

This document contains screenshots for the power analysis for Homework 5.

- Click the “New Study” button to start a new power and sample size analysis.  
or
- Click the “Upload” button to upload a json file with a previous study design that you have saved.

## ◆ GLIMMPSE

General Linear Mixed Model Power and Sample Size

### Design a Study

Welcome to GLIMMPSE. The GLIMMPSE software calculates power and sample size for study designs with normally distributed outcomes. Select one of the options below to begin a power or sample size calculation.

New Study

Start a new design.

Upload

You have previously used GLIMMPSE and wish to work on a saved design.

For a new study: Add title here

◆ GLIMMPSE

General Linear Mixed Model Power and Sample Size

Untitled Study: Study title

Progress  Help  Save  Home 

Please pick a concise title for the study:

\_\_\_\_\_

\_\_\_\_\_



Click the “Power” or “Sample Size” button depending on what you want to solve for.  
In this case, we are solving for power.

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General Linear Mixed Model Power and Sample Size

module5: Solve for

Progress  Help  Save  Home 

Please indicate whether you would like to solve for power or total sample size.  
If you have a rough idea of the number of research participants you will be able to recruit, then solve for power.  
If you have few restrictions on recruitment then you may wish to solve for sample size.

Power

Sample Size



We now move to select the hypothesis test of interest. Thus, we click the Hotelling-Lawley trace.

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General Linear Mixed Model Power and Sample Size

module5: Statistical tests

Progress  Help  Save  Home 

Please choose one or more statistical tests. If you are unsure which to pick, we recommend the Hotelling Lawley Trace test due to its equivalence to a mixed model test.

- Hotelling Lawley Trace
- Pillai-Bartlett Trace
- Wilks Likelihood Ratio
- Box Corrected
- Geisser-Greenhouse Corrected
- Huynh-Feldt Corrected
- Uncorrected



Now we choose the Type I error rate.

A Type I error occurs when a scientist declares a difference when none is present in the population. The Type I error rate is the probability of that kind of error, a false positive, and is often referred to as  $\alpha$  (alpha). A Type I error rate can range from 0 to 1. Although the most commonly used value is 0.05, we recommend 0.01.



**Type I Error Rate**  
0.05

remove



Enter the outcome variable as shown below.

# GLIMMPSE

General Linear Mixed Model Power and Sample Size

module5: Outcomes

Progress Help Save Home

Enter the name of each outcome variable one at a time in the underlined space below. For example, in a study investigating cholesterol-lowering medication, the outcome variables could be HDL, LDL, and total cholesterol.

Note that repeated measurement information will be addressed on the next screen.

Please name the one or more outcomes.

Outcome	remove
SOAM1	



Click the “Define Repeated Measures” button to enter the repeated measures.

GLIMMPSE allows you to define within-participant factors, specified as repeated measures. An independent sampling unit provides one or more observations such that observations from one unit are statistically independent from any other distinct unit while observations from the same unit may be correlated. Repeated measures are present when a response variable is measured on each independent sampling unit on two or more occasions or under two or more conditions. The values of the repeated measures (that is, the levels of the within-participant factors) distinguish the occasions or conditions.

If the study includes repeated measures, click "Add Repeated Measure" and follow the prompts.

You may specify up to 5 repeated measures. Each repeated measure you add will apply to each outcome you specified on the previous page.

Define Repeated Measure



Enter the dimension to be measured as shown below.

What is the name of the dimension you will be measuring?

The text entered in the "Dimension" text box indicates the dimension over which measures were taken (e.g. time, days, locations, etc.). The choice of "Type" indicates whether the repeated measures are numeric (e.g. time), or categorical (e.g. arm, leg, hand).

Dimension:

Brain Region

Cancel Next: Type

Define the type of data related to the variable "Brain Region" as shown below.

What type of data is Brain Region?

Categorical  Numeric

Cancel Back Next: No. Measurements

Enter the spacing values as shown below.

Spacing

If the repeated measures are numeric, the spacing values must be unique nonnegative integers, in ascending order.

Measurement #1 at	0
Measurement #2 at	1

This screen shows a summary of the repeated measures.



GLIMMPSE allows you to define within-participant factors, specified as repeated measures. An independent sampling unit provides one or more observations such that observations from one unit are statistically independent from any other distinct unit while observations from the same unit may be correlated. Repeated measures are present when a response variable is measured on each independent sampling unit on two or more occasions or under two or more conditions. The values of the repeated measures (that is, the levels of the within-participant factors) distinguish the occasions or conditions.



If the study includes repeated measures, click "Add Repeated Measure" and follow the prompts.

You may specify up to 5 repeated measures. Each repeated measure you add will apply to each outcome you specified on the previous page.

Define Repeated Measure

Repeated Measure Dimension	Type	Measurements	Edit	Remove
Brain Region	Categorical	[ "0", "1" ]		

For this example, we do not add clustering.



An independent sampling unit provides one or more observations such that observations from one unit are statistically independent from any other distinct unit while observations from the same unit may be correlated.

