

Chapter 60

The POWER Procedure

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Chapter 60

The POWER Procedure

Overview

Power and sample size analysis enables you to optimize 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 for means
- equivalence tests for means
- confidence intervals for means
- tests of binomial proportions
- multiple regression
- tests of correlation and partial correlation
- one-way analysis of variance
- rank tests for comparing two survival curves

For more complex linear models, see [Chapter 36, “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.

The following sections of this chapter describe how to use PROC POWER and discuss the underlying statistical methodology. The “Getting Started” section on page 3714 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 “Syntax” section on page 3721 describes the syntax of the procedure. The “Details” section on page 3788 summarizes the methods employed by PROC POWER and provides details on several special topics. The “Examples” section on page 3836 illustrates the use of the POWER procedure with several applications.

For more discussion and examples on the main concepts in power and sample size analysis, refer to Castelloe (2000), Castelloe and O’Brien (2001), Muller and Benignus (1992), O’Brien and Muller (1993), and Lenth (2001).

Getting Started

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 machine has an inherently high variability, but its horizontal alignment can be adjusted. The operator agrees to pay for a costly adjustment if you can establish a non-zero 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) using a one-sample t test with a 2-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

using the MEAN= and STDDEV= options and the sample size 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=, NULL=, and SIDES= options specify a 2-sided t test for a mean of 0, assuming a normal distribution with a significance level of $\alpha = 0.05$.

Figure 60.1 shows the output.

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

Figure 60.1. Sample Size Analysis for One-Sample t Test

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 may 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 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 60.2 shows the output, and Figure 60.3 shows the plot.

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 60.2. Sample Size Analysis for One-Sample t Test with Input Ranges

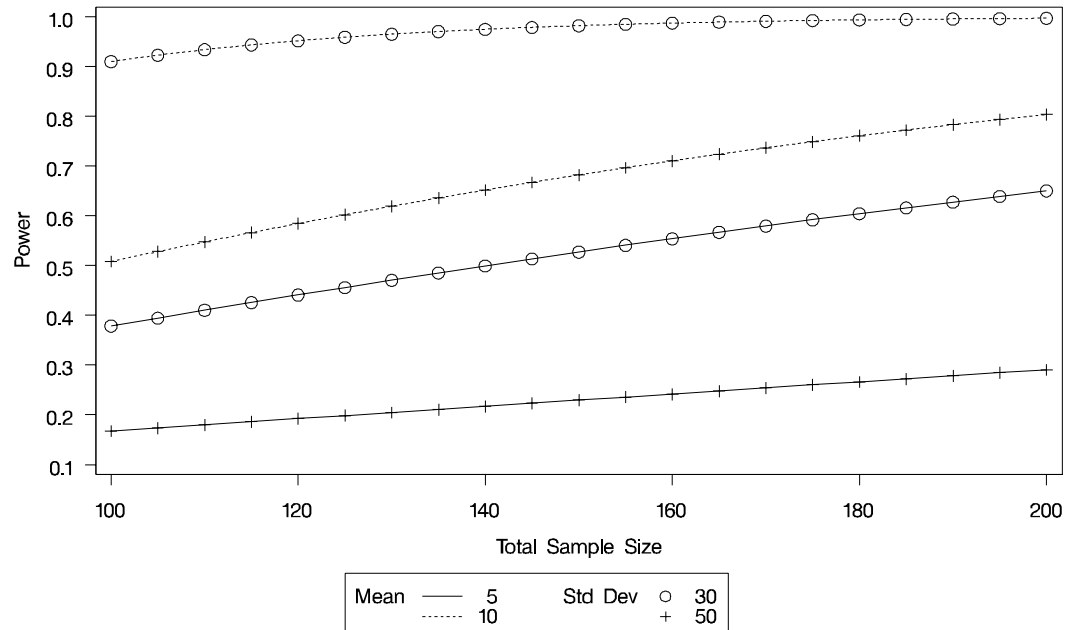


Figure 60.3. Plot of Power versus Sample Size for One-Sample t Test with Input Ranges

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 60.3, 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 using the GROUPMEANS= option. Using the “matched” notation (discussed in the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791), 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 using the GROUPWEIGHTS= option. You could again use the matched notation. But for illustrative purposes, specify the scenarios for each group weight separately 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 2-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 60.4](#).

The POWER Procedure							
Two-sample <i>t</i> 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	

Figure 60.4. Sample Size Analysis for Two-Sample *t* Test Using Group Means

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 wish.

- 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 only specify 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 60.5 shows the new results.

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					
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

Figure 60.5. Sample Size Analysis for Two-Sample t Test Using Mean Differences

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 60.5](#) are lower than those in [Figure 60.4](#) 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

The following statements are available in PROC POWER.

```

PROC POWER < options > ;

MULTREG < options > ;
ONECORR < options > ;
ONESAMPLEFREQ < options > ;
ONESAMPLEMEANS < options > ;

```

```

ONEWAYANOVA < options > ;
PAIREDFREQ < options > ;
PAIREDMEANS < options > ;
TWOSAMPLEFREQ < options > ;
TWOSAMPLEMEANS < options > ;
TWOSAMPLESURVIVAL < options > ;

PLOT < plot-options > < / graph-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 MULTREG, ONECORR, ONESAMPLEFREQ, ONESAMPLEMEANS, ONEWAYANOVA, PAIREDFREQ, PAIREDMEANS, TWOSAMPLEFREQ, TWOSAMPLEMEANS, and TWOSAMPLESURVIVAL.

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 60.1](#) summarizes the basic functions of each statement in PROC POWER. The syntax of each statement in [Table 60.1](#) is described in the following pages.

Table 60.1. Statements in the POWER Procedure

Statement	Description
PROC POWER	invokes the procedure
MULTREG	tests of one or more coefficients in multiple linear regression
ONECORR	Fisher's z test and t test of (partial) correlation
ONESAMPLEFREQ	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
PAIREDFREQ	McNemar's test for paired proportions
PAIREDMEANS	paired t test, confidence interval precision, or equivalence test
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

Table 60.1. (continued)

Statement	Description
TWOSAMPLESURVIVAL	log-rank, Gehan, and Tarone-Ware tests for comparing two survival curves
PLOT	displays plots for previous sample size analysis

See the “[Summary of Analyses](#)” section on page 3789 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.

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 60.2 summarizes categories of options available in the MULTREG statement.

Table 60.2. 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 60.3 summarizes the valid result parameters in the MULTREG statement.

Table 60.3. 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 may use the aliases CONDITIONAL for FIXED and UNCONDITIONAL for RANDOM. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *keyword-list*.

FIXED fixed predictors

RANDOM random (multivariate normal) predictors

NFRACTIONAL

NFRAC

enables fractional input and output for sample sizes. See the “[Sample Size Adjustment Options](#)” section on page 3794 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 wish 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 60.26](#) on page 3801 for further information on minimum NTOTAL values, and see the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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) produces output sorted respectively by

- 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 that 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 that 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 (using the PARTIALCORR= option)
- R^2 for the full and reduced models (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. 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 60.4 summarizes categories of options available in the ONECORR statement.

Table 60.4. Summary of Options in the ONECORR Statement

Task	Options
Define analysis	DIST= TEST=
Specify analysis information	ALPHA= MODEL= NPARTIALVARS= NULL= SIDES=
Specify effects	CORR=
Specify sample size	NTOTAL=
Specify power	POWER=
Control sample size rounding	NFRACTIONAL
Control ordering in output	OUTPUTORDER=

Table 60.5 summarizes the valid result parameters in the ONECORR statement.

Table 60.5. 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 may use the aliases CONDITIONAL for FIXED and UNCONDITIONAL for RANDOM. This option can only be used for DIST=T. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *keyword-list*.

FIXED fixed variables

RANDOM random (bivariate normal) variables

NFRACTIONAL**NFRAC**

enables fractional input and output for sample sizes. See the “[Sample Size Adjustment Options](#)” section on page 3794 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 only be used with the DIST=FISHERZ analysis. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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) produces output sorted respectively by

- MODEL
- SIDES

- NULL
- ALPHA
- NPARTIALVARS
- CORR
- NTOTAL
- POWER

The OUTPUTORDER=SYNTAX option arranges the parameters in the output in the same order that 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 that 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 [“Specifying Value Lists in Analysis Statements”](#) section on page 3791 for information on specifying the *number-list*.

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

Default values of TEST=PEARSON, ALPHA=.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

Default values of TEST=PEARSON, MODEL=RANDOM, ALPHA=.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 of a single binomial proportion.

Summary of Options

Table 60.6 summarizes categories of options available in the ONESAMPLEFREQ statement.

Table 60.6. Summary of Options in the ONESAMPLEFREQ Statement

Task	Options
Define analysis	TEST=
Specify analysis information	ALPHA= NULLPROPORTION= SIDES=
Specify effect	PROPORTION=
Specify sample size	NTOTAL=
Specify power	POWER=
Control sample size rounding	NFRACTIONAL
Choose computational method	METHOD=
Control ordering in output	OUTPUTORDER=

Table 60.7 summarizes the valid result parameters for different analyses in the ONESAMPLEFREQ statement.

Table 60.7. Summary of Result Parameters in the ONESAMPLEFREQ Statement

Analyses	Solve for	Syntax
TEST=ADJZ METHOD=EXACT	Power	POWER = .
TEST=ADJZ 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. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

METHOD=EXACT

METHOD=NORMAL

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

NFRACTIONAL

NFRAC

enables fractional input and output for sample sizes. See the “[Sample Size Adjustment Options](#)” section on page 3794 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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) produces output sorted respectively by

- SIDES
- NULLPROPORTION
- ALPHA
- PROPORTION
- NTOTAL
- POWER

The OUTPUTORDER=SYNTAX option arranges the parameters in the output in the same order that 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 that 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

SIDES= *keyword-list*

specifies the number of sides (or tails) and direction of the statistical test. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *keyword-list*. Valid keywords are

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

The default value is 2.

TEST= ADJZ**TEST= EXACT****TEST= Z**

specifies the statistical analysis. TEST=ADJZ specifies a normal-approximate z test with continuity adjustment. 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.

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

Defaults for the SIDES= and ALPHA= options specify a 2-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

Defaults for the SIDES= and ALPHA= options specify a 2-sided test with a 0.05 significance level.

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

z Test with Continuity Adjustment

Defaults for the SIDES= and ALPHA= options specify a 2-sided test with a 0.05 significance level.

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

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 60.8 summarizes categories of options available in the ONESAMPLEMEANS statement.

Table 60.8. Summary of Options in the ONESAMPLEMEANS Statement

Task	Options
Define analysis	CI= DIST= TEST=
Specify analysis information	ALPHA= LOWER= NULL= SIDES= UPPER=

Table 60.8. (continued)

Task	Options
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 60.9 summarizes the valid result parameters for different analyses in the ONESAMPLEMEANS statement.

Table 60.9. Summary of Result Parameters in the ONESAMPLEMEANS Statement

Analyses	Solve for	Syntax
TEST=T DIST=NORMAL	Power	POWER = .
	Sample size	NTOTAL = .
	Alpha	ALPHA = .
	Mean	MEAN = .
	Standard Deviation	STDDEV = .
TEST=T DIST=LOGNORMAL	Power	POWER = .
	Sample size	NTOTAL = .
TEST=EQUIV	Power	POWER = .
	Sample size	NTOTAL = .
CI=T	Prob(width)	PROBWIDTH = .
	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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 [“Specifying Value Lists in Analysis Statements”](#) section on page 3791 for information on 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 only be used with the CI=T analysis. See the [“Specifying Value Lists in Analysis Statements”](#) section on page 3791 for information on specifying the *number-list*.

LOWER=number-list

specifies the lower equivalence bound for the mean. This option can only be used with the TEST=EQUIV analysis. See the [“Specifying Value Lists in Analysis Statements”](#) section on page 3791 for information on specifying the *number-list*.

MEAN=number-list

specifies the mean, in the original scale. The mean is arithmetic if DIST=NORMAL and geometric if DIST=LOGNORMAL. This option can only be used with the TEST=T and TEST=EQUIV analyses. See the [“Specifying Value Lists in Analysis Statements”](#) section on page 3791 for information on specifying the *number-list*.

NFRACTIONAL**NFRAC**

enables fractional input and output for sample sizes. See the [“Sample Size Adjustment Options”](#) section on page 3794 for information on 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 [“Specifying Value Lists in Analysis Statements”](#) section on page 3791 for information on 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 only be used with the TEST=T analysis. See the [“Specifying Value Lists in Analysis Statements”](#) section on page 3791 for information on 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) produces output sorted respectively by

- SIDES
- NULLMEAN
- LOWER
- UPPER
- ALPHA
- MEAN
- HALFWIDTH
- STDDEV
- CV
- NTOTAL
- POWER
- PROBTYP
- PROBWIDTH

The OUTPUTORDER=SYNTAX option arranges the parameters in the output in the same order that 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 that 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 only be used with the TEST=T and TEST=EQUIV analyses. See the [“Specifying Value Lists in Analysis Statements”](#) section on page 3791 for information on specifying the *number-list*.

PROBTYP= *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 may use the alias GIVENVALIDITY for CONDITIONAL. The PROBTYP= option can only be used with the CI=T analysis. See the [“Specifying Value Lists in Analysis Statements”](#) section on page 3791 for information on 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 PROBTYP= option. Values are expressed as probabilities (for example, 0.9) rather than percentages. This option can only be used with the CI=T analysis. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

SIDES=*keyword-list*

specifies the number of sides (or tails) and direction of the statistical test or confidence interval. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *keyword-list*. Valid keywords and their interpretation for the TEST= analyses are

- 1 1-sided with alternative hypothesis in same direction as effect
- 2 2-sided
- U upper 1-sided with alternative greater than null value
- L lower 1-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 negative infinity and the upper confidence limit. For both of these cases and SIDES=1, the confidence interval computations are equivalent. The SIDES= option can only be used with the TEST=T and CI=T analyses. The default value is 2.

STDDEV=*number-list*

STD=*number-list*

specifies the standard deviation. You can use this option only with DIST=NORMAL. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

TEST

TEST=EQUIV

TEST=T

specifies the statistical analysis. TEST=EQUIV specifies an equivalence test of the mean 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 only be used with the TEST=EQUIV analysis. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

Restrictions on Option Combinations

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

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

Default values for the DIST=, SIDES=, NULLMEAN=, and ALPHA= options specify a 2-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

Default values for the SIDES=, NULLMEAN=, and ALPHA= options specify a 2-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

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 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. The defaults of SIDES=2 and ALPHA=0.05 specify a 2-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 60.10 summarizes categories of options available in the ONEWAYANOVA statement.

Table 60.10. Summary of Options in the ONEWAYANOVA Statement

Task	Options
Define analysis	TEST=
Specify analysis information	ALPHA= CONTRAST= SIDES= NULLCONTRAST=
Specify effects	GROUPMEANS=
Specify variability	STDDEV=

Table 60.10. (continued)

Task	Options
Specify sample size and allocation	GROUPNS= GROUPWEIGHTS= NPERGROUP= NTOTAL=
Specify power	POWER=
Control sample size rounding	NFRACTIONAL
Control ordering in output	OUTPUTORDER=

Table 60.11 summarizes the valid result parameters for different analyses in the ONEWAYANOVA statement.

Table 60.11. Summary of Result Parameters in the ONEWAYANOVA Statement

Analyses	Solve for	Syntax
TEST=CONTRAST	Power Sample size	POWER = . NTOTAL = . NPERGROUP = .
TEST=OVERALL	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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 using

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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 NFRAGMENTAL 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 NFRAGMENTAL option is used. The default value is 1 for each group, amounting to a balanced design. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *grouped-number-list*.

NFRAGMENTAL

NFRAC

enables fractional input and output for sample sizes. See the “[Sample Size Adjustment Options](#)” section on page 3794 for information on the ramifications of the presence (and absence) of the NFRAGMENTAL 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 only be used with the TEST=CONTRAST analysis. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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) produces output sorted respectively by

- 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 that 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 that 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 [“Specifying Value Lists in Analysis Statements”](#) section on page 3791 for information on specifying the *number-list*.

SIDES= *keyword-list*

specifies the number of sides (or tails) and direction of the statistical test. See the [“Specifying Value Lists in Analysis Statements”](#) section on page 3791 for information on specifying the *keyword-list*. Valid keywords are

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

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

STDDEV= *number-list*

STD= *number-list*

specifies the error standard deviation. See the [“Specifying Value Lists in Analysis Statements”](#) section on page 3791 for information on 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 2-sided case and the usual t test for the 1-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 (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 ONEWAYANOVA statement.

One-Degree-of-Freedom Contrast

You can use the NPERGROUP= option in a balanced design. Default values for the SIDES=, NULLCONTRAST=, and ALPHA= options specify a 2-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 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 60.12 summarizes categories of options available in the PAIREFREQ statement.

Table 60.12. Summary of Options in the PAIREFREQ Statement

Task	Options
Define analysis	DIST= TEST=
Specify analysis information	ALPHA= NULLDISCPRORATIO= SIDES=
Specify effects	DISCPROPDIFF= DISCPROPORTIONS= DISCPRORATIO= REFPROPORTION= TOTALPROPDISC=
Specify sample size	NPAIRS=
Specify power	POWER=

Table 60.12. (continued)

Task	Options
Control sample size rounding	NFRACTIONAL
Choose computational method	METHOD=
Control ordering in output	OUTPUTORDER=

Table 60.13 summarizes the valid result parameters in the PAIREDFREQ statement.

Table 60.13. 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

DISCPROPORTIONS=*grouped-number-list*

DISCPS=*grouped-number-list*

specifies the two discordant proportions, p_{10} and p_{01} . See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *grouped-number-list*.

DISCPROPDIFF=*number-list*

DISCPDIFF=*number-list*

specifies the difference $p_{01} - p_{10}$ between discordant proportions. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

DISCPRORATIO=*number-list*

DISCPRATIO=*number-list*

specifies the ratio p_{01}/p_{10} of discordant proportions. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Sample Size Adjustment Options](#)” section on page 3794 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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) produces output sorted respectively by

- SIDES
- NULLDISCPRORATIO
- ALPHA
- DISCPRORPORTIONS
- DISCPRORPDIF
- TOTALPRORDISC
- REFPRORPORTION
- DISCPRORPRATIO

- NPAIRS
- POWER

The OUTPUTORDER=SYNTAX option arranges the parameters in the output in the same order that their corresponding options are specified in the PAIREDFREQ statement. The OUTPUTORDER=REVERSE option arranges the parameters in the output in the reverse of the order that their corresponding options are specified in the PAIREDFREQ 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

REFPROPORTION=*number-list*

REFP=*number-list*

specifies the reference discordant proportion p_{10} . See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

SIDES=*keyword-list*

specifies the number of sides (or tails) and direction of the statistical test or confidence interval. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *keyword-list*. Valid keywords and their interpretation are

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

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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 DISCPROPORTIONDIFF= and TOTALPROPDISC= options)
- ratio of discordant proportions and reference discordant proportion (using the DISCPROPRATIO= and REFPROPORTION= 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. Default values for the TEST=, SIDES=, ALPHA=, and NULLDISCPROPRATIO= options specify a 2-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
    discpropdiff = 0.3
    totalpropdisc = 0.6
    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;
```

McNemar Normal Approximation 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 2-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 60.14 summarizes categories of options available in the PAIREDMEANS statement.

Table 60.14. Summary of Options in the PAIREDMEANS Statement

Task	Options
Define analysis	CI= DIST= TEST=
Specify analysis information	ALPHA= LOWER= NULLDIFF= NULLRATIO= SIDES= UPPER=
Specify effects	HALFWIDTH= MEANDIFF= MEANRATIO= PAIREDMEANS=
Specify variability	CORR= CV= PAIREDCVS= PAIREDSTDDEVS= STDDEV=
Specify sample size	NPAIRS=

Table 60.14. (continued)

Task	Options
Specify power and related probabilities	POWER= PROBTYPE= PROBWIDTH=
Control sample size rounding	NFRACTIONAL
Control ordering in output	OUTPUTORDER=

Table 60.15 summarizes the valid result parameters for different analyses in the PAIREDMEANS statement.

Table 60.15. Summary of Result Parameters in the PAIREDMEANS Statement

Analyses	Solve for	Syntax
TEST=DIFF	Power	POWER = .
	Sample size	NPAIRS = .
TEST=RATIO	Power	POWER = .
	Sample size	NPAIRS = .
TEST=EQUIV_DIFF	Power	POWER = .
	Sample size	NPAIRS = .
TEST=EQUIV_RATIO	Power	POWER = .
	Sample size	NPAIRS = .
CI=DIFF	Prob(width)	PROBWIDTH = .
	Sample size	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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 log-normal 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 only be used with the `CI=DIFF` analysis. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 only be used with the `TEST=EQUIV_DIFF` and `TEST=EQUIV_RATIO` analyses. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 only be used 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

MEANRATIO=number-list

specifies the geometric mean ratio, defined as γ_2/γ_1 . This option can only be used 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

NFRACTIONAL**NFRAC**

enables fractional input and output for sample sizes. See the “[Sample Size Adjustment Options](#)” section on page 3794 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

NULLDIFF=*number-list*

NULLD=*number-list*

specifies the null mean difference. The default value is 0. This option can only be used with the TEST=DIFF analysis. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

NULLRATIO=*number-list*

NULLR=*number-list*

specifies the null mean ratio. The default value is 1. This option can only be used with the TEST=RATIO analysis. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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) produces output sorted respectively by

- SIDES
- NULLDIFF
- NULLRATIO
- LOWER
- UPPER
- ALPHA
- PAIREFREQ
- 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 that 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 that 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. This option can only be used with DIST=LOGNORMAL. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 only be used with DIST=NORMAL. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 may use the alias GIVENVALIDITY for CONDITIONAL. The PROBTYPE= option can only be used with the CI=DIFF analysis. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 PROBTYP= option. Values are expressed as probabilities (for example, 0.9) rather than percentages. This option can only be used with the CI=DIFF analysis. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

SIDES=*keyword-list*

specifies the number of sides (or tails) and direction of the statistical test or confidence interval. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *keyword-list*. Valid keywords and their interpretation for the TEST= analyses are

- 1 1-sided with alternative hypothesis in same direction as effect
- 2 2-sided
- U upper 1-sided with alternative greater than null value
- L lower 1-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 negative 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 only be used with DIST=NORMAL. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 using a two one-sided tests (TOST) analysis (Schuirmann 1987). TEST=EQUIV_RATIO specifies a multiplicative equivalence test of the mean ratio 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 only be used with the TEST=EQUIV_DIFF and TEST=EQUIV_RATIO analyses. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

Restrictions on Option Combinations

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

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

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

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

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

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

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

- common standard deviation (using the STDDEV= option)
- individual standard deviations (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. Default values for the DIST=, SIDES=, NULLDIFF=, and ALPHA= options specify a 2-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. Defaults for the DIST=, SIDES=, NULLRATIO= and ALPHA= options specify a 2-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
    pairedcvs = 0.8 | 0.9
    npairs = 30
    power = .;
run;
```

Additive Equivalence Test for Mean Difference with Normal Data

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

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. The defaults of SIDES=2 and ALPHA=0.05 specify a 2-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;

```

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 60.16 summarizes categories of options available in the TWOSAMPLEFREQ statement.

Table 60.16. Summary of Options in the TWOSAMPLEFREQ Statement

Task	Options
Define analysis	TEST=
Specify analysis information	ALPHA= NULLPROPORTIONDIFF= NULLODDSRATIO= NULLRELATIVERISK= SIDES=
Specify effects	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 60.17 summarizes the valid result parameters for different analyses in the TWOSAMPLEFREQ statement.

Table 60.17. Summary of Result Parameters in the TWOSAMPLEFREQ Statement

Analyses	Solve for	Syntax
TEST=FISHER	Power	POWER = .
	Sample size	NTOTAL = .
		NPERGROUP = .
TEST=LRCHI	Power	POWER = .
	Sample size	NTOTAL = .
		NPERGROUP = .
TEST=PCHI	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, corre-

sponding to the usual $0.05 \times 100\% = 5\%$ level of significance. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *grouped-number-list*.

