

# Mixed Model Power Analysis by Example: Using Free Web-based Software

Western North American Region

International Biometric Society

Sarah M. Kreidler, Keith E. Muller and Deborah H. Glueck

June 20, 2012

# Grant support

2

The progress described was supported by the National Cancer Institute of the National Institutes of Health under award number NCI 3K07CA088811-06S, and by the National Institute of Dental and Craniofacial Research under award NIDCR 1 R01 DE020832-01A1. The content is solely the responsibility of the authors, and does not necessarily represent the official views of the National Cancer Institute, the National Institute of Dental and Craniofacial Research nor the National Institutes of Health.

# Outline

3

- **Motivate the need for GLIMMPSE**
- **Introduce the GLIMMPSE software**
- **Present GLIMMPSE validation results**
- **Demonstrate an ANOVA sample size calculation**

# Outline

4

- **Motivate the need for GLIMMPSE**
- Introduce the GLIMMPSE software
- Present GLIMMPSE validation results
- Demonstrate an ANOVA sample size calculation

# Motivation

5

- Power and sample size calculation is critical for ethical study design.
- Known results are underutilized.
- Our goal: provide a user-friendly tool for calculating power and sample size.

# Outline

6

- Motivate the need for GLIMMPSE
- **Introduce the GLIMMPSE software**
- Present GLIMMPSE validation results
- Demonstrate an ANOVA sample size calculation

# What is GLIMMPSE?

7

- GLIMMPSE is an open-source, online tool for calculating power and sample size for the general linear multivariate model (GLMM) and for a broad class of general linear mixed models (LMM)
  - ▣ <http://glimmpse.samplesizeshop.com/>
- Supported models
  - ▣ GLMM/LMM with Gaussian errors and fixed predictors only
  - ▣ GLMM/LMM with Gaussian errors and fixed predictors plus a single Gaussian covariate

# Related Publications

8

- GLMM with fixed predictors
  - ▣ Muller and Peterson, 1984, *Comp Stat and Data Analysis*
  - ▣ Muller and Barton, 1989, *JASA*
  - ▣ Muller *et al.*, 1992, *JASA*
  - ▣ Muller *et al.*, 2007, *Stats in Med*
  
- GLMM with fixed predictors and a Gaussian covariate
  - ▣ Glueck and Muller, 2003, *Stats in Med*



# Why not SAS or R?

9

- ❑ Need programming expertise to use SAS and R
- ❑ Not all researchers have a SAS license
- ❑ SAS and R not easily accessible via the web

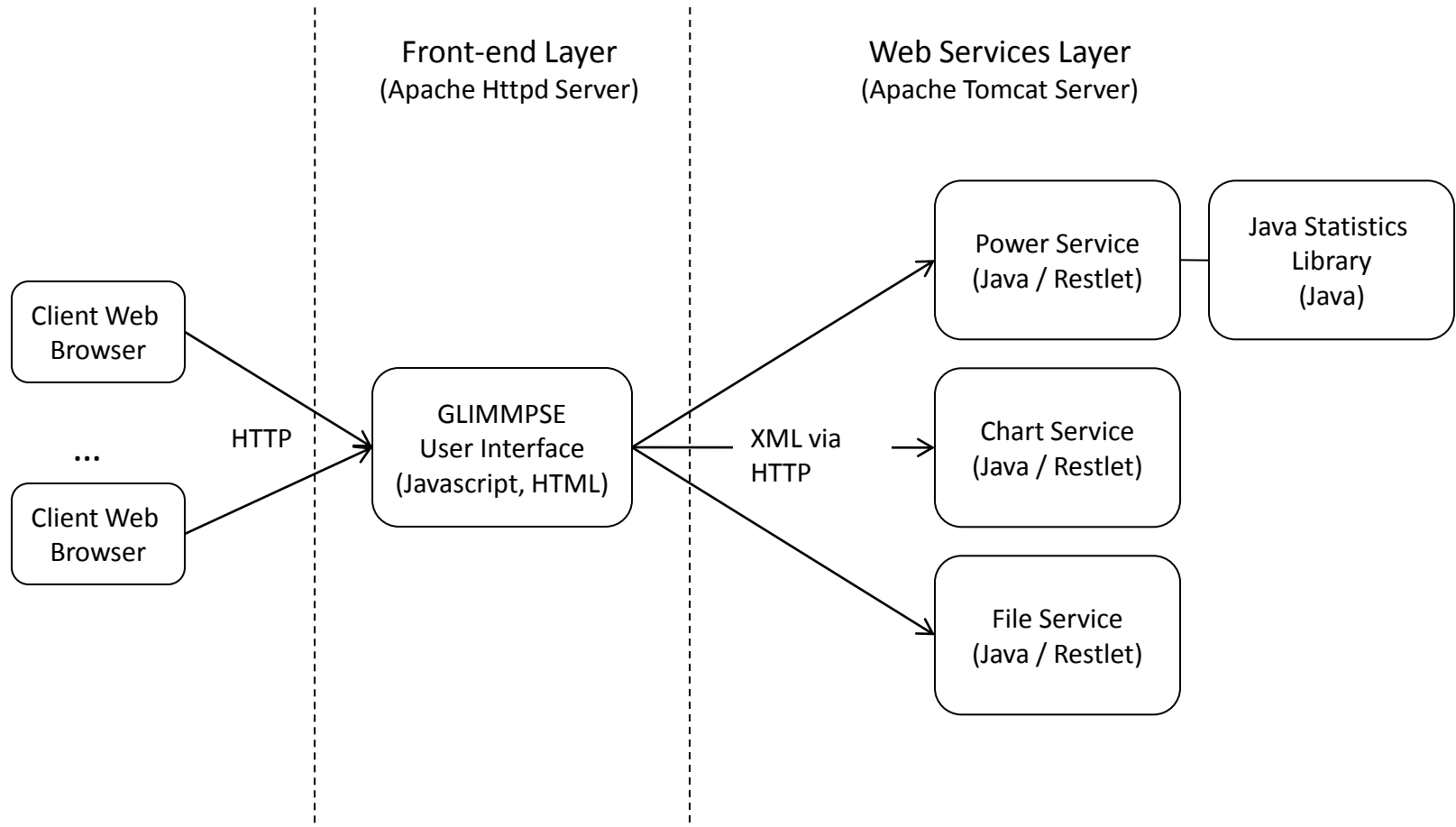
# Why a Web-based Interface?