In a clustered design, the independent sampling unit is a cluster, such as a community, school, or classroom. Observations within a cluster are correlated. The labels for observations within a cluster must be exchangeable. For example, child "ID" within classroom can be reassigned arbitrarily. In contrast, observations across time cannot be reassigned and should not be considered clustered observations. The common correlation between any pair of cluster members is termed the intraclass correlation or intracluster correlation.

To include clustering in the study, click "Add Clustering" and follow the prompts.

You may specify up to 10 levels of clustering.

Add Clustering



Click the “Define Fixed Predictor” to enter the predictors.

Each independent sampling unit has one or more observations which are statistically independent from observations from any other unit.

GLIMMPSE allows you to define fixed predictors which divide the independent sampling unit into groups. One common example of a fixed predictor is treatment, with values placebo and drug, for which the independent sampling unit is randomized to a placebo group or a drug group. Another is gender, with values male or female.

If the design has no fixed predictors, do not define any here.

The design you've described, means that every level of **Genotype** occurs at every level of **Treatment**. This concept applies to every combination of fixed predictors.

Define Fixed Predictor



Enter "treatment" as a predictor.

module5: Fixed predictors Progress  Help  Save  Home

Please name the predictor:

Specify the type of data related to "treatment".

◆ GLIMMPSE

General Linear Mixed Model Power and Sample Size

module5: Fixed predictors

Progress  Help  Save  Home 

What type of data is Treatment?

Nominal

Continuous

Cancel

Back: Data Type

Next: Groups

Enter the groups related to "treatment".

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General Linear Mixed Model Power and Sample Size

module5: Fixed predictors

Progress  Help  Save  Home 

Please name at  
least two groups



Groups:

-  Placebo
-  Chemotherapy

Cancel Back. Type Update predictor

Define the second predictor: "Genotype".

Please name the  
predictor:

Genotype

Cancel Next: Data Type

Specify the type of data.

What type of data is Genotype?

Nominal  Continuous

Cancel Back: Data Type Next: Groups

Enter the groups related to "Genotype".

Please name at least two groups:



Groups:

-  A
-  B
-  C
-  D

Cancel

Back: Type

Update predictor

This screen shows a summary of the fixed predictors.

## GLIMMPSE

General Linear Mixed Model Power and Sample Size

module5: Fixed predictors

Progress  Help  Save  Home 



Each independent sampling unit has one or more observations which are statistically independent from observations from any other unit.

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If the design has no fixed predictors, do not define any here.

The design you've described, means that every level of **Genotype** occurs at every level of **Treatment**. This concept applies to every combination of fixed predictors.

Define Fixed Predictor

### Fixed Predictors

Name	Type	Units	Groups	Remove	Edit
Treatment	NOMINAL		[ "Placebo", "Chemotherapy" ]		
Genotype	NOMINAL		[ "A", "B", "C", "D" ]		



Select the option “No Gaussian Covariate” for this example.

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General Linear Mixed Model Power and Sample Size

module5: Variability due to the gaussian covariate

Progress  Help  Save  Home 



A common experimental design is an analysis of covariance, which includes one or more fixed predictors and one or more continuous control variables, the "covariates." For example, one might run an experiment with 10 males and 10 females, with an indicator variable for gender as a fixed predictor and age as a covariate.

A common special case uses a series of repeated measurements on a continuous outcome. The first measurement, observed prior to treatment, is used as a baseline covariate. The other repeated measurements are outcomes in the general linear multivariate model.

GLIMMPSE can calculate power for hypotheses concerning the fixed predictors, optionally controlling for a single normally distributed covariate. If you plan to include a single normally distributed covariate in your model, use the switch below.

At present, the GLIMMPSE software does not calculate power for multiple normally distributed covariates nor non-normally distributed covariates.

No Gaussian Covariate

Gaussian Covariate



Select the specific study hypothesis as shown below.

Each power or sample size calculation is based on selecting a specific study hypothesis. The options below show the hypotheses which are available for the current study design. Specify the hypothesis that represents your scientific question.

GLIMMSE chooses sensible contrast matrices based on cell means coding. Should you wish to define your own contrast matrices, pick the highest order interaction and choose from the advanced options in the hypothesis components.

Select a hypothesis from the list.

Effects Available for Consideration	Nature of Variation
<input type="radio"/> Treatment x Genotype x Brain Region: Interaction	Between x Between x Within
<input type="radio"/> Treatment x Brain Region: Interaction	Between x Within
<input type="radio"/> Genotype x Brain Region: Interaction	Between x Within
<input type="radio"/> Brain Region: Main Effect	Within
<input checked="" type="radio"/> Treatment x Genotype: Interaction	Between x Between
<input type="radio"/> Treatment: Main Effect	Between
<input type="radio"/> Genotype: Main Effect	Between
<input type="radio"/> Grand Mean	Between

Specify means for:



In this example, “All mean differences zero” was selected to indicate the type of contrast desired.

