



THE  
POWER  
TO KNOW®

# SAS/STAT® 9.2 User's Guide The POWER Procedure (Book Excerpt)



This document is an individual chapter from *SAS/STAT*<sup>®</sup> 9.2 *User's Guide*.

The correct bibliographic citation for the complete manual is as follows: SAS Institute Inc. 2008. *SAS/STAT*<sup>®</sup> 9.2 *User's Guide*. Cary, NC: SAS Institute Inc.

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SAS Institute Inc., SAS Campus Drive, Cary, North Carolina 27513.

1st electronic book, March 2008

2nd electronic book, February 2009

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# Chapter 67

## The POWER Procedure

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## Overview: POWER Procedure

Power and sample size analysis optimizes the resource usage and design of a study, improving chances of conclusive results with maximum efficiency. The POWER procedure performs prospective power and sample size analyses for a variety of goals, such as the following:

- determining the sample size required to get a significant result with adequate probability (power)
- characterizing the power of a study to detect a meaningful effect
- conducting what-if analyses to assess sensitivity of the power or required sample size to other factors

Here *prospective* indicates that the analysis pertains to planning for a future study. This is in contrast to *retrospective* power analysis for a past study, which is not supported by the procedure.

A variety of statistical analyses are covered:

- *t* tests, equivalence tests, and confidence intervals for means
- tests, equivalence tests, and confidence intervals for binomial proportions
- multiple regression
- tests of correlation and partial correlation
- one-way analysis of variance
- rank tests for comparing two survival curves
- logistic regression with binary response
- Wilcoxon-Mann-Whitney (rank-sum) test

For more complex linear models, see Chapter 41, “[The GLMPOWER Procedure](#).”

Input for PROC POWER includes the components considered in study planning:

- design
- statistical model and test
- significance level (alpha)
- surmised effects and variability
- power
- sample size

You designate one of these components by a missing value in the input, in order to identify it as the result parameter. The procedure calculates this result value over one or more scenarios of input values for all other components. Power and sample size are the most common result values, but for some analyses the result can be something else. For example, you can solve for the sample size of a single group for a two-sample *t* test.

In addition to tabular results, PROC POWER produces graphs. You can produce the most common types of plots easily with default settings and use a variety of options for more customized graphics.

For example, you can control the choice of axis variables, axis ranges, number of plotted points, mapping of graphical features (such as color, line style, symbol and panel) to analysis parameters, and legend appearance.

The POWER procedure is one of several tools available in SAS/STAT software for power and sample size analysis. PROC GLMPower supports more complex linear models. The Power and Sample Size application provides a user interface and implements many of the analyses supported in the procedures. See Chapter 41, “[The GLMPower Procedure](#),” and Chapter 68, “[The Power and Sample Size Application](#),” for details.

The following sections of this chapter describe how to use PROC POWER and discuss the underlying statistical methodology. The section “[Getting Started: POWER Procedure](#)” on page 4812 introduces PROC POWER with simple examples of power computation for a one-sample  $t$  test and sample size determination for a two-sample  $t$  test. The section “[Syntax: POWER Procedure](#)” on page 4820 describes the syntax of the procedure. The section “[Details: POWER Procedure](#)” on page 4910 summarizes the methods employed by PROC POWER and provides details on several special topics. The section “[Examples: POWER Procedure](#)” on page 4975 illustrates the use of the POWER procedure with several applications.

For an overview of methodology and SAS tools for power and sample size analysis, see Chapter 19, “[Introduction to Power and Sample Size Analysis](#).” For more discussion and examples, see O’Brien and Castelloe (2007), Castelloe (2000), Castelloe and O’Brien (2001), Muller and Benignus (1992), O’Brien and Muller (1993), and Lenth (2001).

---

## Getting Started: POWER Procedure

---

### Computing Power for a One-Sample $t$ Test

Suppose you want to improve the accuracy of a machine used to print logos on sports jerseys. The logo placement has an inherently high variability, but the horizontal alignment of the machine can be adjusted. The operator agrees to pay for a costly adjustment if you can establish a nonzero mean horizontal displacement in either direction with high confidence. You have 150 jerseys at your disposal to measure, and you want to determine your chances of a significant result (power) by using a one-sample  $t$  test with a two-sided  $\alpha = 0.05$ .

You decide that 8 mm is the smallest displacement worth addressing. Hence, you will assume a true mean of 8 in the power computation. Experience indicates that the standard deviation is about 40.

Use the `ONESAMPLEMEANS` statement in the POWER procedure to compute the power. Indicate power as the result parameter by specifying the `POWER=` option with a missing value (.). Specify your conjectures for the mean and standard deviation by using the `MEAN=` and `STDDEV=` options and for the sample size by using the `NTOTAL=` option. The statements required to perform this analysis are as follows:

```

proc power;
  onesamplemeans
    mean      = 8
    ntotal    = 150
    stddev    = 40
    power     = .;
run;

```

Default values for the `TEST=`, `DIST=`, `ALPHA=`, `NULLMEAN=`, and `SIDES=` options specify a two-sided  $t$  test for a mean of 0, assuming a normal distribution with a significance level of  $\alpha = 0.05$ .

Figure 67.1 shows the output.

**Figure 67.1** Sample Size Analysis for One-Sample  $t$  Test

The POWER Procedure	
One-sample t Test for Mean	
Fixed Scenario Elements	
Distribution	Normal
Method	Exact
Mean	8
Standard Deviation	40
Total Sample Size	150
Number of Sides	2
Null Mean	0
Alpha	0.05
Computed Power	
Power	0.682

The power is about 0.68. In other words, there is about a 2/3 chance that the  $t$  test will produce a significant result demonstrating the machine's average off-center displacement. This probability depends on the assumptions for the mean and standard deviation.

Now, suppose you want to account for some of your uncertainty in conjecturing the true mean and standard deviation by evaluating the power for four scenarios, using reasonable low and high values, 5 and 10 for the mean, and 30 and 50 for the standard deviation. Also, you might be able to measure more than 150 jerseys, and you would like to know under what circumstances you could get by with fewer. You want to plot power for sample sizes between 100 and 200 to visualize how sensitive the power is to changes in sample size for these four scenarios of means and standard deviations. The following statements perform this analysis:

```

proc power;
  onesamplemeans
    mean    = 5 10
    ntotal  = 150
    stddev  = 30 50
    power   = .;
  plot x=n min=100 max=200;
run;

```

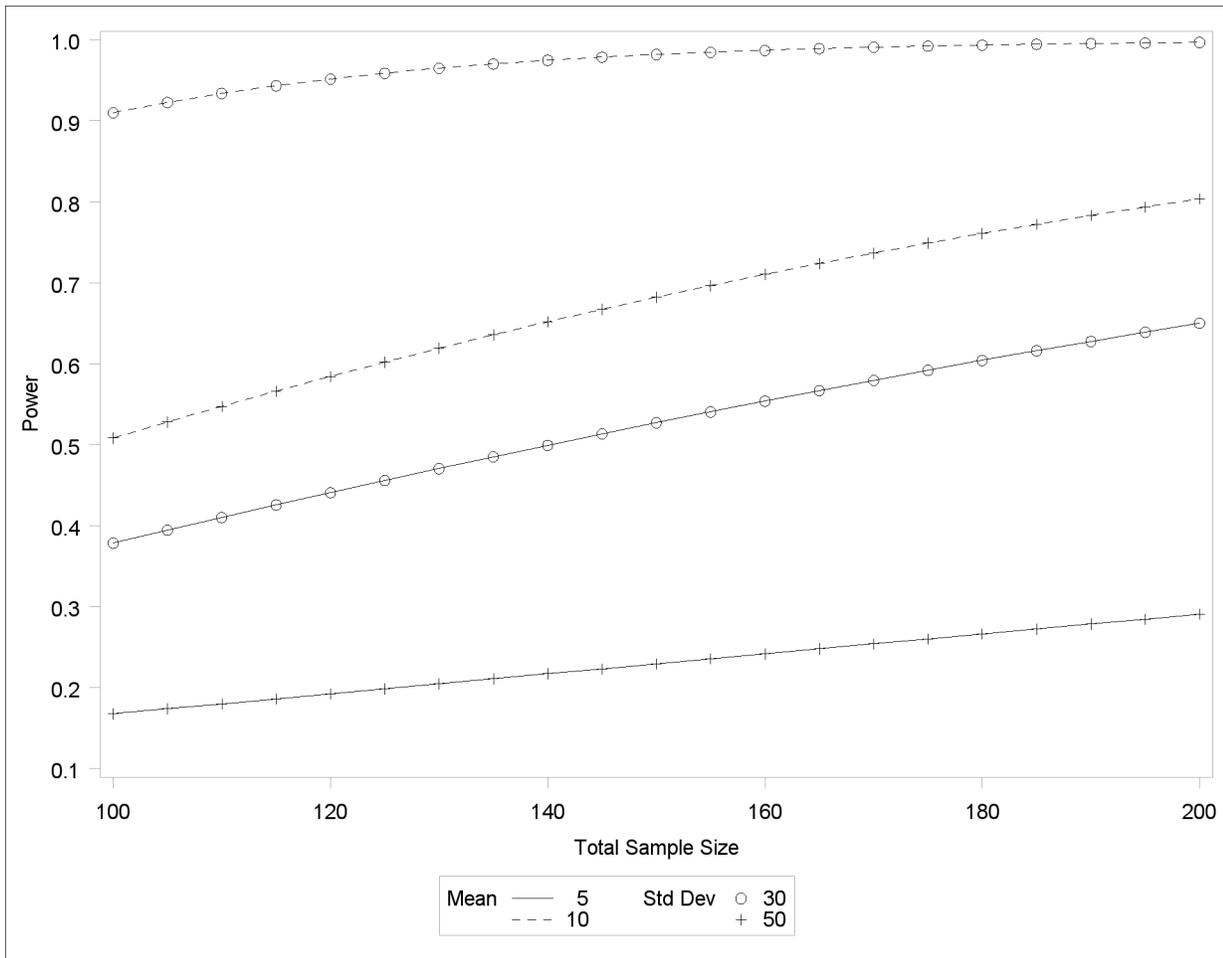
The new mean and standard deviation values are specified by using the **MEAN=** and **STDDEV=** options in the **ONESAMPLEMEANS** statement. The **PLOT** statement with **X=N** produces a plot with sample size on the X axis. (The result parameter, in this case the power, is always plotted on the other axis.) The **MIN=** and **MAX=** options in the **PLOT** statement determine the sample size range.

Figure 67.2 shows the output, and Figure 67.3 shows the plot.

**Figure 67.2** Sample Size Analysis for One-Sample *t* Test with Input Ranges

The POWER Procedure				
One-sample t Test for Mean				
Fixed Scenario Elements				
Distribution				Normal
Method				Exact
Total Sample Size				150
Number of Sides				2
Null Mean				0
Alpha				0.05
Computed Power				
Index	Mean	Std Dev		Power
1	5	30		0.527
2	5	50		0.229
3	10	30		0.982
4	10	50		0.682

**Figure 67.3** Plot of Power versus Sample Size for One-Sample *t* Test with Input Ranges



The power ranges from about 0.23 to 0.98 for a sample size of 150 depending on the mean and standard deviation. In Figure 67.3, the line style identifies the mean, and the plotting symbol identifies the standard deviation. The locations of plotting symbols indicate computed powers; the curves are linear interpolations of these points. The plot suggests sufficient power for a mean of 10 and standard deviation of 30 (for any of the sample sizes) but insufficient power for the other three scenarios.

## Determining Required Sample Size for a Two-Sample *t* Test

In this example you want to compare two physical therapy treatments designed to increase muscle flexibility. You need to determine the number of patients required to achieve a power of at least 0.9 to detect a group mean difference in a two-sample *t* test. You will use  $\alpha = 0.05$  (two-tailed).

The mean flexibility with the standard treatment (as measured on a scale of 1 to 20) is well known to be about 13 and is thought to be between 14 and 15 with the new treatment. You conjecture three alternative scenarios for the means:

1.  $\mu_1 = 13, \mu_2 = 14$
2.  $\mu_1 = 13, \mu_2 = 14.5$
3.  $\mu_1 = 13, \mu_2 = 15$

You conjecture two scenarios for the common group standard deviation:

1.  $\sigma = 1.2$
2.  $\sigma = 1.7$

You also want to try three weighting schemes:

1. equal group sizes (balanced, or 1:1)
2. twice as many patients with the new treatment (1:2)
3. three times as many patients with the new treatment (1:3)

This makes  $3 \times 2 \times 3 = 18$  scenarios in all.

Use the **TWOSAMPLEMEANS** statement in the **POWER** procedure to determine the sample sizes required to give 90% power for each of these 18 scenarios. Indicate total sample size as the result parameter by specifying the **NTOTAL=** option with a missing value (.). Specify your conjectures for the means by using the **GROUPMEANS=** option. Using the “matched” notation (discussed in the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913), enclose the two group means for each scenario in parentheses. Use the **STDDEV=** option to specify scenarios for the common standard deviation. Specify the weighting schemes by using the **GROUPWEIGHTS=** option. You could again use the matched notation. But for illustrative purposes, specify the scenarios for each group weight separately by using the “crossed” notation, with scenarios for each group weight separated by a vertical bar (|). The statements that perform the analysis are as follows:

```
proc power;
  twosamplemeans
    groupmeans = (13 14) (13 14.5) (13 15)
    stddev     = 1.2 1.7
    groupweights = 1 | 1 2 3
    power      = 0.9
    ntotal     = .;
run;
```

Default values for the **TEST=**, **DIST=**, **NULLDIFF=**, **ALPHA=**, and **SIDES=** options specify a two-sided  $t$  test of group mean difference equal to 0, assuming a normal distribution with a significance level of  $\alpha = 0.05$ . The results are shown in [Figure 67.4](#).

**Figure 67.4** Sample Size Analysis for Two-Sample t Test Using Group Means

The POWER Procedure						
Two-sample t Test for Mean Difference						
Fixed Scenario Elements						
Distribution	Normal					
Method	Exact					
Group 1 Weight	1					
Nominal Power	0.9					
Number of Sides	2					
Null Difference	0					
Alpha	0.05					
Computed N Total						
Index	Mean1	Mean2	Std Dev	Weight2	Actual Power	N Total
1	13	14.0	1.2	1	0.907	64
2	13	14.0	1.2	2	0.908	72
3	13	14.0	1.2	3	0.905	84
4	13	14.0	1.7	1	0.901	124
5	13	14.0	1.7	2	0.905	141
6	13	14.0	1.7	3	0.900	164
7	13	14.5	1.2	1	0.910	30
8	13	14.5	1.2	2	0.906	33
9	13	14.5	1.2	3	0.916	40
10	13	14.5	1.7	1	0.900	56
11	13	14.5	1.7	2	0.901	63
12	13	14.5	1.7	3	0.908	76
13	13	15.0	1.2	1	0.913	18
14	13	15.0	1.2	2	0.927	21
15	13	15.0	1.2	3	0.922	24
16	13	15.0	1.7	1	0.914	34
17	13	15.0	1.7	2	0.921	39
18	13	15.0	1.7	3	0.910	44

The interpretation is that in the best-case scenario (large mean difference of 2, small standard deviation of 1.2, and balanced design), a sample size of  $N = 18$  ( $n_1 = n_2 = 9$ ) patients is sufficient to achieve a power of at least 0.9. In the worst-case scenario (small mean difference of 1, large standard deviation of 1.7, and a 1:3 unbalanced design), a sample size of  $N = 164$  ( $n_1 = 41, n_2 = 123$ ) patients is necessary. The Nominal Power of 0.9 in the “Fixed Scenario Elements” table represents the input target power, and the Actual Power column in the “Computed N Total” table is the power at the sample size (N Total) adjusted to achieve the specified sample weighting exactly.

Note the following characteristics of the analysis, and ways you can modify them if you want:

- The total sample sizes are rounded up to multiples of the weight sums (2 for the 1:1 design, 3 for the 1:2 design, and 4 for the 1:3 design) to ensure that each group size is an integer. To request raw fractional sample size solutions, use the **NFRACTIONAL** option.
- Only the group weight that varies (the one for group 2) is displayed as an output column,

while the weight for group 1 appears in the “Fixed Scenario Elements” table. To display the group weights together in output columns, use the matched version of the value list rather than the crossed version.

- If you can specify only differences between group means (instead of their individual values), or if you want to display the mean differences instead of the individual means, use the `MEANDIFF=` option instead of the `GROUPMEANS=` option.

The following statements implement all of these modifications:

```
proc power;
  twosamplemeans
    nfractional
    meandiff      = 1 to 2 by 0.5
    stddev        = 1.2 1.7
    groupweights  = (1 1) (1 2) (1 3)
    power         = 0.9
    ntotal        = .;
run;
```

Figure 67.5 shows the new results.

**Figure 67.5** Sample Size Analysis for Two-Sample  $t$  Test Using Mean Differences

The POWER Procedure	
Two-sample $t$ Test for Mean Difference	
Fixed Scenario Elements	
Distribution	Normal
Method	Exact
Nominal Power	0.9
Number of Sides	2
Null Difference	0
Alpha	0.05

Figure 67.5 continued

Computed Ceiling N Total							
Index	Mean Diff	Std Dev	Weight1	Weight2	Fractional N Total	Actual Power	Ceiling N Total
1	1.0	1.2	1	1	62.507429	0.902	63
2	1.0	1.2	1	2	70.065711	0.904	71
3	1.0	1.2	1	3	82.665772	0.901	83
4	1.0	1.7	1	1	123.418482	0.901	124
5	1.0	1.7	1	2	138.598159	0.901	139
6	1.0	1.7	1	3	163.899094	0.900	164
7	1.5	1.2	1	1	28.961958	0.900	29
8	1.5	1.2	1	2	32.308867	0.906	33
9	1.5	1.2	1	3	37.893351	0.901	38
10	1.5	1.7	1	1	55.977156	0.900	56
11	1.5	1.7	1	2	62.717357	0.901	63
12	1.5	1.7	1	3	73.954291	0.900	74
13	2.0	1.2	1	1	17.298518	0.913	18
14	2.0	1.2	1	2	19.163836	0.913	20
15	2.0	1.2	1	3	22.282926	0.910	23
16	2.0	1.7	1	1	32.413512	0.905	33
17	2.0	1.7	1	2	36.195531	0.907	37
18	2.0	1.7	1	3	42.504535	0.903	43

Note that the Nominal Power of 0.9 applies to the raw computed sample size (Fractional N Total), and the Actual Power column applies to the rounded sample size (Ceiling N Total). Some of the adjusted sample sizes in Figure 67.5 are lower than those in Figure 67.4 because underlying group sample sizes are allowed to be fractional (for example, the first Ceiling N Total of 63 corresponding to equal group sizes of 31.5).

---

## Syntax: POWER Procedure

The following statements are available in PROC POWER:

```

PROC POWER < options > ;
  LOGISTIC < options > ;
  MULTREG < options > ;
  ONECORR < options > ;
  ONESAMPLEFREQ < options > ;
  ONESAMPLEMEANS < options > ;
  ONEWAYANOVA < options > ;
  PAIREDFREQ < options > ;
  PAIREDMEANS < options > ;
  PLOT < plot-options > < / graph-options > ;
  TWOSAMPLEFREQ < options > ;
  TWOSAMPLEMEANS < options > ;
  TWOSAMPLESURVIVAL < options > ;
  TWOSAMPLEWILCOXON < options > ;

```

The statements in the POWER procedure consist of the **PROC POWER** statement, a set of *analysis statements* (for requesting specific power and sample size analyses), and the **PLOT** statement (for producing graphs). The **PROC POWER** statement and at least one of the analysis statements are required. The analysis statements are **LOGISTIC**, **MULTREG**, **ONECORR**, **ONESAMPLEFREQ**, **ONESAMPLEMEANS**, **ONEWAYANOVA**, **PAIREDFREQ**, **PAIREDMEANS**, **TWOSAMPLEFREQ**, **TWOSAMPLEMEANS**, **TWOSAMPLESURVIVAL**, and **TWOSAMPLEWILCOXON**.

You can use multiple analysis statements and multiple **PLOT** statements. Each analysis statement produces a separate sample size analysis. Each **PLOT** statement refers to the previous analysis statement and generates a separate graph (or set of graphs).

The name of an analysis statement describes the framework of the statistical analysis for which sample size calculations are desired. You use options in the analysis statements to identify the result parameter to compute, to specify the statistical test and computational options, and to provide one or more scenarios for the values of relevant analysis parameters.

[Table 67.1](#) summarizes the basic functions of each statement in PROC POWER. The syntax of each statement in [Table 67.1](#) is described in the following pages.

**Table 67.1** Statements in the POWER Procedure

Statement	Description
<b>PROC POWER</b>	invokes the procedure
<b>LOGISTIC</b>	likelihood ratio chi-square test of a single predictor in logistic regression with binary response
<b>MULTREG</b>	tests of one or more coefficients in multiple linear regression

Table 67.1 *continued*

Statement	Description
ONECORR ONESAMPLEFREQ	Fisher's $z$ test and $t$ test of (partial) correlation tests, confidence interval precision, and equivalence tests of a single binomial proportion
ONESAMPLEMEANS	one-sample $t$ test, confidence interval precision, or equivalence test
ONEWAYANOVA	one-way ANOVA including single-degree-of-freedom contrasts
PAIREFREQ PAIREDMEANS	McNemar's test for paired proportions paired $t$ test, confidence interval precision, or equivalence test
PLOT	displays plots for previous sample size analysis
TWOSAMPLEFREQ	chi-square, likelihood ratio, and Fisher's exact tests for two independent proportions
TWOSAMPLEMEANS	two-sample $t$ test, confidence interval precision, or equivalence test
TWOSAMPLESURVIVAL	log-rank, Gehan, and Tarone-Ware tests for comparing two survival curves
TWOSAMPLEWILCOXON	Wilcoxon-Mann-Whitney (rank-sum) test for 2 independent groups

See the section “Summary of Analyses” on page 4910 for a summary of the analyses available and the syntax required for them.

---

## PROC POWER Statement

**PROC POWER** < options > ;

The **PROC POWER** statement invokes the POWER procedure. You can specify the following option.

### PLOTONLY

specifies that only graphical results from the **PLOT** statement should be produced.

---

## LOGISTIC Statement

**LOGISTIC** < options > ;

The **LOGISTIC** statement performs power and sample size analyses for the likelihood ratio chi-square test of a single predictor in binary logistic regression, possibly in the presence of one or

more covariates. All predictor variables are assumed to be independent of each other. So, this analysis is not applicable to studies with correlated predictors—for example, most observational studies (as opposed to randomized studies).

## Summary of Options

Table 67.2 summarizes categories of options available in the LOGISTIC statement.

**Table 67.2** Summary of Options in the LOGISTIC Statement

Task	Options
Define analysis	TEST=
Specify analysis information	ALPHA= COVARIATES= TESTPREDICTOR= VARDIST=
Specify effects	RESPONSEPROB= COVODDSRATIOS= COVREGCOEFFS= DEFAULTUNIT= INTERCEPT= TESTODDSRATIO= TESTREGCOEFF= UNITS=
Specify sample size	NTOTAL=
Specify power	POWER=
Control sample size rounding	NFRACTIONAL
Specify computational method	DEFAULTNBINS= NBINS=
Control ordering in output	OUTPUTORDER=

Table 67.3 summarizes the valid result parameters in the LOGISTIC statement.

**Table 67.3** Summary of Result Parameters in the LOGISTIC Statement

Analyses	Solve For	Syntax
TEST=LRCHI	Power	POWER=.
	Sample size	NTOTAL=.

## Dictionary of Options

**ALPHA=***number-list*

specifies the level of significance of the statistical test. The default is 0.05, corresponding to

the usual  $0.05 \times 100\% = 5\%$  level of significance. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**COVARIATES=***grouped-name-list*

specifies the distributions of any predictor variables in the model but not being tested, using labels specified with the **VARDIST=** option. The distributions are assumed to be independent of each other and of the tested predictor. If this option is omitted, then the tested predictor specified by the **TESTEDPREDICTOR=** option is assumed to be the only predictor in the model. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-name-list*.

**COVODDSRATIOS=***grouped-number-list*

specifies the odds ratios for the covariates in the full model (including variables in the **TESTPREDICTOR=** and **COVARIATES=** options). The ordering of the values corresponds to the ordering in the **COVARIATES=** option. If the response variable is coded as  $Y = 1$  for success and  $Y = 0$  for failure, then the odds ratio for each covariate  $X$  is the odds of  $Y = 1$  when  $X = a$  divided by the odds of  $Y = 1$  when  $X = b$ , where  $a$  and  $b$  are determined from the **DEFAULTUNIT=** and **UNITS=** options. Values must be greater than zero. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**COVREGCOEFFS=***grouped-number-list*

specifies the regression coefficients for the covariates in the full model including the test predictor (as specified by the **TESTPREDICTOR=** option). The ordering of the values corresponds to the ordering in the **COVARIATES=** option. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**DEFAULTNBINS=***number*

specifies the default number of categories (or “bins”) into which the distribution for each predictor variable is divided in internal calculations. Higher values increase computational time and memory requirements but generally lead to more accurate results. Each test predictor or covariate that is absent from the **NBINS=** option derives its bin number from the **DEFAULTNBINS=** option. The default value is **DEFAULTNBINS=10**.

There are two variable distributions for which the number of bins can be overridden internally:

- For an ordinal distribution, the number of ordinal values is always used as the number of bins.
- For a binomial distribution, if the requested number of bins is larger than  $n + 1$ , where  $n$  is the sample size parameter of the binomial distribution, then exactly  $n + 1$  bins are used.

**DEFAULTUNIT=***change-spec*

specifies the default change in the predictor variables assumed for odds ratios specified with the **COVODDSRATIOS=** and **TESTODDSRATIO=** options. Each test predictor or covariate that is absent from the **UNITS=** option derives its change value from the **DEFAULTUNIT=** option. The value must be nonzero. The default value is **DEFAULTUNIT=1**. This option can be used only if at least one of the **COVODDSRATIOS=** and **TESTODDSRATIO=** options is used.

Valid specifications for *change-spec* are as follows:

*number* defines the odds ratio as the ratio of the response variable odds when  $X = a$  to the odds when  $X = a - \textit{number}$  for any constant  $a$ .

<+|->SD defines the odds ratio as the ratio of the odds when  $X = a$  to the odds when  $X = a - \sigma$  (or  $X = a + \sigma$ , if SD is preceded by a minus sign (-)) for any constant  $a$ , where  $\sigma$  is the standard deviation of  $X$  (as determined from the `VARDIST=` option).

*multiple*\*SD defines the odds ratio as the ratio of the odds when  $X = a$  to the odds when  $X = a - \textit{multiple} * \sigma$  for any constant  $a$ , where  $\sigma$  is the standard deviation of  $X$  (as determined from the `VARDIST=` option).

PERCENTILES( $p1, p2$ ) defines the odds ratio as the ratio of the odds when  $X$  is equal to its  $p2 * 100$ th percentile to the odds when  $X$  is equal to its  $p1 * 100$ th percentile (where the percentiles are determined from the distribution specified in the `VARDIST=` option). Values for  $p1$  and  $p2$  must be strictly between 0 and 1.

#### **INTERCEPT=***number-list*

specifies the intercept in the full model (including variables in the `TESTPREDICTOR=` and `COVARIATES=` options). See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

#### **NBINS=**(*“name” = number < . . . “name” = number >*)

specifies the number of categories (or “bins”) into which the distribution for each predictor variable (identified by its *name* from the `VARDIST=` option) is divided in internal calculations. Higher values increase computational time and memory requirements but generally lead to more accurate results. Each predictor variable that is absent from the `NBINS=` option derives its bin number from the `DEFAULTNBINS=` option.

There are two variable distributions for which the `NBINS=` value can be overridden internally:

- For an ordinal distribution, the number of ordinal values is always used as the number of bins.
- For a binomial distribution, if the requested number of bins is larger than  $n + 1$ , where  $n$  is the sample size parameter of the binomial distribution, then exactly  $n + 1$  bins are used.

#### **NFRACTIONAL**

##### **NFRAC**

enables fractional input and output for sample sizes. See the section “[Sample Size Adjustment Options](#)” on page 4916 for information about the ramifications of the presence (and absence) of the `NFRACTIONAL` option.

#### **NTOTAL=***number-list*

specifies the sample size or requests a solution for the sample size with a missing value (`NTOTAL=.`). Values must be at least one. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**OUTPUTORDER=INTERNAL****OUTPUTORDER=REVERSE****OUTPUTORDER=SYNTAX**

controls how the input and default analysis parameters are ordered in the output. **OUTPUTORDER=INTERNAL** (the default) arranges the parameters in the output according to the following order of their corresponding options:

- **DEFAULTNBINS=**
- **NBINS=**
- **ALPHA=**
- **RESPONSEPROB=**
- **INTERCEPT=**
- **TESTPREDICTOR=**
- **TESTODDSRATIO=**
- **TESTREGCOEFF=**
- **COVARIATES=**
- **COVODDSRATIOS=**
- **COVREGCOEFFS=**
- **NTOTAL=**
- **POWER=**

The **OUTPUTORDER=SYNTAX** option arranges the parameters in the output in the same order in which their corresponding options are specified in the **LOGISTIC** statement. The **OUTPUTORDER=REVERSE** option arranges the parameters in the output in the reverse of the order in which their corresponding options are specified in the **LOGISTIC** statement.

**POWER=number-list**

specifies the desired power of the test or requests a solution for the power with a missing value (**POWER=.**). The power is expressed as a probability, a number between 0 and 1, rather than as a percentage. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**RESPONSEPROB=number-list**

specifies the response probability in the full model when all predictor variables (including variables in the **TESTPREDICTOR=** and **COVARIATES=** options) are equal to their means. The log odds of this probability are equal to the intercept in the full model where all predictor are centered at their means. If the response variable is coded as  $Y = 1$  for success and  $Y = 0$  for failure, then this probability is equal to the mean of  $Y$  in the full model when all  $X$ s are equal to their means. Values must be strictly between zero and one. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**TEST=LRCHI**

specifies the likelihood ratio chi-square test of a single model parameter in binary logistic regression. This is the default test option.

**TESTODDSRATIO=number-list**

specifies the odds ratio for the predictor variable being tested in the full model (including variables in the **TESTPREDICTOR=** and **COVARIATES=** options). If the response variable is coded as  $Y = 1$  for success and  $Y = 0$  for failure, then the odds ratio for the  $X$  being tested is the odds of  $Y = 1$  when  $X = a$  divided by the odds of  $Y = 1$  when  $X = b$ , where  $a$  and  $b$  are determined from the **DEFAULTUNIT=** and **UNITS=** options. Values must be greater than zero. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**TESTPREDICTOR=name-list**

specifies the distribution of the predictor variable being tested, using labels specified with the **VARDIST=** option. This distribution is assumed to be independent of the distributions of the covariates as defined in the **COVARIATES=** option. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *name-list*.

**TESTREGCOEFF=number-list**

specifies the regression coefficient for the predictor variable being tested in the full model including the covariates specified by the **COVARIATES=** option. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**UNITS=(“name” = change-spec <... “name” = change-spec >)**

specifies the changes in the predictor variables assumed for odds ratios specified with the **COVODDSRATIOS=** and **TESTODDSRATIO=** options. Each predictor variable whose *name* (from the **VARDIST=** option) is absent from the **UNITS** option derives its change value from the **DEFAULTUNIT=** option. This option can be used only if at least one of the **COVODDSRATIOS=** and **TESTODDSRATIO=** options is used.

Valid specifications for *change-spec* are as follows:

*number* defines the odds ratio as the ratio of the response variable odds when  $X = a$  to the odds when  $X = a - \textit{number}$  for any constant  $a$ .

<+|->SD defines the odds ratio as the ratio of the odds when  $X = a$  to the odds when  $X = a - \sigma$  (or  $X = a + \sigma$ , if SD is preceded by a minus sign (-)) for any constant  $a$ , where  $\sigma$  is the standard deviation of  $X$  (as determined from the **VARDIST=** option).

*multiple*\*SD defines the odds ratio as the ratio of the odds when  $X = a$  to the odds when  $X = a - \textit{multiple} * \sigma$  for any constant  $a$ , where  $\sigma$  is the standard deviation of  $X$  (as determined from the **VARDIST=** option).

PERCENTILES( $p1, p2$ ) defines the odds ratio as the ratio of the odds when  $X$  is equal to its  $p2 * 100$ th percentile to the odds when  $X$  is equal to its  $p1 * 100$ th percentile (where the percentiles are determined from the distribution specified in the **VARDIST=** option). Values for  $p1$  and  $p2$  must be strictly between 0 and 1.

Each unit value must be nonzero.

**VARDIST(“label”)=distribution (parameters)**

defines a distribution for a predictor variable.

For the **VARDIST=** option,

<i>label</i>	identifies the variable distribution in the output and with the <b>COVARIATES=</b> and <b>TESTPREDICTOR=</b> options.
<i>distribution</i>	specifies the distributional form of the variable.
<i>parameters</i>	specifies one or more parameters associated with the distribution.

Choices for distributional forms and their parameters are as follows:

**ORDINAL** (*(values) : (probabilities)*) is an ordered categorical distribution. The *values* are any numbers separated by spaces. The *probabilities* are numbers between 0 and 1 (inclusive) separated by spaces. Their sum must be exactly 1. The number of *probabilities* must match the number of *values*.

**BETA** (*a, b <, l, r >*) is a beta distribution with shape parameters *a* and *b* and optional location parameters *l* and *r*. The values of *a* and *b* must be greater than 0, and *l* must be less than *r*. The default values for *l* and *r* are 0 and 1, respectively.

**BINOMIAL** (*p, n*) is a binomial distribution with probability of success *p* and number of independent Bernoulli trials *n*. The value of *p* must be greater than 0 and less than 1, and *n* must be an integer greater than 0.

**EXPONENTIAL** (*λ*) is an exponential distribution with scale *λ*, which must be greater than 0.

**GAMMA** (*a, λ*) is a gamma distribution with shape *a* and scale *λ*. The values of *a* and *λ* must be greater than 0.

**LAPLACE** (*θ, λ*) is a Laplace distribution with location *θ* and scale *λ*. The value of *λ* must be greater than 0.

**LOGISTIC** (*θ, λ*) is a logistic distribution with location *θ* and scale *λ*. The value of *λ* must be greater than 0.

**LOGNORMAL** (*θ, λ*) is a lognormal distribution with location *θ* and scale *λ*. The value of *λ* must be greater than 0.

**NORMAL** (*θ, λ*) is a normal distribution with mean *θ* and standard deviation *λ*. The value of *λ* must be greater than 0.

**POISSON** (*m*) is a Poisson distribution with mean *m*. The value of *m* must be greater than 0.

**UNIFORM** (*l, r*) is a uniform distribution on the interval [*l, r*], where *l* < *r*.

## Restrictions on Option Combinations

To specify the intercept in the full model, choose one of the following two parameterizations:

- intercept (using the **INTERCEPT=** options)
- Prob( $Y = 1$ ) when all predictors are equal to their means (using the **RESPONSEPROB=** option)

To specify the effect associated with the predictor variable being tested, choose one of the following two parameterizations:

- odds ratio (using the `TESTODDSRATIO=` options)
- regression coefficient (using the `TESTREGCOEFFS=` option)

To describe the effects of the covariates in the full model, choose one of the following two parameterizations:

- odds ratios (using the `COVODDSRATIOS=` options)
- regression coefficients (using the `COVREGCOEFFS=` options)

## Option Groups for Common Analyses

This section summarizes the syntax for the common analyses supported in the `LOGISTIC` statement.

### Likelihood Ratio Chi-Square Test for One Predictor

You can express effects in terms of response probability and odds ratios, as in the following statements:

```
proc power;
  logistic
    vardist("x1a") = normal(0, 2)
    vardist("x1b") = normal(0, 3)
    vardist("x2") = poisson(7)
    vardist("x3a") = ordinal((-5 0 5) : (.3 .4 .3))
    vardist("x3b") = ordinal((-5 0 5) : (.4 .3 .3))
    testpredictor = "x1a" "x1b"
    covariates = "x2" | "x3a" "x3b"
    responseprob = 0.15
    testoddsratio = 1.75
    covoddsratios = (2.1 1.4)
    ntotal = 100
    power = .;
run;
```

The `VARDIST=` options define the distributions of the predictor variables. The `TESTPREDICTOR=` option specifies two scenarios for the test predictor distribution, Normal(10,2) and Normal(10,3). The `COVARIATES=` option specifies two covariates, the first with a Poisson(7) distribution. The second covariate has an ordinal distribution on the values  $-5$ ,  $0$ , and  $5$  with two scenarios for the associated probabilities:  $(.3, .4, .3)$  and  $(.4, .3, .3)$ . The response probability in the full model with all variables equal to zero is specified by the `RESPONSEPROB=` option as  $0.15$ . The odds ratio for a unit decrease in the tested predictor is specified by the `TESTODDSRATIO=` option to be  $1.75$ . Corresponding odds ratios for the two covariates in the full model are specified by the `COVODDSRATIOS=` option to be  $2.1$  and  $1.4$ . The `POWER=.` option requests a solution for the power at a sample size of  $100$  as specified by the `NTOTAL=` option.

Default values of the `TEST=` and `ALPHA=` options specify a likelihood ratio test of the first predictor with a significance level of  $0.05$ . The default of `DEFAULTUNIT=1` specifies that all odds

ratios are defined in terms of unit changes in predictors. The default of `DEFAULTNBINS=10` specifies that each of the three predictor variables is discretized into a distribution with 10 categories in internal calculations.

You can also express effects in terms of regression coefficients, as in the following statements:

```
proc power;
  logistic
    vardist("x1a") = normal(0, 2)
    vardist("x1b") = normal(0, 3)
    vardist("x2") = poisson(7)
    vardist("x3") = ordinal((-5 0 5) : (.3 .4 .3))
    testpredictor = "x1a" "x1b"
    covariates = "x2" | "x3a" "x3b"
    intercept = -6.928162
    testregcoeff = 0.5596158
    covregcoeffs = (0.7419373 0.3364722)
    ntotal = 100
    power = .;
run;
```

The regression coefficients for the tested predictor (`TESTREGCOEFF=0.5596158`) and covariates (`COVREGCOEFFS=(0.7419373 0.3364722)`) are determined by taking the logarithm of the corresponding odds ratios. The intercept in the full model is specified as  $-6.928162$  by the `INTERCEPT=` option. This number is calculated according to the formula at the end of “[Analyses in the LOGISTIC Statement](#)” on page 4922, which expresses the intercept in terms of the response probability, regression coefficients, and predictor means:

$$\text{Intercept} = \log\left(\frac{0.15}{1 - 0.15}\right) - (0.5596158(0) + 0.7419373(7) + 0.3364722(0))$$

---

## MULTREG Statement

**MULTREG** < options > ;

The `MULTREG` statement performs power and sample size analyses for Type III  $F$  tests of sets of predictors in multiple linear regression, assuming either fixed or normally distributed predictors.

### Summary of Options

Table 67.4 summarizes categories of options available in the `MULTREG` statement.

**Table 67.4** Summary of Options in the MULTREG Statement

Task	Options
Define analysis	TEST=
Specify analysis information	ALPHA= MODEL= NFULLPREDICTORS= NOINT NREDUCEDPREDICTORS= NTESTPREDICTORS=
Specify effects	PARTIALCORR= RSQUAREDIFF= RSQUAREFULL= RSQUAREREDUCED=
Specify sample size	NTOTAL=
Specify power	POWER=
Control sample size rounding	NFRACTIONAL
Control ordering in output	OUTPUTORDER=

Table 67.5 summarizes the valid result parameters in the MULTREG statement.

**Table 67.5** Summary of Result Parameters in the MULTREG Statement

Analyses	Solve For	Syntax
TEST=TYPE3	Power	POWER=.
	Sample size	NTOTAL=.

## Dictionary of Options

### **ALPHA=***number-list*

specifies the level of significance of the statistical test. The default is 0.05, corresponding to the usual  $0.05 \times 100\% = 5\%$  level of significance. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### **MODEL=***keyword-list*

specifies the assumed distribution of the tested predictors. **MODEL=FIXED** indicates a fixed predictor distribution. **MODEL=RANDOM** (the default) indicates a joint multivariate normal distribution for the response and tested predictors. You can use the aliases **CONDITIONAL** for **FIXED** and **UNCONDITIONAL** for **RANDOM**. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *keyword-list*.

**FIXED** fixed predictors

**RANDOM** random (multivariate normal) predictors

**NFRACTIONAL****NFRAC**

enables fractional input and output for sample sizes. See the section “[Sample Size Adjustment Options](#)” on page 4916 for information about the ramifications of the presence (and absence) of the **NFRACTIONAL** option.

**NFULLPREDICTORS=number-list****NFULLPRED=number-list**

specifies the number of predictors in the full model, not counting the intercept. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NOINT**

specifies a no-intercept model (for both full and reduced models). By default, the intercept is included in the model. If you want to test the intercept, you can specify the **NOINT** option and simply consider the intercept to be one of the predictors being tested. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NREDUCEDPREDICTORS=number-list****NREDUCEDPRED=number-list****NREDPRED=number-list**

specifies the number of predictors in the reduced model, not counting the intercept. This is the same as the difference between values of the **NFULLPREDICTORS=** and **NTESTPREDICTORS=** options. Note that supplying a value of 0 is the same as specifying an *F* test of a Pearson correlation. This option cannot be used at the same time as the **NTESTPREDICTORS=** option. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NTESTPREDICTORS=number-list****NTESTPRED=number-list**

specifies the number of predictors being tested. This is the same as the difference between values of the **NFULLPREDICTORS=** and **NREDUCEDPREDICTORS=** options. Note that supplying identical values for the **NTESTPREDICTORS=** and **NFULLPREDICTORS=** options is the same as specifying an *F* test of a Pearson correlation. This option cannot be used at the same time as the **NREDUCEDPREDICTORS=** option. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NTOTAL=number-list**

specifies the sample size or requests a solution for the sample size with a missing value (**NTOTAL=.**). The minimum acceptable value for the sample size depends on the **MODEL=**, **NOINT**, **NFULLPREDICTORS=**, **NTESTPREDICTORS=**, and **NREDUCEDPREDICTORS=** options. It ranges from  $p + 1$  to  $p + 3$ , where  $p$  is the value of the **NFULLPREDICTORS** option. See [Table 67.30](#) for further information about minimum **NTOTAL** values, and see the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**OUTPUTORDER=INTERNAL****OUTPUTORDER=REVERSE****OUTPUTORDER=SYNTAX**

controls how the input and default analysis parameters are ordered in the output. **OUTPUTORDER=INTERNAL** (the default) arranges the parameters in the output according to the following order of their corresponding options:

- **MODEL=**
- **NFULLPREDICTORS=**
- **NTESTPREDICTORS=**
- **NREDUCEDPREDICTORS=**
- **ALPHA=**
- **PARTIALCORR=**
- **RSQUAREFULL=**
- **RSQUAREREDUCED=**
- **RSQUAREDIFF=**
- **NTOTAL=**
- **POWER=**

The **OUTPUTORDER=SYNTAX** option arranges the parameters in the output in the same order in which their corresponding options are specified in the **MULTREG** statement. The **OUTPUTORDER=REVERSE** option arranges the parameters in the output in the reverse of the order in which their corresponding options are specified in the **MULTREG** statement.

**PARTIALCORR=number-list****PCORR=number-list**

specifies the partial correlation between the tested predictors and the response, adjusting for any other predictors in the model. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**POWER=number-list**

specifies the desired power of the test or requests a solution for the power with a missing value (**POWER=.**). The power is expressed as a probability, a number between 0 and 1, rather than as a percentage. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**RSQUAREDIFF=number-list****RSQDIFF=number-list**

specifies the difference in  $R^2$  between the full and reduced models. This is equivalent to the proportion of variation explained by the predictors you are testing. It is also equivalent to the squared semipartial correlation of the tested predictors with the response. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**RSQUAREFULL**=*number-list*

**RSQFULL**=*number-list*

specifies the  $R^2$  of the full model, where  $R^2$  is the proportion of variation explained by the model. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**RSQUAREREDUCED**=*number-list*

**RSQREDUCED**=*number-list*

**RSQRED**=*number-list*

specifies the  $R^2$  of the reduced model, where  $R^2$  is the proportion of variation explained by the model. If the reduced model is an empty or intercept-only model (in other words, if **NREDUCEDPREDICTORS**=0 or **NTESTPREDICTORS**=**NFULLPREDICTORS**), then **RSQUAREREDUCED**=0 is assumed. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**TEST**=**TYPE3**

specifies a Type III  $F$  test of a set of predictors adjusting for any other predictors in the model. This is the default test option.

## Restrictions on Option Combinations

To specify the number of predictors, use any two of these three options:

- the number of predictors in the full model (**NFULLPREDICTORS**=)
- the number of predictors in the reduced model (**NREDUCEDPREDICTORS**=)
- the number of predictors being tested (**NTESTPREDICTORS**=)

To specify the effect, choose one of the following parameterizations:

- partial correlation (by using the **PARTIALCORR**= option)
- $R^2$  for the full and reduced models (by using any two of **RSQUAREDIFF**=, **RSQUAREFULL**=, and **RSQUAREREDUCED**=)

## Option Groups for Common Analyses

This section summarizes the syntax for the common analyses supported in the **MULTREG** statement.

### *Type III F Test of a Set of Predictors*

You can express effects in terms of partial correlation, as in the following statements. Default values of the **TEST**=, **MODEL**=, and **ALPHA**= options specify a Type III  $F$  test with a significance level of 0.05, assuming normally distributed predictors.

```

proc power;
  multreg
    model = random
    nfullpredictors = 7
    ntestpredictors = 3
    partialcorr = 0.35
    ntotal = 100
    power = .;
run;

```

You can also express effects in terms of  $R^2$ :

```

proc power;
  multreg
    model = fixed
    nfullpredictors = 7
    ntestpredictors = 3
    rsquarefull = 0.9
    rsquarediff = 0.1
    ntotal = .
    power = 0.9;
run;

```

---

## ONECORR Statement

**ONECORR** < options > ;

The **ONECORR** statement performs power and sample size analyses for tests of simple and partial Pearson correlation between two variables. Both Fisher's  $z$  test and the  $t$  test are supported.

### Summary of Options

Table 67.6 summarizes categories of options available in the **ONECORR** statement.

**Table 67.6** Summary of Options in the **ONECORR** Statement

Task	Options
Define analysis	DIST= TEST=
Specify analysis information	ALPHA= MODEL= NPARTIALVARS= NULLCORR= SIDES=
Specify effects	CORR=
Specify sample size	NTOTAL=

**Table 67.6** *continued*

Task	Options
Specify power	POWER=
Control sample size rounding	NFRACTIONAL
Control ordering in output	OUTPUTORDER=

Table 67.7 summarizes the valid result parameters in the **ONECORR** statement.

**Table 67.7** Summary of Result Parameters in the **ONECORR** Statement

Analyses	Solve For	Syntax
TEST=PEARSON	Power	POWER=.
	Sample size	NTOTAL=.

## Dictionary of Options

### **ALPHA=***number-list*

specifies the level of significance of the statistical test. The default is 0.05, corresponding to the usual  $0.05 \times 100\% = 5\%$  level of significance. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### **CORR=***number-list*

specifies the correlation between two variables, possibly adjusting for other variables as determined by the **NPARTIALVARS=** option. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### **DIST=FISHERZ**

#### **DIST=T**

specifies the underlying distribution assumed for the test statistic. FISHERZ corresponds to Fisher’s *z* normalizing transformation of the correlation coefficient. T corresponds to the *t* transformation of the correlation coefficient. Note that **DIST=T** is equivalent to analyses in the **MULTREG** statement with **NTESTPREDICTORS=1**. The default value is FISHERZ.

### **MODEL=***keyword-list*

specifies the assumed distribution of the first variable when **DIST=T**. The second variable is assumed to have a normal distribution. **MODEL=FIXED** indicates a fixed distribution. **MODEL=RANDOM** (the default) indicates a joint bivariate normal distribution with the second variable. You can use the aliases **CONDITIONAL** for **FIXED** and **UNCONDITIONAL** for **RANDOM**. This option can be used only for **DIST=T**. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *keyword-list*.

**FIXED** fixed variables

**RANDOM** random (bivariate normal) variables

**NFRACTIONAL****NFRAC**

enables fractional input and output for sample sizes. See the section “[Sample Size Adjustment Options](#)” on page 4916 for information about the ramifications of the presence (and absence) of the **NFRACTIONAL** option.

**NPARTIALVARS=number-list****NPVARS=number-list**

specifies the number of variables adjusted for in the correlation between the two primary variables. The default value is 0, corresponding to a simple correlation. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NTOTAL=number-list**

specifies the sample size or requests a solution for the sample size with a missing value (**NTOTAL=.**). Values for the sample size must be at least  $p + 3$  when **DIST=T** and **MODEL=CONDITIONAL**, and at least  $p + 4$  when either **DIST=FISHER** or when **DIST=T** and **MODEL=UNCONDITIONAL**, where  $p$  is the value of the **NPARTIALVARS** option. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NULLCORR=number-list****NULLC=number-list**

specifies the null value of the correlation. The default value is 0. This option can be used only with the **DIST=FISHERZ** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**OUTPUTORDER=INTERNAL****OUTPUTORDER=REVERSE****OUTPUTORDER=SYNTAX**

controls how the input and default analysis parameters are ordered in the output. **OUTPUTORDER=INTERNAL** (the default) arranges the parameters in the output according to the following order of their corresponding options:

- **MODEL=**
- **SIDES=**
- **NULL=**
- **ALPHA=**
- **NPARTIALVARS=**
- **CORR=**
- **NTOTAL=**
- **POWER=**

The **OUTPUTORDER=SYNTAX** option arranges the parameters in the output in the same order in which their corresponding options are specified in the **ONECORR** statement. The **OUTPUTORDER=REVERSE** option arranges the parameters in the output in the reverse of the order in which their corresponding options are specified in the **ONECORR** statement.

**POWER=number-list**

specifies the desired power of the test or requests a solution for the power with a missing value (**POWER=.**). The power is expressed as a probability, a number between 0 and 1, rather than as a percentage. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**SIDES=keyword-list**

specifies the number of sides (or tails) and the direction of the statistical test. Valid keywords are

- 1 one-sided with alternative hypothesis in same direction as effect
- 2 two-sided
- U upper one-sided with alternative greater than null value
- L lower one-sided with alternative less than null value

The default value is 2.

**TEST=PEARSON**

specifies a test of the Pearson correlation coefficient between two variables, possibly adjusting for other variables. This is the default test option.

## Option Groups for Common Analyses

This section summarizes the syntax for the common analyses supported in the **ONECORR** statement.

### *Fisher's z Test for Pearson Correlation*

The following statements demonstrate a power computation for Fisher's z test for correlation. Default values of **TEST=PEARSON**, **ALPHA=0.05**, **SIDES=2**, and **NPARTIALVARS=0** are assumed.

```
proc power;
  onecorr dist=fisherz
    nullcorr = 0.15
    corr = 0.35
    ntotal = 180
    power = .;
run;
```

### *t Test for Pearson Correlation*

The following statements demonstrate a sample size computation for the *t* test for correlation. Default values of **TEST=PEARSON**, **MODEL=RANDOM**, **ALPHA=0.05**, and **SIDES=2** are assumed.

```

proc power;
  onecorr dist=t
    npartialvars = 4
    corr = 0.45
    ntotal = .
    power = 0.85;
run;

```

---

## ONESAMPLEFREQ Statement

**ONESAMPLEFREQ** < options > ;

The **ONESAMPLEFREQ** statement performs power and sample size analyses for exact and approximate tests (including equivalence, noninferiority, and superiority) and confidence interval precision for a single binomial proportion.

### Summary of Options

Table 67.8 summarizes categories of options available in the **ONESAMPLEFREQ** statement.

**Table 67.8** Summary of Options in the **ONESAMPLEFREQ** Statement

Task	Options
Define analysis	CI= TEST=
Specify analysis information	ALPHA= EQUIVBOUNDS= LOWER= MARGIN= NULLPROPORTION= SIDES= UPPER=
Specify effect	HALFWIDTH= PROPORTION=
Specify variance estimation	VAREST=
Specify sample size	NTOTAL=
Specify power and related probabilities	POWER= PROBWIDTH=
Control sample size rounding	NFRACTIONAL
Choose computational method	METHOD=
Control ordering in output	OUTPUTORDER=

Table 67.9 summarizes the valid result parameters for different analyses in the ONESAMPLEFREQ statement.

**Table 67.9** Summary of Result Parameters in the ONESAMPLEFREQ Statement

Analyses	Solve For	Syntax
CI=WILSON	Prob(width)	PROBWIDTH=.
CI=AGRESTICOULL	Prob(width)	PROBWIDTH=.
CI=JEFFREYS	Prob(width)	PROBWIDTH=.
CI=EXACT	Prob(width)	PROBWIDTH=.
CI=WALD	Prob(width)	PROBWIDTH=.
CI=WALD_CORRECT	Prob(width)	PROBWIDTH=.
TEST=ADJZ METHOD=EXACT	Power	POWER=.
TEST=ADJZ METHOD=NORMAL	Power Sample size	POWER=. NTOTAL=.
TEST=EQUIV_ADJZ METHOD=EXACT	Power	POWER=.
TEST=EQUIV_ADJZ METHOD=NORMAL	Power Sample size	POWER=. NTOTAL=.
TEST=EQUIV_EXACT	Power	POWER=.
TEST=EQUIV_Z METHOD=EXACT	Power	POWER=.
TEST=EQUIV_Z METHOD=NORMAL	Power Sample size	POWER=. NTOTAL=.
TEST=EXACT	Power	POWER=.
TEST=Z METHOD=EXACT	Power	POWER=.
TEST=Z METHOD=NORMAL	Power Sample size	POWER=. NTOTAL=.

## Dictionary of Options

### ALPHA=*number-list*

specifies the level of significance of the statistical test. The default is 0.05, corresponding to the usual  $0.05 \times 100\% = 5\%$  level of significance. If the CI= and SIDES=1 options are used, then the value must be less than 0.5. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**CI****CI=AGRESTICOULL | AC****CI=JEFFREYS****CI=EXACT | CLOPPERPEARSON | CP****CI=WALD****CI=WALD\_CORRECT****CI=WILSON | SCORE**

specifies an analysis of precision of a confidence interval for the sample binomial proportion.

The value of the **CI=** option specifies the type of confidence interval. The **CI=AGRESTICOULL** option is a generalization of the “Adjusted Wald / add 2 successes and 2 failures” interval of Agresti and Coull (1998) and is presented in Brown, Cai, and DasGupta (2001). It corresponds to the **TABLES / BINOMIAL (AGRESTICOULL)** option in **PROC FREQ**. The **CI=JEFFREYS** option specifies the equal-tailed Jeffreys prior Bayesian interval, corresponding to the **TABLES / BINOMIAL (JEFFREYS)** option in **PROC FREQ**. The **CI=EXACT** option specifies the exact Clopper-Pearson confidence interval based on enumeration, corresponding to the **TABLES / BINOMIAL (EXACT)** option in **PROC FREQ**. The **CI=WALD** option specifies the confidence interval based on the Wald test (also commonly called the *z* test or normal-approximation test), corresponding to the **TABLES / BINOMIAL (WALD)** option in **PROC FREQ**. The **CI=WALD\_CORRECT** option specifies the confidence interval based on the Wald test with continuity correction, corresponding to the **TABLES / BINOMIAL (CORRECT WALD)** option in **PROC FREQ**. The **CI=WILSON** option (the default) specifies the confidence interval based on the score statistic, corresponding to the **TABLES / BINOMIAL (WILSON)** option in **PROC FREQ**.

Instead of power, the relevant probability for this analysis is the probability of achieving a desired precision. Specifically, it is the probability that the half-width of the confidence interval will be at most the value specified by the **HALFWIDTH=** option.

**EQUIVBOUNDS=***grouped-number-list*

specifies the lower and upper equivalence bounds, representing the same information as the combination of the **LOWER=** and **UPPER=** options but grouping them together. The **EQUIVBOUNDS=** option can be used only with equivalence analyses (**TEST=EQUIV\_ADJZ | EQUIV\_EXACT | EQUIV\_Z**). Values must be strictly between 0 and 1. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**HALFWIDTH=***number-list*

specifies the desired confidence interval half-width. The half-width for a two-sided interval is the length of the confidence interval divided by two. This option can be used only with the **CI=** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**LOWER=***number-list*

specifies the lower equivalence bound for the binomial proportion. The **LOWER=** option can be used only with equivalence analyses (**TEST=EQUIV\_ADJZ | EQUIV\_EXACT | EQUIV\_Z**). Values must be strictly between 0 and 1. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**MARGIN=***number-list*

specifies the equivalence or noninferiority or superiority margin, depending on the analysis.

The **MARGIN=** option can be used with one-sided analyses (**SIDES** = 1 | U | L), in which case it specifies the margin added to the null proportion value in the hypothesis test, resulting in a noninferiority or superiority test (depending on the agreement between the effect and hypothesis directions and the sign of the margin). A test with a null proportion  $p_0$  and a margin  $m$  is the same as a test with null proportion  $p_0 + m$  and no margin.

The **MARGIN=** option can also be used with equivalence analyses (**TEST**=EQUIV\_ADJZ | EQUIV\_EXACT | EQUIV\_Z) when the **NULLPROPORTION=** option is used, in which case it specifies the lower and upper equivalence bounds as  $p_0 - m$  and  $p_0 + m$ , where  $p_0$  is the value of the **NULLPROPORTION=** option and  $m$  is the value of the **MARGIN=** option.

The **MARGIN=** option cannot be used in conjunction with the **SIDES**=2 option. (Instead, specify an equivalence analysis by using **TEST**=EQUIV\_ADJZ or **TEST**=EQUIV\_EXACT or **TEST**=EQUIV\_Z). Also, the **MARGIN=** option cannot be used with the **CI=** option.

Values must be strictly between -1 and 1. In addition, the sum of **NULLPROPORTION** and **MARGIN** must be strictly between 0 and 1 for one-sided analyses, and the derived lower equivalence bound ( $2 * \text{NULLPROPORTION} - \text{MARGIN}$ ) must be strictly between 0 and 1 for equivalence analyses.

See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**METHOD=EXACT****METHOD=NORMAL**

specifies the computational method. **METHOD=EXACT** (the default) computes exact results by using the binomial distribution. **METHOD=NORMAL** computes approximate results by using the normal approximation to the binomial distribution.

**NFRACTIONAL****NFRAC**

enables fractional input and output for sample sizes. This option is invalid when the **METHOD=EXACT** option is specified. See the section “[Sample Size Adjustment Options](#)” on page 4916 for information about the ramifications of the presence (and absence) of the **NFRACTIONAL** option.

**NTOTAL=***number-list*

specifies the sample size or requests a solution for the sample size with a missing value (**NTOTAL**=.). See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NULLPROPORTION=***number-list***NULLP=***number-list*

specifies the null proportion. A value of 0.5 corresponds to the sign test. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**OUTPUTORDER=INTERNAL****OUTPUTORDER=REVERSE****OUTPUTORDER=SYNTAX**

controls how the input and default analysis parameters are ordered in the output. **OUTPUTORDER=INTERNAL** (the default) arranges the parameters in the output according to the following order of their corresponding options:

- **SIDES=**
- **NULLPROPORTION=**
- **ALPHA=**
- **PROPORTION=**
- **NTOTAL=**
- **POWER=**

The **OUTPUTORDER=SYNTAX** option arranges the parameters in the output in the same order in which their corresponding options are specified in the **ONESAMPLEFREQ** statement. The **OUTPUTORDER=REVERSE** option arranges the parameters in the output in the reverse of the order in which their corresponding options are specified in the **ONESAMPLEFREQ** statement.

**POWER=number-list**

specifies the desired power of the test or requests a solution for the power with a missing value (**POWER=.**). The power is expressed as a probability, a number between 0 and 1, rather than as a percentage. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**PROBWIDTH=number-list**

specifies the desired probability of obtaining a confidence interval half-width less than or equal to the value specified by the **HALFWIDTH=** option. A missing value (**PROBWIDTH=.**) requests a solution for this probability. Values are expressed as probabilities (for example, 0.9) rather than percentages. This option can be used only with the **CI=** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**PROPORTION=number-list****P=number-list**

specifies the binomial proportion—that is, the expected proportion of successes in the hypothetical binomial trial. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**SIDES=keyword-list**

specifies the number of sides (or tails) and the direction of the statistical test. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *keyword-list*. Valid keywords are as follows:

- |   |   |
|---|---|
| 1 | one-sided with alternative hypothesis in same direction as effect |
| 2 | two-sided   |

- U upper one-sided with alternative greater than null value
- L lower one-sided with alternative less than null value

If the effect size is zero, then **SIDES=1** is not permitted; instead, specify the direction of the test explicitly in this case with either **SIDES=L** or **SIDES=U**. The default value is 2.

**TEST****TEST= ADJZ****TEST= EQUIV\_ADJZ****TEST= EQUIV\_EXACT****TEST= EQUIV\_Z****TEST= EXACT****TEST= Z**

specifies the statistical analysis. **TEST=ADJZ** specifies a normal-approximate  $z$  test with continuity adjustment. **TEST=EQUIV\_ADJZ** specifies a normal-approximate two-sided equivalence test based on the  $z$  statistic with continuity adjustment and a TOST (two one-sided tests) procedure. **TEST=EQUIV\_EXACT** specifies the exact binomial two-sided equivalence test based on a TOST (two one-sided tests) procedure. **TEST=EQUIV\_Z** specifies a normal-approximate two-sided equivalence test based on the  $z$  statistic without any continuity adjustment, which is the same as the chi-square statistic, and a TOST (two one-sided tests) procedure. **TEST** or **TEST=EXACT** (the default) specifies the exact binomial test. **TEST=Z** specifies a normal-approximate  $z$  test without any continuity adjustment, which is the same as the chi-square test when **SIDES=2**.

**UPPER=number-list**

specifies the upper equivalence bound for the binomial proportion. The **UPPER=** option can be used only with equivalence analyses (**TEST=EQUIV\_ADJZ** | **EQUIV\_EXACT** | **EQUIV\_Z**). Values must be strictly between 0 and 1. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**VAREST=keyword-list**

specifies how the variance is computed in the test statistic for the **TEST=Z**, **TEST=ADJZ**, **TEST=EQUIV\_Z**, and **TEST=EQUIV\_ADJZ** analyses. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *keyword-list*. Valid keywords are as follows:

**NULL** (the default) estimates the variance by using the null proportion(s) (specified by some combination of the **NULLPROPORTION=**, **MARGIN=**, **LOWER=**, and **UPPER=** options). For **TEST=Z** and **TEST=ADJZ**, the null proportion is the value of the **NULLPROPORTION=** option plus the value of the **MARGIN=** option (if it is used). For **TEST=EQUIV\_Z** and **TEST=EQUIV\_ADJZ**, there are two null proportions, corresponding to the lower and upper equivalence bounds, one for each test in the TOST (two one-sided tests) procedure.

**SAMPLE** estimates the variance by using the observed sample proportion.

This option is ignored if the analysis is one other than **TEST=Z**, **TEST=ADJZ**, **TEST=EQUIV\_Z**, or **TEST=EQUIV\_ADJZ**.

## Option Groups for Common Analyses

This section summarizes the syntax for the common analyses supported in the `ONESAMPLEFREQ` statement.

### Exact Test of a Binomial Proportion

The following statements demonstrate a power computation for the exact test of a binomial proportion. Defaults for the `SIDES=` and `ALPHA=` options specify a two-sided test with a 0.05 significance level.

```
proc power;
  onesamplefreq test=exact
    nullproportion = 0.2
    proportion = 0.3
    ntotal = 100
    power = .;
run;
```

### z Test

The following statements demonstrate a sample size computation for the  $z$  test of a binomial proportion. Defaults for the `SIDES=`, `ALPHA=`, and `VAREST=` options specify a two-sided test with a 0.05 significance level that uses the null variance estimate.

```
proc power;
  onesamplefreq test=z method=normal
    nullproportion = 0.8
    proportion = 0.85
    sides = u
    ntotal = .
    power = .9;
run;
```

### z Test with Continuity Adjustment

The following statements demonstrate a sample size computation for the  $z$  test of a binomial proportion with a continuity adjustment. Defaults for the `SIDES=`, `ALPHA=`, and `VAREST=` options specify a two-sided test with a 0.05 significance level that uses the null variance estimate.

```
proc power;
  onesamplefreq test=adjz method=normal
    nullproportion = 0.15
    proportion = 0.1
    sides = 1
    ntotal = .
    power = .9;
run;
```

**Exact Equivalence Test for a Binomial Proportion**

You can specify equivalence bounds by using the `EQUIVBOUNDS=` option, as in the following statements:

```
proc power;
  onesamplefreq test=equiv_exact
    proportion = 0.35
    equivbounds = (0.2 0.4)
    ntotal = 50
    power = .;
run;
```

You can also specify the combination of `NULLPROPORTION=` and `MARGIN=` options:

```
proc power;
  onesamplefreq test=equiv_exact
    proportion = 0.35
    nullproportion = 0.3
    margin = 0.1
    ntotal = 50
    power = .;
run;
```

Finally, you can specify the combination of `LOWER=` and `UPPER=` options:

```
proc power;
  onesamplefreq test=equiv_exact
    proportion = 0.35
    lower = 0.2
    upper = 0.4
    ntotal = 50
    power = .;
run;
```

Note that the three preceding analyses are identical.

**Exact Noninferiority Test for a Binomial Proportion**

A noninferiority test corresponds to an upper one-sided test with a negative-valued margin, as demonstrated in the following statements:

```
proc power;
  onesamplefreq test=exact
    sides = U
    proportion = 0.15
    nullproportion = 0.1
    margin = -0.02
    ntotal = 130
    power = .;
run;
```

### Exact Superiority Test for a Binomial Proportion

A superiority test corresponds to an upper one-sided test with a positive-valued margin, as demonstrated in the following statements:

```
proc power;
  onesamplefreq test=exact
    sides = U
    proportion = 0.15
    nullproportion = 0.1
    margin = 0.02
    ntotal = 130
    power = .;
run;
```

### Confidence Interval Precision

The following statements performs a confidence interval precision analysis for the Wilson score-based confidence interval for a binomial proportion. The default value of the `ALPHA=` option specifies a confidence level of 0.95.

```
proc power;
  onesamplefreq ci=wilson
    halfwidth = 0.1
    proportion = 0.3
    ntotal = 70
    probwidth = .;
run;
```

### Restrictions on Option Combinations

To specify the equivalence bounds for `TEST=EQUIV_ADJZ`, `TEST=EQUIV_EXACT`, and `TEST=EQUIV_Z`, use any of these three option sets:

- lower and upper equivalence bounds, using the `EQUIVBOUNDS=` option
- lower and upper equivalence bounds, using the `LOWER=` and `UPPER=` options
- null proportion (`NULLPROPORTION=`) and margin (`MARGIN=`)

---

## ONESAMPLEMEANS Statement

```
ONESAMPLEMEANS < options > ;
```

The `ONESAMPLEMEANS` statement performs power and sample size analyses for *t* tests, equivalence tests, and confidence interval precision involving one sample.

## Summary of Options

Table 67.10 summarizes categories of options available in the **ONESAMPLEMEANS** statement.

**Table 67.10** Summary of Options in the **ONESAMPLEMEANS** Statement

Task	Options
Define analysis	CI= DIST= TEST=
Specify analysis information	ALPHA= LOWER= NULLMEAN= SIDES= UPPER=
Specify effects	HALFWIDTH= MEAN=
Specify variability	CV= STDDEV=
Specify sample size	NTOTAL=
Specify power and related probabilities	POWER= PROBTYPE= PROBWIDTH=
Control sample size rounding	NFRACTIONAL
Control ordering in output	OUTPUTORDER=

Table 67.11 summarizes the valid result parameters for different analyses in the **ONESAMPLEMEANS** statement.

