

Chapter 568

M×M Cross-Over Designs

Introduction

This module calculates the power for an MxM cross-over design in which each subject receives a sequence of M treatments and is measured at M periods (or time points). The 2x2 cross-over design, the simplest and most common case, is well covered by other **PASS** procedures. We anticipate that users will use this procedure when the number of treatments is greater than or equal to three.

MxM cross-over designs are often created from Latin-squares by letting groups of subjects follow different column of the square. The subjects are randomly assigned to different treatment sequences. The overall design is arranged so that there is balance in that each treatment occurs before and after every other treatment an equal number of times. We refer you to any book on cross-over designs or Latin-squares for more details.

The power calculations used here ignore the complexity of specifying sequence terms in the analysis. Therefore, the data may be thought of as a one-way, repeated measures design. Combining subjects with different treatment sequences makes it more reasonable to assume a simple, circular variance-covariance pattern. Hence, usually, you will assume that all correlations are equal.

This procedure computes power for both the univariate (F-test and F-test with Geisser-Greenhouse correction) and multivariate (Wilks' lambda, Pillai-Bartlett trace, and Hotelling-Lawley trace) approaches.

Impact of Treatment Order, Unequal Variances, and Unequal Correlations

Treatment Order

It is important to understand under what conditions the order of treatment application matters since the design will usually include subjects with different treatment arrangements, although each subject will eventually receive all treatments. Even though the cross-over design requires a *washout* period between each two treatment applications so that the effect of one treatment does not *carryover* to next treatment, it is always a good research practice to try several different treatment orders. **PASS** lets you study this by allowing you to set the means and standard deviations in any order you like.

A brief investigation showed that the order of treatment application only matters when the variances at each treatment are different. The pattern of the correlation matrix does have an impact, but only when the variances are different.

Unequal Variances

PASS lets you investigate the impact of unequal variances on power. Of course, different variance patterns lead to different powers. However, the special point to understand is that when the variances are different, different treatment orders result in different powers as well.

Unequal Correlations

PASS lets you investigate the impact of unequal correlations on power. Of course, different correlation patterns lead to different powers. However, the special point to understand is that when the variances are equal, different treatment orders do not result in different powers. Thus, when the variances are the same, the power values for different treatment orders will remain constant across different treatment orderings.

Conclusions

The above considerations result in the following strategy when using this procedure to power analyze (find the sample size) for a particular design.

1. If the variance is constant across treatments, you can analyze any order and the results will stand for all orderings. For example, for the case $M = 3$, there are six possible orders: ABC, ACB, BAC, BCA, CAB, and CBA. In this case, the resulting sample size will be identical for any order.
2. If the variances are different across treatments (for example, if the variances are treatments with larger means are assumed to be proportionally larger), you should analyze each order separately and then use the average sample size or the maximum sample size. The point is, you cannot simply analyze one order.

Assumptions

The following assumptions are made when using the F -test to analyze a factorial experimental design.

1. The response variable is continuous.
2. The residuals follow the normal probability distribution with mean equal to zero and constant variance.
3. The subjects are independent.

Since in a within-subject design responses coming from the same subject are not independent, assumption 3 must be modified for responses within a subject. Independence between subjects is still assumed.

4. The within-subject covariance matrix is equal for all subjects. In this type of experiment, the repeated measurements on a subject may be thought of as a multivariate response vector having a certain covariance structure.
5. When using an F -test, the within-subject covariance matrix is assumed to be *circular*. One way of defining circularity is that the variances of differences between any two measurements within a subject are constant for all measurements. Since responses that are close together in time (or space) often have a higher correlation than those that are far apart, it is common for this assumption to be violated. This assumption is not necessary for the validity of the three multivariate tests: Wilks' lambda, Pillai-Bartlett trace, or Hotelling-Lawley trace. In fact, their validity does not even require that the variances are equal for all treatments.

Technical Details

General Linear Multivariate Model

This section provides the technical details of the repeated measures designs that can be analyzed by **PASS**. The approximate power calculations outlined in Muller, LaVange, Ramey, and Ramey (1992) are used. Using their notation, for N subjects, the usual general linear multivariate model is

$$Y = XM + R$$

where each row of the residual matrix R is distributed as a multivariate normal

$$\text{row}_k(R) \sim N_p(0, \Sigma)$$

Note that p is the number of levels of the within-subject factor, Y is the matrix of responses, X is the design matrix, M is the matrix of regression parameters (means), and R is the matrix of residuals.

