Chapter 154

Non-Inferiority Tests for Two Means in a Cluster-Randomized Design with Clustering in Only One Arm

Introduction

This procedure computes power and sample size for a *non-inferiority* test in cluster-randomized designs in which the outcome is a continuous normal random variable and clustering occurs in only one arm.

Cluster-randomized designs are those in which whole clusters of subjects (classes, hospitals, communities, etc.) are randomized into a treatment group or a control group. In this case, the means of the two arms (groups), where the second arm is made up of individuals and the first arm is made up of K_i clusters of M_{ij} individuals each, are to be tested using a modified *z* test.

For example, one arm might receive individual intervention (such as medicine) while the other receives this medicine plus some type of group therapy session. The fact that they attend this therapy session implies that they are "clustered". Thus the clustering occurs in only one arm.

It should be noted that we could not find any published results about non-inferiority testing with clusterrandomized designs with clustering in only one group. What we could find were Schuirmann's TOST procedure and a discussion of how to adjust the t-test sample size results given by Campbell and Walters (2014). So, we applied the Campbell and Walters adjustment to Schuirmann's test.

The Statistical Hypotheses

Non-inferiority tests are examples of directional (one-sided) tests. This program module provides the input and output in a format that is convenient for these types of tests. This section will review the specifics of non-inferiority testing.

Remember that in the usual z-test setting, the null (H_0) and alternative (H_1) hypotheses for one-sided tests are defined as follows, assuming that $\delta = \mu_T - \mu_C$ is to be tested. For an *upper-tailed test* we have

$$H_0: \delta \leq 0$$
 versus $H_1: \delta > 0$

Rejecting this test implies that the mean difference is larger than the value δ . This test is called an *upper-tailed test* because it is rejected in samples in which the difference between the sample means is larger than *D*.

Following is an example of a *lower-tailed test*.

$$H_0: \delta \ge 0$$
 versus $H_1: \delta < 0$

Non-inferiority tests are special cases of the above directional tests. It will be convenient to adopt the following specialized notation for the discussion of these tests.

<u>Parameter</u>	<u>PASS Input/Output</u>	Interpretation
μ_T	Not used	<i>Mean</i> of the treatment population. This population is assumed to consist of those who have received the new treatment.
μ_{C}	Not used	<i>Mean</i> of the control population. This population is assumed to consist of those who have received the control (reference) treatment.
ε	NIM	<i>Margin of non-inferiority.</i> This is a tolerance value that defines the magnitude of the amount that is not of practical importance. This may be thought of as the largest change from the baseline that is considered to be trivial. The absolute value is shown to emphasize that this is a magnitude. The sign of the value will be determined by the specific design that is being used.
δ	δ	<i>True difference</i> . This is the value of $\mu_T - \mu_C$, the difference between the means.

Note that the actual values of μ_T and μ_C are not needed. Only their difference is needed for power and sample size calculations.

Non-Inferiority Tests

A *non-inferiority test* tests that the treatment mean is not worse than the control mean by more than the non-inferiority margin. The actual direction of the hypothesis depends on the response variable being studied.

Note that the following definitions work equally well whether the clustered arm is assigned to the treatment group or the control group.

Case 1: High Values Good, Non-Inferiority Test

In this case, higher values are better. The hypotheses are arranged so that rejecting the null hypothesis implies that the treatment mean is no less than a small amount below the reference mean, ε . The value of δ is often set to zero. The following are equivalent sets of hypotheses.

$H_0:\delta \leq -\varepsilon$	versus	$H_1: \delta > -\varepsilon, \ \varepsilon > 0$
$H_0: \mu_T - \mu_C \le -\varepsilon$	versus	$H_1: \ \mu_T - \mu_C > -\varepsilon, \ \varepsilon > 0$
$H_0: \mu_T \leq \mu_C - \varepsilon$	versus	$H_1: \ \mu_T > \mu_C - \varepsilon, \ \varepsilon > 0$

Case 2: High Values Bad, Non-Inferiority Test

In this case, lower values are better. The hypotheses are arranged so that rejecting the null hypothesis implies that the treatment mean is no more than a small amount above the reference mean, ε . The value of δ is often set to zero. The following are equivalent sets of hypotheses.