**Table 67.11** Summary of Result Parameters in the **ONESAMPLEMEANS** Statement

Analyses	Solve For	Syntax
TEST=T DIST=NORMAL	Power Sample size Alpha Mean Standard Deviation	POWER=. NTOTAL=. ALPHA=. MEAN=. STDDEV=.
TEST=T DIST=LOGNORMAL	Power Sample size	POWER=. NTOTAL=.
TEST=EQUIV	Power Sample size	POWER=. NTOTAL=.
CI=T	Prob(width) Sample size	PROBWIDTH=. NTOTAL=.

## Dictionary of Options

### **ALPHA=***number-list*

specifies the level of significance of the statistical test or requests a solution for alpha with a missing value (**ALPHA=.**). The default is 0.05, corresponding to the usual  $0.05 \times 100\% = 5\%$  level of significance. If the **CI=** and **SIDES=1** options are used, then the value must be less than 0.5. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### **CI**

#### **CI=T**

specifies an analysis of precision of the confidence interval for the mean. Instead of power, the relevant probability for this analysis is the probability of achieving a desired precision. Specifically, it is the probability that the half-width of the confidence interval will be at most the value specified by the **HALFWIDTH=** option. If neither the **CI=** option nor the **TEST=** option is used, the default is **TEST=T**.

### **CV=***number-list*

specifies the coefficient of variation, defined as the ratio of the standard deviation to the mean. You can use this option only with **DIST=LOGNORMAL**. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### **DIST=LOGNORMAL**

#### **DIST=NORMAL**

specifies the underlying distribution assumed for the test statistic. **NORMAL** corresponds to the normal distribution, and **LOGNORMAL** corresponds to the lognormal distribution. The default value is **NORMAL**.

### **HALFWIDTH=***number-list*

specifies the desired confidence interval half-width. The half-width is defined as the distance between the point estimate and a finite endpoint. This option can be used only with the **CI=T** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### **LOWER=***number-list*

specifies the lower equivalence bound for the mean. This option can be used only with the **TEST=EQUIV** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### **MEAN=***number-list*

specifies the mean, in the original scale, or requests a solution for the mean with a missing value (**MEAN=.**). The mean is arithmetic if **DIST=NORMAL** and geometric if **DIST=LOGNORMAL**. This option can be used only with the **TEST=T** and **TEST=EQUIV** analyses. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### **NFRACTIONAL**

#### **NFRAC**

enables fractional input and output for sample sizes. See the section “[Sample Size Adjustment](#)”

Options” on page 4916 for information about the ramifications of the presence (and absence) of the **NFRACTIONAL** option.

**NTOTAL=number-list**

specifies the sample size or requests a solution for the sample size with a missing value (**NTOTAL=.**). See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NULLMEAN=number-list**

**NULLM=number-list**

specifies the null mean, in the original scale (whether **DIST=NORMAL** or **DIST=LOGNORMAL**). The default value is 0 when **DIST=NORMAL** and 1 when **DIST=LOGNORMAL**. This option can be used only with the **TEST=T** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**OUTPUTORDER=INTERNAL**

**OUTPUTORDER=REVERSE**

**OUTPUTORDER=SYNTAX**

controls how the input and default analysis parameters are ordered in the output. **OUTPUTORDER=INTERNAL** (the default) arranges the parameters in the output according to the following order of their corresponding options:

- **SIDES=**
- **NULLMEAN=**
- **LOWER=**
- **UPPER=**
- **ALPHA=**
- **MEAN=**
- **HALFWIDTH=**
- **STDDEV=**
- **CV=**
- **NTOTAL=**
- **POWER=**
- **PROBTYPE=**
- **PROBWIDTH=**

The **OUTPUTORDER=SYNTAX** option arranges the parameters in the output in the same order in which their corresponding options are specified in the **ONESAMPLEMEANS** statement. The **OUTPUTORDER=REVERSE** option arranges the parameters in the output in the reverse of the order in which their corresponding options are specified in the **ONESAMPLEMEANS** statement.

**POWER=number-list**

specifies the desired power of the test or requests a solution for the power with a missing value (**POWER=.**). The power is expressed as a probability, a number between 0 and 1, rather than as a percentage. This option can be used only with the **TEST=T** and **TEST=EQUIV** analyses. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**PROBTYPE=keyword-list**

specifies the type of probability for the **PROBWIDTH=** option. A value of **CONDITIONAL** (the default) indicates the conditional probability that the confidence interval half-width is at most the value specified by the **HALFWIDTH=** option, given that the true mean is captured by the confidence interval. A value of **UNCONDITIONAL** indicates the unconditional probability that the confidence interval half-width is at most the value specified by the **HALFWIDTH=** option. You can use the alias **GIVENVALIDITY** for **CONDITIONAL**. The **PROBTYPE=** option can be used only with the **CI=T** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *keyword-list*.

**CONDITIONAL** width probability conditional on interval containing the mean

**UNCONDITIONAL** unconditional width probability

**PROBWIDTH=number-list**

specifies the desired probability of obtaining a confidence interval half-width less than or equal to the value specified by the **HALFWIDTH=** option. A missing value (**PROBWIDTH=.**) requests a solution for this probability. The type of probability is controlled with the **PROBTYPE=** option. Values are expressed as probabilities (for example, 0.9) rather than percentages. This option can be used only with the **CI=T** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**SIDES=keyword-list**

specifies the number of sides (or tails) and the direction of the statistical test or confidence interval. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *keyword-list*. Valid keywords and their interpretation for the **TEST=** analyses are as follows:

- 1 one-sided with alternative hypothesis in same direction as effect
- 2 two-sided
- U upper one-sided with alternative greater than null value
- L lower one-sided with alternative less than null value

For confidence intervals, **SIDES=U** refers to an interval between the lower confidence limit and infinity, and **SIDES=L** refers to an interval between minus infinity and the upper confidence limit. For both of these cases and **SIDES=1**, the confidence interval computations are equivalent. The **SIDES=** option can be used only with the **TEST=T** and **CI=T** analyses. The default value is 2.

**STDDEV=***number-list*

**STD=***number-list*

specifies the standard deviation, or requests a solution for the standard deviation with a missing value (**STDDEV=.**). You can use this option only with **DIST=NORMAL**. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**TEST**

**TEST=EQUIV**

**TEST=T**

specifies the statistical analysis. **TEST=EQUIV** specifies an equivalence test of the mean by using a two one-sided tests (TOST) analysis (Schuirmann 1987). **TEST** or **TEST=T** (the default) specifies a *t* test on the mean. If neither the **TEST=** option nor the **CI=** option is used, the default is **TEST=T**.

**UPPER=***number-list*

specifies the upper equivalence bound for the mean, in the original scale (whether **DIST=NORMAL** or **DIST=LOGNORMAL**). This option can be used only with the **TEST=EQUIV** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

## Restrictions on Option Combinations

To define the analysis, choose one of the following parameterizations:

- a statistical test (by using the **TEST=** option)
- confidence interval precision (by using the **CI=** option)

## Option Groups for Common Analyses

This section summarizes the syntax for the common analyses supported in the **ONESAMPLEMEANS** statement.

### *One-Sample t Test*

The following statements demonstrate a power computation for the one-sample *t* test. Default values for the **DIST=**, **SIDES=**, **NULLMEAN=**, and **ALPHA=** options specify a two-sided test for zero mean with a normal distribution and a significance level of 0.05.

```
proc power;
  onesamplemeans test=t
    mean = 7
    stddev = 3
    ntotal = 50
    power = .;
run;
```

**One-Sample *t* Test with Lognormal Data**

The following statements demonstrate a sample size computation for the one-sample *t* test for lognormal data. Default values for the `SIDES=`, `NULLMEAN=`, and `ALPHA=` options specify a two-sided test for unit mean with a significance level of 0.05.

```
proc power;
  onesamplemeans test=t dist=lognormal
    mean = 7
    cv = 0.8
    ntotal = .
    power = 0.9;
run;
```

**Equivalence Test for Mean of Normal Data**

The following statements demonstrate a power computation for the TOST equivalence test for a normal mean. Default values for the `DIST=` and `ALPHA=` options specify a normal distribution and a significance level of 0.05.

```
proc power;
  onesamplemeans test=equiv
    lower = 2
    upper = 7
    mean = 4
    stddev = 3
    ntotal = 100
    power = .;
run;
```

**Equivalence Test for Mean of Lognormal Data**

The following statements demonstrate a sample size computation for the TOST equivalence test for a lognormal mean. The default of `ALPHA=0.05` specifies a significance level of 0.05.

```
proc power;
  onesamplemeans test=equiv dist=lognormal
    lower = 1
    upper = 5
    mean = 3
    cv = 0.6
    ntotal = .
    power = 0.85;
run;
```

### Confidence Interval for Mean

By default `CI=T` analyzes the conditional probability of obtaining the desired precision, given that the interval contains the true mean, as in the following statements. The defaults of `SIDES=2` and `ALPHA=0.05` specify a two-sided interval with a confidence level of 0.95.

```
proc power;
  onesamplemeans ci = t
    halfwidth = 14
    stddev = 8
    ntotal = 50
    probwidth = .;
run;
```

---

## ONEWAYANOVA Statement

**ONEWAYANOVA** < options > ;

The `ONEWAYANOVA` statement performs power and sample size analyses for one-degree-of-freedom contrasts and the overall  $F$  test in one-way analysis of variance.

### Summary of Options

Table 67.12 summarizes categories of options available in the `ONEWAYANOVA` statement.

**Table 67.12** Summary of Options in the `ONEWAYANOVA` Statement

Task	Options
Define analysis	<code>TEST=</code>
Specify analysis information	<code>ALPHA=</code> <code>CONTRAST=</code> <code>SIDES=</code> <code>NULLCONTRAST=</code>
Specify effects	<code>GROUPMEANS=</code>
Specify variability	<code>STDDEV=</code>
Specify sample size and allocation	<code>GROUPNS=</code> <code>GROUPWEIGHTS=</code> <code>NPERGROUP==</code> <code>NTOTAL=</code>
Specify power	<code>POWER=</code>
Control sample size rounding	<code>NFRACTIONAL</code>
Control ordering in output	<code>OUTPUTORDER=</code>

Table 67.13 summarizes the valid result parameters for different analyses in the `ONEWAYANOVA` statement.

**Table 67.13** Summary of Result Parameters in the `ONEWAYANOVA` Statement

Analyses	Solve For	Syntax
<code>TEST=CONTRAST</code>	Power Sample size	<code>POWER=.</code> <code>NTOTAL=.</code> <code>NPERGROUP==.</code>
<code>TEST=OVERALL</code>	Power Sample size	<code>POWER=.</code> <code>NTOTAL=.</code> <code>NPERGROUP==.</code>

## Dictionary of Options

### **ALPHA=***number-list*

specifies the level of significance of the statistical test. The default is 0.05, corresponding to the usual  $0.05 \times 100\% = 5\%$  level of significance. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### **CONTRAST=** ( *values* ) < ( ... *values* ) >

specifies coefficients for single-degree-of-freedom hypothesis tests. You must provide a coefficient for every mean appearing in the `GROUPMEANS=` option. Specify multiple contrasts either with additional sets of coefficients or with additional `CONTRAST=` options. For example, you can specify two different contrasts of five means by using the following:

```
CONTRAST = (1 -1 0 0 0) (1 0 -1 0 0)
```

### **GROUPMEANS=***grouped-number-list*

#### **GMEANS=***grouped-number-list*

specifies the group means. This option is used to implicitly set the number of groups. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

### **GROUPNS=***grouped-number-list*

#### **GNS=***grouped-number-list*

specifies the group sample sizes. The number of groups represented must be the same as with the `GROUPMEANS=` option. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

### **GROUPWEIGHTS=***grouped-number-list*

#### **GWEIGHTS=***grouped-number-list*

specifies the sample size allocation weights for the groups. This option controls how the total sample size is divided between the groups. Each set of values across all groups represents relative allocation weights. Additionally, if the `NFRACTIONAL` option is not used, the total sample size is restricted to be equal to a multiple of the sum of the group weights (so that

the resulting design has an integer sample size for each group while adhering exactly to the group allocation weights). The number of groups represented must be the same as with the **GROUPMEANS=** option. Values must be integers unless the **NFRACTIONAL** option is used. The default value is 1 for each group, amounting to a balanced design. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

## **NFRACTIONAL**

### **NFRAC**

enables fractional input and output for sample sizes. See the section “[Sample Size Adjustment Options](#)” on page 4916 for information about the ramifications of the presence (and absence) of the **NFRACTIONAL** option.

### **NPERGROUP=number-list**

#### **NPERG=number-list**

specifies the common sample size per group or requests a solution for the common sample size per group with a missing value (**NPERGROUP=.**). Use of this option implicitly specifies a balanced design. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### **NTOTAL=number-list**

specifies the sample size or requests a solution for the sample size with a missing value (**NTOTAL=.**). See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### **NULLCONTRAST=number-list**

#### **NULLC=number-list**

specifies the null value of the contrast. The default value is 0. This option can be used only with the **TEST=CONTRAST** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

## **OUTPUTORDER=INTERNAL**

## **OUTPUTORDER=REVERSE**

## **OUTPUTORDER=SYNTAX**

controls how the input and default analysis parameters are ordered in the output. **OUTPUTORDER=INTERNAL** (the default) arranges the parameters in the output according to the following order of their corresponding options:

- **CONTRAST=**
- **SIDES=**
- **NULLCONTRAST=**
- **ALPHA=**
- **GROUPMEANS=**
- **STDDEV=**
- **GROUPWEIGHTS=**
- **NTOTAL=**

- `NPERGROUP==`
- `GROUPNS=`
- `POWER=`

The `OUTPUTORDER=SYNTAX` option arranges the parameters in the output in the same order in which their corresponding options are specified in the `ONEWAYANOVA` statement. The `OUTPUTORDER=REVERSE` option arranges the parameters in the output in the reverse of the order in which their corresponding options are specified in the `ONEWAYANOVA` statement.

**POWER=***number-list*

specifies the desired power of the test or requests a solution for the power with a missing value (`POWER=.`). The power is expressed as a probability, a number between 0 and 1, rather than as a percentage. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**SIDES=***keyword-list*

specifies the number of sides (or tails) and the direction of the statistical test. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *keyword-list*. Valid keywords are as follows:

- |   |   |
|---|---|
| 1 | one-sided with alternative hypothesis in same direction as effect |
| 2 | two-sided   |
| U | upper one-sided with alternative greater than null value          |
| L | lower one-sided with alternative less than null value             |

This option can be used only with the `TEST=CONTRAST` analysis. The default value is 2.

**STDDEV=***number-list*

**STD=***number-list*

specifies the error standard deviation. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**TEST=CONTRAST**

**TEST=OVERALL**

specifies the statistical analysis. `TEST=CONTRAST` specifies a one-degree-of-freedom test of a contrast of means. The test is the usual  $F$  test for the two-sided case and the usual  $t$  test for the one-sided case. `TEST=OVERALL` specifies the overall  $F$  test of equality of all means. The default is `TEST=CONTRAST` if the `CONTRAST=` option is used, and `TEST=OVERALL` otherwise.

## Restrictions on Option Combinations

To specify the sample size and allocation, choose one of the following parameterizations:

- sample size per group in a balanced design (by using the `NPERGROUP==` option)

- total sample size and allocation weights (by using the `NTOTAL=` and `GROUPWEIGHTS=` options)
- individual group sample sizes (by using the `GROUPNS=` option)

## Option Groups for Common Analyses

This section summarizes the syntax for the common analyses supported in the `ONEWAYANOVA` statement.

### One-Degree-of-Freedom Contrast

You can use the `NPERGROUP==` option in a balanced design, as in the following statements. Default values for the `SIDES=`, `NULLCONTRAST=`, and `ALPHA=` options specify a two-sided test for a contrast value of 0 with a significance level of 0.05.

```
proc power;
  onewayanova test=contrast
    contrast = (1 0 -1)
    groupmeans = 3 | 7 | 8
    stddev = 4
    npergroup = 50
    power = .;
run;
```

You can also specify an unbalanced design with the `NTOTAL=` and `GROUPWEIGHTS=` options:

```
proc power;
  onewayanova test=contrast
    contrast = (1 0 -1)
    groupmeans = 3 | 7 | 8
    stddev = 4
    groupweights = (1 2 2)
    ntotal = .
    power = 0.9;
run;
```

Another way to specify the sample sizes is with the `GROUPNS=` option:

```
proc power;
  onewayanova test=contrast
    contrast = (1 0 -1)
    groupmeans = 3 | 7 | 8
    stddev = 4
    groupns = (20 40 40)
    power = .;
run;
```

### Overall F Test

The following statements demonstrate a power computation for the overall F test in a one-way ANOVA. The default of `ALPHA=0.05` specifies a significance level of 0.05.

```

proc power;
  onewayanova test=overall
    groupmeans = 3 | 7 | 8
    stddev = 4
    npergroup = 50
    power = .;
run;

```

---

## PAIREFREQ Statement

**PAIREFREQ** < options > ;

The **PAIREFREQ** statement performs power and sample size analyses for McNemar's test for paired proportions.

### Summary of Options

Table 67.14 summarizes categories of options available in the **PAIREFREQ** statement.

**Table 67.14** Summary of Options in the PAIREFREQ Statement

Task	Options
Define analysis	DIST= TEST=
Specify analysis information	ALPHA= NULLDISCPRORATIO= SIDES=
Specify effects	PAIREDPROPORTIONS= PROPORTIONDIFF= ODDSRATIO= RELATIVERISK= CORR= DISCPRORATIO= DISCPRORATIO= DISCPRORATIO= REFPROPORTION= TOTALPROPDISC=
Specify sample size	NPAIRS=
Specify power	POWER=
Control sample size rounding	NFRACTIONAL
Choose computational method	METHOD=
Control ordering in output	OUTPUTORDER=

Table 67.15 summarizes the valid result parameters in the PAIREDFREQ statement.

**Table 67.15** Summary of Result Parameters in the PAIREDFREQ Statement

Analyses	Solve For	Syntax
TEST=MCNEMAR METHOD=CONNOR	Power Sample size	POWER=. NPAIRS=.
TEST=MCNEMAR METHOD=EXACT	Power	POWER=.
TEST=MCNEMAR METHOD=MIETTINEN	Power Sample size	POWER=. NPAIRS=.

## Dictionary of Options

### ALPHA=*number-list*

specifies the level of significance of the statistical test. The default is 0.05, corresponding to the usual  $0.05 \times 100\% = 5\%$  level of significance. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### CORR=*number-list*

specifies the correlation  $\phi$  between members of a pair. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### DISCPROPORTIONS=*grouped-number-list*

### DISCPS=*grouped-number-list*

specifies the two discordant proportions,  $p_{10}$  and  $p_{01}$ . See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

### DISCPRPDIFF=*number-list*

### DISCPDIFF=*number-list*

specifies the difference  $p_{01} - p_{10}$  between discordant proportions. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### DISCPRPRATIO=*number-list*

### DISCPRATIO=*number-list*

specifies the ratio  $p_{01}/p_{10}$  of discordant proportions. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### DIST=EXACT\_COND

### DIST=NORMAL

specifies the underlying distribution assumed for the test statistic. EXACT\_COND corresponds to the exact conditional test, based on the exact binomial distribution of the two types of discordant pairs given the total number of discordant pairs. NORMAL corresponds to the conditional test based on the normal approximation to the binomial distribution of the two types of discordant pairs given the total number of discordant pairs. The default value is EXACT\_COND.

**METHOD=CONNOR****METHOD=EXACT****METHOD=MIETTINEN**

specifies the computational method. **METHOD=EXACT** (the default) uses the exact binomial distributions of the total number of discordant pairs and the two types of discordant pairs. **METHOD=CONNOR** uses an approximation from Connor (1987), and **METHOD=MIETTINEN** uses an approximation from Miettinen (1968). The CONNOR and MIETTINEN methods are valid only for **DIST=NORMAL**.

**NFRACTIONAL****NFRAC**

enables fractional input and output for sample sizes. See the section “[Sample Size Adjustment Options](#)” on page 4916 for information about the ramifications of the presence (and absence) of the **NFRACTIONAL** option. This option cannot be used with **METHOD=EXACT**.

**NPAIRS=number-list**

specifies the total number of proportion pairs (concordant and discordant) or requests a solution for the number of pairs with a missing value (**NPAIRS=.**). See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NULLDISCPRORATIO=number-list****NULLDISCPRATIO=number-list****NULLRATIO=number-list****NULLR=number-list**

specifies the null value of the ratio of discordant proportions. The default value is 1. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**ODDSRATIO=number-list****OR=number-list**

specifies the odds ratio  $[p_{.1}/(1 - p_{.1})] / [p_{1.}/(1 - p_{1.})]$ . See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**OUTPUTORDER=INTERNAL****OUTPUTORDER=REVERSE****OUTPUTORDER=SYNTAX**

controls how the input and default analysis parameters are ordered in the output. **OUTPUTORDER=INTERNAL** (the default) arranges the parameters in the output according to the following order of their corresponding options:

- **SIDES=**
- **NULLDISCPRORATIO=**
- **ALPHA=**
- **PAIREDPROPORTIONS=**
- **PROPORTIONDIFF=**

- ODDSRATIO=
- RELATIVERISK=
- CORR=
- DISCPROPORTIONS=
- DISCPROPDIFF=
- TOTALPROPDISC=
- REFPROPORTION=
- DISCPRORATIO=
- NPAIRS=
- POWER=

The **OUTPUTORDER=SYNTAX** option arranges the parameters in the output in the same order in which their corresponding options are specified in the **PAIREFREQ** statement. The **OUTPUTORDER=REVERSE** option arranges the parameters in the output in the reverse of the order in which their corresponding options are specified in the **PAIREFREQ** statement.

**PAIREDPROPORTIONS=***grouped-number-list*

**PPROPORTIONS=***grouped-number-list*

**PAIREDPS=***grouped-number-list*

**PPS=***grouped-number-list*

specifies the two paired proportions,  $p_{1.}$  and  $p_{.1}$ . See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**POWER=***number-list*

specifies the desired power of the test or requests a solution for the power with a missing value (**POWER=.**). The power is expressed as a probability, a number between 0 and 1, rather than as a percentage. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**PROPORTIONDIFF=***number-list*

**PDIFF=***number-list*

specifies the proportion difference  $p_{.1} - p_{1.}$ . See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**REFPROPORTION=***number-list*

**REFP=***number-list*

specifies either the reference first proportion  $p_{1.}$  (when used in conjunction with the **PROPORTIONDIFF=**, **ODDSRATIO=**, or **RELATIVERISK=** option) or the reference discordant proportion  $p_{10}$  (when used in conjunction with the **DISCPROPDIFF=** or **DISCPRORATIO=** option). See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**RELATIVERISK**=*number-list*

**RR**=*number-list*

specifies the relative risk  $p_{.1}/p_{1.}$ . See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**SIDES**=*keyword-list*

specifies the number of sides (or tails) and the direction of the statistical test or confidence interval. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *keyword-list*. Valid keywords and their interpretation are as follows:

- |   |   |
|---|---|
| 1 | one-sided with alternative hypothesis in same direction as effect |
| 2 | two-sided   |
| U | upper one-sided with alternative greater than null value          |
| L | lower one-sided with alternative less than null value             |

If the effect size is zero, then **SIDES**=1 is not permitted; instead, specify the direction of the test explicitly in this case with either **SIDES**=L or **SIDES**=U. The default value is 2.

**TEST**=MCNEMAR

specifies the McNemar test of paired proportions. This is the default test option.

**TOTALPROPDISC**=*number-list*

**TOTALPDISC**=*number-list*

**PDISC**=*number-list*

specifies the sum of the two discordant proportions,  $p_{10} + p_{01}$ . See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

## Restrictions on Option Combinations

To specify the proportions, choose one of the following parameterizations:

- discordant proportions (using the **DISCPROPORTIONS**= option)
- difference and sum of discordant proportions (using the **DISCPROPDIFF**= and **TOTALPROPDISC**=options)
- difference of discordant proportions and reference discordant proportion (using the **DISCPROPDIFF**= and **REFPROPORTION**= options)
- ratio of discordant proportions and reference discordant proportion (using the **DISCPROPRATIO**= and **REFPROPORTION**= options)
- ratio and sum of discordant proportions (using the **DISCPROPRATIO**= and **TOTALPROPDISC**=options)

- paired proportions and correlation (using the `PAIREDPROPORTIONS=` and `CORR=` options)
- proportion difference, reference proportion, and correlation (using the `PROPORTIONDIFF=`, `REFPROPORTION=`, and `CORR=` options)
- odds ratio, reference proportion, and correlation (using the `ODDSRATIO=`, `REFPROPORTION=`, and `CORR=` options)
- relative risk, reference proportion, and correlation (using the `RELATIVERISK=`, `REFPROPORTION=`, and `CORR=` options)

## Option Groups for Common Analyses

This section summarizes the syntax for the common analyses supported in the `PAIREFREQ` statement.

### *McNemar Exact Conditional Test*

You can express effects in terms of the individual discordant proportions, as in the following statements. Default values for the `TEST=`, `SIDES=`, `ALPHA=`, and `NULLDISCPRORATIO=` options specify a two-sided McNemar test for no effect with a significance level of 0.05.

```
proc power;
  pairedfreq dist=exact_cond
    discproportions = 0.15 | 0.45
    npairs = 80
    power = .;
run;
```

You can also express effects in terms of the difference and sum of discordant proportions:

```
proc power;
  pairedfreq dist=exact_cond
    discproppdiff = 0.3
    totalproppdisc = 0.6
    npairs = 80
    power = .;
run;
```

You can also express effects in terms of the difference of discordant proportions and the reference discordant proportion:

```
proc power;
  pairedfreq dist=exact_cond
    discproppdiff = 0.3
    refproportion = 0.15
    npairs = 80
    power = .;
run;
```

You can also express effects in terms of the ratio of discordant proportions and the denominator of the ratio:

```

proc power;
  pairedfreq dist=exact_cond
    discpropratio = 3
    refproportion = 0.15
    npairs = 80
    power = .;
run;

```

You can also express effects in terms of the ratio and sum of discordant proportions:

```

proc power;
  pairedfreq dist=exact_cond
    discpropratio = 3
    totalproprdisc = 0.6
    npairs = 80
    power = .;
run;

```

You can also express effects in terms of the paired proportions and correlation:

```

proc power;
  pairedfreq dist=exact_cond
    pairedproportions = 0.6 | 0.8
    corr = 0.4
    npairs = 45
    power = .;
run;

```

You can also express effects in terms of the proportion difference, reference proportion, and correlation:

```

proc power;
  pairedfreq dist=exact_cond
    proportiondiff = 0.2
    refproportion = 0.6
    corr = 0.4
    npairs = 45
    power = .;
run;

```

You can also express effects in terms of the odds ratio, reference proportion, and correlation:

```

proc power;
  pairedfreq dist=exact_cond
    oddsratio = 2.66667
    refproportion = 0.6
    corr = 0.4
    npairs = 45
    power = .;
run;

```

You can also express effects in terms of the relative risk, reference proportion, and correlation:

```
proc power;
  pairedfreq dist=exact_cond
    relativetrisk = 1.33333
    refproportion = 0.6
    corr = 0.4
    npairs = 45
    power = .;
run;
```

### McNemar Normal Approximation Test

The following statements demonstrate a sample size computation for the normal-approximate McNemar test. The default value for the `METHOD=` option specifies an exact sample size computation. Default values for the `TEST=`, `SIDES=`, `ALPHA=`, and `NULLDISCPRATIO=` options specify a two-sided McNemar test for no effect with a significance level of 0.05.

```
proc power;
  pairedfreq dist=normal method=connor
    discproportions = 0.15 | 0.45
    npairs = .
    power = .9;
run;
```

---

## PAIREDMEANS Statement

**PAIREDMEANS** < options > ;

The **PAIREDMEANS** statement performs power and sample size analyses for *t* tests, equivalence tests, and confidence interval precision involving paired samples.

### Summary of Options

Table 67.16 summarizes categories of options available in the **PAIREDMEANS** statement.

**Table 67.16** Summary of Options in the PAIREDMEANS Statement

Task	Options
Define analysis	CI= DIST= TEST=
Specify analysis information	ALPHA= LOWER= NULLDIFF= NULLRATIO= SIDES=

**Table 67.16** *continued*

Task	Options
Specify effects	UPPER=
	HALFWIDTH=
	MEANDIFF=
	MEANRATIO=
Specify variability	PAIREDMEANS=
	CORR=
	CV=
	PAIREDCVS=
	PAIREDSTDDEVS=
Specify sample size	STDDEV=
	NPAIRS=
Specify power and related probabilities	POWER=
	PROBTYPE=
	PROBWIDTH=
Control sample size rounding	NFRACTIONAL
Control ordering in output	OUTPUTORDER=

Table 67.17 summarizes the valid result parameters for different analyses in the **PAIREDMEANS** statement.

**Table 67.17** Summary of Result Parameters in the **PAIREDMEANS** Statement

Analyses	Solve For	Syntax
<b>TEST=DIFF</b>	Power	<b>POWER=.</b>
	Sample size	<b>NPAIRS=.</b>
<b>TEST=RATIO</b>	Power	<b>POWER=.</b>
	Sample size	<b>NPAIRS=.</b>
<b>TEST=EQUIV_DIFF</b>	Power	<b>POWER=.</b>
	Sample size	<b>NPAIRS=.</b>
<b>TEST=EQUIV_RATIO</b>	Power	<b>POWER=.</b>
	Sample size	<b>NPAIRS=.</b>
<b>CI=DIFF</b>	Prob(width)	<b>PROBWIDTH=.</b>
	Sample size	<b>NPAIRS=.</b>

## Dictionary of Options

### **ALPHA=***number-list*

specifies the level of significance of the statistical test. The default is 0.05, corresponding to the usual  $0.05 \times 100\% = 5\%$  level of significance. If the **CI=** and **SIDES=1** options are used,

then the value must be less than 0.5. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

## CI

### CI=DIFF

specifies an analysis of precision of the confidence interval for the mean difference. Instead of power, the relevant probability for this analysis is the probability of achieving a desired precision. Specifically, it is the probability that the half-width of the observed confidence interval will be at most the value specified by the **HALFWIDTH=** option. If neither the **CI=** option nor the **TEST=** option is used, the default is **TEST=DIFF**.

### CORR=*number-list*

specifies the correlation between members of a pair. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### CV=*number-list*

specifies the coefficient of variation assumed to be common to both members of a pair. The coefficient of variation is defined as the ratio of the standard deviation to the mean. You can use this option only with **DIST=LOGNORMAL**. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### DIST=LOGNORMAL

### DIST=NORMAL

specifies the underlying distribution assumed for the test statistic. **NORMAL** corresponds to the normal distribution, and **LOGNORMAL** corresponds to the lognormal distribution. The default value (also the only acceptable value in each case) is **NORMAL** for **TEST=DIFF**, **TEST=EQUIV\_DIFF**, and **CI=DIFF**; and **LOGNORMAL** for **TEST=RATIO** and **TEST=EQUIV\_RATIO**.

### HALFWIDTH=*number-list*

specifies the desired confidence interval half-width. The half-width is defined as the distance between the point estimate and a finite endpoint. This option can be used only with the **CI=DIFF** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### LOWER=*number-list*

specifies the lower equivalence bound for the mean difference or mean ratio, in the original scale (whether **DIST=NORMAL** or **DIST=LOGNORMAL**). This option can be used only with the **TEST=EQUIV\_DIFF** and **TEST=EQUIV\_RATIO** analyses. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### MEANDIFF=*number-list*

specifies the mean difference, defined as the mean of the difference between the second and first members of a pair,  $\mu_2 - \mu_1$ . This option can be used only with the **TEST=DIFF** and **TEST=EQUIV\_DIFF** analyses. When **TEST=EQUIV\_DIFF**, the mean difference is interpreted as the treatment mean minus the reference mean. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**MEANRATIO=number-list**

specifies the geometric mean ratio, defined as  $\gamma_2/\gamma_1$ . This option can be used only with the **TEST=RATIO** and **TEST=EQUIV\_RATIO** analyses. When **TEST=EQUIV\_RATIO**, the mean ratio is interpreted as the treatment mean divided by the reference mean. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NFRACTIONAL****NFRAC**

enables fractional input and output for sample sizes. See the section “[Sample Size Adjustment Options](#)” on page 4916 for information about the ramifications of the presence (and absence) of the **NFRACTIONAL** option.

**NPAIRS=number-list**

specifies the number of pairs or requests a solution for the number of pairs with a missing value (**NPAIRS=.**). See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NULLDIFF=number-list****NULLD=number-list**

specifies the null mean difference. The default value is 0. This option can be used only with the **TEST=DIFF** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NULLRATIO=number-list****NULLR=number-list**

specifies the null mean ratio. The default value is 1. This option can be used only with the **TEST=RATIO** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**OUTPUTORDER=INTERNAL****OUTPUTORDER=REVERSE****OUTPUTORDER=SYNTAX**

controls how the input and default analysis parameters are ordered in the output. **OUTPUTORDER=INTERNAL** (the default) arranges the parameters in the output according to the following order of their corresponding options:

- **SIDES=**
- **NULLDIFF=**
- **NULLRATIO=**
- **LOWER=**
- **UPPER=**
- **ALPHA=**
- **PAIREDMEANS=**
- **MEANDIFF=**
- **MEANRATIO=**

- HALFWIDTH=
- STDDEV=
- PAIREDSTDDEVS=
- CV=
- PAIREDCVS=
- CORR=
- NPAIRS=
- POWER=
- PROBTYP=
- PROBWIDTH=

The **OUTPUTORDER=SYNTAX** option arranges the parameters in the output in the same order in which their corresponding options are specified in the **PAIREDMEANS** statement. The **OUTPUTORDER=REVERSE** option arranges the parameters in the output in the reverse of the order in which their corresponding options are specified in the **PAIREDMEANS** statement.

**PAIREDCVS=***grouped-number-list*

specifies the coefficient of variation for each member of a pair. Unlike the **CV=** option, the **PAIREDCVS=** option supports different values for each member of a pair. Values must be nonnegative (unless both are equal to zero, which is permitted). This option can be used only with **DIST=LOGNORMAL**. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**PAIREDMEANS=***grouped-number-list*

**PMEANS=***grouped-number-list*

specifies the two paired means, in the original scale. The means are arithmetic if **DIST=NORMAL** and geometric if **DIST=LOGNORMAL**. This option cannot be used with the **CI=DIFF** analysis. When **TEST=EQUIV\_DIFF**, the means are interpreted as the reference mean (first) and the treatment mean (second). See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**PAIREDSTDDEVS=***grouped-number-list*

**PAIREDSTDS=***grouped-number-list*

**PSTDDEVS=***grouped-number-list*

**PSTDS=***grouped-number-list*

specifies the standard deviation of each member of a pair. Unlike the **STDDEV=** option, the **PAIREDSTDDEVS=** option supports different values for each member of a pair. This option can be used only with **DIST=NORMAL**. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**POWER=***number-list*

specifies the desired power of the test or requests a solution for the power with a missing value (**POWER=.**). The power is expressed as a probability, a number between 0 and 1,

rather than as a percentage. This option cannot be used with the **CI=DIFF** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**PROBTYPE=***keyword-list*

specifies the type of probability for the **PROBWIDTH=** option. A value of **CONDITIONAL** (the default) indicates the conditional probability that the confidence interval half-width is at most the value specified by the **HALFWIDTH=** option, given that the true mean difference is captured by the confidence interval. A value of **UNCONDITIONAL** indicates the unconditional probability that the confidence interval half-width is at most the value specified by the **HALFWIDTH=** option. you can use the alias **GIVENVALIDITY** for **CONDITIONAL**. The **PROBTYPE=** option can be used only with the **CI=DIFF** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *keyword-list*.

**CONDITIONAL** width probability conditional on interval containing the mean

**UNCONDITIONAL** unconditional width probability

**PROBWIDTH=***number-list*

specifies the desired probability of obtaining a confidence interval half-width less than or equal to the value specified by the **HALFWIDTH=** option. A missing value (**PROBWIDTH=.**) requests a solution for this probability. The type of probability is controlled with the **PROBTYPE=** option. Values are expressed as probabilities (for example, 0.9) rather than percentages. This option can be used only with the **CI=DIFF** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**SIDES=***keyword-list*

specifies the number of sides (or tails) and the direction of the statistical test or confidence interval. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *keyword-list*. Valid keywords and their interpretation for the **TEST=** analyses are as follows:

- 1 one-sided with alternative hypothesis in same direction as effect
- 2 two-sided
- U upper one-sided with alternative greater than null value
- L lower one-sided with alternative less than null value

For confidence intervals, **SIDES=U** refers to an interval between the lower confidence limit and infinity, and **SIDES=L** refers to an interval between minus infinity and the upper confidence limit. For both of these cases and **SIDES=1**, the confidence interval computations are equivalent. The **SIDES=** option cannot be used with the **TEST=EQUIV\_DIFF** and **TEST=EQUIV\_RATIO** analyses. The default value is 2.

**STDDEV=***number-list*

**STD=***number-list*

specifies the standard deviation assumed to be common to both members of a pair. This option

can be used only with `DIST=NORMAL`. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**TEST****TEST=DIFF****TEST=EQUIV\_DIFF****TEST=EQUIV\_RATIO****TEST=RATIO**

specifies the statistical analysis. `TEST` or `TEST=DIFF` (the default) specifies a paired  $t$  test on the mean difference. `TEST=EQUIV_DIFF` specifies an additive equivalence test of the mean difference by using a two one-sided tests (TOST) analysis (Schuirmann 1987). `TEST=EQUIV_RATIO` specifies a multiplicative equivalence test of the mean ratio by using a TOST analysis. `TEST=RATIO` specifies a paired  $t$  test on the geometric mean ratio. If neither the `TEST=` option nor the `CI=` option is used, the default is `TEST=DIFF`.

**UPPER=***number-list*

specifies the upper equivalence bound for the mean difference or mean ratio, in the original scale (whether `DIST=NORMAL` or `DIST=LOGNORMAL`). This option can be used only with the `TEST=EQUIV_DIFF` and `TEST=EQUIV_RATIO` analyses. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

## Restrictions on Option Combinations

To define the analysis, choose one of the following parameterizations:

- a statistical test (by using the `TEST=` option)
- confidence interval precision (by using the `CI=` option)

To specify the means, choose one of the following parameterizations:

- individual means (by using the `PAIREDMEANS=` option)
- mean difference (by using the `MEANDIFF=` option)
- mean ratio (by using the `MEANRATIO=` option)

To specify the coefficient of variation, choose one of the following parameterizations:

- common coefficient of variation (by using the `CV=` option)
- individual coefficients of variation (by using the `PAIREDCVS=` option)

To specify the standard deviation, choose one of the following parameterizations:

- common standard deviation (by using the `STDDEV=` option)
- individual standard deviations (by using the `PAIREDSTDDEVS=` option)

## Option Groups for Common Analyses

This section summarizes the syntax for the common analyses supported in the `PAIREDMEANS` statement.

### Paired t Test

You can express effects in terms of the mean difference and variability in terms of a correlation and common standard deviation, as in the following statements. Default values for the `DIST=`, `SIDES=`, `NULLDIFF=`, and `ALPHA=` options specify a two-sided test for no difference with a normal distribution and a significance level of 0.05.

```
proc power;
  pairedmeans test=diff
    meandiff = 7
    corr = 0.4
    stddev = 12
    npairs = 50
    power = .;
run;
```

You can also express effects in terms of individual means and variability in terms of correlation and individual standard deviations:

```
proc power;
  pairedmeans test=diff
    pairedmeans = 8 | 15
    corr = 0.4
    pairedstddevs = (7 12)
    npairs = .
    power = 0.9;
run;
```

### Paired t Test of Mean Ratio with Lognormal Data

You can express variability in terms of correlation and a common coefficient of variation, as in the following statements. Defaults for the `DIST=`, `SIDES=`, `NULLRATIO=` and `ALPHA=` options specify a two-sided test of mean ratio = 1 assuming a lognormal distribution and a significance level of 0.05.

```
proc power;
  pairedmeans test=ratio
    meanratio = 7
    corr = 0.3
    cv = 1.2
    npairs = 30
    power = .;
run;
```

You can also express variability in terms of correlation and individual coefficients of variation:

```

proc power;
  pairedmeans test=ratio
    meanratio = 7
    corr = 0.3
    pairedcv = 0.8 | 0.9
    npairs = 30
    power = .;
run;

```

### **Additive Equivalence Test for Mean Difference with Normal Data**

The following statements demonstrate a sample size computation for a TOST equivalence test for a normal mean difference. Default values for the `DIST=` and `ALPHA=` options specify a normal distribution and a significance level of 0.05.

```

proc power;
  pairedmeans test=equiv_diff
    lower = 2
    upper = 5
    meandiff = 4
    corr = 0.2
    stddev = 8
    npairs = .
    power = 0.9;
run;

```

### **Multiplicative Equivalence Test for Mean Ratio with Lognormal Data**

The following statements demonstrate a power computation for a TOST equivalence test for a lognormal mean ratio. Default values for the `DIST=` and `ALPHA=` options specify a lognormal distribution and a significance level of 0.05.

```

proc power;
  pairedmeans test=equiv_ratio
    lower = 3
    upper = 7
    meanratio = 5
    corr = 0.2
    cv = 1.1
    npairs = 50
    power = .;
run;

```

### **Confidence Interval for Mean Difference**

By default `CI=DIFF` analyzes the conditional probability of obtaining the desired precision, given that the interval contains the true mean difference, as in the following statements. The defaults of `SIDES=2` and `ALPHA=0.05` specify a two-sided interval with a confidence level of 0.95.

```

proc power;
  pairedmeans ci = diff
    halfwidth = 4
    corr = 0.35
    stddev = 8
    npairs = 30
    probwidth = .;
run;

```

---

## PLOT Statement

**PLOT** *<plot-options>* *</graph-options>* ;

The **PLOT** statement produces a graph or set of graphs for the sample size analysis defined by the previous analysis statement. The *plot-options* define the plot characteristics, and the *graph-options* are SAS/GRAPH-style options.

## Options

You can specify the following *plot-options* in the **PLOT** statement.

### **INTERPOL=JOIN | NONE**

specifies the type of curve to draw through the computed points. The **INTERPOL=JOIN** option connects computed points by straight lines. The **INTERPOL=NONE** option leaves computed points unconnected.

**KEY=BYCURVE** *<( bycurve-options )>*

**KEY=BYFEATURE** *<( byfeature-options )>*

### **KEY=ONCURVES**

specifies the style of key (or “legend”) for the plot. The default is **KEY=BYFEATURE**, which specifies a key with a column of entries for each plot feature (line style, color, and/or symbol). Each entry shows the mapping between a value of the feature and the value(s) of the analysis parameter(s) linked to that feature. The **KEY=BYCURVE** option specifies a key with each row identifying a distinct curve in the plot. The **KEY=ONCURVES** option places a curve-specific label adjacent to each curve.

You can specify the following *byfeature-options* in parentheses after the **KEY=BYCURVE** option.

### **NUMBERS=OFF | ON**

specifies how the key should identify curves. If **NUMBERS=OFF**, then the key includes symbol, color, and line style samples to identify the curves. If **NUMBERS=ON**, then the key includes numbers matching numeric labels placed adjacent to the curves. The default is **NUMBERS=ON**.

**POS=BOTTOM | INSET**

specifies the position of the key. The **POS=BOTTOM** option places the key below the X axis. The **POS=INSET** option places the key inside the plotting region and attempts to choose the least crowded corner. The default is **POS=BOTTOM**.

You can specify the following *byfeature-options* in parentheses after **KEY=BYFEATURE** option.

**POS=BOTTOM | INSET**

specifies the position of the key. The **POS=BOTTOM** option places the key below the X axis. The **POS=INSET** option places the key inside the plotting region and attempts to choose the least crowded corner. The default is **POS=BOTTOM**.

**MARKERS=ANALYSIS | COMPUTED | NICE | NONE**

specifies the locations for plotting symbols.

The **MARKERS=ANALYSIS** option places plotting symbols at locations corresponding to the values of the relevant input parameter from the analysis statement preceding the **PLOT** statement.

The **MARKERS=COMPUTED** option (the default) places plotting symbols at the locations of actual computed points from the sample size analysis.

The **MARKERS=NICE** option places plotting symbols at tick mark locations (corresponding to the argument axis).

The **MARKERS=NONE** option disables plotting symbols.

**MAX=number | DATAMAX**

specifies the maximum of the range of values for the parameter associated with the “argument” axis (the axis that is *not* representing the parameter being solved for). The default is **DATAMAX**, which specifies the maximum value that occurs for this parameter in the analysis statement that precedes the **PLOT** statement.

**MIN=number | DATAMIN**

specifies the minimum of the range of values for the parameter associated with the “argument” axis (the axis that is *not* representing the parameter being solved for). The default is **DATAMIN**, which specifies the minimum value that occurs for this parameter in the analysis statement that precedes the **PLOT** statement.

**NPOINTS=number****NPTS=number**

specifies the number of values for the parameter associated with the “argument” axis (the axis that is *not* representing the parameter being solved for). You cannot use the **NPOINTS=** and **STEP=** options simultaneously. The default value for typical situations is 20.

**STEP=number**

specifies the increment between values of the parameter associated with the “argument” axis (the axis that is *not* representing the parameter being solved for). You cannot use the **STEP=** and **NPOINTS=** options simultaneously. By default, the **NPOINTS=** option is used instead of the **STEP=** option.

**VARY** ( *feature* <BY *parameter-list*> <, ..., *feature* <BY *parameter-list*>> )

specifies how plot features should be linked to varying analysis parameters. Available plot features are COLOR, LINESSTYLE, PANEL, and SYMBOL. A “panel” refers to a separate plot with a heading identifying the subset of values represented in the plot.

The *parameter-list* is a list of one or more names separated by spaces. Each name must match the name of an analysis option used in the analysis statement preceding the PLOT statement. Also, the name must be the *primary* name for the analysis option—that is, the one listed first in the syntax description.

If you omit the < BY *parameter-list* > portion for a feature, then one or more multivalued parameters from the analysis will be automatically selected for you.

### **X=EFFECT N POWER**

specifies a plot with the requested type of parameter on the X axis and the parameter being solved for on the Y axis. When X=EFFECT, the parameter assigned to the X axis is the one most representative of “effect size.” When X=N, the parameter assigned to the X axis is the sample size. When X=POWER, the parameter assigned to the X axis is the one most representative of “power” (either power itself or a similar probability, such as Prob(Width) for confidence interval analyses). You cannot use the X= and Y= options simultaneously. The default is X=POWER, unless the result parameter is power or Prob(Width), in which case the default is X=N.

You can use the X=N option only when a scalar sample size parameter is used as input in the analysis. For example, X=N can be used with total sample size or sample size per group, or with two group sample sizes when one is being solved for.

Table 67.18 summarizes the parameters representing effect size in different analyses.

**Table 67.18** Effect Size Parameters for Different Analyses

Analysis Statement and Options	Effect Size Parameters
LOGISTIC	None
MULTREG	Partial correlation or $R^2$ difference
ONECORR	Correlation
ONESAMPLEFREQ TEST	Proportion
ONESAMPLEFREQ CI	CI half-width
ONESAMPLEMEANS TEST=T, ONESAMPLEMEANS TEST=EQUIV	Mean
ONESAMPLEMEANS CI=T	CI half-width
ONEWAYANOVA	None
PAIREFREQ	Discordant proportion difference or ratio
PAIREDMEANS TEST=DIFF, PAIREDMEANS TEST=EQUIV_DIFF	Mean difference

Table 67.18 continued

Analysis Statement and Options	Effect Size Parameters
PAIREDMEANS TEST=RATIO, PAIREDMEANS TEST=EQUIV_RATIO	Mean ratio
PAIREDMEANS CI=DIFF	CI half-width
TWOSAMPLEFREQ	Proportion difference, odds ratio, or relative risk
TWOSAMPLEMEANS TEST=DIFF, TWOSAMPLEMEANS TEST=DIFF_SATT, TWOSAMPLEMEANS TEST=EQUIV_DIFF	Mean difference
TWOSAMPLEMEANS TEST=RATIO, TWOSAMPLEMEANS TEST=EQUIV_RATIO	Mean ratio
TWOSAMPLEMEANS CI=DIFF	CI half-width
TWOSAMPLESURVIVAL	Hazard ratio if used, else none
TWOSAMPLEWILCOXON	None

**XOPTS=( *x-options* )**

specifies plot characteristics pertaining to the X axis.

You can specify the following *x-options* in parentheses.

**CROSSREF=NO | YES**

specifies whether the reference lines defined by the **REF=** *x-option* should be crossed with a reference line on the Y axis that indicates the solution point on the curve.

**REF=number-list**

specifies locations for reference lines extending from the X axis across the entire plotting region. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**Y=EFFECT N POWER**

specifies a plot with the requested type of parameter on the Y axis and the parameter being solved for on the X axis. When **Y=EFFECT**, the parameter assigned to the Y axis is the one most representative of “effect size.” When **Y=N**, the parameter assigned to the Y axis is the sample size. When **Y=POWER**, the parameter assigned to the Y axis is the one most representative of “power” (either power itself or a similar probability, such as Prob(Width) for confidence interval analyses). You cannot use the **Y=** and **X=** options simultaneously. By default, the **X=** option is used instead of the **Y=** option.

**YOPTS=( *y-options* )**

specifies plot characteristics pertaining to the Y axis.

You can specify the following *y-options* in parentheses.

**CROSSREF=NO | YES**

specifies whether the reference lines defined by the **REF=** *y-option* should be crossed with a reference line on the X axis that indicates the solution point on the curve.

**REF=number-list**

specifies locations for reference lines extending from the Y axis across the entire plotting region. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

You can specify the following *graph-options* in the **PLOT** statement after a slash (/).

**DESCRIPTION='string'**

specifies a descriptive string of up to 40 characters that appears in the “Description” field of the graphics catalog. The description does not appear on the plots. By default, PROC POWER assigns a description either of the form “Y versus X” (for a single-panel plot) or of the form “Y versus X (S),” where Y is the parameter on the Y axis, X is the parameter on the X axis, and S is a description of the subset represented on the current panel of a multipanel plot.

**NAME='string'**

specifies a name of up to eight characters for the catalog entry for the plot. The default name is PLOT*n*, where *n* is the number of the plot statement within the current invocation of PROC POWER. If the name duplicates the name of an existing entry, SAS/GRAPH software adds a number to the duplicate name to create a unique entry—for example, PLOT11 and PLOT12 for the second and third panels of a multipanel plot generated in the first **PLOT** statement in an invocation of PROC POWER.

---

## TWOSAMPLEFREQ Statement

**TWOSAMPLEFREQ** < *options* > ;

The **TWOSAMPLEFREQ** statement performs power and sample size analyses for tests of two independent proportions. Pearson’s chi-square, Fisher’s exact, and likelihood ratio chi-square tests are supported.

### Summary of Options

Table 67.19 summarizes categories of options available in the **TWOSAMPLEFREQ** statement.

**Table 67.19** Summary of Options in the TWOSAMPLEFREQ Statement

Task	Options
Define analysis	<b>TEST=</b>
Specify analysis information	<b>ALPHA=</b> <b>NULLPROPORTIONDIFF=</b>

**Table 67.19** *continued*

Task	Options
Specify effects	NULLODDSRATIO= NULLRELATIVERISK= SIDES= GROUPPROPORTIONS= ODDSRATIO= PROPORTIONDIFF= REFPROPORTION= RELATIVERISK=
Specify sample size and allocation	GROUPNS= GROUPWEIGHTS= NPERGROUP= NTOTAL=
Specify power	POWER=
Control sample size rounding	NFRACTIONAL
Control ordering in output	OUTPUTORDER=

Table 67.20 summarizes the valid result parameters for different analyses in the TWOSAMPLEFREQ statement.

**Table 67.20** Summary of Result Parameters in the TWOSAMPLEFREQ Statement

Analyses	Solve For	Syntax
TEST=FISHER	Power Sample size	POWER=. NTOTAL=. NPERGROUP=.
TEST=LRCHI	Power Sample size	POWER=. NTOTAL=. NPERGROUP=.
TEST=PCHI	Power Sample size	POWER=. NTOTAL=. NPERGROUP=.

## Dictionary of Options

### ALPHA=*number-list*

specifies the level of significance of the statistical test. The default is 0.05, corresponding to the usual  $0.05 \times 100\% = 5\%$  level of significance. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**GROUPPROPORTIONS**=*grouped-number-list*

**GPROPORTIONS**=*grouped-number-list*

**GROUPPS**=*grouped-number-list*

**GPS**=*grouped-number-list*

specifies the two independent proportions,  $p_1$  and  $p_2$ . See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**GROUPNS**=*grouped-number-list*

**GNS**=*grouped-number-list*

specifies the two group sample sizes. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**GROUPWEIGHTS**=*grouped-number-list*

**GWEIGHTS**=*grouped-number-list*

specifies the sample size allocation weights for the two groups. This option controls how the total sample size is divided between the two groups. Each pair of values for the two groups represents relative allocation weights. Additionally, if the **NFRACTIONAL** option is not used, the total sample size is restricted to be equal to a multiple of the sum of the two group weights (so that the resulting design has an integer sample size for each group while adhering exactly to the group allocation weights). Values must be integers unless the **NFRACTIONAL** option is used. The default value is (1 1), a balanced design with a weight of 1 for each group. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**NFRACTIONAL**

**NFRAC**

enables fractional input and output for sample sizes. See the section “[Sample Size Adjustment Options](#)” on page 4916 for information about the ramifications of the presence (and absence) of the **NFRACTIONAL** option.

**NPERGROUP**=*number-list*

**NPERG**=*number-list*

specifies the common sample size per group or requests a solution for the common sample size per group with a missing value (**NPERGROUP**=.). Use of this option implicitly specifies a balanced design. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NTOTAL**=*number-list*

specifies the sample size or requests a solution for the sample size with a missing value (**NTOTAL**=.). See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NULLODDSRATIO**=*number-list*

**NULLOR**=*number-list*

specifies the null odds ratio. The default value is 1. This option can be used only with the **ODDSRATIO**= option in the **TEST**=PCHI analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NULLPROPORTIONDIFF=***number-list*

**NULLPDIFF=***number-list*

specifies the null proportion difference. The default value is 0. This option can be used only with the [GROUPPROPORTIONS=](#) or [PROPORTIONDIFF=](#) option in the [TEST=PCHI](#) analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NULLRELATIVERISK=***number-list*

**NULLRR=***number-list*

specifies the null relative risk. The default value is 1. This option can be used only with the [RELATIVERISK=](#) option in the [TEST=PCHI](#) analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**ODDSRATIO=***number-list*

**OR=***number-list*

specifies the odds ratio  $[p_2/(1 - p_2)] / [p_1/(1 - p_1)]$ . See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**OUTPUTORDER=INTERNAL**

**OUTPUTORDER=REVERSE**

**OUTPUTORDER=SYNTAX**

controls how the input and default analysis parameters are ordered in the output. [OUTPUTORDER=INTERNAL](#) (the default) arranges the parameters in the output according to the following order of their corresponding options:

- [SIDES=](#)
- [NULLPROPORTIONDIFF=](#)
- [NULLODDSRATIO=](#)
- [NULLRELATIVERISK=](#)
- [ALPHA=](#)
- [GROUPPROPORTIONS=](#)
- [REFPROPORTION=](#)
- [PROPORTIONDIFF=](#)
- [ODDSRATIO=](#)
- [RELATIVERISK=](#)
- [GROUPWEIGHTS=](#)
- [NTOTAL=](#)
- [NPERGROUP=](#)
- [GROUPNS=](#)
- [POWER=](#)

The [OUTPUTORDER=SYNTAX](#) option arranges the parameters in the output in the same order in which their corresponding options are specified in the [TWOSAMPLEFREQ](#) statement. The [OUTPUTORDER=REVERSE](#) option arranges the parameters in the output in the reverse of the order in which their corresponding options are specified in the [TWOSAMPLEFREQ](#) statement.

**POWER=number-list**

specifies the desired power of the test or requests a solution for the power with a missing value (**POWER=.**). The power is expressed as a probability, a number between 0 and 1, rather than as a percentage. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**PROPORTIONDIFF=number-list****PDIFF=number-list**

specifies the proportion difference  $p_2 - p_1$ . See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**REFPROPORTION=number-list****REFP=number-list**

specifies the reference proportion  $p_1$ . See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**RELATIVERISK=number-list****RR=number-list**

specifies the relative risk  $p_2/p_1$ . See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**SIDES=keyword-list**

specifies the number of sides (or tails) and the direction of the statistical test or confidence interval. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *keyword-list*. Valid keywords and their interpretation are as follows:

- 1 one-sided with alternative hypothesis in same direction as effect
- 2 two-sided
- U upper one-sided with alternative greater than null value
- L lower one-sided with alternative less than null value

If the effect size is zero, then **SIDES=1** is not permitted; instead, specify the direction of the test explicitly in this case with either **SIDES=L** or **SIDES=U**. The default value is 2.

**TEST=FISHER****TEST=LRCHI****TEST=PCHI**

specifies the statistical analysis. **TEST=FISHER** specifies Fisher’s exact test. **TEST=LRCHI** specifies the likelihood ratio chi-square test. **TEST=PCHI** (the default) specifies Pearson’s chi-square test.

## Restrictions on Option Combinations

To specify the proportions, choose one of the following parameterizations:

- individual proportions (by using the `GROUPPROPORTIONS=` option)
- difference between proportions and reference proportion (by using the `PROPORTIONDIFF=` and `REFPROPORTION=` options)
- odds ratio and reference proportion (by using the `ODDSRATIO=` and `REFPROPORTION=` options)
- relative risk and reference proportion (by using the `RELATIVERISK=` and `REFPROPORTION=` options)

To specify the sample size and allocation, choose one of the following parameterizations:

- sample size per group in a balanced design (by using the `NPERGROUP=` option)
- total sample size and allocation weights (by using the `NTOTAL=` and `GROUPWEIGHTS=` options)
- individual group sample sizes (by using the `GROUPNS=` option)

## Option Groups for Common Analyses

This section summarizes the syntax for the common analyses supported in the `TWOSAMPLEFREQ` statement.

### *Pearson Chi-Square Test for Two Proportions*

You can use the `NPERGROUP=` option in a balanced design and express effects in terms of the individual proportions, as in the following statements. Default values for the `SIDES=` and `ALPHA=` options specify a two-sided test with a significance level of 0.05.

```
proc power;
  twosamplefreq test=pchi
    groupproportions = (.15 .25)
    nullproportiondiff = .03
    npergroup = 50
    power = .;
run;
```

You can also specify an unbalanced design by using the `NTOTAL=` and `GROUPWEIGHTS=` options and express effects in terms of the odds ratio. The default value of the `NULLODDSRATIO=` option specifies a test of no effect.

```
proc power;
  twosamplefreq test=pchi
    oddsratio = 2.5
    refproportion = 0.3
    groupweights = (1 2)
    ntotal = .
    power = 0.8;
run;
```

You can also specify sample sizes with the `GROUPNS=` option and express effects in terms of relative risks. The default value of the `NULLRELATIVERISK=` option specifies a test of no effect.

```
proc power;
  twosamplefreq test=pchi
    relativetrisk = 1.5
    refproportion = 0.2
    groupns = 40 | 60
    power = .;
run;
```

You can also express effects in terms of the proportion difference. The default value of the `NULLPROPORTIONDIFF=` option specifies a test of no effect, and the default value of the `GROUPWEIGHTS=` option specifies a balanced design.

```
proc power;
  twosamplefreq test=pchi
    proportiondiff = 0.15
    refproportion = 0.4
    ntotal = 100
    power = .;
run;
```

### ***Fisher's Exact Conditional Test for Two Proportions***

The following statements demonstrate a power computation for Fisher's exact conditional test for two proportions. Default values for the `SIDES=` and `ALPHA=` options specify a two-sided test with a significance level of 0.05.

```
proc power;
  twosamplefreq test=fisher
    groupproportions = (.35 .15)
    npergroup = 50
    power = .;
run;
```

### ***Likelihood Ratio Chi-Square Test for Two Proportions***

The following statements demonstrate a sample size computation for the likelihood ratio chi-square test for two proportions. Default values for the `SIDES=` and `ALPHA=` options specify a two-sided test with a significance level of 0.05.

```
proc power;
  twosamplefreq test=lrchi
    oddsratio = 2
    refproportion = 0.4
    npergroup = .
    power = 0.9;
run;
```

## TWOSAMPLEMEANS Statement

**TWOSAMPLEMEANS** < options > ;

The **TWOSAMPLEMEANS** statement performs power and sample size analyses for pooled and unpooled *t* tests, equivalence tests, and confidence interval precision involving two independent samples.

### Summary of Options

Table 67.21 summarizes categories of options available in the **TWOSAMPLEMEANS** statement.

**Table 67.21** Summary of Options in the TWOSAMPLEMEANS Statement

Task	Options
Define analysis	CI= DIST= TEST=
Specify analysis information	ALPHA= LOWER= NULLDIFF= NULLRATIO= SIDES= UPPER=
Specify effects	HALFWIDTH= GROUPMEANS= MEANDIFF= MEANRATIO=
Specify variability	CV= GROUPSTDDEVS== STDDEV=
Specify sample size and allocation	GROUPNS= GROUPWEIGHTS= NPERGROUP= NTOTAL=
Specify power and related probabilities	POWER= PROBTYPE= PROBWIDTH=
Control sample size rounding	NFRACTIONAL
Control ordering in output	OUTPUTORDER=

Table 67.22 summarizes the valid result parameters for different analyses in the **TWOSAMPLEMEANS** statement.

**Table 67.22** Summary of Result Parameters in the TWOSAMPLEMEANS Statement

Analyses	Solve For	Syntax	
TEST=DIFF	Power	POWER=.	
	Sample size	NTOTAL=.	
	Group sample size		NPERGROUP=.
			GROUPNS= <i>n1</i>   .
			GROUPNS= .   <i>n2</i>
			GROUPNS= ( <i>n1</i> .)
	Group weight		GROUPNS= (. <i>n2</i> )
			GROUPWEIGHTS= <i>w1</i>   .
			GROUPWEIGHTS= .   <i>w2</i>
	Alpha		GROUPWEIGHTS= ( <i>w1</i> .)
		GROUPWEIGHTS= (. <i>w2</i> )	
Group mean		ALPHA=.	
		GROUPMEANS= <i>mean1</i>   .	
		GROUPMEANS= .   <i>mean2</i>	
		GROUPMEANS= ( <i>mean1</i> .)	
		GROUPMEANS= (. <i>mean2</i> )	
	Mean difference	MEANDIFF=.	
	Standard deviation	STDDEV=.	
TEST=DIFF_SATT	Power	POWER=.	
	Sample size	NTOTAL=.	
		NPERGROUP=.	
TEST=RATIO	Power	POWER=.	
	Sample size	NTOTAL=.	
		NPERGROUP=.	
TEST=EQUIV_DIFF	Power	POWER=.	
	Sample size	NTOTAL=.	
		NPERGROUP=.	
TEST=EQUIV_RATIO	Power	POWER=.	
	Sample size	NTOTAL=.	
		NPERGROUP=.	
CI=DIFF	Prob(width)	PROBWIDTH=.	
	Sample size	NTOTAL=.	
		NPERGROUP=.	

## Dictionary of Options

### ALPHA=*number-list*

specifies the level of significance of the statistical test or requests a solution for alpha with a missing value (ALPHA=.). The default is 0.05, corresponding to the usual  $0.05 \times 100\% = 5\%$  level of significance. If the CI= and SIDES=1 options are used, then the value must be less than 0.5. See the section “Specifying Value Lists in Analysis Statements” on page 4913

for information about specifying the *number-list*.

## CI

### CI=DIFF

specifies an analysis of precision of the confidence interval for the mean difference, assuming equal variances. Instead of power, the relevant probability for this analysis is the probability that the interval half-width is at most the value specified by the `HALFWIDTH=` option. If neither the `TEST=` option nor the `CI=` option is used, the default is `TEST=DIFF`.

### CV=*number-list*

specifies the coefficient of variation assumed to be common to both groups. The coefficient of variation is defined as the ratio of the standard deviation to the mean. You can use this option only with `DIST=LOGNORMAL`. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### DIST=LOGNORMAL

### DIST=NORMAL

specifies the underlying distribution assumed for the test statistic. `NORMAL` corresponds to the normal distribution, and `LOGNORMAL` corresponds to the lognormal distribution. The default value (also the only acceptable value in each case) is `NORMAL` for `TEST=DIFF`, `TEST=DIFF_SATT`, `TEST=EQUIV_DIFF`, and `CI=DIFF`; and `LOGNORMAL` for `TEST=RATIO` and `TEST=EQUIV_RATIO`.

### GROUPMEANS=*grouped-number-list*

### GMEANS=*grouped-number-list*

specifies the two group means or requests a solution for one group mean given the other. Means are in the original scale. They are arithmetic if `DIST=NORMAL` and geometric if `DIST=LOGNORMAL`. This option cannot be used with the `CI=DIFF` analysis. When `TEST=EQUIV_DIFF`, the means are interpreted as the reference mean (first) and the treatment mean (second). See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

### GROUPNS=*grouped-number-list*

### GNS=*grouped-number-list*

specifies the two group sample sizes or requests a solution for one group sample size given the other. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

### GROUPSTDDEVS=*grouped-number-list*

### GSTDDEVS=*grouped-number-list*

### GROUPSTDS=*grouped-number-list*

### GSTDS=*grouped-number-list*

specifies the standard deviation of each group. Unlike the `STDDEV=` option, the `GROUPSTDDEVS=` option supports different values for each group. It is valid only for the Satterthwaite *t* test (`TEST=DIFF_SATT` `DIST=NORMAL`). See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**GROUPWEIGHTS=***grouped-number-list***GWEIGHTS=***grouped-number-list*

specifies the sample size allocation weights for the two groups, or requests a solution for one group weight given the other. This option controls how the total sample size is divided between the two groups. Each pair of values for the two groups represents relative allocation weights. Additionally, if the **NFRACTIONAL** option is not used, the total sample size is restricted to be equal to a multiple of the sum of the two group weights (so that the resulting design has an integer sample size for each group while adhering exactly to the group allocation weights). Values must be integers unless the **NFRACTIONAL** option is used. The default value is (1 1), a balanced design with a weight of 1 for each group. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**HALFWIDTH=***number-list*

specifies the desired confidence interval half-width. The half-width is defined as the distance between the point estimate and a finite endpoint. This option can be used only with the **CI=DIFF** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**LOWER=***number-list*

specifies the lower equivalence bound for the mean difference or mean ratio, in the original scale (whether **DIST=NORMAL** or **DIST=LOGNORMAL**). Values must be greater than 0 when **DIST=LOGNORMAL**. This option can be used only with the **TEST=EQUIV\_DIFF** and **TEST=EQUIV\_RATIO** analyses. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**MEANDIFF=***number-list*

specifies the mean difference, defined as  $\mu_2 - \mu_1$ , or requests a solution for the mean difference with a missing value (**MEANDIFF=.**). This option can be used only with the **TEST=DIFF**, **TEST=DIFF\_SATT**, and **TEST=EQUIV\_DIFF** analyses. When **TEST=EQUIV\_DIFF**, the mean difference is interpreted as the treatment mean minus the reference mean. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**MEANRATIO=***number-list*

specifies the geometric mean ratio, defined as  $\gamma_2/\gamma_1$ . This option can be used only with the **TEST=RATIO** and **TEST=EQUIV\_RATIO** analyses. When **TEST=EQUIV\_RATIO**, the mean ratio is interpreted as the treatment mean divided by the reference mean. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NFRACTIONAL****NFRAC**

enables fractional input and output for sample sizes. See the section “[Sample Size Adjustment Options](#)” on page 4916 for information about the ramifications of the presence (and absence) of the **NFRACTIONAL** option.