Hypotheses about various sets of regression parameters are tested using

$$H_0: \Theta = \Theta_0$$

$$MD = \Theta$$

where D is an orthonormal contrast matrix and Θ_0 is a matrix of hypothesized values, usually zeros.

Tests of the main effect may be constructed with suitable choices for D . These tests are based on

$$\hat{M} = (X'X)^{-1}X'Y$$

$$\hat{\Theta} = \hat{M}D$$

$$H_{b \times b} = (\hat{\Theta} - \Theta_0)'[C(X'X)^{-1}C']^{-1}(\hat{\Theta} - \Theta_0)$$

$$E_{b \times b} = D'\hat{\Sigma}D \cdot (N - r)$$

$$T_{b \times b} = H + E$$

where r is the rank of X which is, in this case, $p - 1$. Also, C is the scalar 1 and can be ignored in this case.

M×M Cross-Over Designs

Geisser-Greenhouse F-Test

Upon the assumption that Σ has compound symmetry, a size α test of $H_0: \Theta = \Theta_0$ is given by the F ratio

$$F = \frac{\text{tr}(H)/(p-1)}{\text{tr}(E)/[(p-1)(N-p+1)]}$$

with degrees of freedom given by

$$df_1 = p - 1$$

$$df_2 = (p-1)(N-p+1)$$

and noncentrality parameter

$$\lambda = df_1(F)$$

The assumption that Σ has compound symmetry is usually not viable. Box (1954a,b) suggested that adjusting the degrees of freedom of the above F -ratio could compensate for the lack of compound symmetry in Σ . His adjustment has become known as the Geisser-Greenhouse adjustment. Under this adjustment, the modified degrees of freedom and noncentrality parameter are given by

$$df_1 = (p-1)\varepsilon$$

$$df_2 = (p-1)(N-p+1)\varepsilon$$

$$\lambda = (df_1)F\varepsilon$$

where

$$\varepsilon = \frac{\text{tr}(D'\hat{\Sigma}D)^2}{b \text{tr}(D'\hat{\Sigma}DD'\hat{\Sigma}D)}$$

The range of ε is $\frac{1}{b-1}$ to 1. When $\varepsilon = 1$, the matrix is *spherical*. When $\varepsilon = \frac{1}{b-1}$, the matrix differs maximally from sphericity.

The critical value F_{crit} is computed using the expected value of ε to adjust the degrees of freedom. That is, the degrees of freedom of F_{crit} are given by

$$df_1 = (p-1)E(\varepsilon)$$

$$df_2 = (p-1)(N-p+1)E(\varepsilon)$$

where

$$E(\hat{\varepsilon}) = \begin{cases} \varepsilon + \frac{g_1}{N-r} & \text{if } \varepsilon > \frac{g_1}{N-r} \\ \varepsilon/2 & \text{otherwise} \end{cases}$$

$$g_1 = \sum_{i=1}^T f_{ii} \xi_i^2 + \sum_{i \neq j} \frac{f_i \xi_i \xi_j}{(\xi_i - \xi_j)}$$

$$f_i = \frac{\partial \varepsilon}{\partial \xi_i} = \frac{2 \sum \xi_j}{df_1 \sum \xi_j^2} - \frac{2 \lambda_i (\sum \xi_j)^2}{df_1 (\sum \xi_j^2)^2}$$

$$f_{ii} = \frac{\partial^{(2)} \varepsilon}{\partial \xi_i^2} = 2h_1 - 8h_2 + 8h_3 - 2h_4$$

$$h_1 = \frac{2}{df_1 \sum \xi_j^2}$$

$$h_2 = \frac{\xi_i (\sum \xi_j)}{df_1 (\sum \xi_j^2)^2}$$

$$h_3 = \frac{\xi_i^2 (\sum \xi_j)^2}{df_1 (\sum \xi_j^2)^3}$$

$$h_4 = \frac{(\sum \xi_j)^2}{df_1 (\sum \xi_j^2)^2}$$

and the ξ_j 's are the ordered eigenvalues of $D'\Sigma D$.