$H_0: \delta \geq \varepsilon$	versus	$H_1: \delta < \varepsilon, \ \varepsilon > 0$
$H_0: \mu_T - \mu_C \geq \varepsilon$	versus	$H_1: \ \mu_T - \mu_C < \varepsilon, \ \varepsilon > 0$
$H_0: \mu_T \ge \mu_C + \varepsilon$	versus	$H_1: \ \mu_T < \mu_C + \varepsilon, \ \varepsilon > 0$

Technical Details

Our formulation comes from Moerbeek and Wong (2008). They combine two mixed models: one for the arm made up of individuals and a second, more, complicated model for the arm which accounts for the clustering.

The model for the first arm (group 2) is

$$y_i = \beta_0 + x_i'\beta + r_i$$

where y_i is a continuous outcome, x_i is a vector of covariates for subject *i*, β is a vector of effects of these covariates, and r_i is a random error term with expectation zero and variance σ_r^2 .

The mixed model for the second (clustered) arm (group 1) is

$$y_{ij} = \beta_0 + \delta + x'_{ij}\beta + u_i + e_{ij}$$

where y_{ij} is a continuous outcome for subject $i = 1, ..., m_j$ within cluster j = 1, ..., k, δ is the treatment effect to be tested, u_i is a random error term for clusters with expectation zero and variance σ_u^2 , and e_{ij} is a random error term for subjects within a cluster with expectation zero and variance σ_e^2 .

Note that the variance of y_{ij} is $\sigma_u^2 + \sigma_e^2$. The intra-class correlation (ICC) is

$$\rho = \frac{\sigma_u^2}{\sigma_u^2 + \sigma_e^2}$$

These models can be combined into a single mixed model using

$$y_{ij} = \beta_0 + I_{ij}\delta + x'_{ij}\beta + I_{ij}u_i + e_{ij}$$

where I_{ij} is an indicator variable which is equal to one for subjects in the cluster arm and zero for subjects in the other, non-clustered, arm. Note that subjects in the non-clustered arm are assigned to a single "cluster" j = k + 1. Here k is the number of clusters. Note that $\sigma_r^2 \neq \sigma_u^2 + \sigma_e^2$, so the model is heteroscedastic (has unequal variances).

In this model, the treatment effect is measured by the difference in the two treatment means

$$\hat{\delta} = \bar{y}_T - \bar{y}_C$$

The variance of this estimator is

$$\operatorname{var}(\hat{\delta}) = \frac{\overline{m}\sigma_u^2 + \sigma_e^2}{\overline{m}k} + \frac{\sigma_r^2}{N_2} = \sigma_r^2 \left(\theta \,\frac{(\overline{m} - 1)\rho + 1}{\overline{m}k} + \frac{1}{N_2}\right)$$

where \overline{m} is the average cluster size, N_2 is the number of subjects in the non-clustered arm, and

$$\theta = \frac{\sigma_u^2 + \sigma_e^2}{\sigma_r^2}.$$

Using the above, a large sample formula for computing the power of a one-sided test of the significance of the treatment effect at significance level α is given by

$$\operatorname{var}(\hat{\delta}) = \left(\frac{\delta - \varepsilon}{z_{1-\alpha} + z_{Power}}\right)^2$$

For sample size calculation, we assume that the cluster sizes m_j are distributed with a mean cluster size of \overline{m} and a coefficient of variation cluster sizes of *COV*. The accuracy of the variance of the two group means, \overline{Y}_i , can be enhanced by replacing \overline{m} in the numerator of the first term of $\operatorname{var}(\delta)$ with $\overline{m}(COV^2 + 1)$. See Julious (2023) page 86.

Assume that $\delta = \mu_T - \mu_C$ is to be tested using a z-test. The statistical hypotheses are $H_0: \delta \le \varepsilon$ vs. $H_a: \delta > \varepsilon$. The test statistic

$$z = \frac{\bar{y}_T - \bar{y}_C - \varepsilon}{\sqrt{\operatorname{var}(\hat{\delta})}}$$

has an approximate normal distribution for a *subject-level* analysis.

Using the above, a large sample formula for computing the power of a one-sided test of the significance of the treatment effect at significance level α can be derived from

$$\operatorname{var}(\hat{\delta}) = \left(\frac{\delta - \varepsilon}{z_{1-\alpha} + z_{Power}}\right)^2$$

Note that Julious (2023) uses a homoscedastic model that gives the same power values as these when $\theta = 1$. Candlish *et al.* (2018) recommend that the more complicated heteroscedastic model be used because of their findings in a large simulation study.

