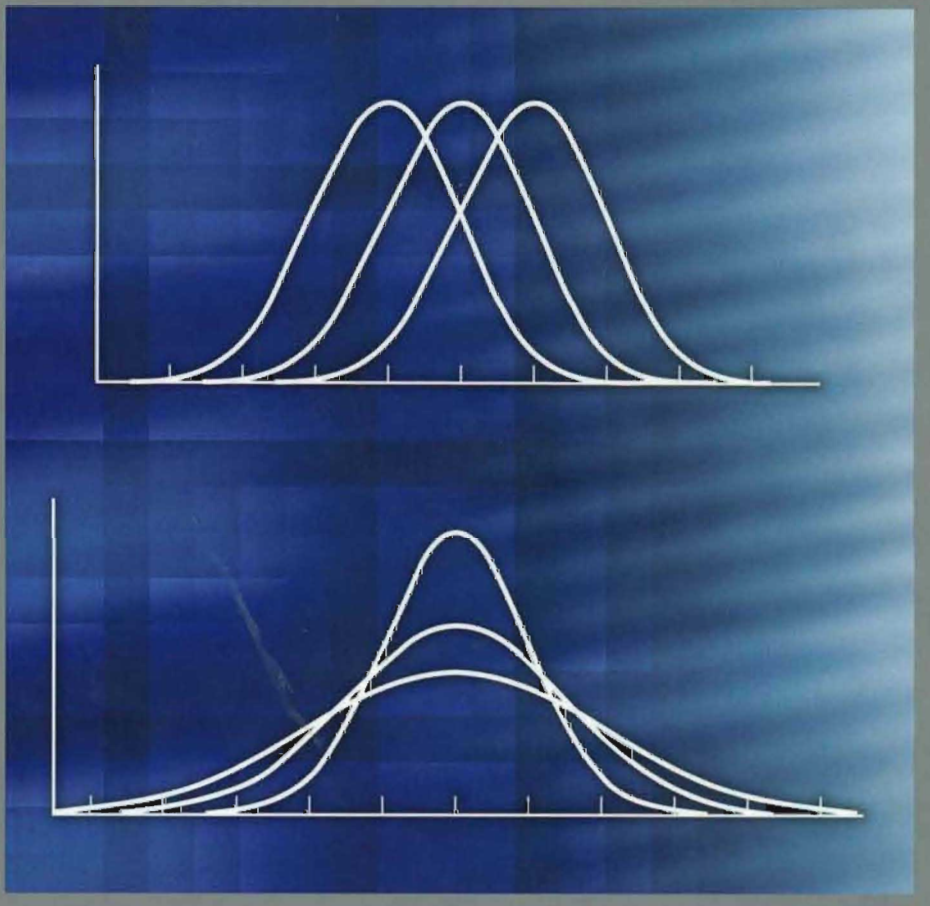
BIOSTATISTICAL ANALYSIS

FIFTH EDITION



JERROLD H. ZAR

STATISTICAL TABLES AND GRAPHS

INTERPOLATION

BIOSTATISTICAL ANALYSIS

Fifth Edition

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Preface

Beginning with the first edition of this book, the goal has been to introduce a broad array of techniques for the examination and analysis of a wide variety of data that may be encountered in diverse areas of biological studies. As such, the book has been called upon to fulfill two purposes. First, it has served as an introductory textbook, assuming no prior knowledge of statistics. Second, it has functioned as a reference work consulted long after formal instruction has ended.

Colleges and universities have long offered an assortment of introductory statistics courses. Some of these courses are without concentration on a particular field in which quantitative data might be collected (and often emphasize mathematics and statistical theory), and some focus on statistical methods of utility to a specific field (such as this book, which has an explicit orientation to the biological sciences). Walker (1929: 148–163) reported that, although the teaching of probability has a much longer history, the first statistics course at a U.S. university or college probably was at Columbia College (renamed Columbia University in 1896) in 1880 in the economics department; followed in 1887 by the second—the first in psychology—at the University of Pennsylvania; in 1889 by the first in anthropology, at Clark University; in 1897 by the first in biology, at Harvard University; in 1898 by the first in mathematics, at the University of Illinois; and in 1900 by the first in education, at Teachers College, Columbia University. In biology, the first courses with statistical content were probably taught by Charles B. Davenport at Harvard (1887–1899), and his *Statistical Methods in Biological Variation*, first published in 1899, may have been the first American book focused on statistics (ibid.: 159).

The material in this book requires no mathematical competence beyond very elementary algebra, although the discussions include many topics that appear seldom, if at all, in other general texts. Some statistical procedures are mentioned though not recommended. This is done for the benefit of readers who may encounter them in research reports or computer software.

Many literature references and footnotes are given throughout most chapters, to provide support for material discussed, to provide historical points, or to direct the reader to sources of additional information. More references are given for controversial and lesser-known topics.

The data in the examples and exercises are largely fictional, though generally realistic, and are intended to demonstrate statistical procedures, not to present actual research conclusions. The exercises at the end of chapters can serve as additional examples of statistical methods, and the answers are given at the back of the book. The sample sizes of most examples and exercises are small in order to conserve space and to enhance the ease of presentation and computation. Although the examples and exercises represent a variety of areas within the biological sciences, they are intended to be understood by biology students and researchers across a diversity of fields.

There are important statistical procedures that involve computations so demanding that they preclude practical execution without appropriate computer software. Basic principles and aspects of the underlying calculations are presented to show how results may be obtained; for even if laborious calculations will be performed by computer, the biologist should be informed enough to interpret properly the computational results. Many statistical packages are available, commercially or otherwise, addressing various subsets of the procedures in this book; but no single package is promoted herein.

A final contribution toward achieving a book with self-sufficiency for most biostatistical needs is the inclusion of a comprehensive set of statistical tables, more extensive than those found in similar texts.

To be useful as a reference, and to allow for differences in content among courses for which it might be used, this book contains much more material than would be covered during one academic term. Therefore, I am sometimes asked to recommend what I consider to be the basic topics for an introduction to the subject. I suggest these book sections (though not necessarily in their entirety) as a core treatment of biostatistical methods, to be augmented or otherwise amended with others of the instructor's preference: 1.1–1.4, 2.1–2.4, 3.1–3.3, 4.1, 4.4–4.6, 6.1–6.4, 7.1–7.4, 7.6–7.7, 8.1–8.5, 8.10–8.11, 9.1–9.3, 10.1–10.4, 11.1–11.4, 12.1–12.4, 14.1, 15.1, 17.1–17.7, 18.1–18.3, 19.1–19.3, 19.9, 20.2–20.4, 22.1–22.3, 22.5, 23.1–23.4; and the introductory paragraph(s) to each of these chapters.

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Acknowledgments

A book of this nature requires, and benefits from, the assistance of many. For the preparation of the early editions, the outstanding library collections of the University of Illinois at Urbana–Champaign were invaluable, and for all editions I am greatly indebted to the library materials and services of Northern Illinois University and its vast book- and journal-collection networks. I also gratefully acknowledge the cooperation of the computer services at Northern Illinois University, which assisted in executing many of the computer programs I prepared to generate some of the appendix tables. For the tables taken from previously published sources, thanks are given for the permission to reprint them, and acknowledgment of each source is given immediately following the appearance of the reprinted material. Additionally, I am pleased to recognize the editorial and production staff at Pearson Education and Laserwords for their valued professional assistance in transforming my manuscript into the published product in hand.

Over many years, teachers, students, and colleagues have aided in leading me to important biostatistical questions and to the material presented in this volume. Special recognition must be made of S. Charles Kendeigh (1904–1986) of the University of Illinois at Urbana–Champaign, who, through considerate mentorship, first made me aware of the value of quantitative analysis of biological data, leading me to produce the first edition; Edward Batschelet (1914–1979), of the University of Zurich, who provided me with kind encouragement and inspiration on statistical matters during the preparation of much of the first two editions; Arthur W. Ghent (1927–2001), University of Illinois at Urbana–Champaign, who was constantly supportive through the first four editions, offering statistical and biological commentary both stimulating and challenging; and Carol J. Feltz (1956–2001), Northern Illinois University, who provided substantive consultation on some major new material for the fourth edition. Prior to publication, the book drew upon the expertise and insights of reviewers, including Raid Amin, University of West Florida; Franklin R. Ampy, Howard University; Sulekha Anand, San José State University; Roxanne Barrows, Hocking College; Thomas Beitinger, University of North Texas; Mark Butler, Old Dominion University; William Caire, University of Central Oklahoma; Gary Cobbs, University of Louisville; Loveday L. Conquest, University of Washington; Todd A. Crowl, Utah State University; Matthew Edwards, University of California, Santa Cruz; Todd Fearer, University of Arkansas-Monticello; Avshalom Gamliel, Wavemetrics, Inc.; Peter Homann, Western Washington University; Robert Huber, Bowling Green State University; James W. Kirchner, University of California, Berkeley; Gary A. Lamberti, University of Notre Dame; David Larsen, University of Missouri, Columbia; David R. McConville, Saint Mary's University of Minnesota; J. Kelly McCoy, Angelo State University; David J. Moriarty, California State Polytechnic University; Mark Rizzardi, Humboldt State University; Michael A. Romano, Western Illinois University; and Thomas A. Wolosz, the State University of New York, Plattsburgh. I also acknowledge my wife, Carol, for her prolonged and consistent patience during the thirty-five years of production of the five editions of this book.

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CHAPTER 1

Data: Types and Presentation

Scientific study involves the systematic collection, organization, analysis, and presentation of knowledge. Many investigations in the biological sciences are quantitative, where knowledge is in the form of numerical observations called *data*. (One numerical observation is a *datum*.*) In order for the presentation and analysis of data to be valid and useful, we must use methods appropriate to the type of data obtained, to the design of the data collection, and to the questions asked of the data; and the limitations of the data, of the data collection, and of the data analysis should be appreciated when formulating conclusions. This chapter, and those that follow, will introduce many concepts relevant to this goal.

The word *statistics* is derived from the Latin for "state," indicating the historical importance of governmental data gathering, which related principally to demographic information (including census data and "vital statistics") and often to their use in military recruitment and tax collecting.†

The term *statistics* is often encountered as a synonym for *data*: One hears of college enrollment statistics (such as the numbers of newly admitted students, numbers of senior students, numbers of students from various geographic locations), statistics of a basketball game (such as how many points were scored by each player, how many fouls were committed), labor statistics (such as numbers of workers unemployed, numbers employed in various occupations), and so on. Hereafter, this use of the word *statistics* will not appear in this book. Instead, it will be used in its other common manner: to refer to the *orderly collection, analysis, and interpretation of data with a view to objective evaluation of conclusions based on the data.* (Section 2.4 will introduce another fundamentally important use of the term *statistic*.)

Statistics applied to biological problems is simply called *biostatistics* or, sometimes, *biometry*‡ (the latter term literally meaning "biological measurement"). Although

*The term *data* is sometimes seen as a singular noun meaning "numerical information." This book refrains from that use.

†Peters (1987: 79) and Walker (1929: 32) attribute the first use of the term *statistics* to a German professor, Gottfried Achenwall (1719–1772), who used the German word *Statistik* in 1749, and the first published use of the English word to John Sinclair (1754–1835) in 1791.

‡The word *biometry*, which literally means "biological measurement," had, since the nineteenth century, been found in several contexts (such as demographics and, later, quantitative genetics: Armitage, 1985; Stigler, 2000), but using it to mean the application of statistical methods to biological information apparently was conceived between 1892 and 1901 by Karl Pearson, along with the name *Biometrika* for the still-important English journal he helped found; and it was first published in the inaugural issue of this journal in 1901 (Snedecor, 1954). The Biometrics Section of the American

their magnitudes relative to each other; or success in learning to run a maze may be recorded as *A*, *B*, or *C*.

It is often true that biological data expressed on the ordinal scale could have been expressed on the interval or ratio scale had exact measurements been obtained (or obtainable). Sometimes data that were originally on interval or ratio scales will be changed to ranks; for example, examination grades of 99, 85, 73, and 66% (ratio scale) might be recorded as A, B, C, and D (ordinal scale), respectively.

Ordinal-scale data contain and convey less information than ratio or interval data, for only relative magnitudes are known. Consequently, quantitative comparisons are impossible (e.g., we cannot speak of a grade of C being half as good as a grade of A, or of the difference between cell sizes 1 and 2 being the same as the difference between sizes 3 and 4). However, we will see that many useful statistical procedures are, in fact, applicable to ordinal data.

(d) Data in Nominal Categories. Sometimes the variable being studied is classified by some qualitative measure it possesses rather than by a numerical measurement. In such cases the variable may be called an *attribute*, and we are said to be dealing with *nominal*, or *categorical*, data. Genetic phenotypes are commonly encountered biological attributes: The possible manifestations of an animal's eye color might be brown or blue; and if human hair color were the attribute of interest, we might record black, brown, blond, or red. As other examples of nominal data (*nominal* is from the Latin word for "name"), people might be classified as male or female, or right-handed or left-handed. Or, plants might be classified as dead or alive, or as with or without fertilizer application. Taxonomic categories also form a nominal classification scheme (for example, plants in a study might be classified as pine, spruce, or fir).

Sometimes, data that might have been expressed on an ordinal, interval, or ratio scale of measurement may be recorded in nominal categories. For example, heights might be recorded as tall or short, or performance on an examination as pass or fail, where there is an arbitrary cut-off point on the measurement scale to separate tall from short and pass from fail.

As will be seen, statistical methods useful with ratio, interval, or ordinal data generally are not applicable to nominal data, and we must, therefore, be able to identify such situations when they occur.

(e) Continuous and Discrete Data. When we spoke previously of plant heights, we were dealing with a variable that could be any conceivable value within any observed range; this is referred to as a *continuous variable*. That is, if we measure a height of 35 cm and a height of 36 cm, an infinite number of heights is possible in the range from 35 to 36 cm: a plant might be 35.07 cm tall or 35.988 cm tall, or 35.3263 cm tall, and so on, although, of course, we do not have devices sensitive enough to detect this infinity of heights. A continuous variable is one for which there is a possible value between any other two values.

However, when speaking of the number of leaves on a plant, we are dealing with a variable that can take on only certain values. It might be possible to observe 27 leaves, or 28 leaves, but 27.43 leaves and 27.9 leaves are values of the variable that are impossible to obtain. Such a variable is termed a *discrete* or *discontinuous variable* (also known as a *meristic variable*). The number of white blood cells in 1 mm^3 of blood, the number of giraffes visiting a water hole, and the number of eggs laid by a grasshopper are all discrete variables. The possible values of a discrete variable generally are consecutive integers, but this is not necessarily so. If the leaves on our

plants are always formed in pairs, then only even integers are possible values of the variable. And the ratio of number of wings to number of legs of insects is a discrete variable that may only have the value of 0, 0.3333..., or 0.6666... (i.e., $\frac{0}{6}$, $\frac{2}{6}$, or $\frac{4}{6}$, respectively).*

Ratio-, interval-, and ordinal-scale data may be either continuous or discrete. Nominal-scale data by their nature are discrete.

1.2 ACCURACY AND SIGNIFICANT FIGURES

Accuracy is the nearness of a measurement to the true value of the variable being measured. *Precision* is not a synonymous term but refers to the closeness to each other of repeated measurements of the same quantity. Figure 1.1 illustrates the difference between accuracy and precision of measurements.

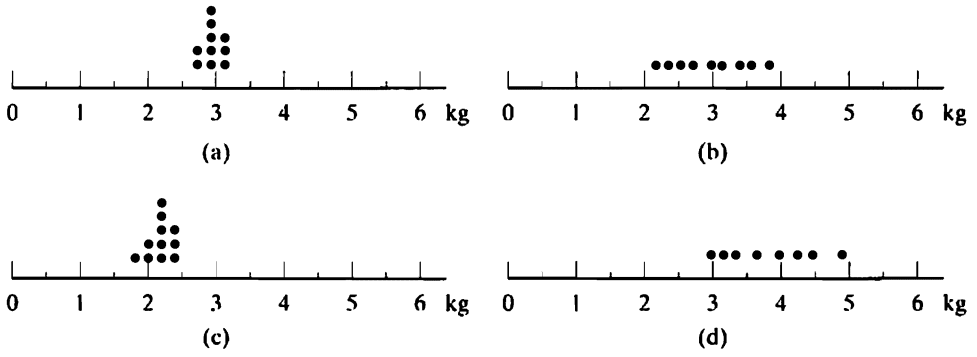

FIGURE 1.1: Accuracy and precision of measurements. A 3-kilogram animal is weighed 10 times. The 10 measurements shown in sample (a) are relatively accurate and precise; those in sample (b) are relatively accurate but not precise; those of sample (c) are relatively precise but not accurate; and those of sample (d) are relatively inaccurate and imprecise.

Human error may exist in the recording of data. For example, a person may miscount the number of birds in a tract of land or misread the numbers on a heart-rate monitor. Or, a person might obtain correct data but record them in such a way (perhaps with poor handwriting) that a subsequent data analyst makes an error in reading them. We shall assume that such errors have not occurred, but there are other aspects of accuracy that should be considered.

Accuracy of measurement can be expressed in numerical reporting. If we report that the hind leg of a frog is 8 cm long, we are stating the number 8 (a value of a continuous variable) as an estimate of the frog's true leg length. This estimate was made using some sort of a measuring device. Had the device been capable of more accuracy, we might have declared that the leg was 8.3 cm long, or perhaps 8.32 cm long. When recording values of continuous variables, it is important to designate the accuracy with which the measurements have been made. By convention, the value 8 denotes a measurement in the range of 7.50000 ... to 8.49999..., the value 8.3 designates a range of 8.25000 ... to 8.34999..., and the value 8.32 implies that the true value lies within the range of 8.31500... to 8.32499.... That is, the reported value is the midpoint of the implied range, and the size of this range is designated by the last decimal place in the measurement. The value of 8 cm implies an ability to

*The ellipsis marks (...) may be read as "and so on." Here, they indicate that $\frac{2}{6}$ and $\frac{4}{6}$ are repeating decimal fractions, which could just as well have been written as 0.3333333333333 ... and 0.6666666666666..., respectively.

determine length within a range of 1 cm, 8.3 cm implies a range of 0.1 cm, and 8.32 cm implies a range of 0.01 cm. Thus, to record a value of 8.0 implies greater accuracy of measurement than does the recording of a value of 8, for in the first instance the true value is said to lie between 7.95000 ... and 8.049999... (i.e., within a range of 0.1 cm), whereas 8 implies a value between 7.50000 ... and 8.49999... (i.e., within a range of 1 cm). To state 8.00 cm implies a measurement that ascertains the frog's limb length to be between 7.99500 ... and 8.00499 ... cm (i.e., within a range of 0.01 cm). Those digits in a number that denote the accuracy of the measurement are referred to as *significant figures*. Thus, 8 has one significant figure, 8.0 and 8.3 each have two significant figures, and 8.00 and 8.32 each have three.

In working with exact values of discrete variables, the preceding considerations do not apply. That is, it is sufficient to state that our frog has four limbs or that its left lung contains thirteen flukes. The use of 4.0 or 13.00 would be inappropriate, for as the numbers involved are exactly 4 and 13, there is no question of accuracy or significant figures.

But there are instances where significant figures and implied accuracy come into play with discrete data. An entomologist may report that there are 72,000 moths in a particular forest area. In doing so, it is probably not being claimed that this is the exact number but an estimate of the exact number, perhaps accurate to two significant figures. In such a case, 72,000 would imply a range of accuracy of 1000, so that the true value might lie anywhere from 71,500 to 72,500. If the entomologist wished to convey the fact that this estimate is believed to be accurate to the nearest 100 (i.e., to three significant figures), rather than to the nearest 1000, it would be better to present the data in the form of *scientific notation*,* as follows: If the number $7.2 \times 10^4 (= 72{,}000)$ is written, a range of accuracy of $0.1 \times 10^4 (= 1000)$ is implied, and the true value is assumed to lie between 71,500 and 72,500. But if 7.20×10^4 were written, a range of accuracy of $0.01 \times 10^4 (= 100)$ would be implied, and the true value would be assumed to be in the range of 71,950 to 72,050. Thus, the accuracy of large values (and this applies to continuous as well as discrete variables) can be expressed succinctly using scientific notation.

Calculators and computers typically yield results with more significant figures than are justified by the data. However, it is good practice—to avoid rounding error—to retain many significant figures until the last step in a sequence of calculations, and on attaining the result of the final step to round off to the appropriate number of figures. A suggestion for the number of figures to report is given at the end of Section 6.2.

1.3 FREQUENCY DISTRIBUTIONS

When collecting and summarizing large amounts of data, it is often helpful to record the data in the form of a *frequency table*. Such a table simply involves a listing of all the observed values of the variable being studied and how many times each value is observed. Consider the tabulation of the frequency of occurrence of sparrow nests in each of several different locations. This is illustrated in Example 1.1, where the observed kinds of nest sites are listed, and for each kind the number of nests observed is recorded. The distribution of the total number of observations among the various categories is termed a *frequency distribution*. Example 1.1 is a frequency table for nominal data, and these data may also be presented graphically by means of a *bar graph* (Figure 1.2), where the height of each bar is proportional to the frequency in the class represented. The widths of all bars in a bar graph should be equal so

*The use of scientific notation—by physicists—can be traced back to at least the 1860s (Miller, 2004b).

EXAMPLE 1.1 The Location of Sparrow Nests: A Frequency Table of Nominal Data

The variable is nest site, and there are four recorded categories of this variable. The numbers recorded in these categories constitute the frequency distribution.

Nest Site	*Number of Nests Observed*
A. Vines	56
B. Building eaves	60
C. Low tree branches	46
D. Tree and building cavities	49

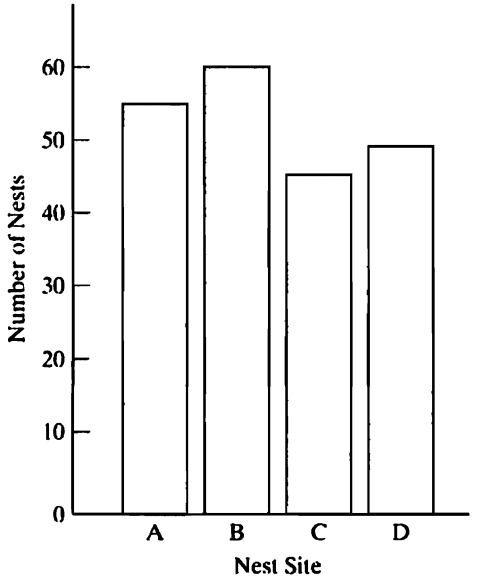

FIGURE 1.2: A bar graph of the sparrow nest data of Example 1.1. An example of a bar graph for nominal data.

that the eye of the reader is not distracted from the differences in bar heights; this also makes the area of each bar proportional to the frequency it represents. Also, the frequency scale on the vertical axis should begin at zero to avoid the apparent differences among bars. If, for example, a bar graph of the data of Example 1.1 were constructed with the vertical axis representing frequencies of 45 to 60 rather than 0 to 60, the results would appear as in Figure 1.3. Huff (1954) illustrates other techniques that can mislead the readers of graphs. It is good practice to leave space between the bars of a bar graph of nominal data, to emphasize the distinctness among the categories represented.

A frequency tabulation of ordinal data might appear as in Example 1.2, which presents the observed numbers of sunfish collected in each of five categories, each category being a degree of skin pigmentation. A bar graph (Figure 1.4) can be prepared for this frequency distribution just as for nominal data.

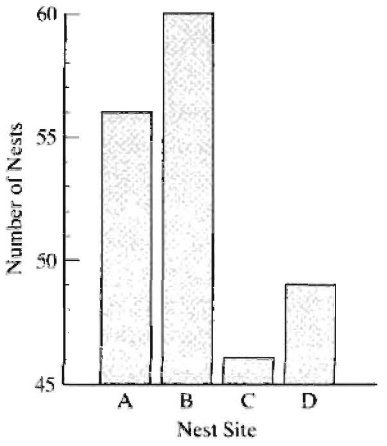

FIGURE 1.3: A bar graph of the sparrow nest data of Example 1.1, drawn with the vertical axis starting at 45. Compare this with Figure 1.1, where the axis starts at 0.

EXAMPLE 1.2 Numbers of Sunfish, Tabulated According to Amount of Black Pigmentation: A Frequency Table of Ordinal Data

The variable is amount of pigmentation, which is expressed by numerically ordered classes. The numbers recorded for the five pigmentation classes compose the frequency distribution.

Pigmentation Class	*Amount of Pigmentation*	*Number of Fish*
0	No black pigmentation	13
1	Faintly speckled	68
2	Moderately speckled	44
3	Heavily speckled	21
4	Solid black pigmentation	8

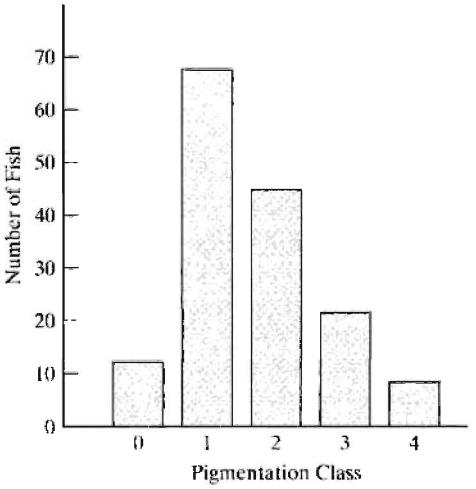

FIGURE 1.4: A bar graph of the sunfish pigmentation data of Example 1.2. An example of a bar graph for ordinal data.

In preparing frequency tables of interval- and ratio-scale data, we can make a procedural distinction between discrete and continuous data. Example 1.3 shows discrete data that are frequencies of litter sizes in foxes, and Figure 1.5 presents this frequency distribution graphically.

EXAMPLE 1.3 Frequency of Occurrence of Various Litter Sizes in Foxes: A Frequency Table of Discrete, Ratio-Scale Data

The variable is litter size, and the numbers recorded for the five litter sizes make up frequency distribution.

Litter Size	*Frequency*
3	10
4	27
5	22
6	4
7	1

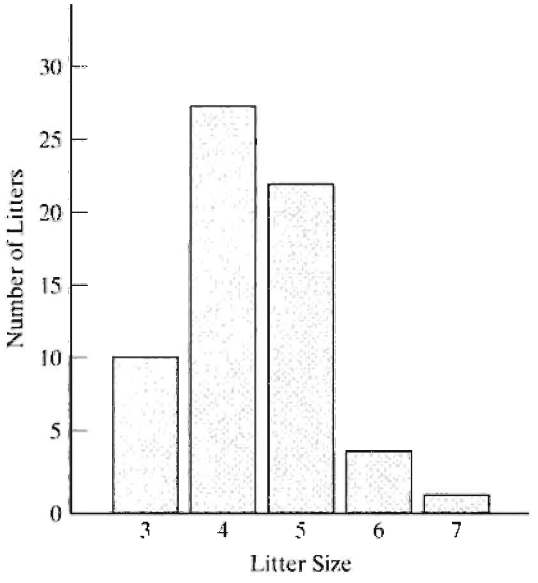

FIGURE 1.5: A bar graph of the fox litter data of Example 1.3. An example of a bar graph for discrete, ratio-scale data.

Example 1.4a shows discrete data that are the numbers of aphids found per clover plant. These data create quite a lengthy frequency table, and it is not difficult to imagine sets of data whose tabulation would result in an even longer list of frequencies. Thus, for purposes of preparing bar graphs, we often cast data into a frequency table by grouping them.

Example 1.4b is a table of the data from Example 1.4a arranged by grouping the data into size classes. The bar graph for this distribution appears as Figure 1.6. Such grouping results in the loss of some information and is generally utilized only to make frequency tables and bar graphs easier to read, and not for calculations performed on

the data. There have been several "rules of thumb" proposed to aid in deciding into how many classes data might reasonably be grouped, for the use of too few groups will obscure the general shape of the distribution. But such "rules" or recommendations are only rough guides, and the choice is generally left to good judgment, bearing in mind that from 10 to 20 groups are useful for most biological work. (See also Doane, 1976.) In general, groups should be established that are equal in the size interval of the variable being measured. (For example, the group size interval in Example 1.4b is four aphids per plant.)

EXAMPLE 1.4a Number of Aphids Observed per Clover Plant: A Frequency Table of Discrete, Ratio-Scale Data

Number of Aphids on a Plant	*Number of Plants Observed*	*Number of Aphids on a Plant*	*Number of Plants Observed*
0	3	20	17
1	1	21	18
2	1	22	23
3	1	23	17
4	2	24	19
5	3	25	18
6	5	26	19
7	7	27	21
8	8	28	18
9	11	29	13
10	10	30	10
11	11	31	14
12	13	32	9
13	12	33	10
14	16	34	8
15	13	35	5
16	14	36	4
17	16	37	1
18	15	38	2
19	14	39	1
		40	0
		41	1
Total number of observations = 424			

Because continuous data, contrary to discrete data, can take on an infinity of values, one is essentially always dealing with a frequency distribution tabulated by groups. If the variable of interest were a weight, measured to the nearest 0.1 mg, a frequency table entry of the number of weights measured to be 48.6 mg would be interpreted to mean the number of weights grouped between 48.5500... and 48.6499... mg (although in a frequency table this class interval is usually written as 48.55–48.65). Example 1.5 presents a tabulation of 130 determinations of the amount of phosphorus, in milligrams per gram, in dried leaves. (Ignore the last two columns of this table until Section 1.4.)

EXAMPLE 1.4b Number of Aphids Observed per Clover Plant: A Frequency Table Grouping the Discrete, Ratio-Scale Data of Example 1.4a

Number of Aphids on a Plant	*Number of Plants Observed*
0–3	6
4–7	17
8–11	40
12–15	54
16–19	59
20–23	75
24–27	77
28–31	55
32–35	32
36–39	8
40–43	1

Total number of observations = 424

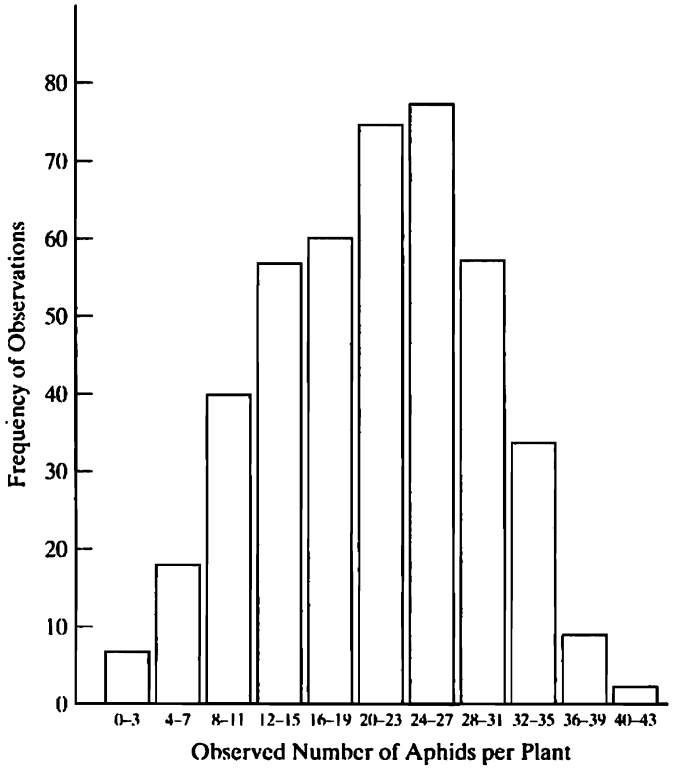

FIGURE 1.6: A bar graph of the aphid data of Example 1.4b. An example of a bar graph for grouped discrete, ratio-scale data.

EXAMPLE 1.5 Determinations of the Amount of Phosphorus in Leaves: A Frequency Table of Continuous Data

Phosphorus (mg/g of leaf)	*Frequency (i.e., number of determinations)*	**Cumulative frequency**	
		Starting with Low Values	*Starting with High Values*
8.15–8.25	2	2	130
8.25–8.35	6	8	128
8.35–8.45	8	16	122
8.45–8.55	11	27	114
8.55–8.65	17	44	103
8.65–8.75	17	61	86
8.75–8.85	24	85	69
8.85–8.95	18	103	45
8.95–9.05	13	116	27
9.05–9.15	10	126	14
9.15–9.25	4	130	4

Total frequency = 130 = n

In presenting this frequency distribution graphically, one can prepare a *histogram*,* which is the name given to a bar graph based on continuous data. This is done in Figure 1.7; note that rather than indicating the range on the horizontal axis, we indicate only the midpoint of the range, a procedure that results in less crowded printing on the graph. Note also that adjacent bars in a histogram are often drawn touching each other, to emphasize the continuity of the scale of measurement, whereas in the other bar graphs discussed they generally are not.

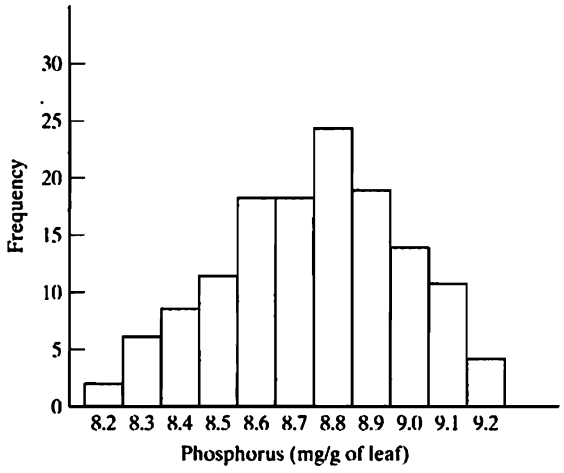

FIGURE 1.7: A histogram of the leaf phosphorus data of Example 1.5. An example of a histogram for continuous data.

*The term *histogram* is from Greek roots (referring to a pole-shaped drawing) and was first published by Karl Pearson in 1895 (David 1995).

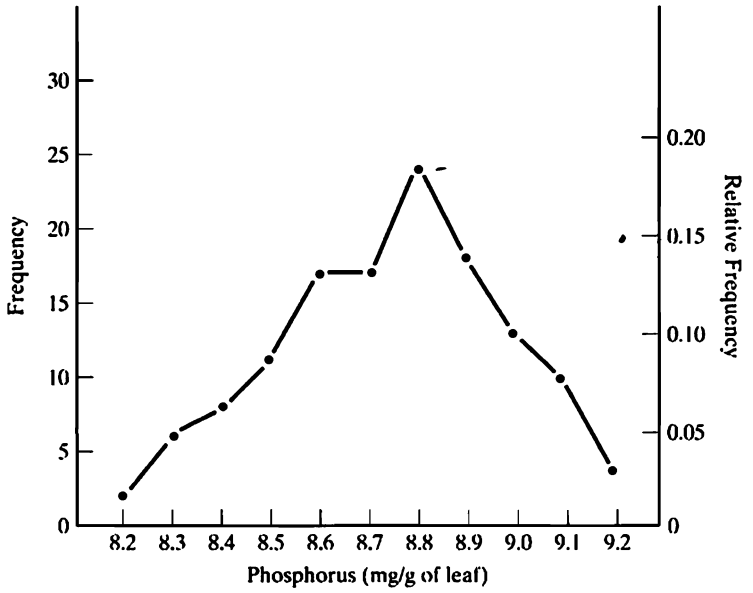

FIGURE 1.8: A frequency polygon for the leaf phosphorus data of Example 1.5.

Often a *frequency polygon* is drawn instead of a histogram. This is done by plotting the frequency of each class as a dot (or other symbol) at the class midpoint and then connecting each adjacent pair of dots by a straight line (Figure 1.8). It is, of course, the same as if the midpoints of the tops of the histogram bars were connected by straight lines. Instead of plotting frequencies on the vertical axis, one can plot *relative frequencies*, or proportions of the total frequency. This enables different distributions to be readily compared and even plotted on the same axes. Sometimes, as in Figure 1.8, frequency is indicated on one vertical axis and the corresponding relative frequency on the other. (Using the data of Example 1.5, the relative frequency for 8.2 mg/g is $2/130 = 0.015$, that for 8.3 mg/g is $6/130 = 0.046$, that for 9.2 mg/g is $4/130 = 0.030$, and so on. The total of all the frequencies is n, and the total of all the relative frequencies is 1.)

Frequency polygons are also commonly used for discrete distributions, but one can argue against their use when dealing with ordinal data, as the polygon implies to the reader a constant size interval horizontally between points on the polygon. Frequency polygons should not be employed for nominal-scale data.

If we have a frequency distribution of values of a continuous variable that falls into a large number of class intervals, the data may be grouped as was demonstrated with discrete variables. This results in fewer intervals, but each interval is, of course, larger. The midpoints of these intervals may then be used in the preparation of a histogram or frequency polygon. The user of frequency polygons is cautioned that such a graph is simply an aid to the eye in following trends in frequency distributions, and one should not attempt to read frequencies between points on the polygon. Also note that the method presented for the construction of histograms and frequency polygons requires that the class intervals be equal. Lastly, the vertical axis (e.g., the frequency scale) on frequency polygons and bar graphs generally should begin with zero, especially if graphs are to be compared with one another. If this is not done, the eye may be misled by the appearance of the graph (as shown for nominal-scale data in Figures 1.2 and 1.3).

1.4 CUMULATIVE FREQUENCY DISTRIBUTIONS

A frequency distribution informs us how many observations occurred for each value (or group of values) of a variable. That is, examination of the frequency table of Example 1.3 (or its corresponding bar graph or frequency polygon) would yield information such as, "How many fox litters of four were observed?", the answer being 27. But if it is desired to ask questions such as, "How many litters of four or more were observed?", or "How many fox litters of five or fewer were observed?", we are speaking of *cumulative frequencies*. To answer the first question, we sum all frequencies for litter sizes four and up, and for the second question, we sum all frequencies from the smallest litter size up through a size of five. We arrive at answers of 54 and 59, respectively.

In Example 1.5, the phosphorus concentration data are cast into two cumulative frequency distributions, one with cumulation commencing at the low end of the measurement scale and one with cumulation being performed from the high values toward the low values. The choice of the direction of cumulation is immaterial, as can be demonstrated. If one desired to calculate the number of phosphorus determinations less than 8.55 mg/g, namely 27, a cumulation starting at the low end might be used, whereas the knowledge of the frequency of determinations greater than 8.55 mg/g, namely 103, can be readily obtained from the cumulation commencing from the high end of the scale. But one can easily calculate any frequency from a low-to-high cumulation (e.g., 27) from its complementary frequency from a high-to-low cumulation (e.g., 103), simply by knowing that the sum of these two frequencies is the total frequency (i.e., $n = 130$); therefore, in practice it is not necessary to calculate both sets of cumulations.

Cumulative frequency distributions are useful in determining medians, percentiles, and other quantiles, as discussed in Sections 3.2 and 4.2. They are not often presented in bar graphs, but *cumulative frequency polygons* (sometimes called *ogives*) are not

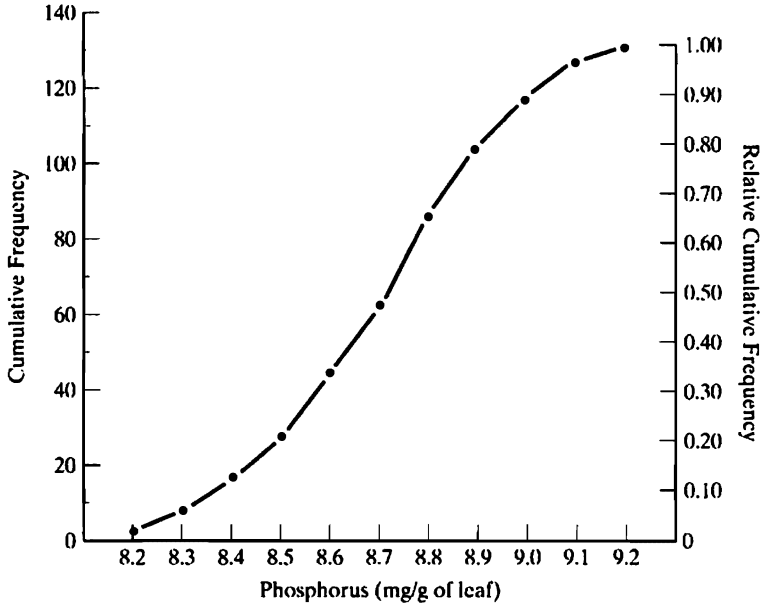

FIGURE 1.9: Cumulative frequency polygon of the leaf phosphorus data of Example 1.5, with cumulation commencing from the lowest to the highest values of the variable.

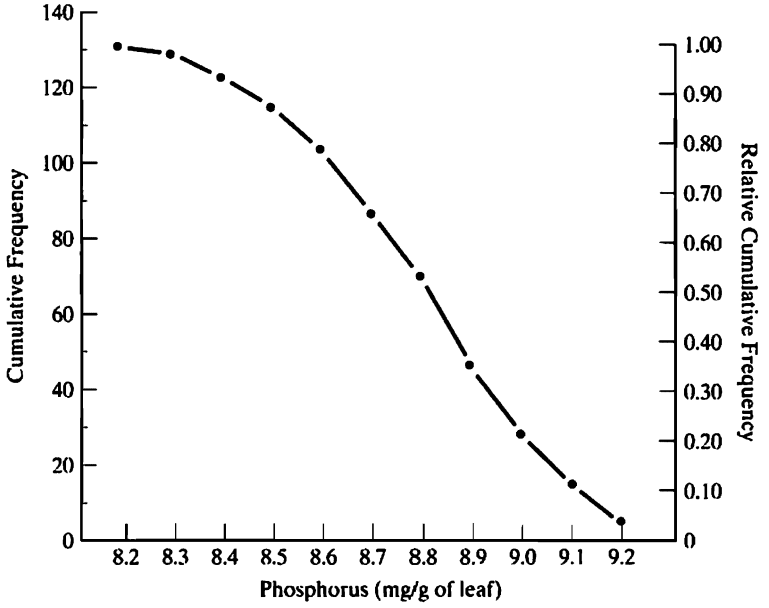

FIGURE 1.10: Cumulative frequency polygon of the leaf phosphorus data of Example 1.5, with cumulation commencing from the highest to the lowest values of the variable.

uncommon. (See Figures 1.9 and 1.10.) Relative frequencies (proportions of the total frequency) can be plotted instead of (or, as in Figures 1.9 and 1.10, in addition to) frequencies on the vertical axis of a cumulative frequency polygon. This enables different distributions to be readily compared and even plotted on the same axes. (Using the data of Example 1.5 for Figure 1.9, the relative cumulative frequency for 8.2 mg/g is $2/130 = 0.015$, that for 8.3 mg/g is $8/130 = 0.062$, and so on. For Figure 1.10, the relative cumulative frequency for 8.2 mg/g is $130/130 = 1.000$, that for 8.3 mg/g is $128/130 = 0.985$, and so on.)

CHAPTER 2

Populations and Samples

The primary objective of a statistical analysis is to infer characteristics of a group of data by analyzing the characteristics of a small sampling of the group. This generalization from the part to the whole requires the consideration of such important concepts as population, sample, parameter, statistic, and random sampling. These topics are discussed in this chapter.

2.1 POPULATIONS

Basic to statistical analysis is the desire to draw conclusions about a group of measurements of a variable being studied. Biologists often speak of a "population" as a defined group of humans or of another species of organisms. Statisticians speak of a *population* (also called a *universe*) as a group of measurements (not organisms) about which one wishes to draw conclusions. It is the latter definition, the statistical definition of *population*, that will be used throughout this book. For example, an investigator may desire to draw conclusions about the tail lengths of bobcats in Montana. All Montana bobcat tail lengths are, therefore, the population under consideration. If a study is concerned with the blood-glucose concentration in three-year-old children, then the blood-glucose levels in all children of that age are the population of interest.

Populations are often very large, such as the body weights of all grasshoppers in Kansas or the eye colors of all female New Zealanders, but occasionally populations of interest may be relatively small, such as the ages of men who have traveled to the moon or the heights of women who have swum the English Channel.

2.2 SAMPLES FROM POPULATIONS

If the population under study is very small, it might be practical to obtain all the measurements in the population. If one wishes to draw conclusions about the ages of all men who have traveled to the moon, it would not be unreasonable to attempt to collect all the ages of the small number of individuals under consideration. Generally, however, populations of interest are so large that obtaining all the measurements is unfeasible. For example, we could not reasonably expect to determine the body weight of every grasshopper in Kansas. What can be done in such cases is to obtain a subset of all the measurements in the population. This subset of measurements constitutes a *sample*, and from the characteristics of samples we can

draw conclusions about the characteristics of the populations from which the samples came.*

Biologists may sample a population that does not physically exist. Suppose an experiment is performed in which a food supplement is administered to 40 guinea pigs, and the sample data consist of the growth rates of these 40 animals. Then the population about which conclusions might be drawn is the growth rates of all the guinea pigs that conceivably might have been administered the same food supplement under identical conditions. Such a population is said to be "imaginary" and is also referred to as "hypothetical" or "potential."

2.3 RANDOM SAMPLING

Samples from populations can be obtained in a number of ways; however, for a sample to be representative of the population from which it came, and to reach valid conclusions about populations by induction from samples, statistical procedures typically assume that the samples are obtained in a *random* fashion. To sample a population randomly requires that each member of the population has an equal and independent chance of being selected. That is, not only must each measurement in the population have an equal chance of being chosen as a member of the sample, but the selection of any member of the population must in no way influence the selection of any other member. Throughout this book, "sample" will always imply "random sample."†

It is sometimes possible to assign each member of a population a unique number and to draw a sample by choosing a set of such numbers at random. This is equivalent to having all members of a population in a hat and drawing a sample from them while blindfolded. Appendix Table B.41 provides 10,000 random digits for this purpose. In this table, each digit from 0 to 9 has an equal and independent chance of appearing anywhere in the table. Similarly, each combination of two digits, from 00 to 99, is found at random in the table, as is each three-digit combination, from 000 to 999, and so on.

Assume that a random sample of 200 names is desired from a telephone directory having 274 pages, three columns of names per page, and 98 names per column. Entering Table B.41 at random (i.e., do not always enter the table at the same place), one might decide first to arrive at a random combination of three digits. If this three-digit number is 001 to 274, it can be taken as a randomly chosen page number (if it is 000 or larger than 274, simply skip it and choose another three-digit number, e.g., the next one on the table). Then one might examine the next digit in the table; if it is a 1, 2, or 3, let it denote a page column (if a digit other than 1, 2, or 3 is encountered, it is ignored, passing to the next digit that is 1, 2, or 3). Then one could look at the next two-digit number in the table; if it is from 01 to 98, let it represent a randomly selected name within that column. This three-step procedure would be performed a total of 200 times to obtain the desired random sample. One can proceed in any direction in the random number table: left to right, right to left, upward, downward, or diagonally; but the direction should be decided on before looking at the table. Computers are capable of quickly generating random numbers (sometimes called "pseudorandom" numbers because the number generation is not perfectly random), and this is how Table B.41 was derived.

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*This use of the terms *population* and *sample* was established by Karl Pearson (1903).

†This concept of random sampling was established by Karl Pearson between 1897 and 1903 (Miller, 2004a).

Very often it is not possible to assign a number to each member of a population, and random sampling then involves biological, rather than simply mathematical, considerations. That is, the techniques for sampling Montana bobcats or Kansas grasshoppers require knowledge about the particular organism to ensure that the sampling is random. Researchers consult relevant books, periodical articles, or reports that address the specific kind of biological measurement to be obtained.

2.4 PARAMETERS AND STATISTICS

Several measures help to describe or characterize a population. For example, generally a preponderance of measurements occurs somewhere around the middle of the range of a population of measurements. Thus, some indication of a population "average" would express a useful bit of descriptive information. Such information is called a *measure of central tendency* (also called a *measure of location*), and several such measures (e.g., the mean and the median) will be discussed in Chapter 3.

It is also important to describe how dispersed the measurements are around the "average." That is, we can ask whether there is a wide spread of values in the population or whether the values are rather concentrated around the middle. Such a descriptive property is called a *measure of variability* (or a *measure of dispersion*), and several such measures (e.g., the range and the standard deviation) will be discussed in Chapter 4.

A quantity such as a measure of central tendency or a measure of dispersion is called a *parameter* when it describes or characterizes a population, and we shall be very interested in discussing parameters and drawing conclusions about them. Section 2.2 pointed out, however, that one seldom has data for entire populations, but nearly always has to rely on samples to arrive at conclusions about populations. Thus, one rarely is able to calculate parameters. However, by random sampling of populations, parameters can be estimated well, as we shall see throughout this book. An estimate of a population parameter is called a *statistic*.* It is statistical convention to represent population parameters by Greek letters and sample statistics by Latin letters; the following chapters will demonstrate this custom for specific examples.

The statistics one calculates will vary from sample to sample for samples taken from the same population. Because one uses sample statistics as estimates of population parameters, it behooves the researcher to arrive at the "best" estimates possible. As for what properties to desire in a "good" estimate, consider the following.

First, it is desirable that if we take an indefinitely large number of samples from a population, the long-run average of the statistics obtained will equal the parameter being estimated. That is, for some samples a statistic may underestimate the parameter of interest, and for others it may overestimate that parameter; but in the long run the estimates that are too low and those that are too high will "average out." If such a property is exhibited by a statistic, we say that we have an *unbiased* statistic or an unbiased estimator.

Second, it is desirable that a statistic obtained from any single sample from a population be very close to the value of the parameter being estimated. This property of a statistic is referred to as *precision*,† *efficiency*, or *reliability*. As we commonly secure only one sample from a population, it is important to arrive at a close estimate of a parameter from a single sample.

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*This use of the terms *parameter* and *statistic* was defined by R. A. Fisher as early as 1922 (Miller, 2004a; Savage, 1976).

†The precision of a sample statistic, as defined here, should not be confused with the precision of a measurement, defined in Section 1.2.

Third, consider that one can take larger and larger samples from a population (the largest sample being the entire population). As the sample size increases, a *consistent* statistic will become a better estimate of the parameter it is estimating. Indeed, if the sample were the size of the population, then the best estimate would be obtained: the parameter itself.

In the chapters that follow, the statistics recommended as estimates of parameters are "good" estimates in the sense that they possess a desirable combination of unbiasedness, efficiency, and consistency.

2.5 OUTLIERS

Occasionally, a set of data will have one or more observations that are so different, relative to the other data in the sample, that we doubt they should be part of the sample. For example, suppose a researcher collected a sample consisting of the body weights of nineteen 20-week-old mallard ducks raised in individual laboratory cages, for which the following 19 data were recorded:

1.87, 3.75, 3.79, 3.82, 3.85, 3.87, 3.90, 3.94, 3.96, 3.99,
3.99, 4.00, 4.03, 4.04, 4.05, 4.06, 4.09, 8.97, and 39.8 kilograms.

Visual inspection of these 19 recorded data casts doubt upon the smallest datum (1.87 kg) and the two largest data (8.97 kg and 39.8 kg) because they differ so greatly from the rest of the weights in the sample. Data in striking disagreement with nearly all the other data in a sample are often called *outliers* or *discordant data*, and the occurrence of such observations generally calls for closer examination.

Sometimes it is clear that an outlier is the result of incorrect recording of data. In the preceding example, a mallard duck weight of 39.8 kg is highly unlikely (to say the least!), for that is about the weight of a 12-year-old boy or girl (and such a duck would probably not fit in one of the laboratory cages). In this case, inspection of the data records might lead us to conclude that this body weight was recorded with a careless placement of the decimal point and should have been 3.98 kg instead of 39.8 kg. And, upon interrogation, the research assistant may admit to weighing the eighteenth duck with the scale set to pounds instead of kilograms, so the metric weight of that animal should have been recorded as 4.07 (not 8.97) kg.

Also, upon further examination of the data-collection process, we may find that the 1.87-kg duck was taken from a wrong cage and was, in fact, only 4 weeks old, not 20 weeks old, and therefore did not belong in this sample. Or, perhaps we find that it was not a mallard duck, but some other bird species (and, therefore, did not belong in this sample). Statisticians say a sample is *contaminated* if it contains a datum that does not conform to the characteristics of the population being sampled. So the weight of a 4-week-old duck, or of a bird of a different species, would be a statistical contaminant and should be deleted from this sample.

There are also instances where it is known that a measurement was faulty—for example, when a laboratory technician spills coffee onto an electronic measuring device or into a blood sample to be analyzed. In such a case, the measurements known to be erroneous should be eliminated from the sample.

However, outlying data can also be correct observations taken from an intended population, collected purely by chance. As we shall see in Section 6.1, when drawing a random sample from a population, it is relatively likely that a datum in the sample will be around the average of the population and very unlikely that a sample datum will be dramatically far from the average. But sample data very far from the average still may be possible.

It should also be noted that in some situations the examination of an outlier may reveal the effect of a previously unsuspected factor. For example, the 1.87-kg duck might, indeed, have been a 20-week-old mallard but suffering from a genetic mutation or a growth-impeding disease deserving of further consideration in additional research.

In summary, it is not appropriate to discard data simply because they appear (to someone) to be unreasonably extreme. However, if there is a very obvious reason for correcting or eliminating a datum, such as the situations described previously, the incorrect data should be corrected or eliminated. In some other cases questionable data can be *accommodated* in statistical analysis, perhaps by employing statistical procedures that give them less weight or analytical techniques that are *robust* in that they are resistant to effects of discrepant data. And in situations when this cannot be done, dubious data will have to remain in the sample (perhaps encouraging the researcher to repeat the experiment with a new set of data).

The idea of rejecting erroneous data dates back over 200 years; and recommendations for formal, objective methods for such rejection began to appear about 150 years ago. Major discussions of outliers, their origin, and treatment (rejection or accommodation) are those of Barnett and Lewis (1994), Beckman and Cook (1983), and Thode (2002: 123–142).

CHAPTER 3

Measures of Central Tendency

In samples, as well as in populations, one generally finds a preponderance of values somewhere around the middle of the range of observed values. The description of this concentration near the middle is an *average*, or a *measure of central tendency* to the statistician. It is also termed a *measure of location*, for it indicates where, along the measurement scale, the sample or population is located. Various measures of central tendency are useful population parameters, in that they describe an important property of populations. This chapter discusses the characteristics of these parameters and the sample statistics that are good estimates of them.

3.1 THE ARITHMETIC MEAN

The most widely used measure of central tendency is the *arithmetic mean*,* usually referred to simply as the *mean*,† which is the measure most commonly called an "average."

Each measurement in a population may be referred to as an X_i (read "X sub i") value. Thus, one measurement might be denoted as X_1, another as X_2, another as X_3, and so on. The subscript i might be any integer value up through N, the total number of X values in the population.‡ The mean of the population is denoted by the Greek letter μ (lowercase mu) and is calculated as the sum of all the X_i values divided by the size of the population.

The calculation of the population mean can be abbreviated concisely by the formula

$$\mu = \frac{\sum_{i=1}^{N} X_i}{N}. \tag{3.1}$$

*As an adjective, *arithmetic* is pronounced with the accent on the third syllable. In early literature on the subject, the adjective *arithmetical* was employed.

†The term *mean* (as applied to the arithmetic mean, as well as to the geometric and harmonic means of Section 3.4) dates from ancient Greece (Walker, 1929: 183), with its current statistical meaning in use by 1755 (Miller, 2004a; Walker, 1929: 176); *central tendency* appeared by the late 1920s (Miller, 2004a).

‡Charles Babbage (1791–1871) (O'Connor and Robertson, 1998) was an English mathematician and inventor who conceived principles used by modern computers—well before the advent of electronics—and who, in 1832, proposed the modern convention of italicizing Latin (also called Roman) letters to denote quantities; nonitalicized letters had already been employed for this purpose for more than six centuries (Miller, 2001).

The Greek letter Σ (capital sigma) means "summation"* and $\sum_{i=1}^{N} X$ means "summation of all X_i values from X_1 through X_N." Thus, for example, $\sum_{i=1}^{4} X_i = X_1 + X_2 + X_3 + X_4$ and $\sum_{i=3}^{5} X_i = X_3 + X_4 + X_5$. Since, in statistical computations, summations are nearly always performed over the entire set of X_i values, this book will assume $\sum X_i$ to mean "sum X_i's over all values of i," simply as a matter of printing convenience, and $\mu = \sum X_i / N$ would therefore designate the same calculation as would $\mu = \sum_{i=1}^{N} X_i / N$.

The most efficient, unbiased, and consistent estimate of the population mean, μ, is the sample mean, denoted as $\overline{X}$ (read as "X bar"). Whereas the size of the population (which we generally do not know) is denoted as N, the size of a sample is indicated by n, and $\overline{X}$ is calculated as

$$\overline{X} = \frac{\sum_{i=1}^{n} X_i}{n} \quad \text{or} \quad \overline{X} = \frac{\sum X_i}{n}, \tag{3.2}$$

which is read "the sample mean equals the sum of all measurements in the sample divided by the number of measurements in the sample."† Example 3.1 demonstrates the calculation of the sample mean. Note that the mean has the same units of measurement as do the individual observations. The question of how many decimal places should be reported for the mean will be answered at the end of Section 6.2; until then we shall simply record the mean with one more decimal place than the data.

EXAMPLE 3.1 A Sample of 24 from a Population of Butterfly Wing Lengths

X_i (in centimeters): 3.3, 3.5, 3.6, 3.6, 3.7, 3.8, 3.8, 3.8, 3.9, 3.9, 3.9, 4.0, 4.0, 4.0, 4.0, 4.1, 4.1, 4.1, 4.2, 4.2, 4.3, 4.3, 4.4, 4.5.

$$\sum X_i = 95.0 \text{ cm}$$
$$n = 24$$
$$\overline{X} = \frac{\sum X_i}{n} = \frac{95.0 \text{ cm}}{24} = 3.96 \text{ cm}$$

*Mathematician Leonhard Euler (1707–1783; born in Switzerland, worked mostly in Russia), in 1755, was the first to use Σ to denote summation (Cajori, 1928/9, Vol. II: 61).

†The modern symbols for plus and minus ("+" and "−") appear to have first appeared in a 1456 unpublished manuscript by German mathematician and astronomer Regiomontanus (Johannes Müller, 1436–1476), with Bohemia-born Johann (Johannes) Widman (1562–1498) the first, in 1489, to use them in print (Cajori, 1928/9, Vol. I: 128, 231–232). The modern equal sign ("=") was invented by Welsh physician and mathematician Robert Recorde (1510–1558), who published it in 1557 (though its use then disappeared in print until 1618), and it was well recognized starting in 1631 (Cajori, ibid.: 298; Gullberg, 1997: 107). Recorde also was the first to use the plus and minus symbols in an English work (Miller, 2004b). Using a horizontal line to express division derives from its use, in denoting fractions, by Arabic author Al-Ḥaṣṣâr in the twelfth century, though it was not consistently employed for several more centuries (Cajori, ibid. I: 269, 310). The slash mark ("/"; also known as a solidus, virgule, or diagonal) was recommended to denote division by the English logician and mathematician Augustus De Morgan (1806–1871) in 1845 (ibid. I: 312–313), and the India-born Swiss author Johann Heinhirch Rahn (1622–1676) proposed, in 1659, denoting division by the symbol "÷", which previously was often used by authors as a minus sign (ibid.: 211, 270; Gullberg, 1997: 105). Many other symbols were used for mathematical operations, before and after these introductions (e.g., Cajori, ibid.: 229–245).

If, as in Example 3.1, a sample contains multiple identical data for several values of the variable, then it may be convenient to record the data in the form of a frequency table, as in Example 3.2. Then X_i can be said to denote each of k different measurements and f_i can denote the frequency with which that X_i occurs in the sample. The sample mean may then be calculated, using the sums of the products of f_i and X_i, as*

$$\overline{X} = \frac{\sum_{i=1}^{k} f_i X_i}{n}. \tag{3.3}$$

Example 3.2 demonstrates this calculation for the same data as in Example 3.1.

EXAMPLE 3.2 The Data from Example 3.1 Recorded as a Frequency Table

X_i (cm)	f_i	$f_i X_i$ (cm)
3.3	1	3.3
3.4	0	0
3.5	1	3.5
3.6	2	7.2
3.7	1	3.7
3.8	3	11.4
3.9	3	11.7
4.0	4	16.0
4.1	3	12.3
4.2	2	8.4
4.3	2	8.6
4.4	1	4.4
4.5	1	4.5
	$\sum f_i = 24$	$\sum f_i X_i = 95.0$ cm

$$k = 13$$

$$\sum_{i=1}^{k} f_i = n = 24$$

$$\overline{X} = \frac{\sum_{i=1}^{k} f_i X_i}{n} = \frac{95.0 \text{ cm}}{24} = 3.96 \text{ cm}$$

$$\text{median} = 3.95 \text{ cm} + \left(\frac{1}{4}\right)(0.1 \text{ cm})$$
$$= 3.95 \text{ cm} + 0.025 \text{ cm}$$
$$= 3.975 \text{ cm}$$

A similar procedure is computing what is called a *weighted mean*, an expression of the average of several means. For example, we may wish to combine the mean of 3.96 cm from the sample of 24 measurements in Example 3.1 with a mean of 3.78 cm from a sample of 30 measurements and a mean of 4.02 cm from a sample of 15. These three means would be from a total of 24 + 30 + 15 = 69 data; and if we had all 69 of the data we could sum them and divide the sum by 69 to obtain the overall mean length. However, that overall mean can be obtained without knowing the 69

*Denoting the multiplication of two quantities (e.g., a and b) by their adjacent placement (i.e., ab) derives from practices in Hindu manuscripts of the seventh century (Cajori, 1928/9, Vol. I: 77, 250). Modern multiplication symbols include a raised dot (as in $a \cdot b$), which was suggested in a 1631 posthumous publication of Thomas Harriot (1560?–1621) and prominently adopted in 1698 by the outstanding mathematician Gottfried Wilhelm Leibniz (1646–1716, in what is now Germany); the St. Andrew's cross (as in $a \times b$), which was used in 1631 by English mathematician William Oughtred (1574–1660) though it was not in general use until more than 200 years later; and the letter X, which was used, perhaps by Oughtred, as early as 1618 (Cajori, ibid.: 251; Gullberg, 1997: 104; Miller 2004b). Johann Rahn's 1659 use of an asterisk-like symbol (as in $a * b$) (Cajori, ibid: 212–213) did not persist but resurfaced in electronic computer languages of the latter half of the twentieth century.

individual measurements, by employing Equation 3.3 with $f_1 = 24$, $X_1 = 3.96$ cm, $f_2 = 30$, $X_2 = 3.78$ cm, $f_3 = 15$, $X_3 = 4.02$ cm, and $n = 69$. This would yield a weighted mean of $\overline{X} = [(24)(3.96\text{ cm}) + (30)(3.78\text{ cm}) + (15)(4.02\text{ cm})]/69 = (268.74\text{ cm})/69 = 3.89\text{ cm}$.

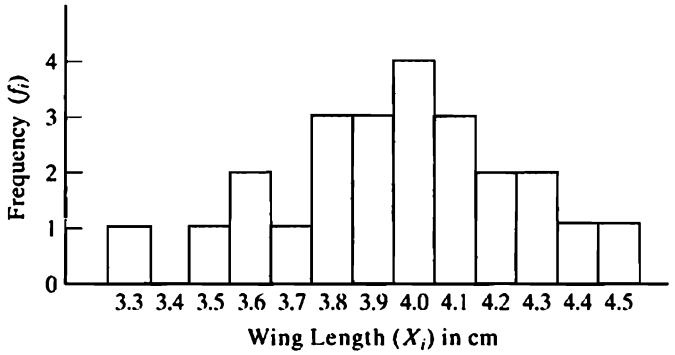


FIGURE 3.1: A histogram of the data in Example 3.2. The mean (3.96 cm) is the center of gravity of the histogram, and the median (3.975 cm) divides the histogram into two equal areas.

If data are plotted as a histogram (Figure 3.1), the mean is the *center of gravity* of the histogram.* That is, if the histogram were made of a solid material, it would balance horizontally with the fulcrum at $\overline{X}$. The mean is applicable to both ratio- and interval-scale data; it should not be used for ordinal data and cannot be used for nominal data.

3.2 THE MEDIAN

The median is typically defined as the middle measurement in an ordered set of data.† That is, there are just as many observations larger than the median as there are smaller. The sample median is the best estimate of the population median. In a symmetrical distribution (such as Figures 3.2a and 3.2b) the sample median is also an unbiased and consistent estimate of μ, but it is not as efficient a statistic as $\overline{X}$ and should not be used as a substitute for $\overline{X}$. If the frequency distribution is asymmetrical, the median is a poor estimate of the mean.

The median of a sample of data may be found by first arranging the measurements in order of magnitude. The order may be either ascending or descending, but ascending order is most commonly used as is done with the samples in Examples 3.1, 3.2, and 3.3. Then, we define the sample median as

$$\text{sample median} = X_{(n+1)/2}. \tag{3.4}$$

*The concept of the mean as the center of gravity was used by L. A. J. Quetelet in 1846 (Walker, 1929: 73).

†The concept of the median was conceived as early as 1816, by K. F. Gauss; enunciated and reinforced by others, including F. Galton in 1869 and 1874; and independently discovered and promoted by G. T. Fechner beginning in 1874 (Walker, 1929: 83–88, 184). It received its name, in English, from F. Galton in 1882 (David, 1995) and, in French, from A. A. Cournot in 1843 (David, 1998a).

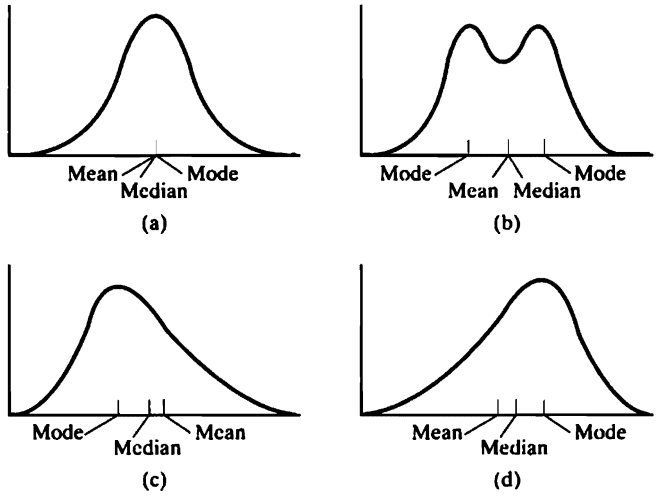


FIGURE 3.2: Frequency distributions showing measures of central tendency. Values of the variable are along the abscissa (horizontal axis), and the frequencies are along the ordinate (vertical axis). Distributions (a) and (b) are symmetrical, (c) is asymmetrical and said to be positively skewed, and (d) is asymmetrical and said to be negatively skewed. Distributions (a), (c), and (d) are unimodal, and distribution b is bimodal. In a unimodal asymmetric distribution, the median lies about one-third the distance between the mean and the mode.*

EXAMPLE 3.3 Life Span for Two Species of Birds in Captivity

The data for each species are arranged in order of magnitude

Species A X_i (mo)	*Species B* X_i (mo)
16	34
32	36
37	38
39	45
40	50
41	54
42	56
50	59
82	69
	91
$n = 9$	$n = 10$
median $= X_{(n+1)/2} = X_{(9+1)/2}$	median $= X_{(n+1)/2} = X_{(10+1)/2}$
$= X_5 = 40$ mo	$= X_{5.5} = 52$ mo
$\overline{X} = 42.11$ mo	$\overline{X} = 53.20$ mo

*An interesting relationship among the mean, median, and standard deviation is shown in Equation 4.21.

If the sample size (n) is odd, then the subscript in Equation 3.4 will be an integer and will indicate which datum is the middle measurement in the ordered sample. For the data of species A in Example 3.3, $n = 9$ and the sample median is $X_{(n+1)/2} = X_{(9+1)/2} = X_5 = 40$ mo. If n is even, then the subscript in Equation 3.4 will be a number midway between two integers. This indicates that there is not a middle value in the ordered list of data; instead, there are two middle values, and the median is defined as the midpoint between them. For the species B data in Example 3.3, $n = 10$ and $X(n + 1)/2 = X_{(10+1)/2} = X_{5.5}$, which signifies that the median is midway between X_5 and X_6, namely a median of (50 mo + 54 mo)/2 = 52 mo.

Note that the median has the same units as each individual measurement. If data are plotted as a frequency histogram (e.g., Figure 3.1), the median is the value of X that divides the area of the histogram into two equal parts. In general, the sample median is a more efficient estimate of the population median when the sample size is large.

If we find the middle value(s) in an ordered set of data to be among identical observations (referred to as *tied* values), as in Example 3.1 or 3.2, a difficulty arises. If we apply Equation 3.4 to these 24 data, then we conclude the median to be $X_{12.5} = 4.0$ cm. But four data are tied at 4.0 cm, and eleven measurements are less than 4.0 cm and nine are greater. Thus, 4.0 cm does not fit the definition above of the median as that value for which there is the same number of data larger and smaller. Therefore, a better definition of the median of a set of data is that value for which no more than half the data are smaller and no more than half are larger.

When the sample median falls among tied observations, we may interpolate to better estimate the population median. Using the data of Example 3.2, we desire to estimate a value below which 50% of the observations in the population lie. Fifty percent of the observations in the sample would be 12 observations. As the first 7 classes in the frequency table include 11 observations and 4 observations are in class 4.0 cm, we know that the desired sample median lies within the range of 3.95 to 4.05 cm. Assuming that the four observations in class 4.0 cm are distributed evenly within the 0.1-cm range of 3.95 to 4.05 cm, then the median will be $\left(\frac{1}{4}\right)(0.1\text{ cm}) = 0.025$ cm into this class. Thus, the median = 3.95 cm + 0.025 cm = 3.975 cm. In general, for the sample median within a class interval containing tied observations,

$$\text{median} = \begin{pmatrix}\text{lower limit}\\ \text{of interval}\end{pmatrix} + \left(\frac{0.5n - \text{cum. freq.}}{\text{no. of observations in interval}}\right)\begin{pmatrix}\text{interval}\\ \text{size}\end{pmatrix}, \quad (3.5)$$

where "cum. freq." refers to the cumulative frequency of the previous classes.* By using this procedure, the calculated median will be the value of X that divides the area of the histogram of the sample into two equal parts. As another example, refer back to Example 1.5, where, by Equation 3.5, median = 8.75 mg/g + {[(0.5)(130) − 61]/24}{0.10 mg/g} = 8.75 mg/g + 0.02 mg/g = 8.77 mg/g.

The median expresses less information than does the mean, for it does not take into account the actual value of each measurement, but only considers the rank of each measurement. Still, it offers advantages in some situations. For example, extremely high or extremely low measurements ("outliers"; Section 2.5) do not affect the median as much as they affect the mean (causing the sample median to be called a "resistant" statistic). Distributions that are not symmetrical around the mean (such as in Figures 3.2c and 3.2d) are said to be *skewed*.† When we deal with skewed

*This procedure was enunciated in 1878 by the German psychologist Gustav Theodor Fechner (1801–1887) (Walker, 1929: 86).

†This term, applied to a distribution and to a curve, was used as early as 1895 by Karl Pearson (Miller, 2004a).

populations and do not want the strong influence of outliers, we may prefer the median to the mean to express central tendency.

Note that in Example 3.3 the researcher would have to wait 82 months to compute a mean life expectancy for species *A* and 91 months for species *B*, whereas the median for species *A* could be determined in only 40 months and in only 52 months for species *B*. Also, to calculate a median one does not need to have accurate data for all members of the sample. If, for example, we did not have the first three data for species *A* accurately recorded, but could state them as "less than 39 months," then the median could have been determined just as readily as if we had all 9 data fully recorded, while calculation of the mean would not have been possible.

The expression "LD fifty" (LD_{50}), used in some areas of biological research, is simply the median lethal dose (and is so named because the median is the 50th percentile, as we shall see in Section 4.2).

The median can be determined not only for interval-scale and ratio-scale data, but also for data on an ordinal scale, data for which the use of the mean usually would not be considered appropriate. But neither the median nor the mean is applicable to nominal data.

3.3 THE MODE

The *mode* is commonly defined as the most frequently occurring measurement in a set of data.* In Example 3.2, the mode is 4.0 cm. But it is perhaps better to define a mode as a measurement of relatively great concentration, for some frequency distributions may have more than one such point of concentration, even though these concentrations might not contain precisely the same frequencies. Thus, a sample consisting of the data 6, 7, 7, 8, 8, 8, 8, 8, 8, 9, 9, 10, 11, 12, 12, 12, 12, 12, 13, 13, and 14 mm would be said to have two modes: at 8 mm and 12 mm. (Some authors would refer to 8 mm as the "major mode" and call 12 mm the "minor mode.") A distribution in which each different measurement occurs with equal frequency is said to have no mode. If two consecutive values of X have frequencies great enough to declare the X values modes, the mode of the distribution may be said to be the midpoint of these two X's; for example, the mode of 3, 5, 7, 7, 7, 8, 8, 8, and 10 liters is 7.5 liters. A distribution with two modes is said to be *bimodal* (e.g., Figure 3.2b) and may indicate a combination of two distributions with different modes (e.g., heights of men and women). Modes are often discerned from histograms or frequency polygons; but we should be aware that the shape of such graphs (such as Figures 1.6, 1.7, and 1.8), and therefore the appearance of modes, may be influenced by the measurement intervals on the horizontal axis.

The sample mode is the best estimate of the population mode. When we sample a symmetrical unimodal population, the mode is an unbiased and consistent estimate of the mean and median (Figure 3.2a), but it is relatively inefficient and should not be so used. As a measure of central tendency, the mode is affected by skewness less than is the mean or the median, but it is more affected by sampling and grouping than these other two measures. The mode, but neither the median nor the mean, may be used for data on the nominal, as well as the ordinal, interval, and ratio scales of measurement. In a unimodal asymmetric distribution (Figures 3.2c and 3.2d), the median lies about one-third the distance between the mean and the mode.

The mode is not often used in biological research, although it is often interesting to report the number of modes detected in a population, if there are more than one.

*The term *mode* was introduced by Karl Pearson in 1895 (David, 1995).

3.4 OTHER MEASURES OF CENTRAL TENDENCY

(a) The Geometric Mean. The *geometric mean* is the nth root* of the product of the n data:

$$\overline{X}_G = \sqrt[n]{X_1 X_2 X_3 \ldots X_n} = \sqrt[n]{\prod_{i=1}^{n} X_i}. \tag{3.6}$$

Capital Greek pi, Π, means "take the product"† in an analogous fashion as Σ indicates "take the sum." The geometric mean may also be calculated as the antilogarithm of the arithmetic mean of the logarithms of the data (where the logarithms may be in any base); this is often more feasible computationally:

$$\overline{X}_G = \text{antilog}\left(\frac{\log X_1 + \log X_2 + \cdots + \log X_n}{n}\right) = \text{antilog}\frac{\sum_{i=1}^{n} \log X_i}{n}. \tag{3.7}$$

The geometric mean is appropriate to use only for ratio-scale data and only when all of the data are positive (that is, greater than zero). If the data are all equal, then the geometric mean, $\overline{X}_G$, is equal to the arithmetic mean, $\overline{X}$ (and also equal to the harmonic mean described below); if the data are not all equal, then‡ $\overline{X}_G < \overline{X}$.

$\overline{X}_G$ is sometimes used as a measure of location when the data are highly skewed to the right (i.e., when there are many more data larger than the arithmetic mean than there are data smaller than the arithmetic mean).

$\overline{X}_G$ is also useful when dealing with data that represent ratios of change. As an illustration of this, Example 3.4 considers changes in the size of a population of organisms over four decades. Each of the original data (population size at the end of a decade) is expressed as a ratio, X_i, of the population size to the population size of the previous decade. The geometric mean of those ratios is computed and may be thought of as representing the average rate of growth per decade (which is the same as a constant rate of compound interest). This example demonstrates that the arithmetic mean of those ratios is $\overline{X} = 1.1650$ (i.e., 16.50% growth) per decade. But over the four decades of population change, this mean would have us calculate a final population size of (10,000)(1.1650)(1.1650)(1.1650)(1.1650) = 18,421, which is *not* the population size recorded at the end of the fourth decade. However, using the geometric mean, $\overline{X}_G$, to indicate the average rate of growth, the final population size would be computed to be (10,000)(1.608)(1.608)(1.608)(1.608) = 18,156, which is the fourth-decade population size that was observed.

*The second footnote in Section 4.5 outlines the origin of the square-root symbol, $\surd$; indicating the cube root as $\sqrt[3]{}$ was suggested by Albert Girard (1595–1632, French-born but studied and worked in the Netherlands) as early as 1629, but this symbol was not generaly used until well into the eighteenth century (Cajori, 1928/9, Vol. I: 371–372). The cube-root symbol eventually was expanded to $\sqrt[n]{}$ to denote the nth root.

†Use of this symbol to indicate taking the product was introduced by René Descartes (Gullberg, 1997: 105).

‡The symbols "<" and ">" (meaning "less than" and "greater than") were inserted by someone else into a 1631 posthumous publication by the English mathematician and astronomer Thomas Harriot (1560?–1621), (Cajori, 1928/9, Vol. I: 199; Gullberg, 1997: 109; Miller, 2004b). The symbols for "less than or equal to" ($\leq$) and "greater than or equal to" ($\geq$) were written as $\leqq$ and $\geqq$ when introduced by the French scientist Pierre Bouguere (1698–1758) in 1734. (Gullberg, 1997: 109).

EXAMPLE 3.4 The Geometric Mean of Ratios of Change

Decade	*Population Size*	*Ratio of Change* X_i
0	10,000	
1	10,500	$\frac{10{,}500}{10{,}000} = 1.05$
2	11,550	$\frac{11{,}550}{10{,}500} = 1.10$
3	13,860	$\frac{13{,}860}{11{,}550} = 1.20$
4	18,156	$\frac{18{,}156}{13{,}860} = 1.31$

$$\overline{X} = \frac{1.05 + 1.10 + 1.20 + 1.31}{4} = \frac{4.66}{4} = 1.1650$$

and $(10{,}000)(0.1650)(1.650)(1.650)(1.650) = 18{,}421$

But,

$$\overline{X}_G = \sqrt[4]{(1.05)(1.10)(1.20)(1.31)} = \sqrt[4]{1.8157} = 1.1608$$

or

$$\overline{X}_G = \text{antilog}\left[\frac{\log(1.05) + \log(1.10) + \log(1.20) + \log(1.31)}{4}\right]$$

$$= \frac{\text{antilog}(0.0212 + 0.0414 + 0.0792 + 0.1173)}{4} = \frac{\text{antilog}(0.2591)}{4}$$

$$= \text{antilog}\, 0.0648 = 1.1608$$

and $(10{,}000)(1.1608)(1.1608)(1.1608)(1.1608) = 18{,}156$

(b) The Harmonic Mean. The *harmonic mean* is the reciprocal of the arithmetic mean of the reciprocals of the data:

$$\overline{X}_H = \frac{1}{\frac{1}{n}\sum \frac{1}{X_i}} = \frac{n}{\sum \frac{1}{X_i}}. \tag{3.8}$$

It may be used for ratio-scale data when no datum is zero. If all of the data are identical, then the harmonic mean, $\overline{X}_H$, is equal to the arithmetic mean, $\overline{X}$ (and equal to the geometric mean, $\overline{X}_G$). If the data are all positive and not identical, then $\overline{X}_H < \overline{X}_G < \overline{X}$.

$\overline{X}_H$ finds use when desiring an average of rates, as described by Croxton, Cowden, and Klein (1967: 182–188). For example, consider that a flock of birds flies from a roosting area to a feeding area 20 km away, flying at a speed of 40 km/hr (which

takes 0.5 hr). The flock returns to the roosting area along the same route (20 km), flying at 20 km/hr (requiring 1 hr of flying time). To ask what the average flying speed was, we might employ Equation 3.2 and calculate the arithmetic mean as $\overline{X} = (40 \text{ km/hr} + 20 \text{ km/hr})/2 = 30 \text{ km/hr}$. However, this answer may not be satisfying, because a total of 40 km was traveled in 1.5 hr, indicating a speed of $(40 \text{ km})/(1.5 \text{ hr}) = 26.7 \text{ km/hr}$. Example 3.5 shows that the harmonic mean ($\overline{X}_G$) is 26.7 km/hr.

EXAMPLE 3.5 The Harmonic Mean of Rates

$$X_1 = 40 \text{ km/hr}, \; X_2 = 20 \text{ km/hr}$$

$$\overline{X} = \frac{40 \text{ km/hr} + 20 \text{ km/hr}}{2} = \frac{60 \text{ km/hr}}{2} = 30 \text{ km/hr}$$

But

$$\overline{X}_H = \frac{2}{\frac{1}{40 \text{ km/hr}} + \frac{1}{20 \text{ km/hr}}} = \frac{2}{0.0250 \text{ hr/km} + 0.0500 \text{ hr/km}}$$

$$= \frac{2}{0.075 \text{ hr/km}} = 26.67 \text{ km/hr}$$

(c) The Range Midpoint. The *range midpoint*, or *midrange*, is a measure of location defined as the point halfway between the minimum and the maximum values in the set of data. It may be used with data measured on the ratio, interval, or ordinal scale; but it is not generally a good estimate of location, for it utilizes relatively little information from the data. (However, the so-called mean daily temperature is often reported as the mean of the minimum and maximum and is, therefore, a range midpoint.)

The midpoint of any two symmetrically located percentiles (see Section 4.2), such as the point midway between the first and third quartiles (i.e., the 25th and 75th percentiles), may be used as a location measure in the same fashion as the range midpoint is used (see Dixon and Massey, 1969: 133–134). Such measures are not as adversely affected by aberrantly extreme values as is the range midpoint, and they may be applied to ratio or interval data. If used with ordinal data, they (and the range midpoint) would be the same as the median.

3.5 CODING DATA

Often in the manipulation of data, considerable time and effort can be saved if *coding* is employed. Coding is the conversion of the original measurements into easier-to-work-with values by simple arithmetic operations. Generally coding employs a *linear transformation* of the data, such as multiplying (or dividing) or adding (or subtracting) a constant. The addition or subtraction of a constant is sometimes termed a translation of the data (i.e., changing the origin), whereas the multiplication or division by a constant causes an expansion or contraction of the scale of measurement.

EXAMPLE 3.6 Coding Data to Facilitate Calculations

Sample 1 (Coding by Subtraction: $A = -840$ g)		**Sample 2 (Coding by Division: $M = 0.001$ liters/ml)**	
X_i (g)	coded $X_i = X_i - 840$ g	X_i (ml)	coded $X_i = (X_i)(0.001 \text{ liters/ml}) = X_i$ liters
842	2	8,000	8.000
844	4	9,000	9.000
846	6	9,500	9.500
846	6	11,000	11.000
847	7	12,500	12.500
848	8	13,000	13.000
849	9		
$\sum X_i = 5922$ g	coded $\sum X_i = 42$ g	$\sum X_i = 63{,}000$ ml	coded $\sum X_i = 63.000$ liters
$\overline{X} = \frac{5922 \text{ g}}{7} = 846$ g	coded $\overline{X} = \frac{42 \text{ g}}{7} = 6$ g	$\overline{X} = 10{,}500$ ml	coded $\overline{X} = 10.500$ liters
$\overline{X} = \text{coded } \overline{X} - A = 6 \text{ g} - (-840 \text{ g}) = 846$ g		$\overline{X} = \text{coded } \frac{\overline{X}}{M} = \frac{10.500 \text{ liters}}{0.001 \text{ liters/ml}} = 10{,}500$ ml	

The first set of data in Example 3.6 are coded by subtracting a constant value of 840 g. Not only is each coded value equal to $X_i - 840$ g, but the mean of the coded values is equal to $\overline{X} - 840$ g. Thus, the easier-to-work-with coded values may be used to calculate a mean that then is readily converted to the mean of the original data, simply by adding back the coding constant.

In Sample 2 of Example 3.6, the observed data are coded by dividing each observation by 1000 (i.e., by multiplying by 0.001).* The resultant mean only needs to be multiplied by the coding factor of 1000 (i.e., divided by 0.001) to arrive at the mean of the original data. As the other measures of central tendency have the same units as the mean, they are affected by coding in exactly the same fashion.

Coding affects the median and mode in the same way as the mean is affected. The widespread use of computers has greatly diminished the need for researchers to

*In 1593, mathematician Christopher Clavius (1538–1612, born in what is now Germany but spent most of his life in what is now Italy; also credited with proposing the currently used Gregorian calendar rules regarding leap years: O'Connor and Robertson, 1996) became the first to use a decimal point to separate units from tenths; in 1617, the Scottish mathematician John Napier (1550–1617) used both points and commas for this purpose (Cajori, 1928/9. Vol. I: 322–323), and the comma is still so used in some parts of the world. In some countries a raised dot has been used—a symbol Americans sometimes employ to denote multiplication.

utilize coding (although computer software may use it). Appendix C presents coding for a variety of statistics.

EXERCISES

3.1. If $X_1 = 3.1\,\text{kg}$, $X_2 = 3.4\,\text{kg}$, $X_3 = 3.6\,\text{kg}$, $X_4 = 3.7\,\text{kg}$, and $X_5 = 4.0\,\text{kg}$, calculate the value of

(a) $\sum_{i=1}^{4} X_i$.

(b) $\sum_{i=2}^{4} X_i$.

(c) $\sum_{i=1}^{5} X_i$.

(d) $\sum X_i$.

3.2. **(a)** Calculate the mean of the five weights in Exercise 3.1.

(b) Calculate the median of those weights.

3.3. The ages, in years, of the faculty members of a university biology department are 32.2, 37.5, 41.7, 53.8, 50.2, 48.2, 46.3, 65.0, and 44.8.

(a) Calculate the mean age of these nine faculty members.

(b) Calculate the median of the ages.

(c) If the person 65.0 years of age retires and is replaced on the faculty with a person 46.5 years old, what is the new mean age?

(d) What is the new median age?

3.4. Consider the following frequency tabulation of leaf weights (in grams):

X_i	f_i
1.85–1.95	2
1.95–2.05	1
2.05–2.15	2
2.15–2.25	3
2.25–2.35	5
2.35–2.45	6
2.45–2.55	4
2.55–2.65	3
2.65–2.75	1

Using the midpoints of the indicated ranges of X_i,

(a) Calculate the mean leaf weight using Equation 3.2, and

(b) Calculate the mean leaf weight using Equation 3.3.

(c) Calculate the median leaf weight using Equation 3.4, and

(d) Calculate the median using Equation 3.5.

(e) Determine the mode of the frequency distribution.

3.5. A fruit was collected from each of eight lemon trees, with the intent of measuring the calcium concentration in the rind (grams of calcium per 100 grams of dry rind). The analytical method used could only detect a concentration of at least 0.80 g/100 g of dry weight. Six of the eight concentrations were measured to be 1.02, 0.98, 0.91, 0.84, 0.87, 1.04 g/100 g of dry weight, and two of the concentrations were known to be less than 0.80 g/100 g of dry weight. What is the median of this sample of eight data?

CHAPTER 4

Measures of Variability and Dispersion

In addition to a description of the central tendency of a set of data, it is generally desirable to have a description of the *variability*, or of the *dispersion*,* of the data. A measure of variability (or measure of dispersion, as it is often called) is an indication of the spread of measurements around the center of the distribution. Measurements that are concentrated around the center of a distribution of data have low variability (low dispersion), whereas data that are very spread out along the measurement scale have high variability (high dispersion). Measures of variability of a population are population parameters, and sample measures of variability are statistics that estimate those parameters.

4.1 THE RANGE

The difference between the highest and lowest measurements in a group of data is termed the *range*.† If sample measurements are arranged in increasing order of magnitude, as if the median were about to be determined, then

$$\text{sample range} = X_n - X_1, \tag{4.1}$$

which is

$$\text{sample range} = \text{largest } X - \text{smallest } X.$$

Sample 1 in Example 4.1 is a hypothetical set of ordered data in which $X_1 = 1.2$ g and $X_n = 2.4$ g. Thus, the range may be expressed as 1.2 to 2.4 g, or as 2.4 g − 1.2 g = 1.2 g. Note that the range has the same units as the individual measurements. Sample 2 in Example 4.1 has the same range as Sample 1.

*The statistical use of this term first appeared in an 1876 publication by Francis Galton (David, 1998a).

†This statistical term dates from an 1848 paper by H. Lloyd (David, 1995). It was already used by the Greek astronomer Hipparchus as a measure of dispersion in the second century B.C.E. (David, 1998b).

EXAMPLE 4.1 Calculation of Measures of Dispersion for Two Hypothetical Samples of 7 Insect Body Weights

Sample 1

X_i (g)	$X_i - \overline{X}$ (g)	$\lvert X_i - \overline{X}\rvert$ (g)	$(X_i - \overline{X})^2$ (g^2)
1.2	−0.6	0.6	0.36
1.4	−0.4	0.4	0.16
1.6	−0.2	0.2	0.04
1.8	0.0	0.0	0.00
2.0	0.2	0.2	0.04
2.2	0.4	0.4	0.16
2.4	0.6	0.6	0.36
$\sum X_i$ = 12.6 g	$\sum(X_i - \overline{X})$ = 0.0 g	$\sum\lvert X_i - \overline{X}\rvert$ = 2.4 g	$\sum(X_i - \overline{X})^2$ = 1.12 g^2

= sum of squared deviations from the mean
= "sum of squares"

$$n = 7;\ \overline{X} = \frac{\sum X_i}{n} = \frac{12.6\text{ g}}{7} = 1.8\text{ g}$$

$$\text{range} = X_7 - X_1 = 2.4\text{ g} - 1.2\text{ g} = 1.2\text{ g}$$

$$\text{interquartile range} = Q_3 - Q_1 = 2.2\text{ g} - 1.4\text{ g} = 0.8\text{ g}$$

$$\text{mean deviation} = \frac{\sum\lvert X_i - \overline{X}\rvert}{n} = \frac{2.4\text{ g}}{7} = 0.34\text{ g}$$

$$\text{variance} = s^2 = \frac{\sum(X_i - \overline{X})^2}{n - 1} = \frac{1.12\text{ g}^2}{6} = 0.1867\text{ g}^2$$

$$\text{standard deviation} = s = \sqrt{0.1867\text{ g}^2} = 0.43\text{ g}$$

Sample 2

X_i (g)	$X_i - \overline{X}$ (g)	$\lvert X_i - \overline{X}\rvert$ (g)	$(X_i - \overline{X})^2$ (g^2)
1.2	−0.6	0.6	0.36
1.6	−0.2	0.2	0.04
1.7	−0.1	0.1	0.01
1.8	0.0	0.0	0.00
1.9	0.1	0.1	0.01
2.0	0.2	0.2	0.04
2.4	0.6	0.6	0.36
$\sum X_i$ = 12.6 g	$\sum(X_i - \overline{X})$ = 0.0 g	$\sum\lvert X_i - \overline{X}\rvert$ = 1.8 g	$\sum(X_i - \overline{X})^2$ = 0.82 g^2

= sum of squared deviations from the mean
= "sum of squares"

$$n = 7;\ \overline{X} = \frac{\sum X_i}{n} = \frac{12.6\text{ g}}{7} = 1.8\text{ g}$$

$$\text{range} = X_7 - X_1 = 2.4\text{ g} - 1.2\text{ g} = 1.2\text{ g}$$

$$\text{interquartile range} = Q_3 - Q_1 = 2.0\,\text{g} - 1.6\,\text{g} = 0.4\,\text{g}$$

$$\text{mean deviation} = \frac{\sum|X_i - \overline{X}|}{n} = \frac{1.8\,\text{g}}{7} = 0.26\,\text{g}$$

$$\text{variance} = s^2 = \frac{\sum(X_i - \overline{X})^2}{n-1} = \frac{0.82\,\text{g}^2}{6} = 0.1367\,\text{g}^2$$

$$\text{standard deviation} = s = \sqrt{0.1367\,\text{g}^2} = 0.37\,\text{g}$$

The range is a relatively crude measure of dispersion, inasmuch as it does not take into account any measurements except the highest and the lowest. Furthermore, it is unlikely that a sample will contain both the highest and lowest values in the population, so the sample range usually underestimates the population range; therefore, it is a biased and inefficient estimator. Nonetheless, it is considered useful by some to present the sample range as an estimate (although a poor one) of the population range. For example, taxonomists are often concerned with having an estimate of what the highest and lowest values in a population are expected to be. Whenever the range is specified in reporting data, however, it is usually a good practice to report another measure of dispersion as well. The range is applicable to ordinal-, interval-, and ratio-scale data.

4.2 DISPERSION MEASURED WITH QUANTILES

Because the sample range is a biased and inefficient estimate of the population range, being sensitive to extremely large and small measurements, alternative measures of dispersion may be desired. Just as the median (Section 3.2) is the value above and below which lies half the set of data, one can define measures, called *quantiles*, above or below which lie other fractional portions of the data.

For example, if the data are divided into four equal parts, we speak of *quartiles*. One-fourth of all the ranked observations are smaller than the first quartile, one-fourth lie between the first and second quartiles, one-fourth lie between the second and third quartiles, and one-fourth are larger than the third quartile. The second quartile is identical to the median. As with the median, the first and third quartiles might be one of the data or the midpoint between two of the data. The first quartile, Q_1, is

$$Q_1 = X_{(n+1)/4}; \tag{4.2}$$

if the subscript, $(n + 1)/4$, is not an integer or half-integer, then it is rounded up to the nearest integer or half-integer. The second quartile is the median, and the subscript on X for the third quartile, Q_3, is

$$n + 1 - (\text{subscript on } X \text{ for } Q_1, \text{ after any rounding}). \tag{4.3}$$

Examining the data in Example 3.3: For species A, $n = 9$, $(n + 1)/4 = 2.5$, and $Q_1 = X_{2.5} = 34.5$ mo; and $Q_3 = X_{10-2.5} = X_{7.5} = 46$ mo. For species B, $n = 10$, $(n + 1)/4 = 2.75$ (which we round up to 3), and $Q_1 = X_3 = 38$ mo, and $Q_3 = X_{11-3} = X_8 = 59$ mo.

The distance between Q_1 and Q_3, the first and third quartiles (i.e., the 25th and 75th percentiles), is known as the *interquartile range* (or *semiquartile range*):

$$\text{interquartile range} = Q_3 - Q_1. \tag{4.4}$$

One may also encounter the *semi-interquartile range*:

$$\text{semi-interquartile range} = \frac{Q_3 - Q_1}{2}, \tag{4.5}$$

also known as the *quartile deviation*.*

If the distribution of data is symmetrical, then 50% of the measurements lie within one quartile deviation above and below the median. For Sample 1 in Example 4.1, $Q_1 = 1.4$ g, $Q_3 = 2.2$ g, and the interquartile range is 2.2 g − 1.4 g = 0.8 g. And for Sample 2, $Q_1 = 1.6$ g, $Q_3 = 2.0$ g, and the interquartile range is 2.0 g − 1.6 g = 0.4 g.

Similarly, values that partition the ordered data set into eight equal parts (or as equal as n will allow) are called *octiles*. The first octile, $\mathbb{O}_1$, is

$$\mathbb{O}_1 = X_{(n+1)/8}; \tag{4.6}$$

and if the subscript, $(n + 1)/8$, is not an integer or half-integer, then it is rounded up to the nearest integer or half-integer. The second, fourth, and sixth octiles are the same as quartiles; that is, $\mathbb{O}_2 = Q_1$, $\mathbb{O}_4 = Q_2$ = median and $\mathbb{O}_6 = Q_3$. The subscript on X for the third octile, $\mathbb{O}_3$, is

$$2(\text{subscript on } X \text{ for } Q_1) - \text{subscript on } X \text{ for } \mathbb{O}_1; \tag{4.7}$$

the subscript on X for the fifth octile, $\mathbb{O}_5$, is

$$n + 1 - \text{subscript on } X \text{ for } \mathbb{O}_3; \tag{4.8}$$

and the subscript on X for the seventh octile, $\mathbb{O}_7$, is

$$n + 1 - \text{subscript on } X \text{ for } \mathbb{O}_1. \tag{4.9}$$

Thus, for the data of Example 3.3: For species A, $n = 9$, $(n + 1)/8 = 1.5$ and $\mathbb{O}_1 = X_{1.5} = 35$ mo; $2(2.5) - 1.5 = 3.5$, so $\mathbb{O}_3 = X_{3.5} = 38$ mo; $n + 1 - 3.5 = 6.5$, so $\mathbb{O}_5 = X_{6.5} = 41.5$ mo; and $n + 1 - 1.5 = 8.5$, so $\mathbb{O}_7 = 61$. For species B, $n = 10$, $(n + 1)/8 = 1.25$ (which we round up to 1.5) and $\mathbb{O}_1 = X_{1.5} = 35$ mo; $2(3) - 1.5 = 4.5$, so $\mathbb{O}_3 = X_{4.5} = 39.5$ mo; $n + 1 - 4.5 = 6.5$, so $\mathbb{O}_5 = X_{6.5} = 41.5$ mo; and $n + 1 - 1.5 = 9.5$, so $\mathbb{O}_7 = 44.5$ mo.

Besides the median, quartiles, and octiles, ordered data may be divided into fifths, tenths, or hundredths by quantities that are respectively called *quintiles*, *deciles*, and *centiles* (the latter also called *percentiles*). Measures that divide a group of ordered data into equal parts are collectively termed *quantiles*.† The expression "LD_{50}," used in some areas of biological research, is simply the 50th percentile of the lethal doses, or the median lethal dose. That is, 50% of the experimental subjects survived this dose, whereas 50% did not. Likewise, "LC_{50}" is the median lethal concentration, or the 50th percentile of the lethal concentrations.

Instead of distance between the 25th and 75th percentiles, distances between other quantiles (e.g., 10th and 90th percentiles) may be used as a dispersion measure. Quantile-based measures of dispersion are valid for ordinal-, interval-, or ratio-scale data, and they do not exhibit the bias and inefficiency of the range.

*This measure was proposed in 1846 by L. A. J. Quetelet (1796–1874); Sir Francis Galton (1822–1911) later called it the "quartile deviation" (Walker, 1929: 84) and, in 1882, used the terms "quartile" and "interquartile range" (David, 1995).

†Sir Francis Galton developed the concept of percentiles, quartiles, deciles, and other quantiles in writings from 1869 to 1885 (Walker, 1929: 86–87, 177, 179). The term *quantile* was introduced in 1940 by M. G. Kendall (David, 1995).

4.3 THE MEAN DEVIATION

As is evident from the two samples in Example 4.1, the range conveys no information about how clustered about the middle of the distribution the measurements are. As the mean is so useful a measure of central tendency, one might express dispersion in terms of deviations from the mean. The sum of all deviations from the mean, that is, $\sum(X_i - \overline{X})$, will always equal zero, however, so such a summation would be useless as a measure of dispersion (as seen in Example 4.1).

Using the absolute values of the deviations from the mean eliminates the negative signs of the deviations, and summing those absolute values results in a quantity that is an expression of dispersion about the mean. Dividing this quantity by n yields a measure known as the *mean deviation*, or *mean absolute deviation*,* of the sample; this measure has the same units as do the data. In Example 4.1, Sample 1 is more variable (or more dispersed, or less concentrated) than Sample 2. Although the two samples have the same range, the mean deviations, calculated as

$$\text{sample mean deviation} = \frac{\sum|X_i - \overline{X}|}{n}, \tag{4.10}$$

express the differences in dispersion.† A different kind of mean deviation can be defined by using the sum of the absolute deviations from the median instead of from the mean.

Mean deviations are seldom encountered, because their utility is far less than that of the statistics in Sections 4.4 and 4.5.

4.4 THE VARIANCE

Another method of eliminating the negative signs of deviations from the mean is to square the deviations. The sum of the squares of the deviations from the mean is often simply called the *sum of squares*, abbreviated SS, and is defined as follows:‡

$$\text{population SS} = \sum(X_i - \mu)^2 \tag{4.11}$$

$$\text{sample SS} = \sum(X_i - \overline{X})^2. \tag{4.12}$$

It can be seen from the above two equations that as a measure of variability, or dispersion, the sum of squares considers how far the X_i's deviate from the mean. In

*The term *mean deviation* is apparently due to Karl Pearson (1857–1936) (Walker, 1929: 55) and *mean absolute deviation*, in 1972, to D. F. Andrews, P. J. Bickel, F. R. Hampel, P. J. Huber, W. H. Rogers, and J. W. Tukey (David, 1995).

†Karl Weierstrass, in 1841, was the first to denote the absolute value of a quantity by enclosing it within two vertical lines (Cajori, 1928/9, Vol. II: p. 123); that is, $|a| = a$ and $|-a| = a$.

‡The modern notation using raised numerals as exponents was introduced by René Descartes in 1637, and many other kinds of notation for exponents were employed before and after that (Cajori, 1928/9, Vol. I: 358; Gullberg, 1997: 134). An 1845 notation of Augustus De Morgan, $a \wedge b$ to indicate a^b (Cajori, ibid.: 358), has reemerged in modern computer use. Nicolas Chuquet (1445–1488) was the first to use negative exponents, and Nicole (also known as Nicolaus) Oresme (1323–1382) was the first to use fractional exponents, though neither of these French mathematicians employed the modern notation of Isaac Newton (1642–1727), the colossal English mathematician, physicist, and astronomer (Cajori, ibid.: 91, 102, 354–355):

$$X^{-a} = \frac{1}{X^a}; \quad X^{\frac{1}{a}} = \sqrt[a]{X}.$$

Using parentheses or brackets to group quantities dates from the mid-sixteenth century, though it was not common mathematical notation until more than two centuries later (ibid.: 392).

Sample 1 of Example 4.1, the sample mean is 1.8 g and it is seen (in the last column) that

$$\begin{aligned}\text{Sample SS} &= (1.2 - 1.8)^2 + (1.4 - 1.8)^2 + (1.6 - 1.8)^2 + (1.8 - 1.8)^2 \\ &\quad + (2.0 - 1.8)^2 + (2.2 - 1.8)^2 + (2.4 - 1.8)^2 \\ &= 0.36 + 0.16 + 0.04 + 0.00 + 0.04 + 0.16 + 0.36 \\ &= 1.12\end{aligned}$$

(where the units are grams^2).* The sum of squares may also be visualized as a measure of the average extent to which the data deviate from each other, for (using the same seven data from Sample 1 in Example 4.1):

$$\begin{aligned}\text{SS} &= [(1.2 - 1.4)^2 + (1.2 - 1.6)^2 + (1.2 - 1.8)^2 + (1.2 - 2.0)^2 \\ &\quad + (1.2 - 2.2)^2 + (1.2 - 2.4)^2 + (1.4 - 1.6)^2 + (1.4 - 1.8)^2 \\ &\quad + (1.4 - 2.0)^2 + (1.4 - 2.2)^2 + (1.4 - 2.4)^2 + (1.6 - 1.8)^2 \\ &\quad + (1.6 - 2.0)^2 + (1.6 - 2.2)^2 + (1.6 - 2.4)^2 + (1.8 - 2.0)^2 \\ &\quad + (1.8 - 2.2)^2 + (1.8 - 2.4)^2 + (2.0 - 2.2)^2 + (2.0 - 2.4)^2 \\ &\quad + (2.2 - 2.4)^2]/7 \\ &= [0.04 + 0.16 + 0.36 + 0.64 + 1.00 + 1.44 + 0.04 + \cdots + 0.04 + 0.16 \\ &\quad + 0.04]/7 \\ &= 7.84/7 = 1.12\end{aligned}$$

(again in grams^2).

The mean sum of squares is called the *variance* (or *mean square*,† the latter being short for *mean squared deviation*), and for a population is denoted by σ^2 ("sigma squared," using the lowercase Greek letter):

$$\sigma^2 = \frac{\sum(X_i - \mu)^2}{N}. \tag{4.14}$$

The best estimate of the population variance, σ^2, is the sample variance, s^2:

$$s^2 = \frac{\sum(X_i - \overline{X})^2}{n - 1}. \tag{4.15}$$

If, in Equation 4.14, we replace μ by $\overline{X}$ and N by n, the result is a quantity that is a biased estimate of σ^2 in that it underestimates σ^2. Dividing the sample sum of squares

*Owing to an important concept in statistics, known as *least squares*, the sum of squared deviations from the mean is smaller than the sum of squared deviations from any other quantity (e.g., the median). Indeed, if Equation 4.12 is applied using some quantity in place of the mean, the resultant "sum of squares" would be

$$SS + nd^2, \tag{4.13}$$

where d is the difference between the mean and the quantity used. For the population sum of squares (defined in Equation 4.11), the relationship would be $SS + Nd^2$.

†The term *mean square* dates back at least to an 1875 publication of Sir George Biddel Airy (1801–1892), Astronomer Royal of England (Walker, 1929: 54). The term *variance* was introduced in 1918 by English statistician Sir Ronald Aylmer Fisher (1890–1962) (ibid.: 189; David, 1995).

by $n - 1$ (called the *degrees of freedom*,* often abbreviated DF), rather than by n, yields an unbiased estimate, and it is Equation 4.15 that should be used to calculate the sample variance.

If all observations in a sample are equal, then there is no variability (that is, no dispersion) and $s^2 = 0$. And s^2 becomes increasingly large as the amount of variability, or dispersion, increases. Because s^2 is a mean sum of squares, it can never be a negative quantity.

The variance expresses the same type of information as does the mean deviation, but it has certain very important mathematical properties relative to probability and hypothesis testing that make it superior. Thus, the mean deviation is very seldom encountered in biostatistical analysis.

The calculation of s^2 can be tedious for large samples, but it can be facilitated by the use of the equality

$$\text{sample SS} = \sum X_i^2 - \frac{\left(\sum X_i\right)^2}{n}. \tag{4.16}$$

This formula is equivalent to Equation 4.12 but is much simpler to work with. Example 4.2 demonstrates its use to obtain a sample sum of squares.

Because the sample variance equals the sample SS divided by DF,

$$s^2 = \frac{\sum X_i^2 - \dfrac{\left(\sum X_i\right)^2}{n}}{n - 1}. \tag{4.17}$$

This last formula is often referred to as a "working formula," or "machine formula," because of its computational advantages. There are, in fact, two major advantages in calculating SS by Equation 4.16 rather than by Equation 4.12. First, fewer computational steps are involved, a fact that decreases chance of error. On many calculators the summed quantities, $\sum X_i$ and $\sum X_i^2$, can both be obtained with only one pass through the data, whereas Equation 4.12 requires one pass through the data to calculate $\overline{X}$ and at least one more pass to calculate and sum the squares of the deviations, $X_i - \overline{X}$. Second, there may be a good deal of rounding error in calculating each $X_i - \overline{X}$, a situation that leads to decreased accuracy in computation, but that is avoided by the use of Equation 4.16.†

For data recorded in frequency tables,

$$\text{sample SS} = \sum f_i X_i^2 - \frac{\left(\sum f_i X_i\right)^2}{n}, \tag{4.18}$$

*Given the sample mean ($\overline{X}$) and sample size (n) in Example 4.1, *degrees of freedom* means that the data could have been weights different from those shown, but when any six (i.e., $n - 1$) of the seven weights are specified, then the seventh weight is also known. The term was first used, though in a different context, by Ronald Aylmer Fisher in 1922 (David, 1955).

†Computational formulas advantageous on calculators may not prove accurate on computers (Wilkinson and Dallal, 1977), largely because computers may use fewer significant figures. (Also see Ling, 1974.) Good computer programs use calculation techniques designed to help avoid rounding errors.

where f_i is the frequency of observations with magnitude X_i. But with a calculator or computer it is often faster to use Equation 4.18 for the individual observations, disregarding the class groupings.

The variance has square units. If measurements are in grams, their variance will be in grams squared, or if the measurements are in cubic centimeters, their variance will be in terms of cubic centimeters squared, even though such squared units have no physical interpretation. The question of how many decimal places to report for the variance will be considered at the end of Section 6.2.

EXAMPLE 4.2 "Machine Formula" Calculation of Variance, Standard Deviation, and Coefficient of Variation (These are the data of Example 4.1)

Sample 1		Sample 2	
X_i (g)	X_i^2 (g^2)	X_i (g)	X_i^2 (g^2)
1.2	1.44	1.2	1.44
1.4	1.96	1.6	2.56
1.6	2.56	1.7	2.89
1.8	3.24	1.8	3.24
2.0	4.00	1.9	3.61
2.2	4.84	2.0	4.00
2.4	5.76	2.4	5.76

$\sum X_i = 12.6\text{ g} \quad \sum X_i^2 = 23.80\text{ g}^2$

$n = 7$

$$\overline{X} = \frac{12.6\text{ g}}{7} = 1.8\text{ g}$$

$$SS = \sum X_i^2 - \frac{(\sum X_i)^2}{n}$$

$$= 23.80\text{ g}^2 - \frac{(12.6\text{ g})^2}{7}$$

$$= 23.80\text{ g}^2 - 22.68\text{ g}^2$$

$$= 1.12\text{ g}^2$$

$$s^2 = \frac{SS}{n-1}$$

$$= \frac{1.12\text{ g}^2}{6} = 0.1867\text{ g}^2$$

$$s = \sqrt{0.1867\text{ g}^2} = 0.43\text{ g}$$

$$V = \frac{s}{\overline{X}} = \frac{0.43\text{ g}}{1.8\text{ g}} = 0.24 = 24\%$$

$\sum X_i = 12.6\text{ g} \quad \sum X_i^2 = 23.50\text{ g}^2$

$n = 7$

$$\overline{X} = \frac{12.6\text{ g}}{7} = 1.8\text{ g}$$

$$SS = 23.50\text{ g}^2 - \frac{(12.6\text{ g})^2}{7}$$

$$= 0.82\text{ g}^2$$

$$s^2 = \frac{0.82\text{ g}^2}{6} = 0.1367\text{ g}^2$$

$$s = \sqrt{0.1367\text{ g}^2} = 0.37\text{ g}$$

$$V = \frac{0.37\text{ g}}{1.8\text{ g}} = 0.21 = 21\%$$

4.5 THE STANDARD DEVIATION

The *standard deviation** is the positive square root† of the variance; therefore, it has the same units as the original measurements. Thus, for a population,

$$\sigma = \sqrt{\frac{\sum X_i^2 - \frac{(\sum X_i)^2}{N}}{N}}. \tag{4.19}$$

And for a sample,‡

$$s = \sqrt{\frac{\sum X_i^2 - \frac{(\sum X_i)^2}{n}}{n-1}}. \tag{4.20}$$

Examples 4.1 and 4.2 demonstrate the calculation of s. This quantity frequently is abbreviated SD, and on rare occasions is called the *root mean square deviation* or *root mean square*. Remember that the standard deviation is, by definition, always a nonnegative quantity.§ The end of Section 6.2 will explain how to determine

*It was the great English statistician Karl Pearson (1857–1936) who coined the term *standard deviation* and its symbol, σ, in 1893, prior to which this quantity was called the *mean error* (Eells, 1926; Walker, 1929: 54–55, 183, 188). In early literature (e.g., by G. U. Yule in 1919), it was termed *root mean square deviation* and acquired the symbol s, and (particularly in the fields of education and psychology) it was occasionally computed using deviations from the median (or even the mode) instead of from the mean (Eells, 1926).

†The square root sign ($\surd$) was introduced by Silesian-born Austrian mathematician Christoff Rudolff (1499–1545) in 1525; by 1637 René Descartes (1596–1650) combined this with a vinculum (a horizontal bar placed above quantities to group them as is done with parentheses or brackets) to obtain the symbol $\sqrt{}$, but Gottfried Wilhelm Leibniz (1646–1716) preferred $\surd(\quad)$, which is still occasionally seen (Cajori, 1928/9, Vol. I: 135, 208, 368, 372, 375). The first footnote in Section 3.4 speaks to the origin of the cube root symbol ($\sqrt[3]{}$).

‡The sample s is actually a slightly biased estimate of the population σ, in that on the average it is a slightly low estimate, especially in small samples. But this fact is generally considered to be offset by the statistic's usefulness. Correction for this bias is sometimes possible (e.g., Bliss, 1967: 131; Dixon and Massey, 1969: 136; Gurland and Tripathi, 1971; Tolman, 1971), but it is rarely employed.

§It can be shown that the median of a distribution is never more than one standard deviation away from the mean (μ); that is,

$$|\text{median} - \mu| \leq \sigma \tag{4.21}$$

(Hotelling and Solomon, 1932; O'Cinneide, 1990; Page and Murty, 1982; Watson, 1994). This is a special case, where $p = 50$, of the relationship

$$\mu - \sigma\sqrt{\frac{1 - p/100}{p/100}} \leq X_p \leq \mu + \sigma\sqrt{\frac{p/100}{1 - p/100}}, \tag{4.22}$$

where X_p is the pth percentile of the distribution (Dharmadhikari, 1991). Also, Page and Murty (1982) have shown these population-parameter relationships between the standard deviation and the range and between the standard deviation and the mean, median, and mode:

$$\text{range}/\sqrt{2n} \leq \sigma \leq \text{range}/2; \tag{4.22a}$$

$$|\text{mode} - \mu| \leq \sigma\sqrt{n/m} \text{ and } |\text{mode} - \text{median}| \leq \sigma(n/m), \tag{4.22b}$$

where m is the number of data at the modal value.

the number of decimal places that may appropriately be recorded for the standard deviation.

4.6 THE COEFFICIENT OF VARIATION

The *coefficient of variation** or *coefficient of variability*, is defined as

$$V = \frac{s}{\overline{X}} \quad \text{or} \quad V = \frac{s}{\overline{X}} \cdot 100\%. \tag{4.23}$$

As $s/\overline{X}$ is generally a small quantity, it is frequently multiplied by 100% in order to express V as a percentage. (The coefficient of variation is often abbreviated as CV.)

As a measure of variability, the variance and standard deviation have magnitudes that are dependent on the magnitude of the data. Elephants have ears that are perhaps 100 times larger than those of mice. If elephant ears were no more variable, relative to their size, than mouse ears, relative to their size, the standard deviation of elephant ear lengths would be 100 times as great as the standard deviation of mouse ear lengths (and the variance of the former would be $100^2 = 10{,}000$ times the variance of the latter). The sample coefficient of variation expresses sample variability relative to the mean of the sample (and is on rare occasion referred to as the "relative standard deviation"). It is called a measure of *relative variability* or *relative dispersion*.

Because s and $\overline{X}$ have identical units, V has no units at all, a fact emphasizing that it is a relative measure, divorced from the actual magnitude or units of measurement of the data. Thus, had the data in Example 4.2 been measured in pounds, kilograms, or tons, instead of grams, the calculated V would have been the same. The coefficient of variation of a sample, namely V, is an estimate of the coefficient of variation of the population from which the sample came (i.e., an estimate of σ/μ). The coefficient of variation may be calculated only for ratio scale data; it is, for example, not valid to calculate coefficients of variation of temperature data measured on the Celsius or Fahrenheit temperature scales. Simpson, Roe, and Lewontin (1960: 89–95) present a good discussion of V and its biological application, especially with regard to zoomorphological measurements.

4.7 INDICES OF DIVERSITY

For nominal-scale data there is no mean or median or ordered measurements to serve as a reference for discussion of dispersion. Instead, we can invoke the concept of *diversity*, the distribution of observations among categories. Consider that sparrows are found to nest in four different types of location (vines, eaves, branches, and cavities). If, out of twenty nests observed, five are found at each of the four locations, then we would say that there was great diversity in nesting sites. If, however, seventeen nests were found in cavities and only one in each of the other three locations, then we would consider the situation to be one of very low nest-site diversity. In other words, observations distributed evenly among categories display high diversity, whereas a set of observations where most of the data occur in very few of the categories is one exhibiting low diversity.

A large number of diversity measures have been introduced, especially for ecological data (e.g., Brower, Zar, and von Ende, 1998: 177–184; Magurran, 2004), a few of which are presented here.

*The term *coefficient of variation* was introduced by the statistical giant Karl Pearson (1857–1936) in 1896 (David, 1995). In early literature the term was variously applied to the ratios of different measures of dispersion and different measures of central tendency (Eells, 1926).

Among the quantitative descriptions of diversity available are those based on a field known as *information theory*.* The underlying considerations of these measures can be visualized by considering *uncertainty* to be synonymous with diversity. If seventeen out of twenty nest sites were to be found in cavities, then one would be relatively certain of being able to predict the location of a randomly encountered nest site. However, if nests were found to be distributed evenly among the various locations (a situation of high nest-site diversity), then there would be a good deal of uncertainty involved in predicting the location of a nest site selected at random. If a set of nominal scale data may be considered to be a random sample, then a quantitative expression appropriate as a measure of diversity is that of Shannon (1948):

$$H' = -\sum_{i=1}^{k} p_i \log p_i \tag{4.24}$$

(often referred to as the Shannon-Wiener diversity index or the Shannon-Weaver index). Here, k is the number of categories and p_i is the proportion of the observations found in category i. Denoting n to be sample size and f_i to be the number of observations in category i, then $p_i = f_i/n$; and an equivalent equation for H' is

$$H' = \frac{n \log n - \sum_{i=1}^{k} f_i \log f_i}{n}, \tag{4.25}$$

a formula that is easier to use than Equation 4.24 because it eliminates the necessity of calculating the proportions (p_i). Published tables of $n \log n$ and $f_i \log f_i$ are available (e.g., Brower, Zar, and von Ende, 1998: 181; Lloyd, Zar, and Karr, 1968). Any logarithmic base may be used to compute H'; bases 10, e, and 2 (in that order of commonness) are the most frequently encountered. A value of H' (or of any other measure of this section except evenness measures) calculated using one logarithmic base may be converted to that of another base; Table 4.1 gives factors for doing this for bases 10, e, and 2. Unfortunately, H' is known to be an underestimate of the diversity in the sampled population (Bowman et al., 1971). However, this bias decreases with increasing sample size. Ghent (1991) demonstrated a relationship between H' and testing hypotheses for equal abundance among the k categories.

The magnitude of H' is affected not only by the distribution of the data but also by the number of categories, for, theoretically, the maximum possible diversity for a set of data consisting of k categories is

$$H'_{\max} = \log k. \tag{4.26}$$

Therefore, some users of Shannon's index prefer to calculate

$$J' = \frac{H'}{H'_{\max}} \tag{4.27}$$

instead of (or in addition to) H', thus expressing the observed diversity as a proportion of the maximum possible diversity. The quantity J' has been termed *evenness* (Pielou, 1966) and may also be referred to as *homogeneity* or *relative diversity*. The measure

*Claude Elwood Shannon (1916–2001) founded what he first called "a mathematical theory of communication" and has become known as "information theory."

TABLE 4.1: Multiplication Factors for Converting among Diversity Measures (H, H', H_{max}, or H'_{max}) Calculated Using Different Logarithmic Bases*

To convert to:	To convert from:		
	Base 2	**Base *e***	**Base 10**
Base 2	1.0000	1.4427	3.3219
Base *e*	0.6931	1.0000	2.3026
Base 10	0.3010	0.4343	1.0000

For example, if $H' = 0.255$ using base 10; H' would be $(0.255)(3.3219) = 0.847$ using base 2.

*The measures J and J' are unaffected by change in logarithmic base.

$1 - J'$ may then be viewed as a measure of *heterogeneity*; it may also be considered a measure of *dominance*, for it reflects the extent to which frequencies are concentrated in a small number of categories. The number of categories in a sample (k) is typically an underestimate of the number of categories in the population from which the sample came, because some categories (especially the rarer ones) are likely to be missed in collecting the sample. Therefore, the sample evenness, J', is typically an overestimate of the population evenness. (That is, J' is a biased statistic.) Example 4.3 demonstrates the calculation of H' and J'.

If a set of data may not be considered a random sample, then Equation 4.24 (or 4.25) is not an appropriate diversity measure (Pielou, 1966). Examples of such

EXAMPLE 4.3 Indices of Diversity for Nominal Scale Data: The Nesting Sites of Sparrows

Category (i)	Observed Frequencies (f_i)
	Sample 1
Vines	5
Eaves	5
Branches	5
Cavities	5

$$H' = \frac{n\log n - \sum f_i \log f_i}{n} = [20\log 20 - (5\log 5 + 5\log 5 + 5\log 5 + 5\log 5)]/20$$

$$= [26.0206 - (3.4949 + 3.4949 + 3.4949 + 3.4949)]/20$$

$$= 12.0410/20 = 0.602$$

$$H'_{max} = \log 4 = 0.602$$

$$J' = \frac{0.602}{0.602} = 1.00$$

	Sample 2
Vines	1
Eaves	1
Branches	1
Cavities	17

$$H' = \frac{n\log n - \sum f_i \log f_i}{n} = [20\log 20 - (1\log 1 + 1\log 1 + 1\log 1 + 17\log 17)]/20$$
$$= [26.0206 - (0 + 0 + 0 + 20.9176)]/20$$
$$= 5.1030/20 = 0.255$$
$$H'_{\max} = \log 4 = 0.602$$
$$J' = \frac{0.255}{0.602} = 0.42$$

	Sample 3
Vines	2
Eaves	2
Branches	2
Cavities	34

$$H' = \frac{n\log n - \sum f_i \log f_i}{n} = [40\log 40 - (2\log 2 + 2\log 2 + 2\log 2 + 34\log 34)]/40$$
$$= [64.0824 - (0.6021 + 0.6021 + 0.6021 + 52.0703)]/40$$
$$= 10.2058/40 = 0.255$$
$$H'_{\max} = \log 4 = 0.602$$
$$J' = \frac{0.255}{0.602} = 0.42$$

situations may be when we have, in fact, data composing an entire population, or data that are a sample obtained nonrandomly from a population. In such a case, one may use the information-theoretic diversity measure of Brillouin (1962: 7–8):*

$$H = \frac{\log\left(\dfrac{n!}{\prod_{i=1}^{k} f_i!}\right)}{n}, \tag{4.28}$$

*The notation $n!$ is read as "n factorial" and signifies the product $(n)(n-1)(n-2)\cdots(2)(1)$. It was proposed by French physician and mathematician Christian Kramp (1760–1826) around 1798; he originally called this function *faculty* ("facultés" in French) but in 1808 accepted the term *factorial* ("factorielle" in French) used by Alsatian mathematician Louis François Antoine Arbogast (1759–1803) (Cajori, 1928/9, Vol. II: 72; Gullberg, 1997: 106; Miller, 2004a; O'Connor and Robertson, 1997). English mathematician Augustus De Morgan (1806–1871) decried the adoption of this symbol as a "barbarism" because it introduced into mathematics a symbol that already had an established meaning in written language, thus giving "the appearance of expressing surprise or admiration" in a mathematical result (Cajori, ibid.: 328).

where Π (capital Greek pi) means to take the product, just as Σ means to take the sum. Equation 4.28 may be written, equivalently, as

$$H = \frac{\log \dfrac{n!}{f_1!f_2!\ldots f_k!}}{n} \tag{4.29}$$

or as

$$H = \frac{(\log n! - \sum \log f_i!)}{n}. \tag{4.30}$$

Table B.40 gives logarithms of factorials to ease this calculation. Other such tables are available, as well (e.g., Brower, Zar, and von Ende 1998: 183; Lloyd, Zar, and Karr, 1968; Pearson and Hartly, 1966: Table 51).* Ghent (1991) discussed the relationship between H and the test of hypotheses about equal abundance among k categories.

The maximum possible Brillouin diversity for a set of n observations distributed among k categories is

$$H_{\max} = \frac{\log n! - (k - d)\log c! - d\log(c + 1)!}{n}, \tag{4.35}$$

where c is the integer portion of n/k, and d is the remainder. (For example, if $n = 17$ and $k = 4$, then $n/k = 17/4 = 4.25$ and $c = 4$ and $d = 0.25$.) The Brillouin-based evenness measure is, therefore,

$$J = \frac{H}{H_{\max}}, \tag{4.36}$$

with $1 - J$ being a dominance measure. When we consider that we have data from an entire population, k is a population measurement, rather than an estimate of one, and J is not a biased estimate as is J'.

For further considerations of these and other diversity measures, see Brower, Zar, and von Ende (1998: Chapter 5B) and Magguran (2004: 100–121).

4.8 CODING DATA

Section 3.5 showed how coding data may facilitate statistical computations of measures of central tendency. Such benefits are even more apparent when calculating SS, s^2,

*For moderate to large n (or f_i), "Stirling's approximation" is excellent (see note after Table B.40):

$$n! = \sqrt{2\pi n}(n/e)^n = \sqrt{2\pi}\sqrt{n}e^{-n}n^n, \tag{4.31}$$

of which this is an easily usable derivation:

$$\log n! = (n + 0.5)\log n - 0.434294n + 0.399090. \tag{4.32}$$

An approximation with only half the error of the above is

$$n! = \sqrt{2\pi}\left(\frac{n + 0.5}{e}\right)^{n+0.5} \tag{4.33}$$

and

$$\log n! = (n + 0.5)\log(n + 0.5) - 0.434294(n + 0.5) + 0.399090. \tag{4.34}$$

This is named for James Stirling, who published something similar to the latter approximation formula in 1730, making an arithmetic improvement in the approximation earlier known by Abraham de Moivre (Kemp, 1989; Pearson, 1924; Walker, 1929: 16).

and s, because of the labor, and concomitant chances of error, involved in the unwieldy squaring of large or small numbers.

When data are coded by adding or subtracting a constant (call it A), the measures of dispersion of Sections 4.1 through 4.5 are not changed from what they were for the data before coding. This is because these measures are based upon deviations, and deviations are not changed by moving the data along the measurement scale (e.g., the deviation between 1 and 10 is the same as the deviation between 11 and 20). Sample 1 in Example 4.4 demonstrates this.

However, when coding by multiplying by a constant (call it M), the measures of dispersion are affected, for the magnitudes of the deviations will be changed. With such coding, the range, mean deviation, and standard deviation are changed by a factor of M, in the same manner as the arithmetic mean and the median are, whereas the sum of squares and variance are changed in accordance with the square of the coding constant (i.e., M^2), and the coefficient of variance is not affected. This is demonstrated in Sample 2 of Example 4.4.

Appendix C presents the results of coding these and many other statistics, where a coded datum is described as

$$[X_i] = MX_i + A. \tag{4.37}$$

EXAMPLE 4.4 Coding Data to Facilitate the Calculation of Measures of Dispersion

Sample 1 (Coding by Subtraction: $A = -840$ g)

Without Coding X_i		*Using Coding* $[X_i]$	
X_i (g)	X_i^2 (g^2)	$[X_i]$ (g)	$[X_i]^2$ (g^2)
842	708,964	2	4
843	710,649	3	9
844	712,336	4	16
846	715,716	6	36
846	715,716	6	36
847	717,409	7	49
848	719,104	8	64
849	720,801	9	81
$\sum X_i = 6765$ g	$\sum X_i^2 = 5{,}720{,}695$ g^2	$\sum[X_i] = 45$ g	$\sum[X_i]^2 = 295$ g^2

$$s^2 = \frac{5720695\ \text{g}^2 - \frac{(6765\ \text{g})^2}{8}}{7}$$
$$= 5.98\ \text{g}^2$$
$$s = 2.45\ \text{g}$$
$$\overline{X} = 845.6\ \text{g}$$
$$V = \frac{s}{\overline{X}} = \frac{2.45\ \text{g}}{845.6\ \text{g}}$$
$$= 0.0029 = 0.29\%$$

$$[s^2] = \frac{295\ \text{g}^2 - \frac{(45\ \text{g})^2}{8}}{7}$$
$$= 5.98\ \text{g}^2$$
$$[s] = 2.44\ \text{g}$$
$$[\overline{X}] = 5.6\ \text{g}$$

Sample 2 (Coding by Division: $M = 0.01$)

Without Coding X_i		*Using Coding* $[X_i]$	
X_i (sec)	X_i^2 (sec^2)	$[X_i]$ (sec)	$[X_i]^2$ (sec^2)
800	640,000	8.00	64.00
900	810,000	9.00	81.00
950	902,500	9.50	90.25
1100	1,210,000	11.00	121.00
1250	1,562,500	12.50	156.25
1300	1,690,000	13.00	169.00
$\sum X_i = 6300$ sec	$\sum X_i^2 = 6{,}815{,}000$ sec^2	$\sum[X_i] = 63.00$ sec	$\sum[X_i]^2 = 681.50$ sec^2

$$s^2 = \frac{6815000 \text{ sec}^2 - \frac{(6300 \text{ sec})^2}{6}}{5}$$

$$= 40{,}000 \text{ sec}^2$$

$$s = 200 \text{ sec}$$

$$\overline{X} = 1050 \text{ sec}$$

$$V = 0.19 = 19\%$$

$$[s^2] = \frac{681.50 \text{ sec}^2 - \frac{(63.00 \text{ sec})^2}{6}}{5}$$

$$= 4 \text{ sec}^2$$

$$[s] = 2.00 \text{ sec}$$

$$[\overline{X}] = 10.50 \text{ sec}$$

$$[V] = 0.19 = 19\%$$

EXERCISES

4.1. Five body weights, in grams, collected from a population of rodent body weights are

66.1, 77.1, 74.6, 61.8, 71.5.

(a) Compute the "sum of squares" and the variance of these data using Equations 4.12 and 4.15, respectively.

(b) Compute the "sum of squares" and the variance of these data by using Equations 4.16 and 4.17, respectively.

4.2. Consider the following data, which are a sample of amino acid concentrations (mg/100 ml) in arthropod hemolymph:

240.6, 238.2, 236.4, 244.8, 240.7, 241.3, 237.9.

(a) Determine the range of the data.

(b) Calculate the "sum of squares" of the data.

(c) Calculate the variance of the data.

(d) Calculate the standard deviation of the data.

(e) Calculate the coefficient of variation of the data.

4.3. The following frequency distribution of tree species was observed in a random sample from a forest:

Species	*Frequency*
White oak	44
Red oak	3
Shagbark hickory	28
Black walnut	12
Basswood	2
Slippery elm	8

(a) Use the Shannon index to express the tree species diversity.

(b) Compute the maximum Shannon diversity possible for the given number of species and individuals.

(c) Calculate the Shannon evenness for these data.

4.4. Assume the data in Exercise 4.3 were an entire population (e.g., all the trees planted around a group of buildings).

(a) Use the Brillouin index to express the tree species diversity.

(b) Compute the maximum Brillouin diversity possible for the given number of species and individuals.

(c) Calculate the Brillouin evenness measure for these data.

CHAPTER 5

Probabilities

Everyday concepts of "likelihood," "predictability," and "chance" are formalized by that branch of mathematics called *probability*. Although earlier work on the subject was done by writers such as Giralamo Cardano (1501–1576) and Galileo Galilei (1564–1642), the investigation of probability as a branch of mathematics sprang in earnest from 1654 correspondence between two great French mathematicians, Blaise Pascal (1623–1662) and Pierre Fermat (1601–1665). These two men were stimulated by the desire to predict outcomes in the games of chance popular among the French nobility of the mid-seventeenth century; we still use the devices of such games (e.g., dice and cards) to demonstrate the basic concepts of probability.*

A thorough discourse on probability is well beyond the scope and intent of this book, but aspects of probability are of biological interest and considerations of probability theory underlie the many procedures for statistical hypothesis testing discussed in the following chapters. Therefore, this chapter will introduce probability concepts that bear the most pertinence to biology and biostatistical analysis. Although mastery of this chapter is not essential to apply the statistical procedures in the remainder of the book, occasionally later reference will be made to it.

Worthwhile presentations of probability specifically for the biologist are found in Batschelet (1976: 441–474); Eason, Coles, and Gettinby (1980: 395–414); and Mosimann (1968).

5.1 COUNTING POSSIBLE OUTCOMES

Suppose a phenomenon can occur in any one of k different ways, but in only one of those ways at a time. For example, a coin has two sides and when tossed will land

*The first published work on the subject of probability and gaming was by the Dutch astronomer, physicist, and mathematician Christiaan (also known as Christianus) Huygens (1629–1695), in 1657 (Asimov, 1982: 138; David, 1962: 113, 133). This, in turn, aroused the interest of other major minds, such as Jacob (also known as Jacques, Jakob, and James) Bernoulli (1654–1705, whose 1713 book was the first devoted entirely to probability), several other members of the remarkable Bernoulli family of Swiss mathematicians, and others such as Abraham de Moivre (1667–1754), Pierre Rémond de Montmort (1678–1719), and Pierre-Simon Laplace (1749–1827) of France. The term *probability* in its modern mathematical sense was used as early as 1718 by de Moivre (Miller, 2004a). For more detailed history of the subject, see David (1962) and Walker (1928: 5–13).

with either the "head" side (H) up or the "tail" side (T) up, but not both. Or, a die has six sides and when thrown will land with either the 1, 2, 3, 4, 5, or 6 side up.* We shall refer to each possible outcome (i.e., H or T with the coin; or 1, 2, 3, 4, 5, or 6 with the die) as an *event*.

If something can occur in any one of k_1 different ways and something else can occur in any one of k_2 different ways, then the number of possible ways for both things to occur is $k_1 \times k_2$. For example, suppose that two coins are tossed, say a silver one and a copper one. There are two possible outcomes of the toss of the silver coin (H or T) and two possible outcomes of the toss of the copper coin (H or T). Therefore, $k_1 = 2$ and $k_2 = 2$ and there are $(k_1)(k_2) = (2)(2) = 4$ possible outcomes of the toss of both coins: both heads, silver head and copper tail, silver tail and copper head, and both tails (i.e., H,H; H,T; T,H; T,T).

Or, consider tossing of a coin together with throwing a die. There are two possible coin outcomes ($k_1 = 2$) and six possible die outcomes ($k_2 = 6$), so there are $(k_1)(k_2) = (2)(6) = 12$ possible outcomes of the two events together:

H,1; H,2; H,3; H,4; H,5; H,6; T,1; T,2; T,3; T,4; T,5; T,6.

If two dice are thrown, we can count six possible outcomes for the first die and six for the second, so there are $(k_1)(k_2) = (6)(6) = 36$ possible outcomes when two dice are thrown:

1,1; 1,2; 1,3; 1,4; 1,5; 1,6;	2,1; 2,2; 2,3; 2,4; 2,5; 2,6;
3,1; 3,2; 3,3; 3,4; 3,5; 3,6;	4,1; 4,2; 4,3; 4,4; 4,5; 4,6;
5,1; 5,2; 5,3; 5,4; 5,5; 5,6;	6,1; 6,2; 6,3; 6,4; 6,5; 6,6.

The preceding counting rule is extended readily to determine the number of ways more than two things can occur together. If one thing can occur in any one of k_1 ways, a second thing in any one of k_2 ways, a third thing in any of k_3 ways, and so on, through an nth thing in any one of k_n ways, then the number of ways for all n things to occur together is

$$(k_1)(k_2)(k_3)\cdots(k_n).$$

Thus, if three coins are tossed, each toss resulting in one of two possible outcomes, then there is a total of

$$(k_1)(k_2)(k_3) = (2)(2)(2) = 8$$

possible outcomes for the three tosses together:

H,H,H; H,H,T; H,T,H; H,T,T; T,H,H, T,H,T; T,T,H; T,T,T.

Similarly, if three dice are thrown, there are $(k_1)(k_2)(k_3) = (6)(6)(6) = 6^3 = 216$ possible outcomes; if two dice and three coins are thrown, there are

*What we recognize as metallic coins originated shortly after 650 B.C.E.—perhaps in ancient Lydia (located on the Aegean Sea in what is now western Turkey). From the beginning, the obverse and reverse sides of coins have had different designs, in earliest times with the obverse commonly depicting animals and, later, deities and rulers (Sutherland, 1992). Dice have long been used for both games and religion. They date from nearly 3000 years B.C.E., with the modern conventional arrangement of dots on the six faces of a cubic die (1 opposite 6, 2 opposite 5, and 3 opposite 4) becoming dominant around the middle of the fourteenth century B.C.E. (David, 1962: 10). Of course, the arrangement of the numbers 1 through 6 on the six faces has no effect on the outcome of throwing a die.

$(k_1)(k_2)(k_3)(k_4)(k_5) = (6)(6)(2)(2)(2) = (6^2)(2^3) = 288$ outcomes; and so on. Example 5.1 gives two biological examples of counting possible outcomes.

EXAMPLE 5.1 Counting Possible Outcomes

(a) A linear arrangement of three deoxyribonucleic acid (DNA) nucleotides is called a triplet. A nucleotide may contain any one of four possible bases: adenine (A), cytosine (C), guanine (G), and thymine (T). How many different triplets are possible?

As the first nucleotide in the triplet may be any one of the four bases (A; C; G; T), the second may be any one of the four, and the third may be any one of the four, there is a total of

$$(k_1)(k_2)(k_3) = (4)(4)(4) = 64 \text{ possible outcomes;}$$

that is, there are 64 possible triplets:

A, A, A; A, A, C; A, A, G; A, A, T;
A, C, A; A, C, C; A, C, G; A, C, T;
A, G, A; A, G, C; A, G, G; A, G, T;
and so on.

(b) If a diploid cell contains three pairs of chromosomes, and one member of each pair is found in each gamete, how many different gametes are possible?

As the first chromosome may occur in a gamete in one of two forms, as may the second and the third chromosomes,

$$(k_1)(k_2)(k_3) = (2)(2)(2) = 2^3 = 8.$$

Let us designate one of the pairs of chromosomes as "long," with the members of the pair being L_1 and L_2; one pair as "short," indicated as S_1 and S_2; and one pair as "midsized," labeled M_1 and M_2. Then the eight possible outcomes may be represented as

L_1, M_1, S_1; L_1, M_1, S_2; L_1, M_2, S_1; L_1, M_2, S_2;
L_2, M_1, S_1; L_2, M_1, S_2; L_2, M_2, S_1; L_2, M_2, S_2.

5.2 PERMUTATIONS

(a) Linear Arrangements. A *permutation** is an arrangement of objects in a specific sequence. For example, a horse (H), cow (C), and sheep (S) could be arranged linearly in six different ways: H,C,S; H,S,C; C,H,S; C,S,H; S,H,C; S,C,H. This set of outcomes may be examined by noting that there are three possible ways to fill the first position in the linear order; but once an animal is placed in this position, there are only two ways to fill the second position; and after animals are placed in the first two positions, there is only one possible way to fill the third position. Therefore, $k_1 = 3$, $k_2 = 2$, and $k_3 = 1$, so that by the method of counting of Section 5.1 there are $(k_1)(k_2)(k_3) = (3)(2)(1) = 6$ ways to align these three animals. We may say that there are six permutations of three distinguishable objects.

*The term *permutation* was invented by Jacob Bernoulli in his landmark posthumous 1713 book on probability (Walker, 1929: 9).

In general, if there are n linear positions to fill with n objects, the first position may be filled in any one of n ways, the second may be filled in any one of $n - 1$ ways, the third in any one of $n - 2$ ways, and so on until the last position, which may be filled in only one way. That is, the filling of n positions with n objects results in ${}_nP_n$ permutations, where

$$ {}_nP_n = n(n - 1)(n - 2)\cdots(3)(2)(1). \tag{5.1} $$

This equation may be written more simply in *factorial* notation as

$$ {}_nP_n = n!, \tag{5.2} $$

where "n factorial" is the product of n and each smaller positive integer*; that is,

$$ n! = n(n - 1)(n - 2)\cdots(3)(2)(1). \tag{5.3} $$

Example 5.2 demonstrates such computation of the numbers of permutations.

EXAMPLE 5.2 The Number of Permutations of Distinct Objects

In how many sequences can six photographs be arranged on a page?

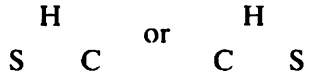
$$ {}_nP_n = 6! = (6)(5)(4)(3)(2)(1) = 720 $$

(b) Circular Arrangements. The numbers of permutations considered previously are for objects arranged on a line. If objects are arranged on a circle, there is no "starting position" as there is on a line, and the number of permutations is

$$ {}_nP'_n = \frac{n!}{n} = (n - 1)!. \tag{5.4} $$

(Observe that the notation ${}_nP'_n$ is used here for circular permutations to distinguish it from the symbol ${}_nP_n$ used for linear permutations.)

Referring again to a horse, a cow, and a sheep, there are ${}_nP'_n = \frac{n!}{n} = (n - 1)! = (3 - 1)! = 2! = 2$ distinct ways in which the three animals could be seated around a table, or arranged around the shore of a pond:



In this example, there is an assumed orientation of the observer, so clockwise and counterclockwise patterns are treated as different. That is, the animals are observed arranged around the top of the table, or observed from above the surface of the pond. But either one of these arrangements would look like the other one if observed from under the table or under the water; and if we did not wish to count the results of these two mirror-image observations as different, we would speak of there being one possible permutation, not two. For example, consider each of the preceding two diagrams to represent three beads on a circular string, one bead in the shape of a horse, one in the shape of a cow, and the other in the shape of a sheep. The two arrangements of H, C, and S shown are not really different, for there is no specific way of viewing the circle; one of the two arrangements turns into the other if the circle is turned over. If $n > 2$ and the orientation of the circle is not specified, then

*See the second footnote in Section 4.7.

the number of permutations of n objects on a circle is

$$ {}_nP''_n = \frac{n!}{2n} = \frac{(n-1)!}{2}. \tag{5.5} $$

(c) Fewer than n Positions. If one has n objects, but fewer than n positions in which to place them, then there would be considerably fewer numbers of ways to arrange the objects than in the case where there are positions for all n. For example, there are ${}_4P_4 = 4! = (4)(3)(2)(1) = 24$ ways of placing a horse (H), cow (C), sheep (S), and pig (P) in four positions on a line. However, there are only twelve ways of linearly arranging these four animals two at a time:

H,C; H,S; H,P; C,H; C,S; C,P; S,H; S,C; S,P; P,H; P,C; P,S.

The number of linear permutations of n objects taken X at a time is*

$$ {}_nP_X = \frac{n!}{(n-X)!}. \tag{5.6} $$

For the preceding example,

$$ {}_4P_2 = \frac{4!}{(4-2)!} = \frac{4!}{2!} = \frac{(4)(3)(2)(1)}{(2)(1)} = 12. $$

Equation 5.2 is a special case of Equation 5.6, where $X = n$; it is important to know that 0! is defined to be 1.†

If the arrangements are circular, instead of linear, then the number of them possible is

$$ {}_nP'_X = \frac{n!}{(n-X)!X}. \tag{5.7} $$

So, for example, there are only $4!/[(4-2)!2] = 6$ different ways of arranging two out of our four animals around a table:

H	H	H	C	C	S
C	S	P	S	P	P

for C seated at the table opposite H is the same arrangement as H seated across from C, S seated with H is the same as H with S, and so on. Example 5.3 demonstrates this further. Equation 5.4 is a special case of Equation 5.7, where $X = n$; and recall that 0! is defined as 1.

EXAMPLE 5.3 The Number of Permutations of n Objects Taken X at a Time: In How Many Different Ways Can a Sequence of Four Slides Be Chosen from a Collection of Six Slides?

$$ {}_nP_X = {}_6P_4 = \frac{6!}{(6-4)!} = \frac{6!}{2!} = \frac{(6)(5)(4)(3)(2)(1)}{(2)(1)} $$
$$ = (6)(5)(4)(3) = 360 $$

*Notation in the form of ${}_nP_X$ to indicate permutations of n items taken X at a time was used prior to 1869 by Harvey Goodwin (Cajori, 1929: 79).

†Why is 0! defined to be 1? In general, $n! = n[(n-1)!]$; for example, $5! = 5(4!)$, $4! = 4(3!)$, $3! = 3(2!)$, and $2! = 2(1!)$. Thus, $1! = 1(0!)$, which is so only if $0! = 1$.

If $n > 2$, then for every circular permutation viewed from above there is a mirror image of that permutation, which would be observed from below. If these two mirror images are not to be counted as different (e.g., if we are dealing with beads of different shapes or colors on a string), then the number of circular permutations is

$$ {}_nP''_X = \frac{n!}{2(n - X)!X}. \tag{5.8} $$

(d) If Some of the Objects Are Indistinguishable. If our group of four animals consisted of two horses (H), a cow (C), and a sheep (S), the number of permutations of the four animals would be twelve:

H,H,C,S; H,H,S,C; H,C,H,S; H,C,S,H; H,S,H,C; H,S,C,H;
C,H,H,S; C,H,S,H; C,S,H,H; S,H,H,C; S,H,C,H; S,C,H,H.

If n_i represents the number of like individuals in category i (in this case the number of animals in species i), then in this example $n_1 = 2$, $n_2 = 1$, and $n_3 = 1$, and we can write the number of permutations as

$$ {}_nP_{n_1,n_2,n_3} = \frac{n!}{n_1!n_2!n_3!} = \frac{4!}{2!1!1!} = 12. $$

If the four animals were two horses (H) and two cows (C), then there would be only six permutations:

H,H,C,C; C,C,H,H; H,C,H,C; C,H,C,H; H,C,C,H; C,H,H,C.

In this case, $n = 4, n_1 = 2$, and $n_2 = 2$, and the number of permutations is calculated to be ${}_nP_{n_1,n_2} = n!/(n_1!n_2!) = 4!/(2!2!) = (4)(3)(2)/[(2)(2)] = 6$.

In general, if n_1 members of the first category of objects are indistinguishable, as are n_2 of the second category, n_3 of the third category, and so on through n_k members of the kth category, then the number of different permutations is

$$ {}_nP_{n_1,n_2,\cdots,n_k} = \frac{n!}{n_1!n_2!\cdots n_k!} \text{ or } \frac{n!}{\prod_{i=1}^{k} n_i!}, \tag{5.9} $$

where the capital Greek letter pi (Π) denotes taking the product just as the capital Greek sigma (Σ, introduced in Section 3.1) indicates taking the sum. This is shown further in Example 5.4.

EXAMPLE 5.4 Permutations with Categories Containing Indistinguishable Members

There are twelve potted plants, six of one species, four of a second species, and two of a third species. How many different linear sequences of species are possible (for example, if arranging the pots on a shelf)?

$$ {}_nP_{n_1,n_2,n_3} = \frac{n}{\prod n_i!} $$

$$ = {}_{12}P_{6,4,2} = \frac{12!}{6!4!2!} $$

$$ = \frac{(12)(11)(10)(9)(8)(7)(6)(5)(4)(3)(2)(1)}{(6)(5)(4)(3)(2)(1)(4)(3)(2)(1)(2)(1)} = 13{,}860. $$

Note that the above calculation could have been simplified by writing

$$\frac{12!}{6!4!2!} = \frac{(12)(11)(10)(9)(8)(7)6!}{6!(4)(3)(2)(2)} = \frac{(12)(11)(10)(9)(8)(7)}{(4)(3)(2)(2)} = 13{,}860.$$

Here, "(1)" is dropped; also, "6!" appears in both the numerator and denominator, thus canceling out.

5.3 COMBINATIONS

In Section 5.2 we considered groupings of objects where the sequence within the groups was important. In many instances, however, only the components of a group, not their arrangement within the group, are important. We saw that if we select two animals from among a horse (H), cow (C), sheep (S), and pig (P), there are twelve ways of arranging the two on a line:

H,C; H,S; H,P; C,H; C,S; C,P; S,H; S,C; S,P; P,H; P,C; P,S.

However, some of these arrangements contain exactly the same kinds of animals, only in different order (e.g., H,C and C,H; H,S and S,H). If the groups of two are important to us, but not the sequence of objects within the groups, then we are speaking of *combinations*,* rather than permutations. Designating the number of combinations of n objects taken X at a time as ${}_nC_X$, we have†

$${}_nC_X = \frac{{}_nP_X}{X!} = \frac{n!}{X!(n - X)!}. \tag{5.10}$$

So for the present example, $n = 4$, $\overline{X} = 2$, and

$${}_4C_2 = \frac{4!}{2!(4 - 2)!} = \frac{4!}{2!2!} = \frac{(4)(3)(2)(1)}{(2)(1)(2)(1)} = \frac{(4)(3)}{2} = 6,$$

the six combinations of the four animals taken two at a time being

H,C; H,S; H,P; C,S; C,P; S,P.

Example 5.5 demonstrates the determination of numbers of combinations for another set of data.

It may be noted that

$${}_nC_n = 1, \tag{5.11}$$

meaning that there is only one way of selecting all n items; and

$${}_nC_1 = n, \tag{5.12}$$

indicating that there are n ways of selecting n items one at a time. Also,

$${}_nC_X = {}_nC_{n-X}, \tag{5.13}$$

*The word *combination* was used in this mathematical sense by Blaise Pascal (1623–1662) in 1654 (Smith, 1953: 528).

†Notation in the form of ${}_nC_X$ to indicate combinations of n items taken X at a time was used by G. Chrystal in 1899 (Cajori, 1929: 80).

EXAMPLE 5.5 Combinations of *n* Objects Taken *X* at a Time

Of a total of ten dogs, eight are to be used in a laboratory experiment. How many different combinations of eight animals may be formed from the ten?

$$_nC_X = {}_{10}C_8 = \frac{10!}{8!(10-8)!} = \frac{10!}{8!2!} = \frac{(10)(9)(8)(7)(6)(5)(4)(3)(2)(1)}{(8)(7)(6)(5)(4)(3)(2)(1)(2)(1)}$$
$$= 45.$$

It should be noted that the above calculations with factorials could have been simplified by writing

$$_{10}C_8 = \frac{10!}{8!2!} = \frac{(10)(9)8!}{8!2!} = \frac{(10)(9)}{2} = 45,$$

so that "8!" appears in both the numerator and denominator, thus canceling each other out.

which means that if we select X items from a group of n, we have at the same time selected the remaining $n - X$ items; that is, an exclusion is itself a selection. For example, if we selected two out of five persons to write a report, we have simultaneously selected three of the five to refrain from writing. Thus,

$$_5C_2 = \frac{5!}{2!(5-2)!} = \frac{5!}{2!3!} = 10 \quad \text{and} \quad {}_5C_{5-2} = {}_5C_3 = \frac{5!}{3!(5-3)!} = \frac{5!}{3!2!} = 10,$$

meaning that there are ten ways to select two out of five persons to perform a task and ten ways to select three out of five persons to be excluded from that task. This question may be addressed by applying Equation 5.9, reasoning that we are asking how many distinguishable arrangements there are of two writers and three nonwriters: $_5P_{2,3} = 5!/(2!3!) = 10$.

The product of combinatorial outcomes may also be employed to address questions such as in Example 5.4. This is demonstrated in Example 5.6.

EXAMPLE 5.6 Products of Combinations

This example provides an alternate method of answering the question of Example 5.4.

There are twelve potted plants, six of one species, four of a second species, and two of a third. How many different linear sequences of species are possible?

There are twelve positions in the sequence, which may be filled by the six members of the first species in this many ways:

$$_{12}C_6 = \frac{12!}{(12-6)!6!} = 924.$$

The remaining six positions in the sequence may be filled by the four members of the second species in this many ways:

$$_6C_4 = \frac{6!}{(6-4)!4!} = 15.$$

And the remaining two positions may be filled by the two members of the third species in only one way:

$$_2C_2 = \frac{2!}{(2-2)!2!} = 1.$$

As each of the ways of filling positions with members of one species exists in association with each of the ways of filling positions with members of each other species, the total different sequences of species is

$$(924)(15)(1) = 13{,}860.$$

From Equation 5.10 it may be noted that, as $_nC_X = {}_nP_X/X!$,

$$_nP_X = X!{}_nC_X. \tag{5.14}$$

It is common mathematical convention to indicate the number of combinations of n objects taken X at a time as $\binom{n}{X}$ instead of $_nC_X$, so for the problem at the beginning of Section 5.3 we could have written*

$$\binom{n}{X} = \binom{4}{2} = \frac{4!}{2!(4-2)!} = 6.$$

Binomial coefficients, which are discussed in Section 24.1, take this form.

5.4 SETS

A *set* is a defined collection of items. For example, a set may be a group of four animals, a collection of eighteen amino acids, an assemblage of twenty-five students, or a group of three genetic traits. Each item in a set is termed an *element*. If a set of animals includes these four elements: horse (H), cow (C), sheep (S), and pig (P), and a second set consists of the elements P, S, H, and C, then we say that the two sets are *equal*, as they contain exactly the same elements. The sequence of elements within sets is immaterial in defining equality or inequality of sets.

If a set consisted of animals H and P, it would be declared a *subset* of the above set (H, C, S, P). A subset is a set, all of whose elements are elements of a larger set.† Therefore, the determination of combinations of X items taken from a set of n items (Section 5.3) is really the counting of possible subsets of items from the set of n items.

In an experiment (or other phenomenon that yields results to observe), there is a set (usually very large) of possible outcomes. Let us refer to this set as the *outcome set*.‡

Each element of the set is one of the possible outcomes of the experiment. For example, if an experiment consists of tossing two coins, the outcome set consists of four elements: H,H; H,T; T,H; T,T, as these are all of the possible outcomes.

A subset of the outcome set is called an *event*. If the outcome set were the possible rolls of a die: 1, 2, 3, 4, 5, 6, an event might be declared to be "even-numbered rolls" (i.e., 2, 4, 6), and another event might be defined as "rolls greater than 4"

*This parenthetical notation for combinations was introduced by Andreas von Ettingshausen in 1826 (Miller, 2004c). Some authors have used a symbol in the form of C_X^n (or ${}^nC_X$) instead of $_nC_X$ for combinations and P_X^n (or ${}^nP_X$) instead of $_nP_X$ for permutations; those symbols will not be used in this book, in order to avoid confusing n with an exponent.

†Utilizing the terms *set* and *subset* in this fashion dates from the last half of the nineteenth century (Miller, 2004a).

‡Also called the *sample space*.

(i.e., 5, 6). In tossing two coins, one event could be "the two coins land differently" (i.e., T,H; H,T), and another event could be "heads do not appear" (i.e., T,T). If the two events in the same outcome set have some elements in common, the two events are said to intersect; and the *intersection* of the two events is that subset composed of those common elements. For example, the event "even-numbered rolls" of a die (2, 4, 6) and the event "rolls greater than 4" (5, 6) have an element in common (namely, the roll 6); therefore 6 is the intersection of the two events. For the events "even-numbered rolls" (2, 4, 6) and "rolls less than 5" (1, 2, 3, 4), the intersection subset consists of those elements of the events that are both even-numbered and less than 5 (namely, 2, 4).*

If two events have no elements in common, they are said to be *mutually exclusive*, and the two sets are said to be *disjoint*. The set that is the intersection of disjoint sets contains no elements and is often called the *empty set* or the *null set*. For example, the events "odd-numbered rolls" and "even-numbered rolls" are mutually exclusive and there are no elements common to both of them.

If we ask what elements are found in either one event or another, or in both of them, we are speaking of the *union* of the two events. The union of the events "even-numbered rolls" and "rolls less than 5" is that subset of the outcome set that contains elements found in either set (or both sets), namely 1, 2, 3, 4, 6.†

Once a subset has been defined, all other elements in the outcome set are said to be the *complement* of that subset. So, if an event is defined as "even-numbered rolls" of a die (2, 4, 6), the complementary subset consists of "odd-numbered rolls" (1, 3, 5). If subset is "rolls less than 5" (1, 2, 3, 4), the complement is the subset consisting of rolls 5 or greater (5, 6).

The above considerations may be presented by what are known as *Venn diagrams*,‡ shown in Figure 5.1.

The rectangle in this diagram denotes the outcome set, the set of all possible outcomes from an experiment or other producer of observations. The circle on the

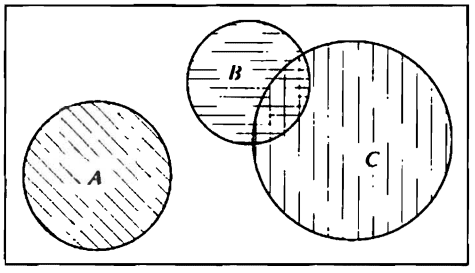


FIGURE 5.1: A Venn diagram showing the relationships among the outcome set represented by the rectangle and the subsets represented by circles *A*, *B*, and *C*. Subsets *B* and *C* intersect, with no intersection with *A*.

*The term *intersection* had been employed in this manner by 1909 (Miller, 2004a). The mathematical symbol for intersection is "∩", first used by Italian mathematician Giuseppe Peano (1858–1932) in 1888 (Miller, 2004a); so, for example, the intersection of set *A* (consisting of 2, 4, 6) and set *B* (consisting of 5, 6) is set $A \cap B$ (consisting of 6).

†The term *union* had been employed in this way by 1912 (Miller, 2004a). The mathematical symbol for union is "∪", first used by Giuseppe Peano in 1888 (Miller, 2004a); so, for example, if set *A* is composed of even-numbered rolls of a die (2, 4, 6), and set *B* is odd-numbered rolls (1, 3, 5), the union of the two sets, namely $A \cup B$, is 2, 4, 6, 1, 3, 5.

‡Named for English mathematical logician John Venn (1834–1923), who in 1880 greatly improved and popularized the diagrams (sometimes called "Euler diagrams") devised by Leonhard Euler (1707–1783) (Gullberg, 1997: 242; O'Connor and Robertson, 2003).

left represents a subset of the outcome set that we shall refer to as event A, the circle in the center signifies a second subset of the outcome set that we shall refer to as event B, and the circle on the right depicts a third subset of the outcome set that we shall call event C. If, for example, an outcome set (the rectangle) is the number of vertebrate animals in a forest, subset A might be animals without legs (namely, snakes), subset B might be mammals, and subset C might be flying animals. Figure 5.1 demonstrates graphically what is meant by union, intersection, mutually exclusive, and complementary sets: The union of B and C (the areas with any horizontal or vertical shading) represents all birds and mammals; the intersection of B and C (the area with both horizontal and vertical shading) represents flying mammals (i.e., bats); the portion of C with only vertical shading represents birds; A is mutually exclusive relative to the union of B and C, and the unshaded area (representing all other vertebrates—namely, amphibians and turtles) is complementary to A, B, and C (and is also mutually exclusive of A, B, and C).

5.5 PROBABILITY OF AN EVENT

As in Section 1.3, we shall define the *relative frequency* of an event as the proportion of the total observations of outcomes that event represents. Consider an outcome set with two elements, such as the possible results from tossing a coin (H; T) or the sex of a person (male; female). If n is the total number of coin tosses and f is the total number of heads observed, then the relative frequency of heads is f/n. Thus, if heads are observed 52 times in 100 coin tosses, the relative frequency is $52/100 = 0.52$ (or 52%). If 275 males occur in 500 human births, the relative frequency of males is $f/n = 275/500 = 0.55$ (or 55%). In general, we may write

$$\text{relative frequency of an event} = \frac{\text{frequency of that event}}{\text{total number of all events}} = \frac{f}{n}. \tag{5.15}$$

The value of f may, of course, range from 0 to n, and the relative frequency may, therefore, range from 0 to 1 (or 0% to 100%). A biological example is given as Example 5.7.

EXAMPLE 5.7 Relative Frequencies

A sample of 852 vertebrate animals is taken randomly from a forest. The sampling was done *with replacement*, meaning that the animals were taken one at a time, returning each one to the forest before the next one was selected. This is done to prevent the sampling procedure from altering the relative frequency in the sampled population. If the sample size is very small compared to the population size, replacement is not necessary. (Recall that random sampling assumes that each individual animal is equally likely to become a part of the sample.)

Vertebrate Subset	*Number*	*Relative Frequency*
amphibians	53	53/852 = 0.06
turtles	41	41/852 = 0.05
snakes	204	204/852 = 0.24
birds	418	418/852 = 0.49
mammals	136	136/852 = 0.16
total	852	1.00

The *probability* of an event is the likelihood of that event expressed either by the relative frequency observed from a large number of data or by knowledge of the system under study. In Example 5.7 the relative frequencies of vertebrate groups have been observed from randomly sampling forest animals. If, for the sake of the present example, we assume that each animal has the same chance of being caught as part of our sample (an unrealistic assumption in nature), we may estimate the probability, P, that the next animal captured will be a snake ($P = 0.24$). Or, using the data of the preceding paragraph, we can estimate that the probability that a human birth will be a male is 0.55, or that the probability of tossing a coin that lands head side up is 0.52. A probability may sometimes be predicted on the basis of knowledge about the system (e.g., the structure of a coin or of a die, or the Mendelian principles of heredity). If we assume that there is no reason why a tossed coin should land "heads" more or less often than "tails," we say there is an equal probability of each outcome: $P(H) = \frac{1}{2}$ and $P(T) = \frac{1}{2}$ states that "the probability of heads is 0.5 and the probability of tails is 0.5."

Probabilities, like relative frequencies, can range from 0 to 1. A probability of 0 means that the event is impossible. For example, in tossing a coin, P(neither H nor T) = 0, or in rolling a die, P(number > 6) = 0. A probability of 1 means that an event is certain. For example, in tossing a coin, P(H or T) = 1; or in rolling a die, $P(1 \leq \text{number} \leq 6) = 1$.*

5.6 ADDING PROBABILITIES

(a) If Events Are Mutually Exclusive. If two events (call them A and B) are mutually exclusive (e.g., legless vertebrates and mammals are disjoint sets in Figure 5.1), then the probability of either event A or event B is the sum of the probabilities of the two events:

$$P(A \text{ or } B) = P(A) + P(B). \tag{5.16}$$

For example, if the probability of a tossed coin landing head up is $\frac{1}{2}$ and the probability of its landing tail up is $\frac{1}{2}$, then the probability of either head or tail up is

$$P(H \text{ or } T) = P(H) + P(T) = \frac{1}{2} + \frac{1}{2} = 1. \tag{5.17}$$

And, for the data in Example 5.7, the probability of selecting, at random, a reptile would be P(turtle or snake) = P(turtle) + P(snake) = 0.05 + 0.24 = 0.29.

This rule for adding probabilities may be extended for more than two mutually exclusive events. For example, the probability of rolling a 2 on a die is $\frac{1}{6}$, the probability of rolling a 4 is $\frac{1}{6}$, and the probability of rolling a 6 is $\frac{1}{6}$; so the probability of rolling an even number is

$$\begin{aligned} P(\text{even number}) = P(2 \text{ or } 4 \text{ or } 6) &= P(2) + P(4) + P(6) \\ &= \frac{1}{6} + \frac{1}{6} + \frac{1}{6} = \frac{3}{6} = \frac{1}{2}. \end{aligned}$$

*A concept related to probability is the *odds* for an event, namely the ratio of the probability of the event occurring and the probability of that event not occurring. For example, if the probability of a male birth is 0.55 (and, therefore, the probability of a female birth is 0.45), then the odds in favor of male births are 0.55/0.45, expressed as "11 to 9."

And, for the data in Example 5.7, the probability of randomly selecting a reptile or amphibian would be $P(\text{turtle}) + P(\text{snake}) + P(\text{amphibian}) = 0.05 + 0.24 + 0.06 = 0.35$.

(b) If Events Are Not Mutually Exclusive. If two events are not mutually exclusive—that is, they intersect (e.g., mammals and flying vertebrates are not disjoint sets in Figure 5.1)—then the addition of the probabilities of the two events must be modified. For example, if we roll a die, the probability of rolling an odd number is

$$P(\text{odd number}) = P(1 \text{ or } 3 \text{ or } 5) = P(1) + P(3) + P(5) = \frac{1}{6} + \frac{1}{6} + \frac{1}{6} = \frac{3}{6} = \frac{1}{2};$$

and the probability of rolling a number less than 4 is

$$P(\text{number} < 4) = P(1 \text{ or } 2 \text{ or } 3) = P(1) + P(2) + P(3) = \frac{1}{6} + \frac{1}{6} + \frac{1}{6} = \frac{3}{6} = \frac{1}{2}.$$

The probability of rolling either an odd number or a number less than 4 obviously is *not* calculated by Equation 5.16, for that equation would yield

$$\begin{aligned} &P(\text{odd number or number} < 4) \\ &\overset{?}{=} P(\text{odd}) + P(\text{number} < 4) \\ &= P[(1 \text{ or } 3 \text{ or } 5) \text{ or } (1 \text{ or } 2 \text{ or } 3)] \\ &= [P(1) + P(3) + P(5)] + [P(1) + P(2) + P(3)] \\ &= \left(\frac{1}{6} + \frac{1}{6} + \frac{1}{6}\right) + \left(\frac{1}{6} + \frac{1}{6} + \frac{1}{6}\right) = 1, \end{aligned}$$

and that would mean that we are certain ($P = 1$) to roll either an odd number or a number less than 4, which would mean that a roll of 4 or 6 is impossible!

The invalidity of the last calculation is due to the fact that the two elements (namely 1 and 3) that lie in both events are counted twice. The subset of elements consisting of rolls 1 and 3 is the intersection of the two events and its probability needs to be subtracted from the preceding computation so that $P(1 \text{ or } 3)$ is counted once, not twice. Therefore, for two intersecting events, A and B, the probability of either A or B is

$$P(A \text{ or } B) = P(A) + P(B) - P(A \text{ and } B). \tag{5.18}$$

In the preceding example,

$$\begin{aligned} &P(\text{odd number or number} < 4) \\ &\quad = P(\text{odd number}) + P(\text{number} < 4) \\ &\qquad - P(\text{odd number and number} < 4) \\ &\quad = P[(1 \text{ or } 3 \text{ or } 5) \text{ or } (1 \text{ or } 2 \text{ or } 3)] - P(1 \text{ or } 3) \\ &\quad = [P(1) + P(3) + P(5)] + [P(1) + P(2) + P(3)] - [P(1) + P(3)] \\ &\quad = \left(\frac{1}{6} + \frac{1}{6} + \frac{1}{6}\right) + \left(\frac{1}{6} + \frac{1}{6} + \frac{1}{6}\right) - \left(\frac{1}{6} + \frac{1}{6}\right) = \frac{4}{6} = \frac{2}{3}. \end{aligned}$$

It may be noted that Equation 5.16 is a special case of Equation 5.18, where $P(A \text{ and } B) = 0$. Example 5.8 demonstrates these probability calculations with a different set of data.

EXAMPLE 5.8 Adding Probabilities of Intersecting Events

A deck of playing cards is composed of 52 cards, with thirteen cards in each of four suits called clubs, diamonds, hearts, and spades. In each suit there is one card each of the following thirteen denominations: ace (A), 2, 3, 4, 5, 6, 7, 8, 9, 10, jack (J), queen (Q), king (K). What is the probability of selecting at random a diamond from the deck of 52 cards?

The event in question (diamonds) is a subset with thirteen elements; therefore,

$$P(\text{diamond}) = \frac{13}{52} = \frac{1}{4} = 0.250.$$

What is the probability of selecting at random a king from the deck?

The event in question (king) has four elements; therefore,

$$P(\text{king}) = \frac{4}{52} = \frac{1}{13} = 0.077.$$

What is the probability of selecting at random a diamond or a king?

The two events (diamonds and kings) intersect, with the intersection having one element (the king of diamonds); therefore,

$$\begin{aligned} P(\text{diamond or king}) &= P(\text{diamond}) + P(\text{king}) - P(\text{diamond and king}) \\ &= \frac{13}{52} + \frac{4}{52} - \frac{1}{52} \\ &= \frac{16}{52} = \frac{4}{13} = 0.308. \end{aligned}$$

If three events are not mutually exclusive, the situation is more complex, yet straightforward. As seen in Figure 5.2, there may be three two-way intersections, shown with vertical shading (A and B; A and C; and B and C), and a three-way

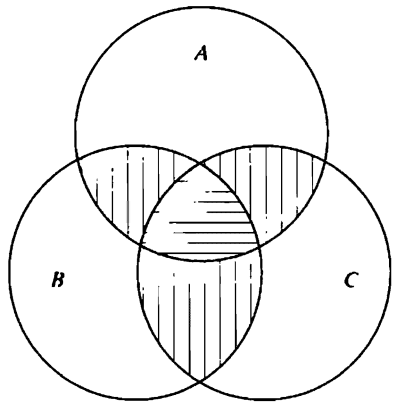


FIGURE 5.2: A Venn diagram showing three intersecting sets: *A*, *B*, and *C*. Here there are three two-way intersections (vertical shading) and one three-way intersection (horizontal shading).

intersection, shown with horizontal shading (A and B and C). If we add the probabilities of the three events, A, B, and C, as $P(A) + P(B) + P(C)$, we are adding the two-way intersections twice. So, we can subtract $P(A \text{ and } B)$, $P(A \text{ and } C)$, and $P(B \text{ and } C)$. Also, the three-way intersection is added three times in $P(A) + P(B) + P(C)$, and subtracted three times by subtracting the three two-way intersections; thus, $P(A \text{ and } B \text{ and } C)$ must be added back into the calculation. Therefore, for three events, not mutually exclusive,

$$\begin{aligned} P(A \text{ or } B \text{ or } C) = {} & P(A) + P(B) + P(C) \\ & - P(A \text{ and } B) - P(A \text{ and } C) - P(B \text{ and } C) \\ & + P(A \text{ and } B \text{ and } C). \end{aligned} \tag{5.19}$$

5.7 MULTIPLYING PROBABILITIES

If two or more events intersect (as A and B in Figure 5.1 and A, B, and C in Figure 5.2), the probability associated with the intersection is the product of the probabilities of the individual events. That is,

$$P(A \text{ and } B) = [P(A)][P(B)], \tag{5.20}$$

$$P(A \text{ and } B \text{ and } C) = [P(A)][P(B)][P(C)], \tag{5.21}$$

and so on.

For example, the probability of a tossed coin landing heads is $\frac{1}{2}$. If two coins are tossed, the probability of *both* coins landing heads is

$$P(H,H) = [P(H)][P(H)] = \left(\frac{1}{2}\right)\left(\frac{1}{2}\right) = \left(\frac{1}{4}\right) = 0.25.$$

This can be verified by examining the outcome set:

H,H; H,T; T,H; T,T,

where $P(H,H)$ is one outcome out of four equally likely outcomes. The probability that 3 tossed coins will land heads is

$$P(H,H,H) = [P(H)][P(H)][P(H)] = \left(\frac{1}{2}\right)\left(\frac{1}{2}\right)\left(\frac{1}{2}\right) = \left(\frac{1}{8}\right) = 0.125.$$

Note, however, that if one or more coins have already been tossed, the probability that the next coin toss (of the same or a different coin) will be heads is simply $\frac{1}{2}$.

5.8 CONDITIONAL PROBABILITIES

There are occasions when our interest will be in determining a *conditional probability*, which is the probability of one event with the stipulation that another event also occurs. An illustration of this, using a deck of 52 playing cards (as described in Example 5.8), would be the probability of selecting a queen, given that the card is a spade. In general, a conditional probability is

$$P(\text{event } A, \text{ given event } B) = \frac{P(A \text{ and } B \text{ jointly})}{P(B)}, \tag{5.22}$$

which can also be calculated as

$$P(\text{event } A, \text{ given event } B) = \frac{\text{frequency of events } A \text{ and } B \text{ jointly}}{\text{frequency of event } B}. \tag{5.23}$$

So, the probability of randomly selecting a queen, with the specification that the card is a spade, is (using Equation 5.22)

$$P(\text{queen, given it is a spade}) = \frac{P(\text{queen of spades})}{P(\text{spade})}$$
$$= (1/52)/(13/52) = 0.02/0.25 = 0.08,$$

which (by Equation 5.23) would be calculated as

$$P(\text{queen, given it is a spade}) = \frac{\text{frequency of queen of spades}}{\text{frequency of spades}}$$
$$= 1/13 = 0.8.$$

Note that this conditional probability is quite different from the probability of selecting a spade, given that the card is a queen, for that would be (by Equation 5.23)

$$P(\text{spade, given it is a queen}) = \frac{\text{frequency of queen of spades}}{\text{frequency of queens}}$$
$$= 1/4 = 0.25.$$

EXERCISES

5.1. A person may receive a grade of either high (H), medium (M), or low (L) on a hearing test, and a grade of either good (G) or poor (P) on a sight test.
(a) How many different outcomes are there if both tests are taken?
(b) What are these outcomes?

5.2. A menu lists three meats, four salads, and two desserts. In how many ways can a meal of one meat, one salad, and one dessert be selected?

5.3. If an organism (e.g., human) has 23 pairs of chromosomes in each diploid cell, how many different gametes are possible for the individual to produce by assortment of chromosomes?

5.4. In how many ways can five animal cages be arranged on a shelf?

5.5. In how many ways can 12 different amino acids be arranged into a polypeptide chain of five amino acids?

5.6. An octapeptide is known to contain four of one amino acid, two of another, and two of a third. How many different amino-acid sequences are possible?

5.7. Students are given a list of nine books and told that they will be examined on the contents of five of them. How many combinations of five books are possible?

5.8. The four human blood types below are genetic phenotypes that are mutually exclusive events. Of 5400 individuals examined, the following frequency of each blood type is observed. What is the relative frequency of each blood type?

Blood Type	*Frequency*
O	2672
A	2041
B	486
AB	201

5.9. An aquarium contains the following numbers of tropical freshwater fishes. What is the relative frequency of each species?

Species	*Number*
Paracheirodon innesi, neon tetra	11
Cheirodon axelrodi, cardinal tetra	6
Pterophyllum scalare, angelfish	4
Pterophyllum altum, angelfish	2
Pterophyllum dumerilii, angelfish	2
Nannostomus marginatus, one-lined pencilfish	2
Nannostomus anomalus golden pencilfish	2

5.10. Use the data of Exercise 5.8, assuming that each of the 5400 has an equal opportunity of being encountered.
- **(a)** Estimate the probability of encountering a person with type A blood.
- **(b)** Estimate the probability of encountering a person who has either type A or type AB blood.

5.11. Use the data of Exercise 5.9, assuming that each individual fish has the same probability of being encountered.
- **(a)** Estimate the probability of encountering an angelfish of the species *Pterophyllum scalare*.
- **(b)** Estimate the probability of encountering a fish belonging to the angelfish genus *Pterophyllum*.

5.12. Either allele A or a may occur at a particular genetic locus. An offspring receives one of its alleles from each of its parents. If one parent possesses alleles A and a and the other parent possesses a and a:
- **(a)** What is the probability of an offspring receiving an A and an a?
- **(b)** What is the probability of an offspring receiving two a alleles?
- **(c)** What is the probability of an offspring receiving two A alleles?

5.13. In a deck of playing cards (see Example 5.8 for a description),
- **(a)** What is the probability of selecting a queen of clubs?
- **(b)** What is the probability of selecting a black (i.e., club or spade) queen?
- **(c)** What is the probability of selecting a black face card (i.e., a black jack, queen, or king)?

5.14. A cage contains six rats, two of them white (W) and four of them black (B); a second cage contains four rats, two white and two black; and a third cage contains five rats, three white and two black. If one rat is selected randomly from each cage,
- **(a)** What is the probability that all three rats selected will be white?
- **(b)** What is the probability that exactly two of the three will be white?
- **(c)** What is the probability of selecting at least two white rats?

5.15. A group of dogs consists of three brown males, two brown females, four white males, four white females, five black males, and four black females. What is the probability of selecting at random
- **(a)** A brown female dog?
- **(b)** A female dog, if the dog is brown?
- **(c)** A brown dog, if the dog is a female?

CHAPTER 6

The Normal Distribution

Commonly, a distribution of interval- or ratio-scale data is observed to have a preponderance of values around the mean with progressively fewer observations toward the extremes of the range of values (see, e.g., Figure 1.5). If n is large, the frequency polygons of many biological data distributions are "bell-shaped"* and look something like Figure 6.1.

Figure 6.1 is a frequency curve for a *normal distribution.*† Not all bell-shaped curves are normal; although biologists are unlikely to need to perform calculations with this equation, it can be noted that a *normal distribution* is defined as one in which height of the curve at X_i is as expressed by the relation:

$$Y_i = \frac{1}{\sigma\sqrt{2\pi}} e^{-(X_i-\mu)^2/2\sigma^2}. \tag{6.1}$$

The height of the curve, Y_i, is referred to as the *normal density*. It is not a frequency, for in a normally distributed population of continuous data the frequency of occurrence of a measurement *exactly* equal to X_i (e.g., exactly equal to 12.5000 cm, or exactly equal to 12.50001 cm) is zero. Equation 6.1 contains two mathematical constants:

*Comparing the curve's shape to that of a bell has been traced as far back as 1872 (Stigler, 1999: 405).

†The normal distribution is sometimes called the *Gaussian distribution*, after [Johann] Karl Friedrich Gauss (1777–1855), a phenomenal German mathematician contributing to many fields of mathematics and for whom the unit of magnetic induction ("gauss") is named. Gauss discussed this distribution in 1809, but the influential French mathematician and astronomer Pierre-Simon Laplace (1749–1827) mentioned it in 1774, and it was first announced in 1733 by mathematician Abraham de Moivre (1667–1754; also spelled De Moivre and Demoivre), who was born in France but emigrated to England at age 21 (after three years in prison) to escape religious persecution as a Protestant (David, 1962: 161–178; Pearson, 1924; Stigler, 1980; Walker, 1934). This situation has been cited as an example of "Stigler's Law of Eponymy," which states that "no scientific discovery is named after its original discoverer" (Stigler, 1980). The distribution was first used, by de Moivre, to approximate a binomial distribution (discussed in Section 24.1) (Stigler, 1999: 407). The adjective *normal* was first used for the distribution by Charles S. Peirce in 1873, and by Wilhelm Lexis and Sir Francis Galton in 1877 (Stigler, 1999: 404–415); Karl Pearson recommended the routine use of that term to avoid "an international question of priority" although it "has the disadvantage of leading people to believe that all other distributions of frequency are in one sense or another 'abnormal'" (Pearson, 1920).

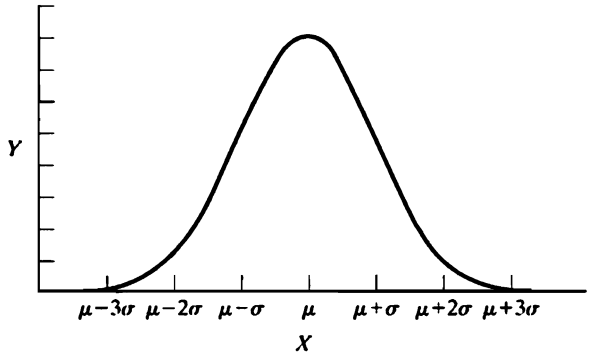


FIGURE 6.1: A normal distribution.

π (lowercase Greek pi),* which equals 3.14159...; and e (the base of Naperian, or natural, logarithms),† which equals 2.71828.... There are also two parameters (μ and σ^2) in the equation. Thus, for any given standard deviation, σ, there are an infinite number of normal curves possible, depending on μ. Figure 6.2a shows normal curves for $\sigma = 1$ and $\mu = 0, 1$, and 2. Likewise, for any given mean, μ, an infinity of normal curves is possible, each with a different value of σ. Figure 6.2b shows normal curves for $\mu = 0$ and $\sigma = 1, 1.5$, and 2.

A normal curve with $\mu = 0$ and $\sigma = 1$ is said to be a *standardized normal curve.* Thus, for a standardized normal distribution,

$$Y_i = 1\sqrt{2\pi}e^{-X_i^2/2}. \tag{6.2}$$

*The lowercase Greek letter pi, π, denotes the ratio between the circumference and the diameter of a circle. This symbol was advanced in 1706 by Wales-born William Jones (1675–1749), after it had been used for over 50 years to represent the circumference (Cajori, 1928/9, Vol. II: 9; Smith, 1953: 312); but it did not gain popularity for this purpose until Swiss Leonhard Euler (1707–1783) began using it in 1736 instead of p (Blatner, 1997: 78; Smith, 1953: 312). According to Gullberg (1997: 85), Jones probably selected this symbol because it is the first letter of the Greek word for "periphery." (See also Section 26.1.) Pi is an "irrational number," meaning that it cannot be expressed as the ratio of two integers. To 20 decimal places its value is 3.14159 26535 89792 33846 (and it may be noted that this number rounded to 10 decimal places is sufficient to obtain, from the diameter, the circumference of a circle as large as the earth's equator to within about a centimeter of accuracy). Beckmann (1977), Blatner (1997), and Dodge (1996) present the history of π and its calculation. By 2000 B.C.E., the Babylonians knew its value to within 0.02. Archimedes of Syracuse (287–212 B.C.E.) was the first to present a procedure to calculate π to any desired accuracy, and he computed it accurate to the third decimal place. Many computational methods were subsequently developed, and π was determined to six decimal places of accuracy by around 500 C.E., to 20 decimal places by around 1600, and to 100 in 1706; 1000 decimal places were reached, using a mechanical calculating machine, before electronic computers joined the challenge in 1949. In the computer era, with advancement of machines and algorithms, one million digits were achieved in 1973, by the end of the 1980s there were calculations accurate to more than a billion digits, and more than one trillion (1,000,000,000,000) digits have now been attained.

†e is an irrational number (as is π; see the preceding footnote). To 20 decimal places e is 2.71828 18284 59045 23536. The symbol, e, for this quantity was introduced by the great Swiss mathematician Leonhard Euler (1707–1783) in 1727 or 1728 and published by him in 1736 (Cajori, 1928/9, Vol. 2: 13; Gullberg, 1997: 85). Johnson and Leeming (1990) discussed the randomness of the digits of e, and Maor (1994) presented a history of this number and its mathematical ramifications. In 2000, e was calculated to 17 billion decimal places (Adrian, 2006: 63).

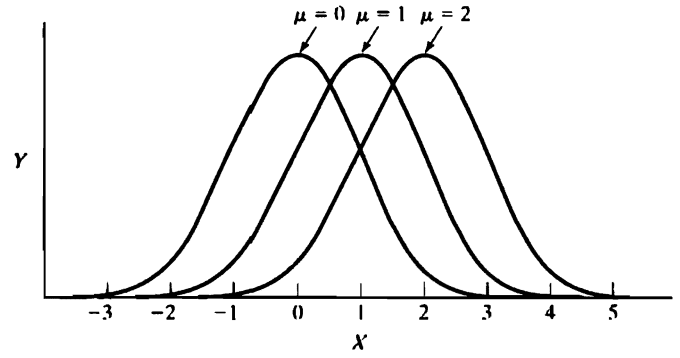


FIGURE 6.2a: Normal distribution with $\sigma = 1$, varying in location with different means (μ).

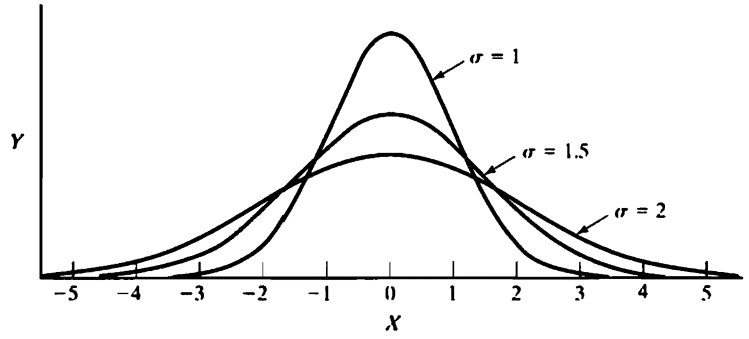


FIGURE 6.2b: Normal distributions with $\mu = 0$, varying in spread with different standard deviations (σ).

6.1 PROPORTIONS OF A NORMAL DISTRIBUTION

If a population of 1000 body weights is normally distributed and has a mean, μ, of 70 kg, one-half of the population (500 weights) is larger than 70 kg and one-half is smaller. This is true simply because the normal distribution is symmetrical. But if we desire to ask what portion of the population is larger than 80 kg, we need to know σ, the standard deviation of the population. If $\sigma = 10$ kg, then 80 kg is one standard deviation larger than the mean, and the portion of the population in question is the shaded area in Figure 6.3a. If, however, $\sigma = 5$ kg, then 80 kg is two standard deviations above μ, and we are referring to a relatively small portion of the population, as shown in Figure 6.3b.

Appendix Table B.2 enables us to determine proportions of normal distributions. For any X_i value from a normal population with mean μ, and standard deviation σ, the value

$$Z = \frac{X_i - \mu}{\sigma} \tag{6.3}$$

tells us how many standard deviations from the mean the X_i value is located. Carrying out the calculation of Equation 6.3 is known as *normalizing*, or *standardizing*, X_i; and Z is known as a *normal deviate*, or a standard score.* The mean of a set of standard scores is 0, and the variance is 1.

*This standard normal curve was introduced in 1899 by W. F. Sheppard (Walker, 1929: 188), and the term *normal deviate* was first used, in 1907, by F. Galton (David, 1995).

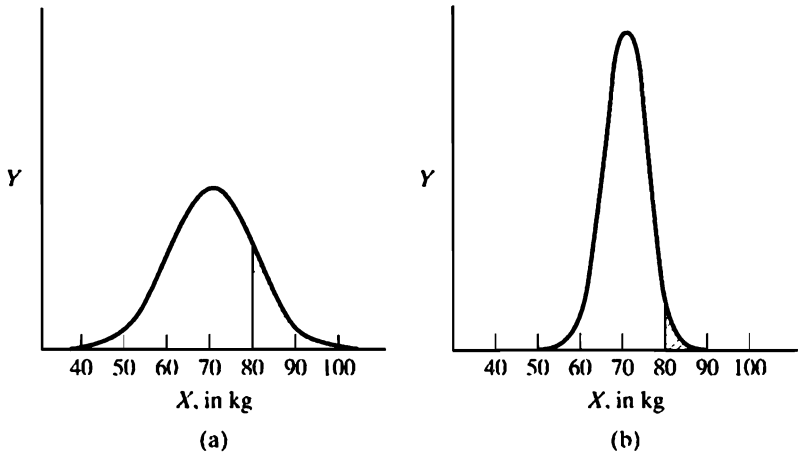


FIGURE 6.3: Two normal distributions with $\mu = 70$ kg. The shaded areas are the portions of the curves that lie above $X = 80$ kg. For distribution (a), $\mu = 70$ kg and $\sigma = 10$ kg; for distribution (b), $\mu = 70$ kg and $\sigma = 5$ kg.

Table B.2 tells us what proportion of a normal distribution lies beyond a given value of Z.* If $\mu = 70$ kg, $\sigma = 10$ kg, and $X_i = 70$ kg, then $Z = (70 \text{ kg} - 70 \text{ kg})/10 \text{ kg} = 0$, and by consulting Table B.2 we see that $P(X_i > 70 \text{ kg}) = P(Z > 0) = 0.5000$.† That is, 0.5000 (or 50.00%) of the distribution is larger than 70 kg. To determine the proportion of the distribution that is greater than 80 kg in weight, $Z = (80 \text{ kg} - 70 \text{ kg})/10 \text{ kg} = 1$, and $P(X_i > 80 \text{ kg}) = P(Z > 1) = 0.1587$ (or 15.87%). This could be stated as being the probability of drawing at random a measurement, X_i, greater than 80 kg from a population with a mean (μ) of 70 kg and a standard deviation (σ) of 10 kg. What, then, is the probability of obtaining, at random, a measurement, X_i, which is less than 80 kg? $P(X_i > 80 \text{ kg}) = 0.1587$, so $P(X_i < 80 \text{ kg}) = 1.0000 - 0.1587 = 0.8413$; that is, if 15.87% of the population is greater than X_i, then 100% − 15.87% (i.e., 84.13% of the population is less than X_i).‡ Example 6.1a presents calculations for determining proportions of a normal distribution lying between a variety of limits.

Note that Table B.2 contains no negative values of Z. However, if we are concerned with proportions in the left half of the distribution, we are simply dealing with areas of the curve that are mirror images of those present in the table. This is demonstrated in Example 6.1b.§

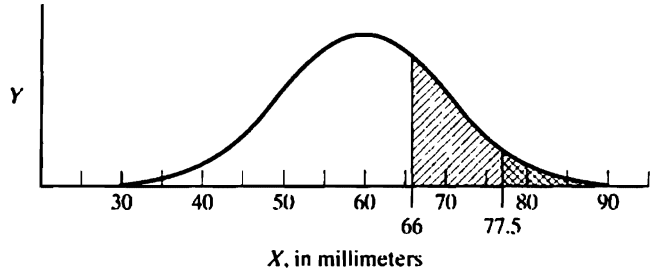
*The first tables of areas under the normal curve were published in 1799 by Christian Kramp (Walker, 1929: 58). Today, some calculators and many computer programs determine normal probabilities (e.g., see Boomsma and Molenaar, 1994).

†Read $P(X_i > 70 \text{ kg})$ as "the probability of an X_i greater than 70 kg"; $P(Z > 0)$ is read as "the probability of a Z greater than 0."

‡The statement that "$P(X_i > 80 \text{ kg}) = 0.1587$, therefore $P(X_i < 80) = 1.0000 - 0.1587$" does not take into account the case of $X_i = 80$ kg. But, as we are considering the distribution at hand to be a continuous one, the probability of X_i being *exactly* 80.000 ... kg (or being *exactly* any other stated value) is practically nil, so these types of probability statements offer no practical difficulties.

§Some old literature avoided referring to negative Z's by expressing the quantity, $Z + 5$, called a *probit*. This term was introduced in 1934 by C. I. Bliss (David, 1995).

EXAMPLE 6.1a Calculating Proportions of a Normal Distribution of Bone Lengths, Where $\mu = 60$ mm and $\sigma = 10$ mm



1. What proportion of the population of bone lengths is larger than 66 mm?

$$Z = \frac{X_i - \mu}{\sigma} = \frac{66\text{ mm} - 60\text{ mm}}{10\text{ mm}} = 0.60$$

$$P(X_i > 66\text{ mm}) = P(Z > 0.60) = 0.2743 \text{ or } 27.43\%$$

2. What is the probability of picking, at random from this population, a bone larger than 66 mm? This is simply another way of stating the quantity calculated in part (1). The answer is 0.2743.
3. If there are 2000 bone lengths in this population, how many of them are greater than 66 mm?

$$(0.2743)(2000) = 549$$

4. What proportion of the population is smaller than 66 mm?

$$P(X_i < 66\text{ mm}) = 1.0000 - P(X_i > 66\text{ mm}) = 1.0000 - 0.2743 = 0.7257$$

5. What proportion of this population lies between 60 and 66 mm? Of the total population, 0.5000 is larger than 60 mm and 0.2743 is larger than 66 mm. Therefore, $0.5000 - 0.2743 = 0.2257$ of the population lies between 60 and 66 mm. That is, $P(60\text{ mm} < X_i < 66\text{ mm}) = 0.5000 - 0.2743 = 0.2257$.
6. What portion of the area under the normal curve lies to the right of 77.5 mm?

$$Z = \frac{77.5\text{ mm} - 60\text{ mm}}{10\text{ mm}} = 1.75$$

$$P(X_i > 77.5\text{ mm}) = P(Z > 1.75) = 0.0401 \text{ or } 4.01\%$$

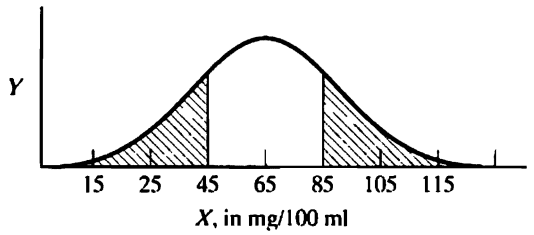
7. If there are 2000 bone lengths in the population, how many of them are larger than 77.5 mm?

$$(0.0401)(2000) = 80$$

8. What is the probability of selecting at random from this population a bone measuring between 66 and 77.5 mm in length?

$$P(66\text{ mm} < X_i < 77.5\text{ mm}) = P(0.60 < Z < 1.75) = 0.2743 - 0.0401 = 0.2342$$

EXAMPLE 6.1b Calculating Proportions of a Normal Distribution of Sucrose Concentrations, Where $\mu = 65$ mg/100 ml and $\sigma = 25$ mg/100 ml



1. What proportion of the population is greater than 85 mg/100 ml?

$$Z = \frac{(X_i - \mu)}{\sigma} = \frac{85 \text{ mg/100 ml} - 65 \text{ mg/100 ml}}{25 \text{ mg/100 ml}} = 0.8$$

$$P(X_i > 85 \text{ mg/100 ml}) = P(Z > 0.8) = 0.2119 \text{ or } 21.19\%$$

2. What proportion of the population is less than 45 mg/100 ml?

$$Z = \frac{45 \text{ mg/100 ml} - 65 \text{ mg/100 ml}}{25 \text{ mg/100 ml}} = -0.80$$

$$P(X_i < 45 \text{ mg/100 ml}) = P(Z < -0.80) = P(Z > 0.80) = 0.2119$$

That is, the probability of selecting from this population an observation less than 0.80 standard deviations below the mean is equal to the probability of obtaining an observation greater than 0.80 standard deviations above the mean.

3. What proportion of the population lies between 45 and 85 mg/100 ml?

$$\begin{aligned} P(45 \text{ mg/100 ml} < X_i < 85 \text{ mg/100 ml}) &= P(-0.80 < Z < 0.80) \\ &= 1.0000 - P(Z < -0.80 \\ &\quad \text{or } Z > 0.80) \\ &= 1.0000 - (0.2119 + 0.2119) \\ &= 1.0000 - 0.4238 \\ &= 0.5762 \end{aligned}$$

Using the preceding considerations of the table of normal deviates (Table B.2), we can obtain the following information for measurements in a normal population:

The interval of $\mu \pm \sigma$ will contain 68.27% of the measurements.*
The interval of $\mu \pm 2\sigma$ will contain 95.44% of the measurements.
The interval of $\mu \pm 2.5\sigma$ will contain 98.76% of the measurements.
The interval of $\mu \pm 3\sigma$ will contain 99.73% of the measurements.
50% of the measurements lie within $\mu \pm 0.67\sigma$.
95% of the measurements lie within $\mu \pm 1.96\sigma$.
97.5% of the measurements lie within $\mu \pm 2.24\sigma$.

*The symbol "±" indicates "plus or minus" and was first published by William Oughtred in 1631 (Cajori, 1928: 245).

99% of the measurements lie within $\mu \pm 2.58\sigma$.
99.5% of the measurements lie within $\mu \pm 2.81\sigma$.
99.9% of the measurements lie within $\mu \pm 3.29\sigma$.

6.2 THE DISTRIBUTION OF MEANS

If random samples of size n are drawn from a normal population, the means of these samples will conform to normal distribution. The distribution of means from a nonnormal population will not be normal but will tend to approximate a normal distribution as n increases in size.* Furthermore, the variance of the distribution of means will decrease as n increases; in fact, the variance of the population of all possible means of samples of size n from a population with variance σ^2 is

$$\sigma_{\overline{X}}^2 = \frac{\sigma^2}{n}. \tag{6.4}$$

The quantity $\sigma_{\overline{X}}^2$ is called the *variance of the mean*. A distribution of sample statistics is called a *sampling distribution*†; therefore, we are discussing the sampling distribution of means.

Since $\sigma_{\overline{X}}^2$ has square units, its square root, $\sigma_{\overline{X}}$, will have the same units as the original measurements (and, therefore, the same units as the mean, μ, and the standard deviation, σ). This value, $\sigma_{\overline{X}}$, is the *standard deviation of the mean*. The standard deviation of a statistic is referred to as a *standard error*; thus, $\sigma_{\overline{X}}$ is frequently called the *standard error of the mean* (sometimes abbreviated SEM), or simply the *standard error* (sometimes abbreviated SE)‡:

$$\sigma_{\overline{X}} = \sqrt{\frac{\sigma^2}{n}} \quad \text{or} \quad \sigma_{\overline{X}} = \frac{\sigma}{\sqrt{n}}. \tag{6.5}$$

Just as $Z = (X_i - \mu)/\sigma$ (Equation 6.3) is a normal deviate that refers to the normal distribution of X_i values,

$$Z = \frac{\overline{X} - \mu}{\sigma_{\overline{X}}} \tag{6.6}$$

is a normal deviate referring to the normal distribution of means ($\overline{X}$ values). Thus, we can ask questions such as: What is the probability of obtaining a random sample of nine measurements with a mean larger than 50.0 cm from a population having a mean of 47.0 cm and a standard deviation of 12.0 cm? This and other examples of the use of normal deviates for the sampling distribution of means are presented in Example 6.2.

As seen from Equation 6.5, to determine $\sigma_{\overline{X}}$ one must know σ^2 (or σ), which is a population parameter. Because we very seldom can calculate population parameters, we must rely on estimating them from random samples taken from the population. The best estimate of $\sigma_{\overline{X}}^2$, the population variance of the mean, is

$$s_{\overline{X}}^2 = \frac{s^2}{n}, \tag{6.7}$$

*This result is known as the *central limit theorem*.

†This term was apparently first used by Ronald Aylmer Fisher in 1922 (Miller, 2004a).

‡This relationship between the standard deviation of the mean and the standard deviation was published by Karl Friedrich Gauss in 1809 (Walker, 1929: 23). The term *standard error* was introduced in 1897 by G. U. Yule (David, 1995), though in a different context (Miller, 2004a).

EXAMPLE 6.2 Proportions of a Sampling Distribution of Means

1. A population of one-year-old children's chest circumferences has $\mu = 47.0$ cm and $\sigma = 12.0$ cm, what is the probability of drawing from it a random sample of nine measurements that has a mean larger than 50.0 cm?

$$\sigma_{\overline{X}} = \frac{12.0 \text{ cm}}{\sqrt{9}} = 4.0 \text{ cm}$$

$$Z = \frac{\overline{X} - \mu}{\sigma_{\overline{X}}} = \frac{50.0 \text{ cm} - 47.0 \text{ cm}}{4.0 \text{ cm}} = 0.75$$

$$P(\overline{X} > 50.0 \text{ cm}) = P(Z > 0.75) = 0.2266$$

2. What is the probability of drawing a sample of 25 measurements from the preceding population and finding that the mean of this sample is less than 40.0 cm?

$$\sigma_{\overline{X}} = \frac{12.0 \text{ cm}}{\sqrt{25}} = 2.4 \text{ cm}$$

$$Z = \frac{40.0 \text{ cm} - 47.0 \text{ cm}}{2.4 \text{ cm}} = -2.92$$

$$P(\overline{X} < 40.0 \text{ cm}) = P(Z < -2.92) = P(Z > 2.92) = 0.0018$$

3. If 500 random samples of size 25 are taken from the preceding population, how many of them would have means larger than 50.0 cm?

$$\sigma_{\overline{X}} = \frac{12.0 \text{ cm}}{\sqrt{25}} = 2.4 \text{ cm}$$

$$Z = \frac{50.0 \text{ cm} - 47.0 \text{ cm}}{2.4 \text{ g}} = 1.25$$

$$P(\overline{X} > 50.0 \text{ cm}) = P(Z > 1.25) = 0.1056$$

Therefore, $(0.1056)(500) = 53$ samples would be expected to have means larger than 50.0 cm.

the sample variance of the mean. Thus,

$$s_{\overline{X}} = \sqrt{\frac{s^2}{n}} \text{ or } s_{\overline{X}} = \frac{s}{\sqrt{n}} \tag{6.8}$$

is an estimate of $\sigma_{\overline{X}}$ and is the sample standard error of the mean. Example 6.3 demonstrates the calculation of $s_{\overline{X}}$.

The importance of the standard error in hypothesis testing and related procedures will be evident in Chapter 7. At this point, however, it can be noted that the magnitude of $s_{\overline{X}}$ is helpful in determining the precision to which the mean and some measures of variability may be reported. Although different practices have been followed by many, we shall employ the following (Eisenhart, 1968). We shall state the standard error to two significant figures (e.g., 2.7 mm in Example 6.3; see Section 1.2 for an explanation

of significant figures). Then the standard deviation and the mean will be reported with the same number of decimal places (e.g., $\overline{X}$ = 137.6 mm in Example 6.3*). The variance may be reported with twice the number of decimal places as the standard deviation.

EXAMPLE 6.3 The Calculation of the Standard Error of the Mean, $s_{\overline{X}}$

The Following are Data for Systolic Blood Pressures, in mm of Mercury, of 12 Chimpanzees.

121
125
128
134
136
138
139
141
144
145
149
151

$\sum X = 1651$ mm

$\sum X^2 = 228{,}111$ mm^2

$n = 12$

$$\overline{X} = \frac{1651 \text{ mm}}{12} = 137.6 \text{ mm}$$

$$SS = 228{,}111 \text{ mm}^2 - \frac{(1651 \text{ mm})^2}{12}$$

$$= 960.9167 \text{ mm}^2$$

$$s^2 = \frac{960.9167 \text{ mm}^2}{11} = 87.3561 \text{ mm}^2$$

$$s = \sqrt{87.3561 \text{ mm}^2} = 9.35 \text{ mm}$$

$$s_{\overline{X}} = \frac{s}{\sqrt{n}} = \frac{9.35 \text{ mm}}{\sqrt{12}} = 2.7 \text{ mm } \textit{or}$$

$$s_{\overline{X}} = \sqrt{\frac{s^2}{n}} = \sqrt{\frac{87.3561 \text{ mm}^2}{12}} = \sqrt{7.2797 \text{ mm}^2} = 2.7 \text{ mm}$$

6.3 INTRODUCTION TO STATISTICAL HYPOTHESIS TESTING

A major goal of statistical analysis is to draw inferences about a population by examining a sample from that population. A very common example of this is the desire to draw conclusions about one or more population means.

We begin by making a concise statement about the population mean, a statement called a *null hypothesis* (abbreviated H_0)† because it expresses the concept of "no difference." For example, a null hypothesis about a population mean (μ) might assert that μ is not different from zero (i.e., μ is equal to zero); and this would be written as

$$H_0: \mu = 0.$$

Or, we could hypothesize that the population mean is not different from (i.e., is equal to) 3.5 cm, or not different from 10.5 kg, in which case we would write H_0: μ = 3.5 cm or H_0: μ = 10.5 kg, respectively.

*In Example 6.3, s is written with more decimal places than the Eisenhart recommendations indicate because it is an intermediate, rather than a final, result; and rounding off intermediate computations may lead to serious rounding error. Indeed, some authors routinely report extra decimal places, even in final results, with the consideration that readers of the results may use them as intermediates in additional calculations.

†The term *null hypothesis* was first published by R. A. Fisher in 1935 (David, 1995; Miller, 2004a; Pearson, 1947). J. Neyman and E. S. Pearson were the first to use the symbol "H_0" and the term *alternate hypothesis*, in 1928 (Pearson, 1947; Miller, 2004a, 2004c). The concept of statistical testing of something akin to a null hypothesis was introduced 300 years ago by John Arbuthnot (1667–1725), a Scottish–English physician and mathematician (Stigler, 1986: 225–226).

If statistical analysis concludes that it is likely that a null hypothesis is false, then an *alternate hypothesis* (abbreviated H_A or H_1) is assumed to be true (at least tentatively). One states a null hypothesis and an alternate hypothesis for each statistical test performed, and all possible outcomes are accounted for by this pair of hypotheses. So, for the preceding examples.*

$$H_0: \mu = 0, \quad H_A: \mu \neq 0;$$
$$H_0: \mu = 3.5 \text{ cm}, \quad H_A: \mu \neq 3.5 \text{ cm};$$
$$H_0: \mu = 10.5 \text{ kg}, \quad H_A: \mu \neq 10.5 \text{ kg}.$$

It must be emphasized that statistical hypotheses are to be stated *before* data are collected to test them. To propose hypotheses after examination of data can invalidate a statistical test. One may, however, legitimately formulate hypotheses *after* inspecting data if a new set of data is then collected with which to test the hypotheses.

(a) Statistical Testing and Probability. Statistical testing of a null hypothesis about μ, the mean of a population, involves calculating $\overline{X}$, the mean of a random sample from that population. As noted in Section 2.1, $\overline{X}$ is the best estimate of μ; but it is only an estimate, and we can ask, What is the probability of an $\overline{X}$ at least as far from the hypothesized μ as is the $\overline{X}$ in the sample, *if* H_0 *is true*? Another way of visualizing this is to consider that, instead of obtaining one sample (of size n) from the population, a large number of samples (each sample of size n) could have been taken from that population. We can ask what proportion of those samples would have had means at least as far as our single sample's mean from the μ specified in the null hypothesis. This question is answered by the considerations of Section 6.2 and is demonstrated in Example 6.4.

EXAMPLE 6.4 Hypothesis Testing of H_0: $\mu = 0$ and H_A: $\mu \neq 0$

The variable, X_i, is the weight change of horses given an antibiotic for two weeks. The following measurements of X_i are those obtained from 17 horses (where a positive weight change signifies a weight gain and a negative weight change denotes a weight loss):

2.0, 1.1, 4.4, −3.1, −1.3, 3.9, 3.2 , −1.6 ,3.5
1.2, 2.5, 2.3, 1.9, 1.8, 2.9, −0.3, and −2.4 kg.

For these 17 data, the sample mean ($\overline{X}$) is 1.29 kg. Although the population variance (σ^2) is typically not known, for the demonstration purpose of this example, σ^2 is said to be 13.4621 kg^2. Then the population standard error of the mean would be

$$\sigma_{\overline{X}} = \sqrt{\frac{\sigma^2}{n}} = \sqrt{\frac{13.4621 \text{ kg}^2}{17}} = \sqrt{0.7919 \text{ kg}^2} = 0.89 \text{ kg}$$

*The symbol "≠" denotes "is not equal to"; Ball (1935: 242) credits Leonhard Euler with its early, if not first, use (though it was first written with a vertical, not a diagonal, line through the equal sign).

and

$$Z = \frac{\overline{X} - \mu}{\sigma_{\overline{X}}} = \frac{1.29 \text{ kg} - 0}{0.89 \text{ kg}} = 1.45.$$

Using Table B.2,

$$P(\overline{X} \geq 1.29 \text{ kg}) = P(Z \geq 1.45) = 0.0735$$

and, because the distribution of Z is symmetrical,

$$P(\overline{X} \leq -1.29 \text{ kg}) = P(Z \leq -1.45) = 0.0735.$$

Therefore,

$$\begin{aligned} &P(\overline{X} \geq 1.29 \text{ kg } \textit{or } \overline{X} \leq -1.29 \text{ kg}) \\ &= P(Z \geq 1.45 \textit{ or } Z \leq -1.45) \\ &= 0.0735 + 0.0735 = 0.1470. \end{aligned}$$

As $0.1470 > 0.05$, do not reject H_0.

In Example 6.4, it is desired to ask whether treating horses with an experimental antibiotic results in a change in body weight. The data shown (X_i values) are the changes in body weight of 17 horses that received the antibiotic, and the statistical hypotheses to be tested are H_0: $\mu = 0$ kg and H_A: $\mu \neq 0$ kg. (As shown in this example, we can write "0" instead of "0 kg" in these hypotheses, because they are statements about *zero* weight change, and *zero* would have the same meaning regardless of whether the horses were weighed in kilograms, milligrams, pounds, ounces, etc.)

These 17 data have a mean of $\overline{X} = 1.29$ kg and they are considered to represent a random sample from a very large number of data, namely the body-weight changes that would result from performing this experiment with a very large number of horses. This large number of potential X_i's is the statistical population. Although one almost never knows the actual parameters of a sampled population, for this introduction to statistical testing let us suppose that the variance of the population sampled for this example is known to be $\sigma^2 = 13.4621 \text{ kg}^2$. Thus, for the population of means that could be drawn from this population of measurements, the standard error of the mean is $\sigma_{\overline{X}} = \sqrt{\sigma^2/n} = \sqrt{13.4621 \text{ kg}^2/17} = \sqrt{0.7919 \text{ kg}^2} = 0.89$ kg (by Equation 6.5). We shall further assume that the population of possible means follows a normal distribution, which is generally a reasonable assumption even when the individual data in the population are not normally distributed.

This hypothesis test may be conceived as asking the following:

> If we have a normal population with $\mu = 0$ kg, and $\sigma_{\overline{X}} = 0.89$ kg, what is the probability of obtaining a random sample of 17 data with a mean ($\overline{X}$) at least as far from 0 kg as 1.29 kg (i.e., at least 1.29 kg larger than 0 kg *or* at least 1.29 kg smaller than 0 kg)?

Section 6.2 showed that probabilities for a distribution of possible means may be ascertained through computations of Z (by Equation 6.6). The preceding null hypothesis is tested in Example 6.4, in which Z may be referred to as our *test statistic* (a computed quantity for which a probability will be determined). In this example, Z is calculated to be 1.45, and Appendix Table B.2 informs us that the probability of a

$Z \geq 1.45$ is 0.0735.* The null hypothesis asks about the deviation of the mean *in either direction* from 0 and, as the normal distribution is symmetrical, we can also say that $P(-Z \leq 1.45) = 0.0735$ and, therefore, $P(|Z| \geq 1.45) = 0.0735 + 0.0735 = 0.1470$. This tells us the probability associated with a $|Z|$ (absolute value of Z) at least as large as the $|Z|$ obtained; and this is the probability of a Z at least as extreme as that obtained, *if* the null hypothesis is true.

It should be noted that this probability,

$$P(|Z| \geq |\text{computed } Z|, \text{ if } H_0 \text{ is true}),$$

is *not* the same as

$$P(H_0 \text{ is true, if } |Z| \geq |\text{computed } Z|),$$

for these are *conditional probabilities*, discussed in Section 5.8. In addition to the playing-card example in that section, suppose a null hypothesis was tested 2500 times, with results as in Example 6.5. By Equation 5.23, the probability of rejecting H_0, *if* H_0 is true, is P(rejecting H_0, if H_0 is true) = (number of rejections of true H_0's)/(number of true H_0's) = 100/2000 = 0.05. And the probability that H_0 is true, *if* H_0 is rejected, is $P(H_0$ true, if H_0 is rejected) = (number of rejections of true H_0's)/(number of rejections of H_0's) = 100/550 = 0.18. These two probabilities (0.05 and 0.18) are decidedly not the same, for they are probabilities based on different conditions.

EXAMPLE 6.5 Probability of Rejecting a True Null Hypothesis

Hypothetical outcomes of testing the same null hypothesis for 2500 random samples of the same size from the same population (where the samples are taken with replacement).

	If H_0 is true	If H_0 is false	Row total
If H_0 is rejected	100	450	550
If H_0 is not rejected	1900	50	1950
Column total	2000	500	2500

Probability that H_0 is rejected if H_0 is true = 100/2000 = 0.05.
Probability that H_0 is true if H_0 is rejected = 100/550 = 0.18.

In hypothesis testing, it is correct to say that the calculated probability (for example, using Z) is

$$P(\text{the data, given } H_0 \text{ is true})$$

and it is *not* correct to say that the calculated probability is

$$P(H_0 \text{ is true, given the data}).$$

Furthermore, in reality we may not be testing H_0: $\mu = 0$ kg in order to conclude that the population mean is *exactly* zero (which it probably is *not*). Rather, we

*Note that "≥" and "≤" are symbols for "greater than or equal to" and "less than or equal to," respectively.

are interested in concluding whether there is a very small difference between the population mean and 0 kg; and what is meant by *very small* will be discussed in Section 6.3(d).

(b) Statistical Errors in Hypothesis Testing. It is desirable to have an objective criterion for drawing a conclusion about the null hypothesis in a statistical test. Even if H_0 is true, random sampling might yield a sample mean ($\overline{X}$) far from the population mean (μ), and a large absolute value of Z would thereby be computed. However, such an occurrence is unlikely, and the larger the $|Z|$, the smaller the probability that the sample came from a population described by H_0. Therefore, we can ask how small a probability (which is the same as asking how large a $|Z|$) will be required to conclude that the null hypothesis is not likely to be true. The probability used as the criterion for rejection of H_0 is called the *significance level*, routinely denoted by α (the lowercase Greek letter alpha).* As indicated below, an α of 0.05 is commonly employed. The value of the test statistic (in this case, Z) corresponding to α is termed the *critical value* of the test statistic. In Appendix Table B.2 it is seen that $P(Z \geq 1.96) = 0.025$; and, inasmuch as the normal distribution is symmetrical, it is also the case that $P(Z \leq -1.96) = 0.025$. Therefore, the critical value for testing the above H_0 at the 0.05 level (i.e., 5% level) of significance is $Z = 1.96$ (see Figure 6.4). These values of Z may be denoted as $Z_{0.025(1)} = 1.96$ and $Z_{0.05(2)} = 1.96$, where the parenthetical number indicates whether one or two tails of the normal distribution are being referred to.

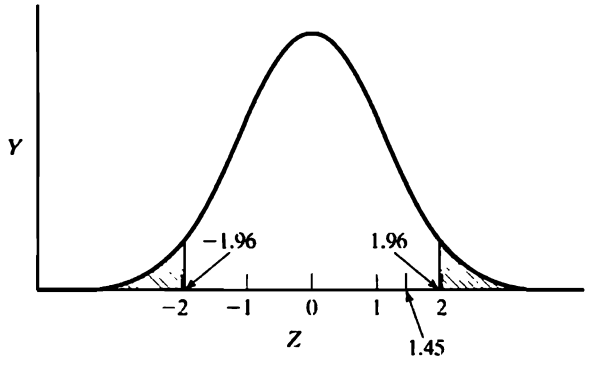


FIGURE 6.4: A normal curve showing (with shading) the 5% of the area under the curve that is the rejection region for the null hypothesis of Example 6.4. This rejection region consists of 2.5% of the curve in the right tail (demarcated by $Z_{0.05(2)} = 1.96$) and 2.5% in the left tail (delineated by $-Z_{0.05(2)} = -1.96$). The calculated test statistic in this example, $Z = 1.45$, does not lie within either tail; so H_0 is not rejected.

So, a calculated Z greater than or equal to 1.96, or less than or equal to -1.96, would be reason to reject H_0, and the shaded portion of Figure 6.4 is known as the "rejection region." The absolute value of the test statistic in Example 6.4 (namely, $|Z| = 1.45$) is not as large as the critical value (i.e., it is neither ≥ 1.9 nor ≤ -1.96), so in this example the null hypothesis is not rejected as a statement about the sampled population.

*David (1955) credits R. A. Fisher as the first to refer to "level of significance," in 1925. Fisher (1925b) also was the first to formally recommend use of the 5% significance level as guidance for drawing a conclusion about the propriety of a null hypothesis (Cowles and Davis, 1982), although he later argued that a fixed significance level should not be used. This use of the Greek "α" first appears in a 1936 publication of J. Neyman and E. S. Pearson (Miller, 2004c).

It is very important to realize that a true null hypothesis will sometimes be rejected, which of course means that an error has been committed in drawing a conclusion about the sampled population. Moreover, this error can be expected to be committed with a frequency of α. The rejection of a null hypothesis when it is in fact true is what is known as a *Type I error* (or "Type 1 error" or "alpha error" or "error of the first kind"). On the other hand, a statistical test will sometimes fail to detect that a H_0 is in fact false, and an erroneous conclusion will be reached by not rejecting H_0. The probability of committing this kind of error (that is, not rejecting H_0 when it is false) is represented by β (the lowercase Greek letter beta). This error is referred to as a *Type II error* (or "Type 2 error" or "beta error" or "error of the second kind"). The *power* of a statistical test is defined as $1 - \beta$: the probability of correctly rejecting the null hypothesis when it is false.* If H_0 is not rejected, some researchers refer to it as having been "accepted," but most consider it better to say "not rejected," for low statistical power often causes failure to reject, and "accept" sounds too definitive. Section 6.3(c) discusses how both the Type I and the Type II errors can be reduced.

Table 6.1 summarizes these two types of statistical errors, and Table 6.2 indicates their probabilities. Because, for a given n, a relatively small probability of a Type I error is associated with a relatively large probability of a Type II error, it is appropriate to ask what the acceptable combination of the two might be. By experience, and by convention, an α of 0.05 is typically considered to be a "small enough chance" of committing a Type I error while not being so small as to result in "too large a chance"of a Type II error (sometimes considered to be around 20%). But the 0.05 level of significance is not sacrosanct. It is an arbitrary, albeit customary, threshold for concluding that there is significant evidence against a null hypothesis. And caution should be exercised in emphatically rejecting a null hypothesis if $p = 0.049$ and not rejecting if $p = 0.051$, for in such borderline cases further examination—and perhaps repetition—of the experiment would be recommended.

TABLE 6.1: The Two Types of Errors in Hypothesis Testing

	If H_0 is true	If H_0 is false
If H_0 is rejected:	Type I error	No error
If H_0 is not rejected:	No error	Type II error

Although 0.05 has been the most widely used significance level, individual researchers may decide whether it is more important to keep one type of error

*The distinction between these two fundamental kinds of statistical errors, and the concept of power, date back to the pioneering work, in England, of Jerzy Neyman (1894–1981; Russian-born, of Polish roots, emigrating as an adult to Poland and then to England, and spending the last half of his life in the United States) and the English statistician Egon S. Pearson (1895–1980) (Lehmann and Reid, 1982; Neyman and Pearson, 1928a; Pearson, 1947). They conceived of the two kinds of errors in 1928 (Lehmann, 1999) and named them, and they formulated the concept of power in 1933 (David, 1995). With some influence by W. S. Gosset ("Student") (Lehmann, 1999), their modifications (e.g., Neyman and Pearson, 1933) of the ideas of the colossal British statistician (1890–1962) R. A. Fisher (1925b) provide the foundations of statistical hypothesis testing. However, from the mid-1930s until his death, Fisher disagreed intensely with the Neyman-Pearson approach, and the hypothesis testing commonly used today is a fusion of the Fisher and the Neyman-Pearson procedures (although this hybridization of philosophies has received criticism—e.g., by Hubbard and Bayarri, 2003). Over the years there has been further controversy regarding hypothesis testing, especially—but not entirely—within the social sciences (e.g., Harlow, Mulaik, and Steiger, 1997). The most extreme critics conclude that hypothesis tests should never be used, while most others advise that they may be employed but only with care to avoid abuse.

TABLE 6.2: The Long-Term Probabilities of Outcomes in Hypothesis Testing

	If H_0 is true	If H_0 is false
If H_0 is rejected	α	$1 - \beta$ ("power")
If H_0 is not rejected	$1 - \alpha$	β

or the other low. In some instances, we may be willing to test with an α greater than 0.05. An example of the later decision could be when there is an adverse health or safety implication if we incorrectly fail to reject a false null hypothesis. So in performing an experiment such as in Example 6.4, perhaps it is deemed important to the continued use of this antibiotic that it not cause a change in body weight; and we want to have a small chance of concluding that the drug causes no weight change when such a decision is incorrect. In other words, we may be especially desirous of avoiding a Type II error. In that case, an α of 0.10 (i.e., 10%) might be used, for that would decrease the probability of a Type II error, although it would concomitantly increase the likelihood of incorrectly rejecting a true H_0 (i.e., committing a Type I error). In other cases, such as indicated in Section 6.3(d), a 0.05 (i.e., 5%) chance of an incorrect rejection of H_0 may be felt to be unacceptably high, so a lower α would be employed in order to reduce the probability of a Type I error (even though that would increase the likelihood of a Type II error).

It is necessary, of course, to state the significance level used when communicating the results of a statistical test. Indeed, rather than simply stating whether the null hypothesis is rejected, it is good procedure to report also the sample size, the test statistic, and the best estimate of the exact probability of the statistic (and such probabilities are obtainable from many computer programs and some calculators, and may be estimated from tables such as those in Appendix B). Note that in Example 6.4, it is reported that $n = 17$, $Z = 1.45$, and $P = 0.1470$, in addition to expressing the conclusion that H_0 is not rejected. In this way, readers of the research results may draw their own conclusions, even if their choice of significance level is different from the author's. It is also good practice to report results regardless of whether H_0 is rejected. Bear in mind, however, that the choice of α is to be made before seeing the data. Otherwise there is a great risk of having the choice influenced by examination of the data, introducing bias instead of objectivity into the proceedings. The best practice generally is to decide on the null and alternate hypotheses, and the significance level, before commencing with data collection and, after performing the statistical test, to express the probability that the sample came from a population for which H_0 is true. It is conventional to refer to rejection of H_0 at the 5% significance level as denoting a "statistically significant" difference between $\overline{X}$ and the μ hypothesized in H_0 (e.g., in Example 6.4, between $\overline{X} = 1.45$ kg and $\mu = 0$ kg).* But, in analyzing biological data, we should consider whether a statistically detected difference reflects a *biologically significant* difference, as will be discussed in Section 6.3(d).

(c) One-Tailed versus Two-Tailed Testing. In Section 6.3(a), Example 6.4 tests whether a population mean was significantly different from a hypothesized value, where the alternate hypothesis embodies difference in either direction (i.e., greater than or less than) from that value. This is known as *two-sided*, or *two-tailed*, testing.

*In reporting research results, some authors have attached an asterisk (*) to a test statistic if it is associated with a probability ≤ 0.05 and two asterisks (**) if the probability is ≤ 0.01, sometimes referring to results at ≤ 0.01 as "highly significant"; but the latter term is best avoided, in preference to reporting the magnitude of p.

for we reject H_0 if Z (the test statistic in this instance) is within either of the two tails of the normal distribution demarcated by the positive and negative critical values of Z (the shaded areas in Figure 6.4).

However, there are cases where there is good scientific justification to test for a significant difference *specifically in one direction only*. That is, on occasion there is a good reason to ask whether a population mean is significantly *larger* than μ_0, and in other situations there is a good rationale for asking whether a population mean is significantly *smaller* than μ_0. Statistical testing that examines difference in only one of the two possible directions is called *one-sided*, or *one-tailed*, testing.

Example 6.4 involved a hypothesis test interested in whether a drug intended to be an antibiotic caused weight change as a side effect of its use. For such a test, H_0 is rejected if Z (the test statistic in this instance) is within the rejection region in either the right-hand *or* the left-hand tail of the normal distribution (i.e., within the shaded areas of Figure 6.4 and Figure 6.5a). However, consider a similar experiment where the purpose of the drug is to cause weight loss. In that case, the statistical hypotheses would be H_0: $\mu \geq 0$ versus H_A: $\mu < 0$. That is, if the drug works as intended and there

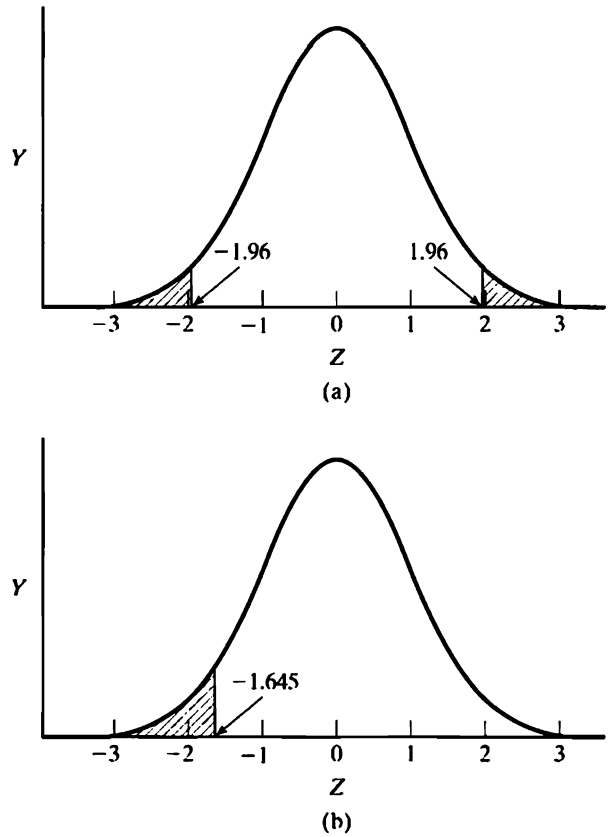


FIGURE 6.5: (a) As in Figure 6.4, a normal curve showing (with shading) the 5% of the area under the curve that is the rejection region for the two-tailed null hypotheses, H_0: $\mu = \mu_0$ versus H_A: $\mu \neq \mu_0$. This rejection region consists of 2.5% of the curve in the right tail (demarcated by $Z_{0.05(2)} = 1.96$), and 2.5% in the left tail (delineated by $-Z_{0.05(2)} = -1.96$). (b) A normal curve showing (with shading) the 5% of the area under the curve that is the rejection region for the one-tailed null hypotheses, H_0: $\mu \geq \mu_0$ vs. H_A: $\mu < \mu_0$. This rejection region consists of 5% of the curve in the left tail (demarcated by $Z_{0.05(1)} = 1.645$).

is a mean weight loss, then H_0 would be rejected; and if the drug does not work (that is, there is a mean weight gain or the mean weight did not change), H_0 would not be rejected. In such a situation, the rejection region would be entirely in one tail of the normal distribution, namely the left-hand tail. This is an example of a *one-tailed test*, whereas Example 6.4 represents a *two-tailed test.*

It can be seen in Appendix B.2 that, if one employs the 5% level of significance, the one-tailed Z value is 1.645. The normal distribution's tail defined by this one-tailed Z is the shaded area of Figure 6.5b. If the calculated Z is within this tail, H_0 is rejected as a correct statement about the population from which this sample came.

Figure 6.5a shows the rejection region of a normal distribution when performing two-tailed testing of H_0: $\mu = \mu_0$ at the 5% significance level (i.e., the same shaded area as in Figure 6.4, namely 2.5% in each tail of the curve); and Figure 6.5b shows the rejection region for one-tailed testing of H_0: $\mu \geq 0$ versus H_A: $\mu < 0$ at the 5% level. (If the experimental drug were intended to result in weight gain, not weight loss, then the rejection region would be in the right-hand tail instead of in the left-hand tail.)

In general, one-tailed hypotheses about a mean are

$$H_0: \mu \geq \mu_0 \text{ and } H_A: \mu < \mu_0,$$

in which case H_0 is rejected if the test statistic is in the left-hand tail of the distribution, *or*

$$H_0: \mu \leq \mu_0 \text{ and } H_A: \mu > \mu_0,$$

in which case H_0 is rejected if the test statistic is in the right-hand tail of the distribution.*

The one-tailed critical value (let's call it $Z_{\alpha(1)}$) is found in Appendix Table B.2. It is always smaller than the two-tailed critical value ($Z_{\alpha(2)}$); for example, at the 5% significance level $Z_{\alpha(1)} = 1.645$ and $Z_{\alpha(2)} = 1.96$. Thus, as will be noted in Section 6.3(d), for a given set of data a one-tailed test is more powerful than a two-tailed test. But it is inappropriate to employ a one-tailed test unless there is a scientific reason for expressing one-tailed, in preference to two-tailed, hypotheses. And recall that *statistical hypotheses are to be declared before examining the data.* Another example of one-tailed testing of a mean is found in Exercise 6.5(a).

(d) What Affects Statistical Power. The power of a statistical testing procedure was defined in Section 6.3(b) as the probability that a test correctly rejects the null hypothesis when that hypothesis is a false statement about the sampled population. It is useful to be aware of what affects the power of a test, and later chapters will show how to estimate the power a test will have and to estimate how small a difference will be detected between a population parameter (e.g., μ) and a hypothesized value (e.g., μ_0).

Figure 6.6a represents a normal distribution of sample means, where each sample was the same size and each sample mean estimates the same population mean. This mean of this distribution is μ_0, the population mean specified in the null hypothesis. This curve is the same as shown in Figure 6.5. As in Figure 6.5, the shaded area in each of the two tails denotes 0.025 of the area under the curve; so both shaded areas compose an area of 0.05, the probability of a Type I error (α).

*Some authors write the first of these two pairs of hypotheses as H_0: $\mu = \mu_0$ and H_A: $\mu < \mu_0$, and the second pair as H_0: $\mu = \mu_0$ and H_A: $\mu > \mu_0$, ignoring mention of the tail that is not of interest.

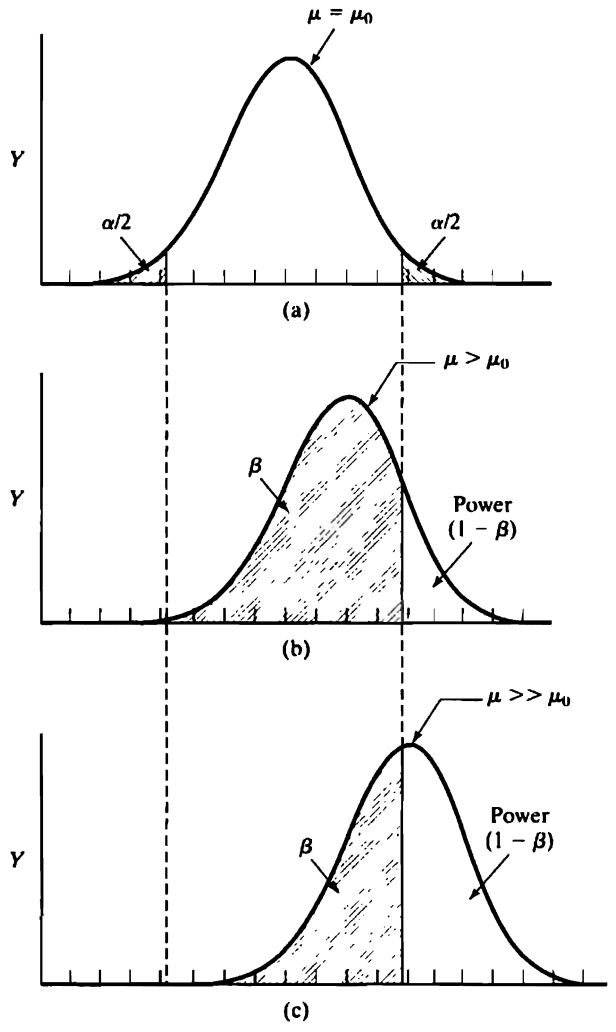


FIGURE 6.6: (a) A normal curve, such as that in Figure 6.4, where μ, the mean of the distribution, is μ_0, the value specified in the null and alternate hypotheses. The shaded area in each of the two tails is 0.025 of the area under the curve, so a total of 0.05 (i.e., 5%) of the curve is the shaded critical region, and α, the probability of a Type I error, is 0.05. (b) The same normal curve, but where μ is larger than μ_0 and the shaded area is the probability of a Type II error (β). (c) The same normal curve, but where μ is much larger than μ_0.

Figure 6.6b is the same normal curve, but with a population mean, μ, different from (i.e., larger than) μ_0. If H_0: $\mu = \mu_0$ is not a true statement about the population, yet we fail to reject H_0, then we have committed a Type II error, the probability of which is β, indicated by the shaded area between the vertical dashed lines in Figure 6.6b. The power of the hypothesis test is defined as $1 - \beta$, which is the unshaded area under this curve.

Figure 6.6c is the same depiction as in Figure 6.6b, but with a population mean, μ, even more different* from μ_0. An important result is that, the farther μ is from the μ_0 specified in H_0, the smaller β becomes and the larger the power becomes.

*The symbol ">" has been introduced as meaning "greater than," and "<" as meaning "less than." The symbols "≫" and "≪" mean "much greater than" and "much less than," respectively.

Figure 6.7 indicates the outcome if a larger α is used, namely 10% instead of 5% (meaning that 5%, instead of 2.5%, of the curve is in each tail). If the probability of a Type I error (α) is increased, then the probability of a Type II error (β) is decreased, and the power of the test is increased.

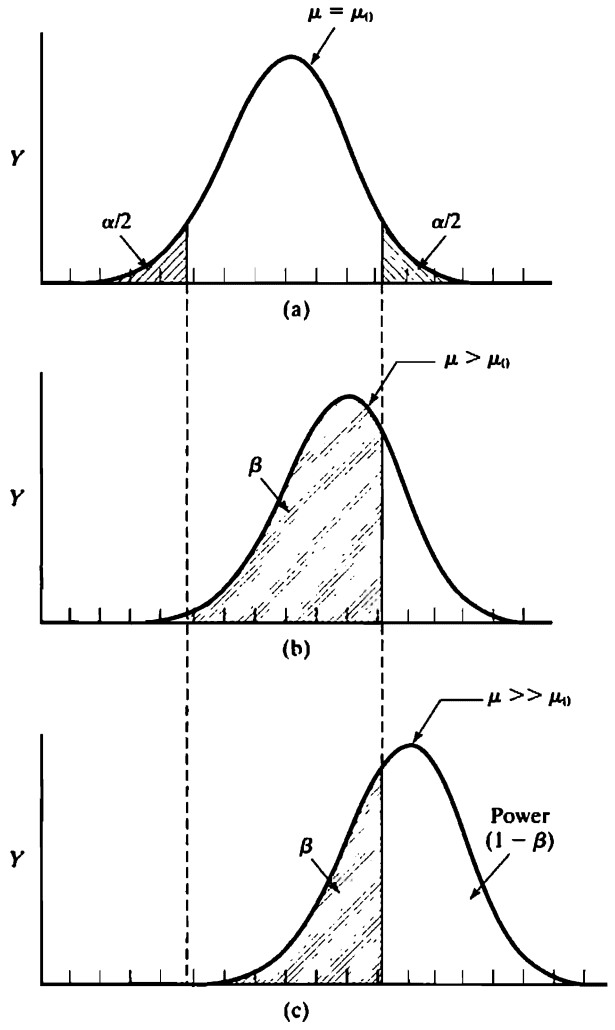


FIGURE 6.7: (a) A normal curve, such as that in Figure 6.6, where μ, the mean of the distribution, is μ_0, the value specified in the null and alternate hypotheses, but where the shaded area in each of the two tails is 0.05 of the area under the curve, so a total of 0.10 (i.e., 10%) of the curve is the shaded critical region, and α, the probability of a Type I error, is 0.10. (b) The same normal curve, but where μ is larger than μ_0 and the shaded area is the probability of a Type II error (β). (c) The same normal curve, but where μ is much larger than μ_0.

Another important outcome is seen by examining Equations 6.5 and 6.6. With larger sample size (n), or with smaller variance (σ^2), the standard error $\sigma_{\bar{X}}$ becomes smaller, which means that the shape of the normal distribution becomes narrower. Figure 6.3 shows an example of this narrowing as the variance decreases in a population of data, and the figures would appear similar if they were for a population of means. So, for a given value of α and of μ, either a smaller σ^2 or a larger n will result in a smaller $\sigma_{\bar{X}}$, which will result in a smaller β and greater power to reject H_0.

In some circumstances, a larger n can be used, but in other situations this would be difficult because of cost or effort. A smaller variance of the sampled population will result if the population is defined as a more homogeneous group of data. In Example 6.4, the experiment could have been performed using only female horses, or only horses of a specified age, or only horses of a specified breed. Then the hypothesis test would be about the specified sex, age, and/or breed, and the population variance would probably be smaller; and this would result in a greater power of the test.

To summarize what influences power,

- For given α, σ^2, and n, power is greater for larger difference between μ and μ_0.
- For given n, σ^2, and difference between μ and μ_0, power is greater for larger α.
- For given α, σ^2, and difference between μ and μ_0, power is greater for larger n.
- For given α, n, and difference between μ and μ_0, power is greater for smaller σ^2.
- For given α, n, σ^2, and difference between μ and μ_0, power is greater for one-tailed than for two-tailed tests (but one-tailed tests may be employed only when the hypotheses are appropriately one-tailed).

(e) Summary of Statistical Hypothesis Testing. Earlier portions of Section 6.3 introduced the principles and practice of testing hypotheses about population parameters, using sample statistics as estimates of those parameters. It is also good practice to report an estimate of the precision with which a parameter has been estimated, by expressing what are known as "confidence limits," which will be introduced in Section 6.4.

To summarize the steps for testing of statistical hypotheses,

1. State H_0 and H_A, using two-tailed or one-tailed hypotheses depending upon the objective of the data analysis.
2. Declare the level of significance, α, to be employed.
3. Collect the data and calculate the test statistic (Z in this chapter).
4. Compare the test statistic to the critical value(s) of that statistic (that is, the value(s) delimiting the rejection region of the statistical distribution of the test statistic). For the testing in this chapter, the critical values are both $Z_{\alpha(2)}$ and $-Z_{\alpha(2)}$ for a two-tailed test and the critical value is $Z_{\alpha(1)}$ for a one-tailed test. If the calculated Z exceeds a critical value, H_0 is rejected.
5. State P, the probability of the test statistic if H_0 is true.
6. State confidence limits (two-tailed or one-tailed) for the population parameter, as discussed in Section 6.4.
7. State conclusion in terms of biological or other practical significance.

6.4 CONFIDENCE LIMITS

Sections 6.3a and 6.3b discussed the distribution of all possible samples of size n from a population with mean μ. It was noted that 5% of the values of Z (by Equation 6.6) for those sample means will be at least as large as $Z_{0.05(2)}$ *or* no larger than $-Z_{0.05(2)}$. This can be expressed as

$$P\left[-Z_{0.05(2)} \leq \frac{\overline{X} - \mu}{\sigma_{\overline{X}}} \leq Z_{0.05(2)}\right] = 95\%, \tag{6.9}$$

and this can be rearranged to read

$$P[\overline{X} - Z_{0.05(2)}\sigma_{\overline{X}} \leq \mu \leq \overline{X} + Z_{0.05(2)}\sigma_{\overline{X}}] = 0.95. \tag{6.10}$$

In general, we can say

$$P[\overline{X} - Z_{\alpha(2)}\sigma_{\overline{X}} \leq \mu \leq \overline{X} + Z_{\alpha(2)}\sigma_{\overline{X}}] = 1 - \alpha. \tag{6.11}$$

The *lower confidence limit* is defined as

$$L_1 = \overline{X} - Z_{\alpha(2)}\sigma_{\overline{X}}, \tag{6.12}$$

and the *upper confidence limit* is

$$L_2 = \overline{X} + Z_{\alpha(2)}\sigma_{\overline{X}}. \tag{6.13}$$

The distance between L_1 and L_2, namely

$$\overline{X} \pm Z_{\alpha(2)}\sigma_{\overline{X}} \tag{6.14}$$

(where "±" is read as "plus or minus"), is called a *confidence interval* (sometimes abbreviated CI).

When referring to a confidence interval, $1 - \alpha$ is known as the *confidence level* (or *confidence coefficient* or *confidence probability*).*

Although $\overline{X}$ is the best estimate of μ, it is only an estimate, and the calculation of a confidence interval for μ allows us to express the precision of this estimate. Example 6.6 demonstrates this for the data of Example 6.4, determining the confidence interval for the mean of the population from which the sample came. As the 95% confidence limits are computed to be −0.45 kg and 3.03 kg, the 95% confidence interval may be expressed as $P(-0.45 \text{ kg} \leq \mu \leq 3.03 \text{ kg}) = 95\%$. This means that, if all possible means of size n ($n = 17$ in this example) were taken from the population and a 95% confidence interval were calculated from each sample, 95% of those intervals would contain μ. (It does *not* mean that there is a 95% probability that the confidence interval computed from the one sample in Example 6.6 includes μ.)

EXAMPLE 6.6 Confidence Limits for the Mean

For the 17 data in Example 6.4, $\overline{X} = 1.29$ kg and $\sigma_{\overline{X}} = 0.89$ kg.
We can calculate the 95% confidence limits for μ using Equations 6.13 and 6.14 and $Z_{0.05(2)} = 1.96$:

$$\begin{aligned} L_1 &= \overline{X} - Z_{\alpha(2)}\sigma_{\overline{X}} \\ &= 1.29 \text{ kg} - (1.96)(0.89 \text{ kg}) \\ &= 1.29 \text{ kg} - 1.74 \text{ kg} = -0.45 \text{ kg} \end{aligned}$$

*We owe the development of confidence intervals to Jerzy Neyman, between 1928 and 1933 (Wang, 2000), although the concept had been enunciated a hundred years before. Neyman introduced the terms *confidence interval* and *confidence coefficient* in 1934 (David, 1995). On rare occasion, biologists may see reference to "fiducial intervals," a concept developed by R. A. Fisher beginning in 1930 and identical to confidence intervals in many, but not all, situations (Pfanzagl, 1978).

$$L_2 = \overline{X} + Z_{\alpha(2)}\sigma_{\overline{X}}$$
$$= 1.29 \text{ kg} + (1.96)(0.89 \text{ kg})$$
$$= 1.29 \text{ kg} + 1.74 \text{ kg} = 3.03 \text{ kg}.$$

So, the 95% confidence interval could be stated as

$$P(-0.45 \text{ kg} \leq \mu \leq 3.03 \text{ kg}).$$

Note that the μ_0 of Example 6.4 (namely 0) is included between L_1 and L_2, indicating that H_0 is not rejected.

As seen in Equation 6.15, a small $\sigma_{\overline{X}}$ will result in a smaller confidence interval, meaning that μ is estimated more precisely when $\sigma_{\overline{X}}$ is small. And, recall from Equation 6.5 that $\sigma_{\overline{X}}$ becomes small as n becomes large. So, in general, a parameter estimate from a large sample is more precise than an estimate of the same parameter from a small sample.

If, instead of a 95% confidence interval, we wished to state an interval that gave us 99% confidence in estimating μ, then $Z_{0.01(2)}$ (which is 2.575) would have been employed instead of $Z_{0.05(2)}$, and we would have computed $L_1 = 1.29 \text{ kg} - (2.575)(0.89 \text{ kg}) = 1.29 \text{ kg} - 2.29 = -1.00$ and $L_2 = 1.29 \text{ kg} + (2.575)(0.89 \text{ kg}) = 1.29 \text{ kg} + 2.29 \text{ kg} = 3.58 \text{ kg}$. It can be seen that a larger confidence level (e.g., 99% instead of 95%) results in a larger width of the confidence interval, evincing the trade-off between confidence and utility. Indeed, if we increase the confidence to 100%, then the confidence interval would be $-\infty$ to ∞, and we would have a statement of great confidence that was useless! Note, also, that it is a two-tailed value of Z (i.e., $Z_{0.05(2)}$) that is used in the computation of a confidence interval when we set confidence limits on both sides of μ.

In summary, a narrower confidence interval will be associated with a smaller standard error ($\sigma_{\overline{X}}$), a larger sample size (n), or a smaller confidence coefficient ($1 - \alpha$).

It is recommended that a $1 - \alpha$ confidence interval be reported for μ whenever results are presented from a hypothesis test at the α significance level. If H_0: $\mu = \mu_0$ is not rejected, then the confidence interval includes μ_0 (as is seen in Example 6.6, where $\mu_0 = 0$ is between L_1 and L_2).

(a) One-Tailed Confidence Limits. In the case of a one-tailed hypothesis test, it is appropriate to determine a one-tailed confidence interval; and, for this, a one-tailed critical value of Z (i.e., $Z_{\alpha(1)}$) is used instead of a two-tailed critical value ($Z_{\alpha(2)}$). For H_0: $\mu \leq \mu_0$ and H_A: $\mu > \mu_0$, the confidence limits for μ are $L_1 = \overline{X} - Z_{\alpha(1)}\sigma_{\overline{X}}$ and $L_2 = \infty$. For H_0: $\mu \geq \mu_0$ and H_A: $\mu < \mu_0$, the confidence limits are $L_1 = -\infty$ and $L_2 = \overline{X} + Z_{\alpha(1)}\sigma_{\overline{X}}$. An example of a one-sided confidence interval is Exercise 6.6(b). If a one-tailed null hypothesis is not rejected, then the associated one-tailed confidence interval includes μ_0.

6.5 SYMMETRY AND KURTOSIS

Chapters 3 and 4 showed how sets of data can be described by measures of central tendency and measures of variability. There are additional characteristics that help describe data sets, and they are sometimes used when we want to know whether a distribution resembles a normal distribution. Two basic features of a distribution of measurements are its *symmetry* and its *kurtosis*. A symmetric distribution (as in

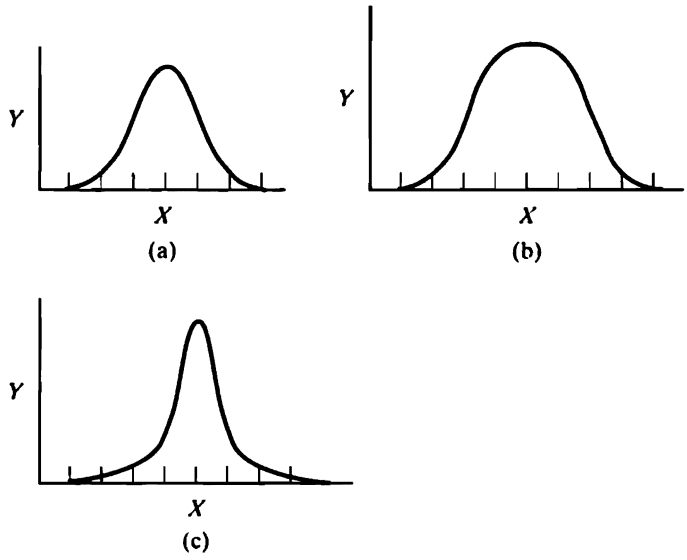


FIGURE 6.8: Symmetric frequency distributions. Distribution (a) is mesokurtic ("normal"), (b) is platykurtic, and (c) is leptokurtic.

distributed populations have $\beta_2 = 3$), some asymmetric distributions have a symmetry measure of 0 and some nonnormal distributions exhibit a kurtosis value of 3 (Thode, 2002: 43).

In practice, researchers seldom calculate these symmetry and kurtosis measures. When they do, however, they should be mindful that using the third and fourth powers of numbers can lead to very serious rounding errors, and they should employ computer programs that use procedures minimizing this problem.

(c) Quantile Measures of Symmetry and Kurtosis. Denoting the ith quartile as Q_i (as in Section 4.2), Q_1 is the first quartile (i.e., the 25% percentile), Q_3 is the third quartile (the 75% percentile), and Q_2 is the second quartile (the 50% percentile, namely the median). A quantile-based expression of skewness (Bowley, 1920: 116; Groeneveld and Meeden, 1984) considers the distance between Q_3 and Q_2 and that between Q_2 and Q_1:

$$\text{Quantile skewness measure} = \frac{(Q_3 - Q_2) - (Q_2 - Q_1)}{(Q_3 - Q_2) + (Q_2 - Q_1)} = \frac{Q_3 + Q_1 - 2Q_2}{Q_3 - Q_1}, \tag{6.18}$$

which is a measure, without units, that may range from -1, for a distribution with extreme left skewness; to 0, for a symmetric distribution; to 1, for a distribution with extreme right skewness. Because Equation 6.18 measures different characteristics of a set of data than $\sqrt{b_1}$ does, these two numerical measures can be very different (and, especially if the skewness is not great, one of the measures can be positive and the other negative).

Instead of using quartiles Q_1 and Q_3, any other symmetric quantiles could be used to obtain a skewness coefficient (Groeneveld and Meeden, 1984), though the

numerical value of the coefficient would not be the same as that of Equation 6.18. For example, the 10th and 90th percentiles could replace Q_1 and Q_3, respectively, in Equation 6.18, along with Q_2 (the median).

A kurtosis measure based on quantiles was proposed by Moors (1988), using octiles: $\mathcal{O}_1$, the first octile, is the 12.5th percentile; $\mathcal{O}_3$, the third octile, is the 37.5th percentile; $\mathcal{O}_5$ is the 62.5th percentile; and $\mathcal{O}_7$ is the 87.5th percentile. Also, $\mathcal{O}_2 = Q_1$, $\mathcal{O}_4 = Q_2$, and $\mathcal{O}_6 = Q_3$. The measure is

$$\text{Quantile kurtosis measure} = \frac{(\mathcal{O}_7 - \mathcal{O}_5) + (\mathcal{O}_3 - \mathcal{O}_1)}{(\mathcal{O}_6 - \mathcal{O}_2)} = \frac{(\mathcal{O}_7 - \mathcal{O}_5) + (\mathcal{O}_3 - \mathcal{O}_1)}{(Q_3 - Q_1)}, \tag{6.19}$$

which has no units and may range from zero, for extreme platykurtosis, to 1.233, for mesokurtosis; to infinity, for extreme leptokurtosis.

Quantile-based measures of symmetry and kurtosis are rarely encountered.

6.6 ASSESSING DEPARTURES FROM NORMALITY

It is sometimes desired to test the hypothesis that a sample came from a population whose members follow a normal distribution. Example 6.7 and Figure 6.9 present a frequency distribution of sample data, and we may desire to know whether the data are likely to have come from a population that had a normal distribution. Comprehensive examinations of statistical methods applicable to such a question have been reported (e.g., by D'Agostino, 1986; Landry and Lepage, 1992; Shapiro, 1986; and Thode, 2002), and a brief overview of some of these techniques will be given here. The latter author discusses about 40 methods for normality testing and notes (ibid.: 143–157) that the power of a testing procedure depends upon the sample size and the nature of the nonnormality that is to be detected (e.g., asymmetry, long-tailedness, short-tailedness).

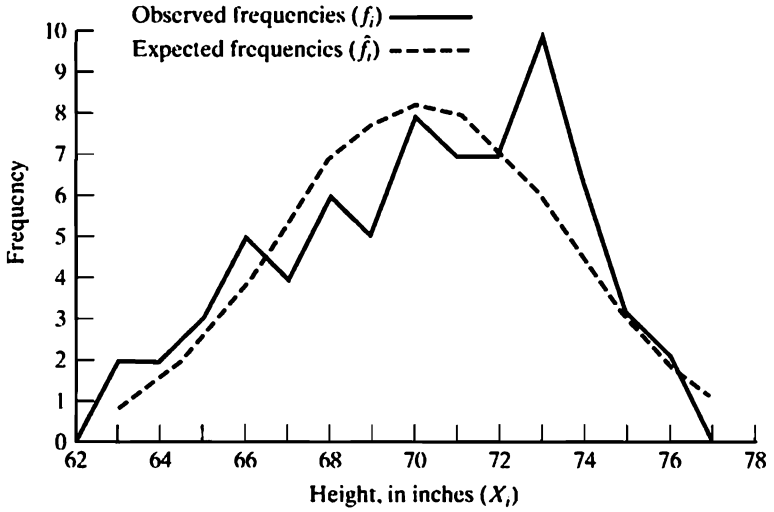


FIGURE 6.9: The frequency polygon for the student height data in Example 6.7 (solid line) with the frequency curve that would be expected if the data followed a normal distribution (broken line).

EXAMPLE 6.7 The Heights of the First 70 Graduate Students in My Biostatistics Course

Height (X_i) (in.)	Observed Frequency (f_i)	Cumulative Frequency (cum. f_i)	f_iX_i (in.)	$f_iX_i^2$ (in.^{2})
63	2	2	126	7,938
64	2	4	128	8,192
65	3	7	195	12,675
66	5	12	330	21,780
67	4	16	268	17,956
68	6	22	408	27,744
69	5	27	345	23,805
70	8	35	560	39,200
71	7	42	497	35,287
72	7	49	504	36,288
73	10	59	730	53,290
74	6	65	444	32,856
75	3	68	225	16,875
76	2	70	152	11,552
	$\Sigma f_i =$ $n = 70$		$\Sigma f_iX_i =$ 4,912 in.	$\Sigma f_iX_i^2 =$ 345,438 in.^{2}

$$SS = \Sigma f_i X_i^2 - \frac{\Sigma(f_i X_i)^2}{n} = 345{,}438 \text{ in.}^2 - \frac{(14{,}912 \text{ in.})^2}{70} = 755.9429 \text{ in.}^2$$

$$s^2 = \frac{SS}{n-1} = \frac{755.9429 \text{ in.}^2}{69} = 10.9557 \text{ in.}^2$$

(a) Graphical Assessment of Normality. Many methods have been used to assess graphically the extent to which a frequency distribution of observed data resembles a normal distribution (e.g., Thode, 2002: 15–40). Recall the graphical representation of a normal distribution as a frequency curve, shown in Figure 6.1. A frequency polygon for the data in Example 6.7 is shown in Figure 6.9, and superimposed on that figure is a dashed curve showing what a normal distribution, with the same number of data (n) mean ($\overline{X}$), and standard deviation (s), would look like. We may wish to ask whether the observed frequencies deviate significantly from the frequencies expected from a normally distributed sample.

Figure 6.10 shows the data of Example 6.7 plotted as a cumulative frequency distribution. A cumulative frequency graph of a normal distribution will be S-shaped (called "sigmoid"). The graph in Figure 6.10 is somewhat sigmoid in shape, but in this visual presentation it is difficult to conclude whether that shape is pronounced enough to reflect normality. So, a different approach is desired. Note that the vertical axis on the left side of the graph expresses cumulative frequencies and the vertical axis

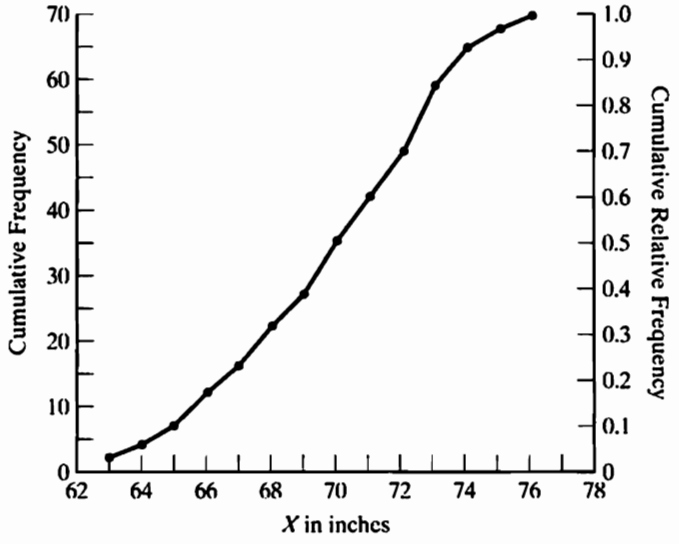


FIGURE 6.10: The cumulative frequency polygon of the student-height data of Example 6.7.

on the right side displays relative frequencies (as introduced in Figure 1.9), and the latter may be thought of as percentiles. For instance, the sample of 70 measurements in Example 6.7 contains 22 data, where $X_i \leq 68$ inches, so 68 in. on the horizontal axis is associated with a cumulative frequency of 22 on the left axis and a cumulative relative frequency of $22/70 = 0.31$ on the right axis; thus, we could say that a height of 68 in. is at the 31st percentile of this sample.

Examination of the relative cumulative frequency distribution is aided greatly by the use of the *normal probability scale*, as in Figure 6.11, rather than the linear scale of Figure 6.10. As the latter figure shows, a given increment in X_i (on the abscissa, the horizontal axis) near the median is associated with a much larger change in relative frequency (on the ordinate, the vertical axis) than is the same increment in X_i at very high or very low relative frequencies. Using the normal-probability scale on the ordinate expands the scale for high and low percentiles and compresses it for percentiles toward the median (which is the 50th percentile). The resulting cumulative frequency plot will be a straight line for a normal distribution. A leptokurtic distribution will appear as a sigmoid (S-shaped) curve on such a plot, and a platykurtic distribution will appear as a reverse S-shape. A negatively skewed distribution will show an upward curve, as the lower portion of an S, and a positively skewed distribution will manifest itself in a shape resembling the upper portion of an S. Figure 6.11 shows the data of Example 6.7 plotted as a cumulative distribution on a normal-probability scale. The curve appears to tend slightly toward leptokurtic.

Graph paper with the normal-probability scale on the ordinate is available commercially, and such graphs are produced by some computer software. One may also encounter graphs with a normal-probability scale on the abscissa and X_i on the ordinate. The shape of the plotted curves will then be converse of those described previously.

(b) Assessing Normality Using Symmetry and Kurtosis Measures. Section 6.5 indicated that a normally distributed population has symmetry and kurtosis parameters

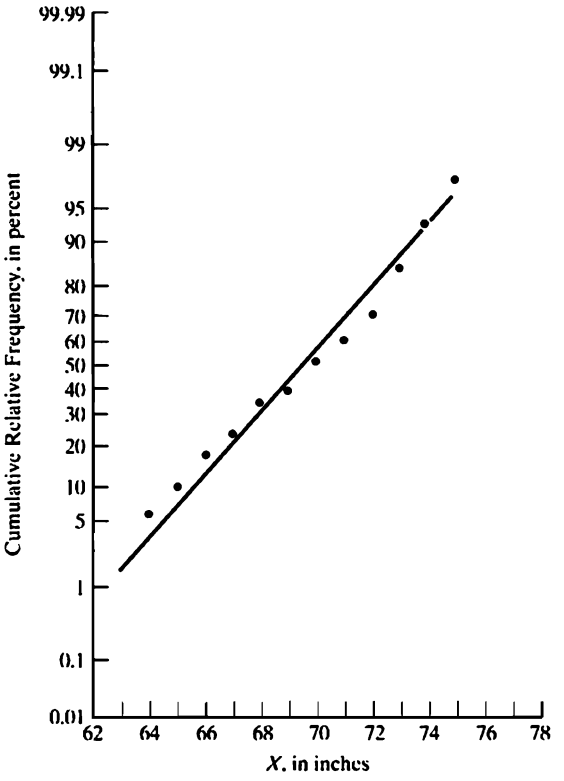


FIGURE 6.11: The cumulative relative frequency distribution for the data of Example 6.7, plotted with the normal probability scale as the ordinate. The expected frequencies (i.e., the frequencies from a normal distribution) would fall on the straight line shown.

of $\sqrt{\beta_1} = 0$ and $\beta_2 = 3$, respectively. Therefore, we can ask whether a sample of data came from a normal population by testing the null hypothesis H_0: $\sqrt{\beta_1} = 0$ (versus the alternate hypothesis, H_A: $\sqrt{\beta_1} \neq 0$) and the hypothesis H_0: $\beta_2 = 3$ (versus H_A: $\beta_2 \neq 3$), as shown in Section 7.16. There are also procedures that employ the symmetry and kurtosis measures simultaneously, to test H_0: The sample came from a normally distributed population versus H_A: The sample came from a population that is not normally distributed (Bowman and Shenton. 1975, 1986; D'Agostino and Pearson, 1973; Pearson, D'Agostino, and Bowman, 1977; Thode, 2002: 54–55, 283).

Statistical testing using these symmetry and kurtosis measures, or the procedure of Section 6.6(d), is generally the best for assessing a distribution's departure from normality (Thode, 2002: 2).

(c) Goodness-of-Fit Assessment of Normality. As will be discussed in Chapter 22, procedures called goodness-of-fit tests are applicable when asking whether a sample of data is likely to have come from a population with a specified distribution. Goodness-of-fit procedures known as chi-square, log-likelihood, and Kolmogorov-Smirnov, or modifications of them, have been used to test the hypothesis of normality (e.g., Zar, 1984: 88–93); and Thode (2002) notes that other goodness-of-fit tests, such as that of Kuiper (1960, which is alluded to in Section 27.18 for other purposes) may also be used. These methods perform poorly, however, in that they possess very low power; and they are not recommended for addressing hypotheses of normality (D'Agostino, 1986; D'Agostino, Belanger, and D'Agostino, 1990; Moore, 1986; Thode, 2002: 152).

(d) Other Methods of Assessing Normality. Shapiro and Wilk (1965) presented a test for normality involving the calculation of a statistic they called W. This computation requires an extensive table of constants, because a different set of $n/2$ constants is needed for each sample size, n. The authors provided a table of these constants and also of critical values of W, but only for n as large as 50. The power of this test has been shown to be excellent when testing for departures from normality (D'Agostino, 1986; Shapiro, Wilk, and Chen, 1968). Royston (1982a, 1982b) provided an approximation that extends the W test to n as large as 2000. Shapiro and Francia (1972) presented a modified procedure (employing a statistic they called W') that allows n to be as large as 99; but Pearson, D'Agostino, and Bowman (1977) noted errors in the published critical values. Among other modifications of W, Rahman and Govindarajulu (1997) offered one (with a test statistic they called $\tilde{W}$) declared to be applicable to any sample size, with critical values provided for n up to 5000. Calculation of W or its modifications is cumbersome and will most likely be done by computer; this test is unusual in that it involves rejection of the null hypothesis of normality if the test statistic is *equal to or less than* the one-tailed critical value.

The performance of the Shapiro-Wilk test is adversely affected by the common situation where there are tied data (i.e., data that are identical, as occur in Example 6.7, where there is more than one observation at each height) (Pearson, D'Agostino, and Bowman, 1977), but modifications of it have addressed that problem (e.g., Royston, 1986, 1989). Statistical testing using the Shapiro-Wilk test, or using symmetry and kurtosis measures (Section 6.6(b)), is generally the preferred method for inquiring whether an underlying population is normally distributed (Thode, 2002: 2).

EXERCISES

6.1. The following body weights were measured in 37 animals:

Weight (X_i) (kg)	*Frequency* (f_i)
4.0	2
4.3	3
4.5	5
4.6	8
4.7	6
4.8	5
4.9	4
5.0	3
5.1	1

(a) Calculate the symmetry measure, $\sqrt{b_1}$.
(b) Calculate the kurtosis measure, b_2.
(c) Calculate the skewness measure based on quantiles.
(d) Calculate the kurtosis measure based on quantiles.

6.2. A normally distributed population of lemming body weights has a mean of 63.5 g and a standard deviation of 12.2 g.
(a) What proportion of this population is 78.0 g or larger?
(b) What proportion of this population is 78.0 g or smaller?
(c) If there are 1000 weights in the population, how many of them are 78.0 g or larger?
(d) What is the probability of choosing at random from this population a weight smaller than 41.0 g?

6.3. **(a)** Considering the population of Exercise 6.2, what is the probability of selecting at random a body weight between 60.0 and 70.0 g?
(b) What is the probability of a body weight between 50.0 and 60.0 g?

6.4. **(a)** What is the standard deviation of all possible means of samples of size 10 which could be drawn from the population in Exercise 6.2?
(b) What is the probability of selecting at random from this population a sample of 10 weights that has a mean greater than 65.0 g?
(c) What is the probability of the mean of a sample of 10 being between 60.0 and 62.0 g?

6.5. The following 18 measurements are obtained of a pollutant in a body of water: 10.25, 10.37, 10.66, 10.47, 10.56, 10.22, 10.44, 10.38, 10.63, 10.40, 10.39, 10.26, 10.32, 10.35, 10.54, 10.33, 10.48, 10.68 milligrams per liter. Although we would not know this in practice, for the sake of this example let us say

we know that the standard error of the mean is $\sigma_{\overline{X}} = 0.24$ mg/liter in the population from which this sample came. The legal limit of this pollutant is 10.00 milligrams per liter.

(a) Test whether the mean concentration in this body of water exceeds the legal limit (i.e., test H_0: $\mu \leq 10.00$ mg/L versus H_A: $\mu > 10.00$ mg/L), using the 5% level of significance.

(b) Calculate the 95% confidence interval for μ.

6.6. The incubation time was measured for 24 alligator eggs. Let's say that these 24 data came from a population with a variance of $\sigma^2 = 89.06$ days^2, and the sample mean is $\overline{X} = 61.4$ days.

(a) Calculate the 99% confidence limits for the population mean.

(b) Calculate the 95% confidence limits for the population mean.

(c) Calculate the 90% confidence limits for the population mean.

CHAPTER 7

One-Sample Hypotheses

This chapter will continue the discussion of Section 6.3 on how to draw inferences about population parameters by testing hypotheses about them using appropriate sample statistics. It will consider hypotheses about each of several population parameters, including the population mean, median, variance, standard deviation, and coefficient of variation. The chapter will also discuss procedures (introduced in Section 6.4) for expressing the confidence one can have in estimating population parameters from sample statistics.

7.1 TWO-TAILED HYPOTHESES CONCERNING THE MEAN

Section 6.4 introduced the concept of statistical testing using a pair of statistical hypotheses, the null and alternate hypotheses, as statements that a population mean (μ) is equal to some specified value (let's call it μ_0):

$$H_0: \quad \mu = \mu_0;$$
$$H_A: \quad \mu \neq \mu_0.$$

For example, let us consider the body temperatures of 25 intertidal crabs that we exposed to air at 24.3° C (Example 7.1). We may wish to ask whether the mean body temperature of members of this species of crab is the same as the ambient air temperature of 24.3° C. Therefore,

$$H_0: \quad \mu = 24.3° \text{ C, and}$$
$$H_A: \quad \mu \neq 24.3° \text{ C.}$$

where the null hypothesis states that the mean of the population of data from which this sample of 25 came is 24.3°C (i.e., μ is "no different from 24.3°C"), and the alternate hypothesis is that the population mean is not equal to (i.e., μ is different from) 24.3°C.

EXAMPLE 7.1 The Two-Tailed *t* Test for Difference between a Population Mean and a Hypothesized Population Mean

Body temperatures (measured in °C) of 25 intertidal crabs placed in air at 24.3°C: 25.8, 24.6, 26.1, 22.9, 25.1, 27.3, 24.0, 24.5, 23.9, 26.2, 24.3, 24.6, 23.3, 25.5, 28.1, 24.8, 23.5, 26.3, 25.4, 25.5, 23.9, 27.0, 24.8, 22.9, 25.4.

$$H_0: \ \mu = 24.3°\text{C}$$

$$H_A: \ \mu \neq 24.3°\text{C}$$

$$\alpha = 0.05$$

$$n = 25$$

$$\overline{X} = 25.03°\text{C}$$

$$s^2 = 1.80(°\text{C})^2$$

$$s_{\overline{X}} = \sqrt{\frac{1.80(°\text{C})^2}{25}} = 0.27°\text{C}$$

$$t = \frac{\overline{X} - \mu}{s_{\overline{X}}} = \frac{25.03°\text{C} - 24.3°\text{C}}{0.27°\text{C}} = \frac{0.73°\text{C}}{0.27°\text{C}} = 2.704$$

$$\nu = 24$$

$$t_{0.05(2),24} = 2.064$$

As $|t| > t_{0.05(2),24}$, reject H_0 and conclude that the sample of 25 body temperatures came from a population whose mean is not 24.3°C.

$$0.01 < P < 0.02 \ [P = 0.012]^*$$

In Section 6.1 (Equation 6.6), $Z = (\overline{X} - \mu)/\sigma_{\overline{X}}$ was introduced as a *normal deviate*, and it was shown how one can determine the probability of obtaining a sample with mean $\overline{X}$ from a population with a specified mean μ. And Section 6.3 discussed how the normal deviate can be used to test hypotheses about a population mean. Note, however, that the calculation of Z requires the knowledge of $\sigma_{\overline{X}}$, which we typically do not have. The best we can do is to calculate $s_{\overline{X}}$ as an estimate of $\sigma_{\overline{X}}$. If n is very, very large, then $s_{\overline{X}}$ is a good estimate of $\sigma_{\overline{X}}$, and we can be

*Throughout the examples in this book, the exact probability of a calculated test statistic (such as t), as determined by computer software, is indicated in brackets. It should not be assumed that the many decimal places given by computer programs are all accurate (McCullough, 1998, 1999); therefore, the book's examples will routinely express these probabilities to only two or three (occasionally four) decimal places. The term "software" was coined by John Wilder Tukey (Leonhardt, 2000).

tempted to calculate Z using this estimate. However, for most biological situations n is insufficiently large to do this; but we can use, in place of the normal distribution (Z), a distribution known as t, the development of which was a major breakthrough in statistical methodology:*

$$t = \frac{\overline{X} - \mu}{s_{\overline{X}}}. \tag{7.1}$$

Because the t-testing procedure is so readily employed, we need not wonder whether n is large enough to use Z; and, in fact, Z is almost never used for hypothesis testing about means.

As do some other distributions to be encountered among statistical methods, the t distribution has different shapes for different values of what is known as *degrees of freedom* (denoted by ν, the lowercase Greek nu).† For hypotheses concerning a mean,

$$\nu = n - 1. \tag{7.2}$$

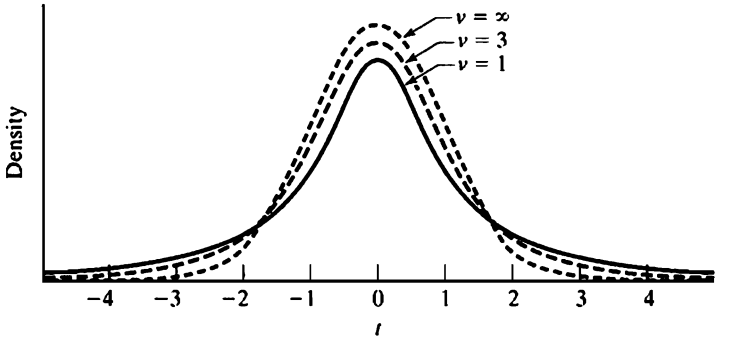


FIGURE 7.1: The t distribution for various degrees of freedom, ν. For $\nu = \infty$, the t distribution is identical to the normal distribution.

Recall that n is the size of the sample (i.e., the number of data from which $\overline{X}$ has been calculated). The influence of ν on the shape of the t distribution is shown in Figure 7.1.

*The t statistic is also referred to as "Student's t" because of William Sealy Gosset (1876–1937), who was an English statistician with the title "brewer" in the Guinness brewery of Dublin. He used the pen name "Student" (under his employer's policy requiring anonymity) to publish noteworthy developments in statistical theory and practice, including ("Student," 1908) the introduction of the distribution that bears his pseudonym. (See Boland, 1984, 2000; Irwin, 1978; Lehmann, 1999; Pearson, 1939; Pearson, Plackett, and Barnard, 1990; Zabell, 2008.) Gosset originally referred to his distribution as z; and, especially between 1922 and 1925, R. A. Fisher (e.g., 1925a, 1925b: 106–113, 117–125; 1928) helped develop its potential in statistical testing while modifying it; Gosset and Fisher then called the modification "t" (Eisenhart, 1979). Gosset was a modest man, but he was referred to as "one of the most original minds in contemporary science" by Fisher (1939a), himself one of the most insightful and influential statisticians of all time. From his first discussions of the t distribution, Gosset was aware that it was strictly applicable only if sampling normally distributed populations, though he surmised that only large deviations from normality would invalidate the use of t (Lehmann, 1999).

†In early writings of the t distribution (during the 1920s and 1930s), the symbol n or f was used for degrees of freedom. This was often confusing because these letters had commonly been used to denote other quantities in statistics so Maurice G. Kendall (1943: 292) recommended ν.

This distribution is leptokurtic (see Section 6.5), having a greater concentration of values around the mean and in the tails than does a normal distribution; but as n (and, therefore, ν) increases, the t distribution tends to resemble a normal distribution more closely, and for $\nu = \infty$ (i.e., for an infinitely large sample*), the t and normal distributions are identical; that is, $t_{\alpha,\infty} = Z_\alpha$.

The mean of the sample of 25 data (body temperatures) shown in Example 7.1 is 25.03°C, and the sample variance is 1.80(°C)^2. These statistics are estimates of the mean and variance of the population from which this sample came. However, this is only one of a very large number of samples of size 25 that could have been taken at random from the population. The distribution of the means of all possible samples with $n = 25$ is the t distribution for $\nu = 24$, which is represented by the curve of Figure 7.2. In this figure, the mean of the t distribution (i.e., $t = 0$) represents the mean hypothesized in H_0 (i.e., $\mu = \mu_0 = 24.3$°C), for, by Equation 7.1, $t = 0$ when $\overline{X} = \mu$. The shaded areas in this figure represent the extreme 5% of the total area under the curve (2.5% in each tail). Thus, an $\overline{X}$ so far from μ that it lies in either of the shaded areas has a probability of less than 5% of occurring by chance alone, and we assume that it occurred because H_0 is, in fact, false. As explained in Section 6.3 regarding the Z distribution, because an extreme t value in either direction from μ will cause us to reject H_0, we are said to be considering a "two-tailed" (or "two-sided") test.

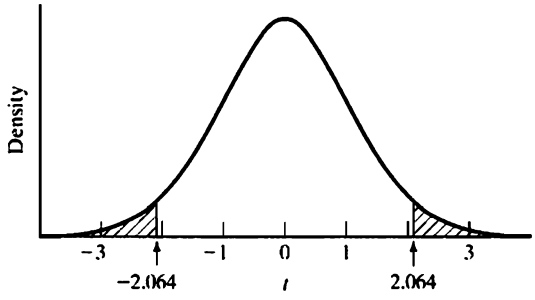


FIGURE 7.2: The t distribution for $\nu = 24$, showing the critical region (shaded area) for a two-tailed test using $\alpha = 0.05$. (The critical value of t is 2.064.)

For $\nu = 24$, we can consult Appendix Table B.3 to find the following two-tailed probabilities (denoted as "$\alpha(2)$") of various values of t:

ν	$\alpha(2)$:	0.50	0.20	0.10	0.05	0.02	0.01
24		0.685	1.318	1.711	2.064	2.492	2.797

Thus, for example, for a two-tailed α of 0.05, the shaded areas of the curve begin at 2.064 t units on either side of μ. Therefore, we can state:

$$P(|t| \geq 2.064) = 0.05.$$

That is, 2.064 and −2.064 are the *critical values* of t; and if t (calculated from Equation 7.1) is equal to or greater than 2.064, or is equal to or less than −2.064, that will be considered reasonable cause to reject H_0 and consider H_A to be a true

*The modern symbol for infinity (∞) was introduced in 1655 by influential English mathematician John Wallis (1616–1703) (Cajori, 1928/9, Vol. 2: 44), but it did not appear again in print until a work by Jacob Bernoulli was published posthumously in 1713 by his nephew Nikolaus Bernoulli (Gullberg, 1997: 30).

statement. That portion of the t distribution beyond the critical values (i.e., the shaded areas in the figure) is called the *critical region*,* or *rejection region*. For the sample of 25 body temperatures (see Example 7.1), $t = 2.704$. As 2.704 lies within the critical region (i.e., $2.704 > 2.064$), H_0 is rejected, and we conclude that the mean body temperature of crabs under the conditions of our experiment is not 24.3°C.

To summarize, the hypotheses for the two-tailed test are

$$H_0: \mu = \mu_0 \quad \text{and} \quad H_A: \mu \neq \mu_0,$$

where μ_0 denotes the hypothesized value to which we are comparing the population mean. (In the above example, $\mu_0 = 24.3$°C.) The test statistic is calculated by Equation 7.1, and if its absolute value is larger than the two-tailed critical value of t from Appendix Table B.3, we reject H_0 and assume H_A to be true. The critical value of t can be abbreviated as $t_{\alpha(2),\nu}$, where $\alpha(2)$ refers to the two-tailed probability of α. Thus, for the preceding example, we could write $t_{0.05(2),24} = 2.064$. In general, for a two-tailed t test,

$$\text{if } |t| \geq t_{\alpha(2),\nu}, \text{ then reject } H_0.$$

Example 7.1 presents the computations for the analysis of the crab data. A t of 2.704 is calculated, which for 24 degrees of freedom lies between the tabled critical values of $t_{0.02(2),24} = 2.492$ and $t_{0.01(2),24} = 2.797$. Therefore, if the null hypothesis, H_0, is a true statement about the population we sampled, the probability of $\overline{X}$ being at least this far from μ is between 0.01 and 0.02; that is, $0.01 < P(|t| \geq 2.704) < 0.02$.† As this probability is less than 0.05, we reject H_0 and declare it is not a true statement. For a consideration of the types of errors involved in rejecting or accepting the null hypothesis, refer to Section 6.4.

Frequently, the hypothesized value in the null and alternate hypotheses is zero. For example, the weights of twelve rats might be measured before and after the animals are placed on a regimen of forced exercise for one week. The change in weight of the animals (i.e., weight after minus weight before) could be recorded, and it might have been found that the mean weight change was −0.65 g (i.e., the mean weight change is a 0.65 g weight loss). If we wished to infer whether such exercise causes any significant change in rat weight, we could state $H_0: \mu = 0$ and $H_A: \mu \neq 0$; Example 7.2 summarizes the t test for this H_0 and H_A. This test is two tailed, for a large $\overline{X} - \mu$ difference in either direction will constitute grounds for rejecting the veracity of H_0.‡

EXAMPLE 7.2 A Two-Tailed Test for Significant Difference between a Population Mean and a Hypothesized Population Mean of Zero

Weight change of twelve rats after being subjected to a regimen of forced exercise. Each weight change (in g) is the weight after exercise minus the weight before.

1.7	$H_0: \mu = 0$
0.7	$H_A: \mu \neq 0$
−0.4	$\alpha = 0.05$

*David (1995) traces the first use of this term to J. Neyman and E. S. Pearson in 1933.

†Some calculators and many computer programs have the capability of determining the probability of a given t (e.g., see Boomsma and Molenaar, 1994). For the present example, we would thereby find that $P(|t| \geq 2.704) = 0.012$.

‡Data that result from the differences between pairs of data (such as measurements before and after an experimental treatment) are discussed further in Chapter 9.

−1.8
0.2
0.9
−1.2
−0.9
−1.8
−1.4
−1.8
−2.0

$n = 12$

$\overline{X} = -0.65\ \text{g}$

$s^2 = 1.5682\ \text{g}^2$

$$s_{\overline{X}} = \sqrt{\frac{1.5682\ \text{g}^2}{12}} = 0.36\ \text{g}$$

$$t = \frac{\overline{X} - \mu}{s_{\overline{X}}} = \frac{-0.65\ \text{g}}{0.36\ \text{g}} = -1.81$$

$\nu = n - 1 = 11$

$t_{0.05(2),11} = 2.201$

Since $|t| < t_{0.05(2),11}$, do not reject H_0.

$$0.05 < P < 0.10\ [P = 0.098]$$

Therefore, we conclude that the exercise does not cause a weight change in the population from which this sample came.

It should be kept in mind that concluding statistical significance is not the same as determining biological significance. In Example 7.1, statistical significance was achieved for a difference of 0.73°C between the mean crab body temperature (25.03°C) and the air temperature (24.3°C). The statistical question posed is whether that magnitude of difference is likely to occur by chance if the null hypothesis of no difference is true. The answer is that it is unlikely (there is only a 0.012 probability) and, therefore, we conclude that H_0 is not true. Now the biological question is whether a difference of 0.73°C is of significance (with respect to the crabs' physiology, to their ecology, or otherwise). If the sample of body temperatures had a smaller standard error, $s_{\overline{X}}$, an even smaller difference would have been declared statistically significant. But is a difference of, say, 0.1°C or 0.01°C of biological importance (even if it is statistically significant)? In Example 7.2, the mean weight change, 0.36 g, was determined not to be significant statistically. But if the sample mean weight change had been 0.8 g (and the standard error had been the same), t would have been calculated to be 2.222 and H_0 would have been rejected. The statistical conclusion would have been that the exercise regime does result in weight change in rats, but the biological question would then be whether a weight change as small as 0.8 g has significance biologically. Thus, assertion of statistical difference should routinely be followed by an assessment of the significance of that difference to the objects of the study (in these examples, to the crabs or to the rats).

(a) Assumptions. The theoretical basis of t testing assumes that sample data came from a normal population, assuring that the mean at hand came from a normal distribution of means. Fortunately, the t test is *robust*,* meaning that its validity is not seriously affected by moderate deviations from this underlying assumption. The test also assumes—as other statistical tests typically do—that the data are a random sample (see Section 2.3).

The adverse effect of nonnormality is that the probability of a Type I error differs substantially from the stated α. Various studies (e.g., Cicchitelli, 1989; Pearson and Please, 1975; and Ractliffe, 1968) have shown that the detrimental effect of nonnormality is greater for smaller α but less for larger n, that there is little effect if

*The term *robustness* was introduced by G. E. P. Box in 1953 (David, 1995).

the distribution is symmetrical, and that for asymmetric distributions the effect is less with strong leptokurtosis than with platykurtosis or mesokurtosis; and the undesirable effect of nonnormality is much less for two-tailed testing than for one-tailed testing (Section 7.2).

It is important to appreciate that a sample used in statistical testing such as that discussed here must consist of truly replicated data, where a *replicate** is defined as the smallest experimental unit to which a treatment is independently applied. In Example 7.1, we desired to draw conclusions about a population of measurements representing a large number of animals (i.e., crabs). Therefore, the sample must consist of measurements (i.e., body temperatures) from n (i.e., 25) animals; it would *not* be valid to obtain 25 body temperatures from a single animal. And, in Example 7.2, 12 individual rats must be used; it would *not* be valid to employ data obtained from subjecting the same animal to the experiment 12 times. Such invalid attempts at replication are discussed by Hurlbert (1984), who named them *pseudoreplication*.

7.2 ONE-TAILED HYPOTHESES CONCERNING THE MEAN

In Section 7.1, we spoke of the hypotheses $H_0: \mu = \mu_0$ and $H_A: \mu \neq \mu_0$, because we were willing to consider a large deviation of $\overline{X}$ in either direction from μ_0 as grounds for rejecting H_0. However, in some instances, our interest lies only in whether $\overline{X}$ is significantly larger (or significantly smaller) than μ_0, and this is termed a "one-tailed" (or "one-sided") test situation. For example, we might be testing a drug hypothesized to cause weight reduction in humans. The investigator is interested only in whether a weight *loss* occurs after the drug is taken. (In Example 7.2, using a two-sided test, we were interested in determining whether either weight loss or weight gain had occurred.) It is important to appreciate that the decision whether to test one-tailed or two-tailed hypotheses must be based on the scientific question being addressed, *before* data are collected.

In the present example, if there is either weight gain or no weight change, the drug will be considered a failure. Therefore, for this one-sided test, we should state $H_0: \mu \geq 0$ and $H_A: \mu < 0$. Here, the null hypothesis states that there is no mean weight loss (i.e., the mean weight change is greater than or equal to zero), and the alternate hypothesis states that there is a mean weight loss (i.e., the mean weight change is less than zero). By examining the alternate hypothesis, H_A, we see that H_0 will be rejected if t is in the left-hand critical region of the t distribution. In general,

$$\text{for } H_A: \mu < \mu_0,$$
$$\text{if } t \leq -t_{\alpha(1),\nu}, \text{ then reject } H_0.^{\dagger}$$

Example 7.3 summarizes such a set of 12 weight change data tested against this pair of hypotheses. From Appendix Table B.3 we find that $t_{0.05(1),11} = 1.796$, and the critical region for this test is shown in Figure 7.3. From this figure, and by examining Appendix Table B.3, we see that $t_{\alpha(1),\nu} = t_{2\alpha(2),\nu}$ or $t_{\alpha(2),\nu} = t_{\alpha/2(1),\nu}$; that is, for example, the critical value of t for a one-sided test at $\alpha = 0.05$ is the same as the critical value of t for a two-sided test at $\alpha = 0.10$.

*The term *replicate*, in the context of experimental design, was introduced by R. A. Fisher in 1926 (Miller, 2004a).

†For one-tailed testing of this H_0, probabilities of t up to 0.25 are indicated in Appendix Table B.3. If $t = 0$, then $P = 0.50$; so if $-t_{0.25(1),\nu} < t < 0$, then $0.25 < P < 0.50$; and if $t > 0$, then $P > 0.50$.

EXAMPLE 7.3 A One-Tailed t Test for the Hypotheses H_0: $\mu \geq 0$ and H_A: $\mu < 0$

The data are weight changes of humans, tabulated after administration of a drug proposed to result in weight loss. Each weight change (in kg) is the weight after minus the weight before drug administration.

0.2
−0.5
−1.3
−1.6
−0.7
0.4
−0.1
0.0
−0.6
−1.1
−1.2
−0.8

$n = 12$

$\overline{X} = -0.61$ kg

$s^2 = 0.4008\ \text{kg}^2$

$$s_{\overline{X}} = \sqrt{\frac{0.4008\ \text{kg}^2}{12}} = 0.18\ \text{kg}$$

$$t = \frac{\overline{X} - \mu}{s_{\overline{X}}} = \frac{-0.61\ \text{kg}}{0.18\ \text{kg}} = -3.389$$

$\nu = n - 1 = 11$

$t_{0.05(1),11} = 1.796.$

If $t \leq -t_{0.05(1),11}$, reject H_0.

Conclusion: reject H_0.

$$0.0025 < P(t \leq -3.389) < 0.005\ [P = 0.0030]$$

We conclude that the drug does cause weight loss.

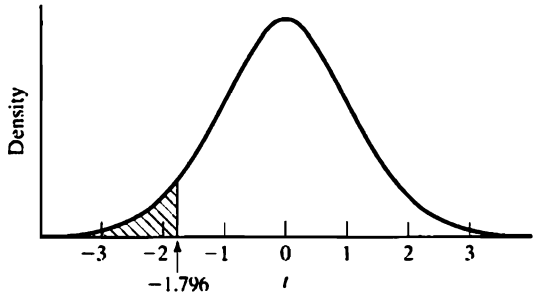


FIGURE 7.3: The distribution of t for $\nu = 11$, showing the critical region (shaded area) for a one-tailed test using $\alpha = 0.05$. (The critical value of t is −1.796.)

If we are interested in whether $\overline{X}$ is significantly *greater* than some value, μ_0, the hypotheses for the one-tailed test are H_0: $\mu \leq \mu_0$ and H_A: $\mu > \mu_0$. For example, a drug manufacturer might advertise that a product dissolves completely in gastric juice within 45 sec. The hypotheses appropriate for testing this claim are H_0: $\mu \leq 45$ sec and H_A: $\mu > 45$ sec, because we are not particularly interested in the possibility that the product dissolves faster than is claimed, but we wish to determine whether its dissolving time is longer than advertised. Thus, the rejection region would be in the right-hand tail, rather than in the left-hand tail (the latter being the case in Example 7.3). The details of such a test are shown in Example 7.4. In general,

for H_A: $\mu > \mu_0$,
if $t \geq t_{\alpha(1),\nu}$, then reject H_0.*

*For this H_0, if $t = 0$, then $P = 0.50$; therefore, if $0 < t < t_{0.25(1),\nu}$, then $0.25 < P < 0.50$, and if $t < 0$, then $P > 0.50$.

EXAMPLE 7.4 The One-Tailed t Test for the Hypotheses H_0: $\mu \leq 45$ sec and H_A: $\mu > 45$ sec

Dissolving times (in sec) of a drug in gastric juice: 42.7, 43.4, 44.6, 45.1, 45.6, 45.9, 46.8, 47.6.

H_0: $\mu \leq 45$ sec
H_A: $\mu > 45$ sec

$\alpha = 0.05$
$n = 8$
$\overline{X} = 45.21$ sec
SS $= 18.8288$ sec^2
$s^2 = 2.6898$ sec^2

$s_{\overline{X}} = 0.58$ sec

$$t = \frac{45.21 \text{ sec} - 45 \text{ sec}}{0.58 \text{ sec}} = 0.36$$

$\nu = 7$

$t_{0.05(1),7} = 1.895$

If $t \geq t_{0.05(1),7}$, reject H_0.

Conclusion: do not reject H_0.

$$P(t \geq 0.36) > 0.25 \; [P = 0.36]$$

We conclude that the mean dissolving time is not greater than 45 sec.

7.3 CONFIDENCE LIMITS FOR THE POPULATION MEAN

When Section 7.1 defined $t = (\overline{X} - \mu)/s_{\overline{X}}$, it was explained that 5% of all possible means from a normally distributed population with mean μ will yield t values that are either larger than $t_{0.05(2),\nu}$ or smaller than $-t_{0.05(2),\nu}$; that is, $|t| \geq t_{0.05(2),\nu}$ for 5% of the means. This connotes that 95% of all t values obtainable lie between the limits of $-t_{0.05(2),\nu}$ and $t_{0.05(2),\nu}$; this may be expressed as

$$P\left[-t_{0.05(2),\nu} \leq \frac{\overline{X} - \mu}{s_{\overline{X}}} \leq t_{0.05(2),\nu}\right] = 0.95. \tag{7.3}$$

It follows from this that

$$P[\overline{X} - t_{0.05(2),\nu}\, s_{\overline{X}} \leq \mu \leq \overline{X} + t_{0.05(2),\nu}\, s_{\overline{X}}] = 0.95. \tag{7.4}$$

The value of the population mean, μ, is not known, but we estimate it as $\overline{X}$, and if we apply Equation 7.4 to many samples from this population, for 95% of the samples the interval between $\overline{X} - t_{0.05(2),\nu}s_{\overline{X}}$ and $\overline{X} + t_{0.05(2),\nu}s_{\overline{X}}$ will include μ. As introduced in Section 6.4, this interval is called the *confidence interval* (abbreviated CI) for μ.

In general, the confidence interval for μ can be stated as

$$P[\overline{X} - t_{\alpha(2),\nu}\, s_{\overline{X}} \leq \mu \leq \overline{X} + t_{\alpha(2),\nu}\, s_{\overline{X}}] = 1 - \alpha. \tag{7.5}$$

As defined in Section 6.4, $\overline{X} - t_{\alpha(2),\nu}\, s_{\overline{X}}$ is called the *lower confidence limit* (abbreviated L_1); and $\overline{X} + t_{\alpha(2),\nu}\, s_{\overline{X}}$ is the *upper confidence limit* (abbreviated L_2); and the two confidence limits can be stated as

$$\overline{X} \pm t_{\alpha(2),\nu}\, s_{\overline{X}} \tag{7.6}$$

(reading "±" to be "plus or minus"). In expressing a confidence interval, we call the quantity $1 - \alpha$ (namely, $1 - 0.05 = 0.95$ in the present example)

the *confidence level* (or the *confidence coefficient*, or the *confidence probability*).*

Although $\overline{X}$ is the best estimate of μ, it is only an estimate (and not necessarily a very good one), and the calculation of the confidence interval for μ provides an expression of the precision of the estimate. Example 7.5, part (a), refers to the data of Example 7.1 and demonstrates the determination of the 95% confidence interval for the mean of the population from which the sample came. As the 95% confidence limits are computed to be $L_1 = 24.47°C$ and $L_2 = 25.59°C$, the 95% confidence interval may be expressed as $P(24.47°C \leq \mu \leq 25.59°C)$. The meaning of this kind of statement is commonly expressed in nonprobabilistic terms as having 95% *confidence* that the interval of 24.47°C to 25.59°C contains μ. This does *not* mean that there is a 95% *probability* that the interval constructed from this one sample contains the population mean, μ; but it does mean that 95% of the confidence limits computed for many independent random samples would bracket μ (or, this could be stated as the probability that the confidence interval from a future sample would contain μ). And, if the μ_0 in H_0 and H_A is within the confidence interval, then H_0 will not be rejected.

EXAMPLE 7.5 Computation of Confidence Intervals and Confidence Limits for the Mean, Using the Data of Example 7.1

(a) At the 95% confidence level:

$\overline{X} = 25.03°C$

$s_{\overline{X}} = 0.27°C$

$t_{0.05(2),24} = 2.064$

$\nu = 24$

$$\begin{aligned} 95\%\text{ confidence interval} &= \overline{X} \pm t_{0.05(2),24}\, s_{\overline{X}} \\ &= 25.03°C \pm (2.064)(0.27°C) \\ &= 25.03°C \pm 0.56°C \end{aligned}$$

$$\begin{aligned} 95\%\text{ confidence limits: } L_1 &= 25.03°C - 0.56°C = 24.47°C \\ L_2 &= 25.03°C + 0.56°C = 25.59°C \end{aligned}$$

(b) At the 99% confidence level:

$t_{0.01(2),24} = 2.797$

$$\begin{aligned} 99\%\text{ confidence interval} &= \overline{X} \pm t_{0.01(2),24}\, s_{\overline{X}} \\ &= 25.03° \pm (2.797)(0.27°C) \\ &= 25.03°C \pm 0.76°C \end{aligned}$$

$$\begin{aligned} 99\%\text{ confidence limits: } L_1 &= 25.03°C - 0.76°C = 24.27°C \\ L_2 &= 25.03°C + 0.76°C = 25.79°C \end{aligned}$$

In both parts (a) and (b), the hypothesized value, $\mu_0 = 24.3°C$ in Example 7.1, lies outside the confidence intervals. This indicates that H_0 would be rejected using either the 5% or the 1% level of significance.

*We owe the development of confidence intervals to Jerzy Neyman, between 1928 and 1933 (Wang, 2000), although the concept had been enunciated a hundred years before. Neyman introduced the terms *confidence interval* and *confidence coefficient* in 1934 (David, 1995). On rare occasion, the biologist may see reference to "fiducial intervals," a concept developed by R. A. Fisher beginning in 1930 and identical to confidence intervals in some, but not all, situations (Pfanzagl, 1978).

The smaller $s_{\overline{Y}}$ is, the smaller will be the confidence interval, meaning that μ is estimated more precisely when $s_{\overline{Y}}$ is small. Also, it can be observed from the calculation of $s_{\overline{Y}}$ (see Equation 6.8) that a large n will result in a small $s_{\overline{Y}}$ and, therefore, a narrower confidence interval. As introduced in Section 6.4, a parameter estimate from a large sample is generally more precise that an estimate of the same parameter from a small sample.

Setting confidence limits around μ has the same underlying assumptions as the testing of hypotheses about μ (Section 7.1a), and violating those assumptions can invalidate the stated level of confidence $(1 - \alpha)$.

If, instead of a 95% confidence interval, it is desired to state a higher level of confidence, say 99%, that L_1 and L_2 encompass the population mean, then $t_{0.01(1),24}$ rather than $t_{0.01(2),24}$ would be employed. From Appendix Table B.3 we find that $t_{0.01(1),24} = 2.797$, so the 99% confidence interval would be calculated as shown in Example 7.5, part (b), where it is determined that $P(24.27^\circ\text{C} \leq \mu \leq 25.79^\circ\text{C}) = 0.99$.

(a) One-Tailed Confidence Limits. As introduced in Section 6.4(a), one-tailed confidence intervals are appropriate in situations that warrant one-tailed hypothesis tests. Such a confidence interval employs a one-tailed critical value of t (i.e., $t_{\alpha(1),\nu}$) instead of a two-tailed critical value ($t_{\alpha(2),\nu}$). For H_0: $\mu \leq \mu_0$ and H_A: $\mu > \mu_0$, the confidence limits for μ are $L_1 = \overline{Y} - t_{\alpha(1),\nu} s_{\overline{Y}}$ and $L_2 = \infty$; and for H_0: $\mu \geq \mu_0$ and H_A: $\mu < \mu_0$, the confidence limits are $L_1 = -\infty$ and $L_2 = \overline{Y} + t_{\alpha(1),\nu} s_{\overline{Y}}$. For the situation in Example 7.4, in which H_0: $\mu \leq 45$ sec and H_A: $\mu > 45$ sec, L_1 would be 45.21 sec − (1.895)(0.58 sec) = 45.21 sec − 1.10 sec = 44.11 and $L_2 = \infty$. And the hypothesized μ_0 (45 sec) lies within the confidence interval, indicating that the null hypothesis is not rejected.

(b) Prediction Limits. While confidence limits express the precision with which a population characteristic is estimated, we can also indicate the precision with which future observations from this population can be predicted.

After calculating $\overline{Y}$ and s^2 from a random sample of n data from a population, we can ask what the mean would be from an additional random sample, of an additional m data, from the same population. The best estimate of the mean of those m additional data would be $\overline{Y}$, and the precision of that estimate may be expressed by this two-tailed *prediction interval* (abbreviated PI):

$$\overline{Y} \pm t_{\alpha(2),\nu} \sqrt{\frac{s^2}{m} + \frac{s^2}{n}}, \tag{7.7}$$

where $\nu = n - 1$ (Hahn and Meeker, 1991: 61–62). If the desire is to predict the value of one additional datum from that population (i.e., $m = 1$), then Equation 7.7 becomes

$$\overline{Y} \pm t_{\alpha(2),\nu} \sqrt{s^2 + \frac{s^2}{n}}. \tag{7.8}$$

The prediction interval will be wider than the confidence interval and will approach the confidence interval as m becomes very large. The use of Equations 7.7 and 7.8 is demonstrated in Example 7.6.

One-tailed prediction intervals are not commonly obtained but are presented in Hahn and Meeker (1991: 63), who also consider another kind of interval: the

tolerance interval, which may be calculated to contain at least a specified proportion (e.g., a specified percentile) of the sampled population; and in Patel (1989), who also discusses simultaneous prediction intervals of means from more than one future sample. The procedure is very much like that of Section 7.3a. If the desire is to obtain only a lower prediction limit, L_1 (while L_2 is considered to be ∞), then the first portion of Equation 7.7 (or 7.8) would be modified to be $\overline{X} - t_{\alpha(1),\nu}$ (i.e., the one-tailed t would be used); and if the intent is to express only an upper prediction limit, L_2 (while regarding L_1 to be $-\infty$), then we would use $\overline{X} + t_{\alpha(1),\nu}$. As an example, Example 7.6 might have asked what the highest mean body temperature is that would be predicted, with probability α, from an additional sample. This would involve calculating L_2 as indicated above, while $L_1 = -\infty$.

EXAMPLE 7.6 Prediction Limits for Additional Sampling from the Population Sampled in Example 7.1

From Example 7.1, which is a sample of 25 crab body temperatures,

$$n = 25,\ \overline{X} = 25.03°\text{C, and } s^2 = 1.80(°\text{C})^2.$$

(a) If we intend to collect 8 additional crab body temperatures from the same population from which the 25 data in Example 7.1 came, then (by Equation 7.7) we can be 95% confident that the mean of those 8 data will be within this prediction interval:

$$\begin{aligned} 25.03°\text{C} \pm t_{0.05(2),24}\sqrt{\frac{1.80(°\text{C})^2}{8} + \frac{1.80(°\text{C})^2}{2}} &= 25.03°\text{C} \pm 2.064(0.545°\text{C}) \\ &= 25.03°\text{C} \pm 1.12°\text{C}. \end{aligned}$$

Therefore, the 95% prediction limits for the predicted mean of these additional data are $L_1 = 23.91°\text{C}$ and $L_2 = 26.15°\text{C}$.

(b) If we intend to collect 1 additional crab body temperature from the same population from which the 25 data in Example 7.1 came, then (by Equation 7.8) we can be 95% confident that the additional datum will be within this prediction interval:

$$\begin{aligned} 25.03°\text{C} \pm t_{0.05(2),24}\sqrt{1.80(°\text{C})^2 + \frac{1.80(°\text{C})^2}{2}} &= 25.03°\text{C} \pm 2.064(1.368°\text{C}) \\ &= 25.03°\text{C} \pm 2.82°\text{C}. \end{aligned}$$

Therefore, the 95% prediction limits for this predicted datum are $L_1 = 22.21°\text{C}$ and $L_2 = 27.85°\text{C}$.

7.4 REPORTING VARIABILITY AROUND THE MEAN

It is very important to provide the reader of a research paper with information concerning the variability of the data reported. But authors of such papers are often unsure of appropriate ways of doing so, and not infrequently do so improperly.

If we wish to describe the population that has been sampled, then the sample mean ($\overline{X}$) and the standard deviation (s) may be reported. The range might also be reported, but in general it should not be stated without being accompanied by another measure of variability, such as s. Such statistics are frequently presented as in Table 7.1 or 7.2.

TABLE 7.1: Tail Lengths (in mm) of Field Mice from Different Localities

Location	n	$\overline{X} \pm$ SD (range in parentheses)
Bedford, Indiana	18	56.22 ± 1.33 (44.8 to 68.9)
Rochester, Minnesota	12	59.61 ± 0.82 (43.9 to 69.8)
Fairfield, Iowa	16	60.20 ± 0.92 (52.4 to 69.2)
Pratt, Kansas	16	53.93 ± 1.24 (46.1 to 63.6)
Mount Pleasant, Michigan	13	55.85 ± 0.90 (46.7 to 64.8)

TABLE 7.2: Evaporative Water Loss of a Small Mammal at Various Air Temperatures. Sample Statistics Are Mean ± Standard Deviation, with Range in Parentheses

	Air Temperature (°C)				
	16.2	24.8	30.7	36.8	40.9
Sample size	10	13	10	8	9
Evaporative water loss (mg/g/hr)	0.611 ± 0.164 (0.49 to 0.88)	0.643 ± 0.194 (0.38 to 1.13)	0.890 ± 0.212 (0.64 to 1.39)	1.981 ± 0.230 (1.50 to 2.36)	3.762 ± 0.641 (3.16 to 5.35)

If it is the author's intention to provide the reader with a statement about the precision of estimation of the population mean, the use of the standard error ($s_{\overline{X}}$) is appropriate. A typical presentation is shown in Table 7.3a. This table might instead be set up to show confidence intervals, rather than standard errors, as shown in Table 7.3b. The standard error is always smaller than the standard deviation. But this is not a reason to report the former in preference to the latter. The determination should be made on the basis of whether the desire is to describe variability within the population or precision of estimating the population mean.

There are three very important points to note about Tables 7.1, 7.2, 7.3a, and 7.3b. First, n should be stated somewhere in the table, either in the caption or in the body of the table. (Thus, the reader has the needed information to convert from SD to SE or from SE to SD, if so desired.) One should always state n when presenting sample statistics ($\overline{X}$, s, $s_{\overline{X}}$, range, etc.), and if a tabular presentation is prepared, it is very good practice to include n somewhere in the table, even if it is mentioned elsewhere in the paper.

Second, the measure of variability is clearly indicated. Not infrequently, an author will state something such as "the mean is 54.2 ± 2.7 g," with no explanation of what "± 2.7" denotes. This renders the statement worthless to the reader, because "± 2.7" will be assumed by some to indicate ± SD, by others to indicate ± SE, by others to

TABLE 7.3a: Enzyme Activities in the Muscle of Various Animals. Data Are $\bar{X} \pm$ SE, with n in Parentheses

	Enzyme Activity (μmole/min/g of tissue)	
Animal	Isomerase	Transketolase
Mouse	0.76 ± 0.09 (4)	0.39 ± 0.04 (4)
Frog	1.53 ± 0.08 (4)	0.18 ± 0.02 (4)
Trout	1.06 ± 0.12 (4)	0.24 ± 0.04 (4)
Crayfish	4.22 ± 0.30 (4)	0.26 ± 0.05 (4)

TABLE 7.3b: Enzyme Activities in the Muscle of Various Animals. Data Are $\bar{X} \pm$ 95% Confidence Limits

		Enzyme Activity (μmole/min/g of tissue)	
Animal	n	Isomerase	Transketolase
Mouse	4	0.76 ± 0.28	0.39 ± 0.13
Frog	4	1.53 ± 0.25	0.18 ± 0.05
Trout	4	1.06 ± 0.38	0.24 ± 0.11
Crayfish	4	4.22 ± 0.98	0.26 ± 0.15

indicate the 95% (or 99%, or other) confidence interval, and by others to indicate the range.* There is no widely accepted convention; one *must* state explicitly what quantity is meant by this type of statement. If such statements of '±" values appear in a table, then the explanation is best included somewhere in the table (either in the caption or in the body of the table), even if it is stated elsewhere in the paper.

Third, the units of measurement of the variable must be clear. There is little information conveyed by stating that the tail lengths of 24 birds have a mean of 8.42 and a standard error of 0.86 if the reader does not know whether the tail lengths were measured in centimeters, or inches, or some other unit. Whenever data appear in tables, the units of measurement should be stated somewhere in the table. Keep in mind that a table should be self-explanatory; one should not have to refer back and forth between the table and the text to determine what the tabled values represent.

Frequently, the types of information given in Tables 7.1, 7.2, 7.3a, and 7.3b are presented in graphs, rather than in tables. In such cases, the measurement scale is typically indicated on the vertical axis, and the mean is indicated in the body of the graph by a short horizontal line or some other symbol. The standard deviation, standard error, or a confidence interval for the mean is commonly indicated on such graphs via a vertical line or rectangle. Often the range is also included, and in such instances the SD or SE may be indicated by a vertical rectangle and the range by a vertical line. Some authors will indicate a confidence interval (generally 95%) in

*In older literature the ± symbol referred to yet another measure, known as the "probable error" (which fell into disuse in the early twentieth century). In a normal curve, the probable error (PE) is 0.6745 times the standard error, because $\bar{X} \pm$ PE includes 50% of the distribution. The term *probable error* was first used in 1815 by German astronomer Friedrich Wilhelm Bessel (1784–1846) (Walker, 1929: 24, 51, 186).

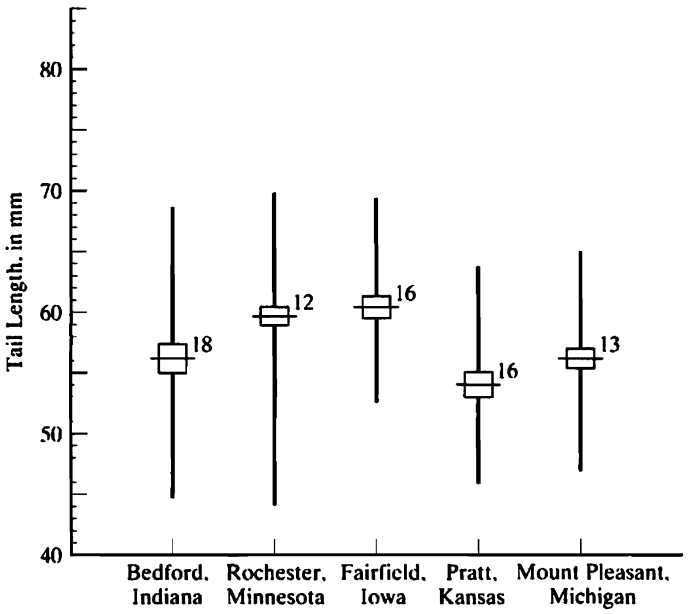


FIGURE 7.4: Tail lengths of male field mice from different localities, indicating the mean, the mean ± standard deviation (vertical rectangle), and the range (vertical line), with the sample size indicated for each location. The data are from Table 7.1.

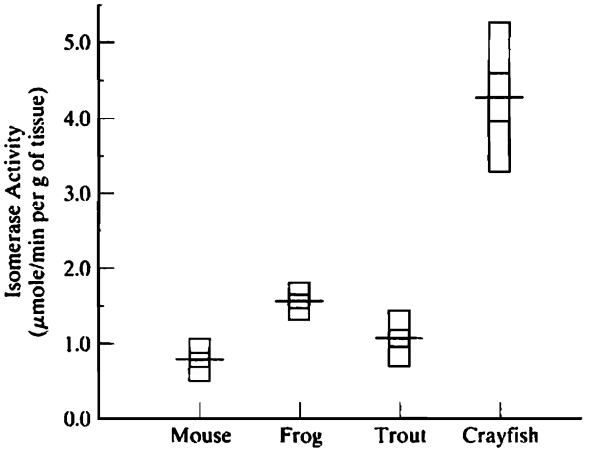


FIGURE 7.5: Levels of muscle isomerase in various animals. Shown is the mean ± standard error (shaded rectangle), and ± the 95% confidence interval (open rectangle). For each sample, $n = 4$. The data are from Tables 7.3a and 7.3b.

addition to the range and either SD or SE. Figures 7.4, 7.5, and 7.6 demonstrate how various combinations of these statistics may be presented graphically.

Instead of the mean and a measure of variability based on the variance, one may present tabular or graphical descriptions of samples using the median and quartiles (e.g., McGill, Tukey, and Larsen, 1978), or the median and its confidence interval. Thus, a graphical presentation such as in Figure 7.4 could have the range indicated by the vertical line, the median by the horizontal line, and the semiquartile range (Section 4.2) by the vertical rectangle. Such a graph is discussed in Section 7.5. Note that when the horizontal axis on the graph represents an interval or ratio scale

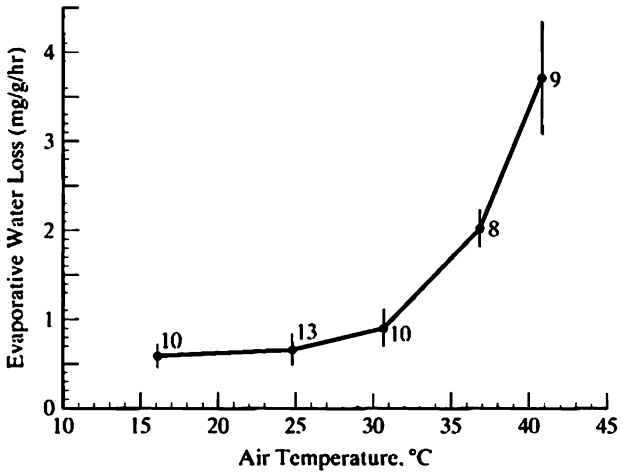


FIGURE 7.6: Evaporative water loss of a small mammal at various air temperatures. Shown at each temperature is the mean ± the standard deviation, and the sample size. The data are from Table 7.2.

variable (as in Figure 7.6), adjacent means may be connected by straight lines to aid in the recognition of trends.

In graphical presentation of data, as in tabular presentation, care must be taken to indicate clearly the following either on the graph or in the caption: The sample size (n), the units of measurement, and what measures of variability (if any) are indicated (e.g., SD, SE, range, 95% confidence interval).

Some authors present $\overline{X} \pm 2s_{\overline{X}}$ in their graphs. An examination of the t table (Appendix Table B.3) will show that, except for small samples, this expression will approximate the 95% confidence interval for the mean. But for small samples, the true confidence interval is, in fact, greater than $\overline{X} \pm 2s_{\overline{X}}$. Thus, the general use of this expression is not to be encouraged, and the calculation of the accurate confidence interval is the wiser practice.

A word of caution is in order for those who determine confidence limits, or SDs or SEs, for two or more means and, by observing whether or not the limits overlap, attempt to determine whether there are differences among the population means. Such a procedure is not generally valid (see Section 8.2); The proper methods for testing for differences between means are discussed in the next several chapters.

7.5 REPORTING VARIABILITY AROUND THE MEDIAN

The median and the lower and upper quartiles (Q_1 and Q_3) form the basis of a graphical presentation that conveys a rapid sense of the middle, the spread, and the symmetry of a set of data. As shown in Figure 7.7, a vertical box is drawn with its bottom at Q_1 and top at Q_3, meaning that the height of the box is the semi-quartile range (Q_3-Q_1). Then, the median is indicated by a horizontal line across the box. Next, a vertical line is extended from the bottom of the box to the smallest datum that is no farther from the box than 1.5 times the interquartile range; and a vertical line is drawn from the top of the box to the largest datum that is no farther from the box than 1.5 times the interquartile range. These two vertical lines, below and above the box, are termed "whiskers," so this graphical representation is called a *box plot* or *box-and-whiskers plot.** If any data are so deviant as to lie beyond the whiskers, they

*The term *box plot* was introduced by John W. Tukey in 1970 (David, 1995).

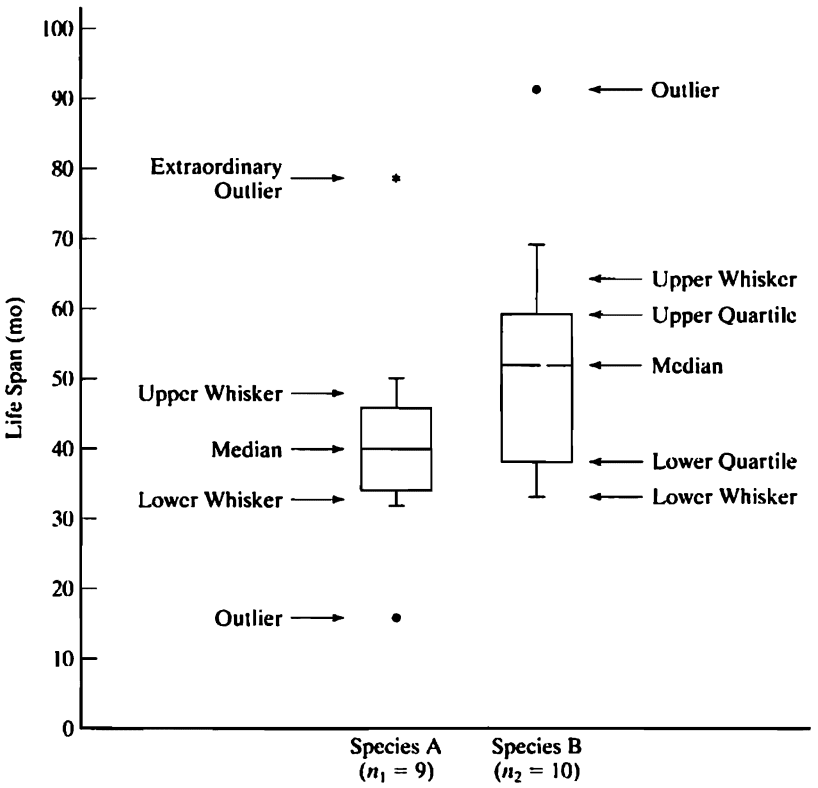


FIGURE 7.7: Box plots for the data of Example 3.3. (The wording with arrows is for instructional purposes and would not otherwise appear in such a graph.)

are termed *outliers* and are placed individually as small circles on the graph. If any are so aberrant as to lie at least 3 times the interquartile range from the box (let's call them "extraordinary outliers"), they may be placed on the graph with a distinctive symbol (such as "*") instead of a circle.* In addition, the size of the data set (n) should be indicated, either near the box plot itself or in the caption accompanying the plot.

Figure 7.7 presents a box plot for the two samples in Example 3.3. For species A, the median = 40 mo, $Q_1 = Q_{10/4} = X_{2.5} = 34.5$ mo, and $Q_3 = X_{10-2.5} = X_{7.5} = 46$ mo. The interquartile range is 46 mo − 34.5 mo = 11.5 mo, so 1.5 times the interquartile range is (1.5)(11.5 mo) = 17.25 mo, and 3 times the interquartile range is (3)(11.5) = 34.5 mo. Therefore, the upper whisker extends from the top of the box up to the largest datum that does not exceed 46 mo + 17.25 mo = 63.25 mo (and that datum is $X_8 = 50$ mo), and the lower whisker extends from the bottom of the box down to the smallest datum that is no smaller than 34.5 mo − 17.25 mo = 17.25 mo (namely, $X_2 = 32$ mo). Two of the data, $X_1 = 16$ mo and $X_9 = 79$ mo, lie farther from the box than the whiskers; thus they are outliers and, as X_9 lies more than 3 times the interquartile range from the box (i.e., is more than 34.5 mo greater than Q_3), it is an extraordinary outlier. Therefore, X_1 is indicated with a circle below the box and X_9 is denoted with a "*" above the box.

*The vertical distances above and below the box by an amount 1.5 times the interquartile range are sometimes called *inner fences*, with those using the factor of 3 being called *outer fences*. Also, the top (Q_3) and bottom (Q_1) of the box are sometimes called the *hinges* of the plot.

For species B, the median = 52 mo, $Q_1 = Q_{11/4} = Q_{2.75}$, which is rounded up to Q_1 = 38 mo, and $Q_3 = X_{11-3} = X_8$ = 59 mo. The interquartile range is 59 mo − 38 mo = 21 mo, so (1.5)(21 mo) = 31.5 mo and (3)(21 mo) = 63 mo. Thus, the upper whisker extends from the box up to the largest datum that does not exceed 59 mo + 21 mo = 80 mo (namely, X_9 = 69 mo), and the lower whisker extends from the box down to the smallest datum that is no smaller than 38 mo − 21 mo = 17 mo (namely, X_1 = 34 mo). As only X_{10} = 91 lies farther from the box than the whiskers, it is the only outlier in the sample of data for species B; it is not an extraordinary outlier because it is not (3)(21 mo), namely 63 mo, above the box.

Box plots are especially useful in visually comparing two or more sets of data. In Figure 7.7, we can quickly discern from the horizontal lines representing the medians that, compared to species A, species B has a greater median life span; and, as the box for species B is larger, that species' sample displays greater variability in life spans. Furthermore, it can be observed that species B has its median farther from the middle of the box, and an upper whisker much longer than the lower whisker, indicating that the distribution of life spans for this species is more skewed toward longer life than is the distribution for species A.

David (1995) attributes the 1970 introduction of box plots to J. W. Tukey, and the capability to produce such graphs appears in many computer software packages. Some authors and some statistical software have used multiplication factors other than 1.5 and 3 to define outliers, some have proposed modifications of box plots to provide additional information (e.g., making the width of each box proportional to the number of data, or to the square root of that number), and some employ quartile determination different from that in Section 4.2. Indeed, Frigge, Hoaglin, and Iglewicz (1989) report that, although common statistical software packages only rarely define the median (Q_2) differently than that presented in Section 3.2, they identified eight ways Q_1 and Q_3 are calculated in various packages. Unfortunately, the different presentations of box plots provide different impressions of the data, and some of the methods of expressing quartiles are not recommended by the latter authors.

7.6 SAMPLE SIZE AND ESTIMATION OF THE POPULATION MEAN

A commonly asked question is, "How large a sample must be taken to achieve a desired precision* in estimating the mean of a population?" The answer is related to the concept of a confidence interval, for a confidence interval expresses the precision of a sample statistic, and the precision increases (i.e., the confidence interval becomes narrower) as the sample size increases.

Let us write Equation 7.6 as $\overline{X} \pm d$, which is to say that $d = t_{\alpha(2),\nu} s_{\overline{X}}$. We shall refer to d as the half-width of the confidence interval, which means that μ is estimated to within $\pm d$. Now, the number of data we must collect to calculate a confidence interval of specified width depends upon: (1) the width desired (for a narrower confidence interval—i.e., more precision in estimating μ—requires a larger sample; (2) the variability in the population (which is estimated by s^2, and larger variability requires larger sample size); and (3) the confidence level specified (for greater confidence—e.g., 99% vs. 95%—requires a larger sample size).

*Recall from Section 2.4 that the precision of a sample statistic is the closeness with which it estimates the population parameter; it is not to be confused with the concept of the precision of a measurement (defined in Section 1.2), which is the nearness of repeated measurements to each

If we have a sample estimate (s^2) of the variance of a normal population, then we can estimate the required sample size for a future sample as

$$n = \frac{s^2 t^2_{\alpha(2),\nu}}{d^2}. \tag{7.9}$$

In this equation, s^2 is the sample variance, estimated with $\nu = n - 1$ degrees of freedom, d is the half-width of the desired confidence interval, and $1 - \alpha$ is the confidence level for the confidence interval. Two-tailed critical values of Student's t, with $\nu = n - 1$ degrees of freedom, are found in Appendix Table B.3.

There is a basic difficulty in solving Equation 7.9, however; the value of $t_{\alpha(2),(n-1)}$ depends upon n, the unknown sample size. The solution may be achieved by iteration—a process of trial and error with progressively more accurate approximations—as shown in Example 7.7. We begin the iterative process of estimation with an initial guess; the closer this initial guess is to the finally determined n, the faster we shall arrive at the final estimate. Fortunately, the procedure works well even if this initial guess is far from the final n (although the process is faster if it is a high, rather than a low, guess).

The reliability of this estimate of n depends upon the accuracy of s^2 as an estimate of the population variance, σ^2. As its accuracy improves with larger samples, one should use s^2 obtained from a sample with a size that is not a very small fraction of the n calculated from Equation 7.9.

EXAMPLE 7.7 Determination of Sample Size Needed to Achieve a Stated Precision in Estimating a Population Mean, Using the Data of Example 7.3

If we specify that we wish to estimate μ with a 95% confidence interval no wider than 0.5 kg, then $d = 0.25$ kg, $1 - \alpha = 0.95$, and $\alpha = 0.05$. From Example 7.3 we have an estimate of the population variance: $s^2 = 0.4008\ \text{kg}^2$.

Let us guess that a sample of 40 is necessary; then,

$$t_{0.05(2),39} = 2.023.$$

So we estimate (by Equation 7.7):

$$n = \frac{(0.4008)(2.023)^2}{(0.25)^2} = 26.2.$$

Next, we might estimate $n = 27$, for which $t_{0.05(2),26} = 2.056$, and we calculate

$$n = \frac{(0.4008)(2.056)^2}{(0.25)^2} = 27.1.$$

Therefore, we conclude that a sample size greater than 27 is required to achieve the specified confidence interval.

7.7 SAMPLE SIZE, DETECTABLE DIFFERENCE, AND POWER IN TESTS CONCERNING THE MEAN

(a) Sample Size Required. If we are to perform a one-sample test as described in Section 7.1 or 7.2, then it is desirable to know how many data should be collected

to detect a specified difference with a specified power. An estimate of the minimum sample size (n) required will depend upon σ^2, the population variance (which can be estimated by s_p^2 from previous similar studies). The beginning of Section 8.4 lists considerations (based upon Lenth, 2001) relevant to the determination of sample size.

We may specify that we wish to perform a t test with a probability of α of committing a Type I error and a probability of β of committing a Type II error; and we can state that we want to be able to detect a difference between μ and μ_0 as small as δ (where μ is the actual population mean and μ_0 is the mean specified in the null hypothesis).* To test at the α significance level with $1 - \beta$ power, the minimum sample size required to detect δ is

$$n = \frac{s^2}{\delta^2}(t_{\alpha,\nu} + t_{\beta(1),\nu})^2, \tag{7.10}$$

where α can be either $\alpha(1)$ or $\alpha(2)$, respectively, depending on whether a one-tailed or two-tailed test is to be used. However, ν depends on n, so n cannot be calculated directly but must be obtained by iteration† (i.e., by a series of estimations, each estimation coming closer to the answer than that preceding). This is demonstrated in Example 7.8.

Equation 7.10 provides better estimates of n when s^2 is a good estimate of the population variance, σ^2, and the latter estimate improves when s^2 is calculated from larger samples. Therefore, it is most desirable that s^2 be obtained from a sample with a size that is not a small fraction of the estimate of n; and it can then be estimated how large an n is needed to repeat the experiment and use the resulting data to test with the designated α, β, and δ.

EXAMPLE 7.8 Estimation of Required Sample Size to Test H_0: $\mu = \mu_0$

How large a sample is needed to reject the null hypothesis of Example 7.2 when sampling from the population in that example? We wish to test at the 0.05 level of significance with a 90% chance of detecting a population mean different from $\mu_0 = 0$ by as little as 1.0 g. In Example 7.2, $s^2 = 1.5682\ \text{g}^2$.

Let us guess that a sample size of 20 would be required. Then, $\nu = 19$, $t_{0.05(2),19} = 2.093$, $\beta = 1 - 0.90 = 0.10$, $t_{0.10(1),19} = 1.328$, and we use Equation 7.8 to calculate

$$n = \frac{1.5682}{(1.0)^2}(2.093 + 1.328)^2 = 18.4.$$

We now use $n = 19$ as an estimate, in which case $\nu = 18$, $t_{0.05(2),18} = 2.101$, $t_{0.10(1),18} = 1.330$, and

$$n = \frac{1.5682}{(1.0)^2}(2.101 + 1.330)^2 = 18.5.$$

Thus, we conclude that a new sample of at least 19 data may be taken from this population to test the above hypotheses with the specified α, β, and δ.

*δ is lowercase Greek delta.

†If the population variance, σ^2, were actually known (a most unlikely situation), rather than estimated by s^2, then Z_α would be substituted for t_α in this and the other computations in this section, and n would be determined in one step instead of iteratively.

(b) Minimum Detectable Difference. By rearranging Equation 7.10, we can ask how small a δ (the difference between μ and μ_0) can be detected by the t test with $1 - \beta$ power, at the α level of significance, using a sample of specified size n:

$$\delta = \sqrt{\frac{s^2}{n}}\left(t_{\alpha,\nu} + t_{\beta(1),\nu}\right), \tag{7.11}$$

where $t_{\alpha,\nu}$ can be either $t_{\alpha(1),\nu}$ or $t_{\alpha(2),\nu}$, depending on whether a one-tailed or two-tailed test is to be performed. The estimation of δ is demonstrated in Example 7.9. Some literature (e.g., Cohen, 1988: 811–814) refers to the "effect size," a concept similar to minimum detectable difference.

EXAMPLE 7.9 Estimation of Minimum Detectable Difference in a One-Sample t Test for H_0: $\mu = \mu_0$

In the two-tailed test of Example 7.2, what is the smallest difference (i.e., difference between μ and μ_0) that is detectable 90% of the time using a sample of 25 data and a significance level of 0.05?

Using Equation 7.9:

$$\begin{aligned}\delta &= \sqrt{\frac{1.5682}{25}}\left(t_{0.05(2),24} + t_{0.10(1),24}\right)\\ &= (0.25)(2.064 + 1.318)\\ &= 0.85 \text{ g.}\end{aligned}$$

(c) Power of One-Sample Testing. If our desire is to express the probability of correctly rejecting a false H_0 about μ, then we seek to estimate the power of a t test. Equation 7.10 can be rearranged to give

$$t_{\beta(1),\nu} = \frac{\delta}{\sqrt{\frac{s^2}{n}}} - t_{\alpha,\nu}, \tag{7.12}$$

where α refers to either $\alpha(2)$ or $\alpha(1)$, depending upon whether the null hypothesis to be tested is two-tailed or one-tailed, respectively. As shown in Example 7.10, for a stipulated δ, α, s^2, and sample size, we can express $t_{\beta(1),\nu}$. Consulting Appendix Table B.3 allows us to convert $t_{\beta(1),\nu}$ to β, but only roughly (e.g., $\beta > 0.25$ in Example 7.10). However, $t_{\beta(1),\nu}$ may be considered to be approximated by $Z_{\beta(1)}$, so Appendix Table B.2 may be used to determine β.* Then, the power of the test is expected to be $1 - \beta$, as shown in Example 7.10. Note that this is the estimated power of a test to be run on a new sample of data from this population, *not* the power of the test performed in Example 7.2.

*Some calculators and computer programs yield β given $t_{\beta,\nu}$. Approximating $t_{\beta(1),\nu}$ by $Z_{\beta(1)}$ apparently yields a β that is an underestimate (and a power that is an overestimate) of no more than 0.01 for ν of at least 11 and no more than 0.02 for ν of at least 7.

EXAMPLE 7.10 Estimation of the Power of a One-Sample *t* Test for H_0: $\mu = \mu_0$

What is the probability of detecting a true difference (i.e., a difference between μ and μ_0) of at least 1.0 g, using $\alpha = 0.05$ for the hypotheses of Example 7.2, if we run the experiment again using a sample of 15 from the same population?

For $n = 15$, $\nu = 14$; $\alpha = 0.05$, $t_{0.05(2),14} = 2.145$, $s^2 = 1.5682\ \text{g}^2$, and $\delta = 1.0$ g; and we use Equation 7.12 to find

$$t_{\beta(1),14} = \frac{1.0}{\sqrt{\frac{1.5682\ \text{g}^2}{15}}} - 2.145$$
$$= 0.948.$$

Consulting Appendix Table B.3 tells us that, for $t_{\beta(1),14} = 0.948$, $0.10 < \beta < 0.25$, so we can say that the power would be $0.75 < 1 - \beta < 0.90$. Alternatively, by considering 0.948 to be a normal deviate and consulting Appendix Table B.2, we conclude that $\beta = 0.17$ and that the power of the test is $1 - \beta = 0.83$. (The exact probabilities, by computer, are $\beta = 0.18$ and power = 0.82.)

When the concept of power was introduced in the discussion "Statistical Errors in Hypothesis Testing" in Section 6.4, it was stated that, for a given sample size (n), α is inversely related to β; that is, the lower the probability of committing a Type I error, the greater the probability of committing a Type II error. It was also noted that α and β can be lowered simultaneously by increasing n. Power is also greater for one-tailed than for two-tailed tests, but recall (from the end of Section 6.4 and from Section 7.2) that power is *not* the criterion for performing a one-tailed instead of a two-tailed test. These relationships are shown in Table 7.4. Table 7.5 shows how power is related to n, s^2, and δ. It can be seen that, for a given s^2 and δ, an increased sample size (n) results in an increase in power. Also, for a given n and δ, power increases as s^2 decreases, so a smaller variability among the data yields greater power. And for a given n and s^2, power increases as δ increases, meaning there is greater power in detecting large differences than there is in detecting small differences.

Often a smaller s^2 is obtained by narrowing the definition of the population of interest. For example, the data of Example 7.2 may vary as much as they do because the sample contains animals of different ages, or of different strains, or of both sexes. It may be wiser to limit the hypothesis, and the sampling, to animals of the same sex and strain and of a narrow range of ages. And power can be increased by obtaining more precise measurements; also, greater power is associated with narrower confidence intervals. A common goal is to test with a power between 0.75 and 0.90.

7.8 SAMPLING FINITE POPULATIONS

In general we assume that a sample from a population is a very small portion of the totality of data in that population. Essentially, we consider that the population is infinite in size, so that the removal of a relatively small number of data from the population does not noticeably affect the probability of selecting further data.

However, if the sample size, n, is an appreciable portion of the population size (a very unusual circumstance), N (say, at least 5%), then we are said to be sampling

TABLE 7.4: Relationship between α, β, Power $(1 - \beta)$, and n, for the Data of Example 7.9
Sample Variance ($s^2 = 1.5682$ g^2) and True Difference ($\delta = 1.0$ g) of Example 7.10, Using Equation 7.12

Two-Tailed Test				One-Tailed Test			
n	α	β	$1 - \beta$	n	α	β	$1 - \beta$
10	0.10	0.25	0.75	10	0.10	0.14	0.86
10	0.05	0.40	0.60	10	0.05	0.25	0.75
10	0.01	0.76	0.24	10	0.01	0.61	0.39
12	0.10	0.18	0.82	12	0.10	0.09	0.91
12	0.05	0.29	0.71	12	0.05	0.18	0.82
12	0.01	0.73	0.27	12	0.01	0.48	0.52
15	0.10	0.10	0.90	15	0.10	0.05	0.95
15	0.05	0.18	0.82	15	0.05	0.10	0.90
15	0.01	0.45	0.55	15	0.01	0.32	0.68
20	0.10	0.04	0.96	20	0.10	0.02	0.98
20	0.05	0.08	0.92	20	0.05	0.04	0.96
20	0.01	0.24	0.76	20	0.01	0.16	0.84

TABLE 7.5: Relationship between n, s^2, δ, and Power (for Testing at $\alpha = 0.05$) for the Hypothesis of Example 7.9, Using Equation 7.10

n	s^2	δ	Power of Two-Tailed Test	Power of One-Tailed Test
Effect of n				
10	1.5682	1.0	0.60	0.75
12	1.5682	1.0	0.71	0.82
15	1.5682	1.0	0.82	0.90
20	1.5682	1.0	0.92	0.96
Effect of s^2				
12	2.0000	1.0	0.60	0.74
12	1.5682	1.0	0.71	0.82
12	1.0000	1.0	0.88	0.94
Effect of δ				
12	1.5682	1.0	0.71	0.82
12	1.5682	1.2	0.86	0.92
12	1.5682	1.4	0.96	0.97

a *finite population*. In such a case, $\overline{X}$ is a substantially better estimate of μ the closer n is to N; specifically,

$$s_{\overline{X}} = \sqrt{\frac{s^2}{n}}\sqrt{1 - \frac{n}{N}} = \sqrt{\left(\frac{s^2}{n}\right)\left(1 - \frac{n}{N}\right)}, \tag{7.13}$$

where n/N is the *sampling fraction* and $1 - n/N$ is referred to as the *finite population correction*.*

Obviously, from Equation 7.13, when n is very small compared to N, then the sampling fraction is almost zero, the finite population correction will be nearly one,

*One may also calculate $1 - n/N$ as $(N - n)/N$.

and $s_{\overline{X}}$ will be nearly $\sqrt{s^2/n}$, just as we have used (Equation 6.8) when assuming the population size, N, to be infinite. As n becomes closer to N, the correction becomes smaller, and $s_{\overline{X}}$ becomes smaller, which makes sense intuitively. If $n = N$, then $1 - n/N = 0$ and $s_{\overline{X}} = 0$, meaning there is no error at all in estimating μ if the sample consists of the entire population; that is, $\overline{X} = \mu$ if $n = N$. In computing confidence intervals when sampling finite populations (i.e., when n is not a negligibly small fraction of N), Equation 7.13 should be used instead of Equation 6.8.

If we are determining the sample size required to estimate the population mean with a stated precision (Section 7.6), and the sample size is an appreciable fraction of the population size, then the required sample size is calculated as

$$m = \frac{n}{1 + (n - 1)/N} \tag{7.14}$$

(Cochran, 1977: 77–78), where n is from Equation 7.9.

7.9 HYPOTHESES CONCERNING THE MEDIAN

In Example 7.2 we examined a sample of weight change data in order to ask whether the mean change in the sampled population was different from zero. Analogously, we may test hypotheses about the population median, M, such as testing H_0: $M = M_0$ against H_A: $M \neq M_0$, where M_0 can be zero or any other hypothesized population median.*

A simple method for testing this two-tailed hypothesis is to determine the confidence limits for the population median, as discussed in Section 23.9, and reject H_0 (with probability $\leq \alpha$ of a Type I error) if $M_0 \leq L_1$ or $M_0 \geq L_2$. This is essentially a binomial test (Section 23.6), where we consider the number of data $< M_0$ as being in one category and the number of data $> M_0$ being in the second category. If either of these two numbers is less than or equal to the critical value in Appendix Table B.27, then H_0 is rejected. (Data equal to M_0 are ignored in this test.)

For one-tailed hypotheses about the median, the binomial test may also be employed. For H_0: $M \geq M_0$ versus H_A: $M < M_0$, H_0 is rejected if the number of data less than M_0 is $\leq$ the one-tailed critical value, $C_{\alpha(1),n}$. For H_0: $M \leq M_0$ versus H_A: $M > M_0$, H_0 is rejected if the number of data greater than M_0 is $\geq n - C_{\alpha(1),n}$.

As an alternative to the binomial test, for either two-tailed or one-tailed hypotheses, we may use the more powerful Wilcoxon signed-rank test. The Wilcoxon procedure is applied as a one-sample median test by ranking the data as described in Section 9.5 and assigning a minus sign to each rank associated with a datum $< M_0$ and a plus sign to each associated with a datum $> M_0$. Any rank equal to M_0 is ignored in this procedure. The sum of the ranks with a plus sign is called T_+ and the sum of the ranks with a minus sign is T_-, with the test then proceeding as described in Section 9.5. The Wilcoxon test assumes that the sampled population is symmetric (in which case the median and mean are identical and this procedure becomes a hypothesis test about the mean as well as about the median, but the one-sample t test is typically a more powerful test about the mean). Section 9.5 discusses this test further.

7.10 CONFIDENCE LIMITS FOR THE POPULATION MEDIAN

The sample median (Section 3.2) is used as the best estimate of M, the population median. Confidence limits for M may be determined by considering the binomial distribution, as discussed in Section 24.9.

*Here M represents the Greek capital letter mu.

HYPOTHESES CONCERNING THE VARIANCE

The sampling distribution of means is a symmetrical distribution, approaching the normal distribution as n increases. But the sampling distribution of variances is not symmetrical, and neither the normal nor the t distribution may be employed to test hypotheses about σ^2 or to set confidence limits around σ^2. However, theory states that

$$\chi^2 = \frac{\nu s^2}{\sigma^2} \tag{7.15}$$

(if the sample came from a population with a normal distribution), where χ^2 represents a statistical distribution* that, like t, varies with the degrees of freedom, ν, where $\nu = n - 1$. Critical values of $\chi^2_{\alpha,\nu}$ are found in Appendix Table B.1.

Consider the pair of two-tailed hypotheses, H_0: $\sigma^2 = \sigma_0^2$ and H_A: $\sigma^2 \neq \sigma_0^2$, where σ_0^2 may be any hypothesized population variance. Then, simply calculate

$$\chi^2 = \frac{\nu s^2}{\sigma_0^2} \quad \text{or, equivalently,} \quad \chi^2 = \frac{SS}{\sigma_0^2}, \tag{7.16}$$

and if the calculated χ^2 is $\geq \chi^2_{\alpha/2,\nu}$ or $\leq \chi^2_{(1-\alpha/2),\nu}$, then H_0 is rejected at the α level of significance. For example, if we wished to test H_0: $\sigma^2 = 1.0(^\circ C)^2$ and H_A: $\sigma^2 \neq 1.0(^\circ C)^2$ for the data of Example 7.1, with $\alpha = 0.05$, we would first calculate $\chi^2 = SS/\sigma_0^2$. In this example, $\nu = 24$ and $s^2 = 1.80(^\circ C)^2$, so $SS = \nu s^2 = 43.20(^\circ C)^2$. Also, as σ^2 is hypothesized to be $1.0(^\circ C)^2$, $\chi^2 = SS/\sigma_0^2 = 43.20(^\circ C)^2/1.0(^\circ C)^2 = 43.20$. Two critical values are to be obtained from the chi-square table (Appendix Table B.1): $\chi^2_{(0.05/2),24} = \chi^2_{0.025,24} = 39.364$ and $\chi^2_{(1-0.05/2),24} = \chi^2_{0.975,24} = 12.401$. As the calculated χ^2 is more extreme than one of these critical values (i.e., the calculated χ^2 is > 39.364), H_0 is rejected, and we conclude that the sample of data was obtained from a population having a variance different from $1.0(^\circ C)^2$.