Wilks' Lambda Approximate F-Test

The hypothesis $H_0: \Theta = \Theta_0$ may be tested using Wilks' likelihood ratio statistic W . This statistic is computed using

$$W = |ET^{-1}|$$

An F approximation to the distribution of W is given by

$$F_{df_1, df_2} = \frac{\eta/df_1}{(1-\eta)/df_2}$$

where

$$\lambda = df_1 F_{df_1, df_2}$$

$$\eta = 1 - W$$

$$df_1 = p - 1$$

$$df_2 = N - p + 1$$

Pillai-Bartlett Trace Approximate F-Test

The hypothesis $H_0: \Theta = \Theta_0$ may be tested using the Pillai-Bartlett Trace. This statistic is computed using

$$T_{PB} = \text{tr}(HT^{-1})$$

A non-central F approximation to the distribution of T_{PB} is given by

$$F_{df_1, df_2} = \frac{\eta/df_1}{(1-\eta)/df_2}$$

where

$$\lambda = df_1 F_{df_1, df_2}$$

$$\eta = \frac{T_{PB}}{s}$$

$$s = 1$$

$$df_1 = p - 1$$

$$df_2 = N - p + 1$$

Hotelling-Lawley Trace Approximate F-Test

The hypothesis $H_0: \Theta = \Theta_0$ may be tested using the Hotelling-Lawley Trace. This statistic is computed using

$$T_{HL} = \text{tr}(HE^{-1})$$

An F approximation to the distribution of T_{HL} is given by

$$F_{df_1, df_2} = \frac{\eta/df_1}{(1-\eta)/df_2}$$

where

$$\lambda = df_1 F_{df_1, df_2}$$

$$\eta = \frac{\frac{T_{HL}}{s}}{1 + \frac{T_{HL}}{s}}$$

$$s = 1$$

$$df_1 = p - 1$$

$$df_2 = N - p + 1$$

The Mean Vector

In the general linear multivariate model presented above, M represents a matrix of regression coefficients. Since you must provide the elements of M , we will discuss its meaning in more detail. Although other structures and interpretations of M are possible, in this module we assume that the elements of M are the cell means. The row of M represents the single group and the columns of M represent the within-group categories.

Consider now an example in which $p = 4$. That is, there is one group of subjects that are each measured four times. The matrix M would appear as follows.

$$M = [\mu_1 \quad \mu_2 \quad \mu_3 \quad \mu_4]$$

To calculate the power of this design, you would need to specify appropriate values of all four means under the alternative hypothesis.

Specifying the M Matrix

When computing the power in a repeated measures analysis of variance, the specification of the M matrix is one of your main tasks. The program cannot do this for you. The calculated power is directly related to your choice. So, your choice for the elements of M must be selected carefully and thoughtfully. When authorization and approval from a government organization is sought, you should be prepared to defend your choice of M . In this section, we will explain how you can specify M .

M×M Cross-Over Designs

Before we begin, it is important that you have in mind exactly what M is. M is a row of means that represent the size of the differences among the means that you want the study or experiment to detect. M gives the means under the alternative hypothesis. Under the null hypothesis, these means are assumed to be equal.

The D Matrix for Within-Subject Contrasts

The D matrix is comprised of contrasts that are applied to the columns of M . The choice of D does not matter as long as it is orthogonal, so an appropriate matrix is generated for you.

Power Calculations

To calculate statistical power, we must determine distribution of the test statistic under the alternative hypothesis which specifies a different value for the regression parameter matrix B . The distribution theory in this case has not been worked out, so approximations must be used. We use the approximations given by Mueller and Barton (1989) and Muller, LaVange, Ramey, and Ramey (1992). These approximations state that under the alternative hypothesis, F_U is distributed as a noncentral F random variable with degrees of freedom and noncentrality shown above. The calculation of the power of a particular test may be summarized as follows

1. Specify values of M , Σ .
2. Determine the critical value using $F_{\text{crit}} = \text{FINV}(1 - \alpha, df_1, df_2)$, where $\text{FINV}()$ is the inverse of the central F distribution and α is the significance level.
3. Compute the noncentrality parameter λ .
4. Compute the power as $\text{Power} = 1 - \text{NCFPROB}(F_{\text{crit}}, df_1, df_2, \lambda)$, where $\text{NCFPROB}()$ is the noncentral F distribution.