**NPERGROUP=***number-list*

**NPERG=***number-list*

specifies the common sample size per group or requests a solution for the common sample size per group with a missing value (**NPERGROUP=.**). Use of this option implicitly specifies a balanced design. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NTOTAL=***number-list*

specifies the sample size or requests a solution for the sample size with a missing value (**NTOTAL=.**). See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NULLDIFF=***number-list*

**NULLD=***number-list*

specifies the null mean difference. The default value is 0. This option can be used only with the **TEST=DIFF** and **TEST=DIFF\_SATT** analyses. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NULLRATIO=***number-list*

**NULLR=***number-list*

specifies the null mean ratio. The default value is 1. This option can be used only with the **TEST=RATIO** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**OUTPUTORDER=INTERNAL**

**OUTPUTORDER=REVERSE**

**OUTPUTORDER=SYNTAX**

controls how the input and default analysis parameters are ordered in the output. **OUTPUTORDER=INTERNAL** (the default) arranges the parameters in the output according to the following order of their corresponding options:

- **SIDES=**
- **NULLDIFF=**
- **NULLRATIO=**
- **LOWER=**
- **UPPER=**
- **ALPHA=**
- **GROUPMEANS=**
- **MEANDIFF=**
- **MEANRATIO=**
- **HALFWIDTH=**
- **STDDEV=**
- **GROUPSTDDEVS==**
- **CV=**

- GROUPWEIGHTS=
- NTOTAL=
- NPERGROUP=
- GROUPNS=
- POWER=
- PROBTTYPE=
- PROBWIDTH=

The **OUTPUTORDER=SYNTAX** option arranges the parameters in the output in the same order in which their corresponding options are specified in the **TWOSAMPLEMEANS** statement. The **OUTPUTORDER=REVERSE** option arranges the parameters in the output in the reverse of the order in which their corresponding options are specified in the **TWOSAMPLEMEANS** statement.

**POWER=number-list**

specifies the desired power of the test or requests a solution for the power with a missing value (**POWER=.**). The power is expressed as a probability, a number between 0 and 1, rather than as a percentage. This option cannot be used with the **CI=DIFF** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**PROBTTYPE=keyword-list**

specifies the type of probability for the **PROBWIDTH=** option. A value of **CONDITIONAL** (the default) indicates the conditional probability that the confidence interval half-width is at most the value specified by the **HALFWIDTH=** option, given that the true mean difference is captured by the confidence interval. A value of **UNCONDITIONAL** indicates the unconditional probability that the confidence interval half-width is at most the value specified by the **HALFWIDTH=** option. you can use the alias **GIVENVALIDITY** for **CONDITIONAL**. The **PROBTTYPE=** option can be used only with the **CI=DIFF** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *keyword-list*.

**CONDITIONAL** width probability conditional on interval containing the mean

**UNCONDITIONAL** unconditional width probability

**PROBWIDTH=number-list**

specifies the desired probability of obtaining a confidence interval half-width less than or equal to the value specified by the **HALFWIDTH=** option. A missing value (**PROBWIDTH=.**) requests a solution for this probability. The type of probability is controlled with the **PROBTTYPE=** option. Values are expressed as probabilities (for example, 0.9) rather than percentages. This option can be used only with the **CI=DIFF** analysis. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**SIDES=keyword-list**

specifies the number of sides (or tails) and the direction of the statistical test or confidence interval. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for

information about specifying the *keyword-list*. Valid keywords and their interpretation for the **TEST=** analyses are as follows:

- 1 one-sided with alternative hypothesis in same direction as effect
- 2 two-sided
- U upper one-sided with alternative greater than null value
- L lower one-sided with alternative less than null value

For confidence intervals, **SIDES=U** refers to an interval between the lower confidence limit and infinity, and **SIDES=L** refers to an interval between minus infinity and the upper confidence limit. For both of these cases and **SIDES=1**, the confidence interval computations are equivalent. The **SIDES=** option cannot be used with the **TEST=EQUIV\_DIFF** and **TEST=EQUIV\_RATIO** analyses. The default value is 2.

**STDDEV=number-list**

**STD=number-list**

specifies the standard deviation assumed to be common to both groups, or requests a solution for the common standard deviation with a missing value (**STDDEV=.**). This option can be used only with **DIST=NORMAL**. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**TEST**

**TEST=DIFF**

**TEST=DIFF\_SATT**

**TEST=EQUIV\_DIFF**

**TEST=EQUIV\_RATIO**

**TEST=RATIO**

specifies the statistical analysis. **TEST** or **TEST=DIFF** (the default) specifies a pooled *t* test on the mean difference, assuming equal variances. **TEST=DIFF\_SATT** specifies a Satterthwaite unpaired *t* test on the mean difference, assuming unequal variances. **TEST=EQUIV\_DIFF** specifies an additive equivalence test of the mean difference by using a two one-sided tests (TOST) analysis (Schuirman 1987). **TEST=EQUIV\_RATIO** specifies a multiplicative equivalence test of the mean ratio by using a TOST analysis. **TEST=RATIO** specifies a pooled *t* test on the mean ratio, assuming equal coefficients of variation. If neither the **TEST=** option nor the **CI=** option is used, the default is **TEST=DIFF**.

**UPPER=number-list**

specifies the upper equivalence bound for the mean difference or mean ratio, in the original scale (whether **DIST=NORMAL** or **DIST=LOGNORMAL**). This option can be used only with the **TEST=EQUIV\_DIFF** and **TEST=EQUIV\_RATIO** analyses. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

## Restrictions on Option Combinations

To define the analysis, choose one of the following parameterizations:

- a statistical test (by using the `TEST=` option)
- confidence interval precision (by using the `CI=` option)

To specify the means, choose one of the following parameterizations:

- individual group means (by using the `GROUPMEANS=` option)
- mean difference (by using the `MEANDIFF=` option)
- mean ratio (by using the `MEANRATIO=` option)

To specify standard deviations in the Satterthwaite  $t$  test (`TEST=DIFF_SATT`), choose one of the following parameterizations:

- common standard deviation (by using the `STDDEV=` option)
- individual group standard deviations (by using the `GROUPSTDDEVS==` option)

To specify the sample sizes and allocation, choose one of the following parameterizations:

- sample size per group in a balanced design (by using the `NPERGROUP=` option)
- total sample size and allocation weights (by using the `NTOTAL=` and `GROUPWEIGHTS=` options)
- individual group sample sizes (by using the `GROUPNS=` option)

## Option Groups for Common Analyses

This section summarizes the syntax for the common analyses supported in the `TWOSAMPLEMEANS` statement.

### *Two-Sample $t$ Test Assuming Equal Variances*

You can use the `NPERGROUP=` option in a balanced design and express effects in terms of the mean difference, as in the following statements. Default values for the `DIST=`, `SIDES=`, `NULLDIFF=`, and `ALPHA=` options specify a two-sided test for no difference with a normal distribution and a significance level of 0.05.

```
proc power;
  twosamplemeans test=diff
    meandiff = 7
    stddev = 12
    npergroup = 50
    power = .;
run;
```

You can also specify an unbalanced design by using the `NTOTAL=` and `GROUPWEIGHTS=` options and express effects in terms of individual group means:

```
proc power;
  twosamplemeans test=diff
    groupmeans = 8 | 15
    stddev = 4
    groupweights = (2 3)
    ntotal = .
    power = 0.9;
run;
```

Another way to specify the sample sizes is with the `GROUPNS=` option:

```
proc power;
  twosamplemeans test=diff
    groupmeans = 8 | 15
    stddev = 4
    groupns = (25 40)
    power = .;
run;
```

### *Two-Sample Satterthwaite $t$ Test Assuming Unequal Variances*

The following statements demonstrate a power computation for the two-sample Satterthwaite  $t$  test allowing unequal variances. Default values for the `DIST=`, `SIDES=`, `NULLDIFF=`, and `ALPHA=` options specify a two-sided test for no difference with a normal distribution and a significance level of 0.05.

```
proc power;
  twosamplemeans test=diff_satt
    meandiff = 3
    groupstddevs = 5 | 8
    groupweights = (1 2)
    ntotal = 60
    power = .;
run;
```

### *Two-Sample Pooled $t$ Test of Mean Ratio with Lognormal Data*

The following statements demonstrate a power computation for the pooled  $t$  test of a lognormal mean ratio. Default values for the `DIST=`, `SIDES=`, `NULLRATIO=`, and `ALPHA=` options specify a two-sided test of mean ratio = 1 assuming a lognormal distribution and a significance level of 0.05.

```
proc power;
  twosamplemeans test=ratio
    meanratio = 7
    cv = 0.8
    groupns = 50 | 70
    power = .;
run;
```

**Additive Equivalence Test for Mean Difference with Normal Data**

The following statements demonstrate a sample size computation for the TOST equivalence test for a normal mean difference. A default value of `GROUPWEIGHTS=(1 1)` specifies a balanced design. Default values for the `DIST=` and `ALPHA=` options specify a significance level of 0.05 and an assumption of normally distributed data.

```
proc power;
  twosamplemeans test=equiv_diff
    lower = 2
    upper = 5
    meandiff = 4
    stddev = 8
    ntotal = .
    power = 0.9;
run;
```

**Multiplicative Equivalence Test for Mean Ratio with Lognormal Data**

The following statements demonstrate a power computation for the TOST equivalence test for a lognormal mean ratio. Default values for the `DIST=` and `ALPHA=` options specify a significance level of 0.05 and an assumption of lognormally distributed data.

```
proc power;
  twosamplemeans test=equiv_ratio
    lower = 3
    upper = 7
    meanratio = 5
    cv = 0.75
    npergroup = 50
    power = .;
run;
```

**Confidence Interval for Mean Difference**

By default `CI=DIFF` analyzes the conditional probability of obtaining the desired precision, given that the interval contains the true mean difference, as in the following statements. The defaults of `SIDES=2` and `ALPHA=0.05` specify a two-sided interval with a confidence level of 0.95.

```
proc power;
  twosamplemeans ci = diff
    halfwidth = 4
    stddev = 8
    groupns = (30 35)
    probwidth = .;
run;
```

---

## TWOSAMPLESURVIVAL Statement

**TWOSAMPLESURVIVAL** < options > ;

The **TWOSAMPLESURVIVAL** statement performs power and sample size analyses for comparing two survival curves. The log-rank, Gehan, and Tarone-Ware rank tests are supported.

### Summary of Options

Table 67.23 summarizes categories of options available in the **TWOSAMPLESURVIVAL** statement.

**Table 67.23** Summary of Options in the TWOSAMPLESURVIVAL Statement

Task	Options
Define analysis	TEST=
Specify analysis information	ALPHA= ACCRUALTIME= FOLLOWUPTIME= TOTALTIME= SIDES=
Specify effects	CURVE= GROUPMEDSURVTIMES= GROUPSURVEXPHAZARDS= GROUPSURVIVAL= HAZARDRATIO= REFSURVEXPHAZARD= REFSURVIVAL=
Specify loss information	GROUPLOSS= GROUPLOSSEXPHAZARDS= GROUPMEDLOSSTIMES=
Specify sample size and allocation	GROUPNS= GROUPWEIGHTS= NPERGROUP= NTOTAL=
Specify power	POWER=
Control sample size rounding	NFRACTIONAL
Specify computational method	NSUBINTERVAL=
Control ordering in output	OUTPUTORDER=

Table 67.24 summarizes the valid result parameters for different analyses in the **TWOSAMPLESURVIVAL** statement.

**Table 67.24** Summary of Result Parameters in the TWOSAMPLESURVIVAL Statement

Analyses	Solve For	Syntax
TEST=GEHAN	Power	POWER=.
	Sample size	NTOTAL=. NPERGROUP=.
TEST=LOGRANK	Power	POWER=.
	Sample size	NTOTAL=. NPERGROUP=.
TEST=TARONEWARE	Power	POWER=.
	Sample size	NTOTAL=. NPERGROUP=.

## Dictionary of Options

**ACCRUALTIME=number-list | MAX**

**ACCTIME=number-list | MAX**

**ACCRUALT=number-list | MAX**

**ACCT=number-list | MAX**

specifies the accrual time. Accrual is assumed to occur uniformly from time 0 to the time specified by the **ACCRUALTIME=** option. If the **GROUPSURVIVAL=** or **REFSURVIVAL=** option is used, then the value of the total time (the sum of accrual and follow-up times) must be less than or equal to the largest time in *each* multipoint (piecewise linear) survival curve. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**ACCRUALTIME=MAX** can be used when each scenario in the analysis contains at least one piecewise linear survival curve (in the **GROUPSURVIVAL=** or **REFSURVIVAL=** option). It causes the accrual time to be automatically set, separately for each scenario, to the maximum possible time supported by the piecewise linear survival curve(s) in that scenario. It is not compatible with the **FOLLOWUPTIME=MAX** option or the **TOTALTIME=** option.

**ALPHA=number-list**

specifies the level of significance of the statistical test. The default is 0.05, corresponding to the usual  $0.05 \times 100\% = 5\%$  level of significance. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**CURVE("label")=points**

defines a survival curve.

For the **CURVE=** option,

*label* identifies the curve in the output and with the **GROUPLOSS=**, **GROUPSURVIVAL=**, and **REFSURVIVAL=** options.

*points* specifies one or more (time, survival) pairs on the curve, where the survival value denotes the probability of surviving until at least the specified time.

A single-point curve is interpreted as exponential, and a multipoint curve is interpreted as piecewise linear. Points can be expressed in either of two forms:

- a series of time:survival pairs separated by spaces. For example:

1:0.9 2:0.7 3:0.6

- a DOLIST of times enclosed in parentheses, followed by a colon (:), followed by a DOLIST of survival values enclosed in parentheses. For example:

(1 to 3 by 1):(0.9 0.7 0.6)

The DOLIST format is the same as in the DATA step.

Points can also be expressed as combinations of the two forms. For example:

1:0.9 2:0.8 (3 to 6 by 1):(0.7 0.65 0.6 0.55)

The points have the following restrictions:

- The time values must be nonnegative and strictly increasing.
- The survival values must be strictly decreasing.
- The survival value at a time of 0 must be equal to 1.
- If there is only one point, then the time must be greater than 0, and the survival value cannot be 0 or 1.

**FOLLOWUPTIME=***number-list* | **MAX**

**FUTIME=***number-list* | **MAX**

**FOLLOWUPT=***number-list* | **MAX**

**FUT=***number-list* | **MAX**

specifies the follow-up time, the amount of time in the study past the accrual time. If the [GROUPSURVIVAL=](#) or [REFSURVIVAL=](#) option is used, then the value of the total time (the sum of accrual and follow-up times) must be less than or equal to the largest time in *each* multipoint (piecewise linear) survival curve. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**FOLLOWUPTIME=MAX** can be used when each scenario in the analysis contains at least one piecewise linear survival curve (in the [GROUPSURVIVAL=](#) or [REFSURVIVAL=](#) option). It causes the follow-up time to be automatically set, separately for each scenario, to the maximum possible time supported by the piecewise linear survival curve(s) in that scenario. It is not compatible with the [ACCRUALTIME=MAX](#) option or the [TOTALTIME=](#) option.

**GROUPLOSS=***grouped-name-list*

**GLOSS=***grouped-name-list*

specifies the exponential loss survival curve for each group, by using labels specified with the [CURVE=](#) option. Loss is assumed to follow an exponential curve, indicating the expected rate of censoring (in other words, loss to follow-up) over time. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-name-list*.

**GROUPLOSSEXPHAZARDS=***grouped-number-list*

**GLOSSEXPHAZARDS=***grouped-number-list*

**GROUPLOSSEXPHS=***grouped-number-list*

**GLOSSEXPHS=***grouped-number-list*

specifies the exponential hazards of the loss in each group. Loss is assumed to follow an exponential curve, indicating the expected rate of censoring (in other words, loss to follow-up) over time. If none of the [GROUPLOSSEXPHAZARDS=](#), [GROUPLOSS=](#), and [GROUPMEDLOSSTIMES=](#) options are used, the default of [GROUPLOSSEXPHAZARDS=\(0 0\)](#) indicates no loss to follow-up. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**GROUPMEDLOSSTIMES=***grouped-number-list*

**GMEDLOSSTIMES=***grouped-number-list*

**GROUPMEDLOSSTS=***grouped-number-list*

**GMEDLOSSTS=***grouped-number-list*

specifies the median times of the loss in each group. Loss is assumed to follow an exponential curve, indicating the expected rate of censoring (in other words, loss to follow-up) over time. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**GROUPMEDSURVTIMES=***grouped-number-list*

**GMEDSURVTIMES=***grouped-number-list*

**GROUPMEDSURVTS=***grouped-number-list*

**GMEDSURVTS=***grouped-number-list*

specifies the median survival times in each group. When the [GROUPMEDSURVTIMES=](#) option is used, the survival curve in each group is assumed to be exponential. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**GROUPNS=***grouped-number-list*

**GNS=***grouped-number-list*

specifies the two group sample sizes. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**GROUPSURVEXPHAZARDS=***grouped-number-list*

**GSURVEXPHAZARDS=***grouped-number-list*

**GROUPSURVEXPHS=***grouped-number-list*

**GEXPHS=***grouped-number-list*

specifies exponential hazard rates of the survival curve for each group. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**GROUPSURVIVAL**=*grouped-name-list*

**GSURVIVAL**=*grouped-name-list*

**GROUPSURV**=*grouped-name-list*

**GSURV**=*grouped-name-list*

specifies the survival curve for each group, by using labels specified with the **CURVE**= option. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-name-list*.

**GROUPWEIGHTS**=*grouped-number-list*

**GWEIGHTS**=*grouped-number-list*

specifies the sample size allocation weights for the two groups. This option controls how the total sample size is divided between the two groups. Each pair of values for the two groups represents relative allocation weights. Additionally, if the **NFRACTIONAL** option is not used, the total sample size is restricted to be equal to a multiple of the sum of the two group weights (so that the resulting design has an integer sample size for each group while adhering exactly to the group allocation weights). Values must be integers unless the **NFRACTIONAL** option is used. The default value is (1 1), a balanced design with a weight of 1 for each group. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

**HAZARDRATIO**=*number-list*

**HR**=*number-list*

specifies the hazard ratio of the second group’s survival curve to the first group’s survival curve. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NFRACTIONAL**

**NFRAC**

enables fractional input and output for sample sizes. See the section “[Sample Size Adjustment Options](#)” on page 4916 for information about the ramifications of the presence (and absence) of the **NFRACTIONAL** option.

**NPERGROUP**=*number-list*

**NPERG**=*number-list*

specifies the common sample size per group or requests a solution for the common sample size per group with a missing value (**NPERGROUP**=.). Use of this option implicitly specifies a balanced design. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NSUBINTERVAL**=*number-list*

**NSUBINTERVALS**=*number-list*

**NSUB**=*number-list*

**NSUBS**=*number-list*

specifies the number of subintervals per unit time to use in internal calculations. Higher values increase computational time and memory requirements but generally lead to more accurate results. The default value is 12. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**NTOTAL=number-list**

specifies the sample size or requests a solution for the sample size with a missing value (**NTOTAL=.**). See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**OUTPUTORDER=INTERNAL****OUTPUTORDER=REVERSE****OUTPUTORDER=SYNTAX**

controls how the input and default analysis parameters are ordered in the output. **OUTPUTORDER=INTERNAL** (the default) arranges the parameters in the output according to the following order of their corresponding options:

- **SIDES=**
- **ACCRUALTIME=**
- **FOLLOWUPTIME=**
- **TOTALTIME=**
- **NSUBINTERVAL=**
- **ALPHA=**
- **REFSURVIVAL=**
- **GROUPSURVIVAL=**
- **REFSURVEXPHAZARD=**
- **HAZARDRATIO=**
- **GROUPSURVEXPHAZARDS=**
- **GROUPMEDSURVTIMES=**
- **GROUPLOSSEXPHAZARDS=**
- **GROUPLOSS=**
- **GROUPMEDLOSSTIMES=**
- **GROUPWEIGHTS=**
- **NTOTAL=**
- **NPERGROUP=**
- **GROUPNS=**
- **POWER=**

The **OUTPUTORDER=SYNTAX** option arranges the parameters in the output in the same order in which their corresponding options are specified in the **TWOSAMPLESURVIVAL** statement. The **OUTPUTORDER=REVERSE** option arranges the parameters in the output in the reverse of the order in which their corresponding options are specified in the **TWOSAMPLESURVIVAL** statement.

**POWER=number-list**

specifies the desired power of the test or requests a solution for the power with a missing value (**POWER=.**). The power is expressed as a probability, a number between 0 and 1, rather than as a percentage. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**REFSURVEXPHAZARD=***number-list*

**REFSURVEXPH=***number-list*

specifies the exponential hazard rate of the survival curve for the first (reference) group. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**REFSURVIVAL=***name-list*

**REFSURV=***name-list*

specifies the survival curve for the first (reference) group, by using labels specified with the **CURVE=** option. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *name-list*.

**SIDES=***keyword-list*

specifies the number of sides (or tails) and the direction of the statistical test or confidence interval. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *keyword-list*. Valid keywords and their interpretation are as follows:

- 1 one-sided with alternative hypothesis in same direction as effect
- 2 two-sided
- U upper one-sided with the alternative hypothesis favoring better survival in the second group
- L lower one-sided with the alternative hypothesis favoring better survival in the first (reference) group

The default value is 2.

**TEST=GEHAN**

**TEST=LOGRANK**

**TEST=TARONEWARE**

specifies the statistical analysis. **TEST=GEHAN** specifies the Gehan rank test. **TEST=LOGRANK** (the default) specifies the log-rank test. **TEST=TARONEWARE** specifies the Tarone-Ware rank test.

**TOTALTIME=***number-list* | **MAX**

**TOTALT=***number-list* | **MAX**

specifies the total time, which is equal to the sum of accrual and follow-up times. If the **GROUPSURVIVAL=** or **REFSURVIVAL=** option is used, then the value of the total time must be less than or equal to the largest time in *each* multipoint (piecewise linear) survival curve. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**TOTALTIME=MAX** can be used when each scenario in the analysis contains at least one piecewise linear survival curve (in the **GROUPSURVIVAL=** or **REFSURVIVAL=** option). It causes the total time to be automatically set, separately for each scenario, to the maximum possible time supported by the piecewise linear survival curve(s) in that scenario. It is not compatible with the **ACCRUALTIME=MAX** option or the **FOLLOWUPTIME=MAX** option.

## Restrictions on Option Combinations

To specify the survival curves, choose one of the following parameterizations:

- arbitrary piecewise linear or exponential curves (by using the `CURVE=` and `GROUPSURVIVAL=` options)
- curves with proportional hazards (by using the `CURVE=`, `REFSURVIVAL=`, and `HAZARDRATIO=` options)
- exponential curves, by using one of the following parameterizations:
  - median survival times (by using the `GROUPMEDSURVTIMES=` option)
  - the hazard ratio and the hazard of the reference curve (by using the `HAZARDRATIO=` and `REFSURVEXPHAZARD=` options)
  - the individual hazards (by using the `GROUPSURVEXPHAZARDS=` option)

To specify the study time, use any two of the following three options:

- accrual time (by using the `ACCRUALTIME=` option)
- follow-up time (by using the `FOLLOWUPTIME=` option)
- total time, the sum of accrual and follow-up times (by using the `TOTALTIME=` option)

To specify the sample size and allocation, choose one of the following parameterizations:

- sample size per group in a balanced design (by using the `NPERGROUP=` option)
- total sample size and allocation weights (by using the `NTOTAL=` and `GROUPWEIGHTS=` options)
- individual group sample sizes (by using the `GROUPNS=` option)

To specify the exponential loss curves, choose one of the following parameterizations:

- a point on the loss curve of each group (by using the `CURVE=` and `GROUPLOSS=` options)
- median loss times (by using the `GROUPMEDLOSSTIMES=` option)
- the individual loss hazards (by using the `GROUPLOSSEXPHAZARDS=` option)

## Option Groups for Common Analyses

This section summarizes the syntax for the common analyses supported in the `TWOSAMPLESURVIVAL` statement.

### Log-Rank Test for Two Survival Curves

You can use the `NPERGROUP=` option in a balanced design and specify piecewise linear or exponential survival curves by using the `CURVE=` and `GROUPSURVIVAL=` options, as in the following statements. Default values for the `SIDES=`, `ALPHA=`, `NSUBINTERVAL=`, and `GROUPLOSSEXPHAZARDS=` options specify a two-sided test with a significance level of 0.05, an assumption of no loss to follow-up, and the use of 12 subintervals per unit time in computations.

```
proc power;
  twosamplesurvival test=logrank
    curve("Control") = (1 2 3):(0.8 0.7 0.6)
    curve("Treatment") = (5):(.6)
    groupsurvival = "Control" | "Treatment"
    accrualtime = 2
    followuptime = 1
    npergroup = 50
    power = .;
run;
```

In the preceding example, the “Control” curve is piecewise linear (since it has more than one point), and the “Treatment” curve is exponential (since it has only one point).

You can also specify an unbalanced design by using the `NTOTAL=` and `GROUPWEIGHTS=` options and specify piecewise linear or exponential survival curves with proportional hazards by using the `CURVE=`, `REFSURVIVAL=`, and `HAZARDRATIO=` options:

```
proc power;
  twosamplesurvival test=logrank
    curve("Control") = (1 2 3):(0.8 0.7 0.6)
    refsurvival = "Control"
    hazardratio = 1.5
    accrualtime = 2
    followuptime = 1
    groupweights = (1 2)
    ntotal = .
    power = 0.8;
run;
```

You can also specify sample sizes with the `GROUPNS=` option and specify exponential survival curves in terms of median survival times:

```
proc power;
  twosamplesurvival test=logrank
    groupmedsurvtimes = (16 22)
    accrualtime = 6
    totaltime = 18
    groupns = 40 | 60
    power = .;
run;
```

You can also specify exponential survival curves in terms of the hazard ratio and reference hazard. The default value of the `GROUPWEIGHTS=` option specifies a balanced design.

```

proc power;
  twosamplesurvival test=logrank
    hazardratio = 1.2
    refsurvexphazard = 0.7
    accrualtime = 2
    totaltime = 4
    ntotal = 100
    power = .;
run;

```

You can also specify exponential survival curves in terms of the individual hazards, as in the following statements:

```

proc power;
  twosamplesurvival test=logrank
    groupsurvexphazards = 0.7 | 0.84
    accrualtime = 2
    totaltime = 4
    ntotal = .
    power = 0.9;
run;

```

### ***Gehan Rank Test for Two Survival Curves***

In addition to the logrank test, you can also specify the Gehan tank test, as in the following statements. Default values for the `SIDES=`, `ALPHA=`, `NSUBINTERVAL=`, and `GROUPLOSSEXPHAZARDS=` options specify a two-sided test with a significance level of 0.05, an assumption of no loss to follow-up, and the use of 12 subintervals per unit time in computations.

```

proc power;
  twosamplesurvival test=gehan
    groupmedsurvtimes = 5 | 7
    accrualtime = 3
    totaltime = 6
    npergroup = .
    power = 0.8;
run;

```

### ***Tarone-Ware Rank Test for Two Survival Curves***

You can also specify the Tarone-Ware tank test, as in the following statements. Default values for the `SIDES=`, `ALPHA=`, `NSUBINTERVAL=`, and `GROUPLOSSEXPHAZARDS=` options specify a two-sided test with a significance level of 0.05, an assumption of no loss to follow-up, and the use of 12 subintervals per unit time in computations.

```

proc power;
  twosamplesurvival test=taroneware
    groupmedsurvtimes = 5 | 7
    accrualtime = 3
    totaltime = 6
    npergroup = 100
    power = .;
run;

```

## TWOSAMPLEWILCOXON Statement

**TWOSAMPLEWILCOXON** < options > ;

The **TWOSAMPLEWILCOXON** statement performs power and sample size analyses for the Wilcoxon-Mann-Whitney test (also called the Wilcoxon rank-sum test, Mann-Whitney-Wilcoxon test, or Mann-Whitney U test) for two independent groups.

Note that the O'Brien-Castelloe approach to computing power for the Wilcoxon test is approximate, based on asymptotic behavior as the total sample size gets large. The quality of the power approximation degrades for small sample sizes; conversely, the quality of the sample size approximation degrades if the two distributions are far apart, so that only a small sample is needed to detect a significant difference. But this degradation is rarely a problem in practical situations, in which experiments are usually performed for relatively close distributions.

### Summary of Options

Table 67.25 summarizes categories of options available in the **TWOSAMPLEWILCOXON** statement.

**Table 67.25** Summary of Options in the TWOSAMPLEWILCOXON Statement

Task	Options
Define analysis	TEST=
Specify analysis information	ALPHA= SIDES=
Specify distributions	VARDIST= VARIABLES=
Specify sample size and allocation	GROUPNS= GROUPWEIGHTS= NPERGROUP= NTOTAL=
Specify power	POWER=
Control sample size rounding	NFRACTIONAL
Specify computational options	NBINS=
Control ordering in output	OUTPUTORDER=

Table 67.26 summarizes the valid result parameters in the **TWOSAMPLEWILCOXON** statement.

**Table 67.26** Summary of Result Parameters in the TWOSAMPLEWILCOXON Statement

Analyses	Solve For	Syntax
TEST=WMW	Power	POWER=.
	Sample size	NTOTAL=.
		NPERGROUP=.

## Dictionary of Options

### **ALPHA=***number-list*

specifies the level of significance of the statistical test. The default is 0.05, corresponding to the usual  $0.05 \times 100\% = 5\%$  level of significance. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### **GROUPNS=***grouped-number-list*

### **GNS=***grouped-number-list*

specifies the two group sample sizes. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

### **GROUPWEIGHTS=***grouped-number-list*

### **GWEIGHTS=***grouped-number-list*

specifies the sample size allocation weights for the two groups. This option controls how the total sample size is divided between the two groups. Each pair of values for the two groups represents relative allocation weights. Additionally, if the **NFRACTIONAL** option is not used, the total sample size is restricted to be equal to a multiple of the sum of the two group weights (so that the resulting design has an integer sample size for each group while adhering exactly to the group allocation weights). Values must be integers unless the **NFRACTIONAL** option is used. The default value is (1 1), a balanced design with a weight of 1 for each group. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-number-list*.

### **NBINS=***number-list*

specifies the number of categories (or “bins”) each variable’s distribution is divided into (unless it is ordinal, in which case the categories remain intact) in internal calculations. Higher values increase computational time and memory requirements but generally lead to more accurate results. However, if the value is too high, then numerical instability can occur. The default value is 1000. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### **NFRACTIONAL**

### **NFRAC**

enables fractional input and output for sample sizes. See the section “[Sample Size Adjustment Options](#)” on page 4916 for information about the ramifications of the presence (and absence) of the **NFRACTIONAL** option.

### **NPERGROUP=***number-list*

### **NPERG=***number-list*

specifies the common sample size per group or requests a solution for the common sample size per group with a missing value (**NPERGROUP=.**). Use of this option implicitly specifies a balanced design. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

### **NTOTAL=***number-list*

specifies the sample size or requests a solution for the sample size with a missing value (**NTOTAL=.**). See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**OUTPUTORDER=INTERNAL****OUTPUTORDER=REVERSE****OUTPUTORDER=SYNTAX**

controls how the input and default analysis parameters are ordered in the output. **OUTPUTORDER=INTERNAL** (the default) arranges the parameters in the output according to the following order of their corresponding options:

- SIDES
- NBINS=
- ALPHA=
- VARIABLES=
- GROUPWEIGHTS=
- NTOTAL=
- NPERGROUP=
- GROUPNS=
- POWER=

The **OUTPUTORDER=SYNTAX** option arranges the parameters in the output in the same order in which their corresponding options are specified in the **TWOSAMPLEWILCOXON** statement. The **OUTPUTORDER=REVERSE** option arranges the parameters in the output in the reverse of the order in which their corresponding options are specified in the **TWOSAMPLEWILCOXON** statement.

**POWER=number-list**

specifies the desired power of the test or requests a solution for the power with a missing value (**POWER=.**). The power is expressed as a probability, a number between 0 and 1, rather than as a percentage. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *number-list*.

**SIDES=keyword-list**

specifies the number of sides (or tails) and the direction of the statistical test. Valid keywords are as follows:

- |   |   |
|---|---|
| 1 | one-sided with alternative hypothesis in same direction as effect |
| 2 | two-sided   |
| U | upper one-sided with alternative greater than null value          |
| L | lower one-sided with alternative less than null value             |

The default value is 2.

**TEST=WMW**

specifies the Wilcoxon-Mann-Whitney test for two independent groups. This is the default test option.

**VARDIST("label")=distribution (parameters)**  
 defines a distribution for a variable.

For the **VARDIST=** option,

*label* identifies the variable distribution in the output and with the **VARIABLES=** option.

*distribution* specifies the distributional form of the variable.

*parameters* specifies one or more parameters associated with the distribution.

Choices for distributional forms and their parameters are as follows:

**ORDINAL** (*(values) : (probabilities)*) is an ordered categorical distribution. The *values* are any numbers separated by spaces. The *probabilities* are numbers between 0 and 1 (inclusive) separated by spaces. Their sum must be exactly 1. The number of *probabilities* must match the number of *values*.

**BETA** (*a, b <, l, r >*) is a beta distribution with shape parameters *a* and *b* and optional location parameters *l* and *r*. The values of *a* and *b* must be greater than 0, and *l* must be less than *r*. The default values for *l* and *r* are 0 and 1, respectively.

**BINOMIAL** (*p, n*) is a binomial distribution with probability of success *p* and number of independent Bernoulli trials *n*. The value of *p* must be greater than 0 and less than 1, and *n* must be an integer greater than 0.

**EXPONENTIAL** (*λ*) is an exponential distribution with scale *λ*, which must be greater than 0.

**GAMMA** (*a, λ*) is a gamma distribution with shape *a* and scale *λ*. The values of *a* and *λ* must be greater than 0.

**LAPLACE** (*θ, λ*) is a Laplace distribution with location *θ* and scale *λ*. The value of *λ* must be greater than 0.

**LOGISTIC** (*θ, λ*) is a logistic distribution with location *θ* and scale *λ*. The value of *λ* must be greater than 0.

**LOGNORMAL** (*θ, λ*) is a lognormal distribution with location *θ* and scale *λ*. The value of *λ* must be greater than 0.

**NORMAL** (*θ, λ*) is a normal distribution with mean *θ* and standard deviation *λ*. The value of *λ* must be greater than 0.

**POISSON** (*m*) is a Poisson distribution with mean *m*. The value of *m* must be greater than 0.

**UNIFORM** (*l, r*) is a uniform distribution on the interval [*l, r*], where *l* < *r*.

**VARIABLES=grouped-name-list**

**VAR=grouped-name-list**

specifies the distributions of two or more variables, using labels specified with the **VARDIST=** option. See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for information about specifying the *grouped-name-list*.

## Restrictions on Option Combinations

To specify the sample size and allocation, choose one of the following parameterizations:

- sample size per group in a balanced design (using the `NPERGROUP=` option)
- total sample size and allocation weights (using the `NTOTAL=` and `GROUPWEIGHTS=` options)
- individual group sample sizes (using the `GROUPNS=` option)

## Option Groups for Common Analyses

This section summarizes the syntax for the common analyses supported in the `TWOSAMPLEWILCOXON` statement.

### *Wilcoxon-Mann-Whitney Test for Comparing Two Distributions*

The following statements performs a power analysis for Wilcoxon-Mann-Whitney tests comparing an ordinal variable with each other type of distribution. Default values for the `ALPHA=`, `NBINS=`, `SIDES=`, and `TEST=` options specify a two-sided test with a significance level of 0.05 and the use of 1000 categories per distribution when discretization is needed.

```
proc power;
  twosamplewilcoxon
    vardist("myordinal") = ordinal ((0 1 2) : (.2 .3 .5))
    vardist("mybeta1") = beta (1, 2)
    vardist("mybeta2") = beta (1, 2, 0, 2)
    vardist("mybinomial") = binomial (.3, 3)
    vardist("myexponential") = exponential (2)
    vardist("mygamma") = gamma (1.5, 2)
    vardist("mylaplace") = laplace (1, 2)
    vardist("mylogistic") = logistic (1, 2)
    vardist("mylognormal") = lognormal (1, 2)
    vardist("mynormal") = normal (3, 2)
    vardist("mypoisson") = poisson (2)
    vardist("myuniform") = uniform (0, 2)
    variables = "myordinal" | "mybeta1" "mybeta2" "mybinomial"
                "myexponential" "mygamma" "mylaplace"
                "mylogistic" "mylognormal" "mynormal"
                "mypoisson" "myuniform"

    ntotal = 40
    power = .;
run;
```

---

## Details: POWER Procedure

---

### Overview of Power Concepts

In statistical hypothesis testing, you typically express the belief that some effect exists in a population by specifying an alternative hypothesis  $H_1$ . You state a null hypothesis  $H_0$  as the assertion that the effect does *not* exist and attempt to gather evidence to reject  $H_0$  in favor of  $H_1$ . Evidence is gathered in the form of sample data, and a statistical test is used to assess  $H_0$ . If  $H_0$  is rejected but there really is *no* effect, this is called a *Type I error*. The probability of a Type I error is usually designated “alpha” or  $\alpha$ , and statistical tests are designed to ensure that  $\alpha$  is suitably small (for example, less than 0.05).

If there really is an effect in the population but  $H_0$  is *not* rejected in the statistical test, then a *Type II error* has been made. The probability of a Type II error is usually designated “beta” or  $\beta$ . The probability  $1 - \beta$  of avoiding a Type II error—that is, correctly rejecting  $H_0$  and achieving statistical significance—is called the *power*. (**NOTE:** Another more general definition of power is the probability of rejecting  $H_0$  for any given set of circumstances, even those corresponding to  $H_0$  being true. The POWER procedure uses this more general definition.)

An important goal in study planning is to ensure an acceptably high level of power. Sample size plays a prominent role in power computations because the focus is often on determining a sufficient sample size to achieve a certain power, or assessing the power for a range of different sample sizes.

Some of the analyses in the POWER procedure focus on *precision* rather than power. An analysis of confidence interval precision is analogous to a traditional power analysis, with “CI Half-Width” taking the place of effect size and “Prob(Width)” taking the place of power. The *CI Half-Width* is the margin of error associated with the confidence interval, the distance between the point estimate and an endpoint. The *Prob(Width)* is the probability of obtaining a confidence interval with *at most* a target half-width.

---

### Summary of Analyses

Table 67.27 gives a summary of the analyses supported in the POWER procedure. The name of the analysis statement reflects the type of data and design. The TEST=, CI=, and DIST= options specify the focus of the statistical hypothesis (in other words, the criterion on which the research question is based) and the test statistic to be used in data analysis.

**Table 67.27** Summary of Analyses

Analysis	Statement	Options
Logistic regression: likelihood ratio chi-square test	LOGISTIC	
Multiple linear regression: Type III $F$ test	MULTREG	
Correlation: Fisher's $z$ test	ONECORR	DIST=FISHERZ
Correlation: $t$ test	ONECORR	DIST=T
Binomial proportion: exact test	ONESAMPLEFREQ	TEST=EXACT
Binomial proportion: $z$ test	ONESAMPLEFREQ	TEST=Z
Binomial proportion: $z$ test with continuity adjustment	ONESAMPLEFREQ	TEST=ADJZ
Binomial proportion: exact equivalence test	ONESAMPLEFREQ	TEST=EQUIV_EXACT
Binomial proportion: $z$ equivalence test	ONESAMPLEFREQ	TEST=EQUIV_Z
Binomial proportion: $z$ test with continuity adjustment	ONESAMPLEFREQ	TEST=EQUIV_ADJZ
Binomial proportion: confidence interval	ONESAMPLEFREQ	CI=AGRESTICOULL  CI=JEFFREYS CI=EXACT CI=WALD CI=WALD_CORRECT CI=WILSON
One-sample $t$ test	ONESAMPLEMEANS	TEST=T
One-sample $t$ test with lognormal data	ONESAMPLEMEANS	TEST=T DIST=LOGNORMAL
One-sample equivalence test for mean of normal data	ONESAMPLEMEANS	TEST=EQUIV
One-sample equivalence test for mean of lognormal data	ONESAMPLEMEANS	TEST=EQUIV DIST=LOGNORMAL
Confidence interval for a mean	ONESAMPLEMEANS	CI=T
One-way ANOVA: one-degree-of-freedom contrast	ONEWAYANOVA	TEST=CONTRAST
One-way ANOVA: overall $F$ test	ONEWAYANOVA	TEST=OVERALL
McNemar exact conditional test	PAIREDFREQ	
McNemar normal approximation test	PAIREDFREQ	DIST=NORMAL

Table 67.27 *continued*

Analysis	Statement	Options
Paired $t$ test	PAIREDMEANS	TEST=DIFF
Paired $t$ test of mean ratio with lognormal data	PAIREDMEANS	TEST=RATIO
Paired additive equivalence of mean difference with normal data	PAIREDMEANS	TEST=EQUIV_DIFF
Paired multiplicative equivalence of mean ratio with lognormal data	PAIREDMEANS	TEST=EQUIV_RATIO
Confidence interval for mean of paired differences	PAIREDMEANS	CI=DIFF
Pearson chi-square test for two independent proportions	TWOSAMPLEFREQ	TEST=PCHI
Fisher's exact test for two independent proportions	TWOSAMPLEFREQ	TEST=FISHER
Likelihood ratio chi-square test for two independent proportions	TWOSAMPLEFREQ	TEST=LRCHI
Two-sample $t$ test assuming equal variances	TWOSAMPLEMEANS	TEST=DIFF
Two-sample Satterthwaite $t$ test assuming unequal variances	TWOSAMPLEMEANS	TEST=DIFF_SATT
Two-sample pooled $t$ test of mean ratio with lognormal data	TWOSAMPLEMEANS	TEST=RATIO
Two-sample additive equivalence of mean difference with normal data	TWOSAMPLEMEANS	TEST=EQUIV_DIFF
Two-sample multiplicative equivalence of mean ratio with lognormal data	TWOSAMPLEMEANS	TEST=EQUIV_RATIO
Two-sample confidence interval for mean difference	TWOSAMPLEMEANS	CI=DIFF
Log-rank test for comparing two survival curves	TWOSAMPLESURVIVAL	TEST=LOGRANK
Gehan rank test for comparing two survival curves	TWOSAMPLESURVIVAL	TEST=GEHAN
Tarone-Ware rank test for comparing two survival curves	TWOSAMPLESURVIVAL	TEST=TARONEWARE
Wilcoxon-Mann-Whitney (rank-sum) test	TWOSAMPLEWILCOXON	

## Specifying Value Lists in Analysis Statements

To specify one or more scenarios for an analysis parameter (or set of parameters), you provide a list of values for the statement option that corresponds to the parameter(s). To identify the parameter you want to solve for, you place missing values in the appropriate list.

There are five basic types of such lists: *keyword-lists*, *number-lists*, *grouped-number-lists*, *name-lists*, and *grouped-name-lists*. Some parameters, such as the direction of a test, have values represented by one or more keywords in a *keyword-list*. Scenarios for scalar-valued parameters, such as power, are represented by a *number-list*. Scenarios for groups of scalar-valued parameters, such as group sample sizes in a multigroup design, are represented by a *grouped-number-list*. Scenarios for named parameters, such as reference survival curves, are represented by a *name-list*. Scenarios for groups of named parameters, such as group survival curves, are represented by a *grouped-name-list*.

The following subsections explain these five basic types of lists.

### Keyword-Lists

A *keyword-list* is a list of one or more keywords separated by spaces. For example, you can specify both two-sided and upper-tailed versions of a one-sample *t* test:

```
SIDES = 2 U
```

### Number-Lists

A *number-list* can be one of two things: a series of one or more numbers expressed in the form of one or more DOLISTs, or a missing value indicator (.).

The DOLIST format is the same as in the DATA step language. For example, for the one-sample *t* test you can specify four scenarios (30, 50, 70, and 100) for a total sample size in any of the following ways.

```
NTOTAL = 30 50 70 100
NTOTAL = 30 to 70 by 20 100
```

A missing value identifies a parameter as the result parameter; it is valid only with options representing parameters you can solve for in a given analysis. For example, you can request a solution for NTOTAL:

```
NTOTAL = .
```

### Grouped-Number-Lists

A *grouped-number-list* specifies multiple scenarios for numeric values in two or more groups, possibly including missing value indicators to solve for a specific group. The list can assume one of two general forms, a “crossed” version and a “matched” version.

**Crossed Grouped-Number-Lists**

The crossed version of a grouped number list consists of a series of *number-lists* (see the section “Number-Lists” on page 4913), one representing each group, with groups separated by a vertical bar (|). The values for each group represent multiple scenarios for that group, and the scenarios for each individual group are crossed to produce the set of all scenarios for the analysis option. For example, you can specify the following six scenarios for the sizes ( $n_1, n_2$ ) of two groups

```
(20, 30)(20, 40)(20, 50)
(25, 30)(25, 40)(25, 50)
```

as follows:

```
GROUPNS = 20 25 | 30 40 50
```

If the analysis can solve for a value in one group given the other groups, then one of the *number-lists* in a *crossed grouped-number-list* can be a missing value indicator (.). For example, in a two-sample  $t$  test you can posit three scenarios for the group 2 sample size while solving for the group 1 sample size:

```
GROUPNS = . | 30 40 50
```

Some analyses can involve more than two groups. For example, you can specify  $2 \times 3 \times 1 = 6$  scenarios for the means of three groups in a one-way ANOVA as follows:

```
GROUPMEANS = 10 12 | 10 to 20 by 5 | 24
```

**Matched Grouped-Number-Lists**

The matched version of a grouped number list consists of a series of numeric lists, each enclosed in parentheses. Each list consists of a value for each group and represents a single scenario for the analysis option. Multiple scenarios for the analysis option are represented by multiple lists. For example, you can express the crossed grouped-number-list

```
GROUPNS = 20 25 | 30 40 50
```

alternatively in a matched format:

```
GROUPNS = (20 30) (20 40) (20 50) (25 30) (25 40) (25 50)
```

The matched version is particularly useful when you want to include only a subset of all combinations of individual group values. For example, you might want to pair 20 only with 50, and 25 only with 30 and 40:

```
GROUPNS = (20 50) (25 30) (25 40)
```

If the analysis can solve for a value in one group given the other groups, then you can replace the value for that group with a missing value indicator (.). If used, the missing value indicator must occur in the same group in every scenario. For example, you can solve for the group 1 sample size (as in the section “[Crossed Grouped-Number-Lists](#)” on page 4914) by using a matched format:

```
GROUPNS = (. 30) (. 40) (. 50)
```

Some analyses can involve more than two groups. For example, you can specify two scenarios for the means of three groups in a one-way ANOVA:

```
GROUPMEANS = (15 24 32) (12 25 36)
```

## Name-Lists

A *name-list* is a list of one or more names in single or double quotes, separated by spaces. For example, you can specify two scenarios for the reference survival curve in a log-rank test:

```
REFSURVIVAL = "Curve A" "Curve B"
```

## Grouped-Name-Lists

A *grouped-name-list* specifies multiple scenarios for names in two or more groups. The list can assume one of two general forms, a “crossed” version and a “matched” version.

### Crossed Grouped-Name-Lists

The crossed version of a grouped name list consists of a series of *name-lists* (see the section “[Name-Lists](#)” on page 4915), one representing each group, with groups separated by a vertical bar (|). The values for each group represent multiple scenarios for that group, and the scenarios for each individual group are crossed to produce the set of all scenarios for the analysis option. For example, you can specify the following six scenarios for the survival curves ( $c_1, c_2$ ) of two groups

```
(“Curve A”, “Curve C”)(“Curve A”, “Curve D”)(“Curve A”, “Curve E”)
(“Curve B”, “Curve C”)(“Curve B”, “Curve D”)(“Curve B”, “Curve E”)
```

as follows:

```
GROUPSURVIVAL = "Curve A" "Curve B" | "Curve C" "Curve D"
                "Curve E"
```

### Matched Grouped-Name-Lists

The matched version of a grouped name list consists of a series of name lists, each enclosed in parentheses. Each list consists of a name for each group and represents a single scenario for the analysis option. Multiple scenarios for the analysis option are represented by multiple lists. For example, you can express the crossed grouped-name-list

```
GROUPSURVIVAL = "Curve A" "Curve B" | "Curve C" "Curve D"
                "Curve E"
```

alternatively in a matched format:

```
GROUPSURVIVAL = ("Curve A" "Curve C")
                 ("Curve A" "Curve D")
                 ("Curve A" "Curve E")
                 ("Curve B" "Curve C")
                 ("Curve B" "Curve D")
                 ("Curve B" "Curve E")
```

The matched version is particularly useful when you want to include only a subset of all combinations of individual group values. For example, you might want to pair “Curve A” only with “Curve C”, and “Curve B” only with “Curve D” and “Curve E”:

```
GROUPSURVIVAL = ("Curve A" "Curve C")
                 ("Curve B" "Curve D")
                 ("Curve B" "Curve E")
```

---

## Sample Size Adjustment Options

By default, PROC POWER rounds sample sizes conservatively (down in the input, up in the output) so that all total sizes (and individual group sample sizes, if a multigroup design) are integers. This is generally considered conservative because it selects the closest realistic design providing *at most* the power of the (possibly fractional) input or mathematically optimized design. In addition, in a multigroup design, all group sizes are adjusted to be multiples of the corresponding group weights. For example, if GROUPWEIGHTS = (2 6), then all group 1 sample sizes become multiples of 2, and all group 2 sample sizes become multiples of 6 (and all total sample sizes become multiples of 8).

With the NFRACTIONAL option, sample size input is not rounded, and sample size output (whether total or groupwise) are reported in two versions, a raw “fractional” version and a “ceiling” version rounded up to the nearest integer.

Whenever an input sample size is adjusted, both the original (“nominal”) and adjusted (“actual”) sample sizes are reported. Whenever computed output sample sizes are adjusted, both the original input (“nominal”) power and the achieved (“actual”) power at the adjusted sample size are reported.

---

## Error and Information Output

The Error column in the main output table provides reasons for missing results and flags numerical results that are bounds rather than exact answers. For example, consider the sample size analysis implemented by the following statements:

```

proc power;
  twosamplefreq test=pchi
    method=normal
    oddsratio= 1.0001
    refproportion=.4
    nulloddsratio=1
    power=.9
    ntotal=.;
run;

```

Figure 67.6 Error Column

The POWER Procedure			
Pearson Chi-square Test for Two Proportions			
Fixed Scenario Elements			
Distribution	Asymptotic normal		
Method	Normal approximation		
Null Odds Ratio	1		
Reference (Group 1) Proportion	0.4		
Odds Ratio	1.0001		
Nominal Power	0.9		
Number of Sides	2		
Alpha	0.05		
Group 1 Weight	1		
Group 2 Weight	1		
Computed N Total			
Actual			
Power	N Total	Error	
0.206	2.15E+09	Solution is a lower bound	

The output in Figure 67.6 reveals that the sample size to achieve a power of 0.9 could not be computed, but that the sample size 2.15E+09 achieves a power of 0.206.

The Info column provides further details about Error column entries, warnings about any boundary conditions detected, and notes about any adjustments to input. Note that the Info column is hidden by default in the main output. You can view it by using the ODS OUTPUT statement to save the output as a data set and the PRINT procedure. For example, the following SAS statements print both the Error and Info columns for a power computation in a two-sample  $t$  test:

```

proc power;
  twosamplemeans
    meandiff= 0 7
    stddev=2
    ntotal=2 5
    power=.;
  ods output output=Power;
run;

proc print noobs data=Power;
  var MeanDiff NominalNTotal NTotal Power Error Info;
run;

```

The output is shown in [Figure 67.7](#).

**Figure 67.7** Error and Info Columns

Mean Diff	Nominal NTotal	NTotal	Power	Error	Info
0	2	2	.	Invalid input	N too small / No effect
0	5	4	0.050		Input N adjusted / No effect
7	2	2	.	Invalid input	N too small
7	5	4	0.477		Input N adjusted

The mean difference of 0 specified with the `MEANDIFF=` option leads to a “No effect” message to appear in the Info column. The sample size of 2 specified with the `NTOTAL=` option leads to an “Invalid input” message in the Error column and an “NTotal too small” message in the Info column. The sample size of 5 leads to an “Input N adjusted” message in the Info column because it is rounded down to 4 to produce integer group sizes of 2 per group.

---

## Displayed Output

If you use the `PLOTONLY` option in the `PROC POWER` statement, the procedure displays only graphical output. Otherwise, the displayed output of the POWER procedure includes the following:

- the “Fixed Scenario Elements” table, which shows all applicable single-valued analysis parameters, in the following order: distribution, method, parameters input explicitly, and parameters supplied with defaults
- an output table showing the following when applicable (in order): the index of the scenario, all multivalued input, ancillary results, the primary computed result, and error descriptions
- plots (if requested)

For each input parameter, the order of the input values is preserved in the output.

Ancillary results include the following:

- Actual Power, the achieved power, if it differs from the input (Nominal) power value
- Actual Prob(Width), the achieved precision probability, if it differs from the input (Nominal) probability value
- Actual Alpha, the achieved significance level, if it differs from the input (Nominal) alpha value
- fractional sample size, if the `NFRACTIONAL` option is used in the analysis statement

If sample size is the result parameter and the NFRACTIONAL option is used in the analysis statement, then both “Fractional” and “Ceiling” sample size results are displayed. Fractional sample sizes correspond to the “Nominal” values of power or precision probability. Ceiling sample sizes are simply the fractional sample sizes rounded up to the nearest integer; they correspond to “Actual” values of power or precision probability.

## ODS Table Names

PROC POWER assigns a name to each table that it creates. You can use these names to reference the table when using the Output Delivery System (ODS) to select tables and create output data sets. These names are listed in [Table 67.28](#). For more information about ODS, see Chapter 20, “Using the Output Delivery System.”

**Table 67.28** ODS Tables Produced by PROC POWER

ODS Table Name	Description	Statement
FixedElements	factoid with single-valued analysis parameters	default*
Output	all input and computed analysis parameters, error messages, and information messages for each scenario	default
PlotContent	data contained in plots, including analysis parameters and indices identifying plot features. (NOTE: This table is saved as a data set and not displayed in PROC POWER output.)	PLOT

\*Depends on input.

The ODS pathnames are created as follows:

- Power.<analysis statement name>< n >.FixedElements
- Power.<analysis statement name>< n >.Output
- Power.<analysis statement name>< n >.PlotContent
- Power.<analysis statement name>< n >.Plot< m >

where

- The Plot< m > objects are the graphs.
- The < n > indexing the analysis statement name is used only if there is more than one instance.
- The < n > indexing the plots increases with every panel in every plot statement, resetting to 1 only at new analysis statements.

---

## Computational Resources

### Memory

In the `TWOSAMPLESURVIVAL` statement, the amount of required memory is roughly proportional to the product of the number of subintervals (specified by the `NSUBINTERVAL=` option) and the total time of the study (specified by the `ACCRUALTIME=`, `FOLLOWUPTIME=`, and `TOTALTIME=` options). If you run out of memory, then you can try either specifying a smaller number of subintervals, changing the time scale to use a longer time unit (for example, years instead of months), or both.

### CPU Time

In the Satterthwaite  $t$  test analysis (`TWOSAMPLEMEANS TEST=DIFF_SATT`), the required CPU time grows as the mean difference decreases relative to the standard deviations. In the `PAIREDFREQ` statement, the required CPU time for the exact power computation (`METHOD=EXACT`) grows with the sample size.

---

## Computational Methods and Formulas

This section describes the approaches used in PROC POWER to compute power for each analysis. The first subsection defines some common notation. The following subsections describe the various power analyses, including discussions of the data, statistical test, and power formula for each analysis. Unless otherwise indicated, computed values for parameters besides power (for example, sample size) are obtained by solving power formulas for the desired parameters.

### Common Notation

Table 67.29 displays notation for some of the more common parameters across analyses. The Associated Syntax column shows examples of relevant analysis statement options, where applicable.

**Table 67.29** Common Notation

Symbol	Description	Associated Syntax
$\alpha$	significance level	ALPHA=
$N$	total sample size	NTOTAL=, NPAIRS=
$n_i$	sample size in $i$ th group	NPERGROUP=, GROUPNS=
$w_i$	allocation weight for $i$ th group (standardized to sum to 1)	GROUPWEIGHTS=
$\mu$	(arithmetic) mean	MEAN=

Table 67.29 continued

Symbol	Description	Associated Syntax
$\mu_i$	(arithmetic) mean in $i$ th group	GROUPMEANS=, PAIREDMEANS=
$\mu_{\text{diff}}$	(arithmetic) mean difference, $\mu_2 - \mu_1$ or $\mu_T - \mu_R$	MEANDIFF=
$\mu_0$	null mean or mean difference (arithmetic)	NULL=, NULLDIFF=
$\gamma$	geometric mean	MEAN=
$\gamma_i$	geometric mean in $i$ th group	GROUPMEANS=, PAIREDMEANS=
$\gamma_0$	null mean or mean ratio (geometric)	NULL=, NULLRATIO=
$\sigma$	standard deviation (or common standard deviation per group)	STDDEV=
$\sigma_i$	standard deviation in $i$ th group	GROUPSTDDEVS=, PAIREDSTDDEVS=
$\sigma_{\text{diff}}$	standard deviation of differences	
CV	coefficient of variation, defined as the ratio of the standard deviation to the (arithmetic) mean	CV=, PAIREDCVS=
$\rho$	correlation	CORR=
$\mu_T, \mu_R$	treatment and reference (arithmetic) means for equivalence test	GROUPMEANS=, PAIREDMEANS=
$\gamma_T, \gamma_R$	treatment and reference geometric means for equivalence test	GROUPMEANS=, PAIREDMEANS=
$\theta_L$	lower equivalence bound	LOWER=
$\theta_U$	upper equivalence bound	UPPER=
$t(\nu, \delta)$	$t$ distribution with d.f. $\nu$ and noncentrality $\delta$	
$F(\nu_1, \nu_2, \lambda)$	$F$ distribution with numerator d.f. $\nu_1$ , denominator d.f. $\nu_2$ , and noncentrality $\lambda$	
$t_{p;\nu}$	$p$ th percentile of $t$ distribution with d.f. $\nu$	
$F_{p;\nu_1,\nu_2}$	$p$ th percentile of $F$ distribution with numerator d.f. $\nu_1$ and denominator d.f. $\nu_2$	
Bin( $N, p$ )	binomial distribution with sample size $N$ and proportion $p$	

A “lower one-sided” test is associated with SIDES=L (or SIDES=1 with the effect smaller than the null value), and an “upper one-sided” test is associated with SIDES=U (or SIDES=1 with the effect larger than the null value).

Owen (1965) defines a function, known as Owen’s  $Q$ , that is convenient for representing terms in

power formulas for confidence intervals and equivalence tests:

$$Q_\nu(t, \delta; a, b) = \frac{\sqrt{2\pi}}{\Gamma(\frac{\nu}{2})2^{\frac{\nu-2}{2}}} \int_a^b \Phi\left(\frac{tx}{\sqrt{\nu}} - \delta\right) x^{\nu-1} \phi(x) dx$$

where  $\phi(\cdot)$  and  $\Phi(\cdot)$  are the density and cumulative distribution function of the standard normal distribution, respectively.

## Analyses in the LOGISTIC Statement

### Likelihood Ratio Chi-Square Test for One Predictor (TEST=LRCHI)

The power computing formula is based on Shieh and O'Brien (1998), Shieh (2000), and Self, Mauritsen, and Ohara (1992).

Define the following notation for a logistic regression analysis:

- $N$  = # subjects (NTOTAL)
- $K$  = # predictors (not counting intercept)
- $\mathbf{x} = (x_1, \dots, x_K)'$  = random variables for predictor vector
- $\boldsymbol{\mu} = (\mu_1, \dots, \mu_K)'$  =  $E\mathbf{x}$  = mean predictor vector
- $\mathbf{x}_i = (x_{i1}, \dots, x_{iK})'$  = predictor vector for subject  $i$  ( $i \in 1, \dots, N$ )
- $Y$  = random variable for response (0 or 1)
- $Y_i$  = response for subject  $i$  ( $i \in 1, \dots, N$ )
- $p_i = \text{Prob}(Y_i = 1 | \mathbf{x}_i)$  ( $i \in 1, \dots, N$ )
- $\phi = \text{Prob}(Y_i = 1 | \mathbf{x}_i = \boldsymbol{\mu})$  (RESPONSEPROB)
- $U_j$  = unit change for  $j$ th predictor (UNITS)
- $OR_j = \text{Odds}(Y_i = 1 | x_{ij} = c) / \text{Odds}(Y_i = 1 | x_{ij} = c - U_j)$  ( $c$  arbitrary,  $i \in 1, \dots, N$ ,  
 $j \in 1, \dots, K$ ) (TESTODDSRATIO if  $j = 1$ , COVODDSRATIOS if  $j > 1$ )
- $\Psi_0$  = intercept in full model (INTERCEPT)
- $\boldsymbol{\Psi} = (\Psi_1, \dots, \Psi_K)'$  = regression coefficients in full model  
( $\Psi_1 = \text{TESTREGCOEFF}$ , others = COVREGCOEFFS)
- $c_j$  = # distinct possible values of  $x_{ij}$  ( $j \in 1, \dots, K$ ) (for any  $i$ ) (NBINS)
- $x_{gj}^*$  =  $g$ th possible value of  $x_{ij}$  ( $g \in 1, \dots, c_j$ ) ( $j \in 1, \dots, K$ )  
(for any  $i$ ) (VARDIST)
- $\pi_{gj} = \text{Prob}(x_{ij} = x_{gj}^*)$  ( $g \in 1, \dots, c_j$ ) ( $j \in 1, \dots, K$ )  
(for any  $i$ ) (VARDIST)
- $C = \prod_{j=1}^K c_j$  = # possible values of  $\mathbf{x}_i$  (for any  $i$ )
- $\mathbf{x}_m^*$  =  $m$ th possible value of  $\mathbf{x}_i$  ( $m \in 1, \dots, C$ )
- $\pi_m = \text{Prob}(\mathbf{x}_i = \mathbf{x}_m^*)$  ( $m \in 1, \dots, C$ )

The logistic regression model is

$$\log\left(\frac{p_i}{1-p_i}\right) = \Psi_0 + \Psi' \mathbf{x}_i$$

The hypothesis test of the first predictor variable is

$$H_0: \Psi_1 = 0$$

$$H_1: \Psi_1 \neq 0$$

Assuming independence among all predictor variables,  $\pi_m$  is defined as follows:

$$\pi_m = \prod_{j=1}^K \pi_{h(m,j)j} \quad (m \in 1, \dots, C)$$

where  $h(m, j)$  is calculated according to the following algorithm:

```

z = m;
do j = K to 1;
    h(m, j) = mod(z - 1, c_j) + 1;
    z = floor((z - 1)/c_j) + 1;
end;
    
```

This algorithm causes the elements of the transposed vector  $\{h(m, 1), \dots, h(m, K)\}$  to vary fastest to slowest from right to left as  $m$  increases, as shown in the following table of  $h(m, j)$  values:

$h(m, j)$	$j$					
	1	2	...	$K-1$	$K$	
1	1	1	...	1	1	
1	1	1	...	1	2	
⋮				⋮		
⋮	1	1	...	1	$c_K$	
⋮	1	1	...	2	1	
⋮	1	1	...	2	2	
⋮				⋮		
$m$	⋮	1	1	...	2	$c_K$
⋮				⋮		
⋮	$c_1$	$c_2$	...	$c_{K-1}$	1	
⋮	$c_1$	$c_2$	...	$c_{K-1}$	2	
⋮				⋮		
$C$	$c_1$	$c_2$	...	$c_{K-1}$	$c_K$	

The  $\mathbf{x}_m^*$  values are determined in a completely analogous manner.

The discretization is handled as follows (unless the distribution is ordinal, or binomial with sample size parameter at least as large as requested number of bins): for  $x_j$ , generate  $c_j$  quantiles at evenly spaced probability values such that each such quantile is at the midpoint of a bin with probability  $\frac{1}{c_j}$ . In other words,

$$x_{gj}^* = \left( \frac{g - 0.5}{c_j} \right) \text{th quantile of relevant distribution,}$$

$$(g \in 1, \dots, c_j)(j \in 1, \dots, K)$$

$$\pi_{gj} = \frac{1}{c_j} \quad (\text{same for all } g)$$

The primary noncentrality for the power computation is

$$\Delta^* = 2 \sum_{m=1}^C \pi_m [b'(\theta_m) (\theta_m - \theta_m^*) - (b(\theta_m) - b(\theta_m^*))]$$

where

$$b'(\theta) = \frac{\exp(\theta)}{1 + \exp(\theta)}$$

$$b(\theta) = \log(1 + \exp(\theta))$$

$$\theta_m = \Psi_0 + \Psi' \mathbf{x}_m^*$$

$$\theta_m^* = \Psi_0^* + \Psi^{*'} \mathbf{x}_m^*$$

where

$$\Psi_0^* = \Psi_0 + \Psi_1 \mu_1 = \text{intercept in reduced model, absorbing the tested predictor}$$

$$\Psi^* = (0, \Psi_2, \dots, \Psi_K)' = \text{coefficients in reduced model}$$

The power is

$$\text{power} = P(\chi^2(1, \Delta^* N) \geq \chi_{1-\alpha}^2(1))$$

Alternative input parameterizations are handled by the following transformations:

$$\Psi_0 = \log\left(\frac{\phi}{1 - \phi}\right) - \Psi' \boldsymbol{\mu}$$

$$\Psi_j = \frac{\log(\text{OR}_j)}{U_j} \quad (j \in 1, \dots, K)$$

## Analyses in the MULTREG Statement

### Type III F Test in Multiple Regression (TEST=TYPE3)

Maxwell (2000) discusses a number of different ways to represent effect sizes (and to compute exact power based on them) in multiple regression. PROC POWER supports two of these, multiple partial correlation and  $R^2$  in full and reduced models.

Let  $p$  denote the total number of predictors in the full model (excluding the intercept), and let  $Y$  denote the response variable. You are testing that the coefficients of  $p_1 \geq 1$  predictors in a set  $X_1$  are 0, controlling for all of the other predictors  $X_{-1}$ , which consists of  $p - p_1 \geq 0$  variables.

The hypotheses can be expressed in two different ways. The first is in terms of  $\rho_{YX_1|X_{-1}}$ , the multiple partial correlation between the predictors in  $X_1$  and the response  $Y$  adjusting for the predictors in  $X_{-1}$ :

$$H_0: \rho_{YX_1|X_{-1}}^2 = 0$$

$$H_1: \rho_{YX_1|X_{-1}}^2 > 0$$

The second is in terms of the multiple correlations in full ( $\rho_{Y|(X_1, X_{-1})}$ ) and reduced ( $\rho_{Y|X_{-1}}$ ) nested models:

$$H_0: \rho_{Y|(X_1, X_{-1})}^2 - \rho_{Y|X_{-1}}^2 = 0$$

$$H_1: \rho_{Y|(X_1, X_{-1})}^2 - \rho_{Y|X_{-1}}^2 > 0$$

Note that the squared values of  $\rho_{Y|(X_1, X_{-1})}$  and  $\rho_{Y|X_{-1}}$  are the population  $R^2$  values for full and reduced models.