It is more common to consider one-tailed hypotheses concerning variances. For the hypotheses H_0: $\sigma^2 \leq \sigma_0^2$ and H_A: $\sigma^2 > \sigma_0^2$, H_0 is rejected if the χ^2 calculated from Equation 7.16 is $\geq \chi^2_{\alpha,\nu}$. For H_0: $\sigma^2 \geq \sigma_0^2$ and H_A: $\sigma^2 < \sigma_0^2$, a calculated χ^2 that is $\leq \chi^2_{(1-\alpha),\nu}$ is grounds for rejecting H_0. For the data of Example 7.4, a manufacturer might be interested in whether the variability in the dissolving times of the drug is greater than a certain value—say, 1.5 sec. Thus, H_0: $\sigma^2 \leq 1.5$ sec^2 and H_A: $\sigma^2 > 1.5$ sec^2 might be tested, as shown in Example 7.11.

EXAMPLE 7.11 A One-Tailed Test for the Hypotheses H_0: $\sigma^2 \leq 1.5$ sec^2 and H_A: $\sigma^2 > 1.5$ sec^2, Using the Data of Example 7.4

$SS = 18.8288$ sec^2

$\nu = 7$

$s^2 = 2.6898$ sec^2

$$\chi^2 = \frac{SS}{\sigma_0^2} = \frac{18.8288 \text{ sec}^2}{1.5 \text{ sec}^2} = 12.553$$

$\chi^2_{0.05,7} = 14.067$

*The Greek letter "chi" (which in lowercase is χ) is pronounced as the "ky" in "sky."

Since $12.553 < 14.067$, H_0 is not rejected.

$$0.05 < P < 0.10 \quad [P = 0.084]$$

We conclude that the variance of dissolving times is no more than 1.5 sec^2.

As is the case for testing hypotheses about a population mean, μ (Sections 7.1 and 7.2), the aforementioned testing of hypotheses about a population variance, σ, depends upon the sample's having come from a population of normally distributed data. However, the F test for variances is not as robust as the t test for means; that is, it is not as resistant to violations of this underlying assumption of normality. The probability of a Type I error will be very different from the specified α if the sampled population is nonnormal, even if it is symmetrical. And, likewise, α will be distorted if there is substantial asymmetry (say, $|\sqrt{b_1}| > 0.6$), even if the distribution is normal (Pearson and Please, 1975).

7.12 CONFIDENCE LIMITS FOR THE POPULATION VARIANCE

Confidence intervals may be determined for many parameters other than the population mean, in order to express the precision of estimates of those parameters.

By employing the χ^2 distribution, we can define an interval within which there is a $1 - \alpha$ chance of including σ^2 in repeated sampling. Appendix Table B.1 tells us the probability of a calculated χ^2 being greater than that in the Table. If we desire to know the two χ^2 values that enclose $1 - \alpha$ of the chi-square curve, we want the portion of the curve between $\chi^2_{(1-\alpha/2),\nu}$ and $\chi^2_{\alpha/2,\nu}$ (for a 95% confidence interval, this would mean the area between $\chi^2_{0.975,\nu}$ and $\chi^2_{0.025,\nu}$). It follows from Equation 7.13 that

$$\chi^2_{(1-\alpha/2),\nu} \leq \frac{\nu s^2}{\sigma^2} \leq \chi^2_{\alpha/2,\nu}, \tag{7.17}$$

and

$$\frac{\nu s^2}{\chi^2_{\alpha/2,\nu}} \leq \sigma^2 \leq \frac{\nu s^2}{\chi^2_{(1-\alpha/2),\nu}}. \tag{7.18}$$

Since $\nu s^2 = SS$, we can also write Equation 7.16 as

$$\frac{SS}{\chi^2_{\alpha/2,\nu}} \leq \sigma^2 \leq \frac{SS}{\chi^2_{(1-\alpha/2),\nu}}. \tag{7.19}$$

Referring back to the data of Example 7.1, we would calculate the 95% confidence interval for σ^2 as follows. As $\nu = 24$ and $s^2 = 1.80(^\circ C)^2$, $SS = \nu s^2 = 43.20(^\circ C)^2$. From Appendix Table B.1, we find $\chi^2_{0.025,24} = 39.364$ and $\chi^2_{0.975,24} = 12.401$. Therefore, $L_1 = SS/\chi^2_{\alpha/2,\nu} = 43.20(^\circ C)^2/39.364 = 1.10(^\circ C)^2$, and $L_2 = SS/\chi^2_{(1-\alpha),\nu} = 43.20(^\circ C)/12.401 = 3.48(^\circ C)^2$. If the null hypothesis H_0: $\sigma^2 = \sigma_0^2$ would have been tested and rejected for some specified variance, σ_0, then σ_0 would be outside of the confidence interval (i.e., σ_0^2 would be either less than L_1 or greater than L_2). Note that the confidence limits, $1.10(^\circ C)^2$ and $3.48(^\circ C)^2$, are not symmetrical around s^2; that is, the distance from L_1 to s^2 is not the same as the distance from s^2 to L_2.

To obtain the $1 - \alpha$ confidence interval for the population standard deviation, simply use the square roots of the confidence limits for σ^2, so that

$$\sqrt{\frac{SS}{\chi^2_{\alpha/2,\nu}}} \le \sigma \le \sqrt{\frac{SS}{\chi^2_{(1-\alpha/2),\nu}}}. \tag{7.20}$$

For the preceding example, the 95% confidence interval for σ would be $\sqrt{1.10(^\circ C)^2} \le \sigma \le \sqrt{3.48(^\circ C)^2}$, or $1.0^\circ C \le \sigma \le 1.9^\circ C$.

The end of Section 7.11 cautioned that testing hypotheses about σ^2 is adversely affected if the sampled population is nonnormal (even if it is symmetrical) or if the population is not symmetrical (even if it is normal). Determination of confidence limits also suffers from this unfavorable effect.

(a) One-Tailed Confidence Limits. In a fashion analogous to estimating a population mean via a one-tailed confidence interval, a one-tailed interval for a population variance is applicable in situations where a one-tailed hypothesis test for the variance is appropriate. For H_0: $\sigma^2 \le \sigma_0^2$ and H_A: $\sigma^2 > \sigma_0^2$, the one-tailed confidence limits for σ^2 are $L_1 = SS/\chi_{\alpha,\nu}$ and $L_2 = \infty$; and for H_0: $\sigma^2 \ge \sigma_0^2$ and H_A: $\sigma^2 < \sigma_0^2$, the confidence limits are $L_1 = 0$ and $L_2 = SS/\chi^2_{1-\alpha,\nu}$. Considering the data in Example 7.4, in which H_0: $\sigma^2 \le 45$ sec^2 and H_A: $\sigma > 45$ sec^2, for 95% confidence, L_1 would be $SS/\chi^2_{0.05,7} = 18.8188 \text{ sec}^2/14.067 = 1.34 \text{ sec}^2$ and $L_2 = \infty$. The hypothesized σ_0^2 (45 sec^2) lies within the confidence interval, indicating that the null hypothesis would not be rejected.

If the desire is to estimate a population's standard deviation (σ) instead of the population variance (σ^2), then simply substitute σ for σ^2 and σ_0 for σ_0^2 above and use the square root of L_1 and L_2 (bearing in mind that $\sqrt{\infty} = \infty$).

(b) Prediction Limits. We can also estimate the variance that would be obtained from an additional random sample of m data from the same population. To do so, the following two-tailed $1 - \alpha$ prediction limits may be determined:

$$L_1 = \frac{s^2}{F_{\alpha(2),n-1,m-1}} \tag{7.21}$$

$$L_2 = s^2 F_{\alpha(2),m-1,n-1} \tag{7.22}$$

(Hahn, 1972; Hahn and Meeker, 1991: 64, who also mention one-tailed prediction intervals; Patel, 1989). A prediction interval for s would be obtained by taking the square roots of the prediction limits for s^2.

The critical values of F, which will be employed many times later in this book, are given in Appendix Table B.4. These will be written in the form F_{α,ν_1,ν_2}, where ν_1 and ν_2 are termed the "numerator degrees of freedom" and "denominator degrees of freedom," respectively (for a reason that will be apparent in Section 8.5). So, if we wished to make a prediction about the variance (or standard deviation) that would be obtained from an additional random sample of 10 data from the population from which the sample in Example 7.1 came, $n = 25$, $n - 1 = 24$, $m = 10$, and $m - 1 = 9$; and to compute the 95% two-tailed prediction interval, we would consult Table B.4 and obtain $F_{\alpha(2),n-1,m-1} = F_{0.05(2),24,9} = 3.61$ and $F_{\alpha(2),m-1,n-1} = F_{0.05(2),9,24} = 2.79$. Thus, the prediction limits would be $L_1 = 1.80(^\circ C)^2/3.61 = 0.50(^\circ C)^2$ and $L_2 = [1.80(^\circ C)^2][2.79] = 5.02(^\circ C)^2$.

7.13 POWER AND SAMPLE SIZE IN TESTS CONCERNING THE VARIANCE

(a) Sample Size Required. We may ask how large a sample would be required to perform the hypothesis tests of Section 7.12 at a specified power. For the hypotheses H_0: $\sigma^2 \leq \sigma_0^2$ versus H_A: $\sigma^2 > \sigma_0^2$, the minimum sample size is that for which

$$\frac{\chi^2_{1-\beta,\nu}}{\chi^2_{\alpha,\nu}} = \frac{\sigma_0^2}{s^2}, \tag{7.23}$$

and this sample size, n, may be found by iteration (i.e., by a directed trial and error), as shown in Example 7.12. The ratio on the left side of Equation 7.23 increases in magnitude as n increases.

EXAMPLE 7.12 Estimation of Required Sample Size to Test H_0: $\sigma^2 \leq \sigma_0^2$ versus H_A: $\sigma^2 > \sigma_0^2$

How large a sample is needed to reject H_0 : $\sigma^2 \leq 1.50$ sec^2, using the data of Example 7.11, if we test at the 0.05 level of significance and with a power of 0.90? (Therefore, $\alpha = 0.05$ and $\beta = 0.10$.)

From Example 7.11, $s^2 = 2.6898$ sec^2. As we have specified $\sigma_0^2 = 1.75$ sec^2, $\sigma_0^2/s^2 = 0.558$.

To begin the iterative process of estimating n, let us guess that a sample size of 30 would be required. Then,

$$\frac{\chi^2_{0.90,29}}{\chi^2_{0.05,29}} = \frac{19.768}{42.557} = 0.465.$$

Because $0.465 < 0.558$, our estimate of n is too low. So we might guess that $n = 50$ is required:

$$\frac{\chi^2_{0.90,49}}{\chi^2_{0.05,49}} = \frac{36.818}{66.339} = 0.555.$$

Because 0.555 is a little less than 0.558, $n = 50$ is a little too low and we might guess $n = 55$, for which $\chi^2_{0.90,54}/\chi^2_{0.05,54} = 41.183/70.153 = 0.571$.

Because 0.571 is greater than 0.558, our estimate of n is high, so we could try $n = 51$, for which $\chi^2_{0.90,50}/\chi^2_{0.05,50} = 37.689/67.505 = 0.558$.

Therefore, we estimate that a sample size of at least 51 is required to perform the hypothesis test with the specified characteristics.

For the hypotheses H_0: $\sigma^2 \geq \sigma_0^2$ versus H_A: $\sigma^2 < \sigma_0^2$, the minimum sample size is that for which

$$\frac{\chi^2_{\beta,\nu}}{\chi^2_{1-\alpha,\nu}} = \frac{\sigma_0^2}{s^2}. \tag{7.24}$$

(b) Power of the Test. If we plan to test the one-tailed hypotheses H_0: $\sigma^2 \leq \sigma_0^2$ versus H_A: $\sigma^2 > \sigma_0^2$, using the α level of significance and a sample size of n, then the power of the test would be

$$1 - \beta = P(\chi^2 \geq \chi^2_{\alpha,\nu}\sigma_0^2/s^2). \tag{7.25}$$

Thus, if the experiment of Example 7.11 were to be repeated with the same sample size, then $n = 8$, $\nu = 7$, $\alpha = 0.05$, $\chi^2_{0.05,9} = 14.067$, $s^2 = 2.6898\ \text{sec}^2$, $\sigma_0^2 = 1.5\ \text{sec}^2$, and the predicted power of the test would be

$$1 - \beta = P[\chi^2 \geq (14.067)(1.5)/2.6898] = P(\chi^2 \geq 7.845).$$

From Appendix Table B.1 we see that, for $\chi^2 \geq 7.845$ with $\nu = 7$, P lies between 0.25 and 0.50 (that is, $0.25 < P < 0.50$). By linear interpolation between $\chi^2_{0.25,7}$ and $\chi^2_{0.50,7}$, we estimate $P(\chi^2 \geq 7.845)$, which is the predicted power of the test, to be 0.38.* If greater power is preferred for this test, we can determine what power would be expected if the experiment were performed with a larger sample size, say $n = 40$. In that case, $\nu = 39$, $\chi^2_{0.05,39} = 54.572$, and the estimate of the power of the test would be

$$1 - \beta = P[\chi^2 \geq (54.572)(1.5)/2.6898] = P(\chi^2 \geq 30.433).$$

Consulting Table B1 for $\nu = 39$, we see that $0.75 < P < 0.90$. By linear interpolation between $\chi^2_{0.75,39}$ and $\chi^2_{0.90,39}$, we estimate $P(\chi^2 \geq 54.572)$, the power of the test, to be 0.82.†

One-tailed testing of H_0: $\sigma^2 \geq \sigma_0^2$ versus H_A: $\sigma^2 \leq \sigma_0^2$ would also employ Equation 7.25. For two-tailed testing of H_0: $\sigma^2 = \sigma_0^2$ versus H_A: $\sigma^2 \neq \sigma_0^2$, substitute $\chi^2_{\alpha/2,\nu}$ for $\chi^2_{\alpha,\nu}$ in Equation 7.25.

7.14 HYPOTHESES CONCERNING THE COEFFICIENT OF VARIATION

Although rarely done, it is possible to ask whether a sample of data is likely to have come from a population with a specified coefficient of variation, call it $(\sigma/\mu)_0$. This amounts to testing of the following pair of two-tailed hypotheses: H_0: $\sigma/\mu = (\sigma/\mu)_0$ and H_A: $\sigma/\mu \neq (\sigma/\mu)_0$. Among the testing procedures proposed, that presented by Miller (1991) works well for a sample size of at least 10 if the sampled population is normal with a mean > 0, with a variance > 0, and with a coefficient of variation, σ/μ, no greater than 0.33. For one-tailed testing (i.e., H_0: $\sigma/\mu \leq (\sigma/\mu)_0$ vs. H_A: $\sigma/\mu > (\sigma/\mu)_0$, or H_0: $\sigma/\mu \geq (\sigma/\mu)_0$ vs. H_A: $\sigma/\mu < (\sigma/\mu)_0$), the test statistic is

$$Z = \frac{\sqrt{n-1}\,[V - (\sigma/\mu)_0]}{(\mu/\sigma)_0\sqrt{0.5 + (\sigma/\mu)_0^2}}, \tag{7.26}$$

the probability of which may be obtained from Appendix Table B.2; or Z may be compared to the critical values of Z_α, read from the last line of Appendix Table B.3. Miller also showed this procedure to yield results very similar to those from a χ^2 approximation by McKay (1932) that, although applicable for n as small as 5, lacks power at such small sample sizes.

Miller and Feltz (1997) present an estimate of the power of this test.

*See the beginning of Appendix B for a discussion of interpolation. In this example, linear interpolation yields $P = 0.38$, harmonic interpolation concludes $P = 0.34$, and the true probability (from appropriate computer software) is $P = 0.35$. So interpolation gave very good approximations.

†The actual probability (via computer) is 0.84, while linear and harmonic interpolations each produced a probability of 0.82, an excellent approximation.

7.15 CONFIDENCE LIMITS FOR THE POPULATION COEFFICIENT OF VARIATION

The $1 - \alpha$ confidence limits for the population coefficient of variation may be estimated as

$$V \pm \frac{V\sqrt{0.5 + V^2}Z_{\alpha/2}}{\sqrt{\nu}}; \tag{7.27}$$

see Miller and Feltz (1997).

7.16 HYPOTHESES CONCERNING SYMMETRY AND KURTOSIS

Section 6.5 introduced the assessment of a population's departure from a normal distribution, including a consideration of a population parameter, $\sqrt{\beta_1}$, for symmetry around the mean and a parameter, β_2, for kurtosis; and their respective sample statistics are $\sqrt{b_1}$ and b_2. Methods will now be discussed for testing hypotheses about a population's symmetry and kurtosis. Such hypotheses are not often employed, but they are sometimes called upon to conclude whether a sampled population follows a normal distribution, and they do appear in some statistical computer packages.

(a) Testing Symmetry around the Mean. The two-tailed hypotheses H_0: $\sqrt{\beta_1} = 0$ versus H_0: $\sqrt{\beta_1} \neq 0$ address the question of whether a sampled population's distribution is symmetrical around its mean. The sample symmetry measure, $\sqrt{b_1}$, is an estimate of $\sqrt{\beta_1}$ and may be calculated by Equation 6.16. Its absolute value may then be compared to critical values, $(\sqrt{b_1})_{\alpha(2),n}$, in Appendix Table B.22.

As an illustration of this, let us say that the data of Example 6.7 yield $\sqrt{b_1} = 0.351$. To test the above H_0 at the 5% level of significance, the critical value from Table B.22 is $(\sqrt{b_1})_{0.05(2),70} = 0.556$. So, H_0 is not rejected and the table indicates that $P(|\sqrt{b_1}| > 0.10)$.

One-tailed testing could be employed if the interest were solely in whether the distribution is skewed to the right (H_0: $\sqrt{\beta_1} \leq 0$ vs. H_0: $\sqrt{\beta_1} > 0$), in which case H_0 would be rejected if $\sqrt{b_1} \geq (\sqrt{b_1})_{\alpha(1),n}$. Or, a one-tailed test of H_0: $\sqrt{\beta_1} \geq 0$ versus H_0: $\sqrt{\beta_1} < 0$ could be used to test specifically whether the distribution is skewed to the left; and H_0 would be rejected if $\sqrt{b_1} \leq -(\sqrt{b_1})_{\alpha(1),n}$.

If the sample size, n, does not appear in Table B.22, a conservative approach (i.e., one with lowered power) would be to use the largest tabled n that is less than the n of our sample; for example, if n were 85, we would use critical values for $n = 80$. Alternatively, a critical value could be estimated, from the table's critical values for n's immediately above and below n under consideration, using linear or harmonic interpolation (see the introduction to Appendix B), with harmonic interpolation appearing to be a little more accurate. There is also a method (D'Agostino, 1970, 1986; D'Agostino, Belanger, and D'Agostino, 1990) by which to approximate the exact probability of H_0.

(b) Testing Kurtosis. Our estimate of a population's kurtosis (β_2) is b_2, given by Equation 6.17. We can ask whether the population is not mesokurtic by the two-tailed hypotheses H_0: $\beta_2 = 3$ versus H_0: $\beta_1 \neq 3$. Critical values for this test are presented in Table B.23, and H_0 is rejected if b_2 is *either* less than the lower-tail critical value for $(b_2)_{\alpha(2),n}$ *or* greater than the upper-tail critical value for $(b_2)_{\alpha(2),n}$.

For the data of Example 6.7, $b_2 = 2.25$. To test the above H_0 at the 5% level of significance, we find that critical values for $n = 70$ do not appear in Table B.23. A conservative procedure (i.e., one with lowered power) is to employ the critical values for the

tabled critical values for the largest n that is less than our sample's n. In our example, this is $n = 50$, and H_0 is rejected if b_2 is *either* less than the lower-tail $(b_2)_{0.05(2),50} = 2.06$ *or* greater than the upper-tail $(b_2)_{0.05(2),50} = 4.36$. In the present example, $b_2 = 2.25$ is neither less than 2.06 nor greater than 4.36, so H_0 is not rejected. And, from Table B.23, we see that $0.05 < P < 0.10$. Rather than using the nearest lower n in Table B.23, we could engage in linear or harmonic interpolation between tabled critical values (see introduction to Appendix B), with harmonic interpolation apparently a little more accurate. There is also a method (D'Agostino, 1970, 1986; D'Agostino, Belanger, and D'Agostino, 1990) to approximate the exact probability of H_0.

One-tailed testing could be employed if the interest is solely in whether the population's distribution is leptokurtic, for which H_0: $\beta_2 \leq 3$ versus H_0: $\beta_2 > 3$ would apply; and H_0 would be rejected if $b_2 \geq$ the upper-tail $(b_2)_{\alpha(1),n}$. Or, if testing specifically whether the distribution is platykurtic, a one-tailed test of H_0: $\beta_2 \geq 3$ versus H_0: $\beta_2 < 3$ would be applicable; and H_0 would be rejected if $b_2 \leq$ the lower-tail $(b_2)_{\alpha(1),n}$.

EXAMPLE 7.13 Two-Tailed Nonparametric Testing of Symmetry Around the Median, Using the Data of Example 6.7 and the Wilcoxon Test of Section 9.5

H_0: The population of data from which this sample came is distributed symmetrically around its median.

H_A: The population is not distributed symmetrically around its median.

$n = 70$; median $= X_{(70+1)/2} = X_{35.5} = 70.5$ in.

X (in.)	d (in.)	f	$\lvert d \rvert$ (in.)	Rank of $\lvert d \rvert$	Signed rank of $\lvert d \rvert$	(f)(Signed rank)
63	−7.5	2	7.5	69.5	−69.5	−139
64	−6.5	2	6.5	67.5	−67.5	−135
65	−5.5	3	5.5	64	−64	−192
66	−4.5	5	4.5	57.5	−57.5	−287.5
67	−3.5	4	3.5	48.5	−48.5	−194
68	−2.5	6	2.5	35.5	−35.5	−213
69	−1.5	5	1.5	21.5	−21.5	−107.5
70	−0.5	8	0.5	8	−8	−64
71	0.5	7	0.5	8	8	56
72	1.5	7	1.5	21.5	21.5	160.5
73	2.5	10	2.5	35.5	35.5	355
74	3.5	6	3.5	48.5	48.5	291
75	4.5	3	4.5	57.5	57.5	172.5
76	5.5	2	5.5	64	64	128
		70				

$T_- = 1332$

$T_+ = 1163$

$T_{0.05(2),70} = 907$ (from Appendix Table B.12)

As neither T_- nor $T_+ < T_{0.05(2),70}$, do not reject H_0. [$P > 0.50$]

(c) Testing Symmetry around the Median. Symmetry of dispersion around the median instead of the mean may be tested nonparametrically by using the Wilcoxon paired-sample test of Section 9.5 (also known as the Wilcoxon signed-rank test). For each datum (X_i) we compute the deviation from the median ($d_i = X_i -$ median) and then analyze the d_i's as in Section 9.5. For the two-tailed test (considering both T_- and T_+ in the Wilcoxon test), the null hypothesis is H_0: The underlying distribution is symmetrical around (i.e., is not skewed from) the median. For a one-tailed test, T_- is the critical value for H_0: The underlying distribution is not skewed to the right of the median; and T_+ is the critical value for H_0: The underlying distribution is not skewed to the left of the median. This test is demonstrated in Example 7.13.

EXERCISES

7.1. The following data are the lengths of the menstrual cycle in a random sample of 15 women. Test the hypothesis that the mean length of human menstrual cycle is equal to a lunar month (a lunar month is 29.5 days).

The data are 26, 24, 29, 33, 25, 26, 23, 30, 31, 30, 28, 27, 29, 26, and 28 days.

7.2. A species of marine arthropod lives in seawater that contains calcium in a concentration of 32 mmole/kg of water. Thirteen of the animals are collected and the calcium concentrations in their coelomic fluid are found to be: 28, 27, 29, 29, 30, 30, 31, 30, 33, 27, 30, 32, and 31 mmole/kg. Test the appropriate hypothesis to conclude whether members of this species maintain a coelomic calcium concentration less than that of their environment.

7.3. Present the following data in a graph that shows the mean, standard error, 95% confidence interval, range, and number of observations for each month.

Table of Caloric Intake (kcal/g of Body Weight) **of Squirrels**

Month	*Number of Data*	*Mean*	*Standard Error*	*Range*
January	13	0.458	0.026	0.289–0.612
February	12	0.413	0.027	0.279–0.598
March	17	0.327	0.018	0.194–0.461

7.4. A sample of size 18 has a mean of 13.55 cm and a variance of 6.4512 cm^2.

(a) Calculate the 95% confidence interval for the population mean.

(b) How large a sample would have to be taken from this population to estimate μ to within 1.00 cm, with 95% confidence?

(c) to within 2.00 cm with 95% confidence?

(d) to within 2.00 cm with 99% confidence?

(e) For the data of Exercise 7.4, calculate the 95% prediction interval for what the mean would be of an additional sample of 10 data from the same population.

7.5. We want to sample a population of lengths and to perform a test of H_0: $\mu = \mu_0$ versus H_A: $\mu \neq \mu_0$, at the 5% significance level, with a 95% probability of rejecting H_0 when $|\mu - \mu_0|$ is at least 2.0 cm. The estimate of the population variance, σ^2, is $s^2 = 8.44$ cm^2.

(a) What minimum sample size should be used?

(b) What minimum sample size would be required if α were 0.01?

(c) What minimum sample size would be required if $\alpha = 0.05$ and power = 0.99?

(d) If $n = 25$ and $\alpha = 0.05$, what is the smallest difference, $|\mu - \mu_0|$, that can be detected with 95% probability?

(e) If $n = 25$ and $\alpha = 0.05$, what is the probability of detecting a difference, $|\mu - \mu_0|$, as small as 2.0 cm?

7.6. There are 200 members of a state legislature. The ages of a random sample of 50 of them are obtained, and it is found that $\bar{X} = 53.87$ yr and $s = 9.89$ yr.

(a) Calculate the 95% confidence interval for the mean age of all members of the legislature.

(b) If the above $\bar{X}$ and s had been obtained from a random sample of 100 from this population, what would the 95% confidence interval for the population mean have been?

7.7. For the data of Exercise 7.4:

(a) Calculate the 95% confidence interval for the population variance.

(b) Calculate the 95% confidence interval for the population standard deviation.

(c) Using the 5% level of significance, test H_0: $\sigma^2 \leq 4.4000$ cm^2 versus H_A: $\sigma^2 > 4.4000$ cm^2.

(d) Using the 5% level of significance, test H_0: $\sigma \geq 3.00$ cm versus H_A : $\sigma < 3.00$ cm.

(e) How large a sample is needed to test H_0: $\sigma^2 \leq 5.0000$ cm^2 if it is desired to test

at the 0.05 level of significance with 75% power?

For the data of Exercise 7.4, calculate the 95% prediction interval for what the variance and standard deviation would be of an additional sample of 20 data from the same population.

7.8. A sample of 100 body weights has $\sqrt{b_1} = 0.375$ and $b_2 = 4.20$.

(a) Test H_0: $\sqrt{\beta_1} = 0$ and H_A: $\sqrt{\beta_1} \neq 0$, at the 5% significance level.

(b) Test H_0: $\beta_2 = 3$ and H_A: $\beta_2 \neq 3$, at the 5% significance level.

CHAPTER 8

Two-Sample Hypotheses

Among the most commonly employed biostatistical procedures is the comparison of two samples to infer whether differences exist between the two populations sampled. This chapter will consider hypotheses comparing two population means, medians, variances (or standard deviations), coefficients of variation, and indices of diversity. In doing so, we introduce another very important sampling distribution, the F distribution—named for its discoverer, R. A. Fisher—and will demonstrate further use of Student's t distribution.

The objective of many two-sample hypotheses is to make inferences about population parameters by examining sample statistics. Other hypothesis-testing procedures, however, draw inferences about populations without referring to parameters. Such procedures are called *nonparametric* methods, and several will be discussed in this and following chapters.

8.1 TESTING FOR DIFFERENCE BETWEEN TWO MEANS

A very common situation for statistical testing is where a researcher desires to infer whether two population means are the same. This can be done by analyzing the difference between the means of samples taken at random from those populations.

Example 8.1 presents the results of an experiment in which adult male rabbits were divided at random into two groups, one group of six and one group of seven.* The members of the first group were given one kind of drug (called "B"), and the

*Sir Ronald Aylmer Fisher (1890–1962) is credited with the first explicit recommendation of the important concept of assigning subjects *at random* to groups for different experimental treatments (Bartlett, 1965; Fisher, 1925b; Rubin, 1990).

members of the second group were given another kind of drug (called "G"). Blood is to be taken from each rabbit and the time it takes the blood to clot is to be recorded.

EXAMPLE 8.1 A Two-Sample *t* Test for the Two-Tailed Hypotheses, H_0: $\mu_1 = \mu_2$ and H_A: $\mu_1 \neq \mu_2$ (Which Could Also Be Stated as H_0: $\mu_1 - \mu_2 = 0$ and H_A: $\mu_1 - \mu_2 \neq 0$). The Data Are Blood-Clotting Times (in Minutes) of Male Adult Rabbits Given One of Two Different Drugs

H_0: $\mu_1 = \mu_2$
H_A: $\mu_1 \neq \mu_2$

Given drug B	*Given drug G*
8.8	9.9
8.4	9.0
7.9	11.1
8.7	9.6
9.1	8.7
9.6	10.4
	9.5

$n_1 = 6$ $n_2 = 7$
$\nu_1 = 5$ $\nu_2 = 6$
$\overline{X}_1 = 8.75$ min $\overline{X}_2 = 9.74$ min
$SS_1 = 1.6950$ min^2 $SS_2 = 4.0171$ min^2

$$s_p^2 = \frac{SS_1 + SS_2}{\nu_1 + \nu_2} = \frac{1.6950 + 4.0171}{5 + 6} = \frac{5.7121}{11} = 0.5193 \text{ min}^2$$

$$s_{\overline{X}_1 - \overline{X}_2} = \sqrt{\frac{s_p^2}{n_1} + \frac{s_p^2}{n_2}} = \sqrt{\frac{0.5193}{6} + \frac{0.5193}{7}} = \sqrt{0.0866 + 0.0742}$$
$$= \sqrt{0.1608} = 0.40 \text{ min}$$

$$t = \frac{\overline{X}_1 - \overline{X}_2}{s_{\overline{X}_1 - \overline{X}_2}} = \frac{8.75 - 9.74}{0.40} = \frac{-0.99}{0.40} = -2.475$$

$t_{0.05(2),\nu} = t_{0.05(2),11} = 2.201$

Therefore, reject H_0.

$$0.02 < P(|t| \geq 2.475) < 0.05 \quad [P = 0.031]$$

We conclude that mean blood-clotting time is not the same for subjects receiving drug B as it is for subjects receiving drug G.

We can ask whether the mean of the population of blood-clotting times of all adult male rabbits who might have been administered drug B (let's call that mean μ_1) is the same as the population mean for blood-clotting times of all adult male rabbits who might have been given drug G (call it μ_2). This would involve the two-tailed hypotheses H_0: $\mu_1 - \mu_2 = 0$ and H_A: $\mu_1 - \mu_2 \neq 0$; and these hypotheses are commonly expressed in their equivalent forms: H_0: $\mu_1 = \mu_2$ and H_A: $\mu_1 \neq \mu_2$. The data from this experiment are presented in Example 8.1.

In this example, a total of 13 members of a biological population (adult male rabbits) were divided at random into two experimental groups, each group to receive treatment with one of the drugs. Another kind of testing situation with two independent samples is where the two groups are predetermined. For example, instead of desiring to test the effect of two drugs on blood-clotting time, a researcher might want to compare the mean blood-clotting time of adult male rabbits to that of adult female rabbits, in which case one of the two samples would be composed of randomly chosen males and the other sample would comprise randomly selected females. In that situation, the researcher would not specify which rabbits will be designated as male and which as female; the sex of each animal (and, therefore, the experimental group to which each is assigned) is determined before the experiment is begun. Similarly, it might have been asked whether the mean blood-clotting time is the same in two strains (or two ages, or two colors) of rabbits. Thus, in Example 8.1 there is random allocation of animals to the two groups to be compared, while in the other examples in this paragraph, there is random sampling of animals within each of two groups that are already established. The statistical hypotheses and the statistical testing procedure are the same in both circumstances.

If the two samples came from two normally distributed populations, and if the two populations have equal variances, then a t value to test such hypotheses may be calculated in a manner analogous to its computation for the one-sample t test introduced in Section 7.1. The t for testing the preceding hypotheses concerning the difference between two population means is

$$t = \frac{\overline{X}_1 - \overline{X}_2}{s_{\overline{X}_1 - \overline{X}_2}}. \tag{8.1}$$

The quantity $\overline{X}_1 - \overline{X}_2$ is the difference between the two sample means; and $s_{\overline{X}_1 - \overline{X}_2}$ is the standard error of the difference between the sample means (explained further below), which is a measure of the variability of the data within the two samples. Therefore, Equation 8.1 compares the differences between two means to the differences among all the data (a concept to be enlarged upon when comparing more than two means—in Chapter 10 and beyond).

The quantity $s_{\overline{X}_1 - \overline{X}_2}$, along with $s^2_{\overline{X}_1 - \overline{X}_2}$, the variance of the difference between the means, needs to be considered further. Both $s^2_{\overline{X}_1 - \overline{X}_2}$ and $s_{\overline{X}_1 - \overline{X}_2}$ are statistics that can be calculated from the sample data and are estimates of the population parameters, $\sigma^2_{\overline{X}_1 - \overline{X}_2}$ and $\sigma_{\overline{X}_1 - \overline{X}_2}$, respectively. It can be shown mathematically that the variance of the difference between two independent variables is equal to the sum of the variances of the two variables, so that $\sigma^2_{\overline{X}_1 - \overline{X}_2} = \sigma^2_{\overline{X}_1} + \sigma^2_{\overline{X}_2}$. Independence means that there is no association correlation between the data in the two populations.* As $\sigma^2_{\overline{X}} = \sigma^2/n$, we can write

$$\sigma^2_{\overline{X}_1 - \overline{X}_2} = \frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}. \tag{8.2}$$

Because the two-sample t test requires that we assume $\sigma_1^2 = \sigma_2^2$, we can write

$$\sigma^2_{\overline{X}_1 - \overline{X}_2} = \frac{\sigma^2}{n_1} + \frac{\sigma^2}{n_2}. \tag{8.3}$$

*If there is a unique relationship between each datum in one sample and a specific datum in another sample, then the data are considered *paired* and the considerations of Chapter 9 apply instead of the methods of the present chapter.

Thus, to calculate the estimate of $\sigma^2_{\overline{X}_1-\overline{X}_2}$, we must have an estimate of σ^2. Since both s_1^2 and s_2^2 are assumed to estimate σ^2, we compute the *pooled variance*, s_p^2, which is then used as the best estimate of σ^2:

$$s_p^2 = \frac{SS_1 + SS_2}{\nu_1 + \nu_2}, \tag{8.4}$$

and

$$s^2_{\overline{X}_1-\overline{X}_2} = \frac{s_p^2}{n_1} + \frac{s_p^2}{n_2}. \tag{8.5}$$

Thus,*

$$s_{\overline{X}_1-\overline{X}_2} = \sqrt{\frac{s_p^2}{n_1} + \frac{s_p^2}{n_2}}, \tag{8.6}$$

and Equation 8.1 becomes

$$t = \frac{\overline{X}_1 - \overline{X}_2}{\sqrt{\frac{s_p^2}{n_1} + \frac{s_p^2}{n_2}}}, \tag{8.7a}$$

which for equal sample sizes (i.e., $n_1 = n_2$, so each sample size may be referred to as n),

$$t = \frac{\overline{X}_1 - \overline{X}_2}{\sqrt{\frac{2s_p^2}{n}}}. \tag{8.7b}$$

Example 8.1 summarizes the procedure for testing the hypotheses under consideration. The critical value to be obtained from Appendix Table B.3 is $t_{\alpha(2),(\nu_1+\nu_2)}$, the two-tailed t value for the α significance level, with $\nu_1 + \nu_2$ degrees of freedom. We shall also write this as $t_{\alpha(2),\nu}$, defining the pooled degrees of freedom to be

$$\nu = \nu_1 + \nu_2 \quad \text{or, equivalently,} \quad \nu = n_1 + n_2 - 2. \tag{8.8}$$

In the two-tailed test, H_0 will be rejected if either $t \geq t_{\alpha(2),\nu}$ or $t \leq -t_{\alpha(2),\nu}$. Another way of stating this is that H_0 will be rejected if $|t| \geq t_{\alpha(2),\nu}$.

This statistical test asks what the probability is of obtaining two independent samples with means ($\overline{X}_1$ and $\overline{X}_2$) at least this different by random sampling from populations whose means (μ_1 and μ_2) are equal. And, if that probability is α or less, then H_0: $\mu_1 = \mu_2$ is rejected and it is declared that there is good evidence that the two population means are different.†

H_0: $\mu_1 = \mu_2$ may be written H_0: $\mu_1 - \mu_2 = 0$ and H_A: $\mu_1 \neq \mu_2$ as H_A: $\mu_1 - \mu_2 \neq 0$; the generalized two-tailed hypotheses are H_0: $\mu_1 - \mu_2 = \mu_0$ and H_A: $\mu_1 - \mu_2 \neq \mu_0$, tested as

$$t = \frac{|\overline{X}_1 - \overline{X}_2| - \mu_0}{s_{\overline{X}_1-\overline{X}_2}}, \tag{8.9}$$

where μ_0 may be any hypothesized difference between population means.

*The standard error of the difference between means may also be calculated as $s_{\overline{X}_1-\overline{X}_2} = \sqrt{Ns_p^2/(n_1n_2)}$, where $N = n_1 + n_2$.

†Instead of testing this hypotheses, a hypothesis of "correlation" (Section 19.11b) could be tested, which would ask whether there is a significant linear relationship between the magnitude of X and the group from which it came. This is not commonly done.

By the procedure of Section 8.9, one can test whether the measurements in one population are a specified amount as large as those in a second population.

(a) One-Tailed Hypotheses about the Difference between Means. One-tailed hypotheses can be tested in situations where the investigator is interested in detecting a difference in only one direction. For example, a gardener may use a particular fertilizer for a particular kind of plant, and a new fertilizer is advertised as being an improvement. Let us say that plant height at maturity is an important characteristic of this kind of plant, with taller plants being preferable. An experiment was run, raising ten plants on the present fertilizer and eight on the new one, with the resultant eighteen plant heights shown in Example 8.2. If the new fertilizer produces plants that are shorter than, or the same height as, plants grown with the present fertilizer, then we shall decide that the advertising claims are unfounded; therefore, the statements of $\mu_1 > \mu_2$ and $\mu_1 = \mu_2$ belong in the same hypothesis, namely the null hypothesis, H_0. If, however, mean plant height is indeed greater with the newer fertilizer, then it shall be declared to be distinctly better, with the alternate hypothesis (H_A: $\mu_1 < \mu_2$) concluded to be the true statement. The t statistic is calculated by Equation 8.1, just as for the two-tailed test. But this calculated t is then compared with the critical value $t_{\alpha(1),\nu}$, rather than with $t_{\alpha(2),\nu}$.

EXAMPLE 8.2 A Two-Sample t Test for the One-Tailed Hypotheses, H_0: $\mu_1 \geq \mu_2$ and H_A: $\mu_1 < \mu_2$ (Which Could Also Be Stated as H_0: $\mu_1 - \mu_2 \geq 0$ and H_A: $\mu_1 - \mu_2 < 0$). The Data Are Heights of Plants, Each Grown with One of Two Different Fertilizers

H_0: $\mu_1 \geq \mu_2$
H_A: $\mu_1 < \mu_2$

Present fertilizer	*Newer fertilizer*
48.2 cm	52.3 cm
54.6	57.4
58.3	55.6
47.8	53.2
51.4	61.3
52.0	58.0
55.2	59.8
49.1	54.8
49.9	
52.6	
$n_1 = 10$	$n_2 = 8$
$\nu_1 = 9$	$\nu_2 = 7$
$\overline{X}_1 = 51.91$ cm	$\overline{X}_2 = 56.55$ cm
$SS_1 = 102.23$ cm^2	$SS_2 = 69.20$ cm^2

$$s_p^2 = \frac{102.23 + 69.20}{9 + 7} = \frac{171.43}{16} = 10.71 \text{ cm}^2$$

$$s_{\overline{X}_1 - \overline{X}_2} = \sqrt{\frac{10.71}{10} + \frac{10.71}{8}} = \sqrt{2.41} = 1.55 \text{ cm}$$

$$t = \frac{\overline{X}_1 - \overline{X}_2}{s_{\overline{X}_1 - \overline{X}_2}} = \frac{51.91 - 56.55}{1.55} = \frac{-4.64}{1.55} = -2.99$$

$t_{0.05(1),16} = 1.746$

As t of -2.99 is less than -1.746, H_0 is rejected.

$$0.0025 < P < 0.005 \quad [P = 0.0043]$$

The mean plant height is greater with the newer fertilizer.

In other cases, the one-tailed hypotheses, H_0: $\mu_1 \leq \mu_2$ and H_A: $\mu_1 > \mu_2$, may be appropriate. Just as introduced in the one-sample testing of Sections 7.1 and 7.2, the following summary of procedures applies to two-sample t testing:

For H_A: $\mu_1 \neq \mu_2$, if $|t| \geq t_{\alpha(2),\nu}$, then reject H_0.

For H_A: $\mu_1 < \mu_2$, if $t \leq -t_{\alpha(1),\nu}$, then reject H_0.*

For H_A: $\mu_1 > \mu_2$, if $t \geq t_{\alpha(1),\nu}$, then reject H_0.†

As indicated in Section 6.3, the null and alternate hypotheses are to be decided upon *before* the data are collected.

Also, H_0: $\mu_1 \leq \mu_2$ and H_A: $\mu_1 > \mu_2$ may be written as H_0: $\mu_1 - \mu_2 \leq 0$ and H_A: $\mu_1 - \mu_2 > 0$, respectively. The generalized hypotheses for this type of one-tailed test are H_0: $\mu_1 - \mu_2 \leq \mu_0$ and H_A: $\mu_1 - \mu_2 > \mu_0$, for which the t is

$$t = \frac{\overline{X}_1 - \overline{X}_2 - \mu_0}{s_{\overline{X}_1 - \overline{X}_2}}, \tag{8.10}$$

and μ_0 may be any specified value of $\mu_1 - \mu_2$.

Lastly, H_0: $\mu_1 \geq \mu_2$ and H_A: $\mu_1 < \mu_2$ may be written as H_0: $\mu_1 - \mu_2 \geq 0$ and H_A: $\mu_1 - \mu_2 < 0$, and the generalized one-tailed hypotheses of this type are H_0: $\mu_1 - \mu_2 \geq \mu_0$ and H_A: $\mu_1 - \mu_2 < \mu_0$, with the appropriate t statistic being that of Equation 8.10. For example, the gardener collecting the data of Example 8.2 may have decided, because the newer fertilizer is more expensive than the other, that it should be used only if the plants grown with it averaged at least 5.0 cm taller than plants grown with the present fertilizer. Then, $\mu_0 = \mu_1 - \mu_2 = -5.0$ cm and, by Equation 8.10, we would calculate $t = (51.91 - 56.55 + 5.0)/1.55 = 0.36/1.55 = 0.232$, which is not $\geq$ the critical value shown in Example 8.2; so H_0: $\mu_1 - \mu_2 \geq -5.0$ cm is not rejected. The following summary of procedures applies to these general hypotheses:

For H_A: $\mu_1 - \mu_2 \neq \mu_0$, if $|t| \geq t_{\alpha(2),\nu}$, then reject H_0.

For H_A: $\mu_1 - \mu_2 < \mu_0$, if $t \leq -t_{\alpha(1),\nu}$, then reject H_0.

For H_A: $\mu_1 - \mu_2 > \mu_0$, if $t \geq t_{\alpha(1),\nu}$, then reject H_0.

*For this one-tailed hypothesis test, probabilities of t up to 0.25 are indicated in Appendix Table B.3. If $t = 0$, then $P = 0.50$; so if $-t_{0.25(1),\nu} < t < 0$, then $0.25 < P < 0.50$; and if $t > 0$ then $P > 0.50$.

†For this one-tailed hypothesis test, $t = 0$ indicates $P = 0.50$; therefore, if $0 < t < t_{0.25(1),\nu}$, then $0.25 < P < 0.50$; and if $t < 0$, then $P > 0.50$.

(b) Violations of the Two-Sample *t*-test Assumptions. The validity of two-sample t testing depends upon two basic assumptions: that the two samples came at random from normal populations and that the two populations had the same variance. Populations of biological data will not have distributions that are exactly normal or variances that are exactly the same. Therefore, it is fortunate that numerous studies, over 70 years, have shown that this t test is robust enough to withstand considerable nonnormality and some inequality of variances. This is especially so if the two sample sizes are equal or nearly equal, particularly when two-tailed hypotheses are tested (e.g., Boneau, 1960; Box, 1953; Cochran, 1947; Havlicek and Peterson, 1974; Posten, Yen, and Owen, 1982; Srivastava, 1958; Stonehouse and Forrester, 1998; Tan, 1982; Welch, 1938) but also in one-tailed testing (Posten, 1992).

In general, the larger and the more equal in size the samples are, the more robust the test will be; and sample sizes of at least 30 provide considerable resistance effects of violating the t-test assumptions when testing at $\alpha = 5\%$ (i.e., the 0.05 level of signficance), regardless of the disparity between σ_1^2 and σ_2^2 (Donaldson, 1968; Ramsey, 1980; Stonehouse and Forrester, 1998); larger sample sizes are needed for smaller α's, smaller n's will suffice for larger significance levels, and larger samples are required for larger differences between σ_1 and σ_2.

Hsu (1938) reported remarkable robustness, even in the presence of very unequal variances and very small samples, if $n_1 = n_2 + 1$ and $\sigma_1^2 > \sigma_2^2$. So, if it is believed (by inspecting s_1^2 and s_2^2) that the population variances (σ_1^2 and σ_2^2) are dissimilar, one might plan experiments that have samples that are unequal in size by 1, where the larger sample comes from the population with the larger variance. But the procedure of Section 8.1c, below, has received a far greater amount of study and is much more commonly employed.

The two-sample t test is very robust to nonnormality if the population variances are the same (Kohr and Games, 1974; Posten, 1992; Posten, Yeh, and Owen, 1982; Ramsey, 1980; Stonehouse and Forrester, 1998; Tomarkin and Serlin, 1986). If the two populations have the same variance and the same shape, the test works well even if that shape is extremely nonnormal (Stonehouse and Forrester, 1998; Tan, 1982). Havlicek and Peterson (1974) specifically discuss the effect of skewness and leptokurtosis.

If the population variances are unequal but the sample sizes are the same, then the probability of a Type I error will tend to be greater than the stated α (Havlicek and Peterson, 1974; Ramsey, 1980), and the test is said to be *liberal*. As seen in Table 8.1a, this departure from α will be less for smaller differences between σ_1^2 and σ_2^2 and for larger sample sizes. (The situation with the most heterogeneous variances is where σ_1^2/σ_2^2 is zero (0) or infinity (∞).)

If the two variances are not equal *and* the two sample sizes are not equal, then the probability of a Type I error will differ from the stated α. If the larger σ^2 is associated with the larger sample, this probability will be less than the stated α (and the test is called *conservative*) and this probability will be greater than the stated α (and the test is called *liberal*) if the smaller sample came from the population with the larger variance (Havlicek and Peterson, 1974; Ramsey, 1980; Stonehouse and Forrester, 1998; Zimmerman, 1987).* The greater the difference between variances, the greater will be the disparity between the probability of a Type I error and the specified α, larger differences will also result in greater departure from α. Table 8.1b

*The reason for this can be seen from Equations 8.4–8.7a: If the larger s_i^2 is coupled with the larger n_i, then the numerator of s_p^2 (which is $\nu_1 s_1^2 + \nu_2 s_2^2$) is greater than if the larger variance is associated with the smaller n. This makes s_p^2 larger, which translates into a larger $s_{\bar{X}_1 - \bar{X}_2}^2$, which produces a smaller t, resulting in a probability of a Type I error lower than the stipulated α.

TABLE 8.1a: Maximum Probabilities of Type I Error when Applying the Two-Tailed *(or, One-Tailed)* t Test to Two Samples of Various Equal Sizes ($n_1 = n_2 = n$), Taken from Normal Populations Having Various Variance Ratios, σ_1^2/σ_2^2

σ_1^2/σ_2^2	n:	3	5	10	15 [16]	20	30	∞
				For $\alpha = 0.05$				
3.33 or 0.300		0.059	0.056	0.054	0.052	0.052	0.051	0.050
5.00 or 0.200		0.064	0.061	0.056	0.054	0.053	0.052	0.050
10.00 or 0.100			0.068	0.059	0.056	0.055	0.053	0.050
∞ or 0		0.109	0.082	0.065	0.060	0.057	0.055	0.050
∞ or 0		*(0.083)*	*(0.068)*	*(0.058)*	*(0.055)*	*(0.054)*	*(0.053)*	*(0.050)*
				For $\alpha = 0.01$				
3.33 or 0.300		0.013	0.013	0.012	[0.011]	0.011	0.011	0.010
5.00 or 0.200		0.015	0.015	0.013	[0.012]	0.011	0.011	0.010
10.00 or 0.100		0.020	0.019	0.015	[0.013]	0.012	0.012	0.010
∞ or 0		0.044	0.028	0.018	[0.015]	0.014	0.013	0.010
∞ or 0		*(0.032)*	*(0.022)*	*(0.015)*	*(0.014)*	*(0.013)*	*(0.012)*	*(0.010)*

These probabilities are gleaned from the extensive analysis of Ramsey (1980), and from Table 1 of Posten, Yeh, and Owen (1982).

shows this for various sample sizes. For example, Table 8.1a indicates that if 20 data are distributed as $n_1 = n_2 = 10$ and the two-tailed t test is performed at the 0.05 significance level, the probability of a Type I error approaches 0.065 for greatly divergent population variances. But in Table 8.1b we see that if $\alpha = 0.05$ is used and 20 data are distributed as $n_1 = 9$ and $n_2 = 11$, then the probability of a Type I error can be as small as 0.042 (if the sample of 11 came from the population with the larger variance) or as large as 0.096 (if the sample of 9 came from the population with the smaller variance).

Section 6.3b explained that a decrease in the probability of the Type I error (α) is associated with an increase in the probability of a Type II error (β); and, because power is $1 - \beta$, an increase in β means a decrease in the power of the test ($1 - \beta$). Therefore, for situations described above as conservative—that is, P(Type I error) $< \alpha$—there will generally be less power than if the population variances were all equal; and when the test is liberal—that is, P(Type I error) $> \alpha$—there will generally be more power than if the variances were equal. (See also Zimmerman and Zumbo, 1993.)

The power of the two-tailed t test is affected very little by small or moderate skewness in the sampled populations, especially if the sample sizes are equal, but there can be a serious effect on one-tailed tests. As for kurtosis, the actual power of the test is less than that discussed in Section 8.4 when the populations are platykurtic and greater when they are leptokurtic, especially for small sample sizes (Boneau, 1960; Glass, Peckham, and Sanders, 1972). The adverse effect of nonnormality is less with large sample sizes (Srivastava, 1958).

(c) The Two-sample t Test with Unequal Variances. As indicated above, the t test for difference between two means is robust to some departure from its underlying assumptions; but it is not dependable when the two population variances are very different. The latter situation is known as the Behrens-Fisher problem, referring to the early work on it by Behrens (1929) and Fisher (e.g., 1939b), and numerous

TABLE 8.1b: Maximum Probabilities of Type I Error when Applying the Two-Tailed *(or One-Tailed)* t Test to Two Samples of Various Unequal Sizes, Taken from Normal Populations Having the Largest Possible Difference between Their Variances

		For $\alpha = 0.05$		For $\alpha = 0.01$	
n_1	n_2	σ_1^2 large	σ_1^2 small	σ_1^2 large	σ_1^2 small
11	9	0.042	0.096	0.0095	0.032
		(0.041)	*(0.079)*	*(0.0088)*	*(0.026)*
22	18	0.036	0.086	0.0068	0.026
		(0.038)	*(0.073)*	*(0.0068)*	*(0.021)*
33	27	0.034	0.082	0.0059	0.024
		(0.037)	*(0.072)*	*(0.0062)*	*(0.020)*
55	45	0.032	0.080	0.0053	0.022
		(0.036)	*(0.070)*	*(0.0057)*	*(0.019)*
12	8	0.025	0.13	0.0045	0.054
		(0.028)	*(0.098)*	*(0.0046)*	*(0.040)*
24	16	0.020	0.12	0.0029	0.044
		(0.025)	*(0.096)*	*(0.0033)*	*(0.034)*
36	24	0.019	0.12	0.0024	0.041
		(0.023)	*(0.094)*	*(0.0029)*	*(0.032)*
60	40	0.018	0.11	0.0021	0.039
		(0.023)	*(0.092)*	*(0.0026)*	*(0.031)*

From Posten, Yeh, and Owen (1982) and Posten (1992).

other studies of this problem have ensued (e.g., Best and Raynor, 1987; Dixon and Massey, 1969: 119; Fisher and Yates, 1963: 60–61;* Gill, 1971; Kim and Cohen, 1998; Lee and Fineberg, 1991; Lee and Gurland, 1975; Satterthwaite, 1946; Scheffé, 1970; Zimmerman and Zumbo, 1993). Several solutions have been proffered, and they give very similar results except for very small samples. One of the easiest, yet reliable, of available procedures is that attributed to Smith (1936) and is often known as the "Welch approximate t"† (Davenport and Webster, 1975; Mehta and Srinivasan, 1971; Wang, 1971; Welch, 1936, 1938, 1947). It has been shown to perform well with respect to Type I error, and it requires no special tables.

The test statistic is that of Equation 8.1 or 8.9, but with $s_{\overline{X}_1 - \overline{X}_2}$ (the standard error of the difference between the means) calculated with the two separate variances instead of with a pooled variance; that is,

$$s'_{\overline{X}_1 - \overline{X}_2} = \sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}} \tag{8.11a}$$

instead of Equation 8.6. And, because $s_{\overline{X}_i} = s_i^2/n_i$ (Equation 6.7), this can be written equivalently as

$$s'_{\overline{X}_1 - \overline{X}_2} = \sqrt{s_{\overline{X}_1}^2 + s_{\overline{X}_2}^2}. \tag{8.11b}$$

*In Fisher and Yates (1963), s refers to the standard error, not the standard deviation.

†Bernard Lewis Welch (1911–1989), English statistician. (See Mardia, 1990.)

Therefore, Equation 8.1 becomes

$$t' = \frac{\overline{X}_1 - \overline{X}_2}{\sqrt{s^2_{\overline{X}_1} + s^2_{\overline{X}_2}}}, \tag{8.11c}$$

Equation 8.11 becomes

$$t' = \frac{\overline{X}_1 - \overline{X}_2 - \mu_0}{\sqrt{s^2_{\overline{X}_1} + s^2_{\overline{X}_2}}}, \tag{8.11d}$$

and two-tailed and one-tailed hypotheses are tested as described earlier for t.

Tables of critical values of t' have been published, but they are not extensive. Satterthwaite (1946) and Scheffé (1970) approximated the distribution of t' well by using t with degrees of freedom of

$$\nu' = \frac{\left(s^2_{\overline{X}_1} + s^2_{\overline{X}_2}\right)^2}{\frac{\left(s^2_{\overline{X}_1}\right)^2}{n_1 - 1} + \frac{\left(s^2_{\overline{X}_2}\right)^2}{n_2 - 1}}. \tag{8.12}$$

These degrees of freedom can be as small as $n_1 - 1$ or $n_2 - 1$, whichever is smaller, and as large as $n_1 + n_2 - 2$. However, ν' is typically not an integer, so the critical value of t' often will not be found in Appendix Table B.3. If ν' is not an integer, the needed critical value, $t_{\alpha,\nu}$, can be obtained via some computer software; or these values can be interpolated from the t's in Table B.3 (the beginning of Appendix B explains interpolation, and at the end of Table B.3 there is an indication of the accuracy of interpolation for t); or, less accurately, the closest integer to ν' (or, to be conservative, the nearest integer less than ν') can be used as the degrees of freedom in Table B.3. The Behrens-Fisher test is demonstrated in Example 8.2a.*

*In the highly unlikely situation where the variances (σ_1^2 and σ_2^2) of the two sampled populations are known, the test for difference between means could be effected with

$$Z = \frac{|\overline{X}_1 - \overline{X}_2| - \mu_0}{\sqrt{\sigma_1^2/n_1 + \sigma_2^2/n_2}}; \tag{8.12a}$$

and it can be recalled that $Z_\alpha = t_{\alpha,\infty}$. If the variance ($\sigma_1^2$) of one of the two populations is known, this test statistic and degrees of freedom may be employed (Maity and Sherman, 2006):

$$t = \frac{|\overline{X}_1 - \overline{X}_2| - \mu_0}{\sqrt{\sigma_1^2/n_1 + s_2^2/n_2}}; \tag{8.12b}$$

$$\nu' = \frac{\left(\sigma_1^2/n_1 + s_2^2/n_2\right)^2}{\frac{s_2^2/n_2}{n_2 - 1}}. \tag{8.12c}$$

EXAMPLE 8.2a The Behrens-Fisher Test for the Two-Tailed Hypotheses, H_0: $\mu_1 = \mu_2$ and H_A: $\mu_1 \neq \mu_2$

The data are the times for seven cockroach eggs to hatch at one laboratory temperature and for eight eggs to hatch at another temperature.

H_0: $\mu_1 = \mu_2$
H_A: $\mu_1 \neq \mu_2$

At 30°C	At 10°C
40 days	36 days
38	45
32	32
37	52
39	59
41	41
35	48
	55

$n_1 = 7$	$n_2 = 8$
$\nu_1 = 6$	$\nu_2 = 7$
$\overline{X}_1 = 37.4$ days	$\overline{X}_2 = 46.0$ days
$SS_1 = 57.71$ days^2	$SS_2 = 612.00$ days^2
$s_1^2 = 9.62$ days^2	$s_2^2 = 87.43$ days^2
$s_{\overline{X}_1}^2 = 1.37$ days^2	$s_{\overline{X}_2}^2 = 10.93$ days^2

$$s'_{\overline{X}_1 - \overline{X}_2} = \sqrt{s_{\overline{X}_1}^2 + s_{\overline{X}_2}^2} = \sqrt{1.37 + 10.83} = 3.51 \text{ days}$$

$$t' = \frac{\overline{X}_1 - \overline{X}_2}{s'_{\overline{X}_1 - \overline{X}_2}} = \frac{37.4 - 46.00}{3.51} = -2.450$$

$$\nu' = \frac{\left(s_{\overline{X}_1}^2 + s_{\overline{X}_2}^2\right)^2}{\frac{\left(s_{\overline{X}_1}^2\right)^2}{\nu_1} + \frac{\left(s_{\overline{X}_2}^2\right)^2}{\nu_2}} = \frac{(1.37 + 10.93)^2}{\frac{(1.37)^2}{6} + \frac{(10.93)^2}{7}} = 8.7$$

$t_{0.05(2),8.7} = 2.274$*

Therefore, reject H_0.

[$P = 0.038$.]*

*These values were obtained by computer.

As with t, the robustness of t' is greater with large and with equal sample sizes. If $\sigma_1^2 = \sigma_2^2$, then either t or t' can be used, but t will be the more powerful procedure (Ramsey, 1980), but generally with only a very slight advantage over t' (Best and Rayner, 1987). If $n_1 = n_2$ and $s_1^2 = s_2^2$, then $t' = t$ and $\nu' = \nu$; but t' is not as powerful and not as robust to nonnormality as t is (Stonehouse and Forrester, 1998; Zimmerman and Zumbo, 1993). However, Best and Rayner (1987) found t' to be much better when the variances and the sample sizes are unequal. They, and Davenport and Webster (1975), reported that the probabilty of a Type I error in the t' test is related to the ratio $(n_2\sigma_1^2)/(n_1\sigma_2^2)$ (let's call this ratio r for the present): When $r > 1$ and $n_1 > n_2$, then this error is near the α specified for the significance test; when $r > 1$ and $n_1 < n_2$, then the error diverges from that α to an extent reflecting the magnitude of r and the difference betwen n_1 and n_2. And, if $r < 1$, then the error is close to the stated α if $n_1 < n_2$, and it departs from that α if $n_1 > n_2$ (differing to a greater extent as the difference between the sample sizes is larger and the size of r is greater). But, larger sample sizes result in less departure from the α used in the hypothesis test.

The effect of heterogeneous variances on the t test can be profound. For example, Best and Rayner (1987) estimated that a t test with $n_1 = 5$ and $n_2 = 15$, and $\sigma_1/\sigma_2 = 4$, has a probabilty of a Type I error using t of about 0.16; and, for those sample sizes when $\sigma_1/\sigma_2 = 0.25$, P(Type I error) is about 0.01; but the probability of that error in those cases is near 0.05 if t' is employed. When the two variances are unequal, the Brown-Forsythe test mentioned in Section 10.1g could also be employed and would be expected to perform similarly to the Behrens-Fisher test, though generally not as well.

If the Behrens-Fisher test concludes difference between the means, a confidence interval for that difference may be obtained in a manner analogous to that in Section 8.2: The procedure is to substitute $s'_{\overline{X}_1 - \overline{X}_2}$ for $s_{\overline{X}_1 - \overline{X}_2}$ and to use ν' instead of ν in Equation 8.14.

Because the t test is adversely affected by heterogeneity of variances, some authors have recommended a two-step testing process: (1) The two sample variances are compared, and (2) only if the two population variances are concluded to be similar should the t test be employed. The similarity of variances may be tested by the procedures of Section 8.5. However, considering that the Behrens-Fisher t' test is so robust to variance inequality (and that the most common variance-comparison test performs very poorly when the distributions are nonnormal or asymmetrical), the routine test of variances is not recommended as a precursor to the testing of means by either t or t' (even though some statistical software packages perform such a test). Gans (1991) and Markowski and Markowski (1990) enlarge upon this conclusion; Moser and Stevens (1992) explain that there is no circumstance when the testing of means using either t or t' is improved by preliminary testing of variances; and Sawilowski (2002) and Wehrhahn and Ogawa (1978) state that the t test's probability of a Type I error may differ greatly from the stated α if such two-step testing is employed.

(d) Which Two-Sample Test to Use. It is very important to inform the reader of a research report specifically what statistical procedures were used in the presentation and analysis of data. It is also generally advisable to report the size (n), the mean ($\overline{X}$), and the variability (variance, standard deviation, or standard error) of each group of data; and confidence limits for each mean and for the difference between the means (Section 8.2) may be expressed if the mean came from a normally distributed population. Visualization of the relative magnitudes of means and measures of variability may be aided by tables or graphs such as described in Section 7.4.

Major choices of statistical methods for comparing two samples are as follows:

- If the two sampled populations are normally distributed and have identical variances (or if they are only slightly to moderately nonnormal and have similar variances): The t test for difference between means is appropriate and preferable. (However, as samples nearly always come from distributions that are not exactly normal with exactly the same variances, conclusions to reject or not reject a null hypothesis should not be considered definitive when the probability associated with t is very near the specified α. For example, if testing at the 5% level of significance, it should not be emphatically declared that H_0 is false if the probability of the calculated t is 0.048. The conclusion should be expressed with caution and, if feasible, the experiment should be repeated—perhaps with more data.)
- If the two sampled populations are distributed normally (or are only slightly to moderately nonnormal), but they have very dissimilar variances: The Behrens-Fisher test of Section 8.1c is appropriate and preferable to compare the two means.
- If the two sampled populations are very different from normally distributed, but they have similar distribution shapes and variances: The Mann-Whitney test of Section 8.11 is appropriate and preferable.
- If the two sampled populations have distributions greatly different from normal and do not have similar distributions and variances: (1) Consider the procedures of Chapter 13 for data that do not exhibit normality and variance equality but that can be transformed into data that are normal and homogeneous of variance; or (2) refer to the procedure mentioned at the end of Section 8.11, which modifies the Mann-Whitney test for Behrens-Fisher situations; or (3) report the mean and variability for each of the samples, perhaps also presenting them in tables and/or graphs (as in Section 7.4), and do not perform hypothesis testing.*

(e) Replication of Data. It is important to use data that are true replicates of the variable to be tested (and recall that a replicate is the smallest experimental unit to which a treatment is independently applied). In Example 8.1 the purpose of the experiment was to ask whether there is a difference in blood-clotting times between persons administered two different drugs. This necessitates obtaining a blood measurement on each of n_1 individuals in the first sample (receiving one of the drugs) and n_2 individuals in the second sample (receiving the other drug). It would not be valid to use n_1 measurements from a single person and n_2 measurements from another person, and to do so would be engaging in what Hurlbert (1984), and subsequently many others, discuss as *pseudoreplication*.

8.2 CONFIDENCE LIMITS FOR POPULATION MEANS

In Section 7.3, we defined the confidence interval for a population mean as $\overline{X} \pm t_{\alpha(2),\nu} s_{\overline{X}}$, where $s_{\overline{X}}$ is the best estimate of $\sigma_{\overline{X}}$ and is calculated as $\sqrt{s^2/n}$. For the

*Another procedure, seldom encountered but highly recommended by Yuen (1974), is to perform the Behrens-Fisher test on *trimmed means* (also known as "truncated means"). A trimmed mean is a sample mean calculated after deleting data from the extremes of the tails of the data distribution. There is no stipulated number of data to be deleted, but it is generally the same number for each tail. The degrees of freedom are those pertaining to the number of data remaining after the deletion.

two-sample situation where we assume that $\sigma_1^2 = \sigma_2^2$, the confidence interval for either μ_1 or μ_2 is calculated using s_p^2 (rather than either s_1^2 or s_2^2) as the best estimate of σ^2, and we use the two-tailed tabled t value with $\nu = \nu_1 + \nu_2$ degrees of freedom. Thus, for μ_i (where i is either 1 or 2, referring to either of the two samples), the $1 - \alpha$ confidence interval is

$$\overline{X}_i \pm t_{\alpha(2),\nu}\sqrt{\frac{s_p^2}{n_i}}. \tag{8.13}$$

For the data of Example 8.1, $\sqrt{s_p^2/n_2} = \sqrt{0.5193\ \text{min}^2/7} = 0.27$ min. Thus, the 95% confidence interval for μ_2 would be 9.74 min $\pm$ (2.201)(0.27 min) = 9.74 min $\pm$ 0.59 min, so that L_1 (the lower confidence limit) = 9.15 min and L_2 (the upper confidence limit) = 10.33 min, and we can declare with 95% confidence that, for the population of blood-clotting times after treatment with drug G, the population mean, μ_2, is no smaller than 9.15 min and no larger than 10.33 min. This may be written as $P(9.15\ \text{min} \leq \mu_2 \leq 10.33\ \text{min}) = 0.95$. The confidence interval for the population mean of data after treatment with drug B would be 8.75 min $\pm(2.201)\sqrt{0.5193\ \text{min}^2/6} = 8.75\ \text{min} \pm 0.64\ \text{min}$; so $L_1 = 8.11$ min and $L_2 = 9.39$ min. Further interpretation of the meaning of the confidence interval for each of these two population means is in Section 7.3.

Confidence limits for the difference between the two population means can also be computed. The $1 - \alpha$ confidence interval for $\mu_1 - \mu_2$ is

$$\overline{X}_1 - \overline{X}_2 \pm t_{\alpha(2),\nu}s_{\overline{X}_1 - \overline{X}_2}. \tag{8.14}$$

Thus, for Example 8.1, the 95% confidence interval for $\mu_1 - \mu_2$ is (8.75 min $-$ 9.74 min) $\pm$ (2.201)(0.40 min) = -0.99 min $\pm$ 0.88 min. Thus, $L_1 = -1.87$ min and $L_2 = -0.11$ min, and we can write $P(-1.87\ \text{min} \leq \mu_1 - \mu_2 \leq -0.11\ \text{min}) = 0.95$.

If H_0: $\mu_1 = \mu_2$ is not rejected, then both samples are concluded to have come from populations having identical means, the common mean being denoted as μ. The best estimate of μ is the "pooled" or "weighted" mean:

$$\overline{X}_p = \frac{n_1\overline{X}_1 + n_2\overline{X}_2}{n_1 + n_2}, \tag{8.15}$$

which is the mean of the combined data from the two samples. Then the $1 - \alpha$ confidence interval for μ is

$$\overline{X}_p \pm t_{\alpha(2),\nu}\sqrt{\frac{s_p^2}{n_1 + n_2}}. \tag{8.16}$$

If H_0 is not rejected, it is the confidence interval of Equation 8.16, rather than those of Equations 8.13 and 8.14, that one would calculate.

As is the case with the t test, these confidence intervals are computed with the assumption that the two samples came from normal populations with the same variance. If the sampled distributions are far from meeting these conditions, then confidence intervals should be eschewed or, if they are reported, they should be presented with the caveat that they are only approximate.

If a separate $1 - \alpha$ confidence interval is calculated for μ_1 and for μ_2, it may be tempting to draw a conclusion about H_0: $\mu_1 = \mu_2$ by observing whether the two confidence intervals overlap. Overlap is the situation where L_1 for the larger mean is less than L_2 for the smaller mean, and such conclusions are made visually

enticing if the confidence intervals are presented in a graph (such as in Figure 7.5) or in a table (e.g., as in Table 7.3b). However, this is *not* a valid procedure for hypothesis testing (e.g., Barr, 1969; Browne, 1979; Ryan and Leadbetter, 2002; Schenker and Gentleman, 2001). If there is no overlap and the population means are consequently concluded to be different, this inference will be associated with a Type I error probability less than the specified α (very much less if the two standard errors are similar); and if there is overlap, resulting in failure to reject H_0, this conclusion will be associated with a probability of a Type II error greater than (i.e., a power less than) if the appropriate testing method were used. As an illustration if this, the data of Example 8.1 yield $L_1 = 8.11$ min and $L_2 = 9.39$ min for the mean of group B and $L_1 = 9.15$ min and $L_2 = 10.33$ min for the mean of group G; and the two confidence intervals overlap even though the null hypothesis is rejected.

(a) One-Tailed Confidence Limits for Difference between Means. If the two-sample t test is performed to assess one-tailed hypotheses (Section 7.2), then it is appropriate to determine a one-tailed confidence interval (as was done in Section 7.3a following a one-tailed one-sample t test). Using one-tailed critical values of t, the following confidence limits apply:

For H_0: $\mu_1 \leq \mu_2$ versus $\mu_1 > \mu_2$, or $\mu_1 - \mu_2 \leq \mu_0$ versus H_0: $\mu_1 - \mu_2 > \mu_0$:

$$L_1 = \overline{X} - \left(t_{\alpha(1),\nu}\right)\left(s_{\overline{X}_1 - \overline{X}_2}\right) \text{ and } L_2 = \infty.$$

For H_0: $\mu_1 \geq \mu_2$ versus $\mu_1 < \mu_2$, or $\mu_1 - \mu_2 \geq \mu_0$ versus $\mu_1 - \mu_2 < \mu_0$:

$$L_1 = -\infty \text{ and } L_2 = \overline{X} + \left(t_{\alpha(1),\nu}\right)\left(s_{\overline{X}_1 - \overline{X}_2}\right).$$

In Example 8.2, one-tailed confidence limits would be $L_1 = -\infty$ and $L_2 = (1.746)(1.55) = 2.71$ cm.

(b) Confidence Limits for Means when Variances Are Unequal. If the population variances are judged to be different enough to warrant using the Behrens-Fisher test (Section 8.1c) for H_0: $\mu_1 = \mu_2$, then the computation of confidence limits is altered from that shown above. If this test rejects the null hypothesis, a confidence interval for each of the two population means (μ_1 and μ_2) and a CI for the difference between the means ($\mu_1 - \mu_2$) should be determined. The $1 - \alpha$ confidence interval for μ_i is obtained as

$$\overline{X}_i \pm t_{\alpha(2),\nu'}\sqrt{\frac{s_i^2}{n_i}}, \text{ which is } \overline{X}_i \pm t_{\alpha(2),\nu'}\sqrt{s_{\overline{X}_i}^2}, \tag{8.17}$$

rather than by Equation 8.13, where ν' is from Equation 8.12. The confidence interval for the difference between the two population means is computed to be

$$\overline{X}_1 - \overline{X}_2 \pm \left(t_{\alpha(2),\nu'}\right)\left(s'_{\overline{X}_1 - \overline{X}_2}\right) \tag{8.18}$$

rather than by Equation 8.14, where $s'_{\overline{X}_1 - \overline{X}_2}$ is from Equation 8.11a or 8.11b. One-tailed confidence intervals are obtained as shown in Section 8.2a above, but using $s'_{\overline{X}_1 - \overline{X}_2}$ instead of $s_{\overline{X}_1 - \overline{X}_2}$. A confidence interval (two-tailed or one-tailed) for $\mu_1 - \mu_2$ includes zero when the associated H_0 is not rejected.

In Example 8.2a, H_0 is rejected, so it is appropriate to determine a 95% CI for μ_1, which is $37.4 \pm 2.274\sqrt{1.37} = 37.4$ days $\pm$ 2.7 days; for μ_2, which is $46.0 \pm 2.274\sqrt{10.93} = 46.0$ days $\pm$ 7.5 days; and for $\mu_1 - \mu_2$, which is $37.4 - 46.0 \pm (2.274)(3.51) = -8.6$ days $\pm$ 7.98 days.

If H_0: $\mu_1 = \mu_2$ is not rejected, then a confidence interval for the common mean, $\overline{X}_p$ (Equation 8.15), may be obtained by using the variance of the combined data from the two samples (call it s_t^2) and the degrees of freedom for those combined data ($\nu_t = n_1 + n_2 - 1$):

$$\overline{X}_p \pm t_{\alpha(2),\nu_t}\sqrt{\frac{s_t^2}{n_1 + n_2}}. \tag{8.19}$$

(c) Prediction Limits. As introduced in Section 7.3b, we can predict statistical characteristics of future sampling from populations from which samples have previously been analyzed. Such a desire might arise with data from an experiment such as in Example 8.1. Data were obtained from six animals treated with one drug and from seven animals treated with a second drug; and the mean blood-clotting times were concluded to be different under these two treatments. Equations 8.14 and 8.18 showed how confidence intervals can be obtained for the difference between means of two samples. It could also be asked what the difference between the means would be of an additional sample of m_1 animals treated with the first drug and a sample of an additional m_2 animals treated with the second.

For those two additional samples the best prediction of the difference between the two sample means would be $\overline{X}_1 - \overline{X}_2$, which in Example 8.1 is 8.75 min $-$ 9.74 min $= -0.99$ min; and there would be a $1 - \alpha$ probability that the difference between the two means would be contained in this prediction interval:

$$\overline{X}_1 - \overline{X}_2 \pm t_{\alpha(2),\nu}\sqrt{s_c^2}, \tag{8.19a}$$

where

$$s_c^2 = \frac{s_p^2}{m_1} + \frac{s_p^2}{n_1} + \frac{s_p^2}{m_2} + \frac{s_p^2}{n_2} \tag{8.19b}$$

(Hahn, 1977). For example, if an additional sample of 10 data were to be obtained for treatment with the first drug and an additional sample of 12 were to be acquired for treatment with the second drug, the 95% prediction limits for the difference between means would employ $s_p^2 = 0.5193\ \text{min}^2$, $n_1 = 6$, $n_2 = 7$, $m_1 = 10$, $m_2 = 12$, $t_{0.05(2),\nu=2.201}$, and $\nu = 11$; and $s_c^2 = 0.51$ min, so the 95% prediction limits would be $L_1 = -2.11$ min and $L_2 = 0.13$ min.

As the above procedure uses the pooled variance, s_p^2, it assumes that the two sampled populations have equal variances. If the two variances are thought to be quite different (the Behrens-Fisher situation discussed in Section 8.1c), then it is preferable to calculate the prediction interval as

$$\overline{X}_1 - \overline{X}_2 \pm t_{\alpha(2),\nu'}\sqrt{s_c^2}, \tag{8.19c}$$

where

$$s_c^2 = \frac{s_1^2}{m_1} + \frac{s_1^2}{n_1} + \frac{s_2^2}{m_2} + \frac{s_2^2}{n_2} \tag{8.19d}$$

2. Sample sizes not large enough to result in detection of a difference of biological importance can expend resources without yielding useful results, *and* sample sizes larger than needed to detect a difference of biological importance can result in unnecessary expenditure of resources.
3. Sample sizes not large enough to detect a difference of biological importance can expose subjects in the study to potentially harmful factors without advancing knowledge, *and* sample sizes larger than needed to detect a difference of biological importance can expose more subjects than necessary to potentially harmful factors or deny them exposure to potentially beneficial ones.

Assuming each sample comes from a normal population and the population variances are similar, we can estimate the minimum sample size to use to achieve desired test characteristics:

$$n \geq \frac{2s_p^2}{\delta^2}(t_{\alpha,\nu} + t_{\beta(1),\nu})^2 \tag{8.22}$$

(Cochran and Cox, 1957: 19–21).* Here, δ is the smallest population difference we wish to detect: $\delta = \mu_1 - \mu_2$ for the hypothesis test for which Equation 8.1 is used; $\delta = |\mu_1 - \mu_2| - \mu_0$ when Equation 8.9 is appropriate; $\delta = \mu_1 - \mu_2 - \mu_0$ when performing a test using Equation 8.10. In Equation 8.22, $t_{\alpha,\nu}$ may be either $t_{\alpha(1),\nu}$ or $t_{\alpha(2),\nu}$, depending, respectively, on whether a one-tailed or two-tailed test is to be performed.

Note that the required sample size depends on the following four quantities:

- δ, the minimum detectable difference between population means.† If we desire to detect a very small difference between means, then we shall need a larger sample than if we wished to detect only large differences.
- σ^2, the population variance. If the variability within samples is great, then a larger sample size is required to achieve a given ability of the test to detect differences between means. We need to know the variability to expect among the data; assuming the variance is the same in each of the two populations sampled, σ^2 is estimated by the pooled variance, s_p^2, obtained from similar studies.
- The significance level, α. If we perform the t test at a low α, then the critical value, $t_{\alpha,\nu}$, will be large and a large n is required to achieve a given ability to detect differences between means. That is, if we desire a low probability of committing a Type I error (i.e., falsely rejecting H_0), then we need large sample sizes.
- The power of the test, $1 - \beta$. If we desire a test with a high probability of detecting a difference between population means (i.e., a low probability of committing a Type II error), then $\beta(1)$ will be small, $t_{\beta(1)}$ will be large, and large sample sizes are required.

Example 8.4 shows how the needed sample size may be estimated. As $t_{\alpha(2),\nu}$ and $t_{\beta(1),\nu}$ depend on n, which is not yet known, Equation 8.22 must be solved iteratively, as we did with Equation 7.10. It matters little if the initial guess for n is inaccurate. Each iterative step will bring the estimate of n closer to the final result (which is

*The method of Section 10.3 may also be used for estimation of sample size, but it offers no substantial advantage over the present procedure.

†δ is lowercase Greek delta. If μ_0 in the statistical hypotheses is not zero (see discussion surrounding Equations 8.9 and 8.10), then δ is the amount by which the absolute value of the difference between the population means differs from μ_0.

declared when two successive iterations fail to change the value of n rounded to the next highest integer). In general, however, fewer iterations are required (i.e., the process is quicker) if one guesses high instead of low.

EXAMPLE 8.4 Estimation of Required Sample Size for a Two-Sample t Test

We desire to test for significant difference between the mean blood-clotting times of persons using two different drugs. We wish to test at the 0.05 level of significance, with a 90% chance of detecting a true difference between population means as small as 0.5 min. The within-population variability, based on a previous study of this type (Example 8.1), is estimated to be 0.52 min^2.

Let us guess that sample sizes of 100 will be required. Then, $\nu = 2(n - 1) = 2(100 - 1) = 198, t_{0.05(2),198} \approx 1.972, \beta = 1 - 0.90 = 0.10, t_{0.10(1),198} = 1.286$, and we calculate (by Equation 8.22):

$$n \geq \frac{2(0.52)}{(0.5)^2}(1.972 + 1.286)^2 = 44.2.$$

Let us now use $n = 45$ to determine $\nu = 2(n - 1) = 88$, $t_{0.05(2),88} = 1.987$, $t_{0.10(1),88} = 1.291$, and

$$n \geq \frac{2(0.52)}{(0.5)^2}(1.987 + 1.291)^2 = 44.7.$$

Therefore, we conclude that each of the two samples should contain at least 45 data.

If n_1 were constrained to be 30, then, using Equation 8.21, the required n_2 would be

$$n_2 = \frac{(44.7)(30)}{2(30) - 44.7} = 88.$$

For a given total number of data ($n_1 + n_2$), maximum test power and robustness occur when $n_1 = n_2$ (i.e., the sample sizes are equal). There are occasions, however, when equal sample sizes are impossible or impractical. If, for example, n_1 were fixed, then we would first determine n by Equation 8.22 and then find the required size of the second sample by Equation 8.21, as shown in Example 8.4. Note, from this example, that a total of $45 + 45 = 90$ data are required in the two equal-sized samples to achieve the desired power, whereas a total of $30 + 88 = 118$ data are needed if the two samples are as unequal as in this example. If $2n - 1 \leq 0$, then see the discussion following Equation 8.21.

(b) Minimum Detectable Difference. Equation 8.22 can be rearranged to estimate how small a population difference (δ, defined above) would be detectable with a given sample size:

$$\delta \geq \sqrt{\frac{2s_p^2}{n}}(t_{\alpha,\nu} + t_{\beta(1),\nu}). \tag{8.23}$$

The estimation of δ is demonstrated in Example 8.5.

EXAMPLE 8.5 Estimation of Minimum Detectable Difference in a Two-Sample *t* Test

In two-tailed testing for significant difference between mean blood-clotting times of persons using two different drugs, we desire to use the 0.05 level of significance and sample sizes of 20. What size difference between means do we have a 90% chance of detecting?

Using Equation 8.23 and the sample variance of Example 8.1, we calculate:

$$\delta = \sqrt{\frac{2(0.5193)}{20}}(t_{0.05(2),38} + t_{0.10(1),38})$$
$$= (0.2279)(2.024 + 1.304) = 0.76 \text{ min.}$$

In a Behrens-Fisher situation (i.e., if we don't assume that $\sigma_1^2 = \sigma_2^2$), Equation 8.23 would employ $\sqrt{s_1^2/n + s_2^2/n}$ instead of $\sqrt{2s_p^2/n}$.

(c) Power of the Test. Further rearrangement of Equation 8.22 results in

$$t_{\beta(1),\nu} \leq \frac{\delta}{\sqrt{\frac{2s_p^2}{n}}} - t_{\alpha,\nu}, \tag{8.24}$$

which is analogous to Equation 7.12 in Section 7.7. On computing $t_{\beta(1),\nu}$, one can consult Appendix Table B.3 to determine $\beta(1)$, whereupon $1 - \beta(1)$ is the power. But this generally will only result in declaring a range of power (e.g., $0.75 <$ power < 0.90). Some computer programs can provide the exact probability of $\beta(1)$, or we may, with only slight overestimation of power (as noted in the footnote in Section 7.7) consider $t_{\beta(1)}$ to be approximated by a normal deviate and may thus employ Appendix Table B.2.

If the two population variances are not assumed to be the same, then $\sqrt{s_1^2/n + s_2^2/n}$ would be used in place of $\sqrt{2s_p^2/n}$ in Equation 8.24.

The above procedure for estimating power is demonstrated in Example 8.6, along with the following method (which will be expanded on in the chapters on analysis of variance). We calculate

$$\phi = \sqrt{\frac{n\delta^2}{4s_p^2}} \tag{8.25}$$

(derived from Kirk, 1995: 182) and ϕ (lowercase Greek phi) is then located in Appendix Figure B.1a, along the lower axis (taking care to distinguish between ϕ's for $\alpha = 0.01$ and $\alpha = 0.05$). Along the top margin of the graph are indicated pooled degrees of freedom, ν, for α of either 0.01 or 0.05 (although the symbol ν_2 is used on the graph for a reason that will be apparent in later chapters). By noting where ϕ vertically intersects the curve for the appropriate ν, one can read across to either the left or right axis to find the estimate of power. As noted in Section 7.7c, the calculated power is an estimate of the probability of rejecting a false null hypothesis in future statistical tests; it is not the probability of rejecting H_0 in tests performed on the present set of data.

EXAMPLE 8.6 Estimation of the Power of a Two-Sample *t* Test

What would be the probability of detecting a true difference of 1.0 min between mean blood-clotting times of persons using the two drugs of Example 8.1, if $n_1 = n_2 = 15$, and $\alpha(2) = 0.05$?

For $n = 15$, $\nu = 2(n - 1) = 28$ and $t_{0.05(2),28} = 2.048$. Using Equation 8.24:

$$t_{\beta(1),28} \leq \frac{1.0}{\sqrt{\frac{2(0.5193)}{15}}} - 2.048 = 1.752.$$

Consulting Appendix Table B.3, we see that, for one-tailed probabilities and $\nu = 28$: $0.025 < P(t \geq 1.752) < 0.05$, so $0.025 < \beta < 0.05$.

$$\text{Power} = 1 - \beta, \text{ so } 0.95 < \text{power} < 0.975.$$

Or, by the normal approximation, we can estimate β by $P(Z \geq 1.752) = 0.04$. So power = 0.96. [The exact figures are $\beta = 0.045$ and power = 0.955.]

To use Appendix Figure B.1, we calculate

$$\phi = \sqrt{\frac{n\delta^2}{4s_p^2}} = \sqrt{\frac{(15)(1.0)}{4(0.5193)}} = 2.69.$$

In the first page of Appendix Figure B.1, we find that $\phi = 2.69$ and $\nu(= \nu_2) = 28$ are associated with a power of about 0.96.

(d) Unequal Sample Sizes. For a given total number of data, $n_1 + n_2$, the two-sample t test has maximum power and robustness when $n_1 = n_2$. However, if $n_1 \neq n_2$, the above procedure for determining minimum detectable difference (Equation 8.23) and power (Equations 8.24 and 8.25) can be performed using the harmonic mean of the two sample sizes (Cohen, 1988: 42):

$$n = \frac{2n_1n_2}{n_1 + n_2}. \tag{8.26}$$

Thus, for example, if $n_1 = 6$ and $n_2 = 7$, then

$$n = \frac{2(6)(7)}{6 + 7} = 6.46.$$

8.5 TESTING FOR DIFFERENCE BETWEEN TWO VARIANCES

If we have two samples of measurements, each sample taken at random from a normal population, we might ask if the variances of the two populations are equal. Consider the data of Example 8.7, where s_1^2, the estimate of σ_1^2, is 21.87 moths^2, and s_2^2, the estimate of σ_2^2, is 12.90 moths^2. The two-tailed hypotheses can be stated as H_0: $\sigma_1^2 = \sigma_2^2$ and H_A: $\sigma_1^2 \neq \sigma_2^2$, and we can ask, What is the probability of taking two samples from two populations having identical variances and having the two sample variances be as different as are s_1^2 and s_2^2? If this probability is rather low (say ≤ 0.05, as in previous chapters), then we reject the veracity of H_0 and conclude that the two samples came from populations having unequal variances. If the probability is greater

than α, we conclude that there is insufficient evidence to conclude that the variances of the two populations are not the same.

(a) Variance-Ratio Test. The hypotheses may be submitted to the two-sample *variance-ratio test*, for which one calculates

$$F = \frac{s_1^2}{s_2^2} \quad \text{or} \quad F = \frac{s_2^2}{s_1^2}, \text{ whichever is larger.*} \tag{8.27}$$

That is, the larger variance is placed in the numerator and the smaller in the denominator. We then ask whether the calculated ratio of sample variances (i.e., F) deviates so far from 1.0 as to enable us to reject H_0 at the α level of significance. For the data in Example 8.7, the calculated F is 1.70. The critical value, $F_{0.05(2),10,9}$, is obtained from Appendix Table B.4 and is found to be 3.59. As $1.70 < 3.59$, we do not reject H_0†.

Note that we consider degrees of freedom associated with the variances in both the numerator and denominator of the variance ratio. Furthermore, it is important to realize that F_{α,ν_1,ν_2} and F_{α,ν_2,ν_1} are not the same (unless, of course, $\nu_1 = \nu_2$), so the numerator and denominator degrees of freedom must be referred to in the correct order.

If $H_0: \sigma_1^2 = \sigma_2^2$ is not rejected, then s_1^2 and s_2^2 are assumed to be estimates of the same population variance, σ^2. The best estimate of this σ^2 that underlies both samples is called the *pooled variance* (introduced as Equation 8.4):

$$s_p^2 = \frac{SS_1 + SS_2}{\nu_1 + \nu_2} = \frac{\nu_1 s_1^2 + \nu_2 s_2^2}{\nu_1 + \nu_2}. \tag{8.28}$$

One-tailed hypotheses may also be submitted to the variance ratio test. For $H_0: \sigma_1^2 \geq \sigma_2^2$ and $H_A: \sigma_1^2 < \sigma_2^2$, s_2^2 is always used as the numerator of the variance ratio; for $H_0: \sigma_1^2 \leq \sigma_2^2$ and $H_A: \sigma_1^2 > \sigma_2^2$, s_1^2 is always used as the numerator. (A look at the alternate hypothesis tells us which variance belongs in the numerator of F in order to make $F > 1$.)

The critical value for a one-tailed test is $F_{\alpha(1),\nu_1,\nu_2}$ from Appendix Table B.4, where ν_1 is the degrees of freedom associated with the numerator of F and ν_2 is the degrees of freedom associated with the denominator. Example 8.8 presents the data submitted to the hypothesis test for whether seeds planted in a greenhouse have less variability in germination time than seeds planted outside.

The variance-ratio test is not a robust test, being severely and adversely affected by sampling nonnormal populations (e.g., Box, 1953; Church and Wike, 1976; Markowski and Markowski, 1990; Pearson, 1932; Tan, 1982), with deviations from mesokurtosis somewhat more important than asymmetry; and in cases of nonnormality the probability of a Type I error can be very much greater than α.

*What we know as the F statistic is a ratio of the variances of two normal distributions and was first described by R. A. Fisher in 1924 (and published in 1928) (Lehmann, 1999); the statistic was named in his honor by G. W. Snedecor (1934: 15).

†Some calculators and many computer programs have the capability of determining the probability of a given F. For the present example, we would thereby find that $P(F \geq 1.70) = 0.44$.

EXAMPLE 8.7 The Two-Tailed Variance Ratio Test for the Hypothesis H_0: $\sigma_1^2 = \sigma_2^2$ and H_A: $\sigma_1^2 \neq \sigma_2^2$. The Data Are the Numbers of Moths Caught During the Night by 11 Traps of One Style and 10 Traps of a Second Style

H_0: $\sigma_1^2 = \sigma_2^2$

H_A: $\sigma_1^2 \neq \sigma_2^2$

$\alpha = 0.05$

Trap type 1	*Trap type 2*
41	52
35	57
33	62
36	55
40	64
46	57
31	56
37	55
34	60
30	59
38	

$n_1 = 11$	$n_2 = 10$
$\nu_1 = 10$	$\nu_2 = 9$
$SS_1 = 218.73$ moths^2	$SS_2 = 116.10$ moths^2
$s_1^2 = 21.87$ moths^2	$s_2^2 = 12.90$ moths^2

$$F = \frac{s_1^2}{s_2^2} = \frac{21.87}{12.90} = 1.70$$

$F_{0.05(2),10,9} = 3.96$

Therefore, do not reject H_0.

$$P(0.20 < F < 0.50)[P = 0.44]$$

$$s_p^2 = \frac{218.73 \text{ moths}^2 + 116.10 \text{ moths}^2}{10 + 9} = 17.62 \text{ moths}^2$$

The conclusion is that the variance of numbers of moths caught is the same for the two kinds of traps.

(b) Other Two-Sample Tests for Variances. A large number of statistical procedures to test differences between variances have been proposed and evaluated (e.g., Brown and Forsythe, 1974c; Church and Wike, 1976; Draper and Hunter, 1969; Levene, 1960; Miller, 1972; O'Neill and Mathews, 2000), often with the goal of avoiding the

EXAMPLE 8.8 A One-Tailed Variance-Ratio Test for the Hypothesis That the Germination Time for Pine Seeds Planted in a Greenhouse Is Less Variable Than for Pine Seeds Planted Outside

H_0: $\sigma_1^2 \geq \sigma_2^2$

H_A: $\sigma_1^2 < \sigma_2^2$

$\alpha = 0.05$

Germination Time (in Days) of Pine Seeds

Greenhouse	*Outside*
69.3	69.5
75.5	64.6
81.0	74.0
74.7	84.8
72.3	76.0
78.7	93.9
76.4	81.2
	73.4
	88.0

$n_1 = 7$	$n_2 = 9$
$\nu_1 = 6$	$\nu_2 = 8$
$SS_1 = 90.57$ days^2	$SS_2 = 700.98$ days^2
$s_1^2 = 15.10$ days^2	$s_2^2 = 87.62$ days^2

$$F = \frac{87.62}{15.10} = 5.80$$

$F_{0.05(1),8,6} = 4.15$

Therefore, reject H_0.

$$0.01 < P(F \geq 5.80) < 0.025 \quad [P = 0.023]$$

The conclusion is that the variance in germination time is less in plants grown in the greenhouse than in those grown outside.

lack of robustness of the variance-ratio test when samples come from nonnormal populations of data. A commonly encountered one is Levene's test, and its various modifications, which is typically less affected by nonnormal distributions than the variance-ratio test is.

The concept is to perform a two-sample t test (two-tailed or one-tailed, as the situation warrants; see Section 8.1), not on the values of X in the two samples but on values of the data after conversion to other quantities. A common conversion is to employ the deviations of each X from its group mean or median; that is, the two-sample t test is performed on $|X_{ij} - \overline{X}_i|$ or on $|X_{ij} -$ median of group $i|$. Other

data conversions, such as the square root or the logarithm of $|X_{ij} - \overline{X}_i|$, have also been examined (Brown and Forsythe, 1974c).

Levene's test is demonstrated in Example 8.9 for two-tailed hypotheses, and X' is used to denote $|X_i - \overline{X}|$. This procedure may also be employed to test one-tailed hypotheses about variances, either H_0: $\sigma_1^2 \geq \sigma_2^2$ vs. H_A: $\sigma_1^2 < \sigma_2^2$, or H_0: $\sigma_1^2 \leq \sigma_2^2$ vs. H_A: $\sigma_1^2 > \sigma_2^2$. This would be done by the one-tailed t-testing described in Section 8.1, using σ^2 in place of μ in the hypothesis statements and using $|X_i - \overline{X}|$ instead of X_i in the computations.

EXAMPLE 8.9 The Two-Sample Levene Test for H_0: $\sigma_1^2 = \sigma_2^2$ and H_A: $\sigma_1^2 \neq \sigma_2^2$. The Data Are Those of Example 8.7

H_0: $\sigma_1^2 = \sigma_2^2$

H_A: $\sigma_1^2 \neq \sigma_2^2$

$\alpha = 0.05$

For group 1: $\Sigma X = 401$ moths, n = 11, $\nu = 10$, $\overline{X} = 36.45$ moths.

For group 2: $\Sigma X = 577$ moths, n = 10, $\nu = 9$, $\overline{X} = 57.70$ moths.

Trap Type 1		*Trap Type 2*	
X_i	$X' = \lvert X_i - \overline{X}\rvert$	X_i	$X' = \lvert X_i - \overline{X}\rvert$
41	4.55	52	5.70
35	1.45	57	0.70
33	3.45	62	4.30
36	0.45	55	2.70
40	3.55	64	6.30
46	9.55	57	0.70
31	5.45	56	1.70
37	0.55	55	2.70
34	2.45	60	2.30
30	6.45	59	1.30
38	1.55		
ΣX_i = 401 moths	$\Sigma X_i' = \Sigma\lvert X_i - \overline{X}\rvert$ = 39.45 moths	ΣX_i = 577 moths	$\Sigma X_i' = \Sigma\lvert X_i - \overline{X}\rvert$ = 28.40 moths

For the absolute values of the deviations from the mean:

$X_1' = 39.45 \text{ moths}/11 = 3.59 \text{ moths}$ $\quad SS_1' = 77.25 \text{ moths}^2$

$X_2' = 28.40 \text{ moths}/10 = 2.84 \text{ moths}$ $\quad SS_2' = 35.44 \text{ moths}^2$

the calculated confidence intervals are only approximations, with the approximation poorer the further from normality the populations are.

Meeker and Hahn (1980) discuss calculation of prediction limits for the variance ratio and provide special tables for that purpose.

8.7 SAMPLE SIZE AND POWER IN TESTS FOR DIFFERENCE BETWEEN TWO VARIANCES

(a) Sample Size Required. In considering the variance-ratio test of Section 8.5, we may ask what minimum sample sizes are required to achieve specified test characteristics. Using the normal approximation recommended by Desu and Raghavarao (1990: 35), the following number of data is needed in each sample to test at the α level of significance with power of $1 - \beta$:

$$n = \left[\frac{Z_\alpha + Z_{\beta(1)}}{\ln\left(\frac{s_1^2}{s_2^2}\right)} \right]^2 + 2. \tag{8.32}$$

For analysts who prefer performing calculations with "common logarithms" (those employing base 10) to using "natural logarithms" (those in base e),* Equation 8.32 may be written equivalently as

$$n = \left[\frac{Z_\alpha + Z_{\beta(1)}}{(2.30259)\log\left(\frac{s_1^2}{s_2^2}\right)} \right]^2 + 2. \tag{8.33}$$

This sample-size estimate assumes that the samples are to be equal in size, which is generally preferable. If, however, it is desired to have unequal sample sizes (which will typically require more total data to achieve a particular power), one may specify that ν_1 is to be m times the size of ν_2; then (after Desu and Raghavarao, 1990: 35):

$$m = \frac{n_1 - 1}{n_2 - 1}, \tag{8.34}$$

$$n_2 = \frac{(m + 1)(n - 2)}{2m} + 2, \tag{8.35}$$

and

$$n_1 = m(n_2 - 1) + 1. \tag{8.36}$$

*In this book, *ln* will denote the natural, or Naperian, logarithm, and *log* will denote the common, or Briggsian, logarithm. These are named for the Scottish mathematician John Napier (1550–1617), who devised and named logarithms, and the English mathematician Henry Briggs (1561–1630), who adapted this computational method to base 10; the German astronomer Johann Kepler (1550–1617) was the first to use the abbreviation "Log," in 1624, and Italian mathematician Bonaventura Cavalieri (1598–1647) was the first to use "log" in 1632 (Cajori, 1928/9, Vol. II: 105–106; Gullber, 1997: 152). Sometimes $\log_e$ and $\log_{10}$ will be seen instead of ln and log, respectively.

As in Section 8.5, determination of whether s_1^2 or s_2^2 is placed in the numerator of the variance ratio in Equation 8.32 depends upon the hypothesis test, and Z_α is either a one-tailed or two-tailed normal deviate depending upon the hypothesis to be tested; n_1 and n_2 correspond to s_1^2 and s_2^2, respectively. This procedure is applicable if the variance ratio is >1.

(b) Power of the Test. We may also estimate what the power of the variance ratio test would be if specified sample sizes were used. If the two sample sizes are the same (i.e., $n = n_1 = n_2$), then Equations 8.32 and 8.33 may be rearranged, respectively, as follows:

$$Z_{\beta(1)} = \sqrt{n - 2}\ln\left(\frac{s_1^2}{s_2^2}\right) - Z_\alpha; \tag{8.37}$$

$$Z_{\beta(1)} = \sqrt{n - 2}(2.30259)\log\left(\frac{s_1^2}{s_2^2}\right) - Z_\alpha. \tag{8.38}$$

After $Z_{\beta(1)}$ is calculated, $\beta(1)$ is determined from the last line of Appendix Table B.3, or from Appendix Table B.2, or from a calculator or computer that gives probability of a normal deviate; and power $= 1 - \beta(1)$. If the two sample sizes are not the same, then the estimation of power may employ

$$Z_{\beta(1)} = \sqrt{\frac{2m(n_2 - 2)}{m + 1}}\ln\left(\frac{s_1^2}{s_2^2}\right) - Z_\alpha \tag{8.39}$$

or

$$Z_{\beta(1)} = \sqrt{\frac{2m(n_2 - 2)}{m + 1}}(2.30259)\log\left(\frac{s_1^2}{s_2^2}\right) - Z_\alpha, \tag{8.40}$$

where m is as in Equation 8.34.

8.8 TESTING FOR DIFFERENCE BETWEEN TWO COEFFICIENTS OF VARIATION

A very useful property of coefficients of variation is that they have no units of measurement. Thus, V's may be compared even if they are calculated from data having different units, as is the case in Example 8.10. And it may be desired to test the null hypothesis that two samples came from populations with the same coefficients of variation.

EXAMPLE 8.10 A Two-Tailed Test for Difference Between Two Coefficients of Variation

H_0: The intrinsic variability of male weights is the same as the intrinsic variability of male heights (i.e., the population coefficients of variation of weight and height are the same, namely H_0: $\sigma_1/\mu_1 = \sigma_2/\mu_2$).

H_0: The intrinsic variability of male weight is not the same as the intrinsic variability of male heights (i.e., the population coefficients of variation of weight and height are not the same, namely H_0: $\sigma_1/\mu_1 \neq \sigma_2/\mu_2$).

(a) The variance-ratio test.

Weight (kg)	*Log of weight*	*Height* (cm)	*Log of height*
72.5	1.86034	183.0	2.26245
71.7	1.85552	172.3	2.23629
60.8	1.78390	180.1	2.25551
63.2	1.80072	190.2	2.27921
71.4	1.85370	191.4	2.28194
73.1	1.86392	169.6	2.22943
77.9	1.89154	166.4	2.22115
75.7	1.87910	177.6	2.24944
72.0	1.85733	184.7	2.26647
69.0	1.83885	187.5	2.27300
		179.8	2.25479

$n_1 = 10$	$n_2 = 11$
$\nu_1 = 9$	$\nu_2 = 10$
$\overline{X}_1 = 70.73$ kg	$\overline{X}_2 = 180.24$ cm
$SS_1 = 246.1610$ kg^2	$SS_2 = 678.9455$ cm^2
$s_1^2 = 27.3512$ kg^2	$s_2^2 = 67.8946$ cm^2
$s_1 = 5.23$ kg	$s_2 = 8.24$ cm
$V_1 = 0.0739$	$V_2 = 0.0457$
$(SS_{log})_1 = 0.00987026$	$(SS_{log})_2 = 0.00400188$
$(s_{log}^2)_1 = 0.0010967$	$(s_{log}^2)_2 = 0.00040019$

$$F = \frac{0.0010967}{0.00040019} = 2.74$$

$F_{0.05(2),9,10} = 3.78$

Therefore, do not reject H_0.

$$0.10 < P < 0.20 \quad [P = 0.13]$$

It is concluded that the coefficient of variation is the same for the population of weights as it is for the population of heights.

(b) The Z test.

$$V_p = \frac{\nu_1 V_1 + \nu_2 V_2}{\nu_1 + \nu_2} = \frac{9(0.0739) + 10(0.0457)}{9 + 10} = \frac{1.1221}{19} = 0.0591$$

$V_p^2 = 0.003493$

$$Z = \frac{V_1 - V_2}{\sqrt{\left(\frac{V_p^2}{\nu_1} + \frac{V_p^2}{\nu_2}\right)(0.5 + V_p^2)}}$$

$$= \frac{0.0739 - 0.0457}{\sqrt{\left(\frac{0.003493}{9} + \frac{0.003493}{10}\right)(0.5 + 0.003493)}}$$

$$= \frac{0.0282}{0.0193} = 1.46$$

$Z_{0.05(2)} = t_{0.05(2),\infty} = 1.960$

Do not reject H_0.

$$0.10 < P < 0.20 \quad [P = 0.14]$$

It is concluded that the coefficient of variation is the same for the population of weights as it is for the population of heights.

Lewontin (1966) showed that

$$F = \frac{\left(s^2_{\log}\right)_1}{\left(s^2_{\log}\right)_2} \text{ or } F = \frac{\left(s^2_{\log}\right)_2}{\left(s^2_{\log}\right)_1} \tag{8.41}$$

may be used for a variance-ratio test, analogously to Equation 8.27. In Equation 8.41, $\left(s^2_{\log}\right)_i$ refers to the variance of the logarithms of the data in Sample i, where logarithms to any base may be employed. This procedure is applicable only if all of the data are positive (i.e., > 0), and it is demonstrated in Example 8.10a. Either two-tailed or one-tailed hypotheses may be tested, as shown in Section 8.5.

This variance-ratio test requires that the logarithms of the data in each sample come from a normal distribution. A procedure advanced by Miller (1991) allows testing when the data, not their logarithms, are from normal distributions (that have positive means and variances). The test statistic, as demonstrated in Example 8.10b, is

$$Z = \frac{V_1 - V_2}{\sqrt{\left(\frac{V_p^2}{\nu_1} + \frac{V_p^2}{\nu_2}\right)(0.5 + V_p^2)}}, \tag{8.42}$$

where

$$V_p = \frac{\nu_1 V_1 + \nu_2 V_2}{\nu_1 + \nu_2} \tag{8.43}$$

is referred to as the "pooled coefficient of variation," which is the best estimate of the population coefficient of variation, σ/μ, that is common to both populations if the null hypothesis of no difference is true.

This procedure is shown, as a two-tailed test, in Example 8.10b. Recall that critical values of Z may be read from the last line of the table of critical values of t (Appendix Table B.3), so $Z_{\alpha(2)} = t_{\alpha(2),\infty}$. One-tailed testing is also possible, in which case the alternate hypothesis would declare a specific direction of difference and one-tailed critical values ($t_{\infty(1),\alpha}$) would be consulted. This test works best if there are at least 10 data in each sample and each population's coefficient of variation is no larger than 0.33. An estimate of the power of the test is given by Miller and Feltz (1997).

8.9 CONFIDENCE LIMITS FOR THE DIFFERENCE BETWEEN TWO COEFFICIENTS OF VARIATION

Miller and Feltz (1997) have provided this $1 - \alpha$ confidence interval for $\sigma_1/\mu_1 - \sigma_2/\mu_2$, where the two sampled populations are normally distributed:

$$V_1 - V_2 \pm Z_{\alpha(2)}\sqrt{\frac{V_1^2}{\nu_1}(0.5 + V_1^2) + \frac{V_2^2}{\nu_1}(0.5 + V_2^2)}. \tag{8.44}$$

8.10 NONPARAMETRIC STATISTICAL METHODS

There is a large body of statistical methods that do not require the estimation of population parameters (such as μ and σ) and that test hypotheses that are not statements about population parameters. These statistical procedures are termed *nonparametric tests.** These are in contrast to procedures such as t tests, which are called *parametric tests* and which do rely upon estimates of population parameters and upon the statement of parameters in the statistical hypotheses. Although they may assume that the sampled populations have the same dispersion or shape, nonparametric methods typically do not make assumptions about the nature of the populations' distributions (e.g., there is no assumption of normality); thus they are sometimes referred to as *distribution-free tests.*† Both parametric and nonparametric tests require that the data have come at random from the sampled populations.

Nonparametric tests (such as the two-sample testing procedure described in Section 8.11) generally may be applied to any situation where we would be justified in employing a parametric test (such as the two-sample t test), as well as in some instances where the assumptions of the latter are untenable. If either the parametric or nonparametric approach is applicable, then the former will generally be more powerful than the latter (i.e., the parametric method will typically have a lower probability of committing a Type II error). However, often the difference in power is not great and can be compensated by a small increase in sample size for the nonparametric test. When the underlying assumptions of a parametric test are seriously violated, then the nonparametric counterpart may be decidedly more powerful.

Most nonparametric statistical techniques convert observed data to the ranks of the data (i.e., their numerical order). For example, measurements of 2.1, 2.3, 2.9, 3.6, and 4.0 kg would be analyzed via their ranks of 1, 2, 3, 4, and 5. A possible disadvantage of this rank transformation of data is that some information is lost (for example, the same ranks would result from measurements of 1.1, 1.3, 2.9, 4.6, and 5.0 kg). A possible advantage is that outliers (see Section 2.5) will have much less influence (for example, the same ranks would result from measurements of 2.1, 2.3, 2.9, 3.6, and 25.0 kg).

It is sometimes counseled that only nonparametric testing may be employed when dealing with ordinal-scale data, but such advice is based upon what Gaito (1980) calls "an old misconception"; this issue is also discussed by Anderson (1961), Gaito (1960), Savage (1957), and Stevens (1968). Interval-scale or ratio-scale measurements are not intrinsically required for the application of parametric testing procedures. Thus parametric techniques may be considered for ordinal-scale data *if* the assumptions of such methods are met—typically, random sampling from normally distributed populations with homogeneity of variances. But ordinal data often come

*The term *nonparametric* was first used by Jacob Wolfowitz in 1942 (David, 1995; Noether, 1984).

†The terms *nonparametric* and *distribution-free* are commonly used interchangeably, but they do not both define exactly the same set of statistical techniques (Noether, 1984).

from nonnormal populations, in which case properly subjecting them to parametric analysis depends upon the robustness of the test to the extent of nonnormality present.

8.11 TWO-SAMPLE RANK TESTING

Several nonparametric procedures, with various characteristics and assumptions, have been proposed for testing differences between the dispersions, or variabilities, of two populations (e.g., see Hettmansperger and McKean, 1998: 118–127; Hollander and Wolfe, 1999: 141–188; Sprent and Smeeton, 2001: 175–185). A far more common desire for nonparametric testing is to compare two populations' central tendencies (i.e., locations on the measurement scale) when underlying assumptions of the t test are not met. The most frequently employed such test is that originally proposed, for equal sample sizes, by Wilcoxon (1945)* and independently presented by Mann and Whitney (1947), for equal or unequal n's. It is called the Wilcoxon-Mann-Whitney test or, more commonly, the Mann-Whitney test.

(a) The Mann-Whitney Test. For this test, as for many other nonparametric procedures, the actual measurements are not employed, but we use instead the ranks of the measurements. The data may be ranked either from the highest to lowest or from the lowest to the highest values. Example 8.11 ranks the measurements from highest to lowest: The greatest height in either of the two groups is given rank 1, the second greatest height is assigned rank 2, and so on, with the shortest height being assigned rank N, where

$$N = n_1 + n_2. \tag{8.45}$$

A Mann-Whitney statistic is then calculated as

$$U = n_1 n_2 + \frac{n_1(n_1 + 1)}{2} - R_1, \tag{8.46}$$

where n_a and n_2 are the number of observations in samples 1 and 2, respectively, and R_1 is the sum of the ranks in sample 1. The Mann-Whitney statistic can also be calculated as

$$U' = n_2 n_1 + \frac{n_2(n_2 + 1)}{2} - R_2 \tag{8.47}$$

(where R_2 is the sum of the ranks of the observations in sample 2), because the labeling of the two samples as 1 and 2 is arbitrary.† If Equation 8.46 has been used to calculate U, then U' can be obtained quickly as

$$U' = n_1 n_2 - U; \tag{8.48}$$

*Wilcoxon may have proposed this test primarily to avoid the drudgery of performing numerous t tests in a time before ubiquitous computer availability (Noether, 1984). Kruskal (1957) gives additional history, including identification of seven independent developments of the procedure Wilcoxon introduced, two of them prior to Wilcoxon, the earliest being by the German psychologist Gustav Deuchler in 1914.

†The Wilcoxon two-sample test (sometimes referred to as the Wilcoxon rank-sum test) uses a test statistic commonly called W, which is R_1 or R_2; the test is equivalent to the Mann-Whitney test, for $U = R_2 - n_2(n_2 + 1)/2$ and $U' = R_1 - n_1(n_1 + 1)/2$. U (or U') is also equal to the number of data in one sample that are exceeded by each datum in the other sample. Note in Example 8.11: For females, ranks 7 and 8 each exceed 6 male ranks and ranks 10, 11, and 12 each exceed all 7 males ranks, for a total of $6 + 6 + 7 + 7 + 7 = 33 = U$; for males, rank 9 exceeds 2 female ranks for a total of $2 = U'$.

EXAMPLE 8.11 The Mann-Whitney Test for Nonparametric Testing of the Two-Tailed Null Hypothesis That There Is No Difference Between the Heights of Male and Female Students

H_0: Male and female students are the same height.

H_A: Male and female students are not the same height.

$\alpha = 0.05$

Heights of males	*Heights of females*	*Ranks of male heights*	*Ranks of female heights*
193 cm	178 cm	1	6
188	173	2	8
185	168	3	10
183	165	4	11
180	163	5	12
175		7	
170		9	
$n_1 = 7$	$n_2 = 5$	$R_1 = 31$	$R_2 = 47$

$$U = n_1 n_2 + \frac{n_1(n_1 + 1)}{2} - R_1$$
$$= (7)(5) + \frac{(7)(8)}{2} - 31$$
$$= 35 + 28 - 31$$
$$= 32$$
$$U' = n_1 n_2 - U$$
$$= (7)(5) - 32$$
$$= 3$$

$U_{0.05(2),7,5} = U_{0.05(2),5,7} = 30$

As $32 > 30$, H_0 is rejected.

$0.01 < P(U \geq 32 \text{ or } U' \leq 3) < 0.02 \quad [P = 0.018]^*$

Therefore, we conclude that height is different for male and female students.

and if Equation 8.47 has been used to compute U', then U can be ascertained as

$$U = n_1 n_2 - U'. \tag{8.49}$$

*In many of the examples in this book, the exact probability of a statistic from a nonparametric test (such as U) will be given within brackets. In some cases, this probability is obtainable from published sources (e.g., Owen, 1962). It may also be given by computer software, in which case there are two cautions: The computer result may not be accurate to the number of decimal places given, and the computer may have used an approximation (such as the normal approximation in the case of U; see Section 8.11d), which may result in a probability departing substantially from the exact probability, especially if the sample sizes are small.

For the two-tailed hypotheses, H_0: male and female students are the same height and H_A: male and female students are not the same height, the calculated U or U'—whichever is larger—is compared with the two-tailed value of $U_{\alpha(2),n_1,n_2}$ found in Appendix Table B.11. This table is set up assuming $n_1 \leq n_2$, so if $n_1 > n_2$, simply use $U_{\alpha(2),n_2,n_1}$ as the critical value. If either U or U' is as great as or greater than the critical value, H_0 is rejected at the α level of significance. A large U or U' will result when a preponderance of the large ranks occurs in one of the samples. As shown in Example 8.11, neither parameters nor parameter estimates are employed in the statistical hypotheses or in the calculations of U and U'.

The values of U in the table are those for probabilities less than or equal to the column headings. Therefore, the U of 32 in Example 8.11 is seen to have a probability of $0.01 < P \leq 0.02$. If the calculated U would have been 31, its probability would have been expressed as $0.02 < P < 0.05$.

We may assign ranks either from large to small data (as in Example 8.11), or from small to large, calling the smallest datum rank 1, the next largest rank 2, and so on. The value of U obtained using one ranking procedure will be the same as the value of U' using the other procedure. In a two-tailed test both U and U' are employed, so it makes no difference from which direction the ranks are assigned.

In summary, we note that after ranking the combined data of the two samples, we calculate U and U' using either Equations 8.46 and 8.48, which requires the determination of R_1, or Equations 8.47 and 8.49, which requires R_2. That is, the sum of the ranks for only one of the samples is needed. However, we may wish to compute both R_1 and R_2 in order to perform the following check on the assignment of ranks (which is especially desirable in the somewhat more complex case of assigning ranks to tied data, as will be shown below):

$$R_1 + R_2 = \frac{N(N + 1)}{2}. \tag{8.50}$$

Thus, in Example 8.11,

$$R_1 + R_2 = 30 + 48 = 78$$

should equal

$$\frac{N(N + 1)}{2} = \frac{12(12 + 1)}{2} = 78.$$

This provides a check on (although it does not guarantee the accuracy of) the assignment of ranks.

Note that hypotheses for the Mann-Whitney test are not statements about parameters (e.g., means or medians) of the two populations. Instead, they address the more general, less specific question of whether the two population distributions of data are the same. Basically, the question asked is whether it is likely that the two samples came at random from the two populations described in the null hypothesis. If samples at least that different would occur with a probability that is small (i.e., less than the significance level, such as 0.05), then H_0 is rejected.

The Mann-Whitney procedure serves to test for difference between medians under certain circumstances (such as when the two sampled populations have symmetrical distributions), but in general it addresses the less specific hypothesis of similarity between the two populations' distributions. The Watson test of Section 26.6 may also be employed when the Mann-Whitney test is applicable, but the latter is easier to perform and is more often found in statistical software.

(b) The Mann-Whitney Test with Tied Ranks. Example 8.12 demonstrates an important consideration encountered in tests requiring the ranking of observations. When two or more observations have exactly the same value, they are said to be *tied*. The rank assigned to each of the tied ranks is the mean of the ranks that would have been assigned to these ranks had they not been tied.* For example, in the present set of data, which are ranked from low to high, the third and fourth lowest values are tied at 32 words per minute, so they are each assigned the rank of $(3 + 4)/2 = 3.5$. The eighth, ninth, and tenth observations are tied at 44 words per minute, so each of them receives the rank of $(8 + 9 + 10)/3 = 9$. Once the ranks have been assigned by this procedure, U and U' are calculated as previously described.

(c) The One-Tailed Mann-Whitney Test. For one-tailed hypotheses we need to declare which tail of the Mann-Whitney distribution is of interest, as this will determine whether U or U' is the appropriate test statistic. This consideration is presented in Table 8.2. In Example 8.12 we have data that were ranked from lowest to highest and the alternate hypothesis states that the data in group 1 are greater in magnitude than those in group 2. Therefore, we need to compute U' and compare it to the one-tailed critical value, $U_{\alpha(1),n_1,n_2}$, from Appendix Table B.11.

TABLE 8.2: The Appropriate Test Statistic for the One-Tailed Mann-Whitney Test

	H_0: Group 1 $\geq$ Group 2 H_A: Group 1 $<$ Group 2	H_0: Group 1 $\leq$ Group 2 H_A: Group 1 $>$ Group 2
Ranking done from low to high	U	U'
Ranking done from high to low	U'	U

(d) The Normal Approximation to the Mann-Whitney Test. Note that Appendix Table B.11 can be used only if the size of the smaller sample does not exceed twenty and the size of the larger sample does not exceed forty. Fortunately, the distribution of U approaches the normal distribution for larger samples. For large n_1 and n_2 we use the fact that the U distribution has a mean of

$$\mu_U = \frac{n_1 n_2}{2}, \tag{8.51}$$

which may be calculated, equivalently, as

$$\mu_U = \frac{U + U'}{2}, \tag{8.51a}$$

and a standard error of

$$\sigma_U = \sqrt{\frac{n_1 n_2 (N + 1)}{12}}, \tag{8.52}$$

*Although other procedures have been proposed to deal with ties, assigning the rank mean has predominated for a long time (e.g., Kendall, 1945).

EXAMPLE 8.12 The One-Tailed Mann-Whitney Test Used to Determine the Effectiveness of High School Training on the Typing Speed of College Students. This Example Also Demonstrates the Assignment of Ranks to Tied Data

H_0: Typing speed is not greater in college students having had high school typing training.

H_A: Typing speed is greater in college students having had high school typing training.

$\alpha = 0.05$

Typing Speed (words per minute)	
With training (rank in parentheses)	*Without training (rank in parentheses)*
44 (9)	32 (3.5)
48 (12)	40 (7)
36 (6)	44 (9)
32 (3.5)	44 (9)
51 (13)	34 (5)
45 (11)	30 (2)
54 (14)	26 (1)
56 (15)	
$n_1 = 8$	$n_2 = 7$
$R_1 = 83.5$	$R_2 = 36.5$

Because ranking was done from low to high and the alternate hypothesis states that the data of group one are larger than the data of group two, use U' as the test statistic (as indicated in Table 8.2).

$$U' = n_2 n_1 + \frac{n_2(n_2 + 1)}{2} - R_2$$

$$= (7)(8) + \frac{(7)(8)}{2} - 36.5$$

$$= 56 + 28 - 36.5$$

$$= 47.5$$

$U_{0.05(1),8,7} = U_{0.05(1),7,8} = 43$

As $47.5 > 43$, reject H_0.

$$0.01 < P < 0.025 \quad [P = 0.012]$$

Consequently, it is concluded that college-student typing speed is greater for students who had typing training in high school.

where $N = n_1 + n_2$, as used earlier. Thus, if a U, or a U', is calculated from data where either n_1 or n_2 is greater than that in Appendix Table B.11, its significance can be determined by computing

$$Z = \frac{U - \mu_U}{\sigma_U} \tag{8.53}$$

or, using a correction for continuity, by

$$Z_c = \frac{|U - \mu_U| - 0.5}{\sigma_U}. \tag{8.54}$$

The continuity correction is included to account for the fact that Z is a continuous distribution, but U is a discrete distribution. However, it appears to be advisable only if the two-tailed P is about 0.05 or greater (as seen from an expansion of the presentation of Lehmann, 1975: 17).

Recalling that the t distribution with $\nu = \infty$ is identical to the normal distribution, the critical value, Z_α, is equal to the critical value, $t_{\alpha,\infty}$. The normal approximation is demonstrated in Example 8.13. When using the normal approximation for two-tailed testing, only U *or* U' (not both) need be calculated. If U' is computed instead of U, then U' is simply substituted for U in Equation 8.53 or 8.54, the rest of the testing procedure remaining the same.

EXAMPLE 8.13 The Normal Approximation to a One-Tailed Mann-Whitney Test to Determine Whether Animals Raised on a Dietary Supplement Reach a Greater Body Weight Than Those Raised on an Unsupplemented Diet

In the experiment, 22 animals (group 1) were raised on the supplemented diet, and 46 were raised on the unsupplemented diet (group 2). The body weights were ranked from 1 (for the smallest weight) to 68 (for the largest weight), and U was calculated to be 282.

H_0: Body weight of animals on the supplemented diet are not greater than those on the unsupplemented diet.

H_A: Body weight of animals on the supplemented diet are greater than those on the unsupplemented diet.

$n_1 = 22, n_2 = 46, N = 68$

$U = 282$

$$U' = n_1 n_2 - U = (22)(46) - 282 = 1012 - 282 = 730$$

$$\mu_U = \frac{n_1 n_2}{2} = \frac{(22)(46)}{2} = 506$$

$$\sigma_U = \sqrt{\frac{n_1 n_2 (N + 1)}{12}} = \sqrt{\frac{(22)(46)(68 + 1)}{12}} = 76.28$$

$$Z = \frac{U' - \mu_U}{\sigma_U} = \frac{224}{76.28} = 2.94$$

For a one-tailed test at $\alpha = 0.05, t_{0.05(1),\infty} = Z_{0.05(1)} = 1.6449$.

As $Z = 2.94 > 1.6449$, reject H_0. $[P = 0.0016]$

So we conclude that the supplemental diet results in greater body weight.

• One-tailed testing may also be performed using the normal approximation. Here one computes either U or U', in accordance with Table 8.2, and uses it in either Equation 8.55 or 8.56, respectively, inserting the correction term (-0.5) if P is about

0.025 or greater:

$$Z_c = \frac{U - \mu_U - 0.5}{\sigma_U}, \text{ if } U \text{ is used, or} \tag{8.55}$$

$$Z_c = \frac{U' - \mu_U - 0.5}{\sigma_U}, \text{ if } U' \text{ is used.} \tag{8.56}$$

The resultant Z_c is then compared to the one-tailed critical value, $Z_{\alpha(1)}$, or, equivalently, $t_{\alpha(1),\infty}$; and if $Z \geq$ the critical value, then H_0 is rejected.*

If tied ranks exist and the normal approximation is utilized, the computations are slightly modified as follows. One should calculate the quantity

$$\sum t = \sum (t_i^3 - t_i), \tag{8.57}$$

where t_i is the number of ties in a group of tied values, and the summation is performed over all groups of ties. Then,

$$\sigma_U = \sqrt{\frac{n_1 n_2}{N^2 - N} \cdot \frac{N^3 - N - \sum t}{12}}, \tag{8.58}$$

and this value is used in place of that from Equation 8.52. (The computation of $\sum t$ is demonstrated, in a similar context, in Example 10.11.)

The normal approximation is best for $\alpha(2) = 0.10$ or 0.05 [or for $\alpha(1) = 0.05$ or 0.025] and is also good for $\alpha(2) = 0.20$ or 0.02 [or for $\alpha(1) = 0.10$ or 0.01], with the approximation improving as sample sizes increase; for more extreme significance levels it is not as reliable, especially if n_1 and n_2 are dissimilar. Fahoome (2002) determined that the normal approximation (Equation 8.53) performed well at the two-tailed 0.05 level of significance (i.e., the probability of a Type I error was between 0.045 and 0.055) for sample sizes as small as 15, and at $\alpha(2) = 0.01$ (for P(Type I error) between 0.009 and 0.011) for n_1 and n_2 of at least 29. Indeed, in many cases with even smaller sample sizes, the normal approximation also yields Type I error probabilities very close to the exact probabilities of U obtained from specialized computer software (especially if there are few or no ties).† Further observations on the accuracy of this approximation are given at the end of Appendix Table B.11.

Buckle, Kraft, and van Eeden (1969) propose another distribution, which they refer to as the "uniform approximation." They show it to be more accurate for $n_1 \neq n_2$, especially when the difference between n_1 and n_2 is great, and especially for small α.

Fix and Hodges (1955) describe an approximation to the Mann-Whitney distribution that is much more accurate than the normal approximation but requires very involved computation. Hodges, Ramsey, and Wechsler (1990) presented a simpler method for a modified normal approximation that provides very good results for probabilities of about 0.001 or greater. Also, the two-sample t test may be applied to the ranks of the data (what is known as using the *rank transformation* of the data), with the probability of the resultant t approaching the exact probability for very large n. But these procedures do not appear to be generally preferable to the normal approximation described above, at least for the probabilities most often of interest.

*By this procedure, Z must be positive in order to reject H_0. If it is negative, then the probability of H_0 being true is $P > 0.50$.

†As a demonstration of this, in Example 8.11 the exact probability is 0.018 and the probability by the normal approximation is 0.019; and for Example 8.12, the exact probability and the normal approximation are both 0.012. In Exercise 8.12, P for U is 0.53 and P for Z is 0.52; and in Exercise 8.13, P for U is 0.41 and P for Z_c is 0.41.

(e) The Mann-Whitney Test with Ordinal Data. The Mann-Whitney test may also be used for ordinal data. Example 8.14 demonstrates this procedure. In this example, 25 undergraduate students were enrolled in an invertebrate zoology course. Each student was guided through the course by one of two teaching assistants, but the same examinations and grading criteria were applied to all students. On the basis of the students' final grades in the course, we wish to test the null hypothesis that students (students in general, not just these 25) perform equally well under both teaching assistants. The variable measured (i.e., the final grade) results in ordinal data, and the hypothesis is amenable to examination by the Mann-Whitney test.

(f) Mann-Whitney Hypotheses Employing a Specified Difference Other Than Zero. Using the two-sample t test, one can examine hypotheses such as H_0: $\mu_1 - \mu_2 = \mu_0$, where μ_0 is not zero. Similarly, the Mann-Whitney test can be applied to hypotheses such as H_0: males are at least 5 cm taller than females (a one-tailed hypothesis with data such as those in Example 8.11) or H_0: the letter grades of students in one course are at least one grade higher that those of students in a second course (a one-tailed hypothesis with data such as those in Example 8.14). In the first hypothesis, one would list all the male heights but list all the female heights after increasing each of them by 5 cm. Then these listed heights would be ranked and the Mann-Whitney analysis would proceed as usual. For testing the second hypothesis, the letter grades for the students in the first course would be listed unchanged, with the grades for the second course increased by one letter grade before listing. Then all the listed grades would be ranked and subjected to the Mann-Whitney test.*

When dealing with ratio- or interval-scale data, it is also possible to propose hypotheses employing a multiplication, rather than an addition, constant. Consider the two-tailed hypothesis H_0: the wings of one species of insect are two times the length of the wings of a second species. We could test this by listing the wing lengths of the first species, listing the wing lengths of the second species after multiplying each length by two, and then ranking the members of the combined two lists and subjecting the ranks to the Mann-Whitney test. The parametric t testing procedure, which assumes equal population variance, ordinarily would be inapplicable for such a hypothesis, because multiplying the data by a constant changes the variance of the data by the square of the constant.

(g) Violations of the Mann-Whitney Test Assumptions. If the underlying assumptions of the parametric analog of a nonparametric test are met, then either procedure may be employed but the parametric test will be the more powerful. The Mann-Whitney test is one of the most powerful of nonparametric tests. When the t-test assumptions are met, the power of the Mann-Whitney test approaches 95.5% (i.e., $3/\pi$) of the power of the t test as sample size increases (Mood, 1954).† And

*To increase these grades by one letter each, a grade of "B" would be changed to an "A," a "C" changed to a "B," and so on; a grade of "A" would have to be increased to a grade not on the original scale (e.g., call it a "Z") and, when ranking, we simply have to keep in mind that this new grade is higher than an "A."

†Mood (1954) credits an earlier statement of this to 1948 lecture notes of E. J. G. Pitman and to a 1950 Dutch publication by H. R. Van der Vaart. The statement that statistical test A is 0.955 as powerful as test B means that the power of test A with sample size of n tends (as n increases) toward having the same power as test B with sample size of $0.955n$; and this is referred to as the *asymptotic relative efficiency* (ARE) of test A compared to test B. Because of its development by Australian statistician Edwin James George Pitman (1897–1993), ARE is often called *Pitman efficiency*, which distinguishes it from a less commonly encountered definition of asymptotic relative

EXAMPLE 8.14 The Mann-Whitney Test for Ordinal Data

H_0: The performance of students is the same under the two teaching assistants.
H_A: Students do not perform equally well under the two teaching assistants.

$\alpha = 0.05$

Teaching Assistant A		Teaching Assistant B	
Grade	*Rank of grade*	*Grade*	*Rank of grade*
A	3	A	3
A	3	A	3
A	3	B+	7.5
A−	6	B+	7.5
B	10	B	10
B	10	B−	12
C+	13.5	C	16.5
C+	13.5	C	16.5
C	16.5	C−	19.5
C	16.5	D	22.5
C−	19.5	D	22.5
		D	22.5
		D	22.5
		D−	25
$n_1 = 11$		$n_2 = 14$	
$R_1 = 114.5$		$R_2 = 210.5$	

$$U = n_1 n_2 + \frac{n_1(n_1 + 1)}{2} - R_1$$
$$= (11)(14) + \frac{(11)(12)}{2} - 114.5$$
$$= 154 + 66 - 114.5$$
$$= 105.5$$

$$U' = n_1 n_2 - U$$
$$= (11)(14) - 105.5$$
$$= 48.5$$

$U_{0.05(2),11,14} = 114$

As $105.5 < 114$, do not reject H_0.

$$0.10 < P(U \geq 105.5 \text{ or } U \leq 48.5) < 0.20$$

Thus, the conclusion is that student performance is the same under both teaching assistants.

efficiency by Bahadur (1967; Blair and Higgins, 1985). Although Pitman efficiency is defined in terms of very large n, it is generally a good expression of relative efficiency of two tests even with small n (Conover, 1999: 112).

for some extremely nonnormal distributions, the Mann-Whitney test is immensely more powerful (Blair and Higgins, 1980a, 1980b; Blair, Higgins, and Smitley, 1980; Hodges and Lehman, 1956). The power of the Mann-Whitney test will never be less than 86.4% of the power of the t test (Conover, 1997: 297; Hodges and Lehman, 1956).

The Mann-Whitney test does not assume normality of the sampled populations as the t test does, but the calculated U is affected not only by the difference between the locations of the two populations along the measurement scale but also by difference between the shapes or dispersons of the two populations' distributions (Boneau, 1962). However, the test is typically employed with the desire to conclude only whether there are differences between measurement locations, in which case it must be assumed that the two sampled populations have the same dispersion and shape, a premise that is often ignored, probably in the belief that the test is more robust to unequal dispersion than is the t test. But the Mann-Whitney test is, indeed, adversely affected by sizable differences in the variances or the shapes of the sampled populations, in that the probability of a Type I error is not the specified α (Fligner and Policello, 1981).* As with the two-sample t test, if the two sample sizes are not equal, and if the larger σ^2 is associated with the larger sample, then the probability of a Type I error will be less than α (and the test is called *conservative*); and if the smaller sample came from the population with the larger variance, then this probability will be greater than α (and the test is called *liberal*) (Zimmerman, 1987). The greater the difference between the variances, the greater the departure from α. In situations where the Mann-Whitney test is conservative, it has more power than the t test (Zimmerman, 1987). The power of the Mann-Whitney test may also be decreased, especially in the presence of outliers, to an extent to which the variances differ; but this decrease is far less than it is with t testing (Zimmerman, 1994, 1996, 1998, 2000). But in some cases unequal variances affect the probability of a Type I error using U more severely than if t or t' were employed (Zimmerman, 1998).

The Mann-Whitney test is included in the guidelines (described in Section 8.1d) for when various two-sample statistical procedures are appropriate.

8.12 TESTING FOR DIFFERENCE BETWEEN TWO MEDIANS

The null hypothesis that two samples came from populations having the same median can be tested by the *median test* described by Mood (1950: 394–395). The procedure is to determine the grand median for all the data in both samples and then to tabulate the numbers of data above and below the grand median in a 2×2 contingency table, as shown in Example 8.15. This contingency table can then be analyzed by the chi-square test of Section 23.3b or G test of Section 23.7.

Example 8.15 demonstrates the median test for the data of Example 8.14. In many cases, such as this one, one or more of the data will be equal to the grand median (in this instance a grade of C+) and, therefore, the number of data above

*Fligner and Policello (1981; Hollander and Wolfe, 1999: 135–139) addressed situations where the sampled populations have dissimilar variances (the "Behrens-Fisher problem" discussed in Section 8.1c), in addition to being nonnormal. They presented a modified Mann-Whitney procedure, requiring that the underlying distributions be symmetrical, along with tables of critical values for use with sample sizes ≤ 12 and with a normal approximation good when the n's are much larger than 12.

EXAMPLE 8.15 The Two-Sample Median Test, Using the Data of Example 8.14

H_0: The two samples came from populations with identical medians (i.e., the median performance is the same under the two teaching assistants).

H_A: The medians of the two sampled populations are not equal.

$\alpha = 0.05$

The median of all 25 measurements in Example 8.14 is $X_{(25+1)2} = X_{13}$ = grade of C+. The following 2 × 2 contingency table is then produced:

Number	*Sample 1*	*Sample 2*	*Total*
Above median	6	6	12
Not above median	3	8	11
Total	9	14	23

Analyzing this contingency table (Section 23.3):

$$X_c^2 = \frac{n\left(|f_{11}f_{22} - f_{12}f_{21}| - \frac{n}{2}\right)^2}{(C_1)(C_2)(R_1)(R_2)} \tag{8.59}$$
$$= 0.473.$$

$$X^2_{0.05,1} = 3.841$$

Therefore, do not reject H_0.

$$0.25 < P < 0.50 \quad [P = 0.49]$$

So it is concluded that the two samples did not come from populations with different medians.

and below the median will be less than the number of original data. Some authors and computer programs have preferred to tabulate the row categories as "above median" and "not above median" (that is, "at or below the median") instead of "above median" and "below median." This will retain in the analysis the original number of data, but it does not test the median-comparison hypothesis as well, and it can produce conclusions very different from those resulting from analyzing the same data categorized as "below median" and "not below median" (i.e., "at or above median"). Others have suggested deleting from the analysis any data that are tied at the grand median. This, too, will give results that may be quite different from the other procedures. If there are many data at the grand median, a good option is to place all data in a contingency table with three, instead of two, rows: "above median," "at median," and "below median."

The median test is about 64% as powerful as the two-sample t test when used on data to which the latter is applicable (Mood, 1954), and about 67% as powerful as the Mann-Whitney test of the preceding section.*

If the two sampled populations have equal variances and shapes, then the Mann-Whitney test (Section 8.11) is a test for difference between medians (Fligner and Policello, 1981).

One can also test whether the difference between two population medians is of a specified magnitude. This would be done in a fashion similar to that indicated in Section 8.11f for the Mann-Whitney test. For example, to hypothesize that the median of population 1 is X units greater than the median of population 2, X would be added to each datum in sample 2 (or X would be subtracted from each datum in sample 1) prior to performing the median test.

8.13 TWO-SAMPLE TESTING OF NOMINAL-SCALE DATA

We may compare two samples of nominal data simply by arranging the data in a $2 \times C$ contingency table and proceeding as described in Chapter 23.

8.14 TESTING FOR DIFFERENCE BETWEEN TWO DIVERSITY INDICES

If the Shannon index of diversity, H' (Section 4.7), is obtained for each of two samples, it may be desired to test the null hypothesis that the diversities of the two sampled populations are equal. Hutcheson (1970) proposed a t test for this purpose:

$$t = \frac{H'_1 - H'_2}{s_{H'_1 - H'_2}}, \tag{8.60}$$

where

$$s_{H'_1 - H'_2} = \sqrt{s^2_{H'_1} + s^2_{H'_2}}. \tag{8.61}$$

The variance of each H' may be approximated by

$$s^2_{H'} = \frac{\sum f_i \log^2 f_i - (\sum f_i \log f_i)^2/n}{n^2} \tag{8.62}$$

(Basharin, 1959; Lloyd, Zar, and Karr, 1968),† where s, f_i, and n are as defined in Section 4.7, and $\log^2 f$ signifies $(\log f)^2$. Logarithms to any base may be used for this calculation, but those to base 10 are most commonly employed. The degrees of freedom associated with the preceding t are approximated by

$$\nu = \frac{\left(s^2_{H'_1} + s^2_{H'_2}\right)^2}{\frac{\left(s^2_{H'_1}\right)^2}{n_1} + \frac{\left(s^2_{H'_2}\right)^2}{n_2}} \tag{8.63}$$

(Hutcheson, 1970).

*As the median test refers to a population parameter in hypothesis testing, it is not a nonparametric test; but it is a distribution-free procedure. Although it does not assume a specific underlying distribution (e.g., normal), it does assume that the two populations have the same shape (a characteristic that is addressed by Schlittgen, 1979).

†Bowman et al. (1971) give an approximation [their Equation (11b)] that is more accurate for very small n.

Example 8.16 demonstrates these computations. If one is faced with many calculations of $s^2_{H'_2}$, the tables of $f_i \log^2 f_i$ provided by Lloyd, Zar, and Karr (1968) will be helpful. One-tailed as well as two-tailed hypotheses may be tested by this procedure. Also, the population diversity indices may be hypothesized to differ by some value, μ_0, other than zero, in which case the numerator of t would be $|H'_1 - H'_2| - \mu_0$.

EXAMPLE 8.16 Comparing Two Indices of Diversity

H_0: The diversity of plant food items in the diet of Michigan blue jays is the same as the diversity of plant food items in the diet of Louisiana blue jays.

H_A: The diversity of plant food items in the diet of Michigan blue jays is not the same as in the diet of Louisiana blue jays.

$\alpha = 0.05$

Michigan Blue Jays

Diet item	f_i	$f_i \log f_i$	$f_i \log^2 f_i$
Oak	47	78.5886	131.4078
Corn	35	54.0424	83.4452
Blackberry	7	5.9157	4.9994
Beech	5	3.4949	2.4429
Cherry	3	1.4314	0.6830
Other	2	0.6021	0.1812
$s_1 = 6$	$n_1 = \sum f_i$ = 99	$\sum f_i \log f_i$ = 144.0751	$\sum f_i \log^2 f_i$ = 223.1595

$$H'_1 = \frac{n \log n - \sum f_i \log f_i}{n} = \frac{197.5679 - 144.0751}{99}$$

$$= 0.5403$$

$$s^2_{H'_1} = \frac{\sum f_i \log^2 f_i - (\sum f_i \log f_i)^2 / n}{n^2} = 0.00137602$$

Louisiana Blue Jays

Diet item	f_i	$f_i \log f_i$	$f_i \log^2 f_i$
Oak	48	80.6996	135.6755
Pine	23	31.3197	42.6489
Grape	11	11.4553	11.9294
Corn	13	14.4813	16.1313
Blueberry	8	7.2247	6.5246
Other	2	0.6021	0.1812
$s_2 = 6$	$n_2 = \sum f_i$ = 105	$\sum f_i \log f_i$ = 145.7827	$\sum f_i \log^2 f_i$ = 213.0909

$$H_2' = \frac{n \log n - \sum f_i \log f_i}{n} = \frac{212.2249 - 145.7827}{105} = 0.6328$$

$$s_{H_2'}^2 = \frac{\sum f_i \log^2 f_i - \left(\sum f_i \log f_i\right)^2 / n}{n^2} = 0.00096918$$

$$s_{H_1' - H_2'} = \sqrt{s_{H_1'}^2 + s_{H_2'}^2} = \sqrt{0.00137602 + 0.00096918} = 0.0484$$

$$t = \frac{H_1' - H_2'}{s_{H_1' - H_2'}} = \frac{-0.0925}{0.0484} = -1.911$$

$$\nu = \frac{\left(s_{H_1'}^2 + s_{H_2'}^2\right)^2}{\frac{\left(s_{H_1'}^2\right)^2}{n_1} + \frac{\left(s_{H_2'}^2\right)^2}{n_2}} = \frac{(0.00137602 + 0.00096918)^2}{\frac{(0.00137602)^2}{99} + \frac{(0.00096918)^2}{105}}$$

$$= \frac{0.000005499963}{0.000000028071} = 196$$

$t_{0.05(2),196} = 1.972$

Therefore, do not reject H_0.

$$0.05 < P < 0.10 \quad [P = 0.057]$$

The conclusion is that the diversity of food items is the same in birds from Michigan and Louisiana.

8.15 CODING DATA

As explained in Section 3.5, coding raw data can sometimes simplify computations. Coding will affect the sample statistics of this chapter (i.e., measures of central tendency and of variability, and their confidence limits) as described in Appendix C. The test statistics and hypothesis-test conclusions in Sections 8.1–8.7 will not be altered by coding, except that coding may not be used in performing the Levene test (Section 8.5b). Neither may coding be used in testing for difference between two coefficients of variation (Section 8.8), except that it is permissible if using the F test and coding by addition (or subtraction, but not multiplication or division). There is no effect of coding on the Mann-Whitney test (Section 8.11) or median test (Section 8.12). And, for testing difference between two diversity indices (Section 8.14), coding by multiplication (or division, but not addition or subtraction) may be employed.

Regarding the topics of Chapters 7 and 9, coding affects the sample statistics (and their confidence limits) as indicated in Appendix C. Coding may be employed for any of the hypothesis tests in those chapters, except that only coding by multiplication (or division, but not addition or subtraction) may be used for testing or coefficients of variation (Section 7.14).

EXERCISES

8.1. Using the following data, test the null hypothesis that male and female turtles have the same mean serum cholesterol concentrations.

Serum Cholesterol (mg/100 ml)

Male	*Female*
220.1	223.4
218.6	221.5
229.6	230.2
228.8	224.3
222.0	223.8
224.1	230.8
226.5	

8.2. It is proposed that animals with a northerly distribution have shorter appendages than animals from a southerly distribution. Test an appropriate hypothesis (by computing t), using the following wing-length data for birds (data are in millimeters).

Northern	*Southern*
120	116
113	117
125	121
118	114
116	116
114	118
119	123
	120

8.3. Two populations of animal body weights are randomly sampled, and $\overline{X}_1 = 4.6$ kg, $s_1^2 = 11.02$ kg^2, $n_1 = 18$, $\overline{X}_2 = 6.0$ kg, $s_2^2 = 4.35$ kg^2, and $n_2 = 26$. Test the hypotheses H_0: $\mu_1 \geq \mu_2$ and H_A: $\mu_1 < \mu_2$ using the Behrens-Fisher test.

8.4. If $\overline{X}_1 = 334.6$ g, $\overline{X}_2 = 349.8$ g, $SS_1 = 364.34$ g^2, $SS_2 = 286.78$ g^2, $n_1 = 19$, and $n_2 = 24$, test the hypothesis that the mean weight of population 2 is more than 10 g greater than the mean weight of population 1.

8.5. For the data of Exercise 8.1:

(a) If the null hypothesis is rejected, compute the 95% confidence limits for μ_1, μ_2, and $\mu_1 - \mu_2$. If H_0 is not rejected, compute the 95% confidence limits for the common population mean, μ_p.

(b) Calculate the 95% prediction interval for the difference between the mean of an additional 25 data from the male population and an additional 20 data from the female population.

8.6. A sample is to be taken from each of two populations from which previous samples of size 14 have had $SS_1 = 244.66$ (km/hr)^2 and $SS_2 = 289.18$ (km/hr)^2. What size sample should be taken from each population in order to estimate $\mu_1 - \mu_2$ to within 2.0 km/hr, with 95% confidence?

8.7. Consider the populations described in Exercise 8.6.

(a) How large a sample should we take from each population if we wish to detect a difference between μ_1 and μ_2 of at least 5.0 km/hr, using a 5% significance level and a t test with 90% power?

(b) If we take a sample of 20 from one population and 22 from the other, what is the smallest difference between μ_1 and μ_2 that we have a 90% probability of detecting with a t test using $\alpha = 0.05$?

(c) If $n_1 = n_2 = 50$, and $\alpha = 0.05$, what is the probability of rejecting H_0: $\mu_1 = \mu_2$ when $\mu_1 - \mu_2$ is as small as 2.0 km/hr?

8.8. The experimental data of Exercise 8.1 might have been collected to determine whether serum cholesterol concentrations varied as much in male turtles as in female turtles. With those data, use the variance-ratio test to assess H_0: $\sigma_1^2 = \sigma_2^2$ versus $\sigma_1^2 \neq \sigma_2^2$.

8.9. Let us propose that wings of a particular bird species vary in length more in the northern part of the species' range than in the southern portion. Use the variance ratio test for H_0: $\sigma_1 \leq \sigma_2$ versus H_A: $\sigma_1 > \sigma_2$ with the data of Exercise 8.2.

8.10. A sample of 21 data from one population has a variance of 38.71 g^2, and a sample of 20 data from a second population has a variance of 21.35 g^2.

(a) Calculate the 95% two-tailed confidence interval for the ratio of σ_1^2/σ_2^2.

(b) How large a sample must be taken from each population if we wish to have a 90% chance of rejecting H_0: $\sigma_1^2 \leq \sigma_2^2$ when H_A: $\sigma_1^2 > \sigma_2^2$ is true and we apply the variance-ratio test at the 5% level of significance?

(c) What would be the power of a variance-ratio test of this H_0, with $\alpha = 0.05$, if sample sizes of 20 were used?

8.11. A sample of twenty-nine plant heights of members of a certain species had $\overline{X}_1 = 10.74$ cm and $s^2 = 14.62$ cm^2, and the heights of a sample of twenty-five from a second species had $\overline{X}_2 = 14.32$ cm and $s^2 = 8.45$ cm^2. Test the null hypothesis that the coefficients of variation of the two sampled populations are the same.

8.12. Using the Mann-Whitney test, test the appropriate hypotheses for the data in Exercise 8.1.

8.13. Using the Mann-Whitney procedure, test the appropriate hypotheses for the data in Exercise 8.2.

8.14. The following data are volumes (in cubic microns) of avian erythrocytes taken from normal (diploid) and intersex (triploid) individuals. Test the hypothesis (using the Mann-Whitney test) that the volume of intersex cells is 1.5 times the volume of normal cells.

Normal	*Intersex*
248	380
236	391
269	377
254	392
249	398
251	374
260	
245	
239	
255	

CHAPTER 9

Paired-Sample Hypotheses

The two-sample testing procedures discussed in Chapter 8 apply when the two samples are independent, independence implying that each datum in one sample is in no way associated with any specific datum in the other sample. However, there are instances when each observation in Sample 1 is in some way physically associated with an observation in Sample 2, so that the data may be said to occur in pairs.

For example, we might wish to test the null hypothesis that the left foreleg and left hindleg lengths of deer are equal. We could make these two measurements on a number of deer, but we would have to remember that the variation among the data might be owing to two possible factors. First, the null hypothesis might be false, there being, in fact, a difference between foreleg and hindleg length. Second, deer are of different sizes, and for each deer the hindleg length is correlated with the foreleg length (i.e., a deer with a large front leg is likely to have a large hind leg). Thus, as Example 9.1 shows, the data can be tabulated in pairs, one pair (i.e., one hindleg measurement and one foreleg measurement) per animal.

9.1 TESTING MEAN DIFFERENCE BETWEEN PAIRED SAMPLES

The two-tailed hypotheses implied by Example 9.1 are $H_0: \mu_1 - \mu_2 = 0$ and $H_A: \mu_1 - \mu_2 \neq 0$ (which, as pointed out in Section 8.1, could also be stated $H_0: \mu_1 = \mu_2$ and $H_A: \mu_1 \neq \mu_2$). However, we can define a mean population difference, μ_d, as $\mu_1 - \mu_2$, and write the hypotheses as $H_0: \mu_d = 0$ and $H_A: \mu_d \neq 0$. Although the use of either μ_d or $\mu_1 - \mu_2$ is correct, the former will be used here when it implies the paired-sample situation.

The test statistic for the null hypothesis is

$$t = \frac{\bar{d}}{s_{\bar{d}}}. \tag{9.1}$$

Therefore, we do not use the original measurements for the two samples, but only the difference within each pair of measurements. One deals, then, with a sample of d_j values, whose mean is $\bar{d}$ and whose variance, standard deviation, and standard error are denoted as $s_{\bar{d}}^2$, s_d, and $s_{\bar{d}}$ respectively. Thus, the *paired-sample t test*, as this procedure may be called, is essentially a one-sample t test, analogous to that described

EXAMPLE 9.1 The Two-Tailed Paired-Sample *t* Test

H_0: $\mu_d = 0$
H_A: $\mu_d \neq 0$
$\alpha = 0.05$

Deer (j)	*Hindleg length* (cm) (X_{1j})	*Foreleg length* (cm) (X_{2j})	*Difference* (cm) ($d_j = X_{1j} - X_{2j}$)
1	142	138	4
2	140	136	4
3	144	147	−3
4	144	139	5
5	142	143	−1
6	146	141	5
7	149	143	6
8	150	145	5
9	142	136	6
10	148	146	2

$n = 10$ $\quad \bar{d} = 3.3$ cm

$s_d^2 = 9.3444$ cm^2 $\quad s_{\bar{d}} = 0.97$ cm

$\nu = n - 1 = 9$ $\quad t = \dfrac{\bar{d}}{s_{\bar{d}}} = \dfrac{3.3}{0.97} = 3.402$

$t_{0.05(2),9} = 2.262$ $\quad$ Therefore, reject H_0.

$$0.005 < P(|t| \geq 3.402) < 0.01 \quad [P = 0.008]$$

in Sections 7.1 and 7.2. In the paired-sample t test, n is the number of differences (i.e., the number of pairs of data), and the degrees of freedom are $\nu = n - 1$. Note that the hypotheses used in Example 9.1 are special cases of the general hypotheses H_0: $\mu_d = \mu_0$ and H_A: $\mu_d \neq \mu_0$, where μ_0 is usually, but not always, zero.

For one-tailed hypotheses with paired samples, one can test either H_0: $\mu_d \geq \mu_0$ and H_A: $\mu_d < \mu_0$, or H_0: $\mu_d \leq \mu_0$ and H_A: $\mu_d > \mu_0$, depending on the question to be asked. Example 9.2 presents data from an experiment designed to test whether a new fertilizer results in an increase of more than 250 kg/ha in crop yield over the old fertilizer. For testing this hypothesis, 18 test plots of the crop were set up. It is probably unlikely to find 18 field plots having exactly the same conditions of soil, moisture, wind, and so on, but it should be possible to set up two plots with similar environmental conditions. If so, then the experimenter would be wise to set up nine pairs of plots, applying the new fertilizer randomly to one plot of each pair and the old fertilizer to the other plot of that pair. As Example 9.2 shows, the statistical hypotheses to be tested are H_0: $\mu_d \leq 250$ kg/ha and H_A: $\mu_d > 250$ kg/ha.

Paired-sample t-testing assumes that each datum in one sample is associated with one, *but only one*, datum in the other sample. So, in the last example, each yield using

EXAMPLE 9.2 A One-Tailed Paired-Sample *t* Test

H_0: $\mu_d \leq 250$ kg/ha

H_A: $\mu_d > 250$ kg/ha

$\alpha = 0.05$

	Crop Yield (kg/ha)		
Plot (j)	*With new fertilizer* (X_{1j})	*With old fertilizer* (X_{2j})	d_j
1	2250	1920	330
2	2410	2020	390
3	2260	2060	200
4	2200	1960	240
5	2360	1960	400
6	2320	2140	180
7	2240	1980	260
8	2300	1940	360
9	2090	1790	300

$n = 9$ $\quad \bar{d} = 295.6$ kg/ha

$s_d^2 = 6502.78\ (\text{kg/ha})^2$ $\quad s_{\bar{d}} = 26.9$ kg/ha

$\nu = n - 1 = 8$ $\quad t = \dfrac{\bar{d} - 250}{s_{\bar{d}}} = 1.695$

$t_{0.05(1),8} = 1.860$ $\quad$ Therefore, do not reject H_0.

$0.05 < P < 0.10 \quad [P = 0.064]$

new fertilizer is paired with only one yield using old fertilizer; and it would have been inappropriate to have some tracts of land large enough to collect two or more crop yields using each of the fertilizers.

The paired-sample t test does not have the normality and equality of variances assumptions of the two-sample t test, but it does assume that the differences, d_i, come from a normally distributed population of differences. If a nonnormal distribution of differences is doubted, the nonparametric test of Section 9.5 should be considered.

If there is, in fact, pairwise association of data from the two samples, then analysis by the two-sample t test will often be less powerful than if the paired-sample t test was employed, and the two-sample test will not have a probability of a Type I error equal to the specified significance level, α. It appears that the latter probability will be increasingly less than α for increasingly large correlation between the pairwise data (and, in the less common situation where there is a negative correlation between the data, the probability will be greater than α); and only a small relationship is needed

to make the paired-sample test advantageous (Hines, 1996; Pollak and Cohen, 1981; Zimmerman, 1997). If the data from Example 9.1 were subjected (inappropriately) to the two-sample t test, rather than to the paired-sample t test, a difference would not have been concluded, and a Type II error would have been committed.

9.2 CONFIDENCE LIMITS FOR THE POPULATION MEAN DIFFERENCE

In paired-sample testing we deal with a sample of differences, d_j, so confidence limits for the mean of a population of differences, μ_d, may be determined as in Section 7.3. In the manner of Equation 7.6, the $1 - \alpha$ confidence interval for μ_d is

$$\bar{d} \pm t_{\alpha(2),\nu} s_{\bar{d}}. \tag{9.2}$$

For example, for the data in Example 9.1, we can compute the 95% confidence interval for μ_d to be $3.3\text{ cm} \pm (2.262)(0.97\text{ cm}) = 3.3\text{ cm} \pm 2.2\text{ cm}$; the 95% confidence limits are $L_1 = 1.1$ cm and $L_2 = 5.5$ cm.

Furthermore, we may ask, as in Section 7.5, how large a sample is required to be $1 - \alpha$ confident in estimating μ_d to within $\pm\ d$ (using Equation 7.7).

9.3 POWER, DETECTABLE DIFFERENCE AND SAMPLE SIZE IN PAIRED-SAMPLE TESTING OF MEANS

By considering the paired-sample test to be a one-sample t test for a sample of differences, we may employ the procedures of Section 7.7 to acquire estimates of required sample size (n), minimum detectable difference (δ), and power ($1 - \beta$), using Equations 7.10, 7.11, and 7.12, respectively.

9.4 TESTING FOR DIFFERENCE BETWEEN VARIANCES FROM TWO CORRELATED POPULATIONS

The tests of Section 8.5 address hypotheses comparing σ_1^2 to σ_2^2 when the two samples of data are independent. For example, if we wanted to compare the variance of the lengths of deer forelegs with the variance of deer hindlegs, we could measure a sample of foreleg lengths of several deer and a sample of hindleg lengths from a different group of deer. As these are independent samples, the variance of the foreleg sample could be compared to the variance of the hindleg sample by the procedures of Section 8.5. However, just as the paired-sample comparison of means is more powerful than independent-sample comparison of means when the data are paired (i.e., when there is an association between each member of one sample and a member of the other sample), there is a variance-comparison test more powerful than those of Section 8.5 if the data are paired (as they are in Example 9.1). This test takes into account the amount of association between the members of the pairs of data, as presented by Snedecor and Cochran (1989: 192–193) based upon a procedure of Pitman (1939). We compute:

$$t = \frac{(F - 1)\sqrt{n - 2}}{2\sqrt{F(1 - r^2)}}. \tag{9.3}$$

Here, n is the sample size common to both samples, r is the correlation coefficient described in Section 19.1 (Equation 19.1), and the degrees of freedom associated with t are $\nu = n - 2$. For a two-tailed test (H_0: $\sigma_1^2 = \sigma_2^2$ vs. H_A: $\sigma_1^2 \neq \sigma_2^2$), either $F = s_1^2/s_2^2$ or $F = s_2^2/s_1^2$ may be used, as indicated in Equation 8.29, and H_0 is rejected if $|t| \geq t_{\alpha(2),\nu}$. This is demonstrated in Example 9.3. For the one-tailed hypotheses, H_0: $\sigma_1^2 \leq \sigma_2^2$ versus H_A: $\sigma_1^2 > \sigma_2^2$, use $F = s_1^2/s_2^2$; for H_0: $\sigma_1^2 \geq \sigma_2^2$ versus H_A: $\sigma_1^2 < \sigma_2^2$, use $F = s_2^2/s_1^2$; and a one-tailed test rejects H_0 if $t \geq t_{\alpha(1),\nu}$.

McCulloch (1987) showed that this t test is adversely affected if the two sampled populations do not have a normal distribution, in that the probability of a Type I error can depart greatly from the stated α. He demonstrated a testing procedure that is very little affected by nonnormality and is only slightly less powerful than t when the underlying populations are normal. It utilizes the differences and the sums of the members of the pairs, just as described in the preceding paragraph; but, instead of the parametric correlation coefficient (r) referred to above, it employs the nonparametric correlation coefficient (r_s) and the associated significance testing of Section 19.9. This technique may be used for two-tailed or one-tailed testing.

EXAMPLE 9.3 Testing for Difference Between the Variances of Two Paired Samples

H_0: $\sigma_1^2 = \sigma_2^2$

H_A: $\sigma_1^2 \neq \sigma_2^2$

$\alpha = 0.05$

Using the paired-sample data of Example 9.1:

$n = 10$; $\nu = 8$

$\sum x^2 = 104.10$; $\sum y^2 = 146.40$

$\sum xy = 83.20$

$s_1^2 = 11.57\ \text{cm}^2$; $s_2^2 = 16.27\ \text{cm}^2$

$F = 11.57\ \text{cm}^2/16.27\ \text{cm}^2 = 0.7111$

Using Equation 19.1, $r = 0.6739$.

Using Equation 9.3:

$t = -0.656$ and $t_{0.05(2),8} = 2.306$, so H_0 is not rejected.

$P > 0.50$ [$P = 0.54$]

9.5 PAIRED-SAMPLE TESTING BY RANKS

The *Wilcoxon paired-sample test* (Wilcoxon, 1945; Wilcoxon and Wilcox, 1964: 9) is a nonparametric analogue to the paired-sample t test, just as the Mann-Whitney test is a nonparametric procedure analogous to the two-sample t test. The literature refers to the test by a variety of names, but usually in conjunction with Wilcoxon's name* and some wording such as "paired sample" or "matched pairs," sometimes together with a phrase like "rank sum" or "signed rank."

Whenever the paired-sample t test is applicable, the Wilcoxon paired-sample test is also applicable. Section 7.9 introduced the Wilcoxon procedure as a nonparametric

*Frank Wilcoxon (1892–1965), American (born in Ireland) chemist and statistician, a major developer of statistical methods based on ranks (Bradley and Hollander, 1978).

one-sample test, but it is also very useful for paired-sample testing, just as the one-sample t and the paired-sample t test are basically the same. If the d_j values are from a normal distribution, then the Wilcoxon test has $3/\pi$ (i.e., 95.5%) of the power in detecting differences as the t test has (Conover, 1999: 363; Mood, 1954). But when the d_j's cannot be assumed to be from a normal distribution, the parametric paired-sample t test should be avoided, for with nonnormality, the Wilcoxon paired-sample test will be more powerful, sometimes much more powerful (Blair and Higgins, 1985). However, the Wilcoxon test assumes the population of differences is symmetrical (which the t test also does, for the normal distribution is symmetrical). The sign test of Section 24.6 could also be used for one-sample testing of the d_j's. It has only $2/\pi$ (64%) of the power of the t test, and only 67% of the power of the Wilcoxon test, when the normality assumption of the t test is met (Conover, 1999: 164). But the sign test does not assume symmetry and is therefore preferable to the Wilcoxon test when the differences come from a very asymmetric population.

Example 9.4 demonstrates the use of the Wilcoxon paired-sample test with the ratio-scale data of Example 9.1, and it is best applied to ratio- or interval-scale data. The testing procedure involves the calculation of differences, as does the paired-sample t test. Then one ranks the absolute values of those differences, from low to high, and affixes the sign of each difference to the corresponding rank. As introduced in Section 8.11, the rank assigned to tied observations is the mean of the ranks that would have been assigned to the observations had they not been tied. Differences of zero are ignored in this test.

Then we sum the ranks having a plus sign (calling this sum T_+) and the ranks with a minus sign (labeling this sum T_-). For a two-tailed test (as in Example 9.4), we reject H_0 if either T_+ or T_- is *less than or equal to* the critical value, $T_{\alpha(2),n}$, from Appendix Table B.12. In doing so, n is the number of differences that are not zero.

Having calculated either T_+ or T_-, the other can be determined as

$$T_- = \frac{n(n+1)}{2} - T_+ \tag{9.4}$$

or

$$T_+ = \frac{n(n+1)}{2} - T_- . \tag{9.5}$$

A different value of T_+ (call it T'_+) or T_- (call it T'_-) will be obtained if rank 1 is assigned to the largest, rather than the smallest, d_i (i.e., the absolute values of the d_j's are ranked from high to low). If this is done, the test statistics are obtainable as

$$T_+ = m(n+1) - T'_+ \tag{9.6}$$

and

$$T_- = m(n+1) - T'_- , \tag{9.7}$$

where m is the number of ranks with the sign being considered.

Pratt (1959) recommended maintaining differences of zero until after ranking, and thereafter ignoring the ranks assigned to the zeros. This procedure may yield slightly better results in some circumstances, though worse results in others (Conover, 1973). If used, then the critical values of Rahe (1974) should be consulted or the normal approximation employed (see the following section) instead of using critical values of T from Appendix Table B.12.

If data are paired, the undesirable use of the Mann-Whitney test, instead of the Wilcoxon paired-sample test, may lead to a greater Type II error, with the concomitant inability to detect actual population differences.

EXAMPLE 9.4 The Wilcoxon Paired-Sample Test Applied to the Data of Example 9.1

H_0: Deer hindleg length is the same as foreleg length.

H_A: Deer hindleg length is not the same as foreleg length.

$\alpha = 0.05$

Deer (j)	*Hindleg length* (cm) (X_{1j})	*Foreleg length* (cm) (X_{2j})	*Difference* ($d_j = X_{1j} - X_{2j}$)	*Rank of* $\lvert d_j \rvert$	*Signed rank of* $\lvert d_j \rvert$
1	142	138	4	4.5	4.5
2	140	136	4	4.5	4.5
3	144	147	−3	3	−3
4	144	139	5	7	7
5	142	143	−1	1	−1
6	146	141	5	7	7
7	149	143	6	9.5	9.5
8	150	145	5	7	7
9	142	136	6	9.5	9.5
10	148	146	2	2	2

$n = 10$

$T_+ = 4.5 + 4.5 + 7 + 7 + 9.5 + 7 + 9.5 + 2 = 51$

$T_- = 3 + 1 = 4$

$T_{0.05(2),10} = 8$

Since $T_- < T_{0.05(2),10}$, H_0 is rejected.

$0.01 < P(T_- \text{ or } T_+ \leq 4) < 0.02 \quad [P = 0.014]$

The Wilcoxon paired-sample test has an underlying assumption that the sampled population of d_j's is symmetrical about the median. Another nonparametric test for paired samples is the sign test (described in Section 24.6), which does not have this assumption but is less powerful if the assumption is met.

Section 8.11f discussed the Mann-Whitney test for hypotheses dealing with differences of specified magnitude. The Wilcoxon paired-sample test can be used in a similar fashion. For instance, it can be asked whether the hindlegs in the population sampled in Example 9.4 are 3 cm longer than the lengths of the forelegs. This can be done by applying the Wilcoxon paired-sample test after subtracting 3 cm from each hindleg length in the sample (or adding 3 cm to each foreleg length).

(a) The One-Tailed Wilcoxon Paired-Sample Test. For one-tailed testing we use one-tailed critical values from Appendix Table B.12 and either T_+ or T_- as follows. For the hypotheses

H_0: Measurements in population 1 $\leq$ measurements in population 2
and H_A: Measurements in population 1 $>$ measurements in population 2,

H_0 is rejected if $T_- \leq T_{\alpha(1),n}$. For the opposite hypotheses:

H_0: Measurements in population 1 $\geq$ measurements in population 2
and H_A: Measurements in population 1 $<$ measurements in population 2,

reject H_0 if $T_+ \leq T_{\alpha(1),n}$.

(b) The Normal Approximation to the Wilcoxon Paired-Sample Test. For data consisting of more than 100 pairs* (the limit of Appendix Table B.12), the significance of T (where either T_+ or T_- may be used for T) may be determined by considering that for such large samples the distribution of T is closely approximated by a normal distribution with a mean of

$$\mu_T = \frac{n(n+1)}{4} \tag{9.8}$$

and a standard error of

$$\sigma_T = \sqrt{\frac{n(n+1)(2n+1)}{24}}. \tag{9.9}$$

Thus, we can calculate

$$Z = \frac{|T - \mu_T|}{\sigma_T}, \tag{9.10}$$

where for T we may use, with identical results, either T_+ or T_-. Then, for a two-tailed test, Z is compared to the critical value, $Z_{\alpha(2)}$, or, equivalently, $t_{\alpha(2),\infty}$ (which for $\alpha = 0.05$ is 1.9600); if Z is greater than or equal to $Z_{\alpha(2)}$, then H_0 is rejected.

A normal approximation with a correction for continuity employs

$$Z_c = \frac{|T - \mu_T| - 0.5}{\sigma_T}. \tag{9.11}$$

As shown at the end of Appendix Table B.12, the normal approximation is better using Z for $\alpha(2)$ from 0.001 to 0.05 and is better using Z_c for $\alpha(2)$ from 0.10 to 0.50.

If there are tied ranks, then use

$$\sigma_T = \sqrt{\frac{n(n+1)(2n+1) - \frac{\sum t}{2}}{24}}, \tag{9.12}$$

where

$$\sum t = \sum (t_i^3 - t_i) \tag{9.13}$$

is the correction for ties introduced in using the normal approximation to the Mann-Whitney test (Equation 8.57), applied here to ties of nonzero differences.

*Fahoome (2002) concluded that the normal approximation also works well for sample sizes smaller than 100. She found that the probability of a Type I error is between 0.045 and 0.055 for two-tailed testing at the 0.05 level of significance with n as small as 10 and is between 0.009 and 0.011 when testing at $\alpha(2) = 0.01$ with n as small as 22. Additional information regarding the accuracy of this approximation is given at the end of Appendix Table B.12.

If we employ the Pratt procedure for handling differences of zero (described above), then the normal approximation is

$$Z = \frac{\left|T - \frac{n(n+1) - m'(m'+1)}{4}\right| - 0.5}{\sqrt{\frac{n(n+1)(2n+1) - m'(m'+1)(2m+1) - \frac{\sum t}{2}}{24}}} \tag{9.14}$$

(Cureton, 1967), where n is the total number of differences (including zero differences), and m' is the number of zero differences; $\sum t$ is as in Equation 9.13, applied to ties other than those of zero differences. We calculate T_+ or T_- by including the zero differences in the ranking and then deleting from considerations both the zero d_j's and the ranks assigned to them. For T in Equation 9.14, either T_+ or T_- may be used. If neither tied ranks nor zero d_j's are present, then Equation 9.14 becomes Equation 9.11.

One-tailed testing may also be performed using the normal approximation (Equation 9.10 or 9.11) or Cureton's procedure (Equation 9.14). The calculated Z is compared to $Z_{\alpha(1)}$ (which is the same as $t_{\alpha(1),\infty}$), and the direction of the arrow in the alternate hypothesis must be examined. If the arrow points to the left ("<"), then H_0 is rejected if $Z \geq Z_{\alpha(1)}$ *and* $T_+ < T_-$; if it points to the right (">"), then reject H_0 if $Z \geq Z_{\alpha(1)}$ *and* $T_+ > T_-$.

Iman (1974a) presents an approximation based on Student's t:

$$t = \frac{T - \mu_T}{\sqrt{\frac{n^2(n+1)(2n+1)}{2(n-1)} - \frac{(T-\mu_T)^2}{n-1}}}, \tag{9.15}$$

with $n - 1$ degrees of freedom. As shown at the end of Appendix Table B.12, this performs slightly better than the normal approximation (Equation 9.10). The test with a correction for continuity is performed by subtracting 0.5 from $|T - \mu_T|$ in both the numerator and denominator of Equation 9.15. This improves the test for $\alpha(2)$ from 0.001 to 0.10, but the uncorrected t is better for $\alpha(2)$ from 0.20 to 0.50. One-tailed t-testing is effected in a fashion similar to that described for Z in the preceding paragraph.*

Fellingham and Stoker (1964) discuss a more accurate approximation, but it requires more computation, and for sample sizes beyond those in Table B.12 the increased accuracy is of no great consequence.

(c) The Wilcoxon Paired-Sample Test for Ordinal Data. The Wilcoxon test nonparametrically examines differences between paired samples when the samples consist of interval-scale or ratio-scale data (such as in Example 9.4), which is legitimate because the paired differences can be meaningfully ordered. However, it may not work well with samples comprising ordinal-scale data because the differences between ordinal scores may not have a meaningful ordinal relationship to each other. For example, each of several frogs could have the intensity of its green skin color recorded on a scale of 1 (very pale green) to 10 (very deep green). Those data would represent an ordinal scale of measurement because a score of 10 indicates a more intense green than a score of 9, a 9 represents an intensity greater than an 8, and so on. Then the skin-color

*When Appendix Table B.12 cannot be used, a slightly improved approximation is effected by comparing the mean of t and Z to the mean of the critical values of t and Z (Iman, 1974a).

intensity could be recorded for these frogs after they were administered hormones for a period of time, and those data would also be ordinal. However, the *differences* between skin-color intensities before and after the hormonal treatment would not necessarily be ordinal data because, for example, the difference between a score of 5 and a score of 2 (a difference of 3) cannot be said to represent a difference in skin color that is greater than the difference between a score of 10 and a score of 8 (a difference of 2).

To deal with such a situation, Kornbrot (1990) presented a modification of the Wilcoxon paired-sample test (which she called the "rank difference test"), along with tables to determine statistical significance of its results.

(d) Wilcoxon Paired-Sample Test Hypotheses about a Specified Difference Other Than Zero. As indicated in Section 9.1, the paired-sample t test can be used for hypotheses proposing that the mean difference is something other than zero. Similarly, the Wilcoxon paired-sample test can examine whether paired differences are centered around a quantity other than zero. Thus, for data such as in Example 9.2, the nonparametric hypotheses could be stated as H_0: crop yield does not increase more than 250 kg/ha with the new fertilizer, versus H_A: crop yield increases more than 250 kg/ha with the new fertilizer. In that case, each datum for the old-fertilizer treatment would be increased by 250 kg/ha (resulting in nine data of 1920, 2020, 2060 kg/ha, etc.) to be paired with the nine new-fertilizer data of 2250, 2410, 2260 kg/ha, and so on. Then, the Wilcoxon paired-sample test would be performed on those nine pairs of data.

With ratio- or interval-scale data, it is also possible to propose hypotheses considering a multiplication, rather than an addition, constant. This concept is introduced at the end of Section 8.11f.

9.6 CONFIDENCE LIMITS FOR THE POPULATION MEDIAN DIFFERENCE

In Section 9.2, confidence limits were obtained for the mean of a population of differences. Given a population of differences, one can also determine confidence limits for the population median. This is done exactly as indicated in Section 7.10; simply consider the observed differences between members of pairs (d_j) as a sample from a population of such differences.

EXERCISES

9.1. Concentrations of nitrogen oxides and of hydrocarbons (recorded in $\mu g/m^3$) were determined in a certain urban area.

(a) Test the hypothesis that both classes of air pollutants were present in the same concentration.

Day	*Nitrogen oxides*	*Hydrocarbons*
1	104	108
2	116	118
3	84	89
4	77	71
5	61	66
6	84	83
7	81	88
8	72	76
9	61	68
10	97	96
11	84	81

(b) Calculate the 95% confidence interval for μ_d.

9.2. Using the data of Exercise 9.1, test the appropriate hypotheses with Wilcoxon's paired-sample test.

9.3. Using the data of Exercise 9.1, test for equality of the variances of the two kinds of air pollutants.

CHAPTER 10

Multisample Hypotheses and the Analysis of Variance

When measurements of a variable are obtained for each of two independently collected samples, hypotheses such as those described in Chapter 8 are appropriate. However, biologists often obtain data in the form of three or more samples, which are from three or more populations, a situation calling for multisample analyses, as introduced in this chapter.

It is tempting to some to test multisample hypotheses by applying two-sample tests to all possible pairs of samples. In this manner, for example, one might proceed to test the null hypothesis H_0: $\mu_1 = \mu_2 = \mu_3$ by testing each of the following hypotheses by the two-sample t test: H_0: $\mu_1 = \mu_2$, H_0: $\mu_1 = \mu_3$, H_0: $\mu_2 = \mu_3$. But such a procedure, employing a series of two-sample tests to address a multisample hypothesis, is invalid.

The calculated test statistic, t, and the critical values we find in the t table are designed to test whether the two sample statistics, $\overline{X}_1$ and $\overline{X}_2$, are likely to have come from the same population (or from two populations with identical means). In properly employing the two-sample test, we could randomly draw two sample means from the same population and wrongly conclude that they are estimates of two different populations' means; but we know that the probability of this error (the Type I error) will be no greater than α. However, consider that three random samples were taken from a single population. In performing the three possible two-sample t tests indicated above, with $\alpha = 0.05$, the probability of wrongly concluding that two of the means estimate different parameters is 14%, considerably greater than α. Similarly, if α is set at 5% and four means are tested, two at a time, by the two-sample t test, there are six pairwise H_0's to be tested in this fashion, and there is a 26% chance of wrongly concluding a difference between one or more of the means. Why is this?

For each two-sample t test performed at the 5% level of significance, there is a 95% probability that we shall correctly conclude not to reject H_0 when the two population means are equal. For the set of three hypotheses, the probability of *correctly* declining to reject all of them is only $0.95^3 = 0.86$. This means that the probability of *incorrectly* rejecting at least one of the H_0's is $1 - (1 - \alpha)^C = 1 - (0.95)^3 = 0.14$, where C

is the number of possible different pairwise combinations of k samples (see footnote to Table 10.1). As the number of means increases, it becomes almost certain that performing all possible two-sample t tests will conclude that some of the sample means estimate different values of μ, even if all of the samples came from the same population or from populations with identical means. Table 10.1 shows the probability of committing a Type I error if multiple t tests are employed to assess differences among more than two means. If, for example, there are 10 sample means, then $k = 10$, $C = 45$, and $1 - 0.95^{45} = 1 - 0.10 = 0.90$ is the probability of at least one Type I error when testing at the 0.05 level of significance. Two-sample tests, it must be emphasized, should *not* be applied to multisample hypotheses. The appropriate procedures are introduced in the following sections.

TABLE 10.1: Probability of Committing at Least One Type I Error by Using Two-Sample t Tests for All C Pairwise Comparisons of k Means*

		Level of Significance, α, Used in the t Tests				
k	C	0.10	0.05	0.01	0.005	0.001
2	1	0.10	0.05	0.01	0.005	0.001
3	3	0.27	0.14	0.03	0.015	0.003
4	6	0.47	0.26	0.06	0.030	0.006
5	10	0.65	0.40	0.10	0.049	0.010
6	15	0.79	0.54	0.14	0.072	0.015
10	45	0.99	0.90	0.36	0.202	0.044
	∞	1.00	1.00	1.00	1.000	1.000

*There are $C = k(k - 1)/2$ pairwise comparisons of k means. This is the number of combinations of k items taken two at a time; see Equation 5.10.

10.1 SINGLE-FACTOR ANALYSIS OF VARIANCE

To test the null hypothesis H_0: $\mu_1 = \mu_2 = \cdots = \mu_k$, where k is the number of experimental groups, or samples, we need to become familiar with the topic of *analysis of variance*, often abbreviated ANOVA (or less commonly, ANOV or AOV). Analysis of variance is a large area of statistical methods, owing its name and much of its early development to R. A. Fisher;* in fact, the F statistic was named in his honor by G. W. Snedecor† (1934: 15). There are many ramifications of analysis of variance considerations, the most common of which will be discussed in this and subsequent chapters. More complex applications and greater theoretical coverage are found in the many books devoted specifically to analysis of variance and experimental design. At this point, it may appear strange that a procedure used for testing the equality of *means* should be named analysis of *variance*, but the reason for this terminology soon will become apparent.

*Sir Ronald Aylmer Fisher (1890–1962), British statistician and geneticist, who introduced the name and basic concept of the technique in 1918 (David, 1995; Street, 1990) and stressed the importance of randomness as discussed in this section. When he introduced analysis of variance, he did so by way of intraclass correlation (Box, 1978: 101), to which it is related (Section 19.12).

†George W. Snedecor (1881–1974), American statistician.

Let us assume that we wish to test whether four different feeds result in different body weights in pigs. Since we are to test for the effect of only one *factor* (feed type) on the variable in question (body weight), the appropriate analysis is termed a single-factor (or "single-criterion" or "single-classification" or "one-way") analysis of variance.* Furthermore, each type of feed is said to be a *level* of the factor. The design of this experiment should have each experimental animal being assigned at random to receive one of the four feeds, with approximately equal numbers of pigs receiving each feed.

As with other statistical testing, it is of fundamental importance that each sample is composed of a random set of data from a population of interest. In Example 10.1, each of four populations consists of body weights of pigs on one of four experimental diets, and 19 pigs were assigned, at random, to the four diets. In other instances, researchers do not actually perform an experiment but, instead, collect data from populations defined other than by the investigator. For example, the interest might be in comparing body weights of four strains of pigs. If that were the case, the strain to which each animal belonged would not have been under the control of the researcher. Instead, he or she would measure a sample of weights for each strain, and the important consideration would be having each of the four samples consist of data assumed to have come at random from one of the four populations of data being studied.

EXAMPLE 10.1 A Single-Factor Analysis of Variance (Model I)

Nineteen pigs are assigned at random among four experimental groups. Each group is fed a different diet. The data are pig body weights, in kilograms, after being raised on these diets. We wish to ask whether pig weights are the same for all four diets.

H_0: $\mu_1 = \mu_2 = \mu_3 = \mu_4$.

H_A: The mean weights of pigs on the four diets are not all equal.

$\alpha = 0.05$

	Feed 1	*Feed 2*	*Feed 3*	*Feed 4*
	60.8	68.7	69.6	61.9
	67.0	67.7	77.1	64.2
	65.0	75.0	75.2	63.1
	68.6	73.3	71.5	66.7
	61.7	71.8		60.3
i	1	2	3	4
n_i	5	5	4	5
$\sum_{j=1}^{n_i} X_{ij}$	323.1	356.5	293.4	316.2
$\overline{X_i}$	64.62	71.30	73.35	63.24

Because the pigs are assigned to the feed groups at random (as with the aid of a random-number table, such as Appendix Table B.41, described in Section 2.3),

*Some authors would here refer to the feed as the "independent variable" and to the weight as the "dependent variable."

the single factor ANOVA is said to represent a *completely randomized experimental design*, or "completely randomized design" (sometimes abbreviated "CRD"). In general, statistical comparison of groups of data works best if each group has the same number of data (a situation referred to as being a *balanced*, or *orthogonal, experimental design*), and the power of the test is heightened by having sample sizes as nearly equal as possible. The present hypothetical data might represent a situation where there were, in fact, five experimental animals in each of four groups, but the body weight of one of the animals (in group 3) was not used in the analysis for some appropriate reason. (Perhaps the animal died, or perhaps it became ill or was discovered to be pregnant, thus introducing a factor other than feed into the experiment.) The performance of the test is also enhanced by having all pigs as similar as possible in all respects except for the experimental factor, diet (i.e., the animals should be of the same breed, sex, and age, should be kept at the same temperature, etc.).

Example 10.1 shows the weights of 19 pigs subjected to this feed experiment, and the null hypothesis to be tested would be H_0: $\mu_1 = \mu_2 = \mu_3 = \mu_4$. Each datum in the experiment may be uniquely represented by the double subscript notation, where X_{ij} denotes datum j in experimental group i. For example, X_{23} denotes the third pig weight in feed group 2, that is, $X_{23} = 74.0$ kg. Similarly, $X_{34} = 96.5$ kg, $X_{41} = 87.9$ kg, and so on. We shall let the mean of group i be denoted by $\overline{X}_i$, and the grand mean of all observations will be designated by $\overline{X}$. Furthermore, n_i will represent the size of sample i, and $N = \sum_{i=1}^{k} n_i$ will be the total number of data in the experiment. The alternate hypothesis for this experiment is H_A: The mean weight of pigs is not the same on these four diets. Note that H_A is *not* $\mu_1 \neq \mu_2 \neq \mu_3 \neq \mu_4$ nor $\mu_1 \neq \mu_2 = \mu_3 = \mu_4$ nor any other specification of which means are different from which; we can only say that, if H_0 is rejected, then there is at least one difference among the four means.*

The four groups in this example (namely, types of feed) represent a nominal-scale variable (see Section 1.1d) in that the groups could be arranged in any sequence. However, in some situations the groups represent a measurement made on a ratio or interval scale (Sections 1.1a and 1.1b). For example, the animal weights of Example 10.1 might have been measured at each of four environmental temperatures or, instead of the groups being different types of feed, the groups might have been different daily amounts of the same kind of feed. In other situations the groups might be expressed on an ordinal scale (Section 1.1c); for example, body weights could be measured at four environmental temperatures defined as cold, medium, warm, and hot, or as quantities of feed defined as very low, low, medium, and high. The analysis of variance of this section is appropriate when the groups are defined on a nominal or ordinal scale. If they represent a ratio or interval scale, the regression procedures of Section 17.7 may be more appropriate, but the latter methods require more levels of the factor than are generally present in an analysis-of-variance experimental design.

(a) Sources of Variation. The statistical technique widely known as *analysis of variance* (ANOVA) examines the several sources of variation among all of the data

*There may be situations where the desired hypothesis is not whether k means are equal to each other, but whether they are all equal to some particular value. Mee, Shah, and Lefante (1987) proposed a procedure for testing H_0: $\mu_1 = \mu_2 = \cdots = \mu_k = \mu_0$, where μ_0 is the specified mean to which all of the other means are to be compared. The alternate hypothesis would be that at least one of the means is different from μ_0 (i.e., H_A: $\mu_i \neq \mu_0$ for at least one i).

in an experiment, by determining a *sum of squares* (meaning "sum of squares of deviations from the mean," a concept introduced in Section 4.4) for each source. Those sums of squares are as shown below.

In an experimental design with k groups, there are n_i data in group i; that is, n_1 designates the number of data in group 1, n_2 the number in group 2, and so on. The total number of data in all k groups will be called N; that is,

$$N = \sum_{i=1}^{k} n_i, \tag{10.1}$$

which in Example 10.1 is $N = 5 + 5 + 4 + 5 = 19$. The sum of squares for all N data is

$$\text{total SS} = \sum_{i=1}^{k} \sum_{j=1}^{n_i} (X_{ij} - \overline{X})^2, \tag{10.2}$$

where X_{ij} is datum j in group i and $\overline{X}$ is the mean of all N data:

$$\overline{X} = \frac{\sum_{i=1}^{k} \sum_{j=1}^{n_i} X_{ij}}{N}. \tag{10.2a}$$

This is the same as considering the N data in all the groups to compose a single group for which the sum of squares is as shown in Equation 4.12. For the data in Example 10.1, these calculations are demonstrated in Example 10.1a.

EXAMPLE 10.1a Sums of Squares and Degrees of Freedom for the Data of Example 10.1.

	Feed 1	*Feed 2*	*Feed 3*	*Feed 4*
$\sum_{j=1}^{n_i} X_{ij}$	323.1	356.5	293.4	316.2
$\overline{X}_i$	64.62	71.30	73.35	63.24

$$\sum_{i=1}^{k} \sum_{j=1}^{n_i} X_{ij} = 60.8 + 67.0 + 65.0 + \cdots + 63.1 + 66.7 + 60.3 = 1289.2$$

$$\overline{X} = \frac{1289.2}{19} = 67.8526$$

$$\begin{aligned}\text{Total SS} &= \sum_{i=1}^{k} \sum_{j=1}^{n_i} (X_{ij} - \overline{X})^2 \\ &= (60.8 - 67.8526)^2 + (67.0 - 67.8526)^2 \\ &\quad + \cdots + (66.7 - 67.8526)^2 + (60.3 - 6.8526)^2 \\ &= 49.7372 + 0.7269 + \cdots + 1.3285 + 57.0418 = 479.6874.\end{aligned}$$

$$\text{total DF} = N - 1 = 19 - 1 = 18$$

$$\text{groups SS} = \sum_{i=1}^{k} n_i(\bar{X}_i - \bar{X})^2$$

$$= 5(64.62 - 67.8526)^2 + 5(71.30 - 67.8526)^2$$
$$+ 4(73.35 - 67.8526)^2 + 5(63.24 - 67.8526)^2$$
$$= 52.2485 + 59.4228 + 120.8856 + 106.3804 = 338.9372$$

$$\text{groups DF} = k - 1$$

$$\text{within-groups (error) SS} = \sum_{i=1}^{k} \left[\sum_{j=1}^{n_i} (X_{ij} - \bar{X}_i)^2 \right]$$
$$= (60.8 - 64.62)^2 + (67.0 - 64.62)^2$$
$$+ \cdots + (66.7 - 63.24)^2 + (60.3 - 63.24)^2$$
$$= 14.5924 + 5.6644 + \cdots + 11.9716 + 8.6436$$
$$= 140.7500$$

or, alternatively,

$$\text{within-groups (error) SS} = \text{Total SS} - \text{Groups SS}$$
$$= 479.6874 - 338.9373 = 140.7501.$$

$$\text{within-groups (error) DF} = \sum_{i=1}^{k} (n_i - 1)$$
$$= (5 - 1) + (5 - 1) + (4 - 1) + (5 - 1) = 15$$

or within-groups (error) DF $= N - k = 19 - 4 = 15$

or within-groups (error) DF = Total DF − Groups DF $= 18 - 3 = 15$.

Note: The quantities involved in the sum-of-squares calculations are carried to several decimal places (as computers typically do) to avoid rounding errors. All of these sums of squares (and the subsequent mean squares) have $(\text{kg})^2$ as units. However, for typographic convenience and ease in reading, the units for ANOVA computations are ordinarily not printed.

The degrees of freedom associated with the total sum of squares are

$$\text{total DF} = N - 1, \tag{10.3}$$

which for the data in Example 10.1 are $19 - 1 = 18$.

A portion of this total amount of variability of the N data is attributable to differences among the means of the k groups; this is referred to as the *among-groups sum of squares* or, simply, as the *groups sum of squares*:

$$\text{groups SS} = \sum_{i=1}^{k} n_i(\bar{X}_i - \bar{X})^2, \tag{10.4}$$

where $\overline{X}_i$ is the mean of the n_i data in sample i and $\overline{X}$ is the mean of all N data. Example 10.1a shows this computation for the data in Example 10.1. Associated with this sum of squares are these degrees of freedom:

$$\text{groups DF} = k - 1, \tag{10.5}$$

which for Example 10.1 are $4 - 1 = 3$.

Furthermore, the portion of the total sum of squares that is not explainable by differences *among* the group means is the variability *within* the groups:

$$\text{within-groups SS} = \sum_{i=1}^{k} \left[\sum_{j=1}^{n_i} (X_{ij} - \overline{X}_i)^2 \right] \tag{10.6}$$

and is commonly called the *error sum of squares*. Within the brackets Equation 4.12 is applied to the data in each one of the k groups, and the within-groups sum of squares is the sum of all k of these applications of Equation 4.12. For the data of Example 10.1, this is shown in Example 10.1a.

The degrees of freedom associated with the within-groups sum of squares are

$$\text{within-groups DF} = \sum_{i=1}^{k} (n_i - 1) = N - k, \tag{10.7}$$

also called the *error DF*, which for Example 10.1 are $4 + 4 + 3 + 4 = 15$ or, equivalently, $19 - 4 = 15$.

The within-groups SS and DF may also be obtained by realizing that they represent the difference between the total variability among the data and the variability among groups:

$$\text{within-groups SS} = \text{total SS} - \text{groups SS} \tag{10.8}$$

and

$$\text{within-groups DF} = \text{total DF} - \text{groups DF}. \tag{10.8a}$$

In summary, each deviation of an observed datum from the grand mean of all data is attributable to a deviation of that datum from its group mean plus the deviation of that group mean from the grand mean; that is,

$$(X_{ij} - \overline{X}) = (X_{ij} - \overline{X}_i) + (\overline{X}_i - \overline{X}). \tag{10.9}$$

Furthermore, sums of squares and degrees of freedom are additive, so

$$\text{total SS} = \text{groups SS} + \text{error SS} \tag{10.10}$$

and

$$\text{total DF} = \text{groups DF} + \text{error DF}. \tag{10.11}$$

(b) "Machine Formulas." The total sum of squares (Equation 10.2) may be calculated readily by a "machine formula" analogous to Equation 4.16:

$$\text{total SS} = \sum_{i=1}^{k} \sum_{j=1}^{n_i} X_{ij}^2 - C, \tag{10.12}$$

where*

$$C = \frac{\left(\sum\sum X_{ij}\right)^2}{N}. \tag{10.13}$$

Example 10.1b demonstrates these calculations.

EXAMPLE 10.1b Sums of Squares and Degrees of Freedom for the Data of Example 10.1, Using Machine Formulas

	Feed 1	*Feed 2*	*Feed 3*	*Feed 4*	
i	1	2	3	4	
n_i	5	5	4	5	
$\sum_{j=1}^{n_i} X_{ij}$	323.1	356.5	293.4	316.2	
$\frac{\left(\sum_{j=1}^{n_i} X_{ij}\right)^2}{n_i}$	20878.7220	25418.4500	21520.8900	19996.4480	$\sum_{i=1}^{k} \frac{\left(\sum_{j=1}^{n_i} X_{ij}\right)}{n_i} = 87814.5500$

$\sum_i \sum_j X_{ij} = 1289.2$ total DF $= N - 1 = 19 - 1 = 18$

$\sum_i \sum_j X_{ij}^2 = 87955.30$ groups DF $= k - 1 = 4 - 1 = 3$

error DF $= N - k = 19 - 4 = 15$

$$C = \frac{\left(\sum_i \sum_j X_{ij}\right)^2}{N} = \frac{(1289.2)^2}{19} = 87475.6126$$

$$\text{total SS} = \sum_i \sum_j X_{ij}^2 - C = 87955.3000 - 87475.6126 = 479.6874$$

$$\text{groups SS} = \sum_{i=1}^{k} \frac{\left(\sum_{j=1}^{n_i}\right)^2}{n_i} - C = 87814.5500 - 87475.6126 = 338.9374$$

$$\text{error SS} = \text{total SS} - \text{groups SS} = 479.68747 - 338.9374 = 140.7500$$

A machine formula for the groups sum of squares (Equation 10.4) is

$$\text{groups SS} = \sum_{i=1}^{k} \frac{\left(\sum_{j=1}^{n_i} X_{ij}\right)^2}{n_i} - C, \tag{10.14}$$

where $\sum_{j=1}^{n_i} X_{ij}$ is the sum of the n_i data from group i.

*The term "machine formula" derives from the formula's utility when using calculating machines. The quantity C is often referred to as a "correction term"—an unfortunate expression, for it implies that some miscalculation needs to be rectified.

The error SS may be calculated as

$$\text{error SS} = \sum_{i=1}^{k}\sum_{j=1}^{n_i} X_{ij}^2 - \sum_{i=1}^{k} \frac{\left(\sum_{j=1}^{n_i} X_{ij}\right)^2}{n_i}, \tag{10.15}$$

which is the machine formula for Equation 10.6.

As shown in Example 10.1b, machine formulas such as these can be very convenient when using simple calculators; but they are of less importance if the statistical computations are performed by computer. As demonstrated in Examples 10.1a and 10.1b, the sums of squares are the same using the two computational formulas.

(c) Testing the Null Hypothesis. Dividing the groups SS or the error SS by the respective degrees of freedom results in a variance, referred to in ANOVA terminology as a *mean square* (abbreviated MS and short for *mean squared deviation from the mean*). Thus,

$$\text{groups MS} = \frac{\text{groups SS}}{\text{groups DF}} \tag{10.16}$$

and

$$\text{error MS} = \frac{\text{error SS}}{\text{error DF}}, \tag{10.17}$$

and the latter quantity, which may also be called the *within-groups mean square*, is occasionally abbreviated as MSE (for "mean square error"). As will be seen below, testing the null hypothesis of equality among population means involves the examination of the groups mean square and the error mean square. Because a mean square is a kind of variance, this procedure is named *analysis of variance*. A total mean square could also be calculated, as (total SS)/(total DF), but it is not used in the ANOVA.

Statistical theory informs us that if the null hypothesis is a true statement about the populations, then the groups MS and the error MS will each be an estimate of σ^2, the variance common to all k populations. But if the k population means are not equal, then the groups MS in the population will be greater than the population's error MS.* Therefore, the test for the equality of means is a one-tailed variance ratio test (introduced in Section 8.5), where the groups MS is always placed in the numerator so as to ask whether it is significantly larger than the error MS:†

$$F = \frac{\text{groups MS}}{\text{error MS}}. \tag{10.18}$$

*Two decades before R. A. Fisher developed analysis of variance techniques, the Danish applied mathematician, Thorvald Nicolai Thiele (1838–1910) presented the concept of comparing the variance among groups to the variance within groups (Thiele, 1897: 41–44). Stigler (1986: 244) reported that an 1860 book by Gustav Theodor Fechner included the most extensive discussion of the concepts of experimental design prior to R. A. Fisher.

†An equivalent computation of F is

$$F = \left(\frac{\text{error DF}}{\text{groups DF}}\right)\left(\frac{\text{(groups SS)/(total SS)}}{1 - \text{(groups SS)/(total SS)}}\right), \tag{10.18a}$$

and Levin, Serlin, and Webne-Behrman (1989) show how ANOVA can be performed by considering the correlation (the topic of Section 19.1) between observations and their group means.

This quantity expresses how the variability of data among groups compares to the variability of data within groups.

The critical value for this test is $F_{\alpha(1),(k-1),(N-k)}$, which is the value of F at the one-tailed significance level α and with numerator degrees of freedom (ν_1 = groups DF) of $k - 1$ and denominator degrees of freedom (ν_2 = error DF) of $N - k$. If the calculated F is as large as, or larger than, the critical value (see Appendix Table B.4), then we reject H_0; and a rejection indicates that the probability is $\leq \alpha$ that the observed data came from populations described by H_0. But remember that all we conclude in such a case is that all the k population means are not equal. To conclude between which means the equalities or inequalities lie, we must turn to the procedures of Chapter 11.

Example 10.1c shows the conclusion of the analysis of variance performed on the data and hypotheses of Example 10.1. Table 10.2 summarizes the single-factor ANOVA calculations.*

EXAMPLE 10.1c The Conclusion of the ANOVA of Example 10.1, Using the Results of Either Example 10.1a or 10.1b

Summary of the Analysis of Variance

Source of variation	*SS*	*DF*	*MS*
Total	479.6874	18	
Groups	338.9374	3	112.9791
Error	140.7500	15	9.3833

$$F = \frac{\text{groups MS}}{\text{error MS}} = \frac{112.9791}{9.3833} = 12.04$$

$F_{0.05(1),3,15} = 3.29$, so reject H_0.

$P < 0.0005$ [$P = 0.00029$]

(d) The Case where $k = 2$. If $k = 2$, then H_0: $\mu_1 = \mu_2$, and either the two-sample t test (Section 8.1) or the single-factor ANOVA may be applied; the conclusions obtained from these two procedures will be identical. The error MS will, in fact, be identical to the pooled variance, s_p^2, in the t test; the groups DF will be $k - 1 = 1$; the F value determined by the analysis of variance will be the square of the t value from the t test; and $F_{\alpha(1),1,(N-2)} = (t_{\alpha(2),(N-2)})^2$. If a one-tailed test between means is required, or if the hypothesis H_0: $\mu_1 - \mu_2 = \mu_0$ is desired for a μ_0 not equal to zero, then the t test is applicable, whereas the ANOVA is not.

*Occasionally the following quantity (or its square root) is called the *correlation ratio*:

$$\eta^2 = \frac{\text{groups SS}}{\text{total SS}}. \tag{10.18b}$$

This is also called *eta squared*, for it is represented using the lowercase Greek letter eta. It is always between 0 and 1, it has no units of measurement, and it expresses the proportion of the total variability of X that is accounted for by the effect of differences among the groups (and is, therefore, reminiscent of the coefficient of determination introduced in Section 17.3a). For Example 10.1, $\eta^2 = 338.9374/479.6874 = 0.71$, or 71%.

TABLE 10.2: Summary of the Calculations for a Single-Factor Analysis of Variance

Source of variation	Sum of squares (SS)	Degrees of freedom (DF)	Mean square (MS)
Total $[X_{ij} - \overline{X}]$	Equation 10.2 or 10.12	$N - 1$	
Groups (i.e., among groups) $[\overline{X}_i - \overline{X}]$	Equation 10.4 or 10.14	$k - 1$	$\frac{\text{groups SS}}{\text{groups DF}}$
Error (i.e., within groups) $[X_{ij} - \overline{X}_i]$	Equation 10.6 or 10.8	$N - k$ or Equation 10.8a	$\frac{\text{error SS}}{\text{error DF}}$

Note: For each source of variation, the bracketed quantity indicates the variation being assessed: k is the number of groups; X_{ij} is datum j in group i; $\overline{X}_i$ is the mean of the data in group i; $\overline{X}$ is the mean of all N data.

(e) ANOVA Using Means and Variances. The above discussion assumes that all the data from the experiment to be analyzed are in hand. It may occur, however, that all we have for each of the k groups is the mean and some measure of variability based on the variances of each group. That is, we may have $\overline{X}_i$ and either SS_i, s_i^2, s_i, or $s_{\overline{X}_i}$ for each group, rather than all the individual values of X_{ij}. For example, we might encounter presentations such as Tables 7.1, 7.2, or 7.3a. If the sample sizes, n_i, are also known, then the single-factor analysis of variance may still be performed, in the following manner.

First, determine the sum of squares or sample variance for each group: recall that

$$SS_i = (n_i - 1)s_i^2 \text{ and } s_i^2 = (s_i)^2 = n_i(s_{\overline{X}_i})^2. \tag{10.19}$$

Then calculate

$$\text{error SS} = \sum_{i=1}^{k} SS_i = \sum_{i=1}^{k} (n_i - 1)s_i^2 \tag{10.20}$$

and

$$\text{groups SS} = \sum_{i=1}^{k} n_i \overline{X}_i^2 - \frac{\left(\sum_{i=1}^{k} n_i \overline{X}_i\right)^2}{\sum_{i=1}^{k} n_i}. \tag{10.21}$$

Knowing the groups SS and error SS, the ANOVA can proceed in the usual fashion.

(f) Fixed-Effects amd Random-Effects ANOVA. In Example 10.1, the biologist designing the experiment was interested in whether all of these particular four feeds have the same effect on pig weight. That is, these four feeds were not randomly selected from a feed catalog but were specifically chosen. When the levels of a factor are specifically chosen one is said to have designed a *fixed-effects model*, or a *Model I*, ANOVA. In such a case, the null hypothesis H_0: $\mu_1 = \mu_2 = \mu_3 = \cdots = \mu_k$ is appropriate.

However, there are instances where the levels of a factor to be tested are indeed chosen at random. For example, we might have been interested in the effect of geographic location of the pigs, rather than the effect of their feed. It is possible that our concern might be with certain specific locations, in which case we would

be employing a fixed-effects mode ANOVA. But we might, instead, be interested in testing the statement that in general there is a difference in pig weights in animals from different locations. That is, instead of being concerned with only the particular locations used in the study, the intent might be to generalize, considering the locations in our study to be a random sample from all possible locations. In this *random-effects model*, or *Model II*, ANOVA,* all the calculations are identical to those for the fixed-effects model, but the null hypothesis is better stated as H_0: there is no difference in pig weight among geographic locations (or H_0: there is no variability in weights among locations). Examination of Equation 10.18 shows that what the analysis asks is whether the variability among locations is greater than the variability within locations. Example 10.2 demonstrates the ANOVA for a random-effects model. The relevant sums of squares could be computed as in Section 10.1a or 10.1b; the machine formulas of Section 10.1b are used in this example. Most biologists will encounter Model I analyses more commonly than Model II situations. When dealing with more than one experimental factor (as in Chapters 12 and 14), the distinction between the two models becomes essential, as it will determine the calculation of F.

(g) Violation of Underlying Assumptions. Recall from Section 8.1b that to test H_0: $\mu_1 = \mu_2$ by the two-sample t test, we assume that $\sigma_1^2 = \sigma_2^2$ and that each of the two samples came at random from a normal population. Similarly, in order to apply the analysis of variance to $\mu_1 = \mu_2 = \cdots = \mu_k$, we assume that $\sigma_1^2 = \sigma_2^2 = \cdots = \sigma_k^2$ and that each of the k samples came at random from a normal population.

However, these conditions are never *exactly* met, so the question becomes how serious the consequences are when there are departures from these underlying assumptions. Fortunately, under many circumstances the analysis of variance is a robust test, meaning that its Type I and Type II error probabilities are not always seriously altered by violation of the test's assumptions. Reports over several decades of research have not agreed on every aspect of this issue, but the following general statements can be made about fixed-effects (i.e., Model I) ANOVA:

As with the two-sample t test (Section 8.1b), the adverse effect of nonnormality is greater with greater departures from normality, but the effect is relatively small if samples sizes are equal, or if the n_i's are unequal but large (with the test less affected by nonnormality as the n_i's increase), or if the variances are equal; and asymmetric distributions have a greater adverse effect than do symmetric distributions (Box and Anderson, 1955; Büning, 1997; Donaldson, 1968; Glass, Peckham, and Sanders, 1972; Harwell et al., 1992; Lix, Keselman, and Keselman, 1996; Srivastava, 1959; Tiku, 1971).

If the variances of the k populations are not equal, the analysis of variance is generally liberal for equal sample sizes, and the extent to which the test is liberal (i.e., the probability of a Type I error exceeds α) increases with greater variance heterogeneity (Büning, 1997; Clinch and Keselman, 1982; Rogan and Keselman, 1977) and decreases with increased sample size (Rogan and Keselman, 1977). Myers and Well (2003: 221) report that this inflation of P(Type I error) is usually less than 0.02 at the 0.05 significance level and less than 0.005 when using $\alpha = 0.01$, when n is at least 5 and the largest variance is no more than four times the smallest variance.

If the group variances are not equal and the n_i's also are unequal, then there can be very serious effects on P(Type I error). The effect will be greater for greater variance heterogeneity (Box, 1954), and if the larger variances are associated with the larger sample sizes (what we shall call a "direct" relationship), the test is conservative

*Also referred to as a components of variance model. The terms *components of variance*, *fixed effects*, *random effects*, *Class I*, and *Class II* for analysis of variance were introduced by Eisenhart (1947).

EXAMPLE 10.2 A Single-Factor Analysis of Variance for a Random-Effects Model (i.e., Model II) Experimental Design

A laboratory employs a technique for determining the phosphorus content of hay. The question arises: "Do phosphorus determinations differ among the technicians performing the analysis?" To answer this question, each of four randomly selected technicians was given five samples from the same batch of hay. The results of the 20 phosphorus determinations (in mg phosphorus/g of hay) are shown.

H_0: Determinations of phosphorus content do not differ among technicians.

H_A: Determinations of phosphorus content do differ among technicians.

$\alpha = 0.05$

	Technician			
	1	2	3	4
	34	37	34	36
	36	36	37	34
	34	35	35	37
	35	37	37	34
	34	37	36	35
Group sums:	173	182	179	176

$$\sum_i \sum_j X_{ij} = 710$$

$$\sum_i \sum_j X_{ij}^2 = 25234$$

$N = 20$

$$C = \frac{(710)^2}{20} = 25205.00$$

total SS $= 25234 - 25205.00 = 29.00$

$$\text{groups (i.e., technicians) SS} = \frac{(173)^2}{5} + \frac{a(182)^2}{5} + \frac{(179)^2}{5} + \frac{(176)^2}{5} - 25205.00$$

$$= 25214.00 - 25205.00 = 9.00$$

error SS $= 29.00 - 9.00 = 20.00$

Source of variation	SS	DF	MS
Total	29.00	19	
Groups (technicians)	9.00	3	3.00
Error	20.00	16	1.25

$$F = \frac{3.00}{1.25} = 2.40$$

$F_{0.05(1),3,16} = 3.24$

Do not reject H_0.

$0.10 < P < 0.25 \quad [P = 0.11]$

(i.e., the probability of a Type I error is less than α), while larger variances affiliated with smaller samples (what we'll call an "inverse" relationship) cause the test to be liberal—that is, P(Type I error) $> \alpha$ (Brown and Forsythe, 1974a; Büning, 1997; Clinch and Keselman, 1982; Donaldson, 1968; Glass, Peckham, and Sanders, 1972; Harwell et al., 1992; Kohr and Games, 1974; Maxwell and Delaney, 2004: 131; Stonehouse and Forrester, 1998; Tomarkin and Serlin, 1986). For example, if testing at $\alpha = 0.05$ and the largest n is twice the size of the smallest, the probability of a Type I error can be as small as 0.006 for a direct relationship between variances and sample sizes and as large as 0.17 for an inverse relationship; if the ratio between the largest and smallest variances is 5, P(Type I error) can be as small as 0.00001 or as large as 0.38, depending upon whether the relationship is direct or inverse, respectively (Scheffé, 1959: 340). This huge distortion of P(Type I error) may be reason to avoid employing the analysis of variance when there is an inverse relationship (if the researcher is primarily concerned about avoiding a Type I error) or when there is a direct relationship (if the principal concern is to evade a Type II error). The adverse effect of heterogeneous variances appears to increase as k increases (Tomarkin and Serlin, 1986).

Recall (Section 6.3b) that a decrease in the probability of the Type I error (α) is associated with an increase in the Type II error (β), and an increase in β means a decrease in the power of the test ($1 - \beta$). Therefore, for situations described above as conservative [i.e., P(Type I error) $< \alpha$], there will generally be less power than if the population variances were all equal; and when the test is liberal [i.e., P(Type I error) $> \alpha$], there will generally be more power than if the variances were equal.

If the sample sizes are all equal, nonnormality generally affects the power of the analysis of variance to only a small extent (Clinch and Keselman, 1982; Glass, Peckham, and Sanders, 1972; Harwell et al., 1992; Tan, 1982), and the effect decreases with increased n (Donaldson, 1968). However, extreme skewness or kurtosis can severely alter (and reduce) the power (Games and Lucas, 1966), and nonnormal kurtosis generally has a more adverse effect than skewness (Sahai and Ageel, 2000: 85). With small samples, for example, very pronounced platykurtosis in the sampled populations will decrease the test's power, and strong leptokurtosis will increase it (Glass, Peckham, and Sanders, 1972). When sample sizes are not equal, the power is much reduced, especially when the large samples have small means (Bochnke, 1984).

The robustness of random-effects (i.e., Model II) analysis of variance (Section 10.1f) has not been studied as much as that of the fixed-effects (Model I) ANOVA. However, the test appears to be robust to departures of normality within the k populations, though not as robust as Model I ANOVA (Sahai, 2000: 86), provided the k groups (levels) of data can be considered to have been selected at random from all possible groups and that the effect of each group on the variable can be considered to be from a normally distributed set of group effects. When the procedure is nonrobust, power appears to be affected more than the probability of a Type I error; and the lack of robustness is not very different if sample sizes are equal or unequal (Tan, 1982; Tan and Wong, 1980). The Model II analysis of variance (as is the case with the Model I ANOVA) also assumes that the k sampled populations have equal variances.

(h) Testing of Multiple Means when Variances Are Unequal. Although testing hypotheses about means via analysis of variance is tolerant to small departures from the assumption of variance homogeneity when the sample sizes are equal, it can yield

very misleading results in the presence of more serious heterogeneity of variances and/or unequal sample sizes. Having unequal variances represents a multisample Behrens-Fisher problem (i.e., an extension of the two-sample Behrens-Fisher situation discussed in Section 8.1c).

Several approaches to this analysis have been proposed (e.g., see Keselman et al., 2000; Lix, Keselman, and Keselman, 1996). A very good one is that described by Welch (1951), which employs

$$F' = \frac{\sum_{i=1}^{k} c_i(\overline{X}_i - \overline{X}_w)^2}{(k-1)\left[1 + \frac{2A(k-2)}{k^2-1}\right]}, \tag{10.22}$$

where

$$c_i = \frac{n_i}{s_i^2} \tag{10.23}$$

$$C = \sum_{i=1}^{k} c_i \tag{10.24}$$

$$\overline{X}_w = \frac{\sum_{i=1}^{k} c_i \overline{X}_i}{C} \tag{10.25}$$

$$A = \sum_{i=1}^{k} \frac{(1 - c_i/C)^2}{\nu_i}, \text{ where } \nu_i = n_i - 1 \tag{10.26}$$

and F' is associated with degrees of freedom of $\nu_1 = k - 1$ and

$$\nu_2 = \frac{k^2 - 1}{3A}, \tag{10.27}$$

which should be rounded to the next lower integer when using Appendix Table B.4. This procedure is demonstrated in Example 10.3.

A modified ANOVA advanced by Brown and Forsythe (1974a, b) also works well:

$$F'' = \frac{\text{groups SS}}{B}, \tag{10.28}$$

EXAMPLE 10.3 Welch's Test for an Analysis-of-Variance Experimental Design with Dissimilar Group Variances

The potassium content (mg of potassium per 100 mg of plant tissue) was measured in five seedlings of each of three varieties of wheat.

H_0: $\mu_1 = \mu_2 = \mu_3$.

H_A: The mean potassium content is not the same for seedlings of all three wheat varieties.

$\alpha = 0.05$

	Variety G	*Variety A*	*Variety L*	
	27.9	24.2	29.1	
	27.0	24.7	27.7	
	26.0	25.6	29.9	
	26.5	26.0	30.7	
	27.0	27.4	28.8	
	27.5	26.1	31.1	
i	1	2	3	
n_i	6	6	6	
ν_i	5	5	5	
$\overline{X}_i$	26.98	25.67	29.55	
s_i^2	0.4617	1.2787	1.6070	
$c_i = n_i/s_i^2$	12.9955	4.6923	3.7337	$C = \sum_i c_i = 21.4215$
$c_i\overline{X}_i$	350.6186	120.4513	110.3308	$\sum_i c_i\overline{X}_i = 581.4007$
$\frac{\left(1 - \frac{c_i}{C}\right)^2}{\nu_i}$	0.0309	0.1220	0.1364	$A = \sum_i \frac{\left(1 - \frac{c_i}{C}\right)^2}{\nu_i} = 0.2893$

$$\overline{X}_w = \frac{\sum_i c_i\overline{X}_i}{C} = \frac{581.4007}{21.4215} = 27.14$$

$$F' = \frac{\sum c_i(\overline{X}_i - \overline{X}_w)^2}{(k-1)\left[1 + \frac{2A(k-2)}{k^2-1}\right]}$$

$$= \frac{12.9955(26.98 - 27.14)^2 + 4.6923(25.67 - 27.14)^2 + 3.7337(29.55 - 27.14)}{(3-1)\left[1 + \frac{2(0.2893)(3-2)}{3^2-1}\right]}$$

$$= \frac{0.3327 + 10.1396 + 21.6857}{2(0.9268)} = \frac{32.4144}{1.8536} = 17.5$$

For critical value of F:

$$\nu_1 = k - 1 = 3 - 1 = 2$$

$$\nu_2 = \frac{k^2 - 1}{3A} = \frac{3^2 - 1}{3(0.2893)} = \frac{8}{0.8679} = 9.22$$

By harmonic interpolation in Appendix Table B.4 or by computer program:

$F_{0.05(1),2,9.22} = 4.22$. So, reject H_0.

$$0.0005 < P < 0.001 \quad [P = 0.0073]$$

where

$$b_i = \left(1 - \frac{n_i}{N}\right)s_i^2, \tag{10.28a}$$

and

$$B = \sum_{i=1}^{k} b_i. \tag{10.29}$$

F'' has degrees of freedom of $\nu_1 = k - 1$ and

$$\nu_2 = \frac{B^2}{\sum_{i=1}^{k} \frac{b_i^2}{\nu_i}}. \tag{10.30}$$

If $k = 2$, both the F' and F'' procedures are equivalent to the t' test. The Welch method (F') has been shown (by Brown and Forsythe, 1974a; Büning, 1997; Dijkstra and Werter, 1981; Harwell et al., 1992; Kohr and Games, 1974; Levy, 1978a; Lix, Keselman, and Keselman, 1996) to generally perform better than F or F'' when population variances are unequal, especially when n_i's are equal. However, the Welch test is liberal if the data come from highly skewed distributions (Clinch and Keselman, 1992; Lix, Keselman, and Keselman, 1996).

Browne and Forsythe (1974a) reported that when variances are equal, the power of F is a little greater than the power of F', and that of F' is a little less than that of F''. But if variances are not equal, F' has greater power than F'' in cases where extremely low and high means are associated with low variances, and the power of F'' is greater than that of F' when extreme means are associated with large variances. Also, in general, F' and F'' are good if all $n_i \geq 10$ and F' is reasonably good if all $n_i \geq 5$.

(i) Which Multisample Test to Use. As with all research reports, the reader should be informed of explicitly what procedures were used for any statistical analysis. And, when results involve the examination of means, that reporting should include the size (n), mean ($\overline{X}$), and variability (e.g., standard deviation or standard error) of each sample. If the samples came from populations having close to normal distributions, then presentation of each sample's confidence limits (Section 10.2) might also be included. Additional interpretation of the results could include displaying the means and measures of variability via tables or graphs such as those described in Section 7.4.

Although it not possible to generalize to all possible situations that might be encountered, the major approaches to comparing the means of k samples, where k is more than two, are as follows:

- If the k sampled populations are normally distributed and have identical variances (or if they are only slightly to moderately nonnormal and have similar variances): The analysis of variance, using F, is appropriate and preferable to test for difference among the means. (However, samples nearly always come from distributions that are not *exactly* normal with *exactly* the same variances, so conclusions to reject or not reject a null hypothesis should not be considered definitive when the probability associated with F is very near the α specified for the hypothesis test; in such a situation the statistical conclusion should be expressed with some caution and, if feasible, the experiment should be repeated (perhaps with more data).

- If the k sampled populations are distributed normally (or are only slightly to moderately nonnormal), but they have very dissimilar variances: The Behrens-Fisher testing of Section 10.1h is appropriate and preferable to compare the k means. If extremely high and low means are associated with small variances, F' is preferable; but if extreme means are associated with large variances, then F'' works better.
- If the k sampled populations are very different from normally distributed, but they have similar distributions and variances: The Kruskal-Wallis test of Section 10.4 is appropriate and preferable.
- If the k sampled populations have distributions greatly different from normal and do not have similar distributions and variances: (1) Consider the procedures of Chapter 13 for data that do not exhibit normality and variance equality but that can be transformed into data that are normal and homogeneous of variance; or (2) report the mean and variability for each of the k samples, perhaps also presenting them in tables and/or graphs (as in Section 7.4), but do not perform hypothesis testing.

(j) Outliers. A small number of data that are much more extreme than the rest of the measurements are called *outliers* (introduced in Section 2.5), and they may cause a sample to depart seriously from the assumptions of normality and variance equality. If, in the experiment of Example 10.1, a pig weight of 652 kg, or 7.12 kg, or 149 kg was reported, the researcher would likely suspect an error. Perhaps the first two of these measurements were the result of the careless reporting of weights of 65.2 kg and 71.2 kg, respectively; and perhaps the third was a weight measured in pounds and incorrectly reported as kilograms. If there is a convincingly explained error such as this, then an offending datum might be readily corrected. Or, if it is believed that a greatly disparate datum is the result of erroneous data collection (e.g., an errant technician, a contaminated reagent, or an instrumentation malfunction), then it might be discarded or replaced. In other cases outliers might be valid data, and their presence may indicate that one should not employ statistical analyses that require population normality and variance equality. There are statistical methods that are sometimes used to detect outliers, some of which are discussed by Barnett and Lewis (1994: Chapter 6), Snedecor and Cochran (1989: 280–281), and Thode (2002: Chapter 6).

True outliers typically will have little or no influence on analyses employing nonparametric two-sample tests (Sections 8.11 and 8.12) or multisample tests (Section 10.4).

10.2 CONFIDENCE LIMITS FOR POPULATION MEANS

When $k > 2$, confidence limits for each of the k population means may be computed in a fashion analogous to that for the case where $k = 2$ (Section 8.2, Equation 8.13), under the same assumptions of normality and homogeneity of variances applicable to the ANOVA. The $1 - \alpha$ confidence interval for μ_i is

$$\overline{X}_i \pm t_{\alpha(2),\nu}\sqrt{\frac{s^2}{n_i}}, \tag{10.31}$$

where s^2 is the error mean square and ν is the error degrees of freedom from the analysis of variance. For example, let us consider the 95% confidence interval for μ_4

in Example 10.1. Here, $\overline{X}_4 = 63.24$ kg, $s^2 = 9.383\ \text{kg}^2$, $n_4 = 5$, and $t_{0.05(2),15} = 2.131$. Therefore, the lower 95% confidence limit, L_1, is $63.24\ \text{kg} - 2.131\sqrt{9.383\ \text{kg}^2/5} = 63.24\ \text{kg} - 3.999\ \text{kg} = 59.24$ kg, and L_2 is $63.24\ \text{kg} + 2.131\sqrt{9.383\ \text{kg}^2/5} = 63.24\ \text{kg} + 3.999\ \text{kg} = 67.24$ kg.

Computing a confidence interval for μ_i would only be warranted if that population mean was concluded to be different from each other population mean. And calculation of a confidence interval for each of the k μ's may be performed only if it is concluded that $\mu_1 \neq \mu_2 \neq \cdots \neq \mu_k$. However, the analysis of variance does not enable conclusions as to which population means are different from which. Therefore, we must first perform multiple comparison testing (Chapter 11), after which confidence intervals may be determined for each different population mean. Confidence intervals for differences between means may be calculated as shown in Section 11.2.

10.3 SAMPLE SIZE, DETECTABLE DIFFERENCE, AND POWER IN ANALYSIS OF VARIANCE

In Section 8.3, dealing with the difference between two means, we saw how to estimate the sample size required to predict a population difference with a specified level of confidence. When dealing with more than two means, we may also wish to determine the sample size necessary to estimate difference between any two population means, and the appropriate procedure will be found in Section 11.2.

In Section 8.4, methods were presented for estimating the power of the two-sample t test, the minimum sample size required for such a test, and the minimum difference between population means that is detectable by such a test. There are also procedures for analysis-of-variance situations, namely for dealing with more than two means. (The following discussion begins with consideration of Model I—fixed-effects model—analyses of variance.)

If H_0 is true for an analysis of variance, then the variance ratio of Equation 10.18 follows the F distribution, this distribution being characterized by the numerator and denominator degrees of freedom (ν_1 and ν_2, respectively). If, however, H_0 is false, then the ratio of Groups MS to error MS follows instead what is known as the *noncentral F distribution*, which is defined by ν_1, ν_2, and a third quantity known as the *noncentrality parameter*. As power refers to probabilities of detecting a false null hypothesis, statistical discussions of the power of ANOVA testing depend upon the noncentral F distribution.

A number of authors have described procedures for estimating the power of an ANOVA, or the required sample size, or the detectable difference among means (e.g., Bausell and Li, 2002; Cohen, 1988: Ch. 8; Tiku, 1967, 1972), but the charts prepared by Pearson and Hartley (1951) provide one of the best of the methods and will be described below.

(a) Power of the Test. Prior to performing an experiment and collecting data from it, it is appropriate and desirable to estimate the power of the proposed test. (Indeed, it is possible that on doing so one would conclude that the power likely will be so low that the experiment needs to be run with many more data or with fewer groups or, perhaps, not run at all.)

Let us specify that an ANOVA involving k groups will be performed at the α significance level, with n data (i.e., replications) per group. We can then estimate the power of the test if we have an estimate of σ^2, the variability within the k populations (e.g., this estimate typically is s^2 from similar experiments, where s^2 is the error MS), and an estimate of the variability among the populations. From this information we

may calculate a quantity called ϕ (lowercase Greek phi), which is related to the noncentrality parameter.

The variability among populations might be expressed in terms of deviations of the k population means, μ_i, from the overall mean of all populations, μ, in which case

$$\phi = \sqrt{\frac{n\sum_{i=1}^{k}(\mu_i - \mu)^2}{k\sigma^2}} \tag{10.32}$$

(e.g., Guenther, 1964: 47; Kirk, 1995: 182). The grand population mean is

$$\mu = \frac{\sum_{i=1}^{k}\mu_i}{k} \tag{10.33}$$

if all the samples are the same size. In practice, we employ the best available estimates of these population means.

Once ϕ has been obtained, we consult Appendix Figure B.1. This figure consists of several pages, each with a different ν_1 (i.e., groups DF) indicated at the upper left of the graph. Values of ϕ are indicated on the lower axis of the graph for both $\alpha = 0.01$ and $\alpha = 0.05$. Each of the curves on a graph is for a different ν_2 (i.e., error DF), for $\alpha = 0.01$ or 0.05, identified on the top margin of a graph. After turning to the graph for the ν_1 at hand, one locates the point at which the calculated ϕ intersects the curve for the given ν_2 and reads horizontally to either the right or left axis to determine the power of the test. This procedure is demonstrated in Example 10.4.

EXAMPLE 10.4 Estimating the Power of an Analysis of Variance When Variability among Population Means Is Specified

A proposed analysis of variance of plant root elongations is to comprise ten roots at each of four chemical treatments. From previous experiments, we estimate σ^2 to be 7.5888 mm^2 and estimate that two of the population means are 8.0 mm, one is 9.0 mm, and one is 12.0 mm. What will be the power of the ANOVA if we test at the 0.05 level of significance?

$$k = 4$$
$$n = 10$$
$$\nu_1 = k - 1 = 3$$
$$\nu_2 = k(n - 1) = 4(9) = 36$$
$$\mu = \frac{8.0 + 8.0 + 9.0 + 12.0}{4} = 9.25$$

$$\phi = \sqrt{\frac{n\sum(\mu_i - \mu)^2}{ks^2}}$$
$$= \sqrt{\frac{10[(8.0 - 9.25)^2 + (8.0 - 9.25)^2 + (9.0 - 9.25)^2 + (12.0 - 9.25)^2]}{4(7.5888)}}$$

$$= \sqrt{\frac{10(10.75)}{4(7.5888)}}$$

$$= \sqrt{3.5414}$$

$$= 1.88$$

In Appendix Figure B.1c, we enter the graph for $\nu_1 = 3$ with $\phi = 1.88, \alpha = 0.05$, and $\nu_2 = 36$ and read a power of about 0.88. Thus, there will be a 12% chance of committing a Type II error in the proposed analysis.

An alternative, and common, way to estimate power is to specify the smallest difference we wish to detect between the two most different population means. Calling this minimum detectable difference δ, we compute

$$\phi = \sqrt{\frac{n\delta^2}{2ks^2}} \tag{10.34}$$

and proceed to consult Appendix Figure B.1 as above, and as demonstrated in Example 10.5. This procedure leads us to the statement that the power will be at least that determined from Appendix Figure B.1 (and, indeed, it typically is greater).

EXAMPLE 10.5 Estimating the Power of an Analysis of Variance When Minimum Detectable Difference Is Specified

For the ANOVA proposed in Example 10.3, we do not estimate the population means, but rather specify that, using ten data per sample, we wish to detect a difference between population means of at least 4.0 mm.

$k = 4$
$\nu_1 = 3$
$n = 10$
$\nu_2 = 36$
$\delta = 4.0$ mm
$s^2 = 7.5888$ mm^2

$$\phi = \sqrt{\frac{n\delta^2}{2ks^2}}$$

$$= \sqrt{\frac{10(4.0)^2}{2(4)(7.5888)}}$$

$$= \sqrt{2.6355}$$

$$= 1.62$$

In Appendix Figure B.1, we enter the graph for $\nu_1 = 3$ with $\phi = 1.62$, $\alpha = 0.05$, and $\nu_2 = 36$ and read a power of about 0.72. That is, there will be a 28% chance of committing a Type II error in the proposed analysis.

It can be seen in Appendix Figure B.1 that power increases rapidly as ϕ increases, and Equations 10.32 and 10.34 show that the power is affected in the following ways:

- Power is greater for greater differences among group means (as expressed by $\Sigma(\mu_i - \mu)^2$ or by the minimum detectable difference, δ).
- Power is greater for larger sample sizes, n_i (and it is greater when the sample sizes are equal).

- Power is greater for fewer groups, k.
- Power is greater for smaller within-group variability, σ^2 (as estimated by s^2, which is the error mean square).
- Power is greater for larger significance levels, α.

These relationships are further demonstrated in Table 10.3a (which shows that for a given total number of data, N, power increases with increased δ and decreases with increased k) and Table 10.3b (in which, for a given sample size, n_i, power is greater for larger δ's and is less for larger k's).

The desirable power in performing a hypothesis test is arbitrary, just as the significance level (α) is arbitrary. A goal of power between 0.75 and 0.90 is often used, with power of 0.80 being common.

TABLE 10.3a: Estimated Power of Analysis of Variance Comparison of Means, with k Samples, with Each Sample of Size $n_i = 20$, with $N = \sum_{i=1}^{k} n_i$ Total Data, and with a Pooled Variance (s^2) of 2.00, for Several Different Minimum Detectable Differences (δ)

	k:	2	3	4	5	6
δ	N:	40	60	80	100	120
1.0		0.59	0.48	0.42	0.38	0.35
1.2		0.74	0.64	0.58	0.53	0.49
1.4		0.86	0.78	0.73	0.68	0.64
1.6		0.94	0.89	0.84	0.81	0.78
1.8		0.97	0.95	0.92	0.90	0.88
2.0		0.99	0.98	0.97	0.95	0.94
2.2		>0.99	0.99	0.99	0.98	0.98
2.4		>0.99	>0.99	>0.99	0.99	0.99

The values of power were obtained from UNISTAT (2003: 473–474).

TABLE 10.3b: Estimated Power of Analysis of Variance Comparison of Means, with k Samples, with the k Sample Sizes (n_i) Totaling $N = \sum_{i=1}^{k} n_i = 60$ Data, and with a Pooled Variance (s^2) of 2.00, for Several Different Minimum Detectable Differences (δ)

	k:	2	3	4	5	6
δ	n_i:	30	20	15	12	10
1.0		0.77	0.48	0.32	0.23	0.17
1.2		0.90	0.64	0.44	0.32	0.24
1.4		0.96	0.78	0.58	0.43	0.32
1.6		0.99	0.89	0.71	0.54	0.42
1.8		>0.99	0.95	0.82	0.66	0.52
2.0		>0.99	0.98	0.90	0.76	0.63
2.2		>0.99	0.99	0.95	0.85	0.72
2.4		>0.99	>0.99	0.98	0.91	0.81

The values of power were obtained from UNISTAT (2003: 473–474).

Estimating the power of a proposed ANOVA may effect considerable savings in time, effort, and expense. For example, such an estimation might conclude that the power is so very low that the experiment, as planned, ought not to be performed. The proposed experimental design might be revised, perhaps by increasing n, or decreasing k, so as to render the results more likely to be conclusive. One may also strive to increase power by decreasing s^2, which may be possible by using experimental subjects that are more homogeneous. For instance, if the 19 pigs in Example 10.1 were not all of the same age and breed and not all maintained at the same temperature, there might well be more weight variability within the four dietary groups than if all 19 were the same in all respects except diet.

As noted for one-sample (Section 7.7) and two-sample (Section 8.4) testing, calculations of power (and of minimum required sample size and minimum detectable difference) and estimates apply to future samples, not to the samples already subjected to the ANOVA. There are both theoretical and practical reasons for this (Hoenig and Heisey, 2001).

(b) Sample Size Required. Prior to performing an analysis of variance, we might ask how many data need to be obtained in order to achieve a desired power. We can specify the power with which we wish to detect a particular difference (say, a difference of biological significance) among the population means and then ask how large the sample from each population must be. This is done, with Equation 10.34, by iteration (i.e., by making an initial guess and repeatedly refining that estimate), as shown in Example 10.6.

How well Equation 10.34 performs depends upon how good an estimate s^2 is of the population variance common to all groups. As the excellence of s^2 as an estimate improves with increased sample size, one should strive to calculate this statistic from a sample with a size that is not a very small fraction of the n estimated from Equation 10.34.

EXAMPLE 10.6 Estimation of Required Sample Size for a One-Way Analysis of Variance

Let us propose an experiment such as that described in Example 10.1. How many replicate data should be collected in each of the four samples so as to have an 80% probability of detecting a difference between population means as small as 3.5 kg, testing at the 0.05 level of significance?

In this situation, $k = 4$, $\nu_1 = k - 1 = 3$, $\delta = 3.5$ kg, and we shall assume (from the previous experiment in Example 10.1) that $s^2 = 9.383$ kg^2 is a good estimate of σ^2.

We could begin by guessing that $n = 15$ is required. Then, $\nu_2 = 4(15 - 1) = 56$, and by Equation 10.34,

$$\phi = \sqrt{\frac{n\delta^2}{2ks^2}} = \sqrt{\frac{15(3.5)^2}{2(4)(9.383)}} = 1.56.$$

Consulting Appendix Figure B.1, the power for the above ν_1, ν_2, α, and ϕ is approximately 0.73. This is a lower power than we desire, so we guess again with a larger n, say $n = 20$:

$$\phi = \sqrt{\frac{20(3.5)^2}{2(4)(9.383)}} = 1.81.$$

Appendix Figure B1 indicates that this ϕ, for $\nu_2 = 4(20 - 1) = 76$, is associated with a power of about 0.84. This power is somewhat higher than we specified, so we could recalculate power using $n = 18$:

$$\phi = \sqrt{\frac{18(3.5)^2}{2(4)(9.383)}} = 1.71$$

and, for $\nu_2 = 4(18 - 1) = 68$, Appendix Figure B.1 indicates a power slightly above 0.80.

Thus, we have estimated that using sample sizes of at least 18 will result in an ANOVA of about 80% for the described experiment. (It will be seen that the use of Appendix Figure B.1 allows only approximate determinations of power; therefore, we may feel more comfortable in specifying that n should be at least 19 for each of the four samples.)

(c) Minimum Detectable Difference. If we specify the significance level and sample size for an ANOVA and the power that we desire the test to have, and if we have an estimate of σ^2, then we can ask what the smallest detectable difference between population means will be. This is sometimes called the "effect size." By entering on Appendix Figure B.1 the specified α, ν_1, and power, we can read a value of ϕ on the bottom axis. Then, by rearrangement of Equation 10.34, the minimum detectable difference is

$$\delta = \sqrt{\frac{2ks^2\phi^2}{n}}. \tag{10.35}$$

Example 10.7 demonstrates this estimation procedure.

EXAMPLE 10.7 Estimation of Minimum Detectable Difference in a One-Way Analysis of Variance

In an experiment similar to that in Example 10.1, assuming that $s^2 = 9.3833\ (\text{kg})^2$ is a good estimate of σ^2, how small a difference between μ's can we have 90% confidence of detecting if $n = 10$ and $\alpha = 0.05$ are used?

As $k = 4$ and $n = 10, \nu_2 = 4(10 - 1) = 36$. For $\nu_1 = 3, \nu_2 = 36, 1 - \beta = 0.90$, and $\alpha = 0.05$, Appendix Figure B.1c gives a ϕ of about 2.0, from which we compute an estimate of

$$\delta = \sqrt{\frac{2ks^2\phi^2}{n}} = \sqrt{\frac{2(4)(9.3833)(2.0)^2}{10}} = 5.5\ \text{kg}.$$

(d) Maximum Number of Groups Testable. For a given α, n, δ, and σ^2, power will decrease as k increases. It may occur that the total number of observations, N, will be limited, and for given ANOVA specifications the number of experimental groups, k, may have to be limited. As Example 10.8 illustrates, the maximum k can be determined by trial-and-error estimation of power, using Equation 10.34.

EXAMPLE 10.8 Determination of Maximum Number of Groups to be Used in a One-Way Analysis of Variance

Consider an experiment such as that in Example 10.1. Perhaps we have six feeds that might be tested, but we have only space and equipment to examine a total of 50 pigs. Let us specify that we wish to test, with $\alpha = 0.05$ and $\beta \leq 0.20$ (i.e., power of at least 80%), and to detect a difference as small as 4.5 kg between population means.

If $k = 6$ were used, then $n = 50/6 = 8.3$ (call it 8), $\nu_1 = 5, \nu_2 = 6(8 - 1) = 42$, and (by Equation 10.34)

$$\phi = \sqrt{\frac{(8)(4.5)^2}{2(6)(9.3833)}} = 1.20,$$

for which Appendix Figure B.1e indicates a power of about 0.55.

If $k = 5$ were used, $n = 50/5 = 10, \nu_1 = 4, \nu_2 = 5(10 - 1) = 45$, and

$$\phi = \sqrt{\frac{(10)(4.5)^2}{2(5)(9.3833)}} = 1.47,$$

for which Appendix Figure B.1d indicates a power of about 0.70.

If $k = 4$ were used, $n = 50/4 = 12.5$ (call it 12), $\nu_1 = 3, \nu_2 = 4(12 - 1) = 44$, and

$$\phi = \sqrt{\frac{(12)(4.5)^2}{2(4)(9.3833)}} = 1.80,$$

for which Appendix Figure B.1c indicates a power of about 0.84.

Therefore, we conclude that no more than four of the feeds should be tested in an analysis of variance if we are limited to a total of 50 experimental pigs.

(e) Random-Effects Analysis of Variance. If the analysis of variance is a random-effects model (described in Section 10.1f), the power, $1 - \beta$, may be determined from

$$F_{(1-\beta),\nu_1,\nu_2} = \frac{\nu_2 s^2 F_{\alpha(1),\nu_1,\nu_2}}{(\nu_2 - 2)(\text{groups MS})} \tag{10.36}$$

(after Scheffé, 1959: 227; Winer, Brown, and Michels, 1979: 246). This is shown in Example 10.9. As with the fixed-effects ANOVA, power is greater with larger n, larger differences among groups, larger α, and smaller s^2.

EXAMPLE 10.9 Estimating the Power of the Random-Effects Analysis of Variance of Example 10.2

$$\text{Groups MS} = 3.00; s^2 = 1.25; \nu_1 = 3, \nu_2 = 16$$

$$F_{\alpha(1),\nu_1,\nu_2} = F_{0.05(1),3,16} = 3.24$$

$$F_{(1-\beta),\nu_1,\nu_2} = \frac{\nu_2 s^2 F_{\alpha(1),\nu_1,\nu_2}}{(\nu_2 - 2)(\text{groups MS})}$$

$$= \frac{(16)(1.25)(3.24)}{(14)(3.00)} = 1.54$$

By consulting Appendix Table B.4, it is seen that an F of 1.54, with degrees of freedom of 3 and 16, is associated with a one-tailed probability between 0.10 and 0.25. (The exact probability is 0.24.) This probability is the power.

To determine required sample size in a random-effects analysis, one can specify values of α, groups MS, s^2, and k. Then, $\nu_1 = k - 1$ and $\nu_2 = k(n - 1)$; and, by iterative trial and error, one can apply Equation 10.36 until the desired power (namely, $1 - \beta$) is obtained.

10.4 NONPARAMETRIC ANALYSIS OF VARIANCE

If a set of data is collected according to a completely randomized design where $k > 2$, it is possible to test nonparametrically for difference among groups. This may be done by the *Kruskal-Wallis test** (Kruskal and Wallis, 1952), often called an "analysis of variance by ranks."† This test may be used in any situation where the parametric single-factor ANOVA (using F) of Section 10.1 is applicable, and it will be $3/\pi$ (i.e., 95.5%) as powerful as the latter; and in other situations its power, relative to F, is never less than 86.4% (Andrews, 1954; Conover 1999: 297). It may also be employed in instances where the latter is not applicable, in which case it may in fact be the more powerful test. The nonparametric analysis is especially desirable when the k samples do not come from normal populations (Keselman, Rogan, and Feir-Walsh, 1977; Krutchkoff, 1998). It also performs acceptably if the populations have no more than slightly different dispersions and shapes; but if the k variances are not the same, then (as with the Mann-Whitney test) the probability of a Type I error departs from the specified α in accordance with the magnitude of those differences (Zimmerman, 2000).‡

As with the parametric analysis of variance (Section 10.1), the Kruskal-Wallis test tends to be more powerful with larger sample sizes, and the power is less when the n_i's are not equal, especially if the large means are associated with the small n_i's (Boehnke, 1984); and it tends to be conservative if the groups with large n_i's have high within-groups variability and liberal if the large samples have low variability (Keselman, Rogan, and Feir-Walsh, 1997). Bochnke (1984) advises against using the Kruskal-Wallis test unless $N > 20$.

If $k = 2$, then the Kruskal-Wallis test is equivalent to the Mann-Whitney test of Section 8.11. Like the Mann-Whitney test, the Kruskal-Wallis procedure does

*William Henry Kruskal (b. 1919), American statistician, and Wilson Allen Wallis (b. 1912), American statistician and econometrician.

†As will be seen, this procedure does not involve variances, but the term *nonparametric analysis of variance* is commonly applied to it in recognition that the test is a nonparametric analog to the parametric ANOVA.

‡Modifications of the Kruskal-Wallis test have been proposed for nonparametric situations where the k variances are not equal (the "Behrens-Fisher problem" addressed parametrically in Section 10.1h) but the k populations are symmetrical (Rust and Fligner, 1984; Conover 1999: 223–224).

not test whether means (or medians or other parameters) may be concluded to be different from each other, but instead addresses the more general question of whether the sampled populations have different distrubutions. However, if the shapes of the distributions are very similar, then the test does become a test for central tendency (and is a test for means if the distributions are symmetric).

The Type I error rate with heterogeneous variances is affected less with the Kruskal-Wallis test than with the parametric analysis of variance if the groups with large variances have small sample sizes (Keselman, Rogan, and Feir-Walsh, 1977; Tomarkin and Serlin, 1986).

Example 10.10 demonstrates the Kruskal-Wallis test procedure. As in other nonparametric tests, we do not use population parameters in statements of hypotheses, and neither parameters nor sample statistics are used in the test calculations. The Kruskal-Wallis test statistic, H, is calculated as

$$H = \frac{12}{N(N+1)} \sum_{i=1}^{k} \frac{R_i^2}{n_i} - 3(N+1), \tag{10.37}$$

where n_i is the number of observations in group i, $N = \sum_{i=1}^{k} n_i$ (the total number of observations in all k groups), and R_i is the sum of the ranks of the n_i observations in group i.* The procedure for ranking data is as presented in Section 8.11 for the Mann-Whitney test. A good check (but not a guarantee) of whether ranks have been assigned correctly is to see whether the sum of all the ranks equals $N(N+1)/2$.

Critical values of H for small sample sizes where $k \leq 5$ are given in Appendix Table B.13. For larger samples and/or for $k > 5$, H may be considered to be approximated by χ^2 with $k - 1$ degrees of freedom. Chi-square, χ^2, is a statistical distribution that is shown in Appendix Table B.1, where probabilities are indicated as column headings and degrees of freedom (ν) designate the rows.

If there are tied ranks, as in Example 10.11, H is a little lower than it should be, and a correction factor may be computed as

$$C = 1 - \frac{\sum t}{N^3 - N}, \tag{10.40}$$

and the corrected value of H is

$$H_c = \frac{H}{C}. \tag{10.41}$$

*Interestingly, H (or H_c of Equation 10.41) could also be computed as

$$H = \frac{\text{groups SS}}{\text{total MS}}, \tag{10.38}$$

applying the procedures of Section 10.1 to the ranks of the data in order to obtain the Groups SS and Total MS. And, because the Total MS is the variance of all N ranks, if there are no ties the Total MS is the variance of the integers from 1 to N, which is

$$\frac{N(N+1)(2N+1)/6 - N^2(N+1)^2/4N}{N-1} \tag{10.38a}$$

The following alternate formula (Pearson and Hartley, 1976: 49) shows that H is expressing the differences among the κ groups' mean ranks ($\bar{R}_i = R_i/n_i$) and the mean of all N ranks, which is $\bar{R} = N(N-1)/2$:

$$H = \frac{12 \sum_{i=1}^{\kappa} n_i(\bar{R}_i - \bar{R})^2}{N(N-1)}. \tag{10.39}$$

EXAMPLE 10.10 The Kruskal-Wallis Single-Factor Analysis of Variance by Ranks

An entomologist is studying the vertical distribution of a fly species in a deciduous forest and obtains five collections of the flies from each of three different vegetation layers: herb, shrub, and tree.

H_0: The abundance of the flies is the same in all three vegetation layers.
H_A: The abundance of the flies is not the same in all three vegetation layers.

$\alpha = 0.05$
The data are as follows (with ranks of the data in parentheses):*

Numbers of Flies/m^3 of Foliage		
Herbs	*Shrubs*	*Trees*
14.0 (15)	8.4 (11)	6.9 (8)
12.1 (14)	5.1 (2)	7.3 (9)
9.6 (12)	5.5 (4)	5.8 (5)
8.2 (10)	6.6 (7)	4.1 (1)
10.2 (13)	6.3 (6)	5.4 (3)
$n_1 = 5$	$n_2 = 5$	$n_3 = 5$
$R_1 = 64$	$R_2 = 30$	$R_3 = 26$

$$N = 5 + 5 + 5 = 15$$

$$H = \frac{12}{N(N+1)} \sum_{i=1}^{k} \frac{R_i^2}{n_1} - 3(N+1)$$

$$= \frac{12}{15(16)} \left[\frac{64^2}{5} + \frac{30^2}{5} + \frac{26^2}{5} \right] - 3(16)$$

$$= \frac{12}{240}[1134.400] - 48$$

$$= 56.720 - 48$$

$$= 8.720$$

$H_{0.05,5,5,5} = 5.780$
Reject H_0.

$$0.005 < P < 0.01$$

*To check whether ranks were assigned correctly, the sum of the ranks (or sum of the rank sums: $64 + 30 + 26 = 120$) is compared to $N(N+1)/2 = 15(16)/2 = 120$. This check will not guarantee that the ranks were assigned properly, but it will often catch errors of doing so.

EXAMPLE 10.11 The Kruskal-Wallis Test with Tied Ranks

A limnologist obtained eight containers of water from each of four ponds. The *p*H of each water sample was measured. The data are arranged in ascending order within each pond. (One of the containers from pond 3 was lost, so $n_3 = 7$, instead of 8; but the test procedure does not require equal numbers of data in each group.) The rank of each datum is shown parenthetically.

H_0: *p*H is the same in all four ponds.
H_A: *p*H is not the same in all four ponds.

$\alpha = 0.05$

Pond 1	*Pond 2*	*Pond 3*	*Pond 4*
7.68 (1)	7.71 (6*)	7.74 (13.5*)	7.71 (6*)
7.69 (2)	7.73 (10*)	7.75 (16)	7.71 (6*)
7.70 (3.5*)	7.74 (13.5*)	7.77 (18)	7.74 (13.5*)
7.70 (3.5*)	7.74 (13.5*)	7.78 (20*)	7.79 (22)
7.72 (8)	7.78 (20*)	7.80 (23.5*)	7.81 (26*)
7.73 (10*)	7.78 (20*)	7.81 (26*)	7.85 (29)
7.73 (10*)	7.80 (23.5*)	7.84 (28)	7.87 (30)
7.76 (17)	7.81 (26*)		7.91 (31)
*Tied ranks.			
$n_1 = 8$	$n_2 = 8$	$n_3 = 7$	$n_4 = 8$
$R_1 = 55$	$R_2 = 132.5$	$R_3 = 145$	$R_4 = 163.5$

$$N = 8 + 8 + 7 + 8 = 31$$

$$H = \frac{12}{N(N+1)} \sum_{i=1}^{k} \frac{R_i^2}{n_i} - 3(N+1)$$

$$= \frac{12}{31(32)} \left[\frac{55^2}{8} + \frac{132.5^2}{8} + \frac{145^2}{7} + \frac{163.5^2}{8} \right] - 3(32)$$

$$= 11.876$$

Number of groups of tied ranks = $m = 7$.

$$\Sigma t = \Sigma(t_i^3 - t_i)$$

$$= (2^3 - 2) + (3^3 - 3) + (3^3 - 3) + (4^3 - 4) + (3^3 - 3) + (2^3 - 2) + (3^3 - 3)$$

$$= 168$$

$$C = 1 - \frac{\Sigma t}{N^3 - N} = 1 - \frac{168}{31^3 - 31} = 1 - \frac{168}{29760} = 0.9944$$

$$H_c = \frac{H}{C} = \frac{11.876}{0.9944} = 11.943$$

$$\nu = k - 1 = 3$$

$\chi^2_{0.05,3} = 7.815$

Reject H_0.

$$0.005 < P < 0.01 \quad [P = 0.0076]$$

or, by Equation 10.43,

$$F = \frac{(N - k)H_c}{(k - 1)(N - 1 - H_c)} = \frac{(31 - 4)(11.943)}{(4 - 1)(31 - 1 - 11.943)} = 5.95$$

$F_{0.05(1),3,26} = 2.98$

Reject H_0.

$$0.0025 < P < 0.005 \quad [P = 0.0031]$$

Here,

$$\sum t = \sum_{i=1}^{m} (t_i^3 - t_i), \tag{10.42}$$

where t_i is the number of ties in the ith group of ties, and m is the number of groups of tied ranks. H_c will differ little from H when the t_i's are very small compared to N.

Kruskal and Wallis (1952) give two approximations that are better than chi-square when the n_i's are small or when significance levels less than 1% are desired; but they are relatively complicated to use. The chi-square approximation is slightly conservative for $\alpha = 0.05$ or 0.10 (i.e., the true Type I probability is a little less than α) and more conservative for $\alpha = 0.01$ (Gabriel and Lachenbruch, 1969): it performs better with larger n_i's. Fahoome (2002) found the probability of a Type I error to be between 0.045 and 0.055 when employing this approximation at the 0.05 significance level if each sample size is at least 11, and between 0.009 and 0.011 when testing at $\alpha = 0.01$ when each $n_i \geq 22$.

Because the χ^2 approximation tends to be conservative, other approximations have been proposed that are better in having Type I error probabilities closer to α. A good alternative is to calculate

$$F = \frac{(N - k)H}{(k - 1)(N - 1 - H)}, \tag{10.43}$$

which is also the test statistic that would be obtained by applying the parametric ANOVA of Section 10.1 to the ranks of the data (Iman, Quade and Alexander, 1975). For the Kruskal-Wallis test, this F gives very good results, being only slightly liberal (with the probability of a Type I error only a little larger than the specified α), and the preferred critical values are F for the given α and degrees of freedom of $\nu_1 = k - 1$ and $\nu_2 = N - k - 1$.* This is demonstrated at the end of Example 10.11.

*A slightly better approximation in some, but not all, cases is to compare

$$\frac{H}{2}\left[1 + \frac{N - k}{N - 1 - H}\right] \text{ to } \frac{(k - 1)F_{\alpha(1),k-1,N-k} + \chi^2_{\alpha,k-1}}{2}. \tag{10.43a}$$

5 TESTING FOR DIFFERENCE AMONG SEVERAL MEDIANS

Section 8.12 presented the *median test* for the two-sample case. This procedure may be expanded to multisample considerations (Mood, 1950: 398–399). The method requires the determination of the grand median of all observations in all k samples considered together. The numbers of data in each sample that are above and below this median are tabulated, and the significance of the resultant $2 \times k$ contingency table is then analyzed, generally by chi-square (Section 23.1), alternatively by the G test (Section 23.7). For example, if there were four populations being compared, the statistical hypotheses would be H_0: all four populations have the same median, and H_A: all four populations do not have the same median. The median test would be the testing of the following contingency table:

	Sample 1	*Sample 2*	*Sample 3*	*Sample 4*	*Total*
Above median	f_{11}	f_{12}	f_{13}	f_{14}	R_1
Below median	f_{21}	f_{22}	f_{23}	f_{24}	R_2
Total	C_1	C_2	C_3	C_4	n

This multisample median test is demonstrated in Example 10.12. Section 8.12 discusses situations where one or more data in the sample are equal to the grand median. Recommended sample sizes are those described is Section 23.4. If H_0 is rejected, than the method of Section 11.7 can be used to attempt to conclude which population medians are different from which.

EXAMPLE 10.12 The Multisample Median Test

H_0: Median elm tree height is the same on all four sides of a building.

H_A: Median elm tree height is not the same on all four sides of a building.

A total of 48 seedlings of the same size were planted at the same time, 12 on each of a building's four sides. The heights, after several years of growth, were as follows:

North	*East*	*South*	*West*
7.1 m	6.9 m	7.8 m	6.4 m
7.2	7.0	7.9	6.6
7.4	7.1	8.1	6.7
7.6	7.2	8.3	7.1
7.6	7.3	8.3	7.6
7.7	7.3	8.4	7.8
7.7	7.4	8.4	8.2
7.9	7.6	8.4	8.4
8.1	7.8	8.6	8.6
8.4	8.1	8.9	8.7
8.5	8.3	9.2	8.8
8.8	8.5	9.4	8.9
medians: 7.7 m	7.35 m	8.4 m	8.0 m

grand median = 7.9 m

The 2×4 contingency table is as follows, with expected frequencies (see Section 23.1) in parentheses:

	North	*East*	*South*	*West*	
Above median	4 (5.5000)	3 (6.0000)	10 (5.5000)	6 (6.0000)	23
Below median	7 (5.5000)	9 (6.0000)	1 (5.5000)	6 (6.0000)	23
Total	11	12	11	12	46

$\chi^2 = 11.182$

$\chi^2_{0.05,3} = 7.815$

Reject H_0.

$0.0005 < P < 0.001$ [$P = 0.00083$]

If the k samples came from populations having the same variance and shape, then the Kruskal-Wallis test may be used as a test for difference among the k population medians.

10.6 HOMOGENEITY OF VARIANCES

Section 8.5 discussed testing the null hypothesis H_0: $\sigma_1^2 = \sigma_2^2$ against the alternate, H_A: $\sigma_1^2 \neq \sigma_2^2$. This pair of two-sample hypotheses can be extended to more than two samples (i.e., $k > 2$) to ask whether all k sample variances estimate the same population variance. The null and alternate hypotheses would then be H_0: $\sigma_1^2 = \sigma_2^2 = \cdots = \sigma_k^2$ and H_0: the k population variances are not all the same. The equality of variances is called homogeneity of variances, or *homoscedasticity*; variance heterogeneity is called *heteroscedasticity*.*

(a) Bartlett's Test. A commonly encountered method employed to test for homogeneity of variances is *Bartlett's test*† (Bartlett, 1937a, 1937b; based on a principle of Neyman and Pearson, 1931). In this procedure, the test statistic is

$$B = (\ln s_p^2)\left(\sum_{i=1}^{k} \nu_i\right) - \sum_{i=1}^{k} \nu_i \ln s_i^2, \tag{10.44}$$

where $\nu_i = n_i - 1$ and n_i is the size of sample i. The pooled variance, s_p^2, is calculated as before as $\sum_{i=1}^{k} SS_i / \sum_{i=1}^{k} \nu_i$. Many researchers prefer to operate with common logarithms (base 10), rather than with natural logarithms (base e);‡ so Equation 10.44 may be written as

$$B = 2.30259[(\log s_p^2)\left(\sum_{i=1}^{k} \nu_i\right) - \sum_{i=1}^{k} \nu_i \log s_i^2]. \tag{10.45}$$

The distribution of B is approximated by the chi-square distribution,§ with $k - 1$ degrees of freedom (Appendix Table B.1), but a more accurate chi-square

*The two terms were introduced by K. Pearson in 1905 (Walker, 1929: 181); since then they have occasionally been spelled *homoskedasticity* and *heteroskedasticity*, respectively.

†Maurice Stevenson Bartlett (1910–2002), English statistician.

‡See footnote in Section 8.7.

§A summary of approximations is given by Nagasenker (1984).

approximation is obtained by computing a correction factor,

$$C = 1 + \frac{1}{3(k-1)}\left(\sum_{i=1}^{k}\frac{1}{\nu_i} - \frac{1}{\sum_{i=1}^{k}\nu_i}\right), \tag{10.46}$$

with the corrected test statistic being

$$B_c = \frac{B}{C}. \tag{10.47}$$

Example 10.13 demonstrates these calculations. The null hypothesis for testing the homogeneity of the variances of four populations may be written symbolically as H_0: $\sigma_1^2 = \sigma_2^2 = \sigma_3^2 = \sigma_4^2$, or, in words, as "the four population variances are homogeneous (i.e., are equal)." The alternate hypothesis can be stated as "The four population variances are not homogeneous (i.e., they are not all equal)," or "There is difference (or heterogeneity) among the four population variances." If H_0 is rejected, the further testing of Section 11.8 will allow us to ask which population variances are different from which.

Bartlett's test is powerful if the sampled populations are normal, but it is very badly affected by nonnormal populations (Box, 1953; Box and Anderson, 1955; Gartside, 1972). If the population distribution is platykurtic, the true α is less than the stated α (i.e., the test is conservative and the probability of a Type II error is increased); if it is leptokurtic, the true α is greater than the stated α (i.e., the probability of a Type I error is increased).

When $k = 2$ and $n_1 = n_2$, Bartlett's test is equivalent to the variance-ratio test of Section 8.5a. However, with two samples of unequal size, the two procedures may yield different results; one will be more powerful in some cases, and the other more powerful in others (Maurais and Ouimet, 1986).

(b) Other Multisample Tests for Variances. Section 8.5b noted that there are other tests for heterogeneity (Levene's test and others) but that all are undesirable in many situations. The Bartlett test remains commendable when the sampled populations are normal, and no procedure is especially good when they are not.

Because of the poor performance of tests for variance homogeneity and the robustness of analysis of variance for multisample testing among means (Section 10.1), it is not recommended that the former be performed as tests of the underlying assumptions of the latter.

HOMOGENEITY OF COEFFICIENTS OF VARIATION

The two-sample procedure of Section 8.8 has been extended by Feltz and Miller (1996) for hypotheses where $k \geq 3$ and each coefficient of variation (V_i) is positive:

$$\chi^2 = \frac{\sum_{i=1}^{k}\nu_i V_i^2 - \dfrac{\left(\sum_{i=1}^{k}\nu_i V_i\right)^2}{\sum_{i=1}^{k}\nu_i}}{V_p^2(0.5 + V_p^2)}, \tag{10.48}$$

EXAMPLE 10.13 Bartlett's Test for Homogeneity of Variances

Nineteen pigs were divided into four groups, and each group was raised on a different food. The data, which are those of Example 10.1, are weights, in kilograms, and we wish to test whether the variance of weights is the same for pigs fed on all four feeds.

H_0: $\sigma_1^2 = \sigma_2^2 = \sigma_3^2 = \sigma_4^2$

H_A: The four population variances are not all equal (i.e., are heterogeneous).

$\alpha = 0.05$

	Feed 1	*Feed 2*	*Feed 3*	*Feed 4*	
	60.8	68.7	69.6	61.9	
	67.0	67.7	77.1	64.2	
	65.0	75.0	75.2	63.1	
	68.6	73.3	71.5	66.7	
	61.7	71.8		60.3	
i	1	2	3	4	
n_i	5	5	4	5	
ν_i	4	4	3	4	$\sum_{i=1}^{k} \nu_i = 15$
SS_i	44.768	37.660	34.970	23.352	$\sum_{i=1}^{k} SS_i = 140.750$
s_i^2	11.192	9.415	11.657	5.838	
$\log s_i^2$	1.0489	0.9738	1.0666	0.7663	
$\nu_i \log s_i^2$	4.1956	3.8952	3.1998	3.0652	$\sum_{i=1}^{k} \nu_i \log s_i^2 = 14.3558$
$1/\nu_i$	0.250	0.250	0.333	0.250	$\sum_{i=1}^{k} 1/\nu_i = 1.083$

$$s_p^2 = \frac{\sum SS_i}{\sum \nu_i} = \frac{140.750}{15} = 9.3833$$

$$\log s_p^2 = 0.9724$$

$$B = 2.30259\left[(\log s_p^2)(\sum \nu_i) - \sum \nu_i \log s_i^2)\right]$$

$$= 2.30259[(0.9724)(15) - 14.3558]$$

$$= 2.30259(0.2302)$$

$$= 0.530$$

$$C = 1 + \frac{1}{3(k-1)} \times \left(\sum \frac{1}{\nu_i} - \frac{1}{\sum \nu_i}\right)$$

$$= 1 + \frac{1}{3(3)}\left(1.083 - \frac{1}{15}\right)$$

$$= 1.113$$

$$B_c = \frac{B}{C} = \frac{0.530}{1.113} = 0.476$$

$$\chi^2_{0.05,3} = 7.815$$

Do not reject H_0.

$0.90 < P < 0.95$ $[P = 0.92]$

EXERCISES

10.1. The following data are weights of food (in kilograms) consumed per day by adult deer collected at different times of the year. Test the null hypothesis that food consumption is the same for all the months tested.

Feb.	*May*	*Aug.*	*Nov.*
4.7	4.6	4.8	4.9
4.9	4.4	4.7	5.2
5.0	4.3	4.6	5.4
4.8	4.4	4.4	5.1
4.7	4.1	4.7	5.6
	4.2	4.8	

10.2. An experiment is to have its results examined by analysis of variance. The variable is temperature (in degrees Celsius), with 12 measurements to be taken in each of five experimental groups. From previous experiments, we estimate the within-groups variability, σ^2, to be $1.54(^\circ C)^2$. If the 5% level of significance is employed, what is the probability of the ANOVA detecting a difference as small as 2.0°C between population means?

10.3. For the experiment of Exercise 10.2, how many replicates are needed in each of the five groups to detect a difference as small as 2.0°C between population means, with 95% power?

10.4. For the experiment of Exercise 10.2, what is the smallest difference between population means that we are 95% likely to detect with an ANOVA using 10 replicates per group?

10.5. Using the Kruskal-Wallis test, test nonparametrically the appropriate hypotheses for the data of Exercise 10.1.

10.6. Three different methods were used to determine the dissolved-oxygen content of lake water. Each of the three methods was applied to a sample of water six times, with the following results. Test the null hypothesis that the three methods yield equally variable results ($\sigma_1^2 = \sigma_2^2 = \sigma_3^2$).

Method 1 (mg/kg)	*Method 2* (mg/kg)	*Method 3* (mg/kg)
10.96	10.88	10.73
10.77	10.75	10.79
10.90	10.80	10.78
10.69	10.81	10.82
10.87	10.70	10.88
10.60	10.82	10.81

10.7. The following statistics were obtained from measurements of the circumferences of trees of four species. Test whether the coefficients of variation of circumferences are the same among the four species.

	Species B	*Species A*	*Species Q*	*Species H*
n:	40	54	58	32
$\overline{X}$ (m):	2.126	1.748	1.350	1.392
s^2 (m^2):	0.488219	0.279173	0.142456	0.203208

where the common coefficient of variation is

$$V_p = \frac{\sum_{i=1}^{k} \nu_i V_i}{\sum_{i=1}^{k} \nu_i}. \tag{10.49}$$

This test statistic approximates the chi-square distribution with $k - 1$ degrees of freedom (Appendix Table B.1) and its computation is shown in Example 10.14. When $k = 2$, the test yields results identical to the two-sample test using Equation 8.42 (and $\chi^2 = Z^2$). As with other tests, the power is greater with larger sample size; for a given sample size, the power is greater for smaller coefficients of variation and for greater differences among coefficients of variation. If the null hypothesis of equal population coefficients of variation is not rejected, then V_p is the best estimate of the coefficient of variation common to all k populations.

EXAMPLE 10.14 Testing for Homogeneity of Coefficients of Variation

For the data of Example 10.1:

H_0: The coefficients of the four sampled populations are the same; i.e., $\sigma_1^2/\mu_1 = \sigma_2^2/\mu_2 = \sigma_3^2/\mu_3 = \sigma_4^2/\mu_4$.

H_A: The coefficients of variation of the four populations are not all the same.

	Feed 1	*Feed 2*	*Feed 3*	*Feed 4*
n_i	5	5	4	5
ν_i	4	4	3	4
$\overline{X}_i$ (kg)	64.62	68.30	73.35	66.64
s_i^2 (kg^2)	11.192	16.665	11.657	9.248
s_i (kg)	3.35	4.08	3.41	3.04
V_i	0.0518	0.0597	0.0465	0.0456

$$\sum_{i=1}^{n} \nu_i = 4 + 4 + 3 + 4 = 15$$

$$\sum_{i=1}^{n} \nu_i V_i = (4)(0.0518) + (4)(0.0597) + (3)(0.0465) + (4)(0.0456) = 0.7679$$

$$V_p = \frac{\sum \nu_i V_i}{\sum \nu_i} = \frac{0.7679}{15} = 0.05119 \qquad V_p^2 = (0.7679)^2 = 0.002620$$

$$\sum_{i=1}^{n} \nu V_i^2 = (4)(0.0518)^2 + (4)(0.0597)^2 + (3)(0.0465)^2 + (4)(0.0456)^2$$
$$= 0.03979$$

$$\chi^2 = \frac{\sum \nu_i V_i^2 - \frac{(\sum \nu_i V_i)^2}{\sum \nu_i}}{V_p^2(0.5 + V_p^2)} = \frac{0.03979 - \frac{(0.7679)^2}{15}}{0.002620(0.5 + 0.002620)} = \frac{0.0004786}{0.001317} = 0.363$$

For chi-square: $\nu = 4 - 1 = 3$; $\chi^2_{0.05,3} = 7.815$. Do not reject H_0.

$$0.90 < P < 0.95 \quad [P = 0.948]$$

Miller and Feltz (1997) reported that this test works best if each sample size (n_i is at least 10 and each coefficient of variation (V_i) is no greater than 0.33; and they describe how the power of the test (and, from such a calculation, the minimum detectable difference and the required sample size) may be estimated.

10.8 CODING DATA

In the parametric ANOVA, coding the data by addition or subtraction of a constant causes no change in any of the sums of squares or mean squares (recall Section 4.8) so the resultant F and the ensuing conclusions are not affected at all. If the coding is performed by multiplying or dividing all the data by a constant, the sums of squares and the mean squares in the ANOVA each will be altered by an amount equal to the square of that constant, but the F value and the associated conclusions will remain unchanged.

A test utilizing ranks (such as the Kruskal-Wallis procedure) will not be affected at all by coding of the raw data. Thus, the coding of data for analysis of variance either parametric or nonparametric, may be employed with impunity, and coding frequently renders data easier to manipulate. Neither will coding of data alter the conclusions from the hypothesis tests in Chapter 11 (multiple comparisons) or Chapters 12, 14, 15, or 16 (further analysis-of-variance procedures). Bartlett's test is also unaffected by coding. The testing of coefficients of variation is unaffected by coding by multiplication or division, but coding by addition or subtraction may not be used. The effect of coding is indicated in Appendix C for many statistics.

10.9 MULTISAMPLE TESTING FOR NOMINAL-SCALE DATA

A $2 \times c$ contingency table may be analyzed to compare frequency distributions of nominal data for two samples. In a like fashion, an $r \times c$ contingency table may be set up to compare frequency distributions of nominal-scale data from r samples. Contingency table procedures are discussed in Chapter 23.

Other procedures have been proposed for multisample analysis of nominal-scale data (e.g., Light and Margolin, 1971; Windsor, 1948).

CHAPTER 11

Multiple Comparisons

The Model I single-factor analysis of variance (ANOVA) of Chapter 10 tests the null hypothesis H_0: $\mu_1 = \mu_2 = \cdots = \mu_k$. However, the rejection of H_0 does not imply that all k population means are different from one another, and we don't know how many differences there are or where differences lie among the k means. For example, if $k = 3$ and H_0: $\mu_1 = \mu_2 = \mu_3$ is rejected, we are not able to conclude whether there is evidence of $\mu_1 \neq \mu_2 = \mu_3$ or of $\mu_1 = \mu_2 \neq \mu_3$ or of $\mu_1 \neq \mu_2 \neq \mu_3$.

The introduction to Chapter 10 explained that it is invalid to employ multiple two-sample t tests to examine the difference among more than two means, for to do so would increase the probability of a Type I error (as shown in Table 10.1). This chapter presents statistical procedures that may be used to compare k means with each other; they are called *multiple-comparison procedures** (MCPs). Except for the procedure known as the least significance difference test, all of the tests referred to in this chapter may be performed even without a preliminary analysis of variance. Indeed, power may be lost if a multiple-comparison test is performed only if the ANOVA concludes a significant difference among means (Hsu, 1996: 177–178; Myers and Well, 2003: 261). And all except the Scheffé test of Section 11.4 are for a set of comparisons to be specified before the collection of data.

The most common principle for multiple-comparison testing is that the significance level, α, is the probability of committing at least one Type I error when making all of the intended comparisons for a set of data. These are said to be a *family* of comparisons, and this error is referred to as *familywise error* (FWE) or, sometimes, *experimentwise error*. Much less common are tests designed to express *comparisonwise error*, the probability of a Type I error in a single comparison.

A great deal has been written about numerous multiple-comparison tests with various objectives, and the output of many statistical computer packages enhances misuse of them (Hsu, 1996: xi). Although there is not unanimity regarding what the "best" procedure is for a given situation, this chapter will present some frequently encountered highly regarded tests for a variety of purposes.

If the desire is to test for differences between members of all possible pairs of means, then the procedures of Section 11.1 would be appropriate, using Section 11.1a

*The term *multiple comparisons* was introduced by D. E. Duncan in 1951 (David, 1995).

if sample sizes are unequal and Section 11.1b if variances are not the same. If the data are to be analyzed to compare the mean of one group (typically called the control) to each of the other group means, then Section 11.3 would be applicable. And if the researcher wishes to examine sample means after the data are collected and compare specific means, or groups of means, of interest, then the testing in Section 11.4 is called for.

Just as with the parametric analysis of variance, the testing procedures of Sections 11.1–11.4 are premised upon there being a normal distribution of the population from which each of the k samples came; but, like the ANOVA, these tests are somewhat robust to deviations from that assumption. However, if it is suspected that the underlying distributions are far from normal, then the analyses of Section 11.5, or data transformations (Chapter 13), should be considered. Multiple-comparison tests are adversely affected by heterogeneous variances among the sampled populations, in the same manner as in ANOVA (Section 10.1g) (Keselman and Toothaker, 1974; Petrinovich and Hardyck, 1969), though to a greater extent (Tukey, 1993).

In multiple-comparison testing—except when comparing means to a control—equal sample sizes are desirable for maximum power and robustness, but the procedures presented can accommodate unequal n's. Petrinovich and Hardyck (1969) caution that the power of the tests is low when sample sizes are less than 10.

This chapter discusses multiple comparisons for the single-factor ANOVA experimental design (Chapter 10).* Applications for other situations are found in Section 12.5 (for the two-factor ANOVA design), 12.7b (for the nonparametric randomized-block ANOVA design), 12.9 (for dichotomous data in randomized blocks), 14.6 (for the multiway ANOVA design), 18.6 and 18.7 (for regression), and 19.8 (for correlation).

11.1 TESTING ALL PAIRS OF MEANS

There are $k(k-1)/2$ different ways to obtain pairs of means from a total of k means.† For example, if $k = 3$, the $k(k-1)/2 = 3(2)/2 = 3$ pairs are μ_1 and μ_2, μ_1 and μ_3, and μ_2 and μ_3; and for $k = 4$, the $k(k-1)/2 = 4(3)/2 = 6$ pairs are μ_1 and μ_2, μ_1 and μ_3, μ_1 and μ_4, μ_2 and μ_3, μ_2 and μ_4, and μ_3 and μ_4. So each of $k(k-1)/2$ null hypotheses may be tested, referring to them as H_0: $\mu_B = \mu_A$, where the subscripts A and B represent each pair of subscripts; each corresponding alternate hypothesis is H_0: $\mu_B \neq \mu_A$.

An excellent way to address these hypotheses is with the *Tukey test* (Tukey, 1953), also known as the honestly significant difference test (HSD test) or wholly significant difference test (WSD test). Example 11.1 demonstrates the Tukey test, utilizing an ANOVA experimental design similar to that in Example 10.1, except that all groups have equal numbers of data (i.e., all of the n_i's are equal). The first step in examining these multiple-comparison hypotheses is to arrange and number all five sample means in order of increasing magnitude. Then pairwise differences between the means, $\overline{X}_A - \overline{X}_B$, are tabulated. Just as a difference between means, divided by

*For nonparametric testing, Conover and Iman (1981) recommend applying methods as those in Sections 11.1–11.4 on the ranks of the data. However Hsu (1996: 177); Sawilowsky, Blair, and Higgins (1999); and Toothaker (1991: 109) caution against doing so.

†The number of combinations of k groups taken 2 at a time is (by Equation 5.10):

$$ {}_kC_2 = \frac{k!}{2!(k-2)!} = \frac{k(k-1)(k-2)!}{2!(k-2)!} = \frac{k(k-1)}{2}. \qquad (11.1) $$

EXAMPLE 11.1 Tukey Multiple Comparison Test with Equal Sample Sizes.

The data are strontium concentrations (mg/ml) in five different bodies of water. First an analysis of variance is performed.

H_0: $\mu_1 = \mu_2 = \mu_3 = \mu_4 = \mu_5$.

H_A: Mean strontium concentrations are not the same in all five bodies of water.

$\alpha = 0.05$

Grayson's Pond	*Beaver Lake*	*Angler's Cove*	*Appletree Lake*	*Rock River*
28.2	39.6	46.3	41.0	56.3
33.2	40.8	42.1	44.1	54.1
36.4	37.9	43.5	46.4	59.4
34.6	37.1	48.8	40.2	62.7
29.1	43.6	43.7	38.6	60.0
31.0	42.4	40.1	36.3	57.3
$\overline{X}_1 = 32.1$ mg/ml	$\overline{X}_2 = 40.2$ mg/ml	$\overline{X}_3 = 44.1$ mg/ml	$\overline{X}_4 = 41.1$ mg/ml	$\overline{X}_5 = 58.3$ mg/ml
$n_1 = 6$	$n_2 = 6$	$n_3 = 6$	$n_4 = 6$	$n_5 = 6$

Source of variation	SS	DF	MS
Total	2437.5720	29	
Groups	2193.4420	4	548.3605
Error	244.1300	25	9.7652

$k = 5, n = 6$

Samples number (i) of ranked means:	1	2	4	3	5
Ranked sample mean ($\overline{X}_i$):	32.1	40.2	41.1	44.1	58.3

To test each H_0: $\mu_B = \mu_A$,

$$SE = \sqrt{\frac{9.7652}{6}} = \sqrt{1.6275} = 1.28.$$

As $q_{0.05,25,k}$ does not appear in Appendix Table B.5, the critical value with the next lower DF is used: $q_{0.05,24,5} = 4.166$.

Comparison B vs. A	*Difference* $(\overline{X}_B - \overline{X}_A)$	SE	q	*Conclusion*
5 vs. 1	58.3 − 32.1 = 26.2	1.28	20.47	Reject H_0: $\mu_5 = \mu_1$
5 vs. 2	58.3 − 40.2 = 18.1	1.28	14.14	Reject H_0: $\mu_5 = \mu_2$
5 vs. 4	58.3 − 41.1 = 17.2	1.28	13.44	Reject H_0: $\mu_5 = \mu_4$
5 vs. 3	58.3 − 44.1 = 14.2	1.28	11.09	Reject H_0: $\mu_5 = \mu_3$
3 vs. 1	44.1 − 32.1 = 12.0	1.28	9.38	Reject H_0: $\mu_3 = \mu_1$
3 vs. 2	44.1 − 40.2 = 3.9	1.28	3.05	Do not reject H_0: $\mu_3 = \mu_2$
3 vs. 4	Do not test			
4 vs. 1	44.1 − 32.1 = 9.0	1.28	7.03	Reject H_0: $\mu_4 = \mu_1$
4 vs. 2	Do not test			
2 vs. 1	40.2 − 32.1 = 8.1	1.28	6.33	Reject H_0: $\mu_2 = \mu_1$

Thus, we conclude that μ_1 is different from the other means, that μ_5 is different from the other means, and that μ_2, μ_4, and μ_3 are indistinguishable from each other: $\mu_1 \neq \mu_2 = \mu_4 = \mu_3 \neq \mu_5$.

the appropriate standard error, yields a t value (Section 8.1), the Tukey test statistic, q, is calculated by dividing a difference between two means by

$$\text{SE} = \sqrt{\frac{s^2}{n}}, \tag{11.2}$$

where n is the number of data in each of groups B and A, and s^2 is the error mean square by ANOVA computation (Equation 10.14). Thus

$$q = \frac{\overline{X}_B - \overline{X}_A}{\text{SE}}, \tag{11.3}$$

which is known as the *studentized range** (and is sometimes designated as T). The null hypothesis H_0: $\overline{X}_B = \overline{X}_A$ is rejected if q is equal to or greater than the critical value, $q_{\alpha,\nu,k}$, from Appendix Table B.5, where ν is the error degrees of freedom (via Equation 10.15, which is $N - k$).

The significance level, α, is the probability of committing at least one Type I error (i.e., the probability of incorrectly rejecting at least one H_0) during the course of comparing all pairs of means. And the Tukey test has good power and maintains the probability of the familywise Type I error at or below the stated α.

The conclusions reached by this multiple-comparison testing may depend upon the order in which the pairs of means are compared. The proper procedure is to compare first the largest mean against the smallest, then the largest against the next smallest, and so on, until the largest has been compared with the second largest. Then one compares the second largest with the smallest, the second largest with the next smallest, and so on. Another important procedural rule is that if no significant difference is found

*E. S. Pearson and H. O. Hartley first used this term in 1953 (David, 1995).

between two means, then it is concluded that no significant difference exists between any means enclosed by those two, and no differences between enclosed means are tested for. Thus, in Example 11.1, because we conclude no difference between population means 3 and 2, no testing is performed to judge the difference between means 3 and 4, or between means 4 and 2. The conclusions in Example 11.1 are that Sample 1 came from a population having a mean different from that of any of the other four sampled populations; likewise, it is concluded that the population mean from which Sample 5 came is different from any of the other population means, and that samples 2, 4, and 3 came from populations having the same means. Therefore, the overall conclusion is that $\mu_1 \neq \mu_2 = \mu_4 = \mu_3 \neq \mu_5$. As a visual aid in Example 11.1, each time a null hypothesis was not rejected, a line was drawn beneath means to connect the two means tested and to encompass any means between them.

The null hypothesis H_0: $\mu_B = \mu_A$ may also be written as $\mu_B - \mu_A = 0$. The hypothesis $\mu_B - \mu_A = \mu_0$, where $\mu_0 \neq 0$, may also be tested; this is done by replacing $\overline{X}_B - \overline{X}_A$ with $|\overline{X}_B - \overline{X}_A| - \mu_0$ in the numerator of Equation 11.3.

Occasionally, a multiple-comparison test, especially if $n_B \neq n_A$, will yield ambiguous results in the form of conclusions of overlapping spans of nonsignificance. For example, one might arrive at the following:

$$\underline{\overline{X}_1 \quad \overline{X}_2 \quad \overline{X}_3 \quad \overline{X}_4}$$

for an experimental design consisting of four groups of data. Here the four samples seem to have come from populations among which there were two different population means: Samples 1 and 2 appear to have been taken from one population, and Samples 2, 3, and 4 from a different population. But this is clearly impossible, for Sample 2 has been concluded to have come from both populations. Because the statistical testing was not able to conclude decisively from which population Sample 2 came, at least one Type II error has been committed. Therefore, it can be stated that $\mu_1 \neq \mu_3 \neq \mu_4$, but it cannot be concluded from which of the two populations Sample 2 came (or if it came from a third population). Repeating the data collection and analysis with a larger number of data might yield more conclusive results.

(a) Multiple Comparisons with Unequal Sample Sizes. If the sizes of the k samples are not equal, the Tukey-Kramer procedure (Kramer, 1956; supported by Dunnett, 1980a; Stoline, 1981; Jaccard, Becker, and Wood, 1984)* is desirable to maintain the probability of a Type I error near α and to operate with good power. For each comparison involving unequal n's, the standard error for use in Equation 11.3 is calculated as

$$\text{SE} = \sqrt{\frac{s^2}{2}\left(\frac{1}{n_B} + \frac{1}{n_A}\right)}, \tag{11.4}$$

which is inserting the harmonic mean of n_B and n_A (Section 3.4b) in place of n in Equation 11.2;† and Equation 11.4 is equivalent to 11.2 when $n_B = n_A$. This test is shown in Example 11.2, using the data of Example 10.1.

*This procedure has been shown to be excellent (e.g., Dunnett, 1980a; Hayter, 1984; Keselman, Murray, and Rogan, 1976; Smith, 1971; Somerville, 1993; Stoline, 1981), with the probability of a familywise Type I error no greater than the stated α.

†Some researchers have replaced n in Equation 11.2 with the harmonic mean of all k samples or with the median or arithmetic mean of the pair of means examined. Dunnett (1980a); Keselman, Murray, and Rogan (1976); Keselman and Rogan (1977); and Smith (1971) concluded the Kramer approach to be superior to those methods, and it is analogous to Equation 8.7a, which is used for two-sample t testing.

EXAMPLE 11.2 The Tukey-Kramer Test with Unequal Sample Sizes

The data (in kg) are those from Equation 10.1.

$k = 4$

s^2 = Error MS = 9.383

Error DF = 15

$q_{0.05,15,4} = 4.076$

Sample number (i) of ranked means:	4	1	2	3
Ranked sample mean ($\overline{X}_i$):	63.24	64.62	71.30	73.35
Sample sizes (n_i):	4	5	5	5

If $n_B = n_A$ (call it n), then $\text{SE} = \sqrt{\frac{s^2}{n}} = \sqrt{\frac{9.383}{5}} = \sqrt{2.111} = 1.453.$

If $n_B \neq n_A$, then $\text{SE} = \sqrt{\frac{s^2}{2}\left(\frac{1}{n_B} + \frac{1}{n_A}\right)} = \sqrt{\frac{0.383}{2}\left(\frac{1}{5} + \frac{1}{4}\right)}$

$= \sqrt{1.877} = 1.370.$

Comparison B vs. A	*Difference* $(\overline{X}_B - \overline{X}_A)$	SE	q	*Conclusion*
3 vs. 4	73.35 − 63.24 = 10.11	1.453	6.958	Reject H_0: $\mu_3 = \mu_4$
3 vs. 1	73.35 − 64.62 = 8.73	1.370	6.371	Reject H_0: $\mu_3 = \mu_1$
3 vs. 2	73.35 − 71.30 = 2.05	1.370	1.496	Do not reject H_0: $\mu_3 = \mu_2$
2 vs. 4	71.30 − 63.24 = 8.06	1.453	5.547	Reject H_0: $\mu_2 = \mu_4$
2 vs. 1	71.30 − 64.62 = 6.68	1.370	4.876	Reject H_0: $\mu_2 = \mu_1$
1 vs. 4	64.62 − 63.24 = 1.38	1.453	0.950	Do not reject H_0: $\mu_1 = \mu_4$

Thus, we conclude that μ_4 and μ_1 are indistinguishable, that μ_2 and μ_3 are indistinguishable, and that μ_4 and μ_1 are different from μ_2 and μ_3: $\mu_4 = \mu_1 \neq \mu_2 = \mu_3$.

(b) Multiple Comparisons with Unequal Variances. Although the Tukey test can withstand some deviation from normality (e.g., Jaccard, Becker, and Wood, 1984), it is less resistant to heterogeneous variances, especially if the sample sizes are not equal. The test is conservative if small n's are associated with small variances and undesirably liberal if small samples come from populations with large variances, and in the presence of both nonnormality and heteroscedasticity the test is very liberal. Many investigations* have determined that the Tukey-Kramer test is also adversely affected by heterogeneous variances.

*These include those of Dunnett (1980b, 1982); Games and Howell (1976); Jaccard, Becker, and Wood (1984); Keselman, Games, and Rogan (1979); Keselman and Rogan (1978); Keselman and Toothaker (1974); Keselman, Toothaker, and Shooter (1975); Ramseyer and Tcheng (1973); Jenkdon and Tamhane (1979).

As a solution to this problem, Games and Howell (1976) proposed the use of the Welch approximation (Section 8.1b) to modify Equation 11.4 to be appropriate when the k population variances are not assumed to be the same or similar:

$$\text{SE} = \sqrt{\frac{1}{2}\left(\frac{s_B^2}{n_B} + \frac{s_A^2}{n_A}\right)}. \tag{11.5}$$

and q will be associated with the degrees of freedom of Equation 8.12; but each sample size should be at least 6. This test maintains the probability of a familywise Type I error around α (though it is sometimes slightly liberal) and it has good power (Games, Keselman, and Rogan, 1981; Keselman, Games, and Rogan, 1979; Keselman and Rogan, 1978; Tamhane, 1979). If the population variances are the same, then the Tukey or Tukey-Kramer test is preferable (Kirk, 1995: 147–148). If there is doubt about whether there is substantial heteroscedacity, it is safer to use the Games and Howell procedure, for if the underlying populations do not have similar variances, that test will be far superior to the Tukey-Kramer test; and if the population variances are similar, the former will have only a little less power than the latter (Levy, 1978c).

(c) Other Multiple-Comparison Methods. Methods other than the Tukey and Tukey-Kramer tests have been employed by statisticians to examine pairwise differences for more than two means. The *Newman-Keuls test* (Newman, 1939; Keuls, 1952), also referred to as the *Student-Newman-Keuls test*, is employed as is the Tukey test, except that the critical values from Appendix Table B.5 are those for $q_{\alpha,\nu,p}$ instead of $q_{\alpha,\nu,k}$, where p is the range of means for a given H_0. So, in Example 11.2, comparing means 3 and 4 would use $p = 4$, comparing means 3 and 1 would call for $p = 3$, and so on (with p ranging from 2 to k). This type of multiple-comparison test is called a *multiple-range test*. There is considerable opinion against using this procedure (e.g., by Einot and Gabriel, 1975; Ramsey, 1978) because it may falsely declare differences with a probability undesirably greater than α.

The *Duncan test* (Duncan, 1955) is also known as the *Duncan new multiple range test* because it succeeds an earlier procedure (Duncan, 1951). It has a different theoretical basis, one that is not as widely accepted as that of Tukey's test, and it has been declared (e.g., by Carmer and Swanson, 1973; Day and Quinn, 1899) to perform poorly. This procedure is executed as is the Student-Newman-Keuls test, except that different critical-value tables are required.

Among other tests, there is also a procedure called the *least significant difference test* (LSD), and there are other tests, such as with *Dunn* or *Bonferroni* in their names (e.g., Howell, 2007: 356–363). The name *wholly significant difference test* (WSD test) is sometimes applied to the Tukey test (Section 11.1) and sometimes as a compromise between the Tukey and Student-Newman-Keuls procedures by employing a critical value midway between $q_{\alpha,\nu,k}$ and $q_{\alpha,\nu,p}$. The Tukey test is preferred here because of its simplicity and generally good performance with regard to Type I and Type II errors.

11.2 CONFIDENCE INTERVALS FOR MULTIPLE COMPARISONS

Expressing a $1 - \alpha$ confidence interval using a sample mean denotes that there is a probability of $1 - \alpha$ that the interval encloses its respective population mean. Once multiple-comparison testing has concluded which of three or more sample

means are significantly different, confidence intervals may be calculated for each different population mean. If one sample mean ($\overline{X}_i$) is concluded to be significantly different from all others, then Equation 10.31 (introduced in Section 10.2) is used:

$$\overline{X}_i \pm t_{\alpha(2),\nu}\sqrt{\frac{s^2}{n_i}}. \tag{10.31}$$

In these calculations, s^2 (essentially a pooled variance) is the same as the error mean square would be for an analysis of variance for these groups of data. If two or more sample means are not concluded to be significantly different, then a pooled mean of those samples is the best estimate of the mean of the population from which those samples came:

$$\overline{X}_p = \frac{\sum n_i \overline{X}_i}{\sum n_i}, \tag{11.6}$$

where the summation is over all samples concluded to have come from the same population. Then the confidence interval is

$$\overline{X}_p \pm t_{\alpha(2),\nu}\sqrt{\frac{s^2}{\sum n_i}}, \tag{11.6a}$$

again summing over all samples whose means are concluded to be indistinguishable. This is analogous to the two-sample situation handled by Equation 8.16, and it is demonstrated in Example 11.3.

If a pair of population means, μ_B and μ_A, are concluded to be different, the $1 - \alpha$ confidence interval for the difference $(\mu_B - \mu_A)$ may be computed as

$$(\overline{X}_B - \overline{X}_A) \pm (q_{\alpha,\nu,k})(\text{SE}). \tag{11.7}$$

Here, as in Section 11.1, ν is the error degrees of freedom appropriate to an ANOVA, k is the total number of means, and SE is obtained from either Equation 11.2 or Equation 11.4, depending upon whether n_B and n_A are equal, or Equation 11.5 if the underlying population variances are not assumed to be equal. This calculation is demonstrated in Example 11.3 for the data in Example 11.1.

(a) Sample Size and Estimation of the Difference between Two Population Means. Section 8.3 showed how to estimate the sample size required to obtain a confidence interval of specified width for a difference between the two population means associated with the two-sample t test. In a multisample situation, a similar procedure may be used with the difference between population means, employing q instead of the t statistic. As in Section 8.3, iteration is necessary, whereby n is determined such that

$$n = \frac{s^2(q_{\alpha,\nu,k})^2}{d^2}. \tag{11.8}$$

Here, d is the half-width of the $1 - \alpha$ confidence interval, s^2 is the estimate of error variance, and k is the total number of means; ν is the error degrees of freedom with the estimated n, namely $\nu = k(n - 1)$.

EXAMPLE 11.3 Confidence Intervals (CI) for the Population Means from Example 11.1

It was concluded in Example 11.1 that $\mu_1 \neq \mu_2 = \mu_4 = \mu_3 \neq \mu_5$. Therefore, we may calculate confidence intervals for μ_1 for $\mu_{2,4,3}$ and for μ_5 (where $\mu_{2,4,3}$ indicates the mean of the common population from which Samples 2, 4, and 3 came).

Using Equation 10.31:

$$95\%\ \text{CI for } \mu_1 = \overline{X}_1 \pm t_{0.05(2),25}\sqrt{\frac{s^2}{n_1}} = 32.1 \pm (2.060)\sqrt{\frac{9.7652}{6}} = 32.1 \text{ mg/ml} \pm 2.6 \text{ mg/ml}.$$

Again using Equation 10.31:

$$95\%\ \text{CI for } \mu_5 = \overline{X}_5 \pm t_{0.05(2),25}\sqrt{\frac{s^2}{n_5}} = 58.3 \text{ mg/ml} \pm 2.6 \text{ mg/ml}.$$

Using Equation 11.6:

$$\overline{X}_p = \overline{X}_{2,4,3} = \frac{n_2\overline{X}_2 + n_4\overline{X}_4 + n_3\overline{X}_3}{n_2 + n_4 + n_3} = \frac{(6)(40.2) + (6)(41.1) + (6)(44.1)}{6 + 6 + 6} = 41.8 \text{ mg/ml}.$$

Using Equation 11.6a:

$$95\%\ \text{CI for } \mu_{2,4,3} = \overline{X}_{2,4,3} \pm t_{0.05(2),25}\sqrt{\frac{s^2}{6 + 6 + 6}} = 41.8 \text{ mg/ml} \pm 1.5 \text{ mg/ml}.$$

Using Equation 11.7:

$$95\%\ \text{CI for } \mu_5 - \mu_{2,4,3} = \overline{X}_5 - \overline{X}_{2,4,3} \pm q_{0.05,25,5}\sqrt{\frac{s^2}{2}\left(\frac{1}{n_5} + \frac{1}{n_2 + n_4 + n_3}\right)}$$
$$= 58.3 - 41.8 \pm (4.166)(1.04)$$
$$= 16.5 \text{ mg/ml} \pm 4.3 \text{ mg/ml}.$$

Using Equation 11.7:

$$95\%\ \text{CI for } \mu_{2,4,3} - \mu_1 = \overline{X}_{2,4,3} - \overline{X}_1 \pm q_{0.05,25,5}\sqrt{\frac{s^2}{2}\left(\frac{1}{n_2 + n_4 + n_3} + \frac{1}{n_1}\right)}$$
$$= 41.8 - 32.1 \pm (4.166)(1.04)$$
$$= 9.7 \text{ mg/ml} \pm 4.3 \text{ mg/ml}.$$

11.3 TESTING A CONTROL MEAN AGAINST EACH OTHER MEAN

Sometimes means are obtained from k groups with the a priori objective of concluding whether the mean of one group, commonly designated as a control, differs significantly from each of the means of the other $k - 1$ groups. Dunnett (1955) provided

an excellent procedure for such testing. Thus, whereas the data described in Section 11.1 were collected with the intent of comparing each sample mean with each other sample mean, the Dunnett test is for multisample data where the objective of the analysis was stated as comparing the control group's mean to the mean of each other group. Tukey's test could be used for this purpose, but it would be less powerful (Myers and Well, 2003: 255). If $k = 2$, Dunnett's test is equivalent to the two-sample t test (Section 8.1).

As in the previous section, s^2 denotes the error mean square, which is an estimate of the common population variance underlying each of the k samples. The Dunnett's test statistic (analogous to that of Equation 11.3) is

$$q' = \frac{\overline{X}_{\text{control}} - \overline{X}_A}{\text{SE}}, \tag{11.9}$$

where the standard error, when the sample sizes are equal, is

$$\text{SE} = \sqrt{\frac{2s^2}{n}}, \tag{11.10}$$

and when the sample sizes are not equal, it is

$$\text{SE} = \sqrt{s^2\left(\frac{1}{n_A} + \frac{1}{n_{\text{control}}}\right)}, \tag{11.11}$$

and when the variances are not equal:

$$\text{SE} = \sqrt{\frac{s_A^2}{n_A} + \frac{s_{\text{control}}^2}{n_{\text{control}}}}. \tag{11.11a}$$

For a two-tailed test, critical values, $q'_{\alpha(2),\nu,k}$, are given in Appendix Table B.7. If $|q'| \geq q'_{\alpha(2),\nu,k}$, then H_0: $\mu_{\text{control}} = \mu_A$ is rejected. Critical values for a one-sample test, $q'_{\alpha(1),\nu,k}$, are given in Appendix Table B.6. In a one-tailed test, H_0: $\mu_{\text{control}} \leq \mu_A$ is rejected if $q' \geq q'_{\alpha(1),\nu,k}$; and H_0: $\mu_{\text{control}} \geq \mu_A$ is rejected if $|q'| \geq q'_{\alpha(1),\nu,k}$ and $\overline{X}_{\text{control}} < \mu_A$ (i.e., if $q \leq -q'_{\alpha(1),\nu,k}$). This is demonstrated in Example 11.4. These critical values ensure that the familywise Type I error = α.

The null hypothesis H_0: $\mu_{\text{control}} = \mu_A$ is a special case of H_0: $\mu_{\text{control}} - 0 = \mu_0$ where $\mu_0 = 0$. However, other values of μ_0 may be placed in the hypothesis, and Dunnett's test would proceed by placing $|\overline{X}_{\text{control}} - \overline{X}_A - \mu_0|$ in the numerator of the q' calculation. In an analogous manner, H_0: $\mu_{\text{control}} - \mu_0 \leq \mu$ (or H_0: $\mu_{\text{control}} - \mu_0 \geq \mu$) may be tested.

When comparison of group means to a control mean is the researcher's stated desire, the sample from the group designated as the control ought to contain more observations than the samples representing the other groups. Dunnett (1955) showed that the optimal size of the control sample typically should be a little less than $\sqrt{k-1}$ times the size of each other sample.

(a) Sample Size and Estimation of the Difference between One Population Mean and the Mean of a Control Population. This situation is similar to that discussed in Section 11.2a, but it pertains specifically to one of the k means being designated as

EXAMPLE 11.4 Dunnett's Test for Comparing the Mean of a Control Group to the Mean of Each Other Group

The yield (in metric tons per hectare) of each of several plots (24 plots, as explained below) of potatoes has been determined after a season's application of a standard fertilizer. Likewise, the potato yields from several plots (14 of them) were determined for each of four new fertilizers. A manufacturer wishes to promote at least one of these four fertilizers by claiming a resultant increase in crop yield. A total of 80 plots is available for use in this experiment.

Optimum allocation of plots among the five fertilizer groups will be such that the control group (let us say that it is group 2) has a little less than $\sqrt{k-1} = \sqrt{4} = 2$ times as many data as each of the other groups. Therefore, it was decided to use $n_2 = 24$ and $n_1 = n_3 = n_4 = m_5 = 14$, for a total N of 80.

Using analysis-of-variance calculations, the error MS (s^2) was found to be 10.42 (metric tons/ha)^2 and the error DF = 75.

$$\text{SE} = \sqrt{10.42\left(\frac{1}{14} + \frac{1}{24}\right)} = 1.1 \text{ metric tons/acre}$$

Group number (i) of ranked means:	1	2	3	4	5
Ranked group mean ($\overline{X}_i$):	17.3	21.7	22.1	23.6	27.8

As the control group (i.e., the group with the standard fertilizer) is group 2, each H_0: $\mu_2 \geq \mu_A$ will be tested against H_A: $\mu_2 < \mu_A$. And for each hypothesis test, $q'_{\alpha,\nu,k} = q'_{0.05(1),75,5}$.

Comparison B vs. A	*Difference* $(\overline{X}_2 - \overline{X}_A)$	SE	$\lvert q' \rvert$	*Conclusion*
2 vs. 1	$21.7 - 17.3 = 4.4$			Because $\overline{X}_2 > \overline{X}_1$, do not reject H_0: $\mu_2 \geq \mu_1$
2 vs. 5	$21.7 - 27.8 = -6.1$	1.1	5.55	Reject H_0: $\mu_2 \geq \mu_5$
2 vs. 4	$21.7 - 23.6 = -1.9$	1.1	1.73	Reject H_0: $\mu_2 \geq \mu_4$
2 vs. 3	Do not test			

We conclude that only fertilizer 5 produces a yield greater than the yield from the control fertilizer (fertilizer 2).

from a control group. The procedure uses this modification of Equation 11.8:

$$n = \frac{2s^2(q'_{\alpha,\nu,k})^2}{d^2}. \tag{11.12}$$

(b) Confidence Intervals for Differences between Control and Other Group Means. Using Dunnett's q' statistic and the SE of Equation 11.10, 11.11, or 11.11a, two-tailed confidence limits can be calculated for the difference between the control mean and each of the other group means:

$$1 - \alpha \text{ CI for } \mu_{\text{control}} - \mu_A = (\overline{X}_{\text{control}} - \overline{X}_A) \pm (q'_{\alpha(2),\nu,k})(\text{SE}). \tag{11.13}$$

One-tailed confidence limits are also possible. The $1 - \alpha$ confidence can be expressed that a difference, $\mu_{\text{control}} - \mu_A$, is not less than (i.e., is at least as large as)

$$(\overline{X}_{\text{control}} - \overline{X}_A) - (q'_{\alpha(1),\nu,k})(\text{SE}), \tag{11.14}$$

or it might be desired to state that the difference is no greater than

$$(\overline{X}_{\text{control}} - \overline{X}_A) + (q'_{\alpha(1),\nu,k})(\text{SE}). \tag{11.15}$$

MULTIPLE CONTRASTS

Inspecting the sample means after performing an analysis of variance can lead to a desire to compare combinations of samples to each other, by what are called *multiple contrasts*. The method of Scheffé* (1953; 1959: Sections 3.4, 3.5) is an excellent way to do this while ensuring a familywise Type I error rate no greater than α.

The data in Example 11.1 resulted in ANOVA rejection of the null hypothesis H_0: $\mu_1 = \mu_2 = \mu_3 = \mu_4 = \mu_5$; and, upon examining the five sample means, perhaps by arranging them in order of magnitude ($\overline{X}_1 < \overline{X}_2 < \overline{X}_4 < \overline{X}_3 < \overline{X}_5$), the researcher might then want to compare the mean strontium concentration in the river (group 5) with that of the bodies of water represented by groups 2, 4, and 3. The relevant null hypothesis would be H_0: $(\mu_2 + \mu_4 + \mu_3)/3 = \mu_5$, which can also be expressed as H_0: $\mu_2/3 + \mu_4/3 + \mu_3/3 - \mu_5 = 0$. The Scheffé test considers that each of the four μ's under consideration is associated with a coefficient, c_i: $c_2 = \frac{1}{3}$, $c_4 = \frac{1}{3}$, $c_3 = \frac{1}{3}$, and $c_5 = -1$ (and the sum of these coefficients is always zero). The test statistic, S, is calculated as

$$S = \frac{\left|\sum c_i \overline{X}_i\right|}{\text{SE}}, \tag{11.16}$$

where

$$\text{SE} = \sqrt{s^2\left(\sum \frac{c_i^2}{n_i}\right)}, \tag{11.17}$$

and the critical value of the test is

$$S_\alpha = \sqrt{(k-1)F_{\alpha(1),k-1,N-k}}\ . \tag{11.18}$$

Also, with these five groups of data, there might be an interest in testing H_0: $\mu_1 - (\mu_2 + \mu_4 + \mu_3)/3 = 0$ or H_0: $(\mu_1 + \mu_5)/2 - (\mu_2 + \mu_4 + \mu_3)/3 = 0$ or H_0: $(\mu_1 + \mu_4)/2 - (\mu_2 + \mu_3)/2 = 0$, or other contrasts. Any number of such hypotheses may be tested, and the familywise Type I error rate is the probability of falsely rejecting at least one of the possible hypotheses. A significant F from an ANOVA of the k groups indicates that there is at least one significant contrast among the groups, although the contrasts that are chosen may not include one to be rejected by the Scheffé test. And if F is not significant, testing multiple contrasts need not be done, for the probability of a Type I error in that testing is not necessarily at α (Hays, 1994: 458). The testing of several of these hypotheses is shown in Example 11.5. In employing the Scheffé test, the decision of which means to compare with which others occurs after inspecting the data, so this is referred to as an a posteriori, or post hoc test.

*Henry Scheffé (1907–1977), American statistician.

EXAMPLE 11.5 Scheffé's Test for Multiple Contrasts, Using the Data of Example 11.1

For $\alpha = 0.05$, the critical value, S_α, for each contrast is (via Equation 11.18) $\sqrt{(k-1)F_{0.05(1),k-1,N-k}}$

$$= \sqrt{(5-1)F_{0.05(1),4,25}}$$
$$= \sqrt{4(2.76)}$$
$$= 3.32.$$

Example 11.1 showed $s^2 = 9.7652$ and $n = 6$.

Contrast	SE	S	*Conclusion*
$\frac{\bar{X}_2 + \bar{X}_3 + \bar{X}_4}{3} - \bar{X}_5$ $= 41.8 - 58.3$ $= -16.5$	$\sqrt{9.7652\left[\frac{\left(\frac{1}{3}\right)^2}{6} + \frac{\left(\frac{1}{3}\right)^2}{6} + \frac{\left(\frac{1}{3}\right)^2}{6} + \frac{(1)^2}{6}\right]} = 1.47$	11.22	Reject H_0: $\frac{\mu_2 + \mu_3 + \mu_4}{3} - \mu_5 = 0$
$\bar{X}_1 - \frac{\bar{X}_2 + \bar{X}_3 + \bar{X}_4}{3}$ $= 32.1 - 41.8$ $= -9.7$	$\sqrt{9.7652\left[\frac{(1)^2}{6} + \frac{\left(\frac{1}{3}\right)^2}{6} + \frac{\left(\frac{1}{3}\right)^2}{6} + \frac{\left(\frac{1}{3}\right)^2}{6}\right]} = 1.47$	6.60	Reject H_0: $\mu_1 - \frac{\mu_2 + \mu_3 + \mu_4}{3} = 0$
$\frac{\bar{X}_1 + \bar{X}_5}{2} - \frac{\bar{X}_2 + \bar{X}_3 + \bar{X}_4}{3}$ $= 45.2 - 41.8$ $= 3.4$	$\sqrt{9.7652\left[\frac{\left(\frac{1}{2}\right)^2}{6} + \frac{\left(\frac{1}{2}\right)^2}{6} + \frac{\left(\frac{1}{3}\right)^2}{6} + \frac{\left(\frac{1}{3}\right)^2}{6} + \frac{\left(\frac{1}{3}\right)^2}{6}\right]} = 1.16$	2.93	Accept H_0: $\frac{\mu_1 + \mu_5}{2} - \frac{\mu_2 + \mu_3 + \mu_4}{3} = 0$
$\frac{\bar{X}_1 + \bar{X}_4}{2} - \frac{\bar{X}_2 + \bar{X}_3}{2}$ $= 36.6 - 42.15$ $= -5.55$	$\sqrt{9.7652\left[\frac{\left(\frac{1}{2}\right)^2}{6} + \frac{\left(\frac{1}{2}\right)^2}{6} + \frac{\left(\frac{1}{2}\right)^2}{6} + \frac{\left(\frac{1}{2}\right)^2}{6}\right]} = 1.28$	4.34	Reject H_0: $\frac{\mu_1 + \mu_4}{2} - \frac{\mu_2 + \mu_3}{2} = 0$

The Scheffé test may also be used to compare one mean with one other. It is then testing the same hypotheses as is the Tukey test. It is less sensitive than the Tukey test to nonnormality and heterogeneity of variances (Hays, 1994: 458, 458; Sahai and Ageel, 2000: 77); but is less powerful and it is recommended that it not be used for pairwise comparisons (e.g., Carmer and Swanson, 1973; Kirk, 1995: 154; Toothaker, 1991: 51, 77, 89–90). Shaffer (1977) described a procedure, more powerful than Scheffé's, specifically for comparing a combination of groups to a group specified as a control.

(a) Multiple Contrasts with Unequal Variances. The Scheffé test is suitable when the samples in the contrast each came from populations with the same variance.

When the population variances differ but the sample sizes are equal, the probability of a Type I error can be different from 0.05 when α is set at 0.05. If the variances *and* the sample sizes are unequal, then (as with the ANOVA, Section 10.1g) the test will be very conservative if the large variances are associated with large sample sizes and very liberal if the small samples come from the populations with the large variances (Keselman and Toothaker, 1974). If the σ_i^2's cannot be assumed to be the same or similar, the procedure of Brown and Forsythe (1974b) may be employed. This is done in a fashion analogous to the two-sample Welch modification of the t test (Section 8.1c), using

$$t' = \frac{\left|\sum c_i \overline{X}_i\right|}{\sqrt{\sum \frac{c_i^2 s_i^2}{n_i}}} \tag{11.19}$$

with degrees of freedom of

$$\nu' = \frac{\left(\sum \frac{c_i^2 s_i^2}{n_i}\right)^2}{\sum \frac{(c_i^2 s_i^2)^2}{n_i^2 (n_i - 1)}}. \tag{11.20}$$

(b) Confidence Intervals for Contrasts. The Scheffé procedure enables the establishment of $1 - \alpha$ confidence limits for a contrast:

$$\sum c_i \overline{X}_i \pm S_\alpha \text{SE} \tag{11.21}$$

(with SE from Equation 11.17). Shaffer's (1977) method produces confidence intervals for a different kind of contrast, that of a group of means with the mean of a control group.

Example 11.6 demonstrates the determination of confidence intervals for two of the statistically significant contrasts of Example 11.5.

11.5 NONPARAMETRIC MULTIPLE COMPARISONS

In the multisample situation where the nonparametric Kruskal-Wallis test (Section 10.4) is appropriate, the researcher usually will desire to conclude which of the samples are significantly different from which others, and the experiment will be run with that goal. This may be done in a fashion paralleling the Tukey test of Section 11.1, by using rank sums instead of means, as demonstrated in Example 11.7. The rank sums, determined as in the Kruskal-Wallis test, are arranged in increasing order of magnitude. Pairwise differences between rank sums are then tabulated, starting with the difference between the largest and smallest rank sums, and proceeding in the same sequence as described in Section 11.1. The standard error is calculated as

$$\text{SE} = \sqrt{\frac{n(nk)(nk + 1)}{12}} \tag{11.22}$$

(Nemenyi, 1963; Wilcoxon and Wilcox, 1964: 10),* and the Studentized range (Appendix Table B.5 to be used is $q_{\alpha,\infty,k}$.)

EXAMPLE 11.6 Confidence Intervals for Multiple Contrasts

The critical value, S_α, for each confidence interval is that of Equation 11.8: $\sqrt{(k-1)F_{\alpha(1),k-1,N-k}}$, and for $\alpha = 0.05$, $S_\alpha = 3.32$ and $s^2 = 9.7652$ as in Example 11.5.

(a) A confidence interval for $\frac{\mu_2 + \mu_3 + \mu_4}{3} - \mu_5$ would employ SE = 1.47 from Example 11.5, and the 95% confidence interval is

$$\left(\frac{\overline{X}_2 + \overline{X}_3 + \overline{X}_4}{3} - \overline{X}_5\right) \pm S_\alpha \text{SE} = -16.5 \pm (3.32)(1.47)$$

$$= -16.5 \text{ mg/ml} \pm 4.9 \text{ mg/ml}$$

$$L_1 = -21.4 \text{ mg/ml}$$

$$L_2 = -11.6 \text{ mg/ml}.$$

(b) A confidence interval for $\mu_1 - \frac{\mu_2 + \mu_3 + \mu_4}{3}$ would employ SE = 1.47 from Example 11.5, and the 95% confidence interval is

$$\left(\overline{X}_1 - \frac{\overline{X}_2 + \overline{X}_3 + \overline{X}_4}{3}\right) \pm S_\alpha \text{SE} = -9.7 \pm (3.32)(1.47)$$

$$= -9.7 \text{ mg/ml} \pm 4.9 \text{ mg/ml}$$

$$L_1 = -14.6 \text{ mg/ml}$$

$$L_2 = -4.8 \text{ mg/ml}.$$

(a) Nonparametric Multiple Comparisons with Unequal Sample Sizes. Multiple-comparison testing such as in Example 11.7 requires that there be equal numbers of data in each of the k groups. If such is not the case, then we may use the procedure of Section 11.7, but a more powerful test is that proposed by Dunn (1964), using a standard error of

$$\text{SE} = \sqrt{\frac{N(N+1)}{12}\left(\frac{1}{n_A} + \frac{1}{n_B}\right)} \tag{11.24}$$

for a test statistic we shall call

$$Q = \frac{\overline{R}_B - \overline{R}_A}{\text{SE}}, \tag{11.25}$$

*Some authors (e.g., Miller 1981: 166) perform this test in an equivalent fashion by considering the difference between mean ranks ($\overline{R}_A$ and $\overline{R}_B$) rather than rank sums (R_A and R_B), in which case the appropriate standard error would be

$$\text{SE} = \sqrt{\frac{k(nk+1)}{12}}. \tag{11.23}$$

EXAMPLE 11.7 Nonparametric Tukey-Type Multiple Comparisons, Using the Nemenyi Test

The data are those from Example 10.10.

$$\text{SE} = \sqrt{\frac{n(nk)(nk+1)}{12}} = \sqrt{\frac{5(15)(16)}{12}} = \sqrt{100} = 10.00$$

Sample number (i) of ranked rank sums:	3	2	1
Rank sum (R_i):	26	30	64

Comparison (B vs. A)	*Difference* ($R_B - R_A$)	SE	q	$q_{0.05,\infty,3}$	*Conclusion*
1 vs. 3	64 − 26 = 38	10.00	3.80	3.314	Reject H_0: Fly abundance is the same at vegetation heights 3 and 1.
1 vs. 2	64 − 30 = 34	10.00	3.40	3.314	Reject H_0: Fly abundance is the same at vegetation heights 2 and 1.
2 vs. 3	30 − 26 = 4	10.00	0.40	3.314	Do not reject H_0: Fly abundance is the same at vegetation heights 3 and 2.

Overall conclusion: Fly abundance is the same at vegetation heights 3 and 2 but is different at height 1.

where $\overline{R}$ indicates a mean rank (i.e., $\overline{R}_A = R_A/n_A$ and $\overline{R}_B = R_B/n_B$). Critical valucs for this test, $Q_{\alpha,k}$, are given in Appendix Table B.15. Applying this procedure to the situation of Example 11.7 yields the same conclusions, but this will not always be the case as this is only an approximate method and conclusions based upon a test statistic very near the critical value should be expressed with reservation. It is advisable to conduct studies that have equal sample sizes so Equation 11.22 or 11.23 may be employed.

If tied ranks are present, then the following is an improvement over Equation 11.24 (Dunn, 1964):

$$\text{SE} = \sqrt{\left(\frac{N(N+1)}{12} - \frac{\sum t}{12(N-1)}\right)\left(\frac{1}{n_A} + \frac{1}{n_B}\right)}. \qquad (11.26)$$

In the latter equation, $\sum t$ is used in the Kruskal-Wallis test when ties are present and is defined in Equation 10.42. The testing procedure is demonstrated in Example 11.8; note that it is the mean ranks ($\overline{R}_i$), rather than the ranks sums (R_i), that are arranged in order of magnitude.

A procedure developed independently by Steel (1960, 1961b) and Dwass (1960) is somewhat more advantageous than the tests of Nemenyi and Dunn (Critchlow and Fligner, 1991; Miller, 1981: 168–169), but it is less convenient to use and it tends to be very conservative and less powerful (Gabriel and Lachenbruch, 1969). And

EXAMPLE 11.8 Nonparametric Multiple Comparisons with Unequal Sample Sizes

The data are those from Example 10.11, where the Kruskal-Wallis test rejected the null hypothesis That water *p*H was the same in all four ponds examined

$\sum t = 168$, as in Example 10.11.

For $n_A = 8$ and $n_B = 8$,

$$\text{SE} = \sqrt{\left(\frac{N(N+1)}{12} - \frac{\sum t}{12(N-1)}\right)\left(\frac{1}{n_A} + \frac{1}{n_B}\right)}$$

$$= \sqrt{\left(\frac{31(32)}{12} - \frac{168}{12(30)}\right)\left(\frac{1}{8} + \frac{1}{8}\right)}$$

$$= \sqrt{20.5500} = 4.53$$

For $n_A = 7$ and $n_B = 8$,

$$\text{SE} = \sqrt{\left(\frac{31(32)}{12} - \frac{168}{12(30)}\right)\left(\frac{1}{7} + \frac{1}{8}\right)} = \sqrt{22.0179} = 4.69.$$

Sample number (i) of ranked means:	1	2	4	3
Rank sum (R_i):	63.24	64.62	71.30	73.35
Sample size (n_i):	8	5	8	7
Mean rank ($\overline{R}_i$)	6.88	16.56	20.44	20.71

To test at the 0.05 significance level, the critical value is $Q_{0.05,4} = 2.639$.

Comparison B vs. A	*Difference* $(\overline{R}_B - \overline{R}_A)$	SE	Q	*Conclusion*
3 vs. 1	20.71 − 6.88 = 13.831	4.69	2.95	Reject H_0: Water *p*H is the same in ponds 3 and 1.
3 vs. 2	20.71 − 16.56 = 4.15	4.69	0.88	Do not reject H_0: Water *p*H is the same in ponds 3 and 2.
3 vs. 4	Do not test			
4 vs. 1	20.44 − 6.88 = 13.56	4.53	2.99	Reject H_0: Water *p*H is the same in ponds 4 and 1.
4 vs. 2	Do not test			
2 vs. 1	16.56 − 6.88 = 9.68	4.53	2.14	Do not reject H_0: Water *p*H is the same in ponds 2 and 1.

Overall conclusion: Water *p*H is the same in ponds 4 and 3 but is different in pond 1, and the relationship of pond 2 to the others is unclear.

this test can lose control of Type I error if the data come from skewed populations (Toothaker, 1991: 108).

(b) Nonparametric Comparisons of a Control to Other Groups. Subsequent to a Kruskal-Wallis test in which H_0 is rejected, a nonparametric analysis may be performed to seek either one-tailed or two-tailed significant differences between one group (designated as the "control") and each of the other groups of data. This is done in a manner paralleling that of the procedure of Section 11.4, but using group rank sums instead of group means. The standard error to be calculated is

$$\text{SE} = \sqrt{\frac{n(nk)(nk + 1)}{6}} \tag{11.27}$$

(Wilcoxon and Wilcox, 1964: 11), and one uses as critical values either $q'_{\alpha(1),\infty,k}$ or $q'_{\alpha(2),\infty,k}$ (from Appendix Table B.6 or Appendix Table B.7, respectively) for one-tailed or two-tailed hypotheses, respectively.*

The preceding nonparametric test requires equal sample sizes. If the n's are not all equal, then the procedure suggested by Dunn (1964) may be employed. By this method, group B is considered to be the control and uses Equation 11.27, where the appropriate standard error is that of Equation 11.26 or 11.28, depending on whether there are ties or no ties, respectively. We shall refer to critical values for this test, which may be two tailed or one tailed, as $Q'_{\alpha,k}$; and they are given in Appendix Table B.16. The test presented by Steel (1959) has drawbacks compared to the procedures above (Miller, 1981: 133).

11.6 NONPARAMETRIC MULTIPLE CONTRASTS

Multiple contrasts, introduced in Section 11.4, can be tested nonparametrically using the Kruskal-Wallis H statistic instead of the F statistic. As an analog of Equation 11.16, we compute

$$S = \frac{\left|\sum c_i \overline{R}_i\right|}{\text{SE}}, \tag{11.29}$$

where c_i is as in Section 11.4, and

$$\text{SE} = \sqrt{\left(\frac{N(N + 1)}{12}\right)\left(\sum \frac{c_i^2}{n_i}\right)}, \tag{11.30}$$

unless there are tied ranks, in which cases we use

$$\text{SE} = \sqrt{\left(\frac{N(N + 1)}{12} - \frac{\sum t}{12(N - 1)}\right)\left(\sum \frac{c_i^2}{n_i}\right)}, \tag{11.31}$$

*If mean ranks, instead of rank sums, are used, then

$$\text{SE} = \sqrt{\frac{k(nk + 1)}{6}}. \tag{11.28}$$

where $\sum t$ is as in Equation 10.42. The critical value for these multiple contrasts is $\sqrt{H_{\alpha,n_1,n_2,\ldots}}$, using Appendix Table B.13 to obtain the critical value of H. If the needed critical value of H is not on that table, then $\chi^2_{\alpha,(k-1)}$ may be used.

11.7 MULTIPLE COMPARISONS AMONG MEDIANS

If the null hypothesis is rejected in a multisample median test (Section 10.5), then it is usually desirable to ascertain among which groups significant differences exist. A Tukey-type multiple comparison test has been provided by Levy (1979), using

$$q = \frac{f_{1B} - f_{1A}}{\text{SE}}. \tag{11.32}$$

As shown in Example 11.19, we employ the values of f_{1j} for each group, where f_{1j} is the number of data in group j that are greater than the grand median. (The values of f_{1j} are the observed frequencies in the first row in the contingency table used in the multisample median test of Section 10.5.) The values of f_{1j} are ranked, and pairwise differences among the ranks are examined as in other Tukey-type tests. The appropriate standard error, when N (the total number of data in all groups) is an even number, is

$$\text{SE} = \sqrt{\frac{n(N+1)}{4N}}, \tag{11.33}$$

and, when N is an odd number, the standard error is

$$\text{SE} = \sqrt{\frac{nN}{4(N-1)}}. \tag{11.34}$$

The critical values to be used are $q_{\alpha,\infty,k}$. This multiple-comparison test appears to possess low statistical power. If the sample sizes are slightly unequal, as in Example 11.9, the test can be used by employing the harmonic mean (see Section 3.4b) of the sample sizes,

$$n = \frac{k}{\sum_{j=1}^{k} \frac{1}{n_j}}, \tag{11.35}$$

for an approximate result.

11.8 MULTIPLE COMPARISONS AMONG VARIANCES

If the null hypothesis that k population variances are all equal (see Section 10.6) is rejected, then we may wish to determine which of the variances differ from which others. Levy (1975a, 1975c) suggests multiple-comparison procedures for this purpose based on a logarithmic transformation of sample variances.

A test analogous to the Tukey test of Section 11.1 is performed by calculating

$$q = \frac{\ln s_B^2 - \ln s_A^2}{\text{SE}}. \tag{11.36}$$

EXAMPLE 11.9 Tukey-Type Multiple Comparison for Differences among Medians, Using the Data of Example 10.12

Sample number (j) of samples ranked by f_{1j}:	2	1	4	3
Ranked f_{1j}:	2	3	6	9
Sample size (n_j):	12	11	12	11

$k = 4$

$N = 11 + 12 + 11 + 12 = 46$

$n = 12$

By Equation 11.35,

$$n = \frac{4}{\frac{1}{12} + \frac{1}{11} + \frac{1}{12} + \frac{1}{11}} = 11.48$$

By Equation 11.36,

$$\text{SE} = \sqrt{\frac{(11.48)(46)}{4(46 - 1)}} = 1.713.$$

H_0: Median of population B = Median of population A.

H_A: Median of population $B \neq$ Median of population A.

Comparison	$f_{1B} - f_{1A}$	SE	q	$q_{0.05,4,\infty}$	*Conclusion*
3 vs. 2	$9 - 2 = 7$	1.713	4.086	3.633	Reject H_0.
3 vs. 1	$9 - 3 = 6$	1.713	3.503	3.633	Do not reject H_0.
3 vs. 4	Do not test				
4 vs. 2	$6 - 2 = 4$	1.713	2.335	3.633	Do not reject H_0.
4 vs. 1	Do not test				
1 vs. 2	Do not test				

Overall conclusion: The medians of populations 3 and 2 (i.e., south and east—see Example 10.12) are not the same; but the test lacks the power to allow clear conclusions about the medians of populations 4 and 1.

where

$$\text{SE} = \sqrt{\frac{2}{\nu}}, \tag{11.37}$$

if both samples being compared are of equal size. If $\nu_A \neq \nu_B$, we can employ

$$\text{SE} = \sqrt{\frac{1}{\nu_B} + \frac{1}{\nu_A}}. \tag{11.38}$$

EXAMPLE 11.10 Tukey-Type Multiple Comparison Test for Differences among Four Variances (i.e., $k = 4$)

i	s_i^2	n_i	ν_i	$\ln s_i^2$
1	2.74 g^2	50	49	1.0080
2	2.83 g^2	48	47	1.0403
3	2.20 g^2	50	49	0.7885
4	6.42 g^2	50	49	1.8594

Sample ranked by variances (i):	3	1	2	4
Logorithm of ranked sample variance ($\ln s_i^2$):	0.7885	1.0080	1.0403	1.8594
Sample degrees of freedom (ν_i):	49	49	47	49

Comparison (B vs. A)	*Difference* ($\ln s_B^2 - \ln s_A^2$)	SE	q	$q_{0.05,\infty,4}$	*Conclusions*
4 vs. 3	1.8594 − 0.7885 = 1.0709	0.202*	5.301	3.633	Reject H_0: $\sigma_4^2 = \sigma_3^2$
4 vs. 1	1.8594 − 1.0080 = 0.8514	0.202	4.215	3.633	Reject H_0: $\sigma_4^2 = \sigma_1^2$
4 vs. 2	1.8594 − 1.0403 = 0.8191	0.204†	4.015	3.633	Reject H_0: $\sigma_4^2 = \sigma_2^2$
2 vs. 3	1.0403 − 0.7885 = 0.2518	0.204	1.234	3.633	Do not reject H_0: $\sigma_2^2 = \sigma_3^2$
2 vs. 1	Do not test				
1 vs. 3	Do not test				

*As $\nu_4 = \nu_3$: $\text{SE} = \sqrt{\frac{2}{\nu}} = \sqrt{\frac{2}{49}} = 0.202.$

†As $\nu_4 \neq \nu_2$: $\text{SE} = \sqrt{\frac{1}{\nu_4} + \frac{1}{\nu_2}} = \sqrt{\frac{1}{49} + \frac{1}{47}} = 0.204.$

Overall conclusion: $\sigma_3^2 = \sigma_1^2 = \sigma_2^2 \neq \sigma_4^2$.

Just as in Sections 11.1 and 11.2, the subscripts A and B refer to the pair of groups being compared; and the sequence of pairwise comparisons must follow that given in those sections. This is demonstrated in Example 11.10.* The critical value for this test is $q_{\alpha,\infty,k}$ (from Appendix Table B.5).

A Newman-Keuls-type test can also be performed using the logarithmic transformation. For this test, we calculate q using Equation 11.36; but the critical value,

*Recall (as in Section 10.6) that "ln" refers to natural logarithms (i.e., logarithms using base e). If one prefers using common logarithms ("log"; logarithms in base 10), then

$$q = \frac{2.30259(\log s_B^2 - \log s_A^2)}{\text{SE}}. \tag{11.39}$$

4 are the same as the means of groups 2 and 3.

(b) Test the hypothesis that the means of groups 2 and 4 are the same as the mean of group 3.

11.6. The following ranks result in a significant Kruskal-Wallis test. Employ nonparametric multiple-range testing to conclude between which of the three groups population differences exist.

Group 1	*Group 2*	*Group 3*
8	10	14
4	6	13
3	9	7
5	11	12
1	2	15

CHAPTER 12

Two-Factor Analysis of Variance

Section 10.1 introduced methods for one-way analysis of variance, which is the analysis of the effects of a factor (such as the type of feed) on a variable (such as the body weight of pigs). The present chapter will discuss how the effects of two factors can be assessed using a single statistical procedure.

The simultaneous analysis to be considered, of the effect of more than one factor on population means, is termed a *factorial analysis of variance*,* and there can be important advantages to such an experimental design. Among them is the fact that a single set of data can suffice for the analysis and it is not necessary to perform a one-way ANOVA for each factor. This may be economical with respect to time, effort, and money; and factorial analysis of variance also can test for the interactive effect of factors. The two-factor analysis of variance is introduced in this chapter. Examination of the effects of more than two factors will be discussed in Chapter 14.

There have been attempts to devise dependable nonparametric statistical tests for experimental designs with two or more factors. For a one-factor ANOVA, the Mann-Whitney test or an ANOVA on the ranks of the data may be employed for nonparametric testing (Section 10.4). But, except for the situation in Section 12.7, nonparametric procedures with more than one factor have not been generally acceptable. For multifactor analyses (this chapter, Chapter 14, and Chapter 15), it has been proposed that a parametric ANOVA may be performed on the ranks of the data (and this rank transformation is employed by some computer packages) or that the Kruskal-Wallis test of Section 10.4 may be expanded. However, Akritas (1990); Blair, Sawilowsky, and Higgins (1987); Brunner and Neumann (1986); McKean and Vidmar (1994); Sawilowsky, Blair, and Higgins (1989); Seaman et al. (1994); Toothaker and

*Some concepts on two-factor analysis of variance were discussed as early as 1899 (Thiele, 1899). In 1926, R. A. Fisher was the first to present compelling arguments for factorial analysis (Box, 1978: 158; Street, 1990).

Chang (1980); and Toothaker and Newman (1994) found that these procedures perform poorly and should not be employed.

12.1 TWO-FACTOR ANALYSIS OF VARIANCE WITH EQUAL REPLICATION

Example 12.1 presents data from an experiment suited to a two-way analysis of variance. The two factors are fixed (as defined in Section 10.1f and discussed further in Section 12.1d). The variable under consideration is blood calcium concentration in birds, and the two factors being simultaneously tested are hormone treatment and sex. Because there are two levels in the first factor (hormone-treated and nontreated) and two levels in the second factor (female and male), this experimental design* is termed a 2×2 (or 2^2) factorial. The two factors are said to be "crossed" because each level of one factor is found in combination with each level of the second factor.† There are $n = 5$ replicate observations (i.e., calcium determinations on each of five birds) for each of the $2 \times 2 = 4$ combinations of the two factors; therefore, there are a total of $N = 2 \times 2 \times 5 = 20$ data in this experiment. In general, it is advantageous to have equal replication (what is sometimes called a "balanced" or "orthogonal" experimental design), but Section 12.2 will consider cases with unequal numbers of data per cell, and Section 12.3 will discuss analyses with only one datum per combination of factors.

For the general case of the two-way factorial analysis of variance, we can refer to one factor as A and to the other as B. Furthermore, let us have a represent the number of levels in factor A, b the number of levels in factor B, and n the number of replicates. A triple subscript on the variable, as X_{ijl}, will enable us to identify uniquely the value that is replicate l of the combination of level i of factor A and level j of factor B. In Example 12.1, $X_{213} = 32.3$ mg/100 ml, $X_{115} = 9.5$ mg/100 ml, and so on. Each combination of a level of factor A with a level of factor B is called a *cell*. The cells may be visualized as the "groups" in a one-factor ANOVA (Section 10.1). There are four cells in Example 12.1: females without hormone treatment, males without hormone treatment, females with hormone treatment, and males with hormone treatment. And there are n replicate data in each cell. For the cell formed by the combination of level i of factor A and level j of factor B, $\overline{X}_{ij}$ denotes the cell mean; for the data in Example 12.1, the mean of a cell is the cell total divided by 5, so $\overline{X}_{11} = 14.88$, $\overline{X}_{12} = 12.12$, $\overline{X}_{21} = 32.52$, and $\overline{X}_{22} = 27.78$ (with the units for each mean being mg/100 ml). The mean of all bn data in level i of factor A is $\overline{X}_{i\cdot}$, and the mean of all an data in level j of factor B is $\overline{X}_{j}$. That is, the mean for the 10 non-hormone-treated birds is $\overline{X}_{1\cdot}$, which is an estimate of the population mean, $\mu_{1\cdot}$; the mean for the hormone-treated birds is $\overline{X}_{2\cdot}$, which estimates $\mu_{2\cdot}$; the mean of the female birds is $\overline{X}_{\cdot 1}$, which estimates $\mu_{\cdot 1}$; and the mean of the male birds is $\overline{X}_{\cdot 2}$, which estimates $\mu_{\cdot 2}$. There are a total of $abn = 20$ data in the experiment, and (just as in the single-factor ANOVA of Section 10.1) the mean of all N data (the "grand mean")

*R. A. Fisher (1890–1962) is credited with creating and promoting the concept of *experimental design* (Savage, 1976), by which is meant the use of statistical considerations in the planning and executing of experiments.

†Two (or more) factors can exist in an ANOVA without being crossed. This will be shown in Chapter 15.

EXAMPLE 12.1 Hypotheses and Data for a Two-Factor Analysis of Variance with Fixed-Effects Factors and Equal Replication

The data are plasma calcium concentrations (in mg/100 ml) of birds of both sexes, half of the birds of each sex being treated with a hormone and half not treated with the hormone.

H_0: There is no effect of hormone treatment on the mean plasma calcium concentration of birds (i.e., $\mu_{\text{no hormone}} = \mu_{\text{hormone}}$ or $\mu_{1\cdot} = \mu_{2\cdot}$).

H_A: There is an effect of hormone treatment on the mean plasma calcium concentration of birds (i.e., $\mu_{\text{no hormone}} \neq \mu_{\text{hormone}}$ or $\mu_{1\cdot} \neq \mu_{2\cdot}$).

H_0: There is no difference in mean plasma calcium concentration between female and male birds (i.e., $\mu_{\text{female}} = \mu_{\text{male}}$ or $\mu_{\cdot 1} = \mu_{\cdot 2}$).

H_A: There is a difference in mean plasma calcium concentration between female and male birds (i.e., $\mu_{\text{female}} \neq \mu_{\text{male}}$ or $\mu_{\cdot 1} \neq \mu_{\cdot 2}$).

H_0: There is no interaction of sex and hormone treatment on the mean plasma calcium concentration of birds.

H_A: There is interaction of sex and hormone treatment on the mean plasma calcium concentration of birds.

$\alpha = 0.05$

No Hormone Treatment		Hormone Treatment	
Female	*Male*	*Female*	*Male*
16.3	15.3	38.1	34.0
20.4	17.4	26.2	22.8
12.4	10.9	32.3	27.8
15.8	10.3	35.8	25.0
9.5	6.7	30.2	29.3

Cell totals: $\sum_{l=1}^{5} X_{11l} = 74.4$ $\sum_{l=1}^{5} X_{12l} = 60.6$ $\sum_{l=1}^{5} X_{21l} = 162.6$ $\sum_{l=1}^{5} X_{22l} = 138.9$

Cell means: $\overline{X}_{11} = 14.88$ $\overline{X}_{12} = 12.12$ $\overline{X}_{21} = 32.52$ $\overline{X}_{22} = 27.78$

is the sum of all the data divided by the total number of data. That is, the grand mean is

$$\overline{X} = \sum_{i=1}^{a} \sum_{j=1}^{b} \sum_{l=1}^{n} X_{ijl}/N. \tag{12.1}$$

(a) Sources of Variation. Recall that the total sum of squares is a measure of variability among all the data in a sample. For the two-factor analysis of variance this is conceptually the same as for the single-factor ANOVA (see Equation 10.2):

$$\text{total SS} = \sum_{i=1}^{a} \sum_{j=1}^{b} \sum_{l=1}^{n} (X_{ijl} - \overline{X})^2, \tag{12.2}$$

with

$$\text{total DF} = N - 1. \tag{12.3}$$

Next we may consider the variability among cells (each cell being a combination of a level of factor A and a level of factor B), handling cells as we did treated "groups" in the single-factor ANOVA (see Equation 10.4):

$$\text{cells SS} = n \sum_{i=1}^{a} \sum_{j=1}^{b} (\overline{X}_{ij} - \overline{X})^2; \tag{12.4}$$

and, as the number of cells is ab,

$$\text{cells DF} = ab - 1. \tag{12.5}$$

Furthermore, the quantity analogous to the within-groups SS in the single-factor ANOVA (Equation 10.6) is

$$\text{within-cells SS} = \sum_{i=1}^{a} \sum_{j=1}^{b} \left[\sum_{l=1}^{n} (X_{ijl} - \overline{X}_{ij})^2 \right], \tag{12.6}$$

which may also be calculated as

$$\text{within-cells SS} = \text{total SS} - \text{cells SS} \tag{12.7}$$

and has degrees of freedom of

$$\text{within-cells DF} = ab(n - 1), \tag{12.8}$$

which is also

$$\text{within-cells DF} = \text{total DF} - \text{cells DF}. \tag{12.9}$$

The terms *Error SS* and *Error DF* are very commonly used for within-cells SS and within-cells DF, respectively.

The calculations indicated above are analogous to those for the one-way analysis of variance (Section 10.1). But a major desire in the two-factor ANOVA is not to consider differences among the cells, but to assess the effects of each of the two factors independently of the other. This is done by considering factor A to be the sole factor in a single-factor ANOVA and then by considering factor B to be the single factor. For factor A this is done as follows:

$$\text{factor } A \text{ SS} = bn \sum_{i=1}^{a} (\overline{X}_{i\cdot} - \overline{X})^2, \tag{12.10}$$

which is associated with degrees of freedom of

$$\text{factor } A \text{ DF} = a - 1. \tag{12.11}$$

Similarly, for factor B,

$$\text{factor } B \text{ SS} = an \sum_{j=1}^{b} (\overline{X}_{\cdot j} - \overline{X})^2, \tag{12.12}$$

for which the degrees of freedom are

$$\text{factor } B \text{ DF} = b - 1. \tag{12.13}$$

In general, the variability among cells is not equal to the variability among levels of factor A plus the variability among levels of factor B (i.e., the result of Equation 12.4 is not equal to the sum of the results from Equations 12.10 and 12.12). The amount of variability not accounted for is that due to the effect of *interaction** between factors A and B. This is designated as the $A \times B$ interaction, and its sum of squares and degrees of freedom are readily calculated as representing the difference between the variability within cells and the variability due to the two factors:

$$A \times B \text{ interaction SS} = \text{cells SS} - \text{factor}A \text{ SS} - \text{factor } B \text{ SS}, \tag{12.14}$$

and

$$A \times B \text{ interaction DF} = \text{cells DF} - \text{factor } A \text{ DF} - \text{factor } B \text{ DF}, \tag{12.15}$$

or, equivalently,

$$\begin{aligned} A \times B \text{ interaction DF} &= (\text{factor } A \text{ DF})(\text{factor } B \text{ DF}) \\ &= (a - 1)(b - 1). \end{aligned} \tag{12.16}$$

Example 12.1a shows the above calculations of sums of squares and degrees of freedom for the data of Example 12.1, and Example 12.2 shows the ANOVA results.

