# Tests for Two Between-Subject Variances in a 2×2M Replicated Cross-Over Design

## Introduction

This procedure calculates power and sample size of tests of between-subject variabilities from a 2×2M replicated cross-over design for the case when the ratio assumed by the null hypothesis is equal to one. This routine deals with the case in which the statistical hypotheses are expressed in terms of the ratio of the between-subject variances.

This design is used to compare two treatments which are administered to subjects in different orders. The design has two treatment sequences. Here, *M* is the number of times a particular treatment is received by a subject.

For example, if M = 2, the design is a 2×4 replicated cross-over. The two sequences might be

sequence 1: C T C T

sequence 2: T C T C

It is assumed that either there is no carry-over from one measurement to the next, or there is an ample washout period between measurements.

## **Technical Details**

This procedure uses the formulation given in Chow, Shao, Wang, and Lokhnygina (2018), pages 213 - 216.

Suppose  $x_{ijkl}$  is the response in the *i*th sequence (*i* = 1, 2), *j*th subject (*j* = 1, ..., *Ni*), *k*th treatment (*k* = T, C), and *l*th replicate (I = 1, ..., M). The mixed effect model analyzed in this procedure is

$$x_{ijkl} = \mu_k + \gamma_{ikl} + S_{ijk} + e_{ijkl}$$

where  $\mu_k$  is the *k*th treatment effect,  $\gamma_{ikl}$  is the fixed effect of the *l*th replicate on treatment *k* in the *i*th sequence,  $S_{ij1}$  and  $S_{ij2}$  are random effects of the *ij*th subject, and  $e_{ijkl}$  is the within-subject error term which is normally distributed with mean 0 and variance  $V_k = \sigma_{Wk}^2$ .

Unbiased estimators of these variances are found after applying an orthogonal transformation matrix *P* to the x's as follows

$$z_{ijk} = P' x_{ijk}$$

where *P* is an *m* × *m* matrix such that *P*'*P* is diagonal and  $var(z_{ijkl}) = \sigma_{Wk}^2$ .

Let  $N_s = N_1 + N_2 - 2$ . In a 2×4 cross-over design the z's become

$$z_{ijk1} = \frac{x_{ijk1} + x_{ijk2}}{2} = \bar{x}_{ijk}.$$

and

$$z_{ijk2} = \frac{x_{ijk1} + x_{ijk2}}{\sqrt{2}} = \bar{x}_{ijk}.$$

In this case, the within-subject variances are estimated as

$$s_{WT}^2 = \frac{1}{N_S(M-1)} \sum_{i=1}^{2} \sum_{j=1}^{N_i} \sum_{l=1}^{M} \left( z_{ijTl} - \bar{z}_{i.Tl} \right)^2$$

and

$$s_{WC}^2 = \frac{1}{N_S(M-1)} \sum_{i=1}^2 \sum_{j=1}^{N_i} \sum_{l=1}^M (z_{ijCl} - \bar{z}_{i.Cl})^2$$

Similarly, the between-subject variances are estimated as

$$s_{BT}^2 = \frac{1}{N_S} \sum_{i=1}^{2} \sum_{j=1}^{N_i} (\bar{x}_{ijT.} - \bar{x}_{i.T.})^2$$

and

$$s_{BC}^2 = \frac{1}{N_S} \sum_{i=1}^{2} \sum_{j=1}^{N_i} (\bar{x}_{ijC.} - \bar{x}_{i.C.})^2$$

where

$$\bar{x}_{i.k.} = \frac{1}{N_i} \sum_{j=1}^{N_i} \bar{x}_{ijk.}$$

Now, since  $E(s_{BK}^2) = \sigma_{BK}^2 + \sigma_{WK}^2/M$ , estimators for the between-subject variance are given by

$$\hat{\sigma}_{BK}^2 = s_{BK}^2 - \hat{\sigma}_{WK}^2 / M$$

The sample between-subject covariance is calculated using

$$s_{BTC}^2 = \frac{1}{N_S} \sum_{i=1}^{2} \sum_{j=1}^{N_i} (\bar{x}_{ijT.} - \bar{x}_{i.T.}) (\bar{x}_{ijC.} - \bar{x}_{i.C.})$$

Using this value, the sample between-subject correlation is easily calculated.