10

- Web browsers are familiar, widely used; requires zero programming
- Java web services is proven technology
  - ▣ Free and cross-platform
  - ▣ Flexible, scalable framework
  - ▣ Encapsulation of power calculation code
  - ▣ Allows for future expansion

# GLIMMPSE Architecture

11



# Software Team

12

- Sarah Kreidler, Tech Lead
- Vijay Chander Akula, Software Engineer
- Uttara Sakhadeo, Software Engineer
- Manual Preparation:
  - ▣ Zacchary Coker-Dukowitz
  - ▣ Brandy Ringham
  - ▣ Yi Guo

# Two Interaction Modes

13

- Guided Mode
- Matrix Mode

# Outline

14

- Motivate the need for GLIMMPSE
- Introduce the GLIMMPSE software
- **Present GLIMMPSE validation results**
- Demonstrate an ANOVA sample size calculation

# GLIMMPSE Accuracy

15

- Maximum absolute deviation (MAD) used to assess accuracy of GLIMMPSE power values
- Compared to results from published power values and values computed with published software
- Compared to simulation

# Validation Results for Fixed Designs

16

Table 2. Accuracy Results for Power Values in GLMM(F) Designs

Example	Mean Calculation CPU Time (sec. $\times 10^{-4}$ )	Mean Simulation CPU Time (sec.)	MAD for GLIMMPSE vs. POWERLIB	MAD for GLIMMPSE vs. Simulation
1	1.3	0.43	$9.5 \times 10^{-7}$	0.010
2	< 0.1	0.38	$2.5 \times 10^{-7}$	0.004
3	2.1	0.41	$9.0 \times 10^{-7}$	0.010
4	8.8	0.46	$9.5 \times 10^{-7}$	0.006
5	3.6	0.74	$9.7 \times 10^{-7}$	0.070
6	2.1	2.11	$9.6 \times 10^{-7}$	0.120
7	< 0.1	1.28	$7.7 \times 10^{-7}$	0.069
8	6.6	42.47	$9.7 \times 10^{-7}$	0.053
9 MB*	< 0.1	1.62	$6.6 \times 10^{-7}$	0.232
9 MEST**	4.2	1.63	$8.4 \times 10^{-7}$	0.045

\* Powers calculated using the  $F$  approximation described by Muller and Barton (1989)

\*\* Powers calculated using the  $F$  approximation described by Muller *et al.* (2007)