The test statistic can be written in terms of the sample multiple partial correlation  $R_{YX_1|X_{-1}}$ ,

$$F = \begin{cases} (N - 1 - p) \frac{R_{YX_1|X_{-1}}^2}{1 - R_{YX_1|X_{-1}}^2}, & \text{intercept} \\ (N - p) \frac{R_{YX_1|X_{-1}}^2}{1 - R_{YX_1|X_{-1}}^2}, & \text{no intercept} \end{cases}$$

or the sample multiple correlations in full ( $R_{Y|(X_1, X_{-1})}$ ) and reduced ( $R_{Y|X_{-1}}$ ) models,

$$F = \begin{cases} (N - 1 - p) \frac{R_{Y|(X_1, X_{-1})}^2 - R_{Y|X_{-1}}^2}{1 - R_{Y|(X_1, X_{-1})}^2}, & \text{intercept} \\ (N - p) \frac{R_{Y|(X_1, X_{-1})}^2 - R_{Y|X_{-1}}^2}{1 - R_{Y|(X_1, X_{-1})}^2}, & \text{no intercept} \end{cases}$$

The test is the usual Type III  $F$  test in multiple regression:

$$\text{Reject } H_0 \text{ if } \begin{cases} F \geq F_{1-\alpha}(p_1, N - 1 - p), & \text{intercept} \\ F \geq F_{1-\alpha}(p_1, N - p), & \text{no intercept} \end{cases}$$

Although the test is invariant to whether the predictors are assumed to be random or fixed, the power is affected by this assumption. If the response and predictors are assumed to have a joint multivariate normal distribution, then the exact power is given by the following formula:

$$\text{power} = \begin{cases} P \left[ \left( \frac{N-1-p}{p_1} \right) \left( \frac{R_{Y|(X_1, X_{-1})}^2}{1 - R_{Y|(X_1, X_{-1})}^2} \right) \geq F_{1-\alpha}(p_1, N - 1 - p) \right], & \text{intercept} \\ P \left[ \left( \frac{N-p}{p_1} \right) \left( \frac{R_{Y|(X_1, X_{-1})}^2}{1 - R_{Y|(X_1, X_{-1})}^2} \right) \geq F_{1-\alpha}(p_1, N - p) \right], & \text{no intercept} \end{cases}$$

$$= \begin{cases} P \left[ R_{Y|(X_1, X_{-1})}^2 \geq \frac{F_{1-\alpha}(p_1, N-1-p)}{F_{1-\alpha}(p_1, N-1-p) + \frac{N-1-p}{p_1}} \right], & \text{intercept} \\ P \left[ R_{Y|(X_1, X_{-1})}^2 \geq \frac{F_{1-\alpha}(p_1, N-p)}{F_{1-\alpha}(p_1, N-p) + \frac{N-p}{p_1}} \right], & \text{no intercept} \end{cases}$$

The distribution of  $R_{Y|(X_1, X_{-1})}^2$  (for any  $\rho_{Y|(X_1, X_{-1})}^2$ ) is given in Chapter 32 of Johnson, Kotz, and Balakrishnan (1995). Sample size tables are presented in Gatsonis and Sampson (1989).

If the predictors are assumed to have fixed values, then the exact power is given by the noncentral  $F$  distribution. The noncentrality parameter is

$$\lambda = N \frac{\rho_{YX_1|X_{-1}}^2}{1 - \rho_{YX_1|X_{-1}}^2}$$

or equivalently,

$$\lambda = N \frac{\rho_{Y|(X_1, X_{-1})}^2 - \rho_{Y|X_{-1}}^2}{1 - \rho_{Y|(X_1, X_{-1})}^2}$$

The power is

$$\text{power} = \begin{cases} P(F(p_1, N - 1 - p, \lambda) \geq F_{1-\alpha}(p_1, N - 1 - p)), & \text{intercept} \\ P(F(p_1, N - p, \lambda) \geq F_{1-\alpha}(p_1, N - p)), & \text{no intercept} \end{cases}$$

The minimum acceptable input value of  $N$  depends on several factors, as shown in [Table 67.30](#).

**Table 67.30** Minimum Acceptable Sample Size Values in the MULTREG Statement

Predictor Type	Intercept in Model?	$p_1 = 1?$	Minimum $N$
Random	Yes	Yes	$p + 3$
Random	Yes	No	$p + 2$
Random	No	Yes	$p + 2$
Random	No	No	$p + 1$
Fixed	Yes	Yes or No	$p + 2$
Fixed	No	Yes or No	$p + 1$

## Analyses in the ONECORR Statement

### Fisher's $z$ Test for Pearson Correlation (TEST=PEARSON DIST=FISHERZ)

Fisher's  $z$  transformation (Fisher 1921) of the sample correlation  $R_{Y|(X_1, X_{-1})}$  is defined as

$$z = \frac{1}{2} \log \left( \frac{1 + R_{Y|(X_1, X_{-1})}}{1 - R_{Y|(X_1, X_{-1})}} \right)$$

Fisher's  $z$  test assumes the approximate normal distribution  $N(\mu, \sigma^2)$  for  $z$ , where

$$\mu = \frac{1}{2} \log \left( \frac{1 + \rho_{Y|(X_1, X_{-1})}}{1 - \rho_{Y|(X_1, X_{-1})}} \right) + \frac{\rho_{Y|(X_1, X_{-1})}}{2(N - 1 - p^*)}$$

and

$$\sigma^2 = \frac{1}{N - 3 - p^*}$$

where  $p^*$  is the number of variables partialled out (Anderson 1984, pp. 132–133) and  $\rho_{Y|(X_1, X_{-1})}$  is the partial correlation between  $Y$  and  $X_1$  adjusting for the set of zero or more variables  $X_{-1}$ .

The test statistic

$$z^* = (N - 3 - p^*)^{\frac{1}{2}} \left[ z - \frac{1}{2} \log \left( \frac{1 + \rho_0}{1 - \rho_0} \right) - \frac{\rho_0}{2(N - 1 - p^*)} \right]$$

is assumed to have a normal distribution  $N(\delta, \nu)$ , where  $\rho_0$  is the null partial correlation and  $\delta$  and  $\nu$  are derived from Section 16.33 of Stuart and Ord (1994):

$$\delta = (N - 3 - p^*)^{\frac{1}{2}} \left[ \frac{1}{2} \log \left( \frac{1 + \rho_{Y|(X_1, X_{-1})}}{1 - \rho_{Y|(X_1, X_{-1})}} \right) + \frac{\rho_{Y|(X_1, X_{-1})}}{2(N - 1 - p^*)} \left( 1 + \frac{5 + \rho_{Y|(X_1, X_{-1})}^2}{4(N - 1 - p^*)} + \frac{11 + 2\rho_{Y|(X_1, X_{-1})}^2 + 3\rho_{Y|(X_1, X_{-1})}^4}{8(N - 1 - p^*)^2} \right) - \frac{1}{2} \log \left( \frac{1 + \rho_0}{1 - \rho_0} \right) - \frac{\rho_0}{2(N - 1 - p^*)} \right]$$

$$\nu = \frac{N - 3 - p^*}{N - 1 - p^*} \left[ 1 + \frac{4 - \rho_{Y|(X_1, X_{-1})}^2}{2(N - 1 - p^*)} + \frac{22 - 6\rho_{Y|(X_1, X_{-1})}^2 - 3\rho_{Y|(X_1, X_{-1})}^4}{6(N - 1 - p^*)^2} \right]$$

The approximate power is computed as

$$\text{power} = \begin{cases} \Phi \left( \frac{\delta - z_{1-\alpha}}{\nu^{\frac{1}{2}}} \right), & \text{upper one-sided} \\ \Phi \left( \frac{-\delta - z_{1-\alpha}}{\nu^{\frac{1}{2}}} \right), & \text{lower one-sided} \\ \Phi \left( \frac{\delta - z_{1-\frac{\alpha}{2}}}{\nu^{\frac{1}{2}}} \right) + \Phi \left( \frac{-\delta - z_{1-\frac{\alpha}{2}}}{\nu^{\frac{1}{2}}} \right), & \text{two-sided} \end{cases}$$

Because the test is biased, the achieved significance level might differ from the nominal significance level. The actual alpha is computed in the same way as the power except with the correlation  $\rho_{Y|(X_1, X_{-1})}$  replaced by the null correlation  $\rho_0$ .

### **t Test for Pearson Correlation (TEST=PEARSON DIST=T)**

The two-sided case is identical to multiple regression with an intercept and  $p_1 = 1$ , which is discussed in the section “Analyses in the MULTREG Statement” on page 4924.

Let  $p^*$  denote the number of variables partialled out. For the one-sided cases, the test statistic is

$$t = (N - 2 - p^*)^{\frac{1}{2}} \frac{R_{YX_1|X_{-1}}}{\left( 1 - R_{YX_1|X_{-1}}^2 \right)^{\frac{1}{2}}}$$

which is assumed to have a null distribution of  $t(N - 2 - p^*)$ .

If the  $X$  and  $Y$  variables are assumed to have a joint multivariate normal distribution, then the exact power is given by the following formula:

$$\text{power} = \begin{cases} P \left[ (N - 2 - p^*)^{\frac{1}{2}} \frac{R_{YX_1|X_{-1}}}{(1 - R_{YX_1|X_{-1}}^2)^{\frac{1}{2}}} \geq t_{1-\alpha}(N - 2 - p^*) \right], & \text{upper one-sided} \\ P \left[ (N - 2 - p^*)^{\frac{1}{2}} \frac{R_{YX_1|X_{-1}}}{(1 - R_{YX_1|X_{-1}}^2)^{\frac{1}{2}}} \leq t_{\alpha}(N - 2 - p^*) \right], & \text{lower one-sided} \end{cases}$$

$$= \begin{cases} P \left[ R_{Y|(X_1, X_{-1})} \geq \frac{t_{1-\alpha}(N - 2 - p^*)}{(t_{1-\alpha}^2(N - 2 - p^*) + N - 2 - p^*)^{\frac{1}{2}}} \right], & \text{upper one-sided} \\ P \left[ R_{Y|(X_1, X_{-1})} \leq \frac{t_{\alpha}(N - 2 - p^*)}{(t_{\alpha}^2(N - 2 - p^*) + N - 2 - p^*)^{\frac{1}{2}}} \right], & \text{lower one-sided} \end{cases}$$

The distribution of  $R_{Y|(X_1, X_{-1})}$  (given the underlying true correlation  $\rho_{Y|(X_1, X_{-1})}$ ) is given in Chapter 32 of Johnson, Kotz, and Balakrishnan (1995).

If the  $X$  variables are assumed to have fixed values, then the exact power is given by the noncentral  $t$  distribution  $t(N - 2 - p^*, \delta)$ , where the noncentrality is

$$\delta = N^{\frac{1}{2}} \frac{\rho_{YX_1|X_{-1}}}{(1 - \rho_{YX_1|X_{-1}}^2)^{\frac{1}{2}}}$$

The power is

$$\text{power} = \begin{cases} P(t(N - 2 - p^*, \delta) \geq t_{1-\alpha}(N - 2 - p^*)), & \text{upper one-sided} \\ P(t(N - 2 - p^*, \delta) \leq t_{\alpha}(N - 2 - p^*)), & \text{lower one-sided} \end{cases}$$

## Analyses in the ONESAMPLEFREQ Statement

### Exact Test of a Binomial Proportion (TEST=EXACT)

Let  $X$  be distributed as  $\text{Bin}(N, p)$ . The hypotheses for the test of the proportion  $p$  are as follows:

$$H_0: p = p_0$$

$$H_1: \begin{cases} p \neq p_0, & \text{two-sided} \\ p > p_0, & \text{upper one-sided} \\ p < p_0, & \text{lower one-sided} \end{cases}$$

The exact test assumes binomially distributed data and requires  $N \geq 1$  and  $0 < p_0 < 1$ . The test statistic is

$$X = \text{number of successes} \sim \text{Bin}(N, p)$$

The significance probability  $\alpha$  is split symmetrically for two-sided tests, in the sense that each tail is filled with as much as possible up to  $\alpha/2$ .

Exact power computations are based on the binomial distribution and computing formulas such as the following from Johnson, Kotz, and Kemp (1992, equation 3.20):

$$P(X \geq C | N, p) = P\left(F_{v_1, v_2} \leq \frac{v_2 p}{v_1(1-p)}\right) \quad \text{where } v_1 = 2C \text{ and } v_2 = 2(N - C + 1)$$

Let  $C_L$  and  $C_U$  denote lower and upper critical values, respectively. Let  $\alpha_a$  denote the achieved (actual) significance level, which for two-sided tests is the sum of the favorable major tail ( $\alpha_M$ ) and the opposite minor tail ( $\alpha_m$ ).

For the upper one-sided case,

$$\begin{aligned} C_U &= \min\{C : P(X \geq C | p_0) \leq \alpha\} \\ \text{Reject } H_0 &\text{ if } X \geq C_U \\ \alpha_a &= P(X \geq C_U | p_0) \\ \text{power} &= P(X \geq C_U | p) \end{aligned}$$

For the lower one-sided case,

$$\begin{aligned} C_L &= \max\{C : P(X \leq C | p_0) \leq \alpha\} \\ \text{Reject } H_0 &\text{ if } X \leq C_L \\ \alpha_a &= P(X \leq C_L | p_0) \\ \text{power} &= P(X \leq C_L | p) \end{aligned}$$

For the two-sided case,

$$\begin{aligned} C_L &= \max\{C : P(X \leq C | p_0) \leq \frac{\alpha}{2}\} \\ C_U &= \min\{C : P(X \geq C | p_0) \leq \frac{\alpha}{2}\} \\ \text{Reject } H_0 &\text{ if } X \leq C_L \text{ or } X \geq C_U \\ \alpha_a &= P(X \leq C_L \text{ or } X \geq C_U | p_0) \\ \text{power} &= P(X \leq C_L \text{ or } X \geq C_U | p) \end{aligned}$$

### ***z Test for Binomial Proportion Using Null Variance (TEST=Z VAREST=NULL)***

For the normal approximation test, the test statistic is

$$Z(X) = \frac{X - Np_0}{[Np_0(1-p_0)]^{\frac{1}{2}}}$$

For the METHOD=EXACT option, the computations are the same as described in the section “[Exact Test of a Binomial Proportion \(TEST=EXACT\)](#)” on page 4928 except for the definitions of the critical values.

For the upper one-sided case,

$$C_U = \min\{C : Z(C) \geq z_{1-\alpha}\}$$

For the lower one-sided case,

$$C_L = \max\{C : Z(C) \leq z_\alpha\}$$

For the two-sided case,

$$C_L = \max\{C : Z(C) \leq z_{\frac{\alpha}{2}}\}$$

$$C_U = \min\{C : Z(C) \geq z_{1-\frac{\alpha}{2}}\}$$

For the METHOD=NORMAL option, the test statistic  $Z(X)$  is assumed to have the normal distribution

$$N\left(\frac{N^{\frac{1}{2}}(p - p_0)}{[p_0(1 - p_0)]^{\frac{1}{2}}}, \frac{p(1 - p)}{p_0(1 - p_0)}\right)$$

The approximate power is computed as

$$\text{power} = \begin{cases} \Phi\left(\frac{z_\alpha + \sqrt{N} \frac{p - p_0}}{\sqrt{\frac{p(1-p)}{p_0(1-p_0)}}}\right), & \text{upper one-sided} \\ \Phi\left(\frac{z_\alpha - \sqrt{N} \frac{p - p_0}}{\sqrt{\frac{p(1-p)}{p_0(1-p_0)}}}\right), & \text{lower one-sided} \\ \Phi\left(\frac{z_{\frac{\alpha}{2}} + \sqrt{N} \frac{p - p_0}}{\sqrt{\frac{p(1-p)}{p_0(1-p_0)}}}\right) + \Phi\left(\frac{z_{\frac{\alpha}{2}} - \sqrt{N} \frac{p - p_0}}{\sqrt{\frac{p(1-p)}{p_0(1-p_0)}}}\right), & \text{two-sided} \end{cases}$$

The approximate sample size is computed in closed form for the one-sided cases by inverting the power equation,

$$N = \left(\frac{z_{\text{power}} \sqrt{p(1-p)} + z_{1-\alpha} \sqrt{p_0(1-p_0)}}{p - p_0}\right)^2$$

and by numerical inversion for the two-sided case.

### ***z Test for Binomial Proportion Using Sample Variance (TEST=Z VAREST=SAMPLE)***

For the normal approximation test using the sample variance, the test statistic is

$$Z_s(X) = \frac{X - Np_0}{[N\hat{p}(1 - \hat{p})]^{\frac{1}{2}}}$$

where  $\hat{p} = X/N$ .

For the METHOD=EXACT option, the computations are the same as described in the section “[Exact Test of a Binomial Proportion \(TEST=EXACT\)](#)” on page 4928 except for the definitions of the critical values.

For the upper one-sided case,

$$C_U = \min\{C : Z_s(C) \geq z_{1-\alpha}\}$$

For the lower one-sided case,

$$C_L = \max\{C : Z_s(C) \leq z_\alpha\}$$

For the two-sided case,

$$C_L = \max\{C : Z_s(C) \leq z_{\frac{\alpha}{2}}\}$$

$$C_U = \min\{C : Z_s(C) \geq z_{1-\frac{\alpha}{2}}\}$$

For the METHOD=NORMAL option, the test statistic  $Z_s(X)$  is assumed to have the normal distribution

$$N\left(\frac{N^{\frac{1}{2}}(p - p_0)}{[p(1-p)]^{\frac{1}{2}}}, 1\right)$$

(see Chow, Shao, and Wang (2003), p. 82).

The approximate power is computed as

$$\text{power} = \begin{cases} \Phi\left(z_\alpha + \sqrt{N} \frac{p-p_0}{\sqrt{p(1-p)}}\right), & \text{upper one-sided} \\ \Phi\left(z_\alpha - \sqrt{N} \frac{p-p_0}{\sqrt{p(1-p)}}\right), & \text{lower one-sided} \\ \Phi\left(z_{\frac{\alpha}{2}} + \sqrt{N} \frac{p-p_0}{\sqrt{p(1-p)}}\right) + \Phi\left(z_{\frac{\alpha}{2}} - \sqrt{N} \frac{p-p_0}{\sqrt{p(1-p)}}\right), & \text{two-sided} \end{cases}$$

The approximate sample size is computed in closed form for the one-sided cases by inverting the power equation,

$$N = p(1-p) \left(\frac{z_{\text{power}} + z_{1-\alpha}}{p - p_0}\right)^2$$

and by numerical inversion for the two-sided case.

### ***z Test for Binomial Proportion with Continuity Adjustment Using Null Variance (TEST=ADJZ VAREST=NULL)***

For the normal approximation test with continuity adjustment, the test statistic is (Pagano and Gauvreau 1993 p. 295):

$$Z_c(X) = \frac{X - Np_0 + 0.5(1_{\{X < Np_0\}}) - 0.5(1_{\{X > Np_0\}})}{[Np_0(1-p_0)]^{\frac{1}{2}}}$$

For the METHOD=EXACT option, the computations are the same as described in the section “Exact Test of a Binomial Proportion (TEST=EXACT)” on page 4928 except for the definitions of the critical values.

For the upper one-sided case,

$$C_U = \min\{C : Z_c(C) \geq z_{1-\alpha}\}$$

For the lower one-sided case,

$$C_L = \max\{C : Z_c(C) \leq z_\alpha\}$$

For the two-sided case,

$$C_L = \max\{C : Z_c(C) \leq z_{\frac{\alpha}{2}}\}$$

$$C_U = \min\{C : Z_c(C) \geq z_{1-\frac{\alpha}{2}}\}$$

For the METHOD=NORMAL option, the test statistic  $Z_c(X)$  is assumed to have the normal distribution  $N(\mu, \sigma^2)$ , where  $\mu$  and  $\sigma^2$  are derived as follows.

For convenience of notation, define

$$k = \frac{1}{2\sqrt{Np_0(1-p_0)}}$$

Then

$$E[Z_c(X)] = 2kNp - 2kNp_0 + kP(X < Np_0) - kP(X > Np_0)$$

and

$$\begin{aligned} \text{Var}[Z_c(X)] &= 4k^2Np(1-p) + k^2[1 - P(X = Np_0)] - k^2[P(X < Np_0) - P(X > Np_0)]^2 \\ &\quad + 4k^2[E(X1_{\{X < Np_0\}}) - E(X1_{\{X > Np_0\}})] - 4k^2Np[P(X < Np_0) - P(X > Np_0)] \end{aligned}$$

The probabilities  $P(X = Np_0)$ ,  $P(X < Np_0)$ , and  $P(X > Np_0)$  and the truncated expectations  $E(X1_{\{X < Np_0\}})$  and  $E(X1_{\{X > Np_0\}})$  are approximated by assuming the normal-approximate distribution of  $X$ ,  $N(Np, Np(1-p))$ . Letting  $\phi(\cdot)$  and  $\Phi(\cdot)$  denote the standard normal PDF and CDF, respectively, and defining  $d$  as

$$d = \frac{Np_0 - Np}{[Np(1-p)]^{\frac{1}{2}}}$$

the terms are computed as follows:

$$P(X = Np_0) = 0$$

$$P(X < Np_0) = \Phi(d)$$

$$P(X > Np_0) = 1 - \Phi(d)$$

$$E(X1_{\{X < Np_0\}}) = Np\Phi(d) - [Np(1-p)]^{\frac{1}{2}}\phi(d)$$

$$E(X1_{\{X > Np_0\}}) = Np[1 - \Phi(d)] + [Np(1-p)]^{\frac{1}{2}}\phi(d)$$

The mean and variance of  $Z_c(X)$  are thus approximated by

$$\mu = k [2Np - 2Np_0 + 2\Phi(d) - 1]$$

and

$$\sigma^2 = 4k^2 \left[ Np(1-p) + \Phi(d)(1-\Phi(d)) - 2(Np(1-p))^{\frac{1}{2}} \phi(d) \right]$$

The approximate power is computed as

$$\text{power} = \begin{cases} \Phi\left(\frac{z_\alpha + \mu}{\sigma}\right), & \text{upper one-sided} \\ \Phi\left(\frac{z_\alpha - \mu}{\sigma}\right), & \text{lower one-sided} \\ \Phi\left(\frac{z_{\frac{\alpha}{2}} + \mu}{\sigma}\right) + \Phi\left(\frac{z_{\frac{\alpha}{2}} - \mu}{\sigma}\right), & \text{two-sided} \end{cases}$$

The approximate sample size is computed by numerical inversion.

### ***z Test for Binomial Proportion with Continuity Adjustment Using Sample Variance (TEST=ADJZ VAREST=SAMPLE)***

For the normal approximation test with continuity adjustment using the sample variance, the test statistic is

$$Z_{cs}(X) = \frac{X - Np_0 + 0.5(1_{\{X < Np_0\}}) - 0.5(1_{\{X > Np_0\}})}{[N\hat{p}(1-\hat{p})]^{\frac{1}{2}}}$$

where  $\hat{p} = X/N$ .

For the METHOD=EXACT option, the computations are the same as described in the section “[Exact Test of a Binomial Proportion \(TEST=EXACT\)](#)” on page 4928 except for the definitions of the critical values.

For the upper one-sided case,

$$C_U = \min\{C : Z_{cs}(C) \geq z_{1-\alpha}\}$$

For the lower one-sided case,

$$C_L = \max\{C : Z_{cs}(C) \leq z_\alpha\}$$

For the two-sided case,

$$C_L = \max\{C : Z_{cs}(C) \leq z_{\frac{\alpha}{2}}\}$$

$$C_U = \min\{C : Z_{cs}(C) \geq z_{1-\frac{\alpha}{2}}\}$$

For the METHOD=NORMAL option, the test statistic  $Z_{cs}(X)$  is assumed to have the normal distribution  $N(\mu, \sigma^2)$ , where  $\mu$  and  $\sigma^2$  are derived as follows.

For convenience of notation, define

$$k = \frac{1}{2\sqrt{Np(1-p)}}$$

Then

$$E[Z_{cs}(X)] \approx 2kNp - 2kNp_0 + kP(X < Np_0) - kP(X > Np_0)$$

and

$$\begin{aligned} \text{Var}[Z_{cs}(X)] \approx & 4k^2Np(1-p) + k^2[1 - P(X = Np_0)] - k^2[P(X < Np_0) - P(X > Np_0)]^2 \\ & + 4k^2[E(X1_{\{X < Np_0\}}) - E(X1_{\{X > Np_0\}})] - 4k^2Np[P(X < Np_0) - P(X > Np_0)] \end{aligned}$$

The probabilities  $P(X = Np_0)$ ,  $P(X < Np_0)$ , and  $P(X > Np_0)$  and the truncated expectations  $E(X1_{\{X < Np_0\}})$  and  $E(X1_{\{X > Np_0\}})$  are approximated by assuming the normal-approximate distribution of  $X$ ,  $N(Np, Np(1-p))$ . Letting  $\phi(\cdot)$  and  $\Phi(\cdot)$  denote the standard normal PDF and CDF, respectively, and defining  $d$  as

$$d = \frac{Np_0 - Np}{[Np(1-p)]^{\frac{1}{2}}}$$

the terms are computed as follows:

$$P(X = Np_0) = 0$$

$$P(X < Np_0) = \Phi(d)$$

$$P(X > Np_0) = 1 - \Phi(d)$$

$$E(X1_{\{X < Np_0\}}) = Np\Phi(d) - [Np(1-p)]^{\frac{1}{2}}\phi(d)$$

$$E(X1_{\{X > Np_0\}}) = Np[1 - \Phi(d)] + [Np(1-p)]^{\frac{1}{2}}\phi(d)$$

The mean and variance of  $Z_{cs}(X)$  are thus approximated by

$$\mu = k[2Np - 2Np_0 + 2\Phi(d) - 1]$$

and

$$\sigma^2 = 4k^2[Np(1-p) + \Phi(d)(1 - \Phi(d)) - 2(Np(1-p))^{\frac{1}{2}}\phi(d)]$$

The approximate power is computed as

$$\text{power} = \begin{cases} \Phi\left(\frac{z_{\alpha} + \mu}{\sigma}\right), & \text{upper one-sided} \\ \Phi\left(\frac{z_{\alpha} - \mu}{\sigma}\right), & \text{lower one-sided} \\ \Phi\left(\frac{z_{\frac{\alpha}{2}} + \mu}{\sigma}\right) + \Phi\left(\frac{z_{\frac{\alpha}{2}} - \mu}{\sigma}\right), & \text{two-sided} \end{cases}$$

The approximate sample size is computed by numerical inversion.

**Exact Equivalence Test of a Binomial Proportion (TEST=EQUIV\_EXACT)**

The hypotheses for the equivalence test are

$$H_0: p < \theta_L \quad \text{or} \quad p > \theta_U$$

$$H_1: \theta_L \leq p \leq \theta_U$$

where  $\theta_L$  and  $\theta_U$  are the lower and upper equivalence bounds, respectively.

The analysis is the two one-sided tests (TOST) procedure as described in Chow, Shao, and Wang (2003) on p. 84, but using exact critical values as on p. 116 instead of normal-based critical values.

Two different hypothesis tests are carried out:

$$H_{a0}: p < \theta_L$$

$$H_{a1}: p \geq \theta_L$$

and

$$H_{b0}: p > \theta_U$$

$$H_{b1}: p \leq \theta_U$$

If  $H_{a0}$  is rejected in favor of  $H_{a1}$  and  $H_{b0}$  is rejected in favor of  $H_{b1}$ , then  $H_0$  is rejected in favor of  $H_1$ .

The test statistic for each of the two tests ( $H_{a0}$  versus  $H_{a1}$  and  $H_{b0}$  versus  $H_{b1}$ ) is

$$X = \text{number of successes} \sim \text{Bin}(N, p)$$

Let  $C_U$  denote the critical value of the exact upper one-sided test of  $H_{a0}$  versus  $H_{a1}$ , and let  $C_L$  denote the critical value of the exact lower one-sided test of  $H_{b0}$  versus  $H_{b1}$ . These critical values are computed in the section “Exact Test of a Binomial Proportion (TEST=EXACT)” on page 4928. Both of these tests are rejected if and only if  $C_U \leq X \leq C_L$ . Thus, the exact power of the equivalence test is

$$\text{power} = P(C_U \leq X \leq C_L)$$

$$= P(X \geq C_U) - P(X \geq C_L + 1)$$

The probabilities are computed using Johnson and Kotz (1970, equation 3.20).

**z Equivalence Test for Binomial Proportion Using Null Variance (TEST=EQUIV\_Z VAREST=NULL)**

The hypotheses for the equivalence test are

$$H_0: p < \theta_L \quad \text{or} \quad p > \theta_U$$

$$H_1: \theta_L \leq p \leq \theta_U$$

where  $\theta_L$  and  $\theta_U$  are the lower and upper equivalence bounds, respectively.

The analysis is the two one-sided tests (TOST) procedure as described in Chow, Shao, and Wang (2003) on p. 84, but using the null variance instead of the sample variance.

Two different hypothesis tests are carried out:

$$H_{a0}: p < \theta_L$$

$$H_{a1}: p \geq \theta_L$$

and

$$H_{b0}: p > \theta_U$$

$$H_{b1}: p \leq \theta_U$$

If  $H_{a0}$  is rejected in favor of  $H_{a1}$  and  $H_{b0}$  is rejected in favor of  $H_{b1}$ , then  $H_0$  is rejected in favor of  $H_1$ .

The test statistic for the test of  $H_{a0}$  versus  $H_{a1}$  is

$$Z_L(X) = \frac{X - N\theta_L}{[N\theta_L(1 - \theta_L)]^{\frac{1}{2}}}$$

The test statistic for the test of  $H_{b0}$  versus  $H_{b1}$  is

$$Z_U(X) = \frac{X - N\theta_U}{[N\theta_U(1 - \theta_U)]^{\frac{1}{2}}}$$

For the METHOD=EXACT option, let  $C_U$  denote the critical value of the exact upper one-sided test of  $H_{a0}$  versus  $H_{a1}$  using  $Z_L(X)$ . This critical value is computed in the section “z Test for Binomial Proportion Using Null Variance (TEST=Z VAREST=NULL)” on page 4929. Similarly, let  $C_L$  denote the critical value of the exact lower one-sided test of  $H_{b0}$  versus  $H_{b1}$  using  $Z_U(X)$ . Both of these tests are rejected if and only if  $C_U \leq X \leq C_L$ . Thus, the exact power of the equivalence test is

$$\begin{aligned} \text{power} &= P(C_U \leq X \leq C_L) \\ &= P(X \geq C_U) - P(X \geq C_L + 1) \end{aligned}$$

The probabilities are computed using Johnson and Kotz (1970, equation 3.20).

For the METHOD=NORMAL option, the test statistic  $Z_L(X)$  is assumed to have the normal distribution

$$N\left(\frac{N^{\frac{1}{2}}(p - \theta_L)}{[\theta_L(1 - \theta_L)]^{\frac{1}{2}}}, \frac{p(1 - p)}{\theta_L(1 - \theta_L)}\right)$$

and the test statistic  $Z_U(X)$  is assumed to have the normal distribution

$$N\left(\frac{N^{\frac{1}{2}}(p - \theta_U)}{[\theta_U(1 - \theta_U)]^{\frac{1}{2}}}, \frac{p(1 - p)}{\theta_U(1 - \theta_U)}\right)$$

(see Chow, Shao, and Wang (2003), p. 84).

The approximate power is computed as

$$\text{power} = \Phi \left( \frac{z_\alpha - \sqrt{N} \frac{p - \theta_U}{\sqrt{\theta_U(1 - \theta_U)}}}{\sqrt{\frac{p(1-p)}{\theta_U(1 - \theta_U)}}} \right) + \Phi \left( \frac{z_\alpha + \sqrt{N} \frac{p - \theta_L}{\sqrt{\theta_L(1 - \theta_L)}}}{\sqrt{\frac{p(1-p)}{\theta_L(1 - \theta_L)}}} \right) - 1$$

The approximate sample size is computed by numerically inverting the power formula, using the sample size estimate  $N_0$  of Chow, Shao, and Wang (2003, p. 85) as an initial guess:

$$N_0 = p(1-p) \left( \frac{z_{1-\alpha} + z_{(1+\text{power})/2}}{0.5(\theta_U - \theta_L) - |p - 0.5(\theta_L + \theta_U)|} \right)^2$$

### ***z Equivalence Test for Binomial Proportion Using Sample Variance (TEST=EQUIV\_Z VAREST=SAMPLE)***

The hypotheses for the equivalence test are

$$H_0: p < \theta_L \quad \text{or} \quad p > \theta_U$$

$$H_1: \theta_L \leq p \leq \theta_U$$

where  $\theta_L$  and  $\theta_U$  are the lower and upper equivalence bounds, respectively.

The analysis is the two one-sided tests (TOST) procedure as described in Chow, Shao, and Wang (2003) on p. 84.

Two different hypothesis tests are carried out:

$$H_{a0}: p < \theta_L$$

$$H_{a1}: p \geq \theta_L$$

and

$$H_{b0}: p > \theta_U$$

$$H_{b1}: p \leq \theta_U$$

If  $H_{a0}$  is rejected in favor of  $H_{a1}$  and  $H_{b0}$  is rejected in favor of  $H_{b1}$ , then  $H_0$  is rejected in favor of  $H_1$ .

The test statistic for the test of  $H_{a0}$  versus  $H_{a1}$  is

$$Z_{sL}(X) = \frac{X - N\theta_L}{[N\hat{p}(1 - \hat{p})]^{1/2}}$$

where  $\hat{p} = X/N$ .

The test statistic for the test of  $H_{b0}$  versus  $H_{b1}$  is

$$Z_{sU}(X) = \frac{X - N\theta_U}{[N\hat{p}(1 - \hat{p})]^{1/2}}$$

For the METHOD=EXACT option, let  $C_U$  denote the critical value of the exact upper one-sided test of  $H_{a0}$  versus  $H_{a1}$  using  $Z_{sL}(X)$ . This critical value is computed in the section “z Test for Binomial Proportion Using Sample Variance (TEST=Z VAREST=SAMPLE)” on page 4930. Similarly, let  $C_L$  denote the critical value of the exact lower one-sided test of  $H_{b0}$  versus  $H_{b1}$  using  $Z_{sU}(X)$ . Both of these tests are rejected if and only if  $C_U \leq X \leq C_L$ . Thus, the exact power of the equivalence test is

$$\begin{aligned} \text{power} &= P(C_U \leq X \leq C_L) \\ &= P(X \geq C_U) - P(X \geq C_L + 1) \end{aligned}$$

The probabilities are computed using Johnson and Kotz (1970, equation 3.20).

For the METHOD=NORMAL option, the test statistic  $Z_{sL}(X)$  is assumed to have the normal distribution

$$N\left(\frac{N^{\frac{1}{2}}(p - \theta_L)}{[p(1-p)]^{\frac{1}{2}}}, 1\right)$$

and the test statistic  $Z_{sU}(X)$  is assumed to have the normal distribution

$$N\left(\frac{N^{\frac{1}{2}}(p - \theta_U)}{[p(1-p)]^{\frac{1}{2}}}, 1\right)$$

(see Chow, Shao, and Wang (2003), p. 84).

The approximate power is computed as

$$\text{power} = \Phi\left(z_\alpha - \sqrt{N} \frac{p - \theta_U}{\sqrt{p(1-p)}}\right) + \Phi\left(z_\alpha + \sqrt{N} \frac{p - \theta_L}{\sqrt{p(1-p)}}\right) - 1$$

The approximate sample size is computed by numerically inverting the power formula, using the sample size estimate  $N_0$  of Chow, Shao, and Wang (2003, p. 85) as an initial guess:

$$N_0 = p(1-p) \left( \frac{z_{1-\alpha} + z_{(1+\text{power})/2}}{0.5(\theta_U - \theta_L) - |p - 0.5(\theta_L + \theta_U)|} \right)^2$$

### **z Equivalence Test for Binomial Proportion with Continuity Adjustment Using Null Variance (TEST=EQUIV\_ADJZ VAREST=NULL)**

The hypotheses for the equivalence test are

$$\begin{aligned} H_0: p < \theta_L \quad \text{or} \quad p > \theta_U \\ H_1: \theta_L \leq p \leq \theta_U \end{aligned}$$

where  $\theta_L$  and  $\theta_U$  are the lower and upper equivalence bounds, respectively.

The analysis is the two one-sided tests (TOST) procedure as described in Chow, Shao, and Wang (2003) on p. 84, but using the null variance instead of the sample variance.

Two different hypothesis tests are carried out:

$$H_{a0}: p < \theta_L$$

$$H_{a1}: p \geq \theta_L$$

and

$$H_{b0}: p > \theta_U$$

$$H_{b1}: p \leq \theta_U$$

If  $H_{a0}$  is rejected in favor of  $H_{a1}$  and  $H_{b0}$  is rejected in favor of  $H_{b1}$ , then  $H_0$  is rejected in favor of  $H_1$ .

The test statistic for the test of  $H_{a0}$  versus  $H_{a1}$  is

$$Z_{cL}(X) = \frac{X - N\theta_L + 0.5(1_{\{X < N\theta_L\}}) - 0.5(1_{\{X > N\theta_L\}})}{\left[ N\hat{\theta}_L(1 - \hat{\theta}_L) \right]^{\frac{1}{2}}}$$

where  $\hat{p} = X/N$ .

The test statistic for the test of  $H_{b0}$  versus  $H_{b1}$  is

$$Z_{cU}(X) = \frac{X - N\theta_U + 0.5(1_{\{X < N\theta_U\}}) - 0.5(1_{\{X > N\theta_U\}})}{\left[ N\hat{\theta}_U(1 - \hat{\theta}_U) \right]^{\frac{1}{2}}}$$

For the METHOD=EXACT option, let  $C_U$  denote the critical value of the exact upper one-sided test of  $H_{a0}$  versus  $H_{a1}$  using  $Z_{cL}(X)$ . This critical value is computed in the section “z Test for Binomial Proportion with Continuity Adjustment Using Null Variance (TEST=ADJZ VAREST=NULL)” on page 4931. Similarly, let  $C_L$  denote the critical value of the exact lower one-sided test of  $H_{b0}$  versus  $H_{b1}$  using  $Z_{cU}(X)$ . Both of these tests are rejected if and only if  $C_U \leq X \leq C_L$ . Thus, the exact power of the equivalence test is

$$\begin{aligned} \text{power} &= P(C_U \leq X \leq C_L) \\ &= P(X \geq C_U) - P(X \geq C_L + 1) \end{aligned}$$

The probabilities are computed using Johnson and Kotz (1970, equation 3.20).

For the METHOD=NORMAL option, the test statistic  $Z_{cL}(X)$  is assumed to have the normal distribution  $N(\mu_L, \sigma_L^2)$ , and  $Z_{cU}(X)$  is assumed to have the normal distribution  $N(\mu_U, \sigma_U^2)$ , where  $\mu_L, \mu_U, \sigma_L^2$ , and  $\sigma_U^2$  are derived as follows.

For convenience of notation, define

$$k_L = \frac{1}{2\sqrt{N\theta_L(1 - \theta_L)}}$$

$$k_U = \frac{1}{2\sqrt{N\theta_U(1 - \theta_U)}}$$

Then

$$\begin{aligned} E[Z_{cL}(X)] &\approx 2k_L Np - 2k_L N\theta_L + k_L P(X < N\theta_L) - k_L P(X > N\theta_L) \\ E[Z_{cU}(X)] &\approx 2k_U Np - 2k_U N\theta_U + k_U P(X < N\theta_U) - k_U P(X > N\theta_U) \end{aligned}$$

and

$$\begin{aligned} \text{Var}[Z_{cL}(X)] &\approx 4k_L^2 Np(1-p) + k_L^2 [1 - P(X = N\theta_L)] - k_L^2 [P(X < N\theta_L) - P(X > N\theta_L)]^2 \\ &\quad + 4k_L^2 [E(X1_{\{X < N\theta_L\}}) - E(X1_{\{X > N\theta_L\}})] - 4k_L^2 Np [P(X < N\theta_L) - P(X > N\theta_L)] \\ \text{Var}[Z_{cU}(X)] &\approx 4k_U^2 Np(1-p) + k_U^2 [1 - P(X = N\theta_U)] - k_U^2 [P(X < N\theta_U) - P(X > N\theta_U)]^2 \\ &\quad + 4k_U^2 [E(X1_{\{X < N\theta_U\}}) - E(X1_{\{X > N\theta_U\}})] - 4k_U^2 Np [P(X < N\theta_U) - P(X > N\theta_U)] \end{aligned}$$

The probabilities  $P(X = N\theta_L)$ ,  $P(X < N\theta_L)$ ,  $P(X > N\theta_L)$ ,  $P(X = N\theta_U)$ ,  $P(X < N\theta_U)$ , and  $P(X > N\theta_U)$  and the truncated expectations  $E(X1_{\{X < N\theta_L\}})$ ,  $E(X1_{\{X > N\theta_L\}})$ ,  $E(X1_{\{X < N\theta_U\}})$ , and  $E(X1_{\{X > N\theta_U\}})$  are approximated by assuming the normal-approximate distribution of  $X$ ,  $N(Np, Np(1-p))$ . Letting  $\phi(\cdot)$  and  $\Phi(\cdot)$  denote the standard normal PDF and CDF, respectively, and defining  $d_L$  and  $d_U$  as

$$\begin{aligned} d_L &= \frac{N\theta_L - Np}{[Np(1-p)]^{\frac{1}{2}}} \\ d_U &= \frac{N\theta_U - Np}{[Np(1-p)]^{\frac{1}{2}}} \end{aligned}$$

the terms are computed as follows:

$$\begin{aligned} P(X = N\theta_L) &= 0 \\ P(X = N\theta_U) &= 0 \\ P(X < N\theta_L) &= \Phi(d_L) \\ P(X < N\theta_U) &= \Phi(d_U) \\ P(X > N\theta_L) &= 1 - \Phi(d_L) \\ P(X > N\theta_U) &= 1 - \Phi(d_U) \\ E(X1_{\{X < N\theta_L\}}) &= Np\Phi(d_L) - [Np(1-p)]^{\frac{1}{2}} \phi(d_L) \\ E(X1_{\{X < N\theta_U\}}) &= Np\Phi(d_U) - [Np(1-p)]^{\frac{1}{2}} \phi(d_U) \\ E(X1_{\{X > N\theta_L\}}) &= Np[1 - \Phi(d_L)] + [Np(1-p)]^{\frac{1}{2}} \phi(d_L) \\ E(X1_{\{X > N\theta_U\}}) &= Np[1 - \Phi(d_U)] + [Np(1-p)]^{\frac{1}{2}} \phi(d_U) \end{aligned}$$

The mean and variance of  $Z_{cL}(X)$  and  $Z_{cU}(X)$  are thus approximated by

$$\begin{aligned} \mu_L &= k_L [2Np - 2N\theta_L + 2\Phi(d_L) - 1] \\ \mu_U &= k_U [2Np - 2N\theta_U + 2\Phi(d_U) - 1] \end{aligned}$$

and

$$\sigma_L^2 = 4k_L^2 \left[ Np(1-p) + \Phi(d_L)(1 - \Phi(d_L)) - 2(Np(1-p))^{\frac{1}{2}} \phi(d_L) \right]$$

$$\sigma_U^2 = 4k_U^2 \left[ Np(1-p) + \Phi(d_U)(1 - \Phi(d_U)) - 2(Np(1-p))^{\frac{1}{2}} \phi(d_U) \right]$$

The approximate power is computed as

$$\text{power} = \Phi\left(\frac{z_\alpha - \mu_U}{\sigma_U}\right) + \Phi\left(\frac{z_\alpha + \mu_L}{\sigma_L}\right) - 1$$

The approximate sample size is computed by numerically inverting the power formula.

### ***z Equivalence Test for Binomial Proportion with Continuity Adjustment Using Sample Variance (TEST=EQUIV\_ADJZ VAREST=SAMPLE)***

The hypotheses for the equivalence test are

$$H_0: p < \theta_L \quad \text{or} \quad p > \theta_U$$

$$H_1: \theta_L \leq p \leq \theta_U$$

where  $\theta_L$  and  $\theta_U$  are the lower and upper equivalence bounds, respectively.

The analysis is the two one-sided tests (TOST) procedure as described in Chow, Shao, and Wang (2003) on p. 84.

Two different hypothesis tests are carried out:

$$H_{a0}: p < \theta_L$$

$$H_{a1}: p \geq \theta_L$$

and

$$H_{b0}: p > \theta_U$$

$$H_{b1}: p \leq \theta_U$$

If  $H_{a0}$  is rejected in favor of  $H_{a1}$  and  $H_{b0}$  is rejected in favor of  $H_{b1}$ , then  $H_0$  is rejected in favor of  $H_1$ .

The test statistic for the test of  $H_{a0}$  versus  $H_{a1}$  is

$$Z_{csL}(X) = \frac{X - N\theta_L + 0.5(1_{\{X < N\theta_L\}}) - 0.5(1_{\{X > N\theta_L\}})}{[N\hat{p}(1 - \hat{p})]^{\frac{1}{2}}}$$

where  $\hat{p} = X/N$ .

The test statistic for the test of  $H_{b0}$  versus  $H_{b1}$  is

$$Z_{csU}(X) = \frac{X - N\theta_U + 0.5(1_{\{X < N\theta_U\}}) - 0.5(1_{\{X > N\theta_U\}})}{[N\hat{p}(1 - \hat{p})]^{\frac{1}{2}}}$$

For the METHOD=EXACT option, let  $C_U$  denote the critical value of the exact upper one-sided test of  $H_{a0}$  versus  $H_{a1}$  using  $Z_{csL}(X)$ . This critical value is computed in the section “z Test for Binomial Proportion with Continuity Adjustment Using Sample Variance (TEST=ADJZ VAREST=SAMPLE)” on page 4933. Similarly, let  $C_L$  denote the critical value of the exact lower one-sided test of  $H_{b0}$  versus  $H_{b1}$  using  $Z_{csU}(X)$ . Both of these tests are rejected if and only if  $C_U \leq X \leq C_L$ . Thus, the exact power of the equivalence test is

$$\begin{aligned} \text{power} &= P(C_U \leq X \leq C_L) \\ &= P(X \geq C_U) - P(X \geq C_L + 1) \end{aligned}$$

The probabilities are computed using Johnson and Kotz (1970, equation 3.20).

For the METHOD=NORMAL option, the test statistic  $Z_{csL}(X)$  is assumed to have the normal distribution  $N(\mu_L, \sigma_L^2)$ , and  $Z_{csU}(X)$  is assumed to have the normal distribution  $N(\mu_U, \sigma_U^2)$ , where  $\mu_L, \mu_U, \sigma_L^2$  and  $\sigma_U^2$  are derived as follows.

For convenience of notation, define

$$k = \frac{1}{2\sqrt{Np(1-p)}}$$

Then

$$\begin{aligned} E[Z_{csL}(X)] &\approx 2kNp - 2kN\theta_L + kP(X < N\theta_L) - kP(X > N\theta_L) \\ E[Z_{csU}(X)] &\approx 2kNp - 2kN\theta_U + kP(X < N\theta_U) - kP(X > N\theta_U) \end{aligned}$$

and

$$\begin{aligned} \text{Var}[Z_{csL}(X)] &\approx 4k^2Np(1-p) + k^2[1 - P(X = N\theta_L)] - k^2[P(X < N\theta_L) - P(X > N\theta_L)]^2 \\ &\quad + 4k^2[E(X1_{\{X < N\theta_L\}}) - E(X1_{\{X > N\theta_L\}})] - 4k^2Np[P(X < N\theta_L) - P(X > N\theta_L)] \\ \text{Var}[Z_{csU}(X)] &\approx 4k^2Np(1-p) + k^2[1 - P(X = N\theta_U)] - k^2[P(X < N\theta_U) - P(X > N\theta_U)]^2 \\ &\quad + 4k^2[E(X1_{\{X < N\theta_U\}}) - E(X1_{\{X > N\theta_U\}})] - 4k^2Np[P(X < N\theta_U) - P(X > N\theta_U)] \end{aligned}$$

The probabilities  $P(X = N\theta_L)$ ,  $P(X < N\theta_L)$ ,  $P(X > N\theta_L)$ ,  $P(X = N\theta_U)$ ,  $P(X < N\theta_U)$ , and  $P(X > N\theta_U)$  and the truncated expectations  $E(X1_{\{X < N\theta_L\}})$ ,  $E(X1_{\{X > N\theta_L\}})$ ,  $E(X1_{\{X < N\theta_U\}})$ , and  $E(X1_{\{X > N\theta_U\}})$  are approximated by assuming the normal-approximate distribution of  $X$ ,  $N(Np, Np(1-p))$ . Letting  $\phi(\cdot)$  and  $\Phi(\cdot)$  denote the standard normal PDF and CDF, respectively, and defining  $d_L$  and  $d_U$  as

$$\begin{aligned} d_L &= \frac{N\theta_L - Np}{[Np(1-p)]^{\frac{1}{2}}} \\ d_U &= \frac{N\theta_U - Np}{[Np(1-p)]^{\frac{1}{2}}} \end{aligned}$$

the terms are computed as follows:

$$P(X = N\theta_L) = 0$$

$$P(X = N\theta_U) = 0$$

$$P(X < N\theta_L) = \Phi(d_L)$$

$$P(X < N\theta_U) = \Phi(d_U)$$

$$P(X > N\theta_L) = 1 - \Phi(d_L)$$

$$P(X > N\theta_U) = 1 - \Phi(d_U)$$

$$E(X1_{\{X < N\theta_L\}}) = Np\Phi(d_L) - [Np(1-p)]^{\frac{1}{2}}\phi(d_L)$$

$$E(X1_{\{X < N\theta_U\}}) = Np\Phi(d_U) - [Np(1-p)]^{\frac{1}{2}}\phi(d_U)$$

$$E(X1_{\{X > N\theta_L\}}) = Np[1 - \Phi(d_L)] + [Np(1-p)]^{\frac{1}{2}}\phi(d_L)$$

$$E(X1_{\{X > N\theta_U\}}) = Np[1 - \Phi(d_U)] + [Np(1-p)]^{\frac{1}{2}}\phi(d_U)$$

The mean and variance of  $Z_{csL}(X)$  and  $Z_{csU}(X)$  are thus approximated by

$$\mu_L = k[2Np - 2N\theta_L + 2\Phi(d_L) - 1]$$

$$\mu_U = k[2Np - 2N\theta_U + 2\Phi(d_U) - 1]$$

and

$$\sigma_L^2 = 4k^2 \left[ Np(1-p) + \Phi(d_L)(1 - \Phi(d_L)) - 2(Np(1-p))^{\frac{1}{2}}\phi(d_L) \right]$$

$$\sigma_U^2 = 4k^2 \left[ Np(1-p) + \Phi(d_U)(1 - \Phi(d_U)) - 2(Np(1-p))^{\frac{1}{2}}\phi(d_U) \right]$$

The approximate power is computed as

$$\text{power} = \Phi\left(\frac{z_\alpha - \mu_U}{\sigma_U}\right) + \Phi\left(\frac{z_\alpha + \mu_L}{\sigma_L}\right) - 1$$

The approximate sample size is computed by numerically inverting the power formula.

### **Wilson Score Confidence Interval for Binomial Proportion (CI=WILSON)**

The two-sided  $100(1 - \alpha)\%$  confidence interval for  $p$  is

$$\frac{X + \frac{z_{1-\alpha/2}^2}{2}}{N + z_{1-\alpha/2}^2} \pm \frac{z_{1-\alpha/2} N^{\frac{1}{2}}}{N + z_{1-\alpha/2}^2} \left( \hat{p}(1 - \hat{p}) + \frac{z_{1-\alpha/2}^2}{4N} \right)^{\frac{1}{2}}$$

So the half-width for the two-sided  $100(1 - \alpha)\%$  confidence interval is

$$\text{half-width} = \frac{z_{1-\alpha/2} N^{\frac{1}{2}}}{N + z_{1-\alpha/2}^2} \left( \hat{p}(1 - \hat{p}) + \frac{z_{1-\alpha/2}^2}{4N} \right)^{\frac{1}{2}}$$

Prob(Width) is calculated exactly by adding up the probabilities of observing each  $X \in \{1, \dots, N\}$  that produces a confidence interval whose half-width is at most a target value  $h$ :

$$\text{Prob(Width)} = \sum_{i=0}^N P(X = i) 1_{\text{half-width} < h}$$

For references and more details about this and all other confidence intervals associated with the CI= option, see “Binomial Proportion” on page 1744 of Chapter 35, “The FREQ Procedure.”

**Agresti-Coull “Add  $k$  Successes and Failures” Confidence Interval for Binomial Proportion (CI=AGRESTICOULL)**

The two-sided  $100(1 - \alpha)\%$  confidence interval for  $p$  is

$$\frac{X + \frac{z_{1-\alpha/2}^2}{2}}{N + z_{1-\alpha/2}^2} \pm z_{1-\alpha/2} \left( \frac{\frac{X + \frac{z_{1-\alpha/2}^2}{2}}{N + z_{1-\alpha/2}^2} \left( 1 - \frac{X + \frac{z_{1-\alpha/2}^2}{2}}{N + z_{1-\alpha/2}^2} \right)}{N + z_{1-\alpha/2}^2} \right)^{\frac{1}{2}}$$

So the half-width for the two-sided  $100(1 - \alpha)\%$  confidence interval is

$$\text{half-width} = z_{1-\alpha/2} \left( \frac{\frac{X + \frac{z_{1-\alpha/2}^2}{2}}{N + z_{1-\alpha/2}^2} \left( 1 - \frac{X + \frac{z_{1-\alpha/2}^2}{2}}{N + z_{1-\alpha/2}^2} \right)}{N + z_{1-\alpha/2}^2} \right)^{\frac{1}{2}}$$

Prob(Width) is calculated exactly by adding up the probabilities of observing each  $X \in \{1, \dots, N\}$  that produces a confidence interval whose half-width is at most a target value  $h$ :

$$\text{Prob(Width)} = \sum_{i=0}^N P(X = i) 1_{\text{half-width} < h}$$

**Jeffreys Confidence Interval for Binomial Proportion (CI=JEFFREYS)**

The two-sided  $100(1 - \alpha)\%$  confidence interval for  $p$  is

$$[L_J(X), U_J(X)]$$

where

$$L_J(X) = \begin{cases} 0, & X = 0 \\ \text{Beta}_{\alpha/2; X+1/2, N-X+1/2}, & X > 0 \end{cases}$$

and

$$U_J(X) = \begin{cases} \text{Beta}_{1-\alpha/2; X+1/2, N-X+1/2}, & X < N \\ 1, & X = N \end{cases}$$

The half-width of this two-sided  $100(1 - \alpha)\%$  confidence interval is defined as half the width of the full interval:

$$\text{half-width} = \frac{1}{2} (U_J(X) - L_J(X))$$

Prob(Width) is calculated exactly by adding up the probabilities of observing each  $X \in \{1, \dots, N\}$  that produces a confidence interval whose half-width is at most a target value  $h$ :

$$\text{Prob(Width)} = \sum_{i=0}^N P(X = i) 1_{\text{half-width} < h}$$

**Exact Clopper-Pearson Confidence Interval for Binomial Proportion (CI=EXACT)**

The two-sided  $100(1 - \alpha)\%$  confidence interval for  $p$  is

$$[L_E(X), U_E(X)]$$

where

$$L_E(X) = \begin{cases} 0, & X = 0 \\ \text{Beta}_{\alpha/2; X, N-X+1}, & X > 0 \end{cases}$$

and

$$U_E(X) = \begin{cases} \text{Beta}_{1-\alpha/2; X+1, N-X}, & X < N \\ 1, & X = N \end{cases}$$

The half-width of this two-sided  $100(1 - \alpha)\%$  confidence interval is defined as half the width of the full interval:

$$\text{half-width} = \frac{1}{2} (U_E(X) - L_E(X))$$

Prob(Width) is calculated exactly by adding up the probabilities of observing each  $X \in \{1, \dots, N\}$  that produces a confidence interval whose half-width is at most a target value  $h$ :

$$\text{Prob(Width)} = \sum_{i=0}^N P(X = i) 1_{\text{half-width} < h}$$

#### **Wald Confidence Interval for Binomial Proportion (CI=WALD)**

The two-sided  $100(1 - \alpha)\%$  confidence interval for  $p$  is

$$\hat{p} \pm z_{1-\alpha/2} \left( \frac{\hat{p}(1 - \hat{p})}{N} \right)^{\frac{1}{2}}$$

So the half-width for the two-sided  $100(1 - \alpha)\%$  confidence interval is

$$\text{half-width} = z_{1-\alpha/2} \left( \frac{\hat{p}(1 - \hat{p})}{N} \right)^{\frac{1}{2}}$$

Prob(Width) is calculated exactly by adding up the probabilities of observing each  $X \in \{1, \dots, N\}$  that produces a confidence interval whose half-width is at most a target value  $h$ :

$$\text{Prob(Width)} = \sum_{i=0}^N P(X = i) 1_{\text{half-width} < h}$$

#### **Continuity-Corrected Wald Confidence Interval for Binomial Proportion (CI=WALD\_CORRECT)**

The two-sided  $100(1 - \alpha)\%$  confidence interval for  $p$  is

$$\hat{p} \pm \left[ z_{1-\alpha/2} \left( \frac{\hat{p}(1 - \hat{p})}{N} \right)^{\frac{1}{2}} + \frac{1}{2N} \right]$$

So the half-width for the two-sided  $100(1 - \alpha)\%$  confidence interval is

$$\text{half-width} = z_{1-\alpha/2} \left( \frac{\hat{p}(1-\hat{p})}{N} \right)^{\frac{1}{2}} + \frac{1}{2N}$$

Prob(Width) is calculated exactly by adding up the probabilities of observing each  $X \in \{1, \dots, N\}$  that produces a confidence interval whose half-width is at most a target value  $h$ :

$$\text{Prob(Width)} = \sum_{i=0}^N P(X = i) 1_{\text{half-width} < h}$$

## Analyses in the ONESAMPLEMEANS Statement

### One-Sample $t$ Test (TEST=T)

The hypotheses for the one-sample  $t$  test are

$$H_0: \mu = \mu_0$$

$$H_1: \begin{cases} \mu \neq \mu_0, & \text{two-sided} \\ \mu > \mu_0, & \text{upper one-sided} \\ \mu < \mu_0, & \text{lower one-sided} \end{cases}$$

The test assumes normally distributed data and requires  $N \geq 2$ . The test statistics are

$$t = N^{\frac{1}{2}} \left( \frac{\bar{x} - \mu_0}{s} \right) \sim t(N-1, \delta)$$

$$t^2 \sim F(1, N-1, \delta^2)$$

where  $\bar{x}$  is the sample mean,  $s$  is the sample standard deviation, and

$$\delta = N^{\frac{1}{2}} \left( \frac{\mu - \mu_0}{\sigma} \right)$$

The test is

$$\text{Reject } H_0 \text{ if } \begin{cases} t^2 \geq F_{1-\alpha}(1, N-1), & \text{two-sided} \\ t \geq t_{1-\alpha}(N-1), & \text{upper one-sided} \\ t \leq t_{\alpha}(N-1), & \text{lower one-sided} \end{cases}$$

Exact power computations for  $t$  tests are discussed in O'Brien and Muller (1993, Section 8.2), although not specifically for the one-sample case. The power is based on the noncentral  $t$  and  $F$  distributions:

$$\text{power} = \begin{cases} P(F(1, N-1, \delta^2) \geq F_{1-\alpha}(1, N-1)), & \text{two-sided} \\ P(t(N-1, \delta) \geq t_{1-\alpha}(N-1)), & \text{upper one-sided} \\ P(t(N-1, \delta) \leq t_{\alpha}(N-1)), & \text{lower one-sided} \end{cases}$$

Solutions for  $N$ ,  $\alpha$ , and  $\delta$  are obtained by numerically inverting the power equation. Closed-form solutions for other parameters, in terms of  $\delta$ , are as follows:

$$\mu = \delta\sigma N^{-\frac{1}{2}} + \mu_0$$

$$\sigma = \begin{cases} \delta^{-1} N^{\frac{1}{2}} (\mu - \mu_0), & |\delta| > 0 \\ \text{undefined}, & \text{otherwise} \end{cases}$$

### One-Sample $t$ Test with Lognormal Data (TEST=T DIST=LOGNORMAL)

The lognormal case is handled by reexpressing the analysis equivalently as a normality-based test on the log-transformed data, by using properties of the lognormal distribution as discussed in Johnson, Kotz, and Balakrishnan (1994, Chapter 14). The approaches in the section “One-Sample  $t$  Test (TEST=T)” on page 4947 then apply.

In contrast to the usual  $t$  test on normal data, the hypotheses with lognormal data are defined in terms of geometric means rather than arithmetic means. This is because the transformation of a null arithmetic mean of lognormal data to the normal scale depends on the unknown coefficient of variation, resulting in an ill-defined hypothesis on the log-transformed data. Geometric means transform cleanly and are more natural for lognormal data.

The hypotheses for the one-sample  $t$  test with lognormal data are

$$H_0: \frac{\gamma}{\gamma_0} = 1$$

$$H_1: \begin{cases} \frac{\gamma}{\gamma_0} \neq 1, & \text{two-sided} \\ \frac{\gamma}{\gamma_0} > 1, & \text{upper one-sided} \\ \frac{\gamma}{\gamma_0} < 1, & \text{lower one-sided} \end{cases}$$

Let  $\mu^*$  and  $\sigma^*$  be the (arithmetic) mean and standard deviation of the normal distribution of the log-transformed data. The hypotheses can be rewritten as follows:

$$H_0: \mu^* = \log(\gamma_0)$$

$$H_1: \begin{cases} \mu^* \neq \log(\gamma_0), & \text{two-sided} \\ \mu^* > \log(\gamma_0), & \text{upper one-sided} \\ \mu^* < \log(\gamma_0), & \text{lower one-sided} \end{cases}$$

where  $\mu^* = \log(\gamma)$ .

The test assumes lognormally distributed data and requires  $N \geq 2$ .

The power is

$$\text{power} = \begin{cases} P(F(1, N-1, \delta^2) \geq F_{1-\alpha}(1, N-1)), & \text{two-sided} \\ P(t(N-1, \delta) \geq t_{1-\alpha}(N-1)), & \text{upper one-sided} \\ P(t(N-1, \delta) \leq t_{\alpha}(N-1)), & \text{lower one-sided} \end{cases}$$

where

$$\delta = N^{\frac{1}{2}} \left( \frac{\mu^* - \log(\gamma_0)}{\sigma^*} \right)$$

$$\sigma^* = [\log(\text{CV}^2 + 1)]^{\frac{1}{2}}$$

### **Equivalence Test for Mean of Normal Data (TEST=EQUIV DIST=NORMAL)**

The hypotheses for the equivalence test are

$$H_0: \mu < \theta_L \quad \text{or} \quad \mu > \theta_U$$

$$H_1: \theta_L \leq \mu \leq \theta_U$$

The analysis is the two one-sided tests (TOST) procedure of Schuirmann (1987). The test assumes normally distributed data and requires  $N \geq 2$ . Phillips (1990) derives an expression for the exact power assuming a two-sample balanced design; the results are easily adapted to a one-sample design:

$$\text{power} = Q_{N-1} \left( (-t_{1-\alpha}(N-1)), \frac{\mu - \theta_U}{\sigma N^{-\frac{1}{2}}}; 0, \frac{(N-1)^{\frac{1}{2}}(\theta_U - \theta_L)}{2\sigma N^{-\frac{1}{2}}(t_{1-\alpha}(N-1))} \right) -$$

$$Q_{N-1} \left( (t_{1-\alpha}(N-1)), \frac{\mu - \theta_L}{\sigma N^{-\frac{1}{2}}}; 0, \frac{(N-1)^{\frac{1}{2}}(\theta_U - \theta_L)}{2\sigma N^{-\frac{1}{2}}(t_{1-\alpha}(N-1))} \right)$$

where  $Q(\cdot, \cdot; \cdot, \cdot)$  is Owen's Q function, defined in the section "[Common Notation](#)" on page 4920.

### **Equivalence Test for Mean of Lognormal Data (TEST=EQUIV DIST=LOGNORMAL)**

The lognormal case is handled by reexpressing the analysis equivalently as a normality-based test on the log-transformed data, by using properties of the lognormal distribution as discussed in Johnson, Kotz, and Balakrishnan (1994, Chapter 14). The approaches in the section "[Equivalence Test for Mean of Normal Data \(TEST=EQUIV DIST=NORMAL\)](#)" on page 4949 then apply.

In contrast to the additive equivalence test on normal data, the hypotheses with lognormal data are defined in terms of geometric means rather than arithmetic means. This is because the transformation of an arithmetic mean of lognormal data to the normal scale depends on the unknown coefficient of variation, resulting in an ill-defined hypothesis on the log-transformed data. Geometric means transform cleanly and are more natural for lognormal data.

The hypotheses for the equivalence test are

$$H_0: \gamma \leq \theta_L \quad \text{or} \quad \gamma \geq \theta_U$$

$$H_1: \theta_L < \gamma < \theta_U$$

$$\text{where } 0 < \theta_L < \theta_U$$

The analysis is the two one-sided tests (TOST) procedure of Schuirmann (1987) on the log-transformed data. The test assumes lognormally distributed data and requires  $N \geq 2$ . Diletti,

Hauschke, and Steinijs (1991) derive an expression for the exact power assuming a crossover design; the results are easily adapted to a one-sample design:

$$\text{power} = Q_{N-1} \left( (-t_{1-\alpha}(N-1)), \frac{\log(\gamma) - \log(\theta_U)}{\sigma^* N^{-\frac{1}{2}}}; 0, \frac{(N-1)^{\frac{1}{2}}(\log(\theta_U) - \log(\theta_L))}{2\sigma^* N^{-\frac{1}{2}}(t_{1-\alpha}(N-1))} \right) - \\ Q_{N-1} \left( (t_{1-\alpha}(N-1)), \frac{\log(\gamma) - \log(\theta_L)}{\sigma^* N^{-\frac{1}{2}}}; 0, \frac{(N-1)^{\frac{1}{2}}(\log(\theta_U) - \log(\theta_L))}{2\sigma^* N^{-\frac{1}{2}}(t_{1-\alpha}(N-1))} \right)$$

where

$$\sigma^* = [\log(\text{CV}^2 + 1)]^{\frac{1}{2}}$$

is the standard deviation of the log-transformed data, and  $Q(\cdot, \cdot; \cdot, \cdot)$  is Owen's Q function, defined in the section "Common Notation" on page 4920.

### Confidence Interval for Mean (CI-T)

This analysis of precision applies to the standard  $t$ -based confidence interval:

$$\left[ \bar{x} - t_{1-\frac{\alpha}{2}}(N-1) \frac{s}{\sqrt{N}}, \quad \bar{x} + t_{1-\frac{\alpha}{2}}(N-1) \frac{s}{\sqrt{N}} \right], \quad \text{two-sided} \\ \left[ \bar{x} - t_{1-\alpha}(N-1) \frac{s}{\sqrt{N}}, \quad \infty \right), \quad \text{upper one-sided} \\ \left( -\infty, \quad \bar{x} + t_{1-\alpha}(N-1) \frac{s}{\sqrt{N}} \right], \quad \text{lower one-sided}$$

where  $\bar{x}$  is the sample mean and  $s$  is the sample standard deviation. The "half-width" is defined as the distance from the point estimate  $\bar{x}$  to a finite endpoint,

$$\text{half-width} = \begin{cases} t_{1-\frac{\alpha}{2}}(N-1) \frac{s}{\sqrt{N}}, & \text{two-sided} \\ t_{1-\alpha}(N-1) \frac{s}{\sqrt{N}}, & \text{one-sided} \end{cases}$$

A "valid" confidence interval captures the true mean. The exact probability of obtaining at most the target confidence interval half-width  $h$ , unconditional or conditional on validity, is given by Beal (1989):

$$\Pr(\text{half-width} \leq h) = \begin{cases} P \left( \chi^2(N-1) \leq \frac{h^2 N(N-1)}{\sigma^2(t_{1-\frac{\alpha}{2}}(N-1))^2} \right), & \text{two-sided} \\ P \left( \chi^2(N-1) \leq \frac{h^2 N(N-1)}{\sigma^2(t_{1-\alpha}(N-1))^2} \right), & \text{one-sided} \end{cases} \\ \Pr(\text{half-width} \leq h \mid \text{validity}) = \begin{cases} \left( \frac{1}{1-\alpha} \right) 2 \left[ Q_{N-1} \left( (t_{1-\frac{\alpha}{2}}(N-1)), 0; 0, b_1 \right) - Q_{N-1} \left( 0, 0; 0, b_1 \right) \right], & \text{two-sided} \\ \left( \frac{1}{1-\alpha} \right) Q_{N-1} \left( (t_{1-\alpha}(N-1)), 0; 0, b_1 \right), & \text{one-sided} \end{cases}$$

where

$$b_1 = \frac{h(N-1)^{\frac{1}{2}}}{\sigma(t_{1-\frac{\alpha}{c}}(N-1))N^{-\frac{1}{2}}}$$

$c$  = number of sides

and  $Q(\cdot, \cdot; \cdot, \cdot)$  is Owen's Q function, defined in the section "Common Notation" on page 4920.