Example 1 – Calculating Power

Suppose a non-inferiority, cluster-randomized study is to be conducted in which one arm (group 2) will receive an individual medical intervention while the other arm (group 1) receives this medicine plus a special group therapy session conducted by a trained therapist. These therapy sessions will be treated as clusters. Here, group 2 (the non-clustered subjects) is the 'control group' and group 1 (the clustered subjects) is the treatment group. The therapy sessions will involve 10 patients with a cluster size COV of 0.65. The point of the study is to determine if the treatment group is non-inferior to the control group.

At the time of the design of the trial, little is known about the variances, so the study will be powered in terms of standardized values. This is accomplished by the setting $\sigma_2 = 1$. The NIM is set to 0.5.

The parameter values are set as follows: alpha = 0.025, N2 = 70, K1 = 4 6 8 10, M1 = 10, COV = 0.65, NIM = 0.5, $\delta = 0.0$, $\sigma_2 = 1$, $\theta = 0.9$, 1.0, 1.1, and $\rho = 0.05$. Power is to be calculated using the standard normal distribution.

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	Power
Assign Group 1 (Clusters) to be the	Treatment Group
Higher Means Are	Better (H1: δ > -NIM, δ = μτ - μc)
Alpha	0.025
Group Allocation	Enter K1 and N2 individually
K1 (Number of Clusters)	4 6 8 10
M1 (Average Cluster Size)	10
COV (Coefficient of Variation of Cluster Sizes)	0.65
N2 (Number of Subjects)	70
NIM (Non-Inferiority Margin)	0.5
δ (Mean Difference = μτ - μc)	0
σ2 (Standard Deviation in Group 2)	1
Θ (Group Variance Ratio = $\sigma 1^2 / \sigma 2^2$)	0.9 1 1.1
ρ (Intracluster Correlation, ICC)	0.05

Output

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

Numeric Reports

Numeric Results	
Solve For:	Power
Group 1 Assignment:	Group 1 has Clusters and is the Treatment Group
Group 2 Assignment:	Group 2 does not have Clusters and is the Control Group
Group Allocation:	Enter K1 and N2 individually
Higher Means Are:	Better
Hypotheses:	H0:δ≤-NIM vs. H1:δ>-NIM

		(Treatine	nt) Clusters	Sample S	Size (Subje	ects)						
Power	Number of Clusters K1	Average Cluster Size M1	Coefficient of Variation of Cluster Sizes COV		Group 2 Control N2		Non- Inferiority Margin -NIM		Group Variance Ratio θ	ICC P	Standard Deviation Group 2 σ2	Alpha
0.57481	4	10	0.65	40	70	110	-0.5	0	0.9	0.05	1	0.025
0.56222	4	10	0.65	40	70	110	-0.5	0	1.0	0.05	1	0.025
).55012	4	10	0.65	40	70	110	-0.5	0	1.1	0.05	1	0.025
).69611	6	10	0.65	60	70	130	-0.5	0		0.05	1	0.025
).68459	6	10	0.65	60	70	130	-0.5	0		0.05	1	0.025
).67335	6	10	0.65	60	70	130	-0.5	0		0.05	1	
).77114	8	10	0.65	80	70	150	-0.5	0		0.05	1	
).76132	8	10	0.65	80	70	150	-0.5	0		0.05	1	
).75163	8	10	0.65	80	70	150	-0.5	0	1.1		1	
0.81996	10	10	0.65	100	70	170	-0.5	0		0.05	1	0.025
0.81173 0.80354	10 10	10 10	0.65 0.65	100 100	70 70	170 170	-0.5 -0.5	0		0.05 0.05	1	0.025 0.025
Power (1 //1	Т	he numbe	pility of rejecting of clusters in the cluster size of	group 1.					itnesis is t	rue.		
COV	Т	he coeffic average	ient of variation cluster size.	n of the clus	ter sizes.	This is		ard deviatio	n of cluste	er size	s divided b	y the
N1, N2,			r of subjects ir	aroune 1 a		1.11						
-NIM		0	of non-inferior	ity. Since h	igher mea	ans are	e better, this	s value is ne	egative an			m
		distance non-inferi he mean matter wh	of non-inferior below the cont or. difference in th nether the treat	ity. Since h rol group m e response ment mean	igher mea ean that t at which (μτ) is as	ans are he trea the po ssociat	e better, this atment mea wer is calcu ed with the	s value is ne in can be ar ulated. δ = μ group with	egative an nd still be ит - µс. No	consid ote tha	dered as it it does no	ot
-ΝΙΜ δ Ə	т	distance non-inferi he mean matter wh clustering he ratio of	of non-inferior below the cont or. difference in th	ity. Since h rol group m e response ment mean rations lead	igher mea ean that t at which (μτ) is as to the sa	ans are he trea the po ssociat me sta	e better, this atment mea wer is calcu ed with the utistical hyp	s value is no in can be an ulated. $\delta = \mu$ group with otheses.	egative an nd still be α ιτ - μc. Να clustering	consid ote that or the	dered as at it does no e group wit	ot h no
δ	T T T	distance non-inferi he mean clustering he ratio of $\sigma 1^2 = \sigma 2^2$ he intractor cluster. In within-clu	of non-inferior below the cont or. difference in th nether the treat g. Both configu the group 1 a	rity. Since h rol group m e response ment mean rations lead nd group 2 · h (ICC). The σu ² / (σu ² - deviation of	igher mea ean that t at which (μτ) is as to the sa variances e correlat + σe²), wh the respo	ans are the trea the po ssociat me sta . In this ion bet here ou onses i	better, this atment mean wer is calcu ed with the tistical hyp s case, Ø = ween a (ra u is the betwon n group 1	s value is no in can be ar ulated. $\delta = \mu$ group with otheses. : ($\sigma u^2 + \sigma e^2$) ndomly sele veen-cluste	egative an nd still be o r - μc. No clustering) / σ2². He ected) pair r standard	consid ote that or the nce, e	dered as at it does no e group wit Ə = 1 implio sponses wi	ot h no es that thin a