EXAMPLE 12.1a Sums of Squares and Degrees of Freedom for the Data of Example 12.1

grand mean: $\overline{X} = (74.4 + 60.6 + 162.6 + 138.9)/20 = 21.825$

treatment means:

no hormone: $\overline{X}_{1\cdot} = (74.4 + 60.6)/10 = 13.50$

hormone: $\overline{X}_{2\cdot} = (162.6 + 138.9)/10 = 30.15$

sex means:

female: $\overline{X}_{\cdot 1} = (74.4 + 162.6)/10 = 23.70$

male: $\overline{X}_{\cdot 2} = (60.6 + 138.9)/10 = 19.95$

$$\text{total SS} = \sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{k=1}^{n}(X_{ijk} - \overline{X})^2$$

$$= (16.3 - 21.825)^2 + (20.4 - 21.825)^2 + \cdots + (29.3 - 21.825)^2$$

$$= 1762.7175$$

$$\text{total DF} = N - 1 = 20 - 1 = 19$$

$$\text{cells SS} = n\sum_{i=1}^{a}\sum_{j=1}^{b}(\overline{X}_{ij} - \overline{X})^2$$

$$= 5\left[(14.88 - 21.825)^2 + (12.12 - 21.825)^2 + (32.52 - 21.825)^2 + (27.78 - 21.825)^2\right]$$

$$= 1461.3255$$

$$\text{cells DF} = ab - 1 = (2)(2) - 1 = 4 - 1 = 3$$

*The term *interaction* was introduced for ANOVA by R. A. Fisher (David, 1995).

$$\text{within-cells (error) SS} = \sum_{i=1}^{a}\sum_{j=1}^{b}\left[\sum_{l=1}^{n}(X_{ijk} - \overline{X}_{ij})^2\right]$$
$$= (16.3 - 14.88)^2 + (20.4 - 14.88)^2$$
$$+ \cdots + (29.3 - 27.78)^2$$
$$= 301.3920$$

or, equivalently,

$$\text{within-cells (error) SS} = \text{Total SS} - \text{Cells SS}$$
$$= 1762.7115 - 1461.3255 = 301.3920$$

$$\text{within-cells (error) DF} = ab(n - 1) = (2)(2)(5 - 1) = (4)(4) = 16$$

or, equivalently,

$$\text{within-cells (error) DF} = \text{total DF} - \text{cells DF} = 19 - 3 = 16$$

$$\text{Factor } A \text{ SS} = bn\sum_{i=1}^{a}(\overline{X}_{i\cdot} - \overline{X})^2$$
$$= (2)(5)\left[(13.50 - 21.825)^2 + (30.15 - 21.825)^2\right]$$
$$= 1386.1125$$

$$\text{factor } A \text{ DF} = a - 1 = 2 - 1 = 1$$

$$\text{factor } B \text{ SS} = an\sum_{j=1}^{b}(\overline{X}_{\cdot j} - \overline{X})^2$$
$$= (2)(5)\left[(23.70 - 21.825)^2 + (19.95 - 21.825)^2\right]$$
$$= 70.3125$$

$$\text{factor } B \text{ DF} = b - 1 = 2 - 1 = 1$$

$$A \times B \text{ interaction SS} = \text{cells SS} - \text{factor } A \text{ SS} - \text{factor } B \text{ SS}$$
$$= 1461.3255 - 1386.1125 - 70.3125 = 4.9005$$

$$A \times B \text{ interaction DF} = \text{cells DF} - \text{factor } A \text{ DF} - \text{factor } B \text{ DF}$$
$$= 3 - 1 - 1 = 1$$

or, equivalently,

$$A \times B \text{ interaction DF} = (\text{factor } A \text{ DF})(\text{factor } B \text{ DF})$$
$$= (2 - 1)(2 - 1) = 1$$

An interaction between two factors means that the effect of one factor is not independent of the presence of a particular level of the other factor. In Example 12.1, no interaction would imply that the difference in the effect of hormone treatment on plasma calcium between males and females is the same under both hormone treatments.* Therefore, interaction among factors is an effect on the variable (e.g.,

*Symbolically, the null hypothesis for interaction effect could be stated as H_0: $\mu_{11} - \mu_{12} = \mu_{21} - \mu_{22}$ or $H_0 : \mu_{11} - \mu_{21} = \mu_{12} - \mu_{22}$, where μ_{ij} is the population mean of the variable in the presence of level i of factor A and level j of factor B.

EXAMPLE 12.2 Two-Factor ANOVA Summary for the Data and Hypotheses of Example 12.1

Analysis of Variance Summary Table			
Source of variation	SS	DF	MS
Total	1762.2175	19	
Cells	1461.3255	3	
Factor *A* (hormone)	1386.1125	1	1386.1125
Factor *B* (sex)	70.3125	1	70.3125
A × *B*	4.9005	1	4.9005
Within-Cells (Error)	301.3920	16	18.8370

For H_0: There is no effect of hormone treatment on the mean plasma calcium concentration of birds in the population sampled.

$$F = \frac{\text{hormone MS}}{\text{within-cells MS}} = \frac{1386.1125}{18.8370} = 73.6$$

$F_{0.05(1),1,16} = 4.49$

Therefore, reject H_0.

$$P < 0.0005 \quad [P = 0.00000022]$$

For H_0: There is no difference in mean plasma calcium concentration between male and female birds in the population sampled.

$$F = \frac{\text{sex MS}}{\text{within-cells MS}} = \frac{70.3125}{18.8370} = 3.73$$

$F_{0.05(1),1,16} = 4.49$

Therefore, do not reject H_0.

$$0.05 < P < 0.10 \quad [P = 0.071]$$

For H_0: There is no interaction of sex and hormone treatment affecting the mean plasma calcium concentration of birds in the population sampled.

$$F = \frac{\text{hormone} \times \text{sex interaction MS}}{\text{within-cells MS}} = \frac{4.9005}{22.8370} = 0.260$$

$F_{0.05(1),1,16} = 4.49$

Therefore, do not reject H_0.

$$P > 0.25 \quad [P = 0.62]$$

plasma calcium) that is in addition to the sum of the effects of each factor considered separately.

For the one-factor ANOVA it was shown (Section 10.1a) how alternative formulas, referred to as "machine formulas," make the sum-of-squares calculations easier because they do not require computing deviations from means, squaring those deviations, and summing the squared deviations. There are also machine formulas for two-factor analyses of variance that avoid the need to calculate grand, cell, and factor means and the several squared deviations associated with them. Familiarity with these formulas is not necessary if the ANOVA calculations are done by an established computer program, but they can be very useful if a calculator is used. These are shown in Section 12.1b.

Table 12.1 summarizes the sums of squares, degrees of freedom, and mean squares for the two-factor analysis of variance.

(b) Machine Formulas. Just as with one-factor analysis of variance (Section 10.1), there are so-called machine formulas for two-factor ANOVA that allow the computation of sums of squares without first calculating overall, cell, within-cell, and factor means. These calculations are shown in Example 12.2a, and they yield the same sums of squares as shown in Example 12.1a.

TABLE 12.1: Summary of the Calculations for a Two-Factor Analysis of Variance with Fixed Effects and Equal Replication

Source of variation	Sum of squares (SS)	Degrees of freedom (DF)	Mean square (MS)
Total $[X_{ijl} - \overline{X}]$	Equation 12.2 or 12.17	$N - 1$	
Cells $[\overline{X}_{ij} - \overline{X}]$	Equation 12.4 or 12.19	$ab - 1$	$\frac{\text{cells SS}}{\text{cells DF}}$
Factor A $[\overline{X}_{i\cdot} - \overline{X}]$	Equation 12.10 or 12.20	$a - 1$	$\frac{\text{factor } A \text{ SS}}{\text{factor } A \text{ DF}}$
Factor B $[\overline{X}_{\cdot j} - \overline{X}]$	Equation 12.12 or 12.21	$b - 1$	$\frac{\text{factor } B \text{ SS}}{\text{factor } B \text{ DF}}$
$A \times B$ interaction	cells SS − factor A SS − factor B SS	$(a - 1)(b - 1)$	$\frac{A \times B \text{ SS}}{A \times B \text{ DF}}$
Within cells (Error) $[X_{ijl} - \overline{X}_{ij}]$	Equation 12.6 or total SS − cells SS	$ab(n - 1)$ or total DF − cells DF	$\frac{\text{error SS}}{\text{error DF}}$

Note: For each source of variation, the bracketed quantity indicates the variation being assessed; a is the number of levels in factor A; b is the number of factors in factor B; n is the number of replicate data in each cell; N is the total number of data (which is abn); X_{ijl} is datum l in the cell formed by level i of factor A and level j of factor B; $\overline{X}_{i\cdot}$ is the mean of the data in level i of factor A; $\overline{X}_{\cdot j}$ is the mean of the data in level j of factor B; $\overline{X}_{ij}$ is the mean of the data in the cell formed by level i of factor A and level j of factor B; and $\overline{X}$ is the mean of all N data.

EXAMPLE 12.2a Using Machine Formulas for the Sums of Squares in Example 12.2

$$\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{l=1}^{l} X_{ijl} = 436.5$$

$$\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{l=1}^{l} X_{ijl}^2 = 11354.31$$

$$\text{total for no hormone} = \sum_{j=1}^{b}\sum_{l=1}^{l} X_{1jl} = 74.4 + 60.6 = 135.0$$

$$\text{total for hormone} = \sum_{j=1}^{2}\sum_{l=1}^{l} X_{2jl} = 162.6 + 138.9 = 301.5$$

$$\text{total for females} = \sum_{i=1}^{a}\sum_{l=1}^{l} X_{i1l} = 74.4 + 162.6 = 237.0$$

$$\text{total for males} = \sum_{i=1}^{a}\sum_{l=1}^{l} X_{i2l} = 60.6 + 138.9 = 199.5$$

$$C = \frac{\left(\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{l=1}^{n} X_{ijl}\right)^2}{N} = \frac{(436.5)^2}{20} = 9526.6125$$

$$\text{total SS} = \sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{l=1}^{n} X_{ijl}^2 - C = 11354.31 - 9526.6125 = 1827.6975$$

$$\text{cells SS7} = \sum_{i=1}^{a}\sum_{j=1}^{b} \frac{\left(\sum_{l=1}^{n} X_{ijl}\right)^2}{n} - C$$

$$= \frac{(74.4)^2 + (60.6)^2 + (162.6)^2 + (138.9)^2}{5} - 9526.6125$$

$$= 1461.3255$$

$$\text{within-cells (i.e., error) SS} = \text{total SS} - \text{cells SS}$$

$$= 1827.6975 - 1461.3255 = 366.3720$$

$$\text{factor A (hormone group) SS} = \frac{\sum_{i=1}^{a}\left(\sum_{j=1}^{b}\sum_{l=1}^{n} X_{ijl}\right)^2}{bn} - C$$

$$= \frac{(\text{sum without hormone})^2 + (\text{sum with hormone})^2}{\text{number of data per hormone group}} - C$$

$$= \frac{(135.0)^2 + (301.5)^2}{(2)(5)} - 9526.6125$$

$$= 1386.1125$$

$$\text{factor } B \text{ (sex) SS} = \frac{\sum_{j=1}^{b}\left(\sum_{i=1}^{a}\sum_{l=1}^{n} X_{ijl}\right)^2}{an} - C$$

$$= \frac{(\text{sum for females})^2 + (\text{sum for males})^2}{\text{number of data per sex}} - C$$

$$= \frac{(237.0)^2 + (199.5)^2}{(2)(5)} - 9526.6125 = 70.3125$$

$$A \times B \text{ interaction SS} = \text{cells SS} - \text{factor } A \text{ SS} - \text{factor } B \text{ SS}$$

$$= 1461.3255 - 1386.1125 - 70.3125 = 4.9005$$

The total variability is expressed by

$$\text{total SS} = \sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{l=1}^{n} X_{ijl}^2 - C, \tag{12.17}$$

where

$$C = \frac{\left(\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{l=1}^{n} X_{ijl}\right)^2}{N}. \tag{12.18}$$

The variability among cells is

$$\text{cells SS} = \frac{\sum_{i=1}^{a}\sum_{j=1}^{b}\left(\sum_{l=1}^{n} X_{ijl}\right)^2}{n} - C. \tag{12.19}$$

And the variability among levels of factor A is

$$\text{factor } A \text{ SS} = \frac{\sum_{i=1}^{a}\left(\sum_{j=1}^{b}\sum_{l=1}^{n} X_{ijl}\right)^2}{bn} - C. \tag{12.20}$$

Simply put, the factor A SS is calculated by considering factor A to be the sole factor in a single-factor analysis of variance of the data. That is, we obtain the sum for each level of factor A (ignoring the fact that the data are also categorized into levels of factor B); the sum of a level is what is in parentheses in Equation 12.20. Then we square each of these level sums and divide the sum of these squares by the number of data per level (i.e., bn). On subtracting the "correction term," C, we arrive at

the factor A SS. If the data were in fact analyzed by a single-factor ANOVA, then the groups SS would indeed be the same as the factor A SS just described, and the groups DF would be what the two-foctor ANOVA considers as factor A DF; but the error SS in the one-way ANOVA would be what the two-factor ANOVA considers as the within-cells SS plus the factor B SS and the interaction sum of squares, and the error DF would be the sum of the within-cells, factor B, and interaction degrees of freedom.

For factor B computations, we simply ignore the division of the data into levels of factor A and proceed as if factor B were the single factor in a one-way ANOVA:

$$\text{factor } B \text{ SS} = \frac{\sum_{j=1}^{b}\left(\sum_{i=1}^{a}\sum_{l=1}^{n} X_{ijl}\right)^2}{an} - C. \tag{12.21}$$

(c) Graphical Display. The cell, column, and row means of Example 12.1 are summarized in Table 12.2. Using these means, the effects of each of the two factors, and the presence of interaction, may be visualized by a graph such as Figure 12.1. We shall refer to the two levels of factor A as A_1 and A_2, and the two levels of

TABLE 12.2: Cell, Row, and Column Means of the Data of Example 12.2 (in mg/100 ml)

	Female (B_1)	Male (B_2)	
No hormone (A_1)	14.9	12.1	13.5
Hormone (A_2)	32.5	27.8	30.2
	23.7	20.0	

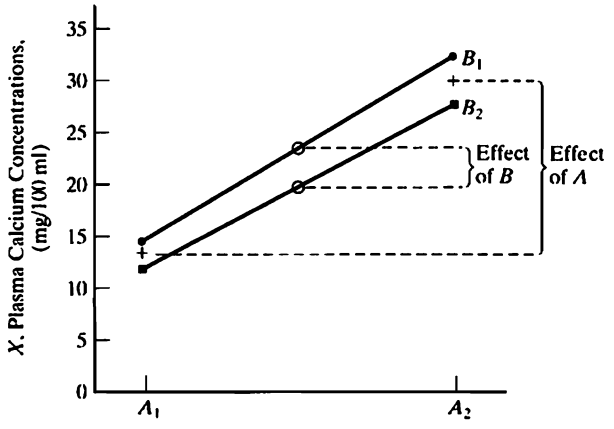


FIGURE 12.1: The means of the two-factor ANOVA data of Example 12.1, as given in Table 12.1. The A_i are the levels of factor A, the B_j are the levels of factor B. A plus sign indicates the mean of an A_i over all (i.e., both) levels of factor B, and an open circle indicates the mean of a B_j over all (i.e., both) levels of factor A.

factor B as B_1 and B_2. The variable, X, is situated on the vertical axis of the figure and on the horizontal axis we indicate A_1 and A_2. The two cell means for B_1 (14.9 and 32.5 mg/100 ml, which are indicated by black circles) are plotted and connected by a line; and the two cell means for B_2 (12.1 and 27.8 mg/100 ml, which are indicated by black squares) are plotted and connected by a second line. The mean of all the data in each level of factor A is indicated with a plus sign, and the mean of all the data in each level of factor B is denoted by an open circle. Then the effect of factor A is observed as the vertical distance between the plus signs; the effect of factor B is expressed as the vertical distance between the open circles; and nonparallelism of the lines indicates interaction between factors A and B. Thus, the ANOVA results of Example 12.1 are readily seen in this plot: there is a large effect of factor A (which is found to be significant by the F statistic) and a small effect of factor B (which is found to be nonsignificant). There is a small interaction effect, indicated in the figure by the two lines departing a little from being parallel (and this effect is also concluded to be nonsignificant). Various possible patterns of such plots are shown in Figure 12.2. Such figures may be drawn for situations with more than two levels within factors. And one may place either factor A or factor B on the horizontal axis; usually the factor with the larger number of levels is placed on this axis, so there are fewer lines to examine.

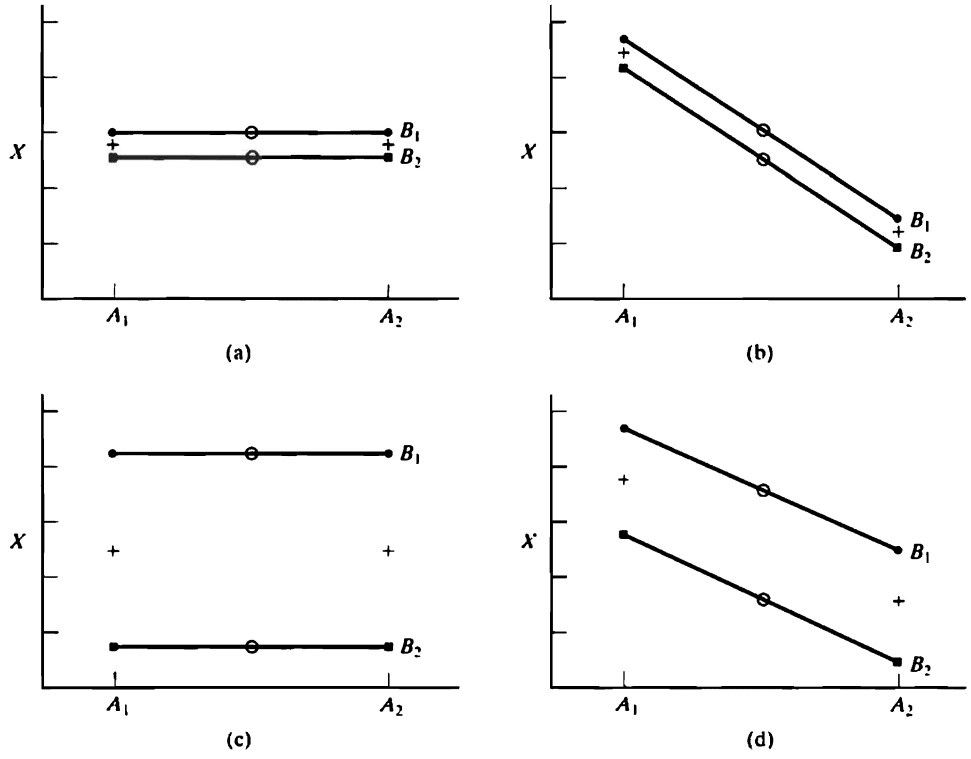


FIGURE 12.2: Means in a two-factor ANOVA, showing various effects of the two factors and their interaction. (a) No effect of factor A (indicated by the plus signs at the same vertical height on the X axis), a small effect of factor B (observed as the circles being only a small distance apart vertically), and no interaction of factors A and B (seen as the lines being parallel). (b) Large effect of factor A, small effect of factor B, and no interaction (which is the situation in Figure 12.1). (c) No effect of A, large effect of B, and no interaction. (d) Large effect of A, large effect of B, and no interaction. (e) No effect of A, no effect of B, but interaction between A and B. (f) Large effect of A, no effect of B, with slight interaction. (g) No effect of A, large effect of B, with large interaction. (h) Effect of A, large effect of B, with large interaction.

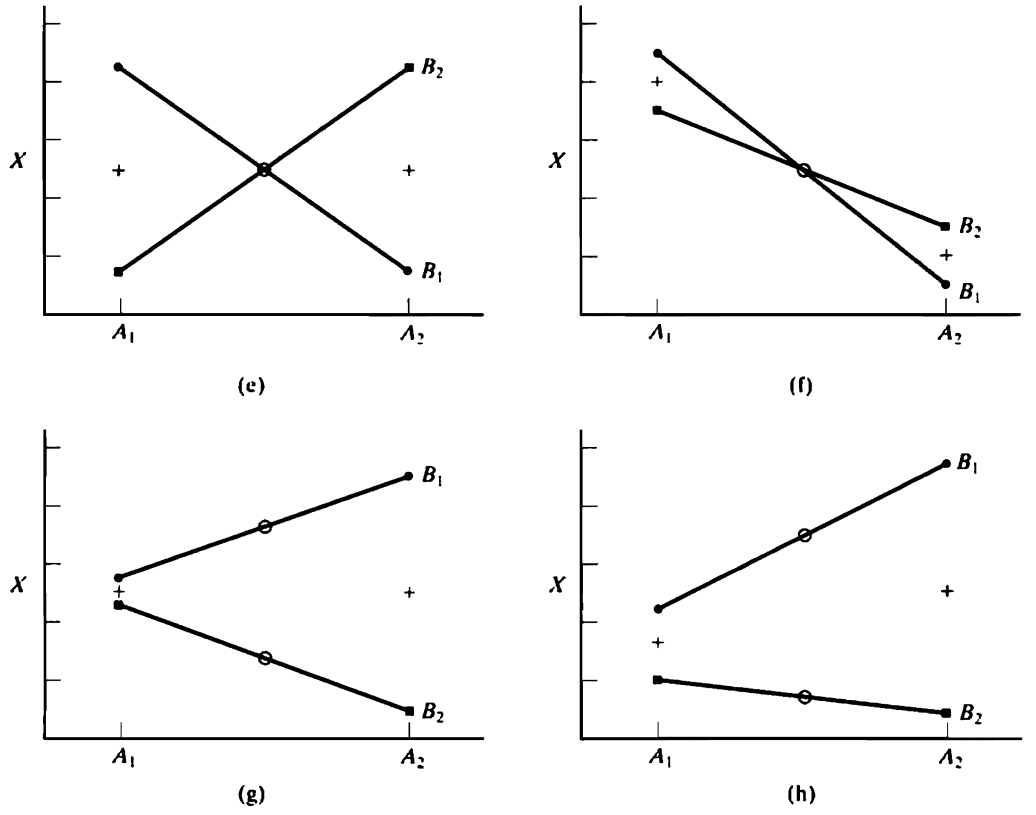


FIGURE 12.2: *(continued)*

(d) Model I ANOVA. Recall, from Section 10.1f, the distinction between fixed and random factors. Example 12.1 is an ANOVA where the levels of both factors are fixed; we did not simply pick these levels at random. A factorial analysis of variance in which all (in this case both) factors are fixed effects is termed a *Model I ANOVA*. In such a model, the null hypothesis of no difference among the levels of a factor is tested using F = factor MS/error MS. In Example 12.2, the appropriate F tests conclude that there is a highly significant effect of the hormone treatment on the mean plasma calcium content, and that there is not a significantly different mean plasma calcium concentration between males and females.

In addition, we can test for significant interaction in a Model I ANOVA by F = interaction MS/error MS and find, in our present example, that there is no significant interaction between the sex of the bird and whether it had the hormone treatment. This is interpreted to mean that the effect of the hormone treatment on calcium is not different in males and females (i.e., the effect of the hormone is not dependent on the sex of the bird). This concept of interaction (or its converse, independence) is analogous to that employed in the analysis of contingency tables (see Chapter 23).

If, in a two-factor analysis of variance, the effects of one or both factors are significant, the interaction effect may or may not be significant. In fact, it is possible to encounter situations where there is a significant interaction even though each of the individual factor effects is judged to be insignificant. A significant interaction implies that the difference among levels of one factor is not constant at all levels of the second factor. Thus, it is generally not useful to speak of a factor effect—even if its F is significant—if there is a significant interaction effect.

TABLE 12.3: Computation of the F Statistic for Tests of Significance in a Two-Factor ANOVA with Replication

Hypothesized effect	Model I (factors A and B both fixed)	Model II (factors A and B both random)	Model III (factor A fixed: factor B random)
Factor A	$\frac{\text{factor } A \text{ MS}}{\text{error MS}}$	$\frac{\text{factor } A \text{ MS}}{A \times B \text{ MS}}$	$\frac{\text{factor } A \text{ MS}}{A \times B \text{ MS}}$
Factor B	$\frac{\text{factor } B \text{ MS}}{\text{error MS}}$	$\frac{\text{factor } B \text{ MS}}{A \times B \text{ MS}}$	$\frac{\text{factor } B \text{ MS}}{\text{error MS}}$
$A \times B$ interaction	$\frac{A \times B \text{ MS}}{\text{error MS}}$	$\frac{A \times B \text{ MS}}{\text{error MS}}$	$\frac{A \times B \text{ MS}}{\text{error MS}}$

(e) Model II ANOVA. If a factorial design is composed only of factors with random levels, then we are said to be employing a *Model II ANOVA* (a relatively uncommon situation). In such a case, where two factors are involved, the appropriate hypothesis testing for significant factor effects is accomplished by calculating F = factor MS/interaction MS (see Table 12.3). We test for the interaction effect, as before, by F = interaction MS/error MS, and it is generally not useful to declare factor effects significant if there is a significant interaction effect. The Model II ANOVA for designs with more than two factors will be discussed in Chapter 14.

(f) Model III ANOVA. If a factorial design has both fixed-effect and random-effect factors, then it is said to be a *mixed-model*,* or a *Model III ANOVA*. The appropriate F statistics are calculated as shown in Table 12.3. Special cases of this will be discussed in Section 12.4. This book observes Voss's (1999) "resolution" of a controversy over the appropriate F for testing a factor effect in mixed models.

(g) Underlying Assumptions. The assumptions underlying the appropriate application of the two-factor analysis of variance are basically those for the single-factor ANOVA (Section 10.1g): The data in each cell came at random from a normally distributed population of measurements and the variance is the same in all of the populations represented by the cells. This population variance is estimated by the within-cells mean square (i.e., the error mean square).

Although these hypothesis tests are robust enough that minor deviations from these assumptions will not appreciably affect them, the probabilities associated with the calculated F values lose dependability as the sampled populations deviate from normality and homoscedasticity, especially if the populations have skewed distributions. If there is doubt about whether the data satisfy these assumptions, then conclusions regarding the rejection of a null hypothesis should not be made if the associated P is near the α specified for the test.

Few alternatives to the ANOVA exist when the underlying assumptions are seriously violated. In a procedure analogous to that described in Section 10.1g for single-factor analysis of variance with heterogeneous group variances, Brown and Forsythe (1974b) present a two-factor ANOVA procedure applicable when the cell variances are not assumed to have come from populations with similar variances. In some cases an appropriate data transformation (Chapter 13) can convert a set of data so the extent of nonnormality and heteroscedasticity is small. As indicated at the end

*The term *mixed model* was introduced by A. M. Mood in 1950 (David, 1995).

of the introduction to this chapter, there appears to be no nonparametric procedures to be strongly recommended for factorial ANOVA, with the exception of that of Section 12.7.

(h) Pooling Mean Squares. If it is not concluded that there is a significant interaction effect, then the interaction MS and the within-cells (i.e., the error) MS are theoretically estimates of the same population variance. Because of this, some authors suggest the pooling of the interaction and within-cells sums of squares and degrees of freedom in such cases. From these pooled SS and DF values, one can obtain a pooled mean square, which then should be a better estimate of the population random error (i.e., within-cell variability) than either the error MS or the interaction MS alone; and the pooled MS will always be a quantity between the interaction MS and the error MS.

The conservative researcher who does not engage in such pooling can be assured that the probability of a Type I error is at the stated α level. But the probability of a Type II error may be greater than is acceptable to some. The chance of the latter type of error is reduced by the pooling described, but confidence in stating the probability of committing a Type I error may be reduced (Brownlee, 1965: 509). Rules of thumb for deciding when to pool have been proposed (e.g., Paull, 1950; Bozivich, Bancroft, and Hartley, 1956), but statistical advice beyond this book should be obtained if such pooling is contemplated. The analyses in this text will proceed according to the conservative nonpooling approach, which Hines (1996), Mead, Bancroft, and Han (1995), and Myers and Well (2003: 333) conclude is generally advisable.

(i) Multiple Comparisons. If significant differences are concluded among the levels of a factor, then the multiple comparison procedures of Section 11.1, 11.2, 11.3, or 11.4 may be employed. For such purposes, s^2 is the within-cells MS, ν is the within-cells DF, and the n of Chapter 11 is replaced in the present situation with the total number of data per level of the factor being tested (i.e., what we have noted in this section as bn data per level of factor A and an data per level of factor B). If there is significant interaction between the two factors, then the means of levels should not be compared. Instead, multiple comparison testing may be performed among cell means.

(j) Confidence Limits for Means. We may compute confidence intervals for population means of levels of a fixed factor by the methods in Section 10.2. The error mean square, s^2, is the within-cells MS of the present discussion; the error degrees of freedom, ν, is the within-cells DF; and n in Section 10.2 is replaced in the present context by the total number of data in the level being examined. Confidence intervals for differences between population means are obtained by the procedures of Section 11.2. This is demonstrated in Example 12.3.

EXAMPLE 12.3 Confidence Limits for the Results of Example 12.2

We concluded that mean plasma calcium concentration is different between birds with the hormone treatment and those without.

$$\overline{X}_1 = \frac{\text{total for nonhormone group}}{\text{number in nonhormone group}} = \frac{135.0 \text{ mg/100 ml}}{10} = 13.50 \text{ mg/100 ml}$$

$$\overline{X}_2 = \frac{\text{total for hormone group}}{\text{number in hormone group}} = \frac{301.5 \text{ mg/100 ml}}{10} = 30.15 \text{ mg/100 ml}$$

where N is the total number of data in all cells.* (For example, in Figure 12.3c, there are two data on row 3, column 1; and (16)(9)/72 = 2. The appropriate hypothesis tests are the same as those in Section 12.1. The sums of squares, degrees of freedom, and mean squares may be calculated by some factorial ANOVA computer programs. Or, the machine formulas referred to in Table 12.1 may be applied with the following modifications: For sums of squares, substitute n_{ij} for n in Equations 12.17 and 12.18, and use

$$\text{cells SS} = \sum_{i=1}^{a}\sum_{j=1}^{b}\frac{\left(\sum_{l=1}^{n_{ij}} X_{ijl}\right)^2}{n_{ij}} : - C , \tag{12.23}$$

$$\text{factor } A \text{ SS} = \sum_{i=1}^{a}\frac{\left(\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl}\right)^2}{n_{ij}} : - C , \tag{12.24}$$

$$\text{factor } B \text{ SS} = \sum_{j=1}^{b}\frac{\left(\sum_{i=1}^{a}\sum_{l=1}^{n_{ij}} X_{ijl}\right)^2}{n_{ij}} : - C , \tag{12.25}$$

$$\text{within-cells (error) DF} = \sum_{i=1}^{a}\sum_{j=1}^{b}(n_{ij} - 1) : . \tag{12.26}$$

(b) Disproportional Replication; Missing Data. In factorial analysis of variance, it is generally advisable to have data with equal replication in the cells (Section 12.1), or at least to have proportional replication (Section 12.2a). If equality or proportionality is not the case, we may employ computer software capable of performing such analyses of variance with disproportional replication (see Section 14.5). Alternatively, if only a very few cells have numbers of data in excess of those representing equal or proportional replications, then data may be deleted, at random, within such cells, so that equality or proportionality is achieved. Then the ANOVA can proceed as usual, as described in Section 12.1 or 12.2a.

If one cell is one datum short of the number required for equal or proportional replication, a value may be estimated† for inclusion in place of the missing datum, as follows (Shearer, 1973):

$$\hat{X}_{ijl} = \frac{aA_i + bB_j - \sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl}}{N + 1 - a - b}, \tag{12.27}$$

*The number of replicates in each of the ab cells need not be checked against Equation 12.22 to determine whether proportional replication is present. One need check only one cell in each of $a - 1$ levels of factor A and one in each of $b - 1$ levels of factor B (Huck and Layne, 1974).

†The estimation of missing values is often referred to as *imputation* and is performed by some computer routines. However, there are many different methods for imputing missing values, especially when more than one datum is missing, and these methods do not all yield the same

where $\hat{X}_{ijl}$ is the estimated value for replicate l in level i of factor A and level j of factor B; A_i is the sum of the other data in level i of factor A; B_j is the sum of the other data in level j of factor B; $\sum\sum\sum X_{ijl}$ is the sum of all the known data, and N is the total number of data (including the missing datum) in the experimental design. For example, if datum X_{124} had been missing in Example 12.1, it could have had a quantity inserted in its place, estimated by Equation 12.27, where $a = 2$, $b = 2$, $N = 20$, $A_i = A_1 =$ the sum of all known data from animals receiving no hormone treatment; $B_j = B_2 =$ the sum of all known data from males; and $\sum\sum\sum X_{ijl} =$ the sum of all 19 known data from both hormone treatments and both sexes. After the missing datum has been estimated, it is inserted into the data set and the ANOVA computations may proceed, with the provision that a missing datum is not counted in determining total and within-cells degrees of freedom. (Therefore, if a datum were missing in Example 12.1, the total DF would have been 18 and the within-cells DF would have been 15.)

If more than one datum is missing (but neither more than 10% of the total number of data nor more data than the number of levels of any factor), then Equation 12.27 could be used iteratively to derive estimates of the missing data (e.g., using cell means as initial estimates). The number of such estimates would not enter into the total or within-cells degrees-of-freedom determinations.

If only a few cells (say, no more than the number of levels in either factor) are each one datum short of the numbers required for equal or proportional replication, then the mean of the data in each such cell may be inserted as an additional datum in that cell. In the latter situation, the analysis proceeds as usual but with the total DF and the within-cells DF each being determined without counting such additional inserted data. Instead of employing these cell means themselves, however, they could be used as starting values for employing Equation 12.27 in iterative fashion. Another procedure for dealing with unequal, and nonproportional, replication is by so-called unweighted means analysis, which employs the harmonic mean of the n_{ij}'s. This will not be discussed here.

None of these procedures is as desirable as when the data are equally or proportionally distributed among the cells.

12.3 TWO-FACTOR ANALYSIS OF VARIANCE WITHOUT REPLICATION

It is generally advisable that a two-factor experimental design have more than one datum in each cell, but situations are encountered in which there is only one datum for each combination of factors (i.e., $n = 1$ for all cells). It is sometimes feasible to collect additional data, to allow the use of the procedures of Section 12.1 or 12.2, but it is also possible to perform a two-factorial ANOVA with nonreplicated data. In a situation of no replication, each datum may be denoted by a double subscript, as X_{ij}, where i denotes a level of factor A and j indicates a level of factor B.

For a levels of factor A and b levels of factor B, the appropriate computations of sums of squares, degrees of freedom, and mean squares are shown directly below. These are analogous to equations in Section 12.1, modified by eliminating n and any summation within cells.

$$\text{total SS} = \sum^{a}\sum^{b}\left(X_{ij} - \overline{X}\right)^2, \tag{12.28}$$

where the mean of all N data (and $N = ab$) is

$$\overline{X} = \frac{\sum_{i=1}^{a}\sum_{j=1}^{b} X_{ij}}{N}. \tag{12.29}$$

Further,

$$\text{factor } A \text{ SS} = b\sum_{i=1}^{a}\left(\overline{X}_{i\cdot} - \overline{X}\right)^2; \tag{12.30}$$

$$\text{factor } B \text{ SS} = a\sum_{j=1}^{a}\left(\overline{X}_{\cdot j} - \overline{X}\right)^2. \tag{12.31}$$

When there is no replication within cells (i.e., $n = 1$), the cells SS of Section 12.1 is identical to the total SS, and the cells DF is the same as the total DF. Consequently, the within-cells sum of squares and degrees of freedom are both zero; that is, with only one datum per cell, there is no variability within cells. The variability among the N data that is not accounted for by the effects of the two factors is the *remainder** variability:

$$\text{remainder SS} = \text{total SS} - \text{factor } A \text{ SS} - \text{factor } B \text{ SS} \tag{12.32}$$

$$\text{remainder DF} = \text{total DF} - \text{factor } A \text{ DF} - \text{factor } B \text{ DF} \tag{12.33}$$

These sums of squares and degrees of freedom, and the relevant mean squares, are summarized in Table 12.4. Note that Equations 12.32 and 12.33 are what are referred to as "interaction" quantities when replication is present; with no replicates it is not possible to assess interaction in the population that was sampled. Table 12.5

TABLE 12.4: Summary of the Calculations for a Two-Factor Analysis of Variance with No Replication

Source of variation	Sum of squares (SS)	Degrees of freedom (DF)	Mean square (MS)
Total $[X_{ij} - \overline{X}]$	Equation 12.27 or 12.34	$N - 1$	
Factor A $[\overline{X}_{i\cdot} - \overline{X}]$	Equation 12.29 or 12.35	$a - 1$	$\frac{\text{factor } A \text{ SS}}{\text{factor } A \text{ DF}}$
Factor B $[\overline{X}_{\cdot j} - \overline{X}]$	Equation 12.30 or 12.26	$b - 1$	$\frac{\text{factor } B \text{ SS}}{\text{factor } B \text{ DF}}$
Remainder	Equation 12.31	$(a - 1)(b - 1)$ or total DF − factor A DF − factor B DF	$\frac{\text{remainder SS}}{\text{remainder DF}}$

Note: For each source of variation, the bracketed quantity indicates the variation being assessed; a is the number of levels in factor A; b is the number of factors in factor B; N is the total number of data (which is ab); X_{ij} is the datum in level i of factor A and level j of factor B; $\overline{X}_{i\cdot}$ is the mean of the data in level i of factor A; $\overline{X}_{\cdot j}$ is the mean of the data in level j of factor B; and $\overline{X}$ is the mean of all N data.

*Some authors refer to "remainder" as "error" or "residual."

TABLE 12.5: Computation of the F Statistic for Tests of Significance in a Two-Factor ANOVA without Replication

(a) If It Is Assumed That There May Be a Significant Interaction Effect

Hypothesized effect	Model I (factors A and B both fixed)	Model II (factors A and B both random)	Model III (factor A fixed; factor B random)
Factor A	Test with caution*	$\frac{\text{factor } A \text{ MS}}{\text{remainder MS}}$	$\frac{\text{factor } A \text{ MS}}{\text{remainder MS}}$
Factor B	Test with caution*	$\frac{\text{factor } B \text{ MS}}{\text{remainder MS}}$	Test with caution*
$A \times B$ interaction	No test possible	No test possible	No test possible

*Analysis can be performed as in Model II, but with increased chance of Type II error.

(b) If It Is Correctly Assumed That There Is No Significant Interaction Effect

Hypothesized effect	Model I	Model II	Model III
Factor A	$\frac{\text{factor } A \text{ MS}}{\text{remainder MS}}$	$\frac{\text{factor } A \text{ MS}}{\text{remainder MS}}$	$\frac{\text{factor } A \text{ MS}}{\text{remainder MS}}$
Factor B	$\frac{\text{factor } B \text{ MS}}{\text{remainder MS}}$	$\frac{\text{factor } B \text{ MS}}{\text{remainder MS}}$	$\frac{\text{factor } B \text{ MS}}{\text{remainder MS}}$
$A \times B$ interaction	No test possible	No test possible	No test possible

summarizes the significance tests that may be performed to test hypotheses about each of the factors. Testing for the effect of each of the two factors in a Model I analysis (or testing for the effect of the random factor in a Model III design) is not advisable if there may, in fact, be interaction between the two factors (and there will be decreased test power); but if a significant difference is concluded, then that conclusion may be accepted. The presence of interaction, also called nonadditivity, may be detectable by the testing procedure of Tukey (1949).

(a) "Machine Formulas." If there is no replication in a two-factor ANOVA, the machine formulas for sums of squares are simplifications of those in Section 12.1b:

$$C = \frac{\left(\sum_{i=1}^{a}\sum_{j=1}^{b} X_{ij}\right)^2}{N}, \tag{12.34}$$

$$\text{total SS} = \sum_{i=1}^{a}\sum_{j=1}^{b} X_{ij}^2 - C, \tag{12.35}$$

$$\text{factor } A \text{ SS} = \frac{\sum_{i=1}^{a}\left(\sum_{j=1}^{b} X_{ij}^2\right)}{b} - C, \tag{12.36}$$

$$\text{factor } B \text{ SS} = \frac{\sum_{j=1}^{b}\left(\sum_{i=1}^{a} X_{ij}^2\right)}{a} - C, \tag{12.37}$$

and the remainder sum of squares is as in Equation 12.32.

(b) Multiple Comparisons and Confidence Limits. In a two-factor ANOVA with no replication, the multiple-comparison and confidence-limit considerations of Sections 12.1i and 12.1j may be applied. However, there is no within-cells (error) mean square or degrees of freedom in the absence of replication. If it can be assumed that there is no interaction between the two factors, then the remainder MS may be employed where s^2 is specified in those sections, the remainder DF is used in place of ν, a is the same as an, and b is the same as bn. If, however, there may be interaction, then multiple comparisons and confidence limits should be avoided.

12.4 TWO-FACTOR ANALYSIS OF VARIANCE WITH RANDOMIZED BLOCKS OR REPEATED MEASURES

The analysis of variance procedure of Section 10.1 (the *completely randomized design*) is for situations where the data are all independent of each other and the experimental units (e.g.,the pigs in Example 10.1) are assigned to the k treatments in a random fashion (that is, random except for striving for equal numbers in each treatment). The following discussion is of two types of ANOVA, for the same null and alternate hypotheses as in Section 10.1, in which each datum in one of the k groups *is* related to one datum in each of the other groups.

(a) Randomized Blocks. To address the hypotheses of Example 10.1, each of four animals from the same litter could be assigned to be raised on each of four diets. The body weights of each set of four animals (i.e., the data for each litter) would be said to constitute a *block*, for the data in a litter are related to each other (namely by having the same mother). With a experimental groups (denoted as k in Chapter 10) and b blocks, there would be $N = ab$ data in the analysis. The concept of blocks is an extension, for more than two groups, the concept of pairs (Section 9.1, which deals with two groups). This experimental plan is called a *randomized-complete-block design*, and each block contains a measurement for each of the a treatments. Only complete blocks will be considered here, so this will simply be called a *randomized-block design*.* When the analysis employs blocks of data within which the data are related, the hypothesis testing of differences among groups can be more powerful than in the completely randomized design.

An illustration of a randomized-block ANOVA is in Example 12.4. The intent of the experiment shown is to determine whether there is a difference among three anesthetic drugs in the time it takes for the anesthetic to take effect when injected intramuscularly into cats of a specified breed. Three cats are obtained from each of five laboratories; because the laboratories may differ in factors such as the food and exercise the animals have had, the three from each laboratory are considered to be a block. Thus, the experiment has $a = 3$ treatment groups and $b = 5$ blocks, and the variable in anesthetic group i and block j is indicated as X_{ij}. The sum of the data in group i can be denoted as $\sum_{j=1}^{b} X_{ij}$, the total of the measurements in block j as $\sum_{i=1}^{a} X_{ij}$, and the sum of all ab data as $N = \sum_{i=1}^{a} \sum_{j=1}^{b} X_{ij}$. In this example, there is only one datum in each of the ab cells (i.e., one per combination of treatment and block), a very common situation when working with randomized blocks.

In Example 12.4, the interest is whether there is any difference among the effects of the different anesthetic drugs, not whether there is any difference due to laboratory source of the animals. (Indeed, the factor defining the blocks is sometimes referred to

*The randomized-block experimental design was developed and so named by R. A. Fisher (1926; David, 1995).

EXAMPLE 12.4 A Randomized Complete Block Analysis of Variance (Model III Two-Factor Analysis of Variance) without Within-Cell Replication

H_0: The mean time for effectiveness is the same for all three anesthetics (i.e., $\mu_1 = \mu_2 = \mu_3$).

H_A: The mean time for effectiveness is not the same for all three anesthetics.

$\alpha = 0.05$

Each block consists of three cats from a single source, and each block is from a different source. Within a block, the cats are assigned one of the anesthetics at random, by numbering the cats 1, 2, and 3 and assigning each of them treatment 1, 2, or 3 at random. For this experiment the randomly designated treatments, from 1 to 3, for each block were as follows, with the anesthetic's time for effect (in minutes) given in parentheses:

	Animal 1	*Animal 2*	*Animal 3*
Block 1:	Treatment 3 (10.75)	Treatment 1 (8.25)	Treatment 2 (11.25)
Block 2:	Treatment 1 (10.00)	Treatment 3 (11.75)	Treatment 2 (12.50)
Block 3:	Treatment 3 (11.25)	Treatment 1 (10.25)	Treatment 2 (12.00)
Block 4:	Treatment 1 (9.50)	Treatment 2 (9.75)	Treatment 3 (9.00)
Block 5:	Treatment 2 (11.00)	Treatment 1 (8.75)	Treatment 3 (10.00)

These data are rearranged as follows in order to tabulate the treatment, block, and grand totals (and, if not using the machine formulas, the treatment, block, and grand means).

Block (j)	*Treatment* (i) 1	2	3	Block Total $\left(\sum_{i=1}^{a} X_{ij}\right)$	Block Mean $\left(\overline{X}_{\cdot j}\right)$
1	8.25	11.25	10.75	30.25	10.08
2	11.00	12.50	11.75	35.25	11.75
3	10.25	12.00	11.25	33.50	11.17
4	9.50	9.75	9.00	28.25	9.42
5	8.75	11.00	10.00	29.75	9.92
Treatment total: $\sum_{j=1}^{b} X_{ij}$	47.75	56.50	52.75		
Treatment mean: $\overline{X}_{i\cdot}$	9.55	11.30	10.55		

Grand total $= \sum_{i=1}^{a}\sum_{j=1}^{b} X_{ij} = 157.00$ Grand mean $= \overline{X} = 10.47$

The sums of squares required in the following table may be obtained using the equations in Section 12.3, as referenced in Table 12.4.

Source of variation	SS	DF	MS
Total	21.7333	14	
Treatments	7.7083	2	3.8542
Blocks	11.0667	4	
Remainder	2.9583	8	0.3698

$$F = \frac{\text{treatments MS}}{\text{remainder MS}} = \frac{3.8542}{0.3698} = 10.4$$

$F_{0.05(1),2,8} = 4.46$, so reject H_0.

$0.005 < P < 0.01$ $[P = 0.0060]$

as a "nuisance factor" or "nuisance variable.") The anesthetics, therefore, are three levels of a fixed-effects factor, and the laboratories are five levels of a random-effects factor. So the completely randomized experimental design calls for a mixed-model (i.e., Model III) analysis of variance (Section 12.1f). Blocking by laboratory is done to account for more of the total variability among all N data than would be accounted for by considering the fixed-factor effects alone. This will decrease the mean square in the denominator of the F that assesses the difference among the treatments, with the intent of making the ANOVA more powerful than if the data were not collected in blocks.

The assignment of an experimental unit to each of the animals in a block should be done at random. For this purpose, Appendix Table B.41 or other source of random numbers may be consulted. In the present example, the experimenter could arbitrarily assign numbers 1, 2, and 3 to each cat from each laboratory. The random-number table should then be entered at a random place, and for each block a random sequence of the numerals 1, 2, and 3 (ignoring all other numbers and any repetition of a 1, 2, or 3) will indicate which treatments should be applied to the animals numbered 1, 2, and 3 in that block. So, in Example 12.4, a sequence of animals numbered 3, 1, 2 was obtained for the first block; 1, 3, 2 for the second; 3, 2, 1 for the third; and so on.

The randomized-block experimental design has found much use in agricultural research, where b plots of ground are designated as blocks and where the environmental (for example, soil and water) conditions are very similar within each block (though not necessarily among blocks). Then a experimental treatments (e.g., fertilizer of pesticide treatment) are applied to random portions of each of the b blocks.

(b) Randomized Blocks with Replication. It is common for the randomized-complete-block experimental design to contain only one datum per cell. That is what is demonstrated in Example 12.4, with the calculation of F executed as shown in the last column of Tables 12.5a and 12.5b. If there are multiple data per cell (what is known as the generalized randomized-block design), this would be handled

as a mixed-model two-factor ANOVA with replication. Doing so would obtain the mean squares and degrees of freedom as indicated earlier in this chapter; and the appropriate F's would be those indicated in the last column of Table 12.3. A case where this would be applicable is where the experiment of Example 12.4 employed a total of six cats—instead of three—from each laboratory, assigning two of the six at random to each of the three treatments.

(c) Repeated Measures. The hypotheses of Example 12.4 could also be tested using an experimental design differing from, but related to, that of randomized blocks. In an experimental procedure using what are called *repeated measures*, each of b experimental animals would be tested with one of the a anesthetic drugs; then, after the effects of the drug had worn off, one of the other anesthetics would be applied to the same animal; and after the effects of that drug were gone, the third drug would be administered to that animal. Thus, b experimental animals would be needed, far fewer than the ab animals required in the randomized-block experiment of Example 12.4, for each block of data contains a successive measurements from the same experimental animal (often referred to as an experimental "subject"). If possible, the application of the a treatments to each of the b subjects should be done in a random sequence, comparable to the randomization within blocks in Section 12.4a. Also, when collecting data for a repeated-measures analysis of variance, sufficient time should be allowed between successive treatments so the effect of a treatment is not contaminated with the effect of the previous treatment (i.e., so there is no "carryover effect" from treatment to treatment).*

Thus, the arrangement of data from a repeated-measures experiment for the hypotheses of Example 12.4 would look exactly like that in that example, except that each of the five blocks of data would be measurements from a single animal, instead of from a animals, from a specified laboratory.

There are some repeated-measures studies where the treatments are not administered in a random sequence to each subject. For example, we might wish to test the effect of a drug on the blood sugar of horses at different times (perhaps at 1, 2, and 5 hours) after the drug's administration. Each of b horses ("subjects") could be given the drug and its blood sugar measured before administering the drug and subsequently at each of the three specified times (so a would be 4). In such a situation, the levels of factor A (the four times) are fixed and are the same for all blocks, and carryover effects are a desired part of the study.†

The repeated-measures experimental design is commonly used by psychological researchers, where the behavioral response of each of several subjects is recorded for each of several experimental circumstances.

(d) Randomized-Block and Repeated-Measures Assumptions. In a randomized-block or repeated-measures experiment, we assume that there are correlations among the measurements within a block or among measurements repeated on a subject. For the randomized-block data in Example 12.4, it may be reasonable to suppose that if an animal is quickly affected by one anesthetic, it will be quickly affected by each

*Although the experiment should be conducted to avoid carryover effects, the times of administering the drug (first, second, or third) could be considered the levels of a third factor, and a three-factor ANOVA could be performed in what is referred to as a "crossover experimental design" (described in Section 14.1a).

†Kirk (1995: 255) calls randomized levels of factor A within blocks a "subjects-by-treatment" experimental design and uses the term *subjects-by-trials* to describe a design where the sequence of application of the levels of factor A to is the same in each block.

of the others. And for the repeated-measures situation described in Section 12.4c, it might well be assumed that the effect of a drug at a given time will be related to the effect at a previous time. However, for the probability of a calculated F to be compared dependably to tabled values of F, there should be equal correlations among all pairs of groups of data. So, for the experiment in Example 12.4, the correlation between the data in groups 1 and 2 is assumed to be the same as the correlation between the data in groups 1 and 3, and the same as that between data in groups 2 and 3. This characteristic, referred to as *compound symmetry*, is related to what statisticians call *sphericity* (e.g., Huynh and Feldt, 1970), or *circularity* (e.g., Rouanet and Lépine, 1970), and it—along with the usual ANOVA assumptions (Section 12.1g)—is an underlying assumption of randomized-block and repeated-measures analyses of variance. Violation of this assumption is, unfortunately, common but difficult to test for, and the investigator should be aware that the Type I error in such tests may be greater than the specified α. An alternative procedure for analyzing data from repeated-measures experiments, one that does not depend upon the sphericity assumption, is *multivariate analysis of variance* (see Chapter 16), which has gained in popularity with the increased availability of computer packages to handle the relatively complex computations. This assumption and this alternative are discussed in major works on analysis of variance and multivariate analysis (e.g., Girden, 1992; Kirk, 1995; Maxwell and Delaney, 2004; O'Brien and Kaiser, 1985; and Stevens, 2002).

If there are missing data, the considerations of Section 12.2b apply. If the experimental design has only one datum for each combination of the factors, and one of the data is missing, then the estimation of Equation 12.26 becomes

$$\hat{X}_{ij} = \frac{aA_i + bB_j - \sum_{i=1}^{a}\sum_{j=1}^{b} X_{ij}}{(a-1)(b-1)}. \tag{12.38}$$

If more than one datum is missing in a block, the entire block can be deleted from the analysis.

(e) More Than One Fixed-Effects Factor. There are many possible experimental designs when the effects of more than one factor are being assessed. One other situation would be where the experiment of Example 12.4 employed blocks as a random-effects factor along with *two* fixed-effects factors, perhaps the drug and the animal's sex. The needed computations of sums of squares, degrees of freedom, and mean squares would likely be performed by computer, and Appendix D (Section D.3b for this hypothetical example) would assist in testing the several hypotheses.

12.5 MULTIPLE COMPARISONS AND CONFIDENCE INTERVALS IN TWO-FACTOR ANALYSIS OF VARIANCE

If a two-factor analysis of variance reveals a significant effect among levels of a fixed-effects factor having more than two levels, then we can determine between which levels the significant difference(s) occur(s). If the desire is to compare all pairs of means for levels in a factor, this may be done using the Tukey test (Section 11.1). The appropriate SE is calculated by Equation 11.2, substituting for n the number of data in each level (i.e., there are bn data in each level of factor A and an data in levels of factor B); s^2 is the within-cells MS and ν is the within-cells degrees of freedom. If there is no replication in the experiment, then we are obliged to use the remainder MS in place of the within-cells MS and to use the remainder DF as ν.

The calculation of confidence limits for the population mean estimated by each significantly different level mean can be performed by the procedures of Section 11.2, as can the computation of confidence limits for differences between members of pairs of significantly different level means.

If it is desired to compare a control mean to each of the other level means, Dunnett's test, described in Section 11.3, may be used; and that section also shows how to calculate confidence limits for the differences between such means. Scheffé's procedure for multiple contrasts (Section 11.4) may also be applied to the levels of a factor, where the critical value in Equation 11.18 employs either a or b in place of k (depending, respectively, on whether the levels of factor A or B are being examined), and the within-cells DF is used in place of $N - k$. In all references to Chapter 11, n in the standard-error computation is to be replaced by the number of data per level, and s^2 and ν are the within-cells MS and DF, respectively.

Multiple-comparison testing and confidence-interval determination are appropriate for levels of a fixed-effects factor but are not used with random-effects factors.

(a) If Interaction Is Significant. On concluding that there is a significant interaction between factors A and B, it is generally not meaningful to test for differences among levels of either of the factors. However, it may be desired to perform multiple comparison testing to seek significant differences among cell means. This can be done with any of the above-mentioned procedures, where n (the number of data per cell) is appropriate instead of the number of data per level. For the Scheffé test critical value (Equation 11.18), k is the number of cells (i.e., $k = ab$) and $N - k$ is the within-cells DF.

(b) Randomized Blocks and Repeated Measures. In randomized-block and repeated-measures experimental designs, the sphericity problem mentioned in Section 12.4d is reason to recommend that multiple-comparison testing not use a pooled variance but, instead, employ the Games and Howell procedure presented in Section 11.1b (Howell, 1997: 471). In doing so, the two sample sizes (n_B and n_A) for calculating SE (in Equation 11.5) will each be b.

An analogous recommendation when the Dunnett test (Section 11.3) is performed would be to use Equation 11.11a in favor of Equation 11.11. And for multiple contrasts, the procedures of Section 11.4a would be followed.

A similar recommendation for confidence limits for each mean is to use the variance associated with that mean instead of a pooled variance. Confidence limits for the difference between two means would employ Equation 11.7.

12.6 SAMPLE SIZE, DETECTABLE DIFFERENCE, AND POWER IN TWO-FACTOR ANALYSIS OF VARIANCE

The concepts and procedures of estimating power, sample size, and minimum detectable difference for a single-factor ANOVA are discussed in Section 10.3, and the same considerations can be applied to fixed-effects factors in a two-factor analysis of variance. (The handling of the fixed factor in a mixed-model ANOVA will be explained in Section 12.6e.)

We can consider either factor A or factor B (or both, but one at a time). Let us say k' is the number of levels of the factor being examined. (That is, $k' = a$ for factor A; $k' = b$ for factor B.) Let us define n' as the number of data in each level. (That is, $n' = bn$ for factor A; $n' = an$ for factor B.) We shall also have s^2 refer

to the within-cells MS. The mean of the population from which level m came is denoted as μ_m.

(a) Power of the Test. We can now generalize equation 10.32 as

$$\phi = \sqrt{\frac{n' \sum_{m=1}^{k'} (\mu_m - \mu)^2}{k's^2}}, \tag{12.39}$$

Equation 10.33 as

$$\mu = \frac{\sum_{m=1}^{k'} \mu_m}{k'}, \tag{12.40}$$

and Equation 10.34 as

$$\phi = \sqrt{\frac{n'\delta^2}{2k's^2}}, \tag{12.41}$$

in order to estimate the power of the analysis of variance in detecting differences among the population means of the levels of the factor under consideration.

After any of the computations of ϕ have taken place, either as above or as below, then we proceed to employ Appendix Figure B.1 just as we did in Section 10.3, with ν_1 being the factor DF (i.e., $k' - 1$), and ν_2 referring to the within-cells (i.e., error) DF.

Later in this book there are examples of ANOVAs where the appropriate denominator for F is some mean square other than the within-cells MS. In such a case, s^2 and ν_2 will refer to the relevant MS and DF.

(b) Sample Size Required. By using Equation 12.41 with a specified significance level, and detectable difference between means, we can determine the necessary minimum number of data per level, n', needed to perform the experiment with a desired power. This is done iteratively, as it was in Example 10.6.

(c) Minimum Detectable Difference. In Example 10.7 we estimated the smallest detectable difference between population means, given the significance level, sample size, and power of a one-way ANOVA. We can pose the same question in the two-factor experiment, generalizing Equation 10.35 as

$$\delta = \sqrt{\frac{2k's^2\phi^2}{n'}}. \tag{12.42}$$

(d) Maximum Number of Levels Testable. The considerations of Example 10.8 can be applied to the two-factor case by using Equation 12.41 instead of Equation 10.34.

(e) Mixed-Model ANOVA. All the preceding considerations of this section can be applied to the fixed factor in a mixed-model (Model III) two-factor analysis of variance with the following modifications.

For factor A fixed, with replication within cells, substitute the interaction MS for the within-cells MS, and use the interaction DF for ν_2.

For factor A fixed, with no replication (i.e., a randomized block experimental design), substitute the remainder MS for the within-cells MS, and use the remainder DF for ν_2. If there is no replication, then $n = 1$, and $n' = b$. (Recall that if there is no replication, we do not test for interaction effect.)

12.7 NONPARAMETRIC RANDOMIZED-BLOCK OR REPEATED-MEASURES ANALYSIS OF VARIANCE

Friedman's* test (1937, 1940) is a nonparametric analysis that may be performed on a randomized-block experimental design, and it is especially useful with data that do not meet the parametric analysis of variance assumptions of normality and homoscedasticity, namely that the k samples (i.e., the k levels of the fixed-effect factor) come from populations that are each normally distributed and have the same variance. Kepner and Robinson (1988) showed that the Friedman test compares favorably with other nonparametric procedures. If the assumptions of the parametric ANOVA are met, the Friedman test will be $3k/[\pi(k + 1)]$ as powerful as the parametric method (van Elteren and Noether, 1959). (For example, the power of the nonparametric test ranges from 64% of the power of the parametric test when $k = 2$, to 72% when $k = 3$, to 87% when $k = 10$, to 95% when k approaches ∞.) If the assumptions of the parametric test are seriously violated, it should not be used and the Friedman test is typically advisable. Where $k = 2$, the Friedman test is equivalent to the sign test (Section 24.6).

In Example 12.5, Friedman's test is applied to the data of Example 12.4. The data within each of the b blocks are assigned ranks. The ranks are then summed for each of the a groups, each rank sum being denoted as R_i. The test statistic, χ_r^2, is calculated as†

$$\chi_r^2 = \frac{12}{ba(a + 1)} \sum_{i=1}^{a} R_i^2 - 3b(a + 1). \tag{12.44}$$

Critical values of χ_r^2, for many values of a and b, are given in Appendix Table B.14.

When $a = 2$, the Wilcoxon paired-sample test (Section 9.5) should be used; if $b = 2$, then the Spearman rank correlation (Section 19.9) should be employed. Appendix Table B.14 should be used when the a and b of an experimental design are contained therein. For a and b beyond this table, the distribution of χ_r^2 may be considered to be approximated by the χ^2 distribution (Appendix Table B.1), with $a - 1$ degrees of freedom. Fahoome (2002) advised that the chi-square approximation is acceptable when b is at least 13 when testing at the 0.05 level of significance and at least 23 when $\alpha = 0.01$ is specified. However, Iman and Davenport (1980) showed that this commonly used approximation tends to be conservative (i.e., it may have a

*Milton Friedman (1912–2006), American economist and winner of the 1976 Nobel Memorial Prize in Economic Science. He is often credited with popularizing the statement, "There's no such thing as a free lunch," and in 1975 he published a book with that title; F. Shapiro reported that Friedman's statement had been in use by others more than 20 years before (Hafner, 2001).

†An equivalent formula is

$$\chi_r^2 = \frac{12\sum_{i=1}^{a}(R_i - \bar{R})^2}{ba(a + 1)} \tag{12.43}$$

(Pearson and Hartley, 1976: 52), showing that we are assessing the difference between the rank sums (R_i) and the mean of the rank sums ($\bar{R}$).

EXAMPLE 12.5 Friedman's Analysis of Variance by Ranks Applied to the Randomized Block Data of Example 12.4

H_0: The time for effectiveness is the same for all three anesthetics.

H_A: The time for effectiveness is not the same for all three anesthetics.

$\alpha = 0.05$

The data from Example 12.4, for the three treatments and five blocks, are shown here, with ranks (1, 2, and 3) within each block shown in parentheses.

	Treatment (i)		
Block (j)	1	2	3
1	8.25	11.25	10.75
	(1)	(3)	(2)
2	11.00	12.50	11.75
	(1)	(3)	(2)
3	10.25	12.00	11.25
	(1)	(3)	(2)
4	9.50	9.75	9.00
	(2)	(3)	(1)
5	8.75	11.00	10.00
	(1)	(3)	(2)
Rank sum (R_i)	6	15	9
Mean rank ($\overline{R}_i$)	1.2	3.0	1.8

$a = 3, \quad b = 5$

$$\chi_r^2 = \frac{12}{ba(a+1)} \sum R_i^2 - 2b(a+1)$$

$$= \frac{12}{(5)(3)(3+1)} \left(6^2 + 15^2 + 9^2\right) - 3(5)(3+1)$$

$$= 0.200(342) - 60 = 8.400$$

$\left(\chi_r^2\right)_{0.05,3,5} = 6.400$

Reject H_0.

$$P < 0.01 \quad [P = 0.0085]$$

$$F_F = \frac{(b-1)\chi_r^2}{b(a-1) - \chi_r^2} = \frac{(5-1)(8.4)}{5(3-1)} - 8.4 = \frac{33.6}{1.6} = 21.0$$

$F_{0.05(1),2,4} = 6.94$

Reject H_0.

$$0.005 < P < 0.01 \quad [P = 0.0076]$$

high likelihood of a Type II error—and, therefore, low power) and that

$$F_F = \frac{(b - 1)\chi_r^2}{b(a - 1) - \chi_r^2} \tag{12.45}$$

is generally superior. To test, H_0, F_F is compared to F (Appendix Table B.4) with degrees of freedom of $a - 1$ and $(a - 1)(b - 1)$.*

Because this nonparametric test employs ranks, it could have been used even if the measurements (in minutes) were not known for the times for the anesthetics to take effect. All that would be needed would be the ranks in each block. In Example 12.4, this would be the knowledge that, for litter 1 (i.e., block 1) drug 1 was effective in a shorter time than was drug 3; and drug 3 acted faster than drug 2; and so on for all b blocks.

Another approach to testing of this experimental design is that of *rank transformation*, by which one ranks all ab data and performs the analysis of variance of Section 12.4 on those ranks (Conover 1974b; Iman and Iman, 1976, 1981; and Iman, Hora, and Conover, 1984). Quade (1979) presented a test that is an extension of the Wilcoxon paired-sample test that may be preferable in some circumstances (Iman, Hora, and Conover, 1984). The rank-transformation procedure, however, often gives results better than those from the Friedman or Quade tests. But its proponents do not recommend that it be routinely employed as an alternative to the parametric ANOVA when it is suspected that the underlying assumptions of the latter do not apply. Instead, they propose that it be employed along with the usual ANOVA and, if both yield the same conclusion, one can feel comfortable with that conclusion.

If tied ranks are present, they may be taken into consideration by computing

$$\left(\chi_r^2\right)_c = \frac{\chi_r^2}{C}, \tag{12.46}$$

(Marascuilo and McSweeney, 1967),† (Kendall, 1962: Chapter 6), where

$$C = 1 - \frac{\sum t}{b(a^3 - a)} \tag{12.48}$$

and $\sum t$ are as defined in Equation 10.42.

The *Kendall coefficient of concordance (W)* is another form of Friedman's χ_r^2:

$$W = \frac{\chi_r^2}{b(a - 1)} \tag{12.49}$$

---

*Iman and Davenport (1980) also show that comparing the mean of χ_r^2 and F_F to the mean of the critical values of χ^2 and F provides an improved approximation when Appendix Table B.14 cannot be used.

†Equivalently,

$$\left(\chi_r^2\right)_c = \frac{\sum_{i=1}^{a} R_i^2 - \frac{\left(\sum_{i=1}^{a} R_i\right)^2}{a}}{\frac{ba(a + 1)}{2} - \frac{\sum t}{2}}. \tag{12.47}$$

(Kendall and Babington Smith, 1939). It is used as a measure of the agreement of rankings within blocks and is considered further in Section 20.16.

(a) Multiple Observations per Cell. In the experiment of Example 12.5, there is one datum for each combination of treatment and block. Although this is the typical situation, one might also encounter an experimental design in which there are multiple observations recorded for each combination of block and treatment group. As in Section 12.1, each combination of level of factor A (group) and level of factor B is called a cell; for n replicate data per cell,

$$\chi_r^2 = \frac{12}{ban^2(na + 1)} \sum_{i=1}^{a} R_i^2 - 3b(na + 1) \tag{12.50}$$

(Marascuilo and McSweeney, 1977: 376–377), with a critical value of $\chi^2_{\alpha,a-1}$. Note that if $n = 1$, Equation 12.50 reduces to Equation 12.44. Benard and van Eltern (1953) and Skillings and Mack (1981) present procedures applicable when there are unequal numbers of data per cell.

(b) Multiple Comparisons. A multiple-comparison analysis applicable to ranked data in a randomized block is similar to the Tukey procedure for ranked data in a one-way ANOVA design (Section 11.5). In this case, Equation 11.3 is used with the difference between rank sums; that is, $R_B - R_A$ in the numerator and

$$\text{SE} = \sqrt{\frac{ba(a + 1)}{12}} \tag{12.51}$$

in the denominator.* (Nemenyi, 1963; Wilcoxon and Wilcox, 1964); and this is used in conjunction with the critical value of $q_{\alpha,\infty,k}$.

If the various groups are to be compared one at a time with a control group, then

$$\text{SE} = \sqrt{\frac{ba(a + 1)}{6}} \tag{12.53}$$

may be used in Dunnett's procedure, in a fashion similar to that explained in Section 11.5b.

The preceding multiple comparisons are applicable to the levels of the fixed-effect factor, not to the blocks (levels of the random-effect factor).

*If desired, mean ranks ($\bar{R}_A = R_A/b$ and $\bar{R}_B = R_B/a$) can be used in the numerator of Equation 11.3, in which case the denominator will be

$$\text{SE} = \sqrt{\frac{a(a + 1)}{12b}}. \tag{12.52}$$

Multiple contrasts, as introduced in Sections 11.4 and 11.6, may be performed using rank sums. We employ Equation 11.29, with*

$$\text{SE} = \sqrt{\frac{ba(a+1)}{12}\left(\sum_i c_i^2\right)}, \tag{12.55}$$

unless there are tied ranks, in which case†

$$\text{SE} = \sqrt{\left(\frac{\dfrac{a(a+1)}{b} - \dfrac{\sum t}{b^2(a-1)}}{12}\right)\left(\sum_i c_i^2\right)} \tag{12.57}$$

(Marascuilo and McSweeney, 1967). The critical value for the multiple contrasts is $\sqrt{(\chi_r^2)_{\alpha,a,b}}$, using Appendix Table B.14 to obtain $(\chi_r^2)_{\alpha,a,b}$. If the needed critical value is not on that table, then $\sqrt{\chi^2_{\alpha,a-1}}$ may be used as an approximation to it.

If there is replication per cell (as in Equation 12.50), the standard errors of this section are modified by replacing a with an and b with bn wherever they appear. (See Marascuilo and McSweeney, 1977: 378.) Norwood et al. (1989) and Skillings and Mack (1981) present multiple-comparison methods applicable when there are unequal numbers of data per cell.

12.8 DICHOTOMOUS NOMINAL-SCALE DATA IN RANDOMIZED BLOCKS OR FROM REPEATED MEASURES

The data for a randomized-block or repeated-measures experimental design may be for a dichotomous variable (i.e., a variable with two possible values: e.g., "present" or "absent," "dead" or "alive," "true" or "false," "left" or "right," "male" or "female," etc.), in which case Cochran's Q test‡ (Cochran, 1950) may be applied. For such an analysis, one value of the attribute is recorded with a "1," and the other with a "0." In Example 12.8, the data are the occurrence or absence of mosquito attacks on humans wearing one of several types of clothing. The null hypothesis is that the proportion of people attacked is the same for each type of clothing worn.

*If mean ranks are used,

$$\text{SE} = \sqrt{\frac{a(a+1)}{12b}\left(\sum_i c_i^2\right)}. \tag{12.54}$$

†If mean ranks are used,

$$\text{SE} = \sqrt{\left(\frac{\dfrac{a(a+1)}{b^2} - \dfrac{\sum t}{b^3(a-1)}}{12}\right)\left(\sum_i c_i^2\right)}. \tag{12.56}$$

‡William Gemmell Cochran (1909–1980), born in Scotland and influential in the United States after some early important work in England (Dempster, 1983; Watson, 1982).

EXAMPLE 12.6 Cochran's *Q* Test

H_0: The proportion of humans attacked by mosquitoes is the same for all five clothing types.

H_A: The proportion of humans attacked by mosquitoes is not the same for all five clothing types.

$\alpha = 0.05$

A person attacked is scored as a "1"; a person not attacked is scored as a "0."

	Clothing Type					
Person (block)	*Light, loose*	*Light, tight*	*Dark, long*	*Dark, short*	*None*	*Totals* (B_j)
1	0	0	0	1	0	1
2*	1	1	1	1	1	*
3	0	0	0	1	1	2
4	1	1	0	1	0	3
5	0	1	1	1	1	4
6	0	1	0	0	1	2
7	0	0	1	1	1	3
8	0	0	1	1	0	2
*Totals** (G_i)	1	3	3	6	4	$\sum_{i=1}^{a} G_i = \sum_{j=1}^{b} B_j = 17$

$a = 5; \quad b = 7^*$

$$Q = \frac{(a-1)\left[\sum_{i=1}^{a} G_i^2 - \frac{\left(\sum_{i=1}^{a} G_i\right)^2}{a}\right]}{\sum_{j=1}^{b} B_j - \frac{\sum_{j=1}^{b} B_j^2}{a}}$$

$$= \frac{(5-1)\left[1+9+9+36+16-\frac{17^2}{5}\right]}{17 - \frac{(1+4+9+16+4+9+4)}{5}} = \frac{52.8}{7.6} = 6.947$$

$\nu = a - 1 = 4$

$\chi^2_{0.05,4} = 9.488$

Therefore, do not reject H_0.

$$0.10 < P < 0.25 \quad [P = 0.14]$$

*The data for block 2 are deleted from the analysis, because 1's occur for all clothing. (See test discussion in Section 12.8.)

For a groups and b blocks, where G_i is the sum of the 1's in group i and B_j is the sum of the 1's in block j,

$$Q = \frac{(a-1)\left[\sum_{i=1}^{a} G_i^2 - \frac{\left(\sum_{i=1}^{a} G_i\right)^2}{a}\right]}{\sum_{j=1}^{b} B_j - \frac{\sum_{j=1}^{b} B_j^2}{a}}. \tag{12.58}$$

Note, as shown in Example 12.8, that $\sum B = \sum G$, which is the total number of 1's in the set of data. This test statistic, Q, is distributed approximately as chi-square with $a - 1$ degree of freedom. Tate and Brown (1970) explain that the value of Q is unaffected by having blocks containing either all 0's or all 1's. Thus, any such block may be disregarded in the calculations. They further point out that the approximation of Q to χ^2 is a satisfactory one only if the number of data is large. These authors suggest as a rule of thumb that a should be at least 4 and ba should be at least 24, where b is the number of blocks remaining after all those containing either all 0's or all 1's are disregarded. For sets of data smaller than these suggestions allow, the analysis may proceed but with caution exercised if Q is near a borderline of significance. In these cases it would be better to use the tables of Tate and Brown (1964) or Patil (1975).

If $a = 2$, then Cochran's test is identical to McNemar's test (Section 24.17), except that the latter employs a correction for continuity.

12.9 MULTIPLE COMPARISONS WITH DICHOTOMOUS RANDOMIZED-BLOCK OR REPEATED-MEASURES DATA

Marascuilo and McSweeney (1967) present a multiple-comparison procedure that may be used for multiple contrasts as well as for pairwise comparisons for data subjected to the Cochran Q test of Section 12.8. It may be performed using group means, $\overline{R}_i = G_i/b$.

For pairwise comparisons, the test statistic is

$$S = \frac{\overline{R}_B - \overline{R}_A}{\text{SE}} \tag{12.59}$$

(which parallels Equation 11.13), where

$$\text{SE} = \sqrt{2\left(\frac{a\sum_j B_j - \sum_j B_j^2}{ab^2(a-1)}\right)}. \tag{12.60}$$

For multiple contrasts, the test statistic is that of Equation 11.16, where $\overline{R}_i$ replaces $\overline{X}_i$ and

$$\text{SE} = \sqrt{\left(\frac{a\sum_j B_j - \sum_j B_j^2}{ab^2(a-1)}\right)\sum_i c_i^2}. \tag{12.61}$$

The critical value for such multiple comparisons is $S_\alpha = \sqrt{\chi^2_{\alpha,a-1}}$.

12.10 INTRODUCTION TO ANALYSIS OF COVARIANCE

Each of the two factors in a two-way ANOVA generally consists of levels that are nominal-scale categories. In Example 10.1, for instance, the variable of interest was the body weight of pigs, and the one factor tested was diet. In a two-factor ANOVA, we might ask about the effect of diet and also introduce the sex of the animal (or the breed) as a second factor, with the levels of sex (or breed) being on a nominal scale.

In the experiment of Example 10.1, we would attempt to employ animals of the same age (and weight), so differences in the measured variable could be attributed to the effect of the diets. However, if the beginning ages (or weights) were markedly not alike, then we might wish to introduce age (or weight) as a second factor. The relationship between ending weight and age (or ending weight and beginning weight) may be thought of as a regression (see Chapter 17), while the relationship between ending weight and diet is a one-way analysis of variance (Chapter 10). The concepts of these two kinds of analyses, and their statistical assumptions, are combined in what is known as *analysis of covariance* (abbreviated ANCOVA),* and the factor that acts as an independent variable in regression is called a *concomitant variable*. This is a large area of statistical methodology beyond the scope of this book but found in many references, including several dealing with experimental design.

EXERCISES

12.1. A study is made of amino acids in the hemolymph of millipedes. For a sample of four males and four females of each of three species, the following concentrations of the amino acid alanine (in mg/100 ml) are determined:

	Species 1	*Species 2*	*Species 3*
Male	21.5	14.5	16.0
	19.6	17.4	20.3
	20.9	15.0	18.5
	22.8	17.8	19.3
Female	14.8	12.1	14.4
	15.6	11.4	14.7
	13.5	12.7	13.8
	16.4	14.5	12.0

(a) Test the hypothesis that there is no difference in mean hemolymph alanine concentration among the three species.

(b) Test the hypothesis that there is no difference between males and females in mean hemolymph alanine concentration.

(c) Test the hypothesis that there is no interaction between sex and species in the mean concentration of alanine in hemolymph.

(d) Prepare a graph of the row, column, and cell means, as done in Figure 12.1, and interpret it in terms of the results of the above hypothesis tests.

(e) If the null hypothesis of part a, above, is rejected, then perform a Tukey test to assess the mean differences among the species.

12.2. Six greenhouse benches were set up as blocks. Within each block, one of each of four varieties of house plants was planted. The plant heights (in centimeters) attained are tabulated as follows. Test the hypothesis that all four varieties of plants reach the same maximum height.

*The first use (and the name) of this statistical technique is attributed to R. A. Fisher prior to 1930 (e.g., Fisher, 1932: 249–262; Yates, 1964).

Block	*Variety 1*	*Variety 2*	*Variety 3*	*Variety 4*
1	19.8	21.9	16.4	14.7
2	16.7	19.8	15.4	13.5
3	17.7	21.0	14.8	12.8
4	18.2	21.4	15.6	13.7
5	20.3	22.1	16.4	14.6
6	15.5	20.8	14.6	12.9

12.3. Consider the data of Exercise 12.2. Nonparametrically test the hypothesis that all four varieties of plants reach the same maximum height.

12.4. A textbook distributor wishes to assess potential acceptance of four general biology textbooks. He asks 15 biology professors to examine the books and to respond as to which ones they would seriously consider for their courses. In the table, a positive response is recorded as 1 and a negative response as a 0. Test the hypothesis that there is no difference in potential acceptance among the four textbooks.

Professor	*Textbook 1*	*Textbook 2*	*Textbook 3*	*Textbook 4*
1	1	1	0	0
2	1	1	0	1
3	1	0	0	0
4	1	1	1	1
5	1	1	0	1
6	0	1	0	0
7	0	1	1	0
8	1	1	1	0
9	0	0	1	0
10	1	0	1	0
11	0	0	0	0
12	1	1	0	1
13	1	0	0	1
14	0	1	1	0
15	1	1	0	0

CHAPTER 13

Data Transformations

Previous chapters have discussed underlying assumptions of several statistical procedures, such as *t*-testing (Sections 7.1a, 8.1d, 8.1e, 9.1), analysis of variance (Sections 10.1g, 10.1i, 12.1g, 12.4d), and parametric multiple comparisons (Chapter 11 introduction). Three assumptions were noted in those chapters: (1) Each sample of data was obtained randomly from the sampled population, (2) each sampled population was normally distributed, and (3) all of the sampled populations had the same variance. These three assumptions will also apply to several statistical procedures discussed in later chapters. If the assumptions are not well satisfied, then the probabilities associated with the test statistics may be incorrect, and conclusions whether to reject the null hypothesis may not be warranted.

If an analysis of variance is to be performed for the effects of two or more factors (i.e., a factorial ANOVA), then it is important to consider the effects of interactions among the factors. For example, in a two-factor analysis of variance (as explained in Chapter 12), the effect of factor A on the variable, X, can be assessed, as can the effect of factor B on that variable. It is also important to examine the interaction effect of the two factors. If the effect of one of the factors on X is the same at all levels of the other factor, then there is no interaction effect, and the effects of the two variables are said to be *additive*.*

It was shown in Section 12.1 that if there is replication within cells in a factorial ANOVA, then the hypothesis of no interaction can be tested, as well as a hypothesis about each of the factors. If, however, there is no replication (Section 12.3), then hypothesis testing is problematic and limited, especially in Model I ANOVA (see Table 12.5). Thus, in the absence of replication, a fourth assumption—that of no interaction (i.e., of additivity)—can be added to the three assumptions mentioned previously.

There are data sets that violate one or more of underlying premises 2, 3, and 4 for which a *transformation* of the data from their original values (X) to values (call them X') that constitute a data set more closely satisfying the assumptions. Also, a reduction in the interaction effect can enhance the power of hypothesis testing for factor effects. For some kinds of data it is known, on theoretical grounds, that a transformation will result in data more amenable to the intended statistical analysis.

*The term *additivity* in this context was introduced by C. Eisenhart in 1947 (David, 1995).

Data transformation will *not* compensate for the absence of random sampling (violation of assumption 1). As with untransformed data, analysis of transformed data can be adversely affected by the presence of outliers (Section 2.5).

Many authors provided early recommendations on the use of data transformations that have become commonly used (e.g., Bartlett, 1947; Box and Cox, 1964; Kendall and Stuart, 1966: 87–96; Thöni, 1967). This chapter will concentrate on three of those transformations: The logarithmic transformation (Section 13.1) is applicable when there is heterogeneity of variances among groups and the group standard deviations are directly proportional to the means, and in cases where two or more factors have a multiplicative (instead of an additive) effect. The square-root transformation (Section 13.2) applies to heteroscedastic data where the group variances are directly proportional to the means, a situation often displayed when the data come from a population of randomly distributed counts. The arcsine transformation (Section 13.3) is germane when the data come from binomial distributions, such as when the data consist of percentages within the limits of 0 and 100% (or, equivalently, proportions within the range of 0 to 1). The transformation of data in regression analysis will be discussed in Section 17.10.

13.1 THE LOGARITHMIC TRANSFORMATION

If the factor effects in an analysis of variance are, in fact, multiplicative instead of additive, then the data will not exhibit additivity, but logarithms of the data will. This is demonstrated in Example 13.1: Example 13.1a shows data for which, for each level of factor B, each datum in factor-A level 2 differs from the corresponding datum in factor-A level 1 by the addition by the same weight (namely, 20 g − 10 g = 10 g and 30 g − 20 g = 10 g), and each datum in level 3 differs from its corresponding level-2 datum by the same amount (i.e., 25 g − 20 g = 5 g and 35 g − 30 g = 5 g). And for factor B, there is a constant difference (20 g − 10 g = 30 g − 20 g = 35 g − 25 g = 10 g) between the two levels, at all three levels of factor A. Thus, in Example 13.1a, no data transformation is needed to achieve additivity. However, in the data of Example 13.1b, the effect of each factor is multiplicative instead of additive. For each level of factor B, the datum in level 2 differs from its corresponding datum in level 1 by a factor of 3 (i.e., 30 g = 3 × 10 g and 60 g = 3 × 20 g); each X in level 3 differs from its level-2 neighbor by a factor of 2 (60 g = 2 × 30 g and 120 g = 2 × 60 g); and there is a multiplicative difference of 2 between the data, at each level of factor A (20 g = 2 × 10 g; 60 g = 2 × 30 g; 120 g = 2 × 60 g) for each of the two levels of factor B. In such a situation, the logarithms of the data will exhibit additivity. This is shown by the logarithmically transformed data of Example 13.1c. In Example 13.1, the six quantities may be data in a 3 × 2 ANOVA without replication or they may represent the six cell means if there is replication.

Figure 13.1 graphs the data in Example 13.1, in the format introduced in Figures 12.1 and 12.2. Figure 13.1a shows the values of X in Example 13.1a. For the two levels of factor B (B_1 and B_2), the line segments are parallel between factor-A levels 1 and 2 (A_1 and A_2) and between levels 2 and 3 (A_2 and A_3), indicating the additive effect of the two factors (i.e., no interaction between the two factors). Figure 13.1b graphs the values of X found in Example 13.1b. In comparing the plots for the two levels of factor B (B_1 and B_2), it is seen that the line segments between the first two levels of factor A (A_1 and A_2) are not parallel, nor are the line segments between the second and third levels of that factor (A_2 and A_3), indicating that the effects of the two factors are not additive (i.e., that there is an interactive effect between factors A and B). Figure 13.1c shows the graph for the data transformed

into their logarithms (Example 13.1c). Here it is seen that the two line segments representing the two levels of factor B are parallel for the comparison of levels 1 and 2 of factor A and for the comparison of levels 2 and 3. Thus, Example 13.1c achieved additivity by using the logarithmic transformation of the data in Example 13.1b.

EXAMPLE 13.1 Additive and Multiplicative Effects

(a) A hypothetical two-way analysis-of-variance design, where the effects of the factors are additive. (Data are in grams.)

	Factor A		
Factor B	*Level 1*	*Level 2*	*Level 3*
Level 1	10	20	25
Level 2	20	30	35

(b) A hypothetical two-way analysis-of-variance design, where the effects of the factors are multiplicative. (Data are in grams.)

	Factor A		
Factor B	*Level 1*	*Level 2*	*Level 3*
Level 1	10	30	60
Level 2	20	60	120

(c) The two-way analysis-of-variance design of Example 13.1b, showing the logarithms (rounded to two decimal places) of the data.

	Factor A		
Factor B	*Level 1*	*Level 2*	*Level 3*
Level 1	1.00	1.48	1.78
Level 2	1.30	1.78	2.08

The logarithmic transformation is also applicable when there is heteroscedasticity and the groups' standard deviations are directly proportional to their means (i.e., there is a constant coefficient of variation among the groups). Such a situation is shown in Example 13.2. This transformation may also convert a positively skewed distribution into a symmetrical one.

Instead of the transformation $X' = \log(X)$, however,

$$X' = \log(X + 1) \tag{13.1}$$

is preferred as the logarithmic transformation on theoretical grounds and is especially preferable when some of the data are small numbers (particularly zero) (Bartlett, 1947). Logarithms in base 10 are generally utilized, but any logarithmic base may be employed. Equation 13.1 is what is used in Example 13.2.

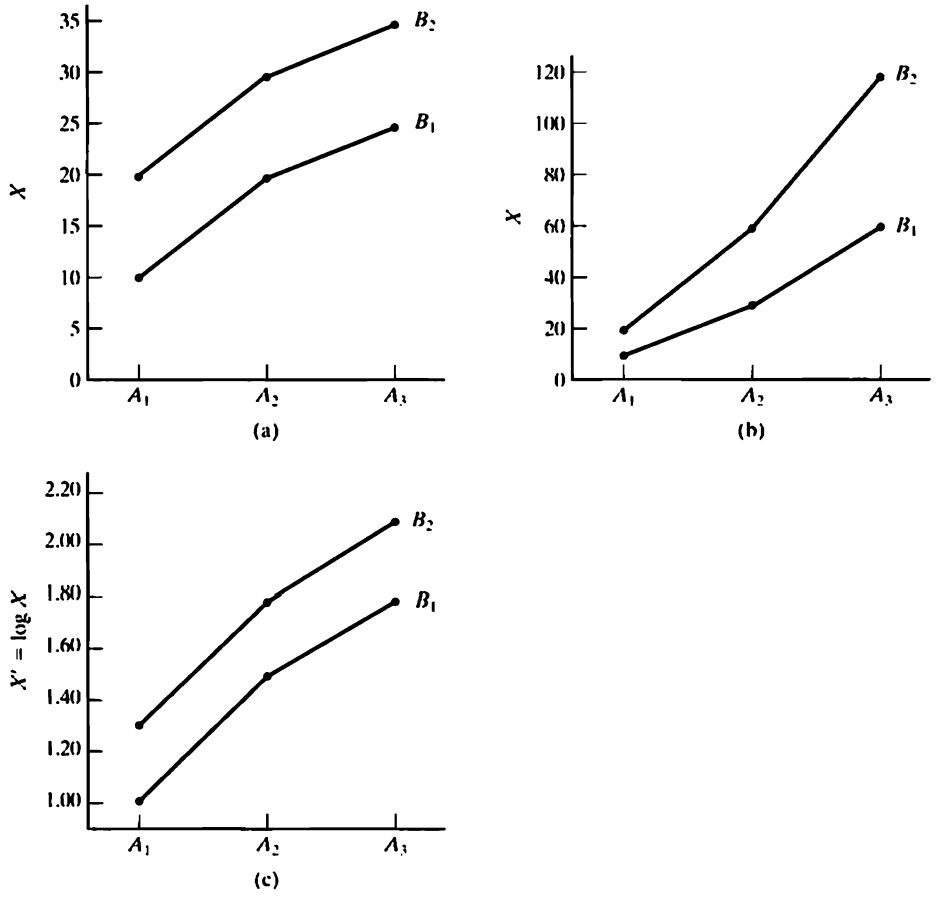


FIGURE 13.1: The effects of the two factors in a 3 × 2 analysis of variance. (a) The data of Example 13.1a, where the parallel line segments reflect lack of interaction between the two factors (i.e., additivity). (b) The data of Example 13.1b, where the nonparallel line segments indicate interaction (i.e., nonadditivity) of the two factors. (c) The data of Example 13.1b transformed to their logarithms and shown as Example 13.1c; the parallelism of these line segments shows that the transformation has resulted in the absence of interaction (i.e., the result is factor additivity).

EXAMPLE 13.2 The Logarithmic Transformation for Data in Which There Is Heterogeneity of Variance and the Standard Deviations Are Directly Proportional to the Means (i.e., the Coefficients of Variation Are the Same)

A prime symbol on a statistic denotes a quantity obtained using the transformed data (e.g., X', s', L').

The original data (leaf lengths, in centimeters):

Group 1	*Group 2*
3.1	7.6
2.9	6.4
3.3	7.5
3.6	6.9
3.5	6.3

$\overline{X}_1 = 3.28$ cm	$\overline{X}_2 = 6.94$ cm
$s_1^2 = 0.0820$ cm^2	$s_2^2 = 0.3630$ cm^2
$s_1 = 0.29$ cm	$s_2 = 0.60$ cm
$V_1 = 0.09$	$V_2 = 0.09$

The logarithmically transformed data, using Equation (13.1):

Group 1	*Group 2*
0.61278	0.93450
0.59106	0.86923
0.63347	0.92942
0.66276	0.89763
0.65321	0.86332
$\overline{X}'_1 = 0.63066$	$\overline{X}'_2 = 0.89882$
$(s_1^2)' = 0.0008586657$	$(s_2^2)' = 0.0010866641$
$s'_1 = 0.02930$	$s'_2 = 0.03296$
$V'_1 = 0.04646$	$V'_2 = 0.03667$
$s'_{\overline{X}_1} = 0.01310$	$s'_{\overline{X}_2} = 0.01474$

Calculating confidence limits for the mean, using the transformed data from Group 1:

$$\text{95\% confidence interval for } \mu'_1 = \overline{X}'_1 \pm (t_{0.05(2),4})(0.01310)$$
$$= 0.63066 \pm (2.776)(0.01310)$$
$$= 0.63066 \pm 0.03637$$

$$L'_1 = 0.59429 \text{ and } L'_2 = 0.66703$$

95% confidence limits for μ_1, in the original units:

$$L_1 = \text{antilog } 0.59429 - 1 = 3.93 - 1 = 2.93 \text{ cm}$$
$$L_2 = \text{antilog } 0.66703 - 1 = 4.65 - 1 = 3.65 \text{ cm}$$

The 95% confidence intervals for μ'_2 and for μ_2 may be calculated in the same manner.

After data transformation, hypothesis testing and expression of confidence intervals may be done on the transformed data. Subtracting 1 from the antilogarithm of the mean of the logarithmically transformed data expresses the sample mean in the units of the original data,* and subtracting 1 from the antilogarithm of each confidence limit for the mean of the transformed data gives the confidence limits for the mean in terms of the nontransformed data. This is demonstrated in Example 13.2. Note that, when performing these calculations on the transformed data, the confidence interval is not symmetrical around the mean in the original units.

*Thöni (1967: 16) has shown that an unbiased estimate of μ would be obtained by adding $(1 - 1/n)s^2$ to the $\overline{X}$ derived by untransforming $\overline{X}'$, where s^2 is the variance of the transformed data. Bias is less for large samples. The antilogarithm of the mean of the transformed data (i.e., the antilogarithm of $(\overline{X}')$ is the geometric mean of the untransformed data (Section 3.4a).

If the distribution of X' is normal, the distribution of X is said to be *lognormal*.*

13.2 THE SQUARE-ROOT TRANSFORMATION

The square-root transformation is applicable when the group variances are directly proportional to the means; that is, when the variances increase as the means increase. This most often occurs in biological data when samples are taken from a Poisson distribution (i.e., when the data consist of counts of randomly occurring objects or events; see Chapter 25 for discussion of the Poisson distribution). Transforming such data by utilizing their square roots results in a sample whose underlying distribution is normal. However, Bartlett (1936) proposed that

$$X' = \sqrt{X + 0.5} \tag{13.2}$$

is preferable to $X' = \sqrt{X}$, especially when there are very small data and/or when some of the observations are zero (see Example 13.3). Actually,

$$X' = \sqrt{X + \frac{3}{8}} \tag{13.3}$$

has even better variance-stabilizing qualities than Equation 13.2 (Kihlberg, Herson, and Schutz, 1972), and Freeman and Tukey (1950) show

$$X' = \sqrt{X} + \sqrt{X + 1} \tag{13.4}$$

to yield similar results but to be preferable for $X \leq 2$.

Equation 13.2 is most commonly employed. Statistical computation may then be performed on the transformed data. The mean of those data can be expressed in terms of the original data by squaring it and then subtracting 0.5, although the resultant statistic is slightly biased.† Budescu and Appelbaum (1981) examined ANOVA for Poisson data and concluded that data transformation is not desirable unless the largest variances are found in the largest samples and the largest sample is more than five times the size of the smallest.

13.3 THE ARCSINE TRANSFORMATION

It is known from statistical theory that percentages from 0 to 100% or proportions from 0 to 1 form a binomial, rather than a normal, distribution, the deviation from normality being great for small or large percentages (0 to 30% and 70 to 100%).‡ If the square root of each proportion, p, in a binomial distribution is transformed to its arcsine (i.e., the angle whose sine is $\sqrt{p}$), then the resultant data will have an underlying distribution that is nearly normal. This transformation,

$$p' = \arcsin \sqrt{p}, \tag{13.5}$$

*The term *lognormal* was introduced by J. H. Gaddam in 1945 (David, 1995).

†Also, an antilogarithmic transformation to obtain $\overline{X}$ in terms of the original units is known to result in a somewhat biased estimator of μ, the estimator being less biased for larger variances of $\overline{X}'$ values.

‡The symbol for percent, "%," appeared around 1650 (Cajori, 1928/1929, Vol. I: 312).

EXAMPLE 13.3 The Square Root Transformation for Poisson Data

Original data (number of parasites in the lungs of 20 frogs allocated to four experimental groups):

	Group 1	*Group 2*	*Group 3*	*Group 4*
	2	6	9	2
	0	4	5	4
	2	8	6	1
	3	2	5	0
	0	4	11	2
$\overline{X}_1$	1.4	4.8	7.2	1.8
s_i^2	1.8	5.2	7.2	2.2

Transformed data; by Equation 13.2:

	Group 1	*Group 2*	*Group 3*	*Group 4*
	1.581	2.550	3.082	1.581
	0.707	2.121	2.345	2.121
	1.581	2.915	2.550	1.225
	1.871	1.581	2.345	0.707
	0.707	2.121	3.391	1.581
$\overline{X}'_i$	1.289	2.258	2.743	1.443
$(s_i^2)'$	0.297	0.253	0.222	0.272
$s'_{\overline{X}_i}$	0.244	0.225	0.211	0.233
$(L'_1)_i$	0.612	1.633	2.157	0.796
$(L'_2)_i$	1.966	2.883	3.329	2.090

On transforming back to original units [e.g., $\overline{X} = (\overline{X}')^2 - 0.5$]:

	Group 1	*Group 2*	*Group 3*	*Group 4*
$\overline{X}_i$	1.2	4.6	7.0	1.6
$(L_1)_i$	−0.1	2.2	4.2	0.1
$(L_2)_i$	3.4	7.8	10.6	3.9

is performed easily with the aid of Appendix Table B.24. For proportions of 0 to 1.00 (i.e., percentages of 0 to 100%), the transformed values will range between 0 and

90 degrees (although some authors' tables present the transformation in terms of radians*).†

The arcsine transformation ("arcsine" is abbreviated "arcsin") frequently is referred to as the "angular transformation," and "inverse sine" or "$\sin^{-1}$" is sometimes written to denote "arcsine."‡

Example 13.4 demonstrates calculations using data submitted to the arcsine transformation. Transformed values (such as means or confidence limits) may be transformed back to proportions, as

$$p = (\sin p')^2; \tag{13.6}$$

and Appendix Table B.25 is useful for this purpose.§ As shown in Section 24.8, confidence limits for proportions will not generally be symmetrical around the mean. This transformation is not as good at the extreme ends of the range of possible values (i.e., near 0 and 100%) as it is elsewhere. If, instead of simply having data consisting of percentages, the researcher knows the count (X) and sample size (n) composing each percentage ($p = X/n$), then the arcsine transformation is improved by replacing $0/n$ with $1/4n$ and n/n with $1 - 1/4n$ (Bartlett, 1937a). Anscombe (1948) proposed an even better transformation:

$$p' = \arcsin \sqrt{\frac{X + \frac{3}{8}}{n + \frac{3}{4}}}. \tag{13.7}$$

And a slight modification of the Freeman and Tukey (1950) transformation, namely,

$$p' = \frac{1}{2}\left[\arcsin\sqrt{\frac{X}{n+1}} + \arcsin\sqrt{\frac{X+1}{n+1}}\right], \tag{13.8}$$

yields very similar results, except for small and large proportions where it appears to be preferable. Determination of transformed proportions, p', by either Equation 13.7 or 13.8 is facilitated by using Appendix Table B.24.

*A radian is $180°/\pi = 57.29577951308232\ldots$ degrees. Expressing angles in radians, instead of degrees, would have Equation 13.5 yield arcsines (p') of 0 to 1.5708 for proportions (p) of 0 to 1; sometimes the use of radians is associated with substituting

$$p' = 2\arcsin\sqrt{p} \tag{13.5a}$$

for Equation 13.5, resulting in values of p' that can range from 0 to 3.1416 (that is, a range of zero to pi). The choice between degrees and radians will not affect the conclusions of statistical procedures employing the arcsine transformation.

†The arcsine transformation is applicable only if the data came from a distribution of data that can lie between 0 and 100% (e.g., not if data are percent increases, which can be greater than 100%).

‡The arcsine of a number is the angle whose sine is that number. (See Section 26.3 for a description of the sine and other trigonometric functions.) The term was initiated in the latter part of the eighteenth century; and the abbreviation "$\sin^{-1}$" was introduced in 1813 by the English astronomer Sir John Frederick William Herschel (1792–1871) (Cajori, 1928/1929, Vol. II: 175–176).

§The mean, $\bar{p}$, that is obtained from $\bar{p}'$ by consulting Appendix Table B.25 is, however, slightly biased. Quenouille (1950) suggests correcting for the bias by adding to $\bar{p}$ the quantity $0.5\cos(2\bar{p}')(1 - e^{-2s^2})$, where s^2 is the variance of the p' values.

EXAMPLE 13.4 The Arcsine Transformation for Percentage Data

Original data (p, the percentage of insects killed in each of seven groups of insects subjected to one of two insecticides):

Insecticide 1 (%)	*Insecticide 2 (%)*
84.2	92.3
88.9	95.1
89.2	90.3
83.4	88.6
80.1	92.6
81.3	96.0
85.8	93.7
$\bar{p}_2 = 84.7\%$	$\bar{p}_2 = 92.7\%$
$s_1^2 = 12.29(\%)^2$	$s_2^2 = 6.73(\%)^2$
$s_1 = 3.5\%$	$s_2 = 2.6\%$

Transformed data (by using Equation 13.5 or Appendix Table B.24) (p'):

Insecticide 1 (°)	*Insecticide 2 (°)*
66.58	73.89
70.54	77.21
70.81	71.85
65.96	70.27
63.51	74.21
64.38	78.46
67.86	75.46
$\bar{p}_1' = 67.09$	$\bar{p}_2' = 74.48$
$(s_1^2)' = 8.0052$	$(s_2^2)' = 8.2193$
$s_1' = 2.83$	$s_2' = 2.87$
$s_{\bar{X}_1}' = 1.07$	$s_{\bar{X}_2}' = 1.08$

Calculating confidence limits:

95% confidence interval for $\mu_1' : \bar{p}_1' \pm (t_{0.05(2),6})(1.07) = 67.09 \pm 2.62$

$$L_1' = 64.47° \text{ and } L_2' = 69.71°$$

By using Appendix Table B.25 to transform backward from L_1', L_2', and p_1':

95% confidence limits for $\mu_1 : L_1 = 81.5\%$ and $L_2 = 88.0\%$.

$$\bar{p}_1 = 84.9\%$$

13.4 OTHER TRANSFORMATIONS

The logarithmic, arcsine, and square-root transformations are those most commonly required to handle nonnormal, heteroscedastic, or nonadditive data. Other transformations are only rarely called for.

If the standard deviations of groups of data are proportional to the square of the means of the groups, then the *reciprocal transformation*,

$$X' = \frac{1}{X}, \tag{13.9}$$

may be employed. (If counts are being transformed, then

$$X' = \frac{1}{X + 1} \tag{13.10}$$

may be used to allow for observations of zero.) See Thöni (1967: 32) for further discussion of the use of this transformation.

If the standard deviations decrease as the group means increase, and/or if the distribution is skewed to the left, then

$$X' = X^2 \tag{13.11}$$

might prove useful.

If the data come from a population with what is termed a "negative binomial distribution," then the use of inverse hyperbolic sines may be called for (see Anscombe, 1948; Bartlett, 1947; Beall, 1940, 1942; Thöni, 1967: 20–24).

Thöni (1967) mentions other, infrequently employed, transformations.

EXERCISES

13.1. Perform the logarithmic transformation on the following data (using Equation 13.1) and calculate the 95% confidence interval for μ. Express the confidence limits in terms of the original units (i.e., ml). The data are 3.67, 4.01, 3.85, 3.92, 3.71, 3.88, 3.74, and 3.82 ml.

13.2. Transform the following proportions by the arcsine transformation (using Appendix Table B.24) and calculate the 95% confidence interval for μ. Express the confidence limits in terms of proportions (using Appendix Table B.25).

0.733, 0.804, 0.746, 0.781, 0.772, and 0.793

13.3. Apply the square-root transformation to the following data (using Equation 13.2) and calculate the 95% confidence interval for μ. Transform the confidence limits back to the units of the original data. The data are 4, 6, 3, 8, 10, 3.

CHAPTER 14

Multiway Factorial Analysis of Variance

Chapter 12 discussed the analysis of the effects on a variable of two factors acting simultaneously. In such a procedure—a two-way, or two-factor, analysis of variance—we can conclude whether either of the factors has a significant effect on the magnitude of the variable and also whether the interaction of the two factors significantly affects the variable. By expanding the considerations of the two-way analysis of variance, we can assess the effects on a variable of the simultaneous application of three or more factors, this being done by what is referred to as multiway factorial analysis of variance.*

It is not unreasonable for a researcher to perform a one-way or two-way analysis of variance by hand (i.e., using a calculator), although computer programs are routinely employed, especially when the experiment consists of a large number of data. However, it has become rare for analyses of variance with more than two factors to be analyzed other than via statistical software, for considerations of time, ease, and accuracy. Therefore, this chapter will presume that established computer programs will be used to perform the necessary calculations, but it will consider the subsequent examination and interpretation of the numerical results of the computer's labor.

14.1 THREE-FACTOR ANALYSIS OF VARIANCE

For a particular variable, we may wish to assess the effects of three factors; let us refer to them as factors A, B, and C. For example, we might desire to determine what effect the following three factors have on the rate of oxygen consumption of crabs: species, temperature, and sex. Example 14.1a shows experimental data collected for crabs of both sexes, representing three species, and measured at three temperatures. For each cell (i.e., each combination of species, temperature, and sex) there was an oxygen consumption datum for each of four crabs (i.e., there were four replicates); therefore, 72 animals were used in the experiment ($N = 2 \times 3 \times 3 \times 4 = 72$).

*The concept of the factorial analysis of variance was introduced by the developer of ANOVA, R. A. Fisher (Bartlett, 1965), and Fisher's first use of the term *factorial* was in 1935 (David, 1995).

EXAMPLE 14.1a A Three-Factor Analysis of Variance (Model I), Where the Variable Is Respiratory Rate of Crabs (in ml O_2/hr)

1 H_0: Mean respiratory rate is the same in all three crab species (i.e., $\mu_1 = \mu_2 = \mu_3$).
H_A: Mean respiratory rate is not the same in all three crab species.

2 H_0: Mean respiratory rate is the same at all three experimental temperatures (i.e., $\mu_{low} = \mu_{med} = \mu_{high}$).
H_A: Mean respiratory rate is not the same at all three experimental temperatures.

3 H_0: Mean respiratory rate is the same for males and females (i.e., $\mu_{\sigma^*} = \mu_{\varphi}$)
H_A: Mean respiratory rate is not the same for males and females (i.e., $\mu_{\sigma^*} \neq \mu_{\varphi}$)

4 H_0: Differences in mean respiratory rate among the three species are independent of (i.e., the population means are the same at) the three experimental temperatures; or, differences in mean respiratory rate among the three temperatures are independent of (i.e., are the same in) the three species. (Testing for $A \times B$ interaction.)
H_A: Differences in mean respiratory rate among the species are not independent of the experimental temperatures.

5 H_0: Differences in mean respiratory rate among the three species are independent of sex (i.e., the population means are the same for both sexes); or, differences in mean respiratory rate between males and females are independent of (i.e., are the same in) the three species. (Testing for $A \times C$ interaction.)
H_A: Differences in mean respiratory rate among the species are not independent of sex.

6 H_0: Differences in mean respiratory rate among the three experimental temperatures are independent of (i.e., the population means are the same in) the two sexes; or, differences in mean respiration rate between the sexes are independent of (i.e., are the same at) the three temperatures. (Testing for $B \times C$ interaction.)
H_A: Differences in mean respiratory rate among the three temperatures are not independent of sex.

7 H_0: Differences in mean respiratory rate among the species (or temperatures, or sexes) are independent of the other two factors. (Testing for $A \times B \times C$ interaction.)
H_A: Differences in mean respiratory rate among the species (or temperature, or sexes) are not independent of the other two factors.

Species 1

Low temp.		*Med. temp.*		*High temp.*	
♂	♀	♂	♀	♂	♀
1.9	1.8	2.3	2.4	2.9	3.0
1.8	1.7	2.1	2.7	2.8	3.1
1.6	1.4	2.0	2.4	3.4	3.0
1.4	1.5	2.6	2.6	3.2	2.7

Species 2

Low temp.		*Med. temp.*		*High temp.*	
♂	♀	♂	♀	♂	♀
2.1	2.3	2.4	2.0	3.6	3.1
2.0	2.0	2.6	2.3	3.1	3.0
1.8	1.9	2.7	2.1	3.4	2.8
2.2	1.7	2.3	2.4	3.2	3.2

Species 3

Low temp.		*Med. temp.*		*High temp.*	
♂	♀	♂	♀	♂	♀
1.1	1.4	2.0	2.4	2.9	3.2
1.2	1.0	2.1	2.6	2.8	2.9
1.0	1.3	1.9	2.3	3.0	2.8
1.4	1.2	2.2	2.2	3.1	2.9

Table 14.1 presents the computer output for the analysis of these experimental results, such output typically giving the sums of squares, degrees of freedom, and mean squares pertaining to the hypotheses to be tested. Some computer programs also give the F values calculated, assuming that the experiment calls for a Model I analysis, which is the case with most biological data, and some present the probability of each F. The major work that the computer software has performed for us is the calculation of the sums of squares. We could easily have arrived at the degrees of freedom for

TABLE 14.1: Computer Output from a Three-Factor Analysis of Variance of the Data Presented in Example 14.1

Source of variation	Sum of squares	DF	Mean square
Factor A	1.81750	2	0.90875
Factor B	24.65583	2	12.32791
Factor C	0.00889	1	0.00889
A × B	1.10167	4	0.27542
A × C	0.37028	2	0.18514
B × C	0.17528	2	0.08764
A × B × C	0.22056	4	0.05514
Error	2.00500	54	0.03713

each factor as the number of levels -1 (so, for factor A, DF $= 3 - 1 = 2$; for factor B, DF $= 3 - 1 = 2$; and for factor C, DF $= 2 - 1 = 1$). The degrees of freedom for each interaction are $A \times B$ DF = factor A DF $\times$ factor B DF $= 2 \times 2 = 4$; $A \times C$ DF = factor A DF $\times$ factor C DF $= 2 \times 1 = 2$; $B \times C$ DF = factor B DF $\times$ factor C DF $= 2 \times 1 = 2$; and $A \times B \times C$ DF = factor A DF $\times$ factor B DF $\times$ factor C DF $= 2 \times 2 \times 1 = 4$. The error DF is, then, the total DF (i.e., $N - 1$) minus all other degrees of freedom. Each needed mean square is then obtained by dividing the appropriate sum of squares by its associated DF. As we are dealing with a Model I (fixed-effects model) ANOVA, the computation of each F value consists of dividing a factor or interaction mean square by the error MS.

Example 14.1b demonstrates testing of the hypotheses stated in Example 14.1a. To test whether oxygen consumption is the same among all three species, the species F (i.e., 24.45) is compared to the critical value, $F_{0.05(1),2,54} \approx 3.17$; because the former exceeds the later, the null hypothesis is rejected.* In a similar fashion, we test the hypothesis concerning each of the other two factors, as well as each of the four hypotheses regarding the interactions of factors, by comparing the calculated F values with the critical values from Appendix Table B.4.

Recall from Chapter 12 that the test for a two-way interaction asks whether differences in the variable among levels of one factor are the same at all levels of the second factor. A test for a three-factor interaction may be thought of as asking if the interaction between any two of the factors is the same at all levels of the third factor. As shown at the conclusion of Example 14.1b, statistical differences among levels of a factor must be expressed with caution if that factor has a significant interaction with another factor.

It is only for a factorial ANOVA with all factors fixed that we compute all F values utilizing the error MS. If any of the factors are random effects, then the analysis becomes more complicated. The proper F calculations for such situations appear in Appendix D.

If there are not equal numbers of replicates in each cell of a factorial analysis of variance design, then the usual ANOVA computations are not valid (see Section 14.5).

A factorial ANOVA experimental design may also include nesting (see Chapter 15 for a discussion of nesting). For example, in Example 14.1 we might have performed two or more respiratory-rate determinations on each of the four animals per cell. Some of the available computer programs for factorial analysis of variance also provide for nested (also called hierarchical) experimental designs.

If one or two of the three factors are measured on an interval or ratio scale, this is an analysis of covariance situation, as described in Section 12.9, and computer programs are available for such analyses. In Example 12.1, for instance, the variable is plasma calcium concentration and two factors are hormone treatment and sex. A third factor might be age, or weight, or hemoglobin concentration, or temperature.

14.2 THE LATIN-SQUARE EXPERIMENTAL DESIGN

A special case of a three-factor analysis of variance is an extension of the randomized-complete-block ANOVA of Section 12.4a or of the repeated-measures ANOVA of Section 12.4c. The two-factor experimental design discussed in Section 12.4a is

*There are no critical values in Appendix Table B.4 for $\nu_2 = 54$, so the values for the next lower degrees of freedom ($\nu_2 = 50$) were utilized. The symbol "$\approx$" indicates "approximately equal to." Alternatively, harmonic interpolation (see introduction to Appendix B) could have been employed: for this example, the interpolation would calculate critical values different from those above by only 0.01. Also, some computer routines can produce critical values.

EXAMPLE 14.1b The Analysis of Variance Summary for the Experiment in Example 14.1a

The following results are obtained for the information in Table 14.1:

For Factor A: $F = \dfrac{0.90875}{0.03713} = 24.45$ For $A \times B$ interaction: $F = \dfrac{0.27542}{0.03713} = 7.42$

For Factor B: $F = \dfrac{12.32791}{0.03713} = 332.02$ For $A \times C$ interaction: $F = \dfrac{0.18514}{0.03713} = 4.99$

For Factor C: $F = \dfrac{0.00889}{0.03713} = 0.24$ For $B \times C$ interaction: $F = \dfrac{0.08764}{0.03713} = 2.36$

For $A \times B \times C$ interaction: $F = \dfrac{0.05514}{0.03713} = 1.49$

Effect in hypothesis	*Calculated* F	*Critical* F *(see footnote 1)*	*Conclusion*	P *(see footnote 2)*
1. Species (Factor A)	24.45	$F_{0.05(1),2,54} \approx 3.17$	Reject H_0	$P \ll 0.00001$
2. Temperature (Factor B)	332.02	$F_{0.05(1),2,54} \approx 3.17$	Reject H_0	$P \ll 0.00001$
3. Sex (Factor C)	0.24	$F_{0.05(1),1,54} \approx 4.03$	Do not reject H_0	$P = 0.63$
4. $A \times B$	7.42	$F_{0.05(1),4,54} \approx 2.56$	Reject H_0	$P = 0.000077$
5. $A \times C$	4.99	$F_{0.05(1),2,54} \approx 3.17$	Reject H_0	$P = 0.010$
6. $B \times C$	2.36	$F_{0.05(1),2,54} \approx 3.17$	Do not reject H_0	$P = 0.10$
7. $A \times B \times C$	1.49	$F_{0.05(1),4,54} \approx 2.56$	Do not reject H_0	$P = 0.22$

[1]There are no critical values in Appendix Table B.4 for $\nu_2 = 54$, so the values for the next lower DF ($\nu_2 = 50$) were used.

[2]These probabilities were obtained from a computer program.

Thus, the hypothesis of equal effects of species and the hypothesis of equal effects of the temperatures are both rejected. However, there is also concluded to be significant interaction between species and temperature, and significant interaction between species and sex. Therefore, it must be realized that, although mean respiratory rates in the sampled populations are concluded to be different for the three species and different at the three temperatures, the differences among species are dependent on both temperature and sex.

composed of a fixed-effects factor (factor A) about which there is a null hypothesis of interest, and a random-effects factor (factor B) whose levels are termed "blocks," and blocking is intended to reduce the unexplained variability among the data. The *Latin-square** experimental design typically consists of a fixed-effects factor of interest

*The term *Latin square* derives from an ancient game of arranging Latin letters in cells within a square. Latin squares were first studied by Swiss mathematician Leonhard Euler (1707–1783) late in his very productive life (Norton, 1939), long before they were employed in analysis of variance. He used the French term *quarré latin*, and A. Cayley may have been the first to use the English term in 1890 (David, 1995); in English it is sometimes written without capitalization.

in hypothesis testing (let us call it factor A) and *two* blocking factors (sometimes referred to as "nuisance factors"), which we shall call factor B and factor C. Having two blocking factors may reduce the remainder MS even further, thus increasing the power of the test for difference among levels of factor A. However, a disadvantage may be that the remainder degrees of freedom are so small that the power of the test is low.

The data in a Latin-square experiment may be displayed conveniently in a tabulation that has the levels of one blocking factor (factor B) as rows and the levels of the other blocking factor (factor C) shown as columns. For example, for three levels of factors A, of factor B, and of factor C, we have the following table:

	Factor C		
Factor B	Level 1	Level 2	Level 3
Level 1	X	X	X
Level 2	X	X	X
Level 3	X	X	X

This table has $3 \times 3 = 9$ cells, and each cell contains one datum: "X." The data to which each of the three levels of factor A are applied can be denoted as A_1, A_2, and A_3; and a Latin square must always contain the same number of levels of each of the three factors. There are 12 possible arrangements for a 3×3 Latin square,* one of which is this:

$$\begin{array}{ccc} A_2 & A_1 & A_3 \\ A_3 & A_2 & A_1 \\ A_1 & A_3 & A_2 \end{array}$$

Example 12.4 represented an experiment designed to test the null hypothesis that the mean time to take effect is the same for three different anesthetics. In a Latin-square arrangement for testing this H_0, one blocking factor could be the source of the animals (factor B, a random-effects factor), and the other could be the source of the drugs (factor C, also a random-effects factor). One of the advantages of a Latin-square design is that it requires fewer data than if a crossed-factor ANOVA were used. For example, for three factors, each consisting of three levels, the Latin square employs nine data; but for a crossed three-factor ANOVA with three levels per factor (see Section 14.1), there would be 27 (i.e., $3^3 = 27$) cells, and 27 data would be required if there were one datum per cell. Therefore, the Latin-square procedure demands far less experimental resources than does a crossed-factor analysis.

In other situations, a block could represent repeated measures on a subject. So the experiment of Example 12.4, which consisted of measurements of effect time for three drugs (factor A, a fixed-effects factor) using animals from three sources (factor B, a random-effects factor), could have been expanded into a Latin-square experiment for each animal tested on three different days (factor C, a repeated-measure factor, for which the experimenter needs to be cautious about avoiding carryover effects, as described in Section 12.4c).

The Latin-square arrangement of treatments (levels of factor A) should be selected at random from all possible arrangements. The experimenter can arrange the rows randomly and the columns randomly, and then assign each level of factor A randomly within each row with the stipulation that each level of factor A appears only once in

*There are 12 configurations possible for a 3×3 Latin square, 576 possible for a 4×4 square, 161,280 for a 5×5 square, 812,851,299 for a 6×6 square, and 61,479,419,904,000 for a 7×7 square.

each column and only once in each row. Several sets of such configurations are listed by Cochran and Cox (1957: 145–146) and Fisher and Yates (1963: 86–89) to facilitate setting up Latin squares. Or, the designation of one of the possible Latin-square configurations may be done by an appropriate computer routine.

A level of factor A is to be assigned to each cell randomly, with the stipulation that each level must appear in each row only once and in each column only once. Also, it must be assumed that there is no interaction between any of the factors (i.e., there must be additivity), and there must be a reasonable expectation that this is so, for there is no good test for interaction in this experimental design.

The only hypothesis generally of interest in a Latin-square analysis is that of equality among the levels of the fixed-effects factor. The total factor-A, factor-B, and factor-C sums of squares are obtained as in other three-factor analyses of variance without replication; because there is only one datum per cell, there are no interactions to be examined. Using a to denote the number of levels in factor A (which is the same as the number of levels in factor B and in factor C), the degrees of freedom for the Latin-square ANOVA are as follows:

$$\text{total DF} = a^2 - 1; \tag{14.1}$$

$$\text{factor } A \text{ DF} = a - 1; \tag{14.2}$$

$$\text{factor } B \text{ DF} = a - 1; \tag{14.3}$$

$$\text{factor } C \text{ DF} = a - 1; \tag{14.4}$$

$$\begin{aligned}\text{remainder DF} &= a^2 - 1 - (a - 1) - (a - 1) - (a - 1) \\ &= (a - 1)(a - 2).\end{aligned} \tag{14.5}$$

The H_0 of no difference among the population means for the a levels of factor A is tested by

$$F = \frac{\text{factor } A \text{ MS}}{\text{remainder MS}}, \tag{14.6}$$

with factor A and remainder DF. Because of the small number of data typically in a Latin-square analysis, it is generally not advisable to proceed if there are missing data. However, a missing datum can be estimated as in Myers and Well (2003: 465) or by some computer software.

The Latin-square design, including situations with data replication, is discussed elsewhere (e.g., Maxwell and Delaney, 2004: 557–561, 611–615; Montgomery, 2005: 136–145; Myers and Well, 2003: 469–477; Snedecor and Cochran, 1989: Section 14.10; Steel, Torrie, and Dickey, 1997: 227–237; and Winer, Brown, and Michels, 1991: Chapter 9).

(a) Crossover Design. Section 12.4c discussed the two-factor ANOVA experimental design where one of the factors is subjects (B, a random-effects factor) upon which repeated measurements are taken, one measurement for each level of the fixed-effects factor (A). It was noted there that enough time should be allowed between successive measurements so there is no carryover effect on X from one measurement to the next on the same subject. As a precaution against there being carryover effects of levels of the fixed-effects factor, the time (the day in the example in Section 12.4c) at which measurements are made on a subject may be considered a third ANOVA factor. Considering subjects and times to be random-effects factors, with no interaction among the three factors, the so-called crossover experimental design takes the form of a Latin square. The crossover design is discussed, for example, in Kirk (1995: 349ff) and Montgomery (2005: 141ff).

(b) Greco-Latin-Square Design. The Latin-square experimental design comprises a fixed-effects factor of interest and two random-effects blocking factors. This concept can be expanded to a design having a fixed-effects factor and *three* blocking factors ("nuisance factors"). This design is rarely encountered. Its reduction of the remainder mean square by using three blocking factors can result in increased power; but the remainder degrees of freedom, $(a - 1)(a - 3)$, are so small that power is decreased. Also, as with Latin squares, this design assumes that there is no interaction among the factors (in this case, among four factors), an assumption that may not be warranted. Greco-Latin-square experiments are described by Cochran and Cox (1957: 132–133); Montgomery (2005: 142–145); Myers and Well (2003: 476–477); and Winer, Brown, and Michels (1991: 680–681, 699–702, 733–734).

14.3 HIGHER-ORDER FACTORIAL ANALYSIS OF VARIANCE

More than three factors may be analyzed simultaneously, but the number of possible interactions to be dealt with will soon become unwieldy as larger analyses are considered (see Table 14.2). For more than three or four factors, prohibitively large amounts of data are needed and interpretations of factor and interaction effects become very difficult.

The major effort in performing an ANOVA is the calculation of the several factor and interaction sums of squares. The factor and interaction degrees of freedom may be obtained as indicated in Section 14.1, and each needed mean square is the relevant sum of squares divided by the respective degrees of freedom. Available computer software provides the needed sums of squares, degrees of freedom, and mean squares. If all factors to be examined are for fixed effects, the F required to test each null hypothesis is obtained by dividing the appropriate factor or interaction mean square by the error MS. If, however, any of the factors represents random effects, then the analysis is more complex and, in some cases, impossible. Appendix D presents the procedures applicable to hypothesis testing in several such cases. See Section 14.5 for consideration of analyses with unequal replication.

If any (but not all) of the factors in a multiway ANOVA are measured on an interval or ratio scale, then we have an analysis of covariance situation (see Section 12.9). If all

TABLE 14.2: Number of Hypotheses Potentially Testable in Factorial Analyses of Variance

	Number of factors			
	2	3	4	5
Main factor	2	3	4	5
2-way interactions	1	3	6	10
3-way interactions		1	4	10
4-way interactions			1	5
5-way interactions				1

Note: The number of mth-order interactions in a k-factor ANOVA is the number of ways k factors can be combined m at a time (see Section 5.3):

$$_kC_m = \frac{k!}{\quad}$$

of the factors are on an interval or ratio scale, then a multiple regression (Chapter 20) may be called for.

14.4 MULTIWAY ANALYSIS OF VARIANCE WITH BLOCKS OR REPEATED MEASURES

Experimental designs can be devised having three or more factors where one or more factors are blocks (see Section 12.4a) or are subjects upon which repeated measures are taken (see Section 12.4c). In such a situation, the analysis may proceed as a factorial ANOVA with the blocking factor or the subjects considered as a random-effects factor. After the sums of squares, degrees of freedom, and mean squares are calculated, an appropriate computer program, or Appendix D, can assist in deriving the appropriate F's to test the hypotheses of interest.

There are also designs in which the same block is applied to some—*but not all*—of the combinations of other factors, and such cases are known as *split-plot* experimental designs. If the same subject is exposed to some—*but not all*—combinations of the other factors, this is one of many kinds of *repeated-measures* designs. Discussions of these topics are found in texts on experimental design such as those of Maxwell and Delaney (2004: Chapters 12–15); Mickey, Dunn, and Clark (2004: Chapter 11); Montgomery (2005: Section 14.5); Myers and Well (2003: Chapter 14); Quinn and Keough (2002: Chapter 11); Snedecor and Cochran (1989, Sections 16.15 and 16.16); Steel, Torrie, and Dickey (1997: Chapter 16); and Winer, Brown, and Michels (1991: Section 5.15, Chapters 7 and 8).

14.5 FACTORIAL ANALYSIS OF VARIANCE WITH UNEQUAL REPLICATION

Although equal replication is always desirable for optimum power and ease of computation in analysis of variance, it is not essential for the performance of the computations in a single-factor ANOVA (Section 10.1). However, all the techniques thus far discussed for ANOVA designs consisting of two or more factors require equal numbers of data per cell (with the exception of the case of proportional replication described in Section 12.2a). For example, the data in Example 14.1 are composed of four replicates in each combination of species, temperature, and sex. If there were five or more replicates in a very small number of cells, then it is not highly criticizable to discard (at random within a cell) those few data necessary to arrive at equal numbers of replicate data. However, a more general approach is available, a procedure by which data suffering from replication inequality can be analyzed and interpreted by analysis-of-variance considerations. The mathematical manipulations involved are sufficiently complex as to be attempted reasonably only by a computer, but it is worthwhile to be aware of the fact that programs for such an analysis are available. (These procedures may employ a type of multiple linear regression—see Section 20.11—and may be referred to as "general linear models.") An introduction to regression methods for ANOVA experimental designs is given by Glantz and Slinker (2001).*

If inequality is due to one or a few cells containing one fewer datum than the others, then a factorial analysis of variance may be performed after inserting an estimate of each missing datum. If one datum is missing, an estimate of its value may be found as follows (Shearer, 1973):

$$\hat{X} = \frac{aA_i + bB_j + cC_l + \cdots - (k-1)\sum X}{N + k - 1 - a - b - c - \cdots}, \tag{14.7}$$

*R. A. Fisher described the relationship between regression and analysis of variance in 1921 (Peters, 1987: 136).

where $\hat{X}$ is the estimated value for a missing datum in level i of factor A, level j of factor B, level l of factor C, and so on; a, b, c, and so on are the numbers of levels in factors A, B, C, and so on, respectively; A is the sum of all the other data in level i of factor A, B is the sum of the other data in level j of factor B, and so on; the summation of $aA_i + bB_j + cC_l + \ldots$ is over all factors; k is the number of factors; $\sum X$ is the sum of all the other data in all levels of all factors; and N is the total number of data (including the missing one) in the experimental design. This estimated value may then be inserted with the other data in the analysis-of-variance computations.

An alternative method of handling experimental designs with one or a few cells containing one fewer datum than the other is much simpler than, but not as desirable as, the aforementioned procedure. For each small cell the mean of the cell's observed data can be inserted as an additional datum. The analysis of variance is then performed as usual, but with the total DF and within-cells DF calculated without including the number of such additional data. (That is, the total and within-cells DF are those appropriate to the set of original observations.) A better estimation procedure for missing data is to use the cell means as starting values for employing Equation 14.7 iteratively, just as with Equation 12.26.

MULTIPLE COMPARISONS AND CONFIDENCE INTERVALS IN MULTIWAY ANALYSIS OF VARIANCE

As we have seen, for each factor a hypothesis may be tested concerning the equality of the population means of levels of that factor. If the null hypothesis of equality is rejected for a fixed-effects factor, then it may be desirable to ascertain between which levels the difference(s) lie(s). This can be done by the multiple-comparison procedures prescribed for two-way analyses of variance in Section 12.5. Also mentioned in that section is the calculation of confidence intervals with respect to level means in a two-factor analysis of variance; those considerations also apply to an ANOVA with more than two factors. It should be remembered that the sample size, n, referred to in Chapters 11 and 12 is replaced in the present context by the total number of data per level (i.e., the number of data used to calculate the level mean); k is replaced by the number of levels of the factor being tested; s^2 will be replaced by the MS appropriate in the denominator of the F ratio used to test for significance of the factor being examined; the degrees of freedom, ν (in q, q', and t) is the DF associated with this MS; and F in Scheffé's test is the same as in the ANOVA.

POWER, DETECTABLE DIFFERENCE, AND SAMPLE SIZE IN MULTIWAY ANALYSIS OF VARIANCE

The principles and procedures of Section 12.6 (for two-way ANOVA) may be readily expanded to multifactor analysis of variance. In Section 12.6, k' is the number of levels of the factor under consideration, n' is the total number of data in each level of that factor, s^2 is the appropriate MS in the denominator of the F used for the desired hypothesis test, ν_2 is the DF associated with that MS, and $\nu_1 = k' - 1$. Then, the power of the ANOVA in detecting differences among level means may be estimated using Equations 12.40–12.42.

Equation 12.42, in place of Equation 10.34, may be used in the fashion shown in Example 10.6, to estimate the minimum number of data per level that would be needed to achieve a specified power, given the significance level and detectable difference desired among means.

Equation 12.43 enables us to estimate the smallest difference among level means detectable with the ANOVA. As indicated in Section 12.6d, we can also use Equation 12.42 to estimate the maximum number of levels testable.

(a) The Mixed-Model ANOVA. The aforementioned procedures are applicable when all the factors are fixed effects (i.e., we have a Model I ANOVA). They may also be applied to any fixed-effects factor in a mixed-model ANOVA, but in such cases we must modify our method as follows.

Consider the appropriate denominator for the F calculated to test for the significance of the factor in question. (See Appendix D.) Then, substitute this denominator for the within-cells MS (s^2); and substitute this denominator DF for ν_2.

EXERCISES

14.1. Use an appropriate computer program to test for all factor and interaction effects in the following $4 \times 3 \times 2$ Model I analysis of variance, where a_i is a level of factor A, b_i is a level of factor B, and c_i is a level of factor C.

	a_1			a_2			a_3			a_4		
	b_1	b_2	b_3	b_1	b_2	b_3	b_1	b_2	b_3	b_1	b_2	b_3
	4.1	4.6	3.7	4.9	5.2	4.7	5.0	6.1	5.5	3.9	4.4	3.7
c_1	4.3	4.9	3.9	4.6	5.6	4.7	5.4	6.2	5.9	3.3	4.3	3.9
	4.5	4.2	4.1	5.3	5.8	5.0	5.7	6.5	5.6	3.4	4.7	4.0
	3.8	4.5	4.5	5.0	5.4	4.5	5.3	5.7	5.0	3.7	4.1	4.4
	4.8	5.6	5.0	4.9	5.9	5.0	6.0	6.0	6.1	4.1	4.9	4.3
c_2	4.5	5.8	5.2	5.5	5.3	5.4	5.7	6.3	5.3	3.9	4.7	4.1
	5.0	5.4	4.6	5.5	5.5	4.7	5.5	5.7	5.5	4.3	4.9	3.8
	4.6	6.1	4.9	5.3	5.7	5.1	5.7	5.9	5.8	4.0	5.3	4.7

14.2. Use an appropriate computer program to test for the effects of all factors and interactions in the following $2 \times 2 \times 2 \times 3$ Model I analysis of variance design, where a_i is a level of factor A, b_i is a level of factor B, c_i is a level of factor C, and d_i is a factor of level D.

	a_1				a_2			
	b_1		b_2		b_1		b_2	
	c_1	c_2	c_1	c_2	c_1	c_2	c_1	c_2
	12.2	13.4	12.2	13.1	10.9	12.1	10.1	11.2
d_1	12.6	13.1	12.4	13.0	11.3	12.0	10.2	10.8
	12.5	13.5	12.3	13.4	11.2	11.7	9.8	10.7
	11.9	12.8	11.8	12.7	10.6	11.3	10.0	10.9
d_2	11.8	12.6	11.9	12.5	10.4	11.1	9.8	10.6
	12.1	12.4	11.6	12.3	10.3	11.2	9.8	10.7
	12.6	13.0	12.5	13.0	11.1	11.9	10.0	10.9
d_3	12.8	12.9	12.7	12.7	11.1	11.8	10.4	10.5
	12.9	13.1	12.4	13.2	11.4	11.7	10.1	10.8

14.3. Using an appropriate computer program, test for all factor and interaction effects in the following Model I 3×2 analysis of variance with unequal replication.

a_1		a_2		a_3	
b_1	b_2	b_1	b_2	b_1	b_2
34.1	35.6	38.6	40.3	41.0	42.1
36.9	36.3	39.1	41.3	41.4	42.7
33.2	34.7	41.3	42.7	43.0	43.1
35.1	35.8	41.4	41.9	43.4	44.8
			40.8		44.5

14.4. A Latin-square experimental design was used to test for the effect of four hormone treatments (A_1, A_2, A_3, and A_4) on the blood calcium levels (measured in mg Ca per 100 ml of blood) of adult farm-raised male ostriches. The two blocking factors are farms (factor B) and analytical methods (factor C). Test the null hypothesis H_0: The mean blood-calcium level is the same with all four hormone treatments.

	Analytical methods			
Farms	C_1	C_2	C_3	C_4
B_1	A_3 12.5	A_4 9.7	A_2 12.0	A_1 9.4
B_2	A_2 10.3	A_3 13.1	A_1 9.5	A_4 13.0
B_3	A_1 8.8	A_2 11.7	A_4 12.4	A_3 14.3
B_4	A_4 10.6	A_1 7.1	A_3 12.0	A_2 10.1

CHAPTER 15

Nested (Hierarchical) Analysis of Variance

Chapters 12 and 14 dealt with analysis-of-variance experimental designs that the statistician refers to as *crossed*. A crossed experiment is one where all possible combinations of levels of the factors exist; the cells of data are formed by each level of one factor being in combination with each level of every other factor. Thus, Example 12.1 is a two-factor crossed experimental design, for each sex is found in combination with each hormone treatment. In Example 14.1, each of the three factors is found in combination with each of the other factors.

In some experimental designs, however, we may have some levels of one factor occurring in combination with the levels of one or more other factors, and other distinctly different levels occurring in combination with others. In Example 15.1a, where blood-cholesterol concentration is the variable, there are two factors: drug type and drug source. Each drug was obtained from two sources, but the two sources are not the same for all the drugs. Thus, the experimental design is not crossed; rather, we say it is *nested* (or *hierarchical*). One factor (drug source) is nested within another factor (drug type). A nested factor, as in the present example, is typically a random-effects factor, and the experiment may be viewed as a modified one-way ANOVA where the levels of this factor (drug source) are samples and the cholesterol measurements within a drug source are called a "subsample."

Sometimes experiments are designed with nesting in order to test a hypothesis about difference among the samples. More typical, however, is the inclusion of a random-effects nested factor in order to account for some within-groups variability and thus make the hypothesis testing for the other factor (usually a fixed-effects factor) more powerful.

15.1 NESTING WITHIN ONE FACTOR

In the experimental design such as in Example 15.1a, the primary concern is to detect population differences among levels of the fixed-effects factor (drug type). We can often employ a more powerful test by nesting a random-effects factor that can account for some of the variability within the groups of interest. The partitioning of the variability in a nested ANOVA may be observed in this example.

(a) Calculations for the Nested ANOVA. Testing the hypotheses in Example 15.1a involves calculating relevant sums of squares and mean squares. This is often done by computer; it can also be accomplished with a calculator as follows

EXAMPLE 15.1a A Nested (Hierarchical) Analysis of Variance

The variable is blood cholesterol concentration in women (in mg/100 ml of plasma). This variable was measured after the administration of one of three different drugs to each of 12 women, and each administered drug was obtained from one of two sources.

	Drug 1		**Drug 2**		**Drug 3**		
	Source A	*Source Q*	*Source D*	*Source B*	*Source L*	*Source S*	
	102	103	108	109	104	105	
	104	104	110	108	106	107	
n_{ij}	2	2	2	2	2	2	$N = 12$
$\sum_{l=1}^{n_{ij}} X_{ijl}$	206	207	218	217	210	212	
$\overline{X}_i$	103	103.5	109	108.5	105	106	$\overline{X} = 105.8333$
n_i	4		4		4		$N = 12$
$\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl}$	413		435		422		$\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl} = 1270$
$\overline{X}_i$	103.25		108.75		105.5		

(see Example 15.1b). In the hierarchical design described, we can uniquely designate each datum by using a triple-subscript notation, where X_{ijl} indicates the lth datum in subgroup j of group i. Thus, in Example 15.1a, $X_{222} = 108$ mg/100 ml, $X_{311} = 104$ mg/100 ml, and so on. For the general case, there are a groups, numbered 1 through a, and b is the number of subgroups in each group. For Example 15.1a, there are three levels of factor A (drug type), and b (the number of levels of factor B, i.e., sources for each drug) is 2. The number of data in subgroup j of group i may be denoted by n_{ij} (2 in this experiment), and the total number of data in group i is n_i (in this example, 4). The total number of observations in the entire experiment is $N = \sum_{i=1}^{k} n_i$ (which could also be computed as $N = \sum_{i=1}^{a}\sum_{j=1}^{b} n_{ij}$). The sum of the data in subgroup j of group i is calculated as $\sum_{l=1}^{n_{ij}} X_{ijl}$; the sum of the data in group i is $\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl}$; and the mean of group i is

$$\overline{X}_i = \frac{\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl}}{n_i}. \tag{15.1}$$

The grand mean of all the data is

$$\overline{X} = \frac{\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl}}{N}. \tag{15.2}$$

EXAMPLE 15.1b Computations for the Nested ANOVA of Example 15.1a

Drug 1		**Drug 2**		**Drug 3**	
Source A	*Source Q*	*Source D*	*Source B*	*Source L*	*Source S*

$$\frac{\left(\sum_{l=1}^{n_{ij}} X_{ijl}\right)^2}{n_{ij}}$$

21218.0 21424.5 23762.0 23544.5 22050.0 22472.0

$$\sum_{i=1}^{a}\sum_{j=1}^{b}\frac{\left(\sum_{l=1}^{n_{ij}} X_{ijl}\right)^2}{n_{ij}} = 134471.0$$

$$\frac{\left(\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl}\right)^2}{n_i}$$

42642.25 47306.25 44521.00

$$\sum_{i=1}^{a}\frac{\left(\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl}\right)^2}{n_i} = 134469.50$$

$$\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} x_{ijl}^2 = 134480.00 \qquad C = \frac{\left(\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl}\right)^2}{N} = \frac{(1270)^2}{12} = 134408.33$$

$$\text{total SS} = \sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl}^2 - C = 134480.00 - 134408.33 = 71.67$$

$$\text{among all subgroups SS} = \sum_{i=1}^{a}\sum_{j=1}^{b}\frac{\left(\sum_{l=1}^{n_{ij}} X_{ijl}\right)^2}{n_{ij}} - C = 134471.00 - 134408.33 = 62.67$$

$$\text{error SS} = \text{total SS} - \text{among all subgroups SS} = 71.67 - 62.67 = 9.00$$

$$\text{groups SS} = \sum_{i=1}^{a}\frac{\left(\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl}\right)^2}{n_i} - C = 134469.50 - 134408.33 = 61.17$$

$$\text{subgroups SS} = \text{among all subgroups SS} - \text{groups SS} = 62.67 - 61.17 = 1.50$$

Source of variation	SS	DF	MS
Total	71.67	11	
Among all subgroups (Sources)	62.67	5	
Groups (Drugs)	61.17	2	30.58
Subgroups	1.50	3	0.50
Error	9.00	6	1.50

H_0: There is no difference among the drug sources in affecting mean blood cholesterol concentration.

H_A: There is difference among the drug sources in affecting mean blood cholesterol concentration.

$$F = \frac{0.50}{1.50} = 0.33. \quad F_{0.05(1),3,6} = 4.76. \quad \text{Do not reject } H_0.$$
$$P > 0.50 \quad [P = 0.80]$$

H_0: There is no difference in mean cholesterol concentrations owing to the three drugs (i.e., $\mu_1 = \mu_2 = \mu_3$).

H_A: There is difference in mean cholesterol concentrations owing to the three drugs.

$$F = \frac{30.58}{0.50} = 61.16. \quad F_{0.05(1),2,3} = 9.55. \quad \text{Reject } H_0.$$
$$0.0025 < P < 0.005 \quad [P = 0.0037]$$

The total sum of squares for this ANOVA design considers the deviations of all the X_{ijl} from $\overline{X}$ and may be calculated as

$$\text{total SS} = \sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}}\left(X_{ijl} - \overline{X}\right)^2 \tag{15.3}$$

or by this "machine formula":

$$\text{total SS} = \sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl}^2 - C, \tag{15.3a}$$

where

$$C = \frac{\left(\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl}\right)^2}{N}. \tag{15.4}$$

For the total variability,

$$\text{total DF} = N - 1. \tag{15.5}$$

The variability among groups (i.e., the deviations $\overline{X}_i - \overline{X}$) is expressed as the "among groups SS" or, simply,

$$\text{groups SS} = \sum_{i=1}^{a} n_i\left(\overline{X}_i - \overline{X}\right)^2 \tag{15.6}$$

or

$$\text{groups SS} = \sum_{i=1}^{a} \frac{\left(\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl}\right)^2}{n_i} - C; \tag{15.6a}$$

and

$$\text{groups DF} = a - 1. \tag{15.7}$$

There is a total of ab subgroups in the design, and, considering them as if they were groups in a one-way ANOVA, we can calculate a measure of the deviations $\overline{X}_{ij} - \overline{X}$ as

$$\text{among all subgroups SS} = \sum_{i=1}^{a}\sum_{i=1}^{b} n_{ij}\left(\overline{X}_{ij} - \overline{X}\right)^2 \tag{15.8}$$

or

$$\text{among all subgroups SS} = \sum_{i=1}^{a}\sum_{j=1}^{b}\frac{\left(\sum_{l=1}^{n_{ij}} X_{ijl}\right)^2}{n_{ij}} - C; \tag{15.8a}$$

and

$$\text{among all subgroups DF} = ab - 1. \tag{15.9}$$

The variability due to the subgrouping within groups is evidenced by the deviations of subgroup means from their group means, $\overline{X}_{ij} - \overline{X}_i$, and the appropriate sum of squares is the "among subgroups within groups" SS, which will be referred to as

$$\text{subgroups SS} = \text{among all subgroups SS} - \text{groups SS}; \tag{15.10}$$

and

$$\text{subgroups DF} = \text{among all subgroups DF} - \text{groups DF} = a(b - 1). \tag{15.11}$$

The within-subgroups, or "error," variability expresses the deviations $X_{ijl} - \overline{X}_{ij}$, namely the deviations of data from their subgroup means; it is essentially the within-cells variability encountered in Chapters 12 and 14. The appropriate sum of squares is obtained by difference:

$$\text{error SS} = \text{total SS} - \text{among all subgroups SS}, \tag{15.12}$$

with

$$\text{error DF} = \text{total DF} - \text{among all subgroups DF} = N - ab. \tag{15.13}$$

The summary of this hierarchical analysis of variance is presented in Table 15.1. Recall that MS = SS/DF. Some similarities may be noted between Tables 12.1 and 15.1, but in the nested ANOVA of Table 15.1 we cannot speak of interaction between the two factors. Calculations for the data and hypotheses of Example 15.1a are shown in Example 15.1b.

(b) Hypothesis Testing in the Nested ANOVA. For the data in Example 15.1a, we can test the null hypothesis that no difference in cholesterol occurs among subgroups (i.e., the source of the drugs has no effect on the mean concentration of blood cholesterol). We do this by examining

$$F = \frac{\text{subgroups MS}}{\text{error MS}}. \tag{15.14}$$

For Example 15.1b, this is $F = 0.50/1.50 = 0.33$; since $F_{0.05(1),3,6} = 4.76$, H_0 is not rejected. (The exact probability of an F at least this large if H_0 is true is 0.80.)

The null hypothesis that there is no difference in cholesterol with the administration of the three different drugs can be tested by

$$F = \frac{\text{groups MS}}{\text{subgroups MS}}, \tag{15.15}$$

which in the present example is $F = 30.58/0.50 = 61.16$. As $F_{0.05(1),2,3} = 9.55$, H_0 is rejected. (The exact probability is 0.0037.) In an experimental design having subgroups nested within groups, as shown here, the groups most often represent a

TABLE 15.1: Summary of Hierarchical (Nested) Single-Factor Analysis of Variance Calculations

Source of variation	SS	DF
Total $[X_{ijl} - \overline{X}]$	$\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl}^2 - C$	N−1
Among all subgroups $[\overline{X}_{ij} - \overline{X}]$	$\sum_{i=1}^{a}\sum_{j=1}^{b}\frac{\left(\sum_{l=1}^{n_{ij}} X_{ijl}\right)^2}{n_{ij}} - C$	ab−1
Groups (i.e., Among groups) $[\overline{X}_i - \overline{X}]$	$\sum_{i=1}^{a}\frac{\left(\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl}\right)^2}{n_i} - C$	a−1
Subgroups (i.e., Among subgroups within groups) $[\overline{X}_{ij} - \overline{X}_i]$	among all subgroups SS− groups SS	a(b−1)
Error (i.e., Within subgroups) $[X_{ijl} - \overline{X}_{ij}]$	total SS− among all subgroups SS	N−ab

Note: $C = \frac{\left(\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{l=1}^{n_{ij}} X_{ijl}\right)^2}{N}$; a = number of groups; b = number of subgroups within each group; n_i = number of data in group i; n_{ij} = number of data in subgroup j for group i; N = total number of data in entire experiment.

fixed-effects factor. But the hypotheses testing is the same if, instead, the groups are a random-effects factor.

If we do not reject the null hypothesis of no difference among subgroups within groups, then the subgroups MS might be considered to estimate the same population variance as does the error MS. Thus, some statisticians suggest that in such cases a pooled mean square can be calculated by pooling the sums of squares and pooling the degrees of freedom for the subgroups variability and the error variability, for this will theoretically provide the ability to perform a more powerful test for differences among groups. (Pooling was previously discussed in Section 12.1h.) However, there is not widespread agreement on this matter, so the suggested procedure is to be conservative and not engage in pooling, at least not without consulting a statistician.

If there are unequal numbers of subgroups in each group, then the analysis becomes more complex, and the preceding calculations are not applicable. This situation is generally submitted to analysis by computer, perhaps by a procedure referred to in Glantz and Slinker (2001).

A hierarchical experimental design might have two (or more) layers of nesting with each subgroup composed of sub-subgroups, thus involving an additional step in the hierarchy. For instance, for the data of Example 15.1a, the different drugs define the groups, the different sources define the subgroups, and if different technicians or different instruments were used to perform the cholesterol analyses within each subgroup, then these technicians or instruments would define the sub-subgroups. Sokal and Rohlf (1995: 288–292) describe the calculations for a design with sub-subgroups, although one generally resorts to computer calculation for hierarchical designs with more than the two steps in the hierarchy discussed in the preceding paragraphs. See Appendix D.4b for assistance in hypothesis testing for one such nested design.

Brits and Lemmer (1990) discuss nonparametric ANOVA with nesting within a single factor.

2 NESTING IN FACTORIAL EXPERIMENTAL DESIGNS

Experimental designs are encountered where there are two or more crossed factors as well as one or more nested factors. For example, in Example 12.1 the two crossed factors are sex and hormone treatment, and five birds of each sex were given each hormone treatment. In addition, the experimenter might have obtained three syringes of blood (that is, three subsamples) from each bird, so that individual birds would be samples and the triplicate blood collections would be subsamples. The birds represent a nested, rather than a crossed, factor because the same animal is not found at every combination of the other two factors. The analysis-of-variance table would then look like that in Example 15.2. The computation of sums of squares could be obtained by computer, and the appropriate hypothesis testing will be that indicated in Appendix D.4c. Some available computer programs can operate with data where there is not equal replication. As shown in Appendix Table D.4c, in a factorial ANOVA with nesting, the determination of F's for hypothesis testing depends upon whether the crossed factors are fixed effects or random effects.

The concept of hierarchical experimental designs could be extended further in this example by considering that each subsample (i.e., each syringe of blood) in Example 15.2 was subjected to two or more (i.e., replicate) chemical analyses. Then chemical analysis would be a factor nested within the syringe factor, syringe nested within animal, and animal nested within the two crossed factors.

EXAMPLE 15.2 An Analysis of Variance with a Random-effects Factor (Animal) Nested within the Two-factor Crossed Experimental Design of Example 12.1

For each of the four combinations of two sexes and two hormone treatments ($a = 2$ and $b = 2$), there are five animals ($c = 5$), from each of which three blood collections are taken ($n = 3$). Therefore, the total number of data collected is $N = abcn = 60$.

Source of variation	SS	DF	MS
Total		$N - 1 = 59$	
Cells		$ab - 1 = 3$	
Hormone treatment (Factor A)	*	$a - 1 = 1$	†
Sex (Factor B)	*	$b - 1 = 1$	†
$A \times B$	*	$(a - 1)(b - 1) = 1$	†
Among all animals		$abc - 1 = 19$	
Cells		$ab - 1 = 3$	
Animals (Within cells) (Factor C)	*	$ab(c - 1) = 16$	†
Error (Within animals)	*	$abc(n - 1) = 40$	†

* These sums of squares can be obtained from appropriate computer software; the other sums of squares in the table might not be given by such a program, or MS might be given but not SS.

† The mean squares can be obtained from an appropriate computer program. Or, they may be obtained from the sums of squares and degrees of freedom (as MS = SS/DF). The degrees of freedom might appear in the computer output, or they may have to be determined by hand. The appropriate F statistics are those indicated in Appendix D.4c.

H_0: There is no difference in mean blood calcium concentration between males and females.

H_A: There is a difference in mean blood calcium concentration between males and females.

$$F = \frac{\text{factor } A \text{ MS}}{\text{factor } C \text{ MS}} \qquad F_{0.05(1),1,16} = 4.49$$

H_0: The mean blood calcium concentration is the same in birds receiving and not receiving the hormone treatment.

H_A: The mean blood calcium concentration is not the same in birds receiving and not receiving the hormone treatment.

$$F = \frac{\text{factor } B \text{ MS}}{\text{factor } C \text{ MS}} \qquad F_{0.05(1),1,16} = 4.49$$

H_0: There is no interactive effect of sex and hormone treatment on mean blood calcium concentration.

H_A: There is interaction between sex and hormone treatment in affecting mean blood calcium concentration.

$$F = \frac{A \times B \text{ MS}}{\text{factor } C \text{ MS}} \qquad F_{0.05(1),1,16} = 4.49$$

H_0: There is no difference in blood calcium concentration among animals within combinations of sex and hormone treatment.

H_A: There is difference in blood calcium concentration among animals within combinations of sex and hormone treatment.

$$F = \frac{\text{factor } C \text{ MS}}{\text{error MS}} \qquad F_{0.05(1),16,40} = 1.90$$

15.3 MULTIPLE COMPARISONS AND CONFIDENCE INTERVALS

Whenever a fixed-effects factor is concluded by an ANOVA to have a significant effect on the variable, we may turn to the question of which of the factor's levels are different from which others. If there are only two levels of the factor, then of course we have concluded that their population means are different by the ANOVA. But if there are more than two levels, then a multiple-comparison test must be employed.

The multiple-comparison procedures usable in nested experimental designs are discussed in Chapter 11, with slight modifications such as those we saw in Sections 12.5 and 14.6. Simply keep the following in mind when employing the tests of Sections 11.1, 11.3, and 11.4:

1. k refers to the number of levels being compared. (In Example 15.1a, $k = a$, the number of levels in factor A. In Example 15.2, $k = a$ when comparing levels of factor A, and $k = b$ when testing levels of factor B.)
2. The sample size, n, refers to the total number of data from which a level mean is calculated. (In Example 15.1a, the sample size $bn = 4$ would be used in place of n. In Example 15.2, we would use $bcn = 30$ to compare level means for factor A and $acn = 30$ for factor B.)

3. The mean square, s^2, refers to the MS in the denominator of the F ratio appropriate to testing the effect in question in the ANOVA. (In Example 15.1a, the subgroups [sources] MS would be used. In Example 15.2, the factor C MS would be used.)
4. The degrees of freedom, ν, for the critical value of q or q' are the degrees of freedom associated with the mean square indicated in item 3. (In Examples 15.1a and 15.2, these would be 3 and 16, respectively.)
5. The critical value of F in the Scheffé test has the same degrees of freedom as it does in the ANOVA for the factor under consideration. (In Example 15.1a, these are 2 and 3. In Example 15.2, they are 1 and 16.)

Once a multiple-comparison test has determined where differences lie among level means, we can express a confidence interval for each different mean, as was done in Sections 11.2, 12.5, and 14.6, keeping in mind the sample sizes, mean squares, and degrees of freedom defined in the preceding list.

15.4 POWER, DETECTABLE DIFFERENCE, AND SAMPLE SIZE IN NESTED ANALYSIS OF VARIANCE

In Sections 12.6 and 14.7, power and sample size for factorial analyses of variance were discussed. The same types of procedures may be employed for a fixed-effects factor within which nesting occurs. As previously used, k' is the number of levels of the factor, n' is the total number of data in each level, and $\nu = k' - 1$. The appropriate mean square, s^2, is that appearing in the denominator of the F ratio used to test that factor in the ANOVA, and ν_2 is the degrees of freedom associated with s^2.

Referring to Section 12.6, the power of a nested ANOVA to detect differences among level means may be estimated using Equations 12.40–12.42 (as in Section 12.6a). Equation 12.41 may be used to estimate the minimum number of data per level that would be needed to achieve a specified power (see Section 12.6b), and Equation 12.42 allows estimation of the smallest detectable difference among level means (see Section 12.6c). Section 12.6d describes how to estimate the maximum number of level means that can be tested.

EXERCISES

15.1. Using the data and conclusions of Example 15.1, perform the following:
- **(a)** Use the Tukey test to conclude which of the three drug means are statistically different from which.
- **(b)** Determine the 95% confidence interval for each significantly different drug mean.

15.2. Three water samples were taken from each of three locations. Two determinations of fluoride content were performed on each of the nine samples. The data are as follows, in milligrams of fluoride per liter of water:

Locations	1			2			3		
Samples	1	2	3	1	2	3	1	2	3
	1.1	1.3	1.2	1.3	1.3	1.4	1.8	2.1	2.2
	1.2	1.1	1.0	1.4	1.5	1.2	2.0	2.0	1.9

- **(a)** Test the hypothesis that there is no difference in mean fluoride content among the samples within locations.
- **(b)** Test the hypothesis that there is no difference in mean fluoride content among the locations.
- **(c)** If the null hypothesis in part (b) is rejected, use the Tukey test to conclude which of the three populations means differ from which.
- **(d)** If the null hypothesis in part (b) is rejected, determine the 95% confidence interval for each different population mean.

CHAPTER 16

Multivariate Analysis of Variance

Chapters 10, 12, 14, and 15 discussed various experimental designs categorized as analysis of variance (ANOVA), wherein a variable is measured in each of several categories, or levels, of one or more factors. The hypothesis testing asked whether the population mean of the variable differed among the levels of each factor. These are examples of what may be termed *univariate analyses of variance*, because they examine the effect of the factor(s) on only one variable.

An expansion of this concept is an experimental design where more than one variable is measured on each experimental subject. In Example 10.1, 19 animals were allocated at random to four experimental groups, and each group was fed a different diet. Thus, diet was the experimental factor, and there were four levels of the factor. In that example, only one variable was measured on each animal: the body weight. But other measurements might have been made on each animal, such as blood cholesterol, blood pressure, or body fat. If two or more variables are measured on each subject in an ANOVA design, we have a *multivariate analysis of variance* (abbreviated MANOVA).*

There are several uses to which multivariate analysis of variance may be put (e.g., Hair et al., 2006: 399–402). This chapter presents a brief introduction to this type of analysis, a multifaceted topic often warranting consultation with knowledgeable practitioners. More extensive coverage is found in many texts on the subject (e.g., Bray and Maxwell, 1985; Hair et al., 2006: Chapter 6; Hand and Taylor, 1987: Chapter 4; Johnson and Wichern, 2002: Chapter 6; Marcoulides and Hershberger, 1997: Chapters 3–4; Sharma, 1996: Chapters 11–12; Srivastava, 2002: Chapter 6; Stevens, 2002: Chapters 4–6; and Tabachnik and Fidell, 2001: Chapter 9). Other multivariate statistical methods are discussed in Chapter 20.

The multivariate analysis-of-variance experimental design discussed here deals with a single factor. There are also MANOVA procedures for blocked, repeated-measures, and factorial experimental designs, as presented in the references just cited.

16.1 THE MULTIVARIATE NORMAL DISTRIBUTION

Recall that univariate analysis of variance assumes that the sample of data for each group of data came from a population of data that were normally distributed, and univariate normal distributions may be shown graphically as in Figures 6.1 and 6.2. In

*Sometimes the variables are referred to as *dependent variables* and the factors as *independent variables* or *criterion variables*.

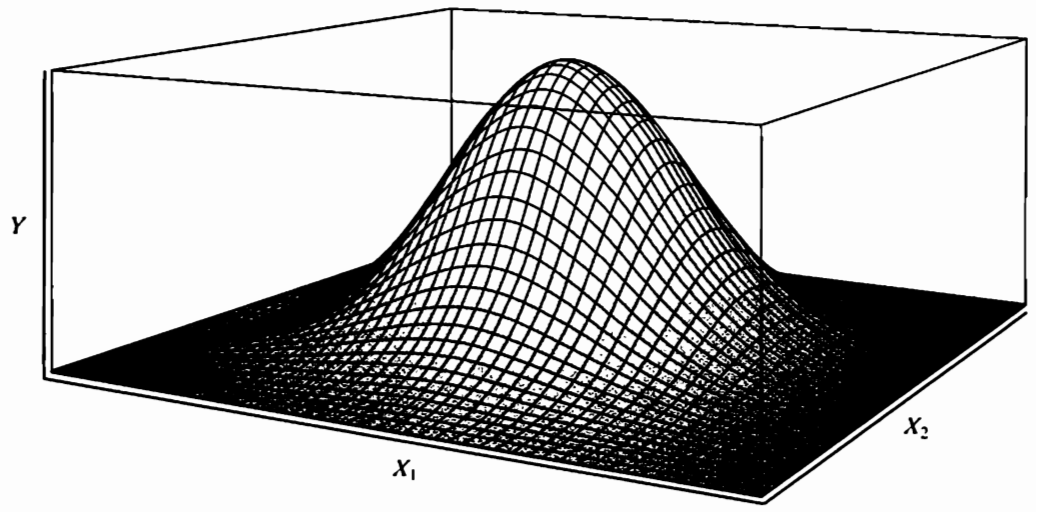


FIGURE 16.1: A bivariate normal distribution, where X_1 and X_2 have identical standard deviations.

such two-dimensional figures, the height of the curve, Y, representing the frequency of observations at a given magnitude of the variable X, is plotted against that value of X; and the highest point of the normal curve is at the mean of X.

The simplest multivariate case is where there are two variables (call them X_1 and X_2) and they can be plotted on a graph with three axes representing Y, X_1, and X_2. The two-variable extension of the single-variable normal curve is a surface representing a *bivariate normal distribution*, such as that shown in Figure 16.1.* The three-dimensional normal surface rises like a hill above a flat floor (where the floor is the plane formed by the two variables, X_1 and X_2), and the highest point of the curved surface is at the means of X_1 and X_2. A plot of more than three dimensions would be required to depict multivariate distributions with more than two measured variables.

Multivariate normality requires, among other characteristics (e.g., Stevens, 2002: 262), that for *each* X_i (in this example, X_i and X_2) there is a normal distribution of Y values. As shown in Figure 6.2a, univariate normal distributions with smaller standard deviations form narrower curves than those with larger standard deviations. Similarly, the hill-shaped bivariate graph of Figure 16.1 will be narrow when the standard deviations of X_1 and X_2 are small and broad when they are large.

Rather than drawing bivariate normal graphs such as Figure 16.1, we may prefer to depict these three-dimensional plots using two dimensions, just as mapmakers represent an elevated or depressed landscape using contour lines. Figure 16.2a shows the distribution of Figure 16.1 with a small plane passing through it parallel to the X_1 and X_2 plane at the base of the graph. A circle is delineated where the small plane intersects the normal-distribution surface. Figure 16.2b shows two planes passing through the normal surface of Figure 16.1 parallel to its base, and their intersections form two concentric circles. If Figures 16.2a and 16.2b are viewed from above the surface, looking straight down toward the plane of X_1 and X_2, those circles would appear as in Figures 16.3a and 16.3b, respectively. Three such intersecting planes would result in three circles, and so on. If the standard deviations

*This three-dimensional surface is what gave rise to the term *bell curve*, named by E. Jeuffret in 1872 (Stigler, 1999: 404).

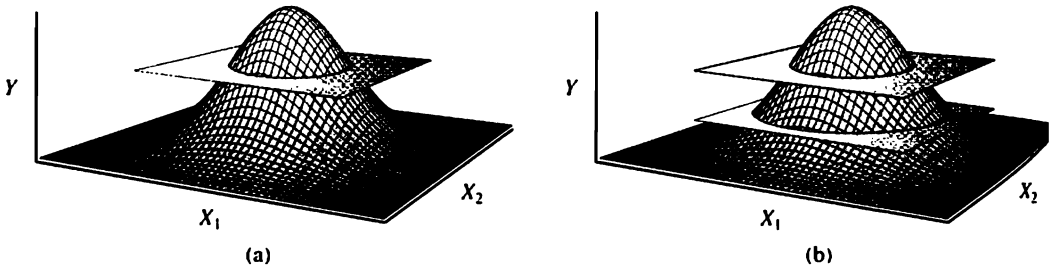


FIGURE 16.2: The bivariate normal distribution of Figure 16.1, with **(a)** an intersecting plane parallel to the X_1-X_2 plane, and **(b)** two intersection planes parallel to the X_1-X_2 plane.

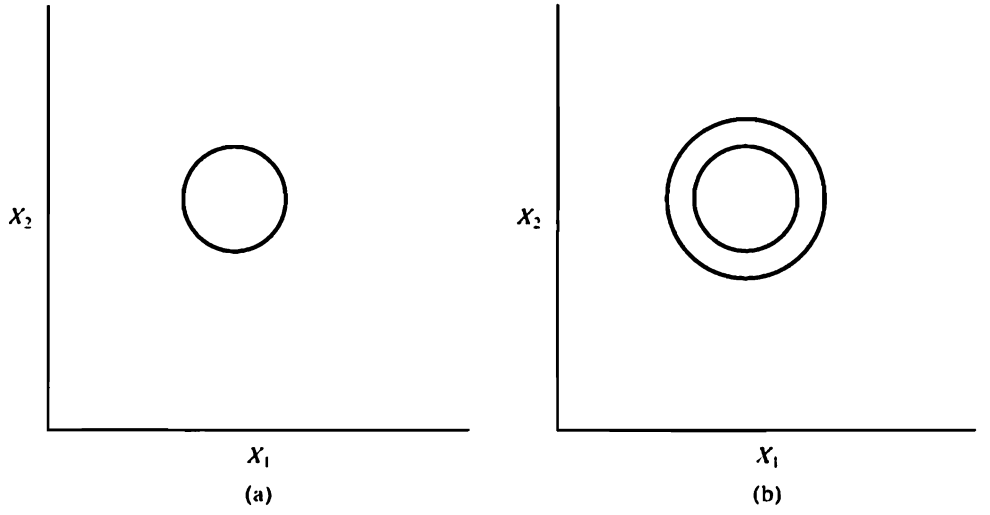


FIGURE 16.3: Representations of Figures 16.2a and 16.2b, showing the circles defined by the intersecting planes.

of X_1 and X_2 are not the same, then parallel planes will intersect the bivariate-normal surface to form ellipses instead of circles. This is shown, for three planes, in Figure 16.4. In such plots, the largest ellipses (or circles, if X_1 and X_2 have equal standard deviations) will be formed nearest the tails of the distribution. Only ellipses (and not circles) will be discussed hereafter, for it is unlikely that the two variables will have exactly the same variances (that is, the same standard deviations).

If an increase in magnitude of one of the two variables is not associated with a change in magnitude of the other, it is said that there is no correlation between X_1 and X_2. If an increase in magnitude of one of the variables *is* associated with either an increase or a decrease in the other, then the two variables are said to be correlated. (Chapter 19 provides a discussion of correlation.) If X_1 and X_2 are not correlated, graphs such as Figure 16.4 will show the long axis of all the ellipses parallel to either the X_1 or X_2 axis of the graph (Figures 16.4a and 16.4b, respectively). If, however, X_1 and X_2 are positively correlated, the ellipses appear as running from the lower left to the upper right of the graph (Figure 16.4c); and if the two variables are negatively correlated, the ellipses run from the lower right to the upper left (Figure 16.4d).

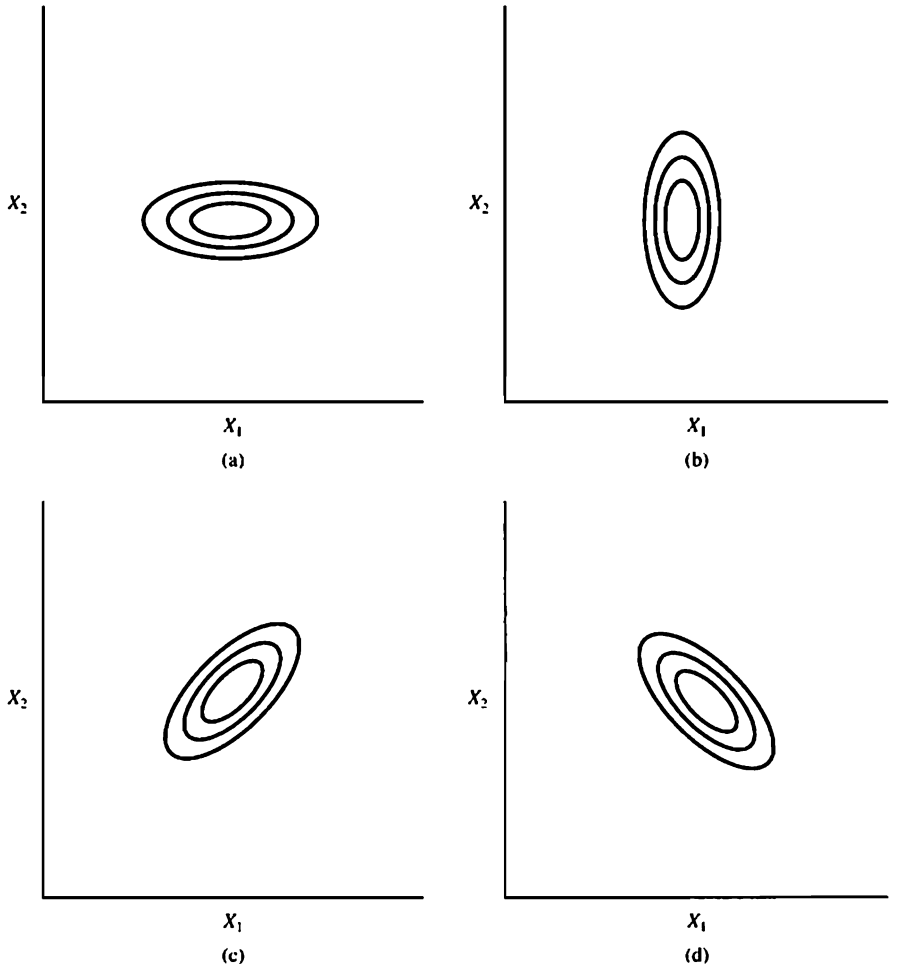


FIGURE 16.4: Representations of bivariate normal distributions where the standard deviations of X_1 and X_2 are not the same. **(a)** X_1 and X_2 are not correlated. **(b)** X_1 and X_2 are not correlated. **(c)** X_1 and X_2 are positively correlated. **(d)** X_1 and X_2 are negatively correlated.

MULTIVARIATE ANALYSIS OF VARIANCE HYPOTHESIS TESTING

At the beginning of the discussion of univariate analysis of variance (Chapter 10), it was explained that, when comparing a variable's mean among more than two groups, to employ multiple t-tests would cause a substantial inflation of α, the probability of a Type I error. In multivariate situations, we desire to compare two or more variables' means among two or more groups, and to do so with multiple ANOVAs would also result in an inflated chance of a Type I error*. Multivariate analysis of variance is a method of comparing the population means for each of the multiple variables of interest at the same time while maintaining the chosen magnitude of Type I error.

A second desirable trait of MANOVA is that it considers the correlation among multiple variables, which separate ANOVAs cannot do. Indeed, if the variables

*For m variables, the probability of a Type I error will range from α, if all of the variables are perfectly correlated, to $1 - (1 - \alpha)^m$, if there is no correlation among them. So, for example, if testing with two variables at the 5% significance level, P(Type I error) = 0.10 (Hair et al., 2006: 400), which can be seen from Table 10.1 by substituting m for C.

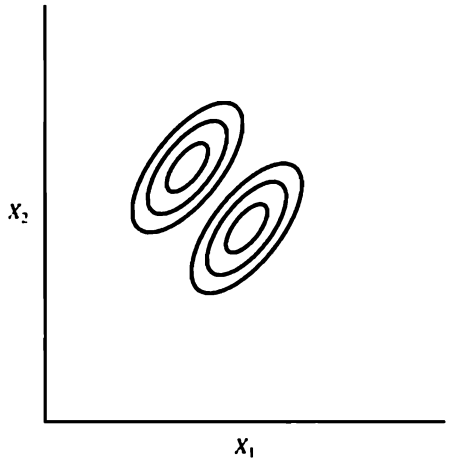


FIGURE 16.5: Two bivariate normal groups of positively correlated data differing in both dimensions.

are correlated, MANOVA may provide more powerful testing than performing a series of separate ANOVAs. (However, if the variables are not correlated, separate ANOVAs may be more powerful than MANOVA.) For example, there are two bivariate distributions depicted in Figure 16.5, with the distribution of variable X_1 being very similar in the two groups and the distribution of X_2 also being very similar in the two groups. Therefore, a univariate ANOVA (or a two-sample t-test) will be unlikely to conclude a difference between the means of the groups for variable X_1 or for variable X_2, but MANOVA may very well conclude the means of the two bivariate distributions to be different.

Third, sometimes group differences for each of several variables are too small to be detected with a series of ANOVAs, but a MANOVA will conclude the groups different by considering the variables jointly. Stevens (2002: 245) cautions to include in the analysis only variables for which there is good rationale, because very small differences between means for most of them may obscure substantial differences for some of them.

In univariate ANOVA with k groups, a typical null hypothesis is

$$H_0: \mu_1 = \mu_2 = \cdots = \mu_k,$$

which says that all k population means are the same. And the corresponding alternate hypothesis is

H_A: The k population means are not all equal.

Recall that H_A does not say that all means are different, only that at least one is different from the others.

Thus, for example, Example 10.1 presented an experiment to ask whether the mean body weight of pigs is the same when the animals are raised on four different feeds. And

H_0: $\mu_1 = \mu_2 = \mu_3 = \mu_4$

H_A: All four population means are not equal.

In a MANOVA with two variables (X_1 and X_2) and k groups, the null hypothesis may be stated as

$$H_0: \mu_{11} = \mu_{12} = \cdots = \mu_{1k} \quad \textit{and} \quad \mu_{21} = \mu_{22} = \cdots = \mu_{2k},$$

where μ_{ij} denotes the population mean of variable i in group j. This H_0 says that the means of variable 1 are the same for all k groups *and* the means of variable 2 are the same for all k groups. The corresponding MANOVA alternate hypothesis is

H_A: The k populations do not have the same group means for variable 1 *and* the same group means for variable 2.

Thus, H_0 is rejected if any of the μ_{1j}'s are concluded to differ from each other *or* if any of the μ_{2j}'s are concluded to differ from each other.

Example 16.1 is similar to Example 10.1, except it comprises two variables (X_1 and X_2): the weight of each animal's body fat and the dry weight of each animal without its body fat. The null hypothesis is that mean weight of body fat is the same on all four diets *and* the mean fat-free dry body weight is the same on all of these diets. (It is *not* being hypothesized that mean body-fat weight is the same as mean fat-free dry body weight!) In this example,

H_0: $\mu_{11} = \mu_{12} = \mu_{13} = \mu_{14}$ *and* $\mu_{21} = \mu_{22} = \mu_{23} = \mu_{24}$

and

H_A: The four feeds do not result in the same mean weight of body fat and the same mean fat-free dry body weight.

If, in the sampled populations, one or more of the six equals signs in H_0 is untrue, then H_0 should be rejected.

There are several methods for comparing means to test MANOVA hypotheses. This chapter will refer to four test statistics employed for this purpose and encountered in MANOVA computer programs. None of these four is considered "best" in all situations. Each captures different characteristics of the differences among means; thus, the four have somewhat different abilities to detect differences in various circumstances. The computations of these test statistics are far from simple and—especially for more than two variables—cannot readily be expressed in algebraic equations. (They are represented with much less effort as matrix calculations, which are beyond the scope of this book.) Therefore, we shall depend upon computer programs to calculate these statistics and shall not attempt to demonstrate the numerical manipulations. It can be noted, however, that the necessary calculations involve total, groups, and error sums of squares (SS, introduced in Section 10.1) and sums of cross products (to be introduced in Section 17.2). And, just as mean squares are derived from sums of squares, quantities known as "covariances" are derived from sums of crossproducts.

The four common MANOVA test statistics are the following.* They are all given by most MANOVA computer software; they often result in the same or very similar conclusions regarding H_0 and operate with similar power (especially with large samples); and they yield identical results when only one variable is being analyzed (a univariate ANOVA) or when $k = 2$.

- *Wilks' lambda.* Wilks' Λ (capital Greek lambda), also called Wilks' likelihood ratio (or Wilks' U),† is the oldest and most commonly encountered multivariate analysis-of-variance statistic, dating from the original formulation of the

*Each of the four MANOVA statistics is a function of what are called *eigenvalues*, or *roots*, of matrices. Matrix algebra is explained in many tests on multivariate statistics, and an introduction to it is given in Section 20.1.

†Named for American statistician Samuel Stanley Wilks (1906–1964), who made numerous contributions to theoretical and applied statistics, including to MANOVA (David and Morrison, 2006).

EXAMPLE 16.1 A Bivariate Analysis of Variance

Several members of a species of sparrow were collected at the same location at four different times of the year. Two variables were measured for each bird: the fat content (in grams) and the fat-free dry weight (in grams). For the statement of the null hypothesis, μ_{ij} denotes the population mean for variable i (where i is 1 or 2) and month j (i.e., j is 1, 2, 3, or 4).

H_0: $\mu_{11} = \mu_{12} = \mu_{13} = \mu_{14}$ *and* $\mu_{21} = \mu_{22} = \mu_{23} = \mu_{24}$

H_A: Sparrows do not have the same weight of fat *and* the same weight of fat-free dry body tissue at these four times of the year.

$\alpha = 0.05$

	December		January		February		March	
	Fat weight	*Lean dry weight*	*Fat weight*	*Lean dry weight*	*Fat weight*	*Lean dry weight*	*Fat weight*	*Lean dry weight*
	2.41	4.57	4.35	5.30	3.98	5.05	1.98	4.19
	2.52	4.11	4.41	5.61	3.48	5.09	2.05	3.81
	2.61	4.79	4.38	5.83	3.36	4.95	2.17	4.33
	2.42	4.35	4.51	5.75	3.52	4.90	2.00	3.70
	2.51	4.36			3.41	5.38	2.02	4.06
$\overline{X}$:	2.49	4.44	4.41	5.62	3.55	5.07	2.04	4.02

Computer computation yields the following output:

Wilks' $\Lambda = 0.0178$, $F = 30.3$, DF = 6, 28, $P \ll 0.0001$.

Reject H_0.

Pillai's trace = 1.0223, $F = 5.23$, DF = 6, 30, $P = 0.0009$.

Reject H_0.

Lawley-Hotelling trace = 52.9847, $F = 115$, DF = 6, 26, $P \ll 0.0001$.

Reject H_0.

Roy's maximum root = 52.9421, $F = 265$, DF = 3, 15, $P \ll 0.0001$.

Reject H_0.

MANOVA procedure (Wilks, 1932). Wilks' Λ is a quantity ranging from 0 to 1; that is, a measure of the amount of variability among the data that *is not* explained by the effect of the levels of the factor.* So, unlike typical test statistics

*Thus, a measure of the proportion of the variability that *is* explained by the levels of the factor is

$$\eta^2 = 1 - \Lambda, \tag{16.1}$$

and η^2 has a meaning like that of R^2 in another kind of multivariate analysis, that of multiple regression or multiple correlation (Section 20.3).

(e.g., F or t or χ^2), H_0 is rejected for *small*, instead of large, values of Λ. Tables of critical values have been published (e.g., Rencher, 2002: 161, 566–573), but computer programs may present Λ transformed into a value of F or χ^2 (tables of which are far more available) with the associated probability (P); as elsewhere, large values of F or χ^2 yield small P's. In Example 16.1, Λ is an expression of the amount of variability among fat weights and among lean dry body weights that is *not* accounted for by the effect of the four times of year.

- *Pillai's trace.* This statistic, based on Pillai (1955), is also called the Pillai-Bartlett trace (or V).* Many authors recommend this statistic as the best test for general use (see Section 16.2a). Large values of V result in rejection of H_0. There are tables of critical values of this statistic (e.g., Rencher, 2002: 166–167, 578–581), but it is often transformed to a value of F.
- *Lawley-Hotelling trace.* This statistic (sometimes symbolized by U) was developed by Lawley (1938) and modified by Hotelling (1951). Tables of critical values exist for this (e.g., Rencher, 2002: 167, 582–686), but it is commonly transformed into values of F.
- *Roy's maximum root.* This is also known by similar names, such as Roy's largest, or greatest, root and sometimes denoted by θ (lowercase Greek theta). This statistic (Roy, 1945) may be compared to critical values (e.g., Rencher, 2002: 165, 574–577), or it may be converted to an F.

Wilks' Λ is a very widely used test statistic for MANOVA, but Olson (1974, 1976, 1979) concluded that Pillai's trace is usually more powerful (see Section 16.2b), and others have found that the Pillai statistic appears to be the most robust and most desirable for general use. If the four MANOVA test statistics do not result in the same conclusion about H_0, further scrutiny of the data may include examination of scatter plots (see Section 17.1), with axes as in Figures 16.5 and 16.6, for correlation among variables. Correlation will suggest favoring the conclusion reached by Pillai's trace, and noncorrelation will suggest relying on Roy's statistic for superior power. In Example 16.1, all four test statistics conclude that H_0 is to be rejected.

(a) Assumptions. As in univariate ANOVA (Section 10.1), the underlying mathematical foundations of MANOVA depend upon certain assumptions. Although it is unlikely that all of the assumptions will be exactly met for a given set of data, it is important to be cognizant of them and of whether the statistical procedures employed are robust to departures from them.

A very important underlying assumption in MANOVA is that the data represent random samples from the populations of interest and that the observations on each subject are independent. In Example 16.1, the body-fat weights of sparrows in each month are assumed to have come at random from the population of body-fat weights of all sparrows from that month from that location, and the lean dry weights at each month are assumed to have come randomly from a population of such weights. Also, the body-fat weight of each subject (i.e., each sparrow) must be independent of the body-fat weight of each other subject, and the lean dry body weights of all the subjects must be independent of each other. MANOVA is invalidated by departure from the assumption of random and independent data.

*A *trace* is the result of a specific mathematical operation on a matrix. See Section 20.1 for more information on matrices.

There are statistical tests for this assumption, such as that which is analogous to the Bartlett test of the homogeneity of variances in the univariate ANOVA (Section 10.6) (Box, 1949, 1950) but which is seriously affected by nonnormality (e.g., Olson, 1974; Stevens, 2002: 271) and thus is not generally recommended. Data transformations (Chapter 13) may be useful to reduce nonnormality or to reduce heterogeneity of variances and covariances. Although MANOVA is typically robust to departures from the variability and variance-correlations assumptions, the Pillai trace (according to Olson, 1974, 1976) is generally the most robust of the four methods.

(b) Power. The power of a MANOVA depends upon a complex set of characteristics, including the extent to which the underlying assumptions (see Section 16.2a) are met. In general, increased sample size is associated with increased power, but power decreases with increase in the number of variables. Thus, if it is desired to employ an experimental design with several variables, larger samples will be needed than would be the case if there were only two variables. Also, as with ANOVA, the power of MANOVA is greater when the population differences between means are larger and when the variability within groups is small. The magnitude of correlations between variables can cause MANOVA to be either more or less powerful than separate ANOVAs. Some MANOVA computer programs calculate power, and Rencher (2002: Section 4.4) and Stevens (2002: 192–202) discuss the estimation of power and of the sample size required in MANOVA. Many computer programs provide a calculation of power, but recall (e.g., Section 10.3) that power estimated from a set of data should be considered as applying to future data sets.

Differences in power among the four test statistics are often not great, but there can be differences. If the group means differ in only one direction (i.e., they are uncorrelated, as in Figure 16.6), a relatively uncommon situation, Roy's statistic is the most powerful of the four, followed—in order of power—by the Lawley-Hotelling trace, Wilks' Λ, and Pillai's trace. However, in the more common situation where the group means differ among more than one dimension (i.e., the variables are correlated, as in Figure 16.5), then the relative powers of these statistics are in the reverse order: The Pillai trace is the most powerful, followed by Wilks' Λ, the Lawley-Hotelling trace, and then Roy's statistic. In intermediate situations, the four statistics tend more toward the latter ordering than the former.

(c) Two-Sample Hypotheses. The preceding four procedures may be used in the case of only two groups, for when $k = 2$ all four will yield the same results. But another test encountered for two-group multivariate analysis is *Hotelling's* T^2 (Hotelling, 1931). This is analogous to the univariate two-group situation, where either ANOVA (Section 10.1) or Student's t (Section 8.1) may be employed.

T^2 is related to the MANOVA statistics of Section 16.2 as follows (Rencher, 2002: 130)*:

$$T^2 = (n_1 + n_2 - 2)\left(\frac{1 - \Lambda}{\Lambda}\right), \tag{16.3}$$

$$T^2 = (n_1 + n_2 - 2)\left(\frac{V}{1 - V}\right), \tag{16.4}$$

*T^2 is also related to the multiple-regression coefficient of determination, R^2 (Equation 20.19), as

$$T^2 = (n_1 + n_2 - 2)\left(\frac{R^2}{1 - R^2}\right). \tag{16.2}$$

$$T^2 = (n_1 + n_2 - 2)\,U, \tag{16.5}$$

$$T^2 = (n_1 + n_2 - 2)\left(\frac{\theta}{1 - \theta}\right), \tag{16.6}$$

where m is the number of variables.

Upon calculation of T^2 (usually by computer), tables of critical values of T^2 (e.g., Rencher, 2002: 558–561) may be consulted, or

$$F = \frac{n_1 + n_2 - m - 1}{(n_1 + n_2 - 2)m}\,T^2 \tag{16.7}$$

may be used, with m and $n_1 + n_2 - m - 1$ degrees of freedom or, equivalently,

$$F = \frac{n_1 + n_2 - m}{(n_1 + n_2 - 1)m}\,T^2 \tag{16.7a}$$

with m and $n_1 + n_2$ degrees of freedom.

Nonparametric testing is also available for two-sample multivariate tests (i.e., as analogs to the univariate Mann-Whitney test, Section 8.11) and for paired-sample tests (analogous to the univariate Wilcoxon or sign tests, Sections 9.5 and 24.6).

16.3 FURTHER ANALYSIS

When a MANOVA rejects H_0, there are procedures that might be employed to expand the analysis of difference among groups (e.g., Bray and Maxwell, 1985: 40–45; Hand and Taylor, 1987: Chapter 5; Hair et al., 2006: 422–426); Hummel and Sligo, 1971; Stevens, 2002: 217–225; Weinfurt, 1995). One approach is to perform a univariate ANOVA on each of the variables (Rencher, 2002: 162–164, followed perhaps by multiple comparisons; see Chapter 11) to test the difference among means for each variable separately. However, this procedure will ignore relationships among the variables, and other criticisms have been raised (e.g., Weinfurt, 1995). Multiple-comparison tests are described in some of the references cited in this discussion.

In univariate ANOVA, one can reject H_0 and have none of the μ's declared different by further analysis (Chapter 11). Similarly, a MANOVA may reject H_0 with subsequent ANOVAs detecting no differences (either because of lack of power or because the interrelations among variables are important in rejection of the multivariate H_0). Some computer programs perform ANOVAs along with a MANOVA.

If $k = 2$ and H_0 is rejected by MANOVA or Hotelling's T^2 test, then two-sample t tests and univariate ANOVAs will yield identical results.

16.4 OTHER EXPERIMENTAL DESIGNS

The data of Example 16.1 are subjected to a multivariate analysis of variance composed of one factor (time of year) and two variables (weight of fat and fat-free dry body weight). This is the same experimental design as the ANOVA of Example 10.1 except that two variables, instead of one, are measured on each animal. A MANOVA may also involve more than two variables. For example, the blood-cholesterol concentration might have been a third variable measured for each of the animals, and the null hypothesis regarding the four factor levels (months) would be

$$H_0: \quad \mu_{11} = \mu_{12} = \mu_{13} = \mu_{14} \quad \text{and} \quad \mu_{21} = \mu_{22} = \mu_{23} = \mu_{24}$$

$$\text{and} \quad \mu_{31} = \mu_{32} = \mu_{33} = \mu_{34}.$$

Other sets of data may be the result of consideration of more than one variable *and* more than one factor. For example, measurements of two or more variables, such as those in Example 16.1, might have been collected for sparrows collected at more than one time of year *and* at more than one geographic location. This would be a multivariate factorial experimental design (which could include an examination of factor interactions), and multivariate versions of repeated-measures and hierarchical analyses of variance are also possible, as is multivariate analysis of covariance (MANCOVA). These are multivariate extensions of the considerations of Chapters 12, 14, and 15 and are discussed in some of the references cited immediately preceding Section 16.1.

Multivariate one-sample testing (analogous to the univariate testing in Section 7.1) and paired-sample testing (analogous to Section 9.1) are possible (e.g., Rencher, 2002: Sections 5.3.2 and 5.7.1).

Analysis of covariance (ANCOVA), introduced in Section 12.9, also may be extended to experimental designs with multiple dependent variables. This is done via MANCOVA, for which computer routines are available.

EXERCISES

16.1. Using multivariate analysis of variance, analyze the following data for the concentration of three amino acids in centipede hemolymph (mg/100 ml), asking whether the mean concentration of these amino acids is the same in males and females:

Male			Female		
	Aspartic			*Aspartic*	
Alanine	*Acid*	*Tyrosine*	*Alanine*	*Acid*	*Tyrosine*
7.0	17.0	19.7	7.3	17.4	22.5
7.3	17.2	20.3	7.7	19.8	24.9
8.0	19.3	22.6	8.2	20.2	26.1
8.1	19.8	23.7	8.3	22.6	27.5
7.9	18.4	22.0	6.4	23.4	28.1
6.4	15.1	18.1	7.1	21.3	25.8
6.6	15.9	18.7	6.4	22.1	26.9
8.0	18.2	21.5	8.6	18.8	25.5

16.2. The following data for deer are for two factors (species and sex), where for each combination of factors there is a measurement of two variables (rate of oxygen consumption, in ml O_2/g/hr, and rate of evaporative water loss, in mg/min). Perform a multivariate analysis of variance to test for equality of the population means of these two variables for each of the two factors and the factor interaction.

Species 1				Species 2			
Female		*Male*		*Female*		*Male*	
0.165	76	0.145	80	0.391	71	0.320	65
0.184	71	0.110	72	0.262	70	0.238	69
0.127	64	0.108	77	0.213	63	0.288	67
0.140	66	0.143	69	0.358	59	0.250	56
0.128	69	0.100	74	0.402	60	0.293	52

CHAPTER 17

Simple Linear Regression

Techniques that consider relationships between two variables are described in this and the following two chapters. Chapter 20 presents the expansion of such techniques to analyze situations where more than two variables may be related to each other.

17.1 REGRESSION VERSUS CORRELATION*

The relationship between two variables may be one of functional dependence of one on the other. That is, the magnitude of one of the variables (the *dependent variable*) is assumed to be determined by—that is, is a function of—the magnitude of the second variable (the *independent variable*), whereas the reverse is not true. For example, in the relationship between blood pressure and age in humans, blood pressure may be considered the dependent variable and age the independent variable; we may reasonably assume that although the magnitude of a person's blood pressure might be a function of age, age is not determined by blood pressure. This is not to say that age is the only biological determinant of blood pressure, but we do consider it to be one determining factor.† The term *dependent* does not necessarily imply a cause-and-effect relationship between the two variables. (See Section 17.4.)

Such a dependence relationship is called a *regression*. The term *simple regression* refers to the simplest kind of regression, one in which only two variables are considered.‡

*The historical developments of regression and correlation are strongly related, owing their discovery—the latter following the former—to Sir Francis Galton, who first developed these procedures during 1875–1885 (Walker, 1929: 103–104, 187); see also the first footnote in Section 19.1. He first used the term *regression* in 1885 (Desmond, 2000).

†Some authors refer to the independent variable as the predictor, regressor, explanatory, or exogenous variable and the dependent variable as the response, criterion, or endogenous variable.

‡In the case of simple regression, the adjective *linear* may be used to refer to the relationship between the two variables being a straight line, but to a statistician it describes the relationship of the parameters discussed in Section 17.2.

Data amenable to simple regression analysis consist of pairs of data measured on a ratio or interval scale. These data are composed of measurements of a dependent variable (Y) that is a random effect and an independent variable (X) that is either a fixed effect or a random effect.* (See Section 10.1f for a review of these concepts.)

It is convenient and informative to graph simple regression data using the ordinate (Y axis) for the dependent variable and the abscissa (X axis) for the independent variable. Such a graph is shown in Figure 17.1 for the $n = 13$ data of Example 17.1, where the data appear as a scatter of 13 points, each point representing a pair of X and Y values.† One pair of X and Y data may be designated as (X_1, Y_1), another as (X_2, Y_2), another as (X_3, Y_3), and so on, resulting in what is called a *scatter plot* of all n of the (X_i, Y_i) data. (The line passing through the data in this figure will be explained in Section 17.2.)

EXAMPLE 17.1 Wing Lengths of 13 Sparrows of Various Ages. The Data Are Plotted in Figure 17.1.

Age (days) (X)	*Wing length* (cm) (Y)
3.0	1.4
4.0	1.5
5.0	2.2
6.0	2.4
8.0	3.1
9.0	3.2
10.0	3.2
11.0	3.9
12.0	4.1
14.0	4.7
15.0	4.5
16.0	5.2
17.0	5.0
$n = 13$	

*On rare occasions, we want to describe a regression relationship where the dependent variable (Y) is recorded on a nominal scale. This requires *logistic regression*, a procedure discussed in Section 24.18.

†Royston (1956) observed that "the basic idea of using co-ordinates to determine the location of a point in space dates back to the Greeks at least, although it was not until the time of Descartes that mathematicians systematically developed the idea." The familiar system of specifying the location of a point by its distance from each of two perpendicular axes (now commonly called the X and Y axes) is referred to as Cartesian coordinates, after the French mathematician and philosopher René Descartes (1596–1650), who wrote under the Latinized version of his name, Renatus Cartesius. His other enduring mathematical introductions included (in 1637) the use of numerals as exponents, the square root sign with a vinculum (i.e., with a horizontal line: $\sqrt{}$), and the use of letters at the end of the alphabet (e.g., X, Y, Z) to denote variables and those near the beginning (e.g., a, b, c) to represent constants (Asimov, 1982: 117; Cajori, 1928: 205, 208, 375).

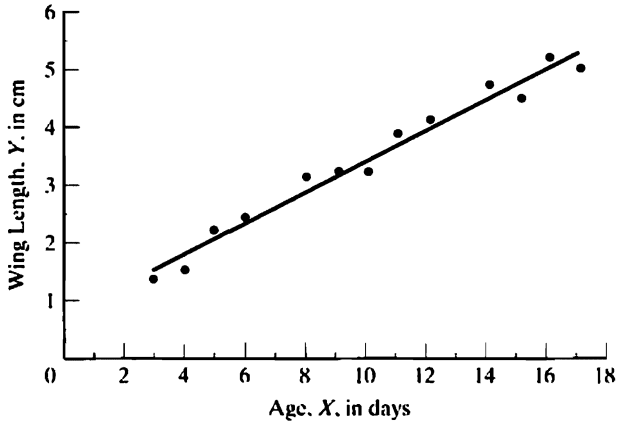


FIGURE 17.1: Sparrow wing length as a function of age. The data are from Example 17.1.

In many kinds of biological data, however, the relationship between two variables is not one of dependence. In such cases, the magnitude of one of the variables changes as the magnitude of the second variable changes, but it is not reasonable to consider there to be an independent and a dependent variable. In such situations, *correlation*, rather than regression, analyses are called for, and both variables are theoretically to be random-effects factors. An example of data suitable for correlation analysis would be measurements of human arm and leg lengths. It might be found that an individual with long arms will in general possess long legs, so a relationship may be describable; but there is no justification in stating that the length of one limb is dependent upon the length of the other. Correlation techniques involving two variables will be discussed in Chapter 19. If more than two variables are being considered, for either correlation or regression, then the appropriate procedures are those found in Chapter 20.

17.2 THE SIMPLE LINEAR REGRESSION EQUATION

The simplest functional relationship of one variable to another in a population is the *simple linear regression*

$$Y_i = \alpha + \beta X_i. \tag{17.1}$$

Here, α and β are population parameters (and, therefore, constants), and this expression will be recognized as the general equation for a straight line.* However, in a population the data are unlikely to be exactly on a straight line, so Y may be said to be related to X by

$$Y_i = \alpha + \beta X_i + \epsilon_i, \tag{17.1a}$$

where ϵ_i (lowercase Greek epsilon) is referred to as an "error," or "residual," which is a departure of an actual Y_i from what Equation 17.1 predicts Y_i to be; and the sum of the ϵ_i's is zero.

*α and β are commonly used for these population parameters, and as such should not be confused with the standard use of the same Greek letters to denote the probabilities of a Type I and Type II error, respectively (see Section 6.3b). Sometimes α and β in regression are designated as β_0 and β_1, respectively. The additive (linear) relationship of the two parameters in Equation 17.1 leads to the term *linear regression equation*. Some examples of nonlinear regression are given in Section 20.14.

Consider the data in Example 17.1, where wing length is the dependent variable and age is the independent variable. From a scatter plot of these data (Figure 17.1), it appears that our sample of measurements from 13 birds represents a population of data in which wing length is linearly related to age. Thus, we would like to estimate the values of α and β that would uniquely describe the functional relationship existing in the population.

If all the data in a scatter diagram such as Figure 17.1 occurred in a straight line, it would be an unusual situation. Generally, as is shown in this figure, there is considerable variability of data around any straight line we might draw through them. What we seek to define is what is commonly termed the "best-fit" line through the data. The criterion for "best fit" that is generally employed utilizes the concept of *least squares*.* Figure 17.2 is an enlarged portion of Figure 17.1. Each value of X will have a corresponding value of Y lying on the line that we might draw through the scatter of data points. This value of Y is represented as $\hat{Y}$ to distinguish it from the Y value actually observed in our sample.† Thus, as Figure 17.2 illustrates, an observed data point is denoted as (X_i, Y_i), and a point on the regression line is $(X_i, \hat{Y}_i)$.

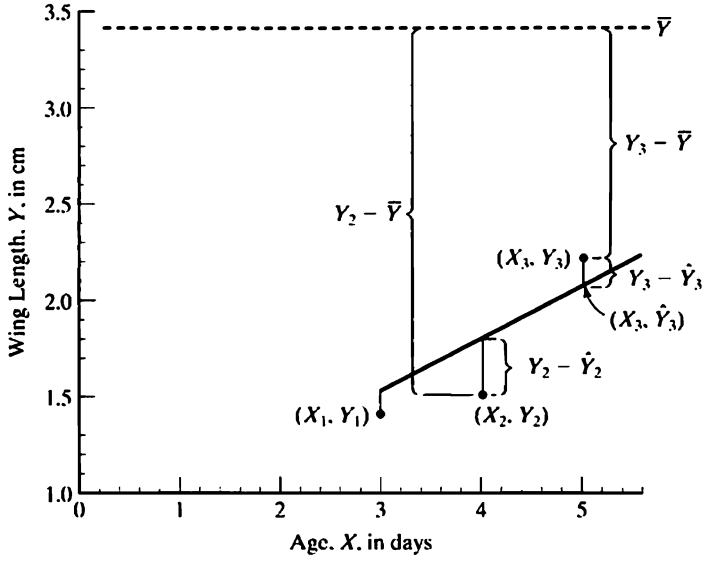


FIGURE 17.2: An enlarged portion of Figure 17.1, showing the partitioning of Y deviations.

The criterion of least squares considers the vertical deviation of each point from the line (i.e., the deviation describable as $Y_i - \hat{Y}_i$) and defines the best-fit line as that which results in the smallest value for the sum of the squares of these deviations for all values of Y_i and $\hat{Y}_i$. That is, $\sum_{i=1}^{n}(Y_i - \hat{Y}_i)^2$ is to be a minimum, where n is the number of data points composing the sample. The sum of squares of these deviations

*The French mathematician Adrien Marie Legendre (1752–1833) published the method now known as least squares (also called ordinary least squares or OLS) in 1805, but the brilliant German mathematician and physicist Karl Friedrich Gauss (1777–1855) claimed—probably truthfully—that he had used it at least 10 years prior to that. (See also Eisenhart, 1978; Seal, 1967.) David (1995) asserts that the term least squares (published in French as moindres quarrés) is properly attributed to Legendre's 1805 publication.

†Statisticians refer to $\hat{Y}$ as "Y hat."

is called the *residual sum of squares* (or, sometimes, the *error sum of squares*) and will be discussed in Section 17.3.*

The only way to determine the population parameters α and β would be to possess all the data for the entire population. Since this is nearly always impossible, we have to estimate these parameters from a sample of n data, where n is the number of pairs of X and Y values. The calculations required to arrive at such estimates, as well as to execute the testing of a variety of important hypotheses, involve the computation of sums of squared deviations from the mean, just as has been encountered in Chapter 10. Recall that the "sum of squares" of X_i values is defined as $\sum(X_i - \overline{X})^2$, which is more easily obtained on a calculator as $\sum X_i^2 - (\sum X_i)^2/n$. It will be convenient to define $x_i = X_i - \overline{X}$, so that this sum of squares can be abbreviated as $\sum x_i^2$, or, more simply, as $\sum x^2$.

Another quantity needed for regression analysis is referred to as the *sum of the cross products* of deviations from the mean:

$$\sum xy = \sum(X_i - \overline{X})(Y_i - \overline{Y}), \tag{17.2}$$

where y denotes a deviation of a Y value from the mean of all Y's just as x denotes a deviation of an X value from the mean of all X's. The sum of the cross products, analogously to the sum of squares, has a simple-to-use "machine formula":

$$\sum xy = \sum X_i Y_i - \frac{(\sum X_i)(\sum Y_i)}{n}, \tag{17.3}$$

and it is recommended that the latter formula be employed if the calculation is not being performed by computer.

(a) The Regression Coefficient. The parameter β is termed the *regression coefficient*, or the *slope* of the best-fit regression line. The best sample estimate of β is

$$b = \frac{\sum xy}{\sum x^2} = \frac{\sum(X_i - \overline{X})(Y_i - \overline{Y})}{\sum(X_i - \overline{X})^2} = \frac{\sum X_i Y_i - \dfrac{(\sum X_i)(\sum Y_i)}{n}}{\sum X_i^2 - \dfrac{(\sum X_i)^2}{n}}. \tag{17.4}$$

Although the denominator in this calculation is always positive, the numerator may be positive, negative, or zero, and the value of b theoretically can range from $-\infty$ to $+\infty$, including zero (see Figure 17.3).

*Another method of regression was proposed in 1757 by Roger Joseph Boscovich (1711–1787, born in what is now Croatia and known also by the Italian name Ruggiero Giuseppe Boscovich). This defined the "best-fit" line as that which minimizes the sum of the absolute values of deviations (that is, $\sum_{i=1}^{n} |Y_i - \hat{Y}_i|$) instead of the sum of squared deviations (Heyde and Seneta, 2001: 82–85). This is referred to as *least absolute deviations* (or LAD). It is rarely seen and employs different (and computationally more difficult) statistical procedures than least-squares regression but may be preferable if there are major outliers or substantial departures from some least-squares assumptions (Section 17.2). A regression method differing from that of least-squares regression and least-absolute-deviations regression is M-*regression* (employing what statisticians call "maximum-likelihood estimation"), described by Birkes and Dodge (1993: Chapter 5), Draper and Smith (1998: Section 25.2), and Huber (2004: Section 7.8) and based upon the concept of Huber (1964). There also exist nonparametric regression methods (Birkes and Dodge, 1993: Chapter 6). These procedures are more robust than least-squares regression and may be preferable when there are prominent outliers or other serious departures from least-squares assumptions.

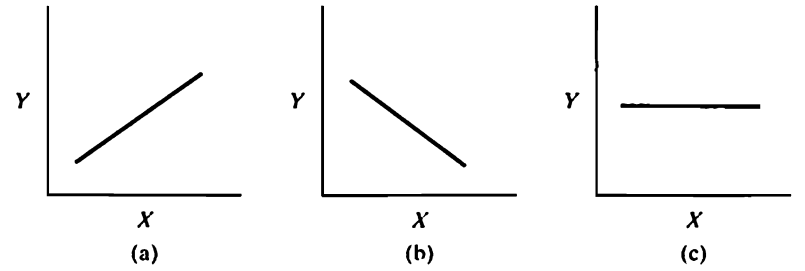


FIGURE 17.3: The slope of a linear regression line may be (a) positive, (b) negative, or (c) zero.

Example 17.2 demonstrates the calculation of b for the data of Example 17.1. Note that the units of b are the units of Y divided by the units of X. The regression coefficient expresses what change in Y is associated, on the average, with a unit change in X. In the present example, $b = 0.270$ cm/day indicates that, for this sample, there is a mean wing growth of 0.270 cm per day for ages 3.0 to 17.0 days. Section 17.5 discusses how to express the precision of b.

EXAMPLE 17.2 The Simple Linear Regression Equation Calculated (Using the "Machine Formula") by the Method of Least Squares, for the Data from the 13 Birds of Example 17.1

$n = 13$

$$\sum X = 3.0 + 4.0 + \cdots + 17.0 = 130.0 \qquad \sum Y = 1.4 + 1.5 + \cdots + 5.0 = 44.4$$

$$\overline{X} = 130.0/13 = 10.0 \qquad \overline{Y} = 44.4/13 = 3.415$$

$$\sum X^2 = 3.0^2 + \cdots + 17.0^2 = 1562.00 \qquad \sum XY = (3.0)(1.4) + \cdots + (17.0)(5.0) = 514.80$$

$$\sum x^2 = 1562.00 - \frac{(130.0)^2}{13} = 1562.00 - 1300.00 = 262.00 \qquad \sum xy = 514.80 - \frac{(130.0)(44.4)}{13} = 514.80 - 444.00 = 70.80$$

$$b = \frac{\sum xy}{\sum x^2} = \frac{70.80}{262.00} = 0.270 \text{ cm/day}$$

$$a = \overline{Y} - b\overline{X} = 3.415 \text{ cm} - (0.270 \text{ cm/day})(10.0 \text{ days})$$

$$= 3.415 \text{ cm} - 2.700 \text{ cm} = 0.715 \text{ cm}$$

So the simple linear regression equation is $\hat{Y} = 0.715 + 0.270X$.

(b) The Y Intercept. An infinite number of lines possess any stated slope, all of them parallel (see Figure 17.4). However, each such line can be defined uniquely by stating, in addition to β, any one point on the line—that is, any pair of coordinates, $(X_i, \hat{Y}_i)$. The point conventionally chosen is the point on the line where $X = 0$. The

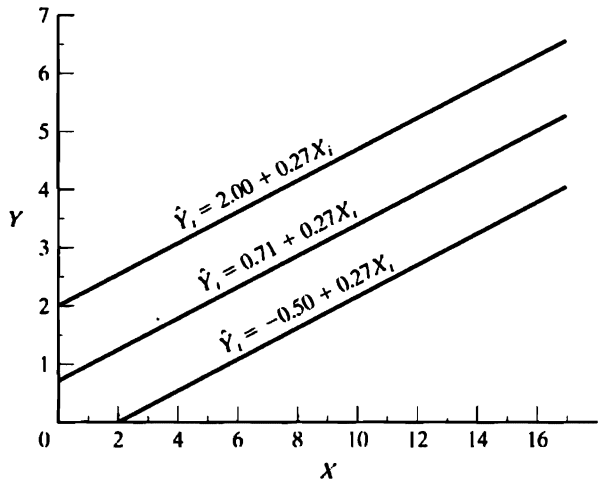


FIGURE 17.4: For any given slope, there exists an infinite number of possible regression lines, each with a different Y intercept. Three of this infinite number are shown here.

value of Y in the population at this point is the parameter α, which is called the *Y intercept.*

It can be shown mathematically that the point $(\overline{X}, \overline{Y})$ always lies on the best-fit regression line. Thus, substituting $\overline{X}$ and $\overline{Y}$ in Equation (17.1), we find that

$$\overline{Y} = \alpha + \beta\overline{X} \tag{17.5}$$

and

$$\alpha = \overline{Y} - \beta\overline{X}. \tag{17.6}$$

The best estimate of the population parameter α is the sample statistic

$$a = \overline{Y} - b\overline{X}. \tag{17.7}$$

The calculation of a is shown in Example 17.2. Note that the Y intercept has the same units as any other Y value. (The precision of the statistic a is considered in Section 17.5.) The sample regression equation (which estimates the population relationship between Y and X stated in Equation 17.1) may be written as

$$\hat{Y}_i = a + bX_i, \tag{17.8}$$

although some authors write

$$\hat{Y}_i = \overline{Y} + b(X_i - \overline{X}), \tag{17.9}$$

which is equivalent.

Figures 17.4 and 17.5 demonstrate that the knowledge of either a or b allows only an incomplete description of a regression function. But by specifying both a and b, a line is uniquely defined. Also, because a and b were calculated using the criterion of least squares, the residual sum of squares from this line is smaller than the residual sum of squares that would result from any other line (i.e., a line with any other a or b) that could be drawn through the data points. This regression line (i.e., the line with this a and b) is not the same line that would result if Y were the independent variable and X the dependent variable.

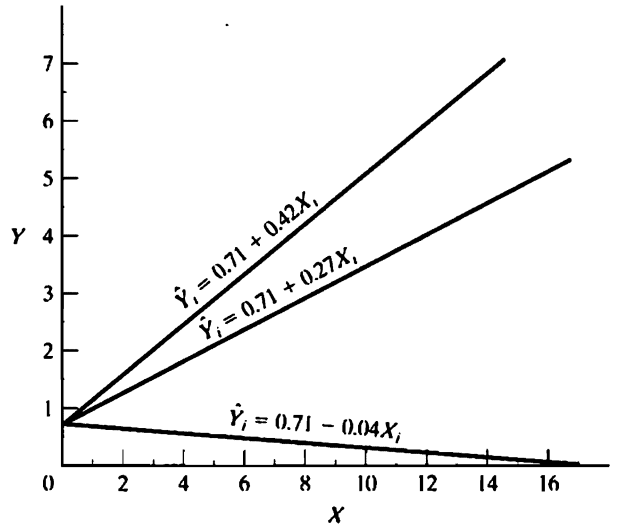


FIGURE 17.5: For any given Y intercept, there exist an infinite number of possible regression lines, each with a different slope. Three of this infinite number are shown here.

(c) Predicting Values of Y. Knowing the parameter estimates a and b for the linear regression equation, we can predict the value of the dependent variable expected in the population at a stated value of X_i. For the regression in Example 17.2, the wing length of a sparrow at 13.0 days of age would be predicted to be

$$\begin{aligned}\hat{Y} &= a + bX_i \\ &= 0.715\text{ cm} + (0.270\text{ cm/day})(13.0\text{ day}) = 4.225\text{ cm.}\end{aligned}$$

The wing length in the population at 7.0 days of age would be estimated to be $\hat{Y} = 0.715\text{ cm} + (0.270\text{ cm/day})(7.0\text{ day}) = 2.605\text{ cm}$, and so on.

To plot a linear regression line graphically, we need to know only two points that lie on the line. We already know two points, namely $(\overline{X}, \overline{Y})$ and $(0, a)$; however, for ease and accuracy in drawing the line by hand, two points that lie near extreme ends of the observed range of X are most useful. For drawing the line in Figure 17.1, the values of $\hat{Y}_i$ for $X_i = 3.0$ days and $X_i = 17.0$ days were used. These were found to be $\hat{Y} = 1.525$ and 5.305 cm, respectively. A regression line should always be drawn using predicted points, and never drawn "by eye."

A word of caution is in order concerning predicting $\hat{Y}_i$ values from a regression equation. Generally, it is an unsafe procedure to extrapolate from a regression equation—that is, to predict $\hat{Y}_i$ values for X_i values outside the observed range of X_i. It would, for example, be unjustifiable to attempt to predict the wing length of a 20-day-old sparrow, or a 1-day-old sparrow, using the regression calculated for birds ranging from 3.0 to 17.0 days in age. Indeed, applying the equation of Example 17.2 to a one-year-old sparrow would predict a wing nearly one meter long! What the linear regression describes is Y as a function of X *within the range of observed values of* X. Thus, a regression equation is often used to interpolate; that is, to estimate a value of Y for an X lying between X's in the sample. But for values of X above or below this range, the function may not be the same (i.e., α and/or β may be different); indeed, the relationship may not even be linear in such ranges, even though it is linear within the observed range. If there is good reason to believe that the described function holds

for X values outside the range of those observed, then we may cautiously extrapolate. Otherwise, beware. A classic example of nonsensical extrapolation was provided in 1874 by Mark Twain (1950: 156):

> In the space of one hundred and seventy-six years the Lower Mississippi has shortened itself two hundred and forty-two miles. That is an average of a trifle over one mile and a third per year [i.e., a slope of -1.375 mi/yr]. Therefore, any calm person, who is not blind or idiotic, can see that in the Old Oölitic Silurian period, just a million years ago next November, the Lower Mississippi River was upward of one million three hundred thousand miles long, and stuck out over the Gulf of Mexico like a fishing rod. And by the same token any person can see that seven hundred and forty-two years from now, the lower Mississippi will be only a mile and three-quarters long, and Cairo [Illinois] and New Orleans [Louisiana] will have joined their streets together, and be plodding comfortably along under a single mayor and a mutual board of aldermen.*

The Y intercept, a, is a statistic that helps specify a regression equation (Equation 17.8). It is, by definition, a predicted value of Y (namely, the $\hat{Y}$ at $X = 0$), but because of the caution against extrapolation, it should not necessarily be considered to represent the magnitude of Y in the population at an X of zero if $X = 0$ is outside the range of X's in the sample. Thus, in Examples 17.1 and 17.2 it should not be proposed that a newly hatched bird in the population (i.e., one 0 days old) has a mean wing length of 0.715 cm.

Section 17.4 discusses the estimation of the error and confidence intervals associated with predicting $\hat{Y}_i$ values.

(d) Assumptions of Regression Analysis. Certain basic assumptions must be met to validly test hypotheses about regressions or to set confidence intervals for regression parameters, although these assumptions are not necessary to compute the regression coefficient, b, the Y intercept, a, and the coefficient of determination, r^2:

1. For each value of X, the values of Y are to have come at random from the sampled population and are to be independent of one another. That is, obtaining a particular Y from the population is in no way dependent upon the obtaining of any other Y.
2. For any value of X in the population there exists a normal distribution of Y values. (This also means that for each value of X there exists in the population a normal distribution of ϵ's.)
3. There is homogeneity of variances in the population; that is, the variances of the distributions of Y values must all be equal to each other. (Indeed, the residual mean square—to be described in Section 17.3—estimates the common variance assumed in the analysis of variance in previous chapters.)
4. In the population, the mean of the Y's at a given X lies on a straight line with the mean of all other Y's at all other X's. That is, the actual relationship between Y and X is linear.
5. The measurements of X were obtained without error. This, of course, is typically impossible; so what we do in practice is assume that the errors in measuring X are negligible, or at least small, compared with errors in measuring Y. If that

*Author Twain concludes by noting that "There is something fascinating about science. One gets such a wholesale return of conjecture out of a trifling investment of fact." It can also be noted that the Silurian period is now considered to have occurred well over 400 million years ago. Even at the time Mark Twain wrote this, scientific opinion placed it at least 20 million years ago.

assumption is not reasonable, other, more complex methods may be considered (Montgomery, Peck, and Vining, 2001: 502).

Violations of assumptions 2, 3, or 4 can sometimes be countered by transformation of data (presented in Section 17.10). Data in violation of assumption 3 will underestimate the residual mean square (Section 17.3) and result in an inflation of the test statistic (F or t), thus increasing the probability of a Type I error (Caudill, 1988). Heteroscedastic data may sometimes be analyzed advantageously by a procedure known as *weighted regression*, which will not be discussed here.

Regression statistics are known to be robust with respect to at least some of these underlying assumptions (e.g., Jacques and Norusis, 1973), so violations of them are not usually of concern unless they are severe. One kind of datum that causes violation of the assumption of normality and homogeneity of variance is the *outlier*, introduced in Section 2.5, which in regression is a recorded measurement that lies very much apart from the trend in the bulk of the data. (For example, in Figure 17.1 a data point at $X = 4$ days and $Y = 4$ cm would have been an outlier.) Procedures known as nonparametric (or distribution-free) regression analyses make no assumptions about underlying statistical distributions. Several versions exist (including regression using ranks) and are discussed by several authors, including Birkes and Dodge (1993: Chapter 6); Cleveland, Mallows, and McRae (1993); Daniel (1990: Chapter 10); Härdle (1990); Hollander and Wolfe (1999: Chapter 9); Montgomery, Peck, and Vining, 2001: Section 7.3); Neave and Worthington (1988: Chapter 10); and Wang and Scott (1994).

(e) Two Kinds of Independent Variables. In regression, measurements of the dependent variable, Y, are considered to be data that have come at random from a population of such data. However, the independent variable, X, may be one of two types.

Section 10.1f spoke of two kinds of factors in analysis of variance: A fixed-effect factor has its levels specifically selected by the experimenter, whereas the levels of a random-effect factor are obtained at random from all possible levels of the factor. Analogously, the values of X in regression may be fixed or random. In Example 17.1, X is a variable with fixed values if the X's were selected by the experimenter (i.e., 13 specific ages of birds were obtained at which to measure wing length). Alternatively, the values of X may have come at random from the sampled population (meaning that the ages were recorded for 13 birds that were selected at random).

Whether the independent variable is random or fixed has no effect on the calculations and hypothesis testing for regression analysis, so the distinction is seldom noted.

17.3 TESTING THE SIGNIFICANCE OF A REGRESSION

The slope, b, of the regression line computed from the sample data expresses quantitatively the straight-line dependence of Y on X in the sample. But what is really desired is information about the functional relationship (if any) in the population from which the sample came. Indeed, the finding of a dependence of Y on X in the sample (i.e., $b \neq 0$) does not necessarily mean that there is a dependence in the population (i.e., $\beta \neq 0$). Consider Figure 17.6, a scatter plot representing a population of data points with no dependence of Y on X; the best-fit regression line for this population would be parallel to the X axis (i.e., the slope, β, would be zero). However, it is possible, by random sampling, to obtain a sample of data points having

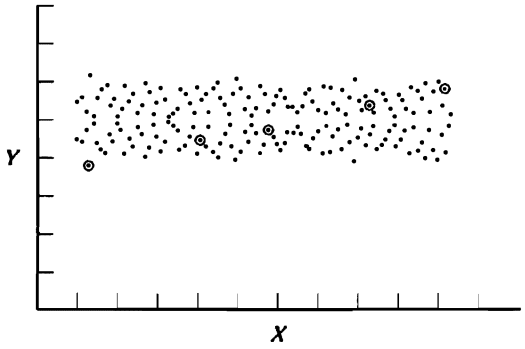


FIGURE 17.6: A hypothetical population of data points, having a regression coefficient, β, of zero. The circled points are a possible sample of five.

the five values circled in the figure. By calculating b for this sample of five, we would estimate that β was positive, even though it is, in fact, zero.

We are not likely to obtain five such points out of this population, but we desire to assess just how likely it is; therefore, we can set up a null hypothesis, H_0: $\beta = 0$, and the alternate hypothesis, H_A: $\beta \neq 0$, appropriate to that assessment. If we conclude that there is a reasonable probability (i.e., a probability greater than the chosen level of significance—say, 5%) that the calculated b could have come from sampling a population with a $\beta = 0$, the H_0 is not rejected. If the probability of obtaining the calculated b is small (say, 5% or less), then H_0 is rejected, and H_A is assumed to be true.

(a) Analysis-of-Variance Testing. The preceding H_0 may be tested by an analysis-of-variance (ANOVA) procedure. First, the overall variability of the dependent variable is calculated by computing the sum of squares of deviations of Y_i values from $\overline{Y}$, a quantity termed the *total sum of squares*:

$$\text{total SS} = \sum(Y_i - \overline{Y})^2 = \sum y^2 = \sum Y_i^2 - \frac{(\sum Y_i)^2}{n}. \tag{17.10}$$

Then we determine the amount of variability among the Y_i values that is attributable to there being a linear regression; this is termed the *linear regression sum of squares*:

$$\text{regression SS} = \sum(\hat{Y}_i - \overline{Y})^2 = \frac{(\sum xy)^2}{\sum x^2} = \frac{\left(\sum X_i Y_i - \dfrac{\sum X_i \sum Y_i}{n}\right)^2}{\sum X_i^2 - \dfrac{(\sum X_i)^2}{n}}; \tag{17.11}$$

because $b = \sum xy / \sum x^2$ (Equation 17.4), this can also be calculated as

$$\text{regression SS} = b \sum xy. \tag{17.12}$$

The value of the regression SS will be equal to that of the total SS only if each data point falls exactly on the regression line, a very unlikely situation. The scatter of data points around the regression line has been alluded to, and the residual, or error, sum

of squares is obtained as

$$\text{residual SS} = \sum(Y_i - \hat{Y}_i)^2 = \text{total SS} - \text{regression SS}. \tag{17.13}$$

Table 17.1 presents the analysis-of-variance summary for testing the hypothesis H_0: $\beta = 0$ against H_A: $\beta \neq 0$. Example 17.3 performs such an analysis for the data from Examples 17.1 and 17.2. The degrees of freedom associated with the total variability of Y_i values are $n - 1$. The degrees of freedom associated with the variability among Y_i's due to regression are always 1 in a simple linear regression. The residual degrees of freedom are calculable as residual DF = total DF − regression DF = $n - 2$. Once the regression and residual mean squares are calculated (MS = SS/DF, as usual), H_0 may be tested by determining

$$F = \frac{\text{regression MS}}{\text{residual MS}}, \tag{17.14}$$

TABLE 17.1: Summary of the Calculations for Testing H_0: $\beta = 0$ against H_A: $\beta \neq 0$ by an Analysis of Variance

Source of variation	Sum of squares (SS)	DF	Mean square (MS)
Total $[Y_i - \overline{Y}]$	$\sum y^2$	$n - 1$	
Linear regression $[\hat{Y}_i - \overline{Y}]$	$\frac{(\sum xy)^2}{\sum x^2}$	1	$\frac{\text{regression SS}}{\text{regression DF}}$
Residual $[Y_i - \hat{Y}_i]$	total SS − regression SS	$n - 2$	$\frac{\text{residual SS}}{\text{residual DF}}$

Note: To test the null hypothesis, we compute F = regression MS/residual MS. The critical value for the test is $F_{\alpha(1),1,(n-2)}$.

EXAMPLE 17.3 Analysis of Variance Testing of H_0: $\beta = 0$ Against H_A: $\beta \neq 0$, Using the Data of Examples 17.1 and 17.2

$n = 13$ $\quad\quad$ $\sum xy = 70.80$ (from Example 17.2)

$\sum Y = 44.4$ $\quad\quad$ $\sum x^2 = 262.00$ (from Example 17.2)

$\sum Y^2 = 171.30$

$$\text{total SS} = \sum y^2 = 171.30 - \frac{(44.4)^2}{13} \quad \text{regression SS} = \frac{(\sum xy)^2}{\sum x^2} = \frac{(70.80)^2}{262.00}$$

$$= 171.30 - 151.6431 \qquad = \frac{5012.64}{262.00}$$

$$= 19.656923 \qquad = 19.132214$$

$\text{total DF} = n - 1 = 12$

Source of variation	SS	DF	MS
Total	19.656923	12	
Linear regression	19.132214	1	19.132214
Residual	0.524709	11	0.047701

$$F = \frac{19.132214}{0.047701} = 401.1$$

$F_{0.05(1),1,11} = 4.84$

Therefore, reject H_0.

$$P \ll 0.0005 \quad [P = 0.00000000053]$$

$$r^2 = \frac{19.132214}{19.656923} = 0.97$$

$s_{Y \cdot X} = \sqrt{0.047701} = 0.218$ cm

which is then compared to the critical value, $F_{\alpha(1),\nu_1,\nu_2}$, where ν_1 = regression DF = 1 and ν_2 = residual DF = $n - 2$.

The residual mean square is often written as $s^2_{Y \cdot X}$, a representation denoting that it is the variance of Y after taking into account the dependence of Y on X. The square root of this quantity (i.e., $s_{Y \cdot X}$) is called the *standard error of estimate* (occasionally termed the "standard error of the regression"). In Example 17.3, $s_{Y \cdot X} = \sqrt{0.047701 \text{ cm}^2} = 0.218$ cm. The standard error of estimate is an overall indication of the accuracy with which the fitted regression function predicts the dependence of Y on X. The magnitude of $s_{Y \cdot X}$ is proportional to the magnitude of the dependent variable, Y, making examination of $s_{Y \cdot X}$ a poor method for comparing regressions. Thus, Dapson (1980) recommends using $s_{Y \cdot X}/\overline{Y}$ (a unitless measure) to examine similarities among two or more regression fits.

The proportion (or percentage) of the total variation in Y that is explained or accounted for by the fitted regression is termed the *coefficient of determination*, r^2, which is often used as a measure of the strength of the straight-line relationship:*

$$r^2 = \frac{\text{regression SS}}{\text{total SS}}; \tag{17.15}$$

r^2 is sometimes referred to as expressing the goodness of fit of the line to the data or as the precision of the regression.

For Example 17.3, $r^2 = 0.97$, or 97%. That portion the total variation not explained by the regression is, of course, $1 - r^2$, or residual SS/total SS, and this is called the *coefficient of nondetermination*, a quantity seldom referred to.† In Example 17.3, $1 - r^2 = 1.00 - 0.97 = 0.03$, or 3%. (The quantity r is the correlation coefficient, to be introduced in Chapter 19.)‡

*However, Ranney and Thigpen (1981) and others caution against declaring r^2 to be a measure of strength of the relationship in cases where X is a fixed-effect variable (see Section 17.2e).

†The standard error of estimate is directly related to the coefficient of nondetermination and to the variability of Y as

$$s_{Y \cdot X} = s_Y \sqrt{(1 - r^2)(n - 1)/(n - 2)}. \tag{17.16}$$

‡Sutton (1990) showed that

$$r^2 = \frac{F}{F + \nu_2}. \tag{17.17}$$

Another good way to express the accuracy of a regression, or to compare accuracies of several regressions, is to compute confidence intervals for predicted values of Y, as described in Section 17.5.

(b) t Testing. The preceding null hypothesis concerning β can also be tested by using Student's t statistic. Indeed, the more general two-tailed hypotheses, H_0: $\beta = \beta_0$ and H_A: $\beta \neq \beta_0$, can be tested in this fashion.* Most frequently, β_0 is zero in these hypotheses, in which case either the analysis of variance or the t test may be employed and the conclusion will be the same. But if any other value of β_0 is hypothesized, then the following procedure is applicable, whereas the analysis of variance is not. Also, the t-testing procedure allows for the testing of one-tailed hypotheses: either H_0: $\beta \leq \beta_0$ and H_A: $\beta > \beta_0$, or H_0: $\beta \geq \beta_0$ and H_A: $\beta < \beta_0$.

Since the t statistic is in general calculated as

$$t = \frac{\text{(parameter estimate)} - \text{(parameter value hypothesized)}}{\text{standard error of parameter estimate}}, \tag{17.18}$$

we need to compute s_b, the standard error of the regression coefficient.

The variance of b is calculated as

$$s_b^2 = \frac{s_{Y \cdot X}^2}{\sum x^2}. \tag{17.19}$$

Therefore,

$$s_b = \sqrt{\frac{s_{Y \cdot X}^2}{\sum x^2}}, \tag{17.20}$$

and

$$t = \frac{b - \beta_0}{s_b}. \tag{17.21}$$

To test H_0: $\beta = 0$ against H_A: $\beta \neq 0$ in Example 17.4, $s_b = 0.0135$ cm/day and $t = 20.000$. The degrees of freedom for this testing procedure are $n - 2$; thus, the critical value in this example, at the 5% significance level, is $t_{0.05(1),11} = 2.201$, and H_0 is rejected. For this two-tailed hypothesis, H_0: $\beta = 0$, either t or F may be employed, with the same result; and $F = t^2$ and $F_{\alpha,1,(n-2)} = t^2_{\alpha(2),(n-2)}$. Section 7.2 presents the relevant concepts and procedures involved in one-tailed hypothesis testing.

17.4 INTERPRETATIONS OF REGRESSION FUNCTIONS

Potential misinterpretation of regression relationships has been alluded to earlier in this chapter and warrants further discussion. If we calculate the two constants, a and b, that define a linear regression question, then we have quantitatively described the average rate of change of Y with a change in X. However, although a mathematical dependence between Y and X has been determined, it must not automatically be assumed that there is a biological cause-and-effect relationship. Causation should be suggested only with insight into the phenomenon being investigated and should not be declared by statistical testing alone. Indeed, it is often necessary to determine the interrelationships among variables beyond the two variables under study, for an observed dependence may, in fact, be due to the influence of one or more variables not

*The use of t for testing regression coefficients emanates from Fisher (1922a).

EXAMPLE 17.4 Use of Student's t to Test H_0: $\beta = 0$ Against H_A: $\beta \neq 0$, Employing the Data of Examples 17.1 and 17.2

$n = 13$

$b = 0.270$ cm/day

$$s_b = \sqrt{\frac{s^2_{Y \cdot X}}{\sum x^2}} = \sqrt{\frac{0.047701}{262.00}} = \sqrt{0.00018206} = 0.0135 \text{ cm/day}$$

$$t = \frac{b - 0}{s_b} = \frac{0.270}{0.0135} = 20.000$$

$t_{0.05(2),11} = 2.201$

Therefore, reject H_0.

$P \ll 0.01$ [$P = 0.00000000027$]

yet analyzed. (The methods of Chapter 20 are often used to attempt to identify such other variables.)

We must also remember that a linear regression function is mathematically nothing more than a straight line forced to fit through a set of data points, and it may not at all describe a natural phenomenon. The biologist may be chagrined when attempting to explain why the observed relationship is well described by a linear function or what biological insights are to be unfolded by the consideration of a particular slope or a particular magnitude of a Y intercept. That is, although a derived regression function often provides a satisfactory and satisfying description of a natural phenomenon, sometimes it does not. Chapters 20 and 21 discuss the fitting of regression models other than $\hat{Y}_i = \alpha + \beta X_i$.

Even if a regression function does not help us to explain the functional anatomy of a natural system, it may still be useful in its ability to predict Y, given X. In the sciences, equations may inaccurately represent natural processes yet may be employed advantageously to predict the magnitude of one variable given the magnitude of an associated variable. Thus, predicting $\hat{Y}$ values (or $\hat{X}$ values; see Section 17.6) and their standard errors is frequently a useful end in itself. But, as stressed in Section 17.2, great caution should be exercised in predicting a $\hat{Y}$ for an X outside the range of the X's used to obtain the regression equation. In addition, while a (the Y intercept) has utility in expressing a regression relationship, expressing a as the predicted value of Y when $X = 0$ may not have biological significance—and may even be meaningless if $X = 0$ lies outside of the range of the observed X's.

If the relationship between two variables is not that of an independent variable and a dependent variable, then correlation analysis (Chapter 19), instead of regression analysis, should be considered.

17.5 CONFIDENCE INTERVALS IN REGRESSION

In many (though not all) cases, knowing the standard error of a statistic allows us to calculate a confidence interval for the parameter being estimated, as

$$\text{confidence interval} = \text{statistic} \pm (t)(\text{SE of statistic}). \tag{17.22}$$

This was first demonstrated in Section 7.3 for the confidence interval for a mean, and it has been used repeatedly in succeeding chapters. In addition, the second significant figure of the standard error of a statistic may be used as an indicator of the precision to which that statistic should be reported (as done with the mean in Section 7.4). The standard error of b has been given by Equation 17.20. For the data in Example 17.4, the second significant figure of $s_b = 0.0135$ cm/day enables us to express b to the third decimal place (i.e., $b = 0.270$ cm/day).

(a) Confidence Interval for the Regression Coefficient. For the $(1 - \alpha)$ confidence limits of β,

$$b \pm t_{\alpha(2),(n-2)}s_b. \tag{17.23}$$

Therefore,

$$L_1 = b - t_{\alpha(2),(n-2)}s_b \tag{17.24}$$

and

$$L_2 = b + t_{\alpha(2),(n-2)}s_b. \tag{17.25}$$

For Example 17.2, the 95% confidence interval for β would be $b \pm t_{0.05(2),11}s_b = 0.270 \pm (2.201)(0.0135) = 0.20 \pm 0.030$ cm/day. Thus, the 95% confidence limits are $L_1 = 0.270 - 0.030 = 0.240$ cm/day and $L_2 = 0.270 + 0.030 = 0.300$ cm/day; and we can state, with 95% confidence (i.e., we state that there is no greater than a 5% chance that we are wrong), that 0.240 cm/day and 0.300 cm/day form an interval that includes the population regression coefficient, β. Figure 17.7 shows, by the broken lines, these confidence limits for the slope of the regression line. Within these limits, the various possible b values rotate the line about the point $(\overline{X}, \overline{Y})$.

(b) Confidence Interval for an Estimated Y. As shown in Section 17.1, a regression equation allows the estimate of the value of Y (namely, $\hat{Y}$) existing in the population

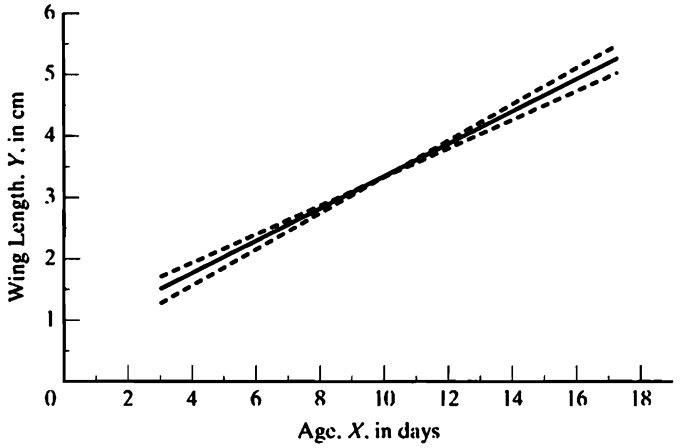


FIGURE 17.7: The regression line from Figure 17.1, showing, by broken lines, the lines with slopes equal to the upper and lower 95% confidence limits for β.

at a given value of X. The standard error of such a population estimate is

$$s_{\hat{Y}_i} = \sqrt{s^2_{Y \cdot X}\left[\frac{1}{n} + \frac{(X_i - \overline{X})^2}{\sum x^2}\right]}. \tag{17.26}$$

Example 17.5a shows how $s_{\hat{Y}_i}$ can be used in Equation 17.22 to calculate confidence intervals. It is apparent from Equation 17.26 that the standard error is a minimum for $X_i = \overline{X}$, and that it increases as estimates are made at values of X_i farther from the mean. If confidence limits were calculated for all points on the regression line, the result would be the curved *confidence bands* shown in Figure 17.8.

EXAMPLE 17.5 Standard Errors of Predicted Values of *Y*

The regression equation derived in Example 17.2 is used for the following considerations. For this regression, $a = 0.72$ cm, $b = 0.270$ cm/day, $\overline{X} = 10.0$ days, $\sum x^2 = 262.00$ days^2, $n = 13$, $s^2_{Y \cdot X} = 0.047701$ cm^2, and $t_{0.05(2),11} = 2.201$.

a. Equation 17.26 is used when we wish to predict the mean value of $\hat{Y}_i$, given X_i, in the entire population. For example, we could ask, "What is the mean wing length of all 13.0-day-old birds in the population under study?"

$$\begin{aligned}\hat{Y}_i &= a + bX_i \\ &= 0.715 + (0.270)(13.0) \\ &= 0.715 + 3.510 \\ &= 4.225 \text{ cm}\end{aligned}$$

$$\begin{aligned}s_{\hat{Y}_i} &= \sqrt{s^2_{Y \cdot X}\left[\frac{1}{n} + \frac{(X_i - \overline{X})^2}{\sum x^2}\right]} \\ &= \sqrt{0.047701\left[\frac{1}{13} + \frac{(13.0 - 10.0)^2}{262.00}\right]} \\ &= \sqrt{(0.047701)(0.111274)} \\ &= 0.073 \text{ cm}\end{aligned}$$

$$\begin{aligned}95\% \text{ confidence interval} &= \hat{Y}_i \pm t_{0.05(2),11} s_{\hat{Y}_i} \\ &= 4.225 \pm (2.201)(0.073) \\ &= 4.225 \pm 0.161 \text{ cm} \\ L_1 &= 4.064 \text{ cm} \\ L_2 &= 4.386 \text{ cm}\end{aligned}$$

b. Equation 17.28 is used when we propose taking an additional sample of m individuals from the population and wish to predict the mean Y value, at a given X, for these m new data. For example, we might ask, "If ten 13.0-day-old birds were taken from the population, what would be their mean wing length?"

$$\hat{Y}_i = 0.715 + (0.270)(13.0) = 4.225 \text{ cm}$$

$$(s_{\hat{Y}_i})_{10} = \sqrt{0.047701\left[\frac{1}{10} + \frac{1}{13} + \frac{(13.0 - 10.0)^2}{262.00}\right]}$$

$$= \sqrt{(0.047701)(0.211274)}$$

$$= 0.100 \text{ cm}$$

$$\text{95\% prediction interval} = \hat{Y}_i \pm t_{0.05(2),11}(s_{\hat{Y}_i})_{10}$$

$$= 4.225 \pm (2.201)(0.100)$$

$$= 4.225 \pm 0.220 \text{ cm}$$

$$L_1 = 4.005 \text{ cm}$$

$$L_2 = 4.445 \text{ cm}$$

c. Equation 17.29 is used when we wish to predict the Y value of a single observation taken from the population as a specified X. For example, we could ask, "If one 13.0-day-old bird were taken from the population, what would be its wing length?"

$$\hat{Y}_i = 0.715 + (0.270)(13.0) = 4.225 \text{ cm}$$

$$(s_{\hat{Y}_i})_1 = \sqrt{0.047701\left[1 + \frac{1}{13} + \frac{(13.0 - 10.0)^2}{262.00}\right]}$$

$$= \sqrt{(0.047701)(1.111274)}$$

$$= 0.230 \text{ cm}$$

$$\text{95\% prediction interval} = \hat{Y}_i \pm t_{0.05(2),11}(s_{\hat{Y}_i})_1$$

$$= 4.225 \pm (2.201)(0.230)$$

$$= 4.225 \pm 0.506 \text{ cm}$$

$$L_1 = 3.719 \text{ cm}$$

$$L_2 = 4.731 \text{ cm}$$

Note from these three examples that the accuracy of prediction increases as does the number of data upon which the prediction is based. For example, predictions about a mean for the entire population will be more accurate than a prediction about a mean from 10 members of the population, which is more accurate than a prediction about a single member of the population.

If $X_i = 0$, then $\hat{Y} = a$ (the Y intercept). Therefore,

$$s_a = \sqrt{s^2_{Y \cdot X}\left[\frac{1}{n} + \frac{\bar{X}^2}{\sum x^2}\right]}. \tag{17.27}$$

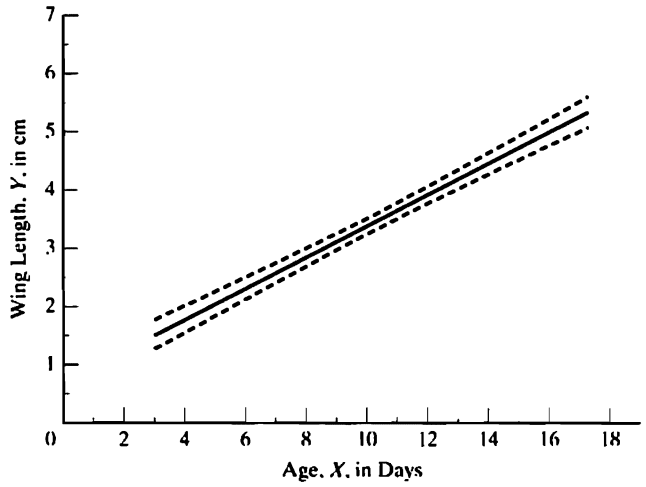


FIGURE 17.8: The 95% confidence bands (broken lines) for the regression line from Figure 17.1 (the regression of Example 17.2).

(c) Prediction Interval for an Estimated *Y*. If we predict a value of $\hat{Y}$ that is the mean of m additional measurements at a given X (Example 17.5b), its standard error would be

$$(s_{\hat{Y}_i})_m = \sqrt{s^2_{Y \cdot X}\left[\frac{1}{m} + \frac{1}{n} + \frac{(X_i - \overline{X})^2}{\sum x^2}\right]}. \tag{17.28}$$

A special case of Equation 17.28, shown as Example 17.5c, exists when it is desired to know the standard error associated with estimating $\hat{Y}_i$ for a single additional measurement at Y_i:

$$(s_{\hat{Y}_i})_1 = \sqrt{s^2_{Y \cdot X}\left[1 + \frac{1}{n} + \frac{(X_i - \overline{X})^2}{\sum x^2}\right]}. \tag{17.29}$$

Equation 17.26 is equal to Equation 17.28 when m approaches infinity. Examples 17.5b and 17.5c demonstrate the use of these standard errors of prediction.

(d) Testing Hypotheses about Estimated *Y* Values. Once we have computed the standard error of a predicted Y, we can test hypotheses about that prediction. For example, we might ask whether the mean population wing length of 13.0-day-old sparrows, call it $\mu_{\hat{Y}_{13.0}}$, is equal to some specified value (two-tailed test) or is greater than (or less than) some specified value (one-tailed test). We simply refer to Equation 17.18, as Example 17.6 demonstrates.

(e) Confidence Interval and Hypothesis Testing for the Residual Mean Square. The sample residual mean square, $s^2_{Y \cdot X}$, is an estimate of the residual mean square in the population, $\sigma^2_{Y \cdot X}$. Confidence limits may be calculated for $\sigma^2_{Y \cdot X}$ as they are for the population variance, σ^2, in Section 7.12. Simply use $\nu = n - 2$, instead of $\nu = n - 1$, and replace σ^2 with $\sigma^2_{Y \cdot X}$ and SS with residual SS in Equation 7.18 or 7.19. Also, a confidence interval for the population standard error of estimate, $\sigma_{Y \cdot X}$, may be obtained by analogy to Equation 7.20. Hypothesis testing for $\sigma^2_{Y \cdot X}$ or $\sigma_{Y \cdot X}$ may be performed by procedures analogous to those of Section 7.11.

EXAMPLE 17.6 Hypothesis Testing with an Estimated *Y* Value

H_0: The mean population wing length of 13.0-day-old birds is not greater than 4 cm (i.e., H_0: $\mu_{\hat{Y}_{13.0}} \leq 4$ cm).

H_A: The mean population wing length of 13.0-day-old birds is greater than 4 cm (i.e., H_A: $\mu_{\hat{Y}_{13.0}} > 4$ cm).

From Example 17.5b, $Y_{13.0} = 4.225$ cm and $s_{\hat{Y}_{13.0}} = 0.073$ cm,

$$t = \frac{4.225 - 4}{0.073} = \frac{0.225}{0.073} = 3.082$$

$t_{0.05(1),11} = 1.796$

Therefore, reject H_0.

$$0.005 < P < 0.01 \quad [P = 0.0052]$$

17.6 INVERSE PREDICTION

Situations exist where we desire to predict the value of the independent variable (X_i) that is to be expected in the population at a specified value of the dependent variable (Y_i), a procedure known as *inverse prediction*. In Example 17.1, for instance, we might ask, "How old is a bird that has a wing 4.5 cm long?" By simple algebraic rearrangement of the linear regression relationship of Equation 17.8, we obtain

$$\hat{X}_i = \frac{Y_i - a}{b}. \tag{17.30}$$

From Figure 17.8, it is clear that, although confidence limits calculated around the predicted $\hat{Y}_i$ are symmetrical above and below $\hat{Y}_i$, confidence limits associated with the predicted $\hat{X}_i$ are not symmetrical to the left and to the right of $\hat{X}_i$. The $1 - \alpha$ confidence limits for the X predicted at a given Y may be calculated as follows, which is demonstrated in Example 17.7:

$$\overline{X} + \frac{b(Y_i - \overline{Y})}{K} \pm \frac{t}{K}\sqrt{s^2_{Y \cdot X}\left[\frac{(Y_i - \overline{Y})^2}{\sum x^2} + K\left(1 + \frac{1}{n}\right)\right]}, \tag{17.31}$$

where* $K = b^2 - t^2 s_b^2$. This computation is a special case of the prediction of the $\hat{X}$ associated with multiple values of Y at that X. For the study of Example 17.1, age can be predicted of m birds to be taken from the population and having a mean body weight of $\overline{Y}_i$:

$$\hat{X}_i = \frac{\overline{Y}_i - a}{b}, \tag{17.32}$$

*Recall that $F_{\alpha(1),1,\nu} = t^2_{\alpha(2),\nu}$. Therefore, we could compute $K = b^2 - Fs_b^2$, where $F = t^2_{\alpha(2),(n-2)} = F_{\alpha(1),1,(n-2)}$. Snedecor and Cochran (1989: 171) presented an alternative, yet equivalent, computation of these confidence limits.

EXAMPLE 17.7 Inverse Prediction

We wish to estimate, with 95% confidence, the age of a bird with a wing length of 4.5 cm.

Predicted age:

$$\hat{X} = \frac{Y_i - a}{b} = \frac{4.5 - 0.715}{0.270} = 14.019 \text{ days}$$

To compute 95% confidence interval:

$t = t_{0.05(2),11} = 2.201$

$$K = b^2 - t^2 s_b^2 = 0.270^2 - (2.201)^2(0.0135)^2 = 0.0720$$

95% confidence interval:

$$\overline{X} + \frac{b(Y_i - \overline{Y})}{K} \pm \frac{t}{K}\sqrt{s_{Y \cdot X}^2\left[\frac{(Y_i - \overline{Y})^2}{\sum x^2} + K\left(1 + \frac{1}{n}\right)\right]}$$

$$= 10.0 + \frac{0.270(4.5 - 3.415)}{0.0720} \pm \frac{2.201}{0.0720}\sqrt{0.047701\left[\frac{(4.5 - 3.415)^2}{262.00} + 0.0720\left(1 + \frac{1}{13}\right)\right]}$$

$$= 10.0 + 4.069 \pm 30.569\sqrt{0.003913}$$

$$= 14.069 \pm 1.912 \text{ days}$$

$L_1 = 12.157$ days

$L_2 = 15.981$ days

where $\overline{Y}_i$ is the mean of the m values of Y_i; and the confidence limits would be calculated as

$$\overline{X} + \frac{b(\overline{Y}_i - \overline{Y})}{K} \pm \frac{t}{K}\sqrt{(s_{Y \cdot X}^2)'\left[\frac{(\overline{Y}_i - \overline{Y})^2}{\sum x^2} + K\left(\frac{1}{m} + \frac{1}{n}\right)\right]}, \tag{17.33}$$

where* $t = t_{\alpha(2),(n+m-3)}$, $K = b^2 - t^2(s_b^2)'$,

$$(s_b^2)' = \frac{(s_{Y \cdot X}^2)'}{\sum x^2}. \tag{17.34}$$

*Alternatively, we may compute $K = b^2 - F(s_b^2)_*$, where $F = t_{\alpha(2),(n+m-3)}^2 = F_{\alpha(1),1,(n+m+3)}$.

and

$$(s^2_{Y \cdot X})' = \text{residual SS} + \sum_{j=1}^{m} (Y_{ij} - \overline{Y}_i)^2/(n + m - 3) \tag{17.35}$$

(Ostle and Malone, 1988: 241; Seber and Lee, 2003: 147–148).

17.7 REGRESSION WITH REPLICATION AND TESTING FOR LINEARITY

If, in Example 17.1, we had wing measurements for more than one bird for at least some of the recorded ages, then we could test the null hypothesis that the population regression is linear.* (Note that true replication requires that there are multiple birds at a given age, not that there are multiple wing measurements on the same bird.) Figure 17.9 presents the data of Example 17.8a. A least-squares, best-fit, linear regression equation can be calculated for any set of at least two data, but neither the equation itself nor the testing for a significant slope (which requires at least three data) indicates whether Y is, in fact, a straight-line function of X in the population sampled.

EXAMPLE 17.8a Regression Data Where There Are Multiple Values of Y for Each Value of X

	Age (yr)	*Systolic blood pressure* (mm Hg)		
i	X_i	Y_{ij}	n_i	$\overline{Y}_i$
1	30	108, 110, 106	3	108.0
2	40	125, 120, 118, 119	4	120.5
3	50	132, 137, 134	3	134.3
4	60	148, 151, 146, 147, 144	5	147.2
5	70	162, 156, 164, 158, 159	5	159.8

$k = 5$; $i = 1$ to 5; $j = 1$ to n_i; $N = 20$

$$\sum\sum X_{ij} = 1050 \qquad \sum\sum Y_{ij} = 2744$$

$$\sum\sum X_{ij}^2 = 59{,}100 \qquad \sum\sum Y_{ij}^2 = 383{,}346 \qquad \sum\sum X_{ij}Y_{ij} = 149{,}240$$

$$\sum x^2 = 3975.00 \qquad \sum y^2 = 6869.20 \qquad \sum xy = 5180.00$$

$$\overline{X} = 52.5 \qquad \overline{Y} = 137.2$$

$$b = \frac{\sum xy}{\sum x^2} = \frac{5180.00}{3975.00} = 1.303 \text{ mm Hg/yr}$$

$$a = \overline{Y} - b\overline{X} = 137.2 - (1.303)(52.5) = 68.79 \text{ mm Hg}$$

Therefore, the least-squares regression line is $\hat{Y}_{ij} = 68.79 + 1.303X_{ij}$.

We occasionally encounter the suggestion that for data such as those in Figure 17.9 the mean Y at each X be utilized for a regression analysis. However, to do so would be to discard information, and such a procedure is not recommended (Freund, 1971).

*Thornby (1972) presents a procedure to test the hypothesis of linearity even when there are not multiple observations of Y. But the computation is rather tedious.

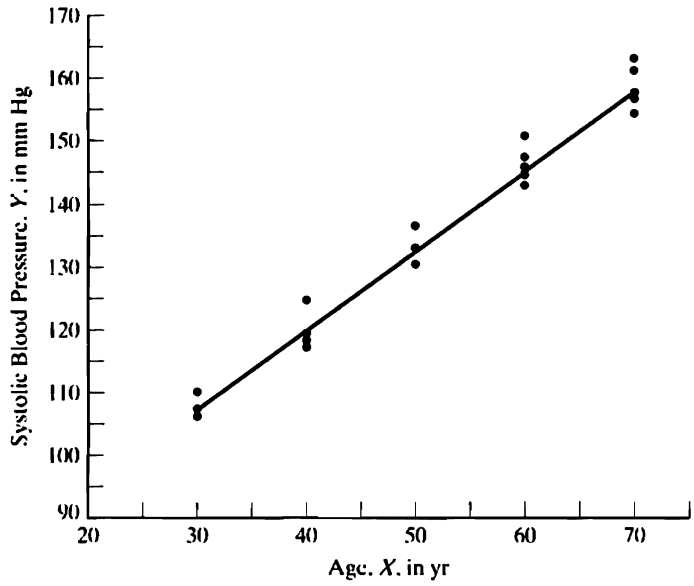


FIGURE 17.9: A regression where there are multiple values of Y for each value of X.

EXAMPLE 17.8b Statistical Analysis of the Regression Data of Example 17.8a

H_0: The population regression is linear.

H_A: The population regression is not linear.

total SS $= \sum y^2 = 6869.20$ total DF $= N - 1 = 19$

$$\text{among-groups SS} = \sum_{i=1}^{k} \frac{\left(\sum_{j=1}^{n_i} Y_{ij}\right)^2}{n_i} - \frac{\left(\sum_{i=1}^{k}\sum_{j=1}^{n_i} Y_{ij}\right)^2}{N}$$

$$= 383{,}228.73 - 376{,}476.80 = 6751.93$$

among-groups DF $= k - 1 = 4$

within-groups SS = total SS − among-groups SS

$= 6869.20 - 6751.93 = 117.27$

within-groups DF = total DF − among-groups DF

$= 19 - 4 = 15$

deviations-from-linearity SS = among-groups SS − regression SS

$= 6751.93 - 6750.29 = 1.64$

deviations-from-linearity DF = among-groups DF − regression DF

$= 4 - 1 = 3$

Source of variation	SS	DF	MS
Total	6869.20	19	
Among groups	6751.93	4	
Linear regression	6750.29	1	
Deviations from linearity	1.64	3	0.55
Within groups	117.27	15	7.82

$$F = \frac{0.55}{7.82} = 0.070$$

Since $F < 1.00$, do not reject H_0.

$$P > 0.25 \quad [P = 0.975]$$

H_0: $\beta = 0$.

H_A: $\beta \neq 0$.

$$\text{regression SS} = \frac{\left(\sum xy\right)^2}{\sum x^2} = \frac{(5180.00)^2}{3975.00} = 6750.29$$

Source of variation	SS	DF	MS
Total	6869.20	19	
Linear regression	6750.29	1	6750.29
Residual	118.91	18	6.61

$$F = \frac{6750.29}{6.61} = 1021.2$$

$F_{0.05(1),1,18} = 4.41$

Therefore, reject H_0.

$$P \ll 0.0005 \quad [P < 0.00000000001]$$

$$r^2 = \frac{6750.29}{6869.20} = 0.98$$

$s_{Y \cdot X} = \sqrt{6.61} = 2.57$ mm Hg

Example 17.8b appropriately analyzes data consisting of multiple Y values at each X value, and Figure 17.9 presents the data graphically. For each of the k unique X_i values, we can speak of each of n_i values of Y (denoted by Y_{ij}) using the double subscript on i exactly as in the one-way analysis of variance (Section 10.1). In Example 17.8a, $n_1 = 3, n_2 = 4, n_3 = 3$, and so on; and $X_{11} = 50$ cm, $Y_{ii} = 108$ mm; $X_{12} = 50$ cm, $Y_{12} = 110$ mm; $X_{13} = 50$ cm, $Y_{13} = 106$ mm; and so on through $X_{55} = 70$ cm, $Y_{55} = 159$ mm. Therefore,

$$\sum xy = \sum_{i=1}^{k} \sum_{j=1}^{n_i} (X_{ij} - \overline{X})(Y_{ij} - \overline{Y}) = \sum\sum X_{ij}Y_{ij} - \frac{\sum X_{ij} \sum Y_{ij}}{N}, \qquad (17.36)$$

where $N = \sum_{i=1}^{k} n_i$ the total number of pairs of data. Also,

$$\sum x^2 = \sum_{i=1}^{k} \sum_{j=1}^{n_i} (X_{ij} - \overline{X})^2 = \sum\sum X_{ij}^2 - \frac{(\sum X_{ij})^2}{N} \tag{17.37}$$

and

$$\text{total SS} = \sum_{i=1}^{k} \sum_{j=1}^{n_i} (Y_{ij} - \overline{Y})^2 = \sum\sum Y_{ij}^2 - C, \tag{17.38}$$

where

$$C = \frac{(\sum\sum Y_{ij})^2}{N} \quad \text{and} \quad N = \sum_{i=1}^{k} n_i. \tag{17.39}$$

Examples 17.8a and 17.8b show the calculations of the regression coefficient, b, the Y intercept a, and the regression and residual sums of squares, using Equations 17.4, 17.7, 17.11, and 17.13, respectively. The total, regression, and residual degrees of freedom are $N - 1$, 1, and $N - 2$, respectively.

As shown in Section 17.3, the analysis of variance for significant slope involves the partitioning of the total variability of Y (i.e., $Y_{ij} - \overline{Y}$) into that variability due to regression ($\hat{Y}_i - \overline{Y}$) and that variability remaining (i.e., residual) after the regression line is fitted ($Y_{ij} - \hat{Y}_i$). However, by considering the k groups of Y values, we can also partition the total variability exactly as we did in the one-way analysis of variance (Sections 10.1a and 10.1b), by describing variability among groups ($\overline{Y}_i - \overline{Y}$) and within groups ($Y_{ij} - \overline{Y}_i$):

$$\text{among-groups SS} = \sum_{i=1}^{k} n_i \left(\overline{Y}_i - \overline{Y}\right)^2 = \sum_{i=1}^{k} \frac{\left(\sum_{j=1}^{n_i} Y_{ij}\right)^2}{n_i} - C, \tag{17.40}$$

$$\text{among-groups DF} = k - 1, \tag{17.41}$$

$$\text{within-groups SS} = \text{total SS} - \text{among-groups SS}, \tag{17.42}$$

$$\text{within-groups DF} = \text{total DF} - \text{among-groups DF} = N - k. \tag{17.43}$$

The variability among groups ($\overline{Y}_i - \overline{Y}$) can also be partitioned. Part of this variability ($\hat{Y}_i - \overline{Y}$) results from the linear regression fit to the data, and the rest ($\overline{Y}_i - \hat{Y}_i$) is due to the deviation of each group of data from the regression line, as shown in Figure 17.10. Therefore,

$$\text{deviations-from-linearity SS} = \text{among-groups SS} - \text{regression SS} \tag{17.44}$$

and

$$\begin{aligned} \text{deviations-from-linearity DF} &= \text{among-groups DF} - \text{regression DF} \\ &= k - 2. \end{aligned} \tag{17.45}$$

Table 17.2 summarizes this partitioning of sums of squares.

Alternatively, and with identical results, we may consider the residual variability ($Y_{ij} - \hat{Y}_i$) to be divisible into two components: within-groups variability ($Y_{ij} - \overline{Y}_i$)

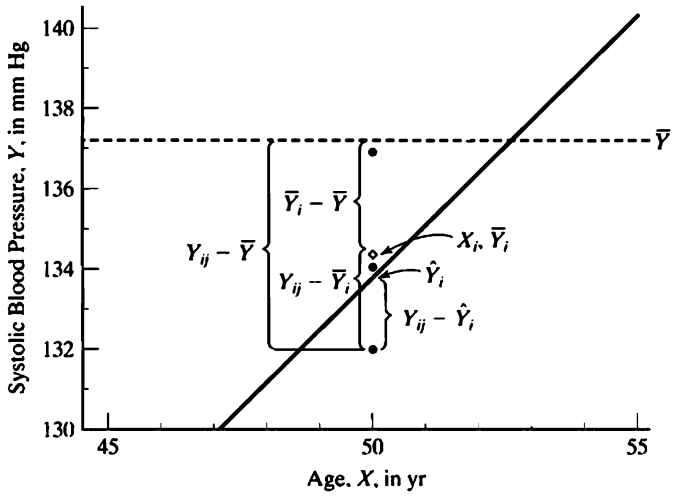


FIGURE 17.10: An enlarged portion of Figure 17.9, showing the partitioning of Y deviations. The mean Y at $X = 50$ yr is 134.3 mm Hg, shown by the symbol "◇"; the mean of all Y's is $\overline{Y}$, shown by a dashed line; Y_{ij} is the jth Y at the ith X; and $\overline{Y}_i$ is the mean of the n_i Y's at X_i.

TABLE 17.2: Summary of the Analyses of Variance Calculations for Testing H_0: the Population Regression Is Linear, and for Testing H_0: $\beta = 0$

Source of variation	*Sum of squares* (SS)	DF	*Mean Square* (MS)
Total $[Y_{ij} - \overline{Y}]$	$\sum y^2$	$N - 1$	
Linear regression $[\hat{Y}_i - \overline{Y}]$	$\dfrac{\left(\sum xy\right)^2}{\sum x^2}$	1	$\dfrac{\text{regression SS}}{\text{regression DF}}$
Residual $[Y_{ij} - \hat{Y}_i]$	total SS − regression SS	$N - 2$	$\dfrac{\text{residual SS}}{\text{residual DF}}$
Among groups $[\overline{Y}_i - \overline{Y}]$	$\displaystyle\sum_{i=1}^{k} \frac{\left(\sum_{j=1}^{n_i} Y_{ij}\right)^2}{n_i} - \frac{\left(\sum_{i=1}^{k}\sum_{j=1}^{n_i} Y_{ij}\right)^2}{N}$	$k - 1$	
Linear regression $[\hat{Y}_i - \overline{Y}]$	$\dfrac{\left(\sum xy\right)^2}{\sum x^2}$	1	
Deviations from linearity $[\overline{Y}_i - \hat{Y}_i]$	among-groups SS − regression SS	$k - 2$	$\dfrac{\text{deviations SS}}{\text{deviations DF}}$
Within groups $[Y_{ij} - \overline{Y}_i]$	total SS − among-groups SS	$N - k$	$\dfrac{\text{within-groups SS}}{\text{within-groups DF}}$

Note: To test H_0: the population regression is linear, we use F = deviations MS/within-groups MS, with a critical value of $F_{\alpha(1),(k-2),(N-k)}$. If the null hypothesis of linearity is rejected, then H_0: $\beta = 0$ is tested using F = regression MS/within-groups MS, with a critical value of $F_{\alpha(1),1,(N-k)}$.

TABLE 17.3: Summary of Analysis of Variance Partitioning of Sources of Variation for Testing Linearity, as an Alternative to That in Table 17.2

Source of variation	DF
Total $[Y_{ij} - \overline{Y}]$	$N - 1$
Among groups $[\overline{Y}_i - \overline{Y}]$	$k - 1$
Within groups $[Y_{ij} - \overline{Y}_i]$	$N - k$
Linear regression $[\hat{Y}_i - \overline{Y}]$	1
Residual $[Y_{ij} - \hat{Y}_i]$	$N - 2$
Within groups $[Y_{ij} - \overline{Y}_i]$	$N - k$
Deviations from linearity $[\overline{Y}_i - \hat{Y}_i]$	$k - 2$

Note: Sums of squares and mean squares are as in Table 17.2.

and deviations-from-linearity $(\overline{Y}_i - \hat{Y}_i)$. This partitioning of sums of squares and degrees of freedom is summarized in Table 17.3.*

If the population relationship between Y and X is a straight line (i.e., "H_0: The population regression is linear" is a true statement), then the deviations-from-linearity MS and the within-groups MS will be estimates of the same variance; if the relationship is not a straight line (H_0 is false), then the deviations-from-linearity MS will be significantly greater than the within-groups MS. Thus, as demonstrated in Example 17.8b,

$$F = \frac{\text{deviations-from-linearity MS}}{\text{within-groups MS}} \tag{17.46}$$

provides a one-tailed test of the null hypothesis of linearity. (If all n_i's are equal, then performing a regression using the k $\overline{Y}$'s will result in the same b and a as will the calculations using all N Y_i's but the significance test for β will be much less powerful and the preceding test for linearity will not be possible.) The power for the test for linearity will be greater for larger numbers of replicate Y's at each X.

If the null hypothesis of linearity is not rejected, then the deviations-from-linearity MS and the within-groups MS may be considered to be estimates of the same population variance. The latter will be the better estimate, as it is based on more degrees of freedom; but an even better estimate is the residual MS, which is $s^2_{Y \cdot X}$, for it constitutes a pooling of the deviations MS and the within-groups MS. Therefore, if a regression is assumed to be linear, $s^2_{Y \cdot X}$ is the appropriate variance to use in the computation of standard errors (e.g., by Equations 17.20, 17.26–17.29) and confidence intervals resulting from them, and this residual mean square $(s^2_{Y \cdot X})$ is also appropriate in testing the hypothesis H_0: $\beta = 0$ (either by Equation 17.14 or by Equations 17.20 and 17.21), as demonstrated in Example 17.8b.

If the population regression is concluded not to be linear, then the investigator can consider the procedures of Section 17.10 or 20.14 or of Chapter 21. If, however, it is desired to test H_0: $\beta = 0$, then the within-groups MS should be substituted for the residual MS $(s^2_{Y \cdot X})$; but it would not be advisable to engage in predictions with the linear-regression equation.

*Some authors refer to deviations from linearity as "lack of fit" and to within-groups variability as "error" or "pure error."

(a) Regression versus Analysis of Variance. Data consisting of replicate values of Y at each of several values of X (such as in Example 17.8) could also be submitted to a single-factor analysis of variance (Chapter 10). This would be done by considering the X's as levels of the factor and the Y's as the data whose means are to be compared (i.e., Y here is the same as X in Chapter 10). This would test H_0: $\mu_1 = \mu_2 = \cdots = \mu_k$ instead of H_0: $\beta = 0$, where k is the number of different values of X (e.g., $k = 5$ in Example 17.8). When there are only two levels of the ANOVA factor (i.e., two different X's in regression), the power of testing these two hypotheses is the same. Otherwise, the regression analysis will be more powerful than the ANOVA (Cottingham, Lennon, and Brown, 2005).

17.8 POWER AND SAMPLE SIZE IN REGRESSION

Although there are basic differences between regression and correlation (see Section 17.1), a set of data for which there is a statistically significant regression coefficient (i.e., H_0: $\beta = 0$ is rejected, as explained in Section 17.3) would also yield a statistically significant correlation coefficient (i.e., we would reject H_0: $\rho = 0$, to be discussed in Section 19.2). In addition, conclusions about the power of a significance test for a regression coefficient can be obtained by estimating power associated with the significance test for the correlation coefficient that would have been obtained from the same set of data.

After performing a regression analysis for a set of data, we may obtain the sample correlation coefficient, r, either from Equation 19.1, or, more simply, as

$$r = b\sqrt{\frac{\sum x^2}{\sum y^2}}, \tag{17.47}$$

or we may take the square root of the coefficient of determination r^2 (Equation 17.15), assigning to it the sign of b. Then, with r in hand, the procedures of Section 19.4 may be employed (Cohen, 1988: 76–77) to estimate power and minimum required sample size for the hypothesis test for the regression coefficient, H_0: $\beta = 0$.

17.9 REGRESSION THROUGH THE ORIGIN

Although not of common biological importance, a special type of regression procedure is called for when we are faced with sets of data for which we know, a priori, that in the population Y will be zero when X is zero (i.e., the population Y intercept is known to be zero). Since the point on the graph with coordinates (0, 0) is termed the *origin* of the graph, this regression situation is known as regression through the origin. In this type of regression analysis, both variables must be measured on a ratio scale, for only such a scale has a true zero (see Section 1.1).

For regression through the origin, the linear regression equation is

$$\hat{Y}_i = bX_i, \tag{17.48}$$

and some of the calculations pertinent to such a regression are as follows:

$$b = \frac{\sum X_i Y_i}{\sum X_i^2}, \tag{17.49}$$

$$\text{total SS} = \sum Y_i^2, \quad \text{with total DF} = n. \tag{17.50}$$

$$\text{regression SS} = \frac{(\sum X_i Y_i)^2}{\sum X_i^2}, \quad \text{with regression DF} = 1, \tag{17.51}$$

$$\text{residual SS} = \text{total SS} - \text{regression SS, with residual DF} = n - 1, \tag{17.52}$$

$$s_b^2 = \frac{s_{Y \cdot X}^2}{\sum X_i^2}, \tag{17.53}$$

where $s_{Y \cdot X}^2$ is residual mean square (residual SS/residual DF). Tests of hypotheses about the slope of the line are performed, as explained earlier in this chapter, with the exception that the preceding values are used; $n - 1$ is used as degrees of freedom whenever $n - 2$ is used for regressions not assumed to pass through the origin. Some statisticians (e.g., Kvålseth, 1985) caution against expressing a coefficient of determination, r^2, for this kind of regression. Bissell (1992) discusses potential difficulties with, and alternatives to, this regression model. A regression line forced through the origin does not necessarily pass through point $(\overline{X}, \overline{Y})$.

(a) Confidence Intervals. For regressions passing through the origin, confidence intervals may be obtained in ways analogous to the procedures in Section 17.5. That is, a confidence interval for the population regression coefficient, β, is calculated using Equation 17.53 for s_b^2 and $n - 1$ degree of freedom in place of $n - 2$. A confidence interval for an estimated $\hat{Y}$ is

$$s_{\hat{Y}} = \sqrt{s_{Y \cdot X}^2 \left(\frac{X_i^2}{\sum X^2} \right)}, \tag{17.54}$$

using the $s_{Y \cdot X}^2$ as in Equation 17.53; a confidence interval for $\hat{Y}_i$ predicted as the mean of m additional measurements at X_i is

$$(s_{\hat{Y}})_m = \sqrt{s_{Y \cdot X}^2 \left(\frac{1}{m} + \frac{X_i^2}{\sum X^2} \right)}; \tag{17.55}$$

and a confidence interval for the $\hat{Y}_i$ predicted for one additional measurement of X_i is

$$(s_{\hat{Y}})_1 = \sqrt{s_{X \cdot Y}^2 \left(1 + \frac{X_i^2}{\sum X^2} \right)} \tag{17.56}$$

(Seber and Lee, 2003: 149).

(b) Inverse Prediction. For inverse prediction (see Section 17.6) with a regression passing through the origin,

$$\hat{X}_i = \frac{Y_i}{b}, \tag{17.57}$$

and the confidence interval for the X_i predicted at a given Y is

$$\overline{X} + \frac{bY_i}{K} \pm \frac{t}{K} \sqrt{s_{Y \cdot X}^2 \left(\frac{Y_i^2}{\sum X_i^2} + K \right)}, \tag{17.58}$$

where $t = t_{\alpha(2),(n-1)}$ and* $K = b^2 - t^2 s_b^2$ (Seber and Lee, 2003: 149).

*Alternatively, $K = b^2 - F s_b^2$, where $F = t_{\alpha(2),(n-1)}^2 = F_{\alpha(1),1,(n-1)}$.

If X is to be predicted for multiple values of Y at that X, then

$$\hat{X}_i = \frac{\overline{Y}_i}{b}, \tag{17.59}$$

where $\overline{Y}_i$ is the mean of m values of Y; and the confidence limits would be calculated as

$$\overline{X} + \frac{b\overline{Y}_i}{K} \pm \frac{t}{K}\sqrt{(s^2_{Y \cdot X})'\left(\frac{\overline{Y}_i^2}{\sum X^2} + \frac{K}{m}\right)}, \tag{17.60}$$

where $t = t_{\alpha(2),(n+m-2)}$ and* $K = b^2 - t^2(s^2_b)'$;

$$(s^2_b)' = \frac{(s^2_{Y \cdot X})'}{\sum X^2}; \tag{17.61}$$

and

$$(s^2_{Y \cdot X})' = \frac{\text{residual SS} + \sum_{j=1}^{m}(Y_{ij} - \overline{Y}_i)^2}{n + m - 2} \tag{17.62}$$

(Seber and Lee, 2003: 149).

17.10 DATA TRANSFORMATIONS IN REGRESSION

As noted in Section 17.2d, the testing of regression hypotheses and the computation of confidence intervals—though not the calculation of a and b—depend upon the assumptions of normality and homoscedasticity, with regard to the values of Y, the dependent variable. Chapter 13 discussed the logarithmic, square-root, and arcsine transformations of data to achieve closer approximations to these assumptions. Consciously striving to satisfy the assumptions often (but without guaranty) appeases the others. The same considerations are applicable to regression data.

Transformation of the independent variable will not affect the distribution of Y, so transformations of X generally may be made with impunity, and sometimes they conveniently convert a curved line into a straight line. However, transformations of Y do affect least-squares considerations and will therefore be discussed. Acton (1966: Chapter 8); Glantz and Slinker (2001: 150–154); Montgomery, Peck, and Vining (2001: 173–193); and Weisberg (2005: Chapter 7) present further discussions of transformations in regression.

If the values of Y are from a Poisson distribution (i.e., the data are counts, especially small counts), then the square-root transformation is usually desirable:

$$Y' = \sqrt{Y + 0.5}, \tag{17.63}$$

where the values of the variable after transformation (Y') are then submitted to regression analysis. (Also refer to Section 13.2.)

If the Y values are from a binomial distribution (e.g., they are proportions or percentages), then the arcsine transformation is appropriate:

$$Y' = \arcsin\sqrt{Y}. \tag{17.64}$$

(See also Section 13.3.) Appendix Table B.24 allows for ready use of this transformation.

*Alternatively, $K = b^2 - F(s^2_b)'$, where $F = t^2_{\alpha(2),(n+m-2)} = F_{\alpha(1),1,(n+m-2)}$.

The most commonly used transformation in regression is the logarithmic transformation (see also Section 13.1), although it is sometimes employed for the wrong reasons. This transformation,

$$Y' = \log Y, \tag{17.65}$$

or

$$Y' = \log(Y + 1), \tag{17.66}$$

is appropriate when there is heteroscedasticity owing to the standard deviation of Y at any X increasing in proportion to the value of X. When this situation exists, it implies that values of Y can be measured more accurately at low than at high values of X. Figure 17.11 shows such data (from Example 17.9) before and after the transformation.

EXAMPLE 17.9 Regression Data Before and After Logarithmic Transformation of Y

Original data (as plotted in Figure 17.11a), indicating the variance of Y (namely, s_Y^2) at each X:

X	Y	s_Y^2
5	10.72, 11.22, 11.75, 12.31	0.4685
10	14.13, 14.79, 15.49, 16.22	0.8101
15	18.61, 19.50, 20.40, 21.37	1.4051
20	24.55, 25.70, 26.92, 28.18	2.4452
25	32.36, 33.88, 35.48, 37.15	4.2526

Transformed data (as plotted in Figure 17.11b), indicating the variance of $\log Y$ (namely, $s_{\log Y}^2$) at each X:

X	$\log Y$	$s_{\log Y}^2$
5	1.03019, 1.04999, 1.07004, 1.09026	0.000668
10	1.15014, 1.16997, 1.19005, 1.21005	0.000665
15	1.26975, 1.29003, 1.30963, 1.32980	0.000665
20	1.39005, 1.40993, 1.43008, 1.44994	0.000665
25	1.51001, 1.52994, 1.54998, 1.56996	0.000666

Many scatter plots of data imply a curved, rather than a straight-line, dependence of Y on X (e.g., Figure 17.11a). Often, logarithmic or other transformations of the values of Y and/or X will result in a straight-line relationship (as Figure 17.11b) amenable to linear regression techniques. *However*, if original, nontransformed values of Y agree with our assumptions of normality and homoscedasticity, then the data resulting from any of the preceding transformations will not abide by these assumptions. This is often not considered, and many biologists employing transformations do so simply to straighten out a curved line and neglect to consider whether the transformed data might indeed be analyzed legitimately by least-squares regression methods. If a transformation may not be used validly to straighten out a curvilinear regression, then Section 20.15 (or perhaps Chapter 21) may be applicable.

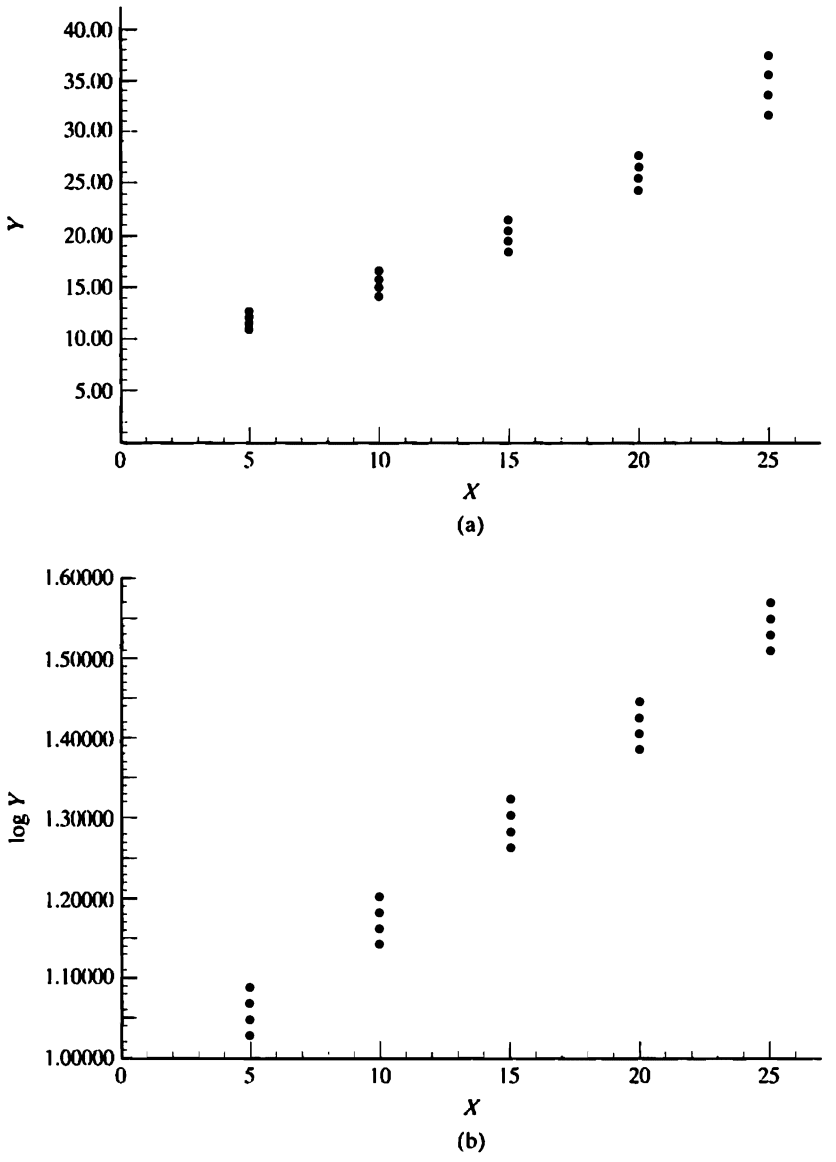


FIGURE 17.11: Regression data (of Example 17.9) exhibiting an increasing variability of Y with increasing magnitude of X. (a) The original data. (b) The data after logarithmic transformation of Y.

Section 13.4 mentions some other, less commonly employed, data transformations. Iman and Conover (1979) discuss rank transformation (i.e., performing a regression of the ranks of Y on the ranks of X).

(a) Examination of Residuals. Since the logarithmic transformation is frequently proposed and employed to try to achieve homoscedasticity, we should consider how a justification for such a transformation might be obtained. If a regression is fitted by least squares, then the sample residuals (i.e., the values of $Y_i - \hat{Y}_i$) may be plotted against their corresponding X's, as in Figure 17.12 (see Draper and Smith, 1998: 62–64). If homoscedasticity exists, then the residuals should be distributed evenly above and below zero (i.e., within the shaded area in Figure 17.12a).

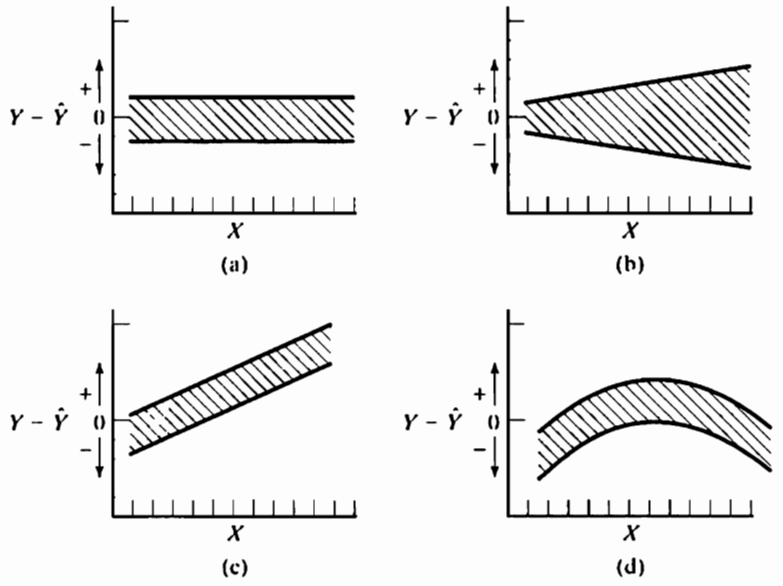


FIGURE 17.12: The plotting of residuals. (a) Data exhibiting homoscedasticity. (b) Data with heteroscedasticity of the sort in Example 17.9. (c) Data for which there was likely an error in the regression calculations, or an additional variable is needed in the regression model. (d) Data for which a linear regression does not accurately describe the relationship between Y and X, and a curvilinear relationship should be considered.

If there is heteroscedasticity due to increasing variability in Y with increasing values of X, then the residuals will form a pattern such as in Figure 17.12b, and a logarithmic transformation might be warranted. If the residuals form a pattern such as in Figure 17.12c, we should suspect that a calculation error has occured or, that an additional important variable should be added to the regression model (see Chapter 20). The pattern in Figure 17.12d indicates that a *linear* regression is an improper model to describe the data; for example, a quadratic regression (see Section 21.2) might be employed.

Glejser (1969) suggests fitting the simple linear regression

$$E_i = a + bX_i, \tag{17.67}$$

where $E_i = |Y_i - \hat{Y}_i|$. A statistically significant b greater than zero indicates Figure 17.12b to be the case, and the logarithmic transformation may be attempted. Then, after the application of the transformation, a plot of the new residuals (i.e., $\log Y_i - \widehat{\log Y_i}$) should be examined and Equation 17.67 fitted, where $E_i = \left|\log Y_i - \widehat{\log Y_i}\right|$. If this regression has a b not significantly different from zero, then we may assume that the transformation was justified. An outlier (see Section 17.2d) will appear on plots such as Figure 17.12 as a point very far outside the pattern indicated by the shaded area.

Tests for normality in the distribution of residuals may be made by using the methods of Section 6.6 (employing $Y_i - \hat{Y}_i$ in place of X_i in that section); graphical examination of normality (as in Figure 6.11) is often convenient.

17.11 THE EFFECT OF CODING DATA

Either X or Y data, or both, may be coded prior to the application of regression analysis, and coding may facilitate computations, especially when the data are very large or very small in magnitude. As shown in Sections 3.5 and 4.8, coding may consist of adding a constant to (or subtracting it from) X, or multiplying (or dividing) X by a constant; or both addition (or subtraction) and multiplication (or division) may be applied simultaneously. Values of Y may be coded in the same fashion; this may even be done simultaneously with the coding of X values, using either the same or different coding constants. If we let M_X and M_Y represent constants by which X and Y, respectively, are to be multiplied, and let A_X and A_Y be constants then to be added to $M_X X$ and $M_Y Y$, respectively, then the transformed variables, $[X]$ and $[Y]$, are

$$[X] = M_X X + A_X \tag{17.68}$$

and

$$[Y] = M_Y Y + A_Y. \tag{17.69}$$

As shown in Appendix C, the slope, b, will not be changed by adding constants to X and/or Y, for such transformations have the effect of simply sliding the scale of one or both axes. But if multiplication factors are used in coding, then the resultant slope, $[b]$, will be equal to $(b)(M_Y/M_X)$. Note that coding in no way alters the value of r^2 or the t or F statistics calculated for hypothesis testing.

A common situation involving multiplicative coding factors is one where the variables were recorded using certain units of measurement, and we want to determine what regression statistics would have resulted if other units of measurement had been used.

For the data in Examples 17.1, 17.2, and 17.3, $a = 0.715$ cm, and $b = 0.270$ cm/day, and $s_{Y \cdot X} = 0.218$ cm. If the wing length data were measured in inches, instead of in centimeters, there would have to be a coding by multiplying by 0.3937 in./cm (for there are 0.3937 inches in one centimeter). By consulting Appendix C, with $M_Y = 0.3937$ in./cm, $A_Y = 0$, $M_X = 1$, and $A_X = 0$, we can calculate that if a regression analysis were run on these data, where X was recorded in inches, the slope would be $[b] = (0.270 \text{ cm/day})(0.3937 \text{ in./cm}) = 0.106$ in./day; the Y intercept would be $[a] = (0.715 \text{ cm})(0.3937 \text{ in./cm}) = 0.281$ in.; and the standard error of estimate would be $s_{Y \cdot X} = (0.3937 \text{ in./cm})(0.218 \text{ cm}) = 0.086$.

A situation employing coding by both adding a constant and multiplying a constant is when we have temperature measurements in degrees Celsius (or Fahrenheit) and wish to determine the regression equation that would have resulted had the data been recorded in degrees Fahrenheit (or Celsius). The appropriate coding constants for use in Appendix C are determined by knowing that Celsius and Fahrenheit temperatures are related as follows:

$$\text{degrees Celsius} = \left(\frac{5}{9}\right)(\text{degrees Fahrenheit}) - \left(\frac{5}{9}\right)(32)$$

$$\text{degrees Fahrenheit} = \left(\frac{9}{5}\right)(\text{degrees Celsius}) + 32.$$

This is summarized elsewhere (Zar, 1968), as are the effects of multiplicative coding on logarithmically transformed data (Zar, 1967).

EXERCISES

17.1. The following data are the rates of oxygen consumption of birds, measured at different environmental temperatures:

Temperature (C)	*Oxygen consumption* (ml/g/hr)
−18.	5.2
−15.	4.7
−10.	4.5
− 5.	3.6
0.	3.4
5.	3.1
10.	2.7
19.	1.8

(a) Calculate a and b for the regression of oxygen consumption rate on temperature.
(b) Test, by analysis of variance, the hypothesis H_0: $\beta = 0$.
(c) Test, by the t test, the hypothesis H_0: $\beta = 0$.
(d) Calculate the standard error of estimate of the regression.
(e) Calculate the coefficient of determination of the regression.
(f) Calculate the 95% confidence limits for β.

17.2. Utilize the regression equation computed for the data of Exercise 17.1.
(a) What is the mean rate of oxygen consumption in the population for birds at 15 C?
(b) What is the 95% confidence interval for this mean rate?
(c) If we randomly chose one additional bird at 15° C from the population, what would its rate of oxygen consumption be estimated to be?
(d) We can be 95% confident of this value lying between what limits?

17.3. The frequency of electrical impulses emitted from electric fish is measured from three fish at each of several temperatures. The resultant data are as follows:

Temperature (C)	*Impulse frequency* (number/sec)
20	225, 230, 239
22	251, 259, 265
23	266, 273, 280
25	287, 295, 302
27	301, 310, 317
28	307, 313, 325
30	324, 330, 338

(a) Compute a and b for the linear regression equation relating impulse frequency to temperature.
(b) Test, by analysis of variance H_0: $\beta = 0$.
(c) Calculate the standard error of estimate of the regression.
(d) Calculate the coefficient of determination of the regression.
(e) Test H_0: The population regression is linear.

CHAPTER 18

Comparing Simple Linear Regression Equations

A regression equation may be calculated for each of two or more samples of data to compare the regression relationships in the populations from which the samples came. We may ask whether the slopes of the regression lines are significantly different (as opposed to whether they may be estimating the same population slope, β). Then, if it is concluded that the slopes of the lines are not significantly different, we may want to test whether the several sets of data are from populations in which the population Y intercepts, as well as the slopes, are the same. In this chapter, procedures for testing differences among regression lines will be presented, as summarized in Figure 18.1.

18.1 COMPARING TWO SLOPES

The comparison of the slopes of two regression lines is demonstrated in Example 18.1. The regression relationship to be studied is the amount of water lost by salamanders maintained at various environmental temperatures. Using the methods of Section 17.2 or 17.7, a regression line is determined using data from each of two species of salamanders. The regression line for 26 animals of species 1 is $10.57 + 2.97X$, and that for 30 animals of species 2 is $24.91 + 2.17X$; these two regression lines are shown in Figure 18.2. Temperature, the independent variable (X), is measured in degrees Celsius, and the dependent variable (Y) is measured in microliters (μl) of water per gram of body weight per hour. Example 18.1 shows the calculations of the slope of each of the two regression lines. In this example, the slope of the line expresses water loss, in μl/g/hr, for each temperature increase of 1 C. The raw data (the 26 X and Y data for species 1 and the 30 pairs of data for species 2) are not shown, but the sums of squares (Σx^2 and Σy^2) and sum of crossproducts (Σxy) for each line are given in this example. (The calculation of the Y intercepts is not shown.)

As shown is Example 18.1, a simple method for testing hypotheses about equality of two population regression coefficients involves the use of Student's t in a fashion analogous to that of testing for differences between two population means (Section 8.1). The test statistic is

$$t = \frac{b_1 - b_2}{s_{b_1 - b_2}}, \tag{18.1}$$

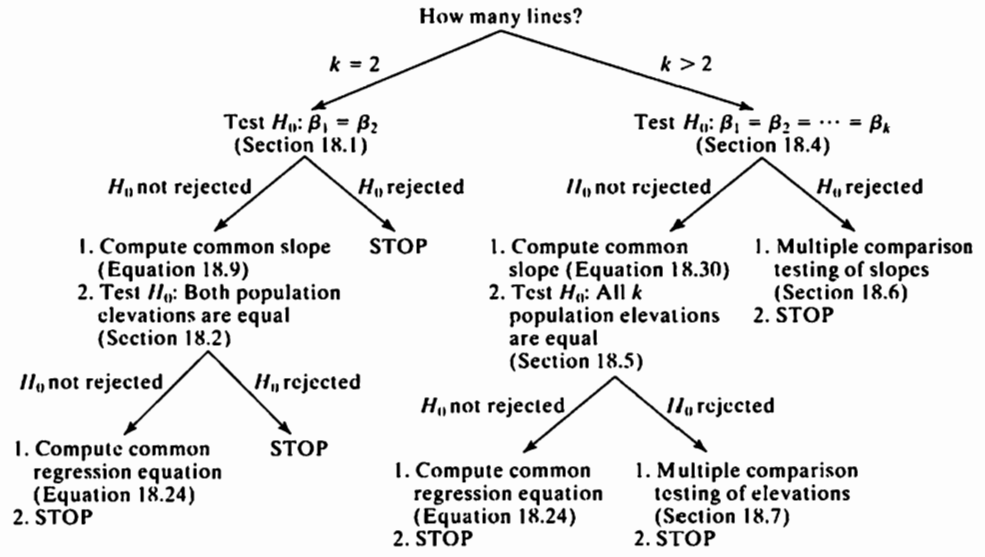


FIGURE 18.1: Flow chart for the comparison of regression lines.

EXAMPLE 18.1 Testing for Difference Between Two Population Regression Coefficients

For each of two species of salamanders, the data are for water loss (Y, measured as μl/g/hr) and environmental temperature (X, in °C).

H_0: $\beta_1 = \beta_2$

H_A: $\beta_1 \neq \beta_2$

For Species 1:

$n = 26$

$\sum x^2 = 1470.8712$

$\sum xy = 4363.1627$

$\sum y^2 = 13299.5296$

$b = \dfrac{4363.1627}{1470.8712} = 2.97$

residual SS $= 13299.5296 - \dfrac{(4363.1627)^2}{1470.8712}$

$= 356.7317$

residual DF $= 26 - 2 = 24$

For Species 2:

$n = 30$

$\sum x^2 = 2272.4750$

$\sum xy = 4928.8100$

$\sum y^2 = 10964.0947$

$b = \dfrac{4928.8100}{2272.4750} = 2.17$

residual SS $= 10964.0947 - \dfrac{(4928.8100)^2}{2272.4750}$

$= 273.9142$

residual DF $= 30 - 2 = 28$

$$(s^2_{Y \cdot X})_p = \frac{356.7317 + 273.9142}{24 + 28} = 12.1278$$

$$s_{b_1 - b_2} = \sqrt{\frac{12.1278}{1470.8712} + \frac{12.1278}{2272.4750}} = 0.1165$$

$$t = \frac{2.97 - 2.17}{0.1165} = 6.867$$

$\nu = 24 + 28 = 52$

Reject H_0 if $|t| \geq t_{\alpha(2),\nu}$

$t_{0.05(2),52} = 2.007$; Reject H_0.

$P < 0.001$ $[P = 0.0000000081]$

Calculation not shown:

$a_1 = 10.57$ $a_2 = 24.91$

where the standard error of the difference between regression coefficients is

$$s_{b_1 - b_2} = \sqrt{\frac{(s^2_{Y \cdot X})_p}{\left(\sum x^2\right)_1} + \frac{(s^2_{Y \cdot X})_p}{\left(\sum x^2\right)_2}}, \tag{18.2}$$

and the pooled residual mean square is calculated as

$$(s^2_{Y \cdot X})_p = \frac{(\text{residual SS})_1 + (\text{residual SS})_2}{(\text{residual DF})_1 + (\text{residual DF})_2}, \tag{18.3}$$

the subscripts 1 and 2 referring to the two regression lines being compared. The critical value of t for this test has $(n_1 - 2) + (n_2 - 2)$ degrees of freedom (i.e., the sum of the two residual degrees of freedom), namely

$$\nu = n_1 + n_2 - 4. \tag{18.4}$$

Just as the t test for difference between means assumes that $\sigma_1^2 = \sigma_2^2$, the preceding t test assumes that $(\sigma^2_{Y \cdot X})_1 = (\sigma^2_{Y \cdot X})_2$. The presence of the latter condition can be tested by the variance ratio test, $F = (s^2_{Y \cdot X})_{\text{larger}}/(s^2_{Y \cdot X})_{\text{smaller}}$; but this is usually not done due to the limitations of that test (see Section 8.5).

The $1 - \alpha$ confidence interval for the difference between two slopes, β_1 and β_2, is

$$(b_1 - b_2) \pm t_{\alpha(2),\nu} s_{b_1 - b_2}, \tag{18.5}$$

where ν is as in Equation 18.4. Thus, for Example 18.1,

$$\begin{aligned} 95\% \text{ confidence interval for } \beta_1 - \beta_2 &= (2.97 - 2.17) \pm (t_{0.05(2),52})(0.1165) \\ &= 0.80 \pm (2.007)(0.1165) \\ &= 0.80\ \mu\text{l/g/hr/°C} \pm 0.23\ \mu\text{l/g/hr/°C}; \end{aligned}$$

and the upper and lower 95% confidence limits for $\beta_1 - \beta_2$ are $L_1 = 0.57\ \mu$l/g/hr/°C and $L_2 = 1.03\ \mu$l/g/hr/°C.

If H_0: $\beta_1 = \beta_2$ is rejected (as in Example 18.1), we may wish to calculate the point where the two lines intersect. The intersection is at

$$X_I = \frac{a_2 - a_1}{b_1 - b_2}, \tag{18.6}$$

at which the value of $\hat{Y}$ may be computed either as

$$\hat{Y}_I = a_1 + b_1 X_I \tag{18.7}$$

or

$$\hat{Y}_I = a_2 + b_2 X_I. \tag{18.8}$$

The point of intersection of the two lines in Example 18.1 is at

$$X_I = \frac{24.91 - 10.57}{2.97 - 2.17} = 17.92°\text{C}$$

and

$$\hat{Y}_I = 1.057 + (2.97)(17.92) = 63.79\ \mu\text{l/g/hr/°C}.$$

Figure 18.2 illustrates this intersection.

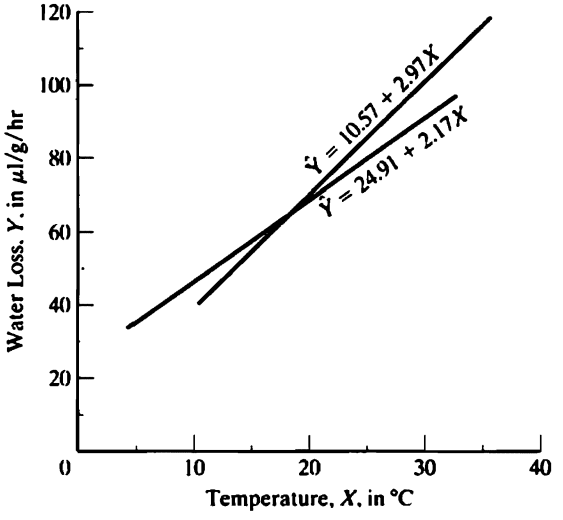


FIGURE 18.2: The two regression lines of Example 18.1. The two slopes are concluded to be significantly different and the two lines are found to intersect at $X_I = 17.92°\text{C}$ and $\hat{Y}_I = 63.79\ \mu\text{l/g/hr}$.

If H_0: $\beta_1 = \beta_2$ is not rejected (as will be shown in Example 18.2), then an estimate of the population regression coefficient, β, underlying both b_1 and b_2 is called the *common* (or *weighted*) *regression coefficient:*

$$b_c = \frac{(\Sigma xy)_1 + (\Sigma xy)_2}{(\Sigma x^2)_1 + (\Sigma x^2)_2} \tag{18.9}$$

or, equivalently (but with more chance of rounding error),

$$b_c = \frac{\left(\Sigma x^2\right)_1 b_1 + \left(\Sigma x^2\right)_2 b_2}{(\Sigma x^2)_1 + (\Sigma x^2)_2}. \tag{18.10}$$

Equation 18.1 is a special case of

$$t = \frac{|b_1 - b_2| - \beta_0}{s_{b_1 - b_2}}, \tag{18.11}$$

namely when $\beta_0 = 0$. By using Equation 18.11, we may test the hypothesis that the difference between two population regression coefficients is a specified magnitude; that is, $H_0: \beta_1 - \beta_2 = \beta_0$ may be tested against $H_A: \beta_1 - \beta_2 \neq \beta_0$.

One-tailed testing is also possible, asking whether one population regression coefficient is greater than the other. If we test $H_0: \beta_1 \geq \beta_2$ and $H_A: \beta_1 < \beta_2$, or $H_0: \beta_1 - \beta_2 \geq \beta_0$ versus $H_A: \beta_1 - \beta_2 < \beta_0$, then H_0 is rejected if $t \leq -t_{\alpha(1),\nu}$; if we test $H_0: \beta_1 \leq \beta_2$ and $H_A: \beta_1 > \beta_2$, or $H_0: \beta_1 - \beta_2 \leq \beta_0$ versus $H_A: \beta_1 - \beta_2 > \beta_0$, then we reject H_0 if $t \geq t_{\alpha(1),\nu}$. In either case, t is computed by Equation 18.1, or by Equation 18.11 if $\beta_0 \neq 0$.

An alternative method of testing $H_0: \beta_1 = \beta_2$ is by the analysis of covariance procedure of Section 18.4. However, if a computer program is not used, the preceding t test generally involves less computational effort.

(a) Power and Sample Size in Comparing Regressions. In Section 17.8 it was explained that the procedure for consideration of power in correlation analysis (Section 19.4) could be used to estimate power and sample size in a regression analysis. Section 19.6 presents power and sample-size estimation when testing for difference between two correlation coefficients. Unfortunately, utilization of that procedure for comparing two regression coefficients is not valid—unless one has the rare case of $\left(\sum x^2\right)_1 = \left(\sum x^2\right)_2$ and $\left(\sum y^2\right)_1 = \left(\sum y^2\right)_2$ (Cohen, 1988: 110).

COMPARING TWO ELEVATIONS

If $H_0: \beta_1 = \beta_2$ is rejected, we conclude that two different populations of data have been sampled. However, if two population regression lines are not concluded to have different slopes (i.e., $H_0: \beta_1 = \beta_2$ is not rejected), then the two lines are assumed to be parallel. In the latter case, we often wish to determine whether the two population regressions have the same elevation (i.e., the same vertical position on a graph) and thus coincide.

To test the null hypothesis that the elevations of the two population regression lines are the same, the following quantities may be used in a t test, as shown in Example 18.2:

sum of squares of X for common regression

$$= A_c = \left(\sum x^2\right)_1 + \left(\sum x^2\right)_2, \tag{18.12}$$

sum of crossproducts for common regression

$$= B_c = \left(\sum xy\right)_1 + \left(\sum xy\right)_2, \tag{18.13}$$

sum of squares of Y for common regression

$$= C_c = \left(\sum y^2\right)_1 + \left(\sum y^2\right)_2, \tag{18.14}$$

residual SS for common regression

$$= SS_c = C_c - \frac{B_c^2}{A_c}, \tag{18.15}$$

$$\text{residual DF for common regression} = \text{DF}_c = n_1 + n_2 - 3, \tag{18.16}$$

and

$$\text{residual MS for common regression} = (s^2_{Y \cdot X})_c = \frac{\text{SS}_c}{\text{DF}_c} \tag{18.17}$$

Then, the appropriate test statistic is

$$t = \frac{(\overline{Y}_1 - \overline{Y}_2) - b_c(\overline{X}_1 - \overline{X}_2)}{\sqrt{(s^2_{Y \cdot X})_c \left[\frac{1}{n_1} + \frac{1}{n_2} + \frac{(\overline{X}_1 - \overline{X}_2)^2}{A_c}\right]}}, \tag{18.18}$$

and the relevant critical value of t is that for $\nu = \text{DF}_c$. Example 18.2 and Figure 18.3 consider the regression of human systolic blood pressure on age for men over 40 years old. A regression equation was fitted for data for men in each of two different occupations. The two-tailed null hypothesis is that in the two sampled populations the regression elevations are the same. This also says that blood pressure is the same in both groups, after accounting for the effect of age. In the example, the H_0 of equal elevations is rejected, so we conclude that men in these two occupations do not have the same blood pressure. As an alternative to this t-testing procedure, the analysis of covariance of Section 18.4 may be used to test this hypothesis, but it generally requires more computational effort unless a computer package is used.

EXAMPLE 18.2 Testing for Difference Between Two Population Regression Coefficients and Elevations

The data are for systolic blood pressure (the dependent variable, Y, in millimeters of mercury [i.e., mm Hg]) and age (the independent variable, X, in years) for men over 40 years of age; the two samples are from different occupations.

For Sample 1:	For Sample 2:
$n = 13$	$n = 15$
$\overline{X} = 54.65$ yr	$\overline{X} = 56.93$ yr
$\overline{Y} = 170.23$ mm Hg	$\overline{Y} = 162.93$ mm Hg
$\sum x^2 = 1012.1923$	$\sum x^2 = 1659.4333$
$\sum xy = 1585.3385$	$\sum xy = 2475.4333$
$\sum y^2 = 2618.3077$	$\sum y^2 = 3848.9333$
$b = 1.57$ mm Hg/yr	$b = 1.49$ mm Hg/yr
$a = 84.6$ mm Hg	$a = 78.0$ mm Hg
residual SS = 135.2833	residual SS = 156.2449
residual DF = 11	residual DF = 13

H_0: $\beta_1 = \beta_2$
H_A: $\beta_1 \neq \beta_2$

$$(s^2_{Y\cdot X})_p = \frac{135.2833 + 156.2449}{11 + 13} = 12.1470$$

$$\nu = 11 + 13 = 24$$

$$s_{b_1 - b_2} = 0.1392$$

$$t = \frac{1.57 - 1.49}{0.1392} = 0.575$$

$t_{0.05(2),24} = 2.064$; do not reject H_0.

$$P > 0.50 \quad [P = 0.57]$$

H_0: The two population regression lines have the same elevation.
H_A: The two population regression lines do not have the same elevation.

$$A_c = 1012.1923 + 1659.4333 = 2671.6256$$

$$B_c = 1585.3385 + 2475.4333 = 4060.7718$$

$$C_c = 2618.3077 + 3848.9333 = 6467.2410$$

$$b_c = \frac{4060.7718}{2671.6256} = 1.520 \text{ mm Hg/yr}$$

$$SS_c = 6467.2410 - \frac{(4060.7718)^2}{2671.6256} = 295.0185$$

$$DF_c = 13 + 15 - 3 = 25$$

$$(s^2_{Y\cdot X})_c = \frac{295.0185}{25} = 11.8007$$

$$t = \frac{(170.23 - 162.93) - 1.520(54.65 - 56.93)}{\sqrt{11.8007\left[\frac{1}{13} + \frac{1}{15} + \frac{(54.65 - 56.93)^2}{2671.6256}\right]}} = \frac{10.77}{1.3105} = 8.218$$

$t_{0.05(2),25} = 2.060$; reject H_0.

$$P < 0.001 \quad [P = 0.0000000072]$$

If it is concluded that two population regressions do not have different slopes but do have different elevations, then the slopes computed from the two samples are both estimates of the common population regression coefficient, and the Y intercepts of the two samples are

$$a_1 = \overline{Y}_1 - b_c\overline{X}_1 \tag{18.19}$$

and

$$a_2 = \overline{Y}_2 - b_c\overline{X}_2, \tag{18.19a}$$

and the two regression equations may be written as

$$\hat{Y}_i = a_1 + b_cX_i \tag{18.20}$$

and

$$\hat{Y}_i = a_2 + b_cX_i \tag{18.20a}$$

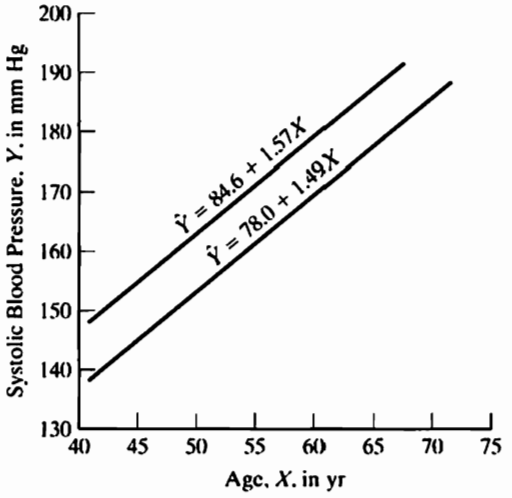


FIGURE 18.3: The two regression lines of Example 18.2.

(though this can be misleading if $X = 0$ is far from the range of X's in the sample). For the two lines in Example 18.2 and Figure 18.3,

$$\hat{Y}_i = 84.6 + 1.52X_i$$

and

$$\hat{Y}_i = 78.0 + 1.52X_i.$$

If it is concluded that two population regressions have neither different slopes nor different elevations, then both sample regressions estimate the same population regression, and this estimate may be expressed using the common regression coefficient, b_c, as well as a common Y intercept:

$$a_c = \overline{Y}_p - b_c\overline{X}_p, \tag{18.21}$$

where the pooled sample means of the two variables may be obtained as

$$\overline{X}_p = \frac{n_1\overline{X}_1 + n_2\overline{X}_2}{n_1 + n_2} \tag{18.22}$$

and

$$\overline{Y}_p = \frac{n_1\overline{Y}_1 + n_2\overline{Y}_2}{n_1 + n_2}. \tag{18.23}$$

Thus, when two samples have been concluded to estimate the same population regression, a single regression equation representing the regression in the sampled population would be

$$\hat{Y}_i = a_c + b_cX_i. \tag{18.24}$$

We may also use t to test one-tailed hypotheses about elevations. For data such as those in Example 18.2 and Figure 18.3, it might have been the case that one occupation was considered to be more stressful, and we may want to determine whether men in that occupation had higher blood pressure than men in the other occupation.

This t test of elevations is preferable to testing for difference between the two population Y intercepts. Difference between Y intercepts would be tested with the null hypothesis $H_0 : \alpha_1 = \alpha_2$, using the sample statistics a_1 and a_2, and could proceed with

$$t = \frac{a_1 - a_2}{s_{a_1 - a_2}}, \tag{18.25}$$

where

$$s_{a_1 - a_2} = \sqrt{(s^2_{Y \cdot X})_p \left[\frac{1}{n_1} + \frac{1}{n_2} + \frac{\overline{X}_1^2}{\left(\sum x^2\right)_1} + \frac{\overline{X}_2^2}{\left(\sum x^2\right)_2} \right]} \tag{18.26}$$

(the latter two equations are a special case of Equations 18.27 and 18.28). However, a test for difference between Y intercepts is generally not as advisable as a test for difference between elevations because it uses a point on each line that may lie far from the observed range of X's. There are many regressions for which the Y intercept has no importance beyond helping to define the line and in fact may be a sample statistic prone to misleading interpretation. In Figure 18.3, for example, discussion of the Y intercepts (and testing hypotheses about them) would require a risky extrapolation of the regression lines far below the range of X for which data were obtained. This would assume that the linear relationship that was determined for ages above 40 years also holds between $X = 0$ and $X = 40$ years, a seriously incorrect assumption in the present case dealing with blood pressures. Also, because the Y intercepts are so far from the mean values of X, their standard errors would be very large, and a test of H_0: $\alpha_1 = \alpha_2$ would lack statistical power.

COMPARING POINTS ON TWO REGRESSION LINES

If the slopes of two regression lines and the elevations of the two lines have not been concluded to be different, then the two lines are estimates of the same population regression line. If the slopes of two lines are not concluded to be different, but their elevations are declared different, then the population lines are assumed to be parallel, and for a given X_i, the corresponding $\hat{Y}_i$ on one line is different from that on the other line.

If the slopes of two population regression lines are concluded different, then the lines are intersecting rather than parallel. In such cases we may wish to test whether a $\hat{Y}$ on one line is the same as the $\hat{Y}$ on the second line at a particular X. For a two-tailed test, we can state the null hypothesis as H_0: $\mu_{\hat{Y}_1} = \mu_{\hat{Y}_2}$ and the alternate as H_A: $\mu_{\hat{Y}_1} \neq \mu_{\hat{Y}_2}$. The test statistic is

$$t = \frac{\hat{Y}_1 - \hat{Y}_2}{s_{\hat{Y}_1 - \hat{Y}_2}}, \tag{18.27}$$

where

$$s_{\hat{Y}_1 - \hat{Y}_2} = \sqrt{(s^2_{Y \cdot X})_p \left[\frac{1}{n_1} + \frac{1}{n_2} + \frac{(X - \overline{X}_1)^2}{\left(\sum x^2\right)_1} + \frac{(X - \overline{X}_2)^2}{\left(\sum x^2\right)_2} \right]}, \tag{18.28}$$

and the degrees of freedom are the pooled degrees of freedom of Equation 18.4. Such a test is demonstrated in Example 18.3.

EXAMPLE 18.3 Testing for Difference Between Points on the Two Nonparallel Regression Lines of Example 18.1 and Figure 18.2. We Are Testing Whether the Volumes (Y) Are Different in the Two Groups at $X = 12$°C

H_0: $\mu_{\hat{Y}_1} = \mu_{\hat{Y}_2}$

H_A: $\mu_{\hat{Y}_1} \neq \mu_{\hat{Y}_2}$

Beyond the statistics given in Example 18.1, we need to know the following:

$$\overline{X}_1 = 22.93°\text{C} \quad \text{and} \quad \overline{X}_2 = 18.95°\text{C}.$$

We then compute:

$$\hat{Y}_1 = 10.57 + (2.97)(12) = 46.21\ \mu\text{l/g/hr}$$

$$\hat{Y}_2 = 24.91 + (2.17)(12) = 50.95\ \mu\text{l/g/hr}$$

$$s_{\hat{Y}_1 - \hat{Y}_2} = \sqrt{12.1278\left[\frac{1}{26} + \frac{1}{30} + \frac{(12 - 22.93)^2}{1470.8712} + \frac{(12 - 18.95)^2}{2272.4750}\right]}$$

$$= \sqrt{2.1135} = 1.45\ \mu\text{l/g/hr}$$

$$t = \frac{46.21 - 50.95}{1.45} = -3.269$$

$$\nu = 26 + 30 - 4 = 52$$

$$t_{0.05(2),52} = 2.007$$

As $|t| > t_{0.05(2),52}$, reject H_0.

$$0.001 < P < 0.002 \quad [P = 0.0019]$$

One-tailed testing is also possible. However, it should be applied with caution, as it assumes that each of the two predicted $\hat{Y}$'s has associated with it the same variance. Therefore, the test works best when the two lines have the same $\overline{X}$, the same $\sum x^2$, and the same n.

18.4 COMPARING MORE THAN TWO SLOPES

If the slopes of more than two regression equations are to be compared, the null hypothesis H_0: $\beta_1 = \beta_2 = \cdots = \beta_k$ may be tested, where k is the number of regressions. The alternate hypothesis would be that, in the k sampled populations, all k slopes are not the same. These hypotheses are analogous to those used in testing whether the means are the same in k samples (Chapter 10). The hypothesis about equality of regression slopes may be tested by a procedure known as *analysis of covariance* (which was introduced in Section 12.10).

Analysis of covariance (ANCOVA) encompasses a large body of statistical methods, and various kinds of ANCOVA are presented in many comprehensive texts, including some of the books cited in the introduction of Chapter 16. The following version of analysis of covariance suffices to test for the equality (sometimes called homogeneity) of regression coefficients (i.e., slopes). Just as an analysis of variance for H_0: $\mu_1 = \mu_2 = \cdots = \mu_k$ assumes that all k population variances are equal

(i.e., $\sigma_1^2 = \sigma_2^2 = \cdots = \sigma_k^2$), the testing of $\beta_1 = \beta_2 = \cdots = \beta_k$ assumes that the residual mean squares in the k populations are all the same (i.e., $(\sigma_{Y \cdot X}^2)_1 = (\sigma_{Y \cdot X}^2)_2 = \cdots = (\sigma_{Y \cdot X}^2)_k$). Heterogeneity of the k residual mean squares can be tested by Bartlett's test (Section 10.6a), but this generally is not done for the same reasons that the test is not often employed as a prelude to analysis-of-variance procedures.

The basic calculations necessary to compare k regression lines require quantities already computed: $\sum x^2$, $\sum xy$, $\sum y^2$ (i.e., total SS), and the residual SS and DF for each computed line (Table 18.1). The values of the k residual sums of squares may then be summed, yielding what we shall call the *pooled residual sum of squares*, SS_p; and the sum of the k residual degrees of freedom is the *pooled residual degrees of freedom*, DF_p. The values of $\sum x^2$, $\sum xy$, and $\sum y^2$ for the k regressions may each be summed, and from these sums a residual sum of squares may be calculated. The latter quantity will be termed the *common residual sum of squares*, SS_c.

TABLE 18.1: Calculations for Testing for Significant Differences Among Slopes and Elevations of k Simple Linear Regression Lines

	$\sum x^2$	$\sum xy$	$\sum y^2$	Residual SS	Residual DF
Regression 1	A_1	B_1	C_1	$SS_1 = C_1 - \frac{B_1^2}{A_1}$	$DF_1 = n_1 - 2$
Regression 2	A_2	B_2	C_2	$SS_2 = C_2 - \frac{B_2^2}{A_2}$	$DF_2 = n_2 - 2$
⋮	⋮	⋮	⋮	⋮	⋮
Regression k	A_k	B_k	C_k	$SS_k = C_k - \frac{B_k^2}{A_k}$	$DF_k = n_k - 2$
Pooled regression				$SS_p = \sum_{i=1}^{k} SS_i$	$DF_p = \sum_{i=1}^{k}(n_i - 2) = \sum_{i=1}^{k} n - 2k$
Common regression	$A_c = \sum_{i=1}^{k} A_i$	$B_c = \sum_{i=1}^{k} B_i$	$C_c = \sum_{i=1}^{k} C_i$	$SS_c = C_c - \frac{B_c^2}{A_c}$	$DF_c = \sum_{i=1}^{k} n_i - k - 1$
Total regression*	A_t	B_t	C_t	$SS_t = C_t - \frac{B_t^2}{A_t}$	$DF_t = \sum_{i=1}^{k} n_i - 2$

* See Section 18.5 for explanation.

To test H_0: $\beta_1 = \beta_2 = \cdots = \beta_k$, we may calculate

$$F = \frac{\left(\frac{SS_c - SS_p}{k - 1}\right)}{\frac{SS_p}{DF_p}}, \tag{18.29}$$

a statistic with numerator and denominator degrees of freedom of $k - 1$ and DF_p, respectively.* Example 18.4 demonstrates this testing procedure for three regression lines calculated from three sets of data (i.e., $k = 3$).

*The quantity $SS_c - SS_p$ is an expression of variability among the k regression coefficients; hence, it is associated with $k - 1$ degrees of freedom.

If H_0: $\beta_1 = \beta_2 = \cdots = \beta_k$ is rejected, then we may wish to employ a multiple comparison test to determine which of the k population slopes differ from which others. This is analogous to the multiple-comparison testing employed after rejecting H_0: $\mu_1 = \mu_2 = \cdots = \mu_k$ (Chapter 11), and it is presented in Section 18.6.

If H_0: $\beta_1 = \beta_2 = \cdots = \beta_k$ is not rejected, then the common regression coefficient, b_c, may be used as an estimate of the β underlying all k samples:

$$b_c = \frac{\sum_{i=1}^{k} (\sum xy)_i}{\sum_{i=1}^{k} (\sum x^2)_i}. \tag{18.30}$$

For Example 18.4, this is $b_c = 2057.66/1381.10 = 1.49$.

EXAMPLE 18.4 Testing for Difference Among Three Regression Functions*

	$\sum x^2$	$\sum xy$	$\sum y^2$	n	b	Residual SS	Residual DF
Regression 1	*430.14*	*648.97*	*1065.34*	*24*	1.51	86.21	22
Regression 2	*448.65*	*694.36*	*1184.12*	*29*	1.55	109.48	27
Regression 3	*502.31*	*714.33*	*1186.52*	*30*	1.42	170.68	28
Pooled regression						366.37	77
Common regression	1381.10	2057.66	3435.98		1.49	370.33	79
Total regression	*2144.06*	*3196.78*	*5193.48*	*83*		427.10	81

* The italicized values are those computed from the raw data; all other values are derived from them.

To test for differences among slopes: H_0, $\beta_1 = \beta_2 = \beta_3$; H_A: All three β's are not equal.

$$F = \frac{\dfrac{370.33 - 366.37}{3 - 1}}{\dfrac{366.37}{77}} = 0.42$$

As $F_{0.05(1),2,77} \cong 3.13$, do not reject H_0.

$$P > 0.25 \quad [P = 0.66]$$

$$b_c = \frac{2057.66}{1381.10} = 1.49$$

To test for differences among elevations,

H_0: The three population regression lines have the same elevation.

H_A: The three lines do not have the same elevation.

$$F = \frac{\dfrac{427.10 - 370.33}{3 - 1}}{\dfrac{370.33}{79}} = 6.06$$

As $F_{0.05(1),2,79} \cong 3.13$, reject H_0.

$$0.0025 < P < 0.005 \quad [P = 0.0036]$$

.5 COMPARING MORE THAN TWO ELEVATIONS

Consider the case where it has been concluded that all k population slopes underlying our k samples of data are equal (i.e., H_0: $\beta_1 = \beta_2 = \cdots = \beta_k$ is not rejected). In this situation, it is reasonable to ask whether all k population regressions are, in fact, identical; that is, whether they have equal elevations as well as slopes, and thus the lines all coincide.

The null hypothesis of equality of elevations may be tested by a continuation of the analysis of covariance considerations outlined in Section 18.4. We can combine the data from all k samples and from the summed data compute $\sum x^2$, $\sum xy$, $\sum y^2$, a residual sum of squares, and residual degrees of freedom; the latter will be called the total residual sum of squares (SS_t) and total residual degrees of freedom (DF_t). (See Table 18.1.) The null hypothesis of equal elevations is tested with

$$F = \frac{\dfrac{SS_t - SS_c}{k - 1}}{\dfrac{SS_c}{DF_c}} \tag{18.31}$$

with $k - 1$ and DF_c degrees of freedom. An example of this procedure is offered in Example 18.4.

If the null hypothesis is rejected, we can then employ multiple comparisons to determine the location of significant differences among the elevations, as described in Section 18.6. If it is not rejected, then all k sample regressions are estimates of the same population regression, and the best estimate of that underlying population regression is given by Equation 18.24 using Equations 18.9 and 18.21.

.6 MULTIPLE COMPARISONS AMONG SLOPES

If an analysis of covariance concludes that k population slopes are not all equal, we may employ a multiple-comparison procedure (Chapter 11) to determine which β's are different from which-others. For example, the Tukey test (Section 11.1) may be employed to test for differences between each pair of β values, by H_0: $\beta_B = \beta_A$ and H_A: $\beta_B \neq \beta_A$, where A and B represent two of the k regression lines.

The test statistic is

$$q = \frac{b_B - b_A}{SE}. \tag{18.32}$$

If $\sum x^2$ is the same for lines A and B, use the standard error

$$SE = \sqrt{\frac{(s^2_{Y \cdot X})_p}{\sum x^2}}. \tag{18.33}$$

If $\sum x^2$ is different for lines A and B, then use

$$\text{SE} = \sqrt{\frac{(s^2_{Y \cdot X})_p}{2}\left[\frac{1}{(\sum x^2)_B} + \frac{1}{(\sum x^2)_A}\right]}. \tag{18.34}$$

The degrees of freedom for determining the critical value of q are the pooled residual DF (i.e., DF_p in Table 18.1). Although it is not mandatory to have first performed the analysis of covariance before applying the multiple-comparison test, such a procedure is commonly followed.

The confidence interval for the difference between the slopes of population regressions A and B is

$$(b_B - b_A) \pm (t_{\alpha,\nu,k})(\text{SE}), \tag{18.35}$$

where $q_{\alpha,\nu,k}$ is from Appendix Table B.5 and ν is the pooled residual DF (i.e., DF_p in Table 18.1).

If one of several regression lines is considered to be a control to which each of the other lines is to be compared, then the procedures of Dunnett's test (introduced in Section 11.3) are appropriate. Here,

$$\text{SE} = \sqrt{\frac{2(s^2_{Y \cdot X})_p}{\sum x^2}} \tag{18.36}$$

if $\sum x^2$ is the same for the control line and the line that is compared to the control line (line A), and

$$\text{SE} = \sqrt{(s^2_{Y \cdot X})_p\left[\frac{1}{(\sum x^2)_A} + \frac{1}{(\sum x^2)_{\text{control}}}\right]} \tag{18.37}$$

if it is not. Either two-tailed or one-tailed hypotheses may be thus tested.

The $1 - \alpha$ confidence interval for the difference between the slopes of the control line and the line that is compared to it (line A) is

$$(b_A - b_{\text{control}}) \pm \left(q'_{\alpha(2),\nu,k}\right)(\text{SE}), \tag{18.38}$$

where $q'_{\alpha(2),\nu,k}$ is from Appendix Table B.6.

To apply Scheffé's procedure (Section 11.4), calculate SE as Equation 18.36 or 18.37, depending on whether $\sum x^2$ is the same for both lines.

18.7 MULTIPLE COMPARISONS AMONG ELEVATIONS

If the null hypothesis $H_0 : \beta_1 = \beta_2 = \cdots = \beta_k$ *has not* been rejected and the null hypothesis of all k elevations being equal *has* been rejected, then multiple-comparison procedures may be applied (see Chapter 11) to conclude between which elevations there are differences in the populations sampled. The test statistic for the Tukey test (Section 11.1) is

$$q = \frac{|(\overline{Y}_A - \overline{Y}_B) - b_c(\overline{X}_A - \overline{X}_B)|}{\text{SE}}, \tag{18.39}$$

with DF_c degrees of freedom (see Table 18.1), where the subscripts A and B refer to the two lines the elevations of which are being compared, b_c is from Equation 18.30,

and

$$\text{SE} = \sqrt{\frac{(s^2_{Y\cdot X})_c}{2}\left[\frac{1}{n_B} + \frac{1}{n_A} + \frac{(\overline{X}_A - \overline{X}_B)^2}{(\sum x^2)_B + (\sum x^2)_A}\right]}. \tag{18.40}$$

If Dunnett's test (Section 11.3) is used to compare the elevation of a regression line (call it line A) and another line considered to be for a control set of data,

$$\text{SE} = \sqrt{(s^2_{Y\cdot X})_c\left[\frac{1}{n_A} + \frac{1}{n_{\text{control}}} + \frac{(\overline{X}_A - \overline{X}_B)^2}{(\sum x^2)_A + (\sum x^2)_{\text{control}}}\right]}. \tag{18.41}$$

Equation 18.41 would also be employed if Scheffé's test (Section 11.4) were being performed on elevations.

18.8 MULTIPLE COMPARISONS OF POINTS AMONG REGRESSION LINES

If it is concluded that there is no significant difference among the slopes of three or more regression lines (i.e., H_0: $\beta_1 = \beta_2 = \cdots = \beta_k$ is not rejected; see Section 18.4), then it would be appropriate to test for differences among elevations (see Sections 18.5 and 18.7). Occasionally, when the above null hypothesis is rejected it is desired to ask whether points on the several regression lines differ at a specific value of X. This can be done, as a multisample extension of Section 18.3, by modifying Equations 18.27 and 18.28. For each line the value of $\hat{Y}$ is computed at the specified X, as

$$\hat{Y}_i = a_i + b_c X \tag{18.42}$$

and a Tukey test is performed for H_0: $\mu_{\hat{Y}_B} = \mu_{\hat{Y}_A}$ as

$$q = \frac{\hat{Y}_B - \hat{Y}_A}{\text{SE}}, \tag{18.43}$$

where

$$\text{SE} = \sqrt{\frac{(s^2_{Y\cdot X})_p}{2}\left[\frac{1}{n_B} + \frac{1}{n_A} + \frac{(X - \overline{X}_A)^2}{(\sum x^2)_B} + \frac{(X - \overline{X}_B)^2}{(\sum x^2)_A}\right]}, \tag{18.44}$$

with DF_p degrees of freedom. An analogous Dunnett or Scheffé test would employ

$$\text{SE} = \sqrt{(s^2_{Y\cdot X})_p\left[\frac{1}{n_B} + \frac{1}{n_A} + \frac{(X - \overline{X}_A)^2}{(\sum x^2)_B} + \frac{(X - \overline{X}_B)^2}{(\sum x^2)_A}\right]}. \tag{18.45}$$

A special case of this testing is where we wish to test for differences among the Y intercepts (i.e., the values of $\hat{Y}$ when $X = 0$), although such a test is rarely appropriate. Equations 18.43 and 18.44 for the Tukey test would become

$$q = \frac{a_B - a_A}{\text{SE}}, \tag{18.46}$$

and

$$\text{SE} = \sqrt{\frac{(s^2_{Y\cdot X})_p}{2}\left[\frac{1}{n_B} + \frac{1}{n_A} + \frac{(\overline{X}_B)^2}{(\sum x^2)_B} + \frac{\left(\overline{X}_A\right)^2}{(\sum x^2)_A}\right]}, \tag{18.47}$$

respectively. The analogous Dunnett or Scheffé test for Y intercepts would employ

$$\text{SE} = \sqrt{(s^2_{Y\cdot X})_p\left[\frac{1}{n_B} + \frac{1}{n_A} + \frac{(\overline{X}_B)^2}{(\sum x^2)_B} + \frac{(\overline{X}_A)^2}{(\sum x^2)_A}\right]}. \tag{18.48}$$

18.9 AN OVERALL TEST FOR COINCIDENTAL REGRESSIONS

It is also possible to perform a single test for the null hypothesis that all k regression lines are coincident; that is, that the β's are all the same *and* that all of the α's are identical. This test would employ

$$F = \frac{\dfrac{\text{SS}_t - \text{SS}_p}{2(k-1)}}{\dfrac{\text{SS}_p}{\text{DF}_p}} \tag{18.49}$$

with $2(k-1)$ and DF_p degrees of freedom. If this F is not significant, then all k sample regressions are concluded to estimate the same population regression, and the best estimate of that population regression is that given by Equation 18.24.

Some statistical workers prefer this test to those of the preceding sections in this chapter. However, if the null hypothesis is rejected, it is still necessary to employ the procedures of the previous sections if we wish to determine whether the differences among the regressions are due to differences among slopes or among elevations.

EXERCISES

18.1. Given:
For Sample 1: $n = 28$, $\sum x^2 = 142.35$, $\sum xy = 69.47$, $\sum y^2 = 108.77$, $\overline{X} = 14.7$, $\overline{Y} = 32.0$.
For Sample 2: $n = 30$, $\sum x^2 = 181.32$, $\sum xy = 97.40$, $\sum y^2 = 153.59$. $\overline{X} = 15.8$, $\overline{Y} = 27.4$.

(a) Test H_0: $\beta_1 = \beta_2$ vs. H_A: $\beta_1 \neq \beta_2$.

(b) If H_0 in part (a) is not rejected, test H_0: The elevations of the two population regressions are the same, versus H_A: The two elevations are not the same.

18.2. Given:
For Sample 1: $n = 33$, $\sum x^2 = 744.32$, $\sum xy = 2341.37$, $\sum y^2 = 7498.91$.
For Sample 2: $n = 34$, $\sum x^2 = 973.14$, $\sum xy = 3147.68$, $\sum y^2 = 10366.97$.
For Sample 3: $n = 29$, $\sum x^2 = 664.42$, $\sum xy = 2047.73$, $\sum y^2 = 6503.32$.
For the total of all 3 samples: $n = 96$, $\sum x^2 = 3146.72$, $\sum xy = 7938.25$, $\sum y^2 = 20599.33$.

(a) Test H_0: $\beta_1 = \beta_2 = \beta_3$, vs. H_A: All three β's are not equal.

(b) If H_0: in part (a) is not rejected, test H_0: The three population regression lines have the same elevation, versus H_A: The lines do not have the same elevation.

CHAPTER 19

Simple Linear Correlation

Chapter 17 introduced simple linear regression, the linear dependence of one variable (termed the dependent variable, Y) on a second variable (called the independent variable, X). In simple linear correlation, we also consider the linear relationship between two variables, but neither is assumed to be functionally dependent upon the other. An example of a correlation situation is the relationship between the wing length and tail length of a particular species of bird. Section 17.1 discussed the difference between regression and correlation. Recall that the adjective *simple* refers to there being only two variables considered simultaneously. Chapter 20 discusses correlation involving more than two variables. Coefficients of correlation are sometimes referred to as *coefficients of association*.

19.1 THE CORRELATION COEFFICIENT

Some authors refer to the two variables in a simple correlation analysis as X_1 and X_2. Here we employ the more common designation of X and Y, which does not, however, imply dependence of Y on X as it does in regression; nor does it imply a cause-and-effect relationship between the two variables. Indeed, correlation analysis yields the same results regardless of which variable is labeled X and which is Y.

The *correlation coefficient* (sometimes called the *simple* correlation coefficient,* indicating that the relationship of only two variables is being examined) is

*It is also called the Pearson product-moment correlation coefficient because of the algebraic expression of the coefficient, and the pioneering work on it, by Karl Pearson (1857–1936), who in 1896 was the first to refer to this measure as a correlation coefficient (David, 1995; Seal, 1967). This followed the major elucidation of the concept of correlation by Sir Francis Galton (1822–1911,

calculated as*

$$r = \frac{\sum xy}{\sqrt{\sum x^2 \sum y^2}} \tag{19.1}$$

(see Section 17.2a for the definition of the abbreviated symbols $\sum x^2$, $\sum y^2$, and $\sum xy$). Among other methods (e.g., Symonds, 1926), Equation 19.1 may be computed by this "machine formula":

$$r = \frac{\sum XY - \dfrac{\sum X \sum Y}{n}}{\sqrt{\left(\sum X^2 - \dfrac{(\sum X)^2}{n}\right)\left(\sum Y^2 - \dfrac{(\sum Y)^2}{n}\right)}}. \tag{19.2}$$

Although the denominator of Equations 19.1 and 19.2 is always positive, the numerator may be positive, zero, or negative, thus enabling r to be either positive, zero, or negative, respectively. A positive correlation implies that for an increase in the value of one of the variables, the other variable also increases in value; a negative correlation indicates that an increase in value of one of the variables is accompanied by a decrease in value of the other variable.† If $\sum xy = 0$, then $r = 0$, and there is zero correlation, denoting that there is no linear association between the magnitudes of the two variables; that is, a change in magnitude of one does not imply a change in magnitude of the other. Figure 19.1 presents these considerations graphically.‡

Also important is the fact that the absolute value of the numerator of Equation 19.1 can never be larger than the denominator. Thus, r can never be greater than 1.0 nor

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cousin of Charles Darwin and proponent of human eugenics) in 1888 (who published it first with the terms *co-relation* and *reversion*). The symbol r can be traced to Galton's 1877–1888 discussion of regression in heredity studies (he later used r to indicate the slope of a regression line), and Galton developed correlation from regression. Indeed, in the early history of correlation, correlation coefficients were called Galton functions. The basic concepts of correlation, however, predated Galton's and Pearson's work by several decades (Pearson, 1920; Rodgers and Nicewander, 1988; Stigler, 1989; Walker, 1929: 92–102, 106, 109–110, 187). The term *coefficient of correlation* was used as early as 1892 by Francis Ysidro Edgeworth (1845–1926; Irish statistician and economist, whose uncle and grand-uncle [sic] was Sir Francis Beaufort, 1774–1857; Beaufort conceived the Beaufort Wind Scale) (Desmond, 2000; Pearson, 1920).

*The computation depicted in Equation 19.2 was first published by Harris (1910). The correlation coefficient may also be calculated as $r = \sum xy/[(n-1)s_X s_Y]$ (Walker, 1929: 111). It is also the case that $|r| = \sqrt{b_Y b_X}$, where b_Y is the regression coefficient if Y is treated as the dependent variable (Section 17.2a) and b_X is the regression coefficient if X is treated as the dependent variable; that is, r is the geometric mean (Section 3.4a) of b_Y and b_X; also, following from Equation 17.15, $|r| = \sqrt{(\text{Regression SS})/(\text{Total SS})}$; see also Rodgers and Nicewander (1988). In literature appearing within a couple of decades of Pearson's work, it was sometimes suggested that a correlation coefficient be computed using deviations from the median instead of from the mean (Eells, 1926; Pearson, 1920), which would result in a quantity not only different from r but without the latter's theoretical and practical advantages.

†The first explanation of negative correlation was in an 1892 paper (on shrimp anatomy) by English marine biologist Walter Frank Raphael Weldon (1860–1906) (Pearson, 1920).

‡Galton published the first two-variable scatter plot of data in 1885 (Rodgers and Nicewander, 1988).

calculated as*

$$r = \frac{\sum xy}{\sqrt{\sum x^2 \sum y^2}} \tag{19.1}$$

(see Section 17.2a for the definition of the abbreviated symbols $\sum x^2$, $\sum y^2$, and $\sum xy$). Among other methods (e.g., Symonds, 1926), Equation 19.1 may be computed by this "machine formula":

$$r = \frac{\sum XY - \dfrac{\sum X \sum Y}{n}}{\sqrt{\left(\sum X^2 - \dfrac{(\sum X)^2}{n}\right)\left(\sum Y^2 - \dfrac{(\sum Y)^2}{n}\right)}}. \tag{19.2}$$

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‡Galton published the first two-variable scatter plot of data in 1885 (Rodgers and Nicewander, 1988).

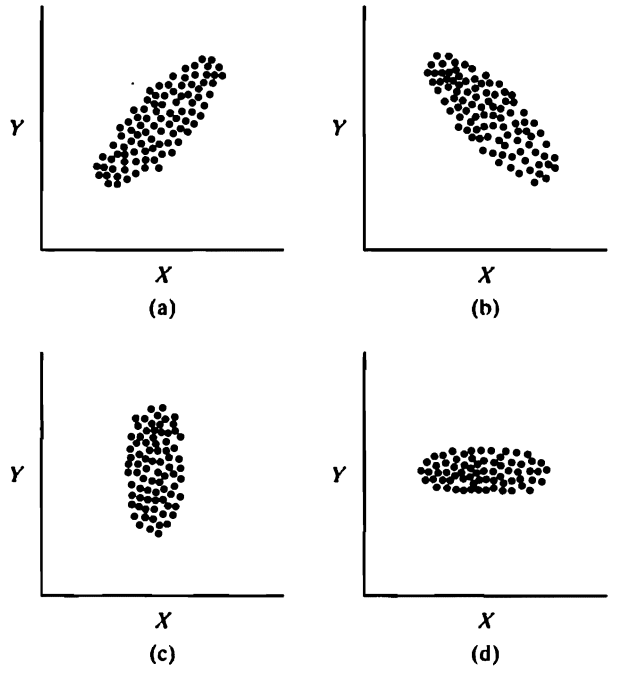

FIGURE 19.1: Simple linear correlation. (a) Positive correlation. (b) Negative correlation. (c) No correlation. (d) No correlation.

less than -1.0. Inspection of this equation further will reveal also that r has no units of measurement, for the units of both X and Y appear in both the numerator and denominator and thus cancel out arithmetically. A regression coefficient, b, may lie in the range of $-\infty \leq b \leq \infty$, and it expresses the magnitude of a change in Y associated with a unit change in X. But a correlation coefficient is unitless and $-1 \leq r \leq 1$. The correlation coefficient is not a measure of quantitative change of one variable with respect to the other, but it is a measure of strength of association between the two variables. That is, a large value of $|r|$ indicates a strong association between X and Y.

The coefficient of determination, r^2, was introduced in Section 17.3 as a measure of how much of the total variability in Y is accounted for by regressing Y on X. In a correlation analysis, r^2 (occasionally called the correlation index) may be calculated simply by squaring the correlation coefficient, r. It may be described as the amount of variability in one of the variables (either Y or X) accounted for by correlating that variable with the second variable.* As in regression analysis, r^2 may be considered to be a measure of the strength of the straight-line relationship.† The calculation of r and r^2 is demonstrated in Example 19.1a. Either r or r^2 can be used to express the strength of the relationship between the two variables.

*As in Section 17.3a, $1 - r^2$ may be referred to as the *coefficient of nondetermination*. A term found in older literature is *coefficient of alienation*: $\sqrt{1 - r^2}$, given by Galton in 1889 and named by T. L. Kelley in 1919 (Walker, 1929: 175).

†Ozer (1985) argued that there are circumstances where $|r|$ is a better coefficient of determination than r^2.

where the standard error of r is calculated by Equation 19.3, and the degrees of freedom are $\nu = n - 2$. (Fisher, 1921, 1925b: 157).* The null hypothesis is rejected if $|t| \geq t_{\alpha(2),\nu}$.

Alternatively, this two-tailed hypothesis may be tested using

$$F = \frac{1 + |r|}{1 - |r|} \tag{19.5}$$

(Cacoullos, 1965), where the critical value is $F_{\alpha(2),\nu,\nu}$. (See Example 19.1b.) Or, critical values of $|r|$ (namely, $r_{\alpha(2),\nu}$) may be read directly from Appendix Table B.17.†

One-tailed hypotheses about the population correlation coefficient may also be tested by the aforementioned procedures. For the hypotheses H_0: $\rho \leq 0$ and H_A: $\rho > 0$, compute either t or F (Equations 19.4 or 19.5, respectively) and reject H_0 if r is positive and either $t \geq t_{\alpha(1),\nu}$, or $F \geq F_{\alpha(1),\nu,\nu}$, or $r \geq r_{\alpha(1),\nu}$. To test H_0: $\rho \geq 0$ vs. H_A: $\rho < 0$, reject H_0 if r is negative and either $|t| \geq t_{\alpha(1),\nu}$, or $F \geq F_{\alpha(1),\nu,\nu}$, or $|r| \geq r_{\alpha(1),\nu}$.

If we wish to test H_0: $\rho = \rho_0$ for any ρ_0 other than zero, however, Equations 19.4 and 19.5 and Appendix Table B.17 are not applicable. Only for $\rho_0 = 0$ can r be considered to have come from a distribution approximated by the normal, and if the distribution of r is not normal, then the t and F statistics may not be validly employed. Fisher (1921, 1925b: 162) dealt with this problem when he proposed a transformation enabling r to be converted to a value, called z, which estimates a population parameter, ζ (lowercase Greek zeta), that *is* normally distributed. The transformation‡ is

$$z = 0.5 \ln\left(\frac{1 + r}{1 - r}\right). \tag{19.9}$$

For values of r between 0 and 1, the corresponding values of Fisher's z will lie between 0 and $+\infty$; and for r's from 0 to -1, the corresponding z's will fall between 0 and $-\infty$.