## ◆ GLIMMPSE

General Linear Mixed Model Power and Sample Size

module5: Between hypothesis

Progress  Help  Save  Home 

What type of contrast do you wish among the levels of the between predictors?

All mean differences zero

A parameter is a characteristic of a population. The parameters of interest are the group means.

The null hypothesis is that all pairwise differences between group means are the same.

Show Advanced Options



This screen gives you the option to select a value different than zero for the contrast comparison constant.

## ◆ GLIMMPSE

General Linear Mixed Model Power and Sample Size

module5: Theta 0

Progress  Help  Save  Home 



A hypothesis compares parameters to a constant, the contrast comparison constant,  $\theta_0$ . This is almost always zero. If you choose a value other than zero, be sure that you understand that the hypothesis you define is scientifically meaningful. Also note that the description and interpretation of your hypothesis given when choosing your contrasts will be affected.



Enter the smallest group size as shown.

## ◆ GLIMMPSE

General Linear Mixed Model Power and Sample Size

module5: Smallest group size

Progress  Help  Save  Home 

Enter the number of independent sampling units in the smallest group in the study. You may enter multiple values for the smallest group size in order to consider a range of total sample sizes.

If you wish to consider fractional group sizes, specify an appropriate integer here and use fractional relative group size values.

Would you like to add another smallest group size?



**Smallest Group Size**

5

remove





Enter the group size ratios as shown below.

For equal group sizes, input a "1" in the block next to each group. This is the default study design.

For unequal group sizes, specify the ratio of the group sizes. For example, consider a design with an active drug group and a placebo group. If twice as many study participants receive the placebo, a value of "2" would be selected for the placebo group, and a value of "1" would be selected for the active drug group.



**Group size ratios**

		Genotype			
		A	B	C	D
Treatment	Placebo	1	1	1	2
	Chemotherapy	1	1	1	2

Enter the mean values for the outcome SOAM1 within each group.

The table below shows the mean values for outcome **SOAM1** within each group in the study. Each group is represented by a row in the table.

Enter the mean values you expect to observe for outcome **SOAM1** within each group. The table should contain at least one value that is non-zero. Also, at least two groups should have means which differ by a scientifically meaningful amount.

Expected mean values, per group, for **SOAM1**

Placebo, A	3.145
Placebo, B	3.145
Placebo, C	3.145
Placebo, D	3.145
Chemotherapy, A	2.125
Chemotherapy, B	2.325
Chemotherapy, C	2.525
Chemotherapy, D	2.975

Set blank values to

value



Enter the scale factor for the means.

## ◆ GLIMMPSE

General Linear Mixed Model Power and Sample Size

module5: Scale factor for the marginal means

Progress  Help  Save  Home 

In power analysis, it is not possible to know the exact values of means before the experiment is observed. Scale factors allow you to consider alternative values for the means by scaling the values entered on the previous screen.

For example, entering the scale factors 0.5, 1, and 2 would compute power for the mean values divided by 2, the mean values as entered, and the mean values multiplied by 2.

Enter a scale factor:

number > 0 

**Scale Factor**

remove

1



Enter the standard deviation.

Enter the standard deviation you expect to observe for each outcome.

Outcome	Standard Deviation
SOAM1	0.2623928



Enter the scale factor variance.

## GLIMMPSE

General Linear Mixed Model Power and Sample Size

module5: Scale factor variance

Progress  Help  Save  Home 

Changes in variability can dramatically affect power and sample size results. It is not possible to know the variability until the experiment is observed. Scale factors allow you to consider alternative values for variability by scaling the calculated covariance matrix. For example, entering the scale factors 0.5, 1, and 2 would compute power for the covariance matrix divided by 2, the covariance matrix as entered, and the covariance matrix multiplied by 2.

You may add up to 10 scale factors.

Choose a number greater than zero



Scale Factor

remove

1



For this example, we don't need to specify the confidence intervals.

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General Linear Mixed Model Power and Sample Size

module5: Confidence intervals

Progress  Help  Save  Home 



If the means ( $\mathbf{B}$ ) or the error covariance ( $\Sigma_e$ ) are sample estimates, then the power values produced from these matrices will be random quantities. To account for this randomness, GLIMMPSE can calculate confidence intervals for power values using the techniques described by Taylor and Muller (1995), Gribbin et al. (2013), and Park (2007).



Include Confidence Intervals

Click the "Calculate" button to see the results.

## GLIMMPSE

General Linear Mixed Model Power and Sample Size

module5: Calculate

Progress  Help  Save  Home 

Calculate

Download result

Results Matrices Design

Design



Hypothesis



Design Dimensions



Parameters



Optional Specifications



We can save results and study design inputs by using the “Save” button.

## ◆ GLIMMPSE

General Linear Mixed Model Power and Sample Size

module5: Calculate

Progress  Help  Save  Home 

Calculate

Download result

Results Matrices Design

Power	Total Sample Size	Means Scale Factor	Variability Scale Factor	Test	Power Method	Type I Error Rate
0.971	50	1	1	Hotelling Lawley Trace	conditional	0.05