A "quality" confidence interval is both sufficiently narrow (half-width  $\leq h$ ) and valid:

$$\begin{aligned}\Pr(\text{quality}) &= \Pr(\text{half-width} \leq h \text{ and validity}) \\ &= \Pr(\text{half-width} \leq h \mid \text{validity})(1 - \alpha)\end{aligned}$$

## Analyses in the ONEWAYANOVA Statement

### One-Degree-of-Freedom Contrast (TEST=CONTRAST)

The hypotheses are

$$\begin{aligned}H_0: c_1\mu_1 + \cdots + c_G\mu_G &= c_0 \\ H_1: \begin{cases} c_1\mu_1 + \cdots + c_G\mu_G \neq c_0, & \text{two-sided} \\ c_1\mu_1 + \cdots + c_G\mu_G > c_0, & \text{upper one-sided} \\ c_1\mu_1 + \cdots + c_G\mu_G < c_0, & \text{lower one-sided} \end{cases}\end{aligned}$$

where  $G$  is the number of groups,  $\{c_1, \dots, c_G\}$  are the contrast coefficients, and  $c_0$  is the null contrast value.

The test is the usual  $F$  test for a contrast in one-way ANOVA. It assumes normal data with common group variances and requires  $N \geq G + 1$  and  $n_i \geq 1$ .

O'Brien and Muller (1993, Section 8.2.3.2) give the exact power as

$$\text{power} = \begin{cases} P(F(1, N - G, \delta^2) \geq F_{1-\alpha}(1, N - G)), & \text{two-sided} \\ P(t(N - G, \delta) \geq t_{1-\alpha}(N - G)), & \text{upper one-sided} \\ P(t(N - G, \delta) \leq t_{\alpha}(N - G)), & \text{lower one-sided} \end{cases}$$

where

$$\delta = N^{\frac{1}{2}} \left( \frac{\sum_{i=1}^G c_i \mu_i - c_0}{\sigma \left( \sum_{i=1}^G \frac{c_i^2}{w_i} \right)^{\frac{1}{2}}} \right)$$

### Overall F Test (TEST=OVERALL)

The hypotheses are

$$\begin{aligned}H_0: \mu_1 &= \mu_2 = \cdots = \mu_G \\ H_1: \mu_i &\neq \mu_j \text{ for some } i, j\end{aligned}$$

where  $G$  is the number of groups.

The test is the usual overall  $F$  test for equality of means in one-way ANOVA. It assumes normal data with common group variances and requires  $N \geq G + 1$  and  $n_i \geq 1$ .

O'Brien and Muller (1993, Section 8.2.3.1) give the exact power as

$$\text{power} = P(F(G-1, N-G, \lambda) \geq F_{1-\alpha}(G-1, N-G))$$

where the noncentrality is

$$\lambda = N \left( \frac{\sum_{i=1}^G w_i (\mu_i - \bar{\mu})^2}{\sigma^2} \right)$$

and

$$\bar{\mu} = \sum_{i=1}^G w_i \mu_i$$

## Analyses in the PAIREDFREQ Statement

### Overview of Conditional McNemar tests

Notation:

		Case		
		Failure	Success	
Control	Failure	$n_{00}$	$n_{01}$	$n_{0\cdot}$
	Success	$n_{10}$	$n_{11}$	$n_{1\cdot}$
		$n_{\cdot 0}$	$n_{\cdot 1}$	$N$

$$n_{00} = \#\{\text{control}=\text{failure}, \text{case}=\text{failure}\}$$

$$n_{01} = \#\{\text{control}=\text{failure}, \text{case}=\text{success}\}$$

$$n_{10} = \#\{\text{control}=\text{success}, \text{case}=\text{failure}\}$$

$$n_{11} = \#\{\text{control}=\text{success}, \text{case}=\text{success}\}$$

$$N = n_{00} + n_{01} + n_{10} + n_{11}$$

$$n_D = n_{01} + n_{10} \equiv \#\text{discordant pairs}$$

$$\hat{\pi}_{ij} = \frac{n_{ij}}{N}$$

$$\pi_{ij} = \text{theoretical population value of } \hat{\pi}_{ij}$$

$$\pi_{1\cdot} = \pi_{10} + \pi_{11}$$

$$\pi_{\cdot 1} = \pi_{01} + \pi_{11}$$

$$\phi = \text{Corr}(\text{control observation}, \text{case observation}) \quad (\text{within a pair})$$

$$\text{DPR} = \text{“discordant proportion ratio”} = \frac{\pi_{01}}{\pi_{10}}$$

$$\text{DPR}_0 = \text{null DPR}$$

Power formulas are given here in terms of the discordant proportions  $\pi_{10}$  and  $\pi_{01}$ . If the input is specified in terms of  $\{\pi_{1\cdot}, \pi_{\cdot 1}, \phi\}$ , then it can be converted into values for  $\{\pi_{10}, \pi_{01}\}$  as follows:

$$\pi_{01} = \pi_{\cdot 1}(1 - \pi_{1\cdot}) - \phi((1 - \pi_{1\cdot})\pi_{1\cdot}(1 - \pi_{\cdot 1})\pi_{\cdot 1})^{\frac{1}{2}}$$

$$\pi_{10} = \pi_{01} + \pi_{1\cdot} - \pi_{\cdot 1}$$

All McNemar tests covered in PROC POWER are *conditional*, meaning that  $n_D$  is assumed fixed at its observed value.

For the usual  $DPR_0 = 1$ , the hypotheses are

$$H_0: \pi_{.1} = \pi_{1.}$$

$$H_1: \begin{cases} \pi_{.1} \neq \pi_{1.}, & \text{two-sided} \\ \pi_{.1} > \pi_{1.}, & \text{upper one-sided} \\ \pi_{.1} < \pi_{1.}, & \text{lower one-sided} \end{cases}$$

The test statistic for both tests covered in PROC POWER (DIST=EXACT\_COND and DIST=NORMAL) is the McNemar statistic  $Q_M$ , which has the following form when  $DPR_0 = 1$ :

$$Q_{M_0} = \frac{(n_{01} - n_{10})^2}{n_{01} + n_{10}}$$

For the conditional McNemar tests, this is equivalent to the square of the  $Z(X)$  statistic for the test of a single proportion (normal approximation to binomial), where the proportion is  $\frac{\pi_{01}}{\pi_{01} + \pi_{10}}$ , the null is 0.5, and “ $N$ ” is  $n_D$  (see, for example, Schork and Williams 1980):

$$\begin{aligned} Z(X) &= \frac{n_{01} - n_D(0.5)}{[n_D 0.5(1 - 0.5)]^{\frac{1}{2}}} \sim N \left( \frac{n^{\frac{1}{2}}_D \left( \frac{\pi_{01}}{\pi_{01} + \pi_{10}} - 0.5 \right)}{[0.5(1 - 0.5)]^{\frac{1}{2}}}, \frac{\frac{\pi_{01}}{\pi_{01} + \pi_{10}} \left( 1 - \frac{\pi_{01}}{\pi_{01} + \pi_{10}} \right)}{0.5(1 - 0.5)} \right) \\ &= \frac{n_{01} - (n_{01} + n_{10})(0.5)}{[(n_{01} + n_{10})0.5(1 - 0.5)]^{\frac{1}{2}}} \\ &= \frac{n_{01} - n_{10}}{[n_{01} + n_{10}]^{\frac{1}{2}}} \\ &= \sqrt{Q_{M_0}} \end{aligned}$$

This can be generalized to a custom null for  $\frac{\pi_{01}}{\pi_{01} + \pi_{10}}$ , which is equivalent to specifying a custom null  $DPR$ :

$$\left[ \frac{\pi_{01}}{\pi_{01} + \pi_{10}} \right]_0 \equiv \left[ \frac{1}{1 + \frac{1}{\frac{\pi_{01}}{\pi_{10}}}} \right]_0 \equiv \frac{1}{1 + \frac{1}{DPR_0}}$$

So, a conditional McNemar test (asymptotic or exact) with a custom null is equivalent to the test of a single proportion  $p_1 \equiv \frac{\pi_{01}}{\pi_{01} + \pi_{10}}$  with a null value  $p_0 \equiv \frac{1}{1 + \frac{1}{DPR_0}}$ , with a sample size of  $n_D$ :

$$H_0: p_1 = p_0$$

$$H_1: \begin{cases} p_1 \neq p_0, & \text{two-sided} \\ p_1 > p_0, & \text{one-sided U} \\ p_1 < p_0, & \text{one-sided L} \end{cases}$$

which is equivalent to

$$H_0: \text{DPR} = \text{DPR}_0$$

$$H_1: \begin{cases} \text{DPR} \neq \text{DPR}_0, & \text{two-sided} \\ \text{DPR} > \text{DPR}_0, & \text{one-sided U} \\ \text{DPR} < \text{DPR}_0, & \text{one-sided L} \end{cases}$$

The general form of the test statistic is thus

$$Q_M = \frac{(n_{01} - n_D p_0)^2}{n_D p_0 (1 - p_0)}$$

The two most common conditional McNemar tests assume either the exact conditional distribution of  $Q_M$  (covered by the DIST=EXACT\_COND analysis) or a standard normal distribution for  $Q_M$  (covered by the DIST=NORMAL analysis).

#### **McNemar Exact Conditional Test (TEST=MCNEMAR DIST=EXACT\_COND)**

For DIST=EXACT\_COND, the power is calculated assuming that the test is conducted by using the exact conditional distribution of  $Q_M$  (conditional on  $n_D$ ). The power is calculated by first computing the conditional power for each possible  $n_D$ . The unconditional power is computed as a weighted average over all possible outcomes of  $n_D$ :

$$\text{power} = \sum_{n_D=0}^N P(n_D) P(\text{Reject } p_1 = p_0 | n_D)$$

where  $n_D \sim \text{Bin}(\pi_{01} + \pi_{10}, N)$ , and  $P(\text{Reject } p_1 = p_0 | n_D)$  is calculated by using the exact method in the section “[Exact Test of a Binomial Proportion \(TEST=EXACT\)](#)” on page 4928.

The achieved significance level, reported as “Actual Alpha” in the analysis, is computed in the same way except by using the actual alpha of the one-sample test in place of its power:

$$\text{actual alpha} = \sum_{n_D=0}^N P(n_D) \alpha^*(p_1, p_0 | n_D)$$

where  $\alpha^*(p_1, p_0 | n_D)$  is the actual alpha calculated by using the exact method in the section “[Exact Test of a Binomial Proportion \(TEST=EXACT\)](#)” on page 4928 with proportion  $p_1$ , null  $p_0$ , and sample size  $n_D$ .

#### **McNemar Normal Approximation Test (TEST=MCNEMAR DIST=NORMAL)**

For DIST=NORMAL, power is calculated assuming the test is conducted by using the normal-approximate distribution of  $Q_M$  (conditional on  $n_D$ ).

For the METHOD=EXACT option, the power is calculated in the same way as described in the section “[McNemar Exact Conditional Test \(TEST=MCNEMAR DIST=EXACT\\_COND\)](#)” on page 4954, except that  $P(\text{Reject } p_1 = p_0 | n_D)$  is calculated by using the exact method in the section

“z Test for Binomial Proportion Using Null Variance (TEST=Z VAREST=NULL)” on page 4929. The achieved significance level is calculated in the same way as described at the end of the section “McNemar Exact Conditional Test (TEST=MCNEMAR DIST=EXACT\_COND)” on page 4954.

For the METHOD=MIETTINEN option, approximate sample size for the one-sided cases is computed according to equation (5.6) in Miettinen (1968):

$$N = \frac{\left\{ z_{1-\alpha}(p_{10} + p_{01}) + z_{power} \left[ (p_{10} + p_{01})^2 - \frac{1}{4}(p_{01} - p_{10})^2(3 + p_{10} + p_{01}) \right]^{\frac{1}{2}} \right\}^2}{(p_{10} + p_{01})(p_{01} - p_{10})^2}$$

Approximate power for the one-sided cases is computed by solving the sample size equation for power, and approximate power for the two-sided case follows easily by summing the one-sided powers each at  $\alpha/2$ :

$$\text{power} = \begin{cases} \Phi \left( \frac{(p_{01} - p_{10})[N(p_{10} + p_{01})]^{\frac{1}{2}} - z_{1-\alpha}(p_{10} + p_{01})}{[(p_{10} + p_{01})^2 - \frac{1}{4}(p_{01} - p_{10})^2(3 + p_{10} + p_{01})]^{\frac{1}{2}}} \right), & \text{upper one-sided} \\ \Phi \left( \frac{-(p_{01} - p_{10})[N(p_{10} + p_{01})]^{\frac{1}{2}} - z_{1-\alpha}(p_{10} + p_{01})}{[(p_{10} + p_{01})^2 - \frac{1}{4}(p_{01} - p_{10})^2(3 + p_{10} + p_{01})]^{\frac{1}{2}}} \right), & \text{lower one-sided} \\ \Phi \left( \frac{(p_{01} - p_{10})[N(p_{10} + p_{01})]^{\frac{1}{2}} - z_{1-\frac{\alpha}{2}}(p_{10} + p_{01})}{[(p_{10} + p_{01})^2 - \frac{1}{4}(p_{01} - p_{10})^2(3 + p_{10} + p_{01})]^{\frac{1}{2}}} \right) + \\ \Phi \left( \frac{-(p_{01} - p_{10})[N(p_{10} + p_{01})]^{\frac{1}{2}} - z_{1-\frac{\alpha}{2}}(p_{10} + p_{01})}{[(p_{10} + p_{01})^2 - \frac{1}{4}(p_{01} - p_{10})^2(3 + p_{10} + p_{01})]^{\frac{1}{2}}} \right), & \text{two-sided} \end{cases}$$

The two-sided solution for  $N$  is obtained by numerically inverting the power equation.

In general, compared to METHOD=CONNOR, the METHOD=MIETTINEN approximation tends to be slightly more accurate but can be slightly anticonservative in the sense of underestimating sample size and overestimating power (Lachin 1992, p. 1250).

For the METHOD=CONNOR option, approximate sample size for the one-sided cases is computed according to equation (3) in Connor (1987):

$$N = \frac{\left\{ z_{1-\alpha}(p_{10} + p_{01})^{\frac{1}{2}} + z_{power} [p_{10} + p_{01} - (p_{01} - p_{10})^2]^{\frac{1}{2}} \right\}^2}{(p_{01} - p_{10})^2}$$

Approximate power for the one-sided cases is computed by solving the sample size equation for power, and approximate power for the two-sided case follows easily by summing the one-sided powers each at  $\alpha/2$ :

$$\text{power} = \begin{cases} \Phi \left( \frac{(p_{01} - p_{10})N^{\frac{1}{2}} - z_{1-\alpha}(p_{10} + p_{01})^{\frac{1}{2}}}{[p_{10} + p_{01} - (p_{01} - p_{10})^2]^{\frac{1}{2}}} \right), & \text{upper one-sided} \\ \Phi \left( \frac{-(p_{01} - p_{10})N^{\frac{1}{2}} - z_{1-\alpha}(p_{10} + p_{01})^{\frac{1}{2}}}{[p_{10} + p_{01} - (p_{01} - p_{10})^2]^{\frac{1}{2}}} \right), & \text{lower one-sided} \\ \Phi \left( \frac{(p_{01} - p_{10})N^{\frac{1}{2}} - z_{1-\frac{\alpha}{2}}(p_{10} + p_{01})^{\frac{1}{2}}}{[p_{10} + p_{01} - (p_{01} - p_{10})^2]^{\frac{1}{2}}} \right) + \\ \Phi \left( \frac{-(p_{01} - p_{10})N^{\frac{1}{2}} - z_{1-\frac{\alpha}{2}}(p_{10} + p_{01})^{\frac{1}{2}}}{[p_{10} + p_{01} - (p_{01} - p_{10})^2]^{\frac{1}{2}}} \right), & \text{two-sided} \end{cases}$$

The two-sided solution for  $N$  is obtained by numerically inverting the power equation.

In general, compared to METHOD=MIETTINEN, the METHOD=CONNOR approximation tends to be slightly less accurate but slightly conservative in the sense of overestimating sample size and underestimating power (Lachin 1992, p. 1250).

## Analyses in the PAIREDMEANS Statement

### Paired $t$ Test (TEST=DIFF)

The hypotheses for the paired  $t$  test are

$$H_0: \mu_{\text{diff}} = \mu_0$$

$$H_1: \begin{cases} \mu_{\text{diff}} \neq \mu_0, & \text{two-sided} \\ \mu_{\text{diff}} > \mu_0, & \text{upper one-sided} \\ \mu_{\text{diff}} < \mu_0, & \text{lower one-sided} \end{cases}$$

The test assumes normally distributed data and requires  $N \geq 2$ . The test statistics are

$$t = N^{\frac{1}{2}} \left( \frac{\bar{d} - \mu_0}{s_d} \right) \sim t(N - 1, \delta)$$

$$t^2 \sim F(1, N - 1, \delta^2)$$

where  $\bar{d}$  and  $s_d$  are the sample mean and standard deviation of the differences and

$$\delta = N^{\frac{1}{2}} \left( \frac{\mu_{\text{diff}} - \mu_0}{\sigma_{\text{diff}}} \right)$$

and

$$\sigma_{\text{diff}} = (\sigma_1^2 + \sigma_2^2 - 2\rho\sigma_1\sigma_2)^{\frac{1}{2}}$$

The test is

$$\text{Reject } H_0 \text{ if } \begin{cases} t^2 \geq F_{1-\alpha}(1, N - 1), & \text{two-sided} \\ t \geq t_{1-\alpha}(N - 1), & \text{upper one-sided} \\ t \leq t_{\alpha}(N - 1), & \text{lower one-sided} \end{cases}$$

Exact power computations for  $t$  tests are given in O'Brien and Muller (1993, Section 8.2.2):

$$\text{power} = \begin{cases} P(F(1, N - 1, \delta^2) \geq F_{1-\alpha}(1, N - 1)), & \text{two-sided} \\ P(t(N - 1, \delta) \geq t_{1-\alpha}(N - 1)), & \text{upper one-sided} \\ P(t(N - 1, \delta) \leq t_{\alpha}(N - 1)), & \text{lower one-sided} \end{cases}$$

**Paired  $t$  Test for Mean Ratio with Lognormal Data (TEST=RATIO)**

The lognormal case is handled by reexpressing the analysis equivalently as a normality-based test on the log-transformed data, by using properties of the lognormal distribution as discussed in Johnson, Kotz, and Balakrishnan (1994, Chapter 14). The approaches in the section “Paired  $t$  Test (TEST=DIFF)” on page 4956 then apply.

In contrast to the usual  $t$  test on normal data, the hypotheses with lognormal data are defined in terms of geometric means rather than arithmetic means.

The hypotheses for the paired  $t$  test with lognormal pairs  $\{Y_1, Y_2\}$  are

$$H_0: \frac{\gamma_2}{\gamma_1} = \gamma_0$$

$$H_1: \begin{cases} \frac{\gamma_2}{\gamma_1} \neq \gamma_0, & \text{two-sided} \\ \frac{\gamma_2}{\gamma_1} > \gamma_0, & \text{upper one-sided} \\ \frac{\gamma_2}{\gamma_1} < \gamma_0, & \text{lower one-sided} \end{cases}$$

Let  $\mu_1^*$ ,  $\mu_2^*$ ,  $\sigma_1^*$ ,  $\sigma_2^*$ , and  $\rho^*$  be the (arithmetic) means, standard deviations, and correlation of the bivariate normal distribution of the log-transformed data  $\{\log Y_1, \log Y_2\}$ . The hypotheses can be rewritten as follows:

$$H_0: \mu_2^* - \mu_1^* = \log(\gamma_0)$$

$$H_1: \begin{cases} \mu_2^* - \mu_1^* \neq \log(\gamma_0), & \text{two-sided} \\ \mu_2^* - \mu_1^* > \log(\gamma_0), & \text{upper one-sided} \\ \mu_2^* - \mu_1^* < \log(\gamma_0), & \text{lower one-sided} \end{cases}$$

where

$$\mu_1^* = \log \gamma_1$$

$$\mu_2^* = \log \gamma_2$$

$$\sigma_1^* = [\log(\text{CV}_1^2 + 1)]^{\frac{1}{2}}$$

$$\sigma_2^* = [\log(\text{CV}_2^2 + 1)]^{\frac{1}{2}}$$

$$\rho^* = \frac{\log\{\rho \text{CV}_1 \text{CV}_2 + 1\}}{\sigma_1^* \sigma_2^*}$$

and  $\text{CV}_1$ ,  $\text{CV}_2$ , and  $\rho$  are the coefficients of variation and the correlation of the original untransformed pairs  $\{Y_1, Y_2\}$ . The conversion from  $\rho$  to  $\rho^*$  is shown in Jones and Miller (1966).

The test assumes lognormally distributed data and requires  $N \geq 2$ . The power is

$$\text{power} = \begin{cases} P(F(1, N-1, \delta^2) \geq F_{1-\alpha}(1, N-1)), & \text{two-sided} \\ P(t(N-1, \delta) \geq t_{1-\alpha}(N-1)), & \text{upper one-sided} \\ P(t(N-1, \delta) \leq t_{\alpha}(N-1)), & \text{lower one-sided} \end{cases}$$

where

$$\delta = N^{\frac{1}{2}} \left( \frac{\mu_1^* - \mu_2^* - \log(\gamma_0)}{\sigma^*} \right)$$

and

$$\sigma^* = (\sigma_1^{*2} + \sigma_2^{*2} - 2\rho^* \sigma_1^* \sigma_2^*)^{\frac{1}{2}}$$

### Additive Equivalence Test for Mean Difference with Normal Data (TEST=EQUIV\_DIFF)

The hypotheses for the equivalence test are

$$H_0: \mu_{\text{diff}} < \theta_L \quad \text{or} \quad \mu_{\text{diff}} > \theta_U$$

$$H_1: \theta_L \leq \mu_{\text{diff}} \leq \theta_U$$

The analysis is the two one-sided tests (TOST) procedure of Schuirmann (1987). The test assumes normally distributed data and requires  $N \geq 2$ . Phillips (1990) derives an expression for the exact power assuming a two-sample balanced design; the results are easily adapted to a paired design:

$$\begin{aligned} \text{power} = & Q_{N-1} \left( (-t_{1-\alpha}(N-1)), \frac{\mu_{\text{diff}} - \theta_U}{\sigma_{\text{diff}} N^{-\frac{1}{2}}}; 0, \frac{(N-1)^{\frac{1}{2}}(\theta_U - \theta_L)}{2\sigma_{\text{diff}} N^{-\frac{1}{2}}(t_{1-\alpha}(N-1))} \right) - \\ & Q_{N-1} \left( (t_{1-\alpha}(N-1)), \frac{\mu_{\text{diff}} - \theta_L}{\sigma_{\text{diff}} N^{-\frac{1}{2}}}; 0, \frac{(N-1)^{\frac{1}{2}}(\theta_U - \theta_L)}{2\sigma_{\text{diff}} N^{-\frac{1}{2}}(t_{1-\alpha}(N-1))} \right) \end{aligned}$$

where

$$\sigma_{\text{diff}} = (\sigma_1^2 + \sigma_2^2 - 2\rho\sigma_1\sigma_2)^{\frac{1}{2}}$$

and  $Q(\cdot, \cdot, \cdot, \cdot)$  is Owen's Q function, defined in the section "Common Notation" on page 4920.

### Multiplicative Equivalence Test for Mean Ratio with Lognormal Data (TEST=EQUIV\_RATIO)

The lognormal case is handled by reexpressing the analysis equivalently as a normality-based test on the log-transformed data, by using properties of the lognormal distribution as discussed in Johnson, Kotz, and Balakrishnan (1994, Chapter 14). The approaches in the section "Additive Equivalence Test for Mean Difference with Normal Data (TEST=EQUIV\_DIFF)" on page 4958 then apply.

In contrast to the additive equivalence test on normal data, the hypotheses with lognormal data are defined in terms of geometric means rather than arithmetic means.

The hypotheses for the equivalence test are

$$H_0: \frac{\gamma_T}{\gamma_R} \leq \theta_L \quad \text{or} \quad \frac{\gamma_T}{\gamma_R} \geq \theta_U$$

$$H_1: \theta_L < \frac{\gamma_T}{\gamma_R} < \theta_U$$

$$\text{where } 0 < \theta_L < \theta_U$$

The analysis is the two one-sided tests (TOST) procedure of Schuirmann (1987) on the log-transformed data. The test assumes lognormally distributed data and requires  $N \geq 2$ . Diletti, Hauschke, and Steinijs (1991) derive an expression for the exact power assuming a crossover design; the results are easily adapted to a paired design:

$$\text{power} = Q_{N-1} \left( (-t_{1-\alpha}(N-1)), \frac{\log\left(\frac{\gamma_T}{\gamma_R}\right) - \log(\theta_U)}{\sigma^* N^{-\frac{1}{2}}}; 0, \frac{(N-1)^{\frac{1}{2}}(\log(\theta_U) - \log(\theta_L))}{2\sigma^* N^{-\frac{1}{2}}(t_{1-\alpha}(N-1))} \right) - Q_{N-1} \left( (t_{1-\alpha}(N-1)), \frac{\log\left(\frac{\gamma_T}{\gamma_R}\right) - \log(\theta_L)}{\sigma^* N^{-\frac{1}{2}}}; 0, \frac{(N-1)^{\frac{1}{2}}(\log(\theta_U) - \log(\theta_L))}{2\sigma^* N^{-\frac{1}{2}}(t_{1-\alpha}(N-1))} \right)$$

where  $\sigma^*$  is the standard deviation of the differences between the log-transformed pairs (in other words, the standard deviation of  $\log(Y_T) - \log(Y_R)$ , where  $Y_T$  and  $Y_R$  are observations from the treatment and reference, respectively), computed as

$$\begin{aligned} \sigma^* &= (\sigma_R^{*2} + \sigma_T^{*2} - 2\rho^* \sigma_R^* \sigma_T^*)^{\frac{1}{2}} \\ \sigma_R^* &= [\log(\text{CV}_R^2 + 1)]^{\frac{1}{2}} \\ \sigma_T^* &= [\log(\text{CV}_T^2 + 1)]^{\frac{1}{2}} \\ \rho^* &= \frac{\log\{\rho \text{CV}_R \text{CV}_T + 1\}}{\sigma_R^* \sigma_T^*} \end{aligned}$$

where  $\text{CV}_R$ ,  $\text{CV}_T$ , and  $\rho$  are the coefficients of variation and the correlation of the original untransformed pairs  $\{Y_T, Y_R\}$ , and  $Q(\cdot, \cdot; \cdot, \cdot)$  is Owen’s Q function. The conversion from  $\rho$  to  $\rho^*$  is shown in Jones and Miller (1966), and Owen’s Q function is defined in the section “Common Notation” on page 4920.

**Confidence Interval for Mean Difference (CI=DIFF)**

This analysis of precision applies to the standard  $t$ -based confidence interval:

$$\begin{aligned} &\left[ \bar{d} - t_{1-\frac{\alpha}{2}}(N-1) \frac{s_d}{\sqrt{N}}, \quad \bar{d} + t_{1-\frac{\alpha}{2}}(N-1) \frac{s_d}{\sqrt{N}} \right], && \text{two-sided} \\ &\left[ \bar{d} - t_{1-\alpha}(N-1) \frac{s_d}{\sqrt{N}}, \quad \infty \right), && \text{upper one-sided} \\ &\left( -\infty, \quad \bar{d} + t_{1-\alpha}(N-1) \frac{s_d}{\sqrt{N}} \right], && \text{lower one-sided} \end{aligned}$$

where  $\bar{d}$  and  $s_d$  are the sample mean and standard deviation of the differences. The “half-width” is defined as the distance from the point estimate  $\bar{d}$  to a finite endpoint,

$$\text{half-width} = \begin{cases} t_{1-\frac{\alpha}{2}}(N-1) \frac{s_d}{\sqrt{N}}, & \text{two-sided} \\ t_{1-\alpha}(N-1) \frac{s_d}{\sqrt{N}}, & \text{one-sided} \end{cases}$$

A “valid” conference interval captures the true mean difference. The exact probability of obtaining at most the target confidence interval half-width  $h$ , unconditional or conditional on validity, is given

by Beal (1989):

$$\Pr(\text{half-width} \leq h) = \begin{cases} P\left(\chi^2(N-1) \leq \frac{h^2 N(N-1)}{\sigma_{\text{diff}}^2 (t_{1-\frac{\alpha}{2}}^2(N-1))}\right), & \text{two-sided} \\ P\left(\chi^2(N-1) \leq \frac{h^2 N(N-1)}{\sigma_{\text{diff}}^2 (t_{1-\alpha}^2(N-1))}\right), & \text{one-sided} \end{cases}$$

$$\Pr(\text{half-width} \leq h \mid \text{validity}) = \begin{cases} \left(\frac{1}{1-\alpha}\right) 2 \left[ Q_{N-1}\left((t_{1-\frac{\alpha}{2}}(N-1)), 0; 0, b_1\right) - Q_{N-1}(0, 0; 0, b_1) \right], & \text{two-sided} \\ \left(\frac{1}{1-\alpha}\right) Q_{N-1}\left((t_{1-\alpha}(N-1)), 0; 0, b_1\right), & \text{one-sided} \end{cases}$$

where

$$\sigma_{\text{diff}} = (\sigma_1^2 + \sigma_2^2 - 2\rho\sigma_1\sigma_2)^{\frac{1}{2}}$$

$$b_1 = \frac{h(N-1)^{\frac{1}{2}}}{\sigma_{\text{diff}}(t_{1-\frac{\alpha}{c}}(N-1))N^{-\frac{1}{2}}}$$

$c$  = number of sides

and  $Q(\cdot, \cdot; \cdot, \cdot)$  is Owen's Q function, defined in the section "Common Notation" on page 4920.

A "quality" confidence interval is both sufficiently narrow (half-width  $\leq h$ ) and valid:

$$\begin{aligned} \Pr(\text{quality}) &= \Pr(\text{half-width} \leq h \text{ and validity}) \\ &= \Pr(\text{half-width} \leq h \mid \text{validity})(1 - \alpha) \end{aligned}$$

## Analyses in the TWOSAMPLEFREQ Statement

### Overview of the $2 \times 2$ Table

Notation:

		Outcome		
		Failure	Success	
Group	1	$n_1 - x_1$	$x_1$	$n_1$
	2	$n_2 - x_2$	$x_2$	$n_2$
		$N - m$	$m$	$N$

$x_1$  = # successes in group 1

$x_2$  = # successes in group 2

$m = x_1 + x_2$  = total # successes

$$\hat{p}_1 = \frac{x_1}{n_1}$$

$$\hat{p}_2 = \frac{x_2}{n_2}$$

$$\hat{p} = \frac{m}{N} = w_1 \hat{p}_1 + w_2 \hat{p}_2$$

The hypotheses are

$$H_0: p_2 - p_1 = p_0$$

$$H_1: \begin{cases} p_2 - p_1 \neq p_0, & \text{two-sided} \\ p_2 - p_1 > p_0, & \text{upper one-sided} \\ p_2 - p_1 < p_0, & \text{lower one-sided} \end{cases}$$

where  $p_0$  is constrained to be 0 for all but the unconditional Pearson chi-square test.

Internal calculations are performed in terms of  $p_1$ ,  $p_2$ , and  $p_0$ . An input set consisting of  $OR$ ,  $p_1$ , and  $OR_0$  is transformed as follows:

$$p_2 = \frac{(OR)p_1}{1 - p_1 + (OR)p_1}$$

$$p_{10} = p_1$$

$$p_{20} = \frac{OR_0 p_{10}}{1 - p_{10} + (OR_0)p_{10}}$$

$$p_0 = p_{20} - p_{10}$$

An input set consisting of  $RR$ ,  $p_1$ , and  $RR_0$  is transformed as follows:

$$p_2 = (RR)p_1$$

$$p_{10} = p_1$$

$$p_{20} = (RR_0)p_{10}$$

$$p_0 = p_{20} - p_{10}$$

Note that the transformation of either  $OR_0$  or  $RR_0$  to  $p_0$  is not unique. The chosen parameterization fixes the null value  $p_{10}$  at the input value of  $p_1$ .

### **Pearson Chi-Square Test for Two Proportions (TEST=PCHI)**

The usual Pearson chi-square test is unconditional. The test statistic

$$z_P = \frac{\hat{p}_2 - \hat{p}_1 - p_0}{\left[ \hat{p}(1 - \hat{p}) \left( \frac{1}{n_1} + \frac{1}{n_2} \right) \right]^{\frac{1}{2}}} = [Nw_1w_2]^{\frac{1}{2}} \frac{\hat{p}_2 - \hat{p}_1 - p_0}{\hat{p}(1 - \hat{p})}$$

is assumed to have a null distribution of  $N(0, 1)$ .

Sample size for the one-sided cases is given by equation (4) in Fleiss, Tytun, and Ury (1980). One-sided power is computed as suggested by Diegert and Diegert (1981) by inverting the sample size formula. Power for the two-sided case is computed by adding the lower-sided and upper-sided powers each with  $\alpha/2$ , and sample size for the two-sided case is obtained by numerically inverting

the power formula. A custom null value  $p_0$  for the proportion difference  $p_2 - p_1$  is also supported.

$$\text{power} = \begin{cases} \Phi \left( \frac{(p_2 - p_1 - p_0)(N w_1 w_2)^{\frac{1}{2}} - z_{1-\alpha} [(w_1 p_1 + w_2 p_2)(1 - w_1 p_1 - w_2 p_2)]^{\frac{1}{2}}}{[w_2 p_1 (1 - p_1) + w_1 p_2 (1 - p_2)]^{\frac{1}{2}}} \right), & \text{upper one-sided} \\ \Phi \left( \frac{-(p_2 - p_1 - p_0)(N w_1 w_2)^{\frac{1}{2}} - z_{1-\alpha} [(w_1 p_1 + w_2 p_2)(1 - w_1 p_1 - w_2 p_2)]^{\frac{1}{2}}}{[w_2 p_1 (1 - p_1) + w_1 p_2 (1 - p_2)]^{\frac{1}{2}}} \right), & \text{lower one-sided} \\ \Phi \left( \frac{(p_2 - p_1 - p_0)(N w_1 w_2)^{\frac{1}{2}} - z_{1-\frac{\alpha}{2}} [(w_1 p_1 + w_2 p_2)(1 - w_1 p_1 - w_2 p_2)]^{\frac{1}{2}}}{[w_2 p_1 (1 - p_1) + w_1 p_2 (1 - p_2)]^{\frac{1}{2}}} \right) + \\ \Phi \left( \frac{-(p_2 - p_1 - p_0)(N w_1 w_2)^{\frac{1}{2}} - z_{1-\frac{\alpha}{2}} [(w_1 p_1 + w_2 p_2)(1 - w_1 p_1 - w_2 p_2)]^{\frac{1}{2}}}{[w_2 p_1 (1 - p_1) + w_1 p_2 (1 - p_2)]^{\frac{1}{2}}} \right), & \text{two-sided} \end{cases}$$

For the one-sided cases, a closed-form inversion of the power equation yield an approximate total sample size

$$N = \frac{\left[ z_{1-\alpha} \{(w_1 p_1 + w_2 p_2)(1 - w_1 p_1 - w_2 p_2)\}^{\frac{1}{2}} + z_{\text{power}} \{w_2 p_1 (1 - p_1) + w_1 p_2 (1 - p_2)\}^{\frac{1}{2}} \right]^2}{w_1 w_2 (p_2 - p_1 - p_0)^2}$$

For the two-sided case, the solution for  $N$  is obtained by numerically inverting the power equation.

### Likelihood Ratio Chi-Square Test for Two Proportions (TEST=LRCHI)

The usual likelihood ratio chi-square test is unconditional. The test statistic

$$z_{LR} = (-1_{\{p_2 < p_1\}}) \sqrt{2N \sum_{i=1}^2 \left[ w_i \hat{p}_i \log \left( \frac{\hat{p}_i}{\hat{p}} \right) + w_i (1 - \hat{p}_i) \log \left( \frac{1 - \hat{p}_i}{1 - \hat{p}} \right) \right]}$$

is assumed to have a null distribution of  $N(0, 1)$  and an alternative distribution of  $N(\delta, 1)$ , where

$$\delta = N^{\frac{1}{2}} (-1_{\{p_2 < p_1\}}) \sqrt{2 \sum_{i=1}^2 \left[ w_i p_i \log \left( \frac{p_i}{w_1 p_1 + w_2 p_2} \right) + w_i (1 - p_i) \log \left( \frac{1 - p_i}{1 - (w_1 p_1 + w_2 p_2)} \right) \right]}$$

The approximate power is

$$\text{power} = \begin{cases} \Phi(\delta - z_{1-\alpha}), & \text{upper one-sided} \\ \Phi(-\delta - z_{1-\alpha}), & \text{lower one-sided} \\ \Phi(\delta - z_{1-\frac{\alpha}{2}}) + \Phi(-\delta - z_{1-\frac{\alpha}{2}}), & \text{two-sided} \end{cases}$$

For the one-sided cases, a closed-form inversion of the power equation yield an approximate total sample size

$$N = \left( \frac{z_{\text{power}} + z_{1-\alpha}}{\delta} \right)^2$$

For the two-sided case, the solution for  $N$  is obtained by numerically inverting the power equation.

### Fisher's Exact Conditional Test for Two Proportions (TEST=FISHER)

Fisher's exact test is conditional on the observed total number of successes  $m$ . Power and sample size computations for the METHOD=WALTERS option are based on a test with similar power properties, the continuity-adjusted arcsine test. The test statistic

$$z_A = (4Nw_1w_2)^{\frac{1}{2}} \left[ \arcsin \left( \left[ \hat{p}_2 + \frac{1}{2Nw_2} (1_{\{\hat{p}_2 < \hat{p}_1\}} - 1_{\{\hat{p}_2 > \hat{p}_1\}}) \right]^{\frac{1}{2}} \right) - \arcsin \left( \left[ \hat{p}_1 + \frac{1}{2Nw_1} (1_{\{\hat{p}_1 < \hat{p}_2\}} - 1_{\{\hat{p}_1 > \hat{p}_2\}}) \right]^{\frac{1}{2}} \right) \right]$$

is assumed to have a null distribution of  $N(0, 1)$  and an alternative distribution of  $N(\delta, 1)$ , where

$$\delta = (4Nw_1w_2)^{\frac{1}{2}} \left[ \arcsin \left( \left[ p_2 + \frac{1}{2Nw_2} (1_{\{p_2 < p_1\}} - 1_{\{p_2 > p_1\}}) \right]^{\frac{1}{2}} \right) - \arcsin \left( \left[ p_1 + \frac{1}{2Nw_1} (1_{\{p_1 < p_2\}} - 1_{\{p_1 > p_2\}}) \right]^{\frac{1}{2}} \right) \right]$$

The approximate power for the one-sided balanced case is given by Walters (1979) and is easily extended to the unbalanced and two-sided cases:

$$\text{power} = \begin{cases} \Phi(\delta - z_{1-\alpha}), & \text{upper one-sided} \\ \Phi(-\delta - z_{1-\alpha}), & \text{lower one-sided} \\ \Phi(\delta - z_{1-\frac{\alpha}{2}}) + \Phi(-\delta - z_{1-\frac{\alpha}{2}}), & \text{two-sided} \end{cases}$$

## Analyses in the TWOSAMPLEMEANS Statement

### Two-Sample t Test Assuming Equal Variances (TEST=DIFF)

The hypotheses for the two-sample  $t$  test are

$$H_0: \mu_{\text{diff}} = \mu_0$$

$$H_1: \begin{cases} \mu_{\text{diff}} \neq \mu_0, & \text{two-sided} \\ \mu_{\text{diff}} > \mu_0, & \text{upper one-sided} \\ \mu_{\text{diff}} < \mu_0, & \text{lower one-sided} \end{cases}$$

The test assumes normally distributed data and common standard deviation per group, and it requires  $N \geq 3$ ,  $n_1 \geq 1$ , and  $n_2 \geq 1$ . The test statistics are

$$t = N^{\frac{1}{2}}(w_1w_2)^{\frac{1}{2}} \left( \frac{\bar{x}_2 - \bar{x}_1 - \mu_0}{s_p} \right) \sim t(N - 2, \delta)$$

$$t^2 \sim F(1, N - 2, \delta^2)$$

where  $\bar{x}_1$  and  $\bar{x}_2$  are the sample means and  $s_p$  is the pooled standard deviation, and

$$\delta = N^{\frac{1}{2}}(w_1w_2)^{\frac{1}{2}} \left( \frac{\mu_{\text{diff}} - \mu_0}{\sigma} \right)$$

The test is

$$\text{Reject } H_0 \text{ if } \begin{cases} t^2 \geq F_{1-\alpha}(1, N-2), & \text{two-sided} \\ t \geq t_{1-\alpha}(N-2), & \text{upper one-sided} \\ t \leq t_{\alpha}(N-2), & \text{lower one-sided} \end{cases}$$

Exact power computations for  $t$  tests are given in O'Brien and Muller (1993, Section 8.2.1):

$$\text{power} = \begin{cases} P(F(1, N-2, \delta^2) \geq F_{1-\alpha}(1, N-2)), & \text{two-sided} \\ P(t(N-2, \delta) \geq t_{1-\alpha}(N-2)), & \text{upper one-sided} \\ P(t(N-2, \delta) \leq t_{\alpha}(N-2)), & \text{lower one-sided} \end{cases}$$

Solutions for  $N$ ,  $n_1$ ,  $n_2$ ,  $\alpha$ , and  $\delta$  are obtained by numerically inverting the power equation. Closed-form solutions for other parameters, in terms of  $\delta$ , are as follows:

$$\begin{aligned} \mu_{\text{diff}} &= \delta\sigma(Nw_1w_2)^{-\frac{1}{2}} + \mu_0 \\ \mu_1 &= \delta\sigma(Nw_1w_2)^{-\frac{1}{2}} + \mu_0 - \mu_2 \\ \mu_2 &= \delta\sigma(Nw_1w_2)^{-\frac{1}{2}} + \mu_0 - \mu_1 \\ \sigma &= \begin{cases} \delta^{-1}(Nw_1w_2)^{\frac{1}{2}}(\mu_{\text{diff}} - \mu_0), & |\delta| > 0 \\ \text{undefined}, & \text{otherwise} \end{cases} \\ w_1 &= \begin{cases} \frac{1}{2} \pm \frac{1}{2} \left[ 1 - \frac{4\delta^2\sigma^2}{N(\mu_{\text{diff}} - \mu_0)^2} \right]^{\frac{1}{2}}, & 0 < |\delta| \leq \frac{1}{2} N^{\frac{1}{2}} \frac{|\mu_{\text{diff}} - \mu_0|}{\sigma} \\ \text{undefined}, & \text{otherwise} \end{cases} \\ w_2 &= \begin{cases} \frac{1}{2} \pm \frac{1}{2} \left[ 1 - \frac{4\delta^2\sigma^2}{N(\mu_{\text{diff}} - \mu_0)^2} \right]^{\frac{1}{2}}, & 0 < |\delta| \leq \frac{1}{2} N^{\frac{1}{2}} \frac{|\mu_{\text{diff}} - \mu_0|}{\sigma} \\ \text{undefined}, & \text{otherwise} \end{cases} \end{aligned}$$

Finally, here is a derivation of the solution for  $w_1$ :

Solve the  $\delta$  equation for  $w_1$  (which requires the quadratic formula). Then determine the range of  $\delta$  given  $w_1$ :

$$\begin{aligned} \min(\delta) &= \begin{cases} 0, & \text{when } w_1 = 0 \text{ or } 1, \text{ if } (\mu_{\text{diff}} - \mu_0) \geq 0 \\ \frac{1}{2} N^{\frac{1}{2}} \frac{(\mu_{\text{diff}} - \mu_0)}{\sigma}, & \text{when } w_1 = \frac{1}{2}, \text{ if } (\mu_{\text{diff}} - \mu_0) < 0 \end{cases} \\ \max(\delta) &= \begin{cases} 0, & \text{when } w_1 = 0 \text{ or } 1, \text{ if } (\mu_{\text{diff}} - \mu_0) < 0 \\ \frac{1}{2} N^{\frac{1}{2}} \frac{(\mu_{\text{diff}} - \mu_0)}{\sigma}, & \text{when } w_1 = \frac{1}{2}, \text{ if } (\mu_{\text{diff}} - \mu_0) \geq 0 \end{cases} \end{aligned}$$

This implies

$$|\delta| \leq \frac{1}{2} N^{\frac{1}{2}} \frac{|\mu_{\text{diff}} - \mu_0|}{\sigma}$$

**Two-Sample Satterthwaite  $t$  Test Assuming Unequal Variances (TEST=DIFF\_SATT)**

The hypotheses for the two-sample Satterthwaite  $t$  test are

$$H_0: \mu_{\text{diff}} = \mu_0$$

$$H_1: \begin{cases} \mu_{\text{diff}} \neq \mu_0, & \text{two-sided} \\ \mu_{\text{diff}} > \mu_0, & \text{upper one-sided} \\ \mu_{\text{diff}} < \mu_0, & \text{lower one-sided} \end{cases}$$

The test assumes normally distributed data and requires  $N \geq 3$ ,  $n_1 \geq 1$ , and  $n_2 \geq 1$ . The test statistics are

$$t = \frac{\bar{x}_2 - \bar{x}_1 - \mu_0}{\left[ \frac{s_1^2}{n_1} + \frac{s_2^2}{n_2} \right]^{\frac{1}{2}}} = N^{\frac{1}{2}} \frac{\bar{x}_2 - \bar{x}_1 - \mu_0}{\left[ \frac{s_1^2}{w_1} + \frac{s_2^2}{w_2} \right]^{\frac{1}{2}}}$$

$$F = t^2$$

where  $\bar{x}_1$  and  $\bar{x}_2$  are the sample means and  $s_1$  and  $s_2$  are the sample standard deviations.

As DiSantostefano and Muller (1995, p. 585) state, the test is based on assuming that under  $H_0$ ,  $F$  is distributed as  $F(1, \nu)$ , where  $\nu$  is given by Satterthwaite's approximation (Satterthwaite 1946),

$$\nu = \frac{\left[ \frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2} \right]^2}{\frac{\left[ \frac{\sigma_1^2}{n_1} \right]^2}{n_1 - 1} + \frac{\left[ \frac{\sigma_2^2}{n_2} \right]^2}{n_2 - 1}} = \frac{\left[ \frac{\sigma_1^2}{w_1} + \frac{\sigma_2^2}{w_2} \right]^2}{\frac{\left[ \frac{\sigma_1^2}{w_1} \right]^2}{Nw_1 - 1} + \frac{\left[ \frac{\sigma_2^2}{w_2} \right]^2}{Nw_2 - 1}}$$

Since  $\nu$  is unknown, in practice it must be replaced by an estimate

$$\hat{\nu} = \frac{\left[ \frac{s_1^2}{n_1} + \frac{s_2^2}{n_2} \right]^2}{\frac{\left[ \frac{s_1^2}{n_1} \right]^2}{n_1 - 1} + \frac{\left[ \frac{s_2^2}{n_2} \right]^2}{n_2 - 1}} = \frac{\left[ \frac{s_1^2}{w_1} + \frac{s_2^2}{w_2} \right]^2}{\frac{\left[ \frac{s_1^2}{w_1} \right]^2}{Nw_1 - 1} + \frac{\left[ \frac{s_2^2}{w_2} \right]^2}{Nw_2 - 1}}$$

So the test is

$$\text{Reject } H_0 \text{ if } \begin{cases} F \geq F_{1-\alpha}(1, \hat{\nu}), & \text{two-sided} \\ t \geq t_{1-\alpha}(\hat{\nu}), & \text{upper one-sided} \\ t \leq t_{\alpha}(\hat{\nu}), & \text{lower one-sided} \end{cases}$$

Exact solutions for power for the two-sided and upper one-sided cases are given in Moser, Stevens, and Watts (1989). The lower one-sided case follows easily by using symmetry. The equations are

as follows:

$$\text{power} = \begin{cases} \int_0^\infty P(F(1, N-2, \lambda) > h(u) F_{1-\alpha}(1, v(u)) | u) f(u) du, & \text{two-sided} \\ \int_0^\infty P(t(N-2, \lambda^{\frac{1}{2}}) > [h(u)]^{\frac{1}{2}} t_{1-\alpha}(v(u)) | u) f(u) du, & \text{upper one-sided} \\ \int_0^\infty P(t(N-2, \lambda^{\frac{1}{2}}) < [h(u)]^{\frac{1}{2}} t_\alpha(v(u)) | u) f(u) du, & \text{lower one-sided} \end{cases}$$

where

$$h(u) = \frac{\left(\frac{1}{n_1} + \frac{u}{n_2}\right) (n_1 + n_2 - 2)}{\left[(n_1 - 1) + (n_2 - 1) \frac{u\sigma_1^2}{\sigma_2^2}\right] \left(\frac{1}{n_1} + \frac{\sigma_2^2}{\sigma_1^2 n_2}\right)}$$

$$v(u) = \frac{\left(\frac{1}{n_1} + \frac{u}{n_2}\right)^2}{\frac{1}{n_1^2(n_1-1)} + \frac{u^2}{n_2^2(n_2-1)}}$$

$$\lambda = \frac{(\mu_{\text{diff}} - \mu_0)^2}{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}$$

$$f(u) = \frac{\Gamma\left(\frac{n_1+n_2-2}{2}\right)}{\Gamma\left(\frac{n_1-1}{2}\right) \Gamma\left(\frac{n_2-1}{2}\right)} \left[\frac{\sigma_1^2(n_2-1)}{\sigma_2^2(n_1-1)}\right]^{\frac{n_2-1}{2}} u^{\frac{n_2-3}{2}} \left[1 + \left(\frac{n_2-1}{n_1-1}\right) \frac{u\sigma_1^2}{\sigma_2^2}\right]^{-\left(\frac{n_1+n_2-2}{2}\right)}$$

The density  $f(u)$  is obtained from the fact that

$$\frac{u\sigma_1^2}{\sigma_2^2} \sim F(n_2 - 1, n_1 - 1)$$

### Two-Sample Pooled $t$ Test of Mean Ratio with Lognormal Data (TEST=RATIO)

The lognormal case is handled by reexpressing the analysis equivalently as a normality-based test on the log-transformed data, by using properties of the lognormal distribution as discussed in Johnson, Kotz, and Balakrishnan (1994, Chapter 14). The approaches in the section “Two-Sample  $t$  Test Assuming Equal Variances (TEST=DIFF)” on page 4963 then apply.

In contrast to the usual  $t$  test on normal data, the hypotheses with lognormal data are defined in terms of geometric means rather than arithmetic means. The test assumes equal coefficients of variation in the two groups.

The hypotheses for the two-sample  $t$  test with lognormal data are

$$H_0: \frac{\gamma_2}{\gamma_1} = \gamma_0$$

$$H_1: \begin{cases} \frac{\gamma_2}{\gamma_1} \neq \gamma_0, & \text{two-sided} \\ \frac{\gamma_2}{\gamma_1} > \gamma_0, & \text{upper one-sided} \\ \frac{\gamma_2}{\gamma_1} < \gamma_0, & \text{lower one-sided} \end{cases}$$

Let  $\mu_1^*$ ,  $\mu_2^*$ , and  $\sigma^*$  be the (arithmetic) means and common standard deviation of the corresponding normal distributions of the log-transformed data. The hypotheses can be rewritten as follows:

$$H_0: \mu_2^* - \mu_1^* = \log(\gamma_0)$$

$$H_1: \begin{cases} \mu_2^* - \mu_1^* \neq \log(\gamma_0), & \text{two-sided} \\ \mu_2^* - \mu_1^* > \log(\gamma_0), & \text{upper one-sided} \\ \mu_2^* - \mu_1^* < \log(\gamma_0), & \text{lower one-sided} \end{cases}$$

where

$$\mu_1^* = \log \gamma_1$$

$$\mu_2^* = \log \gamma_2$$

The test assumes lognormally distributed data and requires  $N \geq 3$ ,  $n_1 \geq 1$ , and  $n_2 \geq 1$ .

The power is

$$\text{power} = \begin{cases} P(F(1, N-2, \delta^2) \geq F_{1-\alpha}(1, N-2)), & \text{two-sided} \\ P(t(N-2, \delta) \geq t_{1-\alpha}(N-2)), & \text{upper one-sided} \\ P(t(N-2, \delta) \leq t_{\alpha}(N-2)), & \text{lower one-sided} \end{cases}$$

where

$$\delta = N^{\frac{1}{2}}(w_1 w_2)^{\frac{1}{2}} \left( \frac{\mu_2^* - \mu_1^* - \log(\gamma_0)}{\sigma^*} \right)$$

$$\sigma^* = [\log(\text{CV}^2 + 1)]^{\frac{1}{2}}$$

### Additive Equivalence Test for Mean Difference with Normal Data (TEST=EQUIV\_DIFF)

The hypotheses for the equivalence test are

$$H_0: \mu_{\text{diff}} < \theta_L \quad \text{or} \quad \mu_{\text{diff}} > \theta_U$$

$$H_1: \theta_L \leq \mu_{\text{diff}} \leq \theta_U$$

The analysis is the two one-sided tests (TOST) procedure of Schuirmann (1987). The test assumes normally distributed data and requires  $N \geq 3$ ,  $n_1 \geq 1$ , and  $n_2 \geq 1$ . Phillips (1990) derives an expression for the exact power assuming a balanced design; the results are easily adapted to an unbalanced design:

$$\text{power} = Q_{N-2} \left( (-t_{1-\alpha}(N-2)), \frac{\mu_{\text{diff}} - \theta_U}{\sigma N^{-\frac{1}{2}}(w_1 w_2)^{-\frac{1}{2}}}; 0, \frac{(N-2)^{\frac{1}{2}}(\theta_U - \theta_L)}{2\sigma N^{-\frac{1}{2}}(w_1 w_2)^{-\frac{1}{2}}(t_{1-\alpha}(N-2))} \right) -$$

$$Q_{N-2} \left( (t_{1-\alpha}(N-2)), \frac{\mu_{\text{diff}} - \theta_L}{\sigma N^{-\frac{1}{2}}(w_1 w_2)^{-\frac{1}{2}}}; 0, \frac{(N-2)^{\frac{1}{2}}(\theta_U - \theta_L)}{2\sigma N^{-\frac{1}{2}}(w_1 w_2)^{-\frac{1}{2}}(t_{1-\alpha}(N-2))} \right)$$

where  $Q(\cdot, \cdot; \cdot, \cdot)$  is Owen's Q function, defined in the section "Common Notation" on page 4920.

**Multiplicative Equivalence Test for Mean Ratio with Lognormal Data (TEST=EQUIV\_RATIO)**

The lognormal case is handled by reexpressing the analysis equivalently as a normality-based test on the log-transformed data, by using properties of the lognormal distribution as discussed in Johnson, Kotz, and Balakrishnan (1994, Chapter 14). The approaches in the section “[Additive Equivalence Test for Mean Difference with Normal Data \(TEST=EQUIV\\_DIFF\)](#)” on page 4967 then apply.

In contrast to the additive equivalence test on normal data, the hypotheses with lognormal data are defined in terms of geometric means rather than arithmetic means.

The hypotheses for the equivalence test are

$$H_0: \frac{\gamma_T}{\gamma_R} \leq \theta_L \quad \text{or} \quad \frac{\gamma_T}{\gamma_R} \geq \theta_U$$

$$H_1: \theta_L < \frac{\gamma_T}{\gamma_R} < \theta_U$$

where  $0 < \theta_L < \theta_U$

The analysis is the two one-sided tests (TOST) procedure of Schuirmann (1987) on the log-transformed data. The test assumes lognormally distributed data and requires  $N \geq 3$ ,  $n_1 \geq 1$ , and  $n_2 \geq 1$ . Diletti, Hauschke, and Steinijans (1991) derive an expression for the exact power assuming a crossover design; the results are easily adapted to an unbalanced two-sample design:

$$\text{power} = Q_{N-2} \left( (-t_{1-\alpha}(N-2)), \frac{\log\left(\frac{\gamma_T}{\gamma_R}\right) - \log(\theta_U)}{\sigma^* N^{-\frac{1}{2}}(w_1 w_2)^{-\frac{1}{2}}}; 0, \frac{(N-2)^{\frac{1}{2}}(\log(\theta_U) - \log(\theta_L))}{2\sigma^* N^{-\frac{1}{2}}(w_1 w_2)^{-\frac{1}{2}}(t_{1-\alpha}(N-2))} \right) -$$

$$Q_{N-2} \left( (t_{1-\alpha}(N-2)), \frac{\log\left(\frac{\gamma_T}{\gamma_R}\right) - \log(\theta_L)}{\sigma^* N^{-\frac{1}{2}}(w_1 w_2)^{-\frac{1}{2}}}; 0, \frac{(N-2)^{\frac{1}{2}}(\log(\theta_U) - \log(\theta_L))}{2\sigma^* N^{-\frac{1}{2}}(w_1 w_2)^{-\frac{1}{2}}(t_{1-\alpha}(N-2))} \right)$$

where

$$\sigma^* = [\log(\text{CV}^2 + 1)]^{\frac{1}{2}}$$

is the (assumed common) standard deviation of the normal distribution of the log-transformed data, and  $Q(\cdot, \cdot; \cdot, \cdot)$  is Owen's Q function, defined in the section “[Common Notation](#)” on page 4920.

**Confidence Interval for Mean Difference (CI=DIFF)**

This analysis of precision applies to the standard  $t$ -based confidence interval:

$$\left[ (\bar{x}_2 - \bar{x}_1) - t_{1-\frac{\alpha}{2}}(N-2) \frac{s_p}{\sqrt{N w_1 w_2}}, \right. \\ \left. (\bar{x}_2 - \bar{x}_1) + t_{1-\frac{\alpha}{2}}(N-2) \frac{s_p}{\sqrt{N w_1 w_2}} \right], \quad \text{two-sided}$$

$$\left[ (\bar{x}_2 - \bar{x}_1) - t_{1-\alpha}(N-2) \frac{s_p}{\sqrt{N w_1 w_2}}, \infty \right), \quad \text{upper one-sided}$$

$$\left( -\infty, (\bar{x}_2 - \bar{x}_1) + t_{1-\alpha}(N-2) \frac{s_p}{\sqrt{N w_1 w_2}} \right], \quad \text{lower one-sided}$$

where  $\bar{x}_1$  and  $\bar{x}_2$  are the sample means and  $s_p$  is the pooled standard deviation. The “half-width” is defined as the distance from the point estimate  $\bar{x}_2 - \bar{x}_1$  to a finite endpoint,

$$\text{half-width} = \begin{cases} t_{1-\frac{\alpha}{2}}(N-2) \frac{s_p}{\sqrt{N w_1 w_2}}, & \text{two-sided} \\ t_{1-\alpha}(N-2) \frac{s_p}{\sqrt{N w_1 w_2}}, & \text{one-sided} \end{cases}$$

A “valid” confidence interval captures the true mean. The exact probability of obtaining at most the target confidence interval half-width  $h$ , unconditional or conditional on validity, is given by Beal (1989):

$$\Pr(\text{half-width} \leq h) = \begin{cases} P \left( \chi^2(N-2) \leq \frac{h^2 N(N-2)(w_1 w_2)}{\sigma^2(t_{1-\frac{\alpha}{c}}^2(N-2))} \right), & \text{two-sided} \\ P \left( \chi^2(N-2) \leq \frac{h^2 N(N-2)(w_1 w_2)}{\sigma^2(t_{1-\alpha}^2(N-2))} \right), & \text{one-sided} \end{cases}$$

$$\Pr(\text{half-width} \leq h \mid \text{validity}) = \begin{cases} \left(\frac{1}{1-\alpha}\right) 2 \left[ Q_{N-2} \left( (t_{1-\frac{\alpha}{c}}(N-2)), 0; 0, b_2 \right) - Q_{N-2}(0, 0; 0, b_2) \right], & \text{two-sided} \\ \left(\frac{1}{1-\alpha}\right) Q_{N-2} \left( (t_{1-\alpha}(N-2)), 0; 0, b_2 \right), & \text{one-sided} \end{cases}$$

where

$$b_2 = \frac{h(N-2)^{\frac{1}{2}}}{\sigma(t_{1-\frac{\alpha}{c}}(N-2))N^{-\frac{1}{2}}(w_1 w_2)^{-\frac{1}{2}}}$$

$c$  = number of sides

and  $Q(\cdot, \cdot; \cdot, \cdot)$  is Owen’s Q function, defined in the section “Common Notation” on page 4920.

A “quality” confidence interval is both sufficiently narrow (half-width  $\leq h$ ) and valid:

$$\begin{aligned} \Pr(\text{quality}) &= \Pr(\text{half-width} \leq h \text{ and validity}) \\ &= \Pr(\text{half-width} \leq h \mid \text{validity})(1 - \alpha) \end{aligned}$$

### Analyses in the TWOSAMPLESURVIVAL Statement

#### Rank Tests for Two Survival Curves (TEST=LOGRANK, TEST=GEHAN, TEST=TARONEWARE)

The method is from Lakatos (1988) and Cantor (1997, pp. 83–92).

Define the following notation:

$X_j(i)$  =  $i$ th input time point on survival curve for group  $j$

$S_j(i)$  = input survivor function value corresponding to  $X_j(i)$

$h_j(t)$  = hazard rate for group  $j$  at time  $t$

$\Psi_j(t)$  = loss hazard rate for group  $j$  at time  $t$

$\lambda_j$  = exponential hazard rate for group  $j$

$R$  = hazard ratio of group 2 to group 1  $\equiv$  (assumed constant) value of  $\frac{h_2(t)}{h_1(t)}$

$m_j$  = median survival time for group  $j$

$b$  = number of subintervals per time unit

$T$  = accrual time

$\tau$  = postaccrual follow-up time

$L_j$  = exponential loss rate for group  $j$

$XL_j$  = input time point on loss curve for group  $j$

$SL_j$  = input survivor function value corresponding to  $XL_j$

$mL_j$  = median survival time for group  $j$

$r_i$  = rank for  $i$ th time point

Each survival curve can be specified in one of several ways.

- For exponential curves:
  - a single point  $(X_j(1), S_j(1))$  on the curve
  - median survival time
  - hazard rate
  - hazard ratio (for curve 2, with respect to curve 1)
- For piecewise linear curves with proportional hazards:
  - a set of points  $\{(X_1(1), S_1(1)), (X_1(2), S_1(2)), \dots\}$  (for curve 1)
  - hazard ratio (for curve 2, with respect to curve 1)
- For arbitrary piecewise linear curves:
  - a set of points  $\{(X_j(1), S_j(1)), (X_j(2), S_j(2)), \dots\}$

A total of  $M$  evenly spaced time points  $\{t_0 = 0, t_1, t_2, \dots, t_M = T + \tau\}$  are used in calculations, where

$$M = \text{floor}((T + \tau)b)$$

The hazard function is calculated for each survival curve at each time point. For an exponential curve, the (constant) hazard is given by one of the following, depending on the input parameteriza-

tion:

$$h_j(t) = \begin{cases} \lambda_j \\ \lambda_1 R \\ \frac{-\log(\frac{1}{2})}{m_j} \\ \frac{-\log(S_j(1))}{X_j(1)} \\ \frac{-\log(S_1(1))}{X_1(1)} R \end{cases}$$

For a piecewise linear curve, define the following additional notation:

$$t_i^- = \text{largest input time } X \text{ such that } X \leq t_i$$

$$t_i^+ = \text{smallest input time } X \text{ such that } X > t_i$$

The hazard is computed by using linear interpolation as follows:

$$h_j(t_i) = \frac{S_j(t_i^-) - S_j(t_i^+)}{[S_j(t_i^+) - S_j(t_i^-)] [t_i - t_i^-] + S_j(t_i^-) [t_i^+ - t_i^-]}$$

With proportional hazards, the hazard rate of group 2's curve in terms of the hazard rate of group 1's curve is

$$h_2(t) = h_1(t)R$$

Hazard function values  $\{\Psi_j(t_i)\}$  for the loss curves are computed in an analogous way from  $\{L_j, XL_j, SL_j, mL_j\}$ .

The expected number at risk  $N_j(i)$  at time  $i$  in group  $j$  is calculated for each group and time points 0 through  $M - 1$ , as follows:

$$N_j(0) = Nw_j$$

$$N_j(i + 1) = N_j(i) \left[ 1 - h_j(t_i) \left(\frac{1}{b}\right) - \Psi_j(t_i) \left(\frac{1}{b}\right) - \left(\frac{1}{b(T + \tau - t_i)}\right) 1_{\{t_i > \tau\}} \right]$$

Define  $\theta_i$  as the ratio of hazards and  $\phi_i$  as the ratio of expected numbers at risk for time  $t_i$ :

$$\theta_i = \frac{h_2(t_i)}{h_1(t_i)}$$

$$\phi_i = \frac{N_2(i)}{N_1(i)}$$

The expected number of deaths in each subinterval is calculated as follows:

$$D_i = [h_1(t_i)N_1(i) + h_2(t_i)N_2(i)] \left(\frac{1}{b}\right)$$

The rank values are calculated as follows according to which test statistic is used:

$$r_i = \begin{cases} 1, & \text{log-rank} \\ \frac{N_1(i) + N_2(i)}{\sqrt{N_1(i) + N_2(i)}}, & \text{Gehan} \\ \sqrt{N_1(i) + N_2(i)}, & \text{Tarone-Ware} \end{cases}$$

The distribution of the test statistic is approximated by  $N(E, 1)$  where

$$E = \frac{\sum_{i=0}^{M-1} D_i r_i \left[ \frac{\phi_i \theta_i}{1 + \phi_i \theta_i} - \frac{\phi_i}{1 + \phi_i} \right]}{\sqrt{\sum_{i=0}^{M-1} D_i r_i^2 \frac{\phi_i}{(1 + \phi_i)^2}}}$$

Note that  $N^{\frac{1}{2}}$  can be factored out of the mean  $E$ , and so it can be expressed equivalently as

$$E = N^{\frac{1}{2}} E^* = N^{\frac{1}{2}} \left[ \frac{\sum_{i=0}^{M-1} D_i^* r_i^* \left[ \frac{\phi_i \theta_i}{1 + \phi_i \theta_i} - \frac{\phi_i}{1 + \phi_i} \right]}{\sqrt{\sum_{i=0}^{M-1} D_i^* r_i^{*2} \frac{\phi_i}{(1 + \phi_i)^2}}} \right]$$

where  $E^*$  is free of  $N$  and

$$\begin{aligned} D_i^* &= [h_1(t_i)N_1^*(i) + h_2(t_i)N_2^*(i)] \left( \frac{1}{b} \right) \\ r_i^* &= \begin{cases} 1, & \text{log-rank} \\ \frac{N_1^*(i) + N_2^*(i)}{\sqrt{N_1^*(i) + N_2^*(i)}}, & \text{Gehan} \\ \sqrt{N_1^*(i) + N_2^*(i)}, & \text{Tarone-Ware} \end{cases} \\ N_j^*(0) &= w_j \\ N_j^*(i+1) &= N_j^*(i) \left[ 1 - h_j(t_i) \left( \frac{1}{b} \right) - \Psi_j(t_i) \left( \frac{1}{b} \right) - \left( \frac{1}{b(T + \tau - t_i)} \right) 1_{\{t_i > \tau\}} \right] \end{aligned}$$

The approximate power is

$$\text{power} = \begin{cases} \Phi \left( -N^{\frac{1}{2}} E^* - z_{1-\alpha} \right), & \text{upper one-sided} \\ \Phi \left( N^{\frac{1}{2}} E^* - z_{1-\alpha} \right), & \text{lower one-sided} \\ \Phi \left( -N^{\frac{1}{2}} E^* - z_{1-\frac{\alpha}{2}} \right) + \Phi \left( N^{\frac{1}{2}} E^* - z_{1-\frac{\alpha}{2}} \right), & \text{two-sided} \end{cases}$$

Note that the upper and lower one-sided cases are expressed differently than in other analyses. This is because  $E^* > 0$  corresponds to a higher survival curve in group 1 and thus, by the convention used in PROC power for two-group analyses, the lower side.

For the one-sided cases, a closed-form inversion of the power equation yield an approximate total sample size

$$N = \left( \frac{z_{\text{power}} + z_{1-\alpha}}{E^*} \right)^2$$

For the two-sided case, the solution for  $N$  is obtained by numerically inverting the power equation.