Covariance Matrix Assumptions

The following assumptions are made when using the F -test. These assumptions are not needed when using one of the three multivariate tests.

In order to use the F ratio to test hypotheses, certain assumptions are made about the distribution of the residuals e_{ijk} . Specifically, it is assumed that the residuals for each subject, $e_{ij1}, e_{ij2}, \dots, e_{ijT}$, are distributed as a multivariate normal with means equal to zero and covariance matrix Σ_{ij} . Two additional assumptions are made about these covariance matrices. First, they are assumed to be equal for all subjects. That is, it is assumed that $\Sigma_{11} = \Sigma_{12} = \dots = \Sigma_{Gn} = \Sigma$. Second, the covariance matrix is assumed to have a particular form called *circularity*. A covariance matrix is *circular* if there exists a matrix A such that

$$\Sigma = A + A' + \lambda I_T$$

where I_T is the identity matrix of order T , and λ is a constant.

This property may also be defined as

$$\sigma_{ii} + \sigma_{jj} - 2\sigma_{ij} = 2\lambda$$

M×M Cross-Over Designs

One type of matrix that is circular is one that has *compound symmetry*. A matrix with this property has all elements on the main diagonal equal and all elements off the main diagonal equal. An example of a covariance matrix with compound symmetry is

$$\Sigma = \begin{bmatrix} \sigma^2 & \rho\sigma^2 & \rho\sigma^2 & \cdots & \rho\sigma^2 \\ \rho\sigma^2 & \sigma^2 & \rho\sigma^2 & \cdots & \rho\sigma^2 \\ \rho\sigma^2 & \rho\sigma^2 & \sigma^2 & \cdots & \rho\sigma^2 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ \rho\sigma^2 & \rho\sigma^2 & \rho\sigma^2 & \cdots & \sigma^2 \end{bmatrix}$$

or, with actual numbers,

$$\begin{bmatrix} 9 & 2 & 2 & 2 \\ 2 & 9 & 2 & 2 \\ 2 & 2 & 9 & 2 \\ 2 & 2 & 2 & 9 \end{bmatrix}$$

Covariance Patterns

In a repeated measures design with N subjects, each measured M times, observations within a single subject may be correlated, and a pattern for their covariance must be specified. In this case, the overall covariance matrix will have the block-diagonal form:

$$V = \begin{pmatrix} V_1 & 0 & 0 & \cdots & 0 \\ 0 & V_2 & 0 & \cdots & 0 \\ 0 & 0 & V_3 & \cdots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \cdots & V_N \end{pmatrix},$$

where V_i is the $M \times M$ covariance submatrices corresponding to the i^{th} subject. The $\mathbf{0}$'s represent $M \times M$ matrices of zeros giving zero covariances for observations on different subjects. This routine allows the specification of two different covariance matrix types: All ρ 's Equal and AR(1), Banded(1), and Banded(2).

All ρ 's Equal (Compound Symmetry)

A compound symmetry covariance model assumes that all covariances are equal, and all variances on the diagonal are equal. That is

$$\Sigma = \sigma^2 \begin{pmatrix} 1 & \rho & \rho & \rho & \cdots & \rho \\ \rho & 1 & \rho & \rho & \cdots & \rho \\ \rho & \rho & 1 & \rho & \cdots & \rho \\ \rho & \rho & \rho & 1 & \cdots & \rho \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\ \rho & \rho & \rho & \rho & \cdots & 1 \end{pmatrix}_{M \times M}$$

where σ^2 is the subject variance and ρ is the correlation between observations on the same subject.

M×M Cross-Over Designs

AR(1)

An AR(1) (autoregressive order 1) covariance model assumes that all variances on the diagonal are equal and that covariances t time periods apart are equal to $\rho^t\sigma^2$. That is

$$\Sigma = \sigma^2 \begin{pmatrix} 1 & \rho & \rho^2 & \rho^3 & \dots & \rho^{M-1} \\ \rho & 1 & \rho & \rho^2 & \dots & \rho^{M-2} \\ \rho^2 & \rho & 1 & \rho & \dots & \rho^{M-3} \\ \rho^3 & \rho^2 & \rho & 1 & \dots & \rho^{M-4} \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\ \rho^{M-1} & \rho^{M-2} & \rho^{M-3} & \rho^{M-4} & \dots & 1 \end{pmatrix}_{M \times M}$$

where σ^2 is the residual variance and ρ is the correlation between observations on the same subject.