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*As an aside, t may also be computed as follows (Martín Andrés, Herranz Tejedor, and Silva Mato, 1995): Consider all N data (where $N = n_1 + n_2$) to be a sample of measurements, and associate with each datum either 0, if the datum is a value of X, or 1, if it is a value of Y; consider this set of N zeros and ones to be a second sample of data. Then calculate t for the two samples, as would be done in a two-sample t-test (Section 8.1). This concept will be used in Section 19.11b.

†Critical values of r may also be calculated as

$$r_{\alpha,\nu} = \sqrt{\frac{t^2_{\alpha,\nu}}{t^2_{\alpha,\nu} + \nu}}, \tag{19.6}$$

where α may be either one tailed or two tailed, and $\nu = n - 2$. If a regression analysis is performed, rather than a correlation analysis, the probability of rejection of H_0: $\beta = 0$ is identical to the probability of rejecting H_0: $\rho = 0$. Also, r is related to b as

$$r = \frac{s_X}{s_Y} b, \tag{19.7}$$

where s_X and s_Y are the standard deviations of X and Y, respectively.

‡z is also equal to $r + r^3/3 + r^5/5 \ldots$ and is a quantity that mathematicians recognize as the inverse hyperbolic tangent of r, namely $z = \tanh^{-1} r$. The transformation of z to r, given in Appendix Table B.19, is

$$r = \tanh z \quad \text{or} \quad r = \frac{e^{2z} - 1}{e^{2z} + 1}. \tag{19.8}$$

For convenience, we may utilize Appendix Table B.18 to avoid having to perform the computation of Equation 19.8 to transform r to z.*

For the hypothesis H_0: $\rho = \rho_0$, then we calculate a normal deviate, as

$$Z = \frac{z - \zeta_0}{\sigma_z}, \tag{19.10}$$

where z is the transform of r; ζ_0 is the transform of the hypothesized coefficient, ρ_0; and the standard error of z is approximated by

$$\sigma_z = \sqrt{\frac{1}{n - 3}} \tag{19.11}$$

(Fisher, 1925b: 162), an approximation that improves as n increases.

In Example 19.1a, $r = 0.870$ was calculated. If we had desired to test H_0: $\rho = 0.750$, we would have proceeded as shown in Example 19.2. Recall that the critical value of a normal deviate may be obtained readily from the bottom line of the t table (Appendix Table B.3), because $Z_{\alpha(2)} = t_{\alpha(2),\infty}$.

EXAMPLE 19.2 Testing H_0: $\rho = \rho_0$, Where $\rho_0 \neq 0$

$r = 0.870$

$n = 12$

H_0: $\rho = 0.750$; H_A: $\rho \neq 0.750$.

$$z = 0.5 \ln\left(\frac{1 + 0.870}{1 - 0.870}\right) = 1.3331$$

$\zeta_0 = 0.9730$

$$Z = \frac{z - \zeta_0}{\sqrt{\frac{1}{n - 3}}} = \frac{1.3331 - 0.9730}{\sqrt{\frac{1}{9}}} = \frac{0.3601}{0.3333} = 1.0803$$

$Z_{0.05(2)} = t_{0.05(2),\infty} = 1.960$

Therefore, do not reject H_0.

$0.20 < P < 0.50$ $[P = 0.28]$

One-tailed hypotheses may also be tested, using $Z_{\alpha(1)}$ (or $t_{\alpha(1),\infty}$) as the critical value. For H_0: $\rho \leq \rho_0$ and H_A: $\rho > \rho_0$, H_0 is rejected if $Z \geq Z_{\alpha(1)}$, and for H_0: $\rho \geq \rho_0$ versus H_A: $\rho < \rho_0$, H_0 is rejected if $Z \leq -Z_{\alpha(1)}$.

If the variables in correlation analysis have come from a bivariate normal distribution, as often may be assumed, then we may employ the aforementioned procedures, as well as those that follow. Sometimes only one of the two variables may be assumed to have been obtained randomly from a normal population. It may be possible to employ a data transformation (see Section 17.10) to remedy this situation. If that cannot be done, then the hypothesis H_0: $\rho = 0$ (or its associated one-tailed hypotheses) may be tested, but none of the other testing procedures of this chapter (except for the

*As noted at the end of Section 19.7, there is a slight and correctable bias in z. Unless n is very small, however, this correction will be insignificant and may be ignored.

methods of Section 19.9) are valid. If neither variable came from a normal population and data transformations do not improve this condition, then we may turn to the procedures of Section 19.9.

19.3 CONFIDENCE INTERVALS FOR THE POPULATION CORRELATION COEFFICIENT

Confidence limits on ρ may be determined by a procedure related to Equation 19.5; the lower and upper confidence limits are

$$L_1 = \frac{(1 + F_\alpha)r + (1 - F_\alpha)}{(1 + F_\alpha) + (1 - F_\alpha)r} \tag{19.12}$$

and

$$L_2 = \frac{(1 + F_\alpha)r - (1 - F_\alpha)}{(1 + F_\alpha) - (1 - F_\alpha)r}, \tag{19.13}$$

respectively, where $F_\alpha = F_{\alpha(2),\nu,\nu}$ and $\nu = n - 2$ (Muddapur, 1988).* This is shown in Example 19.3.

Fisher's transformation may be used to approximate these confidence limits, although the confidence interval will generally be larger than that from the foregoing procedure, and the confidence coefficient may occasionally (and undesirably) be less than $1 - \alpha$ (Jeyaratnam, 1992). By this procedure, we convert r to z (using Equation 9.8 or Appendix Table B.18); then the $1 - \alpha$ confidence limits may be computed for ζ:

$$z \pm Z_{\alpha(2)}\sigma_z \tag{19.16}$$

or, equivalently,

$$z \pm t_{\alpha(2),\infty}\sigma_z. \tag{19.17}$$

The lower and upper confidence limits, L_1 and L_2, are both z values and may be transformed to r values, using Appendix Table B.19 or Equation 19.9. Example 19.3 demonstrates this procedure. Note that although the confidence limits for ζ are symmetrical, the confidence limits for ρ are not.

19.4 POWER AND SAMPLE SIZE IN CORRELATION

(a) Power in Correlation. If we test H_0: $\rho = 0$ at the α significance level, with a sample size of n, then we may estimate the probability of correctly rejecting H_0 when ρ_0 is in fact a specified value other than zero. This is done by using the Fisher z transformation for the critical value of r and for the sample r (from Appendix Table B.18 or Equation 19.8); let us call these two transformed values z_α and z, respectively. Then, the power of the test for H_0: $\rho = 0$ is $1 - \beta(1)$, where $\beta(1)$ is the one-tailed probability of the normal deviate

$$Z_{\beta(1)} = (z - z_\alpha)\sqrt{n - 3}. \tag{19.18}$$

*Jeyaratnam (1992) asserts that the same confidence limits are obtained by

$$L_1 = \frac{r - w}{1 - rw} \quad \text{and} \tag{19.14}$$

$$L_2 = \frac{r + w}{1 + rw}, \tag{19.15}$$

where w is $r_{\alpha,\nu}$ from Equation 19.6 using the two-tailed $t_{\alpha(2),\nu}$.

EXAMPLE 19.3 Setting Confidence Limits for a Correlation Coefficient. This Example Uses the Data of Example 19.1a

$r = 0.870$, $n = 12$, $\nu = 10$, $\alpha = 0.05$

For the 95% confidence interval for ρ:

$F_\alpha = F_{0.05(2),10,10} = 3.72$; so

$$L_1 = \frac{(1 + F_\alpha)r + (1 - F_\alpha)}{(1 + F_\alpha) + (1 - F_\alpha)r} = \frac{4.11 - 2.72}{4.72 - 2.37} = 0.592$$

$$L_2 = \frac{(1 + F_\alpha)r - (1 - F_\alpha)}{(1 + F_\alpha) - (1 - F_\alpha)r} = \frac{4.11 + 2.72}{4.72 + 2.37} = 0.963.$$

For the Fisher approximation:

$r = 0.870$; therefore, $z = 1.3331$ (from Appendix Table B.18).

$$\sigma_z = \sqrt{\frac{1}{n - 3}} = 0.3333$$

$$\begin{aligned} \text{95\% confidence interval for } \zeta &= z \pm Z_{0.05(2)}\sigma_z \\ &= z \pm t_{0.05(2),\infty}\sigma_z \\ &= 1.3331 \pm (1.9600)(0.3333) \\ &= 1.3331 \pm 0.6533 \end{aligned}$$

$L_1 = 0.680$; $L_2 = 1.986$

These confidence limits are in terms of z. For the 95% confidence limits for ρ, transform L_1 and L_2 from z to r (using Appendix Table B.19): $L_1 = 0.592$, $L_2 = 0.963$.

Instead of using the Appendix table, this confidence-limit transformation from z to r may be done using Equation 19.9:

$$L_1 = \frac{e^{2(0.680)} - 1}{e^{2(0.680)} + 1} = \frac{2.8962}{4.8962} = 0.592$$

$$L_2 = \frac{e^{2(1.986)} - 1}{e^{2(1.986)} + 1} = \frac{52.0906}{54.0906} = 0.963.$$

(Cohen, 1988: 546), as demonstrated in Example 19.4. This procedure may be used for one-tailed as well as two-tailed hypotheses, so α may be either $\alpha(1)$ or $\alpha(2)$, respectively.

(b) Sample Size for Correlation Hypothesis Testing. If the desired power is stated, then we can ask how large a sample is required to reject H_0: $\rho = 0$ if it is truly false with a specified $\rho_0 \neq 0$. This can be estimated (Cohen, 1988: 546) by calculating

$$n = \left(\frac{Z_{\beta(1)} + Z_\alpha}{\zeta_0}\right)^2 + 3, \tag{19.19}$$

where ζ_0 is the Fisher transformation of the ρ_0 specified, and the significance level, α, can be either one-tailed or two-tailed. This procedure is shown in Example 19.5a.

EXAMPLE 19.4 Determination of Power of the Test of H_0: $\rho = 0$ in Example 19.1b

$n = 12$; $\nu = 10$

$r = 0.870$, so $z = 1.3331$

$r_{0.05(2),10} = 0.576$, so $z_{0.05} = 0.6565$

$$Z_{\beta(1)} = (1.3331 - 0.6565)\sqrt{12 - 3}$$
$$= 2.03$$

From Appendix Table B.2, $P(Z \geq 2.03) = 0.0212 = \beta$. Therefore, the power of the test is $1 - \beta = 0.98$.

EXAMPLE 19.5a Determination of Required Sample Size in Testing H_0: $\rho = 0$

We desire to reject H_0: $\rho = 0$ 99% of the time when $|\rho| \geq 0.5$ and the hypothesis is tested at the 0.05 level of significance. Therefore, $\beta(1) = 0.01$ and (from the last line of Appendix Table B.3) and $Z_{\beta(1)} = 2.3263$; $\alpha(2) = 0.05$ and $Z_{\alpha(2)} = 1.9600$; and, for $r = 0.5$, $z = 0.5493$.

Then

$$n = \left(\frac{2.3263 + 1.9600}{0.5493}\right)^2 + 3 = 63.9,$$

so a sample of size at least 64 should be used.

(c) Hypothesizing ρ Other Than 0. For the two-tailed hypothesis H_0: $\rho = \rho_0$, where $\rho_0 \neq 0$, the power of the test is determined from

$$Z_{\beta(1)} = |z - z_0| - z_{\alpha(2)}\sqrt{n - 3} \tag{19.20}$$

instead of from Equation 19.18; here, z_0 is the Fisher transformation of ρ_0. One-tailed hypotheses may be addressed using $\alpha(1)$ in place of $\alpha(2)$ in Equation 19.20.

(d) Sample Size for Confidence Limits. After we calculate a sample correlation coefficient, r, as an estimate of a population correlation coefficient, ρ, we can estimate how large a sample would be needed from this population to determine a confidence interval for ρ that is no greater than a specified size.

The confidence limits in Example 19.5b, determined from a sample of $n = 12$, define a confidence interval having a width of $0.963 - 0.592 = 0.371$. We could ask how large a sample from this population would be needed to state a confidence interval no wider than 0.30. As shown in Example 19.5b, this sample size may be estimated by the iterative process (introduced in Section 7.7a) of applying Equations 19.12 and 19.13. Because the desired size of the confidence interval (0.30) is smaller than the confidence-interval width obtained from the sample of size 12 in Example 19.3 (0.371), we know that a sample larger than 12 would be needed. Example 19.5b shows the confidence interval calculated for $n = 15$ (0.31), which is a little larger than desired; a confidence interval is calculated for $n = 16$, which is found to be the size desired (0.30). If the same process is used for determining the sample size needed to obtain a confidence interval no larger than 0.20, it is estimated that n would have to be at least 30.

EXAMPLE 19.5b Determination of Required Sample Size in Expressing Confidence Limits for a Correlation Coefficient

If a calculated r is 0.870 (as in Example 19.1a), and a 95% confidence interval no wider than 0.30 is desired for estimating ρ, the following iterative process may be employed:

If $n = 15$ were used, then $\nu = 13$, and $F_{0.05(2),13,13} = 3.12$, so

$$L_1 = \frac{(1 + F_\alpha)r + (1 - F_\alpha)}{(1 + F_\alpha) + (1 - F_\alpha)r} = \frac{(4.12)(0.870) - 2.12}{4.12 - (2.12)(0.870)} = \frac{3.584 - 2.12}{4.12 - 1.844}$$

$$= \frac{1.464}{2.276} = 0.643$$

$$L_2 = \frac{(1 + F_\alpha)r - (1 - F_\alpha)}{(1 + F_\alpha) - (1 - F_\alpha)r} = \frac{(4.12)(0.870) + 2.12}{4.12 + (2.12)(0.870)} = \frac{3.584 + 2.12}{4.12 + 1.844}$$

$$= \frac{5.704}{5.964} = 0.956$$

and the width of the confidence interval is $L_2 - L_1 = 0.956 - 0.643 = 0.31$, which is a little larger than desired, so larger n is needed.

If $n = 20$ were used, then $\nu = 18$, and $F_{0.05(2),18,18} = 2.60$, so

$$L_1 = \frac{(1 + F_\alpha)r + (1 - F_\alpha)}{(1 + F_\alpha) + (1 - F_\alpha)r} = \frac{(3.60)(0.870) - 1.60}{3.60 - (1.60)(0.870)} = \frac{3.132 - 1.60}{3.60 - 1.392}$$

$$= \frac{1.532}{2.208} = 0.694$$

$$L_2 = \frac{(1 + F_\alpha)r - (1 - F_\alpha)}{(1 + F_\alpha) - (1 - F_\alpha)r} = \frac{3.132 + 1.60}{3.60 + 1.392} = \frac{4.732}{4.992} = 0.948$$

and the width of the confidence interval is $L_2 - L_1 = 0.948 - 0.694 = 0.25$, which is smaller than that desired, so a smaller n may be used.

If $n = 16$ were used, then $\nu = 14$, and $F_{0.05(2),14,14} = 2.98$, so

$$L_1 = \frac{(1 + F_\alpha)r + (1 - F_\alpha)}{(1 + F_\alpha) + (1 - F_\alpha)r} = \frac{(3.98)(0.870) - 1.98}{3.98 - (1.98)(0.870)} = \frac{3.463 - 1.98}{3.98 - 1.723}$$

$$= \frac{1.483}{2.257} = 0.657$$

$$L_2 = \frac{(1 + F_\alpha)r - (1 - F_\alpha)}{(1 + F_\alpha) - (1 - F_\alpha)r} = \frac{3.463 + 1.98}{3.98 + 1.723} = \frac{5.443}{5.703} = 0.954$$

and the width of the confidence interval is $L_2 - L_1 = 0.954 - 0.657 = 0.30$, so it is estimated that a sample size of at least 16 should be used to obtain the desired confidence interval.

To calculate the desired confidence interval using the Fisher transformation, $r = 0.870$; $z = 1.3331$ (e.g., from Appendix Table B.18); $Z_{0.05(2)} = 1.9600$.

If $n = 15$ were used, then $\sigma_z = \sqrt{\frac{1}{15 - 3}} = 0.2887$.

The 95% confidence interval for ζ is $1.3331 \pm (1.9600)(0.2887) = 1.3331 \pm 0.5658$.

The confidence limits are

$L_1 = 0.7672$; $L_2 = 1.8990$

For the 95% confidence interval for ρ, transform this L_1 and L_2 for z to L_1 and L_2 for r (e.g., using Appendix Table B.19):

$L_1 = 0.645$; $L_2 = 0.956$

and the width of the confidence interval is estimated to be $0.956 - 0.645 = 0.31$, which is a little larger than that desired, so a larger n should be used.

If $n = 16$ were used, then $\sigma_z = \sqrt{\frac{1}{16 - 3}} = 0.2774$.

For the 95% confidence interval for $\zeta = 1.3331 \pm (1.9600)(0.2774)$
$= 1.3331 \pm 0.5437$

and $L_1 = 0.7894$; $L_2 = 1.8768$

For the 95% confidence interval for ρ, transform the z'a to r':

The confidence limits are

$L_1 = 0.658$; $L_2 = 0.954$

and the width of the confidence interval is estimated to be $0.954 - 0.658 = 0.30$, so it is estimated that a sample size of at least 16 should be used.

19.5 COMPARING TWO CORRELATION COEFFICIENTS

Hypotheses (either one-tailed or two-tailed) about two correlation coefficients may be tested by the use of

$$Z = \frac{z_1 - z_2}{\sigma_{z_1 - z_2}}, \tag{19.21}$$

where

$$\sigma_{z_1 - z_2} = \sqrt{\frac{1}{n_1 - 3} + \frac{1}{n_2 - 3}}. \tag{19.22}$$

If $n_1 = n_2$, then Equation 19.22 reduces to

$$\sigma_{z_1 - z_2} = \sqrt{\frac{2}{n - 3}}, \tag{19.23}$$

where n is the size of each sample. The use of the Fisher z transformation both normalizes the underlying distribution of each of the correlation coefficients, r_1 and r_2, and stabilizes the variances of these distributions (Winterbottom, 1979). The multisample hypothesis test recommended by Paul (1988), and presented in Section 19.7, may be used for the two-tailed two-sample hypothesis mentioned previously. It tends to result in a probability of Type I error that is closer to the specified α; but, as it also tends to be larger than α, I do not recommend it for the two-sample case. The preferred procedure for testing the two-tailed hypotheses, H_0: $\rho_1 = \rho_2$ versus H_A: $\rho_1 = \rho_2$, is to employ Equation 19.21, as shown in Example 19.6.* One-tailed hypotheses may be tested using one-tailed critical values, namely $Z_{\alpha(1)}$.

*A null hypothesis such as H_0: $\rho_1 - \rho_2 = \rho_0$, where $\rho_0 \neq 0$, might be tested by substituting $|z_1 - z_2| - \zeta_0$ for the numerator in Equation 19.21, but no utility for such a test is apparent.

EXAMPLE 19.6 Testing the Hypothesis H_0: $\rho_1 = \rho_2$

For a sample of 98 bird wing and tail lengths, a correlation coefficient of 0.78 was calculated. A sample of 95 such measurements from a second bird species yielded a correlation coefficient of 0.84. Let us test for the equality of the two population correlation coefficients.

$H_0: \rho_1 = \rho_2$; $H_A: \rho_1 \neq \rho_2$

$r_1 = 0.78$ $r_2 = 0.84$

$z_1 = 1.0454$ $z_2 = 1.2212$

$n_1 = 98$ $n_2 = 95$

$$Z = \frac{1.0454 - 1.2212}{\sqrt{\frac{1}{n_1 - 3} + \frac{1}{n_2 - 3}}} = \frac{-0.1758}{0.1463} = -1.202$$

$Z_{0.05(2)} = t_{0.05(2),\infty} = 1.960$

Therefore, do not reject H_0.

$$0.20 < P < 0.50 \quad [P = 0.23]$$

The common correlation coefficient may then be computed as

$$z_w = \frac{(n_1 - 3)z_1 + (n_2 - 3)z_2}{(n_1 - 3) + (n_2 - 3)} = \frac{(95)(1.0454) + (92)(1.2212)}{95 + 92} = 1.1319$$

$r_w = 0.81$.

Occasionally we want to test for equality of two correlation coefficients that are not independent. For example, if Sample 1 in Example 19.6 were data from a group of 98 young birds, and Sample 2 were from 95 of these birds when they were older (three of the original birds having died or escaped), the two sets of data should not be considered to be independent. Procedures for computing r_1 and r_2, taking dependence into account, are reviewed by Steiger (1980).

(a) Common Correlation Coefficient. As in Example 19.6, a conclusion that $\rho_1 = \rho_2$ would lead us to say that both of our samples came from the same population of data, or from two populations with identical correlation coefficients. In such a case, we may combine the information from the two samples to calculate a better estimate of a single underlying ρ. Let us call this estimate the *common*, or *weighted*, *correlation coefficient*. We obtain it by converting

$$z_w = \frac{(n_1 - 3)z_1 + (n_2 - 3)z_2}{(n_1 - 3) + (n_2 - 3)} \tag{19.24}$$

to its corresponding r value, r_w, as shown in Example 19.6. If both samples are of equal size (i.e., $n_1 = n_2$), then the previous equation reduces to

$$z_w = \frac{z_1 + z_2}{2}. \tag{19.25}$$

Appendix Table B.19 gives the conversion of z_w to the common correlation coefficient, r_w (which estimates the common population coefficient, ρ). Paul (1988) has shown that if ρ is less than about 0.5, then a better estimate of that parameter utilizes

$$z_w = \frac{(n_1 - 1)z_1' + (n_2 - 1)z_2'}{(n_1 - 1) + (n_2 - 1)}, \tag{19.26}$$

where

$$z_i' = z_i - \frac{3z_i + r_i}{4(n_i - 1)} \tag{19.27}$$

and z_i is the z in Equation 19.8 (Hotelling, 1953).

We may test hypotheses about the common correlation coefficient (H_0: $\rho = 0$ versus H_A: $\rho \neq 0$, or H_0: $\rho = \rho_0$ versus H_A: $\rho \neq \rho_0$, or similar one-tailed tests) by Equation 19.33 or 19.34.

19.6 POWER AND SAMPLE SIZE IN COMPARING TWO CORRELATION COEFFICIENTS

The power of the preceding test for difference between two correlation coefficients is estimated as $1 - \beta$, where β is the one-tailed probability of the normal deviate calculated as

$$Z_{\beta(1)} = \frac{|z_1 - z_2|}{\sigma_{z_1 - z_2}} - Z_\alpha \tag{19.28}$$

(Cohen, 1988: 546–547), where α may be either one-tailed or two-tailed and where $Z_{\alpha(1)}$ or $Z_{\alpha(2)}$ is most easily read from the last line of Appendix Table B.3. Example 19.7 demonstrates this calculation for the data of Example 19.6.

EXAMPLE 19.7 Determination of the Power of the Test of H_0: $\rho_1 = \rho_2$ in Example 19.6

$z_1 = 1.0454 \qquad z_2 = 1.2212$

$\sigma_{z_1 - z_2} = 0.1463$

$Z_\alpha = Z_{0.05(2)} = 1.960$

$$Z_{\beta(1)} = \frac{|1.0454 - 1.2212|}{0.1463} - 1.960$$
$$= 1.202 - 1.960$$
$$= -0.76$$

From Appendix Table B.2,

$$\beta = P(Z \geq -0.76) = 1 - P(Z \leq -0.76) = 1 - 0.2236 = 0.78.$$

Therefore,

$$\text{power} = 1 - \beta = 1 - 0.78 = 0.22.$$

If we state a desired power to detect a specified difference between transformed correlation coefficients, then the sample size required to reject H_0 when testing at the α level of significance is

$$n = 2\left(\frac{Z_\alpha + Z_{\beta(1)}}{z_1 - z_2}\right)^2 + 3 \tag{19.29}$$

(Cohen, 1988: 547). This is shown in Example 19.8.

The test for difference between correlation coefficients is most powerful for $n_1 = n_2$, and the proceding estimation is for a sample size of n in both samples. Sometimes the size of one sample is fixed and cannot be manipulated, and we then ask how large the second sample must be to achieve the desired power. If n_1 is fixed and n is determined by Equation 19.29, then (by considering n to be the harmonic mean of n_1 and n_2),

$$n_2 = \frac{n_1(n + 3) - 6n}{2n_1 - n - 3} \tag{19.30}$$

(Cohen, 1988: 137).*

EXAMPLE 19.8 Estimating the Sample Size Necessary for the Test of H_0: $\rho_1 = \rho_2$

Let us say we wish to be 90% confident of detecting a difference, $z_1 - z_2$, as small as 0.5000 when testing H_0: $\rho_1 = \rho_2$ at the 5% significance level. Then $\beta(1) = 0.10, \alpha(2) = 0.05$, and

$$n = 2\left(\frac{1.9600 + 1.2816}{0.5000}\right)^2 + 3$$
$$= 87.1.$$

So sample sizes of at least 88 should be used.

19.7 COMPARING MORE THAN TWO CORRELATION COEFFICIENTS

If k samples have been obtained and an r has been calculated for each, we often want to conclude whether or not all samples came from populations having identical ρ's. If H_0: $\rho_1 = \rho_2 = \cdots = \rho_k$ is not rejected, then all samples might be combined and one value of r calculated to estimate the single population ρ. As Example 19.9 shows, the testing of this hypothesis involves transforming each r to a z value. We may then calculate

$$\chi^2 = \sum_{i=1}^{k}(n_i - 3)z_i^2 - \frac{\left[\sum_{i=1}^{k}(n_i - 3)z_i\right]^2}{\sum_{i=1}^{k}(n_i - 3)}, \tag{19.31}$$

which may be considered to be a chi-square value with $k - 1$ degrees of freedom.†

(a) Common Correlation Coefficient. If H_0 is not rejected, then all k sample correlation coefficients are concluded to estimate a common population ρ. A common r (also known as a weighted mean of r) may be obtained from transforming the

*If the denominator in Equation 19.30 is ≤ 0, then we must either increase n_1 or change the desired power, significance level, or detectable difference in order to solve for n_2.

†Equation 19.31 is a computational convenience for

$$\chi^2 = \sum(n_i - 3)(z_i - z_w)^2, \tag{19.31a}$$

where z_w is a weighted mean of z shown in Equation 19.32.

EXAMPLE 19.9 Testing a Three-Sample Hypothesis Concerning Correlation Coefficients

Given the following:

$n_1 = 24 \quad n_2 = 29 \quad n_3 = 32$
$r_1 = 0.52 \quad r_2 = 0.56 \quad r_3 = 0.87$

To test:

H_0: $\rho_1 = \rho_2 = \rho_3$.
H_A: All three population correlation coefficients are not equal.

i	r_i	z_i	z_i^2	n_i	$n_i - 3$	$(n_i - 3)z_i$	$(n_i - 3)z_i^2$
1	0.52	0.5763	0.3321	24	21	12.1023	6.9741
2	0.56	0.6328	0.4004	29	26	16.4528	10.4104
3	0.87	1.3331	1.7772	32	29	38.6599	51.5388
Sums:					76	67.2150	68.9233

$$\chi^2 = \sum(n_i - 3)z_i^2 - \frac{[\sum(n_i - 3)z_i]^2}{\sum(n_i - 3)}$$

$$= 68.9233 - \frac{(67.2150)^2}{76}$$

$$= 9.478$$

$$\nu = k - 1 = 2$$

$\chi^2_{0.05,2} = 5.991$
Therefore, reject H_0.

$$0.005 < P < 0.01 \quad [P = 0.0087]$$

If H_0 had not been rejected, it would have been appropriate to calculate the common correlation coefficient:

$$z_w = \frac{\sum(n_i - 3)z_i}{\sum(n_i - 3)} = \frac{67.2150}{76} = 0.884$$

$$r_w = 0.71.$$

weighted mean z value,

$$z_w = \frac{\sum_{i=1}^{k}(n_i - 3)z_i}{\sum_{i=1}^{k}(n_i - 3)}, \tag{19.32}$$

to its corresponding r value (let's call it r_w), as shown in Example 19.9. This transformation is that of Equation 19.8 and is given in Appendix Table B.19. If H_0 is not rejected, we may test H_0: $\rho = 0$ versus H_A: $\rho \neq 0$ by the method attributed to Neyman

(1959) by Paul (1988):

$$Z = \frac{\sum_{i=1}^{k} n_i r_i}{\sqrt{N}}, \tag{19.33}$$

where $N = \sum_{i=1}^{k} n_i$, and rejecting H_0 if $|Z| \geq Z_{\alpha(2)}$. For one-tailed testing, H_0: $\rho \leq 0$ versus H_A: $\rho > 0$ is rejected if $Z \geq Z_{\alpha(1)}$; and H_0: $\rho \geq 0$ versus H_A: $\rho < 0$ is rejected if $Z \leq -Z_{\alpha(1)}$.

For the hypotheses H_0: $\rho = \rho_0$ versus H_A: $\rho \neq \rho_0$, the transformation of Equation 19.8 is applied to convert ρ_0 to ζ_0. Then (from Paul, 1988),

$$Z = (z_w - \zeta_0)\sqrt{\sum_{i=1}^{n}(n_i - 3)} \tag{19.34}$$

is computed and H_0 is rejected if $|Z| \geq Z_{\alpha(2)}$. For one-tailed testing, H_0: $\rho \leq \rho_0$ is rejected if $Z \geq Z_{\alpha(1)}$ or H_0: $\rho \geq \rho_0$ is rejected if $Z \leq -Z_{\alpha(1)}$.

If correlations are not independent, then they may be compared as described by Steiger (1980).

(b) Overcoming Bias. Fisher (1958: 205) and Hotelling (1953) have pointed out that the z transformation is slightly biased, in that each z will be a little inflated. This minor systematic error is likely to have only negligible effects on our previous considerations, but it is inclined to have adverse effects on the testing of multisample hypotheses, for in the latter situations several values of z_i, and therefore several small errors, are being summed. Such a hypothesis test and the estimation of a common correlation coefficient are most improved by correcting for bias when sample sizes are small or there are many samples in the analysis.

Several corrections for bias are available. Fisher recommended subtracting

$$\frac{r}{2(n-1)}$$

from z, whereas Hotelling determined that better corrections to z are available, such as subtracting

$$\frac{3z + r}{4(n-1)}.$$

However, Paul (1988) recommends a test that performs better than one employing such corrections for bias. It uses

$$\chi^2_P = \sum_{i=1}^{k} \frac{n_i(r_i - r_w)^2}{(1 - r_i r_w)^2} \tag{19.35}$$

with $k - 1$ degrees of freedom. Example 19.10 demonstrates this test.

If the multisample null hypothesis is not rejected, then ρ, the underlying population correlation coefficient, may be estimated by calculating z_w via Equation 19.32 and converting it to r_w. As an improvement, Paul (1988) determined that $n_i - 1$ should be used in place of $n_i - 3$ in the latter equation if ρ is less than about 0.5. Similarly, to compare ρ to a specified value, ρ_0, $n_i - 1$ would be used instead of $n_i - 3$ in Equation 19.34 if ρ is less than about 0.5.

EXAMPLE 19.10 The Hypothesis Testing of Example 19.9, Employing Correction for Bias

$$\chi^2_P = \sum_{i=1}^{k} \frac{n_i(r_i - r_w)^2}{(1 - r_i r_w)^2}$$

$$= \frac{24(0.52 - 0.71)^2}{[1 - (0.52)(0.71)]^2} + \frac{29(0.56 - 0.71)^2}{[1 - (0.56)(0.71)]^2} + \frac{32(0.87 - 0.71)^2}{[1 - (0.87)(0.71)]^2}$$

$$= 2.1774 + 1.7981 + 5.6051$$

$$= 9.5806$$

$$\chi^2_{0.05,2} = 5.991$$

Therefore, reject H_0.

$$0.005 < P < 0.01 \quad [P = 0.0083]$$

19.8 MULTIPLE COMPARISONS AMONG CORRELATION COEFFICIENTS

If the null hypothesis of the previous section (H_0: $\rho_1 = \rho_2 = \cdots = \rho_k$) is rejected, it is typically of interest to determine which of the k correlation coefficients are different from which others. This can be done, again using Fisher's z transformation (Levy, 1976).

In the fashion of Section 11.1 (where multiple comparisons were made among means), we can test each pair of correlation coefficients, r_B and r_A, by a Tukey-type test, if $n_B = n_A$:

$$q = \frac{z_B - z_A}{\text{SE}}. \tag{19.36}$$

where

$$\text{SE} = \sqrt{\frac{1}{n - 3}} \tag{19.37}$$

and n is the size of each sample. If the sizes of the two samples, A and B, are not equal, then we can use

$$\text{SE} = \sqrt{\frac{1}{2}\left(\frac{1}{n_B - 3} + \frac{1}{n_A - 3}\right)}. \tag{19.38}$$

The appropriate critical value for this test is $q_{\alpha,\infty,k}$ (from Appendix Table B.5). This test is demonstrated in Example 19.11.

It is typically unnecessary in multiple comparison testing to employ the correction for bias described at the end of Section 19.7.

(a) Comparing a Control Correlation Coefficient to Each Other Correlation Coefficient. The foregoing methods enable us to compare each correlation coefficient with each other coefficient. If, instead, we desire only to compare each coefficient to one

EXAMPLE 19.11 Tukey-Type Multiple Comparison Testing Among the Three Correlation Coefficients in Example 19.9

Samples ranked by correlation coefficient (i):	1	2	3
Ranked correlation coefficients (r_i):	0.52	0.56	0.87
Ranked transformed coefficients (z_i):	0.5763	0.6328	1.3331
Sample size (n_i):	24	29	32

Comparison B vs. A	*Difference* $z_B - z_A$	SE	q	$q_{0.05,\infty,3}$	*Conclusion*
3 vs. 1	$1.3331 - 0.5763 = 0.7568$	0.203	3.728	3.314	Reject H_0: $\rho_3 = \rho_1$
3 vs. 2	$1.3331 - 0.6328 = 0.7003$	0.191	3.667	3.314	Reject H_0: $\rho_3 = \rho_2$
2 vs. 1	$0.6328 - 0.5763 = 0.0565$	0.207	0.273	3.314	Do not reject H_0: $\rho_2 = \rho_1$

Overall conclusion: $\rho_1 = \rho_2 \neq \rho_3$

particular coefficient (call it the correlation coefficient of the "control" set of data), then a procedure analogous to the Dunnett test of Section 11.3 may be employed (Huitema, 1974).

Let us designate the control set of data as B, and each other group of data, in turn, as A. Then we compute

$$q = \frac{z_B - z_A}{\text{SE}}, \tag{19.39}$$

for each A, in the same sequence as described in Section 11.3. The appropriate standard error is

$$\text{SE} = \sqrt{\frac{2}{n - 3}} \tag{19.40}$$

if samples A and B are of the same size, or

$$\text{SE} = \sqrt{\frac{1}{n_B - 3} + \frac{1}{n_A - 3}} \tag{19.41}$$

if $n_A \neq n_B$. The critical value is $q'_{\alpha(1),\infty,p}$ (from Appendix Table B.6) or $q'_{\alpha(2),\infty,p}$ (from Appendix Table B.7) for the one-tailed or two-tailed test, respectively.

(b) Multiple Contrasts Among Correlation Coefficients. Section 11.4 introduced the concepts and procedures of multiple contrasts among means; these are multiple comparisons involving groups of means. In a similar fashion, multiple contrasts may be examined among correlation coefficients (Marascuilo, 1971: 454–455). We again employ the z transformation and calculate, for each contrast, the test statistic

$$S = \frac{\left|\sum_i c_i z_i\right|}{\text{SE}}, \tag{19.42}$$

where

$$\text{SE} = \sqrt{\sum_i c_i^2 \sigma_{z_i}^2} \tag{19.43}$$

and c_i is a contrast coefficient, as described in Section 11.4. (For example, if we wished to test the hypothesis H_0: $(\rho_1 + \rho_2)/2 - \rho_3 = 0$, then $c_1 = \frac{1}{2}$, $c_2 = \frac{1}{2}$, and $c_3 = -1$.) The critical value for this test is

$$S_\alpha = \sqrt{\chi^2_{\alpha.(k-1)}}. \tag{19.44}$$*

19.9 RANK CORRELATION

If we have data obtained from a bivariate population that is far from normal, then the correlation procedures discussed thus far are generally inapplicable. Instead, we may operate with the ranks of the measurements for each variable. Two different *rank correlation* methods are commonly encountered, that proposed by Spearman (1904) and that of Kendall† (1938). And, these procedures are also applicable if the data are ordinal.

Example 19.12 demonstrates Spearman's rank correlation procedure. After each measurement of a variable is ranked, as done in previously described nonparametric testing procedures, Equation 19.1 can be applied to the ranks to obtain the *Spearman rank correlation coefficient*, r_s. However, a computation that is often simpler is

$$r_s = 1 - \frac{6\sum_{i=1}^{n} d_i^2}{n^3 - n}. \tag{19.46}$$‡

*Because $\chi^2_{\alpha,\nu} = \nu F_{\alpha(1),\nu,\infty}$, it is equivalent to write

$$S_\alpha = \sqrt{(k-1)F_{\alpha(1).(k-1).\infty}}. \tag{19.45}$$

but Equation 19.44 is preferable because it engenders less rounding error in the calculations.

†Charles Edward Spearman (1863–1945), English psychologist and statistician, an important researcher on intelligence and on the statistical field known as factor analysis (Cattell, 1978). Sir Maurice George Kendall (1907–1983), English statistician contributing to many fields (Bartholomew, 1983; David and Fuller, 2007; Ord, 1984; Stuart, 1984). Kruskal (1958) noted that the early development of the method promoted by Kendall began 41 years prior to the 1938 paper. Karl Pearson observed that Sir Francis Galton considered the correlation of ranks even before developing correlation of variables (Walker, 1929: 128).

‡As the sum of n ranks is $n(n+1)/2$, Equation 19.1 may be rewritten for rank correlation as

$$r_s = \frac{\sum_{i=1}^{n} (\text{rank of } X_i)(\text{rank of } Y_i) - \dfrac{n(n+1)^2}{4}}{\sqrt{\left(\sum_{i=1}^{n} (\text{rank of } X_i)^2 - \dfrac{n(n+1)^2}{4}\right)\left(\sum_{i=1}^{n} (\text{rank of } Y_i)^2 - \dfrac{n(n+1)^2}{4}\right)}}. \tag{19.47}$$

Instead of using differences between ranks of pairs of X and Y, we may use the sums of the ranks for each pair, where S_i = rank of X_i + rank of Y_i (Meddis, 1984: 227; Thomas, 1989):

$$r_s = \frac{6\sum S_i^2}{n^3 - n} - \frac{7n + 5}{n - 1}. \tag{19.48}$$

EXAMPLE 19.12 Spearman Rank Correlation for the Relationship Between the Scores of Ten Students on a Mathematics Aptitude Examination and a Biology Aptitude Examination

Student (i)	Mathematics examination score (X_i)	Rank of X_i	Biology examination score (Y_i)	Rank of Y_i	d_i	d_i^2
1	57	3	83	7	−4	16
2	45	1	37	1	0	0
3	72	7	41	2	5	25
4	78	8	84	8	0	0
5	53	2	56	3	−1	1
6	63	5	85	9	−4	16
7	86	9	77	6	3	9
8	98	10	87	10	0	0
9	59	4	70	5	−1	1
10	71	6	59	4	2	4

$n = 10$

$\sum d_i^2 = 72$

$$r_s = 1 - \frac{6\sum d_i^2}{n^3 - n}$$

$$= 1 - \frac{6(72)}{10^3 - 10}$$

$$= 1 - 0.436$$

$$= 0.564$$

To test H_0: $\rho_s = 0$; H_A: $\rho_s \neq 0$.

$(r_s)_{0.05(2),10} = 0.648$ (from Appendix Table B.20)

Therefore, do not reject H_0.

$P = 0.10$

where d_i is a difference between X and Y ranks: d_i = rank of X_i − rank of Y_i.* The value of r_s, as an estimate of the population rank correlation coefficient, ρ_s, may range from −1 to +1, and it has no units; however, its value is not to be expected to be the same as the value of r that might have been calculated for the original data instead of their ranks.

Appendix Table B.20 may be used to assess the significance of r_s. A comment following that table refers to approximating the exact probability of r_s. If n is greater than that provided for in that table, then r_s may be used in place of r in the hypothesis

*Spearman (1904) also presented a rank-correlation method, later (Spearman, 1906) called the "footrule" coefficient. Instead of using the squares of the d_i's, as r_s does, this coefficient employs the absolute values of the d_i's:

$$r_f = 1 - \frac{3\sum |d_i|}{n^2 - 1}. \tag{19.48a}$$

However, r_f typically does not range from −1 to 1; its lower limit is −0.5 if n is odd and, if n is even, it is −1 when $n = 2$ and rapidly approaches −0.5 as n increases (Kendall, 1970: 32–33).

testing procedures of Section 19.2.* If either the Spearman or the parametric correlation analysis (Section 19.2) is applicable, the former is $9/\pi^2 = 0.91$ times as powerful as the latter (Daniel, 1990: 362; Hotelling and Pabst, 1936; Kruskal, 1958).†

(a) Correction for Tied Data. If there are tied data, then they are assigned average ranks as described before (e.g., Section 8.11) and r_s is better calculated either by Equation 19.1 applied to the ranks (Iman and Conover, 1978) or as

$$(r_s)_c = \frac{(n^3 - n)/6 - \sum d_i^2 - \sum t_X - \sum t_Y}{\sqrt{[(n^3 - n)/6 - 2\sum t_X][(n^3 - n)/6 - 2\sum t_Y]}} \tag{19.50}$$

(Kendall, 1962: 38; Kendall and Gibbons, 1990: 44; Thomas, 1989). Here,

$$\sum t_X = \frac{\sum(t_i^3 - t_i)}{12}, \tag{19.51}$$

where t_i is the number of tied values of X in a group of ties, and

$$\sum t_Y = \frac{\sum(t_i^3 - t_i)}{12}, \tag{19.52}$$

where t_i is the number of tied Y's in a group of ties; this is demonstrated in Example 19.13. If $\sum t_X$ and $\sum t_Y$ are zero, then Equation 19.50 is identical to Equation 19.46. Indeed, the two equations differ appreciably only if there are numerous tied data.

Computationally, it is simpler to apply Equation 19.1 to the ranks to obtain $(r_s)_c$ when ties are present.

(b) Other Hypotheses, Confidence Limits, Sample Size, and Power. If $n \geq 10$ and $\rho_s \leq 0.9$, then the Fisher z transformation may be used for Spearman coefficients, just as it was in Sections 19.2 through 19.6, for testing several additional kinds of hypotheses (including multiple comparisons), estimating power and sample size, and setting confidence limits around ρ_s. But in doing so it is recommended that $1.060/(n - 3)$ be used instead of $1/(n - 3)$ in the variance of z (Fieller, Hartley, and Pearson, 1957, 1961). That is,

$$(\sigma_z)_s = \sqrt{\frac{1.060}{n - 3}} \tag{19.53}$$

should be used for the standard error of z (instead of Equation 19.11).

(c) The Kendall Rank Correlation Coefficient. In addition to some rarely encountered rank-correlation procedures (e.g., see Kruskal, 1958), the Kendall

*In this discussion, r_s will be referred to as an unbiased estimate of a population correlation coefficient, ρ_s, although that is not strictly true (Daniel, 1990: 365; Gibbons and Chakraborti, 2003: 432; Kruskall, 1958).

†Zimmerman (1994b) presented a rank-correlation procedure that he asserted is slightly more powerful than the Spearman r_s method. Martín Andrés, Herranz Tejedor, and Silva Mato (1995) showed a relationship between the Spearman rank correlation and the Wilcoxon-Mann-Whitney test of Section 8.11. The Spearman statistic is related to the coefficient of concordance, W (Section 19.13), for two groups of ranks:

$$W = (r_s + 1)/2. \tag{19.49}$$

EXAMPLE 19.13 The Spearman Rank Correlation Coefficient, Computed for the Data of Example 19.1

X	*Rank of* X	Y	*Rank of* Y	d_i	d_i^2
10.4	4	7.4	5	−1	1
10.8	8.5	7.6	7	1.5	2.25
11.1	10	7.9	11	−1	1
10.2	1.5	7.2	2.5	−1	1
10.3	3	7.4	5	−2	4
10.2	1.5	7.1	1	0.5	0.25
10.7	7	7.4	5	2	4
10.5	5	7.2	2.5	2.5	6.25
10.8	8.5	7.8	9.5	−1	1
11.2	11	7.7	8	3	9
10.6	6	7.8	9.5	−3.5	12.25
11.4	12	8.3	12	0	0

$n = 12$ $\qquad r_s = 1 - \dfrac{6\sum d_i^2}{n^3 - n}$

$\sum d_i^2 = 42.00$ $\qquad = 1 - \dfrac{6(42.00)}{1716}$

$= 1 - 0.147$

$= 0.853$

To test H_0: $\rho_s = 0$; H_A: $\rho_s \neq 0$,

$(r_s)_{0.05(2),12} = 0.587$ (from Appendix Table B.20)

Therefore, reject H_0.

$$P < 0.001$$

To employ the correction for ties (see Equation 19.50):

among the X's there are two measurements of 10.2 cm and two of 10.8 cm, so

$$\sum t_X = \frac{(2^3 - 2) + (2^3 - 2)}{12} = 1;$$

among the Y's there are two measurements tied at 7.2 cm, three at 7.4 cm, and two at 7.8 cm, so

$$\sum t_Y = \frac{(2^3 - 2) + (3^3 - 3) + (2^3 - 2)}{12} = 3;$$

therefore,

$$(r_s)_c = \frac{(12^3 - 12)/6 - 42.00 - 1 - 3}{\sqrt{[(12^3 - 12)/6 - 2(1)][(12^3 - 12)/6 - 2(3)]}} = \frac{242}{284.0} = 0.852;$$

and the hypothesis test proceeds exactly as above.

rank-correlation method is often used* (see, e.g., Daniel, 1990: 365–381; Kendall and Gibbons, 1938, 1990: 3–8; Siegel and Castellan, 1988: 245–254). The sample Kendall correlation coefficient is commonly designated as τ (lowercase Greek tau, an exceptional use of a Greek letter to denote a sample statistic).†

The correlation statistic τ for a set of paired X and Y data is a measure of the extent to which the order of the X's differs from the order of the Y's. Its calculation will not be shown here, but this coefficient may be determined—with identical results—either from the data or from the ranks of the data.

For example, these six ranks of X's and six ranks of Y's are in exactly the same order:

X:	1	2	3	4	5	6
Y:	1	2	3	4	5	6

and τ would be calculated to be 1, just as r_s would be 1, for there is perfect agreement of the orders of the ranks of X's and Y's. However, the following Y ranks are in the reverse sequence of the X ranks:

X:	1	2	3	4	5	6
Y:	6	5	4	3	2	1

and τ would be -1, just as r_s would be, for there is an exact reversal of the relationship between the X's and Y's. And, just as with r_s, τ will be closer to zero the further the X and Y ranks are from either perfect agreement or an exact reversal of agreement; but the values of τ and r_s will not be the same except when $\tau = -1$ or 1.

The performances of the Spearman and Kendall coefficients for hypothesis testing are very similar, but the former may be a little better, especially when n is large (Chow, Miller, and Dickinson, 1974), and for a large n the Spearman measure is also easier to calculate than the Kendall. Jolliffe (1981) describes the use of the runs-up-and-down test of Section 25.8 to perform nonparametric correlation testing in situations where r_s and τ are ineffective.

19.10 WEIGHTED RANK CORRELATION

The rank correlation of Section 19.9 gives equal emphasis to each pair of data. There are instances, however, when our interest is predominantly in whether there is correlation among the largest (or smallest) ranks in the two populations. In such cases we should prefer a procedure that will give stronger weight to intersample agreement on which items have the smallest (or largest) ranks, and Quade and Salama (1992) refer to such a method as *weighted rank correlation* (a concept they introduced in Salama and Quade, 1982).

In Example 19.14, a study has determined the relative importance of eight ecological factors (e.g., aspects of temperature and humidity, diversity of ground cover, abundance of each of several food sources) in the success of a particular species of bird in a particular habitat. A similar study ranked the same ecological factors for a second species in that habitat, and the desire is to ask whether the same ecological factors are most important for both species. We want to ask whether there is a positive correlation between the factors most important to one species and the factors most important to the other species. Therefore, a one-tailed weighted correlation analysis is called for.

*The idea of this correlation measure was presented as early as 1899 in a posthumous publication of the German philosopher, physicist, and psychologist Gustav Theodor Fechner (1801–1887) (Kruskal, 1958).

†It is much less frequently designated as T, t, r_k, or $\hat{\tau}$.

EXAMPLE 19.14 A Top-Down Correlation Analysis, Where for Each of Two Bird Species, Eight Ecological Factors Are Weighted in Terms of Their Importance to the Success of the Birds in a Given Habitat

H_0: The same ecological factors are most important to both species.
H_A: The same ecological factors are not most important to both species.

	Rank		Savage number (S_i)		
Factor (i)	*Species 1*	*Species 2*	*Species 1*	*Species 2*	$(S_i)_1(S_i)_2$
A	1	1	2.718	2.718	7.388
B	2	2	1.718	1.718	2.952
C	3	3	1.218	1.218	1.484
D	4	7	0.885	0.268	0.237
E	5	8	0.635	0.125	0.079
F	6	6	0.435	0.435	0.189
G	7	5	0.268	0.635	0.170
H	8	4	0.125	0.885	0.111
Sum			8.002	8.002	12.610

$n = 20$

$$\sum_{i=1}^{n}(S_i)_1(S_i)_2 = 12.610$$

$$r_T = \frac{\sum_{i=1}^{n}(S_i)_1(S_i)_2 - n}{(n - S_1)}$$

$$= \frac{12.610 - 8}{8 - 2.718} = 0.873$$

$$0.005 < P < 0.01$$

A correlation analysis performed on the pairs of ranks would result in a Spearman rank correlation coefficient of $r_s = 0.548$, which is not significantly different from zero. (The one-tailed probability is $0.05 < P < 0.10$.) Iman (1987) and Iman and Conover (1987) propose weighting the ranks by replacing them with the sums of reciprocals known as Savage scores (Savage, 1956). For a given sample size, n, the ith Savage score is

$$S_i = \sum_{j=i}^{n} \frac{1}{j}. \tag{19.54}$$

Thus, for example, if $n = 4$, then $S_1 = 1/1 + 1/2 + 1/3 + 1/4 = 2.083, S_2 = 1/2 + 1/3 + 1/4 = 1.083, S_3 = 1/3 + 1/4 = 0.583$, and $S_4 = 1/4 = 0.250$. A check on arithmetic is that $\sum_{i=1}^{n} S_i = n$; for this example, $n = 4$ and $2.083 + 1.083 + 0.583 + 0.250 = 3.999$. Table 19.1 gives Savage scores for n of 3 through 20. Scores for larger n are readily computed; but, as rounding errors will be compounded in the summation, it is wise to employ extra decimal places in such calculations. If there are tied ranks, then we may use the mean of the Savage scores for the positions of the tied data. For example, if $n = 4$ and ranks 2 and 3 are tied, then use $(1.083 + 0.583)/2 = 0.833$ for both S_2 and S_3.

TABLE 19.1: Savage Scores, S_i, for Various Sample Sizes, n

n	i =	1	2	3	4	5	6	7	8	9	10
3		1.833	0.833	0.333							
4		2.083	1.083	0.583	0.250						
5		2.283	1.283	0.783	0.450	0.200					
6		2.450	1.450	0.950	0.617	0.367	0.167				
7		2.593	1.593	1.093	0.756	0.510	0.310	0.143			
8		2.718	1.718	1.218	0.885	0.635	0.435	0.268	0.125		
9		2.829	1.829	1.329	0.996	0.746	0.546	0.379	0.236	0.111	
10		2.929	1.929	1.429	1.096	0.846	0.646	0.479	0.336	0.211	0.100
11		3.020	2.020	1.520	1.187	0.937	0.737	0.570	0.427	0.302	0.191
12		3.103	2.103	1.603	1.270	1.020	0.820	0.653	0.510	0.385	0.274
13		3.180	2.180	1.680	1.347	1.097	0.897	0.730	0.587	0.462	0.351
14		3.252	2.251	1.752	1.418	1.168	0.968	0.802	0.659	0.534	0.423
15		3.318	2.318	1.818	1.485	1.235	1.035	0.868	0.725	0.600	0.489
16		3.381	2.381	1.881	1.547	1.297	1.097	0.931	0.788	0.663	0.552
17		3.440	2.440	1.940	1.606	1.356	1.156	0.990	0.847	0.722	0.611
18		3.495	2.495	1.995	1.662	1.412	1.212	1.045	0.902	0.777	0.666
19		3.548	2.548	2.048	1.714	1.464	1.264	1.098	0.955	0.830	0.719
20		3.598	2.598	2.098	1.764	1.514	1.314	1.148	1.005	0.880	0.769

n	i =	11	12	13	14	15	16	17	18	19	20
11		0.091									
12		0.174	0.083								
13		0.251	0.160	0.077							
14		0.323	0.232	0.148	0.071						
15		0.389	0.298	0.215	0.138	0.067					
16		0.452	0.361	0.278	0.201	0.129	0.062				
17		0.510	0.420	0.336	0.259	0.188	0.121	0.059			
18		0.566	0.475	0.392	0.315	0.244	0.177	0.114	0.056		
19		0.619	0.528	0.445	0.368	0.296	0.230	0.167	0.108	0.053	
20		0.669	0.578	0.495	0.418	0.346	0.280	0.217	0.158	0.103	0.050

The Pearson correlation coefficient of Equation 19.1 may then be calculated using the Savage scores, a procedure that Iman and Conover (1985, 1987) call "top-down correlation"; we shall refer to the top-down correlation coefficient as r_T. Alternatively, if there are no ties among the ranks of either of the two samples, then

$$r_T = \frac{\sum_{i=1}^{n} (S_i)_1 (S_i)_2 - n}{(n - S_1)}, \tag{19.55}$$

where $(S_i)_1$ and $(S_i)_2$ are the ith Savage scores in Samples 1 and 2, respectively; this is demonstrated in Example 19.14, where it is concluded that there is significant agreement between the two rankings for the most important ecological factors. (As indicated previously, if all factors were to receive equal weight in the analysis of this

set of data, a nonsignificant Spearman rank correlation coefficient would have been calculated.)*

Significance testing of r_T refers to testing H_0: $\rho_T \leq 0$ against H_A: $\rho_T > 0$ and may be effected by consulting Appendix Table B.21, which gives critical values for r_T. For sample sizes greater than those appearing in this table, a one-tailed normal approximation may be employed (Iman and Conover, 1985, 1987):

$$Z = \frac{r_T}{\sqrt{n - 1}}. \tag{19.56}$$

The top-down correlation coefficient, r_T, is 1.0 when there is perfect agreement among the ranks of the two sets of data. If the ranks are completely opposite in the two samples, then $r_T = -1.0$ only if $n = 2$; it approaches -0.645 as n increases. If we wished to perform a test that was especially sensitive to agreement at the bottom, instead of the top, of the list of ranks, then the foregoing procedure would be performed by assigning the larger Savage scores to the larger ranks.

If there are more than two groups of ranks, then see the procedure at the end of Section 20.16.

CORRELATION WITH NOMINAL-SCALE DATA

(a) Both Variables Are Dichotomous. *Dichotomous* normal-scale data are data recorded in two nominal categories (e.g., observations might be recorded as male or female, dead or alive, with or without thorns), and Chapters 23 and 24 contain discussions of several aspects of the analysis of such data. Data collected for a dichotomous variable may be presented in the form of a table with two rows and two columns (a "2 × 2 contingency table"; see Section 23.3). The data of Example 19.15, for instance, may be cast into a 2 × 2 table, as shown. We shall set up such tables by having f_{11} and f_{22} be the frequencies of agreement between the two variables (where f_{ij} is the frequency in row i and column j).

Many measures of association of two dichotomous variables have been suggested (e.g., Conover, 1999: Section 4.4; Everitt, 1992: Section 3.6; Gibbons and Chakraborti, 2003: Section 14.3). So-called *contingency coefficients*,† such as

$$\sqrt{\frac{\chi^2}{\chi^2 + n}} \tag{19.57}$$

and

$$\sqrt{\frac{\frac{\chi^2}{n}}{1 + \frac{\chi^2}{n}}}, \tag{19.57a}$$

*Procedures other than the use of Savage scores may be used to assign differential weights to the ranks to be analyzed: some give more emphasis to the lower ranks and some give less (Quade and Salama, 1992). Savage scores are recommended as an intermediate strategy.

†A term coined by Karl Pearson (Walker, 1958).

EXAMPLE 19.15 Correlation for Dichotomous Nominal-Scale Data. Data Are Collected to Determine the Degree of Association, or Correlation, Between the Presence of a Plant Disease and the Presence of a Certain Species of Insect

Case	*Presence of plant disease*	*Presence of insect*
1	+	+
2	+	+
3	−	−
4	−	+
5	+	+
6	−	+
7	−	−
8	+	+
9	−	+
10	−	−
11	+	+
12	−	−
13	+	+
14	−	+

The data may be tabulated in the following 2 × 2 contingency table:

	Plant Disease		
Insect	*Present*	*Absent*	*Total*
Present	6	4	10
Absent	0	4	4
Total	6	8	14

$$\phi_1 = \frac{f_{11}f_{22} - f_{12}f_{21}}{\sqrt{C_1C_2R_1R_2}}$$

$$= \frac{(6)(4) - (4)(0)}{\sqrt{(6)(8)(10)(4)}}$$

$$= 0.55$$

$$Q = \frac{f_{11}f_{22} - f_{12}f_{21}}{f_{11}f_{22} + f_{12}f_{21}} = \frac{(6)(4) - (4)(0)}{(6)(4) + (4)(0)} = 1.00$$

$$r_n = \frac{(f_{11} + f_{22}) - (f_{12} - f_{21})}{(f_{11} + f_{22}) + (f_{12} + f_{21})} = \frac{(6 + 4) - (4 + 0)}{(6 + 4) + (4 + 0)} = \frac{10 - 4}{10 + 4} = 0.43$$

employ the χ^2 statistic of Section 23.3. However, they have drawbacks, among them the lack of the desirable property of ranging between 0 and 1. [They are indeed zero when $\chi^2 = 0$ (i.e., when there is no association between the two variables), but the coefficients can never reach 1, even if there is complete agreement between the two variables.]

The Cramér, or phi, coefficient* (Cramér, 1946: 44),

$$\phi = \sqrt{\frac{\chi^2}{n}}, \tag{19.58}$$

does range from 0 to 1 (as does ϕ^2, which may also be used as a measure of association).† It is based upon χ^2 (uncorrected for continuity), as obtained from Equation 23.1, or, more readily, from Equation 23.6. Therefore, we can write

$$\phi_1 = \frac{f_{11}f_{22} - f_{12}f_{21}}{\sqrt{C_1C_2R_1R_2}}, \tag{19.59}$$

where R_i is the sum of the frequencies in row i and C_j is the sum of column j. This measure is preferable to Equation 19.58 because it can range from -1 to $+1$, thus expressing not only the strength of an association between variables but also the direction of the association (as does r). If $\phi = 1$, all the data in the contingency table lie in the upper left and lower right cells (i.e., $f_{12} = f_{21} = 0$). In Example 19.15 this would mean there was complete agreement between the presence of both the disease and the insect; either both were always present or both were always absent. If $f_{11} = f_{22} = 0$, all the data lie in the upper right and lower left cells of the contingency table, and $\phi = -1$. The measure ϕ may also be considered as a correlation coefficient, for it is equivalent to the r that would be calculated by assigning a numerical value to members of one category of each variable and another numerical value to members of the second category. For example, if we replace each "+" with 0, and each "−" with 1, in Example 19.15, we would obtain (by Equation 19.1) $r = 0.55$.‡

*Harald Cramér (1893–1985) was a distinguished Swedish mathematician (Leadbetter, 1988). This measure is commonly symbolized by the lowercase Greek phi ϕ—pronounced "fy" as in "simplify"—and is a sample statistic, not a population parameter as a Greek letter typically designates. (It should, of course, not be confused with the quantity used in estimating the power of a statistical test, which is discussed elsewhere in this book.) This measure is what Karl Pearson called "mean square contingency" (Walker, 1929: 133).

†ϕ may be used as a measure of association between rows and columns in contingency tables larger than 2×2, as

$$\phi = \sqrt{\frac{\chi^2}{n(k-1)}}, \tag{19.58a}$$

where k is the number of rows or the number of columns, whichever is smaller (Cramér, 1946: 443); ϕ^2 is also known as the *mean square contingency* (Cramér 1946: 282).

‡If the two rows and two columns of data are arranged so $C_2 \geq R_2$ (as is the case in Example 19.15), the maximum possible ϕ is

$$\phi_{\max} = \sqrt{\frac{R_2C_1}{R_1C_2}}: \tag{19.59a}$$

$\phi = 0.55$ is, in fact, ϕ_{max} for marginal totals of 10, 4, 6, and 8, but if the data in Example 19.15 had been $f_{11} = 5$, $f_{12} = 5$, $f_{21} = 1$, and $f_{22} = 3$, ϕ would have been 0.23, resulting in $\phi/\phi_{max} = 0.42$. Some researchers have used ϕ/ϕ_{max} as an index of association, but Davenport and El-Sanhurry (1991) identified a disadvantage of doing so.

The statistic ϕ is also preferred over the previous coefficients of this section because it is amenable to hypothesis testing. The significance of ϕ (i.e., whether it indicates that an association exists in the sampled population) can be assessed by considering the significance of the contingency table. If the frequencies are sufficiently large (see Section 23.6), the significance of χ_c^2 (chi-square with the correction for continuity) may be determined. The variance of ϕ is given by Kendall and Stuart (1979: 572).

The Yule coefficient of association (Yule 1900, 1912),*

$$Q = \frac{f_{11}f_{22} - f_{12}f_{21}}{f_{11}f_{22} + f_{12}f_{21}}, \tag{19.60}$$

ranges from -1 (if either f_{11} or f_{22} is zero) to $+1$ (if either f_{12} or f_{21} is zero). The variance of Q is given by Kendall and Stuart (1979: 571).

A better measure is that of Ives and Gibbons (1967). It may be expressed as a correlation coefficient,

$$r_n = \frac{(f_{11} + f_{22}) - (f_{12} + f_{21})}{(f_{11} + f_{22}) + (f_{12} + f_{21})}. \tag{19.61}$$

The interpretation of positive and negative values of r_n (which can range from -1 to $+1$) is just as for ϕ.

The expression of significance of r_n involves statistical testing which will be described in Chapter 24. The binomial test (Section 24.5) may be utilized, with a null hypothesis of H_0: $p = 0.5$, using cases of perfect agreement and cases of disagreement as the two categories. Alternatively, the sign test (Section 24.6), the Fisher exact test (Section 24.16), or the chi-square contingency test (Section 23.3) could be applied to the data.

Tetrachoic correlation is a situation where each of two nominal-scale variables has two categories because of an artificial dichotomy (Glass and Hopkins, 1996: 136–137; Howell, 2007: 284–285; Sheskin, 2004: 997–1000).† For example, data might be collected to ask whether there is a correlation between the height of children, recorded as "tall" or "short," and their performance on an intelligence test, recorded as "high" or "low." Underlying each of these two dichotomous variables is a spectrum of measurements, and observations are placed in the categories by an arbitrary definition of *tall*, *short*, *high*, and *low*. (If there are more than two categories of one or both variables, the term *polychoric correlation* may be used.) Therefore, the categories of X and the categories of Y may be considered to represent ordinal scales of measurement.

The tetrachoic correlation coefficient, r_t, is an estimate of what the correlation coefficient, r, of Section 9.1 would be if the continuous data (ratio-scale or interval-scale) were known for the underlying distributions; it ranges from -1 to 1. It is rarely encountered, largely because it is a very poor estimate (it has a large standard error and is adversely affected by nonnormality). The calculation of r_t, and its use in hypothesis testing, is discussed by Sheskin (2004: 998–1000).

(b) One Variable Is Dichotomous. *Point-biserial correlation* is the term used for a correlation between Y, a variable measured on a continuous scale (i.e., a ratio or

*Q is one of several measures of association discussed by British statistician George Udny Yule (1871–1951). He called it Q in honor of Lambert Adolphe Jacques Quetelet (1796–1874), a pioneering Belgian statistician and astronomer who was a member of more than 100 learned societies, including the American Statistical Association (of which he was the first foreign member elected after its formation in 1839); Quetelet worked on measures of association as early as 1832 (Walker, 1929: 130–131).

†This coefficient was developed by Karl Pearson (1901).

interval scale, not an ordinal scale), and X, a variable recorded in two nominal-scale categories.* Although this type of correlation analysis has been employed largely in the behavioral sciences (e.g., Glass and Hopkins, 1996: 364–365, 368–369; Howell, 1997: 279–283, 2007: 277–281; Sheskin, 2004: 990–993), it can also have application with biological data. If it is Y, instead of X, that has two nominal-scale categories, then logistic regression (Section 24.18) may be considered.

Example 19.16 utilizes point-biserial correlation to express the degree to which the blood-clotting time in humans is related to the type of drug that has been administered. In this example, the data of Example 8.1 are tabulated denoting the use of one drug (drug B) by an X of 0 and the use of the other drug (drug G) by an X of 1. The dichotomy may be recorded by any two numbers, with identical results, but employing 0 and 1 provides the simplest computation.

Then a point-biserial correlation coefficient, r_{pb}, is calculated by applying Equation 19.1 or, equivalently, Equation 19.2 to the pairs of X and Y data. The sign of r_{pb} depends upon which category of X is designated as 0; in Example 19.16, r_{pb} is positive, but it would have been negative if drug B had been recorded as 1 and drug G as 0. The coefficient r_{pb} can range from -1 to 1, and it is zero when the means of the two groups of Y's are the same (i.e., $\overline{Y}_1 = \overline{Y}_0$; see the next paragraph).

A computation with equivalent results is

$$r_{pb} = \frac{\overline{Y}_1 - \overline{Y}_0}{s_Y}\sqrt{\frac{n_1 n_0}{N(N-1)}}. \tag{19.62}$$

where $\overline{Y}_0$ is the mean of all n_0 of the Y data associated with $X = 0$, $\overline{Y}_1$ is the mean of the n_1 Y data associated with $X = 1$, $N = n_0 + n_1$, and s_Y is the standard deviation of all N values of Y.†

By substituting r_{pb} for r and N for n, Equations 19.3 and 19.4 may be used for a point-biserial correlation coefficient, and hypothesis testing may proceed as in Section 19.2.

Hypothesis testing involving the population point-biserial correlation coefficient, ρ_{pb}, yields the same results as testing for the difference between two population means (Section 8.1). If an analysis of this kind of data has been done by a t test on sample means, as in Example 8.1, then determination of the point-biserial correlation coefficient may be accomplished by

$$r_{pb} = \sqrt{\frac{t^2}{t^2 + N - 2}}. \tag{19.63}$$

If variable X consists of more than two nominal-scale categories and Y is a continuous variable, then the expression of association between Y and X may be called a *point-polyserial correlation* (Olsson, Drasgow, and Dorans, 1982), a rarely encountered analytical situation not discussed here.

Biserial correlation involves a variable (Y) measured on a continuous scale and differs from point-biserial correlation in the nature of nominal-scale variable X (Glass and Hopkins, 1996: 134–136; Howell, 1997: 286–288, 2007: 284–285; Sheskin, 2004: 995–997). In this type of correlation, the nominal-scale categories are artificial. For

*This procedure was presented and named by Karl Pearson in 1901 (Glass and Hopkins, 1996: 133).

†Although this is a correlation, not a regression, situation, it can be noted that a regression line (calculated via Section 17.1) would run from $\overline{Y}_0$ to $\overline{Y}_1$, and it would have a slope of $\overline{Y}_1 - \overline{Y}_0$ and a Y intercept of $\overline{Y}_0$.

EXAMPLE 19.16 Point-Biserial Correlation, Using Data of Example 8.1

H_0: There is no correlation between blood-clotting time and drug. (H_0: $\rho_{pb} = 0$)
H_A: There is correlation between blood-clotting time and drug. (H_A: $\rho_{pb} \neq 0$)
For variable X, drug B is represented by $X = 0$ and drug G by $X = 1$; Y is the time (in minutes) for blood to clot.

X	Y			
0	8.8			
0	8.4	$n_0 = 6$	$n_1 = 7$	$N = 13$
0	7.9	$\sum X = 7$	$\sum Y = 120.70$	
0	8.7	$\sum X^2 = 7$	$\sum Y^2 = 1129.55$	
0	9.1	$\sum x^2 = 3.2308$	$\sum y^2 = 8.8969$	
0	9.6	$\sum XY = 68.2$		
1	9.9	$\sum xy = 3.2077$		
1	9.0			
1	11.1			
1	9.6			
1	8.7			
1	10.4			
1	9.5			

$$r_{pb} = \frac{3.2077}{\sqrt{(3.2308)(8.8969)}} = 0.5983, \quad r_{pb}^2 = 0.3580$$

$$t = \frac{0.5983}{\sqrt{\frac{1 - 0.3580}{13 - 2}}} = \frac{0.5983}{0.2416} = 2.476$$

$$t_{0.05(2),11} = 2.201$$

Therefore, reject H_0.

$$0.02 < P < 0.05 \quad [P = 0.031]$$

This is the same result as obtained comparing the mean clotting times of the two drug groups (Example 8.1).

example, mice in a diet experiment might be recorded as heavy or light in weight by declaring a particular weight as being the dividing point between "heavy" and "light" (and X behaves like an ordinal-scale variable).

This correlation coefficient, r_b, may be obtained by Equation 9.1 or 9.2, as is r_{pb}, and will be larger than r_{pb} except that when r_{pb} is zero, r_b is also zero. Because X represents an ordered measurement scale, $X = 0$ should be used for the smaller measurement (e.g., "light" in the previous example) and $X = 1$ for the larger measurement (e.g., "heavy"). If there are more than two ranked categories of

X, the term *polyserial correlation* may be applied (Olsson, Drasgow, and Dorans, 1982).

However, the calculated biserial correlation coefficient is adversely affected if the distribution underlying variable X is not normal; indeed, with nonnormality, $|r_b|$ can be much greater than 1. The correlation r_b is an estimate of the correlation coefficient of Section 9.1 that would have been obtained if X were the measurements from the underlying normal distribution. The calculation of, and hypothesis testing with, this coefficient is discussed by Sheskin (2004: 995–996).

INTRACLASS CORRELATION

In some correlation situations it is not possible to designate one variable as X and one as Y. Consider the data in Example 19.17, where the intent is to determine whether there is a relationship between the weights of identical twins. Although the weight data clearly exist in pairs, the placement of a member in each pair in the first or in the second column is arbitrary, in contrast to the paired-sample testing of Section 9.1, where all the data in the first column have something in common and all the data in the second column have something in common. When pairs of data occur as in Example 19.17, we may employ *intraclass correlation*, a concept generally approached by analysis-of-variance considerations (specifically, Model II single-factor ANOVA (Section 10.1f). Aside from assuming random sampling from a bivariate normal distribution, this procedure also assumes that the population variances are equal.

If we consider each of the pairs in our example as groups in an ANOVA (i.e., $k = 7$), with each group containing two observations (i.e., $n = 2$), then we may calculate mean squares to express variability both between and within the k groups (see Section 10.1). Then the *intraclass correlation coefficient* is defined as

$$r_I = \frac{\text{groups MS} - \text{error MS}}{\text{groups MS} + \text{error MS}}, \tag{19.64}$$

this statistic being an estimate of the population intraclass correlation coefficient, ρ_I. To test H_0: $\rho_I = 0$ versus H_0: $\rho_I \neq 0$, we may utilize

$$F = \frac{\text{groups MS}}{\text{error MS}}, \tag{19.65}$$

a statistic associated with groups DF and error DF for the numerator and denominator, respectively.* If the measurements are equal within each group, then error MS = 0, and $r_I = 1$ (a perfect positive correlation). If there is more variability within groups than there is between groups, then r_I will be negative. The smallest it may be, however, is $-1/(n - 1)$; therefore, only if $n = 2$ (as in Example 19.17) can r_I be as small as -1.

We are not limited to pairs of data (i.e., situations where $n = 2$) to speak of intraclass correlation. Consider, for instance, expanding the considerations of Example 19.17 into a study of weight correspondence among triplets instead of twins. Indeed, n need not even be equal for all groups. We might, for example, ask whether there is a relationship among adult weights of brothers; here, some families might

*If desired, F may be calculated first, followed by computing

$$r_I = (F - 1)/(F + 1). \tag{19.66}$$

Also, if $n > 2$, then

$$\sigma_{z_I} = \sqrt{\frac{n}{2(n-1)(k-2)}} \tag{19.74}$$

(Fisher, 1958: 219), and

$$\sigma_{z_1 - z_2} = \sqrt{\frac{\frac{n}{k_1 - 2} + \frac{n}{k_2 - 2}}{2(n-1)}} \tag{19.75}$$

(Zerbe and Goldgar, 1980). Nonparametric measures of intraclass correlation have been proposed (e.g., Rothery, 1979).

19.13 CONCORDANCE CORRELATION

If the intent of collecting pairs of data is to assess reproducibility or agreement of data sets, an effective technique is that which Lin (1989, 1992, 2000) refers to as *concordance correlation*. For example, the staff of an analytical laboratory might wish to know whether measurements of a particular substance are the same using two different instruments, or when performed by two different technicians.

In Example 19.18, the concentration of lead was measured in eleven specimens of brain tissue, where each specimen was analyzed by two different atomic-absorption spectrophotometers. These data are presented in Figure 19.2. If the scales of the two axes are the same, then perfect reproducibility of assay would be manifested by the data falling on a 45° line intersecting the origin of the graph (the line as shown in Figure 19.2), and concordance correlation assesses how well the data follow that 45° line.

The concordance correlation coefficient, r_c, is

$$r_c = \frac{2\sum xy}{\sum x^2 + \sum y^2 + n(\overline{X} - \overline{Y})^2}. \tag{19.76}$$

This coefficient can range from -1 to $+1$, and its absolute value cannot be greater than the Pearson correlation coefficient, r; so it can be stated that $-1 \leq -|r| \leq r_c \leq |r| \leq 1$; and $r_c = 0$ only if $r = 0$.

Hypothesis testing is not recommended with r_c (Lin, 1992), but a confidence interval may be obtained for the population parameter ρ_c of which r_c is an estimate. To do so, the Fisher transformation (Equation 19.8) is applied to r_c to obtain a transformed value we shall call z_c; and the standard error of z_c is obtained as

$$\sigma_{z_c} = \sqrt{\frac{\frac{(1-r^2)r_c^2}{(1-r_c^2)r^2} + \frac{2r_c^3(1-r_c)U}{r(1-r_c^2)^2} - \frac{r_c^4U^2}{2r^2(1-r_c^2)^2}}{n-2}}, \tag{19.77}$$

where

$$U = \frac{\sqrt{n}(\overline{X} - \overline{Y})^2}{\sqrt{\sum x^2 \sum y^2}}. \tag{19.78}$$

This computation is shown in Example 19.18.

Furthermore, we might ask whether two concordance correlations are significantly different. For example, consider that the between-instrument reproducibility analyzed in Example 19.18 was reported for very experienced technicians, and a set of data

EXAMPLE 19.18 Reproducibility of Analyses of Lead Concentrations in Brain Tissue (in Micrograms of Lead per Gram of Tissue), Using Two Different Atomic-Absorption Spectrophotometers

	Tissue Lead (μg/g)	
Tissue sample (i)	*Spectrophotometer A* (X_i)	*Spectrophotometer B* (Y_i)
1	0.22	0.21
2	0.26	0.23
3	0.30	0.27
4	0.33	0.27
5	0.36	0.31
6	0.39	0.33
7	0.41	0.37
8	0.44	0.38
9	0.47	0.40
10	0.51	0.43
11	0.55	0.47

$n = 11$

$\sum X = 4.24$ $\quad \sum Y = 3.67$ $\quad \sum XY = 1.5011$

$\sum X^2 = 1.7418$ $\quad \sum Y^2 = 1.2949$ $\quad \sum xy = 0.08648$

$\sum x^2 = 0.10747$ $\quad \sum y^2 = 0.07045$

$\overline{X} = 0.385$ $\quad \overline{Y} = 0.334$

$$r_c = \frac{2\sum xy}{\sum x^2 + \sum y^2 + n(\overline{X} - \overline{Y})^2}$$

$$= \frac{2(0.08648)}{0.10747 + 0.07045 + 11(0.385 - 0.334)^2} = \frac{0.17296}{0.20653}$$

$$= 0.8375; \quad r_c^2 = 0.7014$$

$$r = \frac{\sum xy}{\sqrt{\sum x^2 \sum y^2}} = 0.9939; \quad r^2 = 0.9878$$

For $r_c = 0.8375, z_c = 1.213$ (from Appendix Table B.18, by interpolation)

$$U = \frac{\sqrt{n}(\overline{X} - \overline{Y})^2}{\sqrt{\sum x^2 \sum y^2}} = \frac{(3.31662)(0.051)^2}{\sqrt{(0.10747)(0.07045)}} = 0.09914$$

$$\sigma_{z_c} = \sqrt{\frac{\dfrac{(1 - r^2)r_c^2}{(1 - r_c^2)r^2} + \dfrac{2r_c^3(1 - r_c)U}{r(1 - r_c^2)^2} - \dfrac{r_c^4U^2}{2r^2(1 - r_c^2)^2}}{n - 2}}$$

$$= \sqrt{\frac{\dfrac{(1 - 0.9878)(0.7014)}{(1 - 0.7014)(0.9878)} + \dfrac{2(0.8375)^3(1 - 0.8375)(0.09914)}{(0.9939)(1 - 0.7014)} - \dfrac{(0.8375)^4(0.09914)^2}{2(0.9878)(1 - 0.7014)}}{11 - 2}}$$

$$= \sqrt{\frac{0.0291 + 0.06377 - 0.002447}{9}} = 0.0245$$

95% confidence interval for ζ_c:

$$z_c \pm Z_{0.05(2)}\sigma_{z_c} = 1.213 \pm (1.960)(0.0610) = 1.213 \pm 0.120$$

$$L_1 = 1.093; \quad L_2 = 1.333.$$

For the 95% confidence limits for ρ_c, the foregoing confidence limits for ζ_c are transformed (as with Appendix Table B.19) to

$$L_1 = 0.794; \quad L_2 = 0.870.$$

was also collected for novice analysts. In order to ask whether the measure of reproducibility (namely, r_c) is different for the highly experienced and the less experienced workers, we can employ the hypothesis testing of Section 19.5. For this, we obtain r_c for the data from the experienced technicians (call it r_1) and another r_c (call it r_2) for the data from the novices. Then each r_c is transformed

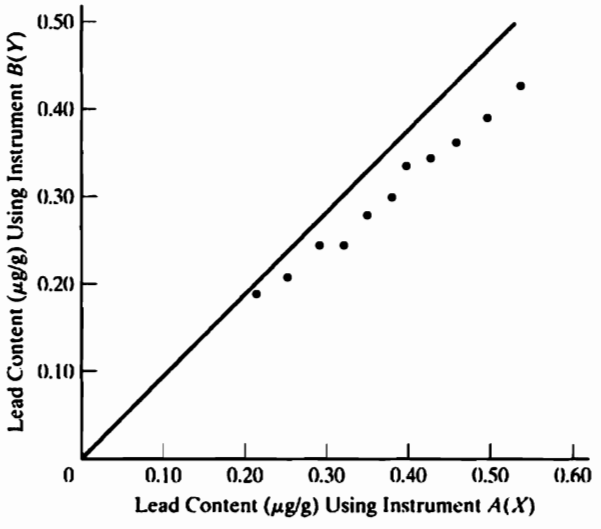

FIGURE 19.2: Lead concentrations in brain tissue (μg/g), determined by two different analytical instruments. The data are from Example 19.18 and are shown with a 45° line through the origin.

to its corresponding z_c (namely, z_1 and z_2) and the standard error to be used in Equation 19.21 is

$$\sigma_{z_1 - z_2} = \sqrt{\sigma_{z_1}^2 + \sigma_{z_2}^2}, \tag{19.79}$$

where each σ_z^2 is obtained as the square of the σ_{z_c} in Equation 19.77.

Lin (1989) has shown that this method of assessing reproducibility is superior to comparison of coefficients of variation (Section 8.8), to the paired-t test (Section 9.1), to regression (Section 17.2), to Pearson correlation (Section 19.1), and to intraclass correlation (Section 19.12). And he has shown the foregoing hypothesis test to be robust with n as small as 10; however (Lin and Chinchilli, 1996), the two coefficients to be compared should have come from populations with similar ranges of data. Lin (1992) also discusses the sample-size requirement for this coefficient; and Barnhart, Haber, and Song (2002) expand concordance correlation to more than two sets of data.

14 THE EFFECT OF CODING

Except for the procedures in Sections 19.11 and 19.12, coding of the raw data will have no effect on the correlation coefficients presented in this chapter, on their z transformations, or on any statistical procedures regarding those coefficients and transformations. See Appendix C for information about the use of coding in Sections 19.11 and 19.12.

EXERCISES

1. Measurements of serum cholesterol (mg/100 ml) and arterial calcium deposition (mg/100 g dry weight of tissue) were made on 12 animals. The data are as follows:

Calcium (X)	*Cholesterol* (Y)
59	298
52	303
42	233
59	287
24	236
24	245
40	265
32	233
63	286
57	290
36	264
24	239

(a) Calculate the correlation coefficient.
(b) Calculate the coefficient of determination.
(c) Test H_0: $\rho = 0$ versus H_A: $\rho \neq 0$.
(d) Set 95% confidence limits on the correlation coefficient.

2. Using the data from Exercise 19.1:
(a) Test H_0: $\rho \leq 0$ versus H_A: $\rho > 0$.
(b) Test H_0: $\rho = 0.50$ versus H_A: $\rho \neq 0.50$.

19.3. Given: $r_1 = -0.44, n_1 = 24, r_2 = -0.40, n_2 = 30$.
(a) Test H_0: $\rho_1 = \rho_2$ versus H_A: $\rho_1 \neq \rho_2$.
(b) If H_0 in part (a) is not rejected, compute the common correlation coefficient.

19.4. Given: $r_1 = 0.45, n_1 = 18, r_2 = 0.56, n_2 = 16$. Test H_0: $\rho_1 \geq \rho_2$ versus H_A: $\rho_1 < \rho_2$.

19.5. Given: $r_1 = 0.85, n_1 = 24, r_2 = 0.78, n_2 = 32, r_3 = 0.86, n_3 = 31$.
(a) Test H_0: $\rho_1 = \rho_2 = \rho_3$, stating the appropriate alternate hypothesis.
(b) If H_0 in part (a) is not rejected, compute the common correlation coefficient.

19.6. **(a)** Calculate the Spearman rank correlation coefficient for the data of Exercise 19.1.
(b) Test H_0: $\rho_s = 0$ versus H_A: $\rho_s \neq 0$.

19.7. Two different laboratories evaluated the efficacy of each of seven pharmaceuticals in treating hypertension in women, ranking them as shown below.

Drug	*Lab 1 rank*	*Lab 2 rank*
L	1	1
P	2	3
Pr	3	2
D	4	4
E	5	7
A	6	6
H	7	5

CHAPTER 20

Multiple Regression and Correlation

The previous three chapters discussed the analyses of regression and correlation relationships between two variables (*simple* regression and correlation). This chapter will extend those kinds of analyses to regressions and correlations examining the interrelationships among three or more variables (*multiple* regression and correlation).

In *multiple regression*, one of the variables is considered to be functionally dependent upon at least one of the others. *Multiple correlation* is a situation when none of the variables is deemed to be dependent on another.*

The computations required for multiple-regression and multiple-correlation analyses would be very arduous, and in many cases prohibitive, without the computer capability that is widely available for this task. Therefore, the mathematical operations used to obtain regression and correlation coefficients, and to perform relevant hypothesis tests, will not be emphasized here. Section 20.1 summarizes the kinds of calculations that a computer program will typically perform and present, but that information is not necessary for understanding the statistical procedures discussed in the remainder of this chapter, including the interpretation of the results of the computer's work.

Though uncommon, there are cases where the dependent variable is recorded on a nominal scale (not on a ratio or interval scale), most often a scale with two nominal categories (e.g., male and female, infected and not infected, successful and unsuccessful). The analyses of this chapter are not applicable for such data. Instead, a procedure known as *logistic regression* (Section 24.18) may be considered.

*Much development in multiple correlation theory began in the late nineteenth century by several pioneers, including Karl Pearson (1857–1936) and his colleague, George Udny Yule (1871–1951) (Pearson 1967). (Pearson first called partial regression coefficients "double regression coefficients," and Yule later called them "net regression coefficients.") Pearson was the first to use the terms *multiple correlation*, in 1908, and *multiple correlation coefficient*, in 1914 (David, 1995).

Multiple regression is a major topic in theoretical and applied statistics; only an introduction is given here, and consultation with a statistical expert is often advisable.*

20.1 INTERMEDIATE COMPUTATIONAL STEPS

There are certain quantities that a computer program for multiple regression and/or correlation must calculate. Although we shall not concern ourselves with the mechanics of computation, intermediate steps in the calculating procedures are indicated here so the user will not be a complete stranger to them if they appear in the computer output. Among the many different programs available for multiple regression and correlation, some do not print all the following intermediate results, or they may do so only if the user specifically asks for them to appear in the output.

Consider n observations of M variables (the variables being referred to as X_1 through X_M; (see Example 20.1a)). If one of the M variables is considered to be dependent upon the others, then we may eventually designate that variable as Y, but the program will perform most of its computations simply considering all M variables as X's numbered 1 through M.

The sum of the observations of each of the M variables is calculated as

$$\sum_{j=1}^{n} X_{1j} \quad \sum_{j=1}^{n} X_{2j} \quad \cdots \quad \sum_{j=1}^{n} X_{Mj}. \tag{20.1}$$

For simplicity, let us refrain from indexing the $\sum$'s and assume that summations are always performed over all n sets of data. Thus, the sums of the variables could be denoted as

$$\sum X_1 \quad \sum X_2 \quad \cdots \quad \sum X_M. \tag{20.2}$$

Sums of squares and sums of cross products are calculated just as for simple regression, or correlation, for each of the M variables. The following sums, often referred to as *raw sums of squares* and *raw sums of cross products*, may be presented in computer output in the form of a matrix, or two-dimensional array:

$$\begin{array}{cccc} \sum X_1^2 & \sum X_1X_2 & \sum X_1X_3 & \cdots \sum X_1X_M \\ \sum X_2X_1 & \sum X_2^2 & \sum X_2X_3 & \cdots \sum X_2X_M \\ \sum X_3X_1 & \sum X_3X_2 & \sum X_3^2 & \cdots \sum X_3X_M \\ \vdots & \vdots & \vdots & \vdots \\ \sum X_MX_1 & \sum X_MX_2 & \sum X_MX_3 & \cdots \sum X_M^2. \end{array} \tag{20.3}$$

As $\sum X_iX_k = \sum X_kX_i$, this matrix is said to be symmetrical about the diagonal running from upper left to lower right.† Therefore, this array, and those that follow,

*Greater discussion of multiple regression and correlation, often with explanation of the underlying mathematical procedures and alternate methods, can be found in many texts, such as Birkes and Dodge (1993); Chatterjee and Hadi (2006); Draper and Smith (1998); Glantz and Slinker (2001); Hair et al. (2006: Chapter 4); Howell (2007: Chapter 15); Kutner, Nachtsheim, and Neter (2004); Mickey, Dunn, and Clark (2004); Montgomery, Peck, and Vining (2006); Pedhazur (1997); Seber and Lee (2003); Tabachnik and Fidell (2001: Chapter 5); and Weisberg (2005).

†We shall refer to the values of a pair of variables as X_i and X_k.

EXAMPLE 20.1a The $n \times M$ Data Matrix for a Hypothetical Multiple Regression or Correlation ($n = 33$; $M = 5$)

	Variable (i)				
j	1 (° C)	2 (cm)	3 (mm)	4 (min)	5 (ml)
1	6	9.9	5.7	1.6	2.12
2	1	9.3	6.4	3.0	3.39
3	−2	9.4	5.7	3.4	3.61
4	11	9.1	6.1	3.4	1.72
5	−1	6.9	6.0	3.0	1.80
6	2	9.3	5.7	4.4	3.21
7	5	7.9	5.9	2.2	2.59
8	1	7.4	6.2	2.2	3.25
9	1	7.3	5.5	1.9	2.86
10	3	8.8	5.2	0.2	2.32
11	11	9.8	5.7	4.2	1.57
12	9	10.5	6.1	2.4	1.50
13	5	9.1	6.4	3.4	2.69
14	−3	10.1	5.5	3.0	4.06
15	1	7.2	5.5	0.2	1.98
16	8	11.7	6.0	3.9	2.29
17	−2	8.7	5.5	2.2	3.55
18	3	7.6	6.2	4.4	3.31
19	6	8.6	5.9	0.2	1.83
20	10	10.9	5.6	2.4	1.69
21	4	7.6	5.8	2.4	2.42
22	5	7.3	5.8	4.4	2.98
23	5	9.2	5.2	1.6	1.84
24	3	7.0	6.0	1.9	2.48
25	8	7.2	5.5	1.6	2.83
26	8	7.0	6.4	4.1	2.41
27	6	8.8	6.2	1.9	1.78
28	6	10.1	5.4	2.2	2.22
29	3	12.1	5.4	4.1	2.72
30	5	7.7	6.2	1.6	2.36
31	1	7.8	6.8	2.4	2.81
32	8	11.5	6.2	1.9	1.64
33	10	10.4	6.4	2.2	1.82

are sometimes presented as a half-matrix, such as

$$\begin{matrix} \sum X_1^2 & & & \\ \sum X_2 X_1 & \sum X_2^2 & & \\ \sum X_3 X_1 & \sum X_3 X_2 & \sum X_3^2 & \\ \vdots & \vdots & \vdots & \\ \sum X_M X_1 & \sum X_M X_2 & \sum X_M X_3 & \cdots \sum X_M^2. \end{matrix} \tag{20.4}$$

If a raw sum of squares, $\sum X_i^2$, is reduced by $(\sum X_i)^2/n$, we have a sum of squares that has previously (Section 17.2) been symbolized as $\sum x^2$, referring to $\sum\sum(X_{ij} - \overline{X}_i)^2$. Similarly, a raw sum of cross products, $\sum X_i X_k$, if diminished by $\sum X_i \sum X_k/n$, yields $\sum x_i x_k$, which represents $\sum(X_{ij} - \overline{X}_i)(X_{kj} - \overline{X}_k)$. These quantities are known as *corrected* sums of squares and *corrected* sums of crossproducts, respectively, and they may be presented as the following matrix:

$$\begin{matrix} \sum x_1^2 & \sum x_1x_2 & \sum x_1x_3 & \cdots & \sum x_1x_M \\ \sum x_2x_1 & \sum x_2^2 & \sum x_2x_3 & \cdots & \sum x_2x_M \\ \sum x_3x_1 & \sum x_3x_2 & \sum x_3^2 & \cdots & \sum x_3x_M \\ \vdots & \vdots & \vdots & & \vdots \\ \sum x_Mx_1 & \sum x_Mx_2 & \sum x_Mx_3 & \cdots & \sum x_M^2. \end{matrix} \tag{20.5}$$

From Matrix 20.5, it is simple to calculate a matrix of simple correlation coefficients, for r_{ik} (representing the correlation between variables i and k) $= \sum x_i x_k \Big/ \sqrt{\sum x_i^2 \sum x_k^2}$ (Equation 19.1):

$$\begin{matrix} r_{11} & r_{12} & r_{13} & \cdots & r_{1M} \\ r_{21} & r_{22} & r_{23} & \cdots & r_{2M} \\ r_{31} & r_{32} & r_{33} & \cdots & r_{3M} \\ \vdots & \vdots & \vdots & & \vdots \\ r_{M1} & r_{M2} & r_{M3} & \cdots & r_{MM}. \end{matrix} \tag{20.6}$$

Each element in the diagonal of this matrix (i.e., r_{ii}) is equal to 1.0, for there will always be a perfect positive correlation between a variable and itself (see Example 20.1b).

EXAMPLE 20.1b A Matrix of Simple Correlation Coefficients, as It Might Appear as Computer Output (from the Data of Example 20.1a)

	1	2	3	4	5
1	1.00000	0.32872	0.16767	0.05191	−0.73081
2	0.32872	1.00000	−0.14550	0.18033	−0.21204
3	0.16767	−0.14550	1.00000	0.24134	−0.05541
4	0.05191	0.18033	0.24134	1.00000	0.31267
5	−0.73081	−0.21204	−0.05541	0.31267	1.00000

The final major manipulation necessary before the important regression or correlation statistics of the following sections can be obtained is the computation of the *inverse* of a matrix. The process of inverting a matrix will not be explained here; it is to two-dimensional algebra what taking the reciprocal is to ordinary, one-dimensional algebra.* While inverting a matrix of moderate size is too cumbersome to be performed easily by hand, it may be readily accomplished by computer. A

*The plural of *matrix* is *matrices*. As a shorthand notation, statisticians may refer to an entire matrix by a boldface letter, and the inverse of the matrix by that letter's reciprocal. So, Matrices

multiple-regression or correlation program may invert the corrected sum of squares and crossproducts matrix, Matrix 20.5, resulting in a symmetrical matrix symbolized

$$\begin{matrix} c_{11} & c_{12} & c_{13} & \cdots & c_{1M} \\ c_{21} & c_{22} & c_{23} & \cdots & c_{2M} \\ \vdots & \vdots & \vdots & & \vdots \\ c_{M1} & c_{M2} & c_{M3} & \cdots & c_{MM}. \end{matrix} \tag{20.7}$$

Or the correlation matrix, Matrix 20.6, may be inverted, yielding a different array of values, which we may designate

$$\begin{matrix} d_{11} & d_{12} & d_{13} & \cdots & d_{1M} \\ d_{21} & d_{22} & d_{23} & \cdots & d_{2M} \\ d_{31} & d_{32} & d_{33} & \cdots & d_{3M} \\ \vdots & \vdots & \vdots & & \vdots \\ d_{M1} & d_{M2} & d_{M3} & \cdots & d_{MM}. \end{matrix} \tag{20.8}$$

Computer routines might compute either Matrix 20.7 or 20.8; the choice is unimportant because the two are interconvertible:

$$c_{ik} = \frac{d_{ik}}{\sqrt{\sum x_i^2 \sum x_k^2}}, \tag{20.9}$$

or, equivalently,

$$c_{ik} = \frac{r_{ik} d_{ik}}{\sum x_i x_k}. \tag{20.10}$$

From manipulations of these types of arrays, a computer program can derive the sample statistics and components of analysis of variance described in the following sections. If partial correlation coefficients are desired (Section 20.7), the matrix inversion takes place as shown. If partial regression analysis is desired (Sections 20.2–20.4), then inversion is performed only on the $M - 1$ rows and $M - 1$ columns corresponding to the independent variables in either Matrix 20.5 or 20.6.

THE MULTIPLE-REGRESSION EQUATION

Recall, from Section 17.2, that a simple linear regression for a population of paired variables is the relationship

$$Y_i = \alpha + \beta X_i. \tag{17.1}$$

In this relationship, Y and X represent the dependent and independent variables, respectively; β is the regression coefficient in the sampled population; and α (the Y intercept) is the predicted value of Y in the population when X is zero. And the subscript i in this equation indicates the ith pair of X and Y data in the sample.

In some situations, however, Y may be considered dependent upon more than one variable. Thus,

$$Y_j = \alpha + \beta_1 X_{1j} + \beta_2 X_{2j} \tag{20.11}$$

20.3, 20.5, and 20.6 might be referred to by the symbols $\mathbf{X}$, $\mathbf{x}$, and $\mathbf{r}$, respectively; and Matrices 20.7 and 20.8 could be written, respectively, as $\mathbf{c} = \mathbf{x}^{-1}$ and $\mathbf{d} = \mathbf{r}^{-1}$. David (2006) gives A. C. Aitken primary credit for introducing matrix algebra into statistics in 1931.

may be proposed, implying that one variable (Y) is linearly dependent upon a second variable (X_1) and that Y is also linearly dependent upon a third variable (X_2). Here, i denotes the ith independent variable, and X_{ij} specifies the jth observation of variable i. In this particular multiple regression model, we have one dependent variable and two independent variables.* The two population parameters β_1 and β_2 are termed *partial regression coefficients*: β_1 expresses how much Y would change for a unit change in X_1, if X_2 were held constant. It is sometimes said that β_1 is a measure of the relationship of Y to X_1 after "controlling for" X_2; that is, it is a measure of the extent to which Y is related to X_1 after removing the effect of X_2. Similarly, β_2 describes the rate of change of Y as X_2 changes, with X_1 being held constant. β_1 and β_2 are called partial regression coefficients, then, because each expresses only part of the dependence relationship. The Y intercept, α, is the value of Y when *both* X_1 and X_2 are zero. Whereas Equation 17.1 mathematically represents a line (which may be presented on a two-dimensional graph), Equation 20.11 defines a plane (which may be plotted on a three-dimensional graph). A regression with m independent variables defines an m-dimensional surface, sometimes referred to as a "response surface" or "hyperplane."

The population data whose relationship is described by Equation 20.11 will probably not all lie exactly on a plane, so this equation may be expressed as

$$Y_j = \alpha + \beta_1 X_{1j} + \beta_2 X_{2j} + \epsilon_j; \tag{20.12}$$

ϵ_j, the "residual," or "error," is the amount by which Y_j differs from what is predicted by $\alpha + \beta_1 X_{1j} + \beta_2 X_{2j}$, where the sum of all ϵ's is zero, the ϵ's are assumed to be normally distributed, and each partial regression coefficient, β_i, estimates the change of Y in the population when there is a change of one unit (e.g., a change of 1 centimeter, 1 minute, or 1 milliliter) in X_i and no change in the other X's.

If we sample the population containing the three variables (Y, X_1, and X_2) in Equation 20.11, we can compute sample statistics to estimate the population parameters in the model. The multiple-regression function derived from a sample of data would be

$$\hat{Y}_j = a + b_1 X_{1j} + b_2 X_{2j}. \tag{20.13}$$

The sample statistics a, b_1, and b_2 are estimates of the population parameters α, β_1, and β_2, respectively, where each partial regression coefficient b_i is the expected change in Y in the population for a change of one unit in X_i if all of the other $m - 1$ independent variables are held constant, and a is the expected population value of Y when each X_i is zero. (Often, the sample Y intercept, a, is represented by b_0 and the population Y intercept is represented as β_0 instead of α.)

Theoretically, in multiple-regression analyses there is no limit to m, the number of independent variables (X_i) that can be proposed as influencing the dependent variable (Y), as long as $n \geq m + 2$. (There will be computational limitations, however.) The general population model, of which Equation 20.12 is the special case for $m = 2$, is†

$$Y_j = \alpha + \beta_1 X_{1j} + \beta_2 X_{2j} + \beta_3 X_{3j} + \cdots + \beta_m X_{mj} + \epsilon_j. \tag{20.14}$$

---

*"*Dependence* in a regression context refers to mathematical, not necessarily biological, dependence. Sometimes the independent variables are called "predictor" or "regressor" or "explanatory" or "exogenous" variables, and the dependent variable may be referred to as the "response" or "criterion" or "endogenous" variable.

†This equation reflects that multiple regression is a special case of what mathematical statisticians call the *general linear model*. Multiple correlation, simple regression and correlation, analysis of variance, and analysis of covariance are also special cases of that model.

or, more succinctly,

$$Y_j = \alpha + \sum_{i=1}^{m} \beta_i X_{ij} + \epsilon_j, \tag{20.15}$$

where m is the number of independent variables. This model is said to be one of *multiple linear regression* because of the linear (i.e., additive) arrangement of the parameters (α and β_i) in the model. The sample regression equation, containing the statistics used to estimate the population parameters when there are m independent variables, would be

$$\hat{Y}_j = a + b_1 X_{1j} + b_2 X_{2j} + b_3 X_{3j} + \cdots + b_m X_{mj}, \tag{20.16}$$

or

$$\hat{Y}_j = a + \sum_{i=1}^{m} b_i X_{ij}. \tag{20.17}$$

At least $m + 2$ data points are required to perform a multiple regression analysis, where m is the number of independent variables determining each data point.

The criterion for defining the "best fit" multiple regression equation is most commonly that of *least squares*,* which—as described in Section 17.2 for simple regression—represents the regression equation with the minimum residual sum of squares† (i.e., the minimum value of $\sum_{j=1}^{n}(Y_j - \hat{Y}_j)^2$). The idea of the least-squares fit of a plane (or hyperplane) through data is an extension of the least-squares concept discussed in Section 17.2 regarding the fit of a line through data.

From the analysis shown in Example 20.1c,‡ we arrive at a regression function having partial regression coefficients of $b_1 = -0.129$ ml/°C, $b_2 = -0.019$ ml/cm, $b_3 = -0.05$ ml/mm, $b_4 = 0.209$ ml/min, and a Y intercept of $a = 2.96$ ml.§ Thus we can write the regression function as $\hat{Y} = 2.96 - 0.129X_1 - 0.019X_2 - 0.05X_3 + 0.209X_4$.

*The statistics in Equation 20.16, derived by the method of least squares, are known to statisticians as *best linear unbiased estimates* (BLUE) because they are unbiased estimates of the population parameters of interest (see Section 2.4), the equation is a linear combination of terms, and the statistics are "best" in the sense of having the smallest variance of any linear unbiased estimates.

†Another criterion that could be used—with different associated statistical procedures—is that of *least absolute deviations*, which would involve minimizing $\sum_{j=1}^{n} |Y_j - \hat{Y}_j|$ (see Birkes and Dodge, 1993; Chapter 2; Bloomfield and Steiger, 1983). As indicated in a Section 17.2 footnote, this procedure may be beneficial when there are outlier data, and—as indicated in that footnote—an intermediate regression method is what is known as *M-regression*.

‡It should be noted that a computer program's output may display results with symbols different from those commonly found in publications such as this book. For example, n might be represented by N, t by T, and r by R; and X_1, X_2, and so on might be written as $X(1)$, $X(2)$, and so on or by $X1$, $X2$, $X3$, and so on. Numbers, especially very large or very small numbers, might be shown in "scientific notation"; for example, 0.0001234 might be displayed as 1.234×10^{-4} or $1.234 \times 10 - 4$ or 0.1234E−3. Users of computer programs should also be aware that some programs, particularly older ones, employ a small enough number of significant figures to cause sizable round-off errors to accumulate through the series of calculations noted in Section 20.1. Such errors may be especially severe if the variables have greatly different magnitudes or if there is considerable multicollinearity (described on Section 20.4).

§By examining the magnitude of the standard errors of the four partial regression coefficients (namely, 0.021287, 0.056278, 0.20727, and 0.067034), we observe that their second significant figures are at the third, third, second, and third decimal places, respectively, making it appropriate to state the four coefficients to those precisions. (See the beginning of Section 17.5.)

EXAMPLE 20.1c A Computer Fit of a Multiple-Regression Equation to the Data of Example 20.1a, Where Variable 5 Is the Dependent Variable

Regression model:

$Y = \alpha + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \beta_4 X_4$

For each i (where $i = 1, 2, 3, 4$),

$H_0: \beta_i = 0$

$H_A: \beta_i \neq 0$

Variable i	b_i	s_{b_i}	t	ν	b_i'
X_1	−0.12932	0.021287	−6.075	28	−0.73176
X_2	−0.018785	0.056278	−0.334	28	−0.41108
X_3	−0.046215	0.20727	−0.223	28	−0.26664
X_4	0.20876	0.067034	3.114	28	0.36451

Y intercept: $a = 2.9583$

Therefore, b_1 is an estimate of the relationship between Y and X_1 after removing the effects on Y of X_2, X_3, and X_4 (i.e., holding those three independent variables constant). So, in this example, an increase of 1° Celsius in variable 1 is predicted to be associated with a 0.129-ml decrease in volume in variable 5 (which is variable Y in this example) if there is no change in variables X_2, X_3, and X_4. Similarly, b_2 estimates the relationship between Y and X_2 after removing the effects of X_1, X_3, and X_4; and so on.

Section 20.4a will explain that, if independent variables are highly correlated with each other, then the interpretation of partial regression coefficients becomes questionable, as does the testing of hypotheses about the coefficients.

20.3 ANALYSIS OF VARIANCE OF MULTIPLE REGRESSION OR CORRELATION

A computer program for multiple regression analysis will typically include an analysis of variance (ANOVA), as shown in Example 20.1d, to test the null hypothesis that all partial regression coefficients (β_i) are zero against the alternate hypothesis that at least one of the β_i's is not zero. This analysis of variance is analogous to that in the case of simple regression (Section 17.3a), in that the total sum of squares and degrees of freedom are separated into two components: (1) the sum of squares and degrees of freedom due to multiple regression, and (2) the residual sum of squares and degrees of freedom; the multiple-regression mean square and the residual mean square are obtained from those quantities. The total sum of squares is an expression of the total amount of variability among the Y values (namely, $Y_j - \overline{Y}$), the regression sum of squares expresses the variability among the Y values that is attributable to the regression being fit (that is, $\hat{Y}_j - \overline{Y}$), and the residual sum of squares tells us about the amount of variability among the Y's that remains after fitting the regression ($Y_j - \hat{Y}_j$). The needed sums of squares, degrees of freedom, and means squares are summarized in Table 20.1. The expressions given in that table for sums of squares are the defining equations; the actual computations of these quantities may involve the use of formulas more suitable to the calculating machine.

EXAMPLE 20.1d A Computer Analysis of Variance for the Multiple Regression Data of Example 20.1a

H_0: $\beta_1 = \beta_2 = \beta_3 = \beta_4 = 0$

H_A: β_1 and/or β_2 and/or β_3 and/or $\beta_4 \neq 0$

Source of Variation	SS	DF	MS
Total	14.747	32	
Multiple regression	9.7174	4	2.4294
Residual	5.0299	28	0.17964

$F = 13.5$, with DF of 4 and 28

$F_{0.05(1),4,28} = 2.71$, so reject H_0.

$P \ll 0.0005 \quad [P = 2.99 \times 10^{-6}]$

Coefficient of determination: $R^2 = 0.65893$

Adjusted coefficient of determination: $R_a^2 = 0.61021$

Multiple correlation coefficient: $R = 0.81175$

Standard error of estimate: $s_{Y \cdot 1,2,3,4} = 0.42384$

TABLE 20.1: Definitions of the Appropriate Sums of Squares, Degrees of Freedom, and Mean Squares Used in Multiple Regression or Multiple Correlation Analysis of Variance

Source of variation	Sum of squares (SS)	DF*	Mean square (MS)
Total	$\sum(Y_j - \overline{Y})^2$	$n - 1$	
Regression	$\sum(\hat{Y}_j - \overline{Y}_j)^2$	m	$\frac{\text{regression SS}}{\text{regression DF}}$
Residual	$\sum(Y_j - \hat{Y}_j)^2$	$n - m - 1$	$\frac{\text{residual SS}}{\text{residual DF}}$

*n = total number of data points (i.e., total number of Y values); m = number of independent variables in the regression model.

Note that a multiple-regression ANOVA (Table 20.1) becomes a simple-regression ANOVA (Table 17.1) when m, the number of independent variables, is 1.

If we assume Y to be functionally dependent on each of the X's, then we are dealing with multiple regression. If no such dependence is implied, then any of the $M = m + 1$ variables could be designated as Y for the purposes of utilizing the computer program; this is a case of *multiple correlation*. In either situation, we can test the hypothesis that there is no interrelationship among the variables, as

$$F = \frac{\text{regression MS}}{\text{residual MS}}. \tag{20.18}$$

The numerator and denominator degrees of freedom for this variance ratio are the regression DF and the residual DF, respectively. For multiple regression, this F tests

$$H_0: \beta_1 = \beta_2 = \cdots = \beta_M = 0,$$

which may be written as

$$H_0: \beta_i = 0 \text{ for all } i\text{'s},$$

against

$$H_A: \beta_i \neq 0 \text{ for one or more } i\text{'s}.$$

The ratio,

$$R^2 = \frac{\text{regression SS}}{\text{total SS}} \tag{20.19}$$

or, equivalently,

$$R^2 = 1 - \frac{\text{residual SS}}{\text{total SS}} \tag{20.20}$$

is the *coefficient of determination* for a multiple regression or correlation, or the *coefficient of multiple determination*.* In a regression situation, it is an expression of the proportion of the total variability in Y that is attributable to the dependence of Y on all the X_i's, as defined by the regression model fit to the data. In the case of correlation, R^2 may be considered to be amount of variability in any one of the M variables that is accounted for by correlating it with all of the other $M - 1$ variables; the quantity $1 - R^2$ is called the *coefficient of nondetermination*, the portion of the variability in one of the variables that is *not* accounted for by its correlation with the other variables.

Healy (1984) and others caution against using R^2 as a measure of "goodness of fit" of a given regression model; and one should not attempt to employ R^2 to compare regressions with different m's and different amounts of replication. An acceptable measure of goodness of fit is what is referred to as the *adjusted coefficient of determination*†.

$$R_a^2 = 1 - \frac{\text{residual MS}}{\text{total MS}}, \tag{20.22}$$

*R^2 may also be calculated as (Sutton, 1990)

$$R^2 = \frac{F}{F + \nu_2/\nu_1}. \tag{20.21}$$

Expressing R^2 may not be appropriate for regression models with no Y intercept, and various authors—and some computer programs—have used the symbol R^2 to denote somewhat different quantities (Kvålseth, 1985).

†Huberty and Mourad (1980) note that several adjustments to R^2 have been proposed and credit the first appearance of R_a^2, a very good one, to Ezekiel (1930: 225–226), who termed it an "index of determination" to distinguish it from the coefficient of determination. They also distinguish between a coefficient of determination when the purpose is multiple correlation (R_a^2), on the one hand, and one (which they attribute to G. E. Nicholson, in 1948, and F. M. Lord, in 1950) that they recommend where the objective is prediction via multiple regression, on the other hand:

$$R_{NL}^2 = 1 - \left(\frac{n + m + 1}{n - m - 1}\right)\left(\frac{n - 1}{n}\right)\left(1 - R^2\right). \tag{20.21a}$$

The difference between R_a^2 and R_{NL}^2 increases as m increases and decreases as n increases.

which is

$$R_a^2 = 1 - \frac{n - 1}{n - m - 1}(1 - R^2). \tag{20.23}$$

R_a^2 increases only if an added X_i results in an improved fit of the regression to the data, whereas R^2 always increases with the addition of an X_i (or it is unchanged if the b_i associated with the X_i is zero). Therefore, R^2 tends to be an overestimate of the population coefficient of determination (ρ^2), with the magnitude of the overestimate greater with smaller n or larger m, and R_a^2 is a better estimate of ρ^2. Because R_a^2 is smaller than R^2, it is sometimes called the "shrunken R^2." If ρ^2 is near zero, the calculated R_a^2 may be negative (in which case it should be expressed as zero). R_a^2 is useful for comparing regression equations that have different numbers of independent variables.

The square root of the coefficient of determination is referred to as the *multiple correlation coefficient*:*

$$R = \sqrt{R^2}. \tag{20.24}$$

R is also equal to the Pearson correlation coefficient, r, for the correlation of the observed values of Y_j with the respective predicted values, $\hat{Y}_j$. For multiple correlation the F of Equation 20.18 allows us to draw inference about the population multiple correlation coefficient, ρ, by testing H_0: $\rho = 0$ against H_A: $\rho \neq 0$.

In a multiple-correlation analysis, Equation 20.18 provides the test for whether the multiple-correlation coefficient is zero in the sampled population. In the case of a multiple regression analysis, Equation 20.18 tests the null hypothesis of no dependence of Y on any of the independent variables, X_i; that is, H_0: $\beta_1 = \beta_2 = \cdots = \beta_m = 0$ (vs. H_A: All m population partial regression coefficients are not equal to zero). Once R^2 has been calculated, the following computation of F may be used as an alternative to Equation 20.18:

$$F = \left(\frac{R^2}{1 - R^2}\right)\left(\frac{\text{residual DF}}{\text{regression DF}}\right), \tag{20.25}$$

and F (from either Equation 20.18 or 20.25 provides a test of H_0: $\rho^2 = 0$ versus H_A: $\rho^2 \neq 0$.

The square root of the residual mean square is the *standard error of estimate* for the multiple regression:

$$s_{Y \cdot 1,2,\ldots,m} = \sqrt{\text{residual MS}}. \tag{20.26}$$

As the residual MS is often called the error MS, $s_{Y \cdot 1,2,\ldots,m}$ is sometimes termed the root mean square error. The subscript $(Y \cdot 1,2,\ldots,m)$ refers to the mathematical dependence of variable Y on the independent variables 1 through m.

The addition of a variable, X_i, to a regression model increases the regression sum of squares and decreases the residual sum of squares (unless the associated b_i is zero, in which case these sums of squares are unchanged). It is important to ask, however, whether an increase in regression sum of squares is important (i.e., whether the added variable contributes useful information to our analysis). The regression degrees of

*G. U. Yule, in 1897, was the first to use R to denote the multiple correlation coefficient (Walker, 1929: 112). R. A. Fisher described the distribution of this statistic in 1928 (Lehmann, 1999). R can never be less than the coefficient of correlation between Y and any of the X_i's (Darlington, 1990: 53).

which is

$$R_a^2 = 1 - \frac{n - 1}{n - m - 1}(1 - R^2). \tag{20.23}$$

R_a^2 increases only if an added X_i results in an improved fit of the regression to the data, whereas R^2 always increases with the addition of an X_i (or it is unchanged if the b_i associated with the X_i is zero). Therefore, R^2 tends to be an overestimate of the population coefficient of determination (ρ^2), with the magnitude of the overestimate greater with smaller n or larger m, and R_a^2 is a better estimate of ρ^2. Because R_a^2 is smaller than R^2, it is sometimes called the "shrunken R^2." If ρ^2 is near zero, the calculated R_a^2 may be negative (in which case it should be expressed as zero). R_a^2 is useful for comparing regression equations that have different numbers of independent variables.

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In a multiple-correlation analysis, Equation 20.18 provides the test for whether the multiple-correlation coefficient is zero in the sampled population. In the case of a multiple regression analysis, Equation 20.18 tests the null hypothesis of no dependence of Y on any of the independent variables, X_i; that is, H_0: $\beta_1 = \beta_2 = \cdots = \beta_m = 0$ (vs. H_A: All m population partial regression coefficients are not equal to zero). Once R^2 has been calculated, the following computation of F may be used as an alternative to Equation 20.18:

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The addition of a variable, X_i, to a regression model increases the regression sum of squares and decreases the residual sum of squares (unless the associated b_i is zero, in which case these sums of squares are unchanged). It is important to ask, however, whether an increase in regression sum of squares is important (i.e., whether the added variable contributes useful information to our analysis). The regression degrees of

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freedom also increase and the residual degrees of freedom also decrease with the addition of a variable and therefore the regression mean square might decrease and/or the residual mean square might increase, and F might be reduced. This issue is addressed in Sections 20.4 and 20.6.

(a) Assumptions of Multiple Regression Analysis. The underlying assumptions of multiple regression are analogous to those of simple regression (Section 17.2d):

1. The values of Y have come at random from the sampled population and are independent of one another.
2. For any combination of values of the X_i's in the population, there is a normal distribution of Y values. (Thus, for each of the combinations of X_i's, there is in the population a normal distribution of ϵ's.)
3. There is homogeneity of variances; that is, the variances of the population distributions of Y values for all combinations of X_i's are all equal to each other. (The residual mean square, $s^2_{Y\cdot 1,2,\ldots,m}$ is the estimate of this common variance.)
4. The independent variables, X_i's, are fixed-effects factors (Section 17.2e), the measurements of which were obtained with no error or with errors negligible compared to the magnitude of errors in measuring Y.

These assumptions do not impact the calculation of regression statistics (a, b_i, R^2), but they do underlie the performance of hypothesis testing and the expression of confidence intervals. Fortunately, regression analysis is robust to some deviation from these assumptions, especially if n is large.

Chatterjee and Hadi (2006: Chapter 4) discuss graphical examination of data for purposes including assessment of departures from assumptions, and some computer programs will provide analysis of residuals (i.e., $Y_i - \hat{Y}_i$ vs. X_i) as introduced in Section 17.10a. Data transformations for variables in multiple regression may assist in meeting the regression assumptions, as in the case of simple regression (Section 17.10) (e.g., Chatterjee and Hadi, 2006: Chapter 6; Cohen et al., 2003: Section 6.4).

There are regression methods, not commonly encountered, to which the foregoing assumptions do not apply. As mentioned in Section 17.2, these include nonparametric regression, least-absolute-deviations regression, and M-regression (Birkes and Dodge, 1993: Chapters 5 and 6; Cleveland, Mallows, and McRae, 1993; Draper and Smith, 1998: Chapter 25; Hollander and Wolfe, 1999: Chapter 9; Huber, 2004: Chapter 7; Kutner, Nachtsheim, and Neter, 2004: 449–558; Montgomery, Peck, and Vining, 2006: Section 7.3; Wang and Scott, 1994).

20.4 HYPOTHESES CONCERNING PARTIAL REGRESSION COEFFICIENTS

In employing simple regression (Section 17.3), it is generally desired to test H_0: $\beta = \beta_0$, a two-tailed null hypothesis where β_0 is most often zero. If, in multiple regression, Equation 20.18 yields a significant F (i.e., H_0: $\beta_1 = \beta_2 = \cdots = \beta_m = 0$ is rejected), then we have concluded that at least one β_i is different from zero and its associated X_i contributes to explaining Y. In that case, each of the partial regression coefficients in a multiple-regression equation may be submitted to an analogous hypothesis, H_0: $\beta_i = \beta_0$, where, again, the test is usually two-tailed and the constant is most frequently zero. For H_0: $\beta_i = 0$, Student's t may be computed as

$$t = \frac{b_i}{s_{b_i}} \tag{20.27}$$

and considerations of Section 17.3b indicate how one-tailed tests and cases where $\beta_0 \neq 0$ would be handled.*

We may obtain both b_i and s_{b_i} from the computer output shown in Example 20.1c. In the particular computer program employed for this example, the t value is also calculated for each b_i. If it had not been, then Equation 20.27 would have been applied. (Some computer programs present the square of this t value and call it a "partial F value.") The residual degrees of freedom are used for this test.

If the standard errors are not given by the computer program being utilized, then they may be calculated as

$$s_{b_i} = \sqrt{s^2_{Y \cdot 1,2,\ldots,m} c_{ii}}, \tag{20.28}$$

where $s^2_{Y \cdot 1,2,\ldots,m}$ is the square of the standard error of estimate, which is simply the residual mean square, and c_{ii} is defined in Section 20.1. Knowing s_{b_i}, we can obtain a $1 - \alpha$ confidence interval for a partial regression coefficient, β_i, as

$$b_i \pm t_{\alpha(2),\nu} s_{b_i}, \tag{20.29}$$

where ν is the residual degrees of freedom.

In general, a significant F value in testing for dependence of Y on all X_i's (by Equation 20.18) will be associated with significance of some of the β_i's being concluded by t-testing; but it is possible to have a significant F without any significant t's, or, in rarer cases, significant t's without a significant F (Cohen et al. 2003: 90; Cramer, 1972; Draper and Smith, 1998: 146–147; Geary and Leser, 1968). These situations can occur when there is a high degree of multicollinearity (see Section 20.4a), and, in general, H_0: $\beta_i = 0$ should not be tested if there is not a significant F for the multiple-regression model.

Section 20.6 discusses methods for concluding which of the m independent variables should be kept in the multiple-regression model and which should be deleted because they do not contribute significantly to the magnitude of Y. Those procedures may be considered if any of the partial regression coefficients are found to be nonsignificant (i.e., at least one H_0: $\beta_i = 0$ is not rejected).

Cohen and colleagues (2003: 94–95) discuss power analysis for partial regression coefficients and provide a special table for this purpose. Various rules of thumb have been presented for sample sizes desirable for testing multiple-regression hypotheses; Green (1991) critiqued several such "rules." These tend to be very general. For example, Hair et al. (2006: 194–197) provide the following recommendations for testing partial regression coefficients at the 0.05 significance level with a power of at least 0.80: a minimum n of 50, preferably 100, and a minimum n-to-i ratio of 5 : 1, preferably 15 : 1 to 20 : 1—or up to 50 : 1 if the procedure of Section 20.6e is used. (As with other statistical methods, specifying a smaller significance level, or a greater power, requires larger samples.) If a reasonable set of independent variables is concluded to contribute to the determination of Y, then power may not be a concern; if not, it might be wise to repeat the experiment with these recommended sample sizes. Conferring with a statistical consultant may help determine how to proceed.

(a) Multicollinearity. If independent variables, say X_1 and X_2, are highly correlated, then the partial regression coefficients associated with them (b_1 and b_2) may not be assumed to reflect the dependence of Y on X_1 or Y on X_2 that exists in the population.

*The distribution of partial regression coefficients (and partial correlation coefficients, Section 20.7) was described by R. A. Fisher at the urging of W. S. Gosset ("Student") (Lehmann, 1999).

Statisticians call correlation between independent variables *multicollinearity* (and sometimes, if it is between only two X_i's, it is termed *collinearity*). It is also known as *intercorrelation* or *nonorthogonality* or *illconditioning* between variables. In practice, multicollinearity is of little consequence if it is not great. But if the multicollinearity is substantial, then standard errors of the partial regression coefficients of the correlated X_i's will be large (and confidence intervals of the b_i's will be wide), significance testing will possess low power, and the interpretation of the effects of those X_i's on Y (and conclusions about the associated b_i's and t's) may be spurious or ambiguous.

Consequential multicollinearity may be suspected

- if a regression coefficient appears unreasonable (such as being unreasonable in sign or magnitude or having an insignificant t even though its X is expected to have a considerable effect on Y);
- if the F for the overall regression is significant with α much lower than the stated significance level but none of the β's are concluded to be different from zero;
- if there are significant t's without a significant F;
- if some correlation coefficients for pairs of X_i's are very high (some researchers would say >0.80 or, especially, >0.90), as observed in Matrix 20.6;
- if R^2 is much greater than $\sum_{i=1}^{m} r_{Yi}^2$, where r_{Yi}^2 represents the simple correlation of the dependent variable (Y) on an independent variable (X_i);
- if there is a great change in the b_i's associated with the other variables when a variable is added to or deleted from the regression model;
- if there is a large difference in regression coefficients upon the addition or deletion of data.

Multicollinearity is more likely with a large number of independent variables, and the adverse effect of multicollinearity may be especially pronounced if the range of any of the X_i's is narrow.* Texts such as Glantz and Slinker (2001: Chapter 5) and Hair et al. (2006: 206–207) discuss both the assessment of multicollinearity by analysis such as what is called tolerance (or its inverse, the variance inflation factor, VIF), and the reduction of multicollinearity (e.g., by deletion of one or more correlated variables from the equation).

Singularity is extreme multicollinearity, when there is a perfect correlation (i.e., $r = 1.0$ or $r = -1.0$) between two (or more) variables. In this situation, a multiple-regression analysis cannot be performed until one (or more) of the perfectly correlated variables is removed from consideration.

When multicollinearity is present, standard errors of partial regression coefficients (s_{b_i}'s) may be large, meaning that the b_i's are imprecise estimates of the relationships in the population. As a consequence, a b_i may not be declared statistically significant from zero (as by the above t test), even when Y and X_i are related in the population. With highly correlated X_i's the overall F for the regression model can be significant even when the t tests for the individual X_i's are not (Berry and Feldman, 1985: 42–43; Bertrand and Holder, 1988; Hamilton, 1987; Kendall and Stuart, 1979; 367; Routledge, 1990). An additional deleterious effect of multicollinearity is that it may lead to increased roundoff error in the computation of regression statistics.

*If the intercorrelation is great, we may be unable to calculate the partial regression coefficients at all, for it may not be possible to perform the matrix inversion described in Section 20.1.

STANDARDIZED PARTIAL REGRESSION COEFFICIENTS

Users of multiple-regression analysis may encounter *standardized partial regression coefficients*.* The common definition of such a coefficient employs the standard deviation of Y (namely S_Y) and of X_i (namely S_{X_i}):

$$b_i' = b_i\left(\frac{s_{X_i}}{s_Y}\right), \quad \text{or, equivalently,} \quad b_i' = b_i\sqrt{\frac{\sum x_i^2}{\sum y^2}}. \tag{20.30}$$

A standardized partial regression coefficient, b_i', is the partial regression coefficient that would result from using Y/s_Y in place of Y and, for that i, using $X/s_{\hat{X}}$ in place of X: or, equivalently from using $(Y - \overline{Y})/s_{\hat{Y}}$ in place of Y and, for that i, using $(X - \overline{X})/s_{\hat{X}}$ in place of X. These coefficients are sometimes reported as indicators of the relative importance of the independent variables (X_i's) in determining the value of the dependent variable Y (if the X_i's are uncorrelated).

These coefficients are unitless, so they are especially useful indicators when X_i's are on different measurement scales; a b_i' with a large absolute value is indicative of its associated X_i having a high degree of influence on Y. Many multiple-regression computer programs include standardized regression coefficients, and some also include their standard errors. A test of H_0: $\beta_i' = 0$ is typically not performed, however, for it would tell the user no more than a test performed for H_0: $\beta_i = 0$; that is, the probability associated with the former null hypothesis is equal to the probability associated with the latter. Standardized partial regression coefficients suffer from the same problems with multicollinearity as do partial regression coefficients (see Section 20.4a).

SELECTING INDEPENDENT VARIABLES

Example 20.1c shows the statistics for the least-squares best-fit equation for the data of Example 20.1a. However, although the data consisted of four independent variables, it should not be assumed that each of the four has a consequential effect on the magnitude of the dependent variable.

Challenges facing the user of multiple regression analysis include concluding which of the independent variables have a significant effect on Y in the population sampled. It is desired to employ a regression equation with as many of the independent variables as required to provide a good determination of which of these variables effect a significant change of Y in the population and to enable accurate prediction of Y. However, the resultant regression equation should comprise as few variables as are necessary for this purpose so as to minimize the time, energy, and expense expended in collecting further data or performing further calculations with the selected regression equation, to optimize statistical estimates (the variances of b_i and $\hat{Y}_j$ may increase unacceptably if nonsignificant variables are included), and, we hope, to simplify the interpretations of the resultant regression equation; a smaller number of variables will also tend to increase the precision of predicted Y's (Draper and Smith, 1998: 327).

The following statistical procedures are important if the intent of the analysis is to predict Y from a group of significantly influential X_i's. However, if the goal is to describe, and help understand, biological relationships underlying the magnitude of Y, then some analysts have argued that biological considerations, in addition to

*These are sometimes called beta coefficients (β_i) but should not be confused with the population parameters (β_i) estimated by b_i.

automated statistical rules, should be employed when deciding which variables to add to or delete from the regression model.

A number of procedures have been proposed to conclude which is, in some objective way, the "best" (or at least a very good) regression model. The various methods do not necessarily arrive at the same conclusions on this question, and there is not universal agreement among statisticians as to which is most advantageous. Indeed, because of drawbacks such as those noted later, some data analysts recommend against using any of them. However, inasmuch as they are commonly found in research publications and computer output, they are summarized here for the reader's benefit.

This section will discuss common methods that have been used for concluding which of the m independent variables should be included in the model, but consultation with a professional statistician may be beneficial in many cases. Deciding, by statistical processes, which of m independent variables should remain in a multiple-regression model is discussed in the references cited in the footnote at the end of the introduction to this chapter, such as in Chatterjee, Hadi, and Price (2000: Chapter 11); Draper and Smith (1998: Chapter 15); Glantz and Slinker (2001: Chapter 6); Hair et al. (2006: 209–214); Kutner, Nachtsheim, and Neter (2004: Chapter 9); and Seber and Lee (2003: Chapter 12).

Each of the methods in Sections 20.6b, 20.6c, and 20.6e involves more than one null hypothesis about partial regression coefficients. However, the several hypothesis tests performed on a set of data are not independent, so the probability of Type I errors may be substantially different from α, especially if the ratio of n to m is small. (See Section 20.4 for recommended sample sizes.) There is no consensus regarding how to correct for this, but many suggest that the same nominal significance level (α) should be used for testing each of the H_0's (though the method described later as "stepwise" might proceed otherwise, as indicated in Section 20.6e).

(a) Fitting All Possible Equations. One procedure would start by fitting a regression equation that contains all the independent variables. In the present example this would involve fitting an equation using all four X_i's. Then a regression fit would be calculated for each of the four different equations containing three of the four independent variables, a regression would be fit for each of the six possible equations comprising two of the X_i's, and a simple regression (that is, with one X_i) would be done using each of the four independent variables. After fitting all 15 of these regression equations, we could choose the one resulting in the lowest residual mean square, or, equivalently, the largest R_a^2 (which is preferable to using R^2) or smallest standard error of estimate.

This is often referred to as "all subsets regression." There are drawbacks to such a procedure, however. First, many regression equations must be calculated,* the number being $2^m - 1$. Thus, if $m = 5$, there would be a total of 31 regressions to be fit; if $m = 8$, then 255 regressions would be called for; if $m = 10$, the goal would be to choose among 1023 regression equations; and so on. A second difficulty with considering the very large number of all possible regressions is that of declaring an objective method for determining which among these many equations is to be considered to be the "best." Thirdly, if one regression equation is determined to be the "best" (perhaps by examining R^2, R_a^2, or $s^2_{Y\cdot 1,2,3,\ldots,m}$, or by a method referred to in Section 20.6f), there is the challenge of concluding whether that equation is

*This calculation is, by Equation 5.10 or 24.2, the number of ways that n items can be combined, one a time, two at a time, and so on.

significantly better than the one deemed "second best." Also, this procedure may result in a regression with substantial multicollinearity.

(b) Backward Elimination of Variables. If a multiple regression equation is fitted using all m independent variables in a set of data (as done in Example 20.1c), then we might ask whether any of those variables have insignificant influence on Y in the sampled population and thus may be eliminated from the equation. The hypothesis H_0: $\beta_i = 0$ may be examined for each of the m partial regression coefficients. If all m of these hypothesis tests are rejected, it may be concluded that all of the X's have a significant effect on Y and none of them should be deleted from the regression model. However, if any $|t|$ values are less than the critical value, $t_{\alpha(2),\nu}$, where ν is the residual degrees of freedom ($n - m - 1$, in the model being considered at this step of the process),* then the independent variable associated with the t with the lowest absolute value is deleted from the model and a new multiple-regression equation may be fitted using the remaining $m - 1$ independent variables. The null hypothesis H_0: $\beta_i = 0$ is then tested for each partial regression coefficient in this new model, and if any of the $|t|$ values are less than the critical value, then one more variable is deleted and a new multiple-regression analysis performed.

As demonstrated in Example 20.1c, this procedure is repeated in what is termed a stepwise fashion, until all b_i's in the equation are concluded to estimate β_i's that are different from zero. Each time a variable is thus deleted from the regression model, the regression MS decreases slightly and the residual MS increases slightly and R^2 decreases (unless that variable's partial regression coefficient is zero, in which case there is no change).

(c) Forward Addition of Variables. Another stepwise procedure (often called forward selection) is to begin with the smallest possible regression model (i.e., one with only one independent variable; in other words, a simple regression) and gradually work up to the multiple-regression model incorporating the largest number of significantly important variables. It is first determined which is the "best" simple-regression model for the data, such as by fitting all m simple regressions and selecting the one for which b_i has the largest value of $|t|$. If none of the b_i's is significant, then it is concluded that no population relationship has been detected between Y and the X_i's and the procedure proceeds no further. If at least one b_i is significant, then a fit would be effected for each of the regressions possessing the X already selected and one of the other X's, and the equation with the largest $|t|$ associated with one of the other X's would be chosen. In a similar fashion, the "best" regression equation can be determined with one X in addition to the two already chosen, and so on. At each step, $|t|$ is compared to the critical value $t_{\alpha(2),\nu}$, where ν is the residual degrees of freedom ($n - m - 1$) at that step.†

Because the relationships among variables change as each one is added, it is not warranted to declare the importance of each variable to be indicated by the sequence in which it is added to the regression model.

(d) Backward Elimination versus Forward Addition. Mantel (1970) described how a "step-up" forward-selection process (Section 20.6c) can involve more computational

*Some computer programs express the critical value as $F_{\alpha(1),1,\nu}$, which is equal to $t^2_{\alpha(2),\nu}$ and, in the context of backward elimination, might be referred to as the "F to remove."

†If F (a "partial F," which is t^2) is used as the test statistic, some computer routines call the critical value ($F_{\alpha(1),1,\nu}$) the "F to enter."

EXAMPLE 20.1e Backward Elimination of Variables in Multiple-Regression Analysis, Using the Data from Example 20.1a

As shown in Example 20.1c, the multiple regression analysis for the model $\hat{Y} = \alpha + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \beta_4 X_4$ yields the following statistics:

Variable	b_i	s_{b_i}	t	ν
X_1	−0.12932	0.021287	−6.075	28
X_2	−0.018785	0.056278	−0.334	28
X_3	−0.046215	0.20727	−0.223	28
X_4	0.20876	0.067034	3.114	28
	$a = 2.9583$			

The critical value for testing $H_0: \beta_j = 0$ against $H_A: \beta_j \neq 0$ is $t_{0.05(2),28} = 2.048$. Therefore, H_0 would be rejected for β_1 and β_4, but not for β_2 or β_3. Of the t tests for the latter two, the t for testing the significance of β_3 has the smaller absolute value. Therefore, $\beta_3 X_3$ is deleted from the model, leaving $\hat{Y} = \alpha + \beta_1 X_1 + \beta_2 X_2 + \beta_4 X_4$. The data are then subjected to a multiple-regression analysis using this model with three independent variables, and the following statistics are obtained:

Variable	b_i	s_{b_i}	t	ν
X_1	−0.13047	0.020312	−6.423	29
X_2	−0.015424	0.053325	−0.289	29
X_4	0.20450	0.063203	3.236	29
	$a = 2.6725$			

The critical value for testing the significance of these partial regression coefficients is $t_{0.05(2),29} = 2.045$. Therefore, $H_0: \beta_j = 0$ would be rejected for β_1 and for β_4, but not for β_2. Therefore, $\beta_2 X_2$ is deleted from the regression model, leaving $\hat{Y} = \alpha + \beta_1 X_1 + \beta_4 X_4$. The analysis of the data using this model, with two independent variables, yields the following statistics:

Variable	b_i	s_{b_i}	t	ν
X_1	−0.13238	0.018913	−6.999	30
X_4	0.20134	0.061291	3.285	30
	$a = 2.5520$			

The critical value for testing $H_0: \beta_j = 0$ against $H_0: \beta_j \neq 0$ is $t_{0.05(2),30} = 2.042$. Therefore, both β_1 and β_4 are concluded to be different from zero, and $\hat{Y} = 2.552 - 0.132 X_1 + 0.201 X_4$ is the final model.

effort, and is fraught with more theoretical deficiencies, than is the "step-down" backward-elimination method (Section 20.6b). The step-up procedure might require as many as ${}_{m+1}C_2$ regressions to be fit (see, e.g., Equation 5.10 or 24.2)*; so if $m = 5$, there would be as many as 15 regression equations to examine, if $m = 8$, there would be as many as 36, and so on. However, the step-down method will never involve the fitting of more than m regressions. Also, forward selection will not identify situations where the addition of a significant X fails to recognize that a previously added X is no longer deemed to significant, it may fail to identify significant independent variables when multicollinearity is present (Hamilton, 1987; Mantel, 1970), and it may yield erroneous conclusions when dealing with dummy variables (described in Section 20.10) with more than two categories (Cohen, 1991). The backward-elimination method is generally preferred to the forward-addition process.

(e) Stepwise Regression. The procedures of Sections 20.6b and 20.6c are stepwise in their execution, but the process very commonly named stepwise is one that employs *both* the addition and the elimination of independent variables in order to conclude which of the variables should be in the multiple-regression model. The process begins as does the step-up method; but whenever an X is added, the b associated with each of the X's thus far in the model is examined to see whether it has a nonsignificant t. If any of them do, then the term with the smallest $|t|$ is eliminated at that step. No more than one X is added or removed at each step, as is the case in the step-down and step-up procedures.

Many statisticians consider this method of variable selection to be preferable to the step-up (Section 20.6c) or step-down (Section 20.6b) method, though others have serious reservations about all three of these procedures (Henderson and Denison, 1989). Some computer software for stepwise regression will allow the user to employ t (or F) with the α for adding a variable to the regression equation different from the α used to remove a variable from the model (so, for example, one might use $\alpha = 0.05$ for adding a variable and $\alpha = 0.10$ for eliminating a variable); but the α for adding should not be greater than the α for removing.

Some computer programs contain routines for performing the addition and/or elimination of variables automatically by one or more of the three stepwise procedures just described. But if a computer program does not do this, the user can determine which variable should be added or deleted at each step, and after each addition or deletion, resubmit the data for computer analysis.

(f) Other Methods. Some computer software presents other methods and criteria to select the "best" set of independent variables for a given set of data. Two such procedures employ statistics known as Mallows C_p, which is closely related to R_a^2 (Kennard, 1971),† and PRESS (predicted error sum of squares). These are described in references such as those cited in the footnote at the end of the introduction to this chapter.

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*The number obtained as ${}_{m+1}C_2$ is called a *triangular number*. It is the sum of the consecutive integers from 1 to m and gets its name from the arrangement of objects in rows: one object in the first row, two in the second row, and so on through the mth row.

†C. L. Mallows introduced C_p in 1964; it was published by Gorman and Toman (1966). Mallows (1973) credited its conception to discussions with Cuthbert Daniel late in 1963, and he used the symbol C to honor the latter colleague. The symbol p is used by many authors to denote the number of independent variables (as m is used in this book).

20.7 PARTIAL CORRELATION

When the interest is in the relationship among all M variables, with none of them considered dependent upon the others, then the multiple-correlation coefficient, R, reflects the overall relationship of all M variables. But we may desire to examine the variables two at a time. We could calculate a simple correlation coefficient, r, for each pair of variables (i.e., what Example 20.1b presents to us). But the problem with considering simple correlations of all variables, two at a time, is that such correlations will fail to take into account the interactions of any of the other variables on the two in question. *Partial correlation* addresses this problem by considering the correlation between each pair of variables while holding constant the effect of each of the other variables.* Symbolically, a partial correlation coefficient for a situation considering three variables (sometimes called a first-order partial correlation coefficient) would be $r_{ik \cdot l}$, which refers to the correlation between variables i and k, considering that variable l does not change its value (i.e., we have eliminated any effect of the interaction of variable l on the relationship between variables i and k). For four variables, a partial correlation coefficient, $r_{ik \cdot lp}$ (sometimes called a second-order partial correlation coefficient), expresses the correlation between variables i and k, assuming that variables l and p were held at constant values. In general, a partial correlation coefficient might be referred to as $r_{ik \cdots}$, meaning the correlation between variables i and k, holding all other variables constant (i.e., removing, or "partialling out" the effects of the other variables).

Another way to visualize partial correlation with three variables (i.e., $M = 3$) is as follows. In a regression of variable X_i on X_l, a set of residuals $(X_i - \hat{X}_i)$ will result; and the regression of X_k on X_l will yield another set of residuals $(X_k - \hat{X}_k)$. The correlation between these two sets of residuals will be the partial correlation coefficient, $r_{ik \cdot l}$.

For three variables, partial correlation coefficients may be calculated from simple correlation coefficients as

$$r_{ik \cdot l} = \frac{r_{ik} - r_{il} r_{kl}}{\sqrt{(1 - r_{il}^2)(1 - r_{kl}^2)}}. \tag{20.31}$$

For more than three variables, the calculations become quite burdensome, and computer assistance is routinely employed. If a partial regression coefficient, b_i, has been obtained for the regression of Y on X_i, the partial correlation coefficient $r_{Yi \cdots}$ can be determined from the t obtained for that b_i as

$$r_{Yi \cdots} = \sqrt{\frac{t^2}{t^2 + \nu}}, \text{ where } \nu = n - M \tag{20.32}$$

(Algina and Seaman, 1984). So, for example (see Examples 20.1b and 20.1c),

$$r_{Y4 \cdots} = \sqrt{\frac{(3.114)^2}{(3.114)^2 + 28}} = 0.5072.$$

*The first (in 1892) to extend the concept of correlation to more than two variables was Francis Ysidro Edgeworth (1845–1926), a statistician and economist who was born in Ireland and spent most of his career at Oxford University (Desmond, 2000; Stigler, 1978). Karl Pearson was the first to express what we now call multiple and partial correlation coefficients; in 1897 he proposed the term *partial correlation*, in contrast to *total correlation* (i.e., what we now call simple correlation), and in preference to what G. U. Yule termed *nett* (a British variant of the word *net*) and *gross* correlation, respectively (Snedecor, 1954; Walker, 1929: 109, 111, 185).

A computer program providing partial correlation coefficients will generally do so in the form of a matrix, such as in Example 20.2:

$$\begin{matrix} 1.00 & r_{12\cdots} & r_{13\cdots} & \cdots & r_{1M\cdots} \\ r_{21\cdots} & 1.00 & r_{23\cdots} & \cdots & r_{2M\cdots} \\ r_{31\cdots} & r_{32\cdots} & 1.00 & \cdots & r_{3M\cdots} \\ \vdots & \vdots & \vdots & & \vdots \\ r_{M1\cdots} & r_{M2\cdots} & r_{M3\cdots} & \cdots & 1.00. \end{matrix} \tag{20.33}$$

To test H_0: $\rho_{ik\cdots} = 0$, we may employ

$$t = \frac{r_{ik\cdots}}{s_{r_{ik\cdots}}}, \tag{20.34}$$

where

$$s_{r_{ik\cdots}} = \sqrt{\frac{1 - r_{ik\cdots}^2}{n - M}} \tag{20.35}$$

and M is the total number of variables in the multiple correlation.* The statistical significance of a partial correlation coefficient (i.e., the test of H_0: $\rho_{ik\cdots} = 0$) may also be determined by employing Appendix Table B.17 for $n - M$ degrees of freedom. One-tailed hypotheses may be performed as for simple correlation coefficients (Section 19.2). If a multiple-regression and a multiple-correlation analysis were performed on the same data, the test conclusion for H_0: $\beta_i = 0$ would be identical to the test conclusion for H_0: $\rho_{ik\cdots} = 0$ (by either t testing or "partial F" testing), where variable k is the dependent variable. Hypotheses such as H_0: $\rho_{ik\cdots} = \rho_0$, or similar one-tailed hypotheses, where $\rho_0 \neq 0$, may be testing using the z transformation (Section 19.2).

EXAMPLE 20.2 A Matrix of Partial Correlation Coefficients, as It Might Appear as Computer Output (from the Data of Example 20.1a)

	1	2	3	4	5
1	1.00000	0.19426	0.12716	0.33929	−0.75406
2	0.19426	1.00000	−0.26977	0.23500	−0.06296
3	0.12716	−0.26977	1.00000	0.26630	−0.04210
4	0.33929	0.23500	0.26630	1.00000	0.50720
5	−0.75406	−0.06296	−0.04210	0.50720	1.00000

Cohen et al. (2003: 94–95) present power estimation, with a needed table, for partial correlation. Serlin and Harwell (1993) assess several nonparametric methods for three-variable partial correlation without the assumption of normality.

*This test statistic may also be calculated as

$$t = \sqrt{\frac{(n - M)(r_{ik\cdots}^2)}{1 - r^2}} \tag{20.36}$$

(a) Semipartial Correlation. Another correlation concept, not as commonly encountered as partial correlation, is that of *semipartial correlation* (Cohen et al., 2003: 72–73, 84–85; Howell, 2007: Section 15.7; Pedhazur, 1997: 174–180), sometimes called *part correlation*. This is the correlation between two of M variables (where $M > 2$) where the effects of all other variables are removed from only one of the two. For example, if $M = 3$, the first-order coefficient of the semipartial correlation between variables X_1 and X_2, with the influence of variable X_3 removed ("partialled out") from X_2 but not from X_1, is

$$r_{1(2.3)} = \frac{r_{12} - r_{13}r_{23}}{\sqrt{1 - r_{23}}}, \tag{20.36a}$$

and the second-order semipartial correlation coefficient for the relationship between X_1 and X_2, with the influence of X_3 and X_4 removed could be designated as $r_{1(2.34)}$. A generalized notation for a semipartial correlation is $r_{i(k\cdots)}$, meaning the correlation between X_i and X_k, removing the effect on X_k of all the other variables. A simple method of calculating a semipartial correlation coefficient was given by Algina and Seaman (1984) as

$$r_{i(k\cdots)} = t_i^2\sqrt{\frac{\text{error MS}}{\text{total SS}}}. \tag{20.36b}$$

The absolute value of the coefficient of semipartial correlation between two variables is always less than the absolute value of the coefficient of partial correlation between those two variables, except that the two coefficients are equal if there is zero correlation between X_i and any variable other than X_k (Darlington, 1990: 56).

A hypothesis test for a population semipartial correlation coefficient being different from zero would exhibit the same probability as a test for the partial correlation coefficient (or the partial regression coefficient, or the standardized partial regression coefficient) being different from zero for the same two variables (Cohen et al., 2003: 89).

20.8 PREDICTING *Y* VALUES

Having fitted a multiple-regression equation to a set of data, we may desire to calculate the Y value to be expected at a particular combination of X_i values. Consider the a and b_i values determined in Example 20.2 for an equation of the form $\hat{Y} = a + b_1X_1 + b_4X_4$. Then the predicted value at $X_1 = 7°C$ and $X_4 = 2.0$ min, for example, would be $\hat{Y} = 2.552 - (0.132)(7) + (0.201)(2.0) = 2.03$ ml. Such predictions may be done routinely if there is a significant regression (i.e., the F from Equation 20.18 is significant), although, as with simple linear regression (Section 17.2), it is unwise to predict Y for X_i's outside the ranges of the X_i's used to obtain the regression statistics.

In the consideration of the standard error of such a predicted Y, the reader may refer to Section 17.5b (Equation 17.26) for the calculations appropriate when $m = 1$. The following is the standard error of a mean Y predicted from a multiple regression equation:

$$s_{\hat{Y}} = \sqrt{s^2_{Y\cdot 1,2,\ldots,m}\left[\frac{1}{n} + \sum_{i=1}^{m}\sum_{k=1}^{m} c_{ik}x_ix_k\right]}. \tag{20.37}$$

In this equation, $x_i = X_i - \overline{X}_i$, where X_i is the value of independent variable i at which Y is to be predicted, $\overline{X}_i$ is the mean of the observed values of variable i that were used to calculate the regression equation, and c_{ik} is from Matrix 20.7.

Thus, for the value of Y just predicted, we can solve Equation 20.37 as shown in Example 20.3.

EXAMPLE 20.3 The Standard Error of a Predicted *Y*

For the equation $\hat{Y} = 2.552 - 0.132X_1 + 0.201X_2$, derived from the data of Example 20.1a, where X_1 is the variable in column 1 of the data matrix, X_2 is the variable in column 4, and Y is the variable in column 5, we obtain the following quantities needed to solve Equation 20.37:

$$s^2_{Y\cdot 1,2} = 0.16844, \quad n = 33, \quad \overline{X} = 4.4546,$$
$$\overline{X}_2 = 2.5424, \quad \sum x_1^2 = 472.18, \quad \sum x_2^2 = 44.961,$$
$$d_{11} = 1.0027, \quad d_{12} = -0.052051, \quad d_{21} = -0.052051, \quad d_{22} = 1.0027.$$

By employing Equation 20.9, each d_{ik} is converted to a c_{ik}, resulting in

$$c_{11} = 0.0021236, \quad c_{12} = -0.00035724, \quad c_{21} = -0.00035724, \quad c_{22} = 0.022302.$$

What is the mean population value of Y at $X_1 = 7°C$ and $X_4 = 2.0$ min?

$$\hat{Y} = 2.552 - (0.132)(7) + (0.201)(2.0) = 2.030 \text{ ml}$$

What is the standard error of the mean population value of Y at $X_1 = 7°C$ and $X_4 = 2.0$ min? [Equation 20.37 is used.]

$$\begin{aligned} s^2_{\hat{Y}} &= 0.16844\left[\frac{1}{33} + (0.0021236)(7 - 4.4546)^2\right. \\ &\quad + (-0.00035724)(7 - 4.4546)(2.0 - 2.5424) \\ &\quad + (-0.00035724)(2.0 - 2.5424)(7 - 4.4546) \\ &\quad \left. + (0.022302)(2.0 - 2.5424)^2\right] \\ &= 0.16844\left(\frac{1}{33} + 0.0213066\right) \\ &= 0.008693 \text{ ml}^2 \\ s_{\hat{Y}} &= \sqrt{0.008693 \text{ ml}^2} = 0.093 \text{ ml} \end{aligned}$$

As $t_{0.05(2),30} = 2.042$, the 95% prediction interval for the predicted Y is $2.030 \pm (2.042)(0.093)$ ml $= 2.030 \pm 0.190$ ml.

What is the predicted value of one additional Y value taken from the population at $X_1 = 7°C$ and $X_4 = 2.0$ min?

$$\hat{Y} = 2.552 - (0.132)(7) + (0.201)(2.0) = 2.030 \text{ ml}$$

What is the standard error of the predicted value of one additional Y value taken from the population at $X_1 = 7°C$ and $X_4 = 2.0$ min? [Equation 20.39 is used.]

$$\begin{aligned} s_{\hat{Y}} &= \sqrt{0.16844\left[1 + \frac{1}{33} + 0.0213066\right]} \\ &= 0.421 \text{ ml} \end{aligned}$$

As $t_{0.05(2),30} = 2.042$, the 95% prediction interval for the preceding predicted $\hat{Y}$ is $2.03 \pm (2.042)(0.421)$ ml $= 2.03 \pm 0.86$ ml.

What is the predicted value of the mean of 10 additional values of Y taken from the population at $X_1 = 7°C$ *and* $X_4 = 2.0$ *min?*

$$\hat{Y} = 2.552 - (0.132)(7) + (0.201)(2.0) = 2.030 \text{ ml}$$

What is the standard error of the predicted value of the mean of 10 additional values of Y taken from the population at $X_1 = 7°C$ *and* $X_4 = 2.0$ *min?* [Equation 20.40 is used.]

$$s_{\hat{Y}} = \sqrt{0.16844\left[\frac{1}{10} + \frac{1}{33} + 0.0213066\right]}$$
$$= 0.16 \text{ ml}$$

As $t_{0.05(2),30} = 2.042$, the 95% prediction interval for the predicted Y is $2.03 \pm (2.042)(0.16)$ ml $= 2.03 \pm 0.33$ ml.

A special case of Equation 20.37 is where each $X_i = 0$. The Y in question is then the Y intercept, a, and

$$s_a = \sqrt{s^2_{Y \cdot 1,2,\ldots,m}\left[\frac{1}{n} + \sum_{i=1}^{m}\sum_{k=1}^{m} c_{ik}\bar{X}_i\bar{X}_k\right]}. \tag{20.38}$$

To predict the value of Y that would be expected if one additional set of X_i were obtained, we may use Equation 20.16, and the standard error of this prediction is

$$(s_{\hat{Y}})_1 = \sqrt{s^2_{Y \cdot 1,2,\ldots,m}\left[1 + \frac{1}{n} + \sum_{i=1}^{m}\sum_{k=1}^{m} c_{ik}x_i x_k\right]}, \tag{20.39}$$

as Example 20.3 shows. This situation is a special case of predicting the mean Y to be expected from obtaining p additional sets of X_i, where the X_1's in all sets are equal, the X_2's in all sets are equal, and so on. Such a calculation is performed in Example 20.3, using

$$(s_{\hat{Y}})_p = \sqrt{s^2_{Y \cdot 1,2,\ldots,m}\left[\frac{1}{p} + \frac{1}{n} + \sum_{i=1}^{m}\sum_{k=1}^{m} c_{ik}x_i x_k\right]}. \tag{20.40}$$

Adding an independent variable, X_i, to a regression model increases each of the standard errors, $s_{\hat{Y}}$, in this section. Therefore, it is desirable to be assured that all variables included are important in predicting $\hat{Y}$ (see Section 20.6).

20.9 TESTING DIFFERENCE BETWEEN TWO PARTIAL REGRESSION COEFFICIENTS

If two partial regression coefficients, b_i and b_k, have the same units of measurement, it may occasionally be of interest to test H_0: $\beta_i - \beta_k = \beta_0$. This can be done by using

$$t = \frac{|b_i - b_k| - \beta_0}{s_{b_i - b_k}}. \tag{20.41}$$

When $\beta_0 = 0$ is hypothesized, this may be written as

$$t = \frac{b_i - b_k}{s_{b_i - b_k}} \tag{20.42}$$

and the null hypothesis can be written as H_0: $\beta_i = \beta_k$. The standard error of the difference between two partial regression coefficients is*

$$s_{b_i - b_k} = \sqrt{s^2_{Y \cdot 1.2 \ldots m}[c_{ii} + c_{kk} - 2c_{ik}]} \tag{20.43}$$

and the degrees of freedom for this test are $n - m - 1$.

Testing other hypotheses about partial regression coefficients is discussed by Chatterjee, Hadi, and Price (2006: Section 3.9).

"DUMMY" VARIABLES

It is sometimes useful to introduce into a multiple regression model one or more additional variables in order to account for the effects of one or more nominal-scale variables on the dependent variable, Y. For example, we might be considering fitting the model $\hat{Y}_j = a + b_1 X_{1j} + b_2 X_{2j}$, where Y is diastolic blood pressure in a species of bear, X_1 is age, and X_2 is body weight. In addition, we might be interested in determining the effect (if any) of the animal's sex on blood pressure. Our regression model could then be expanded to $\hat{Y}_j = a + b_1 X_{1j} + b_2 X_{2j} + b_3 X_{3j}$, where X_3 is a "dummy variable," or "indicator variable," with one of two possible values: for example, set $X_3 = 0$ if the data are for a male and $X_3 = 1$ if the data are for a female. By using this dummy variable, we can test whether sex is a significant determinant of blood pressure (by the considerations of Section 20.4 for testing H_0: $\beta_3 = 0$). If it is, then the use of the model with all three independent variables will yield significantly more accurate Y values than the preceding model with only two independent variables, if the regression equation is used for predicting blood pressure.

If there are three levels of the nominal-scale variable, then two dummies would be needed in the regression model. For example, if we were considering the blood pressure of both sexes and of three subspecies of this bear species, then we might fit the model $\hat{Y}_j = a + b_1 X_{1j} + b_2 X_{2j} + b_3 X_{3j} + b_4 X_{4j} + b_5 X_{5j}$, where X_1, X_2, and X_3 are as before and X_4 and X_5 specify the subspecies. For example, subspecies 1 could be denoted by $X_4 = 0$ and $X_5 = 0$, subspecies 2 by $X_4 = 0$ and $X_5 = 1$, and subspecies 3 by $X_4 = 1$ and $X_5 = 0$. When L levels (i.e., nominal scale categories) of a variable are to be represented by dummy variables, $L - 1$ dummy variables are required. So, in the preceding examples, when $L = 2$ sexes, 1 dummy variable is needed; when $L = 3$ subspecies, 2 dummy variables must be used. Each dummy variable is set to either 0 or 1 for each Y (e.g., 0 or 1 for sex; and 0&0, 0&1, or 1&0 for subspecies), and, for a given Y, the sum of the 0's and 1's may not exceed 1 (so, for example, a dummy two-variable combination of 0&0, 0&1, or 1&0 is acceptable, but 1&1 is not). Further considerations of dummy variables are found in Chatterjee and Hadi (2006: Chapter 5), Draper and Smith (1998: Chapter 14), Hardy (1993), and Pedhazur (1997: 343–360).

When $L > 2$, it is inadvisable to employ stepwise regression by the forward-selection process of Section 20.6c (Cohen, 1991). If the dependent variable, Y, is the

*This could also be written as

$$s_{b_i - b_k} = \sqrt{s^2_{b_i} + s^2_{b_k} + 2s^2_{Y \cdot 1.2 \ldots m} c_{ik}}. \tag{20.43a}$$

dummy variable, appropriate procedures are more complicated and may involve the use of what is known as *logistic regression* (Section 24.18).

20.11 INTERACTION OF INDEPENDENT VARIABLES

It may be proposed that two or more independent variables interact in affecting the dependent variable, Y, a concept encountered in Chapters 12 and 14 when discussing factorial analysis of variance. For example, we may propose this regression model:

$$Y_j = \alpha + \beta_1 X_{1j} + \beta_2 X_{2j} + \beta_3 X_{1j} X_{2j} + \epsilon_j. \tag{20.44}$$

The regression analysis would proceed by treating X_1X_2 as a third independent variable (i.e., as if it were X_3); and rejecting H_0: $\beta_3 = 0$ would indicate a significant interaction between X_1 and X_2, meaning that the magnitude of the effect of X_1 on Y is dependent upon X_2 and the magnitude of the effect of X_2 on Y is dependent upon X_1. By using linear-regression equations that include interaction terms, a great variety of analysis-of-variance experimental designs can be analyzed (even those with unequal replication per cell), and this is a technique employed by some computer programs. Many ramifications of interactions in multiple regression are covered by Aiken and West (1991) and in many of the texts cited in the footnote at the end of the introduction to this chapter. Interaction, the joint effect on Y of two or more X's, should not be confused with correlation among X's ("multicollinearity," discussed in Section 20.4a).

20.12 COMPARING MULTIPLE REGRESSION EQUATIONS

Often we want to determine whether the multiple regressions from two or more sets of data, all containing the same variables, are estimating the same population regression function. We may test the null hypothesis that all the sample regression equations estimate the same population regression model by an extension of the considerations of Section 18.9. For a total of k regressions, the pooled residual sum of squares, SS_p, is the sum of all k residual sums of squares; and the pooled residual degrees of freedom, DF_p, is the sum of all k residual degrees of freedom. We then can combine the data from all k regressions and calculate a regression for this totality of data. The resulting total residual sum of squares and total degrees of freedom will be referred to as SS_t and DF_t, respectively.

The test of the null hypothesis (that there is a single set of population parameters underlying all k sample regressions) is

$$F = \frac{\dfrac{SS_t - SS_p}{(m + 1)(k - 1)}}{\dfrac{SS_p}{DF_p}}, \tag{20.45}$$

a statistic with $(m + 1)(k - 1)$ and DF_p degrees of freedom, Example 20.4 demonstrates this procedure.

We may also employ the concept of parallelism in multiple regression as we did in simple regression. A simple linear regression may be represented as a line on a two-dimensional graph, and two such lines are said to be parallel if the vertical distance between them is constant for all values of the independent variable, meaning that the regression coefficients (i.e., slopes) of the two lines are the same. A multiple regression with two independent variables may be visualized as a plane in three-dimensional space. Two planes are parallel if the vertical distance between them is

the same for all combinations of the independent variables, in which case each of the partial regression coefficients for one regression is equal to the corresponding coefficient of the second regression, with only the Y intercepts possibly differing.

EXAMPLE 20.4 Comparing Multiple Regressions

Let us consider three multiple regressions, each fitted to a different sample of data, and each containing the same dependent variable and the same four independent variables. (Therefore, $m = 4$ and $k = 3$.) The residual sums of squares from each of the regressions are 437.8824, 449.2417, and 411.3548, respectively.

If the residual degrees of freedom for each of the regressions are 41, 32, and 38, respectively (that is, the three sample sizes were 46, 37, and 43, respectively), then the pooled residual sum of squares, SS_p, is 1298.4789, and the pooled residual degrees of freedom, DF_p, is 111.

Then, we combine the 126 data from all three samples and fit to these data a multiple regression having the same variables as the three individual regressions fitted previously. From this multiple regression let us say we have a total residual sum of squares, SS_t, of 1577.3106. The total residual degrees of freedom, DF_t, is 121.

Then we test H_0: All three sample regression functions estimate the same population regression, against H_A: All three sample regression functions do not estimate the same population regression:

$$F = \frac{\dfrac{SS_t - SS_p}{(m + 1)(k - 1)}}{\dfrac{SS_p}{DF_p}}$$

$$= \frac{\dfrac{1577.3106 - 1298.4789}{(5)(2)}}{\dfrac{1298.4789}{111}}$$

$$= 2.38.$$

The degrees of freedom associated with F are 10 and 111.

Since $F_{0.05(1),10,111} \cong 1.93$, reject H_0.

$$0.01 < P < 0.025 \quad [P = 0.013]$$

In general, two or more multiple regressions are said to be parallel if they all have the same β_1, β_2, β_3, and so on. This may be tested by a straightforward extension of the procedure in Section 18.4. The residual sums of squares for all k regressions are summed to give the pooled residual sum of squares, SS_p; the pooled residual degrees of freedom are

$$DF_p = \sum_{i=1}^{k} n_i - k(m + 1). \tag{20.46}$$

Additionally, we calculate a residual sum of squares for the "combined" regression in the following manner. Each element in a corrected sum-of-squares and sum-of-cross-products matrix (Matrix 20.5) is formed by summing all those elements from the k regressions. For example, element $\sum x_1^2$ for the combined regression is formed as

$(\sum x_1^2)_1 + (\sum x_1^2)_2 + (\sum x_1^2)_3 + \cdots + (\sum x_1^2)_k$, and element $\sum x_1 x_2$ is formed as $(\sum x_1 x_2)_1 + (\sum x_1 x_2)_2 + \cdots + (\sum x_1 x_2)_k$. The residual sum of squares obtained from the multiple regression analysis using the resulting matrix is the "common" residual sum of squares, SS_c: the degrees of freedom associated with it are

$$DF_c = \sum_{i=1}^{k} n_i - k - m. \tag{20.47}$$

Then the null hypothesis of all k regressions being parallel is tested by

$$F = \frac{\dfrac{SS_c - SS_p}{k - 1}}{\dfrac{SS_p}{DF_p}}, \tag{20.48}$$

with $k - 1$ and DF_p degrees of freedom.

If the null hypothesis is not rejected, we conclude that the independent variables affect the dependent variable in the same manner in all k regressions; we also conclude that all k regressions are parallel. Now we may ask whether the elevations of the k regressions are all the same. Here we proceed by an extension of the method in Section 18.5. The data for all k regressions are pooled together and one overall regression is fitted. The residual sum of squares of this regression is the total residual sum of squares, SS_t, which is associated with degrees of freedom of

$$DF_t = \sum_{i=1}^{k} n_t - m - 1. \tag{20.49}$$

(The latter degrees of freedom do not enter the calculation of F.)

Then the hypothesis of no difference among the k elevations is tested by

$$F = \frac{\dfrac{SS_t - SS_c}{k - 1}}{\dfrac{SS_c}{DF_c}}, \tag{20.50}$$

with $k - 1$ and DF_c degrees of freedom.

20.13 MULTIPLE REGRESSION THROUGH THE ORIGIN

As an expansion of the simple linear regression model presented in Section 17.9, we might propose a multiple regression model where $\alpha = 0$; that is, when all $X_i = 0$, then $Y = 0$:

$$\hat{Y}_j = \beta_1 X_{1j} + \beta_2 X_{2j} + \cdots + \beta_m X_{mj}. \tag{20.51}$$

This will be encountered only rarely in biological work, but it is worth noting that some multiple-regression computer programs are capable of handling this model.* Striking differences in the computer output will be that total DF = n, regression DF = m (the number of parameters in the model), and residual DF = $n - m$. Also, an *inverse pseudocorrelation matrix* may appear in the computer output in place of an inverse correlation or inverse sum-of-squares and sum-of-cross-products matrix. This

*Hawkins (1980) explains how a regression can be fitted through the origin using the output from a computer program for fitting a regression not assumed to pass through the origin.

regression model is legitimate only if each variable (i.e., Y and each X_i) is measured on a ratio scale (as defined in Section 1.1).

NONLINEAR REGRESSION

Regression models such as

$$Y_i = \alpha + \beta X_i, \tag{17.1}$$

$$Y_j = \alpha + \beta_1 X_{1j} + \beta_2 X_{2j} + \cdots + \beta_m X_{mj}, \tag{20.14}$$

or

$$Y_i = \alpha + \beta_1 X_i + \beta_2 X_i^2 + \cdots + \beta_m X_i^m \tag{21.2}$$

are more completely symbolized as

$$Y_i = \alpha + \beta X_i + \epsilon_i, \tag{20.52}$$

$$Y_j = \alpha + \beta_1 X_{1j} + \beta_2 X_{2j} + \cdots + \beta_m X_{mj} + \epsilon_j, \tag{20.53}$$

or

$$Y_i = \alpha + \beta_1 X_i + \beta_2 X_i^2 + \cdots + \beta_m X_i^m + \epsilon_i, \tag{20.54}$$

respectively, where ϵ is the *residual* (or "error"), the difference between the value of Y predicted from the equation and the true value of Y in the population. All three of the preceding regression models are termed *linear* models because their parameters (i.e., α, β, and ϵ) appear in an additive fashion. However, cases do arise where the investigator wishes to fit to the data a model that is nonlinear with regard to its parameters. Such models might be those such as "exponential growth,"

$$Y_i = \alpha\beta^{X_i} + \epsilon_i \tag{20.55}$$

or

$$Y = \alpha e^{\gamma X_i} + \epsilon_i; \tag{20.56}$$

"exponential decay,"

$$Y_i = \alpha\beta^{-X_i} + \epsilon_i \tag{20.57}$$

or

$$Y_i = \alpha e^{-\gamma X_i} + \epsilon_i; \tag{20.58}$$

"asymptotic regression,"

$$Y_i = \alpha - \beta\delta^{X_i} + \epsilon_i \tag{20.59}$$

or

$$Y_i = \alpha - \beta(e^{-\gamma X_i}) + \epsilon_i; \tag{20.60}$$

or "logistic growth,"

$$Y_i = \frac{\alpha}{1 + \beta\delta^{X_i}} + \epsilon_i; \tag{20.61}$$

where the various Greek letters are parameters in the model. (See Snedecor and Cochran, 1989: 399, for graphs of such functions.) Other nonlinear models would be those in which the residuals were not additive, but, for example, might be multiplicative:

$$Y_i = \beta X_i \epsilon_i. \tag{20.62}$$

Sometimes a nonlinear model may be transformed into a linear one. For example, we may transform

$$Y_i = \alpha X_i^{\beta} \epsilon_i \tag{20.63}$$

by taking the logarithm of each side of the equation, acquiring a model that is linear in its parameters:

$$\log Y_i = \log \alpha + \beta \log X_i + \log \epsilon_i. \tag{20.64}$$

Transformations must be employed with careful consideration, however, so that the assumption of homogeneity of variance is not violated.

Biologists at times wish to fit nonlinear equations, some much more complex than the examples given, and computer programs are available for many of them. Such programs fall into two general groups. First are programs written to fit a particular model or a family of models, and the use of the program is little if any more complicated than the use of a multiple-linear-regression program. Second are general programs that can handle any of a wide variety of models. To use the latter type of program, however, requires the user to submit a good deal of information, perhaps the partial derivatives of the regression function with respect to each parameter in the model (thus, consulting with a statistician would be in order).

Nonlinear regression programs typically involve some sort of an iterative procedure, *iteration* being the utilization of a set of parameter estimates to arrive at a set of somewhat better parameter estimates, using the new estimates to derive better estimates, and so on. Thus, many of these programs require the user to submit initial estimates of (i.e., to guess the values of) the parameters in the model being fitted.

The program output for a nonlinear regression analysis is basically similar to much of the output from multiple-linear-regression analyses. Most importantly, the program should provide estimates of the parameters in the model (i.e., the statistics in the regression equation), the standard error of each of these statistics, and an analysis-of-variance summary including at least the regression and residual SS and DF. If regression and residual MS are not presented in the output, they may be calculated by dividing the appropriate SS by its associated DF. An F test of significance of the entire regression (or correlation) and the coefficient of determination may be obtained by means of Equations 20.18 and 20.19, respectively. Testing whether a parameter in the model is equal to a hypothesized value may be effected by a t test similar to those previously used for simple and partial regression coefficients (e.g., Section 20.4). Kvålseth (1985) and others warn that the computation of R^2 may be inappropriate in nonlinear regression.

Further discussions of nonlinear regression are found in Bates and Watts (1988), Berry and Feldman (1985: 51–64), Seber and Wild (1989), Snedecor and Cochran (1989: Chapter 19), and some of the books cited in the footnote at the end of the introduction to this chapter.

20.15 DESCRIPTIVE VERSUS PREDICTIVE MODELS

Often, it is hoped that a regression model implies a biological dependence (i.e., a cause and effect) in nature, and that this dependence is supported by the mathematical relationship described by the regression equation. However, regression equations are at times useful primarily as a means of predicting the value of a variable, if the

values of a number of associated variables are known. For example, we may desire to predict the weight (call it variable Y) of a mammal, given the length of the femur (variable X). Perhaps a polynomial regression such as

$$\hat{Y}_i = a + b_1 X_i + b_2 X_i^2 + b_3 X_i^3 + b_4 X_i^4 \tag{20.65}$$

might be found to fit the data rather well. (See Chapter 21 for details of polynomial regression.) Or perhaps we wish to predict a man's blood pressure (call it variable Y) as accurately as we can by using measurements of his weight (variable W), his age (variable A), and his height (variable H). By deriving additional regression terms composed of combinations and powers of the three measured independent variables, we might conclude the statistical significance of each term in an equation such as

$$\begin{aligned}\hat{Y}_i = a &+ b_1 W_i + b_2 A_i + b_3 H_i + b_4 W_i^2 + b_5 H_i^2 + b_6 W_i^3 \\ &+ b_7 W_i A_i + b_8 H_i A_i + b_9 W_i^3 A_i.\end{aligned} \tag{20.66}$$

Equations such as 20.65 and 20.66 might have statistically significant partial regression coefficients. They might also have associated with them small standard errors of estimate, meaning that the standard error of predicted Y_i's (and, therefore, the prediction intervals) would be small. Thus, these would be good regression equations for purposes of prediction; but this does not imply that the fourth power of femur length has any natural significance in determining mammal weights, or that terms such as $H_i A_i$ or $W_i^3 A_i$ have any *biological* significance relative to human blood pressure.

To realize a regression function that describes underlying biological phenomena, the investigator must possess a good deal of knowledge about the interrelationships in nature among the variables in the model. Is it indeed reasonable to assume underlying relationships to be linear, or is there a logical basis for seeking to define a particular nonlinear relationship? (For example, forcing a linear model to fit a set of data in no way "proves" that the underlying biological relationships are, in fact, linear.) Are the variables included in the model meaningful choices? (For example, we might find a significant regression of variable A on variable B, whereas a third variable, C, is actually causing the changes in both A and B.) Statistical analysis is only a tool; it cannot be depended upon when applied to incomplete or fallacious biological information.

CONCORDANCE: RANK CORRELATION AMONG SEVERAL VARIABLES

The concept of nonparametric analysis of the correlation between two variables (Section 19.9) can be expanded to consider association among more than two. Such multivariate association is measurable nonparametrically by a statistic known as *Kendall's coefficient of concordance** (Kendall and Gibbons, 1990: Chapter 6; Kendall and Babbington Smith, 1939.)† To demonstrate, let us expand the considerations of Examples 19.1a and 19.13 to examine whether there is concordance (i.e., association) among the magnitudes of wing, tail, and bill lengths in birds of a particular species. Example 20.5 shows such data, for which we determine the ranks for each of the three variables (just as we did for each of the two variables in Example 19.13).

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*Maurice George Kendall (1907–1983), English statistician.

†Wallis (1939) introduced this statistic independently, calling it the "correlation ratio," and designating it by η_r^2 (where η is the lowercase Greek eta).

EXAMPLE 20.5 Kendall's Coefficient of Concordance

H_0: In the sampled population, there is no association among the three variables (wing, tail, and bill lengths).

H_0: In the sampled population, there is a relationship among wing, tail, and bill lengths.

Birds (i)	**Wing Length** (cm)		**Tail Length** (cm)		**Bill Length** (mm)		*Sums of ranks* (R_i)
	Data	*Ranks*	*Data*	*Ranks*	*Data*	*Ranks*	
1	10.4	4	7.4	5	17	5.5	14.5
2	10.8	8.5	7.6	7	17	5.5	21
3	11.1	10	7.9	11	20	9.5	30.5
4	10.2	1.5	7.2	2.5	14.5	2	6
5	10.3	3	7.4	5	15.5	3	11
6	10.2	1.5	7.1	1	13	1	3.5
7	10.7	7	7.4	5	19.5	8	20
8	10.5	5	7.2	2.5	16	4	11.5
9	10.8	8.5	7.8	9.5	21	11	29
10	11.2	11	7.7	8	20	9.5	28.5
11	10.6	6	7.8	9.5	18	7	22.5
12	11.4	12	8.3	12	22	12	36

$M = 3$

$n = 12$

Without correction for ties:

$$W = \frac{\sum R_i^2 - \frac{(\sum R_i)^2}{n}}{\frac{M^2(n^3 - n)}{12}}$$

$$= \frac{(14.5^2 + 21^2 + 30.5^2 + \cdots + 36^2) - \frac{(14.5 + 21 + 30.5 + \cdots + 36)^2}{12}}{\frac{3^2(12^3 - 12)}{12}}$$

$$= \frac{5738.5 - \frac{(234)^2}{12}}{\frac{15444}{12}}$$

$$= \frac{1175.5}{1287} = 0.913$$

$$\chi_r^2 = M(n - 1)W$$

$$= (3)(12 - 1)(0.913)$$

$$= 30.129$$

From Appendix Table B.14, $(X_r^2)_{0.05,3,12} = 6.167$.

Reject H_0: $P \ll 0.001$.

Incorporating the correction for ties:

In group 1 (wing length): there are 2 data tied at 10.2 cm

(i.e., $t_1 = 2$); there are 2 data tied at 10.8 cm (i.e., $t_2 = 2$).

In group 2 (tail length): there are 2 data tied at 7.2 cm

(i.e., $t_3 = 2$); there are 3 data tied at 7.4 cm (i.e., $t_4 = 3$); there are 2 data tied at 7.8 cm (i.e., $t_5 = 2$).

In group 3 (bill length): there are 2 data tied at 17 mm (i.e., $t_6 = 2$); there are 2 data tied at 20 mm (i.e., $t_7 = 2$).

Considering all seven groups of ties,

$$\begin{aligned}\sum t &= \sum_{i=1}^{7}(t_i^3 - t_i) \\ &= (2^3 - 2) + (2^3 - 2) + (2^3 - 2) + (3^3 - 3) \\ &\quad + (2^3 - 2) + (2^3 - 2) + (2^3 - 2) = 60\end{aligned}$$

and

$$W_c = \frac{1175.5}{\dfrac{15444 - 3(60)}{12}} = \frac{1175.5}{1272} = 0.924.$$

Then, to test the significance of W_c:

$$\begin{aligned}(\chi_r^2)_c &= M(n - 1)W_c \\ &= (3)(12 - 1)(0.924) = 30.492.\end{aligned}$$

For these data, the same conclusion is reached with W_c as with W, namely: Reject H_0; and $P \ll 0.001$.

Several computational formulas for the coefficient of concordance are found in various texts. Two that are easy to use are

$$W = \frac{\sum(R_i - \bar{R})^2}{\dfrac{M^2(n^3 - n)}{12}} \tag{20.67}$$

and, equivalently,

$$W = \frac{\sum R_i^2 - \dfrac{(\sum R_i)^2}{n}}{\dfrac{M^2(n^3 - n)}{12}}. \tag{20.68}$$

where M is the number of variables being correlated, and n is the number of data per variable. The numerators of Equations 20.67 and 20.68 are simply the sum of squares of the n rank sums, R_i, using Equations 4.12 and 4.16, respectively.*

The value of W may range from 0 (when there is no association and, consequently, the R_i's are equal and the sum of squares of R_i is zero) to 1 (when there is complete agreement among the rankings of all n groups and there is the maximum possible sum of squares for M variables). In Example 20.5 there is a very high level of concordance ($W = 0.913$), indicating that a bird with a large measurement for one of the variables is likely to have a large measurement for each of the other two variables.

We can ask whether a calculated sample W is significant; that is, whether it represents an association different from zero in the population of data that was sampled (Kendall and Gibbons, 1990: 224–227). The latter authors give tables of probabilities of W, but a simple way to assess the significance of W without such tables is to use the relationship between this coefficient and the Friedman X_r^2 (Section 12.7). Using the notation from the present section (Kendall and Babbington Smith, 1939),

$$\chi_r^2 = M(n - 1)W. \tag{20.69}$$

Thus, we can convert a calculated W to its equivalent χ_r^2 and then employ our table of critical values of χ_r^2 (Appendix Table B.14). This is demonstrated in Example 20.5. If either n or M is larger than that found in this table, then χ_r^2 may be assumed to be approximated by χ^2 with $n - 1$ degrees of freedom, and Appendix Table B.1 is used.

(a) The Coefficient of Concordance with Tied Ranks. If there are tied ranks within any of the M groups, then mean ranks are assigned as in previous discussions (e.g., Section 8.11, Example 8.14). Then W is computed with a correction for ties,

$$W_c = \frac{\sum R_i^2 - \dfrac{\left(\sum R_i\right)^2}{n}}{\dfrac{M^2(n^3 - n) - M\sum t}{12}}, \tag{20.70}$$

where

$$\sum t = \sum_{i=1}^{m} (t_i^3 - t_i), \tag{20.71}$$

t_i is the number of ties in the ith group of ties, and m is the number of groups of tied ranks.† This computation of W_c is demonstrated in Example 20.5. W_c will not differ appreciably from W unless the numbers of tied data are great.

(b) The Coefficient of Concordance for Assessing Agreement. A common use of Kendall's coefficient of concordance is to express the intensity of agreement among several rankings. In Example 20.6, each of the three ten-year-old girls has been asked to rank the palatability of six flavors of ice cream. We wish to ask whether ten-year-old girls, in the population from which this sample came, agree upon the rankings.

*Kendall and Gibbons (1990: 123) present W with this correlation for continuity, noting that it does not appreciably alter the resultant W: Subtract 1 from the numerator and add 2 to the denominator of Equation 20.67 or 20.68.

†As in Equation 20.70, when ties are present, the denominator in Equations 20.68 and 20.69 would incorporate the subtraction of $M\sum t$ prior to dividing by 12.

EXAMPLE 20.6 Kendall's Coefficient of Concordance Used to Assess Agreement

Each of three girls ranked her taste preference for each of six flavors of ice cream (chocolate-chip, chocolate, spumoni, vanilla, butter-pecan, Neapolitan.)

H_0: There is no agreement in flavor preference.

H_A: There is agreement in flavor preference.

	Flavors (i)						
Girl	CC	C	S	V	BP	N	
1	5	1	3	2	4	6	
2	6	2	3	1	5	4	
3	6	3	2	1	4	5	
Rank sum (R_i)	17	6	8	4	13	15	$\sum R_i = 63$

$M = 3$

$n = 6$

$$W = \frac{\sum R_i^2 - \dfrac{(\sum R_i)^2}{n}}{\dfrac{M^2(n^3 - n)}{12}}$$

$$= \frac{17^2 + 6^2 + 8^2 + 4^2 + 13^2 + 15^2 - \dfrac{63^2}{6}}{\dfrac{3^2(6^3 - 6)}{12}} = \frac{137.50}{157.50} = 0.873$$

$$\chi_r^2 = M(n - 1)W = (3)(6 - 1)(0.873) = 13.095$$

Using Appendix Table B.14, $(\chi_r^2)_{0.05,3,6} = 7.000$. Therefore, reject H_0. The conclusion is that there is agreement in flavor preferences.

$$P < 0.001$$

(c) The Relationship Between W and r_s. Not only Kendall's W related to Friedman's X_r^2 (Equation 20.69), but it is related to the mean value of all possible Spearman rank correlation coefficients that would be obtained from all possible pairs of variables. These correlation coefficients may be listed in a matrix array:

$$\begin{matrix} (r_s)_{11} & (r_s)_{12} & (r_s)_{13} & \cdots & (r_s)_{1M} \\ (r_s)_{21} & (r_s)_{22} & (r_s)_{23} & \cdots & (r_s)_{2M} \\ (r_s)_{31} & (r_s)_{32} & (r_s)_{33} & \cdots & (r_s)_{3M} \\ \vdots & \vdots & \vdots & & \vdots \\ \vdots & \vdots & \vdots & & \vdots \\ \vdots & \vdots & \vdots & & \vdots \\ (r_s)_{M1} & (r_s)_{M2} & (r_s)_{M3} & \cdots & (r_s)_{MM}, \end{matrix} \tag{20.72}$$

a form similar to that of Matrix 20.6. As in Matrix 20.6, each element of the diagonal, $(r_s)_{ii}$, is equal to 1.0, and each element below the diagonal is duplicated above the diagonal, as $(r_s)_{ik} = (r_s)_{ki}$. There are $M!/[2(M - 2)!]$ different r_s's possible for M variables.*

In Example 20.5, we are speaking of three r_s's: $(r_s)_{12}$, the r_s for wing length and tail length; $(r_s)_{13}$, the r_s for wing and bill lengths; and $(r_s)_{23}$, the r_s for tail and bill lengths. The Spearman rank correlation coefficient matrix, using correction for ties (Equation 19.50), would be

$$\begin{matrix} 1.000 & & \\ 0.852 & 1.000 & \\ 0.917 & 0.890 & 1.000. \end{matrix}$$

For Example 20.6, the r_s matrix would be

$$\begin{matrix} 1.000 & & \\ 0.771 & 1.000 & \\ 0.771 & 0.886 & 1.000. \end{matrix}$$

Denoting the mean of r_s as $\overline{r_s}$, the relationship with W (if there are no tied ranks) is

$$W = \frac{(M - 1)\overline{r_s} + 1}{M}; \tag{20.73}$$

therefore,

$$\overline{r_s} = \frac{MW - 1}{M - 1}. \tag{20.74}$$

If there are ties, then the preceding two equations relate W_c and $(\overline{r_s})_c$ in the same fashion as W and $\overline{r_s}$ are related. While the possible range of W is 0 to 1, $\overline{r_s}$ may range from $-1/(M - 1)$ to 1. For Example 20.5, $(\overline{r_s})_c = (0.852 + 0.917 + 0.890)/3 = 0.886$, and Equation 20.73 yields $W = 0.924$. And for Example 20.6, $\overline{r_s} = 0.809$, and Equation 20.73 gives $W = 0.873$.

If $M = 2$ (i.e., there are only two variables, or rankings, being correlated, as in Examples 19.12 or 19.13), then either r_s or W might be computed; and

$$W = \frac{\overline{r_s} + 1}{2}, \tag{20.75}$$

and

$$r_s = 2W_c - 1. \tag{20.76}$$

When $M = 2$, the use of r_s is preferable, for there are more thorough tables of critical values available.

If significant concordance is concluded for each of two groups of data, we may wish to ask if the agreement within each group is the same for both groups. For example, the data in Example 20.6 are for ice cream flavor preference as assessed by girls, and we might have a similar set of data for the preference exhibited by boys of the same age for these same flavors; and if there were significant concordance among girls as well as significant agreement among boys, we might wish to ask whether the consensus among girls is the same as that among boys. A test for this purpose was presented by Schucany and Frawley (1973), with elaboration by Li and Schucany (1975). However, the hypothesis test is not always conclusive

*That is, M things taken two at a time. (See Equation 5.10.)

with regard to concordance between two groups and it has received criticism by Hollander and Sethuraman (1978), who proposed a different procedure. Serlin and Marascuilo (1983) reexamined both approaches as well as multiple comparison testing.

(d) Top-Down Concordance. Section 19.10 discussed a weighted-correlation procedure called "top-down correlation," a two-sample test allowing us to give emphasis to those items ranked high (or low). An analogous situation can occur when there are more than two groups of ranks. For example, for the data of Example 20.6 we might have desired to know whether the girls in the sampled population agree on the most favored ice-cream flavors, with our having relatively little interest in whether they agree on the least appealing flavors. As with the correlation situation, we may employ the Savage scores, S_i, of Equation 19.54 (and Table 19.1), and a concordance test statistic is

$$C_T = \frac{1}{M^2(n - S_1)}\left(\sum_{i=1}^{n} R_i^2 - M^2 n\right), \tag{20.77}$$

the significance of which may be assessed by

$$\chi_T^2 = M(n - 1)C_T, \tag{20.78}$$

by comparing it to the chi-square distribution (Appendix Table B.1) with $n - 1$ degrees of freedom (Iman and Conover, 1987). Here, n and M are as in the preceding concordance computations: Each of M groups has n ranks. R_i is the sum of the Savage scores, across the M groups, at rank position i; and S_1 is Savage score 1 (see Section 19.10). This is demonstrated in Example 20.7. In this example, it is concluded that there is agreement among the girls regarding the most tasty ice cream flavors. We could instead have asked whether there was agreement as to the least tasty flavors. This would have been done by assigning Savage scores in reverse order (i.e., $S_1 = 2.450$ assigned to rank 6, S_2 to rank 5, and so on). If this were done we would have found that $C_T = 0.8222$ and $\chi_T^2 = 12.333$, which would have resulted in a rejection of the null hypothesis of no agreement regarding the least liked flavors ($0.025 < P < 0.05$; $P = 0.030$).

EXAMPLE 20.7 Top-down Concordance, Using the Data of Example 20.6 to Ask Whether There Was Significant Agreement Among Children Regarding the Most Desirable Ice Cream Flavors. The Table of Data Shows the Savage Scores in Place of the Ranks of Example 20.6.

H_0: There is no agreement regarding the most preferred flavors.
H_A: There is agreement regarding the most preferred flavors.

	Flavors (i)					
Girl	CC	C	S	V	BP	N
1	0.367	2.450	0.950	1.450	0.617	0.167
2	0.167	1.450	0.950	2.450	0.367	0.617
3	0.167	0.950	1.450	2.450	0.617	0.367
R_i	0.701	4.850	3.350	6.350	1.601	1.151

$$C_T = \frac{1}{M^2(n - S_1)}\left(\sum_{i=1}^{n} R_i^2 - M^2 n\right)$$

$$= \frac{1}{3^2(6 - 2.450)}\left[0.701^2 + 4.850^2 + 3.350^2 + 6.350^2 + 1.601^2 + 1.151^2 - (3^2)(6)\right]$$

$$= 0.03130[79.4469 - 54] = 0.03130(25.4469) = 0.7965$$

$$\chi_T^2 = 3(6 - 1)C_T$$

$$= (15)(0.7965) = 11.948$$

$\nu = n - 1 = 5$

$\chi^2_{0.05,5} = 11.070$

Reject H_0.

$0.025 < P < 0.05 \quad [P = 0.036]$

EXERCISES

20.1. Given the following data:

$Y(g)$	X_1 (m)	X_2 (cm)	X_3 (m^2)	X_4 (cm)
51.4	0.2	17.8	24.6	18.9
72.0	1.9	29.4	20.7	8.0
53.2	0.2	17.0	18.5	22.6
83.2	10.7	30.2	10.6	7.1
57.4	6.8	15.3	8.9	27.3
66.5	10.6	17.6	11.1	20.8
98.3	9.6	35.6	10.6	5.6
74.8	6.3	28.2	8.8	13.1
92.2	10.8	34.7	11.9	5.9
97.9	9.6	35.8	10.8	5.5
88.1	10.5	29.6	11.7	7.8
94.8	20.5	26.3	6.7	10.0
62.8	0.4	22.3	26.5	14.3
81.6	2.3	37.9	20.0	0.5

(a) Fit the multiple regression model $Y = \alpha + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \beta_4 X_4$ to the data, computing the sample partial regression coefficients and Y intercept.

(b) By analysis of variance, test the hypothesis that there is no significant multiple regression relationship.

(c) If H_0 is rejected in part (b), compute the standard error of each partial regression coefficient and test each H_0: $\beta_i = 0$.

(d) Calculate the standard error of estimate and the coefficient of determination.

(e) What is the predicted mean population value of Y at $X_1 = 5.2$ m, $X_2 = 21.3$ cm, $X_3 = 19.7$ m^2, and $X_4 = 12.2$ cm?

(f) What are the 95% confidence limits for the $\hat{Y}$ of part (e)?

(g) Test the hypothesis that the mean population value of Y at the X_i's stated in part (e) is greater than 50.0 g.

20.2. Subject the data of Exercise 20.1 to a stepwise regression analysis.

20.3. Analyze the five variables in Exercise 20.1 as a multiple correlation.

(a) Compute the multiple-correlation coefficient.

(b) Test the null hypothesis that the population multiple-correlation coefficient is zero.

(c) Compute the partial correlation coefficient for each pair of variables.

(d) Determine which of the calculated partial correlation coefficients estimate population partial correlation coefficients that are different from zero.

20.4. The following values were obtained for three multiple regressions of the form $\hat{Y} = a + b_1 X_1 + b_2 X_2 + b_3 X_3$. Test the null hypothesis that each

of the three sample regressions estimates the same population regression function.

Regression	*Residual sum of squares*	*Residual degrees of freedom*
1	44.1253	24
2	56.7851	27
3	54.4288	21
All data combined	171.1372	

Each of five research papers was read by each of four reviewers. Each reviewer then ranked the quality of the five papers, as follows:

	Papers				
	1	2	3	4	5
Reviewer 1	5	4	3	1	2
Reviewer 2	4	5	3	2	1
Reviewer 3	5	4	1	2	3
Reviewer 4	5	3	2	4	1

(a) Calculate the Kendall coefficient of concordance.

(b) Test whether the rankings by the four reviewers are in agreement.

CHAPTER 21

Polynomial Regression

A specific type of multiple regression is that concerning a *polynomial* expression:

$$Y_i = \alpha + \beta_1 X_i + \beta_2 X_i^2 + \beta_3 X_i^3 + \cdots + \beta_m X_i^m + \epsilon_i, \tag{21.1}$$

a model with parameters estimated in the expression

$$\hat{Y}_i = a + b_1 X_i + b_2 X_i^2 + b_3 X_i^3 + \cdots + b_m X_i^m, \tag{21.2}$$

for which a more concise symbolism is

$$\hat{Y}_i = a + \sum_{j=1}^{m} b_j X_i^j. \tag{21.3}$$

If $m = 1$, then the polynomial regression reduces to a simple linear regression (with Equations 21.1 and 21.2 becoming Equations 17.1a and 17.8, respectively).

As shown in Example 21.1, a polynomial equation such as Equation 21.2 deals with only two variables: the dependent variable, Y, and the independent variable, X. Additional terms in the polynomial equation consist of powers of X as if they are additional independent variables. That is, Equation 21.2 may be expressed as $\hat{Y}_j = a + b_1 X_{1j} + b_2 X_{2j} + b_3 X_{3j} + \cdots + b_m X_{mj}$, where, corresponding to the terms in Equation 21.2, X_{1j} is X_j, X_{2j} is X_j^2, X_{3j} is X_j^3, and so on, and X_{mj} is X_j^m.

The highest power in a polynomial equation, m, is known as the *degree* or *order* of the equation. There may be an underlying biological relationship warranting description by a polynomial model, but this is unlikely to involve an equation with an exponent larger than 2 or 3. The more common objective of polynomial regression, especially when $m > 2$, is to obtain an equation with which to predict the population value of Y at a specified X.

Polynomial regression is discussed in greater detail in Cohen et al. (2003: Section 6.2), von Eye and Schuster (1998: Chapter 7), and some of the books noted in the introduction to Chapter 20 (e.g., Draper and Smith, 1998: Chapter 12; Glantz and Slinker, 2001: 91–96; Kutner, Nachtsheim, and Neter, 2004: Section 8.1).

21.1 POLYNOMIAL CURVE FITTING

A polynomial equation may be analyzed by submitting values of Y, X, X^2, X^3, and so on to multiple regression computer programs.* There are also computer programs

*Serious rounding errors can readily arise when dealing with powers of X_i, and these problems can often be reduced by coding (see Appendix C). A commonly recommended coding is to subtract $\overline{X}$ (i.e., to use $X_i - \overline{X}$ in place of X_i); this is known as *centering* the data (e.g., Cohen et al., 2003: Section 6.2.3; Ryan, 1997: Sections 3.2.4 and 4.2.1). Coding, such as described in Appendix C, should be attempted with rounding-error in polynomial regression.

EXAMPLE 21.1 Stepwise Polynomial Regression

The following shows the results of a polynomial-regression analysis, by forward addition of terms, of data collected from a river, where X is the distance from the mouth of the river (in kilometers) and Y is the concentration of iron in the water (in micrograms per liter).

X (km)	Y (μg/L)
1.22	40.9
1.34	41.8
1.51	42.4
1.66	43.0
1.72	43.4
1.93	43.9
2.14	44.3
2.39	44.7
2.51	45.0
2.78	45.1
2.97	45.4
3.17	46.2
3.32	47.0
3.50	48.6
3.53	49.0
3.85	49.7
3.95	50.0
4.11	50.8
4.18	51.1

$n = 19$

First, a linear regression is fit to the data ($m = 1$), resulting in

$a = 37.389$, $b = 3.1269$, and $s_b = 0.15099$.

To test H_0: $\beta = 0$ against H_A: $\beta \neq 0$, $t = \frac{b}{s_b} = 20.709$, with $\nu = 17$.

As $t_{0.05(2),17} = 2.110$, H_0 is rejected.

Then, a quadratic (second-power) regression is fit to the data ($m = 2$), resulting in

$$a = 40.302, \quad b_1 = 0.66658, \quad s_{b_1} = 0.91352$$
$$b_2 = 0.45397, \quad s_{b_2} = 0.16688.$$

To test H_0: $\beta_2 = 0$ against H_A: $\beta_2 \neq 0$, $t = 2.720$, with $\nu = 16$.

As $t_{0.05(2),16} = 2.120$, H_0 is rejected.

Then, a cubic (third-power) regression is fit to the data ($m = 3$), resulting in

$$a = 32.767, \quad b_1 = 10.411, \quad s_{b_1} = 3.9030$$
$$b_2 = -3.3868, \quad s_{b_2} = 1.5136$$
$$b_3 = 0.47011, \quad s_{b_3} = 0.18442.$$

To test H_0: $\beta_3 = 0$ against H_A: $\beta_3 \neq 0, t = 2.549$, with $\nu = 15$.
As $t_{0.05(2),15} = 2.131$, H_0 is rejected.

Then, a quartic (fourth-power) regression is fit to the data ($m = 4$), resulting in

$$\begin{aligned} a &= 6.9265, & b_1 &= 55.835, & s_{b_1} &= 12.495 \\ & & b_2 &= -31.487, & s_{b_2} &= 7.6054 \\ & & b_3 &= 7.7625, & s_{b_3} &= 1.9573 \\ & & b_4 &= -0.67507, & s_{b_4} &= 0.18076. \end{aligned}$$

To test H_0: $\beta_4 = 0$ against H_A: $\beta_4 \neq 0, t = 3.735$, with $\nu = 14$.
As $t_{0.05(2),14} = 2.145$, H_0 is rejected.

Then, a quintic (fifth-power) regression is fit to the data ($m = 5$), resulting in

$$\begin{aligned} a &= 36.239, & b_1 &= -9.1615, & s_{b_1} &= 49.564 \\ & & b_2 &= 23.387, & s_{b_2} &= 41.238 \\ & & b_3 &= -14.346, & s_{b_3} &= 16.456 \\ & & b_4 &= 3.5936, & s_{b_4} &= 3.1609 \\ & & b_5 &= -0.31740, & s_{b_5} &= 0.23467. \end{aligned}$$

To test H_0: $\beta_5 = 0$ against H_A: $\beta_5 \neq 0, t = 1.353$, with $\nu = 13$.
As $t_{0.05(2),13} = 2.160$, do not reject H_0.

Therefore, it appears that a quartic polynomial is an appropriate regression function for the data. But to be more confident, we add one more term beyond the quintic to the model (i.e., a sextic, or sixth-power, polynomial regression is fit to the data; $m = 6$), resulting in

$$\begin{aligned} a &= 157.88, & b_1 &= -330.98, & s_{b_1} &= 192.28 \\ & & b_2 &= 364.04, & s_{b_2} &= 201.29 \\ & & b_3 &= -199.36, & s_{b_3} &= 108.40 \\ & & b_4 &= 58.113, & s_{b_4} &= 31.759 \\ & & b_5 &= -8.6070, & s_{b_5} &= 4.8130 \\ & & b_6 &= 0.50964, & s_{b_6} &= 0.29560. \end{aligned}$$

To test H_0: $\beta_6 = 0$ against H_A: $\beta_6 \neq 0, t = 1.724$, with $\nu = 12$.
As $t_{0.05(2),12} = 2.179$, do not reject H_0.

In concluding that the quartic regression is a desirable fit to the data, we have $\hat{Y} = 6.9265 + 55.835X - 31.487X^2 + 7.7625X^3 - 0.67507X^4$. See Figure 21.1 for graphical presentation of the preceding polynomial equations.

that will perform polynomial regression with the input of only Y and X data (with the program calculating the powers of X instead of the user having to submit them as computer input).

The power, m, for fitting a polynomial to the data may be no greater than $n - 1$*; but m's larger than 4 or 5 are very seldom warranted.

The appropriate maximum m may be determined in one of two ways. One is the backward-elimination multiple-regression procedure of Section 20.6b. This would involve beginning with the highest-order term (the term with the largest m) in which

*If $m = n - 1$, the curve will fit perfectly to the data (i.e., $R^2 = 1$). For example, it can be observed that for two data ($n = 2$), a linear regression line ($m = 1$) will pass perfectly through the two data points; for $n = 3$, the quadratic curve from a second-order polynomial regression ($m = 2$) will fit perfectly through the three data points; and so on.

we have any interest. But, except for occasional second- or third-order equations, this m is difficult to specify meaningfully before the analysis.

The other procedure, which is more commonly used, is that of forward-selection multiple regression (Section 20.6c). A simple linear regression ($\hat{Y}_i = a + bX_i$) is fit to the data as in Figure 21.1a. Then a second-degree polynomial (known as a *quadratic* equation, $\hat{Y}_i = a + b_1X_i + b_2X_i^2$) is fit, as shown in Figure 21.1b. The next step would be to fit a third-degree polynomial (called a *cubic* equation, $\hat{Y}_i = a + b_1X_i + b_2X_i^2 + b_3X_i^3$), and the stepwise process of adding terms could continue beyond that. But at each step we ask whether adding the last term significantly improved the polynomial-regression equation. This "improvement" may be assessed by the t test for H_0: $\beta_j = 0$ (Section 20.4), where b_j, the sample estimate of β_j, is the partial-regression coefficient in the last term added.*

At each step of adding a term, rejection of H_0: $\beta = 0$ for the last term added indicates that the term significantly improves the model; and it is recommended practice that, at each step, each previous (i.e., lower-order) term is retained even if its b is no longer significant. If the H_0 is *not* rejected, then the final model might be expressed without the last term, as the equation assumed to appropriately describe the mathematical relationship between Y and X. But, as done in Example 21.1, some would advise carrying the analysis one or two terms beyond the point where the preceding H_0 is not rejected, to reduce the possibility that significant terms are being neglected inadvertently. For example, it is possible to not reject H_0: $\beta_3 = 0$, but by testing further to reject H_0: $\beta_4 = 0$. A polynomial regression may be fit through the origin using the considerations of Section 20.13.

After arriving at a final equation in a polynomial regression analysis, it may be desired to predict values of Y at a given value of X. This can be done by the procedures of Section 20.8, by which the precision of a predicted $\hat{Y}$ (expressed by a standard error or confidence interval) may also be computed. Indeed, prediction is often the primary goal of a polynomial regression (see Section 20.15) and biological interpretation is generally difficult, especially for $m > 2$.

It is very dangerous to extrapolate by predicting Y's beyond the range of the observed X's, and this is even more unwise than in the case of simple regression or other multiple regression. It should also be noted that use of polynomial regression can be problematic, especially for m larger than 2, because X_i is correlated with powers of X_i (i.e., with X_i^2, X_i^3, and so on), so the analysis may be very adversely affected by multicollinearity (Section 20.4a).

The concept of polynomial regression may be extended to the study of relationships of Y to more than one independent variable. For example, equations such as these may be analyzed by considering them to be multiple regressions:

$$\hat{Y} = a + b_1X_1 + b_2X_1^2 + b_3X_2 + b_4X_1X_2$$
$$\hat{Y} = a + b_1X_1 + b_2X_1^2 + b_3X_2 + b_4X_2^2 + b_5X_1X_2.$$

*This hypothesis may also be tested by

$$F = \frac{(\text{Regression SS for model of degree } m) - (\text{Regression SS for model of degree } m - 1)}{\text{Residual MS for the model of degree } m}, \tag{21.4}$$

with a numerator DF of 1 and a denominator DF that is the residual DF for the m-degree model, and this gives results the same as from the t test.

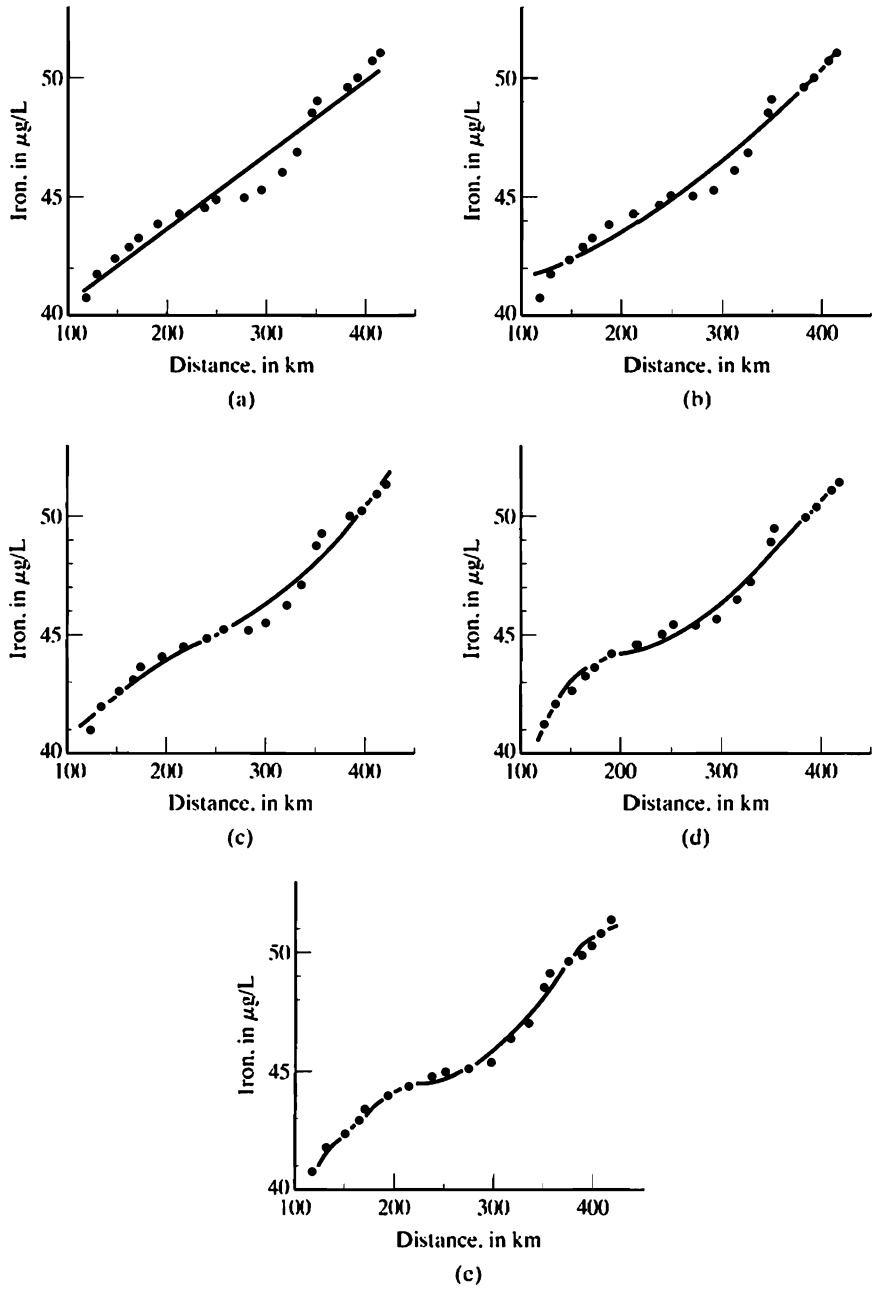

FIGURE 21.1: Fitting polynomial regression models. Each of the following regressions is fit to the 19 data points of Example 21.1. (a) Linear: $\hat{Y} = 37.389 + 3.1269X$. (b) Quadratic: $\hat{Y} = 40.302 + 0.66658X + 0.45397X^2$. (c) Cubic: $\hat{Y} = 32.767 + 10.411X - 3.3868X^2 + 0.47011X^3$. (d) Quartic: $\hat{Y} = 6.9265 + 55.835X - 31.487X^2 + 7.7625X^3 - 0.67507X^4$. (e) Quintic $\hat{Y} = 36.239 - 9.1615X + 23.387X^2 - 14.346X^3 + 3.5936X^4 - 0.31740X^5$. The stepwise analysis of Example 21.1 concludes that the quartic equation provides the appropriate fit; that is, the quintic expression does not provide a significant improvement in fit over the quartic.

In these examples, the term X_1X_2 represents interaction between the two independent variables. Because there is more than one independent variable, there is no clear sequence of adding one term at a time in a forward-selection procedure, and some other method (such as in Section 20.6e) would have to be employed to strive for the best set of terms to compose the multiple-regression model.

QUADRATIC REGRESSION

The most common polynomial regression is the second-order, or *quadratic*, regression:

$$Y_i = \alpha + \beta_1 X_i + \beta_2 X_i^2 + \epsilon_i \tag{21.5}$$

with three population parameters, α, β_1, and β_2, to be estimated by three regression statistics, a, b_1, and b_2, respectively, in the quadratic equation

$$\hat{Y}_i = a + b_1 X_i + b_2 X_i^2. \tag{21.6}$$

The geometric shape of the curve represented by Equation 21.6 is a *parabola.* An example of a quadratic regression line is shown in Figure 21.2. If b_2 is negative as shown in Figure 21.2, the parabola will be concave downward. If b_2 is positive (as shown in Figure 21.1b), the curve will be concave upward. Therefore, one-tailed hypotheses may be desired: Rejection of H_0: $\beta_2 \geq 0$ would conclude a parabolic relationship in the population that is concave downward ($\beta_2 < 0$), and rejecting H_0: $\beta_2 \leq 0$ would indicate the curve is concave upward in the population ($\beta_2 > 0$).

(a) Maximum and Minimum Values of Y_i. A common interest in polynomial regression analysis, especially where $m = 2$ (quadratic), is the determination of a maximum or minimum value of Y_i (Bliss 1970: Section 14.4; Studier, Dapson, and Bigelow, 1975). A maximum value of Y_i is defined as one that is greater than those Y_i's that are close to it; and a minimum Y_i is one that is less than the nearby Y_i's. If, in a quadratic regression (Equation 21.6), the coefficient b_2 is negative, then there will be a maximum, as shown in Figure 21.2. If b_2 is positive, there will be a minimum (as is implied in Figure 21.1b). It may be desired to determine what the maximum or minimum value of Y_i is and what the corresponding value of X_i is.

The maximum or minimum of a quadratic equation is at the following value of the independent variable:

$$\hat{X}_0 = \frac{-b_1}{2b_2}. \tag{21.7}$$

Placing $\hat{X}_0$ in the quadratic equation (Equation 21.6), we find that

$$\hat{Y}_0 = a - \frac{b_1^2}{4b_2}. \tag{21.8}$$

Thus, in Figure 21.2, the maximum is at

$$\hat{X}_0 = \frac{-17.769}{2(-7.74286)} = 1.15 \text{ hr},$$

at which

$$\hat{Y}_0 = 1.39 - \frac{(17.769)^2}{4(-7.74286)} = 11.58 \text{ mg/100 ml}.$$

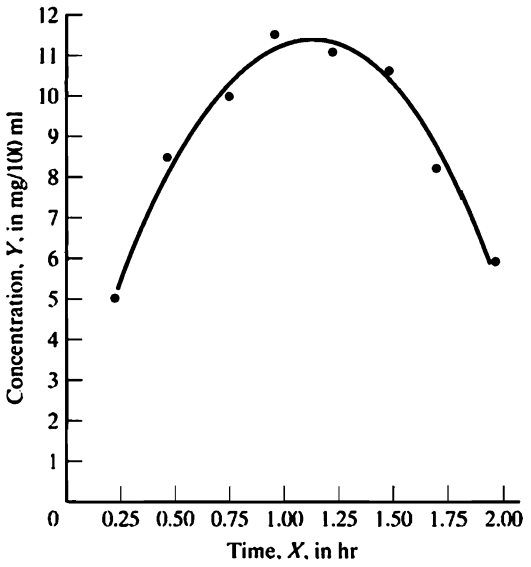

FIGURE 21.2: Quadratic fit to eight data points resulting in the equation $\hat{Y}_i = 1.39 + 17.769X_i - 7.74286X_i^2$.

A confidence interval for a maximum or minimum $\hat{Y}_0$ may be computed by the procedures of Section 20.8.

EXERCISES

21.1. The following measurements are the concentrations of leaf stomata (in numbers of stomata per square millimeter) and the heights of leaves above the ground (in centimeters). Subject the data to a polynomial regression analysis by stepwise addition of terms.

Y	X
(number/mm^2)	(cm)
4.5	21.4
4.4	21.7
4.6	22.3
4.7	22.9
4.5	23.2
4.4	23.8
4.5	24.8
4.2	25.4
4.4	25.9
4.2	27.2
3.8	27.4
3.4	28.0
3.1	28.9
3.2	29.2
3.0	29.8

21.2. Consider the following data, where X is temperature (in degrees Celsius) and Y is the concentration of a mineral in insect hemolymph (in millimoles per liter).

X	Y
(°C)	(mmole/L)
3.0	2.8
5.0	4.9
8.0	6.7
14.0	7.6
21.0	7.2
25.0	6.1
28.0	4.7

(a) Fit a quadratic equation to these data.
(b) Test for significance of the quadratic term.
(c) Estimate the mean population value of $\hat{Y}_i$ at $X_i = 10.0°C$ and compute the 95% confidence interval for the estimate.
(d) Determine the values of X and Y at which the quadratic function is maximum.

CHAPTER 22

Testing for Goodness of Fit

This chapter and the next concentrate on some statistical methods designed for use with nominal-scale data. As nominal data are counts of items or events in each of several categories, procedures for their analysis are sometimes referred to as *enumeration statistical methods*. This chapter deals with methods that address how well a sample of observations from a population of data conforms to the population's distribution of observations expressed by a null hypothesis. These procedures, which compare frequencies in a sample to frequencies hypothesized in the sampled population, are called *goodness-of-fit tests*. In testing such hypotheses, the widely used chi-square statistic* (χ^2) will be discussed, as will the more recently developed log-likelihood ratio introduced in Section 22.7. Goodness of fit for ordered categories (as contrasted with nominal-scale categories) is addressed by the Kolmogorov-Smirnov test of Section 22.8 or by the Watson test of Section 27.5.

*The symbol for chi-square is χ^2, where the Greek lowercase letter chi (χ) is pronounced as the "ky" in "sky" (see Appendix A). Some authors use the notation X^2 instead of χ^2, which avoids employing a Greek letter for something other than a population parameter; but this invites confusion with the designation of X^2 as the square of an observation, X; so the symbol χ^2 will be used in this book. Karl Pearson (1900) pioneered the use of this statistic for goodness-of-fit analysis, and David (1995) credits him with the first use of the terms *chi-squared* and *goodness of fit* at that time. Pearson and R. A Fisher subsequently expanded the theory and application of chi-square (Lancaster, 1969: Chapter 1). *Chi-squared* is the term commonly preferred to *chi-square* by British writers.

Karl Pearson (1857–1936) was a remarkable British mathematician. Walker (1958) notes that Pearson has been referred to as "the founder of the science of statistics"; she called Pearson's development of statistical thinking and practice "an achievement of fantastic proportions" and said of his influence on others: "Few men in all the history of science have stimulated so many other people to cultivate and enlarge the fields they had planted." Karl Pearson, Walter Frank, and Francis Galton founded the British journal *Biometrika*, which was first issued in October 1901 and which still influences statistics in many areas. Pearson edited this journal for 35 years, succeeded for 30 years by his son, Egon Sharpe Pearson, himself a powerful contributor to statistical theory and application (see Bartlett, 1981).

CHI-SQUARE GOODNESS OF FIT FOR TWO CATEGORIES

It is often desired to obtain a sample of nominal scale data and to infer whether the population from which it came conforms to a specified distribution. For example, a plant geneticist might raise 100 progeny from a cross that is hypothesized to result in a 3:1 phenotypic ratio of yellow-flowered to green-flowered plants. Perhaps this sample of 100 is composed of 84 yellow-flowered plants and 16 green-flowered plants, although the hypothesis indicates an expectation of 75 yellow- and 25 green-flowered plants. The sampled population is the flower colors of all possible offspring from parent plants of the kind used in the experiment. The question of interest, then, is whether the observed frequencies (84 and 16) deviate significantly from the frequencies (75 and 25) expected from sampling this population.

The following chi-square statistic may be used as a measure of how much an observed sample distribution of nominal-scale data differs from a hypothesized distribution:

$$\chi^2 = \sum_{i=1}^{k} \frac{(f_i - \hat{f}_i)^2}{\hat{f}_i}. \qquad (22.1)^*$$

Here, f_i is the frequency (that is, the number of counts) observed in category i, $\hat{f}_i$ is the frequency expected in category i if the null hypothesis is true,† and the summation is performed over all k categories of data. For the aforementioned flower-color data, which are in two categories, Example 22.1 shows the two observed frequencies (f_1 and f_2), the two expected frequencies ($\hat{f}_1$ and $\hat{f}_2$), and the null and alternate hypotheses (H_0 and H_A). The expected frequency, $\hat{f}_i$, for each category may be calculated by multiplying the total number of observations, n, by the proportion of the total that the null hypothesis specifies for each category. Therefore, for the two flower colors in this example, $\hat{f}_1 = (100)(\frac{3}{4}) = 75$ and $\hat{f}_2 = (100)(\frac{1}{4}) = 25$.

Examining Equation 22.1 shows that larger disagreement between observed and expected frequencies (i.e., larger $f_i - \hat{f}_i$ values) will result in a larger χ^2 value. Thus, this type of calculation is referred to as a measure of *goodness of fit* (although it might better have been named a measure of "poorness of fit"). A calculated χ^2 value can be as small as zero, in the case of a perfect fit (i.e., each f_i value equals its corresponding $\hat{f}_i$), or very large if the fit is very bad; it can never be a negative value.

It is fundamentally important to appreciate that the chi-square statistic is calculated using the actual frequencies observed. It is not valid to convert the data to percentages

*Equation 22.1 can be rewritten as

$$\chi^2 = \sum_{i=1}^{k} \frac{f_i^2}{\hat{f}_i} - n. \qquad (22.2)$$

where n is the sum of all the f_i's, namely the total number of observations in the sample. Although this formula renders the calculation of χ^2 a little easier, it has the disadvantage of not enabling us to examine each contribution to χ^2 [i.e., each $(f_i - \hat{f}_i)^2/\hat{f}_i$], and, as shown in Section 22.4, such an examination is an aid in determining how we might subdivide an overall chi-square analysis into component chi-square analyses for additional data collection. Thus, Equation 22.2 is seldom encountered.

†The symbol $\hat{f}$ is pronounced "f hat."

EXAMPLE 22.1 Calculation of Chi-Square Goodness of Fit, of Data Consisting of the Colors of 100 Flowers, to a Hypothesized Color Ratio of 3:1

H_0: The sample data came from a population having a 3 : 1 ratio of yellow to green flowers.

H_A: The sample data came from a population not having a 3 : 1 ratio of yellow to green flowers.

The data recorded are the 100 observed frequencies, f_i, in each of the two flower-color categories, with the frequencies expected under the null hypothesis, $\hat{f}_i$, in parentheses.

	Category (flower color)		
	Yellow	*Green*	*n*
f_i	84	16	100
$(\hat{f}_i)$	*(75)*	*(25)*	

Degrees of freedom $= \nu = k - 1 = 2 - 1 = 1$

$$\chi^2 = \sum \frac{(f_i - \hat{f}_i)^2}{\hat{f}_i} = \frac{(84 - 75)^2}{75} + \frac{(16 - 25)^2}{25}$$

$$= \frac{9^2}{75} + \frac{9^2}{25}$$

$$= 1.080 + 3.240$$

$$= 4.320$$

$\chi^2_{0.05,1} = 3.841$

Therefore, reject H_0.

$$0.025 < P < 0.05 \quad [P = 0.038]$$

An improved procedure is presented in Section 22.2 (Example 22.2).

and attempt to submit the percentages to Equation 22.1. An additional consideration in calculating chi-square is described in Section 22.2.

Critical values of χ^2 are given in Appendix Table B.1. For chi-square goodness-of-fit testing, the degrees of freedom, ν, are $k - 1$, so in the present example $\nu = 2 - 1 = 1$, and the first line of Appendix Table B.1 is consulted to decide whether the null hypothesis, H_0, should be rejected. As in most hypothesis testing, a calculated χ^2 greater than or equal to the critical value causes rejection of H_0.

In Example 22.1, χ^2 is calculated to be 4.320 and the critical value is $\chi^2_{0.05,1} = 3.841$. This means that the probability of obtaining a sample of data diverging at least this far from the hypothesized distribution, *if* the null hypothesis is true, is less than 0.05. Therefore, if testing is being performed at the 5% significance level, H_0 is rejected and declared not to be a true statement about the distribution of flower colors in the sampled population. Indeed, examination of the first line of Appendix Table B.1

indicates that this probability lies between 0.025 and 0.05 (which we can express as $0.025 < P < 0.05$).*

The numbers of items in the two categories may be expressed as proportions (or percentages): In Example 22.1, yellow-flowered plants compose 0.84 (i.e., 84%) of the sample, and 0.16 (i.e., 16%) are green flowered. Confidence intervals for such proportions are discussed in Section 24.8.

CHI-SQUARE CORRECTION FOR CONTINUITY

Chi-square values obtained from actual data, using Equation 22.1, belong to a discrete, or discontinuous, distribution, in that they can take on only certain values. For instance, in Example 22.1 we calculated a chi-square value of 4.320 for $f_1 = 84, f_2 = 16, \hat{f}_1 = 75$, and $\hat{f}_2 = 25$. If we had observed $f_1 = 83$ and $f_2 = 17$, the calculated chi-square value would have been $(83 - 75)^2/75 + (17 - 25)^2/25 = 0.8533 + 2.5600 = 3.413$; for $f_1 = 82$ and $f_2 = 18, \chi^2 = 2.613$; and so on. These chi-square values obviously form a discrete distribution, for results between 4.320 and 3.413 or between 3.413 and 2.613 are not possible with the given $\hat{f}_i$ values. However, the theoretical χ^2 distribution, from which Appendix Table B.1 is derived, is a continuous distribution; that is, for example, all values of χ^2 between 2.613 and 4.320 are possible. Thus, our need to determine the probability of a calculated χ^2 can be met only approximately by consulting Appendix Table B.1, and our conclusions are not taking place exactly at the level of α which we set. This situation would be unfortunate were it not for the fact that the approximation is a very good one, except when $\nu = 1$ (and in the instances described in Section 22.5). In the case of $\nu = 1$, it is usually recommended to use the *Yates correction for continuity* (Yates, 1934),† where the absolute value of each deviation of f_i from $\hat{f}_i$ is reduced by 0.5. That is,

$$\chi_c^2 = \sum_{i=1}^{2} \frac{(|f_i - \hat{f}_i| - 0.5)^2}{\hat{f}_i}, \tag{22.3}$$

where χ_c^2 denotes the chi-square value calculated with the correction for continuity.

This correction is demonstrated in Example 22.2, which presents the determination of χ_c^2 for the data of Example 22.1. For this example, the use of χ_c^2 yields the same conclusion as is arrived at without the correction for continuity, but this will not always be the case. Without the continuity correction, the calculated χ^2 may be inflated enough to cause us to reject H_0, whereas the corrected χ_c^2 value might not. In other words, not correcting for continuity may cause us to commit the Type I error with a probability greater than the stated α. The Yates correction should routinely be used when $\nu = 1$; it is not applicable for $\nu > 1$. For very large n, the effect of discontinuity is small, even for $\nu = 1$, and in such cases the Yates correction will

*Some calculators and computer programs have the capability of determining the exact probability of a given χ^2. For the present example, we would thereby find that $P(\chi^2 \geq 4.320) = 0.038$.

†Although English statistician Frank Yates (1902–1994) deserves the credit for suggesting this correction for chi-square testing, it had previously been employed in other statistical contexts (Pearson, 1947). R. A. Fisher associated it with Yates's name in 1936 (David, 1995). This was one of many important contributions Yates made over a distinguished 59-year publishing career, and he was also one of the earliest users of electronic computers to summarize and analyze data (Dyke, 1995). The correction should not be applied in the very rare situations where the numerator of χ^2 is *increased*, instead of decreased, by its use (that is, when $|f_i - \hat{f}_i| < 0.25$).

change the calculated chi-square very little. Its use remains appropriate with $\nu = 1$, however, regardless of n.

EXAMPLE 22.2 Chi-Square Goodness of Fit, Using the Yates Correction for Continuity

For the hypothesis and data of Example 22.1:

	Category (flower color)		
	Yellow	*Green*	n
f_i	84	16	100
$(\hat{f}_i)$	*(75)*	*(25)*	

$$\nu = k - 1 = 2 - 1 = 1$$

$$\chi_c^2 = \sum_{i=1}^{2} \frac{(|f_i - \hat{f}_i| - 0.5)^2}{\hat{f}_i} = \frac{(|84 - 75| - 0.5)^2}{75} + \frac{(|16 - 25| - 0.5)^2}{25}$$

$$= 0.9633 + 2.8900 = 3.853$$

$\chi^2_{0.05,1} = 3.841$.

Therefore, reject H_0.

$$0.025 < P < 0.05 \quad [P = 0.0497]$$

For $k = 2$, if H_0 involves a 1 : 1 ratio,

$$\chi^2 = \frac{(f_1 - f_2)^2}{n} \tag{22.4}$$

may be used in place of Equation 22.1, and

$$\chi_c^2 = \frac{(|f_1 - f_2| - 1)^2}{n} \tag{22.5}$$

may be used instead of Equation 22.3. In these two shortcut equations, $\hat{f}_1$ and $\hat{f}_2$ need not be calculated, thus avoiding the concomitant rounding errors.

If, when $\nu = 1$, the chi-square calculation is performed by a computer, the user should be aware whether the continuity correction is employed.

22.3 CHI-SQUARE GOODNESS OF FIT FOR MORE THAN TWO CATEGORIES

Example 22.1 demonstrated chi-square goodness-of-fit testing when there are two categories of data (i.e., $k = 2$). This kind of analysis may be extended readily to sets of data with larger numbers of categories, as Example 22.3 exemplifies. Here, 250 plants were examined ($n = 250$), and their seeds were classified into four categories ($k = 4$). The calculated χ^2, using Equation 22.1, is 8.972. (This book will routinely express a calculated chi-square to at least three decimal places, for that is the accuracy of the table of critical values, Appendix Table B.1. Therefore, to help avoid rounding errors, intermediate calculations, including those of $\hat{f}_i$, will be performed to four or more decimal places.)

EXAMPLE 22.3 Chi-square Goodness of Fit for $k = 4$

H_0: The sample comes from a population having a 9 : 3 : 3 : 1 ratio of yellow-smooth to yellow-wrinkled to green-smooth to green-wrinkled seeds.

H_A: The sample comes from a population not having a 9 : 3 : 3 : 1 ratio of the above four seed phenotypes.

The sample data are recorded as observed frequencies, f_i, with the frequencies expected under the null hypothesis, $\hat{f}_i$, in parentheses.

	Yellow smooth	*Yellow wrinkled*	*Green smooth*	*Green wrinkled*	n
f_i	152	39	53	6	250
$(\hat{f}_i)$	*(140.6250)*	*(46.8750)*	*(46.8750)*	*(15.6250)*	

$$\nu = k - 1 = 3$$

$$\chi^2 = \frac{11.3750^2}{140.6250} + \frac{7.8750^2}{46.8750} + \frac{6.1250^2}{46.8750} + \frac{9.6250^2}{15.6250}$$

$$= 0.9201 + 1.3230 + 0.8003 + 5.9290$$

$$= 8.972$$

$\chi^2_{0.05,3} = 7.815$

Therefore, reject H_0.

$$0.025 < P < 0.05 \quad [P = 0.030]$$

It has already been pointed out that larger χ^2 values will result from larger differences between f_i and $\hat{f}_i$, but large calculated χ^2 values may also simply be the result of a large number of classes of data, because the calculation involves the summing over all classes. Thus, in considering the significance of a calculated χ^2, the value of k must be taken into account. What is done is to consider the degrees of freedom* (ν). For the chi-square goodness-of-fit testing discussed in this chapter, $\nu = k - 1$. Thus, in Example 22.3 $\nu = 4 - 1 = 3$, while the calculated χ^2 is 8.972. Entering Appendix Table B.1 in the row for $\nu = 3$, it is seen that $P(\chi^2 \geq 7.815) = 0.05$ and $P(\chi^2 \geq 9.348) = 0.025$. Therefore, $0.025 < P(\chi^2 \geq 8.972) < 0.05$; and, if testing at the 5% significance level, we would reject the null hypothesis that the sample came from a population having a 9 : 3 : 3 : 1 ratio of yellow-smooth to yellow-wrinkled to green-smooth to green-wrinkled seeds. The tabled critical values may be denoted as $\chi^2_{\alpha,\nu}$; thus, for example, we can write $\chi^2_{0.05,3} = 7.815$ and $\chi^2_{0.025,3} = 0.348$.

When we say the degrees of freedom are $k - 1$, we are stating that, given the frequencies in any $k - 1$ of the categories, we can determine the frequency in the remaining category. This is so because n is known, and the sum of the frequencies in all k categories equals n. In other words, there is "freedom" to assign frequencies to only $k - 1$ categories. It may also be noted that the degrees of freedom are k minus

*This term was introduced by R. A. Fisher, in 1922, while discussing contingency tables (see Chapter 23) (David, 1995).

the number of sample constants used to calculate the expected frequencies. In the present examples, only one constant, n, was so used, so $\nu = k - 1$.

22.4 SUBDIVIDING CHI-SQUARE GOODNESS OF FIT

In Example 22.3, the chi-square analysis detected a difference between the observed and expected frequencies too great to be attributed to chance, and the null hypothesis was rejected. This conclusion may be satisfactory in some instances, but in many cases the investigator will wish to perform further analysis.

For the example under consideration, the null hypothesis is that the sample came from a population having a 9 : 3 : 3 : 1 phenotypic ratio. If the chi-square analysis had not led to a rejection of the hypothesis, we would proceed no further. But since H_0 was rejected, we may wish to ask whether the significant disagreement between observed and expected frequencies was concentrated in certain of the categories, or whether the difference was due to the effects of the data in all of the classes. The four individual contributions to the chi-square value are 0.9201, 1.3230, 0.8003, and 5.9290; and the contribution resulting from the last class (the green-wrinkled seeds) contributes a relatively large amount to the size of the calculated χ^2. Thus we see that the nonconformity of the sample frequencies to those expected from a population with a 9 : 3 : 3 : 1 ratio is due largely to the magnitude of the discrepancy between f_4 and $\hat{f}_4$.

This line of thought can be examined as shown in Example 22.4. First, we test H_0: f_1, f_2, and f_3 came from a population having a 9:3:3 ratios with H_A: The frequencies in the first three categories came from a population having a phenotypic ratio other than 9 : 3 : 3. This null hypothesis is not rejected, indicating that the frequencies in the first three categories conform acceptably well to those predicted by H_0. Then we can test the frequency of green-wrinkled seeds against the combined frequencies for the other three phenotypes, under the null hypothesis of a 1 : 15 ratio. The calculated χ^2 value causes us to reject this hypothesis, however, and we draw the conclusion that the nonconformity of the data in Example 22.3 to the hypothesized frequencies is due primarily to the observed frequency of green-wrinkled seeds. In the latter hypothesis test, χ^2_c is employed instead of χ^2 because $\nu = 1$.

EXAMPLE 22.4 Chi-Square Goodness of Fit, Subdividing the Chi-Square Analysis of Example 22.3

H_0: The sample came from a population with a 9 : 3 : 3 ratio of the first three phenotypes in Example 22.2.

H_A: The sample came from a population not having a 9 : 3 : 3 ratio of the first three phenotypes in Example 22.2.

	Seed Characteristics			
	Yellow smooth	*Yellow wrinkled*	*Green smooth*	n
f_i	152	39	53	244
$(\hat{f}_i)$	*(146.4000)*	*(48.8000)*	*(48.8000)*	

$\nu = k - 1 = 2$

$$\chi^2 = \frac{5.6000^2}{146.4000} + \frac{-9.8000^2}{48.8000} + \frac{4.2000^2}{48.8000}$$
$$= 0.2142 + 1.9680 + 0.3615$$
$$= 2.544$$

$\chi^2_{0.05,2} = 5.991$

Therefore, do not reject H_0.

$$0.25 < P < 0.50 \quad [P = 0.28]$$

H_0: The sample came from a population with a 1 : 15 ratio of green-wrinkled to other seed phenotypes.

H_A: The sample came from a population not having the 1 : 15 ratio stated in H_0.

	Seed Characteristics		
	Green wrinkled	*Others*	n
f_i	6	244	250
$(\hat{f}_i)$	*(15.6250)*	*(234.3750)*	

$\nu = k - 1 = 1$

$$\chi^2_c = \sum_{i=1}^{2} \frac{(|f_i - \hat{f}_i| - 0.5)^2}{\hat{f}_i} = \frac{(9.6250 - 0.5)^2}{15.6250} + \frac{(9.6250 - 0.5)^2}{234.3750}$$
$$= 5.3290 + 0.3553 = 5.684$$

$\chi^2_{0.05,1} = 3.841$

Therefore, reject H_0.

$$0.01 < P < 0.025 \quad [P = 0.017]$$

Note: It is not proper to test statistical hypotheses that were stated *after* examining the data to be tested. Therefore, the analyses described in this section should be considered only a guide to developing hypotheses that subdivide a goodness-of-fit analysis. And the newly proposed hypotheses should then be stated in advance of their being tested with a new set of data.

CHI-SQUARE GOODNESS OF FIT WITH SMALL FREQUENCIES

In order for us to assign a probability to the results of a chi-square goodness-of-fit test, and thereby assess the statistical significance of the test, the calculated χ^2 must be a close approximation to the theoretical distribution that is summarized in Appendix Table B.1. This approximation is quite acceptable as long as the expected frequencies are not too small. If $\hat{f}_i$ values are very small, however, the calculated χ^2 is biased in that it is larger than the theoretical χ^2 it is supposed to estimate, and there is a tendency to reject the null hypothesis with a probability greater than α. This is

undesirable, and statisticians have attempted to define in a convenient manner what would constitute $\hat{f}_i$'s that are "too small."

For decades a commonly applied general rule was that no expected frequency should be less than 5.0,* even though it has long been known that it is tolerable to have a few $\hat{f}_i$'s considerably smaller than that (e.g., Cochran, 1952, 1954). By a review of previous recommendations and an extensive empirical analysis, Roscoe and Byars (1971) reached conclusions that provide less restrictive guidelines for chi-square goodness-of-fit testing. They and others have found that the test is remarkably robust when testing for a uniform distribution—that is, for H_0: In the population, the frequencies in all k categories are equal—in which case $\hat{f}_i = n/k$. In this situation, it appears that it is acceptable to have expected frequencies as small as 1.0 for testing at α as small as 0.05, or as small as 2.0 for α as small as 0.01. The chi-square test works nearly as well when there is moderate departure from a uniform distribution in H_0, and the average expected frequencies may be as small as those indicated for a uniform distribution. And even with great departure from uniform, it appears that the average expected frequency (i.e., n/k) may be as small as 2.0 for testing at α as low as 0.05 and as small as 4.0 for α as small as 0.01. Koehler and Larntz (1980) suggested that the chi-square test is applicable for situations where $k \geq 3, n \geq 10$, and $n^2/k \geq 10$. Users of goodness-of-fit testing can be comfortable if their data fit both the Roscoe and Byars and the Koehler and Larntz guidelines. These recommendations are for situations where there are more than two categories. If $k = 2$, then it is wise to have $\hat{f}_i$'s of at least 5.0, or to use the binomial test as indicated in the next paragraph.

The chi-square calculation can be employed if the data for the classes with offensively low $\hat{f}_i$ values are simply eliminated from H_0 and the subsequent analysis. Or, certain of the classes of data might be meaningfully combined so as to result in all $\hat{f}_i$ values being large enough to proceed with the analysis. Such modified procedures are not to be recommended as routine practice, however. Rather, the experimenter should strive to obtain a sufficiently large n for the analysis to be performed. When $k = 2$ and each f_i is small, the use of the binomial test (Section 24.5) is preferable to chi-square analysis. [Similarly, use of the multinomial, rather than the binomial, distribution is appropriate when $k > 2$ and the f_i's are small; however, this is a tedious procedure and will not be demonstrated here (Radlow and Alf, 1975).]

22.6 HETEROGENEITY CHI-SQUARE TESTING FOR GOODNESS OF FIT

It is sometimes the case that a number of sets of data are being tested against the same null hypothesis, and we wish to decide whether we may combine all of the sets in order to perform one overall chi-square analysis. As an example, let us examine some of the classic data of Gregor Mendel†(1865). In one series of 10 experiments,

*Some statisticians have suggested lower limits as small as 1.0 and others recommend limits as large as 20.0 (as summarized by Cressie and Read, 1989; Tate and Hyer, 1973), with lower $\hat{f}_i$'s acceptable in some cases where the $\hat{f}_i$'s are all equal.

†Born Johann Mendel (1822–1884), he was an Augustinian monk (taking the name *Gregor* when entering the monastery), an Austrian schoolteacher, and a pioneer in biological experimentation and its quantitative analysis—although his data have been called into question by statisticians (Edwards, 1986; Fisher, 1936). His research was unappreciated until sixteen years after his death.

Mendel obtained pea plants with either yellow or green seeds, with the frequency of yellow-seed plants and green-seed plants shown in Example 22.5.* The data from each of the 10 samples are tested against the null hypothesis that there is a 3-to-1 ratio of plants with yellow seeds to plants with green seeds in the population from which the sample came. H_0 is not rejected in any of the 10 experiments, so it is reasonable to test a null hypothesis examining heterogeneity, that all 10 samples could have come from the same population (or from more than one population having the same ratios). This new hypothesis may be tested by the procedure called *heterogeneity chi-square* analysis (sometimes referred to as "interaction" chi-square analysis or even "homogeneity analysis"). In addition to performing the 10 separate chi-squares tests, we total all 10 f_i values and total all 10 $\hat{f}_i$ values and perform a chi-square test on these totals. But in totaling these values, commonly called *pooling* them, we must assume that all ten samples came from the same population (or from populations having identical seed-color ratios). If this assumption is true, we say that the samples are *homogeneous*. If this assumption is false, the samples are said to be *heterogeneous*, and the chi-square analysis on the pooled data would not be justified. So we are faced with the desirability of testing for heterogeneity, using the null hypothesis that the samples could have come from the same population (i.e., H_0: The samples are homogeneous).

Testing for heterogeneity among replicated goodness-of-fit tests is based on the fact that the sum of chi-square values is itself a chi-square value. If the samples are indeed homogeneous, then the total of the individual chi-square values should be close to the chi-square for the total frequencies. In Example 22.5, the total chi-square is 7.1899, with a total of 10 degrees of freedom; and the chi-square of the totals is 0.1367, with 1 degree of freedom. The absolute value of the difference between these two chi-squares is itself a chi-square (called the *heterogeneity chi-square*), 7.053, with $\nu = 10 - 1 = 9$.

Consulting Appendix Table B.1, we see that for the heterogeneity chi-square, $\chi^2_{0.05,9} = 16.9$, so H_0 is not rejected. Thus we conclude that the 10 samples could have come from the same population and that their frequencies might justifiably be pooled. The Yates correction for continuity may not be applied in a heterogeneity chi-square analysis (Cochran, 1942; Lancaster, 1949). But if we conclude that the sample data may be pooled, we should then analyze these pooled data using the correction for

EXAMPLE 22.5 Heterogeneity Chi-Square Analysis

The data are the number of pea plants with yellow seeds and the number with green seeds, in each of 10 plant-breeding experiments.

The null hypothesis for each experiment is that the population sampled has a 3 : 1 ratio of plants with yellow seeds to plants with green seeds.

The null hypothesis for the heterogeneity chi-square test is that all 10 samples of data came from the same population (or from populations with the same ratios).

For each experiment, the observed frequencies, f_i, are given, with the frequencies, $\hat{f}_i$, predicted by the null hypothesis within parentheses.

*These ten data sets come from what Mendel (1865) collectively called "Experiment 2," in which, he reports, "258 plants yielded 8023 seeds, 6022 yellow and 2001 green; their ratio, therefore, is 3.01 : 1." (He was expressing that 6022/2001 = 3.01.)

Experiment	*Plants with yellow seeds*	*Plants with green seeds*	*Total plants* (n)	*Uncorrected chi-square**	ν
1	25	11	36	0.5926	1
	(27.0000)	*(9.0000)*			
2	32	7	39	1.0342	1
	(29.2500)	*(9.7500)*			
3	14	5	19	0.0175	1
	(14.2500)	*(4.7500)*			
4	70	27	97	0.4158	1
	(72.7500)	*(24.2500)*			
5	24	13	37	2.0270	1
	(27.7500)	*(9.2500)*			
6	20	6	26	0.0513	1
	(19.5000)	*(6.5000)*			
7	32	13	45	0.3630	1
	(33.7500)	*(11.2500)*			
8	44	9	53	1.8176	1
	(39.7500)	*(13.2500)*			
9	50	14	64	0.3333	1
	(48.0000)	*(16.0000)*			
10	44	18	62	0.5376	1
	(46.5000)	*(15.5000)*			
Total of chi-squares				7.1899	10
Chi-square of totals (i.e., pooled chi-square)	355 *(358.5000)*	123 *(119.5000)*	478	0.1367	1
Heterogeneity chi-square				7.0532	9

$\chi^2_{0.05,9} = 16.919$.
Do not reject the homogeneity null hypothesis. $0.50 < P < 0.75$ [$P = 0.63$]

* In heterogeneity analysis, chi-square is computed *without* correction for continuity.

Pooled chi-square with continuity correction: $\chi^2_c = 0.1004$ and $\chi^2_{0.05,1} = 3.841$.
Do not reject H_0 of 3 : 1 ratio. $0.50 < P < 0.75$ [$P = 0.75$]

continuity. Thus, for Example 22.5, $\chi^2_c = 0.128$, rather than $\chi^2 = 0.137$, should be used, once it has been determined that the samples are homogeneous and the data may be pooled. Heterogeneity testing may also be done using the log-likelihood statistic, G (Section 22.7), instead of χ^2.

Example 22.6 demonstrates how we can be misled by pooling heterogeneous samples without testing for acceptable homogeneity. If the six samples shown were pooled and a chi-square computed ($\chi^2 = 0.2336$), we would not reject the null hypothesis. But such a procedure would have ignored the strong indication obtainable

EXAMPLE 22.6 Hypothetical Data for Heterogeneity Chi-Square Analysis, Demonstrating Misleading Results from the Pooling of Heterogeneous Samples

H_0: The sample population has a 1 : 1 ratio of right- to left-handed men.

H_A: The sampled population does not have a 1 : 1 ratio of right- to left-handed men.

Sample frequencies observed, f_i, are listed, with the frequencies predicted by H_0 ($\hat{f}_i$) in parentheses.

Sample	*Right-handed*	*Left-handed*	*n*	*Uncorrected chi-square*	*ν*
1	3 *(7.0000)*	11 *(7.0000)*	14	4.5714	1
2	4 *(8.0000)*	12 *(8.0000)*	16	4.0000	1
3	5 *(10.0000)*	15 *(10.0000)*	20	5.0000	1
4	14 *(9.0000)*	4 *(9.0000)*	18	5.5556	1
5	13 *(8.5000)*	4 *(8.5000)*	17	4.7647	1
6	17 *(11.0000)*	5 *(11.0000)*	22	6.5455	1
Total of chi-squares				30.4372	6
Chi-square of totals (i.e., pooled chi-square)	56 *(53.5000)*	51 *(53.5000)*	107	0.2336	1
Heterogeneity chi-square				30.2036	5

$\chi^2_{0.05,5} = 11.070.$

Reject H_0 for homogeneity. $P < 0.001$ [$P = 0.000013$]

Therefore, we are not justified in performing a goodness-of-fit analysis on the pooled data.

from the heterogeneity analysis ($P < 0.001$) that the samples came from more than one population. The appearance of the data in this example suggests that Samples 1, 2, and 3 came from one population, and Samples 4, 5, and 6 came from another, possibilities that can be reexamined with new data.

It is also important to realize that the pooling of homogeneous data can, in some cases, result in a more powerful analysis. Example 22.7 presents hypothetical data for four replicate chi-square analyses. None of the individual chi-square tests detects a significant deviation from the null hypothesis; but on pooling them, the chi-square test performed on the larger number of data does reject H_0. The nonsignificant

EXAMPLE 22.7 Hypothetical Data for Heterogeneity Chi-Square Analysis, Demonstrating How Nonsignificant Sample Frequencies Can Result in Significant Pooled Frequencies

For each sample, and for the pooled sample:

H_0: The sampled population has equal frequencies of right- and left-handed men.

H_A: The sampled population does not have equal frequencies of right- and left-handed men.

For heterogeneity testing:

H_0: All the samples came from the same population.

H_A: The samples came from at least two different populations.

For each sample, the observed frequencies, f_i, are given, together with the expected frequencies, $\hat{f}_i$, in parentheses.

Sample	*Right-handed*	*Left-handed*	n	*Uncorrected chi-square*	ν
1	15 *(11.0000)*	7 *(11.0000)*	22	2.9091	1
2	16 *(12.0000)*	8 *(12.0000)*	24	2.6667	1
3	12 *(8.5000)*	5 *(8.5000)*	17	2.8824	1
4	13 *(9.0000)*	5 *(9.0000)*	18	3.5556	1
Total of chi-squares				12.0138	4
Chi-square of totals (pooled chi-square)	56 *(40.5000)*	25 *(40.5000)*	81	11.8642	1
Heterogeneity chi-square				0.1496	3

$\chi^2_{0.05,3} = 7.815$.

The homogeneity H_0 is not rejected. $0.975 < P < 0.99$ $[P = 0.985]$

Therefore, we are justified in pooling the four sets of data. On doing so, $\chi^2_c = 11.111$, DF = 1, $P = 0.00086$, H_0 is rejected.

heterogeneity chi-square shows that we are justified in pooling the replicates in order to analyze a single set of data with a large n.

22.7 THE LOG-LIKELIHOOD RATIO FOR GOODNESS OF FIT

The *log-likelihood ratio* is applicable to goodness-of-fit analysis in circumstances having data for which chi-square may be employed. The log-likelihood ratio,*

*Proposed by Wilks (1935), based upon concepts of Neyman and Pearson (1928a, 1928b). This procedure, often referred to simply as the *likelihood ratio* (abbreviated LR), considers the ratio between two likelihoods (i.e., probabilities). Referring to Example 22.3, one likelihood is the likelihood of the population containing the same proportions that the sample has of the data

$\sum f_i \ln(f_i/\hat{f}_i)$, may also be written as $\sum f_i \ln f_i - \sum f_i \ln \hat{f}$. Twice this quantity, a value called G, approximates the χ^2 distribution.* Thus†

$$G = 2\sum f_i \ln \frac{f_i}{\hat{f}_i} \quad \text{or} \quad G = 4.60517 \sum f_i \log \frac{f_i}{\hat{f}_i}, \tag{22.6}$$

or, equivalently,

$$G = 2\left[\sum f_i \ln f_i - \sum f_i \ln \hat{f}_i\right] \quad \text{or} \quad G = 4.60517\left[\sum f_i \log f_i - \sum f_i \log \hat{f}_i\right] \tag{22.7}$$

is applicable as a test for goodness of fit, utilizing Appendix Table B.1 with the same degrees of freedom as would be used for chi-square testing. Example 22.8 demonstrates the G test for the data of Example 22.3. In this case, the same conclusion is reached using G and χ^2, but this will not always be so.

EXAMPLE 22.8 Calculation of the *G* Statistic for the Log-Likelihood Ratio Goodness-of-Fit Test. The Data and the Hypotheses Are Those of Example 22.3

	Yellow smooth	*Yellow wrinkled*	*Green smooth*	*Green wrinkled*	n
f_i	152	39	53	6	250
$(\hat{f}_i)$	*(140.6250)*	*(46.8750)*	*(46.8750)*	*(15.6250)*	

$$\nu = k - 1 = 3$$

$$G = 4.60517\left[\sum f_i \log f_i - \sum f_i \log \hat{f}_i\right]$$

$$= 4.60517[(152)(2.18184) + (39)(1.59106) + (53)(1.72428) + (6)(0.77815) - (152)(2.14806) - (39)(1.67094) - (53)(1.67094) - (6)(1.19382)]$$

$$= 4.60517[331.63968 + 62.05134 + 91.38684 + 4.66890 - 326.50512 - 65.16666 - 88.55982 - 7.16292]$$

$$= 4.60517[2.35224]$$

$$= 10.832^{\ddagger}$$

$\chi^2_{0.05,3} = 7.815$

Therefore, reject H_0.

$$0.01 < P < 0.025 \quad [P = 0.013]$$

‡Using natural logarithms (see Equations 22.6 or 22.7) yields the same value of G.

in the four categories. And the other is the likelihood of the population containing the proportions, in the four categories, that are stated in the null hypothesis. The ratio of the first likelihood to the second will be larger for greater departures of population proportions from the proportions observed in the sample.

*G also appears in the literature written as G^2 and occasionally as *likelihood ratio* χ^2; it is sometimes referred to as a measure of *deviance*.

†As noted in the Section 8.7 footnote, "ln" refers to natural logarithm (in base e) and "log" to common logarithm (in base 10). Many modern calculators can employ either.

Williams (1976) recommended G be used in preference to χ^2 whenever any $|f_i - \hat{f}_i| \geq \hat{f}_i$. The two methods often yield the same conclusions, especially when n is large; when they do not, some statisticians prefer G; others recommend χ^2, for while G may result in a more powerful test in some cases, χ^2 tends to provide a test that operates much closer to the stated level of α (e.g., Chapman, 1976; Cressie and Read, 1989; Hutchinson, 1979; Larntz, 1978; Lawal, 1984; Moore, 1986; Rudas, 1986), with the probability of a Type I error often far above α when employing G.

When $\nu = 1$, the Yates correction for continuity is applied in a fashion analogous to that in chi-square analysis in Section 22.2. The procedure is to make each f_i closer to $\hat{f}_i$ by 0.5 and to apply Equation 22.7 (or Equation 22.6) using these modified f_i's. This is demonstrated in Example 22.9.

EXAMPLE 22.9 The *G* Test for Goodness of Fit for Two Categories, for the Hypotheses and Data of Example 22.1

(a) Without the Yates correction for continuity:

	Category (flower color)		
	Yellow	*Green*	n
f_i	84	16	100
$(\hat{f}_i)$	*(75)*	*(25)*	

$$\nu = k - 1 = 2 - 1 = 1$$

$$G = 4.60517[(84)(1.92428) + (16)(1.20412) - (84)(1.87506) - (16)(1.39794)]$$
$$= 4.60517[1.03336] = 4.759$$

$\chi^2_{0.05,1} = 3.841$
Therefore, reject H_0.

$$0.025 < P < 0.05 \quad [P = 0.029]$$

(b) With the Yates correction for continuity:

	Category (flower color)		
	Yellow	*Green*	n
f_i	84	16	100
$(\hat{f}_i)$	*(75)*	*(25)*	
Modified f_i	83.5	16.5	

$$\nu = k - 1 = 2 - 1 = 1$$

$$G_c = 4.60517[(83.5)(1.92169) + (16.5)(1.21748) - (83.5)(1.87506) - (16.5)(1.39794)]$$
$$= 4.60517[0.916015] \doteq 4.218$$

$\chi^2_{0.05,1} = 3.841$
Therefore, reject H_0.

$$0.025 < P < 0.05 \quad [P = 0.040]$$

KOLMOGOROV-SMIRNOV GOODNESS OF FIT

This chapter has thus far dealt with goodness-of-fit tests applicable to nominal-scale data. This section will present goodness-of-fit testing for data measured on a ratio, interval, or ordinal scale.

Example 22.10 presents data that are measurements of the height above the ground at which each of 15 moths was found on the trunk of a 25-meter-tall tree. For each height, X_i, the observed frequency is f_i, which is the number of moths found at that height. The Kolmogorov-Smirnov goodness-of-fit test (Kolmogorov, 1933; Smirnov, 1939a, 1939b), also called the Kolmogorov-Smirnov one-sample test, examines how well an observed cumulative frequency distribution conforms to an

EXAMPLE 22.10 Two-Tailed Kolmogorov-Smirnov Goodness of Fit for Continuous Ratio-Scale Data, Vertical Distribution of Moths on a Tree Trunk

H_0: Moths are distributed uniformly from ground level to height of 25 m.
H_A: Moths are not distributed uniformly from ground level to height of 25 m.

Each X_i is a height (in meters) at which a moth was observed on the tree trunk.

i	X_i	f_i	F_i	rel F_i	rel $\hat{F}_i$	D_i	D'_i
1	1.4	1	1	0.0667	0.0560	0.0107	0.0560
2	2.6	1	2	0.1333	0.1040	0.0293	0.0373
3	3.3	1	3	0.2000	0.1320	0.0680	0.0013
4	4.2	1	4	0.2667	0.1680	0.0987	0.0320
5	4.7	1	5	0.3333	0.1880	0.1453	0.0787
6	5.6	2	7	0.4667	0.2240	0.2427	0.1093
7	6.4	1	8	0.5333	0.2560	0.2773	0.2107
8	7.7	1	9	0.6000	0.3080	0.2920	0.2253
9	9.3	1	10	0.6667	0.3720	0.2947	0.2280
10	10.6	1	11	0.7333	0.4240	0.3093	0.2427
11	11.5	1	12	0.8000	0.4600	0.3400	0.2733
12	12.4	1	13	0.8667	0.4960	0.3707	0.3040
13	18.6	1	14	0.9333	0.7440	0.1893	0.1227
14	22.3	1	15	1.0000	0.8920	0.1080	0.0413

$n = 15$
$\max D_i = D_{12} = |0.8667 - 0.4960| = |0.3707| = 0.3707$
$\max D'_i = D'_{12} = |0.8000 - 0.4960| = |0.3040| = 0.3040$
$D = 0.3707$
$D_{0.05(2),15} = 0.33760$
Therefore, reject H_0.

$$0.02 < P < 0.05$$

expected frequency distribution.* (Section 1.4 introduced the concept of a cumulative frequency distribution.) The test considers how likely it is to obtain the observed data distribution at random from a population having the distribution specified in the null hypotheses.

For the test applicable to continuous data (i.e., ratio-scale or interval-scale data), the observed frequencies are arranged in ascending order and each cumulative observed frequency, F_i, is obtained as the sum of the observed frequencies from f_1 up to and including f_i. (For example, F_{10} is the sum of f_1 through f_{10}.) And from these cumulative frequencies the *cumulative relative observed frequencies* are determined as

$$\text{rel } F_i = \frac{F_i}{n}, \tag{22.8}$$

where n, which is $\sum f_i$, is the number of data in the sample. Thus, rel F_i is simply the proportion of the data that are measurements $\leq X_i$. For the data being discussed, n is 15, so, for example, rel $F_{10} = 11/15 = 0.7333$.

Then, for each X_i, the *cumulative relative expected frequency*, $\hat{F}_i$, is calculated as follows (where *expected* refers to the distribution specified in the null hypothesis). In Example 22.10, H_0 proposes a uniform distribution of moths over the heights 0 to 25 meters, so rel $\hat{F}_i = X_i/25$ m (for example, $\hat{F}_{10} = 10.6$ m/25 m = 0.4240). If, in a similar study, the null hypothesis were a uniform distribution over heights 1 to 25 m from the ground, then rel $\hat{F}_i$ would be $(X_i - 1)/24$ m.

The test statistic, D, for the Kolmogorov-Smirnov goodness-of-fit is obtained by first calculating both

$$D_i = |\text{rel } F_i - \text{rel } \hat{F}_i| \tag{22.9}$$

and

$$D'_i = |\text{rel } F_{i-1} - \text{rel } \hat{F}_i| \tag{22.10}$$

for each i. For the data under consideration, for example, $D_{10} = |0.7333 - 0.4240| = 0.3093$ and $D'_{10} = |0.6667 - 0.4240| = 0.2427$. In using Equation 22.10 it is important to know that $F_0 = 0$, so $D'_1 = \text{rel } \hat{F}_1$ (and in Example 22.10, $D'_1 = |0 - 0.0560| = 0.0560$). Then the test statistic is

$$D = \max[(\max D_i), (\max D'_i)], \tag{22.11}$$

which means "D is the largest value of D_i or the largest value of D'_i, whichever is larger." Critical values for this test statistic are referred to as $D_{\alpha,n}$ in Appendix Table B.9. If $D \geq D_{\alpha,n}$, then H_0 is rejected at the α level of significance.

Figure 22.1 demonstrates why it is necessary to examine both D_i and D'_i in comparing an observed to a hypothesized cumulative frequency distribution for continuous data. (See also D'Agostino and Noether, 1973; Fisz, 1963: Section 12.5A;

*The name of the test honors the two Russian mathematicians who developed its underlying concepts and procedures: Andrei Nikolaevich Kolmogorov (1903–1987) and Nikolai Vasil'evich Smirnov (1900–1906). Körner (1996: 190) reported that "Kolmogorov worked in such a large number of mathematical fields that eleven experts were required to describe his work for his London Mathematical Society obituary." Kolmogorov originated the test for the one-sample situation discussed here, and Smirnov described a two-sample test to assess how well two observed cumulative frequency distributions represent population distributions that coincide. (See, e.g., Daniel, 1990: Section 8.3; Hollander and Wolfe, 1999: Section 5.4; Siegel and Castellan, 1988: 144–151, 166; and Sprent and Smeeton, 2001: 185–187, for discussion of the Kolmogorov-Smirnov two-sample test.)

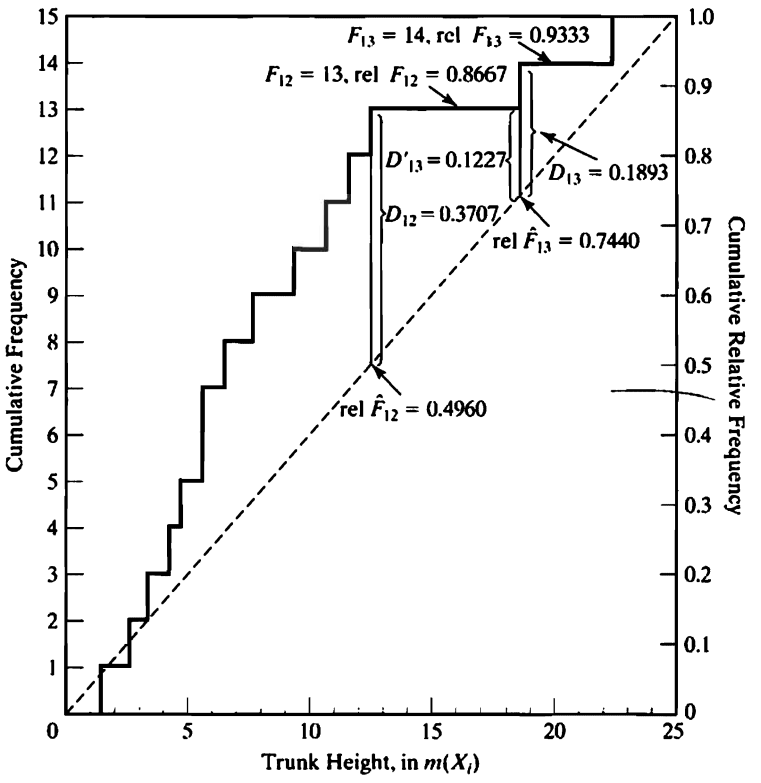

FIGURE 22.1: Graphical representation of Example 22.10, Kolmogorov-Smirnov goodness-of-fit testing for continuous data. The solid line plots the observed frequencies, and the dashed line shows the expected frequencies.

Gibbons and Chakraborti, 2003: Section 4.3.) What is sought is the maximum deviation between the observed distribution, F (which looks like a staircase when graphed), and the hypothesized distribution, $\hat{F}$. (The distribution of $\hat{F}$ appears as a straight line if H_0 proposes a uniform distribution; but other distributions, such as a normal distribution, may be hypothesized.) For each $\hat{F}_i$, we must consider the vertical distance $D_i = |F_i - \hat{F}_i|$, which occurs at the left end of a step, as well as the vertical distance $D'_i = |F_{i-1} - \hat{F}_i|$, which is at the right end of a step.

A lesser-known, but quite good, alternative for the Kolmogorov-Smirnov test for goodness of fit of continuous data is the Watson goodness-of-fit test. It is discussed in Section 27.5 as being especially suited for data on a circular scale, but it is applicable as well to data on a linear scale such as in the present section. Other alternatives have been proposed, including those that have special emphasis on the differences in the tails of the distributions (Calitz, 1987).

(a) Correction for Increased Power. For small sample sizes (say, $n \leq 25$), the power of Kolmogorov-Smirnov testing can be increased impressively by employing the correction expounded by Harter, Khamis, and Lamb (1984) and Khamis (1990, 1993). For each i, Equation 22.8 is modified to

$$\text{rel } \mathcal{F}_i = \frac{F_i}{n + 1} \tag{22.12}$$

and

$$\text{rel } \mathcal{F}'_i = \frac{F_i - 1}{n - 1}. \tag{22.13}$$

Then, differences analogous to D_i and D'_i of Equations 22.9 and 22.10, respectively, are obtained as

$$D_{0,i} = \left|\text{rel } \mathcal{F}'_i - \text{rel } \hat{F}_i\right| \tag{22.14}$$

$$D_{1,i} = \left|\text{rel } \mathcal{F}'_i - \text{rel } \hat{F}_i\right|. \tag{22.15}$$

For these two statistics, the subscripts 0 and 1 are denoted as δ (lowercase Greek delta), so the developers of this procedure call it the δ-corrected Kolmogorov-Smirnov goodness-of-fit test.

The test statistic is either max $D_{0,i}$ or max $D_{1,i}$, whichever leads to the higher level of significance (i.e., the smaller probability). Appendix Table B.10 gives critical values for $D_{\delta,n}$ for various levels of α. This test is demonstrated in Example 22.11. Although in this example the conclusion is the same as with the uncorrected Kolmogorov-Smirnov test (Example 22.10), this is not always so. However, Khamis (1990) reported that if $n > 20$, the results of this corrected Kolmogorov-Smirnov method are practically indistinguishable from those from the uncorrected procedure, and in such cases either the uncorrected or corrected test may be used.

EXAMPLE 22.11 δ-corrected Kolmogorov-Smirnov Goodness of Fit

The hypotheses and data are those of Example 22.10.

i	X_i	F_i	rel $\hat{F}_i$	rel $\mathcal{F}_i$	$D_{0,i}$	rel $\mathcal{F}'_i$	$D_{1,i}$
1	1.4	1	0.0560	0.0625	0.0065	0.0000	0.0560
2	2.6	2	0.1040	0.1250	0.0210	0.0714	0.0326
3	3.3	3	0.1320	0.1875	0.0555	0.1429	0.0109
4	4.2	4	0.1680	0.2500	0.0820	0.2143	0.0463
5	4.7	5	0.1880	0.3125	0.1245	0.2857	0.0977
6	5.6	7	0.2240	0.4375	0.2135	0.4286	0.2046
7	6.4	8	0.2560	0.5000	0.2440	0.5000	0.2440
8	7.7	9	0.3080	0.5625	0.2545	0.5714	0.2634
9	9.3	10	0.3720	0.6250	0.2530	0.6429	0.2709
10	10.6	11	0.4240	0.6875	0.2635	0.7143	0.2903
11	11.5	12	0.4600	0.7500	0.2900	0.7857	0.3257
12	12.4	13	0.4960	0.8125	0.3165	0.8571	0.3611
13	18.6	14	0.7440	0.8750	0.1310	0.9286	0.1846
14	22.3	15	0.8920	0.9375	0.0455	1.0000	0.1080

$n = 15$
max $D_{0,i} = D_{0,12} = 0.3165$, which has a probability of $0.05 < P < 0.10$
max $D_{1,i} = D_{1,12} = 0.3611$, which has a probability of $0.02 < P < 0.05$
Therefore, reject H_0: $0.02 < P < 0.05$.

The δ-corrected procedure can result in a test with a Type I error slightly greater than α; Khamis (2000) presented an adjustment to remedy this. Feltz (1998) discussed similar corrections that have more power in some circumstances.

(b) Sample Size Required. When it is planned to apply a Kolmogorov-Smirnov test to continuous data, it may be asked how large a sample is needed to be able to detect a significant difference of a given magnitude between an observed and a hypothesized cumulative frequency distribution. All that need be done is to seek the desired minimum detectable difference in the body of the table of critical values of D (Appendix Table B.9), for the selected significance level, α. For example, to be able to detect a difference as small as 0.30 between an observed and a hypothesized cumulative relative frequency distribution, at a significance level of 0.05, a sample of of at least 20 would be needed, for $D_{0.05,19} = 0.30143$, which is larger than 0.30, and $D_{0.05,20} = 0.29408$, which is smaller than 0.30. If the desired difference is not in the table, then the nearest smaller one is used. Thus, for a study such as that in Example 22.10, it is estimated that at least 20 moths would have to be observed to be able to detect, at the 5% significance level, a difference between the cumulative frequency distributions—a difference of either D or D'—as small as 0.30.

If the desired detectable difference is beyond the $D_{\alpha,n}$ values in Appendix Table B.9 (i.e., the difference is $< D_{\alpha,160}$), then we know that the required sample size is greater than 160. This sample size may be estimated by employing the values of d_α at the end of Appendix Table B.9.* If we wish to detect a difference as small as Δ, then the sample size should be at least†

$$n = \frac{d_\alpha^2}{\Delta^2}. \tag{22.17}$$

For example, if the collector of data in Example 22.11 had desired to be able to detect a difference, D_i or D_i', as small as 0.10, a sample size of at least 185 moth observations should have been obtained, for

$$n = \frac{(1.35810)^2}{(0.10)^2} = 184.4.$$

(c) Discrete or Grouped Data. Ordinal data, such as in Example 22.12, are not measurements on a continuous scale and should not be analyzed by the Kolmogorov-Smirnov procedures discussed previously. But the following method is applicable.

Example 22.12 shows the results of an experiment in which cats were given a choice of five foods, identical in all respects except moisture content. A total of 40 observations were recorded. The experiment was performed in a fashion that ensured that all 40 were independent; this was done by using 40 cats, each given a choice among the five foods (not, for example, by using eight cats with each cat being given five opportunities to choose among the food types), and the cats were subjected to the experiment one at a time, so no individual's actions would influence another's.

*These values at the end of Appendix Table B.9 are

$$d_\alpha = \sqrt{\frac{-\ln \alpha}{2}}. \tag{22.16}$$

†Δ is the capital Greek letter delta.

EXAMPLE 22.12 Kolmogorov-Smirnov Goodness-of-Fit Test for Discrete Ordered Data

H_0: Cats have no preference along a food-moisture gradient.
H_A: Cats do have preference along a food-moisture gradient.

Food Moisture (i)	f_i	$\hat{f}_i$	F_i	$\hat{F}_i$	d_i
1 (driest)	5	8	5	8	3
2	6	8	11	16	5
3	7	8	18	24	6
4	10	8	28	32	4
5 (moistest)	12	8	40	40	0

$n = 40$; $k = 5$
$d_{\max} = d_3 = 6$
$(d_{\max})_{0.05,5,40} = 8$
Therefore, do not reject H_0.

$$[0.10 < P < 0.20]$$

The food moisture is expressed on an ordinal scale, for although we can say that food 1 is drier than food 2 and food 2 is drier than food 3, we cannot say that the difference in moisture between foods 1 and 2 is quantitatively equal to the difference between foods 2 and 3. That is, we can speak only of relative magnitudes, and not quantitative measurements, of the foods' moisture contents.

The null hypothesis of equal preference for the five food types could be tested by chi-square goodness of fit (Section 22.3), and this would be appropriate if the five foods were nominal-scale categories (for example, different brands or different recipes). But the present data are in categories that have a rational order, and the null hypothesis is that there is no preference along the gradient of food moisture (that is, no preference among the five moisture categories arranged in ascending order).

The data are observed frequencies, f_i, namely the numbers of animals choosing each of the five food types. The expected frequencies, $\hat{f}_i$, are the numbers expected if the null hypothesis is true. In the present example, hypothesizing no preferred food type, a uniform distribution (i.e., a frequency of eight in each of the five categories) would be expected.

For the Kolmogorov-Smirnov goodness-of-fit test, cumulative observed frequencies (F_i) and cumulative expected frequencies ($\hat{F}_i$) are calculated for categories 1 through k. (In Example 22.12, $k = 5$.) The cumulative frequency for category i is the sum of all frequencies from categories 1 through i (in Example 22.12, the frequencies for food as moist as, or moister than, i).

For each category, i, the absolute value of difference between the two cumulative frequency distributions is determined:

$$d_i = |F_i - \hat{F}_i| \ . \tag{22.18}$$

The largest d_i is the test statistic; let us call it $d_{\max}$.

Critical values of d_{max} are found in Appendix Table B.8 (which requires that in the experiment n, the total number of data, is a multiple of k, the number of categories).* Also, the tabled critical values are for situations where all of the expected frequencies, $\hat{f}_i$, are equal, but the table also works well for unequal $\hat{f}_i$ if the inequality is not great (Pettitt and Stephens, 1977).

The d_{max} procedure is also appropriate when data are recorded on a continuous scale but are grouped into broad categories on that scale so $f_i > 1$ for several f_i's. For such data, or for ordinal data, the test appropriate for ungrouped continuous data (using D) is conservative (e.g., Noether, 1963; Pettitt and Stephens, 1977), meaning that the testing is occurring at an α smaller—perhaps much smaller—than that stated, and the probability of a Type II error is inflated; that is, the power of the test is reduced. Therefore, use of d_{max} is preferred to using D for grouped or ordinal data.†

Example 22.13 shows how the data of Example 22.10 would look had the investigator recorded them in 5-meter ranges of trunk heights. Note that power is lost (and H_0 is not rejected) by grouping the data, and grouping should be avoided or minimized whenever possible.

When applicable (that is, when the categories are ordered), the Kolmogorov-Smirnov test is more powerful than the chi-square test when n is small or when $\hat{f}_i$

EXAMPLE 22.13 Kolmogorov-Smirnov Goodness-of-Fit Test for Continuous, But Grouped, Data

The hypotheses are as in Example 22.10, with that example's data recorded in 5-meter segments of tree height (where, for example, 5–10 m denotes a height of at least 5 m but less than 10 m).

i	Trunk height (X_i)	f_i	$\hat{f}_i$	F_i	$\hat{F}_i$	d_i
1	0–5 m	5	3	5	3	2
2	5–10 m	5	3	10	6	4
3	10–15 m	5	3	13	9	4
4	15–20 m	1	3	14	12	2
5	20–25 m	1	3	15	15	0

$n = 15$; $k = 5$
$d_{max} = 4$
$(d_{max})_{0.05,5,15} = 5$
Therefore, do not reject H_0.

$$[0.10 < P < 0.20]$$

*If n is not evenly divisible by k, then, conservatively, the critical value for the nearest larger n in the table may be used. (However, that critical value might not exist in the table.)

†The first footnote of this section refers to the Kolmogorov-Smirnov two-sample test, which also yields conservative results if applied to discrete data (Noether, 1963).

values are small, and often in other cases.* Another advantage of the Kolmogorov-Smirnov test over chi-square is that it is not adversely affected by small expected frequencies (see Section 22.5).

EXERCISES

22.1. Consult Appendix Table B.1

(a) What is the probability of computing a χ^2 at least as large as 3.452 if DF = 2 and the null hypothesis is true?

(b) What is $P(\chi^2 \geq 8.668)$ if $\nu = 5$?

(c) What is $\chi^2_{0.05,4}$?

(d) What is $\chi^2_{0.01,8}$?

22.2. Each of 126 individuals of a certain mammal species was placed in an enclosure containing equal amounts of each of six different foods. The frequency with which the animals chose each of the foods was:

Food item (i)	f_i
N	13
A	26
W	31
G	14
M	28
C	14

(a) Test the hypothesis that there is no preference among the food items.

(b) If the null hypothesis is rejected, ascertain which of the foods are preferred by this species.

22.3. A sample of hibernating bats consisted of 44 males and 54 females. Test the hypothesis that the hibernating population consists of equal numbers of males and females.

22.4. In attempting to determine whether there is a 1 : 1 sex ratio among hibernating bats, samples were taken from four different locations in a cave:

Location	*Males*	*Females*
V	44	54
D	31	40
E	12	18
M	15	16

By performing a heterogeneity chi-square analysis, determine whether the four samples may justifiably be pooled. If they may, pool them and retest the null hypothesis of equal sex frequencies.

22.5. Test the hypothesis and data of Exercise 22.2 using the log-likelihood G.

22.6. A straight line is drawn on the ground perpendicular to the shore of a body of water. Then the locations of ground arthropods of a certain species are measured along a 1-meter-wide band on either side of the line. Use the Kolmogorov-Smirnov procedure on the following data to test the null hypothesis of uniform distribution of this species from the water's edge to a distance of 10 meters inland.

Distance from water (m)	*Number observed*	*Distance from* (m)	*Number observed*
0.3	1	3.4	1
0.6	1	4.1	1
1.0	1	4.6	1
1.1	1	4.7	1
1.2	1	4.8	1
1.4	1	4.9	1
1.6	1	4.9	1
1.9	1	5.3	1
2.1	1	5.8	1
2.2	1	6.4	1
2.4	1	6.8	1
2.6	1	7.5	1
2.8	1	7.7	1
3.0	1	8.8	1
3.1	1	9.4	1

22.7. For a two-tailed Kolmogorov-Smirnov goodness-of-fit test with continuous data at the 5% level of significance, how large a sample is necessary to detect a difference as small as 0.25 between cumulative relative frequency distributions?

*A chi-square goodness-of-fit test performed on the data of Example 22.12, for H_0: There is no preference among the five food categories, would disregard the order of the categories and would yield $\chi^2 = 4.250$; and the log-likelihood goodness of fit would result in $G = 4.173$. Each of those statistics would be associated with a probability between 0.25 and 0.50.

28. A bird feeder is placed at each of six different heights. It is recorded which feeder was selected by each of 18 cardinals. Using the Kolmogorov-Smirnov procedure for discrete data, test the null hypothesis that each feeder height is equally desirable to cardinals.

Feeder height	*Number observed*
1 (lowest)	2
2	3
3	3
4	4
5	4
6 (highest)	2

CHAPTER 23

Contingency Tables

Enumeration data may be collected simultaneously for two nominal-scale variables. These data may be displayed in what is known as a *contingency table*, where the r rows of the table represent the r categories of one variable and the c columns indicate the c categories of the other variable; thus, there are rc "cells" in the table. (This presentation of data is also known as a *cross tabulation* or *cross classification*.)

Example 23.1a is of a contingency table of two rows and four columns, and may be referred to as a 2 × 4 ("two by four") table having (2)(4) = 8 cells. A sample of 300 people has been obtained from a specified population (let's say members of an actors' professional association), and the variables tabulated are each person's sex and each person's hair color. In this 2 × 4 table, the number of people in the sample with each of the eight combinations of sex and hair color is recorded in one of the eight cells of the table. These eight data could also be recorded in a 4 × 2 contingency table, with the four hair colors appearing as rows and the two sexes as columns, and that would not change the statistical hypothesis tests or the conclusions that result from them. As with previous statistical tests, the total number of data in the sample is designated as n.

EXAMPLE 23.1 A 2 × 4 Contingency Table for Testing the Independence of Hair Color and Sex in Humans

(a) H_0: Human hair color is independent of sex in the population sampled.
H_A: Human hair color is not independent of sex in the population sampled.

$\alpha = 0.05$

	Hair color				
Sex	*Black*	*Brown*	*Blond*	*Red*	**Total**
Male	32	43	16	9	100 (= R_1)
Female	55	65	64	16	200 (= R_2)
Total	87 (= C_1)	108 (= C_2)	80 (= C_3)	25 (= C_4)	300 (= n)

(b) The observed frequency, f_{ij}, in each cell is shown, with the frequency expected if H_0 is true (i.e., $\hat{f}_{ij}$) in parentheses.

	Hair color				
Sex	*Black*	*Brown*	*Blond*	*Red*	**Total**
Male	32 *(29.0000)*	43 *(36.0000)*	16 *(26.6667)*	9 *(8.3333)*	100 (= R_1)
Female	55 *(58.0000)*	65 *(72.0000)*	64 *(53.3333)*	16 *(16.6667)*	200 (= R_2)
Total	87 (= C_1)	108 (= C_2)	80 (= C_3)	25 (= C_4)	300 (= n)

$$\chi^2 = \sum\sum \frac{(f_{ij} - \hat{f}_{ij})^2}{\hat{f}_{ij}}$$

$$= \frac{(32 - 29.0000)^2}{29.0000} + \frac{(43 - 36.0000)^2}{36.0000} + \frac{(16 - 26.6667)^2}{26.6667}$$
$$+ \frac{(9 - 8.3333)^2}{8.3333} + \frac{(55 - 58.0000)^2}{58.0000} + \frac{(65 - 72.0000)^2}{72.0000}$$
$$+ \frac{(64 - 53.3333)^2}{53.3333} + \frac{(16 - 16.6667)^2}{16.6667}$$
$$= 0.3103 + 1.3611 + 4.2667 + 0.0533 + 0.1552 + 0.6806 + 2.1333 + 0.0267 = 8.987$$

$$\nu = (r - 1)(c - 1) = (2 - 1)(4 - 1) = 3$$

$$\chi^2_{0.05,3} = 7.815$$

Therefore, reject H_0.

$$0.025 < P < 0.05 \quad [P = 0.029]$$

The hypotheses to be tested in this example may be stated in any of these three ways:

H_0: In the sampled population, a person's hair color is independent of that person's sex (that is, a person's hair color is not associated with the person's sex), and

H_A: In the sampled population, a person's hair color is not independent of that person's sex (that is, a person's hair color is associated with the person's sex), *or*

H_0: In the sampled population, the ratio of males to females is the same for people having each of the four hair colors, and

H_A: In the sampled population, the ratio of males to females is not the same for people having each of the four hair colors; *or*

H_0: In the sampled population, the proportions of people with the four hair colors is the same for both sexes, and

H_A: In the sampled population, the proportions of people with the four hair colors is not the same for both sexes.

In order to test the stated hypotheses, the sample of data in this example could have been collected in a variety of ways:

- It could have been stipulated, in advance of collecting the data, that a specified number of males would be taken at random from all the males in the population and a specified number of females would be taken at random from all the females in the population. Then the hair color of the people in the sample would be recorded for each sex. That is what was done for Example 23.1a, where it was decided, before the data were collected, that the sample would consist of 100 males and 200 females.
- It could have been stipulated, in advance of collecting the data, that a specified number of people with each hair color would be taken at random from all persons in the population with that hair color. Then the sex of the people in the sample would be recorded for each hair color.
- It could have been stipulated, in advance of collecting, that a sample of n people would be taken at random from the population, without specifying how many of each sex would be in the sample or how many of each hair color would be in the sample. Then the sex and hair color of each person would be recorded.

For most contingency-table situations, the same statistical testing procedure applies to any one of these three methods of obtaining the sample of n people, and the same result is obtained. However, when dealing with the smallest possible contingency table, namely one with only two rows and two columns (Section 23.3), an additional sampling strategy may be encountered that calls for a different statistical procedure.

Section 23.8 will introduce procedures for analyzing contingency tables of more than two dimensions, where frequencies are tabulated simultaneously for more than two variables.

23.1 CHI-SQUARE ANALYSIS OF CONTINGENCY TABLES

The most common procedure for analyzing contingency table data uses the chi-square statistic.* Recall that for the computation of chi-square one utilizes observed and expected frequencies (and never proportions or percentages). For the goodness-of-fit analysis introduced in Section 22.1, f_i denoted the frequency observed in category i of the variable under study. In a contingency table, we have two variables under consideration, and we denote an observed frequency as f_{ij}. Using the double subscript, f_{ij} refers to the frequency observed in row i and column j of the contingency table. In Example 23.1, the value in row 1 column 1 is denoted as f_{11}, that in row 2 column 3 as f_{23}, and so on. Thus, $f_{11} = 32, f_{12} = 43, f_{13} = 16, \ldots, f_{23} = 64$, and $f_{24} = 16$.

The total frequency in row i of the table is denoted as R_i and is obtained as $R_i = \sum_{j=1}^{c} f_{ij}$. Thus, $R_1 = f_{11} + f_{12} + f_{13} + f_{14} = 100$, which is the total number of males in the sample, and $R_2 = f_{21} + f_{22} + f_{23} + f_{24} = 200$, which is the total number of females in the sample. The column totals, C_j, are obtained by analogous

*The early development of chi-square analysis of contingency tables is credited to Karl Pearson (1904) and R. A. Fisher (1922). In 1904, Pearson was the first to use the term "contingency table" (David, 1995).

and it is in this way that the $\hat{f}_{ij}$ values in Example 23.1b were obtained. Note that we can check for arithmetic errors in our calculations by observing that $R_i = \sum_{j=1}^{c} f_{ij} = \sum_{j=1}^{c} \hat{f}_{ij}$ and $C_j = \sum_{i=1}^{r} f_{ij} = \sum_{i=1}^{r} \hat{f}_{ij}$. That is, the row totals of the expected frequencies equal the row totals of the observed frequencies, and the column totals of the expected frequencies equal the column totals of the observed frequencies.

Once χ^2 has been calculated, its significance can be ascertained from Appendix Table B.1, but to do so we must determine the degrees of freedom of the contingency table.

The degrees of freedom for a chi-square calculated from contingency-table data are*

$$\nu = (r - 1)(c - 1). \tag{23.5}$$

In Example 23.1, which is a 2×4 table, $\nu = (2 - 1)(4 - 1) = 3$. The calculated statistic is 9.987 and the critical value is $\chi^2_{0.05,3} = 7.815$, so the null hypothesis is rejected.

It is good to calculate expected frequencies and other intermediate results to at least four decimal places and to round to three decimal places after arriving at the value of χ^2. Barnett and Lewis (1994: 431–440) and Simonoff (2003: 228–234) discuss outliers in contingency-table data.

(a) Comparing Proportions. Hypotheses for data in a contingency table with only two rows (or only two columns) often refer to ratios or proportions. In Example 23.1, the null hypothesis could have been stated as, "In the sampled population, the sex ratio is the same for each hair color" or as "In the sampled population, the proportion of males is the same for each hair color." The comparison of two proportions is discussed in Sections 23.3b and 24.10; and the comparison of more than two proportions is further discussed in Sections 24.13–24.15.

23.2 VISUALIZING CONTINGENCY-TABLE DATA

Among the ways to present contingency-table data in graphical form is a method known as a *mosaic* display.†

In Chapter 1, nominal-scale data were presented in a bar graph in Figure 1.2. The categories of the nominal-scale variable appear on one axis of the graph (typically the horizontal axis, as in Figure 1.2), and the number of observations is on the other

*In the early days of contingency-table analysis, K. Pearson and R. A. Fisher disagreed vehemently over the appropriate degrees of freedom to employ; Fisher's (1922) view has prevailed (Agresti, 2002: 622; Savage, 1976), as has his use of the term *degrees of freedom*.

†The current use of mosaic displays is attributed to Hartigan and Kleiner (1981). In an historical review of rectangular presentations of data, Friendly (2002) credits the English astronomer Edmond (a.k.a. Edmund) Halley (1656–1742), famous for his 1682 observation of the comet that bears his name, with the first use of rectangular areas in the data representation for two independent variables (which, however, were not variables for a contingency table). Further developments in the visual use of rectangular areas took place in France and Germany in the early 1780s; a forerunner of mosaic graphs was introduced in 1844 by French civil engineer Charles Joseph Minard (1791–1870), and what resembled the modern mosaic presentation was first used in 1877 by German statistician Georg von Mayr (1841–1925). In 1977, French cartographer Jacques Bertin (1918–) used graphs very similar to the mosaics of Hartigan and Kleiner.

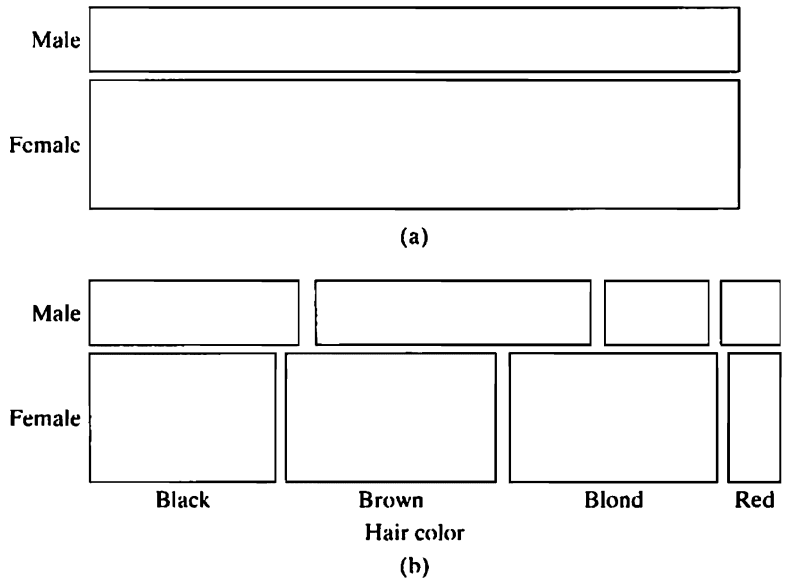

FIGURE 23.1: A mosaic display for the contingency-table data of Example 23.1. (a) The first step displays two horizontal bars of equal width with the height of one of them representing the number of males and the height of the other representing the number of females in the sample. (b) The second step divides each of the two horizontal bars into four tiles, with the width of each tile depicting the frequency in the sample of a hair color among the individuals of one of the sexes.

axis. The lengths of the bars in the graph are representations of the frequencies of occurrence of observations in the data categories; and, when bars are of equal width, the areas of the bars also depict those frequencies.

Figure 23.1 demonstrates visualizing the data in Example 23.1 and shows the two-step process of preparing a mosaic display. The first step is to prepare Figure 23.1a, which is a graph reflecting the numbers of males and females in the sample of data described in Example 23.1. Of the 300 data, 100 are males and 200 are females, so the bar for females is two times as high as the bar for males. (The bars are graphed horizontally to reflect the rows in the Example 23.1 contingency table, but they could have been drawn vertically instead.) The bars are drawn with equal widths, so their areas also express visually the proportion of the 300 data in each sex category, with the lower (female) bar having two times the area of the upper (male) bar.

The second step, shown in Figure 23.1b, is to divide each sex's horizontal bar into four segments representing the relative frequencies of the four hair colors within that sex. For example, black hair among males was exhibited by $32/100 = 0.32$ of the males in the sample, so black is depicted by a bar segment that is 32% of the width of the male bar; and $16/200 = 0.08$ of the sample's females had red hair, so the red-hair segment for females is 8% of the width of the female bar. These bar segments are often referred to as *tiles*, and there will be a tile for each of the $r \times c$ cells in the contingency table. Mosaic displays are usually, but not necessarily, drawn with small gaps between adjacent tiles.

If the boundaries of the tiles for the two bars were perfectly aligned vertically, that would indicate that the $r \times c$ frequencies were in perfect agreement with the

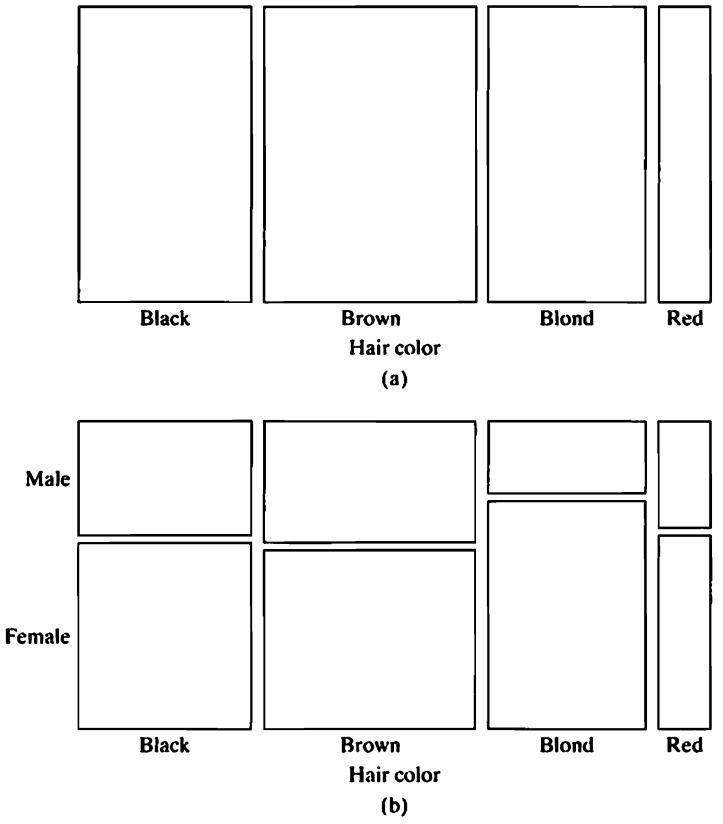

FIGURE 23.2: A mosaic display for the contingency-table data of Example 23.1. (a) The first step displays four vertical bars of equal height, one for each of the hair colors in the sample, with the width of the bars expressing the relative frequencies of the hair colors. (b) The second step divides each of the four vertical bars into two tiles, with the length of each tile depicting the frequency of a members of a sex among the individuals of one of the hair colors.

null hypothesis. The more out of alignment the tiles are, the less likely it is that the sampled population conforms to that specified in H_0.

In Figure 23.1, the data of Example 23.1 were displayed graphically by showing the frequency of each hair color within each sex. Alternatively, the data could be presented as the frequency of each sex for each hair color. This is shown in Figure 23.2. In Figure 23.2a, the widths of the four vertical bars represent the relative frequencies of the four hair colors in the sample, and Figure 23.2b divides each of those four bars into two segments (tiles) with sizes reflecting the proportions of males and females with each hair color.

Either graphical depiction (Figure 23.1b or 23.2b) is legitimate, with the choice depending upon the visual emphasis the researcher wants to give to each of the variables.

Mosaic displays may also be presented for contingency tables having more than two rows *and* more than two columns (such as Exercise 23.4 at the end of this chapter). Friendly (1994, 1995, 1999, 2002) described how the interpretation of mosaic graphs can be enhanced by shading or coloring the tiles to emphasize the degree to which observed frequencies differ from expected frequencies in the cells of the contingency table; and mosaic presentations are also used for contingency tables with more than two dimensions (which are introduced in Section 23.8).

2 × 2 CONTINGENCY TABLES

The smallest possible contingency table is that consisting of two rows and two columns. It is referred to as a 2 × 2 ("two by two") table or a fourfold table, and it is often encountered in biological research. By Equation 23.5, the degrees of freedom for 2 × 2 tables is $(2 - 1)(2 - 1) = 1$.

The information in a 2 × 2 contingency table may be displayed as

f_{11}	f_{12}	R_1
f_{21}	f_{22}	R_2
C_1	C_2	n

where f_{ij} denotes the frequency observed in row i and column j, R_i is the sum of the two frequencies in row i, C_j is the sum of the two frequencies in column j, and n is the total number of data in the sample. (The sample size, n, is the sum of all four of the f_{ij}'s, is the sum of the two row totals, and is the sum of the two column totals.) The row totals, R_1 and R_2, are said to occupy one margin of the table, and the column totals, C_1 and C_2, are said to occupy an adjacent margin of the table.

There are different experimental designs that result in data that can be arranged in contingency tables, depending upon the nature of the populations from which the samples come. As described by Barnard (1947) and others, these can be categorized on the basis of whether the marginal totals are set by the experimenter before the data are collected.

(a) No Margin Fixed. There are situations where only the size of the sample (n) is declared in advance of data collection, and neither the row totals nor the column totals are prescribed.* In Example 23.2a, the experimenter decided that the total number of data in the sample would be $n = 70$, but there was no specification prior to the data collection of what the total number of boys, of girls, of right-handed children, or of left-handed children would be. A sample of 70 was taken at random from a population of children (perhaps of a particular age of interest), and then the numbers of right-handed boys, right-handed girls, left-handed boys, and left-handed girls were recorded as shown in this example. The statistical analysis shown in Example 23.2b will be discussed in Section 23.3d.

EXAMPLE 23.2 A 2 × 2 Contingency Table with No Fixed Margins

(a) H_0: In the sampled population, handedness is independent of sex.
H_A: In the sampled population, handedness is not independent of sex.

$\alpha = 0.05$

	Boys	*Girls*	*Total*
Left-handed	6	12	18
Right-handed	28	24	52
Total	34	36	70

*This kind of experimental design is sometimes referred to as a double dichotomy or as representing a multinomial sampling distribution, and the resulting test as a test of association or test of independence.

(b) Using Equation 23.6 (Equation 23.1 could also be used, with the same result),

$$\chi^2 = \frac{n(f_{11}f_{22} - f_{12}f_{21})^2}{R_1R_2C_1C_2}$$
$$= \frac{70[(6)(24) - (12)(28)]^2}{(18)(52)(34)(36)}$$
$$= 2.2524.$$

$\nu = 1$; $\chi^2_{0.05,1} = 3.841$

Therefore, do not reject H_0.

$$0.10 < P < 0.25 \quad [P = 0.22]$$

(b) One Margin Fixed. Some experimental designs not only specify the sample size, n, but also indicate—prior to collecting data—how many data in the sample will be in each row (or how many will be in each column).* Thus, in Example 23.2a, it could have been declared, before counting how many children were in each of the four categories, how many boys would be taken at random from all the boys in the population and how many girls would be taken at random from the girls in the population. Or the column totals might have been fixed, stating how many right-handed children and how many left-handed children would be selected from their respective populations.

Another example of a contingency table with one pair of marginal totals fixed is shown in Example 23.3a. In this study, it was decided to collect, at random, 24 mice of species 1 and 25 of species 2, and the researcher recorded the number of mice of each species that were infected with a parasite of interest.

EXAMPLE 23.3 A 2 × 2 Contingency Table with One Fixed Margin

(a) H_0: The proportion of the population infected with an intestinal parasite is the same in two species of mouse.

H_A: The proportion of the population infected with an intestinal parasite is not the same in two species of mouse.

$\alpha = 0.05$

	Species 1	*Species 2*	*Total*
With parasite	18	10	28
Without parasite	6	15	21
Total	24	25	49

*This experimental design is often called a comparative trial, the resulting test a test of homogeneity, and the underlying distributions binomial distributions (which will be discussed further in Chapter 24).

summations: $C_j = \sum_{i=1}^{r} f_{ij}$. For example, the total number of blonds in the sample data is $C_3 = \sum_{i=1}^{2} f_{i3} = f_{13} + f_{23} = 80$, the total number of redheads is $C_4 = \sum_{i=1}^{2} f_{i4} = 25$, and so on. The total number of observations in all cells of the table is called the grand total and is $\sum_{i=1}^{r} \sum_{j=1}^{c} f_{ij} = f_{11} + f_{12} + f_{13} + \cdots + f_{23} + f_{24} = 300$, which is n, the size of our sample. The computation of the grand total may be written in several other notations: $\sum_i \sum_j f_{ij}$ or $\sum_{i,j} f_{ij}$, or simply $\sum\sum f_{ij}$. When no indices are given on the summation signs, we assume that the summation of all values in the sample is desired.

The most common calculation of chi-square analysis of contingency tables is

$$\chi^2 = \sum\sum \frac{(f_{ij} - \hat{f}_{ij})^2}{\hat{f}_{ij}}. \tag{23.1}$$

In this formula, similar to Equation 22.1 for chi-square goodness of fit, $\hat{f}_{ij}$ refers to the frequency expected in a row i column j if the null hypothesis is true.* If, in Example 23.1a, hair color is in fact independent of sex, then $\frac{100}{300} = \frac{1}{3}$ of all black-haired people would be expected to be males and $\frac{200}{300} = \frac{2}{3}$ would be expected to be females. That is, $\hat{f}_{11} = \frac{100}{300}(87) = 29$ (the expected number of black-haired males), $\hat{f}_{21} = \frac{200}{300}(87) = 58$ (the expected number of black-haired females), $\hat{f}_{12} = \frac{100}{300}(108) = 36$ (the expected number of brown-haired males), and so on.

This may also be explained by the probability rule introduced in Section 5.7: The probability of two independent events occurring at once is the product of the probabilities of the two events. Thus, if having black hair is independent of being male, then the probability of a person being both black-haired and male is the probability of a person being black-haired multiplied by the probability of a person being male, namely $\left(\frac{87}{300}\right) \times \left(\frac{100}{300}\right)$, which is 0.0966667. This means that the expected number of black-haired males in a sample of 300 is $(0.0966667)(300) = 29.0000$. In general, the frequency expected in a cell of a contingency table is

$$\hat{f}_{ij} = \left(\frac{R_i}{n}\right)\left(\frac{C_j}{n}\right)n, \tag{23.3}$$

which reduces to the commonly encountered formula,

$$\hat{f}_{ij} = \frac{(R_i)(C_j)}{n}, \tag{23.4}$$

*Just as Equation 22.2 is equivalent to Equation 22.1 for chi-square goodness of fit, the following are mathematically equivalent to Equation 23.1 for contingency tables:

$$\chi^2 = \sum\sum \frac{f_{ij}^2}{\hat{f}_{ij}} - n \tag{23.2}$$

and

$$\chi^2 = n\left(\sum\sum \frac{f_{ij}^2}{R_i C_j} - 1\right). \tag{23.2a}$$

These formulas are computationally simpler than Equation 23.1, the latter not even requiring the calculation of expected frequencies; however, they do not allow for the examination of the contributions to the computed chi-square, the utility of which will be seen in Section 23.6.

(b) Using Equation 23.6 (Equation 23.1 could also be used, with the same result),

$$\chi^2 = \frac{n(f_{11}f_{22} - f_{12}f_{21})^2}{R_1R_2C_1C_2}$$

$$= \frac{49[(18)(15) - (10)(6)]^2}{(28)(21)(24)(25)}$$

$$= 6.1250.$$

$$0.01 < P < 0.025 \quad [P = 0.013]$$

If one margin is fixed, hypotheses might be expressed in terms of proportions. For Example 23.3a, the null hypothesis could be stated as H_0: In the sampled population, the proportion of infected mice is the same in species 1 and species 2. The statistical analysis shown in Example 23.3b will be discussed in Section 23.3d. Additional statistical procedures for dealing with proportions are discussed in Chapter 24.

(c) Both Margins Fixed. In some cases (which are very uncommon), both margins in the contingency table are fixed.* That is, R_1, R_2, C_1, C_2, and n are all set before the collection of data.

Data for such a 2 × 2 table are shown in Example 23.4a, where an ecologist wanted to compare the ability of two species of snails to tolerate the current of a stream and adhere to the stream's substrate. The researcher labeled 30 snails that were clinging to the bottom of the stream, 19 of them selected at random from a population of snails of one species and 11 selected at random from a population of snails of a second species. These 30 individuals were then observed as the current washed over them, and it was decided before the experiment began that data collection would end when more than half of the 30 (that is, 16) yielded to the current and were swept downstream.

EXAMPLE 23.4 A 2 × 2 Contingency Table with Two Fixed Margins

(a) H_0: The ability of snails to resist the current is no different between the two species.

H_A: The ability of snails to resist the current is different between the two species.

$\alpha = 0.05$

The four marginal totals are set before performing the experiment, and the four cell frequencies are collected from the experiment.

	Resisted	*Yielded*	
Species 1	12	7	19
Species 2	2	9	11
	14	16	30

*The sampling in this experimental design comes from what is known as a hypergeometric distribution, about which more will be said in Sections 24.2 and 24.16, and the experimental design is sometimes called an independence trial.

(b) Using Equation 23.7 (Equation 23.1 could also be used, with the same result, if $f_{ij} - \hat{f}_{ij}$ is replaced by $|f_{ij} - \hat{f}_{ij}| - 0.5$), the chi-square with the Yates correction for continuity is

$$\chi_c^2 = \frac{n\left(|f_{11}f_{22} - f_{12}f_{21}| - \frac{n}{2}\right)^2}{R_1R_2C_1C_2}$$

$$= \frac{30\left[|(12)(9) - (7)(2)| - \frac{30}{2}\right]^2}{(19)(11)(14)(16)}$$

$$= 3.999.$$

$\nu = 1$

$\chi^2_{0.05,1} = 3.841.$

Therefore, reject H_0.

$$0.025 < P < 0.05 \quad [P = 0.046]$$

(c) Using Equation 23.7b, the chi-square with the Cochran-Haber correction for continuity is calculated as follows:

$m_1 = R_2 = 11,\ m_2 = C_1 = 14$

$\hat{f} = m_1m_2/n = (11)(14)/30 = 5.13$

$f = f_{21} = 2;\ d = |f - \hat{f}| = |2 - 5.13| = 3.13$

$2\hat{f} = 2(5.13) = 10.26;$

As $f < 2\hat{f}, D = 3.0$

$$\chi_H^2 = \frac{n^3D^2}{R_1R_2C_1C_2}$$

$$= \frac{(30)^3(3.0)^2}{(19)(11)(14)(16)}$$

$$= 5.191.$$

As $\chi^2_{0.05,1} = 3.841$, reject H_0.

$$0.01 < P < 0.025 \quad [P = 0.023]$$

Thus, prior to collecting the data, the number of snails of each species was decided upon (as 19 and 11), *and* the total numbers of snails dislodged by the current (16 and 14) were specified. Other illustrations of 2 × 2 tables with both margins fixed are provided in Examples 24.20 and 24.21 and Exercises 24.20 and 24.21. The statistical analysis demonstrated in Example 23.4b will be discussed in Section 23.3d.

(d) Analysis of 2 × 2 Contingency Tables. Contingency-table hypotheses may be examined by chi-square, as shown in Section 23.1, calculating χ^2 with Equation 23.1 with the expected frequencies ($\hat{f}_{ij}$) obtained via Equation 23.4. However, for a 2 × 2

table, the following is a simpler computation,* for it does not require that the expected frequencies be determined, and it avoids rounding error associated with calculating $\hat{f}_{ij}$ and $f_{ij} - \hat{f}_{ij}$:

$$\chi^2 = \frac{n(f_{11}f_{22} - f_{12}f_{21})^2}{R_1R_2C_1C_2}. \tag{23.6}$$

As with goodness of fit (Section 22.1), chi-square values that are calculated come from a discrete distribution, but they are to be compared (such as by Appendix Table B.1) to chi-square values from a continuous distribution. Thus, statisticians may recommend that a correction for continuity be applied when $\nu = 1$ (which is the case when dealing with a 2 × 2 contingency table). More than 20 continuity corrections have been proposed; the most commonly considered is the Yates (1934) correction† (as was used in Section 22.2 for goodness of fit), which is the modification of Equation 23.1 by substituting $|f_{ij} - \hat{f}_{ij}| - 0.5$ for $f_{ij} - \hat{f}_{ij}$ or, equivalently, using the following instead of Equation 23.6:

$$\chi_c^2 = \frac{n\left(|f_{11}f_{22} - f_{12}f_{21}| - \frac{n}{2}\right)^2}{R_1R_2C_1C_2}. \tag{23.7}$$

This is the calculation employed in Example 23.4b, and its use approximates the two-tailed Fisher exact test discussed in Section 24.16b.

Haber (1980) showed that there are other correction methods that often perform better than that of Yates, which tends to be conservative (in that it has a probability less than α of a Type I error and has lower power than a nonconservative test). He proposed using a procedure based on a principle expounded by Cochran (1942, 1952). In the Cochran-Haber method (demonstrated in Example 23.4c), the smallest of the four expected frequencies is determined; using Equation 23.4, this frequency is

$$\hat{f} = \frac{m_1m_2}{n}, \tag{23.7a}$$

where m_1 is the smallest of the four marginal totals and m_2 is the smaller of the two totals in the other margin. In Example 23.4, the smallest marginal total, m_1, is 11, which is a row total; and m_2 is, therefore, the smaller of the two column totals, namely 14. Then the absolute difference between this expected frequency ($\hat{f}$) and its corresponding observed frequency (f) is $d = |f - \hat{f}|$; and

- If $f \leq 2\hat{f}$, then define D = the largest multiple of 0.5 that is $<d$; and
- If $f > 2\hat{f}$, then define $D = d - 0.5$.

The chi-square with the Cochran-Haber correction is

$$\chi_H^2 = \frac{n^3D^2}{R_1R_2C_1C_2}. \tag{23.7b}$$

*Richardson (1994) attributed Equation 23.6 to Fisher (1922). Upton (1982) reported a "slight" improvement if $n - 1$ is employed in place of n.

†Pearson (1947) points out that Yates's use of this correction for chi-square analysis was employed as early as 1921 for other statistical purposes. The continuity correction for 2 × 2 tables should *not* be used in the very rare instances that its inclusion increases, instead of decreases, the numerator (that is, when $|f_{11} - f_{22}| < n/2$).

If $f > 2\hat{f}$, then the Cochran-Haber-corrected chi-square (χ^2_H) is the same as the chi-square with the Yates correction (χ^2_c). Also, if either $C_1 = C_2$ or $R_a = R_2$, then $\chi^2_H = \chi^2_c$.

A great deal has been written about 2×2 contingency-table testing.* For example, it has been reported that the power of chi-square testing increases with larger n or with more similarity between the two totals in a margin, and that the difference between results using chi-square and a continuity-corrected chi-square is less for large n.

In addition, many authors have reported that, for 2×2 tables having no fixed margin or only one fixed margin, χ^2_c provides a test that is very, very conservative (that is, the probability of a Type I error is far less than that indicated by referring to the theoretical chi-square distribution—such as in Appendix Table B.1), with relatively low power; and they recommend that it should not be used for such sets of data. The use of χ^2 instead of χ^2_c will occasionally result in a test that is somewhat liberal (i.e., the probability of a Type I error is a little greater than that indicated by the chi-square distribution, though it will typically be closer to the latter distribution than χ^2_c will be); this liberalism is more pronounced when the two row totals are very different or the two column totals are very different.

For many decades there has been debate and disagreement over the appropriate statistical procedure for each of the aforementioned three sampling models for data in a 2×2 contingency table, with arguments presented on both theoretical and empirical grounds. There is still no consensus, and some believe there never will be,† but there is significant agreement on the following:

- If the 2×2 table has no margin fixed or only one margin fixed, then use χ^2. This is demonstrated in Examples 23.2b and 23.3b.
- If the 2×2 table has both margins fixed, then use χ^2_c or χ^2_H, as demonstrated in Example 23.4, or use the Fisher exact test of Section 24.16. As noted after Equation 23.7b, there are situations in which χ^2_c and χ^2_H are equal; otherwise, χ^2_H is routinely a better approximation of the Fisher exact test and is preferred to χ^2_c.

Computer software may present χ^2 or a continuity-corrected χ^2_c, or both, and the user must decide which one of these two test statistics to use (such as by the guidelines just given).

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*This paragraph and the next are a summary of the findings in many publications, such as those cited in the footnote that follows this one.

†Those promoting the analysis of any of the three models by using chi-square with the Yates correction for continuity (χ^2_c), or the Fisher exact test of Section 24.16, include Camilli (1990), Cox (1984), Fisher (1935), Kendall and Stuart (1979), Martín Andrés (1991), Mehta and Hilton (1993), Upton (1992), and Yates (1984). Among those concluding that χ^2_c should not be employed for all three models are Barnard (1947, 1979); Berkson (1978); Camilli and Hopkins (1978); Conover (1974); D'Agostino, Chase, and Belanger (1988); Garside and Mack (1976); Grizzle (1967); Haber (1980, 1982, 1987, 1990); Haviland (1990); Kempthorne (1979); Kroll (1989); Liddell (1976); Parshall and Kromrey (1996); Pearson (1947); Plackett (1964); Richardson (1990, 1994); Starmer, Grizzle, and Sen (1974); Storer and Kim (1990); and Upton (1982). Other procedures for testing 2×2 tables have been proposed (e.g., see Martín Andrés and Silva Mato (1994); Martín Andrés and Tapia Garcia (2004); and Overall, Rhoades, and Starbuck (1987)).

(e) One-Tailed Testing. The preceding hypotheses are two-tailed, which is the typical situation. However, one-tailed hypotheses (where a one-tailed hypothesis is specified before data are collected) are possible for data in 2×2 tables. In Example 23.2, the hypotheses could have been stated as follows:

H_0: In the sampled population, the proportion of left-handed children is the same or greater for boys compared to girls.

H_A: In the sampled population, the proportion of left-handed children is less for boys than for girls.

If the direction of the difference in the sample is that indicated in the null hypothesis (i.e., if $f_{11}/C_1 \geq f_{12}/C_2$), then H_0 cannot be rejected and the one-tailed analysis proceeds no further. However, if the direction of the difference in the sample is not in the direction of the null hypothesis (as in Example 23.2, where $6/34 < 12/36$), then it can be asked whether that difference is likely to indicate a difference in that direction in the population. In this example, one-tailed hypotheses could also have been stated as follows:

H_0: In the sampled population, the proportion of boys is the same or less for left-handed compared to right-handed children.

H_A: In the sampled population, the proportion of boys is greater for left-handed than for right-handed children.

This would ask whether the sample proportion f_{11}/R_1 (namely, 6/18) resulted from a population proportion less than or equal to the population proportion estimated by f_{21}/R_2 (i.e., 28/52).

Consistent with the preceding recommendations for two-tailed hypothesis testing, the following can be advised for one-tailed testing: For 2×2 tables in which no margin or only one margin is fixed, test by using one-half of the chi-square probability (for example, employing the critical value $\chi^2_{0.10,1}$ for testing at $\alpha = 0.05$), by dividing the resultant P by 2, or by using one-tailed values for Z in the normal approximation of Section 24.10. For tables with two fixed margins, the Fisher exact test of Section 24.16 is the preferred method of analysis, though if $R_1 = R_2$ or $C_1 = C_2$, we may calculate χ^2_c or, preferably, χ^2_H, and proceed as indicated previously for situations with one fixed margin. If neither $R_1 = R_2$ nor $C_1 = C_2$, using χ^2_H or χ^2_c yields a very poor approximation to the one-tailed Fisher exact test and is not recommended.

CONTINGENCY TABLES WITH SMALL FREQUENCIES

Section 22.5 discussed bias in chi-square goodness-of-fit testing when expected frequencies are "too small." As with goodness-of-fit testing, for a long time many statisticians (e.g., Fisher, 1925b) advised that chi-square analysis of contingency tables be employed only if each of the expected frequencies was at least 5.0—even after there was evidence that such analyses worked well with smaller frequencies (e.g., Cochran, 1952, 1954). The review and empirical analysis of Roscoe and Byars (1971) offer more useful guidelines. Although smaller sample sizes are likely to work well, a secure practice is to have the mean expected frequency be at least 6.0 when testing with α as small as 0.05, and at least 10.0 for $\alpha = 0.01$. Requiring an average expected frequency of at least 6 is typically less restrictive than stipulating that each $\hat{f}_{ij}$ be at least 5. Since the mean expected frequency is n/rc, the minimum sample size for

testing at the 0.05 significance level should be at least $n = 6rc = 6(2)(4) = 48$ for a 2×4 contingency table (such as in Example 23.1) and at least $6(2)(2) = 24$ for a 2×2 table (as in Exercises 23.2, 23.3, 23.4, and 23.5).

If any of the expected frequencies are smaller than recommended, then one or more rows or columns containing an offensively low $\hat{f}_{ij}$ might be discarded, or rows or columns might be combined to result in $\hat{f}_{ij}$'s of sufficient magnitude. However, such practices are not routinely advised, for they disregard information that can be important to the hypothesis testing. When possible, it is better to repeat the experiment with a sufficiently large n to ensure large enough expected frequencies. Some propose employing the log-likelihood ratio of Section 23.7 as a test less affected than chi-square by low frequencies, but this is not universally suggested. If both margins are fixed in a 2×2 contingency table, then the Fisher exact test of Section 24.16 is highly recommended when frequencies are small.

23.5 HETEROGENEITY TESTING OF 2 × 2 TABLES

Testing for heterogeneity of replicate samples in goodness-of-fit analysis was discussed in Section 22.6. An analogous procedure may be used with contingency-table data, as demonstrated in Example 23.5. Here, data set 1 is the data from Example 23.2, and each of the three other sets of data is a sample obtained by the same data-collection procedure for the purpose of testing the same hypothesis. Heterogeneity testing asks whether all four of the data sets are likely to have come from the same population of data. In this example, a calculation of χ^2 was done, as in Section 23.3a, for each of the four contingency tables; and H_0 was not rejected for any of the data sets. This failure to reject H_0 might reflect low power of the test due to small sample sizes, so it would be helpful to use the heterogeneity test to conclude whether it would be reasonable to combine the four sets of data and perform a more powerful test of H_0 with the pooled number of data.

EXAMPLE 23.5 A Heterogeneity Chi-Square Analysis of Four 2 × 2 Contingency Tables, Where Data Set 1 Is That of Example 23.2

(a) H_0: In the sampled population, handedness is independent of sex.
H_A: In the sampled population, handedness is not independent of sex.
$\alpha = 0.05$

Data Set 1

From the data of Example 23.2, $\chi^2 = 2.2523$, DF = 1, $0.10 < P < 0.25$.

Data Set 2

	Boys	*Girls*	*Total*	
Left-handed	4	7	11	
Right-handed	25	13	38	
Total	29	20	49	$\chi^2 = 3.0578$, DF = 1, $0.05 < P < 0.10$

Data Set 3

	Boys	*Girls*	*Total*	
Left-handed	7	10	17	
Right-handed	27	18	45	
Total	34	28	62	$\chi^2 = 1.7653$, DF = 1, $0.10 < P < 0.25$

Data Set 4

	Boys	*Girls*	*Total*	
Left-handed	4	7	11	
Right-handed	22	14	36	
Total	26	21	47	$\chi^2 = 2.0877$, DF = 1, $0.10 < P < 0.25$

(b) H_0: The four samples are homogeneous.
H_A: The four samples are heterogeneous.

Data Sets 1–4 Pooled

	Boys	*Girls*	*Total*	
Left-handed	21	36	57	$\chi^2 = 8.9505$
Right-handed	102	69	171	DF = 1
Total	123	105	228	

χ^2 for Data Set 1:	2.2523	DF = 1
χ^2 for Data Set 2:	3.0578	DF = 1
χ^2 for Data Set 3:	1.7653	DF = 1
χ^2 for Data Set 4:	2.0877	DF = 1
Total chi-square:	9.1631	DF = 4
Chi-square of pooled data:	8.9505	DF = 1
Heterogeneity chi-square	0.2126	DF = 3

For heterogeneity testing (using $\chi^2 = 0.2126$):
$\chi^2_{0.05,3} = 7.815$.
Therefore, do not reject H_0.

$$0.975 < P < 0.99 \quad [P = 0.98]$$

(c) H_0: In the sampled population, handedness is independent of sex.
H_A: In the sampled population, handedness is not independent of sex.

$\alpha = 0.05$

	Data Sets 1–4 Pooled		
	Boys	*Girls*	*Total*
Left-handed	21	36	57
Right-handed	102	69	171
Total	123	105	228

$\chi^2_{0.05,1} = 3.841$

$\chi^2 = 8.9505$; therefore, reject H_0.

$0.001 < P < 0.005$ [$P = 0.0028$]

In the test for heterogeneity, chi-square is calculated for each of the samples; these four separate χ^2 values are shown in Example 23.5a, along with the χ^2 for the contingency table formed by the four sets of data combined. The χ^2 values for the four separate contingency tables are them summed (to obtain what may be called a total chi-square, which is 9.1631), and the degrees of freedom for the four tables are also summed (to obtain a total DF, which is 4), as shown in Example 23.5b. The test for heterogeneity employs a chi-square value that is the absolute difference between the total chi-square and the chi-square from the table of combined data, with degrees of freedom that are the difference between the total degrees of freedom and the degrees of freedom from the table of combined data. In the present example, the heterogeneity χ^2 is 0.2126, with 3 degrees of freedom. That chi-square is associated with a probability much greater than 0.05, so H_0 is not rejected and it is concluded that the data of the four samples may be combined.

Example 23.5c considers the contingency table formed by combining the data of all four of the original tables and tests the same hypothesis of independence that was tested for each of the original tables. When the heterogeneity test fails to reject H_0, pooling of the data is generally desirable because it allows contingency-table analysis with a larger n.

Heterogeneity testing with 2×2 tables is performed without the chi-square correction for continuity, except when both margins are fixed, in which case χ^2_c is used for the combined data while χ^2 is used for all other steps in the analysis (Cochran, 1942; Lancaster, 1949). The heterogeneity test may also be performed for contingency tables with more than two rows or columns. To test for heterogeneity, the log-likelihood ratio, G (Section 23.7), may be used instead of χ^2.

23.6 SUBDIVIDING CONTINGENCY TABLES

In Example 23.1, the analysis of a 2×4 contingency table, it was concluded that there was a significant difference in human hair-color frequencies between males and females. Expressing the percent males and percent females in each column, as in Example 23.6a, and examining Figures 23.1 and 23.2 shows that the proportion of males in the blond column is prominently less than in the other columns. (Examining the data in this fashion can be helpful, although frequencies, not proportions, are used for the hypothesis test.)

EXAMPLE 23.6a The Data of Example 23.1, Where for Each Hair Color the Percent Males and Percent Females Are Indicated

	Hair color				
Sex	*Black*	*Brown*	*Blond*	*Red*	**Total**
Male	32 (37%)	43 (40%)	16 (20%)	9 (36%)	100
Female	55 (63%)	65 (60%)	64 (80%)	16 (64%)	200
Total	87	108	80	25	300

In Example 23.1, the null hypothesis that the four hair colors are independent of sex was rejected.

Thus, it might be suspected that the significant χ^2 calculated in Example 23.1 was due largely to the frequencies in column 3 of the table. To pursue that supposition, the data in column 3 may be momentarily ignored and the remaining 2×3 table considered; this is done in Example 23.6b. The nonsignificant χ^2 for this table supports the null hypothesis that these three hair colors are independent of sex in the population from which the sample came. Then, in Example 23.6c, a 2×2 table is formed by considering blond versus all other hair colors combined. For this table, the null hypothesis of independence is rejected.

EXAMPLE 23.6b The 2×3 Contingency Table Formed from Columns 1, 2, and 4 of the Original 2×4 Table. $\hat{f}_{ij}$ Values for the Cells of the 2×3 Table Are Shown in Parentheses

H_0: The occurrence of black, brown, and red hair is independent of sex.
H_A: The occurrence of black, brown, and red hair is not independent of sex.

$\alpha = 0.05$

	Hair color			
Sex	*Black*	*Brown*	*Red*	**Total**
Male	32 *(33.2182)*	43 *(41.2364)*	9 *(9.5455)*	84
Female	55 *(53.7818)*	65 *(66.7636)*	16 *(15.4545)*	136
Total	87	108	25	220

$\chi^2 = 0.245$ with DF = 2

$\chi^2_{0.05,2} = 5.991$

Therefore, do not reject H_0.

$$0.75 < P < 0.90 \quad [P = 0.88]$$

EXAMPLE 23.6c The 2 × 2 Contingency Table Formed by Combining Columns 1, 2, and 4 of the Original Table

H_0: Occurrence of blond and nonblond hair color is independent of sex.

H_A: Occurrence of blond and nonblond hair color is not independent of sex.

$\alpha = 0.05$

	Hair color		
Sex	*Blond*	*Nonblond*	**Total**
Male	16	84	100
Female	64	136	200
Total	80	220	300

$\chi^2 = 8.727$

DF = 1

$\chi^2_{0.05,1} = 3.841$

Therefore, reject H_0.

$$0.001 < P < 0.005 \quad [P = 0.0036]$$

By the described series of subdivisions and column combinations of the original contingency table, we see evidence suggesting that, among the four hair colors in the population, blond occurs between the sexes with relative frequencies different from those of the other colors. However, it is not strictly proper to test statistical hypotheses developed after examining the data to be tested. Therefore, the analysis of a subdivided contingency table should be considered only as a guide to developing hypotheses. Hypotheses suggested by this analysis then can be tested by obtaining a new set of data from the population of interest and stating those hypotheses in advance of the testing.

23.7 THE LOG-LIKELIHOOD RATIO FOR CONTINGENCY TABLES

The log-likelihood ratio was introduced in Section 22.7, where the G statistic (sometimes called G^2) was presented as an alternative to chi-square for goodness-of-fit testing. The G test may also be applied to contingency tables (Neyman and Pearson,

1928a, 1928b; Wilks, 1935), where

$$G = 2\left[\sum_i \sum_j f_{ij} \ln\left(\frac{f_{ij}}{\hat{f}_{ij}}\right)\right], \tag{23.8}$$

which, without the necessity of calculating expected frequencies, may readily be computed as

$$G = 2\left[\sum_i \sum_j f_{ij} \ln f_{ij} - \sum_i R_i \ln R_i - \sum_j C_j \ln C_j + n \ln n\right]. \tag{23.9}$$

If common logarithms (denoted by "log") are used instead of natural logarithms (indicated as "ln"), then use 4.60517 instead of 2 prior to the left bracket. Because G is approximately distributed as χ^2, Appendix Table B.1 may be used with $(r-1)(c-1)$ degrees of freedom. In Example 23.7, the contingency table of Example 23.1 is analyzed using the G statistic, with very similar results.

EXAMPLE 23.7 The G Test for the Contingency Table Data of Example 23.1

H_0: Hair color is independent of sex.
H_A: Hair color is not independent of sex.

$\alpha = 0.05$

	Hair color				
Sex	*Black*	*Brown*	*Blond*	*Red*	**Total**
Male	32	43	16	9	100
Female	55	65	64	16	200
Total	87	108	80	25	300

$$\begin{aligned}
G &= 4.60517\left[\sum\sum f_{ij} \log f_{ij} - \sum R_i \log R_i - \sum C_j \log C_j + n \log n\right] \\
&= 4.60517[(32)(1.50515) + (43)(1.63347) + (16)(1.20412) + (9)(0.95424) \\
&\quad + (55)(1.74036) + (65)(1.81291) + (64)(1.80618) + (16)(1.20412) \\
&\quad - (100)(2.00000) - (200)(2.30103) - (87)(1.93952) \\
&\quad - (108)(2.03342) - (80)(1.90309) - (25)(1.39794) + (300)(2.47712)] \\
&= 4.60517(2.06518) \\
&= 9.510 \text{ with DF} = 3
\end{aligned}$$

$\chi^2_{0.05,3} = 7.815$

Therefore, reject H_0.

$$0.01 < P < 0.025 \quad [P = 0.023]$$

In the case of a 2×2 table, the Yates correction for continuity (see Sections 23.3c and 23.3d) is applied by making each f_{ij} 0.5 closer to $\hat{f}_{ij}$. This may be accomplished (without calculating expected frequencies) as follows: If $f_{11}f_{22} - f_{12}f_{21}$ is negative add 0.5 to f_{11} and f_{22} and subtract 0.5 from f_{12} and f_{21}; if $f_{11}f_{22} - f_{12}f_{21}$ is positive subtract 0.5 from f_{11} and f_{22} and add 0.5 to f_{12} and f_{21}; then Equation 23.8 or 23.9 is applied using these modified values of f_{11}, f_{12}, f_{21}, and f_{22}.

Williams (1976) recommended that G be used in preference to χ^2 whenever $|f_{ij} - \hat{f}_{ij}| \geq \hat{f}_{ij}$ for any cell. Both χ^2 and G commonly result in the same conclusion for the hypothesis test, especially when n is large. When they do not, some statisticians favor employing G, and its use is found in some research reports and computer software. However, many others (e.g., Agresti, 2002: 24, 396; Agresti and Yang, 1987; Berry and Mielke, 1988; Hosmane, 1986; Hutchinson, 1979; Koehler, 1986; Larntz, 1978; Margolin and Light, 1974; Stelzl, 2000; Upton, 1982) have concluded that the χ^2 procedure is preferable to G; and generally it more closely refers to the probability of a Type I error.

23.8 MULTIDIMENSIONAL CONTINGENCY TABLES

Thus far, this chapter has considered two-dimensional contingency tables (tables with rows and columns as the two dimensions), where each of the two dimensions represents a nominal-scale variable. However, categorical data may also be collected and tabulated with respect to three or more nominal-scale variables, resulting in what are called multidimensional contingency tables—that is, tables with three or more dimensions (e.g., see Christensen, 1990; Everitt, 1992: Chapter 4; Fienberg, 1970, 1980; Goodman, 1970; Simonoff, 2003: Chapter 8). An example would be data from a study similar to that in Example 23.1, but where eye color is a third variable—in addition to the variables hair color and sex.

As the number of dimensions increases, so does the complexity of the analysis, and various interactions of variables are potentially of interest. Multidimensional contingency tables may be analyzed by extensions of the χ^2 and G testing discussed earlier in this chapter, as will be indicated in this section. Computer-program libraries often include provision for the analysis of such tables, including by utilizing what are known as *log-linear models*,* a large body of statistical procedures (e.g., see Everitt, 1992: Chapter 5; Fienberg, 1970, 1980; Howell, 2007: Chapter 17; Kennedy, 1992; Knoke and Burke, 1980; Tabachnik and Fidell, 2001: Chapter 7).

Figure 23.3 shows a three-dimensional contingency table. The three "rows" are species, the four "columns" are geographic locations, and the two "tiers" (or "layers") are presence and absence of a disease. If a sample is obtained containing individuals of these species, from these locations, and with and without the disease in question, then observed frequencies can be recorded in the 24 cells of this $3 \times 4 \times 2$ contingency table. We shall refer to the observed frequency in row i, column j, and tier l as f_{ijl}. We shall refer to the number of rows, columns, and tiers as r, c, and t, respectively. The sum of the frequencies in row i will be designated R_i, the sum in column j as C_j, and the sum in tier l as T_l. Friendly (1994, 1999), Hartigan and Kleiner (1981, 1984),

*Log-linear models are mathematical representations that also underlie analysis of variance (Chapters 10, 12, 14, 15, and 16) and multiple regression (Chapter 20). The term *log-linear model* was introduced in 1969 by Y. M. M. Bishop and S. E. Fienberg (David, 1995).

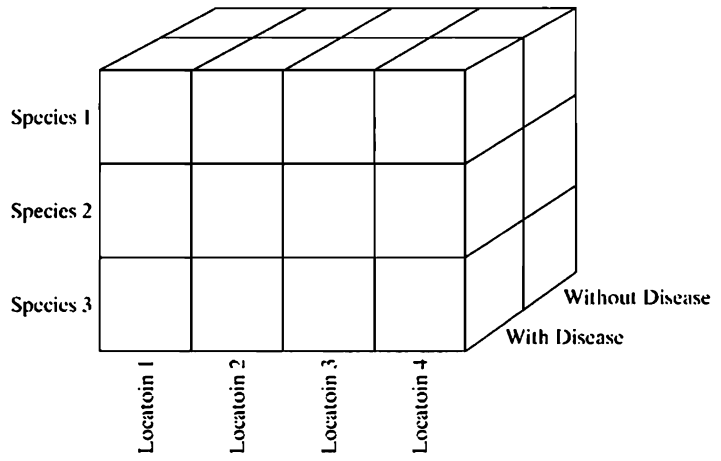

FIGURE 23.3: A three-dimensional contingency table, where the three rows are species, the four columns are locations, and the two tiers are occurrence of a disease. An observed frequency, f_{ijl}, will be recorded in each combination of row, column, and tier.

and Simonoff (2003: 329) discuss mosaic displays for contingency tables with more than two dimensions, and such graphical presentations can make multidimensional contingency table data easier to visualize and interpret than if they are presented only in tabular format.

Example 23.8 presents a $2 \times 2 \times 2$ contingency table where data (f_{ijl}) are collected as described previously, but only for two species and two locations. Note that throughout the following discussions the sum of the expected frequencies for a given row, column, or tier equals the sum of the observed frequencies for that row, column, or tier.

EXAMPLE 23.8 Test for Mutual Independence in a $2 \times 2 \times 2$ Contingency Table

H_0: Disease occurrence, species, and location are all mutually independent in the population sampled.

H_A: Disease occurrence, species, and location are not all mutually independent in the population sampled.

The observed frequencies (f_{ijl}):

	Disease present		**Disease absent**		**Species totals**
	Location 1	*Location 2*	*Location 1*	*Location 2*	($r = 2$)
Species 1	44	12	38	10	$R_1 = 104$
Species 2	28	22	20	18	$R_2 = 88$
Disease totals ($t = 2$):	$T_1 = 106$		$T_2 = 86$		*Grand total:*
Location totals: ($c = 2$):	$C_1 = 130, C_2 = 62$				$n = 192$

The expected frequencies ($\hat{f}_{ijl}$):

	Disease present		Disease absent		
	Location 1	*Location 2*	*Location 1*	*Location 2*	**Species totals**
Species 1	38.8759	18.5408	31.5408	15.0425	$R_1 = 104$
Species 2	32.8950	15.6884	26.6884	12.7283	$R_2 = 88$
Disease totals:	$T_1 = 106$		$T_2 = 86$		*Grand total:*
Location totals:	$C_1 = 130, C_2 = 62$				$n = 192$

$$\chi^2 = \sum\sum\sum \frac{(f_{ijl} - \hat{f}_{ijl})^2}{\hat{f}_{ijl}}$$

$$\chi^2 = \frac{(44 - 38.8759)^2}{38.8759} + \frac{(12 - 18.5408)^2}{18.5408} + \frac{(38 - 31.5408)^2}{31.5408} + \frac{(10 - 15.0425)^2}{15.0425} + \frac{(28 - 32.8950)^2}{32.8950} + \frac{(22 - 15.6884)^2}{15.6884} + \frac{(20 - 26.6884)^2}{26.6884} + \frac{(18 - 12.7283)^2}{12.7283}$$

$$= 0.6754 + 2.3075 + 1.3228 + 1.6903 + 0.7284 + 2.5392 + 1.6762 + 2.1834$$

$$= 13.123$$

$$\nu = rct - r - c - t + 2 = (2)(2)(2) - 2 - 2 - 2 + 2 = 4$$

$$\chi^2_{0.05,4} = 9.488$$

Reject H_0.

$$0.01 < P < 0.025 \quad [P = 0.011]$$

(a) Mutual Independence. We can test more than one null hypothesis using multidimensional contingency-table data. An overall kind of hypothesis is that which states mutual independence among all the variables. Another way of expressing this H_0 is that there are no interactions (either three-way or two-way) among any of the variables. For this hypothesis, the expected frequency in row i, column j, and tier l is

$$\hat{f}_{ijl} = \frac{R_i C_j T_l}{n^2}, \tag{23.10}$$

where n is the total of all the frequencies in the entire contingency table.

null hypothesis is tested by computing

$$\chi^2 = \sum_{i=1}^{r}\sum_{j=1}^{c}\sum_{l=1}^{t}\frac{(f_{ijl} - \hat{f}_{ijl})^2}{\hat{f}_{ijl}}, \tag{23.11}$$

which is a simple extension of the chi-square calculation for a two-dimensional table (by Equation 23.1). The degrees of freedom for this test are the sums of the degrees of freedom for all interactions:

$$\nu = (r-1)(c-1)(t-1) + (r-1)(c-1) + (r-1)(t-1) + (c-1)(t-1), \tag{23.12}$$

which is equivalent to

$$\nu = rct - r - c - t + 2. \tag{23.13}$$

(b) Partial Independence. If the preceding null hypothesis is not rejected, then we conclude that all three variables are mutually independent and the analysis proceeds no further. If, however, H_0 is rejected, then we may test further to conclude between which variables dependencies and independencies exist. For example, we may test whether one of the three variables is independent of the other two, a situation known as *partial independence.**

For the hypothesis of rows being independent of columns and tiers, we need total frequencies for rows and total frequencies for combinations of columns and tiers. Designating the total frequency in column j and tier l as $(CT)_{jl}$, expected frequencies are calculated as

$$\hat{f}_{ijl} = \frac{R_i(CT)_{jl}}{n}, \tag{23.14}$$

and Equation 23.11 is used with degrees of freedom

$$\nu = (r-1)(c-1)(t-1) + (r-1)(c-1) + (r-1)(t-1), \tag{23.15}$$

which is equivalent to

$$\nu = rct - ct - r + 1. \tag{23.16}$$

For the null hypothesis of columns being independent of rows and tiers, we compute expected frequencies using column totals, C_j, and the totals for row and tier combinations, $(RT)_{il}$:

$$\hat{f}_{ijl} = \frac{C_j(RT)_{il}}{n}, \tag{23.17}$$

and

$$\nu = rct - rt - c + 1. \tag{23.18}$$

And, for the null hypothesis of tiers being independent of rows and columns, we use tier totals, T_l, and the totals for row and column combinations, $(RC)_{ij}$:

$$\hat{f}_{ijl} = \frac{T_l(RC)_{ij}}{n}; \tag{23.19}$$

$$\nu = rct - rc - t + 1. \tag{23.20}$$

*A different hypothesis is that of *conditional independence*, where two of the variables are said to be independent in each level of the third (but each may have dependence on the third). This is discussed in the references cited at the beginning of this section.

In Example 23.9, all three pairs of hypotheses for partial independence are tested. In one of the three (the last), H_0 is not rejected; thus we conclude that presence of disease is independent of species and location. However, the hypothesis test of Example 23.8 concluded that all three variables are not independent of each other. Therefore, we suspect that species and location are not independent. The independence of these two variables may be tested using a two-dimensional contingency table, as described earlier, in Section 23.3, and demonstrated in Example 23.10. In the present case, the species-location interaction is tested by way of a 2×2 contingency table, and we conclude that these two factors are not independent (i.e., species occurrence depends on geographic location).

In general, hypotheses to be tested should be stated before the data are collected. But the hypotheses proposed in Example 23.10 were suggested *after* the data were examined. Therefore, instead of accepting the present conclusion of the analysis in Example 23.10, such a conclusion should be reached by testing this pair of hypotheses upon obtaining a new set of data from the population of interest and stating the hypotheses in advance of the testing.

EXAMPLE 23.9 Test for Partial Independence in a $2 \times 2 \times 2$ Contingency Table. As the H_0 of Overall Independence Was Rejected in Example 23.8, We May Test the Following Three Pairs of Hypotheses

H_0: Species is independent of location and disease.
H_A: Species is not independent of location and disease.

The expected frequencies ($\hat{f}_{ijl}$):

	Disease present		Disease absent		
	Location 1	*Location 2*	*Location 1*	*Location 2*	**Species totals**
Species 1	39.0000	18.4167	31.4167	15.1667	$R_1 = 104$
Species 2	33.0000	15.5833	26.5833	12.8333	$R_2 = 88$
Location and disease totals:	$(CT)_{11} = 72$	$(CT)_{12} = 34$	$(CT)_{21} = 58$	$(CT)_{22} = 28$	*Grand total:* $n = 192$

$$\chi^2 = \frac{(44 - 39.0000)^2}{39.0000} + \frac{(12 - 18.4167)^2}{18.4167} + \frac{(38 - 31.4167)^2}{31.4167} + \cdots + \frac{(18 - 12.8333)^2}{12.8333}$$

$$= 0.6410 + 2.2357 + 1.3795 + 1.7601 + 0.7576 + 2.6422 + 1.6303 + 2.0801$$

$$= 13.126$$

$$\nu = rct - ct - r + 1 = (2)(2)(2) - (2)(2) - 2 + 1 = 3$$

$$\chi^2_{0.05,3} = 7.815$$

Reject H_0. Species is not independent of location and presence of disease.

$$0.005 < P < 0.001 \quad [P = 0.0044]$$

H_0: Location is independent of species and disease.

H_A: Location is not independent of species and disease.

The expected frequencies ($\hat{f}_{ijl}$):

	Disease present		**Disease absent**		
	Species 1	*Species 2*	*Species 1*	*Species 2*	**Location totals**
Location 1	37.91677	33.8542	32.5000	25.7292	$C_1 = 130$
Location 2	18.0833	16.1458	15.5000	12.2708	$C_2 = 62$
Species and disease totals:	$(RT)_{11} = 56$	$(RT)_{12} = 50$	$(RT)_{21} = 48$	$(RT)_{22} = 38$	*Grand total:* $n = 192$

$$\chi^2 = \frac{(44 - 37.9167)^2}{37.9167} + \frac{(28 - 33.8542)^2}{33.8542} + \cdots + \frac{(18 - 12.2708)^2}{12.2708}$$

$$= 0.9760 + 1.0123 + 0.9308 + 1.2757 + 2.0464 + 2.1226 + 1.9516 + 2.6749$$

$$= 12.990 \text{ .}$$

$$\nu = rct - rt - c + 1 = (2)(2)(2) - (2)(2) - 2 + 1 = 3$$

$$\chi^2_{0.05,3} = 7.815$$

Reject H_0. Location is not independent of species and presence of disease.

$$0.001 < P < 0.005 \quad [P = 0.0047]$$

H_0: Presence of disease is independent of species and location.

H_A: Presence of disease is not independent of species and location.