## **Testing Variance Inequality**

The following three sets of statistical hypotheses are used to test for between-subject variance inequality.

$$H_0: \frac{\sigma_{BT}^2}{\sigma_{BC}^2} \ge 1 \quad \text{versus} \quad H_1: \frac{\sigma_{BT}^2}{\sigma_{BC}^2} < 1,$$
$$H_0: \frac{\sigma_{BT}^2}{\sigma_{BC}^2} \le 1 \quad \text{versus} \quad H_1: \frac{\sigma_{BT}^2}{\sigma_{BC}^2} > 1,$$
$$H_0: \frac{\sigma_{BT}^2}{\sigma_{BC}^2} = 1 \quad \text{versus} \quad H_1: \frac{\sigma_{BT}^2}{\sigma_{BC}^2} \neq 1,$$

Let  $\eta = \sigma_{BT}^2 - \sigma_{BC}^2$  be the parameter of interest. The test statistic is  $\hat{\eta} = \hat{\sigma}_{BT}^2 - \hat{\sigma}_{BC}^2$ .

#### **Two-Sided Test**

For the two-sided test, compute two limits,  $\hat{\eta}_L$  and  $\hat{\eta}_U$ , using

$$\hat{\eta}_L = \hat{\eta} - \sqrt{\Delta_L}$$
 $\hat{\eta}_U = \hat{\eta} + \sqrt{\Delta_U}$ 

Reject the null hypothesis if  $\hat{\eta}_L > 0$  is or  $\hat{\eta}_U < 0$ .

The  $\Delta s$  are given by

$$\Delta_{L} = \lambda_{1}^{2}h\left(\frac{\alpha}{2}, N_{s} - 1\right) + \lambda_{2}^{2}h\left(1 - \frac{\alpha}{2}, N_{s} - 1\right) + h\left(\frac{\alpha}{2}, N_{s}(M - 1)\right)\frac{\hat{\sigma}_{WT}^{4}}{M^{2}} + h\left(1 - \frac{\alpha}{2}, N_{s}(M - 1)\right)\frac{\hat{\sigma}_{WC}^{4}}{M^{2}}$$
$$\Delta_{U} = \lambda_{1}^{2}h\left(1 - \frac{\alpha}{2}, N_{s} - 1\right) + \lambda_{2}^{2}h\left(\frac{\alpha}{2}, N_{s} - 1\right) + h\left(1 - \frac{\alpha}{2}, N_{s}(M - 1)\right)\frac{\hat{\sigma}_{WT}^{4}}{M^{2}} + h\left(\frac{\alpha}{2}, N_{s}(M - 1)\right)\frac{\hat{\sigma}_{WC}^{4}}{M^{2}}$$

where

$$h(A,B) = \left(1 - \frac{B}{\chi^2_{A,B}}\right)^2$$
$$\lambda_i^2 = \left(\frac{s_{BT}^2 - s_{BC}^2 \pm \sqrt{(s_{BT}^2 + s_{BC}^2)^2 - 4(R0)s_{BTC}^4}}{2}\right) \text{ for } i = 1,2$$

and  $\chi^2_{A,B}$  is the upper quantile of the Chi-square distribution with *B* degrees of freedom.

### **One-Sided Test**

For the lower, one-sided test, compute the limit,  $\hat{\eta}_U$ , using

$$\hat{\eta}_U = \hat{\eta} + \sqrt{\Delta_U}$$

Reject the null hypothesis if  $\hat{\eta}_U < 0$ .