NFRACTIONAL

NFRAC

enables fractional input and output for sample sizes. See the “[Sample Size Adjustment Options](#)” section on page 3794 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

NULLODDSRATIO=*number-list*

NULLOR=*number-list*

specifies the null odds ratio. The default value is 1. This option can only be used along with the ODDSRATIO= option in the TEST=PCHI analysis. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

NULLPROPORTIONDIFF=*number-list*

NULLPDIFF=*number-list*

specifies the null proportion difference. The default value is 0. This option can only be used along with the GROUPPROPORTIONS= or PROPORTIONDIFF= option in the TEST=PCHI analysis. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

NULLRELATIVERISK=*number-list*

NULLRR=*number-list*

specifies the null relative risk. The default value is 1. This option can only be used along with the RELATIVERISK= option in the TEST=PCHI analysis. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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) produces output sorted respectively by

- SIDES
- NULLDIFF
- 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 that 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 that 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

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

specifies the proportion difference $p_2 - p_1$. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

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

specifies the reference proportion p_1 . See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

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

specifies the relative risk p_2/p_1 . See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

SIDES= *keyword-list*

specifies the number of sides (or tails) and direction of the statistical test or confidence interval. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *keyword-list*. Valid keywords and their interpretation are

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

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 (using the GROUPPROPORTIONS= option)
- difference between proportions and reference proportion (using the PROPORTIONDIFF and REFPROPORTION= options)
- odds ratio and reference proportion (using the ODDSRATIO= and REFPROPORTION= options)
- relative risk and reference proportion (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 (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 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. Default values for the SIDES= and ALPHA= options specify a 2-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 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

Default values for the SIDES= and ALPHA= options specify a 2-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

Default values for the SIDES= and ALPHA= options specify a 2-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 60.18 summarizes categories of options available in the TWOSAMPLEMEANS statement.

Table 60.18. 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 60.19 summarizes the valid result parameters for different analyses in the TWOSAMPLEMEANS statement.

Table 60.19. Summary of Result Parameters in the TWOSAMPLEMEANS Statement

Analyses	Solve for	Syntax
TEST=DIFF	Power	POWER = .
	Sample size	NTOTAL = . NPERGROUP = .
	Group sample size	GROUPNS = <i>n1</i> .
		GROUPNS = . <i>n2</i>
		GROUPNS = (<i>n1</i> .) GROUPNS = (. <i>n2</i>)
	Group weight	GROUPWEIGHTS = <i>w1</i> .
		GROUPWEIGHTS = . <i>w2</i>
		GROUPWEIGHTS = (<i>w1</i> .)
		GROUPWEIGHTS = (. <i>w2</i>)
	Alpha	ALPHA = .
Group mean	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. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 log-normal 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 NFRAC 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 NFRAC option is used. The default value is (1 1), a balanced design with a weight of 1 for each group. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 only be used with the CI=DIFF analysis. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 only be used with the TEST=EQUIV_DIFF and TEST=EQUIV_RATIO analyses. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 only be used 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

MEANRATIO= *number-list*

specifies the geometric mean ratio, defined as γ_2/γ_1 . This option can only be used 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

NFRAC**NFRAC**

enables fractional input and output for sample sizes. See the “[Sample Size Adjustment Options](#)” section on page 3794 for information on the ramifications of the presence (and absence) of the NFRAC 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

NULLDIFF= *number-list*

NULLD= *number-list*

specifies the null mean difference. The default value is 0. This option can only be used with the TEST=DIFF and TEST=DIFF_SATT analyses. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

NULLRATIO= *number-list*

NULLR= *number-list*

specifies the null mean ratio. The default value is 1. This option can only be used with the TEST=RATIO analysis. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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) produces output sorted respectively by

- SIDES
- NULLDIFF
- NULLRATIO
- LOWER
- UPPER
- ALPHA
- GROUPMEANS
- MEANDIFF
- MEANRATIO
- HALFWIDTH
- STDDEV
- GROUPSTDDEVS
- CV
- GROUPWEIGHTS
- NTOTAL
- NPERGROUP

- GROUPNS
- POWER
- PROBTYP
- PROBWIDTH

The OUTPUTORDER=SYNTAX option arranges the parameters in the output in the same order that 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 that 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

PROBTYP=*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 may use the alias GIVENVALIDITY for CONDITIONAL. The PROBTYP= option can only be used with the CI=DIFF analysis. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 PROBTYP= option. Values are expressed as probabilities (for example, 0.9) rather than percentages. This option can only be used with the CI=DIFF analysis. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

SIDES=*keyword-list*

specifies the number of sides (or tails) and direction of the statistical test or confidence interval. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *keyword-list*. Valid keywords and their interpretation for the TEST= analyses are

1 1-sided with alternative hypothesis in same direction as effect

- 2 2-sided
- U upper 1-sided with alternative greater than null value
- L lower 1-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 negative 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

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 only be used with DIST=NORMAL. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 unpooled *t* test on the mean difference, assuming unequal variances. TEST=EQUIV_DIFF specifies an additive equivalence test of the mean difference using a two one-sided tests (TOST) analysis (Schirman 1987). TEST=EQUIV_RATIO specifies a multiplicative equivalence test of the mean ratio 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 only be used with the TEST=EQUIV_DIFF and TEST=EQUIV_RATIO analyses. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

Restrictions on Option Combinations

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

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

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

- individual group means (using the GROUPMEANS= option)
- mean difference (using the MEANDIFF= option)
- mean ratio (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 (using the STDDEV= option)
- individual group standard deviations (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 (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 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. Default values for the DIST=, SIDES=, NULLDIFF=, and ALPHA= options specify a 2-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 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

Default values for the DIST=, SIDES=, NULLDIFF=, and ALPHA= options specify a 2-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

Default values for the DIST=, SIDES=, NULLRATIO=, and ALPHA= options specify a 2-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

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

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. The defaults of SIDES=2 and ALPHA=0.05 specify a 2-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 60.20 summarizes categories of options available in the TWOSAMPLESURVIVAL statement.

Table 60.20. 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 60.21 summarizes the valid result parameters for different analyses in the TWOSAMPLESURVIVAL statement.

Table 60.21. 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***ACCTIME=***number-list***ACCRUALT=***number-list***ACCT=***number-list*

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= options are 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

CURVE("label")=points

defines a survival curve.

For the CURVE= option,

<i>label</i>	identifies the curve in the output and with the GROUPLOSS=, GROUPSURVIVAL=, and REFSURVIVAL= options.
<i>points</i>	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 language.

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*

FUTIME=*number-list*

FOLLOWUPT=*number-list*

FUT=*number-list*

specifies the follow-up time, the amount of time in the study past the accrual time. If the **GROUPSURVIVAL=** or **REFSURVIVAL=** options are 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

GROUPLOSS= *grouped-name-list*

GLOSS= *grouped-name-list*

specifies the exponential loss survival curve for each group, using labels specified with the **CURVE=** option. Loss is assumed to follow an exponential curve, indicating the expected rate of loss to follow-up over time. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 loss to follow-up over time. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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, using labels specified with the `CURVE=` option. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *grouped-name-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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

NFRACTIONAL

NFRAC

enables fractional input and output for sample sizes. See the “[Sample Size Adjustment Options](#)” section on page 3794 for information on the ramifications of

the presence (and absence) of the NFRACTIONAL option.

NPARGROUP= *number-list*

NPARG= *number-list*

specifies the common sample size per group or requests a solution for the common sample size per group with a missing value (NPARGROUP=.). Use of this option implicitly specifies a balanced design. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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) produces output sorted respectively by

- 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 that 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 that 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

REFSURVIVAL= *name-list*

REFSURV= *name-list*

specifies the survival curve for the first (reference) group, using labels specified with the CURVE= option. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *name-list*.

SIDES=*keyword-list*

specifies the number of sides (or tails) and direction of the statistical test or confidence interval. See the “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *keyword-list*. Valid keywords and their interpretation are

- | | |
|---|---|
| 1 | 1-sided with alternative hypothesis in same direction as effect |
| 2 | 2-sided |
| U | upper 1-sided with the alternative hypothesis favoring better survival in the second group |
| L | lower 1-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*

TOTALT=*number-list*

specifies the total time, which is equal to the sum of accrual and follow-up times. If the GROUPSURVIVAL= or REFSURVIVAL= options are 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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

Restrictions on Option Combinations

To specify the survival curves, choose one of the following parameterizations:

- arbitrary piecewise linear or exponential curves (using the CURVE= and GROUPSURVIVAL= options)
- curves with proportional hazards (using the CURVE=, REFSURVIVAL=, and HAZARDRATIO= options)
- exponential curves, using one of the following parameterizations:
 - median survival times (using the GROUPMEDSURVTIMES= option)
 - the hazard ratio and the hazard of the reference curve (using the HAZARDRATIO= and REFSURVEXPHAZARD= options)
 - the individual hazards (using the GROUPSURVEXPHAZARDS= option)

To specify the study time, use any two of the following three options:

- accrual time (using the ACCRUALTIME= option)
- follow-up time (using the FOLLOWUPTIME= option)
- total time, the sum of accrual and follow-up times (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 (using the NPERGROUP= option)
- total sample size and allocation weights (using the NTOTAL= and GROUPWEIGHTS= options)
- individual group sample sizes (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 (using the CURVE= and GROUPLOSS= options)

- median loss times (using the GROUPMEDLOSSTIMES= option)
- the individual loss hazards (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 using the CURVE= and GROUPSURVIVAL= options. Default values for the SIDES=, ALPHA=, NSUBINTERVAL=, and GROUPLOSSEXPHAZARDS= options specify a 2-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 using the NTOTAL= and GROUPWEIGHTS= options and specify piecewise linear or exponential survival curves with proportional hazards 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.

```

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

Default values for the SIDES=, ALPHA=, NSUBINTERVAL=, and GROUPLOSSEXPHAZARDS= options specify a 2-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

Default values for the `SIDES=`, `ALPHA=`, `NSUBINTERVAL=`, and `GROUPLOSSEXPHAZARDS=` options specify a 2-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;
```

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

INTERPOL=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`

NUMBERS=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

POS=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 the **KEY=BYFEATURE** option.

POS=BOTTOM

POS=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

MARKERS=COMPUTED

MARKERS=NICE

MARKERS=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

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 the maximum value occurring for this parameter in the analysis statement preceding the **PLOT** statement.

MIN=number

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 the minimum value occurring for this parameter in the analysis statement preceding 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, LINESTYLE, 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 multi-valued parameters from the analysis will be automatically selected for you.

X=EFFECT**X=N****X=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 only use the X=N option 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 60.22 summarizes the parameters representing effect size in different analyses.

Table 60.22. Effect Size Parameters For Different Analyses

Analysis Statement and Options	Effect Size Parameters
MULTREG	Partial correlation or R^2 difference
ONECORR	Correlation
ONESAMPLEFREQ	Proportion

Table 60.22. (continued)

Analysis Statement and Options	Effect Size Parameters
ONESAMPLEMEANS TEST=T, ONESAMPLEMEANS TEST=EQUIV	Mean
ONESAMPLEMEANS CI=T	CI half-width
ONEWAYANOVA	none
PAIREDFREQ	Discordant proportion difference or ratio
PAIREDMEANS TEST=DIFF, PAIREDMEANS TEST=EQUIV_DIFF	Mean difference
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

XOPTS= (*x-options*)

specifies plot characteristics pertaining to the x-axis.

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

CROSSREF=NO

CROSSREF=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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on specifying the *number-list*.

Y=EFFECT**Y=N****Y=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

CROSSREF=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 “[Specifying Value Lists in Analysis Statements](#)” section on page 3791 for information on 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.

Details

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 1 error*. The probability of a Type 1 error is usually designated “alpha” or α , and statistical tests are designed to ensure that α 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 2 error* has been made. The probability of a Type 2 error is usually designated “beta” or β . The probability $1 - \beta$ of avoiding a Type 2 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 60.23 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 60.23. Summary of Analyses

Statement	Options	
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
One-sample t test	ONESAMPLEMEANS	TEST=T
One-sample t test with log- normal data	ONESAMPLEMEANS	TEST=T DIST=LOGNORMAL
One-sample equivalence test for mean of normal data	ONESAMPLEMEANS	TEST=EQUIV

Table 60.23. (continued)

Statement	Options	
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
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

Table 60.23. (continued)

Statement	Options
Two-sample confidence interval for mean difference	TWOSAMPLEMEANS CI=DIFF
Log-rank test for comparing two survival curves	TWOSAMPLESURVIVATEST=LOGRANK
Gehan rank test for comparing two survival curves	TWOSAMPLESURVIVATEST=GEHAN
Tarone-Ware rank test for comparing two survival curves	TWOSAMPLESURVIVATEST=TARONEWARE

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 wish 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 2-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 “[Number-lists](#)” section on page 3791), one representing each group, each 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 wish to include only a subset of all combinations of individual group values. For example, you may 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 “[Crossed Grouped-number-lists](#)” section on page 3792) 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 “[Name-lists](#)” section on page 3793), one representing each group, each 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 wish to include only a subset of all combinations of individual group values. For example, you may 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 group-wise) 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 explains 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
    oddsratio= 1.0001
    refproportion=.4
    nulloddsratio=1
    power=.9
    ntotal=.;
run;
```

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

Figure 60.6. Error Column

The output in [Figure 60.6](#) 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 Information column provides further details about Error entries, warnings about any boundary conditions detected, and notes about any adjustments to input. Note that the Information 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
```

```

      stdev=2
      ntotal=2 5
      power=. ;
      ods output output=Power;
proc print noobs data=Power;
      var MeanDiff NominalNTotal NTotal Power Error Info;
run;

```

The output is shown in [Figure 60.7](#).

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

Figure 60.7. Error and Information Columns

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 only displays 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 NFRATIONAL option is used in the analysis statement

If sample size is the result parameter and the NFRATIONAL 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 60.24](#). For more information on ODS, see [Chapter 15](#), “Using the Output Delivery System.”

Table 60.24. 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 path names 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 $\langle n \rangle$ indexing the analysis statement name is only used if there is more than one instance.
- The $\langle n \rangle$ 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).

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 60.25 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 60.25. Common Notation

Symbol	Description	Associated Syntax
α	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=
μ	(arithmetic) mean	MEAN=
μ_i	(arithmetic) mean in i th group	GROUPMEANS=, PAIREDMEANS=
μ_{diff}	(arithmetic) mean difference, $\mu_2 - \mu_1$ or $\mu_T - \mu_R$	MEANDIFF=

Table 60.25. (continued)

Symbol	Description	Associated Syntax
μ_0	null mean or mean difference (arithmetic)	NULL=, NULLDIFF=
γ	geometric mean	MEAN=
γ_i	geometric mean in i th group	GROUPMEANS=, PAIREDMEANS=
γ_0	null mean or mean ratio (geometric)	NULL=, NULLRATIO=
σ	standard deviation (or common standard deviation per group)	STDDEV=
σ_i	standard deviation in i th group	GROUPSTDDEVS=, PAIREDSTDDEVS=
σ_{diff}	standard deviation of differences	
CV	coefficient of variation, defined as the ratio of the standard deviation to the (arithmetic) mean	CV=, PAIREDCVS=
ρ	correlation	CORR=
μ_T, μ_R	treatment and reference (arithmetic) means for equivalence test	GROUPMEANS=, PAIREDMEANS=
γ_T, γ_R	treatment and reference geometric means for equivalence test	GROUPMEANS=, PAIREDMEANS=
θ_L	lower equivalence bound	LOWER=
θ_U	upper equivalence bound	UPPER=
$t(\nu, \delta)$	t distribution with d.f. ν and noncentrality δ	
$F(\nu_1, \nu_2, \lambda)$	F distribution with numerator d.f. ν_1 , denominator d.f. ν_2 , and noncentrality λ	
$t_{p;\nu}$	p th percentile of t distribution with d.f. ν	
$F_{p;\nu_1,\nu_2}$	p th percentile of F distribution with numerator d.f. ν_1 and denominator d.f. ν_2	
$\text{Bin}(N, p)$	binomial distribution with sample size N and proportion p	

A “lower 1-sided” test is associated with SIDES=L (or SIDES=1 with the effect smaller than the null value), and an “upper 1-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 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 Y 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 is comprised 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} :

$$\begin{aligned} H_0 &: \rho_{YX_1|X_{-1}}^2 = 0 \\ H_1 &: \rho_{YX_1|X_{-1}}^2 > 0 \end{aligned}$$

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:

$$\begin{aligned} H_0 &: \rho_{Y|(X_1, X_{-1})}^2 - \rho_{Y|X_{-1}}^2 = 0 \\ H_1 &: \rho_{Y|(X_1, X_{-1})}^2 - \rho_{Y|X_{-1}}^2 > 0 \end{aligned}$$

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:

$$\begin{aligned} \text{power} &= \begin{cases} P \left[\left(\frac{N-1-p}{p_1} \right) \left(\frac{R_{Y|X_1, X_{-1}}^2}{1-R_{Y|X_1, X_{-1}}^2} \right) \geq F_{1-\alpha}(p_1, N-1-p) \right], & \text{intercept} \\ P \left[\left(\frac{N-p}{p_1} \right) \left(\frac{R_{Y|X_1, X_{-1}}^2}{1-R_{Y|X_1, X_{-1}}^2} \right) \geq F_{1-\alpha}(p_1, N-p) \right], & \text{no intercept} \end{cases} \\ &= \begin{cases} P \left[R_{Y|X_1, X_{-1}}^2 \geq \frac{F_{1-\alpha}(p_1, N-1-p)}{F_{1-\alpha}(p_1, N-1-p) + \frac{N-1-p}{p_1}} \right], & \text{intercept} \\ P \left[R_{Y|X_1, X_{-1}}^2 \geq \frac{F_{1-\alpha}(p_1, N-p)}{F_{1-\alpha}(p_1, N-p) + \frac{N-p}{p_1}} \right], & \text{no intercept} \end{cases} \end{aligned}$$

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

$$\lambda = N \frac{\rho_{Y X_1 | X_{-1}}^2}{1 - \rho_{Y X_1 | X_{-1}}^2}$$

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 60.26](#).

Table 60.26. 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 ρ_0 is the null partial correlation and δ and ν are derived from section 16.33 of Stuart and Ord (1994):

$$\begin{aligned} \delta = & (N - 3 - p^*)^{\frac{1}{2}} \left[\frac{1}{2} \log \left(\frac{1 + \rho_{Y|(X_1, X_{-1})}}{1 - \rho_{Y|(X_1, X_{-1})}} \right) + \right. \\ & \frac{\rho_{Y|(X_1, X_{-1})}}{2(N - 1 - p^*)} \left(1 + \frac{5 + \rho_{Y|(X_1, X_{-1})}^2}{4(N - 1 - p^*)} + \right. \\ & \left. \left. \frac{11 + 2\rho_{Y|(X_1, X_{-1})}^2 + 3\rho_{Y|(X_1, X_{-1})}^4}{8(N - 1 - p^*)^2} \right) \right] \end{aligned}$$

$$\nu = \frac{N-3-p^*}{N-1-p^*} \left[1 + \frac{4 - \rho_{Y|(X_1, X_{-1})}^2}{2(N-1-p^*)} + \frac{22 - 6\rho_{Y|(X_1, X_{-1})}^2 - 3\rho_{Y|(X_1, X_{-1})}^4}{6(N-1-p^*)^2} \right] - \frac{1}{2} \log \left(\frac{1 + \rho_0}{1 - \rho_0} \right) - \frac{\rho_0}{2(N-1-p^*)}$$

The approximate power is computed as

$$\text{power} = \begin{cases} \Phi \left(\frac{\delta - z_{1-\alpha}}{\nu^{\frac{1}{2}}} \right), & \text{upper 1-sided} \\ \Phi \left(\frac{-\delta - z_{1-\alpha}}{\nu^{\frac{1}{2}}} \right), & \text{lower 1-sided} \\ \Phi \left(\frac{\delta - z_{1-\frac{\alpha}{2}}}{\nu^{\frac{1}{2}}} \right) + \Phi \left(\frac{-\delta - z_{1-\frac{\alpha}{2}}}{\nu^{\frac{1}{2}}} \right), & \text{2-sided} \end{cases}$$

Because the test is biased, the achieved significance level may 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 ρ_0 .

t Test for Pearson Correlation (TEST=PEARSON DIST=T)

The 2-sided case is identical to multiple regression with an intercept and $p_1 = 1$, which is discussed in the “Analyses in the MULTREG Statement” section on page 3800.

Let p^* denote the number of variables partialled out. For the 1-sided cases, the test statistic is

$$t = (N - 2 - p^*)^{\frac{1}{2}} \frac{R_{YX_1|X_{-1}}}{(1 - R_{YX_1|X_{-1}}^2)^{\frac{1}{2}}}$$

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:

$$\text{power} = \begin{cases} P \left[(N - 2 - p^*)^{\frac{1}{2}} \frac{R_{YX_1|X_{-1}}}{(1 - R_{YX_1|X_{-1}}^2)^{\frac{1}{2}}} \geq t_{1-\alpha}(N - 2 - p^*) \right], & \text{upper 1-sided} \\ P \left[(N - 2 - p^*)^{\frac{1}{2}} \frac{R_{YX_1|X_{-1}}}{(1 - R_{YX_1|X_{-1}}^2)^{\frac{1}{2}}} \leq t_{\alpha}(N - 2 - p^*) \right], & \text{lower 1-sided} \end{cases}$$

$$= \begin{cases} P \left[R_{Y|(X_1, X_{-1})} \geq \frac{t_{1-\alpha}(N-2-p^*)}{\left(t_{1-\alpha}^2(N-2-p^*) + \frac{1}{N-2-p^*}\right)^{\frac{1}{2}}} \right], & \text{upper 1-sided} \\ P \left[R_{Y|(X_1, X_{-1})} \leq \frac{t_{\alpha}(N-2-p^*)}{\left(t_{\alpha}^2(N-2-p^*) + \frac{1}{N-2-p^*}\right)^{\frac{1}{2}}} \right], & \text{lower 1-sided} \end{cases}$$

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

$$\delta = N^{\frac{1}{2}} \frac{\rho_{YX_1|X_{-1}}}{\left(1 - \rho_{YX_1|X_{-1}}^2\right)^{\frac{1}{2}}}$$

The power is

$$\text{power} = \begin{cases} P(t(N-2-p^*, \delta) \geq t_{1-\alpha}(N-2-p^*)), & \text{upper 1-sided} \\ P(t(N-2-p^*, \delta) \leq t_{\alpha}(N-2-p^*)), & \text{lower 1-sided} \end{cases}$$

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:

$$H_0 : p = p_0$$

$$H_1 : \begin{cases} p \neq p_0, & \text{2-sided} \\ p > p_0, & \text{upper 1-sided} \\ p < p_0, & \text{lower 1-sided} \end{cases}$$

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 α is split symmetrically for 2-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 and Kotz (1970, equation 3.20):

$$P(X \geq C | N, p) = P\left(F_{\nu_1, \nu_2} \leq \frac{\nu_2 p}{\nu_1(1-p)}\right)$$

where $\nu_1 = 2C$ and $\nu_2 = 2(N - C + 1)$

Let C_L and C_U denote lower and upper critical values, respectively. Let α_a denote the achieved (actual) significance level, which for 2-sided tests is the sum of the favorable major tail (α_M) and the opposite minor tail (α_m).

For the upper 1-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 1-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 2-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 (TEST=Z)

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 “Exact Test of a Binomial Proportion (TEST=EXACT)” section on page 3804 except for the definitions of the critical values.