The expected frequencies ($\hat{f}_{ijl}$):

	Species 1		**Species 2**		
	Location 1	*Location 2*	*Location 1*	*Location 2*	**Disease totals**
Disease present	45.2708	12.1458	26.5000	22.0833	$T_1 = 106$
Disease absent	36.7292	9.8542	21.5000	17.9167	$T_2 = 86$
Species and location totals:	$(RC)_{11} = 82$	$(RC)_{12} = 22$	$(RC)_{21} = 48$	$(RC)_{22} = 40$	*Grand total:* $n = 192$

$$\chi^2 = \frac{(44 - 45.2708)^2}{45.2708} + \frac{(12 - 12.1458)^2}{12.1458} + \cdots + \frac{(18 - 17.9167)^2}{17.9167}$$
$$= 0.0357 + 0.0018 + 0.0849 + 0.0003 + 0.0440 + 0.0022 + 0.1047 + 0.0004$$
$$= 0.274$$

$\nu = rct - rc - t + 1 = (2)(2)(2) - (2)(2) - 2 + 1 = 3$

$\chi^2_{0.05,3} = 7.815$

Do not reject H_0.

$0.95 < P < 0.975 \quad [P = 0.96]$

EXAMPLE 23.10 Test for Independence of Two Variables, Following Tests for Partial Dependence

The hypothesis test of Example 23.8 concluded that all three variables are not mutually independent, while the last test in Example 23.9 concluded that presence of disease is independent of species and location. Therefore, it is desirable (and permissible) to test the following two-dimensional contingency table:

H_0: Species occurrence is independent of location.

H_A: Species occurrence is not independent of location.

	Location 1	*Location 2*	*Total*
Species 1	82	22	104
Species 2	48	40	88
Total	130	62	192

$\chi^2 = 12.874$

$\nu = (r - 1)(c - 1) = 1$

$\chi^2_{0.05,1} = 3.841$

Reject H_0.

$P < 0.001 \quad [P = 0.00033]$

(c) The Log-Likelihood Ratio. The log-likelihood ratio of Section 23.7 can be expanded to contingency tables with more than two dimensions. While some authors have chosen this procedure over chi-square testing and it is found in some statistical computer packages, others (e.g., Haber, 1984; Hosmane, 1987; Koehler, 1986; Larntz, 1978; Rudas, 1986; and Stelzl, 2000) have concluded that χ^2 is preferable. With χ^2 in contrast to G, the probability of a Type I error is generally closer to α.

EXERCISES

23.1. Consider the following data for the abundance of a certain species of bird.

(a) Using chi-square, test the null hypothesis that the ratio of numbers of males to females was the same in all four seasons.

(b) Apply the G test to that hypothesis.

Sex	*Spring*	*Summer*	*Fall*	*Winter*
Males	163	135	71	43
Females	86	77	40	38

23.2. The following data are frequencies of skunks found with and without rabies in two different geographic areas.

(a) Using chi-square, test the null hypothesis that the incidence of rabies in skunks is the same in both areas.

(b) Apply the G test to that hypothesis.

Area	*With rabies*	*Without rabies*
E	14	29
W	12	38

23.3. Data were collected as in Exercise 23.2, but with the additional tabulation of the sex of each skunk recorded, as follows. Test for mutual independence; and, if H_0 is rejected, test for partial independence.

	With rabies		**Without rabies**	
Area	*Male*	*Female*	*Male*	*Female*
E	42	33	55	63
W	84	51	34	48

23.4. A sample of 150 was obtained of men with each of three types of cancer, and the following data are the frequencies of blood types for the men.

(a) Using chi-square, test the null hypothesis that, in the sampled population, the frequency distribution of the three kinds of cancer is the same for men with each of the four blood types (which is the same as testing the H_0 that the frequency distribution of the four blood types is the same in men with each of the three kinds of cancer).

(b) Apply the G test to the same hypothesis.

	Blood type				
Cancer type	*O*	*A*	*B*	*AB*	**Total**
Colon	61	65	18	6	$R_1 = 150$
Lung	69	57	15	9	$R_2 = 150$
Prostate	73	60	12	5	$R_3 = 150$

CHAPTER 24

Dichotomous Variables

This chapter will concentrate on nominal-scale data that come from a population with only two categories. As examples, members of a mammal litter might be classified as male or female, victims of a disease as dead or alive, trees in an area as "deciduous" or "evergreen," or progeny as color-blind or not color-blind. A nominal-scale variable having two categories is said to be *dichotomous*. Such variables have already been discussed in the context of goodness of fit (Chapter 22) and contingency tables (Chapter 23).

The proportion of the population belonging to one of the two categories is denoted as p (here departing from the convention of using Greek letters for population parameters). Therefore, the proportion of the population belonging to the second class is $1 - p$, and the notation $q = 1 - p$ is commonly employed. For example, if 0.5 (i.e., 50%) of a population were male, then we would know that 0.5 (i.e., $1 - 0.5$) of the population were female, and we could write $p = 0.5$ and $q = 0.5$; if 0.4 (i.e., 40%) of a population were male, then 0.6 (i.e., 60%) of the population were female, and we could write $p = 0.4$ and $q = 0.6$.

If we took a random sample of ten from a population where $p = q = 0.5$, then we might expect that the sample would consist of five males and five females. However, we should not be too surprised to find such a sample consisting of six males and four females, or four males and six females, although neither of these combinations would be expected with as great a frequency as samples possessing the population sex ratio of 5 : 5. It would, in fact, be possible to obtain a sample of ten with nine males and one female, or even one consisting of all males, but the probabilities of such samples being encountered by random chance are relatively low.

If we were to obtain a large number of samples from the population under consideration, the frequency of samples consisting of no males, one male, two males, and so on would be described by the *binomial distribution* (sometimes referred to as the "Bernoulli distribution"*). Let us now examine binomial probabilities.

BINOMIAL PROBABILITIES

Consider a population consisting of two categories, where p is the proportion of individuals in one of the categories and $q = 1 - p$ is the proportion in the other. Then the probability of selecting at random from this population a member of the first category is p, and the probability of selecting a member of the second category is q.†

For example, let us say we have a population of female and male animals, in proportions of $p = 0.4$ and $q = 0.6$, respectively, and we take a random sample of two individuals from the population. The probability of the first being a female is p (i.e., 0.4) and the probability of the second being a female is also p. As the probability of two independent (i.e., mutually exclusive) events both occurring is the product of the probabilities of the two separate events (Section 5.7), the probability of having two females in a sample of two is $(p)(p) = p^2 = 0.16$; the probability of the sample of two consisting of two males is $(q)(q) = q^2 = 0.36$.

What is the probability of the sample of two consisting of one male and one female? This could occur by the first individual being a female and the second a male (with a probability of pq) or by the first being a male and the second a female (which would occur with a probability of qp). The probability of either of two mutually exclusive outcomes is the sum of the probabilities of each outcome (Section 5.6), so the probability of one female and one male in the sample is $pq + qp = 2pq = 2(0.4)(0.6) = 0.48$. Note that $0.16 + 0.36 + 0.48 = 1.00$.

Now consider another sample from this population, one where $n = 3$. The probability of all three individuals being female is $ppp = p^3 = (0.4)^3 = 0.064$. The probability of two females and one male is ppq (for a sequence of ♀ ♀ ♂) + pqp (for ♀ ♂ ♀) + qpp (for ♂ ♀ ♀), or $3p^2q = 3(0.4)^2(0.6) = 0.288$. The probability of one female and two males is pqq (for ♀ ♂ ♂) + qpq (for ♂ ♀ ♂) + qqp (for ♂ ♂ ♀), or $3pq^2 = 3(0.4)(0.6)^2 = 0.432$. And, finally, the probability of all three being males is $qqq = q^3 = (0.6)^3 = 0.216$. Note that $p^3 + 3p^2q + 3pq^2 + q^3 = 0.064 + 0.288 + 0.432 + 0.216 = 1.000$ (meaning that there is a 100% probability—that is, it is certain—that the three animals will be in one of these three combinations of sexes).

If we performed the same exercise with $n = 4$, we would find that the probability of four females is $p^4 = (0.4)^4 = 0.0256$, the probability of three females (and one male) is $4p^3q = 4(0.4)^3(0.6) = 0.1536$, the probability of two females is $6p^2q^2 = 0.3456$,

*The binomial formula in the following section was first described, in 1676, by English scientist-mathematician Sir Isaac Newton (1642–1727), more than 10 years after he discovered it (Gullberg, 1997: 776). Its first proof, for positive integer exponents, was given by the Swiss mathematician Jacques (also known as Jacob, Jakob, or James) Bernoulli (1654–1705), in a 1713 posthumous publication; thus, each observed event from a binomial distribution is sometimes called a Bernoulli trial. Jacques Bernoulli's nephew, Nicholas Bernoulli (1687–1759), is given credit for editing that publication and writing a preface for it, but Hald (1984) explains that in 1713 Nicholas also presented an improvement to his uncle's binomial theorem. David (1995) attributes the first use of the term *binomial distribution* to G. U. Yule, in 1911.

†This assumes "sampling with replacement." That is, each individual in the sample is taken at random from the population and then is returned to the population before the next member of the sample is selected at random. Sampling without replacement is discussed in Section 24.2. If the population is very large compared to the size of the sample, then sampling with and without replacement are indistinguishable in practice.

the probability of one female is $4pq^3 = 0.3456$, and the probability of no females (i.e., all four are male) is $q^4 = 0.1296$. (The sum of these five terms is 1.0000, a good arithmetic check.)

If a random sample of size n is taken from a binomial population, then the probability of X individuals being in one category (and, therefore, $n - X$ individuals in the second category) is

$$P(X) = \binom{n}{X} p^X q^{n-X}. \tag{24.1}$$

In this equation, $p^X q^{n-X}$ refers to the probability of sample consisting of X items, each having a probability of p, and $n - X$ items, each with probability q. The *binomial coefficient*,

$$\binom{n}{X} = \frac{n!}{X!(n - X)!}, \tag{24.2}$$

is the number of ways X items of one kind can be arranged with $n - X$ items of a second kind, or, in other words, it is ${}_nC_X$, the number of possible *combinations* of n items divided into one group of X items and a second group of $n - X$ items. (See Section 5.3 for a discussion of combinations and Equation 5.3 explaining the factorial notation, "!".) Therefore, Equation 24.1 can be written as

$$P(X) = \frac{n!}{X!(n - X)!} p^X q^{n-X}. \tag{24.3}$$

Thus, $\binom{n}{X} p^X q^{n-X}$ is the Xth term in the expansion of $(p + q)^n$, and Table 24.1 shows this expansion for powers up through 6. Note that for any power, n, the sum of the two exponents in any term is n. Furthermore, the first term will always be p^n, the second will always contain $p^{n-1}q$, the third will always contain $p^{n-2}q^2$, and so on, with the last term always being q^n. The sum of all the terms in a binomial expansion will always be 1.0, for $p + q = 1$, and $(p + q)^n = 1^n = 1$.

As for the coefficients of these terms in the binomial expansion, the Xth term of the nth power expansion can be calculated by Equation 24.3. Furthermore, the examination of these coefficients as shown in Table 24.2 has been deemed interesting for centuries. This arrangement is known as *Pascal's triangle*.* We can see from this

TABLE 24.1: Expansion of the Binomial, $(p + q)^n$

n	$(p + q)^n$
1	$p + q$
2	$p^2 + 2pq + q^2$
3	$p^3 + 3p^2q + 3pq^2 + q^3$
4	$p^4 + 4p^3q + 6p^2q^2 + 4pq^3 + q^4$
5	$p^5 + 5p^4q + 10p^3q^2 + 10p^2q^3 + 5pq^4 + q^5$
6	$p^6 + 6p^5q + 15p^4q^2 + 20p^3q^3 + 15p^2q^4 + 6pq^5 - q^6$

*Blaise Pascal (1623–1662), French mathematician and physicist and one of the founders of probability theory (in 1654, immediately before abandoning mathematics to become a religious recluse). He had his triangular binomial coefficient derivation published in 1665, although knowledge of the triangular properties appears in Chinese writings as early as 1303 (Cajori, 1954; David, 1962; Gullberg 1997: 141; Struik, 1967: 79). Pascal also invented (at age 19) a mechanical adding and subtracting machine which, though patented in 1649, proved too expensive to be practical to construct (Asimov, 1982: 130–131). His significant contributions to the study of fluid pressures have been honored by naming the international unit of pressure the pascal, which is a pressure of one

TABLE 24.2: Binomial Coefficient, ${}_nC_X$

n	$X = 0$	1	2	3	4	5	6	7	8	9	10	Sum of coefficients
1	1	1										$2 = 2^1$
2	1	2	1									$4 = 2^2$
3	1	3	3	1								$8 = 2^3$
4	1	4	6	4	1							$16 = 2^4$
5	1	5	10	10	5	1						$32 = 2^5$
6	1	6	15	20	15	6	1					$64 = 2^6$
7	1	7	21	35	35	21	7	1				$128 = 2^7$
8	1	8	28	56	70	56	28	8	1			$256 = 2^8$
9	1	9	36	84	126	126	84	36	9	1		$512 = 2^9$
10	1	10	45	120	210	252	210	120	45	10	1	$1024 = 2^{10}$

triangular array that any binomial coefficient is the sum of two coefficients on the line above it, namely,

$$\binom{n}{X} = \binom{n-1}{X-1} + \binom{n-1}{X}. \tag{24.4}$$

This can be more readily observed if we display the triangular array as follows:

$$\begin{array}{ccccccccccc}
 & & & & & 1 & & & & & \\
 & & & & 1 & & 1 & & & & \\
 & & & 1 & & 2 & & 1 & & & \\
 & & 1 & & 3 & & 3 & & 1 & & \\
 & 1 & & 4 & & 6 & & 4 & & 1 & \\
1 & & 5 & & 10 & & 10 & & 5 & & 1
\end{array}$$

Also note that the sum of all coefficients for the nth power binomial expansion is 2^n. Appendix Table B.26a presents binomial coefficients for much larger n's and X's, and they will be found useful later in this chapter.

Thus, we can calculate probabilities of category frequencies occurring in random samples from a binomial population. If, for example, a sample of five (i.e., $n = 5$) is taken from a population composed of 50% males and 50% females (i.e., $p = 0.5$ and $q = 0.5$) then Example 24.1 shows how Equation 24.3 is used to determine the probability of the sample containing 0 males, 1 male, 2 males, 3 males, 4 males, and 5 males. These probabilities are found to be 0.03125, 0.15625, 0.31250, 0.31250, 0.15625, and 0.03125, respectively. This enables us to state that if we took 100 random samples of five animals each from the population, about three of the samples [i.e., $(0.03125)(100) = 3.125$ of them] would be expected to contain all females, about 16 [i.e., $(0.15625)(100) = 15.625$] to contain one male and four females, 31 [i.e., $(0.31250)(100)$] to consist of two males and three females, and so on. If we took 1400 random samples of five, then $(0.03125)(1400) = 43.75$ [i.e., about 44] of them would be expected to contain all females, and so on. Figure 24.1a shows graphically

newton per square meter (where a newton—named for Sir Isaac Newton—is the unit of force representing a one-kilogram mass accelerating at the rate of one meter per second per second). Pascal is also the name of a computer programming language developed in 1970 by Niklaus Wirth. The relationship of Pascal's triangle to ${}_nC_X$ was first published in 1685 by the English mathematician John Wallis (1616–1703) (David, 1962: 123–124).

EXAMPLE 24.1 Computing Binomial Probabilities, $P(X)$, Where $n = 5$, $p = 0.5$, and $q = 0.5$ (Following Equation 24.3)

X	$P(X)$
0	$\frac{5!}{0!5!}(0.5^0)(0.5^5) = (1)(1.0)(0.03125) = 0.03125$
1	$\frac{5!}{1!4!}(0.5^1)(0.5^4) = (5)(0.5)(0.0625) = 0.15625$
2	$\frac{5!}{2!3!}(0.5^2)(0.5^3) = (10)(0.25)(0.125) = 0.31250$
3	$\frac{5!}{3!2!}(0.5^3)(0.5^2) = (10)(0.125)(0.25) = 0.31250$
4	$\frac{5!}{4!1!}(0.5^4)(0.5^1) = (5)(0.0625)(0.5) = 0.15625$
5	$\frac{5!}{5!0!}(0.5^5)(0.5^0) = (1)(0.03125)(1.0) = 0.03125$

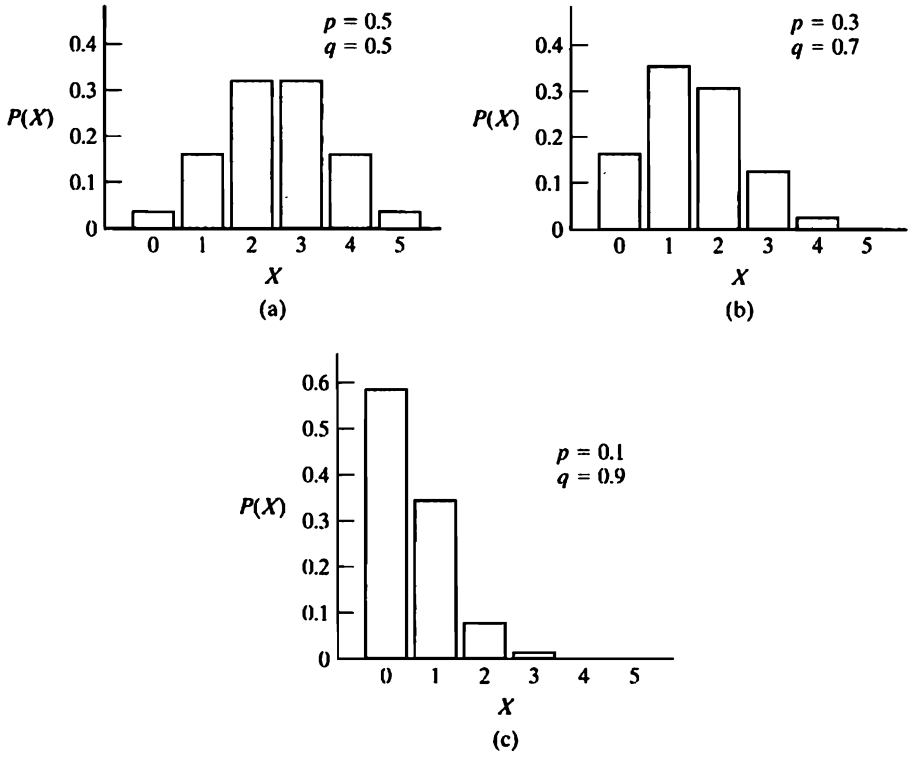

FIGURE 24.1: The binomial distribution, for $n = 5$. (a) $p = q = 0.5$. (b) $p = 0.3$, $q = 0.7$. (c) $p = 0.1$ $q = 0.9$. These graphs were drawn utilizing the proportions given by Equation 24.1.

the binomial distribution for $p = q = 0.5$, for $n = 5$. Note, from Figure 24.1a and Example 24.1, that when $p = q = 0.5$ the distribution is symmetrical [i.e., $P(0) = P(n), P(1) = P(n - 1)$, etc.], and Equation 24.3 becomes

$$P(X) = \frac{n!}{X!(n - X)!}0.5^n. \tag{24.5}$$

Appendix Table B.26b gives binomial probabilities for $n = 2$ to $n = 20$, for $p = 0.5$.

Example 24.2 presents the calculation of binomial probabilities for the case where $n = 5, p = 0.3$, and $q = 1 - 0.3 = 0.7$. Thus, if we were sampling a population consisting of 30% males and 70% females, 0.16807 (i.e., 16.807%) of the samples would be expected to contain no males, 0.36015 to contain one male and four females, and so on. Figure 24.1b presents this binomial distribution graphically, whereas Figure 24.1c shows the distribution where $p = 0.1$ and $q = 0.9$.

EXAMPLE 24.2 Computing Binomial Probabilities, $P(X)$, Where $n = 5$, $p = 0.4$, and $q = 0.7$ (Following Equation 24.3)

X	$P(X)$
0	$\frac{5!}{0!5!}(0.3^0)(0.7^5) = (1)(1.0)(0.16807) = 0.16807$
1	$\frac{5!}{1!4!}(0.3^1)(0.7^4) = (5)(0.3)(0.2401) = 0.36015$
2	$\frac{5!}{2!3!}(0.3^2)(0.7^3) = (10)(0.09)(0.343) = 0.30870$
3	$\frac{5!}{3!2!}(0.3^3)(0.7^2) = (10)(0.027)(0.49) = 0.13230$
4	$\frac{5!}{4!1!}(0.3^4)(0.7^1) = (5)(0.0081)(0.7) = 0.02835$
5	$\frac{5!}{5!0!}(0.3^5)(0.7^0) = (1)(0.00243)(1.0) = 0.00243$

For calculating binomial probabilities for large n, it is often convenient to employ logarithms. For this reason, Appendix Table B.40, a table of logarithms of factorials, is provided. Alternatively, it is useful to note that the denominator of Equation 24.3 cancels out much of the numerator, so that it is possible to simplify the computation of $P(X)$, especially in the tails of the distribution (i.e., for low X and for high X), as shown in Example 24.3. If p is very small, then the use of the Poisson distribution (Section 25.1), should be considered.*

The mean of a binomial distribution of counts X is

$$\mu_X = np, \tag{24.6}$$

*Raff (1956) and Molenaar (1969a, 1969b) discuss several approximations to the binomial distribution, including the normal and Poisson distributions.

EXAMPLE 24.3 Computing Binomial Probabilities, $P(X)$, with $n = 400$, $p = 0.02$, and $q = 0.98$

(Many calculators can operate with large powers of numbers; otherwise, logarithms may be used.)

X	$P(X)$
0	$\frac{n!}{0!(n-0)!}p^0q^{n-0} = q^n = 0.98^{400} = 0.00031$
1	$\frac{n!}{1!(n-1)!}p^1q^{n-1} = npq^{n-1} = (400)(0.02)(0.98^{399}) = 0.00253$
2	$\frac{n!}{2!(n-2)!}p^2q^{n-2} = \frac{n(n-1)}{2!}p^2q^{n-2}$ $= \frac{(400)(399)}{2}(0.02^2)(0.98^{398}) = 0.01028$
3	$\frac{n!}{3!(n-3)!}p^3q^{n-3} = \frac{n(n-1)(n-2)}{3!}p^3q^{n-3}$ $= \frac{(400)(399)(398)}{(3)(2)}(0.02^3)(0.98^{397}) = 0.02784$

and so on.

the variance* of X is

$$\sigma_X^2 = npq, \tag{24.8}$$

and the standard deviation of X is

$$\sigma_X = \sqrt{npq}. \tag{24.9}$$

Thus, if we have a binomially distributed population where p (e.g., the proportion of males) $= 0.5$ and q (e.g., the proportion of females) $= 0.5$ and we take 10 samples from that population, the mean of the 10 X's (i.e., the mean number of males per sample) would be expected to be $np = (10)(0.05) = 5$ and the standard deviation of the 10 X's would be expected to be $\sqrt{npq} = \sqrt{(10)(0.5)(0.5)} = 1.58$. Our concern typically is with the distribution of the expected probabilities rather than the expected X's, as will be explained in Section 24.3.

24.2 THE HYPERGEOMETRIC DISTRIBUTION

Binomial probabilities (Section 24.1) may result from what is known as "sampling with replacement." This means that after an item is randomly removed from the

*A measure of symmetry (see Section 6.5a) for a binomial distribution is

$$\gamma_1 = \frac{q - p}{\sqrt{npq}}, \tag{24.7}$$

so it can be seen that $\gamma_1 = 0$ only when $p = q = 0.05$, $\gamma_1 > 0$ implies a distribution skewed to the right (as in Figures 24.1b and 24.1c) and $\gamma_1 < 0$ indicates a distribution skewed to the left.

population to be part of the sample it is returned to the population before randomly selecting another item for inclusion in the sample. (This assumes that after the item is returned to the population it has the same chance of being selected again as does any other member of the population; in many biological situations—such as catching a mammal in a trap—this is not so.) Sampling with replacement ensures that the probability of selecting an item belonging to a specific one of the binomial categories remains constant. If sampling from an actual population is performed without replacement, then selecting an item from the first category reduces p and increases q (and, if the selected item were from the second category, then q would decrease and p would increase). Binomial probabilities may also arise from sampling "hypothetical" populations (introduced in Section 2.2), such as proportions of heads and tails from all possible coin tosses or of males and females in all possible fraternal twins.

Probabilities associated with sampling without replacement follow the *hypergeometric distribution* instead of the binomial distribution. The probability of obtaining a sample of n items from a hypergeometric distribution, where the sample consists of X items in one category and $n - X$ items in a second category, is

$$P(X) = \frac{\binom{N_1}{X}\binom{N_2}{n-X}}{\binom{N_T}{n}} \tag{24.10}$$

$$= \frac{N_1!N_2!n!(N_T - n)!}{X!(N_1 - X)!(n - X)!(N_2 - n + X)!N_T!}. \tag{24.11}$$

Here, N_T is the total number of items in the population, N_1 in category 1 and N_2 in category 2. For example, we could ask what the probability is of forming a sample consisting of three women and two men by taking five people at random from a group of eight women and six men. As $N_1 = 8, N_2 = 6, N_T = 14, n = 5$, and $X = 3$, the probability is

$$P(X) = \frac{\binom{8}{3}\binom{6}{2}}{\binom{14}{5}}$$

$$= \frac{8!\,6!\,5!X\,9!}{3!\,5!\,2!\,4!\,14!}$$

$$= \frac{(8\cdot 7\cdot 6\cdot 5\cdot 4\cdot 3\cdot 2)(6\cdot 5\cdot 4\cdot 3\cdot 2)(5\cdot 4\cdot 3\cdot 2)(9\cdot 8\cdot 7\cdot 6\cdot 5\cdot 4\cdot 3\cdot 2)}{(3\cdot 2)(5\cdot 4\cdot 3\cdot 2)(2)(4\cdot 3\cdot 2)(14\cdot 13\cdot 12\cdot 11\cdot 10\cdot 9\cdot 8\cdot 7\cdot 6\cdot 5\cdot 4\cdot 3\cdot 2)}$$

$$= 0.4196.$$

If the population is very large compared to the size of the sample, then the result of sampling with replacement is indistinguishable from that of sampling without replacement, and the hypergeometric distribution approaches—and is approximated by—the binomial distribution. Table 24.3 compares the binomial distribution with $p = 0.01$ and $n = 100$ to three hypergeometric distributions with the same p and n but with different population sizes. It can be seen that for larger N_T the hypergeometric is closer to the binomial distribution.

TABLE 24.3: The Hypergeometric Distribution Where N_1, the Number of Items of One Category, Is 1% of the Population Size, N_T; and the Binomial Distribution with $p = 0.01$; the Sample Size, n, Is 100 in Each Case

X	$P(X)$ for hypergeometric: $N_T = 1000, N_1 = 10$	$P(X)$ for hypergeometric: $N_T = 2000, N_1 = 20$	$P(X)$ for hypergeometric: $N_T = 5000, N_1 = 50$	$P(X)$ for binomial: $p = 0.01$
0	0.34693	0.35669	0.36235	0.36603
1	0.38937	0.37926	0.37347	0.36973
2	0.19447	0.18953	0.18670	0.18486
3	0.05691	0.05918	0.06032	0.06100
4	0.01081	0.01295	0.01416	0.01494
5	0.00139	0.00211	0.00258	0.00290
6	0.00012	0.00027	0.00038	0.00046
>6	0.00000	0.00001	0.00004	0.00008
Total	1.00000	1.00000	1.00000	1.00000

24.3 SAMPLING A BINOMIAL POPULATION

Let us consider a population of N individuals: Y individuals in one category and $N - Y$ in the second category. Then the proportion of individuals in the first category is

$$p = \frac{Y}{N} \tag{24.12}$$

and the proportion in the second is

$$q = 1 - p \quad \text{or} \quad q = \frac{N - Y}{N}. \tag{24.13}$$

If a sample of n observations is taken from this population, with replacement, and X observations are in one category and $n - X$ are in the other, then the population parameter p is estimated by the sample statistic

$$\hat{p} = \frac{X}{n}, \tag{24.14}$$

which is the proportion of the sample that is in the first category.* The estimate of q is

$$\hat{q} = 1 - p \quad \text{or} \quad \hat{q} = \frac{n - X}{n}, \tag{24.15}$$

which is the proportion of the sample occurring in the second category. In Example 24.4 we have $X = 4$ and $n = 20$, so $\hat{p} = 4/20 = 0.20$ and $\hat{q} = 1 - p = 0.80$.

If our sample of 20 were returned to the population (or if the population were extremely large), and we took another sample of 20, and repeated this multiple sampling procedure many times, we could obtain many calculations of $\hat{p}$, each estimating the population parameter p. If, in the population, $p = 0$, then obviously any sample from that population would have $\hat{p} = 0$; and if $p = 1.0$, then each and

*Placing the symbol "^" above a letter is statistical convention for denoting an estimate of the quantity which that letter denotes. Thus, $\hat{p}$ refers to an estimate of p, and the statistic $\hat{q}$ is a sample estimate of the population parameter q. Routinely, $\hat{p}$ is called "p hat" and $\hat{q}$ is called "q hat."

EXAMPLE 24.4 Sampling a Binomial Population

From a population of male and female spiders, a sample of 20 is taken, which contains 4 males and 16 females.

$n = 20$

$X = 4$

By Equation 24.14,

$$\hat{p} = \frac{X}{n} = \frac{4}{20} = 0.20.$$

Therefore, we estimate that 20% of the population are males and, by Equation 24.15,

$$\hat{q} = 1 - \hat{p} = 1 - 0.20 = 0.80$$

or

$$\hat{q} = \frac{n - X}{n} = \frac{20 - 4}{20} = \frac{16}{20} = 0.80,$$

so we estimate that 80% of the population are females.

The variance of the estimate $\hat{p}$ (or of $\hat{q}$) is, by Equation 24.17,

$$s_{\hat{p}}^2 = \frac{\hat{p}\hat{q}}{n - 1} = \frac{(0.20)(0.80)}{20 - 1} = 0.008421.$$

If we consider that the sample consists of four 1's and sixteen 0's, then $\sum X = 4$, $\sum X^2 = 4$, and the variance of the twenty 1's and 0's is, by Equation 4.17, $s^2 = (4 - 4^2/20)/(20 - 1) = 0.168421$, and the variance of the mean, by Equation 6.7, is $s_{\bar{X}}^2 = 0.168421/20 = 0.008421$.

The standard error (or standard deviation) of $\hat{p}$ (or of $\hat{q}$) is, by Equation 24.21, $s_{\hat{p}} = \sqrt{0.008421} = 0.092$.

every $\hat{p}$ would be 1.0. However, if p is neither 0 nor 1.0, then all the many samples from the population would not have the same values of $\hat{p}$. The variance of all possible $\hat{p}$'s is

$$\sigma_{\hat{p}}^2 = \frac{pq}{n}, \tag{24.16}$$

which can be estimated from our sample as

$$s_{\hat{p}}^2 = \frac{\hat{p}\hat{q}}{n - 1}. \tag{24.17}$$

This variance is essentially a variance of means, so Equation 24.16 is analogous to Equation 6.4, and Equation 24.17 to Equation 6.7. In Example 24.4 it is shown that the latter is true. The variance of $\hat{q}$ is the same as the variance of $\hat{p}$; that is

$$\sigma_{\hat{q}}^2 = \sigma_{\hat{p}}^2 \tag{24.18}$$

and

$$s_{\hat{q}}^2 = s_{\hat{p}}^2. \tag{24.19}$$

The standard error of $\hat{p}$ (or of $\hat{q}$), also called the standard deviation, is

$$\sigma_{\hat{p}} = \sqrt{\frac{pq}{n}}, \tag{24.20}$$

which is estimated from a sample as*

$$s_{\hat{p}} = \sqrt{\frac{\hat{p}\hat{q}}{n-1}}. \tag{24.21}$$

The possible values of $\sigma^2_{\hat{p}}$, $\sigma^2_{\hat{q}}$, $\sigma_{\hat{p}}$, and $\sigma_{\hat{q}}$ range from a minimum of zero when either $\hat{p}$ or $\hat{q}$ is zero, to a maximum when $\hat{p} = \hat{q} = 0.5$; and $s^2_{\hat{p}}$, $s^2_{\hat{q}}$, $s_{\hat{p}}$, and $s_{\hat{q}}$ can range from a minimum of zero when either $\hat{p}$ or $\hat{q}$ is zero, to a maximum when $\hat{p} = \hat{q} = 0.5$.

(a) Sampling Finite Populations†. If n is a substantial portion of the entire population of size N, and sampling is without replacement, then a finite population correction is called for (just like that found in Section 7.7) in estimating $\sigma^2_{\hat{p}}$ or $\sigma_{\hat{p}}$:

$$s^2_{\hat{p}} = \frac{\hat{p}\hat{q}}{n-1}\left(1 - \frac{n}{N}\right) \tag{24.23}$$

and

$$s_{\hat{p}} = \sqrt{\frac{\hat{p}\hat{q}}{n-1}\left(1 - \frac{n}{N}\right)}, \tag{24.24}$$

when n/N is called the *sampling fraction*, and $1 - n/N$ is the *finite population correction*, the latter also being written as $(N - n)/N$. As N becomes very large compared to n, Equation 24.23 approaches Equation 24.17 and Equation 24.24 approaches 24.21.

We can estimate Y, the total number of occurrences in the population in the first category, as

$$\hat{Y} = \hat{p}N; \tag{24.25}$$

and the variance and standard error of this estimate are

$$s^2_{\hat{Y}} = \frac{N(N-n)\hat{p}\hat{q}}{n-1} \tag{24.26}$$

and

$$s_{\hat{Y}} = \sqrt{\frac{N(N-n)\hat{p}\hat{q}}{n-1}}, \tag{24.27}$$

respectively.

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*We often see

$$s_{\hat{p}} = \sqrt{\frac{\hat{p}\hat{q}}{n}} \tag{24.22}$$

used to estimate $\sigma_{\hat{p}}$. Although it is an underestimate, when n is large the difference between Equations 24.21 and 24.22 is slight.

†These procedures are from Cochran (1977: 52). When sampling from finite populations, the data follow the hypergeometric (Section 24.2), rather than the binomial, distribution.

GOODNESS OF FIT FOR THE BINOMIAL DISTRIBUTION

(a) When p Is Hypothesized to Be Known. In some biological situations the population proportions, p and q, might be postulated, as from theory. For example, theory might tell us that 50% of mammalian sperm contain an X chromosome, whereas 50% contain a Y chromosome, and we can expect a 1 : 1 sex ratio among the offspring. We may wish to test the hypothesis that our sample came from a binomially distributed population with equal sex frequencies. We may do this as follows, by the goodness-of-fit testing introduced in Chapter 22.

Let us suppose that we have tabulated the sexes of the offspring from 54 litters of five animals each (Example 24.5). Setting $p = q = 0.5$, the proportion of each possible litter composition can be computed by the procedures of Example 24.1, using Equation 24.3, or they can be read directly from Appendix Table B.26b. From these proportions, we can tabulate expected frequencies, and then can subject observed and expected frequencies of each type of litter to a chi-square goodness-of-fit analysis (see Section 22.1), with $k - 1$ degrees of freedom (k being the number of classes of X). In Example 24.5, we do not reject the null hypothesis, and therefore we conclude that the sampled population is binomial with $p = 0.5$.

EXAMPLE 24.5 Goodness of Fit of a Binomial Distribution, When p Is Postulated

The data consist of observed frequencies of females in 54 litters of five offspring per litter. $X = 0$ denotes a litter having no females, $X = 1$ a litter having one female, and so on; f is the observed number of litters, and $\hat{f}$ is the number of litters expected if the null hypothesis is true. Computation of the values of $\hat{f}$ requires the values of $P(X)$, as obtained in Example 24.1.

H_0: The sexes of the offspring reflect a binomial distribution with $p = q = 0.5$.

H_A: The sexes of the offspring do not reflect a binomial distribution with $p = q = 0.5$.

X_i	f_i	$\hat{f}_i$
0	3	(0.03125)(54) = 1.6875
1	10	(0.15625)(54) = 8.4375
2	14	(0.31250)(54) = 16.8750
3	17	(0.31250)(54) = 16.8750
4	9	(0.15625)(54) = 8.4375
5	1	(0.03125)(54) = 1.6875

$$\chi^2 = \frac{(3 - 1.6875)^2}{1.6875} + \frac{(10 - 8.4375)^2}{8.4375} + \frac{(14 - 16.8750)^2}{16.8750}$$
$$+ \frac{(17 - 16.8750)^2}{16.8750} + \frac{(9 - 8.4375)^2}{8.4375} + \frac{(1 - 1.6875)^2}{1.6875}$$
$$= 1.0208 + 0.2894 + 0.4898 + 0.0009 + 0.0375 + 0.2801 = 2.1185$$

$\nu = k - 1 = 6 - 1 = 5$

$\chi^2_{0.05,5} = 11.070$

Therefore, do not reject H_0.

$$0.75 < P < 0.90 \quad [P = 0.83]$$

To avoid bias in this chi-square computation, no expected frequency should be less than 1.0 (Cochran, 1954). If such small frequencies occur, then frequencies in the appropriate extreme classes of X may be pooled to arrive at sufficiently large $\hat{f}_i$ values. Such pooling was not necessary in Example 24.5, as no $\hat{f}_i$ was less than 1.0. But it will be shown in Example 24.6.

EXAMPLE 24.6 Goodness of Fit of a Binomial Distribution, When p Is Estimated from the Sample Data

The data consist of observed frequencies of left-handed persons in 75 samples of eight persons each. $X = 0$ denotes a sample with no left-handed persons, $X = 1$ a sample with one left-handed person, and so on; f is the observed number of samples, and $\hat{f}$ is the number of samples expected if the null hypothesis is true. Each $\hat{f}$ is computed by multiplying 75 by $P(X)$, where $P(X)$ is obtained from Equation 24.3 by substituting $\hat{p}$ and $\hat{q}$ for p and q, respectively.

H_0: The frequencies of left- and right-handed persons in the population follow a binomial distribution.

H_A: The frequencies of left- and right-handed persons in the population do not follow a binomial distribution.

$$\overline{X} = \frac{\sum f_i X_i}{\sum f_i} = \frac{96}{75} = 1.2800$$

$$\hat{p} = \frac{\overline{X}}{n} = \frac{1.2800}{8} = 0.16 = \text{probability of a person being left-handed}$$

$$\hat{q} = 1 - \hat{p} = 0.84 = \text{probability of a person being right-handed}$$

X_i	f_i		$f_i X_i$	$\hat{f}_i$	
0	21		0	$\frac{8!}{0!8!}(0.16^0)(0.84^8)(75) = (0.24788)(75) = 18.59$	
1	26		26	$(0.37772)(75) = 28.33$	
2	19		38	$(0.25181)(75) = 18.89$	
3	6		18	$(0.09593)(75) = 7.19$	
4	2	3	8	$(0.02284)(75) = 1.71$	1.99
5	0		0	$(0.00348)(75) = 0.26$	
6	1		6	$(0.00033)(75) = 0.02$	
7	0		0	$(0.00002)(75) = 0.00$	
8	0		0	$(0.00000)(75) = 0.00$	
	75		96		

Note: The extremely small $\hat{f}$ values of 0.00, 0.00, 0.02, and 0.26 are each less than 1.00. So they are combined with the adjacent $\hat{f}$ of 1.71. This results in an $\hat{f}$ of 1.99 for a corresponding f of 3.

$$\sum f_i = 75$$

$$\sum f_i X_i = 96$$

$$\chi^2 = \frac{(21 - 18.59)^2}{18.59} + \frac{(26 - 28.33)^2}{28.33} + \frac{(19 - 18.89)^2}{18.89} + \frac{(6 - 7.19)^2}{7.19} + \frac{(3 - 1.99)^2}{1.99}$$

$$= 1.214$$

$$\nu = k - 2 = 5 - 2 = 3$$

$$\chi^2_{0.05,3} = 7.815$$

Therefore, do not reject H_0.

$$0.50 < P < 0.75 \quad [P = 0.7496]$$

The G statistic (Section 22.7) may be calculated in lieu of chi-square, with the summation being executed over all classes except those where not only $f_i = 0$ but also all more extreme f_i's are zero. The Kolmogorov-Smirnov statistic of Section 22.8 could also be used to determine the goodness of fit. Heterogeneity testing (Section 22.6) may be performed for several sets of data hypothesized to have come from a binomial distribution.

If the preceding null hypothesis had been rejected, we might have looked in several directions for a biological explanation. The rejection of H_0 might have indicated that the population p was, in fact, not 0.5. Or, it might have indicated that the underlying distribution was not binomial. The latter possibility may occur when membership of an individual in one of the two possible categories is dependent upon another individual in the sample. In Example 24.5, for instance, identical twins (or other multiple identical births) might have been a common occurrence in the species in question. In that case, if one member of a litter was found to be female, then there would be a greater-than-expected chance of a second member of the litter being female.

(b) When p Is Not Assumed to Be Known. Commonly, we do not postulate the value of p in the population but estimate it from a sample of data. As shown in Example 24.7, we may do this by calculating

$$\hat{p} = \frac{\sum_{i=1}^{k} f_i X_i \Big/ \sum_{i=1}^{k} f_i}{n}. \tag{24.28}$$

It then follows that $\hat{q} = 1 - \hat{p}$.

The values of $\hat{p}$ and $\hat{q}$ may be substituted in Equation 24.3 in place of p and q, respectively. Thus, expected frequencies may be calculated for each X, and a chi-square goodness-of-fit analysis may be performed as it was in Example 24.5. In such a procedure, however, ν is $k - 2$ rather than $k - 1$, because two constants

(n and $\hat{p}$) must be obtained from the sample, and ν is, in general, determined as k minus the number of such constants. The G statistic (Section 22.7) may be employed when p is not known, but the Kolmogorov-Smirnov test (Section 22.8) is very conservative in such cases and should be avoided.

The null hypothesis for such a test would be that the sampled population was distributed binomially, with the members of the population occuring independently of one another.

24.5 THE BINOMIAL TEST AND ONE-SAMPLE TEST OF A PROPORTION

With the ability to determine binomial probabilities, a simple procedure may be employed for goodness-of-fit testing of nominal data distributed between two categories. This method is especially welcome as an alternative to chi-square goodness of fit where the expected frequencies are small (see Section 22.5). If p is very small, then the Poisson distribution (Section 25.1) may be used; and it is simpler to employ when n is very large. Because the binomial distribution is discrete, this procedure is conservative in that the probability of a Type I error is $\leq \alpha$.

(a) One-Tailed Testing. Animals might be introduced one at a time into a passageway at the end of which each has a choice of turning either to the right or to the left. A substance, perhaps food, is placed out of sight to the left or right; the direction is randomly determined (as by the toss of a coin). We might state a null hypothesis, that there is no tendency for animals to turn in the direction of the food, against the alternative, that the animals prefer to turn toward the food. If we consider p to be the probability of turning toward the food, then the hypothesis (one-tailed) would be stated as $H_0: p \leq 0.5$ and $H_A: p > 0.5$, and such an experiment might be utilized, for example, to determine the ability of the animals to smell the food. We may test H_0 as shown in Example 24.7. In this procedure, we determine the probability of obtaining, at random, a distribution of data deviating as much as, or more than, the observed data. In Example 24.7, the most likely distribution of data in a sample of twelve from a population where p, in fact, was 0.5, would be six left and six right. The samples deviating from a 6 : 6 ratio even more than our observed sample (having a 10 : 2 ratio) would be those possessing eleven left, one right, and twelve left, zero right.

EXAMPLE 24.7 A One-Tailed Binomial Test

Twelve animals were introduced, one at a time, into a passageway at the end of which they could turn to the left (where food was placed out of sight) or to the right. We wish to determine if these animals came from a population in which animals would choose the left more often than the right (perhaps because they were able to smell the food).

Thus, $n = 12$, the number of animals; X is the number of animals turning left; and p is the probability of animals in the sampled population that would turn left.

$H_0: p \leq 0.5$ and $H_A: p > 5$

In this example, $P(X)$ is obtained either from Appendix Table B.26b or by Equation 24.3.

(a) The test using binomial probabilities

X	$P(X)$
0	0.00024
1	0.00293
2	0.01611
3	0.05371
4	0.12085
5	0.19336
6	0.22559
7	0.19336
8	0.12085
9	0.05371
10	0.01611
11	0.00293
12	0.00024

On performing the experiment, ten of the twelve animals turned to the left and two turned to the right. If H_0 is true, $P(X \geq 10) = 0.01611 + 0.00293 + 0.00024 = 0.01928$. As this probability is less than 0.05, reject H_0.

(b) The test using a confidence limit

This test could also be performed by using the upper confidence limit of p as a critical value. For example, by Equation 24.35, with a one-tailed F,

$$X = pn = (0.5)(12) = 6,$$

$$\nu_1' = 2(6 + 1) = 14,$$

$$\nu_2' = 2(12 - 6) = 12,$$

$$F_{0.05(1),14,12} = 2.64, \text{ and}$$

$$L_2 = \frac{(6 + 1)(2.64)}{12 - 6 + (6 + 1)(2.64)} = 0.755.$$

Because the observed $\hat{p}$ (namely $X/n = 10/12 = 0.833$) exceeds the critical value (0.755), we reject H_0.

(c) A simpler alternative

Appendix Table B.27 can be consulted for $n - 12$ and $\alpha(1) = 0.05$ and to find an upper critical value of $n - C_{0.05(1),n} = 12 - 2 = 10$. As an X of 10 falls within the range of $\hat{p} \geq n - C_{0.05(1),12}, n$, H_0 is rejected; and (by examining the column headings) $0.01 < P(X \geq 10) < 0.25$).

The general one-tailed hypotheses are $H_0: p \leq p_0$ and $H_A: p > p_0$, or $H_0: p \geq p_0$ and $H_A: p < p_0$, where p_0 need not be 0.5. The determination of the probability of $\hat{p}$

as extreme as, or more extreme than, that observed is shown in Example 24.8, where the expected frequencies, $P(X)$, are obtained either from Appendix Table B.26b or by Equation 24.3. If the resultant probability is less than or equal to α, then H_0 is rejected. A simple procedure for computing this P when $p_0 = 0.5$ is shown in Section 24.6.

Alternatively, a critical value for the one-tailed binomial test may be found using the confidence-limit determinations of Section 24.8. This is demonstrated in Example 24.7b, using a one-tailed F for the confidence interval presented in Section 24.8a. If $H_A: p > 0.5$ (as in Example 24.7), then Equation 24.35 is used to obtain the upper critical value as the critical value for the test. If the alternative hypothesis had been $H_A: p > 0.5$, then Equation 24.29 would have been appropriate, calculating the lower confidence limit to be considered the critical value. Or the needed upper or lower confidence limit could be obtained using a one-tailed Z for the procedure of Section 24.8c. Employing the confidence limits of Section 24.8b is not recommended.

A simpler alternative, demonstrated as Example 24.8c, is to consult Appendix Table B.27 to obtain the lower confidence limit, $C_{\alpha(1),n}$, for one-tailed probabilities, $\alpha(1)$. If $H_A: p < 0.5$, then H_0 is rejected if $X \leq C_{\alpha(1),n}$, where $X = np$. If $H_A: p > 0.5$ (as in Example 24.7), then H_0 is rejected if $X > n - C_{\alpha(1),n}$.

(b) Two-Tailed Testing. The preceding experiment might have been performed without expressing an interest specifically in whether the animals were attracted toward the introduced substance. Thus, there would be no reason for considering a preference for only one of the two possible directions, and we would be dealing with two-tailed hypotheses, $H_0: p = 0.5$ and $H_A: p \neq 0.5$. The testing procedure would be identical to that in Example 24.7, except that we desire to know $P(X \leq 2 \text{ or } X \geq 10)$. This is the probability of a set of data deviating *in either direction* from the expected as much as or more than those data observed. This is shown in Example 24.8. The general two-tailed hypotheses are $H_0: p = p_0$ and $H_A: p \neq p_0$. If $p_0 = 0.5$, a simplified computation of P is shown in Equation 24.5.

Instead of enumerating the several values of $P(X)$ required, we could determine critical values for the two-tailed binomial test as the two-tailed confidence limits described in Section 24.8. If the observed $\hat{p}$ lies outside the interval formed by L_1 and L_2, then H_0 is rejected. This is demonstrated in Example 24.8b, using the confidence limits of Section 24.8a. If the hypothesized p is 0.5, then ν_1 and ν_2 are the same for L_1 and L_2; therefore, the required critical value of F is the same for both confidence limits. This is shown in Example 24.8a, where $\nu_1 = \nu_1'$, $\nu_2 = \nu_2'$, and $F_{0.05(2),14,12}$ is used for both L_1 and L_2. The confidence-limit calculation of Section 24.8c can also be used, but employing Section 24.8b is not recommended.

A simpler two-tailed binomial test is possible using Appendix Table B.27, as demonstrated in Example 24.8c. If the observed count, $X = pn$, is either $\leq C_{\alpha(2),\nu}$ or $\geq n - C_{\alpha(2),n}$, then H_0 is rejected.

(c) Normal and Chi-Square Approximations. Some researchers have used the normal approximation to the binomial distribution to perform the two-tailed test (for $H_0: p = p_0$ versus $H_A: p \neq p_0$) or the one-tailed test (either $H_0: p \leq p_0$ versus $H_A: p > p_0$, or $H_0: p \geq p_0$ versus $H_A: p < p_0$). The test statistic is

$$Z = \frac{X - np_0}{\sqrt{np_0q_0}}, \tag{24.29}$$

EXAMPLE 24.8 A Two-Tailed Binomial Test

The experiment is as described in Example 24.7, except that we have no a priori interest in the animals' turning either toward or away from the introduced substance.

H_0: $p = 0.5$
H_A: $p \neq 0.5$

$n = 12$

(a) The probabilities of X, for $X = 0$ through $X = 12$, are given in Example 24.7.

$$\begin{aligned} P(X \geq 10 \text{ or } X \leq 2) &= 0.01611 + 0.00293 + 0.00024 + 0.01611 \\ &\quad + 0.00293 + 0.00024 \\ &= 0.03856 \end{aligned}$$

As this probability is less than 0.05, reject H_0.

(b) Alternatively, this test could be performed by using the confidence limits as critical values. By Equations 24.34 and 24.35, we have

$$X = pn = (0.5)(12) = 6,$$

and for L_1 we have

$$\nu_1 = 2(12 - 6 + 1) = 14$$
$$\nu_2 = 2(6) = 12$$
$$F_{0.05(2),14,12} = 3.21$$
$$L_1 = \frac{6}{6 + (12 - 6 + 1)(3.21)} = 0.211,$$

and for L_2 we have

$$\nu'_1 = 2(6 + 1) = 14$$
$$\nu'_2 = 2(12 - 6) = 12$$
$$F_{0.05(2),14,12} = 3.21$$
$$L_2 = \frac{(6 + 1)(3.21)}{12 - 6 + (6 + 1)(3.21)} = 0.789.$$

As the observed $\hat{p}$ (namely $X/n = 10/12 = 0.833$) lies outside the range of 0.211 to 0.789, we reject H_0.

(c) A simpler procedure uses Appendix Table B.27 to obtain critical values of $C_{0.05(2),6} = 2$ and $n - C_{0.05(2),6} = 12 - 2 = 10$. As $X = 10$, H_0 is rejected; and $0.02 < P(X \leq 2 \text{ or } X > 10) < 0.05$.

where $X = n\hat{p}$, the number of observations in one of the two categories, and np_0 is the number of observations expected in that category if H_0 is true. Equivalently, this

may be expressed as

$$Z = \frac{p - p_0}{\sqrt{p_0 q_0 / n}}. \tag{24.30}$$

The two-tailed null hypothesis, $H_0 : p = p_0$ (tested in Example 24.9), is rejected if $|Z| > Z_{\alpha(2)}$; the one-tailed $H_0 : p \leq p_0$ is rejected if $|Z| > Z_{\alpha(1)}$, and $H_0 : p \geq p_0$ is rejected if $|Z| < Z_{\alpha(1)}$.

EXAMPLE 24.9 The Normal Approximation to the Binomial Test

For the normal approximation to the binomial test of Example 24.8, using the data of Example 24.7, $H_0: p = 0.5$; $H_A: p \neq 0.5$; $p_0 = 0.5$; $n = 12$; $X = 10$; $\hat{p} = 10/12 = 0.8333$.

Using Equation 24.29,

$$Z = \frac{X - np_0}{\sqrt{np_0 q_0}} = \frac{10 - 6}{\sqrt{(12)(0.5)(0.5)}} = \frac{4}{1.7321} = 2.3098$$

$$Z_{0.05(2)} = 1.9600$$

Therefore, reject H_0.

$$0.02 < P < 0.05 \quad [0.021]$$

$$Z_c = \frac{|X - np_0| - 0.5}{\sqrt{np_0 q_0}} = \frac{|10 - 6| - 0.5}{\sqrt{(12)(0.5)(0.5)}} = \frac{3.5}{1.7321} = 2.0207$$

$$0.02 < P < 0.05 \quad [0.043]$$

Using Equation 24.30,

$$Z = \frac{p - p_0}{\sqrt{p_0 q_0 / n}} = \frac{0.8333 - 0.5000}{\sqrt{(0.5)(0.5/12)}} = \frac{0.3333}{0.0208} = 2.3093$$

$$0.02 < P < 0.05 \quad [0.021]$$

$$Z_c = \frac{|p - p_0| - 0.5/n}{\sqrt{p_0 q_0 / n}} = \frac{|0.8333 - 0.5000| - 0.5/12}{\sqrt{(0.5)(0.5/12)}}$$

$$= \frac{0.3333 - 0.0417}{0.0208} = 2.0208$$

$$0.02 < P < 0.05 \quad [0.043]$$

The test may also be performed with a correction for continuity, by bringing np_0 closer by 0.5 to X in Equation 24.29 or by bringing p_0 nearer by $0.5/n$ to p in Equation 24.30. This is shown in Example 24.9, where the probability using Z_c is seen to be closer than $P(Z)$ to the probability determined by the binomial test.

The two-tailed (but not the one-tailed) test can be effected as a chi-square goodness of fit in accordance with Section 22.1 (with the continuity correction shown in Section 22.2). For two-tailed hypotheses, Z testing is equivalent to chi-square

testing, for $Z^2 = \chi^2$ (and, if $Z_c^2 = \chi_c^2$). However, Ramsey and Ramsey (1988) concluded that the approximation is not as powerful as the binomial test.

The normal approximation to the binomial test and the chi-square goodness-of-fit test does not work well when n is small. Section 22.5 recommends that $\hat{f}_1$ and $\hat{f}_2$ be at least 5 for the chi-square procedure; the equivalent statement for the normal approximation to the binomial test is that $p_0 n$ and $q_0 n$ should be at least 5.

THE SIGN TEST

For two samples where interval- or ratio scale data occur in pairs, hypotheses of no difference between the means of the two samples may be tested by the t test shown in Section 9.1. If paired data are measured on an ordinal scale, the nonparametric *sign test** can be useful; it may be employed whenever the Wilcoxon paired-sample test (Section 9.5) is appropriate, although it is not as powerful as the latter. The sign test may also be used with interval- or ratio-scale data, but in those circumstances it is not as powerful as the paired t test and it does not express hypotheses in terms of population means.

The actual differences between members of a pair are not utilized in the sign test; only the direction (or sign) of each difference is tabulated. In Example 24.10, all that need be recorded is whether each hindleg length is greater than, equal to, or less than its corresponding foreleg length; we do this by recording +, 0, or −, respectively. We then ask what the probability is of the observed distribution, or a more extreme distribution, of + and − signs if the null hypothesis is true. (A difference of zero is deleted from the analysis, so n is here defined as the number of differences having a sign.†) The analysis proceeds as a binomial test with $H_0: p = 0.5$, and the null hypothesis tested is, essentially, that in the population the median difference is zero (i.e., the population frequencies of positive differences and negative differences are the same), but it differs from the median test of Section 8.12 in that the data in the two samples are paired.

In performing a binomial test with $p_0 = q_0 = 0.5$, which is always the case with the sign test, the exact probability, P, may be obtained by the following simple considerations. As introduced in Equation 24.5, for a given n the probability of a specified X is 0.5^n times the binomial coefficient. And binomial coefficients are defined in Equation 24.2 and presented in Table 24.2 and Appendix Table B.26a. In performing the binomial or sign test, we sum binomial terms in one or both tails of the distribution, and if $p_0 = q_0 = 0.5$, then this is the same as multiplying 0.5^n by the sum of the binomial coefficients in the one or two tails. Examining Example 24.10, what is needed is the sum of the probabilities in the two tails defined by $X \leq 2$ and $X \geq 8$. Thus, we may sum the coefficients, ${}_{10}C_X$, for $X \leq 2$ and $X \geq 8$, and multiply that sum by 0.5^{10} or, equivalently, divide the sum by 2^{10}. For this example, the binomial coefficients are 1, 10, 45, 45, 10, and 1, so the probability of H_0 being a true statement about the sampled population is

$$\frac{1 + 10 + 45 + 45 + 10 + 1}{2^{10}} = \frac{112}{1024} = 0.1094.$$

*The sign test was first employed by Scottish physician and mathematician John Arbuthnott (1667–1735), and his 1710 publication is perhaps the earliest report of something resembling a statistical hypothesis (Noether, 1984).

†Methods have been described specifically for situations where there are many differences of zero (Coakley and Heise, 1996; Fong et al., 2003; Wittkowski, 1998).

EXAMPLE 24.10 The Sign Test for the Paired-Sample Data of Examples 9.1 and 9.4.

Deer	*Hindleg length* (cm)	*Foreleg length* (cm)	*Difference*
1	142	138	+
2	140	136	+
3	144	147	−
4	144	139	+
5	142	143	−
6	146	141	+
7	149	143	+
8	150	145	+
9	142	136	+
10	148	146	+

H_0: There is no difference between hindleg and foreleg length in deer. ($p = 0$)

H_A: There is a difference between hindleg and foreleg length in deer. ($p \neq 0$)

$n = 10$, and there are 8 positive differences and 2 negative differences.

Using Appendix Table B.26b for $n = 10$ and $p = 0.50$,

$$\begin{aligned} &P(X \leq 2 \text{ or } X \geq 8) \\ &= 0.04395 + 0.00977 + 0.00098 + 0.04395 + 0.00977 + 0.00098 \\ &= 0.1094. \end{aligned}$$

As the probability is greater than 0.05, do not reject H_0.

Using binomial coefficients,

$$\frac{1 + 10 + 45 + 45 + 10 + 1}{2^{10}} = \frac{112}{1024} = 0.1094.$$

Using Appendix Table B.27 for $n = 10$, the critical values are $C_{0.05(2),10} = 1$ and $n - C_{0.05(2),10} = 10 - 1 = 9$. As neither $X = 2$ nor $X = 8$ is as small as 1 or as large as 9, H_0 is not rejected; and by consulting Appendix Table B.27, we state $0.10 < P < 0.20$.

This calculation can be more accurate than summing the six individual binomial probabilities, as shown in Example 24.10, for it avoids rounding error.

An extension of the sign test to nonparametric testing for blocked data from more than two groups is found in the form of the Friedman test (Section 12.7).

Immediately prior to Section 9.5a, it is noted that the Wilcoxon paired-sample test can be applied to hypotheses expressing differences of specified magnitude. The sign test can be used in a similar fashion. For instance, it can be asked whether the hindlegs in the population sampled in Example 24.10 are 3 cm longer than the lengths of the forelegs. This can be done by applying the sign test after subtracting 3 cm from each hindleg length in the sample (or adding 3 cm to each foreleg length).

24.7 POWER, DETECTABLE DIFFERENCE, AND SAMPLE SIZE FOR THE BINOMIAL AND SIGN TESTS

The power of, and required sample size for, the binomial test may be determined by examining the cumulative binomial distribution. As the sign test is essentially a binomial test with p hypothesized to be 0.5 (see Section 24.6), its power and sample size may be assessed in the same manner as for the binomial test.

(a) Power of the Test. If a binomial test is performed at significance level α and with sample size n, we can estimate the power of the test (i.e., the probability of correctly rejecting H_0) as follows. First we determine the critical value(s) of X for the test. For a one-tailed test of H_0: $p \leq p_0$ versus H_A: $p > p_0$, the critical value is the smallest value of X for which the probability of that X or a larger X is $\leq \alpha$. (In Example 24.7a this is found to be $X = 10$.) For a one-tailed test of H_0: $p \leq p_0$ versus H_A: $p > p_0$, the critical value is the largest X for which the probability of that X or of a smaller X is $\leq \alpha$. Then we examine the binomial distribution for the observed proportion, $\hat{p}$, from our sample. The power of the test is $\geq$ the probability of an X at least as extreme as the critical value referred to previously.* This is demonstrated in Example 24.11.

EXAMPLE 24.11 Determination of the Power of the One-Tailed Binomial Test of Example 24.7a

In Example 24.7, H_0: $p \leq 0.5$ and $\hat{p} = X/n = 10/12 = 0.833$. And $X = 10$ is the critical value, because $P(X \geq 10) < 0.05$, but $P(X \geq 11) > 0.05$.

Using Equation 24.3, $P(X)$ for X's of 10 through 12 is calculated for the binomial distribution having $p = 0.833$ and $n = 12$:

X	$P(X)$
10	0.296
11	0.269
12	0.112

Thus, the power when performing this test on a future set of such data is estimated to be $\geq 0.296 + 0.269 + 0.112 = 0.68$.

For a two-tailed test of H_0: $p = p_0$ versus H_A: $p \neq p_0$, there are two critical values of X, one that cuts off $\alpha/2$ of the binomial distribution in each tail. Knowing these two X's, we examine the binomial distribution for $\hat{p}$, and the power of the test is the probability in the latter distribution that X is at least as extreme as the critical values. This is demonstrated in Example 24.12.

Cohen (1988: Section 5.4) presents tables to estimate sample size requirements in the sign test.

(b) Normal Approximation for Power. Having performed a binomial test or a sign test, it may be estimated what the power would be if the same test were

*If the critical X delineates a probability of exactly α in the tail of the distribution, then the power is equal to that computed; if the critical value defines a tail of less than α, then the power is greater than that calculated.

EXAMPLE 24.12 Determination of the Power of the Two-Tailed Sign Test of Example 24.10

In Example 24.10, H_0: $p = 0.50$, the critical values are 1 and 9, and $\hat{p} = X/n = 8/10 = 0.800$.

Using Equation 24.3, $P(X)$ is calculated for all X's equal to or more extreme than the critical values, for the binomial distribution having $p = 0.800$ and $n = 10$:

X	$P(X)$
0	0.000
1	0.000
9	0.269
10	0.112

Therefore, the power of performing this test on a future set of data is $\geq 0.000 + 0.000 + 0.269 + 0.112 = 0.38$.

performed on a future set of data taken from the same population. As noted earlier (e.g., Sections 7.7 and 8.7), this is not an estimate of the power of the test already performed; it is an estimate of the power of this test performed on a new set of data obtained from the same population. It has been noted in the preceding discussions of the binomial distribution that normal approximations to that distribution are generally poor and inadvisable. However, rough estimates of power are often sufficient in planning data collection. If n is not small and the best estimate of the population proportion, p, is not near 0 or 1, then an approximation of the power of a binomial or sign test can be calculated as

$$\text{power} = P\left[Z \leq \frac{p_0 - p}{\sqrt{\frac{pq}{n}}} - Z_{\alpha(2)}\sqrt{\frac{p_0q_0}{pq}}\right] + P\left[Z \geq \frac{p_0 - p}{\sqrt{\frac{pq}{n}}} + Z_{\alpha(2)}\sqrt{\frac{p_0q_0}{pq}}\right] \tag{24.31}$$

(Marascuilo and McSweeney, 1977: 62). Here p_0 is the population proportion in the hypothesis to be tested, $q_0 = 1 - p_0$, p is the true population proportion (or our best estimate of it), $q = 1 - p$, $Z_{\alpha(2)} = t_{\alpha(2),\infty}$, and the probabilities of Z are found in Appendix Table B.2, using the considerations of Section 6.1. This is demonstrated in Example 24.13.

For the one-tailed test, H_0: $p \leq p_0$ versus H_A: $p > p_0$, the estimated power is

$$\text{power} = P\left[Z \geq \frac{p_0 - p}{\sqrt{\frac{pq}{n}}} + Z_{\alpha(1)}\sqrt{\frac{p_0q_0}{pq}}\right]; \tag{24.31a}$$

EXAMPLE 24.13 Estimation of Power in a Two-Tailed Binomial Test, Using the Normal Approximation

To test $H_0: p = 0.5$ versus $H_A: p \neq 0.5$, using $\alpha = 0.05$ (so $Z_{0.05(2)} = 1.9600$) and a sample size of 50, when p in the population is actually 0.5:
Employing Equation 24.31,

$$\text{power} = P\left[Z \leq \frac{p_0 - p}{\sqrt{\frac{pq}{n}}} - Z_{\alpha(2)}\sqrt{\frac{p_0q_0}{pq}}\right] + P\left[Z \geq \frac{p_0 - p}{\sqrt{\frac{pq}{n}}} + Z_{\alpha(2)}\sqrt{\frac{p_0q_0}{pq}}\right]$$

$$= P\left[Z \leq \frac{0.5 - 0.4}{\sqrt{\frac{(0.4)(0.6)}{50}}} - Z_{\alpha(2)}\sqrt{\frac{(0.5)(0.5)}{(0.4)(0.6)}}\right] + P\left[Z \geq \frac{0.5 - 0.4}{\sqrt{\frac{(0.4)(0.6)}{50}}} + Z_{\alpha(2)}\sqrt{\frac{(0.5)(0.5)}{(0.4)(0.6)}}\right]$$

$$= P[Z \leq 1.4434 - (1.9600)(1.0206)] + P[Z \geq 1.4434 + (1.9600)(1.0206)]$$
$$= P[Z \leq 1.4434 - 2.0004] + P[Z \leq 1.4434 + 2.0004]$$
$$= P[Z \leq -0.56] + P[Z \geq 3.44] = P[Z \geq 0.56] + P[Z \geq 3.44]$$
$$= 0.29 + 0.00 = 0.29.$$

and for the one-tailed hypotheses, $H_0: p \geq p_0$ versus $H_A: p < p_0$,

$$\text{power} = P\left[Z \leq \frac{p_0 - p}{\sqrt{\frac{pq}{n}}} - Z_{\alpha(1)}\sqrt{\frac{p_0q_0}{pq}}\right]. \tag{24.31b}$$

(c) Sample Size Required and Minimum Detectable Difference. Prior to designing an experiment, an estimate of the needed sample size may be obtained by specifying

α and the minimum difference between p_0 and p that is desired to be detected with a given power.

If p is not very near 0 or 1, this may be done with a normal approximation, with the understanding that this will result only in a rough estimate. Depending upon the hypothesis to be tested, Equation 24.31, 24.31a, or 24.31b may be used to estimate power for any sample size (n) that appears to be a reasonable guess. If the calculated power is less than desired, then the calculation is repeated with a larger n; if it is greater than that desired, the calculation is repeated with a smaller n. This repetitive process (called iteration) is performed until the specified power is obtained from the equation, at which point n is the estimate of the required sample size.

An estimate of the required n may be obtained without iteration, when one-tailed testing is to be performed. Equations 24.31a and 24.31b can be rearranged as follows (Simonoff, 2003, 59–60):

For $H_0: p \leq p_0$ versus $H_A: p > p_0$,

$$n = \left(\frac{Z_{\alpha(1)}\sqrt{p_0 q_0} - Z_{\beta(1)}\sqrt{pq}}{p_0 - p} \right)^2; \tag{24.32}$$

and for $H_0: p \geq p_0$ versus $H_A: p < p_0$,

$$n = \left(\frac{Z_{\alpha(1)}\sqrt{p_0 q_0} + Z_{\beta(1)}\sqrt{pq}}{p_0 - p} \right)^2. \tag{24.32a}$$

Levin and Chen (1999) have shown that these two equations provide values of n that tend to be underestimates, and they present estimates that are often better.

If p is not very near 0 or 1, we can specify α, power, and n, and employ iteration to obtain a rough estimate of the smallest difference between p_0 and p that can be detected in a future experiment.

A reasonable guess of this minimum detectable difference, $p_0 - p$, may be inserted into Equation 24.31, 24.31a, or 24.31b (depending upon the hypothesis to be tested), and the calculated power is then examined. If the power is less than that specified, then the calculation is performed again, using a larger value of $p_0 - p$; if the calculated power is greater than the specified power, the computation is performed again, using a smaller $p_0 - p$. This iterative process, involving increasing or decreasing $p_0 - p$ in the equation, is repeated until the desired power is achieved, at which point the $p_0 - p$ used to calculate that power is the minimum detectable difference sought.

Or, to estimate the minimum detectable difference for one-tailed testing, either Equation 24.32 or 24.32a (depending upon the hypotheses) may be rearranged to give

$$p_0 - p = \frac{Z_{\alpha(1)}\sqrt{p_0 q_0} - Z_{\beta(1)}\sqrt{pq}}{\sqrt{n}}, \tag{24.33}$$

or

$$p_0 - p = \frac{Z_{\alpha(1)}\sqrt{p_0 q_0} + Z_{\beta(1)}\sqrt{pq}}{\sqrt{n}}, \tag{24.33a}$$

respectively.

24.8 CONFIDENCE LIMITS FOR A POPULATION PROPORTION

Confidence intervals for the binomial parameter, p, can be calculated by a very large number of methods.* Among them are the following:

(a) Clopper-Pearson Interval. A confidence interval for p may be computed (Agresti and Coull, 1998; Bliss, 1967: 199–201; Brownlee, 1965: 148–149; Fleiss, Levin, and Paik, 2003: 25) using a relationship between the F distribution and the binomial distribution (Clopper and Pearson, 1934). As demonstrated in Example 24.14a, the lower confidence limit for p is

$$L_1 = \frac{X}{X + (n - X + 1)F_{\alpha(2),\nu_1,\nu_2}}, \tag{24.34}$$

where $\nu_1 = 2(n - X + 1)$ and $\nu_2 = 2X$. And the upper confidence limit for p is

$$L_2 = \frac{(X + 1)F_{\alpha(2),\nu_1',\nu_2'}}{n - X + (X + 1)F_{\alpha(2),\nu_1',\nu_2'}}, \tag{24.35}$$

with $\nu_1' = 2(X + 1)$, which is the same as $\nu_2 + 2$, and $\nu_2' = 2(n - X)$, which is equal to $\nu_1 - 2$.

The interval specified by L_1 and L_2 is one of many referred to as an "exact" confidence interval, because it is based upon an exact distribution (the binomial distribution) and not upon an approximation of a distribution. But it is not exact in the sense of specifying an interval that includes p with a probability of exactly $1 - \alpha$. Indeed, the aforementioned interval includes p with a probability of *at least* $1 - \alpha$, and the probability might be much greater than $1 - \alpha$. (So a confidence interval calculated in this fashion using $\alpha = 0.05$, such as in Example 24.14a, will contain p with a probability of 95% *or greater*.) Because this interval tends to be larger than necessary for $1 - \alpha$ confidence, it is said to be a *conservative* confidence interval (although the conservatism is less when n is large).

(b) Wald Interval. This commonly encountered approximation for the confidence interval, based upon the normal distribution,† is shown in Exercise 24.14b:

$$\hat{p} \pm Z_{\alpha(2)}\sqrt{\frac{\hat{p}\hat{q}}{n}}. \tag{24.36}$$

But this approximation can yield unsatisfactory results, especially when p is near 0 or 1 or when n is small. (Although the approximation improves somewhat as n or $\hat{p}\hat{q}$ increases, it still performs less well than the method discussed in Section 24.8c.)

One problem with this confidence interval is that it overestimates the precision of estimating p (and thus is said to be "liberal." That is, the interval includes p less

*Many of these are discussed by Agresti and Coull (1998); Blyth (1986); Böhning (1994); Brown, Cai, and DasGupta (2002); Fujino (1980); Newcombe (1998a); and Vollset (1993).

†Brownlee (1965: 136) credits Abraham de Moivre as the first to demonstrate, in 1733, the approximation of the binomial distribution by the normal distribution. Agresti (2002: 15) refers to this as one of the first confidence intervals proposed for any parameter, citing Laplace (1812: 283).

EXAMPLE 24.14 Determination of 95% Confidence Interval for the Binomial Population Parameter, p

One hundred fifty birds were randomly collected from a population, and there were 65 females in the sample. What proportion of the population is female?

$$n = 150, \quad X = 65$$

$$\hat{p} = \frac{X}{n} = \frac{65}{150} = 0.4333, \quad \hat{q} = 1 - \hat{p} = 1 - 0.4333 = 0.5667$$

(a) The Clopper-Pearson Confidence Interval:

For the lower 95% confidence limit,

$$\nu_1 = 2(n - X + 1) = 2(150 - 65 + 1) = 172$$

$$\nu_2 = 2X = 2(65) = 130$$

$$F_{0.05(2),172,130} \approx F_{0.05(2),140,120} = 1.42$$

$$L_1 = \frac{X}{X + (n - X + 1)F_{0.05(2),172,130}}$$

$$\approx \frac{65}{65 + (150 - 65 + 1)(1.42)} = 0.347.$$

For the upper 95% confidence limit,

$$\nu_1' = 2(X + 1) = 2(65 + 1) = 132$$

$$\text{or } \nu_1' = \nu_2 + 2 = 130 + 2 = 132$$

$$\nu_2' = 2(n - X) = 2(150 - 65) = 170$$

$$\text{or } \nu_2' = \nu_1 - 2 = 172 - 2 = 170$$

$$F_{0.05(2),132,170} \approx F_{0.05(2),120,160} = 1.39$$

$$L_2 = \frac{(X + 1)F_{0.05(2),132,170}}{n - X + (X + 1)F_{0.05(2),132,170}}$$

$$\approx \frac{(65 + 1)(1.39)}{150 - 65 + (65 + 1)(1.39)} = 0.519.$$

Therefore, we can state the 95% confidence interval as

$$P(0.347 \leq p \leq 0.519) = 0.95,$$

which is to say that there is 95% confidence that the interval between 0.347 and 0.519 includes the population parameter p.

Note: In this example, the required critical values of F have degrees of freedom (172 and 130 for L_1, and 132 and 170 for L_2) that are not in Appendix Table B.4. So the next lower available degrees of freedom were used, which is generally an acceptable procedure. Exact critical values from an appropriate computer program

are $F_{0.05(2),172,130} = 1.387$ and $F_{0.05(2),132,170} = 1.376$, yielding $L_1 = 0.353$ and $L_2 = 0.514$, which are results very similar to those just given.

(b) The Wald Confidence Interval:

$$Z_{0.05(2)} = 1.9600$$

$$\hat{p} \pm Z_{\alpha(2)}\sqrt{\frac{\hat{p}\hat{q}}{n}}$$

$$= 0.4333 \pm 1.9600\sqrt{\frac{(0.4333)(0.5667)}{150}} = 0.4333 \pm 0.0793$$

$$L_1 = 0.354, \quad L_2 = 0.513$$

(c) The Adjusted Wald Confidence Interval:

$$Z^2_{0.05(2)} = 1.9600^2 = 3.8416; \quad Z^2_{0.05(2)}/2 = 1.9600^2/2 = 1.9208$$

$$\text{adjusted } X \text{ is } \tilde{X} = X + Z^2_{0.05(2)}/2 = 65 + 1.9208 = 66.9208$$

$$\text{adjusted } n \text{ is } \tilde{n} = n + Z^2_{0.05(2)} = 150 + 3.8416 = 153.8416$$

$$\text{adjusted } \hat{p} \text{ is } \tilde{p} = \frac{\tilde{X}}{\tilde{n}} = \frac{66.9208}{153.8416} = 0.4350, \quad \hat{q} = 0.5650$$

$$95\% \text{ confidence interval for } p \text{ is } \tilde{p} \pm Z_{0.05(2)}\sqrt{\frac{\tilde{p}\tilde{q}}{\tilde{n}}}$$

$$= 0.4350 \pm 1.9600\sqrt{\frac{(0.4350)(0.5650)}{153.8416}} = 0.4350 \pm 0.0783$$

$$L_1 = 0.357, \quad L_2 = 0.513$$

than $1 - \alpha$ of the time (e.g., less than 95% of the time when $\alpha = 0.05$). Another objection is that the calculated confidence interval is always symmetrical around $\hat{p}$ (that is, it has a lower limit as far from $\hat{p}$ as the upper limit is), although a binomial distribution is skewed (unless $p = 0.50$; see Figure 24.1). This forced symmetry can result in a calculated L_1 that is less than 0 or an L_2 greater than 1, which would be unreasonable. Also, when $\hat{p}$ is 0 or 1, no confidence interval is calculable; the upper and lower confidence limits are both calculated to be $\hat{p}$.

Though it is commonly encountered, many authors* have noted serious disadvantages of Equation 24.36 (even with application of a continuity correction), have strongly discouraged its use, and have discussed some approximations that perform much better.

(c) Adjusted Wald Interval. A very simple, and very good, modification of the Wald interval (called an "adjusted Wald interval" by Agresti and Caffo, 2000, and Agresti

*See, for example: Agresti and Caffo (2000); Agresti and Coull (1998); Blyth (1986); Brown, Cai, and DasGupta (2001, 2002); Fujino (1980); Newcombe (1998a); Schader and Schmid (1990); and Vollset (1993). Fleiss, Levin, and Paik (2003: 28–29) present a normal approximation more complicated than, but apparently more accurate than, Equation 24.36.

and Coull, 1998) substitutes* $\tilde{X} = X + Z^2_{\alpha(2)}/2$ for X and $\tilde{n} = n + Z^2_{\alpha(2)}$ for n in Equation 24.36,† as shown in Example 24.14c; then, $\tilde{p} = \tilde{X}/\tilde{n}$, and $\tilde{q} = 1 - \tilde{p}$.

The probability of this confidence interval containing the population parameter is much closer to $1 - \alpha$ than the intervals in Sections 28.4a and 28.4b, although that probability may be a little below or a little above $1 - \alpha$ in individual cases. And neither L_1 nor L_2 is as likely as with the nonadjusted Wald interval to appear less than 0 or greater than 1.

(d) Which Interval to Use. Because n is fairly large in Example 24.14, and $\hat{p}$ and $\hat{q}$ are close to 0.5, the confidence limits do not vary appreciably among the aforementioned procedures. However, the following general guidelines emerge from the many studies performed on confidence intervals for the binomial parameter, p, although there is not unanimity of opinion:

- If it is desired that there is probability of at least $1 - \alpha$ that the interval from L_1 to L_2 includes p, even if the interval might be very conservative (i.e., the probability might be much greater than $1 - \alpha$), then the Clopper-Pearson interval (Section 24.8a) should be used.
- If it is desired that the probability is close to $1 - \alpha$ that the interval from L_1 to L_2 includes p, even though it might be either a little above or a little below $1 - \alpha$, then the adjusted Wald interval (Section 24.8c) is preferable. Another approximation is that of Wilson (1927) and is sometimes called the "score interval" (with different, but equivalent, formulas given by Agresti and Coull, 2000 and Newcombe, 1998a); and it yields results similar to those of the adjusted Wald interval.
- The nonadjusted Wald interval (Section 24.8b) should not be used.
- None of these confidence-interval calculations works acceptably when $X = 0$ (that is, when $\hat{p} = 0$) or when $X = 1$ (that is, when $\hat{p} = 1$). The following exact confidence limits (Blyth, 1986; Fleiss, Levin, and Paik, 2003: 23; Sprent and Smeeton, 2001: 81; Vollset, 1993) should be used in those circumstances‡:

$$\text{If } X = 0: \qquad L_1 = 0 \text{ and } L_2 = 1 - \sqrt[n]{\alpha(1)} \tag{24.37}$$

$$\text{If } X = 1: \qquad L_1 = \sqrt[n]{\alpha(1)} \text{ and } L_2 = 1. \tag{24.38}$$

One-tailed confidence intervals can be determined via the considerations presented in Sections 6.4a and 7.3a and the use of a one-tailed critical value for F or Z.

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*The symbol above the X and n is called a tilde (pronounced "til-duh"); $\tilde{X}$ is read as "X tilde" and $\tilde{n}$ as "n tilde."

†For a 95% confidence interval, $Z_{\alpha(2)} = 1.9600$, $Z^2_{0.05(2)} = 3.8416$, and $Z^2_{0.05(2)}/2 = 1.9208$; so it is often recommended to simply use $X + 2$ in place of X and $n + 4$ in place of n, which yields very good results. For the data of Example 24.14, this would give the same confidence limits as in Example 24.14c: $L_1 = 0.357$ and $L_2 = 0.513$.

‡The notation $\sqrt[n]{X}$ represents the nth root of X, which may also be written as $X^{1/n}$, so $\sqrt[n]{\alpha(1)}$ may be seen written as $[\alpha(1)]^{1/n}$. It can also be noted that negative exponents represent reciprocals: $X^{-a} = 1/X^a$. This modern notation for fractional and negative powers was introduced by Sir Isaac Newton (1642–1727) in 1676, although the notion of fractional powers was conceived much earlier, such as by French writer Nicole Oresme (ca. 1323–1382) (Cajori, 1928–1929: Vol. I: 91, 354, 355).

There are computer programs and published tables that provide confidence limits for p, but users of them should be confident in the computational method employed to obtain the results.

(e) Confidence Limits with Finite Populations. It is usually considered that the size of a sampled population (N) is *very much* larger than the size of the sample (n), as if the population size was infinite. If, however, n is large compared to N (i.e., the sample is a large portion of the population), it is said that the population is finite. As n approaches N, the estimation of p becomes more accurate, and the calculation of confidence limits by the adjusted Wald method (or by the Wald method) improves greatly by converting the lower confidence limit, L_1, to $(L_1)_c$ and the upper confidence limit, L_2, to $(L_2)_c$, as follows (Burstein, 1975):

$$(L_1)_c = \frac{\tilde{X} - 0.5}{\tilde{n}} - \left(\frac{\tilde{X} - 0.5}{\tilde{n}} - L_1\right)\sqrt{\frac{N - \tilde{n}}{N - 1}} \tag{24.39}$$

$$(L_2)_c = \frac{\tilde{X} + \tilde{X}/\tilde{n}}{\tilde{n}} + \left(L_2 - \frac{\tilde{X} + \tilde{X}/\tilde{n}}{\tilde{n}}\right)\sqrt{\frac{N - \tilde{n}}{N - 1}}. \tag{24.40}$$

The more $(N - n)/(N - 1)$ differs from 1.0, the more the confidence limits from Equations 24.39 and 24.40 will be preferable to those that do not consider the sample population to be finite.

(f) Sample Size Requirements. A researcher may wish to estimate, for a given $\hat{p}$, how large a sample is necessary to produce a confidence interval of a specified width.

Section 24.8b presents a procedure (although often a crude one) for calculating a confidence interval for p when p is not close to 0 or 1. That normal approximation can be employed, with $\hat{p}$ and $\hat{q}$ obtained from an existing set of data, to provide a rough estimate of the number of data (n) that a future sample from the same population must contain to obtain a confidence interval where both L_1 and L_2 are at a designated distance, δ, from p:

$$n = \frac{Z^2_{0.05(2)}\hat{p}\hat{q}}{\delta^2} \tag{24.41}$$

(Cochran, 1977: 75–76; Hollander and Wolfe, 1999: 30), where $Z_{0.05(2)}$ is a two-tailed normal deviate. If we do not have an estimate of p, then a conservative estimate of the required n can be obtained by inserting 0.5 for $\hat{p}$ and for $\hat{q}$ in Equation 24.41.

If the sample size, n, is not a small portion of the population size, N, then the required sample size is smaller than the n determined by Equation 24.41 and can be estimated as

$$m = \frac{n}{1 + (n - 1)/N} \tag{24.42}$$

(Cochran, 1977: 75–76).

For the confidence intervals of Sections 24.8a and 24.8c, a much better estimate of the needed sample size may be obtained by iteration. For a given $\hat{p}$, a value of n may be proposed, from Equation 24.41 or otherwise. (Equation 24.41 will yield an underestimate of n.) Then the confidence limits are calculated. If the confidence interval is wider than desired, perform the calculation again with a larger n; and if it is

narrower than desired, try again with a smaller n. This process can be repeated until an estimate of the required n is obtained for the interval width desired.

24.9 CONFIDENCE INTERVAL FOR A POPULATION MEDIAN

The confidence limits for a population median* may be obtained by considering a binomial distribution with $p = 0.5$. The procedure thus is related to the binomial and sign tests in earlier sections of this chapter and may conveniently use Appendix Table B.27. That table gives $C_{\alpha,n}$, and from this we can state the confidence interval for a median to be

$$P(X_i \leq \text{population median} \leq X_j) \geq 1 - \alpha, \tag{24.43}$$

where

$$i = C_{\alpha(2),n} + 1 \tag{24.44}$$

and

$$j = n - C_{\alpha(2),n} \tag{24.45}$$

(e.g., MacKinnon, 1964), if the data are arranged in order of magnitude (so that X_i is the smallest measurement and X_j is the largest). The confidence limits, therefore, are $L_1 = X_i$ and $L_2 = X_j$. Because of the discreteness of the binomial distribution, the confidence will typically be a little greater than the $1 - \alpha$ specified. This procedure is demonstrated in Example 24.14a.

EXAMPLE 24.14a A Confidence Interval for a Median

Let us determine a 95% confidence interval for the median of the population from which each of the two sets of data in Example 3.3 came, where the population median was estimated to be 40 mo for species A and 52 mo for species B.

For species $A, n = 9$, so (from Appendix Table B.27) $C_{0.05(2),9} = 1$ and $n - C_{0.05(2),9} = 9 - 1 = 8$. The confidence limits are, therefore, X_i and X_j, where $i = 1 + 1 = 2$ and $j = 8$; and we can state

$$P(X_2 \leq \text{population median} \leq X_8) \geq 0.95$$

or

$$P(36 \text{ mo} \leq \text{population median} \leq 43 \text{ mo}) \geq 0.95.$$

For species $B, n = 10$, and Appendix Table B.27 informs us that $C_{0.05(2),10} = 1$; therefore, $n - C_{0.05(2),10} = 10 - 1 = 9$. The confidence limits are X_i and X_j, where $i = 1 + 1 = 2$ and $j = 9$; thus,

$$P(X_2 \leq \text{population median} \leq X_9) \geq 0.95.$$

or

$$P(36 \text{ mo} \leq \text{population median} \leq 69 \text{ mo}) \geq 0.95.$$

Hutson (1999) discussed calculation of confidence intervals for quantiles other than the median.

*Such confidence intervals were first discussed by William R. Thompson in 1936 (Noether, 1984).

(a) A Large-Sample Approximation. For samples larger than appearing in Appendix Table B.27, an excellent approximation of the lower confidence limit (based on Hollander and Wolfe, 1999: Section 3.6), is derived from the normal distribution as

$$L_1 = X_i, \tag{24.46}$$

where

$$i = \frac{n - Z_{\alpha(2)}\sqrt{n}}{2} \tag{24.47}$$

rounded to the nearest integer, and $Z_{\alpha(2)}$ is the two-tailed normal deviate read from Appendix Table B.2. (Recall that $Z_{\alpha(2)} = t_{\alpha(2),\infty}$, and so may be read from the last line of Appendix Table B.3.) The upper confidence limit is

$$L_2 = X_{n-i+1}. \tag{24.48}$$

By this method we approximate a confidence interval for the population median with confidence $\geq 1 - \alpha$.

TESTING FOR DIFFERENCE BETWEEN TWO PROPORTIONS

Two proportions may be compared by casting the underlying data in a 2×2 contingency table and considering that one margin of the table is fixed (Section 23.3b). For example, in Example 23.3 the column totals (the total data for each species) are fixed and the proportion of mice afflicted with the parasite are $\hat{p}_1 = 18/24 = 0.75$ for species 1 and $\hat{p}_2 = 10/25 = 0.40$ for species 2. The null hypothesis (H_0: $p_1 = p_2$) may be tested using the normal distribution (as shown in Example 24.15), by computing

$$Z = \frac{\hat{p}_1 - \hat{p}_2}{\sqrt{\frac{\bar{p}\bar{q}}{n_1} + \frac{\bar{p}\bar{q}}{n_2}}}. \tag{24.49}$$

Here, $\bar{p}$ is the proportion of parasitized mice obtained by pooling all n data:

$$\frac{X_1 + X_2}{n_1 + n_2} \tag{24.50}$$

or, equivalently, as

$$\frac{n_1\hat{p}_1 + n_2\hat{p}_2}{n_1 + n_2}, \tag{24.51}$$

and $\bar{q} = 1 - \bar{p}$.

A null hypothesis may propose a difference other than zero between two proportions. With p_0 the specified difference, H_0: $|p_1 - p_2| = p_0$ may be tested by replacing the numerator* of Equation 24.49 with $|p_1 - p_2| - p_0$.

One-tailed testing is also possible (with $p_0 = 0$ or $p_0 \neq 0$) and is effected in a fashion analogous to that used for testing difference between two means (Section 8.1a). This is demonstrated in Example 24.15b, where the alternate hypothesis is that the parasite infects a higher proportion of fish in species 1 than in species 2, and also in Example 24.15c.

*If p_0 is not zero in H_0 and H_A, in some cases a somewhat more powerful test has been reported if the denominator of Equation 24.49 is replaced by $\sqrt{\hat{p}_1\hat{q}_1/n_1 + \hat{p}_2\hat{q}_2/n_2}$ (Agresti, 2002: 77; Eberhardt and Fligner, 1977).

EXAMPLE 24.15 Testing for Difference Between Two Proportions

Using the data of Example 23.3,

$$\hat{p}_1 = X_1/n_1 = 18/24 = 0.75$$
$$\hat{p}_2 = X_2/n_2 = 10/25 = 0.40$$
$$\bar{p} = (18 + 10)/(24 + 25) = 28/49 = 0.5714$$
$$\bar{q} = 1 - 0.5714 = 0.4286.$$

(a) The two-tailed test for $H_0: p_1 = p_2$ versus $H_A: p_1 \neq p_2$

$$Z = \frac{\hat{p}_1 - \hat{p}_2}{\sqrt{\frac{\bar{p}\,\bar{q}}{n_1} + \frac{\bar{p}\,\bar{q}}{n_2}}}$$

$$= \frac{0.75 - 0.40}{\sqrt{\frac{(0.5714)(0.4286)}{24} + \frac{(0.5714)(0.4286)}{25}}}$$

$$= \frac{0.35}{\sqrt{0.1414}} = 2.4752$$

For $\alpha = 0.05$, $Z_{0.05(2)} = 1.9600$ and H_0 is rejected.

$$0.01 < P < 0.02 \quad [P = 0.013]$$

(b) The one-tailed test for $H_0: p_1 \leq p_2$ versus $H_A: p_1 > p_2$

For $\alpha = 0.05$, $Z_{0.05(1)} = 1.6449$. Because $Z > 1.6449$ and the difference (0.35) is in the direction of the alternate hypothesis, H_0 is rejected.

$$0.005 < P < 0.01 \quad [P = 0.007]$$

(c) The one-tailed test for $H_0: p_1 \geq p_2$ versus $H_A: p_1 < p_2$

For $\alpha = 0.05$, $Z_{0.05(1)} = 1.6449$. Because $Z > 1.6449$ but the difference (0.35) is not in the direction of the alternate hypothesis, H_0 is not rejected.

Important note: Three pairs of hypotheses are tested in this example. This is done only for demonstration of the test, for in practice it would be proper to test only one of these pairs of hypotheses for a given set of data. The decision of which one of the three pairs of hypotheses to use should be made on the basis of the biological question being asked and is to be made *prior to* the collection of the data.

If the preceding hypotheses pertain to a sample of n_1 proportions and a second sample of n_2 proportions, then the t test of Section 8.1 can be used in conjunction with the data transformation of Section 13.3.

24.11 CONFIDENCE LIMITS FOR THE DIFFERENCE BETWEEN PROPORTIONS

When a proportion ($\hat{p}_1$) is obtained by sampling one population, and a proportion ($\hat{p}_2$) is from another population, confidence limits for the difference between the two population proportions ($p_1 - p_2$) can be calculated by many methods.* The most common are these:

(a) Wald Interval. A confidence interval may be expressed in a fashion analogous to the Wald interval for a single proportion (which is discussed in Section 24.8b):

$$\hat{p}_1 - \hat{p}_2 \pm Z_{\alpha(2)}\sqrt{\frac{\hat{p}_1\hat{q}_1}{n_1} + \frac{\hat{p}_2\hat{q}_2}{n_2}}, \tag{24.52}$$

where $\hat{p}_1 = X_1/n_1$, $\hat{p}_2 = X_2/n_2$, $\hat{q}_1 = 1 - \hat{p}_1$, and $\hat{q}_2 = 1 - \hat{p}_2$.

Though commonly used, this calculation of confidence limits yields poor results, even when sample sizes are large. These confidence limits include $\hat{p}_1 - \hat{p}_2$ less than $1 - \alpha$ of the time (e.g., less than 95% of the time when expressing a 95% confidence interval), and thus they are said to be "liberal." The confidence limits include $\hat{p}_1 - \hat{p}_2$ *much* less than $1 - \alpha$ of the time when $\hat{p}_1$ and $\hat{p}_2$ are near 0 or 1. Also, Equation 24.52 produces confidence limits that are always symmetrical around $\hat{p}_1 - \hat{p}_2$, whereas (unless $\hat{p}_1 - \hat{p}_2 = 0.50$) the distance between the lower confidence limit (L_1) and $\hat{p}_1 - \hat{p}_2$ should be different than the distance between $\hat{p}_1 - \hat{p}_2$ and the upper limit (L_2). This unrealistic symmetry can produce a calculated L_1 that is less than 0 or greater than 1, which would be an unreasonable result. In addition, when both $\hat{p}_1$ and $\hat{p}_2$ are either 0 or 1, a confidence interval cannot be calculated by this equation. Therefore, this calculation (as is the case of Equation 24.36 in Section 24.8b) generally is not recommended.

(b) Adjusted Wald Interval. Agresti and Caffo (2000) have shown that it is far preferable to employ an "adjusted" Wald interval (analogous to that in the one-sample situation of Section 24.8c), where Equation 24.52 is employed by substituting† $\tilde{X}_i = X_i + Z^2_{\alpha(2)}/4$ for X_i and $\tilde{n}_i = n_i Z^2_{\alpha(2)}/2$ for n_i. As shown in Example 24.15a, the adjusted confidence interval is obtained by using $\tilde{p}_i = \tilde{X}_i/\tilde{n}_i$ in place of $\hat{p}_i$ in Equation 24.52. This adjusted Wald confidence interval avoids the undesirable severe liberalism obtainable with the unadjusted interval, although it can be slightly conservative (i.e., have a probability of a little greater than $1 - \alpha$ of containing $p_1 - p_2$) when $\tilde{p}_1$ and $\tilde{p}_2$ are both near 0 or 1.

Newcombe (1998b) discussed a confidence interval that is a modification of the one-sample interval based upon Wilson (1927) and mentioned in Section 24.8d. It is said to produce results similar to those of the adjusted Wald interval.

(c) Sample Size Requirements. If the statistics $\hat{p}_1$ and $\hat{p}_2$ are obtained from sampling two populations, it may be desired to estimate how many data must be collected from those populations to calculate a confidence interval of specified width for $p_1 - p_2$. The following may be derived from the calculation of the Wald interval

*A large number of them are discussed by Agresti and Caffo (2000), Agresti and Coull (1998), Blyth (1986), Hauck and Anderson (1986), Newcombe (1998b), and Upton (1982).

†For a 95% confidence interval, $Z^2_{\alpha(2)}/4 = (1.9600)^2/4 = 0.9604$ and $Z^2_{\alpha(2)}/2 = (1.9600)^2/2 = 1.9208$, so using $X_i + 1$ in place of X_i and $n_i + 2$ in place of n_i yields very good results.

EXAMPLE 24.15a Confidence Interval for the Difference Between Two Population Proportions

For the 95% adjusted Wald confidence interval using the data of Example 23.3,

$$Z_{0.05(2)} = 1.9600,$$

$$\text{so } (1.9600)^2/4 = 0.9604 \text{ and } (1.9600)^2/2 = 1.9208$$

$$X_1 = 18, \text{so } \tilde{X}_1 = 18 + 0.9604 = 18.9604$$

$$X_2 = 10, \text{so } \tilde{X}_2 = 10 + 0.9604 = 10.9604$$

$$n_1 = 24, \text{so } \tilde{n}_1 = 24 + 1.9208 = 25.9208$$

$$n_2 = 25, \text{so } \tilde{n}_2 = 25 + 1.9208 = 26.9208$$

$$\tilde{p}_1 = 18.9604/25.9208 = 0.7315 \text{ and } \tilde{q}_1 = 1 - 0.7315 = 0.2685$$

$$\tilde{p}_2 = 10.9604/26.9208 = 0.4071 \text{ and } \tilde{q}_1 = 1 - 0.4071 = 0.5929$$

$$95\% \text{ CI for } p_1 - p_2 = \tilde{p}_1 - \tilde{p}_2 \pm Z_{0.05(2)}\sqrt{\frac{\tilde{p}_1\tilde{q}_1}{\tilde{n}_1} + \frac{\tilde{p}_2\tilde{q}_2}{\tilde{n}_2}}$$

$$= 0.7315 - 0.4071 \pm 1.9600\sqrt{\frac{(0.7315)(0.2685)}{25.9208} + \frac{(0.4071)(0.5929)}{26.9208}}$$

$$= 0.3244 \pm 1.9600\sqrt{0.0076 + 0.0090} = 0.3244 \pm 0.2525$$

$$L_1 = 0.07; \quad L_2 = 0.58.$$

(Section 24.11a) for equal sample sizes ($n = n_1 = n_2$):

$$n = Z^2_{\alpha(2)}\left[\frac{\hat{p}_1\hat{q}_1 + \hat{p}_2\hat{q}_2}{(\hat{p}_1 - \hat{p}_2)^2}\right]. \tag{24.53}$$

This is an underestimate of the number of data needed, and a better estimate may be obtained by iteration, using the adjusted Wald interval (Section 24.11b). For the given $\hat{p}_1$ and $\hat{p}_2$, a speculated value of n is inserted into the computation of the adjusted Wald interval in place of n_1 and n_2. If the calculated confidence interval is wider than desired, the adjusted Wald calculation is performed again with a larger n; if it is narrower than desired, the calculation is executed with a smaller n. This process is repeated until n is obtained for the interval width desired.

The iteration using the adjusted Wald equation may also be performed with one of the future sample sizes specified, in which case the process estimates the size needed for the other sample.

24.12 POWER, DETECTABLE DIFFERENCE, AND SAMPLE SIZE IN TESTING DIFFERENCE BETWEEN TWO PROPORTIONS

(a) Power of the Test. If the test of $H_0: p_1 = p_2$ versus $H_A: p_1 \neq p_2$ is to be performed at the α significance level, with n_1 data in sample 1 and n_2 data in sample 2, and if the two samples come from populations actually having proportions of p_1

and p_2, respectively, then an estimate of power is

$$\text{power} = P\left[Z \leq \frac{-Z_{\alpha(2)}\sqrt{\bar{p}\,\bar{q}/n_1 + \bar{p}\,\bar{q}/n_2} - (p_1 - p_2)}{\sqrt{p_1q_1/n_1 + p_2q_2/n_2}}\right] + P\left[Z \geq \frac{Z_{\alpha(2)}\sqrt{\bar{p}\,\bar{q}/n_1 + \bar{p}\,\bar{q}/n_2} - (p_1 - p_2)}{\sqrt{p_1q_1/n_1 + p_2q_2/n_2}}\right] \tag{24.54}$$

(Marascuilo and McSweeney, 1977: 111), where

$$\bar{p} = \frac{n_1p_1 + n_2p_2}{n_1 + n_2}, \tag{24.55}$$

$$q_1 = 1 - p_1, \tag{24.56}$$

$$q_2 = 1 - p_2, \tag{24.57}$$

and

$$\bar{q} = 1 - \bar{p}. \tag{24.58}$$

The calculation is demonstrated in Example 24.16.

For the one-tailed test of H_0: $p_1 \geq p_2$ versus H_A: $p_1 < p_2$, the estimated power is

$$\text{power} = P\left[Z \leq \frac{-Z_{\alpha(1)}\sqrt{\bar{p}\,\bar{q}/n_1 + \bar{p}\,\bar{q}/n_2} - (p_1 - p_2)}{\sqrt{p_1q_1/n_1 + p_2q_2/n_2}}\right]; \tag{24.59}$$

and for the one-tailed hypotheses, H_0: $p_1 \leq p_2$ versus H_A: $p_1 > p_2$,

$$\text{power} = P\left[Z \geq \frac{Z_{\alpha(1)}\sqrt{\bar{p}\,\bar{q}/n_1 + \bar{p}\,\bar{q}/n_2} - (p_1 - p_2)}{\sqrt{p_1q_1/n_1 + p_2q_2/n_2}}\right]. \tag{24.60}$$

These power computations are based on approximations to the Fisher exact test (Section 24.16) and tend to produce a conservative result. That is, the power is likely to be greater than that calculated.

(b) Sample Size Required and Minimum Detectable Difference. Estimating the sample size needed in a future comparison of two proportions, with a specified power, has been discussed by several authors,* using a normal approximation. Such an estimate may also be obtained by iteration analogous to that of Section 24.7c.

*See, for example, Casagrande, Pike, and Smith (1978); Cochran and Cox (1957: 27); and Fleiss, Levin, and Paik (2003: 72). Also, Hornick and Overall (1980) reported that the following computation of Cochran and Cox (1957: 27) yields good results and appears not to have a tendency to be conservative:

$$n = \left(Z_\alpha + Z_{\beta(1)}\right)^2 \Big/ \left[2\left(\arcsin\sqrt{p_1} - \arcsin\sqrt{p_2}\right)\right], \tag{24.61}$$

where the arcsines are expressed in radians.

EXAMPLE 24.16 Estimation of Power in a Two-Tailed Test Comparing Two Proportions

We propose to test $H_0: p_1 = p_2$ versus $H_A: p_1 \neq p_2$, with $\alpha = 0.05$, $n_1 = 50$, and $n_2 = 45$, where in the sampled populations $p_1 = 0.75$ and $p_2 = 0.50$. The power of the test can be estimated as follows.

We first compute (by Equation 24.55):

$$\bar{p} = \frac{(50)(0.75) + (45)(0.50)}{50 + 45} = 0.6316 \quad \text{and} \quad \bar{q} = 1 - \bar{p} = 0.3684.$$

Then

$$\frac{\bar{p}\,\bar{q}}{n_1} = \frac{(0.6316)(0.3684)}{50} = 0.0047; \quad \frac{\bar{p}\,\bar{q}}{n_2} = 0.0052;$$

$$\frac{p_1 q_1}{n_1} = \frac{(0.75)(0.25)}{50} = 0.0038; \quad \frac{p_2 q_2}{n_2} = \frac{(0.50)(0.50)}{45} = 0.0056;$$

$$Z_{0.05(2)} = 1.9600;$$

and, using Equation 24.64,

$$\text{power} = P\left[Z \leq \frac{-1.9600\sqrt{0.0047 + 0.0052} - (0.75 - 0.50)}{\sqrt{0.0038 + 0.0056}}\right] + P\left[Z \geq \frac{1.9600\sqrt{0.0047 + 0.0052} - (0.75 - 0.50)}{\sqrt{0.0038 + 0.0056}}\right]$$

$$= P(Z \leq -4.59) + P(Z \geq -0.57)$$
$$= P(Z \geq -4.59) + [1 - P(Z \geq 0.57)]$$
$$= 0.0000 + [1.0000 - 0.2843]$$
$$= 0.72.$$

The estimation procedure uses Equation 24.54, 24.59, or 24.60, depending upon the null hypothesis to be tested. The power is thus determined for the difference $(p_1 - p_2)$ desired to be detected between two population proportions. This is done using equal sample sizes $(n_1 = n_2)$ that are a reasonable guess of the sample size that is required from each of the two populations. If the power thus calculated is less than desired, then the calculation is repeated using a larger sample size. If the calculated power is greater than the desired power, the computation is performed again but using a smaller sample size. Such iterative calculations are repeated until the specified power has been obtained, and the last n used in the calculation is the estimate of the sample size required in each of the two samples.

The samples from the two populations should be of the same size $(n_1 = n_2)$ for the desired power to be calculated with the fewest total number of data $(n_1 + n_2)$. Fleiss, Tytun, and Ury (1980), Levin and Chen (1999), and Ury and Fleiss (1980) discuss the estimation of n_1 and n_2 when acquiring equal sample sizes is not practical.

In a similar manner, n, α, and power may be specified, and the minimum detectable difference $(p_1 - p_2)$ may be estimated. This is done by iteration, using Equation 24.54, 24.59, or 24.60, depending upon the null hypothesis to be tested. A reasonable guess of the minimum detectable difference can be entered into the equation and, if the calculated power is less than that desired, the computation is repeated with a larger $(p_1 - p_2)$; if the calculated power is greater than that desired, the computation is repeated by inserting a smaller $p_1 - p_2$ into the equation; and when the desired power is obtained from the equation, the $p_1 - p_2$ last used in the calculation is an expression of the estimated minimum detectable difference.

Ury (1982) described a procedure for estimating one of the two population proportions if n, α, the desired power, and the other population proportion are specified.

24.13 COMPARING MORE THAN TWO PROPORTIONS

Comparison of proportions may be done by contingency-table analysis. For example, the null hypothesis of Example 23.1 could be stated as, "The proportions of males and females are the same among individuals of each of the four hair colors."

Alternatively, an approximation related to the normal approximation is applicable (if n is large and neither p nor q is very near 1). Using this approximation, one tests H_0: $p_1 = p_2 = \cdots = p_k$ against the alternative hypothesis that all k proportions are not the same, as

$$\chi^2 = \sum_{i=1}^{k} \frac{(X_i - n_i\bar{p})^2}{n_i\bar{p}\,\bar{q}} \tag{24.62}$$

(Pazer and Swanson, 1972: 187–190). Here,

$$\bar{p} = \frac{\sum_{i=1}^{k} X_i}{\sum_{i=1}^{k} n_i} \tag{24.63}$$

is a pooled proportion, $\bar{q} = 1 - \bar{q}$, and χ^2 has $k - 1$ degrees of freedom. Example 24.17 demonstrates this procedure, which is equivalent to χ^2 testing of a contingency table with two rows (or two columns).

We can instead test whether k p's are equal not only to each other but to a specified constant, p_0 (i.e., H_0: $p_1 = p_2 = \cdots = p_k = p_0$). This is done by computing

$$\chi^2 = \sum_{i=1}^{k} \frac{(X_i - n_i p_0)^2}{n_i p_0(1 - p_0)}, \tag{24.64}$$

which is then compared to the critical value of χ^2 for k (rather than $k - 1$) degrees of freedom (Kulkarni and Shah, 1995, who also discuss one-tailed testing of H_0, where H_A is that $p_i \neq p_0$ for at least one i).

If each of the several proportions to be compared to each other is the mean of a set of proportions, then we can use the multisample testing procedures of Chapters 10, 11, 12, 14, and 15. To do so, the individual data should be transformed as suggested in Section 13.3, preferably by Equation 13.7 or 13.8, if possible.

EXAMPLE 24.17 Comparing Four Proportions, Using the Data of Example 23.1

$$n_1 = 87,\ X_1 = 32,\ \hat{p}_1 = \frac{32}{87} = 0.368,\ \hat{q}_1 = 0.632$$

$$n_2 = 108, X_2 = 43,\ \hat{p}_2 = \frac{43}{108} = 0.398,\ \hat{q}_2 = 0.602$$

$$n_3 = 80, X_3 = 16,\ \hat{p}_3 = \frac{16}{80} = 0.200,\ \hat{q}_3 = 0.800$$

$$n_4 = 25,\ X_4 = 9,\ \hat{p}_4 = \frac{9}{25} = 0.360,\ \hat{q}_4 = 0.640$$

$$\bar{p} = \frac{\sum X_i}{\sum n_i} = \frac{32 + 43 + 16 + 9}{87 + 108 + 80 + 25} = \frac{100}{300} = \frac{1}{3}$$

$$\bar{q} = 1 - \bar{p} = \frac{2}{3}$$

$$\chi^2 = \sum \frac{(X_i - n_i\bar{p})^2}{n_i\bar{p}\,\bar{q}}$$

$$= \frac{\left[132 - (87)\left(\frac{1}{3}\right)\right]^2}{(87)\left(\frac{1}{3}\right)\left(\frac{2}{3}\right)} + \frac{\left[43 - (108)\left(\frac{1}{3}\right)\right]^2}{(108)\left(\frac{1}{3}\right)\left(\frac{2}{3}\right)} + \frac{\left[16 - (80)\left(\frac{1}{3}\right)\right]^2}{(80)\left(\frac{1}{3}\right)\left(\frac{2}{3}\right)}$$

$$+ \frac{\left[9 - (25)\left(\frac{1}{3}\right)\right]^2}{(25)\left(\frac{1}{3}\right)\left(\frac{2}{3}\right)}$$

$$= 0.4655 + 2.0417 + 6.4000 + 0.0800$$

$$= 8.987 \text{ (which is the same } \chi^2 \text{ as in Example 23.1)}$$

$$\nu = k - 1 = 4 - 1 = 3$$

$$\chi^2_{0.05,3} = 7.815$$

Therefore, reject H_0.

$$0.025 < P < 0.05 \quad [P = 0.029]$$

Note how the calculated χ^2 compares with that in Example 23.1; the two procedures yield the same results for contingency tables with two rows or two columns.

Finally, it should be noted that comparing several p's yields the same results as one compared the associated q's.

MULTIPLE COMPARISONS FOR PROPORTIONS

(a) Comparisons of All Pairs of Proportions. If the null hypothesis $H_0: p_1 = p_2 = \cdots = p_k$ (see Section 24.13) is rejected, then we may desire to determine specifically which population proportions are different from which others. The following procedure (similar to that of Levy, 1975a) allows for testing analogous to the Tukey test introduced in Section 11.1. An angular transformation (Section 13.3) of each sample proportion is to be used. If $\hat{p}$, but not X and n, is known, then Equation 13.5 may be used. If, however, X and n are known, then either Equation 13.7 or 13.8 is preferable. (The latter two equations give similar results, except for small or large $\hat{p}$, where Equation 13.8 is probably better.)

As shown in Example 24.18, the multiple comparison procedure is similar to that in Chapter 11 (the Tukey test being in Section 11.1). The standard error for each comparison is, in degrees,*

$$\text{SE} = \sqrt{\frac{820.70}{n + 0.5}} \tag{24.65}$$

EXAMPLE 24.18 Tukey-Type Multiple Comparison Testing Among the Four Proportions of Example 24.17

Samples ranked by proportion (i):	3	4	1	2
Ranked sample proportions ($p_i = X_i/n_i$):	16/80 = 0.200	9/25 = 0.360	32/87 = 0.368	43/108 = 0.398
Ranked transformed proportions (p'_i, in degrees):	26.85	37.18	37.42	39.18

Comparison *B vs. A*	*Difference* $p'_B - p'_A$	SE	q	$q_{0.05,\infty,4}$	*Conclusion*
2 vs. 3	39.18 − 26.85 = 12.33	2.98	4.14	3.633	Reject $H_0: p_2 = p_3$
2 vs. 4	39.18 − 37.18 = 2.00	4.46	0.45	3.633	Do not reject H_0: $p_2 = p_4$
2 vs. 1	Do not test				
1 vs. 3	37.42 − 26.85 = 10.57	3.13	3.38	3.633	Do not reject H_0: $p_1 = p_3$
1 vs. 4	Do not test				
4 vs. 3	Do not test				

Overall conclusion: $p_4 = p_1 = p_2$ and $p_3 = p_4 = p_1$, which is the kind of ambiguous result described at the end of Section 11.1. By chi-square analysis (Example 23.6) it was concluded that $p_3 \neq p_4 = p_1 = p_2$; it is likely that the present method lacks power for this set of data.

Equation 13.8 is used for the transformations. For sample 3, for example, $X/(n + 1) = 16/81 = 0.198$ and $(X + 1)/(n + 1) = 17/81 = 0.210$, so $p'_3 = \frac{1}{2}[\arcsin\sqrt{0.198} + \arcsin\sqrt{0.210}] = \frac{1}{2}[26.4215 + 27.2747] = 26.848$. If we use Appendix Table B.24 to obtain the two needed arcsines, we have $p'_3 = \frac{1}{2}[26.42 + 27.27] = 26.845$.

*The constant 820.70 square degrees results from $(180°/2\pi)^2$, which follows from the variances reported by Anscombe (1948) and Freeman and Tukey (1950).

if the two samples being compared are the same size, or

$$\text{SE} = \sqrt{\frac{410.35}{n_A + 0.5} + \frac{410.35}{n_B + 0.5}} \tag{24.66}$$

if they are not. The critical value is $q_{\alpha,\infty,k}$ (from Appendix Table B.5).

Use of the normal approximation to the binomial is possible in multiple-comparison testing (e.g., Marascuilo, 1971: 380–382); but the preceding procedure is preferable, even though it—and the methods to follow in this section—may lack desirable power.

(b) Comparison of a Control Proportion to Each Other Proportion. A procedure analogous to the Dunnett test of Section 11.3 may be used as a multiple comparison test where instead of comparing all pairs of proportions we desire to compare one proportion (designated as the "control") to each of the others. Calling the control group B, and each other group, in turn, A, we compute the Dunnett test statistic:

$$q = \frac{p'_B - p'_A}{\text{SE}}. \tag{24.67}$$

Here, the proportions have been transformed as earlier in this section, and the appropriate standard error is

$$\text{SE} = \sqrt{\frac{1641.40}{n + 0.5}} \tag{24.68}$$

if Samples A and B are the same size, or

$$\text{SE} = \sqrt{\frac{820.70}{n_A + 0.5} + \frac{820.70}{n_B + 0.5}} \tag{24.69}$$

if $n_A \neq n_B$. The critical value is $q'_{\alpha(1),\infty,p}$ (from Appendix Table B.6) or $q'_{\alpha(2),\infty,p}$ (from Appendix Table B.7) for one-tailed or two-tailed testing, respectively.

(c) Multiple Contrasts Among Proportions. The Scheffé procedure for multiple contrasts among means (Section 11.4) may be adapted to proportions by using angular transformations as done earlier in this section. For each contrast, we calculate

$$S = \frac{\left|\sum_i c_i p'_i\right|}{\text{SE}}, \tag{24.70}$$

where

$$\text{SE} = \sqrt{820.70 \sum_i \frac{c_i^2}{n_i + 0.5}}, \tag{24.71}$$

and c_i is a contrast coefficient as described in Section 11.4. For example, if we wished to test the hypothesis H_0: $(p_1 + p_2 + p_4)/3 - p_3 = 0$, then $c_1 = \frac{1}{3}, c_2 = \frac{1}{3}, c_3 = -1$, and $c_4 = \frac{1}{3}$.

TRENDS AMONG PROPORTIONS

In a $2 \times c$ contingency table (2 rows and c columns), the columns may have a natural quantitative sequence. For example, they may represent different ages, different lengths of time after a treatment, different sizes, different degrees of infection, or different intensities of a treatment. In Example 24.19, the columns represent three age classes of women, and the data are the frequencies with which the 104 women in the sample exhibit a particular skeletal condition. The chi-square contingency-table analysis of Section 23.1 tests the null hypothesis that the occurrence of this condition is independent of age class (i.e., that the population proportion, p, of women with the condition is the same for all three age classes). It is seen, in Example 24.19a, that this hypothesis is rejected, so we conclude that in the sampled population there is a relationship between the two variables (age class and skeletal condition).

EXAMPLE 24.19 Testing for Linear Trend in a 2 × 3 Contingency Table. The Data Are the Frequencies of Occurrence of a Skeletal Condition in Women, Tabulated by Age Class

	Age class			
	Young	*Medium*	*Older*	*Total*
Condition present	6	16	18	40
Condition absent	22	28	14	64
Total	28	44	32	104
$\hat{p}_j$	0.2143	0.3636	0.5625	
X_j	−1	0	1	

(a) Comparison of proportions

H_0: In the sampled population, the proportion of women with this condition is the same for all three age classes.

H_A: In the sampled population, the proportion of women with this condition is not the same for all three age classes.

$$\hat{f}_{11} = (40)(28)/104 = 10.7692,\ \hat{f}_{12} = (40)(44)/104 = 16.9231, \ldots,$$
$$\hat{f}_{23} = (64)(28)/104 = 19.6923$$

$$\chi^2 = \sum_{i=1}^{r}\sum_{j=1}^{c} \frac{(f_{ij} - \hat{f}_{ij})^2}{\hat{f}_{ij}}$$
$$= \frac{(6 - 10.7692)^2}{10.7692} + \frac{(16 - 16.9231)^2}{16.9231} + \cdots + \frac{(14 - 19.6923)^2}{19.6923}$$
$$= 2.1121 + 0.0504 + 2.6327 + 1.3200 + 0.0315 + 1.6454$$
$$= 7.7921$$

(b) Test for trend

H_0: In the sampled population, there is a linear trend among these three age categories for the proportion of women with this condition.

H_A: In the sampled population, there is not a linear trend among these three age categories for the proportion of women with this condition.

$$\chi_t^2 = \frac{n}{R_1 R_2} \cdot \frac{\left(n\sum_{j=1}^{c} f_{1,j}X_j - R_1\sum_{j=1}^{c} C_jX_j\right)^2}{n\sum_{j=1}^{c} C_jX_j^2 - \left(\sum_{j=1}^{c} C_jX_j\right)^2}$$

$$= \frac{104}{(40)(64)} \cdot \frac{\{104[(6)(-1) + (16)(0) + (18)(1)] - 40[(28)(-1) + (44)(0) + (32)(1)]\}^2}{104[(28)(-1^2) + (44)(0^2) + (32)(1^2)] - [(28)(-1) + (44)(0) + (32)(1)]^2}$$

$$= 0.04062 \cdot \frac{(1248 - 160)^2}{6240 - 16}$$

$$= (0.04062)(190.1902) = 7.726$$

	Chi-square	ν	P
Total	$\chi^2 = 7.792$	2	$0.01 < P < 0.025$ $[P = 0.020]$
Linear trend	$\chi_t^2 = 7.726$	1	
Departure from linear trend	$\chi_d^2 = 0.066$	1	$0.75 < P < 0.90$ $[P = 0.80]$

In addition, we may ask whether the difference among the three age classes follows a linear trend; that is, whether there is either a greater occurrence of the condition of interest in women of greater age or a lesser occurrence with greater age. The question of linear trend in a $2 \times n$ contingency table may be addressed by the method promoted by Armitage (1955, 1971: 363–365) and Armitage, Berry, and Matthews (2002: 504–509). To do so, the magnitudes of ages expressed by the age classes may be designated by consecutive equally spaced ordinal scores: X. For example, the "young," "medium," and "older" categories in the present example could be indicated by X's of 1, 2, and 3; or by 0, 1, and 2; or by -1, 0, and 1; or by 0.5, 1, and 1.5; or by 3, 5, and 7; and so on. The computation for trend is made easier if the scores are consecutive integers centered on zero, so scores of -1, 0, and 1 are used in Example 24.19. (If the number of columns, c, were 4, then X's such as -2, -1, 1, and 2, or 1, 0, 2, and 3 could be used.)

The procedure divides the contingency-table chi-square into component parts, somewhat as sum-of-squares partitioning is done in analysis of variance. The chi-square of Equation 23.1 may be referred to as the total chi-square, a portion of which can be identified as being due to a linear trend:

$$\text{chi-square for linear trend} = \chi_t^2 = \frac{n}{R_1 R_2} \cdot \frac{\left(n\sum_{j=1}^{c} f_{1,j}X_j - R_1\sum_{j=1}^{c} C_jX_j\right)^2}{n\sum_{j=1}^{c} C_jX_j^2 - \left(\sum_{j=1}^{c} C_jX_j\right)^2}, \quad (24.72)$$

and the remainder is identified as not being due to a linear trend:

$$\text{chi-square for departure from linear trend} = \chi^2_d = \chi^2 - \chi^2_l. \qquad (24.73)$$

Associated with these three chi-square values are degrees of freedom of $c - 1$ for χ^2, 1 for χ^2_l and $c - 2$ for χ^2_d.* This testing for trend among proportions is more powerful than the chi-square test for difference among the c proportions, so a trend might be identified even if the latter chi-square test concludes no significant difference among the proportions.

If, in Example 24.19, the data in the second column (16 and 28) were for older women and the data in the third column (18 and 14) were for medium-aged women, the total chi-square would have been the same, but χ^2_l would have been 0.899 [$P = 0.34$], and it would have been concluded that there was no linear trend with age.

In Example 24.19, the presence of a physical condition was analyzed in reference to an ordinal scale of measurement ("young," "medium," and "older"). In other situations, an interval or ratio scale may be encountered. For example, the three columns might have represented age classes of known quantitative intervals. If the three categories were equal intervals of "20.0–39.9 years," "40.0–59.9 years,"and "60.0–79.9 years," then the X's could be set as equally spaced values (for example, as -1, 0, and 1) the same as in Example 24.19. However, if the intervals were unequal in size, such as "20.0–29.9 years," "30.0–49.9 years,"and "50.0–79.9 years," then the X's should reflect the midpoints of the intervals, such as by 25, 40, and 65; or (with the subtraction of 25 years) by 0, 15, and 40; or (with subtraction of 40 years) by -15, 0, and 25.

THE FISHER EXACT TEST

In the discussion of 2×2 contingency tables, Section 23.3c described contingency tables that have two fixed margins, and Section 23.3d recommended analyzing such tables using a contingency-corrected chi-square (χ^2_c or χ^2_H), or a procedure known as the *Fisher exact test.*† The test using chi-square corrected for continuity is an approximation of the Fisher exact test, with χ^2_H the same as χ^2_c or routinely a better approximation than χ^2_c.

The Fisher exact test is based upon hypergeometric probabilities (see Section 24.2). The needed calculations can be tedious, but some statistical computer programs (e.g., Zar, 1987, and some statistical packages) can perform the test. Although this book recommends this test only for 2×2 tables having both margins fixed, some researchers use it for the other kinds of 2×2 tables (see Section 23.3d).

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*Armitage (1955) explained that this procedure may be thought of as a regression of the sample proportions, $\hat{p}_j$, on the ordinal scores, X_j, where the $\hat{p}_j$'s are weighted by the column totals, C_j; or as a regression of n pairs of Y and X, where Y is 1 for each of the observations in row 1 and is 0 for each of the observations in row 2.

†Named for Sir Ronald Aylmer Fisher (1890–1962), a monumental statistician recognized as a principal founder of modern statistics, with extremely strong influence in statistical theory and methods, including many areas of biostatistics (see, for example, Rao, 1992). At about the same time he published this procedure (Fisher, 1934: 99–101; 1935), it was also presented by Yates (1934) and Irwin (1935), so it is sometimes referred to as the Fisher-Yates test or Fisher-Irwin test. Yates (1984) observed that Fisher was probably aware of the exact-test procedure as early as 1926. Although often referred to as a statistician, R. A. Fisher also had a strong reputation as a biologist (e.g., Neyman, 1967), publishing—from 1912 to 1962—140 papers on genetics as well as 129 on statistics and 16 on other topics (Barnard, 1990).

The probability of a given 2 × 2 table is

$$P = \frac{\binom{R_1}{f_{11}}\binom{R_2}{f_{21}}}{\binom{n}{C_1}}, \tag{24.74}$$

which is identical to

$$P = \frac{\binom{C_1}{f_{11}}\binom{C_2}{f_{12}}}{\binom{n}{R_1}}. \tag{24.75}$$

From Equation 24.11, both Equations 24.74 and 24.75 reduce to

$$P = \frac{R_1!\,R_2!\,C_1!\,C_2!}{f_{11}!\,f_{21}!\,f_{12}!\,f_{22}!\,n!}, \tag{24.76}$$

and it will be seen that there is advantage in expressing this as

$$P = \frac{\dfrac{R_1!\,R_2!\,C_1!\,C_2!}{n!}}{f_{11}!\,f_{12}!\,f_{21}!\,f_{22}!}. \tag{24.77}$$

(a) One-Tailed Testing. Consider the data of Example 23.4. If species 1 is naturally found in more rapidly moving waters, it would be reasonable to propose that it is better adapted to resist current, and the test could involve one-tailed hypotheses: H_0: The proportion of snails of species 1 resisting the water current is no greater than (i.e., less than or equal to) the proportion of species 2 withstanding the current, and H_A: The proportion of snails of species 1 resisting the current is greater than the proportion of species 2 resisting the current. The Fisher exact test proceeds as in Example 24.20.

EXAMPLE 24.20 A One-Tailed Fisher Exact Test, Using the Data of Example 23.4

H_0: The proportion of snails of species 1 able to resist the experimental water current is no greater than the proportion of species 2 snails able to resist the current.

H_A: The proportion of snails of species 1 able to resist the experimental water current is greater than the proportion of species 2 snails able to resist the current.

	Resisted	Yielded	
Species 1	12	7	19
Species 2	2	9	11
	14	16	30

Expressing the proportion of each species resisting the current in the sample,

	Resisted	*Yielded*	*Total*
Species 1	0.63	0.37	1.00
Species 2	0.18	0.82	1.00

The sample data are in the direction of H_A, in that the species 1 sample has a higher proportion of resistant snails than does the species 2 sample. But are the data significantly in that direction? (If the data were not in the direction of H_A, the conclusion would be that H_0 cannot be rejected, and the analysis would proceed no further.) The probability of the observed table of data is

$$P = \frac{\dfrac{R_1!\,R_2!\,C_1!\,C_2!}{n!}}{f_{11}!\,f_{12}!\,f_{21}!\,f_{22}!}$$

$$= \frac{\dfrac{19!\,11!\,14!\,16!}{30!}}{12!\,7!\,2!\,9!}$$

$$= \text{antilog}\,[(\log 19! + \log 11! + \log 14! + \log 16! - \log 30!) - (\log 12! + \log 7! + \log 2! + \log 9!)]$$

$$= \text{antilog}\,[(17.08509 + 7.60116 + 10.94041 + 13.32062 - 32.42366) - (8.68034 + 3.70243 + 0.30103 + 5.55976)]$$

$$= \text{antilog}\,[16.52362 - 18.24356]$$

$$= \text{antilog}\,[-1.71994]$$

$$= \text{antilog}\,[0.28006 - 2.00000]$$

$$= 0.01906.$$

There are two tables with data more extreme than the observed data; they are as follows:

Table A:

13	6	19
1	10	11
14	16	30

$$P = \frac{\dfrac{19!\,11!\,14!\,16!}{30!}}{13!\,6!\,1!\,10!}$$

$$= \text{antilog}\,[16.52362 - (\log 13! + \log 6! + \log 1! + \log 10!)]$$

$$= \text{antilog}\,[-2.68776]$$

$$= 0.00205$$

Table B:

14	5	19
0	11	11
14	16	30

$$P = \frac{\frac{19!\,11!\,14!\,16!}{30!}}{14!\,5!\,0!\,11!}$$

$$= \text{antilog}\,[16.52362 - (\log 14! + \log 5! + \log 0! + \log 11!)]$$

$$= \text{antilog}\,[-4.09713]$$

$$= 0.00008$$

To summarize the probability of the original table and of the two more extreme tables (where f_0 in each table is the smallest of the four frequencies in that table),

	f_0	P
Original table	2	0.01906
More extreme table A	1	0.00205
More extreme table B	0	0.00008
Entire tail		0.02119

Therefore, if the null hypothesis is true, the probability of the array of data in the observed table or in more extreme tables is 0.02119. As this probability is less than 0.05, H_0 is rejected.

Note that if the hypotheses had been H_0: Snail species 2 has no greater ability to resist current than species 1 and H_A: Snail species 2 has greater ability to resist current than species 1, then we would have observed that the sample data are *not* in the direction of H_A and would not reject H_0, without even computing probabilities.

Instead of computing this exact probability of H_0, we may consult Appendix Table B.28, for $n = 30$, $m_1 = 11$, $m_2 = 14$; and the one-tailed critical values of f, for $\alpha = 0.05$, are 2 and 8. As the observed f in the cell corresponding to $m_1 = 11$ and $m_2 = 14$ is 2, H_0 may be rejected.

The probability of the observed contingency table occurring by chance, given the row and column totals, may be computed using Equation 24.76 or 24.77. Then the probability is calculated for each possible table having observed data more extreme that those of the original table. If the smallest observed frequency in the original table is designated as f_0 (which is 2 in Example 24.20), the more extreme tables are those that have smaller values of f_0 (which would be 1 and 0 in this example). (If the smallest observed frequency occurs in two cells of the table, then f_0 is designated to be the one with the smaller frequency diagonally opposite of it.)

The null hypothesis is tested by examining the sum of the probabilities of the observed table and of all the more extreme tables. This procedure yields the exact probability (hence the name of the test) of obtaining this set of tables by chance if the null hypothesis is true; and if this probability is less than or equal to the significance level, α, then H_0 is rejected.

Note that the quantity $R_1!R_2!C_1!C_2!/n!$ appears in each of the probability calculations using Equation 24.76 and therefore need be computed only once. It is only the value of $f_{11}!f_{12}!f_{21}!f_{22}!$ that needs to be computed anew for each table. To undertake these computations, the use of logarithms is advised for all but the smallest tables; and Appendix Table B.40 provides logarithms of factorials. It is also obvious that, unless the four cell frequencies are small, this test calculation is tedious without a computer.

An alternative to computing the exact probability in the Fisher exact test of 2×2 tables is to consult Appendix Table B.28 to obtain critical values with which to test null hypotheses for n up to 30. We examine the four marginal frequencies, R_1, R_2, C_1, and C_2; and we designate the smallest of the four as m_1. If m_1 is a row total, then we call the smaller of the two column totals m_2; if m_1 is a column total, then the smaller row total is m_2. In Example 24.20, $m_1 = R_2$ and $m_2 = C_1$; and the one-tailed critical values in Appendix Table B.28, for $\alpha = 0.05$, are 2 and 8. The observed frequency in the cell corresponding to marginal totals m_1 and m_2 is called f; and if f is equal to or more extreme than 2 or 8 (i.e., if $f \leq 2$ or $f \geq 8$), then H_0 is rejected. However, employing tables of critical values results in expressing a range of probabilities associated with H_0; and a noteworthy characteristic of the exact test—namely the exact probability—is absent.

Bennett and Nakamura (1963) published tables for performing an exact test of 2×3 tables where the three column (or row) totals are equal and n is as large as 60. Computer programs have been developed to perform exact testing of $r \times c$ tables where r and/or c is greater than 2.

Feldman and Kluger (1963) demonstrated a simpler computational procedure for obtaining the probabilities of tables more extreme than those of the observed table. It will not be presented here because the calculations shown on this section and in Section 24.16c are straightforward and because performance of the Fisher exact test is so often performed via computer programs.

(b) Two-Tailed Testing. For data in a 2×2 contingency table, the Fisher exact test may also be used to test two-tailed hypotheses, particularly when both margins of the table are fixed. Example 24.21 demonstrates this for the data and hypotheses of Example 23.4. What is needed is the sum of the probabilities of the observed table and of all tables more extreme in the same direction as the observed data. This is the probability obtained for the one-tailed test shown in Example 24.20. If either $R_1 = R_2$ or $C_1 = C_2$, then the two-tailed probability is two times the one-tailed probability. Otherwise, it is not, and the probability for the second tail is computed as follows.*

Again designating f_0 to be the smallest of the four observed frequencies and m_1 to be the smallest of the four marginal frequencies in the original table, a 2×2 table is formed by replacing f_0 with $m_1 - 0$, and *this is the most extreme table in the second tail. This is shown as Table C in Example 24.21. The probability of that table is calculated with Equation 24.76 or 24.77; if it is greater than the probability of the original table, then the two-tailed probability equals the one-tailed probability and the computation is complete. If the probability of the newly formed table is not greater than that of the original table, then it contributes to the probability of the second tail and the calculations continue. The probability of the next less extreme table is*

*Some (e.g., Dupont, 1986) recommend that the two-tailed probability should be determined as two times the one-tailed probability. Others (e.g., Lloyd, 1998) argue against that calculation, and that practice is not employed here; and it can be noted that the second tail may be much smaller than the first and such a doubling procedure could result in a computed two-tailed probability that is greater than 1.

Note that the quantity $R_1!R_2!C_1!C_2!/n!$ appears in each of the probability calculations using Equation 24.76 and therefore need be computed only once. It is only the value of $f_{11}!f_{12}!f_{21}!f_{22}!$ that needs to be computed anew for each table. To undertake these computations, the use of logarithms is advised for all but the smallest tables; and Appendix Table B.40 provides logarithms of factorials. It is also obvious that, unless the four cell frequencies are small, this test calculation is tedious without a computer.

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(b) Two-Tailed Testing. For data in a 2×2 contingency table, the Fisher exact test may also be used to test two-tailed hypotheses, particularly when both margins of the table are fixed. Example 24.21 demonstrates this for the data and hypotheses of Example 23.4. What is needed is the sum of the probabilities of the observed table and of all tables more extreme in the same direction as the observed data. This is the probability obtained for the one-tailed test shown in Example 24.20. If either $R_1 = R_2$ or $C_1 = C_2$, then the two-tailed probability is two times the one-tailed probability. Otherwise, it is not, and the probability for the second tail is computed as follows.*

Again designating f_0 to be the smallest of the four observed frequencies and m_1 to be the smallest of the four marginal frequencies in the original table, a 2×2 table is formed by replacing f_0 with $m_1 - 0$, and this is the most extreme table in the second tail. This is shown as Table C in Example 24.21. The probability of that table is calculated with Equation 24.76 or 24.77; if it is greater than the probability of the original table, then the two-tailed probability equals the one-tailed probability and the computation is complete. If the probability of the newly formed table is not greater than that of the original table, then it contributes to the probability of the second tail and the calculations continue. The probability of the next less extreme table is

*Some (e.g., Dupont, 1986) recommend that the two-tailed probability should be determined as two times the one-tailed probability. Others (e.g., Lloyd, 1998) argue against that calculation, and that practice is not employed here; and it can be noted that the second tail may be much smaller than the first and such a doubling procedure could result in a computed two-tailed probability that is greater than 1.

EXAMPLE 24.21 A Two-Tailed Fisher Exact Test, Using the Data and Hypotheses of Example 23.4

The probability of the observed table was found, in Example 24.20, to be 0.01906, and the one-tailed probability was calculated to be 0.02119. In determining the one-tailed probability, the smallest cell frequency (f_0) in the most extreme table (Table B) was 0, and the smallest marginal frequency (m_1) was 11. So $m_1 - f_0 = 11 - 0 = 11$ is inserted in place of f_0 to form the most extreme table in the opposite tail:

Table C:

3	16	19
11	0	11
14	16	30

the probability of which is

$$P = \frac{19!\,11!\,14!\,16!}{30!\,3!\,16!\,11!\,0!}$$

$= 0.00000663$, which is rounded to 0.00001.

The less extreme tables that are in the second tail, and have probabilities less than the probability of the observed table, are these two:

Table D:

4	15	19	
10	1	11	$P = 0.00029$
14	16	30	cumulative $P = 0.00001 + 0.00029 = 0.00030$

Table E:

5	14	19	
9	2	11	$P = 0.00440$
14	16	30	cumulative $P = 0.00030 + 0.00440 = 0.00470$

The next less extreme table is this:

Table F:

6	13	19	
8	3	11	$P = 0.03079$
14	16	30	cumulative $P = 0.00470 + 0.03079 = 0.03549$

The Table F cumulative probability (0.03549) is larger than the probability of the original table (0.02119), so the Table F probability is not considered a relevant part of the second tail. The second tail consists of the following:

	f_0	P
Table C	3	0.00001
Table D	4	0.00029
Table E	5	0.00440
Entire second tail		0.00470

and the two-tailed P is, therefore, 0.02119 + 0.00470 = 0.02589. As this is less than 0.05, we may reject H_0. Note that χ^2_H in Example 23.4 has a probability close to that of this Fisher exact test.

If using Appendix Table B.28, $n = 30, m_1 = 11, m_2 = 14$, and the f corresponding to m_1 and m_2 in the observed table is 2. As the two-tailed critical values of f, for $\alpha = 0.05$, are 2 and 9, H_0 is rejected.

determined; that table (Table D in Example 24.21) has cell frequency f_0 increased by 1, keeping the marginal frequencies the same. The two probabilities calculated for the second tail are summed and, if the sum is no greater than the probability of the original table, that cell frequency is again increased by 1 and a new probability computed. This process is continued as long as the sum of the probabilities in that tail is no greater than the probability of the original table.

(c) Probabilities Using Binomial Coefficients. Ghent (1972), Leslie (1955), Leyton (1968), and Sakoda and Cohen (1957) have shown how the use of binomial coefficients can eliminate much of the laboriousness of Fisher-exact-test computations, and Ghent (1972) and Carr (1980) have expanded these considerations to tables with more than two rows and/or columns. Using Appendix Table B.26a, this computational procedure requires much less effort than the use of logarithms of factorials, and it is at least as accurate. It may be employed for moderately large sample sizes, limited by the number of digits on one's calculator.

Referring back to Equation 24.75, the probability of a given 2 × 2 table is seen to be the product of two binomial coefficients divided by a third. The numerator of Equation 24.75 consists of one binomial coefficient representing the number of ways C_1 items can be combined f_{11} at a time (or f_{21} at a time, which is equivalent) and a second coefficient expressing the number of ways C_2 items can be combined f_{12} at a time (or, equivalently, f_{22} at a time). And the denominator denotes the number of ways n items can be combined R_1 at a time (or R_2 at a time). Appendix Table B.26a provides a large array of binomial coefficients, and the proper selection of those required leads to simple computation of the probability of a 2 × 2 table. (See Section 5.3 for discussion of combinations.)

The procedure is demonstrated in Example 24.22, for the data in Example 24.20. Consider the first row of the contingency table and determine the largest f_{11} and the smallest f_{12} that are possible without exceeding the row totals and column totals. These are $f_{11} = 14$ and $f_{12} = 5$, which sum to the row total of 19. (Other frequencies, such as 15 and 4, also add to 19, but the frequencies in the first column are limited to 14.) In a table where $f_{11} < f_{12}$, switch the two columns of the 2 × 2 table before performing these calculations.

EXAMPLE 24.22 The Fisher Exact Tests of Examples 24.20 and 24.21, Employing the Binomial-Coefficient Procedure

The observed 2 × 2 contingency table is

12	7	19
2	9	11
14	16	30

The top-row frequencies, f_{11} and f_{12}, of all contingency tables possible with the observed row and column totals, and their associated binomial coefficients and coefficient products, are as follows. The observed contingency table is indicated by "*".

		Binomial coefficient				Coefficient product	
f_{11}	f_{12}	$C_1 = 14$		$C_2 = 16$			
14	5	1.	×	4,368.	=	4,368	
13	6	14.	×	8,008.	=	112,112	1,157,520
12*	7*	91.	×	11,440.	=	1,041,040*	
11	8	364.	×	12,870.	=	4,684,680	
10	9	1,001.	×	11,440.	=	11,451,440	
9	10	2,002.	×	8,008.	=	16,032,016	
8	11	3,003.	×	4,368.	=	13,117,104	
7	12	3,432.	×	1,820.	=	6,246,240	
6	13	3,003.	×	560.	=	1,681,680	
5	14	2,002.	×	120.	=	240,240	
4	15	1,001.	×	16.	=	16,016	256,620
3	16	364.	×	1.	=	364	
						54,627,300	

One-tailed probability: $\frac{1,157,520}{54,627,300} = 0.02119$

Probability associated with the opposite tail: $\frac{256,620}{54,627,300} = 0.00470$

Two-tailed probability: 0.02589

We shall need to refer to the binomial coefficients for what Appendix Table B.26a refers to as $n = 14$ and $n = 16$, for these are the two column totals (C_1 and C_2) in the contingency table in Example 24.20. We record, from Appendix Table B.26a, the binomial coefficient for $n = C_1 = 14$ and $X = f_{11} = 14$ (which is 1), the coefficient for $n = C_2 = 16$ and $X = f_{12} = 5$ (which is 4,368), and the product of the two coefficients (which is 4,368).

Then we record the binomial coefficients of the next less extreme table; that is, the one with $f_{11} = 13$ and $f_{12} = 6$ (that is, coefficients of 14 and 8,008) and their product (i.e., 112,112). This process is repeated for each possible table until f_{11} can be no

smaller (and f_{12} can be no larger): that is, $f_{11} = 3$ and $f_{12} = 16$. The sum of all the coefficient products (54,627,300 in this example) is the number of ways n things may be combined R_1 at a time (where n is the total of the frequencies in the 2×2 table); this is the binomial coefficient for n (the total frequency) and $X = R_1$ (and in the present example this coefficient is ${}_{30}C_{11} = 54{,}627{,}300$). Determining this coefficient is a good arithmetic check against the sum of the products of the several coefficients of individual contingency tables.

Dividing the coefficient product for a contingency table by the sum of the products yields the probability of that table. Thus, the table of observed data in Example 24.20 has $f_{11} = 14$ and $f_{12} = 5$, and we may compute 1,041,040/54,627,300 = 0.01906, exactly the probability obtained in Example 24.20 using logarithms of factorials. The probability of the one-tailed test employs the sum of those coefficient products equal to or smaller than the product for the observed table and in the same tail as the observed table. In the present example, this tail would include products 4,368, 112,112, and 1,041,040, the sum of which is 1,157,520, and 1,157,520/54,627,300 = 0.02119, which is the probability calculated in Example 24.20. To obtain the probability for the two-tailed test, we add to the one-tailed probability the probabilities of all tables in the opposite tail that have coefficient products equal to or less than that of the observed table. In our example these products are 240,240, 16,016, and 364, their sum is 256,620, and 256,620/54,627,300 = 0.00470; the probabilities of the two tails are 0.02119 and 0.00470, which sum to the two-tailed probability of 0.02589 (which is what was calculated in Example 24.21).

PAIRED-SAMPLE TESTING OF NOMINAL-SCALE DATA

(a) Data in a 2×2 Table. Nominal-scale data may come from paired samples. A 2×2 table containing data that are *dichotomous* (i.e., the nominal-scale variable has two possible values) may be analyzed by the *McNemar test* (McNemar, 1947).

For example, assume that we wish to test whether two skin lotions are equally effective in relieving a poison-ivy rash. Both of the lotions might be tested on each of 50 patients with poison-ivy rashes on both arms, by applying one lotion to one arm and the other lotion to the other arm (using, for each person, a random selection of which arm gets which lotion). The results of the experiment can be summarized in a table such as in Example 24.23, where the results for each of the 50 patients consist of a pair of data (i.e., the outcomes of using the two lotions on each patient). As with other 2×2 tables (such as in Section 23.3), the datum in row i and column j will be designated as f_{ij}. Thus, $f_{11} = 12$, $f_{12} = 5$, $f_{21} = 11$, and $f_{22} = 22$; and the total of the four frequencies is $n = 50$. The two-tailed null hypothesis is that, in the sampled population of people who might be treated with these two medications, the proportion of them that would obtain relief from lotion A (call it p_1) is the same as the proportion receiving relief from lotion B (call it p_2); that is, H_0: $p_1 = p_2$ (vs. H_A: $p_1 \neq p_2$). In the sample, 12 patients (f_{11}) experienced relief from both lotions and 22 (f_{22}) had relief from neither lotion. The proportion of people in the sample who experienced relief from lotion A is $\hat{p}_1 = (f_{11} + f_{21})/n = (12 + 11)/50 = 0.46$, and the proportion benefiting from lotion B is $\hat{p}_2 = (f_{11} + f_{12})/n = (12 + 5)/50 = 0.34$. The sample estimate of $p_1 - p_2$ is

$$\hat{p}_1 - \hat{p}_2 = \frac{f_{11} + f_{21}}{n} - \frac{f_{11} + f_{12}}{n} = \frac{f_{11}}{n} + \frac{f_{21}}{n} - \frac{f_{11}}{n} - \frac{f_{12}}{n} = \frac{f_{21}}{n} - \frac{f_{12}}{n}. \tag{24.78}$$

That is, of the four data in the 2 × 2 table, only f_{12} and f_{21} are needed to test the hypotheses. The test is essentially a goodness-of-fit procedure (Section 22.1) where we ask whether the ratio of f_{12} to f_{21} departs significantly from 1 : 1. Thus, the hypotheses could also be stated as H_0: $\psi = 1$ and H_A: $\psi \neq 1$, where* ψ is the population ratio estimated by f_{12}/f_{21}.

The goodness-of-fit test for this example could proceed using Equation 22.1, but for this hypothesis it is readily performed via

$$\chi^2 = \frac{(f_{12} - f_{21})^2}{f_{12} + f_{21}}, \tag{24.79}$$

which is equivalent to using the normal deviate for a two-tailed test:

$$Z = \frac{|f_{12} - f_{21}|}{\sqrt{f_{12} + f_{21}}}. \tag{24.80}$$

Because χ^2 and Z are continuous distributions and the data to be analyzed are counts (i.e., integers), some authors have employed corrections for continuity. A common one is the Yates correction for continuity (introduced in Section 22.2). This is accomplished using Equation 22.3 or, equivalently, with

$$\chi_c^2 = \frac{(|f_{12} - f_{21}| - 1)^2}{f_{12} + f_{21}}, \tag{24.81}$$

which is the same as employing

$$Z_c = \frac{|f_{12} - f_{21}| - 1}{\sqrt{f_{12} + f_{21}}}. \tag{24.82}$$

The calculation of χ_c^2 for this test is demonstrated in Example 24.23.

A McNemar test using χ^2 operates with the probability of a Type I error much closer to α than testing with χ_c^2, although that probability will occasionally be a little greater than α. That is, the test can be liberal, rejecting H_0 more often than it should at the α level of significance. Use of χ_c^2 will routinely result in a test that is conservative, rejecting H_0 less often than it should and having less power than employing χ^2. Often, as in Example 24.23, the same conclusion is reached using the test with and without a correction for continuity. Bennett and Underwood (1970) and others have advised that the continuity correction should not generally be used.

Because this test employs only two of the four tabulated data (f_{12} and f_{21}), the results are the same regardless of the magnitude of the other two counts (f_{11} and f_{22}), which are considered as tied data and ignored in the analysis. If f_{12} and f_{21} are small, this test does not work well. If $f_{12} + f_{21} \leq 10$, the binomial test (Section 24.5) is recommended, with $n = f_{12} + f_{21}$ and $X = f_{12}$ (or f_{21}).

Another type of data amenable to McNemar testing results from the situation where experimental responses are recorded before and after some event, in which case the procedure may be called the "McNemar test for change." For example, we might record whether students saying the plan to pursue a career in microbiology,

*The symbol ψ is the lowercase Greek letter psi. (See Appendix A.)

EXAMPLE 24.23 McNemar's Test for Paired-Sample Nominal Scale Data

H_0: The proportion of persons experiencing relief is the same with both lotions (i.e., $H_0: p_1 = p_2$).

H_A: The proportion of persons experiencing relief is not the same with both lotions (i.e., $H_0: p_1 \neq p_2$).

$\alpha = 0.05$
$n = 50$

	Lotion A	
Lotion B	*Relief*	*No relief*
Relief	12	5
No relief	11	22

$$\chi^2 = \frac{(f_{12} - f_{21})^2}{(f_{12} - f_{21})} = \frac{(5 - 11)^2}{5 + 11} = 2.250$$

$\nu = 1$, $\chi^2_{0.05,1} = 3.841$. Therefore, do not reject H_0.

$$0.10 < P < 0.25 \quad [P = 0.13]$$

Alternatively, and with the same result,

$$Z = \frac{|f_{12} - f_{21}|}{\sqrt{f_{12} + f_{21}}} = \frac{|5 - 1|}{\sqrt{5 + 11}} = 1.500,$$

$Z_{0.05(2)} = 1.900$. Therefore, do not reject H_0.

$$0.10 < P < 0.20 \quad [P = 0.13]$$

With a correction for continuity,

$$\chi^2_c = \frac{(|f_{12} - f_{21}| - 1)^2}{(f_{12} - f_{21})} = \frac{(|5 - 11| - 1)^2}{5 + 11} = 1.562.$$

Do not reject H_0.

$$0.10 < P < 0.25 \quad [P = 0.21]$$

Alternatively, and with the same result,

$$Z_c = \frac{|f_{12} - f_{21}| - 1}{\sqrt{f_{12} + f_{21}}} = \frac{|5 - 1| - 1}{\sqrt{5 + 11}} = 1.250.$$

Do not reject H_0.

$$0.20 < P < 0.50 \quad [P = 0.21]$$

before and after an internship experience in microbiology laboratory. The column headings could be "yes" and "no" before the internship, and the row designations then would be "yes" and "no" after the internship.

The McNemar test should not be confused with 2 × 2 contingency-table analysis (Section 23.3). Contingency-table data are analyzed using a null hypothesis of independence between rows and columns, whereas in the case of data subjected to the McNemar test, there is intentional association between the row and column data.

(b) The One-Tailed McNemar Test. Using the normal deviate (Z) as the test statistic, one-tailed hypotheses can be tested. So, for example, the hypotheses for a poison ivy-treatment experiment could be H_0: The proportion of people experiencing relief with lotion A is not greater than (i.e., is less than or equal to) the proportion having relief with lotion B, versus H_A : The proportion of people experiencing relief with lotion A is greater than the proportion obtaining relief with lotion B. And H_0 would be rejected if Z (or Z_c, if using the continuity correction) were greater than or equal to $Z_{\alpha(1)}$ *and* $f_{21} > f_{12}$.

(c) Power and Sample Size for the McNemar Test. The ability of the McNemar test to reject a null hypothesis, when the hypothesis is false, may be estimated by computing

$$Z_{\beta(1)} = \frac{\sqrt{n}\sqrt{p}(\psi - 1) - Z_\alpha\sqrt{\psi + 1}}{\sqrt{(\psi + 1) - p(\psi - 1)^2}} \tag{24.83}$$

(Connett, Smith, and McHugh, 1987). Here, n is the number of pairs to be used (i.e., $n = f_{11} + f_{12} + f_{21} + f_{22}$); p is an estimate, as from a pilot study, of the proportion f_{12}/n or f_{21}/n, whichever is smaller; ψ is the magnitude of difference desired to be detected by the hypothesis test, expressed as the ratio in the population of either f_{12} to f_{21}, or f_{21} to f_{12}, whichever is larger; and Z_α is $Z_{\alpha(2)}$ or $Z_{\alpha(1)}$, depending upon whether the test is two-tailed or one-tailed, respectively. Then, using Appendix Table B.2 or the last line in Appendix Table B.3 (i.e., for t with $\nu = \infty$), determine $\beta(1)$; and the estimated power of the test is $1 - \beta(1)$. This estimation procedure is demonstrated in Example 24.24.

Similarly, we can estimate the sample size necessary to perform a McNemar test with a specified power:

$$n = \frac{\left[Z_\alpha\sqrt{\psi + 1} + Z_{\beta(1)}\sqrt{(\psi + 1) - p(\psi - 1)^2}\right]^2}{p(\psi - 1)^2} \tag{24.84}$$

(Connett, Smith, and McHugh, 1987). This is demonstrated in Example 24.25

(d) Data in Larger Tables. The McNemar test may be extended to square tables larger than 2 × 2 (Bowker, 1948; Maxwell, 1970). What we test is whether the upper right corner of the table is symmetrical with the lower left corner. This is done by ignoring the data along the diagonal containing f_{ii} (i.e., row 1, column 1; row 2, column 2; etc.). We compute

$$\chi^2 = \sum_{i=1}^{r}\sum_{j>i}\frac{(f_{ij} - f_{ji})^2}{f_{ij} + f_{ji}}, \tag{24.85}$$

where, as before, f_{ij} is the observed frequency in row i and column j, and the degrees of freedom are

$$\nu = \frac{r(r - 1)}{2}, \tag{24.86}$$

EXAMPLE 24.24 Determination of Power of the McNemar Test

Considering the data of Example 24.23 to be from a pilot study, what would be the probability of rejecting H_0 if 200 pairs of data were used in a future study, if the test were performed at the 0.05 level of significance and if the population ratio of f_{21} to f_{12} were at least 2?

From the pilot study, using $n = 51$ pairs of data, $f_{12/n} = 6/51 = 0.1176$ and $f_{21/n} = 10/51 = 0.1961$; so $p = 0.1176$. We specify $\alpha(2) = 0.05$, so $Z_{0.05(2)} = 1.9600$ (from the last line of Appendix Table B.3). And we also specify a new sample size of $n = 200$ and $\psi = 2$. Therefore,

$$Z_{\beta(1)} = \frac{\sqrt{n}\sqrt{p}(\psi - 1) - Z_{\alpha(2)}\sqrt{\psi + 1}}{\sqrt{(\psi + 1) - p(\psi - 1)^2}}$$

$$= \frac{\sqrt{200}\sqrt{0.1176}(2 - 1) - 1.9600\sqrt{2 + 1}}{\sqrt{(2 + 1) - 0.1176(2 - 1)^2}}$$

$$= \frac{(14.1421)(0.3429)(1) - 1.9600(1.7321)}{\sqrt{3 - (0.1176)(1)}}$$

$$= \frac{4.8493 - 3.3949}{\sqrt{2.8824}} = \frac{1.4544}{1.6978} = 0.86.$$

From Appendix Table B.2, if $Z_{\beta(1)} = 0.86$, then $\beta(1) = 0.19$; therefore, power [i.e., $1 - \beta(1)$] is $1 - 0.19 = 0.81$.

From Appendix Table B.3, if $Z_{\beta(1)}$ [i.e., $t_{\beta(1),\infty}$] is 0.86, then $\beta(1)$ lies between 0.25 and 0.10, and the power [i.e., $1 - \beta(1)$] lies between 0.75 and 0.90. [$\beta(1) = 0.19$ and power = 0.81.]

and where r is the number of rows (or, equivalently, the number of columns) in the table of data. This is demonstrated in Example 24.26.

Note that Equation 24.85 involves the testing of a series of 1 : 1 ratios by what is essentially an expansion of Equation 24.79. Each of these 1 : 1 ratios derives from a unique pairing of the r categories taken two at a time. Recall (Equation 5.10) that the number of ways that r items can be combined two at a time is ${}_rC_2 = r!/[2(r - 2)!]$. So, in Example 24.26, where there are three categories, there are ${}_3C_2 = 3!/[2(3 - 2)!] = 3$ pairings, resulting in three terms in the χ^2 summation. If there were four categories of religion, then the summation would involve ${}_4C_2 = 4!/[2(4 - 2)!] = 6$ pairings, and 6 χ^2 terms; and so on. For data of this type in a 2×2 table, Equation 24.85 becomes Equation 24.79, and Equation 24.86 yields $\nu = 1$.

(e) Testing for Effect of Treatment Order. If two treatments are applied sequentially to a group of subjects, we might ask whether the response to each treatment depended on the order in which the treatments were administered. For example, suppose we have two medications for the treatment of poison-ivy rash, but, instead of the situation in Example 24.23, they are to be administered orally rather than by external

EXAMPLE 24.25 Determination of Sample Size for the McNemar Test

Considering the data of Example 24.23 to be from a pilot study, how many pairs of data would be needed to have a 90% probability of rejecting the two-tailed H_0 if a future test were performed at the 0.05 level of significance and the ratio of f_{21} to f_{12} in the population were at least 2?

As in Example 24.24, $p = 0.1176$ and $Z_{\alpha(2)} = 1.9600$. In addition, we specify that $\psi = 2$ and that the power of the test is to be 0.90 [so $\beta(1) = 0.10$]. Therefore, the required sample size is

$$n = \frac{\left[Z_{\alpha(2)}\sqrt{\psi + 1} + Z_{\beta(1)}\sqrt{(\psi + 1) - p(\psi - 1)^2}\right]^2}{p(\psi - 1)^2}$$

$$= \frac{\left[1.9600\sqrt{2 + 1} + 1.2816\sqrt{(2 + 1) - (0.1176)(2 - 1)^2}\right]^2}{(0.1176)(2 - 1)^2}$$

$$= \frac{[1.9600(1.7321) + 1.2816(1.6978)]^2}{0.1176} = \frac{(5.5708)^2}{0.1176} = 263.9.$$

Therefore, at least 264 pairs of data should be used.

application to the skin. Thus, in this example, both arms receive medication at the same time, but the oral medications must be given at different times.

Gart (1969a) provides the following procedure to test for the difference in response between two sequentially applied treatments and to test whether the order of application had an effect on the response. The following 2 × 2 contingency table is used to test for a treatment effect:

	Order of Application of Treatments A and B		
	A, then B	*B, then A*	*Total*
Response with first treatment	f_{11}	f_{12}	R_1
Response with second treatment	f_{21}	f_{22}	R_2
Total	C_1	C_2	n

By redefining the rows, the following 2 × 2 table may be used to test the null hypothesis of no difference in response due to order of treatment application:

	Order of Application of Treatments A and B		
	A, then B	*B, then A*	*Total*
Response with treatment A	f_{11}	f_{12}	R_1
Response with treatment B	f_{21}	f_{22}	R_2
Total	C_1	C_2	n

EXAMPLE 24.26 McNemar's Test for a 3 × 3 Table of Nominal-Scale Data

H_0: Of men who adopt a religion different from that of their fathers, a change from one religion to another is as likely as a change from the latter religion to the former.

H_A: Of men who adopt a religion different from that of their fathers, a change from one religion to another is not as likely as a change from the latter religion to the former.

Man's	Man's Father's Religion		
Religion	*Protestant*	*Catholic*	*Jewish*
Protestant	173	20	7
Catholic	15	51	2
Jewish	5	3	24

$r = 3$

$$\chi^2 = \sum_{i=1}^{r} \sum_{j>i} \frac{(f_{ij} - f_{ji})^2}{f_{ij} + f_{ji}}$$

$$= \frac{(f_{12} - f_{21})^2}{f_{12} - f_{21}} + \frac{(f_{13} - f_{31})^2}{f_{13} - f_{31}} + \frac{(f_{23} - f_{32})^2}{f_{23} - f_{32}}$$

$$= \frac{(20 - 15)^2}{20 + 15} + \frac{(7 - 5)^2}{7 + 5} + \frac{(2 - 3)^2}{2 + 3}$$

$$= 0.7143 + 0.3333 + 0.2000$$

$$= 1.248$$

$$\nu = \frac{r(r-1)}{2} = \frac{3(2)}{2} = 3$$

$\chi^2_{0.05,3} = 7.815$

Do not reject H_0.

$$0.50 < P < 0.75 \, [P = 0.74]$$

These two contingency tables have one fixed margin (the column totals are fixed; Section 23.3b) and they may be tested by chi-square, which is shown in Example 24.27. One-tailed hypotheses may be tested as described in Section 23.3e.

EXAMPLE 24.27 Gart's Test for Effect of Treatment and Treatment Order

H_0: The two oral medications have the same effect on relieving poison-ivy rash.

H_A: The two oral medications do not have the same effect on relieving poison-ivy rash.

	Order of Application of Medications A and B		
	A, then B	*B, then A*	*Total*
Response with 1st medication	14	6	20
Response with 2nd medication	4	12	16
Total	18	18	36

Using Equation 23.6,

$$\chi^2 = \frac{n(f_{11}f_{22} - f_{12}f_{21})^2}{R_1R_2C_1C_2}$$

$$= \frac{36[(14)(12) - (6)(4)]^2}{(20)(16)(18)(18)} = 7.200.$$

$\chi^2_{0.05,1} = 3.841$; reject H_0.

That is, it is concluded that there is a difference in response to the two medications, regardless of the order in which they are administered.

$$0.005 < P < 0.01 \quad [P = 0.0073]$$

H_0: The order of administration of the two oral medications does not affect their abilities to relieve poison-ivy rash.

H_A: The order of administration of the two oral medications does affect their abilities to relieve poison-ivy rash.

	Order of Application of Medications A and B		
	A, then B	*B, then A*	*Total*
Response with medication A	14	12	26
Response with medication B	4	6	10
Total	18	18	36

$$\chi^2 = \frac{36[(14)(6) - (12)(4)]^2}{(26)(10)(18)(18)} = 0.554$$

$\chi^2_{0.05,1} = 3.841$; do not reject H_0.

That is, it is concluded that the effects of the two medications are not affected by the order in which they are administered.

$$0.25 < P < 0.50 \quad [P = 0.46]$$

LOGISTIC REGRESSION

Previous discussions of regression (Chapters 17, 20, and 21) considered data measured on a continuous (i.e., ratio or interval) scale, where there are measurements of a dependent variable (Y) associated with measurements of one or more independent variables (X's). However, there are situations (commonly involving clinical, epidemiological, or sociological data) where the dependent variable is measured on a nominal scale; that is, where the data are in two or more categories. For example, a sample of men could be examined for the presence of arterial plaque, and this information is recorded together with the age of each man. The mean age of men with plaque and the mean of those without plaque could be compared via a two-sample t test (Section 8.1). But the data can be analyzed in a different fashion, deriving a quantitative expression of the relationship between the presence of plaque and the age of the subject and allowing for the prediction of the probability of plaque at a specified age.

Regression data with Y recorded on a dichotomous scale do not meet the assumptions of the previously introduced regression methods, assumptions such as that the Y's and residuals (ϵ's; Section 20.2) have come from a normal distribution at each value of X and have the same variance at all values of X. So another statistical procedure must be sought. The most frequently employed analysis of such data is *logistic regression*.*

A brief introduction to logistic regression is given here, employing terminology largely analogous to that in Chapters 17 and 20.† Because of the intense calculations required, users of this regression technique will depend upon computer programs, which are found in several statistical computer packages, and will typically benefit from consultation with a statistician familiar with the procedures.

(a) Simple Logistic Regression. The simplest—and most common—logistic regression situation is where the categorical data (Y) are binomial, also known as *dichotomous* (i.e., the data consist of each observation recorded as belonging in one of two categories). Each value of Y is routinely recorded as "1" or "0" and might, for example, refer to a characteristic as being "present" (1) or "absent" (0), or to subjects being "with" (1) or "without" (0) a disease.‡

Logistic regression considers the probability (p) of encountering a Y of 1 at a given X in the population that was sampled. So, for example, p could be the probability of

*A similar procedure, but one that is less often preferred, is known as *discriminant analysis*. What statisticians refer to as the *general linear model* underlies several statistical techniques, including analysis of variance, analysis of covariance, multivariate analysis of variance, linear regression, logistic regression, and discriminant analysis.

†Logistic regression is a wide-ranging topic and is covered in portions of comprehensive books on regression (e.g., Chatterjee and Hadi, 2006: Chapter 12; Glantz and Slinker, 2001: Chapter 12; Hair et al., 2006: Chapter 5; Kutner, Nachtsheim, and Neter, 2004: Chapter 14; Meyers, Gamst, and Guarino, 2006: Chapter 6A and 6B; Montgomery, Peck, and Vining, 2001: Section 14.2; Pedhazur, 1997: Chapter 17; Vittinghoff et al., 2005: Chapter 6); in books on the analysis of categorical data (e.g., Agresti, 2002: Chapters 5 and 6; Agresti, 2007: Chapters 4 and 5; Fleiss, Levin, and Paik, 2003: Chapter 11); and in works that concentrate specifically on logistic regression (e.g., Garson, 2006; Hosmer and Lemeshow, 2000; Kleinbaum and Klein, 2002; Menard, 2002; Pampel, 2000).

‡Designating observations of Y as "0" or "1" is thus an example of using a "dummy variable," first described in Section 20.10. Any two integers could be used, but 0 and 1 are almost always employed, and this results in the mean of the Y's being the probability of $Y = 1$.

encountering a member of the population that has a specified characteristic present, or the proportion that has a specified disease.

The logistic regression relationship in a population is

$$p = \frac{e^{\alpha+\beta X}}{1 + e^{\alpha+\beta X}}, \tag{24.87}$$

where e is the mathematical constant introduced in Chapter 6. This equation may also be written, equivalently, using the abbreviation "exp" for an exponent on e:

$$p = \frac{\exp(\alpha + \beta X)}{1 + \exp(\alpha + \beta X)}, \tag{24.87a}$$

or, equivalently, as

$$p = \frac{1}{1 + e^{-(\alpha+\beta X)}} \text{ or } p = \frac{1}{1 + \exp[-(\alpha + \beta X)]}. \tag{24.87b}$$

The parameter α is often seen written as β_0.

The sample regression equations corresponding to these expressions of population regression are, respectively,

$$\hat{p} = \frac{e^{a+bX}}{1 + e^{a+bX}}, \tag{24.88}$$

$$\hat{p} = \frac{\exp(a + bX)}{1 + \exp(a + bX)}, \tag{24.88a}$$

$$\hat{p} = \frac{1}{1 + e^{-(a+bX)}} \text{ or } \hat{p} = \frac{1}{1 + \exp[-(a + bX)]}; \tag{24.88b}$$

and a is often written as b_0.

Logistic regression employs the concept of the *odds* of an event (briefly mentioned in Section 5.5), namely the probability of the event occurring expressed relative to the probability of the event not occurring. Using the designations $p = P(Y = 1)$ and $q = 1 - p = P(Y = 0)$, the odds can be expressed by these four equivalent statements:

$$\frac{P(Y = 1)}{1 - P(Y = 1)} \text{ or } \frac{P(Y = 1)}{P(Y = 0)} \text{ or } \frac{p}{1 - p} \text{ or } \frac{p}{q}, \tag{24.89}$$

and the fourth will be employed in the following discussion.

A probability, p, must lie within a limited range ($0 \leq p \leq 1$).* However, odds, p/q, have no upper limit. For example, if $p = 0.1$, odds $= 0.1/0.9 = 0.11$; if $p = 0.5$, odds $= 0.5/0.5 = 1$; if $p = 0.9$, odds $= 0.9/0.1 = 9$; if $p = 0.97$, odds $= 0.97/0.03 = 32.3$; and so on. Expanding the odds terminology, if, for example, a population contains 60% females and 40% males, it is said that the odds are 0.60/0.40 = "6 to 4" or "1.5 to 1" *in favor of* randomly selecting a female from the population, or 1.5 to 1 *against* selecting a male.

In order to obtain a linear model using the regression terms α and βX, statisticians utilize the natural logarithm of the odds, a quantity known as a *logit*; this is sometimes

*If a linear regression were performed on p versus X, predicted values of $\hat{p}$ could be less than 0 or greater than 1, an untenable outcome. This is another reason why logistic regression should be used when dealing with a categorical dependent variable.

referred to as a "logit transformation" of the dependent variable:

$$\text{logit} = \ln(\text{odds}) = \ln\left(\frac{p}{q}\right). \tag{24.90}$$

For $0 < \text{odds} < 1.0$, the logit is a negative number (and it becomes farther from 0 the closer the odds are to 0); for odds = 0.5, the logit is 0; and for odds > 0, the logit is a positive number (and it becomes farther from 0 the closer the odds are to 1).

Using the logit transformation, the population linear regression equation and sample regression equations are, respectively,

$$\text{logit for } p = \alpha + \beta X \tag{24.91}$$

and

$$\text{logit for } \hat{p} = a + bX. \tag{24.92}$$

This linear relationship is shown in Figure 24.2b. Determining a and b for Equation 24.92 is performed by an iterative process termed *maximum likelihood estimation*, instead of by the least-squares procedure used in the linear regressions of previous chapters. The term maximum likelihood refers to arriving at the a and b that are most likely to estimate the population parameters underlying the observed sample of data.

As with the regression procedures previously discussed, the results of a logistic regression analysis will include a and b as estimates of the population parameters α and β, respectively. Computer output will routinely present these, with the standard error of b (namely, s_b), confidence limits for β, and a test of H_0: $\beta = 0$. In logistic regression there are no measures corresponding to the coefficient of determination (r^2) in linear regression analysis (Section 17.3), but some authors have suggested statistics to express similar concepts.

For a logistic relationship, a plot of p versus X will display an S-shaped curve rising from the lower left to the upper right, such as that in Figure 24.2a. In such a graph, p is near zero for very small values of X, it increases gradually as X increases, then it increases much more rapidly with further increase in X, and then it increases at a slow rate for larger X's, gradually approaching 1.0. Figure 24.2a is a graph for a logistic equation with $\alpha = -2.0$ and $\beta = 1.0$. The graph would shift to the left by 1 unit of X for each increase of α by 1, and the rise in p would be steeper with a larger β. If β were negative instead of positive, the curve would be a reverse S shape, rising from the lower right to the upper left of the graph, instead of from the lower left to the upper right.*

For a 1-unit increase in X, the odds increase by a factor of e^{β}. If, for example, $\beta = 1.0$, then the odds for $X = 4$ would be $e^{1.0}$ (namely, 2.72) times the odds for $X = 3$. And a one-unit increase in X will result in a unit increase in the logit of p. So, if $\beta = 1.0$, then the logit for $X = 4$ would be 1.0 larger than the logit for $X = 3$. If β is negative, then the odds and logit decrease instead of increase.

Once the logistic-regression relationship is determined for a sample of data, it may be used to predict the probability of X for a given X. Equation 24.92 yields a logit of p for the specified X; then

$$\text{odds} = e^{\text{logit}} \tag{24.93}$$

*Another representation of binary Y data in an S-shaped relationship to X is that of *probits*, based upon a cumulative normal distribution. The use of logits is simpler and is preferred by many.

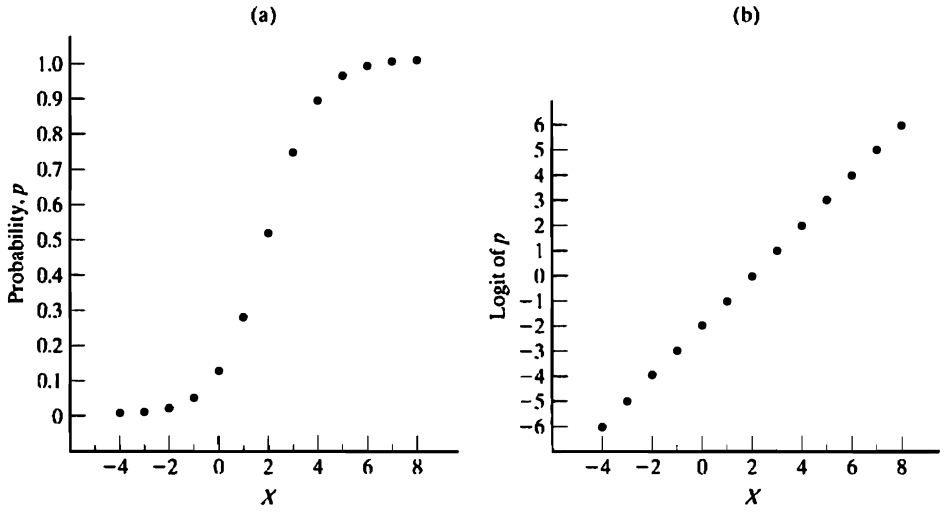

FIGURE 24.2: Logistic regression, where $\alpha = -2.0$ and $\beta = 1.0$. (a) The relationship of $p = 1/[1 + e^{-(\alpha+\beta X)}]$ to X. (b) The relationship of the logit of p to X.

and

$$\hat{p} = \frac{\text{odds}}{1 + \text{odds}}. \tag{24.94}$$

If n is large, the hypothesis H_0: $\beta = 0$ may be tested using

$$Z = \frac{b}{s_b}, \tag{24.95}$$

which is analogous to the linear-regression test of that hypothesis using t (Section 17.3b). This is known as the Wald test*; sometimes, with exactly the same result, the test statistic used is $\chi^2 = Z^2$, with 1 degree of freedom. In further analogy with linear regression, confidence limits for β are obtainable as

$$b \pm Z_{\alpha(2)} s_b. \tag{24.96}$$

Assessing H_0: $\beta = 0$ and expressing a confidence interval for β may also be done using a computer-intensive process known as likelihood-ratio, or log-likelihood, testing. It has been noted (e.g., by Hauck and Donner, 1977; Menard, 2002: 43; Pampel, 2000: 30) that when b is large, its standard error (s_b) is inflated, thereby increasing the probability of a Type II error in a Wald test (and thus decreasing the power of the test). Therefore, it is sometimes recommended that the likelihood-ratio test be used routinely in preference to the commonly encountered Wald test. For the same reason, likelihood-ratio confidence limits can be recommended over those obtained by Equation 24.96. The interpretation of logistic-regression coefficients is discussed more fully in the references cited in the second footnote in Section 24.18.

In recommending an adequate number of data for logistic-regression analysis, some authors have suggested that n be large enough that there are at least 10 observations of $Y = 1$ and at least 10 of $Y = 0$.

*Named for Hungarian-born, Vienna-educated, American mathematician and econometrician Abraham Wald (1902–1950).

(b) Multiple Logistic Regression. Just as the concepts and procedures of linear regression with one independent variable, X (Chapter 17), can be expanded into those of linear regression with more than one X (Chapter 20), the basic ideas of logistic regression with one X (Section 24.18a) can be enlarged to those of logistic regression with more than one X. Expanding Equations 24.87–24.87b to equations for multiple logistic regression with m independent variables, $\alpha + \beta X$ is replaced with $\alpha + \Sigma_{i=1}^{m}\beta_i X_i$, which is $\alpha + \beta_1 X_1 + \beta_2 X_2 + \cdots + \beta_m X_m$; and, in Equations 24.88–24.88b, $a + bX$ is replaced with $a + \Sigma_{i=1}^{m} b_i X_i$, which is $a + b_1 X_1 + b_2 X_2 + \cdots + b_m X_m$. Analogous to multiple linear regression, β_i expresses the change in ln(logit) for a 1-unit change in X_i, with the effects of the other X_i's held constant. Further interpretation of logistic partial-regression coefficients is discussed in the references cited in the second footnote of Section 24.18.

The statistical significance of the overall multiple logistic regression model is tested via $H_0: \beta_1 = \beta_2 = \cdots = \beta_m$, which is analogous to the analysis-of-variance testing in multiple linear regression (Section 20.3). The significance of each partial-regression coefficient is tested via $H_0: \beta_i = 0$. As with multiple liner regression, $H_0: \beta_1 = \beta_2 = \cdots = \beta_m$ can be rejected while none of the significance tests of individual partial-regression coefficients result in rejection of $H_0: \beta_i = 0$ (especially when the conservative Wald test is used).

The standardized partial-regression coefficients in multiple linear regression (Section 20.5) cannot be computed for logistic regression, but some authors have proposed similar coefficients. Also, there is no perfect logistic-regression analog to coefficients of determination (R^2 and R_a^2 in Section 20.3). Several measures have been suggested by various authors to express the concept of such a coefficient; sometimes they are referred to as "pseudo-R^2" values (and some do not have 1.0 as their maximum). Just as with multiple linear-regression analysis, multiple logistic regression is adversely affected by multicolinearity (see Section 20.4a). Logistic analysis does not work well with small numbers of data, and some authors recommend that the sample be large enough that there are at least $10m$ 0's and at least $10m$ 1's for the dependent variable. And, as is the case of multiple linear regression, multiple logistic regression is adversely affected by outliers.

(c) Other Models of Logistic Regression. Though not commonly encountered, the dependent variable can be one that has more than two categories. This is known as a *polytomous* (or "polychotomous" or "multinomial") variable. Also, the dependent variable can be one that is measured on an ordinal scale but recorded in nominal-scale categories. For example, subjects could be classified as "underweight," "normal weight," and "overweight."

Logistic regression may also be performed when an independent variable (X) is recorded on a dichotomous nominal scale. For example, the dependent variable could be recorded as hair loss ($Y = 1$) or no hair loss ($Y = 0$) in men, with the independent variable (X) being exposed ($X = 1$) or not exposed ($X = 0$) to a certain drug or radiation treatment. Such data can be subjected to a 2×2 contingency-table analysis (Section 23.3), where the null hypothesis is that the proportion (p) of men with loss of hair is the same in the treated and nontreated groups. Using logistic regression, however, the null hypothesis is that hair loss is statistically dependent upon receiving the treatment and the relationship between p and whether treatment was applied is quantified.

In multiple logistic regression, one or more of the X's may be recorded on a dichotomous scale. So, for example, Y could be recorded as hair loss or no hair loss, X_1 could

be age (measured on a continuous scale), and X_2 could be sex (a dichotomous variable: male or female). Indeed, using dummy variables (introduced in Section 20.10), X's can be recorded on a nominal scale with more than two categories. If all m of the independent variables are nominal and Y is dichotomous, the data could be arranged in a $2 \times m$ contingency table, but different hypotheses would be tested thereby.

It is also possible to perform stepwise multiple logistic regression (analogous to the procedures of Section 20.6) in order to determine which of the X's should be in the final regression model, logistic regression with polynomial terms (analogous to Chapter 21), and logistic regression with interaction of independent variables (analogous to Section 20.11).

EXERCISES

24.1. If, in a binomial population, $p = 0.3$ and $n = 6$, what proportion of the population does $X = 2$ represent?

24.2. If, in a binomial population, $p = 0.22$ and $n = 5$, what is the probability of $X = 4$?

24.3. Determine whether the following data, where $n = 4$, are likely to have come from a binomial population with $p = 0.25$:

X	f
0	30
1	51
2	33
3	10
4	2

24.4. Determine whether the following data, where $n = 4$, are likely to have come from a binomial population:

X	f
0	20
1	41
2	33
3	11
4	4

24.5. A randomly selected male mouse of a certain species was placed in a cage with a randomly selected male mouse of a second species, and it was recorded which animal exhibited dominance over the other. The experimental procedure was performed, with different pairs of animals, a total of twenty times, with individuals from species 1 being dominant six times and those from species 2 being dominant fourteen times. Test the null hypothesis that there is no difference in the ability of members of either species to dominate.

24.6. A hospital treated 412 skin cancer patients over a period of time. Of these, 197 were female. Using the normal approximation to the binomial test, test the hypothesis that equal numbers of males and females seek treatment for skin cancer.

24.7. Test the null hypothesis of Exercise 22.3, using the binomial test normal approximation.

24.8. Ten students were given a mathematics aptitude test in a quiet room. The same students were given a similar test in a room with background music. Their performances were as follows. Using the sign test, test the hypothesis that the music has no effect on test performance.

Student	*Score without music*	*Score with music*
1	114	112
2	121	122
3	136	141
4	102	107
5	99	96
6	114	109
7	127	121
8	150	146
9	129	127
10	130	128

24.9. Estimate the power of the hypothesis test of Exercise 24.5 if $\alpha = 0.05$.

24.10. Using the normal approximation, estimate the power of the hypothesis test of Exercise 24.6 if $\alpha = 0.05$.

24.11. In a random sample of 30 boys, 18 have curly hair. Determine the 95% confidence limits for the proportion of curly-haired individuals in the population of boys that was sampled.

(a) Determine the Clopper-Pearson interval.
(b) Determine the Wald interval.
(c) Determine the adjusted Wald interval.

. In a random sample of 1215 animals, 62 exhibited a certain genetic defect. Determine the 95% confidence interval for the proportion of the population displaying this defect.
(a) Determine the Clopper-Pearson interval.
(b) Determine the Wald interval.
(c) Determine the adjusted Wald interval.

. From this sample of 14 measurements, determine the 90% confidence limits for the population median running speed of monkeys: 28.3, 29.1, 29.5, 20.1, 30.2, 31.4, 32.2, 32.8, 33.1, 33.2, 33.6, 34.5, 34.7, and 34.8 km/hr.

. Using the data of Exercise 23.3, test H_0: $p_1 = p_2$ versus H_A: $p_1 \neq p_2$.

. Using the data of Example 23.3, determine the 95% adjusted Wald confidence limits for $p_1 - p_2$.

. Using the data of Exercise 23.1, test the null hypothesis that there is the same proportion of males in all four seasons.

. If the null hypothesis in Exercise 24.16 is rejected, perform a Tukey-type multiple-comparison test to conclude which population proportions are different from which. (Use Equation 13.7 for the standard error.)

. A new type of heart valve has been developed and is implanted in 63 dogs that have been raised on various levels of exercise. The numbers of valve transplants that succeed are tabulated as follows.
(a) Is the proportion of successful implants the same for dogs on all exercise regimens?
(b) Is there a trend with amount of exercise in the proportion of successful implants?

	Amount of exercise				
Implant	*None*	*Slight*	*Moderate*	*Vigorous*	*Total*
Successful	8	9	17	14	48
Unsuccessful	7	3	3	2	15
Total	15	12	20	16	63

. In investigating the cold tolerance of adults of a species of tropical butterfly, 68 of the butterflies (32 females and 36 males) were subjected to a cold temperature until half of the 68 had died. Twenty of the females survived, as did 14 of the males, with the data tabulated as follows:

	Females	*Males*	
Alive	20	14	34
Dead	12	22	34
	32	36	68

Prior to performing the experiment and collecting the data, it was stated that H_0: females are as likely as males to survive the experimental temperature, and H_A: Females and males are not equally likely to survive.
(a) Use the Fisher exact test for the one-tailed hypotheses.
(b) Use chi-square with the Yates correction for continuity (Sections 23.3c and 23.3d) for the two-tailed hypotheses.
(c) Use chi-square with the Cochran-Haber correction for continuity (Sections 23.3c and 23.3d) for the two-tailed hypotheses.
(d) Use the Fisher exact test for the two-tailed hypotheses.

24.20. Thirteen snakes of species S and 17 of species E were placed in an enclosure containing 14 mice of species M and 16 of species U. Each of the 30 snakes ate one of the 30 mice, and the following results were recorded:

	Snakes S	*Snakes E*	
Mice M	3	11	14
Mice U	10	6	16
	13	17	30

Prior to performing the experiment and collecting the data, it was decided whether the interest was in a one-tailed or two-tailed test. The one-tailed test hypotheses would be H_0: Under the conditions of this experiment, snakes of species E are not more likely than species S to eat mice of species M (i.e., they are less likely or equally likely to do so), and H_A: Snakes of species E are more likely to eat mice of species M. The two-tailed hypotheses would be H_0: Under the conditions of this experiment, snakes of species S and species E are equally likely to eat mice of species M, and H_A: Snakes of species S and species E are not equally likely to eat mice of species M.
(a) Use the Fisher exact test for the one-tailed hypotheses.
(b) Use chi-square with the Yates correction for continuity (Sections 23.3c and 23.3d) for the two-tailed hypotheses.
(c) Use chi-square with the Cochran-Haber correction for continuity.
(d) Use the Fisher exact test for the two-tailed hypotheses.

24.21. One hundred twenty-two pairs of brothers, one member of each pair overweight and the other of normal weight, were examined for presence of varicose veins. Use the McNemar test for the data below to test the hypothesis that there is no relationship between being overweight and developing varicose veins (i.e., that the same proportion of overweight men as normal weight men possess varicose veins). In the following data tabulation "v.v." stands for "varicose veins."

Normal Weight	**Overweight**	
	With v.v.	*Without v.v.*
With v.v.	19	5
Without v.v.	12	86

$n = 12$

CHAPTER 25

Testing for Randomness

A *random distribution* of objects in space is one in which each one of equal portions of the space has the same probability of containing an object, and the occurrence of an object in no way influences the occurrence of any of the other objects. A biological example in one-dimensional space could be the linear distribution of blackbirds along the top of a fence, an example in two-dimensional space could be the distribution of cherry trees in a forest, and an example in three-dimensional space could be the distribution of unicellular algae in water.* A random distribution of events in time is one in which each period of time of given length (e.g., an hour or a day) has an equal chance of containing an event, and the occurrence of any one of the events is independent of the occurrence of any of the other events. An example of events in periods of time could be the numbers of heart-attack patients entering a hospital each day.

25.1 POISSON PROBABILITIES

The *Poisson distribution*† is important in describing *random* occurrences when the probability of an occurrence is small. The terms of the Poisson distribution are

$$P(X) = \frac{e^{-\mu}\mu^X}{X!} \tag{25.1a}$$

or, equivalently,

$$P(X) = \frac{\mu^X}{e^{\mu}X!}, \tag{25.1b}$$

*An extensive coverage of the description and analysis of spatial pattern is given by Upton and Fingleton (1985).

†Also known as *Poisson's law* and named for Siméon Denis Poisson (1781–1840), a French mathematician, astronomer, and physicist (Féron, 1978). He is often credited with the first report of this distribution in a 1837 publication. However, Dale (1989) reported that it appeared earlier in an 1830 memoir of an 1829 presentation by Poisson, and Abraham de Moivre (1667–1754) apparently described it in 1718 (David, 1962: 168; Stigler, 1982). It was also described independently by others, including "Student" (W. S. Gosset, 1976–1937) during 1906–1909 (Boland, 2000; Haight, 1967: 117). Poisson's name might have first been attached to this distribution, in contrast to his being merely cited, by H.E. Soper in 1914 (David, 1995).

where $P(X)$ is the probability of X occurrences in a unit of space (or time) and μ is the population mean number of occurrences in the unit of space (or time). Thus,

$$P(0) = e^{-\mu}, \tag{25.2}$$

$$P(1) = e^{-\mu}\mu, \tag{25.3}$$

$$P(2) = \frac{e^{-\mu}\mu^2}{2}, \tag{25.4}$$

$$P(3) = \frac{e^{-\mu}\mu^3}{(3)(2)}, \tag{25.5}$$

$$P(4) = \frac{e^{-\mu}\mu^4}{(4)(3)(2)}, \tag{25.6}$$

and so on, where $P(0)$ is the probability of no occurrences in the unit space, $P(1)$ is the probability of exactly one occurrence in the unit space, and so on. Figure 25.1 presents some Poisson probabilities graphically.

In calculating a series of Poisson probabilities, as represented by the preceding five equations, a simple computational expedient is available:

$$P(X) = \frac{P(X-1)\mu}{X}. \tag{25.7}$$

Example 25.1 demonstrates these calculations for predicting how many plants will have no beetles, how many will have one beetle, how many will have two beetles, and so on, if 80 beetles are distributed randomly among 50 plants.

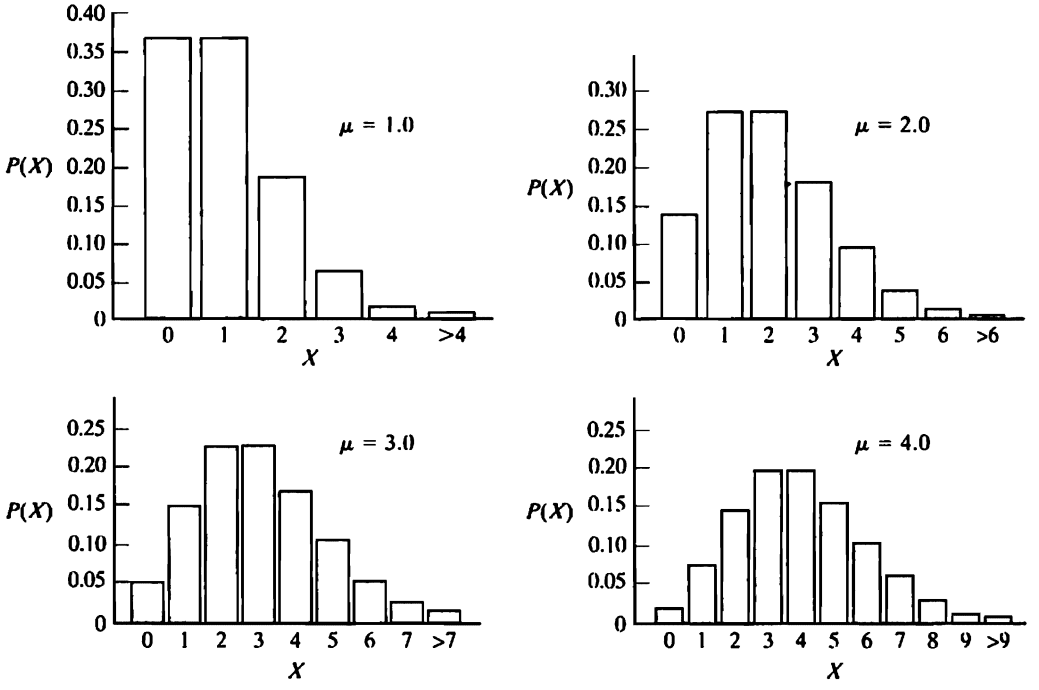

FIGURE 25.1: The Poisson distribution for various values of μ. These graphs were prepared by using Equation 25.1.

EXAMPLE 25.1 Frequencies from a Poisson Distribution

There are 50 plants in a greenhouse. If 80 leaf-eating beetles are introduced and they randomly land on the plants, what are the expected numbers of beetles per plant?

$$n = 50$$

$$\mu = \frac{80 \text{ beetles}}{50 \text{ plants}} = 1.6 \text{ beetles/plant}$$

Using Equation 25.2, $P(0) = e^{-\mu} = e^{-1.6} = 0.20190$; thus, 20.190% of the plants—that is, (0.20190)(50) = 10.10 (about 10)—are expected to have no beetles. The probabilities of plants with $X_i = 1, 2, 3, \ldots$ beetles are as follows, using Equation 25.7 (although Equation 25.1a or 25.1b could be used instead):

Number of beetles X	*Poisson probability* $P(X)$	**Estimated number of plants** $\hat{f} = [P(X)][n]$	$\hat{f}$ *rounded*
0	0.20190	(0.20190)(50) = 10.10	10
1	(0.20190)(1.6)/1 = 0.32304	(0.32304)(50) = 16.15	16
2	(0.32304)(1.6)/2 = 0.25843	(0.25843)(50) = 12.92	13
3	(0.25843)(1.6)/3 = 0.13783	(0.13783)(50) = 6.89	7
4	(0.13783)(1.6)/4 = 0.05513	(0.05513)(50) = 2.76	3
5	(0.05513)(1.6)/5 = 0.01764	(0.01764)(50) = 0.88	1
≤ 5	0.99397	49.70	50
≥ 6	1.00000 − 0.99397 = 0.00603	(0.00603)(50) = 0.30	0
		50.00	50

The Poisson distribution is appropriate when there is a small probability of a single event, as reflected in a small μ, and this distribution is very similar to the binomial distribution where n is large and p is small. For example, Table 25.1 compares the Poisson distribution where $\mu = 1$ with the binomial distribution where $n = 100$ and $p = 0.01$ (and, therefore, $\mu = np = 1$). Thus, the Poisson distribution has importance in describing binomially distributed events having low probability. Another interesting property of the Poisson distribution is that $\sigma^2 = \mu$; that is, the variance and the mean are equal.

CONFIDENCE LIMITS FOR THE POISSON PARAMETER

Confidence limits for the Poisson distribution parameter, μ, may be obtained as follows. The lower $1 - \alpha$ confidence limit is

$$L_1 = \frac{\chi^2_{(1-\alpha/2),\nu}}{2}, \tag{25.8}$$

where $\nu = 2X$; and the upper $1 - \alpha$ confidence limit is

$$L_2 = \frac{\chi^2_{\alpha/2,\nu}}{2}. \tag{25.9}$$

TABLE 25.1: The Poisson Distribution Where $\mu = 1$ Compared with the Binomial Distribution Where $n = 100$ and $p = 0.01$ (i.e., with $\mu = 1$) and the Binomial Distribution Where $n = 10$ and $p = 0.1$ (i.e., with $\mu = 1$)

X	$P(X)$ for Poisson: $\mu = 1$	$P(X)$ for binomial: $n = 100, p = 0.01$	$P(X)$ for binomial: $n = 10, p = 0.1$
0	0.36788	0.36603	0.34868
1	0.36788	0.36973	0.38742
2	0.18394	0.18486	0.19371
3	0.06131	0.06100	0.05740
4	0.01533	0.01494	0.01116
5	0.00307	0.00290	0.00149
6	0.00050	0.00046	0.00014
7	0.00007	0.00006	0.00001
>7	0.00001	0.00002	0.00000
Total	1.00000	1.00000	1.00001

where $\nu = 2(X + 1)$ (Pearson and Hartley, 1966: 81). This is demonstrated in Example 25.2. L_1 and L_2 are the confidence limits for the population mean and for the population variance. Confidence limits for the population standard deviation, σ, are simply the square roots of L_1 and L_2. The confidence limits, L_1 and L_2 (or their square roots), are not symmetrical around the parameter to which they refer. This procedure is a fairly good approximation. If confidence limits are desired to be accurate to more decimal places than given by the available critical values of χ^2, we may engage in the more tedious process of examining the tails of the Poisson distribution (e.g., see Example 25.3) to determine the value of X that cuts off $\alpha/2$ of each tail. Baker (2002) and Schwertman and Martinez (1994) discuss several approximations to L_1 and L_2, but the best of them require more computational effort than do the exact limits given previously, and they are all poor estimates of those limits.

EXAMPLE 25.2 Confidence Limits for the Poisson Parameter

An oak leaf contains four galls. Assuming that there is a random occurrence of galls on oak leaves in the population, estimate with 95% confidence the mean number of galls per leaf in the population.

The population mean, μ, is estimated as $X = 4$ galls/leaf.

The 95% confidence limits for μ are

$$L_1 = \frac{\chi^2_{(1-\alpha/2),\nu}}{2}, \quad \text{where} \quad \nu = 2X = 2(4) = 8$$

$$L_1 = \frac{\chi^2_{0.975,8}}{2} = \frac{2.180}{2} = 1.1 \text{ galls/leaf}$$

$$L_2 = \frac{\chi^2_{\alpha/2,\nu}}{2}, \quad \text{where} \quad \nu = 2(X + 1) = 2(4 + 1) = 10$$

$$L_2 = \frac{\chi^2_{0.025,10}}{2} = \frac{20.483}{2} = 10.2 \text{ galls/leaf}$$

Therefore, we can state

$$P(1.1 \text{ galls/leaf} \leq \mu \leq 10.2 \text{ galls/leaf}) \geq 0.95$$

and

$$P(1.1 \text{ galls/leaf} \leq \sigma^2 \leq 10.2 \text{ galls/leaf}) \geq 0.95;$$

and, using the square roots of L_1 and L_2,

$$P(1.0 \text{ galls/leaf} \leq \sigma \leq 3.2 \text{ galls/leaf}) \geq 0.95.$$

GOODNESS OF FIT FOR THE POISSON DISTRIBUTION

The goodness of fit of a set of data to the Poisson distribution is a test of the null hypothesis that the data are distributed randomly within the space that was sampled. This may be tested by chi-square (Section 22.3), as was done with the binomial distribution in Section 24.4. When tabulating the observed frequencies (f_i) and the expected frequencies ($\hat{f}_i$), the frequencies in the tails of the distribution should be pooled so no $\hat{f}_i$ is less than 1.0 (Cochran, 1954). The degrees of freedom are $k - 2$ (where k is the number of categories of X remaining after such pooling). Example 25.3 fits a set of data to a Poisson distribution, using the sample mean, $\overline{X}$, as an estimate of μ in Equations 25.2 and 25.7. The G statistic (Section 22.7) may be used for goodness-of-fit analysis instead of chi-square. It will give equivalent results when n/k is large; if n/k is very small, G is preferable to χ^2 (Rao and Chakravarti, 1956).

If μ were known for the particular population sampled, or if it were desired to assume a certain value of μ, then the parameter would not have to be estimated by $\overline{X}$, and the degrees of freedom for χ^2 for G goodness-of-fit testing would be $k - 1$. For example, if the 50 plants in Example 25.1 were considered the only plants of interest and 80 beetles were distributed among them, μ would be 80/50 = 1.6. Then the observed number of beetles per plant could be counted and those numbers compared to the expected frequencies ($\hat{f}$) determined in Example 25.1 for a random distribution. It is only when this parameter is specified that the Kolmogorov-Smirnov goodness-of-fit procedure (Section 22.8) may be applied (Massey, 1951).

EXAMPLE 25.3 Fitting the Poisson Distribution

Thirty plots of ground were examined within an abandoned golf course, each plot being the same size; a total of 74 weeds were counted in the 30 plots. The frequency f is the number of plots found to contain X weeds; $P(X)$ is the probability of X weeds in a plot if the distribution of weeds is random within the golf course.

H_0: The weeds are distributed randomly.

H_A: The weeds are not distributed randomly.

$n = 30$

$$\overline{X} = \frac{74 \text{ weeds}}{30 \text{ plots}} = 2.47 \text{ weeds/plot}$$

$$P(0) = e^{-\overline{X}} = e^{-2.47} = 0.08458$$

X	f	fX	$P(X)$	$\hat{f} = [P(X)][n]$
0	2	0	0.08458	2.537
1	1	1	(0.08458)(2.47)/1 = 0.20891	6.267
2	13	26	(0.20891)(2.47)/2 = 0.25800	7.740
3	10	30	(0.25800)(2.47)/3 = 0.21242	6.373
4	3	12	(0.21242)(2.47)/4 = 0.13116	3.935
5	1	5	(0.13116)(2.47)/5 = 0.06479	1.944
6	0	0	(0.06479)(2.47)/6 = 0.02667	0.800
	30	74	0.98653	29.596

The last $\hat{f}$ calculated (for $X = 6$) is less than 1.0, so the calculation of $\hat{f}$'s proceeds no further. The sum of the seven calculated $\hat{f}$'s is 25.596, so $P(X > 6) = 30 - 25.596 = 0.404$ and the $\hat{f}$'s of 0.800 and 0.404 are summed to 1.204 to obtain an $\hat{f}$ that is no smaller than 1.0.*

Then the chi-square goodness of fit would proceed as in Section 22.3:

X:	0	1	2	3	4	5	≥ 6	n
f:	2	1	13	10	3	1	0	30
$\hat{f}$:	2.537	6.267	7.740	6.373	3.935	1.944	1.204	

$$\chi^2 = \frac{(2 - 2.537)^2}{2.537} + \frac{(1 - 6.267)^2}{6.267} + \frac{(13 - 7.740)^2}{7.740} + \frac{(10 - 6.373)^2}{6.373} + \frac{(3 - 3.935)^2}{3.935} + \frac{(1 - 1.944)^2}{1.944} + \frac{(0 - 1.204)^2}{1.204}$$

$$= 0.114 + 4.427 + 3.575 + 2.064 + 0.222 + 0.458 + 1.204$$

$$= 12.064$$

$$\nu = k - 2 = 7 - 2 = 5$$

$$\chi^2_{0.05,5} = 11.070.$$

Therefore, reject H_0.

$$0.025 < P < 0.05$$

*$P(X) > 6$ could also have been obtained by adding all of the $P(X)$'s in the preceding table, which would result in a sum of 0.98653; and (0.98653)(30) = 29.596.

The null hypothesis in Poisson goodness-of-fit testing is that the distribution of objects in space (or events in time) is random.

- A *random* distribution of objects in a space is one in which each object has the same probability of occurring in each portion of the space; that is, the occurrence of each object is independent of the occurrence of any other object. There are

these two kinds of deviation from randomness that will cause rejection of the null hypothesis:

- A *uniform* distribution of objects in a space is one in which there is equal distance between adjacent objects, as if they are repelling each other.
- A *contagious* distribution* (also referred to as a "clumped," "clustered," "patchy," or "aggregated" distribution) in a space is one in which objects are more likely than in a random distribution to occur in the vicinity of other objects, as if they are attracting each other.

Figures 25.2 and 25.3 show examples of these three kinds of distributions.

If a population has a random (Poisson) distribution, the variance is the same as the mean: that is, $\sigma^2 = \mu$ and $\sigma^2/\mu = 1.0$.† If the distribution is more uniform than random (said to be "underdispersed"), $\sigma^2 < \mu$ and $\sigma^2/\mu < 1.0$; and if the distribution is distributed contagiously ("overdispersed"), $\sigma^2 > \mu$ and $\sigma^2/\mu > 1.0$.

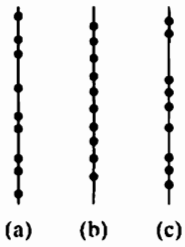

FIGURE 25.2: Distributions in one-dimensional space (i.e., along a line): (a) random (Poisson), in which $\sigma^2 = \mu$; (b) uniform, in which $\sigma^2 < \mu$; (c) contagious, in which $\sigma^2 > \mu$.

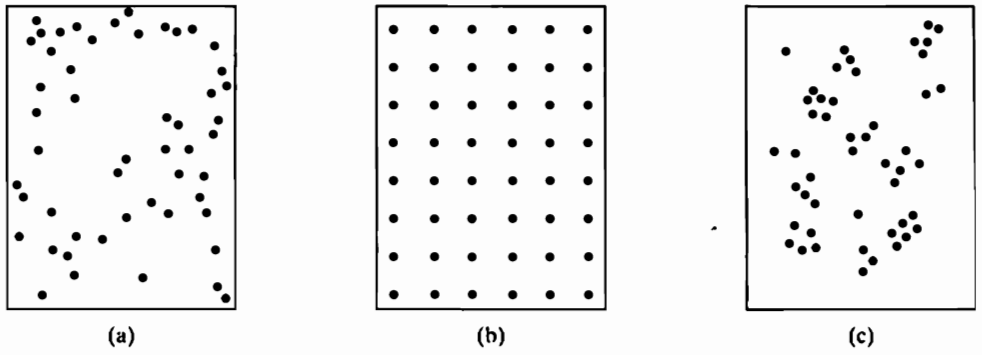

FIGURE 25.3: Distributions in two-dimensional space: (a) random (Poisson), in which $\sigma^2 = \mu$; (b) uniform, in which $\sigma^2 < \mu$; (c) contagious, in which $\sigma^2 > \mu$.

*A mathematical distribution that is sometimes used to describe contagious distributions of biological data is the *negative binomial distribution*, which is described, for example, by Ludwig and Reynolds (1988: 24–26, 32–35) and Pielou (1977: 278–281), and by Ross and Preece (1985), who credit a 1930 French paper by G. Polya with the first use of the term *contagious* in this context. David (1995) reported that "negative binomial distribution" is a term first used by M. Greenwood and G. U. Yule, in 1920.

†Although a population with a random distribution will always have its mean equal to its variance, Hurlbert (1990), Pielou (1967: 155), and others have emphasized that not every population with $\mu = \sigma^2$ has a random distribution.

The investigator generally has some control over the size of the space, or the length of the time interval, from which counts are recorded. So a plot size twice as large as that in Example 25.3 might have been used, in which case each f would most likely have been twice the size as in this example, with $\overline{X}$ of 4.94, instead of 2.47. In analyses using the Poisson distribution, it is desirable to use a sample distribution with a fairly small mean—let us say certainly below 10, preferably below 5, and ideally in the neighborhood of 1. If the mean is too large, then the Poisson too closely resembles the binomial, as well as the normal, distribution. If it is too small, however, then the number of categories, k, with appreciable frequencies will be too small for sensitive analysis.

Graphical testing of goodness of fit is sometimes encountered. The reader may consult Gart (1969b) for such considerations.

25.4 THE POISSON DISTRIBUTION FOR THE BINOMIAL TEST

The binomial test was introduced in Section 24.5 as a goodness-of-fit test for counts in two categories. If n is large, the binomial test is unwieldy. If p is small, it may be convenient to use the Poisson distribution, for it becomes very similar to the binomial distribution at such p's.

(a) One-Tailed Testing. Let us consider the following example. It is assumed (as from a very large body of previous information) that a certain type of genetic mutation naturally occurs in an insect population with a frequency of 0.0020 (i.e., on average in 20 out of 10,000 insects). On exposing a large number of these insects to a particular chemical, we wish to ask whether that chemical increases the rate of this mutation. Thus, we state H_0: $p \leq 0.0020$ and H_A: $p > 0.0020$. (The general one-tailed hypotheses of this sort would be H_0: $p \leq p_0$ and H_A: $p > p_0$, where p_0 is the proportion of interest in the statistical hypotheses. If we had reason to ask whether some treatment reduced the natural rate of mutations, then the one-tailed test would have used H_0: $p \geq p_0$ and H_A: $p < p_0$.)

As an example, if performing this exposure experiment for the hypotheses H_0: $p_0 \leq 0.0020$ and H_A: $p_0 > 0.0020$ yielded 28 of the mutations of interest in 8000 insects observed, then the sample mutation rate is $\hat{p} = X/n = 28/8000 = 0.0035$. The question is whether the rate of 0.0035 is significantly greater than 0.0020. If we conclude that there is a low probability (i.e., $\leq \alpha$) of a sample rate being at least as large as 0.0035 when the sample is taken at random from a population having a rate of 0.0020, then H_0 is to be rejected.

The hypotheses could also be stated in terms of numbers, instead of proportions, as H_0: $\mu \leq \mu_0$ and H_A: $\mu > \mu_0$, where $\mu_0 = p_0 n$ (which is $0.0020 \times 8000 = 16$ in this example).

By substituting $p_0 n$ for μ in Equation 25.1, we determine the probability of observing $X = 28$ mutations if our sample came from a population with $p_0 = 0.0020$. To test the hypothesis at hand, we determine the probability of observing $X \geq 28$ mutations in a sample. (If the alternate hypothesis being considered were H_A: $p < p_0$, then we would compute the probability of mutations less than or equal to the number observed.) If the one-tailed probability is less than or equal to α, then H_0 is rejected at the α level of significance. This process is shown in Examples 25.4 and 25.5a.

EXAMPLE 25.4 Poisson Probabilities for Performing the Binomial Test with a Very Small Proportion

$p_0 = 0.0020$

$n = 8000$

We substitute $p_0 n = (0.0020)(8000) = 16$ for μ in Equation 25.1 to compute the following*:

For lower tail of distribution			For upper tail of distribution		
X	$P(X)$	*Cumulative* $P(X)$	X	$P(X)$	*Cumulative* $P(X)$
0	0.00000	0.00000	23	0.02156	0.05825
1	0.00000	0.00000	24	0.01437	0.03669
2	0.00001	0.00001	25	0.00920	0.02232
3	0.00008	0.00009	26	0.00566	0.01312
4	0.00031	0.00040	27	0.00335	0.00746
5	0.00098	0.00138	28	0.00192	0.00411
6	0.00262	0.00400	29	0.00106	0.00219
7	0.00599	0.00999	30	0.00056	0.00113
8	0.01199	0.02198	31	0.00029	0.00057
9	0.02131	0.04329	32	0.00015	0.00028
10	0.03410	0.07739	33	0.00007	0.00013
			34	0.00003	0.00006
			35	0.00002	0.00003
			36	0.00001	0.00001
			37	0.00000	0.00000

The cumulative probability is the probability in the indicated tail. For example, $P(X \leq 10) = 0.07739$ and $P(X \geq 25) = 0.02232$. This series of computations terminates when we reach a $P(X)$ that is zero to the number of decimal places used.

*For example, using Equation 25.1a, $P(X = 28) = \frac{e^{-16}16^{28}}{28!} = 0.00192$; and $P(X = 29) = \frac{e^{-16}16^{29}}{29!} = 0.00106$.

(b) Two-Tailed Testing. If there is no reason, a priori, to hypothesize that a change in mutation rate would be in one specified direction (e.g., an increase) from the natural rate, then a two-tailed test is appropriate. The probability of the observed number of mutations is computed as shown in Example 25.4. Then we calculate and sum all the probabilities (in both tails) that are equal to or smaller than that of the observed. This is demonstrated in Example 25.5b.

(c) Power of the Test. Recall that the power of a statistical test is the probability of that test rejecting a null hypothesis that is in fact a false statement about the

EXAMPLE 25.5a A One-Tailed Binomial Test for a Proportion from a Poisson Population, Using the Information of Example 25.4

H_0: $p \leq 0.0020$
H_A: $p > 0.0020$
$\alpha = 0.05$
$n = 8000$
$X = 28$
$p_0 n = (0.0020)(8000) = 16$

Therefore, we could state

H_0: $\mu \leq 16$
H_A: $\mu > 16$.

From Example 25.4, we see that $P(X = 28) = 0.00192$ and $P(X \geq 28) = 0.00411$. As $0.00411 < 0.05$, reject H_0.

EXAMPLE 25.5b A Two-Tailed Binomial Test for a Proportion from a Poisson Population, Using the Information of Example 25.4

H_0: $p = 0.0020$
H_A: $p \neq 0.0020$
$\alpha = 0.05$
$n = 8000$
$X = 28$
$p_0 n = (0.0020)(8000) = 16$

Therefore, we can state

H_0: $\mu = 16$
H_A: $\mu \neq 16$.

From Example 25.4, we see that $P(X = 28) = 0.00192$.

The sum of the probabilities in one tail that are ≤ 0.00192 is 0.00411; the sum of the probabilities in the other tail that are ≤ 0.00192 is 0.00138. Therefore, the probability of obtaining these data from a population where H_0 is true is $0.00411 + 0.00138 = 0.00549$.

As $0.00549 < 0.05$, reject H_0.

population. We can determine the power of the preceding test when it is performed with a sample size of n at a significance level of α. For a one-tailed test, we first determine the critical value of X (i.e., the smallest X that delineates a proportion of the Poisson distribution $\leq \alpha$). Examining the distribution of Example 25.4, for example, for $\alpha = 0.05$, we see that the appropriate X is 24 [for $P(X \geq 24) = 0.037$), while $P(X \geq 23) = 0.058$]. We then examine the Poisson distribution having the

sample X replace μ in Equation 25.1. The power of the test is $\geq$ the probability of an X at least as extreme as the critical value of X.*

For a two-tailed hypothesis, we identify one critical value of X as the smallest X that cuts off $\leq \alpha/2$ of the distribution in the upper tail and one as the largest X that cuts off $\leq \alpha/2$ of the lower tail. In Example 25.6, these two critical values for $\alpha = 0.05$ (i.e., $\alpha/2 = 0.025$) are $X = 25$ and $X = 8$ [as $P(X \geq 25) = 0.022$ and $P(X \leq 8) = 0.022$]. Then we examine the Poisson distribution having the sample X replace μ in Equation 25.1. As shown in Example 25.6, the power of the two-tailed test is at least as large as the probability of X in the latter Poisson distribution being more extreme than either of the critical values. That is, power $\geq P(X \geq$ upper critical value$) + P(X \leq$ lower critical value).

COMPARING TWO POISSON COUNTS

If we have two counts, X_1 and X_2, each from a population with a Poisson distribution, we can ask whether they are likely to have come from the same population (or from populations with the same mean). The test of H_0: $\mu_1 = \mu_2$ (against H_A: $\mu_1 \neq \mu_2$) is related to the binomial test with $p = 0.50$ (Przyborowski and Wilenski, 1940; Pearson and Hartley, 1966: 78–79), so that Appendix Table B.27 can be utilized, using $n = X_1 + X_2$. For the two-tailed test, H_0 is rejected if either X_1 or X_2 is $\leq$ the critical value, $C_{\alpha(2),n}$. This is demonstrated in Example 25.7.

For a one-tailed test of H_0: $\mu_1 \leq \mu_2$ against H_A: $\mu_1 > \mu_2$, we reject H_0 if $X_1 > X_2$ and $X_2 \leq C_{\alpha(1),n}$, where $n = X_1 + X_2$. For H_0: $\mu_1 \geq \mu_2$ and H_A: $\mu_1 < \mu_2$, H_0 is rejected if $X_1 < X_2$ and $X_1 \leq C_{\alpha(1),n}$, where $n = X_1 + X_2$.

This procedure results in conservative testing, and if n is at least 5, then a normal approximation should be used (Detre and White, 1970; Przyborowski and Wilenski, 1940; Sichel, 1973). For the two-tailed test,

$$Z = \frac{|X_1 - X_2|}{\sqrt{X_1 + X_2}} \tag{25.10}$$

is considered a normal deviate, so the critical value is $Z_{\alpha(2)}$ (which can be read as $t_{\alpha(2),\infty}$ at the end of Appendix Table B.3). This is demonstrated in Example 25.7.

For a one-tailed test,

$$Z = \frac{X_1 - X_2}{\sqrt{X_1 - X_2}}. \tag{25.11}$$

For H_0: $\mu_1 \leq \mu_2$ versus H_A: $\mu_1 > \mu_2$, H_0 is rejected if $X_1 > X_2$ and $Z \geq Z_{\alpha(1)}$. For H_0: $\mu_1 \geq \mu_2$ versus H_A: $\mu_1 < \mu_2$, H_0 is rejected if $X_1 < X_2$ and $Z \leq -Z_{\alpha(1)}$.

The normal approximation is sometimes seen presented with a correction for continuity, but Pirie and Hamdan (1972) concluded that this produces results that are excessively conservative and the test has very low power.

An alternative normal approximation, based on a square-root transformation (Anscombe, 1948) is

$$Z = \left| \sqrt{2X_1 + \frac{3}{4}} - \sqrt{2X_2 + \frac{3}{4}} \right| \tag{25.12}$$

*If the critical value delineates exactly α of the tail of the Poisson distribution, then the test's power is exactly what was calculated; if the critical value cuts off $< \alpha$ of the tail, then the power is $>$ that calculated.

EXAMPLE 25.6 Estimation of the Power of the Small-Probability Binomial Tests of Examples 25.5a and 25.5b, Using $\alpha = 0.05$

Substituting $X = 28$ for μ in Equation 25.1, we compute the following*:

For lower tail of distribution			For upper tail of distribution		
X	$P(X)$	*Cumulative* $P(X)$	X	$P(X)$	*Cumulative* $P(X)$
0	0.000	0.000	24	0.060	0.798
1	0.000	0.000	25	0.067	0.738
2	0.000	0.000	26	0.072	0.671
3	0.000	0.000	27	0.075	0.599
3	0.000	0.000	28	0.075	0.524
5	0.000	0.000	29	0.073	0.449
6	0.000	0.000	30	0.068	0.376
7	0.000	0.000	31	0.061	0.308
8	0.000	0.000	32	0.054	0.247
			33	0.045	0.193
			34	0.037	0.148
			35	0.030	0.111
			36	0.023	0.081
			37	0.018	0.058
			38	0.013	0.040
			39	0.009	0.027
			40	0.007	0.018
			41	0.004	0.011
			42	0.003	0.007
			43	0.002	0.004
			44	0.001	0.002
			45	0.001	0.001
			46	0.000	0.000

The critical value for the one-tailed test of Example 25.5a is $X = 24$. The power of this test is $>P(X \geq 24)$ in the preceding distribution. That is, the power is >0.798.

The critical values for the two-tailed test of Example 25.5b are 25 and 8. The power of this test is $>P(X \geq 25) + P(X \leq 8) = 0.738 + 0.000$. That is, the power is >0.738.

*For example, using Equation 25.1a, $P(X = 24) = \frac{e^{-28}28^{24}}{24!} = 0.06010$; and $P(X = 25) = \frac{e^{-28}28^{25}}{25!} = 0.06731$.

(Best, 1975). It may be used routinely in place of Equation 25.10, and it has superior power when testing at $\alpha < 0.05$. Equation 25.12 is for a two-tailed test; for one-tailed testing, use

$$Z = \sqrt{2X_1 + \frac{3}{4}} - \sqrt{2X_2 + \frac{3}{4}}, \tag{25.13}$$

with the same procedure to reject H_0 as with Equation 25.11.

EXAMPLE 25.7 A Two-Sample Test with Poisson Data

One fish is found to be infected with 13 parasites and a second fish with 220. Assuming parasites are distributed randomly among fish, test whether these two fish are likely to have come from the same population. (If the two were of different species, or sexes, then we could ask whether the two species, or sexes, are equally infected.) The test is two-tailed for hypotheses H_0: $\mu_1 = \mu_2$ and H_A: $\mu_1 \neq \mu_2$.

Using Appendix Table B.27 for $n = X_1 + X_2 = 13 + 22 = 35$, we find a critical value of $C_{0.05(2),35} = 11$. Because neither X_1 nor X_2 is ≤ 11, H_0 is not rejected. Using the smaller of the two X's, we conclude that the probability is between 0.20 and 0.50 that a fish with 13 parasites and one with 22 parasites come from the same Poisson population (or from two Poisson populations having the same mean).

Using the normal approximation of Equation 25.10,

$$Z = \frac{|X_1 - X_2|}{\sqrt{X_1 + X_2}} = \frac{|13 - 22|}{\sqrt{13 + 22}} = \frac{9}{5.916} = 1.521$$

$Z_{0.05(2)} = t_{0.05(2),\infty} = 1.960.$

Therefore, do not reject H_0.

$$0.10 < P < 0.20 \quad [P = 0.13]$$

SERIAL RANDOMNESS OF NOMINAL-SCALE CATEGORIES

Representatives of two different nominal-scale categories may appear serially in space or time, and their randomness of occurrence may be assessed as in the following example. Members of two species of antelopes are observed drinking along a river, and their linear order is as shown in Example 25.8. We may ask whether the sequence of occurrence of members of the two species is random (as opposed to the animals either forming groups with individuals of the same species or shunning members of the same species). A sequence of like elements, bounded on either side by either unlike elements or no elements, is termed a *run*. Thus, any of the following arrangements of five members of antelope species A and seven members of species B would be considered to consist of five runs:

BAABBBAAABBB, or *BBAAAABBBBAB*, or *BABAAAABBBBB*, or *BAAABAABBBBB*, and so on.

To test the null hypothesis of randomness, we may use the *runs test*.* If n_1 is the total number of elements of the first category (in the present example, the number of antelope of species A), n_2 the number of antelope of species B, and u the number of runs in the entire sequence, then the critical values, $u_{\alpha(2),n_1,n_2}$, can be read from Appendix Table B.29 for cases where both $n_1 \leq 30$ and $n_2 \leq 30$. The critical values in this table are given in pairs; if the u in the sample is $\leq$ the first member of the pair *or* $\geq$ the second, then H_0 is rejected.

*From its inception the runs test has also been considered to be a nonparametric test of whether two samples come from the same population (e.g., Wald and Wolfowitz, 1940), but as a two-sample test it has very poor power and the Mann-Whitney test of Section 8.11 is preferable.

EXAMPLE 25.8 The Two-Tailed Runs Test with Elements of Two Kinds

Members of two species of antelopes (denoted as species A and B) are drinking along a river in the following order: *AABBAABBBBAAABBBBAABBB*.

H_0: The distribution of members of the two species along the river is random.
H_A: The distribution of members of the two species along the river is not random.

For species A, $n_1 = 9$; for species B, $n_2 = 13$; and $u = 9$.

$u_{0.05(2),9,13} = 6$ and 17 (from Appendix Table B.29)

As u is neither ≤ 6 nor ≥ 17, do not reject H_0.

$$0.10 \leq P \leq 0.20$$

The power of the runs test increases with sample size.* Although Appendix Table B.29 cannot be employed if either n_1 or n_2 is larger than 30, for such samples the distribution of u approaches normality with a mean of

$$\mu_u = \frac{2n_1n_2}{N} + 1 \tag{25.14}$$

and a standard deviation of

$$\sigma_u = \sqrt{\frac{2n_1n_2(2n_1n_2 - N)}{N^2(N - 1)}}, \tag{25.15}$$

where $N = n_1 + n_2$ (Brownlee, 1965: 226–230; Wald and Wolfowitz, 1940). And the statistic

$$Z_c = \frac{|u - \mu_u| - 0.5}{\sigma_u} \tag{25.16}$$

may be considered a normal deviate, with $Z_{\alpha(2)}$ being the critical value for the test. (The 0.5 in the numerator of Z_c is a correction for continuity.)

Using Equation 25.16, the runs test may be extended to data with more than two categories (Wallis and Roberts, 1956: 571), for, in general,

$$\mu_u = \frac{N(N + 1) - \sum n_i^2}{N} \tag{25.17}$$

and

$$\sigma_u = \sqrt{\frac{\sum n_i^2\left[\sum n_i^2 + N(N + 1)\right] - 2N\sum n_i^3 - N^3}{N^2(N - 1)}}, \tag{25.18}$$

where n_i is the number of items in category i, N is the total number of items (i.e., $N = \sum n_i$), and the summations are over all categories. (For two categories,

*Mogull (1994) has shown that the runs test should not used in the unusual case of a sample consisting entirely of runs of two (for example, a sample consisting of *BBAABBAABBAABB*). In such situations the runs test is incapable of concluding departures from randomness; it has very low power, and the power *decreases* with increased sample size.

Equations 25.17 and 25.18 are equivalent to Equations 25.14 and 25.15, respectively.) O'Brien (1976) and O'Brien and Dyck (1985) present a runs test, for two or more categories, that utilizes more information from the data, and is more powerful, than the above procedure.

(a) One-Tailed Testing. There are two ways in which a distribution of nominal-scale categories can be nonrandom: (a) The distribution may have fewer runs than would occur at random, in which case the distribution is more clustered, or contagious, than random; (b) the distribution may have more runs than would occur at random, indicating a tendency toward a uniform distribution.

To test for the one-tailed situation of contagion, we state H_0: The elements in the population are not distributed contagiously, versus H_A: The elements in the population are distributed contagiously; and H_0 would be rejected at the $\alpha(1)$ significance level if $u \leq$ the lower of the pair of critical values in Appendix Table B.29. Thus, had the animals in Example 25.8 been arranged *AAAAABBBBBBAAAABBBBBBB*, then $u = 4$ and the one-tailed 5% critical value would be the lower value of $u_{0.05(1),9,13}$, which is 7; as $4 < 7$, H_0 is rejected and the distribution is concluded to be clustered. In using the normal approximation, H_0 is rejected if $Z_c \geq Z_{\alpha(1)}$ and $u \leq \mu_u$.

To test for uniformity, we use H_0: The elements in the population are not uniformly distributed versus H_A: The elements in the population are uniformly distributed. If $u \geq$ the upper critical value in Appendix Table B.29 for $\alpha(1)$, then H_0 is rejected. If the animals in Example 25.8 had been arranged as *ABABABBABABBABABBABBAB*, then $u = 18$, which is greater than the upper critical value of $u_{0.05(1),9,13}$ (which is 16); therefore, H_0 would have been rejected. If the normal approximation were used, H_0 would be rejected if $Z_c \geq Z_{\alpha(1)}$ and $u \geq \mu_u$.

(b) Centrifugal and Centripetal Patterns. Occasionally, nonrandomness in the sequential arrangement of two nominal-scale categories is characterized by one of the categories being predominant toward the ends of the series and the other toward the center. In the following sequence, for example,

AAAABAABBBBBBABBBBBAABBAAAAA

the *A*'s are more common toward the termini of the sequence, and the *B*'s are more common toward the center of the sequence. Such a situation might be the pattern of two species of plants along a line transect from the edge of a marsh, through the center of the marsh, to the opposite edge. Or we might observe the occurrence of diseased and healthy birds in a row of cages, each cage containing one bird. Ghent (1993) refers to this as a *centrifugal* pattern of *A*'s and a *centripetal* pattern of *B*'s and presents a statistical test to detect such distributions of observations.

SERIAL RANDOMNESS OF MEASUREMENTS: PARAMETRIC TESTING

Biologists may encounter continuous data that have been collected serially in space or time. For example, rates of conduction might be measured at successive lengths along a nerve. A null hypothesis of no difference in conduction rate as one examines successive portions essentially is stating that all the measurements obtained are a random sample from a population of such measurements.

Example 25.9 presents data consisting of dissolved oxygen measurements of a water solution determined on the same instrument every five minutes. The desire

EXAMPLE 25.9 The Mean Square Successive Difference Test

An instrument for measuring dissolved oxygen is used to record a measurement every five minutes from a container of lake water. It is desired to know whether the differences in measurements are random or whether they are systematic. (If the latter, it could be due to the dissolved oxygen content in the water changing, or the instrument's response changing, or to both.) The data (in ppm) are as follows, recorded in the sequence in which they were obtained: 9.4, 9.3, 9.3, 9.2, 9.3, 9.2, 9.1, 9.3, 9.2, 9.1, 9.1.

H_0: Consecutive measurements obtained on the lake water with this instrument have random variability.

H_A: Consecutive measurements obtained on the lake water with this instrument have nonrandom variability and are serially correlated.

$n = 11$

$s^2 = 0.01018\ (\text{ppm})^2$

$$s_*^2 = \frac{(9.3 - 9.4)^2 + (9.3 - 9.3)^2 + (9.2 - 9.3)^2 + \ldots + (9.1 - 9.1)^2}{2(11 - 1)}$$

$$= 0.00550$$

$$C = 1 - \frac{0.00550}{0.01018} = 1 - 0.540 = 0.460$$

$C_{0.05,11} = 0.452$

Therefore, reject H_0.

$$0.025 < P < 0.05$$

is to conclude whether fluctuations in measurements are random or whether they indicate a nonrandom instability in the measuring device (or in the solution). The null hypothesis that the sequential variability among measurements is random may be subjected to the *mean square successive difference* test, a test that assumes normality in the underlying distribution. In this procedure, we calculate the sample variance, s^2, which is an estimate of the population variance, σ^2, as introduced in Section 4.4:

$$s^2 = \frac{\sum_{i=1}^{n}(X_i - \overline{X})^2}{n - 1}, \tag{4.15}$$

or

$$s^2 = \frac{\sum_{i=1}^{n} X_i^2 - \frac{\left(\sum_{i=1}^{n} X_i\right)^2}{n}}{n - 1}. \tag{4.17}$$

If the null hypothesis is true, then another estimate of σ^2 is

$$s_*^2 = \frac{\sum_{i=1}^{n-1}(X_{i+1} - X_i)^2}{2(n - 1)} \tag{25.19}$$

(von Neumann et al., 1941). Therefore, the ratio s_*^2/s^2 should equal 1 when H_0 is true. Using Young's (1941) notation, the test statistic is

$$C = 1 - \frac{s_*^2}{s^2}, \tag{25.20}$$

and if this value equals or exceeds the critical value $C_{\alpha,n}$, in Appendix Table B.30, we reject the null hypothesis of serial randomness.* The mean square successive difference test considers the one-tailed alternate hypothesis that measurements are serially correlated.

For n larger than those in Appendix Table B.30, the hypothesis may be tested by a normal approximation:

$$Z = \frac{C}{\sqrt{\frac{n-2}{n^2-1}}} \tag{25.22}$$

(von Neumann et al., 1941), with the value of the calculated Z being compared with the critical value of $Z_{\alpha(1)} = t_{\alpha(1),\infty}$. This approximation is very good for $\alpha = 0.05$, for n as small as 10; for $\alpha = 0.10, 0.25$, or 0.025, for n as small as 25; and for $\alpha = 0.01$ and 0.005, for n of at least 100.

SERIAL RANDOMNESS OF MEASUREMENTS: NONPARAMETRIC TESTING

If we do not wish to assume that a sample of serially obtained measurements came from a normal population, then the procedure of Section 25.7 should not be employed. Instead, there are nonparametric methods that address hypotheses about serial patterns.

(a) Runs Up and Down: Two-Tailed Testing. We may wish to test the null hypothesis that successive directions of change in serial data tend to occur randomly, with the alternate hypothesis stating the directions of change occur *either* in clusters (that is, where an increase from one datum to another is likely to be followed by another increase, and a decrease in the magnitude of the variable is likely to be followed by another decrease) *or* with a tendency toward regular alternation of increases and decreases (i.e., an increase is likely to be followed by a decrease, and vice versa). In the series of n data, we note whether datum $i + 1$ is larger than datum i (and denote this as a positive change, indicated as "+") or is smaller than datum i (which is referred to as a negative change, indicated as "−"). By a nonparametric procedure presented by Wallis and Moore (1941), the series of +'s and −'s is examined and we determine the number of runs of +'s and −'s, calling this number u as we did in Section 25.6. Appendix Table B.31 presents pairs of critical values for u, where for the two-tailed test for deviation from randomness one would reject H_0 if u were *either* ≤ the first member of the pair *or* ≥ the second member of the pair.

*Equations 4.15 and 25.19 may be combined so that C can be computed as

$$C = 1 - \frac{\sum_{i=1}^{n-1}(X_i - X_{i+1})^2}{2(\mathrm{SS})}, \tag{25.21}$$

where SS is the numerator of either Equation 4.15 or 4.17.

For sample sizes larger than those in Table B.31, a normal approximation may be employed (Edgington, 1961; Wallis and Moore, 1941) using Equation 25.16, where

$$\mu_u = \frac{2n - 1}{3} \tag{25.23}$$

and

$$\sigma_u = \sqrt{\frac{16n - 29}{90}}. \tag{25.24}$$

The runs-up-and-down test may be used for ratio, interval, or ordinal data and is demonstrated in Example 25.10. It is most powerful when no adjacent data are the same; if there are identical adjacent data, as in Example 25.10, then indicate the progression from each adjacent datum to the next as "0" and determine the mean of all the u's that would result from all the different conversions of the 0's to either +'s or −'s. Levene (1952) discussed the power of this test.

EXAMPLE 25.10 Testing of Runs Up and Down

Data are measurements of temperature in a rodent burrow at noon on successive days.

H_0: The successive positive and negative changes in temperature measurements are random.

H_A: The successive positive and negative changes in the series of temperature measurements are not random.

Day	*Temperature* (°C)	*Difference*
1	20.2	
2	20.4	+
3	20.1	−
4	20.3	+
5	20.5	+
6	20.7	+
7	20.5	−
8	20.4	−
9	20.8	+
10	20.8	0
11	21.0	+
12	21.7	+

$n = 12$

If the difference of 0 is counted as +, then $u = 5$; if the 0 is counted as −, then $u = 7$; mean $u = 6$.

For $\alpha = 0.05$, the critical values are $u_{0.05(2),12} = 4$ and 11.

H_0 is not rejected; $0.25 < P \leq 0.50$.

(b) Runs Up and Down: One-Tailed Testing. In a fashion similar to that in Section 25.6a, a one-tailed test would address one of two situations. One is where H_0: In the sampled population, the successive positive and negative changes in the series of data are not clustered (i.e., are not contagious), and H_A: In the sampled population, the successive positive and negative changes in the series of data are clustered (i.e., are contagious). For this test, H_0 would be rejected if $u \leq$ the first member of the pair of one-tailed critical values in Appendix Table B.31; if the test is performed using the normal approximation, H_0 would be rejected if $|Z_c \geq Z_{\alpha(1)}|$ and $u \leq \mu_u$. The other one-tailed circumstance is where H_0: In the sampled population, the successive positive and negative changes in the series of data do not alternate regularly (i.e., are not uniform), versus H_A: In the sampled population, the series of data do alternate regularly (i.e., are uniform). H_0 would be rejected if $u \geq$ the second member of the pair of one-tailed critical values; if the test uses the normal approximation, H_0 would be rejected if $Z_c \geq Z_{\alpha(1)}$ and $u \geq \mu_u$.

(c) Runs Above and Below the Median. Another method of assessing randomness of ratio-, interval-, or ordinal-scale measurements examines the pattern of their distribution with respect to the set of data. We first determine the median of the sample (as explained in Section 3.2). Then we record each datum as being either above (+) or below (−) the median. If a sample datum is equal to the median, it is discarded from the analysis. We then record u, the number of runs, in the resulting sequence of +'s and −'s. The test then proceeds as the runs test of Section 25.6. This is demonstrated, for two-tailed hypotheses, in Example 25.11; common one-tailed hypotheses are those inquiring into contagious (i.e., clumped) distributions of data above or below the median.

EXAMPLE 25.11 Runs Above and Below the Median

The data and hypotheses are those of Example 25.10.
The median of the 12 data is determined to be 20.5 C.
The sequence of data, indicating whether they are above (+) or below (−) the median, is − − − − 0 + 0 − + + ++.
For the runs test, $n_1 = 5, n_2 = 5, u = 4$.
The critical values are $u_{0.05(2),5,5} = 2$ and 10; therefore, do not reject H_0; $0.20 < P \leq 0.50$.

Although the test for runs up and down and the test for runs above and below the median may both be considered nonparametric alternatives to the parametric means square successive difference test of Section 25.7, the latter runs test often resembles the parametric test more than the former runs test does. The test for runs up and down works well to detect long-term trends in the data, unless there are short-term random fluctuations superimposed upon those trends. The other two tests tend to perform better in detecting long-term patterns in the presence of short-term randomness (A. W. Ghent, personal communication).

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$$\mu_u = \frac{2n - 1}{3} \tag{25.23}$$

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Data are measurements of temperature in a rodent burrow at noon on successive days.

H_0: The successive positive and negative changes in temperature measurements are random.

H_A: The successive positive and negative changes in the series of temperature measurements are not random.

Day	*Temperature* (°C)	*Difference*
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2	20.4	+
3	20.1	−
4	20.3	+
5	20.5	+
6	20.7	+
7	20.5	−
8	20.4	−
9	20.8	+
10	20.8	0
11	21.0	+
12	21.7	+

$n = 12$

If the difference of 0 is counted as +, then $u = 5$; if the 0 is counted as −, then $u = 7$; mean $u = 6$.

For $\alpha = 0.05$, the critical values are $u_{0.05(2),12} = 4$ and 11.

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(c) Runs Above and Below the Median. Another method of assessing randomness of ratio-, interval-, or ordinal-scale measurements examines the pattern of their distribution with respect to the set of data. We first determine the median of the sample (as explained in Section 3.2). Then we record each datum as being either above (+) or below (−) the median. If a sample datum is equal to the median, it is discarded from the analysis. We then record u, the number of runs, in the resulting sequence of +'s and −'s. The test then proceeds as the runs test of Section 25.6. This is demonstrated, for two-tailed hypotheses, in Example 25.11; common one-tailed hypotheses are those inquiring into contagious (i.e., clumped) distributions of data above or below the median.

EXAMPLE 25.11 Runs Above and Below the Median

The data and hypotheses are those of Example 25.10.
The median of the 12 data is determined to be 20.5° C.
The sequence of data, indicating whether they are above (+) or below (−) the median, is − − − − 0 + 0 − + + ++.
For the runs test, $n_1 = 5, n_2 = 5, u = 4$.
The critical values are $u_{0.05(2),5,5} = 2$ and 10; therefore, do not reject H_0; $0.20 < P \leq 0.50$.

Although the test for runs up and down and the test for runs above and below the median may both be considered nonparametric alternatives to the parametric means square successive difference test of Section 25.7, the latter runs test often resembles the parametric test more than the former runs test does. The test for runs up and down works well to detect long-term trends in the data, unless there are short-term random fluctuations superimposed upon those trends. The other two tests tend to perform better in detecting long-term patterns in the presence of short-term randomness (A. W. Ghent, personal communication).

EXERCISES

25.1. If, in a Poisson distribution, $\mu = 1.5$, what is $P(0)$? What is $P(5)$?

25.2. A solution contains bacterial viruses in a concentration of 5×10^8 bacterial-virus particles per milliliter. In the same solution are 2×10^8 bacteria per milliliter. If there is a random distribution of virus among the bacteria,

(a) What proportion of the bacteria will have no virus particles?

(b) What proportion of the bacteria will have virus particles?

(c) What proportion of the bacteria will have at least two virus particles?

(d) What proportion of the bacteria will have three virus particles?

25.3. Fifty-seven men were seated in an outdoor area with only their arms exposed. After a period of time, the number of mosquito bites (X) on each man's arms was recorded, as follows, where f is the number of men with X bites. Test the null hypothesis that mosquitoes bite these men at random.

X	f
0	8
1	17
2	18
3	11
4	3
≥ 5	0

25.4. We wish to compile a list of certain types of human metabolic diseases that occur in more than 0.01% of the population. A random sample of 25,000 infants reveals five infants with one of these diseases. Should that disease be placed on our list?

25.5. A biologist counts 112 diatoms in a milliliter of lake water, and 134 diatoms are counted in a milliliter of a second collection of lake water. Test the hypothesis that the two water collections came from the same lake (or from lakes with the same mean diatom concentrations).

25.6. An economic entomologist rates the annual incidence of damage by a certain beetle as mild (M) or heavy (H). For a 27-year period he records the following: *H M M M H H M M H M H H H M M H H H M M H H M M M M*. Test the null hypothesis that the incidence of heavy damage occurs randomly over the years.

25.7. The following data are the magnitudes of fish kills along a certain river (measured in kilograms of fish killed) over a period of years. Test the null hypothesis that the magnitudes of the fish kills were randomly distributed over time.

Year	*Kill* (kg)
1955	147.4
1956	159.8
1957	155.2
1958	161.3
1959	173.2
1960	191.5
1961	198.2
1962	166.0
1963	171.7
1964	184.9
1965	177.6
1966	162.8
1967	177.9
1968	189.6
1969	206.9
1970	221.5

25.8. Analyze the data of Exercise 25.7 nonparametrically to test for serial randomness.

CHAPTER 26

Circular Distributions: Descriptive Statistics

26.1 DATA ON A CIRCULAR SCALE

In Section 1.1b, an interval scale of measurement was defined as a scale with equal intervals but with no true zero point. A special type of interval scale is a circular scale, where not only is there no true zero, but any designation of high or low values is arbitrary. A common example of a circular scale of measurement is compass direction (Figure 26.1a), where a circle is said to be divided into 360 equal intervals, called degrees,* and for which the zero point is arbitrary. There is no physical justification for a direction of north to be designated 0 (or 360) degrees, and a direction of 270° cannot be said to be a "larger" direction than 90°.†

Another common circular scale is time of day (Fig. 26.1b), where a day is divided into 24 equal intervals, called hours, but where the designation of midnight as the zero or starting point is arbitrary. One hour of a day corresponds to 15° (i.e., 360°/24) of a circle, and 1° of a circle corresponds to four minutes of a day. Other time divisions, such as weeks and years (see Figure 26.1c), also represent circular scales of measurement.

*A degree is divided into 60 minutes (i.e., 1° = 60′) and a minute into 60 seconds (1′ = 60″). A number system based upon 60 is termed *sexagesimal*, and we owe the division of the circle into 360 degrees—and the 60-minute hour and 60-second minute—to the ancient Babylonians (about 3000 years ago). The use of the modern symbols (° and ′ and ″) appears to date from the 1570s (Cajori, 1928–1929, Vol. II: 146).

†Occasionally one will encounter angular measurements expressed in radians instead of in degrees. A radian is the angle that is subtended by an arc of a circle equal in length to the radius of the circle. As a circle's circumference is 2π times the radius, a radian is $360°/2\pi = 180°/\pi = 57.29577951°$ (or 57 deg, 17 min, 44.8062 sec). The term *radian* was first used, in 1873, by James Thomson, brother of Baron William Thomson (Lord Kelvin), the famous Scottish mathematician and physicist (Cajori, 1928–1929, Vol. II: 147). A direction measured clockwise, from 0° at north, is called an *azimuth*. Rarely, a direction is recorded as an angular measurement called a *grad*: a right angle (90°) is divided into 100 grads, so a grad is 0.9 of a degree.

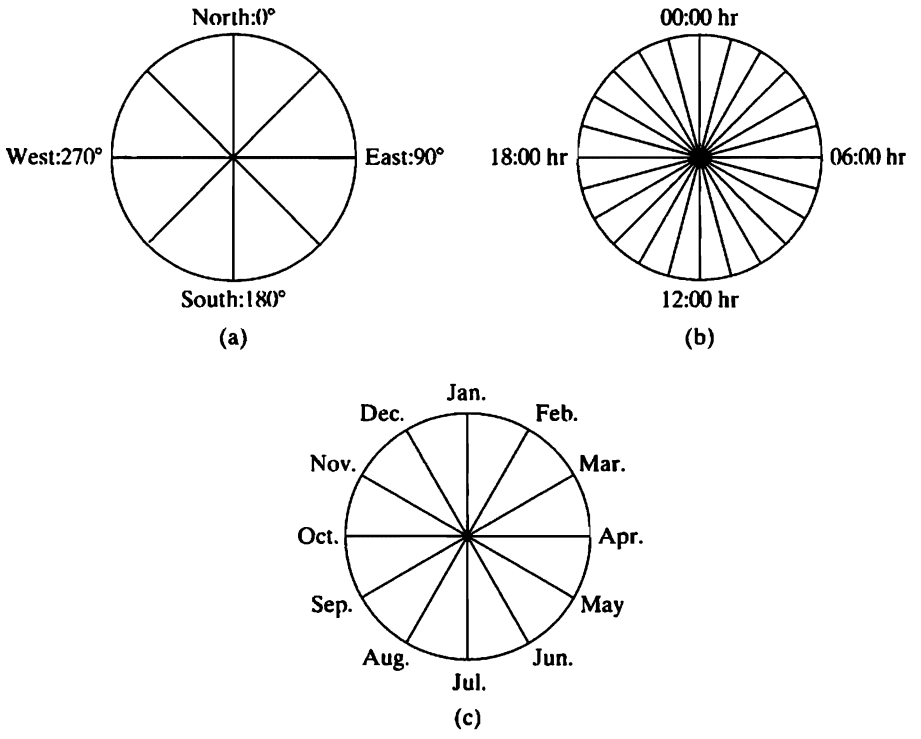


FIGURE 26.1: Common circular scales of measurement. (a) Compass directions. (b) Times of day. (c) Days of the year (with the first day of each month shown).

In general, X time units may be converted to an angular direction (a, in degrees), where X has been measured on a circular scale having k time units in the full cycle:

$$a = \frac{(360°)(X)}{k}. \tag{26.1}$$

For example, to convert a time of day (X, in hours) to an angular direction, $k = 24$ hr; to convert a day of the week to an angular direction, number the seven days from some arbitrary point (e.g., Sunday = day 1) and use Equation 26.1 with $k = 7$; to convert the Xth day of the year to an angular direction, $k = 365$ (or, $k = 366$ in a leap year); to convert a month of the year, $k = 12$; and so on.* Such conversions are demonstrated in Example 26.1.

Data from circular distributions generally may *not* be analyzed using the statistical methods presented earlier in this book. This is so for theoretical reasons as well as for empirically obvious reasons stemming from the arbitrariness of the zero point on the circular scale. For example, consider three compass directions—10°, 30°, and 350°,

*Equation 26.1 gives angular directions corresponding to the ends of time periods (e.g., the end of the Xth day of the year). If some other point in a time period is preferred, the equation can be adjusted accordingly. For example, noon can be considered on the Xth day of the year by using $X-0.5$ in place of X. If the same point is used in each time period (e.g., always using either noon or midnight), then the statistical procedures of this and the following chapter will be unaffected by the choice of point. (However, graphical procedures, as in Section 26.2, will of course be affected, in the form of a rotation of the graph if Equation 26.1 is adjusted. If, for example, we considered noon on the Xth day of the year, the entire graph would be rotated about half a degree counterclock-

EXAMPLE 26.1 Conversions of Times Measured on a Circular Scale to Corresponding Angular Directions

By Equation 26.1,

$$a = \frac{(360°)(X)}{k}.$$

1. Given a time of day of 06:00 hr (which is one-fourth of the 24-hour clock and should correspond, therefore, to one-fourth of a circle),

$$X = 6 \text{ hr}, k = 24 \text{ hr}, \text{ and}$$
$$a = (360°)(6 \text{ hr})/24 \text{ hr} = 90°.$$

2. Given a time of day of 06:15 hr,

$$X = 6.25 \text{ hr}, k = 24 \text{ hr}, \text{ and}$$
$$a = (360°)(6.25 \text{ hr})/24 \text{ hr} = 93.75°.$$

3. Given the 14th day of February, being the 45th day of the year,

$$X = 45 \text{ days}, k = 365 \text{ days}, \text{ and}$$
$$a = (360°)(45 \text{ days})/365 \text{ days} = 44.38°.$$

for which we wish to calculate an arithmetic mean. The arithmetic mean calculation of $(10° + 30° + 350°)/3 = 390°/3 = 130°$ is clearly absurd, for all data are northerly directions and the computed mean is southeasterly.

This chapter introduces some basic considerations useful in calculating descriptive statistics for circular data, and Chapter 27 discusses tests of hypotheses.* Statistical methods have also been developed for data that occur on a sphere (which are of particular interest to earth scientists).‡

2 GRAPHICAL PRESENTATION OF CIRCULAR DATA

Circular data are often presented as a scatter diagram, where the scatter is shown on the circumference of a circle. Figure 26.2 shows such a graph for the data of Example 26.2. If frequencies of data are too large to be plotted conveniently on a scatter diagram, then a bar graph, or histogram, may be drawn. This is demonstrated in Figure 26.3, for the data presented in Example 26.3. Recall that in a histogram, the length, as well as the area, of each bar is an indication of the frequency observed at each plotted value of the variable (Section 1.3). Occasionally, as shown in Figure 26.4, a histogram is seen presented with sectors, instead of bars, composing the graph; this is sometimes called a *rose diagram*. Here, the radii forming the outer boundaries

*More extensive reviews of methods for circular data include Batschelet†(1965, 1972, 1981), Fisher (1993), Jammalamadaka and SenGupta (2001), Mardia (1972a, 1981), and Mardia and Jupp (2000).

†Edward Batschelet (1914–1979), Swiss biomathematician, was one of the most influential writers in developing, explaining, and promulgating circular statistical methods, particularly among biologists.

‡Notable discussions of the statistical analysis of sperical data are as follows: Batschelet (1981: Chapter 11); Fisher, Lewis, and Embleton (1987); Mardia (1972a: Chapters 8 and 9); Mardia and Jupp (2000: Chapters 9, 10, etc.); Upton and Fingleton (1989: Chapter 10); and Watson (1983).

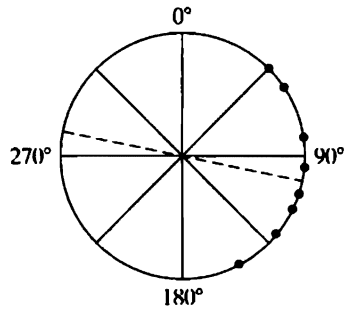


FIGURE 26.2: A circular scatter diagram for the data of Example 26.2. (The dashed line defines the median as explained in Section 26.6.)

EXAMPLE 26.2 A Sample of Circular Data. These Data Are Plotted in Figure 26.2

Eight trees are found leaning in the following compass directions: 45°, 55°, 81°, 96°, 110°, 117°, 132°, 154°.

of the sectors are proportional to the frequencies being represented, but the areas of the sectors are not. Since it is likely that the areas will be judged by eye to represent the frequencies, the reader of the graph is being misled, and this type of graphical presentation is not recommended. However, a true-area rose diagram can be obtained by plotting the square roots of frequencies as radii.*

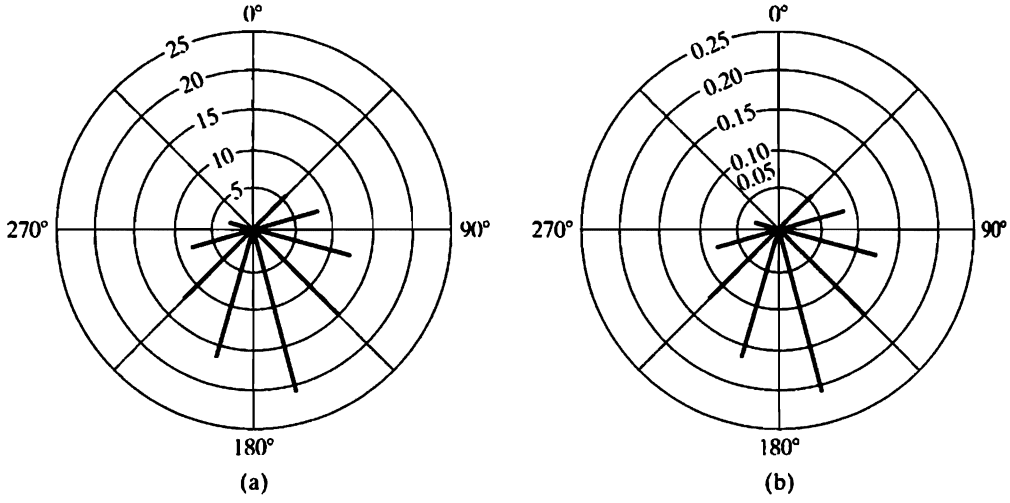


FIGURE 26.3: (a) Circular histogram for the data of Example 26.3 where the concentric circles represent frequency increments of 5. (b) A relative frequency histogram for the data of Example 26.3 with the concentric circles representing relative frequency increments of 0.05.

*The earliest user of rose diagrams was the founder of modern nursing and pioneer social and health statistician, Florence Nightingale (1820–1910), in 1858. She employed true-area colored diagrams, which she termed "coxcombs," to indicate deaths from various causes over months of the year (Fisher, 1993: 5–6). (Nightingale gained much fame for her work with the British Army during the Crimean War.)

EXAMPLE 26.3 A Sample of Circular Data, Presented as a Frequency Table, Where a_i Is an Angle and f_i Is the Observed Frequency of a_i. These Data Are Plotted in Figure 26.3

a_i (deg)	f_i	Relative f_i
0–30	0	0.00
30–60	6	0.06
60–90	9	0.09
90–120	13	0.12
120–150	15	0.14
150–180	22	0.21
180–210	17	0.16
210–240	12	0.11
240–270	8	0.08
270–300	3	0.03
300–330	0	0.00
330–360	0	0.00
n = 105		Total = 1.00

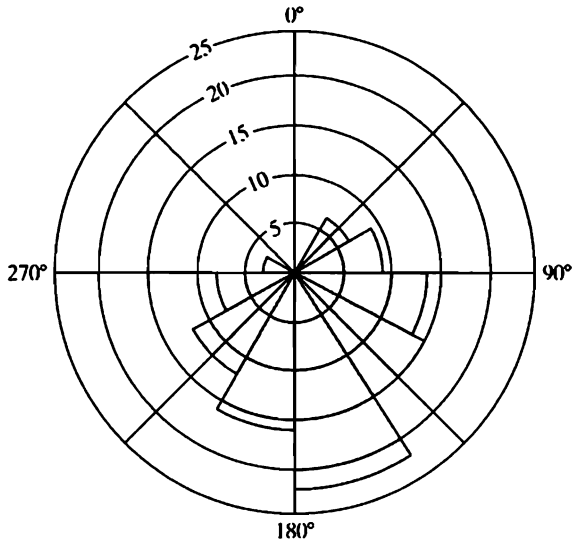


FIGURE 26.4: A rose diagram of the data of Example 26.3, utilizing sectors instead of bars. This procedure is not recommended unless square roots of the frequencies are employed (see Section 26.2).

Another manner of expressing circular frequency distributions graphically is shown in Figure 26.5. Here, the length of each bar of the histogram represents a frequency, as in Figure 26.3(a), but the bars extend from the circumference of a circle instead of from the center. In addition, an arrow extending from the circle's center toward the circumference indicates both the direction and the length of the mean vector, and this expresses visually both the mean angle and a measure of data concentration (as explained in Sections 26.4 and 26.5).

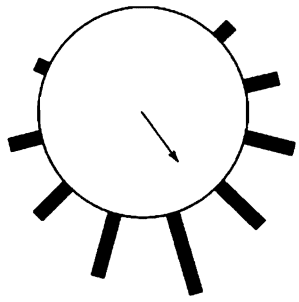


FIGURE 26.5: Circular histogram for the data of Example 26.3, including an arrow depicting the mean angle ($\bar{a}$) and a measure of dispersion (r).

A histogram of circular data can also be plotted as a linear histogram (see Section 1.3), with degrees on the horizontal axis and frequencies (or relative frequencies) on the vertical axis. But the impression on the eye may vary with the arbitrary location of the origin of the horizontal axis, and (unless the range of data is small—say, no more than 180°) the presentation of Figure 26.3 or Figure 26.5 is preferable.

26.3 TRIGONOMETRIC FUNCTIONS

A great many of the procedures that follow in this chapter and the next require the determination of basic trigonometric functions. Consider that a circle (perhaps representing a compass face) is drawn on rectangular coordinates (as on common graph paper) with the center as the origin (i.e., zero) of both a vertical X axis and a horizontal Y axis; this is what is done in Figure 26.6.

There are two methods that can be used to locate any point on a plane (such as a sheet of paper). One is to specify X and Y (as done previously in discussing regression and correlation in Chapters 17 and 19). However, with circular data it is conventional to use a vertical, instead of a horizontal, X axis. This second method

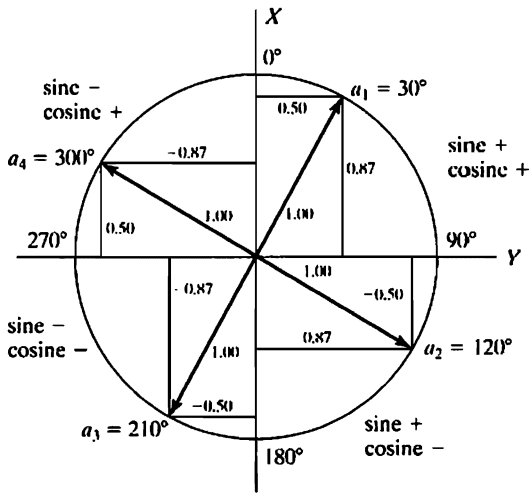


FIGURE 26.6: A unit circle, showing four points and their polar (a and r) and rectangular (X and Y) coordinates.

specifies both the angle, a, with respect to some starting direction (say, clockwise from the top of the X axis, namely "north") and the straight-line distance, r, from some reference point (the center of the circle). This pair of numbers, a and r, is known as the "polar coordinates" of a point.* Thus, for example, in Figure 26.6, point 1 is uniquely identified by polar coordinates $a = 30°$ and $r = 1.00$, point 2 by $a = 120°$ and $r = 1.00$, and so on. If the radius of the circle is specified to be 1 unit, as in Figure 26.6, the circle is called a *unit circle.*

If a is negative, it is expressing a direction *counterclockwise* from zero. It may be added to 360° to yield the equivalent positive angle; thus, for example, $-60° = 360° - 60° = 300°$. An angle greater than 360° is equivalent to the number of degrees by which it exceeds 360° or a multiple of 360°. So, for example, $450° = 450° - 360° = 90°$ and $780° = 780° - 360° - 360° = 60°$.

The first-mentioned method of locating points on a graph referred to the X and Y axes. By this method, point 1 in Figure 26.6 is located by the "rectangular coordinates" $X = 0.87$ and $Y = 0.50$, point 2 by $X = -0.50$ and $Y = 0.87$, point 3 by $X = -0.87$ and $Y = -0.50$, and point 4 by $X = 0.50$ and $Y = -0.87$. The *cosine* (abbreviated "cos") of an angle is defined as the ratio of the X and the r associated with the circular measurement:

$$\cos a = \frac{X}{r}, \tag{26.2}$$

while the *sine* (abbreviated "sin") of the angle is the ratio of the associated Y and r:

$$\sin a = \frac{Y}{r}. \tag{26.3}$$

Thus, for example, the sine of a_1 in Figure 26.6 is $\sin 30° = 0.50/1.00 = 0.50$, and its cosine is $\cos 30° = 0.87/1.00 = 0.87$. Also, $\sin 120° = 0.87/1.00 = 0.87$, $\cos 120° = -0.50/1.00 = -0.50$, and so on. Sines and cosines (two of the most used "trigonometric† functions") are readily available in published tables, and many electronic calculators give them (and sometimes convert between polar and rectangular coordinates as well). The sines of 0° and 180° are zero, angles between 0° and 180° have sines that are positive, and the sines are negative for $180° < a < 360°$. The cosine is zero for 90° and 270°, with positive cosines obtained for $0° < a < 90°$ and for $270° < a < 360°$, and negative cosines for angles between 90° and 270°.

A third trigonometric function is the *tangent:*‡

$$\tan a = \frac{Y}{X} = \frac{\sin a}{\cos a}. \tag{26.5}$$

*This use of the symbol r has no relation to the r that denotes a sample correlation coefficient (Section 19.1).

†*Trigonometry* refers, literally, to the measurement of triangles (such as the triangles that emanate from the center of the circle in Figure 26.6).

‡The angle having a tangent of Y/X is known as the arctangent (abbreviated *arctan*) of Y/X. As noted at the end of Section 26.3, a given tangent can be obtained from either of two different angles. If $X \geq 0$, then $a = \arctan(Y/X)$; if $X < 0$, then $a = \arctan(Y/X) + 180°$. The *cotangent* is the reciprocal of the tangent, namely

$$\cot a = \frac{X}{Y} = \frac{\cos a}{\sin a}. \tag{26.4}$$

On the circle, two different angles have the same sine, two have the same cosine, and two have the same tangent:

$$\sin a = \sin(180° - a)$$
$$\cos a = \cos(360° - a)$$
$$\tan a = \tan(180° + a).$$

We shall see later that rectangular coordinates, X and Y, may also be used in conjunction with mean angles just as they are with individual angular measurements.*

26.4 THE MEAN ANGLE

If a sample consists of n angles, denoted as a_1 through a_n, then the mean of these angles, $\bar{a}$, is to be an estimate of the mean angle, μ_a in the sampled population. To compute the sample mean angle, $\bar{a}$, we first consider the rectangular coordinates of the mean angle:

$$X = \frac{\sum_{i=1}^{n} \cos a_i}{n} \tag{26.6}$$

and

$$Y = \frac{\sum_{i=1}^{n} \sin a_i}{n}. \tag{26.7}$$

Then, the quantity

$$r = \sqrt{X^2 + Y^2} \tag{26.8}$$

is computed;† this is the length of the mean vector, which will be further discussed in Section 26.5. The value of $\bar{a}$ is determined as the angle having the following cosine and sine:

$$\cos \bar{a} = \frac{X}{r} \tag{26.9}$$

and

$$\sin \bar{a} = \frac{Y}{r}. \tag{26.10}$$

Example 26.4 demonstrates these calculations. It is also true that

$$\tan \bar{a} = \frac{Y}{X} = \frac{\sin \bar{a}}{\cos \bar{a}}. \tag{26.11}$$

If $r = 0$, the mean angle is undefined and we conclude that there is no mean direction.

*Over time, many different symbols and abbreviations have been used for trigonometric functions. The abbreviations *sin.* and *tan.* were established in the latter half of the sixteenth century, and the periods were dropped early in the next century (Cajori, 1928–1929, Vol. II: 150, 158). The cosine was first known as the "sine of the complement"—because the cosine of a equals the sine of $90° - a$ for angles from 0° to 90°—and the English writer E. Gunter changed "complementary sine" to "cosine" and "complementary tangent" to "cotangent" in 1620 (ibid.: 157).

†This use of the symbol r has no relation to the r that denotes a sample correlation coefficient (Section 19.1).

If the circular data are times instead of angles, then the mean time corresponding to the mean angle may be determined from a manipulation of Equation 26.1:

$$\overline{X} = \frac{ka}{360^\circ}. \tag{26.12}$$

EXAMPLE 26.4 Calculating the Mean Angle for the Data of Example 26.2

a_i (deg)	$\sin a_i$	$\cos a_i$
45	0.70711	0.70711
55	0.81915	0.57358
81	0.98769	0.15643
96	0.99452	−0.10453
110	0.93969	−0.34202
117	0.89101	−0.45399
132	0.74315	−0.66913
154	0.43837	−0.89879
	$\sum \sin a_i = 6.52069$	$\sum \cos a_i = -1.03134$
	$Y = \frac{\sum \sin a_i}{n}$	$X = \frac{\sum \cos a_i}{n}$
	$= 0.81509$	$= -0.12892$

$n = 8$

$$r = \sqrt{X^2 + Y^2} = \sqrt{(-0.12892)^2 + (0.81509)^2} = \sqrt{0.68099} = 0.82522$$

$$\cos \bar{a} = \frac{X}{r} = \frac{-0.12892}{0.82522} = -0.15623$$

$$\sin \bar{a} = \frac{Y}{r} = \frac{0.81509}{0.82522} = 0.98772$$

The angle with this sine and cosine is $\bar{a} = 99^\circ$.

So, to determine a mean time of day, $\overline{X}$, from a mean angle, $\bar{a}$, $\overline{X} = (24 \text{ hr})(\bar{a})/360^\circ$. For example, a mean angle of 270° on a 24-hour clock corresponds to $\overline{X} = (24 \text{ hr})(270^\circ)/360^\circ = 18{:}00$ hr (also denoted as 6:00 P.M.).

If the sine of a is S, then it is said that the *arcsine* of S is a; for example, the sine of 30° is 0.50, so the arcsine of 0.50 is 30°. If the cosine of a is C, then the *arccosine* of C is a; for example, the cosine of 30° is 0.866, so the arccosine of 0.866 is 30°. And, if the tangent of a is T, then the *arctangent* of T is a; for example, the tangent of 30° is 0.577, so the arctangent of 0.577 is 30°*

(a) Grouped Data. Circular data are often recorded in a frequency table (as in Example 26.3). For such data, the following computations are convenient alternatives

*The arcsine is also referred to as the "inverse sine" and can be abbreviated "arcsin" or $\sin^{-1}$; the arccosine can be designated as "arccos" or $\cos^{-1}$, and the arctangent as "arctan" or $\tan^{-1}$.

to Equations 26.6 and 25.7, respectively:

$$X = \frac{\sum f_i \cos a_i}{n} \tag{26.13}$$

$$Y = \frac{\sum f_i \sin a_i}{n} \tag{26.14}$$

(which are analogous to Equation 3.3 for linear data). In these equations, a_i is the midpoint of the measurement interval recorded (e.g., $a_2 = 45°$ in Example 26.3, which is the midpoint of the second recorded interval, $30 - 60°$), f_i is the frequency of occurrence of data within that interval (e.g., $f_2 = 6$ in that example), and $n = \sum f_i$. Example 26.5 demonstrates the determination of $\bar{a}$ for the grouped data (where f_i is not 0) of Example 26.3.

EXAMPLE 26.5 Calculating the Mean Angle for the Data of Example 26.3

a_i	f_i	$\sin a_i$	$f_i \sin a_i$	$\cos a_i$	$f_i \cos a_i$
45°	6	0.70711	4.24266	0.70711	4.24266
75°	9	0.96593	8.69337	0.25882	2.32938
105°	13	0.96593	12.55709	−0.25882	−3.36466
135°	15	0.70711	10.60665	−0.70711	−10.60665
165°	22	0.25882	5.69404	−0.96593	−21.25046
195°	17	−0.25882	−4.39994	−0.96593	−16.42081
225°	12	−0.70711	−8.48532	−0.70711	−8.48532
255°	8	−0.96593	−7.72744	−0.25882	−2.07056
285°	3	−0.96593	−2.89779	0.25882	0.77646

$n = 105$ $\quad \sum f_i \sin a_i = 18.28332$ $\quad \sum f_i \cos a_i = -54.84996$

$$Y = \frac{\sum f_i \sin a_i}{n} = 0.17413 \qquad X = \frac{\sum f_i \cos a_i}{n} = -0.52238$$

$$r = \sqrt{X^2 + Y^2} = \sqrt{(-0.52238)^2 + (0.17413)^2} = 0.55064$$

$$\cos \bar{a} = \frac{X}{r} = \frac{-0.52238}{0.55064} = -0.94868$$

$$\sin \bar{a} = \frac{Y}{r} = \frac{0.17413}{0.55064} = 0.31623$$

The angle with this cosine and sine is $\bar{a} = 162°$.

There is a bias in computing r from grouped data, in that the result is too small. A correction for this is available (Batschelet, 1965: 16–17, 1981: 37–40; Mardia, 1972a: 78–79; Mardia and Jupp, 2000: 23; Upton and Fingleton, 1985: 219), which may be applied when the distribution is unimodal and does not deviate greatly from symmetry. For data grouped into equal intervals of d degrees each,

$$r_c = cr, \tag{26.15}$$

where r_c is the corrected r, and c is a correction factor,

$$c = \frac{\frac{d\pi}{360^\circ}}{\sin\left(\frac{d}{2}\right)}. \tag{26.16}$$

The correction is insignificant for intervals smaller than 30°. This correction is for the quantity r; the mean angle, $\bar{a}$, requires no correction for grouping.

ANGULAR DISPERSION

When dealing with circular data, it is desirable to have a measure, analogous to those of Chapter 4 for a linear scale, to describe the dispersion of the data.

We can define the *range* in a circular distribution of data as the smallest arc (i.e., the smallest portion of the circle's circumference) that contains all the data in the distribution. For example, in Figure 26.7a, the range is zero; in Figure 26.7b, the shortest arc is from the data point at 38° to the datum at 60°, making the range 22°; in Figure 26.7c, the data are found from 10° to 93°, with a range of 83°; in Figure 26.7d, the data run from 322° to 135°, with a range of 173°; in Figure 26.7e, the shortest arc containing all the data is that running clockwise from 285° to 171°, namely an arc of 246°; and in Figure 26.7f, the range is 300°. For the data of Example 26.4, the range is 109° (as the data run from 45° to 154°).

Another measure of dispersion is seen by examining Figure 26.7; the value of r (by Equation 26.8, and indicated by the length of the broken line) varies inversely with the amount of dispersion in the data. Therefore, r is a measure of concentration. It has no units and it may vary from 0 (when there is so much dispersion that a mean angle cannot be described) to 1.0 (when all the data are concentrated at the same direction). (An r of 0 does not, however, necessarily indicate a uniform distribution. For example, the data of Figure 26.8 would also yield $r = 0$). A line specified by both its direction and length is called a *vector*, so r is sometimes called the length of the mean vector.

In Section 3.1 the mean on a linear scale was noted to be the center of gravity of a group of data. Similarly, the tip of the mean vector (i.e., the quantity r), in the direction of the mean angle ($\bar{a}$) lies at the center of gravity. (Consider that each circle in Figure 26.7 is a disc of material of negligible weight, and each datum is a dot of unit weight. The disc, held parallel to the ground, would balance at the tip of the arrow in the figure. In Figure 26.7f, $r = 0$ and the center of gravity is the center of the circle.)

Because r is a measure of concentration, $1-r$ is a measure of dispersion. Lack of dispersion would be indicated by $1-r = 0$, and maximum dispersion by $1-r = 1.0$. As a measure of dispersion reminiscent of those for linear data, Mardia (1972a: 45), Mardia and Jupp (2000: 18), and Upton and Fingleton (1985: 218) defined *circular variance*:

$$S^2 = 1 - r. \tag{26.17}$$

Batschelet (1965, 1981: 34) defined *angular variance:*

$$s^2 = 2(1 - r) \tag{26.18}$$

as being a closer analog to linear variance (Equation 4.15). While S^2 may range from 0 to 1, and s^2 from 0 to 2, an S^2 of 1 or an s^2 of 2 does not necessarily indicate a uniform distribution of data around the circle because, as noted previously, $r = 0$

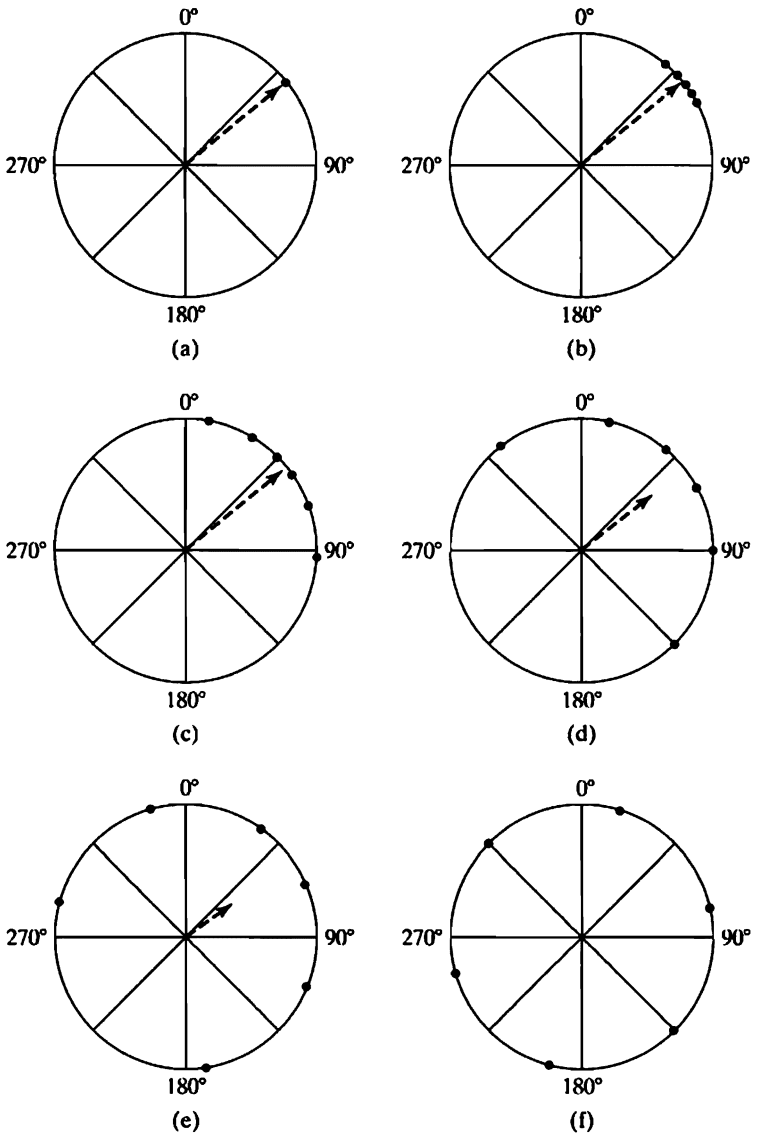


FIGURE 26.7: Circular distributions with various amounts of dispersion. The direction of the broken-line arrow indicates the mean angle, which is 50° in each case, and the length of the arrow expresses r (Equation 26.8), a measure of concentration. The magnitude of r varies inversely with the amount of dispersion, and that the values of s and s_0 vary directly with the amount of dispersion. (a) $r = 1.00, s = 0°, s_0 = 0°$. (b) $r = 0.99, s = 8.10°, s_0 = 8.12°$. (c) $r = 0.90, s = 25.62°, s_0 = 26.30°$. (d) $r = 0.60, s = 51.25°, s_0 = 57.91°$. (e) $r = 0.30, s = 67.79°, s_0 = 88.91$. (f) $r = 0.00, s = 81.03°, s_0 = \infty$. (By the method of Section 27.1, the magnitude of r is statistically significant in Figs. a, b, and c, but not in d, e, and f.)

does not necessarily indicate a uniform distribution. The variance measure

$$s_0^2 = -2 \ln r \tag{26.19}$$

is a statistic that ranges from 0 to ∞ (Mardia, 1972a: 24). These three dispersion measures are in radians squared. To express them in degrees squared, multiply each by $(180°/\pi)^2$.

Measures analogous to the linear standard deviation include the "mean angular deviation," or simply the *angular deviation*, which is

$$s = \frac{180^\circ}{\pi}\sqrt{2(1 - r)}, \tag{26.20}$$

in degrees.* This ranges from a minimum of zero (e.g., Fig. 26.7a) to a maximum of 81.03° (e.g., Fig. 26.7f).† Mardia (1972a: 24, 74) defines *circular standard deviation* as

$$s_0 = \frac{180^\circ}{\pi}\sqrt{-2\ln r} \tag{26.21}$$

degrees; or, employing common, instead of natural, logarithms:

$$s_0 = \frac{180^\circ}{\pi}\sqrt{-4.60517\log r} \tag{26.22}$$

degrees. This is analogous to the standard deviation, s, on a linear scale (Section 4.5) in that it ranges from zero to infinity (see Fig. 26.7). For large r, the values of s and s_0 differ by no more than 2 degrees for r as small as 0.80, by no more than 1 degree for r as small as 0.87, and by no more than 0.1 degree for r as small as 0.97. It is intuitively reasonable that a measure of angular dispersion should have a finite upper limit, so s is the dispersion measure preferred in this book. Appendix Tables B.32 and B.33 convert r to s and s_0, respectively. If the data are grouped, then s and s_0 are biased in being too high, so r_c (by Equation 26.15) can be used in place of r. For the data of Example 26.4 (where $r = 0.82522$), $s = 34^\circ$ and $s_0 = 36^\circ$; for the data of Example 26.5 (where $r = 0.55064$), $s = 54^\circ$ and $s_0 = 63^\circ$.

Dispersion measures analogous to the linear mean deviation (Section 4.3) utilize absolute deviations of angles from the mean or median (e.g., Fisher, 1993: 36).

Measures of symmetry and kurtosis on a circular scale, analogous to those that may be calculated on a linear scale (Section 6.5), are discussed by Batschelet (1965: 14–15, 1981: 54–44); Mardia (1972a: 36–38, 74–76), and Mardia and Jupp (2000: 22, 31, 145–146).

THE MEDIAN AND MODAL ANGLES

In a fashion analogous to considerations for linear scales of measurement (Sections 3.2 and 3.3), we can determine the sample median and mode of a set of data on a circular scale.

To find the *median angle*, we first determine which diameter of the circle divides the data into two equal-sized groups. The median angle is the angle indicated by that diameter's radius that is nearer to the majority of the data points. If n is even, the median is nearly always midway between two of the data. In Example 26.2, a diameter extending from 103° to 289° divides the data into two groups of four each (as indicated by the dashed line in Fig. 26.2). The data are concentrated around 103°, rather than 289°, so the sample median is 103°. If n is odd, the median will almost always be one of the data points or 180° opposite from one. If the data in Example 26.2 had been seven in number—with the 45° lacking—then the diameter line would have run through 110° and 290°, and the median would have been 110°.

Though uncommon, it is possible for a set of angular data to have more than one angle fit this definition of median. In such a case, Otieno and Anderson-Cook (2003)

*Simply delete the constant, $180^\circ/\pi$, in this and in the following equations if the measurement is desired in radians rather than degrees.

†This is a range of 0 to 1.41 radians.

recommend calculating the estimate of the population median as the mean of the two or more medians fitting the definition. Mardia (1972a: 29–30) shows how the median is estimated, analogously to Equation 3.5, when it lies within a group of tied data. If a sample has the data equally spaced around the circle (as in Fig. 26.7f), then the median, as well as the mean, is undefined.

The *modal angle* is defined as is the mode for linear scale data (Section 3.3). Just as with linear data, there may be more than one mode or there may be no modes.

26.7 CONFIDENCE LIMITS FOR THE POPULATION MEAN AND MEDIAN ANGLES

The confidence limits of the mean of angles may be expressed as

$$\bar{a} \pm d. \tag{26.23}$$

That is, the lower confidence limit is $L_1 = \bar{a} - d$ and the upper confidence limit is $L_2 = \bar{a} + d$. For n as small as 8, the following method may be used (Upton, 1986). For $r \leq 0.9$,

$$d = \arccos\left[\frac{\sqrt{\dfrac{2n(2R^2 - n\chi^2_{\alpha,1})}{4n - \chi^2_{\alpha,1}}}}{R}\right] \tag{26.24}$$

and for $r \geqslant 0.9$,

$$d = \arccos\left[\frac{\sqrt{n^2 - (n^2 - R^2)e^{\chi^2_{\alpha,1}/n}}}{R}\right], \tag{26.25}$$

where

$$R = nr. \tag{26.26}$$

This is demonstrated in Examples 26.6 and 27.3.* As this procedure is only approximate, d—and confidence limits—should not be expressed to fractions of a degree. This procedure is based on the von Mises distribution, a circular analog of the normal distribution.† Batschelet (1972: 86; Zar, 1984: 665–666) presents nomograms that yield similar results.

*As shown in these examples, a given cosine is associated with two different angles: a and $360° - a$; the smaller of the two is to be used.

†Richard von Mises (1883–1953), a physicist and mathematician, was born in the Austro-Hungarian Empire and moved to Germany, Turkey, and the United States because of two world wars (Geiringer, 1978). He introduced this distribution (von Mises, 1918), and it was called "circular normal" by Gumbel, Greenwood, and Durand (1953), and later by others, because of its similarity to the linear-scale normal distribution. It is described mathematically by Batschelet (1981: 279–282), Fisher (1993: 48–56), Jammalamadaka and SenGupta (2001: 35–42), Mardia (1972a: 122–127), Mardia and Jupp (2000: 36, 68–71, 85–88, 167–173), and Upton and Fingleton (1985: 277–229).

EXAMPLE 26.6 The 95% Confidence Interval for the Data of Example 26.4

$n = 8$

$\bar{a} = 99°$

$r = 0.82522$

$R = nr = (8)(0.82522) = 6.60108$

$\chi^2_{0.05,1} = 3.841$

Using Equation 26.24:

$$d = \arccos\left[\frac{\sqrt{\frac{2n\left(2R^2 - n\chi^2_{\alpha,1}\right)}{4n - \chi^2_{\alpha,1}}}}{R}\right]$$

$$= \arccos\left[\frac{\sqrt{\frac{2(8)[2(6.60108)^2 - 8(3.841)]}{4(8) - 3.841}}}{6.60108}\right]$$

$$= \arccos 0.89883$$

$$= 26° \text{ or } 360° - 26° = 334°.$$

The 95% confidence interval is $99° \pm 26°$; $L_1 = 73°$ and $L_2 = 125°$.

Confidence limits for the median angle may be obtained by the procedure of Section 24.8. The median is determined as in Section 26.6. Then the data are numbered 1 through n, with 1 representing the datum farthest from the median in a counterclockwise direction and n denoting the datum farthest in a clockwise direction.

AXIAL DATA

Although not common, circular data may be encountered that are bimodal and have their two modes diametrically opposite on the circle. An example of such data is shown in Figure 26.8, where there is a group of seven angular data opposite a group of eight data (with the data shown as small black circles). Such measurements are known as *axial data*, and it is desirable to calculate the angle that best describes the circle diameter that runs through the two groups of data. Determining the mean angle ($\bar{a}$) of the diameter in one direction means that the mean angle of the diameter in the other direction is $\bar{a} + 180°$.

These 15 measurements are given in Example 26.7 and resulted from the following experiment: A river flows in a generally southeasterly–northwesterly direction. Fifteen fish, of a species that prefers shallow water at river edges, were released in the middle of the river. Then it was recorded which direction from the point of release each of the fish traveled.

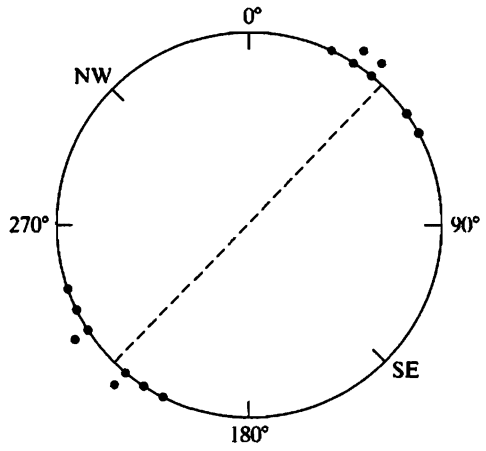


FIGURE 26.8: A bimodal circular distribution, showing the data of Example 26.7.

EXAMPLE 26.7 The Data of Fig. 26.8, and Their Axial Mean

a_i (degrees)	modulo $2a_i$ (degrees)	$\sin 2a_i$	$\cos 2a_i$
35	70	0.93964	0.34202
40	80	0.98481	0.17365
40	80	0.98481	0.17365
45	90	1.00000	0.00000
45	90	1.00000	0.00000
55	110	0.93969	−0.34202
60	120	0.86602	−0.50000
215	70	0.93964	0.34202
220	80	0.98481	0.17365
225	90	1.00000	0.00000
225	90	1.00000	0.00000
235	110	0.93969	−0.34202
235	110	0.93969	−0.34202
240	120	0.86602	−0.50000
245	130	0.76604	−0.64279
	$n = 15$	$\Sigma \sin 2a_i$	$\Sigma \cos 2a_i$
		$= 14.15086$	$= -1.46386$
		$Y = -0.94339$	$X = -0.09759$

$r = 0.94842$

$\sin \bar{a} = 0.99470$

$\cos \bar{a} = -0.10290$

The angle ($2\bar{a}$) with this sine and cosine is 95.9°; so $\bar{a} = 95.9°/2 = 48°$.
Also: $\tan 2\bar{a} = Y/X = -9.66687$; and, since $C < 0$, $\bar{a} = \arctan -9.66687 + 180° = -84.1° + 180° = 95.9°$; so $\bar{a} = 48°$.

The statistical procedure is to calculate the mean angle (Section 26.4) after doubling each of the data (that is, to find the mean of $2a_i$). It will be noted that doubling of an angle greater than 180° will result in an angle greater than 360°; in that case, 360° is subtracted from the doubled angle. (This results in angles that are said to be "modulo 360°.") The doubling of angles for axial data is also appropriate for calculating other statistics, such as those in Sections 26.5–26.7, and for the statistical testing in Chapter 27.

The mean angle of 48° determined in Example 26.7 indicates that a line running from 48° to 228° (that is, from 48° to 48° + 180°) is the axis of the bimodal data (shown as a dashed line in Fig. 26.8).

THE MEAN OF MEAN ANGLES

If a mean is determined for each of several groups of angles, then we have a set of mean angles. Consider the data in Example 26.8. Here, a mean angle, $\bar{a}$, has been calculated for each of k samples of circular data, using the procedure of Section 26.4. If, now, we desire to determine the grand mean of these several means, it is not appropriate to consider each of the sample means as an angle and employ the method of Section 26.4. To do so would be to assume that each mean had a vector length, r, of 1.0 (i.e., that an angular deviation, s, of zero was the case in each of the k samples), a most unlikely situation. Instead, we shall employ the procedure promulgated by Batschelet* (1978, 1981: 201–202), whereby the grand mean has rectangular coordinates

$$\overline{X} = \frac{\sum_{j=1}^{k} X_j}{k} \tag{26.27}$$

and

$$\overline{Y} = \frac{\sum_{j=1}^{k} Y_j}{k}, \tag{26.28}$$

where X_j and Y_j are the quantities X and Y, respectively, applying Equations 26.6 and 26.7 to sample j; k is the total number of samples. If we do not have X and Y for each sample, but we have $\bar{a}$ and r (polar coordinates) for each sample, then

$$\overline{X} = \frac{\sum_{j=1}^{k} r_j \cos \bar{a}_j}{k} \tag{26.29}$$

and

$$\overline{Y} = \frac{\sum_{j=1}^{k} r_j \sin \bar{a}_j}{k}. \tag{26.30}$$

*Batschelet (1981: 198) refers to statistical analysis of a set of angles as a first-order analysis and the analysis of a set of mean angles as a second-order analysis.

Having obtained $\overline{X}$ and $\overline{Y}$, we may substitute them for X and Y, respectively, in Equations 26.8, 26.9, and 26.10 (and 26.11, if desired) in order to determine $\bar{a}$, which is the grand mean. For this calculation, all n_j's (sample sizes) should be equal, although unequal sample sizes do not appear to seriously affect the results (Batschelet, 1981: 202).

Figure 26.9 shows the individual means and the grand mean for Example 26.8. (By the hypothesis testing of Section 27.1, we would conclude that there is in this example no significant mean direction for Samples 5 and 7. However, the data from these two samples should not be deleted from the present analysis.)

Batschelet (1981: 144, 262–265) discussed confidence limits for the mean of mean angles.

EXAMPLE 26.8 The Mean of a Set of Mean Angles

Under particular light conditions, each of seven butterflies is allowed to fly from the center of an experimental chamber ten times. From the procedures of Section 26.4, the values of $\bar{a}$ and r for each of the seven samples of data are as follows.

$k = 7; \quad n = 10$

Sample (j)	$\bar{a}_j$	r_j	$X_j = r_j \cos \bar{a}_j$	$Y_j = r_j \sin \bar{a}_j$
1	160°	0.8954	−0.84140	0.30624
2	169	0.7747	−0.76047	0.14782
3	117	0.4696	−0.21319	0.41842
4	140	0.8794	−0.67366	0.56527
5	186	0.3922	−0.39005	−0.04100
6	134	0.6952	−0.48293	0.50009
7	171	0.3338	−0.32969	0.05222
			−3.69139	1.94906

$$\overline{X} = \frac{\sum r_j \cos \bar{a}_j}{k} = \frac{-3.69139}{7} = -0.52734$$

$$\overline{Y} = \frac{\sum r_j \sin \bar{a}_j}{k} = \frac{1.94906}{7} = 0.27844$$

$$r = \sqrt{\overline{X}^2 + \overline{Y}^2} = \sqrt{0.35562} = 0.59634$$

$$\cos \bar{a} = \frac{\overline{X}}{r} = \frac{-0.52734}{0.59634} = -0.88429$$

$$\sin \bar{a} = \frac{\overline{Y}}{r} = \frac{0.27844}{0.59634} = 0.46691$$

Therefore, $\bar{a} = 152°$.

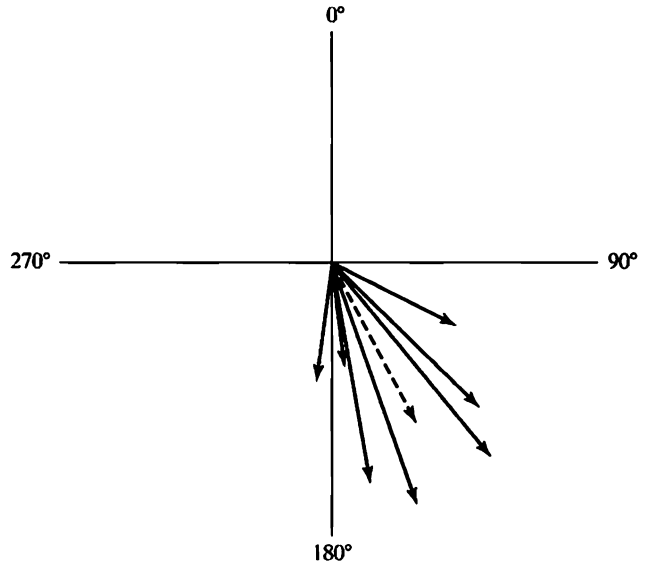


FIGURE 26.9: The data of Example 26.8. Each of the seven vectors in this sample is itself a mean vector. The mean of these seven means is indicated by the broken line.

EXERCISES

26.1. Twelve nests of a particular bird species were recorded on branches extending in the following directions from the trunks of trees:

Direction		*Frequency*
N:	0°	2
NE:	45°	4
E:	90°	3
SE:	135°	1
S:	180°	1
SW:	225°	1
W:	270°	0
NW:	315°	0

(a) Compute the sample mean direction.
(b) Compute the angular deviation for the data.
(c) Determine 95% confidence limits for the population mean.
(d) Determine the sample median direction.

26.2. A total of 15 human births occurred as follows:

1:15 A.M. 4:40 A.M. 5:30 A.M. 6:50 A.M.
2:00 A.M. 11:00 A.M. 4:20 A.M. 5:10 A.M.
4:30 A.M. 5:15 A.M. 10:30 A.M. 8:55 A.M.
6:10 A.M. 2:45 A.M. 3:10 A.M.

(a) Compute the mean time of birth.
(b) Compute the angular deviation for the data.
(c) Determine 95% confidence limits for the population mean time.
(d) Determine the sample median time.

CHAPTER 27

Circular Distributions: Hypothesis Testing

Armed with the procedures in Chapter 26 and the information contained in the basic statistics of circular distributions (primarily $\bar{a}$ and r), we can now examine a number of methods for testing hypotheses about populations measured on a circular scale.

27.1 TESTING SIGNIFICANCE OF THE MEAN ANGLE

(a) The Rayleigh Test for Uniformity. We can place more confidence in $\bar{a}$ as an estimate of the population mean angle, μ_a, if s is small, than if it is large. This is identical to stating that $\bar{a}$ is a better estimate of μ_a if r is large than if r is small. What is desired is a method of asking whether there is, in fact, a mean direction for the population of data that were sampled, for even if there is no mean direction (i.e., the circular distribution is uniform) in the population, a random sample might still display a calculable mean. The test we require is that concerning H_0: The sampled population is uniformly distributed around a circle versus H_A: The population is not a uniform circular distribution. This may be tested by the *Rayleigh test**. As circular uniformity implies there is no mean direction, the Rayleigh test may also be said to test H_0: $\rho = 0$ versus H_A: $\rho \neq 0$, where ρ is the population mean vector length.

*Named for Lord Rayleigh [John William Strutt, Third Baron Rayleigh (1842–1919)], a physicist and applied mathematician who gained his greatest fame for discovering and isolating the chemical element argon (winning him the Nobel Prize in physics in 1904), although some of his other contributions to physics were at least as important (Lindsay, 1976). He was a pioneering worker with directional data beginning in 1880 (Fisher, 1993: 10; Moore, 1980; Rayleigh, 1919).

The Rayleigh test asks how large a sample r must be to indicate confidently a nonuniform population distribution. A quantity referred to as "Rayleigh's R" is obtainable as

$$R = nr, \tag{27.1}$$

and the so-called "Rayleigh's z" may be utilized for testing the null hypothesis of no population mean direction:

$$z = \frac{R^2}{n} \quad \text{or} \quad z = nr^2. \tag{27.2}$$

Appendix Table B.34 presents critical values of $z_{\alpha,n}$. Also an excellent approximation of the probability of Rayleigh's R is*

$$P = \exp\left[\sqrt{1 + 4n + 4(n^2 - R^2)} - (1 + 2n)\right] \tag{27.4}$$

(derived from Greenwood and Durand, 1955). This calculation is accurate to three decimal places for n as small as 10 and to two decimal places for n as small as 5.† The Rayleigh test assumes sampling from a von Mises distribution, a circular analog of the linear normal distribution. (See von Mises footnote to Section 26.7.)

If H_0 is rejected by Rayleigh's test, we may conclude that there is a mean population direction (see Example 27.1), and if H_0 is not rejected, we may conclude the population distribution to be uniform around the circle; but only if we may assume that the population distribution does not have more than one mode. (For example, the data in Example 26.7 and Figure 26.8 would result in a Rayleigh test failing to reject H_0. While these data have no mean direction, they are not distributed uniformly around the circle, and they are not unimodal.)

EXAMPLE 27.1 Rayleigh's Test for Circular Uniformity, Applied to the Data of Example 26.2

These data are plotted in Figure 26.2.

H_0: $\rho = 0$ (i.e., the population is uniformly distributed around the circle).

H_A: $\rho \neq 0$ (i.e., the population is not distributed uniformly around the circle).

Following Example 26.4:

$n = 8$

$r = 0.82522$

$R = nr = (8)(0.82522) = 6.60176$

$$z = \frac{R^2}{n} = \frac{(6.60176)^2}{8} = 5.448.$$

Using Appendix Table B.34, $z_{0.05,8} = 2.899$. Reject H_0. $0.001 < P < 0.002$

*Recall the following notation:

$$\exp[C] = e^C. \tag{27.3}$$

†A simpler, but less accurate, approximation for P is to consider $2z$ as a chi-square with 2 degrees of freedom (Mardia, 1972a: 113; Mardia and Jupp, 2000: 92). This is accurate to two decimal places for n as small as about 15.

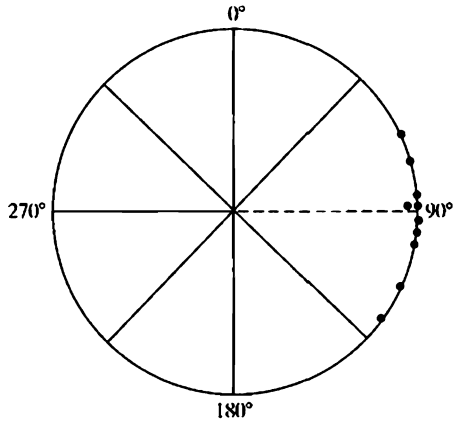


FIGURE 27.1: The data for the V test of Example 27.2. The broken line indicates the expected mean angle (94°).

Section 26.8 explains how axially bimodal data—such as in Figure 26.8—can be transformed into unimodal data, thereafter to be subjected to Rayleigh testing and other procedures requiring unimodality. What is known as "Rao's spacing test" (Batschelet, 1981: 66–69; Rao, 1976) is particularly appropriate when circular data are neither unimodal nor axially bimodal, and Russell and Levitin (1994) have produced excellent tables for its use.

(b) Modified Rayleigh Test for Uniformity versus a Specified Mean Angle. The Rayleigh test looks for any departure from uniformity. A modification of that test (Durand and Greenwood, 1958; Greenwood and Durand, 1955) is available for use when the investigator has reason to propose, *in advance*, that if the sampled distribution is not uniform it will have a specified mean direction. In Example 27.2 (and presented graphically in Figure 27.1), ten birds were released at a site directly west of their home. Therefore, the statistical analysis may include the suspicion that such birds will tend to fly directly east (i.e., at an angle of 90°). The testing procedure considers H_0: The population directions are uniformly distributed versus H_A: The directions in the population are not uniformly distributed and $\mu_a = 90°$. By using additional information, namely the proposed mean angle, this test is more powerful than Rayleigh's test (Batschelet, 1972; 1981: 60).

The preceding hypotheses are tested by a modified Rayleigh test that we shall refer to as the *V test*, in which the test statistic is computed as

$$V = R\cos(\bar{a} - \mu_0), \tag{27.5}$$

where μ_0 is the mean angle proposed. The significance of V may be ascertained from

$$u = V\sqrt{\frac{2}{n}}. \tag{27.6}$$

Appendix Table B.35 gives critical values of $u_{\alpha,n}$, a statistic which, for large sample sizes, approaches a one-tailed normal deviate, $Z_{\alpha(1)}$, especially in the neighborhood of probabilities of 0.05. If the data are grouped, then R may be determined from r_c (Equation 26.15) rather than from r.

(c) One-Sample Test for the Mean Angle. The Rayleigh test and the V test are nonparametric methods for testing for uniform distribution of a population

EXAMPLE 27.2 The *V* Test for Circular Uniformity Under the Alternative of Nonuniformity and a Specified Mean Direction

H_0: The population is uniformly distributed around the circle (i.e., H_0: $\rho = 0$).

H_A: The population is not uniformly distributed around the circle (i.e., H_A: $\rho \neq 0$), but has a mean of 90°.

a_i (deg)	$\sin a_i$	$\cos a_i$
66	0.91355	0.40674
75	0.96593	0.25882
86	0.99756	0.06976
88	0.99939	0.03490
88	0.99939	0.03490
93	0.99863	0.05234
97	0.99255	0.12187
101	0.98163	0.19081
118	0.88295	0.46947
130	0.76604	0.64279
$n = 10$	$\sum \sin a_i = 9.49762$	$\sum \cos a_i = -0.67216$

$$Y = \frac{9.49762}{10} = 0.94976$$

$$X = -\frac{0.67216}{10} = -0.06722$$

$$r = \sqrt{(-0.06722)^2 + (0.94976)^2} = 0.95214$$

$$\sin \bar{a} = \frac{Y}{r} = 0.99751$$

$$\cos \bar{a} = \frac{X}{r} = -0.07060$$

$$\bar{a} = 94°.$$

$$R = (10)(0.95214) = 9.5214$$

$$V = R\cos(94° - 90°)$$

$$= 9.5214\cos(4°)$$

$$= (9.5214)(0.99756)$$

$$= 9.498$$

$$u = V\sqrt{\frac{2}{n}}$$

$$= (9.498)\sqrt{\frac{2}{10}}$$

$$= 4.248$$

Using Appendix Table B.35, $u_{0.05,10} = 1.648$. Reject H_0. $P < 0.0005$.

of data around the circle. (See Batschelet, 1981: Chapter 4, for other tests of the null hypothesis of randomness.) If it is desired to test whether the population mean angle is equal to a specified value, say μ_0, then we have a one-sample test situation analogous to that of the one-sample t test for data on a linear scale (Section 7.1). The hypotheses are

$$H_0: \mu_a = \mu_0$$

and

$$H_A: \mu_a \neq \mu_0,$$

and H_0 is tested simply by observing whether μ_0 lies within the $1 - \alpha$ confidence interval for μ_a. If μ_a lies outside the confidence interval, then H_0 is rejected. Section 26.7 describes the determination of confidence intervals for the population mean angle, and Example 27.3 demonstrates the hypothesis-testing procedure.*

EXAMPLE 27.3 The One-Sample Test for the Mean Angle, Using the Data of Example 27.2

H_0: The population has a mean of 90° (i.e., $\mu_a = 90°$).
H_A: The population mean is not 90° (i.e., $\mu_a \neq 90°$).

The computation of the following is given in Example 27.2:

$r = 0.95$

$\bar{a} = 94°$

Using Equation 26.25, for $\alpha = 0.05$ and $n = 10$:

$R = nr = (10)(0.95) = 9.5$

$\chi^2_{0.05,1} = 3.841$

$$d = \arccos\left[\frac{\sqrt{n^2 - (n^2 - R^2)e^{\chi^2_{\alpha,1}/n}}}{R}\right]$$

$$= \arccos\left[\frac{\sqrt{10^2 - (10^2 - 9.5^2)e^{3.841/10}}}{9.5}\right]$$

$$= \arccos[0.9744]$$

$$= 13°, \text{or } 360° - 13° = 347°.$$

Thus, the 95% confidence interval for μ_a is $94° \pm 13°$.

As this confidence interval does contain the hypothesized mean ($\mu_0 = 90°$), do not reject H_0.

*For demonstration purposes (Examples 27.2 and 27.3) we have applied the V test and the one-sample test for the mean angle to the same set of data. In practice this would not be done. Deciding which test to employ would depend, respectively, on whether the intention is to test for circular uniformity or to test whether the population mean angle is a specified value.

TESTING SIGNIFICANCE OF THE MEDIAN ANGLE

(a) The Hodges-Ajne Test for Uniformity. A simple alternative to the Rayleigh test (Section 27.1) is the so-called *Hodges-Ajne test*,* which does not assume sampling from a specific distribution. This is called an "omnibus test" because it works well for unimodal, bimodal, and multimodal distributions. If the underlying distribution is that assumed by the Rayleigh test, then the latter procedure is the more powerful.

Given a sample of circular data, we determine the smallest number of data that occur within a range of 180°. As shown in Example 27.4, this is readily done by drawing a line through the center of the circle (i.e., drawing a diameter) and rotating that line around the center until there is the greatest possible difference between the numbers of data on each side of the line. If, for example, the diameter line were vertical (i.e., through 0° and 180°), there would be 10 data on one side of it and 14 on the other; if the line were horizontal (i.e., through 90° and 270°), then there would be 3.5 points on one side and 20.5 points on the other; and if the diameter were rotated slightly counterclockwise from horizontal (shown as a dashed line in the figure in Example 27.4), then there would be 3 data on one side and 21 on the other, and no line will split the data with fewer data on one side and more on the other. The test statistic, which we shall call m, is the smallest number of data that can be partitioned on one side of a diameter; in Example 27.4, $m = 3$.

The probability of an m at least this small, under the null hypothesis of circular uniformity, is

$$P = \frac{(n - 2m)\binom{n}{m}}{2^{n-1}} = \frac{(n - 2m)\dfrac{n!}{m!(n - m)!}}{2^{n-1}} \tag{27.7}$$

(Hodges, 1955), using the binomial coefficient notation of Equation 24.2. Instead of computing this probability, we may refer to Appendix Table B.36, which gives critical values for m as a function of n and α. (It can be seen from this table that in order to test at the 5% significance level, we must have a sample of at least nine data.) For $n > 50$, P may be determined by the following approximation:

$$P \approx \frac{\sqrt{2\pi}}{A}\exp\left[\frac{-\pi^2}{8A^2}\right], \tag{27.8}$$

where

$$A = \frac{\pi\sqrt{n}}{2(n - 2m)} \tag{27.9}$$

(Ajne, 1968); the accuracy of this approximation is indicated at the end of Appendix Table B.36.

(b) Modified Hodges-Ajne Test for Uniformity versus a Specified Angle. Just as (in Section 27.1b) the V test is a modification of the Rayleigh test to test for circular uniformity against an alternative that proposes a specified angle, a test presented by Batschelet (1981: 64–66) is a modification of the Hodges-Ajne test to test

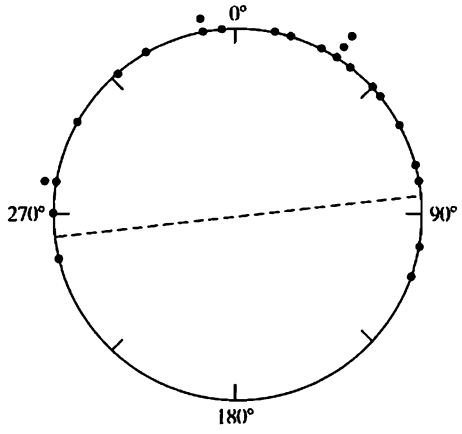
*This procedure was presented by Ajne (1968). Shortly thereafter, Bhattacharyya and Johnson (1969) showed that his test is identical to a test given by Hodges (1955) for a different purpose.

EXAMPLE 27.4 The Hodges-Ajne Test for Circular Uniformity

H_0: The population is uniformly distributed around the circle.

H_A: The population is not uniformly distributed around the circle.

This sample of 24 data is collected: 10°, 15°, 25°, 30°, 30°, 30°, 35°, 45°, 50°, 60°, 75°, 80°, 100°, 110°, 255°, 270°, 280°, 280°, 300°, 320°, 330°, 350°, 350°, 355°.



$n = 24; m = 3$

For $\alpha = 0.05$, the critical value (from Appendix Table B.36) is $m_{0.05,24} = 4$; reject H_0. $0.002 < P \leq 0.005$.

$$\text{Exact probability} = P = \frac{(n - 2m)\binom{n}{m}}{2^{n-1}} = \frac{(n - 2m)\dfrac{n!}{m!(n - m)!}}{2^{n-1}}$$

$$= \frac{(24 - 6)\dfrac{24!}{3!\,21!}}{2^{23}} = 0.0043$$

For comparison, the Rayleigh test for these data would yield $\bar{a} = 12°$, $r = 0.563, R = 13.513, z = 7.609, P < 0.001$.

nonparametrically for uniformity against an alternative that specifies an angle. For the Batschelet test, we count the number of data that lie within ±90° of the specified angle; let us call this number m' and the test statistic is

$$C = n - m'. \tag{27.10}$$

We may proceed by performing a two-tailed binomial test (Section 24.5), with $p = 0.5$ and with C counts in one category and m' counts in the other. As shown in the figure in Example 27.5, this may be visualized as drawing a diameter line perpendicular to the radius extending in the specified angle and counting the data on either side of that line.

(c) A Binomial Test. A nonparametric test to conclude whether the population median angle is equal to a specified value may be performed as follows. Count the number of observed angles on either side of a diameter through the hypothesized angle and subject these data to the binomial test of Section 24.5, with $p = 0.5$.

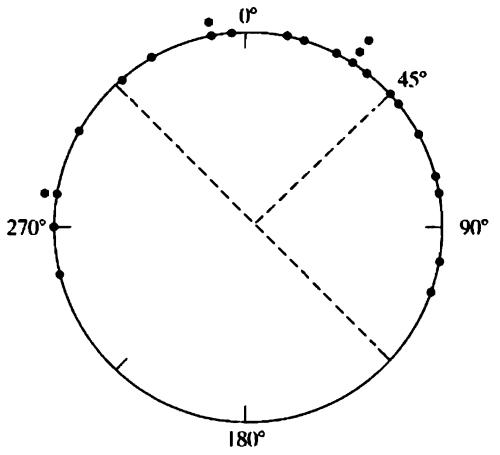
EXAMPLE 27.5 The Batschelet Test for Circular Uniformity

H_0: The population is uniformly distributed around the circle.

H_A: The population is not uniformly distributed around the circle, but is concentrated around 45°.

The data are those of Example 27.4.

$n = 24; p = 0.5; m' = 19; C = 5$



For the binomial test of Section 24.5, using Appendix Table B.27, $C_{0.05(2),24} = 6$, reject H_0, $0.005 < P \leq 0.01$; by the procedure shown in Example 24.8a, the exact probability would be $P = 0.00661$.

TESTING SYMMETRY AROUND THE MEDIAN ANGLE

The symmetry of a distribution around the median may be tested nonparametrically using the Wilcoxon paired-sample test (also known as the Wilcoxon signed-rank test) of Section 9.5. For each angle (X_i) we calculate the deviation of X_i from the median (i.e., $d_i = X_i -$ median), and we then analyze the d_i's as explained in Section 9.5. This is shown in Example 27.6 for a two-tailed test, where H_0: The underlying distribution is not skewed from the median. A one-tailed test could be used to ask whether the distribution was skewed in a specific direction from the median. (T_- would be the test statistic for H_0: The distribution is not skewed clockwise from the median, and T_+ would be the test statistic for H_0: The distribution is not skewed counterclockwise from the median.)

EXAMPLE 27.6 Testing for Symmetry Around the Median Angle, for the Data of Example 27.6

H_0: The underlying distribution is symmetrical around the median.

H_A: The underlying distribution is not symmetrical around the median.

For the 8 data below, the median is 161.5°.

Using the Wilcoxon signed-rank test:

X_i	$d_i = X_i - \text{median}$	Rank of $\lvert d_i \rvert$	Signed rank of $\lvert d_i \rvert$
97°	−64.5°	8	−8
104°	−57.5°	7	−7
121°	−40.5°	5	−5
159°	−2.5°	1.5	−1.5
164°	2.5°	1.5	1.5
172°	10.5°	3	3
195°	33.5°	4	4
213°	51.5°	6	6

$T_+ = 1.5 + 3 + 4 + 6 = 14.5$

$T_- = 8 + 7 + 5 + 1.5 = 21.5$

$T_{0.05(2),8} = 3$

Neither T_+ nor T_- is $< T_{0.05(2),8}$, so do not reject H_0. $P > 0.50$

27.4 TWO-SAMPLE AND MULTISAMPLE TESTING OF MEAN ANGLES

(a) Two-Sample Testing. It is common to consider the null hypothesis H_0: $\mu_1 = \mu_2$, where μ_1 and μ_2 are the mean angles for each of two circular distributions (see Example 27.7). Watson and Williams (1956, with an improvement by Stephens, 1972) proposed a test that utilizes the statistic

$$F = K\frac{(N - 2)(R_1 + R_2 - R)}{N - R_1 - R_2}, \tag{27.11}$$

where $N = n_1 + n_2$. In this equation, R is Rayleigh's R calculated by Equation 27.1 with the data from the two samples being combined; R_1 and R_2 are the values of Rayleigh's R for the two samples considered separately. K is a factor, obtained from Appendix Table B.37, that corrects for bias in the F calculation; in that table we use the weighted mean of the two vector lengths for the column headed r:

$$r_w = \frac{n_1 r_1 + n_2 r_2}{N} = \frac{R_1 + R_2}{N}. \tag{27.12}$$

The critical value for this test is $F_{\alpha(1),1,N-2}$. Alternatively,

$$t = \sqrt{K\frac{(N - 2)(R_1 + R_2 - R)}{N - R_1 - R_2}} \tag{27.13}$$

may be compared with $t_{\alpha(2),N-2}$. This test may be used for r_w as small as 0.75, if $N/2 \geq 25$. (Batschelet, 1981: 97, 321; Mardia 1972a: 155; Mardia and Jupp, 2000: 130). The underlying assumptions of the test are discussed at the end of this section.

EXAMPLE 27.7 The Watson-Williams Test for Two Samples

H_0: $\mu_1 = \mu_2$
H_A: $\mu_1 \neq \mu_2$

Sample 1			Sample 2		
a_i (deg)	$\sin a_i$	$\cos a_i$	a_i (deg)	$\sin a_i$	$\cos a_i$
94	0.99756	−0.06976	77	0.97437	0.22495
65	0.90631	0.42262	70	0.93969	0.34202
45	0.70711	0.70711	61	0.87462	0.48481
52	0.78801	0.61566	45	0.70711	0.70711
38	0.61566	0.78801	50	0.76604	0.64279
47	0.73135	0.68200	35	0.57358	0.81915
73	0.95630	0.29237	48	0.74314	0.66913
82	0.99027	0.13917	65	0.90631	0.42262
90	1.00000	0.00000	36	0.58779	0.80902
40	0.64279	0.76604			
87	0.99863	0.05234			
$n_1 = 11$	$\sum \sin a_i$	$\sum \cos a_i$	$n_2 = 9$	$\sum \sin a_i$	$\sum \cos a_i$
	$= 9.33399$	$= 4.39556$		$= 7.07265$	$= 5.12160$
	$Y = 0.84854$, $X = 0.39960$			$Y = 0.78585$, $X = 0.56907$	
	$r_1 = 0.93792$			$r_2 = 0.97026$	
	$\sin \bar{a}_1 = 0.90470$			$\sin \bar{a}_2 = 0.80994$	
	$\cos \bar{a}_1 = 0.42605$			$\cos \bar{a}_2 = 0.58651$	
	$\bar{a}_1 = 65°$			$\bar{a}_2 = 54°$	
	$R_1 = 10.31712$			$R_2 = 8.73234$	

By combining the twenty data from both samples:

$$\sum \sin a_i = 9.33399 + 7.07265 = 16.40664$$

$$\sum \cos a_i = 4.39556 + 5.12160 = 9.51716$$

$$N = 11 + 9 = 20$$

$$Y = \frac{16.40664}{20} = 0.82033$$

$$X = \frac{9.51716}{20} = 0.47586$$

$$r = 0.94836$$

$$R = 18.96720$$

$$r_w = \frac{10.31712 + 8.73234}{20} = 0.952; K = 1.0251$$

$$F = K\frac{(N-2)(R_1+R_2-R)}{N-R_1-R_2}$$
$$= (1.0351)\frac{(20-2)(10.31712+8.73234-18.96720)}{20-10.31712-8.73234}$$
$$= (1.0351)\frac{1.48068}{0.95054}$$
$$= 1.61$$

$F_{0.05(1),1,18} = 4.41$.

Therefore, do not reject H_0.

$$0.10 < P < 0.25 \quad [P = 0.22]$$

Thus, we conclude that the two sample means estimate the same population mean, and the best estimate of this population mean is obtained as

$$\sin\bar{a} = \frac{Y}{r} = 0.86500$$
$$\cos\bar{a} = \frac{X}{r} = 0.50177$$
$$\bar{a} = 60°.$$

The data may be grouped as long as the grouping interval is $\leq 10°$. See Batschelet (1972; 1981: Chapter 6) for a review of other two-sample testing procedures. Mardia (1972a: 156–158) and Mardia and Jupp (2000: 130) give a procedure for an approximate confidence interval for $\mu_1 - \mu_2$.

(b) Multisample Testing. The Watson-Williams test can be generalized to a multisample test for testing H_0: $\mu_1 = \mu_2 = \cdots = \mu_k$, a hypothesis reminiscent of analysis of variance considerations for linear data (Section 10.1). In multisample tests with circular data (such as Example 27.8),

$$F = K\frac{(N-k)\left(\sum_{j=1}^{k} R_j - R\right)}{(k-1)\left(N - \sum_{j=1}^{k} R_j\right)}. \tag{27.14}$$

Here, k is the number of samples, R is the Rayleigh's R for all k samples combined, and $N = \sum_{j=1}^{n} n_j$. The correction factor, K, is obtained from Appendix Table B.37, using

$$r_w = \frac{\sum_{j=1}^{k} n_j r_j}{N} = \frac{\sum_{j=1}^{k} R_j}{N}. \tag{27.15}$$

The critical value for this test is $F_{\alpha(1),k-1,N-k}$. Equation 27.15 (and, thus this test) may be used for r_w as small as 0.45 if $N/k \geq 6$ (Batschelet, 1981: 321; Mardia, 1972a: 163; Mardia and Jupp, 2000: 135). If the data are grouped, the grouping interval should be

EXAMPLE 27.8 The Watson-Williams Test for Three Samples

H_0: All three samples are from populations with the same mean angle.
H_A: All three samples are not from populations with the same mean angle.

Sample 1			Sample 2		
a_1 (deg)	$\sin a_i$	$\cos a_i$	a_i (deg)	$\sin a_i$	$\cos a_i$
135	0.70711	−0.70711	150	0.50000	−0.86603
145	0.57358	−0.81915	130	0.76604	−0.64279
125	0.81915	−0.57358	175	0.08716	−0.99619
140	0.64279	−0.76604	190	−0.17365	−0.98481
165	0.25882	−0.96593	180	0.00000	−1.00000
170	0.17365	−0.98481	220	−0.64279	−0.76604
$n_1 = 6$	$\sum \sin a_i$	$\sum \cos a_i$	$n_2 = 6$	$\sum \sin a_i$	$\sum \cos a_i$
	$= 3.17510$	$= -4.81662$		$= 0.53676$	$= -5.25586$
	$\bar{a}_1 = 147°$			$\bar{a}_2 = 174°$	
	$r_1 = 0.96150$			$r_2 = 0.88053$	
	$R_1 = 5.76894$			$R_2 = 5.28324$	

Sample 3		
a_i (deg)	$\sin a_i$	$\cos a_i$
140	0.64279	−0.76604
165	0.25882	−0.96593
185	−0.08715	−0.99619
180	0.00000	−1.00000
125	0.81915	−0.57358
175	0.08716	−0.99619
140	0.64279	−0.76604
$n_3 = 7$	$\sum \sin a_i$	$\sum \cos a_i$
	$= 2.36356$	$= -6.06397$
	$\bar{a}_3 = 159°$	
	$r_3 = 0.92976$	
	$R_3 = 6.50832$	

$k = 3$

$N = 6 + 6 + 7 = 19$

For all 19 data:

$\sum \sin a_i = 3.17510 + 0.53676 + 2.36356 = 6.07542$

$\sum \cos a_i = -4.81662 - 5.25586 - 6.06397 = -16.13645$

$Y = 0.31976$

$X = -0.84929$

$$r = 0.90749$$

$$R = 17.24231$$

$$r_w = \frac{5.76894 + 5.28324 + 6.50832}{19} = 0.924$$

$$F = K\frac{(N - k)(\sum R_j - R)}{(k - 1)(N - \sum R_j)}$$

$$= (1.0546)\frac{(19 - 3)(5.76894 + 5.28324 + 6.50832 - 17.24231)}{(3 - 1)(19 - 5.76894 - 5.28324 - 6.50832)}$$

$$= (1.0546)\frac{5.09104}{2.87900}$$

$$= 1.86$$

$$\nu_1 = k - 1 = 2$$

$$\nu_2 = N - k = 16$$

$$F_{0.05(1),2,16} = 3.63.$$

Therefore, do not reject H_0.

$$0.10 < P < 0.25 \quad [P = 0.19]$$

Thus, we conclude that the three sample means estimate the same population mean, and the best estimate of that population mean is obtained as

$$\sin \bar{a} = \frac{Y}{r} = 0.35236$$

$$\cos \bar{a} = \frac{X}{r} = -0.93587$$

$$\bar{a} = 159°.$$

no larger than 10°. Upton (1976) presents an alternative to the Watson-Williams test that relies on χ^2, instead of F, but the Watson-Williams procedure is a little simpler to use.

The Watson-Williams tests (for two or more samples) are parametric and assume that each of the samples came from a population conforming to what is known as the von Mises distribution, a circular analog to the normal distribution of linear data. (See the second footnote in Section 26.7.) In addition, the tests assume that the population dispersions are all the same. Fortunately, the tests are robust to departures from these assumptions. But if the underlying assumptions are known to be violated severely (as when the distributions are not unimodal), we should be wary of their use. In the two-sample case, the nonparametric test of Section 27.5 is preferable to the Watson-Williams test when the assumptions of the latter are seriously unmet.

Stephens (1982) developed a test with characteristics of a hierarchical analysis of variance of circular data, and Harrison and Kanji (1988) and Harrison, Kanji, and Gadsden (1986) present two-factor ANOVA (including the randomized block design).

Batschelet (1981: 122–126), Fisher (1993: 131–133), Jammalamadake and SenGupta (2001: 128–130), Mardia (1972a: 158–162, 165–166), and Stephens (1972) discuss testing of equality of population concentrations.

NONPARAMETRIC TWO-SAMPLE AND MULTISAMPLE TESTING OF ANGLES

If data are grouped—Batschelet (1981: 110) recommends a grouping interval larger than 10°—then contingency-table analysis may be used (as introduced in Section 23.1) as a two-sample test. The runs test of Section 27.18 may be used as a two-sample test, but it is not as powerful for that purpose as are the procedures below, and it is best reserved for testing the hypothesis in Section 27.18.

(a) Watson's Test. Among the nonparametric procedures applicable to two samples of circular data (e.g., see Batschelet, 1972, 1981: Chapter 6; Fisher, 1993: Section 5.3; Mardia, 1972a: Section 2.4; Mardia and Jupp, 2000: Section 8.3) are the median test of Section 27.6 and the Watson test.

The Watson test, a powerful procedure developed by Watson* (1962), is recommended in place of the Watson-Williams two-sample test of Section 27.4 when at least one of the sampled populations is not unimodal or when there are other considerable departures from the assumptions of the latter test. It may be used on grouped data if the grouping interval is no greater than 5° (Batschelet, 1981: 115).

The data in each sample are arranged in ascending order, as demonstrated in Example 27.9. For the two sample sizes, n_1 and n_2, let us denote the ith observation in Sample 1 as a_{1i} and the jth datum in Sample 2 as a_{2j}. Then, for the data in Example 27.9, $a_{11} = 35°$, $a_{21} = 75°$, $a_{12} = 45°$, $a_{22} = 80°$, and so on. The total number of data is $N = n_1 + n_2$. The cumulative relative frequencies for the observations in Sample 1 are i/n_1, and those for Sample 2 are j/n_2. As shown in the present example, we then define values of d_k (where k runs from 1 through N) as the differences between the two cumulative relative frequency distributions. The test statistic, called the Watson U^2, is computed as

$$U^2 = \frac{n_1 n_2}{N^2} \sum_{k=1}^{N} (d_k - \bar{d})^2, \tag{27.16a}$$

where $\bar{d} = \Sigma d_k / N$; or, equivalently, as

$$U^2 = \frac{n_1 n_2}{N^2} \left[\sum_{k=1}^{N} d_k^2 - \frac{\left(\sum_{k=1}^{N} d_k \right)^2}{N} \right]. \tag{27.16b}$$

Critical values of U^2_{α,n_1,n_2} are given in Appendix Table B.38a bearing in mind that $U^2_{\alpha,n_1,n_2} = U^2_{\alpha,n_2,n_1}$.

Watson's U^2 is especially useful for circular data because the starting point for determining the cumulative frequencies is immaterial. It may also be used in any situation with linear data that are amenable to Mann-Whitney testing (Section 8.11), but it is generally not recommended as a substitute for the Mann-Whitney test; the latter is easier to perform and has access to more extensive tables of critical values, and the former may declare significance because group dispersions are different.

*Geoffrey Stuart Watson (1921–1998), outstanding Australian-born statistician (Mardia, 1998).

EXAMPLE 27.9 Watson's U^2 Test for Nonparametric Two-Sample Testing

H_0: The two samples came from the same population, or from two populations having the same direction.

H_A: The two samples did not come from the same population, or from two populations having the same directions.

Sample 1			Sample 2				
i	a_{1i} (deg)	$\frac{i}{n_1}$	j	a_{2j} (deg)	$\frac{j}{n_2}$	$d_k = \frac{i}{n_1} - \frac{j}{n_2}$	d_k^2
1	35	0.1000			0.0000	0.1000	0.0100
2	45	0.2000			0.0000	0.2000	0.0400
3	50	0.3000			0.0000	0.3000	0.0900
4	55	0.4000			0.0000	0.4000	0.1600
5	60	0.5000			0.0000	0.5000	0.2500
6	70	0.6000			0.0000	0.6000	0.3600
		0.6000	1	75	0.0909	0.5091	0.2592
		0.6000	2	80	0.1818	0.4182	0.1749
7	85	0.7000			0.1818	0.5182	0.2685
		0.7000	3	90	0.2727	0.4273	0.1826
8	95	0.8000			0.2727	0.5273	0.2780
		0.8000	4	100	0.3636	0.4364	0.1904
9	105	0.9000			0.3636	0.5364	0.2877
		0.9000	5	110	0.4546	0.4454	0.1984
10	120	1.0000			0.4546	0.5454	0.2975
		1.0000	6	130	0.5455	0.4545	0.2066
		1.0000	7	135	0.6364	0.3636	0.1322
		1.0000	8	140	0.7273	0.2727	0.0744
		1.0000	9	150	0.8182	0.1818	0.0331
		1.0000	10	155	0.9091	0.0909	0.0083
		1.0000	11	165	1.0000	0.0000	0.0000
$n_1 = 10$			$n_2 = 11$			$\sum d_k = 7.8272$	$\sum d_k^2 = 3.5018$

$N = n_1 + n_2 = 21$

$$U^2 = \frac{n_1 n_2}{N^2}\left[\sum d_k^2 - \frac{(\sum d_k)^2}{N}\right]$$

$$= \frac{(10)(11)}{21^2}\left[3.5018 - \frac{(7.8272)^2}{21}\right]$$

$$= 0.1458$$

$U^2_{0.05,10,11} = 0.1856$

Do not reject H_0.

$0.10 < P < 0.20$

(b) Watson's Test with Ties. If there are some tied data (i.e., there are two or more observations having the same numerical value), then the Watson two-sample test is modified as demonstrated in Example 27.10. We define t_{1i} as the number of data in

EXAMPLE 27.10 Watson's U^2 Test for Data Containing Ties

H_0: The two samples came from the same population, or from two populations having the same directions.

H_A: The two samples did not come from the same population, or from two populations having the same directions.

i	a_{1i}	t_{1i}	m_{1i}	$\frac{m_{1i}}{n_1}$	j	a_{2j}	t_{2j}	m_{2j}	$\frac{m_{2j}}{n_2}$	$d_k = \frac{m_{1i}}{n_1} - \frac{m_{2j}}{n_2}$	d_k^2	t_k
				0.0000	1	30°	1	1	0.1000	−0.1000	0.0100	1
				0.0000	2	35	1	2	0.2000	−0.2000	0.0400	1
1	40°	1	1	0.0833					0.2000	−0.1167	0.0136	1
2	45	1	2	0.1667					0.2000	−0.0333	0.0011	1
3	50	1	3	0.2500	3	50	1	3	0.3000	−0.0500	0.0025	2
4	55	1	4	0.3333					0.3000	0.0333	0.0011	1
				0.3333	4	60	1	4	0.4000	−0.0667	0.0044	1
				0.3333	5	65	2	6	0.6000	−0.2677	0.0711	2
5	70	1	5	0.4167					0.6000	−0.1833	0.0336	1
				0.4167	6	75	1	7	0.7000	−0.2833	0.0803	1
6	80	2	7	0.5833	7	80	1	8	0.8000	−0.2167	0.0470	3
				0.5833	8	90	1	9	0.9000	−0.3167	0.1003	1
7	95	1	8	0.6667					0.9000	−0.2333	0.0544	1
				0.6667	9	100	1	10	1.0000	−0.3333	0.1111	1
8	105	1	9	0.7500					1.0000	−0.2500	0.0625	1
9	110	2	11	0.9167					1.0000	−0.0833	0.0069	2
10	120	1	12	1.0000					1.0000	0.0000	0.0000	1
	$n_1 = 12$					$n_2 = 10$				$\sum t_k d_k = -3.5334$	$\sum t_k d_k^2 = 0.8144$	

$N = 12 + 10 = 22$

$$U^2 = \frac{n_1 n_2}{N^2}\left[\sum t_k d_k^2 - \frac{(\sum t_k d_k)^2}{N}\right]$$

$$= \frac{(12)(10)}{22^2}\left[0.8144 - \frac{(-3.5334)^2}{22}\right]$$

$$= 0.0612$$

$U^2_{0.05,10,12} = 0.2246$

Do not reject H_0.

$P > 0.50$

Sample 1 with a value of a_{1i} and t_{2j} as the number of data in Sample 2 that have a value of a_{2j}. Additionally, m_{1i} and m_{2j} are the cumulative number of data in Samples 1 and 2, respectively; so the cumulative relative frequencies are m_{1i}/n_1 and m_{2j}/n_2, respectively. As in Section 27.5a, d_k represents a difference between two cumulative distributions; and each t_k is the total number of data, in both samples, at each a_{ij}. The test statistic is

$$U^2 = \frac{n_1 n_2}{N^2}\left[\sum_{k=1}^{N} t_k d_k^2 - \frac{\left(\sum_{k=1}^{N} t_k d_k\right)^2}{N}\right]. \tag{27.17}$$

(c) Wheeler and Watson Test. Another nonparametric test for the null hypothesis of no difference between two circular distributions is one presented by Wheeler and Watson (1964; developed independently by Mardia, 1967). This procedure ranks all N data and for each a calculates what is termed a *uniform score* or *circular rank*:

$$d = \frac{(360°)(\text{rank of } a)}{N}. \tag{27.18}$$

This spaces all of the data equally around the circle. Then

$$C_i = \sum_{j=1}^{n_i} \cos d_j \tag{27.19}$$

and

$$S_i = \sum_{j=1}^{n_i} \sin d_j, \tag{27.20}$$

where i refers to *either* sample 1 or 2; it does not matter which one of the two samples is used for this calculation. The test statistic is

$$W = \frac{2(N-1)(C_i^2 + S_i^2)}{n_1 n_2}. \tag{27.21}$$

Critical values of W have been published for some sample sizes (Batschelet, 1981: 344; Mardia, 1967; Mardia and Jupp, 2000: 375–376; Mardia and Spurr, 1973). It has also been shown that W approaches a χ^2 distribution with 2 degrees of freedom for large N. This approximation works best for significance levels no less than 0.025 and has been deemed acceptable by Batschelet (1981: 103) if N is larger than 17, by Fisher (1993: 123) if n_1 and n_2 are each at least 10, and by Mardia and Spurr (1973) if N is greater than 20. This approximation should not be used if there are tied data or if the two sample dispersions are very different (Batschelet 1981: 103). An approximation related to the F distribution has been proposed (Mardia, 1967; Mardia and Jupp, 2000: 148–149) as preferable for some sample sizes.

This test is demonstrated in Example 27.11. This example shows C_i and S_i for each of the two samples, but C and S are only needed from one of the samples in order to perform the test.

EXAMPLE 27.11 The Wheeler and Watson Two-Sample Test for the Data of Example 27.9

H_0: The two samples came from the same population, or from two populations having the same directions.

H_A: The two samples did not come from the same population, or from two populations having the same directions.

$n_1 = 10, n_2 = 11$, and $N = 21$

$$\frac{360^\circ}{N} = \frac{360^\circ}{21} = 17.1429^\circ$$

Sample 1			Sample 2		
Direction (degrees)	*Rank of direction*	*Circular rank* (degrees)	*Direction* (degrees)	*Rank of direction*	*Circular rank* (degrees)
35	1	17.14			
45	2	34.29			
50	3	51.43			
55	4	68.57			
60	5	85.71			
70	6	102.86			
			75	7	120.00
			80	8	137.14
85	9	154.29			
			90	10	171.43
95	11	188.57			
			100	12	205.71
105	13	222.86			
			110	14	240.00
120	15	257.14			
			130	16	274.29
			135	17	291.43
			140	18	308.57
			150	19	325.71
			160	20	342.86
			165	21	360.00
$C_1 = -0.2226$			$C_2 = 0.2226$		
$S_1 = 3.1726$			$S_2 = -3.1726$		

$$W = \frac{2(N-1)(C_1^2 + S_1^2)}{n_1 n_2}$$

$$= \frac{2(21-1)[(-0.2226)^2 + (3.1726)^2]}{(10)(11)} = 3.678$$

$\nu = 2$

$\chi^2_{0.05,2} = 5.991$

Do not reject H_0.

$0.10 < P < 0.25$

(b) Multisample Testing. The Wheeler and Watson test may also be applied to more than two samples. The procedure is as before, where all N data from all k samples are ranked and (by Equation 27.18) the circular rank, d, is calculated for each datum. Equations 27.19 and 27.20 are applied to each sample, and

$$W = 2\sum_{i=1}^{k}\left[\frac{C_i^2 + S_i^2}{n_i}\right]. \tag{27.22}$$

Some critical values for $k = 3$ have been published (Batschelet, 1981: 345; Mardia, 1970b; Mardia and Spurr, 1973). For large sample sizes, W may be considered to approximate χ^2 with $2(k - 1)$ degrees of freedom. This approximation is considered adequate by Fisher (1993: 123) if each n_i is at least 10 and by Mardia and Spurr (1973) if N is greater than 20.

Maag (1966) extended the Watson U^2 test to $k > 2$, but critical values are not available. Comparison of more than two medians may be effected by the procedure in Section 27.6.

If the data are in groups with a grouping interval larger than 10, then an $r \times c$ contingency table analysis may be performed, for r samples in c groups; see Section 23.1 for this analytical procedure.

27.6 TWO-SAMPLE AND MULTISAMPLE TESTING OF MEDIAN ANGLES

The following comparison of two or more medians is presented by Fisher (1933: 114), who states it as applicable if each sample size is at least 10 and all data are within 90° of the grand median (i.e., the median of all N data from all k samples). If we designate m_i to be the number of data in sample i that lie between the grand median and the grand median $-$ 90°, and $M = \sum_{i=1}^{k} m_i$, then

$$\frac{N^2}{M(N - M)}\sum_{i=1}^{k}\frac{m_i^2}{n_i} - \frac{NM}{N - M} \tag{27.23}$$

is a test statistic that may be compared to χ^2 with $k - 1$ degrees of freedom.*

If "H_0: All k population medians are equal" is not rejected, then the grand median is the best estimate of the median of each of the k populations.

27.7 TWO-SAMPLE AND MULTISAMPLE TESTING OF ANGULAR DISTANCES

Angular distance is simply the shortest distance, in angles, between two points on a circle. For example, the angular distance between 95° and 120° is 25°, between 340° and 30° is 50°, and between 190° and 5° is 175°. In general, we shall refer to the angular distance between angles a_1 and a_2 as $d_{a_1 - a_2}$. (Thus, $d_{95\ -\ 120^\circ} = 25^\circ$, and so on.)

*The same results are obtained if m_i is defined as the number of data in sample i that lie between the grand median and the grand median + 90°.

Angular distances are useful in drawing inferences about departures of data from a specified direction. We may observe travel directions of animals trained to travel in a particular compass direction (perhaps "homeward"), or of animals confronted with the odor of food coming from a specified direction. If dealing with times of day we might speak of the time of a physiological or behavioral activity in relation to the time of a particular stimulus.

(a) Two-Sample Testing. If a specified angle (e.g., direction or time of day) is μ_0, we may ask whether the mean of a sample of data, $\bar{a}$, significantly departs from μ_0 by testing the one-sample hypothesis, H_0: $\mu_a = \mu_0$, as explained in Section 27.1c. However, we may have two samples, Sample 1 and Sample 2, each of which has associated with it a specified angle of interest, μ_1 and μ_2, respectively (where μ_1 and μ_2 need not be the same). We may ask whether the angular distances for Sample 1 ($d_{a_{1i}-\mu_1}$) are significantly different from those for Sample 2 ($d_{a_{2i}-\mu_2}$). As shown in Example 27.12, we can rank the angular distances of both samples combined and then perform a Mann-Whitney test (see Section 8.11). This was suggested by Wallraff (1979).

EXAMPLE 27.12 Two-Sample Testing of Angular Distances

Birds of both sexes are transported away from their homes and released, with their directions of travel tabulated. The homeward direction for each sex is 135°.

H_0: Males and females orient equally well toward their homes.

H_A: Males and females do not orient equally well toward their homes.

Males			Females		
Direction traveled	*Angular distance*	*Rank*	*Direction traveled*	*Angular distance*	*Rank*
145°	10°	6	160°	25°	12.5
155	20	11	135	0	1
130	5	2.5	145	10	6
145	10	6	150	15	9.5
145	10	6	125	10	6
160	25	12.5	120	15	9.5
140	5	2.5			
		46.5			44.5

For the two-tailed Mann-Whitney test:

$n_1 = 7, R_1 = 46.5$

$n_2 = 6, R_2 = 44.5$

$$U = n_1 n_2 + \frac{n_1(n_1 + 1)}{2} - R_1 = (7)(6) + \frac{7(8)}{2} - 46.5 = 23.5$$

$$U' = n_1 n_2 - U = (7)(6) - 23.5 = 18.5$$

$U_{0.05(2),7,6} = U_{0.05(2),6,7} = 36.$

Do not reject H_0.

$P > 0.20$

The procedure could be performed as a one-tailed instead of a two-tailed test, if there were reason to be interested in whether the angular distances in one group were greater than those in the other.

(b) Multisample Testing. If more than two samples are involved, then the angular deviations of all of them are pooled and ranked, whereupon the Kruskal-Wallis test (Section 10.4) may be applied, followed if necessary by nonparametric multiple-comparison testing (Section 11.5).

27.8 TWO-SAMPLE AND MULTISAMPLE TESTING OF ANGULAR DISPERSION

The Wallraff (1979) procedure of analyzing angular distances (Section 27.7) may be applied to testing for angular dispersion. The angular distances of concern for Sample 1 are $d_{a_{1i}-\bar{a}_1}$ and those for Sample 2 are $d_{a_{2i}-\bar{a}_2}$. Thus, just as measures of dispersion for linear data may refer to deviations of the data from their mean (Sections 4.3 and 4.4), here we consider the deviations of circular data from their mean.

The angular distances of the two samples may be pooled and ranked for application of the Mann-Whitney test, which may be employed for either two-tailed (Example 27.13) or one-tailed testing.

EXAMPLE 27.13 Two-Sample Testing for Angular Dispersion

The times of day that males and females are born are tabulated. The mean time of day for each sex is determined (to the nearest 5 min) as in Section 26.4. (For males, $\bar{a}_1$ = 7:55 A.M.; for females, $\bar{a}_2$ = 8:15 A.M.)

H_0: The times of day of male births are as variable as the times of day of female births.

H_A: The times of day of male births do not have the same variability as the times of day of female births.

Male			Female		
Time of day	*Angular distance*	*Rank*	*Time of day*	*Angular distance*	*Rank*
05:10 hr	2:45 hr	11	08:15 hr	0:00 hr	1
06:30	1:25	4	10:20	2:05	8.5
09:40	1:45	6	09:45	1:30	5
10:20	2:25	10	06:10	2:05	8.5
04:20	3:35	13	04:05	4:10	14
11:15	3:20	12	07:50	0:25	2
			09:00	0:45	3
			10:10	1:55	7
		$R_1 = 56$			$R_2 = 49$

For the two-tailed Mann-Whitney test:

$$n_1 = 6, R_1 = 56$$

$$n_2 = 8, R_2 = 49$$

$$U = n_1 n_2 + \frac{n_1(n_1 + 1)}{2} - R_1 = (6)(8) + \frac{6(7)}{2} - 56 = 13$$

$U' = n_1n_2 - U = (6)(8) - 13 = 35$

$U_{0.05(2),6,8} = 40.$

Do not reject H_0.

$P = 0.20$

If we wish to compare the dispersions of more than two samples, then the aforementioned Mann-Whitney procedure may be expanded by using the Kruskal-Wallis test (Section 10.4), followed if necessary by nonparametric multiple comparisons (Section 11.5).

PARAMETRIC ANALYSIS OF THE MEAN OF MEAN ANGLES

A set of n angles, a_i, has a mean angle, $\bar{a}$, and an associated mean vector length, r. This set of data may be referred to as a *first-order sample.* A set of k such means may be referred to as a *second-order sample.* Section 26.9 discussed the computation of the mean of a second-order sample, namely the mean of a set of means. We can also test the statistical significance of a mean of means.

For a second-order sample of k mean angles, $\overline{X}$ can be obtained with either Equation 26.27 or 26.29 and $\overline{Y}$ with either Equation 26.28 or 26.30. Assuming that the second-order sample comes from a bivariate normal distribution (i.e., a population in which the X_j's follow a normal distribution, and the Y_j's are also normally distributed), a testing procedure due to Hotelling* (1931) may be applied.