# Outline

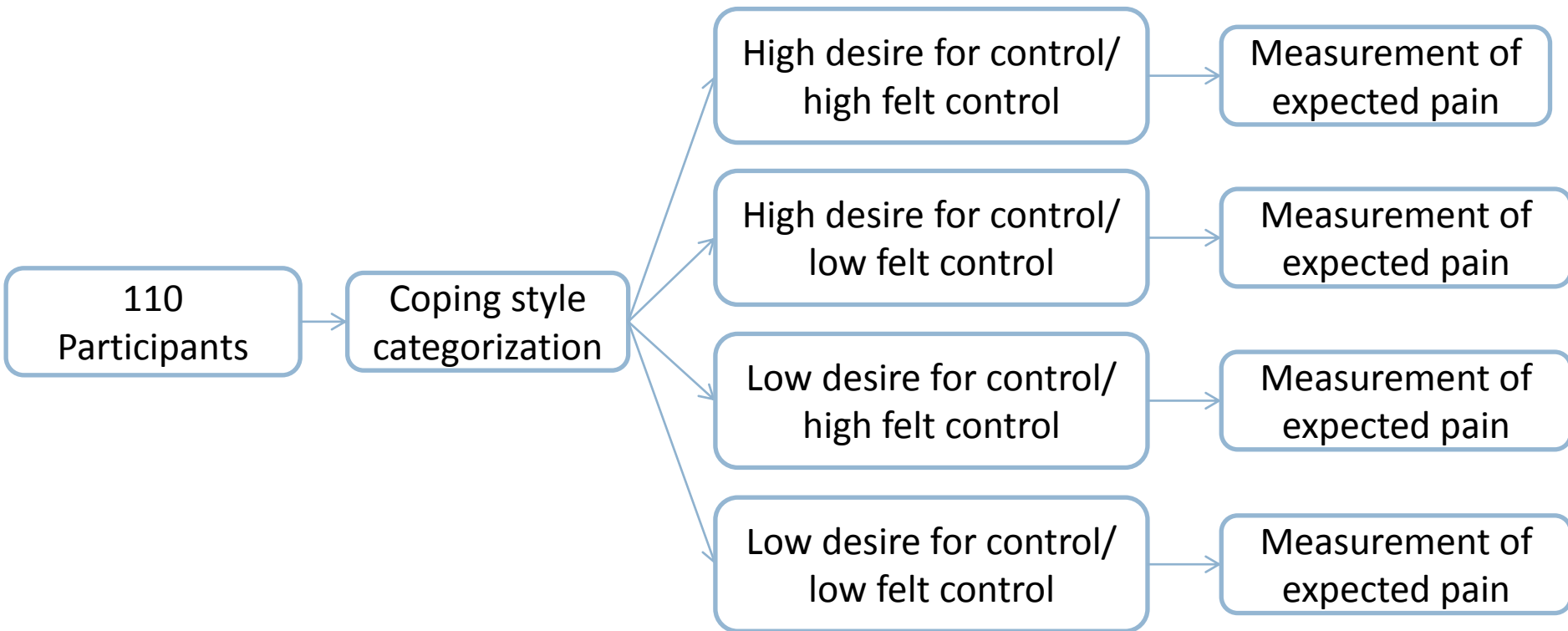
17

- Motivate the need for GLIMMPSE
- Introduce the GLIMMPSE software
- Present GLIMMPSE validation results
- **Demonstrate an ANOVA sample size calculation**

# Power Calculation in Practice: ANOVA

18

Law *et al.* (1994) studied coping style and expectations of pain with dental treatment



# Hypothesis of Interest

19

- Do pre-manipulation expectations of pain with dental treatment differ across individuals with different coping styles?
- ANOVA with four coping styles and a single outcome of expected pain

# GLIMMPSE Guided Mode

20

## Start Your Study Design

Select one of the options below to begin your power or sample size estimate.

Guided Study Design	Matrix Study Design	Upload a Study Design
Build common study designs including ANOVA, ANCOVA, and regression with guidance from the study design wizard. This mode is designed for more applied researchers including physicians, nurses, and other principal investigators.	Directly enter the matrices for the general linear model. This mode is designed for users with advanced statistical training.	If you have previously saved a study design from GLIMMPSE, you may upload it here. Click browse to select your study design file.
<input type="button" value="Select"/>	<input type="button" value="Select"/>	<input type="text"/> <input type="button" value="Browse_"/>

Click the select button to enter guided mode

# Select a Sample Size Calculation

21

**Start**

Type I Error

Design

Coefficients


Contrasts


Null Hypothesis


Variability

Options

Results

 Save Design

 Help

 Cancel

**Which value are you solving for?**

To begin your calculation, please indicate whether you would like to solve for power or total sample size.

If you have a rough idea of the number of subjects you will be able to recruit, then solving for power may be more beneficial.

If you have fewer restrictions on recruitment and would like to ensure a well-powered study, then solving for sample size is likely to be more useful.

☐ Power

☒ Total Sample Size

Previous

Next

# Enter the Power Values Desired

22

**Start**

Type I Error

Design

Coefficients


Contrasts


Null Hypothesis


Variability

Options

Results

 Save Design

 Help

 Cancel

**Power Values**

Enter the desired power values in the list below. Power values are decimals between 0 and 1, with higher values indicating a greater likelihood of correctly rejecting your null hypothesis. Common values are 0.8 or 0.9.