For the upper 1-sided case,

$$C_U = \min\{C : Z(C) \geq z_{1-\alpha}\}$$

For the lower 1-sided case,

$$C_L = \max\{C : Z(C) \leq z_\alpha\}$$

For the 2-sided case,

$$\begin{aligned} C_L &= \max\{C : Z(C) \leq z_{\frac{\alpha}{2}}\} \\ C_U &= \min\{C : Z(C) \geq z_{1-\frac{\alpha}{2}}\} \end{aligned}$$

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

$$\text{power} = \begin{cases} \Phi\left(\frac{z_{\alpha} + \sqrt{N} \frac{p - p_0}{\sqrt{p_0(1 - p_0)}}}{\sqrt{\frac{p(1 - p)}{p_0(1 - p_0)}}}\right), & \text{upper 1-sided} \\ \Phi\left(\frac{z_{\alpha} - \sqrt{N} \frac{p - p_0}{\sqrt{p_0(1 - p_0)}}}{\sqrt{\frac{p(1 - p)}{p_0(1 - p_0)}}}\right), & \text{lower 1-sided} \\ \Phi\left(\frac{z_{\frac{\alpha}{2}} + \sqrt{N} \frac{p - p_0}{\sqrt{p_0(1 - p_0)}}}{\sqrt{\frac{p(1 - p)}{p_0(1 - p_0)}}}\right) + \Phi\left(\frac{z_{\frac{\alpha}{2}} - \sqrt{N} \frac{p - p_0}{\sqrt{p_0(1 - p_0)}}}{\sqrt{\frac{p(1 - p)}{p_0(1 - p_0)}}}\right), & \text{2-sided} \end{cases}$$

The approximate sample size is computed in closed form for the 1-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 2-sided case.

z Test for Binomial Proportion with Continuity Adjustment (TEST=ADJZ)

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 “Exact Test of a Binomial Proportion (TEST=EXACT)” section on page 3804 except for the definitions of the critical values.

For the upper 1-sided case,

$$C_U = \min\{C : Z_c(C) \geq z_{1-\alpha}\}$$

For the lower 1-sided case,

$$C_L = \max\{C : Z_c(C) \leq z_\alpha\}$$

For the 2-sided case,

$$\begin{aligned} C_L &= \max\{C : Z_c(C) \leq z_{\frac{\alpha}{2}}\} \\ C_U &= \min\{C : Z_c(C) \geq z_{1-\frac{\alpha}{2}}\} \end{aligned}$$

For the METHOD=NORMAL option, the test statistic $Z_c(X)$ is assumed to have the normal distribution $N(\mu, \sigma^2)$ where μ and σ^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

$$\begin{aligned} \text{Var}[Z_c(X)] &= \frac{p(1-p)}{p_0(1-p_0)} + k^2 [1 - P(X = Np_0)] \\ &\quad - k^2 [P(X < Np_0) - P(X > Np_0)]^2 \\ &\quad + 4k^2 [E(X1_{\{X < Np_0\}}) - E(X1_{\{X > Np_0\}})] \\ &\quad - 4k^2 Np [P(X < Np_0) - P(X > Np_0)] \end{aligned}$$

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:

$$\begin{aligned} P(X = Np_0) &= 0 \\ P(X < Np_0) &= \Phi(d) \end{aligned}$$

$$\begin{aligned}
 P(X > Np_0) &= 1 - \Phi(d) \\
 E(X1_{\{X < Np_0\}}) &= Np\Phi(d) - [Np(1-p)]^{\frac{1}{2}}\phi(d) \\
 E(X1_{\{X > Np_0\}}) &= Np[1 - \Phi(d)] + [Np(1-p)]^{\frac{1}{2}}\phi(d)
 \end{aligned}$$

The mean and variance of $Z_c(X)$ are thus approximated by

$$\mu = k [2Np - 2Np_0 + 2\Phi(d) - 1]$$

and

$$\sigma^2 = 4k^2 [Np(1-p) + \Phi(d)(1 - \Phi(d)) - 2(Np(1-p))^{\frac{1}{2}}\phi(d)]$$

The approximate power is computed as

$$\text{power} = \begin{cases} \Phi\left(\frac{z_{\alpha} + \mu}{\sigma}\right), & \text{upper 1-sided} \\ \Phi\left(\frac{z_{\alpha} - \mu}{\sigma}\right), & \text{lower 1-sided} \\ \Phi\left(\frac{z_{\frac{\alpha}{2}} + \mu}{\sigma}\right) + \Phi\left(\frac{z_{\frac{\alpha}{2}} - \mu}{\sigma}\right), & \text{2-sided} \end{cases}$$

Analyses in the ONESAMPLEMEANS Statement

One-sample t Test (TEST=T)

The hypotheses for the one-sample t test are

$$\begin{aligned}
 H_0 &: \mu = \mu_0 \\
 H_1 &: \begin{cases} \mu \neq \mu_0, & \text{2-sided} \\ \mu > \mu_0, & \text{upper 1-sided} \\ \mu < \mu_0, & \text{lower 1-sided} \end{cases}
 \end{aligned}$$

The test assumes normally distributed data and requires $N \geq 2$. The test statistics are

$$\begin{aligned}
 t &= N^{\frac{1}{2}} \left(\frac{\bar{x} - \mu_0}{s} \right) \sim t(N - 1, \delta) \\
 t^2 &\sim F(1, N - 1, \delta^2)
 \end{aligned}$$

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

$$\text{Reject } H_0 \text{ if } \begin{cases} t^2 \geq F_{1-\alpha}(1, N-1), & \text{2-sided} \\ t \geq t_{1-\alpha}(N-1), & \text{upper 1-sided} \\ t \leq t_{\alpha}(N-1), & \text{lower 1-sided} \end{cases}$$

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:

$$\text{power} = \begin{cases} P(F(1, N-1, \delta^2) \geq F_{1-\alpha}(1, N-1)), & \text{2-sided} \\ P(t(N-1, \delta) \geq t_{1-\alpha}(N-1)), & \text{upper 1-sided} \\ P(t(N-1, \delta) \leq t_{\alpha}(N-1)), & \text{lower 1-sided} \end{cases}$$

Solutions for N , α , and δ are obtained by numerically inverting the power equation. Closed-form solutions for other parameters, in terms of δ , are as follows:

$$\begin{aligned} \mu &= \delta \sigma N^{-\frac{1}{2}} + \mu_0 \\ \sigma &= \begin{cases} \delta^{-1} N^{\frac{1}{2}} (\mu - \mu_0), & |\delta| > 0 \\ \text{undefined}, & \text{otherwise} \end{cases} \end{aligned}$$

One-sample t Test with Lognormal Data (TEST=T DIST=LOGNORMAL)

The lognormal case is handled by re-expressing the analysis equivalently as a normality-based test on the log-transformed data, using properties of the lognormal distribution as discussed in Johnson and Kotz (1970, chapter 14). The approaches in the “One-sample t Test (TEST=T)” section on page 3808 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

$$\begin{aligned} H_0 &: \frac{\gamma}{\gamma_0} = 1 \\ H_1 &: \begin{cases} \frac{\gamma}{\gamma_0} \neq 1, & \text{2-sided} \\ \frac{\gamma}{\gamma_0} > 1, & \text{upper 1-sided} \\ \frac{\gamma}{\gamma_0} < 1, & \text{lower 1-sided} \end{cases} \end{aligned}$$

Let μ^* and σ^* be the (arithmetic) mean and standard deviation of the normal distribution of the log-transformed data. The hypotheses can be rewritten as follows:

$$H_0 : \mu^* = \log(\gamma_0)$$

$$H_1 : \begin{cases} \mu^* \neq \log(\gamma_0), & \text{2-sided} \\ \mu^* > \log(\gamma_0), & \text{upper 1-sided} \\ \mu^* < \log(\gamma_0), & \text{lower 1-sided} \end{cases}$$

where $\mu^* = \log(\gamma)$.

The test assumes lognormally distributed data and requires $N \geq 2$.

The power is

$$\text{power} = \begin{cases} P(F(1, N-1, \delta^2) \geq F_{1-\alpha}(1, N-1)), & \text{2-sided} \\ P(t(N-1, \delta) \geq t_{1-\alpha}(N-1)), & \text{upper 1-sided} \\ P(t(N-1, \delta) \leq t_{\alpha}(N-1)), & \text{lower 1-sided} \end{cases}$$

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

$$H_0 : \mu < \theta_L \text{ or } \mu > \theta_U$$

$$H_1 : \theta_L \leq \mu \leq \theta_U$$

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 "Common Notation" section on page 3798.

Equivalence Test for Mean of Lognormal Data (TEST=EQUIV DIST=LOGNORMAL)

The lognormal case is handled by re-expressing the analysis equivalently as a normality-based test on the log-transformed data, using properties of the lognormal distribution as discussed in Johnson and Kotz (1970, chapter 14). The approaches in the “[Equivalence Test for Mean of Normal Data \(TEST=EQUIV DIST=NORMAL\)](#)” section on page 3810 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

$$H_0 : \gamma \leq \theta_L \text{ or } \gamma \geq \theta_U$$

$$H_1 : \theta_L < \gamma < \theta_U$$

$$\text{where } 0 < \theta_L < \theta_U$$

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:

$$\begin{aligned} \text{power} = & Q_{N-1} \left((-t_{1-\alpha}(N-1)), \frac{\log(\gamma) - \log(\theta_U)}{\sigma^* N^{-\frac{1}{2}}}; \right. \\ & \left. 0, \frac{(N-1)^{\frac{1}{2}}(\log(\theta_U) - \log(\theta_L))}{2\sigma^* N^{-\frac{1}{2}}(t_{1-\alpha}(N-1))} \right) - \\ & Q_{N-1} \left((t_{1-\alpha}(N-1)), \frac{\log(\gamma) - \log(\theta_L)}{\sigma^* N^{-\frac{1}{2}}}; \right. \\ & \left. 0, \frac{(N-1)^{\frac{1}{2}}(\log(\theta_U) - \log(\theta_L))}{2\sigma^* N^{-\frac{1}{2}}(t_{1-\alpha}(N-1))} \right) \end{aligned}$$

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 “[Common Notation](#)” section on page 3798.

Confidence Interval for Mean (CI=T)

This analysis of precision applies to the standard t -based confidence interval:

$$\begin{cases} \left[\bar{x} - t_{1-\frac{\alpha}{2}}(N-1)\frac{s}{\sqrt{N}}, \bar{x} + t_{1-\frac{\alpha}{2}}(N-1)\frac{s}{\sqrt{N}} \right], & \text{2-sided} \\ \left(\bar{x} - t_{1-\alpha}(N-1)\frac{s}{\sqrt{N}}, \infty \right), & \text{upper 1-sided} \\ \left(-\infty, \bar{x} + t_{1-\alpha}(N-1)\frac{s}{\sqrt{N}} \right], & \text{lower 1-sided} \end{cases}$$

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,

$$\text{half-width} = \begin{cases} t_{1-\frac{\alpha}{2}}(N-1)\frac{s}{\sqrt{N}}, & \text{2-sided} \\ t_{1-\alpha}(N-1)\frac{s}{\sqrt{N}}, & \text{1-sided} \end{cases}$$

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):

$$\begin{aligned} \Pr(\text{half-width} \leq h) &= \begin{cases} P\left(\chi^2(N-1) \leq \frac{h^2 N(N-1)}{\sigma^2(t_{1-\frac{\alpha}{2}}^2(N-1))}\right), & \text{2-sided} \\ P\left(\chi^2(N-1) \leq \frac{h^2 N(N-1)}{\sigma^2(t_{1-\alpha}^2(N-1))}\right), & \text{1-sided} \end{cases} \\ \Pr(\text{half-width} \leq h \mid \text{validity}) &= \begin{cases} \left(\frac{1}{1-\alpha}\right) 2 \left[Q_{N-1}\left((t_{1-\frac{\alpha}{2}}(N-1)), 0; 0, b_1\right) - Q_{N-1}(0, 0; 0, b_1) \right], & \text{2-sided} \\ \left(\frac{1}{1-\alpha}\right) Q_{N-1}\left((t_{1-\alpha}(N-1)), 0; 0, b_1\right), & \text{1-sided} \end{cases} \end{aligned}$$

where

$$\begin{aligned} b_1 &= \frac{h(N-1)^{\frac{1}{2}}}{\sigma(t_{1-\frac{\alpha}{2}}(N-1))N^{-\frac{1}{2}}} \\ c &= \text{number of sides} \end{aligned}$$

and $Q(\cdot, \cdot; \cdot, \cdot)$ is Owen’s Q function, defined in the “Common Notation” section on page 3798.

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

$$H_0 : c_1\mu_1 + \cdots + c_G\mu_G = c_0$$

$$H_1 : \begin{cases} c_1\mu_1 + \cdots + c_G\mu_G \neq c_0, & \text{2-sided} \\ c_1\mu_1 + \cdots + c_G\mu_G > c_0, & \text{upper 1-sided} \\ c_1\mu_1 + \cdots + c_G\mu_G < c_0, & \text{lower 1-sided} \end{cases}$$

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

$$\text{power} = \begin{cases} P(F(1, N - G, \delta^2) \geq F_{1-\alpha}(1, N - G)), & \text{2-sided} \\ P(t(N - G, \delta) \geq t_{1-\alpha}(N - G)), & \text{upper 1-sided} \\ P(t(N - G, \delta) \leq t_{\alpha}(N - G)), & \text{lower 1-sided} \end{cases}$$

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

$$H_0 : \mu_1 = \mu_2 = \cdots = \mu_G$$

$$H_1 : \mu_i \neq \mu_j \text{ for some } i, j$$

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

$$\begin{aligned}
 n_{00} &= \#\{\text{control=failure, case=failure}\} \\
 n_{01} &= \#\{\text{control=failure, case=success}\} \\
 n_{10} &= \#\{\text{control=success, case=failure}\} \\
 n_{11} &= \#\{\text{control=success, case=success}\} \\
 N &= n_{00} + n_{01} + n_{10} + n_{11} \\
 n_D &= n_{01} + n_{10} \equiv \#\text{ discordant pairs} \\
 \hat{\pi}_{ij} &= \frac{n_{ij}}{N} \\
 \pi_{ij} &= \text{theoretical population value of } \hat{\pi}_{ij} \\
 \pi_{1\cdot} &= \pi_{10} + \pi_{11} \\
 \pi_{\cdot 1} &= \pi_{01} + \pi_{11} \\
 OR &= \text{“odds ratio”} = \frac{\pi_{01}}{\pi_{10}} \\
 OR_0 &= \text{null odds ratio}
 \end{aligned}$$

All McNemar tests covered in PROC POWER are *conditional*, meaning that n_D is assumed fixed at its observed value.

For the usual $OR_0 = 0$, the hypotheses are

$$\begin{aligned}
 H_0 & : \pi_{\cdot 1} = \pi_{1\cdot} \\
 H_1 & : \begin{cases} \pi_{\cdot 1} \neq \pi_{1\cdot}, & \text{2-sided} \\ \pi_{\cdot 1} > \pi_{1\cdot}, & \text{upper 1-sided} \\ \pi_{\cdot 1} < \pi_{1\cdot}, & \text{lower 1-sided} \end{cases}
 \end{aligned}$$

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 $OR_0 = 0$:

$$Q_{M_0} = \frac{(n_{01} - n_{10})^2}{n_{01} + n_{10}}$$

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, e.g., Schork and Williams 1980):

$$\begin{aligned}
 Z(X) & = \frac{n_{01} - n_D(0.5)}{[n_D 0.5(1 - 0.5)]^{\frac{1}{2}}} \sim N \left(\frac{n_D^{\frac{1}{2}} \left(\frac{\pi_{01}}{\pi_{01} + \pi_{10}} - 0.5 \right)}{[0.5(1 - 0.5)]^{\frac{1}{2}}}, \frac{\frac{\pi_{01}}{\pi_{01} + \pi_{10}} \left(1 - \frac{\pi_{01}}{\pi_{01} + \pi_{10}} \right)}{0.5(1 - 0.5)} \right) \\
 & = \frac{n_{01} - (n_{01} + n_{10})(0.5)}{[(n_{01} + n_{10})0.5(1 - 0.5)]^{\frac{1}{2}}} \\
 & = \frac{n_{01} - n_{10}}{[n_{01} + n_{10}]^{\frac{1}{2}}} \\
 & = \sqrt{Q_{M_0}}
 \end{aligned}$$

This can be generalized to a custom null for $\frac{\pi_{01}}{\pi_{01} + \pi_{10}}$, which is equivalent to specifying a custom odds ratio:

$$\left[\frac{\pi_{01}}{\pi_{01} + \pi_{10}} \right]_0 \equiv \left[\frac{1}{1 + \frac{1}{\frac{\pi_{01}}{\pi_{10}}}} \right]_0 \equiv \frac{1}{1 + \frac{1}{OR_0}}$$

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 $p_0 \equiv \frac{1}{1 + \frac{1}{OR_0}}$, with a sample size of n_D :

$$\begin{aligned}
 H_0 & : p_1 = p_0 \\
 H_1 & : \begin{cases} p_1 \neq p_0, & \text{2-sided} \\ p_1 > p_0, & \text{1-sided U} \\ p_1 < p_0, & \text{1-sided L} \end{cases}
 \end{aligned}$$

which is equivalent to

$$H_0 : OR = OR_0$$

$$H_1 : \begin{cases} OR \neq OR_0, & \text{2-sided} \\ OR > OR_0, & \text{1-sided U} \\ OR < OR_0, & \text{1-sided L} \end{cases}$$

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 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 using the exact method in the “Exact Test of a Binomial Proportion (TEST=EXACT)” section on page 3804.

The achieved significance level, reported as Actual Alpha in the analysis, is computed in the same way except 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 using the exact method in the “Exact Test of a Binomial Proportion (TEST=EXACT)” section on page 3804 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 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 “McNemar Exact Conditional Test (TEST=MCNEMAR DIST=EXACT_COND)” section on page 3816, except that $P(\text{Reject } p_1 = p_0 | n_D)$ is calculated using the exact method in the “z Test for Binomial Proportion (TEST=Z)” section on page 3805. The achieved significance level is calculated in the same way as described at the end of the “McNemar Exact Conditional Test (TEST=MCNEMAR DIST=EXACT_COND)” section on page 3816.

For the METHOD=MIETTINEN option, approximate sample size for the 1-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 1-sided cases is computed by solving the sample size equation for power, and approximate power for the 2-sided case follows easily by summing the 1-sided powers each at $\alpha/2$:

$$\text{power} = \begin{cases} \Phi \left(\frac{(p_{01} - p_{10})[N(p_{10} + p_{01})]^{\frac{1}{2}} - z_{1-\alpha}(p_{10} + p_{01})}{[(p_{10} + p_{01})^2 - \frac{1}{4}(p_{01} - p_{10})^2(3 + p_{10} + p_{01})]^{\frac{1}{2}}} \right), & \text{upper 1-sided} \\ \Phi \left(\frac{-(p_{01} - p_{10})[N(p_{10} + p_{01})]^{\frac{1}{2}} - z_{1-\alpha}(p_{10} + p_{01})}{[(p_{10} + p_{01})^2 - \frac{1}{4}(p_{01} - p_{10})^2(3 + p_{10} + p_{01})]^{\frac{1}{2}}} \right), & \text{lower 1-sided} \\ \Phi \left(\frac{(p_{01} - p_{10})[N(p_{10} + p_{01})]^{\frac{1}{2}} - z_{1-\frac{\alpha}{2}}(p_{10} + p_{01})}{[(p_{10} + p_{01})^2 - \frac{1}{4}(p_{01} - p_{10})^2(3 + p_{10} + p_{01})]^{\frac{1}{2}}} \right) + \\ \Phi \left(\frac{-(p_{01} - p_{10})[N(p_{10} + p_{01})]^{\frac{1}{2}} - z_{1-\frac{\alpha}{2}}(p_{10} + p_{01})}{[(p_{10} + p_{01})^2 - \frac{1}{4}(p_{01} - p_{10})^2(3 + p_{10} + p_{01})]^{\frac{1}{2}}} \right), & \text{2-sided} \end{cases}$$

The 2-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 may 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 1-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 1-sided cases is computed by solving the sample size equation for power, and approximate power for the 2-sided case follows easily by summing the 1-sided powers each at $\alpha/2$:

$$\text{power} = \begin{cases} \Phi \left(\frac{(p_{01}-p_{10})N^{\frac{1}{2}} - z_{1-\alpha}(p_{10}+p_{01})^{\frac{1}{2}}}{[p_{10}+p_{01}-(p_{01}-p_{10})^2]^{\frac{1}{2}}} \right), & \text{upper 1-sided} \\ \Phi \left(\frac{-(p_{01}-p_{10})N^{\frac{1}{2}} - z_{1-\alpha}(p_{10}+p_{01})^{\frac{1}{2}}}{[p_{10}+p_{01}-(p_{01}-p_{10})^2]^{\frac{1}{2}}} \right), & \text{lower 1-sided} \\ \Phi \left(\frac{(p_{01}-p_{10})N^{\frac{1}{2}} - z_{1-\frac{\alpha}{2}}(p_{10}+p_{01})^{\frac{1}{2}}}{[p_{10}+p_{01}-(p_{01}-p_{10})^2]^{\frac{1}{2}}} \right) + \\ \Phi \left(\frac{-(p_{01}-p_{10})N^{\frac{1}{2}} - z_{1-\frac{\alpha}{2}}(p_{10}+p_{01})^{\frac{1}{2}}}{[p_{10}+p_{01}-(p_{01}-p_{10})^2]^{\frac{1}{2}}} \right), & \text{2-sided} \end{cases}$$

The 2-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

$$H_0 : \mu_{\text{diff}} = \mu_0$$

$$H_1 : \begin{cases} \mu_{\text{diff}} \neq \mu_0, & \text{2-sided} \\ \mu_{\text{diff}} > \mu_0, & \text{upper 1-sided} \\ \mu_{\text{diff}} < \mu_0, & \text{lower 1-sided} \end{cases}$$

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

$$\text{Reject } H_0 \quad \text{if } \begin{cases} t^2 \geq F_{1-\alpha}(1, N-1), & \text{2-sided} \\ t \geq t_{1-\alpha}(N-1), & \text{upper 1-sided} \\ t \leq t_{\alpha}(N-1), & \text{lower 1-sided} \end{cases}$$

Exact power computations for t tests are given in O'Brien and Muller (1993, section 8.2.2):

$$\text{power} = \begin{cases} P(F(1, N-1, \delta^2) \geq F_{1-\alpha}(1, N-1)), & \text{2-sided} \\ P(t(N-1, \delta) \geq t_{1-\alpha}(N-1)), & \text{upper 1-sided} \\ P(t(N-1, \delta) \leq t_{\alpha}(N-1)), & \text{lower 1-sided} \end{cases}$$

Paired t Test for Mean Ratio with Lognormal Data (TEST=RATIO)

The lognormal case is handled by re-expressing the analysis equivalently as a normality-based test on the log-transformed data, using properties of the lognormal distribution as discussed in Johnson and Kotz (1970, chapter 14). The approaches in the “Paired t Test (TEST=DIFF)” section on page 3818 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

$$\begin{aligned} H_0 &: \frac{\gamma_2}{\gamma_1} = \gamma_0 \\ H_1 &: \begin{cases} \frac{\gamma_2}{\gamma_1} \neq \gamma_0, & \text{2-sided} \\ \frac{\gamma_2}{\gamma_1} > \gamma_0, & \text{upper 1-sided} \\ \frac{\gamma_2}{\gamma_1} < \gamma_0, & \text{lower 1-sided} \end{cases} \end{aligned}$$

Let μ_1^* , μ_2^* , σ_1^* , σ_2^* , and ρ^* 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:

$$\begin{aligned} H_0 &: \mu_2^* - \mu_1^* = \log(\gamma_0) \\ H_1 &: \begin{cases} \mu_2^* - \mu_1^* \neq \log(\gamma_0), & \text{2-sided} \\ \mu_2^* - \mu_1^* > \log(\gamma_0), & \text{upper 1-sided} \\ \mu_2^* - \mu_1^* < \log(\gamma_0), & \text{lower 1-sided} \end{cases} \end{aligned}$$

where

$$\begin{aligned} \mu_1^* &= \log \gamma_1 \\ \mu_2^* &= \log \gamma_2 \\ \sigma_1^* &= [\log(\text{CV}_1^2 + 1)]^{\frac{1}{2}} \end{aligned}$$

$$\begin{aligned}\sigma_2^* &= [\log(\text{CV}_2^2 + 1)]^{\frac{1}{2}} \\ \rho^* &= \frac{\log\{\rho\text{CV}_1\text{CV}_2 + 1\}}{\sigma_1^*\sigma_2^*}\end{aligned}$$

and CV_1 , CV_2 , and ρ are the coefficients of variation and the correlation of the original untransformed pairs $\{Y_1, Y_2\}$. The conversion from ρ to ρ^* is shown in Jones and Miller (1966).