The sums of squares and crossproducts of the k means are

$$\sum x^2 = \sum X_j^2 - \frac{(\sum X_j)^2}{k}, \tag{27.24}$$

$$\sum y^2 = \sum Y_j^2 - \frac{(\sum Y_j)^2}{k}, \tag{27.25}$$

and

$$\sum xy = \sum X_jY_j - \frac{\sum X_j \sum Y_j}{k}, \tag{27.26}$$

where $\sum$ in each instance refers to a summation over all k means (i.e., $\sum = \sum_{j=1}^{k}$).

Then, we can test the null hypothesis that there is no mean direction (i.e., H_0: $\rho = 0$) in the population from which the second-order sample came by using as a test statistic

$$F = \frac{k(k-2)}{2}\left[\frac{\overline{X}^2\sum y^2 - 2\overline{X}\,\overline{Y}\sum xy + \overline{Y}^2\sum x^2}{\sum x^2\sum y^2 - (\sum xy)^2}\right], \tag{27.27}$$

with the critical value being the one-tailed F with degrees of freedom of 2 and $k - 2$ (Batschelet, 1978; 1981: 144–150). This test is demonstrated in Example 27.14, using the data from Example 26.8.

*Harold Hotelling (1895–1973), American mathematical economist and statistician. He owed his life, and thus the achievements of an impressive career, to a zoological mishap. While attending the University of Washington he was called to military service in World War I and appointed to care for mules. One of his charges (named Dynamite) broke Hotelling's leg, thus preventing the young soldier from accompanying his division to France where the unit was annihilated in battle (Darnell, 1988).

EXAMPLE 27.14 The Second-Order Analysis for Testing the Significance of the Mean of the Sample Means in Example 26.8

H_0: There is no mean population direction (i.e., $\rho = 0$).
H_A: There is a mean population direction (i.e., $\rho \neq 0$).

$k = 7, \quad \overline{X} = -0.52734, \quad \overline{Y} = 0.27844$

$\sum X_j = -3.69139, \quad \sum X_j^2 = 2.27959, \quad \sum x^2 = 0.33297$

$\sum Y_j = 1.94906, \quad \sum Y_j^2 = 0.86474, \quad \sum y^2 = 0.32205$

$\sum X_j Y_j = -1.08282, \quad \sum xy = -0.05500$

$$F = \frac{7(7-2)}{2}\left[\frac{(-0.52734)^2(0.32205) - 2(-0.52734)(0.27844)(-0.05500) + (0.27844)^2(0.33297)}{(0.33297)(0.32205) - (-0.05500)^2}\right]$$
$$= 16.66$$

$F_{0.05(1),2,5} = 5.79$
Reject H_0.

$$0.005 < P < 0.01$$

And, from Example 26.8, we see that the population mean angle is estimated to be 152°.

This test assumes the data are not grouped. The assumption of bivariate normality is a serious one. Although the test appears robust against departures due to kurtosis, the test may be badly affected by departures due to extreme skewness, rejecting a true H_0 far more often than indicated by the significance level, α (Everitt, 1979; Mardia, 1970a).

27.10 NONPARAMETRIC ANALYSIS OF THE MEAN OF MEAN ANGLES

The Hotelling testing procedure of Section 27.9 requires that the k $\overline{X}$'s come from a normal distribution, as do the k $\overline{Y}$'s. Although we may assume the test to be robust to some departure from this bivariate normality, there may be considerable nonnormality in a sample, in which case a nonparametric method is preferable.

Moore (1980) has provided a nonparametric modification of the Rayleigh test, which can be used to test a sample of mean angles; it is demonstrated in Example 27.15. The k vector lengths are ranked, so that r_1 is the smallest and r_k is the largest. We shall call the ranks i (where i ranges from 1 through k) and compute

$$X = \frac{\sum_{i=1}^{k} i \cos \bar{a}_i}{k} \tag{27.28}$$

$$Y = \frac{\sum_{i=1}^{k} i \sin \bar{a}_i}{k} \tag{27.29}$$

$$R' = \sqrt{\frac{X^2 + Y^2}{k}}. \tag{27.30}$$

EXAMPLE 27.15 Nonparametric Second-Order Analysis for Significant Direction in the Sample of Means of Example 26.8

H_0: The population from which the sample of means came is uniformly distributed around the circle (i.e., $\rho = 0$).

H_A: The population of means is not uniformly distributed around the circle (i.e., $\rho \neq 0$).

Sample rank (i)	r_i	a_i	$\cos \bar{a}_i$	$\sin \bar{a}_i$	$i \cos \bar{a}_i$	$i \sin \bar{a}_i$
1	0.3338	171°	−0.98769	0.15643	−0.98769	0.15643
2	0.3922	186	−0.99452	−0.10453	−1.98904	−0.20906
3	0.4696	117	−0.45399	0.04570	−1.36197	2.67302
4	0.6962	134	−0.69466	0.71934	−2.77863	2.87736
5	0.7747	169	−0.98163	0.19081	−4.90814	0.95404
6	0.8794	140	−0.76604	0.64279	−4.59627	3.85673
7	0.8954	160	−0.93969	0.34202	−6.57785	2.39414
					−23.19959	12.70266

$k = 7$

$$X = \frac{\sum i \cos \bar{a}_i}{k} = \frac{-23.19959}{7} = -3.31423$$

$$Y = \frac{\sum i \sin \bar{a}_i}{k} = \frac{12.70266}{7} = 1.81467$$

$$R' = \sqrt{\frac{X^2 + Y^2}{k}} = \sqrt{\frac{(-3.31423)^2 + (1.81467)^2}{7}} = \sqrt{2.03959} = 1.428$$

$R'_{0.05,7} = 1.066$

Therefore, reject H_0.

$P < 0.001$

The test statistic, R', is then compared to the appropriate critical value, $R'_{\alpha,n}$, in Appendix Table B.39.

(a) Testing with Weighted Angles. The Moore modification of the Rayleigh test can also be used when we have a sample of angles, each of which is weighted. We may then perform the ranking of the angles by the weights, instead of by the vector lengths, r. For example, the data of Example 26.2 could be ranked by the amount of leaning. Or, if we are recording the direction each of several birds flies from a release point, the weights could be the distances flown. (If the birds disappear at the horizon, then the weights of their flight angles are all the same.)

PARAMETRIC TWO-SAMPLE ANALYSIS OF THE MEAN OF MEAN ANGLES

Batschelet (1978, 1981: 150–154) explained how the Hotelling (1931) procedure of Section 27.9 can be extended to consider the hypothesis of equality of the means of

two populations of means (assuming each population to be bivariate normal). We proceed as in Section 27.9, obtaining an $\overline{X}$ and $\overline{Y}$ for each of the two samples ($\overline{X}_1$ and $\overline{Y}_1$ for Sample 1, and $\overline{X}_2$ and $\overline{Y}_2$ for Sample 2). Then, we apply Equations 27.24, 27.25, and 27.26 to each of the two samples, obtaining $(\sum x^2)_1$, $(\sum xy)_1$, and $(\sum y^2)_1$ for Sample 1, and $(\sum x^2)_2$, $(\sum xy)_2$, and $(\sum y^2)_2$ for Sample 2.

Then we calculate

$$\left(\sum x^2\right)_c = \left(\sum x^2\right)_1 + \left(\sum x^2\right)_2; \tag{27.31}$$

$$\left(\sum y^2\right)_c = \left(\sum y^2\right)_1 + \left(\sum y^2\right)_2; \tag{27.32}$$

$$(\sum xy)_c = (\sum xy)_1 + (\sum xy)_2; \tag{27.33}$$

and the null hypothesis of the two population mean angles being equal is tested by

$$F = \frac{N-3}{2\left(\frac{1}{k_1}+\frac{1}{k_2}\right)}\left[\frac{(\overline{X}_1-\overline{X}_2)^2(\sum y^2)_c - 2(\overline{X}_1-\overline{X}_2)(\overline{Y}_1-\overline{Y}_2)(\sum xy)_c + (\overline{Y}_1-\overline{Y}_2)^2(\sum x^2)_c}{(\sum x^2)_c(\sum y^2)_c - (\sum xy)_c^2}\right], \tag{27.34}$$

where $N = k_1 + k_2$, and F is one-tailed with 2 and $N - 3$ degrees of freedom. This test is shown in Example 27.16, using the data of Figure 27.2.

EXAMPLE 27.16 Parametric Two-Sample Second-Order Analysis for Testing the Difference Between Mean Angles

We have two samples, each consisting of mean directions and vector lengths, as shown in Figure 27.2. Sample 1 is the data from Examples 26.8 and 27.14, where

$$k_1 = 7; \quad \overline{X}_1 = -0.52734; \quad \overline{Y}_1 = 0.27844; \quad \bar{a}_1 = 152°;$$

$$\left(\sum x^2\right)_1 = 0.33297; \quad \left(\sum y^2\right)_1 = 0.32205; \quad (\sum xy)_1 = -0.05500.$$

Sample 2 consists of the following 10 data:

j	$\bar{a}_j$	r_j
1	115°	0.9394
2	127	0.6403
3	143	0.3780
4	103	0.6671
5	130	0.8210
6	147	0.5534
7	107	0.8334
8	137	0.8139
9	127	0.2500
10	121	0.8746

Applying the calculations of Examples 26.8 and 27.14, we find

$$k_2 = 10; \quad \sum r_j \cos a_j = -3.66655; \quad \sum r_j \sin a_j = 5.47197;$$

$$\overline{X}_2 = -0.36660; \quad \overline{Y}_2 = 0.54720; \quad \bar{a}_2 = 124°.$$

$\left(\sum x^2\right)_2 = 0.20897$; $\left(\sum y^2\right)_2 = 0.49793$; $(\sum xy)_2 = -0.05940$.

Then, we can test

H_0: $\mu_1 = \mu_2$ (The means of the populations from which these two samples came are equal.)

H_A: $\mu_1 \neq \mu_2$ (The two population means are not equal.)

$N = 7 + 10$

$$\left(\sum x^2\right)_c = 0.33297 + 0.20897 = 0.54194$$

$$\left(\sum y^2\right)_c = 0.32205 + 0.49793 = 0.81998$$

$$(\sum xy)_c = -0.05500 + (-0.05940) = -0.11440$$

$$F = \frac{(17 - 3)}{2\left(\frac{1}{7} + \frac{1}{10}\right)} \times \left[\frac{\begin{array}{l}[-0.52734 - (-0.36660)]^2(0.81998) \\ \quad - 2[-0.52734 - (-0.36660)](0.27844 - 0.54720)(-0.11440) \\ \quad\quad + (0.27844 - 0.54720)^2(0.54194)\end{array}}{(0.54194)(0.81998) - (-0.11440)^2}\right]$$

$= 4.69$

$F_{0.05(1),2,14} = 3.74$.

Reject H_0.

$0.025 < P < 0.05$ $[P = 0.028]$

The two-sample Hotelling test is robust to departures from the normality assumption (far more so than is the one-sample test of Section 27.9), the effect of nonnormality being slight conservatism (i.e., rejecting a false H_0 a little less frequently than indicated by the significance level, α) (Everitt, 1979). The two samples should be of the same size, but departure from this assumption does not appear to have serious consequences (Batschelet, 1981: 202).

NONPARAMETRIC TWO-SAMPLE ANALYSIS OF THE MEAN OF MEAN ANGLES

The parametric test of Section 27.11 is based on sampled populations being bivariate normal and the two populations having variances and covariances in common, unlikely assumptions to be strictly satisfied in practice. While the test is rather robust to departures from these assumptions, employing a nonparametric test may be employed to assess whether two second-order populations have the same directional orientation.

Batschelet (1978; 1981: 154–156) presented the following nonparametric procedure (suggested by Mardia, 1967) as an alternative to the Hotelling test of Section 27.11. First compute the grand mean vector, pooling all data from both samples. Then, the X coordinate of the grand mean is subtracted from the X coordinate of each of the data in both samples, and the Y of the grand mean is subtracted from the Y of each of the data. (This maneuver determines the direction of each datum from the

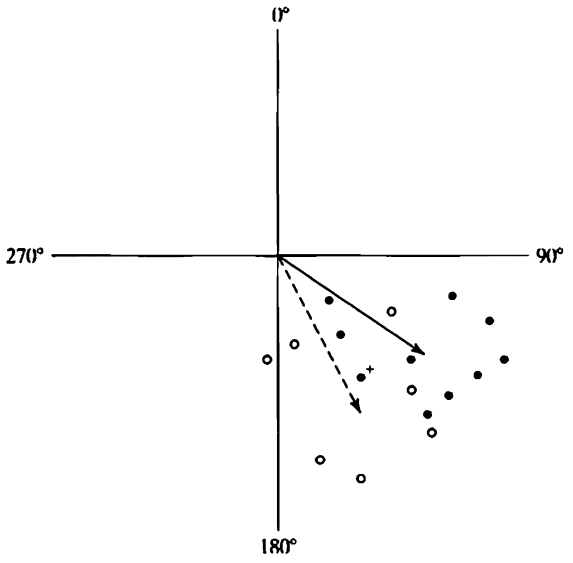


FIGURE 27.2: The data of Example 27.16. The open circles indicate the ends of the seven mean vectors of Sample 1 (also shown in Figure 26.9), with the mean of these seven indicated by the broken-line vector. The solid circles indicate the 10 data of Sample 2, with their mean shown as a solid-line vector. (The "+" indicates the grand mean vector of all seventeen data, which is used in Example 27.17.)

grand mean.) As shown in Example 27.17, the resulting vectors are then tested by a nonparametric two-sample test (as in Section 27.5). This procedure requires that the data not be grouped.

EXAMPLE 27.17 Nonparametric Two-Sample Second-Order Analysis, Using the Data of Example 27.16

H_0: The two samples came from the same population, or from two populations with the same directions.

H_A: The two samples did not come from the same population, nor from two populations with the same directions.

Total number of vectors $= 7 + 10 = 17$

To determine the grand mean vector (which is shown in Figure 27.2):

$$\sum r_j \cos a_j = (-3.69139) + (-3.66655) = -7.35794$$

$$\sum r_j \sin a_j = 1.94906 + 5.47197 = 7.42103$$

$$\overline{X} = \frac{-7.35794}{17} = -0.43282$$

$$\overline{Y} = \frac{7.42103}{17} = 0.43653$$

$\overline{X}$ and $\overline{Y}$ are all that we need to define the grand mean; however, if we wish we can also determine the length and direction of the grand mean vector:

$$r = \sqrt{\overline{X}^2 + \overline{Y}^2} = \sqrt{(-0.43282)^2 + (0.43653)^2} = 0.61473$$

$$\cos \bar{a} = \frac{-0.43282}{0.61473} = -0.70408$$

$$\sin \bar{a} = \frac{0.43653}{0.61473} = 0.71012$$

$$\bar{a} = 135°.$$

Returning to the hypothesis test, we subtract the foregoing $\overline{X}$ from the X, and the $\overline{Y}$ from the Y, for each of the 17 data, arriving at 17 new vectors, as follows:

Sample 1

Datum	X	$X - \overline{X}$	Y	$Y - \overline{Y}$	*New a*
1	−0.84140	−0.40858	0.30624	−0.13029	184°
2	−0.76047	−0.32765	0.14782	−0.28871	210
3	−0.21319	0.21963	0.41842	−0.01811	20
4	−0.67366	−0.24084	0.56527	0.12874	137
5	−0.39005	0.04277	−0.04100	−0.47753	276
6	−0.48293	−0.05011	0.50009	0.06356	107
7	−0.32969	0.10313	0.05222	−0.38431	290

Sample 2

Datum	X	$X - \overline{X}$	Y	$Y - \overline{Y}$	*New a*
1	−0.39701	0.03581	0.85139	0.41485	86°
2	−0.38534	0.04748	0.51137	0.07484	75
3	−0.30188	0.13084	0.22749	−0.20904	320
4	−0.15006	0.28276	0.65000	0.21347	48
5	−0.52773	−0.09491	0.62892	0.19239	108
6	−0.46412	−0.03130	0.30140	−0.13513	230
7	−0.24366	0.18916	0.79698	0.36045	68
8	−0.59525	−0.16243	0.55508	0.11855	127
9	−0.15045	0.28237	0.19966	−0.23687	334
10	−0.45045	−0.01763	0.74968	0.31315	92

Now, using Watson's two-sample test (Section 27.5) on these new angles:

	Sample 1		**Sample 2**				
i	a_{1i}	i/n_1	j	a_{2j}	j/n_2	d_k	d_k^2
1	20	0.1429			0.0000	0.1429	0.0204
		0.1429	1	48	0.1000	0.0429	0.0018
		0.1429	2	68	0.2000	−0.0571	0.0033
		0.1429	3	75	0.3000	−0.1571	0.0247
		0.1429	4	86	0.4000	−0.2571	0.0661
		0.1429	5	92	0.5000	−0.3571	0.1275
2	107	0.2857			0.5000	−0.2143	0.0459
		0.2857	6	108	0.6000	−0.3143	0.0988
		0.2857	7	127	0.7000	−0.4143	0.1716
3	137	0.4286			0.7000	−0.2714	0.0737
4	184	0.5714			0.7000	−0.1286	0.0165
5	210	0.7143			0.7000	0.0143	0.0002
		0.7143	8	230	0.8000	−0.0857	0.0073
6	276	0.8571			0.8000	0.0571	0.0033

7	290	1.0000			0.8000	0.2000	0.0400
		1.0000	9	320	0.9000	0.1000	0.0100
		1.0000	10	334	1.0000	0.0000	0.0000
	$n_1 = 7$		$n_2 = 10$			Σd_k	Σd_k^2
						$= -1.6998$	$= 0.7111$

$$N = 7 + 10 = 17$$

$$U^2 = \frac{n_1 n_2}{N}\left[\Sigma d_k^2 - \frac{(\Sigma d_k)^2}{N}\right]$$

$$= \frac{(7)(10)}{17^2}\left[0.7111 - \frac{(-1.6998)^2}{17}\right]$$

$$= 0.1311$$

$U^2_{0.05,7,10} = 0.1866$

Do not reject H_0.

$$0.10 < P < 0.20$$

27.13 PARAMETRIC PAIRED-SAMPLE TESTING WITH ANGLES

The paired-sample experimental design was introduced in Chapter 9 for linear data, and Section 9.1 showed how the analysis of two samples having paired data could be reduced to a one-sample test employing the differences between members of pairs.

Circular data in two samples might also be paired, in which case the one-sample Hotelling test of Section 27.9 may be used after forming a single sample of data from the differences between the paired angles. If a_{ij} is the jth angle in the ith sample, then a_{1j} and a_{2j} are a pair of data. A single set of rectangular coordinates, X's and Y's, is formed by computing

$$X_j = \cos a_{2j} - \cos a_{1j} \tag{27.35}$$

and

$$Y_j = \sin a_{2j} - \sin a_{1j}. \tag{27.36}$$

Then the procedure of Section 27.9 may be applied, as shown in Example 27.18 (where k is the number of pairs).

EXAMPLE 27.18 The Hotelling Test for Paired Samples of Angles

Ten birds are marked for individual identification, and we record on which side of a tree each bird sits to rest in the morning and in the afternoon. We wish to test the following.

H_0: The side of a tree on which birds sit is the same in the morning and in the afternoon.

H_A: The side of a tree on which birds sit is not the same in the morning and in the afternoon.

	Morning			Afternoon			Difference		
Bird (j)	Direction (a_{1j})	$\sin a_{1j}$	$\cos a_{1j}$	Direction (a_{2j})	$\sin a_{2j}$	$\cos a_{2j}$	Y_j	X_j	X_jY_j
1	105°	0.9659	−0.2588	205°	−0.4226	−0.9063	−1.3885	−0.6475	0.8991
2	120	0.8660	−0.5000	210	−0.5000	−0.8660	−1.3660	−0.3660	0.5000
3	135	0.7071	−0.7071	235	−0.8192	−0.5736	−1.5263	0.1335	−0.2038
4	95	0.9962	−0.0872	245	−0.9063	−0.4226	−1.9025	−0.3354	0.6381
5	155	0.4226	−0.9063	260	−0.9848	−0.1736	−1.4074	0.7327	−1.0312
6	170	0.1736	−0.9848	255	−0.9659	−0.2588	−1.1395	0.7260	−0.8273
7	160	0.3420	−0.9397	240	−0.8660	−0.5000	−1.2080	0.4397	−0.5312
8	155	0.4226	−0.9063	245	−0.9063	−0.4226	−1.3289	0.4837	−0.6428
9	120	0.8660	−0.5000	210	−0.5000	−0.8660	−1.3660	−0.3660	0.5000
10	115	0.9063	−0.4226	200	−0.3420	−0.9397	−1.2483	−0.5171	0.6455

$k = 10$

$\overline{X} = 0.0284$

$\overline{Y} = -1.3881$

$\Sigma Y_j = -13.8814$ $\Sigma X_j = 0.2836$

$\Sigma Y_j^2 = 19.6717$ $\Sigma X_j^2 = 2.5761$ $\Sigma X_jY_j = -0.0536$

$$\sum x^2 = 2.5761 - \frac{(0.2836)^2}{10} = 2.5681$$

$$\sum y^2 = 19.6717 - \frac{(-13.8814)^2}{10} = 0.4024$$

$$\sum xy = -0.0536 - \frac{(0.2836 - 13.8814)}{10} = 0.3402$$

$$F = \frac{k(k-2)}{2}\left[\frac{\overline{X}^2\Sigma y^2 - 2\overline{X}\,\overline{Y}\Sigma xy + \overline{Y}^2\Sigma x^2}{\Sigma x^2\Sigma y^2 - (\Sigma xy)^2}\right]$$

$$F = \frac{10(10-2)}{2}\left[\frac{(0.0284)^2(0.4024) - 2(0.0284)(-1.3881) \times (0.3402) + (-1.3881)^2(2.5681)}{(2.5681)(0.4024) - (0.3402)^2}\right]$$

$$= 217$$

$F_{0.05(1),2,8} = 4.46.$

Reject H_0.

$$P \ll 0.0005 \quad [P = 0.00000011]$$

If each member of a pair of data is a mean angle ($\bar{a}$) from a sample, with an associated vector length (r), then we are dealing with a second-order analysis. The aforementioned Hotelling test may be applied if the following computations are used in place of Equations 27.35 and 27.36, respectively:

$$X_j = r_{2j}\cos\bar{a}_{2j} - r_{1j}\cos\bar{a}_{1j} \tag{27.37}$$

$$Y_j = r_{2j}\sin\bar{a}_{2j} - r_{ij}\sin\bar{a}_{1j}. \tag{27.38}$$

27.14 NONPARAMETRIC PAIRED-SAMPLE TESTING WITH ANGLES

Circular data in a paired-sample experimental design may be tested nonparametrically by forming a single sample of the paired differences, which can then be subjected to the Moore test of Section 27.10. We calculate rectangular coordinates (X_j and Y_j) for each paired difference, as done in Equations 27.35 and 27.36. Then, for each of the j paired differences, we compute

$$r_j = \sqrt{X_j^2 + Y_j^2}, \tag{27.39}$$

$$\cos a_j = \frac{X_j}{r_j}, \tag{27.40}$$

$$\sin a_j = \frac{Y_j}{r_j}. \tag{27.41}$$

Then the values of r_j are ranked, with ranks (i) running from 1 through n, and we complete the analysis using Equations 27.28, 27.29, and 27.30 and Appendix Table B.39, substituting n for k. The procedure is demonstrated in Example 27.19.

If each member of a pair of circular-scale data is a mean angle, $\bar{a}_j$, with an associated vector length, r_j, then we modify the preceding analysis. Calculate X_j and Y_j by Equations 27.37 and 27.38, respectively, instead of by Equations 27.35 and 27.36, respectively. Then apply Equations 27.39 through 27.41 and Equations 27.28 through 27.30 to complete the analysis (where k is the number of paired means).

27.15 PARAMETRIC ANGULAR CORRELATION AND REGRESSION

The correlation of two variables, each measured on a linear scale, was discussed in Chapter 19, with linear-scale regression being introduced in Chapter 17. Correlation involving angular data may be of two kinds: Either both variables are measured on a circular scale (a situation sometimes termed "angular-angular," or "spherical," correlation), or one variable is on a circular scale with the other measured on a linear scale (sometimes called an "angular-linear," or "cylindrical," correlation). The study of biological rhythms deals essentially with the rhythmic dependence (i.e., regression) of a linear scale variable (e.g., a measure of biological activity, such as body temperature) on a circular scale variable (namely, time).

(a) Angular-Angular Correlation. Correlation measures developed for correlation between two angular variables were for years characterized by serious deficiencies, such as not distinguishing between positive and negative relationships (e.g., see the review by Jupp and Mardia, 1980). However, Fisher and Lee (1983) presented a correlation coefficient analogous to the familiar parametric correlation coefficient of

EXAMPLE 27.19 The Moore Test for Paired Data on a Circular Scale of Measurement

Ten birds are marked for individual identification, and we record on which side of a tree each bird sits to rest in the morning and in the afternoon. (The data are the same as in Example 27.18.) We wish to test the following:

H_0: The side of a tree on which birds sit is the same in the morning and in the afternoon.

H_A: The side of a tree on which birds sit is not the same in the morning and in the afternoon.

	Morning			Afternoon			Difference					
Bird (j)	Direction (a_{1j})	$\sin a_{1j}$	$\cos a_{1j}$	Direction (a_{2j})	$\sin a_{2j}$	$\cos a_{2j}$	Y_j	X_j	r_j	$\sin a_j$	$\cos a_j$	Rank of r_j (i)
1	105°	0.9659	−0.2588	205°	−0.4226	−0.9063	−1.3885	−0.6475	1.5321	−0.9063	−0.4226	7.5
2	120	0.8660	−0.5000	210	−0.5000	−0.8660	−1.3660	−0.3660	1.4142	−0.9659	−0.2588	4.5
3	135	0.7071	−0.7071	235	−0.8192	−0.5736	−1.5263	0.1335	1.5321	−0.9962	0.0871	7.5
4	95	0.9962	−0.0872	245	−0.9063	−0.4226	−1.9025	−0.3354	1.9318	−0.9848	−0.1736	10
5	155	0.4226	−0.9063	260	−0.9848	−0.1736	−1.4074	0.7327	1.5867	−0.8870	0.4618	9
6	170	0.1736	−0.9848	255	−0.9659	−0.2588	−1.1395	0.7260	1.3511	−0.8434	0.5373	2
7	160	0.3420	−0.9397	240	−0.8660	−0.5000	−1.2080	0.4397	1.2855	−0.9397	0.3420	1
8	155	0.4226	−0.9063	245	−0.9063	−0.4226	−1.3289	0.4837	1.4152	−0.9390	0.3418	6
9	120	0.8660	−0.5000	210	−0.5000	−0.8660	−1.3660	−0.3660	1.4142	−0.9659	−0.2588	4.5
10	115	0.9063	−0.4226	200	−0.3420	−0.9397	−1.2483	−0.5171	1.3512	−0.9238	−0.3827	3

$$n = 10$$

$$X = \frac{\sum_{i=1}^{n} i \cos a_i}{n} = \frac{1(0.3420) + 2(0.5373) + \cdots + 10(-0.1736)}{10}$$

$$= -0.0106$$

$$Y = \frac{\sum_{i=1}^{n} i \sin a_i}{n} = \frac{1(-0.9397) + 2(-0.8434) + \cdots + 10(-0.9848)}{10}$$

$$= -5.1825$$

$$R' = \sqrt{\frac{X^2 + Y^2}{n}} = \sqrt{\frac{(-0.0106)^2 + (-5.1825)^2}{10}} = \sqrt{2.685842} = 1.639$$

$R'_{0.05,10} = 1.048.$

Reject H_0.

$$P < 0.001$$

Section 19.1*; it is†

$$r_{aa} = \frac{\sum_{i=1}^{n-1}\sum_{j=i+1}^{n} \sin(a_i - a_j)\sin(b_i - b_j)}{\sqrt{\sum_{i=1}^{n-1}\sum_{j=i+1}^{n} \sin^2(a_i - a_j) \sum_{i=1}^{n-1}\sum_{j=i+1}^{n} \sin^2(b_i - b_j)}}, \tag{27.43}$$

where the ith pair of data is denoted as a_i, b_i‡.

Upton and Fingleton (1989: 303) gave a relatively simple method to test the significance of r_{aa}—that is, to test whether the sample of data came from a population having a correlation coefficient, ρ_{aa}, different from zero. The procedure involves computing r_{aa} an additional n times for the sample, each time eliminating a different one of the n pairs of a and b data.§

Then a mean and variance of these n additional r_{aa}'s is calculated (let's call the mean $\bar{r}_{aa}$, and the variance $s^2_{r_{aa}}$); and confidence limits for ρ_{aa} are obtained as

$$L_1 = nr_{aa} - (n-1)\bar{r}_{aa} - Z_{\alpha(2)}\sqrt{\frac{s^2_{r_{aa}}}{n}} \tag{27.45}$$

and

$$L_2 = nr_{aa} - (n-1)\bar{r}_{aa} + Z_{\alpha(2)}\sqrt{\frac{s^2_{r_{aa}}}{n}}. \tag{27.46}$$

If the confidence interval (i.e., the interval between L_1 and L_2) does *not* include zero, then H_0: $\rho_{aa} = 0$ is rejected in favor of H_A: $\rho_{aa} \neq 0$. The computation of r_{aa}, and testing its significance, is shown in Example 27.20.

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*Results identical to those from Equation 19.1 may be obtained by

$$r = \frac{\sum_{i=1}^{n-1}\sum_{j=i+1}^{n} (X_i - X_j)(Y_i - Y_j)}{\sqrt{\sum_{i=1}^{n-1}\sum_{j=i+1}^{n} (X_i - X_j)^2 \sum_{i=1}^{n-1}\sum_{j=i+1}^{n} (Y_i - Y_j)^2}}. \tag{27.42}$$

†The notation "$\sin^2(a_i - a_j)$" means "$[\sin(a_i - a_j)]^2$."

‡Fisher (1993: 151) gives an alternate computation of r_{aa} as

$$\frac{4\left[\left(\sum_{i=1}^{n}\cos a_i \cos b_i\right)\left(\sum_{i=1}^{n}\sin a_i \sin b_i\right) - \left(\sum_{i=1}^{n}\cos a_i \sin b_i\right)\left(\sum_{i=1}^{n}\sin a_i \cos b_i\right)\right]}{\sqrt{\left[n^2 - \left(\sum_{i=1}^{n}\cos(2a_i)\right)^2 - \left(\sum_{i=1}^{n}\sin(2a_i)\right)^2\right]\left[n^2 - \left(\sum_{i=1}^{n}\cos(2b_i)\right)^2 - \left(\sum_{i=1}^{n}\sin(2b_i)\right)^2\right]}}. \tag{27.44}$$

§This involves what statisticians call the *jackknife* technique (introduced by Quenouille, 1956), named in 1964 by R. G. Miller (David, 1995).

EXAMPLE 27.20 Angular-Angular Correlation

We wish to assess the relationship between the orientation of insects and the direction of a light source.

H_0: $\rho_{aa} = 0$; H_A: $\rho_{aa} \neq 0$

	Insect	Light
i	a_i	b_i
1	145°	120°
2	190°	180°
3	310°	330°
4	210°	225°
5	80°	55°

$n = 5$; the computations proceed as follows:

i	j	$a_i - a_j$	$b_i - b_j$	$\sin(a_i - a_j)$	$\sin(b_i - b_j)$	$\sin(a_i - a_j) \times \sin(b_i - b_j)$	$\sin^2(a_i - a_j)$	$\sin^2(b_i - b_j)$
1	2	−45°	−60°	−0.70711	−0.86603	0.61237	0.50000	0.75001
1	3	−165°	−210°	−0.25882	0.50000	−0.12941	0.06699	0.25000
1	4	−65°	−105°	−0.90631	−0.96593	0.87543	0.82140	0.93302
1	5	65°	65°	0.90631	0.90631	0.82140	0.82140	0.82140
2	3	−120°	−150°	−0.86603	−0.50000	0.43302	0.75001	0.25000
2	4	−20°	−45°	−0.34202	−0.70711	0.24185	0.11698	0.50000
2	5	110°	125°	0.93969	0.81915	0.76975	0.88302	0.67101
3	4	100°	105°	0.98481	0.96593	0.95126	0.96985	0.93302
3	5	230°	275°	−0.76604	−0.99619	0.76312	0.58682	0.99239
4	5	130°	170°	0.76604	0.17365	0.13302	0.58682	0.03015
					Sum:	5.47181	6.10329	6.13100

$$r_{aa} = \frac{\sum_{i=1}^{n-1}\sum_{j=i+1}^{n} \sin(a_i - a_j)\sin(b_i - b_j)}{\sqrt{\sum_{i=1}^{n-1}\sum_{j=i+1}^{n} \sin^2(a_i - a_j) \sum_{i=1}^{n-1}\sum_{j=i+1}^{n} \sin^2(b_i - b_j)}}$$

$$= \frac{5.47181}{\sqrt{(6.10329)(6.13100)}} = \frac{5.47181}{\sqrt{37.41927}} = \frac{5.47181}{6.11713} = 0.8945$$

Five r_{aa}'s computed for the above data, each with a different pair of data deleted:

i deleted:	1	2	3	4	5
r_{aa}	0.90793	0.87419	0.92905	0.89084	0.87393

$\bar{r}_{aa} = 0.89519$; $s^2_{r_{aa}} = 0.0005552$

$nr_{aa} - (n - 1)\bar{r}_{aa} = (5)(0.8945) - (5 - 1)(0.89519) = 0.8917$

$$Z_{0.05(2)}\sqrt{\frac{s^2_{r_{aa}}}{n}} = 1.9600\sqrt{\frac{0.0005552}{5}} = 1.9600(0.0105) = 0.0206$$

$L_1 = 0.8917 - 0.0206 = 0.8711$

$L_2 = 0.8917 + 0.0206 = 0.9123.$

As this confidence interval does not encompass zero, reject H_0.

(b) Angular-Linear Correlation. Among the procedures proposed for correlating an angular variable (a) with a linear variable (X) is one by Mardia (1976). Using Equation 19.1, determine coefficients for the correlation between X and the sine of a (call it r_{XS}), the correlation between X and the cosine of a (call it r_{XC}), and the correlation between the cosine and the sine of a (call it r_{CS}). Then, the angular-linear correlation coefficient is

$$r_{al} = \sqrt{\frac{r^2_{XC} + r^2_{XS} - 2r_{XC}r_{XS}r_{CS}}{1 - r^2_{CS}}}. \tag{27.47}$$

For angular-linear correlation, the correlation coefficient lies between 0 and 1 (i.e., there is no negative correlation). If n is large, then the significance of the correlation coefficient may be assessed by comparing nr^2_{al} to χ^2_2 (Batschelet, 1981: 193). This procedure is shown in Example 27.21. It is not known how large n must be for the chi-square approximation to give good results, and Fisher (1993: 145) recommends a different (laborious) method for assessing significance of the test statistic.

EXAMPLE 27.21 Angular-Linear Correlation

For a sampled population of animals, we wish to examine the relationship between distance traveled and direction traveled.

$H_0: \rho_{al} = 0$; $H_A: \rho_{al} \neq 0$

$\alpha = 0.05$

i	X distance (km)	a_i direction (deg)	$\sin a_i$	$\cos a_i$
1	48	190	−0.17364	−0.98481
2	55	160	0.34202	−0.93969
3	26	210	−0.50000	−0.86603
4	23	225	−0.70711	−0.70711
5	22	220	−0.64279	−0.76604
6	62	140	0.64279	−0.76604
7	64	120	0.86603	−0.50000

$n = 7$

$\sum X_i = 300$ kilometers; $\sum X_i^2 = 14{,}958$ km^2

$\sum \sin a_i = -0.17270$ degrees; $\sum \sin^2 a_i = 2.47350$ deg^2

$\sum \cos a_i = -5.52972$ degrees; $\sum \cos^2 a_i = 4.52652$ deg^2

"Sum of squares" of $X = \sum x^2 = 14{,}958 - 300^2/7 = 2100.86$ km^2

"Sum of squares" of $\sin a_i = 2.47350 - (-0.17270)^2/7 = 2.46924$ deg^2

"Sum of squares" of $\cos a_i = 4.52652 - (-5.52972)^2/7 = 0.15826$ deg^2

"Sum of cross products" of X and $\cos a_i = (48)(-0.98481) + (55)(-0.93969) + \cdots + (64)(-0.50000) - (300)(-5.52972)/7 = -234.08150 - (-236.98800) = 2.90650$ deg-km

"Sum of cross products" of X and $\sin a_i = (48)(-0.17364) + (55)(0.34202) + \cdots + (64)(0.86603) - (300)(-0.17270)/7 = 62.35037 - (-7.40143) = 69.75180$ deg-km

"Sum of cross products" of $\cos a_i$ and $\sin a_i = (-0.98481)(-0.17364) + (-0.93969)(0.34202) + \cdots + (-0.50000)(0.86603) - (-5.52972)(-0.17270)/7 = 0.34961 - 0.13643 = -0.21318$ deg-km

$r_{XC} = 0.15940$; $r_{XC}^2 = 0.02541$

$r_{XS} = 0.96845$; $r_{XS}^2 = 0.93789$

$r_{CS} = 0.34104$; $r_{CS}^2 = 0.11630$

$$r_{al}^2 = \frac{r_{XC}^2 + r_{XS}^2 - 2r_{XC}r_{XS}r_{CS}}{1 - r_{CS}^2}$$

$$= \frac{0.02541 + 0.93789 - 2(0.15940)(0.96845)(0.34104)}{1 - 0.11630}$$

$$= \frac{0.85801}{0.88370} = 0.97093$$

$r_{al} = \sqrt{0.97093} = 0.9854$

$nr_{al}^2 = (7)(0.97093) = 6.797.$

$\chi^2_{0.05,2} = 5.991$; reject H_0; $0.025 < P < 0.05$

(c) Regression. Linear-circular regression, in which the dependent variable (Y) is linear and the independent variable (a) circular, may be analyzed, by the regression methods of Chapter 20, as

$$Y_i = b_0 + b_1 \cos a_i + b_2 \sin a_i \tag{27.48}$$

(Fisher, 1993: 139–140), where b_0 is the Y-intercept and b_1 and b_2 are partial regression coefficients.

In circular-linear regression, where a is the dependent variable and Y the independent variable, the situation is rather more complicated and is discussed by Fisher (1993: 155–168). Regression where both the dependent and independent variables

are on a circular scale (angular-angular regression), or where there is a circular dependent variable and both circular and linear independent variables, has received little attention in the statistical literature (Fisher, 1993: 168; Lund, 1999).

(d) Rhytomometry. The description of biological rhythms may be thought of as a regression (often called *periodic regression*) of the linear variable on time (a circular variable). Excellent discussions of such regression are provided by Batschelet (1972; 1974; 1981: Chapter 8), Bliss (1970: Chapter 17), Bloomfield (1976), and Nelson et al. (1979).

The *period*, or length, of the cycle* is often stated in advance. Parameters to be estimated in the regression are the *amplitude* of the rhythm (which is the range from the minimum to the maximum value of the linear variable)† and the *phase angle*, or *acrophase*, of the cycle (which is the point on the circular time scale at which the linear variable is maximum). If the period is also a parameter to be estimated, then the situation is more complex and one may resort to the broad area of *time series analysis* (e.g., Fisher, 1993: 172–189). Some biological rhythms can be fitted, by least-squares regression, by a sine (or cosine) curve; and if the rhythm does not conform well to such a symmetrical functional relationship, then a "harmonic analysis" (also called a "Fourier analysis") may be employed.

27.16 NONPARAMETRIC ANGULAR CORRELATION

(a) Angular-Angular Correlation. A nonparametric correlation procedure proposed by Mardia (1975) employs the ranks of circular measurements as follows. If pair i of circular data is denoted by measurements a_i and b_i, then these two statistics are computed:

$$r' = \frac{\left\{\sum_{i=1}^{n} \cos[C(\text{rank of } a_i - \text{rank of } b_i)]\right\}^2 + \left\{\sum_{i=1}^{n} \sin[C(\text{rank of } a_i - \text{rank of } b_i)]\right\}^2}{n^2} \tag{27.49}$$

$$r'' = \frac{\left\{\sum_{i=1}^{n} \cos[C(\text{rank of } a_i + \text{rank of } b_i)]\right\}^2 + \left\{\sum_{i=1}^{n} \sin[C(\text{rank of } a_i + \text{rank of } b_i)]\right\}^2}{n^2}, \tag{27.50}$$

where

$$C = \frac{360°}{n}; \tag{27.51}$$

and Fisher and Lee (1982) showed that

$$(r_{aa})_s = r' - r'' \tag{27.52}$$

*A rhythm with one cycle every twenty-four hours is said to be "circadian" (from the Latin *circa*, meaning "about" and *diem*, meaning "day"); a rhythm with a seven-day period is said to be "circaseptan"; a rhythm with a fourteen-day period is "circadiseptan"; one with a period of one year is "circannual" (Halberg and Lee, 1974).

†The amplitude is often defined as half this range.

is, for circular data, analogous to the Spearman rank correlation coefficient of Section 19.9. For n of 8 or more, we may calculate

$$(n - 1)(r_{aa})_s$$

and compare it to the critical value of

$$A + B/n,$$

using A and B from Table 27.1 (which yields excellent approximations to the values given by Fisher and Lee, 1982). This procedure is demonstrated in Example 27.22.

TABLE 27.1: Constants A and B for Critical Values for Nonparametric Angular-Angular Correlation

$\alpha(2)$:	0.20	0.10	0.05	0.02	0.01
$\alpha(1)$:	0.10	0.05	0.025	0.01	0.005
A:	1.61	2.30	2.99	3.91	4.60
B:	1.52	2.00	2.16	1.60	1.60

EXAMPLE 27.22 Nonparametric Angular-Angular Correlation

For a population of birds sampled, we wish to correlate the direction toward which they attempt to fly in the morning with that in the evening.

$H_0: (\rho_{aa})_s = 0; H_A: (\rho_{aa})_s \neq 0$

$\alpha = 0.05$

	Direction					
Bird i	Evening a_i	Morning b_i	Rank of a_i	Rank of b_i	Rank difference	Rank sum
1	30°	60°	4.5	5	−0.5	9.5
2	10°	50°	2	4	−2	6
3	350°	10°	8	2	6	10
4	0°	350°	1	8	−7	9
5	340°	330°	7	7	0	14
6	330°	0°	6	1	5	7
7	20°	40°	3	3	0	6
8	30°	70°	4.5	6	−1.5	10.5

$n = 8; C = 360°/n = 45°$

$$r' = \frac{\left\{\sum_{i=1}^{n} \cos[C(\text{rank of } a_i - \text{rank of } b_i)]\right\}^2 + \left\{\sum_{i=1}^{n} \sin[C(\text{rank of } a_i - \text{rank of } b_i)]\right\}^2}{n^2}$$

$$= \Big(\{\cos[45°(-0.5)] + \cos[45°(-2)] + \cdots + \cos[45°(-1.5)]\}^2 + \{\sin[45°(-0.5)] + \sin[45°(-1)] + \cdots + \sin[45°(-1.5)]\}^2\Big)/8^2$$

$$= 0.3654$$

$$r'' = \frac{\left\{\sum_{i=1}^{n} \cos[C(\text{rank of } a_i + \text{rank of } b_i)]\right\}^2 + \left\{\sum_{i=1}^{n} \sin[C(\text{rank of } a_i + \text{rank of } b_i)]\right\}^2}{n^2}$$

$$= \Big(\{\cos[45^\circ(9.5)] + \cos[45^\circ(6)] + \cdots + \cos[45^\circ(10.5)]\}^2$$

$$+ \{\sin[45^\circ(9.5)] + \sin[45^\circ(6)] + \cdots + \sin[45^\circ(10.5)]\}^2\Big)/8^2$$

$$= 0.0316$$

$$(r_{aa})_s = r' - r'' = 0.3654 - 0.0316 = 0.3338$$

$$(n-1)(r_{aa})_s = (8-1)(0.3338) = 2.34$$

For $\alpha(2) = 0.05$ and $n = 8$, the critical value is estimated to be

$$A + B/n = 2.99 + 2.16/8 = 3.26.$$

As $2.34 < 3.26$, do not reject H_0.

We may also compute critical values for other significance levels:

for $\alpha(2) = 0.20$: $1.61 + 1.52/8 = 1.80$;

for $\alpha(2) = 0.10$: $2.30 + 2.00/8 = 2.55$;

therefore, $0.10 < P < 0.20$.

Fisher and Lee (1982) also described a nonparametric angular-angular correlation that is analogous to the Kendall rank correlation mentioned in Section 19.9c (see also Upton and Fingleton, 1989).

(b) Angular-Linear Correlation. Mardia (1976) presented a ranking procedure for correlation between a circular and a linear variable, which is analogous to the Spearman rank correlation in Section 19.9. (See also Fisher, 1993: 140–141; Mardia and Jupp, 2000: 246–248.)

27.17 GOODNESS-OF-FIT TESTING FOR CIRCULAR DISTRIBUTIONS

Either χ^2 or G may be used to test the goodness of fit of a theoretical to an observed circular frequency distribution. (See Chapter 22 for general aspects of goodness-of-fit methods.) The procedure is to determine each expected frequency, $\hat{f}_i$, corresponding to each observed frequency, f_i, in each category, i. For the data of Example 26.3, for instance, we might hypothesize a uniform distribution of data among the 12 divisions of the data. The test of this hypothesis is presented in Example 27.23. Batschelet (1981: 72) recommends grouping the data so that no expected frequency is less than 4 in using chi-square. All of the k categories do not have to be the same size. If

they are (as in Example 27.23, where each category is 30° wide), Fisher (1993: 67) recommends that n/k be at least 2.

EXAMPLE 27.23 Chi-Square Goodness of Fit for the Circular Data of Example 26.3

H_0: The data in the population are distributed uniformly around the circle.

H_A: The data in the population are not distributed uniformly around the circle.

a_i (deg)	f_i	$\hat{f}_i$
0–30	0	8.7500
30–60	6	8.7500
60–90	9	8.7500
90–120	13	8.7500
120–150	15	8.7500
150–180	22	8.7500
180–210	17	8.7500
210–240	12	8.7500
240–270	8	8.7500
270–300	3	8.7500
300–330	0	8.7500
330–360	0	8.7500

$k = 12 \quad n = 105$

$\hat{f}_i = 105/12 = 8.7500$ for all i

$$\chi^2 = \frac{(0 - 8.7500)^2}{8.7500} + \frac{(6 - 8.7500)^2}{8.7500} + \frac{(9 - 8.7500)^2}{8.7500} + \cdots + \frac{(0 - 8.7500)^2}{8.7500}$$
$$= 8.7500 + 0.8643 + 0.0071 + \cdots + 8.7500$$
$$= 66.543$$

$\nu = k - 1 = 11$

$\chi^2_{0.05,11} = 19.675$

Reject H_0. $P \ll 0.001$ [$P = 0.00000000055$]

Recall that goodness-of-fit testing by the chi-square or G statistic does not take into account the sequence of categories that occurs in the data distribution. In Section 22.8, the Kolmogorov-Smirnov test was introduced in preference to chi-square when the categories of data are, in fact, ordered. Unfortunately, the Kolmogorov-Smirnov test yields different results for different starting points on a circular scale; however, a

modification of this test by Kuiper (1960) provides a goodness-of-fit test, the results of which are unrelated to the starting point on a circle.

If data are not grouped, the Kuiper test is preferred to the chi-square procedure. It is discussed by Batschelet (1965: 26–27; 1981: 76–79), Fisher (1993: 66–67), Mardia (1972a: 173–180), Mardia and Jupp (2000: 99–103). Among others, another goodness-of-fit test applicable to circular distributions of ungrouped data (Watson, 1961, 1962, 1995), is often referred to as the *Watson one-sample U^2 test*, which is demonstrated in Example 27.24. To test the null hypothesis of uniformity, first transform each angular measurement, a_i, by dividing it by 360°:

$$u_i = \frac{a_i}{360°}. \tag{27.53}$$

Then the following quantities are obtained for the set of n values of u_i : $\sum u_i, \sum u_i^2, \bar{u}$, and $\sum iu_i$. The test statistic, called "Watson's U^2," is

$$U^2 = \sum u_i^2 - \frac{\left(\sum u_i\right)^2}{n} - \frac{2}{n}\sum iu_i + (n+1)\,\bar{u} + \frac{n}{12} \tag{27.54}$$

(Mardia, 1972a: 182; Mardia and Jupp, 2000: 103–105). Critical values for this test are $U^2_{\alpha,n}$ in Appendix Table B38b. Kuiper's test and Watson's test appear to be very similar in power (Stephens, 1969b; Mardia and Jupp, 2000: 115). Lockhart and Stephens (1985) discussed the use of Watson's U^2 for goodness of fit to the von Mises distribution and provided tables for that application.

EXAMPLE 27.24 Watson's Goodness-of-Fit Testing Using the Data of Example 26.2

H_0: The sample data come from a population uniformly distributed around the circle.

H_A: The sample data do not come from a population uniformly distributed around the circle.

i	a_i	u_i	u_i^2	iu_i
1	45°	0.1250	0.0156	0.1250
2	55°	0.1528	0.0233	0.3056
3	81°	0.2250	0.0506	0.6750
4	96°	0.2667	0.0711	1.0668
5	110°	0.3056	0.0934	1.5280
6	117°	0.3250	0.1056	1.9500
7	132°	0.3667	0.1345	2.5669
8	154°	0.4278	0.1830	3.4224
$n = 8$		$\sum u_i$ =2.1946	$\sum u_i^2$ =0.6771	$\sum iu_i$ =11.6397

$$\bar{u} = \frac{\sum u_i}{n} = \frac{2.1946}{8} = 0.2743$$

$$U^2 = \sum u_i^2 - \frac{(\sum u_i)^2}{n} - \frac{2}{n}\sum i u_i + (n+1)\bar{u} + \frac{n}{12}$$

$$= 0.6771 - \frac{(2.1946)^2}{8} - \frac{2}{8}(11.6397) + (8+1)(0.2743) + \frac{8}{12}$$

$$= 0.6771 - 0.6020 - 2.9099 + 2.4687 + 0.6667$$

$$= 0.3006$$

$U^2_{0.05,7} = 0.179$

Therefore, reject H_0. $0.002 < P < 0.005$.

SERIAL RANDOMNESS OF NOMINAL-SCALE CATEGORIES ON A CIRCLE

When dealing with the occurrence of members of two nominal-scale categories along a linear space or time, the runs test of Section 25.6 is appropriate. A runs test is also available for spatial or temporal measurements that are on a circular scale. This test may also be employed as a two-sample test, but the tests of Sections 27.4 and 27.5 are more powerful for that purpose; the circular runs test is best reserved for testing the hypothesis of random distribution of members of two categories around a circle.

We define a run on a circle as a sequence of like elements, bounded on each side by unlike elements. Similar to Section 25.6, we let n_1 be the total number of elements in the first category, n_2 the number of elements in the second category, and u the number of runs in the entire sequence of elements. For the runs test on a linear scale (Section 25.6), the number of runs may be even or odd; however, on a circle the number of runs is always even: half of the runs (i.e., $u/2$) consist of elements belonging to one of the categories, and there are also $u/2$ runs of elements of the other category.

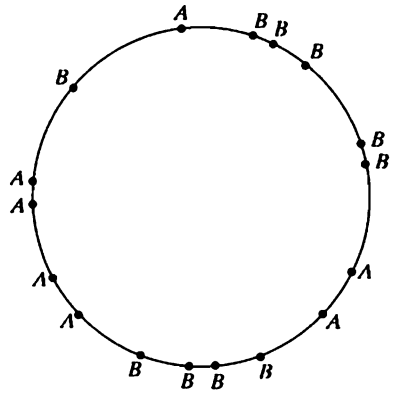
The null hypothesis may be tested by analysis of the following 2×2 contingency table (Stevens, 1939), where $u' = u/2$:

u'	$n_1 - u'$	n_1
$n_2 - u'$	$u' - 1$	$n_2 - 1$
n_2	$n_1 - 1$	$n_1 + n_2 - 1$

This should be done by the Fisher exact test of Section 24.16, as demonstrated in Example 27.25. For that test, m_1, m_2, n, and f are as defined in Section 24.16 and at the end of Appendix Table B.28. For two-tailed testing, as in Example 27.25, the second pair of critical values in that table are used.

EXAMPLE 27.25 The Two-Tailed Runs Test on a Circle

Members of the two antelope species of Example 25.8 (referred to as species A and B) are observed drinking on the shore of a pond in the following sequence:



H_0: The distribution of members of the two species around the pond is random.

H_A: The distribution of members of the two species around the pond is not random.

$n_1 = 7, n_2 = 10, u = 6, u' = 3$

3	4	7
7	2	9
10	6	16

To use Appendix Table B.28, $m_1 = 6$, $m_2 = 7$, $f = 4$, $n = 17$. For a two-tailed test, the critical values of f for $\alpha = 0.05$ are 0 and 5. Therefore, we do not reject H_0; $P \geq 0.20$.

If one or both sample sizes exceed those in Table B.28, then this 2×2 contingency table may be subjected to analysis by chi-square, but a correction for continuity should be used (Section 23.3c). Ghent and Zar (1992) discuss normal approximations for circular runs testing.

Although this discussion and Example 27.25 depict a distribution around a circle, the testing procedure is appropriate if the physical arrangement of observations is in the shape of an ellipse, a rectangle, or any other closed figure—however irregular—providing that the figure is everywhere wider than the spacing of the elements along its periphery; and it may also be used for data that are conceptually circular, such as clock times or compass directions.

(a) One-Tailed Testing. For one-tailed testing we use the first pair of critical values in Appendix Table B.28. We can test specifically whether the population is nonrandom due to clustering (also known as contagion) in the following manner. We state H_0: In the population the members of each of the two groups are not clustered (i.e., not distributed contagiously) around the circle and H_A: In the population the members of each of the two groups are clustered (i.e., distributed contagiously) around the circle;

and if $f \leq$ the first member of the pair of one-tailed critical values, then H_0 is rejected. In using a normal approximation, this H_0 is rejected if $Z \geq Z_{\alpha(1)}$ and $u' \leq \mu_{u'}$.

If our interest is specifically whether the population distribution is nonrandom owing to a tendency toward being uniform, then we state H_0: In the population the members of each of the two groups do not tend to be uniformly distributed around the circle versus H_A: In the population the members of each of the two groups tend to be uniformly distributed around the circle; and if $f \geq$ the second member of the one-tailed pair of critical values then H_0 is rejected. If a normal approximation is employed, this H_0 is rejected if $Z \geq Z_{\alpha(1)}$ and $u' \geq \mu_{u'}$.

EXERCISES

27.1. Consider the data of Exercise 26.1. Test the null hypothesis that the population is distributed uniformly around the circle (i.e., $\rho = 0$).

27.2. Consider the data of Exercise 26.2. Test the null hypothesis that time of birth is distributed uniformly around the clock (i.e., $\rho = 0$).

27.3. Trees are planted in a circle to surround a cabin and protect it from prevailing west (i.e., 270°) winds. The trees suffering the greatest wind damage are the eleven at the following directions.

(a) Using the V test, test the null hypothesis that tree damage is independent of wind direction, versus the alternate hypothesis that tree damage is concentrated around 270°.

(b) Test H_0: $\mu_a = 270°$ vs. H_A: $\mu_a \neq 270°$.

285°	295°	335°
240	275	260
280	310	300
255	260	

27.4. Test nonparametrically for uniformity, using the data of Exercise 27.1.

27.5. Test nonparametrically for the data and experimental situation of Exercise 27.3.

27.6. The direction of the spring flight of a certain bird species was recorded as follows in eight individuals released in full sunlight and seven individuals released under overcast skies:

Sunny	*Overcast*
350°	340°
340	305
315	255
10	270
20	305
355	320
345	335
360	

Using the Watson-Williams test, test the null hypothesis that the mean flight direction in this species is the same under both cloudy and sunny skies.

27.7. Using the data of Exercise 27.6, test nonparametrically the hypothesis that birds of the species under consideration fly in the same direction under sunny as well as under cloudy skies.

27.8. Times of arrival at a feeding station of members of three species of hummingbirds were recorded as follows:

Species 1	*Species 2*	*Species 3*
05:40 hr	05:30 hr	05:35 hr
07:15	07:20	08:10
09:00	09:00	08:15
11:20	09:40	10:15
15:10	11:20	14:20
17:25	15:00	15:35
	17:05	16:05
	17:20	
	17:40	

Test the null hypothesis that members of all three species have the same mean time of visiting the feeding station.

27.9. For the data in Exercise 27.6, the birds were released at a site from which their home lies due north (i.e., in a compass direction of 0°). Test whether birds orient homeward better under sunny skies than under cloudy skies.

27.10. For the data in Exercise 27.6, test whether the variability in flight direction is the same under both sky conditions.

27.11. The following data, for each of nine experimental animals, are the time of day when body temperature is greatest and the time of day when heart rate is greatest.

(a) Determine and test the correlation of these two times of day.

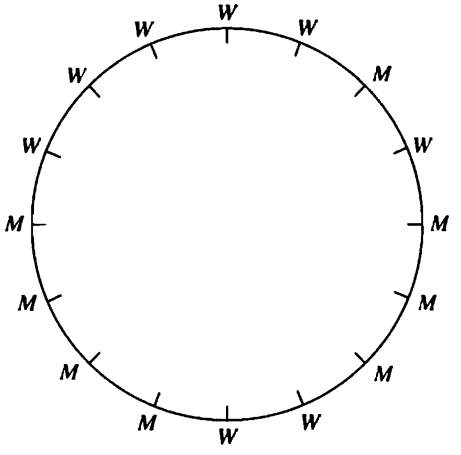
(b) Perform nonparametric correlation analysis on these data.

Animal i	Time of day: Body temperature a_i	Time of day: Heart rate b_i
1	09:50	10:40
2	10:20	09:30
3	11:40	11:10
4	08:40	08:30
5	09:10	08:40
6	10:50	09:10
7	13:20	12:50
8	13:10	13:30
9	12:40	13:00

27.12. For a sample of nine human births, the following are the times of day of the births and the ages of the mothers. Test whether there is correlation between these two variables.

Birth i	Age (yr) X_i	Time of day (hr:min) a_i
1	23	06:25
2	22	07:20
3	19	07:05
4	25	08:15
5	28	15:40
6	24	09:25
7	31	18:20
8	17	07:30
9	27	16:10

27.13. Eight men (M) and eight women (W) were asked to sit around a circular conference table; they did so in the following configuration (see figure). Test whether there is evidence that members of the same sex tend to sit next to each other.



APPENDIX A

The Greek Alphabet

Many Greek letters are commonly used in statistical and other scientific writing. English pronunciations are expressed below, guided largely by *Webster's Third New International Dictionary, Unabridged*, Merriam-Webster, 2002 (online at unabridged.merriam-webster.com, July 2, 2008). Most of these letters' names and pronunciations used by English speakers are different from those of Greek speakers (Papanastasiou, 2003). Those Greek letters used in this book appear, alphabetically by their English names, in the index.

Capital Greek letter	Lowercase Greek letter[1]	English name	Common English pronunciation[2]	Alternate English pronunciation[2]
A	α	alpha	al-fuh	
B	β	beta	bay-tuh	bee-tuh[3]
Γ	γ	gamma	gam-uh	
Δ	δ	delta	del-tuh	
E	ϵ	epsilon	ehp-suh-lahn	ehp-suh-l'n
Z	ζ	zeta	zay-tuh	zee-tuh[3]
H	η	eta	ay-tuh	ee-tuh[3]
Θ	θ	theta	thay-tuh	thee-tuh[3]
I	ι	iota	I-oh-tuh	ee-oh-tuh[3]
K	κ	kappa	kap-uh	
Λ	λ	lambda	lam-duh	
M	μ	mu	myoo	moo
N	ν	nu	noo	nyoo
Ξ	ξ	xi	zI	ksI *or* ksee[3]
O	o	omicron	oh-muhk-rahn	ah-muhk-rahn *or* ah-muhk-r'n
Π	π	pi	pI	
P	ρ	rho	ro[3]	
Σ	σ	sigma	sig-muh	
T	τ	tau	tau	taw
Υ	υ	upsilon	up-suhl-ahn	up-suhl-uhn or yoop-suhl-ahn
Φ	ϕ	phi	fI	
X	χ	chi	kI	

Capital Greek letter	Lowercase Greek letter[1]	English name	Common English pronunciation[2]	Alternate English pronunciation[2]
Ψ	ψ	psi	sI	psI *or* psee[3]
Ω	ω	omega	oh-meh-guh[4]	oh-may-guh[4] *or* oh-mee-guh[4]

[1] Less commonly encountered are these variants: epsilon, ε; theta ϑ; pi, ϖ; rho, ϱ; sigma, ς; phi, φ.

[2] In this table, accented syllables are underlined and the following pronunciation guide is used: *a* is as in *jam*; *ah* is as *a* in *calm*; *au* is as *ou* in loud; *aw* is as in *paw*; *ay* is as in *bay*; *ee* is as in *meet*; *eh* is as *e* in *met*; *I* is as in *idea*; *i* is as in *still*; *oh* is as *o* in *lone*; *oo* is as in *tool*; *th* is as in *thin*; *uh* is as *u* in *up*.

[3] This pronunciation is similar to that of Greek speakers (Papanastasiou, 2003).

[4] These pronunciations usually have the accent on the second syllable, but occasionally the accent is placed on the first syllable.

APPENDIX B

Statistical Tables and Graphs

INTERPOLATION

INTERPOLATION

In some of the statistical tables that follow (viz. Appendix Tables B.3, B.4, B.5, B.6, B.7, B.17), a critical value might be required for degrees of freedom not shown in the table, or a probability not in the table is needed for a test statistic. In such instances, interpolation may be used to compute an estimate of the required critical value or probability.

Linear Interpolation. Let us say that we desire a critical value for ν degrees of freedom, where $a < \nu < b$; let us call it C_ν. We first determine the proportion $p = (\nu - a)/(b - a)$. Then, the required critical value is determined as $C_\nu = C_b + p(C_a - C_b)$.

For example, consider $F_{0.05(2),1,260}$, which lies between $F_{0.05(2),1,200} = 5.10$ and $F_{0.05(2),1,300} = 5.07$ in Appendix Table B.4. We calculate $p = (260 - 200)/(300 - 200) = 0.600$; then our estimate is $F_{0.05(2),1,260} = C_\nu = 5.07 + (0.600)(5.10 - 5.07) = 5.07 + 0.02 = 5.09$.

Similarly, we can use linear interpolation to estimate the probability (let's call it P) associated with a test statistic (let's call it C). If, for example, we wish to know the probability of a chi-square at least as large as $\chi^2 = 7.845$, for 7 degrees of freedom ($\nu = 7$). Appendix Table B.1 shows us that P lies between 0.25 and 0.50. According to the table, $\chi^2_{0.050,7} = 6.346$ (let's call this a and use P_a to designate the probability, 0.50, associated with a) and $\chi^2_{0.025,7} = 9.037$ (let's call this b and use P_b to designate the associated probability, 0.25). We proceed as follows: $p = (C - a)/(b - a) = (7.845 - 6.346)/(9.037 - 6.346) = 1.4990/2.6910 = 0.557$, and the estimated probability is $P = P_b + p(P_a - P_b) = 0.25 + (0.557)(0.50 - 0.25) = 0.39$. That is, linear interpolation yields $\chi^2_{0.39,7} = 7.845$.

Linear interpolation cannot be used when $b = \infty$, but harmonic interpolation (below) can be.

Harmonic Interpolation. A more accurate interpolation procedure for critical-value determination is one that uses the reciprocals of degrees of freedom. (Because reciprocals of large numbers are small numbers, it is good practice to use 100 times each reciprocal, and this is what will be demonstrated here.) Let us say we desire a critical value for ν degrees of freedom, where $a < \nu < b$; call it C_ν. We first determine $p = (100/a - 100/\nu)/(100/a - 100/b)$. Then $C_\nu = C_b + (1 - p)(C_a - C_b)$.

For example, let us consider the above example of desiring $F_{0.05(2),1,260}$. We calculate $p = (100/200 - 100/260)/(100/200 - 100/300) = 0.692$; then the estimate is $F_{0.05(2),1,260} = C_\nu = 5.07 + (1 - 0.692)(5.10 - 5.07) = 5.07 + 0.01 = 5.08$.

Similarly, we can use harmonic interpolation to estimate the probability (let's call it P) associated with a test statistic (let's call it C). If, for example, we wish to know the probability of a chi-square at least as large as $\chi^2 = 7.845$, for 7 degrees of freedom ($\nu = 7$). Table B.1 shows us that P lies between 0.25 and 0.50. This table tells us that $\chi^2_{0.50,7} = 6.346$ (let's call this a and use P_a to designate the probability, 0.50, associated with a) and $\chi^2_{0.025,7} = 9.037$ (let's call this b and use P_b to designate its probability, 0.25). We proceed as follows: $p = (100/a - 100/C)/(100/a - 100/b) = (100/6.346 - 100/7.845)/(100/6.346 - 100/9.037) = (15.7580 - 12.7470)/(15.7580 - 11.0656) = 0.642$, and the estimated probability is $P = P_b + (1 - p)(P_a - P_b) = 0.25 + (1 - 0.642)(0.50 - 0.25) = 0.34$. That is, harmonic interpolation yields $\chi^2_{0.34,7} = 7.845$.

Harmonic interpolation is especially useful when $b = \infty$. For example, to determine $t_{0.01(2),2800}$, which lies between $t_{0.01(2),1000} = 2.581$ and $t_{0.01(2),\infty} = 2.5758$ in Appendix Table B.3, we calculate $p = (100/1000 - 100/2800)/(100/1000 - 100/\infty) = 0.0643/0.1000 = 0.6430$. Then, $t_{0.01(2),2800} = C_\nu = 2.5758 + (1 - 0.6430)(2.581 - 2.5758) = 2.5758 + 0.0019 = 2.578$. (Note that $100/\infty = 0$.)

TABLE B.1: Critical Values of the Chi-Square (χ^2) Distribution

ν	α: 0.999	0.995	0.99	0.975	0.95	0.90	0.75	0.50	0.25	0.10	0.05	0.025	0.01	0.005	0.001
1	0.000	0.000	0.000	0.001	0.004	0.016	0.102	0.455	1.323	2.706	3.841	5.024	6.635	7.879	10.828
2	0.002	0.010	0.020	0.051	0.103	0.211	0.575	1.386	2.773	4.605	5.991	7.378	9.210	10.597	13.816
3	0.024	0.072	0.115	0.216	0.352	0.584	1.213	2.366	4.108	6.251	7.815	9.348	11.345	12.838	16.266
4	0.091	0.207	0.297	0.484	0.711	1.064	1.923	3.357	5.385	7.779	9.488	11.143	13.277	14.860	18.467
5	0.210	0.412	0.554	0.831	1.145	1.610	2.675	4.351	6.626	9.236	11.070	12.833	15.086	16.750	20.515
6	0.381	0.676	0.872	1.237	1.635	2.204	3.455	5.348	7.841	10.645	12.592	14.449	16.812	18.548	22.458
7	0.599	0.989	1.239	1.690	2.167	2.833	4.255	6.346	9.037	12.017	14.067	16.013	18.475	20.278	24.322
8	0.857	1.344	1.646	2.180	2.733	3.490	5.071	7.344	10.219	13.362	15.507	17.535	20.090	21.955	26.124
9	1.152	1.735	2.088	2.700	3.325	4.168	5.899	8.343	11.389	14.684	16.919	19.023	21.666	23.589	27.877
10	1.479	2.156	2.558	3.247	3.940	4.865	6.737	9.342	12.549	15.987	18.307	20.483	23.209	25.188	29.588
11	1.834	2.603	3.053	3.816	4.575	5.578	7.584	10.341	13.701	17.275	19.675	21.920	24.725	26.757	31.264
12	2.214	3.074	3.571	4.404	5.226	6.304	8.438	11.340	14.845	18.549	21.026	23.337	26.217	28.300	32.909
13	2.617	3.565	4.107	5.009	5.892	7.042	9.299	12.340	15.984	19.812	22.362	24.736	27.688	29.819	34.528
14	3.041	4.075	4.660	5.629	6.571	7.790	10.165	13.339	17.117	21.064	23.685	26.119	29.141	31.319	36.123
15	3.483	4.601	5.229	6.262	7.261	8.547	11.037	14.339	18.245	22.307	24.996	27.488	30.578	32.801	37.697
16	3.942	5.142	5.812	6.908	7.962	9.312	11.912	15.338	19.369	23.542	26.296	28.845	32.000	34.267	39.252
17	4.416	5.697	6.408	7.564	8.672	10.085	12.792	16.338	20.489	24.769	27.587	30.191	33.409	35.718	40.790
18	4.905	6.265	7.015	8.231	9.390	10.865	13.675	17.338	21.605	25.989	28.869	31.526	34.805	37.156	42.312
19	5.407	6.844	7.633	8.907	10.117	11.651	14.562	18.338	22.718	27.204	30.144	32.852	36.191	38.582	43.820
20	5.921	7.434	8.260	9.591	10.851	12.443	15.452	19.337	23.828	28.412	31.410	34.170	37.566	39.997	45.315
21	6.447	8.034	8.897	10.283	11.591	13.240	16.344	20.337	24.935	29.615	32.671	35.479	38.932	41.401	46.797
22	6.983	8.643	9.542	10.982	12.338	14.041	17.240	21.337	26.039	30.813	33.924	36.781	40.289	42.796	48.268
23	7.529	9.260	10.196	11.689	13.091	14.848	18.137	22.337	27.141	32.007	35.172	38.076	41.638	44.181	49.728
24	8.085	9.886	10.856	12.401	13.848	15.659	19.037	23.337	28.241	33.196	36.415	39.364	42.980	45.559	51.179
25	8.649	10.520	11.524	13.120	14.611	16.473	19.939	24.337	29.339	34.382	37.652	40.646	44.314	46.928	52.620
26	9.222	11.160	12.198	13.844	15.379	17.292	20.843	25.336	30.435	35.563	38.885	41.923	45.642	48.290	54.052
27	9.803	11.808	12.879	14.573	16.151	18.114	21.749	26.336	31.528	36.741	40.113	43.195	46.963	49.645	55.476
28	10.391	12.461	13.565	15.308	16.928	18.939	22.657	27.336	32.620	37.916	41.337	44.461	48.278	50.993	56.892
29	10.986	13.121	14.256	16.047	17.708	19.768	23.567	28.336	33.711	39.087	42.557	45.722	49.588	52.336	58.301
30	11.588	13.787	14.953	16.791	18.493	20.599	24.478	29.336	34.800	40.256	43.773	46.979	50.892	53.672	59.703
31	12.196	14.458	15.655	17.539	19.281	21.434	25.390	30.336	35.887	41.422	44.985	48.232	52.191	55.003	61.098
32	12.811	15.134	16.362	18.291	20.072	22.271	26.304	31.336	36.973	42.585	46.194	49.480	53.486	56.328	62.487
33	13.431	15.815	17.074	19.047	20.867	23.110	27.219	32.336	38.058	43.745	47.400	50.725	54.776	57.648	63.870
34	14.057	16.501	17.789	19.806	21.664	23.952	28.136	33.336	39.141	44.903	48.602	51.966	56.061	58.964	65.247
35	14.688	17.192	18.509	20.569	22.465	24.797	29.054	34.336	40.223	46.059	49.802	53.203	57.342	60.275	66.619
36	15.324	17.887	19.233	21.336	23.269	25.643	29.973	35.336	41.304	47.212	50.998	54.437	58.619	61.581	67.985
37	15.965	18.586	19.960	22.106	24.075	26.492	30.893	36.336	42.383	48.363	52.192	55.668	59.893	62.883	69.346
38	16.611	19.289	20.691	22.878	24.884	27.343	31.815	37.335	43.462	49.513	53.384	56.896	61.162	64.181	70.703
39	17.262	19.996	21.426	23.654	25.695	28.196	32.737	38.335	44.539	50.660	54.572	58.120	62.428	65.476	72.055
40	17.916	20.707	22.164	24.433	26.509	29.051	33.660	39.335	45.616	51.805	55.758	59.342	63.691	66.766	73.402
41	18.576	21.421	22.906	25.215	27.326	29.907	34.585	40.335	46.692	52.949	56.942	60.561	64.950	68.053	74.745
42	19.239	22.138	23.650	25.999	28.144	30.765	35.510	41.335	47.766	54.090	58.124	61.777	66.206	69.336	76.084
43	19.906	22.859	24.398	26.785	28.965	31.625	36.436	42.335	48.840	55.230	59.304	62.990	67.459	70.616	77.419
44	20.576	23.584	25.148	27.575	29.787	32.487	37.363	43.335	49.913	56.369	60.481	64.201	68.710	71.893	78.750
45	21.251	24.311	25.901	28.366	30.612	33.350	38.291	44.335	50.985	57.505	61.656	65.410	69.957	73.166	80.077
46	21.929	25.041	26.657	29.160	31.439	34.215	39.220	45.335	52.056	58.641	62.830	66.617	71.201	74.437	81.400
47	22.610	25.775	27.416	29.956	32.268	35.081	40.149	46.335	53.127	59.774	64.001	67.821	72.443	75.704	82.720
48	23.295	26.511	28.177	30.755	33.098	35.949	41.079	47.335	54.196	60.907	65.171	69.023	73.683	76.969	84.037

TABLE B.1 (cont.): Critical Values of the Chi-Square (χ^2) Distribution

ν	α: 0.999	0.995	0.99	0.975	0.95	0.90	0.75	0.50	0.25	0.10	0.05	0.025	0.01	0.005	0.001
49	23.983	27.249	28.941	31.555	33.930	36.818	42.010	48.335	55.265	62.038	66.339	70.222	74.919	78.231	85.351
50	24.674	27.991	29.707	32.357	34.764	37.689	42.942	49.335	56.334	63.167	67.505	71.420	76.154	79.490	86.661
51	25.368	28.735	30.475	33.162	35.600	38.560	43.874	50.335	57.401	64.295	68.669	72.616	77.386	80.747	87.968
52	26.065	29.481	31.246	33.968	36.437	39.433	44.808	51.335	58.468	65.422	69.832	73.810	78.616	82.001	89.272
53	26.765	30.230	32.019	34.776	37.276	40.308	45.741	52.335	59.534	66.548	70.993	75.002	79.843	83.253	90.573
54	27.468	30.981	32.793	35.586	38.116	41.183	46.676	53.335	60.600	67.673	72.153	76.192	81.069	84.502	91.872
55	28.173	31.735	33.570	36.398	38.958	42.060	47.610	54.335	61.665	68.796	73.311	77.380	82.292	85.749	93.168
56	28.881	32.491	34.350	37.212	39.801	42.937	48.546	55.335	62.729	69.919	74.468	78.567	83.513	86.994	94.461
57	29.592	33.248	35.131	38.027	40.646	43.816	49.482	56.335	63.793	71.040	75.624	79.752	84.733	88.236	95.751
58	30.305	34.008	35.913	38.844	41.492	44.696	50.419	57.335	64.857	72.160	76.778	80.936	85.950	89.477	97.039
59	31.021	34.770	36.698	39.662	42.339	45.577	51.356	58.335	65.919	73.279	77.931	82.117	87.166	90.715	98.324
60	31.738	35.535	37.485	40.482	43.188	46.459	52.294	59.335	66.981	74.397	79.082	83.298	88.379	91.952	99.607
61	32.459	36.301	38.273	41.303	44.038	47.342	53.232	60.335	68.043	75.514	80.232	84.476	89.591	93.186	100.888
62	33.181	37.068	39.063	42.126	44.889	48.226	54.171	61.335	69.104	76.630	81.381	85.654	90.802	94.419	102.166
63	33.906	37.838	39.855	42.950	45.741	49.111	55.110	62.335	70.165	77.745	82.529	86.830	92.010	95.649	103.442
64	34.633	38.610	40.649	43.776	46.595	49.996	56.050	63.335	71.225	78.860	83.675	88.004	93.217	96.878	104.716
65	35.362	39.383	41.444	44.603	47.450	50.883	56.990	64.335	72.285	79.973	84.821	89.177	94.422	98.105	105.988
66	36.093	40.158	42.240	45.431	48.305	51.770	57.931	65.335	73.344	81.085	85.965	90.349	95.626	99.330	107.258
67	36.826	40.935	43.038	46.261	49.162	52.659	58.872	66.335	74.403	82.197	87.108	91.519	96.828	100.554	108.526
68	37.561	41.713	43.838	47.092	50.020	53.548	59.814	67.335	75.461	83.308	88.250	92.689	98.028	101.776	109.791
69	38.298	42.494	44.639	47.924	50.879	54.438	60.756	68.334	76.519	84.418	89.391	93.856	99.228	102.996	111.055
70	39.036	43.275	45.442	48.758	51.739	55.329	61.698	69.334	77.577	85.527	90.531	95.023	100.425	104.215	112.317
71	39.777	44.058	46.246	49.592	52.600	56.221	62.641	70.334	78.634	86.635	91.670	96.189	101.621	105.432	113.577
72	40.520	44.843	47.051	50.428	53.462	57.113	63.585	71.334	79.690	87.743	92.808	97.353	102.816	106.648	114.835
73	41.264	45.629	47.858	51.265	54.325	58.006	64.528	72.334	80.747	88.850	93.945	98.516	104.010	107.862	116.092
74	42.010	46.417	48.666	52.103	55.189	58.900	65.472	73.334	81.803	89.956	95.081	99.678	105.202	109.074	117.346
75	42.757	47.206	49.475	52.942	56.054	59.795	66.417	74.334	82.858	91.061	96.217	100.839	106.393	110.286	118.599
76	43.507	47.997	50.286	53.782	56.920	60.690	67.362	75.334	83.913	92.166	97.351	101.999	107.583	111.495	119.850
77	44.258	48.788	51.097	54.623	57.786	61.586	68.307	76.334	84.968	93.270	98.484	103.158	108.771	112.704	121.100
78	45.010	49.582	51.910	55.466	58.654	62.483	69.252	77.334	86.022	94.374	99.617	104.316	109.958	113.911	122.348
79	45.764	50.376	52.725	56.309	59.522	63.380	70.198	78.334	87.077	95.476	100.749	105.473	111.144	115.117	123.594
80	46.520	51.172	53.540	57.153	60.391	64.278	71.145	79.334	88.130	96.578	101.879	106.629	112.329	116.321	124.839
81	47.277	51.969	54.357	57.998	61.261	65.176	72.091	80.334	89.184	97.680	103.010	107.783	113.512	117.524	126.083
82	48.036	52.767	55.174	58.845	62.132	66.076	73.038	81.334	90.237	98.780	104.139	108.937	114.695	118.726	127.324
83	48.796	53.567	55.993	59.692	63.004	66.976	73.985	82.334	91.289	99.880	105.267	110.090	115.876	119.927	128.565
84	49.557	54.368	56.813	60.540	63.876	67.876	74.933	83.334	92.342	100.980	106.395	111.242	117.057	121.126	129.804
85	50.320	55.170	57.634	61.389	64.749	68.777	75.881	84.334	93.394	102.079	107.522	112.393	118.236	122.325	131.041
86	51.085	55.973	58.456	62.239	65.623	69.679	76.829	85.334	94.446	103.177	108.648	113.544	119.414	123.522	132.277
87	51.850	56.777	59.279	63.089	66.498	70.581	77.777	86.334	95.497	104.275	109.773	114.693	120.591	124.718	133.512
88	52.617	57.582	60.103	63.941	67.373	71.484	78.726	87.334	96.548	105.372	110.898	115.841	121.767	125.913	134.745
89	53.386	58.389	60.928	64.793	68.249	72.387	79.675	88.334	97.599	106.469	112.022	116.989	122.942	127.106	135.978
90	54.155	59.196	61.754	65.647	69.126	73.291	80.625	89.334	98.650	107.565	113.145	118.136	124.116	128.299	137.208
91	54.926	60.005	62.581	66.501	70.003	74.196	81.574	90.334	99.700	108.661	114.268	119.282	125.289	129.491	138.438
92	55.698	60.815	63.409	67.356	70.882	75.100	82.524	91.334	100.750	109.756	115.390	120.427	126.462	130.681	139.666
93	56.472	61.625	64.238	68.211	71.760	76.006	83.474	92.334	101.800	110.850	116.511	121.571	127.633	131.871	140.893
94	57.246	62.437	65.068	69.068	72.640	76.912	84.425	93.334	102.850	111.944	117.632	122.715	128.803	133.059	142.119
95	58.022	63.250	65.898	69.925	73.520	77.818	85.376	94.334	103.899	113.038	118.752	123.858	129.973	134.247	143.344

TABLE B.1 (cont.): Critical Values of the Chi-Square (χ^2) Distribution

ν	α: 0.999	0.995	0.99	0.975	0.95	0.90	0.75	0.50	0.25	0.10	0.05	0.025	0.01	0.005	0.001
96	58.799	64.063	66.730	70.783	74.401	78.725	86.327	95.334	104.948	114.131	119.871	125.000	131.141	135.433	144.567
97	59.577	64.878	67.562	71.642	75.282	79.633	87.278	96.334	105.997	115.223	120.990	126.141	132.309	136.619	145.789
98	60.356	65.694	68.396	72.501	76.164	80.541	88.229	97.334	107.045	116.315	122.108	127.282	133.476	137.803	147.010
99	61.137	66.510	69.230	73.361	77.046	81.449	89.181	98.334	108.093	117.407	123.225	128.422	134.642	138.987	148.230
100	61.918	67.328	70.065	74.222	77.929	82.358	90.133	99.334	109.141	118.498	124.342	129.561	135.807	140.169	149.449
101	62.701	68.146	70.901	75.083	78.813	83.267	91.085	100.334	110.189	119.589	125.458	130.700	136.971	141.351	150.667
102	63.484	68.965	71.737	75.946	79.697	84.177	92.038	101.334	111.236	120.679	126.574	131.838	138.134	142.532	151.884
103	64.269	69.785	72.575	76.809	80.582	85.088	92.991	102.334	112.284	121.769	127.689	132.975	139.297	143.712	153.099
104	65.055	70.606	73.413	77.672	81.468	85.998	93.944	103.334	113.331	122.858	128.804	134.111	140.459	144.891	154.314
105	65.841	71.428	74.252	78.536	82.354	86.909	94.897	104.334	114.378	123.947	129.918	135.247	141.620	146.070	155.528
106	66.629	72.251	75.092	79.401	83.240	87.821	95.850	105.334	115.424	125.035	131.031	136.382	142.780	147.247	156.740
107	67.418	73.075	75.932	80.267	84.127	88.733	96.804	106.334	116.471	126.123	132.144	137.517	143.940	148.424	157.952
108	68.207	73.899	76.774	81.133	85.015	89.645	97.758	107.334	117.517	127.211	133.257	138.651	145.099	149.599	159.162
109	68.998	74.724	77.616	82.000	85.903	90.558	98.712	108.334	118.563	128.298	134.369	139.784	146.257	150.774	160.372
110	69.790	75.550	78.458	82.867	86.792	91.471	99.666	109.334	119.608	129.385	135.480	140.917	147.414	151.948	161.581
111	70.582	76.377	79.302	83.735	87.681	92.385	100.620	110.334	120.654	130.472	136.591	142.049	148.571	153.122	162.788
112	71.376	77.204	80.146	84.604	88.570	93.299	101.575	111.334	121.699	131.558	137.701	143.180	149.727	154.294	163.995
113	72.170	78.033	80.991	85.473	89.461	94.213	102.530	112.334	122.744	132.643	138.811	144.311	150.882	155.466	165.201
114	72.965	78.862	81.836	86.342	90.351	95.128	103.485	113.334	123.789	133.729	139.921	145.441	152.037	156.637	166.406
115	73.761	79.692	82.682	87.213	91.242	96.043	104.440	114.334	124.834	134.813	141.030	146.571	153.191	157.808	167.610
116	74.558	80.522	83.529	88.084	92.134	96.958	105.396	115.334	125.878	135.898	142.138	147.700	154.344	158.977	168.813
117	75.356	81.353	84.377	88.955	93.026	97.874	106.352	116.334	126.923	136.982	143.246	148.829	155.496	160.146	170.016
118	76.155	82.185	85.225	89.827	93.918	98.790	107.307	117.334	127.967	138.066	144.354	149.957	156.648	161.314	171.217
119	76.955	83.018	86.074	90.700	94.811	99.707	108.263	118.334	129.011	139.149	145.461	151.084	157.800	162.481	172.418
120	77.755	83.852	86.923	91.573	95.705	100.624	109.220	119.334	130.055	140.233	146.567	152.211	158.950	163.648	173.617
121	78.557	84.686	87.773	92.446	96.598	101.541	110.176	120.334	131.098	141.315	147.674	153.338	160.100	164.814	174.816
122	79.359	85.521	88.624	93.320	97.493	102.458	111.133	121.334	132.142	142.398	148.779	154.464	161.250	165.980	176.014
123	80.162	86.356	89.475	94.195	98.387	103.376	112.089	122.334	133.185	143.480	149.885	155.589	162.398	167.144	177.212
124	80.965	87.192	90.327	95.070	99.283	104.295	113.046	123.334	134.228	144.562	150.989	156.714	163.546	168.308	178.408
125	81.770	88.029	91.180	95.946	100.178	105.213	114.004	124.334	135.271	145.643	152.094	157.839	164.694	169.471	179.604
126	82.575	88.866	92.033	96.822	101.074	106.132	114.961	125.334	136.313	146.724	153.198	158.962	165.841	170.634	180.799
127	83.381	89.704	92.887	97.698	101.971	107.051	115.918	126.334	137.356	147.805	154.302	160.086	166.987	171.796	181.993
128	84.188	90.543	93.741	98.576	102.867	107.971	116.876	127.334	138.398	148.885	155.405	161.209	168.133	172.957	183.186
129	84.996	91.383	94.596	99.453	103.765	108.891	117.834	128.334	139.440	149.965	156.508	162.331	169.278	174.118	184.379
130	85.804	92.223	95.451	100.331	104.662	109.811	118.792	129.334	140.482	151.045	157.610	163.453	170.423	175.278	185.571
131	86.613	93.063	96.307	101.210	105.560	110.732	119.750	130.334	141.524	152.125	158.712	164.575	171.567	176.438	186.762
132	87.423	93.904	97.163	102.089	106.459	111.652	120.708	131.334	142.566	153.204	159.814	165.696	172.711	177.597	187.953
133	88.233	94.746	98.021	102.968	107.357	112.573	121.667	132.334	143.608	154.283	160.915	166.816	173.854	178.755	189.142
134	89.044	95.588	98.878	103.848	108.257	113.495	122.625	133.334	144.649	155.361	162.016	167.936	174.996	179.913	190.331
135	89.856	96.431	99.736	104.729	109.156	114.417	123.584	134.334	145.690	156.440	163.116	169.056	176.138	181.070	191.520
136	90.669	97.275	100.595	105.609	110.056	115.338	124.543	135.334	146.731	157.518	164.216	170.175	177.280	182.226	192.707
137	91.482	98.119	101.454	106.491	110.956	116.261	125.502	136.334	147.772	158.595	165.316	171.294	178.421	183.382	193.894
138	92.296	98.964	102.314	107.372	111.857	117.183	126.461	137.334	148.813	159.673	166.415	172.412	179.561	184.538	195.080
139	93.111	99.809	103.174	108.254	112.758	118.106	127.421	138.334	149.854	160.750	167.514	173.530	180.701	185.693	196.266
140	93.926	100.655	104.034	109.137	113.659	119.029	128.380	139.334	150.894	161.827	168.613	174.648	181.840	186.847	197.451

Table B.1 was prepared using Equation 26.4.6 of Zelen and Severo (1964). The chi-square values were calculated to six decimal places and then rounded to three decimal places.

Examples:

$$\chi^2_{0.05,12} = 21.026 \quad \text{and} \quad \chi^2_{0.0,138} = 61.162$$

For large degrees of freedom (ν), critical values of χ^2 can be approximated very well by

$$\chi^2_{\alpha,\nu} = \nu\left(1 - \frac{2}{9\nu} + Z_{\alpha(1)}\sqrt{\frac{2}{9\nu}}\right)^3$$

(Wilson and Hilferty, 1931). It is for this purpose that the values of $Z_{\alpha(1)}$ are given below (from White, 1970).

α:	0.999	0.995	0.99	0.975	0.95	0.90	0.75
$Z_{\alpha(1)}$:	−3.09023	−2.57583	−2.32635	−1.95996	−1.64485	−1.28155	−0.67449

α:	0.50	0.25	0.10	0.05	0.025	0.01	0.005	0.001
$Z_{\alpha(1)}$:	0.00000	0.67449	1.28155	1.64485	1.95996	2.32635	2.57583	3.09023

The percent error, that is, (approximation − true value)/true value × 100%, resulting from the use of this approximation is as follows:

ν	α: 0.999	0.995	0.99	0.975	0.95	0.90	0.75	0.50	0.25	0.10	0.05	0.025	0.01	0.005	0.001
30	−0.7	−0.3	−0.2	−0.1	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.1	0.2
100	−0.1	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*
140	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*

where the asterisk indicates a percent error the absolute value of which is less than 0.05%. Zar (1978) and Lin (1988a) discuss this and other approximations for $\chi^2_{\alpha,\nu}$.

For one degree of freedom, the χ^2 distribution is related to the normal distribution (Appendix Table B.2) and the t distribution (Appendix Table B.3) as*

$$\chi^2_{\alpha,1} = \left(Z_{\alpha(2)}\right)^2 = \left(t_{\alpha(2),\infty}\right)^2.$$

For example, $\chi^2_{0.05,1} = 3.841$, and $(Z_{0.05(2)})^2 = (t_{0.05(2),\infty})^2 = (1.9600)^2 = 3.8416$.

The relationship between χ^2 and F (Appendix Table B.4) is

$$\chi^2_{\alpha,\nu} = \nu F_{\alpha(1),\nu,\infty}.$$

For example, $\chi^2_{0.05,9} = 16.919$, and $(9)(F_{0.05(1),9,\infty}) = (9)(1.88) = 16.92$.

TABLE B.2: Proportions of the Normal Curve (One-Tailed)
This table gives the proportion of the normal curve in the right-hand tail that lies at or beyond (i.e., is at least as extreme as) a given normal deviate; for example, $Z = |(X_i - \mu)|/\sigma$ or $Z = |(\bar{X} - \mu)|/\sigma_{\bar{X}}$. For example, the proportion of a normal distribution for which $Z \geq 1.51$ is 0.0655.

Z	0	1	2	3	4	5	6	7	8	9	Z
0.0	0.5000	0.4960	0.4920	0.4880	0.4840	0.4801	0.4761	0.4721	0.4681	0.4641	0.0
0.1	0.4602	0.4562	0.4522	0.4483	0.4443	0.4404	0.4364	0.4325	0.4286	0.4247	0.1
0.2	0.4207	0.4168	0.4129	0.4090	0.4052	0.4013	0.3974	0.3936	0.3897	0.3859	0.2
0.3	0.3821	0.3783	0.3745	0.3707	0.3669	0.3632	0.3594	0.3557	0.3520	0.3483	0.3
0.4	0.3446	0.3409	0.3372	0.3336	0.3300	0.3264	0.3228	0.3192	0.3156	0.3121	0.4
0.5	0.3085	0.3050	0.3015	0.2981	0.2946	0.2912	0.2877	0.2843	0.2810	0.2776	0.5
0.6	0.2743	0.2709	0.2676	0.2643	0.2611	0.2578	0.2546	0.2514	0.2483	0.2451	0.6
0.7	0.2420	0.2389	0.2358	0.2327	0.2297	0.2266	0.2236	0.2207	0.2177	0.2148	0.7
0.8	0.2119	0.2090	0.2061	0.2033	0.2005	0.1977	0.1949	0.1922	0.1894	0.1867	0.8
0.9	0.1841	0.1814	0.1788	0.1762	0.1736	0.1711	0.1685	0.1660	0.1635	0.1611	0.9
1.0	0.1587	0.1562	0.1539	0.1515	0.1492	0.1469	0.1446	0.1423	0.1401	0.1379	1.0
1.1	0.1357	0.1335	0.1314	0.1292	0.1271	0.1251	0.1230	0.1210	0.1190	0.1170	1.1
1.2	0.1151	0.1131	0.1112	0.1093	0.1075	0.1056	0.1038	0.1020	0.1003	0.0985	1.2
1.3	0.0968	0.0951	0.0934	0.0918	0.0901	0.0885	0.0869	0.0853	0.0838	0.0823	1.3
1.4	0.0808	0.0793	0.0778	0.0764	0.0749	0.0735	0.0721	0.0708	0.0694	0.0681	1.4
1.5	0.0668	0.0655	0.0643	0.0630	0.0618	0.0606	0.0594	0.0582	0.0571	0.0559	1.5
1.6	0.0548	0.0537	0.0526	0.0516	0.0505	0.0495	0.0485	0.0475	0.0465	0.0455	1.6
1.7	0.0446	0.0436	0.0427	0.0418	0.0409	0.0401	0.0392	0.0384	0.0375	0.0367	1.7
1.8	0.0359	0.0351	0.0344	0.0336	0.0329	0.0322	0.0314	0.0307	0.0301	0.0294	1.8
1.9	0.0287	0.0281	0.0274	0.0268	0.0262	0.0256	0.0250	0.0244	0.0239	0.0233	1.9
2.0	0.0228	0.0222	0.0217	0.0212	0.0207	0.0202	0.0197	0.0192	0.0188	0.0183	2.0
2.1	0.0179	0.0174	0.0170	0.0166	0.0162	0.0158	0.0154	0.0150	0.0146	0.0143	2.1
2.2	0.0139	0.0136	0.0132	0.0129	0.0125	0.0122	0.0119	0.0116	0.0113	0.0110	2.2
2.3	0.0107	0.0104	0.0102	0.0099	0.0096	0.0094	0.0091	0.0089	0.0087	0.0084	2.3
2.4	0.0082	0.0080	0.0078	0.0075	0.0073	0.0071	0.0069	0.0068	0.0066	0.0064	2.4
2.5	0.0062	0.0060	0.0059	0.0057	0.0055	0.0054	0.0052	0.0051	0.0049	0.0048	2.5
2.6	0.0047	0.0045	0.0044	0.0043	0.0041	0.0040	0.0039	0.0038	0.0037	0.0036	2.6
2.7	0.0035	0.0034	0.0033	0.0032	0.0031	0.0030	0.0029	0.0028	0.0027	0.0026	2.7
2.8	0.0026	0.0025	0.0024	0.0023	0.0023	0.0022	0.0021	0.0021	0.0020	0.0019	2.8
2.9	0.0019	0.0018	0.0018	0.0017	0.0016	0.0016	0.0015	0.0015	0.0014	0.0014	2.9
3.0	0.0013	0.0013	0.0013	0.0012	0.0012	0.0011	0.0011	0.0011	0.0010	0.0010	3.0
3.1	0.0010	0.0009	0.0009	0.0009	0.0008	0.0008	0.0008	0.0008	0.0007	0.0007	3.1
3.2	0.0007	0.0007	0.0006	0.0006	0.0006	0.0006	0.0006	0.0005	0.0005	0.0005	3.2
3.3	0.0005	0.0005	0.0005	0.0004	0.0004	0.0004	0.0004	0.0004	0.0004	0.0003	3.3
3.4	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0003	0.0002	3.4
3.5	0.0002	0.0002	0.0002	0.0002	0.0002	0.0002	0.0002	0.0002	0.0002	0.0002	3.5
3.6	0.0002	0.0002	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	3.6
3.7	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	3.7
3.8	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	3.8

Table B.2 was prepared using an algorithm of Hastings (1955: 187). Probabilities for values of Z in between those shown in this table may be obtained by either linear or harmonic interpolation. David (2005) presented a brief history of tables related to the normal distribution.

Critical values of Z may be found in Appendix Table B.3 as $Z_\alpha = t_{\alpha,\infty}$. For example, $Z_{0.05(2)} = t_{0.05(2),\infty} = 1.9600$. These critical values are related to those of χ^2 and F as

$$Z_{\alpha(2)} = t_{\alpha(2),\infty} = \sqrt{F_{\alpha(1),1,\infty}} = \sqrt{\chi^2_{\alpha,1}}$$

(first described by R. A. Fisher in 1924 and published in 1928; Lehmann, 1999).

Many computer programs and calculators can generate these proportions. Also, there are many quick and easy approximations. For example, we can compute

$$P = \left[1 - \sqrt{1 - e^{-c^2}}\right]/2,$$

where setting $c = 0.806z(1 - 0.018z)$ (Hamaker, 1978) yields P dependable to the third decimal place for z as small as about 0.2, and using $c = z/(1.237 + 0.0249z)$ (Lin, 1988b) achieves that accuracy for z as small as about 0.1. Hawkes's (1982) formulas are accurate to within 1 in the fifth decimal place, though they require more computation.

Table B.3 was prepared using Equations 26.7.3 and 26.7.4 of Zelen and Severo (1964), except for the values at infinity degrees of freedom, which are adapted from White (1970). Except for the values at infinity degrees of freedom, t was calculated to eight decimal places and then rounded to three decimal places.

Examples:

$$t_{0.05(2),13} = 2.160 \quad \text{and} \quad t_{0.01(1),19} = 2.539$$

If a critical value is needed for degrees of freedom not on this table, one may conservatively employ the next smaller ν that is on the table. Or, the needed critical value, for $\nu < 1000$, may be calculated by linear interpolation, with an error of no more than 0.001. If a little more accuracy is desired, or if the needed ν is >1000, then harmonic interpolation should be used.

Critical values of t for infinity degrees of freedom are related to critical values of Z and χ^2 as

$$t_{\alpha(1),\infty} = Z_{\alpha(1)} \quad \text{and} \quad t_{\alpha(2),\infty} = Z_{\alpha(2)} = \sqrt{\chi^2_{\alpha,1}}.$$

The accuracy of arithmetic and harmonic interpolation of t is within 0.002 for ν at least as large as that shown below.

	$\alpha(2)$:	0.50	0.20	0.10	0.05	0.02	0.01	0.005	0.002	0.001
	$\alpha(1)$:	0.25	0.10	0.05	0.025	0.01	0.005	0.0025	0.001	0.0005
Arithmetic		3	4	5	6	7	7	9	9	10
Harmonic		2	3	4	4	5	5	6	7	7

TABLE B.3: Critical Values of the t Distribution

ν	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	1.000	3.078	6.314	12.706	31.821	63.657	127.321	318.309	636.619
2	0.816	1.886	2.920	4.303	6.965	9.925	14.089	22.327	31.599
3	0.765	1.638	2.353	3.182	4.541	5.841	7.453	10.215	12.924
4	0.741	1.533	2.132	2.776	3.747	4.604	5.598	7.173	8.610
5	0.727	1.476	2.015	2.571	3.365	4.032	4.773	5.893	6.869
6	0.718	1.440	1.943	2.447	3.143	3.707	4.317	5.208	5.959
7	0.711	1.415	1.895	2.365	2.998	3.499	4.029	4.785	5.408
8	0.706	1.397	1.860	2.306	2.896	3.355	3.833	4.501	5.041
9	0.703	1.383	1.833	2.262	2.821	3.250	3.690	4.297	4.781
10	0.700	1.372	1.812	2.228	2.764	3.169	3.581	4.144	4.587
11	0.697	1.363	1.796	2.201	2.718	3.106	3.497	4.025	4.437
12	0.695	1.356	1.782	2.179	2.681	3.055	3.428	3.930	4.318
13	0.694	1.350	1.771	2.160	2.650	3.012	3.372	3.852	4.221
14	0.692	1.345	1.761	2.145	2.624	2.977	3.326	3.787	4.140
15	0.691	1.341	1.753	2.131	2.602	2.947	3.286	3.733	4.073
16	0.690	1.337	1.746	2.120	2.583	2.921	3.252	3.686	4.015
17	0.689	1.333	1.740	2.110	2.567	2.898	3.222	3.646	3.965
18	0.688	1.330	1.734	2.101	2.552	2.878	3.197	3.610	3.922
19	0.688	1.328	1.729	2.093	2.539	2.861	3.174	3.579	3.883
20	0.687	1.325	1.725	2.086	2.528	2.845	3.153	3.552	3.850
21	0.686	1.323	1.721	2.080	2.518	2.831	3.135	3.527	3.819
22	0.686	1.321	1.717	2.074	2.508	2.819	3.119	3.505	3.792
23	0.685	1.319	1.714	2.069	2.500	2.807	3.104	3.485	3.768
24	0.685	1.318	1.711	2.064	2.492	2.797	3.091	3.467	3.745
25	0.684	1.316	1.708	2.060	2.485	2.787	3.078	3.450	3.725
26	0.684	1.315	1.706	2.056	2.479	2.779	3.067	3.435	3.707
27	0.684	1.314	1.703	2.052	2.473	2.771	3.057	3.421	3.690
28	0.683	1.313	1.701	2.048	2.467	2.763	3.047	3.408	3.674
29	0.683	1.311	1.699	2.045	2.462	2.756	3.038	3.396	3.659
30	0.683	1.310	1.697	2.042	2.457	2.750	3.030	3.385	3.646
31	0.682	1.309	1.696	2.040	2.453	2.744	3.022	3.375	3.633
32	0.682	1.309	1.694	2.037	2.449	2.738	3.015	3.365	3.622
33	0.682	1.308	1.692	2.035	2.445	2.733	3.008	3.356	3.611
34	0.682	1.307	1.691	2.032	2.441	2.728	3.002	3.348	3.601
35	0.682	1.306	1.690	2.030	2.438	2.724	2.996	3.340	3.591
36	0.681	1.306	1.688	2.028	2.434	2.719	2.990	3.333	3.582
37	0.681	1.305	1.687	2.026	2.431	2.715	2.985	3.326	3.574
38	0.681	1.304	1.686	2.024	2.429	2.712	2.980	3.319	3.566
39	0.681	1.304	1.685	2.023	2.426	2.708	2.976	3.313	3.558
40	0.681	1.303	1.684	2.021	2.423	2.704	2.971	3.307	3.551
41	0.681	1.303	1.683	2.020	2.421	2.701	2.967	3.301	3.544
42	0.680	1.302	1.682	2.018	2.418	2.698	2.963	3.296	3.538
43	0.680	1.302	1.681	2.017	2.416	2.695	2.959	3.291	3.532
44	0.680	1.301	1.680	2.015	2.414	2.692	2.956	3.286	3.526
45	0.680	1.301	1.679	2.014	2.412	2.690	2.952	3.281	3.520
46	0.680	1.300	1.679	2.013	2.410	2.687	2.949	3.277	3.515
47	0.680	1.300	1.678	2.012	2.408	2.685	2.946	3.273	3.510
48	0.680	1.299	1.677	2.011	2.407	2.682	2.943	3.269	3.505
49	0.680	1.299	1.677	2.010	2.405	2.680	2.940	3.265	3.500
50	0.679	1.299	1.676	2.009	2.403	2.678	2.937	3.261	3.496

TABLE B.3 (cont.): Critical Values of the t Distribution

ν	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
52	0.679	1.298	1.675	2.007	2.400	2.674	2.932	3.255	3.488
54	0.679	1.297	1.674	2.005	2.397	2.670	2.927	3.248	3.480
56	0.679	1.297	1.673	2.003	2.395	2.667	2.923	3.242	3.473
58	0.679	1.296	1.672	2.002	2.392	2.663	2.918	3.237	3.466
60	0.679	1.296	1.671	2.000	2.390	2.660	2.915	3.232	3.460
62	0.678	1.295	1.670	1.999	2.388	2.657	2.911	3.227	3.454
64	0.678	1.295	1.669	1.998	2.386	2.655	2.908	3.223	3.449
66	0.678	1.295	1.668	1.997	2.384	2.652	2.904	3.218	3.444
68	0.678	1.294	1.668	1.995	2.382	2.650	2.902	3.214	3.439
70	0.678	1.294	1.667	1.994	2.381	2.648	2.899	3.211	3.435
72	0.678	1.293	1.666	1.993	2.379	2.646	2.896	3.207	3.431
74	0.678	1.293	1.666	1.993	2.378	2.644	2.894	3.204	3.427
76	0.678	1.293	1.665	1.992	2.376	2.642	2.891	3.201	3.423
78	0.678	1.292	1.665	1.991	2.375	2.640	2.889	3.198	3.420
80	0.678	1.292	1.664	1.990	2.374	2.639	2.887	3.195	3.416
82	0.677	1.292	1.664	1.989	2.373	2.637	2.885	3.193	3.413
84	0.677	1.292	1.663	1.989	2.372	2.636	2.883	3.190	3.410
86	0.677	1.291	1.663	1.988	2.370	2.634	2.881	3.188	3.407
88	0.677	1.291	1.662	1.987	2.369	2.633	2.880	3.185	3.405
90	0.677	1.291	1.662	1.987	2.368	2.632	2.878	3.183	3.402
92	0.677	1.291	1.662	1.986	2.368	2.630	2.876	3.181	3.399
94	0.677	1.291	1.661	1.986	2.367	2.629	2.875	3.179	3.397
96	0.677	1.290	1.661	1.985	2.366	2.628	2.873	3.177	3.395
98	0.677	1.290	1.661	1.984	2.365	2.627	2.872	3.175	3.393
100	0.677	1.290	1.660	1.984	2.364	2.626	2.871	3.174	3.390
105	0.677	1.290	1.659	1.983	2.362	2.623	2.868	3.170	3.386
110	0.677	1.289	1.659	1.982	2.361	2.621	2.865	3.166	3.381
115	0.677	1.289	1.658	1.981	2.359	2.619	2.862	3.163	3.377
120	0.677	1.289	1.658	1.980	2.358	2.617	2.860	3.160	3.373
125	0.676	1.288	1.657	1.979	2.357	2.616	2.858	3.157	3.370
130	0.676	1.288	1.657	1.978	2.355	2.614	2.856	3.154	3.367
135	0.676	1.288	1.656	1.978	2.354	2.613	2.854	3.152	3.364
140	0.676	1.288	1.656	1.977	2.353	2.611	2.852	3.149	3.361
145	0.676	1.287	1.655	1.976	2.352	2.610	2.851	3.147	3.359
150	0.676	1.287	1.655	1.976	2.351	2.609	2.849	3.145	3.357
160	0.676	1.287	1.654	1.975	2.350	2.607	2.846	3.142	3.352
170	0.676	1.287	1.654	1.974	2.348	2.605	2.844	3.139	3.349
180	0.676	1.286	1.653	1.973	2.347	2.603	2.842	3.136	3.345
190	0.676	1.286	1.653	1.973	2.346	2.602	2.840	3.134	3.342
200	0.676	1.286	1.653	1.972	2.345	2.601	2.839	3.131	3.340
250	0.675	1.285	1.651	1.969	2.341	2.596	2.832	3.123	3.330
300	0.675	1.284	1.650	1.968	2.339	2.592	2.828	3.118	3.323
350	0.675	1.284	1.649	1.967	2.337	2.590	2.825	3.114	3.319
400	0.675	1.284	1.649	1.966	2.336	2.588	2.823	3.111	3.315
450	0.675	1.283	1.648	1.965	2.335	2.587	2.821	3.108	3.312
500	0.675	1.283	1.648	1.965	2.334	2.586	2.820	3.107	3.310
600	0.675	1.283	1.647	1.964	2.333	2.584	2.817	3.104	3.307
700	0.675	1.283	1.647	1.963	2.332	2.583	2.816	3.102	3.304
800	0.675	1.283	1.647	1.963	2.331	2.582	2.815	3.100	3.303
900	0.675	1.282	1.647	1.963	2.330	2.581	2.814	3.099	3.301
1000	0.675	1.282	1.646	1.962	2.330	2.581	2.813	3.098	3.300
∞	0.6745	1.2816	1.6449	1.9600	2.3263	2.5758	2.8070	3.0902	3.2905

TABLE B.4: Critical Values of the *F* Distribution

ν_1 = Numerator DF = 1

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	5.83	39.9	161.	648.	4050.	16200.	64800.	405000.	1620000.
2	2.57	8.53	18.5	38.5	98.5	199.	399.	999.	2000.
3	2.02	5.54	10.1	17.4	34.1	55.6	89.6	167.	267.
4	1.81	4.54	7.71	12.2	21.2	31.3	45.7	74.1	106.
5	1.69	4.06	6.61	10.0	16.3	22.8	31.4	47.2	63.6
6	1.62	3.78	5.99	8.81	13.7	18.6	24.8	35.5	46.1
7	1.57	3.59	5.59	8.07	12.2	16.2	21.1	29.2	37.0
8	1.54	3.46	5.32	7.57	11.3	14.7	18.8	25.4	31.6
9	1.51	3.36	5.12	7.21	10.6	13.6	17.2	22.9	28.0
10	1.49	3.29	4.96	6.94	10.0	12.8	16.0	21.0	25.5
11	1.47	3.23	4.84	6.72	9.65	12.2	15.2	19.7	23.7
12	1.46	3.18	4.75	6.55	9.33	11.8	14.5	18.6	22.2
13	1.45	3.14	4.67	6.41	9.07	11.4	13.9	17.8	21.1
14	1.44	3.10	4.60	6.30	8.86	11.1	13.5	17.1	20.2
15	1.43	3.07	4.54	6.20	8.68	10.8	13.1	16.6	19.5
16	1.42	3.05	4.49	6.12	8.53	10.6	12.8	16.1	18.9
17	1.42	3.03	4.45	6.04	8.40	10.4	12.6	15.7	18.4
18	1.41	3.01	4.41	5.98	8.29	10.2	12.3	15.4	17.9
19	1.41	2.99	4.38	5.92	8.18	10.1	12.1	15.1	17.5
20	1.40	2.97	4.35	5.87	8.10	9.94	11.9	14.8	17.2
21	1.40	2.96	4.32	5.83	8.02	9.83	11.8	14.6	16.9
22	1.40	2.95	4.30	5.79	7.95	9.73	11.6	14.4	16.6
23	1.39	2.94	4.28	5.75	7.88	9.63	11.5	14.2	16.4
24	1.39	2.93	4.26	5.72	7.82	9.55	11.4	14.0	16.2
25	1.39	2.92	4.24	5.69	7.77	9.48	11.3	13.9	16.0
26	1.38	2.91	4.23	5.66	7.72	9.41	11.2	13.7	15.8
27	1.38	2.90	4.21	5.63	7.68	9.34	11.1	13.6	15.6
28	1.38	2.89	4.20	5.61	7.64	9.28	11.0	13.5	15.5
29	1.38	2.89	4.18	5.59	7.60	9.23	11.0	13.4	15.3
30	1.38	2.88	4.17	5.57	7.56	9.18	10.9	13.3	15.2
35	1.37	2.85	4.12	5.48	7.42	8.98	10.6	12.9	14.7
40	1.36	2.84	4.08	5.42	7.31	8.83	10.4	12.6	14.4
45	1.36	2.82	4.06	5.38	7.23	8.71	10.3	12.4	14.1
50	1.35	2.81	4.03	5.34	7.17	8.63	10.1	12.2	13.9
60	1.35	2.79	4.00	5.29	7.08	8.49	9.96	12.0	13.5
70	1.35	2.78	3.98	5.25	7.01	8.40	9.84	11.8	13.3
80	1.34	2.77	3.96	5.22	6.96	8.33	9.75	11.7	13.2
90	1.34	2.76	3.95	5.20	6.93	8.28	9.68	11.6	13.0
100	1.34	2.76	3.94	5.18	6.90	8.24	9.62	11.5	12.9
120	1.34	2.75	3.92	5.15	6.85	8.18	9.54	11.4	12.8
140	1.33	2.74	3.91	5.13	6.82	8.14	9.48	11.3	12.7
160	1.33	2.74	3.90	5.12	6.80	8.10	9.44	11.2	12.6
180	1.33	2.73	3.89	5.11	6.78	8.08	9.40	11.2	12.6
200	1.33	2.73	3.89	5.10	6.76	8.06	9.38	11.2	12.5
300	1.33	2.72	3.87	5.07	6.72	8.00	9.30	11.0	12.4
500	1.33	2.72	3.86	5.05	6.69	7.95	9.23	11.0	12.3
∞	1.32	2.71	3.84	5.02	6.64	7.88	9.14	10.8	12.1

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 2

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	7.50	49.5	200.	800.	5000.	20000.	80000.	500000.	2000000.
2	3.00	9.00	19.0	39.0	99.0	199.	399.	999.	2000.
3	2.28	5.46	9.55	16.0	30.8	49.8	79.9	149.	237.
4	2.00	4.32	6.94	10.6	18.0	26.3	38.0	61.2	87.4
5	1.85	3.78	5.79	8.43	13.3	18.3	25.0	37.1	49.8
6	1.76	3.46	5.14	7.26	10.9	14.5	19.1	27.0	34.8
7	1.70	3.26	4.74	6.54	9.55	12.4	15.9	21.7	27.2
8	1.66	3.11	4.46	6.06	8.65	11.0	13.9	18.5	22.7
9	1.62	3.01	4.26	5.71	8.02	10.1	12.5	16.4	19.9
10	1.60	2.92	4.10	5.46	7.56	9.43	11.6	14.9	17.9
11	1.58	2.86	3.98	5.26	7.21	8.91	10.8	13.8	16.4
12	1.56	2.81	3.89	5.10	6.93	8.51	10.3	13.0	15.3
13	1.55	2.76	3.81	4.97	6.70	8.19	9.84	12.3	14.4
14	1.53	2.73	3.74	4.86	6.51	7.92	9.47	11.8	13.7
15	1.52	2.70	3.68	4.77	6.36	7.70	9.17	11.3	13.2
16	1.51	2.67	3.63	4.69	6.23	7.51	8.92	11.0	12.7
17	1.51	2.64	3.59	4.62	6.11	7.35	8.70	10.7	12.3
18	1.50	2.62	3.55	4.56	6.01	7.21	8.51	10.4	11.9
19	1.49	2.61	3.52	4.51	5.93	7.09	8.35	10.2	11.6
20	1.49	2.59	3.49	4.46	5.85	6.99	8.21	9.95	11.4
21	1.48	2.57	3.47	4.42	5.78	6.89	8.08	9.77	11.2
22	1.48	2.56	3.44	4.38	5.72	6.81	7.96	9.61	11.0
23	1.47	2.55	3.42	4.35	5.66	6.73	7.86	9.47	10.8
24	1.47	2.54	3.40	4.32	5.61	6.66	7.77	9.34	10.6
25	1.47	2.53	3.39	4.29	5.57	6.60	7.69	9.22	10.5
26	1.46	2.52	3.37	4.27	5.53	6.54	7.61	9.12	10.3
27	1.46	2.51	3.35	4.24	5.49	6.49	7.54	9.02	10.2
28	1.46	2.50	3.34	4.22	5.45	6.44	7.48	8.93	10.1
29	1.45	2.50	3.33	4.20	5.42	6.40	7.42	8.85	9.99
30	1.45	2.49	3.32	4.18	5.39	6.35	7.36	8.77	9.90
35	1.44	2.46	3.27	4.11	5.27	6.19	7.14	8.47	9.52
40	1.44	2.44	3.23	4.05	5.18	6.07	6.99	8.25	9.25
45	1.43	2.42	3.20	4.01	5.11	5.97	6.86	8.09	9.04
50	1.43	2.41	3.18	3.97	5.06	5.90	6.77	7.96	8.88
60	1.42	2.39	3.15	3.93	4.98	5.79	6.63	7.77	8.65
70	1.41	2.38	3.13	3.89	4.92	5.72	6.53	7.64	8.49
80	1.41	2.37	3.11	3.86	4.88	5.67	6.46	7.54	8.37
90	1.41	2.36	3.10	3.84	4.85	5.62	6.41	7.47	8.28
100	1.41	2.36	3.09	3.83	4.82	5.59	6.37	7.41	8.21
120	1.40	2.35	3.07	3.80	4.79	5.54	6.30	7.32	8.10
140	1.40	2.34	3.06	3.79	4.76	5.50	6.26	7.26	8.03
160	1.40	2.34	3.05	3.78	4.74	5.48	6.22	7.21	7.97
180	1.40	2.33	3.05	3.77	4.73	5.46	6.20	7.18	7.93
200	1.40	2.33	3.04	3.76	4.71	5.44	6.17	7.15	7.90
300	1.39	2.32	3.03	3.73	4.68	5.39	6.11	7.07	7.80
500	1.39	2.31	3.01	3.72	4.65	5.35	6.06	7.00	7.72
∞	1.39	2.30	3.00	3.69	4.61	5.30	5.99	6.91	7.60

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 3

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	8.20	53.6	216.	864.	5400.	21600.	86500.	540000.	2160000.
2	3.15	9.16	19.2	39.2	99.2	199.	399.	999.	2000.
3	2.36	5.39	9.28	15.4	29.5	47.5	76.1	141.	225.
4	2.05	4.19	6.59	9.98	16.7	24.3	35.0	56.2	80.1
5	1.88	3.62	5.41	7.76	12.1	16.5	22.4	33.2	44.4
6	1.78	3.29	4.76	6.60	9.78	12.9	16.9	23.7	30.5
7	1.72	3.07	4.35	5.89	8.45	10.9	13.8	18.8	23.5
8	1.67	2.92	4.07	5.42	7.59	9.60	12.0	15.8	19.4
9	1.63	2.81	3.86	5.08	6.99	8.72	10.7	13.9	16.8
10	1.60	2.73	3.71	4.83	6.55	8.08	9.83	12.6	15.0
11	1.58	2.66	3.59	4.63	6.22	7.60	9.17	11.6	13.7
12	1.56	2.61	3.49	4.47	5.95	7.23	8.65	10.8	12.7
13	1.55	2.56	3.41	4.35	5.74	6.93	8.24	10.2	11.9
14	1.53	2.52	3.34	4.24	5.56	6.68	7.91	9.73	11.3
15	1.52	2.49	3.29	4.15	5.42	6.48	7.63	9.34	10.8
16	1.51	2.46	3.24	4.08	5.29	6.30	7.40	9.01	10.3
17	1.50	2.44	3.20	4.01	5.19	6.16	7.21	8.73	9.99
18	1.49	2.42	3.16	3.95	5.09	6.03	7.04	8.49	9.69
19	1.49	2.40	3.13	3.90	5.01	5.92	6.89	8.28	9.42
20	1.48	2.38	3.10	3.86	4.94	5.82	6.76	8.10	9.20
21	1.48	2.36	3.07	3.82	4.87	5.73	6.64	7.94	8.99
22	1.47	2.35	3.05	3.78	4.82	5.65	6.54	7.80	8.82
23	1.47	2.34	3.03	3.75	4.76	5.58	6.45	7.67	8.66
24	1.46	2.33	3.01	3.72	4.72	5.52	6.36	7.55	8.51
25	1.46	2.32	2.99	3.69	4.68	5.46	6.29	7.45	8.39
26	1.45	2.31	2.98	3.67	4.64	5.41	6.22	7.36	8.27
27	1.45	2.30	2.96	3.65	4.60	5.36	6.16	7.27	8.16
28	1.45	2.29	2.95	3.63	4.57	5.32	6.10	7.19	8.07
29	1.45	2.28	2.93	3.61	4.54	5.28	6.05	7.12	7.98
30	1.44	2.28	2.92	3.59	4.51	5.24	6.00	7.05	7.89
35	1.43	2.25	2.87	3.52	4.40	5.09	5.80	6.79	7.56
40	1.42	2.23	2.84	3.46	4.31	4.98	5.66	6.59	7.33
45	1.42	2.21	2.81	3.42	4.25	4.89	5.55	6.45	7.15
50	1.41	2.20	2.79	3.39	4.20	4.83	5.47	6.34	7.01
60	1.41	2.18	2.76	3.34	4.13	4.73	5.34	6.17	6.81
70	1.40	2.16	2.74	3.31	4.07	4.66	5.26	6.06	6.67
80	1.40	2.15	2.72	3.28	4.04	4.61	5.19	5.97	6.57
90	1.39	2.15	2.71	3.26	4.01	4.57	5.14	5.91	6.49
100	1.39	2.14	2.70	3.25	3.98	4.54	5.11	5.86	6.43
120	1.39	2.13	2.68	3.23	3.95	4.50	5.05	5.78	6.34
140	1.38	2.12	2.67	3.21	3.92	4.47	5.01	5.73	6.28
160	1.38	2.12	2.66	3.20	3.91	4.44	4.98	5.69	6.23
180	1.38	2.11	2.65	3.19	3.89	4.42	4.95	5.66	6.19
200	1.38	2.11	2.65	3.18	3.88	4.41	4.94	5.63	6.16
300	1.38	2.10	2.63	3.16	3.85	4.36	4.88	5.56	6.08
500	1.37	2.09	2.62	3.14	3.82	4.33	4.84	5.51	6.01
∞	1.37	2.08	2.61	3.12	3.78	4.28	4.77	5.42	5.91

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 4

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	8.58	55.8	225.	900.	5620.	22500.	90000.	562000.	2250000.
2	3.23	9.24	19.2	39.2	99.2	199.	399.	999.	2000.
3	2.39	5.34	9.12	15.1	28.7	46.2	73.9	137.	218.
4	2.06	4.11	6.39	9.60	16.0	23.2	33.3	53.4	76.1
5	1.89	3.52	5.19	7.39	11.4	15.6	21.0	31.1	41.5
6	1.79	3.18	4.53	6.23	9.15	12.0	15.7	21.9	28.1
7	1.72	2.96	4.12	5.52	7.85	10.1	12.7	17.2	21.4
8	1.66	2.81	3.84	5.05	7.01	8.81	10.9	14.4	17.6
9	1.63	2.69	3.63	4.72	6.42	7.96	9.74	12.6	15.1
10	1.59	2.61	3.48	4.47	5.99	7.34	8.89	11.3	13.4
11	1.57	2.54	3.36	4.28	5.67	6.88	8.25	10.3	12.2
12	1.55	2.48	3.26	4.12	5.41	6.52	7.76	9.63	11.2
13	1.53	2.43	3.18	4.00	5.21	6.23	7.37	9.07	10.5
14	1.52	2.39	3.11	3.89	5.04	6.00	7.06	8.62	9.95
15	1.51	2.36	3.06	3.80	4.89	5.80	6.80	8.25	9.48
16	1.50	2.33	3.01	3.73	4.77	5.64	6.58	7.94	9.08
17	1.49	2.31	2.96	3.66	4.67	5.50	6.39	7.68	8.75
18	1.48	2.29	2.93	3.61	4.58	5.37	6.23	7.46	8.47
19	1.47	2.27	2.90	3.56	4.50	5.27	6.09	7.27	8.23
20	1.47	2.25	2.87	3.51	4.43	5.17	5.97	7.10	8.02
21	1.46	2.23	2.84	3.48	4.37	5.09	5.86	6.95	7.83
22	1.45	2.22	2.82	3.44	4.31	5.02	5.76	6.81	7.67
23	1.45	2.21	2.80	3.41	4.26	4.95	5.67	6.70	7.52
24	1.44	2.19	2.78	3.38	4.22	4.89	5.60	6.59	7.39
25	1.44	2.18	2.76	3.35	4.18	4.84	5.53	6.49	7.27
26	1.44	2.17	2.74	3.33	4.14	4.79	5.46	6.41	7.16
27	1.43	2.17	2.73	3.31	4.11	4.74	5.40	6.33	7.06
28	1.43	2.16	2.71	3.29	4.07	4.70	5.35	6.25	6.97
29	1.43	2.15	2.70	3.27	4.04	4.66	5.30	6.19	6.89
30	1.42	2.14	2.69	3.25	4.02	4.62	5.25	6.12	6.82
35	1.41	2.11	2.64	3.18	3.91	4.48	5.07	5.88	6.51
40	1.40	2.09	2.61	3.13	3.83	4.37	4.93	5.70	6.30
45	1.40	2.07	2.58	3.09	3.77	4.29	4.83	5.56	6.13
50	1.39	2.06	2.56	3.05	3.72	4.23	4.75	5.46	6.01
60	1.38	2.04	2.53	3.01	3.65	4.14	4.64	5.31	5.82
70	1.38	2.03	2.50	2.97	3.60	4.08	4.56	5.20	5.70
80	1.38	2.02	2.49	2.95	3.56	4.03	4.50	5.12	5.60
90	1.37	2.01	2.47	2.93	3.53	3.99	4.45	5.06	5.53
100	1.37	2.00	2.46	2.92	3.51	3.96	4.42	5.02	5.48
120	1.37	1.99	2.45	2.89	3.48	3.92	4.36	4.95	5.39
140	1.36	1.99	2.44	2.88	3.46	3.89	4.32	4.90	5.33
160	1.36	1.98	2.43	2.87	3.44	3.87	4.30	4.86	5.29
180	1.36	1.98	2.42	2.86	3.43	3.85	4.27	4.83	5.26
200	1.36	1.97	2.42	2.85	3.41	3.84	4.26	4.81	5.23
300	1.35	1.96	2.40	2.83	3.38	3.80	4.21	4.75	5.15
500	1.35	1.96	2.39	2.81	3.36	3.76	4.17	4.69	5.09
∞	1.35	1.94	2.37	2.79	3.32	3.72	4.11	4.62	5.00

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 5

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	8.82	57.2	230.	922.	5760.	23100.	92200.	576000.	2310000.
2	3.28	9.29	19.3	39.3	99.3	199.	399.	999.	2000.
3	2.41	5.31	9.01	14.9	28.2	45.4	72.6	135.	214.
4	2.07	4.05	6.26	9.36	15.5	22.5	32.3	51.7	73.6
5	1.89	3.45	5.05	7.15	11.0	14.9	20.2	29.8	39.7
6	1.79	3.11	4.39	5.99	8.75	11.5	14.9	20.8	26.6
7	1.71	2.88	3.97	5.29	7.46	9.52	12.0	16.2	20.2
8	1.66	2.73	3.69	4.82	6.63	8.30	10.3	13.5	16.4
9	1.62	2.61	3.48	4.48	6.06	7.47	9.12	11.7	14.1
10	1.59	2.52	3.33	4.24	5.64	6.87	8.29	10.5	12.4
11	1.56	2.45	3.20	4.04	5.32	6.42	7.67	9.58	11.2
12	1.54	2.39	3.11	3.89	5.06	6.07	7.20	8.89	10.4
13	1.52	2.35	3.03	3.77	4.86	5.79	6.82	8.35	9.66
14	1.51	2.31	2.96	3.66	4.69	5.56	6.51	7.92	9.11
15	1.49	2.27	2.90	3.58	4.56	5.37	6.26	7.57	8.66
16	1.48	2.24	2.85	3.50	4.44	5.21	6.05	7.27	8.29
17	1.47	2.22	2.81	3.44	4.34	5.07	5.87	7.02	7.98
18	1.46	2.20	2.77	3.38	4.25	4.96	5.72	6.81	7.71
19	1.46	2.18	2.74	3.33	4.17	4.85	5.58	6.62	7.48
20	1.45	2.16	2.71	3.29	4.10	4.76	5.46	6.46	7.27
21	1.44	2.14	2.68	3.25	4.04	4.68	5.36	6.32	7.10
22	1.44	2.13	2.66	3.22	3.99	4.61	5.26	6.19	6.94
23	1.43	2.11	2.64	3.18	3.94	4.54	5.18	6.08	6.80
24	1.43	2.10	2.62	3.15	3.90	4.49	5.11	5.98	6.68
25	1.42	2.09	2.60	3.13	3.85	4.43	5.04	5.89	6.56
26	1.42	2.08	2.59	3.10	3.82	4.38	4.98	5.80	6.46
27	1.42	2.07	2.57	3.08	3.78	4.34	4.92	5.73	6.37
28	1.41	2.06	2.56	3.06	3.75	4.30	4.87	5.66	6.28
29	1.41	2.06	2.55	3.04	3.73	4.26	4.82	5.59	6.21
30	1.41	2.05	2.53	3.03	3.70	4.23	4.78	5.53	6.13
35	1.40	2.02	2.49	2.96	3.59	4.09	4.60	5.30	5.85
40	1.39	2.00	2.45	2.90	3.51	3.99	4.47	5.13	5.64
45	1.38	1.98	2.42	2.86	3.45	3.91	4.37	5.00	5.49
50	1.37	1.97	2.40	2.83	3.41	3.85	4.30	4.90	5.37
60	1.37	1.95	2.37	2.79	3.34	3.76	4.19	4.76	5.20
70	1.36	1.93	2.35	2.75	3.29	3.70	4.11	4.66	5.08
80	1.36	1.92	2.33	2.73	3.26	3.65	4.05	4.58	4.99
90	1.35	1.91	2.32	2.71	3.23	3.62	4.01	4.53	4.92
100	1.35	1.91	2.31	2.70	3.21	3.59	3.97	4.48	4.87
120	1.35	1.90	2.29	2.67	3.17	3.55	3.92	4.42	4.79
140	1.34	1.89	2.28	2.66	3.15	3.52	3.89	4.37	4.74
160	1.34	1.88	2.27	2.65	3.13	3.50	3.86	4.33	4.69
180	1.34	1.88	2.26	2.64	3.12	3.48	3.84	4.31	4.66
200	1.34	1.88	2.26	2.63	3.11	3.47	3.82	4.29	4.64
300	1.33	1.87	2.24	2.61	3.08	3.43	3.77	4.22	4.56
500	1.33	1.86	2.23	2.59	3.05	3.40	3.73	4.18	4.51
∞	1.33	1.85	2.21	2.57	3.02	3.35	3.68	4.10	4.42

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 6

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	8.98	58.2	234.	937.	5860.	23400.	93700.	586000.	2340000.
2	3.31	9.33	19.3	39.3	99.3	199.	399.	999.	2000.
3	2.42	5.28	8.94	14.7	27.9	44.8	71.7	133.	211.
4	2.08	4.01	6.16	9.20	15.2	22.0	31.5	50.5	71.9
5	1.89	3.40	4.95	6.98	10.7	14.5	19.6	28.8	38.5
6	1.78	3.05	4.28	5.82	8.47	11.1	14.4	20.0	25.6
7	1.71	2.83	3.87	5.12	7.19	9.16	11.5	15.5	19.3
8	1.65	2.67	3.58	4.65	6.37	7.95	9.83	12.9	15.7
9	1.61	2.55	3.37	4.32	5.80	7.13	8.68	11.1	13.3
10	1.58	2.46	3.22	4.07	5.39	6.54	7.87	9.93	11.7
11	1.55	2.39	3.09	3.88	5.07	6.10	7.27	9.05	10.6
12	1.53	2.33	3.00	3.73	4.82	5.76	6.80	8.38	9.74
13	1.51	2.28	2.92	3.60	4.62	5.48	6.44	7.86	9.07
14	1.50	2.24	2.85	3.50	4.46	5.26	6.14	7.44	8.53
15	1.48	2.21	2.79	3.41	4.32	5.07	5.89	7.09	8.10
16	1.47	2.18	2.74	3.34	4.20	4.91	5.68	6.80	7.74
17	1.46	2.15	2.70	3.28	4.10	4.78	5.51	6.56	7.43
18	1.45	2.13	2.66	3.22	4.01	4.66	5.36	6.35	7.18
19	1.44	2.11	2.63	3.17	3.94	4.56	5.23	6.18	6.95
20	1.44	2.09	2.60	3.13	3.87	4.47	5.11	6.02	6.76
21	1.43	2.08	2.57	3.09	3.81	4.39	5.01	5.88	6.59
22	1.42	2.06	2.55	3.05	3.76	4.32	4.92	5.76	6.44
23	1.42	2.05	2.53	3.02	3.71	4.26	4.84	5.65	6.30
24	1.41	2.04	2.51	2.99	3.67	4.20	4.76	5.55	6.18
25	1.41	2.02	2.49	2.97	3.63	4.15	4.70	5.46	6.07
26	1.41	2.01	2.47	2.94	3.59	4.10	4.64	5.38	5.98
27	1.40	2.00	2.46	2.92	3.56	4.06	4.58	5.31	5.89
28	1.40	2.00	2.45	2.90	3.53	4.02	4.53	5.24	5.80
29	1.40	1.99	2.43	2.88	3.50	3.98	4.48	5.18	5.73
30	1.39	1.98	2.42	2.87	3.47	3.95	4.44	5.12	5.66
35	1.38	1.95	2.37	2.80	3.37	3.81	4.27	4.89	5.39
40	1.37	1.93	2.34	2.74	3.29	3.71	4.14	4.73	5.19
45	1.36	1.91	2.31	2.70	3.23	3.64	4.05	4.61	5.04
50	1.36	1.90	2.29	2.67	3.19	3.58	3.98	4.51	4.93
60	1.35	1.87	2.25	2.63	3.12	3.49	3.87	4.37	4.76
70	1.34	1.86	2.23	2.59	3.07	3.43	3.79	4.28	4.64
80	1.34	1.85	2.21	2.57	3.04	3.39	3.74	4.20	4.56
90	1.33	1.84	2.20	2.55	3.01	3.35	3.70	4.15	4.50
100	1.33	1.83	2.19	2.54	2.99	3.33	3.66	4.11	4.45
120	1.33	1.82	2.18	2.52	2.96	3.28	3.61	4.04	4.37
140	1.32	1.82	2.16	2.50	2.93	3.26	3.58	4.00	4.32
160	1.32	1.81	2.16	2.49	2.92	3.24	3.55	3.97	4.28
180	1.32	1.81	2.15	2.48	2.90	3.22	3.53	3.94	4.25
200	1.32	1.80	2.14	2.47	2.89	3.21	3.52	3.92	4.22
300	1.32	1.79	2.13	2.45	2.86	3.17	3.47	3.86	4.15
500	1.31	1.79	2.12	2.43	2.84	3.14	3.43	3.81	4.10
∞	1.31	1.77	2.10	2.41	2.80	3.09	3.37	3.74	4.02

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 7

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.10	58.9	237.	948.	5930.	23700.	94900.	593000.	2370000.
2	3.34	9.35	19.4	39.4	99.4	199.	399.	999.	2000.
3	2.43	5.27	8.89	14.6	27.7	44.4	71.0	132.	209.
4	2.08	3.98	6.09	9.07	15.0	21.6	31.0	49.7	70.7
5	1.89	3.37	4.88	6.85	10.5	14.2	19.1	28.2	37.6
6	1.78	3.01	4.21	5.70	8.26	10.8	14.0	19.5	24.9
7	1.70	2.78	3.79	4.99	6.99	8.89	11.2	15.0	18.7
8	1.64	2.62	3.50	4.53	6.18	7.69	9.49	12.4	15.1
9	1.60	2.51	3.29	4.20	5.61	6.88	8.36	10.7	12.8
10	1.57	2.41	3.14	3.95	5.20	6.30	7.56	9.52	11.2
11	1.54	2.34	3.01	3.76	4.89	5.86	6.97	8.66	10.1
12	1.52	2.28	2.91	3.61	4.64	5.52	6.51	8.00	9.28
13	1.50	2.23	2.83	3.48	4.44	5.25	6.15	7.49	8.63
14	1.49	2.19	2.76	3.38	4.28	5.03	5.86	7.08	8.11
15	1.47	2.16	2.71	3.29	4.14	4.85	5.62	6.74	7.68
16	1.46	2.13	2.66	3.22	4.03	4.69	5.41	6.46	7.33
17	1.45	2.10	2.61	3.16	3.93	4.56	5.24	6.22	7.04
18	1.44	2.08	2.58	3.10	3.84	4.44	5.09	6.02	6.78
19	1.43	2.06	2.54	3.05	3.77	4.34	4.96	5.85	6.57
20	1.43	2.04	2.51	3.01	3.70	4.26	4.85	5.69	6.38
21	1.42	2.02	2.49	2.97	3.64	4.18	4.75	5.56	6.21
22	1.41	2.01	2.46	2.93	3.59	4.11	4.66	5.44	6.07
23	1.41	1.99	2.44	2.90	3.54	4.05	4.58	5.33	5.94
24	1.40	1.98	2.42	2.87	3.50	3.99	4.51	5.23	5.82
25	1.40	1.97	2.40	2.85	3.46	3.94	4.44	5.15	5.71
26	1.39	1.96	2.39	2.82	3.42	3.89	4.38	5.07	5.62
27	1.39	1.95	2.37	2.80	3.39	3.85	4.33	5.00	5.53
28	1.39	1.94	2.36	2.78	3.36	3.81	4.28	4.93	5.45
29	1.38	1.93	2.35	2.76	3.33	3.77	4.24	4.87	5.38
30	1.38	1.93	2.33	2.75	3.30	3.74	4.19	4.82	5.31
35	1.37	1.90	2.29	2.68	3.20	3.61	4.02	4.59	5.04
40	1.36	1.87	2.25	2.62	3.12	3.51	3.90	4.44	4.85
45	1.35	1.85	2.22	2.58	3.07	3.43	3.81	4.32	4.71
50	1.34	1.84	2.20	2.55	3.02	3.38	3.74	4.22	4.60
60	1.33	1.82	2.17	2.51	2.95	3.29	3.63	4.09	4.44
70	1.33	1.80	2.14	2.47	2.91	3.23	3.56	3.99	4.32
80	1.32	1.79	2.13	2.45	2.87	3.19	3.50	3.92	4.24
90	1.32	1.78	2.11	2.43	2.84	3.15	3.46	3.87	4.18
100	1.32	1.78	2.10	2.42	2.82	3.13	3.43	3.83	4.13
120	1.31	1.77	2.09	2.39	2.79	3.09	3.38	3.77	4.06
140	1.31	1.76	2.08	2.38	2.77	3.06	3.35	3.72	4.01
160	1.31	1.75	2.07	2.37	2.75	3.04	3.32	3.69	3.97
180	1.31	1.75	2.06	2.36	2.74	3.02	3.30	3.67	3.94
200	1.30	1.75	2.06	2.35	2.73	3.01	3.29	3.65	3.92
300	1.30	1.74	2.04	2.33	2.70	2.97	3.24	3.59	3.85
500	1.30	1.73	2.03	2.31	2.68	2.94	3.20	3.54	3.80
∞	1.29	1.72	2.01	2.29	2.64	2.90	3.15	3.47	3.72

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 8

ν_2 = Denom. DF	α(2): 0.50 α(1): 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.19	59.4	239.	957.	5980.	23900.	95700.	598000.	2390000.
2	3.35	9.37	19.4	39.4	99.4	199.	399.	999.	2000.
3	2.44	5.25	8.85	14.5	27.5	44.1	70.5	131.	208.
4	2.08	3.95	6.04	8.98	14.8	21.4	30.6	49.0	69.7
5	1.89	3.34	4.82	6.76	10.3	14.0	18.8	27.6	36.9
6	1.78	2.98	4.15	5.60	8.10	10.6	13.7	19.0	24.3
7	1.70	2.75	3.73	4.90	6.84	8.68	10.9	14.6	18.2
8	1.64	2.59	3.44	4.43	6.03	7.50	9.24	12.0	14.6
9	1.60	2.47	3.23	4.10	5.47	6.69	8.12	10.4	12.4
10	1.56	2.38	3.07	3.85	5.06	6.12	7.33	9.20	10.9
11	1.53	2.30	2.95	3.66	4.74	5.68	6.74	8.35	9.76
12	1.51	2.24	2.85	3.51	4.50	5.35	6.29	7.71	8.94
13	1.49	2.20	2.77	3.39	4.30	5.08	5.93	7.21	8.29
14	1.48	2.15	2.70	3.29	4.14	4.86	5.64	6.80	7.78
15	1.46	2.12	2.64	3.20	4.00	4.67	5.40	6.47	7.37
16	1.45	2.09	2.59	3.12	3.89	4.52	5.20	6.19	7.02
17	1.44	2.06	2.55	3.06	3.79	4.39	5.03	5.96	6.73
18	1.43	2.04	2.51	3.01	3.71	4.28	4.89	5.76	6.48
19	1.42	2.02	2.48	2.96	3.63	4.18	4.76	5.59	6.27
20	1.42	2.00	2.45	2.91	3.56	4.09	4.65	5.44	6.09
21	1.41	1.98	2.42	2.87	3.51	4.01	4.55	5.31	5.92
22	1.40	1.97	2.40	2.84	3.45	3.94	4.46	5.19	5.78
23	1.40	1.95	2.37	2.81	3.41	3.88	4.38	5.09	5.65
24	1.39	1.94	2.36	2.78	3.36	3.83	4.31	4.99	5.54
25	1.39	1.93	2.34	2.75	3.32	3.78	4.25	4.91	5.43
26	1.38	1.92	2.32	2.73	3.29	3.73	4.19	4.83	5.34
27	1.38	1.91	2.31	2.71	3.26	3.69	4.14	4.76	5.25
28	1.38	1.90	2.29	2.69	3.23	3.65	4.09	4.69	5.18
29	1.37	1.89	2.28	2.67	3.20	3.61	4.04	4.64	5.11
30	1.37	1.88	2.27	2.65	3.17	3.58	4.00	4.58	5.04
35	1.36	1.85	2.22	2.58	3.07	3.45	3.83	4.36	4.78
40	1.35	1.83	2.18	2.53	2.99	3.35	3.71	4.21	4.59
45	1.34	1.81	2.15	2.49	2.94	3.28	3.62	4.09	4.45
50	1.33	1.80	2.13	2.46	2.89	3.22	3.55	4.00	4.34
60	1.32	1.77	2.10	2.41	2.82	3.13	3.45	3.86	4.19
70	1.32	1.76	2.07	2.38	2.78	3.08	3.37	3.77	4.08
80	1.31	1.75	2.06	2.35	2.74	3.03	3.32	3.70	4.00
90	1.31	1.74	2.04	2.34	2.72	3.00	3.28	3.65	3.94
100	1.30	1.73	2.03	2.32	2.69	2.97	3.25	3.61	3.89
120	1.30	1.72	2.02	2.30	2.66	2.93	3.20	3.55	3.82
140	1.30	1.71	2.01	2.28	2.64	2.91	3.17	3.51	3.77
160	1.29	1.71	2.00	2.27	2.62	2.88	3.14	3.48	3.73
180	1.29	1.70	1.99	2.26	2.61	2.87	3.12	3.45	3.70
200	1.29	1.70	1.98	2.26	2.60	2.86	3.11	3.43	3.68
300	1.29	1.69	1.97	2.23	2.57	2.82	3.06	3.38	3.61
500	1.28	1.68	1.96	2.22	2.55	2.79	3.03	3.33	3.56
∞	1.28	1.67	1.94	2.19	2.51	2.74	2.97	3.27	3.48

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 9

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.26	59.9	241.	963.	6020.	24100.	96400.	602000.	2410000.
2	3.37	9.38	19.4	39.4	99.4	199.	399.	999.	2000.
3	2.44	5.24	8.81	14.5	27.3	43.9	70.1	130.	207.
4	2.08	3.94	6.00	8.90	14.7	21.1	30.3	48.5	69.0
5	1.89	3.32	4.77	6.68	10.2	13.8	18.5	27.2	36.3
6	1.77	2.96	4.10	5.52	7.98	10.4	13.4	18.7	23.9
7	1.69	2.72	3.68	4.82	6.72	8.51	10.7	14.3	17.8
8	1.63	2.56	3.39	4.36	5.91	7.34	9.03	11.8	14.3
9	1.59	2.44	3.18	4.03	5.35	6.54	7.92	10.1	12.1
10	1.56	2.35	3.02	3.78	4.94	5.97	7.14	8.96	10.6
11	1.53	2.27	2.90	3.59	4.63	5.54	6.56	8.12	9.48
12	1.51	2.21	2.80	3.44	4.39	5.20	6.11	7.48	8.66
13	1.49	2.16	2.71	3.31	4.19	4.94	5.76	6.98	8.03
14	1.47	2.12	2.65	3.21	4.03	4.72	5.47	6.58	7.52
15	1.46	2.09	2.59	3.12	3.89	4.54	5.23	6.26	7.11
16	1.44	2.06	2.54	3.05	3.78	4.38	5.04	5.98	6.77
17	1.43	2.03	2.49	2.98	3.68	4.25	4.87	5.75	6.49
18	1.42	2.00	2.46	2.93	3.60	4.14	4.72	5.56	6.24
19	1.41	1.98	2.42	2.88	3.52	4.04	4.60	5.39	6.03
20	1.41	1.96	2.39	2.84	3.46	3.96	4.49	5.24	5.85
21	1.40	1.95	2.37	2.80	3.40	3.88	4.39	5.11	5.69
22	1.39	1.93	2.34	2.76	3.35	3.81	4.30	4.99	5.55
23	1.39	1.92	2.32	2.73	3.30	3.75	4.22	4.89	5.43
24	1.38	1.91	2.30	2.70	3.26	3.69	4.15	4.80	5.31
25	1.38	1.89	2.28	2.68	3.22	3.64	4.09	4.71	5.21
26	1.37	1.88	2.27	2.65	3.18	3.60	4.03	4.64	5.12
27	1.37	1.87	2.25	2.63	3.15	3.56	3.98	4.57	5.04
28	1.37	1.87	2.24	2.61	3.12	2.52	3.93	4.50	4.96
29	1.36	1.86	2.22	2.59	3.09	3.48	3.89	4.45	4.89
30	1.36	1.85	2.21	2.57	3.07	3.45	3.85	4.39	4.82
35	1.35	1.82	2.16	2.50	2.96	3.32	3.68	4.18	4.57
40	1.34	1.79	2.12	2.45	2.89	3.22	3.56	4.02	4.38
45	1.33	1.77	2.10	2.41	2.83	3.15	3.47	3.91	4.25
50	1.32	1.76	2.07	2.38	2.78	3.09	3.40	3.82	4.14
60	1.31	1.74	2.04	2.33	2.72	3.01	3.30	3.69	3.98
70	1.31	1.72	2.02	2.30	2.67	2.95	3.23	3.60	3.88
80	1.30	1.71	2.00	2.28	2.64	2.91	3.17	3.53	3.80
90	1.30	1.70	1.99	2.26	2.61	2.87	3.13	3.48	3.74
100	1.29	1.69	1.97	2.24	2.59	2.85	3.10	3.44	3.69
120	1.29	1.68	1.96	2.22	2.56	2.81	3.06	3.38	3.62
140	1.29	1.68	1.95	2.21	2.54	2.78	3.02	3.34	3.57
160	1.28	1.67	1.94	2.19	2.52	2.76	3.00	3.31	3.54
180	1.28	1.67	1.93	2.19	2.51	2.74	2.98	3.28	3.51
200	1.28	1.66	1.93	2.18	2.50	2.73	2.96	3.26	3.49
300	1.27	1.65	1.91	2.16	2.47	2.69	2.92	3.21	3.42
500	1.27	1.64	1.90	2.14	2.44	2.66	2.88	3.16	3.37
∞	1.27	1.63	1.88	2.11	2.41	2.62	2.83	3.10	3.30

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 10

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.32	60.2	242.	969.	6060.	24200.	96900.	606000.	2420000.
2	3.38	9.39	19.4	39.4	99.4	199.	399.	999.	2000.
3	2.44	5.23	8.79	14.4	27.2	43.7	69.8	129.	206.
4	2.08	3.92	5.96	8.84	14.5	21.0	30.0	48.1	68.3
5	1.89	3.30	4.74	6.62	10.1	13.6	18.3	26.9	35.9
6	1.77	2.94	4.06	5.46	7.87	10.3	13.2	18.4	23.5
7	1.69	2.70	3.64	4.76	6.62	8.38	10.5	14.1	17.5
8	1.63	2.54	3.35	4.30	5.81	7.21	8.87	11.5	14.0
9	1.59	2.42	3.14	3.96	5.26	6.42	7.77	9.89	11.8
10	1.55	2.32	2.98	3.72	4.85	5.85	6.99	8.75	10.3
11	1.52	2.25	2.85	3.53	4.54	5.42	6.41	7.92	9.24
12	1.50	2.19	2.75	3.37	4.30	5.09	5.97	7.29	8.43
13	1.48	2.14	2.67	3.25	4.10	4.82	5.62	6.80	7.81
14	1.46	2.10	2.60	3.15	3.94	4.60	5.33	6.40	7.31
15	1.45	2.06	2.54	3.06	3.80	4.42	5.10	6.08	6.91
16	1.44	2.03	2.49	2.99	3.69	4.27	4.90	5.81	6.57
17	1.43	2.00	2.45	2.92	3.59	4.14	4.73	5.58	6.29
18	1.42	1.98	2.41	2.87	3.51	4.03	4.59	5.39	6.05
19	1.41	1.96	2.38	2.82	3.43	3.93	4.46	5.22	5.84
20	1.40	1.94	2.35	2.77	3.37	3.85	4.35	5.08	5.66
21	1.39	1.92	2.32	2.73	3.31	3.77	4.26	4.95	5.50
22	1.39	1.90	2.30	2.70	3.26	3.70	4.17	4.83	5.36
23	1.38	1.89	2.27	2.67	3.21	3.64	4.09	4.73	5.24
24	1.38	1.88	2.25	2.64	3.17	3.59	4.03	4.64	5.13
25	1.37	1.87	2.24	2.61	3.13	3.54	3.96	4.56	5.03
26	1.37	1.86	2.22	2.59	3.09	3.49	3.91	4.48	4.94
27	1.36	1.85	2.20	2.57	3.06	3.45	3.85	4.41	4.86
28	1.36	1.84	2.19	2.55	3.03	3.41	3.81	4.35	4.78
29	1.35	1.83	2.18	2.53	3.00	3.38	3.76	4.29	4.71
30	1.35	1.82	2.16	2.51	2.98	3.34	3.72	4.24	4.65
35	1.34	1.79	2.11	2.44	2.88	3.21	3.56	4.03	4.39
40	1.33	1.76	2.08	2.39	2.80	3.12	3.44	3.87	4.21
45	1.32	1.74	2.05	2.35	2.74	3.04	3.35	3.76	4.08
50	1.31	1.73	2.03	2.32	2.70	2.99	3.28	3.67	3.97
60	1.30	1.71	1.99	2.27	2.63	2.90	3.18	3.54	3.82
70	1.30	1.69	1.97	2.24	2.59	2.85	3.11	3.45	3.71
80	1.29	1.68	1.95	2.21	2.55	2.80	3.05	3.39	3.64
90	1.29	1.67	1.94	2.19	2.52	2.77	3.01	3.34	3.58
100	1.28	1.66	1.93	2.18	2.50	2.74	2.98	3.30	3.53
120	1.28	1.65	1.91	2.16	2.47	2.71	2.94	3.24	3.46
140	1.28	1.64	1.90	2.14	2.45	2.68	2.90	3.20	3.42
160	1.27	1.64	1.89	2.13	2.43	2.66	2.88	3.17	3.38
180	1.27	1.63	1.88	2.12	2.42	2.64	2.86	3.14	3.35
200	1.27	1.63	1.88	2.11	2.41	2.63	2.84	3.12	3.33
300	1.26	1.62	1.86	2.09	2.38	2.59	2.80	3.07	3.27
500	1.26	1.61	1.85	2.07	2.36	2.56	2.76	3.02	3.22
∞	1.25	1.60	1.83	2.05	2.32	2.52	2.71	2.96	3.14

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 11

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.37	60.5	243.	973.	6080.	24300.	97300.	608000.	2430000.
2	3.39	9.40	19.4	39.4	99.4	199.	399.	999.	2000.
3	2.45	5.22	8.76	14.4	27.1	43.5	69.5	129.	205.
4	2.08	3.91	5.94	8.79	14.5	20.8	29.8	47.7	67.8
5	1.89	3.28	4.70	6.57	9.96	13.5	18.1	26.6	35.5
6	1.77	2.92	4.03	5.41	7.79	10.1	13.1	18.2	23.2
7	1.69	2.68	3.60	4.71	6.54	8.27	10.4	13.9	17.2
8	1.63	2.52	3.31	4.24	5.73	7.10	8.73	11.4	13.8
9	1.58	2.40	3.10	3.91	5.18	6.31	7.63	9.72	11.6
10	1.55	2.30	2.94	3.66	4.77	5.75	6.86	8.59	10.1
11	1.52	2.23	2.82	3.47	4.46	5.32	6.29	7.76	9.05
12	1.49	2.17	2.72	3.32	4.22	4.99	5.85	7.14	8.25
13	1.47	2.12	2.63	3.20	4.02	4.72	5.50	6.65	7.63
14	1.46	2.07	2.57	3.09	3.86	4.51	5.21	6.26	7.13
15	1.44	2.04	2.51	3.01	3.73	4.33	4.98	5.94	6.73
16	1.43	2.01	2.46	2.93	3.62	4.18	4.79	5.67	6.40
17	1.42	1.98	2.41	2.87	3.52	4.05	4.62	5.44	6.12
18	1.41	1.95	2.37	2.81	3.43	3.94	4.48	5.25	5.89
19	1.40	1.93	2.34	2.76	3.36	3.84	4.35	5.08	5.68
20	1.39	1.91	2.31	2.72	3.29	3.76	4.24	4.94	5.50
21	1.39	1.90	2.28	2.68	3.24	3.68	4.15	4.81	5.35
22	1.38	1.88	2.26	2.65	3.18	3.61	4.06	4.70	5.21
23	1.37	1.87	2.24	2.62	3.14	3.55	3.99	4.60	5.09
24	1.37	1.85	2.22	2.59	3.09	3.50	3.92	4.51	4.98
25	1.36	1.84	2.20	2.56	3.06	3.45	3.85	4.42	4.88
26	1.36	1.83	2.18	2.54	3.02	3.40	3.80	4.35	4.79
27	1.35	1.82	2.17	2.51	2.99	3.36	3.75	4.28	4.71
28	1.35	1.81	2.15	2.49	2.96	3.32	3.70	4.22	4.63
29	1.35	1.80	2.14	2.48	2.93	3.29	3.66	4.16	4.56
30	1.34	1.79	2.13	2.46	2.91	3.25	3.61	4.11	4.50
35	1.33	1.76	2.07	2.39	2.80	3.12	3.45	3.90	4.25
40	1.32	1.74	2.04	2.33	2.73	3.03	3.33	3.75	4.07
45	1.31	1.72	2.01	2.29	2.67	2.96	3.25	3.64	3.94
50	1.30	1.70	1.99	2.26	2.63	2.90	3.18	3.55	3.83
60	1.29	1.68	1.95	2.22	2.56	2.82	3.08	3.42	3.68
70	1.29	1.66	1.93	2.18	2.51	2.76	3.00	3.33	3.58
80	1.28	1.65	1.91	2.16	2.48	2.72	2.95	3.27	3.50
90	1.28	1.64	1.90	2.14	2.45	2.68	2.91	3.22	3.44
100	1.27	1.64	1.89	2.12	2.43	2.66	2.88	3.18	3.40
120	1.27	1.63	1.87	2.10	2.40	2.62	2.83	3.12	3.33
140	1.27	1.62	1.86	2.09	2.38	2.59	2.80	3.08	3.28
160	1.26	1.61	1.85	2.07	2.36	2.57	2.78	3.05	3.25
180	1.26	1.61	1.84	2.07	2.35	2.56	2.76	3.02	3.22
200	1.26	1.60	1.84	2.06	2.34	2.54	2.74	3.00	3.20
300	1.26	1.59	1.82	2.04	2.31	2.51	2.70	2.95	3.14
500	1.25	1.58	1.81	2.02	2.28	2.48	2.66	2.91	3.09
∞	1.25	1.57	1.79	1.99	2.25	2.43	2.61	2.84	3.01

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 12

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.41	60.7	244.	977.	6110.	24400.	97700.	611000.	2440000.
2	3.39	9.41	19.4	39.4	99.4	199.	399.	999.	2000.
3	2.45	5.22	8.74	14.3	27.1	43.4	69.3	128.	204.
4	2.08	3.90	5.91	8.75	14.4	20.7	29.7	47.4	67.4
5	1.89	3.27	4.68	6.52	9.89	13.4	18.0	26.4	35.2
6	1.77	2.90	4.00	5.37	7.72	10.0	12.9	18.0	23.0
7	1.68	2.67	3.57	4.67	6.47	8.18	10.3	13.7	17.0
8	1.62	2.50	3.28	4.20	5.67	7.01	8.61	11.2	13.6
9	1.58	2.38	3.07	3.87	5.11	6.23	7.52	9.57	11.4
10	1.54	2.28	2.91	3.62	4.71	5.66	6.75	8.45	9.94
11	1.51	2.21	2.79	3.43	4.40	5.24	6.18	7.63	8.88
12	1.49	2.15	2.69	3.28	4.16	4.91	5.74	7.00	8.09
13	1.47	2.10	2.60	3.15	3.96	4.64	5.40	6.52	7.48
14	1.45	2.05	2.53	3.05	3.80	4.43	5.12	6.13	6.99
15	1.44	2.02	2.48	2.96	3.67	4.25	4.88	5.81	6.59
16	1.43	1.99	2.42	2.89	3.55	4.10	4.69	5.55	6.26
17	1.41	1.96	2.38	2.82	3.46	3.97	4.52	5.32	5.98
18	1.40	1.93	2.34	2.77	3.37	3.86	4.38	5.13	5.75
19	1.40	1.91	2.31	2.72	3.30	3.76	4.26	4.97	5.55
20	1.39	1.89	2.28	2.68	3.23	3.68	4.15	4.82	5.37
21	1.38	1.87	2.25	2.64	3.17	3.60	4.06	4.70	5.21
22	1.37	1.86	2.23	2.60	3.12	3.54	3.97	4.58	5.08
23	1.37	1.84	2.20	2.57	3.07	3.47	3.89	4.48	4.96
24	1.36	1.83	2.18	2.54	3.03	3.42	3.83	4.39	4.85
25	1.36	1.82	2.16	2.51	2.99	3.37	3.76	4.31	4.75
26	1.35	1.81	2.15	2.49	2.96	3.33	3.71	4.24	4.66
27	1.35	1.80	2.13	2.47	2.93	3.28	3.66	4.17	4.58
28	1.34	1.79	2.12	2.45	2.90	3.25	3.61	4.11	4.51
29	1.34	1.78	2.10	2.43	2.87	3.21	3.56	4.05	4.44
30	1.34	1.77	2.09	2.41	2.84	3.18	3.52	4.00	4.38
35	1.32	1.74	2.04	2.34	2.74	3.05	3.36	3.79	4.13
40	1.31	1.71	2.00	2.29	2.66	2.95	3.25	3.64	3.95
45	1.30	1.70	1.97	2.25	2.61	2.88	3.16	3.53	3.82
50	1.30	1.68	1.95	2.22	2.56	2.82	3.09	3.44	3.71
60	1.29	1.66	1.92	2.17	2.50	2.74	2.99	3.32	3.57
70	1.28	1.64	1.89	2.14	2.45	2.68	2.92	3.23	3.46
80	1.27	1.63	1.88	2.11	2.42	2.64	2.87	3.16	3.39
90	1.27	1.62	1.86	2.09	2.39	2.61	2.83	3.11	3.33
100	1.27	1.61	1.85	2.08	2.37	2.58	2.80	3.07	2.28
120	1.26	1.60	1.83	2.05	2.34	2.54	2.75	3.02	3.22
140	1.26	1.59	1.82	2.04	2.31	2.52	2.72	2.98	3.17
160	1.26	1.59	1.81	2.03	2.30	2.50	2.69	2.95	3.14
180	1.25	1.58	1.81	2.02	2.28	2.48	2.67	2.92	3.11
200	1.25	1.58	1.80	2.01	2.27	2.47	2.66	2.90	3.09
300	1.25	1.57	1.78	1.99	2.24	2.43	2.61	2.85	3.02
500	1.24	1.56	1.77	1.97	2.22	2.40	2.58	2.81	2.97
∞	1.24	1.55	1.75	1.94	2.18	2.36	2.53	2.74	2.90

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 13

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.44	60.9	245.	980.	6130.	24500.	98000.	613000.	2450000.
2	3.40	9.41	19.4	39.4	99.4	199.	399.	999.	2000.
3	2.45	5.21	8.73	14.3	27.0	43.3	69.1	128.	204.
4	2.08	3.89	5.89	8.71	14.3	20.6	29.5	47.2	67.1
5	1.89	3.26	4.66	6.49	9.82	13.3	17.9	26.2	34.9
6	1.77	2.89	3.98	5.33	7.66	9.95	12.8	17.8	22.7
7	1.68	2.65	3.55	4.63	6.41	8.10	10.1	13.6	16.8
8	1.62	2.49	3.26	4.16	5.61	6.94	8.51	11.1	13.4
9	1.58	2.36	3.05	3.83	5.05	6.15	7.43	9.44	11.3
10	1.54	2.27	2.89	3.58	4.65	5.59	6.66	8.32	9.80
11	1.51	2.19	2.76	3.39	4.34	5.16	6.09	7.51	8.74
12	1.49	2.13	2.66	3.24	4.10	4.84	5.66	6.89	7.96
13	1.47	2.08	2.58	3.12	3.91	4.57	5.31	6.41	7.35
14	1.45	2.04	2.51	3.01	3.75	4.36	5.03	6.02	6.86
15	1.43	2.00	2.45	2.92	3.61	4.18	4.80	5.71	6.47
16	1.42	1.97	2.40	2.85	3.50	4.03	4.61	5.44	6.14
17	1.41	1.94	2.35	2.79	3.40	3.90	4.44	5.22	5.86
18	1.40	1.92	2.31	2.73	3.32	3.79	4.30	5.03	5.63
19	1.39	1.89	2.28	2.68	3.24	3.70	4.18	4.87	5.43
20	1.38	1.87	2.25	2.64	3.18	3.61	4.07	4.72	5.25
21	1.37	1.86	2.22	2.60	3.12	3.54	3.98	4.60	5.10
22	1.37	1.84	2.20	2.56	3.07	3.47	3.89	4.49	4.97
23	1.36	1.83	2.18	2.53	3.02	3.41	3.82	4.39	4.84
24	1.36	1.81	2.15	2.50	2.98	3.35	3.75	4.30	4.74
25	1.35	1.80	2.14	2.48	2.94	3.30	3.69	4.22	4.64
26	1.35	1.79	2.12	2.45	2.90	3.26	3.63	4.14	4.55
27	1.34	1.78	2.10	2.43	2.87	3.22	3.58	4.08	4.47
28	1.34	1.77	2.09	2.41	2.84	3.18	3.53	4.01	4.40
29	1.33	1.76	2.08	2.39	2.81	3.15	3.49	3.96	4.33
30	1.33	1.75	2.06	2.37	2.79	3.11	3.45	3.91	4.27
35	1.32	1.72	2.01	2.30	2.69	2.98	3.29	3.70	4.02
40	1.31	1.70	1.97	2.25	2.61	2.89	3.17	3.55	3.85
45	1.30	1.68	1.94	2.21	2.55	2.82	3.08	3.44	3.71
50	1.29	1.66	1.92	2.18	2.51	2.76	3.01	3.35	3.61
60	1.28	1.64	1.89	2.13	2.44	2.68	2.91	3.23	3.46
70	1.27	1.62	1.86	2.10	2.40	2.62	2.84	3.14	3.36
80	1.27	1.61	1.84	2.07	2.36	2.58	2.79	3.07	3.29
90	1.26	1.60	1.83	2.05	2.33	2.54	2.75	3.02	3.23
100	1.26	1.59	1.82	2.04	2.31	2.52	2.72	2.99	3.19
120	1.26	1.58	1.80	2.01	2.28	2.48	2.67	2.93	3.12
140	1.25	1.57	1.79	2.00	2.26	2.45	2.64	2.89	3.07
160	1.25	1.57	1.78	1.99	2.24	2.43	2.62	2.86	3.04
180	1.25	1.56	1.77	1.98	2.23	2.42	2.60	2.83	3.01
200	1.24	1.56	1.77	1.97	2.22	2.40	2.58	2.82	2.99
300	1.24	1.55	1.75	1.95	2.19	2.37	2.54	2.76	2.93
500	1.24	1.54	1.74	1.93	2.17	2.34	2.50	2.72	2.88
∞	1.23	1.52	1.72	1.90	2.13	2.29	2.45	2.66	2.81

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 14

ν_2 = Denom. DF	α(2): 0.50 α(1): 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.47	61.1	245.	983.	6140.	24600.	98300.	614000.	2460000.
2	3.41	9.42	19.4	39.4	99.4	199.	399.	999.	2000.
3	2.45	5.20	8.71	14.3	26.9	43.2	69.0	128.	203.
4	2.08	3.88	5.87	8.68	14.2	20.5	29.4	46.9	66.8
5	1.89	3.25	4.64	6.46	9.77	13.2	17.8	26.1	34.7
6	1.76	2.88	3.96	5.30	7.60	9.88	12.7	17.7	22.6
7	1.68	2.64	3.53	4.60	6.36	8.03	10.1	13.4	16.6
8	1.62	2.48	3.24	4.13	5.56	6.87	8.43	10.9	13.3
9	1.57	2.35	3.03	3.80	5.01	6.09	7.35	9.33	11.1
10	1.54	2.26	2.86	3.55	4.60	5.53	6.58	8.22	9.67
11	1.51	2.18	2.74	3.36	4.29	5.10	6.02	7.41	8.62
12	1.48	2.12	2.64	3.21	4.05	4.77	5.58	6.79	7.84
13	1.46	2.07	2.55	3.08	3.86	4.51	5.24	6.31	7.23
14	1.44	2.02	2.48	2.98	3.70	4.30	4.96	5.93	6.75
15	1.43	1.99	2.42	2.89	3.56	4.12	4.73	5.62	6.36
16	1.42	1.95	2.37	2.82	3.45	3.97	4.54	5.35	6.03
17	1.41	1.93	2.33	2.75	3.35	3.84	4.37	5.13	5.76
18	1.40	1.90	2.29	2.70	3.27	3.73	4.23	4.94	5.53
19	1.39	1.88	2.26	2.65	3.19	3.64	4.11	4.78	5.33
20	1.38	1.86	2.22	2.60	3.13	3.55	4.00	4.64	5.15
21	1.37	1.84	2.20	2.56	3.07	3.48	3.91	4.51	5.00
22	1.36	1.83	2.17	2.53	3.02	3.41	3.82	4.40	4.87
23	1.36	1.81	2.15	2.50	2.97	3.35	3.75	4.30	4.75
24	1.35	1.80	2.13	2.47	2.93	3.30	3.68	4.21	4.64
25	1.35	1.79	2.11	2.44	2.89	3.25	3.62	4.13	4.54
26	1.34	1.77	2.09	2.42	2.86	3.20	3.56	4.06	4.46
27	1.34	1.76	2.08	2.39	2.82	3.16	3.51	3.99	4.38
28	1.33	1.75	2.06	2.37	2.79	3.12	3.46	3.93	4.30
29	1.33	1.75	2.05	2.36	2.77	3.09	3.42	3.88	4.24
30	1.33	1.74	2.04	2.34	2.74	3.06	3.38	3.82	4.18
35	1.31	1.70	1.99	2.27	2.64	2.93	3.22	3.62	3.93
40	1.30	1.68	1.95	2.21	2.56	2.83	3.10	3.47	3.76
45	1.29	1.66	1.92	2.17	2.51	2.76	3.02	3.36	3.63
50	1.28	1.64	1.89	2.14	2.46	2.70	2.95	3.27	3.52
60	1.27	1.62	1.86	2.09	2.39	2.62	2.85	3.15	3.38
70	1.27	1.60	1.84	2.06	2.35	2.56	2.78	3.06	3.28
80	1.26	1.59	1.82	2.03	2.31	2.52	2.73	3.00	3.20
90	1.26	1.58	1.80	2.02	2.29	2.49	2.69	2.95	3.14
100	1.25	1.57	1.79	2.00	2.27	2.46	2.65	2.91	3.10
120	1.25	1.56	1.78	1.98	2.23	2.42	2.61	2.85	3.03
140	1.24	1.55	1.76	1.96	2.21	2.40	2.58	2.81	2.99
160	1.24	1.55	1.75	1.95	2.20	2.38	2.55	2.78	2.95
180	1.24	1.54	1.75	1.94	2.18	2.36	2.53	2.76	2.93
200	1.24	1.54	1.74	1.93	2.17	2.35	2.52	2.74	2.91
300	1.23	1.53	1.72	1.91	2.14	2.31	2.47	2.69	2.84
500	1.23	1.52	1.71	1.89	2.12	2.28	2.44	2.64	2.79
∞	1.22	1.50	1.69	1.87	2.08	2.24	2.39	2.58	2.72

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 15

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.49	61.2	246.	985.	6160.	24600.	98500.	616000.	2460000.
2	3.41	9.42	19.4	39.4	99.4	199.	399.	999.	2000.
3	2.46	5.20	8.70	14.3	26.9	43.1	68.8	127.	203.
4	2.08	3.87	5.86	8.66	14.2	20.4	29.3	46.8	66.5
5	1.89	3.24	4.62	6.43	9.72	13.1	17.7	25.9	34.5
6	1.76	2.87	3.94	5.27	7.56	9.81	12.7	17.6	22.4
7	1.68	2.63	3.51	4.57	6.31	7.97	9.98	13.3	16.5
8	1.62	2.46	3.22	4.10	5.52	6.81	8.35	10.8	13.1
9	1.57	2.34	3.01	3.77	4.96	6.03	7.28	9.24	11.0
10	1.53	2.24	2.85	3.52	4.56	5.47	6.51	8.13	9.56
11	1.50	2.17	2.72	3.33	4.25	5.05	5.95	7.32	8.52
12	1.48	2.10	2.62	3.18	4.01	4.72	5.52	6.71	7.74
13	1.46	2.05	2.53	3.05	3.82	4.46	5.17	6.23	7.13
14	1.44	2.01	2.46	2.95	3.66	4.25	4.89	5.85	6.65
15	1.43	1.97	2.40	2.86	3.52	4.07	4.67	5.54	6.26
16	1.41	1.94	2.35	2.79	3.41	3.92	4.47	5.27	5.94
17	1.40	1.91	2.31	2.72	3.31	3.79	4.31	5.05	5.67
18	1.39	1.89	2.27	2.67	3.23	3.68	4.17	4.87	5.44
19	1.38	1.86	2.23	2.62	3.15	3.59	4.05	4.70	5.24
20	1.37	1.84	2.20	2.57	3.09	3.50	3.94	4.56	5.07
21	1.37	1.83	2.18	2.53	3.03	3.43	3.85	4.44	4.92
22	1.36	1.81	2.15	2.50	2.98	3.36	3.76	4.33	4.78
23	1.35	1.80	2.13	2.47	2.93	3.30	3.69	4.23	4.66
24	1.35	1.78	2.11	2.44	2.89	3.25	3.62	4.14	4.56
25	1.34	1.77	2.09	2.41	2.85	3.20	3.56	4.06	4.46
26	1.34	1.76	2.07	2.39	2.81	3.15	3.50	3.99	4.37
27	1.33	1.75	2.06	2.36	2.78	3.11	3.45	3.92	4.29
28	1.33	1.74	2.04	2.34	2.75	3.07	3.40	3.86	4.22
29	1.32	1.73	2.03	2.32	2.73	3.04	3.36	3.80	4.15
30	1.32	1.72	2.01	2.31	2.70	3.01	3.32	3.75	4.09
35	1.31	1.69	1.96	2.23	2.60	2.88	3.16	3.55	3.85
40	1.30	1.66	1.92	2.18	2.52	2.78	3.04	3.40	3.68
45	1.29	1.64	1.89	2.14	2.46	2.71	2.96	3.29	3.55
50	1.28	1.63	1.87	2.11	2.42	2.65	2.89	3.20	3.45
60	1.27	1.60	1.84	2.06	2.35	2.57	2.79	3.08	3.30
70	1.26	1.59	1.81	2.03	2.31	2.51	2.72	2.99	3.20
80	1.26	1.57	1.79	2.00	2.27	2.47	2.67	2.93	3.12
90	1.25	1.56	1.78	1.98	2.24	2.44	2.63	2.88	3.07
100	1.25	1.56	1.77	1.97	2.22	2.41	2.60	2.84	3.02
120	1.24	1.55	1.75	1.94	2.19	2.37	2.55	2.78	2.96
140	1.24	1.54	1.74	1.93	2.17	2.35	2.52	2.74	2.91
160	1.24	1.53	1.73	1.92	2.15	2.33	2.49	2.71	2.88
180	1.23	1.53	1.72	1.91	2.14	2.31	2.48	2.69	2.85
200	1.23	1.52	1.72	1.90	2.13	2.30	2.46	2.67	2.83
300	1.23	1.51	1.70	1.88	2.10	2.26	2.42	2.62	2.77
500	1.22	1.50	1.69	1.86	2.07	2.23	2.38	2.58	2.72
∞	1.22	1.49	1.67	1.83	2.04	2.19	2.33	2.51	2.65

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 16

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.52	61.3	246.	987.	6170.	24700.	98700.	617000.	2470000.
2	3.41	9.43	19.4	39.4	99.4	199.	399.	999.	2000.
3	2.46	5.20	8.69	14.2	26.8	43.0	68.7	127.	202.
4	2.08	3.86	5.84	8.63	14.2	20.4	29.2	46.6	66.2
5	1.88	3.23	4.60	6.40	9.68	13.1	17.6	25.8	34.3
6	1.76	2.86	3.92	5.24	7.52	9.76	12.6	17.4	22.3
7	1.68	2.62	3.49	4.54	6.28	7.91	9.91	13.2	16.4
8	1.62	2.45	3.20	4.08	5.48	6.76	8.29	10.8	13.0
9	1.57	2.33	2.99	3.74	4.92	5.98	7.21	9.15	10.9
10	1.53	2.23	2.83	3.50	4.52	5.42	6.45	8.05	9.46
11	1.50	2.16	2.70	3.30	4.21	5.00	5.89	7.24	8.43
12	1.48	2.09	2.60	3.15	3.97	4.67	5.46	6.63	7.65
13	1.46	2.04	2.51	3.03	3.78	4.41	5.11	6.16	7.05
14	1.44	2.00	2.44	2.92	3.62	4.20	4.84	5.78	6.57
15	1.42	1.96	2.38	2.84	3.49	4.02	4.61	5.46	6.18
16	1.41	1.93	2.33	2.76	3.37	3.87	4.42	5.20	5.86
17	1.40	1.90	2.29	2.70	3.27	3.75	4.25	4.99	5.59
18	1.39	1.87	2.25	2.64	3.19	3.64	4.11	4.80	5.36
19	1.38	1.85	2.21	2.59	3.12	3.54	3.99	4.64	5.16
20	1.37	1.83	2.18	2.55	3.05	3.46	3.89	4.49	4.99
21	1.36	1.81	2.16	2.51	2.99	3.38	3.79	4.37	4.84
22	1.36	1.80	2.13	2.47	2.94	3.31	3.71	4.26	4.71
23	1.35	1.78	2.11	2.44	2.89	3.25	3.63	4.16	4.59
24	1.34	1.77	2.09	2.41	2.85	3.20	3.56	4.07	4.48
25	1.34	1.76	2.07	2.38	2.81	3.15	3.50	3.99	4.39
26	1.33	1.75	2.05	2.36	2.78	3.11	3.45	3.92	4.30
27	1.33	1.74	2.04	2.34	2.75	3.07	3.40	3.86	4.22
28	1.32	1.73	2.02	2.32	2.72	3.03	3.35	3.80	4.15
29	1.32	1.72	2.01	2.30	2.69	2.99	3.31	3.74	4.08
30	1.32	1.71	1.99	2.28	2.66	2.96	3.27	3.69	4.02
35	1.30	1.67	1.94	2.21	2.56	2.83	3.11	3.48	3.78
40	1.29	1.65	1.90	2.15	2.48	2.74	2.99	3.34	3.61
45	1.28	1.63	1.87	2.11	2.43	2.66	2.90	3.23	3.48
50	1.27	1.61	1.85	2.08	2.38	2.61	2.84	3.14	3.38
60	1.26	1.59	1.82	2.03	2.31	2.53	2.74	3.02	3.23
70	1.26	1.57	1.79	2.00	2.27	2.47	2.67	2.93	3.13
80	1.25	1.56	1.77	1.97	2.23	2.43	2.62	2.87	3.06
90	1.25	1.55	1.76	1.95	2.21	2.39	2.58	2.82	3.00
100	1.24	1.54	1.75	1.94	2.19	2.37	2.55	2.78	2.96
120	1.24	1.53	1.73	1.92	2.15	2.33	2.50	2.72	2.89
140	1.23	1.52	1.72	1.90	2.13	2.30	2.47	2.68	2.84
160	1.23	1.52	1.71	1.89	2.11	2.28	2.44	2.65	2.81
180	1.23	1.51	1.70	1.88	2.10	2.26	2.42	2.63	2.78
200	1.23	1.51	1.69	1.87	2.09	2.25	2.41	2.61	2.76
300	1.22	1.49	1.68	1.85	2.06	2.21	2.36	2.56	2.70
500	1.22	1.49	1.66	1.83	2.04	2.19	2.33	2.52	2.65
∞	1.21	1.47	1.64	1.80	2.00	2.14	2.28	2.45	2.58

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 17

ν_2 = Denom. DF	α(2): 0.50 α(1): 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.53	61.5	247.	989.	6180.	24700.	98900.	618000.	2470000.
2	3.42	9.43	19.4	39.4	99.4	199.	399.	999.	2000.
3	2.46	5.19	8.68	14.2	26.8	42.9	68.6	127.	202.
4	2.08	3.86	5.83	8.61	14.1	20.3	29.1	46.5	66.0
5	1.88	3.22	4.59	6.38	9.64	13.0	17.5	25.7	34.2
6	1.76	2.85	3.91	5.22	7.48	9.71	12.5	17.4	22.1
7	1.67	2.61	3.48	4.52	6.24	7.87	9.85	13.1	16.3
8	1.61	2.45	3.19	4.05	5.44	6.72	8.23	10.7	12.9
9	1.57	2.32	2.97	3.72	4.89	5.94	7.16	9.08	10.8
10	1.53	2.22	2.81	3.47	4.49	5.38	6.40	7.98	9.38
11	1.50	2.15	2.69	3.28	4.18	4.96	5.84	7.17	8.34
12	1.47	2.08	2.58	3.13	3.94	4.63	5.40	6.57	7.57
13	1.45	2.03	2.50	3.00	3.75	4.37	5.06	6.09	6.97
14	1.44	1.99	2.43	2.90	3.59	4.16	4.79	5.71	6.49
15	1.42	1.95	2.37	2.81	3.45	3.98	4.56	5.40	6.11
16	1.41	1.92	2.32	2.74	3.34	3.83	4.37	5.14	5.79
17	1.39	1.89	2.27	2.67	3.24	3.71	4.21	4.92	5.52
18	1.38	1.86	2.23	2.62	3.16	3.60	4.07	4.74	5.29
19	1.37	1.84	2.20	2.57	3.08	3.50	3.94	4.58	5.09
20	1.37	1.82	2.17	2.52	3.02	3.42	3.84	4.44	4.92
21	1.36	1.80	2.14	2.48	2.96	3.34	3.74	4.31	4.77
22	1.35	1.79	2.11	2.45	2.91	3.27	3.66	4.20	4.64
23	1.35	1.77	2.09	2.42	2.86	3.21	3.58	4.10	4.52
24	1.34	1.76	2.07	2.39	2.82	3.16	3.52	4.02	4.41
25	1.33	1.75	2.05	2.36	2.78	3.11	3.46	3.94	4.32
26	1.33	1.73	2.03	2.34	2.75	3.07	3.40	3.86	4.23
27	1.33	1.72	2.02	2.31	2.71	3.03	3.35	3.80	4.15
28	1.32	1.71	2.00	2.29	2.68	2.99	3.30	3.74	4.08
29	1.32	1.71	1.99	2.27	2.66	2.95	3.26	3.68	4.02
30	1.31	1.70	1.98	2.26	2.63	2.92	3.22	3.63	3.96
35	1.30	1.66	1.92	2.18	2.53	2.79	3.06	3.43	3.72
40	1.29	1.64	1.89	2.13	2.45	2.70	2.95	3.28	3.54
45	1.28	1.62	1.86	2.09	2.39	2.62	2.86	3.17	3.41
50	1.27	1.60	1.83	2.06	2.35	2.57	2.79	3.09	3.31
60	1.26	1.58	1.80	2.01	2.28	2.49	2.69	2.96	3.17
70	1.25	1.56	1.77	1.97	2.23	2.43	2.62	2.88	3.07
80	1.25	1.55	1.75	1.95	2.20	2.39	2.57	2.81	3.00
90	1.24	1.54	1.74	1.93	2.17	2.35	2.53	2.76	2.94
100	1.24	1.53	1.73	1.91	2.15	2.33	2.50	2.73	2.89
120	1.23	1.52	1.71	1.89	2.12	2.29	2.45	2.67	2.83
140	1.23	1.51	1.70	1.87	2.10	2.26	2.42	2.63	2.78
160	1.23	1.50	1.69	1.86	2.08	2.24	2.40	2.60	2.75
180	1.22	1.50	1.68	1.85	2.07	2.22	2.38	2.58	2.72
200	1.22	1.49	1.67	1.84	2.06	2.21	2.36	2.56	2.70
300	1.22	1.48	1.66	1.82	2.03	2.17	2.32	2.50	2.64
500	1.21	1.47	1.64	1.80	2.00	2.14	2.28	2.46	2.59
∞	1.21	1.46	1.62	1.78	1.97	2.10	2.23	2.40	2.52

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 18

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.55	61.6	247.	990.	6190.	24800.	99100.	619000.	2480000.
2	3.42	9.44	19.4	39.4	99.4	199.	399.	999.	2000.
3	2.46	5.19	8.67	14.2	26.8	42.9	68.5	127.	202.
4	2.08	3.85	5.82	8.59	14.1	20.3	29.0	46.3	65.8
5	1.88	3.22	4.58	6.36	9.61	13.0	17.4	25.6	34.0
6	1.76	2.85	3.90	5.20	7.45	9.66	12.4	17.3	22.0
7	1.67	2.61	3.47	4.50	6.21	7.83	9.79	13.1	16.2
8	1.61	2.44	3.17	4.03	5.41	6.68	8.18	10.6	12.8
9	1.56	2.31	2.96	3.70	4.86	5.90	7.11	9.01	10.7
10	1.53	2.22	2.80	3.45	4.46	5.34	6.35	7.91	9.30
11	1.50	2.14	2.67	3.26	4.15	4.92	5.79	7.11	8.27
12	1.47	2.08	2.57	3.11	3.91	4.59	5.36	6.51	7.50
13	1.45	2.02	2.48	2.98	3.72	4.33	5.02	6.03	6.90
14	1.43	1.98	2.41	2.88	3.56	4.12	4.74	5.66	6.43
15	1.42	1.94	2.35	2.79	3.42	3.95	4.51	5.35	6.04
16	1.40	1.91	2.30	2.72	3.31	3.80	4.32	5.09	5.72
17	1.39	1.88	2.26	2.65	3.21	3.67	4.16	4.87	5.45
18	1.38	1.85	2.22	2.60	3.13	3.56	4.02	4.68	5.23
19	1.37	1.83	2.18	2.55	3.05	3.46	3.90	4.52	5.03
20	1.36	1.81	2.15	2.50	2.99	3.38	3.79	4.38	4.86
21	1.36	1.79	2.12	2.46	2.93	3.31	3.70	4.26	4.71
22	1.35	1.78	2.10	2.43	2.88	3.24	3.62	4.15	4.58
23	1.34	1.76	2.08	2.39	2.83	3.18	3.54	4.05	4.46
24	1.34	1.75	2.05	2.36	2.79	3.12	3.47	3.96	4.35
25	1.33	1.74	2.04	2.34	2.75	3.08	3.41	3.88	4.26
26	1.33	1.72	2.02	2.31	2.72	3.03	3.36	3.81	4.17
27	1.32	1.71	2.00	2.29	2.68	2.99	3.31	3.75	4.10
28	1.32	1.70	1.99	2.27	2.65	2.95	3.26	3.69	4.02
29	1.31	1.69	1.97	2.25	2.63	2.92	3.22	3.63	3.96
30	1.31	1.69	1.96	2.23	2.60	2.89	3.18	3.58	3.90
35	1.29	1.65	1.91	2.16	2.50	2.76	3.02	3.38	3.66
40	1.28	1.62	1.87	2.11	2.42	2.66	2.90	3.23	3.49
45	1.27	1.60	1.84	2.07	2.36	2.59	2.82	3.12	3.36
50	1.27	1.59	1.81	2.03	2.32	2.53	2.75	3.04	3.26
60	1.26	1.56	1.78	1.98	2.25	2.45	2.65	2.91	3.11
70	1.25	1.55	1.75	1.95	2.20	2.39	2.58	2.83	3.01
80	1.24	1.53	1.73	1.92	2.17	2.35	2.53	2.76	2.94
90	1.24	1.52	1.72	1.91	2.14	2.32	2.49	2.71	2.88
100	1.23	1.52	1.71	1.89	2.12	2.29	2.46	2.68	2.84
120	1.23	1.50	1.69	1.87	2.09	2.25	2.41	2.62	2.78
140	1.22	1.50	1.68	1.85	2.07	2.22	2.38	2.58	2.73
160	1.22	1.49	1.67	1.84	2.05	2.20	2.35	2.55	2.70
180	1.22	1.48	1.66	1.83	2.04	2.19	2.34	2.53	2.67
200	1.22	1.48	1.66	1.82	2.03	2.18	2.32	2.51	2.65
300	1.21	1.47	1.64	1.80	1.99	2.14	2.28	2.46	2.59
500	1.21	1.46	1.62	1.78	1.97	2.11	2.24	2.41	2.54
∞	1.20	1.44	1.60	1.75	1.93	2.06	2.19	2.35	2.47

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 19

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.57	61.7	248.	992.	6200.	24800.	99200.	620000.	2480000.
2	3.42	9.44	19.4	39.4	99.4	199.	399.	999.	2000.
3	2.46	5.19	8.67	14.2	26.7	42.8	68.4	127.	201.
4	2.08	3.85	5.81	8.58	14.0	20.2	28.9	46.2	65.7
5	1.88	3.21	4.57	6.34	9.58	12.9	17.4	25.5	33.9
6	1.76	2.84	3.88	5.18	7.42	9.62	12.4	17.2	21.9
7	1.67	2.60	3.46	4.48	6.18	7.79	9.74	13.0	16.1
8	1.61	2.43	3.16	4.02	5.38	6.64	8.13	10.5	12.8
9	1.56	2.30	2.95	3.68	4.83	5.86	7.06	8.95	10.7
10	1.53	2.21	2.79	3.44	4.43	5.31	6.31	7.86	9.23
11	1.49	2.13	2.66	3.24	4.12	4.89	5.75	7.06	8.20
12	1.47	2.07	2.56	3.09	3.88	4.56	5.32	6.45	7.43
13	1.45	2.01	2.47	2.96	3.69	4.30	4.98	5.98	6.84
14	1.43	1.97	2.40	2.86	3.53	4.09	4.70	5.60	6.37
15	1.41	1.93	2.34	2.77	3.40	3.91	4.47	5.29	5.98
16	1.40	1.90	2.29	2.70	3.28	3.76	4.28	5.04	5.66
17	1.39	1.87	2.24	2.63	3.19	3.64	4.12	4.82	5.40
18	1.38	1.84	2.20	2.58	3.10	3.53	3.98	4.63	5.17
19	1.37	1.82	2.17	2.53	3.03	3.43	3.86	4.47	4.97
20	1.36	1.80	2.14	2.48	2.96	3.35	3.76	4.33	4.80
21	1.35	1.78	2.11	2.44	2.90	3.27	3.66	4.21	4.65
22	1.35	1.77	2.08	2.41	2.85	3.21	3.58	4.10	4.52
23	1.34	1.75	2.06	2.37	2.80	3.15	3.50	4.00	4.41
24	1.33	1.74	2.04	2.35	2.76	3.09	3.44	3.92	4.30
25	1.33	1.73	2.02	2.32	2.72	3.04	3.38	3.84	4.21
26	1.32	1.71	2.00	2.29	2.69	3.00	3.32	3.77	4.12
27	1.32	1.70	1.99	2.27	2.66	2.96	3.27	3.70	4.04
28	1.31	1.69	1.97	2.25	2.63	2.92	3.22	3.64	3.97
29	1.31	1.68	1.96	2.23	2.60	2.88	3.18	3.59	3.91
30	1.31	1.68	1.95	2.21	2.57	2.85	3.14	3.53	3.85
35	1.29	1.64	1.89	2.14	2.47	2.72	2.98	3.33	3.61
40	1.28	1.61	1.85	2.09	2.39	2.63	2.87	3.19	3.44
45	1.27	1.59	1.82	2.04	2.34	2.56	2.78	3.08	3.31
50	1.26	1.58	1.80	2.01	2.29	2.50	2.71	2.99	3.21
60	1.25	1.55	1.76	1.96	2.22	2.42	2.61	2.87	3.06
70	1.24	1.54	1.74	1.93	2.18	2.36	2.54	2.78	2.96
80	1.24	1.52	1.72	1.90	2.14	2.32	2.49	2.72	2.89
90	1.23	1.51	1.70	1.88	2.11	2.28	2.45	2.67	2.83
100	1.23	1.50	1.69	1.87.	2.09	2.26	2.42	2.63	2.79
120	1.22	1.49	1.67	1.84	2.06	2.22	2.37	2.58	2.73
140	1.22	1.48	1.66	1.83	2.04	2.19	2.34	2.54	2.68
160	1.22	1.48	1.65	1.82	2.02	2.17	2.32	2.51	2.65
180	1.21	1.47	1.64	1.81	2.01	2.15	2.30	2.48	2.62
200	1.21	1.47	1.64	1.80	2.00	2.14	2.28	2.46	2.60
300	1.21	1.46	1.62	1.77	1.97	2.10	2.24	2.41	2.54
500	1.20	1.45	1.61	1.76	1.94	2.07	2.20	2.37	2.49
∞	1.20	1.43	1.59	1.73	1.90	2.03	2.15	2.31	2.42

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 20

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.58	61.7	248.	993.	6210.	24800.	99300.	621000.	2480000.
2	3.43	9.44	19.4	39.4	99.4	199.	399.	999.	2000.
3	2.46	5.18	8.66	14.2	26.7	42.8	68.3	126.	201.
4	2.08	3.84	5.80	8.56	14.0	20.2	28.9	46.1	65.5
5	1.88	3.21	4.56	6.33	9.55	12.9	17.3	25.4	33.8
6	1.76	2.84	3.87	5.17	7.40	9.59	12.3	17.1	21.8
7	1.67	2.59	3.44	4.47	6.16	7.75	9.70	12.9	16.0
8	1.61	2.42	3.15	4.00	5.36	6.61	8.09	10.5	12.7
9	1.56	2.30	2.94	3.67	4.81	5.83	7.02	8.90	10.6
10	1.52	2.20	2.77	3.42	4.41	5.27	6.27	7.80	9.17
11	1.49	2.12	2.65	3.23	4.10	4.86	5.71	7.01	8.14
12	1.47	2.06	2.54	3.07	3.86	4.53	5.28	6.40	7.37
13	1.45	2.01	2.46	2.95	3.66	4.27	4.94	5.93	6.78
14	1.43	1.96	2.39	2.84	3.51	4.06	4.66	5.56	6.31
15	1.41	1.92	2.33	2.76	3.37	3.88	4.44	5.25	5.93
16	1.40	1.89	2.28	2.68	3.26	3.73	4.25	4.99	5.61
17	1.39	1.86	2.23	2.62	3.16	3.61	4.09	4.78	5.34
18	1.38	1.84	2.19	2.56	3.08	3.50	3.95	4.59	5.12
19	1.37	1.81	2.16	2.51	3.00	3.40	3.83	4.43	4.92
20	1.36	1.79	2.12	2.46	2.94	3.32	3.72	4.29	4.75
21	1.35	1.78	2.10	2.42	2.88	3.24	3.63	4.17	4.60
22	1.34	1.76	2.07	2.39	2.83	3.18	3.54	4.06	4.47
23	1.34	1.74	2.05	2.36	2.78	3.12	3.47	3.96	4.36
24	1.33	1.73	2.03	2.33	2.74	3.06	3.40	3.87	4.25
25	1.33	1.72	2.01	2.30	2.70	3.01	3.34	3.79	4.16
26	1.32	1.71	1.99	2.28	2.66	2.97	3.28	3.72	4.07
27	1.32	1.70	1.97	2.25	2.63	2.93	3.23	3.66	3.99
28	1.31	1.69	1.96	2.23	2.60	2.89	3.19	3.60	3.92
29	1.31	1.68	1.94	2.21	2.57	2.86	3.14	3.54	3.86
30	1.30	1.67	1.93	2.20	2.55	2.82	3.11	3.49	3.80
35	1.29	1.63	1.88	2.12	2.44	2.69	2.95	3.29	3.56
40	1.28	1.61	1.84	2.07	2.37	2.60	2.83	3.14	3.39
45	1.27	1.58	1.81	2.03	2.31	2.53	2.74	3.04	3.26
50	1.26	1.57	1.78	1.99	2.27	2.47	2.68	2.95	3.16
60	1.25	1.54	1.75	1.94	2.20	2.39	2.58	2.83	3.02
70	1.24	1.53	1.72	1.91	2.15	2.33	2.51	2.74	2.92
80	1.23	1.51	1.70	1.88	2.12	2.29	2.46	2.68	2.85
90	1.23	1.50	1.69	1.86	2.09	2.25	2.42	2.63	2.79
100	1.23	1.49	1.68	1.85	2.07	2.23	2.38	2.59	2.75
120	1.22	1.48	1.66	1.82	2.03	2.19	2.34	2.53	2.68
140	1.22	1.47	1.65	1.81	2.01	2.16	2.31	2.49	2.64
160	1.21	1.47	1.64	1.80	1.99	2.14	2.28	2.47	2.60
180	1.21	1.46	1.63	1.79	1.98	2.12	2.26	2.44	2.58
200	1.21	1.46	1.62	1.78	1.97	2.11	2.25	2.42	2.56
300	1.20	1.45	1.61	1.75	1.94	2.07	2.20	2.37	2.49
500	1.20	1.44	1.59	1.74	1.92	2.04	2.17	2.33	2.45
∞	1.19	1.42	1.57	1.71	1.88	2.00	2.12	2.27	2.37

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 22

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.61	61.9	249.	995.	6220.	24900.	99600.	622000.	2490000.
2	3.43	9.45	19.5	39.5	99.5	199.	399.	999.	2000.
3	2.46	5.18	8.65	14.1	26.6	42.7	68.2	126.	201.
4	2.08	3.84	5.79	8.53	14.0	20.1	28.7	45.9	65.3
5	1.88	3.20	4.54	6.30	9.51	12.8	17.2	25.3	33.6
6	1.76	2.83	3.86	5.14	7.35	9.53	12.3	17.0	21.7
7	1.67	2.58	3.43	4.44	6.11	7.69	9.62	12.8	15.9
8	1.61	2.41	3.13	3.97	5.32	6.55	8.02	10.4	12.6
9	1.56	2.29	2.92	3.64	4.77	5.78	6.95	8.80	10.5
10	1.52	2.19	2.75	3.39	4.36	5.22	6.20	7.71	9.06
11	1.49	2.11	2.63	3.20	4.06	4.80	5.64	6.92	8.04
12	1.46	2.05	2.52	3.04	3.82	4.48	5.21	6.32	7.27
13	1.44	1.99	2.44	2.92	3.62	4.22	4.87	5.85	6.68
14	1.42	1.95	2.37	2.81	3.46	4.01	4.60	5.48	6.21
15	1.41	1.91	2.31	2.73	3.33	3.83	4.37	5.17	5.83
16	1.39	1.88	2.25	2.65	3.22	3.68	4.18	4.91	5.52
17	1.38	1.85	2.21	2.59	3.12	3.56	4.02	4.70	5.25
18	1.37	1.82	2.17	2.53	3.03	3.45	3.88	4.51	5.03
19	1.36	1.80	2.13	2.48	2.96	3.35	3.76	4.35	4.83
20	1.35	1.78	2.10	2.43	2.90	3.27	3.66	4.21	4.67
21	1.35	1.76	2.07	2.39	2.84	3.19	3.56	4.09	4.52
22	1.34	1.74	2.05	2.36	2.78	3.12	3.48	3.98	4.39
23	1.33	1.73	2.02	2.33	2.74	3.06	3.41	3.89	4.27
24	1.33	1.71	2.00	2.30	2.70	3.01	3.34	3.80	4.17
25	1.32	1.70	1.98	2.27	2.66	2.96	3.28	3.72	4.07
26	1.32	1.69	1.97	2.24	2.62	2.92	3.22	3.65	3.99
27	1.31	1.68	1.95	2.22	2.59	2.88	3.17	3.58	3.91
28	1.31	1.67	1.93	2.20	2.56	2.84	3.13	3.52	3.84
29	1.30	1.66	1.92	2.18	2.53	2.80	3.08	3.47	3.77
30	1.30	1.65	1.91	2.16	2.51	2.77	3.04	3.42	3.71
35	1.28	1.62	1.85	2.09	2.40	2.64	2.89	3.22	3.48
40	1.27	1.59	1.81	2.03	2.33	2.55	2.77	3.07	3.31
45	1.26	1.57	1.78	1.99	2.27	2.47	2.68	2.96	3.18
50	1.25	1.55	1.76	1.96	2.22	2.42	2.62	2.88	3.08
60	1.24	1.53	1.72	1.91	2.15	2.33	2.52	2.75	2.94
70	1.23	1.51	1.70	1.88	2.11	2.28	2.45	2.67	2.84
80	1.23	1.49	1.68	1.85	2.07	2.23	2.39	2.61	2.77
90	1.22	1.48	1.66	1.83	2.04	2.20	2.35	2.56	2.71
100	1.22	1.48	1.65	1.81	2.02	2.17	2.32	2.52	2.67
120	1.21	1.46	1.63	1.79	1.99	2.13	2.28	2.46	2.60
140	1.21	1.45	1.62	1.77	1.97	2.11	2.24	2.42	2.56
160	1.21	1.45	1.61	1.76	1.95	2.09	2.22	2.39	2.52
180	1.20	1.44	1.60	1.75	1.94	2.07	2.20	2.37	2.50
200	1.20	1.44	1.60	1.74	1.93	2.06	2.19	2.35	2.48
300	1.20	1.43	1.58	1.72	1.89	2.02	2.14	2.30	2.41
500	1.19	1.42	1.56	1.70	1.87	1.99	2.11	2.26	2.37
∞	1.18	1.40	1.54	1.67	1.83	1.95	2.05	2.19	2.30

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 24

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.63	62.0	249.	997.	6230.	24900.	99800.	623000.	2490000.
2	3.43	9.45	19.5	39.5	99.5	199.	399.	999.	2000.
3	2.46	5.18	8.64	14.1	26.6	42.6	68.1	126.	200.
4	2.08	3.83	5.77	8.51	13.9	20.0	28.7	45.8	65.0
5	1.88	3.19	4.53	6.28	9.47	12.8	17.1	25.1	33.4
6	1.75	2.82	3.84	5.12	7.31	9.47	12.2	16.9	21.5
7	1.67	2.58	3.41	4.41	6.07	7.64	9.56	12.7	15.8
8	1.60	2.40	3.12	3.95	5.28	6.50	7.95	10.3	12.5
9	1.56	2.28	2.90	3.61	4.73	5.73	6.89	8.72	10.4
10	1.52	2.18	2.74	3.37	4.33	5.17	6.14	7.64	8.96
11	1.49	2.10	2.61	3.17	4.02	4.76	5.58	6.85	7.95
12	1.46	2.04	2.51	3.02	3.78	4.43	5.16	6.25	7.19
13	1.44	1.98	2.42	2.89	3.59	4.17	4.82	5.78	6.60
14	1.42	1.94	2.35	2.79	3.43	3.96	4.55	5.41	6.13
15	1.41	1.90	2.29	2.70	3.29	3.79	4.32	5.10	5.75
16	1.39	1.87	2.24	2.63	3.18	3.64	4.13	4.85	5.44
17	1.38	1.84	2.19	2.56	3.08	3.51	3.97	4.63	5.18
18	1.37	1.81	2.15	2.50	3.00	3.40	3.83	4.45	4.95
19	1.36	1.79	2.11	2.45	2.92	3.31	3.71	4.29	4.76
20	1.35	1.77	2.08	2.41	2.86	3.22	3.61	4.15	4.59
21	1.34	1.75	2.05	2.37	2.80	3.15	3.51	4.03	4.44
22	1.33	1.73	2.03	2.33	2.75	3.08	3.43	3.92	4.31
23	1.33	1.72	2.01	2.30	2.70	3.02	3.35	3.82	4.20
24	1.32	1.70	1.98	2.27	2.66	2.97	3.29	3.74	4.09
25	1.32	1.69	1.96	2.24	2.62	2.92	3.23	3.66	4.00
26	1.31	1.68	1.95	2.22	2.58	2.87	3.17	3.59	3.92
27	1.31	1.67	1.93	2.19	2.55	2.83	3.12	3.52	3.84
28	1.30	1.66	1.91	2.17	2.52	2.79	3.07	3.46	3.77
29	1.30	1.65	1.90	2.15	2.49	2.76	3.03	3.41	3.70
30	1.29	1.64	1.89	2.14	2.47	2.73	2.99	3.36	3.64
35	1.28	1.60	1.83	2.06	2.36	2.60	2.83	3.16	3.41
40	1.26	1.57	1.79	2.01	2.29	2.50	2.72	3.01	3.24
45	1.26	1.55	1.76	1.96	2.23	2.43	2.63	2.90	3.11
50	1.25	1.54	1.74	1.93	2.18	2.37	2.56	2.82	3.01
60	1.24	1.51	1.70	1.88	2.12	2.29	2.46	2.69	2.87
70	1.23	1.49	1.67	1.85	2.07	2.23	2.39	2.61	2.77
80	1.22	1.48	1.65	1.82	2.03	2.19	2.34	2.54	2.70
90	1.22	1.47	1.64	1.80	2.00	2.15	2.30	2.50	2.64
100	1.21	1.46	1.63	1.78	1.98	2.13	2.27	2.46	2.60
120	1.21	1.45	1.61	1.76	1.95	2.09	2.23	2.40	2.53
140	1.20	1.44	1.60	1.74	1.93	2.06	2.19	2.36	2.49
160	1.20	1.43	1.59	1.73	1.91	2.04	2.17	2.33	2.45
180	1.20	1.43	1.58	1.72	1.90	2.02	2.15	2.31	2.43
200	1.19	1.42	1.57	1.71	1.89	2.01	2.13	2.29	2.41
300	1.19	1.41	1.55	1.69	1.85	1.97	2.09	2.24	2.35
500	1.18	1.40	1.54	1.67	1.83	1.94	2.05	2.20	2.30
∞	1.18	1.38	1.52	1.64	1.79	1.90	2.00	2.13	2.23

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 26

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.64	62.1	249.	999.	6240.	25000.	99900.	624000.	2500000.
2	3.44	9.45	19.5	39.5	99.5	199.	399.	999.	2000.
3	2.46	5.17	8.63	14.1	26.6	42.6	68.0	126.	200.
4	2.08	3.83	5.76	8.49	13.9	20.0	28.6	45.6	64.9
5	1.88	3.18	4.52	6.26	9.43	12.7	17.1	25.0	33.3
6	1.75	2.81	3.83	5.10	7.28	9.43	12.1	16.8	21.4
7	1.67	2.57	3.40	4.39	6.04	7.60	9.50	12.7	15.7
8	1.60	2.40	3.10	3.93	5.25	6.46	7.90	10.2	12.4
9	1.55	2.27	2.89	3.59	4.70	5.69	6.84	8.66	10.3
10	1.52	2.17	2.72	3.34	4.30	5.13	6.09	7.57	8.89
11	1.48	2.09	2.59	3.15	3.99	4.72	5.54	6.78	7.87
12	1.46	2.03	2.49	3.00	3.75	4.39	5.11	6.19	7.12
13	1.44	1.97	2.41	2.87	3.56	4.13	4.77	5.72	6.53
14	1.42	1.93	2.33	2.77	3.40	3.92	4.50	5.35	6.07
15	1.40	1.89	2.27	2.68	3.26	3.75	4.27	5.04	5.69
16	1.39	1.86	2.22	2.60	3.15	3.60	4.09	4.79	5.37
17	1.38	1.83	2.17	2.54	3.05	3.47	3.92	4.57	5.11
18	1.36	1.80	2.13	2.48	2.97	3.36	3.79	4.39	4.89
19	1.35	1.78	2.10	2.43	2.89	3.27	3.67	4.23	4.70
20	1.35	1.76	2.07	2.39	2.83	3.18	3.56	4.09	4.53
21	1.34	1.74	2.04	2.34	2.77	3.11	3.47	3.97	4.38
22	1.33	1.72	2.01	2.31	2.72	3.04	3.38	3.86	4.25
23	1.32	1.70	1.99	2.28	2.67	2.98	3.31	3.77	4.14
24	1.32	1.69	1.97	2.25	2.63	2.93	3.24	3.68	4.03
25	1.31	1.68	1.95	2.22	2.59	2.88	3.18	3.60	3.94
26	1.31	1.67	1.93	2.19	2.55	2.84	3.13	3.53	3.85
27	1.30	1.65	1.91	2.17	2.52	2.79	3.08	3.47	3.78
28	1.30	1.64	1.90	2.15	2.49	2.76	3.03	3.41	3.71
29	1.29	1.63	1.88	2.13	2.46	2.72	2.99	3.35	3.64
30	1.29	1.63	1.87	2.11	2.44	2.69	2.95	3.30	3.58
35	1.27	1.59	1.82	2.04	2.33	2.56	2.79	3.10	3.35
40	1.26	1.56	1.77	1.98	2.26	2.46	2.67	2.96	3.18
45	1.25	1.54	1.74	1.94	2.20	2.39	2.59	2.85	3.05
50	1.24	1.52	1.72	1.91	2.15	2.33	2.52	2.76	2.95
60	1.23	1.50	1.68	1.86	2.08	2.25	2.42	2.64	2.81
70	1.22	1.48	1.65	1.82	2.03	2.19	2.35	2.56	2.71
80	1.22	1.47	1.63	1.79	2.00	2.15	2.30	2.49	2.64
90	1.21	1.45	1.62	1.77	1.97	2.12	2.26	2.44	2.58
100	1.21	1.45	1.61	1.76	1.95	2.09	2.23	2.41	2.54
120	1.20	1.43	1.59	1.73	1.92	2.05	2.18	2.35	2.48
140	1.20	1.42	1.57	1.72	1.89	2.02	2.15	2.31	2.43
160	1.19	1.42	1.57	1.70	1.88	2.00	2.12	2.28	2.40
180	1.19	1.41	1.56	1.69	1.86	1.98	2.10	2.26	2.37
200	1.19	1.41	1.55	1.68	1.85	1.97	2.09	2.24	2.35
300	1.18	1.39	1.53	1.66	1.82	1.93	2.04	2.18	2.29
500	1.18	1.38	1.52	1.64	1.79	1.90	2.01	2.14	2.24
∞	1.17	1.37	1.50	1.61	1.76	1.86	1.95	2.08	2.17

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 28

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.66	62.2	250.	1000.	6250.	25000.	100000.	625000.	2500000.
2	3.44	9.46	19.5	39.5	99.5	199.	399.	999.	2000.
3	2.46	5.17	8.62	14.1	26.5	42.5	67.9	126.	200.
4	2.08	3.82	5.75	8.48	13.9	19.9	28.5	45.5	64.7
5	1.88	3.18	4.50	6.24	9.40	12.7	17.0	24.9	33.2
6	1.75	2.81	3.82	5.08	7.25	9.39	12.1	16.7	21.3
7	1.66	2.56	3.39	4.38	6.02	7.57	9.45	12.6	15.6
8	1.60	2.39	3.09	3.91	5.22	6.43	7.86	10.2	12.3
9	1.55	2.26	2.87	3.58	4.67	5.65	6.80	8.60	10.2
10	1.51	2.16	2.71	3.33	4.27	5.10	6.05	7.52	8.82
11	1.48	2.08	2.58	3.13	3.96	4.68	5.49	6.73	7.81
12	1.46	2.02	2.48	2.98	3.72	4.36	5.07	6.14	7.05
13	1.43	1.96	2.39	2.85	3.53	4.10	4.73	5.67	6.47
14	1.42	1.92	2.32	2.75	3.37	3.89	4.46	5.30	6.01
15	1.40	1.88	2.26	2.66	3.24	3.72	4.23	4.99	5.63
16	1.39	1.85	2.21	2.58	3.12	3.57	4.05	4.74	5.32
17	1.37	1.82	2.16	2.52	3.03	3.44	3.89	4.53	5.05
18	1.36	1.79	2.12	2.46	2.94	3.33	3.75	4.34	4.83
19	1.35	1.77	2.08	2.41	2.87	3.24	3.63	4.18	4.64
20	1.34	1.75	2.05	2.37	2.80	3.15	3.52	4.05	4.47
21	1.33	1.73	2.02	2.33	2.74	3.08	3.43	3.93	4.33
22	1.33	1.71	2.00	2.29	2.69	3.01	3.35	3.82	4.20
23	1.32	1.69	1.97	2.26	2.64	2.95	3.27	3.72	4.08
24	1.31	1.68	1.95	2.23	2.60	2.90	3.20	3.63	3.98
25	1.31	1.67	1.93	2.20	2.56	2.85	3.14	3.56	3.89
26	1.30	1.66	1.91	2.17	2.53	2.80	3.09	3.49	3.80
27	1.30	1.64	1.90	2.15	2.49	2.76	3.04	3.42	3.72
28	1.29	1.63	1.88	2.13	2.46	2.72	2.99	3.36	3.65
29	1.29	1.62	1.87	2.11	2.44	2.69	2.95	3.31	3.59
30	1.29	1.62	1.85	2.09	2.41	2.66	2.91	3.26	3.53
35	1.27	1.58	1.80	2.02	2.30	2.53	2.75	3.06	3.30
40	1.26	1.55	1.76	1.96	2.23	2.43	2.64	2.91	3.13
45	1.25	1.53	1.73	1.92	2.17	2.36	2.55	2.80	3.00
50	1.24	1.51	1.70	1.89	2.12	2.30	2.48	2.72	2.90
60	1.23	1.49	1.66	1.83	2.05	2.22	2.38	2.60	2.76
70	1.22	1.47	1.64	1.80	2.01	2.16	2.31	2.51	2.66
80	1.21	1.45	1.62	1.77	1.97	2.11	2.26	2.45	2.59
90	1.21	1.44	1.60	1.75	1.94	2.08	2.22	2.40	2.53
100	1.20	1.43	1.59	1.74	1.92	2.05	2.19	2.36	2.49
120	1.20	1.42	1.57	1.71	1.89	2.01	2.14	2.30	2.42
140	1.19	1.41	1.56	1.69	1.86	1.99	2.11	2.26	2.38
160	1.19	1.40	1.55	1.68	1.85	1.97	2.08	2.23	2.35
180	1.19	1.40	1.54	1.67	1.83	1.95	2.06	2.21	2.32
200	1.18	1.39	1.53	1.66	1.82	1.94	2.05	2.19	2.30
300	1.18	1.38	1.51	1.64	1.79	1.90	2.00	2.14	2.24
500	1.17	1.37	1.50	1.62	1.76	1.87	1.97	2.10	2.19
∞	1.17	1.35	1.48	1.59	1.72	1.82	1.91	2.03	2.12

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 30

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.67	62.3	250.	1000.	6260.	25000.	100000.	626000.	2500000.
2	3.44	9.46	19.5	39.5	99.5	199.	399.	999.	2000.
3	2.47	5.17	8.62	14.1	26.5	42.5	67.8	125.	200.
4	2.08	3.82	5.75	8.46	13.8	19.9	28.5	45.4	64.6
5	1.88	3.17	4.50	6.23	9.38	12.7	17.0	24.9	33.1
6	1.75	2.80	3.81	5.07	7.23	9.36	12.0	16.7	21.2
7	1.66	2.56	3.38	4.36	5.99	7.53	9.41	12.5	15.5
8	1.60	2.38	3.08	3.89	5.20	6.40	7.82	10.1	12.2
9	1.55	2.25	2.86	3.56	4.65	5.62	6.76	8.55	10.2
10	1.51	2.16	2.70	3.31	4.25	5.07	6.01	7.47	8.76
11	1.48	2.08	2.57	3.12	3.94	4.65	5.46	6.68	7.75
12	1.45	2.01	2.47	2.96	3.70	4.33	5.03	6.09	7.00
13	1.43	1.96	2.38	2.84	3.51	4.07	4.70	5.63	6.42
14	1.41	1.91	2.31	2.73	3.35	3.86	4.42	5.25	5.95
15	1.40	1.87	2.25	2.64	3.21	3.69	4.20	4.95	5.58
16	1.38	1.84	2.19	2.57	3.10	3.54	4.01	4.70	5.27
17	1.37	1.81	2.15	2.50	3.00	3.41	3.85	4.48	5.01
18	1.36	1.78	2.11	2.44	2.92	3.30	3.71	4.30	4.78
19	1.35	1.76	2.07	2.39	2.84	3.21	3.59	4.14	4.59
20	1.34	1.74	2.04	2.35	2.78	3.12	3.49	4.00	4.42
21	1.33	1.72	2.01	2.31	2.72	3.05	3.40	3.88	4.28
22	1.32	1.70	1.98	2.27	2.67	2.98	3.31	3.78	4.15
23	1.32	1.69	1.96	2.24	2.62	2.92	3.24	3.68	4.03
24	1.31	1.67	1.94	2.21	2.58	2.87	3.17	3.59	3.93
25	1.31	1.66	1.92	2.18	2.54	2.82	3.11	3.52	3.84
26	1.30	1.65	1.90	2.16	2.50	2.77	3.06	3.44	3.75
27	1.30	1.64	1.88	2.13	2.47	2.73	3.00	3.38	3.68
28	1.29	1.63	1.87	2.11	2.44	2.69	2.96	3.32	3.61
29	1.29	1.62	1.85	2.09	2.41	2.66	2.92	3.27	3.54
30	1.28	1.61	1.84	2.07	2.39	2.63	2.88	3.22	3.49
35	1.27	1.57	1.79	2.00	2.28	2.50	2.72	3.02	3.25
40	1.25	1.54	1.74	1.94	2.20	2.40	2.60	2.87	3.08
45	1.24	1.52	1.71	1.90	2.14	2.33	2.51	2.76	2.96
50	1.23	1.50	1.69	1.87	2.10	2.27	2.45	2.68	2.86
60	1.22	1.48	1.65	1.82	2.03	2.19	2.35	2.55	2.71
70	1.21	1.46	1.62	1.78	1.98	2.13	2.28	2.47	2.62
80	1.21	1.44	1.60	1.75	1.94	2.08	2.22	2.41	2.54
90	1.20	1.43	1.59	1.73	1.92	2.05	2.18	2.36	2.49
100	1.20	1.42	1.57	1.71	1.89	2.02	2.15	2.32	2.44
120	1.19	1.41	1.55	1.69	1.86	1.98	2.11	2.26	2.38
140	1.19	1.40	1.54	1.67	1.84	1.96	2.07	2.22	2.33
160	1.18	1.39	1.53	1.66	1.82	1.93	2.05	2.19	2.30
180	1.18	1.39	1.52	1.65	1.81	1.92	2.03	2.17	2.27
200	1.18	1.38	1.52	1.64	1.79	1.91	2.01	2.15	2.25
300	1.17	1.37	1.50	1.62	1.76	1.87	1.97	2.10	2.19
500	1.17	1.36	1.48	1.60	1.74	1.84	1.93	2.05	2.14
∞	1.16	1.34	1.46	1.57	1.70	1.79	1.88	1.99	2.07

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 40

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.71	62.5	251.	1010.	6290.	25100.	101000.	629000.	2510000.
2	3.45	9.47	19.5	39.5	99.5	199.	399.	999.	2000.
3	2.47	5.16	8.59	14.0	26.4	42.3	67.5	125.	199.
4	2.08	3.80	5.72	8.41	13.7	19.8	28.2	45.1	64.1
5	1.88	3.16	4.46	6.18	9.29	12.5	16.8	24.6	32.7
6	1.75	2.78	3.77	5.01	7.14	9.24	11.9	16.4	21.0
7	1.66	2.54	3.34	4.31	5.91	7.42	9.26	12.3	15.2
8	1.59	2.36	3.04	3.84	5.12	6.29	7.68	9.92	12.0
9	1.54	2.23	2.83	3.51	4.57	5.52	6.62	8.37	9.94
10	1.51	2.13	2.66	3.26	4.17	4.97	5.88	7.30	8.55
11	1.47	2.05	2.53	3.06	3.86	4.55	5.33	6.52	7.55
12	1.45	1.99	2.43	2.91	3.62	4.23	4.91	5.93	6.81
13	1.42	1.93	2.34	2.78	3.43	3.97	4.57	5.47	6.23
14	1.41	1.89	2.27	2.67	3.27	3.76	4.30	5.10	5.77
15	1.39	1.85	2.20	2.59	3.13	3.58	4.08	4.80	5.40
16	1.37	1.81	2.15	2.51	3.02	3.44	3.89	4.54	5.09
17	1.36	1.78	2.10	2.44	2.92	3.31	3.73	4.33	4.83
18	1.35	1.75	2.06	2.38	2.84	3.20	3.59	4.15	4.61
19	1.34	1.73	2.03	2.33	2.76	3.11	3.47	3.99	4.42
20	1.33	1.71	1.99	2.29	2.69	3.02	3.37	3.86	4.25
21	1.32	1.69	1.96	2.25	2.64	2.95	3.27	3.74	4.11
22	1.31	1.67	1.94	2.21	2.58	2.88	3.19	3.63	3.98
23	1.31	1.66	1.91	2.18	2.54	2.82	3.12	3.53	3.87
24	1.30	1.64	1.89	2.15	2.49	2.77	3.05	3.45	3.76
25	1.29	1.63	1.87	2.12	2.45	2.72	2.99	3.37	3.67
26	1.29	1.61	1.85	2.09	2.42	2.67	2.93	3.30	3.59
27	1.28	1.60	1.84	2.07	2.38	2.63	2.88	3.23	3.51
28	1.28	1.59	1.82	2.05	2.35	2.59	2.84	3.18	3.44
29	1.27	1.58	1.81	2.03	2.33	2.56	2.79	3.12	3.38
30	1.27	1.57	1.79	2.01	2.30	2.52	2.76	3.07	3.32
35	1.25	1.53	1.74	1.93	2.19	2.39	2.60	2.87	3.09
40	1.24	1.51	1.69	1.88	2.11	2.30	2.48	2.73	2.92
45	1.23	1.48	1.66	1.83	2.05	2.22	2.39	2.62	2.79
50	1.22	1.46	1.63	1.80	2.01	2.16	2.32	2.53	2.69
60	1.21	1.44	1.59	1.74	1.94	2.08	2.22	2.41	2.55
70	1.20	1.42	1.57	1.71	1.89	2.02	2.15	2.32	2.45
80	1.19	1.40	1.54	1.68	1.85	1.97	2.10	2.26	2.38
90	1.19	1.39	1.53	1.66	1.82	1.94	2.06	2.21	2.32
100	1.18	1.38	1.52	1.64	1.80	1.91	2.02	2.17	2.28
120	1.18	1.37	1.50	1.61	1.76	1.87	1.98	2.11	2.21
140	1.17	1.36	1.48	1.60	1.74	1.84	1.94	2.07	2.17
160	1.17	1.35	1.47	1.58	1.72	1.82	1.92	2.04	2.13
180	1.16	1.34	1.46	1.57	1.71	1.80	1.90	2.02	2.11
200	1.16	1.34	1.46	1.56	1.69	1.79	1.88	2.00	2.09
300	1.15	1.32	1.43	1.54	1.66	1.75	1.84	1.94	2.02
500	1.15	1.31	1.42	1.52	1.63	1.72	1.80	1.90	1.98
∞	1.14	1.30	1.39	1.48	1.59	1.67	1.74	1.84	1.90

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 50

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.74	62.7	252.	1010.	6300.	25200.	101000.	630000.	2520000.
2	3.46	9.47	19.5	39.5	99.5	199.	399.	999.	2000.
3	2.47	5.15	8.58	14.0	26.4	42.2	67.4	125.	198.
4	2.08	3.80	5.70	8.38	13.7	19.7	28.1	44.9	63.8
5	1.88	3.15	4.44	6.14	9.24	12.5	16.7	24.4	32.5
6	1.75	2.77	3.75	4.98	7.09	9.17	11.8	16.3	20.8
7	1.66	2.52	3.32	4.28	5.86	7.35	9.17	12.2	15.1
8	1.59	2.35	3.02	3.81	5.07	6.22	7.59	9.80	11.8
9	1.54	2.22	2.80	3.47	4.52	5.45	6.54	8.26	9.81
10	1.50	2.12	2.64	3.22	4.12	4.90	5.80	7.19	8.43
11	1.47	2.04	2.51	3.03	3.81	4.49	5.25	6.42	7.43
12	1.44	1.97	2.40	2.87	3.57	4.17	4.83	5.83	6.69
13	1.42	1.92	2.31	2.74	3.38	3.91	4.50	5.37	6.11
14	1.40	1.87	2.24	2.64	3.22	3.70	4.23	5.00	5.66
15	1.38	1.83	2.18	2.55	3.08	3.52	4.00	4.70	5.29
16	1.37	1.79	2.12	2.47	2.97	3.37	3.81	4.45	4.98
17	1.36	1.76	2.08	2.41	2.87	3.25	3.65	4.24	4.72
18	1.34	1.74	2.04	2.35	2.78	3.14	3.52	4.06	4.50
19	1.33	1.71	2.00	2.30	2.71	3.04	3.40	3.90	4.31
20	1.32	1.69	1.97	2.25	2.64	2.96	3.29	3.77	4.15
21	1.32	1.67	1.94	2.21	2.58	2.88	3.20	3.64	4.00
22	1.31	1.65	1.91	2.17	2.53	2.82	3.12	3.54	3.88
23	1.30	1.64	1.88	2.14	2.48	2.76	3.04	3.44	3.76
24	1.29	1.62	1.86	2.11	2.44	2.70	2.98	3.36	3.66
25	1.29	1.61	1.84	2.08	2.40	2.65	2.91	3.28	3.57
26	1.28	1.59	1.82	2.05	2.36	2.61	2.86	3.21	3.49
27	1.28	1.58	1.81	2.03	2.33	2.57	2.81	3.14	3.41
28	1.27	1.57	1.79	2.01	2.30	2.53	2.76	3.09	3.34
29	1.27	1.56	1.77	1.99	2.27	2.49	2.72	3.03	3.28
30	1.26	1.55	1.76	1.97	2.25	2.46	2.68	2.98	3.22
35	1.24	1.51	1.70	1.89	2.14	2.33	2.52	2.78	2.98
40	1.23	1.48	1.66	1.83	2.06	2.23	2.40	2.64	2.82
45	1.22	1.46	1.63	1.79	2.00	2.16	2.31	2.53	2.69
50	1.21	1.44	1.60	1.75	1.95	2.10	2.24	2.44	2.59
60	1.20	1.41	1.56	1.70	1.88	2.01	2.14	2.32	2.45
70	1.19	1.39	1.53	1.66	1.83	1.95	2.07	2.23	2.35
80	1.18	1.38	1.51	1.63	1.79	1.90	2.02	2.16	2.28
90	1.18	1.36	1.49	1.61	1.76	1.87	1.98	2.11	2.22
100	1.17	1.35	1.48	1.59	1.74	1.84	1.94	2.08	2.18
120	1.16	1.34	1.46	1.56	1.70	1.80	1.89	2.02	2.11
140	1.16	1.33	1.44	1.55	1.67	1.77	1.86	1.98	2.06
160	1.15	1.32	1.43	1.53	1.66	1.75	1.83	1.95	2.03
180	1.15	1.32	1.42	1.52	1.64	1.73	1.81	1.92	2.00
200	1.15	1.31	1.41	1.51	1.63	1.71	1.80	1.90	1.98
300	1.14	1.29	1.39	1.48	1.59	1.67	1.75	1.85	1.92
500	1.14	1.28	1.38	1.46	1.57	1.64	1.71	1.80	1.87
∞	1.13	1.26	1.35	1.43	1.52	1.59	1.65	1.73	1.79

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 60

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.76	62.8	252.	1010.	6310.	25300.	101000.	631000.	2530000.
2	3.46	9.47	19.5	39.5	99.5	199.	399.	999.	2000.
3	2.47	5.15	8.57	14.0	26.3	42.1	67.3	124.	198.
4	2.08	3.79	5.69	8.36	13.7	19.6	28.0	44.7	63.6
5	1.87	3.14	4.43	6.12	9.20	12.4	16.6	24.3	32.4
6	1.74	2.76	3.74	4.96	7.06	9.12	11.7	16.2	20.7
7	1.65	2.51	3.30	4.25	5.82	7.31	9.12	12.1	15.0
8	1.59	2.34	3.01	3.78	5.03	6.18	7.54	9.73	11.8
9	1.54	2.21	2.79	3.45	4.48	5.41	6.49	8.19	9.72
10	1.50	2.11	2.62	3.20	4.08	4.86	5.75	7.12	8.34
11	1.47	2.03	2.49	3.00	3.78	4.45	5.20	6.35	7.35
12	1.44	1.96	2.38	2.85	3.54	4.12	4.78	5.76	6.61
13	1.42	1.90	2.30	2.72	3.34	3.87	4.44	5.30	6.04
14	1.40	1.86	2.22	2.61	3.18	3.66	4.17	4.94	5.58
15	1.38	1.82	2.16	2.52	3.05	3.48	3.95	4.64	5.21
16	1.36	1.78	2.11	2.45	2.93	3.33	3.76	4.39	4.91
17	1.35	1.75	2.06	2.38	2.83	3.21	3.60	4.18	4.65
18	1.34	1.72	2.02	2.32	2.75	3.10	3.47	4.00	4.43
19	1.33	1.70	1.98	2.27	2.67	3.00	3.35	3.84	4.24
20	1.32	1.68	1.95	2.22	2.61	2.92	3.24	3.70	4.08
21	1.31	1.66	1.92	2.18	2.55	2.84	3.15	3.58	3.93
22	1.30	1.64	1.89	2.14	2.50	2.77	3.07	3.48	3.81
23	1.30	1.62	1.86	2.11	2.45	2.71	2.99	3.38	3.69
24	1.29	1.61	1.84	2.08	2.40	2.66	2.92	3.29	3.59
25	1.28	1.59	1.82	2.05	2.36	2.61	2.86	3.22	3.50
26	1.28	1.58	1.80	2.03	2.33	2.56	2.81	3.15	3.42
27	1.27	1.57	1.79	2.00	2.29	2.52	2.76	3.08	3.34
28	1.27	1.56	1.77	1.98	2.26	2.48	2.71	3.02	3.27
29	1.26	1.55	1.75	1.96	2.23	2.45	2.67	2.97	3.21
30	1.26	1.54	1.74	1.94	2.21	2.42	2.63	2.92	3.15
35	1.24	1.50	1.68	1.86	2.10	2.28	2.47	2.72	2.91
40	1.22	1.47	1.64	1.80	2.02	2.18	2.35	2.57	2.75
45	1.21	1.44	1.60	1.76	1.96	2.11	2.26	2.46	2.62
50	1.20	1.42	1.58	1.72	1.91	2.05	2.19	2.38	2.52
60	1.19	1.40	1.53	1.67	1.84	1.96	2.09	2.25	2.38
70	1.18	1.37	1.50	1.63	1.78	1.90	2.01	2.16	2.28
80	1.17	1.36	1.48	1.60	1.75	1.85	1.96	2.10	2.20
90	1.17	1.35	1.46	1.58	1.72	1.82	1.92	2.05	2.15
100	1.16	1.34	1.45	1.56	1.69	1.79	1.89	2.01	2.10
120	1.16	1.32	1.43	1.53	1.66	1.75	1.84	1.95	2.04
140	1.15	1.31	1.41	1.51	1.63	1.72	1.80	1.91	1.99
160	1.15	1.30	1.40	1.50	1.61	1.69	1.77	1.88	1.95
180	1.14	1.29	1.39	1.48	1.60	1.68	1.75	1.85	1.93
200	1.14	1.29	1.39	1.47	1.58	1.66	1.74	1.83	1.90
300	1.13	1.27	1.36	1.45	1.55	1.62	1.69	1.78	1.84
500	1.13	1.26	1.35	1.42	1.52	1.58	1.65	1.73	1.79
∞	1.12	1.24	1.32	1.39	1.47	1.53	1.59	1.66	1.71

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 70

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.77	62.9	252.	1010.	6320.	25300.	101000.	632000.	2530000.
2	3.46	9.48	19.5	39.5	99.5	199.	399.	999.	2000.
3	2.47	5.15	8.57	14.0	26.3	42.1	67.2	124.	198.
4	2.08	3.79	5.68	8.35	13.6	19.6	28.0	44.6	63.4
5	1.87	3.14	4.42	6.11	9.18	12.4	16.6	24.3	32.3
6	1.74	2.76	3.73	4.94	7.03	9.09	11.7	16.1	20.6
7	1.65	2.51	3.29	4.24	5.80	7.28	9.07	12.1	14.9
8	1.59	2.33	2.99	3.77	5.01	6.15	7.49	9.67	11.7
9	1.54	2.20	2.78	3.43	4.46	5.38	6.45	8.13	9.65
10	1.50	2.10	2.61	3.18	4.06	4.83	5.71	7.07	8.28
11	1.46	2.02	2.48	2.99	3.75	4.41	5.16	6.30	7.29
12	1.44	1.95	2.37	2.83	3.51	4.09	4.74	5.71	6.55
13	1.41	1.90	2.28	2.70	3.32	3.84	4.41	5.26	5.98
14	1.39	1.85	2.21	2.60	3.16	3.62	4.14	4.89	5.53
15	1.38	1.81	2.15	2.51	3.02	3.45	3.91	4.59	5.16
16	1.36	1.77	2.09	2.43	2.91	3.30	3.73	4.34	4.85
17	1.35	1.74	2.05	2.36	2.81	3.18	3.57	4.13	4.60
18	1.34	1.71	2.00	2.30	2.72	3.07	3.43	3.95	4.38
19	1.33	1.69	1.97	2.25	2.65	2.97	3.31	3.79	4.19
20	1.32	1.67	1.93	2.20	2.58	2.88	3.20	3.66	4.03
21	1.31	1.65	1.90	2.16	2.52	2.81	3.11	3.54	3.88
22	1.30	1.63	1.88	2.13	2.47	2.74	3.03	3.43	3.76
23	1.29	1.61	1.85	2.09	2.42	2.68	2.95	3.34	3.64
24	1.28	1.60	1.83	2.06	2.38	2.63	2.89	3.25	3.54
25	1.28	1.58	1.81	2.03	2.34	2.58	2.83	3.17	3.45
26	1.27	1.57	1.79	2.01	2.30	2.53	2.77	3.10	3.37
27	1.27	1.56	1.77	1.98	2.27	2.49	2.72	3.04	3.29
28	1.26	1.55	1.75	1.96	2.24	2.45	2.67	2.98	3.22
29	1.26	1.54	1.74	1.94	2.21	2.42	2.63	2.92	3.16
30	1.25	1.53	1.72	1.92	2.18	2.38	2.59	2.87	3.10
35	1.23	1.49	1.66	1.84	2.07	2.25	2.43	2.67	2.86
40	1.22	1.46	1.62	1.78	1.99	2.15	2.31	2.53	2.70
45	1.21	1.43	1.59	1.74	1.93	2.08	2.22	2.42	2.57
50	1.20	1.41	1.56	1.70	1.88	2.02	2.15	2.33	2.47
60	1.19	1.38	1.52	1.64	1.81	1.93	2.05	2.21	2.33
70	1.18	1.36	1.49	1.60	1.75	1.86	1.97	2.12	2.22
80	1.17	1.34	1.46	1.57	1.71	1.82	1.92	2.05	2.15
90	1.16	1.33	1.44	1.55	1.68	1.78	1.88	2.00	2.09
100	1.16	1.32	1.43	1.53	1.66	1.75	1.84	1.96	2.05
120	1.15	1.31	1.41	1.50	1.62	1.71	1.79	1.90	1.98
140	1.14	1.29	1.39	1.48	1.60	1.68	1.76	1.86	1.93
160	1.14	1.29	1.38	1.47	1.58	1.65	1.73	1.83	1.90
180	1.14	1.28	1.37	1.46	1.56	1.64	1.71	1.80	1.87
200	1.13	1.27	1.36	1.45	1.55	1.62	1.69	1.78	1.85
300	1.13	1.26	1.34	1.42	1.51	1.58	1.64	1.72	1.78
500	1.12	1.24	1.32	1.39	1.48	1.54	1.60	1.68	1.73
∞	1.11	1.22	1.29	1.36	1.43	1.49	1.54	1.60	1.65

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 80

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.78	62.9	253.	1010.	6330.	25300.	101000.	633000.	2530000.
2	3.46	9.48	19.5	39.5	99.5	199.	399.	999.	2000.
3	2.47	5.15	8.56	14.0	26.3	42.1	67.1	124.	198.
4	2.08	3.78	5.67	8.33	13.6	19.5	27.9	44.6	63.3
5	1.87	3.13	4.41	6.10	9.16	12.3	16.5	24.2	32.2
6	1.74	2.75	3.72	4.93	7.01	9.06	11.6	16.1	20.5
7	1.65	2.50	3.29	4.23	5.78	7.25	9.04	12.0	14.8
8	1.59	2.33	2.99	3.76	4.99	6.12	7.46	9.63	11.6
9	1.54	2.20	2.77	3.42	4.44	5.36	6.42	8.09	9.61
10	1.50	2.09	2.60	3.17	4.04	4.80	5.68	7.03	8.23
11	1.46	2.01	2.47	2.97	3.73	4.39	5.13	6.26	7.25
12	1.44	1.95	2.36	2.82	3.49	4.07	4.71	5.68	6.51
13	1.41	1.89	2.27	2.69	3.30	3.81	4.38	5.22	5.94
14	1.39	1.84	2.20	2.58	3.14	3.60	4.11	4.86	5.49
15	1.37	1.80	2.14	2.49	3.00	3.43	3.89	4.56	5.12
16	1.36	1.77	2.08	2.42	2.89	3.28	3.70	4.31	4.81
17	1.35	1.74	2.03	2.35	2.79	3.15	3.54	4.10	4.56
18	1.33	1.71	1.99	2.29	2.70	3.04	3.40	3.92	4.34
19	1.32	1.68	1.96	2.24	2.63	2.95	3.28	3.76	4.15
20	1.31	1.66	1.92	2.19	2.56	2.86	3.18	3.62	3.99
21	1.30	1.64	1.89	2.15	2.50	2.79	3.08	3.50	3.84
22	1.30	1.62	1.86	2.11	2.45	2.72	3.00	3.40	3.72
23	1.29	1.61	1.84	2.08	2.40	2.66	2.93	3.30	3.60
24	1.28	1.59	1.82	2.05	2.36	2.60	2.86	3.22	3.50
25	1.28	1.58	1.80	2.02	2.32	2.55	2.80	3.14	3.41
26	1.27	1.56	1.78	1.99	2.28	2.51	2.74	3.07	3.33
27	1.26	1.55	1.76	1.97	2.25	2.47	2.69	3.00	3.25
28	1.26	1.54	1.74	1.94	2.22	2.43	2.64	2.94	3.18
29	1.25	1.53	1.73	1.92	2.19	2.39	2.60	2.89	3.12
30	1.25	1.52	1.71	1.90	2.16	2.36	2.56	2.84	3.06
35	1.23	1.48	1.65	1.82	2.05	2.22	2.40	2.64	2.83
40	1.22	1.45	1.61	1.76	1.97	2.12	2.28	2.49	2.66
45	1.21	1.42	1.57	1.72	1.91	2.05	2.19	2.38	2.53
50	1.20	1.40	1.54	1.68	1.86	1.99	2.12	2.30	2.43
60	1.18	1.37	1.50	1.63	1.78	1.90	2.02	2.17	2.29
70	1.17	1.35	1.47	1.59	1.73	1.84	1.94	2.08	2.18
80	1.16	1.33	1.45	1.55	1.69	1.79	1.89	2.01	2.11
90	1.16	1.32	1.43	1.53	1.66	1.75	1.84	1.96	2.05
100	1.15	1.31	1.41	1.51	1.63	1.72	1.81	1.92	2.01
120	1.14	1.29	1.39	1.48	1.60	1.68	1.76	1.86	1.94
140	1.14	1.28	1.38	1.46	1.57	1.65	1.72	1.82	1.89
160	1.13	1.27	1.36	1.45	1.55	1.62	1.69	1.79	1.85
180	1.13	1.27	1.35	1.43	1.53	1.61	1.67	1.76	1.83
200	1.13	1.26	1.35	1.42	1.52	1.59	1.66	1.74	1.80
300	1.12	1.24	1.32	1.39	1.48	1.55	1.61	1.68	1.74
500	1.11	1.23	1.30	1.37	1.45	1.51	1.56	1.63	1.68
∞	1.10	1.21	1.27	1.33	1.40	1.45	1.50	1.56	1.60

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 90

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.79	63.0	253.	1010.	6330.	25300.	101000.	633000.	2530000.
2	3.46	9.48	19.5	39.5	99.5	199.	399.	999.	2000.
3	2.47	5.15	8.56	14.0	26.3	42.0	67.1	124.	197.
4	2.08	3.78	5.67	8.33	13.6	19.5	27.9	44.5	63.2
5	1.87	3.13	4.41	6.09	9.14	12.3	16.5	24.2	32.1
6	1.74	2.75	3.72	4.92	7.00	9.04	11.6	16.1	20.4
7	1.65	2.50	3.28	4.22	5.77	7.23	9.01	12.0	14.8
8	1.59	2.32	2.98	3.75	4.97	6.10	7.44	9.60	11.6
9	1.53	2.19	2.76	3.41	4.43	5.34	6.40	8.06	9.57
10	1.49	2.09	2.59	3.16	4.03	4.79	5.66	7.00	8.20
11	1.46	2.01	2.46	2.96	3.72	4.37	5.11	6.23	7.21
12	1.43	1.94	2.36	2.81	3.48	4.05	4.69	5.65	6.48
13	1.41	1.89	2.27	2.68	3.28	3.79	4.36	5.19	5.91
14	1.39	1.84	2.19	2.57	3.12	3.58	4.09	4.83	5.45
15	1.37	1.80	2.13	2.48	2.99	3.41	3.86	4.53	5.09
16	1.36	1.76	2.07	2.40	2.87	3.26	3.68	4.28	4.78
17	1.34	1.73	2.03	2.34	2.78	3.13	3.52	4.07	4.53
18	1.33	1.70	1.98	2.28	2.69	3.02	3.38	3.89	4.31
19	1.32	1.68	1.95	2.23	2.61	2.93	3.26	3.73	4.12
20	1.31	1.65	1.91	2.18	2.55	2.84	3.16	3.60	3.96
21	1.30	1.63	1.88	2.14	2.49	2.77	3.06	3.48	3.81
22	1.29	1.62	1.86	2.10	2.43	2.70	2.98	3.37	3.69
23	1.29	1.60	1.83	2.07	2.39	2.64	2.90	3.28	3.57
24	1.28	1.58	1.81	2.03	2.34	2.58	2.84	3.19	3.47
25	1.27	1.57	1.79	2.01	2.30	2.53	2.78	3.11	3.38
26	1.27	1.56	1.77	1.98	2.26	2.49	2.72	3.04	3.30
27	1.26	1.54	1.75	1.95	2.23	2.45	2.67	2.98	3.22
28	1.26	1.53	1.73	1.93	2.20	2.41	2.62	2.92	3.15
29	1.25	1.52	1.72	1.91	2.17	2.37	2.58	2.86	3.09
30	1.25	1.51	1.70	1.89	2.14	2.34	2.54	2.81	3.03
35	1.23	1.47	1.64	1.81	2.03	2.20	2.38	2.61	2.80
40	1.21	1.44	1.60	1.75	1.95	2.10	2.26	2.47	2.63
45	1.20	1.41	1.56	1.70	1.89	2.03	2.17	2.36	2.50
50	1.19	1.39	1.53	1.67	1.84	1.97	2.10	2.27	2.40
60	1.18	1.36	1.49	1.61	1.76	1.88	1.99	2.14	2.25
70	1.17	1.34	1.46	1.57	1.71	1.81	1.92	2.05	2.15
80	1.16	1.33	1.44	1.54	1.67	1.77	1.86	1.98	2.08
90	1.15	1.31	1.42	1.52	1.64	1.73	1.82	1.93	2.02
100	1.15	1.30	1.40	1.50	1.61	1.70	1.78	1.89	1.97
120	1.14	1.28	1.38	1.47	1.58	1.66	1.73	1.83	1.90
140	1.13	1.27	1.36	1.45	1.55	1.62	1.70	1.79	1.86
160	1.13	1.26	1.35	1.43	1.53	1.60	1.67	1.75	1.82
180	1.13	1.26	1.34	1.42	1.51	1.58	1.65	1.73	1.79
200	1.12	1.25	1.33	1.41	1.50	1.56	1.63	1.71	1.77
300	1.11	1.23	1.31	1.38	1.46	1.52	1.58	1.65	1.70
500	1.11	1.22	1.29	1.35	1.43	1.48	1.53	1.60	1.65
∞	1.10	1.20	1.26	1.31	1.38	1.43	1.47	1.52	1.56

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 100

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.80	63.0	253.	1010.	6330.	25300.	101000.	633000.	2530000.
2	3.47	9.48	19.5	39.5	99.5	199.	399.	999.	2000.
3	2.47	5.14	8.55	14.0	26.2	42.0	67.1	124.	197.
4	2.08	3.78	5.66	8.32	13.6	19.5	27.9	44.5	63.2
5	1.87	3.13	4.41	6.08	9.13	12.3	16.5	24.1	32.1
6	1.74	2.75	3.71	4.92	6.99	9.03	11.6	16.0	20.4
7	1.65	2.50	3.27	4.21	5.75	7.22	8.99	12.0	14.8
8	1.58	2.32	2.97	3.74	4.96	6.09	7.42	9.57	11.6
9	1.53	2.19	2.76	3.40	4.41	5.32	6.38	8.04	9.54
10	1.49	2.09	2.59	3.15	4.01	4.77	5.64	6.98	8.17
11	1.46	2.01	2.46	2.96	3.71	4.36	5.09	6.21	7.19
12	1.43	1.94	2.35	2.80	3.47	4.04	4.67	5.63	6.45
13	1.41	1.88	2.26	2.67	3.27	3.78	4.34	5.17	5.88
14	1.39	1.83	2.19	2.56	3.11	3.57	4.07	4.81	5.43
15	1.37	1.79	2.12	2.47	2.98	3.39	3.85	4.51	5.06
16	1.36	1.76	2.07	2.40	2.86	3.25	3.66	4.26	4.76
17	1.34	1.73	2.02	2.33	2.76	3.12	3.50	4.05	4.50
18	1.33	1.70	1.98	2.27	2.68	3.01	3.36	3.87	4.28
19	1.32	1.67	1.94	2.22	2.60	2.91	3.24	3.71	4.10
20	1.31	1.65	1.91	2.17	2.54	2.83	3.14	3.58	3.93
21	1.30	1.63	1.88	2.13	2.48	2.75	3.04	3.46	3.79
22	1.29	1.61	1.85	2.09	2.42	2.69	2.96	3.35	3.66
23	1.29	1.59	1.82	2.06	2.37	2.62	2.89	3.25	3.55
24	1.28	1.58	1.80	2.02	2.33	2.57	2.82	3.17	3.45
25	1.27	1.56	1.78	2.00	2.29	2.52	2.76	3.09	3.36
26	1.27	1.55	1.76	1.97	2.25	2.47	2.70	3.02	3.27
27	1.26	1.54	1.74	1.94	2.22	2.43	2.65	2.96	3.20
28	1.25	1.53	1.73	1.92	2.19	2.39	2.60	2.90	3.13
29	1.25	1.52	1.71	1.90	2.16	2.36	2.56	2.84	3.06
30	1.25	1.51	1.70	1.88	2.13	2.32	2.52	2.79	3.01
35	1.23	1.47	1.63	1.80	2.02	2.19	2.36	2.59	2.77
40	1.21	1.43	1.59	1.74	1.94	2.09	2.24	2.44	2.60
45	1.20	1.41	1.55	1.69	1.88	2.01	2.15	2.33	2.47
50	1.19	1.39	1.52	1.66	1.82	1.95	2.08	2.25	2.37
60	1.18	1.36	1.48	1.60	1.75	1.86	1.97	2.12	2.23
70	1.16	1.34	1.45	1.56	1.70	1.80	1.90	2.03	2.13
80	1.16	1.32	1.43	1.53	1.65	1.75	1.84	1.96	2.05
90	1.15	1.30	1.41	1.50	1.62	1.71	1.80	1.91	1.99
100	1.14	1.29	1.39	1.48	1.60	1.68	1.76	1.87	1.95
120	1.14	1.28	1.37	1.45	1.56	1.64	1.71	1.81	1.88
140	1.13	1.26	1.35	1.43	1.53	1.60	1.67	1.76	1.83
160	1.13	1.26	1.34	1.42	1.51	1.58	1.64	1.73	1.79
180	1.12	1.25	1.33	1.40	1.49	1.56	1.62	1.70	1.76
200	1.12	1.24	1.32	1.39	1.48	1.54	1.60	1.68	1.74
300	1.11	1.22	1.30	1.36	1.44	1.50	1.55	1.62	1.67
500	1.10	1.21	1.28	1.34	1.41	1.46	1.51	1.57	1.62
∞	1.09	1.18	1.24	1.30	1.36	1.40	1.44	1.49	1.53

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 120

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.80	63.1	253.	1010.	6340.	25400.	101000.	634000.	2540000.
2	3.47	9.48	19.5	39.5	99.5	199.	399.	999.	2000.
3	2.47	5.14	8.55	13.9	26.2	42.0	67.0	124.	197.
4	2.08	3.78	5.66	8.31	13.6	19.5	27.8	44.4	63.1
5	1.87	3.12	4.40	6.07	9.11	12.3	16.4	24.1	32.0
6	1.74	2.74	3.70	4.90	6.97	9.00	11.6	16.0	20.3
7	1.65	2.49	3.27	4.20	5.74	7.19	8.96	11.9	14.7
8	1.58	2.32	2.97	3.73	4.95	6.06	7.39	9.53	11.5
9	1.53	2.18	2.75	3.39	4.40	5.30	6.35	8.00	9.49
10	1.49	2.08	2.58	3.14	4.00	4.75	5.61	6.94	8.12
11	1.46	2.00	2.45	2.94	3.69	4.34	5.07	6.18	7.14
12	1.43	1.93	2.34	2.79	3.45	4.01	4.65	5.59	6.41
13	1.41	1.88	2.25	2.66	3.25	3.76	4.31	5.14	5.84
14	1.39	1.83	2.18	2.55	3.09	3.55	4.04	4.77	5.39
15	1.37	1.79	2.11	2.46	2.96	3.37	3.82	4.47	5.02
16	1.35	1.75	2.06	2.38	2.84	3.22	3.63	4.23	4.72
17	1.34	1.72	2.01	2.32	2.75	3.10	3.47	4.02	4.46
18	1.33	1.69	1.97	2.26	2.66	2.99	3.34	3.84	4.25
19	1.32	1.67	1.93	2.20	2.58	2.89	3.22	3.68	4.06
20	1.31	1.64	1.90	2.16	2.52	2.81	3.11	3.54	3.90
21	1.30	1.62	1.87	2.11	2.46	2.73	3.02	3.42	3.75
22	1.29	1.60	1.84	2.08	2.40	2.66	2.93	3.32	3.62
23	1.28	1.59	1.81	2.04	2.35	2.60	2.86	3.22	3.51
24	1.28	1.57	1.79	2.01	2.31	2.55	2.79	3.14	3.41
25	1.27	1.56	1.77	1.98	2.27	2.50	2.73	3.06	3.32
26	1.26	1.54	1.75	1.95	2.23	2.45	2.68	2.99	3.24
27	1.26	1.53	1.73	1.93	2.20	2.41	2.62	2.92	3.16
28	1.25	1.52	1.71	1.91	2.17	2.37	2.58	2.86	3.09
29	1.25	1.51	1.70	1.89	2.14	2.33	2.53	2.81	3.03
30	1.24	1.50	1.68	1.87	2.11	2.30	2.49	2.76	2.97
35	1.22	1.46	1.62	1.79	2.00	2.16	2.33	2.56	2.73
40	1.21	1.42	1.58	1.72	1.92	2.06	2.21	2.41	2.56
45	1.20	1.40	1.54	1.68	1.85	1.99	2.12	2.30	2.44
50	1.19	1.38	1.51	1.64	1.80	1.93	2.05	2.21	2.34
60	1.17	1.35	1.47	1.58	1.73	1.83	1.94	2.08	2.19
70	1.16	1.32	1.44	1.54	1.67	1.77	1.87	1.99	2.09
80	1.15	1.31	1.41	1.51	1.63	1.72	1.81	1.92	2.01
90	1.15	1.29	1.39	1.48	1.60	1.68	1.76	1.87	1.95
100	1.14	1.28	1.38	1.46	1.57	1.65	1.73	1.83	1.90
120	1.13	1.26	1.35	1.43	1.53	1.61	1.68	1.77	1.83
140	1.13	1.25	1.33	1.41	1.50	1.57	1.64	1.72	1.78
160	1.12	1.24	1.32	1.39	1.48	1.55	1.61	1.69	1.75
180	1.12	1.23	1.31	1.38	1.47	1.53	1.59	1.66	1.72
200	1.11	1.23	1.30	1.37	1.45	1.51	1.57	1.64	1.69
300	1.10	1.21	1.28	1.34	1.41	1.46	1.51	1.58	1.62
500	1.10	1.19	1.26	1.31	1.38	1.42	1.47	1.53	1.57
∞	1.08	1.17	1.22	1.27	1.32	1.36	1.40	1.45	1.48

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 140

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.81	63.1	253.	1010.	6340.	25400.	101000.	634000.	2540000.
2	3.47	9.48	19.5	39.5	99.5	199.	399.	999.	2000.
3	2.47	5.14	8.55	13.9	26.2	42.0	67.0	124.	197.
4	2.08	3.77	5.65	8.30	13.5	19.4	27.8	44.4	63.0
5	1.87	3.12	4.39	6.06	9.10	12.3	16.4	24.0	31.9
6	1.74	2.74	3.70	4.90	6.96	8.98	11.5	15.9	20.3
7	1.65	2.49	3.26	4.19	5.72	7.18	8.94	11.9	14.7
8	1.58	2.31	2.96	3.72	4.93	6.05	7.37	9.50	11.5
9	1.53	2.18	2.74	3.38	4.39	5.28	6.33	7.97	9.46
10	1.49	2.08	2.57	3.13	3.98	4.73	5.59	6.92	8.09
11	1.46	2.00	2.44	2.94	3.68	4.32	5.05	6.15	7.11
12	1.43	1.93	2.33	2.78	3.44	4.00	4.63	5.57	6.38
13	1.41	1.87	2.25	2.65	3.24	3.74	4.29	5.11	5.81
14	1.39	1.82	2.17	2.54	3.08	3.53	4.02	4.75	5.36
15	1.37	1.78	2.11	2.45	2.95	3.36	3.80	4.45	5.00
16	1.35	1.75	2.05	2.37	2.83	3.21	3.61	4.20	4.69
17	1.34	1.71	2.00	2.31	2.73	3.08	3.45	3.99	4.44
18	1.33	1.69	1.96	2.25	2.65	2.97	3.32	3.81	4.22
19	1.32	1.66	1.92	2.19	2.57	2.87	3.20	3.66	4.03
20	1.31	1.64	1.89	2.15	2.50	2.79	3.09	3.52	3.87
21	1.30	1.62	1.86	2.10	2.44	2.71	3.00	3.40	3.73
22	1.29	1.60	1.83	2.07	2.39	2.65	2.92	3.29	3.60
23	1.28	1.58	1.81	2.03	2.34	2.59	2.84	3.20	3.49
24	1.27	1.57	1.78	2.00	2.30	2.53	2.77	3.11	3.38
25	1.27	1.55	1.76	1.97	2.26	2.48	2.71	3.03	3.29
26	1.26	1.54	1.74	1.94	2.22	2.43	2.66	2.96	3.21
27	1.26	1.53	1.72	1.92	2.18	2.39	2.60	2.90	3.13
28	1.25	1.51	1.71	1.90	2.15	2.35	2.56	2.84	3.06
29	1.24	1.50	1.69	1.88	2.12	2.32	2.51	2.79	3.00
30	1.24	1.49	1.68	1.86	2.10	2.28	2.47	2.74	2.94
35	1.22	1.45	1.61	1.77	1.98	2.15	2.31	2.53	2.71
40	1.21	1.42	1.57	1.71	1.90	2.05	2.19	2.39	2.54
45	1.19	1.39	1.53	1.66	1.84	1.97	2.10	2.27	2.41
50	1.18	1.37	1.50	1.63	1.79	1.91	2.03	2.19	2.31
60	1.17	1.34	1.46	1.57	1.71	1.81	1.92	2.06	2.16
70	1.16	1.32	1.42	1.53	1.65	1.75	1.84	1.96	2.06
80	1.15	1.30	1.40	1.49	1.61	1.70	1.79	1.90	1.98
90	1.14	1.28	1.38	1.47	1.58	1.66	1.74	1.84	1.92
100	1.14	1.27	1.36	1.45	1.55	1.63	1.70	1.80	1.87
120	1.13	1.26	1.34	1.42	1.51	1.58	1.65	1.74	1.80
140	1.12	1.24	1.32	1.39	1.48	1.55	1.61	1.69	1.75
160	1.12	1.23	1.31	1.38	1.46	1.52	1.58	1.66	1.71
180	1.11	1.22	1.30	1.36	1.45	1.50	1.56	1.63	1.68
200	1.11	1.22	1.29	1.35	1.43	1.49	1.54	1.61	1.66
300	1.10	1.20	1.26	1.32	1.39	1.44	1.49	1.55	1.59
500	1.09	1.18	1.24	1.29	1.35	1.40	1.44	1.49	1.53
∞	1.08	1.16	1.20	1.25	1.30	1.33	1.37	1.41	1.44

TABLE B.4 (cont.): Critical Values of the *F* Distribution

ν_1 = Numerator DF = 200

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.82	63.2	254.	1020.	6350.	25400.	102000.	635000.	2540000.
2	3.47	9.49	19.5	39.5	99.5	199.	399.	999.	2000.
3	2.47	5.14	8.54	13.9	26.2	41.9	66.9	124.	197.
4	2.08	3.77	5.65	8.29	13.5	19.4	27.7	44.3	62.9
5	1.87	3.12	4.39	6.05	9.08	12.2	16.4	24.0	31.8
6	1.74	2.73	3.69	4.88	6.93	8.95	11.5	15.9	20.2
7	1.65	2.48	3.25	4.18	5.70	7.15	8.90	11.8	14.6
8	1.58	2.31	2.95	3.70	4.91	6.02	7.33	9.45	11.4
9	1.53	2.17	2.73	3.37	4.36	5.26	6.29	7.93	9.40
10	1.49	2.07	2.56	3.12	3.96	4.71	5.56	6.87	8.04
11	1.46	1.99	2.43	2.92	3.66	4.29	5.01	6.10	7.06
12	1.43	1.92	2.32	2.76	3.41	3.97	4.59	5.52	6.33
13	1.40	1.86	2.23	2.63	3.22	3.71	4.26	5.07	5.76
14	1.38	1.82	2.16	2.53	3.06	3.50	3.99	4.71	5.31
15	1.37	1.77	2.10	2.44	2.92	3.33	3.77	4.41	4.95
16	1.35	1.74	2.04	2.36	2.81	3.18	3.58	4.16	4.64
17	1.34	1.71	1.99	2.29	2.71	3.05	3.42	3.95	4.39
18	1.32	1.68	1.95	2.23	2.62	2.94	3.28	3.77	4.17
19	1.31	1.65	1.91	2.18	2.55	2.85	3.16	3.61	3.98
20	1.30	1.63	1.88	2.13	2.48	2.76	3.06	3.48	3.82
21	1.29	1.61	1.84	2.09	2.42	2.68	2.96	3.36	3.68
22	1.28	1.59	1.82	2.05	2.36	2.62	2.88	3.25	3.55
23	1.28	1.57	1.79	2.01	2.32	2.56	2.81	3.16	3.44
24	1.27	1.56	1.77	1.98	2.27	2.50	2.74	3.07	3.34
25	1.26	1.54	1.75	1.95	2.23	2.45	2.68	2.99	3.24
26	1.26	1.53	1.73	1.92	2.19	2.40	2.62	2.92	3.16
27	1.25	1.52	1.71	1.90	2.16	2.36	2.57	2.86	3.09
28	1.25	1.50	1.69	1.88	2.13	2.32	2.52	2.80	3.02
29	1.24	1.49	1.67	1.86	2.10	2.29	2.48	2.74	2.95
30	1.24	1.48	1.66	1.84	2.07	2.25	2.44	2.69	2.89
35	1.22	1.44	1.60	1.75	1.96	2.11	2.27	2.49	2.66
40	1.20	1.41	1.55	1.69	1.87	2.01	2.15	2.34	2.49
45	1.19	1.38	1.51	1.64	1.81	1.93	2.06	2.23	2.36
50	1.18	1.36	1.48	1.60	1.76	1.87	1.99	2.14	2.26
60	1.16	1.33	1.44	1.54	1.68	1.78	1.88	2.01	2.11
70	1.15	1.30	1.40	1.50	1.62	1.71	1.80	1.92	2.00
80	1.14	1.28	1.38	1.47	1.58	1.66	1.74	1.85	1.93
90	1.13	1.27	1.36	1.44	1.55	1.62	1.70	1.79	1.86
100	1.13	1.26	1.34	1.42	1.52	1.59	1.66	1.75	1.82
120	1.12	1.24	1.32	1.39	1.48	1.54	1.60	1.68	1.74
140	1.11	1.22	1.30	1.36	1.45	1.51	1.56	1.64	1.69
160	1.11	1.21	1.28	1.35	1.42	1.48	1.53	1.60	1.65
180	1.10	1.21	1.27	1.33	1.41	1.46	1.51	1.57	1.62
200	1.10	1.20	1.26	1.32	1.39	1.44	1.49	1.55	1.60
300	1.09	1.18	1.23	1.28	1.35	1.39	1.43	1.48	1.52
500	1.08	1.16	1.21	1.25	1.31	1.35	1.38	1.43	1.46
∞	1.07	1.13	1.17	1.21	1.25	1.28	1.30	1.34	1.36

TABLE B.4 (cont.): Critical Values of the F Distribution

ν_1 = Numerator DF = ∞

ν_2 = Denom. DF	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	9.85	63.3	254.	1020.	6370.	25500.	102000.	637000.	2550000.
2	3.48	9.49	19.5	39.5	99.5	199.	399.	999.	2000.
3	2.47	5.13	8.53	13.9	26.1	41.8	66.8	123.	196.
4	2.08	3.76	5.63	8.26	13.5	19.3	27.6	44.0	62.6
5	1.87	3.11	4.37	6.02	9.02	12.1	16.3	23.8	31.6
6	1.74	2.72	3.67	4.85	6.88	8.88	11.4	15.7	20.0
7	1.65	2.47	3.23	4.14	5.65	7.08	8.81	11.7	14.4
8	1.58	2.29	2.93	3.67	4.86	5.95	7.25	9.33	11.3
9	1.53	2.16	2.71	3.33	4.31	5.19	6.21	7.81	9.26
10	1.48	2.06	2.54	3.08	3.91	4.64	5.47	6.76	7.91
11	1.45	1.97	2.40	2.88	3.60	4.23	4.93	6.00	6.93
12	1.42	1.90	2.30	2.72	3.36	3.90	4.51	5.42	6.20
13	1.40	1.85	2.21	2.60	3.17	3.65	4.18	4.97	5.64
14	1.38	1.80	2.13	2.49	3.00	3.44	3.91	4.60	5.19
15	1.36	1.76	2.07	2.40	2.87	3.26	3.69	4.31	4.83
16	1.34	1.72	2.01	2.32	2.75	3.11	3.50	4.06	4.52
17	1.33	1.69	1.96	2.25	2.65	2.98	3.34	3.85	4.27
18	1.32	1.66	1.92	2.19	2.57	2.87	3.20	3.67	4.05
19	1.30	1.63	1.88	2.13	2.49	2.78	3.08	3.51	3.87
20	1.29	1.61	1.84	2.09	2.42	2.69	2.97	3.38	3.71
21	1.28	1.59	1.81	2.04	2.36	2.61	2.88	3.26	3.56
22	1.28	1.57	1.78	2.00	2.31	2.55	2.80	3.15	3.43
23	1.27	1.55	1.76	1.97	2.26	2.48	2.72	3.05	3.32
24	1.26	1.53	1.73	1.94	2.21	2.43	2.65	2.97	3.22
25	1.25	1.52	1.71	1.91	2.17	2.38	2.59	2.89	3.13
26	1.25	1.50	1.69	1.88	2.13	2.33	2.54	2.82	3.05
27	1.24	1.49	1.67	1.85	2.10	2.29	2.48	2.75	2.97
28	1.24	1.48	1.65	1.83	2.06	2.25	2.44	2.69	2.90
29	1.23	1.47	1.64	1.81	2.03	2.21	2.39	2.64	2.84
30	1.23	1.46	1.62	1.79	2.01	2.18	2.35	2.59	2.78
35	1.20	1.41	1.56	1.70	1.89	2.04	2.18	2.38	2.54
40	1.19	1.38	1.51	1.64	1.80	1.93	2.06	2.23	2.37
45	1.18	1.35	1.47	1.59	1.74	1.85	1.97	2.12	2.23
50	1.16	1.33	1.44	1.55	1.68	1.79	1.89	2.03	2.13
60	1.15	1.29	1.39	1.48	1.60	1.69	1.78	1.89	1.98
70	1.13	1.27	1.35	1.44	1.54	1.62	1.69	1.79	1.87
80	1.12	1.24	1.32	1.40	1.49	1.56	1.63	1.72	1.79
90	1.12	1.23	1.30	1.37	1.46	1.52	1.58	1.66	1.72
100	1.11	1.21	1.28	1.35	1.43	1.49	1.54	1.62	1.67
120	1.10	1.19	1.25	1.31	1.38	1.43	1.48	1.54	1.59
140	1.09	1.18	1.23	1.28	1.35	1.39	1.43	1.49	1.53
160	1.08	1.16	1.21	1.26	1.32	1.36	1.40	1.45	1.49
180	1.08	1.15	1.20	1.24	1.30	1.33	1.37	1.42	1.45
200	1.07	1.14	1.19	1.23	1.28	1.31	1.35	1.39	1.42
300	1.06	1.11	1.15	1.18	1.22	1.25	1.27	1.30	1.33
500	1.05	1.09	1.11	1.14	1.16	1.18	1.20	1.23	1.24
∞	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

Appendix Table B.4 was prepared using Equations 26.6.4, 26.6.5, 26.6.8, 26.6.11, 26.6.12, 26.4.6, and 26.4.14 of Zelen and Severo (1964). Values of F were calculated to a relative error $\leq 10^{-8}$ and then were rounded to three significant figures.

Examples:

$$F_{0.05(1),2,18} = 3.55, \quad F_{0.01(1),8,10} = 5.06 \quad \text{and} \quad F_{0.05(2),20,40} = 2.07$$

If a critical value is needed for degrees of freedom not on this table, we may conservatively employ the next smaller degrees of freedom that are on the table. Or, the needed critical value may be obtained by linear

interpolation, with an error no greater than 0.01 for $\alpha(1) \geq 0.01$ and no greater than 0.02 for $\alpha(1) < 0.01$. If a little more accuracy is desired, or if $\nu_1 > 200$ or $\nu_2 > 500$, harmonic interpolation should be used.

Note that $P(F_{\nu_1,\nu_2}) = 1 - P(1/F_{\nu_2,\nu_1})$.

For example,

$$P(F_{2,28} \geq 2.50) = 0.10 \quad \text{and} \quad P(1/F_{28,2} \leq 2.50) = 0.90$$

F is related to t, Z, and χ^2 as

$$F_{\alpha(1),1,\nu} = \left(t_{\alpha(2),\nu}\right)^2; \; F_{\alpha(1),1,\infty} = \left(Z_{\alpha(2)}\right)^2; \; F_{\alpha(1),\nu,\infty} = \chi^2_{\alpha,\nu}/\nu.$$

Also,

$$F_{\alpha,\nu_1,\nu_2} = 1/F_{\alpha,\nu_2,\nu_1}.$$

Mantel (1966) and George (1987) discuss approximating the F distribution using binomial probabilities.

TABLE B.5: Critical Values of the q Distribution, for the Tukey Test

$\alpha = 0.50$

ν	$k:2$	3	4	5	6	7	8	9	10
1	1.414	2.338	2.918	3.335	3.658	3.920	4.139	4.327	4.491
2	1.155	1.908	2.377	2.713	2.973	3.184	3.361	3.513	3.645
3	1.082	1.791	2.230	2.545	2.789	2.987	3.152	3.294	3.418
4	1.048	1.737	2.163	2.468	2.704	2.895	3.055	3.193	3.313
5	1.028	1.705	2.124	2.423	2.655	2.843	3.000	3.135	3.253
6	1.015	1.685	2.098	2.394	2.623	2.809	2.964	3.097	3.214
7	1.006	1.670	2.080	2.375	2.601	2.785	2.938	3.070	3.186
8	0.9990	1.659	2.067	2.359	2.584	2.767	2.920	3.051	3.165
9	0.9938	1.651	2.057	2.347	2.572	2.753	2.905	3.035	3.149
10	0.9897	1.645	2.049	2.338	2.561	2.742	2.893	3.023	3.137
11	0.9863	1.639	2.042	2.330	2.553	2.733	2.884	3.014	3.127
12	0.9836	1.635	2.037	2.324	2.546	2.726	2.876	3.005	3.118
13	0.9812	1.631	2.032	2.319	2.540	2.719	2.870	2.998	3.111
14	0.9792	1.628	2.028	2.314	2.535	2.714	2.864	2.993	3.105
15	0.9775	1.625	2.025	2.310	2.531	2.709	2.859	2.987	3.099
16	0.9760	1.623	2.022	2.307	2.527	2.705	2.855	2.983	3.095
17	0.9747	1.621	2.020	2.304	2.524	2.702	2.851	2.979	3.091
18	0.9735	1.619	2.018	2.301	2.521	2.699	2.848	2.976	3.087
19	0.9724	1.618	2.015	2.299	2.518	2.696	2.845	2.973	3.084
20	0.9715	1.616	2.013	2.297	2.516	2.693	2.842	2.970	3.081
24	0.9685	1.611	2.007	2.290	2.509	2.685	2.834	2.961	3.071
30	0.9656	1.606	2.001	2.284	2.501	2.678	2.825	2.952	3.062
40	0.9626	1.602	1.996	2.277	2.494	2.670	2.817	2.943	3.053
60	0.9597	1.597	1.990	2.270	2.486	2.662	2.808	2.934	3.043
120	0.9568	1.592	1.984	2.264	2.479	2.654	2.799	2.925	3.034
∞	0.9539	1.588	1.978	2.257	2.472	2.645	2.791	2.915	3.024

ν	$k:11$	12	13	14	15	16	17	18	19
1	4.637	4.767	4.885	4.992	5.091	5.182	5.266	5.345	5.420
2	3.762	3.867	3.963	4.049	4.129	4.203	4.271	4.335	4.395
3	3.528	3.626	3.715	3.797	3.871	3.940	4.004	4.064	4.120
4	3.419	3.515	3.601	3.680	3.752	3.819	3.881	3.939	3.993
5	3.357	3.451	3.535	3.613	3.684	3.749	3.811	3.867	3.920
6	3.317	3.409	3.493	3.569	3.639	3.704	3.764	3.820	3.873
7	3.288	3.380	3.463	3.538	3.608	3.672	3.732	3.788	3.840
8	3.267	3.358	3.440	3.515	3.585	3.648	3.708	3.763	3.815
9	3.250	3.341	3.423	3.498	3.567	3.630	3.689	3.744	3.796
10	3.237	3.328	3.410	3.484	3.552	3.616	3.674	3.729	3.781
11	3.227	3.317	3.398	3.472	3.540	3.604	3.662	3.717	3.769
12	3.219	3.308	3.389	3.463	3.531	3.594	3.652	3.706	3.757
13	3.211	3.300	3.381	3.455	3.523	3.585	3.643	3.698	3.749
14	3.204	3.293	3.375	3.448	3.515	3.578	3.636	3.690	3.741
15	3.199	3.288	3.369	3.442	3.509	3.572	3.630	3.684	3.735
16	3.194	3.283	3.364	3.436	3.504	3.567	3.624	3.678	3.729
17	3.190	3.278	3.359	3.432	3.499	3.562	3.620	3.673	3.724
18	3.186	3.274	3.355	3.428	3.495	3.558	3.615	3.669	3.719
19	3.183	3.271	3.352	3.424	3.491	3.554	3.611	3.665	3.715
20	3.179	3.268	3.348	3.421	3.488	3.550	3.608	3.661	3.712
24	3.170	3.258	3.338	3.410	3.477	3.539	3.596	3.650	3.700
30	3.160	3.248	3.327	3.400	3.466	3.528	3.585	3.639	3.688
40	3.150	3.238	3.317	3.389	3.456	3.517	3.574	3.627	3.677
60	3.141	3.228	3.306	3.378	3.444	3.505	3.562	3.615	3.665
120	3.131	3.217	3.296	3.367	3.433	3.494	3.551	3.603	3.653
∞	3.121	3.207	3.285	3.356	3.422	3.482	3.538	3.591	3.640

TABLE B.5 (cont.): Critical Values of the q Distribution, for the Tukey Test

$\alpha = 0.50$

ν	k : 20	22	24	26	28	30	32	34	36
1	5.489	5.616	5.731	5.835	5.930	6.017	6.098	6.173	6.244
2	4.451	4.554	4.646	4.730	4.807	4.878	4.943	5.004	5.061
3	4.172	4.269	4.356	4.434	4.507	4.573	4.634	4.691	4.745
4	4.044	4.138	4.222	4.298	4.368	4.432	4.492	4.547	4.599
5	3.970	4.062	4.145	4.220	4.288	4.352	4.410	4.464	4.515
6	3.922	4.014	4.095	4.169	4.237	4.299	4.357	4.411	4.461
7	3.889	3.979	4.060	4.133	4.200	4.262	4.319	4.372	4.422
8	3.864	3.953	4.033	4.106	4.174	4.234	4.291	4.344	4.394
9	3.844	3.933	4.013	4.086	4.152	4.214	4.270	4.323	4.372
10	3.829	3.917	3.997	4.069	4.135	4.196	4.253	4.305	4.354
11	3.816	3.904	3.984	4.056	4.122	4.183	4.239	4.291	4.340
12	3.806	3.894	3.973	4.045	4.110	4.171	4.227	4.279	4.328
13	3.797	3.884	3.964	4.035	4.101	4.162	4.218	4.269	4.318
14	3.789	3.877	3.956	4.027	4.092	4.153	4.209	4.261	4.309
15	3.783	3.870	3.949	4.020	4.085	4.145	4.201	4.253	4.302
16	3.777	3.864	3.942	4.014	4.079	4.139	4.195	4.246	4.295
17	3.772	3.859	3.937	4.009	4.073	4.133	4.189	4.241	4.289
18	3.767	3.854	3.932	4.003	4.069	4.128	4.184	4.236	4.284
19	3.763	3.850	3.928	3.999	4.064	4.124	4.180	4.231	4.279
20	3.759	3.846	3.995	3.995	4.060	4.120	4.175	4.227	4.275
24	3.748	3.834	3.912	3.983	4.048	4.107	4.162	4.214	4.262
30	3.736	3.822	3.899	3.970	4.035	4.094	4.149	4.200	4.248
40	3.724	3.809	3.887	3.957	4.021	4.080	4.135	4.186	4.234
60	3.711	3.797	3.874	3.944	4.008	4.067	4.121	4.172	4.220
120	3.699	3.784	3.861	3.930	3.994	4.053	4.107	4.157	4.204
∞	3.686	3.771	3.847	3.916	3.979	4.037	4.091	4.141	4.188

ν	k : 38	40	50	60	70	80	90	100
1	6.310	6.372	6.637	6.847	7.021	7.169	7.297	7.411
2	5.115	5.165	5.379	5.550	5.690	5.810	5.914	6.006
3	4.795	4.842	5.043	5.202	5.335	5.447	5.544	5.630
4	4.647	4.693	4.888	5.043	5.171	5.280	5.374	5.458
5	4.563	4.608	4.799	4.951	5.077	5.184	5.277	5.359
6	4.500	4.552	4.741	4.891	5.016	5.121	5.213	5.294
7	4.469	4.513	4.700	4.850	4.973	5.078	5.169	5.249
8	4.440	4.484	4.671	4.819	4.941	5.045	5.136	5.215
9	4.418	4.462	4.647	4.794	4.916	5.020	5.110	5.189
10	4.400	4.444	4.629	4.775	4.897	5.000	5.090	5.169
11	4.386	4.429	4.613	4.760	4.881	4.984	5.073	5.152
12	4.374	4.417	4.600	4.747	4.867	4.970	5.059	5.138
13	4.364	4.406	4.590	4.736	4.856	4.959	5.048	5.126
14	4.355	4.397	4.581	4.726	4.846	4.949	5.037	5.116
15	4.347	4.390	4.573	4.718	4.838	4.940	5.029	5.107
16	4.340	4.383	4.566	4.710	4.831	4.932	5.021	5.099
17	4.334	4.377	4.559	4.704	4.824	4.926	5.014	5.092
18	4.329	4.372	4.554	4.698	4.818	4.920	5.008	5.086
19	4.324	4.367	4.549	4.693	4.813	4.914	5.003	5.081
20	4.320	4.363	4.545	4.689	4.808	4.910	4.998	5.076
24	4.307	4.349	4.530	4.674	4.793	4.894	4.982	5.060
30	4.293	4.335	4.515	4.659	4.778	4.878	4.966	5.044
40	4.279	4.321	4.500	4.644	4.762	4.862	4.950	5.027
60	4.264	4.306	4.485	4.627	4.745	4.845	4.932	5.009
120	4.249	4.290	4.469	4.610	4.727	4.827	4.914	4.990
∞	4.232	4.274	4.450	4.591	4.707	4.806	4.892	4.968

TABLE B.5 (cont.): Critical Values of the q Distribution, for the Tukey Test

$\alpha = 0.20$

ν	k: 2	3	4	5	6	7	8	9	10
1	4.353	6.615	8.075	9.138	9.966	10.64	11.21	11.70	12.12
2	2.667	3.820	4.559	5.098	5.521	5.867	6.158	6.409	6.630
3	2.316	3.245	3.833	4.261	4.597	4.872	5.104	5.305	5.481
4	2.168	3.004	3.527	3.907	4.205	4.449	4.655	4.832	4.989
5	2.087	2.872	3.358	3.712	3.988	4.214	4.405	4.570	4.715
6	2.036	2.788	3.252	3.588	3.850	4.065	4.246	4.403	4.540
7	2.001	2.731	3.179	3.503	3.756	3.962	4.136	4.287	4.419
8	1.976	2.689	3.126	3.440	3.686	3.886	4.055	4.201	4.330
9	1.956	2.658	3.085	3.393	3.633	3.828	3.994	4.136	4.261
10	1.941	2.632	3.053	3.355	3.590	3.782	3.944	4.084	4.206
11	1.928	2.612	3.027	3.325	3.557	3.745	3.905	4.042	4.162
12	1.918	2.596	3.006	3.300	3.529	3.715	3.872	4.007	4.126
13	1.910	2.582	2.988	3.279	3.505	3.689	3.844	3.978	4.095
14	1.902	2.570	2.973	3.261	3.485	3.667	3.820	3.953	4.069
15	1.896	2.560	2.960	3.246	3.467	3.648	3.800	3.931	4.046
16	1.891	2.551	2.948	3.232	3.452	3.631	3.782	3.912	4.026
17	1.886	2.543	2.938	3.220	3.439	3.617	3.766	3.895	4.008
18	1.882	2.536	2.930	3.210	3.427	3.604	3.753	3.881	3.993
19	1.878	2.530	2.922	3.200	3.416	3.592	3.740	3.867	3.979
20	1.874	2.524	2.914	3.192	3.407	3.582	3.729	3.855	3.966
24	1.864	2.507	2.892	3.166	3.377	3.549	3.694	3.818	3.927
30	1.853	2.490	2.870	3.140	3.348	3.517	3.659	3.781	3.887
40	1.843	2.473	2.848	3.114	3.318	3.484	3.624	3.743	3.848
60	1.833	2.456	2.826	3.089	3.290	3.452	3.589	3.707	3.809
120	1.822	2.440	2.805	3.063	3.260	3.420	3.554	3.669	3.770
∞	1.812	2.424	2.784	3.037	3.232	3.389	3.520	3.632	3.730

ν	k: 11	12	13	14	15	16	17	18	19
1	12.50	12.84	13.14	13.43	13.68	13.93	14.14	14.35	14.54
2	6.826	7.002	7.162	7.308	7.442	7.566	7.682	7.790	7.891
3	5.637	5.778	5.906	6.023	6.131	6.230	6.323	6.410	6.491
4	5.128	5.253	5.367	5.471	5.566	5.655	5.738	5.815	5.888
5	4.844	4.960	5.066	5.162	5.251	5.334	5.411	5.482	5.550
6	4.663	4.773	4.873	4.965	5.049	5.128	5.201	5.269	5.333
7	4.537	4.643	4.739	4.827	4.908	4.984	5.054	5.120	5.181
8	4.444	4.547	4.640	4.726	4.805	4.877	4.945	5.009	5.069
9	4.372	4.473	4.564	4.647	4.724	4.796	4.862	4.924	4.982
10	4.316	4.414	4.503	4.585	4.660	4.730	4.795	4.856	4.913
11	4.270	4.366	4.454	4.534	4.608	4.677	4.741	4.801	4.857
12	4.231	4.327	4.413	4.492	4.565	4.633	4.696	4.755	4.810
13	4.199	4.293	4.379	4.457	4.529	4.596	4.658	4.716	4.770
14	4.172	4.265	4.349	4.426	4.498	4.564	4.625	4.683	4.737
15	4.148	4.240	4.324	4.400	4.471	4.536	4.597	4.654	4.707
16	4.127	4.218	4.301	4.377	4.447	4.512	4.572	4.628	4.681
17	4.109	4.199	4.282	4.357	4.426	4.490	4.550	4.606	4.659
18	4.093	4.182	4.264	4.339	4.407	4.471	4.531	4.586	4.638
19	4.078	4.167	4.248	4.323	4.391	4.454	4.513	4.569	4.620
20	4.065	4.154	4.234	4.308	4.376	4.439	4.498	4.552	4.604
24	4.024	4.111	4.190	4.262	4.329	4.391	4.448	4.502	4.552
30	3.982	4.068	4.145	4.216	4.281	4.342	4.398	4.451	4.500
40	3.941	4.025	4.101	4.170	4.234	4.293	4.348	4.399	4.447
60	3.900	3.982	4.056	4.124	4.186	4.244	4.297	4.347	4.395
120	3.859	3.938	4.011	4.077	4.138	4.194	4.246	4.295	4.341
∞	3.817	3.895	3.966	4.030	4.089	4.144	4.195	4.242	4.287

TABLE B.5 (cont.): Critical Values of the q Distribution, for the Tukey Test

$\alpha = 0.20$

ν	k: 20	22	24	26	28	30	32	34	36
1	14.72	15.06	15.36	15.63	15.88	16.11	16.32	16.52	16.71
2	7.986	8.162	8.320	8.463	8.594	8.715	8.827	8.931	9.029
3	6.568	6.709	6.835	6.951	7.057	7.154	7.244	7.328	7.407
4	5.956	6.082	6.195	6.298	6.392	6.479	6.560	6.635	6.706
5	5.613	5.730	5.835	5.931	6.019	6.100	6.175	6.245	6.311
6	5.393	5.504	5.604	5.695	5.779	5.856	5.927	5.994	6.056
7	5.239	5.346	5.442	5.530	5.610	5.684	5.753	5.817	5.877
8	5.125	5.228	5.322	5.407	5.485	5.557	5.624	5.686	5.744
9	5.037	5.138	5.229	5.312	5.388	5.459	5.524	5.585	5.641
10	4.967	5.066	5.155	5.237	5.311	5.380	5.444	5.504	5.559
11	4.910	5.007	5.095	5.175	5.248	5.316	5.379	5.437	5.492
12	4.862	4.958	5.044	5.123	5.196	5.262	5.324	5.382	5.436
13	4.822	4.917	5.002	5.080	5.151	5.217	5.278	5.335	5.388
14	4.787	4.881	4.965	5.042	5.113	5.178	5.238	5.295	5.347
15	4.757	4.850	4.934	5.010	5.080	5.144	5.204	5.260	5.312
16	4.731	4.823	4.906	4.981	5.050	5.114	5.174	5.229	5.281
17	4.708	4.799	4.881	4.956	5.025	5.088	5.147	5.202	5.253
18	4.688	4.778	4.859	4.934	5.002	5.065	5.123	5.177	5.228
19	4.669	4.759	4.840	4.914	4.981	5.044	5.102	5.156	5.206
20	4.652	4.742	4.822	4.895	4.963	5.025	5.082	5.136	5.186
24	4.599	4.687	4.766	4.838	4.904	4.964	5.021	5.073	5.122
30	4.546	4.632	4.710	4.779	4.844	4.903	4.958	5.010	5.058
40	4.493	4.576	4.652	4.720	4.783	4.841	4.895	4.945	4.993
60	4.439	4.520	4.594	4.661	4.722	4.778	4.831	4.880	4.925
120	4.384	4.463	4.535	4.600	4.659	4.714	4.765	4.812	4.857
∞	4.329	4.405	4.475	4.537	4.595	4.648	4.697	4.743	4.786

ν	k: 38	40	50	60	70	80	90	100
1	16.88	17.05	17.74	18.30	18.76	19.15	19.49	19.79
2	9.121	9.207	9.576	9.869	10.11	10.32	10.50	10.66
3	7.481	7.551	7.849	8.086	8.283	8.450	8.596	8.725
4	6.771	6.834	7.100	7.313	7.489	7.639	7.769	7.885
5	6.372	6.430	6.678	6.877	7.041	7.181	7.303	7.411
6	6.115	6.170	6.406	6.595	6.751	6.885	7.001	7.103
7	5.934	5.987	6.214	6.397	6.548	6.676	6.788	6.887
8	5.799	5.851	6.072	6.249	6.395	6.520	6.629	6.725
9	5.695	5.745	5.961	6.134	6.277	6.399	6.506	6.600
10	5.612	5.661	5.873	6.042	6.182	6.302	6.407	6.499
11	5.544	5.592	5.800	5.967	6.105	6.223	6.326	6.416
12	5.487	5.535	5.740	5.904	6.040	6.156	6.257	6.347
13	5.438	5.486	5.689	5.850	5.985	6.100	6.200	6.288
14	5.397	5.444	5.644	5.804	5.937	6.051	6.150	6.237
15	5.361	5.407	5.606	5.764	5.896	6.008	6.106	6.193
16	5.329	5.375	5.572	5.729	5.859	5.971	6.068	6.154
17	5.301	5.347	5.542	5.698	5.827	5.938	6.034	6.119
18	5.276	5.321	5.515	5.670	5.798	5.908	6.004	6.089
19	5.254	5.299	5.491	5.645	5.772	5.881	5.976	6.061
20	5.233	5.278	5.469	5.622	5.749	5.857	5.951	6.035
24	5.169	5.212	5.400	5.549	5.674	5.780	5.872	5.954
30	5.103	5.146	5.329	5.475	5.597	5.701	5.791	5.871
40	5.037	5.078	5.257	5.399	5.518	5.619	5.708	5.786
60	4.969	5.009	5.183	5.321	5.437	5.535	5.621	5.697
120	4.899	4.938	5.106	5.240	5.352	5.447	5.530	5.603
∞	4.826	4.864	5.026	5.155	5.262	5.353	5.433	5.503

TABLE B.5 (cont.): Critical Values of the q Distribution, for the Tukey Test

$\alpha = 0.10$

ν	k: 2	3	4	5	6	7	8	9	10
1	8.929	13.44	16.36	18.49	20.15	21.51	22.64	23.62	24.48
2	4.130	5.733	6.773	7.538	8.139	8.633	9.049	9.409	9.725
3	3.328	4.467	5.199	5.738	6.162	6.511	6.806	7.062	7.287
4	3.015	3.976	4.586	5.035	5.388	5.679	5.926	6.139	6.327
5	2.850	3.717	4.264	4.664	4.979	5.238	5.458	5.648	5.816
6	2.748	3.559	4.065	4.435	4.726	4.966	5.168	5.344	5.499
7	2.680	3.451	3.931	4.280	4.555	4.780	4.972	5.137	5.283
8	2.630	3.374	3.834	4.169	4.431	4.646	4.829	4.987	5.126
9	2.592	3.316	3.761	4.084	4.337	4.545	4.721	4.873	5.007
10	2.563	3.270	3.704	4.018	4.264	4.465	4.636	4.783	4.913
11	2.540	3.234	3.658	3.965	4.205	4.401	4.568	4.711	4.838
12	2.521	3.204	3.621	3.922	4.156	4.349	4.511	4.652	4.776
13	2.505	3.179	3.589	3.885	4.116	4.305	4.464	4.602	4.724
14	2.491	3.158	3.563	3.854	4.081	4.267	4.424	4.560	4.680
15	2.479	3.140	3.540	3.828	4.052	4.235	4.390	4.524	4.641
16	2.469	3.124	3.520	3.804	4.026	4.207	4.360	4.492	4.608
17	2.460	3.110	3.503	3.784	4.004	4.183	4.334	4.464	4.579
18	2.452	3.098	3.488	3.767	3.984	4.161	4.311	4.440	4.554
19	2.445	3.087	3.474	3.751	3.966	4.142	4.290	4.418	4.531
20	2.439	3.078	3.462	3.736	3.950	4.124	4.271	4.398	4.510
24	2.420	3.047	3.423	3.692	3.900	4.070	4.213	4.336	4.445
30	2.400	3.017	3.386	3.648	3.851	4.016	4.155	4.275	4.381
40	2.381	2.988	3.349	3.605	3.803	3.963	4.099	4.215	4.317
60	2.363	2.959	3.312	3.562	3.755	3.911	4.042	4.155	4.254
120	2.344	2.930	3.276	3.520	3.707	3.859	3.987	4.096	4.191
∞	2.326	2.902	3.240	3.478	3.661	3.808	3.931	4.037	4.129

ν	k: 11	12	13	14	15	16	17	18	19
1	25.24	25.92	26.54	27.10	27.62	28.10	28.54	28.96	29.35
2	10.01	10.26	10.49	10.70	10.89	11.07	11.24	11.39	11.54
3	7.487	7.667	7.832	7.982	8.120	8.249	8.368	8.479	8.584
4	6.495	6.645	6.783	6.909	7.025	7.133	7.233	7.327	7.414
5	5.966	6.101	6.223	6.336	6.440	6.536	6.626	6.710	6.789
6	5.637	5.762	5.875	5.979	6.075	6.164	6.247	6.325	6.398
7	5.413	5.530	5.637	5.735	5.826	5.910	5.988	6.061	6.130
8	5.250	5.362	5.464	5.558	5.644	5.724	5.799	5.869	5.935
9	5.127	5.234	5.333	5.423	5.506	5.583	5.655	5.723	5.786
10	5.029	5.134	5.229	5.317	5.397	5.472	5.542	5.607	5.668
11	4.951	5.053	5.146	5.231	5.309	5.382	5.450	5.514	5.573
12	4.886	4.986	5.077	5.160	5.236	5.308	5.374	5.436	5.495
13	4.832	4.930	5.019	5.100	5.176	5.245	5.311	5.372	5.429
14	4.786	4.882	4.970	5.050	5.124	5.192	5.256	5.316	5.373
15	4.746	4.841	4.927	5.006	5.079	5.147	5.209	5.269	5.324
16	4.712	4.805	4.890	4.968	5.040	5.107	5.169	5.227	5.282
17	4.682	4.774	4.858	4.935	5.005	5.071	5.133	5.190	5.244
18	4.655	4.746	4.829	4.905	4.975	5.040	5.101	5.158	5.211
19	4.631	4.721	4.803	4.879	4.948	5.012	5.073	5.129	5.182
20	4.609	4.699	4.780	4.855	4.924	4.987	5.047	5.103	5.155
24	4.541	4.628	4.708	4.780	4.847	4.909	4.966	5.021	5.071
30	4.474	4.559	4.635	4.706	4.770	4.830	4.886	4.939	4.988
40	4.408	4.490	4.564	4.632	4.695	4.752	4.807	4.857	4.905
60	4.342	4.421	4.493	4.558	4.619	4.675	4.727	4.775	4.821
120	4.276	4.353	4.422	4.485	4.543	4.597	4.647	4.694	4.738
∞	4.211	4.285	4.351	4.412	4.468	4.519	4.568	4.612	4.654

TABLE B.5 (cont.): Critical Values of the q Distribution, for the Tukey Test

$\alpha = 0.10$

ν	k : 20	22	24	26	28	30	32	34	36
1	29.71	30.39	30.99	31.54	32.04	32.50	32.93	33.33	33.71
2	11.68	11.93	12.16	12.36	12.55	12.73	12.89	13.04	13.18
3	8.683	8.864	9.029	9.177	9.314	9.440	9.557	9.666	9.768
4	7.497	7.650	7.789	7.914	8.029	8.135	8.234	8.326	8.412
5	6.863	7.000	7.123	7.236	7.340	7.435	7.523	7.606	7.683
6	6.467	6.593	6.708	6.812	6.908	6.996	7.078	7.155	7.227
7	6.195	6.315	6.422	6.521	6.611	6.695	6.773	6.845	6.913
8	5.997	6.111	6.214	6.308	6.395	6.475	6.549	6.618	6.683
9	5.846	5.956	6.055	6.146	6.229	6.306	6.378	6.444	6.507
10	5.726	5.833	5.930	6.017	6.098	6.173	6.242	6.307	6.368
11	5.630	5.734	5.828	5.914	5.992	6.065	6.132	6.196	6.255
12	5.550	5.652	5.744	5.827	5.904	5.976	6.042	6.103	6.161
13	5.483	5.583	5.673	5.755	5.830	5.900	5.965	6.025	6.082
14	5.426	5.524	5.612	5.693	5.767	5.836	5.899	5.959	6.014
15	5.376	5.473	5.560	5.639	5.713	5.780	5.843	5.901	5.956
16	5.333	5.428	5.515	5.593	5.665	5.732	5.793	5.851	5.905
17	5.295	5.389	5.474	5.552	5.623	5.689	5.750	5.806	5.860
18	5.262	5.355	5.439	5.515	5.585	5.650	5.711	5.767	5.820
19	5.232	5.324	5.407	5.483	5.552	5.616	5.676	5.732	5.784
20	5.205	5.296	5.378	5.453	5.522	5.586	5.645	5.700	5.752
24	5.119	5.208	5.287	5.360	5.427	5.489	5.546	5.600	5.650
30	5.034	5.120	5.197	5.267	5.332	5.392	5.447	5.499	5.547
40	4.949	5.032	5.107	5.174	5.236	5.294	5.347	5.397	5.444
60	4.864	4.944	5.015	5.081	5.141	5.196	5.247	5.295	5.340
120	4.779	4.856	4.924	4.987	5.044	5.097	5.146	5.192	5.235
∞	4.694	4.767	4.832	4.892	4.947	4.997	5.044	5.087	5.128

ν	k : 38	40	50	60	70	80	90	100
1	34.06	34.38	35.79	36.91	37.83	38.62	39.30	39.91
2	13.31	13.44	13.97	14.40	14.75	15.05	15.31	15.54
3	9.864	9.954	10.34	10.65	10.91	11.12	11.31	11.48
4	8.493	8.569	8.896	9.156	9.373	9.557	9.718	9.860
5	7.756	7.825	8.118	8.353	8.548	8.715	8.859	8.988
6	7.294	7.358	7.630	7.848	8.029	8.184	8.319	8.438
7	6.976	7.036	7.294	7.500	7.672	7.818	7.946	8.059
8	6.744	6.801	7.048	7.245	7.409	7.550	7.672	7.780
9	6.566	6.621	6.859	7.050	7.208	7.343	7.461	7.566
10	6.425	6.479	6.709	6.895	7.048	7.180	7.295	7.396
11	6.310	6.363	6.588	6.768	6.918	7.047	7.158	7.258
12	6.215	6.267	6.487	6.663	6.810	6.936	7.045	7.142
13	6.135	6.186	6.402	6.575	6.719	6.842	6.949	7.045
14	6.067	6.116	6.329	6.499	6.641	6.762	6.868	6.961
15	6.008	6.057	6.266	6.433	6.573	6.692	6.796	6.888
16	5.956	6.004	6.210	6.376	6.513	6.631	6.734	6.825
17	5.910	5.958	6.162	6.325	6.461	6.577	6.679	6.769
18	5.870	5.917	6.118	6.280	6.414	6.529	6.630	6.719
19	5.833	5.880	6.079	6.239	6.372	6.486	6.585	6.674
20	5.801	5.847	6.044	6.203	6.335	6.447	6.546	6.633
24	5.697	5.741	5.933	6.086	6.214	6.324	6.419	6.503
30	5.593	5.636	5.821	5.969	6.093	6.198	6.291	6.372
40	5.488	5.529	5.708	5.850	5.969	6.071	6.160	6.238
60	5.382	5.422	5.593	5.730	5.844	5.941	6.026	6.102
120	5.275	5.313	5.476	5.606	6.715	5.808	5.888	5.960
∞	5.166	5.202	5.357	5.480	5.582	5.669	5.745	5.812

TABLE B.5 (cont.): Critical Values of the q Distribution, for the Tukey Test

$\alpha = 0.05$

ν	k: 2	3	4	5	6	7	8	9	10
1	17.97	26.98	32.82	37.08	40.41	43.12	45.40	47.36	49.07
2	6.085	8.331	9.798	10.88	11.74	12.44	13.03	13.54	13.99
3	4.501	5.910	6.825	7.502	8.037	8.478	8.853	9.177	9.462
4	3.927	5.040	5.757	6.287	6.707	7.053	7.347	7.602	7.826
5	3.635	4.602	5.218	5.673	6.033	6.330	6.582	6.802	6.995
6	3.461	4.339	4.896	5.305	5.628	5.895	6.122	6.319	6.493
7	3.344	4.165	4.681	5.060	5.359	5.606	5.815	5.998	6.158
8	3.261	4.041	4.529	4.886	5.167	5.399	5.597	5.767	5.918
9	3.199	3.949	4.415	4.756	5.024	5.244	5.432	5.595	5.739
10	3.151	3.877	4.327	4.654	4.912	5.124	5.305	5.461	5.599
11	3.113	3.820	4.256	4.574	4.823	5.028	5.202	5.353	5.487
12	3.082	3.773	4.199	4.508	4.751	4.950	5.119	5.265	5.395
13	3.055	3.735	4.151	4.453	4.690	4.885	5.049	5.192	5.318
14	3.033	3.702	4.111	4.407	4.639	4.829	4.990	5.131	5.254
15	3.014	3.674	4.076	4.367	4.595	4.782	4.940	5.077	5.198
16	2.998	3.649	4.046	4.333	4.557	4.741	4.897	5.031	5.150
17	2.984	3.628	4.020	4.303	4.524	4.705	4.858	4.991	5.108
18	2.971	3.609	3.997	4.277	4.495	4.673	4.824	4.956	5.071
19	2.960	3.593	3.977	4.253	4.469	4.645	4.794	4.924	5.038
20	2.950	3.578	3.958	4.232	4.445	4.620	4.768	4.896	5.008
24	2.919	3.532	3.901	4.166	4.373	4.541	4.684	4.807	4.915
30	2.888	3.486	3.845	4.102	4.302	4.464	4.602	4.720	4.824
40	2.858	3.442	3.791	4.039	4.232	4.389	4.521	4.635	4.735
60	2.829	3.399	3.737	3.977	4.163	4.314	4.441	4.550	4.646
120	2.800	3.356	3.685	3.917	4.096	4.241	4.363	4.468	4.560
∞	2.772	3.314	3.633	3.858	4.030	4.170	4.286	4.387	4.474

ν	k: 11	12	13	14	15	16	17	18	19
1	50.59	51.96	53.20	54.33	55.36	56.32	57.22	58.04	58.83
2	14.39	14.75	15.08	15.38	15.65	15.91	16.14	16.37	16.57
3	9.717	9.946	10.15	10.35	10.53	10.69	10.84	10.98	11.11
4	8.027	8.208	8.373	8.525	8.664	8.794	8.914	9.028	9.134
5	7.168	7.324	7.466	7.596	7.717	7.828	7.932	8.030	8.122
6	6.649	6.789	6.917	7.034	7.143	7.244	7.338	7.426	7.508
7	6.302	6.431	6.550	6.658	6.759	6.852	6.939	7.020	7.097
8	6.054	6.175	6.287	6.389	6.483	6.571	6.653	6.729	6.802
9	5.867	5.983	6.089	6.186	6.276	6.359	6.437	6.510	6.579
10	5.722	5.833	5.935	6.028	6.114	6.194	6.269	6.339	6.405
11	5.605	5.713	5.811	5.901	5.984	6.062	6.134	6.202	6.265
12	5.511	5.615	5.710	5.798	5.878	5.953	6.023	6.089	6.151
13	5.431	5.533	5.625	5.711	5.789	5.862	5.931	5.995	6.055
14	5.364	5.463	5.554	5.637	5.714	5.786	5.852	5.915	5.974
15	5.306	5.404	5.493	5.574	5.649	5.720	5.785	5.846	5.904
16	5.256	5.352	5.439	5.520	5.593	5.662	5.727	5.786	5.843
17	5.212	5.307	5.392	5.471	5.544	5.612	5.675	5.734	5.790
18	5.174	5.267	5.352	5.429	5.501	5.568	5.630	5.688	5.743
19	5.140	5.231	5.315	5.391	5.462	5.528	5.589	5.647	5.701
20	5.108	5.199	5.282	5.357	5.427	5.493	5.553	5.610	5.663
24	5.012	5.099	5.179	5.251	5.319	5.381	5.439	5.494	5.545
30	4.917	5.001	5.077	5.147	5.211	5.271	5.327	5.379	5.429
40	4.824	4.904	4.977	5.044	5.106	5.163	5.216	5.266	5.313
60	4.732	4.808	4.878	4.942	5.001	5.056	5.107	5.154	5.199
120	4.641	4.714	4.781	4.842	4.898	4.950	4.998	5.044	5.086
∞	4.552	4.622	4.685	4.743	4.796	4.845	4.891	4.934	4.974

TABLE B.5 (cont.): Critical Values of the q Distribution, for the Tukey Test

$\alpha = 0.05$

ν	k: 20	22	24	26	28	30	32	34	36
1	59.56	60.91	62.12	63.22	64.23	65.15	66.01	66.81	67.56
2	16.77	17.13	17.45	17.75	18.02	18.27	18.50	18.72	18.92
3	11.24	11.47	11.68	11.87	12.05	12.21	12.36	12.50	12.63
4	9.233	9.418	9.584	9.736	9.875	10.00	10.12	10.23	10.34
5	8.208	8.368	8.512	8.643	8.764	8.875	8.979	9.075	9.165
6	7.587	7.730	7.861	7.979	8.088	8.189	8.283	8.370	8.452
7	7.170	7.303	7.423	7.533	7.634	7.728	7.814	7.895	7.972
8	6.870	6.995	7.109	7.212	7.307	7.395	7.477	7.554	7.625
9	6.644	6.763	6.871	6.970	7.061	7.145	7.222	7.295	7.363
10	6.467	6.582	6.686	6.781	6.868	6.948	7.023	7.093	7.159
11	6.326	6.436	6.536	6.628	6.712	6.790	6.863	6.930	6.994
12	6.209	6.317	6.414	6.503	6.585	6.660	6.731	6.796	6.858
13	6.112	6.217	6.312	6.398	6.478	6.551	6.620	6.684	6.744
14	6.029	6.132	6.224	6.309	6.387	6.459	6.526	6.588	6.647
15	5.958	6.059	6.149	6.233	6.309	6.379	6.445	6.506	6.564
16	5.897	5.995	6.084	6.166	6.241	6.310	6.374	6.434	6.491
17	5.842	5.940	6.027	6.107	6.181	6.249	6.313	6.372	6.427
18	5.794	5.890	5.977	6.055	6.128	6.195	6.258	6.316	6.371
19	5.752	5.846	5.932	6.009	6.081	6.147	6.209	6.267	6.321
20	5.714	5.807	5.891	5.968	6.039	6.104	6.165	6.222	6.275
24	5.594	5.683	5.764	5.838	5.906	5.968	6.027	6.081	6.132
30	5.475	5.561	5.638	5.709	5.774	5.833	5.889	5.941	5.990
40	5.358	5.439	5.513	5.581	5.642	5.700	5.753	5.803	5.849
60	5.241	5.319	5.389	5.453	5.512	5.566	5.617	5.664	5.708
120	5.126	5.200	5.266	5.327	5.382	5.434	5.481	5.526	5.568
∞	5.012	5.081	5.144	5.201	5.253	5.301	5.346	5.388	5.427

ν	k: 38	40	50	60	70	80	90	100
1	68.26	68.92	71.73	73.97	75.82	77.40	78.77	79.98
2	19.11	19.28	20.05	20.66	21.16	21.59	21.96	22.29
3	12.75	12.87	13.36	13.76	14.08	14.36	14.61	14.82
4	10.44	10.53	10.93	11.24	11.51	11.73	11.92	12.09
5	9.250	9.330	9.674	9.949	10.18	10.38	10.54	10.69
6	8.529	8.601	8.913	9.163	9.370	9.548	9.702	9.839
7	8.043	8.110	8.400	8.632	8.824	8.989	9.133	9.261
8	7.693	7.756	8.029	8.248	8.430	8.586	8.722	8.843
9	7.428	7.488	7.749	7.958	8.132	8.281	8.410	8.526
10	7.220	7.279	7.529	7.730	7.897	8.041	8.166	8.276
11	7.053	7.110	7.352	7.546	7.708	7.847	7.968	8.075
12	6.916	6.970	7.205	7.394	7.552	7.687	7.804	7.909
13	6.800	6.854	7.083	7.267	7.421	7.552	7.667	7.769
14	6.702	6.754	6.979	7.159	7.309	7.438	7.550	7.650
15	6.618	6.669	6.888	7.065	7.212	7.339	7.449	7.546
16	6.544	6.594	6.810	6.984	7.128	7.252	7.360	7.457
17	6.479	6.529	6.741	6.912	7.054	7.176	7.283	7.377
18	6.422	6.471	6.680	6.848	6.989	7.109	7.213	7.307
19	6.371	6.419	6.626	6.792	6.930	7.048	7.152	7.244
20	6.325	6.373	6.576	6.740	6.877	6.994	7.097	7.187
24	6.181	6.226	6.421	6.579	6.710	6.822	6.920	7.008
30	6.037	6.080	6.267	6.417	6.543	6.650	6.744	6.827
40	5.893	5.934	6.112	6.255	6.375	6.477	6.566	6.645
60	5.750	5.789	5.958	6.093	6.206	6.303	6.387	6.462
120	5.607	5.644	5.802	5.929	6.035	6.126	6.205	6.275
∞	5.463	5.498	5.646	5.764	5.863	5.947	6.020	6.085

TABLE B.5 (cont.): Critical Values of the q Distribution, for the Tukey Test

$\alpha = 0.025$

ν	k: 2	3	4	5	6	7	8	9	10
1	35.99	54.00	65.69	74.22	80.87	86.29	90.85	94.77	98.20
2	8.776	11.94	14.01	15.54	16.75	17.74	18.58	19.31	19.95
3	5.907	7.661	8.808	9.660	10.34	10.89	11.37	11.78	12.14
4	4.943	6.244	7.088	7.716	8.213	8.625	8.976	9.279	9.548
5	4.474	5.558	6.257	6.775	7.186	7.527	7.816	8.068	8.291
6	4.199	5.158	5.772	6.226	6.586	6.884	7.138	7.359	7.554
7	4.018	4.897	5.455	5.868	6.194	6.464	6.695	6.895	7.072
8	3.892	4.714	5.233	5.616	5.919	6.169	6.382	6.568	6.732
9	3.797	4.578	5.069	5.430	5.715	5.950	6.151	6.325	6.479
10	3.725	4.474	4.943	5.287	5.558	5.782	5.972	6.138	6.285
11	3.667	4.391	4.843	5.173	5.433	5.648	5.831	5.989	6.130
12	3.620	4.325	4.762	5.081	5.332	5.540	5.716	5.869	6.004
13	3.582	4.269	4.694	5.004	5.248	5.449	5.620	5.769	5.900
14	3.550	4.222	4.638	4.940	5.178	5.374	5.540	5.684	5.811
15	3.522	4.182	4.589	4.885	5.118	5.309	5.471	5.612	5.737
16	3.498	4.148	4.548	4.838	5.066	5.253	5.412	5.550	5.672
17	3.477	4.118	4.512	4.797	5.020	5.204	5.361	5.496	5.615
18	3.458	4.092	4.480	4.761	4.981	5.162	5.315	5.448	5.565
19	3.442	4.068	4.451	4.728	4.945	5.123	5.275	5.405	5.521
20	3.427	4.047	4.426	4.700	4.914	5.089	5.238	5.368	5.481
24	3.381	3.983	4.347	4.610	4.816	4.984	5.126	5.250	5.358
30	3.337	3.919	4.271	4.523	4.720	4.881	5.017	5.134	5.238
40	3.294	3.858	4.197	4.439	4.627	4.780	4.910	5.022	5.120
60	3.251	3.798	4.124	4.356	4.536	4.682	4.806	4.912	5.006
120	3.210	3.739	4.053	4.276	4.447	4.587	4.704	4.805	4.894
∞	3.170	3.682	3.984	4.197	4.361	4.494	4.605	4.700	4.784

ν	k: 11	12	13	14	15	16	17	18	19
1	101.3	104.0	106.5	108.8	110.8	112.7	114.5	116.2	117.7
2	20.52	21.03	21.49	21.91	22.30	22.67	23.01	23.32	23.62
3	12.46	12.75	13.01	13.26	13.48	13.69	13.88	14.06	14.23
4	9.788	10.01	10.20	10.39	10.55	10.71	10.85	10.99	11.11
5	8.490	8.670	8.834	8.984	9.124	9.253	9.374	9.486	9.593
6	7.729	7.887	8.031	8.163	8.286	8.399	8.506	8.605	8.698
7	7.230	7.373	7.504	7.624	7.735	7.839	7.935	8.025	8.111
8	6.879	7.011	7.132	7.244	7.347	7.443	7.532	7.616	7.695
9	6.617	6.742	6.856	6.961	7.058	7.148	7.232	7.311	7.385
10	6.416	6.534	6.643	6.742	6.834	6.920	7.000	7.075	7.146
11	6.256	6.369	6.473	6.568	6.657	6.739	6.815	6.887	6.955
12	6.125	6.235	6.335	6.427	6.512	6.591	6.665	6.734	6.799
13	6.017	6.123	6.220	6.309	6.392	6.468	6.539	6.607	6.670
14	5.926	6.029	6.123	6.210	6.290	6.364	6.434	6.499	6.560
15	5.848	5.949	6.041	6.125	6.203	6.276	6.344	6.407	6.467
16	5.781	5.879	5.969	6.052	6.128	6.199	6.265	6.328	6.386
17	5.722	5.818	5.907	5.987	6.062	6.132	6.197	6.258	6.315
18	5.670	5.765	5.852	5.931	6.004	6.073	6.137	6.197	6.253
19	5.624	5.718	5.803	5.881	5.954	6.020	6.083	6.142	6.198
20	5.583	5.675	5.759	5.836	5.907	5.974	6.036	6.093	6.148
24	5.455	5.543	5.623	5.697	5.764	5.827	5.886	5.941	5.994
30	5.330	5.414	5.490	5.560	5.624	5.684	5.740	5.792	5.841
40	5.208	5.288	5.360	5.426	5.487	5.544	5.597	5.646	5.693
60	5.089	5.164	5.232	5.295	5.352	5.406	5.456	5.503	5.546
120	4.972	5.043	5.107	5.166	5.221	5.271	5.318	5.362	5.403
∞	4.858	4.925	4.985	5.041	5.092	5.139	5.183	5.224	5.262

TABLE B.5 (cont.): Critical Values of the q Distribution, for the Tukey Test

$\alpha = 0.025$

ν	k: 20	22	24	26	28	30	32	34	36
1	119.2	121.9	124.3	126.5	128.6	130.4	132.1	133.7	135.2
2	23.89	24.41	24.87	25.29	25.67	26.03	26.35	26.66	26.95
3	14.39	14.69	14.95	15.19	15.41	15.62	15.81	15.99	16.15
4	11.23	11.46	11.66	11.84	12.00	12.16	12.30	12.44	12.56
5	9.693	9.878	10.04	10.20	10.34	10.47	10.59	10.70	10.80
6	8.787	8.949	9.097	9.231	9.355	9.469	9.575	9.674	9.767
7	8.191	8.339	8.473	8.595	8.708	8.812	8.909	8.999	9.084
8	7.769	7.907	8.031	8.145	8.250	8.346	8.436	8.520	8.599
9	7.455	7.585	7.702	7.809	7.908	7.999	8.084	8.163	8.237
10	7.212	7.335	7.447	7.549	7.643	7.729	7.810	7.885	7.956
11	7.019	7.137	7.244	7.341	7.431	7.514	7.592	7.664	7.732
12	6.861	6.974	7.078	7.172	7.258	7.338	7.413	7.483	7.548
13	6.730	6.840	6.939	7.031	7.115	7.192	7.265	7.332	7.396
14	6.619	6.726	6.823	6.911	6.993	7.069	7.139	7.204	7.266
15	6.523	6.628	6.723	6.809	6.889	6.962	7.031	7.095	7.155
16	6.441	6.543	6.636	6.721	6.799	6.870	6.938	7.000	7.059
17	6.370	6.469	6.560	6.644	6.720	6.790	6.856	6.917	6.975
18	6.306	6.404	6.493	6.575	6.650	6.720	6.784	6.844	6.900
19	6.250	6.347	6.434	6.514	6.588	6.656	6.719	6.779	6.835
20	6.200	6.295	6.381	6.460	6.532	6.600	6.662	6.720	6.775
24	6.043	6.133	6.215	6.290	6.359	6.423	6.482	6.538	6.589
30	5.888	5.974	6.052	6.123	6.188	6.248	6.305	6.357	6.406
40	5.737	5.818	5.891	5.958	6.020	6.077	6.130	6.179	6.226
60	5.588	5.664	5.733	5.797	5.584	5.908	5.958	6.004	6.048
120	5.442	5.513	5.578	5.637	5.691	5.741	5.788	5.831	5.872
∞	5.299	5.365	5.425	5.480	5.530	5.577	5.620	5.660	5.698

ν	k: 38	40	50	60	70	80	90	100
1	136.6	137.9	143.6	148.1	151.8	154.9	157.7	160.0
2	27.22	27.47	28.55	29.42	30.13	30.74	31.27	31.74
3	16.31	16.46	17.08	17.59	18.00	18.36	18.67	18.95
4	12.68	12.79	13.27	13.65	13.96	14.23	14.47	14.68
5	10.91	11.00	11.40	11.72	11.99	12.21	12.41	12.59
6	9.855	9.938	10.30	10.58	10.81	11.02	11.19	11.35
7	9.164	9.239	9.563	9.822	10.04	10.23	10.38	10.53
8	8.673	8.743	9.044	9.286	9.487	9.660	9.810	9.944
9	8.307	8.373	8.657	8.885	9.076	9.238	9.381	9.507
10	8.023	8.086	8.356	8.574	8.755	8.911	9.046	9.167
11	7.796	7.856	8.116	8.325	8.499	8.648	8.779	8.894
12	7.610	7.668	7.919	8.120	8.289	8.433	8.559	8.671
13	7.455	7.512	7.755	7.950	8.113	8.253	8.375	8.484
14	7.324	7.379	7.615	7.806	7.965	8.101	8.220	8.325
15	7.212	7.265	7.496	7.682	7.837	7.970	8.086	8.189
16	7.115	7.167	7.393	7.574	7.726	7.856	7.969	8.070
17	7.030	7.081	7.302	7.480	7.628	7.756	7.868	7.966
18	6.954	7.005	7.221	7.396	7.543	7.667	7.777	7.874
19	6.887	6.936	7.150	7.322	7.465	7.589	7.696	7.792
20	6.827	6.876	7.086	7.255	7.397	7.518	7.624	7.718
24	6.639	6.685	6.885	7.046	7.180	7.296	7.397	7.486
30	6.453	6.497	6.686	6.839	6.965	7.075	7.171	7.255
40	6.270	6.311	6.489	6.633	6.753	6.855	6.945	7.025
60	6.089	6.127	6.295	6.429	6.540	6.636	6.720	6.795
120	5.910	5.946	6.101	6.225	6.329	6.418	6.495	6.564
∞	5.733	5.766	5.909	6.023	6.118	6.199	6.270	6.333

TABLE B.5 (cont.): Critical Values of the q Distribution, for the Tukey Test

$\alpha = 0.01$

ν	k: 2	3	4	5	6	7	8	9	10
1	90.03	135.0	164.3	185.6	202.2	215.8	227.2	237.0	245.6
2	14.04	19.02	22.29	24.72	26.63	28.20	29.53	30.68	31.69
3	8.261	10.62	12.17	13.33	14.24	15.00	15.64	16.20	16.69
4	6.512	8.120	9.173	9.958	10.58	11.10	11.55	11.93	12.27
5	5.702	6.976	7.804	8.421	8.913	9.321	9.669	9.972	10.24
6	5.243	6.331	7.033	7.556	7.973	8.318	8.613	8.869	9.097
7	4.949	5.919	6.543	7.005	7.373	7.679	7.939	8.166	8.368
8	4.746	5.635	6.204	6.625	6.960	7.237	7.474	7.681	7.863
9	4.596	5.428	5.957	6.348	6.658	6.915	7.134	7.325	7.495
10	4.482	5.270	5.769	6.136	6.428	6.669	6.875	7.055	7.213
11	4.392	5.146	5.621	5.970	6.247	6.476	6.672	6.842	6.992
12	4.320	5.046	5.502	5.836	6.101	6.321	6.507	6.670	6.814
13	4.260	4.964	5.404	5.727	5.981	6.192	6.372	6.528	6.667
14	4.210	4.895	5.322	5.634	5.881	6.085	6.258	6.409	6.543
15	4.168	4.836	5.252	5.556	5.796	5.994	6.162	6.309	6.439
16	4.131	4.786	5.192	5.489	5.722	5.915	6.079	6.222	6.349
17	4.099	4.742	5.140	5.430	5.659	5.847	6.007	6.147	6.270
18	4.071	4.703	5.094	5.379	5.603	5.788	5.944	6.081	6.201
19	4.046	4.670	5.054	5.334	5.554	5.735	5.889	6.022	6.141
20	4.024	4.639	5.018	5.294	5.510	5.688	5.839	5.970	6.087
24	3.956	4.546	4.907	5.168	5.374	5.542	5.685	5.809	5.919
30	3.889	4.455	4.799	5.048	5.242	5.401	5.536	5.653	5.756
40	3.825	4.367	4.696	4.931	5.114	5.265	5.392	5.502	5.559
60	3.762	4.282	4.595	4.818	4.991	5.133	5.253	5.356	5.447
120	3.702	4.200	4.497	4.709	4.872	5.005	5.118	5.214	5.299
∞	3.643	4.120	4.403	4.603	4.757	4.882	4.987	5.078	5.157

ν	k: 11	12	13	14	15	16	17	18	19
1	253.2	260.0	266.2	271.8	277.0	281.8	286.3	290.4	294.3
2	32.59	33.40	34.13	34.81	35.43	36.00	36.53	37.03	37.50
3	17.13	17.53	17.89	18.22	18.52	18.81	19.07	19.32	19.55
4	12.57	12.84	13.09	13.32	13.53	13.73	13.91	14.08	14.24
5	10.48	10.70	10.89	11.08	11.24	11.40	11.55	11.68	11.81
6	9.301	9.485	9.653	9.808	9.951	10.08	10.21	10.32	10.43
7	8.548	8.711	8.860	8.997	9.124	9.242	9.353	9.456	9.554
8	8.027	8.176	8.312	8.436	8.552	8.659	8.760	8.854	8.943
9	7.647	7.784	7.910	8.025	8.132	8.232	8.325	8.412	8.495
10	7.356	7.485	7.603	7.712	7.812	7.906	7.993	8.076	8.153
11	7.128	7.250	7.362	7.465	7.560	7.649	7.732	7.809	7.883
12	6.943	7.060	7.167	7.265	7.356	7.441	7.520	7.594	7.665
13	6.791	6.903	7.006	7.101	7.188	7.269	7.345	7.417	7.485
14	6.664	6.772	6.871	6.962	7.047	7.126	7.199	7.268	7.333
15	6.555	6.660	6.757	6.845	6.927	7.003	7.074	7.142	7.204
16	6.462	6.564	6.658	6.744	6.823	6.898	6.967	7.032	7.093
17	6.381	6.480	6.572	6.656	6.734	6.806	6.873	6.937	6.997
18	6.310	6.407	6.497	6.579	6.655	6.725	6.792	6.854	6.912
19	6.247	6.342	6.430	6.510	6.585	6.654	6.719	6.780	6.837
20	6.191	6.285	6.371	6.450	6.523	6.591	6.654	6.714	6.771
24	6.017	6.106	6.186	6.261	6.330	6.394	6.453	6.510	6.563
30	5.849	5.932	6.008	6.078	6.143	6.203	6.259	6.311	6.361
40	5.686	5.764	5.835	5.900	5.961	6.017	6.069	6.119	6.165
60	5.528	5.601	5.667	5.728	5.785	5.837	5.886	5.931	5.974
120	5.375	5.443	5.505	5.562	5.614	5.662	5.708	5.750	5.790
∞	5.227	2.590	5.348	5.400	5.448	5.493	5.535	5.574	5.611

TABLE B.5 (cont.): Critical Values of the q Distribution, for the Tukey Test

$\alpha = 0.01$

ν	k: 20	22	24	26	28	30	32	34	36
1	298.0	304.7	310.8	316.3	321.3	326.0	330.3	334.3	338.0
2	37.95	38.76	39.49	40.15	40.76	41.32	41.84	42.33	42.78
3	19.77	20.17	20.53	20.86	21.16	21.44	21.70	21.95	22.17
4	14.40	14.68	14.93	15.16	15.37	15.57	15.75	15.92	16.08
5	11.93	12.16	12.36	12.54	12.71	12.87	13.02	13.15	13.28
6	10.54	10.73	10.91	11.06	11.21	11.34	11.47	11.58	11.69
7	9.646	9.815	9.970	10.11	10.24	10.36	10.47	10.58	10.67
8	9.027	9.182	9.322	9.450	9.569	9.678	9.779	9.874	9.964
9	8.573	8.717	8.847	8.966	9.075	9.177	9.271	9.360	9.443
10	8.226	8.361	8.483	8.595	8.698	8.794	8.883	8.966	9.044
11	7.952	8.080	8.196	8.303	8.400	8.491	8.575	8.654	8.728
12	7.731	7.853	7.964	8.066	8.159	8.246	8.327	8.402	8.473
13	7.548	7.665	7.772	7.870	7.960	8.043	8.121	8.193	8.262
14	7.395	7.508	7.611	7.705	7.792	7.873	7.948	8.018	8.084
15	7.264	7.374	7.474	7.566	7.650	7.728	7.800	7.869	7.932
16	7.152	7.258	7.356	7.445	7.527	7.602	7.673	7.739	7.802
17	7.053	7.158	7.253	7.340	7.420	7.493	7.563	7.627	7.687
18	6.968	7.070	7.163	7.247	7.325	7.398	7.465	7.528	7.587
19	6.891	6.992	7.082	7.166	7.242	7.313	7.379	7.440	7.498
20	6.823	6.922	7.011	7.092	7.168	7.237	7.302	7.362	7.419
24	6.612	6.705	6.789	6.865	6.936	7.001	7.062	7.119	7.173
30	6.407	6.494	6.572	6.644	6.710	6.772	6.828	6.881	6.932
40	6.209	6.289	6.362	6.429	6.490	6.547	6.600	6.650	6.697
60	6.015	6.090	6.158	6.220	6.277	6.330	6.378	6.424	6.467
120	5.827	5.897	5.959	6.016	6.069	6.117	6.162	6.204	6.244
∞	5.645	5.709	5.766	5.818	5.866	5.911	5.952	5.990	6.026

ν	k: 38	40	50	60	70	80	90	100
1	341.5	344.8	358.9	370.1	379.4	387.3	394.1	400.1
2	43.21	43.61	45.33	46.70	47.83	48.80	49.64	50.38
3	22.39	22.59	23.45	24.13	24.71	25.19	25.62	25.99
4	16.23	16.37	16.98	17.46	17.86	18.02	18.50	18.77
5	13.40	13.52	14.00	14.39	14.72	14.99	15.23	15.45
6	11.80	11.90	12.31	12.65	12.92	13.16	13.37	13.55
7	10.77	10.85	11.23	11.52	11.77	11.99	12.17	12.34
8	10.05	10.13	10.47	10.75	10.97	11.17	11.34	11.49
9	9.521	9.594	9.912	10.17	10.38	10.57	10.73	10.87
10	9.117	9.187	9.486	9.726	9.927	10.10	10.25	10.39
11	8.798	8.864	9.148	9.377	9.568	9.732	9.875	10.00
12	8.539	8.603	8.875	9.094	9.277	9.434	9.571	9.693
13	8.326	8.387	8.648	8.859	9.035	9.187	9.318	9.436
14	8.146	8.204	8.457	8.661	8.832	8.978	9.106	9.219
15	7.992	8.049	8.295	8.492	8.658	8.800	8.924	9.035
16	7.860	7.916	8.154	8.347	8.507	8.646	8.767	8.874
17	7.745	7.799	8.031	8.219	8.377	8.511	8.630	8.735
18	7.643	7.696	7.924	8.107	8.261	8.393	8.508	8.611
19	7.553	7.605	7.828	8.008	8.159	8.288	8.401	8.502
20	7.473	7.523	7.742	7.919	8.067	8.194	8.305	8.404
24	7.223	7.270	7.476	7.642	7.780	7.900	8.004	8.097
30	6.978	7.023	7.215	7.370	7.500	7.611	7.709	7.796
40	6.740	6.782	6.960	7.104	7.225	7.328	7.419	7.500
60	6.507	6.546	6.710	6.843	6.954	7.050	7.133	7.207
120	6.281	6.316	6.467	6.588	6.689	6.776	6.852	6.919
∞	6.060	6.092	6.228	6.338	6.429	6.507	6.575	6.636

TABLE B.5 (cont.): Critical Values of the q Distribution, for the Tukey Test

$\alpha = 0.005$

ν	k: 2	3	4	5	6	7	8	9	10
1	180.1	270.1	328.5	371.2	404.4	431.6	454.4	474.0	491.1
2	19.93	26.97	31.60	35.02	37.73	39.95	41.83	43.46	44.89
3	10.55	13.50	15.45	16.91	18.06	19.01	19.83	20.53	21.15
4	7.916	9.814	11.06	11.99	12.74	13.35	13.88	14.33	14.74
5	6.751	8.196	9.141	9.847	10.41	10.88	11.28	11.63	11.93
6	6.105	7.306	8.088	8.670	9.135	9.522	9.852	10.14	10.40
7	5.699	6.750	7.429	7.935	8.339	8.674	8.961	9.211	9.433
8	5.420	6.370	6.981	7.435	7.797	8.097	8.354	8.578	8.777
9	5.218	6.096	6.657	7.074	7.405	7.680	7.915	8.120	8.303
10	5.065	5.888	6.412	6.800	7.109	7.365	7.584	7.775	7.944
11	4.945	5.727	6.222	6.588	6.878	7.119	7.325	7.505	7.664
12	4.849	5.597	6.068	6.416	6.693	6.922	7.118	7.288	7.439
13	4.770	5.490	5.943	6.277	6.541	6.760	6.947	7.111	7.255
14	4.704	5.401	5.838	6.160	6.414	6.626	6.805	6.962	7.101
15	4.647	5.325	5.750	6.061	6.308	6.511	6.685	6.837	6.971
16	4.599	5.261	5.674	5.977	6.216	6.413	6.582	6.729	6.859
17	4.557	5.205	5.608	5.903	6.136	6.329	6.493	6.636	6.763
18	4.521	3.156	5.550	5.839	6.067	6.255	6.415	6.554	6.678
19	4.488	5.113	5.500	5.783	6.005	6.189	6.346	6.482	6.603
20	4.460	5.074	5.455	5.732	5.951	6.131	6.285	6.418	6.537
24	4.371	4.955	5.315	5.577	5.783	5.952	6.096	6.221	6.332
30	4.285	4.841	5.181	5.428	5.621	5.780	5.914	6.031	6.135
40	4.202	4.731	5.053	5.284	5.465	5.614	5.739	5.848	5.944
60	4.122	4.625	4.928	5.146	5.316	5.454	5.571	5.673	5.762
120	4.045	4.523	4.809	5.013	5.172	5.301	5.410	5.504	5.586
∞	3.970	4.424	4.694	4.886	5.033	5.154	5.255	5.341	5.418

ν	k: 11	12	13	14	15	16	17	18	19
1	506.3	520.0	532.4	543.6	554.0	563.6	572.5	580.9	588.7
2	46.16	47.31	48.35	49.30	50.17	50.99	51.74	52.45	53.12
3	21.70	22.20	22.66	23.08	23.46	23.82	24.15	24.46	24.76
4	15.10	15.42	15.72	15.99	16.24	16.48	16.70	16.90	17.09
5	12.21	12.46	12.69	12.90	13.09	13.27	13.44	13.60	13.75
6	10.63	10.83	11.02	11.20	11.36	11.51	11.65	11.78	11.90
7	9.632	9.812	9.977	10.13	10.27	10.40	10.52	10.64	10.75
8	8.955	9.117	9.265	9.401	9.527	9.644	9.754	9.857	9.953
9	8.466	8.614	8.749	8.874	8.990	9.097	9.198	9.292	9.381
10	8.096	8.234	8.360	8.476	8.583	8.683	8.777	8.865	8.947
11	7.807	7.937	8.055	8.164	8.265	8.359	8.447	8.530	8.608
12	7.575	7.697	7.810	7.914	8.009	8.099	8.183	8.261	8.335
13	7.384	7.502	7.609	7.708	7.800	7.886	7.965	8.040	8.111
14	7.225	7.338	7.442	7.537	7.625	7.707	7.784	7.856	7.924
15	7.091	7.200	7.300	7.392	7.477	7.556	7.630	7.699	7.765
16	6.976	7.081	7.178	7.267	7.349	7.426	7.498	7.566	7.629
17	6.876	6.979	7.072	7.159	7.239	7.314	7.384	7.449	7.511
18	6.788	6.888	6.980	7.064	7.142	7.215	7.283	7.347	7.407
19	6.711	6.809	6.898	6.981	7.057	7.128	7.195	7.257	7.316
20	6.642	6.738	6.826	6.907	6.981	7.051	7.116	7.177	7.235
24	6.431	6.520	6.602	6.677	6.747	6.812	6.872	6.930	6.983
30	6.227	6.310	6.387	6.456	6.521	6.581	6.638	6.691	6.741
40	6.030	6.108	6.179	6.244	6.304	6.360	6.412	6.461	6.507
60	5.841	5.913	5.979	6.039	6.094	6.146	6.194	6.239	6.281
120	5.660	5.726	5.786	5.842	5.893	5.940	5.984	6.025	6.064
∞	5.485	5.546	5.602	5.652	5.699	5.742	5.783	5.820	5.856

TABLE B.5 (cont.): Critical Values of the q Distribution, for the Tukey Test

$\alpha = 0.005$

ν	k: 20	22	24	26	28	30	32	34	36
1	596.0	609.5	621.7	632.6	642.7	652.0	660.6	668.5	676.0
2	53.74	54.89	55.92	56.86	57.73	58.52	59.26	59.95	60.59
3	25.03	25.54	26.00	26.42	26.80	27.15	27.48	27.79	28.07
4	17.28	17.61	17.91	18.19	18.44	18.68	18.89	19.09	19.28
5	13.89	14.14	14.38	14.59	14.79	14.96	15.13	15.29	15.44
6	12.02	12.23	12.43	12.61	12.77	12.92	13.06	13.19	13.32
7	10.85	11.03	11.21	11.36	11.50	11.64	11.76	11.88	11.99
8	10.04	10.22	10.37	10.51	10.64	10.76	10.87	10.97	11.07
9	9.465	9.620	9.761	9.890	10.01	10.12	10.22	10.32	10.41
10	9.026	9.170	9.302	9.422	9.532	9.635	9.730	9.820	9.904
11	8.682	8.818	8.941	9.055	9.159	9.256	9.345	9.430	9.509
12	8.405	8.534	8.652	8.759	8.858	8.950	9.036	9.116	9.191
13	8.178	8.302	8.414	8.516	8.611	8.699	8.781	8.857	8.929
14	7.988	8.107	8.215	8.314	8.404	8.489	8.568	8.641	8.710
15	7.827	7.942	8.046	8.141	8.229	8.311	8.387	8.458	8.524
16	7.689	7.800	7.901	7.994	8.078	8.158	8.231	8.300	8.365
17	7.569	7.677	7.775	7.865	7.948	8.024	8.096	8.163	8.226
18	7.464	7.570	7.665	7.753	7.833	7.908	7.978	8.043	8.104
19	7.372	7.474	7.568	7.653	7.732	7.805	7.873	7.937	7.996
20	7.289	7.390	7.481	7.565	7.642	7.713	7.780	7.842	7.901
24	7.034	7.128	7.213	7.291	7.362	7.429	7.491	7.549	7.603
30	6.788	6.875	6.954	7.026	7.093	7.154	7.212	7.265	7.316
40	6.550	6.631	6.704	6.770	6.832	6.889	6.942	6.991	7.038
60	6.321	6.396	6.462	6.523	6.580	6.632	6.861	6.726	6.769
120	6.101	6.169	6.230	6.286	6.337	6.385	6.428	6.470	6.508
∞	5.889	5.951	6.006	6.057	6.103	6.146	6.186	6.223	6.258

ν	k: 38	40	50	60	70	80	90	100
1	683.0	689.6	717.8	740.2	758.8	774.5	788.2	800.3
2	61.19	61.76	64.19	66.13	67.74	69.10	70.29	71.35
3	28.34	28.60	29.68	30.55	31.27	31.88	32.42	32.90
4	19.46	19.63	20.36	20.93	21.42	21.83	22.18	22.50
5	15.58	15.71	16.27	16.72	17.09	17.41	17.69	17.94
6	13.43	13.54	14.02	14.40	14.71	14.98	15.21	15.43
7	12.09	12.18	12.60	12.93	13.21	13.44	13.65	13.84
8	11.16	11.25	11.63	11.93	12.18	12.39	12.58	12.75
9	10.49	10.58	10.92	11.20	11.43	11.63	11.80	11.96
10	9.983	10.06	10.38	10.64	10.86	11.04	11.20	11.35
11	9.583	9.654	9.957	10.20	10.41	10.59	10.74	10.88
12	9.262	9.328	9.617	9.850	10.04	10.21	10.36	10.49
13	8.997	9.061	9.337	9.560	9.747	9.907	10.05	10.17
14	8.775	8.837	9.103	9.317	9.497	9.652	9.787	9.907
15	8.587	8.647	8.904	9.111	9.285	9.434	9.565	9.680
16	8.425	8.483	8.733	8.933	9.102	9.247	9.373	9.486
17	8.285	8.341	8.583	8.779	8.943	9.084	9.206	9.316
18	8.162	8.217	8.452	8.643	8.803	8.940	9.061	9.167
19	8.053	8.106	8.337	8.523	8.679	8.813	8.931	9.036
20	7.956	8.008	8.234	8.416	8.569	8.700	8.815	8.917
24	7.655	7.704	7.914	8.083	8.226	8.348	8.455	8.551
30	7.364	7.409	7.603	7.760	7.893	8.006	8.105	8.193
40	7.082	7.123	7.302	7.447	7.568	7.672	7.763	7.845
60	6.808	6.846	7.010	7.143	7.252	7.347	7.431	7.504
120	6.545	6.580	6.728	6.846	6.946	7.032	7.107	7.173
∞	6.291	6.322	6.454	6.561	6.649	6.725	6.792	6.850

TABLE B.5 (cont.): Critical Values of the q Distribution, for the Tukey Test

$\alpha = 0.001$

ν	k: 2	3	4	5	6	7	8	9	10
1	900.3	1351.	1643.	1856.	2022.	2158.	2272.	2370.	2455.
2	44.69	60.42	70.77	78.43	84.49	89.46	93.67	97.30	100.5
3	18.28	23.32	26.65	29.13	31.11	32.74	34.12	35.33	36.39
4	12.18	14.99	16.84	18.23	19.34	20.26	21.04	21.73	22.33
5	9.714	11.67	12.96	13.93	14.71	15.35	15.90	16.38	16.81
6	8.427	9.960	10.97	11.72	12.32	12.83	13.26	13.63	13.97
7	7.648	8.930	9.763	10.40	10.90	11.32	11.68	11.99	12.27
8	7.130	8.250	8.978	9.522	9.958	10.32	10.64	10.91	11.15
9	6.762	7.768	8.419	8.906	9.295	9.619	9.897	10.14	10.36
10	6.487	7.411	8.006	8.450	8.804	9.099	9.352	9.573	9.769
11	6.275	7.136	7.687	8.098	8.426	8.699	8.933	9.138	9.319
12	6.106	6.917	7.436	7.821	8.127	8.383	8.601	8.793	8.962
13	5.970	6.740	7.231	7.595	7.885	8.126	8.333	8.513	8.673
14	5.856	6.594	7.062	7.409	7.685	7.915	8.110	8.282	8.434
15	5.760	6.470	6.920	7.252	7.517	7.736	7.925	8.088	8.234
16	5.678	6.365	6.799	7.119	7.374	7.585	7.766	7.923	8.063
17	5.608	6.275	6.695	7.005	7.250	7.454	7.629	7.781	7.916
18	5.546	6.196	6.604	6.905	7.143	7.341	7.510	7.657	7.788
19	5.492	6.127	6.525	6.817	7.049	7.242	7.405	7.549	7.676
20	5.444	6.065	6.454	6.740	6.966	7.154	7.313	7.453	7.577
24	5.297	5.877	6.238	6.503	6.712	6.884	7.031	7.159	7.272
30	5.156	5.698	6.033	6.278	6.470	6.628	6.763	6.880	6.984
40	5.022	5.528	5.838	6.063	6.240	6.386	6.509	6.616	6.711
60	4.894	5.365	5.653	5.860	6.022	6.155	6.268	6.366	6.451
120	4.771	5.211	5.476	5.667	5.815	5.937	6.039	6.128	6.206
∞	4.654	5.063	5.309	5.484	5.619	5.730	5.823	5.903	5.973

ν	k: 11	12	13	14	15	16	17	18	19
1	2532.	2600.	2662.	2718.	2770.	2818.	2863.	2904.	2943.
2	103.3	105.9	108.2	110.4	112.3	114.2	115.9	117.4	118.9
3	37.34	38.20	38.98	39.69	40.35	40.97	41.54	42.07	42.58
4	22.87	23.36	23.81	24.21	24.59	24.94	25.27	25.58	25.87
5	17.18	17.53	17.85	18.13	18.41	18.66	18.89	19.10	19.31
6	14.27	14.54	14.79	15.01	15.22	15.42	15.60	15.78	15.94
7	12.52	12.74	12.95	13.14	13.32	13.48	13.64	13.78	13.92
8	11.36	11.56	11.74	11.91	12.06	12.21	12.34	12.47	12.59
9	10.55	10.73	10.89	11.03	11.18	11.30	11.42	11.54	11.64
10	9.946	10.11	10.25	10.39	10.52	10.64	10.75	10.85	10.95
11	9.482	9.630	9.766	9.892	10.01	10.12	10.22	10.31	10.41
12	9.115	9.254	9.381	9.498	9.606	9.707	9.802	9.891	9.975
13	8.817	8.948	9.068	9.178	9.281	9.376	9.466	9.550	9.629
14	8.571	8.696	8.809	8.914	9.012	9.103	9.188	9.267	9.343
15	8.365	8.483	8.592	8.693	8.786	8.872	8.954	9.030	9.102
16	8.189	8.303	8.407	8.504	8.593	8.676	8.755	8.828	8.897
17	8.037	8.148	8.248	8.342	8.427	8.508	8.583	8.654	8.720
18	7.906	8.012	8.110	8.199	8.283	8.361	8.434	8.502	8.567
19	7.790	7.893	7.988	8.075	8.156	8.232	8.303	8.369	8.432
20	7.688	7.788	7.880	7.966	8.044	8.118	8.186	8.251	8.312
24	7.374	7.467	7.551	7.629	7.701	7.768	7.831	7.890	7.946
30	7.077	7.162	7.239	7.310	7.375	7.437	7.494	7.548	7.599
40	6.796	6.872	6.942	7.007	7.067	7.122	7.174	7.223	7.269
60	6.528	6.598	6.661	6.720	6.774	6.824	6.871	6.914	6.956
120	6.276	6.339	6.396	6.448	6.496	6.542	6.583	6.623	6.660
∞	6.036	6.092	6.144	6.191	6.234	6.274	6.312	6.347	6.380

TABLE B.5 (cont.): Critical Values of the q Distribution, for the Tukey Test

$\alpha = 0.001$

ν	k: 20	22	24	26	28	30	32	34	36
1	2980.	3047.	3108.	3163.	3213.	3260.	3303.	3343.	3380.
2	120.3	122.9	125.2	127.3	129.3	131.0	132.7	134.2	135.7
3	43.05	43.92	44.70	45.42	46.07	46.68	47.24	47.77	48.26
4	26.14	26.65	27.10	27.51	27.89	28.24	28.57	28.88	29.16
5	19.51	19.86	20.19	20.48	20.75	21.01	21.24	21.46	21.66
6	16.09	16.38	16.64	16.87	17.08	17.28	17.47	17.64	17.81
7	14.04	14.29	14.50	14.70	14.88	15.05	15.20	15.35	15.49
8	12.70	12.91	13.09	13.26	13.42	13.57	13.71	13.84	13.96
9	11.75	11.93	12.10	12.25	12.39	12.53	12.65	12.77	12.87
10	11.03	11.20	11.36	11.50	11.63	11.75	11.87	11.97	12.07
11	10.49	10.65	10.79	10.92	11.04	11.16	11.26	11.35	11.45
12	10.06	10.20	10.34	10.46	10.57	10.68	10.78	10.87	10.96
13	9.704	9.843	9.969	10.09	10.19	10.29	10.39	10.47	10.55
14	9.414	9.546	9.666	9.776	9.878	9.972	10.06	10.14	10.22
15	9.170	9.296	9.411	9.517	9.613	9.703	9.788	9.867	9.940
16	8.963	9.084	9.194	9.295	9.388	9.475	9.556	9.631	9.702
17	8.784	8.900	9.007	9.104	9.194	9.277	9.355	9.429	9.497
18	8.628	8.741	8.844	8.938	9.025	9.106	9.181	9.251	9.318
19	8.491	8.601	8.701	8.792	8.876	8.955	9.028	9.096	9.161
20	8.370	8.477	8.574	8.663	8.745	8.821	8.892	8.959	9.021
24	7.999	8.097	8.185	8.267	8.342	8.411	8.476	8.537	8.594
30	7.647	7.735	7.816	7.890	7.958	8.021	8.080	8.135	8.188
40	7.312	7.393	7.466	7.533	7.594	7.651	7.704	7.754	7.801
60	6.995	7.067	7.133	7.193	7.248	7.299	7.347	7.392	7.433
120	6.695	6.760	6.818	6.872	6.921	6.966	7.008	7.048	7.085
∞	6.411	6.469	6.520	6.568	6.611	6.651	6.689	6.723	6.756

ν	k: 38	40	50	60	70	80	90	100
1	3415.	3448.	3589.	3701.	3794.	3873.	3941.	4002.
2	137.0	138.3	143.7	148.0	151.6	154.7	157.4	159.7
3	48.72	49.16	51.02	52.51	53.75	54.81	55.72	56.53
4	29.43	29.68	30.78	31.65	32.37	32.98	33.52	34.00
5	21.86	22.03	22.82	23.45	23.97	24.41	24.80	25.15
6	17.96	18.10	18.73	19.22	19.64	20.00	20.31	20.58
7	15.62	15.74	16.27	16.69	17.04	17.35	17.61	17.85
8	14.07	14.18	14.64	15.01	15.32	15.59	15.82	16.02
9	12.97	13.07	13.49	13.82	14.10	14.34	14.55	14.74
10	12.16	12.25	12.63	12.94	13.20	13.42	13.61	13.78
11	11.53	11.62	11.97	12.25	12.49	12.70	12.88	13.04
12	11.03	11.11	11.44	11.71	11.94	12.13	12.29	12.45
13	10.63	10.70	11.01	11.27	11.48	11.66	11.82	11.97
14	10.30	10.37	10.66	10.91	11.11	11.28	11.43	11.57
15	10.01	10.08	10.37	10.59	10.79	10.96	11.10	11.23
16	9.769	9.833	10.11	10.34	10.52	10.68	10.82	10.95
17	9.562	9.623	9.888	10.10	10.29	10.44	10.58	10.70
18	9.381	9.440	9.696	9.904	10.08	10.23	10.36	10.48
19	9.221	9.279	9.528	9.730	9.899	10.04	10.17	10.29
20	9.081	9.137	9.379	9.575	9.740	9.881	10.01	10.12
24	8.648	8.700	8.921	9.100	9.250	9.380	9.494	9.596
30	8.237	8.283	8.484	8.647	8.783	8.901	9.004	9.096
40	7.845	7.887	8.067	8.214	8.337	8.442	8.535	8.618
60	7.473	7.510	7.671	7.802	7.911	8.005	8.088	8.161
120	7.121	7.153	7.296	7.411	7.507	7.590	7.662	7.726
∞	6.787	6.816	6.941	7.041	7.124	7.196	7.259	7.314

Table B.5 is reprinted, with permission of the author, from the more extensive Table B.2 of H. L. Harter (1970).