The  $\Delta_U$  is given by

$$\Delta_{U} = h(1 - \alpha, N_{s} - 1)\lambda_{1}^{2} + h(\alpha, N_{s} - 1)\lambda_{2}^{2} + h(1 - \alpha, N_{s}(M - 1))\frac{\hat{\sigma}_{WT}^{4}}{M^{2}} + h(\alpha, N_{s}(M - 1))\frac{\hat{\sigma}_{WC}^{4}}{M^{2}}$$

#### Power

#### **Two-Sided Test**

The power of the two-sided test is given by

Power = 
$$1 - \Phi\left(z_{1-\frac{\alpha}{2}} - \frac{(R_1 - 1)\sigma_{BC}^2}{\sqrt{\sigma^{*2}/N_s}}\right) + \Phi\left(z_{\alpha/2} - \frac{(R_1 - 1)\sigma_{BC}^2}{\sqrt{\sigma^{*2}/N_s}}\right)$$

where

$$R_{1} = \frac{\sigma_{BT}^{2}}{\sigma_{BC}^{2}}$$

$$\sigma_{BT}^{2} = R_{1}\sigma_{BC}^{2}$$

$$\sigma^{*2} = 2\left[\left(\sigma_{BT}^{2} + \frac{\sigma_{WT}^{2}}{M}\right)^{2} + \left(\sigma_{BC}^{2} + \frac{\sigma_{WC}^{2}}{M}\right)^{2} + \frac{\sigma_{WT}^{4}}{M^{2}(M-1)} + \frac{\sigma_{WC}^{4}}{M^{2}(M-1)} - 2R_{1}\sigma_{BC}^{4}\rho^{2}\right]$$

where *R1* is the value of the variance ratio stated by the alternative hypothesis and  $\Phi(x)$  is the standard normal CDF.

A simple binary search algorithm can be applied to the power function to obtain an estimate of the necessary sample size.

### **One-Sided Test**

The power of the lower, one-sided test,  $H_0: \frac{\sigma_{BT}^2}{\sigma_{BC}^2} \ge 1$  versus  $H_1: \frac{\sigma_{BT}^2}{\sigma_{BC}^2} < 1$ , is given by

Power = 
$$\Phi\left(z_{\alpha} - \frac{(R_1 - 1)\sigma_{BC}^2}{\sqrt{\sigma^{*2}/N_s}}\right)$$

The power of the upper, one-sided test,  $H_0: \frac{\sigma_{BT}^2}{\sigma_{BC}^2} \le 1$  versus  $H_1: \frac{\sigma_{BT}^2}{\sigma_{BC}^2} > 1$ , is given by

Power = 
$$1 - \Phi\left(z_{1-\alpha} - \frac{(R_1 - 1)\sigma_{BC}^2}{\sqrt{\sigma^{*2}/N_s}}\right)$$

## Example 1 – Finding Sample Size

A company has developed a generic drug for treating rheumatism and wants to compare it to the standard drug in terms of the between-subject variability. A 2 x 4 cross-over design will be used to test the inequality using a two-sided test.

Company researchers set the variance ratio under the null hypothesis to 1, the significance level to 0.05, the power to 0.90, M to 2, and the actual variance ratio values between 0.6 and 1.4. They also set  $\sigma^2 BC = 0.4$ ,  $\sigma^2 wT = 0.2$ ,  $\sigma^2 wc = 0.3$ , and  $\rho = 0.75$ . They want to investigate the range of required sample size values assuming that the two sequence sample sizes are equal.

## 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
Alternative Hypothesis	Two-Sided (H1: σ²вт/σ²вс ≠ 1)
Power	0.90
Alpha	0.05
Sequence Allocation	Equal (N1 = N2)
M (Number of Replicates)	2
R1 (Actual Variance Ratio)	0.6 0.7 0.9 1.1 1.3 1.4
σ²вс (Control Variance)	0.4
σ²wт (Treatment Variance)	0.2
σ²wc (Control Variance)	0.3
ρ (Treatment, Control Correlation)	0.75