## Analyses in the TWOSAMPLEWILCOXON Statement

### *Wilcoxon-Mann-Whitney Test for Comparing Two Distributions (TEST=WMW)*

The power approximation in this section is applicable to the Wilcoxon-Mann-Whitney (WMW) test as invoked with the WILCOXON option in the PROC NPAR1WAY statement of the NPAR1WAY

procedure. The approximation is based on O'Brien and Castelloe (2006) and an estimator called  $\widehat{WMW}_{\text{odds}}$ . See O'Brien and Castelloe (2006) for a definition of  $\widehat{WMW}_{\text{odds}}$ , which need not be derived in detail here for purposes of explaining the power formula.

Let  $Y_1$  and  $Y_2$  be independent observations from any two distributions that you want to compare using the WMW test. For purposes of deriving the asymptotic distribution of  $\widehat{WMW}_{\text{odds}}$  (and consequently the power computation as well), these distributions must be formulated as ordered categorical (“ordinal”) distributions.

If a distribution is continuous, it can be discretized using a large number of categories with negligible loss of accuracy. Each nonordinal distribution is divided into  $b$  categories, where  $b$  is the value of the NBINS parameter, with breakpoints evenly spaced on the probability scale. That is, each bin contains an equal probability  $1/b$  for that distribution. Then the breakpoints across both distributions are pooled to form a collection of  $C$  bins (heretofore called “categories”), and the probabilities of bin membership for each distribution are recalculated. The motivation for this method of binning is to avoid degenerate representations of the distributions—that is, small handfuls of large probabilities among mostly empty bins—as can be caused by something like an evenly spaced grid across raw values rather than probabilities.

After the discretization process just mentioned, there are now two ordinal distributions, each with a set of probabilities across a common set of  $C$  ordered categories. For simplicity of notation, assume (without loss of generality) the response values to be  $1, \dots, C$ . Represent the conditional probabilities as

$$\tilde{p}_{ij} = \text{Prob}(Y_i = j \mid \text{group} = i), i \in \{1, 2\} \quad \text{and} \quad j \in \{1, \dots, C\}$$

and the group allocation weights as

$$w_i = \frac{n_i}{N} = \text{Prob}(\text{group} = i), \quad i \in \{1, 2\}$$

The joint probabilities can then be calculated simply as

$$p_{ij} = \text{Prob}(\text{group} = i, Y_i = j) = w_i \tilde{p}_{ij}, i \in \{1, 2\} \quad \text{and} \quad j \in \{1, \dots, C\}$$

The next step in the power computation is to compute the probabilities that a randomly chosen pair of observations from the two groups is concordant, discordant, or tied. It is useful to define these probabilities as functions of the terms  $Rs_{ij}$  and  $Rd_{ij}$ , defined as follows, where  $Y$  is a random observation drawn from the joint distribution across groups and categories:

$$\begin{aligned} Rs_{ij} &= \text{Prob}(Y \text{ is concordant with cell}(i, j)) + \frac{1}{2}\text{Prob}(Y \text{ is tied with cell}(i, j)) \\ &= \text{Prob}((\text{group} < i \text{ and } Y < j) \text{ or } (\text{group} > i \text{ and } Y > j)) + \\ &\quad \frac{1}{2}\text{Prob}(\text{group} \neq i \text{ and } Y = j) \\ &= \sum_{g=1}^2 \sum_{c=1}^C w_g \tilde{p}_{gc} \left[ \mathbf{I}_{(g-i)(c-j) > 0} + \frac{1}{2}\mathbf{I}_{g \neq i, c=j} \right] \end{aligned}$$

and

$$\begin{aligned}
 Rd_{ij} &= \text{Prob}(Y \text{ is discordant with cell}(i, j)) + \frac{1}{2}\text{Prob}(Y \text{ is tied with cell}(i, j)) \\
 &= \text{Prob}((\text{group} < i \text{ and } Y > j) \text{ or } (\text{group} > i \text{ and } Y < j)) + \\
 &\quad \frac{1}{2}\text{Prob}(\text{group} \neq i \text{ and } Y = j) \\
 &= \sum_{g=1}^2 \sum_{c=1}^C w_g \tilde{p}_{gc} \left[ \mathbf{I}_{(g-i)(c-j) < 0} + \frac{1}{2}\mathbf{I}_{g \neq i, c=j} \right]
 \end{aligned}$$

For an independent random draw  $Y_1, Y_2$  from the two distributions,

$$\begin{aligned}
 P_c &= \text{Prob}(Y_1, Y_2 \text{ concordant}) + \frac{1}{2}\text{Prob}(Y_1, Y_2 \text{ tied}) \\
 &= \sum_{i=1}^2 \sum_{j=1}^C w_i \tilde{p}_{ij} R_{sij}
 \end{aligned}$$

and

$$\begin{aligned}
 P_d &= \text{Prob}(Y_1, Y_2 \text{ discordant}) + \frac{1}{2}\text{Prob}(Y_1, Y_2 \text{ tied}) \\
 &= \sum_{i=1}^2 \sum_{j=1}^C w_i \tilde{p}_{ij} R_{dij}
 \end{aligned}$$

Then

$$WMW_{\text{odds}} = \frac{P_c}{P_d}$$

Proceeding to compute the theoretical standard error associated with  $WMW_{\text{odds}}$  (that is, the population analogue to the sample standard error),

$$SE(WMW_{\text{odds}}) = \frac{2}{P_d} \left[ \sum_{i=1}^2 \sum_{j=1}^C w_i \tilde{p}_{ij} (WMW_{\text{odds}} R_{dij} - R_{sij})^2 / N \right]^{\frac{1}{2}}$$

Converting to the natural log scale and using the delta method,

$$SE(\log(WMW_{\text{odds}})) = \frac{SE(WMW_{\text{odds}})}{WMW_{\text{odds}}}$$

The next step is to produce a “smoothed” version of the  $2 \times C$  cell probabilities that conforms to the null hypothesis of the Wilcoxon-Mann-Whitney test (in other words, independence in the  $2 \times C$  contingency table of probabilities). Let  $SE_{H_0}(\log(WMW_{\text{odds}}))$  denote the theoretical standard error of  $\log(WMW_{\text{odds}})$  assuming  $H_0$ .

Finally we have all of the terms needed to compute the power, using the noncentral chi-square and normal distributions:

$$\text{power} = \begin{cases} P\left(Z \geq \frac{SE_{H_0}(\log(WM W_{\text{odds}}))}{SE(\log(WM W_{\text{odds}}))} z_{1-\alpha} - \delta^* N^{\frac{1}{2}}\right), & \text{upper one-sided} \\ P\left(Z \leq \frac{SE_{H_0}(\log(WM W_{\text{odds}}))}{SE(\log(WM W_{\text{odds}}))} z_{\alpha} - \delta^* N^{\frac{1}{2}}\right), & \text{lower one-sided} \\ P\left(\chi^2(1, (\delta^*)^2 N) \geq \left[\frac{SE_{H_0}(\log(WM W_{\text{odds}}))}{SE(\log(WM W_{\text{odds}}))}\right]^2 \chi^2_{1-\alpha}(1)\right), & \text{two-sided} \end{cases}$$

where

$$\delta^* = \frac{\log(WM W_{\text{odds}})}{N^{\frac{1}{2}} SE(\log(WM W_{\text{odds}}))}$$

is the primary noncentrality—that is, the “effect size” that quantifies how much the two conjectured distributions differ.  $Z$  is a standard normal random variable,  $\chi^2(df, nc)$  is a noncentral  $\chi^2$  random variable with degrees of freedom  $df$  and noncentrality  $nc$ , and  $N$  is the total sample size.

## Examples: POWER Procedure

### Example 67.1: One-Way ANOVA

This example deals with the same situation as in [Example 41.1](#) of Chapter 41, “[The GLMPOWER Procedure](#).”

Hocking (1985, p. 109) describes a study of the effectiveness of electrolytes in reducing lactic acid buildup for long-distance runners. You are planning a similar study in which you will allocate five different fluids to runners on a 10-mile course and measure lactic acid buildup immediately after the run. The fluids consist of water and two commercial electrolyte drinks, EZDure and LactoZap, each prepared at two concentrations, low (EZD1 and LZ1) and high (EZD2 and LZ2).

You conjecture that the standard deviation of lactic acid measurements given any particular fluid is about 3.75, and that the expected lactic acid values will correspond roughly to those in [Table 67.31](#). You are least familiar with the LZ1 drink and hence decide to consider a range of reasonable values for that mean.

**Table 67.31** Mean Lactic Acid Buildup by Fluid

Water	EZD1	EZD2	LZ1	LZ2
35.6	33.7	30.2	29 or 28	25.9

You are interested in four different comparisons, shown in [Table 67.32](#) with appropriate contrast coefficients.

**Table 67.32** Planned Comparisons

Comparison	Contrast Coefficients				
	Water	EZD1	EZD2	LZ1	LZ2
Water versus electrolytes	4	-1	-1	-1	-1
EZD versus LZ	0	1	1	-1	-1
EZD1 versus EZD2	0	1	-1	0	0
LZ1 versus LZ2	0	0	0	1	-1

For each of these contrasts you want to determine the sample size required to achieve a power of 0.9 for detecting an effect with magnitude in accord with [Table 67.31](#). You are not yet attempting to choose a single sample size for the study, but rather checking the range of sample sizes needed for individual contrasts. You plan to test each contrast at  $\alpha = 0.025$ . In the interests of reducing costs, you will provide twice as many runners with water as with any of the electrolytes; in other words, you will use a sample size weighting scheme of 2:1:1:1:1. Use the `ONEWAYANOVA` statement in the `POWER` procedure to compute the sample sizes.

The statements required to perform this analysis are as follows:

```
proc power;
  onewayanova
    groupmeans = 35.6 | 33.7 | 30.2 | 29 28 | 25.9
    stddev = 3.75
    groupweights = (2 1 1 1 1)
    alpha = 0.025
    ntotal = .
    power = 0.9
    contrast = (4 -1 -1 -1 -1) (0 1 1 -1 -1)
              (0 1 -1 0 0) (0 0 0 1 -1);
run;
```

The `NTOTAL=` option with a missing value (.) indicates total sample size as the result parameter. The `GROUPMEANS=` option with values from [Table 67.31](#) specifies your conjectures for the means. With only one mean varying (the LZ1 mean), the “crossed” notation is simpler, showing scenarios for each group mean, separated by vertical bars (|). See the section “[Specifying Value Lists in Analysis Statements](#)” on page 4913 for more details on crossed and matched notations for grouped values. The contrasts in [Table 67.32](#) are specified with the `CONTRAST=` option, by using the “matched” notation with each contrast enclosed in parentheses. The `STDDEV=`, `ALPHA=`, and `POWER=` options specify the error standard deviation, significance level, and power. The `GROUPWEIGHTS=` option specifies the weighting schemes. Default values for the `NULLCONTRAST=` and `SIDES=` options specify a two-sided  $t$  test of the contrast equal to 0. See [Output 67.1.1](#) for the results.

**Output 67.1.1** Sample Sizes for One-Way ANOVA Contrasts

The POWER Procedure												
Single DF Contrast in One-Way ANOVA												
Fixed Scenario Elements												
Method											Exact	
Alpha											0.025	
Standard Deviation											3.75	
Group Weights											2 1 1 1 1	
Nominal Power											0.9	
Number of Sides											2	
Null Contrast Value											0	
Computed N Total												
Index	-----Contrast-----					-----Means-----					Actual Power	N Total
1	4	-1	-1	-1	-1	35.6	33.7	30.2	29	25.9	0.947	30
2	4	-1	-1	-1	-1	35.6	33.7	30.2	28	25.9	0.901	24
3	0	1	1	-1	-1	35.6	33.7	30.2	29	25.9	0.929	60
4	0	1	1	-1	-1	35.6	33.7	30.2	28	25.9	0.922	48
5	0	1	-1	0	0	35.6	33.7	30.2	29	25.9	0.901	174
6	0	1	-1	0	0	35.6	33.7	30.2	28	25.9	0.901	174
7	0	0	0	1	-1	35.6	33.7	30.2	29	25.9	0.902	222
8	0	0	0	1	-1	35.6	33.7	30.2	28	25.9	0.902	480

The sample sizes in [Output 67.1.1](#) range from 24 for the comparison of water versus electrolytes to 480 for the comparison of LZ1 versus LZ2, both assuming the smaller LZ1 mean. The sample size for the latter comparison is relatively large because the small mean difference of  $28 - 25.9 = 2.1$  is hard to detect.

The Nominal Power of 0.9 in the “Fixed Scenario Elements” table in [Output 67.1.1](#) represents the input target power, and the Actual Power column in the “Computed N Total” table is the power at the sample size (N Total) adjusted to achieve the specified sample weighting. Note that all of the sample sizes are rounded up to multiples of 6 to preserve integer group sizes (since the group weights add up to 6). You can use the `NFRACTIONAL` option in the `ONEWAYANOVA` statement to compute raw fractional sample sizes.

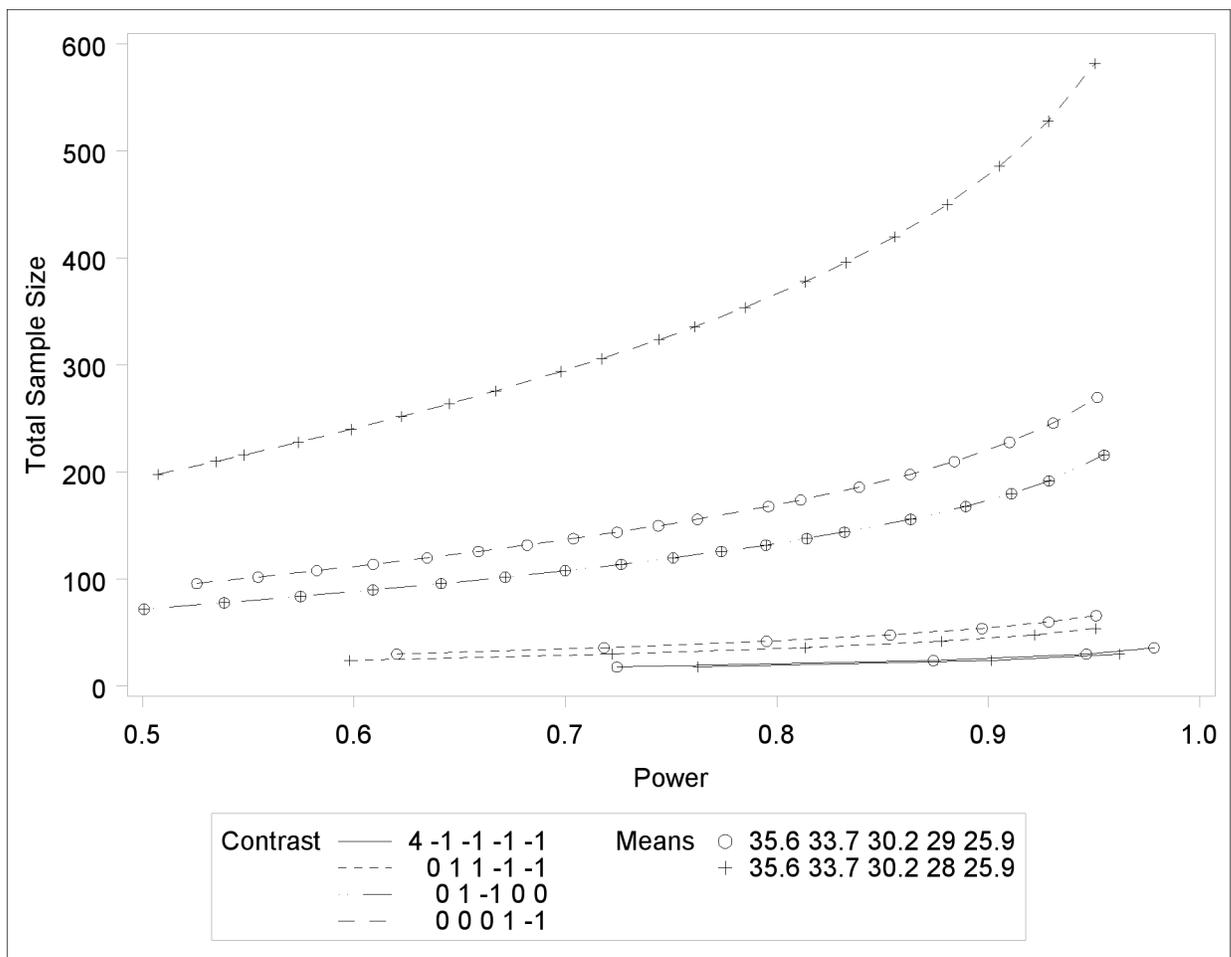
Suppose you want to plot the required sample size for the range of power values from 0.5 to 0.95. First, define the analysis by specifying the same statements as before, but add the `PLOTONLY` option to the `PROC POWER` statement to disable the nongraphical results. Next, specify the `PLOT` statement with `X=POWER` to request a plot with power on the X axis. (The result parameter, here sample size, is always plotted on the other axis.) Use the `MIN=` and `MAX=` options in the `PLOT` statement to specify the power range. The following statements produce the plot shown in [Output 67.1.2](#).

```

proc power plotonly;
  onewayanova
    groupmeans = 35.6 | 33.7 | 30.2 | 29 28 | 25.9
    stddev = 3.75
    groupweights = (2 1 1 1 1)
    alpha = 0.025
    ntotal = .
    power = 0.9
    contrast = (4 -1 -1 -1 -1) (0 1 1 -1 -1)
              (0 1 -1 0 0) (0 0 0 1 -1);
  plot x=power min=.5 max=.95;
run;

```

**Output 67.1.2** Plot of Sample Size versus Power for One-Way ANOVA Contrasts



In [Output 67.1.2](#), the line style identifies the contrast, and the plotting symbol identifies the group means scenario. The plot shows that the required sample size is highest for the (0 0 0 1 -1) contrast, corresponding to the test of LZ1 versus LZ2 that was previously found to require the most resources, in either cell means scenario.

Note that some of the plotted points in [Output 67.1.2](#) are unevenly spaced. This is because the plotted points are the *rounded* sample size results at their corresponding *actual* power levels. The

range specified with the `MIN=` and `MAX=` values in the `PLOT` statement corresponds to *nominal* power levels. In some cases, actual power is substantially higher than nominal power. To obtain plots with evenly spaced points (but with *fractional* sample sizes at the computed points), you can use the `NFRACTIONAL` option in the analysis statement preceding the `PLOT` statement.

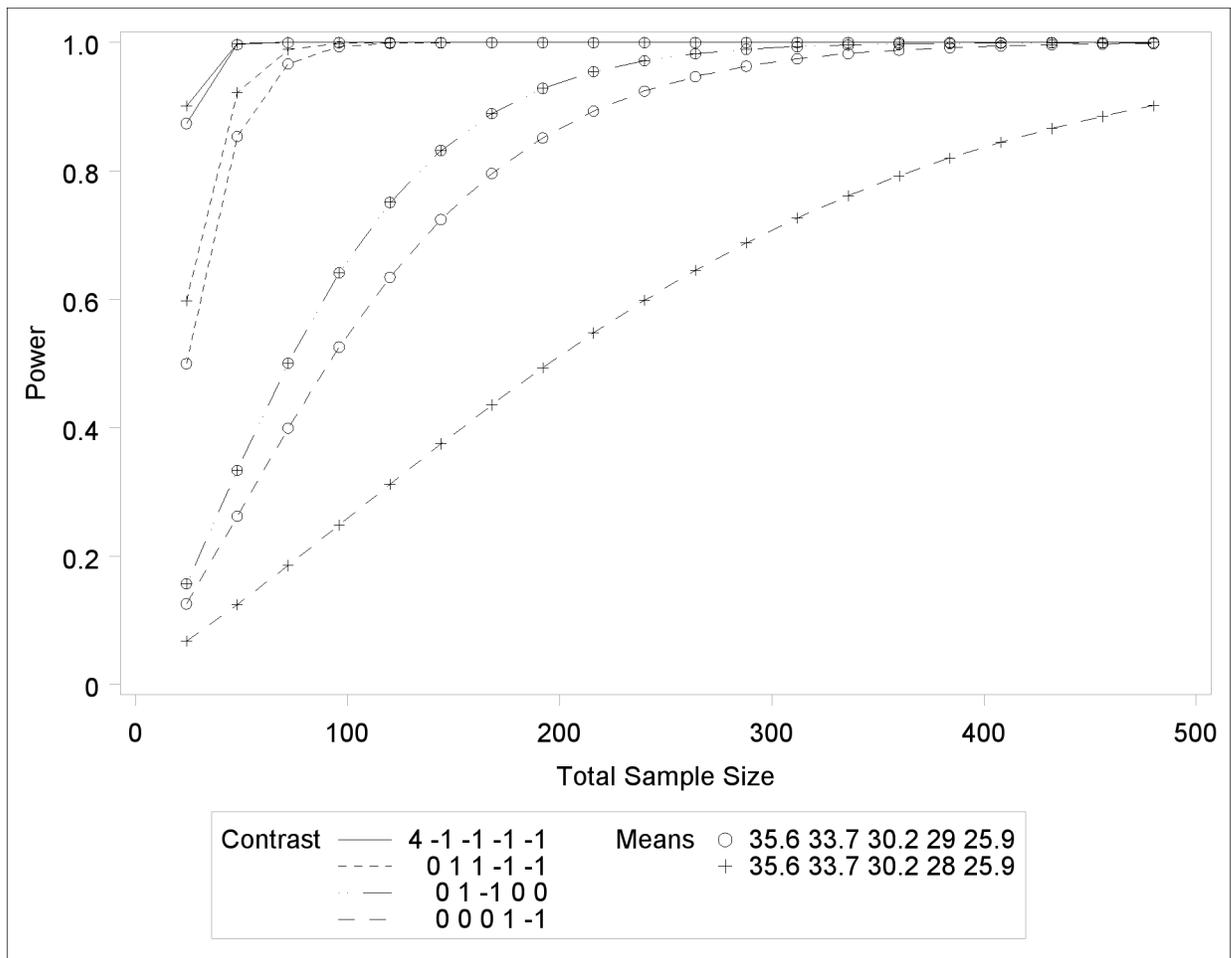
Finally, suppose you want to plot the power for the range of sample sizes you will likely consider for the study (the range of 24 to 480 that achieves 0.9 power for different comparisons). In the `ONEWAYANOVA` statement, identify power as the result (`POWER=.`), and specify `NTOTAL=24`. The following statements produce the plot:

```
proc power plotonly;
  onewayanova
    groupmeans = 35.6 | 33.7 | 30.2 | 29 28 | 25.9
    stddev = 3.75
    groupweights = (2 1 1 1 1)
    alpha = 0.025
    ntotal = 24
    power = .
    contrast = (4 -1 -1 -1 -1) (0 1 1 -1 -1)
              (0 1 -1 0 0) (0 0 0 1 -1);
  plot x=n min=24 max=480;
run;
```

The `X=N` option in the `PLOT` statement requests a plot with sample size on the X axis.

Note that the value specified with the `NTOTAL=24` option is not used. It is overridden in the plot by the `MIN=` and `MAX=` options in the `PLOT` statement, and the `PLOTONLY` option in the `PROC POWER` statement disables nongraphical results. But the `NTOTAL=` option (along with a value) is still needed in the `ONEWAYANOVA` statement as a placeholder, to identify the desired parameterization for sample size.

[Output 67.1.3](#) shows the resulting plot.

**Output 67.1.3** Plot of Power versus Sample Size for One-Way ANOVA Contrasts

Although [Output 67.1.2](#) and [Output 67.1.3](#) surface essentially the same computations for practical power ranges, they each provide a different quick visual assessment. [Output 67.1.2](#) reveals the range of required sample sizes for powers of interest, and [Output 67.1.3](#) reveals the range of achieved powers for sample sizes of interest.

### Example 67.2: The Sawtooth Power Function in Proportion Analyses

For many common statistical analyses, the power curve is monotonically increasing: the more samples you take, the more power you achieve. However, in statistical analyses of discrete data, such as tests of proportions, the power curve is often nonmonotonic. A small increase in sample size can result in a *decrease* in power, a decrease that is sometimes substantial. The explanation is that the actual significance level (in other words, the achieved Type I error rate) for discrete tests strays below the target level and varies with sample size. The power loss from a decrease in the Type I error rate can outweigh the power gain from an increase in sample size. The example discussed here demonstrates this “sawtooth” phenomenon. For additional discussion on the topic, see Chernick and Liu (2002).

Suppose you have a new scheduling system for an airline, and you want to determine how many flights you must observe to have at least an 80% chance of establishing an improvement in the proportion of late arrivals on a specific travel route. You will use a one-sided exact binomial proportion test with a null proportion of 30%, the frequency of late arrivals under the previous scheduling system, and a nominal significance level of  $\alpha = 0.05$ . Well-supported predictions estimate the new late arrival rate to be about 20%, and you will base your sample size determination on this assumption.

The POWER procedure does not currently compute exact sample size directly for the exact binomial test. But you can get an initial estimate by computing the approximate sample size required for a  $z$  test. Use the `ONESAMPLEFREQ` statement in the POWER procedure with `TEST=Z` and `METHOD=NORMAL` to compute the approximate sample size to achieve a power of 0.8 by using the  $z$  test. The following statements perform the analysis:

```
proc power;
  onesamplefreq test=z method=normal
    sides          = 1
    alpha          = 0.05
    nullproportion = 0.3
    proportion     = 0.2
    ntotal        = .
    power         = 0.8;
run;
```

The `NTOTAL=` option with a missing value (.) indicates sample size as the result parameter. The `SIDES=1` option specifies a one-sided test. The `ALPHA=`, `NULLPROPORTION=`, and `POWER=` options specify the significance level of 0.05, null value of 0.3, and target power of 0.8, respectively. The `PROPORTION=` option specifies your conjecture of 0.3 for the true proportion.

**Output 67.2.1** Approximate Sample Size for  $z$  Test of a Proportion

The POWER Procedure		
Z Test for Binomial Proportion		
Fixed Scenario Elements		
Method	Normal approximation	
Number of Sides		1
Null Proportion		0.3
Alpha		0.05
Binomial Proportion		0.2
Nominal Power		0.8
Variance Estimate	Null Variance	
Computed N Total		
Actual Power	N	Total
0.800	119	

The results, shown in [Output 67.2.1](#), indicate that you need to observe about  $N=119$  flights to have an 80% chance of rejecting the hypothesis of a late arrival proportion of 30% or higher, if the true proportion is 20%, by using the  $z$  test. A similar analysis ([Output 67.2.2](#)) reveals an approxi-

mate sample size of  $N=129$  for the  $z$  test with continuity correction, which is performed by using `TEST=ADJZ`:

```
proc power;
  onesamplefreq test=adjz method=normal
    sides          = 1
    alpha          = 0.05
    nullproportion = 0.3
    proportion     = 0.2
    ntotal         = .
    power          = 0.8;
run;
```

### Output 67.2.2 Approximate Sample Size for $z$ Test with Continuity Correction

The POWER Procedure		
Z Test for Binomial Proportion with Continuity Adjustment		
Fixed Scenario Elements		
Method	Normal approximation	
Number of Sides		1
Null Proportion		0.3
Alpha		0.05
Binomial Proportion		0.2
Nominal Power		0.8
Variance Estimate	Null Variance	
	Computed N	Total
	Actual	N
	Power	Total
	0.801	129

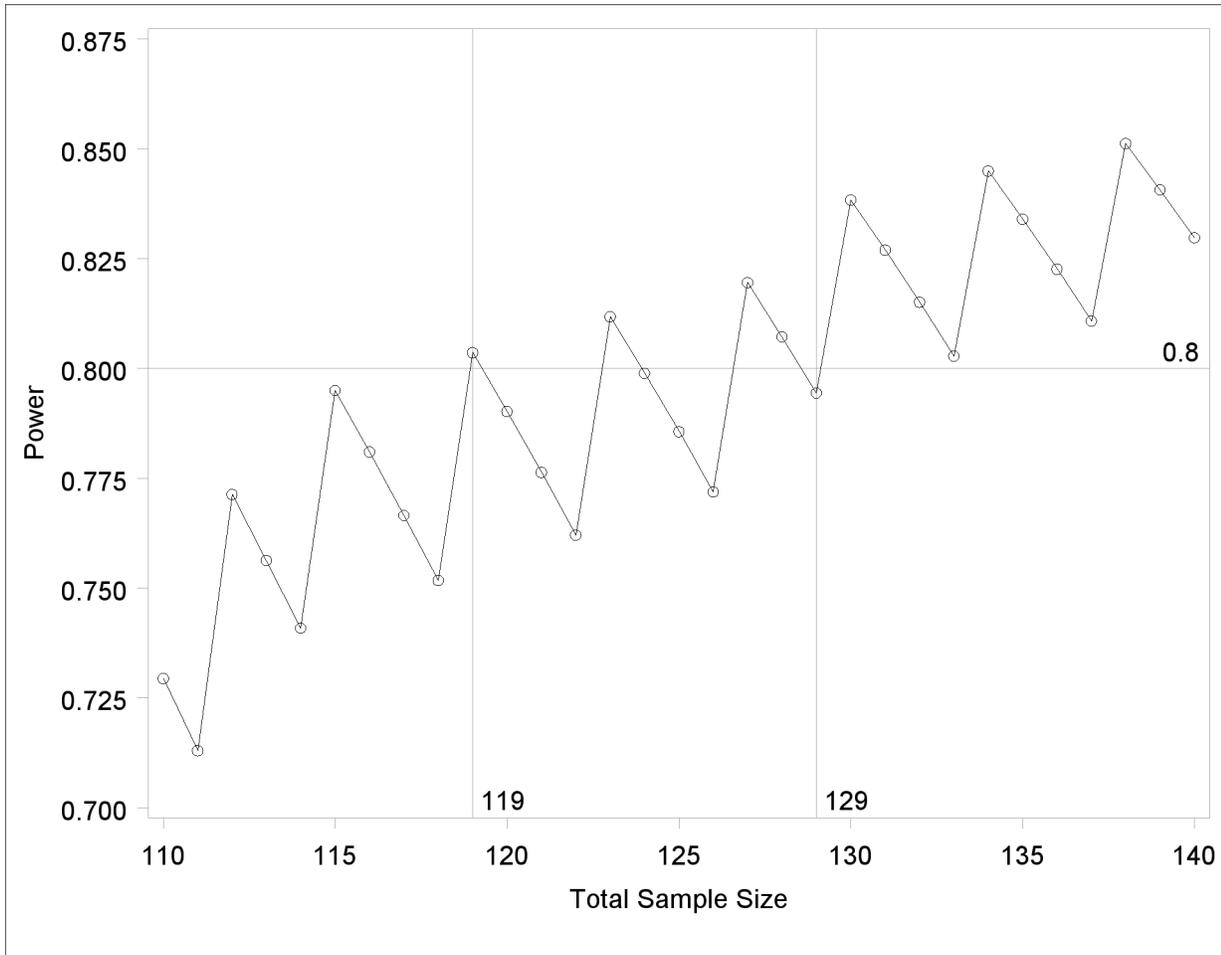
Based on the approximate sample size results, you decide to explore the power of the exact binomial test for sample sizes between 110 and 140. The following statements produce the plot:

```
proc power plotonly;
  onesamplefreq test=exact
    sides          = 1
    alpha          = 0.05
    nullproportion = 0.3
    proportion     = 0.2
    ntotal         = 119
    power          = .;
  plot x=n min=110 max=140 step=1
    yopts=(ref=.8) xopts=(ref=119 129);
run;
```

The `TEST=EXACT` option in the `ONESAMPLEFREQ` statement specifies the exact binomial test, and the missing value (.) for the `POWER=` option indicates power as the result parameter. The `PLOTONLY` option in the `PROC POWER` statement disables nongraphical output. The `PLOT`

statement with  $X=N$  requests a plot with sample size on the X axis. The **MIN=** and **MAX=** options in the **PLOT** statement specify the sample size range. The **YOPTS=(REF=)** and **XOPTS=(REF=)** options add reference lines to highlight the approximate sample size results. The **STEP=1** option produces a point at each integer sample size. The sample size value specified with the **NTOTAL=** option in the **ONESAMPLEFREQ** statement is overridden by the **MIN=** and **MAX=** options in the **PLOT** statement. [Output 67.2.3](#) shows the resulting plot.

**Output 67.2.3** Plot of Power versus Sample Size for Exact Binomial Test



Note the sawtooth pattern in [Output 67.2.3](#). Although the power surpasses the target level of 0.8 at  $N=119$ , it decreases to 0.79 with  $N=120$  and further to 0.76 with  $N=122$  before rising again to 0.81 with  $N=123$ . Not until  $N=130$  does the power stay above the 0.8 target. Thus, a more conservative sample size recommendation of 130 might be appropriate, depending on the precise goals of the sample size determination.

In addition to considering alternative sample sizes, you might also want to assess the sensitivity of the power to inaccuracies in assumptions about the true proportion. The following statements produce a plot including true proportion values of 0.18 and 0.22. They are identical to the previous statements except for the additional true proportion values specified with the **PROPORTION=** option in the **ONESAMPLEFREQ** statement.

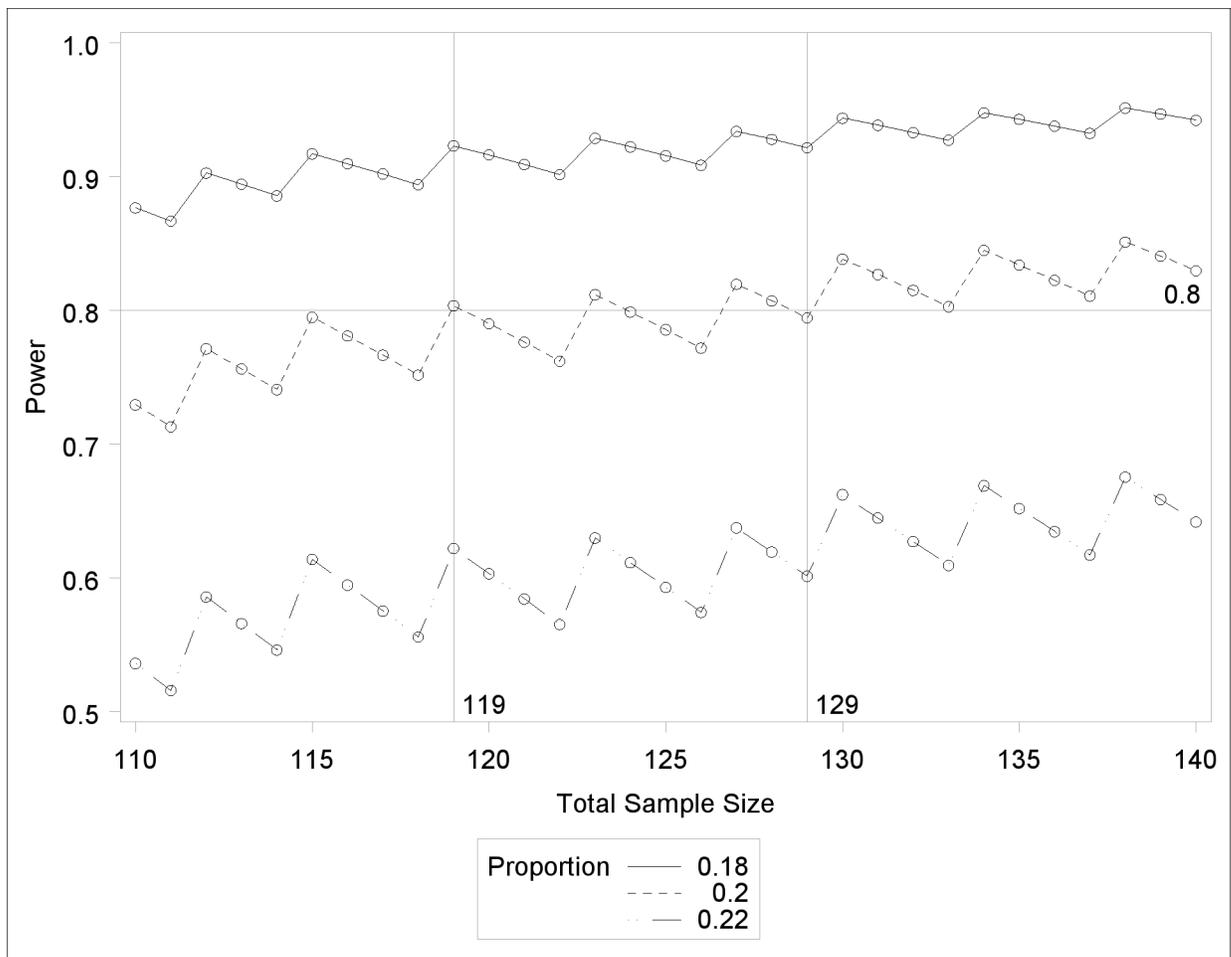
```

proc power plotonly;
  onesamplefreq test=exact
    sides          = 1
    alpha          = 0.05
    nullproportion = 0.3
    proportion      = 0.18 0.2 0.22
    ntotal         = 119
    power          = .;
  plot x=n min=110 max=140 step=1
       yopts=(ref=.8) xopts=(ref=119 129);
run;

```

Output 67.2.4 shows the resulting plot.

**Output 67.2.4** Plot for Assessing Sensitivity to True Proportion Value



The plot reveals a dramatic sensitivity to the true proportion value. For  $N=119$ , the power is about 0.92 if the true proportion is 0.18, and as low as 0.62 if the proportion is 0.22. Note also that the power jumps occur at the same sample sizes in all three curves; the curves are only shifted and stretched vertically. This is because spikes and valleys in power curves are invariant to the true proportion value; they are due to changes in the critical value of the test.

A closer look at some ancillary output from the analysis sheds light on this property of the sawtooth pattern. You can add an ODS OUTPUT statement to save the plot content corresponding to [Output 67.2.3](#) to a data set:

```
proc power plotonly;
  ods output plotcontent=PlotData;
  onesamplefreq test=exact
    sides          = 1
    alpha          = 0.05
    nullproportion = 0.3
    proportion     = 0.2
    ntotal        = 119
    power         = .;
  plot x=n min=110 max=140 step=1
       yopts=(ref=.8) xopts=(ref=119 129);
run;
```

The PlotData data set contains parameter values for each point in the plot. The parameters include underlying characteristics of the putative test. The following statements print the critical value and actual significance level along with sample size and power:

```
proc print data=PlotData;
  var NTotal LowerCritVal Alpha Power;
run;
```

[Output 67.2.5](#) shows the plot data.

## Output 67.2.5 Numerical Content of Plot

Obs	NTotal	Lower CritVal	Alpha	Power
1	110	24	0.0356	0.729
2	111	24	0.0313	0.713
3	112	25	0.0446	0.771
4	113	25	0.0395	0.756
5	114	25	0.0349	0.741
6	115	26	0.0490	0.795
7	116	26	0.0435	0.781
8	117	26	0.0386	0.767
9	118	26	0.0341	0.752
10	119	27	0.0478	0.804
11	120	27	0.0425	0.790
12	121	27	0.0377	0.776
13	122	27	0.0334	0.762
14	123	28	0.0465	0.812
15	124	28	0.0414	0.799
16	125	28	0.0368	0.786
17	126	28	0.0327	0.772
18	127	29	0.0453	0.820
19	128	29	0.0404	0.807
20	129	29	0.0359	0.794
21	130	30	0.0493	0.838
22	131	30	0.0441	0.827
23	132	30	0.0394	0.815
24	133	30	0.0351	0.803
25	134	31	0.0480	0.845
26	135	31	0.0429	0.834
27	136	31	0.0384	0.823
28	137	31	0.0342	0.811
29	138	32	0.0466	0.851
30	139	32	0.0418	0.841
31	140	32	0.0374	0.830

Note that whenever the critical value changes, the actual  $\alpha$  jumps up to a value close to the nominal  $\alpha=0.05$ , and the power also jumps up. Then while the critical value stays constant, the actual  $\alpha$  and power slowly decrease. The critical value is independent of the true proportion value. So you can achieve a locally maximal power by choosing a sample size corresponding to a spike on the sawtooth curve, and this choice is locally optimal *regardless* of the unknown value of the true proportion. Locally optimal sample sizes in this case include 115, 119, 123, 127, 130, and 134.

As a point of interest, the power does not always jump sharply and decrease gradually. The shape of the sawtooth depends on the direction of the test and the location of the null proportion relative to 0.5. For example, if the direction of the hypothesis in this example is reversed (by switching true and null proportion values) so that the rejection region is in the upper tail, then the power curve exhibits sharp decreases and gradual increases. The following statements are similar to those producing the plot in [Output 67.2.3](#) but with values of the `PROPORTION=` and `NULLPROPORTION=` options switched:

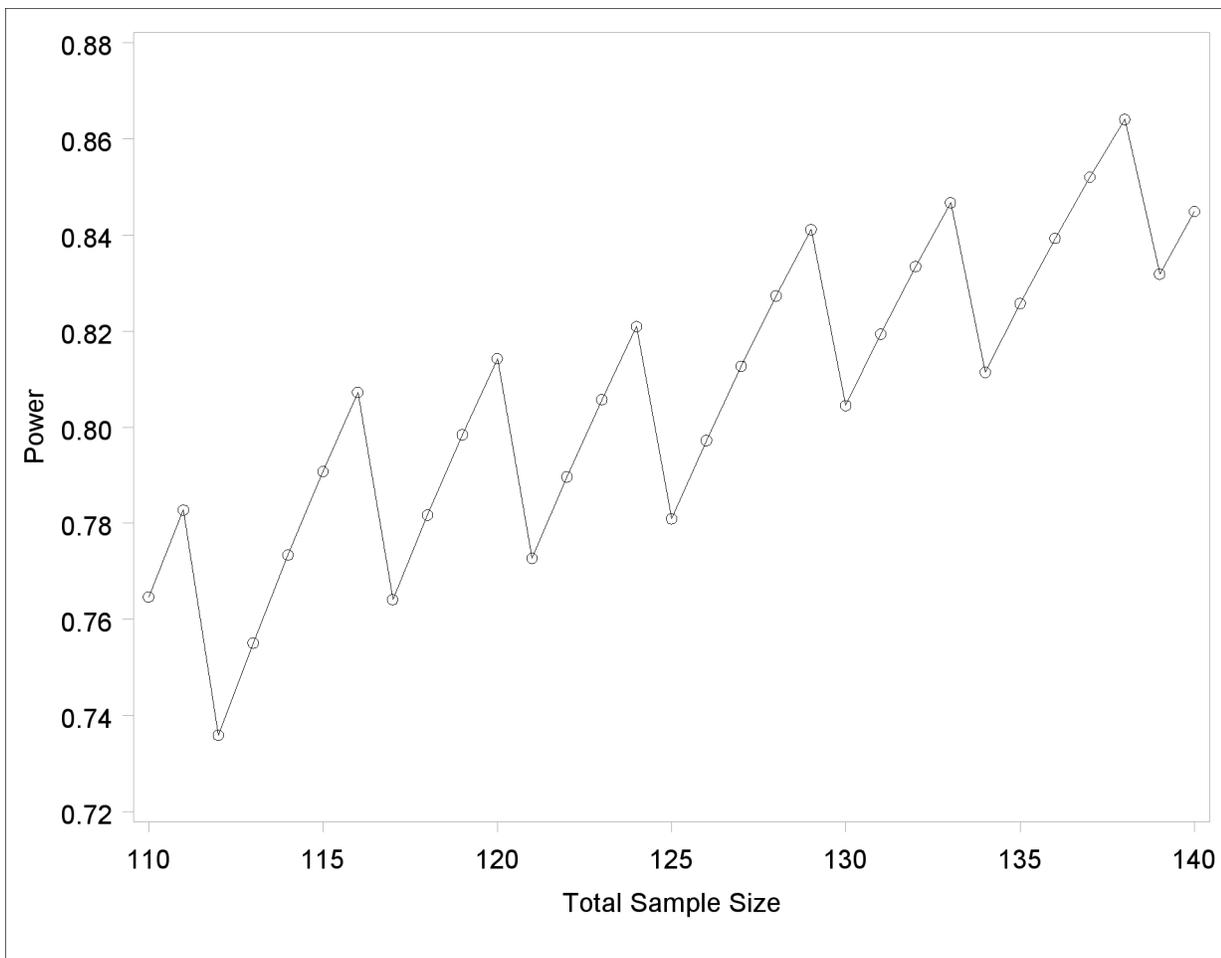
```

proc power plotonly;
  onesamplefreq test=exact
    sides          = 1
    alpha          = 0.05
    nullproportion = 0.2
    proportion     = 0.3
    ntotal         = 119
    power          = .;
  plot x=n min=110 max=140 step=1;
run;

```

The resulting plot is shown in [Output 67.2.6](#).

**Output 67.2.6** Plot of Power versus Sample Size for Another One-sided Test



Finally, two-sided tests can lead to even more irregular power curve shapes, since changes in lower and upper critical values affect the power in different ways. The following statements produce a plot of power versus sample size for the scenario of a two-sided test with high alpha and a true proportion close to the null value:

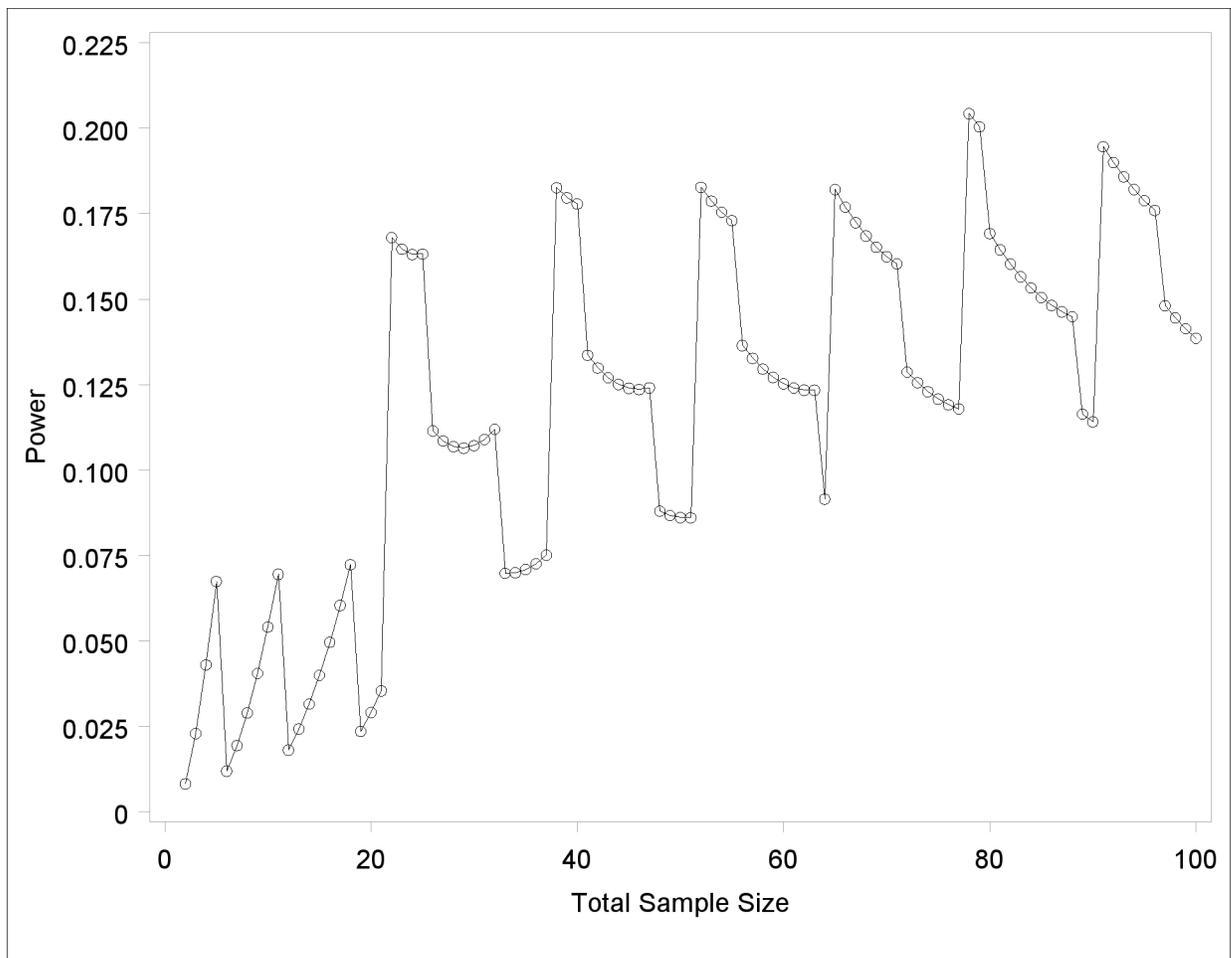
```

proc power plotonly;
  onesamplefreq test=exact
    sides          = 2
    alpha          = 0.2
    nullproportion = 0.1
    proportion     = 0.09
    ntotal         = 10
    power          = .;
  plot x=n min=2 max=100 step=1;
run;

```

Output 67.2.7 shows the resulting plot.

**Output 67.2.7** Plot of Power versus Sample Size for a Two-Sided Test



Due to the irregular shapes of power curves for proportion tests, the question “Which sample size should I use?” is often insufficient. A sample size solution produced directly in PROC POWER reveals the smallest possible sample size to achieve your target power. But as the examples in this section demonstrate, it is helpful to consult graphs for answers to questions such as the following:

- Which sample size will guarantee that all higher sample sizes also achieve my target power?

- Given a candidate sample size, can I increase it slightly to achieve locally maximal power, or perhaps even decrease it and get higher power?

---

### Example 67.3: Simple AB/BA Crossover Designs

Crossover trials are experiments in which each subject is given a sequence of different treatments. They are especially common in clinical trials for medical studies. The reduction in variability from taking multiple measurements on a subject allows for more precise treatment comparisons. The simplest such design is the AB/BA crossover, in which each subject receives each of two treatments in a randomized order.

Under certain simplifying assumptions, you can test the treatment difference in an AB/BA crossover trial by using either a paired or two-sample  $t$  test (or equivalence test, depending on the hypothesis). This example will demonstrate when and how you can use the `PAIREDMEANS` statement in `PROC POWER` to perform power analyses for AB/BA crossover designs.

Senn (1993, Chapter 3) discusses a study comparing the effects of two bronchodilator medications in treatment of asthma, by using an AB/BA crossover design. Suppose you want to plan a similar study comparing two new medications, “Xilodol” and “Brantium.” Half of the patients would be assigned to sequence AB, getting a dose of Xilodol in the first treatment period, a wash-out period of one week, and then a dose of Brantium in the second treatment period. The other half would be assigned to sequence BA, following the same schedule but with the drugs reversed. In each treatment period you would administer the drugs in the morning and then measure peak expiratory flow (PEF) at the end of the day, with higher PEF representing better lung function.

You conjecture that the mean and standard deviation of PEF are about  $\mu_A = 310$  and  $\sigma_A = 40$  for Xilodol and  $\mu_B = 330$  and  $\sigma_B = 55$  for Brantium, and that each pair of measurements on the same subject will have a correlation of about 0.3. You want to compute the power of both one-sided and two-sided tests of mean difference, with a significance level of  $\alpha = 0.01$ , for a sample size of 100 patients and also plot the power for a range of 50 to 200 patients. Note that the allocation ratio of patients to the two sequences is irrelevant in this analysis.

The choice of statistical test depends on which assumptions are reasonable. One possibility is a  $t$  test. A paired or two-sample  $t$  test is valid when there is no carryover effect and no interactions between patients, treatments, and periods. See Senn (1993, Chapter 3) for more details. The choice between a paired or a two-sample test depends on what you assume about the period effect. If you assume no period effect, then a paired  $t$  test is the appropriate analysis for the design, with the first member of each pair being the Xilodol measurement (regardless of which sequence the patient belongs to). Otherwise the two-sample  $t$  test approach is called for, since this analysis adjusts for the period effect by using an extra degree of freedom.

Suppose you assume no period effect. Then you can use the `PAIREDMEANS` statement in `PROC POWER` with the `TEST=DIFF` option to perform a sample size analysis for the paired  $t$  test. Indicate power as the result parameter by specifying the `POWER=` option with a missing value (.). Specify the conjectured means and standard deviations for each drug by using the `PAIREDMEANS=` and `PAIREDSTDDEVS=` options and the correlation by using the `CORR=` option. Specify both one- and two-sided tests by using the `SIDES=` option, the significance level by using the `ALPHA=` op-

tion, and the sample size (in terms of number of pairs) by using the `NPAIRS=` option. Generate a plot of power versus sample size by specifying the `PLOT` statement with `X=N` to request a plot with sample size on the X axis. (The result parameter, here power, is always plotted on the other axis.) Use the `MIN=` and `MAX=` options in the `PLOT` statement to specify the sample size range (as numbers of pairs).

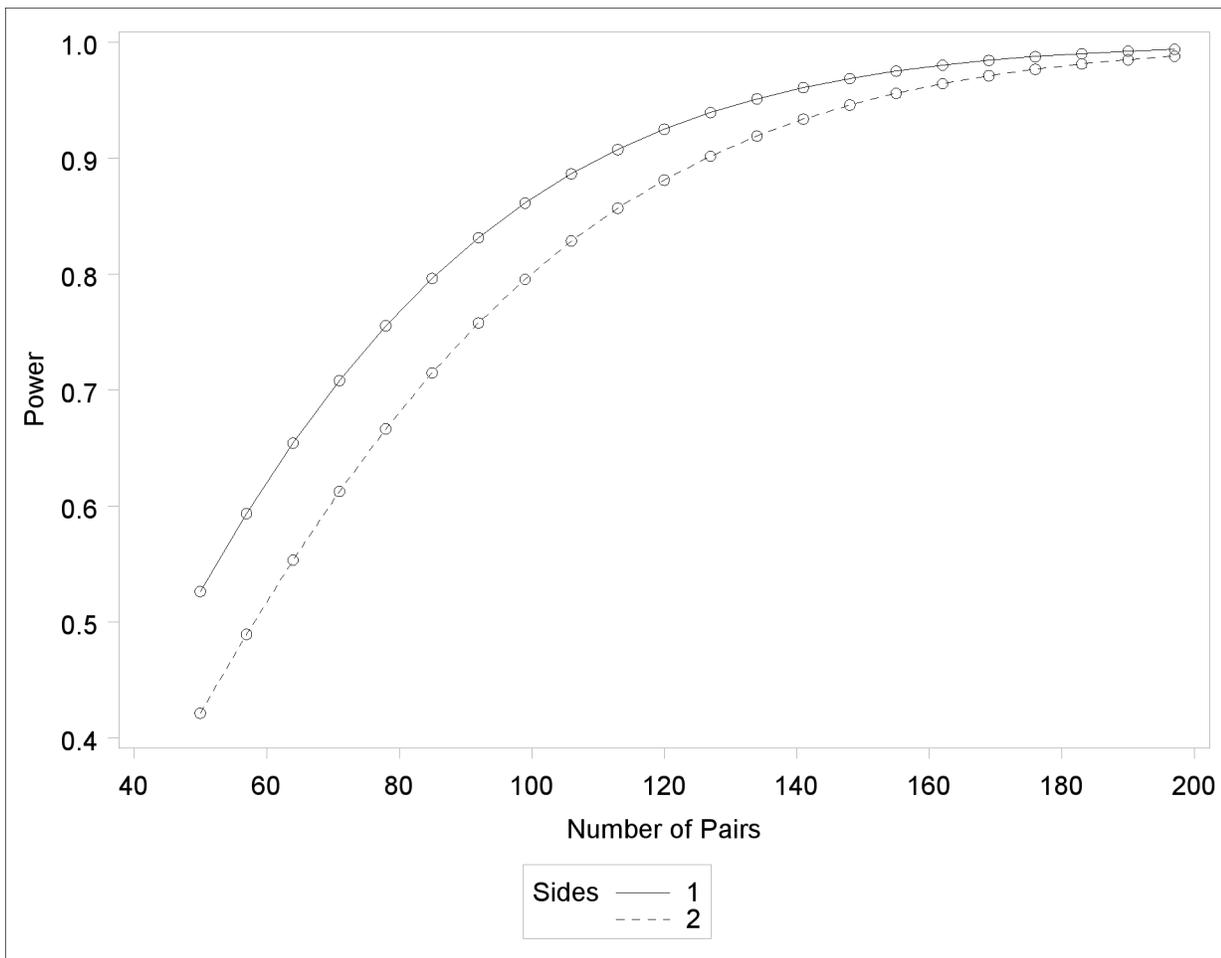
The following statements perform the sample size analysis:

```
proc power;
  pairedmeans test=diff
    pairedmeans = (330 310)
    pairedstddevs = (40 55)
    corr = 0.3
    sides = 1 2
    alpha = 0.01
    npairs = 100
    power = .;
  plot x=n min=50 max=200;
run;
```

Default values for the `NULLDIFF=` and `DIST=` options specify a null mean difference of 0 and the assumption of normally distributed data. The output is shown in [Output 67.3.1](#) and [Output 67.3.2](#).

#### Output 67.3.1 Power for Paired *t* Analysis of Crossover Design

The POWER Procedure		
Paired t Test for Mean Difference		
Fixed Scenario Elements		
Distribution		Normal
Method		Exact
Alpha		0.01
Mean 1		330
Mean 2		310
Standard Deviation 1		40
Standard Deviation 2		55
Correlation		0.3
Number of Pairs		100
Null Difference		0
Computed Power		
Index	Sides	Power
1	1	0.865
2	2	0.801

**Output 67.3.2** Plot of Power versus Sample Size for Paired  $t$  Analysis of Crossover Design

The “Computed Power” table in [Output 67.3.1](#) shows that the power with 100 patients is about 0.8 for the two-sided test and 0.87 for the one-sided test with the alternative of larger Brantium mean. In [Output 67.3.2](#), the line style identifies the number of sides of the test. The plotting symbols identify locations of actual computed powers; the curves are linear interpolations of these points. The plot demonstrates how much higher the power is in the one-sided test than in the two-sided test for the range of sample sizes.

Suppose now that instead of detecting a difference between Xilodol and Brantium, you want to establish that they are similar—in particular, that the absolute mean PEF difference is at most 35. You might consider this goal if, for example, one of the drugs has fewer side effects and if a difference of no more than 35 is considered clinically small. Instead of a standard  $t$  test, you would conduct an *equivalence test* of the treatment mean difference for the two drugs. You would test the hypothesis that the true difference is less than  $-35$  or more than  $35$  against the alternative that the mean difference is between  $-35$  and  $35$ , by using an additive model and a two one-sided tests (“TOST”) analysis.

Assuming no period effect, you can use the `PAIREDMEANS` statement with the `TEST=EQUIV_DIFF` option to perform a sample size analysis for the paired equivalence test. Indicate power as the result parameter by specifying the `POWER=` option with a missing value (.).

Use the `LOWER=` and `UPPER=` options to specify the equivalence bounds of  $-35$  and  $35$ . Use the `PAIREDMEANS=`, `PAIREDSTDDEVS=`, `CORR=`, and `ALPHA=` options in the same way as in the  $t$  test at the beginning of this example to specify the remaining parameters.

The following statements perform the sample size analysis:

```
proc power;
  pairedmeans test=equiv_add
    lower      = -35
    upper      = 35
  pairedmeans = (330 310)
  pairedstddevs = (40 55)
  corr         = 0.3
  alpha        = 0.01
  npairs       = 100
  power        = .;
run;
```

The default option `DIST=NORMAL` specifies an assumption of normally distributed data. The output is shown in [Output 67.3.3](#).

**Output 67.3.3** Power for Paired Equivalence Test for Crossover Design

The POWER Procedure	
Equivalence Test for Paired Mean Difference	
Fixed Scenario Elements	
Distribution	Normal
Method	Exact
Lower Equivalence Bound	-35
Upper Equivalence Bound	35
Alpha	0.01
Reference Mean	330
Treatment Mean	310
Standard Deviation 1	40
Standard Deviation 2	55
Correlation	0.3
Number of Pairs	100
Computed Power	
Power	0.598

The power for the paired equivalence test with 100 patients is about 0.6.

## Example 67.4: Noninferiority Test with Lognormal Data

The typical goal in noninferiority testing is to conclude that a new treatment or process or product is not appreciably worse than some standard. This is accomplished by convincingly rejecting a one-sided null hypothesis that the new treatment is appreciably worse than the standard. When designing such studies, investigators must define precisely what constitutes “appreciably worse.”

You can use the POWER procedure for sample size analyses for a variety of noninferiority tests, by specifying custom, one-sided null hypotheses for common tests. This example illustrates the strategy (often called Blackwelder’s scheme; Blackwelder 1982) by comparing the means of two independent lognormal samples. The logic applies to one-sample, two-sample, and paired-sample problems involving normally distributed measures and proportions.

Suppose you are designing a study hoping to show that a new (less expensive) manufacturing process does not produce appreciably more pollution than the current process. Quantifying “appreciably worse” as 10%, you seek to show that the mean pollutant level from the new process is less than 110% of that from the current process. In standard hypothesis testing notation, you seek to reject

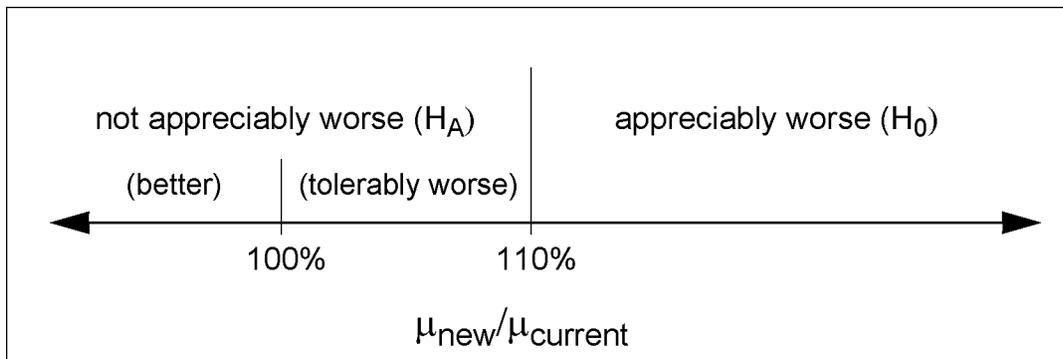
$$H_0: \frac{\mu_{\text{new}}}{\mu_{\text{current}}} \geq 1.10$$

in favor of

$$H_A: \frac{\mu_{\text{new}}}{\mu_{\text{current}}} < 1.10$$

This is described graphically in Figure 67.8. Mean ratios below 100% are better levels for the new process; a ratio of 100% indicates absolute equivalence; ratios of 100–110% are “tolerably” worse; and ratios exceeding 110% are appreciably worse.

**Figure 67.8** Hypotheses for the Pollutant Study



An appropriate test for this situation is the common two-group  $t$  test on log-transformed data. The hypotheses become

$$H_0: \log(\mu_{\text{new}}) - \log(\mu_{\text{current}}) \geq \log(1.10)$$

$$H_A: \log(\mu_{\text{new}}) - \log(\mu_{\text{current}}) < \log(1.10)$$

Measurements of the pollutant level will be taken by using laboratory models of the two processes and will be treated as independent lognormal observations with a coefficient of variation ( $\sigma/\mu$ )

between 0.5 and 0.6 for both processes. You will end up with 300 measurements for the current process and 180 for the new one. It is important to avoid a Type I error here, so you set the Type I error rate to 0.01. Your theoretical work suggests that the new process will actually reduce the pollutant by about 10% (to 90% of current), but you need to compute and graph the power of the study if the new levels are actually between 70% and 120% of current levels.

Implement the sample size analysis by using the `TWOSAMPLEMEANS` statement in PROC POWER with the `TEST=RATIO` option. Indicate power as the result parameter by specifying the `POWER=` option with a missing value (.). Specify a series of scenarios for the mean ratio between 0.7 and 1.2 by using the `MEANRATIO=` option. Use the `NULLRATIO=` option to specify the null mean ratio of 1.10. Specify `SIDES=L` to indicate a one-sided test with the alternative hypothesis stating that the mean ratio is *lower* than the null value. Specify the significance level, scenarios for the coefficient of variation, and the group sample sizes by using the `ALPHA=`, `CV=`, and `GROUPNS=` options. Generate a plot of power versus mean ratio by specifying the `PLOT` statement with the `X=EFFECT` option to request a plot with mean ratio on the X axis. (The result parameter, here power, is always plotted on the other axis.) Use the `STEP=` option in the `PLOT` statement to specify an interval of 0.05 between computed points in the plot.

The following statements perform the desired analysis:

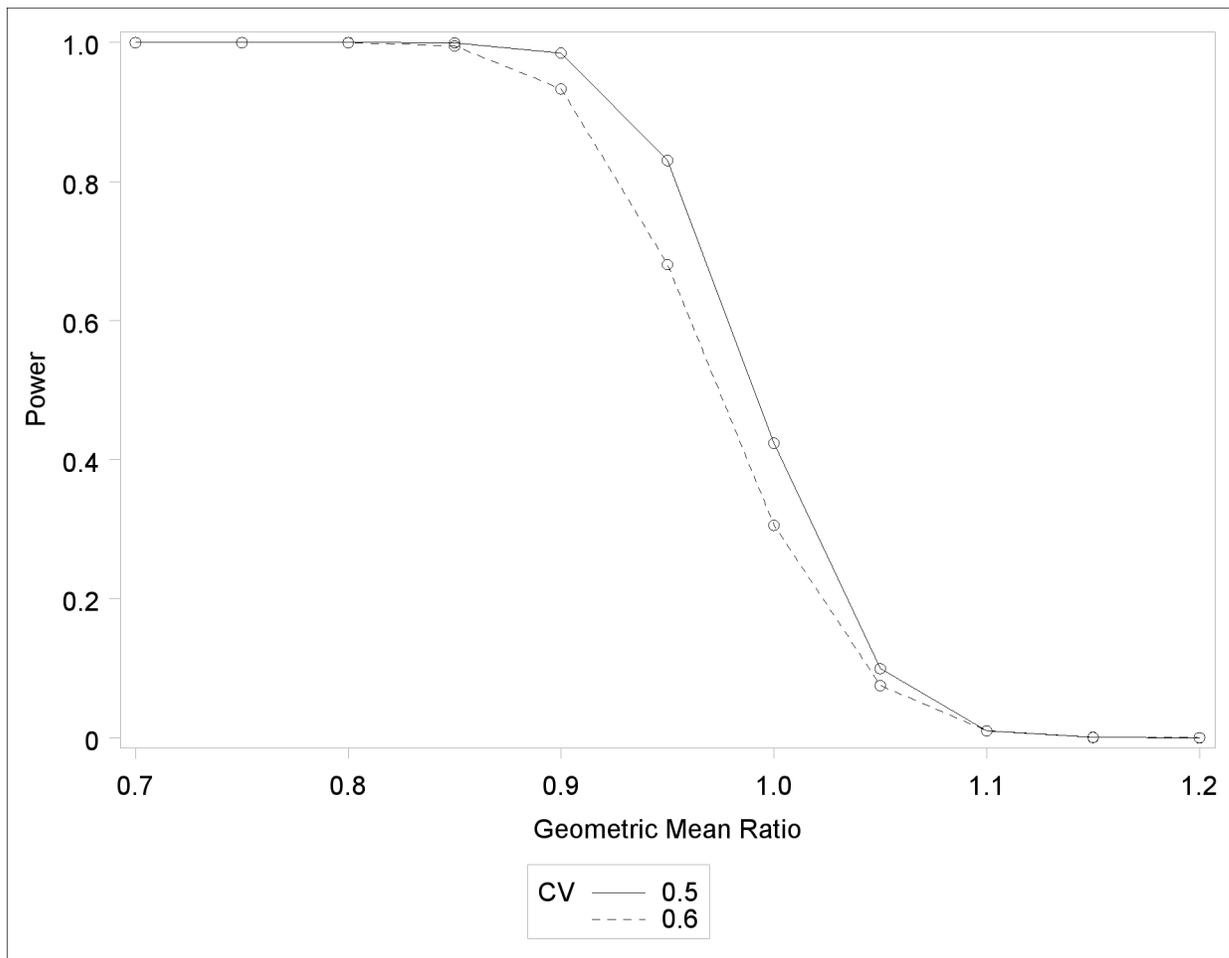
```
proc power;
  twosamplemeans test=ratio
    meanratio = 0.7 to 1.2 by 0.1
    nullratio = 1.10
    sides      = L
    alpha      = 0.01
    cv         = 0.5 0.6
    groupns    = (300 180)
    power      = .;
  plot x=effect step=0.05;
run;
```

Note the use of `SIDES=L`, which forces computations for cases that need a rejection region that is opposite to the one providing the most one-tailed power; in this case, it is the lower tail. Such cases will show power that is less than the prescribed Type I error rate. The default option `DIST=LOGNORMAL` specifies the assumption of lognormally distributed data. The default `MIN=` and `MAX=` options in the plot statement specify an X axis range identical to the effect size range in the `TWOSAMPLEMEANS` statement (mean ratios between 0.7 and 1.2).