Banded(1)

A Banded(1) (banded order 1) covariance model assumes that all variances on the diagonal are equal, covariances for observations one time period apart are equal to $\rho\sigma^2$, and covariances for measurements greater than one time period apart are equal to zero. That is

$$\Sigma = \sigma^2 \begin{pmatrix} 1 & \rho & 0 & 0 & \dots & 0 \\ \rho & 1 & \rho & 0 & \dots & 0 \\ 0 & \rho & 1 & \rho & \dots & 0 \\ 0 & 0 & \rho & 1 & \dots & 0 \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & 0 & \dots & 1 \end{pmatrix}_{M \times M}$$

where σ^2 is the residual variance and ρ is the correlation between observations on the same subject.

Banded(2)

A Banded(2) (banded order 2) covariance model assumes that all variances on the diagonal are equal, covariances for observations one or two time periods apart are equal to $\rho\sigma^2$, and covariances for measurements greater than two time period apart are equal to zero. That is

$$\Sigma = \sigma^2 \begin{pmatrix} 1 & \rho & \rho & 0 & \dots & 0 \\ \rho & 1 & \rho & \rho & \dots & 0 \\ \rho & \rho & 1 & \rho & \dots & 0 \\ 0 & \rho & \rho & 1 & \dots & 0 \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & 0 & \dots & 1 \end{pmatrix}_{M \times M}$$

where σ^2 is the residual variance and ρ is the correlation between observations on the same subject.

Example 1 – Determining Sample Size

Researchers are planning a study of the impact of a new drug on heart rate. They want to investigate three treatments: placebo (P), low dose (L), and higher dose (H) of the new drug. They decide to use a 3x3 cross-over design with six possible treatment sequences: PLH, PHL, HPL, HLP, LPH, and LHP. They will assign an equal number of subjects to each sequence. Hence, the final sample size will be the next multiple of six above the N found by PASS. For example, an N of 32 would be rounded up to 36.

They anticipate little difference between the placebo and the low dose. However, they expect that the high dose will reduce the heart rate about 10%. They decide to use the mean values of 80, 80, and 72.

Similar studies have found a standard deviation of 15. To allow for a sensitivity analysis of the standard deviation, they will use three standard deviations: 13, 15, and 17.

The researchers assume that all correlations among the measurements at different time points within a subject will be equal to 0.5. To allow for a sensitivity analysis of the correlation, they will use three correlations: 0.4, 0.5, and 0.6.

They decide to use the F-test statistic with the Geisser-Greenhouse correction.

The test will be conducted at the 0.05 significance level. What sample size is necessary to achieve 90% power over a range of possible means and standard deviations?

Setup

If the procedure window is not already open, use the PASS Home window to open it. The parameters for this example are listed below and are stored in the **Example 1** settings file. To load these settings to the procedure window, click **Open Example Settings File** in the Help Center or File menu.

Design Tab	
Solve For	Sample Size
Test Statistic	Univariate: Geisser-Greenhouse F-Test
Power.....	0.90
Alpha.....	0.05
M (Periods, Treatments)	3
μ 's ($\mu_1, \mu_2, \dots, \mu_M$).....	List
μ 's List.....	80 80 72
K (Means Multiplier).....	1
Pattern of σ 's Across Time.....	Equal: $\sigma = \sigma_1 = \sigma_2 = \dots = \sigma_M$
σ (Standard Deviation).....	13 15 17
Pattern of ρ 's Across Time	All ρ's Equal
ρ (Correlation).....	0.4 0.5 0.6

Output

Click the Calculate button to perform the calculations and generate the following output.