Examples:

$$q_{0.05,24,3} = 5.532 \quad \text{and} \quad q_{0.01,20,5} = 5.294$$

If a critical value is needed for degrees of freedom not on this table, we may conservatively use the next lower degrees of freedom in the table. The required critical value may be estimated by harmonic interpolation. See Harter (1960) for further considerations of interpolation.

TABLE B.6: Critical Values of q' for the One-Tailed Dunnett's Test

	$\alpha = 0.05$								
ν	k : 2	3	4	5	6	7	8	9	10
5	2.02	2.44	2.68	2.85	2.98	3.08	3.16	3.24	3.30
6	1.94	2.34	2.56	2.71	2.83	2.92	3.00	3.07	3.12
7	1.89	2.27	2.48	2.62	2.73	2.82	2.89	2.95	3.01
8	1.86	2.22	2.42	2.55	2.66	2.74	2.81	2.87	2.92
9	1.83	2.18	2.37	2.50	2.60	2.68	2.75	2.81	2.86
10	1.81	2.15	2.34	2.47	2.56	2.64	2.70	2.76	2.81
11	1.80	2.13	2.31	2.44	2.53	2.60	2.67	2.72	2.77
12	1.78	2.11	2.29	2.41	2.50	2.58	2.64	2.69	2.74
13	1.77	2.09	2.27	2.39	2.48	2.55	2.61	2.66	2.71
14	1.76	2.08	2.25	2.37	2.46	2.53	2.59	2.64	2.69
15	1.75	2.07	2.24	2.36	2.44	2.51	2.57	2.62	2.67
16	1.75	2.06	2.23	2.34	2.43	2.50	2.56	2.61	2.65
17	1.74	2.05	2.22	2.33	2.42	2.49	2.54	2.59	2.64
18	1.73	2.04	2.21	2.32	2.41	2.48	2.53	2.58	2.62
19	1.73	2.03	2.20	2.31	2.40	2.47	2.52	2.57	2.61
20	1.72	2.03	2.19	2.30	2.39	2.46	2.51	2.56	2.60
24	1.71	2.01	2.17	2.28	2.36	2.43	2.48	2.53	2.57
30	1.70	1.99	2.15	2.25	2.33	2.40	2.45	2.50	2.54
40	1.68	1.97	2.13	2.23	2.31	2.37	2.42	2.47	2.51
60	1.67	1.95	2.10	2.21	2.28	2.35	2.39	2.44	2.48
120	1.66	1.93	2.08	2.18	2.26	2.32	2.37	2.41	2.45
∞	1.64	1.92	2.06	2.16	2.23	2.29	2.34	2.38	2.42
	$\alpha = 0.01$								
ν	k : 2	3	4	5	6	7	8	9	10
5	3.37	3.90	4.21	4.43	4.60	4.73	4.85	4.94	5.03
6	3.14	3.61	3.88	4.07	4.21	4.33	4.43	4.51	4.59
7	3.00	3.42	3.66	3.83	3.96	4.07	4.15	4.23	4.30
8	2.90	3.29	3.51	3.67	3.79	3.88	3.96	4.03	4.09
9	2.82	3.19	3.40	3.55	3.66	3.75	3.82	3.89	3.94
10	2.76	3.11	3.31	3.45	3.56	3.64	3.71	3.78	3.83
11	2.72	3.06	3.25	3.38	3.48	3.56	3.63	3.69	3.74
12	2.68	3.01	3.19	3.32	3.42	3.50	3.56	3.62	3.67
13	2.65	2.97	3.15	3.27	3.37	3.44	3.51	3.56	3.61
14	2.62	2.94	3.11	3.23	3.32	3.40	3.46	3.51	3.56
15	2.60	2.91	3.08	3.20	3.29	3.36	3.42	3.47	3.52
16	2.58	2.88	3.05	3.17	3.26	3.33	3.39	3.44	3.48
17	2.57	2.86	3.03	3.14	3.23	3.30	3.36	3.41	3.45
18	2.55	2.84	3.01	3.12	3.21	3.27	3.33	3.38	3.42
19	2.54	2.83	2.99	3.10	3.18	3.25	3.31	3.36	3.40
20	2.53	2.81	2.97	3.08	3.17	3.23	3.29	3.34	3.38
24	2.49	2.77	2.92	3.03	3.11	3.17	3.22	3.27	3.31
30	2.46	2.72	2.87	2.97	3.05	3.11	3.16	3.21	3.24
40	2.42	2.68	2.82	2.92	2.99	3.05	3.10	3.14	3.18
60	2.39	2.64	2.78	2.87	2.94	3.00	3.04	3.08	3.12
120	2.36	2.60	2.73	2.82	2.89	2.94	2.99	3.03	3.06
∞	2.33	2.56	2.68	2.77	2.84	2.89	2.93	2.97	3.00

Values in Table B.6 are reprinted, with the permission of the author ad publisher, from the tables of C. W. Dunnelt (1955, *J. Amer. Statist. Assoc.* 50: 1096–1121.)

Examples:

$$q'_{0.05(1),16,4} = 2.23 \quad \text{and} \quad q'_{0.01(1),24,3} = 2.77$$

If a critical value is required for degrees of freedom not on this table, we may conservatively use the critical value with the next lower degrees of freedom. Or, the critical value may be estimated by harmonic interpolation.

Values in Table B.7 are reprinted, with the permission of the author and editor, from the tables of C. W. Dunnett (1964, Biometrics 20: 482–491).

Examples:

$$q'_{0.05(2),30,5} = 2.58 \quad \text{and} \quad q'_{0.01(2),20,4} = 3.29$$

If a critical value is required for degrees of freedom not on this table, we may conservatively use the critical value with the next lower degrees of freedom. Or, the critical value may be estimated by harmonic interpolation.

TABLE B.7: Critical Values of q' for the Two-Tailed Dunnett's Test

	$\alpha = 0.05$													
v	k: 2	3	4	5	6	7	8	9	10	11	12	13	16	21
5	2.57	3.03	3.29	3.48	3.62	3.73	3.82	3.90	3.97	4.03	4.09	4.14	4.26	4.42
6	2.45	2.86	3.10	3.26	3.39	3.49	3.57	3.64	3.71	3.76	3.81	3.86	3.97	4.11
7	2.36	2.75	2.97	3.12	3.24	3.33	3.41	3.47	3.53	3.58	3.63	3.67	3.78	3.91
8	2.31	2.67	2.88	3.02	3.13	3.22	3.29	3.35	3.41	3.46	3.50	3.54	3.64	3.76
9	2.26	2.61	2.81	2.95	3.05	3.14	3.20	3.26	3.32	3.36	3.40	3.44	3.53	3.65
10	2.23	2.57	2.76	2.89	2.99	3.07	3.14	3.19	3.24	3.29	3.33	3.36	3.45	3.57
11	2.20	2.53	2.72	2.84	2.94	3.02	3.08	3.14	3.19	3.23	3.27	3.30	3.39	3.50
12	2.18	2.50	2.68	2.81	2.90	2.98	3.04	3.09	3.14	3.18	3.22	3.25	3.34	3.45
13	2.16	2.48	2.65	2.78	2.87	2.94	3.00	3.06	3.10	3.14	3.18	3.21	3.29	3.40
14	2.14	2.46	2.63	2.75	2.84	2.91	2.97	3.02	3.07	3.11	3.14	3.18	3.26	3.36
15	2.13	2.44	2.61	2.73	2.82	2.89	2.95	3.00	3.04	3.08	3.12	3.15	3.23	3.33
16	2.12	2.42	2.59	2.71	2.80	2.87	2.92	2.97	3.02	3.06	3.09	3.12	3.20	3.30
17	2.11	2.41	2.58	2.69	2.78	2.85	2.90	2.95	3.00	3.03	3.07	3.10	3.18	3.27
18	2.10	2.40	2.56	2.68	2.76	2.83	2.89	2.94	2.98	3.01	3.05	3.08	3.16	3.25
19	2.09	2.39	2.55	2.66	2.75	2.81	2.87	2.92	2.96	3.00	3.03	3.06	3.14	3.23
20	2.09	2.38	2.54	2.65	2.73	2.80	2.86	2.90	2.95	2.98	3.02	3.05	3.12	3.22
24	2.06	2.35	2.51	2.61	2.70	2.76	2.81	2.86	2.90	2.94	2.97	3.00	3.07	3.16
30	2.04	2.32	2.47	2.58	2.66	2.72	2.77	2.82	2.86	2.89	2.92	2.95	3.02	3.11
40	2.02	2.29	2.44	2.54	2.62	2.68	2.73	2.77	2.81	2.85	2.87	2.90	2.97	3.06
60	2.00	2.27	2.41	2.51	2.58	2.64	2.69	2.73	2.77	2.80	2.83	2.86	2.92	3.00
120	1.98	2.24	2.38	2.47	2.55	2.60	2.65	2.69	2.73	2.76	2.79	2.81	2.87	2.95
∞	1.96	2.21	2.35	2.44	2.51	2.57	2.61	2.65	2.69	2.72	2.74	2.77	2.83	2.91
	$\alpha = 0.01$													
v	k: 2	3	4	5	6	7	8	9	10	11	12	13	16	21
5	4.03	4.63	4.98	5.22	5.41	5.56	5.69	5.80	5.89	5.98	6.05	6.12	6.30	6.52
6	3.71	4.21	4.51	4.71	4.87	5.00	5.10	5.20	5.28	5.35	5.41	5.47	5.62	5.81
7	3.50	3.95	4.21	4.39	4.53	4.64	4.74	4.82	4.89	4.95	5.01	5.06	5.19	5.36
8	3.36	3.77	4.00	4.17	4.29	4.40	4.48	4.56	4.62	4.68	4.73	4.78	4.90	5.05
9	3.25	3.63	3.85	4.01	4.12	4.22	4.30	4.37	4.43	4.48	4.53	4.57	4.68	4.82
10	3.17	3.53	3.74	3.88	3.99	4.08	4.16	4.22	4.28	4.33	4.37	4.42	4.52	4.65
11	3.11	3.45	3.65	3.79	3.89	3.98	4.05	4.11	4.16	4.21	4.25	4.29	4.30	4.52
12	3.05	3.39	3.58	3.71	3.81	3.89	3.96	4.02	4.07	4.12	4.16	4.19	4.29	4.41
13	3.01	3.33	3.52	3.65	3.74	3.82	3.89	3.94	3.99	4.04	4.08	4.11	4.20	4.32
14	2.98	3.29	3.47	3.59	3.69	3.76	3.83	3.88	3.93	3.97	4.01	4.05	4.13	4.24
15	2.95	3.25	3.43	3.55	3.64	3.71	3.78	3.83	3.88	3.92	3.95	3.99	4.07	4.18
16	2.92	3.22	3.39	3.51	3.60	3.67	3.73	3.78	3.83	3.87	3.91	3.94	4.02	4.13
17	2.90	3.19	3.36	3.47	3.56	3.63	3.69	3.74	3.79	3.83	3.86	3.90	3.98	4.08
18	2.88	3.17	3.33	3.44	3.53	3.60	3.66	3.71	3.75	3.79	3.83	3.86	3.94	4.04
19	2.86	3.15	3.31	3.42	3.50	3.57	3.63	3.68	3.72	3.76	3.79	3.83	3.90	4.00
20	2.85	3.13	3.29	3.40	3.48	3.55	3.60	3.65	3.69	3.73	3.77	3.80	3.87	3.97
24	2.80	3.07	3.22	3.32	3.40	3.47	3.52	3.57	3.61	3.64	3.68	3.70	3.78	3.87
30	2.75	3.01	3.15	3.25	3.33	3.39	3.44	3.49	3.52	3.56	3.59	3.62	3.69	3.78
40	2.70	2.95	3.09	3.19	3.26	3.32	3.37	3.41	3.44	3.48	3.51	3.53	3.60	3.68
60	2.66	2.90	3.03	3.12	3.19	3.25	3.29	3.33	3.37	3.40	3.42	3.45	3.51	3.59
120	2.62	2.85	2.97	3.06	3.12	3.18	3.22	3.26	3.29	3.32	3.35	3.37	3.43	3.51
∞	2.58	2.79	2.92	3.00	3.06	3.11	3.15	3.19	3.22	3.25	3.27	3.29	3.35	3.42

TABLE B.8: Critical Values of d_{max} for the Kolmogorov-Smirnov Goodness-of-Fit for Discrete or Grouped Data

		$\alpha(2)$: < 0.50	0.20	0.10	0.05	0.02	0.01	0.005	0.002	0.001
k	n	$\alpha(1)$: < 0.25	0.10	0.05	0.025	0.01	0.005	0.0025	0.001	0.0005
3	3	2	2	2	3	3	3	3	3	3
3	6	2	3	3	3	4	4	4	5	5
3	9	2	3	4	4	4	5	5	5	6
3	12	3	4	4	4	5	5	6	6	7
3	15	3	4	4	5	6	6	6	7	7
3	18	3	4	5	5	6	6	7	7	8
3	21	3	4	5	6	6	7	7	8	8
3	24	3	5	5	6	7	7	8	8	9
3	27	3	5	6	6	7	8	8	9	9
3	30	4	5	6	7	8	8	9	9	10
3	33	4	5	6	7	8	8	9	10	10
3	35	4	5	6	7	8	9	9	10	11
3	39	4	6	7	7	8	9	10	11	11
3	42	4	6	7	8	9	9	10	11	12
3	45	4	6	7	8	9	10	10	11	12
3	48	4	6	7	8	9	10	11	12	12
3	51	4	6	7	8	10	10	11	12	13
3	54	4	6	8	9	10	11	11	12	13
3	57	5	7	8	9	10	11	12	13	13
3	60	5	7	8	9	10	11	12	13	14
3	63	5	7	8	9	10	11	12	13	14
3	66	5	7	8	9	10	11	12	13	14
3	69	5	7	8	9	11	12	13	14	14
3	72	5	7	8	9	11	12	13	14	15
3	75	4	7	8	10	11	12	13	14	15
3	78	5	7	9	10	11	12	13	14	15
3	81	5	7	9	10	11	13	13	15	16
3	84	5	7	9	10	12	13	14	15	16
3	87	4	7	9	10	12	13	14	15	16
3	90	4	7	9	10	12	13	14	15	16
3	93	4	7	9	11	12	13	14	15	16
3	96	4	7	9	10	12	13	14	15	16
3	99	4	7	9	10	12	13	14	15	16
4	4	2	2	3	3	3	3	4	4	4
4	8	2	3	4	4	4	5	5	5	5
4	12	3	4	4	5	5	6	6	6	7
4	16	3	4	5	5	6	6	7	7	8
4	20	3	4	5	6	6	7	7	8	8
4	24	4	5	6	6	7	8	8	9	9
4	28	4	5	6	7	7	8	9	9	10
4	32	4	5	6	7	8	9	9	10	10
4	36	4	6	7	7	8	9	10	10	11
4	40	4	6	7	8	9	9	10	11	12
4	44	5	6	7	8	9	10	11	11	12
4	48	5	6	7	8	10	10	11	12	13
4	52	5	7	8	9	10	11	11	12	13
4	56	5	7	8	9	10	11	12	13	13
4	60	5	7	8	9	10	11	12	13	14
4	64	5	7	8	9	11	12	13	14	14
4	68	5	7	9	10	11	12	13	14	15
4	72	5	7	9	10	11	12	13	14	15
4	76	5	8	9	10	11	12	13	14	15
4	80	5	8	9	10	11	12	13	15	15
4	84	5	7	9	10	12	13	14	15	16
4	88	5	7	9	10	12	13	14	15	16
4	92	5	7	9	10	12	13	14	16	16
4	96	5	7	9	10	12	13	14	16	17
4	100	5	8	9	11	12	13	14	16	17
5	5	2	3	3	3	4	4	4	4	4
5	10	3	3	4	4	5	5	5	6	6

TABLE B.8 (cont.): Critical Values of d_{max} for the Kolmogorov-Smirnov Goodness-of-Fit for Discrete or Grouped Data

k	n	$\alpha(2)$: < 0.50 $\alpha(1)$: < 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
5	15	3	4	5	5	6	6	7	7	7
5	20	4	5	5	6	7	7	7	8	8
5	25	4	5	6	6	7	8	8	9	9
5	30	4	5	6	7	8	8	9	10	10
5	35	4	6	7	7	8	9	10	10	11
5	40	5	6	7	8	9	10	10	11	12
5	45	5	6	7	8	9	10	11	12	12
5	50	5	7	8	9	10	11	11	12	13
5	55	5	7	8	9	10	11	12	13	14
5	60	5	7	8	9	11	12	12	13	14
5	65	5	7	9	10	11	12	13	14	14
5	70	6	8	9	10	11	12	13	14	15
5	75	6	8	9	10	12	13	14	15	15
5	80	5	8	9	11	12	13	14	15	16
5	85	5	8	9	11	12	13	14	15	16
5	90	6	8	10	11	12	13	14	15	16
5	95	6	8	9	11	12	13	14	16	17
5	100	5	8	9	11	12	14	15	16	17
6	6	2	3	3	4	4	4	4	5	5
6	12	3	4	4	5	5	6	6	6	7
6	18	3	4	5	6	6	7	7	8	8
6	24	4	5	6	6	7	8	8	9	9
6	30	4	6	6	7	8	9	9	10	10
6	36	5	6	7	8	9	9	10	11	11
6	42	5	6	7	8	9	10	11	11	12
6	48	5	7	8	9	10	11	11	12	13
6	54	5	7	8	9	10	11	12	13	14
6	60	6	7	9	10	11	12	13	13	14
6	66	6	8	9	10	11	12	13	14	15
6	72	6	8	9	10	12	13	13	14	15
6	78	6	8	9	11	12	13	14	15	16
6	84	6	8	9	11	12	13	14	15	16
6	90	5	8	10	11	13	14	15	16	16
6	96	6	8	10	11	13	14	15	16	17
7	7	3	3	4	4	4	5	5	5	5
7	14	3	4	5	5	6	6	7	7	7
7	21	4	5	6	6	7	7	8	8	9
7	28	4	5	6	7	8	8	9	10	10
7	35	5	6	7	8	9	9	10	11	11
7	42	5	6	7	8	9	10	11	12	12
7	49	5	7	8	9	10	11	12	12	13
7	56	6	7	8	9	11	12	12	13	14
7	63	6	8	9	10	11	12	13	14	15
7	70	6	8	9	10	12	13	13	15	15
7	77	6	8	9	11	12	13	14	15	16
7	84	6	8	10	12	12	13	14	15	16
7	91	6	8	10	11	13	14	15	16	17
7	98	6	8	10	11	13	14	15	16	17
8	8	3	3	4	4	5	5	5	5	6
8	16	3	4	5	6	6	7	7	7	8
8	24	4	5	6	7	7	8	8	9	9
8	32	4	6	7	7	8	9	10	10	11
8	40	5	6	7	8	9	10	11	11	12
8	48	5	7	8	9	10	11	12	12	13
8	56	6	7	9	10	11	12	12	13	14
8	64	6	8	9	10	11	12	13	14	15
8	72	6	8	9	11	12	13	14	15	15
8	80	6	8	10	11	12	13	14	15	16
8	88	6	8	10	11	13	14	15	16	17
8	95	6	9	10	11	13	14	15	16	17

TABLE B.8 (cont.): Critical Values of d_{max} for the Kolmogorov-Smirnov Goodness-of-Fit for Discrete or Grouped Data

k	n	$\alpha(2)$: < 0.50 $\alpha(1)$: < 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
9	9	3	4	4	4	5	5	5	6	6
9	18	4	5	5	6	7	7	7	8	8
9	27	4	6	6	7	8	8	9	10	10
9	36	5	6	7	8	9	10	10	11	11
9	45	5	7	8	9	10	11	11	12	13
9	54	6	7	9	10	11	11	12	13	14
9	63	6	8	9	10	11	12	13	14	15
9	72	6	8	10	11	12	13	14	15	16
9	81	6	8	10	11	13	13	14	15	16
9	90	6	9	10	11	13	14	15	16	17
9	99	6	9	10	12	13	14	15	17	18
10	10	3	4	4	5	5	5	6	6	6
10	20	4	5	6	6	7	7	8	8	9
10	30	4	6	7	7	8	9	9	10	11
10	40	5	7	8	8	9	10	11	11	12
10	50	6	7	8	9	10	11	12	13	13
10	60	6	8	9	10	11	12	13	14	15
10	70	6	8	10	11	12	13	14	15	15
10	80	6	9	10	11	13	14	14	16	16
10	90	6	9	10	12	13	14	15	16	17
10	100	6	9	10	12	13	14	15	17	18
11	11	3	4	4	5	5	6	6	6	7
11	22	4	5	6	6	7	8	8	9	9
11	33	5	6	7	8	9	9	10	11	11
11	44	5	7	8	9	10	11	11	12	13
11	55	6	8	9	10	11	12	12	13	14
11	66	6	8	9	11	12	13	14	15	15
11	77	6	9	10	11	12	13	14	15	16
11	88	6	9	10	12	13	14	15	16	17
11	99	6	9	10	12	13	14	16	17	18
12	12	3	4	5	5	6	6	6	7	7
12	24	4	5	6	7	8	8	9	9	10
12	36	5	6	7	8	9	10	10	11	12
12	48	6	7	8	9	10	11	12	13	13
12	60	6	8	9	10	11	12	13	14	15
12	72	6	9	10	11	12	13	14	15	16
12	84	7	9	10	11	13	14	15	16	17
12	96	7	9	10	12	13	14	15	17	18
13	13	3	4	5	5	6	6	6	7	7
13	26	4	6	6	7	8	8	9	10	10
13	39	5	7	8	8	9	10	11	11	12
13	52	6	8	9	10	11	12	12	13	14
13	65	6	8	9	11	12	13	14	15	15
13	78	7	9	10	11	13	14	14	16	16
13	91	7	9	11	12	13	14	15	16	17
14	14	3	4	5	5	6	6	7	7	7
14	28	5	6	7	7	8	9	9	10	10
14	42	5	7	8	9	10	10	11	12	12
14	56	6	8	9	10	11	12	13	14	14
14	70	7	8	10	11	12	13	14	15	16
14	84	7	9	10	12	13	14	15	16	17
14	98	7	9	11	12	13	15	16	17	18
15	15	4	4	5	6	6	7	7	7	8
15	30	5	6	7	8	8	9	10	10	11
14	45	6	7	8	9	10	11	12	12	13
15	60	6	8	9	10	12	12	13	14	15
15	75	7	9	10	11	13	14	14	15	16
15	90	7	9	11	12	13	14	15	16	17
16	16	4	5	5	6	6	7	7	8	8
16	32	5	6	7	8	9	9	10	11	11

TABLE B.8 (cont.): Critical Values of d_{max} for the Kolmogorov-Smirnov Goodness-of-Fit for Discrete or Grouped Data

k	n	$\alpha(2)$: < 0.50 $\alpha(1)$: < 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
16	48	6	7	8	9	10	11	12	13	13
16	64	6	8	10	11	12	13	14	15	15
16	80	7	9	10	11	13	14	15	16	17
16	96	7	9	11	12	14	15	16	17	18
17	17	4	5	5	6	7	7	7	8	8
17	34	5	6	7	8	9	10	10	11	11
17	51	6	8	9	10	11	12	12	13	14
17	68	7	9	10	11	12	13	14	15	16
17	85	7	9	10	12	13	14	15	16	17
18	18	4	5	6	6	7	7	8	8	8
18	36	5	7	7	8	9	10	10	11	12
18	54	6	8	9	10	11	12	13	14	14
18	72	7	9	10	11	13	13	14	15	16
18	90	7	9	11	12	13	14	15	17	17
19	19	4	5	6	6	7	7	8	8	9
19	38	5	7	8	8	9	10	11	11	12
19	57	6	8	9	10	11	12	13	14	15
19	76	7	9	10	11	13	14	15	16	16
19	95	7	9	11	12	14	15	16	17	18
20	20	4	5	6	6	7	8	8	9	9
20	40	5	7	8	9	10	10	11	12	12
20	60	6	8	9	10	12	13	13	14	15
20	80	7	9	10	12	13	14	15	16	17
20	100	7	9	11	12	14	15	16	17	18
21	21	4	5	6	7	7	8	8	9	9
21	42	5	7	8	9	10	11	11	12	13
21	63	7	8	10	11	12	13	14	15	15
21	84	7	9	11	12	13	14	15	16	17
22	22	4	5	6	7	7	8	8	9	9
22	44	6	7	8	9	10	11	12	12	13
22	66	7	9	10	11	12	13	14	15	16
22	88	7	9	11	12	13	15	15	17	17
23	23	4	5	6	7	8	8	9	9	9
23	46	6	7	8	9	10	11	12	13	13
23	69	7	9	10	11	12	13	14	15	16
23	92	7	9	11	12	14	15	16	17	18
24	24	4	6	6	7	8	8	9	9	10
24	48	6	8	9	10	11	11	12	13	14
24	72	7	9	10	11	13	14	14	16	16
24	96	7	10	11	12	14	15	16	17	18
25	25	4	6	6	7	8	8	9	10	10
25	50	6	8	9	10	11	12	12	13	14
25	75	7	9	10	11	13	14	15	16	16
25	100	7	10	11	12	14	15	16	17	18
26	26	5	6	7	7	8	9	9	10	10
26	52	6	8	9	10	11	12	13	13	14
26	78	7	9	11	12	13	14	15	16	17
27	27	5	6	7	7	8	9	9	10	10
27	54	6	8	9	10	11	12	13	14	14
27	81	7	9	11	12	13	14	15	16	17
28	28	5	6	7	7	8	9	9	10	11
28	56	6	8	9	10	11	12	13	14	15
28	84	7	9	11	12	13	14	15	16	17
29	29	5	6	7	8	8	9	10	10	11
29	58	6	8	9	10	12	12	13	14	15
29	87	7	10	11	12	14	15	16	17	17
30	30	5	6	7	8	9	9	10	10	11
30	60	7	8	10	11	12	13	13	14	15
30	90	7	9	11	12	14	15	16	17	18
31	31	5	6	7	8	9	9	10	11	11

TABLE B.8 (cont.): Critical Values of d_{max} for the Kolmogorov-Smirnov Goodness-of-Fit for Discrete or Grouped Data

k	n	$\alpha(2)$: < 0.50	0.20	0.10	0.05	0.02	0.01	0.005	0.002	0.001
		$\alpha(1)$: < 0.25	0.10	0.05	0.025	0.01	0.005	0.0025	0.001	0.0005
31	62	7	9	10	11	12	13	14	15	15
31	93	7	9	11	12	14	15	16	17	18
32	32	5	6	7	8	9	9	10	11	11
32	64	7	9	10	11	12	13	14	15	16
32	96	7	10	11	12	14	15	16	17	18
33	33	5	6	7	8	9	10	10	11	11
33	66	7	9	10	11	12	13	14	15	16
33	99	7	10	11	13	14	15	16	17	18
34	34	5	7	7	8	9	10	10	11	12
34	68	7	9	10	11	13	13	14	15	16
35	35	5	7	8	8	9	10	11	11	12
35	70	7	9	10	11	13	14	14	16	16
36	36	5	7	8	8	9	10	11	11	12
36	72	7	9	10	11	13	14	15	16	16
37	37	5	7	8	9	10	10	11	12	12
37	74	7	9	11	12	13	14	15	16	17
38	38	5	7	8	9	10	10	11	12	12
38	76	7	9	11	12	13	14	15	16	17
39	39	6	7	8	9	10	10	11	12	12
39	78	7	9	11	12	13	14	15	16	17
40	40	6	7	8	9	10	11	11	12	13
40	80	7	9	11	12	13	14	15	16	17
41	41	6	7	8	9	10	11	11	12	13
41	82	7	10	11	12	13	14	15	16	17
42	42	6	7	8	9	10	11	11	12	13
42	84	7	10	11	12	14	15	15	17	17
43	43	6	7	8	9	10	11	12	12	13
43	86	8	10	11	12	13	15	16	17	18
44	44	6	7	8	9	10	11	12	13	13
44	88	7	10	11	12	14	15	16	17	18
45	45	6	8	9	9	10	11	12	13	13
45	90	7	10	11	12	14	15	16	17	18
46	46	6	8	9	10	11	11	12	13	13
46	92	7	10	11	13	14	15	16	17	18
47	47	6	8	9	10	11	11	12	13	14
47	94	8	10	11	13	14	15	16	17	18
48	48	6	8	9	10	11	12	12	13	14
48	96	7	10	11	13	14	15	16	18	18
49	49	6	8	9	10	11	12	12	13	14
49	98	8	10	11	13	14	15	16	18	19
50	50	6	8	9	10	11	12	13	13	14
50	100	7	10	11	13	14	15	16	18	19

These critical values were determined by the method used in Pettitt and Stephens (1977) by modifying a computer program kindly provided by A. N. Pettitt.

Examples:

$$(d_{max})_{0.05(2),30,90} = 11 \quad \text{and} \quad (d_{max})_{0.01(1),25,75} = 13$$

Appendix Table B.8 is applicable when all expected frequencies are equal; it also works well with expected frequencies that are slightly to moderately unequal (Pettitt and Stephens 1977).

Note: The values of d_{max} shown have probabilities slightly less than their column headings. Therefore, for example, $0.02 < P(d_{max} = 12, \text{ for } k = 30, \text{ and } n = 90) < 0.05$.

TABLE B.9: Critical Values of D for the Kolmogorov-Smirnov Goodness-of-Fit Test for Continuous Distributions

n	$\alpha(2)$: < 0.50 $\alpha(1)$: < 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	0.75000	0.90000	0.95000	0.97500	0.99000	0.99500	0.99750	0.99900	0.99950
2	0.50000	0.68377	0.77639	0.84189	0.90000	0.92929	0.95000	0.96838	0.97764
3	0.43529	0.56481	0.63604	0.70760	0.78456	0.82900	0.86428	0.90000	0.92063
4	0.38209	0.49265	0.56522	0.62394	0.68887	0.73424	0.77639	0.82217	0.85047
5	0.34319	0.44698	0.50945	0.56328	0.62718	0.66853	0.70543	0.75000	0.78137
6	0.31447	0.41037	0.46799	0.51926	0.57741	0.61661	0.65287	0.69571	0.72479
7	0.29312	0.38148	0.43607	0.48342	0.53844	0.57581	0.60975	0.65071	0.67930
8	0.27567	0.35831	0.40962	0.45427	0.50654	0.54179	0.57429	0.61368	0.64098
9	0.26082	0.33910	0.38746	0.43001	0.47960	0.51332	0.54443	0.58210	0.60846
10	0.24809	0.32260	0.36866	0.40925	0.45662	0.48893	0.51872	0.55500	0.58042
11	0.23709	0.30829	0.35242	0.39122	0.43670	0.46770	0.49639	0.53135	0.55588
12	0.22748	0.29577	0.33815	0.37543	0.41918	0.44905	0.47672	0.51047	0.53422
13	0.21901	0.28470	0.32549	0.36143	0.40362	0.43247	0.45921	0.49189	0.51490
14	0.21146	0.27481	0.31417	0.34890	0.38970	0.41762	0.44352	0.47520	0.49753
15	0.20465	0.26589	0.30397	0.33760	0.37713	0.40420	0.42934	0.46011	0.48182
16	0.19844	0.25778	0.29472	0.32733	0.36571	0.39201	0.41644	0.44637	0.46750
17	0.19277	0.25039	0.28627	0.31796	0.35528	0.38086	0.40464	0.43380	0.45440
18	0.18757	0.24360	0.27851	0.30936	0.34569	0.37062	0.39380	0.42224	0.44234
19	0.18277	0.23735	0.27136	0.30143	0.33685	0.36117	0.38379	0.41156	0.43119
20	0.17833	0.23156	0.26473	0.29408	0.32866	0.35241	0.37451	0.40165	0.42085
21	0.17421	0.22617	0.25858	0.28724	0.32104	0.34426	0.36588	0.39243	0.41122
22	0.17036	0.22115	0.25283	0.28087	0.31394	0.33666	0.35782	0.38382	0.40223
23	0.16676	0.21646	0.24746	0.27490	0.30728	0.32954	0.35027	0.37575	0.39380
24	0.16338	0.21205	0.24242	0.26931	0.30104	0.32286	0.34318	0.36817	0.38588
25	0.16021	0.20790	0.23768	0.26404	0.29516	0.31657	0.33651	0.36104	0.37843
26	0.15721	0.20399	0.23320	0.25908	0.28962	0.31063	0.33022	0.35431	0.37139
27	0.15437	0.20030	0.22898	0.25438	0.28438	0.30502	0.32426	0.34794	0.36473
28	0.15169	0.19680	0.22497	0.24993	0.27942	0.29971	0.31862	0.34190	0.35842
29	0.14914	0.19348	0.22117	0.24571	0.27471	0.29466	0.31327	0.33617	0.35242
30	0.14672	0.19032	0.21756	0.24170	0.27023	0.28986	0.30818	0.33072	0.34672
31	0.14442	0.18732	0.21412	0.23788	0.26596	0.28529	0.30333	0.32553	0.34129
32	0.14222	0.18445	0.21085	0.23424	0.26189	0.28094	0.29870	0.32058	0.33611
33	0.14012	0.18171	0.20771	0.23076	0.25801	0.27677	0.29428	0.31584	0.33115
34	0.13811	0.17909	0.20472	0.22743	0.25429	0.27279	0.29005	0.31131	0.32641
35	0.13618	0.17659	0.20185	0.22425	0.25073	0.26897	0.28600	0.30697	0.32187
36	0.13434	0.17418	0.19910	0.22119	0.24732	0.26532	0.28211	0.30281	0.31751
37	0.13257	0.17188	0.19646	0.21826	0.24404	0.26180	0.27838	0.29882	0.31333
38	0.13086	0.16966	0.19392	0.21544	0.24089	0.25843	0.27480	0.29498	0.30931
39	0.12923	0.16753	0.19148	0.21273	0.23786	0.25518	0.27135	0.29128	0.30544
40	0.12765	0.16547	0.18913	0.21012	0.23494	0.25205	0.26803	0.28772	0.30171
41	0.12613	0.16349	0.18687	0.20760	0.23213	0.24904	0.26482	0.28429	0.29811
42	0.12466	0.16158	0.18468	0.20517	0.22941	0.24613	0.26173	0.28097	0.29465
43	0.12325	0.15974	0.18257	0.20283	0.22679	0.24332	0.25875	0.27778	0.29130
44	0.12188	0.15796	0.18053	0.20056	0.22426	0.24060	0.25587	0.27468	0.28806
45	0.12056	0.15623	0.17856	0.19837	0.22181	0.23798	0.25308	0.27169	0.28493
46	0.11927	0.15457	0.17665	0.19625	0.21944	0.23544	0.25038	0.26880	0.28190
47	0.11803	0.15295	0.17481	0.19420	0.21715	0.23298	0.24776	0.26600	0.27896
48	0.11683	0.15139	0.17301	0.19221	0.21493	0.23059	0.24523	0.26328	0.27611
49	0.11567	0.14987	0.17128	0.19028	0.21277	0.22828	0.24277	0.26065	0.27335
50	0.11453	0.14840	0.16959	0.18841	0.21068	0.22604	0.24039	0.25809	0.27067
51	0.11344	0.14697	0.16796	0.18659	0.20864	0.22386	0.23807	0.25561	0.26807
52	0.11237	0.14558	0.16637	0.18482	0.20667	0.22174	0.23582	0.25319	0.26555
53	0.11133	0.14423	0.16483	0.18311	0.20475	0.21968	0.23364	0.25085	0.26309
54	0.11032	0.14292	0.16332	0.18144	0.20289	0.21768	0.23151	0.24857	0.26070
55	0.10934	0.14164	0.16186	0.17981	0.20107	0.21574	0.22944	0.24635	0.25837
56	0.10839	0.14040	0.16044	0.17823	0.19930	0.21384	0.22742	0.24419	0.25611
57	0.10746	0.13919	0.15906	0.17669	0.19758	0.21199	0.22546	0.24208	0.25390
58	0.10655	0.13801	0.15771	0.17519	0.19590	0.21020	0.22355	0.24003	0.25175
59	0.10566	0.13686	0.15639	0.17373	0.19427	0.20844	0.22169	0.23803	0.24966
60	0.10480	0.13573	0.15511	0.17231	0.19267	0.20673	0.21987	0.23608	0.24761
61	0.10396	0.13464	0.15385	0.17091	0.19112	0.20506	0.21809	0.23418	0.24562
62	0.10314	0.13357	0.15263	0.16956	0.18960	0.20343	0.21636	0.23232	0.24367
63	0.10234	0.13253	0.15144	0.16823	0.18812	0.20184	0.21467	0.23051	0.24177

TABLE B.9 (cont.): Critical Values of D for the Kolmogorov-Smirnov Goodness-of-Fit Test for Continuous Distributions

n	$\alpha(2)$: < 0.50 $\alpha(1)$: < 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
64	0.10155	0.13151	0.15027	0.16693	0.18667	0.20029	0.21302	0.22873	0.23991
65	0.10079	0.13052	0.14913	0.16567	0.18525	0.19877	0.21141	0.22700	0.23810
66	0.10004	0.12954	0.14802	0.16443	0.18387	0.19729	0.20983	0.22531	0.23633
67	0.09931	0.12859	0.14693	0.16322	0.18252	0.19584	0.20829	0.22365	0.23459
68	0.09859	0.12766	0.14587	0.16204	0.18119	0.19442	0.20678	0.22204	0.23289
69	0.09789	0.12675	0.14483	0.16088	0.17990	0.19303	0.20530	0.22045	0.23123
70	0.09721	0.12586	0.14381	0.15975	0.17863	0.19167	0.20386	0.21890	0.22961
71	0.09653	0.12499	0.14281	0.15864	0.17739	0.19034	0.20244	0.21738	0.22802
72	0.09588	0.12413	0.14183	0.15755	0.17618	0.18903	0.20105	0.21589	0.22646
73	0.09523	0.12329	0.14087	0.15649	0.17499	0.18776	0.19970	0.21444	0.22493
74	0.09460	0.12247	0.13993	0.15544	0.17382	0.18650	0.19837	0.21301	0.22343
75	0.09398	0.12167	0.13901	0.15442	0.17268	0.18528	0.19706	0.21161	0.22196
76	0.09338	0.12088	0.13811	0.15342	0.17155	0.18408	0.19578	0.21024	0.22053
77	0.09278	0.12011	0.13723	0.15244	0.17045	0.18290	0.19453	0.20889	0.21912
78	0.09220	0.11935	0.13636	0.15147	0.16938	0.18174	0.19330	0.20757	0.21773
79	0.09162	0.11860	0.13551	0.15052	0.16832	0.18060	0.19209	0.20628	0.21637
80	0.09106	0.11787	0.13467	0.14960	0.16728	0.17949	0.19091	0.20501	0.21504
81	0.09051	0.11716	0.13385	0.14868	0.16626	0.17840	0.18974	0.20376	0.21373
82	0.08997	0.11645	0.13305	0.14779	0.16526	0.17732	0.18860	0.20253	0.21245
83	0.08944	0.11576	0.13226	0.14691	0.16428	0.17627	0.18748	0.20133	0.21119
84	0.08891	0.11508	0.13148	0.14605	0.16331	0.17523	0.18638	0.20015	0.20995
85	0.08840	0.11442	0.13072	0.14520	0.16236	0.17421	0.18530	0.19898	0.20873
86	0.08790	0.11376	0.12997	0.14437	0.16143	0.17321	0.18423	0.19784	0.20753
87	0.08740	0.11311	0.12923	0.14355	0.16051	0.17223	0.18319	0.19672	0.20635
88	0.08691	0.11248	0.12850	0.14274	0.15961	0.17126	0.18216	0.19562	0.20520
89	0.08643	0.11186	0.12779	0.14195	0.15873	0.17031	0.18115	0.19453	0.20406
90	0.08596	0.11125	0.12709	0.14117	0.15786	0.16938	0.18016	0.19347	0.20294
91	0.08550	0.11064	0.12640	0.14040	0.15700	0.16846	0.17918	0.19242	0.20184
92	0.08504	0.11005	0.12572	0.13965	0.15616	0.16755	0.17822	0.19138	0.20076
93	0.08459	0.10947	0.12506	0.13891	0.15533	0.16666	0.17727	0.19037	0.19969
94	0.08415	0.10889	0.12440	0.13818	0.15451	0.16579	0.17634	0.18937	0.19865
95	0.08371	0.10833	0.12375	0.13746	0.15371	0.16493	0.17542	0.18838	0.19761
96	0.08328	0.10777	0.12312	0.13675	0.15291	0.16408	0.17452	0.18741	0.19660
97	0.08286	0.10722	0.12249	0.13606	0.15214	0.16324	0.17363	0.18646	0.19560
98	0.08245	0.10668	0.12187	0.13537	0.15137	0.16242	0.17275	0.18552	0.19461
99	0.08204	0.10615	0.12126	0.13469	0.15061	0.16162	0.17189	0.18460	0.19364
100	0.08163	0.10563	0.12067	0.13403	0.14987	0.16081	0.17104	0.18368	0.19268
102	0.08084	0.10460	0.11949	0.13273	0.14841	0.15925	0.16938	0.18190	0.19081
104	0.08008	0.10361	0.11836	0.13146	0.14700	0.15773	0.16777	0.18017	0.18900
106	0.07933	0.10264	0.11725	0.13023	0.14562	0.15625	0.16620	0.17848	0.18723
108	0.07861	0.10170	0.11618	0.12904	0.14429	0.15482	0.16467	0.17685	0.18551
110	0.07790	0.10079	0.11513	0.12787	0.14299	0.15342	0.16319	0.17525	0.18384
112	0.07722	0.09990	0.11411	0.12674	0.14172	0.15207	0.16174	0.17370	0.18222
114	0.07655	0.09903	0.11312	0.12564	0.14049	0.15074	0.16034	0.17219	0.18063
116	0.07590	0.09818	0.11215	0.12457	0.13929	0.14945	0.15897	0.17072	0.17909
118	0.07527	0.09736	0.11121	0.12352	0.13812	0.14820	0.15763	0.16929	0.17759
120	0.07465	0.09656	0.11029	0.12250	0.13697	0.14697	0.15633	0.16789	0.17612
122	0.07404	0.09577	0.10940	0.12150	0.13586	0.14578	0.15506	0.16652	0.17469
124	0.07345	0.09501	0.10852	0.12053	0.13477	0.14461	0.15382	0.16519	0.17329
126	0.07288	0.09426	0.10767	0.11958	0.13371	0.14347	0.15261	0.16389	0.17193
128	0.07232	0.09353	0.10684	0.11866	0.13268	0.14236	0.15142	0.16262	0.17060
130	0.07177	0.09282	0.10602	0.11775	0.13166	0.14128	0.15027	0.16138	0.16930
132	0.07123	0.09213	0.10523	0.11687	0.13068	0.14021	0.14914	0.16017	0.16802
134	0.07071	0.09144	0.10445	0.11600	0.12971	0.13918	0.14804	0.15898	0.16678
136	0.07019	0.09078	0.10369	0.11516	0.12876	0.13816	0.14696	0.15782	0.16556
138	0.06969	0.09013	0.10294	0.11433	0.12784	0.13717	0.14590	0.15669	0.16437
140	0.06920	0.08949	0.10221	0.11352	0.12693	0.13620	0.14487	0.15558	0.16321
142	0.06872	0.08887	0.10150	0.11273	0.12604	0.13524	0.14385	0.15449	0.16207
144	0.06825	0.08826	0.10080	0.11195	0.12517	0.13431	0.14286	0.15343	0.16095
146	0.06778	0.08766	0.10012	0.11119	0.12432	0.13340	0.14189	0.15238	0.15986
148	0.06733	0.08707	0.09944	0.11044	0.12349	0.13250	0.14094	0.15136	0.15879
150	0.06689	0.8650	0.09879	0.10971	0.12267	0.13163	0.14001	0.15036	0.15774

TABLE B.9 (cont.): Critical Values of D for the Kolmogorov-Smirnov Goodness-of-Fit Test for Continuous Distributions

n	$\alpha(2)$: < 0.50 $\alpha(1)$: < 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
152	0.06646	0.08593	0.09814	0.10900	0.12187	0.13077	0.13909	0.14938	0.15671
154	0.06603	0.08538	0.09751	0.10830	0.12109	0.12993	0.13820	0.14842	0.15570
156	0.06561	0.08484	0.09689	0.10761	0.12032	0.12910	0.13732	0.14747	0.15471
158	0.06520	0.08430	0.09628	0.10693	0.11956	0.12829	0.13645	0.14655	0.15374
160	0.06480	0.08378	0.09569	0.10627	0.11882	0.12749	0.13561	0.14564	0.15278
d_α	0.83255	1.07298	1.22387	1.35810	1.51743	1.62762	1.73082	1.85846	1.94947
A_α	−0.042554	0.002557	0.052556	0.112820	0.205662	0.284642	0.370673	0.494581	0.595698

Table B.9 was prepared using Equation 3.0 of Birnbaum and Tingey (1951). The values of $D_{\alpha,n}$ were computed to eight decimal places and then rounded to five decimal places.

Examples:

$$D_{0.05(2),20} = 0.29408 \quad \text{and} \quad D_{0.01(1),55} = 0.20107$$

For large n, critical values of $D_{\alpha(2),n}$ can be approximated by

$$D_{\alpha(2),n} = \sqrt{\frac{-\ln(\alpha/2)}{2n}}$$

(Smirnov, 1939a) or, more accurately, by either

$$D_{\alpha(2),n} = \sqrt{\frac{-\ln(\alpha/2)}{2n}} - \frac{0.16693}{n}$$

or

$$D_{\alpha(2),n} = \sqrt{\frac{-\ln(\alpha/2)}{2n}} - \frac{0.16693}{n} - \frac{A_\alpha}{\sqrt{n^3}}$$

(Miller, 1956), where

$$A_\alpha = 0.09037\left[-\log\left(\frac{\alpha}{2}\right)\right]^{3/2} + 0.01515\left[\log\left(\frac{\alpha}{2}\right)\right]^2 + 0.08467\left(\frac{\alpha}{2}\right) - 0.11143.$$

For the significance levels, α, in Table D.9, the appropriate values of A_α at given at the end of the table.

These approximations are for critical values of D for two-tailed testing. To obtain critical D's for one-tailed tests, insert the one-tailed α in these equations instead of the two-tailed α.

The accuracy of each of these three approximations is shown below as percent error, where percent error = (approximate $D_{\alpha,n}$ − exact $D_{\alpha,n}$)/(exact $D_{\alpha,n}$) × 100%.

For the first approximating equation,*

n	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
20	4.4%	3.6%	3.4%	3.3%	3.2%	3.3%	3.3%	3.5%	3.6%
50	2.8	2.3	2.1	1.9	1.9	1.8	1.8	1.8	1.9
100	2.0	1.6	1.4	1.3	1.2	1.2	1.2	1.2	1.2
160	1.6	1.3	1.1	1.0	1.0	0.9	0.9	0.9	0.9

*The first approximation may also be written as

$$D_{\alpha,n} = \frac{d_\alpha}{\sqrt{n}},$$

where

$$d_\alpha = \sqrt{(-\ln\alpha)/2}$$

is given at the bottom of Table B.9.

For the second approximating equation,

	$\alpha(2)$: 0.50	0.20	0.10	0.05	0.02	0.01	0.005	0.002	0.001
n	$\alpha(1)$: 0.25	0.10	0.05	0.025	0.01	0.005	0.0025	0.001	0.0005
10	0.6%	0.0*	0.5%	0.9%	1.4%	1.9%	2.3%	2.9%	3.3%
20	0.3	0.0*	0.2	0.4	0.7	0.9	1.1	1.4	1.6
50	0.1	0.0*	0.1	0.2	0.3	0.4	0.4	0.5	0.6
100	0.1	0.0*	0.0*	0.1	0.1	0.2	0.2	0.3	0.3
160	0.0*	0.0*	0.0*	0.0*	0.1	0.1	0.1	0.2	0.2

For the third approximating equation:

	$\alpha(2)$: 0.50	0.20	0.10	0.05	0.02	0.01	0.005	0.002	0.001
n	$\alpha(1)$: 0.25	0.10	0.05	0.025	0.01	0.005	0.0025	0.001	0.0005
5	−0.1%	−0.2%	0.0*	0.1	0.1%	0.1%	3.3%	0.5%	0.5%
10	−0.1	0.0*	0.2%	0.0*	0.0*	0.1	0.0*	0.1	0.1
20	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*	0.0*

*This percent error is less than 0.05%.

TABLE B.10: Critical Values of D_δ for the δ-Corrected Kolmogorov-Smirnov Goodness-of-Fit Test for Continuous Distributions

n	δ	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
3	0	0.23875	0.35477	0.41811	0.46702	0.53456	0.57900	0.61428	0.63000	0.67063
	1	0.38345	0.53584	0.63150	0.70760	0.78456	0.82900	0.86428	0.90000	0.92063
4	0	0.23261	0.33435	0.39075	0.44641	0.50495	0.54210	0.57722	0.62216	0.65046
	1	0.33126	0.46154	0.53829	0.60468	0.68377	0.71409	0.77639	0.82217	0.85047
5	0	0.22665	0.31556	0.37359	0.42174	0.47692	0.51576	0.54981	0.58914	0.61682
	1	0.29930	0.41172	0.48153	0.34273	0.61133	0.63692	0.69887	0.74881	0.76133
6	0	0.21803	0.30244	0.35522	0.40045	0.45440	0.48988	0.52240	0.56231	0.58954
	1	0.27516	0.37706	0.44074	0.49569	0.55969	0.60287	0.64167	0.68777	0.71966
7	0	0.20935	0.28991	0.33905	0.38294	0.43337	0.46761	0.49932	0.53714	0.56345
	1	0.25645	0.35066	0.40892	0.46010	0.51968	0.55970	0.59646	0.64081	0.67126
8	0	0.20148	0.27828	0.32538	0.36697	0.41522	0.44819	0.47834	0.51499	0.54065
	1	0.24149	0.32925	0.38365	0.43160	0.48732	0.52519	0.56000	0.60194	0.63114
9	0	0.19475	0.26794	0.31325	0.35277	0.39922	0.43071	0.45983	0.49525	0.51997
	1	0.22919	0.31157	0.36287	0.40794	0.46067	0.49652	0.52953	0.56963	0.59760
10	0	0.18913	0.25884	0.30221	0.34022	0.38481	0.41517	0.44329	0.47747	0.50148
	1	0.21881	0.29668	0.34525	0.38798	0.43809	0.47220	0.50373	0.54207	0.56889
11	0	0.18381	0.25071	0.29227	0.32894	0.37187	0.40122	0.42835	0.46147	0.48475
	1	0.20981	0.28388	0.33008	0.37084	0.41864	0.45127	0.48146	0.51823	0.54408
12	0	0.17878	0.24325	0.28330	0.31869	0.36019	0.38856	0.41484	0.44696	0.46954
	1	0.20190	0.27269	0.31686	0.35588	0.40167	0.43208	0.46197	0.49737	0.52235
13	0	0.17410	0.23639	0.27515	0.30935	0.34954	0.37703	0.40254	0.43372	0.45570
	1	0.19487	0.26279	0.30520	0.34265	0.38668	0.41680	0.44475	0.47889	0.50292
14	0	0.16976	0.23010	0.26767	0.30081	0.33980	0.36649	0.39127	0.42159	0.44298
	1	0.18859	0.25395	0.29478	0.33086	0.37331	0.40238	0.42936	0.46237	0.48563
15	0	0.16575	0.22430	0.26077	0.29296	0.33083	0.35679	0.38090	0.41043	0.43129
	1	0.18293	0.24600	0.28541	0.32026	0.36128	0.38940	0.41551	0.44748	0.47001
16	0	0.16204	0.21895	0.23439	0.28570	0.32256	0.34784	0.37132	0.40012	0.42043
	1	0.17778	0.23879	0.27692	0.31065	0.35039	0.37764	0.40296	0.43398	0.45591
17	0	0.15859	0.21397	0.24847	0.27897	0.31489	0.33953	0.36245	0.39055	0.41041
	1	0.19308	0.23221	0.26918	0.30189	0.34045	0.36691	0.39151	0.42168	0.44298
18	0	0.15537	0.20933	0.24296	0.27270	0.30773	0.33181	0.35419	0.38164	0.40106
	1	0.16875	0.22617	0.26208	0.29386	0.33134	0.35707	0.38101	0.41037	0.43114
19	0	0.15235	0.20498	0.23781	0.26685	0.30108	0.32459	0.34647	0.37332	0.39235
	1	0.16475	0.22060	0.25553	0.28646	0.32295	0.34801	0.37133	0.39995	0.42020
20	0	0.14948	0.20089	0.23298	0.26137	0.29484	0.31784	0.33924	0.36633	0.38414
	1	0.16104	0.21544	0.24947	0.27961	0.31518	0.33962	0.36237	0.39031	0.41008
21	0	0.14678	0.19705	0.22844	0.25622	0.28898	0.31149	0.33246	0.35822	0.37645
	1	0.15758	0.21064	0.24384	0.27325	0.30796	0.33182	0.35404	0.38134	0.40067
22	0	0.14422	0.19343	0.22416	0.25136	0.28346	0.30552	0.32607	0.35133	0.36921
	1	0.15435	0.20616	0.23859	0.26732	0.30123	0.32456	0.34628	0.37298	0.39189
23	0	0.14179	0.19001	0.22012	0.24679	0.27825	0.29989	0.32005	0.34483	0.36239
	1	0.15132	0.20197	0.23367	0.26176	0.29494	0.31776	0.33902	0.36516	0.38365
24	0	0.13949	0.18677	0.21630	0.24245	0.27333	0.29456	0.31435	0.33868	0.35593
	1	0.14848	0.19804	0.22906	0.25656	0.28904	0.31138	0.33221	0.35782	0.37597
25	0	0.13730	0.18370	0.21268	0.23835	0.26866	0.28951	0.30895	0.33285	0.34980
	1	0.14579	0.19433	0.21472	0.25166	0.28349	0.30539	0.32580	0.35091	0.36875
26	0	0.13522	0.18077	0.20924	0.23445	0.26423	0.28472	0.30382	0.32733	0.34398
	1	0.14326	0.19084	0.22063	0.24704	0.27825	0.29973	0.31980	0.34441	0.36187
27	0	0.13323	0.17799	0.20596	0.23074	0.26001	0.28016	0.29895	0.32206	0.33845
	1	0.14086	0.18753	0.21676	0.24267	0.27330	0.29439	0.31403	0.33823	0.35541

TABLE B.10 (cont.): Critical Values of D_δ for the δ-Corrected Kolmogorov-Smirnov Goodness-of-Fit Test for Continuous Distributions

n	δ	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
28	0	0.13133	0.17533	0.20283	0.22721	0.25600	0.27582	0.29430	0.31704	0.33319
	1	0.13858	0.18440	0.21309	0.23853	0.26861	0.28933	0.30864	0.33242	0.34927
29	0	0.12951	0.17280	0.19985	0.22383	0.25217	0.27168	0.28987	0.31227	0.32818
	1	0.13641	0.18142	0.20961	0.23461	0.26417	0.28452	0.30351	0.32688	0.34349
30	0	0.12777	0.17037	0.19700	0.22061	0.24851	0.36772	0.28564	0.30770	0.32335
	1	0.13435	0.17859	0.20630	0.23088	0.25994	0.27996	0.29863	0.32162	0.33794
31	0	0.12610	0.16805	0.19427	0.21752	0.24501	0.26393	0.28157	0.30333	0.31875
	1	0.13238	0.17589	0.20314	0.22732	0.25391	0.27561	0.29399	0.31662	0.33268
32	0	0.12450	0.16582	0.19166	0.21457	0.24165	0.26030	0.27771	0.29915	0.31436
	1	0.13051	0.17332	0.20014	0.22393	0.25207	0.27146	0.28955	0.31184	0.32764
33	0	0.12295	0.16368	0.18915	0.21173	0.23843	0.25683	0.27399	0.29513	0.31015
	1	0.12871	0.17086	0.19726	0.22069	0.24840	0.26750	0.28532	0.30728	0.32286
34	0	0.12147	0.16162	0.18674	0.20901	0.23534	0.25348	0.27042	0.29127	0.30609
	1	0.12699	0.16850	0.19451	0.21759	0.24490	0.26371	0.28127	0.30296	0.31827
35	0	0.12004	0.15964	0.18442	0.20639	0.23237	0.25027	0.26698	0.28757	0.30219
	1	0.12534	0.16625	0.19188	0.21462	0.24154	0.26008	0.27740	0.29873	0.31388
36	0	0.11866	0.15774	0.18218	0.20387	0.22951	0.24718	0.26368	0.28401	0.29844
	1	0.12375	0.16408	0.18935	0.21278	0.23831	0.25660	0.27368	0.29472	0.30968
37	0	0.11733	0.15590	0.18003	0.20144	0.22676	0.24421	0.26050	0.28057	0.29481
	1	0.12223	0.16200	0.18692	0.20904	0.23522	0.25326	0.27011	0.29087	0.30558
38	0	0.11604	0.15413	0.17796	0.19910	0.22410	0.24134	0.25743	0.27726	0.29135
	1	0.12076	0.16000	0.18459	0.20642	0.23225	0.25005	0.26668	0.28717	0.30172
39	0	0.11480	0.15242	0.17595	0.19684	0.22154	0.23857	0.25447	0.27406	0.28800
	1	0.11935	0.15808	0.18234	0.20389	0.22938	0.24096	0.26334	0.28361	0.29799
40	0	0.11360	0.15076	0.17402	0.19465	0.21907	0.23589	0.25161	0.27098	0.28474
	1	0.11798	0.15622	0.18018	0.20145	0.22663	0.24399	0.26020	0.28019	0.29439
41	0	0.11243	0.14916	0.17215	0.19254	0.21667	0.23331	0.24884	0.26799	0.28162
	1	0.11667	0.15443	0.17810	0.19910	0.22397	0.24112	0.25713	0.27688	0.29092
42	0	0.11130	0.14761	0.17034	0.19050	0.21436	0.23081	0.24617	0.26511	0.27880
	1	0.11540	0.15270	0.17608	0.19684	0.22141	0.23835	0.25418	0.27369	0.28758
43	0	0.11021	0.14611	0.16858	0.18852	0.21212	0.22839	0.24358	0.26232	0.27564
	1	0.11417	0.15103	0.17414	0.19465	0.21893	0.23568	0.25132	0.27061	0.28433
44	0	0.10915	0.14466	0.16688	0.18661	0.20995	0.22604	0.24108	0.29962	0.27277
	1	0.11298	0.14942	0.17226	0.19253	0.21654	0.23310	0.24857	0.26764	0.28120
45	0	0.10812	0.14325	0.16524	0.18475	0.20785	0.22377	0.23865	0.25700	0.27004
	1	0.11183	0.14786	0.17044	0.19049	0.21423	0.23060	0.24590	0.26476	0.27815
46	0	0.10712	0.14188	0.16364	0.18295	0.20581	0.22157	0.23629	0.25445	0.26737
	1	0.11072	0.14635	0.16858	0.18851	0.21199	0.22818	0.24331	0.26198	0.27524
47	0	0.10615	0.14055	0.16208	0.18120	0.20383	0.21943	0.23401	0.25199	0.26477
	1	0.10964	0.14488	0.16697	0.18659	0.20982	0.22584	0.24081	0.25928	0.27242
48	0	0.10520	0.13926	0.16058	0.17950	0.20190	0.21735	0.23179	0.24959	0.26225
	1	0.10859	0.14346	0.16532	0.18473	0.20772	0.22357	0.23839	0.25666	0.26966
49	0	0.10428	0.13800	0.15911	0.17785	0.20003	0.21534	0.22963	0.24725	0.25991
	1	0.10737	0.14208	0.16371	0.18293	0.20568	0.22137	0.23604	0.25413	0.26701
50	0	0.10339	0.13678	0.15769	0.17624	0.19822	0.21337	0.22753	0.24500	0.25742
	1	0.10659	0.14074	0.16216	0.18117	0.20370	0.21924	0.23376	0.25167	0.26441

These critical values were kindly provided by H. J. Khamis, by the method described in Khamis (1990).

TABLE B.11: Critical Values of the Mann-Whitney *U* Distribution

n_1	n_2	$\alpha(2)$: 0.20 $\alpha(1)$: 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	1	—	—	—	—	—	—	—	—
	2	—	—	—	—	—	—	—	—
	3	—	—	—	—	—	—	—	—
	4	—	—	—	—	—	—	—	—
	5	—	—	—	—	—	—	—	—
	6	—	—	—	—	—	—	—	—
	7	—	—	—	—	—	—	—	—
	8	—	—	—	—	—	—	—	—
	9	9	—	—	—	—	—	—	—
	10	10	—	—	—	—	—	—	—
	11	11	—	—	—	—	—	—	—
	12	12	—	—	—	—	—	—	—
	13	13	—	—	—	—	—	—	—
	14	14	—	—	—	—	—	—	—
	15	15	—	—	—	—	—	—	—
	16	16	—	—	—	—	—	—	—
	17	17	—	—	—	—	—	—	—
	18	18	—	—	—	—	—	—	—
	19	18	19	—	—	—	—	—	—
	20	19	20	—	—	—	—	—	—
	21	20	21	—	—	—	—	—	—
	22	21	22	—	—	—	—	—	—
	23	22	23	—	—	—	—	—	—
	24	23	24	—	—	—	—	—	—
	25	24	25	—	—	—	—	—	—
	26	25	26	—	—	—	—	—	—
	27	26	27	—	—	—	—	—	—
	28	27	28	—	—	—	—	—	—
	29	27	29	—	—	—	—	—	—
	30	28	30	—	—	—	—	—	—
	31	29	31	—	—	—	—	—	—
	32	30	32	—	—	—	—	—	—
	33	31	33	—	—	—	—	—	—
	34	32	34	—	—	—	—	—	—
	35	33	35	—	—	—	—	—	—
	36	34	36	—	—	—	—	—	—
	37	35	37	—	—	—	—	—	—
	38	36	38	—	—	—	—	—	—
	39	36	38	39	—	—	—	—	—
1	40	37	39	40	—	—	—	—	—
2	2	—	—	—	—	—	—	—	—
	3	6	—	—	—	—	—	—	—
	4	8	—	—	—	—	—	—	—
	5	9	10	—	—	—	—	—	—
	6	11	12	—	—	—	—	—	—
	7	10	14	—	—	—	—	—	—
	8	14	15	16	—	—	—	—	—
	9	16	17	18	—	—	—	—	—
	10	17	19	20	—	—	—	—	—
	11	19	21	22	—	—	—	—	—
	12	20	22	23	—	—	—	—	—
	13	22	24	25	26	—	—	—	—
	14	23	25	27	28	—	—	—	—
	15	25	27	29	30	—	—	—	—
	16	27	29	31	32	—	—	—	—
	17	28	31	32	34	—	—	—	—
	18	30	32	34	36	—	—	—	—
	19	31	34	36	37	38	—	—	—
2	20	33	36	38	39	40	—	—	—

TABLE B.11 (cont.): Critical Values of the Mann-Whitney *U* Distribution

n_1	n_2	$\alpha(2)$: 0.20 $\alpha(1)$: 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
2	21	34	37	39	41	42	—	—	—
	22	36	39	41	43	44	—	—	—
	23	37	41	43	45	46	—	—	—
	24	39	42	45	47	48	—	—	—
	25	41	44	47	49	50	—	—	—
	26	42	46	48	51	52	—	—	—
	27	44	47	50	52	53	54	—	—
	28	45	49	52	54	55	56	—	—
	29	47	51	54	56	57	58	—	—
	30	48	53	55	58	59	60	—	—
	31	50	54	57	60	61	62	—	—
	32	51	56	59	62	63	64	—	—
	33	53	58	61	64	65	66	—	—
	34	55	59	63	65	67	68	—	—
	35	56	61	64	67	69	70	—	—
	36	58	63	66	69	71	72	—	—
	37	59	64	68	71	73	74	—	—
	38	61	66	70	73	75	76	—	—
	39	62	68	71	75	76	77	—	—
2	40	64	69	73	77	78	79	—	—
3	3	8	9	—	—	—	—	—	—
	4	11	12	—	—	—	—	—	—
	5	13	14	15	—	—	—	—	—
	6	15	16	17	—	—	—	—	—
	7	15	19	20	21	—	—	—	—
	8	19	21	22	24	—	—	—	—
	9	22	23	25	26	27	—	—	—
	10	24	26	27	29	30	—	—	—
	11	26	28	30	32	33	—	—	—
	12	28	31	32	34	35	36	—	—
	13	30	33	35	37	38	39	—	—
	14	32	35	37	40	41	42	—	—
	15	35	38	40	42	43	44	—	—
	16	37	40	42	45	46	47	—	—
	17	39	42	45	47	49	50	51	—
	18	41	45	47	50	52	53	54	—
	19	43	47	50	53	54	56	57	—
	20	45	49	52	55	57	58	60	—
	21	48	52	55	58	60	61	62	63
	22	50	54	57	60	62	64	65	66
	23	52	56	60	63	65	67	68	69
	24	54	59	62	66	68	69	71	72
	25	56	61	65	68	70	72	74	75
	26	58	63	67	71	73	75	77	78
	27	60	66	70	74	76	78	79	80
	28	63	68	72	76	79	80	82	83
	29	65	70	74	79	81	83	85	86
	30	67	73	77	81	84	86	88	89
	31	69	75	79	84	87	89	91	92
	32	71	77	82	87	89	91	94	95
	33	73	80	84	89	92	94	96	98
	34	76	82	87	92	95	97	99	101
	35	78	84	89	94	97	100	102	103
	36	80	87	92	97	100	103	105	106
	37	82	89	94	100	103	105	108	109
	38	84	91	97	102	105	108	111	112
	39	86	94	99	105	108	111	113	115
3	40	89	96	102	107	111	114	116	118

TABLE B.11 (cont.): Critical Values of the Mann-Whitney *U* Distribution

n_1	n_2	$\alpha(2)$: 0.20 $\alpha(1)$: 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
4	4	13	15	16	—	—	—	—	—
	5	16	18	19	20	—	—	—	—
	6	19	21	22	23	24	—	—	—
	7	20	24	25	27	28	—	—	—
	8	25	27	28	30	31	32	—	—
	9	27	30	32	33	35	36	—	—
	10	30	33	35	37	38	39	40	—
	11	33	36	38	40	42	43	44	—
	12	36	39	41	43	45	46	48	—
	13	39	42	44	47	49	50	51	52
	14	41	45	47	50	52	53	55	56
	15	44	48	50	53	55	57	59	60
	16	47	50	53	57	59	60	62	63
	17	50	53	57	60	62	64	66	67
	18	52	56	60	63	66	67	69	71
	19	55	59	63	67	69	71	73	74
	20	58	62	66	70	72	75	77	78
	21	61	65	69	73	76	78	80	82
	22	63	68	72	77	79	82	84	85
	23	66	71	75	80	83	85	88	89
	24	69	74	79	83	86	89	91	93
	25	72	77	82	87	90	92	95	97
	26	74	80	85	90	93	96	98	100
	27	77	83	88	93	96	99	102	104
	28	80	86	91	96	100	103	106	108
	29	83	89	94	100	103	106	109	111
	30	85	92	97	103	107	110	113	115
	31	88	95	100	106	110	113	117	119
	32	91	98	104	110	114	117	120	122
	33	94	101	107	113	117	120	124	126
	34	96	104	110	116	120	124	127	130
	35	99	107	113	120	124	127	131	133
	36	102	110	116	123	127	131	135	137
	37	105	113	119	126	131	134	138	141
	38	107	116	122	130	134	138	142	144
	39	110	118	125	133	137	141	145	148
4	40	113	121	129	136	141	145	149	152
5	5	20	21	23	24	25	—	—	—
	6	23	25	27	28	29	30	—	—
	7	24	29	30	32	34	35	—	—
	8	30	32	34	36	38	39	40	—
	9	33	36	38	40	42	43	44	45
	10	37	39	42	44	46	47	49	50
	11	40	43	46	48	50	52	53	54
	12	43	47	49	52	54	56	58	59
	13	47	50	53	56	58	60	62	63
	14	50	54	57	60	63	64	67	68
	15	53	57	61	64	67	69	71	72
	16	57	61	65	68	71	73	75	77
	17	60	65	68	72	75	77	80	81
	18	63	68	72	76	79	81	84	86
	19	67	72	76	80	83	86	88	90
	20	70	75	80	84	87	90	93	95
	21	73	79	83	88	91	94	97	99
	22	77	82	87	92	96	98	102	104
	23	80	86	91	96	100	103	106	108
	24	84	90	95	100	104	107	110	113
5	25	87	93	98	104	108	111	115	117

TABLE B.11 (cont.): Critical Values of the Mann-Whitney *U* Distribution

n_1	n_2	$\alpha(2)$: 0.20 $\alpha(1)$: 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
5	26	90	97	102	108	112	115	119	121
	27	94	100	106	112	119	120	123	126
	28	97	104	110	116	120	124	128	130
	29	100	107	113	120	124	128	132	135
	30	104	111	117	124	128	132	136	139
	31	107	115	121	128	133	136	141	144
	32	110	118	125	132	137	141	145	148
	33	114	122	128	136	141	145	150	153
	34	117	125	132	140	145	149	154	157
	35	120	129	136	144	149	153	158	161
	36	124	132	140	148	153	158	163	166
	37	127	136	144	152	157	162	167	170
	38	130	140	147	156	161	166	171	175
	39	134	143	151	160	165	170	176	179
5	40	137	147	155	164	169	174	180	184
6	6	27	29	31	33	34	35	—	—
	7	29	34	36	38	39	40	42	—
	8	35	38	40	42	44	45	47	48
	9	39	42	44	47	49	50	52	53
	10	43	46	49	52	54	55	57	58
	11	47	50	53	57	59	60	62	64
	12	51	55	58	61	63	65	68	69
	13	55	59	62	66	68	70	73	74
	14	59	63	67	71	73	75	78	79
	15	63	67	71	75	78	80	83	85
	16	67	71	75	80	83	85	88	90
	17	71	76	80	84	87	90	93	95
	18	74	80	84	89	92	95	98	100
	19	78	84	89	94	97	100	103	106
	20	82	88	93	98	102	105	108	111
	21	86	92	97	103	107	110	114	116
	22	90	96	102	108	111	115	119	121
	23	94	101	106	112	116	120	124	126
	24	98	105	111	117	121	125	129	132
	25	102	109	115	121	126	130	134	137
	26	106	113	119	126	131	134	139	142
	27	110	117	124	131	135	139	144	147
	28	114	122	128	135	140	144	149	152
	29	118	126	132	140	145	149	154	157
	30	122	130	137	145	150	154	159	163
	31	125	134	141	149	154	159	164	168
	32	129	138	146	154	159	164	169	173
	33	133	142	150	158	164	169	174	178
	34	137	147	154	163	169	174	179	183
	35	141	151	159	168	173	179	185	188
	36	145	155	163	172	178	184	190	194
	37	149	159	167	177	183	188	195	199
	38	153	163	172	182	188	193	200	204
	39	157	167	176	186	193	198	205	209
6	40	161	172	181	191	197	203	210	214
7	7	36	38	41	43	45	46	48	49
	8	40	43	46	49	50	52	54	55
	9	45	48	51	54	56	58	60	61
	10	49	53	56	59	61	63	65	67
	11	54	58	61	65	67	69	71	73
	12	58	63	66	70	72	75	77	79
	13	63	67	71	75	78	80	83	85
	14	67	72	76	81	83	86	89	91
7	15	72	77	81	86	89	92	95	97

TABLE B.11 (cont.): Critical Values of the Mann-Whitney *U* Distribution

n_1	n_2	$\alpha(2)$: 0.20 $\alpha(1)$: 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
7	16	76	82	86	91	94	97	101	103
	17	81	86	91	96	100	103	106	109
	18	85	91	96	102	105	108	112	115
	19	90	96	101	107	111	114	118	120
	20	94	101	106	112	116	120	124	126
	21	99	106	111	117	122	125	129	132
	22	103	110	116	123	127	131	135	138
	23	108	115	121	128	132	136	141	144
	24	112	120	126	133	138	142	147	150
	25	117	125	131	139	143	148	153	156
	26	121	129	136	144	149	153	158	162
	27	126	134	141	149	154	159	164	168
	28	130	139	146	154	160	164	170	174
	29	135	144	151	160	165	170	176	179
	30	139	149	156	165	170	176	181	185
	31	144	153	161	170	176	181	187	191
	32	148	158	166	175	181	187	193	197
	33	153	163	171	181	187	192	199	203
	34	157	168	176	186	192	198	204	209
	35	162	172	181	191	198	203	210	215
	36	166	177	186	196	203	209	216	221
	37	171	182	191	202	208	215	222	227
	38	175	187	196	207	214	220	227	232
	39	180	191	201	212	219	226	233	238
7	40	184	196	206	217	225	231	239	244
8	8	45	49	51	55	57	58	60	62
	9	50	54	57	61	63	65	67	68
	10	56	60	63	67	69	71	74	75
	11	61	65	69	73	75	77	80	82
	12	66	70	74	79	81	84	87	89
	13	71	76	80	84	87	90	93	95
	14	76	81	86	90	94	96	100	102
	15	81	87	91	96	100	103	106	109
	16	86	92	97	102	106	109	113	115
	17	91	97	102	108	112	115	119	122
	18	96	103	108	114	118	122	126	129
	19	101	108	114	120	124	128	132	135
	20	106	113	119	126	130	134	139	142
	21	112	119	125	132	136	140	145	148
	22	117	124	131	138	142	147	152	155
	23	122	130	136	144	149	153	158	162
	24	127	135	142	150	155	159	165	168
	25	132	140	147	155	161	165	171	175
	26	137	146	153	161	167	172	177	181
	27	142	151	159	167	173	178	184	188
	28	147	156	164	173	179	184	190	195
	29	152	162	170	179	185	190	197	201
	30	157	167	175	185	191	197	203	208
	31	162	172	181	191	197	203	210	214
	32	167	178	187	197	203	209	216	221
	33	172	183	192	203	209	215	223	227
	34	177	188	198	208	215	222	229	234
	35	182	194	203	214	221	228	235	241
	36	188	199	209	220	228	234	242	247
	37	193	205	215	226	234	240	248	254
	38	198	210	220	232	240	247	255	260
	39	203	215	226	238	246	253	261	267
8	40	208	221	231	244	252	259	268	273
9	9	56	60	64	67	70	72	74	76
	10	62	66	70	74	77	79	82	83
9	11	68	72	76	81	83	86	89	91

TABLE B.11 (cont.): Critical Values of the Mann-Whitney *U* Distribution

n_1	n_2	$\alpha(2)$: 0.20 $\alpha(1)$: 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
9	12	73	78	82	87	90	93	96	98
	13	79	84	89	94	97	100	103	106
	14	85	90	95	100	104	107	111	113
	15	90	96	101	107	111	114	118	120
	16	96	102	107	113	117	121	125	128
	17	101	108	114	120	124	128	132	135
	18	107	114	120	126	131	135	139	142
	19	113	120	126	133	138	142	146	150
	20	118	126	132	140	144	149	154	157
	21	124	132	139	146	151	155	161	164
	22	130	138	145	153	158	162	168	172
	23	135	144	151	159	164	169	175	179
	24	141	150	157	166	171	176	182	186
	25	147	156	163	172	178	183	189	193
	26	152	162	170	179	185	190	196	201
	27	158	168	176	185	191	197	203	208
	28	164	174	182	192	198	204	211	215
	29	169	179	188	198	205	211	218	222
	30	175	185	194	205	212	218	225	230
	31	180	191	201	211	218	224	232	237
	32	186	197	207	218	225	231	239	244
	33	192	203	213	224	232	238	246	251
	34	197	209	219	231	238	245	253	259
	35	203	215	226	237	245	252	260	266
	36	209	221	232	244	252	259	267	273
	37	214	227	238	250	258	266	275	280
	38	220	233	244	257	265	273	282	288
	39	225	239	250	263	272	280	289	295
9	40	231	245	257	270	279	286	296	302
10	10	68	73	77	81	84	87	90	92
	11	74	79	84	88	92	94	98	100
	12	81	86	91	96	99	102	106	108
	13	87	93	97	103	106	110	113	116
	14	93	99	104	110	114	117	121	124
	15	99	106	111	117	121	125	129	132
	16	106	112	118	124	129	133	137	140
	17	112	119	125	132	136	140	145	148
	18	118	125	132	139	143	148	153	156
	19	124	132	138	146	151	155	161	164
	20	130	138	145	153	158	163	168	172
	21	137	145	152	160	166	170	176	180
	22	143	152	159	167	173	178	184	188
	23	149	158	166	175	180	186	192	196
	24	155	165	173	182	188	193	200	204
	25	161	171	179	189	195	201	207	212
	26	168	178	186	196	202	208	215	220
	27	174	184	193	203	210	216	223	228
	28	180	191	200	210	217	223	231	236
	29	186	197	207	217	224	231	238	244
	30	192	204	213	224	232	238	246	252
	31	199	210	220	232	239	246	254	259
	32	205	217	227	239	246	253	262	267
	33	211	223	234	246	254	261	269	275
	34	217	230	241	253	261	268	277	283
	35	223	236	247	260	268	276	285	291
	36	229	243	254	267	276	284	293	299
	37	236	249	261	274	283	291	300	307
	38	242	256	268	281	290	299	308	315
	39	248	262	275	289	298	306	316	323
10	40	254	269	281	296	305	314	324	331

TABLE B.11 (cont.): Critical Values of the Mann-Whitney *U* Distribution

n_1	n_2	$\alpha(2)$: 0.20 $\alpha(1)$: 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
11	11	81	87	91	96	100	103	106	109
	12	88	94	99	104	108	111	115	117
	13	95	101	106	112	116	119	123	126
	14	102	108	114	120	124	128	132	135
	15	108	115	121	128	132	136	141	144
	16	115	122	129	135	140	144	149	152
	17	122	130	136	143	148	152	158	161
	18	129	137	143	151	156	161	166	170
	19	136	144	151	159	164	169	175	178
	20	142	151	158	167	172	177	183	187
	21	149	158	166	174	180	185	191	196
	22	156	165	173	182	188	193	200	204
	23	163	172	180	190	196	202	208	213
	24	169	179	188	198	204	210	217	222
	25	176	186	195	205	212	218	225	230
	26	183	194	203	213	220	226	234	239
	27	190	201	210	221	228	234	242	247
	28	196	208	218	229	236	243	251	256
	29	203	215	225	236	244	251	259	265
	30	210	222	232	244	252	259	267	273
	31	217	229	240	252	260	267	276	282
	32	223	236	247	260	268	275	284	290
	33	230	243	255	267	276	283	293	299
	34	237	250	262	275	284	292	301	307
	35	244	257	269	283	292	300	309	316
	36	250	265	277	290	300	308	318	325
	37	257	272	284	298	308	316	326	333
	38	264	279	291	306	316	324	335	342
	39	271	286	299	314	323	332	343	350
11	40	277	293	306	321	331	341	351	359
12	12	95	102	107	113	117	120	124	127
	13	103	109	115	121	125	129	133	136
	14	110	117	123	130	134	138	143	146
	15	117	125	131	138	143	147	152	155
	16	125	132	139	146	151	156	161	165
	17	132	140	147	155	160	165	170	174
	18	139	148	155	163	169	173	179	183
	19	147	156	163	172	177	182	188	193
	20	154	163	171	180	186	191	198	202
	21	161	171	179	188	194	200	207	211
	22	169	179	187	197	203	209	216	220
	23	176	186	195	205	212	218	225	230
	24	183	194	203	213	220	227	234	239
	25	191	202	211	222	229	235	243	248
	26	198	209	219	230	238	244	252	258
	27	205	217	227	239	246	253	261	267
	28	213	225	235	247	255	262	270	276
	29	220	232	243	255	263	271	279	285
	30	227	240	251	264	272	279	288	295
	31	235	248	259	272	280	288	297	304
	32	242	256	267	280	289	297	307	313
	33	249	263	275	289	298	306	316	322
	34	257	271	283	297	306	315	325	332
	35	264	279	291	305	315	323	334	341
	36	271	286	299	314	323	332	343	350
	37	278	294	307	322	332	341	352	359
	38	286	302	315	330	340	350	361	368
	39	293	309	323	339	349	359	370	378
12	40	300	317	331	347	358	367	379	387

TABLE B.11 (cont.): Critical Values of the Mann-Whitney *U* Distribution

n_1	n_2	$\alpha(2)$: 0.20 $\alpha(1)$: 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
13	13	111	118	124	130	135	139	143	146
	14	119	126	132	139	144	148	153	157
	15	127	134	141	148	153	158	163	167
	16	134	143	149	157	163	167	173	177
	17	142	151	158	166	172	177	183	187
	18	150	159	167	175	181	186	192	197
	19	158	167	171	184	190	196	202	207
	20	166	176	184	193	200	205	212	217
	21	174	184	193	202	209	215	222	227
	22	182	192	201	211	218	224	232	237
	23	190	201	210	220	227	234	241	247
	24	198	209	218	229	237	243	251	256
	25	205	217	227	238	246	253	261	266
	26	213	225	236	247	255	262	270	276
	27	221	234	244	256	264	271	280	286
	28	229	242	253	265	273	281	290	296
	29	237	250	261	274	283	290	300	306
	30	245	258	270	283	292	300	309	316
	31	253	267	278	292	301	309	319	326
	32	260	275	287	301	310	319	329	336
	33	268	283	296	310	319	328	338	346
	34	276	291	304	319	329	337	348	355
	35	284	299	313	328	338	347	358	365
	36	292	308	321	337	347	356	367	375
	37	300	316	330	346	356	366	377	385
	38	308	324	338	355	365	375	387	395
	39	315	332	347	363	374	385	397	405
13	40	323	341	355	372	384	394	406	415
14	14	127	135	141	149	154	161	164	167
	15	136	144	151	159	164	169	174	178
	16	144	153	160	168	174	179	185	189
	17	153	161	169	178	184	189	195	199
	18	161	170	178	187	194	199	206	210
	19	169	179	188	197	203	209	216	221
	20	178	188	197	207	213	219	226	231
	21	186	197	206	216	223	229	237	242
	22	195	206	215	226	233	240	247	253
	23	203	215	224	235	243	250	258	263
	24	212	223	234	245	253	260	268	274
	25	220	232	243	255	263	270	278	284
	26	228	241	252	264	272	280	289	295
	27	237	250	261	274	282	290	299	306
	28	245	259	270	283	292	300	309	316
	29	254	268	279	293	302	310	320	327
	30	262	276	289	302	312	320	330	337
	31	271	285	298	312	321	330	340	348
	32	279	294	307	321	331	340	351	358
	33	287	303	316	331	341	350	361	369
	34	296	312	325	341	351	360	371	379
	35	304	320	334	350	361	370	382	390
	36	313	329	343	360	370	380	392	400
	37	321	338	353	369	380	390	402	411
	38	329	347	362	379	390	400	413	421
	39	338	356	371	388	400	410	423	432
14	40	346	364	380	398	410	420	433	442
15	15	145	153	161	169	174	179	185	189
	16	154	163	170	179	185	190	197	201
	17	163	172	180	189	195	201	208	212
	18	172	182	190	200	206	212	219	224
	19	181	191	200	210	216	223	230	235
15	20	190	200	210	220	227	233	241	246

TABLE B.11 (cont.): Critical Values of the Mann-Whitney *U* Distribution

n_1	n_2	$\alpha(2)$: 0.20 $\alpha(1)$: 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
15	21	199	210	219	230	237	244	252	257
	22	208	219	229	240	248	255	263	269
	23	217	229	239	251	258	265	274	280
	24	226	238	249	261	269	276	285	291
	25	235	247	258	271	279	287	296	302
	26	244	257	268	281	290	298	307	313
	27	253	266	278	291	300	308	318	325
	28	262	276	288	301	311	319	329	336
	29	271	285	297	312	321	330	340	347
	30	280	294	307	322	331	340	351	358
	31	288	304	317	332	342	351	362	369
	32	297	313	327	342	352	362	373	381
	33	306	323	336	352	363	372	384	392
	34	315	332	346	362	373	383	395	403
	35	324	341	356	372	383	394	406	414
	36	333	351	366	382	394	404	417	425
	37	342	360	375	393	404	415	428	436
	38	351	369	385	403	415	425	439	448
	39	360	379	395	413	425	436	449	459
15	40	369	388	404	423	435	447	460	470
16	16	163	173	181	190	196	202	208	213
	17	173	183	191	201	207	213	220	225
	18	182	193	202	212	218	224	232	237
	19	192	203	212	222	230	236	244	249
	20	201	213	222	233	241	247	255	261
	21	211	223	233	244	252	259	267	273
	22	221	233	243	255	263	270	279	285
	23	230	243	253	266	274	281	290	296
	24	240	253	264	276	285	293	302	308
	25	249	263	274	287	296	304	314	320
	26	259	273	284	298	307	315	325	332
	27	268	283	295	309	318	327	337	344
	28	278	292	305	319	329	338	348	356
	29	287	302	315	330	340	349	360	367
	30	297	312	326	341	351	360	372	379
	31	306	322	336	352	362	372	383	391
	32	316	332	346	362	373	383	395	403
	33	325	342	357	373	384	394	406	415
	34	335	352	367	384	395	406	418	427
	35	344	362	377	395	406	417	429	438
	36	354	372	388	405	417	428	441	450
	37	363	382	398	416	428	439	453	462
	38	373	392	408	427	439	451	464	474
	39	382	402	418	437	450	462	476	485
16	40	392	412	429	448	461	473	487	497
17	17	183	193	202	212	219	225	232	238
	18	193	204	213	224	231	237	245	250
	19	203	214	224	235	242	249	257	263
	20	213	225	235	247	254	261	270	275
	21	223	236	246	258	266	273	282	288
	22	233	246	257	269	278	285	294	300
	23	244	257	268	281	289	297	306	313
	24	254	267	279	292	301	309	319	325
	25	264	278	290	303	313	321	331	338
	26	274	288	301	315	324	333	343	350
	27	284	299	312	326	336	345	355	363
	28	294	309	322	337	348	357	368	375
	29	304	320	333	349	359	369	380	388
17	30	314	330	344	360	371	380	392	400

TABLE B.11 (cont.): Critical Values of the Mann-Whitney *U* Distribution

n_1	n_2	$\alpha(2)$: 0.20 $\alpha(1)$: 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
17	31	324	341	355	371	382	392	404	413
	32	334	351	366	383	394	404	417	425
	33	344	362	377	394	406	416	429	438
	34	354	372	388	405	417	428	441	450
	35	365	383	399	417	429	440	453	462
	36	375	393	410	428	440	452	465	475
	37	385	404	420	439	452	464	478	487
	38	395	414	431	451	464	476	490	500
	39	405	425	442	462	475	487	502	512
17	40	415	435	453	473	487	499	514	525
18	18	204	215	225	236	243	250	258	263
	19	214	226	236	248	255	257	271	277
	20	225	237	248	260	268	275	284	287
	21	236	248	259	272	280	288	297	303
	22	246	260	271	284	292	300	310	316
	23	257	271	282	296	305	313	323	329
	24	268	282	294	308	317	325	336	343
	25	278	293	306	320	329	338	348	356
	26	289	304	317	332	341	350	361	369
	27	300	315	328	344	354	363	374	382
	28	310	326	340	355	366	376	387	395
	29	321	337	351	367	378	388	400	408
	30	331	348	363	379	390	401	413	421
	31	342	359	374	391	403	413	426	434
	32	353	370	386	403	415	426	438	447
	33	363	382	397	415	427	438	451	460
	34	374	393	409	427	439	451	464	473
	35	385	404	420	439	451	463	477	487
	36	395	415	432	451	464	475	490	500
	37	406	426	443	463	476	488	502	513
	38	416	437	454	475	488	500	515	526
	39	427	448	466	486	500	513	528	539
18	40	438	459	477	498	512	525	541	552
19	19	226	238	248	260	268	276	284	291
	20	237	250	261	273	281	289	298	304
	21	248	261	273	286	294	302	312	318
	22	259	273	285	298	307	315	325	332
	23	270	285	297	311	320	329	339	346
	24	282	296	309	323	333	342	352	360
	25	293	308	321	336	346	355	366	373
	26	304	320	333	348	359	368	379	387
	27	315	331	345	361	371	381	393	401
	28	326	343	357	373	384	394	406	415
	29	338	355	369	386	397	407	420	428
	30	349	366	381	398	410	421	433	442
	31	360	378	393	411	423	434	447	456
	32	371	390	405	423	436	447	460	469
	33	382	401	417	436	448	460	474	483
	34	393	413	429	448	461	473	487	497
19	35	405	424	441	461	474	486	500	511
	36	416	436	453	473	487	499	514	524
	37	427	448	465	486	500	512	527	538
	38	438	459	477	498	512	525	541	552
	39	449	471	489	511	525	538	554	565
	40	—	482	502	523	538	551	568	579

TABLE B.11 (cont.): Critical Values of the Mann-Whitney U Distribution

n_1	n_2	$\alpha(2)$: 0.20 $\alpha(1)$: 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
20	20	249	262	273	286	295	303	312	319
	21	260	274	286	299	308	317	326	333
	22	272	276	299	313	322	330	341	348
	23	284	299	311	326	335	344	355	362
	24	296	311	324	339	349	358	369	377
	25	307	323	337	352	362	372	383	391
	26	319	335	349	365	376	386	397	405
	27	331	348	362	378	389	399	411	420
	28	343	360	374	391	403	413	425	434
	29	354	372	387	404	416	427	440	449
	30	366	384	400	418	430	440	454	463
	31	378	396	412	431	443	454	468	477
	32	389	409	425	444	456	468	482	492
	33	401	421	438	457	470	482	496	506
	34	413	433	450	470	483	495	510	520
	35	425	445	463	483	497	509	524	534
	36	436	457	475	496	510	523	538	549
	37	448	469	488	509	523	536	552	563
	38	—	482	501	522	537	550	566	577
	39	—	*494*	513	535	550	564	580	592
20	40	—	*506*	526	548	563	577	594	606

The preceding values were derived, with permission of the publisher, from the tables of Milton (1964, *J. Amer. Statist. Assoc.* 59: 925–934), with the italicized values derived from Wilcoxon, Katti, and Wilcox (1970). Each U has a probability of no more than that indicated in its column heading; for example, for $n_1 = 20$ and $n_2 = 21$, the two-tailed probability of $U = 299$ is $0.01 < P < 0.02$.

Examples:

$$U_{0.05(2),5,8} = 34 \quad \text{and} \quad U_{0.05(1),10,8} = U_{0.05(1),8,10} = 60$$

For the Mann-Whitney test involving n_1 and/or n_2 larger than those in this table, the normal approximation of Section 8.11d may be used. For example, using the normal approximation when $n_1 \geq 20$ and $n_2 \geq 40$ results in two-tailed testing at a P(Type I error) < 0.005 different (lower) from α for $\alpha = 0.10$ or 0.05 and the P(Type I error) is no more than about 0.0005 different from (higher than) α for $\alpha = 0.02$ or 0.01. Fahoome (2002) determined that the approximation results in a probability of a Type I error between 0.045 and 0.055 when testing at the two-tailed 0.05 significance level and n_1 and n_2 of at least 15, and a probability between 0.009 and 0.011 when $\alpha(2) = 0.01$ and n_1 and $n_2 \geq 29$. Wilcoxon, Katti, and Wilcox (1970) gave critical values for larger sample sizes for Wilcoxon's two-sample T, where $T = n_1 n_2 + n_1(n_1 + 1)/2 - U$, but they are generally not needed thanks to this approximation.

TABLE B.12: Critical Values of the Wilcoxon *T* Distribution
***Note*: Contrary to most other tables of critical values, *low* values of *T* are associated with *low* probabilities (α); see Section 9.5**

n	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.001 0.005
4	2	0						
5	4	2	0					
6	6	3	2	0				
7	9	5	3	2	0			
8	12	8	5	3	1	0		
9	16	10	8	5	3	1	0	
10	20	14	10	8	5	3	1	
11	24	17	13	10	7	5	3	0
12	29	21	17	13	9	7	5	1
13	35	26	21	17	12	9	7	2
14	40	31	25	21	15	12	9	4
15	47	36	30	25	19	15	12	6
16	54	42	35	29	23	19	15	8
17	61	48	41	34	27	23	19	11
18	69	55	47	40	32	27	23	14
19	77	62	53	46	37	32	27	18
20	86	69	60	52	43	37	32	21
21	95	77	67	58	49	42	37	25
22	104	86	75	65	55	48	42	30
23	114	94	83	73	62	54	48	35
24	125	104	91	81	69	61	54	40
25	136	113	100	89	76	68	60	45
26	148	124	110	98	84	75	67	51
27	160	134	119	107	92	83	74	57
28	172	145	130	116	101	91	82	64
29	185	157	140	126	110	100	90	71
30	198	169	151	137	120	109	98	78
31	212	181	163	147	130	118	107	86
32	226	194	175	159	140	128	116	94
33	241	207	187	170	151	138	126	102
34	257	221	200	182	162	148	136	111
35	272	235	213	195	173	159	146	120
36	289	250	227	208	185	171	157	130
37	305	265	241	221	198	182	168	140
38	323	281	256	235	211	194	180	150
39	340	297	271	249	224	207	192	161
40	358	313	286	264	238	220	204	172
41	377	330	302	279	252	233	217	183
42	396	348	319	294	266	247	230	195
43	416	365	336	310	281	261	244	207
44	436	384	353	327	296	276	258	220
45	456	402	371	343	312	291	272	233
46	477	422	389	361	328	307	287	246
47	499	441	407	378	345	322	302	260
48	521	462	426	396	362	339	318	274
49	543	482	446	415	379	355	334	289
50	566	503	466	434	397	373	350	304
51	590	525	486	453	416	390	367	319
52	613	547	507	473	434	408	384	335
53	638	569	529	494	454	427	402	351
54	668	592	550	514	473	445	420	368
55	688	615	573	536	493	465	438	385
56	714	639	595	557	514	484	457	402
57	740	664	618	579	535	504	477	420
58	767	688	642	602	556	525	497	438
59	794	714	666	625	578	546	517	457
60	822	739	690	648	600	567	537	476

TABLE B.12 (cont.): Critical Values of the Wilcoxon T Distribution

n	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.001 0.005
61	850	765	715	672	623	589	558	495
62	879	792	741	697	646	611	580	515
63	908	819	767	721	669	634	602	535
64	938	847	793	747	693	657	624	556
65	968	875	820	772	718	681	647	577
66	998	903	847	798	742	705	670	599
67	1029	932	875	825	768	729	694	621
68	1061	962	903	852	793	754	718	643
69	1093	992	931	879	819	779	742	666
70	1126	1022	960	907	846	805	767	689
71	1159	1053	990	936	873	831	792	712
72	1192	1084	1020	964	901	858	818	736
73	1226	1116	1050	994	928	884	844	761
74	1261	1148	1081	1023	957	912	871	786
75	1296	1181	1112	1053	986	940	898	811
76	1331	1214	1144	1084	1015	968	925	836
77	1367	1247	1176	1115	1044	997	953	862
78	1403	1282	1209	1147	1075	1026	981	889
79	1440	1316	1242	1179	1105	1056	1010	916
80	1478	1351	1276	1211	1136	1086	1039	943
81	1516	1387	1310	1244	1168	1116	1069	971
82	1554	1423	1345	1277	1200	1147	1099	999
83	1593	1459	1380	1311	1232	1178	1129	1028
84	1632	1496	1415	1345	1265	1210	1160	1057
85	1672	1533	1451	1380	1298	1242	1191	1086
86	1712	1571	1487	1415	1332	1275	1223	1116
87	1753	1609	1524	1451	1366	1308	1255	1146
88	1794	1648	1561	1487	1400	1342	1288	1177
89	1836	1688	1599	1523	1435	1376	1321	1208
90	1878	1727	1638	1560	1471	1410	1355	1240
91	1921	1767	1676	1597	1507	1445	1389	1271
92	1964	1808	1715	1635	1543	1480	1423	1304
93	2008	1849	1755	1674	1580	1516	1458	1337
94	2052	1891	1795	1712	1617	1552	1493	1370
95	2097	1933	1836	1752	1655	1589	1529	1404
96	2142	1976	1877	1791	1693	1626	1565	1438
97	2187	2019	1918	1832	1731	1664	1601	1472
98	2233	2062	1960	1872	1770	1702	1638	1507
99	2280	2106	2003	1913	1810	1740	1676	1543
100	2327	2151	2045	1955	1850	1779	1714	1578

Each T in Appendix Table B.12 has a probability less than or equal to the α in its column heading.

Appendix Table B.12 is taken, with permission of the publisher, from the more extensive table of R. L. McCornack (1965, *J. Amer. Statist. Assoc.* 60: 864–871).

Examples:

$$T_{0.05(2),16} = 29 \quad \text{and} \quad T_{0.01(1),62} = 646.$$

For performing the Wilcoxon paired-sample test when $n > 100$, we may use the normal approximation (Section 9.5). The accuracy of this approximation is expressed below as follows: critical T from approximation—true critical T. In parentheses is the accuracy of the approximation with the continuity correction.

$\alpha(2)$: n	0.50	0.20	0.10	0.05	0.02	0.01	0.005	0.001
20	0(0)	1(1)	0(0)	0(−1)	−1(−1)	−2(−2)	−3(−3)	−5(−5)
40	1(1)	1(1)	1(1)	0(−1)	−2(−2)	−2(−3)	−3(−4)	−7(−8)
60	1(0)	1(1)	1(1)	0(0)	−2(−2)	−2(−3)	−4(−4)	−9(−9)
80	1(0)	1(1)	1(0)	0(−1)	−2(−2)	−4(−4)	−5(−5)	−10(−10)
100	1(1)	1(0)	1(1)	−1(−1)	−2(−3)	−4(−4)	−6(−7)	−11(−11)

The accuracy of the t approximation of Section 9.5 is similarly expressed here:

$\alpha(2)$: n	0.50	0.20	0.10	0.05	0.02	0.01	0.005	0.001
20	0(−1)	1(0)	0(0)	1(0)	1(1)	2(1)	2(1)	4(3)
40	1(0)	0(0)	1(0)	1(0)	1(1)	2(2)	3(3)	5(4)
60	0(−1)	0(0)	1(0)	1(1)	2(1)	3(2)	4(3)	6(5)
80	0(−1)	0(0)	0(0)	1(0)	2(2)	3(2)	4(4)	7(7)
100	0(0)	0(−1)	1(0)	0(0)	2(2)	3(3)	4(4)	8(7)

TABLE B.13: Critical Values of the Kruskal-Wallis *H* Distribution

n_1	n_2	n_3	n_4	α: 0.10	0.05	0.02	0.01	0.005	0.002	0.001
2	2	2		4.571						
3	2	1		4.286						
3	2	2		4.500	4.714					
3	3	1		4.571	5.143					
3	3	2		4.556	5.361	6.250				
3	3	3		4.622	5.600	6.489	7.200	7.200		
4	2	1		4.500						
4	2	2		4.458	5.333	6.000				
4	3	1		4.056	5.208					
4	3	2		4.511	5.444	6.144	6.444	7.000		
4	3	3		4.709	5.791	6.564	6.745	7.318	8.018	
4	4	1		4.167	4.967	6.667	6.667			
4	4	2		4.555	5.455	6.600	7.036	7.282	7.855	
4	4	3		4.545	5.598	6.712	7.144	7.598	8.227	8.909
4	4	4		4.654	5.692	6.962	7.654	8.000	8.654	9.269
5	2	1		4.200	5.000					
5	2	2		4.373	5.160	6.000	6.533			
5	3	1		4.018	4.960	6.044				
5	3	2		4.651	5.251	6.124	6.909	7.182		
5	3	3		4.533	5.648	6.533	7.079	7.636	8.048	8.727
5	4	1		3.987	4.985	6.431	6.955	7.364		
5	4	2		4.541	5.273	6.505	7.205	7.573	8.114	8.591
5	4	3		4.549	5.656	6.676	7.445	7.927	8.481	8.795
5	4	4		4.619	5.657	6.953	7.760	8.189	8.868	9.168
5	5	1		4.109	5.127	6.145	7.309	8.182		
5	5	2		4.623	5.338	6.446	7.338	8.131	6.446	7.338
5	5	3		4.545	5.705	6.866	7.578	8.316	8.809	9.521
5	5	4		4.523	5.666	7.000	7.823	8.523	9.163	9.606
5	5	5		4.940	5.780	7.220	8.000	8.780	9.620	9.920
6	1	1		—						
6	2	1		4.200	4.822					
6	2	2		4.545	5.345	6.182	6.982			
6	3	1		3.909	4.855	6.236				
6	3	2		4.682	5.348	6.227	6.970	7.515	8.182	
6	3	3		4.538	5.615	6.590	7.410	7.872	8.628	9.346
6	4	1		4.038	4.947	6.174	7.106	7.614		
6	4	2		4.494	5.340	6.571	7.340	7.846	8.494	8.827
6	4	3		4.604	5.610	6.725	7.500	8.033	8.918	9.170
6	4	4		4.595	5.681	6.900	7.795	8.381	9.167	9.861
6	5	1		4.128	4.990	6.138	7.182	8.077	8.515	
6	5	2		4.596	5.338	6.585	7.376	8.196	8.967	9.189
6	5	3		4.535	5.602	6.829	7.590	8.314	9.150	9.669
6	5	4		4.522	5.661	7.018	7.936	8.643	9.458	9.960
6	5	5		4.547	5.729	7.110	8.028	8.859	9.771	10.271
6	6	1		4.000	4.945	6.286	7.121	8.165	9.077	9.692
6	6	2		4.438	5.410	6.667	7.467	8.210	9.219	9.752
6	6	3		4.558	5.625	6.900	7.725	8.458	9.458	10.150
6	6	4		4.548	5.724	7.107	8.000	8.754	9.662	10.342
6	6	5		4.542	5.765	7.152	8.124	8.987	9.948	10.524
6	6	6		4.643	5.801	7.240	8.222	9.170	10.187	10.889
7	7	7		4.594	5.819	7.332	8.378	9.373	10.516	11.310
8	8	8		4.595	5.805	7.355	8.465	9.495	10.805	11.705
2	2	1	1		—					
2	2	2	1		5.357	5.679				
2	2	2	2		5.667	6.167	6.667	6.667		
3	1	1	1		—					
3	2	1	1		5.143					
3	2	2	1		5.556	5.833	6.500			
3	2	2	2		5.544	6.333	6.978	7.133	7.533	
3	3	1	1		5.333	6.333				

TABLE B.13 (cont.): Critical Values of the Kruskal-Wallis *H* Distribution

n_1	n_2	n_3	n_4	α: 0.10	0.05	0.02	0.01	0.005	0.002	0.001
3	3	2	1	5.689	6.244	6.689	7.200	7.400		
3	3	2	2	5.745	6.527	7.182	7.636	7.873	8.018	8.455
3	3	3	1	5.655	6.600	7.109	7.400	8.055	8.345	
3	3	3	2	5.879	6.727	7.636	8.105	8.379	8.803	9.030
3	3	3	3	6.026	7.000	7.872	8.538	8.897	9.462	9.513
4	1	1	1	—						
4	2	1	1	5.250	5.833					
4	2	2	1	5.533	6.133	6.667	7.000			
4	2	2	2	5.755	6.545	7.091	7.391	7.964	8.291	
4	3	1	1	5.067	6.178	6.711	7.067			
4	3	2	1	5.591	6.309	7.018	7.455	7.773	8.182	
4	3	2	2	5.750	6.621	7.530	7.871	8.273	8.689	8.909
4	3	3	1	5.589	6.545	7.485	7.758	8.212	8.697	9.182
4	3	3	2	5.872	6.795	7.763	8.333	8.718	9.167	8.455
4	3	3	3	6.016	6.984	7.995	8.659	9.253	9.709	10.016
4	4	1	1	5.182	5.945	7.091	7.909	7.909		
4	4	2	1	5.568	6.386	7.364	7.886	8.341	8.591	8.909
4	4	2	2	5.808	6.731	7.750	8.346	8.692	9.269	9.462
4	4	3	1	5.692	6.635	7.660	8.231	8.583	9.038	9.327
4	4	3	2	5.901	6.874	7.951	8.621	9.165	9.615	9.945
4	4	3	3	6.019	7.038	8.181	8.876	9.495	10.105	10.467
4	4	4	1	5.564	6.725	7.879	8.588	9.000	9.478	9.758
4	4	4	2	5.914	6.957	8.157	8.871	9.486	10.043	10.429
4	4	4	3	6.042	7.142	8.350	9.075	9.742	10.542	10.929
4	4	4	4	6.088	7.235	8.515	9.287	9.971	10.809	11.338
2	1	1	1	1 —						
2	2	1	1	1 5.786						
2	2	2	1	1 6.250	6.750					
2	2	2	2	1 6.600	7.133	7.533	7.533			
2	2	2	2	2 6.982	7.418	8.073	8.291	8.727	8.727	
3	1	1	1	1 —						
3	2	1	1	1 6.139	6.583					
3	2	2	1	1 6.511	6.800	7.400	7.600			
3	2	2	2	1 6.709	7.309	7.836	8.127	8.327	8.618	
3	2	2	2	2 6.955	7.682	8.303	8.682	8.985	9.273	9.364
3	3	1	1	1 6.311	7.111	7.467				
3	3	2	1	1 6.600	7.200	7.892	8.073	8.345		
3	3	2	2	1 6.788	7.591	8.258	8.576	8.924	9.167	9.303
3	3	2	2	2 7.026	7.910	8.667	9.115	9.474	9.769	10.026
3	3	3	1	1 6.788	7.576	8.242	8.424	8.848	9.455	9.455
3	3	3	2	1 6.910	7.769	8.590	9.051	9.410	9.769	9.974
3	3	3	2	2 7.121	8.044	9.011	9.505	9.890	10.330	10.637
3	3	3	3	1 7.077	8.000	8.879	9.451	9.846	10.286	10.549
3	3	3	3	2 7.210	8.200	9.267	9.876	10.333	10.838	11.171
3	3	3	3	3 7.333	8.333	9.467	10.200	10.733	10.267	11.667

Each tabled H in Appendix Table B.13 has a probability less than or equal to the α in its column heading.

The values of H in Appendix Table B.13 were determined from *Selected Tables in Mathematical Statistics*, Volume III, pp. 320–384, by permission of the American Mathematical Society. © 1975 by the American Mathematical Society (Iman, Quade, and Alexander, 1975).

Examples:

$$H_{0.05,4,3,2} = 5.444 \quad \text{and} \quad H_{0.01,4,4,5} = H_{0.01,5,4,4} = 7.760$$

Approximations are available (Section 10.4) for larger sample sizes.

TABLE B.14: Critical Values of the Friedman χ_r^2 Distribution

a (M)*	b (n)	α: 0.50	0.20	0.10	0.05	0.02	0.01	0.005	0.002	0.001
3	2	3.000	4.000							
3	3	2.667	4.667		6.000					
3	4	2.000	4.500	6.000	6.500			8.000		
3	5	2.800	3.600	5.200	6.400		8.400			10.000
3	6	2.330	4.000	5.33	7.000	8.330	9.000		10.330	12.000
3	7	2.000	3.714	5.429	7.143	8.000	8.857	10.286	11.143	12.286
3	8	2.250	4.000	5.250	6.250	7.750	9.000	9.750	12.000	12.250
3	9	2.000	3.556	5.556	6.222	8.000	9.556	10.667	11.556	12.667
3	10	1.800	3.800	5.000	6.200	7.800	9.600	10.400	12.200	12.600
3	11	1.636	3.818	4.909	6.545	7.818	9.455	10.364	11.636	13.273
3	12	1.500	3.500	5.167	6.167	8.000	9.500	10.167	12.167	12.500
3	13	1.846	3.846	4.769	6.000	8.000	9.385	10.308	11.538	12.923
3	14	1.714	3.571	5.143	6.143	8.143	9.000	10.429	12.000	13.286
3	15	1.733	3.600	4.933	6.400	8.133	8.933	10.000	12.133	12.933
4	2	3.600	5.400		6.000					
4	3	3.400	5.400	6.600	7.400	8.200	9.000		9.000	
4	4	3.000	4.800	6.300	7.800	8.400	9.600		10.200	11.100
4	5	3.000	5.160	6.360	7.800	9.240	9.960	10.920	11.640	12.600
4	6	3.000	4.800	6.400	7.600	9.400	10.200	11.400	12.200	12.800
4	7	2.829	4.886	6.429	7.800	9.343	10.371	11.400	12.771	13.800
4	8	2.550	4.800	6.300	7.650	9.450	10.350	11.850	12.900	13.800
4	9			6.467	7.800	9.133	10.867	12.067		14.467
4	10			6.360	7.800	9.120	10.800	12.000		14.640
4	11			6.382	7.909	9.327	11.073	12.273		14.891
4	12			6.400	7.900	9.200	11.100	12.300		15.000
4	13			6.415	7.965	7.369	11.123	12.323		15.277
4	14			6.343	7.386	9.343	11.143	12.514		15.257
4	15			6.440	8.040	9.400	11.240	12.520		15.400
5	2			7.200	7.600	8.000	8.000			
5	3			7.467	8.533	9.600	10.133	10.667		11.467
5	4			7.600	8.800	9.500	11.200	12.000		13.200
5	5			7.680	8.960	10.240	11.680	12.480		14.400
5	6			7.733	9.067	10.400	11.867	13.067		15.200
5	7			7.771	9.143	10.514	12.114	13.257		15.657
5	8			7.800	9.300	10.600	12.300	13.500		16.000
5	9			7.733	9.244	10.667	12.444	13.689		16.356
5	10			7.760	9.280	10.720	12.480	13.480		16.480
6	2			8.286	9.143	9.429	9.714	10.000		
6	3			8.714	9.857	10.810	11.762	12.524		13.286
6	4			9.000	10.286	11.429	12.714	13.571		15.286
6	5			9.000	10.486	11.743	13.229	14.257		16.429
6	6			9.048	10.571	12.000	13.619	14.762		17.048
6	7			9.122	10.674	12.061	13.857	15.000		17.612
6	8			9.143	10.714	12.214	14.000	15.286		18.000
6	9			9.127	10.778	12.302	14.143	15.476		18.270
6	10			9.143	10.800	12.343	14.299	15.600		18.514

*For Kendall's coefficient of concordance, W, use the column headings in parentheses.

Each χ_r^2 in Appendix Table B.14 has a probability less than or equal to the α in its column heading.

For $a = 3$, and for $a = 4$, with $b \leq 8$, the values of χ_r^2 in Appendix Table B.14 were determined from the exact probabilities of D. B. Owen, *Handbook of Statistical Tables*, © 1962, U.S. Department of Energy, published by Addision-Wesley, Reading, Massachusetts, Table 14.1, pp. 408–409; reprinted with permission. Critical values for a with $b > 8$, and for $a = 5$ and 6, were taken, with permission of the publisher, from Martin, LeBlanc, and Toan (1993).

Examples:

$$(\chi_r^2)_{0.05,3,6} = 7.000 \quad \text{and} \quad W_{0.05,4,3} = 7.400$$

TABLE B.15: Critical Values of Q for Nonparametric Multiple-Comparison Testing

k	α: 0.50	0.20	0.10	0.05	0.02	0.01	0.005	0.002	0.001
2	0.674	1.282	1.645	1.960	2.327	2.576	2.807	3.091	3.291
3	1.383	1.834	2.128	2.394	2.713	2.936	3.144	3.403	3.588
4	1.732	2.128	2.394	2.639	2.936	3.144	3.342	3.588	3.765
5	1.960	2.327	2.576	2.807	3.091	3.291	3.481	3.719	3.891
6	2.128	2.475	2.713	2.936	3.209	3.403	3.588	3.820	3.988
7	2.261	2.593	2.823	3.038	3.304	3.494	3.675	3.902	4.067
8	2.369	2.690	2.914	3.124	3.384	3.570	3.748	3.972	4.134
9	2.461	2.773	2.992	3.197	3.453	3.635	3.810	4.031	4.191
10	2.540	2.845	3.059	3.261	3.512	3.692	3.865	4.083	4.241
11	2.609	2.908	3.119	3.317	3.565	3.743	3.914	4.129	4.286
12	2.671	2.965	3.172	3.368	3.613	3.789	3.957	4.171	4.326
13	2.726	3.016	3.220	3.414	3.656	3.830	3.997	4.209	4.363
14	2.777	3.062	3.264	3.456	3.695	3.868	4.034	4.244	4.397
15	2.823	3.105	3.304	3.494	3.731	3.902	4.067	4.276	4.428
16	2.866	3.144	3.342	3.529	3.765	3.935	4.098	4.305	4.456
17	2.905	3.181	3.376	3.562	3.796	3.965	4.127	4.333	4.483
18	2.942	3.215	3.409	3.593	3.825	3.993	4.154	4.359	4.508
19	2.976	3.246	3.439	3.622	3.852	4.019	4.179	4.383	4.532
20	3.008	3.276	3.467	3.649	3.878	4.044	4.203	4.406	4.554
21	3.038	3.304	3.494	3.675	3.902	4.067	4.226	4.428	4.575
22	3.067	3.331	3.519	3.699	3.925	4.089	4.247	4.448	4.595
23	3.094	3.356	3.543	3.722	3.947	4.110	4.268	4.468	4.614
24	3.120	3.380	3.566	3.744	3.968	4.130	4.287	4.486	4.632
25	3.144	3.403	3.588	3.765	3.988	4.149	4.305	4.504	4.649

Appendix Table B.15 was prepared using Equation 26.2.23 of Zelen and Severo (1964), which determines Q_α such that $P(Q_\alpha) \leq \alpha(1)/[k(k-1)]$, where Q_α is a normal deviate (Appendix Table B.2). (This procedure is a form of what is known as a Bonferroni calculation.)

Examples:

$$Q_{0.05,4} = 2.639 \quad \text{and} \quad Q_{0.10,5} = 2.576$$

TABLE B.16: Critical Values of Q' for Nonparametric Multiple-Comparison Testing with a Control

k	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
2	0.674	1.282	1.645	1.960	2.327	2.576	2.807	3.091	3.291
3	1.150	1.645	1.960	2.242	2.576	2.807	3.024	3.291	3.481
4	1.383	1.834	2.128	2.394	2.713	2.936	3.144	3.403	3.588
5	1.534	1.960	2.242	2.498	2.807	3.024	3.227	3.481	3.662
6	1.645	2.054	2.327	2.576	2.879	3.091	3.291	3.540	3.719
7	1.732	2.128	2.394	2.639	2.936	3.144	3.342	3.588	3.765
8	1.803	2.190	2.450	2.690	2.983	3.189	3.384	3.628	3.803
9	1.863	2.242	2.498	2.735	3.024	3.227	3.421	3.662	3.836
10	1.915	2.287	2.540	2.773	3.059	3.261	3.453	3.692	3.865
11	1.960	2.327	2.576	2.807	3.091	3.291	3.481	3.719	3.891
12	2.001	2.362	2.609	2.838	3.119	3.317	3.506	3.743	3.914
13	2.037	2.394	2.639	2.866	3.144	3.342	3.529	3.765	3.935
14	2.070	2.424	2.666	2.891	3.168	3.364	3.551	3.785	3.954
15	2.101	2.450	2.690	2.914	3.189	3.384	3.570	3.803	3.972
16	2.128	2.475	2.713	2.936	3.209	3.403	3.588	3.820	3.988
17	2.154	2.498	2.735	2.955	3.227	3.421	3.605	3.836	4.003
18	2.178	2.520	2.755	2.974	3.245	3.437	3.621	3.851	4.018
19	2.201	2.540	2.773	2.992	3.261	3.453	3.635	3.865	4.031
20	2.222	2.558	2.791	3.008	3.276	3.467	3.649	3.878	4.044
21	2.242	2.576	2.807	3.024	3.291	3.481	3.662	3.891	4.056
22	2.261	2.593	2.823	3.038	3.304	3.494	3.675	3.902	4.067
23	2.278	2.609	2.838	3.052	3.317	3.506	3.687	3.914	4.078
24	2.295	2.624	2.852	3.066	3.330	3.518	3.698	3.924	4.088
25	2.311	2.639	2.866	3.078	3.342	3.529	3.709	3.935	4.098

Appendix Table B.16 was prepared using Equation 26.2.23 of Zelen and Severo (1964), which determines Q'_α such that $P(Q'_\alpha) \leq \alpha(2)/[(k-1)] = \alpha(1)/(k-1)$, where Q'_α is a normal deviate. (This procedure is a form of what is known as a Bonferroni calculation.)

Examples:

$$Q_{0.05(2),9} = 2.735 \quad \text{and} \quad Q_{0.01(1),12} = 3.119$$

TABLE B.17: Critical Values of the Correlation Coefficient, r

ν	α: 0.50 α: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
1	0.707	0.951	0.988	0.997	1.000	1.000	1.000	1.000	1.000
2	0.500	0.800	0.900	0.950	0.980	0.990	0.995	0.998	0.999
3	0.404	0.687	0.805	0.878	0.934	0.959	0.974	0.986	0.991
4	0.347	0.608	0.729	0.811	0.882	0.917	0.942	0.963	0.974
5	0.309	0.551	0.669	0.755	0.833	0.875	0.906	0.935	0.951
6	0.281	0.507	0.621	0.707	0.789	0.834	0.870	0.905	0.925
7	0.260	0.472	0.582	0.666	0.750	0.798	0.836	0.875	0.898
8	0.242	0.443	0.549	0.632	0.715	0.765	0.805	0.847	0.872
9	0.228	0.419	0.521	0.602	0.685	0.735	0.776	0.820	0.847
10	0.216	0.398	0.497	0.576	0.658	0.708	0.750	0.795	0.823
11	0.206	0.380	0.476	0.553	0.634	0.684	0.726	0.772	0.801
12	0.197	0.365	0.457	0.532	0.612	0.661	0.703	0.750	0.780
13	0.189	0.351	0.441	0.514	0.592	0.641	0.683	0.730	0.760
14	0.182	0.338	0.426	0.497	0.574	0.623	0.664	0.711	0.742
15	0.176	0.327	0.412	0.482	0.558	0.606	0.647	0.694	0.725
16	0.170	0.317	0.400	0.468	0.542	0.590	0.631	0.678	0.708
17	0.165	0.308	0.389	0.456	0.529	0.575	0.616	0.662	0.693
18	0.160	0.299	0.378	0.444	0.515	0.561	0.602	0.648	0.679
19	0.156	0.291	0.369	0.433	0.503	0.549	0.589	0.635	0.665
20	0.152	0.284	0.360	0.423	0.492	0.537	0.576	0.622	0.652
21	0.148	0.277	0.352	0.413	0.482	0.526	0.565	0.610	0.640
22	0.145	0.271	0.344	0.404	0.472	0.515	0.554	0.599	0.629
23	0.141	0.265	0.337	0.396	0.462	0.505	0.543	0.588	0.618
24	0.138	0.260	0.330	0.388	0.453	0.496	0.534	0.578	0.607
25	0.136	0.255	0.323	0.381	0.445	0.487	0.524	0.568	0.597
26	0.133	0.250	0.317	0.374	0.437	0.479	0.515	0.559	0.588
27	0.131	0.245	0.311	0.367	0.430	0.471	0.507	0.550	0.579
28	0.128	0.241	0.306	0.361	0.423	0.463	0.499	0.541	0.570
29	0.126	0.237	0.301	0.355	0.416	0.456	0.491	0.533	0.562
30	0.124	0.233	0.296	0.349	0.409	0.449	0.484	0.526	0.554
31	0.122	0.229	0.291	0.344	0.403	0.442	0.477	0.518	0.546
32	0.120	0.225	0.287	0.339	0.397	0.436	0.470	0.511	0.539
33	0.118	0.222	0.283	0.334	0.392	0.430	0.464	0.504	0.532
34	0.116	0.219	0.279	0.329	0.386	0.424	0.458	0.498	0.525
35	0.115	0.216	0.275	0.325	0.381	0.418	0.452	0.492	0.519
36	0.113	0.213	0.271	0.320	0.376	0.413	0.446	0.486	0.513
37	0.111	0.210	0.267	0.316	0.371	0.408	0.441	0.480	0.507
38	0.110	0.207	0.264	0.312	0.367	0.403	0.435	0.474	0.501
39	0.108	0.204	0.261	0.308	0.362	0.398	0.430	0.469	0.495
40	0.107	0.202	0.257	0.304	0.358	0.393	0.425	0.463	0.490
41	0.106	0.199	0.254	0.301	0.354	0.389	0.420	0.458	0.484
42	0.104	0.197	0.251	0.297	0.350	0.384	0.416	0.453	0.479
43	0.103	0.195	0.248	0.294	0.346	0.380	0.411	0.449	0.474
44	0.102	0.192	0.246	0.291	0.342	0.376	0.407	0.444	0.469
45	0.101	0.190	0.243	0.288	0.338	0.372	0.403	0.439	0.465
46	0.100	0.188	0.240	0.285	0.335	0.368	0.399	0.435	0.460
47	0.099	0.186	0.238	0.282	0.331	0.365	0.395	0.431	0.456
48	0.098	0.184	0.235	0.279	0.328	0.361	0.391	0.427	0.451
49	0.097	0.182	0.233	0.276	0.325	0.358	0.387	0.423	0.447
50	0.096	0.181	0.231	0.273	0.322	0.354	0.384	0.419	0.443
52	0.094	0.177	0.226	0.268	0.316	0.348	0.377	0.411	0.435
54	0.092	0.174	0.222	0.263	0.310	0.341	0.370	0.404	0.428
56	0.090	0.171	0.218	0.259	0.305	0.336	0.364	0.398	0.421
58	0.089	0.168	0.214	0.254	0.300	0.330	0.358	0.391	0.414
60	0.087	0.165	0.211	0.250	0.295	0.325	0.352	0.385	0.408

TABLE B.17 (cont.): Critical Values of the Correlation Coefficient, r

ν	α: 0.50 α: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
62	0.086	0.162	0.207	0.246	0.290	0.320	0.347	0.379	0.402
64	0.084	0.160	0.204	0.242	0.286	0.315	0.342	0.374	0.396
66	0.083	0.157	0.201	0.239	0.282	0.310	0.337	0.368	0.390
68	0.082	0.155	0.198	0.235	0.278	0.306	0.332	0.363	0.385
70	0.081	0.153	0.195	0.232	0.274	0.302	0.327	0.358	0.380
72	0.080	0.151	0.193	0.229	0.270	0.298	0.323	0.354	0.375
74	0.079	0.149	0.190	0.226	0.266	0.294	0.319	0.349	0.370
76	0.078	0.147	0.188	0.223	0.263	0.290	0.315	0.345	0.365
78	0.077	0.145	0.185	0.220	0.260	0.286	0.311	0.340	0.361
80	0.076	0.143	0.183	0.217	0.257	0.283	0.307	0.336	0.357
82	0.075	0.141	0.181	0.215	0.253	0.280	0.304	0.333	0.328
84	0.074	0.140	0.179	0.212	0.251	0.276	0.300	0.329	0.349
86	0.073	0.138	0.177	0.210	0.248	0.273	0.297	0.325	0.345
88	0.072	0.136	0.174	0.207	0.245	0.270	0.293	0.321	0.341
90	0.071	0.135	0.173	0.205	0.242	0.267	0.290	0.318	0.338
92	0.070	0.133	0.171	0.203	0.240	0.264	0.287	0.315	0.334
94	0.070	0.132	0.169	0.201	0.237	0.262	0.284	0.312	0.331
96	0.069	0.131	0.167	0.199	0.235	0.259	0.281	0.308	0.327
98	0.068	0.129	0.165	0.197	0.232	0.256	0.279	0.305	0.324
100	0.068	0.128	0.164	0.195	0.230	0.254	0.276	0.303	0.321
105	0.066	0.125	0.160	0.190	0.225	0.248	0.270	0.296	0.314
110	0.064	0.122	0.156	0.186	0.220	0.242	0.264	0.289	0.307
115	0.063	0.119	0.153	0.182	0.215	0.237	0.258	0.283	0.300
120	0.062	0.117	0.150	0.178	0.210	0.232	0.253	0.277	0.294
125	0.060	0.114	0.147	0.174	0.206	0.228	0.248	0.272	0.289
130	0.059	0.112	0.144	0.171	0.202	0.223	0.243	0.267	0.283
135	0.058	0.110	0.141	0.168	0.199	0.219	0.239	0.262	0.278
140	0.057	0.108	0.139	0.165	0.195	0.215	0.234	0.257	0.273
145	0.056	0.106	0.136	0.162	0.192	0.212	0.230	0.253	0.269
150	0.055	0.105	0.134	0.159	0.189	0.208	0.227	0.249	0.264
160	0.053	0.101	0.130	0.154	0.183	0.202	0.220	0.241	0.256
170	0.052	0.098	0.126	0.150	0.177	0.196	0.213	0.234	0.249
180	0.050	0.095	0.122	0.145	0.172	0.190	0.207	0.228	0.242
190	0.049	0.093	0.119	0.142	0.168	0.185	0.202	0.222	0.236
200	0.048	0.091	0.116	0.138	0.164	0.181	0.197	0.216	0.230
250	0.043	0.081	0.104	0.124	0.146	0.162	0.176	0.194	0.206
300	0.039	0.074	0.095	0.113	0.134	0.148	0.161	0.177	0.188
350	0.036	0.068	0.088	0.105	0.124	0.137	0.149	0.164	0.175
400	0.034	0.064	0.082	0.098	0.116	0.128	0.140	0.154	0.164
450	0.032	0.060	0.077	0.092	0.109	0.121	0.132	0.145	0.154
500	0.030	0.057	0.074	0.088	0.104	0.115	0.125	0.138	0.146
600	0.028	0.052	0.067	0.080	0.095	0.105	0.114	0.126	0.134
700	0.026	0.048	0.062	0.074	0.088	0.097	0.106	0.116	0.124
800	0.024	0.045	0.058	0.069	0.082	0.091	0.099	0.109	0.116
900	0.022	0.043	0.055	0.065	0.077	0.086	0.093	0.103	0.109
1000	0.021	0.041	0.052	0.062	0.073	0.081	0.089	0.098	0.104

The values in Appendix Table B.17 were computed using Equation 19.4 and Table B.3.
Examples:

$$r_{0.05(2),25} = 0.381 \quad \text{and} \quad r_{0.01(1),30} = 0.409$$

If we require a critical value for degrees of freedom not on this table, the critical value for the next lower degrees of freedom in the table may be conservatively used. Or, linear or harmonic interpolation may be used. If $\nu > 1000$, then use harmonic interpolation, setting the critical value equal to zero for $\nu = \infty$.
Also note:

$$T_{\alpha,\nu} = \sqrt{\frac{t_{\alpha,\nu}}{t_{\alpha,\nu} + \nu}}$$

TABLE B.18: Fisher's z Transformation for Correlation Coefficients, r

r	0	1	2	3	4	5	6	7	8	9	r
0.000	0.0000	0.0010	0.0020	0.0030	0.0040	0.0050	0.0060	0.0070	0.0080	0.0090	0.000
0.010	0.0100	0.0110	0.0120	0.0130	0.0140	0.0150	0.0160	0.0170	0.0180	0.0190	0.010
0.020	0.0200	0.0210	0.0220	0.0230	0.0240	0.0250	0.0260	0.0270	0.0280	0.0290	0.020
0.030	0.0300	0.0310	0.0320	0.0330	0.0340	0.0350	0.0360	0.0370	0.0380	0.0390	0.030
0.040	0.0400	0.0410	0.0420	0.0430	0.0440	0.0450	0.0460	0.0470	0.0480	0.0490	0.040
0.050	0.0500	0.0510	0.0520	0.0530	0.0541	0.0551	0.0561	0.0571	0.0581	0.0591	0.050
0.060	0.0601	0.0611	0.0621	0.0631	0.0641	0.0651	0.0661	0.0671	0.0681	0.0691	0.060
0.070	0.0701	0.0711	0.0721	0.0731	0.0741	0.0751	0.0761	0.0772	0.0782	0.0792	0.070
0.080	0.0802	0.0812	0.0822	0.0832	0.0842	0.0852	0.0862	0.0872	0.0882	0.0892	0.080
0.090	0.0902	0.0913	0.0923	0.0933	0.0943	0.0953	0.0963	0.0973	0.0983	0.0993	0.090
0.100	0.1003	0.1013	0.1024	0.1034	0.1044	0.1054	0.1064	0.1074	0.1084	0.1094	0.100
0.110	0.1104	0.1115	0.1125	0.1135	0.1145	0.1155	0.1165	0.1175	0.1186	0.1196	0.110
0.120	0.1206	0.1216	0.1226	0.1236	0.1246	0.1257	0.1267	0.1277	0.1287	0.1297	0.120
0.130	0.1307	0.1318	0.1328	0.1338	0.1348	0.1358	0.1368	0.1379	0.1389	0.1399	0.130
0.140	0.1409	0.1419	0.1430	0.1440	0.1450	0.1460	0.1470	0.1481	0.1491	0.1501	0.140
0.150	0.1511	0.1522	0.1532	0.1542	0.1552	0.1563	0.1573	0.1583	0.1593	0.1604	0.150
0.160	0.1614	0.1624	0.1634	0.1645	0.1655	0.1655	0.1675	0.1686	0.1696	0.1706	0.160
0.170	0.1717	0.1727	0.1737	0.1748	0.1758	0.1768	0.1779	0.1789	0.1799	0.1809	0.170
0.180	0.1820	0.1830	0.1840	0.1851	0.1861	0.1872	0.1882	0.1892	0.1903	0.1913	0.180
0.190	0.1923	0.1934	0.1944	0.1955	0.1965	0.1975	0.1986	0.1996	0.2006	0.2017	0.190
0.200	0.2027	0.2038	0.2048	0.2059	0.2069	0.2079	0.2090	0.2100	0.2111	0.2121	0.200
0.210	0.2132	0.2142	0.2153	0.2163	0.2174	0.2184	0.2195	0.2205	0.2216	0.2226	0.210
0.220	0.2237	0.2247	0.2258	0.2268	0.2279	0.2289	0.2300	0.2310	0.2321	0.2331	0.220
0.230	0.2342	0.2352	0.2363	0.2374	0.2384	0.2395	0.2405	0.2416	0.2427	0.2437	0.230
0.240	0.2448	0.2458	0.2469	0.2480	0.2490	0.2501	0.2512	0.2522	0.2533	0.2543	0.240
0.250	0.2554	0.2565	0.2575	0.2586	0.2597	0.2608	0.2618	0.2629	0.2640	0.2650	0.250
0.260	0.2661	0.2672	0.2683	0.2693	0.2704	0.2715	0.2726	0.2736	0.2747	0.2758	0.260
0.270	0.2769	0.2779	0.2790	0.2801	0.2812	0.2823	0.2833	0.2844	0.2855	0.2866	0.270
0.280	0.2877	0.2888	0.2899	0.2909	0.2920	0.2931	0.2942	0.2953	0.2964	0.2975	0.280
0.290	0.2986	0.2997	0.3008	0.3018	0.3029	0.3040	0.3051	0.3062	0.3073	0.3084	0.290
0.300	0.3095	0.3106	0.3117	0.3128	0.3139	0.3150	0.3161	0.3172	0.3183	0.3194	0.300
0.310	0.3205	0.3217	0.3228	0.3239	0.3250	0.3261	0.3272	0.3283	0.3294	0.3305	0.310
0.320	0.3316	0.3328	0.3339	0.3350	0.3361	0.3372	0.3383	0.3395	0.3406	0.3417	0.320
0.330	0.3428	0.3440	0.3451	0.3462	0.3473	0.3484	0.3496	0.3507	0.3518	0.3530	0.330
0.340	0.3541	0.3552	0.3564	0.3575	0.3586	0.3598	0.3609	0.3620	0.3632	0.3643	0.340
0.350	0.3654	0.3666	0.3677	0.3689	0.3700	0.3712	0.3723	0.3734	0.3746	0.3757	0.350
0.360	0.3769	0.3780	0.3792	0.3803	0.3815	0.3826	0.3838	0.3850	0.3861	0.3873	0.360
0.370	0.3884	0.3896	0.3907	0.3919	0.3931	0.3942	0.3954	0.3966	0.3977	0.3989	0.370
0.380	0.4001	0.4012	0.4024	0.4036	0.4047	0.4059	0.4071	0.4083	0.4094	0.4106	0.380
0.390	0.4118	0.4130	0.4142	0.4153	0.4165	0.4177	0.4189	0.4201	0.4213	0.4225	0.390
0.400	0.4236	0.4248	0.4260	0.4272	0.4284	0.4296	0.4308	0.4320	0.4332	0.4344	0.400
0.410	0.4356	0.4368	0.4380	0.4392	0.4404	0.4416	0.4428	0.4441	0.4453	0.4465	0.410
0.420	0.4477	0.4489	0.4501	0.4513	0.4526	0.4538	0.4550	0.4562	0.4574	0.4587	0.420
0.430	0.4599	0.4611	0.4624	0.4636	0.4648	0.4660	0.4673	0.4685	0.4698	0.4710	0.430
0.440	0.4722	0.4735	0.4747	0.4760	0.4772	0.4784	0.4797	0.4809	0.4822	0.4834	0.440
0.450	0.4847	0.4860	0.4872	0.4885	0.4897	0.4910	0.4922	0.4935	0.4948	0.4960	0.450
0.460	0.4973	0.4986	0.4999	0.5011	0.5024	0.5037	0.5049	0.5062	0.5075	0.5088	0.460
0.470	0.5101	0.5114	0.5126	0.5139	0.5152	0.5165	0.5178	0.5191	0.5204	0.5217	0.470
0.480	0.5230	0.5243	0.5256	0.5269	0.5282	0.5295	0.5308	0.5321	0.5334	0.5347	0.480
0.490	0.5361	0.5374	0.5387	0.5400	0.5413	0.5427	0.5440	0.5453	0.5466	0.5480	0.490
0.500	0.5493	0.5506	0.5520	0.5533	0.5547	0.5560	0.5573	0.5587	0.5600	0.5614	0.500
0.510	0.5627	0.5641	0.5654	0.5668	0.5681	0.5695	0.5709	0.5722	0.5736	0.5750	0.510
0.520	0.5763	0.5777	0.5791	0.5805	0.5818	0.5832	0.5846	0.5860	0.5874	0.5888	0.520
0.530	0.5901	0.5915	0.5929	0.5943	0.5957	0.5971	0.5985	0.5999	0.6013	0.6027	0.530
0.540	0.6042	0.6056	0.6070	0.6084	0.6098	0.6112	0.6127	0.6141	0.6155	0.6169	0.540

TABLE B.18 (cont.): Fisher's z Transformation for Correlation Coefficients, r

r	0	1	2	3	4	5	6	7	8	9	r
0.550	0.6184	0.6198	0.6213	0.6227	0.6241	0.6256	0.6270	0.6285	0.6299	0.6314	0.550
0.560	0.6328	0.6343	0.6358	0.6372	0.6387	0.6401	0.6416	0.6431	0.6446	0.6460	0.560
0.570	0.6475	0.6490	0.6505	0.6520	0.6535	0.6550	0.6565	0.6580	0.6595	0.6610	0.570
0.580	0.6625	0.6640	0.6655	0.6670	0.6685	0.6700	0.6716	0.6731	0.6746	0.6761	0.580
0.590	0.6777	0.6792	0.6807	0.6823	0.6838	0.6854	0.6869	0.6885	0.6900	0.6916	0.590
0.600	0.6931	0.6947	0.6963	0.6978	0.6994	0.7010	0.7026	0.7042	0.7057	0.7073	0.600
0.610	0.7089	0.7105	0.7121	0.7137	0.7153	0.7169	0.7185	0.7201	0.7218	0.7234	0.610
0.620	0.7250	0.7266	0.7283	0.7299	0.7315	0.7332	0.7348	0.7365	0.7381	0.7398	0.620
0.630	0.7414	0.7431	0.7447	0.7464	0.7481	0.7497	0.7514	0.7531	0.7548	0.7565	0.630
0.640	0.7582	0.7599	0.7616	0.7633	0.7650	0.7667	0.7684	0.7701	0.7718	0.7736	0.640
0.650	0.7753	0.7770	0.7788	0.7805	0.7823	0.7840	0.7858	0.7875	0.7893	0.7910	0.650
0.660	0.7928	0.7946	0.7964	0.7981	0.7999	0.8017	0.8035	0.8053	0.8071	0.8089	0.660
0.670	0.8107	0.8126	0.8144	0.8162	0.8180	0.8199	0.8217	0.8236	0.8254	0.8273	0.670
0.680	0.8291	0.8310	0.8328	0.8347	0.8366	0.8385	0.8404	0.8422	0.8441	0.8460	0.680
0.690	0.8480	0.8499	0.8518	0.8537	0.8556	0.8576	0.8595	0.8614	0.8634	0.8653	0.690
0.700	0.8673	0.8693	0.8712	0.8732	0.8752	0.8772	0.8792	0.8812	0.8832	0.8852	0.700
0.710	0.8872	0.8892	0.8912	0.8933	0.8953	0.8973	0.8994	0.9014	0.9035	0.9056	0.710
0.720	0.9076	0.9097	0.9118	0.9139	0.9160	0.9181	0.9202	0.9223	0.9245	0.9266	0.720
0.730	0.9287	0.9309	0.9330	0.9352	0.9373	0.9395	0.9417	0.9439	0.9461	0.9483	0.730
0.740	0.9505	0.9527	0.9549	0.9571	0.9594	0.9616	0.9639	0.9661	0.9684	0.9707	0.740
0.750	0.9730	0.9752	0.9775	0.9798	0.9822	0.9845	0.9868	0.9891	0.9915	0.9938	0.750
0.760	0.9962	0.9986	1.0010	1.0034	1.0058	1.0082	1.0106	1.0130	1.0154	1.0179	0.760
0.770	1.0203	1.0228	1.0253	1.0277	1.0302	1.0327	1.0352	1.0378	1.0403	1.0428	0.770
0.780	1.0454	1.0479	1.0505	1.0531	1.0557	1.0583	1.0609	1.0635	1.0661	1.0688	0.780
0.790	1.0714	1.0741	1.0768	1.0795	1.0822	1.0849	1.0876	1.0903	1.0931	1.0958	0.790
0.800	1.0986	1.1014	1.1042	1.1070	1.1098	1.1127	1.1155	1.1184	1.1212	1.1241	0.800
0.810	1.1270	1.1299	1.1329	1.1358	1.1388	1.1417	1.1447	1.1477	1.1507	1.1538	0.810
0.820	1.1568	1.1599	1.1630	1.1660	1.1691	1.1723	1.1754	1.1786	1.1817	1.1849	0.820
0.830	1.1881	1.1914	1.1946	1.1979	1.2011	1.2044	1.2077	1.2111	1.2144	1.2178	0.830
0.840	1.2212	1.2246	1.2280	1.2314	1.2349	1.2384	1.2419	1.2454	1.2490	1.2526	0.840
0.850	1.2561	1.2598	1.2634	1.2671	1.2707	1.2744	1.2782	1.2819	1.2857	1.2895	0.850
0.860	1.2933	1.2972	1.3011	1.3050	1.3089	1.3129	1.3169	1.3209	1.3249	1.3290	0.860
0.870	1.3331	1.3372	1.3414	1.3456	1.3498	1.3540	1.3583	1.3626	1.3670	1.3713	0.870
0.880	1.3758	1.3802	1.3847	1.3892	1.3938	1.3984	1.4030	1.4077	1.4124	1.4171	0.880
0.890	1.4219	1.4268	1.4316	1.4365	1.4415	1.4465	1.4516	1.4566	1.4618	1.4670	0.890
0.900	1.4722	1.4775	1.4828	1.4882	1.4937	1.4992	1.5047	1.5103	1.5160	1.5217	0.900
0.910	1.5275	1.5334	1.5393	1.5453	1.5513	1.5574	1.5636	1.5698	1.5762	1.5825	0.910
0.920	1.5890	1.5956	1.6022	1.6089	1.6157	1.6226	1.6296	1.6366	1.6438	1.6510	0.920
0.930	1.6584	1.6658	1.6734	1.6811	1.6888	1.6967	1.7047	1.7129	1.7211	1.7295	0.930
0.940	1.7380	1.7467	1.7555	1.7645	1.7736	1.7828	1.7923	1.8019	1.8116	1.8216	0.940
0.950	1.8318	1.8421	1.8527	1.8635	1.8745	1.8857	1.8972	1.9090	1.9210	1.9333	0.950
0.960	1.9459	1.9588	1.9721	1.9856	1.9996	2.0139	2.0287	2.0439	2.0595	2.0756	0.960
0.970	2.0923	2.1095	2.1273	2.1457	2.1648	2.1847	2.2054	2.2269	2.2494	2.2729	0.970
0.980	2.2975	2.3234	2.3507	2.3795	2.4101	2.4426	2.4774	2.5147	2.5549	2.5987	0.980
0.990	2.6466	2.6995	2.7587	2.8257	2.9030	2.9944	3.1062	3.2502	3.4531	3.7997	0.990

Appendix Table B.18 was produced using Equation 19.8. *Example:* For $r = 0.641$, $z = 0.7599$.

TABLE B.19: Correlation Coefficients, *r*, Corresponding to Fisher's *z* Transformation

z	0	1	2	3	4	5	6	7	8	9	*z*
0.00	0.0000	0.0010	0.0020	0.0030	0.0040	0.0050	0.0060	0.0070	0.0080	0.0090	0.00
0.01	0.0100	0.0110	0.0120	0.0130	0.0140	0.0150	0.0160	0.0170	0.0180	0.0190	0.01
0.02	0.0200	0.0210	0.0220	0.0230	0.0240	0.0250	0.0260	0.0270	0.0280	0.0290	0.02
0.03	0.0300	0.0310	0.0320	0.0330	0.0340	0.0350	0.0360	0.0370	0.0380	0.0390	0.03
0.04	0.0400	0.0410	0.0420	0.0430	0.0440	0.0450	0.0460	0.0470	0.0480	0.0490	0.04
0.05	0.0500	0.0510	0.0520	0.0530	0.0539	0.0549	0.0559	0.0569	0.0579	0.0589	0.05
0.06	0.0599	0.0609	0.0619	0.0629	0.0639	0.0649	0.0659	0.0669	0.0679	0.0689	0.06
0.07	0.0699	0.0709	0.0719	0.0729	0.0739	0.0749	0.0759	0.0768	0.0778	0.0788	0.07
0.08	0.0798	0.0808	0.0818	0.0828	0.0838	0.0848	0.0858	0.0868	0.0878	0.0888	0.08
0.09	0.0898	0.0907	0.0917	0.0927	0.0937	0.0947	0.0957	0.0967	0.0977	0.0987	0.09
0.10	0.0997	0.1007	0.1016	0.1026	0.1036	0.1046	0.1056	0.1066	0.1076	0.1086	0.10
0.11	0.1096	0.1105	0.1115	0.1125	0.1135	0.1145	0.1155	0.1165	0.1175	0.1184	0.11
0.12	0.1194	0.1204	0.1214	0.1224	0.1234	0.1244	0.1253	0.1263	0.1273	0.1283	0.12
0.13	0.1293	0.1303	0.1312	0.1322	0.1332	0.1342	0.1352	0.1361	0.1371	0.1381	0.13
0.14	0.1391	0.1401	0.1411	0.1420	0.1430	0.1440	0.1450	0.1460	0.1469	0.1479	0.14
0.15	0.1489	0.1499	0.1508	0.1518	0.1528	0.1538	0.1547	0.1557	0.1567	0.1577	0.15
0.16	0.1586	0.1596	0.1606	0.1616	0.1625	0.1635	0.1645	0.1655	0.1664	0.1674	0.16
0.17	0.1684	0.1694	0.1703	0.1713	0.1723	0.1732	0.1742	0.1752	0.1761	0.1771	0.17
0.18	0.1781	0.1790	0.1800	0.1810	0.1820	0.1829	0.1839	0.1849	0.1858	0.1868	0.18
0.19	0.1877	0.1887	0.1897	0.1906	0.1916	0.1926	0.1935	0.1945	0.1955	0.1964	0.19
0.20	0.1974	0.1983	0.1993	0.2003	0.2012	0.2022	0.2031	0.2041	0.2051	0.2060	0.20
0.21	0.2070	0.2079	0.2089	0.2098	0.2108	0.2117	0.2127	0.2137	0.2146	0.2156	0.21
0.22	0.2165	0.2175	0.2184	0.2194	0.2203	0.2213	0.2222	0.2232	0.2241	0.2251	0.22
0.23	0.2260	0.2270	0.2279	0.2289	0.2298	0.2308	0.2317	0.2327	0.2336	0.2346	0.23
0.24	0.2355	0.2364	0.2374	0.2383	0.2393	0.2402	0.2412	0.2421	0.2430	0.2440	0.24
0.25	0.2449	0.2459	0.2468	0.2477	0.2487	0.2496	0.2506	0.2515	0.2524	0.2534	0.25
0.26	0.2543	0.2552	0.2562	0.2571	0.2580	0.2590	0.2599	0.2608	0.2618	0.2627	0.26
0.27	0.2636	0.2646	0.2655	0.2664	0.2673	0.2683	0.2692	0.2701	0.2711	0.2720	0.27
0.28	0.2729	0.2738	0.2748	0.2757	0.2766	0.2775	0.2784	0.2794	0.2803	0.2812	0.28
0.29	0.2821	0.2831	0.2840	0.2849	0.2858	0.2867	0.2876	0.2886	0.2895	0.2904	0.29
0.30	0.2913	0.2922	0.2931	0.2941	0.2950	0.2959	0.2968	0.2977	0.2986	0.2995	0.30
0.31	0.3004	0.3013	0.3023	0.3032	0.3041	0.3050	0.3059	0.3068	0.3077	0.3086	0.31
0.32	0.3095	0.3104	0.3113	0.3122	0.3131	0.3140	0.3149	0.3158	0.3167	0.3176	0.32
0.33	0.3185	0.3194	0.3203	0.3212	0.3221	0.3230	0.3239	0.3248	0.3257	0.3266	0.33
0.34	0.3275	0.3284	0.3293	0.3302	0.3310	0.3319	0.3328	0.3337	0.3346	0.3355	0.34
0.35	0.3364	0.3373	0.3381	0.3390	0.3399	0.3408	0.3417	0.3426	0.3435	0.3443	0.35
0.36	0.3452	0.3461	0.3470	0.3479	0.3487	0.3496	0.3505	0.3514	0.3522	0.3531	0.36
0.37	0.3540	0.3549	0.3557	0.3566	0.3575	0.3584	0.3592	0.3601	0.3610	0.3618	0.37
0.38	0.3627	0.3636	0.3644	0.3653	0.3662	0.3670	0.3679	0.3688	0.3696	0.3705	0.38
0.39	0.3714	0.3722	0.3731	0.3739	0.3748	0.3757	0.3765	0.3774	0.3782	0.3791	0.39
0.40	0.3799	0.3808	0.3817	0.3825	0.3834	0.3842	0.3851	0.3859	0.3868	0.3876	0.40
0.41	0.3885	0.3893	0.3902	0.3910	0.3919	0.3927	0.3936	0.3944	0.3952	0.3961	0.41
0.42	0.3969	0.3978	0.3986	0.3995	0.4003	0.4011	0.4020	0.4028	0.4036	0.4045	0.42
0.43	0.4053	0.4062	0.4070	0.4078	0.4087	0.4095	0.4103	0.4112	0.4120	0.4128	0.43
0.44	0.4136	0.4145	0.4153	0.4161	0.4170	0.4178	0.4186	0.4194	0.4203	0.4211	0.44
0.45	0.4219	0.4227	0.4235	0.4244	0.4252	0.4260	0.4268	0.4276	0.4285	0.4293	0.45
0.46	0.4301	0.4309	0.4317	0.4325	0.4333	0.4342	0.4350	0.4358	0.4366	0.4374	0.46
0.47	0.4382	0.4390	0.4398	0.4406	0.4414	0.4422	0.4430	0.4438	0.4446	0.4454	0.47
0.48	0.4462	0.4470	0.4478	0.4486	0.4494	0.4502	0.4510	0.4518	0.4526	0.4534	0.48
0.49	0.4542	0.4550	0.4558	0.4566	0.4574	0.4582	0.4590	0.4598	0.4605	0.4613	0.49
0.50	0.4621	0.4629	0.4637	0.4645	0.4653	0.4660	0.4668	0.4676	0.4684	0.4692	0.50
0.51	0.4699	0.4707	0.4715	0.4723	0.4731	0.4738	0.4746	0.4754	0.4762	0.4769	0.51
0.52	0.4777	0.4785	0.4792	0.4800	0.4808	0.4815	0.4823	0.4831	0.4838	0.4846	0.52
0.53	0.4854	0.4861	0.4869	0.4877	0.4884	0.4892	0.4900	0.4907	0.4915	0.4922	0.53
0.54	0.4930	0.4937	0.4945	0.4953	0.4960	0.4968	0.4975	0.4983	0.4990	0.4998	0.54
0.55	0.5005	0.5013	0.5020	0.5028	0.5035	0.5043	0.5050	0.5057	0.5065	0.5072	0.55
0.56	0.5080	0.5087	0.5095	0.5102	0.5109	0.5117	0.5124	0.5132	0.5139	0.5146	0.56
0.57	0.5154	0.5161	0.5168	0.5176	0.5183	0.5190	0.5198	0.5205	0.5212	0.5219	0.57
0.58	0.5227	0.5234	0.5241	0.5248	0.5256	0.5263	0.5270	0.5277	0.5285	0.5292	0.58
0.59	0.5299	0.5306	0.5313	0.5320	0.5328	0.5335	0.5342	0.5349	0.5356	0.5363	0.59

TABLE B.19 (cont.): Correlation Coefficients, r, Corresponding to Fisher's z Transformation

z	0	1	2	3	4	5	6	7	8	9	z
0.60	0.5370	0.5378	0.5385	0.5392	0.5399	0.5406	0.5413	0.5420	0.5427	0.5434	0.60
0.61	0.5441	0.5448	0.5455	0.5462	0.5469	0.5476	0.5483	0.5490	0.5497	0.5504	0.61
0.62	0.5511	0.5518	0.5525	0.5532	0.5539	0.5546	0.5553	0.5560	0.5567	0.5574	0.62
0.63	0.5581	0.5587	0.5594	0.5601	0.5608	0.5615	0.5622	0.5629	0.5635	0.5642	0.63
0.64	0.5649	0.5656	0.5663	0.5669	0.5676	0.5683	0.5690	0.5696	0.5703	0.5710	0.64
0.65	0.5717	0.5723	0.5730	0.5737	0.5744	0.5750	0.5757	0.5764	0.5770	0.5777	0.65
0.66	0.5784	0.5790	0.5797	0.5804	0.5810	0.5817	0.5823	0.5830	0.5837	0.5843	0.66
0.67	0.5850	0.5856	0.5863	0.5869	0.5876	0.5883	0.5889	0.5896	0.5902	0.5909	0.67
0.68	0.5915	0.5922	0.5928	0.5935	0.5941	0.5948	0.5954	0.5961	0.5967	0.5973	0.68
0.69	0.5980	0.5986	0.5993	0.5999	0.6005	0.6012	0.6018	0.6025	0.6031	0.6037	0.69
0.70	0.6044	0.6050	0.6056	0.6063	0.6069	0.6075	0.6082	0.6088	0.6094	0.6100	0.70
0.71	0.6107	0.6113	0.6119	0.6126	0.6132	0.6138	0.6144	0.6150	0.6157	0.6163	0.71
0.72	0.6169	0.6175	0.6181	0.6188	0.6194	0.6200	0.6206	0.6212	0.6218	0.6225	0.72
0.73	0.6231	0.6237	0.6243	0.6249	0.6255	0.6261	0.6267	0.6273	0.6279	0.6285	0.73
0.74	0.6291	0.6297	0.6304	0.6310	0.6316	0.6322	0.6328	0.6334	0.6340	0.6346	0.74
0.75	0.6351	0.6357	0.6363	0.6369	0.6375	0.6381	0.6387	0.6393	0.6399	0.6405	0.75
0.76	0.6411	0.6417	0.6423	0.6428	0.6434	0.6440	0.6446	0.6452	0.6458	0.6463	0.76
0.77	0.6469	0.6475	0.6481	0.6487	0.6492	0.6498	0.6504	0.6510	0.6516	0.6521	0.77
0.78	0.6527	0.6533	0.6539	0.6544	0.6550	0.6556	0.6561	0.6567	0.6573	0.6578	0.78
0.79	0.6584	0.6590	0.6595	0.6601	0.6607	0.6612	0.6618	0.6624	0.6629	0.6635	0.79
0.80	0.6640	0.6646	0.6652	0.6657	0.6663	0.6668	0.6674	0.6679	0.6685	0.6690	0.80
0.81	0.6696	0.6701	0.6707	0.6712	0.6718	0.6723	0.6729	0.6734	0.6740	0.6745	0.81
0.82	0.6751	0.6756	0.6762	0.6767	0.6772	0.6778	0.6783	0.6789	0.6794	0.6799	0.82
0.83	0.6805	0.6810	0.6815	0.6821	0.6826	0.6832	0.6837	0.6842	0.6847	0.6853	0.83
0.84	0.6858	0.6863	0.6869	0.6874	0.6879	0.6884	0.6890	0.6895	0.6900	0.6905	0.84
0.85	0.6911	0.6916	0.6921	0.6926	0.6932	0.6937	0.6942	0.6947	0.6952	0.6957	0.85
0.86	0.6963	0.6968	0.6973	0.6978	0.6983	0.6988	0.6993	0.6998	0.7004	0.7009	0.86
0.87	0.7014	0.7019	0.7024	0.7029	0.7034	0.7039	0.7044	0.7049	0.7054	0.7059	0.87
0.88	0.7064	0.7069	0.7074	0.7079	0.7084	0.7089	0.7094	0.7099	0.7104	0.7109	0.88
0.89	0.7114	0.7119	0.7124	0.7129	0.7134	0.7139	0.7143	0.7148	0.7153	0.7158	0.89
0.90	0.7163	0.7168	0.7173	0.7178	0.7182	0.7187	0.7192	0.7197	0.7202	0.7207	0.90
0.91	0.7211	0.7216	0.7221	0.7226	0.7230	0.7235	0.7240	0.7245	0.7249	0.7254	0.91
0.92	0.7259	0.7264	0.7268	0.7273	0.7278	0.7283	0.7287	0.7292	0.7297	0.7301	0.92
0.93	0.7306	0.7311	0.7315	0.7320	0.7325	0.7329	0.7334	0.7338	0.7343	0.7348	0.93
0.94	0.7352	0.7357	0.7361	0.7366	0.7371	0.7375	0.7380	0.7384	0.7389	0.7393	0.94
0.95	0.7398	0.7402	0.7407	0.7411	0.7416	0.7420	0.7425	0.7429	0.7434	0.7438	0.95
0.96	0.7443	0.7447	0.7452	0.7456	0.7461	0.7465	0.7469	0.7474	0.7478	0.7483	0.96
0.97	0.7487	0.7491	0.7496	0.7500	0.7505	0.7509	0.7513	0.7518	0.7522	0.7526	0.97
0.98	0.7531	0.7535	0.7539	0.7544	0.7548	0.7552	0.7557	0.7561	0.7565	0.7569	0.98
0.99	0.7574	0.7578	0.7582	0.7586	0.7591	0.7595	0.7599	0.7603	0.7608	0.7612	0.99
1.0	0.7616	0.7658	0.7699	0.7739	0.7779	0.7818	0.7857	0.7895	0.7932	0.7969	1.0
1.1	0.8005	0.8041	0.8076	0.8110	0.8144	0.8178	0.8210	0.8243	0.8274	0.8306	1.1
1.2	0.8337	0.8367	0.8397	0.8426	0.8455	0.8483	0.8511	0.8538	0.8565	0.8591	1.2
1.3	0.8617	0.8643	0.8668	0.8692	0.8717	0.8741	0.8764	0.8787	0.8809	0.8832	1.3
1.4	0.8854	0.8875	0.8896	0.8917	0.8937	0.8957	0.8977	0.8996	0.9015	0.9033	1.4
1.5	0.9051	0.9069	0.9087	0.9104	0.9121	0.9138	0.9154	0.9170	0.9186	0.9201	1.5
1.6	0.9217	0.9232	0.9246	0.9261	0.9275	0.9289	0.9302	0.9316	0.9329	0.9341	1.6
1.7	0.9354	0.9366	0.9379	0.9391	0.9402	0.9414	0.9425	0.9436	0.9447	0.9458	1.7
1.8	0.9468	0.9478	0.9488	0.9498	0.9508	0.9517	0.9527	0.9536	0.9545	0.9554	1.8
1.9	0.9562	0.9571	0.9579	0.9587	0.9595	0.9603	0.9611	0.9618	0.9626	0.9633	1.9
2.0	0.9640	0.9647	0.9654	0.9661	0.9667	0.9674	0.9680	0.9687	0.9693	0.9699	2.0
2.1	0.9705	0.9710	0.9716	0.9721	0.9727	0.9732	0.9737	0.9743	0.9748	0.9753	2.1
2.2	0.9757	0.9762	0.9767	0.9771	0.9776	0.9780	0.9785	0.9789	0.9793	0.9797	2.2
2.3	0.9801	0.9805	0.9809	0.9812	0.9816	0.9820	0.9823	0.9827	0.9830	0.9833	2.3
2.4	0.9837	0.9840	0.9843	0.9846	0.9849	0.9852	0.9855	0.9858	0.9861	0.9863	2.4

TABLE B.19 (cont.): Correlation Coefficients, r, Corresponding to Fisher's z Transformation

z	0	1	2	3	4	5	6	7	8	9	z
2.5	0.9866	0.9869	0.9871	0.9874	0.9876	0.9879	0.9881	0.9884	0.9886	0.9888	2.5
2.6	0.9890	0.9892	0.9895	0.9897	0.9899	0.9901	0.9903	0.9905	0.9906	0.9908	2.6
2.7	0.9910	0.9912	0.9914	0.9915	0.9917	0.9919	0.9920	0.9922	0.9923	0.9925	2.7
2.8	0.9926	0.9928	0.9929	0.9931	0.9932	0.9933	0.9935	0.9936	0.9937	0.9938	2.8
2.9	0.9940	0.9941	0.9942	0.9943	0.9944	0.9945	0.9946	0.9947	0.9949	0.9950	2.9
3.0	0.9951	0.9952	0.9952	0.9953	0.9954	0.9955	0.9956	0.9957	0.9958	0.9959	3.0
3.1	0.9959	0.9960	0.9961	0.9962	0.9963	0.9963	0.9964	0.9965	0.9965	0.9966	3.1
3.2	0.9967	0.9967	0.9968	0.9969	0.9969	0.9970	0.9971	0.9971	0.9972	0.9972	3.2
3.3	0.9973	0.9973	0.9974	0.9974	0.9975	0.9975	0.9976	0.9976	0.9977	0.9977	3.3
3.4	0.9978	0.9978	0.9979	0.9979	0.9979	0.9980	0.9980	0.9981	0.9981	0.9981	3.4
3.5	0.9982	0.9982	0.9982	0.9983	0.9983	0.9984	0.9984	0.9984	0.9984	0.9985	3.5
3.6	0.9985	0.9985	0.9986	0.9986	0.9986	0.9986	0.9987	0.9987	0.9987	0.9988	3.6
3.7	0.9988	0.9988	0.9988	0.9988	0.9989	0.9989	0.9989	0.9989	0.9990	0.9990	3.7
3.8	0.9990	0.9990	0.9990	0.9991	0.9991	0.9991	0.9991	0.9991	0.9991	0.9992	3.8
3.9	0.9992	0.9992	0.9992	0.9992	0.9992	0.9993	0.9993	0.9993	0.9993	0.9993	3.9
4.0	0.9993	0.9993	0.9994	0.9994	0.9994	0.9994	0.9994	0.9994	0.9994	0.9994	4.0
4.1	0.9995	0.9995	0.9995	0.9995	0.9995	0.9995	0.9995	0.9995	0.9995	0.9995	4.1
4.2	0.9996	0.9996	0.9996	0.9996	0.9996	0.9996	0.9996	0.9996	0.9996	0.9996	4.2
4.3	0.9996	0.9996	0.9996	0.9997	0.9997	0.9997	0.9997	0.9997	0.9997	0.9997	4.3
4.4	0.9997	0.9997	0.9997	0.9997	0.9997	0.9997	0.9997	0.9997	0.9997	0.9997	4.4
4.5	0.9998	0.9998	0.9998	0.9998	0.9998	0.9998	0.9998	0.9998	0.9998	0.9998	4.5
4.6	0.9998	0.9998	0.9998	0.9998	0.9998	0.9998	0.9998	0.9998	0.9998	0.9998	4.6
4.7	0.9998	0.9998	0.9998	0.9998	0.9998	0.9999	0.9999	0.9999	0.9999	0.9999	4.7
4.8	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	4.8
4.9	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	4.9

$$r = \tanh z = \frac{e^{2z} - 1}{e^{2z} + 1}$$

Example:

$$z = 2.42, \quad r = 0.9843$$

TABLE B.20: Critical Values of the Spearman Rank-Correlation Coefficient, r_S

n	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
4	0.600	1.000	1.000						
5	0.500	0.800	0.900	1.000	1.000				
6	0.371	0.657	0.829	0.886	0.943	1.000	1.000		
7	0.321	0.571	0.714	0.786	0.893	0.929	0.964	1.000	1.000
8	0.310	0.524	0.643	0.738	0.833	0.881	0.905	0.952	0.976
9	0.267	0.483	0.600	0.700	0.783	0.833	0.867	0.917	0.933
10	0.248	0.455	0.564	0.648	0.745	0.794	0.830	0.879	0.903
11	0.236	0.427	0.536	0.618	0.709	0.755	0.800	0.845	0.873
12	0.217	0.406	0.503	0.587	0.678	0.727	0.769	0.818	0.846
13	0.209	0.385	0.484	0.560	0.648	0.703	0.747	0.791	0.824
14	0.200	0.367	0.464	0.538	0.626	0.679	0.723	0.771	0.802
15	0.189	0.354	0.446	0.521	0.604	0.654	0.700	0.750	0.779
16	0.182	0.341	0.429	0.503	0.582	0.635	0.679	0.729	0.762
17	0.176	0.328	0.414	0.485	0.566	0.615	0.662	0.713	0.748
18	0.170	0.317	0.401	0.472	0.550	0.600	0.643	0.695	0.728
19	0.165	0.309	0.391	0.460	0.535	0.584	0.628	0.677	0.712
20	0.161	0.299	0.380	0.447	0.520	0.570	0.612	0.662	0.696
21	0.156	0.292	0.370	0.435	0.508	0.556	0.599	0.648	0.681
22	0.152	0.284	0.361	0.425	0.496	0.544	0.586	0.634	0.667
23	0.148	0.278	0.353	0.415	0.486	0.532	0.573	0.622	0.654
24	0.144	0.271	0.344	0.406	0.476	0.521	0.562	0.610	0.642
25	0.142	0.265	0.337	0.398	0.466	0.511	0.551	0.598	0.630
26	0.138	0.259	0.331	0.390	0.457	0.501	0.541	0.587	0.619
27	0.136	0.255	0.324	0.382	0.448	0.491	0.531	0.577	0.608
28	0.133	0.250	0.317	0.375	0.440	0.483	0.522	0.567	0.598
29	0.130	0.245	0.312	0.368	0.433	0.475	0.513	0.558	0.589
30	0.128	0.240	0.306	0.362	0.425	0.467	0.504	0.549	0.580
31	0.126	0.236	0.301	0.356	0.418	0.459	0.496	0.541	0.571
32	0.124	0.232	0.296	0.350	0.412	0.452	0.489	0.533	0.563
33	0.121	0.229	0.291	0.345	0.405	0.446	0.482	0.525	0.554
34	0.120	0.225	0.287	0.340	0.399	0.439	0.475	0.517	0.547
35	0.118	0.222	0.283	0.335	0.394	0.433	0.468	0.510	0.539
36	0.116	0.219	0.279	0.330	0.388	0.427	0.462	0.504	0.533
37	0.114	0.216	0.275	0.325	0.383	0.421	0.456	0.497	0.526
38	0.113	0.212	0.271	0.321	0.378	0.415	0.450	0.491	0.519
39	0.111	0.210	0.267	0.317	0.373	0.410	0.444	0.485	0.513
40	0.110	0.207	0.264	0.313	0.368	0.405	0.439	0.479	0.507
41	0.108	0.204	0.261	0.309	0.364	0.400	0.433	0.473	0.501
42	0.107	0.202	0.257	0.305	0.359	0.395	0.428	0.468	0.495
43	0.105	0.199	0.254	0.301	0.355	0.391	0.423	0.463	0.490
44	0.104	0.197	0.251	0.298	0.351	0.386	0.419	0.458	0.484
45	0.103	0.194	0.248	0.294	0.347	0.382	0.414	0.453	0.479
46	0.102	0.192	0.246	0.291	0.343	0.378	0.410	0.448	0.474
47	0.101	0.190	0.243	0.288	0.340	0.374	0.405	0.443	0.469
48	0.100	0.188	0.240	0.285	0.336	0.370	0.401	0.439	0.465
49	0.098	0.186	0.238	0.282	0.333	0.366	0.397	0.434	0.460
50	0.097	0.184	0.235	0.279	0.329	0.363	0.393	0.430	0.456
51	0.096	0.182	0.233	0.276	0.326	0.359	0.390	0.426	0.451
52	0.095	0.180	0.231	0.274	0.323	0.356	0.386	0.422	0.447
53	0.095	0.179	0.228	0.271	0.320	0.352	0.382	0.418	0.443
54	0.094	0.177	0.226	0.268	0.317	0.349	0.379	0.414	0.439
55	0.093	0.175	0.224	0.266	0.314	0.346	0.375	0.411	0.435
56	0.092	0.174	0.222	0.264	0.311	0.343	0.372	0.407	0.432
57	0.091	0.172	0.220	0.261	0.308	0.340	0.369	0.404	0.428
58	0.090	0.171	0.218	0.259	0.306	0.337	0.366	0.400	0.424
59	0.089	0.169	0.216	0.257	0.303	0.334	0.363	0.397	0.421
60	0.089	0.168	0.214	0.255	0.300	0.331	0.360	0.394	0.418
61	0.088	0.166	0.213	0.252	0.298	0.329	0.357	0.391	0.414
62	0.087	0.165	0.211	0.250	0.296	0.326	0.354	0.388	0.411
63	0.086	0.163	0.209	0.248	0.293	0.323	0.351	0.385	0.408

TABLE B.20 (cont.): Critical Values of the Spearman Rank-Correlation Coefficient, r_s

	$\alpha(2)$:	0.50	0.20	0.10	0.05	0.02	0.01	0.005	0.002	0.001
n	$\alpha(1)$:	0.25	0.10	0.05	0.025	0.01	0.005	0.0025	0.001	0.0005
64		0.086	0.162	0.207	0.246	0.291	0.321	0.348	0.382	0.405
65		0.085	0.161	0.206	0.244	0.289	0.318	0.346	0.379	0.402
66		0.084	0.160	0.204	0.243	0.287	0.316	0.343	0.376	0.399
67		0.084	0.158	0.203	0.241	0.284	0.314	0.341	0.373	0.396
68		0.083	0.157	0.201	0.239	0.282	0.311	0.338	0.370	0.393
69		0.082	0.156	0.200	0.237	0.280	0.309	0.336	0.368	0.390
70		0.082	0.155	0.198	0.235	0.278	0.307	0.333	0.365	0.388
71		0.081	0.154	0.197	0.234	0.276	0.305	0.331	0.363	0.385
72		0.081	0.153	0.195	0.232	0.274	0.303	0.329	0.360	0.382
73		0.080	0.152	0.194	0.230	0.272	0.301	0.327	0.358	0.380
74		0.080	0.151	0.193	0.229	0.271	0.299	0.324	0.355	0.377
75		0.079	0.150	0.191	0.227	0.269	0.297	0.322	0.353	0.375
76		0.078	0.149	0.190	0.226	0.267	0.295	0.320	0.351	0.372
77		0.078	0.148	0.189	0.224	0.265	0.293	0.318	0.349	0.370
78		0.077	0.147	0.188	0.223	0.264	0.291	0.316	0.346	0.368
79		0.077	0.146	0.186	0.221	0.262	0.289	0.314	0.344	0.365
80		0.076	0.145	0.185	0.220	0.260	0.287	0.312	0.342	0.363
81		0.076	0.144	0.184	0.219	0.259	0.285	0.310	0.340	0.361
82		0.075	0.143	0.183	0.217	0.257	0.284	0.308	0.338	0.359
83		0.075	0.142	0.182	0.216	0.255	0.282	0.306	0.336	0.357
84		0.074	0.141	0.181	0.215	0.254	0.280	0.305	0.334	0.355
85		0.074	0.140	0.180	0.213	0.252	0.279	0.303	0.332	0.353
86		0.074	0.139	0.179	0.212	0.251	0.277	0.301	0.330	0.351
87		0.073	0.139	0.177	0.211	0.250	0.276	0.299	0.328	0.349
88		0.073	0.138	0.176	0.210	0.248	0.274	0.298	0.327	0.347
89		0.072	0.137	0.175	0.209	0.247	0.272	0.296	0.325	0.345
90		0.072	0.136	0.174	0.207	0.245	0.271	0.294	0.323	0.343
91		0.072	0.135	0.173	0.206	0.244	0.269	0.293	0.321	0.341
92		0.071	0.135	0.173	0.205	0.243	0.268	0.291	0.319	0.339
93		0.071	0.134	0.172	0.204	0.241	0.267	0.290	0.318	0.338
94		0.070	0.133	0.171	0.203	0.240	0.265	0.288	0.316	0.336
95		0.070	0.133	0.170	0.202	0.239	0.264	0.287	0.314	0.334
96		0.070	0.132	0.169	0.201	0.238	0.262	0.285	0.313	0.332
97		0.069	0.131	0.168	0.200	0.236	0.261	0.284	0.311	0.331
98		0.069	0.130	0.167	0.199	0.235	0.260	0.282	0.310	0.329
99		0.068	0.130	0.166	0.198	0.234	0.258	0.281	0.308	0.327
100		0.068	0.129	0.165	0.197	0.233	0.257	0.279	0.307	0.326

For the table entries through $n = 11$ in Appendix Table B.20, the exact distribution of Σd^2 was used (Owen, 1962: 400–406). For $n = 12$, the exact distribution of de Jonge and van Montfort (1972) was used; for n's of 13 through 16, the exact distributions of Otten (1973) were used; and for $n = 12$–18, the exact distributions of Franklin (1988a) were used. For larger n, the Pearson-curve approximations described by Olds (1938) were employed, with the excellent accuracy of results discussed elsewhere (Franklin, 1988b, 1989; Zar, 1972).

Examples:

$$(r_s)_{0.05(2),9} = 0.700 \quad \text{and} \quad (r_s)_{0.01(2),52} = 0.356$$

For n larger than those in this table, we may utilize either Appendix Table B.17 or, equivalently, Equation 19.4. The accuracy of this procedure is discussed by Zar (1972).

The critical values in this table are the probabilities ≤ the column headings.

The exact probability of r_s can be estimated as the probability of a normal deviate (see Section 6.1),

$$Z = r_s\sqrt{n - 1},$$

or by substituting r_s for r in calculating t via Equations 19.3 and 19.4. Iman and Conover (1978) reported that the use of Z is conservative (i.e., the probability of a Type I error is less than α) for $\alpha > 0.05$ and liberal (probability greater than α) for $\alpha < 0.05$, whereas t behaves in the opposite fashion; and an even better estimate is obtained by averaging the probability of Z and the probability of t. Fahoome (2002) advised that, for $\alpha = 0.05$, $P(Z)$ lies between 0.045 and 0.055 if n is at least 12; and, for $\alpha = 0.01$, $P(Z)$ is between 0.009 and 0.011 for n of at least 40. It appears inadvisable to use these approximations for probabilities as small as 0.001 unless n is at least 60.

TABLE B.21: Critical Values of the Top-Down Correlation Coefficient, r_T

n	$\alpha(1)$: 0.25	0.10	0.05	0.025	0.01	0.005	0.001	0.0005
3	0.786	1.000	1.000	1.000	1.000	1.000	1.000	1.000
4	0.478	0.870	0.942	1.000	1.000	1.000	1.000	1.000
5	0.752	0.905	0.959	0.977	1.000	1.000	1.000	1.000
6	0.324	0.676	0.810	0.887	0.943	0.969	1.000	1.000
7	0.271	0.622	0.738	0.836	0.906	0.934	0.977	0.991
8	0.245	0.575	0.692	0.779	0.865	0.904	0.960	0.972
9	0.228	0.530	0.654	0.742	0.826	0.871	0.936	0.953
10	0.245	0.492	0.620	0.707	0.793	0.840	0.913	0.933
11	0.204	0.461	0.539	0.677	0.762	0.812	0.890	0.913
12	0.195	0.435	0.560	0.650	0.735	0.786	0.868	0.893
13	0.186	0.412	0.535	0.625	0.711	0.762	0.847	0.873
14	0.179	0.393	0.513	0.602	0.689	0.740	0.827	0.854
15		0.389	0.486	0.565	0.680	0.688	0.826	
16		0.376	0.470	0.546	0.656	0.665	0.798	
17		0.364	0.454	0.528	0.635	0.644	0.773	
18		0.353	0.440	0.512	0.615	0.625	0.750	
19		0.343	0.428	0.497	0.598	0.607	0.728	
20		0.334	0.416	0.433	0.581	0.591	0.709	
21		0.325	0.405	0.470	0.566	0.576	0.691	
22		0.317	0.395	0.459	0.552	0.562	0.674	
23		0.310	0.386	0.448	0.538	0.549	0.659	
24		0.303	0.377	0.438	0.526	0.537	0.644	
25		0.297	0.368	0.428	0.515	0.526	0.631	
26		0.291	0.361	0.419	0.504	0.515	0.618	
27		0.285	0.354	0.411	0.494	0.505	0.606	
28		0.280	0.347	0.403	0.484	0.496	0.595	
29		0.275	0.340	0.395	0.475	0.487	0.584	
30		0.270	0.334	0.388	0.466	0.478	0.574	

For n through 14, the critical values were determined from the exact distributions of Iman and Conover (1985) and Iman (1987). For $15 \leq n \leq 30$, the critical values are reprinted, with permission of the publisher, from Iman and Conover, copyright 1987, *Technometrics* 29: 351–357; all rights reserved. For $n > 30$, the normal approximation may be employed:

$$Z = r_T \sqrt{n - 1}.$$

TABLE B.22: Critical Values of the Symmetry Measure, $\sqrt{b_1}$

n	$\alpha(2)$: 0.10 $\alpha(1)$: 0.05	0.05 0.025	0.02 0.01	0.01 0.005
20	0.772	0.940	1.150	1.304
25	0.711	0.866	1.059	1.200
30	0.662	0.806	0.986	1.117
35	0.521	0.756	0.923	1.044
40	0.588	0.714	0.871	0.985
45	0.559	0.679	0.826	0.934
50	0.534	0.647	0.788	0.889
60	0.492	0.596	0.724	0.816
70	0.459	0.556	0.673	0.758
80	0.432	0.522	0.632	0.710
90	0.409	0.494	0.597	0.670
100	0.390	0.470	0.567	0.636
125	0.351	0.422	0.508	0.569
150	0.322	0.387	0.465	0.519
175	0.299	0.359	0.430	0.481
200	0.280	0.336	0.403	0.449
250	0.251	0.301	0.361	0.402
300	0.230	0.275	0.329	0.366
350	0.213	0.255	0.305	0.339
400	0.200	0.239	0.285	0.317
450	0.188	0.225	0.269	0.299
500	0.179	0.214	0.355	0.283

Values in Appendix Table B.22 are reprinted from E. S. Pearson and H. O. Hartley (eds.), *Biometrika Tables for Statisticians. Volume I*, 1976, p. 207, by permission of the Oxford University Press.

TABLE B.23: Critical Values of the Kurtosis Measure, b_2

	Lower Tail				Upper Tail			
	$\alpha(2)$: 0.01	0.02	0.05	0.10	0.10	0.05	0.02	0.01
n	$\alpha(1)$: 0.005	0.01	0.025	0.05	0.05	0.025	0.01	0.005
20	1.58	1.64	1.73	1.83	4.18	4.68	5.38	5.91
30	1.73	1.79	1.89	1.98	4.12	4.57	5.20	5.69
40	1.83	1.89	1.99	2.07	4.06	4.46	5.04	5.48
50	1.91	1.95	2.06	2.15	4.00	4.36	4.88	5.28
75	2.05	2.08	2.19	2.27	3.87	4.17	4.59	4.90
100	2.13	2.18	2.27	2.35	3.77	4.03	4.39	4.66
125	2.19	2.24	2.32	2.40	3.70	3.93	4.24	4.48
150	2.24	2.29	2.37	2.45	3.65	3.86	4.13	4.34
175	2.28	2.34	2.41	2.48	3.61	3.79	4.04	4.23
200	2.32	2.37	2.44	2.51	3.57	3.75	3.98	4.16
250	—	2.42	—	2.55	3.52	—	3.87	—
300	—	2.46	—	2.59	3.47	—	3.79	—
400	—	2.52	—	2.64	3.41	—	3.67	—
500	—	2.57	—	2.67	3.37	—	3.60	—
600	—	2.60	—	2.70	3.34	—	3.54	—
700	—	2.62	—	2.72	3.31	—	3.50	—
800	—	2.65	—	2.74	3.29	—	3.46	—
900	—	2.66	—	2.75	3.28	—	3.43	—
1000	—	2.68	—	2.76	3.26	—	3.41	—
2000	—	2.77	—	2.83	3.18	—	3.28	—

Values in Appendix Table B.23 are reprinted from E. S. Pearson and H. O. Hartley (eds.), *Biometrika Tables for Statisticians. Volume I*, 1976, p. 208, by permission of the Oxford University Press.

TABLE B.24: The Arcsine Transformation, p'

p	0	1	2	3	4	5	6	7	8	9	p
0.000	0.00	0.57	0.81	0.99	1.15	1.28	1.40	1.52	1.62	1.72	0.000
0.001	1.81	1.90	1.99	2.07	2.14	2.22	2.29	2.36	2.43	2.50	0.001
0.002	2.56	2.63	3.69	2.75	2.81	2.87	2.92	2.98	3.03	3.09	0.002
0.003	3.14	3.19	3.24	3.29	3.34	3.39	3.44	3.49	3.53	3.58	0.003
0.004	3.63	3.67	3.72	3.76	3.80	3.85	3.89	3.93	3.97	4.01	0.004
0.005	4.05	4.10	4.14	4.17	4.21	4.25	4.29	4.33	4.37	4.41	0.005
0.006	4.44	4.48	4.52	4.55	4.59	4.62	4.66	4.70	4.73	4.76	0.006
0.007	4.80	4.83	4.87	4.90	4.93	4.97	5.00	5.03	5.07	5.10	0.007
0.008	5.13	5.16	5.20	5.23	5.26	5.29	5.32	5.35	5.38	5.41	0.008
0.009	5.44	5.47	5.50	5.53	5.56	5.59	5.62	5.65	5.68	5.71	0.009
0.01	5.74	6.02	6.29	6.55	6.80	7.03	7.27	7.49	7.71	7.92	0.01
0.02	3.13	8.33	8.53	8.72	8.91	9.10	9.28	9.46	9.63	9.80	0.02
0.03	9.97	10.14	10.30	10.47	10.63	10.78	10.94	11.09	11.24	11.39	0.03
0.04	11.54	11.68	11.83	11.97	12.11	12.25	12.38	12.52	12.66	12.79	0.04
0.05	12.92	13.05	13.18	13.31	13.44	13.56	13.69	13.81	13.94	14.06	0.05
0.06	14.18	14.30	14.42	14.54	14.65	14.77	14.89	15.00	15.12	15.23	0.06
0.07	15.34	15.45	15.56	15.68	15.79	15.89	16.00	16.11	16.22	16.32	0.07
0.08	16.43	16.54	16.64	16.74	16.85	16.95	17.05	17.15	17.26	17.36	0.08
0.09	17.46	17.56	17.66	17.76	17.85	17.95	18.05	18.15	18.24	18.34	0.09
0.10	18.43	18.53	18.63	18.72	18.81	18.91	19.00	19.09	19.19	19.28	0.10
0.11	19.37	19.46	19.55	19.64	19.73	19.82	19.91	20.00	20.09	20.18	0.11
0.12	20.27	20.36	20.44	20.53	20.62	20.70	20.79	20.88	20.96	21.05	0.12
0.13	21.13	21.22	21.30	21.39	21.47	21.56	21.64	21.72	21.81	21.89	0.13
0.14	21.97	22.06	22.14	22.22	22.30	22.38	22.46	22.54	22.63	22.71	0.14
0.15	22.79	22.87	22.95	23.03	23.11	23.18	23.26	23.34	23.42	23.50	0.15
0.16	23.58	23.66	23.73	23.81	23.89	23.97	24.04	24.12	24.20	24.27	0.16
0.17	24.35	24.43	24.50	24.58	24.65	24.73	24.80	24.88	24.95	25.03	0.17
0.18	25.10	25.18	25.25	25.33	25.40	25.47	25.55	25.62	25.70	25.77	0.18
0.19	25.84	25.91	25.99	26.06	26.13	26.21	26.28	26.35	26.42	26.49	0.19
0.20	26.57	26.64	26.71	26.78	26.85	26.92	26.99	27.06	27.13	27.20	0.20
0.21	27.27	27.35	27.42	27.49	27.56	27.62	27.69	27.76	27.83	27.90	0.21
0.22	27.97	28.04	28.11	28.18	28.25	28.32	28.39	28.45	28.52	28.59	0.22
0.23	28.66	28.73	28.79	28.86	28.93	29.00	29.06	29.13	29.20	29.27	0.23
0.24	29.33	29.40	29.47	29.53	29.60	29.67	29.73	29.80	29.87	29.93	0.24
0.25	30.00	30.07	30.13	30.20	30.26	30.33	30.40	30.46	30.53	30.59	0.25
0.26	30.66	30.72	30.79	30.85	30.92	30.98	31.05	31.11	31.18	31.24	0.26
0.27	31.31	31.37	31.44	31.50	31.56	31.63	31.69	31.76	31.82	31.88	0.27
0.28	31.95	32.01	32.08	32.14	32.20	32.27	32.33	32.39	32.46	32.52	0.28
0.29	32.58	32.65	32.71	32.77	32.83	32.90	32.96	33.02	33.09	33.15	0.29
0.30	33.21	33.27	33.34	33.40	33.46	33.52	33.58	33.65	33.71	33.77	0.30
0.31	33.83	33.90	33.96	34.02	34.08	34.14	34.20	34.27	34.33	34.39	0.31
0.32	34.45	34.51	34.57	34.63	34.70	34.76	34.82	34.88	34.94	35.00	0.32
0.33	35.06	35.12	35.18	35.24	35.30	35.37	35.43	35.49	35.55	35.61	0.33
0.34	35.67	35.73	35.79	35.85	35.91	35.97	36.03	36.09	36.15	36.21	0.34
0.35	36.27	36.33	36.39	36.45	36.51	36.57	36.63	36.69	36.75	36.81	0.35
0.36	36.87	36.93	36.99	37.05	37.11	37.17	37.23	37.29	37.35	37.41	0.36
0.37	37.46	37.52	37.58	37.64	37.70	37.76	37.82	37.88	37.94	38.00	0.37
0.38	38.06	38.12	38.17	38.23	38.29	38.35	38.41	38.47	38.53	38.59	0.38
0.39	38.65	38.70	38.76	38.82	38.88	38.94	39.00	39.06	39.11	39.17	0.39
0.40	39.23	39.29	39.35	39.41	39.47	39.52	39.58	39.64	39.70	39.76	0.40
0.41	39.82	39.87	39.93	39.99	40.05	40.11	40.16	40.22	40.28	40.34	0.41
0.42	40.40	40.45	40.51	40.57	40.63	40.69	40.74	40.80	40.86	40.92	0.42
0.43	40.98	41.03	41.09	41.15	41.21	41.27	41.32	41.38	41.44	41.50	0.43
0.44	41.55	41.61	41.67	41.73	41.78	41.84	41.90	41.96	42.02	42.07	0.44
0.45	42.13	42.19	42.25	42.30	42.36	42.42	42.48	42.53	42.59	42.65	0.45
0.46	42.71	42.76	42.82	42.88	42.94	42.99	43.05	43.11	43.17	43.22	0.46
0.47	43.28	43.94	43.39	43.45	43.51	43.57	43.62	43.68	43.74	43.80	0.47
0.48	43.83	43.91	43.97	44.03	44.08	44.14	44.20	44.26	44.31	44.37	0.48
0.49	44.43	44.48	44.54	44.60	44.66	44.71	44.77	44.83	44.89	44.94	0.49
0.50	45.00	45.06	45.11	45.17	45.23	45.29	45.34	45.40	45.46	45.52	0.50
0.51	45.57	45.63	45.69	45.74	45.80	45.86	45.92	45.97	46.03	46.09	0.51
0.52	46.15	46.20	46.26	46.32	46.38	46.43	46.49	46.55	46.61	46.66	0.52
0.53	46.72	46.78	46.83	46.89	46.95	47.01	47.06	47.12	47.18	47.24	0.53

TABLE B.24 (cont.): The Arcsine Transformation, p'

p	0	1	2	3	4	5	6	7	8	9	p
0.54	47.29	47.35	47.41	47.47	47.52	47.58	47.64	47.70	47.75	47.81	0.54
0.55	47.87	47.93	47.98	48.04	48.10	48.16	48.22	48.27	48.33	48.39	0.55
0.56	48.45	48.50	48.56	48.62	48.68	48.73	48.79	48.85	48.91	48.97	0.56
0.57	49.02	49.08	49.14	49.20	49.26	49.31	49.37	49.43	49.49	49.55	0.57
0.58	49.60	49.66	49.72	49.78	49.84	49.89	49.95	50.01	50.07	50.13	0.58
0.59	50.18	50.24	50.30	50.36	50.42	50.48	50.53	50.59	50.65	50.71	0.59
0.60	50.77	50.83	50.89	50.94	51.00	51.06	51.12	51.18	51.24	51.30	0.60
0.61	51.35	51.41	51.47	51.53	51.59	51.65	51.71	51.77	51.83	51.88	0.61
0.62	51.94	52.00	52.06	52.12	52.18	52.24	52.30	52.36	52.42	52.48	0.62
0.63	52.54	52.59	52.65	52.71	52.77	52.83	52.89	52.95	53.01	53.07	0.63
0.64	53.13	53.19	53.25	53.31	53.37	53.43	53.49	53.55	53.61	53.67	0.64
0.65	53.73	53.79	53.85	53.91	53.97	54.03	54.09	54.15	54.21	54.27	0.65
0.66	54.33	54.39	54.45	54.51	54.57	54.63	54.70	54.76	54.82	54.88	0.66
0.67	54.94	55.00	55.06	55.12	55.18	55.24	55.30	55.37	55.43	55.49	0.67
0.68	55.55	55.61	55.67	55.73	55.80	55.86	55.92	55.98	56.04	56.10	0.68
0.69	56.17	56.23	56.29	56.35	56.42	56.48	56.54	56.60	56.66	56.73	0.69
0.70	56.79	56.85	56.91	56.98	57.04	57.10	57.17	57.23	57.29	57.35	0.70
0.71	57.42	57.48	57.54	57.61	57.67	57.73	57.80	57.86	57.92	57.99	0.71
0.72	58.05	58.12	58.18	58.24	58.31	58.37	58.44	58.50	58.56	58.63	0.72
0.73	58.69	58.76	58.82	58.89	58.95	59.02	59.08	59.15	59.21	59.28	0.73
0.74	59.34	59.41	59.47	59.54	59.60	59.67	59.74	59.80	59.87	59.93	0.74
0.75	60.00	60.07	60.13	60.20	60.27	60.33	60.40	60.47	60.53	60.60	0.75
0.76	60.67	60.73	60.80	60.87	60.94	61.00	61.07	61.14	61.21	61.27	0.76
0.77	61.34	61.41	61.48	61.55	61.61	61.68	61.75	61.82	61.89	61.96	0.77
0.78	62.03	62.10	62.17	62.24	62.31	62.38	62.44	62.51	62.58	62.65	0.78
0.79	62.73	62.80	62.87	62.94	63.01	63.08	63.15	63.22	63.29	63.36	0.79
0.80	63.43	63.51	63.58	63.65	63.72	63.79	63.87	63.94	64.01	64.09	0.80
0.81	64.16	64.23	64.30	64.38	64.45	64.53	64.60	64.67	64.75	64.82	0.81
0.82	64.90	64.97	65.05	65.12	65.20	65.27	65.35	65.42	65.50	65.57	0.82
0.83	65.65	65.73	65.80	65.88	65.96	66.03	66.11	66.19	66.27	66.34	0.83
0.84	66.42	66.50	66.58	66.66	66.74	66.82	66.89	66.97	67.05	67.13	0.84
0.85	67.21	67.29	67.37	67.46	67.54	67.62	67.70	67.78	67.86	67.94	0.85
0.86	68.03	68.11	68.19	68.28	68.36	68.44	68.53	68.61	68.70	68.78	0.86
0.87	68.87	68.95	69.04	69.12	69.21	69.30	69.38	69.47	69.56	69.64	0.87
0.88	69.73	69.82	69.91	70.00	70.09	70.18	70.27	70.36	70.45	70.54	0.88
0.89	70.63	70.72	70.81	70.91	71.00	71.09	71.19	71.28	71.37	71.47	0.89
0.90	71.57	71.66	71.76	71.85	71.95	72.05	72.15	72.24	72.34	72.44	0.90
0.91	72.54	72.64	72.74	72.85	72.95	73.05	73.15	73.26	73.36	73.46	0.91
0.92	73.57	73.68	73.78	73.89	74.00	74.11	74.21	74.32	74.44	74.55	0.92
0.93	74.66	74.77	74.88	75.00	75.11	75.23	75.35	75.46	75.58	75.70	0.93
0.94	75.82	75.94	76.06	76.19	76.31	76.44	76.56	76.69	76.82	76.95	0.94
0.95	77.08	77.21	77.34	77.48	77.62	77.75	77.89	78.03	78.17	78.32	0.95
0.96	78.46	78.61	78.76	78.91	79.06	79.22	79.37	79.53	79.70	79.86	0.96
0.97	80.03	80.20	80.37	80.54	80.72	80.90	81.09	81.28	81.47	81.67	0.97
0.98	81.87	82.08	82.29	82.51	82.73	82.97	83.20	83.45	83.71	83.98	0.98
0.990	84.26	84.29	84.32	84.35	84.38	84.41	84.44	84.47	84.50	84.53	0.990
0.991	84.56	84.59	84.62	84.65	84.68	84.71	84.74	84.77	84.80	84.84	0.991
0.992	84.87	84.90	84.93	84.97	85.00	85.03	85.07	85.10	85.13	85.17	0.992
0.993	85.20	85.24	85.27	85.30	85.34	85.38	85.41	85.45	85.48	85.32	0.993
0.994	85.56	85.59	85.63	85.67	85.71	85.75	85.79	85.83	85.86	85.90	0.994
0.995	85.95	83.99	86.03	86.07	86.11	86.15	86.20	86.24	86.28	86.33	0.995
0.996	86.37	86.42	86.47	86.51	86.56	86.61	86.66	86.71	86.76	86.81	0.996
0.997	86.86	86.91	86.97	87.02	87.08	87.13	87.19	87.25	87.31	87.37	0.997
0.998	87.44	87.50	87.57	87.64	87.71	87.78	87.86	87.93	88.01	88.10	0.998
0.999	88.19	88.28	88.38	88.48	88.60	88.72	88.85	89.01	89.19	89.43	0.999
1.000	90.00										

By Equation 13.5,

$$p' = \arcsin\sqrt{p}$$

Examples:

$p = 0.712$, $p' = 57.54$ and $p = 0.9921$, $p' = 84.90$

TABLE B.25: Proportions, p, Corresponding to Arcsine Transformations, p'

p'	0	1	2	3	4	5	6	7	8	9	p'
0.0	0.0000	0.0000	0.0000	0.0000	0.0000	0.0001	0.0001	0.0001	0.0002	0.0002	0.0
1.0	0.0003	0.0004	0.0004	0.0005	0.0006	0.0007	0.0008	0.0009	0.0010	0.0011	1.0
2.0	0.0012	0.0013	0.0015	0.0016	0.0018	0.0019	0.0021	0.0022	0.0024	0.0026	2.0
3.0	0.0027	0.0029	0.0031	0.0033	0.0035	0.0037	0.0039	0.0042	0.0044	0.0046	3.0
4.0	0.0049	0.0051	0.0054	0.0056	0.0059	0.0062	0.0064	0.0067	0.0070	0.0073	4.0
5.0	0.0076	0.0079	0.0082	0.0085	0.0089	0.0092	0.0095	0.0099	0.0102	0.0106	5.0
6.0	0.0109	0.0113	0.0117	0.0120	0.0124	0.0128	0.0132	0.0136	0.0140	0.0144	6.0
7.0	0.0149	0.0153	0.0157	0.0161	0.0166	0.0170	0.0175	0.0180	0.0184	0.0189	7.0
8.0	0.0194	0.0199	0.0203	0.0208	0.0213	0.0218	0.0224	0.0229	0.0234	0.0239	8.0
9.0	0.0245	0.0250	0.0256	0.0261	0.0267	0.0272	0.0278	0.0284	0.0290	0.0296	9.0
10.0	0.0302	0.0308	0.0314	0.0320	0.0326	0.0332	0.0338	0.0345	0.0351	0.0358	10.0
11.0	0.0364	0.0371	0.0377	0.0384	0.0391	0.0397	0.0404	0.0411	0.0418	0.0425	11.0
12.0	0.0432	0.0439	0.0447	0.0454	0.0461	0.0468	0.0476	0.0483	0.0491	0.0498	12.0
13.0	0.0506	0.0514	0.0521	0.0529	0.0537	0.0345	0.0553	0.0561	0.0669	0.0577	13.0
14.0	0.0585	0.0593	0.0602	0.0610	0.0618	0.0627	0.0635	0.0644	0.0653	0.0661	14.0
15.0	0.0670	0.0679	0.0687	0.0696	0.0705	0.0714	0.0723	0.0732	0.0741	0.0751	15.0
16.0	0.0760	0.0769	0.0778	0.0788	0.0797	0.0807	0.0816	0.0826	0.0835	0.0845	16.0
17.0	0.0855	0.0865	0.0874	0.0884	0.0894	0.0904	0.0914	0.0924	0.0934	0.0945	17.0
18.0	0.0955	0.0965	0.0976	0.0986	0.0996	0.1007	0.1017	0.1028	0.1039	0.1049	18.0
19.0	0.1060	0.1071	0.1082	0.1092	0.1103	0.1114	0.1125	0.1136	0.1147	0.1159	19.0
20.0	0.1170	0.1181	0.1192	0.1204	0.1215	0.1225	0.1238	0.1249	0.1261	0.1273	20.0
21.0	0.1284	0.1296	0.1308	0.1320	0.1331	0.1343	0.1355	0.1367	0.1379	0.1391	21.0
22.0	0.1403	0.1415	0.1428	0.1440	0.1452	0.1464	0.1477	0.1489	0.1502	0.1514	22.0
23.0	0.1527	0.1539	0.1552	0.1565	0.1577	0.1590	0.1603	0.1616	0.1628	0.1641	23.0
24.0	0.1654	0.1667	0.1680	0.1693	0.1707	0.1720	0.1733	0.1746	0.1759	0.1773	24.0
25.0	0.1786	0.1799	0.1813	0.1826	0.1840	0.1853	0.1867	0.1881	0.1894	0.1908	25.0
26.0	0.1922	0.1935	0.1949	0.1963	0.1977	0.1991	0.2005	0.2019	0.2033	0.2047	26.0
27.0	0.2061	0.2075	0.2089	0.2104	0.2118	0.2132	0.2146	0.2161	0.2175	0.2190	27.0
28.0	0.2204	0.2219	0.2233	0.2248	0.2262	0.2277	0.2291	0.2306	0.2321	0.2336	28.0
29.0	0.2350	0.2365	0.2380	0.2395	0.2410	0.2425	0.2440	0.2455	0.2470	0.2485	29.0
30.0	0.2500	0.2515	0.2530	0.2545	0.2561	0.2576	0.2591	0.2607	0.2622	0.2637	30.0
31.0	0.2653	0.2668	0.2684	0.2699	0.2715	0.2730	0.2746	0.2761	0.2777	0.2792	31.0
32.0	0.2808	0.2824	0.2840	0.2855	0.2871	0.2887	0.2903	0.2919	0.2934	0.2950	32.0
33.0	0.2966	0.2982	0.2998	0.3014	0.3030	0.3046	0.3062	0.3079	0.3095	0.3111	33.0
34.0	0.3127	0.3143	0.3159	0.3176	0.3192	0.3208	0.3224	0.3241	0.3257	0.3274	34.0
35.0	0.3290	0.3306	0.3323	0.3339	0.3356	0.3372	0.3389	0.3405	0.3422	0.3438	35.0
36.0	0.3455	0.3472	0.3488	0.3505	0.3521	0.3538	0.3555	0.3572	0.3588	0.3605	36.0
37.0	0.3622	0.3639	0.3655	0.3672	0.3689	0.3706	0.3723	0.3740	0.3757	0.3773	37.0
38.0	0.3790	0.3807	0.3824	0.3841	0.3858	0.3875	0.3892	0.3909	0.3926	0.3943	38.0
39.0	0.3960	0.3978	0.3995	0.4012	0.4029	0.4046	0.4063	0.4080	0.4097	0.4115	39.0
40.0	0.4132	0.4149	0.4166	0.4183	0.4201	0.4218	0.4235	0.4252	0.4270	0.4287	40.0
41.0	0.4304	0.4321	0.4339	0.4356	0.4373	0.4391	0.4408	0.4425	0.4443	0.4460	41.0
42.0	0.4677	0.4495	0.4512	0.4529	0.4547	0.4564	0.4582	0.4599	0.4616	0.4634	42.0
43.0	0.4651	0.4669	0.4686	0.4703	0.4721	0.4738	0.4756	0.4773	0.4791	0.4808	43.0
44.0	0.4826	0.4843	0.4860	0.4878	0.4895	0.4913	0.4930	0.4948	0.4965	0.4983	44.0
45.0	0.5000	0.5017	0.5035	0.5052	0.5070	0.5087	0.5105	0.5122	0.5140	0.5157	45.0
46.0	0.5174	0.5192	0.5209	0.5227	0.5244	0.5262	0.5279	0.5297	0.5314	0.5331	46.0
47.0	0.5349	0.5366	0.5384	0.5401	0.5418	0.5436	0.5453	0.5471	0.5488	0.5505	47.0
48.0	0.5523	0.5540	0.5557	0.5575	0.5592	0.5609	0.5627	0.5644	0.5661	0.5679	48.0
49.0	0.5696	0.5713	0.5730	0.5748	0.5765	0.5782	0.5799	0.5817	0.5834	0.5851	49.0
50.0	0.5868	0.5885	0.5903	0.5920	0.5937	0.5954	0.5971	0.5988	0.6003	0.6022	50.0
51.0	0.6040	0.6057	0.6074	0.6091	0.6108	0.6125	0.6142	0.6159	0.6176	0.6193	51.0
52.0	0.6210	0.6227	0.6243	0.6260	0.6277	0.6294	0.6311	0.6328	0.6345	0.6361	52.0
53.0	0.6378	0.6395	0.6412	0.6428	0.6445	0.6462	0.6479	0.6495	0.6512	0.6528	53.0
54.0	0.6545	0.6562	0.6578	0.6595	0.6611	0.6628	0.6644	0.6661	0.6677	0.6694	54.0
55.0	0.6710	0.6726	0.6743	0.6759	0.6776	0.6792	0.6808	0.6824	0.6841	0.6857	55.0
56.0	0.6873	0.6889	0.6905	0.6921	0.6938	0.6954	0.6970	0.6986	0.7002	0.7018	56.0
57.0	0.7034	0.7050	0.7066	0.7081	0.7097	0.7113	0.7129	0.7145	0.7160	0.7176	57.0
58.0	0.7192	0.7208	0.7223	0.7239	0.7254	0.7270	0.7285	0.7301	0.7316	0.7332	58.0
59.0	0.7347	0.7363	0.7378	0.7393	0.7409	0.7424	0.7439	0.7455	0.7470	0.7485	59.0

TABLE B.25 (cont.): Proportions, p, Corresponding to Arcsine Transformations, p'

p'	0	1	2	3	4	5	6	7	8	9	p'
60.0	0.7500	0.7515	0.7530	0.7545	0.7560	0.7575	0.7590	0.7605	0.7620	0.7635	60.0
61.0	0.7650	0.7664	0.7679	0.7694	0.7709	0.7723	0.7738	0.7752	0.7767	0.7781	61.0
62.0	0.7796	0.7810	0.7825	0.7839	0.7854	0.7868	0.7882	0.7896	0.7911	0.7925	62.0
63.0	0.7939	0.7953	0.7967	0.7981	0.7995	0.8009	0.8023	0.8037	0.8051	0.8065	63.0
64.0	0.8078	0.8092	0.8106	0.8119	0.8133	0.8147	0.8160	0.8174	0.8187	0.8201	64.0
65.0	0.8214	0.8227	0.8241	0.8254	0.8267	0.8280	0.8293	0.8307	0.8320	0.8333	65.0
66.0	0.8346	0.8359	0.8372	0.8384	0.8397	0.8410	0.8423	0.8435	0.8448	0.8461	66.0
67.0	0.8473	0.8486	0.8498	0.8511	0.8523	0.8536	0.8548	0.8560	0.8572	0.8585	67.0
68.0	0.8597	0.8609	0.8621	0.8633	0.8645	0.8657	0.8659	0.8680	0.8692	0.8704	68.0
69.0	0.8716	0.8727	0.8739	0.8751	0.8762	0.8774	0.8785	0.8796	0.8808	0.8819	69.0
70.0	0.8830	0.8841	0.8853	0.8864	0.8875	0.8886	0.8897	0.8908	0.8918	0.8929	70.0
71.0	0.8940	0.8951	0.8961	0.8972	0.8983	0.8993	0.9004	0.9014	0.9024	0.9035	71.0
72.0	0.9045	0.9055	0.9066	0.9076	0.9086	0.9096	0.9106	0.9116	0.9126	0.9135	72.0
73.0	0.9145	0.9155	0.9165	0.9174	0.9184	0.9193	0.9203	0.9212	0.9222	0.9231	73.0
74.0	0.9240	0.9249	0.9259	0.9268	0.9277	0.9286	0.9295	0.9304	0.9313	0.9321	74.0
75.0	0.9330	0.9339	0.9347	0.9356	0.9365	0.9373	0.9382	0.9390	0.9398	0.9407	75.0
76.0	0.9415	0.9423	0.9431	0.9439	0.9447	0.9455	0.9463	0.9471	0.9479	0.9486	76.0
77.0	0.9494	0.9502	0.9509	0.9517	0.9524	0.9532	0.9539	0.9546	0.9553	0.9581	77.0
78.0	0.9568	0.9575	0.9582	0.9589	0.9596	0.9603	0.9609	0.9616	0.9623	0.9629	78.0
79.0	0.9636	0.9642	0.9649	0.9653	0.9662	0.9668	0.9674	0.9680	0.9686	0.9692	79.0
80.0	0.9698	0.9704	0.9710	0.9716	0.9722	0.9728	0.9733	0.9739	0.9744	0.9750	80.0
81.0	0.9755	0.9761	0.9766	0.9771	0.9776	0.9782	0.9787	0.9792	0.9797	0.9801	81.0
82.0	0.9806	0.9811	0.9816	0.9820	0.9825	0.9830	0.9834	0.9839	0.9843	0.9847	82.0
83.0	0.9851	0.9856	0.9860	0.9864	0.9868	0.9872	0.9876	0.9880	0.9833	0.9887	83.0
84.0	0.9891	0.9894	0.9898	0.9901	0.9903	0.9908	0.9911	0.9915	0.9918	0.9921	84.0
85.0	0.9924	0.9927	0.9930	0.9933	0.9935	0.9938	0.9941	0.9944	0.9946	0.9949	85.0
86.0	0.9951	0.9954	0.9956	0.9958	0.9961	0.9963	0.9965	0.9967	0.9969	0.9971	86.0
87.0	0.9973	0.9974	0.9976	0.9978	0.9979	0.9981	0.9982	0.9984	0.9985	0.9987	87.0
88.0	0.9988	0.9989	0.9990	0.9991	0.9992	0.9993	0.9994	0.9995	0.9996	0.9996	88.0
89.0	0.9997	0.9998	0.9998	0.9999	0.9999	0.9999	1.0000	1.0000	1.0000	1.0000	89.0
90.0	1.0000										

By Equation 13.6,

$$p = (\sin p')^2$$

Examples:

$$p' = 46.2,\ p = 0.5209 \quad \text{and} \quad p' = 85.3,\ p = 0.9933$$

TABLE B.26a: Binomial Coefficients, $_nC_X$

X	$n = 1$	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	X
0	*1*	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
1	*1*	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	1
2		1	3	6	10	15	21	28	36	45	55	66	78	91	105	120	136	2
3			1	4	10	20	35	56	84	120	165	220	286	364	455	560	680	3
4				1	5	15	35	70	126	210	330	495	715	1001	1365	1820	2380	4
5					1	6	21	56	126	252	462	792	1287	2002	3003	4368	6188	5
6						1	7	28	84	210	462	924	1716	3003	5005	8008	12376	6
7							1	8	36	120	330	792	1716	3432	6435	11440	19448	7
8								1	9	45	165	495	1287	3003	6435	12870	24310	8
9									1	10	55	220	715	2002	5005	11440	24310	9
10										1	11	66	286	1001	3003	8008	19448	10
11											1	12	78	364	1365	4368	12376	11
12												1	13	91	455	1820	6188	12
13													1	14	105	560	2380	13

X	$n = 18$	19	20	21	22	23	24	25	26	27	28	29	X
0	1	1	1	1	1	1	1	1	1	1	1	1	0
1	18	19	20	21	22	23	24	25	26	27	28	29	1
2	153	171	190	210	231	253	276	300	325	351	378	406	2
3	816	969	1140	1330	1540	1771	2024	2300	2600	2925	3276	3654	3
4	3060	3876	4845	5985	7315	8855	10626	12650	14950	17550	20475	23751	4
5	8568	11628	15504	20349	26334	33649	42504	53130	65780	80730	98280	118755	5
6	18564	27132	38760	54264	74613	100947	134596	177100	230230	296010	376740	475020	6
7	31824	50388	77520	116280	170544	245157	346104	480700	657800	888030	1184040	1560780	7
8	43758	75582	125970	203490	319770	490314	735471	1081575	1562275	2220075	3108105	4292145	8
9	48620	92378	167960	293930	497420	817190	1307504	2042975	3124550	4686825	6906900	10015005	9
10	43758	92378	184756	352716	646646	1144066	1961256	3268760	5311735	8436285	13123110	20030010	10
11	31824	75582	167960	352716	705432	1352078	2496144	4457400	7726160	13037895	21474180	34597290	11
12	18564	50388	125970	293930	646646	1352078	2704156	5200300	9657700	17383860	30421755	51895935	12
13	8568	27132	77520	203490	497420	1144066	2496144	5200300	10400600	20058300	37442160	67863915	13
14	3060	11628	38760	116280	319770	817190	1961256	4457400	9657700	20058300	40116600	77558760	14
15	816	3876	15504	54264	170544	490314	1307504	3268760	7726160	17383860	37442160	77558760	15
16	153	969	4845	20349	74613	245157	735471	2042975	5311735	13037895	30421755	67863915	16
17	18	171	1140	5985	26334	100947	346104	1081575	3124550	8436285	21474180	51895935	17

TABLE B.26a (cont.): Binomial Coefficients, $_nC_X$

X	$n = 30$	31	32	33	34	35	36	37	38	X
0	1	1	1	1	1	1	1	1	1	0
1	30	31	32	33	34	35	36	37	38	1
2	435	465	496	528	561	595	630	666	703	2
3	4060	4495	4960	5456	5984	6545	7140	7770	8436	3
4	27405	31465	35960	40920	46376	52360	58905	66045	73815	4
5	142506	169911	201376	237336	278256	324632	376992	435897	501942	5
6	593775	736281	906192	1107568	1344904	1623160	1947792	2324784	2760681	6
7	2035800	2629575	3365856	4272048	5379616	6724520	8347680	10295472	12620256	7
8	5852925	7888725	10518300	13884156	18156204	23535820	30260340	38608020	48903492	8
9	14307150	20160075	28048800	38567100	52451256	70607460	94143280	124403620	163011640	9
10	30045015	44352165	64512240	92561040	131128140	183579396	254186856	348330136	472733756	10
11	54627300	84672315	129024480	193536720	286097760	417225900	600805296	854992152	1203322288	11
12	86493225	141120525	225792840	354817320	548354040	834451800	1251677700	1852482996	2707475148	12
13	119759850	206253075	347373600	573166440	927983760	1476337800	2310789600	3562467300	5414950296	13
14	145422675	265182525	471435600	818809200	1391975640	2319959400	3796297200	6107086800	9669554100	14
15	155117520	300540195	565722720	1037158320	1855967520	3247943160	5567902560	9364199760	15471286560	15
16	145422675	300540195	601080390	1166803110	2203961430	4059928950	7307872110	12875774670	22239974430	16
17	119759850	265182525	565722720	1166803110	2333606220	4537567650	8597496600	15905368710	28781143380	17
18	86493225	206253075	471435600	1037158320	2203961430	4537567650	9075135300	17672631900	33578000610	18
19	54627300	141120525	347373600	818809200	1855967520	4059928950	8597496600	17672631900	35345263800	19
20	30045015	84672315	225792840	573166440	1391975640	3247943160	7307872110	15905368710	33578000610	20
21	14307150	44352165	129024480	354817320	927983760	2319959400	5567902560	12875774670	28781143380	21
22	5852925	20160075	64512240	193536720	548354040	1476337800	3796297200	9364199760	22239974430	22

TABLE B.26a (cont.): Binomial Coefficients, $_nC_X$

X	$n = 39$	40	41	42	43	44	45	46	X
0	1	1	1	1	1	1	1	1	0
1	39	40	41	42	43	44	45	46	1
2	741	780	820	861	903	946	990	1035	2
3	9139	9880	10660	11480	12341	13244	14190	15180	3
4	82251	91390	101270	111930	123410	135751	148995	163185	4
5	575757	658008	749398	850668	962598	1086008	1221759	1370754	5
6	3262623	3838380	4496388	5245786	6096454	7059052	8145060	9366819	6
7	15380937	18643560	22481940	26978328	32224114	38320568	45379620	53524680	7
8	61523748	76904685	95548245	118030185	145008513	177232627	215553195	260932815	8
9	211915132	273438880	350343565	445891810	563921995	708930508	886163135	1101716330	9
10	635745396	847660528	1121099408	1471442973	1917334783	2481256778	3190187286	4076350421	10
11	1676056044	2311801440	3159461968	4280561376	5752004349	7669339132	10150595910	13340783196	11
12	3910797436	5586853480	7898654920	11058116888	15338678264	21090682613	28760021745	38910617655	12
13	8122425444	12033222880	1762007630	25518731280	36576848168	51915526432	73006209045	101766230790	13
14	15084504396	23206929840	35240152720	52860229080	78378960360	114955808528	166871334960	239877544005	14
15	25140840660	40225345056	63432274896	98672427616	151532656696	229911617056	344867425584	511738760544	15
16	37711260990	62852101650	103077446706	166509721602	265182149218	416714805914	646626422970	991493848554	16
17	51021117810	88732378800	151584480450	254661927156	421171648758	686353797976	1103068603890	1749695026860	17
18	62359143990	113380261800	202112640600	353697121050	608359048206	1029530696964	1715884494940	2818953098830	18
19	68923264410	131282408400	244662670200	446775310800	800472431850	1408831480056	2438362177020	4154246671960	19
20	68923264410	137846528820	269128937220	513791607420	960566918220	1761039350070	3169870830126	5608233007146	20
21	62359143990	131282408400	269128937220	538257874440	1052049481860	2012616400080	3773655750150	6943526580276	21
22	51021117810	113380261800	244662670200	513791607420	1052049481860	2104098963720	4116715363800	7890371113950	22
23	37711260990	88732378800	202112640600	446775310800	960566918220	2012616400080	4116715363800	8233430727600	23
24	25140840660	62852101650	151584480450	353697121050	800472431850	1761039350070	3773655750150	7890371113950	24
25	15084504396	40225345056	103077446706	254661927156	608359048206	1408831480056	3169870830126	6943526580276	25

Shown are binomial coefficients, $_nC_X = \binom{n}{X}$, which are the numbers of combinations of n items taken X at a time. For each n, the array of binomial coefficients is symmetrical; the middle of the array is shown in italics, and the coefficient for X is the same as for $n - X$. *For example*, $_{18}C_{13} = {}_{18}C_5 = 8568$ and $_{46}C_{44} = {}_{46}C_2 = 1035$.

TABLE B.26b: Proportions of the Binomial Distribution for $p = q = 0.5$

X	$n = 1$	2	3	4	5	6	7	8	9	10	X
0	0.50000	0.25000	0.12500	0.06250	0.03125	0.01563	0.00781	0.00391	0.00195	0.00098	0
1	0.50000	0.50000	0.37500	0.25000	0.15625	0.09375	0.05469	0.03125	0.01758	0.00977	1
2		0.25000	0.37500	0.37500	0.31250	0.23438	0.16406	0.10938	0.07031	0.04395	2
3			0.12500	0.25000	0.31250	0.31250	0.27344	0.21875	0.16406	0.11719	3
4				0.05230	0.15625	0.23438	0.27344	0.27344	0.24609	0.20508	4
5					0.03125	0.09375	0.16406	0.21875	0.24609	0.24608	5
6						0.01563	0.05469	0.10938	0.16406	0.20508	6
7							0.00781	0.03125	0.07031	0.11719	7
8								0.00391	0.01758	0.04395	8
9									0.00195	0.00977	9
10										0.00098	10
X	$n = 11$	12	13	14	15	16	17	18	19	20	X
0	0.00049	0.00024	0.00012	0.00006	0.00003	0.00002	0.00001	0.00000	0.00000	0.00000	0
1	0.00537	0.00293	0.00159	0.00085	0.00046	0.00024	0.00013	0.00007	0.00004	0.00002	1
2	0.02686	0.01611	0.00952	0.00333	0.00320	0.00183	0.00104	0.00058	0.00033	0.00018	2
3	0.08057	0.05371	0.03491	0.02222	0.01389	0.00854	0.00519	0.00311	0.00185	0.00109	3
4	0.16113	0.12085	0.08728	0.06110	0.04166	0.02777	0.01816	0.01167	0.00739	0.00462	4
5	0.22559	0.19336	0.15710	0.12219	0.09164	0.06665	0.04721	0.03268	0.02218	0.01479	5
6	0.22559	0.22559	0.20947	0.18329	0.15274	0.12219	0.09442	0.07082	0.05175	0.03696	6
7	0.16113	0.19336	0.20947	0.20947	0.19638	0.17456	0.14838	0.12140	0.09611	0.07393	7
8	0.08057	0.12085	0.15710	0.18329	0.19638	0.19638	0.18547	0.16692	0.14416	0.12013	8
9	0.02686	0.05371	0.06728	0.12219	0.15274	0.17456	0.18547	0.18547	0.17620	0.16018	9
10	0.00537	0.01611	0.03491	0.06110	0.09164	0.12219	0.14838	0.16692	0.17620	0.17620	10
11	0.00049	0.00293	0.00952	0.02222	0.04166	0.06665	0.09442	0.12140	0.14416	0.16018	11
12		0.00024	0.00159	0.00555	0.01389	0.02777	0.04721	0.07082	0.09611	0.12013	12
13			0.00012	0.00085	0.00320	0.00854	0.01816	0.03268	0.05175	0.07393	13
14				0.00006	0.00046	0.00183	0.00519	0.01167	0.02218	0.03696	14
15					0.00003	0.00024	0.00104	0.00311	0.00739	0.01479	15
16						0.00002	0.00013	0.00058	0.00185	0.00462	16
17							0.00001	0.00007	0.00033	0.00109	17
18								0.00000	0.00004	0.00018	18
19									0.00000	0.00002	19
20										0.00000	20

$$P(X) = \frac{n!}{X!(n - X)!} p^X (1 - p)^{n-X}$$

TABLE B.27: Critical Values of C for the Sign Test or the Binomial Test with $p = 0.5$

n	$\alpha(2)$: .50 / $\alpha(1)$: .25	.20 / .10	.10 / .05	.05 / .025	.02 / .01	.01 / .005	.005 / .0025	.002 / .001	.001 / .0005
2	—	—	—	—	—	—	—	—	—
3	0	—	—	—	—	—	—	—	—
4	0	0	—	—	—	—	—	—	—
5	1	0	0	—	—	—	—	—	—
6	1	0	0	0	—	—	—	—	—
7	2	1	0	0	0	—	—	—	—
8	2	1	1	0	0	0	—	—	—
9	2	2	1	1	0	0	0	—	—
10	3	2	1	1	0	0	0	0	—
11	3	2	2	1	1	0	0	0	0
12	4	3	2	2	1	1	0	0	0
13	4	3	3	2	1	1	1	0	0
14	5	4	3	2	2	1	1	1	0
15	5	4	3	3	2	2	1	1	1
16	6	4	4	3	2	2	2	1	1
17	6	5	4	4	3	2	2	1	1
18	7	5	5	4	3	3	2	2	1
19	7	6	5	4	4	3	3	2	2
20	7	6	5	5	4	3	3	2	2
21	8	7	6	5	4	4	3	3	2
22	8	7	6	5	5	4	4	3	3
23	9	7	7	6	5	4	4	3	3
24	9	8	7	6	5	5	4	4	3
25	10	8	7	7	6	5	5	4	4
26	10	9	8	7	6	6	5	4	4
27	11	9	8	7	7	6	5	5	4
28	11	10	9	8	7	6	6	5	5
29	12	10	9	8	7	7	6	5	5
30	12	10	10	9	8	7	6	6	5
31	13	11	10	9	8	7	7	6	6
32	13	11	10	9	8	8	7	6	6
33	14	12	11	10	9	8	8	7	6
34	14	12	11	10	9	9	8	7	7
35	15	13	12	11	10	9	8	8	7
36	15	13	12	11	10	9	9	8	7
37	15	14	13	12	10	10	9	8	8
38	16	14	13	12	11	10	9	9	8
39	16	15	13	12	11	11	10	9	8
40	17	15	14	13	12	11	10	9	9
41	17	15	14	13	12	11	11	10	9
42	18	16	15	14	13	12	11	10	10
43	18	16	15	14	13	12	11	11	10
44	19	17	16	15	13	13	12	11	10
45	19	17	16	15	14	13	12	11	11
46	20	18	16	15	14	13	13	12	11
47	20	18	17	16	15	14	13	12	11
48	21	19	17	16	15	14	13	12	12
49	21	19	18	17	15	15	14	13	12
50	22	19	18	17	16	15	14	13	13
101	46	43	41	40	38	37	35	34	33
102	47	44	42	40	38	37	36	35	34
103	47	44	42	41	39	37	36	35	34
104	48	44	43	41	39	38	37	35	34
105	48	45	43	41	40	38	37	36	35
106	49	45	44	42	40	39	38	36	35
107	49	46	44	42	41	39	38	37	36
108	49	46	44	43	41	40	38	37	36
109	50	47	45	43	41	40	39	37	36
110	50	47	45	44	42	41	39	38	37

n	$\alpha(2)$: .50 / $\alpha(1)$: .25	.20 / .10	.10 / .05	.05 / .025	.02 / .01	.01 / .005	.005 / .0025	.002 / .001	.001 / .0005
51	22	20	19	18	16	15	15	14	13
52	23	20	19	18	17	16	15	14	13
53	23	21	20	18	17	16	15	14	14
54	24	21	20	19	18	17	16	15	14
55	24	22	20	19	18	17	16	15	14
56	24	22	21	20	18	17	17	16	15
57	25	23	21	20	19	18	17	16	15
58	25	23	22	21	19	18	17	16	16
59	26	24	22	21	20	19	18	17	16
60	26	24	23	21	20	19	18	17	16
61	27	24	23	22	20	20	19	18	17
62	27	25	24	22	21	20	19	18	17
63	28	25	24	23	21	20	19	18	18
64	28	26	24	23	22	21	20	19	18
65	29	26	25	24	22	21	20	19	18
66	29	27	23	24	23	22	21	20	19
67	30	27	26	25	23	22	21	20	19
68	30	28	26	25	23	22	22	20	20
69	31	28	27	25	24	23	22	21	20
70	31	29	27	26	24	23	22	21	20
71	32	29	28	26	25	24	23	22	21
72	32	30	28	27	25	24	23	22	21
73	33	30	28	27	26	25	24	22	22
74	33	30	29	28	26	25	24	23	22
75	34	31	29	28	26	25	24	23	22
76	34	31	30	28	27	26	25	24	23
77	35	32	30	29	27	26	25	24	23
78	35	32	31	29	28	27	26	24	24
79	36	33	31	30	28	27	26	25	24
80	36	33	32	30	29	28	27	25	24
81	36	34	32	31	29	28	27	26	25
82	37	34	33	31	30	28	27	26	25
83	37	35	33	32	30	29	28	27	26
84	38	35	33	32	30	29	28	27	26
85	38	36	34	32	31	30	29	27	26
86	39	36	34	33	31	30	29	28	27
87	39	37	35	33	32	31	29	28	27
88	40	37	35	34	32	31	30	29	28
89	40	37	36	34	33	31	30	29	28
90	41	38	36	35	33	32	31	29	29
91	41	38	37	35	33	32	31	30	29
92	42	39	37	36	34	33	32	30	29
93	42	39	38	36	34	33	32	31	30
94	43	40	38	37	35	34	32	31	30
95	43	40	38	37	35	34	33	32	31
96	44	41	39	37	36	34	33	32	31
97	44	41	39	38	36	35	34	32	31
98	45	42	40	38	37	35	34	33	32
99	45	42	40	39	37	36	35	33	32
100	46	43	41	39	37	36	35	34	33
151	70	67	64	62	60	59	57	56	54
152	71	67	65	63	61	59	58	56	55
153	71	68	65	63	61	60	58	56	55
154	72	68	66	64	62	60	59	57	56
155	72	69	66	64	62	61	59	57	56
156	73	69	67	65	63	61	60	58	57
157	73	69	67	65	63	61	60	58	57
158	74	70	68	66	63	62	60	59	57
159	74	70	68	66	64	62	61	59	58
160	75	71	69	67	64	63	61	60	58

TABLE B.27 (cont.): Critical Values of C for the Sign Test or the Binomial Test with $p = 0.5$

n	$\alpha(2)$: .50	.20	.10	.05	.02	.01	.005	.002	.001	n	$\alpha(2)$: .50	.20	.10	.05	.02	.01	.005	.002	.001
	$\alpha(1)$: .25	.10	.05	.025	.01	.005	.0025	.001	.0005		$\alpha(1)$: .25	.10	.05	.025	.01	.005	.0025	.001	.0005
111	51	48	46	44	42	41	40	38	37	161	75	71	69	67	65	63	62	60	59
112	51	48	46	45	43	41	40	39	38	162	76	72	70	68	65	64	62	60	59
113	52	49	47	45	43	42	41	39	38	163	76	72	70	68	66	64	63	61	60
114	52	49	47	46	44	42	41	40	39	164	77	73	70	68	66	65	63	61	60
115	53	50	48	46	44	43	42	40	39	165	77	73	71	69	67	65	64	62	60
116	53	50	48	46	45	43	42	40	39	166	78	74	71	69	67	65	64	62	61
117	54	51	49	47	45	44	42	41	40	167	78	74	72	70	68	66	64	63	61
118	54	51	49	47	45	44	43	41	40	168	79	75	72	70	68	66	65	63	62
119	55	52	50	48	46	45	43	42	41	169	79	75	73	71	68	67	65	63	62
120	55	52	50	48	46	45	44	42	41	170	80	76	73	71	69	67	66	64	63
121	56	52	50	49	47	45	44	43	42	171	80	76	74	72	69	68	66	64	63
122	56	53	51	49	47	46	45	43	42	172	81	77	74	72	70	68	67	65	64
123	57	53	51	50	48	46	45	43	42	173	81	77	75	73	70	69	67	65	64
124	57	54	52	50	48	47	45	44	43	174	82	78	75	73	71	69	68	66	64
125	58	54	52	51	49	47	46	44	43	175	82	78	76	74	71	70	68	66	65
126	58	55	53	51	49	48	46	45	44	176	83	79	76	74	72	70	68	67	65
127	59	55	53	51	49	48	47	45	44	177	83	79	77	74	72	70	69	67	66
128	59	56	54	52	50	48	47	46	45	178	83	79	77	75	73	71	69	67	66
129	60	56	54	52	50	49	48	46	45	179	84	80	78	75	73	71	70	68	67
130	60	57	55	53	51	49	48	46	45	180	84	80	78	76	73	72	70	68	67
131	61	57	55	53	51	50	49	47	46	181	85	81	78	76	74	72	71	69	67
132	61	58	56	54	52	50	49	47	46	182	85	81	79	77	74	73	71	69	68
133	62	58	56	54	52	51	49	48	47	183	86	82	79	77	75	73	72	70	68
134	62	59	56	55	53	51	50	48	47	184	86	82	80	78	75	74	72	70	69
135	63	59	57	55	53	52	50	49	48	185	87	83	80	78	76	74	72	71	69
136	63	60	57	56	53	52	51	49	48	186	87	83	81	79	76	74	73	71	70
137	64	60	58	56	54	52	51	50	48	187	88	84	81	79	77	75	73	71	70
138	64	60	58	57	54	53	52	50	49	188	88	84	82	80	77	75	74	72	71
139	65	61	59	57	55	53	52	50	49	189	89	85	82	80	78	76	74	72	71
140	65	61	59	57	55	54	52	51	50	190	89	85	83	81	78	76	75	73	71
141	65	62	60	58	56	54	53	51	50	191	90	86	83	81	78	77	75	73	72
142	66	62	60	58	56	55	53	52	51	192	90	86	84	81	79	77	76	74	72
143	66	63	61	59	57	55	54	52	51	193	91	87	84	82	79	78	76	74	73
144	67	63	61	59	57	56	54	53	51	194	91	87	85	82	80	78	77	75	73
145	67	64	62	60	58	56	55	53	52	195	92	88	85	83	80	79	77	75	74
146	68	64	62	60	58	56	55	53	52	196	92	88	85	83	81	79	77	75	74
147	68	65	63	61	58	57	56	54	53	197	93	89	86	84	81	79	78	76	75
148	69	65	63	61	59	57	56	54	53	198	93	89	86	84	82	80	78	76	75
149	69	66	63	62	59	58	56	55	54	199	94	89	87	85	82	80	79	77	75
150	70	66	64	62	60	58	57	55	54	200	94	90	87	85	83	81	79	77	76
201	95	90	88	86	83	81	80	78	76	251	119	114	111	109	106	104	102	100	99
202	95	91	88	86	83	82	80	78	77	252	120	115	112	109	107	105	103	101	99
203	96	91	89	87	84	82	81	79	77	253	120	115	112	110	107	105	103	101	99
204	96	92	89	87	84	83	81	79	78	254	121	116	113	110	107	106	104	101	100
205	97	92	90	87	85	83	81	79	78	255	121	116	113	111	108	106	104	102	100
206	97	93	90	88	85	84	82	80	78	256	122	117	114	111	108	106	105	102	101
207	98	93	91	88	86	84	82	80	79	257	122	117	114	112	109	107	105	103	101
208	98	94	91	89	86	84	83	81	79	258	123	118	115	112	109	107	106	103	102
209	99	94	92	89	87	85	83	81	80	259	123	118	115	113	110	108	106	104	102
210	99	95	92	90	87	85	84	82	80	260	124	119	116	113	110	108	106	104	103
211	100	95	93	90	88	86	84	82	81	261	124	119	116	114	111	109	107	105	103
212	100	96	93	91	88	86	85	83	81	262	125	120	117	114	111	109	107	105	103
213	101	96	94	91	89	87	85	83	82	263	125	120	117	115	112	110	108	106	104
214	101	97	94	92	89	87	86	83	82	264	126	121	118	115	112	110	108	106	104
215	102	97	94	92	89	88	86	84	82	265	126	121	118	116	113	111	109	106	105
216	102	98	95	93	90	88	86	84	83	266	126	122	119	116	113	111	109	107	105
217	103	98	95	93	90	89	87	85	83	267	127	122	119	117	114	111	110	107	106
218	103	99	96	94	91	89	87	85	84	268	127	123	120	117	114	112	110	108	106
219	104	99	96	94	91	89	88	86	84	269	128	123	120	117	114	112	111	108	107
220	104	99	97	94	92	90	88	86	85	270	128	123	120	118	115	113	111	109	107

TABLE B.27 (cont.): Critical Values of C for the Sign Test or the Binomial Test with $p = 0.5$

n	$\alpha(2)$: .50 / $\alpha(1)$: .25	.20 / .10	.10 / .05	.05 / .025	.02 / .01	.01 / .005	.005 / .0025	.002 / .001	.001 / .0005
221	104	100	97	95	92	90	89	87	85
222	105	100	98	95	93	91	89	87	86
223	105	101	98	96	93	91	90	88	86
224	106	101	99	96	94	92	90	88	86
225	106	102	99	97	94	92	91	88	87
226	107	102	100	97	95	93	91	89	87
227	107	103	100	98	95	93	91	89	88
228	108	103	101	98	95	94	92	90	88
229	108	104	101	99	96	94	92	90	89
230	109	104	102	99	96	95	93	91	89
231	109	105	102	100	97	95	93	91	90
232	110	105	102	100	97	95	94	92	90
233	110	106	103	101	98	96	94	92	90
234	111	106	103	101	98	96	95	92	91
235	111	107	104	101	99	97	95	93	91
236	112	107	104	102	99	97	95	93	92
237	112	108	105	102	100	98	96	94	92
238	113	108	105	103	100	98	96	94	93
239	113	109	106	103	101	99	97	95	93
240	114	109	106	104	101	99	97	95	94
241	114	110	107	104	101	100	98	96	94
242	115	110	107	105	102	100	98	96	94
243	115	111	108	105	102	100	99	96	95
244	116	111	108	106	103	101	99	97	95
245	116	111	109	106	103	101	100	97	96
246	117	112	109	107	104	102	100	98	96
247	117	112	110	107	104	102	100	98	97
248	118	113	110	108	105	103	101	99	97
249	118	113	111	108	105	103	101	99	98
250	119	114	111	109	106	104	102	100	98
301	144	138	135	133	129	127	125	123	121
302	144	139	136	133	130	128	126	123	121
303	145	139	136	133	130	128	126	124	122
304	145	140	137	134	131	129	127	124	122
305	146	140	137	134	131	129	127	125	123
306	146	141	138	135	132	130	127	125	123
307	147	141	138	135	132	130	128	125	124
308	147	142	139	136	133	130	128	126	124
309	148	142	139	136	133	131	129	126	125
310	148	143	140	137	134	131	129	127	125
311	149	143	140	137	134	132	130	127	126
312	149	144	140	138	134	132	130	128	126
313	150	144	141	138	135	133	131	128	126
314	150	145	141	139	135	133	131	129	127
315	151	145	142	139	136	134	132	129	127
316	151	146	142	140	136	134	132	130	128
317	151	146	143	140	137	135	133	130	128
318	152	147	143	141	137	135	133	131	129
319	152	147	144	141	138	136	133	131	129
320	153	148	144	141	138	136	134	131	130
321	153	148	145	142	139	136	134	132	130
322	154	149	145	142	139	137	135	132	131
323	154	149	146	143	140	137	135	133	131
324	155	149	146	143	140	138	136	133	131
325	155	150	147	144	141	138	136	134	132
326	156	150	147	144	141	139	137	134	132
327	156	151	148	145	141	139	137	135	133
328	157	151	148	145	142	140	138	135	133
329	157	152	149	146	142	140	138	136	134
330	158	152	149	146	143	141	139	136	134

n	$\alpha(2)$: .50 / $\alpha(1)$: .25	.20 / .10	.10 / .05	.05 / .025	.02 / .01	.01 / .005	.005 / .0025	.002 / .001	.001 / .0005
271	129	124	121	118	115	113	111	109	107
272	129	124	121	119	116	114	112	110	108
273	130	125	122	119	116	114	112	110	108
274	130	125	122	120	117	115	113	110	109
275	131	126	123	120	117	115	113	111	109
276	131	126	123	121	118	116	114	111	110
277	132	127	124	121	118	116	114	112	110
278	132	127	124	122	119	117	115	112	111
279	133	128	125	122	119	117	115	113	111
280	133	128	125	123	120	117	116	113	112
281	134	129	126	123	120	118	116	114	112
282	134	129	126	124	120	118	116	114	112
283	135	130	127	124	121	119	117	115	113
284	135	130	127	124	121	119	117	115	113
285	136	131	128	125	122	120	118	115	114
286	136	131	128	125	122	120	118	116	114
287	137	132	129	126	123	121	119	116	115
288	137	132	129	126	123	121	119	117	115
289	138	133	130	127	124	122	120	117	116
290	138	133	130	127	124	122	120	118	116
291	139	134	130	128	125	123	121	118	117
292	139	134	131	128	125	123	121	119	117
293	140	135	131	129	126	123	122	119	117
294	140	135	132	129	126	124	122	120	118
295	141	135	132	130	127	124	122	120	118
296	141	136	133	130	127	125	123	120	119
297	142	136	133	131	127	125	123	121	119
298	142	137	134	131	128	126	124	121	120
299	143	137	134	132	128	126	124	122	120
300	143	138	135	132	129	127	125	122	121
351	168	162	159	156	153	150	148	146	144
352	169	163	160	157	153	151	149	146	144
353	169	163	160	157	154	151	149	147	145
354	170	164	161	158	154	152	150	147	145
355	170	164	161	158	155	152	150	147	146
356	171	165	161	159	155	153	151	148	146
357	171	165	162	159	156	153	151	148	146
358	172	166	162	159	156	154	151	149	147
359	172	166	163	160	156	154	152	149	147
360	173	167	163	160	157	155	152	150	148
361	173	167	164	161	157	155	153	150	148
362	174	168	164	161	158	156	153	151	149
363	174	168	165	162	158	156	154	151	149
364	175	169	165	162	159	156	154	152	150
365	175	169	166	163	159	157	155	152	150
366	176	170	166	163	160	157	155	152	151
367	176	170	167	164	160	158	156	153	151
368	177	171	167	164	161	158	156	153	152
369	177	171	168	165	161	159	157	154	152
370	178	172	168	165	162	159	157	154	152
371	178	172	169	166	162	160	158	155	153
372	178	173	169	166	163	160	158	155	153
373	179	173	170	167	163	161	158	156	154
374	179	174	170	167	164	161	159	156	154
375	180	174	171	168	164	162	159	157	155
376	180	175	171	168	164	162	160	157	155
377	181	175	172	168	165	163	160	158	156
378	181	176	172	169	165	163	161	158	156
379	182	176	172	169	166	163	161	158	157
380	182	177	173	170	166	164	162	155	157

TABLE B.27 (cont.): Critical Values of C for the Sign Test or the Binomial Test with $p = 0.5$

n	$\alpha(2)$: .50 / $\alpha(1)$: .25	.20 / .10	.10 / .05	.05 / .025	.02 / .01	.01 / .005	.005 / .0025	.002 / .001	.001 / .0005
331	158	153	150	147	143	141	139	136	135
332	159	153	150	147	144	142	139	137	135
333	159	154	150	148	144	142	140	137	136
334	160	154	151	148	145	142	140	138	136
335	160	155	151	149	145	143	141	138	136
336	161	155	152	149	146	143	141	139	137
337	161	156	152	150	146	144	142	139	137
338	162	156	153	150	147	144	142	140	138
339	162	157	153	150	147	145	143	140	138
340	163	157	154	151	148	145	143	141	139
341	163	158	154	151	148	146	144	141	139
342	164	158	155	152	149	146	144	141	140
343	164	159	155	152	149	147	145	142	140
344	165	159	156	153	149	147	145	142	141
345	165	160	156	153	150	148	145	143	141
346	166	160	157	154	150	148	146	143	141
347	166	161	157	154	151	149	146	144	142
348	167	161	158	155	151	149	147	144	142
349	167	162	158	155	152	149	147	145	143
350	168	162	159	156	152	150	148	145	143
401	193	187	183	180	176	174	171	169	167
402	193	187	184	180	177	174	172	169	167
403	194	188	184	181	177	175	172	170	168
404	194	188	184	181	178	175	173	170	168
405	195	189	185	182	178	176	173	170	168
406	195	189	185	182	179	176	174	171	169
407	196	190	186	183	179	177	174	171	169
408	196	190	186	183	180	177	175	172	170
409	197	191	187	184	180	177	175	172	170
410	197	191	187	184	180	178	176	173	171
411	198	192	188	185	181	178	176	173	171
412	198	192	188	185	181	179	177	174	172
413	199	192	189	186	182	179	177	174	172
414	199	193	189	186	182	180	177	175	173
415	200	193	190	187	183	180	178	175	173
416	200	194	190	187	183	181	178	176	174
417	201	194	191	187	184	181	179	176	174
418	201	195	191	188	184	182	179	176	174
419	202	195	192	188	185	182	180	177	175
420	202	196	192	189	185	183	180	177	175
421	203	196	193	189	186	183	181	178	176
422	203	197	193	190	186	184	181	178	176
423	204	197	194	190	187	184	182	179	177
424	204	198	194	191	187	185	182	179	177
425	205	198	195	191	188	185	183	180	178
426	205	199	195	192	188	185	183	180	178
427	206	199	196	192	188	186	184	181	179
428	206	200	196	193	189	186	184	181	179
429	207	200	196	193	189	187	184	182	179
430	207	201	197	194	190	187	185	182	180
431	207	201	197	194	190	188	185	182	180
432	208	202	198	195	191	188	186	183	181
433	208	202	198	195	191	189	186	183	181
434	209	203	199	196	192	189	187	184	182
435	209	203	199	196	192	190	187	184	182
436	210	204	200	197	193	190	188	185	183
437	210	204	200	197	193	191	188	185	183
438	211	205	201	198	194	191	189	186	184
439	211	205	201	198	194	192	189	186	184
440	212	206	202	198	195	192	190	187	185

n	$\alpha(2)$: .50 / $\alpha(1)$: .25	.20 / .10	.10 / .05	.05 / .025	.02 / .01	.01 / .005	.005 / .0025	.002 / .001	.001 / .0005
381	183	177	173	170	167	164	162	159	157
382	183	177	174	171	167	165	163	160	158
383	184	178	174	171	168	165	163	160	158
384	184	178	175	172	168	166	164	161	159
385	185	179	175	172	169	166	164	161	159
386	185	179	176	173	169	167	164	162	160
387	186	180	176	173	170	167	165	162	160
388	186	180	177	174	170	168	165	163	161
389	187	181	177	174	171	168	166	163	161
390	187	181	178	175	171	169	166	164	162
391	188	182	178	175	172	169	167	164	162
392	188	182	179	176	172	170	167	164	162
393	189	183	179	176	172	170	168	165	163
394	189	183	180	177	173	170	168	165	163
395	190	184	180	177	173	171	169	166	164
396	190	184	181	178	174	171	169	166	164
397	191	185	181	178	174	172	170	167	165
398	191	185	182	178	175	172	170	167	165
399	192	186	182	179	175	173	171	168	166
400	192	186	183	179	176	173	171	168	166
451	217	211	207	204	200	197	195	192	190
452	218	211	208	204	200	198	195	192	190
453	218	212	208	205	201	198	196	193	191
454	219	212	208	205	201	199	196	193	191
455	219	213	209	206	202	199	197	194	191
456	220	213	209	206	202	200	197	194	192
457	220	214	210	207	203	200	198	195	192
458	221	214	210	207	203	200	198	195	193
459	221	215	211	208	204	201	198	195	193
460	222	215	211	208	204	201	199	196	194
461	222	216	212	208	205	202	199	196	194
462	223	216	212	209	205	202	200	197	195
463	223	217	213	209	205	203	200	197	195
464	224	217	213	210	206	203	201	198	196
465	224	218	214	210	206	204	201	198	196
466	225	218	214	211	207	204	202	199	197
467	225	219	215	211	207	205	202	199	197
468	226	219	215	212	208	205	203	200	197
469	226	220	216	212	208	206	203	200	198
470	227	220	216	213	209	206	204	201	198
471	227	221	217	213	209	207	204	201	199
472	228	221	217	214	210	207	205	201	199
473	228	222	218	214	210	208	205	202	200
474	229	222	218	215	211	208	205	202	200
475	229	223	219	215	211	208	206	203	201
476	230	223	219	216	212	209	206	203	201
477	230	224	220	216	212	209	207	204	202
478	231	224	220	217	213	210	207	204	202
479	231	224	221	217	213	210	208	205	203
480	232	225	221	218	214	211	208	205	203
481	232	225	221	218	214	211	209	206	203
482	233	226	222	218	214	212	209	206	204
483	233	226	222	219	215	212	210	207	204
484	234	227	223	219	215	213	210	207	205
485	234	227	223	220	216	213	211	208	205
486	235	228	224	220	216	214	211	208	206
487	235	228	224	221	217	214	212	208	206
488	236	229	225	221	217	215	212	209	207
489	236	229	225	222	218	215	212	209	207
490	237	230	226	222	218	216	213	210	208

TABLE B.27 (cont.): Critical Values of C for the Sign Test or the Binomial Test with $p = 0.5$

n	$\alpha(2)$: .50 / $\alpha(1)$: .25	.20 / .10	.10 / .05	.05 / .025	.02 / .01	.01 / .005	.005 / .0025	.002 / .001	.001 / .0005
441	212	206	202	199	195	192	190	187	185
442	213	207	203	199	196	193	191	188	185
443	213	207	203	200	196	193	191	188	186
444	214	207	204	200	197	194	191	188	186
445	214	208	204	201	197	194	192	189	187
446	215	208	205	201	197	195	192	189	187
447	215	209	205	202	198	195	193	190	188
448	216	209	206	202	198	196	193	190	188
449	216	210	206	203	199	196	194	191	189
450	217	210	207	203	199	197	194	191	189
501	242	235	231	228	223	221	218	215	213
502	242	236	232	228	224	221	219	215	213
503	243	236	232	229	224	222	219	216	214
504	243	237	233	229	225	222	220	216	214
505	244	237	233	229	225	223	220	217	215
506	244	238	234	230	226	223	220	217	215
507	245	238	234	230	226	224	221	218	216
508	245	239	234	231	227	224	221	218	216
509	246	239	235	231	227	224	222	219	216
510	246	240	235	232	228	225	222	219	217
511	247	240	236	232	228	225	223	220	217
512	247	241	236	233	229	226	223	220	218
513	248	241	237	233	229	226	224	221	218
514	248	241	237	234	230	227	224	221	219
515	249	242	238	234	230	227	225	221	219
516	249	242	238	235	231	228	225	222	220
517	250	243	239	235	231	228	226	222	220
518	250	243	239	236	232	229	226	223	221
519	251	244	240	236	232	229	227	223	221
520	251	244	240	237	232	230	227	224	222
521	252	245	241	237	233	230	227	224	222
522	252	245	241	238	233	231	228	225	222
523	253	246	242	238	234	231	228	225	223
524	253	246	242	239	234	232	229	226	223
525	254	247	243	239	235	232	229	226	224
526	254	247	243	240	235	232	230	227	224
527	255	248	244	240	236	233	230	227	225
528	255	248	244	240	236	233	231	228	225
529	256	249	245	241	237	234	231	228	226
530	256	249	245	241	237	234	232	228	226
531	257	250	246	242	238	235	232	229	227
532	257	250	246	242	238	235	233	229	227
533	258	251	247	243	239	236	233	230	228
534	258	251	247	243	239	236	234	230	228
535	259	252	247	244	240	237	234	231	229
536	259	252	248	244	240	237	235	231	229
537	260	253	248	245	241	238	235	232	229
538	260	253	249	245	241	238	235	232	230
539	261	254	249	246	242	239	236	233	230
540	261	254	250	246	242	239	236	233	231
541	262	255	250	247	242	240	237	234	231
542	262	255	251	247	243	240	237	234	232
543	263	256	251	248	243	241	238	235	232
544	263	256	252	248	244	241	238	235	233
545	264	257	252	249	244	241	239	235	233
546	264	257	253	249	245	242	239	236	234
547	265	258	253	250	245	242	240	236	234
548	265	258	254	250	246	243	240	237	235
549	266	258	254	251	246	243	241	237	235
550	266	259	255	251	247	244	241	238	235

n	$\alpha(2)$: .50 / $\alpha(1)$: .25	.20 / .10	.10 / .05	.05 / .025	.02 / .01	.01 / .005	.005 / .0025	.002 / .001	.001 / .0005
491	237	230	226	223	219	216	213	210	208
492	238	231	227	223	219	216	214	211	209
493	238	231	227	224	220	217	214	211	209
494	239	232	228	224	220	217	215	212	209
495	239	232	228	225	221	218	215	212	210
496	239	233	229	225	221	218	216	213	210
497	240	233	229	226	222	219	216	213	211
498	240	234	230	226	222	219	217	214	211
499	241	234	230	227	223	220	217	214	212
500	241	235	231	227	223	220	218	214	212
551	267	259	255	252	247	244	242	238	236
552	267	260	256	252	248	245	242	239	236
553	268	260	256	252	248	245	243	239	237
554	268	261	257	253	249	246	243	240	237
555	269	261	257	253	249	246	243	240	238
556	269	262	258	254	250	247	244	241	238
557	270	262	258	254	250	247	244	241	239
558	270	263	259	255	251	248	245	242	239
559	271	263	259	255	251	248	245	242	240
560	271	264	260	256	251	249	246	242	240
561	272	264	260	256	252	249	246	243	241
562	272	265	261	257	252	249	247	243	241
563	272	265	261	257	253	250	247	244	242
564	273	266	261	258	253	250	248	244	242
565	273	266	262	258	254	251	248	245	242
566	274	267	262	259	254	251	249	245	243
567	274	267	263	259	255	252	249	246	243
568	275	268	263	260	255	252	250	246	244
569	275	268	264	260	256	253	250	247	244
570	276	269	264	261	256	253	251	247	245
571	276	269	265	261	257	254	251	248	245
572	277	270	265	262	257	254	251	248	246
573	277	270	266	262	258	255	252	249	246
574	278	271	266	263	258	255	252	249	247
575	278	271	267	263	259	256	253	249	247
576	279	272	267	263	259	256	253	250	248
577	279	272	268	264	260	257	254	250	248
578	280	273	268	264	260	257	254	251	249
579	280	273	269	265	261	258	255	251	249
580	281	274	269	265	261	258	255	252	249
581	281	274	270	266	261	258	256	252	250
582	282	275	270	266	262	259	256	253	250
583	282	275	271	267	262	259	257	253	251
584	283	276	271	267	263	260	257	254	251
585	283	276	272	268	263	260	258	254	252
586	284	276	272	268	264	261	258	255	252
587	284	277	273	269	264	261	259	255	253
588	285	277	273	269	265	262	259	256	253
589	285	278	274	270	265	262	259	256	254
590	286	278	274	270	266	263	260	257	254
591	286	279	275	271	266	263	260	257	255
592	287	279	275	271	267	264	261	257	255
593	287	280	275	272	267	264	261	258	255
594	288	280	276	272	268	265	262	258	256
595	288	281	276	273	268	265	262	259	256
596	289	281	277	273	269	266	263	259	257
597	289	282	277	274	269	266	263	260	257
598	290	282	278	274	270	267	264	260	258
599	290	283	278	275	270	267	264	261	258
600	291	283	279	275	271	267	265	261	259

TABLE B.27 (cont.): Critical Values of C for the Sign Test or the Binomial Test with $p = 0.5$

n	$\alpha(2)$: .50 $\alpha(1)$: .25	.20 .10	.10 .05	.05 .025	.02 .01	.01 .005	.005 .0025	.002 .001	.001 .0005	n	$\alpha(2)$: .50 $\alpha(1)$: .25	.20 .10	.10 .05	.05 .025	.02 .01	.01 .005	.005 .0025	.002 .001	.001 .0005
601	291	284	279	275	271	268	265	262	259	651	316	308	304	300	295	292	289	285	283
602	292	284	280	276	271	268	266	262	260	652	316	309	304	300	295	292	289	286	283
603	292	285	280	276	272	269	266	263	260	653	317	309	304	300	296	293	290	286	284
604	293	285	281	277	272	269	267	263	261	654	317	310	305	301	296	293	290	287	284
605	293	286	281	277	273	270	267	264	261	655	318	310	305	301	297	294	291	287	284
606	294	286	282	278	273	270	267	264	262	656	318	311	306	302	297	294	291	287	285
607	294	287	282	278	274	271	268	264	262	657	319	311	306	302	298	295	292	288	285
608	295	287	283	279	274	271	268	265	262	658	319	312	307	303	298	295	292	288	286
609	295	288	283	279	275	272	269	265	263	659	320	312	307	303	299	295	293	289	286
610	296	288	284	280	275	272	269	266	263	660	320	313	308	304	299	296	293	289	287
611	296	289	284	280	276	273	270	266	264	661	321	313	308	304	300	296	293	290	287
612	297	289	285	281	276	273	270	267	264	662	321	314	309	305	300	297	294	290	288
613	297	290	285	281	277	274	271	267	265	663	322	314	309	305	301	297	294	291	288
614	298	290	286	282	277	274	271	268	265	664	322	314	310	306	301	298	295	291	289
615	298	291	286	282	278	275	272	268	266	665	323	315	310	306	302	298	295	292	289
616	299	291	287	283	278	275	272	269	266	666	323	315	311	307	302	299	296	292	290
617	299	292	287	283	279	276	273	269	267	667	324	316	311	307	302	299	296	293	290
618	300	292	288	284	279	276	273	270	267	668	324	316	312	308	303	300	297	293	291
619	300	293	288	284	280	276	274	270	268	669	325	317	312	308	303	300	297	294	291
620	301	293	289	285	280	277	274	271	268	670	325	317	313	309	304	301	298	294	291
621	301	294	289	285	281	277	275	271	269	671	326	318	313	309	304	301	298	295	292
622	302	294	289	286	281	278	275	272	269	672	326	318	314	310	305	302	299	295	292
623	302	295	290	286	281	278	276	272	269	673	327	319	314	310	305	302	299	295	293
624	303	295	290	287	282	279	276	272	270	674	327	319	315	311	306	303	300	296	293
625	303	295	291	287	282	279	276	273	270	675	328	320	315	311	306	303	300	296	294
626	304	296	291	287	283	280	277	273	271	676	328	320	316	312	307	304	301	297	294
627	304	296	292	288	283	280	277	274	271	677	329	321	316	312	307	304	301	297	295
628	305	297	292	288	284	281	278	274	272	678	329	321	317	312	308	304	301	298	295
629	305	297	293	289	284	281	278	275	272	679	330	322	317	313	308	305	302	298	296
630	306	298	293	289	285	282	279	275	273	680	330	322	318	313	309	305	302	299	296
631	306	298	294	290	285	282	279	276	273	681	331	323	318	314	309	306	303	299	297
632	307	299	294	290	286	283	280	276	274	682	331	323	319	314	310	306	303	300	297
633	307	299	295	291	286	283	280	277	274	683	332	324	319	315	310	307	304	300	298
634	308	300	295	291	287	284	281	277	275	684	332	324	319	315	311	307	304	301	298
635	308	300	296	292	287	284	281	278	275	685	333	325	320	316	311	308	305	301	298
636	308	301	296	292	288	285	282	278	276	686	333	325	320	316	312	308	305	302	299
637	309	301	297	293	288	285	282	279	276	687	334	326	321	317	312	309	306	302	299
638	309	302	297	293	289	285	283	279	276	688	334	326	321	317	313	309	306	303	300
639	310	302	298	294	289	286	283	279	277	689	335	327	322	318	313	310	307	303	300
640	310	303	298	294	290	286	284	280	277	690	335	327	322	318	313	310	307	303	301
641	311	303	299	295	290	287	284	280	278	691	336	328	323	319	314	311	308	304	301
642	311	304	299	295	291	287	284	281	278	692	336	328	323	319	314	311	308	304	302
643	312	304	300	296	291	288	285	281	279	693	337	329	324	320	315	312	309	305	302
644	312	305	300	296	291	288	285	282	279	694	337	329	324	320	315	312	309	305	303
645	313	305	301	297	292	289	286	282	280	695	338	330	325	321	316	313	310	306	303
646	313	306	301	297	292	289	286	283	280	696	338	330	325	321	316	313	310	306	304
647	314	306	302	298	293	290	287	283	281	697	339	331	326	322	317	314	310	307	304
648	314	307	302	298	293	290	287	284	281	698	339	331	326	322	317	314	311	307	305
649	315	307	303	299	294	291	288	284	282	699	340	332	327	323	318	314	311	308	305
650	315	308	303	299	294	291	288	285	282	700	340	332	327	323	318	315	312	308	306
701	341	333	328	324	319	315	312	309	306	751	365	357	352	348	343	339	336	332	329
702	341	333	328	324	319	316	313	309	306	752	366	357	352	348	343	340	337	333	330
703	342	334	329	325	320	316	313	310	307	753	366	358	353	349	344	340	337	333	330
704	342	334	329	325	320	317	314	310	307	754	367	358	353	349	344	341	337	334	331
705	343	334	330	325	321	317	314	311	308	755	367	359	354	350	345	341	338	334	331
706	343	335	330	326	321	318	315	311	308	756	368	359	354	350	345	342	338	335	332
707	344	335	331	326	322	318	315	311	309	757	368	360	355	351	346	342	339	335	332
708	344	336	331	327	322	319	316	312	309	758	369	360	355	351	346	343	339	336	333
709	345	336	332	327	323	319	316	312	310	759	369	361	356	352	346	343	340	336	333
710	345	337	332	328	323	320	317	313	310	760	370	361	356	352	347	344	340	336	334

TABLE B.27 (cont.): Critical Values of C for the Sign Test or the Binomial Test with $p = 0.5$

n	$\alpha(2)$: .50 $\alpha(1)$: .25	.20 .10	.10 .05	.05 .025	.02 .01	.01 .005	.005 .0025	.002 .001	.001 .0005	n	$\alpha(2)$: .50 $\alpha(1)$: .25	.20 .10	.10 .05	.05 .025	.02 .01	.01 .005	.005 .0025	.002 .001	.001 .0005
711	346	337	333	328	324	320	317	313	311	761	370	362	357	352	347	344	341	337	334
712	346	338	333	329	324	321	318	314	311	762	371	362	357	353	348	344	341	337	335
713	346	338	334	329	324	321	318	314	312	763	371	363	358	353	348	345	342	338	335
714	347	339	334	330	325	322	319	315	312	764	372	363	358	354	349	345	342	338	336
715	347	339	335	330	325	322	319	315	313	765	372	364	359	354	349	346	343	339	336
716	348	340	335	331	326	323	319	316	313	766	373	364	359	355	350	346	343	339	337
717	348	340	335	331	326	323	320	316	313	767	373	365	360	355	350	347	344	340	337
718	349	341	336	332	327	324	320	317	314	768	374	365	360	356	351	347	344	340	337
719	349	341	336	332	327	324	321	317	314	769	374	366	361	356	351	348	345	341	338
720	350	342	337	333	328	324	321	318	315	770	375	366	361	357	352	348	345	341	338
721	350	342	337	333	328	325	322	318	315	771	375	367	362	357	352	349	346	342	339
722	351	343	338	334	329	325	322	319	316	772	376	367	362	358	353	349	346	342	339
723	351	343	338	334	329	326	323	319	316	773	376	368	363	358	353	350	347	343	340
724	352	344	339	335	330	326	323	319	317	774	377	368	363	359	354	350	347	343	340
725	352	344	339	335	330	327	324	320	317	775	377	369	364	359	354	351	347	344	341
726	353	345	340	336	331	327	324	320	318	776	378	369	364	360	355	351	348	344	341
727	353	345	340	336	331	328	325	321	318	777	378	370	365	360	355	352	348	344	342
728	354	346	341	337	332	328	325	321	319	778	379	370	365	361	356	352	349	345	342
729	354	346	341	337	332	329	326	322	319	779	379	371	366	361	356	353	349	345	343
730	355	347	342	338	333	329	326	322	320	780	380	371	366	362	357	353	350	346	343
731	355	347	342	338	333	330	327	323	320	781	380	372	367	362	357	354	350	346	344
732	356	348	343	338	334	330	327	323	321	782	381	372	367	363	357	354	351	347	344
733	356	348	343	339	334	331	328	324	321	783	381	373	367	363	358	354	351	347	345
734	357	349	344	339	335	331	328	324	321	784	382	373	368	364	358	355	352	348	345
735	357	349	344	340	335	332	328	325	322	785	382	374	368	364	359	355	352	348	345
736	358	350	345	340	335	332	329	325	322	786	383	374	369	365	359	356	353	349	346
737	358	350	345	341	336	333	329	326	323	787	383	375	369	365	360	356	353	349	346
738	359	351	346	341	336	333	330	326	323	788	384	375	370	365	360	357	354	350	347
739	359	351	346	342	337	334	330	327	324	789	384	376	370	366	361	357	354	350	347
740	360	352	347	342	337	334	331	327	324	790	385	376	371	366	361	358	355	351	348
741	360	352	347	343	338	334	331	327	325	791	385	376	371	367	362	358	355	351	348
742	361	353	348	343	338	335	332	328	325	792	386	377	372	367	362	359	356	352	349
743	361	353	348	344	339	335	332	328	326	793	386	377	372	368	363	359	356	352	349
744	362	354	349	344	339	336	333	329	326	794	386	378	373	368	363	360	356	353	350
745	362	354	349	345	340	336	333	329	327	795	387	378	373	369	364	360	357	353	350
746	363	354	350	345	340	337	334	330	327	796	387	379	374	369	364	361	357	353	351
747	363	355	350	346	341	337	334	330	328	797	388	379	374	370	365	361	358	354	351
748	364	355	351	346	341	338	335	331	328	798	388	380	375	370	365	362	358	354	352
749	364	356	351	347	342	338	335	331	329	799	389	380	375	371	366	362	359	355	352
750	365	356	351	347	342	339	336	332	329	800	389	381	376	371	366	363	359	355	353
801	390	381	376	372	367	363	360	356	353	851	415	406	401	396	391	387	384	379	377
802	390	382	377	372	367	364	360	356	353	852	415	406	401	396	391	387	384	380	377
803	391	382	377	373	368	364	361	357	354	853	416	407	401	397	392	388	385	380	377
804	391	383	378	373	368	365	361	357	354	854	416	407	402	397	392	388	385	381	378
805	392	383	378	374	369	365	362	358	355	855	417	408	402	398	393	389	385	381	378
806	392	384	379	374	369	365	362	358	355	856	417	408	403	398	393	389	386	382	379
807	393	384	379	375	369	366	363	359	356	857	418	409	403	399	393	390	386	382	379
808	393	385	380	375	370	366	363	359	356	858	418	409	404	399	394	390	387	383	380
809	394	385	380	376	370	367	364	360	357	859	419	410	404	400	394	391	387	383	380
810	394	386	381	376	371	367	364	360	357	860	419	410	405	400	395	391	388	384	381
811	395	386	381	377	371	368	365	361	358	861	420	411	405	401	395	392	388	384	381
812	395	387	382	377	372	368	365	361	358	862	420	411	406	401	396	392	389	385	382
813	396	387	382	378	372	369	366	361	359	863	421	412	406	402	396	393	389	385	382
814	396	388	383	378	373	369	366	362	359	864	421	412	407	402	397	393	390	386	383
815	397	388	383	379	373	370	366	362	360	865	422	413	407	403	397	394	390	386	383
816	397	389	384	379	374	370	367	363	360	866	422	413	408	403	398	394	391	387	384
817	398	389	384	379	374	371	367	363	361	867	423	414	408	404	398	395	391	387	384
818	398	390	384	380	375	371	368	364	361	868	423	414	409	404	399	395	392	388	385
819	399	390	385	380	375	372	368	364	361	869	424	415	409	405	399	396	392	388	385
820	399	391	385	381	376	372	369	365	362	870	424	415	410	405	400	396	393	388	386

TABLE B.27 (cont.): Critical Values of C for the Sign Test or the Binomial Test with $p = 0.5$

n	$\alpha(2)$: .50 $\alpha(1)$: .25	.20 .10	.10 .05	.05 .025	.02 .01	.01 .005	.005 .0025	.002 .001	.001 .0005	n	$\alpha(2)$: .50 $\alpha(1)$: .25	.20 .10	.10 .05	.05 .025	.02 .01	.01 .005	.005 .0025	.002 .001	.001 .0005
821	400	391	386	381	376	373	369	365	362	871	425	416	410	406	400	397	393	389	386
822	400	392	386	382	377	373	370	366	363	872	425	416	411	406	401	397	394	389	386
823	401	392	387	382	377	374	370	366	363	873	426	417	411	407	401	397	394	390	387
824	401	393	387	383	378	374	371	367	364	874	426	417	412	407	402	398	395	390	387
825	402	393	388	383	378	375	371	367	364	875	427	418	412	408	402	398	395	391	388
826	402	394	388	384	379	375	372	368	365	876	427	418	413	408	403	399	395	391	388
827	403	394	389	384	379	375	372	368	365	877	428	419	413	408	403	399	396	392	389
828	403	395	389	385	380	376	373	369	366	878	428	419	414	409	404	400	396	392	389
829	404	395	390	385	380	376	373	369	366	879	429	420	414	409	404	400	397	393	390
830	404	396	390	386	381	377	374	370	367	880	429	420	415	410	405	401	397	393	390
831	405	396	391	386	381	377	374	370	367	881	429	420	415	410	405	401	398	394	391
832	405	397	391	387	381	378	375	370	368	882	430	421	416	411	405	402	398	394	391
833	406	397	392	387	382	378	375	371	368	883	430	421	416	411	406	402	399	395	392
834	406	397	392	388	382	379	375	371	369	884	431	422	417	412	406	403	399	395	392
835	407	398	393	388	383	379	376	372	369	885	431	422	417	412	407	403	400	396	393
836	407	398	393	389	383	380	376	372	369	886	432	423	418	413	407	404	400	396	393
837	408	399	394	389	384	380	377	373	370	887	432	423	418	413	408	404	401	397	394
838	408	399	394	390	384	381	377	373	370	888	433	424	418	414	408	405	401	397	394
839	409	400	395	390	385	381	378	374	371	889	433	424	419	414	409	405	402	397	394
840	409	400	395	391	385	382	378	374	371	890	434	425	419	415	409	406	402	398	395
841	410	401	396	391	386	382	379	375	372	891	434	425	420	415	410	406	403	398	395
842	410	401	396	392	386	383	379	375	372	892	435	426	420	416	410	407	403	399	396
843	411	402	397	392	387	383	380	376	373	893	435	426	421	416	411	407	404	399	396
844	411	402	397	393	387	384	380	376	373	894	436	427	421	417	411	408	404	400	397
845	412	403	398	393	388	384	381	377	374	895	436	427	422	417	412	408	405	400	397
846	412	403	398	394	388	385	381	377	374	896	437	428	422	418	412	408	405	401	398
847	413	404	399	394	389	385	382	378	375	897	437	428	423	418	413	409	405	401	398
848	413	404	399	394	389	386	382	378	375	898	438	429	423	419	413	409	406	402	399
849	414	405	400	395	390	386	383	379	376	899	438	429	424	419	414	410	406	402	399
850	414	405	400	395	390	386	383	379	376	900	439	430	424	420	414	410	407	403	400
901	439	430	425	420	415	411	407	403	400	951	464	455	449	444	439	435	431	427	424
902	440	431	425	421	415	411	408	404	401	952	465	455	450	445	439	435	432	427	424
903	440	431	426	421	416	412	408	404	401	953	465	456	450	445	440	436	432	428	425
904	441	432	426	422	416	412	409	405	402	954	466	456	451	446	440	436	433	428	425
905	441	432	427	422	417	413	409	405	402	955	466	457	451	446	441	437	433	429	426
906	442	433	427	423	417	413	410	406	403	956	467	457	452	447	441	437	434	429	426
907	442	433	428	423	417	414	410	406	403	957	467	458	452	447	442	438	434	430	427
908	443	434	428	423	418	414	411	406	403	958	468	458	453	448	442	438	435	430	427
909	443	434	429	424	418	415	411	407	404	959	468	459	453	448	442	439	435	431	428
910	444	435	429	424	419	415	412	407	404	960	469	459	454	449	443	439	436	431	428
911	444	435	430	425	419	416	412	408	405	961	469	460	454	449	443	440	436	432	429
912	445	436	430	425	420	416	413	408	405	962	470	460	454	450	444	440	436	432	429
913	445	436	431	426	420	417	413	409	406	963	470	461	455	450	444	441	437	433	429
914	446	437	431	426	421	417	414	409	406	964	471	461	455	451	445	441	437	433	430
915	446	437	432	427	421	418	414	410	407	965	471	462	456	451	445	442	438	434	430
916	447	438	432	427	422	418	415	410	407	966	472	462	456	452	446	442	438	434	431
917	447	438	433	428	422	419	415	411	408	967	472	463	457	452	446	442	439	434	431
918	448	439	433	428	423	419	416	411	408	968	473	463	457	453	447	443	439	435	432
919	448	439	434	429	423	419	416	412	409	969	473	464	458	453	447	443	440	435	432
920	449	440	434	429	424	420	416	412	409	970	473	464	458	453	448	444	440	436	433
921	449	440	435	430	424	420	417	413	410	971	474	465	459	454	448	444	441	436	433
922	450	441	435	430	425	421	417	413	410	972	474	465	459	454	449	445	441	437	434
923	450	441	436	431	425	421	418	414	411	973	475	466	460	455	449	445	442	437	434
924	451	442	436	431	426	422	418	414	411	974	475	466	460	455	450	446	442	438	435
925	451	442	436	432	426	422	419	415	412	975	476	466	461	456	450	446	443	438	435

TABLE B.27 (cont.): Critical Values of C for the Sign Test or the Binomial Test with $p = 0.5$

n	$\alpha(2)$: .50 / $\alpha(1)$: .25	.20 / .10	.10 / .05	.05 / .025	.02 / .01	.01 / .005	.005 / .0025	.002 / .001	.001 / .0005
926	452	443	437	432	427	423	419	415	412
927	452	443	437	433	427	423	420	415	412
928	453	443	438	433	428	424	420	416	413
929	453	444	438	434	428	424	421	416	413
930	454	444	439	434	429	425	421	417	414
931	454	445	439	435	429	425	422	417	414
932	455	445	440	435	430	426	422	418	415
933	455	446	440	436	430	426	423	418	415
934	456	446	441	436	430	427	423	419	416
935	456	447	441	437	431	427	424	419	416
936	457	447	442	437	431	428	424	420	417
937	457	448	442	438	432	428	425	420	417
938	458	448	443	438	432	429	425	421	418
939	458	449	443	438	433	429	426	421	418
940	459	449	444	439	433	430	426	422	419
941	459	450	444	439	434	430	426	422	419
942	460	450	445	440	434	430	427	423	420
943	460	451	445	440	435	431	427	423	420
944	461	451	446	441	435	431	428	424	420
945	461	452	446	441	436	432	428	424	421
946	462	452	447	442	436	432	429	425	421
947	462	453	447	442	437	433	429	425	422
948	463	453	448	443	437	433	430	425	422
949	463	454	448	443	438	434	430	426	423
950	464	454	449	444	438	434	431	426	423

n	$\alpha(2)$: .50 / $\alpha(1)$: .25	.20 / .10	.10 / .05	.05 / .025	.02 / .01	.01 / .005	.005 / .0025	.002 / .001	.001 / .0005
976	476	467	461	456	451	447	443	439	436
977	477	467	462	457	451	447	444	439	436
978	477	468	462	457	452	448	444	440	437
979	478	468	463	458	452	448	445	440	437
980	478	469	463	458	453	449	445	441	438
981	479	469	464	459	453	449	446	441	438
982	479	470	464	459	454	450	446	442	438
983	480	470	465	460	454	450	447	442	439
984	480	471	465	460	455	451	447	443	439
985	481	471	466	461	455	451	447	443	440
986	481	472	466	461	455	452	448	444	440
987	482	472	467	462	456	452	448	444	441
988	482	473	467	462	456	453	449	444	441
989	483	473	468	463	457	453	449	445	442
990	483	474	468	463	457	453	450	445	442
991	484	474	469	464	458	454	450	446	443
992	484	475	469	464	458	454	451	446	443
993	485	475	470	465	459	455	451	447	444
994	485	476	470	465	459	455	452	447	444
995	486	476	471	466	460	456	452	448	445
996	486	477	471	466	460	456	453	448	445
997	487	477	472	467	461	457	453	449	446
998	487	478	472	467	461	457	454	449	446
999	488	478	473	468	462	458	454	450	447
1000	488	479	473	468	462	458	455	450	447

Appendix Table B.27 was prepared by considering binomial probabilities, such as those in Table B.26b, where the probability of a lower critical value, $C_{\alpha,n}$, is $< \alpha(2)$; upper critical values are $n - C_{\alpha,n}$.

Example:

$C_{0.01,950} = 434$, with $950 - 434 = 516$ as the upper critical value

TABLE B.28: Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
2	1	1	0, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
3	1	1	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
4	1	1	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
4	1	2	0, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
4	2	2	0, 2	0, 2	0, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
5	1	1	–, 1	–, 1	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
5	1	2	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
5	2	2	0, 2	0, 2	–, 2	–, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
6	1	1	–, 1	–, 1	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
6	1	2	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
6	1	3	0, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
6	2	2	0, 2	0, 2	–, 2	–, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
6	2	3	0, 2	0, 2	0, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
6	3	3	1, 2	0, 3	0, 3	0, 3	0, 3	0, 3	0, 3	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
7	1	1	–, 1	–, 1	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
7	1	2	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
7	1	3	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
7	2	2	0, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
7	2	3	0, 2	0, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
7	3	3	0, 2	0, 2	0, 3	0, 3	–, 3	–, 3	–, 3	–, 3	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
8	1	1	–, 1	–, 1	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
8	1	2	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
8	1	3	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
8	1	4	0, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
8	2	2	–, 1	–, 1	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
8	2	3	0, 2	0, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
8	2	4	0, 2	0, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
8	3	3	0, 2	0, 2	0, 3	0, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
8	3	4	1, 2	0, 3	0, 3	0, 3	0, 3	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
8	4	4	1, 3	1, 3	0, 4	0, 4	0, 4	0, 4	0, 4	0, 4	0, 4	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
9	1	1	–, 1	–, 1	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
9	1	2	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
9	1	3	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
9	1	4	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
9	2	2	–, 1	–, 1	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
9	2	3	0, 2	0, 2	–, 2	–, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
9	2	4	0, 2	0, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
9	3	3	0, 2	0, 2	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
9	3	4	0, 2	0, 3	0, 3	0, 3	–, 3	–, 3	–, 3	–, 3	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
9	4	4	1, 3	0, 3	0, 3	0, 4	0, 4	0, 4	0, 4	0, 4	–, 4	–, 4	–, 4	–, 4	–, –	–, –	–, –	–, –	–, –	–, –

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
10	1	1	–,1	–,1	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
10	1	2	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
10	1	3	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
10	1	4	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
10	1	5	0,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
10	2	2	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
10	2	3	0,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
10	2	4	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
10	2	5	0,2	0,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
10	3	3	0,2	0,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–
10	3	4	0,2	0,2	0,3	0,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
10	3	5	1,2	0,3	0,3	0,3	0,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
10	4	4	1,3	0,3	0,3	0,3	0,4	0,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–
10	4	5	1,3	0,4	0,4	0,4	0,4	0,4	0,4	0,4	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
10	5	5	2,3	1,4	1,4	0,5	0,5	0,5	0,5	0,5	0,5	0,5	0,5	0,5	0,5	–,–	–,–	–,–	–,–	–,–
11	1	1	–,1	–,1	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
11	1	2	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
11	1	3	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
11	1	4	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
11	1	5	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
11	2	2	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
11	2	3	–,1	–,1	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
11	2	4	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
11	2	5	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
11	3	3	0,2	0,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–
11	3	4	0,2	0,2	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
11	3	5	0,2	0,3	0,3	0,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
11	4	4	0,2	0,3	0,3	0,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–
11	4	5	1,3	0,3	0,3	0,4	0,4	0,4	0,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
11	5	5	1,3	1,4	1,4	0,4	0,4	0,4	0,5	0,5	0,5	0,5	–,5	–,5	–,5	–,5	–,–	–,–	–,–	–,–
12	1	1	–,1	–,1	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
12	1	2	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
12	1	3	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
12	1	4	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
12	1	5	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
12	1	6	0,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
12	2	2	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
12	2	3	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
12	2	4	0,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
12	2	5	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
12	2	6	0,2	0,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
12	3	3	0,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
12	3	4	0,2	0,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
12	3	5	0,2	0,3	0,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
12	3	6	1,2	0,3	0,3	0,3	0,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
12	4	4	0,2	0,3	0,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–
12	4	5	1,3	0,3	0,3	0,4	0,4	0,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
12	4	6	1,3	0,4	0,4	0,4	0,4	0,4	0,4	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
12	5	5	1,3	1,4	0,4	0,4	0,4	0,4	0,4	0,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,–	–,–
12	5	6	2,3	1,4	1,4	0,5	0,5	0,5	0,5	0,5	0,5	0,5	0,5	–,–	–,–	–,–	–,–	–,–	–,–	–,–
12	6	6	2,4	1,5	1,5	1,5	1,5	1,5	1,5	0,6	0,6	0,6	0,6	0,6	0,6	0,6	0,6	–,–	–,–	–,–
13	1	1	–,1	–,1	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
13	1	2	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
13	1	3	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
13	1	4	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
13	1	5	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
13	1	6	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
13	2	2	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
13	2	3	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
13	2	4	0,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
13	2	5	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
13	2	6	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
13	3	3	0,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–
13	3	4	0,2	0,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
13	3	5	0,2	0,3	0,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
13	3	6	0,2	0,3	0,3	0,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
13	4	4	0,2	0,3	0,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–
13	4	5	1,3	0,3	0,3	0,4	0,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–	–,–	–,–
13	4	6	1,3	0,3	0,4	0,4	0,4	0,4	0,4	–,4	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
13	5	5	1,3	0,3	0,4	0,4	0,4	0,4	0,4	–,4	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5
13	5	6	1,3	1,4	1,4	0,4	0,4	0,5	0,5	0,5	0,5	–,5	–,5	–,5	–,5	–,5	–,–	–,–	–,–	–,–
13	6	6	2,4	1,4	1,5	1,5	1,5	0,5	0,5	0,5	0,6	0,6	0,6	0,6	0,6	0,6	–,6	–,6	–,6	–,6
14	1	1	–,1	–,1	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	1	2	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	1	3	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	1	4	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	1	5	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	1	6	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	1	7	0,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	2	2	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
14	2	3	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	2	4	0,1	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	2	5	0,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	2	6	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	2	7	0,2	0,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	3	3	0,2	–,2	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–
14	3	4	0,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	3	5	0,2	0,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	3	6	0,2	0,3	0,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	3	7	1,2	0,3	0,3	0,3	0,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	4	4	0,2	0,3	–,3	–,3	–,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4
14	4	5	0,2	0,3	0,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–
14	4	6	1,3	0,3	0,3	0,4	0,4	0,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	4	7	1,3	0,4	0,4	0,4	0,4	0,4	0,4	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	5	5	1,3	0,3	0,4	0,4	0,4	0,4	–,4	–,4	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5
14	5	6	1,3	1,4	0,4	0,4	0,4	0,4	0,5	0,5	–,5	–,5	–,5	–,5	–,5	–,5	–,–	–,–	–,–	–,–
14	5	7	2,3	1,4	1,4	0,5	0,5	0,5	0,5	0,5	0,5	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
14	6	6	2,4	1,4	1,4	1,5	0,5	0,5	0,5	0,5	0,5	0,6	0,6	0,6	–,6	–,6	–,6	–,6	–,6	–,6
14	6	7	2,4	1,5	1,5	1,5	1,5	0,6	0,6	0,6	0,6	0,6	0,6	0,6	0,6	0,6	–,–	–,–	–,–	–,–
14	7	7	3,4	2,5	2,5	1,6	1,6	1,6	1,6	1,6	1,6	0,7	0,7	0,7	0,7	0,7	0,7	0,7	0,7	0,7
15	1	1	–,1	–,1	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
15	1	2	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
15	1	3	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
15	1	4	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
15	1	5	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
15	1	6	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
15	1	7	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
15	2	2	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–
15	2	3	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
15	2	4	–,1	–,1	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
15	2	5	0,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
15	2	6	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
15	2	7	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
15	3	3	0,1	–,2	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–
15	3	4	0,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–
15	3	5	0,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
15	3	6	0,2	0,3	0,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
15	3	7	0,2	0,3	0,3	0,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
15	4	4	0,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4
15	4	5	0,2	0,3	0,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
15	4	6	1,3	0,3	0,3	0,4	0,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
15	4	7	1,3	0,3	0,4	0,4	0,4	0,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
15	5	5	1,3	0,3	0,3	0,4	0,4	−,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5
15	5	6	1,3	0,3	0,4	0,4	0,4	0,4	0,4	0,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,−	−,−
15	5	7	1,3	1,4	1,4	0,4	0,5	0,5	0,5	0,5	0,5	−,5	−,5	−,5	−,−	−,−	−,−	−,−	−,−	−,−
15	6	6	1,4	1,4	1,4	0,4	0,5	0,5	0,5	0,5	0,5	−,5	−,6	−,6	−,6	−,6	−,6	−,6	−,6	−,6
15	6	7	2,4	1,4	1,5	1,5	1,5	0,5	0,5	0,5	0,6	0,6	0,6	0,6	−,6	−,6	−,6	−,6	−,−	−,−
15	7	7	2,4	2,5	1,5	1,5	1,6	1,6	1,6	1,6	0,6	0,6	0,6	0,7	0,7	0,7	0,7	0,7	−,7	−,7
16	1	1	−,1	−,1	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	1	2	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	1	3	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	1	4	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	1	5	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	1	6	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	1	7	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	1	8	0,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	2	2	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−
16	2	3	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	2	4	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	2	5	0,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	2	6	0,2	0,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	2	7	0,2	0,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	2	8	0,2	0,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	3	3	−,1	−,1	−,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−
16	3	4	0,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−
16	3	5	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	3	6	0,2	0,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	3	7	0,2	0,3	0,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	3	8	1,2	0,3	0,3	0,3	0,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	4	4	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4
16	4	5	0,2	0,3	0,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−
16	4	6	0,2	0,3	0,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−
16	4	7	1,3	0,3	0,3	0,4	0,4	0,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	4	8	1,3	0,4	0,4	0,4	0,4	0,4	0,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	5	5	1,3	0,3	0,3	0,4	−,4	−,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5
16	5	6	1,3	0,3	0,4	0,4	0,4	0,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,−	−,−
16	5	7	1,3	1,4	0,4	0,4	0,4	0,5	0,5	0,5	−,5	−,5	−,5	−,5	−,5	−,5	−,−	−,−	−,−	−,−
16	5	8	2,3	1,4	1,4	0,5	0,5	0,5	0,5	0,5	0,5	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
16	6	6	1,4	1,4	0,4	0,4	0,4	0,5	0,5	0,5	−,5	−,5	−,5	−,5	−,6	−,6	−,6	−,6	−,6	−,6
16	6	7	2,4	1,4	1,4	1,5	0,5	0,5	0,5	0,5	0,6	0,6	−,6	−,6	−,6	−,6	−,6	−,6	−,6	−,6

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
16	6	8	2,4	1,5	1,5	1,5	1,5	0,6	0,6	0,6	0,6	0,6	0,6	0,6	0,6	–,–	–,–	–,–	–,–	–,–
16	7	7	2,4	2,5	1,5	1,5	1,5	1,6	0,6	0,6	0,6	0,6	0,6	0,6	0,7	0,7	–,7	–,7	–,7	–,7
16	7	8	3,4	2,5	2,5	1,6	1,6	1,6	1,6	1,6	0,7	0,7	0,7	0,7	0,7	0,7	0,7	0,7	0,7	–,–
16	8	8	3,5	2,6	2,6	2,6	2,6	1,7	1,7	1,7	1,7	1,7	1,7	0,8	0,8	0,8	0,8	0,8	0,8	0,8
17	1	1	–,1	–,1	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	1	2	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	1	3	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	1	4	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	1	5	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	1	6	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	1	7	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	1	8	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	2	2	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–
17	2	3	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	2	4	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	2	5	0,1	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	2	6	0,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	2	7	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	2	8	0,2	0,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	3	3	–,1	–,1	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–
17	3	4	0,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–
17	3	5	0,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	3	6	0,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	3	7	0,2	0,3	0,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	3	8	0,2	0,3	0,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	4	4	0,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4
17	4	5	0,2	0,3	–,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–
17	4	6	0,2	0,3	0,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–	–,–	–,–
17	4	7	1,3	0,3	0,3	0,4	0,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	4	8	1,3	0,3	0,4	0,4	0,4	0,4	–,4	–,4	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
17	5	5	0,2	0,3	0,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,5	–,5	–,5	–,5	–,5	–,5
17	5	6	1,3	0,3	0,4	0,4	0,4	–,4	–,4	–,4	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5
17	5	7	1,3	1,4	0,4	0,4	0,4	0,5	0,5	0,5	–,5	–,5	–,5	–,5	–,5	–,5	–,–	–,–	–,–	–,–
17	5	8	1,3	1,4	1,4	0,4	0,5	0,5	0,5	0,5	–,5	–,5	–,5	–,5	–,–	–,–	–,–	–,–	–,–	–,–
17	6	6	1,4	1,4	0,4	0,4	0,4	0,5	0,5	0,5	–,5	–,5	–,5	–,5	–,6	–,6	–,6	–,6	–,6	–,6
17	6	7	1,3	1,4	1,4	0,4	0,5	0,5	0,5	0,5	0,5	–,6	–,6	–,6	–,6	–,6	–,6	–,6	–,6	–,6
17	6	8	2,4	1,4	1,5	1,5	1,5	0,5	0,5	0,5	0,6	0,6	0,6	0,6	–,6	–,6	–,–	–,–	–,–	–,–
17	7	7	2,4	1,4	1,5	1,5	1,5	0,5	0,6	0,6	0,6	0,6	0,6	0,6	–,6	–,6	–,7	–,7	–,7	–,7
17	7	8	2,4	2,5	1,5	1,5	1,6	1,6	1,6	1,6	0,6	0,6	0,7	0,7	0,7	0,7	0,7	–,7	–,7	–,7
17	8	8	3,5	2,5	2,6	2,6	1,6	1,6	1,6	1,7	1,7	1,7	0,7	0,7	0,7	0,7	0,8	0,8	0,8	0,8

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
18	1	1	–,1	–,1	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	1	2	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	1	3	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	1	4	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	1	5	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	1	6	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	1	7	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	1	8	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	1	9	0,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	2	2	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–
18	2	3	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	2	4	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	2	5	–,1	–,1	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	2	6	0,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	2	7	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	2	8	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	2	9	0,2	0,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	3	3	–,1	–,1	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–
18	3	4	0,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–
18	3	5	0,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	3	6	0,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	4	6	0,2	0,3	0,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–
18	4	7	1,3	0,3	0,3	0,4	–,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	4	8	1,3	0,3	0,4	0,4	0,4	0,4	–,4	–,4	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	4	9	1,3	0,4	0,4	0,4	0,4	0,4	0,4	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	5	5	0,2	0,3	0,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,5	–,5	–,5	–,5	–,5	–,5
18	5	6	1,3	0,3	0,3	0,4	0,4	–,4	–,4	–,4	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5
18	5	7	1,3	0,3	0,4	0,4	0,4	–,4	–,4	–,4	–,5	–,5	–,5	–,5	–,5	–,5	–,–	–,–	–,–	–,–
18	5	8	1,3	1,4	0,4	0,4	0,4	0,5	0,5	0,5	–,5	–,5	–,5	–,5	–,–	–,–	–,–	–,–	–,–	–,–
18	5	9	2,3	1,4	1,4	0,5	0,5	0,5	0,5	0,5	0,5	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
18	6	6	1,3	0,3	0,4	0,4	0,4	0,5	0,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,6	–,6	–,6	–,6
18	6	7	1,4	1,4	1,4	0,4	0,5	0,5	0,5	0,5	–,5	–,5	–,6	–,6	–,6	–,6	–,6	–,6	–,6	–,6
18	6	8	2,4	1,4	1,5	1,5	0,5	0,5	0,5	0,5	0,6	0,6	–,6	–,6	–,6	–,6	–,6	–,6	–,–	–,–
18	6	9	2,4	1,5	1,5	1,5	1,5	0,6	0,6	0,6	0,6	0,6	0,6	0,6	0,6	–,–	–,–	–,–	–,–	–,–
18	7	7	2,4	1,4	1,5	1,5	0,5	0,5	0,5	0,5	0,6	0,6	–,6	–,6	–,6	–,6	–,7	–,7	–,7	–,7
18	7	8	2,4	2,5	1,5	1,5	1,5	1,6	0,6	0,6	0,6	0,6	0,6	0,7	0,7	0,7	–,7	–,7	–,7	–,7
18	7	9	3,4	2,5	2,5	1,6	1,6	1,6	1,6	1,6	0,7	0,7	0,7	0,7	0,7	0,7	0,7	–,–	–,–	–,–
18	8	8	3,5	2,5	2,5	2,6	1,6	1,6	1,6	1,7	0,7	0,7	0,7	0,7	0,7	0,7	0,7	0,8	–,8	–,8
18	8	9	3,5	2,6	2,6	2,6	2,6	1,7	1,7	1,7	1,7	1,7	1,7	0,8	0,8	0,8	0,8	0,8	0,8	0,8
18	9	9	4,5	3,6	3,6	2,7	2,7	2,7	2,7	1,8	1,8	1,8	1,8	1,8	1,8	1,8	1,8	0,9	0,9	0,9

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
19	1	1	–,1	–,1	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	1	2	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	1	3	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	1	4	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	1	5	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	1	6	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	1	7	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	1	8	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	1	9	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	2	2	–,1	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–
19	2	3	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	2	4	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	2	5	–,1	–,1	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	2	6	0,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	2	7	0,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	2	8	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	2	9	0,2	0,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	3	3	–,1	–,1	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–
19	3	4	0,1	–,2	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–
19	3	5	0,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	3	6	0,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	3	7	0,2	0,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	3	8	0,2	0,3	0,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	3	9	0,2	0,3	0,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	4	4	0,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4
19	4	5	0,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–
19	4	6	0,2	0,3	0,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–
19	4	7	0,2	0,3	0,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–	–,–	–,–
19	4	8	1,3	0,3	0,3	0,4	0,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	4	9	1,3	0,3	0,4	0,4	0,4	0,4	–,4	–,4	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	5	5	0,2	0,3	0,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,5	–,5	–,5	–,5	–,5	–,5
19	5	6	1,3	0,3	0,3	0,4	–,4	–,4	–,4	–,4	–,4	–,4	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5
19	5	7	1,3	0,3	0,4	0,4	0,4	–,4	–,4	–,4	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,–	–,–
19	5	8	1,3	1,4	0,4	0,4	0,4	0,5	0,5	0,5	–,5	–,5	–,5	–,5	–,5	–,5	–,–	–,–	–,–	–,–
19	5	9	1,3	1,4	1,4	0,4	0,5	0,5	0,5	0,5	–,5	–,5	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
19	6	6	1,3	0,3	0,4	0,4	0,4	–,4	–,4	–,4	–,5	–,5	–,5	–,5	–,5	–,5	–,6	–,6	–,6	–,6
19	6	7	1,4	1,4	0,4	0,4	0,4	0,5	0,5	0,5	–,5	–,5	–,5	–,5	–,6	–,6	–,6	–,6	–,6	–,6
19	6	8	2,4	1,4	1,4	1,5	0,5	0,5	0,5	0,5	0,6	0,6	–,6	–,6	–,6	–,6	–,6	–,6	–,–	–,–
19	6	9	2,4	1,4	1,5	1,5	1,5	0,5	0,5	0,6	0,6	0,6	0,6	–,6	–,6	–,6	–,–	–,–	–,–	–,–
19	7	7	2,4	1,4	1,4	1,5	0,5	0,5	0,5	0,5	0,6	0,6	–,6	–,6	–,6	–,6	–,6	–,6	–,7	–,7

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
19	7	8	2,4	1,4	1,5	1,5	1,5	0,5	0,6	0,6	0,6	0,6	0,6	−,6	−,7	−,7	−,7	−,7	−,7	−,7
19	7	9	2,4	2,5	1,5	1,5	1,6	1,6	1,6	0,6	0,6	0,6	0,7	0,7	0,7	0,7	−,7	−,7	−,7	−,7
19	8	8	2,5	2,5	1,5	1,5	1,6	1,6	1,6	0,6	0,7	0,7	0,7	0,7	0,7	0,7	−,7	−,7	−,8	−,8
19	8	9	3,5	2,5	2,6	2,6	1,6	1,6	1,7	1,7	1,7	1,7	0,7	0,7	0,7	0,8	0,8	0,8	0,8	0,8
19	9	9	3,5	3,6	2,6	2,6	2,7	2,7	1,7	1,7	1,7	1,8	1,8	1,8	1,8	0,8	0,8	0,8	0,8	0,9
20	1	1	−,1	−,1	−,1	−,1	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	1	2	−,1	−,1	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	1	3	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	1	4	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	1	5	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	1	6	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	1	7	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	1	8	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	1	9	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	1	10	0,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	2	2	−,1	−,1	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−
20	2	3	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	2	4	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	2	5	−,1	−,1	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	2	6	0,1	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	2	7	0,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	2	8	0,2	0,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	2	9	0,2	0,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	2	10	0,2	0,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	3	3	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3
20	3	4	0,1	−,2	−,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−
20	3	5	0,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−
20	3	6	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	3	7	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	3	8	0,2	0,3	0,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	3	9	0,2	0,3	0,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	3	10	1,2	0,3	0,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	4	4	0,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4
20	4	5	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−
20	4	6	0,2	0,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−
20	4	7	0,2	0,3	0,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−
20	4	8	1,3	0,3	0,3	0,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	4	9	1,3	0,3	0,4	0,4	0,4	0,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	4	10	1,3	0,4	0,4	0,4	0,4	0,4	0,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
20	5	5	0,2	0,3	0,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
20	5	6	0, 2	0, 3	0, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5
20	5	7	1, 3	0, 3	0, 4	0, 4	0, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, −	−, −
20	5	8	1, 3	0, 3	0, 4	0, 4	0, 4	0, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, −	−, −	−, −	−, −
20	5	9	1, 3	1, 4	0, 4	0, 4	0, 4	0, 5	0, 5	0, 5	−, 5	−, 5	−, 5	−, 5	−, −	−, −	−, −	−, −	−, −	−, −
20	5	10	2, 3	1, 4	1, 4	0, 5	0, 5	0, 5	0, 5	0, 5	0, 5	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
20	6	6	1, 3	0, 3	0, 4	0, 4	0, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6
20	6	7	1, 4	1, 4	0, 4	0, 4	0, 4	0, 5	0, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6
20	6	8	1, 4	1, 4	1, 4	0, 4	0, 5	0, 5	0, 5	0, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6
20	6	9	2, 4	1, 4	1, 5	1, 5	0, 5	0, 5	0, 5	0, 5	0, 6	0, 6	−, 6	−, 6	−, 6	−, 6	−, −	−, −	−, −	−, −
20	6	10	2, 4	1, 5	1, 5	1, 5	1, 5	0, 6	0, 6	0, 6	0, 6	0, 6	0, 6	−, −	−, −	−, −	−, −	−, −	−, −	−, −
20	7	7	1, 3	1, 4	1, 4	0, 4	0, 5	0, 5	0, 5	0, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 7	−, 7
20	7	8	2, 4	1, 4	1, 5	1, 5	0, 5	0, 5	0, 6	0, 6	0, 6	0, 6	−, 6	−, 6	−, 6	−, 6	−, 7	−, 7	−, 7	−, 7
20	7	9	2, 4	2, 5	1, 5	1, 5	1, 6	1, 6	0, 6	0, 6	0, 6	0, 6	0, 7	0, 7	0, 7	0, 7	−, 7	−, 7	−, 7	−, 7
20	7	10	3, 4	2, 5	2, 5	1, 6	1, 6	1, 6	1, 6	0, 7	0, 7	0, 7	0, 7	0, 7	0, 7	0, 7	0, 7	−, −	−, −	−, −
20	8	8	2, 5	2, 5	1, 5	1, 5	1, 6	1, 6	0, 6	0, 6	0, 6	0, 6	0, 7	0, 7	0, 7	0, 7	−, 7	−, 7	−, 7	−, 7
20	8	9	3, 5	2, 5	2, 6	2, 6	1, 6	1, 6	1, 6	1, 7	0, 7	0, 7	0, 7	0, 7	0, 7	0, 7	0, 8	0, 8	−, 8	−, 8
20	8	10	3, 5	2, 6	2, 6	2, 6	2, 6	1, 7	1, 7	1, 7	1, 7	1, 7	1, 7	0, 8	0, 8	0, 8	0, 8	0, 8	0, 8	0, 8
20	9	9	3, 5	3, 6	2, 6	2, 6	2, 6	2, 7	1, 7	1, 7	1, 7	1, 8	1, 8	1, 8	0, 8	0, 8	0, 8	0, 8	0, 8	0, 8
20	9	10	4, 5	3, 6	3, 6	2, 7	2, 7	2, 7	2, 7	1, 8	1, 8	1, 8	1, 8	1, 8	1, 8	0, 9	0, 9	0, 9	0, 9	0, 9
20	10	10	4, 6	3, 7	3, 7	3, 7	3, 7	2, 8	2, 8	2, 8	2, 8	1, 9	1, 9	1, 9	1, 9	1, 9	1, 9	1, 9	1, 9	0, 10
21	1	1	−, 1	−, 1	−, 1	−, 1	−, 1	−, 1	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	1	2	−, 1	−, 1	−, 1	−, 1	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	1	3	−, 1	−, 1	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	1	4	−, 1	−, 1	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	1	5	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	1	6	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	1	7	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	1	8	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	1	9	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	1	10	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	2	2	−, 1	−, 1	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −
21	2	3	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	2	4	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	2	5	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	2	6	0, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	2	7	0, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	2	8	0, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	2	9	0, 2	0, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	2	10	0, 2	0, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
21	3	3	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
21	3	4	−,1	−,1	−,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−
21	3	5	0,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−
21	3	6	0,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
21	3	7	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
21	3	8	0,2	0,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
21	3	9	0,2	0,3	0,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
21	3	10	0,2	0,3	0,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
21	4	4	0,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4
21	4	5	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4
21	4	6	0,2	0,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−
21	4	7	0,2	0,3	0,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−
21	4	8	0,2	0,3	0,3	0,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
21	4	9	1,3	0,3	0,3	0,4	0,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
21	4	10	1,3	0,3	0,4	0,4	0,4	0,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
21	5	5	0,2	0,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5
21	5	6	0,2	0,3	0,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5
21	5	7	1,3	0,3	0,3	0,4	0,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,−	−,−
21	5	8	1,3	0,3	0,4	0,4	0,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,−	−,−	−,−	−,−
21	5	9	1,3	1,4	0,4	0,4	0,4	0,5	0,5	0,5	−,5	−,5	−,5	−,5	−,−	−,−	−,−	−,−	−,−	−,−
21	5	10	1,3	1,4	1,4	0,4	0,5	0,5	0,5	0,5	−,5	−,5	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
21	6	6	1,3	0,3	0,4	0,4	0,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,6	−,6
21	6	7	1,3	0,3	0,4	0,4	0,4	0,5	−,5	−,5	−,5	−,5	−,5	−,5	−,6	−,6	−,6	−,6	−,6	−,6
21	6	8	1,4	1,4	0,4	0,4	0,5	0,5	0,5	0,5	−,5	−,5	−,6	−,6	−,6	−,6	−,6	−,6	−,6	−,6
21	6	9	2,4	1,4	1,4	1,5	0,5	0,5	0,5	0,5	0,6	0,6	−,6	−,6	−,6	−,6	−,6	−,6	−,−	−,−
21	6	10	2,4	1,4	1,5	1,5	1,5	0,5	0,6	0,6	0,6	0,6	0,6	−,6	−,6	−,6	−,−	−,−	−,−	−,−
21	7	7	1,4	1,4	0,4	0,4	0,5	0,5	0,5	0,5	−,5	−,5	−,6	−,6	−,6	−,6	−,6	−,6	−,6	−,6
21	7	8	2,4	1,4	1,5	1,5	0,5	0,5	0,5	0,6	0,6	0,6	−,6	−,6	−,6	−,6	−,7	−,7	−,7	−,7
21	7	9	2,4	1,4	1,5	1,5	1,5	0,6	0,6	0,6	0,6	0,6	0,6	0,7	−,7	−,7	−,7	−,7	−,7	−,7
21	7	10	2,4	2,5	1,5	1,5	1,6	1,6	1,6	0,6	0,7	0,7	0,7	0,7	0,7	0,7	−,7	−,7	−,−	−,−
21	8	8	2,5	2,5	1,5	1,5	1,5	1,6	0,6	0,6	0,6	0,6	0,7	0,7	−,7	−,7	−,7	−,7	−,7	−,7
21	8	9	2,5	2,5	1,5	1,6	1,6	1,6	1,6	0,6	0,7	0,7	0,7	0,7	0,7	0,7	−,8	−,8	−,8	−,8
21	8	10	3,5	2,5	2,6	2,6	1,6	1,6	1,7	1,7	1,7	0,7	0,7	0,7	0,8	0,8	0,8	0,8	0,8	−,8
21	9	9	3,5	2,5	2,6	2,6	1,6	1,6	1,7	1,7	1,7	0,7	0,7	0,7	0,8	0,8	0,8	0,8	0,8	−,8
21	9	10	3,5	3,6	2,6	2,6	2,7	2,7	1,7	1,7	1,8	1,8	1,8	1,8	0,8	0,8	0,8	0,8	0,9	0,9
21	10	10	4,6	3,6	3,7	3,7	2,7	2,7	2,8	2,8	1,8	1,8	1,8	1,8	1,9	1,9	1,9	1,9	0,9	0,9
22	1	1	−,1	−,1	−,1	−,1	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
22	1	2	−,1	−,1	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
22	1	3	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
22	1	4	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
22	1	5	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
22	1	6	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	1	7	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	1	8	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	1	9	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	1	10	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	1	11	0,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	2	2	–,1	–,1	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–
22	2	3	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	2	4	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	2	5	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	2	6	–,1	–,1	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	2	7	0,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	2	8	0,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	2	9	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	2	10	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	2	11	0,2	0,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	3	3	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3
22	3	4	–,1	–,1	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–
22	3	5	0,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–
22	3	6	0,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	3	7	0,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	3	8	0,2	0,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	3	9	0,2	0,3	0,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	3	10	0,2	0,3	0,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	3	11	1,2	0,3	0,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	4	4	0,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4
22	4	5	0,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4
22	4	6	0,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–
22	4	7	0,2	0,3	0,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–
22	4	8	0,2	0,3	0,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–	–,–	–,–
22	4	9	1,3	0,3	0,3	0,4	0,4	–,4	–,4	–,4	–,4	–,4	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	4	10	1,3	0,3	0,4	0,4	0,4	0,4	–,4	–,4	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	4	11	1,3	0,4	0,4	0,4	0,4	0,4	0,4	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	5	5	0,2	0,3	–,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,5	–,5	–,5	–,5
22	5	6	0,2	0,3	0,3	–,3	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,4	–,5	–,5	–,5	–,5	–,5	–,5
22	5	7	1,3	0,3	0,3	0,4	–,4	–,4	–,4	–,4	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5
22	5	8	1,3	0,3	0,4	0,4	0,4	–,4	–,4	–,4	–,5	–,5	–,5	–,5	–,5	–,5	–,–	–,–	–,–	–,–
22	5	9	1,3	1,4	0,4	0,4	0,4	0,5	0,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,–	–,–	–,–	–,–
22	5	10	1,3	1,4	0,4	0,4	0,5	0,5	0,5	0,5	–,5	–,5	–,5	–,5	–,–	–,–	–,–	–,–	–,–	–,–
22	5	11	2,3	1,4	1,4	0,5	0,5	0,5	0,5	0,5	0,5	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
22	6	6	1,3	0,3	0,4	0,4	–,4	–,4	–,4	–,4	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,6	–,6
22	6	7	1,3	0,3	0,4	0,4	0,4	–,4	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,5	–,6	–,6	–,6	–,6
22	6	8	1,4	1,4	0,4	0,4	0,4	0,5	0,5	–,5	–,5	–,5	–,6	–,6	–,6	–,6	–,6	–,6	–,6	–,6
22	6	9	1,4	1,4	1,4	0,4	0,5	0,5	0,5	0,5	–,6	–,6	–,6	–,6	–,6	–,6	–,6	–,6	–,–	–,–
22	6	10	2,4	1,4	1,5	1,5	0,5	0,5	0,5	0,6	0,6	0,6	–,6	–,6	–,6	–,6	–,–	–,–	–,–	–,–
22	6	11	2,4	1,5	1,5	1,5	1,5	0,6	0,6	0,6	0,6	0,6	0,6	–,–	–,–	–,–	–,–	–,–	–,–	–,–
22	7	7	1,4	1,4	0,4	0,4	0,5	0,5	0,5	–,5	–,5	–,5	–,6	–,6	–,6	–,6	–,6	–,6	–,6	–,6
22	7	8	2,4	1,4	1,4	1,5	0,5	0,5	0,5	0,6	–,6	–,6	–,6	–,6	–,6	–,6	–,7	–,7	–,7	–,7
22	7	9	2,4	1,4	1,5	1,5	0,5	0,5	0,6	0,6	0,6	0,6	–,6	–,6	–,7	–,7	–,7	–,7	–,7	–,7
22	7	10	2,4	2,5	1,5	1,5	1,6	1,6	0,6	0,6	0,6	0,7	0,7	0,7	0,7	–,7	–,7	–,7	–,7	–,7
22	7	11	3,4	2,5	2,5	1,6	1,6	1,6	1,6	0,7	0,7	0,7	0,7	0,7	0,7	0,7	0,7	–,–	–,–	–,–
22	8	8	2,4	1,4	1,5	1,5	1,5	0,5	0,6	0,6	0,6	0,6	0,6	–,6	–,7	–,7	–,7	–,7	–,7	–,7
22	8	9	2,5	2,5	1,5	1,5	1,6	1,6	0,6	0,6	0,7	0,7	0,7	0,7	0,7	–,7	–,7	–,7	–,8	–,8
22	8	10	3,5	2,5	2,6	1,6	1,6	1,6	1,6	1,7	0,7	0,7	0,7	0,7	0,7	0,8	0,8	0,8	–,8	–,8
22	8	11	3,5	2,6	2,6	2,6	2,6	1,7	1,7	1,7	1,7	0,8	0,8	0,8	0,8	0,8	0,8	0,8	0,8	–,–
22	9	9	3,5	2,5	2,6	1,6	1,6	1,6	1,7	1,7	0,7	0,7	0,7	0,7	0,8	0,8	0,8	0,8	–,8	–,8
22	9	10	3,5	3,6	2,6	2,6	2,7	2,7	1,7	1,7	1,7	1,8	0,8	0,8	0,8	0,8	0,8	0,8	0,9	0,9
22	9	11	4,5	3,6	3,6	2,7	2,7	2,7	2,7	1,8	1,8	1,8	1,8	1,8	1,8	0,9	0,9	0,9	0,9	0,9
22	10	10	4,6	3,6	3,7	2,7	2,7	2,7	2,7	2,8	1,8	1,8	1,8	1,8	1,8	1,9	0,9	0,9	0,9	0,9
22	10	11	4,6	3,7	3,7	3,7	3,7	2,8	2,8	2,8	2,8	1,9	1,9	1,9	1,9	1,9	1,9	1,9	1,9	0,10
22	11	11	5,6	4,7	4,7	3,8	3,8	3,8	3,8	2,9	2,9	2,9	2,9	2,9	2,9	1,10	1,10	1,10	1,10	1,10
23	1	1	–,1	–,1	–,1	–,1	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	1	2	–,1	–,1	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	1	3	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	1	4	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	1	5	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	1	6	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	1	7	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	1	8	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	1	9	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	1	10	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	1	11	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	2	2	–,1	–,1	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–
23	2	3	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	2	4	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	2	5	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	2	6	–,1	–,1	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	2	7	0,1	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	2	8	0,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	2	9	0,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	2	10	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	2	11	0,2	0,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
23	3	3	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3
23	3	4	–,1	–,1	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–
23	3	5	0,1	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
23	3	6	0, 2	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
23	3	7	0, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
23	3	8	0, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
23	3	9	0, 2	0, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
23	3	10	0, 2	0, 3	0, 3	−, 3	−, 3	−, 3	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
23	3	11	0, 2	0, 3	0, 3	−, 3	−, 3	−, 3	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
23	4	4	0, 2	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4
23	4	5	0, 2	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4
23	4	6	0, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −
23	4	7	0, 2	0, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −
23	4	8	0, 2	0, 3	0, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −
23	4	9	1, 3	0, 3	0, 3	0, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
23	4	10	1, 3	0, 3	0, 3	0, 4	0, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
23	4	11	1, 3	0, 3	0, 4	0, 4	0, 4	0, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
23	5	5	0, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5
23	5	6	0, 2	0, 3	0, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5
23	5	7	0, 2	0, 3	0, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5
23	5	8	1, 3	0, 3	0, 4	0, 4	0, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, −	−, −
23	5	9	1, 3	0, 3	0, 4	0, 4	0, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, −	−, −	−, −	−, −
23	5	10	1, 3	1, 4	0, 4	0, 4	0, 4	0, 5	0, 5	0, 5	−, 5	−, 5	−, 5	−, 5	−, −	−, −	−, −	−, −	−, −	−, −
23	5	11	1, 3	1, 4	1, 4	0, 4	0, 5	0, 5	0, 5	0, 5	−, 5	−, 5	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
23	6	6	1, 2	0, 3	0, 4	0, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6
23	6	7	1, 3	0, 3	0, 4	0, 4	0, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6
23	6	8	1, 4	1, 4	0, 4	0, 4	0, 4	0, 5	0, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6
23	6	9	1, 4	1, 4	0, 4	0, 4	0, 5	0, 5	0, 5	0, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6
23	6	10	2, 4	1, 4	1, 4	1, 5	0, 5	0, 5	0, 5	0, 6	0, 6	0, 6	−, 6	−, 6	−, 6	−, 6	−, −	−, −	−, −	−, −
23	6	11	2, 4	1, 4	1, 5	1, 5	1, 5	0, 5	0, 6	0, 6	0, 6	0, 6	0, 6	−, 6	−, 6	−, 6	−, −	−, −	−, −	−, −
23	7	7	1, 4	1, 4	0, 4	0, 4	0, 4	0, 5	0, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6
23	7	8	1, 4	1, 4	1, 4	0, 4	0, 5	0, 5	0, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 7	−, 7
23	7	9	2, 4	1, 4	1, 5	1, 5	0, 5	0, 5	0, 6	0, 6	0, 6	0, 6	−, 6	−, 6	−, 6	−, 6	−, 7	−, 7	−, 7	−, 7
23	7	10	2, 4	2, 5	1, 5	1, 5	1, 5	1, 6	0, 6	0, 6	0, 6	0, 6	0, 7	0, 7	−, 7	−, 7	−, 7	−, 7	−, 7	−, 7
23	7	11	2, 4	2, 5	1, 5	1, 5	1, 6	1, 6	1, 6	0, 6	0, 7	0, 7	0, 7	0, 7	0, 7	0, 7	−, 7	−, 7	−, −	−, −
23	8	8	2, 4	1, 4	1, 5	1, 5	0, 5	0, 5	0, 6	0, 6	0, 6	0, 6	−, 6	−, 6	−, 7	−, 7	−, 7	−, 7	−, 7	−, 7
23	8	9	2, 5	2, 5	1, 5	1, 5	1, 6	1, 6	0, 6	0, 6	0, 6	0, 7	0, 7	0, 7	−, 7	−, 7	−, 7	−, 7	−, 8	−, 8
23	8	10	2, 5	2, 5	2, 5	1, 6	1, 6	1, 6	1, 6	0, 6	0, 7	0, 7	0, 7	0, 7	0, 7	0, 8	−, 8	−, 8	−, 8	−, 8

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
23	8	11	3, 5	2, 5	2, 6	2, 6	1, 6	1, 6	1, 7	1, 7	1, 7	0, 7	0, 7	0, 7	0, 8	0, 8	0, 8	0, 8	−, 8	−, 8
23	9	9	3, 5	2, 5	2, 5	1, 6	1, 6	1, 6	1, 6	1, 7	0, 7	0, 7	0, 7	0, 7	0, 7	0, 8	−, 8	−, 8	−, 8	−, 8
23	9	10	3, 5	2, 5	2, 6	2 6	1, 6	1, 7	1, 7	1, 7	1, 7	0, 7	0, 8	0, 8	0, 8	0, 8	0, 8	0, 8	0, 8	−, 8
23	9	11	3, 5	3, 6	2, 6	2, 7	2, 7	2, 7	1, 7	1, 7	1, 8	1, 8	1, 8	1, 8	0, 8	0, 8	0, 9	0, 9	0, 9	0, 9
23	10	10	3, 6	3, 6	2, 6	2, 7	2, 7	2, 7	1, 7	1, 7	1, 8	1, 8	1, 8	1, 8	0, 8	0, 8	0, 9	0, 9	0, 9	0, 9
23	10	11	4, 6	3, 6	3, 7	2, 7	2, 7	2, 7	2, 8	2, 8	1, 8	1, 8	1, 9	1, 9	1, 9	1, 9	0, 9	0, 9	0, 9	0, 9
23	11	11	4, 6	4, 7	3, 7	3, 8	3, 8	3, 8	2, 8	2, 8	2, 9	2, 9	2, 9	1, 9	1, 9	1, 9	1, 10	1, 10	1, 10	1, 10
24	1	1	−, 1	−, 1	−, 1	−, 1	−, 1	−, 1	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	1	2	−, 1	−, 1	−, 1	−, 1	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	1	3	−, 1	−, 1	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	1	4	−, 1	−, 1	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	1	5	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	1	6	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	1	7	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	1	8	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	1	9	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	1	10	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	1	11	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	1	12	0, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	2	2	−, 1	−, 1	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −
24	2	3	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	2	4	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	2	5	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	2	6	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	2	7	0, 1	−, 2	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	2	8	0, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	2	9	0, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	2	10	0, 2	0, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	2	11	0, 2	0, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	2	12	0, 2	0, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	3	3	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3
24	3	4	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, −	−, −
24	3	5	0, 1	−, 2	−, 2	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, −	−, −	−, −	−, −
24	3	6	0, 2	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, −	−, −	−, −	−, −	−, −	−, −
24	3	7	0, 2	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	3	8	0, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	3	9	0, 2	0, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	3	10	0, 2	0, 3	0, 3	−, 3	−, 3	−, 3	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	3	11	0, 2	0, 3	0, 3	−, 3	−, 3	−, 3	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	3	12	1, 2	0, 3	0, 3	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
24	4	4	0, 1	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4
24	4	5	0, 2	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4
24	4	6	0, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −
24	4	7	0, 2	0, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −
24	4	8	0, 2	0, 3	0, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −
24	4	9	0, 2	0, 3	0, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	4	10	1, 3	0, 3	0, 3	0, 4	0, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	4	11	1, 3	0, 3	0, 4	0, 4	0, 4	0, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	4	12	1, 3	0, 4	0, 4	0, 4	0, 4	0, 4	0, 4	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	5	5	0, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5
24	5	6	0, 2	0, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5
24	5	7	0, 2	0, 3	0, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5
24	5	8	1, 3	0, 3	0, 3	0, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, −	−, −
24	5	9	1, 3	0, 3	0, 4	0, 4	0, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, −	−, −	−, −	−, −
24	5	10	1, 3	1, 4	0, 4	0, 4	0, 4	0, 5	0, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, −	−, −	−, −	−, −	−, −	−, −
24	5	11	1, 3	1, 4	0, 4	0, 4	0, 5	0, 5	0, 5	0, 5	−, 5	−, 5	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	5	12	2, 3	1, 4	1, 4	0, 5	0, 5	0, 5	0, 5	0, 5	0, 5	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	6	6	0, 2	0, 3	0, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5
24	6	7	1, 3	0, 3	0, 4	0, 4	0, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6
24	6	8	1, 3	0, 3	0, 4	0, 4	0, 4	0, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6
24	6	9	1, 4	1, 4	0, 4	0, 4	0, 5	0, 5	0, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6
24	6	10	1, 3	1, 4	1, 4	0, 4	0, 5	0, 5	0, 5	0, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, −	−, −
24	6	11	2, 4	1, 4	1, 5	1, 5	0, 5	0, 5	0, 5	0, 6	0, 6	0, 6	−, 6	−, 6	−, 6	−, 6	−, −	−, −	−, −	−, −
24	6	12	2, 4	1, 5	1, 5	1, 5	1, 5	0, 6	0, 6	0, 6	0, 6	0, 6	0, 6	−, −	−, −	−, −	−, −	−, −	−, −	−, −
24	7	7	1, 3	0, 3	0, 4	0, 4	0, 4	0, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6
24	7	8	1, 4	1, 4	0, 4	0, 4	0, 5	0, 5	0, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 7	−, 7
24	7	9	2, 4	1, 4	1, 5	1, 5	0, 5	0, 5	0, 5	0, 6	0, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 7	−, 7	−, 7	−, 7
24	7	10	2, 4	1, 4	1, 5	1, 5	1, 5	0, 5	0, 6	0, 6	0, 6	0, 6	0, 6	−, 6	−, 7	−, 7	−, 7	−, 7	−, 7	−, 7
24	7	11	2, 4	2, 5	1, 5	1, 5	1, 6	1, 6	0, 6	0, 6	0, 6	0, 7	0, 7	0, 7	0, 7	−, 7	−, 7	−, 7	−, 7	−, 7
24	7	12	3, 4	2, 5	2, 5	1, 6	1, 6	1, 6	1, 6	0, 7	0, 7	0, 7	0, 7	0, 7	0, 7	0, 7	−, −	−, −	−, −	−, −
24	8	8	2, 4	1, 4	1, 5	1, 5	0, 5	0, 5	0, 5	0, 6	0, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 7	−, 7	−, 7	−, 7
24	8	9	2, 4	1, 4	1, 5	1, 5	1, 5	0, 5	0, 6	0, 6	0, 6	0, 7	0, 7	0, 7	−, 7	−, 7	−, 7	−, 7	−, 7	−, 7
24	8	10	2, 5	2, 5	1, 5	1, 6	1, 6	1, 6	0, 6	0, 6	0, 7	0, 7	0, 7	0, 7	0, 7	−, 7	−, 8	−, 8	−, 8	−, 8
24	8	11	3, 5	2, 5	2, 6	1, 6	1, 6	1, 6	1, 7	1, 7	0, 7	0, 7	0, 7	0, 7	0, 8	0, 8	0, 8	0, 8	−, 8	−, 8
24	8	12	3, 5	2, 6	2, 6	2, 6	2, 6	1, 7	1, 7	1, 7	1, 7	0, 8	0, 8	0, 8	0, 8	0, 8	0, 8	0, 8	0, 8	−, −
24	9	9	2, 5	2, 5	1, 5	1, 6	1, 6	1, 6	1, 6	0, 6	0, 7	0, 7	0, 7	0, 7	0, 7	−, 7	−, 8	−, 8	−, 8	−, 8
24	9	10	3, 5	2, 5	2, 6	1, 6	1, 6	1, 6	1, 7	1, 7	0, 7	0, 7	0, 7	0, 8	0, 8	0, 8	0, 8	−, 8	−, 8	−, 8
24	9	11	3, 5	3, 6	2, 6	2, 7	2, 7	1, 7	1, 7	1, 7	1, 8	1, 8	0, 8	0, 8	0, 8	0, 8	0, 8	0, 9	0, 9	0, 9
24	9	12	4, 5	3, 6	2, 7	2, 7	2, 7	2, 7	2, 7	1, 8	1, 8	1, 8	1, 8	1, 8	1, 8	0, 9	0, 9	0, 9	0, 9	0, 9
24	10	10	3, 6	3, 6	2, 6	2, 7	2, 7	1, 7	1, 7	1, 7	1, 8	1, 8	0, 8	0, 8	0, 8	0, 8	0, 9	0, 9	0, 9	0, 9
24	10	11	4, 6	3, 6	3, 7	2, 7	2, 7	2, 7	2, 8	2, 8	1, 8	1, 8	1, 8	1, 9	1, 9	1, 9	0, 9	0, 9	0, 9	0, 9
24	10	12	4, 6	3, 7	3, 7	2, 8	2, 8	2, 8	2, 8	2, 8	2, 8	1, 9	1, 9	1, 9	1, 9	1, 9	1, 9	0, 10	0, 10	0, 10
24	11	11	4, 6	4, 7	3, 7	3, 8	2, 8	2, 8	2, 8	2, 8	2, 9	2, 9	1, 9	1, 9	1, 9	1, 9	1, 9	1, 10	0, 10	0, 10
24	11	12	5, 6	4, 7	3, 8	3, 8	3, 8	3, 8	3, 8	2, 9	2, 9	2, 9	2, 9	1, 10	1, 10	1, 10	1, 10	1, 10	1, 10	1, 10
24	12	12	5, 7	4, 8	4, 8	3, 9	3, 9	3, 9	3, 9	3, 9	3, 9	2, 10	2, 10	2, 10	2, 10	2, 10	2, 10	1, 11	1, 11	1, 11

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
25	1	1	−,1	−,1	−,1	−,1	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	1	2	−,1	−,1	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	1	3	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	1	4	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	1	5	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	1	6	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	1	7	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	1	8	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	1	9	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	1	10	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	1	11	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	1	12	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	2	2	−,1	−,1	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−
25	2	3	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−
25	2	4	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	2	5	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	2	6	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	2	7	−,1	−,1	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	2	8	0,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	2	9	0,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	2	10	0,2	0,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	2	11	0,2	0,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	2	12	0,2	0,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	3	3	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3
25	3	4	−,1	−,1	−,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−
25	3	5	0,1	−,2	−,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−
25	3	6	0,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−
25	3	7	0,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	3	8	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	3	9	0,2	0,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	3	10	0,2	0,3	0,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	3	11	0,2	0,3	0,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	3	12	0,2	0,3	0,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	4	4	0,1	−,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4
25	4	5	0,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4
25	4	6	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−
25	4	7	0,2	0,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−
25	4	8	0,2	0,3	0,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−
25	4	9	0,2	0,3	0,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−
25	4	10	1,3	0,3	0,3	0,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
25	4	11	1,3	0,3	0,4	0,4	0,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	4	12	1,3	0,3	0,4	0,4	0,4	0,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	5	5	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,5	−,5
25	5	6	0,2	0,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5
25	5	7	0,2	0,3	0,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5
25	5	8	1,3	0,3	0,3	0,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,−	−,−
25	5	9	1,3	0,3	0,4	0,4	0,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,−	−,−	−,−	−,−
25	5	10	1,3	0,3	0,4	0,4	0,4	0,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,−	−,−	−,−	−,−
25	5	11	1,3	1,4	0,4	0,4	0,4	0,5	0,5	0,5	−,5	−,5	−,5	−,5	−,−	−,−	−,−	−,−	−,−	−,−
25	5	12	1,3	1,4	1,4	0,4	0,5	0,5	0,5	0,5	−,5	−,5	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
25	6	6	0,2	0,3	0,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5
25	6	7	1,3	0,3	0,4	0,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,6	−,6	−,6	−,6
25	6	8	1,3	0,3	0,4	0,4	0,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,6	−,6	−,6	−,6	−,6	−,6
25	6	9	1,4	1,4	0,4	0,4	0,4	0,5	0,5	−,5	−,5	−,5	−,6	−,6	−,6	−,6	−,6	−,6	−,6	−,6
25	6	10	1,4	1,4	1,4	0,4	0,5	0,5	0,5	−,5	−,6	−,6	−,6	−,6	−,6	−,6	−,6	−,6	−,−	−,−
25	6	11	2,4	1,4	1,5	1,5	0,5	0,5	0,5	0,6	0,6	0,6	−,6	−,6	−,6	−,6	−,−	−,−	−,−	−,−
25	6	12	2,4	1,4	1,5	1,5	1,5	0,5	0,6	0,6	0,6	0,6	0,6	−,6	−,−	−,−	−,−	−,−	−,−	−,−
25	7	7	1,3	0,3	0,4	0,4	0,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,6	−,6	−,6	−,6	−,6	−,6
25	7	8	1,4	1,4	0,4	0,4	0,5	0,5	0,5	−,5	−,5	−,5	−,6	−,6	−,6	−,6	−,6	−,6	−,7	−,7
25	7	9	1,3	1,4	1,4	0,5	0,5	0,5	0,5	0,6	−,6	−,6	−,6	−,6	−,6	−,6	−,7	−,7	−,7	−,7
25	7	10	2,4	1,4	1,5	1,5	0,5	0,5	0,6	0,6	0,6	−,6	−,6	−,6	−,7	−,7	−,7	−,7	−,7	−,7
25	7	11	2,4	2,5	1,5	1,5	1,6	1,6	0,6	0,6	0,6	0,7	0,7	0,7	−,7	−,7	−,7	−,7	−,7	−,7
25	7	12	2,4	2,5	1,5	1,6	1,6	1,6	1,6	0,6	0,7	0,7	0,7	0,7	0,7	−,7	−,7	−,7	−,−	−,−
25	8	8	2,4	1,4	1,5	0,5	0,5	0,5	0,5	0,6	−,6	−,6	−,6	−,6	−,6	−,6	−,7	−,7	−,7	−,7
25	8	9	2,4	1,4	1,5	1,5	0,5	0,5	0,6	0,6	0,6	−,6	−,6	−,6	−,7	−,7	−,7	−,7	−,7	−,7
25	8	10	2,5	2,5	1,5	1,5	1,6	1,6	0,6	0,6	0,7	0,7	0,7	0,7	−,7	−,7	−,7	−,7	−,8	−,8
25	8	11	3,5	2,5	2,5	1,6	1,6	1,6	1,6	1,7	0,7	0,7	0,7	0,7	0,7	0,8	−,8	−,8	−,8	−,8
25	8	12	3,5	2,5	2,6	1,6	1,6	1,6	1,7	1,7	0,7	0,7	0,7	0,8	0,8	0,8	0,8	0,8	−,8	−,8
25	9	9	2,5	2,5	1,5	1,5	1,6	1,6	0,6	0,6	0,7	0,7	0,7	0,7	−,7	−,7	−,8	−,8	−,8	−,8
25	9	10	3,5	2,5	2,6	1,6	1,6	1,6	1,7	1,7	0,7	0,7	0,7	0,7	0,8	0,8	−,8	−,8	−,8	−,8
25	9	11	3,5	2,5	2,6	1,6	1,6	1,7	1,7	1,7	1,7	0,7	0,8	0,8	0,8	0,8	0,8	0,9	0,9	−,9
25	9	12	3,5	3,6	2,6	2,7	2,7	2,7	1,7	1,7	1,8	1,8	1,8	0,8	0,8	0,8	0,9	0,9	0,9	0,9
25	10	10	3,5	2,5	2,6	1,6	1,7	1,7	1,7	1,7	1,7	1,8	0,8	0,8	0,8	0,8	0,8	0,9	0,9	0,9
25	10	11	3,6	3,6	2,6	2,7	2,7	2,7	1,7	1,7	1,8	1,8	1,8	0,8	0,8	0,9	0,9	0,9	0,9	0,9
25	10	12	4,6	3,6	3,7	2,7	2,7	2,8	2,8	2,8	1,8	1,8	1,9	1,9	1,9	1,9	0,9	0,9	0,9	0,9
25	11	11	4,6	3,6	3,7	2,7	2,7	2,8	2,8	2,8	1,8	1,8	1,9	1,9	1,9	1,9	0,9	0,9	0,10	0,10
25	11	12	4,6	4,7	3,7	3,8	3,8	2,8	2,8	2,8	2,9	2,9	1,9	1,9	1,9	1,9	1,10	1,10	1,10	1,10
25	12	12	5,7	4,7	4,8	3,8	3,8	3,9	3,9	3,9	2,9	2,9	2,10	2,10	2,10	2,10	1,10	1,10	1,11	1,11
26	1	1	−,1	−,1	−,1	−,1	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	1	2	−,1	−,1	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
26	1	3	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	1	4	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	1	5	−,1	−,1	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	1	6	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	1	7	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	1	8	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	1	9	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	1	10	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	1	11	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	1	12	−,1	−,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	1	13	0,1	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	2	2	−,1	−,1	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−
26	2	3	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−
26	2	4	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	2	5	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	2	6	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	2	7	−,1	−,1	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	2	8	0,1	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	2	9	0,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	2	10	0,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	2	11	0,2	0,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	2	12	0,2	0,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	2	13	0,2	0,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	3	3	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3
26	3	4	−,1	−,1	−,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−
26	3	5	−,1	−,1	−,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−
26	3	6	0,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−
26	3	7	0,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	3	8	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	3	9	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	3	10	0,2	0,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	3	11	0,2	0,3	0,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	3	12	0,2	0,3	0,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	3	13	1,2	0,3	0,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
26	4	4	0,1	−,2	−,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4
26	4	5	0,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4
26	4	6	0,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−
26	4	7	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−
26	4	8	0,2	0,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−
26	4	9	0,2	0,3	0,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
26	4	10	1, 2	0, 3	0, 3	0, 4	–, 4	–, 4	–, 4	–, 4	–, 4	–, 4	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
26	4	11	1, 3	0, 3	0, 3	0, 4	0, 4	–, 4	–, 4	–, 4	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
26	4	12	1, 3	0, 3	0, 4	0, 4	0, 4	–, 4	–, 4	–, 4	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
26	4	13	1, 3	0, 4	0, 4	0, 4	0, 4	0, 4	0, 4	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
26	5	5	0, 2	–, 2	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, 4	–, 4	–, 4	–, 4	–, 4	–, 4	–, 4	–, 4	–, 5	–, 5
26	5	6	0, 2	0, 3	–, 3	–, 3	–, 3	–, 3	–, 4	–, 4	–, 4	–, 4	–, 4	–, 4	–, 4	–, 4	–, 5	–, 5	–, 5	–, 5
26	5	7	0, 2	0, 3	0, 3	–, 3	–, 4	–, 4	–, 4	–, 4	–, 4	–, 4	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5
26	5	8	0, 2	0, 3	0, 3	–, 4	–, 4	–, 4	–, 4	–, 4	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5
26	5	9	1, 3	0, 3	0, 4	0, 4	0, 4	–, 4	–, 4	–, 4	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, –	–, –
26	5	10	1, 3	0, 3	0, 4	0, 4	0, 4	–, 4	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, –	–, –	–, –	–, –
26	5	11	1, 3	1, 4	0, 4	0, 4	0, 4	0, 5	0, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, –	–, –	–, –	–, –	–, –	–, –
26	5	12	1, 3	1, 4	0, 4	0, 4	0, 5	0, 5	0, 5	0, 5	–, 5	–, 5	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
26	5	13	2, 3	1, 4	1, 4	0, 5	0, 5	0, 5	0, 5	0, 5	0, 5	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
26	6	6	0, 2	0, 3	0, 3	–, 3	–, 3	–, 4	–, 4	–, 4	–, 4	–, 4	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5
26	6	7	1, 3	0, 3	0, 4	0, 4	–, 4	–, 4	–, 4	–, 4	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 6	–, 6
26	6	8	1, 3	0, 3	0, 4	0, 4	0, 4	–, 4	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 6	–, 6	–, 6	–, 6
26	6	9	1, 4	1, 4	0, 4	0, 4	0, 4	0, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 6	–, 6	–, 6	–, 6	–, 6	–, 6
26	6	10	1, 4	1, 4	0, 4	0, 4	0, 5	0, 5	0, 5	–, 5	–, 5	–, 5	–, 6	–, 6	–, 6	–, 6	–, 6	–, 6	–, 6	–, 6
26	6	11	2, 4	1, 4	1, 4	1, 5	0, 5	0, 5	0, 5	0, 6	–, 6	–, 6	–, 6	–, 6	–, 6	–, 6	–, –	–, –	–, –	–, –
26	6	12	2, 4	1, 4	1, 5	1, 5	0, 5	0, 5	0, 6	0, 6	0, 6	0, 6	–, 6	–, 6	–, 6	–, 6	–, –	–, –	–, –	–, –
26	6	13	2, 4	1, 5	1, 5	1, 5	1, 5	0, 6	0, 6	0, 6	0, 6	0, 6	0, 6	–, –	–, –	–, –	–, –	–, –	–, –	–, –
26	7	7	1, 3	0, 3	0, 4	0, 4	0, 4	–, 4	–, 5	–, 5	–, 5	–, 5	–, 5	–, 5	–, 6	–, 6	–, 6	–, 6	–, 6	–, 6
26	7	8	1, 4	1, 4	0, 4	0, 4	0, 5	0, 5	0, 5	–, 5	–, 5	–, 5	–, 6	–, 6	–, 6	–, 6	–, 6	–, 6	–, 6	–, 6
26	7	9	1, 4	1, 4	1, 4	0, 4	0, 5	0, 5	0, 5	–, 5	–, 6	–, 6	–, 6	–, 6	–, 6	–, 6	–, 7	–, 7	–, 7	–, 7
26	7	10	2, 4	1, 4	1, 5	1, 5	0, 5	0, 5	0, 6	0, 6	0, 6	–, 6	–, 6	–, 6	–, 7	–, 7	–, 7	–, 7	–, 7	–, 7
26	7	11	2, 4	1, 4	1, 5	1, 5	1, 5	0, 5	0, 6	0, 6	0, 6	0, 7	0, 7	–, 7	–, 7	–, 7	–, 7	–, 7	–, 7	–, 7
26	7	12	2, 4	2, 5	1, 5	1, 5	1, 6	1, 6	0, 6	0, 6	0, 7	0, 7	0, 7	0, 7	–, 7	–, 7	–, 7	–, 7	–, –	–, –
26	7	13	3, 4	2, 5	2, 5	1, 6	1, 6	1, 6	1, 6	0, 7	0, 7	0, 7	0, 7	0, 7	0, 7	–, –	–, –	–, –	–, –	–, –
26	8	8	1, 3	1, 4	1, 4	0, 4	0, 5	0, 5	0, 5	0, 6	–, 6	–, 6	–, 6	–, 6	–, 6	–, 6	–, 7	–, 7	–, 7	–, 7
26	8	9	2, 4	1, 4	1, 5	1, 5	0, 5	0, 5	0, 6	0, 6	0, 6	–, 6	–, 6	–, 6	–, 7	–, 7	–, 7	–, 7	–, 7	–, 7
26	8	10	2, 5	2, 5	1, 5	1, 5	1, 6	1, 6	0, 6	0, 6	0, 6	0, 7	0, 7	0, 7	–, 7	–, 7	–, 7	–, 7	–, 8	–, 8
26	8	11	2, 5	2, 5	1, 5	1, 6	1, 6	1, 6	1, 6	0, 6	0, 7	0, 7	0, 7	0, 7	0, 7	–, 7	–, 8	–, 8	–, 8	–, 8
26	8	12	3, 5	2, 5	2, 6	1, 6	1, 6	1, 6	1, 7	1, 7	0, 7	0, 7	0, 7	0, 7	0, 8	0, 8	0, 8	–, 8	–, 8	–, 8
26	8	13	3, 5	2, 6	2, 6	1, 7	1, 7	1, 7	1, 7	1, 7	1, 7	0, 8	0, 8	0, 8	0, 8	0, 8	0, 8	0, 8	–, –	
26	9	9	2, 5	2, 5	1, 5	1, 5	1, 6	1, 6	0, 6	0, 6	0, 6	0, 7	0, 7	0, 7	–, 7	–, 7	–, 7	–, 7	–, 8	–, 8
26	9	10	2, 5	2, 5	1, 5	1, 6	1, 6	1, 6	1, 6	0, 6	0, 7	0, 7	0, 7	0, 7	0, 7	0, 8	–, 8	–, 8	–, 8	–, 8
26	9	11	3, 5	2, 5	2, 6	1, 6	1, 6	1, 7	1, 7	1, 7	0, 7	0, 7	0, 8	0, 8	0, 8	0, 8	0, 8	–, 8	–, 8	–, 8
26	9	12	3, 5	3, 6	2, 6	2, 7	2, 7	1, 7	1, 7	1, 7	1, 8	1, 8	0, 8	0, 8	0, 8	0, 8	0, 9	0, 9	0, 9	0, 9
26	9	13	4, 5	3, 6	2, 7	2, 7	2, 7	2, 7	2, 7	1, 8	1, 8	1, 8	1, 8	0, 9	0, 9	0, 9	0, 9	0, 9	0, 9	0, 9
26	10	10	3, 5	2, 5	2, 6	1, 6	1, 6	1, 7	1, 7	1, 7	0, 7	0, 7	0, 8	0, 8	0, 8	0, 8	0, 8	–, 8	–, 9	–, 9