## Output

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

Numeric Results

Pow	or	Sequence Sample Size		Number of	Between-Subject Variance		Within-Subject Variance		Between- Subject (Treatment, Control)		
Target	Actual	 	N2	N	Replicates M	Ratio R1	Control σ²вс	Treatment σ²wτ	Control σ²wc	Correlation P	Alpha
).9	0.9008	142	142	284	2	0.6	0.4	0.2	0.3	0.75	0.05
0.9	0.9001	259	259	518	2	0.7	0.4	0.2	0.3	0.75	0.05
).9	0.9000	2527	2527	5054	2	0.9	0.4	0.2	0.3	0.75	0.05
).9	0.9000	2816	2816	5632	2	1.1	0.4	0.2	0.3	0.75	0.05
0.9	0.9007	356	356	712	2	1.3	0.4	0.2	0.3	0.75	0.05
).9	0.9002	214	214	428	2	1.4	0.4	0.2	0.3	0.75	0.05
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Actual F N1 N2 N M		hypothe The actua target p The num The num The total The num subject. The value The betw The within	esis. al power ower. ber of sul number ber of sul per of rep e of the b een-subj n-subject	achieved ojects in of subject olicates. etween	d. Because N1 sequence 1. sequence 2. tts. $N = N1 + N$ That is, it is the subject variance nce of measurem	and N2 a I2. e number ce ratio at rements in hents in th	of times a to the control of times a to the control of the control of the treatment	, this value is reatment mea power is calcu I group. t group.	usually slig	htly larger than	
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#### **Summary Statements**

A 2x2M replicated cross-over design will be used to test whether the between-subject variance of the treatment ( $\sigma^2 BT$ ) is different from the between-subject variance of the control ( $\sigma^2 BC$ ) by testing whether the between-subject variance ratio ( $\sigma^2 BT / \sigma^2 BC$ ) is different from 1 (H0:  $\sigma^2 BT / \sigma^2 BC = 1$  versus H1:  $\sigma^2 BT / \sigma^2 BC \neq 1$ ). Each subject will alternate treatments (T and C), with an assumed wash-out period between measurements to avoid carry-over. With 2 replicate pairs, each subject will be measured 4 times. For those in the Sequence 1 group, the first treatment will be C, and the sequence is [C T C T]. For those in the Sequence 2 group, the first treatment will be T, and the sequence is [T C T C]. The comparison will be made using a two-sided, variance-difference test (treatment minus control) as described in Chow, Shao, Wang, and Lokhnygina (2018), with a Type I error rate ( $\alpha$ ) of 0.05. For the control group, the between-subject variance ( $\sigma^2 BC$ ) is assumed to be 0.4, and the within-subject variance is assumed to be 0.3. The within-subject variance of the treatment group is assumed to be 0.2. The between-subject variance of the treatment group is assumed to be 0.4 with 90% power, the number of subjects needed will be 142 in Group/Sequence 1, and 142 in Group/Sequence 2.

#### Dropout-Inflated Sample Size

	Sample Size			I	pout-Infla Enrollmer ample Siz	Expected Number of Dropouts			
Dropout Rate	N1	N2	N	N1'	N2'	N'	D1	D2	D
20%	142	142	284	178	178	356	36	36	72
20%	259	259	518	324	324	648	65	65	130
20%	2527	2527	5054	3159	3159	6318	632	632	1264
20%	2816	2816	5632	3520	3520	7040	704	704	1408
20%	356	356	712	445	445	890	89	89	178
20%	214	214	428	268	268	536	54	54	108

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.
N1, N2, and N	The evaluable sample sizes at which power is computed. If N1 and N2 subjects are evaluated out of the
	N1' and N2' subjects that are enrolled in the study, the design will achieve the stated power.
N1', N2', and N'	The number of subjects that should be enrolled in the study in order to obtain N1, N2, and N evaluable
	subjects, based on the assumed dropout rate. After solving for N1 and N2, N1' and N2' are calculated by
	inflating N1 and N2 using the formulas N1' = N1 / (1 - DR) and N2' = N2 / (1 - DR), with N1' and N2'
	always rounded up. (See Julious, S.A. (2010) pages 52-53, or Chow, S.C., Shao, J., Wang, H., and
	Lokhnygina, Y. (2018) pages 32-33.)
D1, D2, and D	The expected number of dropouts. $D1 = N1' - N1$ , $D2 = N2' - N2$ , and $D = D1 + D2$ .