Numeric Reports

Numeric Results

Solve For: [Sample Size](#)
 Test: Geisser-Greenhouse Corrected F-Test
 μ 's: 80 80 72
 σ 's: All Equal
 ρ 's: All Equal

Power	Sample Size N	Number of Periods and Treatments M	Means Multiplier K	Standard Deviation of Means σ_m	Standard Deviation σ	Within- Subject Correlation ρ	Alpha
0.9011	32	3	1	3.77	13	0.4	0.05
0.9014	27	3	1	3.77	13	0.5	0.05
0.9017	22	3	1	3.77	13	0.6	0.05
0.9012	42	3	1	3.77	15	0.4	0.05
0.9073	36	3	1	3.77	15	0.5	0.05
0.9054	29	3	1	3.77	15	0.6	0.05
0.9045	54	3	1	3.77	17	0.4	0.05
0.9024	45	3	1	3.77	17	0.5	0.05
0.9078	37	3	1	3.77	17	0.6	0.05

Power The probability of rejecting a false null hypothesis when the alternative hypothesis is true.
 N The total number of subjects in the study.
 M The number of time points at which each subject is measured. This is also the number of periods and the number of treatments.
 K The effect size multiplier. The original means are all multiplied by this value, resulting in a corresponding change in the effect size.
 σ_m Standard Deviation of Means. The magnitude of differences among the hypothesized means.
 σ The standard deviation across subjects at a given time point.
 ρ The (auto)correlation between observations made on a subject at the first and second time points.
 Alpha The probability of rejecting a true null hypothesis.

Summary Statements

A 3-period, 3-treatment cross-over design will be used to test whether there is a difference in the 3 means. The comparison will be made using a Geisser-Greenhouse corrected F-test with a Type I error rate (α) of 0.05. The group means under the null hypothesis are assumed to be equal. The standard deviation across subjects at the same period is assumed to be 13. The assumed pattern of the covariance matrix is 'all correlations equal' (compound symmetry) with a correlation of 0.4 between adjacent time point measurements. To detect group means of '80 80 72' (or a standard deviation of means of 3.77) with 90% power, the needed number of subjects is 32 (each measured 3 times).

M×M Cross-Over Designs

Dropout-Inflated Sample Size

Dropout Rate	Sample Size N	Dropout- Inflated Enrollment Sample Size N'	Expected Number of Dropouts D
20%	32	40	8
20%	27	34	7
20%	22	28	6
20%	42	53	11
20%	36	45	9
20%	29	37	8
20%	54	68	14
20%	45	57	12
20%	37	47	10

Dropout Rate	The percentage of subjects (or items) that are expected to be lost at random during the course of the study and for whom no response data will be collected (i.e., will be treated as "missing"). Abbreviated as DR.
N	The evaluable sample size at which power is computed. If N subjects are evaluated out of the N' subjects that are enrolled in the study, the design will achieve the stated power.
N'	The total number of subjects that should be enrolled in the study in order to obtain N evaluable subjects, based on the assumed dropout rate. After solving for N, N' is calculated by inflating N using the formula $N' = N / (1 - DR)$, with N' always rounded up. (See Julious, S.A. (2010) pages 52-53, or Chow, S.C., Shao, J., Wang, H., and Lohknygina, Y. (2018) pages 32-33.)
D	The expected number of dropouts. $D = N' - N$.

Dropout Summary Statements

Anticipating a 20% dropout rate, 40 subjects should be enrolled to obtain a final sample size of 32 subjects.