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
26	10	11	3, 6	3, 6	2, 6	2, 7	2, 7	1, 7	1, 7	1, 7	1, 8	1, 8	0, 8	0, 8	0, 8	0, 8	0, 9	0, 9	0, 9	0, 9
26	10	12	4, 6	3, 6	3, 7	2, 7	2, 7	2, 8	2, 8	1, 8	1, 8	1, 8	1, 8	1, 9	1, 9	0, 9	0, 9	0, 9	0, 9	0, 9
26	10	13	4, 6	3, 7	3, 7	2, 8	2, 8	2, 8	2, 8	2, 8	1, 9	1, 9	1, 9	1, 9	1, 9	1, 9	1, 9	0, 10	0, 10	0, 10
26	11	11	4, 6	3, 6	3, 7	2, 7	2, 7	2, 8	2, 8	1, 8	1, 8	1, 8	1, 9	1, 9	1, 9	0, 9	0, 9	0, 9	0, 9	0, 9
26	11	12	4, 6	4, 7	3, 7	3, 8	2, 8	2, 8	2, 8	2, 8	2, 9	1, 9	1, 9	1, 9	1, 9	1, 9	1, 10	1, 10	0, 10	0, 10
26	11	13	5, 6	4, 7	3, 8	3, 8	3, 8	2, 9	2, 9	2, 9	2, 9	2, 9	2, 9	1, 10	1, 10	1, 10	1, 10	1, 10	1, 10	1, 10
26	12	12	5, 7	4, 7	3, 8	3, 8	3, 8	3, 9	2, 9	2, 9	2, 9	2, 9	2, 9	2, 10	1, 10	1, 10	1, 10	1, 10	1, 10	1, 11
26	12	13	5, 7	4, 8	4, 8	3, 9	3, 9	3, 9	3, 9	3, 9	2, 10	2, 10	2, 10	2, 10	2, 10	2, 10	1, 11	1, 11	1, 11	1, 11
26	13	13	6, 7	5, 8	4, 9	4, 9	4, 9	3, 10	3, 10	3, 10	3, 10	3, 10	3, 10	2, 11	2, 11	2, 11	2, 11	2, 11	2, 11	1, 12
27	1	1	–, 1	–, 1	–, 1	–, 1	–, 1	–, 1	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	1	2	–, 1	–, 1	–, 1	–, 1	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	1	3	–, 1	–, 1	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	1	4	–, 1	–, 1	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	1	5	–, 1	–, 1	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	1	6	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	1	7	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	1	8	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	1	9	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	1	10	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	1	11	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	1	12	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	1	13	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	2	2	–, 1	–, 1	–, 1	–, 1	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, –	–, –	–, –	–, –
27	2	3	–, 1	–, 1	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –
27	2	4	–, 1	–, 1	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	2	5	–, 1	–, 1	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	2	6	–, 1	–, 1	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	2	7	–, 1	–, 1	–, 2	–, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	2	8	0, 1	–, 2	–, 2	–, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	2	9	0, 2	–, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	2	10	0, 2	–, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	2	11	0, 2	0, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	2	12	0, 2	0, 2	–, 2	–, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	2	13	0, 2	0, 2	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	3	3	–, 1	–, 1	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3
27	3	4	–, 1	–, 1	–, 2	–, 2	–, 2	–, 2	–, 2	–, 2	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, –	–, –
27	3	5	–, 1	–, 1	–, 2	–, 2	–, 2	–, 2	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, –	–, –	–, –	–, –
27	3	6	0, 1	–, 2	–, 2	–, 2	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, –	–, –	–, –	–, –	–, –	–, –
27	3	7	0, 2	–, 2	–, 2	–, 2	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
27	3	8	0, 2	–, 2	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, 3	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
27	3	9	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
27	3	10	0,2	0,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
27	3	11	0,2	0,3	0,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
27	3	12	0,2	0,3	0,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
27	3	13	0,2	0,3	0,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
27	4	4	−,1	−,1	−,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4
27	4	5	0,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4
27	4	6	0,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4
27	4	7	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−
27	4	8	0,2	0,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−
27	4	9	0,2	0,3	0,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−
27	4	10	0,2	0,3	0,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
27	4	11	1,3	0,3	0,3	0,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
27	4	12	1,3	0,3	0,4	0,4	0,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
27	4	13	1,3	0,3	0,4	0,4	0,4	0,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
27	5	5	0,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,5	−,5
27	5	6	0,2	−,2	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5
27	5	7	0,2	0,3	0,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5
27	5	8	0,2	0,3	0,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5
27	5	9	1,3	0,3	0,3	0,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,−	−,−
27	5	10	1,3	0,3	0,4	0,4	0,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,−	−,−	−,−	−,−
27	5	11	1,3	0,3	0,4	0,4	0,4	0,5	−,5	−,5	−,5	−,5	−,5	−,5	−,−	−,−	−,−	−,−	−,−	−,−
27	5	12	1,3	1,4	0,4	0,4	0,5	0,5	0,5	0,5	−,5	−,5	−,5	−,5	−,−	−,−	−,−	−,−	−,−	−,−
27	5	13	1,3	1,4	1,4	0,4	0,5	0,5	0,5	0,5	−,5	−,5	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
27	6	6	0,2	0,3	0,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5
27	6	7	1,2	0,3	0,4	0,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,6	−,6
27	6	8	1,3	0,3	0,4	0,4	0,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,6	−,6	−,6	−,6
27	6	9	1,3	0,3	0,4	0,4	0,4	0,5	−,5	−,5	−,5	−,5	−,5	−,5	−,6	−,6	−,6	−,6	−,6	−,6
27	6	10	1,4	1,4	0,4	0,4	0,5	0,5	0,5	−,5	−,5	−,5	−,6	−,6	−,6	−,6	−,6	−,6	−,6	−,6
27	6	11	1,4	1,4	1,4	0,4	0,5	0,5	0,5	−,5	−,6	−,6	−,6	−,6	−,6	−,6	−,6	−,6	−,−	−,−
27	6	12	2,4	1,4	1,5	1,5	0,5	0,5	0,5	0,6	0,6	−,6	−,6	−,6	−,6	−,6	−,−	−,−	−,−	−,−
27	6	13	2,4	1,4	1,5	1,5	1,5	0,5	0,6	0,6	0,6	0,6	−,6	−,6	−,−	−,−	−,−	−,−	−,−	−,−
27	7	7	1,3	0,3	0,4	0,4	0,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,6	−,6	−,6	−,6
27	7	8	1,4	0,4	0,4	0,4	0,4	0,5	−,5	−,5	−,5	−,5	−,6	−,6	−,6	−,6	−,6	−,6	−,6	−,6
27	7	9	1,4	1,4	0,4	0,4	0,5	0,5	0,5	−,5	−,6	−,6	−,6	−,6	−,6	−,6	−,6	−,6	−,7	−,7
27	7	10	2,4	1,4	1,5	0,5	0,5	0,5	0,5	0,6	−,6	−,6	−,6	−,6	−,6	−,6	−,7	−,7	−,7	−,7
27	7	11	2,4	1,4	1,5	1,5	0,5	0,5	0,6	0,6	0,6	−,6	−,6	−,6	−,7	−,7	−,7	−,7	−,7	−,7
27	7	12	2,4	2,5	1,5	1,5	1,6	1,6	0,6	0,6	0,6	0,7	0,7	0,7	−,7	−,7	−,7	−,7	−,7	−,7
27	7	13	2,4	2,5	1,5	1,6	1,6	1,6	1,6	0,6	0,7	0,7	0,7	0,7	0,7	−,7	−,7	−,7	−,−	−,−
27	8	8	1,4	1,4	0,4	0,4	0,5	0,5	0,5	−,5	−,6	−,6	−,6	−,6	−,6	−,6	−,7	−,7	−,7	−,7

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
27	8	9	2, 4	1, 4	1, 5	0, 5	0, 5	0, 5	0, 6	0, 6	0, 6	−, 6	−, 6	−, 6	−, 7	−, 7	−, 7	−, 7	−, 7	−, 7
27	8	10	2, 4	1, 4	1, 5	1, 5	1, 5	0, 6	0, 6	0, 6	0, 6	0, 7	−, 7	−, 7	−, 7	−, 7	−, 7	−, 7	−, 7	−, 7
27	8	11	2, 5	2, 5	1, 5	1, 6	1, 6	1, 6	0, 6	0, 6	0, 7	0, 7	0, 7	0, 7	−, 7	−, 7	−, 8	−, 8	−, 8	−, 8
27	8	12	3, 5	2, 5	2, 6	1, 6	1, 6	1, 6	1, 6	1, 7	0, 7	0, 7	0, 7	0, 7	0, 8	0, 8	−, 8	−, 8	−, 8	−, 8
27	8	13	3, 5	2, 5	2, 6	1, 6	1, 6	1, 7	1, 7	1, 7	0, 7	0, 7	0, 8	0, 8	0, 8	0, 8	0, 8	0, 8	−, 8	−, 8
27	9	9	2, 4	1, 4	1, 5	1, 5	1, 5	0, 6	0, 6	0, 6	0, 6	0, 7	−, 7	−, 7	−, 7	−, 7	−, 7	−, 7	−, 8	−, 8
27	9	10	2, 5	2, 5	1, 5	1, 6	1, 6	1, 6	0, 6	0, 6	0, 7	0, 7	0, 7	0, 7	−, 7	−, 7	−, 8	−, 8	−, 8	−, 8
27	9	11	3, 5	2, 5	2, 6	1, 6	1, 6	1, 6	1, 7	1, 7	0, 7	0, 7	0, 7	0, 8	0, 8	0, 8	−, 8	−, 8	−, 8	−, 8
27	9	12	3, 5	2, 5	2, 6	1, 6	1, 7	1, 7	1, 7	1, 7	1, 7	1, 8	0, 8	0, 8	0, 8	0, 8	0, 8	0, 9	−, 9	−, 9
27	9	13	3, 5	3, 6	2, 6	2, 7	2, 7	1, 7	1, 7	1, 7	1, 8	1, 8	1, 8	0, 8	0, 8	0, 8	0, 9	0, 9	0, 9	0, 9
27	10	10	3, 5	2, 5	2, 6	1, 6	1, 6	1, 7	1, 7	1, 7	0, 7	0, 7	0, 8	0, 8	0, 8	0, 8	−, 8	−, 8	−, 8	−, 8
27	10	11	3, 6	3, 6	2, 6	2, 7	2, 7	1, 7	1, 7	1, 7	1, 8	1, 8	0, 8	0, 8	0, 8	0, 8	0, 9	0, 9	0, 9	−, 9
27	10	12	3, 6	3, 6	2, 6	2, 7	2, 7	1, 7	1, 7	1, 8	1, 8	1, 8	1, 8	0, 8	0, 9	0, 9	0, 9	0, 9	0, 9	0, 9
27	10	13	4, 6	3, 6	3, 7	2, 7	2, 7	2, 8	2, 8	2, 8	1, 8	1, 8	1, 9	1, 9	1, 9	1, 9	0, 9	0, 9	0, 10	0, 10
27	11	11	3, 6	3, 6	2, 7	2, 7	2, 7	1, 7	1, 8	1, 8	1, 8	1, 8	1, 8	1, 9	0, 9	0, 9	0, 9	0, 9	0, 9	0, 9
27	11	12	4, 6	3, 6	3, 7	2, 7	2, 8	2, 8	2, 8	2, 8	1, 8	1, 9	1, 9	1, 9	1, 9	1, 9	0, 9	0, 9	0, 10	0, 10
27	11	13	4, 6	4, 7	3, 7	3, 8	3, 8	2, 8	2, 8	2, 9	2, 9	2, 9	1, 9	1, 9	1, 10	1, 10	1, 10	1, 10	0, 10	0, 10
27	12	12	4, 7	4, 7	3, 7	3, 8	3, 8	2, 8	2, 8	2, 9	2, 9	2, 9	1, 9	1, 9	1, 10	1, 10	1, 10	1, 10	1, 10	0, 10
27	12	13	5, 7	4, 7	4, 8	3, 8	3, 8	3, 9	3, 9	2, 9	2, 9	2, 10	2, 10	2, 10	2, 10	1, 10	1, 10	1, 10	1, 11	1, 11
27	13	13	5, 7	5, 8	4, 8	4, 9	4, 9	3, 9	3, 9	3, 10	3, 10	2, 10	2, 10	2, 10	2, 11	2, 11	2, 11	2, 11	1, 11	1, 11
28	1	1	−, 1	−, 1	−, 1	−, 1	−, 1	−, 1	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
28	1	2	−, 1	−, 1	−, 1	−, 1	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
28	1	3	−, 1	−, 1	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
28	1	4	−, 1	−, 1	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
28	1	5	−, 1	−, 1	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
28	1	6	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
28	1	7	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
28	1	8	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
28	1	9	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
28	1	10	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
28	1	11	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
28	1	12	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
28	1	13	−, 1	−, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
28	1	14	0, 1	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
28	2	2	−, 1	−, 1	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −
28	2	3	−, 1	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −
28	2	4	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
28	2	5	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
28	2	6	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
28	2	7	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
28	2	8	−,1	−,1	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	2	9	0,2	−,2	−,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	2	10	0,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	2	11	0,2	−,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	2	12	0,2	0,2	−,2	−,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	2	13	0,2	0,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	2	14	0,2	0,2	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	3	3	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3
28	3	4	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−
28	3	5	−,1	−,1	−,2	−,2	−,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−
28	3	6	0,1	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−
28	3	7	0,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	3	8	0,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	3	9	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	3	10	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	3	11	0,2	0,3	−,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	3	12	0,2	0,3	0,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	3	13	0,2	0,3	0,3	−,3	−,3	−,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	3	14	1,2	0,3	0,3	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	4	4	−,1	−,1	−,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4
28	4	5	0,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4
28	4	6	0,2	−,2	−,2	−,2	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4
28	4	7	0,2	−,2	−,3	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−
28	4	8	0,2	0,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−
28	4	9	0,2	0,3	0,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−
28	4	10	0,2	0,3	0,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	4	11	1,3	0,3	0,3	0,4	−,4	−,4	−,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	4	12	1,3	0,3	0,3	0,4	0,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	4	13	1,3	0,3	0,4	0,4	0,4	−,4	−,4	−,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	4	14	1,3	0,4	0,4	0,4	0,4	0,4	0,4	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	5	5	0,2	−,2	−,2	−,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,5	−,5
28	5	6	0,2	−,2	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5
28	5	7	0,2	0,3	−,3	−,3	−,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5
28	5	8	0,2	0,3	0,3	−,3	−,4	−,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5
28	5	9	1,3	0,3	0,3	0,4	−,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,−	−,−
28	5	10	1,3	0,3	0,4	0,4	0,4	−,4	−,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,−	−,−	−,−	−,−
28	5	11	1,3	0,3	0,4	0,4	0,4	−,4	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,5	−,−	−,−	−,−	−,−
28	5	12	1,3	1,4	0,4	0,4	0,4	0,5	0,5	−,5	−,5	−,5	−,5	−,5	−,−	−,−	−,−	−,−	−,−	−,−
28	5	13	1,3	1,4	0,4	0,4	0,5	0,5	0,5	0,5	−,5	−,5	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−
28	5	14	2,3	1,4	1,4	0,5	0,5	0,5	0,5	0,5	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−	−,−

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
28	6	6	0,2	0,3	0,3	-,3	-,3	-,3	-,4	-,4	-,4	-,4	-,4	-,4	-,5	-,5	-,5	-,5	-,5	-,5
28	6	7	0,2	0,3	0,3	-,3	-,4	-,4	-,4	-,4	-,5	-,5	-,5	-,5	-,5	-,5	-,5	-,5	-,6	-,6
28	6	8	1,3	0,3	0,4	0,4	-,4	-,4	-,4	-,4	-,5	-,5	-,5	-,5	-,5	-,5	-,6	-,6	-,6	-,6
28	6	9	1,3	0,3	0,4	0,4	0,4	-,4	-,5	-,5	-,5	-,5	-,5	-,5	-,6	-,6	-,6	-,6	-,6	-,6
28	6	10	1,4	1,4	0,4	0,4	0,4	0,5	0,5	-,5	-,5	-,5	-,6	-,6	-,6	-,6	-,6	-,6	-,6	-,6
28	6	11	1,4	1,4	0,4	0,4	0,5	0,5	0,5	-,5	-,6	-,6	-,6	-,6	-,6	-,6	-,6	-,6	-,-	-,-
28	6	12	2,4	1,4	1,4	1,5	0,5	0,5	0,5	0,6	-,6	-,6	-,6	-,6	-,6	-,6	-,-	-,-	-,-	-,-
28	6	13	2,4	1,4	1,5	1,5	0,5	0,5	0,6	0,6	0,6	0,6	-,6	-,6	-,6	-,6	-,-	-,-	-,-	-,-
28	6	14	2,4	1,5	1,5	1,5	1,5	0,6	0,6	0,6	0,6	0,6	0,6	-,-	-,-	-,-	-,-	-,-	-,-	-,-
28	7	7	1,3	0,3	0,4	0,4	0,4	-,4	-,4	-,4	-,5	-,5	-,5	-,5	-,5	-,5	-,6	-,6	-,6	-,6
28	7	8	1,3	0,3	0,4	0,4	0,4	0,5	-,5	-,5	-,5	-,5	-,5	-,5	-,6	-,6	-,6	-,6	-,6	-,6
28	7	9	1,4	1,4	0,4	0,4	0,5	0,5	0,5	-,5	-,5	-,5	-,6	-,6	-,6	-,6	-,6	-,6	-,7	-,7
28	7	10	1,3	1,4	1,4	0,5	0,5	0,5	0,5	0,6	-,6	-,6	-,6	-,6	-,6	-,6	-,7	-,7	-,7	-,7
28	7	11	2,4	1,4	1,5	1,5	0,5	0,5	0,6	0,6	0,6	-,6	-,6	-,6	-,7	-,7	-,7	-,7	-,7	-,7
28	7	12	2,4	1,4	1,5	1,5	1,5	0,6	0,6	0,6	0,6	0,7	0,7	-,7	-,7	-,7	-,7	-,7	-,7	-,7
28	7	13	2,4	2,5	1,5	1,5	1,6	1,6	0,6	0,6	0,7	0,7	0,7	0,7	-,7	-,7	-,7	-,7	-,-	-,-
28	7	14	3,4	2,5	2,5	1,6	1,6	1,6	1,6	0,7	0,7	0,7	0,7	0,7	0,7	-,-	-,-	-,-	-,-	-,-
28	8	8	1,4	1,4	0,4	0,4	0,5	0,5	0,5	-,5	-,6	-,6	-,6	-,6	-,6	-,6	-,6	-,6	-,7	-,7
28	8	9	2,4	1,4	1,5	0,5	0,5	0,5	0,5	0,6	-,6	-,6	-,6	-,6	-,6	-,6	-,7	-,7	-,7	-,7
28	8	10	2,4	1,4	1,5	1,5	0,5	0,5	0,6	0,6	0,6	-,6	-,7	-,7	-,7	-,7	-,7	-,7	-,7	-,7
28	8	11	2,5	2,5	1,5	1,5	1,6	1,6	0,6	0,6	0,7	0,7	0,7	0,7	-,7	-,7	-,7	-,7	-,8	-,8
28	8	12	2,5	2,5	1,5	1,6	1,6	1,6	1,6	0,6	0,7	0,7	0,7	0,7	0,7	-,7	-,8	-,8	-,8	-,8
28	8	13	3,5	2,5	2,6	1,6	1,6	1,6	1,7	1,7	0,7	0,7	0,7	0,8	0,8	0,8	-,8	-,8	-,8	-,8
28	8	14	3,5	2,6	2,6	1,7	1,7	1,7	1,7	1,7	1,7	0,8	0,8	0,8	0,8	0,8	0,8	0,8	0,8	-,-
28	9	9	2,4	1,4	1,5	1,5	0,5	0,5	0,6	0,6	0,6	-,6	-,7	-,7	-,7	-,7	-,7	-,7	-,7	-,7
28	9	10	2,5	2,5	1,5	1,6	1,6	1,6	0,6	0,6	0,7	0,7	0,7	0,7	-,7	-,7	-,8	-,8	-,8	-,8
28	9	11	3,5	2,5	2,6	1,6	1,6	1,6	1,7	1,7	0,7	0,7	0,7	0,8	0,8	0,8	-,8	-,8	-,8	-,8
28	9	12	3,5	2,5	2,6	1,6	1,6	1,7	1,7	1,7	0,7	0,7	0,8	0,8	0,8	0,8	0,8	-,8	-,9	-,9
28	9	13	3,5	3,6	2,6	2,7	2,7	1,7	1,7	1,7	1,8	1,8	0,8	0,8	0,8	0,8	0,9	0,9	0,9	0,9
28	9	14	4,5	3,6	2,7	2,7	2,7	1,8	1,8	1,8	1,8	1,8	1,8	0,9	0,9	0,9	0,9	0,9	0,9	0,9
28	10	10	3,5	2,5	2,6	1,6	1,6	1,6	1,7	1,7	0,7	0,7	0,7	0,8	0,8	0,8	-,8	-,8	-,8	-,8
28	10	11	3,5	2,5	2,6	1,6	1,7	1,7	1,7	1,7	0,7	0,8	0,8	0,8	0,8	0,8	0,8	0,9	-,9	-,9
28	10	12	3,6	3,6	2,6	2,7	2,7	1,7	1,7	1,7	1,8	1,8	0,8	0,8	0,8	0,9	0,9	0,9	0,9	0,9
28	10	13	4,6	3,6	3,7	2,7	2,7	2,8	2,8	1,8	1,8	1,8	1,9	1,9	0,9	0,9	0,9	0,9	0,9	0,10
28	10	14	4,6	3,7	3,7	2,8	2,8	2,8	2,8	2,8	1,9	1,9	1,9	1,9	1,9	1,9	0,10	0,10	0,10	0,10
28	11	11	3,6	3,6	2,6	2,7	2,7	1,7	1,7	1,8	1,8	1,8	0,8	0,8	0,9	0,9	0,9	0,9	0,9	0,9
28	11	12	4,6	3,6	3,7	2,7	2,7	2,8	2,8	1,8	1,8	1,8	1,9	1,9	1,9	0,9	0,9	0,9	0,10	0,10
28	11	13	4,6	4,7	3,7	3,8	2,8	2,8	2,8	2,9	1,9	1,9	1,9	1,9	1,9	1,10	1,10	0,10	0,10	0,10
28	11	14	5,6	4,7	3,8	3,8	3,8	2,9	2,9	2,9	2,9	2,9	2,9	1,10	1,10	1,10	1,10	1,10	1,10	0,11
28	12	12	4,7	4,7	3,7	3,8	2,8	2,8	2,8	2,9	2,9	1,9	1,9	1,9	1,9	1,10	1,10	0,10	0,10	0,10
28	12	13	5,7	4,7	3,8	3,8	3,8	3,9	2,9	2,9	2,9	2,10	2,10	2,10	1,10	1,10	1,10	1,10	1,11	1,11
28	12	14	5,7	4,8	4,8	3,9	3,9	3,9	3,9	2,10	2,10	2,10	2,10	2,10	2,10	1,11	1,11	1,11	1,11	1,11
28	13	13	5,7	5,8	4,8	4,9	3,9	3,9	3,9	3,10	2,10	2,10	2,10	2,10	2,10	2,11	1,11	1,11	1,11	1,11
28	13	14	6,7	5,8	4,9	4,9	4,9	3,10	3,10	3,10	3,10	2,11	2,11	2,11	2,11	2,11	2,11	2,11	2,11	2,11
28	14	14	6,8	5,9	5,9	4,10	4,10	4,10	4,10	3,11	3,11	3,11	3,11	3,11	3,11	2,12	2,12	2,12	2,12	2,12

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
29	1	1	–,1	–,1	–,1	–,1	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	1	2	–,1	–,1	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	1	3	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	1	4	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	1	5	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	1	6	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	1	7	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	1	8	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	1	9	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	1	10	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	1	11	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	1	12	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	1	13	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	1	14	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	2	2	–,1	–,1	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–
29	2	3	–,1	–,1	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–
29	2	4	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	2	5	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	2	6	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	2	7	–,1	–,1	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	2	8	–,1	–,1	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	2	9	0,1	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	2	10	0,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	2	11	0,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	2	12	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	2	13	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	2	14	0,2	0,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	3	3	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3
29	3	4	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–
29	3	5	–,1	–,1	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–
29	3	6	0,1	–,2	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–
29	3	7	0,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–
29	3	8	0,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	3	9	0,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	3	10	0,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	3	11	0,2	0,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	3	12	0,2	0,3	0,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
29	3	13	0,2	0,3	0,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
29	3	14	0, 2	0, 3	0, 3	−, 3	−, 3	−, 3	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
29	4	4	−, 1	−, 1	−, 2	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4
29	4	5	0, 1	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4
29	4	6	0, 2	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4
29	4	7	0, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −
29	4	8	0, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −
29	4	9	0, 2	0, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −
29	4	10	0, 2	0, 3	0, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −
29	4	11	0, 2	0, 3	0, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
29	4	12	1, 3	0, 3	0, 3	0, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
29	4	13	1, 3	0, 3	0, 4	0, 4	0, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
29	4	14	1, 3	0, 3	0, 4	0, 4	0, 4	0, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
29	5	5	0, 2	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5
29	5	6	0, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5
29	5	7	0, 2	0, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5
29	5	8	0, 2	0, 3	0, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5
29	5	9	1, 2	0, 3	0, 3	0, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, −	−, −
29	5	10	1, 3	0, 3	0, 4	0, 4	0, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, −	−, −	−, −	−, −
29	5	11	1, 3	0, 3	0, 4	0, 4	0, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, −	−, −	−, −	−, −
29	5	12	1, 3	1, 4	0, 4	0, 4	0, 4	0, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, −	−, −	−, −	−, −	−, −	−, −
29	5	13	1, 3	1, 4	0, 4	0, 4	0, 5	0, 5	0, 5	0, 5	−, 5	−, 5	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
29	5	14	1, 3	1, 4	1, 4	0, 4	0, 5	0, 5	0, 5	0, 5	−, 5	−, 5	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
29	6	6	0, 2	0, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5
29	6	7	0, 2	0, 3	0, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5
29	6	8	1, 3	0, 3	0, 4	0, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6
29	6	9	1, 3	0, 3	0, 4	0, 4	0, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6
29	6	10	1, 4	0, 4	0, 4	0, 4	0, 4	0, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6
29	6	11	1, 4	1, 4	0, 4	0, 4	0, 5	0, 5	0, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6
29	6	12	1, 3	1, 4	1, 4	0, 4	0, 5	0, 5	0, 5	0, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, −	−, −
29	6	13	2, 4	1, 4	1, 5	1, 5	0, 5	0, 5	0, 5	0, 6	0, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, −	−, −	−, −	−, −
29	6	14	2, 4	1, 4	1, 5	1, 5	1, 5	0, 5	0, 6	0, 6	0, 6	0, 6	−, 6	−, 6	−, −	−, −	−, −	−, −	−, −	−, −
29	7	7	1, 3	0, 3	0, 4	0, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6
29	7	8	1, 3	0, 3	0, 4	0, 4	0, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6
29	7	9	1, 4	1, 4	0, 4	0, 4	0, 5	0, 5	0, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 7	−, 7
29	7	10	1, 4	1, 4	0, 4	0, 4	0, 5	0, 5	0, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 7	−, 7	−, 7	−, 7

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
29	7	11	2, 4	1, 4	1, 5	0, 5	0, 5	0, 5	0, 6	0, 6	–, 6	–, 6	–, 6	–, 6	–, 7	–, 7	–, 7	–, 7	–, 7	–, 7
29	7	12	2, 4	1, 4	1, 5	1, 5	0, 5	0, 5	0, 6	0, 6	0, 6	–, 6	–, 7	–, 7	–, 7	–, 7	–, 7	–, 7	–, 7	–, 7
29	7	13	2, 4	2, 5	1, 5	1, 5	1, 6	1, 6	0, 6	0, 6	0, 6	0, 7	0, 7	0, 7	–, 7	–, 7	–, 7	–, 7	–, –	–, –
29	7	14	2, 4	2, 5	1, 5	1, 6	1, 6	1, 6	1, 6	0, 6	0, 7	0, 7	0, 7	0, 7	0, 7	–, 7	–, –	–, –	–, –	–, –
29	8	8	1, 4	1, 4	0, 4	0, 4	0, 5	0, 5	0, 5	–, 5	–, 5	–, 5	–, 6	–, 6	–, 6	–, 6	–, 6	–, 6	–, 7	–, 7
29	8	9	1, 3	1, 4	1, 4	0, 5	0, 5	0, 5	0, 5	0, 6	–, 6	–, 6	–, 6	–, 6	–, 6	–, 6	–, 7	–, 7	–, 7	–, 7
29	8	10	2, 4	1, 4	1, 5	0, 5	0, 5	0, 5	0, 6	0, 6	0, 6	–, 6	–, 6	–, 6	–, 7	–, 7	–, 7	–, 7	–, 7	–, 7
29	8	11	2, 4	1, 4	1, 5	1, 5	1, 6	0, 6	0, 6	0, 6	0, 6	0, 7	–, 7	–, 7	–, 7	–, 7	–, 7	–, 7	–, 8	–, 8
29	8	12	2, 5	2, 5	1, 5	1, 6	1, 6	1, 6	0, 6	0, 6	0, 7	0, 7	0, 7	0, 7	–, 7	–, 7	–, 8	–, 8	–, 8	–, 8
29	8	13	3, 5	2, 5	2, 6	1, 6	1, 6	1, 6	1, 7	1, 7	0, 7	0, 7	0, 7	0, 7	0, 8	0, 8	–, 8	–, 8	–, 8	–, 8
29	8	14	3, 5	2, 5	2, 6	1, 6	1, 6	1, 7	1, 7	1, 7	0, 7	0, 7	0, 8	0, 8	0, 8	0, 8	0, 8	–, 8	–, 8	–, 8
29	9	9	2, 4	1, 4	1, 5	0, 5	0, 5	0, 5	0, 6	0, 6	0, 6	–, 6	–, 7	–, 7	–, 7	–, 7	–, 7	–, 7	–, 7	–, 7
29	9	10	2, 5	2, 5	1, 5	1, 6	1, 6	0, 6	0, 6	0, 6	0, 7	0, 7	0, 7	–, 7	–, 7	–, 7	–, 8	–, 8	–, 8	–, 8
29	9	11	2, 5	2, 5	1, 5	1, 6	1, 6	1, 6	0, 6	0, 6	0, 7	0, 7	0, 7	0, 8	0, 8	–, 8	–, 8	–, 8	–, 8	–, 8
29	9	12	3, 5	2, 5	2, 6	1, 6	1, 6	1, 7	1, 7	1, 7	0, 7	0, 7	0, 8	0, 8	0, 8	0, 8	–, 8	–, 8	–, 8	–, 8
29	9	13	3, 5	3, 6	2, 6	2, 7	1, 7	1, 7	1, 7	1, 7	1, 8	1, 8	0, 8	0, 8	0, 8	0, 8	0, 9	0, 9	–, 9	–, 9
29	9	14	3, 5	3, 6	2, 6	2, 7	2, 7	1, 7	1, 7	1, 8	1, 8	1, 8	1, 8	0, 8	0, 8	0, 9	0, 9	0, 9	0, 9	0, 9
29	10	10	2, 5	2, 5	1, 5	1, 6	1, 6	1, 6	0, 6	0, 7	0, 7	0, 7	0, 7	0, 8	0, 8	–, 8	–, 8	–, 8	–, 8	–, 8
29	10	11	3, 5	2, 5	2, 6	1, 6	1, 6	1, 7	1, 7	1, 7	0, 7	0, 7	0, 8	0, 8	0, 8	0, 8	–, 8	–, 8	–, 9	–, 9
29	10	12	3, 6	3, 6	2, 6	2, 7	2, 7	1, 7	1, 7	1, 7	1, 8	1, 8	0, 8	0, 8	0, 8	0, 8	0, 9	0, 9	0, 9	–, 9
29	10	13	3, 6	3, 6	2, 7	2, 7	2, 7	1, 7	1, 8	1, 8	1, 8	1, 8	1, 8	1, 9	0, 9	0, 9	0, 9	0, 9	0, 9	0, 9
29	10	14	4, 6	3, 6	3, 7	2, 7	2, 7	2, 8	2, 8	1, 8	1, 8	1, 9	1, 9	1, 9	1, 9	0, 9	0, 9	0, 9	0, 10	0, 10
29	11	11	3, 6	3, 6	2, 6	2, 7	2, 7	1, 7	1, 7	1, 7	1, 8	1, 8	0, 8	0, 8	0, 8	0, 9	0, 9	0, 9	0, 9	–, 9
29	11	12	4, 6	3, 6	2, 7	2, 7	2, 7	2, 8	1, 8	1, 8	1, 8	1, 8	1, 9	1, 9	0, 9	0, 9	0, 9	0, 9	0, 9	0, 10
29	11	13	4, 6	3, 6	3, 7	2, 7	2, 8	2, 8	2, 8	1, 8	1, 9	1, 9	1, 9	1, 9	1, 9	0, 9	0, 10	0, 10	0, 10	0, 10
29	11	14	4, 6	4, 7	3, 7	3, 8	3, 8	2, 8	2, 8	2, 9	2, 9	1, 9	1, 9	1, 9	1, 10	1, 10	1, 10	1, 10	0, 10	0, 10
29	12	12	4, 6	3, 6	3, 7	2, 7	2, 8	2, 8	2, 8	1, 8	1, 9	1, 9	1, 9	1, 9	1, 9	1, 10	0, 10	0, 10	0, 10	0, 10
29	12	13	4, 7	4, 7	3, 7	3, 8	3, 8	2, 8	2, 9	2, 9	2, 9	1, 9	1, 9	1, 9	1, 10	1, 10	1, 10	1, 10	0, 10	0, 10
29	12	14	5, 7	4, 7	4, 8	3, 8	3, 8	3, 9	3, 9	2, 9	2, 9	2, 10	2, 10	2, 10	1, 10	1, 10	1, 11	1, 11	1, 11	1, 11
29	13	13	5, 7	4, 7	4, 8	3, 8	3, 9	3, 9	3, 9	2, 9	2, 10	2, 10	2, 10	2, 10	1, 10	1, 10	1, 11	1, 11	1, 11	1, 11
29	13	14	5, 7	5, 8	4, 8	4, 9	4, 9	3, 9	3, 9	3, 10	3, 10	2, 10	2, 10	2, 10	2, 11	2, 11	2, 11	1, 11	1, 11	1, 11
29	14	14	6, 8	5, 8	5, 9	4, 9	4, 9	4, 10	4, 10	3, 10	3, 10	3, 11	3, 11	3, 11	2, 11	2, 11	2, 12	2, 12	2, 12	2, 12
30	1	1	–, 1	–, 1	–, 1	–, 1	–, 1	–, 1	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
30	1	2	–, 1	–, 1	–, 1	–, 1	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
30	1	3	–, 1	–, 1	–, 1	–, 1	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
30	1	4	–, 1	–, 1	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
30	1	5	–, 1	–, 1	–, 1	–, 1	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.5.0		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
30	1	6	–,1	–,1	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	1	7	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	1	8	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	1	9	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	1	10	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	1	11	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	1	12	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	1	13	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	1	14	–,1	–,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	1	15	0,1	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	2	2	–,1	–,1	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–
30	2	3	–,1	–,1	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–
30	2	4	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	2	5	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	2	6	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	2	7	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	2	8	–,1	–,1	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	2	9	0,1	–,2	–,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	2	10	0,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	2	11	0,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	2	12	0,2	–,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	2	13	0,2	0,2	–,2	–,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	2	14	0,2	0,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	2	15	0,2	0,2	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	3	3	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3
30	3	4	–,1	–,1	–,2	–,2	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3
30	3	5	–,1	–,1	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–
30	3	6	0,1	–,2	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–
30	3	7	0,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–
30	3	8	0,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	3	9	0,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	3	10	0,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	3	11	0,2	0,3	–,3	–,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	3	12	0,2	0,3	–,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	3	13	0,2	0,3	0,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	3	14	0,2	0,3	0,3	–,3	–,3	–,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	3	15	1,2	0,3	0,3	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–	–,–
30	4	4	–,1	–,1	–,2	–,2	–,2	–,2	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,3	–,4	–,4	–,4	–,4

TABLE B.28 (cont.): Critical Values for Fisher's Exact Test

n	m_1	m_2	α: 0.50		0.20		0.10		0.05		0.02		0.01		0.005		0.002		0.001	
30	4	5	0, 1	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4
30	4	6	0, 2	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4
30	4	7	0, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −
30	4	8	0, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −
30	4	9	0, 2	0, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −
30	4	10	0, 2	0, 3	0, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −
30	4	11	0, 2	0, 3	0, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
30	4	12	1, 3	0, 3	0, 3	0, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
30	4	13	1, 3	0, 3	0, 4	0, 4	0, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
30	4	14	1, 3	0, 3	0, 4	0, 4	0, 4	−, 4	−, 4	−, 4	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
30	4	15	1, 3	0, 4	0, 4	0, 4	0, 4	0, 4	0, 4	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
30	5	5	0, 2	−, 2	−, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4
30	5	6	0, 2	−, 2	−, 3	−, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5
30	5	7	0, 2	0, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5
30	5	8	0, 2	0, 3	0, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5
30	5	9	0, 2	0, 3	0, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5
30	5	10	1, 3	0, 3	0, 3	0, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, −	−, −
30	5	11	1, 3	0, 3	0, 4	0, 4	0, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, −	−, −	−, −	−, −
30	5	12	1, 3	0, 3	0, 4	0, 4	0, 4	0, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, −	−, −	−, −	−, −	−, −	−, −
30	5	13	1, 3	1, 4	0, 4	0, 4	0, 4	0, 5	0, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, −	−, −	−, −	−, −	−, −	−, −
30	5	14	1, 3	1, 4	0, 4	0, 4	0, 5	0, 5	0, 5	0, 5	−, 5	−, 5	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
30	5	15	2, 3	1, 4	1, 4	0, 5	0, 5	0, 5	0, 5	0, 5	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −	−, −
30	6	6	0, 2	0, 3	−, 3	−, 3	−, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5
30	6	7	0, 2	0, 3	0, 3	−, 3	−, 4	−, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5
30	6	8	1, 2	0, 3	0, 4	0, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6
30	6	9	1, 3	0, 3	0, 4	0, 4	0, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6
30	6	10	1, 3	0, 3	0, 4	0, 4	0, 4	0, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6
30	6	11	1, 4	1, 4	0, 4	0, 4	0, 5	0, 5	0, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6
30	6	12	1, 4	1, 4	0, 4	0, 4	0, 5	0, 5	0, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, −	−, −
30	6	13	2, 4	1, 4	1, 5	1, 5	0, 5	0, 5	0, 5	0, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, −	−, −	−, −	−, −
30	6	14	2, 4	1, 4	1, 5	1, 5	0, 5	0, 5	0, 6	0, 6	0, 6	0, 6	−, 6	−, 6	−, −	−, −	−, −	−, −	−, −	−, −
30	6	15	2, 4	1, 5	1, 5	1, 5	1, 5	0, 6	0, 6	0, 6	0, 6	0, 6	0, 6	−, −	−, −	−, −	−, −	−, −	−, −	−, −
30	7	7	1, 3	0, 3	0, 4	0, 4	−, 4	−, 4	−, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6
30	7	8	1, 3	0, 3	0, 4	0, 4	0, 4	−, 4	−, 5	−, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6
30	7	9	1, 4	1, 4	0, 4	0, 4	0, 4	0, 5	−, 5	−, 5	−, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6
30	7	10	1, 4	1, 4	0, 4	0, 4	0, 5	0, 5	0, 5	−, 5	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 7	−, 7	−, 7	−, 7
30	7	11	2, 4	1, 4	1, 5	0, 5	0, 5	0, 5	0, 5	0, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 6	−, 7	−, 7	−, 7	−, 7
30	7	12	2, 4	1, 4	1, 5	1, 5	0, 5	0, 5	0, 6	0, 6	0, 6	−, 6	−, 6	−, 6	−, 7	−, 7	−, 7	−, 7	−, 7	−, 7
30	7	13	2, 4	2, 5	1, 5	1, 5	1, 6	0, 6	0, 6	0, 6	0, 6	0, 7	0, 7	−, 7	−, 7	−, 7	−, 7	−, 7	−, 7	−, 7
30	7	14	2, 4	2, 5	1, 5	1, 6	1, 6	1, 6	0, 6	0, 6	0, 7	0, 7	0, 7	0, 7	−, 7	−, 7	−, 7	−, 7	−, −	−, −

TABLE B.29: Critical Values of u for the Runs Test

n_1	n_2	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
2	3	2, 4	–, 5	–, –	–, –	–, –	–, –	–, –	–, –	–, –
	4	2, 5	–, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
	5	2, –	2, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
	6	2, –	2, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
	7	3, –	2, –	–, –	–, –	–, –	–, –	–, –	–, –	–, –
	8	3, –	2, –	2, –	–, –	–, –	–, –	–, –	–, –	–, –
	9	3, –	2, –	2, –	–, –	–, –	–, –	–, –	–, –	–, –
	10	3, –	2, –	2, –	–, –	–, –	–, –	–, –	–, –	–, –
	11	3, –	2, –	2, –	–, –	–, –	–, –	–, –	–, –	–, –
	12	3, –	2, –	2, –	2, –	–, –	–, –	–, –	–, –	–, –
	13	3, –	2, –	2, –	2, –	–, –	–, –	–, –	–, –	–, –
	14	3, –	2, –	2, –	2, –	–, –	–, –	–, –	–, –	–, –
	15	3, –	2, –	2, –	2, –	–, –	–, –	–, –	–, –	–, –
	16	3, –	2, –	2, –	2, –	–, –	–, –	–, –	–, –	–, –
	17	3, –	2, –	2, –	2, –	–, –	–, –	–, –	–, –	–, –
	18	3, –	2, –	2, –	2, –	–, –	–, –	–, –	–, –	–, –
	19	3, –	3, –	2, –	2, –	2, –	–, –	–, –	–, –	–, –
	20	3, –	3, –	2, –	2, –	2, –	–, –	–, –	–, –	–, –
	21	4, –	3, –	2, –	2, –	2, –	–, –	–, –	–, –	–, –
	22	4, –	3, –	2, –	2, –	2, –	–, –	–, –	–, –	–, –
	23	4, –	3, –	2, –	2, –	2, –	–, –	–, –	–, –	–, –
	24	4, –	3, –	2, –	2, –	2, –	–, –	–, –	–, –	–, –
	25	4, –	3, –	2, –	2, –	2, –	–, –	–, –	–, –	–, –
	26	4, –	3, –	2, –	2, –	2, –	–, –	–, –	–, –	–, –
	27	4, –	3, –	2, –	2, –	2, –	2, –	–, –	–, –	–, –
	28	4, –	3, –	2, –	2, –	2, –	2, –	–, –	–, –	–, –
	29	4, –	3, –	2, –	2, –	2, –	2, –	–, –	–, –	–, –
2	30	4, –	3, –	2, –	2, –	2, –	2, –	–, –	–, –	–, –
3	3	2, 6	2, 6	–, –	–, –	–, –	–, –	–, –	–, –	–, –
	4	3, 6	2, 7	–, 7	–, –	–, –	–, –	–, –	–, –	–, –
	5	3, 7	2, 7	2, –	–, –	–, –	–, –	–, –	–, –	–, –
	6	3, 7	2, –	2, –	2, –	–, –	–, –	–, –	–, –	–, –
	7	3, 7	3, –	2, –	2, –	–, –	–, –	–, –	–, –	–, –
	8	4, 7	3, –	2, –	2, –	–, –	–, –	–, –	–, –	–, –
	9	4, –	3, –	2, –	2, –	2, –	–, –	–, –	–, –	–, –
	10	4, –	3, –	3, –	2, –	2, –	–, –	–, –	–, –	–, –
	11	4, –	3, –	3, –	2, –	2, –	–, –	–, –	–, –	–, –
	12	4, –	3, –	3, –	2, –	2, –	2, –	–, –	–, –	–, –
	13	4, –	3, –	3, –	2, –	2, –	2, –	–, –	–, –	–, –
	14	4, –	3, –	3, –	3, –	2, –	2, –	–, –	–, –	–, –
	15	4, –	4, –	3, –	3, –	2, –	2, –	2, –	–, –	–, –
	16	4, –	4, –	3, –	3, –	2, –	2, –	2, –	–, –	–, –
	17	4, –	4, –	3, –	3, –	2, –	2, –	2, –	–, –	–, –
	18	4, –	4, –	3, –	3, –	2, –	2, –	2, –	–, –	–, –
	19	4, –	4, –	3, –	3, –	2, –	2, –	2, –	–, –	–, –
	20	4, –	4, –	3, –	3, –	2, –	2, –	2, –	–, –	–, –
	21	5, –	4, –	3, –	3, –	2, –	2, –	2, –	2, –	–, –
	22	5, –	4, –	4, –	3, –	2, –	2, –	2, –	2, –	–, –
	23	5, –	4, –	4, –	3, –	3, –	2, –	2, –	2, –	–, –
3	24	5, –	4, –	4, –	3, –	3, –	2, –	2, –	2, –	–, –

TABLE B.29 (cont.): Critical Values of u for the Runs Test

n_1	n_2	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
3	25	5, –	4, –	4, –	3, –	3, –	2, –	2, –	2, –	–, –
	26	5, –	4, –	4, –	3, –	3, –	2, –	2, –	2, –	–, –
	27	5, –	4, –	4, –	3, –	3, –	2, –	2, –	2, –	2, –
	28	5, –	4, –	4, –	3, –	3, –	2, –	2, –	2, –	2, –
	29	5, –	4, –	4, –	3, –	3, –	2, –	2, –	2, –	2, –
3	30	5, –	4, –	4, –	3, –	3, –	2, –	2, –	2, –	2, –
4	4	3, 7	2, 8	2, 8	–, –	–, –	–, –	–, –	–, –	–, –
	5	3, 6	3, 8	2, 9	2, 9	–, 9	–, –	–, –	–, –	–, –
	6	4, 8	3, 9	3, 9	2, 9	2, –	–, –	–, –	–, –	–, –
	7	4, 8	3, 9	3, 9	2, –	2, –	–, –	–, –	–, –	–, –
	8	4, 8	3, 9	3, –	3, –	2, –	2, –	–, –	–, –	–, –
	9	5, 9	4, 9	3, –	3, –	2, –	2, –	–, –	–, –	–, –
	10	5, 9	4, –	3, –	3, –	2, –	2, –	2, –	–, –	–, –
	11	5, 9	4, –	3, –	3, –	2, –	2, –	2, –	–, –	–, –
	12	5, 9	4, –	4, –	3, –	3, –	2, –	2, –	–, –	–, –
	13	5, 9	4, –	4, –	3, –	3, –	2, –	2, –	2, –	–, –
	14	5, 9	4, –	4, –	3, –	3, –	2, –	2, –	2, –	–, –
	15	6, –	4, –	4, –	3, –	3, –	3, –	2, –	2, –	–, –
	16	6, –	5, –	4, –	4, –	3, –	3, –	2, –	2, –	2, –
	17	6, –	5, –	4, –	4, –	3, –	3, –	2, –	2, –	2, –
	18	6, –	5, –	4, –	4, –	3, –	3, –	2, –	2, –	2, –
	19	6, –	5, –	4, –	4, –	3, –	3, –	2, –	2, –	2, –
	20	6, –	5, –	4, –	4, –	3, –	3, –	3, –	2, –	2, –
	21	6, –	5, –	4, –	4, –	3, –	3, –	3, –	2, –	2, –
	22	6, –	5, –	4, –	4, –	3, –	3, –	3, –	2, –	2, –
	23	6, –	5, –	4, –	4, –	4, –	3, –	3, –	2, –	2, –
	24	6, –	5, –	5, –	4, –	4, –	3, –	3, –	2, –	2, –
	25	6, –	5, –	5, –	4, –	4, –	3, –	3, –	2, –	2, –
	26	6, –	5, –	5, –	4, –	4, –	3, –	3, –	2, –	2, –
	27	6, –	5, –	5, –	4, –	4, –	3, –	3, –	3, –	2, –
	28	6, –	6, –	5, –	4, –	4, –	3, –	3, –	3, –	2, –
	29	6, –	6, –	5, –	4, –	4, –	4, –	3, –	3, –	2, –
4	30	6, –	6, –	5, –	4, –	4, –	4, –	3, –	3, –	2, –
5	5	4, 8	3, 9	3, 9	2, 10	2, 10	–, –	–, –	–, –	–, –
	6	4, 9	3, 9	3, 10	3, 10	2, 11	2, 11	–, 11	–, –	–, –
	7	5, 9	4, 10	3, 10	3, 11	2, 11	2, –,	–, –	–, –	–, –
	8	5, 9	4, 10	3, 11	3, 11	2, –	2, –	2, –	–, –	–, –
	9	5, 10	4, 10	4, 11	3, –	3, –	2, –	2, –	2, –	–, –
	10	6, 10	5, 11	4, 11	3, –	3, –	3, –	2, –	2, –	–, –
	11	6, 10	5, 11	4, –	4, –	3, –	3, –	2, –	2, –	2, –
	12	6, 10	5, 11	4, –	4, –	3, –	3, –	2, –	2, –	2, –
	13	6, 10	5, 11	4, –	4, –	3, –	3, –	3, –	2, –	2, –
	14	6, 10	5, –	5, –	4, –	3, –	3, –	3, –	2, –	2, –
	15	6, 11	5, –	5, –	4, –	4, –	3, –	3, –	2, –	2, –
	16	7, 11	6, –	5, –	4, –	4, –	3, –	3, –	2, –	2, –
	17	7, 11	6, –	5, –	4, –	4, –	3, –	3, –	3, –	2, –
	18	7, 11	6, –	5, –	5, –	4, –	4, –	3, –	3, –	2, –
	19	7, 11	6, –	5, –	5, –	4, –	4, –	3, –	3, –	2, –
	20	7, 11	6, –	5, –	5, –	4, –	4, –	3, –	3, –	3, –
	21	7, 11	6, –	5, –	5, –	4, –	4, –	3, –	3, –	3, –
	22	7, –	6, –	6, –	5, –	4, –	4, –	4, –	3, –	3, –
	23	7, –	6, –	6, –	5, –	4, –	4, –	4, –	3, –	3, –
5	24	7, –	6, –	6, –	5, –	4, –	4, –	4, –	3, –	3, –

TABLE B.29 (cont.): Critical Values of u for the Runs Test

n_1	n_2	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
5	25	8, –	6, –	6, –	5, –	4, –	4, –	4, –	3, –	3, –
	26	8, –	6, –	6, –	5, –	5, –	4, –	4, –	3, –	3, –
	27	8, –	6, –	6, –	5, –	5, –	4, –	4, –	3, –	3, –
	28	8, –	6, –	6, –	5, –	5, –	4, –	4, –	3, –	3, –
	29	8, –	7, –	6, –	6, –	5, –	4, –	4, –	4, –	3, –
5	30	8, –	7, –	6, –	6, –	5, –	4, –	4, –	4, –	3, –
6	6	5, 9	4, 10	3, 11	3, 11	2, 12	2, 12	2, 12	–, –	–, –
	7	5, 8	4, 11	4, 11	3, 12	3, 12	2, 13	2, 13	–, 13	–, –
	8	6, 10	5, 11	4, 12	3, 12	3, 13	3, 13	2, 13	2, –	–, –
	9	6, 10	5, 11	4, 12	4, 13	3, 13	3, –	2, –	2, –	2, –
	10	6, 11	5, 12	5, 12	4, 13	3, –	3, –	3, –	2, –	2, –
	11	7, 11	5, 12	5, 13	4, 13	4, –	3, –	3, –	2, –	2, –
	12	7, 11	6, 12	5, 13	4, 13	4, –	3, –	3, –	3, –	2, –
	13	7, 12	6, 12	5, 13	5, –	4, –	3, –	3, –	3, –	2, –
	14	7, 12	6, 13	5, 13	5, –	4, –	4, –	3, –	3, –	2, –
	15	7, 12	6, 13	6, –	5, –	4, –	4, –	3, –	3, –	3, –
	16	8, 12	6, 13	6, –	5, –	4, –	4, –	4, –	3, –	3, –
	17	8, 12	6, 13	6, –	5, –	5, –	4, –	4, –	3, –	3, –
	18	8, 12	7, 13	6, –	5, –	5, –	4, –	4, –	3, –	3, –
	19	8, 12	7, –	6, –	6, –	5, –	4, –	4, –	3, –	3, –
	20	8, 12	7, –	6, –	6, –	5, –	4, –	4, –	4, –	3, –
	21	8, 12	7, –	6, –	6, –	5, –	5, –	4, –	4, –	3, –
	22	8, 13	7, –	6, –	6, –	5, –	5, –	4, –	4, –	3, –
	23	8, 13	7, –	6, –	6, –	5, –	5, –	4, –	4, –	3, –
	24	8, 13	7, –	7, –	6, –	5, –	5, –	4, –	4, –	4, –
	25	8, 13	8, –	7, –	6, –	5, –	5, –	4, –	4, –	4, –
	26	9, 13	8, –	7, –	6, –	6, –	5, –	5, –	4, –	4, –
	27	9, 13	8, –	7, –	6, –	6, –	5, –	5, –	4, –	4, –
	28	9, 13	8, –	7, –	6, –	6, –	5, –	5, –	4, –	4, –
	29	9, 13	8, –	7, –	6, –	6, –	5, –	5, –	4, –	4, –
6	30	9, 13	8, –	7, –	6, –	6, –	5, –	5, –	4, –	4, –
7	7	6, 10	5, 11	4, 12	3, 13	3, 13	3, 13	2, 14	2, 14	–, –
	8	6, 11	5, 12	4, 13	4, 13	3, 14	3, 14	3, 14	2, 15	2, 15
	9	7, 11	5, 12	5, 13	4, 14	4, 14	3, 15	3, 15	2, 15	2, –
	10	7, 12	6, 13	5, 13	5, 14	4, 15	3, 15	3, 15	3, –	2, –
	11	7, 12	6, 13	5, 14	5, 14	4, 15	4, 15	3, –	3, –	2, –
	12	8, 12	6, 13	6, 14	5, 14	4, 15	4, –	3, –	3, –	3, –
	13	8, 12	7, 14	6, 14	5, 15	5, –	4, –	4, –	3, –	3, –
	14	8, 13	7, 14	6, 14	5, 15	5, –	4, –	4, –	3, –	3, –
	15	8, 13	7, 14	6, 15	6, 15	5, –	4, –	4, –	3, –	3, –
	16	8, 13	7, 14	6, 15	6, –	5, –	5, –	4, –	4, –	3, –
	17	9, 13	7, 14	7, 15	6, –	5, –	5, –	4, –	4, –	3, –
	18	9, 14	8, 14	7, 15	6, –	5, –	5, –	4, –	4, –	4, –
	19	9, 14	8, 15	7, 15	6, –	6, –	5, –	5, –	4, –	4, –
	20	9, 14	8, 15	7, –	6, –	6, –	5, –	5, –	4, –	4, –
7	21	9, 14	8, 15	7, –	7, –	6, –	5, –	5, –	4, –	4, –

TABLE B.29 (cont.): Critical Values of u for the Runs Test

n_1	n_2	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
7	22	9, 14	8, 15	7, –	7, –	6, –	5, –	5, –	4, –	4, –
	23	10, 14	8, 15	8, –	7, –	6, –	6, –	5, –	5, –	4, –
	24	10, 14	8, 15	8, –	7, –	6, –	6, –	5, –	5, –	4, –
	25	10, 14	8, –	8, –	7, –	6, –	6, –	5, –	5, –	4, –
	26	10, 14	8, –	8, –	7, –	6, –	6, –	5, –	5, –	4, –
	27	10, 14	9, –	8, –	7, –	6, –	6, –	6, –	5, –	5, –
	28	10, 14	9, –	8, –	7, –	7, –	6, –	6, –	5, –	5, –
	29	10, 14	9, –	8, –	8, –	7, –	6, –	6, –	5, –	5, –
7	30	10, 14	9, –	8, –	8, –	7, –	6, –	6, –	5, –	5, –
8	8	7, 11	5, 13	5, 13	4, 14	4, 14	3, 15	3, 15	2, 16	2, 16
	9	7, 10	6, 13	5, 14	5, 14	4, 15	3, 15	3, 16	3, 16	2, 17
	10	7, 12	6, 13	6, 14	5, 15	4, 15	4, 16	3, 16	3, 17	3, 17
	11	8, 13	7, 14	6, 15	5, 15	5, 16	4, 16	4, 17	3, 17	3, –
	12	8, 13	7, 14	6, 15	6, 16	5, 16	4, 17	4, 17	3, –	3, –
	13	8, 13	7, 15	6, 15	6, 16	5, 17	5, 17	4, 17	4, –	3, –
	14	9, 14	7, 15	7, 16	6, 16	5, 17	5, 17	4, –	4, –	3, –
	15	9, 14	8, 15	7, 16	6, 16	5, 17	5, –	5, –	4, –	4, –
	16	9, 14	8, 15	7, 16	6, 17	6, 17	5, –	5, –	4, –	4, –
	17	9, 14	8, 16	7, 16	7, 17	6, –	5, –	5, –	4, –	4, –
	18	10, 14	8, 16	8, 16	7, 17	6, –	6, –	5, –	4, –	4, –
	20	10, 15	9, 16	8, 17	7, 17	6, –	6, –	5, –	5, –	4, –
	21	10, 15	9, 16	8, 17	7, –	7, –	6, –	6, –	5, –	5, –
	22	10, 15	9, 16	8, 17	8, –	7, –	6, –	6, –	5, –	5, –
	23	10, 15	9, 16	8, 17	8, –	7, –	6, –	6, –	5, –	5, –
	24	11, 16	9, 16	8, 17	8, –	7, –	6, –	6, –	5, –	5, –
	25	11, 16	9, 17	9, –	8, –	7, –	7, –	6, –	5, –	5, –
	26	11, 16	10, 17	9, –	8, –	7, –	7, –	6, –	6, –	5, –
	27	11, 16	10, 17	9, –	8, –	7, –	7, –	6, –	6, –	5, –
	28	11, 16	10, 17	9, –	8, –	8, –	7, –	6, –	6, –	5, –
	29	11, 16	10, 17	9, –	8, –	8, –	7, –	6, –	6, –	5, –
8	30	11, 16	10, 17	9, –	8, –	8, –	7, –	7, –	6, –	6, –
9	9	8, 12	6, 14	6, 14	5, 15	4, 16	4, 16	3, 17	3, 17	3, 17
	10	8, 13	7, 14	6, 15	5, 16	5, 16	4, 17	4, 17	3, 18	3, 18
	11	8, 13	7, 15	6, 15	6, 16	5, 17	5, 17	4, 18	3, 18	3, 19
	12	9, 14	7, 15	7, 16	6, 16	5, 17	5, 18	4, 18	4, 19	3, 19
	13	9, 14	8, 15	7, 16	6, 17	6, 18	5, 18	5, 18	4, 19	4, 19
	14	9, 14	8, 16	7, 17	7, 17	6, 18	5, 18	5, 19	4, 19	4, –
	15	10, 15	8, 16	8, 17	7, 18	6, 18	6, 19	5, 19	4, –	4, –
	16	10, 15	9, 16	8, 17	7, 18	6, 18	6, 19	5, 19	5, –	4, –
	17	10, 15	9, 17	8, 17	7, 18	7, 19	6, 19	5, –	5, –	4, –
	18	10, 16	9, 17	8, 18	8, 18	7, 19	6, –	6, –	5, –	5, –
	19	11, 16	9, 17	8, 18	8, 18	7, 19	6, –	6, –	5, –	5, –
	20	11, 16	10, 17	9, 18	8, 18	7, 19	7, –	6, –	5, –	5, –
	21	11, 16	10, 18	9, 18	8, 19	7, –	7, –	6, –	6, –	5, –
	22	11, 16	10, 18	9, 18	8, 19	7, –	7, –	6, –	6, –	5, –
	23	12, 16	10, 18	9, 18	8, 19	8, –	7, –	6, –	6, –	5, –
	24	12, 17	10, 18	9, 18	9, 19	8, –	7, –	7, –	6, –	6, –
	25	12, 17	10, 18	10, 19	9, 19	8, –	7, –	7, –	6, –	6, –
	26	12, 17	10, 18	10, 19	9, –	8, –	7, –	7, –	6, –	6, –
	27	12, 17	11, 18	10, 19	9, –	8, –	8, –	7, –	6, –	6, –
	28	12, 17	11, 18	10, 19	9, –	8, –	8, –	7, –	6, –	6, –
	29	12, 17	11, 18	10, 19	9, –	8, –	8, –	7, –	7, –	6, –
9	30	12, 18	11, 18	10, 19	9, –	8, –	8, –	7, –	7, –	6, –

TABLE B.29 (cont.): Critical Values of u for the Runs Test

n_1	n_2	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
10	10	9, 13	7, 15	6, 16	6, 16	5, 17	5, 17	4, 18	4, 18	3, 19
	11	9, 12	8, 15	7, 16	6, 17	5, 18	5, 18	4, 19	4, 19	3, 19
	12	9, 14	8, 16	7, 17	7, 17	6, 18	5, 19	5, 19	4, 20	4, 20
	13	10, 15	8, 16	8, 17	7, 18	6, 19	5, 19	5, 20	4, 20	4, 20
	14	10, 15	9, 17	8, 17	7, 18	6, 19	6, 19	5, 20	5, 20	4, 21
	15	10, 16	9, 17	8, 18	7, 18	7, 19	6, 20	6, 20	5, 21	5, 21
	16	11, 16	9, 17	8, 18	8, 19	7, 20	6, 20	6, 20	5, 21	5, –
	17	11, 16	10, 18	9, 18	8, 19	7, 20	6, 20	6, 20	5, 21	5, –
	18	11, 16	10, 18	9, 19	8, 19	7, 20	7, 21	6, 21	6, –	5, –
	19	12, 17	10, 18	9, 19	8, 20	8, 20	7, 21	6, 21	6, –	5, –
	20	12, 17	10, 18	9, 19	9, 20	8, 20	7, 21	7, –	6, –	6, –
	21	12, 17	10, 18	10, 19	9, 20	8, 21	7, 21	7, –	6, –	6, –
	22	12, 17	11, 19	10, 20	9, 20	8, 21	8, –	7, –	6, –	6, –
	23	12, 18	11, 19	10, 20	9, 20	8, 21	8, –	7, –	6, –	6, –
	24	12, 18	11, 19	10, 20	9, 20	8, 21	8, –	7, –	7, –	6, –
	25	13, 18	11, 19	10, 20	10, 20	9, –	8, –	7, –	7, –	6, –
	26	13, 18	11, 20	10, 20	10, 21	9, –	8, –	8, –	7, –	6, –
	27	13, 18	12, 20	11, 20	10, 21	9, –	8, –	8, –	7, –	7, –
	28	13, 18	12, 20	11, 20	10, 21	9, –	8, –	8, –	7, –	7, –
	29	13, 18	12, 20	11, 20	10, 21	9, –	9, –	8, –	7, –	7, –
10	30	14, 18	12, 20	11, 20	10, 21	9, –	9, –	8, –	8, –	7, –
11	11	9, 15	8, 16	7, 17	7, 17	6, 18	5, 19	5, 19	4, 20	4, 20
	12	10, 15	9, 16	8, 17	7, 18	6, 19	6, 19	5, 20	5, 20	4, 21
	13	10, 16	9, 17	8, 18	7, 19	6, 19	6, 20	5, 20	5, 21	4, 21
	14	11, 16	9, 17	8, 18	8, 19	7, 20	6, 20	6, 21	5, 21	5, 22
	15	11, 16	10, 18	9, 19	8, 19	7, 20	7, 21	6, 21	5, 22	5, 22
	16	11, 17	10, 18	9, 19	8, 20	7, 21	7, 21	6, 22	6, 22	5, 23
	17	12, 17	10, 18	9, 19	9, 20	8, 21	7, 22	7, 22	6, 22	5, 23
	18	12, 17	10, 19	10, 20	9, 20	8, 21	7, 22	7, 22	6, 23	6, 23
	19	12, 18	11, 19	10, 20	9, 21	8, 22	8, 22	7, 22	6, 23	6, –
	20	12, 18	11, 19	10, 20	9, 21	8, 22	8, 22	7, 23	7, 23	6, –
	21	13, 18	11, 20	10, 20	10, 21	9, 22	8, 22	7, 23	7, –	6, –
	22	13, 18	11, 20	10, 21	10, 22	9, 22	8, 23	8, 23	7, –	6, –
	23	13, 19	12, 20	11, 21	10, 22	9, 22	8, 23	8, 23	7, –	7, –
	24	13, 19	12, 20	11, 21	10, 22	9, 22	9, 23	8, –	7, –	7, –
	25	14, 19	12, 20	11, 21	10, 22	9, 23	9, 23	8, –	7, –	7, –
	26	14, 19	12, 21	11, 22	10, 22	10, 23	9, –	8, –	8, –	7, –
	27	14, 19	12, 21	11, 22	11, 22	10, 23	9, –	8, –	8, –	7, –
	28	14, 20	13, 21	12, 22	11, 22	10, 23	9, –	9, –	8, –	7, –
	29	14, 20	13, 21	12, 22	11, 22	10, 23	9, –	9, –	8, –	8, –
11	30	14, 20	13, 21	12, 22	11, 22	10, –	10, –	9, –	8, –	8, –
12	12	10, 16	9, 17	8, 18	7, 19	7, 19	6, 20	5, 21	5, 21	4, 22
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	17	12, 18	11, 19	10, 20	9, 21	8, 22	8, 22	7, 23	6, 24	6, 24
	18	13, 18	11, 20	10, 21	9, 21	8, 22	8, 23	7, 23	7, 24	6, 24
	19	13, 18	11, 20	10, 21	10, 22	9, 23	8, 23	7, 24	7, 24	6, 25
	20	13, 19	12, 20	11, 21	10, 22	9, 23	8, 23	8, 24	7, 24	7, 25
12	21	14, 19	12, 21	11, 22	10, 22	9, 23	9, 24	8, 24	7, 25	7, 25

TABLE B.29 (cont.): Critical Values of u for the Runs Test

n_1	n_2	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
12	22	14, 19	12, 21	11, 22	10, 22	9, 23	9, 24	8, 24	7, 25	7, –
	23	14, 20	12, 21	11, 22	11, 23	10, 24	9, 24	8, 24	8, 25	7, –
	24	14, 20	13, 21	12, 22	11, 23	10, 24	9, 24	9, 25	8, –	7, –
	25	14, 20	13, 22	12, 22	11, 23	10, 24	9, 24	9, 25	8, –	8, –
	26	15, 20	13, 22	12, 23	11, 23	10, 24	10, 25	9, 25	8, –	8, –
	27	15, 20	13, 22	12, 23	11, 24	10, 24	10, 25	9, 25	8, –	8, –
	28	15, 21	13, 22	12, 23	12, 24	11, 24	10, 25	9, –	9, –	8, –
	29	15, 21	14, 22	13, 23	12, 24	11, 24	10, 25	10, –	9, –	8, –
12	30	15, 21	14, 22	13, 23	12, 24	11, 25	10, 25	10, –	9, –	8, –
13	13	11, 17	10, 18	9, 19	8, 20	7, 21	7, 21	6, 22	5, 23	5, 23
	14	12, 17	10, 19	9, 20	9, 20	8, 21	7, 22	7, 22	6, 23	5, 24
	15	12, 18	11, 19	10, 20	9, 21	8, 22	7, 22	7, 23	6, 24	6, 24
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	17	13, 19	11, 20	10, 21	10, 22	9, 23	8, 23	7, 24	7, 25	6, 25
	18	13, 19	12, 20	11, 21	10, 22	9, 23	8, 24	8, 24	7, 25	7, 25
	19	14, 19	12, 21	11, 22	10, 23	9, 24	9, 24	8, 25	7, 25	7, 26
	20	14, 20	12, 21	11, 22	10, 23	10, 24	9, 24	8, 25	8, 26	7, 26
	21	14, 20	13, 22	12, 22	11, 23	10, 24	9, 25	9, 25	8, 26	7, 26
	22	15, 20	13, 22	12, 23	11, 24	10, 24	9, 25	9, 26	8, 26	7, 27
	23	15, 20	13, 22	12, 23	11, 24	10, 25	10, 25	9, 26	8, 26	8, 27
	24	15, 21	13, 22	12, 23	11, 24	10, 25	10, 26	9, 26	8, 27	8, 27
	25	15, 21	14, 23	13, 24	12, 24	11, 25	10, 26	9, 26	9, 27	8, 27
	26	16, 21	14, 23	13, 24	12, 24	11, 26	10, 26	10, 26	9, 27	8, –
	27	16, 21	14, 23	13, 24	12, 25	11, 26	10, 26	10, 26	9, 27	9, –
	28	16, 22	14, 23	13, 24	12, 25	11, 26	11, 26	10, 27	9, –	9, –
	29	16, 22	14, 24	13, 24	13, 25	12, 26	11, 26	10, 27	9, –	9, –
13	30	16, 22	15, 24	14, 24	13, 25	12, 26	11, 26	10, 27	10, –	9, –
14	14	12, 18	11, 19	10, 20	9, 21	8, 22	7, 23	7, 23	6, 24	6, 24
	15	13, 16	11, 20	10, 21	9, 22	8, 23	8, 23	7, 24	7, 24	6, 25
	16	13, 19	11, 20	11, 21	10, 22	9, 23	8, 24	8, 24	7, 25	6, 25
	17	14, 19	12, 21	11, 22	10, 23	9, 24	8, 24	8, 25	7, 25	7, 26
	18	14, 20	12, 21	11, 22	10, 23	9, 24	9, 25	8, 25	7, 26	7, 26
	19	14, 20	13, 22	12, 23	11, 23	10, 24	9, 25	8, 26	8, 26	7, 27
	20	15, 20	13, 22	12, 23	11, 24	10, 25	9, 25	9, 26	8, 27	7, 27
	21	15, 21	13, 22	12, 23	11, 24	10, 25	10, 26	9, 26	8, 27	8, 28
	22	15, 21	14, 23	12, 24	12, 24	11, 26	10, 26	9, 27	9, 27	8, 28
	23	16, 21	14, 23	13, 24	12, 25	11, 26	10, 26	10, 27	9, 28	8, 28
	24	16, 22	14, 23	13, 24	12, 25	11, 26	10, 27	10, 27	9, 28	8, 28
	25	16, 22	14, 24	13, 24	12, 25	11, 26	11, 27	10, 28	9, 28	9, 28
	26	16, 22	15, 24	14, 25	13, 26	12, 26	11, 27	10, 28	9, 28	9, 29
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	28	17, 23	15, 24	14, 25	13, 26	12, 27	11, 28	11, 28	10, 29	9, 29
	29	17, 23	15, 24	14, 26	13, 26	12, 27	12, 28	11, 28	10, 29	9, –
14	30	17, 23	15, 25	14, 26	13, 26	12, 27	12, 28	11, 28	10, 29	10, –
15	15	13, 19	12, 20	11, 21	10, 22	9, 23	8, 24	8, 24	7, 25	6, 26
	16	14, 19	12, 21	11, 22	10, 23	9, 24	9, 24	8, 25	7, 26	7, 26
	17	14, 20	12, 21	11, 22	11, 23	10, 24	9, 25	8, 26	8, 26	7, 27
	18	14, 20	13, 22	12, 23	11, 24	10, 25	9, 25	9, 26	8, 27	7, 27
	19	15, 21	13, 22	12, 23	11, 24	10, 25	10, 26	9, 27	8, 27	8, 28
	20	15, 21	13, 23	12, 24	12, 25	11, 26	10, 26	9, 27	8, 28	8, 28
	21	16, 21	14, 23	13, 24	12, 25	11, 26	10, 27	10, 27	9, 28	8, 29
	22	16, 22	14, 24	13, 25	12, 25	11, 26	10, 27	10, 28	9, 28	8, 29
	23	16, 22	14, 24	13, 25	12, 26	11, 27	11, 27	10, 28	9, 29	9, 29
15	24	16, 22	15, 24	14, 25	13, 26	12, 27	11, 28	10, 28	10, 29	9, 30

TABLE B.29 (cont.): Critical Values of u for the Runs Test

n_1	n_2	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
15	25	17, 23	15, 24	14, 26	13, 26	12, 27	11, 28	11, 29	10, 29	9, 30
	26	17, 23	15, 25	14, 26	13, 27	12, 28	11, 28	11, 29	10, 30	9, 30
	27	17, 23	16, 25	14, 26	14, 27	12, 28	12, 28	11, 29	10, 30	10, 30
	28	18, 24	16, 25	15, 26	14, 27	13, 28	12, 29	11, 29	10, 30	10, 30
	29	18, 24	16, 26	15, 26	14, 27	13, 28	12, 29	11, 30	11, 30	10, 31
15	30	18, 24	16, 26	15, 27	14, 28	13, 28	12, 29	12, 30	11, 30	10, 31
16	16	14, 20	12, 22	11, 23	11, 23	10, 24	9, 25	8, 26	8, 26	7, 27
	17	15, 18	13, 22	12, 23	11, 24	10, 25	9, 26	9, 26	8, 27	7, 28
	18	15, 21	13, 23	12, 24	11, 25	10, 26	10, 26	9, 27	8, 28	8, 28
	19	15, 21	14, 23	13, 24	12, 25	11, 26	10, 27	9, 27	9, 28	8, 29
	20	16, 22	14, 24	13, 25	12, 25	11, 26	10, 27	10, 28	9, 29	8, 29
	21	16, 22	14, 24	13, 25	12, 26	11, 27	11, 28	10, 28	9, 29	9, 30
	22	17, 23	15, 24	14, 25	13, 26	12, 27	11, 28	10, 29	9, 29	9, 30
	23	17, 23	15, 25	14, 26	13, 27	12, 28	11, 28	11, 29	10, 30	9, 30
	24	17, 23	15, 25	14, 26	13, 27	12, 28	12, 29	11, 29	10, 30	9, 31
	25	17, 24	16, 25	15, 26	14, 27	13, 28	12, 29	11, 30	10, 30	10, 31
	26	18, 24	16, 26	15, 27	14, 28	13, 29	12, 29	11, 30	11, 31	10, 31
	27	18, 24	16, 26	15, 27	14, 28	13, 29	12, 30	12, 30	11, 31	10, 32
	28	18, 24	16, 26	15, 27	14, 28	13, 29	13, 30	12, 30	11, 31	10, 32
	29	19, 25	17, 26	16, 28	15, 28	14, 30	13, 30	12, 31	11, 32	11, 32
16	30	19, 25	17, 27	16, 28	15, 29	14, 30	13, 30	12, 31	11, 32	11, 32
17	17	15, 21	13, 23	12, 24	11, 25	10, 26	10, 26	9, 27	8, 28	8, 28
	18	16, 21	14, 23	13, 24	12, 25	11, 26	10, 27	9, 27	9, 28	8, 29
	19	16, 22	14, 24	13, 25	12, 26	11, 27	10, 27	10, 28	9, 29	8, 29
	20	16, 22	15, 24	13, 25	13, 26	11, 27	11, 28	10, 29	9, 29	9, 30
	21	17, 23	15, 25	14, 26	13, 27	12, 28	11, 28	10, 29	10, 30	9, 30
	22	17, 23	15, 25	14, 26	13, 27	12, 28	11, 29	11, 30	10, 30	9, 31
	23	17, 24	16, 25	15, 27	14, 27	13, 29	12, 29	11, 30	10, 31	10, 31
	24	18, 24	16, 26	15, 27	14, 28	13, 29	12, 30	11, 30	11, 31	10, 32
	25	18, 24	16, 26	15, 27	14, 28	13, 29	12, 30	12, 31	11, 31	10, 32
	26	18, 25	17, 26	15, 28	14, 29	13, 30	13, 30	12, 31	11, 32	10, 32
	27	19, 25	17, 27	16, 28	15, 29	14, 30	13, 31	12, 31	11, 32	11, 33
	28	19, 25	17, 27	16, 28	15, 29	14, 30	13, 31	12, 32	12, 32	11, 33
	29	19, 26	17, 27	16, 28	15, 29	14, 30	13, 31	13, 32	12, 33	11, 33
17	30	20, 26	18, 28	17, 29	16, 30	14, 31	14, 32	13, 32	12, 33	11, 33
18	18	16, 22	14, 24	13, 25	12, 26	11, 27	11, 27	10, 28	9, 29	9, 29
	19	16, 20	15, 24	14, 25	13, 26	12, 27	11, 28	10, 29	9, 30	9, 30
	20	17, 23	15, 25	14, 26	13, 27	12, 28	11, 29	11, 29	10, 30	9, 31
	21	17, 23	15, 25	14, 26	13, 27	12, 28	12, 29	11, 30	10, 31	10, 31
	22	18, 24	16, 26	15, 27	14, 28	13, 29	12, 30	11, 30	10, 31	10, 32
	23	18, 24	16, 26	15, 27	14, 28	13, 29	12, 30	12, 31	11, 32	10, 32
	24	18, 25	17, 27	15, 28	14, 29	13, 30	13, 30	12, 31	11, 32	10, 33
	25	19, 25	17, 27	16, 28	15, 29	14, 30	13, 31	12, 32	11, 32	11, 33
	26	19, 25	17, 27	16, 28	15, 29	14, 30	13, 31	12, 32	12, 33	11, 33
	27	19, 26	18, 28	16, 29	15, 30	14, 31	13, 32	13, 32	12, 33	11, 34
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	29	20, 26	18, 28	17, 29	16, 30	15, 32	14, 32	13, 33	12, 34	12, 34
18	30	20, 27	18, 29	17, 30	16, 31	15, 32	14, 32	14, 33	13, 34	12, 34

TABLE B.29 (cont.): Critical Values of u for the Runs Test

n_1	n_2	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
19	19	17, 23	15, 25	14, 26	13, 27	12, 28	11, 29	11, 29	10, 30	9, 31
	20	17, 24	16, 25	14, 27	13, 27	12, 29	12, 29	11, 30	10, 31	10, 31
	21	18, 24	16, 26	15, 27	14, 28	13, 29	12, 30	11, 31	11, 31	10, 32
	22	18, 25	16, 26	15, 28	14, 29	13, 30	12, 30	12, 31	11, 32	10, 32
	23	19, 25	17, 27	16, 28	15, 29	13, 30	13, 31	12, 32	11, 32	11, 33
	24	19, 25	17, 27	16, 28	15, 29	14, 31	13, 31	12, 32	11, 33	11, 33
	25	19, 26	17, 28	16, 29	15, 30	14, 31	13, 32	13, 32	12, 33	11, 34
	26	20, 26	18, 28	17, 29	16, 30	14, 31	14, 32	13, 33	12, 34	11, 34
	27	20, 26	18, 28	17, 30	16, 31	15, 32	14, 32	13, 33	12, 34	12, 35
	28	20, 27	18, 29	17, 30	16, 31	15, 32	14, 33	14, 34	13, 34	12, 35
	29	21, 27	19, 29	18, 30	17, 31	15, 32	15, 33	14, 34	13, 35	12, 35
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20	20	18, 24	16, 26	15, 27	14, 28	13, 29	12, 30	11, 31	11, 31	10, 32
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	28	21, 28	19, 30	18, 31	17, 32	16, 33	15, 34	14, 34	13, 35	13, 36
	29	21, 28	19, 30	18, 31	17, 32	16, 33	15, 34	14, 35	13, 36	13, 36
20	30	22, 28	20, 30	18, 32	17, 32	16, 34	15, 34	15, 35	14, 36	13, 37
21	21	19, 25	17, 27	16, 28	15, 29	14, 30	13, 31	12, 32	11, 33	11, 33
	22	19, 26	17, 28	16, 29	15, 30	14, 31	13, 32	13, 32	12, 33	11, 34
	23	20, 26	18, 28	17, 29	16, 30	14, 31	14, 32	13, 33	12, 34	11, 35
	24	20, 27	18, 29	17, 30	16, 31	15, 32	14, 33	13, 34	12, 34	12, 35
	25	21, 27	19, 29	17, 30	16, 31	15, 32	14, 33	14, 34	13, 35	12, 36
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	27	21, 28	19, 30	18, 31	17, 32	16, 33	15, 34	14, 35	13, 36	13, 36
	28	22, 28	20, 30	18, 32	17, 33	16, 34	15, 35	15, 35	14, 36	13, 37
	29	22, 29	20, 31	19, 32	18, 33	16, 34	16, 35	15, 36	14, 37	13, 37
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22	22	20, 26	18, 28	17, 29	16, 30	14, 32	14, 32	13, 33	12, 34	11, 35
	23	20, 24	18, 29	17, 30	16, 31	15, 32	14, 33	13, 34	12, 35	12, 35
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	28	22, 29	20, 31	19, 32	18, 33	17, 35	16, 35	15, 36	14, 37	13, 38
	29	23, 29	21, 31	19, 33	18, 34	17, 35	16, 36	15, 37	14, 38	14, 38
22	30	23, 30	21, 32	20, 33	19, 34	17, 35	16, 36	16, 37	15, 38	14, 39
23	23	21, 27	19, 29	17, 31	16, 32	15, 33	14, 34	14, 34	13, 35	12, 36
	24	21, 28	19, 30	18, 31	17, 32	16, 33	15, 34	14, 35	13, 36	13, 36
	25	22, 28	20, 30	18, 32	17, 33	16, 34	15, 35	14, 35	14, 36	13, 37
	26	22, 29	20, 31	19, 32	18, 33	16, 34	16, 35	15, 36	14, 37	13, 38
	27	23, 29	20, 31	19, 33	18, 34	17, 35	16, 36	15, 36	14, 37	14, 38
	28	23, 30	21, 32	20, 33	18, 34	17, 35	16, 36	16, 37	15, 38	14, 39
	29	23, 30	21, 32	20, 33	19, 35	17, 36	17, 37	16, 37	15, 38	14, 39
23	30	24, 30	21, 33	20, 34	19, 35	18, 36	17, 37	16, 38	15, 39	15, 39

TABLE B.29 (cont.): Critical Values of u for the Runs Test

n_1	n_2	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
24	24	22, 28	20, 30	18, 32	17, 33	16, 34	15, 35	15, 35	14, 36	13, 37
	25	22, 26	20, 31	19, 32	18, 33	17, 34	16, 35	15, 36	14, 37	13, 38
	26	23, 29	20, 31	19, 33	18, 34	17, 35	16, 36	15, 37	14, 38	14, 38
	27	23, 30	21, 32	20, 33	19, 34	17, 36	16, 36	16, 37	15, 38	14, 39
	28	23, 30	21, 32	20, 34	19, 35	18, 36	17, 37	16, 38	15, 39	14, 39
	29	24, 31	22, 33	20, 34	19, 35	18, 36	17, 37	16, 38	15, 39	15, 40
24	30	24, 31	22, 33	21, 35	20, 36	18, 37	17, 38	17, 39	16, 40	15, 40
25	25	23, 29	21, 31	19, 33	18, 34	17, 35	16, 36	15, 37	14, 38	14, 38
	26	23, 30	21, 32	20, 33	19, 34	17, 36	16, 37	16, 37	15, 38	14, 39
	27	24, 30	21, 33	20, 34	19, 35	18, 36	17, 37	16, 38	15, 39	14, 39
	28	24, 31	22, 33	21, 34	19, 35	18, 37	17, 38	16, 38	15, 39	15, 40
	29	24, 31	22, 33	21, 35	20, 36	18, 37	18, 38	17, 39	16, 40	15, 41
25	30	25, 32	23, 34	21, 35	20, 36	19, 38	18, 39	17, 39	16, 40	15, 41
26	26	24, 30	21, 33	20, 34	19, 35	18, 36	17, 37	16, 38	15, 39	14, 40
	27	24, 28	22, 33	21, 34	19, 36	18, 37	17, 38	16, 39	15, 39	15, 40
	28	25, 31	22, 34	21, 35	20, 36	19, 37	18, 38	17, 39	16, 40	15, 41
	29	25, 32	23, 34	21, 35	20, 37	19, 38	18, 39	17, 40	16, 41	16, 41
26	30	25, 32	23, 35	22, 36	21, 37	19, 38	18, 39	18, 40	17, 41	16, 42
27	27	25, 31	22, 34	21, 35	20, 36	19, 37	18, 38	17, 39	16, 40	15, 41
	28	25, 32	23, 34	21, 36	20, 37	19, 38	18, 39	17, 40	16, 41	16, 41
	29	25, 32	23, 35	22, 36	21, 37	19, 39	19, 39	18, 40	17, 41	16, 42
27	30	26, 33	24, 35	22, 37	21, 38	20, 39	19, 40	18, 41	17, 42	16, 43
28	28	25, 33	23, 35	22, 36	21, 37	19, 39	19, 39	18, 40	17, 41	16, 42
	29	26, 30	24, 35	22, 37	21, 38	20, 39	19, 40	18, 41	17, 42	16, 43
28	30	26, 34	24, 36	23, 37	22, 38	20, 40	19, 41	18, 41	17, 42	17, 43
29	29	26, 34	24, 36	23, 37	22, 38	20, 40	19, 41	19, 41	17, 43	17, 43
29	30	27, 34	25, 36	23, 38	22, 39	21, 40	20, 41	19, 42	18, 43	17, 44
30	30	27, 35	25, 37	24, 38	23, 39	21, 41	20, 42	19, 43	18, 44	18, 44

Appendix Table B.29 was prepared using the procedure described by Brownlee (1965: 225–226) and Swed and Eisenhart (1943).

Example:

$$u_{0.05(2),24,30} = 20 \quad \text{and} \quad 36$$

The pairs of critical values are consulted as described in Section 25.6. The probability of a u found in the table is less than or equal to its column heading and greater than the next smaller column heading. For example, the two-tailed probability for $n_1 = 25$, $n_2 = 26$, and $u = 20$ is $0.05 < P \leq 0.10$; the two-tailed probability for $n_1 = 20$, $n_2 = 30$, and $u = 15$ is $0.002 < P \leq 0.005$; and the one-tailed probability for $n_1 = 24$, $n_2 = 25$, and $u = 21$ is $0.10 < P \leq 0.25$. For n larger than 30, use the normal approximation of Section 25.6.

TABLE B.30: Critical Values of C for the Mean Square Successive Difference Test

n	α: 0.25	0.10	0.05	0.025	0.01	0.005	0.0025	0.001	0.0005
8	0.2,23	0.4,09	0.5,09	0.5,87	0.6,68	0.7,16	0.7,56	0.7,99	0.8,25
9	0.2,12	0.3,91	0.4,88	0.5,65	0.6,45	0.6,94	0.7,35	0.7,79	0.8,07
10	0.2,03	0.3,74	0.4,69	0.5,44	0.6,24	0.6,73	0.7,14	0.7,60	0.7,88
11	0.1,94	0.3,60	0.4,52	0.5,26	0.6,04	0.6,53	0.6,94	0.7,40	0.7,70
12	0.1,87	0.3,47	0.4,36	0.5,09	0.5,86	0.6,34	0.6,76	0.7,22	0.7,52
13	0.1,80	0.3,35	0.4,22	0.4,93	0.5,69	0.6,17	0.6,58	0.7,05	0.7,35
14	0.1,74	0.3,25	0.4,09	0.4,78	0.5,53	0.6,01	0.6,42	0.6,89	0.7,19
15	0.1,69	0.3,15	0.3,97	0.4,65	0.5,39	0.5,86	0.6,27	0.6,73	0.7,04
16	0.1,64	0.3,06	0.3,86	0.4,53	0.5,25	0.5,72	0.6,12	0.6,58	0.6,89
17	0.1,59	0.2,98	0.3,76	0.4,41	0.5,13	0.5,58	0.5,99	0.6,45	0.6,75
18	0.1,55	0.2,90	0.3,67	0.4,31	0.5,01	0.5,46	0.5,86	0.6,32	0.6,62
19	0.1,51	0.2,83	0.3,58	0.4,21	0.4,90	0.5,35	0.5,74	0.6,19	0.6,50
20	0.1,48	0.2,76	0.3,50	0.4,12	0.4,80	0.5,24	0.5,63	0.6,08	0.6,38
21	0.1,44	0.2,70	0.3,43	0.4,03	0.4,70	0.5,13	0.5,52	0.5,97	0.6,27
22	0.1,41	0.2,64	0.3,35	0.3,95	0.4,61	0.5,04	0.5,42	0.5,86	0.6,16
23	0.1,38	0.2,59	0.3,29	0.3,87	0.4,52	0.4,94	0.5,32	0.5,76	0.6,06
24	0.1,35	0.2,54	0.3,22	0.3,80	0.4,44	0.4,86	0.5,23	0.5,66	0.5,96
25	0.1,33	0.2,49	0.3,16	0.3,73	0.4,36	0.4,77	0.5,14	0.5,57	0.5,87
26	0.1,30	0.2,45	0.3,11	0.3,66	0.4,29	0.4,69	0.5,06	0.5,49	0.5,78
27	0.1,28	0.2,40	0.3,05	0.3,60	0.4,22	0.4,62	0.4,98	0.5,40	0.5,69
28	0.1,26	0.2,36	0.3,00	0.3,54	0.4,15	0.4,55	0.4,90	0.5,32	0.5,61
29	0.1,23	0.2,32	0.2,95	0.3,49	0.4,09	0.4,48	0.4,83	0.5,25	0.5,53
30	0.1,21	0.2,29	0.2,91	0.3,43	0.4,02	0.4,41	0.4,76	0.5,17	0.5,46
31	0.1,20	0.2,25	0.2,86	0.3,38	0.3,97	0.4,35	0.4,70	0.5,10	0.5,38
32	0.1,18	0.2,22	0.2,82	0.3,33	0.3,91	0.4,29	0.4,63	0.5,04	0.5,31
33	0.1,16	0.2,18	0.2,78	0.3,29	0.3,86	0.4,23	0.4,57	0.4,97	0.5,25
34	0.1,14	0.2,15	0.2,74	0.3,24	0.3,80	0.4,18	0.4,51	0.4,91	0.5,18
35	0.1,13	0.2,12	0.2,71	0.3,20	0.3,76	0.4,12	0.4,46	0.4,85	0.5,12
36	0.1,11	0.2,10	0.2,67	0.3,16	0.3,71	0.4,07	0.4,40	0.4,79	0.5,06
37	0.1,10	0.2,07	0.2,64	0.3,12	0.3,66	0.4,02	0.4,35	0.4,74	0.5,00
38	0.1,08	0.2,04	0.2,60	0.3,08	0.3,62	0.3,97	0.4,30	0.4,68	0.4,95
39	0.1,07	0.2,02	0.2,57	0.3,04	0.3,57	0.3,93	0.4,25	0.4,63	0.4,89
40	0.1,06	0.1,99	0.2,54	0.3,01	0.3,53	0.3,88	0.4,20	0.4,58	0.4,84
41	0.1,04	0.1,97	0.2,51	0.2,97	0.3,49	0.3,84	0.4,15	0.4,53	0.4,79
42	0.1,03	0.1,95	0.2,48	0.2,94	0.3,45	0.3,80	0.4,11	0.4,48	0.4,74
43	0.1,02	0.1,92	0.2,45	0.2,90	0.3,42	0.3,76	0.4,07	0.4,44	0.4,69
44	0.1,01	0.1,90	0.2,43	0.2,87	0.3,38	0.3,72	0.4,02	0.4,39	0.4,64
45	0.1,00	0.1,88	0.2,40	0.2,84	0.3,35	0.3,68	0.3,98	0.4,35	0.4,60
46	0.0,99	0.1,86	0.2,38	0.2,81	0.3,31	0.3,64	0.3,94	0.4,31	0.4,55
47	0.0,98	0.1,84	0.2,35	0.2,79	0.3,28	0.3,61	0.3,91	0.4,26	0.4,51
48	0.0,97	0.1,82	0.2,33	0.2,76	0.3,25	0.3,57	0.3,87	0.4,22	0.4,47
49	0.0,96	0.1,81	0.2,30	0.2,73	0.3,22	0.3,54	0.3,83	0.4,19	0.4,43
50	0.0,95	0.1,79	0.2,28	0.2,70	0.3,19	0.3,51	0.3,80	0.4,15	0.4,39
52	0.0,93	0.1,75	0.2,24	0.2,65	0.3,13	0.3,44	0.3,73	0.4,08	0.4,31
54	0.0,91	0.1,72	0.2,20	0.2,61	0.3,07	0.3,38	0.3,67	0.4,01	0.4,24
56	0.0,90	0.1,69	0.2,16	0.2,56	0.3,02	0.3,33	0.3,61	0.3,94	0.4,17
58	0.0,88	0.1,66	0.2,12	0.2,52	0.2,97	0.3,27	0.3,55	0.3,88	0.4,11
60	0.0,87	0.1,64	0.2,09	0.2,48	0.2,92	0.3,22	0.3,49	0.3,82	0.4,05
62	0.0,85	0.1,61	0.2,06	0.2,44	0.2,88	0.3,17	0.3,44	0.3,76	0.3,99
64	0.0,84	0.1,58	0.2,03	0.2,40	0.2,84	0.3,13	0.3,39	0.3,71	0.3,93
66	0.0,83	0.1,56	0.2,00	0.2,37	0.2,79	0.3,08	0.3,34	0.3,66	0.3,87
68	0.0,81	0.1,54	0.1,97	0.2,33	0.2,76	0.3,04	0.3,30	0.3,61	0.3,82
70	0.0,80	0.1,52	0.1,94	0.2,30	0.2,72	0.3,00	0.3,25	0.3,56	0.3,77

TABLE B.30 (cont.): Critical Values of C for the Mean Square Successive Difference Test

n	α: 0.25	0.10	0.05	0.025	0.01	0.005	0.0025	0.001	0.0005
72	0.0,79	0.1,50	0.1,91	0.2,27	0.2,68	0.2,96	0.3,21	0.3,51	0.3,72
74	0.0,78	0.1,48	0.1,89	0.2,24	0.2,65	0.2,92	0.3,17	0.3,47	0.3,68
76	0.0,77	0.1,46	0.1,86	0.2,21	0.2,61	0.2,88	0.3,13	0.3,42	0.3,63
78	0.0,76	0.1,44	0.1,84	0.2,18	0.2,58	0.2,85	0.3,09	0.3,38	0.3,59
80	0.0,75	0.1,42	0.1,82	0.2,16	0.2,55	0.2,81	0.3,05	0.3,34	0.3,55
82	0.0,74	0.1,40	0.1,80	0.2,13	0.2,52	0.2,78	0.3,02	0.3,31	0.3,51
84	0.0,73	0.1,39	0.1,77	0.2,11	0.2,49	0.2,75	0.2,98	0.3,27	0.3,47
86	0.0,72	0.1,37	0.1,75	0.2,08	0.2,46	0.2,72	0.2,95	0.3,23	0.3,43
88	0.0,71	0.1,36	0.1,73	0.2,06	0.2,44	0.2,69	0.2,92	0.3,20	0.3,39
90	0.0,70	0.1,34	0.1,72	0.2,04	0.2,41	0.2,66	0.2,89	0.3,16	0.3,36
92	0.0,69	0.1,33	0.1,70	0.2,02	0.2,38	0.2,63	0.2,86	0.3,13	0.3,32
94	0.0,68	0.1,31	0.1,68	0.2,00	0.2,36	0.2,60	0.2,83	0.3,10	0.3,29
96	0.0,67	0.1,30	0.1,66	0.1,98	0.2,33	0.2,58	0.2,80	0.3,07	0.3,26
98	0.0,65	0.1,29	0.1,65	0.1,96	0.2,31	0.2,55	0.2,77	0.3,04	0.3,23
100	0.0,64	0.1,27	0.1,63	0.1,94	0.2,29	0.2,53	0.2,75	0.3,01	0.3,20
105		0.1,24	0.1,59	0.1,89	0.2,24	0.2,47	0.2,68	0.2,94	0.3,12
110		0.1,21	0.1,56	0.1,85	0.2,19	0.2,41	0.2,62	0.2,88	0.3,05
115		0.1,19	0.1,52	0.1,81	0.2,14	0.2,36	0.2,57	0.2,82	0.2,99
120		0.1,16	0.1,49	0.1,77	0.2,10	0.2,31	0.2,52	0.2,76	0.2,93
125		0.1,14	0.1,46	0.1,74	0.2,05	0.2,27	0.2,47	0.2,71	0.2,87
130		0.1,11	0.1,43	0.1,70	0.2,02	0.2,23	0.2,42	0.2,66	0.2,82
135		0.1,09	0.1,41	0.1,67	0.1,98	0.2,19	0.2,38	0.2,61	0.2,77
140		0.1,07	0.1,38	0.1,64	0.1,94	0.2,15	0.2,34	0.2,56	0.2,72
145		0.1,05	0.1,36	0.1,61	0.1,91	0.2,11	0.2,30	0.2,52	0.2,68
150		0.1,02	0.1,33	0.1,59	0.1,88	0.2,08	0.2,26	0.2,48	0.2,63

Appendix Table B.30 was prepared by the method outlined in Young (1941). *Examples*:

$$C_{0.05,60} = 0.209 \quad \text{and} \quad C_{0.01,68} = 0.276$$

For n greater than shown in the table, the normal approximation (Equation 25.22) may be utilized. This approximation is excellent, especially for α near 0.05, as shown in the following tabulation. The following table considers the absolute difference between the exact critical value of C and the value of C calculated from the normal approximation. Given in the table are the minimum sample sizes necessary to achieve such absolute differences of various specified magnitudes.

Absolute Difference	α = 0.25	0.10	0.05	0.025	0.01	0.005	0.0025	0.001	0.0005
≤ 0.002	30	35	8	35	70	90	120		
≤ 0.005	20	20	8	20	45	60	80	100	120
≤ 0.010	15	10	8	15	30	40	50	60	80
≤ 0.020	8	8	8	8	20	25	30	40	45

TABLE B.31: Critical Values, u, for the Runs-Up-and-Down Test

n	$\alpha(2)$: 0.50 $\alpha(1)$: 0.25	0.20 0.10	0.10 0.05	0.05 0.025	0.02 0.01	0.01 0.005	0.005 0.0025	0.002 0.001	0.001 0.0005
4	1, -	1, -	-, -	-, -	-, -	-, -	-, -	-, -	-, -
5	2, -	1, -	1, -	1, -	-, -	-, -	-, -	-, -	-, -
6	2, 5	2, -	1, -	1, -	1, -	1, -	-, -	-, -	-, -
7	3, 6	2, -	2, -	2, -	1, -	1, -	1, -	1, -	1, -
8	3, 7	3, 7	2, -	2, -	2, -	1, -	1, -	1, -	1, -
9	4, 7	3, 8	3, 8	2, -	2, -	2, -	2, -	1, -	1, -
10	5, 8	4, 9	3, 9	3, -	3, -	2, -	2, -	2, -	2, -
11	5, 9	4, 10	4, 10	4, 10	3, -	3, -	3, -	2, -	2, -
12	6, 10	5, 10	4, 11	4, 11	4, -	3, -	3, -	3, -	2, -
13	6, 10	6, 11	5, 12	5, 12	4, 12	4, -	3, -	3, -	3, -
14	7, 11	6, 12	6, 12	5, 13	5, 13	4, 13	4, -	4, -	3, -
15	8, 12	7, 13	6, 13	6, 14	3, 14	5, 14	4, -	4, -	4, -
16	8, 12	7, 13	7, 14	6, 14	6, 15	5, 15	5, 15	5, -	4, -
17	9, 13	8, 14	7, 15	7, 15	6, 16	6, 16	5, 16	5, -	5, -
18	10, 14	8, 15	8, 15	7, 16	7, 16	6, 17	6, 17	6, 17	5, -
19	10, 15	9, 10	8, 16	8, 17	7, 17	7, 18	7, 18	6, 18	6, 18
20	11, 15	10, 16	9, 17	8, 17	8, 18	7, 18	7, 19	7, 19	6, 19
21	11, 16	10, 17	10, 18	9, 18	8, 19	8, 19	8, 20	7, 20	7, 20
22	12, 17	11, 18	10, 18	10, 19	9, 20	8, 20	8, 20	8, 21	7, 21
23	13, 17	12, 18	11, 19	10, 20	10, 20	9, 21	9, 21	8, 22	8, 22
24	13, 18	12, 19	11, 20	11, 20	10, 21	10, 22	9, 22	9, 22	8, 23
25	14, 19	13, 20	12, 21	11, 21	11, 22	10, 22	10, 23	9, 23	9, 23
26	15, 29	13, 21	13, 21	12, 22	11, 23	11, 23	10, 24	10, 24	9, 24
27	15, 20	14, 21	13, 22	13, 23	12, 23	11, 24	11, 24	10, 25	10, 25
28	16, 21	15, 22	14, 23	13, 23	12, 24	12, 25	11, 25	11, 26	10, 26
29	17, 21	15, 23	14, 24	14, 24	13, 25	12, 25	12, 26	11, 26	11, 27
30	17, 22	16, 24	15, 24	14, 25	13, 26	13, 26	12, 27	12, 27	11, 28
31	18, 23	16, 24	16, 25	15, 26	14, 26	13, 27	13, 27	12, 28	12, 28
32	18, 24	17, 25	16, 26	15, 26	15, 27	14, 28	14, 28	13, 29	12, 29
33	19, 24	18, 26	17, 26	16, 27	15, 28	15, 29	14, 29	13, 30	13, 30
34	20, 25	18, 26	17, 27	17, 28	16, 29	15, 29	15, 30	14, 20	14, 31
35	20, 26	19, 27	18, 28	17, 29	16, 29	16, 30	15, 31	15, 31	14, 32
36	21, 26	20, 28	19, 29	18, 29	17, 30	16, 31	16, 31	15, 32	15, 32
37	22, 27	20, 29	19, 29	18, 20	18, 31	17, 32	16, 32	16, 33	15, 33
38	22, 28	21, 29	20, 30	19, 31	18, 32	17, 32	17, 33	16, 33	16, 34
39	23, 28	21, 30	20, 31	20, 32	19, 32	18, 33	17, 34	17, 34	16, 35
40	24, 29	22, 31	21, 32	20, 32	19, 33	19, 34	18, 34	17, 35	17, 35
41	24, 30	23, 31	22, 32	21, 33	20, 34	19, 35	19, 34	18, 36	17, 36
42	25, 30	23, 32	22, 33	21, 34	20, 35	20, 35	19, 36	18, 37	18, 37
43	26, 31	24, 33	23, 34	22, 35	21, 35	20, 36	20, 37	19, 37	18, 38
44	26, 32	24, 33	23, 34	23, 35	22, 36	21, 37	20, 37	20, 38	19, 39
45	27, 33	25, 34	24, 35	23, 36	22, 37	22, 38	21, 38	20, 39	20, 39
46	27, 33	26, 35	25, 36	24, 37	23, 38	22, 38	21, 39	21, 40	20, 40
47	28, 34	26, 36	25, 37	24, 37	23, 38	23, 39	22, 40	21, 40	21, 41
48	29, 35	27, 36	26, 37	25, 38	24, 39	23, 40	23, 40	22, 41	21, 42
49	29, 35	28, 37	27, 38	26, 39	25, 40	24, 41	23, 41	22, 42	22, 42
50	30, 36	28, 38	27, 39	26, 40	25, 41	24, 41	24, 42	23, 43	22, 43

Appendix Table B.31 was prepared using the recursion algorithm attributed to André (1883; Bradley, 1968: 281) in order to ascertain the probability of a particular u, after which it was determined what value of u would yield a cumulative tail probability $\leq \alpha$. *Note:* The α represented by each u in the table is less than or equal to that in the column heading and greater than the next smaller column heading. For example, if $n = 9$ and $u = 3$ for a two-tailed test, $0.05 < P \leq 0.10$; if $n = 15$ and $u = 7$ for u one-tailed test for uniformity, $0.05 < P \leq 0.10$.

The normal approximation of Section 25.8 will correctly reject H_0 at the indicated one-tailed and two-tailed significance levels for sample sizes as small as these:

$\alpha(2)$:	0.50	0.20	0.10	0.05	0.02	0.01	0.005	0.002	0.001
$\alpha(1)$:	0.25	0.10	0.05	0.025	0.01	0.005	0.0025	0.001	0.0005
n:	5	4	9	11	13	15	19	20	20

TABLE B.32: Angular Deviation, *s*, As a Function of Vector Length, *r*

r	0	1	2	3	4	5	6	7	8	9
0.00	81.0285	80.9879	80.9474	80.9068	80.8662	80.8256	80.7850	80.7444	80.7037	80.6630
0.01	80.6223	80.5816	80.5408	80.5000	80.4593	80.4185	80.3776	80.3368	80.2959	80.2550
0.02	80.2141	80.1731	80.1322	80.0912	80.0502	80.0092	79.9682	79.9271	79.8860	79.8449
0.03	79.8038	79.7626	79.7215	79.6803	79.6391	79.5978	79.5566	79.5153	79.4740	79.4327
0.04	79.3914	79.3500	79.3086	79.2672	79.2258	79.1843	79.1429	79.1014	79.0599	79.0183
0.05	78.9768	78.9352	78.8936	78.8520	78.8103	78.7687	78.7270	78.6853	78.6435	78.6018
0.06	78.5600	78.5182	78.4764	78.4345	78.3927	78.3508	78.3089	78.2670	78.2250	78.1830
0.07	78.1410	78.0990	78.0569	78.0149	77.9728	77.9307	77.8885	77.8464	77.8042	77.7620
0.08	77.7198	77.6775	77.6353	77.5930	77.5506	77.5083	77.4659	77.4235	77.3811	77.3387
0.09	77.2962	77.2537	77.2112	77.1687	77.1262	77.0836	77.0410	76.9984	76.9557	76.9130
0.10	76.8703	76.8276	76.7849	76.7421	76.6993	76.6565	76.6137	76.5708	76.5279	76.4850
0.11	76.4421	76.3991	76.3562	76.3132	76.2701	76.2271	76.1840	76.1409	76.0978	76.0546
0.12	76.0114	75.9582	75.9250	75.8818	75.8385	75.7952	75.7519	75.7085	75.6651	75.6217
0.13	75.5783	75.5349	75.4914	75.4479	75.4044	75.3608	75.3172	75.2737	75.2300	75.1864
0.14	75.1427	75.0990	75.0553	75.0115	74.9678	74.9240	74.8801	74.8363	74.7924	74.7485
0.15	74.7045	74.6606	74.6166	74.5726	74.5286	74.4845	74.4404	74.3963	74.3522	74.3080
0.16	74.2638	74.2196	74.1754	74.1311	74.0868	74.0425	73.9981	73.9537	73.9093	73.8649
0.17	73.8204	73.7760	73.7314	73.6869	73.6423	73.5978	73.5531	73.5085	73.4638	73.4191
0.18	73.3744	73.3296	73.2849	73.2401	73.1952	73.1503	73.1055	73.0605	73.0156	72.9706
0.19	72.9256	72.8805	72.8355	72.7904	72.7453	72.7002	72.6550	72.6098	72.5646	72.5193
0.20	72.4741	72.4287	72.3834	72.3380	72.2926	72.2472	72.2018	72.1563	72.1108	72.0652
0.21	72.0197	71.9741	71.9285	71.8828	71.8371	71.7914	71.7457	71.6999	71.6541	71.6083
0.22	71.5624	71.5165	71.4706	71.4247	71.3787	71.3327	71.2866	71.2406	71.1945	71.1483
0.23	71.1022	71.0560	71.0098	70.9635	70.9173	70.8710	70.8246	70.7783	70.7319	70.6854
0.24	70.6390	70.5925	70.5460	70.4994	70.4528	70.4062	70.3596	70.3129	70.2662	70.2195
0.25	70.1727	70.1259	70.0791	70.0322	69.9853	69.9384	69.8914	69.8445	69.7975	69.7504
0.26	69.7033	69.6562	69.6091	69.5619	69.5147	69.4674	69.4202	69.3729	69.3255	69.2782
0.27	69.2307	69.1833	69.1358	69.0883	69.0408	68.9933	68.9456	68.8980	68.8504	68.8027
0.28	68.7549	68.7072	68.6594	68.6115	68.5637	68.5158	68.4678	68.4199	68.3719	68.3239
0.29	68.2758	68.2277	68.1796	68.1314	68.0832	68.0350	67.9867	67.9384	67.8901	67.8417
0.30	67.7933	67.7448	67.6964	67.6478	67.5993	67.5507	67.5021	67.4535	67.4048	67.3560
0.31	67.3073	67.2585	67.2097	67.1608	67.1119	67.0630	67.0140	66.9650	66.9160	66.8669
0.32	66.8178	66.7686	66.7195	66.6702	66.6210	66.5717	66.5223	66.4730	66.4236	66.3741
0.33	66.3246	66.2751	66.2256	66.1760	66.1264	66.0767	66.0270	65.9773	65.9275	65.8777
0.34	65.8278	65.7779	65.7280	65.6781	65.6281	65.5780	65.5279	65.4778	65.4277	65.3775
0.35	65.3272	65.2770	65.2267	65.1763	65.1259	65.0755	65.0250	64.9745	64.9240	64.8734
0.36	64.8228	64.7721	64.7214	64.6707	64.6199	64.5691	64.5182	64.4673	64.4164	64.3654
0.37	64.3143	64.2533	64.2122	64.1610	64.1098	64.0586	64.0074	63.9561	63.9047	63.8533
0.38	63.8019	63.7504	63.6989	63.6473	63.5957	63.5441	63.4924	63.4407	63.3889	63.3371
0.39	63.2852	63.2334	63.1814	63.1294	63.0774	63.0253	62.9732	62.9211	62.8689	62.8167
0.40	62.7644	62.7121	62.6597	62.6073	62.5548	62.5023	62.4498	62.3972	62.3445	62.2919
0.41	62.2391	62.1854	62.1336	62.0807	62.0278	61.9749	61.9219	61.8688	61.8158	61.7626
0.42	61.7094	61.6562	61.6030	61.5496	61.4963	61.4429	61.3894	61.3359	61.2824	61.2288
0.43	61.1751	61.1215	61.0677	61.0139	60.9601	60.9063	60.8523	60.7984	60.7443	60.6903
0.44	60.6361	60.5820	60.5278	60.4735	60.4192	60.3648	60.3104	60.2560	60.2015	60.1469
0.45	60.0923	60.0377	59.9830	59.9282	59.8734	59.8185	59.7636	59.7087	59.6537	59.5986
0.46	59.5435	59.4884	59.4332	59.3779	59.3226	59.2672	59.2118	59.1563	59.1008	59.0452
0.47	58.9896	58.9339	58.8782	58.8224	58.7666	58.7107	58.6548	58.5988	58.5427	58.4866
0.48	58.4305	58.3743	58.3180	58.2617	58.2053	58.1489	58.0924	58.0358	57.9792	57.9226
0.49	57.8659	57.8091	57.7523	57.6954	57.6385	57.5815	57.5245	57.4674	57.4102	57.3530

TABLE B.32 (cont.): Angular Deviation, s, As a Function of Vector Length, r

r	0	1	2	3	4	5	6	7	8	9
0.50	57.2958	57.2384	57.1811	57.1236	57.0661	57.0086	56.9510	56.8933	56.8356	56.7778
0.51	56.7199	56.6620	55.5040	56.5460	56.4879	56.4298	56.3716	56.3133	56.2550	56.1966
0.52	56.1382	56.0797	56.0211	55.9625	55.9038	55.8450	55.7862	55.7273	55.6684	55.6094
0.53	55.5503	55.4912	55.4320	55.3727	55.3134	55.2540	55.1946	55.1351	55.0755	55.0159
0.54	54.9562	54.8964	54.8366	54.7767	54.7167	54.6567	54.5966	54.5364	54.4762	54.4159
0.55	54.3555	54.2951	54.2346	54.1741	54.1134	54.0527	53.9920	53.9311	53.8702	53.8092
0.56	53.7482	53.6871	53.6259	53.5647	53.5033	53.4419	53.3805	53.3189	53.2573	53.1957
0.57	53.1339	53.0721	53.0102	52.9482	52.8862	52.8241	52.7619	52.6997	52.6373	52.5749
0.58	52.5124	52.4499	52.3873	52.3246	52.2618	52.1989	52.1360	52.0730	52.0099	51.9468
0.59	51.8835	51.8202	51.7568	51.6934	51.6298	51.5662	51.5025	51.4387	51.3749	51.3109
0.60	51.2469	51.1828	51.1186	51.0544	50.9900	50.9256	50.8611	50.7965	50.7318	50.6671
0.61	50.6023	50.5373	50.4723	50.4073	50.3421	50.2768	50.2115	50.1461	50.0806	50.0150
0.62	49.9493	49.8835	49.8177	49.7517	49.6857	49.6196	49.5534	49.4871	49.4207	49.3542
0.63	49.2877	49.2210	49.1543	49.0875	49.0205	48.9535	48.8864	48.8192	48.7519	48.6846
0.64	48.6171	48.5495	48.4818	48.4141	48.3462	48.2783	48.2102	48.1421	48.0739	48.0055
0.65	47.9371	47.8685	47.7999	47.7312	47.6624	47.5934	47.5244	47.4553	47.3861	47.3167
0.66	47.2473	47.1778	47.1081	47.0384	46.9686	46.8986	46.8286	46.7584	46.6882	46.6178
0.67	46.5473	46.4767	46.4060	46.3353	46.2643	46.1933	46.1222	46.0510	45.9796	45.9082
0.68	45.8366	45.7549	45.6932	45.6213	45.5492	45.4771	45.4049	45.3325	45.2600	45.1875
0.69	45.1147	45.0419	44.9690	44.8959	44.8227	44.7494	44.6760	44.6025	44.5288	44.4550
0.70	44.3811	44.3071	44.2329	44.1586	44.0842	44.0097	43.9351	43.8603	43.7854	43.7103
0.71	43.6352	43.5599	43.4844	43.4089	43.3332	43.2574	43.1814	43.1053	43.0291	42.9527
0.72	42.8762	42.7996	42.7228	42.6459	42.5689	42.4917	42.4144	42.3369	42.2593	42.1815
0.73	42.1036	42.0256	41.9474	41.8691	41.7906	41.7120	41.6332	41.5543	41.4752	41.3960
0.74	41.3166	41.2370	41.1573	41.0775	40.9975	40.9174	40.8371	40.7566	40.6760	40.5952
0.75	40.5142	40.4331	40.3519	40.2704	40.1888	40.1070	40.0251	39.9430	39.8607	39.7783
0.76	39.6957	39.6129	39.5299	39.4468	39.3635	39.2800	39.1963	39.1125	39.0285	38.9443
0.77	38.8599	38.7753	38.6906	38.6056	38.5205	38.4352	38.3497	38.2640	38.1781	38.0920
0.78	38.0057	37.9192	37.8326	37.7457	37.6586	37.5714	37.4839	37.3962	37.3083	37.2202
0.79	37.1319	37.0434	36.9547	36.8657	36.7766	36.6872	36.5976	36.5078	36.4178	36.3275
0.80	36.2370	36.1463	36.0554	35.9642	35.8728	35.7812	35.6893	35.5972	35.5049	35.4123
0.81	35.3195	35.2264	35.1331	35.0396	34.9457	34.8517	34.7573	34.6628	34.5679	34.4728
0.82	34.3775	34.2818	34.1859	34.0898	33.9933	33.8966	33.7997	33.7024	33.6048	33.5070
0.83	33.4089	33.3105	33.2118	33.1128	33.0135	32.9139	32.8140	32.7138	32.6133	32.5125
0.84	32.4114	32.3099	32.2082	32.1061	32.0037	31.9009	31.7979	31.6945	31.5907	31.4806
0.85	31.3822	31.2774	31.1723	31.0668	30.9609	30.8547	30.7481	30.6412	30.5339	30.4262
0.86	30.3181	30.2096	30.1007	29.9915	29.8818	29.7718	29.6613	29.5504	29.4391	29.3274
0.87	29.2152	29.1026	28.9896	28.8762	28.7623	28.6479	28.5331	28.4178	28.3020	28.1858
0.88	28.0691	27.9519	27.8342	27.7160	27.5973	27.4781	27.3584	27.2381	27.1173	26.9960
0.89	26.8741	26.7517	26.6287	26.5051	26.3810	26.2562	26.1309	26.0050	25.8784	25.7513
0.90	25.6234	25.4950	25.3659	25.2362	25.1058	24.9746	24.8428	24.7104	24.5771	24.4432
0.91	24.3085	24.1731	24.0369	23.9000	23.7622	23.6237	23.4843	23.3441	23.2030	23.0611
0.92	22.9183	22.7746	22.6300	22.4845	22.3380	22.1906	22.0421	21.8927	21.7422	21.5907
0.93	21.4381	21.2844	21.1296	20.9737	20.8166	20.6583	20.4988	20.3380	20.1759	20.0126
0.94	19.8478	19.6817	19.5142	19.3453	19.1748	19.0029	18.8293	18.6542	18.4773	18.2988
0.95	18.1185	17.9364	17.7524	17.5666	17.3787	17.1887	16.9967	16.8024	16.6059	16.4070
0.96	16.2057	16.0018	15.7954	15.5861	15.3741	15.1590	14.9409	14.7196	14.4948	14.2666
0.97	14.0345	13.7987	13.5587	13.3144	13.0655	12.8117	12.5529	12.2886	12.0185	11.7422
0.98	11.4592	11.1690	10.8711	10.5648	10.2494	9.9239	9.5874	9.2387	8.8763	8.4984
0.99	8.1029	7.6871	7.2474	6.7794	6.2765	5.7296	5.1247	4.4382	3.6238	2.5625
1.00	0.0000									

Values of s are given in degrees, by Equation 26.20.

TABLE B.33: Circular Standard Deviation, s_0, as a Function of Vector Length, r

r	0	1	2	3	4	5	6	7	8	9
0.00	∞	212.9639	201.9968	195.2961	190.3990	186.5119	183.2748	180.4925	178.0473	175.8622
0.01	173.8843	172.0755	170.4075	168.8585	167.4115	166.0531	164.7723	163.5600	162.4087	161.3121
0.02	160.2649	159.2623	158.3005	157.3760	156.4857	155.6270	154.7974	153.9950	153.2178	152.4640
0.03	151.7323	151.0212	150.3295	149.6560	148.9998	148.3597	147.7351	147.1250	146.5287	145.9456
0.04	145.3750	144.8163	144.2690	143.7326	143.2066	142.6905	142.1839	141.6865	141.1979	140.7177
0.05	140.2456	139.7813	139.3245	138.8749	138.4324	137.9966	137.5672	137.1442	136.7273	136.3162
0.06	135.9109	135.5110	135.1165	134.7272	134.3430	133.9636	133.5889	133.2189	132.8533	132.4290
0.07	132.1350	131.7822	131.4333	131.0883	130.7472	130.4097	130.0759	129.7455	129.4186	129.0951
0.08	128.7748	128.4578	128.1438	127.8329	127.5250	127.2200	126.9178	126.6184	126.3218	126.0278
0.09	125.7364	125.4476	125.1612	124.8774	124.5959	124.3167	124.0399	123.7654	123.4930	123.2228
0.10	122.9548	122.6888	122.4249	122.1630	121.9031	121.6452	121.3891	121.1349	120.8825	120.6320
0.11	120.3832	120.1361	119.8908	119.6472	119.4052	119.1648	118.9261	118.6889	118.4533	118.2192
0.12	117.9866	117.7554	117.5258	117.2975	117.0707	116.8452	116.6211	116.3984	116.1770	115.9569
0.13	115.7381	115.5205	115.3042	115.0891	114.8753	114.6626	114.4511	114.2408	114.0316	113.8236
0.14	113.6166	113.4108	113.2060	113.0023	112.7997	112.5981	112.3976	112.1980	111.9995	111.8019
0.15	111.6054	111.4097	111.2151	111.0213	110.8285	110.6367	110.4457	110.2556	110.0664	109.8780
0.16	109.6906	109.5039	109.3182	109.1332	108.9491	108.7657	108.5832	108.4015	108.2205	108.0404
0.17	107.8609	107.6823	107.5044	107.3272	107.1508	106.9751	106.8000	106.6258	106.4522	106.2793
0.18	106.1070	105.9355	105.7646	105.5944	105.4248	105.2559	105.0877	104.9200	104.7530	104.5866
0.19	104.4209	104.2557	104.0911	103.9272	103.7638	103.6010	103.4388	103.2772	103.1161	102.9556
0.20	102.7957	102.6362	102.4774	102.3191	102.1613	102.0040	101.8473	101.6911	101.5354	101.3802
0.21	101.2255	101.0714	100.9177	100.7645	100.6118	100.4595	100.3078	100.1565	100.0057	99.8553
0.22	99.7054	99.5560	99.4070	99.2585	99.1104	98.9628	98.8155	98.6688	98.5224	98.3765
0.23	98.2310	98.0859	97.9412	97.7969	97.6531	97.5096	97.3665	97.2239	97.0816	96.9397
0.24	96.7982	96.6571	96.5164	96.3760	96.2360	96.0964	95.9571	95.8182	95.6797	95.5415
0.25	95.4037	95.2663	95.1292	94.9924	94.8560	94.7199	94.5841	94.4487	94.3136	94.1789
0.26	94.0445	93.9104	93.7766	93.6432	93.5100	93.3772	93.2447	93.1125	92.9806	92.8490
0.27	92.7177	92.5867	92.4560	92.3257	92.1956	92.0657	91.9362	91.8070	91.6781	91.5494
0.28	91.4210	91.2929	91.1651	91.0375	90.9102	90.7832	90.6565	90.5300	90.4038	90.2778
0.29	90.1521	90.0267	89.9015	89.7766	89.6519	89.5275	89.4033	89.2794	89.1557	89.0322
0.30	88.9090	88.7861	88.6634	88.5409	88.4186	88.2966	88.1748	88.0533	87.9320	87.8109
0.31	87.6900	87.5693	87.4489	87.3287	87.2087	87.0889	86.9694	86.8500	86.7309	86.6120
0.32	86.4933	86.3748	86.2565	86.1384	86.0205	85.9028	85.7853	85.6680	85.5509	85.4340
0.33	85.3173	85.2008	85.0845	84.9684	84.8525	84.7367	84.6212	84.5058	84.3906	84.2757
0.34	84.1608	84.0462	83.9317	83.8175	83.7034	83.5895	83.4757	83.3621	83.2487	83.1355
0.35	83.0224	82.9095	82.7968	82.6843	82.5719	82.4597	82.3476	82.2357	82.1240	82.0124
0.36	81.9010	81.7897	81.6786	81.5676	81.4568	81.3462	81.2357	81.1254	81.0152	80.9052
0.37	80.7953	80.6855	80.5759	80.4665	80.3572	80.2480	80.1390	80.0301	79.9214	79.8128
0.38	79.7043	79.5960	79.4878	79.3798	79.2719	79.1641	79.0565	78.9490	78.8416	78.7343
0.39	78.6272	78.5202	78.4133	78.3066	78.2000	78.0935	77.9872	77.8809	77.7748	77.6688
0.40	77.5629	77.4572	77.3516	77.2460	77.1470	77.0354	76.9302	76.8252	76.7202	76.6154
0.41	76.5107	76.4061	76.3016	76.1973	76.0930	75.9888	75.8848	75.7809	75.6770	75.5733
0.42	75.4697	75.3662	75.2628	75.1594	75.0562	74.9531	74.8501	74.7472	74.6444	74.5417
0.43	74.4391	74.3366	74.2342	74.1319	74.0296	73.9275	73.8255	73.7235	73.6217	73.5199
0.44	73.4183	73.3167	73.2152	73.1138	73.0125	72.9113	72.8101	72.7091	72.6081	72.5072
0.45	72.4064	72.3057	72.2051	72.1046	72.0041	71.9037	71.8034	71.7032	71.6030	71.5030
0.46	71.4030	71.3031	71.2033	71.1035	71.0038	70.9042	70.8047	70.7052	70.6058	70.5065
0.47	70.4073	70.3081	70.2090	70.1100	70.0110	69.9121	69.8133	69.7146	69.6159	69.5173
0.48	69.4187	69.3202	69.2218	69.1234	69.0251	68.9269	68.8287	68.7306	68.6326	68.5346
0.49	68.4367	68.3388	68.2410	68.1433	68.0456	67.9479	67.8504	67.7528	67.6554	67.5580

TABLE B.33 (cont.): Circular Standard Deviation, s_0, as a Function of Vector Length, r

r	0	1	2	3	4	5	6	7	8	9
0.50	67.4606	67.3633	67.2661	67.1689	67.0718	66.9747	66.8776	66.7806	66.6837	66.5868
0.51	66.4900	66.3932	66.2965	66.1998	66.1031	66.0065	65.9100	65.8135	65.7170	65.6206
0.52	65.5243	65.4279	65.3316	65.2354	65.1392	65.0431	64.9469	64.8509	64.7548	64.6588
0.53	64.5629	64.4670	64.3711	64.2752	64.1794	64.0837	63.9879	63.8922	63.7966	63.7009
0.54	63.6053	63.5098	63.4143	63.3188	63.2233	63.1279	63.0325	62.9371	62.8417	62.7464
0.55	62.6511	62.5559	62.4607	62.3655	62.2703	62.1751	62.0800	61.9849	61.8899	61.7948
0.56	61.6998	61.6048	61.5098	61.4149	61.3199	61.2250	61.1301	61.0353	60.9404	60.8456
0.57	60.7508	60.6560	60.5612	60.4664	60.3717	60.2770	60.1823	60.0876	59.9929	59.8982
0.58	59.8036	59.7089	59.6143	59.5197	59.4251	59.3305	59.2359	59.1414	59.0468	58.9523
0.59	58.8577	58.7632	58.6687	58.5742	58.4797	58.3852	58.2907	58.1962	58.1017	58.0072
0.60	57.9127	57.8182	57.7238	57.6293	57.5348	57.4404	57.3459	57.2514	57.1570	57.0625
0.61	56.9680	56.8736	56.7791	56.6846	56.5902	56.4957	56.4012	56.3067	56.2122	56.1177
0.62	56.0232	55.9287	55.8342	55.7396	55.6451	55.5505	55.4560	55.3614	55.2668	55.1722
0.63	55.0776	54.9830	54.8884	54.7938	54.6991	54.6044	54.5097	54.4150	54.3203	54.2256
0.64	54.1308	54.0361	53.9413	53.8465	53.7517	53.6568	53.5619	53.4671	53.3722	53.2772
0.65	53.1823	53.0873	52.9923	52.8973	52.8022	52.7071	52.6120	52.5169	524217	52.3266
0.66	52.2313	52.1361	52.0408	51.9455	51.8502	51.7548	51.6594	51.5640	51.4685	51.3730
0.67	51.2775	51.1819	51.0863	50.9907	50.8950	50.7993	50.7035	50.6077	50.5119	50.4160
0.68	50.3201	50.2241	50.1281	50.0321	49.9360	49.8398	49.7437	49.6474	49.5512	49.4549
0.69	49.3585	49.2621	49.1656	49.0691	48.9725	48.8759	48.7792	48.6825	48.5858	48.4889
0.70	48.3920	48.2951	48.1981	48.1011	48.0039	47.9068	47.8095	47.7123	47.6149	47.5175
0.71	47.4200	47.3225	47.2249	47.1272	47.0295	46.9317	46.8338	46.7359	46.6379	46.5398
0.72	46.4417	46.3435	46.2452	46.1468	46.0484	45.9499	45.8513	45.7527	45.6539	45.5551
0.73	45.4562	45.3573	45.2582	45.1591	45.0599	44.9606	44.8612	44.7617	44.6622	44.5625
0.74	44.4628	44.3630	44.2631	44.1631	44.0630	43.9628	43.8625	43.7621	43.6617	43.5611
0.75	43.4604	43.3597	43.2588	43.1578	43.0568	42.9556	42.8543	42.7529	42.6515	42.5499
0.76	42.4482	42.3463	42.2444	42.1424	42.0402	41.9380	41.8356	41.7331	41.6305	41.5277
0.77	41.4249	41.3219	41.2188	41.1156	41.0122	40.9087	40.8051	40.7014	40.5975	40.4935
0.78	40.3894	40.2851	40.1807	40.0761	39.9715	39.8666	39.7617	39.6565	39.5513	39.4459
0.79	39.3403	39.2346	39.1288	39.0228	38.9166	38.8103	38.7038	38.5972	38.4904	38.3834
0.80	38.2763	38.1690	38.0615	37.9539	37.8461	37.7381	37.6300	37.5217	37.4132	37.3045
0.81	37.1956	37.0865	36.9773	36.8679	36.7583	36.6484	36.5384	36.4282	36.3178	36.2072
0.82	36.0964	35.9854	35.8742	35.7628	35.6511	35.5393	35.4272	35.3149	35.2024	35.0896
0.83	34.9767	34.8635	34.7501	34.6364	34.5225	34.4084	34.2940	34.1793	34.0645	33.9493
0.84	33.8340	33.7183	33.6024	33.4863	33.3698	33.2531	33.1362	33.0189	32.9014	32.7836
0.85	32.6655	32.5471	32.4285	32.3095	32.1902	32.0707	31.9508	31.8306	31.7101	31.5893
0.86	31.4682	31.3467	31.2249	31.1028	30.9803	30.8575	30.7343	30.6108	30.4869	30.3627
0.87	30.2381	30.1131	29.9877	29.8620	29.7359	29.6094	29.4825	29.3552	29.2274	29.0993
0.88	28.9708	28.8418	28.7124	28.5825	28.4522	28.3215	28.1903	28.0586	27.9265	27.7938
0.89	27.6607	27.5271	27.3930	27.2584	27.1233	26.9877	26.8515	26.7148	26.5775	26.4397
0.90	26.3013	26.1623	26.0227	25.8826	25.7418	25.6004	25.4584	25.3158	25.1725	25.0285
0.91	24.8839	24.7386	24.5925	24.4458	24.2984	24.1502	24.0012	23.8515	23.7011	23.5498
0.92	23.3977	23.2448	23.0910	22.9364	22.7808	22.6244	22.4671	22.3088	22.1496	21.9894
0.93	21.8282	21.6660	21.5027	21.3384	21.1729	21.0062	20.8286	20.6697	20.4996	20.3283
0.94	20.1556	19.9817	19.8064	19.6298	19.4517	19.2722	190912	18.9087	18.7246	18.5.388
0.95	18.3513	18.1622	17.9712	17.7784	17.5837	17.3870	17.1882	16.9874	16.7843	16.5790
0.96	16.3714	16.1612	15.9486	15.7333	15.5152	15.2943	15.0703	14.8432	14.6128	14.3790
0.97	14.1415	13.9003	13.6550	13.4055	13.1516	12.8929	12.6292	12.3601	12.0854	11.8045
0.98	11.5171	11.2226	10.9205	10.6101	10.2907	99614	9.6212	9.2689	8.9030	8.5218
0.99	8.1232	7.7044	7.2620	6.7912	6.2859	5.7368	5.1298	4.4414	3.6255	2.5630
1.00	0.0000									

Values of s_0 are given in degrees, by Equation 26.21.

TABLE B.34: Circular Values of z for Rayleigh's Test for Circular Uniformity

n	α: 0.50	0.20	0.10	0.05	0.02	0.01	0.005	0.002	0.001
6	0.734	1.639	2.274	2.865	3.576	4.058	4.491	4.985	5.297
7	0.727	1.634	2.278	2.885	3.627	4.143	4.617	5.181	5.556
8	0.723	1.631	2.281	2.899	3.665	4.205	4.710	5.322	5.743
9	0.719	1.628	2.283	2.910	3.694	4.252	4.780	5.430	5.885
10	0.717	1.626	2.285	2.919	3.716	4.289	4.835	5.514	5.996
11	0.715	1.625	2.287	2.926	3.735	4.319	4.879	5.582	6.085
12	0.713	1.623	2.288	2.932	3.750	4.344	4.916	5.638	6.158
13	0.711	1.622	2.289	2.937	3.763	4.265	4.947	5.685	6.219
14	0.710	1.621	2.290	2.941	3.774	4.383	4.973	5.725	6.271
15	0.709	1.620	2.291	2.945	3.784	4.398	4.996	5.759	6.316
16	0.708	1.620	2.292	2.948	3.792	4.412	5.015	5.789	6.354
17	0.707	1.619	2.292	2.951	3.799	4.423	5.033	5.815	6.388
18	0.706	1.619	2.293	2.954	3.806	4.434	5.048	5.838	6.418
19	0.705	1.618	2.293	2.956	3.811	4.443	5.061	5.858	6.445
20	0.705	1.618	2.294	2.958	3.816	4.451	5.074	5.877	6.469
21	0.704	1.617	2.294	2.960	3.821	4.459	5.085	5.893	6.491
22	0.704	1.617	2.295	2.961	3.825	4.466	5.095	5.908	6.510
23	0.703	1.616	2.295	2.963	3.829	4.472	5.104	5.922	6.528
24	0.703	1.616	2.295	2.964	3.833	4.478	5.112	5.935	6.544
25	0.702	1.616	2.296	2.966	3.836	4.483	5.120	5.946	6.559
26	0.702	1.616	2.296	2.967	3.839	4.488	5.127	5.957	6.573
27	0.702	1.615	2.296	2.968	3.842	4.492	5.133	5.966	6.586
28	0.701	1.615	2.296	2.969	3.844	4.496	5.139	5.975	6.598
29	0.701	1.615	2.297	2.970	3.847	4.500	5.145	5.984	6.609
30	0.701	1.615	2.297	2.971	3.849	4.504	5.150	5.992	6.619
32	0.700	1.614	2.297	2.972	3.853	4.510	5.159	6.006	6.637
34	0.700	1.614	2.297	2.974	3.856	4.516	5.168	6.018	6.654
36	0.700	1.614	2.298	2.975	3.859	4.521	5.175	6.030	6.668
38	0.699	1.614	2.298	2.976	3.862	4.525	5.182	6.039	6.681
40	0.699	1.613	2.298	2.977	3.865	4.529	5.188	6.048	6.692
42	0.699	1.613	2.298	2.978	3.867	4.533	5.193	6.056	6.703
44	0.698	1.613	2.299	2.979	3.869	4.536	5.198	6.064	6.712
46	0.698	1.613	2.299	2.979	3.871	4.539	5.202	6.070	6.721
48	0.698	1.613	2.299	2.980	3.873	4.542	5.206	6.076	6.729
50	0.698	1.613	2.299	2.981	3.874	4.545	5.210	6.082	6.736
55	0.697	1.612	2.299	2.982	3.878	4.550	5.218	6.094	6.752
60	0.697	1.612	2.300	2.983	3.881	4.555	5.225	6.104	6.765
65	0.697	1.612	2.300	2.984	3.883	4.559	5.231	6.113	6.776
70	0.696	1.612	2.300	2.985	3.885	4.562	5.235	6.120	6.786
75	0.696	1.612	2.300	2.986	3.887	4.565	5.240	6.127	6.794
80	0.696	1.611	2.300	2.986	3.889	4.567	5.243	6.132	6.801
90	0.696	1.611	2.301	2.987	3.891	4.572	5.249	6.141	6.813
100	0.695	1.611	2.301	2.988	3.893	4.575	5.254	6.149	6.822
120	0.695	1.611	2.301	2.990	3.896	4.580	5.262	6.160	6.837
140	0.695	1.611	2.301	2.990	3.899	4.584	5.267	6.168	6.847
160	0.695	1.610	2.301	2.991	3.900	4.586	5.271	6.174	6.855
180	0.694	1.610	2.302	2.992	3.902	4.588	5.274	6.178	6.861
200	0.694	1.610	2.302	2.992	3.903	4.590	5.276	6.182	6.865
300	0.694	1.610	2.302	2.993	3.906	4.595	5.284	6.193	6.879
500	0.694	1.610	2.302	2.994	3.908	4.599	5.290	6.201	6.891
∞	0.6931	1.6094	2.3026	2.9957	3.9120	4.6052	5.2983	6.2146	6.9078

The values in Appendix Table B.34 were computed using Durand and Greenwood's Equation 6 (1958). This procedure was found to give slightly more accurate results than Durand and Greenwood's Equation 4, distinctly better results than the Pearson curve approximation, and very much better results than the chi-square approximation (Stephens, 1969a). By examining the exact critical values of Greenwood and Durand (1955), we see that the preceding tabled values for $\alpha = 0.05$ are accurate to the third decimal place for n as small as 8, and for $\alpha = 0.01$ for n as small as 10. For n as small as 6, none of the tabled values for $\alpha = 0.05$ or 0.01 has a relative error greater than 0.3%.

Examples:

$$Z_{0.05,80} = 2.986 \quad \text{and} \quad Z_{0.01,32} = 4.510$$

As n increases, the critical values become closer to $\chi^2_{\alpha,2}/2$.

TABLE B.35: Critical Values of u for the V Test of Circular Uniformity

n	α: 0.25	0.10	0.05	0.025	0.01	0.005	0.0025	0.001	0.0005
8	0.688	1.296	1.649	1.947	2.280	2.498	2.691	2.916	3.066
9	0.687	1.294	1.649	1.948	2.286	2.507	2.705	2.937	3.094
10	0.685	1.293	1.648	1.950	2.290	2.514	2.716	2.954	3.115
11	0.684	1.292	1.648	1.950	2.293	2.520	2.725	2.967	3.133
12	0.684	1.291	1.648	1.951	2.296	2.525	2.732	2.978	3.147
13	0.683	1.290	1.647	1.952	2.299	2.529	2.738	2.987	3.159
14	0.682	1.290	1.647	1.953	2.301	2.532	2.743	2.995	3.169
15	0.682	1.289	1.647	1.953	2.302	2.535	2.748	3.002	3.177
16	0.681	1.289	1.647	1.953	2.304	2.538	2.751	3.008	3.185
17	0.681	1.288	1.647	1.954	2.305	2.540	2.755	3.013	3.191
18	0.681	1.288	1.647	1.954	2.306	2.542	2.758	3.017	3.197
19	0.680	1.287	1.647	1.954	2.308	2.544	2.761	3.021	3.202
20	0.680	1.287	1.646	1.955	2.308	2.546	2.763	3.025	3.207
21	0.680	1.287	1.646	1.955	2.309	2.547	2.765	3.028	3.211
22	0.679	1.287	1.646	1.955	2.310	2.549	2.767	3.031	3.215
23	0.679	1.286	1.646	1.955	2.311	2.550	2.769	3.034	3.218
24	0.679	1.286	1.646	1.956	2.311	2.551	2.770	3.036	3.221
25	0.679	1.286	1.646	1.956	2.312	2.552	2.772	3.038	3.224
26	0.679	1.286	1.646	1.956	2.313	2.553	2.773	3.040	3.227
27	0.678	1.286	1.646	1.956	2.313	2.554	2.775	3.042	3.229
28	0.678	1.285	1.646	1.956	2.314	2.555	2.776	3.044	3.231
29	0.678	1.285	1.646	1.956	2.314	2.555	2.777	3.046	3.233
30	0.678	1.285	1.646	1.957	2.315	2.556	2.778	3.047	3.235
32	0.678	1.285	1.646	1.957	2.315	2.557	2.780	3.050	3.239
34	0.678	1.285	1.646	1.957	2.316	2.558	2.781	3.052	3.242
36	0.677	1.285	1.646	1.957	2.316	2.559	2.783	3.054	3.245
38	0.677	1.284	1.646	1.957	2.317	2.560	2.784	3.056	3.247
40	0.677	1.284	1.646	1.957	2.317	2.561	2.785	3.058	3.249
42	0.677	1.284	1.646	1.958	2.318	2.562	2.786	3.060	3.251
44	0.677	1.284	1.646	1.958	2.318	2.562	2.787	3.061	3.253
46	0.677	1.284	1.646	1.958	2.319	2.563	2.788	3.062	3.255
48	0.677	1.284	1.645	1.958	2.319	2.564	2.789	3.063	3.256
50	0.677	1.284	1.645	1.958	2.319	2.564	2.790	3.065	3.258
55	0.676	1.284	1.645	1.958	2.320	2.565	2.791	3.067	3.261
60	0.676	1.283	1.645	1.958	2.320	2.566	2.793	3.069	3.263
65	0.676	1.283	1.645	1.958	2.321	2.567	2.794	3.071	3.265
70	0.676	1.283	1.645	1.958	2.321	2.567	2.795	3.072	3.267
75	0.676	1.283	1.645	1.959	2.322	2.568	2.796	3.073	3.269
80	0.676	1.283	1.645	1.959	2.322	2.568	2.796	3.074	3.270
90	0.676	1.283	1.645	1.959	2.322	2.569	2.797	3.076	3.272
100	0.676	1.283	1.645	1.959	2.323	2.570	2.798	3.077	3.274
120	0.675	1.282	1.645	1.959	2.323	2.571	2.800	3.080	3.277
140	0.675	1.282	1.645	1.959	2.324	2.572	2.801	3.081	3.279
160	0.675	1.282	1.645	1.959	2.324	2.572	2.802	3.082	3.280
180	0.675	1.282	1.645	1.959	2.324	2.573	2.802	3.083	3.282
200	0.675	1.282	1.645	1.959	2.325	2.573	2.803	3.084	3.282
300	0.675	1.282	1.645	1.960	2.325	2.574	2.804	3.086	3.285
∞	0.6747	1.2818	1.6449	1.9598	2.3256	2.5747	2.8053	3.0877	3.2873

The values in Appendix Table B.35 were computed using Durand and Greenwood's Equation 7 (1958).
Examples:

$$u_{0.05,25} = 1.646 \quad \text{and} \quad u_{0.01,20} = 2.308$$

TABLE B.36: Critical Values of m for the Hodges-Ajne Test for Circular Uniformity

n	$\alpha \leq 0.50$	0.20	0.10	0.05	0.02	0.01	0.005	0.002	0.001
4	0								
5	0								
6	0	0							
7	0	0							
8	1	0	0						
9	1	0	0	0					
10	1	1	0	0	0				
11	2	1	1	0	0				
12	2	1	1	0	0	0			
13	3	2	1	1	0	0	0		
14	3	2	1	1	0	0	0	0	
15	3	2	2	1	1	0	0	0	0
16	4	3	2	2	1	1	0	0	0
17	4	3	2	2	1	1	1	0	0
18	4	3	3	2	2	1	1	0	0
19	5	4	3	3	2	2	1	1	0
20	5	4	3	3	2	2	1	1	1
21	6	4	4	3	3	2	2	1	1
22	6	5	4	4	3	2	2	2	1
23	6	5	4	4	3	3	2	2	1
24	7	6	5	4	3	3	3	2	2
25	7	6	5	5	4	3	3	2	2
26	8	6	6	5	4	4	3	3	2
27	8	7	6	5	4	4	4	3	3
28	8	7	6	6	5	4	4	3	3
29	9	7	7	6	5	5	4	4	3
30	9	8	7	6	6	5	4	4	3
31	10	8	7	7	6	5	5	4	4
32	10	9	8	7	6	6	5	4	4
33	11	9	8	7	7	6	5	5	4
34	11	9	9	8	7	6	6	5	5
35	11	10	9	8	7	7	6	5	5
36	12	10	9	9	8	7	6	6	5
37	12	11	10	9	8	7	7	6	6
38	13	11	10	9	8	8	7	6	6
39	13	11	10	10	9	8	7	7	6
40	13	12	11	10	9	8	8	7	7
41	14	12	11	10	9	9	8	7	7
42	14	13	12	11	10	9	9	8	7
43	15	13	12	11	10	9	9	8	8
44	15	13	12	12	11	10	9	8	8
45	16	14	13	12	11	10	10	9	8
46	16	14	13	12	11	11	10	9	9
47	16	15	14	13	12	11	10	10	9
48	17	15	14	13	12	11	11	10	9
49	17	15	14	13	12	12	11	10	10
50	18	16	15	14	13	12	11	11	10

The critical values in Appendix Table B.36 are the values of m for which $P \leq \alpha$, where P is calculated by Equation 27.7, which is from Hodges (1955). To determine P for $n > 50$, we may use the approximation shown as Equation 27.8, which is from Ajne (1968). The accuracy of the approximation is shown below, as true probability—approximate probability for the largest true probability $\leq \alpha$:

n	α: 0.50	0.20	0.10	0.05	0.02	0.01	0.005	0.002′	0.001
30	0.0026	−0.0029	−0.0047	−0.0038	−0.0038	−0.0021	−0.00089	−0.00089	−0.00029
40	0.0016	−0.0020	−0.0034	−0.0032	−0.0021	−0.0030	−0.00095	−0.00052	−0.00052
50	0.0039	−0.0017	−0.0027	−0.0026	−0.0019	−0.0012	−0.00063	−0.00063	−0.00029

TABLE B.37: Correction Factor, K, for the Watson and Williams Test

r	0	1	2	3	4	5	6	7	8	9
0.00		188.4989	94.7472	63.5015	47.8749	38.4992	32.2498	27.7851	24.4367	21.8325
0.01	19.7489	18.0444	16.6239	15.4219	14.3916	13.4986	12.7173	12.0278	11.4150	10.8667
0.02	10.3731	9.9266	9.5206	9.1500	8.8103	8.4976	8.2091	7.9419	7.6938	7.4628
0.03	7.2472	7.0455	6.8564	6.6787	6.5115	6.3539	6.2050	6.0641	5.9306	5.8040
0.04	5.6837	5.5693	5.4603	5.3564	5.2572	5.1625	5.0718	4.9850	4.9017	4.8219
0.05	4.7453	4.6717	4.6009	4.5328	4.4672	4.4039	4.3430	4.2841	4.2273	4.1724
0.06	4.1194	4.0680	4.0184	3.9703	3.9237	3.8785	3.8347	3.7922	3.7510	3.7109
0.07	3.6720	3.6342	3.5974	3.5616	3.5268	3.4930	3.4600	3.4278	3.3965	3.3666
0.08	3.3362	3.3072	3.2789	3.2512	3.2243	3.1979	3.1722	3.1470	3.1224	3.0984
0.09	3.0749	3.0519	3.0294	3.0074	2.9858	2.9648	2.9441	2.9239	2.9041	2.8846
0.10	2.8656	2.8469	2.8286	2.8107	2.7931	2.7758	2.7589	2.7423	2.7259	2.7099
0.11	2.6942	2.6787	2.6636	2.6487	2.6340	2.6196	2.6055	2.5915	2.5779	2.5644
0.12	2.5512	2.5382	2.5254	2.5128	2.5004	2.4882	2.4762	2.4644	2.4528	2.4413
0.13	2.4301	2.4189	2.4080	2.3972	2.3866	2.3762	2.3658	2.3557	2.3457	2.3358
0.14	2.3261	2.3165	2.3070	2.2977	2.2885	2.2794	2.2705	2.2616	2.2529	2.2443
0.15	2.2358	2.2275	2.2192	2.2110	2.2030	2.1950	2.1872	2.1794	2.1718	2.1642
0.16	2.1567	2.1494	2.1421	2.1349	2.1278	2.1208	2.1138	2.1070	2.1002	2.0935
0.17	2.0868	2.0803	2.0738	2.0674	2.0611	2.0549	2.0487	2.0426	2.0365	2.0305
0.18	2.0246	2.0188	2.0130	2.0072	2.0016	1.9960	1.9904	1.9849	1.9795	1.9741
0.19	1.9688	1.9635	1.9583	1.9532	1.9481	1.9430	1.9380	1.9331	1.9282	1.9233
0.20	1.9185	1.9137	1.9090	1.9043	1.8997	1.8951	1.8906	1.8861	1.8817	1.8772
0.21	1.8729	1.8685	1.8643	1.8600	1.8558	1.8516	1.8475	1.8434	1.8393	1.8353
0.22	1.8313	1.8274	1.8234	1.8195	1.8157	1.8119	1.8081	1.8043	1.8006	1.7969
0.23	1.7933	1.7896	1.7860	1.7825	1.7789	1.7754	1.7719	1.7685	1.7651	1.7617
0.24	1.7583	1.7550	1.7516	1.7484	1.7451	1.7419	1.7386	1.7355	1.7323	1.7292
0.25	1.7261	1.7230	1.7199	1.7169	1.7138	1.7108	1.7079	1.7049	1.7020	1.6991
0.26	1.6962	1.6933	1.6905	1.6877	1.6849	1.6821	1.6793	1.6766	1.6739	1.6712
0.27	1.6685	1.6658	1.6632	1.6606	1.6579	1.6554	1.6528	1.6502	1.6477	1.6452
0.28	1.6427	1.6402	1.6377	1.6353	1.6328	1.6304	1.6280	1.6256	1.6233	1.6209
0.29	1.6186	1.6162	1.6139	1.6116	1.6094	1.6071	1.6048	1.6026	1.6004	1.5982
0.30	1.5960	1.5938	1.5916	1.5895	1.5873	1.5852	1.5831	1.5810	1.5789	1.5768
0.31	1.5748	1.5727	1.5707	1.5687	1.5667	1.5647	1.5627	1.5607	1.5587	1.5568
0.32	1.5548	1.5529	1.5510	1.5491	1.5472	1.5453	1.5434	1.5416	1.5397	1.5379
0.33	1.5360	1.5342	1.5324	1.5306	1.5288	1.5270	1.5253	1.5235	1.5217	1.5200
0.34	1.5183	1.5165	1.5148	1.5131	1.5114	1.5097	1.5081	1.5064	1.5047	1.5031
0.35	1.5014	1.4998	1.4982	1.4966	1.4950	1.4934	1.4918	1.4902	1.4886	1.4871
0.36	1.4855	1.4839	1.4824	1.4809	1.4793	1.4778	1.4763	1.4748	1.4733	1.4718
0.37	1.4703	1.4689	1.4674	1.4659	1.4645	1.4630	1.4616	1.4602	1.4587	1.4573
0.38	1.4559	1.4545	1.4531	1.4517	1.4503	1.4490	1.4476	1.4462	1.4449	1.4435
0.39	1.4422	1.4408	1.4395	1.4382	1.4368	1.4355	1.4342	1.4329	1.4316	1.4303
0.40	1.4290	1.4277	1.4265	1.4252	1.4239	1.4227	1.4214	1.4202	1.4189	1.4177
0.41	1.4165	1.4152	1.4140	1.4128	1.4116	1.4104	1.4092	1.4080	1.4068	1.4056
0.42	1.4044	1.4033	1.4021	1.4009	1.3998	1.3986	1.3975	1.3963	1.3952	1.3940
0.43	1.3929	1.3918	1.3907	1.3895	1.3884	1.3873	1.3862	1.3851	1.3840	1.3829
0.44	1.3818	1.3808	1.3797	1.3786	1.3775	1.3765	1.3754	1.3744	1.3733	1.3723
0.45	1.3712	1.3702	1.3691	1.3681	1.3671	1.3660	1.3650	1.3640	1.3630	1.3620
0.46	1.3610	1.3600	1.3590	1.3580	1.3570	1.3560	1.3550	1.3540	1.3530	1.3521
0.47	1.3511	1.3501	1.3492	1.3482	1.3472	1.3463	1.3453	1.3444	1.3434	1.3425
0.48	1.3416	1.3406	1.3397	1.3388	1.3378	1.3369	1.3360	1.3351	1.3342	1.3333
0.49	1.3324	1.3315	1.3306	1.3297	1.3288	1.3279	1.3270	1.3261	1.3252	1.3243
0.50	1.3235	1.3226	1.3217	1.3209	1.3200	1.3191	1.3183	1.3174	1.3166	1.3157
0.51	1.3148	1.3140	1.3132	1.3123	1.3115	1.3106	1.3098	1.3090	1.3081	1.3073
0.52	1.3065	1.3057	1.3049	1.3040	1.3032	1.3024	1.3016	1.3008	1.3000	1.2992
0.53	1.2984	1.2976	1.2968	1.2960	1.2952	1.2944	1.2936	1.2929	1.2921	1.2913
0.54	1.2905	1.2897	1.2890	1.2882	1.2874	1.2867	1.2859	1.2851	1.2844	1.2836
0.55	1.2829	1.2821	1.2814	1.2806	1.2799	1.2791	1.2784	1.2776	1.2769	1.2762
0.56	1.2754	1.2747	1.2740	1.2732	1.2725	1.2718	1.2710	1.2703	1.2696	1.2689
0.57	1.2682	1.2674	1.2667	1.2660	1.2653	1.2646	1.2639	1.2632	1.2625	1.2618
0.58	1.2611	1.2604	1.2597	1.2590	1.2583	1.2576	1.2569	1.2562	1.2555	1.2548
0.59	1.2542	1.2535	1.2528	1.2521	1.2514	1.2508	1.2501	1.2494	1.2487	1.2481

TABLE B.37 (cont.): Correction Factor, K, for the Watson and Williams Test

r	0	1	2	3	4	5	6	7	8	9
0.60	1.2474	1.2467	1.2461	1.2454	1.2447	1.2441	1.2434	1.2428	1.2421	1.2414
0.61	1.2408	1.2401	1.2395	1.2388	1.2382	1.2375	1.2369	1.2362	1.2356	1.2350
0.62	1.2343	1.2337	1.2330	1.2324	1.2318	1.2311	1.2305	1.2298	1.2292	1.2286
0.63	1.2280	1.2273	1.2267	1.2261	1.2254	1.2248	1.2242	1.2236	1.2230	1.2223
0.64	1.2217	1.2211	1.2205	1.2199	1.2193	1.2186	1.2180	1.2174	1.2168	1.2162
0.65	1.2156	1.2150	1.2144	1.2138	1.2132	1.2126	1.2120	1.2114	1.2108	1.2102
0.66	1.2096	1.2090	1.2084	1.2078	1.2072	1.2066	1.2060	1.2054	1.2048	1.2042
0.67	1.2036	1.2030	1.2024	1.2018	1.2013	1.2007	1.2001	1.1995	1.1989	1.1983
0.68	1.1977	1.1972	1.1966	1.1960	1.1954	1.1948	1.1943	1.1937	1.1931	1.1925
0.69	1.1920	1.1914	1.1908	1.1902	1.1897	1.1891	1.1885	1.1879	1.1874	1.1868
0.70	1.1862	1.1857	1.1851	1.1845	1.1840	1.1834	1.1828	1.1823	1.1817	1.1811
0.71	1.1806	1.1800	1.1794	1.1789	1.1783	1.1777	1.1772	1.1766	1.1761	1.1755
0.72	1.1749	1.1744	1.1738	1.1733	1.1727	1.1721	1.1716	1.1710	1.1705	1.1699
0.73	1.1694	1.1688	1.1682	1.1677	1.1671	1.1666	1.1660	1.1655	1.1649	1.1644
0.74	1.1638	1.1633	1.1627	1.1621	1.1616	1.1610	1.1605	1.1599	1.1594	1.1588
0.75	1.1583	1.1577	1.1572	1.1566	1.1561	1.1555	1.1550	1.1544	1.1539	1.1533
0.76	1.1528	1.1522	1.1517	1.1511	1.1505	1.1500	1.1494	1.1489	1.1483	1.1478
0.77	1.1472	1.1467	1.1461	1.1456	1.1450	1.1445	1.1439	1.1434	1.1428	1.1423
0.78	1.1417	1.1412	1.1406	1.1401	1.1395	1.1389	1.1384	1.1378	1.1373	1.1367
0.79	1.1362	1.1356	1.1351	1.1345	1.1340	1.1334	1.1328	1.1323	1.1317	1.1312
0.80	1.1306	1.1300	1.1295	1.1289	1.1284	1.1278	1.1272	1.1267	1.1261	1.1256
0.81	1.1250	1.1244	1.1239	1.1233	1.1227	1.1222	1.1216	1.1210	1.1205	1.1199
0.82	1.1193	1.1188	1.1182	1.1176	1.1170	1.1165	1.1159	1.1153	1.1147	1.1142
0.83	1.1136	1.1130	1.1124	1.1119	1.1113	1.1107	1.1101	1.1095	1.1090	1.1084
0.84	1.1078	1.1072	1.1066	1.1060	1.1054	1.1049	1.1043	1.1037	1.1031	1.1025
0.85	1.1019	1.1013	1.1007	1.1001	1.0995	1.0989	1.0983	1.0977	1.0971	1.0965
0.86	1.0959	1.0953	1.0947	1.0941	1.0935	1.0928	1.0922	1.0916	1.0910	1.0904
0.87	1.0898	1.0892	1.0885	1.0879	1.0873	1.0867	1.0861	1.0854	1.0848	1.0842
0.88	1.0835	1.0829	1.0823	1.0816	1.0810	1.0804	1.0797	1.0791	1.0785	1.0778
0.89	1.0772	1.0765	1.0759	1.0752	1.0746	1.0740	1.0733	1.0727	1.0720	1.0713
0.90	1.0707	1.0700	1.0694	1.0687	1.0681	1.0674	1.0667	1.0661	1.0654	1.0647
0.91	1.0641	1.0634	1.0627	1.0621	1.0614	1.0607	1.0601	1.0594	1.0587	1.0580
0.92	1.0573	1.0567	1.0560	1.0553	1.0546	1.0539	1.0533	1.0526	1.0519	1.0512
0.93	1.0505	1.0498	1.0491	1.0484	1.0477	1.0470	1.0463	1.0456	1.0449	1.0443
0.94	1.0436	1.0429	1.0422	1.0414	1.0407	1.0400	1.0393	1.0386	1.0379	1.0372
0.95	1.0365	1.0358	1.0351	1.0344	1.0337	1.0330	1.0322	1.0315	1.0308	1.0301
0.96	1.0294	1.0287	1.0279	1.0272	1.0265	1.0258	1.0251	1.0243	1.0236	1.0229
0.97	1.0222	1.0214	1.0207	1.0200	1.0192	1.0185	1.0178	1.0170	1.0163	1.0156
0.98	1.0148	1.0141	1.0134	1.0126	1.0119	1.0112	1.0104	1.0097	1.0089	1.0082
0.99	1.0075	1.0067	1.0060	1.0052	1.0045	1.0037	1.0030	1.0022	1.000*	1.000*

*No correction is needed for $r \geq 0.998$.

Values of K were determined as $1 + 3/8k$, where k was obtained using Equation 6.3.14 of Mardia (1972: 155), and Equations 9.8.1–9.8.4 of Olver (1964).

Examples:

$r = 0.743$, $K = 1.1621$ and $r = 0.814$, $K = 1.227$

TABLE B.38a: Critical Values of Watson's Two-Sample U^2

n_1	n_2	α : 0.50	0.20	0.10	0.05	0.02	0.01	0.005	0.002	0.001
4	4	0.1172	0.1875	—	—	—	—	—	—	—
4	5	0.0815	0.2037	0.2037	—	—	—	—	—	—
4	6	0.0875	0.1333	0.2167	0.2167	—	—	—	—	—
4	7	0.0844	0.1299	0.1688	0.2273	—	—	—	—	—
4	8	0.0903	0.1319	0.1632	0.2361	—	—	—	—	—
4	9	0.0855	0.1282	0.1752	0.2436	0.2436	—	—	—	—
4	10	0.0804	0.1232	0.1571	0.2018	0.2500	—	—	—	—
4	11	0.0828	0.1253	0.1556	0.1949	0.2556	—	—	—	—
4	12	0.0781	0.1302	0.1563	0.2031	0.2604	0.2604	—	—	—
4	13	0.0792	0.1244	0.1538	0.1855	0.2647	0.2647	—	—	—
4	14	0.0780	0.1227	0.1534	0.1931	0.2298	0.2685	—	—	—
4	15	0.0789	0.1228	0.1561	0.1807	0.2228	0.2719	0.2719	—	—
4	16	0.0781	0.1250	0.1531	0.1836	0.2281	0.2750	0.2750	—	—
4	17	0.0775	0.1223	0.1531	0.1839	0.2330	0.2778	0.2778	—	—
4	18	0.0764	0.1212	0.1490	0.1818	0.2197	0.2481	0.2803	—	—
4	19	0.0755	0.1213	0.1533	0.1796	0.2220	0.2517	0.2826	—	—
4	20	0.0764	0.1201	0.1535	0.1842	0.2264	0.2451	0.2847	—	—
4	21	0.0752	0.1200	0.1514	0.1819	0.2143	0.2486	0.2867	0.2867	—
4	22	0.0756	0.1211	0.1508	0.1823	0.2185	0.2517	0.2885	0.2885	—
4	23	0.0751	0.1194	0.1508	0.1814	0.2177	0.2394	0.2636	0.2901	—
4	24	0.0755	0.1202	0.1499	0.1797	0.2184	0.2411	0.2660	0.2917	—
4	25	0.0752	0.1200	0.1497	0.1814	0.2152	0.2441	0.2600	0.2931	—
4	26	0.0752	0.1191	0.1486	0.1816	0.2175	0.2396	0.2624	0.2944	—
4	27	0.0753	0.1189	0.1505	0.1786	0.2151	0.2360	0.2646	0.2957	0.2957
4	28	0.0748	0.1203	0.1496	0.1775	0.2165	0.2388	0.2667	0.2969	0.2969
4	29	0.0749	0.1198	0.1491	0.1794	0.2165	0.2369	0.2557	0.2980	0.2980
4	30	0.0745	0.1196	0.1493	0.1797	0.2140	0.2395	0.2578	0.2990	0.2990
5	5	0.0890	0.1610	0.2250	0.2250	—	—	—	—	—
5	6	0.0848	0.1333	0.1818	0.2424	—	—	—	—	—
5	7	0.0855	0.1284	0.1712	0.1998	0.2569	—	—	—	—
5	8	0.0846	0.1308	0.1654	0.2154	0.2692	—	—	—	—
5	9	0.0798	0.1242	0.1591	0.1909	0.2798	0.2798	—	—	—
5	10	0.0836	0.1236	0.1609	0.1956	0.2409	0.2889	0.2889	—	—
5	11	0.0810	0.1241	0.1560	0.1901	0.2287	0.2969	0.2969	—	—
5	12	0.0784	0.1235	0.1549	0.1863	0.2255	0.2608	0.3039	—	—
5	13	0.0777	0.1256	0.1563	0.1837	0.2298	0.2692	0.3102	—	—
5	14	0.0782	0.1218	0.1534	0.1820	0.2211	0.2571	0.2767	0.3158	—
5	15	0.0782	0.1235	0.1515	0.1835	0.2248	0.2515	0.2835	0.3208	—
5	16	0.0766	0.1206	0.1552	0.1825	0.2230	0.2552	0.2897	0.3254	—
5	17	0.0761	0.1199	0.1520	0.1820	0.2205	0.2472	0.2782	0.3295	0.3295
5	18	0.0763	0.1208	0.1536	0.1797	0.2164	0.2464	0.2715	0.3333	0.3333
5	19	0.0754	0.1201	0.1517	0.1824	0.2193	0.2526	0.2745	0.3052	0.3368
5	20	0.0760	0.1216	0.1520	0.1824	0.2200	0.2416	0.2664	0.3096	0.3400
5	21	0.0755	0.1195	0.1510	0.1810	0.2206	0.2448	0.2712	0.2990	0.3429
5	22	0.0756	0.1201	0.1524	0.1820	0.2191	0.2426	0.2689	0.3033	0.3457
5	23	0.0755	0.1196	0.1513	0.1811	0.2178	0.2451	0.2737	0.2960	0.3209
5	24	0.0747	0.1195	0.1511	0.1810	0.2190	0.2437	0.2736	0.2983	0.3241

TABLE B.38a (cont.): Critical Values of Watson's Two-Sample U^2

n_1	n_2	α : 0.50	0.20	0.10	0.05	0.02	0.01	0.005	0.002	0.001
5	25	0.0754	0.1197	0.1517	0.1810	0.2168	0.2461	0.2674	0.3021	0.3272
5	26	0.0749	0.1186	0.1514	0.1806	0.2189	0.2447	0.2675	0.2943	0.3176
5	27	0.0748	0.1193	0.1508	0.1804	0.2165	0.2443	0.2674	0.2975	0.3207
5	28	0.0746	0.1188	0.1512	0.1802	0.2170	0.2417	0.2694	0.2937	0.3136
5	29	0.0743	0.1189	0.1510	0.1802	0.2171	0.2443	0.2666	0.2970	0.3153
5	30	0.0743	0.1189	0.1512	0.1802	0.2160	0.2419	0.2678	0.2979	0.3181
6	6	0.0880	0.1319	0.1713	0.2060	0.2639	—	—	—	—
6	7	0.0806	0.1209	0.1538	0.1941	0.2821	0.2821	—	—	—
6	8	0.0833	0.1265	0.1607	0.1964	0.2455	0.2976	0.2976	—	—
6	9	0.0815	0.1259	0.1556	0.1926	0.2321	0.2617	0.3111	—	—
6	10	0.0771	0.1260	0.1563	0.1896	0.2313	0.2479	0.3229	0.3229	—
6	11	0.0784	0.1212	0.1569	0.1872	0.2246	0.2620	0.2888	0.3333	—
6	12	0.0802	0.1242	0.1551	0.1829	0.2261	0.2593	0.2747	0.3426	0.3426
6	13	0.0769	0.1215	0.1538	0.1849	0.2213	0.2497	0.2780	0.3509	0.3509
6	14	0.0768	0.1220	0.1536	0.1839	0.2250	0.2506	0.2821	0.3196	0.3583
6	15	0.0762	0.1217	0.1524	0.1852	0.2201	0.2487	0.2730	0.3058	0.3651
6	16	0.0758	0.1212	0.1534	0.1823	0.2235	0.2500	0.2789	0.3078	0.3357
6	17	0.0750	0.1211	0.1526	0.1833	0.2199	0.2472	0.2745	0.3129	0.3427
6	18	0.0760	0.1211	0.1535	0.1840	0.2199	0.2461	0.2739	0.2998	0.3295
6	19	0.0751	0.1200	0.1523	0.1832	0.2204	0.2498	0.2744	0.3060	0.3298
6	20	0.0747	0.1196	0.1526	0.1824	0.2196	0.2490	0.2734	0.3077	0.3333
6	21	0.0758	0.1205	0.1523	0.1834	0.2205	0.2475	0.2734	0.3057	0.3369
6	22	0.0749	0.1204	0.1518	0.1824	0.2202	0.2473	0.2752	0.3036	0.3260
6	23	0.0745	0.1194	0.1514	0.1824	0.2194	0.2469	0.2729	0.3073	0.3273
6	24	0.0743	0.1194	0.1519	0.1826	0.2206	0.2484	0.2715	0.3056	0.3289
6	25	0.0744	0.1191	0.1514	0.1819	0.2202	0.2473	0.2731	0.3015	0.3277
6	26	0.0739	0.1188	0.1510	0.1815	0.2198	0.2464	0.2710	0.3047	0.3265
6	27	0.0741	0.1193	0.1515	0.1822	0.2200	0.2469	0.2731	0.3053	0.3281
6	28	0.0737	0.1190	0.1507	0.1821	0.2201	0.2467	0.2731	0.3039	0.3270
6	29	0.0736	0.1189	0.1511	0.1816	0.2200	0.2473	0.2719	0.3038	0.3258
6	30	0.0736	0.1193	0.1509	0.1823	0.2194	0.2471	0.2725	0.3045	0.3262
7	7	0.0791	0.1345	0.1578	0.1986	0.2511	0.3036	0.3036	—	—
7	8	0.0794	0.1198	0.1556	0.1817	0.2246	0.2722	0.3222	—	—
7	9	0.0786	0.1223	0.1560	0.1818	0.2215	0.2552	0.2909	0.3385	—
7	10	0.0773	0.1227	0.1546	0.1866	0.2269	0.2622	0.2773	0.3529	0.3529
7	11	0.0771	0.1219	0.1551	0.1839	0.2214	0.2532	0.2806	0.3225	0.3657
7	12	0.0764	0.1216	0.1541	0.1855	0.2256	0.2519	0.2757	0.3083	0.3772
7	13	0.0765	0.1216	0.1545	0.1842	0.2227	0.2523	0.2776	0.3150	0.3479
7	14	0.0761	0.1228	0.1568	0.1840	0.2248	0.2530	0.2744	0.3210	0.3337
7	15	0.0754	0.1213	0.1525	0.1845	0.2235	0.2503	0.2780	0.3118	0.3378
7	16	0.0753	0.1203	0.1530	0.1848	0.2236	0.2508	0.2772	0.3113	0.3432
7	17	0.0749	0.1204	0.1526	0.1827	0.2227	0.2500	0.2752	0.3109	0.3340
7	18	0.0749	0.1200	0.1524	0.1841	0.2235	0.2502	0.2768	0.3117	0.3346
7	20	0.0743	0.1198	0.1526	0.1832	0.2219	0.2499	0.2780	0.3081	0.3330
7	21	0.0751	0.1203	0.1534	0.1840	0.2224	0.2496	0.2782	0.3123	0.3336
7	22	0.0743	0.1196	0.1518	0.1832	0.2221	0.2512	0.2763	0.3090	0.3341
7	23	0.0739	0.1194	0.1522	0.1832	0.2226	0.2499	0.2780	0.3103	0.3327
8	8	0.0781	0.1250	0.1563	0.1836	0.2256	0.2500	0.2959	0.3438	—

TABLE B.38a (cont.): Critical Values of Watson's Two-Sample U^2

n_1	n_2	$\alpha = 0.50$	0.20	0.10	0.05	0.02	0.01	0.005	0.002	0.001
8	9	0.0784	0.1225	0.1552	0.1863	0.2255	0.2582	0.2827	0.3627	0.3627
8	10	0.0775	0.1220	0.1546	0.1852	0.2220	0.2491	0.2796	0.3359	0.3796
8	11	0.0766	0.1220	0.1543	0.1842	0.2249	0.2524	0.2799	0.3194	0.3529
8	12	0.0766	0.1208	0.1557	0.1854	0.2229	0.2521	0.2807	0.3167	0.3396
8	13	0.0754	0.1212	0.1532	0.1853	0.2237	0.2531	0.2778	0.3135	0.3446
8	14	0.0751	0.1205	0.1530	0.1855	0.2224	0.2516	0.2796	0.3137	0.3381
8	15	0.0746	0.1210	0.1536	0.1855	0.2232	0.2507	0.2783	0.3130	0.3341
8	16	0.0761	0.1220	0.1542	0.1854	0.2222	0.2531	0.2795	0.3156	0.3417
8	17	0.0747	0.1200	0.1529	0.1841	0.2241	0.2524	0.2782	0.3124	0.3388
8	18	0.0748	0.1199	0.1528	0.1840	0.2244	0.2513	0.2813	0.3152	0.3397
8	19	0.0742	0.1196	0.1527	0.1839	0.2243	0.2526	0.2799	0.3145	0.3384
8	20	0.0741	0.1196	0.1527	0.1839	0.2239	0.2527	0.2795	0.3134	0.3393
9	9	0.0770	0.1250	0.1552	0.1867	0.2251	0.2663	0.2855	0.3404	0.3843
9	10	0.0760	0.1216	0.1544	0.1860	0.2257	0.2538	0.2865	0.3205	0.3614
9	11	0.0764	0.1208	0.1542	0.1845	0.2249	0.2552	0.2814	0.3168	0.3410
9	12	0.0767	0.1217	0.1543	0.1852	0.2257	0.2540	0.2804	0.3157	0.3395
9	13	0.0755	0.1205	0.1532	0.1850	0.2247	0.2526	0.2798	0.3187	0.3389
9	14	0.0752	0.1201	0.1532	0.1843	0.2243	0.2526	0.2809	0.3168	0.3409
9	15	0.0757	0.1201	0.1535	0.1850	0.2245	0.2541	0.2831	0.3152	0.3393
9	16	0.0744	0.1200	0.1533	0.1850	0.2244	0.2539	0.2822	0.3172	0.3439
10	10	0.0750	0.1225	0.1545	0.1850	0.2250	0.2545	0.2825	0.3170	0.3450
10	11	0.0756	0.1215	0.1544	0.1856	0.2237	0.2548	0.2791	0.3172	0.3405
10	12	0.0758	0.1212	0.1534	0.1848	0.2246	0.2545	0.2818	0.3155	0.3409
10	13	0.0749	0.1204	0.1532	0.1853	0.2254	0.2542	0.2816	0.3184	0.3452
10	14	0.0749	0.1201	0.1535	0.1847	0.2252	0.2550	0.2823	0.3181	0.3439
10	15	0.0747	0.1211	0.1536	0.1856	0.2256	0.2549	0.2837	0.3189	0.3440
11	11	0.0760	0.1211	0.1541	0.1857	0.2262	0.2540	0.2826	0.3194	0.3442
11	12	0.0751	0.1206	0.1535	0.1851	0.2253	0.2543	0.2839	0.3182	0.3439
11	13	0.0746	0.1206	0.1532	0.1853	0.2255	0.2546	0.2838	0.3193	0.3461
12	12	0.0752	0.1215	0.1528	0.1863	0.2266	0.2558	0.2844	0.3192	0.3438
13	13	0.070	0.117	0.150	0.183	0.225	0.257	0.288	0.329	0.360
14	14	0.070	0.117	0.151	0.183	0.226	0.258	0.289	0.330	0.361
16	16	0.070	0.117	0.151	0.184	0.227	0.259	0.291	0.332	0.364
18	18	0.070	0.117	0.151	0.184	0.228	0.260	0.292	0.334	0.366
20	20	0.069	0.117	0.151	0.185	0.228	0.261	0.293	0.335	0.367
25	25	0.069	0.117	0.152	0.185	0.229	0.262	0.295	0.338	0.370
30	30	0.069	0.117	0.152	0.186	0.230	0.263	0.296	0.339	0.372
35	35	0.069	0.117	0.152	0.186	0.231	0.264	0.297	0.340	0.373
40	40	0.069	0.117	0.152	0.186	0.231	0.264	0.298	0.341	0.374
50	50	0.069	0.117	0.152	0.187	0.231	0.265	0.299	0.343	0.376
60	60	0.069	0.117	0.152	0.187	0.232	0.266	0.299	0.343	0.377
80	80	0.069	0.117	0.152	0.187	0.232	0.266	0.300	0.344	0.378
100	100	0.069	0.117	0.152	0.187	0.233	0.267	0.300	0.345	0.378
∞	∞	0.0710	0.1167	0.1518	0.1869	0.2333	0.2684	0.3035	0.3500	0.3851

The four-decimal-place critical values in Table B.38a (except for sample sizes of infinity) were obtained from distributions of U^2 calculated using the method described by Burr (1964). The three-decimal-place critical values shown were computed by the approximation of Tiku (1965), using the computer algorithms of Best and Roberts (1975), Bhattacharjee (1970), International Business Machines (1968: 362), and Odeh and Evans (1974). The critical values for sample sizes of infinity were computed as

$$U^2_{\alpha,\infty,\infty} = \left(\frac{1}{2\pi^2}\right)\left[\ln\left(\frac{\alpha}{2}\right) - \ln\left\{1 + \left(\frac{\alpha}{2}\right)^3\right\}\right]$$

(Watson 1962) and should be used if sample sizes are greater than 100.

Examples:

$$U^2_{0.05,6,8} = 0.1964 \quad \text{and} \quad U^2_{0.01,10,12} = 0.2545$$

TABLE B.38b: Critical Values of Watson's One-Sample U^2

n	α: 0.50	0.20	0.10	0.05	0.02	0.01	0.005	0.002	0.001
4	0.074	0.116	0.144	0.171	0.205	0.230	0.254	0.286	0.310
5	0.073	0.116	0.146	0.175	0.211	0.238	0.264	0.299	0.324
6	0.072	0.117	0.147	0.177	0.215	0.243	0.271	0.307	0.334
7	0.071	0.117	0.148	0.179	0.218	0.247	0.275	0.313	0.341
8	0.071	0.117	0.149	0.180	0.220	0.250	0.279	0.317	0.346
9	0.071	0.117	0.149	0.181	0.221	0.252	0.281	0.321	0.350
10	0.070	0.117	0.150	0.182	0.223	0.253	0.284	0.323	0.353
11	0.070	0.117	0.150	0.182	0.224	0.255	0.285	0.325	0.356
12	0.070	0.117	0.150	0.183	0.225	0.256	0.287	0.327	0.358
13	0.070	0.117	0.150	0.183	0.225	0.257	0.288	0.329	0.360

The values of U_n^2 in Appendix Table B.38b were obtained with the approximation of Tiku (1965). For $n > 13$, Table B.38a may be employed using $U_n^2 = U_{n,n}^2$.

Examples:

$$U_{0.05,9}^2 = 0.181 \quad \text{and} \quad U_{0.01,25}^2 = 0.262$$

TABLE B.39: Critical Values of R' for the Moore Test for Circular Uniformity

n	α: 0.50	0.10	0.05	0.025	0.01	0.005	0.001
2	0.791	1.049	1.053	1.060	1.061	1 061	1.061
3	0.693	1.039	1.095	1.124	1.143	1.149	1.154
4	0.620	1.008	1.090	1.146	1.192	1.212	1.238
5	0.588	0.988	1.084	1.152	1.216	1.250	1.298
6	0.568	0.972	1.074	1.152	1.230	1.275	1.345
7	0.556	0.959	1.055	1.150	1.238	1.291	1.373
8	0.546	0.949	1.059	1.148	1.242	1.300	1.397
9	0.538	0.940	1.053	1.145	1.245	1.307	1.416
10	0.532	0.934	1.048	1.144	1.248	1.313	1.432
12	0.523	0.926	1.042	1.140	1.252	1.322	1.456
14	0.518	0.920	1.037	1.136	1.252	1.325	1.470
16	0.514	0.914	1.031	1.132	1.250	1.327	1.480
18	0.510	0.910	1.027	1.129	1.248	1.328	1.487
20	0.507	0.906	1.024	1.127	1.247	1.329	1.492
22	0.505	0.903	1.022	1.126	1.246	1.330	1.496
24	0.503	0.901	1.021	1.125	1.246	1.331	1.499
26	0.502	0.899	1.019	1.124	1.246	1.332	1.501
28	0.500	0.897	1.018	1.124	1.246	1.333	1.502
30	0.499	0.896	1.016	1.123	1.245	1.334	1.502
40	0.494	0.891	1.012	1.119	1.243	1.332	1.504
50	0.489	0.887	1.007	1.115	1.241	1.329	1.506
80	0.487	0.883	1.005	1.113	1.240	1.329	1.508
100	0.495	0.881	1.004	1.112	1.240	1.329	1.509
∞	0.481	0.876	0.999	1.109	1.239	1.329	1.517

Values in Appendix Table B.39 were taken, with permission of the publisher, from Table 1 of Moore (1980, *Biometrika* 67: 175–180).

Examples:

$$R'_{0.05,24} = 1.021 \quad \text{and} \quad R'_{0.10,30} = 0.896$$

TABLE B.40: Common Logarithms of Factorials

X	0	1	2	3	4	5	6	7	8	9
0	0.00000	0.00000	0.30103	0.77815	1.38021	2.07918	2.85733	3.70243	4.60552	5.55976
10	6.55976	7.60116	8.68034	9.79428	10.94041	12.11650	13.32062	14.55107	15.80634	17.08509
20	18.38612	19.70834	21.05077	22.41249	23.79271	25.19065	26.60562	28.03698	29.48414	30.94654
30	32.42366	33.91502	35.42017	36.93869	38.47016	40.01423	41.57054	43.13874	44.71852	46.30959
40	47.91165	49.52443	51.14768	52.78115	54.42460	56.07781	57.74057	59.41267	61.09391	62.78410
50	64.48307	66.19065	67.90665	69.63092	71.36332	73.10368	74.85187	76.60774	78.37117	80.14202
60	81.92017	83.70550	85.49790	87.29724	89.10342	90.91633	92.73587	94.56195	96.39446	98.23331
70	100.07841	101.92966	103.78700	105.65032	107.51955	109.39461	111.27543	113.16192	115.05401	116.95164
80	118.85473	120.76321	122.67703	124.59610	126.52038	128.44980	130.38430	132.32382	134.26830	136.21769
90	138.17194	140.13098	142.09477	144.06325	146.03638	148.01410	149.99637	151.98314	153.97437	155.97000
100	157.97000	159.97433	161.98293	163.99576	166.01280	168.03399	170.05929	172.08867	174.12210	176.15952
110	178.20092	180.24624	182.29546	184.34854	186.40544	188.46614	190.53060	192.59878	194.67067	196.74621
120	198.82539	200.90818	202.99454	205.08444	207.17787	209.27478	211.37515	213.47895	215.58616	217.69675
130	219.81069	221.92796	224.04854	226.17239	228.29949	230.42983	232.56337	234.70009	236.83997	238.98298
140	241.12911	243.27833	245.43062	247.58595	249.74432	251.90568	254.07004	256.23735	258.40762	260.58080
150	262.75689	264.93587	267.11771	269.30241	271.48993	273.68026	275.87338	278.06928	280.26794	282.46934
160	284.67346	286.88028	289.08980	291.30198	293.51683	295.73431	297.95442	300.17714	302.40245	304.63033
170	306.86078	309.09378	311.32931	313.56735	315.80790	318.05094	320.29645	322.54443	324.79485	327.04770
180	329.30297	331.56065	333.82072	336.08317	338.34799	340.61516	342.88467	345.15652	347.43067	349.70714
190	351.98589	354.26692	356.55022	358.83578	361.12358	363.41362	365.70587	368.00034	370.29701	372.59586
200	374.89689	377.20008	379.50544	381.81293	384.12256	386.43432	388.74818	391.06415	393.38222	395.70236
210	398.02458	400.34887	402.67520	405.00358	407.33399	409.66643	412.00089	414.33735	416.67580	419.01625
220	421.35867	423.70306	426.04941	428.39772	430.74797	433.10015	435.45426	437.81028	440.16822	442.52805
230	444.88978	447.25339	449.61888	451.98624	454.35545	456.72652	459.09943	461.47418	463.85076	466.22916
240	468.60937	470.99139	473.37520	475.76081	478.14820	480.53736	482.92830	485.32100	487.71545	490.11165
250	492.50959	494.90926	497.31066	499.71378	502.11861	504.52516	506.93340	509.34333	511.75495	514.16825
260	516.58322	518.99986	521.41816	523.83812	526.25972	528.68297	531.10785	533.53436	535.96250	538.39225
270	540.82361	543.25658	545.69115	548.12731	550.56506	553.00440	555.44531	557.88779	560.33183	562.77743
280	565.22459	567.67330	570.12355	572.57533	575.02865	577.48350	579.93986	582.39775	584.85714	587.31804
290	589.78043	592.24433	594.70971	597.17658	599.64492	602.11475	604.58604	607.05879	609.53301	612.00868
300	614.48580	616.96437	619.44438	621.92582	624.40869	626.89299	629.37871	631.86585	634.35440	636.84436
310	639.33572	641.82848	644.32264	646.81818	649.31511	651.81342	654.31311	656.81417	659.31660	661.82039
320	664.32554	666.83204	669.33990	671.84910	674.35965	676.87153	679.38475	681.89929	684.41517	686.93236
330	689.45088	691.97071	694.49184	697.01429	699.53803	702.06308	704.58942	707.11705	709.64597	712.17616
340	714.70764	717.24040	719.77442	722.30972	724.84628	727.38410	729.92317	732.46350	735.00508	737.54791

TABLE B.40 (cont.): Common Logarithms of Factorials

X	0	1	2	3	4	5	6	7	8	9
350	740.09197	742.63728	745.18382	747.73160	750.28060	752.83083	755.38228	757.93495	760.48883	763.04393
360	765.60023	768.15774	770.71644	773.27635	775.83745	778.39975	780.96323	783.52789	786.09374	788.66077
370	791.22897	793.79834	796.36889	798.94059	801.51347	804.08750	806.66268	809.23903	811.81652	814.39516
380	816.97494	819.55587	822.13793	824.72113	827.30546	829.89092	832.47751	835.06522	837.65405	840.24400
390	842.83506	845.42724	848.02053	850.61492	853.21042	855.80701	858.40471	861.00350	863.60338	866.20435
400	868.80641	871.40956	874.01378	876.61909	879.22547	881.83293	884.44145	887.05105	889.66171	892.27343
410	894.88621	897.50006	900.11495	902.73090	905.34790	907.96595	910.58504	913.20518	915.82636	918.44857
420	921.07182	923.69610	926.32141	928.94776	931.57512	934.20351	936.83292	939.46335	942.09479	944.72725
430	947.36072	949.99519	952.63068	955.26717	957.90466	960.54314	963.18263	965.82311	968.46459	971.10705
440	973.75050	976.39494	979.04037	981.68677	984.33415	986.98251	989.63185	992.28215	994.93343	997.58568
450	1000.23889	1002.89307	1005.54821	1008.20430	1010.86136	1013.51937	1016.17834	1018.83825	1021.49912	1024.16093
460	1026.82369	1029.48739	1032.15203	1034.81761	1037.48413	1040.15158	1042.81997	1045.48929	1048.15953	1050.83070
470	1053.50280	1056.17582	1058.84977	1061.52463	1064.20040	1066.87710	1069.55471	1072.23322	1074.91265	1077.59299
480	1080.27423	1082.95637	1085.63942	1088.32337	1091.00821	1093.69395	1096.38059	1099.06812	1101.75654	1104.44585
490	1107.13604	1109.82713	1112.51909	1115.21194	1117.90567	1120.60027	1123.29575	1125.99211	1128.68934	1131.38744

If $\log X!$ is needed for $X > 499$, consult Lloyd, Zar, and Karr (1968) or Pearson and Hartley (1966: Table 51), or note that "Stirling's approximation" is excellent, being accurate to about two decimal places for n as small as 10:

$$\log X! = (X + 0.5)\log X - 0.434294X + 0.39909;$$

and this approximation is even better, having half the error:

$$\log X! = (X + 0.5)\log(X + 0.5) - 0.434294(X + 0.5) + 0.399090$$

(Kemp, 1989; Tweddle, 1984).

Walker (1934) notes that Abraham de Moivre was aware of this approximation before Stirling. Thus we have another example of "Stigler's Law of Eponymy" (see the second footnote in Chapter 6).

TABLE B.41: Ten Thousand Random Digits

	00–04	05–09	10–14	15–19	20–24	25–29	30–34	35–39	40–44	45–49
00	22808	04391	45529	53968	57136	98228	85485	13801	68194	56382
01	49305	36965	44849	64987	59501	35141	50159	57369	76913	75739
02	81934	19920	73316	69243	69605	17022	53264	83417	55193	92929
03	10840	13508	48120	22467	54505	70536	91206	81038	22418	34800
04	99555	73289	59605	37105	24621	44100	72832	12268	97089	68112
05	32677	45709	62337	35132	45128	96761	08745	53388	98353	46724
06	09401	75407	27704	11569	52842	83543	44750	03177	50511	15301
07	73424	31711	65519	74869	56744	40864	75315	89866	96563	75142
08	37075	81378	59472	71858	86903	66860	03757	32723	54273	45477
09	02060	37158	55244	44812	45369	78939	08048	28036	40946	03898
10	94719	43565	40028	79866	43137	28063	52513	66405	71511	66135
11	70234	48272	59621	88778	16536	36505	41724	24776	63971	01685
12	07972	71752	92745	86465	01845	27416	50519	48458	68460	63113
13	58521	64882	26993	48104	61307	73933	17214	44827	88306	78177
14	32580	45202	21148	09684	39411	04892	02055	75276	51831	85686
15	88796	30829	35009	22695	23694	11220	71006	26720	39476	60538
16	31525	82746	78935	82980	61236	28940	96341	13790	66247	33839
17	02747	35989	70387	89571	34570	17002	79223	96817	31681	15207
18	46651	28987	20625	61347	63981	41085	67412	29053	00724	14841
19	43598	14436	33521	55637	39789	26560	66404	71802	18763	80560
20	30596	92319	11474	64546	60030	73795	60809	24016	29166	36059
21	56198	64370	85771	62633	78240	05766	32419	35769	14057	80674
22	68266	67544	06464	84956	18431	04015	89049	15098	12018	89338
23	31107	28597	65102	75599	17496	87590	68848	33021	69855	54015
24	37555	05069	38680	87274	55152	21792	77219	48732	03377	01160
25	90463	27249	43845	94391	12145	36882	48906	52336	00780	74407
26	99189	88731	93531	52638	54989	04237	32978	59902	05463	09245
27	37631	74016	89072	59598	55356	27346	80856	80875	52850	36548
28	73829	21651	50141	76142	72303	06694	61697	76662	23745	96282
29	15634	89428	47090	12094	42134	62381	87236	90118	53463	46969
30	00571	45172	78532	63863	98597	15742	41967	11821	91389	07476
31	83374	10184	56384	27050	77700	13875	96607	76479	80535	17454
32	78666	85645	13181	08700	08289	62956	64439	39150	95690	18555
33	47890	88197	21368	65254	35917	54035	83028	84636	38186	50581
34	56238	13559	79344	83198	94642	35165	40188	21456	67024	62771
35	36369	32234	38129	59963	99237	72648	66504	99065	61161	16186
36	42934	34578	28968	74028	42164	56647	76806	61023	33099	48293
37	09010	15226	43474	30174	26727	39317	48508	55438	85336	40762
38	83897	90073	72941	85613	85569	24183	08247	15946	02957	68504
39	82206	01230	93252	89045	25141	91943	75531	87420	99012	80751
40	14175	32992	49046	41272	94040	44929	98531	27712	05106	35242
41	58968	88367	70927	74765	18635	85122	27722	95388	61523	91745
42	62601	04595	76926	11007	67631	64641	07994	04639	39314	83126
43	97030	71165	47032	85021	65554	66774	21560	04121	57297	85415
44	89074	31587	21360	41673	71192	85795	82757	52928	62586	02179
45	07806	81312	81215	99858	26762	28993	74951	64680	50934	32011
46	91540	86466	13229	76624	44092	96604	08590	89705	03424	48033
47	99279	27334	33804	77988	93592	90708	56780	70097	39907	51006
48	63224	05074	83941	25034	43516	22840	35230	66048	80754	46302
49	98361	97513	27529	66419	35328	19738	82366	38573	50967	72754

TABLE B.41 (cont.): Ten Thousand Random Digits

	00–04	05–09	10–14	15–19	20–24	25–29	30–34	35–39	40–44	45–49
50	27791	82504	33523	27623	16597	32089	81596	78429	14111	68245
51	33147	46058	92388	10150	63224	26003	56427	29945	44546	50233
52	67243	10454	40269	44324	46013	00061	21622	68213	47749	76398
53	78176	70368	95523	09134	31178	33857	26171	07063	41984	99310
54	70199	70547	94431	45423	48695	01370	68065	61982	20200	27066
55	19840	01143	18606	07622	77282	68422	70767	33026	15135	91212
56	32970	28267	17695	20571	50227	69447	45535	16845	68283	15919
57	43233	53872	68520	70013	31395	60361	39034	59444	17066	07418
58	08514	23921	16685	89184	71512	82239	72947	69523	75618	79826
59	28595	51196	96108	84384	80359	02346	60581	01488	63177	47496
60	83334	81552	88223	29934	68663	23726	18429	84855	26897	94782
61	66112	95787	84997	91207	67576	27496	01603	22395	41546	68178
62	25245	14749	30653	42355	88625	37412	87384	09392	11273	28116
63	21861	22185	41576	15238	92294	50643	69848	48020	19785	41518
64	74506	40569	90770	40812	57730	84150	91500	53850	52104	37988
65	23271	39549	33042	10661	37312	50914	73027	21010	76788	64037
66	08548	16021	64715	08275	50987	67327	11431	31492	86970	47335
67	14236	80869	90798	85659	10079	28535	35938	10710	67046	74021
68	55270	49583	86467	40633	27952	27187	35058	66628	94372	75665
69	02301	05524	91801	23647	51330	35677	05972	90729	26650	81684
70	72843	03767	62590	92077	91552	76853	45812	15503	93138	87788
71	49248	43346	29503	22494	08051	09035	75802	63967	74257	00046
72	62598	99092	87806	42727	30659	10118	83000	96198	47155	00361
73	27510	69457	98616	62172	07056	61015	22159	65590	51082	34912
74	84167	66640	69100	22944	19833	23961	80834	37418	42284	12951
75	14722	88488	54999	55244	03301	37344	01053	79305	94771	95215
76	46696	05477	32442	18738	43021	72933	14995	30408	64043	67834
77	13938	09867	28949	94761	38419	38695	90165	82841	75399	09932
78	48778	56434	42495	07050	35250	09660	56192	34793	36146	96806
79	00571	71281	01563	66448	94560	55920	31580	26640	91262	30863
80	96050	57641	21798	14917	21836	15053	33566	51177	91786	12610
81	30870	81575	14019	07831	81840	25506	29358	88668	42742	62048
82	59153	29135	00712	73025	14263	17253	95662	75535	26170	95240
83	78283	70379	54969	05821	26485	28990	40207	00434	38863	61892
84	12175	95800	41106	93962	06245	00883	65337	75506	66294	62241
85	14192	39242	17961	29448	84078	14545	39417	83649	26495	41672
86	69060	38669	00849	24991	84252	41611	62773	63024	57079	59283
87	46154	11705	29355	71523	21377	36745	00766	21549	51796	81340
88	93419	54353	41269	07014	28352	77594	57293	59219	26098	63041
89	13201	04017	68889	81388	60829	46231	46161	01360	25839	52380
90	62264	99963	98226	29972	95169	07546	01574	94986	06123	52804
91	58030	30054	27479	70354	12351	33761	94357	81081	74418	74297
92	81242	26739	92304	81425	29052	37708	49370	46749	59613	50749
93	16372	70531	92036	54496	50521	83872	30064	67555	40354	23671
94	54191	04574	58634	91370	40041	77649	42030	42547	47593	07435
95	15933	92602	19496	18703	63380	58017	14665	88867	84807	44672
96	21518	77770	53826	97114	82062	34592	87400	64938	75540	54751
97	34524	64627	92997	21198	14976	07071	91566	44335	83237	24335
98	46557	67780	59432	23250	63352	43890	07109	07911	85956	62699
99	31929	13996	05126	83561	03244	33635	26952	01638	22788	26393

TABLE B.41 (cont.): Ten Thousand Random Digits

	50–54	55–59	60–64	65–69	70–74	75–79	80–84	85–89	90–94	95–99
00	53330	26487	85005	06384	13822	83736	95876	71355	31226	56063
01	96990	62825	97110	73006	32661	63408	03893	10333	41902	69175
02	30385	16588	63609	09132	53081	14478	50813	22887	03746	10289
03	75252	66905	60536	13408	25158	35825	10447	47375	89249	91238
04	52615	66504	78496	90443	84414	31981	88768	49629	15174	99795
05	39992	51082	74547	31022	71980	40900	84729	34286	96944	49502
06	51788	87155	13272	92461	06466	25392	22330	17336	42528	78628
07	88569	35645	50602	94043	35316	66344	78064	89651	89025	12722
08	14513	34794	44976	71244	60548	03041	03300	46389	25340	23804
09	50257	53477	24546	01377	20292	85097	00660	39561	62367	61424
10	35170	69025	46214	27085	83416	48597	19494	49380	28469	77549
11	22225	83437	43912	30337	75784	77689	60425	85588	93438	61343
12	90103	12542	97828	85859	85859	64101	00924	89012	17889	01154
13	68240	89649	85705	18937	30114	89827	89460	01998	81745	31281
14	01589	18335	24024	39498	82052	07868	49486	25155	61730	08946
15	36375	61694	90654	16475	92703	59561	45517	90922	93357	00207
16	11237	60921	51162	74153	94774	84150	39274	10089	45020	09624
17	48667	68353	40567	79819	48551	26789	07281	14669	00576	17435
18	99286	42806	02956	73762	04419	21676	67533	50553	21115	26742
19	44651	48349	13003	39656	99757	74964	00141	21387	66777	68533
20	83251	70164	05732	66842	77717	25305	36218	85600	23736	06629
21	41551	54630	88759	10085	48806	08724	50685	95638	20829	37264
22	68990	51280	51368	73661	21764	71552	69654	17776	51935	53169
23	63393	76820	33106	23322	16783	35630	50938	90047	97577	27699
24	93317	87564	32371	04190	27608	40658	11517	19646	82335	60088
25	48546	41090	69890	58014	04093	39286	12253	55859	83853	15023
26	31435	57566	99741	77250	43165	31150	20735	57406	85891	04806
27	56405	29392	76998	66849	29175	11641	85284	89978	73169	62140
28	70102	50882	85960	85955	03828	69417	55854	63173	60485	00327
29	92746	32004	52242	94763	32955	39848	09724	30029	45196	67606
30	67737	34389	57920	47081	60714	04935	48278	90687	99290	18554
31	35606	76646	14813	51114	52492	46778	08156	22372	59999	43938
32	64836	28649	45759	45788	43183	25275	25300	21548	33941	66314
33	86319	92367	37873	48993	71443	22768	69124	65611	79267	49709
34	90632	32314	24446	60301	31376	13575	99663	81929	39343	17648
35	83752	51966	43895	03129	37539	72989	52393	45542	70344	96712
36	56755	21142	86355	33569	63096	66780	97539	75150	25718	33724
37	14100	28857	60648	86304	97397	97210	74842	87483	51558	52883
38	69227	24872	48057	29318	74385	02097	63266	26950	73173	53025
39	77718	56967	36560	87155	26021	70903	32086	11722	32053	63723
40	09550	38799	88929	80877	87779	99905	17122	25985	16866	76005
41	12404	42453	88609	89148	85892	96045	10310	45021	62023	70061
42	07985	27418	92734	80000	58969	99011	73815	49705	68076	69605
43	58124	53830	08705	20916	46048	30342	86530	72608	93074	80937
44	46173	77223	75661	57691	24055	27568	41227	58542	73196	44886
45	13476	72301	85793	80516	59479	66985	24801	84009	71317	87321
46	82472	98647	17053	94591	36790	42275	51154	77765	01115	09331
47	55370	63433	80653	30739	68821	46854	41939	38962	20703	69424
48	89274	74795	82231	69384	53605	67860	01309	27273	76316	54253
49	55242	74511	62992	17981	17323	79325	35238	21393	13114	70084

Many computer programs can generate random numbers (actually *pseudorandom numbers*, for the sequence of digits will repeat—but commonly only after about two billion uses of the random-number generator; McCullough, 1998).

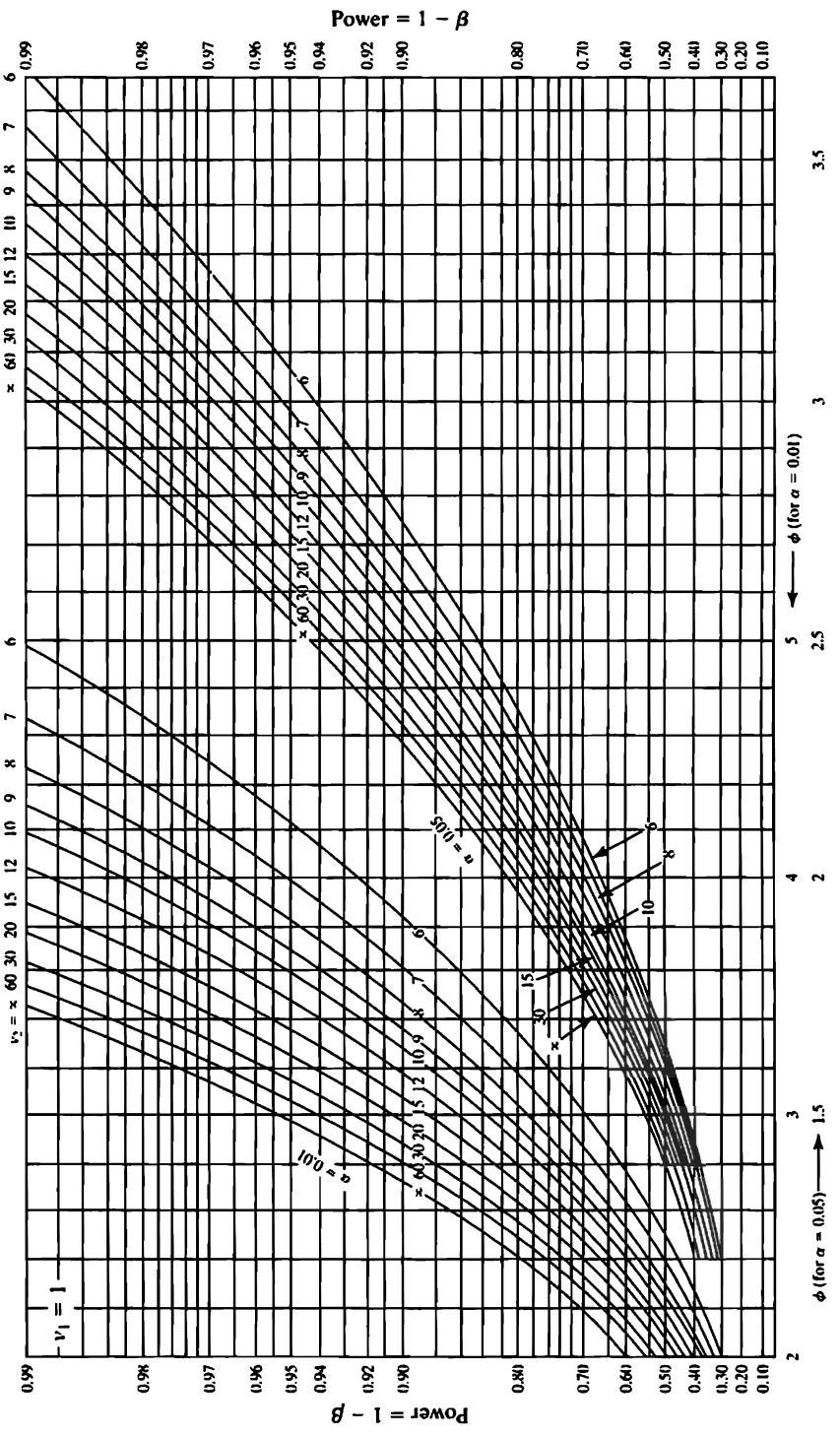


FIGURE B.1a: Power and sample size in analysis of variance; $\nu_1 = 1$.

Note: In this figure (for $\nu_1 = 1$), the curves for $\alpha = 0.05$ and $\alpha = 0.01$ are positioned the reverse of what they are in Figures B.1b–1h.

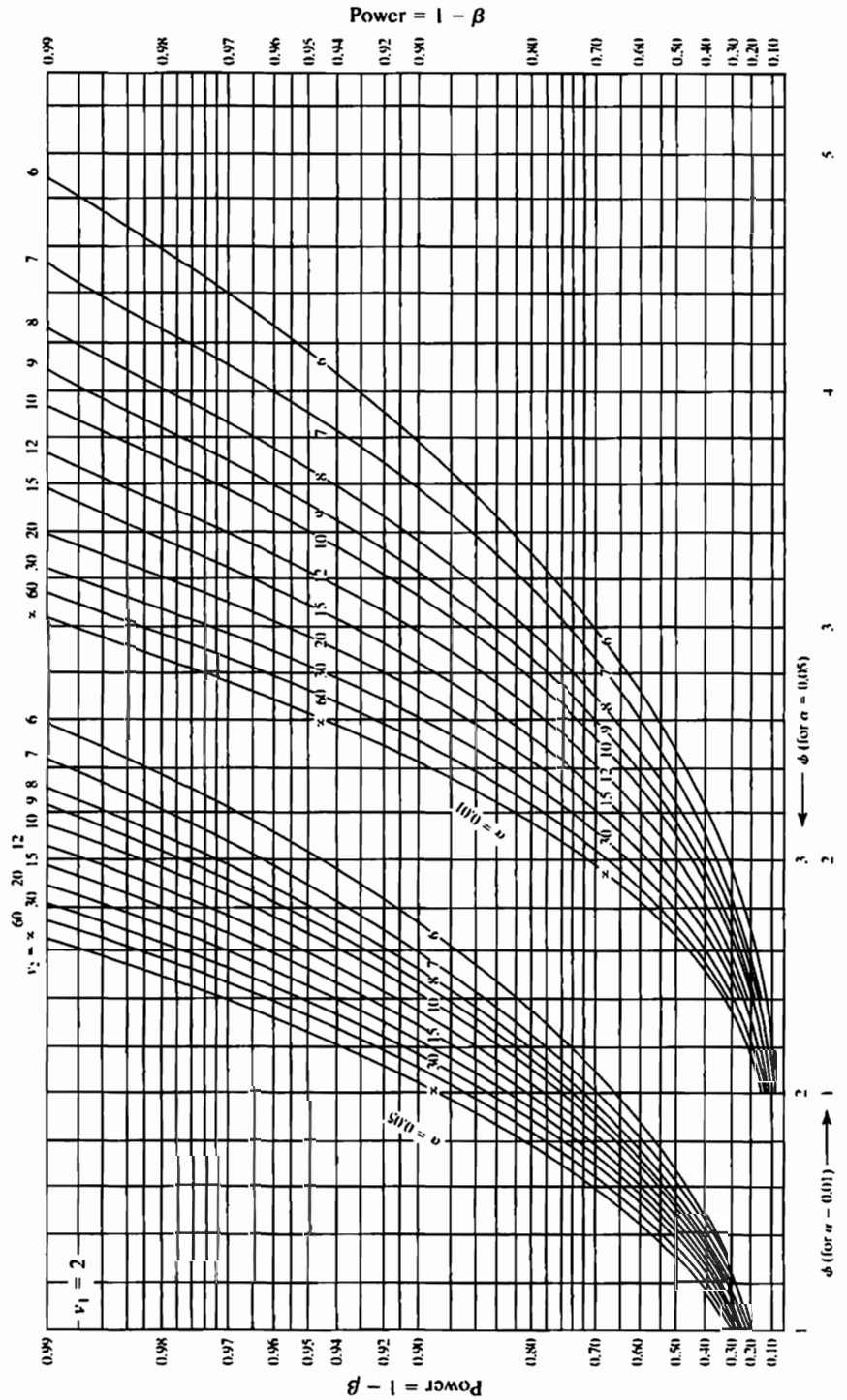


FIGURE B.1b: Power and sample size in analysis of variance; $\nu_1 = 2$.

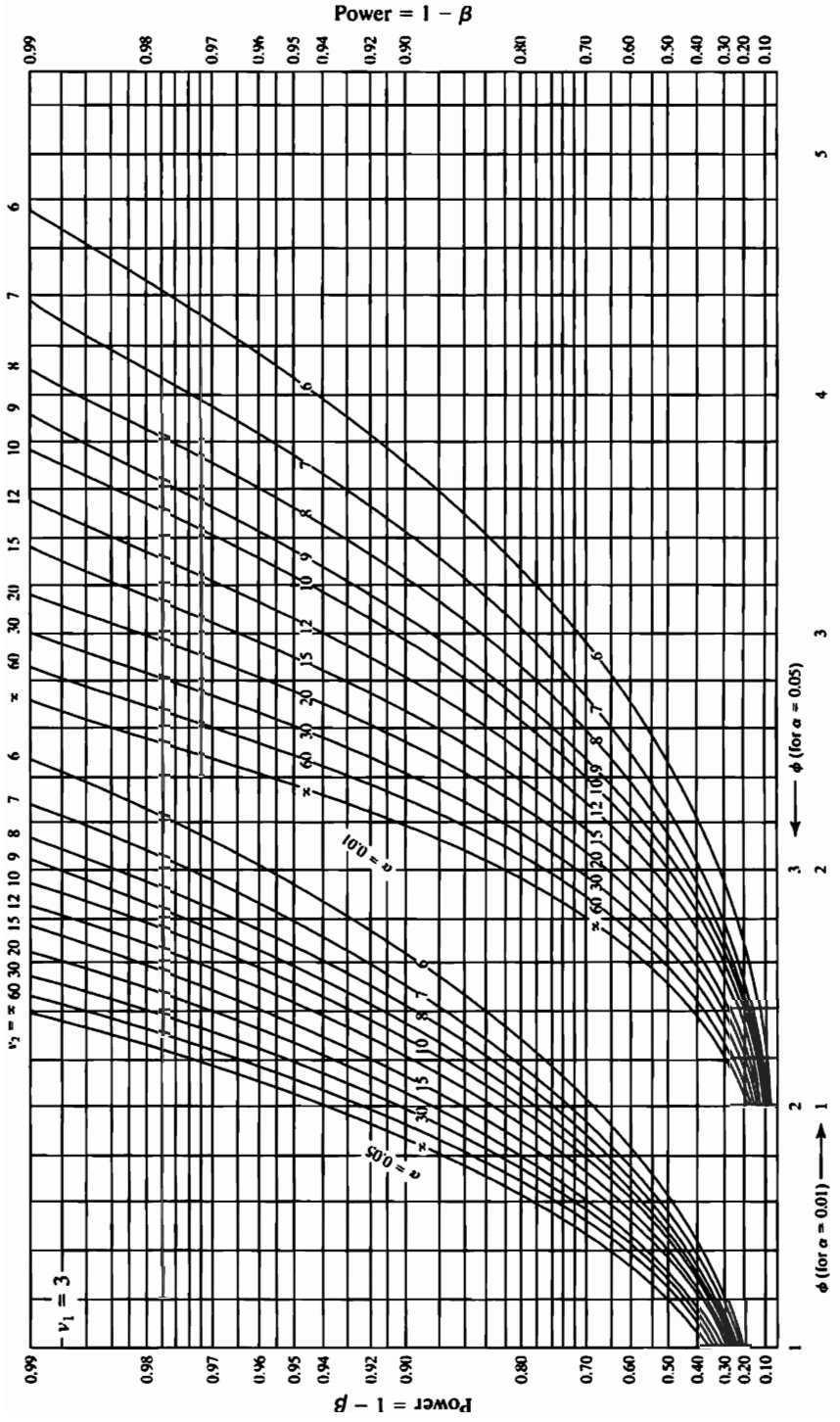


FIGURE B.1c: Power and sample size in analysis of variance: $\nu_1 = 3$.

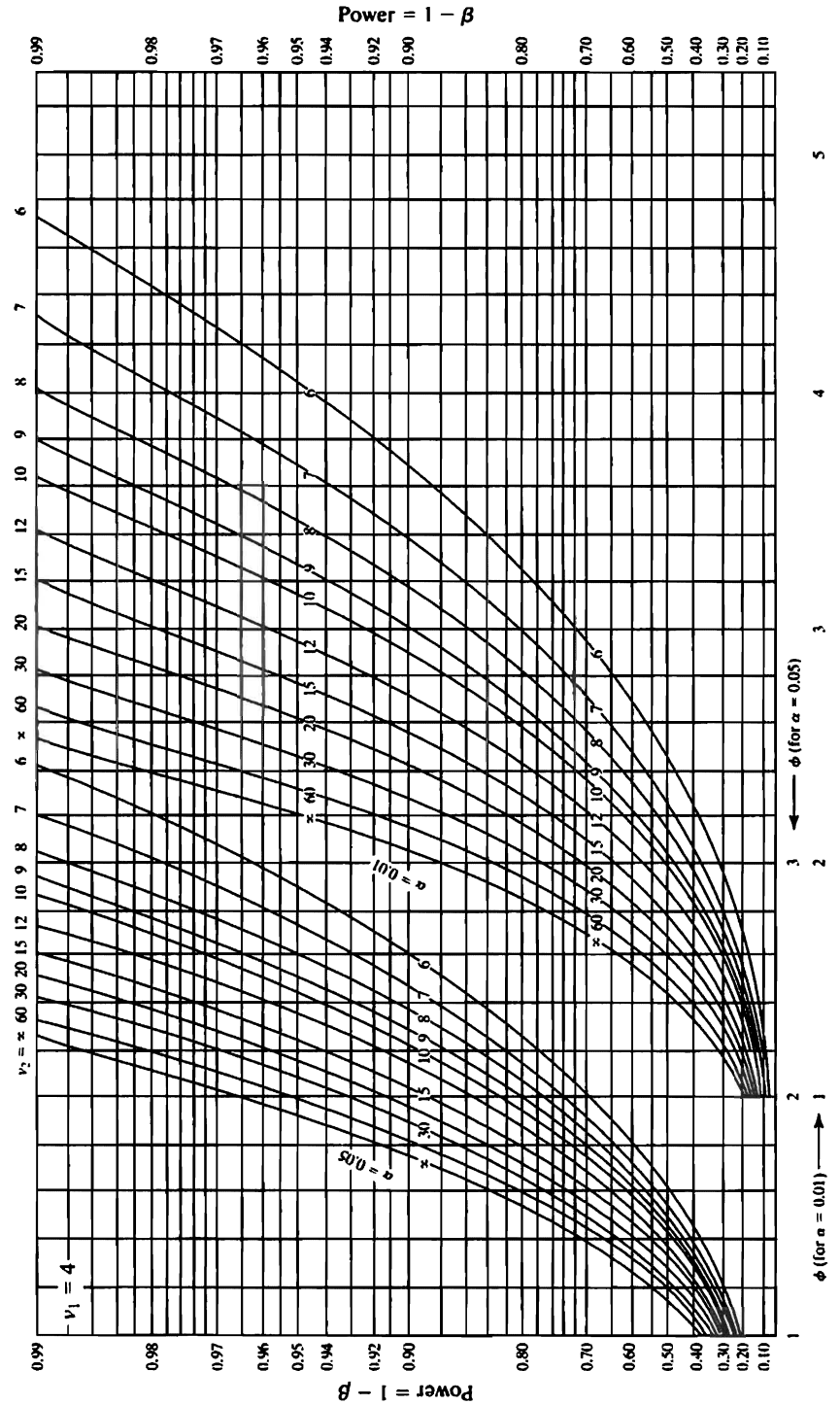


FIGURE B.1d: Power and sample size in analysis of variance: $\nu_1 = 4$.

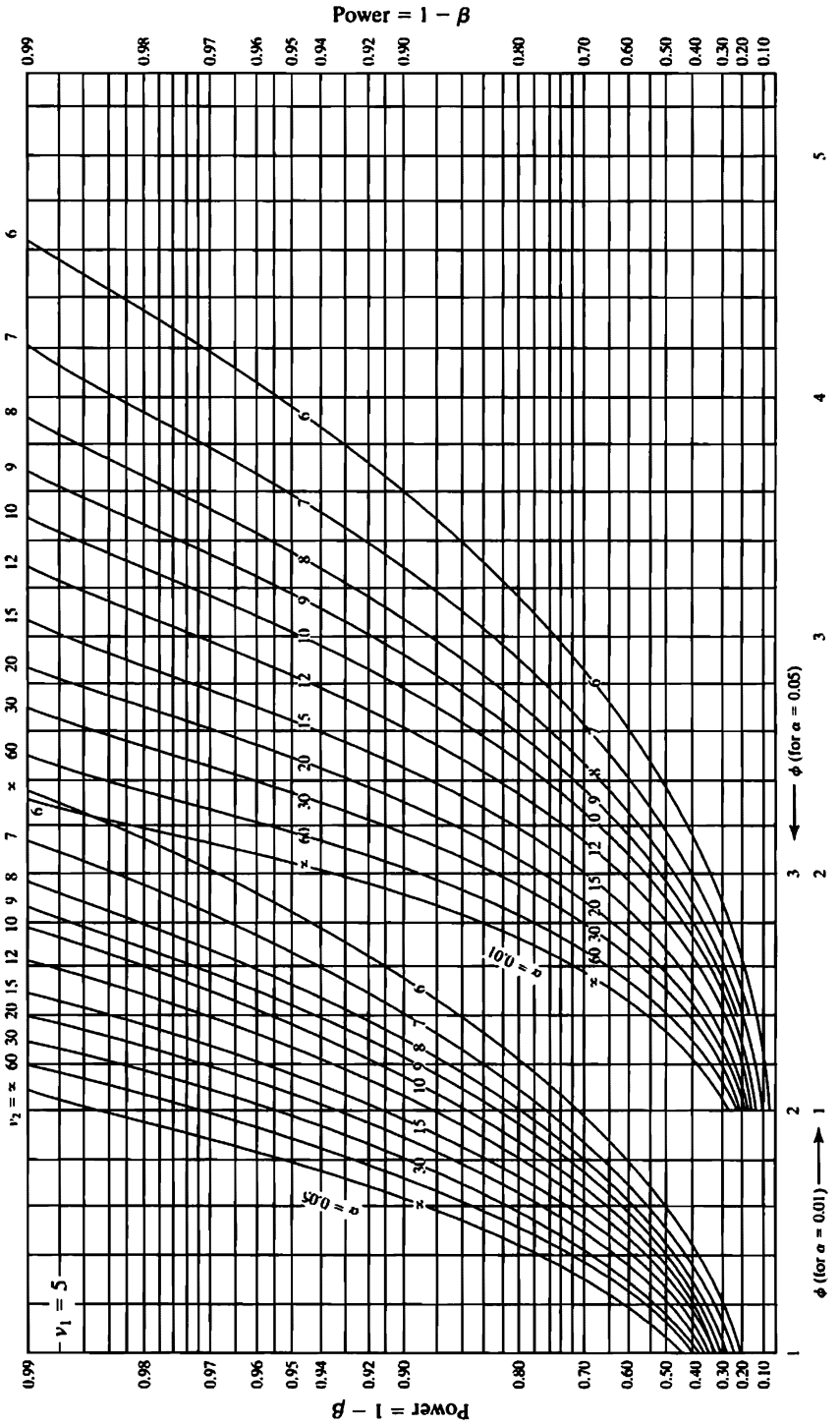


FIGURE B.1e: Power and sample size in analysis of variance: $\nu_1 = 5$.

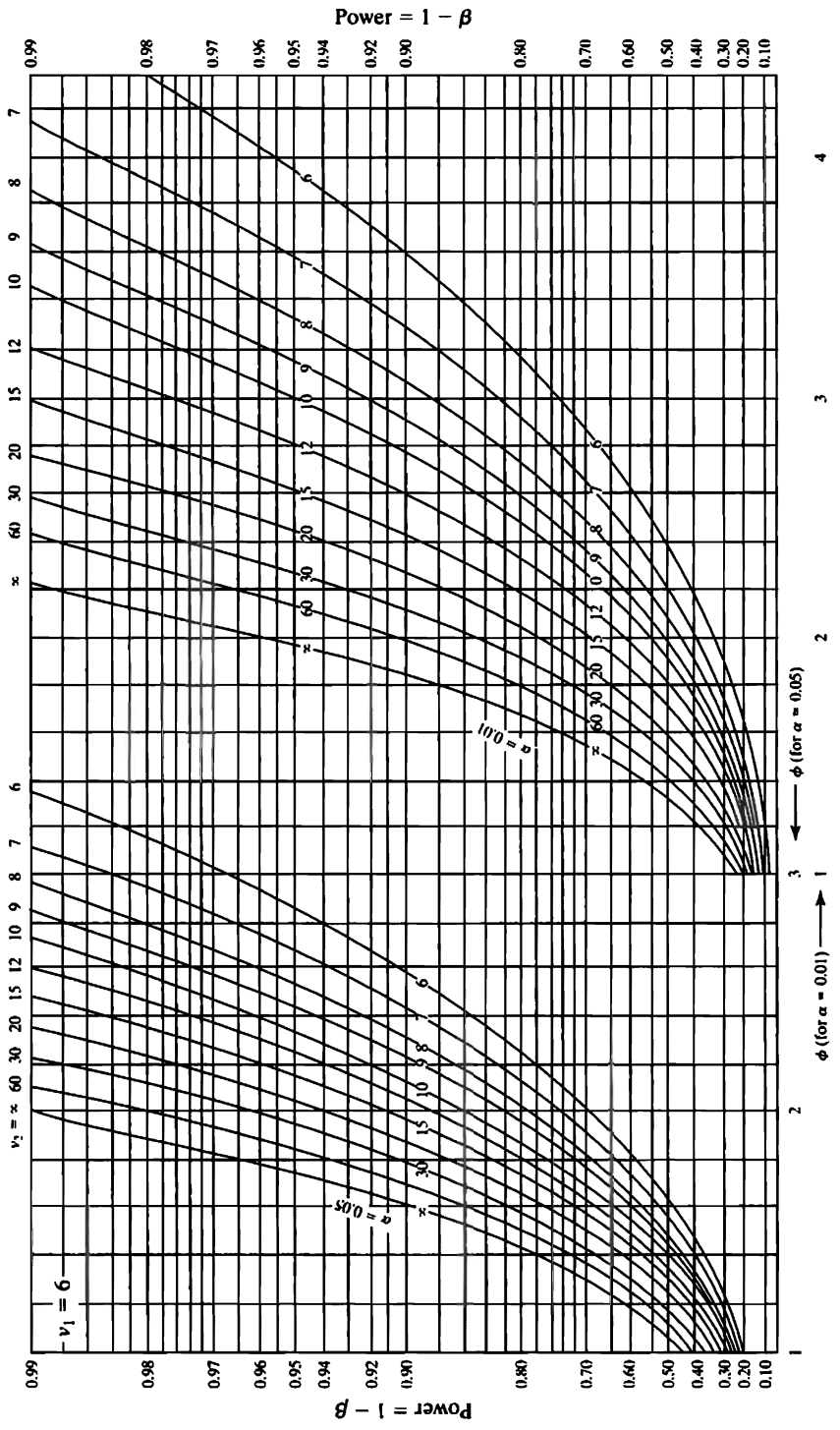


FIGURE B.1f: Power and sample size in analysis of variance: $\nu_1 = 6$.

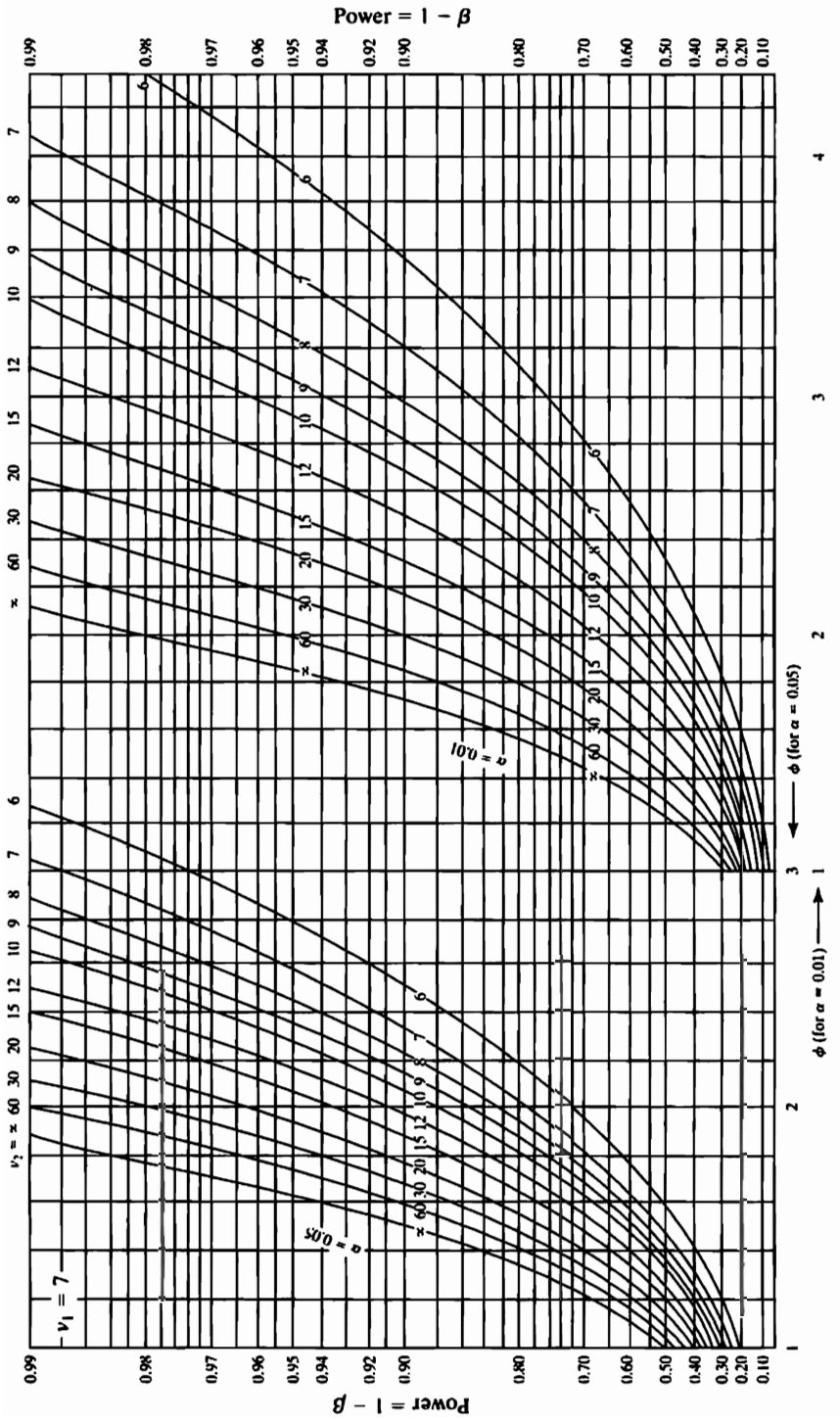


FIGURE B.1g: Power and sample size in analysis of variance: $\nu_1 = 7$.

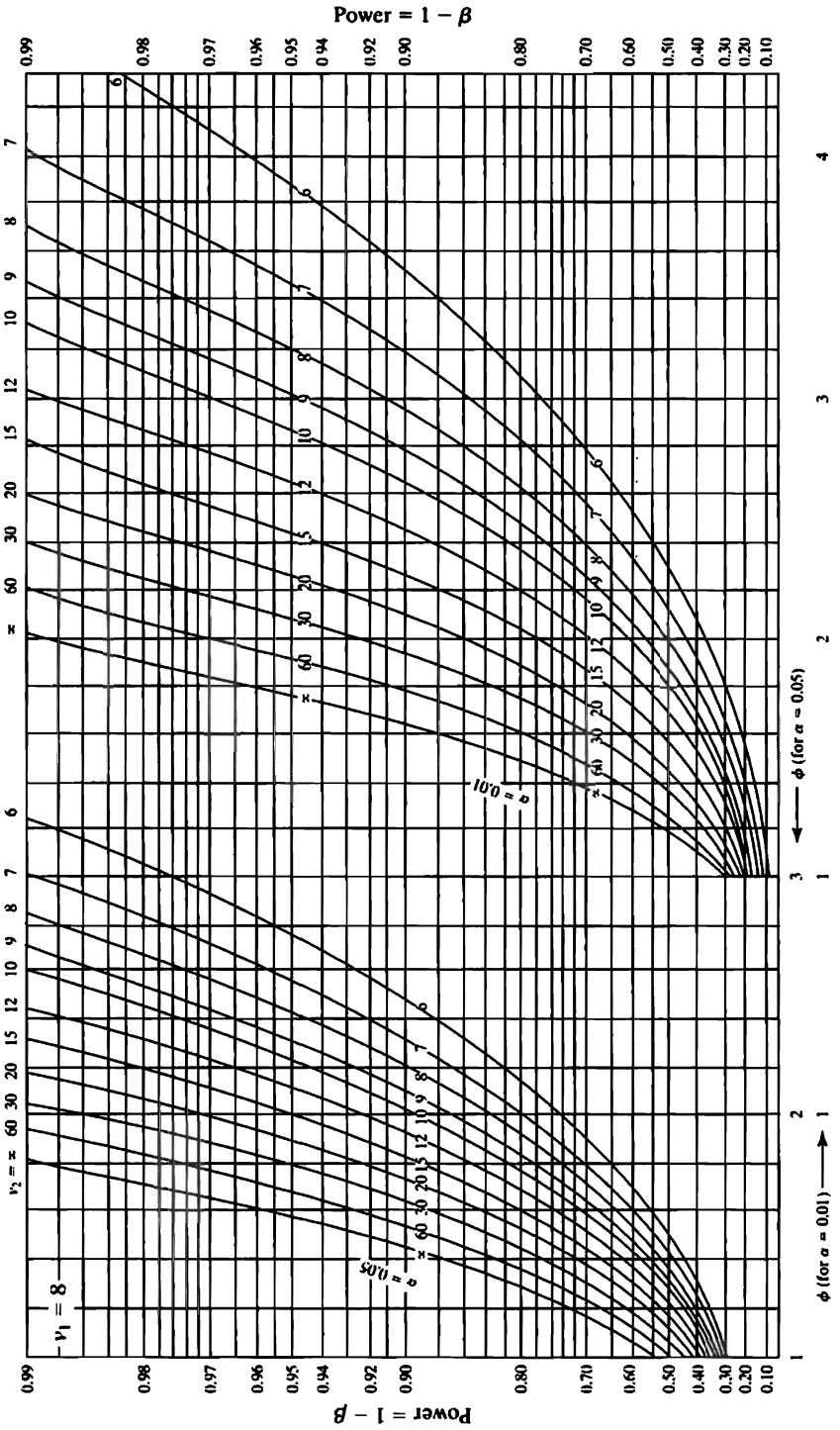


FIGURE B.1h: Power and sample size in analysis of variance: $\nu_1 = 8$.

The graphs in Figs. B.1a through B.1h were presented by Pearson and Hartley (1951, *Biometrika* 38: 112–130) as an improvement over those of Tang (1938) and are reprinted with permission of the *Biometrika* Trustees.

APPENDIX C

The Effects of Coding Data

The concept of coding, as an aid to computation with very large or very small data, was introduced in Section 3.5. The following table indicates the sections in this book where various statistics receive their first major discussion. The coded value of each statistic is indicated by brackets (where, for example, $[\overline{X}]$ is the sample mean calculated from coded data, where coding is done by multiplying each datum by M and then adding A. The second column of the table shows how to obtain the statistic that would have been calculated from the original, noncoded data; and the third column shows how a statistic from noncoded data can be converted to the statistic that would be obtained by coding the data.

For example, if each datum, X, in a sample with an arithmetic mean of 0.15 is multiplied by 10 (i.e., $M = 10$) and then 2 is added to the result (i.e., $A = 2$), the coded arithmetic mean would be $[\overline{X}] = M\overline{X} + A = (10)(0.15) + 2 = 3.5$. Conversely, if it is found that the mean of the coded data is 3.5, then the mean of the uncoded data would be $\overline{X} = ([\overline{X}] - A)/M = (3.5 - 2)/10 = 0.15$. If there is no multiplicative coding, then $M = 1$; and, if there is no additive coding, then $A = 0$.

For simple regression statistics (Chapter 17), M_X and A_X pertain to the independent variable, X, and M_Y and A_Y apply to the dependent variable, Y.

Coding for confidence limits or prediction limits for a statistic employs the same M and A as used for that statistic.

Text Section	Statistic	Value after Coding		Value before Coding
3.1	Arithmetic mean, $\overline{X}$	$[\overline{X}] = M\overline{X} + A$		$\overline{X} = \frac{[\overline{X}]-A}{M}$
3.2	Median	Same as	$\overline{X}$	(above)
3.3	Mode	Same as	$\overline{X}$	(above)
3.4a	Geometric mean, $\overline{X}_G$	$[\overline{X}_G] = M\overline{X}_G$		$\overline{X}_G = \frac{[\overline{X}_G]}{M}$
3.4b	Harmonic mean, $\overline{X}_H$	$[\overline{X}_H] = M\overline{X}_H$		$\overline{X}_H = \frac{[\overline{X}_H]}{M}$
3.5c	Range midpoint	Same as	$\overline{X}$	(above)
4.1	Range	Same as	s	(below)
4.2	Interquartile range	Same as	s	(below)
4.3	Mean deviation	Same as	s	(below)
4.4	Sum of squares, SS	$[SS] = M^2\,SS$		$SS = \frac{[SS]}{M^2}$
4.4	Variance, s^2	$[s^2] = M^2s^2$		$s^2 = \frac{[s^2]}{M^2}$
4.5	Standard deviation, s	$[s] = Ms$		$s = \frac{[s]}{M}$
6.2	Standard error of mean, $s_{\overline{X}}$	$[s_{\overline{X}}] = Ms_{\overline{X}}$		$s_{\overline{X}} = \frac{[s_{\overline{X}}]}{M}$

Text Section	Statistic	Value after Coding	Value before Coding
7.3	Confidence limits, L_1 and L_2 dealing with means	$[L_i] = ML_i + A$	$L_i = \frac{[L_i]-A}{M}$
17.2a	Regression coefficient,* b	$[b] = \frac{bM_Y}{M_X}$	$b = \frac{[b]M_X}{M_Y}$
17.2b	Y-intercept.* a	$[a] =$ $aM_Y - [b]A_X - A_Y$	$a =$ $\frac{[a]+[b]A_X-A_Y}{M_Y}$
17.3a	Standard error of estimate	$[s_{Y.X}] = M_Y[s_{Y.X}]$	$s_{Y.X} = \frac{[s_{Y.X}]}{M_Y}$
17.3b	Standard error of b: s_b	$[s_b] = \frac{s_b M_Y}{M_X}$	$s_b = \frac{s_b M_X}{M_Y}$
17.5b	Standard error of a: s_a	$[s_a] = s_a M_Y$	$s_a = \frac{s_a}{M_Y}$

The following quantites, in the book sections indicated, are not changed by coding the data from which they are calculated: **Section 4.6:** Coefficient of variation,† V; **4.7:** Shannon diversity index,† H'; **4.7:** Shannon evenness index,† J'; **6.1:** Normal deviate, Z; **6.5a:** Symmetry, $\sqrt{b_1}$; **6.5b:** Kurtosis, b_2; **7.1:** Student's t; **7.11:** Chi-square, χ^2; **7.15:** Confidence limits, L_i, dealing with variances; **8.1c:** Behrens-Fisher/Welch t'; **8.5:** Variance ratio, F; **8.11:** Mann-Whitney U and U'; **8.11d:** Sum of ranks, R; Mean of U; Standard error of U; Number of tied data in a group of ties: t_i **9.5:** Wilcoxon T_+ and T_-; **9.5b:** Mean of T; Standard error of T; **10.1a:** Correlation ratio, η^2; **10.1f:** Welch's F'; **10.1f:** Brown and Forsythe's F''; **10.3a:** Power function, ϕ; **10.3c:** Mimimum detectable difference, δ; **10.4:** Kruskal-Wallis H and H_c; **10.6:** Bartlett's B; **11.1:** Tukey-test studentized range, q; **11.3:** Dunnett's multiple-comparison statistic, q'; **11.4:** Scheffé's multiple-contrast statistic, S; **11.5:** Dunn's multiple-comparison statistic, Q; **12.7:** Friedman's χ_r^2 and $(\chi_r^2)_c$; **16.2:** Wilks' Λ (U) and η^2; Pillai's trace, V; Lawley-Hotelling tace, U; Roy's maximum root, θ; **16.2c:** Hotelling's T^2; **17.3a:** Coefficient of determination, r^2; **Chapter 19:** All correlation coefficients (e.g., r), except those in Sections 19.11a,† 19.11b, 19.12† and their standard errors (e.g., s_r); also, all Fisher z transformations of correlation coefficient and standard errors of z; **20.1:** Element of inverse correlation matrix, d_{ik}; **20.3:** Multiple coefficient of determination, R^2; Adjusted multiple coefficient of determination, R_a^2; Multiple correlation coefficient, R; **20.5:** Standardized partial regression coefficient, b_i'; Standard error of s_{b_i}; **20.16:** Kendall coefficient of concordance, W, W_c and C_T; **25.7:** mean square successive difference statistic, C; **25.8:** nonparametric runs test statistic, u.

In general, nominal-scale variables (most of Chapters 22–25) and circular variables (Chapters 26–27) should not be submitted to data coding.

* For regression through the origin (Section 17.9), both A_X and A_Y must be zero; that is, coding by an addition constant may not be used.

† In these cases, coding may only be performed with $A = 0$.

APPENDIX D

Analysis-of-Variance Hypothesis Testing

When an analysis-of-variance (ANOVA) experimental design has more than one factor, then the appropriate F values (and degrees of freedom) depend upon which of the factors are fixed and which are random effects (see Section 12.1), and which factors (if any) are nested within which (see Chapter 15). Shown below in Section D.1 is a procedure that enables us to determine the appropriate Fs and DFs for a given experimental design. It is a simplification of the procedures outlined by Bennett and Franklin (1954: 413–415), Hicks (1982: 214–223), Kirk (1995: 402–406), Scheffé (1959: 284–289), and Winer, Brown, and Michels (1991: 369–377) and is the method used to produce the contents of Sections D.2 through D.5. If we have one of the experimental designs of Sections D.2–D.4, the Fs and DFs are given therein; if the design is not found in those pages, then the procedures of Section D.1 may be used to determine the Fs and DFs appropriate to the ANOVA.

D.1 DETERMINATION OF APPROPRIATE *F*s AND DEGREES OF FREEDOM

The example given here is an analysis-of-variance design with three factors, A, B, and C, where factor A is a fixed effect, factor B is a random effect, and C is a random effect that is nested within combinations of factors A and B. This is the ANOVA that is the fourth example in Section D.4d. The following steps are followed, and a table is prepared as indicated.

1. Assign to each factor a unique letter and subscript. If a factor is nested (or is a block in a split-plot design or is a subject in a mixed within-subjects design) within one or more other factors, place the subscript(s) of the latter factor(s) in parentheses. For the present example, we would write A_i, B_j, $C_{l(ij)}$.
2. Prepare a table as follows:
   A. Row labels are the factors, with their subscripts (and the factor interactions, if any, with their subscripts), and a row for error (i.e., within cells) labeled "e", with all factor subscripts in parentheses. Factors, interactions, and error will be referred to collectively as "effects."
   B. Column headings are the factor subscripts, with an indication of whether each is associated with a fixed-effects factor or a random-effects factor.

   For our example,

Effect	*A Fixed* i	*B Random* j	*C Random* l
A_i			
B_j			
$[AB]_{ij}$			
$C_{l(ij)}$			
$e_{(ijl)}$			

3. The body of the table is filled in as follows:
   A. Examine each column corresponding to a fixed-effects factor. (In our example, only column i is so examined.) For each such column, enter a "0" in each row that the column subscript appears outside parentheses in the row subscript. (In our example, enter "0" in rows A_i and $[AB]_{ij}$ of column i.)

B. Enter "1" in every other position of the table.

For our example,

Effect	A Fixed i	B Random j	C Random l
A_i	0	1	1
B_j	1	1	1
$[AB]_{ij}$	0	1	1
$C_{l(ij)}$	1	1	1
$e_{(ijl)}$	1	1	1

4. For each row, list all effects that contain all the subscripts of the row label. In our example,

Effect	A Fixed i	B Random j	C Random l	Effect list
A_i	0	1	1	$A + AB + C + e$
B_j	1	1	1	$B + AB + C + e$
$[AB]_{ij}$	0	1	1	$AB + C + e$
$C_{l(ij)}$	1	1	1	$C + e$
$e_{(ijl)}$	1	1	1	e

5. For each effect, locate the row corresponding to each effect in the effect list and do the following for each such row:

   A. Ignore a zero in a column headed by a subscript in the row label, and if there is a zero in that row, then delete that effect from the effect list.

   B. Locate the table row corresponding to each factor or interaction in the effect list. If there is a zero in that row, other then in the columns headed by the subscripts in the row label, then delete that factor or interaction from the list.

   In our example, we examine row A_i by ignoring column i. Our factor and interaction list consists of B, C, AB, and e. None of these rows contain zeros, so we retain the entire list.

   We examine row B_j by ignoring column j. Our list of factors and interactions consists of B, C, AB, and e. Rows B_j, $C_{l(ij)}$, and e_{ijl} contain no zeros, but row $[AB]_{ij}$ has a zero. Therefore, we delete AB from our list for row B_j.

   We similarly examine row $[AB]_{ij}$ by ignoring columns i and j; row $C_{l(ij)}$ by ignoring columns i, j, and l; and row $e_{(ijl)}$ by ignoring columns i, j, and l. No items are deleted from the factor and interaction lists for these rows.

   As a result, we have the following:

Effect	Effect list
A_i	$A + AB + C + e$
B_j	$B + C + e$
$[AB]_{ij}$	$AB + C + e$
$C_{l(ij)}$	$C + e$
$e_{(ijl)}$	e

6. The appropriate F is determined as follows:

   A. The numerator for F is the mean square (MS) for the effect (factor or interaction) in question. The numerator degrees of freedom (DF) are the DF associated with the numerator MS.

   B. The denominator for F is the mean square for the effect having the same effect list as does the numerator effect, with the exception of not having the numerator effect in the effect list. The denominator degrees of freedom are the DF associated with the denominator MS.

   To test for the significance of factor A in our example, MS_A would be the numerator. As factor A has an effect list of A, AB, C, e, we desire in the denominator the mean square for the effect having an effect list

of AB, C, e; therefore, the denominator is MS_{AB} and

$$F = \frac{MS_A}{MS_{AB}}.$$

To test for the significance of factor B, place MS_B in the numerator of F. Because factor B has an effect list of B, C, e, the denominator of F needs to be the mean square for the effect having an effect list of C, e, meaning that the denominator is to be MS_C, and

$$F = \frac{MS_B}{MS_C}.$$

To test for the significance of factor interaction AB, we place MS_{AB} in the numerator of F; and, as AB has an effect list of AB, C, e, we need in the denominator the MS for the effect with an effect list of C, e; so we use MS_C in the denominator, and

$$F = \frac{MS_{AB}}{MS_C}.$$

To test for the significance of factor C, we place MS_C in the numerator of F. As factor C has an effect list of C, e, the denominator should be the MS for the effect containing only e in its effect list. Therefore,

$$F = \frac{MS_C}{MS_e}.$$

Occasionally, as in examples (*c*) and (*d*) in Section D.3, there is no single effect that has the effect list required in step 6.B above. If this is the case, then a combination of effect lists may be considered as an approximate procedure (Satterthwaite, 1946).

For the example in Section D.3c, steps 1–5 above yield the following effect list:

Effect	*Effect list*
A_i	$A + AB + AC + ABC + e$
B_j	$B + BC + e$
C_l	$C + BC + e$
$[AB]_{ij}$	$AB + ABC + e$
$[AC]_{il}$	$AC + ABC + e$
$[BC]_{jl}$	$BC + e$
$[ABC]_{ijl}$	$ABC + e$
$e_{(ijl)}$	e

To test for the significance of factor A in that example, we place MS_A in the numerator of F and observe that the associated effect list is A, AB, AC, ABC, e, and we require a denominator MS associated with an effect list of AB, AC, ABC, e. We note that if we add the effect lists for effect AB (namely AB, ABC, e) and effect AC (i.e., AC, ABC, e) and then subtract the list for effect ABC (namely, ABC, e), we have the desired list (AB, AC, ABC, e). Thus, we place in the denominator of F the combination of mean squares associated with the combination of effect lists used, namely $MS_{AB} + MS_{AC} - MS_{ABC}$. Therefore,

$$F = \frac{MS_A}{MS_{AB} + MS_{AC} - MS_{ABC}}.$$

(This statistic is sometimes referred to as a "quasi-F" and may—albeit rarely—be negative. In that case, treat it as if it were zero.)

If a combination of mean squares is used as the denominator of F, then the denominator degrees of freedom are

$$\frac{(\text{denominator of } F)^2}{\sum_i [(MS_i)^2/DF_i]},$$

where the summation takes place over all the mean squares in the denominator of F.

For our example, the numerator DF for testing the significance of factor A is DF_A, and the denominator DF is

$$\frac{(MS_{AB} + MS_{AC} - MS_{ABC})^2}{\frac{(MS_{AB})^2}{DF_{AB}} + \frac{(MS_{AC})^2}{DF_{AC}} + \frac{(MS_{ABC})^2}{DF_{ABC}}}.$$

In the following series of tables, mean squares for factors are denoted as MS_A, MS_B, and so on; mean squares for interaction among factors are indicated as MS_{AB}, MS_{AC}, MS_{ABC}, and so on; and the error mean square is denoted by MS_e. Degrees of freedom (DF) are indicated with the same subscripts as the mean squares.

If an analysis of variance has only one replicate per cell, the calculation of MS_e is not possible, the quantity calculated as the "remainder" MS being the MS for the highest-order interaction. If we assume that the highest-order interaction MS is insignificant, the remainder MS may be used in place of the error MS in the F calculation and other procedures where MS_e is called for.

D.2 TWO-FACTOR ANALYSIS OF VARIANCE

(a) Factors *A* and *B* Both Fixed (See Example 12.1.)

Source of variation	F	ν_1	ν_2
A	MS_A/MS_e	DF_A	DF_e
B	MS_B/MS_e	DF_B	DF_e
AB	MS_{AB}/MS_e	DF_{AB}	DF_e

(b) Factor *A* Fixed; Factor *B* Random (See Example 12.4.)

Source of variation	F	ν_1	ν_2
A	MS_A/MS_{AB}	DF_A	DF_{AB}
B	MS_B/MS_e	DF_B	DF_e
AB	MS_{AB}/MS_e	DF_{AB}	DF_e

(c) Factors *A* and *B* Both Random

Source of variation	F	ν_1	ν_2
A	MS_A/MS_{AB}	DF_A	DF_{AB}
B	MS_B/MS_{AB}	DF_B	DF_{AB}
AB	MS_{AB}/MS_e	DF_{AB}	DF_e

D.3 THREE-FACTOR ANALYSIS OF VARIANCE

(a) Factors *A*, *B* and *C* All Fixed (See Example 14.1.)

Source of variation	F	ν_1	ν_2
A	MS_A/MS_e	DF_A	DF_e
B	MS_B/MS_e	DF_B	DF_e
C	MS_C/MS_e	DF_C	DF_e
AB	MS_{AB}/MS_e	DF_{AB}	DF_e
AC	MS_{AC}/MS_e	DF_{AC}	DF_e
BC	MS_{BC}/MS_e	DF_{BC}	DF_e
ABC	MS_{ABC}/MS_e	DF_{ABC}	DF_e

(b) Factors A and B Fixed; Factor C Random

Source of variation	F	ν_1	ν_2
A	$MS_A/MS_{AC\cdot}$	DF_A	$DF_{AC\cdot}$
B	$MS_B/MS_{BC\cdot}$	DF_B	$DF_{BC\cdot}$
C	$MS_{C\cdot}/MS_e$	$DF_{C\cdot}$	DF_e
AB	$MS_{AB}/MS_{ABC\cdot}$	DF_{AB}	$DF_{ABC\cdot}$
AC	$MS_{AC\cdot}/MS_e$	$DF_{AC\cdot}$	DF_e
BC	$MS_{BC\cdot}/MS_e$	$DF_{BC\cdot}$	DF_e
ABC	$MS_{ABC\cdot}/MS_e$	$DF_{ABC\cdot}$	DF_e

(c) Factor A Fixed; Factors B and C Random

Source of variation	F	ν_1	ν_2
A	$MS_A/(MS_{AB} + MS_{AC\cdot} - MS_{ABC\cdot})$	DF_A	$\dfrac{(MS_{AB}+MS_{AC\cdot}-MS_{ABC\cdot})^2}{(MS_{AB})^2/DF_{AB}+(MS_{AC\cdot})^2/DF_{AC\cdot}+(MS_{ABC\cdot})^2/DF_{ABC\cdot}}$
B	$MS_B/MS_{BC\cdot}$	DF_B	$DF_{BC\cdot}$
C	$MS_{C\cdot}/MS_{BC\cdot}$	$DF_{C\cdot}$	$DF_{BC\cdot}$
AB	$MS_{AB}/MS_{ABC\cdot}$	DF_{AB}	$DF_{ABC\cdot}$
AC	$MS_{AC\cdot}/MS_{ABC\cdot}$	$DF_{AC\cdot}$	$DF_{ABC\cdot}$
BC	$MS_{BC\cdot}/MS_e$	$DF_{BC\cdot}$	DF_e
ABC	$MS_{ABC\cdot}/MS_e$	DF_{ABC}	DF_e

(d) Factors A, B, C All Random

Source of variation	F	ν_1	ν_2
A	$MS_A/(MS_{AB} + MS_{AC\cdot} - MS_{ABC\cdot})$	DF_A	$\dfrac{(MS_{AB}+MS_{AC\cdot}-MS_{ABC\cdot})^2}{(MS_{AB})^2/DF_{AB}+(MS_{AC\cdot})^2/DF_{AC\cdot}+(MS_{ABC\cdot})^2/DF_{ABC\cdot}}$
B	$MS_B/(MS_{AB} + MS_{BC\cdot} - MS_{ABC\cdot})$	DF_B	$\dfrac{(MS_{AB}+MS_{BC\cdot}-MS_{ABC\cdot})^2}{(MS_{AB})^2/DF_{AB}+(MS_{BC\cdot})^2/DF_{BC\cdot}+(MS_{ABC\cdot})^2/DF_{ABC\cdot}}$
C	$MS_{C\cdot}/(MS_{AC\cdot} + MS_{BC\cdot} - MS_{ABC\cdot})$	$DF_{C\cdot}$	$\dfrac{(MS_{AC\cdot}+MS_{BC\cdot}-MS_{ABC\cdot})^2}{(MS_{AC\cdot})^2/DF_{AC\cdot}+(MS_{BC\cdot})^2/DF_{BC\cdot}+(MS_{ABC\cdot})^2/DF_{ABC\cdot}}$
AB	$MS_{AB}/MS_{ABC\cdot}$	DF_{AB}	$DF_{ABC\cdot}$
AC	$MS_{AC}/MS_{ABC\cdot}$	$DF_{AC\cdot}$	$DF_{ABC\cdot}$
BC	$MS_{BC}/MS_{ABC\cdot}$	DF_{BC}	$DF_{ABC\cdot}$
ABC	$MS_{ABC\cdot}/MS_e$	$DF_{ABC\cdot}$	DF_e

D.4 NESTED ANALYSIS OF VARIANCE

(a) Factor A either Fixed or Random; Factor B Random and Nested within Factor A (See Example 15.1.)

Source of variation	F	ν_1	ν_2
A	MS_A/MS_B	DF_A	DF_B
B	MS_B/MS_e	DF_B	DF_e

(b) Factor *A* Either Fixed or Random; Factor *B* Random and Nested within Factor *A*; Factor *C* Random and Nested within Factor *B*

Source of variation	F	ν_1	ν_2
A	MS_A/MS_B	DF_A	DF_B
B	MS_B/MS_C	DF_B	DF_C
C	MS_C/MS_e	DF_C	DF_e

(c) Factors *A* and *B* Fixed; Factor *C* Random and Nested within Factors *A* and *B* (See Example 15.2.)

Source of variation	F	ν_1	ν_2
A	MS_A/MS_C	DF_A	DF_C
B	MS_B/MS_C	DF_B	DF_C
AB	MS_{AB}/MS_C	DF_{AB}	DF_C
C	MS_C/MS_e	DF_C	DF_e

(d) Factor *A* Fixed; Factor *B* Random; Factor *C* Random and Nested within Factors *A* and *B*

Source of variation	F	ν_1	ν_2
A	MS_A/MS_{AB}	DF_A	DF_{AB}
B	MS_B/MS_C	DF_B	DF_C
AB	MS_{AB}/MS_C	DF_{AB}	DF_C
C	MS_C/MS_e	DF_C	DF_e

(e) Factors *A* and *B* Random; Factor *C* Random and Nested within Factors *A* and *B*

Source of variation	F	ν_1	ν_2
A	MS_A/MS_{AB}	DF_A	DF_{AB}
B	MS_B/MS_{AB}	DF_B	DF_{AB}
AB	MS_{AB}/MS_C	DF_{AB}	DF_C
C	MS_C/MS_e	DF_C	DF_e

Answers to Exercises

Chapter 3

3.1. **(a)** 13.8 kg; **(b)** 10.7 kg; **(c)** 17.8 kg; **(d)** 17.8 kg.

3.2. **(a)** 3.56 kg; **(b)** 3.6 kg.

3.3. **(a)** 46.63 yr; **(b)** 46.3 yr; **(c)** 44.58 yr; **(d)** 46.3 yr.

3.4. **(a)** 2.33 g; **(b)** 2.33 g; **(c)** 2.4 g; **(d)** 2.358 g; **(e)** 2.4 g.

3.5. 0.89 g/100 g.

Chapter 4

4.1. **(a)** SS = 156.028 g^2, s^2 = 39.007 g^2; **(b)** same as (a).

4.2. **(a)** Range = 236.4 mg/100 ml to 244.8 mg/100 ml = 8.4 mg/100 ml; **(b)** SS = 46.1886 $(mg/100\ ml)^2$; **(c)** s^2 = 7.6981 $(mg/100\ ml)^2$; **(d)** s = 2.77 mg/100 ml; **(e)** V = 0.0115 = 1.15%.

4.3. $k = 6, n = 97$; **(a)** H' = 0.595; **(b)** H'_{max} = 0.778; **(c)** J' = 0.76.

4.4. $k = 6, n = 97$; **(a)** H = 0.554; **(b)** c = 16, d = 0.1667, H_{max} = 0.741; **(c)** J = 0.75.

Chapter 5

5.1. **(a)** (3)(2) = 6; **(b)** H,G H,P M,G M,P L,G L,P.

5.2. (3)(4)(2) = 24.

5.3. 2^{23} = 8,388,608.

5.4. ${}_5P_5 = 5!$ = 120.

5.5. ${}_{12}P_5 = 12!/7!$ = 95,040.

5.6. ${}_8P_{4,2,2} = 8!/[4!2!2!]$ = 420.

5.7. ${}_9C_5 = 9!/(5!4!)$ = 126.

5.8. O: 0.49; A: 0.38; B: 0.09; AB: 0.04.

5.9. n = 29; 0.38, 0.21, 0.14, 0.07, 0.07, 0.07, 0.07.

5.10. **(a)** P = 0.38; **(b)** P = 0.38 + 0.04 = 0.42.

5.11. **(a)** $P = 4/29$ = 0.14; **(b)** $P = 4/29 + 2/29 + 2/29$ = 0.28.

5.12. **(a)** $P = \left(\frac{1}{2}\right)(1) = \left(\frac{1}{2}\right)$ = 0.5; **(b)** $P = \left(\frac{1}{2}\right)(1) = \left(\frac{1}{2}\right)$ = 0.5; **(c)** $P = \left(\frac{1}{2}\right)(0) = 0$.

5.13. **(a)** $P = \left(\frac{1}{13}\right)\left(\frac{1}{4}\right) = \frac{1}{52}$ = 0.019; **(b)** $P = \left(\frac{1}{4} + \frac{1}{4}\right)\left(\frac{1}{13}\right) = \frac{1}{26}$ = 0.038;

(c) $P = \left(\frac{1}{2}\right)\left(\frac{3}{13}\right) = \frac{3}{26}$ = 0.12.

5.14. **(a)** P(all 3 white) = $[P(W)][P(W)][P(W)] = \left(\frac{2}{6}\right)\left(\frac{2}{4}\right)\left(\frac{3}{5}\right) = \frac{12}{120}$ = 0.10; **(b)** P(2 white) = $[P(W)][P(W)][P(B)] + [P(W)][P(B)][P(W)] + [P(B)][P(W)][P(W)] = \left(\frac{2}{6}\right)\left(\frac{2}{4}\right)\left(\frac{2}{5}\right) + \left(\frac{2}{6}\right)\left(\frac{2}{4}\right)\left(\frac{3}{5}\right) + \left(\frac{4}{6}\right)\left(\frac{2}{4}\right)\left(\frac{3}{5}\right) = \frac{8}{120} + \frac{12}{120} + \frac{24}{120} = \frac{44}{120}$ = 0.37.

(c) P(2 or 3 white) = 0.10 + 0.37 = 0.47.

5.15. **(a)** $P = 3/22$ = 0.14; **(b)** $P = 2/5$ = 0.40; **(c)** $P = 3/10$ = 0.30.

Chapter 6

6.1. $\sum f_i = n$ = 37, $\overline{X}$ = 4.6514, $\sum(X_i - \overline{X})^2$ = 2.2922, $\sum(X_i - \overline{X})^3$ = −0.4049, $\sum(X_i - \overline{X})^4$ = 0.5110, **(a)** $\sqrt{b_1}$ = −0.71. **(b)** b_2 = 3.60. **(c)** $Q_1 = X_{9.5}$ = 4.5 km, $Q_2 = M = X_{19}$ = 4.7 kg, $Q_3 = X_{28.5}$ = 4.8 kg; skewness = −0.100 **(d)** $\mathcal{O}_1 = X_5$ = 4.3 kg, $\mathcal{O}_2 = Q_1$ = 4.5 kg, $\mathcal{O}_3 = X_{12}$ = 4.6 kg; $\mathcal{O}_5 = X_{26}$ = 4.8 kg, $\mathcal{O}_6 = Q_3$ = 4.8 kg, $\mathcal{O}_7 = X_{33}$ = 4.9 kg; kurtosis = 1.333.

6.2. **(a)** Z = (78.0 g − 63.5 g)/12.2 g = 1.19, $P(X \geq 78.0\ g) = P(Z \geq 1.19)$ = 0.1170; **(b)** $P(X \leq 78.0\ g) = 1.0000 - P(X \geq 78.0\ g)$ = 1.000 − 0.1170 = 0.8830; **(c)** (0.1170)(1000) = 117; **(d)** Z = (41.0 g − 63.5 g)/12.2 g = −1.84, $P(X \leq 41.0\ g) = P(Z \leq -1.84)$ = 0.0329

6.3. **(a)** $P(X \leq 60.0\ g) = P(Z \leq -0.29)$ = 0.3859, $P(X \geq 70.0\ g) = P(Z \geq 0.53)$ = 0.2981, $P(60.0\ g \leq X \leq 70.0\ g)$ = 1.0000 − 0.3859 − 0.2981 = 0.3160; **(b)** $P(X \leq 60.0\ g) = P(Z \leq -0.29)$ = 0.3859, $P(X \leq 50.0\ g) = P(Z \leq -1.11)$ = 0.1335, $P(50.0\ g \leq X \leq 60.0\ g) = P(-1.11 \leq Z \leq -0.29)$ = 0.3859 − 0.1335 = 0.2524.

6.4. **(a)** $\sigma_{\overline{X}} = \sigma/\sqrt{n}$ = 12.2 g/$\sqrt{10}$ = 3.86 g; **(b)** Z = (65.0 g − 63.5)/3.86 g = 0.39, $P(\overline{X} \geq 65.0\ g) = P(Z \geq 0.39)$ = 0.3483; **(c)** $P(\overline{X} \leq 62.0\ g) = P(Z \leq -0.39)$ = 0.3483, $P(\overline{X} \leq 60.0\ g) = P(Z \leq -0.91)$ = 0.1814, $P(60.0\ g \leq \overline{X} \leq 62.0\ g)$ = 0.3483 − 0.1814 = 0.1669.

6.5. **(a)** $\overline{X}$ = 10.43 g/L; Z = (10.43 mg/L − 10.00 mg/L)/0.24 mg/L = 1.79; $P(Z \geq 10.00\ mg/L)$ = 0.0367; as 0.0367 < 0.05, reject H_0. **(b)** $Z_{0.05(1)}$ = 1.645, L_1 = 10.43 mg/L −

$(1.645)(0.24\ \text{mg/L}) = 10.04\ \text{mg/L}$, $L_2 = \infty$; $\mu_0 = 10.00\ \text{mg/L}$, $10.00\ \text{mg/L} < 10.04\ \text{mg/L}$ so H_0 is rejected.

6.6. $\sigma_{\overline{X}} = \sqrt{89.06\ \text{days}^2/24} = 3.71$ days; **(a)** for 99% confidence, $Z_{0.010(2)} = 2.575$, $L_1 = 61.4\ \text{days} - (2.575)(1.93\ \text{days}) = 61.4\ \text{days} - 4.9\ \text{days} = 56.5$ days, $L_2 = 61.4\ \text{days} + 4.9\ \text{days} = 66.3$ days; **(b)** for 95% confidence, $Z_{0.05(2)} = 1.960$, $L_1 = 57.6$ days, $L_2 = 65.2$ days; **(c)** for 90% confidence, $Z_{0.10(2)} = 1.645$, $L_1 = 58.2$ days, $L_2 = 64.6$ days.

Chapter 7

7.1. H_0: $\mu = 29.5$ days, H_A: $\mu \neq 29.5$ days, $\overline{X} = 27.7$ days, $s_{\overline{X}} = 0.708$ days, $n = 15$, $t = 2.542$, $\nu = 15 - 1 = 14$, $t_{0.05(2),14} = 2.145$, $0.02 < P(|t| \geq 2.542) < 0.05$ [$P = 0.023$]; therefore, reject H_0 and conclude that the sample came from a population with a mean that is not 29.5 days.

7.2. H_0: $\mu \geq 32$ mmole/kg, H_A: $\mu < 32$ mmole/kg, $\overline{X} = 29.77$ mmole/kg, $s_{\overline{X}} = 0.5$ mmole/kg, $n = 13$, $t = -4.46$, $\nu = 12$, $t_{0.05(1),12} = 1.782$, $P(t < -4.46) < 0.0005$ [$P = 0.00039$]; therefore, reject H_0 and conclude that the sample came from a population with a mean less than 32 mmole/kg.

7.3. Graph, which includes three 95% confidence intervals: 0.458 ± 0.057 kcal/g; 0.413 ± 0.059 kcal/g; 0.327 ± 0.038 kcal/g.

7.4. **(a)** 13.55 ± 1.26 cm; **(b)** $n = 28$; **(c)** $n = 9$; **(d)** $n = 15$. **(e)** For $\overline{X}$ of second sample, $m = 10$: $L_1 = 13.55\ \text{cm} - 2.11\ \text{cm} = 11.44$ cm, $L_2 = 13.55\ \text{cm} + 2.11\ \text{cm} = 15.66$ cm.

7.5. **(a)** $n = 30$; **(b)** $n = 41$; **(c)** $n = 42$; **(d)** $d = 2.2$ cm; **(e)** $t_{\beta(1),24} = 1.378$, $0.05 < \beta < 0.10$, so $0.90 <$ power < 0.95; or, by normal approximation, $\beta = 0.08$ and power $= 0.92$ [$\beta = 0.09$ and power $= 0.91$].

7.6. **(a)** $N = 200$, $n = 50$, $s^2 = 97.8121\ \text{yr}^2$, $t_{0.05(2),49} = 2.010$; $s_{\overline{X}} = 1.2113$ yr. 95% confidence interval $= 53.87 \pm 2.43$ yr; **(b)** $t_{0.05(2),99} = 1.984$; $s_{\overline{X}} = 0.6993$ yr, 95% confidence interval $= 53.87 \pm 1.39$ yr.

7.7. **(a)** $s^2 = 6.4512$, $n = 18$, SS $= 109.6704\ \text{cm}^2$; $\chi^2_{0.025,17} = 30.191$, $\chi^2_{0.975,17} = 7.564$; $L_1 = 3.6326\ \text{cm}^2$, $L_2 = 14.4990\ \text{cm}^2$. **(b)** $s = 2.54$ cm; $L_1 = 1.91$ cm, $L_2 = 3.81$ cm. **(c)** $\chi^2 = 24.925$, $\chi^2_{0.05,17} = 27.587$; 24.925 is not > 27.587, so do not reject H_0; $0.05 < P < 0.10$ [$P = 0.096$]. **(d)** $\sigma^2 = 9.000\ \text{cm}^2$, $\chi^2 = 12.186$, $\chi^2_{0.95,17} = 8.672$; 12.186 is not < 8.672, so do not reject H_0; $0.10 < P < 0.25$ [$P = 0.21$]. **(e)** $\sigma_0^2/s^2 = 0.682$; by trial and error: $n = 71$, $\nu = 70$, $\chi^2_{0.75,70}/\chi^2_{0.05,70} = 61.698/90.531 = 0.9682$. **(f)** For s^2 of new sample, $m = 20$: $F_{0.05(2),19,17} = 2.63$, $F_{0.05(2),17,19} = 2.57$, $L_1 = 6.4512\ \text{cm}^2/2.57 = 2.51\ \text{cm}^2$, $L_2 = (6.4512\ \text{cm}^2)(2.63) = 16.97\ \text{cm}^2$; for s: $L_1 = 1.58$ cm, $L_2 = 4.12$ cm).

7.8. **(a)** Do not reject H_0; $P > 0.10$ **(b)** Reject H_0; $0.02 < P < 0.05$.

Chapter 8

8.1. H_0: $\mu_1 = \mu_2$, H_A: $\mu_1 \neq \mu_2$, $n_1 = 7$, $\text{SS}_1 = 108.6171\ (\text{mg/100 ml})^2$, $\overline{X}_1 = 224.24$ mg/100 ml, $\nu_1 = 6$, $n_2 = 6$, $\text{SS}_2 = 74.7533\ (\text{mg/100 ml})^2$, $\overline{X}_2 = 225.67$ mg/100 ml, $\nu_2 = 5$, $s_p^2 = 16.6700\ (\text{mg/100 ml})^2$, $s_{\overline{X}_1 - \overline{X}_2} = 2.27$ mg/100 ml, $t = -0.630$, $t_{0.05(2),11} = 2.201$; therefore, do not reject H_0; $P > 0.50$ [$P = 0.54$].

8.2. H_0: $\mu_1 \geq \mu_2$, H_A: $\mu_1 < \mu_2$, $n_1 = 7$, $\text{SS}_1 = 98.86\ \text{mm}^2$, $\nu_1 = 6$, $\overline{X}_1 = 117.9$ mm, $n_2 = 8$, $\text{SS}_2 = 62.88\ \text{mm}^2$, $\nu_2 = 7$, $\overline{X}_2 = 118.1$ mm, $s_p^2 = 12.44\ \text{mm}^2$, $s_{\overline{X}_1 - \overline{X}_2} = 1.82$ mm, $t = -0.11$, $t_{0.05(1),13} = 1.771$; therefore, do not reject H_0; $P > 0.25$ [$P = 0.46$].

8.3. H_0: $\mu_1 \geq \mu_2$, H_0: $\mu_1 < \mu_2$, $\overline{X}_1 = 4.6$ kg, $s_1^2 = 11.02\ \text{kg}^2$, $n_1 = 18$; $\nu_1 = 17$, $\overline{X}_2 = 6.0\ \text{kg}^2$, $s_2^2 = 4.35\ \text{kg}^2$, $n_2 = 26$, $\nu_2 = 25$, $s_{\overline{X}_1 - \overline{X}_2} = 0.88$ kg, $t = -1.59$, $t_{0.05(1),42} = 1.682$; therefore, do not reject H_0, $0.05 < P < 0.10$ [$P = 0.060$].

8.4. H_0: $\mu_2 - \mu_1 \leq 10$ g, H_A: $\mu_2 - \mu_1 > 10$ g, $\overline{X}_1 = 334.6$ g, $\text{SS}_1 = 364.34\ \text{g}^2$, $n_1 = 19$, $\nu_1 = 18$, $\overline{X}_2 = 349.8$ g, $\text{SS}_2 = 286.78\ \text{g}^2$, $n_2 = 24$, $\nu_2 = 23$, $s_p^2 = 15.88\ \text{g}^2$, $s_{\overline{X}_1 - \overline{X}_2} = 1.22$ g, $t = 4.26$, $t_{0.05(1),41} = 1.683$ therefore, reject H_0 and conclude that μ_2 is at least 10 g greater than μ_1; $P < 0.0005$ [$P = 0.00015$].

8.5. **(a)** H_0 is not rejected; $\overline{X}_p = 224.90$ mg/100 ml; $t_{0.05(2),11} = 2.201$; $s_p^2 = 16.6700\ (\text{mg/100 ml})^2$; 95% confidence interval $= 22.490 \pm \sqrt{16.5700/13} = 224.90 \pm 1.13$; $L_1 = 223.77$ mg/100 ml, $L_2 = 226.03$ mg/100 ml. **(b)** $\overline{X}_1 - \overline{X}_2 = -3.43$ mg/100 ml; $s_c^2 = 6.6601\ (\text{mg/100 ml})^2$; 95% prediction interval $= -3.43 \pm 2.201\sqrt{6.6601} = -3.43 \pm 5.68$; $L_1 = -9.29$ mg/100 ml, $L_2 = 2.25$ mg/100 ml.

8.6. $s_p^2 = (244.66 + 289.18)/(13 + 13) = 20.53(\text{km/hr})^2$; $d = 2.0$ km/hr. If we guess

$n = 50$, then $\nu = 2(50 - 1) = 98$, $t_{0.05(2),98} = 1.984$, and $n = 40.4$. Then, guess $n = 41$; $\nu = 80$, $t_{0.05(2),80} = 1.990$, and $n = 40.6$. So, the desired $n = 41$.

8.7. **(a)** If we guess $n = 25$, then $\nu = 2(24) = 48$. $t_{0.05(2),48} = 2.011$, $t_{0.10(1),48} = 1.299$, and $n = 18.0$. Then, guess $n = 18$; $\nu = 34$, $t_{0.05(2),34} = 2.032$, $t_{0.10(1),34} = 1.307$, and $n = 18.3$. So, the desired sample size is $n = 19$. **(b)** $n = 20.95$, $\nu = 40$, $t_{0.05(2),40} = 2.021$, $t_{0.10(1),40} = 1.303$, and $\delta = 4.65$ km/hr. **(c)** $n = 50$, $\nu = 98$, $t_{0.05(2),98} = 1.984$, and $t_{\beta(1),98} = 0.223$; $\beta > 0.25$, so power < 0.75 (or, by the normal approximation, $\beta = 0.41$, so power $= 0.59$).

8.8. $n_1 = 7, \nu_1 = 6, s_1^2 = 18.1029\ (\text{mg}/100\ \text{ml})^2$, $n_2 = 6, \nu_2 = 5, s_2^2 = 14.9507\ (\text{mg}/100\ \text{ml})^2$; $F = 1.21$, $F_{0.05(2),6,5} = 6.98$; do not reject H_0; $P > 0.50$ [$P = 0.85$].

8.9. $n_1 = 7, \nu_1 = 6, s_1^2 = 16.48\ \text{mm}^2$, $n_2 = 8, \nu_2 = 7$, $s_2^2 = 8.98\ \text{mm}^2$; $F = 1.83$, $F_{0.05(2),6,7} = 3.87$; do not reject H_0; $0.10 < P < 0.25$ [$P = 0.22$].

8.10. $n_1 = 21, \nu_1 = 20, s_1^2 = 38.71\ \text{g}^2$, $n_2 = 20, \nu_2 = 19$, $s_2^2 = 21.35\ \text{g}^2$, $s_1^2/s_2^2 = 1.81$. **(a)** $F_{0.05(2),20,19} = 2.51$, $F_{0.05(2),19,20} = 2.48$; $L_1 = 0.72\ \text{g}^2$, $L_2 = 4.49\ \text{g}^2$. **(b)** $Z_{0.05(1)} = 1.6449$, $Z_{0.10(1)} = 1.2816$, $n = 26.3$ (so a sample of at least 27 should be taken from each population). **(c)** $Z_{\beta(1)} = 0.87$, $\beta(1) = 0.19$, power $= 0.81$.

8.11. H_0: $\sigma_1/\mu_1 = \sigma_2/\mu_2$, H_A: $\sigma_1/\mu_1 \neq \sigma_2/\mu_2$; $s_1 = 3.82$ cm, $V_1 = 0.356$, $s_2 = 2.91$ cm, $V_2 = 0.203$; $V_p = 0.285$; $Z = 2.533$, $Z_{0.05(2)} = 1.960$; reject H_0; $0.01 < P < 0.02$ [$P = 0.013$].

8.12. H_0: Male and female turtles have the same serum cholesterol concentrations; H_A: Male and female turtles do not have the same serum cholesterol concentrations.

Male ranks	*Female ranks*
2	5
1	3
11	12
10	8
4	6
7	13
9	

$R_1 = 44, n_1 = 7, R_2 = 47, n_2 = 6$; $U = 26$; $U' = (7)(6) - 26 = 16$; $U_{0.05(2),7,6} = U_{0.05(2),6,7} = 36$; therefore, do not reject H_0; $P > 0.20$ [$P = 0.53$].

8.13. H_0: Northern birds do not have shorter wings than southern birds; H_A: Northern birds have shorter wings than southern birds.

Northern ranks	*Southern ranks*
11.5	5
1	7
15	13
8.5	2.5
5	5
2.5	8.5
10	14
	11.5

$R_1 = 53.5, n_1 = 7, n_2 = 8$; $U = 30.5$; $U' = 25.5$; $U_{0.05(1),7,8} = 43$; therefore, do not reject H_0; $P > 0.10$ [$P \approx 0.41$].

8.14. H_0: Intersex cells have 1.5 times the volume of normal cells; H_A: Intersex cells do not have 1.5 times the volume of normal cells.

Normal × 1.5	*Rank*	*Intersex*	*Rank*
372	4	380	9
354	1	391	13
403.5	16	377	8
381	10	392	14
373.5	5	398	15
376.5	7	374	6
390	12		
367.5	3		
358.5	2		
382.5	11		

$R_1 = 71, n_1 = 10, n_2 = 6$; $U = 44$, $U' = 16$; $U_{0.05(2),10,6} = 49$; therefore, do not reject H_0; $0.10 < P < 0.20$.

Chapter 9

9.1. H_0: $\mu_d = 0$, H_A: $\mu_d \neq 0$; $\bar{d} = -2.09\ \mu\text{g}/\text{m}^3$, $s_{\bar{d}} = 1.29\ \mu\text{g}/\text{m}^3$. **(a)** $t = -1.62, n = 11, \nu = 10$, $t_{0.05(2),10} = 2.228$; therefore, do not reject H_0: $0.10 < P < 0.20$ [$P = 0.14$]. **(b)** 95% confidence interval for $\mu_d = -2.09 \pm (2.228)(1.29) = -2.09 \pm 2.87$; $L_1 = -4.96\ \mu\text{g}/\text{m}^3$, $L_2 = 0.78\ \mu\text{g}/\text{m}^3$.

9.2.

d_i	*Signed rank*
−4	−5.5
−2	−3
−5	−7.5
6	9
−5	−7.5
1	1.5
−7	−10.5
−4	−5.5
−7	−10.5
1	1.5
3	4

$T = 9 + 1.5 + 1.5 + 4 = 16$; $T_{0.05(2),11} = 10$; since T is not ≤ 10, do not reject H_0; $0.10 < P < 0.20$.

9.3. $s_1^2 = 285.21\ (\mu g/m^3)^2, s_2^2 = 270.36\ (\mu g/m^3)^2$; F = 1.055; r = 0.9674; t = 0.317; $t_{0.05(2),9} = 2.262$; do not reject H_0: $\sigma_1^2 = \sigma_2^2$; $P > 0.50$ [$P = 0.76$].

Chapter 10

10.1. H_0: $\mu_1 = \mu_2 = \mu_3 = \mu_4$; H_A: The mean food consumption is not the same for all four months; $F = 0.7688/0.0348 = 22.1$; $F_{0.05(1),3,18} = 3.16$; reject H_0; $P < 0.0005$ [$P = 0.0000029$].

10.2. $k = 5, \nu_1 = 4, n = 12, \nu_2 = 55, \sigma^2 = 1.54(°C)^2$, $\delta = 2.0°C$; $\phi = 1.77$; from Appendix Figure B.1d we find that the power is about 0.88.

10.3. $n = 16$, for which $\nu_2 = 75$ and $\phi = 2.04$. (The power is a little greater than 0.95; for $n = 15$ the power is about 0.94.)

10.4. $\nu_2 = 45$, power = 0.95, $\phi = 2.05$; minimum detectable difference is about 2.5°C.

10.5. H_0: The amount of food consumed is the same during all four months; H_A: The amount of food consumed is not the same during all four months; $n_1 = 5, n_2 = 6, n_3 = 6, n_4 = 5$; $R_1 = 69.5$, $R_2 = 23.5, R_3 = 61.5, R_4 = 98.5$; $N = 22$; $H = 17.08$; $\chi^2_{0.05,3} = 7.815$; reject H_0; $P \ll 0.001$. H_c (i.e., H corrected for ties) would be obtained as $\sum t = 120$, $C = 0.9887$, $H_c = 17.28$. $F = 27.9$, $F_{0.05(1),3,17} = 3.20$; reject H_0; $P \ll 0.0005$ [$P = 0.00000086$].

10.6. H_0: $\sigma_1^2 = \sigma_2^2 = \sigma_3^2$; H_A: The three population variances are not all equal; $B = 5.94517$, $C = 1.0889$, $B_c = B/C = 5.460$; $\chi^2_{0.05,2} = 5.991$; do not reject H_0; $0.05 < P < 0.10$ [$P = 0.065$].

10.7. H_0: $\mu_1/\sigma_1 = \mu_2/\sigma_2 = \mu_3/\sigma_3 = \mu_4/\sigma_4$; $s_1 = 0.699, V_1 = 0.329, s_2 = 0.528, V_2 = 0.302, s_3 = 0.377, V_3 = 0.279, s_4 = 0.451, V_4 = 0.324$; $V_p = 0.304$; $\chi^2 = 1.320$, $\chi^2_{0.05,3} = 7.815$; do not reject H_0; $0.50 < P < 0.75$ [$P = 0.72$].

Chapter 11

11.1. **(a, b)** Ranked sample means: 14.8 16.2 20.2; $k = 3, n = 8, \alpha = 0.05, s^2 = 8.46, \nu = 21$ (which is not in Appendix Table B.5, so use $\nu = 20$, which is in the table); reject H_0: $\mu_2 = \mu_1$; reject H_0: $\mu_2 = \mu_3$; do not reject H_0: $\mu_3 = \mu_1$. Therefore, the overall conclusion is $\mu_1 = \mu_3 \neq \mu_2$. **(c)** $\overline{X}_p = \overline{X}_{1,3} = 15.5, t_{0.05(2),21} = 2.080$, $n_1 + n_2 = 16$, 95% CI for $\mu_{1,3} = 15.5 \pm 1.5$; 95% CI for $\mu_2 = 20.2 \pm 2.1$; $\overline{X}_{1,3} - \overline{X}_2 = -4.7$, SE = 1.03, 95% CI for $\mu_{1,3} - \mu_2 = -4.7 \pm 3.2$.

11.2. $\overline{X}_1 = 4.82, n_1 = 5; \overline{X}_2 = 4.33, n_2 = 6; \overline{X}_3 = 4.67$, $n_3 = 6; \overline{X}_4 = 5.24, n_4 = 5; s^2 = 0.0348; \nu = 18$; $q_{0.05,18,4} = 3.997$; conclusion: $\mu_2 \neq \mu_3 = \mu_1 \neq \mu_4$.

11.3. Means, sample sizes, and $q_{0.05,18,14}$ as in Exercise 11.2; $s_1^2 = 0.0170, s_2^2 = 0.0307, s_3^2 = 0.0227$, $s_4^2 = 0.0730$, conclusion: $\mu_2 \neq \mu_3 = \mu_1 \neq \mu_4$.

11.4. Ranked sample means: 60.62, 69.30, 86.24, 100.35; sample sizes of 5, 5, 5, and 4, respectively; $k = 4$, $\nu = 15, \alpha = 0.05, s^2 = 8.557$; control group is group 1; $q'_{0.05(2),15,4} = 2.61$; reject H_0: $\mu_4 = \mu_1$, reject H_0: $\mu_3 = \mu_1$, reject H_0: $\mu_2 = \mu_1$. Overall conclusion: The mean of the control population is different from the mean of each other population.

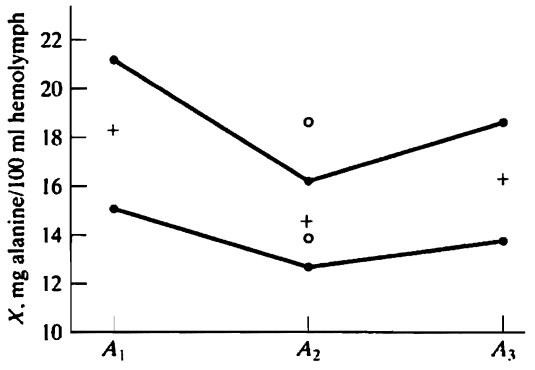
11.5. Ranked sample means: 60.62, 69.30, 86.24, 100.35; sample sizes of 5, 5, 5, and 4, respectively; $k = 4$, $\nu = 15, \alpha = 0.05, s^2 = 8.557$; critical value of S is 3.14; for H_0: $(\mu_1 + \mu_4)/2 - (\mu_2 + \mu_3)/2 = 0$, $S = 8.4$, reject H_0; for H_0: $(\mu_2 + \mu_4)/2 - \mu_3 = 0, S = 13.05$, reject H_0.

11.6. $R_1 = 21, R_2 = 38, R_3 = 61$. Overall conclusion: The variable being measured is the same magnitude in populations 1 and 2. The variable is of different magnitude in population 3.

Chapter 12

12.1. **(a)** H_0: There is no difference in mean hemolymph alanine among the three species; H_A: There is difference in mean hemolymph alanine among the three species; $F = 27.6304/2.1121 = 13.08$; $F_{0.05(1),2,18} = 3.55$; reject H_0; $P < 0.0005$ [$P = 0.00031$]. **(b)** H_0: There is no difference in mean hemolymph alanine between males and females; H_A: There is difference in mean hemolymph alanine between males and females; $F = 138.7204/2.1121 = 65.68$; $F_{0.05(1),1,18} = 4.41$ reject H_0; $P \ll 0.0005$ [$P = 0.00000020$]. **(c)** H_0: There is no species × sex interaction in mean hemolymph alanine; H_A: There is species × sex interaction in mean hemolymph alanine;

$F = 3.4454/2.1121 = 1.63$; $F_{0.05(1),2,18} = 3.55$; do not reject H_0; $0.10 < P < 0.25$ [$P = 0.22$].
(d) See graph below; the wide vertical distance between the open circles indicates difference between sexes; the vertical distances among the plus signs indicates difference among the three species;



the parallelism of the male and female lines indicates no interaction effect. **(e)** Ranked sample means: 14.43 16.13 18.14 (means 2, 3, and 1, respectively); $k = 3$; $n = 8$; $\alpha = 0.05$; $s^2 = 2.1121$; $\nu = 18$; reject H_0: $\mu_1 = \mu_2$, reject H_0: $\mu_1 = \mu_3$, do not reject H_0: $\mu_3 = \mu_2$.

12.2. H_0: All four plant varieties reach the same mean height (i.e., H_0: $\mu_1 = \mu_2 = \mu_3 = \mu_4$); H_A: All four plant varieties do not reach the same mean height; $F = 62.8461/0.4351 = 144$; $F_{0.05(1),3,15} = 3.29$; reject H_0; $P \ll 0.0005$ [$P < 10^{-10}$].

12.3. H_0: All four plant varieties reach the same height; H_A: All four plant varieties do not reach the same height; $R_1 = 18$, $R_2 = 24$, $R_3 = 12$, $R_4 = 6$; $\chi^2_{0.05,3} = 7.815$; reject H_0; $P < 0.001$.

12.4. H_0: There is no difference in potential acceptance among the three textbooks; H_A: The three textbooks do not have the same potential acceptance; $a = 4$, $b = 13$ (blocks 4 and 11 are deleted from the analysis); $Q = 5.53$; $\nu = 3$; $\chi^2_{0.05,3} = 7.815$; do not reject H_0; $0.10 < P < 0.25$ [$P = 0.14$].

Chapter 13

13.1. $\overline{X}' = 0.68339$, $s'_{\overline{X}} = 0.00363$; $L'_1 = 0.67481$, $L'_2 = 0.69197$; $L_1 = 3.73$ ml, $L_2 = 3.92$ ml.

13.2. $\overline{X}' = 61.48$, $s'_{\overline{X}} = 0.76$; $L'_1 = 59.53$, $L'_2 = 63.43$; $L_1 = 0.742$, $L_2 = 0.800$.

13.3. $\overline{X}' = 2.4280$, $s'_{\overline{X}} = 0.2329$; $L'_1 = 1.8292$, $L'_2 = 3.0268$; $L_1 = 2.85$, $L_2 = 8.66$.

Chapter 14

14.1. H_0: No effect of factor A; H_A: Factor A has an effect; $F = 10.2901/0.0805 = 127.8$; as $F_{0.05(1),3,72} \cong 2.74$, H_0 is rejected; $P \ll 0.0005$ [$P < 10^{-12}$]. H_0: No effect of factor B; $F = 3.8295/0.0805 = 47.6$; as $F_{0.05(1),2,72} \cong 3.13$, H_0 is rejected; $P \ll 0.0005$ [$P < 10^{-13}$]. H_0: No effect of factor C; $F = 4.2926/0.0805 = 53.3$; as $F_{0.05(1),1,72} \cong 3.98$, H_0 is rejected; $P \ll 0.0005$ [$P < 10^{-9}$]. H_0: No interaction between factors A and B; H_A: There is $A \times B$ interaction; $F = 0.1182/0.0805 = 1.47$; as $F_{0.05(1),6,72} \cong 2.23$, H_0 is not rejected; $P > 0.25$ [$P = 0.20$]. H_0: No interaction between factors A and C; $F = 0.6159/0.0805 = 7.65$; as $F_{0.05(1),3,72} \cong 2.74$, H_0 is rejected; $P < 0.0005$ [$P = 0.00017$]. H_0: No interaction between factors B and C; $F = 0.0039/0.0805 = 0.048$; as $F_{0.05(1),2,72} \cong 1.41$, H_0 is not rejected; $P > 0.25$ [$P = 0.95$]. H_0: No interaction between factors A, B, and C; $F = 0.1459/0.0805 = 1.81$; as $F_{0.05(1),6,72} \cong 2.23$, H_0 is not rejected; $0.10 < P < 0.25$ [$P = 0.11$].

14.2. H_0: No effect of factor A; H_A: Factor A has an effect; $F = 56.00347/0.03198 = 1751$; reject H_0; $P \ll 0.0005$ [$P < 10^{-14}$]. H_0: No effect of factor B; $F = 4.65125/0.03198 = 145.4$; reject H_0; $P \ll 0.0005$ [$P < 10^{-13}$]. H_0: No effect of factor C; $F = 8.6125/0.03198 = 269.3$; reject H_0: $P \ll 0.0005$ [$P < 10^{-13}$]. H_0: No effect of factor D; $F = 2.17056/0.03198 = 67.9$; reject H_0; $P \ll 0.0005$ [$P < 10^{-14}$]. H_0: No interaction between factors A and B; $F = 2.45681/0.03198 = 76.8$; reject H_0; $P \ll 0.0005$ [$P < 10^{-11}$]. H_0: No interaction between factors A and C; $F = 0.05014/0.03198 = 1.57$; do not reject H_0; $0.10 < P < 0.25$ [$P = 0.22$]. H_0: No interaction between factors A and D; $F = 0.06889/0.03198 = 2.15$; do not reject H_0; $0.10 < P < 0.25$ [$P = 0.13$]. H_0: No interaction between factors B and C; $F = 0.01681/0.03198 = 0.53$; do not reject H_0; $P > 0.25$ [$P = 0.47$]. H_0: No interaction between factors B and D; $F = 0.15167/0.03198 = 4.74$; reject H_0; $0.01 < P < 0.025$. H_0: No interaction between factor C and D; $F = 0.26000/0.03198 = 8.13$; reject H_0; $0.0005 < P < 0.001$ [$P = 0.00091$]. H_0: No interaction among factors A, B, and C; $F = 0.00125/0.03198 = 0.039$; do not reject H_0; $P > 0.25$ [$P = 0.84$]. H_0: No interaction among factors A, B, and D; $F = 0.14222/0.03198 = 2.11$; do not reject H_0; $0.10 < P < 0.25$ [$P = 0.13$]. H_0: No interaction among factors B, C, and D; $F = 0.00222/0.03198 = 0.069$; do not reject H_0; $P >$

0.25 [$P = 0.093$]. H_0: No interaction among factors A, B, C, and D; $F = 0.01167/0.03198 = 0.36$; do not reject H_0; $P > 0.25$ [$P = 0.70$].

14.3. H_0: No effect of factor A; H_A: There is an effect of factor A; $F = 239.39048/2.10954 = 113.5$; as $F_{0.05(1),1,22} = 4.30$, reject H_0; $P \ll 0.0005$ [$P < 10^{-9}$]. H_0: No effect of factor B; $F = 8.59013/2.10954 = 4.07$; as $F_{0.05(1),1,22} = 4.30$; do not reject H_0; $0.05 < P < 0.10$ [$P = 0.056$]. H_0: No interaction between factors A and B; $F = 0.10440/2.10954 = 0.05$; as $F_{0.05(1),1,22} = 4.30$, do not reject H_0; $P > 0.25$ [$P = 0.83$].

14.4. For Factor A: SS = 37.4719, DF = 3, MS = 12.4906; for remainder: SS = 3.5287, MS = 0.5881, DF = 6; $F = 21.2$; $F_{0.05(1),3,6} = 4.76$; $0.01 < P < 0.0025$; $P = 0.0014$; reject H_0.

Chapter 15

15.1. **(a)** $q_{\alpha,\nu,k} = q_{0.05,3,3} = 5.910$; $s^2 = 0.50$; SE = 0.3536; reject H_0: $\mu_2 = \mu_1$, $q = 15.56$ [$0.001 < P < 0.005$]; reject H_0 : $\mu_2 = \mu_3$, $q = 9.19$ [$0.01 < P < 0.025$], reject H_0: $\mu_3 = \mu_1$, $q = 6.35$ [$0.025 < P < 0.05$]. **(b)** $t_{0.05(2),3} = 3.182$; 95% CI = $\overline{X}_i \pm 1.13$ mg/100 ml.

15.2. **(a)** H_0: The mean fluoride concentrations are the same for all three samples at a given location; H_A: The mean fluoride concentrations are not the same for all three samples at a given location; $F = 0.008333/0.01778 = 0.469$; as $F < 1.0$, so do not reject H_0; $P > 0.25$ [$P = 0.82$]. **(b)** H_0: The mean fluoride concentration is the same at all three locations; H_A: The mean fluoride concentration is not the same at all three locations: $F = 1.1850/0.008333 = 142$; $F_{0.05(1),2,6} = 5.14$; reject H_0; $P \ll 0.0005$ [$P = 0.0000086$]. **(c)** $q_{\alpha,\nu,k} = q_{0.05,6,3} = 4.339$; $s^2 = 0.08333$; SE = 0.0373; $\overline{X}_1 = 1.15$, $\overline{X}_2 = 1.35$, $\overline{X}_3 = 2.00$; reject H_0: $\mu_3 = \mu_1$, $q = 22.79$ [$P < 0.001$]; reject H_0: $\mu_3 = \mu_2$, $q = 17.43$ [$P < 0.001$], reject H_0: $\mu_2 = \mu_1$, $q = 5.36$ [$0.01 < P < 0.025$]. **(d)** $t_{0.05(2),6} = 2.447$; 95% confidence interval (mg/L): $\overline{X}_i \pm 0.09$.

Chapter 16

16.1. H_0: $\mu_{11} = \mu_{12} = \mu_{13}$ and $\mu_{21} = \mu_{22} = \mu_{23}$; Wilks' $\Lambda = 0.0872$, Pillai's trace = 0.9128, Lawley-Hotelling trace = 10.4691, Roy's maximum root = 10.4681; for each, $F = 41.8723$, $P \ll 0.0001$; reject H_0.

16.2. For species, H_0: $\mu_{11} = \mu_{12}$ and $\mu_{21} = \mu_{22}$; Wilks' $\Lambda = 0.1820$, Pillai's trace = 0.8180, Lawley-Hotelling trace = 4.4956, Roy's maximum root = 4.4956; for each, $F = 33.7167$, $P \ll 0.0001$; reject H_0. For sex, H_0: $\mu_{11} = \mu_{12}$ and $\mu_{21} = \mu_{22}$; Wilks' $\Lambda = 0.8295$, Pillai's trace = 0.1705, Lawley-Hotelling trace = 0.2055, Roy's maximum root = 0.2055; for each, $F = 1.5415$, $P = 0.2461$; do not reject H_0. For species × sex interaction, H_0: There is no interaction; Wilks' $\Lambda = 0.8527$, Pillai's trace = 0.1473, Lawley-Hotelling trace = 0.1727, Roy's maximum root = 0.1727; for each, $F = 1.2954$, $P = 0.3027$; do not reject H_0.

Chapter 17

17.1. **(a)** $b = -0.0878$ ml/g/hr/°C, $a = 3.78$ ml/g/hr. **(b)** H_0: $\beta = 0$, H_A: $\beta \neq 0$; $F = 309$; reject H_0; $P \ll 0.0005$ [$P = 0.0000022$]. **(c)** H_0: $\beta = 0$, H_A: $\beta \neq 0$; $t = -17.6$; reject H_0: $P \ll 0.001$ [$P = 0.0000022$]. **(d)** $s_{Y \cdot X} = 0.17$ ml/g/hr; **(e)** $r^2 = 0.98$; **(f)** 95% confidence interval for $\beta = -0.0878 \pm 0.0122$; $L_1 = -0.1000$ ml/g/hr/°C, $L_2 = -0.0756$ ml/g/hr/°C.

17.2. **(a)** $\hat{Y} = 3.47 - (0.0878)(15) = 2.15$ ml/g/hr. **(b)** $s_{\hat{Y}} = 0.1021$ ml/g/hr; $L_1 = 1.90$ ml/g/hr, $L_2 = 2.40$ ml/g/hr. **(c)** $\hat{Y} = 2.15$ ml/g/hr. **(d)** $s_{\hat{Y}} = 0.1960$ ml/g/hr; $L_1 = 1.67$ ml/g/hr, $L_2 = 2.63$ ml/g/hr.

17.3. **(a)** $b = 9.73$ impulses/sec/°C, $a = 44.2$ impulses/sec. **(b)** H_0: $\beta = 0$, H_A: $\beta \neq 0$; $F = 311$; reject H_0; $P \ll 0.0005$ [$P < 10^{-13}$]. **(c)** $s_{Y \cdot X} = 8.33$ impulses/sec. **(d)** $r^2 = 0.94$. **(e)** H_0: The population regression is linear; H_A: The population regression is not linear; $F = 1.78$, do not reject H_0; $0.10 < P < 0.25$ [$P = 0.18$].

Chapter 18

18.1. **(a)** H_0: $\beta_1 = \beta_2$; $b_1 = 0.488$, $b_2 = 0.537$; $s_{b_1 - b_2} = 0.202$; $t = -0.243$; as $t_{0.05(2),54} = 2.005$, do not reject H_0; $P > 0.50$ [$P = 0.81$]. **(b)** H_0: The elevations of the two population regressions are the same; H_A: The elevations of the two population regressions are not the same; $b_c = 0.516$; $t = 10.7$; as $t_{0.05(2),55} \cong 2.004$, reject H_0; $P \ll 0.001$ [$P = 2 \times 10^{-14}$].

18.2. **(a)** H_0: $\beta_1 = \beta_2 = \beta_3$; H_A: All three β's are not equal; $F = 0.84$; as $F_{0.05(1),2,90} = 3.10$, do not reject H_0; $P > 0.25$ [$P = 0.44$]; $b_c = 3.16$. **(b)** H_0: The three population regression lines have the same elevation; H_A: The three lines do not all have the same elevation; $F = 4.61$; as $F_{0.05(1),2,90} = 3.10$, reject H_0; $0.01 < P < 0.025$ [$P = 0.012$].

Chapter 19

19.1. **(a)** $r = 0.86$. **(b)** $r^2 = 0.73$. **(c)** H_0: $\rho = 0$; H_A: $\rho \neq 0$; $s_r = 0.16$; $t = 5.38$; as $t_{0.05(2),10} = 2.228$; reject H_0; $P < 0.001$ [$P = 0.00032$]. Or: $r = 0.86$, $r_{0.05(2),10} = 0.576$; reject H_0; $P < 0.001$. Or: $F = 13.29$, $F_{0.05(2),10,10} = 3.72$; reject H_0: $P < 0.001$. **(d)** $L_1 = 0.56$, $L_2 = 0.96$.

19.2. **(a)** H_0: $\rho \leq 0$; H_A: $\rho > 0$; $r = 0.86$; $t = 5.38$; $t_{0.05(1),10} = 1.812$; reject H_0; $P < 0.0005$ [$P = 0.00016$]. Or: $r_{0.05(1),10} = 0.497$; reject H_0; $P < 0.0005$. Or: $F = 13.29$; $F_{0.05(1),10,10} = 2.98$; reject H_0: $P < 0.0005$. **(b)** H_0: $\rho = 0.50$; H_A: $\rho \neq 0.50$; $r = 0.86$; $z = 1.2933$; $\zeta_0 = 0.5493$; $\sigma_z = 0.3333$; $Z = 2.232$; $Z_{0.05(2)} = 1.960$; reject H_0; $0.02 < P < 0.05$ [$P = 0.026$].

19.3. **(a)** H_0: $\rho_1 = \rho_2$; H_A: $\rho_1 \neq \rho_2$; $z_1 = -0.4722$. $z_2 = -0.4236$; $\sigma_{z_1 - z_2} = 0.2910$; $Z = -0.167$; $Z_{0.05(2)} = 1.960$; do not reject H_0; $P > 0.50$ [$P = 0.87$]. **(b)** $z_w = -0.4449$; $r_w = -0.42$.

19.4. H_0: $\rho_1 \geq \rho_2$; H_A: $\rho_1 < \rho_2$; $z_1 = 0.4847$, $z_2 = 0.6328$; $\sigma_{z_1 - z_2} = 0.3789$; $Z = -0.3909$; $Z_{0.05(1)} = 1.645$; do not reject H_0; $P > 0.25$ [$P = 0.35$].

19.5. **(a)** H_0: $\rho_1 = \rho_2 = \rho_3$; H_A: The three population correlation coefficients are not all the same; $\chi^2 = 111.6607 - (92.9071)^2/78 = 0.998$; $\chi^2_{0.05,2} = 5.991$; do not reject H_0; $0.50 < P < 0.75$ [$P = 0.61$]. $\chi^2_P = 1.095$, $0.50 < P < 0.75$ [$P = 0.58$]. **(b)** $z_w = 92.9071/78 = 1.1911$; $r_w = 0.83$.

19.6. **(a)** $\sum d_i^2 = 88.00$, $r_s = 0.69$; **(b)** H_0: $\rho_s = 0$; H_A: $\rho_s \neq 0$; as $(r_s)_{0.05(2),12} = 0.587$, reject H_0; $0.01 < P < 0.02$.

19.7. **(a)** $r_T = 0.914$; **(b)** reject H_0; $0.005 < P < 0.01$.

19.8. **(a)** $r_n = (16 - 7)/(16 + 7) = 0.39$. **(b)** H_0: There is no correlation between the type of institution a college president heads and the type of institution he or she attended as a undergraduate; H_A: There is a correlation between the type of school headed and the type attended. By Fisher exact test (using Appendix Table B.28): $n = 23$, $m_1 = 9$, $m_2 = 11$, $f = 2$, critical $f_{0.05(2)} = 1$ and 7; as f is not ≤ 1 and is not ≥ 7, do not reject H_0.

19.9. **(a)** $r_I = (0.000946 - 0.00213)/(0.000946 + 0.001213) = -0.12$. **(b)** H_0: There is no correlation between corticosterone determinations from the same laboratory (i.e., $\rho_I = 0$); H_A: There is no correlation between corticosterone determinations from the same laboratory (i.e., $\rho_I \neq 0$); $F = 0.000946/0.001213 = 0.78$; since $F_{0.05(1),3,4} = 6.59$, do not reject H_0; $P > 0.25$ [$P = 0.56$].

19.10. **(a)** $r_c = 0.9672$. **(b)** $z_c = 2.0470$, $r = 0.9991$, $U = 0.2502$, $\sigma_{z_c} = 0.2135$; for ζ_c: $L_1 = 1.6285$, $L_2 = 2.4655$; for ρ_c: $L_1 = 0.926$, $L_2 = 0.986$.

Chapter 20

20.1. **(a)** $\hat{Y} = -30.14 + 2.07X_1 + 2.58X_2 + 0.64X_3 + 1.11X_4$. **(b)** H_0: No population regression; H_A: There is a population regression; $F = 90.2$, $F_{0.05(1),4,9} = 3.63$, reject H_0, $P \ll 0.0005$ [$P = 0.00000031$]. **(c)** H_0: $\beta_1 = 0$, H_A: $\beta_1 \neq 0$; $t_{0.05(2),9} = 2.262$; "*" below denotes significance:

i	b_i	s_{b_i}	$t = \frac{b_i}{s_{b_i}}$	*Conclusion*
1	2.07	0.46	4.50*	Reject H_0.
2	2.58	0.74	3.49*	Reject H_0.
3	0.64	0.46	1.39	Do not reject H_0.
4	1.11	0.76	1.46	Do not reject H_0.

(d) $s_{Y \cdot 1,2,3,4} = 3.11$ g; $R^2 = 0.9757$. **(e)** $\overline{Y} = 61.73$ g. **(f)** $s_{\hat{Y}} = 2.9549$ g, $L_1 = 55.0$ g, $L_2 = 68.4$ g. **(g)** H_0: $\mu_Y \leq 50.0$ g, H_A: $\mu_Y > 50.0$ g, $t = 3.970$; $t_{0.05(1),9} = 1.833$, reject H_0; $0.001 < P < 0.0025$ [$P = 0.0016$].

20.2. (1) With X_1, X_2, X_3, and X_4 in the model, see Exercise 20.1c. (2) Delete X_3. With X_1, X_2, and X_4 in the model, $t_{0.05(2),10} = 2.228$ and:

i	b_i	t
1	1.48	9.15*
2	1.73	4.02*
4	0.21	0.50
	$a = 16.83$	

(3) Delete X_4. With X_1 and X_2 in the model, $t_{0.05(2),11} = 2.201$ and:

i	b_i	t
1	1.48	9.47*
2	1.53	13.19*
	$a = 24.96$	

(4) Therefore, the final equation is $\hat{Y} = 24.96 + 1.48X_1 + 1.53X_2$.

20.3. **(a)** $R = 0.9878$. **(b)** $F = 90.2$, $F_{0.05(1),4,9} = 3.63$, reject H_0: There is no population correlation among the five variables; $P \ll 0.0005$ [$P = 0.00000031$]. **(c)** Partial correlation coefficients:

	1	2	3	4	5
1	1.0000				
2	−0.9092*	1.0000			
3	−0.8203*	−0.8089*	1.0000		
4	−0.7578*	−0.9094*	−0.8724*	1.0000	
5	0.8342*	0.7583*	0.4183	0.4342	1.0000

(d) From Appendix Table B.17, $r_{0.05(2),9} = 0.602$, and the significant partial correlation coefficients are indicated with asterisks in part (c).

20.4. H_0: Each of the three sample regressions estimates the same population regression; H_A: Each of the three sample regressions does not estimate the same population regression; $F = 0.915$; as $F_{0.05(1),8,72} = 2.07$, do not reject H_0; $P > 0.25$ [$P = 0.51$].

20.5. **(a)** $W = 0.675$. **(b)** H_0: There is no agreement among the four faculty reviewers; H_A: There is agreement among the four faculty reviewers; $\chi_r^2 = 10.800$; $(\chi_r^2)_{0.05,4,5} = 7.800$; reject H_0; $0.005 < P < 0.01$.

Chapter 21

21.1. In each step, H_0: $\beta_i = 0$ versus H_A: $\beta_i \neq 0$ is tested, where i is the highest term in the polynomial expression. An asterisk indicates H_0 is rejected. (1) Linear regression: $\hat{Y} = 8.8074 - 0.18646X$; $t = 7.136$*; $t_{0.05(2),13} = 2.160$. (2) Quadratic regression: $\hat{Y} = -14.495 + 1.6595X - 0.036133X^2$; $t = 5.298$*; $t_{0.05(2),12} = 2.179$. (3) Cubic regression: $\hat{Y} = -33.810 + 3.9550X - 0.12649X^2 + 0.0011781X^3$; $t = 0.374$; $t_{0.05(2),11} = 2.201$. (4) Quartic regression: $\hat{Y} = 525.30 - 84.708X + 5.1223X^2 - 0.13630X^3 + 0.0013443X^4$; $t = 0.911$; $t_{0.05(2),10} = 2.28$. Therefore, the quadratic expression is concluded to be the "best."

21.2. **(a)** $\hat{Y} = 1.00 + 0.851X - 0.0259X^2$. **(b)** H_0: $\beta_2 = 0$; H_A: $\beta_2 \neq 0$; $F = 69.4$; $F_{0.05(1),1,4} = 7.71$; reject H_0; $0.001 < P < 0.0025$ [$P = 0.0011$]. **(c)** $\hat{Y} = 6.92$ eggs/cm^2; $s_{\hat{Y}} = 0.26$ eggs/cm^2; 95% confidence interval = 6.92 ± 0.72 eggs/cm^2. **(d)** $\hat{X}_0 = 16.43$°C; $\hat{Y}_0 = 7.99$ eggs/ cm^2. **(e)** For $\hat{X}_0$: 95% confidence interval = 16.47 ± 0.65°C; for $\hat{Y}_0$: 95% confidence interval = 7.99 ± 0.86 eggs/cm^2.

Chapter 22

22.1. **(a)** For $\nu = 2$, $P(\chi^2 \geq 3.452)$ is between 0.10 and 0.25 [$P = 0.18$]; **(b)** For $\nu = 5$, $0.10 < (\chi^2 \geq 8.668) < 0.25$ [$P = 0.12$]; **(c)** $\chi^2_{0.05,4} = 9.488$; **(d)** $\chi^2_{0.01,8} = 20.090$.

22.2. **(a)** $\chi^2 = 16.000$, $\nu = 5$, $0.005 < P < 0.01$ [$P = 0.0068$]. As $P < 0.05$, reject H_0 of equal food item preference. **(b)** By grouping food items N, G, and C; $n = 41$, and for H_0: Equal food preference, $\chi^2 = 0.049$, $\nu = 2$, $0.975 < P < 0.99$ [$P = 0.98$]; as $P > 0.05$, H_0 is not rejected. By grouping food items A, W, and M; $n = 85$, and for H_0: Equal food preference, $\chi^2 = 0.447$, $\nu = 2$, $0.75 < P < 0.90$ [$P = 0.80$]; as $P > 0.05$, H_0 is not rejected. By considering food items N, G, and C as one group and items A, W, and M as a second group, and H_0: Equal preference for the two groups, $\chi_c^2 = 14.675$, $\nu = 1$, $P < 0.001$ [$P = 0.00013$]; H_0 is rejected.

22.3. $\chi_c^2 = 0.827$, $\nu = 1$, $0.25 < P < 0.50$ [$P = 0.36$]. As $P > 0.05$, do not reject H_0: The population consists in equal numbers of males and females.

22.4.

Location	*Males*	*Females*	χ^2	ν
1	44	54	1.020	1
2	31	40	1.141	1
3	12	18	1.200	1
4	15	16	0.032	1
Total of chi-squares			3.393	4
Pooled chi-square 102	128		2.939	1
Heterogeneity chi-square			0.454	3

$0.90 < P < 0.95$

Because P(heterogeneity χ^2) > 0.05, the four samples may be pooled with the following results: $\chi_c^2 = 2.717$, $\nu = 1$, $0.05 < P < 0.10$ [$P = 0.099$]; $P > 0.05$, so do not reject H_0: Equal numbers of males and females in the population.

22.5. $G = 16.188$, $\nu = 5$, $0.005 < P < 0.01$ [$P = 0.0063$]; $P < 0.05$, so reject H_0 of no difference in food preference.

22.6. H_0: There is a uniform distribution of the animals from the water's edge to a distance of 10 meters upland; max $D_i = 0.24333$, max $D_i' = 0.2033$, $D = 0.2433$; $D_{0.05(2),31} = 0.23788$; reject H_0, $0.02 < P < 0.05$.

22.7. $D_{0.05,27} = 0.25438$ and $D_{0.05,28} = 0.24993$, so a sample size of at least 28 is called for.

22.8. $d_{\max} = 1$; $(d_{\max})_{0.05,6,18} = 6$; do not reject H_0: The feeders are equally desirable to the birds; $P > 0.50$.

Chapter 23

23.1. **(a)** $\hat{f}_{11} = 157.1026, \hat{f}_{12} = 133.7580, \hat{f}_{13} = 70.0337, \hat{f}_{14} = 51.1057, \hat{f}_{21} = 91.8974, \hat{f}_{22} = 78.2420, \hat{f}_{23} = 40.9663, \hat{f}_{24} = 29.8943, R_1 = 412, R_2 = 241, C_1 = 249, C_2 = 212, C_3 = 111, C_4 = 81, n = 653$; $\chi^2 = 0.2214 + 0.0115 + 0.0133 + 1.2856 + 0.3785 + 0.0197 + 0.0228 + 2.1978 = 4.151$; $\nu = (2 - 1)(4 - 1) = 3$; $\chi^2_{0.05,3} = 7.815, 0.10 < P(\chi^2 \geq 4.156) < 0.25$ [$P = 0.246$]; $P > 0.05$, do not reject H_0. **(b)** $G = 4.032, \nu = 3, \chi^2_{0.05,3} = 7.815, 0.25 < P(\chi^2 \geq 4.032) < 0.50$ [$P = 0.26$]; $P > 0.05$, do not reject H_0.

23.2. **(a)** $f_{11} = 14, f_{12} = 29, f_{21} = 12, f_{22} = 38, R_1 = 43, R_2 = 50, C_1 = 26, C_2 = 67, n = 93$; $\chi^2 = 0.8407, \nu = 1$; $\chi^2_{0.05,1} = 3.841, 0.25 < P(\chi^2 \geq 0.8407) < 0.50$; as $P > 0.05$, do not reject H_0 [$P = 0.36$]. **(b)** $G = 0.8395, \nu = 1$; $\chi^2_{0.05,1} = 3.841, 0.25 < P(\chi^2 \geq 0.8395) < 0.50$; as $P > 0.05$, do not reject H_0 [$P = 0.36$].

23.3. H_0: Sex, area, and occurrence of rabies are mutually independent; $\chi^2 = 33.959$; $\nu = 4$; $\chi^2_{0.05,4} = 9.488$; reject H_0; $P < 0.001$ [$P = 0.00000076$]. H_0: Area is independent of sex and rabies; $\chi^2 = 23.515$; $\nu = 3$; $\chi^2_{0.05,3} = 7.815$; reject H_0; $P < 0.001$ [$P = 0.000032$]. H_0: Sex is independent of area and rabies; $\chi^2 = 11.130$; $\nu = 3$; reject H_0; $0.01 < P < 0.25$ [$P = 0.011$]. H_0: Rabies is independent of area and sex; $\chi^2 = 32.170$; $\nu = 3$; reject H_0; $P < 0.001$ [$P = 0.00000048$].

23.4. **(a)** $R_1 = R_2 = R_3 = 150, C_1 = 203, C_2 = 182, C_3 = 45, C_4 = 20, n = 450$; $\hat{f}_{11} = \hat{f}_{21} = \hat{f}_{31} = 67.6667, \hat{f}_{12} = \hat{f}_{22} = \hat{f}_{32} = 60.6667, \hat{f}_{13} = \hat{f}_{23} = \hat{f}_{33} = 15.0000, \hat{f}_{14} = \hat{f}_{24} = \hat{f}_{34} = 6.6667$; $\chi^2 = 4.141$; $\nu = (2)(3) = 6$; $\chi^2_{0.05,6} = 12.592$; $0.50 < P < 0.75$ [$P = 0.66$]; do not reject H_0. **(b)** $G = 4.141$, same probability and conclusion as part (a).

Chapter 24

24.1. $P(X = 2) = 0.32413$.

24.2. $P(X = 4) = 0.00914$.

24.3. H_0: The sampled population is binomial with $p = 0.25$; H_A: The sampled population is not binomial with $p = 0.25$; $\sum f_i = 126$; $F_1 = (0.31641)(126) = 39.868, F_2 = 53.157, F_3 = 26.578, F_4 = 5.907, F_5 = 0.493$; combine F_4 and F_5 and combine f_4 and f_5; $\chi^2 = 11.524, \nu = k - 1 = 3, \chi^2_{0.05,3} = 7.815$; reject H_0; $0.005 < P < 0.01$ [$P = 0.0092$].

24.4. H_0: The sampled population is binomial; H_A: The sampled population is not binomial; $\hat{p} = \frac{156}{109}/4 = 0.3578$; $\chi^2 = 3.186, \nu = k - 2 = 3, \chi^2_{0.05,3} = 7.815$; do not reject H_0; $0.25 < P < 0.50$ [$P = 0.36$].

24.5. H_0: $p = 0.5$; H_A: $p \neq 0.5$; $n = 20$; $P(X \leq 6 \text{ or } X \geq 14) = 0.11532$; since this probability is greater than 0.05, do not reject H_0.

24.6. H_0: $p = 0.5$; H_A: $p \neq 0.5$; $\hat{p} = \frac{197}{412} = 0.4782$; $Z = -0.888$; $Z_c = 0.838$; $Z_{0.05(2)} = t_{0.05(2),\infty} = 1.960$; therefore, do not reject H_0; $P \approx 0.37$ [$P = 0.40$].

24.7. H_0: $p = 0.5$; H_A: $p \neq 0.5$; $X = 44$; $Z = -1.0102$; $Z_{0.05(2)} = t_{0.05(2),\infty} = 1.960$; do not reject H_0; $0.20 < P < 0.50$ [$P = 0.30$].

24.8. H_0: $p = 0.5$; H_A: $p \neq 0.5$; number of positive differences = 7; for $n = 10$ and $p = 0.5$; $P(X \leq 3 \text{ or } X \geq 7) = 0.34378$; since this probability is greater than 0.05, do not reject H_0.

24.9. $n = 20, p = 0.50$; critical values are 5 and 15; $\hat{p} = 6/20 = 0.30$, power = $0.00080 + 0.00684 + 0.02785 + 0.07160 + 0.13042 + 0.17886 + 0.00004 + 0.00001 = 0.42$.

24.10. $p_0 = 0.50, p = 0.4782, n = 412$; power = $P(Z < -1.08) + P(Z > 2.84) = 0.1401 + 0.0023 = 0.14$.

24.11. $X = 18, n = 30, \hat{p} = 0.600$ **(a)** $F_{0.05(2),26,36} \approx F_{0.05(2),26,35} = 2.04, L_1 = 0.404$; $F_{0.05(2),38,24} \approx F_{0.05(2),30,24} = 2.21, L_2 = 0.778$. Using exact probabilities of F: $F_{0.05(2),26,36} = 2.025, L_1 = 0.406$; $F_{0.05(2),28,34} = 2.156, L_2 = 0.773$. **(b)** $Z_{0.05(2)} = 1.9600$, confidence interval is $0.600 \pm (1.9600)(0.0894), L_1 = 0.425, L_2 = 0.775$. **(c)** $\tilde{X} = 19.92, \tilde{n} = 33.84, \tilde{p} = 0.589$, confidence interval is $0.589 \pm (1.9600)(0.0846), L_1 = 0.423, L_2 = 0.755$.

24.12. $X = 62, n = 1215, \hat{p} = 0.051$ **(a)** $F_{0.05(2),2308,124} \approx F_{0.05(2),\infty,120} = 1.31, L_1 = 0.039$; $F_{0.05(2),126,2306} \approx F_{0.05(2),120,\infty} = 1.27, L_2 = 0.065$. Using exact probabilities of F: $F_{0.05(2),2308,124} = 1.312, L_1 = 0.039$; $F_{0.05(2),126,2306} = 1.271, L_2 = 0.061$. **(b)** $Z_{0.05(2)} = 1.9600$, confidence interval is $0.051 \pm (1.9600)(0.0631), L_1 = 0.039, L_2 = 0.063$. **(c)** $\tilde{X} = 63.92, \tilde{n} = 1218.84, \tilde{p} = 0.052$. confidence interval is $0.052 \pm (1.9600)(0.00638), L_1 = 0.039, L_2 = 0.065$.

24.13. sample median = 32.5 km/hr, $i = 4, j = 1$, $P(29.5 \text{ km/hr} \leq \text{population median} \leq 33.6 \text{ km/hr}) = 0.90$.

24.14. $\hat{p}_1 = 0.7500, \hat{p}_2 = 0.4000, \overline{p} = 0.5714, \overline{q} = 0.4286$, SE = 0.1414, $Z = 2.475$, $0.01 < P < 0.02$, reject H_0 [$P = 0.013$].

24.15. $\widetilde{X}_1 = 18.96, \tilde{n}_1 = 25.92, \tilde{p}_1 = 0.7315, \widetilde{X}_2 = 10.96, \tilde{n}_2 = 26.92, \tilde{p}_2 = 0.4071$. SE = 0.1286, 95% confidence interval = 32.444 ± 0.2521, $L_1 = 0.372$, $L_2 = 0.576$.

24.16. H_0: $p_1 = p_2 = p_3 = p_4$, H_A: All four population proportions are not equal; $X_1 = 163$, $X_2 = 135$, $X_3 = 71$, $X_4 = 43$, $n_1 = 249$, $n_2 = 212$, $n_3 = 111$, $n_4 = 81$; $\hat{p}_1 = 0.6546, \hat{p}_2 = 0.6368, \hat{p}_3 = 0.6396, \hat{p}_4 = 0.5309$; $\overline{p} = 412/653 = 0.6309$, $\chi^2 = 0.6015 + 0.0316 + 0.0364 + 3.4804 = 4.150$, $\chi^2_{0.05,3} = 7.815$; do not reject H_0; $0.10 < P < 0.25$ [$P = 0.246$].

24.17. H_0: $p_1 = p_2 = p_3 = p_4$ is not rejected. So multiple-comparison testing is not done.

24.18. **(a)** P of original table = 0.02965; P of next more extreme table (i.e., where $f_{11} = 21$) = 0.01037; P of next more extreme table (i.e., where $f_{11} = 22$) = 0.00284; and so on with total P for that tail = 0.0435; H_0 is rejected. **(b)** $\chi^2_c = 2.892$, $0.05 < P < 0.10$ [$P = 0.089$], H_0 is not rejected. **(c)** $\chi^2_H = 2.892$, $0.05 < P < 0.10$ [$P = 0.089$], H_0 is not rejected. **(d)** Since $R_1 = R_2$, the two-tailed P is 2 times the one-tailed P; two-tailed $P = 2(0.0435) = 0.087$, H_0 is not rejected.

24.19. **(a)** P of original table = 0.02034; P of next most extreme table (i.e., where $f_{11} = 2$) = 0.00332; P of next most extreme table (i.e., where $f_{11} = 1$) = 0.00021; and so on, with a total P for that tail = 0.02787, H_0 is rejected. **(b)** $\chi^2_c = 3.593$, $0.05 < P < 0.10$ [$P = 0.057$], H_0 is not rejected. **(c)** $\chi^2_H = 4.909$, $0.025 < P < 0.05$ [$P = 0.027$], and H_0 is not rejected. **(d)** For the most extreme table in the tail opposite from that in part **(a)**, $f_{11} = 13$ and $f_{12} = 1$, $P = 0.00000$; for next more extreme table, $f_{11} = 12$, $P = 0.00001$; for the next more extreme table, $f_{11} = 11$, $P = 0.00027$; and so on through each of the tables in this tail with a probability less than 0.02034; sum of the tables' probabilities in the second tail = 0.00505; sum of the probabilities of the two tails = 0.02787 + 0.00505 = 0.03292; H_0 is rejected.

24.20. H_0: There is no difference in frequency of occurrence of varicose veins between overweight and normal weight men; H_A: There is a difference in frequency of occurrence of varicose veins between overweight men and normal weight men; $f_{11} = 19, f_{12} = 5, f_{21} = 12, f_{22} = 86$, $n = 122$; $\chi^2_c = 2.118$; $\chi^2_{0.05,1} = 3.841$; do not reject H_0; $0.10 < P < 0.25$ [$P = 0.15$].

Chapter 25

25.1. If $\mu = 1.5$, $P(X = 0) = 0.2231$ and $P(X = 5) = 0.0141$.

25.2. $\mu = \frac{5}{2} = 2.5$ viruses per bacterium. **(a)** $P(X = 0) = 0.0821$. **(b)** $P(X > 0) = 1.0000 - P(X = 0) = 1.0000 - 0.0821 = 0.9197$. **(c)** $P(X \geq 2) = 1.0000 - P(X = 0) - P(X = 1) = 1.0000 - 0.0821 - 0.2052 = 0.7127$. **(d)** $P(X = 3) = 0.2138$.

25.3. H_0: Biting mosquitoes select the men randomly; H_A: Biting mosquitoes do not select the mean randomly. $\overline{X} = \sum f_i X_i = 98/57 = 1.7193$; $\chi^2 = 3.060$, $\nu = 6 - 2 = 4$, $\chi^2_{0.05,4} = 7.815$; do not reject H: $0.50 < P < 0.75$ [$P = 0.55$]

25.4. H_0: $p \leq 0.00010$; H_A: $p > 0.00010$; $p_0 = 0.00010$; $n = 25{,}000$; $p_0 n = 2.5$; $X = 5$; $P(X \geq 5) = 0.1087$; do not reject H_0; do not include this disease on the list.

25.5. H_0: $\mu_1 = \mu_2$; H_A: $\mu_1 \neq \mu_2$; $X_1 = 112, X_2 = 134$; $Z = 1.40$; $Z_{0.05(2)} = 1.9600$; do not reject H_0; $0.10 < P < 0.20$ [$P = 0.16$].

25.6. H_0: The incidence of heavy damage is random over the years; H_A: The incidence of heavy damage is not random over the years; $n_1 = 14$, $n_2 = 13$, $u = 12$, $u_{0.05,14,13} = 9$ and 20. As 12 is neither ≤ 9 nor ≥ 20; do not reject H_0; $P = 0.50$.

25.7. H_0: The magnitude of fish kills is randomly distributed over time; H_A: The magnitude of fish kills is not randomly distributed over time; $n = 16$, $s^2 = 400.25$, $s^2_* = 3126.77/30 = 104.22$; $C = 0.740$, $C_{0.05,16} = 0.386$; reject H_0; $P < 0.0005$.

25.8. H_0: The data are sequentially random; H_A: The data are not sequentially random; $n = 16$, $u = 7$; critical values = 6 and 14; do not reject H_0; $0.05 < P \leq 0.10$.

Chapter 26

26.1. $n = 12$, $Y = 0.48570$, $X = 0.20118$, $r = 0.52572$ ($c = 1.02617$, $r_c = 0.53948$). **(a)** $\overline{a} = 68°$. **(b)** $s = 56°$ (using correction for grouping, $s = 55°$), $s' = 65°$ (using correction for grouping, $s' = 64°$). **(c)** $68° \pm 47°$ (using correction for grouping, $68° \pm 46°$). **(d)** median = 67.5°.

26.2. $n = 15$, $Y = 0.76319$, $X = 0.12614$, $r = 0.77354$. **(a)** a = 5:22 A.M. **(b)** s = 2:34 hr. **(c)** 5:22 hr ± 1:38 hr. **(d)** median = 5:10 A.M.

Chapter 27

27.1. H_0: $\rho = 0$; H_A: $\rho \neq 0$; $r = 0.526$; $R = 6.309$; $z = 3.317$, $z_{0.05,12} = 2.932$; reject H_0; $0.02 < P < 0.05$.

27.2. H_0: $\rho = 0$, H_A: $\rho \neq 0$; $r = 0.774$; $R = 11.603$; $z = 8.975$, $z_{0.05,15} = 2.945$; reject H_0; $P < 0.001$.

27.3. H_0: $\rho = 0$; H_A: $\rho \neq 0$; $n = 11$, $Y = -0.88268$, $X = 0.17138$, $r = 0.89917$, $\bar{a} = 281°$, $R = 9.891$, $\mu_0 = 270°$. **(a)** $V = 9.709$, $u = 4.140$, $u_{0.05,11} = 1.648$; reject H_0; $P < 0.0005$. **(b)** H_0: $\mu_a = 270°$, H_A: $\mu_a \neq 270°$, 95% confidence interval for $\mu_a = 281° \pm 19°$, so do not reject H_0.

27.4. $n = 12, m = 2, m_{0.05,12} = 0$, do not reject H_0; $0.20 < P \leq 0.50$.

27.5. $n = 11, m' = 0, C = 11, C_{0.05(2),11} = 1$, reject H_0; $P < 0.001$.

27.6. H_0: Mean flight direction is the same under the two sky conditions; H_A: Mean flight direction is not the same under the two sky conditions; $n_1 = 8, n_2 = 7, R_1 = 7.5916, R_2 = 6.1130$, $\bar{a}_1 = 352°, \bar{a}_2 = 305°, N = 15, r_w = 0.914$, $R = 12.5774$; $F = 12.01, F_{0.05(1),1,13} = 4.67$; reject H_0; $0.0025 < P < 0.005$ [$P = 0.004$].

27.7. H_0: The flight direction is the same under the two sky conditions; H_A: The flight direction is not the same under the two sky conditions; $n_1 = 8$, $n_2 = 7, N = 15$; $\sum d_k = -2.96429$. $\sum d_k^2 = 1.40243, U^2 = 0.2032, U^2_{0.05,8,7} = 0.1817$; do not reject H_0: $0.02 < P < 0.05$.

27.8. H_0: Members of all three hummingbird species have the same mean time of feeding at the feeding station; H_A: Members of all three species do not have the same mean time of feeding at the feeding station; $n_1 = 6, n_2 = 9, n_3 = 7, N = 22$; $R_1 = 2.965, R_2 = 3.938, R_3 = 3.868$; $\bar{a}_1 = 10{:}30$ hr, $\bar{a}_2 = 11{:}45$ hr, $\bar{a}_3 = 11{:}10$ hr; $r_w = 0.490, F = 0.206, F_{0.05(1),2,19} = 3.54$; do not reject H_0; $P > 0.25$ [$P = 0.82$]. Therefore, all three $\bar{a}_i$'s estimate the same μ_a, the best estimate of which is 11:25 hr.

27.9. H_0: Birds do not orient better when skies are sunny than when cloudy; H_A: Birds do orient better when skies are sunny than when cloudy. Angular distances for group 1 (sunny): 10, 20, 45, 10, 20, 5, 15, and 0°; for group 2 (cloudy): 20, 55, 105, 90, 55, 40, and 25°. For the one-tailed Mann-Whitney test: $n_1 = 8, n_2 = 7, R_1 = 40, U = 52$, $U_{0.05(1),8,7} = 43$; reject H_0; $P = 0.0025$.

27.10. H_0: Variability in flight direction is the same under both sky conditions; H_A: Variability in flight direction is not the same under both sky conditions; $\bar{a}_1 = 352°, \bar{a}_2 = 305°$; angular distances for group 1 (sunny): 2, 12, 37, 18, 28, 3, 7, and 8°, and for group 2 (cloudy): 35, 0, 50, 35, 0, 15, and 30°; for the two-tailed Mann-Whitney test: $R_1 = 58, U = 34, U' = 22, U_{0.05(2),8,7} = 46$; reject H_0; $P < 0.001$.

27.11. **(a)** H_0: $\rho_{aa} = 0$; H_A: $\rho_{aa} \neq 0$; $r_{aa} = 0.9244$; $\bar{r}_{aa} = 0.9236$; $s^2_{r_{aa}} = 0.0004312$; $L_1 = 0.9169$, $L_2 = 0.9440$; reject H_0. **(b)** H_0: $(\rho_{aa})_s = 0$, H_A: $(\rho_{aa}) \neq 0$; $r' = 0.453, r'' = 0.009, (r_{aa})_s = 0.365$; $(n-1)(r_{aa})_s = 2.92$, for $\alpha(2) = 0.05$ the critical value is 3.23; do not reject H_0; for $\alpha(2) = 0.10$, the critical value is 2.52, so $0.05 < P < 0.10$.

27.12. H_0: $\rho_{al} = 0$; H_A: $\rho_{al} \neq 0$; $r_{al} = 0.833, nr^2_{al} = 6.24$, $\chi^2_{0.05,2} = 5.991$, reject H_0.

27.13. H_0: The distribution is not contagious; H_A: The distribution is contagious; $n_1 = 8, n_2 = 8, u = 6$, $u' = 3$; using Appendix Table B.28: $m_1 = 7$, $m_2 = 7, f = 2, n = 15$, critical values are 1 and 6, so do not reject H_0; $P \geq 0.50$.

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Page numbers are given for the first or major occurences of terms, topics and symbols, and italicized page numbers refer to especially informative sites.

In this index, the abbreviation "approx." means "approximation"; "c.l." means "confidence limit(s)"; "coef." means "coefficient(s)"; "correl." means "correlation"; "c.v." means "critical value"; "dist." means "distribution(s)"; "et al." (for Latin et alibi) means "and elsewhere"; "ff" means "and following"; "hyp." means "hypotheses"; "int. calc." means "intermediate calculation"; "p." means "population"; "prop." means "proportion(s)"; "regr." means "regression"; "s." means "sample"; and "stat." means "statistic(s)." As indicated in the text, a bar (" $\bar{}$ ") over a symbol designates its mean, a carat ("^") over a symbol designates its estimated or predicted value, and brackets ("[ ]") surrounding a single symbol refer to its value after coding.