Summary Statements

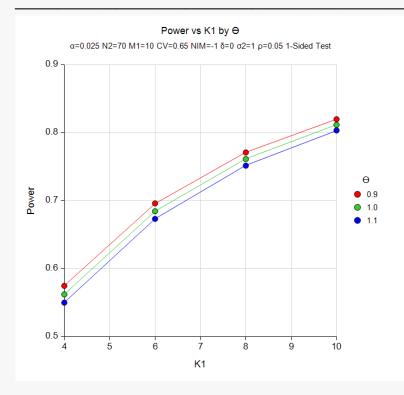
A parallel, two-group design (where higher means are considered to be better), with cluster-randomized subjects in Group 1 only (the treatment group), and no clustering in Group 2 (the control group), will be used to test whether the treatment mean (μ T) of Group 1 is non-inferior to the control mean (μ C) of Group 2, with a non-inferiority margin of -0.5 (H0: $\delta \le -0.5$ versus H1: $\delta > -0.5$, $\delta = \mu$ T - μ C). The comparison will be made using a one-sided mixed model test, with a Type I error rate (α) of 0.025. For Group 2 (the control group), the subject-to-subject standard deviation is assumed to be 1. The Group 1 (treatment) to Group 2 (control) variance ratio is assumed to be 0.9. For Group 1 (the treatment group), the intracluster correlation coefficient is assumed to be 0.05, and the coefficient of variation of cluster sizes is assumed to be 0.65. To detect a mean difference (μ T - μ C) of 0, with 4 clusters of 10 subjects per cluster in the treatment group (Group 1) (totaling 40 subjects), and 70 subjects in the control group (Group 2), the power is 0.57481.

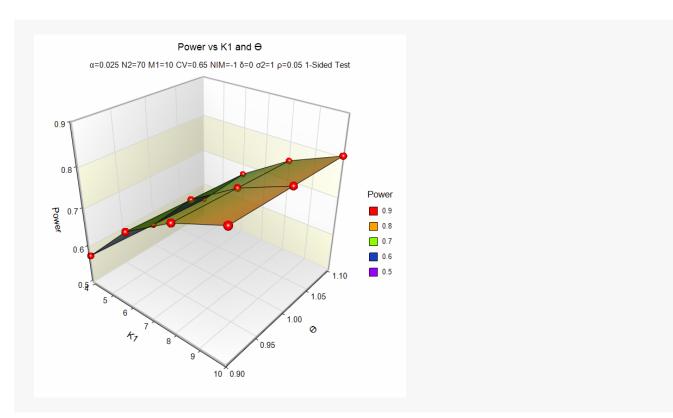
References	
,	d Wong, W.K. 2008. 'Sample size formulae for trials comparing group and individual treatments in del.' Statistics in Medicine, Vol. 27, pages 2850-2864.
	A. 2023. Sample Sizes for Clinical Trials. Second Edition. CRC Press. New York.
	Klar, N. 2000. Design and Analysis of Cluster Randomization Trials in Health Research. Arnold.