Output 67.4.1 and Output 67.4.2 show the results.

**Output 67.4.1** Power for Noninferiority Test of Ratio

The POWER Procedure				
Two-sample t Test for Mean Ratio				
Fixed Scenario Elements				
Distribution				Lognormal
Method				Exact
Number of Sides				L
Null Geometric Mean Ratio				1.1
Alpha				0.01
Group 1 Sample Size				300
Group 2 Sample Size				180
Computed Power				
	Index	Geo Mean Ratio	CV	Power
	1	0.7	0.5	>.999
	2	0.7	0.6	>.999
	3	0.8	0.5	>.999
	4	0.8	0.6	>.999
	5	0.9	0.5	0.985
	6	0.9	0.6	0.933
	7	1.0	0.5	0.424
	8	1.0	0.6	0.306
	9	1.1	0.5	0.010
	10	1.1	0.6	0.010
	11	1.2	0.5	<.001
	12	1.2	0.6	<.001

**Output 67.4.2** Plot of Power versus Mean Ratio for Noninferiority Test

The “Computed Power” table in [Output 67.4.1](#) shows that power exceeds 0.90 if the true mean ratio is 90% or less, as surmised. But power is unacceptably low (0.31–0.42) if the processes happen to be truly equivalent. Note that the power is identical to the alpha level (0.01) if the true mean ratio is 1.10 and below 0.01 if the true mean ratio is appreciably worse (>110%). In [Output 67.4.2](#), the line style identifies the coefficient of variation. The plotting symbols identify locations of actual computed powers; the curves are linear interpolations of these points.

### Example 67.5: Multiple Regression and Correlation

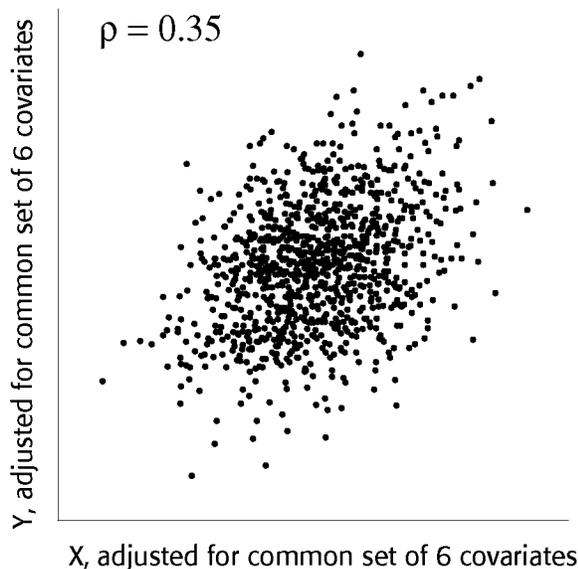
You are working with a team of preventive cardiologists investigating whether elevated serum homocysteine levels are linked to atherosclerosis (plaque buildup) in coronary arteries. The planned analysis is an ordinary least squares regression to assess the relationship between total homocysteine level (tHcy) and a plaque burden index (PBI), adjusting for six other variables: age, gender, plasma levels of folate, vitamin B<sub>6</sub>, vitamin B<sub>12</sub>, and a serum cholesterol index. You will regress PBI on tHcy and the six other predictors (plus the intercept) and use a Type III *F* test to assess whether

tHcy is a significant predictor after adjusting for the others. You wonder whether 100 subjects will provide adequate statistical power.

This is a correlational study at a single time. Subjects will be screened so that about half will have had a heart problem. All eight variables will be measured during one visit. Most clinicians are familiar with simple correlations between two variables, so you decide to pose the statistical problem in terms of estimating and testing the partial correlation between  $X_1 = \text{tHcy}$  and  $Y = \text{PBI}$ , controlling for the six other predictor variables ( $R_{YX_1|X_{-1}}$ ). This greatly simplifies matters, especially the elicitation of the conjectured effect.

You use partial regression plots like that shown in [Figure 67.9](#) to teach the team that the partial correlation between PBI and tHcy is the correlation of two sets of residuals obtained from ordinary regression models, one from regressing PBI on the six covariates and the other from regressing tHcy on the same covariates. Thus each subject has “expected” tHcy and PBI values based on the six covariates. The cardiologists believe that subjects whose tHcy is relatively higher than expected will also have a PBI that is relatively higher than expected. The partial correlation quantifies that adjusted association just as a standard simple correlation does with the unadjusted linear association between two variables.

**Figure 67.9** Partial Regression Plot



Based on previously published studies of various coronary risk factors and after viewing a set of scatterplots showing various correlations, the team surmises that the true partial correlation is likely to be at least 0.35.

You want to compute the statistical power for a sample size of  $N = 100$  by using  $\alpha = 0.05$ . You also want to plot power for sample sizes between 50 and 150. Use the `MULTREG` statement to compute the power and the `PLOT` statement to produce the graph. Since the predictors are observed rather than fixed in advanced, and a joint multivariate normal assumption seems tenable, use `MODEL=RANDOM`. The following statements perform the power analysis:

```

proc power;
  multreg
    model = random
    nfullpredictors = 7
    ntestpredictors = 1
    partialcorr = 0.35
    ntotal = 100
    power = .;
  plot x=n min=50 max=150;
run;

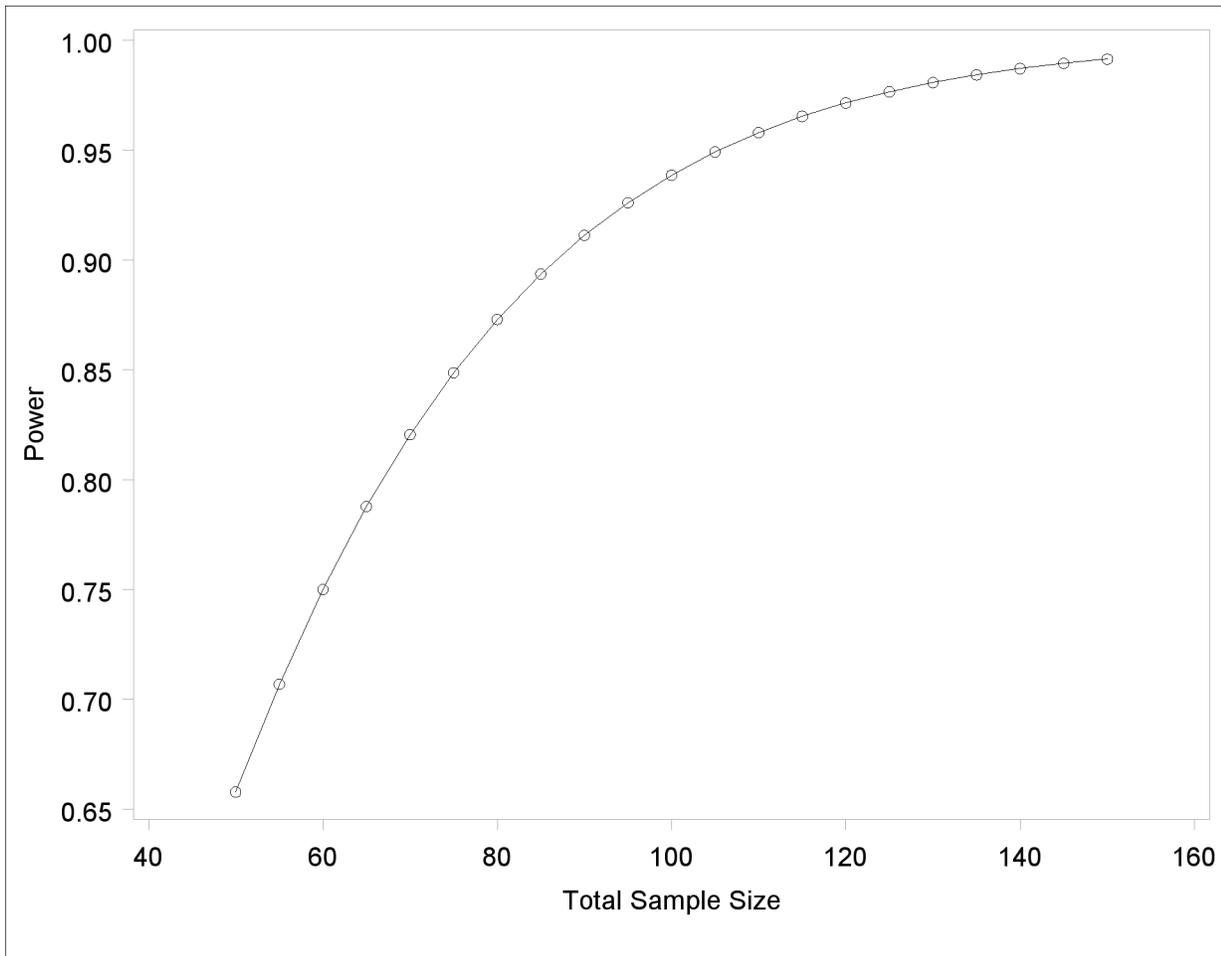
```

The `POWER=.` option identifies power as the parameter to compute. The `NFULLPREDICTORS=` option specifies seven total predictors (not including the intercept), and the `NTESTPREDICTORS=` option indicates that one of those predictors is being tested. The `PARTIALCORR=` and `NTOTAL=` options specify the partial correlation and sample size, respectively. The default value for the `ALPHA=` option sets the significance level to 0.05. The `X=N` option in the plot statement requests a plot of sample size on the X axis, and the `MIN=` and `MAX=` options specify the sample size range.

Output 67.5.1 shows the output, and Output 67.5.2 shows the plot.

#### Output 67.5.1 Power Analysis for Multiple Regression

The POWER Procedure	
Type III F Test in Multiple Regression	
Fixed Scenario Elements	
Method	Exact
Model	Random X
Number of Predictors in Full Model	7
Number of Test Predictors	1
Partial Correlation	0.35
Total Sample Size	100
Alpha	0.05
Computed Power	
Power	
0.939	

**Output 67.5.2** Plot of Power versus Sample Size for Multiple Regression

For the sample size  $N = 100$ , the study is almost balanced with respect to Type I and Type II error rates, with  $\alpha = 0.05$  and  $\beta = 1 - 0.937 = 0.063$ . The study thus seems well designed at this sample size.

Now suppose that in a follow-up meeting with the cardiologists, you discover that their specific intent is to demonstrate that the (partial) correlation between PBI and tHcy is greater than 0.2. You suggest changing the planned data analysis to a one-sided Fisher's  $z$  test with a null correlation of 0.2. The following statements perform a power analysis for this test:

```
proc power;
  onecorr dist=fisherz
    npvars = 6
    corr = 0.35
    nullcorr = 0.2
    sides = 1
    ntotal = 100
    power = .;
run;
```

The `DIST=FISHERZ` option in the `ONECORR` statement specifies Fisher's  $z$  test. The `NPARTIALVARS=` option specifies that six additional variables are adjusted for in the partial correlation. The `CORR=` option specifies the conjectured correlation of 0.35, and the `NULLCORR=` option indicates the null value of 0.2. The `SIDES=` option specifies a one-sided test.

Output 67.5.3 shows the output.

**Output 67.5.3** Power Analysis for Fisher's  $z$  Test

The POWER Procedure		
Fisher's $z$ Test for Pearson Correlation		
Fixed Scenario Elements		
Distribution	Fisher's $z$ transformation of $r$	
Method	Normal approximation	
Number of Sides	1	
Null Correlation	0.2	
Number of Variables Partialled Out	6	
Correlation	0.35	
Total Sample Size	100	
Nominal Alpha	0.05	
Computed Power		
	Actual	
	Alpha	Power
	0.05	0.466

The power for Fisher's  $z$  test is less than 50%, the decrease being mostly due to the smaller effect size (relative to the null value). When asked for a recommendation for a new sample size goal, you compute the required sample size to achieve a power of 0.95 (to balance Type I and Type II errors) and 0.85 (a threshold deemed to be minimally acceptable to the team). The following statements perform the sample size determination:

```
proc power;
  onecorr dist=fisherz
    npvars = 6
    corr = 0.35
    nullcorr = 0.2
    sides = 1
    ntotal = .
    power = 0.85 0.95;
run;
```

The `NTOTAL=.` option identifies sample size as the parameter to compute, and the `POWER=` option specifies the target powers.

**Output 67.5.4** Sample Size Determination for Fisher's z Test

The POWER Procedure				
Fisher's z Test for Pearson Correlation				
Fixed Scenario Elements				
Distribution			Fisher's z transformation of r	
Method			Normal approximation	
Number of Sides				1
Null Correlation				0.2
Number of Variables Partialled Out				6
Correlation				0.35
Nominal Alpha				0.05
Computed N Total				
Index	Nominal Power	Actual Alpha	Actual Power	N Total
1	0.85	0.05	0.850	280
2	0.95	0.05	0.950	417

The results in [Output 67.5.4](#) reveal a required sample size of 417 to achieve a power of 0.95 and a required sample size of 280 to achieve a power of 0.85.

---

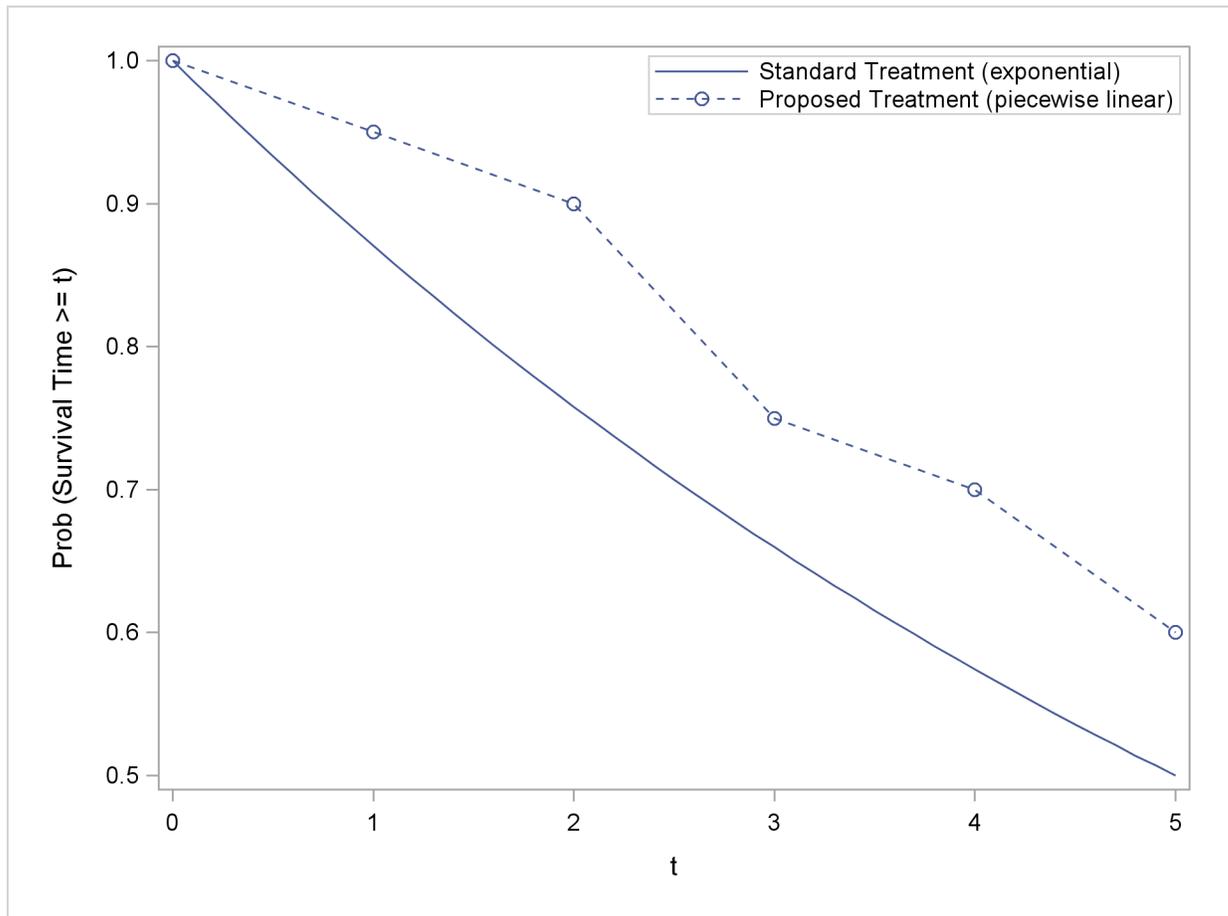
## Example 67.6: Comparing Two Survival Curves

You are consulting for a clinical research group planning a trial to compare survival rates for proposed and standard cancer treatments. The planned data analysis is a log-rank test to nonparametrically compare the overall survival curves for the two treatments. Your goal is to determine an appropriate sample size to achieve a power of 0.8 for a two-sided test with  $\alpha = 0.05$  by using a balanced design.

The survival curve for patients on the standard treatment is well known to be approximately exponential with a median survival time of five years. The research group conjectures that the new proposed treatment will yield a (nonexponential) survival curve similar to the dashed line in [Figure 67.6.1](#).

Patients will be accrued uniformly over two years and then followed for an additional three years past the accrual period. Some loss to follow-up is expected, with roughly exponential rates that would result in about 50% loss with the standard treatment within 10 years. The loss to follow-up with the proposed treatment is more difficult to predict, but 50% loss would be expected to occur sometime between years 5 and 20.

## Output 67.6.1 Survival Curves



Use the `TWOSAMPLESURVIVAL` statement with the `TEST=LOGRANK` option to compute the required sample size for the log-rank test. The following statements perform the analysis:

```
proc power;
  twosamplesurvival test=logrank
    curve("Standard") = 5 : 0.5
    curve("Proposed") = (1 to 5 by 1):(0.95 0.9 0.75 0.7 0.6)
    groupsurvival = "Standard" | "Proposed"
    accrualtime = 2
    followuptime = 3
    groupmedlosstimes = 10 | 20 5
    power = 0.8
    npergroup = .;
run;
```

The `CURVE=` option defines the two survival curves. The “Standard” curve has only one point, specifying an exponential form with a survival probability of 0.5 at year 5. The “Proposed” curve is a piecewise linear curve defined by the five points shown in Figure 67.6.1. The `GROUPSURVIVAL=` option assigns the survival curves to the two groups, and the `ACCRUALTIME=` and `FOLLOWUPTIME=` options specify the accrual and follow-up times. The `GROUPMEDLOSSTIMES=` option specifies the years at which 50% loss is expected to occur.

The **POWER=** option specifies the target power, and the **NPERGROUP=.** option identifies sample size per group as the parameter to compute. Default values for the **SIDES=** and **ALPHA=** options specify a two-sided test with  $\alpha = 0.05$ .

Output 67.6.2 shows the results.

**Output 67.6.2** Sample Size Determination for Log-Rank Test

The POWER Procedure				
Log-Rank Test for Two Survival Curves				
Fixed Scenario Elements				
Method	Lakatos normal approximation			
Accrual Time	2			
Follow-up Time	3			
Group 1 Survival Curve	Standard			
Form of Survival Curve 1	Exponential			
Group 2 Survival Curve	Proposed			
Form of Survival Curve 2	Piecewise Linear			
Group 1 Median Loss Time	10			
Nominal Power	0.8			
Number of Sides	2			
Number of Time Sub-Intervals	12			
Alpha	0.05			
Computed N Per Group				
	Index	Median Loss Time 2	Actual Power	N Per Group
	1	20	0.800	228
	2	5	0.801	234

The required sample size per group to achieve a power of 0.8 is 228 if the median loss time is 20 years for the proposed treatment. Only six more patients are required in each group if the median loss time is as short as five years.

---

### Example 67.7: Confidence Interval Precision

An investment firm has hired you to help plan a study to estimate the success of a new investment strategy called “IntuiVest.” The study involves complex simulations of market conditions over time, and it tracks the balance of a hypothetical brokerage account starting with \$50,000. Each simulation is very expensive in terms of computing time. You are asked to determine an appropriate number of simulations to estimate the average change in the account balance at the end of three years. The goal is to have a 95% chance of obtaining a 90% confidence interval whose half-width is at most \$1,000. That is, the firm wants to have a 95% chance of being able to correctly claim at the end of the study

that “Our research shows with 90% confidence that IntuiVest yields a profit of \$X +/- \$1,000 at the end of three years on an initial investment of \$50,000 (under simulated market conditions).”

The probability of achieving the desired precision (that is, a small interval width) can be calculated either unconditionally or conditionally given that the true mean is captured by the interval. You decide to use the conditional form, considering two of its advantages:

- The conditional probability is usually lower than the unconditional probability for the same sample size, meaning that the conditional form is generally conservative.
- The overall probability of achieving the desired precision *and* capturing the true mean is easily computed as the product of the half-width probability and the confidence level. In this case, the overall probability is  $0.95 \times 0.9 = 0.855$ .

Based on some initial simulations, you expect a standard deviation between \$25,000 and \$45,000 for the ending account balance. You will consider both of these values in the sample size analysis.

As mentioned in the section “[Overview of Power Concepts](#)” on page 4910, an analysis of confidence interval precision is analogous to a traditional power analysis, with “CI Half-Width” taking the place of effect size and “Prob(Width)” taking the place of power. In this example, the target CI Half-Width is 1000, and the desired Prob(Width) is 0.95.

In addition to computing sample sizes for a half-width of \$1,000, you are asked to plot the required number of simulations for a range of half-widths between \$500 and \$2,000. Use the [ONESAMPLEMEANS](#) statement with the [CI=T](#) option to implement the sample size determination. The following statements perform the analysis:

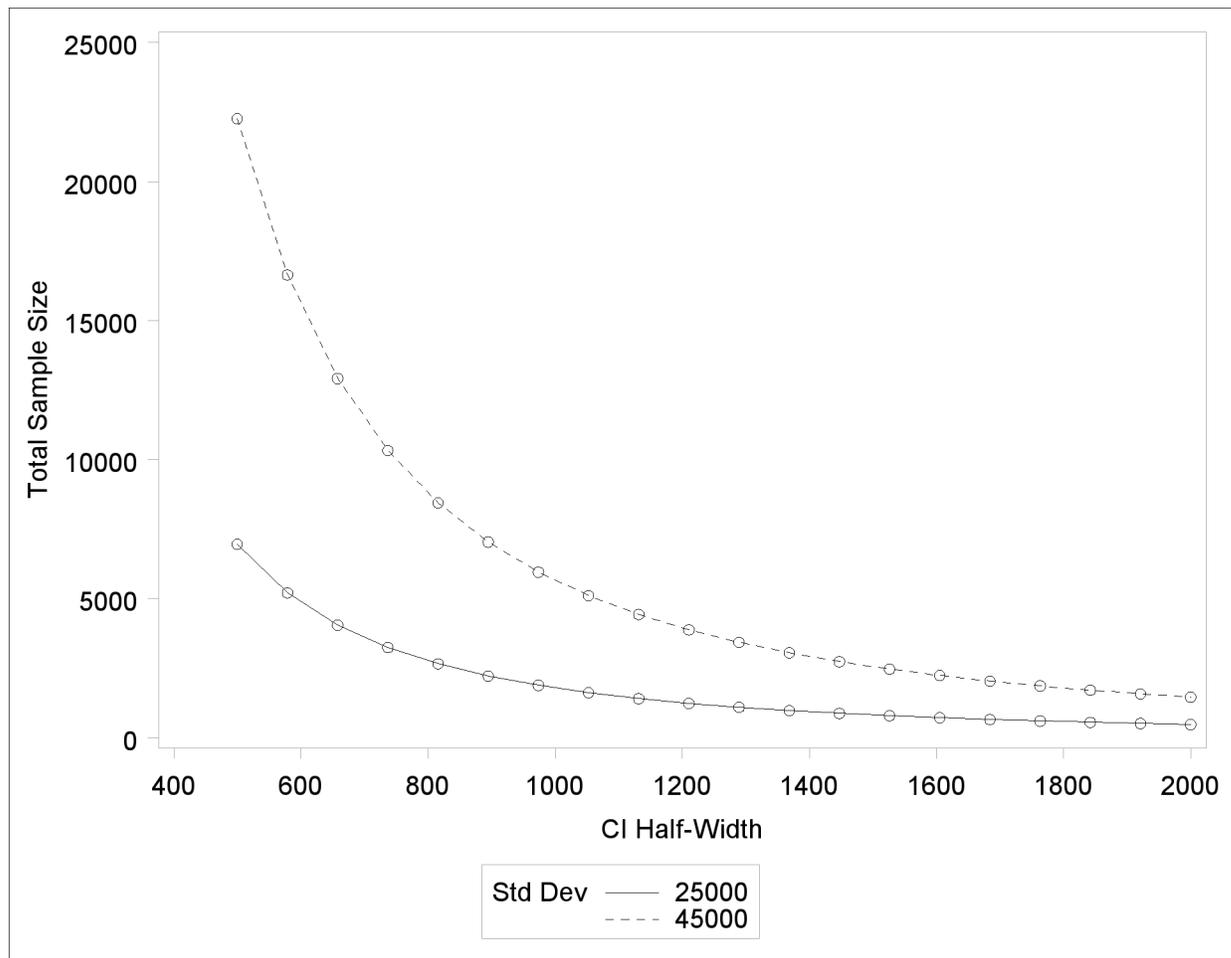
```
proc power;
  onesamplemeans ci=t
    alpha = 0.1
    halfwidth = 1000
    stddev = 25000 45000
    probwidth = 0.95
    ntotal = .;
  plot x=effect min=500 max=2000;
run;
```

The [NTOTAL=.](#) option identifies sample size as the parameter to compute. The [ALPHA=0.1](#) option specifies a confidence level of  $1 - \alpha = 0.9$ . The [HALFWIDTH=](#) option specifies the target half-width, and the [STDDEV=](#) option specifies the conjectured standard deviation values. The [PROBWIDTH=](#) option specifies the desired probability of achieving the target precision. The default value [PROBTYPE=CONDITIONAL](#) specifies that this probability is conditional on the true mean being captured by the interval. The default of [SIDES=2](#) indicates a two-sided interval.

[Output 67.7.1](#) shows the output, and [Output 67.7.2](#) shows the plot.

**Output 67.7.1** Sample Size Determination for Confidence Interval Precision

The POWER Procedure			
Confidence Interval for Mean			
Fixed Scenario Elements			
Distribution		Normal	
Method		Exact	
Alpha		0.1	
CI Half-Width		1000	
Nominal Prob(Width)		0.95	
Number of Sides		2	
Prob Type		Conditional	
Computed N Total			
Index	Std Dev	Actual Prob (Width)	N Total
1	25000	0.951	1788
2	45000	0.950	5652

**Output 67.7.2** Plot of Sample Size versus Confidence Interval Half-Width

The number of simulations required in order to have a 95% chance of obtaining a half-width of at most 1000 is between 1788 and 5652, depending on the standard deviation. The plot reveals that more than 20,000 simulations would be required for a half-width of 500, assuming the higher standard deviation.

---

### Example 67.8: Customizing Plots

This example demonstrates various ways you can modify and enhance plots:

- assigning analysis parameters to axes
- fine-tuning a sample size axis
- adding reference lines
- linking plot features to analysis parameters

- choosing key (legend) styles
- modifying symbol locations

The example plots are all based on a sample size analysis for a two-sample  $t$  test of group mean difference. You start by computing the sample size required to achieve a power of 0.9 by using a two-sided test with  $\alpha = 0.05$ , assuming the first mean is 12, the second mean is either 15 or 18, and the standard deviation is either 7 or 9.

Use the `TWOSAMPLEMEANS` statement with the `TEST=DIFF` option to compute the required sample sizes. Indicate total sample size as the result parameter by supplying a missing value (`.`) with the `NTOTAL=` option. Use the `GROUPMEANS=`, `STDDEV=`, and `POWER=` options to specify values of the other parameters. The following statements perform the sample size computations:

```
proc power;
  twosamplemeans test=diff
    groupmeans   = 12 | 15 18
    stddev       = 7 9
    power        = 0.9
    ntotal       = .;
run;
```

Default values for the `NULLDIFF=`, `SIDES=`, `GROUPWEIGHTS=`, and `DIST=` options specify a null mean difference of 0, two-sided test, balanced design, and assumption of normally distributed data, respectively.

Output 67.8.1 shows that the required sample size ranges from 60 to 382, depending on the unknown standard deviation and second mean.

**Output 67.8.1** Computed Sample Sizes

The POWER Procedure				
Two-sample t Test for Mean Difference				
Fixed Scenario Elements				
Distribution			Normal	
Method			Exact	
Group 1 Mean			12	
Nominal Power			0.9	
Number of Sides			2	
Null Difference			0	
Alpha			0.05	
Group 1 Weight			1	
Group 2 Weight			1	
Computed N Total				
Index	Mean2	Std Dev	Actual Power	N Total
1	15	7	0.902	232
2	15	9	0.901	382
3	18	7	0.904	60
4	18	9	0.904	98

## Assigning Analysis Parameters to Axes

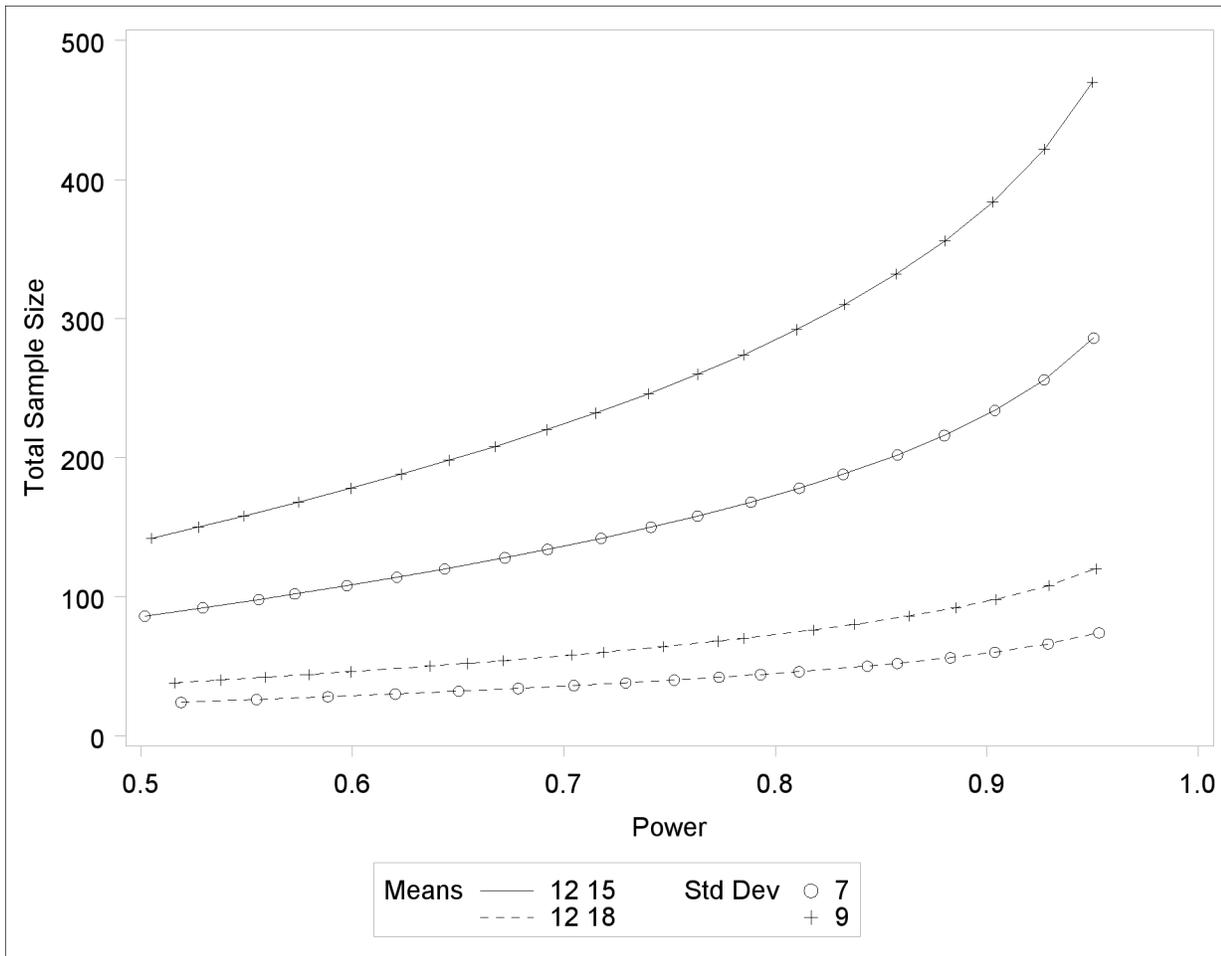
Use the **PLOT** statement to produce plots for all power and sample size analyses in PROC POWER. For the sample size analysis described at the beginning of this example, suppose you want to plot the required sample size on the Y axis against a range of powers between 0.5 and 0.95 on the X axis. The **X=** and **Y=** options specify which parameter to plot against the result and which axis to assign to this parameter. You can use either the **X=** or the **Y=** option, but not both. Use the **X=POWER** option in the **PLOT** statement to request a plot with power on the X axis. The result parameter, here total sample size, is always plotted on the other axis. Use the **MIN=** and **MAX=** options to specify the range of the axis indicated with either the **X=** or the **Y=** option. Here, specify **MIN=0.5** and **MAX=0.95** to specify the power range. The following statements produce the plot:

```
proc power plotonly;
  twosamplemeans test=diff
    groupmeans    = 12 | 15 18
    stddev        = 7 9
    power         = 0.9
    ntotal        = .;
  plot x=power min=0.5 max=0.95;
run;
```

Note that the value (0.9) of the **POWER=** option in the **TWOSAMPLEMEANS** statement is only a placeholder when the **PLOTONLY** option is used and both the **MIN=** and **MAX=** options are used, because the values of the **MIN=** and **MAX=** options override the value of 0.9. But the **POWER=** option itself is still required in the **TWOSAMPLEMEANS** statement, to provide a complete specification of the sample size analysis.

The resulting plot is shown in [Output 67.8.2](#).

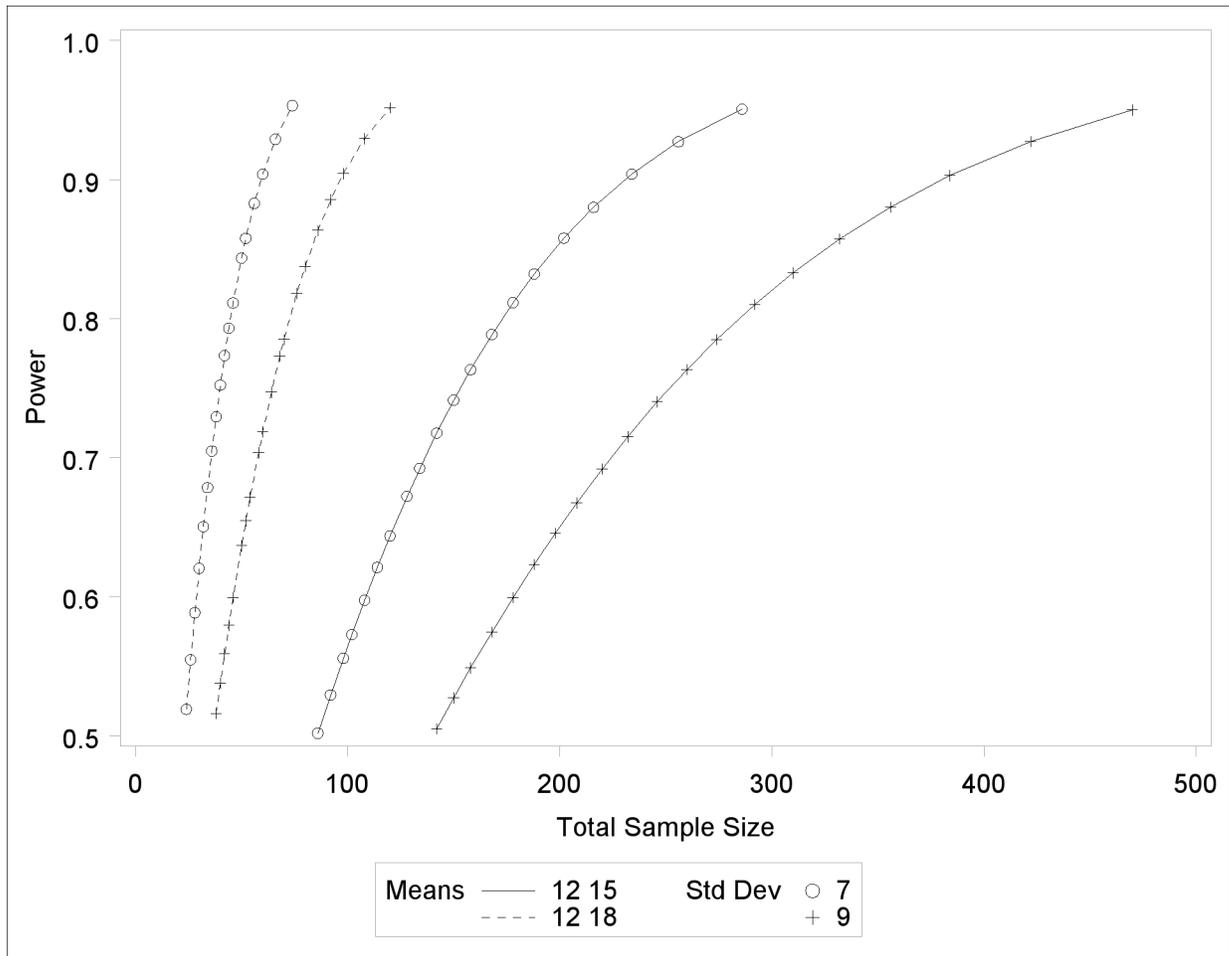
Output 67.8.2 Plot of Sample Size versus Power



The line style identifies the group means scenario, and the plotting symbol identifies the standard deviation scenario. The locations of plotting symbols indicate computed sample sizes; the curves are linear interpolations of these points. By default, each curve consists of approximately 20 computed points (sometimes slightly more or less, depending on the analysis).

If you would rather plot power on the Y axis versus sample size on the X axis, you have two general strategies to choose from. One strategy is to use the **Y=** option instead of the **X=** option in the **PLOT** statement:

```
plot y=power min=0.5 max=0.95;
```

**Output 67.8.3** Plot of Power versus Sample Size using First Strategy

Note that the resulting plot ([Output 67.8.3](#)) is essentially a mirror image of [Output 67.8.2](#). The axis ranges are set such that each curve in [Output 67.8.3](#) contains similar values of Y instead of X. Each plotted point represents the computed value of the X axis at the input value of the Y axis.

A second strategy for plotting power versus sample size (when originally solving for sample size) is to invert the analysis and base the plot on computed power for a given range of sample sizes. This strategy works well for monotonic power curves (as is the case for the  $t$  test and most other continuous analyses). It is advantageous in the sense of preserving the traditional role of the Y axis as the computed parameter. A common way to implement this strategy is as follows:

- Determine the range of sample sizes sufficient to cover at the desired power range for all curves (where each “curve” represents a scenario for standard deviation and second group mean).
- Use this range for the X axis of a plot.

To determine the required sample sizes for target powers of 0.5 and 0.95, change the values in the `POWER=` option as follows to reflect this range:

```

proc power;
  twosamplemeans test=diff
    groupmeans   = 12 | 15 18
    stddev       = 7 9
    power        = 0.5 0.95
    ntotal       = .;
run;

```

Output 67.8.4 reveals that a sample size range of 24 to 470 is approximately sufficient to cover the desired power range of 0.5 to 0.95 for all curves (“approximately” because the actual power at the rounded sample size of 24 is slightly higher than the nominal power of 0.5).

**Output 67.8.4** Computed Sample Sizes

The POWER Procedure						
Two-sample t Test for Mean Difference						
Fixed Scenario Elements						
Distribution	Normal					
Method	Exact					
Group 1 Mean	12					
Number of Sides	2					
Null Difference	0					
Alpha	0.05					
Group 1 Weight	1					
Group 2 Weight	1					
Computed N Total						
Index	Mean2	Std Dev	Nominal Power	Actual Power	N Total	
1	15	7	0.50	0.502	86	
2	15	7	0.95	0.951	286	
3	15	9	0.50	0.505	142	
4	15	9	0.95	0.950	470	
5	18	7	0.50	0.519	24	
6	18	7	0.95	0.953	74	
7	18	9	0.50	0.516	38	
8	18	9	0.95	0.952	120	

To plot power on the Y axis for sample sizes between 20 and 500, use the `X=N` option in the `PLOT` statement with `MIN=20` and `MAX=500`:

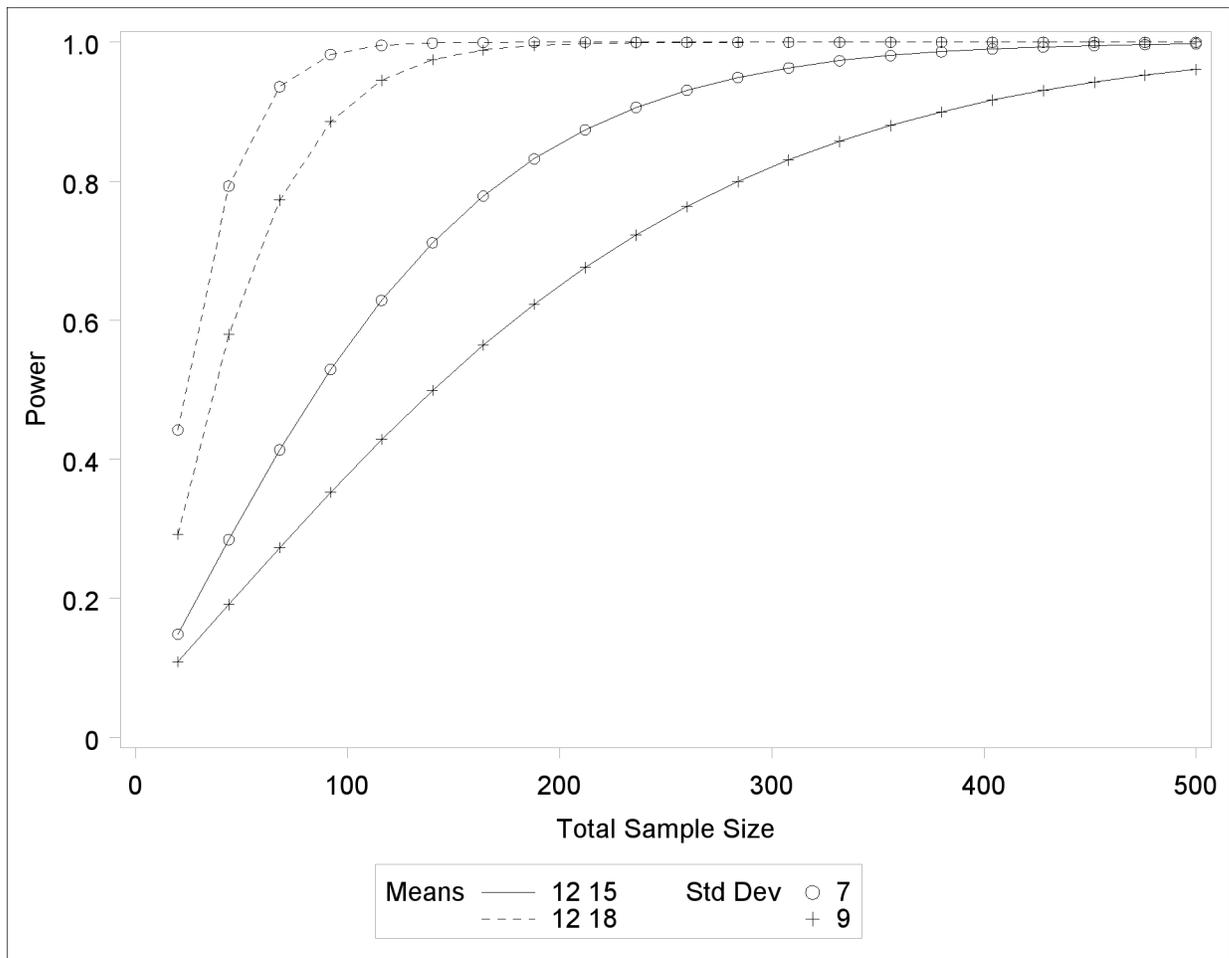
```

proc power plotonly;
  twosamplemeans test=diff
    groupmeans   = 12 | 15 18
    stddev       = 7 9
    power        = .
    ntotal       = 200;
  plot x=n min=20 max=500;
run;

```

Each curve in the resulting plot in [Output 67.8.5](#) covers at least a power range of 0.5 to 0.95.

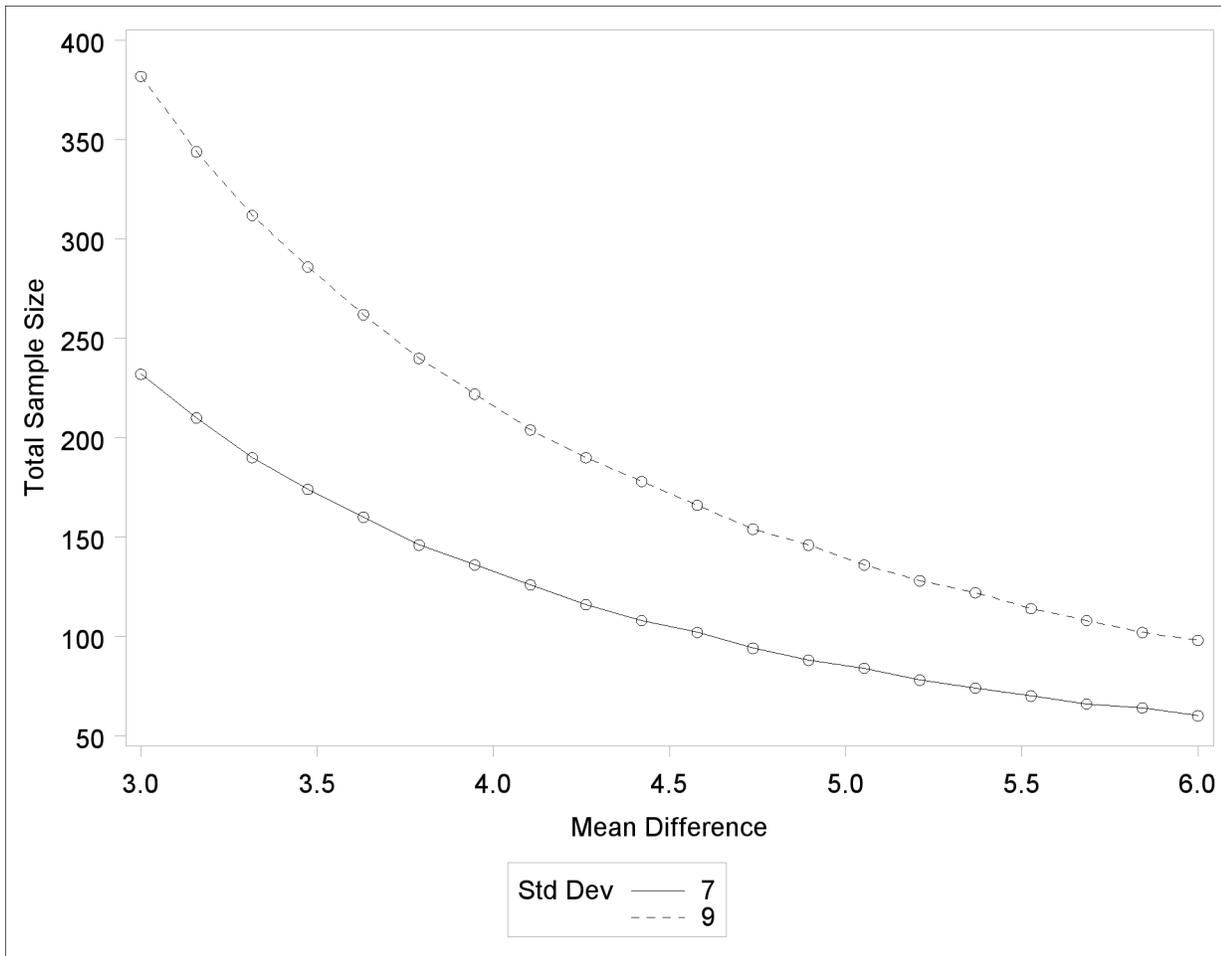
**Output 67.8.5** Plot of Power versus Sample Size Using Second Strategy



Finally, suppose you want to produce a plot of sample size versus effect size for a power of 0.9. In this case, the “effect size” is defined to be the mean difference. You need to reparameterize the analysis by using the `MEANDIFF=` option instead of the `GROUPMEANS=` option to produce a plot, since each plot axis must be represented by a scalar parameter. Use the `X=EFFECT` option in the `PLOT` statement to assign the mean difference to the X axis. The following statements produce a plot of required sample size to detect mean differences between 3 and 6:

```
proc power plotonly;
  twosamplemeans test=diff
    meandiff      = 3 6
    stddev        = 7 9
    power         = 0.9
    ntotal        = .;
  plot x=effect min=3 max=6;
run;
```

The resulting plot [Output 67.8.6](#) shows how the required sample size decreases with increasing mean difference.

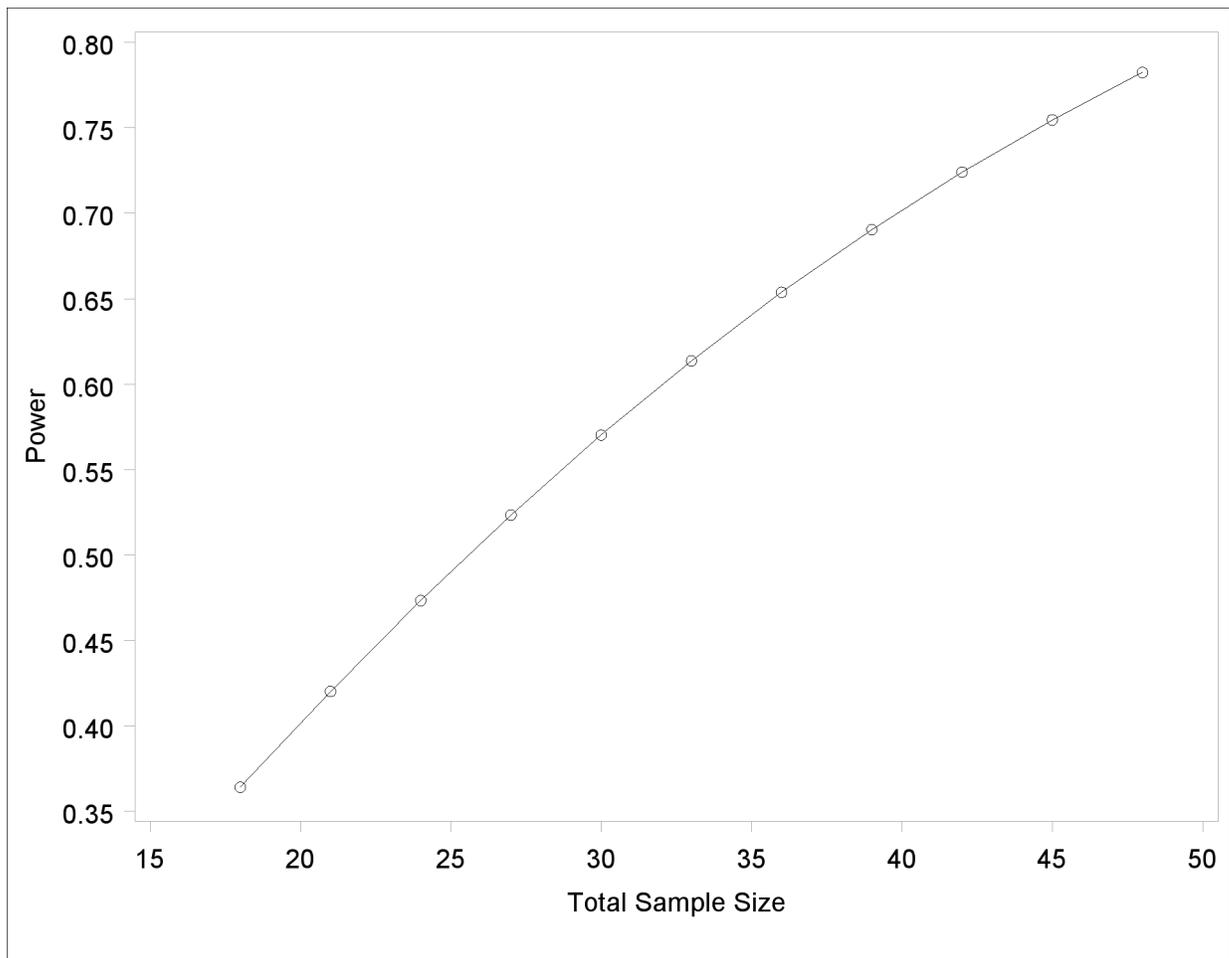
**Output 67.8.6** Plot of Sample Size versus Mean Difference

### Fine-Tuning a Sample Size Axis

Consider the following plot request for a sample size analysis similar to the one in [Output 67.8.1](#) but with only a single scenario, and with unbalanced sample size allocation of 2:1:

```
proc power plotonly;
  ods output plotcontent=PlotData;
  twosamplemeans test=diff
    groupmeans = 12 | 18
    stddev      = 7
    groupweights = 2 | 1
    power       = .
    ntotal      = 20;
  plot x=n min=20 max=50 npoints=20;
run;
```

The `MIN=`, `MAX=`, and `NPOINTS=` options in the `PLOT` statement request a plot with 20 points between 20 and 50. But the resulting plot ([Output 67.8.7](#)) appears to have only 11 points, and they range from 18 to 48.

**Output 67.8.7** Plot with Overlapping Points

The reason that this plot has fewer points than usual is due to the rounding of sample sizes. If you do not use the **NFRACTIONAL** option in the analysis statement (here, the **TWOSAMPLEMEANS** statement), then the set of sample size points determined by the **MIN=**, **MAX=**, **NPOINTS=**, and **STEP=** options in the **PLOT** statement can be rounded to satisfy the allocation weights. In this case, they are rounded down to the nearest multiples of 3 (the sum of the weights), and many of the points overlap. To see the overlap, you can print the **NominalNTotal** (unadjusted) and **NTotal** (rounded) variables in the **PlotContent** ODS object (here saved to a data set called **PlotData**):

```
proc print data=PlotData;
  var NominalNTotal NTotal;
run;
```

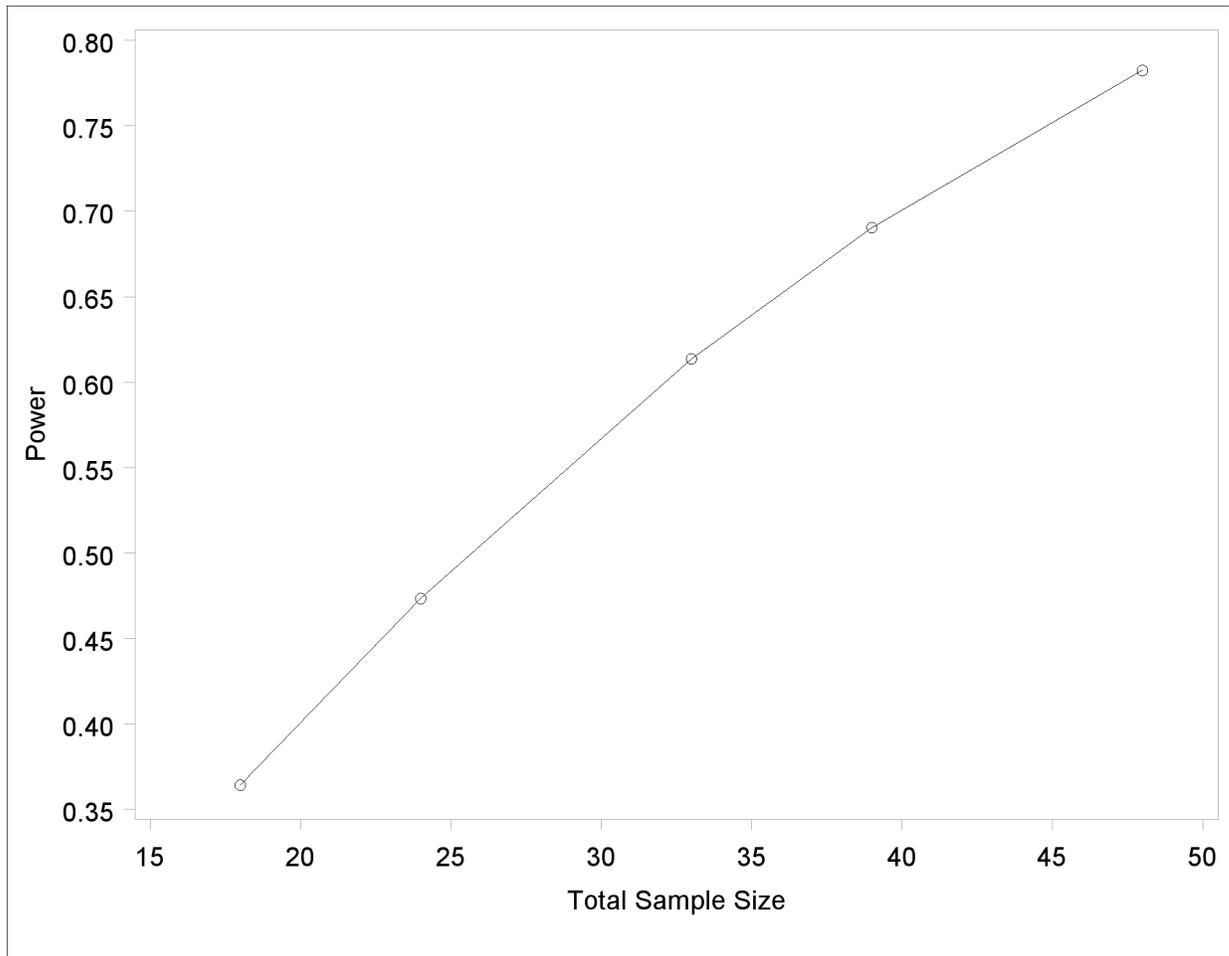
The output is shown in [Output 67.8.8](#).

**Output 67.8.8** Sample Sizes

	Obs	Nominal NTotal	NTotal
	1	18.0	18
	2	19.6	18
	3	21.2	21
	4	22.7	21
	5	24.3	24
	6	25.9	24
	7	27.5	27
	8	29.1	27
	9	30.6	30
	10	32.2	30
	11	33.8	33
	12	35.4	33
	13	36.9	36
	14	38.5	36
	15	40.1	39
	16	41.7	39
	17	43.3	42
	18	44.8	42
	19	46.4	45
	20	48.0	48

Besides overlapping of sample size points, another peculiarity that might occur without the `NFRACTIONAL` option is unequal spacing—for example, in the plot in [Output 67.8.9](#), created with the following statements:

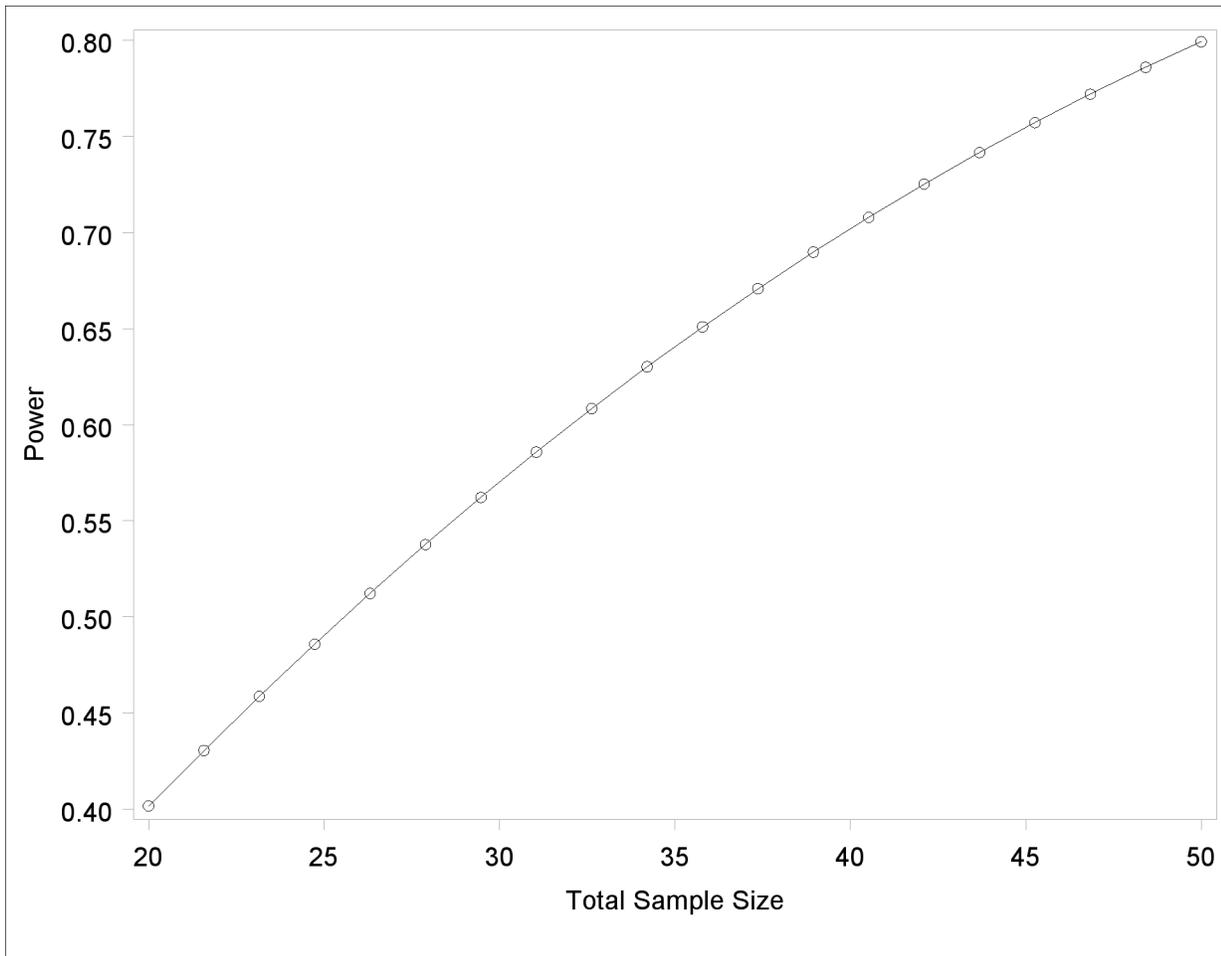
```
proc power plotonly;
  twosamplemeans test=diff
    groupmeans = 12 | 18
    stddev      = 7
    groupweights = 2 | 1
    power       = .
    ntotal      = 20;
  plot x=n min=20 max=50 npoints=5;
run;
```

**Output 67.8.9** Plot with Unequally Spaced Points

If you want to guarantee evenly spaced, nonoverlapping sample size points in your plots, you can either (1) use the **NFRACTIONAL** option in the analysis statement preceding the **PLOT** statement or (2) use the **STEP=** option and provide values for the **MIN=**, **MAX=**, and **STEP=** options in the **PLOT** statement that are multiples of the sum of the allocation weights. Note that this sum is simply 1 for one-sample and paired designs and 2 for balanced two-sample designs. So any integer step value works well for one-sample and paired designs, and any even step value works well for balanced two-sample designs. Both of these strategies will avoid rounding adjustments.