#### **Dropout Summary Statements**

Anticipating a 20% dropout rate, 178 subjects should be enrolled in Group 1, and 178 in Group 2, to obtain final group sample sizes of 142 and 142, respectively.

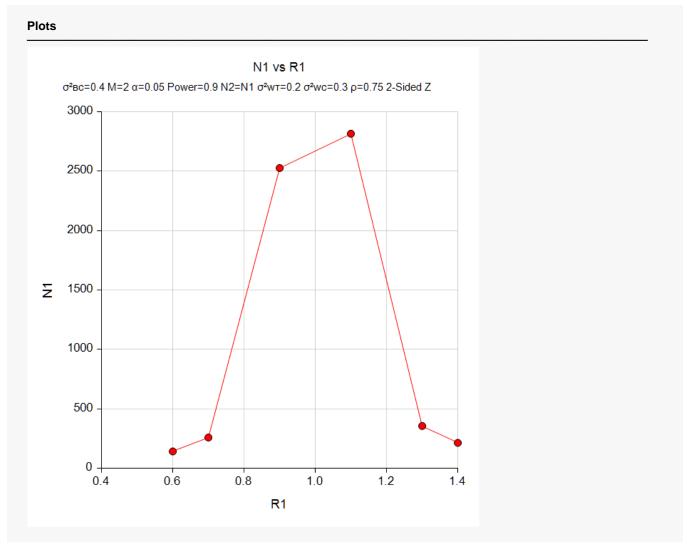
#### References

Chow, S.C., Shao, J., Wang, H., and Lokhnygina, Y. 2018. Sample Size Calculations in Clinical Research, Third Edition. Taylor & Francis/CRC. Boca Raton, Florida.

Chow, S.C., and Liu, J.P. 2014. Design and Analysis of Clinical Trials, Third Edition. John Wiley & Sons. Hoboken, New Jersey.

This report gives the sample sizes for the indicated scenarios.

### **Plots Section**



This plot shows the relationship between sample size and R1.

Tests for Two Between-Subject Variances in a 2×2M Replicated Cross-Over Design

## Example 2 – Validation using Chow and Liu (2014)

We will use an example from Chow and Liu (2014) page 517 to validate this procedure.

In this example, significance level = 0.05, power = 0.80, M = 2,  $\sigma BT$  = 0.3,  $\sigma BC$  = 0.4,  $\sigma WT$  = 0.2,  $\sigma WC$  = 0.3, and  $\rho$  = 0.75. From these values, we find that R1 = 0.5625. The resulting sample size is found to be 66 per sequence.

## 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.

Solve For	Sample Size
Alternative Hypothesis	Two-Sided (H1: σ²вт/σ²вс ≠ 1)
Power	0.80
Alpha	0.05
Sequence Allocation	Equal (N1 = N2)
M (Number of Replicates)	2
R1 (Actual Variance Ratio)	0.5625
σ²вс (Control Variance)	0.16
σ²wτ (Treatment Variance)	0.04
σ <sup>2</sup> wc (Control Variance)	0.09
ρ (Treatment, Control Correlation)	0.75

## Output

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

		Solve For:Sample SizeHypotheses:H0: $\sigma^2 B \tau / \sigma^2 B c = 1$ vs. H1: $\sigma^2 B \tau / \sigma^2 B c \neq 1$												
Power		Sequence Sample Size		Number of	Between-Subject Variance		Within-Subject Variance		Between- Subject (Treatment,					
Fower		Actual	 N1	N2	N	Replicates	Ratio R1	Control σ²вс	Treatment σ²wτ	Control	Control) Correlation ρ	Alpha		

The sample sizes match Chow and Liu (2014).