The test assumes lognormally distributed data and requires $N \geq 2$. The power is

$$\text{power} = \begin{cases} P(F(1, N-1, \delta^2) \geq F_{1-\alpha}(1, N-1)), & \text{2-sided} \\ P(t(N-1, \delta) \geq t_{1-\alpha}(N-1)), & \text{upper 1-sided} \\ P(t(N-1, \delta) \leq t_{\alpha}(N-1)), & \text{lower 1-sided} \end{cases}$$

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

$$\begin{aligned}H_0 &: \mu_{\text{diff}} < \theta_L \quad \text{or} \quad \mu_{\text{diff}} > \theta_U \\ H_1 &: \theta_L \leq \mu_{\text{diff}} \leq \theta_U\end{aligned}$$

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 "Common Notation" section on page 3798.

Multiplicative Equivalence Test for Mean Ratio with Lognormal Data (TEST=EQUIV_RATIO)

The lognormal case is handled by re-expressing the analysis equivalently as a normality-based test on the log-transformed data, using properties of the lognormal distribution as discussed in Johnson and Kotz (1970, chapter 14). The approaches in the “Additive Equivalence Test for Mean Difference with Normal Data (TEST=EQUIV_DIFF)” section on page 3820 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:

$$\begin{aligned} \text{power} = & Q_{N-1} \left((-t_{1-\alpha}(N-1)), \frac{\log\left(\frac{\gamma_T}{\gamma_R}\right) - \log(\theta_U)}{\sigma^* N^{-\frac{1}{2}}}; \right. \\ & \left. 0, \frac{(N-1)^{\frac{1}{2}}(\log(\theta_U) - \log(\theta_L))}{2\sigma^* N^{-\frac{1}{2}}(t_{1-\alpha}(N-1))} \right) - \\ & Q_{N-1} \left((t_{1-\alpha}(N-1)), \frac{\log\left(\frac{\gamma_T}{\gamma_R}\right) - \log(\theta_L)}{\sigma^* N^{-\frac{1}{2}}}; \right. \\ & \left. 0, \frac{(N-1)^{\frac{1}{2}}(\log(\theta_U) - \log(\theta_L))}{2\sigma^* N^{-\frac{1}{2}}(t_{1-\alpha}(N-1))} \right) \end{aligned}$$

where σ^* 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 CV_R , CV_T , and ρ 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 ρ to ρ^* is shown in Jones and Miller (1966), and Owen's Q function is defined in the "Common Notation" section on page 3798.

Confidence Interval for Mean Difference (CI=DIFF)

This analysis of precision applies to the standard t -based confidence interval:

$$\begin{cases} \left[\bar{d} - t_{1-\frac{\alpha}{2}}(N-1)\frac{s_d}{\sqrt{N}}, \bar{d} + t_{1-\frac{\alpha}{2}}(N-1)\frac{s_d}{\sqrt{N}} \right], & \text{2-sided} \\ \left[\bar{d} - t_{1-\alpha}(N-1)\frac{s_d}{\sqrt{N}}, \infty \right), & \text{upper 1-sided} \\ \left(-\infty, \bar{d} + t_{1-\alpha}(N-1)\frac{s_d}{\sqrt{N}} \right], & \text{lower 1-sided} \end{cases}$$

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,

$$\text{half-width} = \begin{cases} t_{1-\frac{\alpha}{2}}(N-1)\frac{s_d}{\sqrt{N}}, & \text{2-sided} \\ t_{1-\alpha}(N-1)\frac{s_d}{\sqrt{N}}, & \text{1-sided} \end{cases}$$

A "valid" confidence 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):

$$\begin{aligned} \Pr(\text{half-width} \leq h) &= \begin{cases} P\left(\chi^2(N-1) \leq \frac{h^2 N(N-1)}{\sigma_{\text{diff}}^2 (t_{1-\frac{\alpha}{2}}^2(N-1))}\right), & \text{2-sided} \\ P\left(\chi^2(N-1) \leq \frac{h^2 N(N-1)}{\sigma_{\text{diff}}^2 (t_{1-\alpha}^2(N-1))}\right), & \text{1-sided} \end{cases} \\ \Pr(\text{half-width} \leq h \mid \text{validity}) &= \begin{cases} \left(\frac{1}{1-\alpha}\right) 2 \left[Q_{N-1}\left((t_{1-\frac{\alpha}{2}}(N-1)), 0; 0, b_1\right) - Q_{N-1}(0, 0; 0, b_1) \right], & \text{2-sided} \\ \left(\frac{1}{1-\alpha}\right) Q_{N-1}\left((t_{1-\alpha}(N-1)), 0; 0, b_1\right), & \text{1-sided} \end{cases} \end{aligned}$$

where

$$\begin{aligned} \sigma_{\text{diff}} &= (\sigma_1^2 + \sigma_2^2 - 2\rho\sigma_1\sigma_2)^{\frac{1}{2}} \\ b_1 &= \frac{h(N-1)^{\frac{1}{2}}}{\sigma_{\text{diff}}(t_{1-\frac{\alpha}{2}}(N-1))N^{-\frac{1}{2}}} \\ c &= \text{number of sides} \end{aligned}$$

and $Q(\cdot, \cdot; \cdot, \cdot)$ is Owen's Q function, defined in the "Common Notation" section on page 3798.

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 2×2 Table

Notation:

		Group 2		
		Failure	Success	
Group 1	Failure	x_1	x_2	m
	Success	$n_1 - x_1$	$n_2 - x_2$	$N - m$
		n_1	n_2	N

$$x_1 = \text{\# successes in group 1}$$

$$x_2 = \text{\# successes in group 2}$$

$$m = x_1 + x_2 = \text{total \# successes}$$

$$\hat{p}_1 = \frac{x_1}{n_1}$$

$$\hat{p}_2 = \frac{x_2}{n_2}$$

$$\hat{p} = \frac{m}{N} = w_1\hat{p}_1 + w_2\hat{p}_2$$

The hypotheses are

$$H_0 : p_2 - p_1 = p_0$$

$$H_1 : \begin{cases} p_2 - p_1 \neq p_0, & \text{2-sided} \\ p_2 - p_1 > p_0, & \text{upper 1-sided} \\ p_2 - p_1 < p_0, & \text{lower 1-sided} \end{cases}$$

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:

$$\begin{aligned} p_2 &= (RR)p_1 \\ p_{10} &= p_1 \\ p_{20} &= (RR_0)p_{10} \\ p_0 &= p_{20} - p_{10} \end{aligned}$$

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 1-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 2-sided case is computed by adding the lower-sided and upper-sided powers each with $\alpha/2$, and sample size for the 2-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.

$$\text{power} = \begin{cases} \Phi \left(\frac{(p_2 - p_1 - p_0)(Nw_1w_2)^{\frac{1}{2}} - z_{1-\alpha} [(w_1p_1 + w_2p_2)(1 - w_1p_1 - w_2p_2)]^{\frac{1}{2}}}{[w_2p_1(1-p_1) + w_1p_2(1-p_2)]^{\frac{1}{2}}} \right), & \text{upper 1-sided} \\ \Phi \left(\frac{-(p_2 - p_1 - p_0)(Nw_1w_2)^{\frac{1}{2}} - z_{1-\alpha} [(w_1p_1 + w_2p_2)(1 - w_1p_1 - w_2p_2)]^{\frac{1}{2}}}{[w_2p_1(1-p_1) + w_1p_2(1-p_2)]^{\frac{1}{2}}} \right), & \text{lower 1-sided} \\ \Phi \left(\frac{(p_2 - p_1 - p_0)(Nw_1w_2)^{\frac{1}{2}} - z_{1-\frac{\alpha}{2}} [(w_1p_1 + w_2p_2)(1 - w_1p_1 - w_2p_2)]^{\frac{1}{2}}}{[w_2p_1(1-p_1) + w_1p_2(1-p_2)]^{\frac{1}{2}}} \right) + \\ \Phi \left(\frac{-(p_2 - p_1 - p_0)(Nw_1w_2)^{\frac{1}{2}} - z_{1-\frac{\alpha}{2}} [(w_1p_1 + w_2p_2)(1 - w_1p_1 - w_2p_2)]^{\frac{1}{2}}}{[w_2p_1(1-p_1) + w_1p_2(1-p_2)]^{\frac{1}{2}}} \right), & \text{2-sided} \end{cases}$$

For the 1-sided cases, a closed-form inversion of the power equation yield an approximate total sample size

$$N = \frac{\left[z_{1-\alpha} \{ (w_1p_1 + w_2p_2)(1 - w_1p_1 - w_2p_2) \}^{\frac{1}{2}} + z_{\text{power}} \{ w_2p_1(1 - p_1) + w_1p_2(1 - p_2) \}^{\frac{1}{2}} \right]^2}{w_1w_2(p_2 - p_1 - p_0)^2}$$

For the 2-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

$$\text{power} = \begin{cases} \Phi(\delta - z_{1-\alpha}), & \text{upper 1-sided} \\ \Phi(-\delta - z_{1-\alpha}), & \text{lower 1-sided} \\ \Phi\left(\delta - z_{1-\frac{\alpha}{2}}\right) + \Phi\left(-\delta - z_{1-\frac{\alpha}{2}}\right), & \text{2-sided} \end{cases}$$

For the 1-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 2-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 1-sided balanced case is given by Walters (1979) and is easily extended to the unbalanced and 2-sided cases:

$$\text{power} = \begin{cases} \Phi(\delta - z_{1-\alpha}), & \text{upper 1-sided} \\ \Phi(-\delta - z_{1-\alpha}), & \text{lower 1-sided} \\ \Phi\left(\delta - z_{1-\frac{\alpha}{2}}\right) + \Phi\left(-\delta - z_{1-\frac{\alpha}{2}}\right), & \text{2-sided} \end{cases}$$

Analyses in the TWOSAMPLEMEANS Statement

Two-sample t Test Assuming Equal Variances (TEST=DIFF)

The hypotheses for the two-sample t test are

$$H_0 : \mu_{\text{diff}} = \mu_0$$

$$H_1 : \begin{cases} \mu_{\text{diff}} \neq \mu_0, & \text{2-sided} \\ \mu_{\text{diff}} > \mu_0, & \text{upper 1-sided} \\ \mu_{\text{diff}} < \mu_0, & \text{lower 1-sided} \end{cases}$$

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

$$t = N^{\frac{1}{2}}(w_1 w_2)^{\frac{1}{2}} \left(\frac{\bar{x}_2 - \bar{x}_1 - \mu_0}{s_p} \right) \sim t(N - 2, \delta)$$

$$t^2 \sim F(1, N - 2, \delta^2)$$

where \bar{x}_1 and \bar{x}_2 are the sample means and s_p is the pooled standard deviation, and

$$\delta = N^{\frac{1}{2}}(w_1 w_2)^{\frac{1}{2}} \left(\frac{\mu_{\text{diff}} - \mu_0}{\sigma} \right)$$

The test is

$$\text{Reject } H_0 \text{ if } \begin{cases} t^2 \geq F_{1-\alpha}(1, N - 2), & \text{2-sided} \\ t \geq t_{1-\alpha}(N - 2), & \text{upper 1-sided} \\ t \leq t_{\alpha}(N - 2), & \text{lower 1-sided} \end{cases}$$

Exact power computations for t tests are given in O'Brien and Muller (1993, section 8.2.1):

$$\text{power} = \begin{cases} P(F(1, N - 2, \delta^2) \geq F_{1-\alpha}(1, N - 2)), & \text{2-sided} \\ P(t(N - 2, \delta) \geq t_{1-\alpha}(N - 2)), & \text{upper 1-sided} \\ P(t(N - 2, \delta) \leq t_{\alpha}(N - 2)), & \text{lower 1-sided} \end{cases}$$

Solutions for N , n_1 , n_2 , α , and δ are obtained by numerically inverting the power equation. Closed-form solutions for other parameters, in terms of δ , 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 δ equation for w_1 (which requires the quadratic formula). Then determine the range of δ given w_1 :

$$\begin{aligned}\min_{w_1}(\delta) &= \begin{cases} 0, & \text{when } w_1 = 0 \text{ or } 1, \text{ if } (\mu_{\text{diff}} - \mu_0) \geq 0 \\ \frac{1}{2}N^{\frac{1}{2}}\frac{(\mu_{\text{diff}} - \mu_0)}{\sigma}, & \text{when } w_1 = \frac{1}{2}, \text{ if } (\mu_{\text{diff}} - \mu_0) < 0 \end{cases} \\ \max_{w_1}(\delta) &= \begin{cases} 0, & \text{when } w_1 = 0 \text{ or } 1, \text{ if } (\mu_{\text{diff}} - \mu_0) < 0 \\ \frac{1}{2}N^{\frac{1}{2}}\frac{(\mu_{\text{diff}} - \mu_0)}{\sigma}, & \text{when } w_1 = \frac{1}{2}, \text{ if } (\mu_{\text{diff}} - \mu_0) \geq 0 \end{cases}\end{aligned}$$

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

$$\begin{aligned}H_0 &: \mu_{\text{diff}} = \mu_0 \\ H_1 &: \begin{cases} \mu_{\text{diff}} \neq \mu_0, & \text{2-sided} \\ \mu_{\text{diff}} > \mu_0, & \text{upper 1-sided} \\ \mu_{\text{diff}} < \mu_0, & \text{lower 1-sided} \end{cases}\end{aligned}$$

The test assumes normally distributed data and requires $N \geq 3$, $n_1 \geq 1$, and $n_2 \geq 1$. The test statistics are

$$\begin{aligned}t &= \frac{\bar{x}_2 - \bar{x}_1 - \mu_0}{\left[\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2} \right]^{\frac{1}{2}}} = N^{\frac{1}{2}} \frac{\bar{x}_2 - \bar{x}_1 - \mu_0}{\left[\frac{s_1^2}{w_1} + \frac{s_2^2}{w_2} \right]^{\frac{1}{2}}} \\ F &= t^2\end{aligned}$$

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 ν 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 ν 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

$$\text{Reject } H_0 \text{ if } \begin{cases} F \geq F_{1-\alpha}(1, \hat{\nu}), & \text{2-sided} \\ t \geq t_{1-\alpha}(\hat{\nu}), & \text{upper 1-sided} \\ t \leq t_{\alpha}(\hat{\nu}), & \text{lower 1-sided} \end{cases}$$

Exact solutions for power for the 2-sided and upper 1-sided cases are given in Moser, Stevens, and Watts (1989). The lower 1-sided case follows easily using symmetry. The equations are as follows:

$$\text{power} = \begin{cases} \int_0^{\infty} P(F(1, N-2, \lambda) > h(u)F_{1-\alpha}(1, v(u))|u) f(u)du, & \text{2-sided} \\ \int_0^{\infty} P\left(t(N-2, \lambda^{\frac{1}{2}}) > [h(u)]^{\frac{1}{2}} t_{1-\alpha}(v(u))|u\right) f(u)du, & \text{upper 1-sided} \\ \int_0^{\infty} P\left(t(N-2, \lambda^{\frac{1}{2}}) < [h(u)]^{\frac{1}{2}} t_{\alpha}(v(u))|u\right) f(u)du, & \text{lower 1-sided} \end{cases}$$

where

$$h(u) = \frac{\left(\frac{1}{n_1} + \frac{u}{n_2}\right)(n_1 + n_2 - 2)}{\left[(n_1 - 1) + (n_2 - 1)\frac{u\sigma_1^2}{\sigma_2^2}\right]\left(\frac{1}{n_1} + \frac{\sigma_2^2}{\sigma_1^2 n_2}\right)}$$

$$v(u) = \frac{\left(\frac{1}{n_1} + \frac{u}{n_2}\right)^2}{\frac{1}{n_1^2(n_1-1)} + \frac{u^2}{n_2^2(n_2-1)}}$$

$$\lambda = \frac{(\mu_{\text{diff}} - \mu_0)^2}{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}$$

$$f(u) = \frac{\Gamma\left(\frac{n_1+n_2-2}{2}\right)}{\Gamma\left(\frac{n_1-1}{2}\right)\Gamma\left(\frac{n_2-1}{2}\right)} \left[\frac{\sigma_1^2(n_2-1)}{\sigma_2^2(n_1-1)}\right]^{\frac{n_2-1}{2}} \cdot u^{\frac{n_2-3}{2}} \left[1 + \left(\frac{n_2-1}{n_1-1}\right) \frac{u\sigma_1^2}{\sigma_2^2}\right]^{-\left(\frac{n_1+n_2-2}{2}\right)}$$

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 re-expressing the analysis equivalently as a normality-based test on the log-transformed data, using properties of the lognormal distribution as discussed in Johnson and Kotz (1970, chapter 14). The approaches in the “Two-sample t Test Assuming Equal Variances (TEST=DIFF)” section on page 3826 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

$$H_0 : \frac{\gamma_2}{\gamma_1} = \gamma_0$$

$$H_1 : \begin{cases} \frac{\gamma_2}{\gamma_1} \neq \gamma_0, & \text{2-sided} \\ \frac{\gamma_2}{\gamma_1} > \gamma_0, & \text{upper 1-sided} \\ \frac{\gamma_2}{\gamma_1} < \gamma_0, & \text{lower 1-sided} \end{cases}$$

Let μ_1^* , μ_2^* , and σ^* 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:

$$H_0 : \mu_2^* - \mu_1^* = \log(\gamma_0)$$

$$H_1 : \begin{cases} \mu_2^* - \mu_1^* \neq \log(\gamma_0), & \text{2-sided} \\ \mu_2^* - \mu_1^* > \log(\gamma_0), & \text{upper 1-sided} \\ \mu_2^* - \mu_1^* < \log(\gamma_0), & \text{lower 1-sided} \end{cases}$$

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

$$\text{power} = \begin{cases} P(F(1, N-2, \delta^2) \geq F_{1-\alpha}(1, N-2)), & \text{2-sided} \\ P(t(N-2, \delta) \geq t_{1-\alpha}(N-2)), & \text{upper 1-sided} \\ P(t(N-2, \delta) \leq t_{\alpha}(N-2)), & \text{lower 1-sided} \end{cases}$$

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:

$$\text{power} = Q_{N-2} \left((-t_{1-\alpha}(N-2)), \frac{\mu_{\text{diff}} - \theta_U}{\sigma N^{-\frac{1}{2}}(w_1 w_2)^{-\frac{1}{2}}}; \right. \\ \left. 0, \frac{(N-2)^{\frac{1}{2}}(\theta_U - \theta_L)}{2\sigma N^{-\frac{1}{2}}(w_1 w_2)^{-\frac{1}{2}}(t_{1-\alpha}(N-2))} \right) - \\ Q_{N-2} \left((t_{1-\alpha}(N-2)), \frac{\mu_{\text{diff}} - \theta_L}{\sigma N^{-\frac{1}{2}}(w_1 w_2)^{-\frac{1}{2}}}; \right. \\ \left. 0, \frac{(N-2)^{\frac{1}{2}}(\theta_U - \theta_L)}{2\sigma N^{-\frac{1}{2}}(w_1 w_2)^{-\frac{1}{2}}(t_{1-\alpha}(N-2))} \right)$$

where $Q(\cdot, \cdot; \cdot, \cdot)$ is Owen's Q function, defined in the "Common Notation" section on page 3798.

**Multiplicative Equivalence Test for Mean Ratio with Lognormal Data
(TEST=EQUIV_RATIO)**

The lognormal case is handled by re-expressing the analysis equivalently as a normality-based test on the log-transformed data, using properties of the lognormal distribution as discussed in Johnson and Kotz (1970, chapter 14). The approaches in the “Additive Equivalence Test for Mean Difference with Normal Data (TEST=EQUIV_DIFF)” section on page 3830 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:

$$\begin{aligned} \text{power} = & Q_{N-2} \left((-t_{1-\alpha}(N-2)), \frac{\log\left(\frac{\gamma_T}{\gamma_R}\right) - \log(\theta_U)}{\sigma^* N^{-\frac{1}{2}}(w_1 w_2)^{-\frac{1}{2}}}; \right. \\ & \left. 0, \frac{(N-2)^{\frac{1}{2}}(\log(\theta_U) - \log(\theta_L))}{2\sigma^* N^{-\frac{1}{2}}(w_1 w_2)^{-\frac{1}{2}}(t_{1-\alpha}(N-2))} \right) - \\ & Q_{N-2} \left((t_{1-\alpha}(N-2)), \frac{\log\left(\frac{\gamma_T}{\gamma_R}\right) - \log(\theta_L)}{\sigma^* N^{-\frac{1}{2}}(w_1 w_2)^{-\frac{1}{2}}}; \right. \\ & \left. 0, \frac{(N-2)^{\frac{1}{2}}(\log(\theta_U) - \log(\theta_L))}{2\sigma^* N^{-\frac{1}{2}}(w_1 w_2)^{-\frac{1}{2}}(t_{1-\alpha}(N-2))} \right) \end{aligned}$$

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 “Common Notation” section on page 3798.

Confidence Interval for Mean Difference (CI=DIFF)

This analysis of precision applies to the standard t -based confidence interval:

$$\begin{aligned} & \left[(\bar{x}_2 - \bar{x}_1) - t_{1-\frac{\alpha}{2}}(N-2) \frac{s_p}{\sqrt{Nw_1w_2}}, \right. \\ & \quad \left. (\bar{x}_2 - \bar{x}_1) + t_{1-\frac{\alpha}{2}}(N-2) \frac{s_p}{\sqrt{Nw_1w_2}} \right], \quad \text{2-sided} \\ & \left[(\bar{x}_2 - \bar{x}_1) - t_{1-\alpha}(N-2) \frac{s_p}{\sqrt{Nw_1w_2}}, \infty \right), \quad \text{upper 1-sided} \\ & \left(-\infty, (\bar{x}_2 - \bar{x}_1) + t_{1-\alpha}(N-2) \frac{s_p}{\sqrt{Nw_1w_2}} \right], \quad \text{lower 1-sided} \end{aligned}$$

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,

$$\text{half-width} = \begin{cases} t_{1-\frac{\alpha}{2}}(N-2) \frac{s_p}{\sqrt{Nw_1w_2}}, & \text{2-sided} \\ t_{1-\alpha}(N-2) \frac{s_p}{\sqrt{Nw_1w_2}}, & \text{1-sided} \end{cases}$$

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):

$$\begin{aligned} \Pr(\text{half-width} \leq h) &= \begin{cases} P\left(\chi^2(N-2) \leq \frac{h^2 N(N-2)(w_1w_2)}{\sigma^2(t_{1-\frac{\alpha}{2}}^2(N-2))}\right), & \text{2-sided} \\ P\left(\chi^2(N-2) \leq \frac{h^2 N(N-2)(w_1w_2)}{\sigma^2(t_{1-\alpha}^2(N-2))}\right), & \text{1-sided} \end{cases} \\ \Pr(\text{half-width} \leq h \mid \text{validity}) &= \begin{cases} \left(\frac{1}{1-\alpha}\right) 2 \left[Q_{N-2}\left((t_{1-\frac{\alpha}{2}}(N-2)), 0; 0, b_2\right) - Q_{N-2}(0, 0; 0, b_2) \right], & \text{2-sided} \\ \left(\frac{1}{1-\alpha}\right) Q_{N-2}\left((t_{1-\alpha}(N-2)), 0; 0, b_2\right), & \text{1-sided} \end{cases} \end{aligned}$$

where

$$\begin{aligned} b_2 &= \frac{h(N-2)^{\frac{1}{2}}}{\sigma(t_{1-\frac{\alpha}{2}}(N-2))N^{-\frac{1}{2}}(w_1w_2)^{-\frac{1}{2}}} \\ c &= \text{number of sides} \end{aligned}$$

and $Q(\cdot, \cdot; \cdot, \cdot)$ is Owen’s Q function, defined in the “[Common Notation](#)” section on page 3798.