The following statements implement the first strategy to create the plot in [Output 67.8.10](#), by using the **NFRACTIONAL** option in the **TWOSAMPLEMEANS** statement:

```
proc power plotonly;
  twosamplemeans test=diff
    nfractional
    groupmeans    = 12 | 18
    stddev        = 7
    groupweights  = 2 | 1
    power         = .
    ntotal        = 20;
  plot x=n min=20 max=50 npoints=20;
run;
```

**Output 67.8.10** Plot with Fractional Sample Sizes

To implement the second strategy, use multiples of 3 for the `STEP=`, `MIN=`, and `MAX=` options in the `PLOT` statement (because the sum of the allocation weights is  $2 + 1 = 3$ ). The following statements use `STEP=3`, `MIN=18`, and `MAX=48` to create a plot that looks identical to the plot in [Output 67.8.7](#) but suffers no overlapping of points:

```
proc power plotonly;
  twosamplemeans test=diff
    groupmeans = 12 | 18
    stddev      = 7
    groupweights = 2 | 1
    power       = .
    ntotal      = 20;
  plot x=n min=18 max=48 step=3;
run;
```

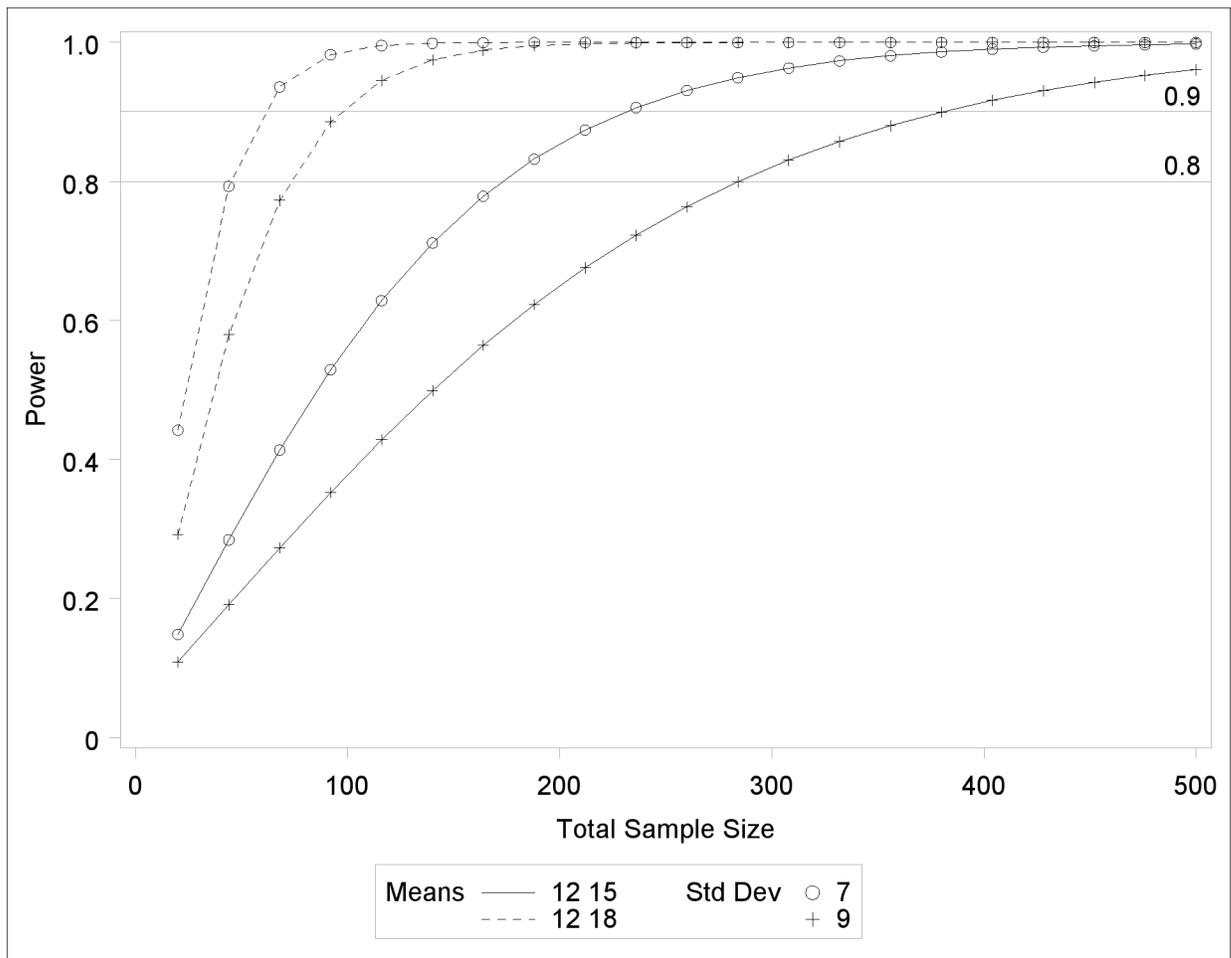
### Adding Reference Lines

Suppose you want to add reference lines to highlight `power=0.8` and `power=0.9` on the plot in [Output 67.8.5](#). You can add simple reference lines by using the `YOPTS=` option and `REF=` subop-

tion in the `PLOT` statement to produce [Output 67.8.11](#), with the following statements:

```
proc power plotonly;
  twosamplemeans test=diff
    groupmeans = 12 | 15 18
    stddev     = 7 9
    power      = .
    ntotal     = 100;
  plot x=n min=20 max=500
    yopts=(ref=0.8 0.9);
run;
```

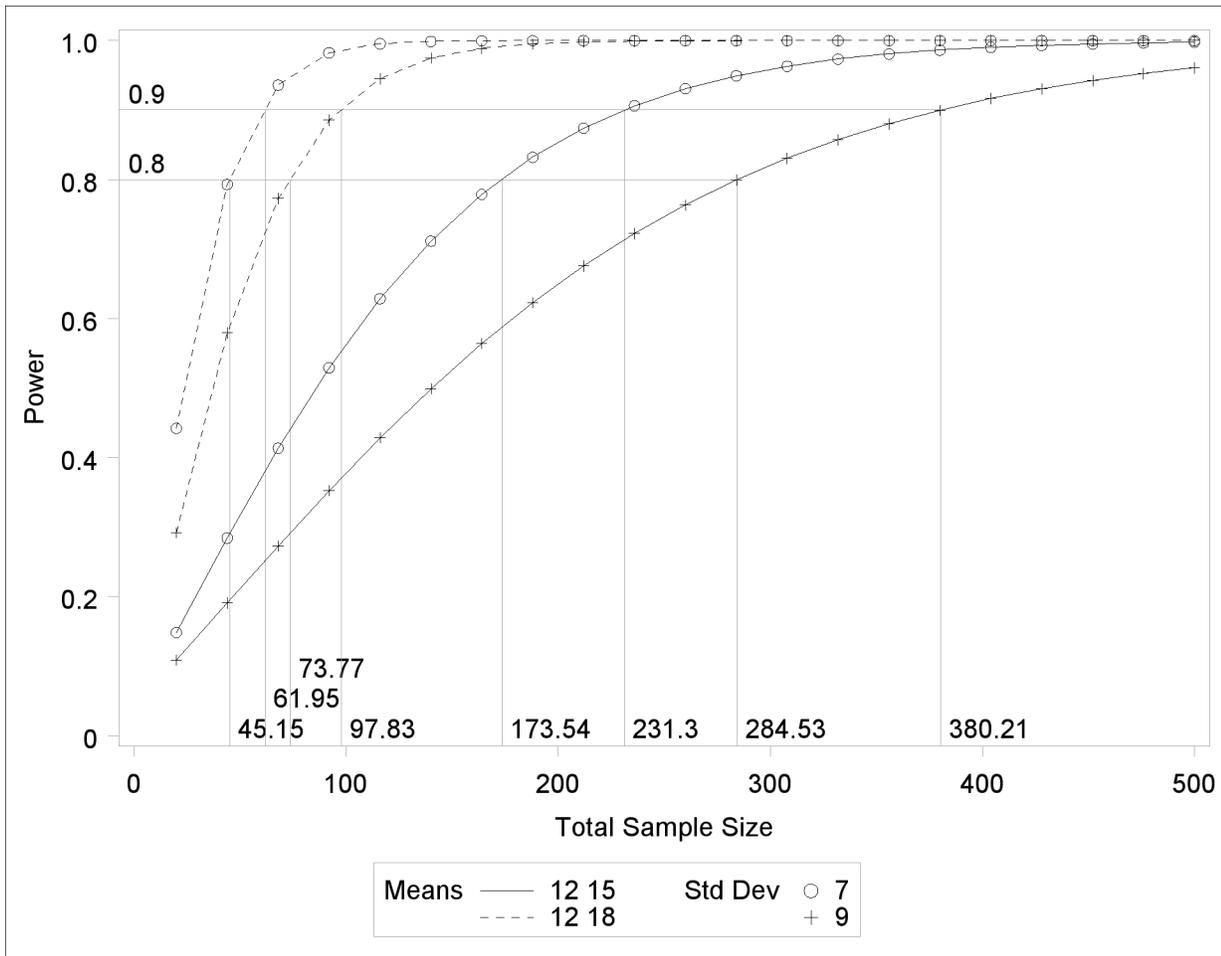
**Output 67.8.11** Plot with Simple Reference Lines on Y Axis



Or you can specify `CROSSREF=YES` to add reference lines that intersect each curve and cross over to the other axis:

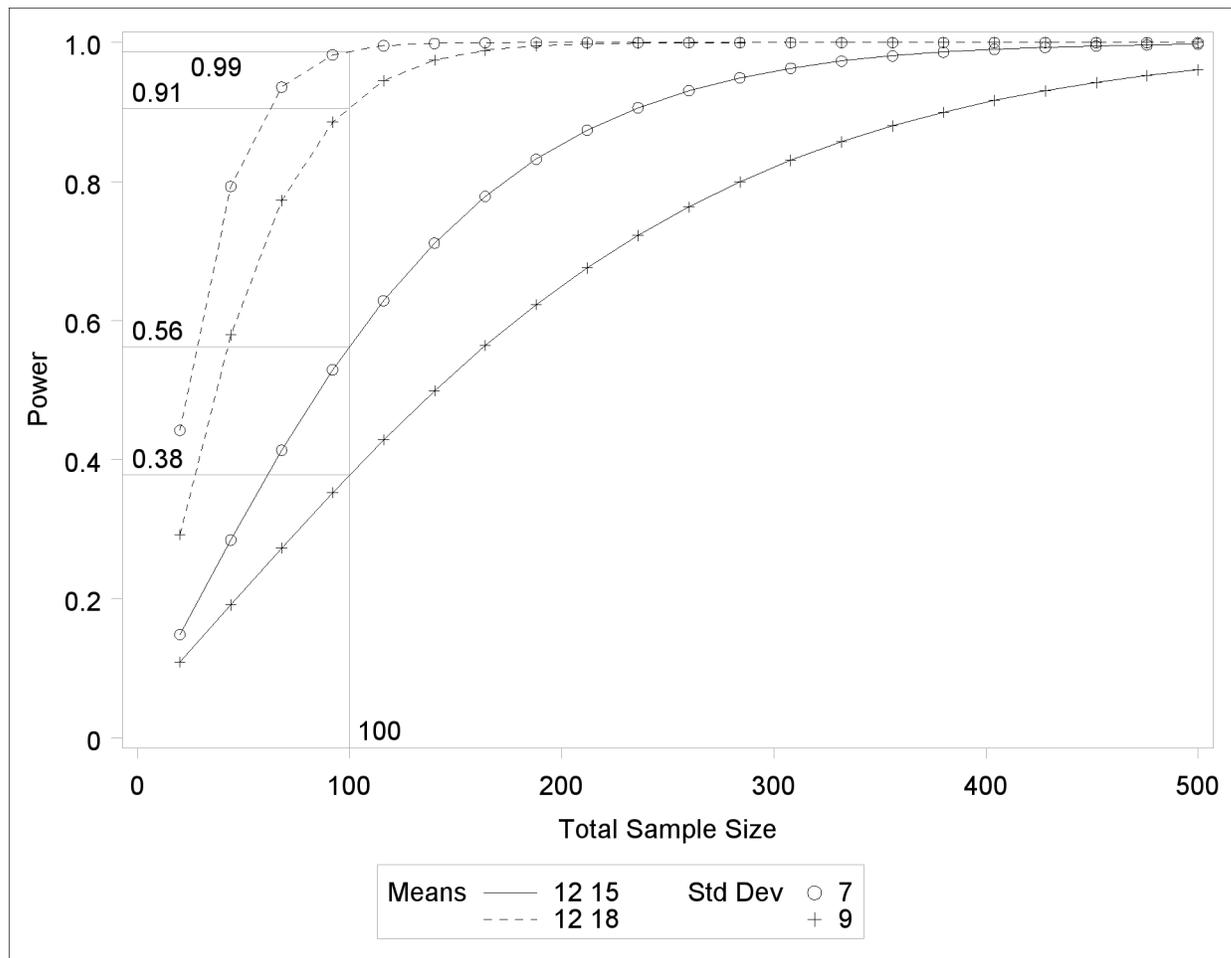
```
plot x=n min=20 max=500
  yopts=(ref=0.8 0.9 crossref=yes);
```

The resulting plot is shown in [Output 67.8.12](#).

**Output 67.8.12** Plot with CROSSREF=YES Style Reference Lines from Y Axis

You can also add reference lines for the X axis by using the `XOPTS=` option instead of the `YOPTS=` option. For example, the following `PLOT` statement produces [Output 67.8.13](#), which has crossing reference lines highlighting the sample size of 100:

```
plot x=n min=20 max=500
     xopts=(ref=100 crossref=yes);
```

**Output 67.8.13** Plot with CROSSREF=YES Style Reference Lines from X Axis

### Linking Plot Features to Analysis Parameters

You can use the **VARY** option in the **PLOT** statement to specify which of the following features you want to associate with analysis parameters.

- line style
- plotting symbol
- color
- panel

You can specify mappings between each of these features and one or more analysis parameters, or you can simply choose a subset of these features to use (and rely on default settings to associate these features with multiple-valued analysis parameters).

Suppose you supplement the sample size analysis in [Output 67.8.5](#) to include three values of alpha, by using the following statements:

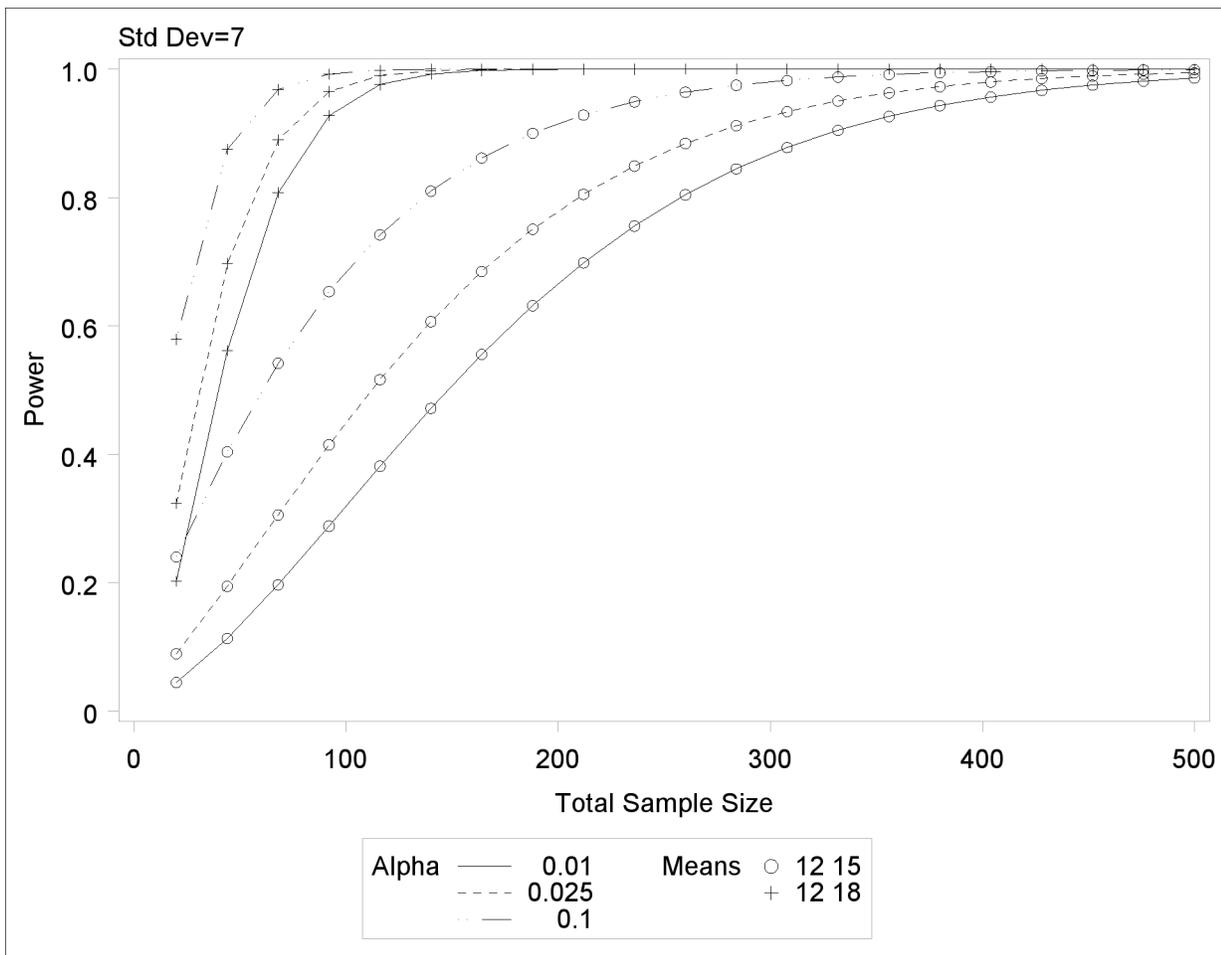
```

proc power plotonly;
  twosamplemeans test=diff
    groupmeans = 12 | 15 18
    stddev      = 7 9
    alpha       = 0.01 0.025 0.1
    power       = .
    ntotal     = 100;
  plot x=n min=20 max=500;
run;

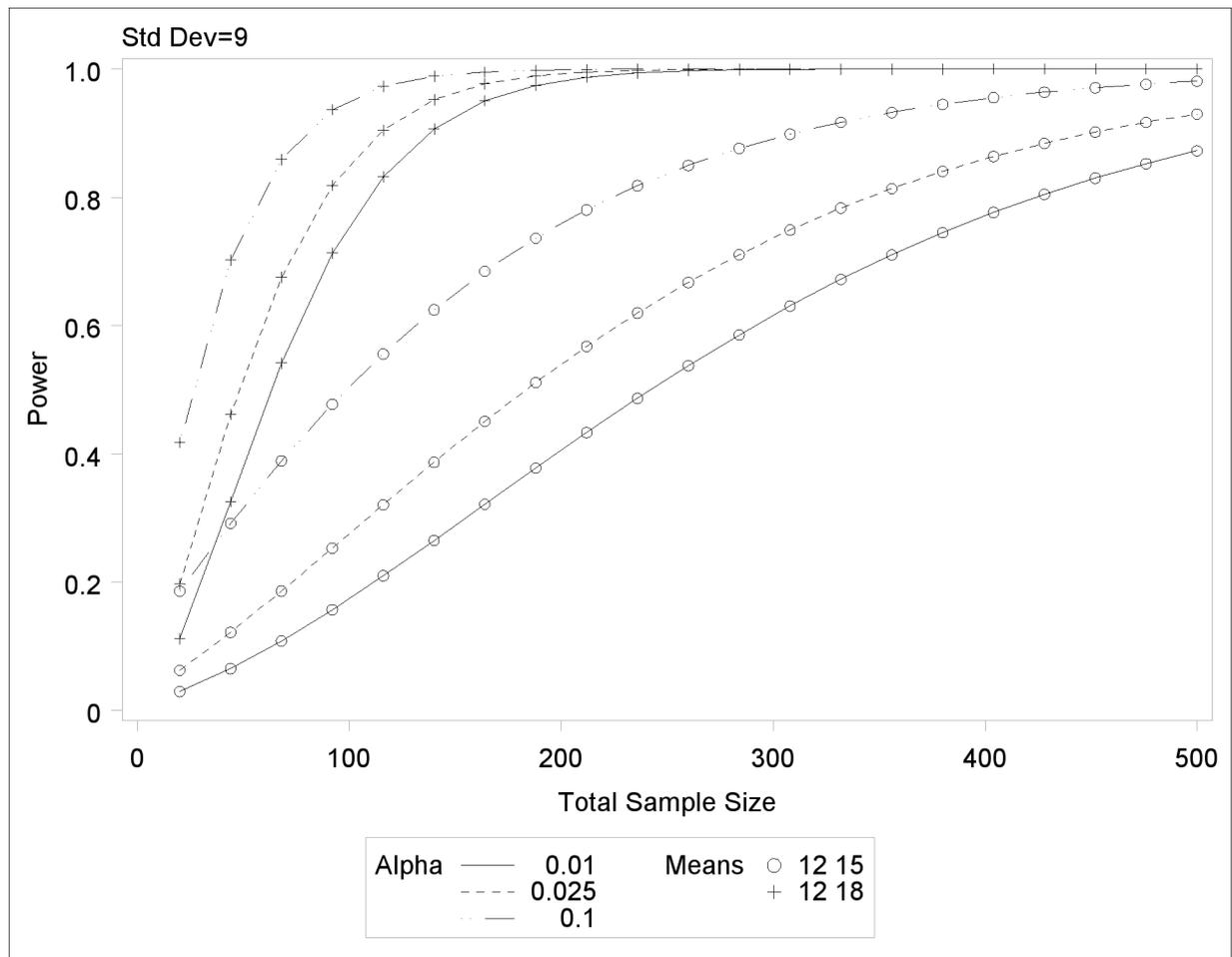
```

The defaults for the **VARY** option in the **PLOT** statement specify line style varying by the **ALPHA=** parameter, plotting symbol varying by the **GROUPMEANS=** parameter, panel varying by the **STDDEV=** parameter, and color remaining constant. The resulting plot, consisting of two panels, is shown in [Output 67.8.14](#).

**Output 67.8.14** Plot with Default VARY Settings



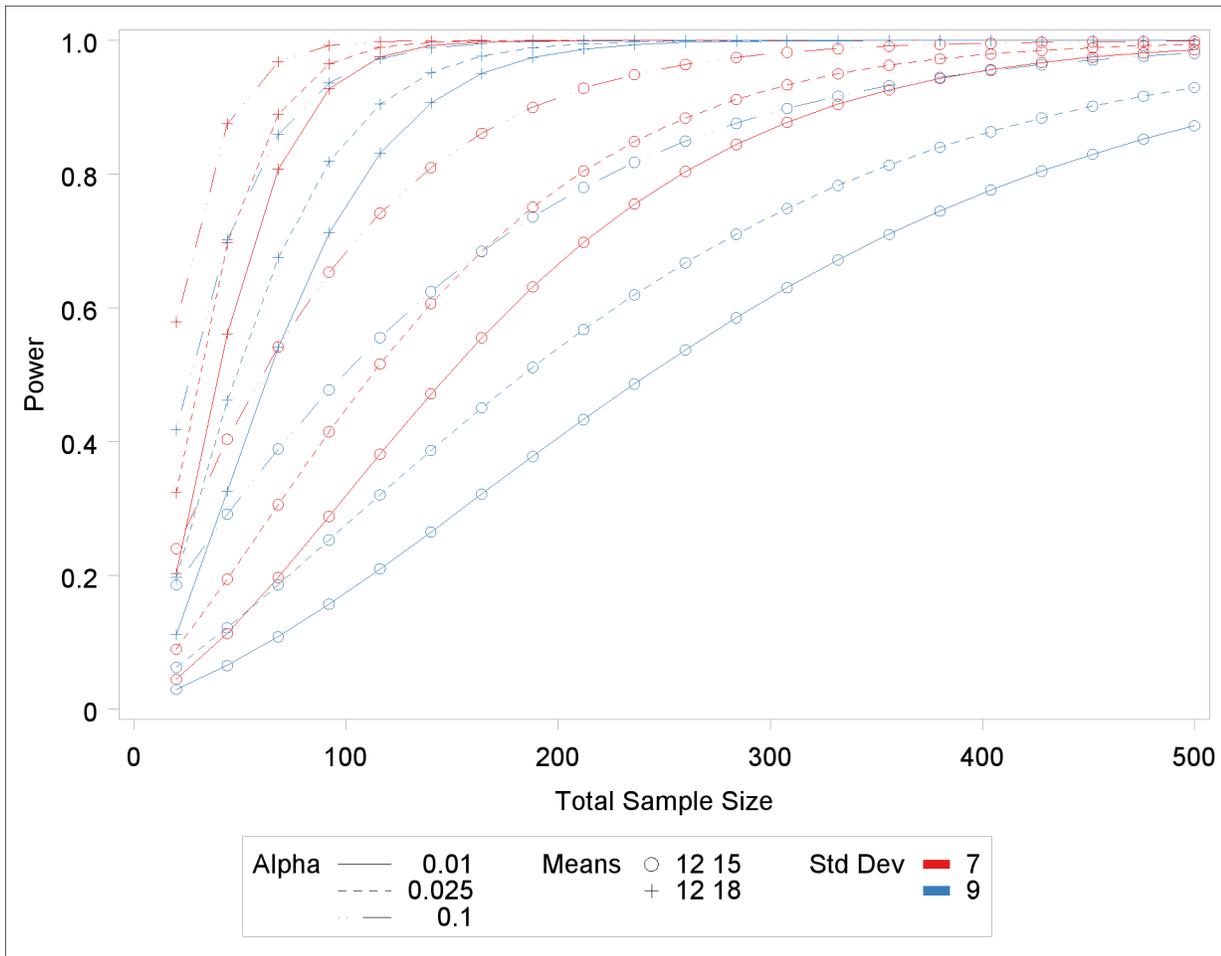
Output 67.8.14 continued



Suppose you want to produce a plot with only one panel that varies color in addition to line style and plotting symbol. Include the `LINESTYLE`, `SYMBOL`, and `COLOR` keywords in the `VARY` option in the `PLOT` statement, as follows, to produce the plot in [Output 67.8.15](#):

```
plot x=n min=20 max=500
    vary (linestyle, symbol, color);
```

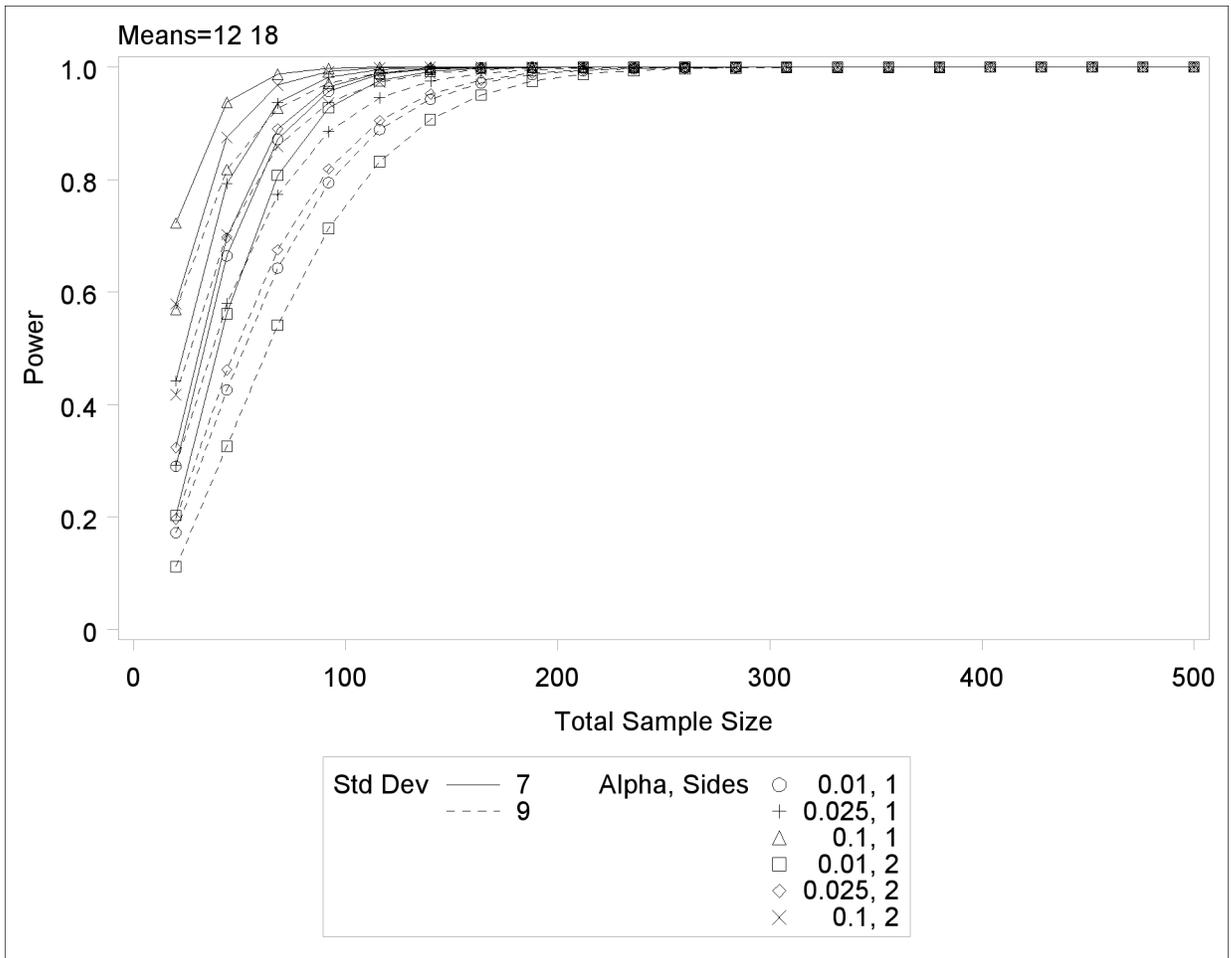
Output 67.8.15 Plot with Varying Color Instead of Panel

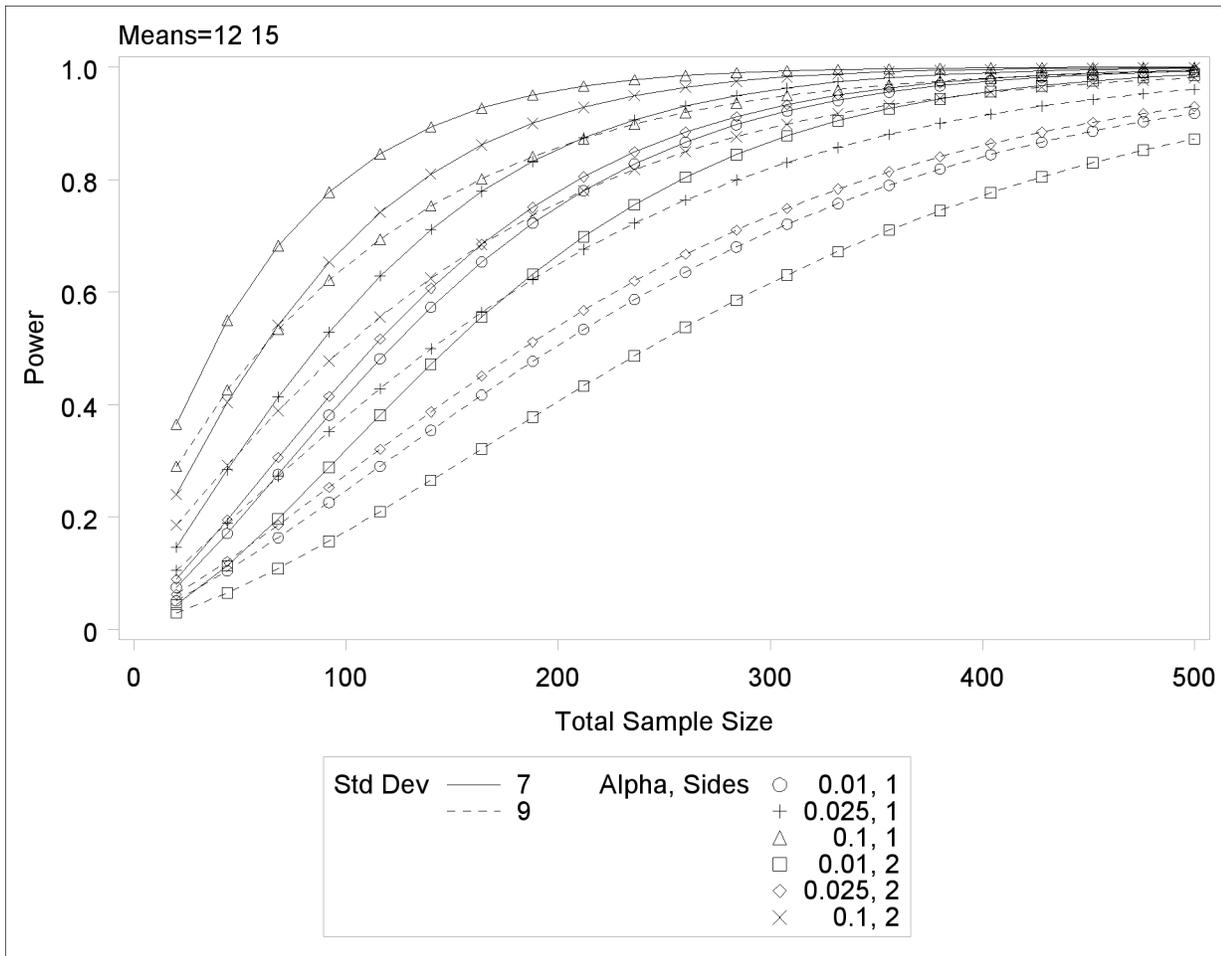


Finally, suppose you want to specify which features are used *and* which analysis parameters they are linked to. The following `PLOT` statement produces a two-panel plot (shown in [Output 67.8.16](#)) in which line style varies by standard deviation, plotting symbol varies by both alpha and sides, and panel varies by means:

```
plot x=n min=20 max=500
    vary (linestyle by stddev,
        symbol by alpha sides,
        panel by groupmeans);
```

**Output 67.8.16** Plot with Features Explicitly Linked to Parameters



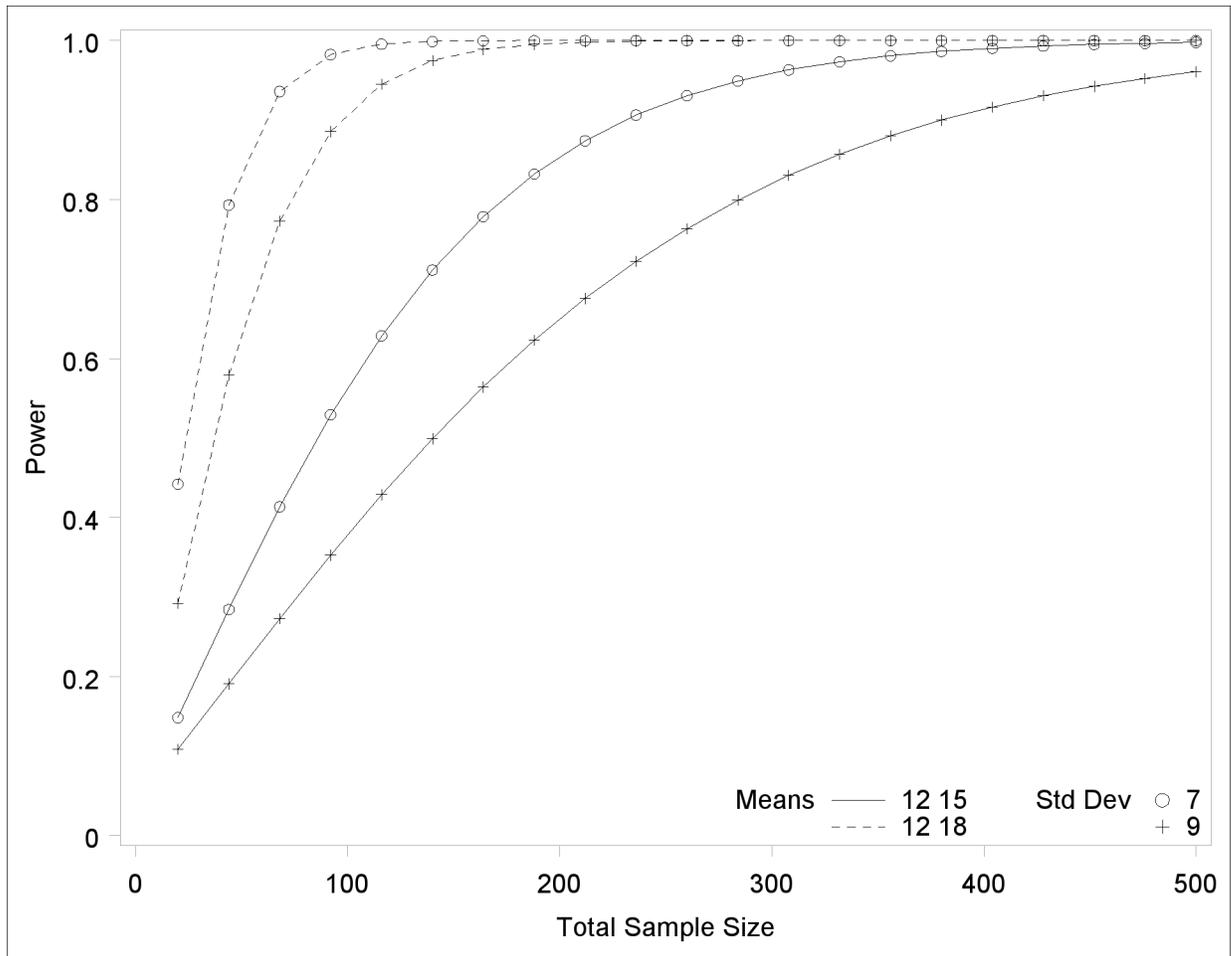
Output 67.8.16 *continued*

## Choosing Key (Legend) Styles

The default style for the key (or “legend”) is one that displays the association between levels of features and levels of analysis parameters, located below the X axis. For example, [Output 67.8.5](#) demonstrates this style of key.

You can reproduce [Output 67.8.5](#) with the same key but a different location, inside the plotting region, by using the `POS=INSET` option within the `KEY=BYFEATURE` option in the `PLOT` statement. The following statements product the plot in [Output 67.8.17](#):

```
proc power plotonly;
  twosamplemeans test=diff
    groupmeans = 12 | 15 18
    stddev     = 7 9
    power      = .
    ntotal     = 200;
  plot x=n min=20 max=500
    key = byfeature(pos=inset);
run;
```

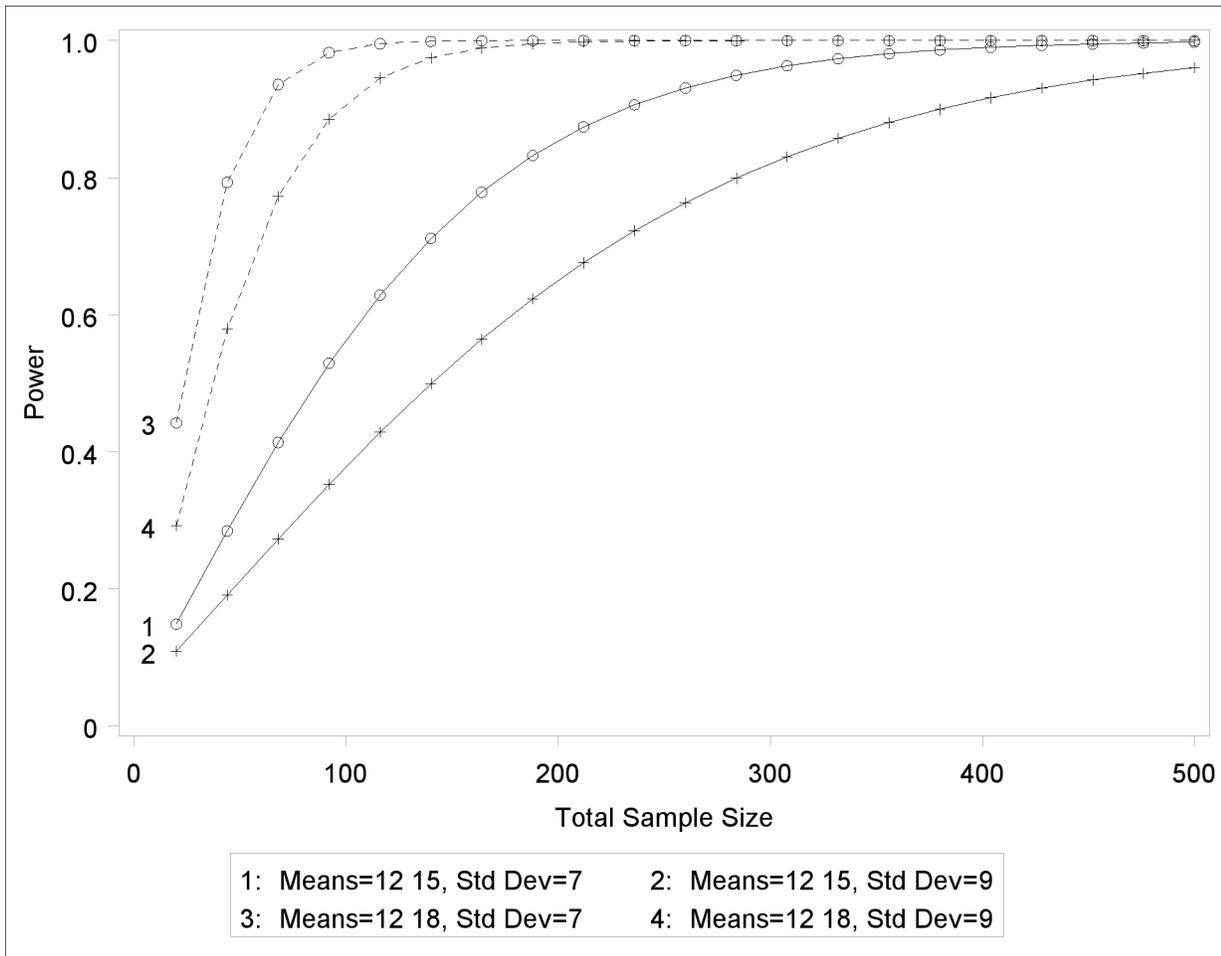
**Output 67.8.17** Plot with a By-Feature Key inside the Plotting Region

Alternatively, you can specify a key that identifies each individual curve separately by number by using the `KEY=BYCURVE` option in the `PLOT` statement:

```
plot x=n min=20 max=500
      key = bycurve;
```

The resulting plot is shown in [Output 67.8.18](#).

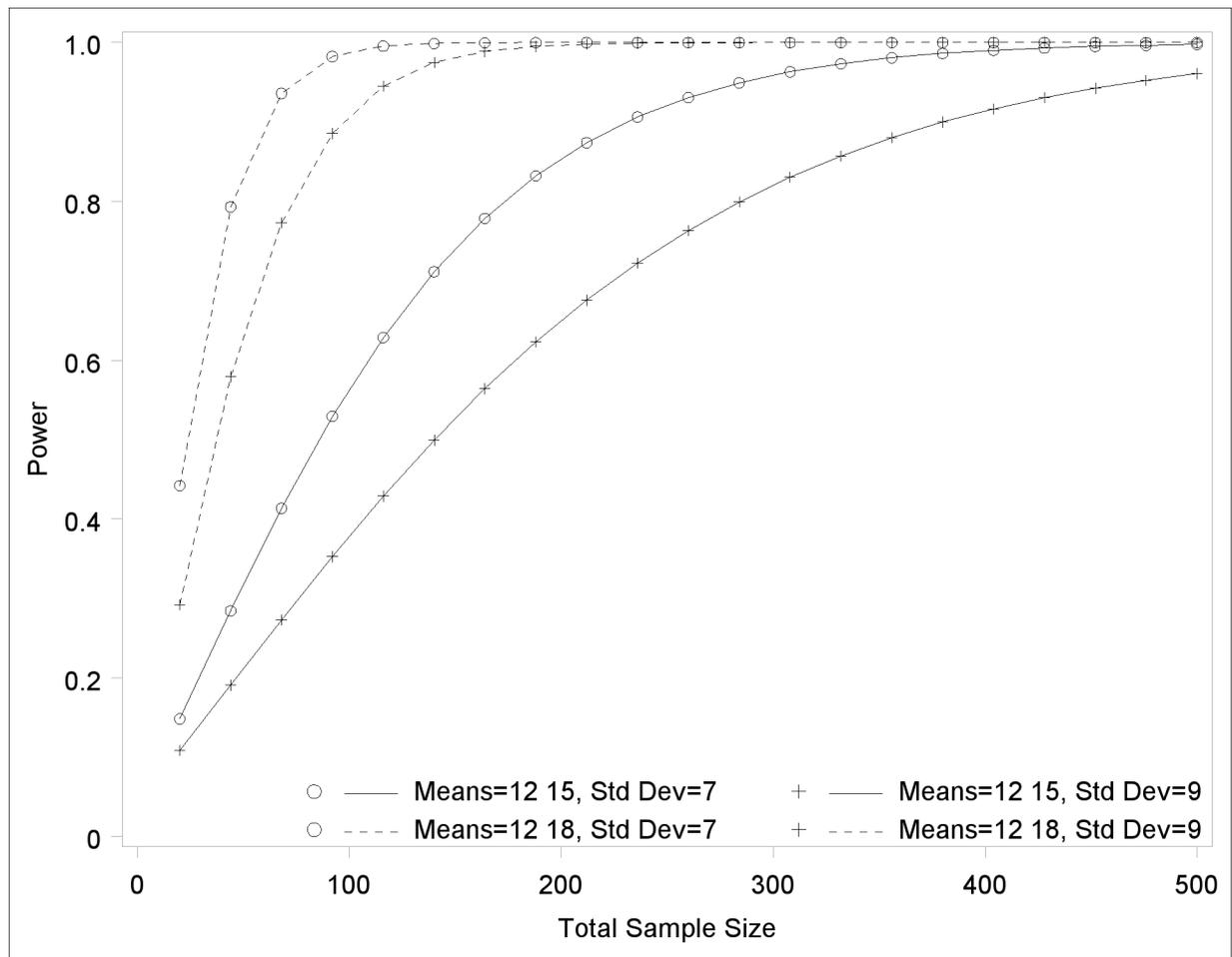
Output 67.8.18 Plot with a Numbered By-Curve Key



Use the `NUMBERS=OFF` option within the `KEY=BYCURVE` option to specify a nonnumbered key that identifies curves with samples of line styles, symbols, and colors:

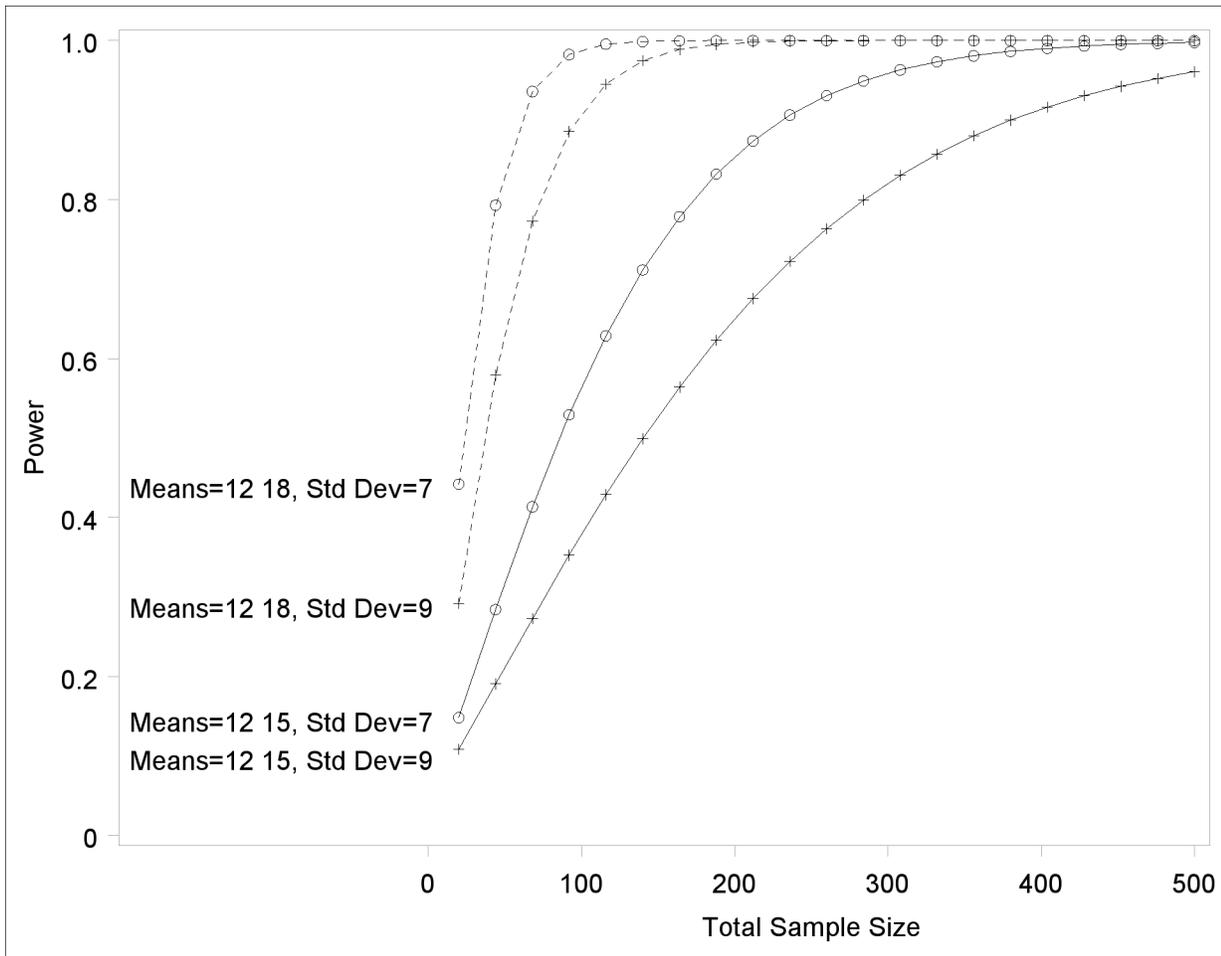
```
plot x=n min=20 max=500
      key = bycurve(numbers=off pos=inset);
```

The `POS=INSET` suboption places the key within the plotting region. The resulting plot is shown in [Output 67.8.19](#).

**Output 67.8.19** Plot with a Nonnumbered By-Curve Key

Finally, you can attach labels directly to curves with the `KEY=ONCURVES` option. The following `PLOT` statement produces [Output 67.8.20](#):

```
plot x=n min=20 max=500
      key = oncurves;
```

**Output 67.8.20** Plot with Directly Labeled Curves**Modifying Symbol Locations**

The default locations for plotting symbols are the points computed directly from the power and sample size algorithms. For example, [Output 67.8.5](#) shows plotting symbols corresponding to computed points. The curves connecting these points are interpolated (as indicated by the `INTERPOL=` option in the `PLOT` statement).

You can modify the locations of plotting symbols by using the `MARKERS=` option in the `PLOT` statement. The `MARKERS=ANALYSIS` option places plotting symbols at locations corresponding to the input specified in the analysis statement preceding the `PLOT` statement. You might prefer this as an alternative to using reference lines to highlight specific points. For example, you can reproduce [Output 67.8.5](#), but with the plotting symbols located at the sample sizes shown in [Output 67.8.1](#), by using the following statements:

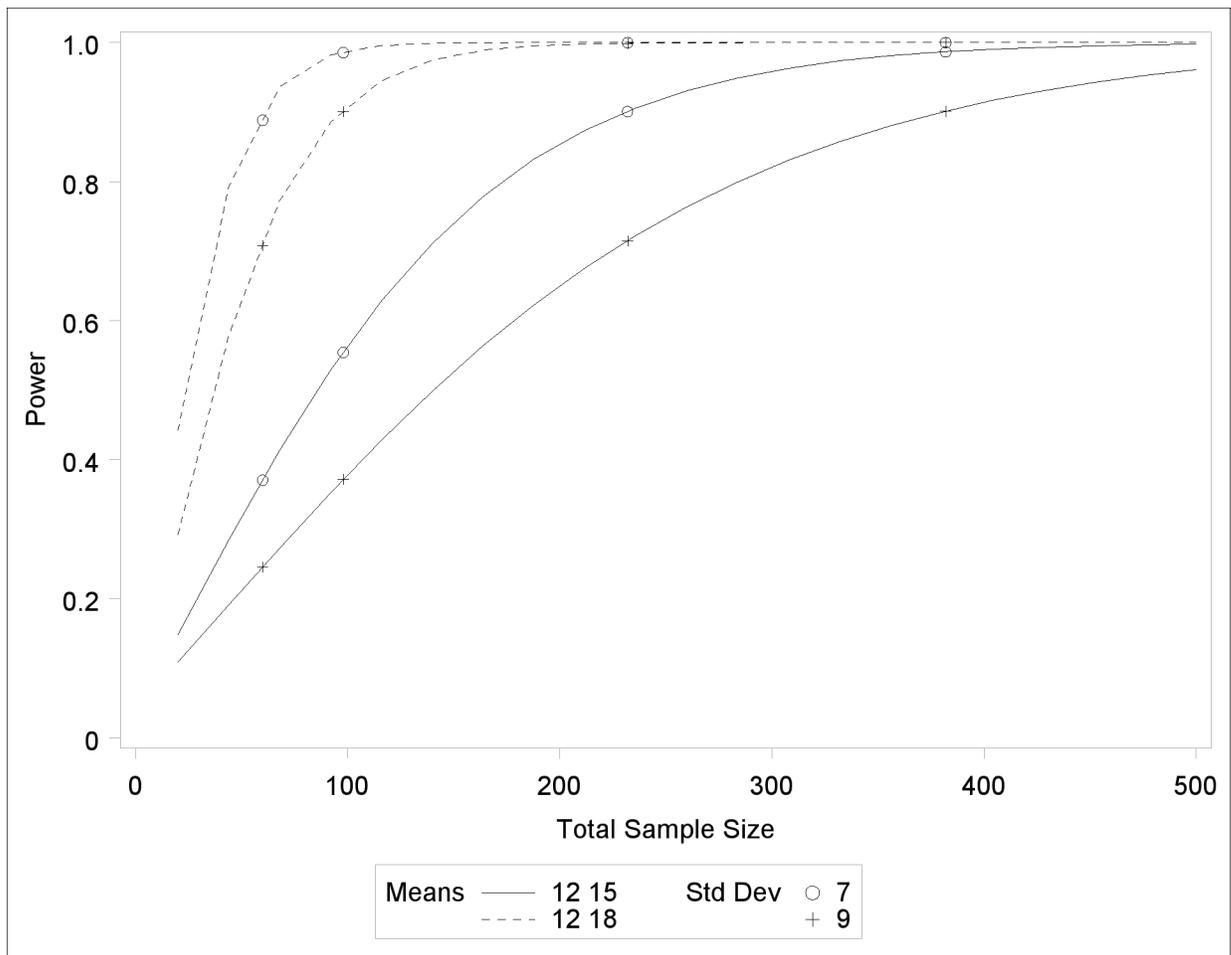
```

proc power plotonly;
  twosamplemeans test=diff
    groupmeans = 12 | 15 18
    stddev      = 7 9
    power       = .
    ntotal      = 232 382 60 98;
  plot x=n min=20 max=500
    markers=analysis;
run;

```

The analysis statement here is the `TWOSAMPLEMEANS` statement. The `MARKERS=ANALYSIS` option in the `PLOT` statement causes the plotting symbols to occur at sample sizes specified by the `NTOTAL=` option in the `TWOSAMPLEMEANS` statement: 232, 382, 60, and 98. The resulting plot is shown in [Output 67.8.21](#).

**Output 67.8.21** Plot with `MARKERS=ANALYSIS`



You can also use the `MARKERS=NICE` option to align symbols with the tick marks on one of the axes (the X axis when the `X=` option is used, or the Y axis when the `Y=` option is used):

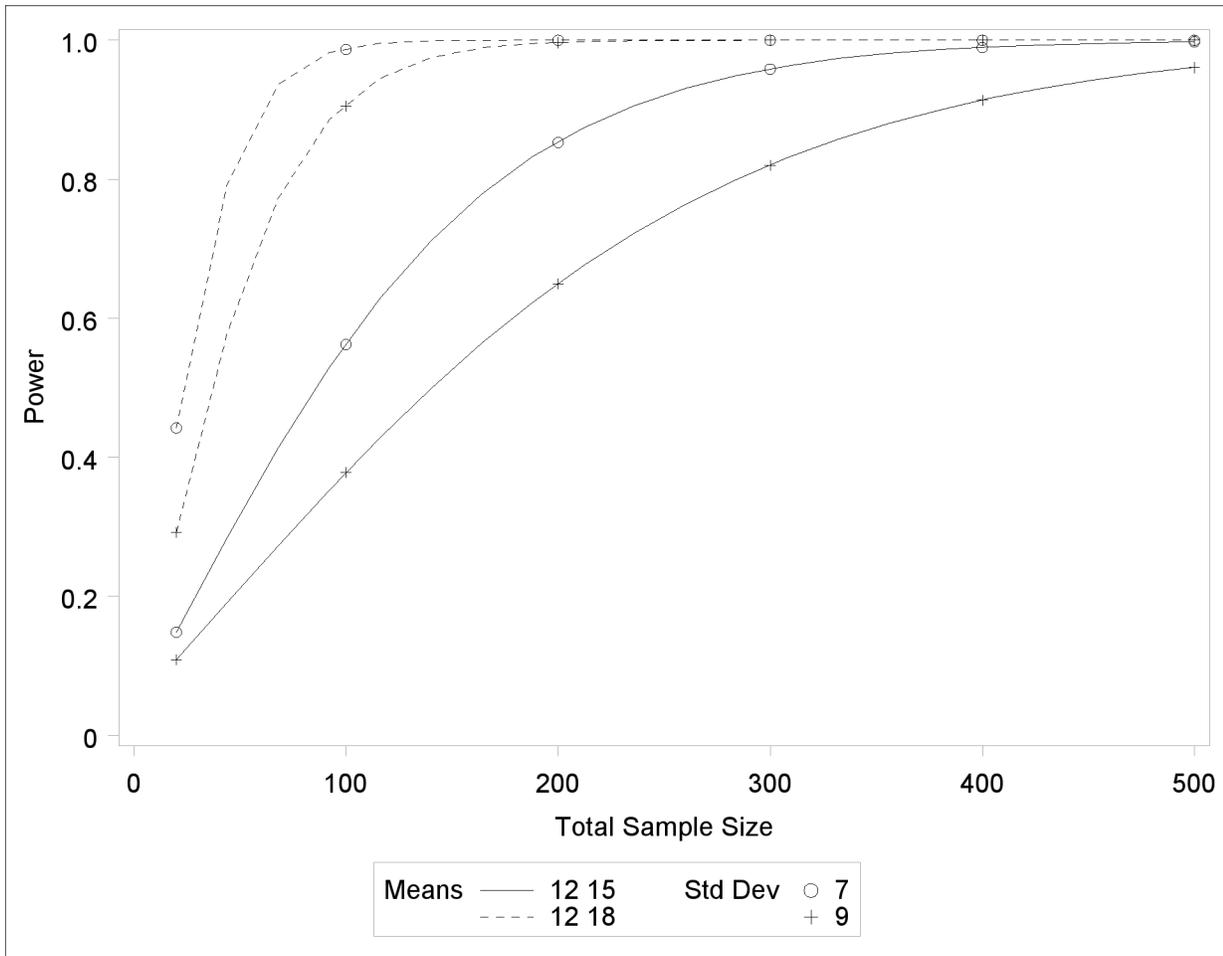
```

plot x=n min=20 max=500
  markers=nice;

```

The plot created by this `PLOT` statement is shown in [Output 67.8.22](#).

**Output 67.8.22** Plot with `MARKERS=NICE`



Note that the plotting symbols are aligned with the tick marks on the X axis because the `X=` option is specified.

## Example 67.9: Binary Logistic Regression with Independent Predictors

Suppose you are planning an industrial experiment similar to the analysis in “[Getting Started: LOGISTIC Procedure](#)” on page 3258 of Chapter 51, “[The LOGISTIC Procedure](#),” but for a different type of ingot. The primary test of interest is the likelihood ratio chi-square test of the effect of heating time on the readiness of the ingots for rolling. Ingot will be randomized independently into one of four different heating times (5, 10, 15, and 20 minutes) with allocation ratios 2:3:3:2 and three different soaking times (2, 4, and 6 minutes) with allocation ratios 2:2:1. The mass of each ingot will be measured as a covariate.

You want to know how many ingots you must sample to have a 90% chance of detecting an odds

ratio as small as 1.2 for a five-minute heating time increase. The odds ratio is defined here as the odds of the ingot not being ready given a heating time of  $h$  minutes divided by the odds given a heating time of  $h - 5$  minutes, for any time  $h$ . You will use a significance level of  $\alpha = 0.1$  to balance Type I and Type II errors since you consider their importance to be roughly equal.

The distributions of heating time and soaking time are determined by the design, but you must conjecture the distribution of ingot mass. Suppose you expect its distribution to be approximately normal with mean 4 kg and standard deviation between 1 kg and 2 kg.

You are powering the study for an odds ratio of 1.2 for the heating time, but you must also conjecture odds ratios for soaking time and mass. You suspect that the odds ratio for a unit increase in soaking time is about 1.4, and the odds ratio for a unit increase in mass is between 1 and 1.3.

Finally, you must provide a guess for the average probability of an ingot not being ready for rolling, averaged across all possible design profiles. Existing data suggest that this probability lies between 0.15 and 0.25.

You decide to evaluate sample size at the two extremes of each parameter for which you conjectured a range. Use the following statements to perform the sample size determination:

```
proc power;
  logistic
    vardist("Heat") = ordinal((5 10 15 20) : (0.2 0.3 0.3 0.2))
    vardist("Soak") = ordinal((2 4 6) : (0.4 0.4 0.2))
    vardist("Mass1") = normal(4, 1)
    vardist("Mass2") = normal(4, 2)
    testpredictor = "Heat"
    covariates = "Soak" | "Mass1" "Mass2"
    responseprob = 0.15 0.25
    testoddsratio = 1.2
    units= ("Heat" = 5)
    covoddsratios = 1.4 | 1 1.3
    alpha = 0.1
    power = 0.9
    ntotal = .;
run;
```

The **VARDIST=** option is used to define the distributions of the predictor variables. The distributions of heating and soaking times are defined by the experimental design, with ordinal probabilities derived from the allocation ratios. The two conjectured standard deviations for the ingot mass are represented in the Mass1 and Mass2 distributions. The **TESTPREDICTOR=** option identifies the predictor being tested, and the **COVARIATES=** option specifies the scenarios for the remaining predictors in the model (soaking time and mass). The **RESPONSEPROB=** option specifies the overall response probability, and the **TESTODDSRATIO=** and **UNITS=** options indicate the odds ratio and increment for heating time. The **COVODDSRATIOS=** option specifies the scenarios for the odds ratios of soaking time and mass. The default **DEFAULTUNIT=1** option specifies a unit change for both of these odds ratios. The **ALPHA=** option sets the significance level, and the **POWER=** option defines the target power. Finally, the **NTOTAL=** option with a missing value (.) identifies the parameter to solve for.

Output 67.9.1 shows the results.

**Output 67.9.1** Sample Sizes for Test of Heating Time in Logistic Regression

The POWER Procedure										
Likelihood Ratio Chi-Square Test for One Predictor										
Fixed Scenario Elements										
Method		Shieh-O'Brien approximation								
Alpha		0.1								
Test Predictor		Heat								
Odds Ratio for Test Predictor		1.2								
Unit for Test Pred Odds Ratio		5								
Nominal Power		0.9								
Computed N Total										
Index	Response Prob	-Covariates-	--Cov ORs-	-Cov Units-	Total N	Actual Power	N	Total		
								Bins	Total	
1	0.15	Soak	Mass1	1.4	1.0	1	1	120	0.900	1878
2	0.15	Soak	Mass1	1.4	1.3	1	1	120	0.900	1872
3	0.15	Soak	Mass2	1.4	1.0	1	1	120	0.900	1878
4	0.15	Soak	Mass2	1.4	1.3	1	1	120	0.900	1857
5	0.25	Soak	Mass1	1.4	1.0	1	1	120	0.900	1342
6	0.25	Soak	Mass1	1.4	1.3	1	1	120	0.900	1348
7	0.25	Soak	Mass2	1.4	1.0	1	1	120	0.900	1342
8	0.25	Soak	Mass2	1.4	1.3	1	1	120	0.900	1369

The required sample size ranges from 1342 to 1878, depending on the unknown true values of the overall response probability, mass standard deviation, and soaking time odds ratio. The overall response probability clearly has the largest influence among these parameters, with a sample size increase of almost 40% going from 0.25 to 0.15.

**Example 67.10: Wilcoxon-Mann-Whitney Test**

Consider a hypothetical clinical trial to treat interstitial cystitis (IC), a painful, chronic inflammatory condition of the bladder with no known cause that most commonly affects women. Two treatments will be compared: lidocaine alone (“lidocaine”) versus lidocaine plus a fictitious experimental drug called Mironel (“Mir+lido”). The design is balanced, randomized, double-blind, and female-only. The primary outcome is a measure of overall improvement at week 4 of the study, measured on a seven-point Likert scale as shown in [Table 67.33](#).

**Table 67.33** Self-Report Improvement Scale

“Compared to when I started this study, my condition is:”	
much worse	−3
worse	−2
slightly worse	−1
the same	0
slightly better	+1
better	+2
much better	+3

The planned data analysis is a one-sided Wilcoxon-Mann-Whitney test with  $\alpha = 0.05$  where the alternative hypothesis represents greater improvement for “Mir+lido.”

You are asked to graphically assess the power of the planned trial for sample sizes between 100 and 250, assuming that the conditional outcome probabilities given treatment are equal to the values in Table 67.34.

**Table 67.34** Conjectured Conditional Probabilities

Treatment	Response						
	−3	−2	−1	0	+1	+2	+3
lidocaine	0.01	0.04	0.20	0.50	0.20	0.04	0.01
Mir+lido	0.01	0.03	0.15	0.35	0.30	0.10	0.06

Use the following statements to compute the power at sample sizes of 100 and 250 and generate a power curve:

```
proc power;
  twosamplewilcoxon
    vardist("lidocaine") = ordinal ((−3 −2 −1 0 1 2 3) :
                                   (.01 .04 .20 .50 .20 .04 .01))
    vardist("Mir+lido") = ordinal ((−3 −2 −1 0 1 2 3) :
                                   (.01 .03 .15 .35 .30 .10 .06))
    variables = "lidocaine" | "Mir+lido"
    sides = u
    ntotal = 100 250
    power = .;
    plot step=10;
run;
```

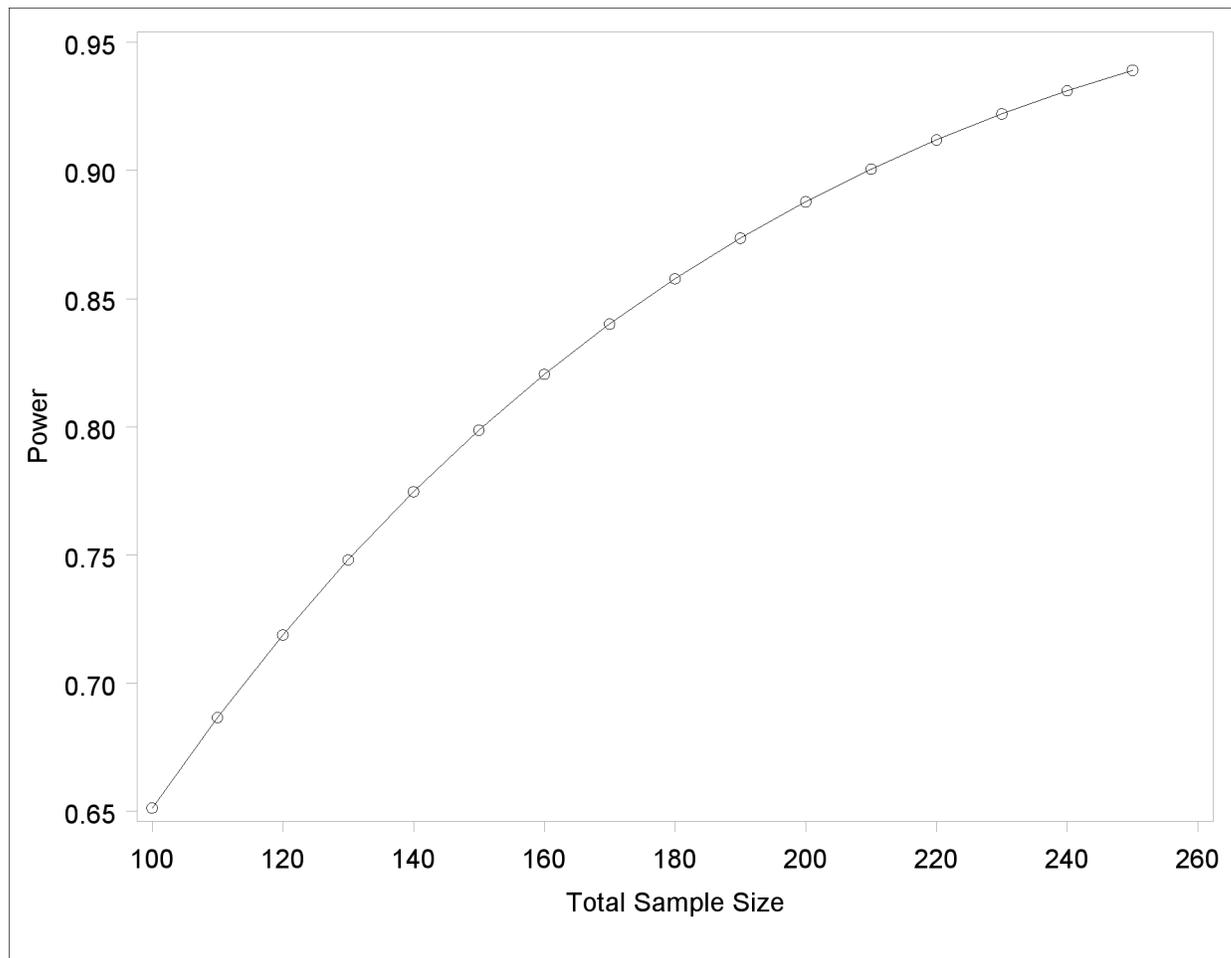
The **VARDIST=** option is used to define the distribution for each treatment, and the **VARIABLES=** option specifies the distributions to compare. The **SIDES=U** option corresponds to the alternative hypothesis that the second distribution (“Mir+lido”) is more favorable. The **NTOTAL=** option specifies the total sample sizes of interest, and the **POWER=** option with a missing value (.) identifies the parameter to solve for. The default **GROUPWEIGHTS=** and **ALPHA=** options specify a balanced design and significance level  $\alpha = 0.05$ .

The `STEP=10` option in the `PLOT` statement requests a point for each sample size increment of 10. The default values for the `X=`, `MIN=`, and `MAX=` plot options specify a sample size range of 100 to 250 (the same as in the analysis) for the X axis.

The tabular and graphical results are shown in [Output 67.10.1](#) and [Output 67.10.2](#), respectively.

**Output 67.10.1** Power Values for Wilcoxon-Mann-Whitney Test

The POWER Procedure		
Wilcoxon-Mann-Whitney Test		
Fixed Scenario Elements		
Method	O'Brien-Castelloe approximation	
Number of Sides	U	
Group 1 Variable	lidocaine	
Group 2 Variable	Mir+lido	
Pooled Number of Bins	7	
Alpha	0.05	
Group 1 Weight	1	
Group 2 Weight	1	
NBins Per Group	1000	
Computed Power		
Index	N	
	Total	Power
1	100	0.651
2	250	0.939

**Output 67.10.2** Plot of Power versus Sample Size for Wilcoxon Power Analysis

The achieved power ranges from 0.651 to 0.939, increasing with sample size.

---

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