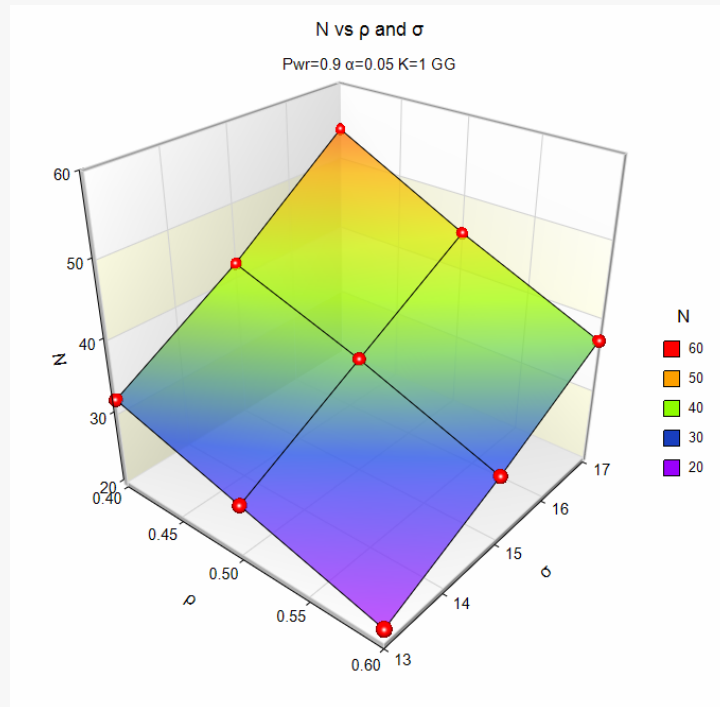
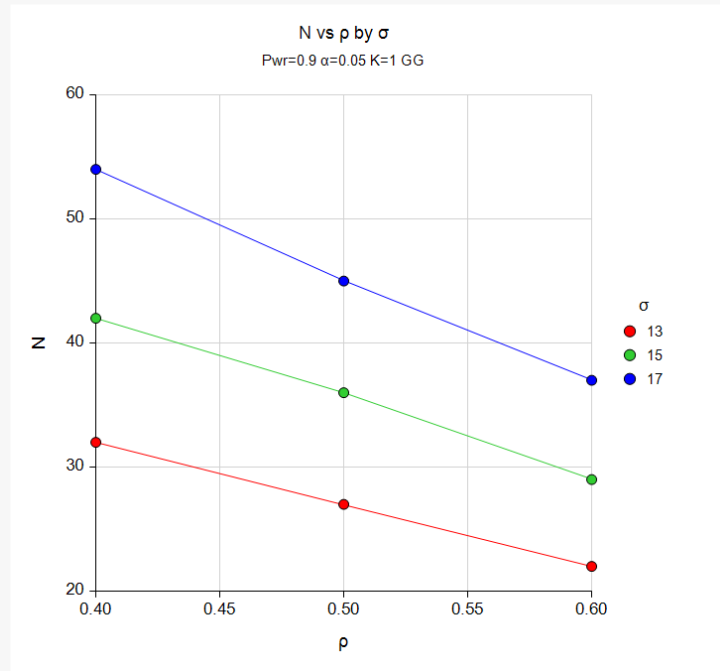
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This report gives the power for each value of the other parameters. The definitions are shown in the report.

Plots Section

Plots



The plots show the relationship between N , ρ , and σ when the other parameters in the design are held constant.

Example 2 – Validation using PASS’s Repeated Measures Procedure

To validate this procedure, we will run the first scenario through **PASS**’s Repeated Measures Analysis procedure. We did this and obtained the following report.

Design Report

Solve For: [Sample Size Based on the Geisser-Greenhouse Corrected F-Test \(All Terms\)](#)

Term*	Test	Power	Sample Size		Effect Multiplier K	Standard Deviation of Effects σ_m	Standard Deviation σ	Effect Size σ_m / σ	Alpha
			Average Group n	Total N					
W1 (3)	GG F	0.90853	33	33	1	3.77124	5.81378	0.64867	0.05

* The numbers in parentheses represent the number of levels associated with the factor.

Setup

If the procedure window is not already open, use the PASS Home window to open it. The parameters for this example are listed below and are stored in the **Example 2** settings file. To load these settings to the procedure window, click **Open Example Settings File** in the Help Center or File menu.

Design Tab

Solve For	Sample Size
Test Statistic	Univariate: Geisser-Greenhouse F-Test
Power.....	0.90
Alpha.....	0.05
M (Periods, Treatments)	3
μ i's ($\mu_1, \mu_2, \dots, \mu_M$).....	List
μ i's List.....	80 80 72
K (Means Multiplier).....	1
Pattern of σ 's Across Time.....	Equal: $\sigma = \sigma_1 = \sigma_2 = \dots = \sigma_M$
σ (Standard Deviation).....	13
Pattern of ρ 's Across Time.....	All ρ's Equal
ρ (Correlation).....	0.4

Output

Click the Calculate button to perform the calculations and generate the following output.

Numeric Results

Solve For: [Sample Size](#)
 Test: Geisser-Greenhouse Corrected F-Test
 μ 's: 80 80 72
 σ 's: All Equal
 ρ 's: All Equal

Power	Sample Size N	Number of Periods and Treatments M	Means Multiplier K	Standard Deviation of Means σ_m	Standard Deviation σ	Within- Subject Correlation ρ	Alpha
0.9011	32	3	1	3.77	13	0.4	0.05

This procedure has very similar results to that of the previously validated procedure.