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
λ_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
τ	=	post-accrual 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 parameterization:

$$h_j(t) = \begin{cases} \lambda_j \\ \lambda_1 R \\ \frac{-\log(\frac{1}{2})}{m_j} \\ \frac{-\log(S_j(1))}{X_j(1)} \\ \frac{-\log(S_1(1))}{X_1(1)} R \end{cases}$$

For a piecewise linear curve, define the following additional notation:

$$\begin{aligned} t_i^- &= \text{largest input time } X \text{ such that } X \leq t_i \\ t_i^+ &= \text{smallest input time } X \text{ such that } X > t_i \end{aligned}$$

The hazard is computed 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:

$$\begin{aligned} N_j(0) &= Nw_j \\ N_j(i+1) &= N_j(i) \left[1 - h_j(t_i) \left(\frac{1}{b}\right) - \Psi_j(t_i) \left(\frac{1}{b}\right) - \left(\frac{1}{b(T + \tau - t_i)}\right) 1_{\{t_i > \tau\}} \right] \end{aligned}$$

Define θ_i as the ratio of hazards and ϕ_i as the ratio of expected numbers at risk for time t_i :

$$\begin{aligned} \theta_i &= \frac{h_2(t_i)}{h_1(t_i)} \\ \phi_i &= \frac{N_2(i)}{N_1(i)} \end{aligned}$$

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

$$\text{power} = \begin{cases} \Phi \left(-N^{\frac{1}{2}} E^* - z_{1-\alpha} \right), & \text{upper 1-sided} \\ \Phi \left(N^{\frac{1}{2}} E^* - z_{1-\alpha} \right), & \text{lower 1-sided} \\ \Phi \left(-N^{\frac{1}{2}} E^* - z_{1-\frac{\alpha}{2}} \right) + \Phi \left(N^{\frac{1}{2}} E^* - z_{1-\frac{\alpha}{2}} \right), & \text{2-sided} \end{cases}$$

Note that the upper and lower 1-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 2-group analyses, the lower side.

For the 1-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 2-sided case, the solution for N is obtained by numerically inverting the power equation.

Examples

Example 60.1. One-Way ANOVA

This example deals with the same situation as in Example 36.1 on page 2169 of Chapter 36, “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 race. 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 60.27. You are least familiar with the LZ1 drink and hence decide to consider a range of reasonable values for that mean.

Table 60.27. 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 60.28 with appropriate contrast coefficients.

Table 60.28. 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 60.27. 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 60.27](#) 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 a vertical bar (|). See the [“Specifying Value Lists in Analysis Statements”](#) section on page 3791 for more details on crossed and matched notations for grouped values. The contrasts in [Table 60.28](#) are specified with the `CONTRAST` option, 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 `NULL=` and `SIDES=` options specify a 2-sided t test of the contrast equal to 0. See [Output 60.1.1](#) for the output.

Output 60.1.1. 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 60.1.1](#) 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 60.1.1](#) 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 NFRAC 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.

```
proc power plotonly;
  onewayanova
    groupmeans = 35.6 | 33.7 | 30.2 | 29 28 | 25.9
    stdddev = 3.75
```

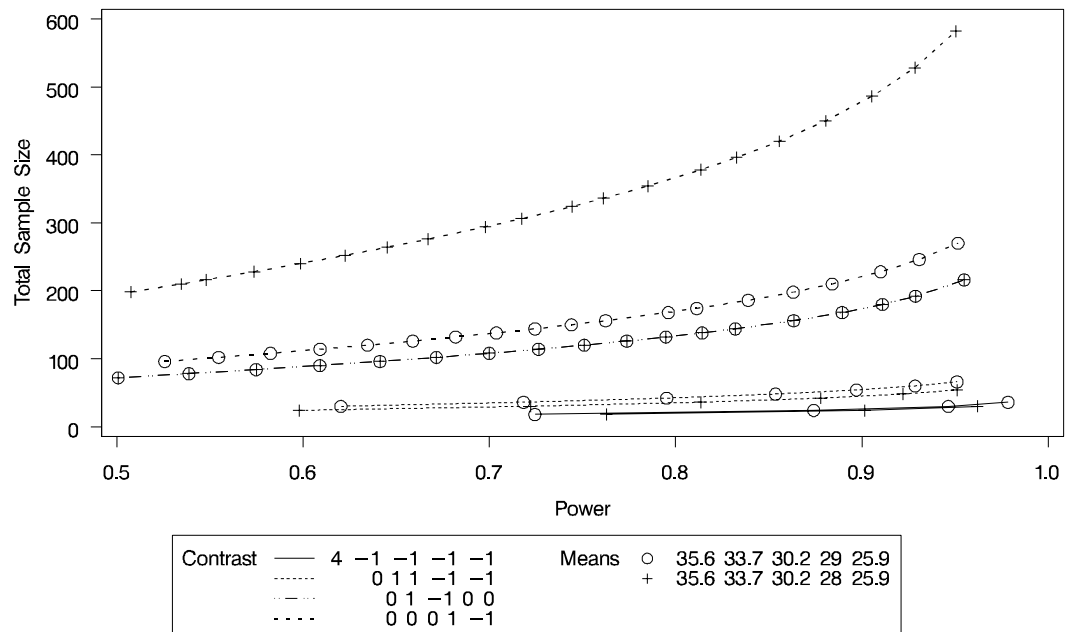
```

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;

```

See [Output 60.1.2](#) for the resulting plot.

Output 60.1.2. Plot of Sample Size versus Power for One-Way ANOVA Contrasts



In [Output 60.1.2](#), 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 60.1.2](#) 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 correspond 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 dif-

ferent comparisons). In the ONEWAYANOVA statement, identify power as the result (POWER=.), and specify NTOTAL=24. The following statements produce the plot:

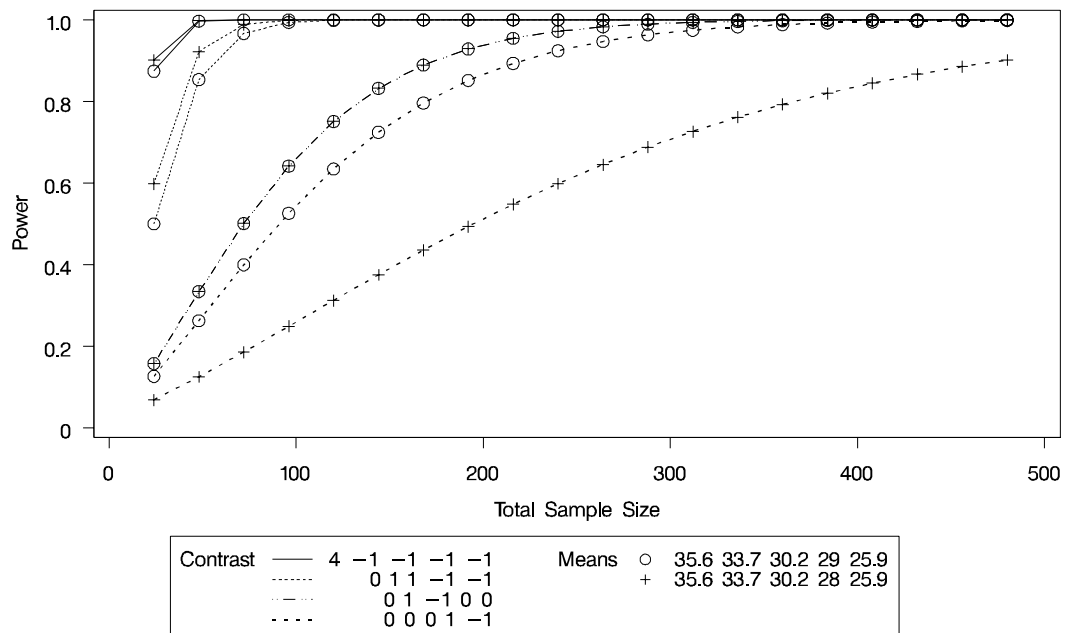
```
proc power plotonly;
  onewayanova
    groupmeans = 35.6 | 33.7 | 30.2 | 29 28 | 25.9
    stddev = 3.75
    groupweights = (2 1 1 1 1)
    alpha = 0.025
    ntotal = 24
    power = .
    contrast = (4 -1 -1 -1 -1) (0 1 1 -1 -1)
              (0 1 -1 0 0) (0 0 0 1 -1);
  plot x=n min=24 max=480;
run;
```

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.

See [Output 60.1.3](#) for the plot.

Output 60.1.3. Plot of Power versus Sample Size for One-Way ANOVA Contrasts



Although [Output 60.1.2](#) and [Output 60.1.3](#) surface essentially the same computations for practical power ranges, they each provide a different quick visual assessment. [Output 60.1.2](#) reveals the range of required sample sizes for powers of interest, and [Output 60.1.3](#) reveals the range of achieved powers for sample sizes of interest.

Example 60.2. 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 non-monotonic. 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 1 error rate) for discrete tests strays below the target level and varies with sample size. The power loss from a decrease in the Type 1 error rate may outweigh the power gain from an increase in sample size. The example discussed in this section demonstrates this “sawtooth” phenomenon. For additional discussion on the topic, refer to 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 1-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 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 1-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. The PROPORTION= option specifies your conjecture of 0.3 for the true proportion.

Output 60.2.1. 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	
Computed N Total		
Actual Power	N	Total
0.800		119

The results, shown in [Output 60.2.1](#), 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%, using the z test. A similar analysis ([Output 60.2.2](#)) reveals an approximate sample size of $N=129$ for the z test with continuity correction, which performed 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 60.2.2. 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
Computed N Total		
Actual Power	N Total	
0.801	129	

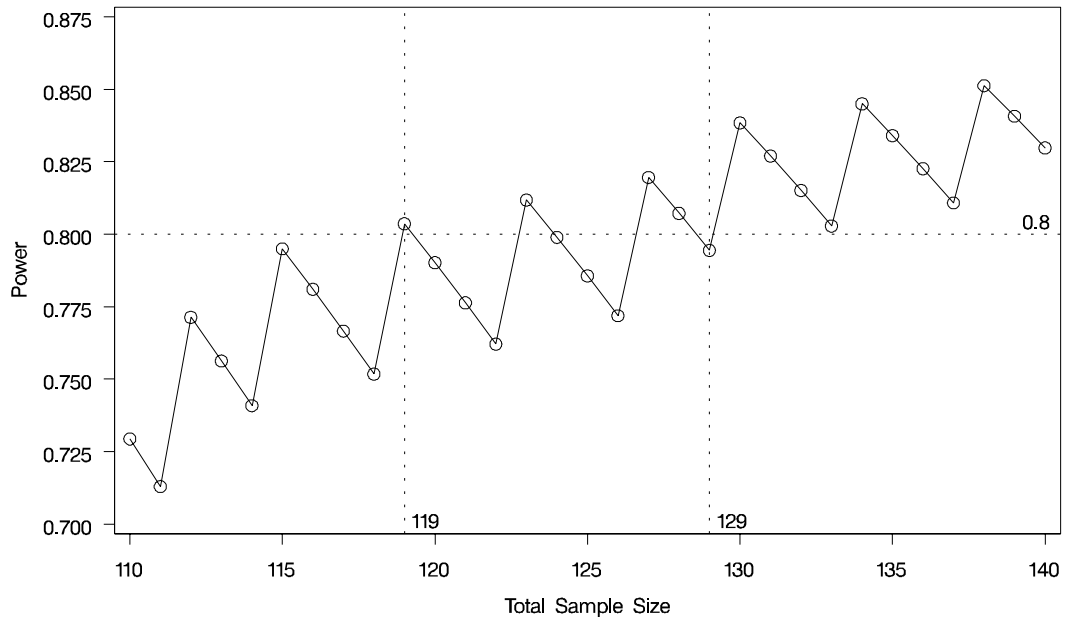
Based on the approximate sample size results, you decide to explore the power of the exact binomial test for sample sizes between 110 and 140. The following statements produce the plot:

```
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 60.2.3](#) shows the plot.

Output 60.2.3. Plot of Power versus Sample Size for Exact Binomial Test



Note the sawtooth pattern in [Output 60.2.3](#). 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 may 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
```

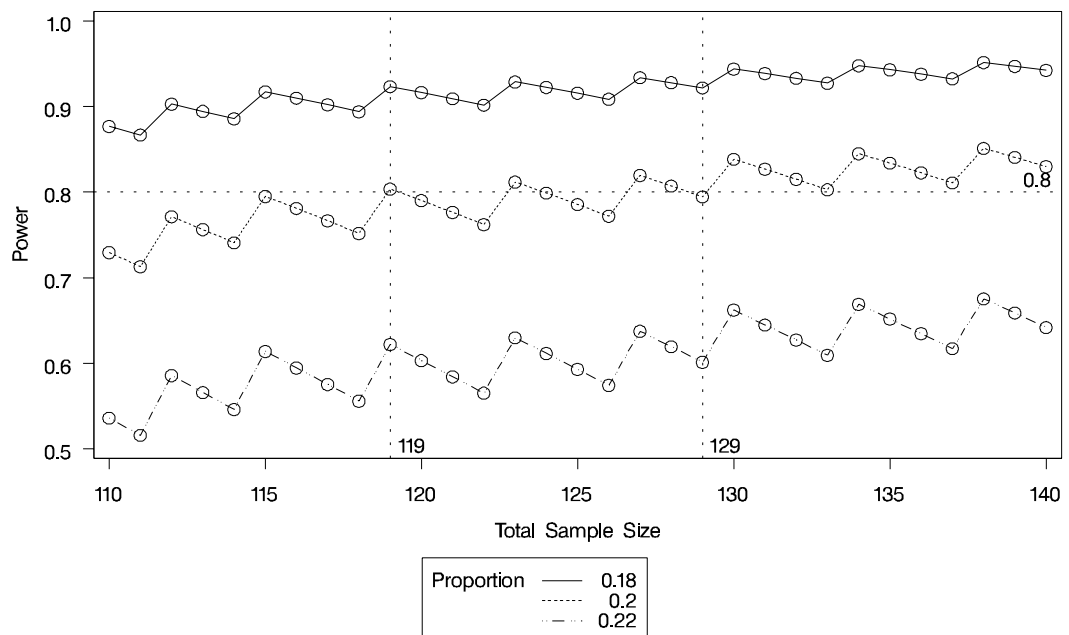
```

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 60.2.4 shows the plot.

Output 60.2.4. 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 0.22, and as low as 0.62 if the proportion is 0.18. 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 60.2.3 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 including 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 60.2.5 shows the plot data.

Output 60.2.5. Numerical Content of Plot

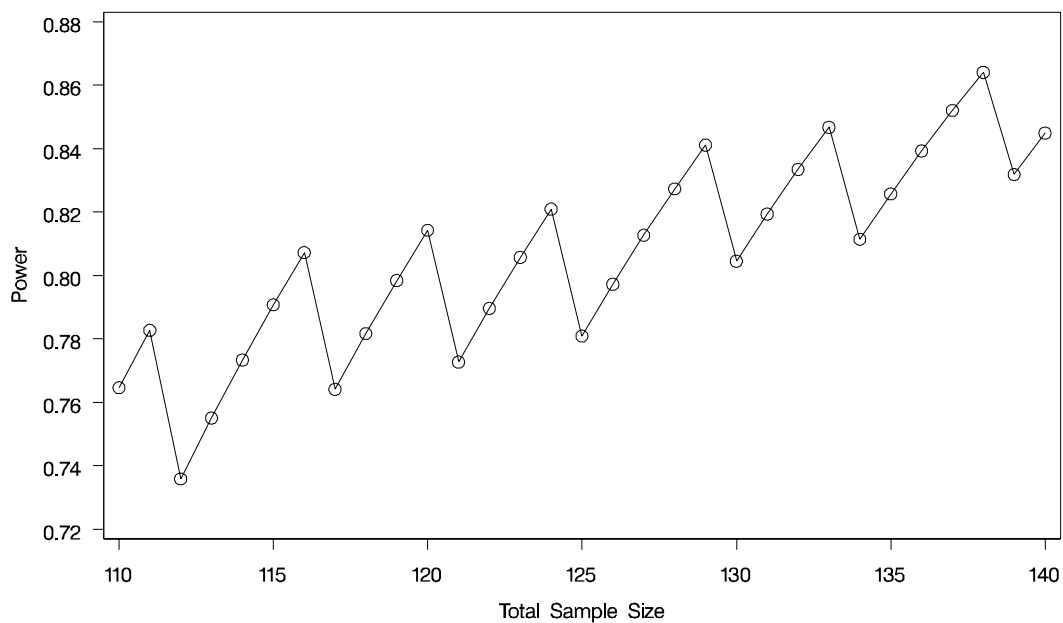
Obs	NTotal	Lower CritVal	Alpha	Power
1	110	24	0.0356	0.729
2	111	24	0.0313	0.713
3	112	25	0.0446	0.771
4	113	25	0.0395	0.756
5	114	25	0.0349	0.741
6	115	26	0.0490	0.795
7	116	26	0.0435	0.781
8	117	26	0.0386	0.767
9	118	26	0.0341	0.752
10	119	27	0.0478	0.804
11	120	27	0.0425	0.790
12	121	27	0.0377	0.776
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 α 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 α 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 60.2.3](#) 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;
```

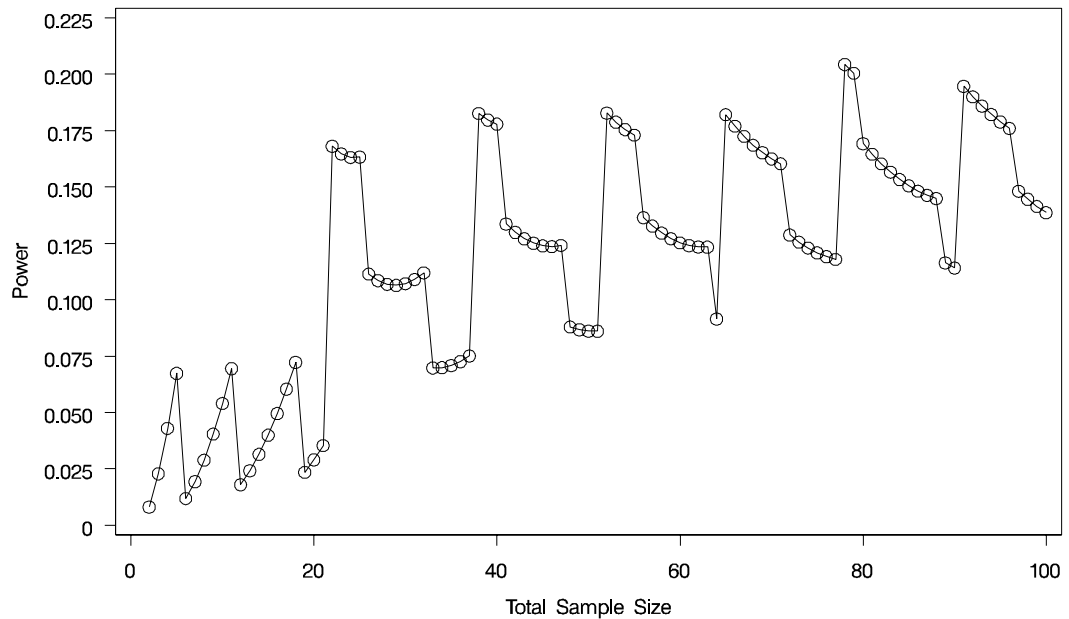
The resulting plot is shown in [Output 60.2.6](#).

Output 60.2.6. Plot of Power versus Sample Size for Another 1-Sided Test

Finally, 2-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 2-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;
```

The resulting plot is shown in [Output 60.2.7](#).

Output 60.2.7. Plot of Power versus Sample Size for a 2-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 60.3. 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 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, 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 1-sided and 2-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 carry-over 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 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 using the PAIREDMEANS= and PAIREDSTDDEVS= options and the correlation using the CORR= option. Specify both 1- and 2-sided tests using the SIDES= option, the significance level using the ALPHA= option, and the sample size (in terms of number of pairs) 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
```

```

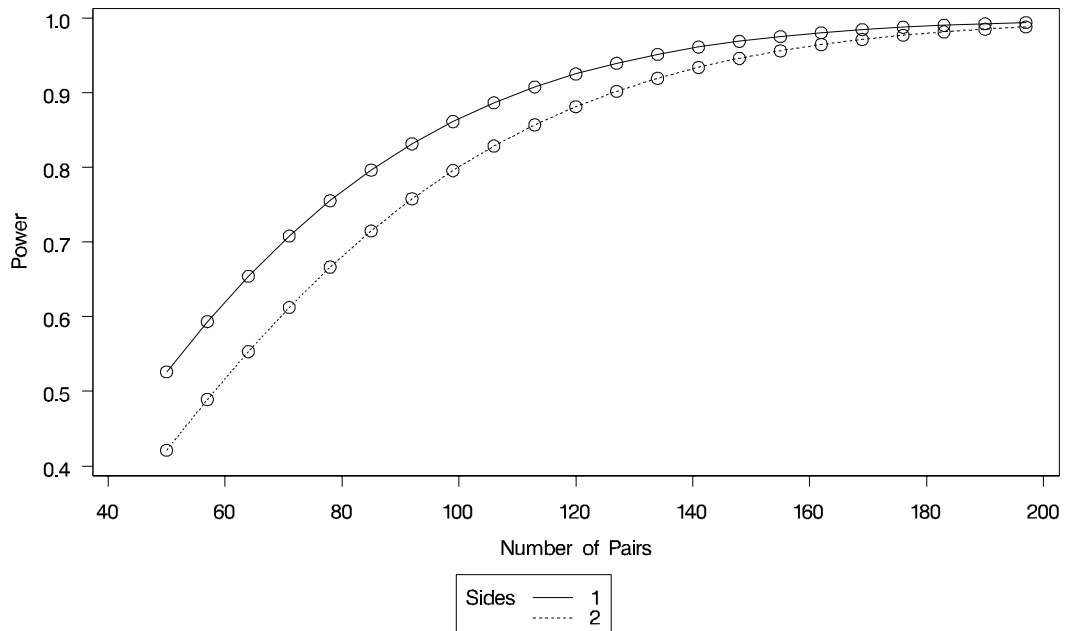
alpha          = 0.01
npairs         = 100
power          = .;
plot x=n min=50 max=200;
run;

```

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 60.3.1](#) and [Output 60.3.2](#).

Output 60.3.1. 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 60.3.2. Plot of Power versus Sample Size for Paired *t* Analysis of Crossover Design

The Computed Power table in [Output 60.3.1](#) shows that the power with 100 patients is about 0.8 for the 2-sided test and 0.87 for the 1-sided test with the alternative of larger Brantium mean. In [Output 60.3.2](#), 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 for the 1-sided test than the 2-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, 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 60.3.3](#).

Output 60.3.3. 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 60.4. 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 1-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, 1-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 60.8](#). 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.