This report shows the power for each of the scenarios.

Plots Section

Plots





These plots show the power versus the number of clusters by the group variance ratio.

Example 2 – Validation using a Previously Validated Procedure

This procedure will be validated using the results of the previously validated procedure: **Non-Inferiority Tests for Two Means in a Cluster-Randomized Design**. In order to create a validation example, the cluster size of one group will be set to one.

Note that the previous procedure uses the non-central t distribution for calculations while this procedure uses the normal distribution. This will make the power values slightly different.

The parameter values are set as follows: *alpha* = 0.025, K1 = 70, M1 = 1, K2 = 8, M2 = 10, *COV* = 0, NIM = 0.5, δ = 0.0, σ = 1, and ρ = 0.05. The resulting power is calculated to be 0.78794.

Setup of the Validation Procedure

If the **Non-Inferiority Tests for Two Means in a Cluster-Randomized Design** 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 **Validation of Only One Clustered Arm Procedure** 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	Power
Higher Means Are	Better (Ha: δ > -NIM)
Test Statistic	T-Test Based on Number of Subjects
Alpha	0.025
K1 (Number of Clusters)	70
M1 (Average Cluster Size)	1
K2 (Number of Clusters)	8
M2 (Average Cluster Size)	10
COV of Cluster Sizes	0
NIM (Non-Inferiority Margin)	0.5
δ (Mean Difference = μ1 - μ2)	0
σ (Standard Deviation)	1
ρ (Intracluster Correlation, ICC)	0.05

Validation Output

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

Solve For Groups: Test Stati Higher Mo Hypothes	stic: eans Are	T-T Bet	Treatm est with ter	n DF Ba	: Contro sed on I H1: δ >	Number o	f Subje	cts						
		mber luster		с	luster S	Size	Sa	ample S	Size	Mean	Non- Inferiority	Standard	100	
Power				C 	luster \$ M2	Size COV		ample S N2	Size N	Mean Difference δ		Standard Deviation σ	ICC P	Alpha

PASS calculates the power value as 0.78794.

Setup

Now the parameter values of the current procedure are set as follows: alpha = 0.025, N2 = 70, K1 = 8, M1 = 10, COV = 0, NIM = 0.5, $\delta = 0.0$, $\sigma 2 = 1$, $\theta = 1$, and $\rho = 0.05$.

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	Power
Assign Group 1 (Clusters) to be the	Treatment Group
Higher Means Are	Βetter (H1: δ > -NIM, δ = μτ - μc)
Alpha	0.025
Group Allocation	Enter K1 and N2 individually
K1 (Number of Clusters)	8
M1 (Average Cluster Size)	10
COV (Coefficient of Variation of Cluster Sizes)	0
N2 (Number of Subjects)	70
NIM (Non-Inferiority Margin)	0.5
δ (Mean Difference = μ τ - μ c)	0
σ 2 (Standard Deviation in Group 2)	1
Θ (Group Variance Ratio = $\sigma 1^2 / \sigma 2^2$)	1
ρ (Intracluster Correlation, ICC)	0.05

Output

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

Solve Fo	or:	Power										
Group 1	Assignment:	Group 1 h	nas Clusters and	is the Treatm	nent Group							
	Assignment:		does not have Cl		the Contro	I Group	1					
Group Al	llocation:	Enter K1	and N2 individua	ally								
	leans Are:	Better										
Hypothes	ses:	H0: δ ≤ -N	NIM vs. H1:δ:	> -NIM								
	Group 1	(Trootmo)										
	Group 1		nt) Clusters		ize (Subje	ects)	Non-		Group		Standard	
Power	Group 1 Number of Clusters K1	(Treatmen Average Cluster Size M1				ects) Total N	Non- Inferiority Margin -NIM	Mean Difference δ	Group Variance Ratio θ	ICC P	Standard Deviation Group 2 σ2	Alpha

PASS calculates a power of 0.79308. The difference between this value and the previous value of 0.78794 is 0.00514. This slight difference occurs because the other procedure uses the non-central t distribution for its power calculation, but this procedure uses the normal distribution.