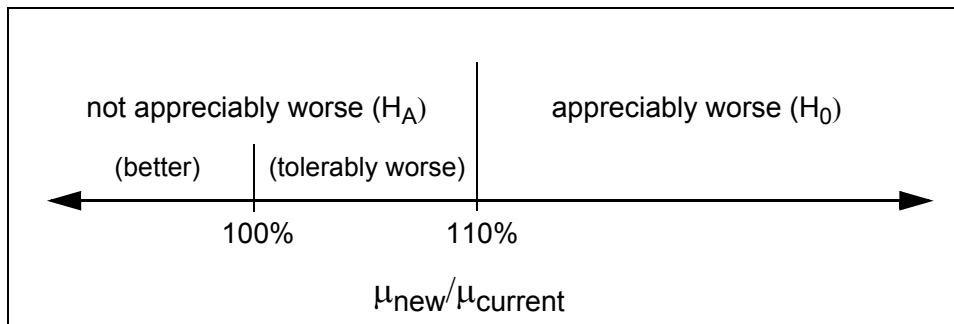


Figure 60.8. Hypotheses for the Pollutant Study

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 using laboratory models of the two processes and will be treated as independent lognormal observations with a coefficient of variation (σ/μ) 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 1 error here, so you set the Type 1 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 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 using the MEANRATIO= option. Use the NULLRATIO= option to specify the null mean ratio of 1.10. Specify SIDES=L to indicate a 1-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 using the ALPHA=, CV=, and GROUPNS= options. Generate a plot of power versus mean ratio by specifying the PLOT statement with X=EFFECT 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;
```

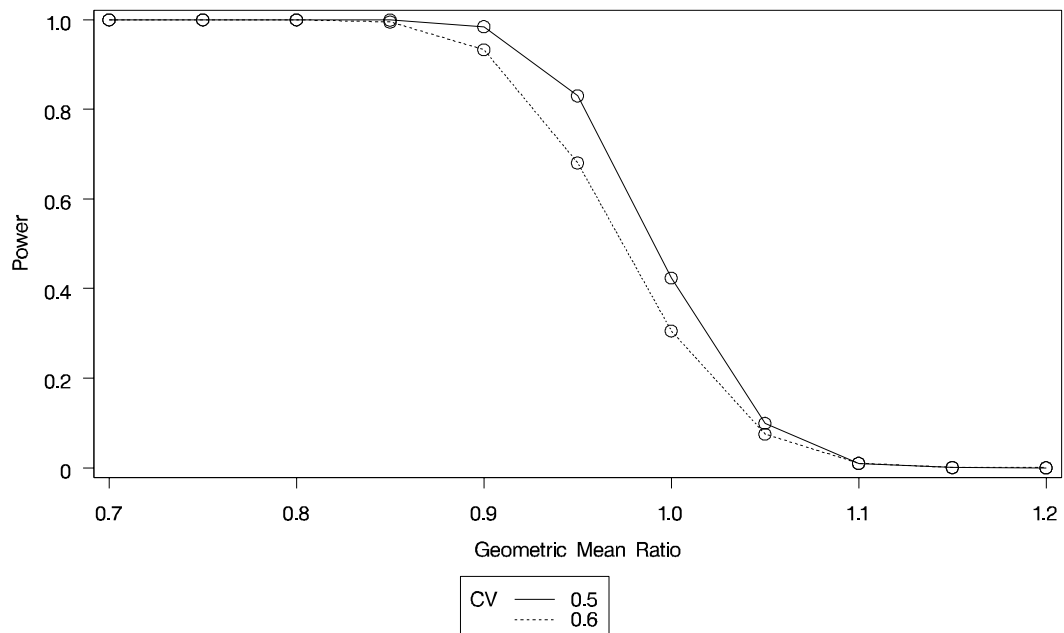
Note the use of SIDES=L, which forces computations for cases that need a rejection region that is opposite to the one providing the most one-tailed power; in this case, it is the lower tail. Such cases will show power that is less than the prescribed Type 1 error rate. The default option DIST=LOGNORMAL 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).

See the output in [Output 60.4.1](#) and [Output 60.4.2](#).

Output 60.4.1. 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				I
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 60.4.2. Plot of Power versus Mean Ratio for Noninferiority Test



The Computed Power table in [Output 60.4.1](#) 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 60.4.2](#), 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 60.5. 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, vitamins B₆ and B₁₂, 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 60.9 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 who are relatively higher than expected on tHcy will also be relatively higher than expected on PBI. The partial correlation quantifies that adjusted association just like a standard simple correlation does with the unadjusted linear association between two variables.

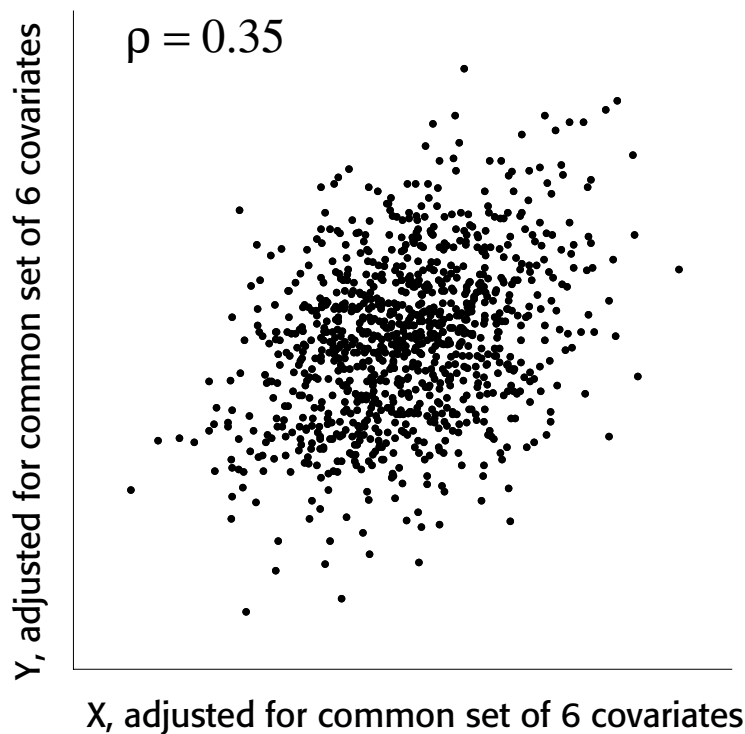


Figure 60.9. Partial Regression Plot

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 $N = 100$, 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;

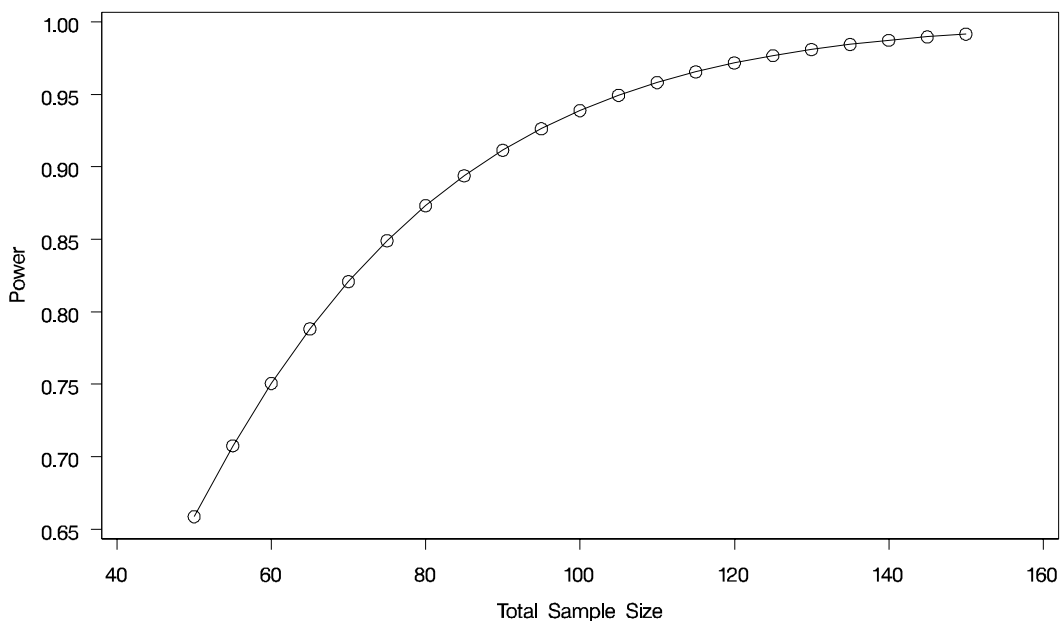
```

The `POWER=.` option identifies power as the parameter to compute. The `NFULLPREDICTORS=` option specifies 7 total predictors (not including the intercept), and the `NTESTPREDICTORS=` option indicates that 1 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 60.5.1](#) shows the output, and [Output 60.5.2](#) shows the plot.

Output 60.5.1. 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 60.5.2. Plot of Power versus Sample Size for Multiple Regression

For the sample size $N = 100$, the study is almost balanced with respect to Type 1 and Type 2 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 1-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 NPVARS= option specifies that 6 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 1-sided test.

Output 60.5.3 shows the output.

Output 60.5.3. 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 1 and Type 2 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 60.5.4. Sample Size Determination for Fisher's z Test

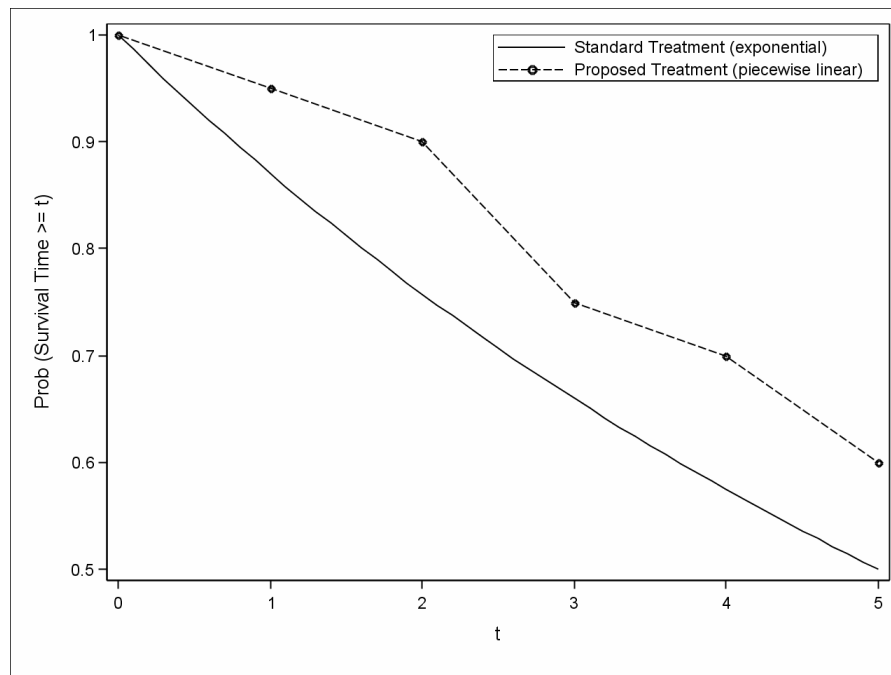
The POWER Procedure				
Fisher's z Test for Pearson Correlation				
Fixed Scenario Elements				
Distribution			Fisher's z transformation of r	
Method			Normal approximation	
Number of Sides				1
Null Correlation				0.2
Number of Variables Partialled Out				6
Correlation				0.35
Nominal Alpha				0.05
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 60.5.4](#) reveal a required sample size of 417 to achieve a power of 0.95 and 280 to achieve a power of 0.85.

Example 60.6. 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 2-sided test with $\alpha = 0.05$ 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 [Output 60.6.1](#). 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 60.6.1. 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 [Output 60.6.1](#). 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 2-sided test with $\alpha = 0.05$.

Output 60.6.2 shows the results.

Output 60.6.2. 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	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 60.7. 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 “[Overview of Power Concepts](#)” section on page 3788, 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;
```

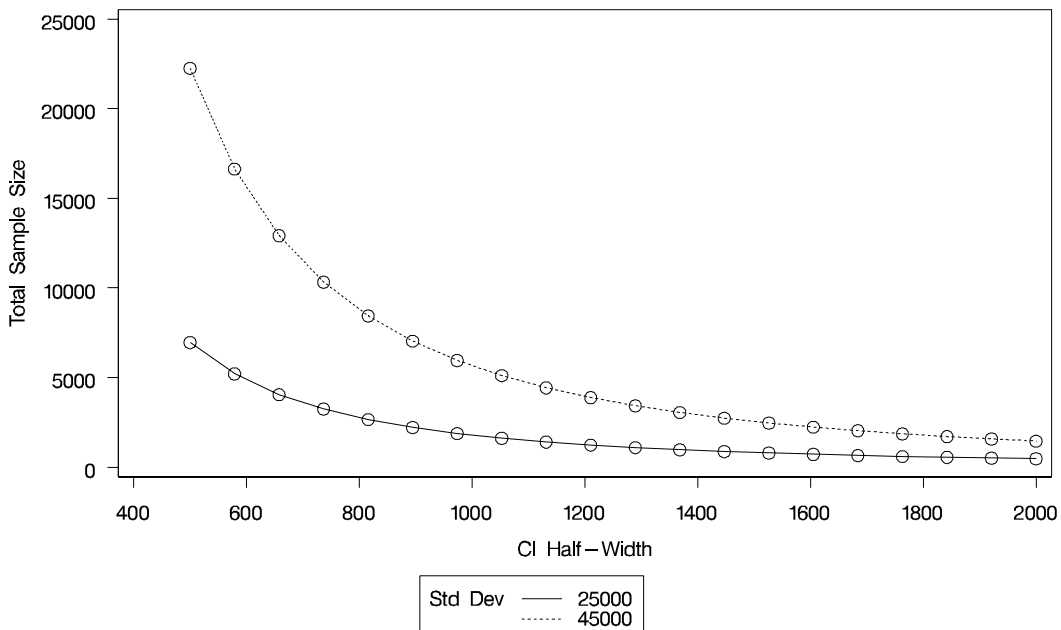
The NTOTAL=. option identifies sample size as the parameter to compute. The ALPHA=0.1 option specifies a confidence level of $1 - \alpha = 0.9$. The HALFWIDTH= option specifies the target half-width, and the STDDEV= option specifies the conjectured standard deviation values. The PROBWIDTH= option specifies the desired probability of achieving the target precision. The default value PROBTYP=CONDITIONAL specifies that this probability is conditional on the true mean being captured by the interval. The default of SIDES=2 indicates a 2-sided interval.

[Output 60.7.1](#) shows the output, and [Output 60.7.2](#) shows the plot.

Output 60.7.1. 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 60.7.2. Plot of Sample Size vs. 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 over 20,000 simulations would be required for a half-width of 500 assuming the higher standard deviation.

Example 60.8. Customizing Plots

The example in this section 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 using a 2-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= option 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, 2-sided test, balanced design, and assumption of normally distributed data.

[Output 60.8.1](#) shows that the required sample size ranges from 60 to 382 depending on the unknown standard deviation and second mean.

Output 60.8.1. 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 Y= option, but not both. Use the X=POWER option in 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.

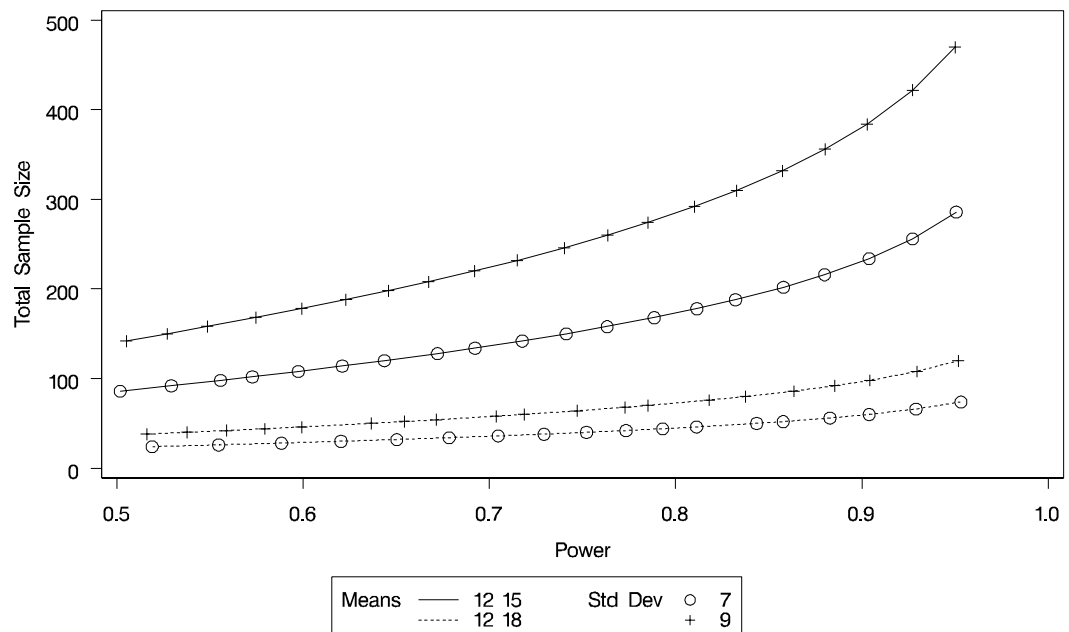
```
proc power plotonly;
  twosamplemeans test=diff
    groupmeans    = 12 | 15 18
    stddev        = 7 9
    power         = 0.9
    ntotal        = .;
  plot x=power min=0.5 max=0.95;
run;
```

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 60.8.2](#).

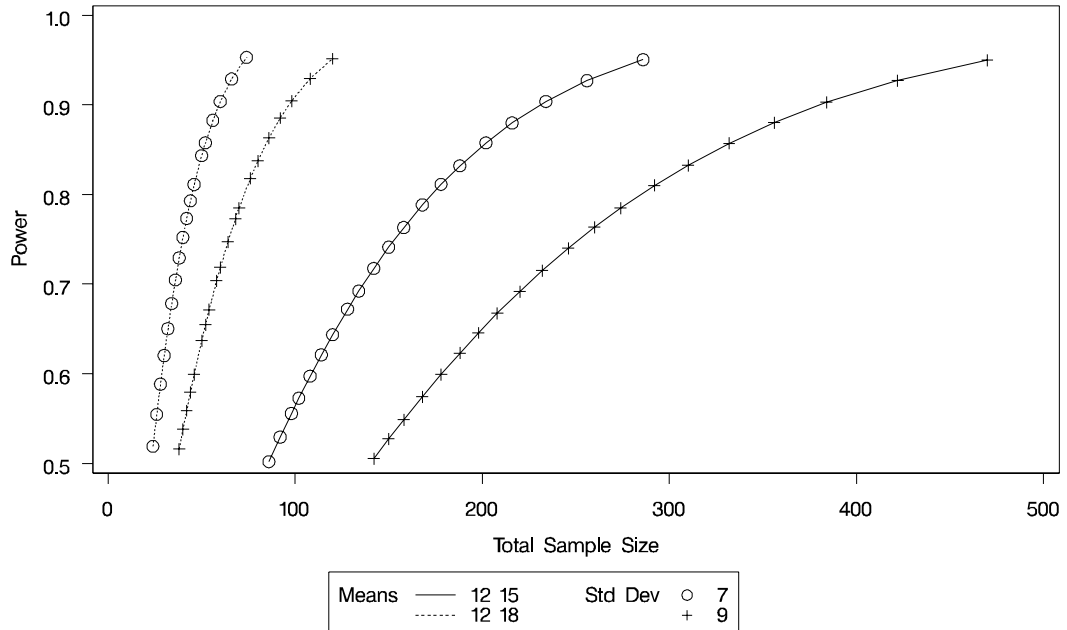
Output 60.8.2. Plot of Sample Size versus Power



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 60.8.3. Plot of Power versus Sample Size using First Strategy

Note that the resulting plot ([Output 60.8.3](#)) is essentially a mirror image of [Output 60.8.2](#). The axis ranges are set such that each curve in [Output 60.8.3](#) 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

- 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 to reflect this range:

```
proc power;
  twosamplemeans test=diff
    groupmeans   = 12 | 15 18
    stddev       = 7 9
```

```

power          = 0.5 0.95
ntotal        = .;
run;

```

Output 60.8.4 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 60.8.4. 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	

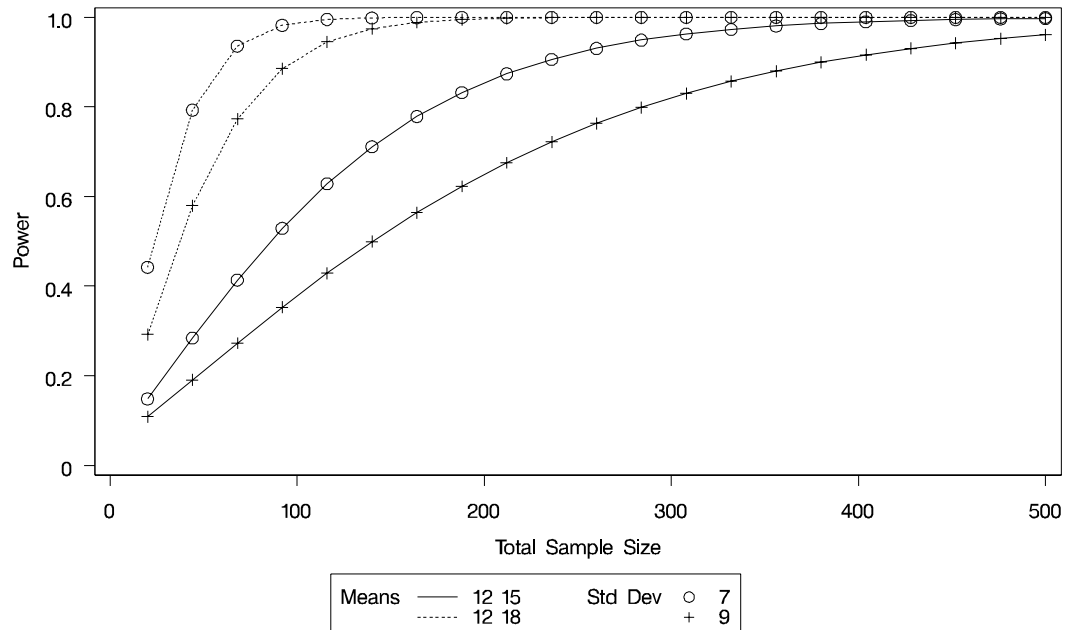
To plot power on the y-axis for sample sizes between 20 and 500, use the X=N option in the PLOT statement with MIN=20 and MAX=500:

```

proc power plotonly;
  twosamplemeans test=diff
    groupmeans = 12 | 15 18
    stddev     = 7 9
    power      = .
    ntotal     = 200;
  plot x=n min=20 max=500;
run;

```

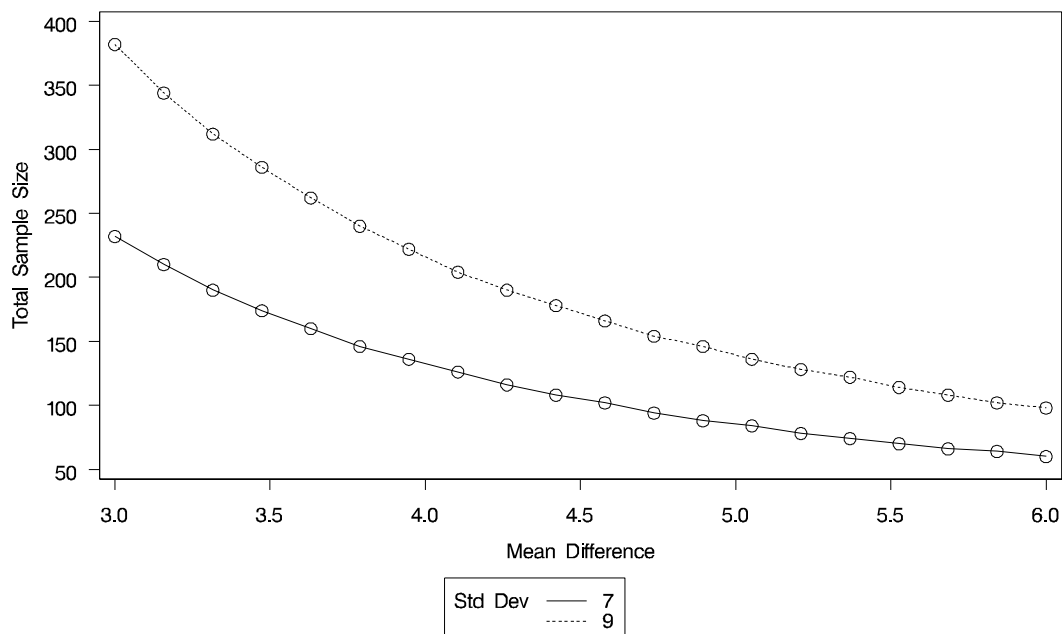
Each curve in the resulting plot in Output 60.8.5 covers at least a power range of 0.5 to 0.95.

Output 60.8.5. 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 60.8.6](#) shows how the required sample size decreases with increasing mean difference.

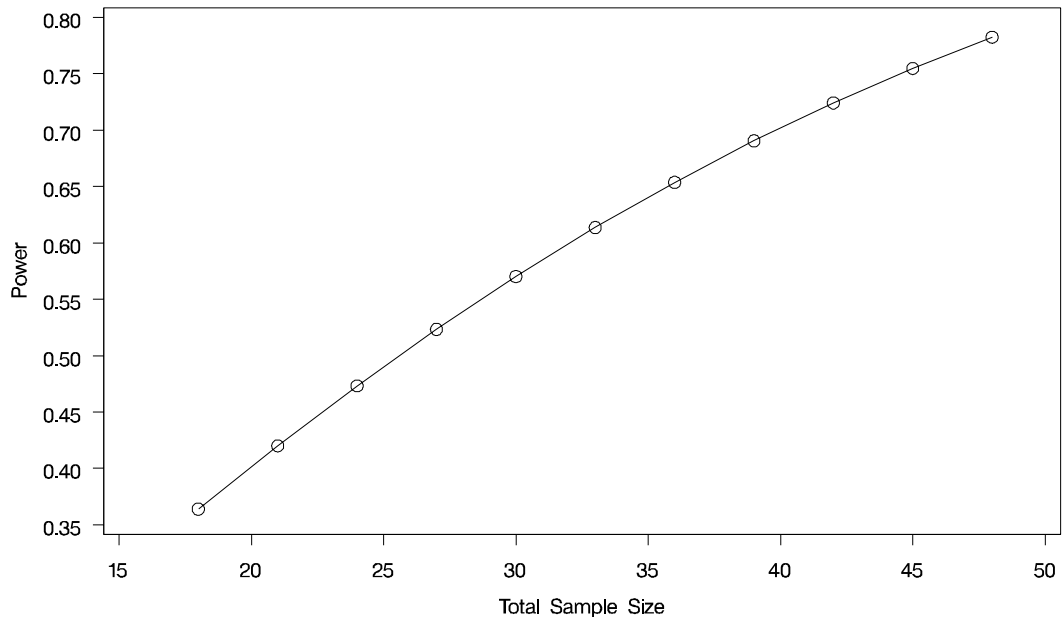
Output 60.8.6. Plot of Sample Size versus Mean Difference

Fine-Tuning a Sample Size Axis

Consider the following plot request for a sample size analysis similar to the one in [Output 60.8.1](#) 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 60.8.7](#)) appears to have only 11 points, and they range from 18 to 48.

Output 60.8.7. 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 may 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;
```

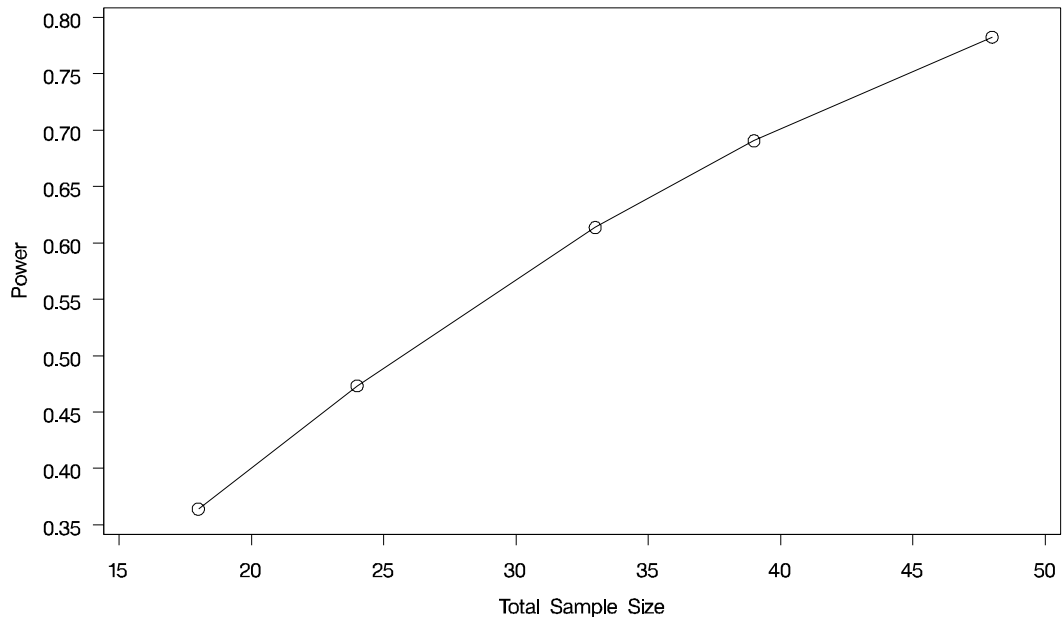
The output is shown in [Output 60.8.8](#).

Output 60.8.8. 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 60.8.9](#), created with the following statements.

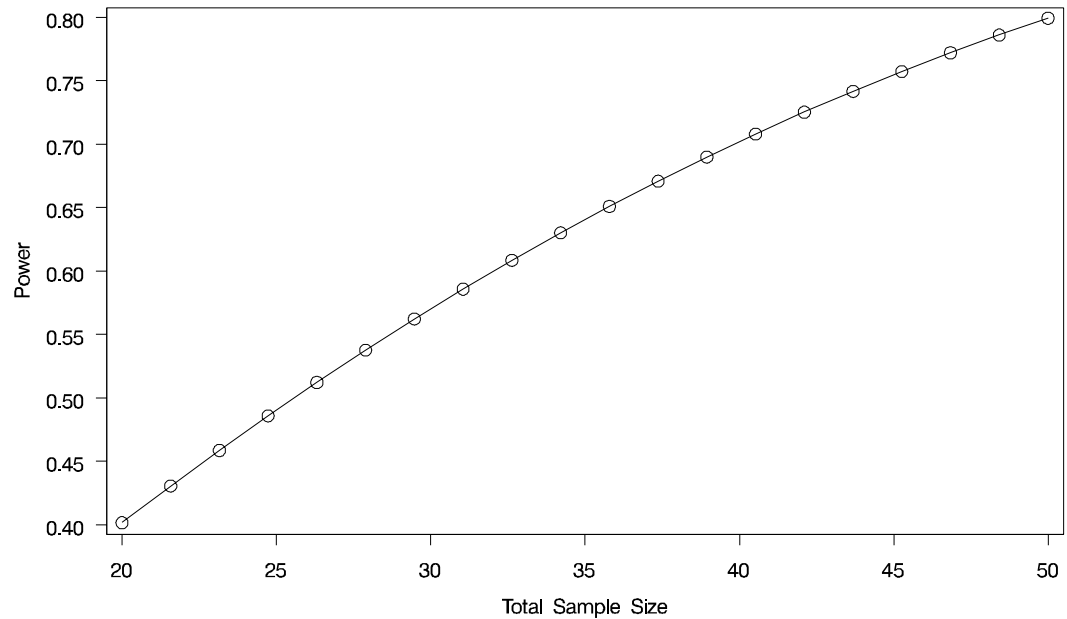
```
proc power plotonly;
  twosamplemeans test=diff
    groupmeans    = 12 | 18
    stddev        = 7
    groupweights  = 2 | 1
    power         = .
    ntotal        = 20;
  plot x=n min=20 max=50 npoints=5;
run;
```

Output 60.8.9. 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 60.8.10](#), 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 60.8.10. 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 [Output 60.8.7](#) 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

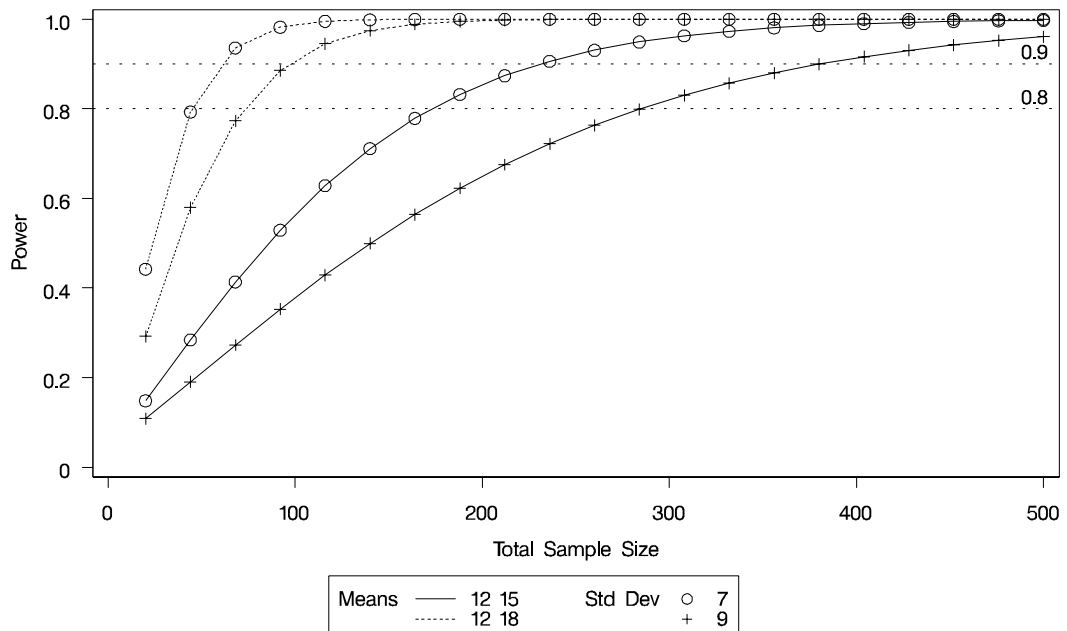
Suppose you want to add reference lines to highlight power=0.8 and power=0.9 on the plot in [Output 60.8.5](#). You can add simple reference lines using the YOPTS= option and REF= suboption in the PLOT statement to produce [Output 60.8.11](#), using the following statements.

```
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 60.8.11. 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:

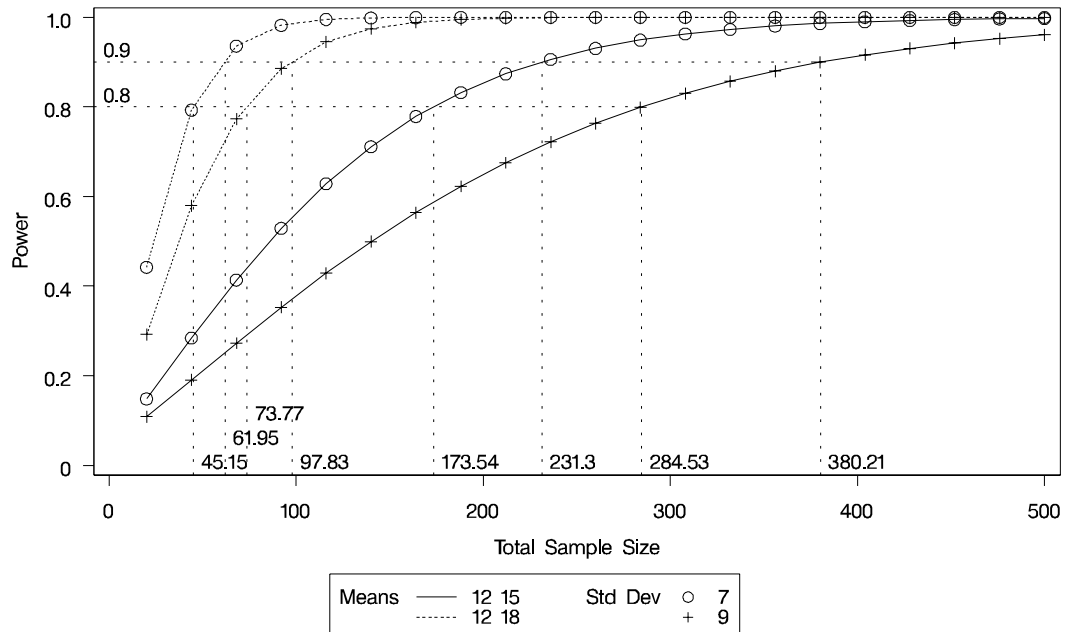
```

plot x=n min=20 max=500
yopts=(ref=0.8 0.9 crossref=yes);

```

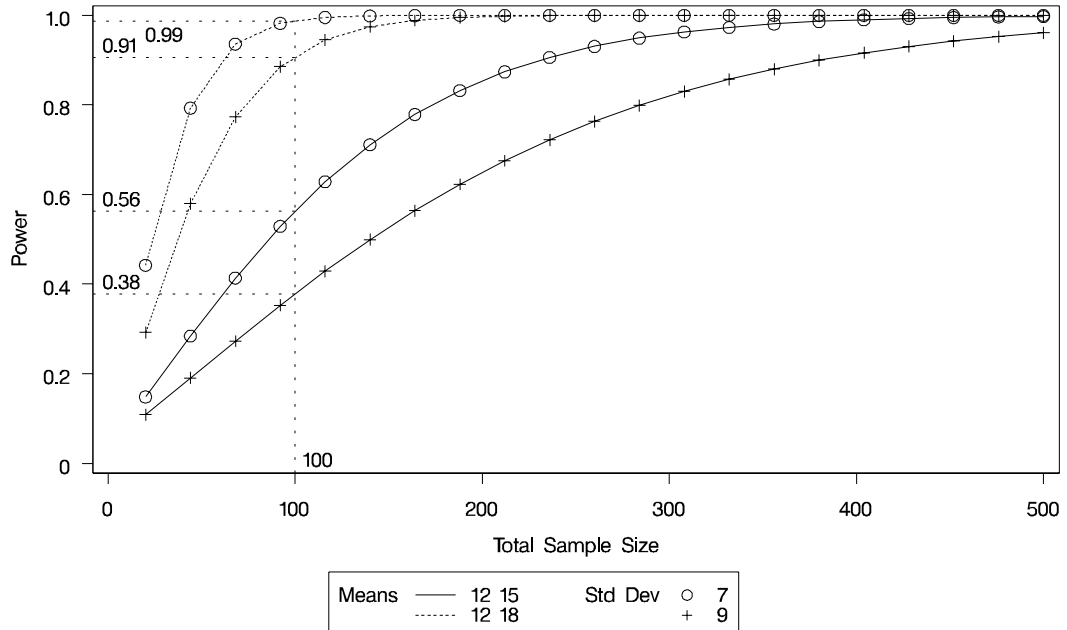
The resulting plot is shown in [Output 60.8.12](#).

Output 60.8.12. 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 60.8.13](#), which has crossing reference lines highlighting the sample size of 100.

```
plot x=n min=20 max=500
      xopts=(ref=100 crossref=yes);
```

Output 60.8.13. 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 wish 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).

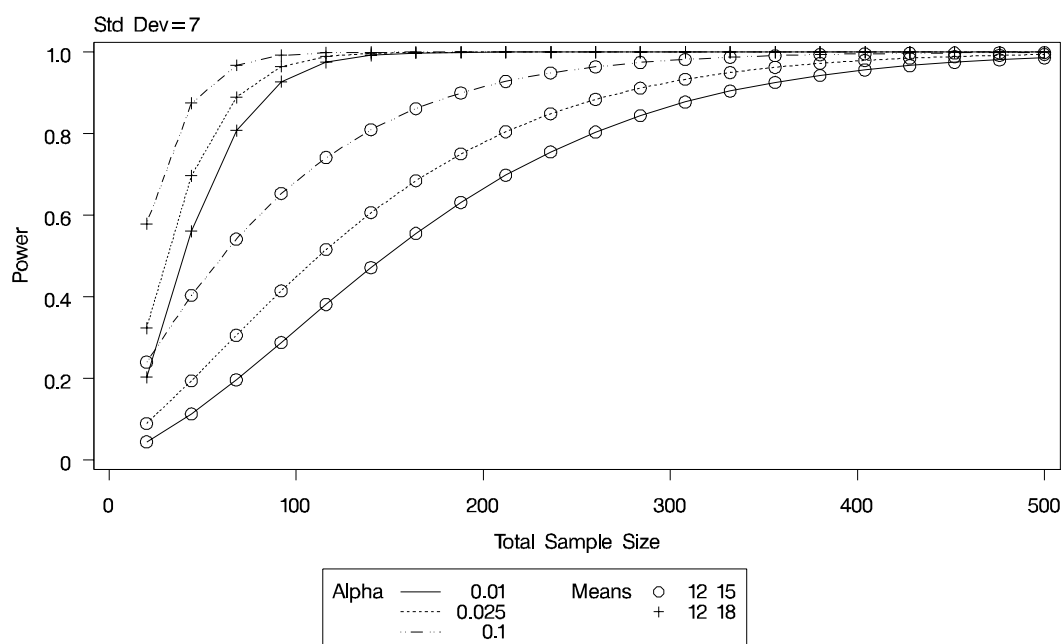
Suppose you supplement the sample size analysis in [Output 60.8.5](#) to include three values of alpha, using the following statements.

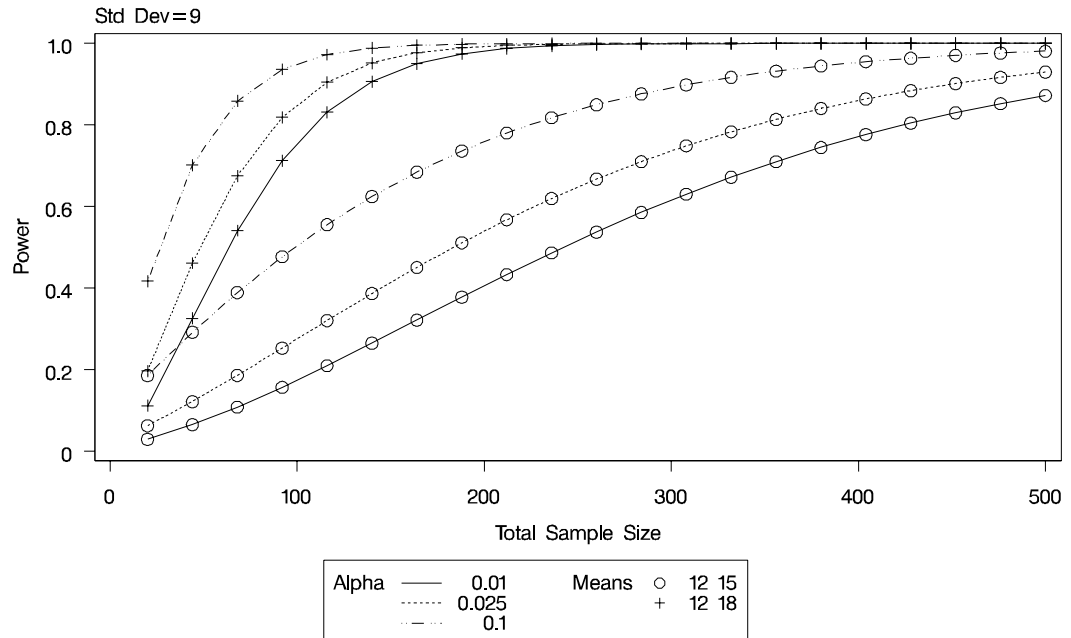
```
proc power plotonly;
  twosamplemeans test=diff
    groupmeans    = 12 | 15 18
    stddev        = 7 9
    alpha         = 0.01 0.025 0.1
    power         = .
    ntotal        = 100;
```

```
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 60.8.14](#) and [Output 60.8.15](#).

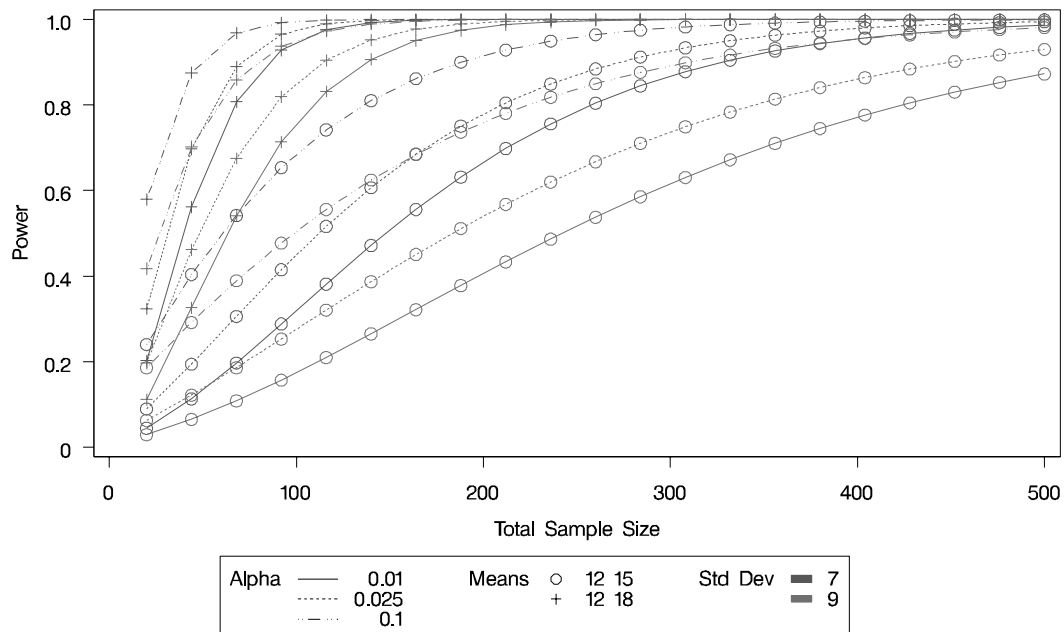
Output 60.8.14. Plot with Default VARY Settings: Panel 1 of 2



Output 60.8.15. Plot with Default VARY Settings: Panel 2 of 2

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 60.8.16](#).

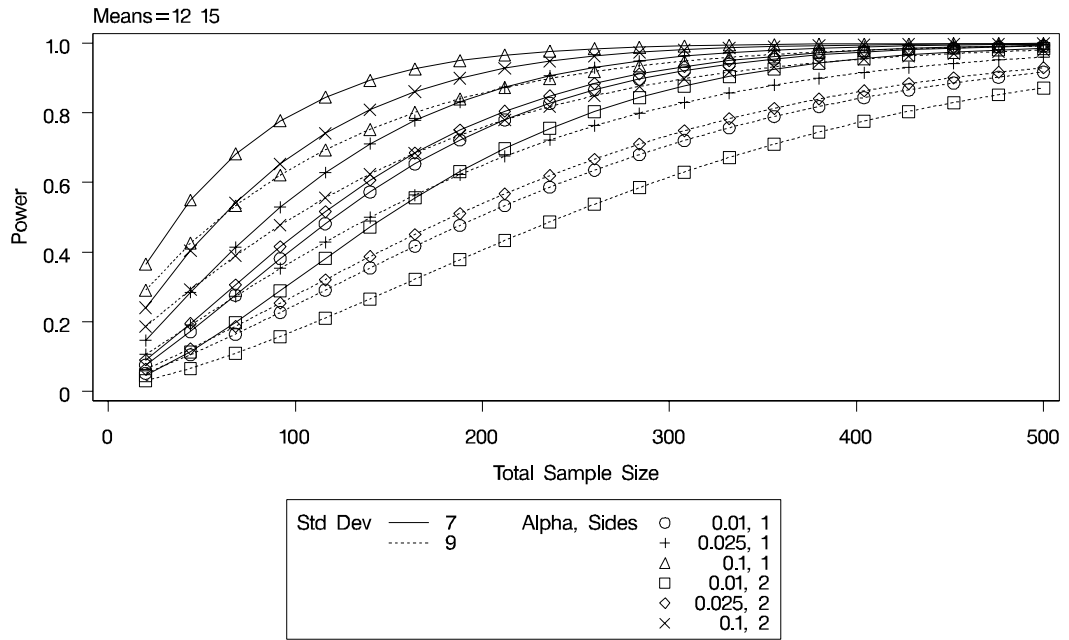
```
plot x=n min=20 max=500
    vary (linestyle, symbol, color);
```

Output 60.8.16. Plot with Varying Color Instead of Panel

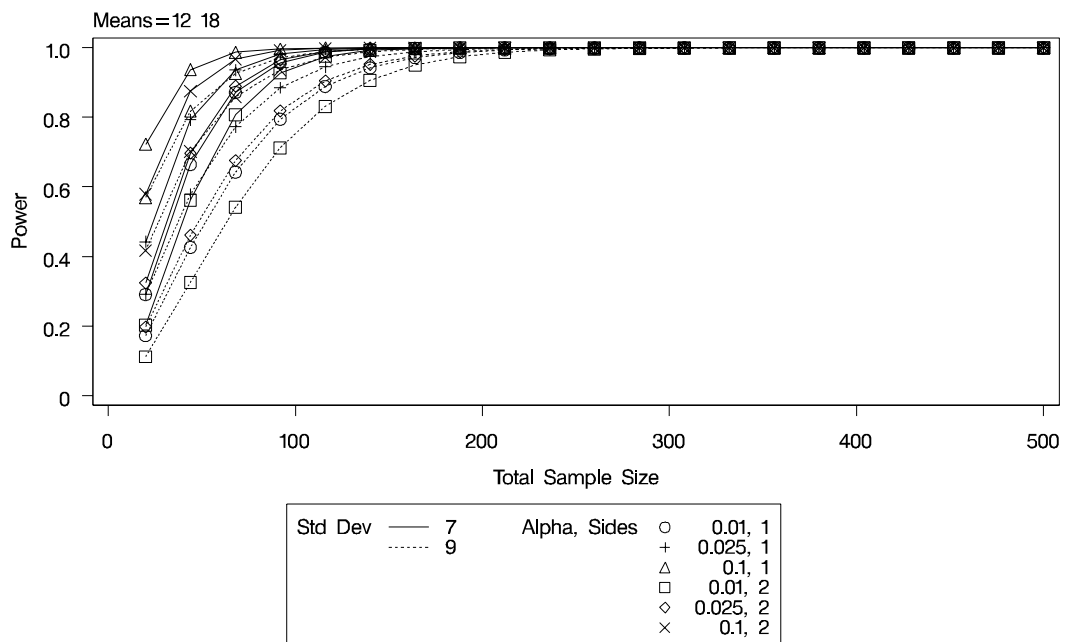
Finally, suppose you want to specify which features are used *and* which analysis parameters they are linked to. The following PLOT statement produces a two-panel plot (shown in [Output 60.8.17](#) and [Output 60.8.18](#)) in which line style varies by standard deviation, plotting symbol varies by both 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 60.8.17. Plot with Features Explicitly Linked to Parameters: Panel 1 of 2



Output 60.8.18. Plot with Features Explicitly Linked to Parameters: Panel 2 of 2



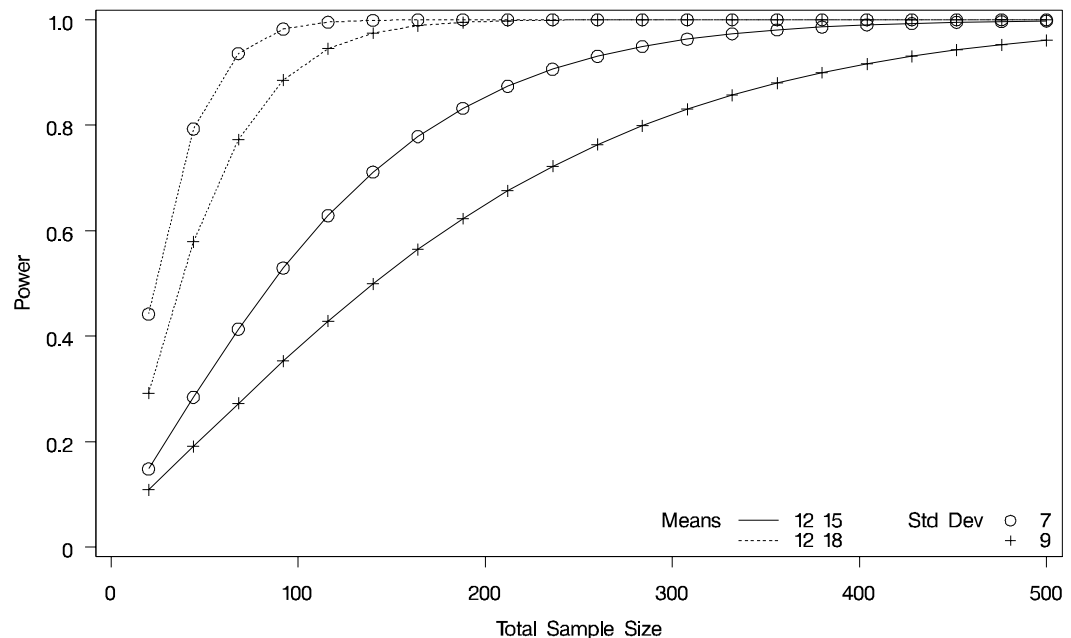
Choosing Key (Legend) Styles

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 60.8.5](#) demonstrates this style of key.

You can reproduce [Output 60.8.5](#) with the same key but a different location, inside the plotting region, using the POS=INSET option within the KEY=BYFEATURE option in the PLOT statement. The following statements product the plot in [Output 60.8.19](#).

```
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 60.8.19. Plot with a By-Feature Key Inside the Plotting Region

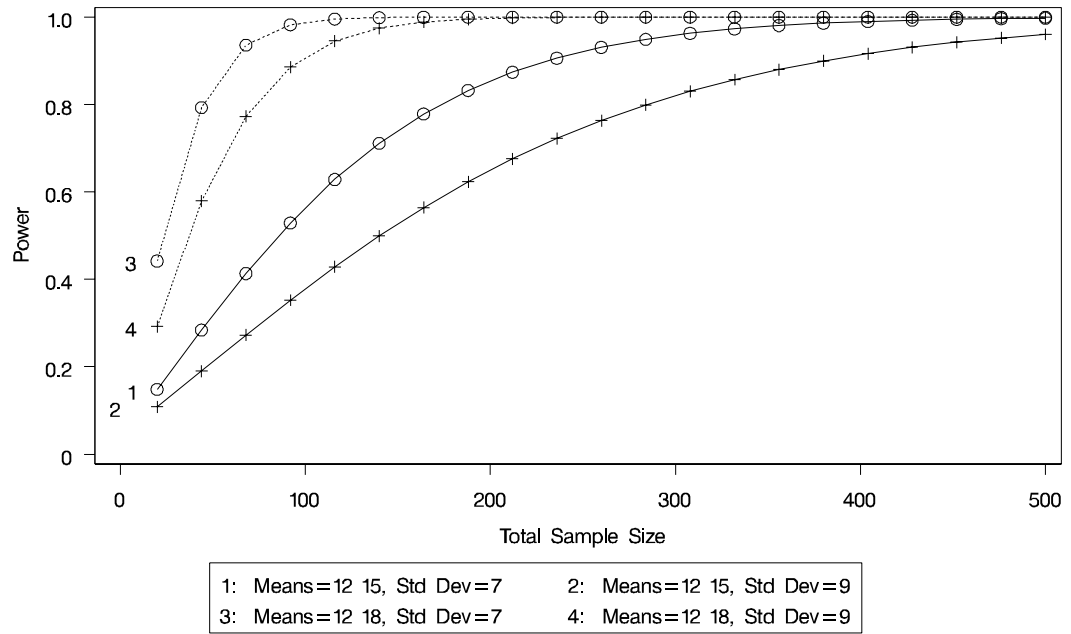


Alternatively, you can specify a key that identifies each individual curve separately by number using the KEY=BYCURVE option in the PLOT statement:

```
plot x=n min=20 max=500
  key = bycurve;
```

The resulting plot is shown in [Output 60.8.20](#).

Output 60.8.20. Plot with a Numbered By-Curve Key

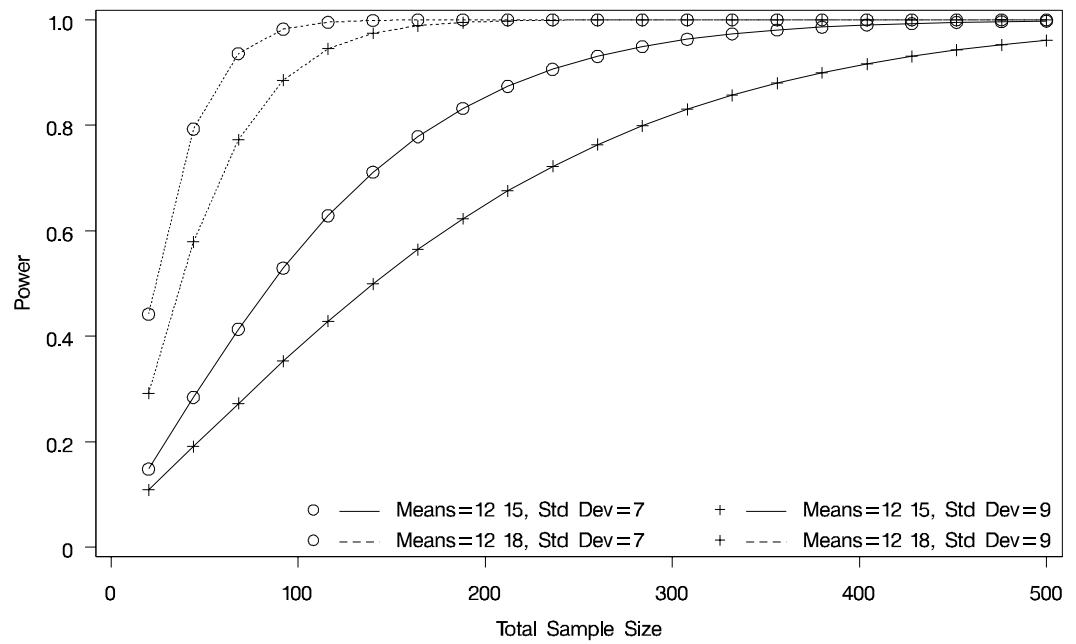


Use the `NUMBERS=OFF` option within the `KEY=BYCURVE` option to specify a nonnumbered key that identifies curves with samples of line styles, symbols, and colors:

```
plot x=n min=20 max=500
     key = bycurve(numbers=off pos=inset);
```

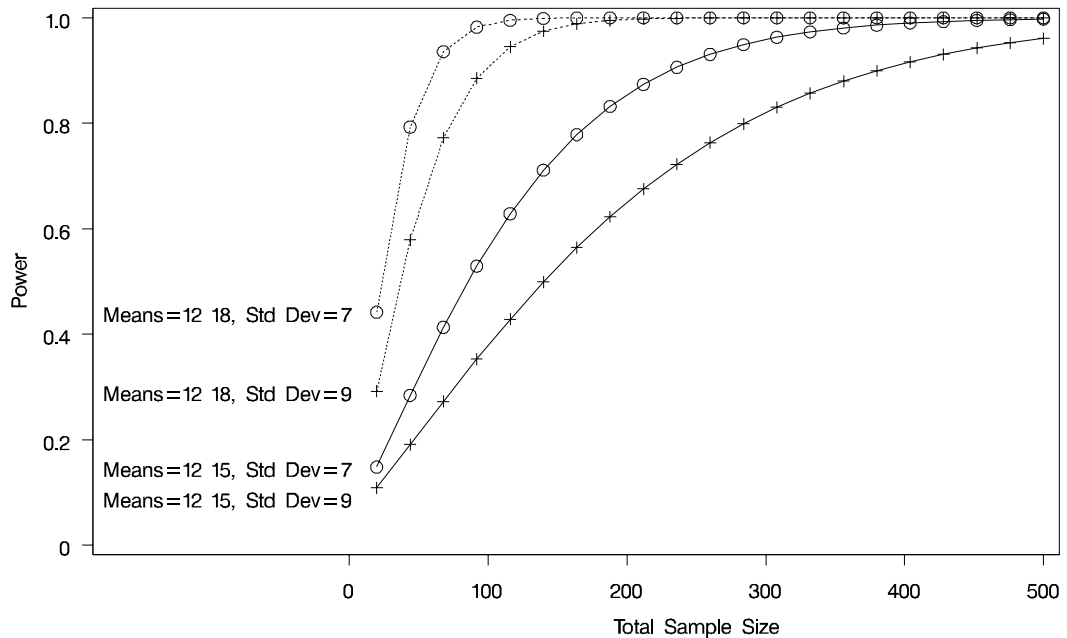
The `POS=INSET` suboption places the key within the plotting region. The resulting plot is shown in [Output 60.8.21](#).

Output 60.8.21. 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 60.8.22](#).

```
plot x=n min=20 max=500
     key = oncurves;
```

Output 60.8.22. 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 60.8.5](#) shows plotting symbols corresponding to computed points. The curves connecting these points are interpolated (as indicated by the INTERPOL= option in the PLOT statement).

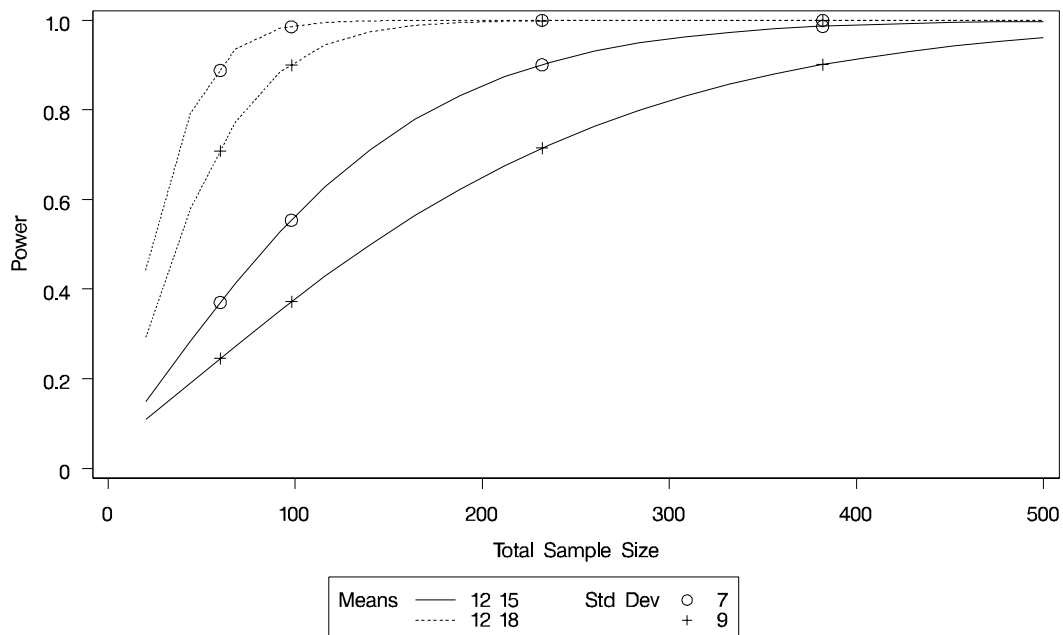
You can modify the locations of plotting symbols using the MARKERS= option in the plot statement. The MARKERS=ANALYSIS option places plotting symbols at locations corresponding to the input specified in the analysis statement preceding the PLOT statement. You may prefer this as an alternative to using reference lines to highlight specific points. For example, you can reproduce [Output 60.8.5](#), but with the plotting symbols located at the sample sizes shown in [Output 60.8.1](#), 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 60.8.23](#).

Output 60.8.23. Plot with MARKERS=ANALYSIS

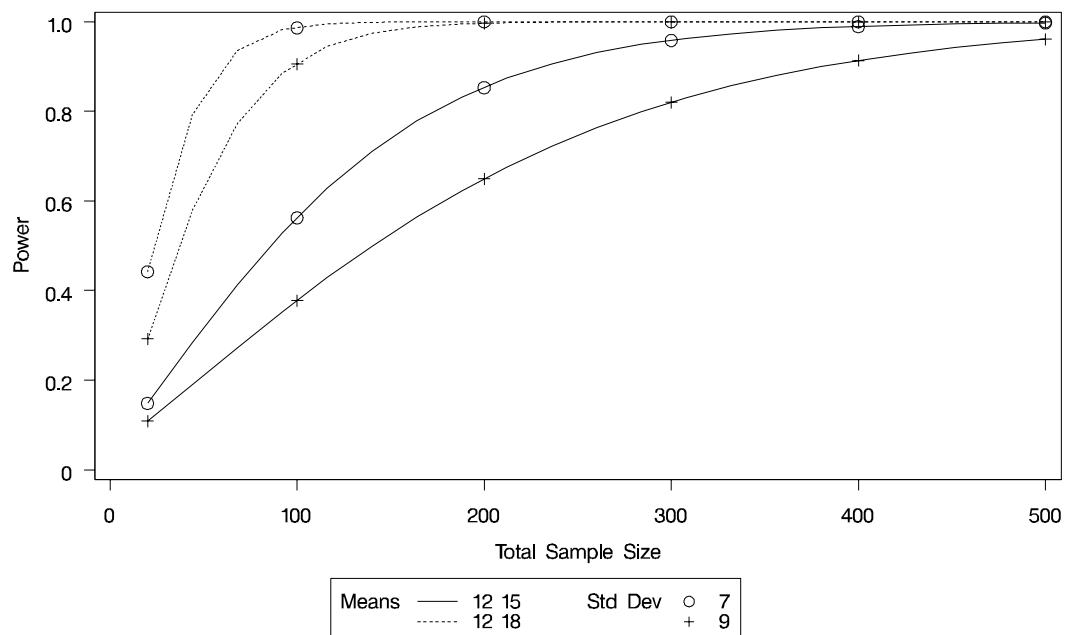


You can also use the MARKERS=NICE option to align symbols with the tick marks on one of the axes (the x-axis when the X= option is used, or the y-axis when the Y= is used):

```
plot x=n min=20 max=500
     markers=nice;
```

The plot created by this PLOT statement is shown in [Output 60.8.24](#).

Output 60.8.24. 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.

References

- Anderson, T.W. (1984), *An Introduction to Multivariate Statistical Analysis*, Second Edition, New York: John Wiley & Sons.
- Beal, S.L. (1989), "Sample Size Determination for Confidence Intervals on the Population Means and on the Difference between Two Population Means," *Biometrics*, 45, 969–977.
- Blackwelder, W.C. (1982), "'Proving the Null Hypothesis' in Clinical Trials," *Controlled Clinical Trials*, 3, 345–353.
- Cantor, A. B. (1997), *Extending SAS[®] Survival Analysis Techniques for Medical Research*, Cary, NC: SAS Institute Inc.
- Castelloe, J.M. (2000), "Sample Size Computations and Power Analysis with the SAS[®] System," *Proceedings of the Twenty-fifth Annual SAS Users Group International Conference*, Paper 265-25, Cary, NC: SAS Institute Inc.
- Castelloe, J.M. and O'Brien, R.G. (2001), "Power and Sample Size Determination for Linear Models," *Proceedings of the Twenty-sixth Annual SAS Users Group International Conference*, Paper 240-26. Cary, NC: SAS Institute Inc.

- Chernick, M.R. and Liu, C.Y. (2002), "The Saw-Toothed Behavior of Power Versus Sample Size and Software Solutions: Single Binomial Proportion Using Exact Methods," *The American Statistician*, 56, 149–155.
- Connor, R.J. (1987), "Sample Size for Testing Differences in Proportions for the Paired-Sample Design," *Biometrics*, 43, 207–211.
- Diegert, C. and Diegert, K.V. (1981), "Note on Inversion of Casagrande-Pike-Smith Approximate Sample-Size Formula for Fisher-Irwin Test on 2 X 2 Tables," *Biometrics*, 37, 595.
- Diletti, D., Hauschke, D., and Steinijans, V.W. (1991), "Sample Size Determination for Bioequivalence Assessment by Means of Confidence Intervals," *International Journal of Clinical Pharmacology, Therapy and Toxicology*, 29, 1–8.
- DiSantostefano, R.L. and Muller, K.E. (1995), "A Comparison of Power Approximations for Satterthwaite's Test," *Communications in Statistics — Simulation and Computation*, 24 (3), 583–593.
- Fisher, R.A. (1921), "On the 'Probable Error' of a Coefficient of Correlation Deduced from a Small Sample," *Metron*, 1, 3–32.
- Fleiss, J.L., Tytun, A. and Ury, H.K. (1980), "A Simple Approximation for Calculating Sample Sizes for Comparing Independent Proportions," *Biometrics*, 36, 343–346.
- Gatsonis, C. and Sampson, A.R. (1989), "Multiple Correlation: Exact Power and Sample Size Calculations," *Psychological Bulletin*, 106, 516–524.
- Hocking, R.R. (1985), *The Analysis of Linear Models*, Monterey, CA: Brooks/Cole Publishing Company.
- Johnson, N.L. and Kotz, S. (1970), *Distributions in Statistics: Continuous Univariate Distributions — 1*, New York: John Wiley & Sons.
- Johnson, N.L. Kotz, S. and Balakrishnan, N. (1995), *Continuous Univariate Distributions, Volume 2*, Second Edition, New York: John Wiley & Sons.
- Jones R.M. and Miller, K.S. (1966), "On the Multivariate Lognormal Distribution," *Journal of Industrial Mathematics*, 16, 63–76.
- Lachin, J.M. (1992), "Power and Sample Size Evaluation for the McNemar Test with Application to Matched Case-Control Studies," *Statistics in Medicine*, 11, 1239–1251.
- Lakatos, E. (1988), "Sample Sizes Based on the Log-Rank Statistic in Complex Clinical Trials," *Biometrics*, 44, 229–241.
- Lenth, R.V. (2001), "Some Practical Guidelines for Effective Sample Size Determination," *The American Statistician*, 55, 187–193.
- Maxwell, S.E. (2000), "Sample Size and Multiple Regression Analysis," *Psychological Methods*, 5, 434–458.
- Miettinen, O.S. (1968), "The Matched Pairs Design in the Case of All-or-None Responses," *Biometrics*, 339–352.

- Moser, B.K., Stevens, G.R., and Watts, C.L. (1989), "The Two-Sample T Test Versus Satterthwaite's Approximate F Test," *Communications in Statistics A — Theory and Methods*, 18, 3963–3975.
- Muller, K.E. and Benignus, V.A. (1992), "Increasing Scientific Power with Statistical Power," *Neurotoxicology and Teratology*, 14, 211–219.
- O'Brien, R.G. and Muller, K.E. (1993), "Unified Power Analysis for t -Tests Through Multivariate Hypotheses," in *Applied Analysis of Variance in Behavioral Science*, ed. L.K. Edwards, New York: Marcel Dekker, Chapter 8, 297–344.
- Owen, D.B. (1965), "A Special Case of a Bivariate Non-Central t -Distribution," *Biometrika*, 52, 437–446.
- Pagano, M. and Gauvreau, K. (1993), *Principles of Biostatistics*, Belmont, CA: Wadsworth, Inc.
- Phillips, K.F. (1990), "Power of the Two One-Sided Tests Procedure in Bioequivalence," *Journal of Pharmacokinetics and Biopharmaceutics*, 18, 137–144.
- Satterthwaite, F.W. (1946), "An Approximate Distribution of Estimates of Variance Components," *Biometrics Bulletin*, 2, 110–114.
- Schork, M. and Williams, G. (1980), "Number of Observations Required for the Comparison of Two Correlated Proportions," *Communications in Statistics—Simulation and Computation* 9, 349–357.
- Schuirmann, D.J. (1987), "A Comparison of the Two One-Sided Tests Procedure and the Power Approach for Assessing the Equivalence of Average Bioavailability," *Journal of Pharmacokinetics and Biopharmaceutics*, 15, 657–680.
- Senn, S. (1993), *Cross-over Trials in Clinical Research*, New York: John Wiley & Sons, Inc.
- Stuart, A. and Ord, J.K. (1994), *Kendall's Advanced Theory of Statistics, Volume 1: Distribution Theory*, Sixth Edition, Baltimore: Edward Arnold Publishers Ltd.
- Walters, D.E. (1979). "In Defence of the Arc Sine Approximation," *The Statistician*, 28, 219–232.

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