Type the decimal into the listbox and click enter. To remove an item, highlight it and click the "Delete" button

Power Values:

Add

Delete

0.9

Previous

Next

# Enter Type I Error Values

23

Start

**Type I Error**

Predictors

Outcomes


Hypotheses


Differences Between Means


Variability

Options

Results

 Save Design

 Help

 Cancel

## Type I Error

Type I error indicates the probability of incorrectly identifying a significant difference when there is none (i.e. rejecting a true null hypothesis). Type I error values should be decimals between 0 and 1. The most commonly used values are 0.01, 0.05, and 0.1.

Enter the type I error values into the text box and hit enter. You may enter up to 5 values. To remove a value, select it in the list and click the "Delete" button.

Type I Error Values:

Add

Delete

0.01

Previous

Next

# Enter Fixed Predictors

24

Start

Type I Error

**Predictors**

Outcomes

Hypotheses

Differences Between  
Means

Variability

Options

Results

 Save Design

 Help

 Cancel

## Categorical Predictors

In the table below, specify any categorical predictors. Categorical predictors take on a set number of possible values (i.e. categories). A common example of a categorical predictor is treatment group, where research participants may be randomized to a placebo or an active drug group.

Enter the names of all categorical predictors in the left text box. For example, one might enter "drug" and "gender" as predictors.

For each predictor, highlight the predictor name from the list on the left below the "Predictor" text box, and type its associated category names in the "Categories" text box.

For the example above, you would highlight "drug", then enter "placebo" and "active" as categories. Next, you would highlight "gender" and type "male" and "female" as categories.

Predictor	Category
<input type="text"/>	<input type="text"/>
<input type="button" value="Add"/>	<input type="button" value="Add"/>
<input type="button" value="Delete"/>	<input type="button" value="Delete"/>
<div>coping style</div>	<div>high desire / low felt high desire / high felt low desire / low felt low desire / high felt</div>

Previous

Next



# Enter Study Outcomes

25

Start

Type I Error

Predictors

**Outcomes**

Hypotheses

Differences Between Means

Variability

Options

Results

## Outcomes

Please enter your outcome variables in the table below. Outcomes are the dependent variables in your study. For example, in a study investigating cholesterol-lowering medication, the outcome could be serum cholesterol levels.

Outcomes:


Add


Delete


expected pain

Previous

Next

 Save Design

 Help

 Cancel

# Select Primary Study Hypothesis

26

Start

Type I Error

Predictors

Outcomes


**Hypotheses**


Differences Between Means


Variability

Options

Results

 Save Design

 Help

 Cancel

## Hypotheses

Based on your study design so far, listed below are some potential hypotheses you may wish to test. Select the hypothesis which most closely resembles your primary study hypothesis. This hypothesis will be used to determine power for your study.

☒ The outcomes will differ by coping style

Previous

Next

# Specify Clinically Meaningful Differences

27

Start

Type I Error

Predictors

Outcomes

Hypotheses

**Differences  
Between Means**

Variability

Options

Results

## Estimated Means

In the table below, enter the approximate means you expect to see for each group in your study. You can enter mean values for each of the outcomes you specified. The groups are listed along the left hand side of the table, and the outcomes are listed across the top. When you are finished, click next to continue.

coping style	expected pain
high desire / low felt	<input type="text" value="5"/>
high desire / high felt	<input type="text" value="0"/>
low desire / low felt	<input type="text" value="0"/>
low desire / high felt	<input type="text" value="0"/>

Previous

Next

 Save Design




 Help

 Cancel

# Specify Variability in Expected Pain

28

Start	<b>Variability in Observed Outcomes</b>  On this screen, you will provide values to indicate the amount of variability in your outcome measures. This is typically reported as standard deviation values in the literature.  What is the standard deviation for the following outcomes?  expected pain <input type="text" value="7.6"/>
Type I Error	
Predictors	
Outcomes	
Hypotheses	
Differences Between Means	
<b>Variability</b>	<div>Previous</div> <div>Next</div>
Options	
Results	

 Save Design  
 Help  
 Cancel

# Additional Options...

29

- Scale factors for regression coefficients and variability
- Confidence intervals
- Statistical tests
- Power curves

# Power Results

30

Start

Type I Error

Predictors

Outcomes


Hypotheses


Differences Between Means


Variability

Options

**Results**

 Save Design

 Help

 Cancel

## Power Results

Test	Actual Power	Total Sample Size	Beta Scale	Sigma Scale	Alpha	Nominal Power	Power Method	Quantile
unirep	0.9017	244	1.0	1.0	0.01	0.9000	conditional	
unirep	0.9217	132	1.0	0.5	0.01	0.9000	conditional	
unirep	0.9061	488	1.0	2.0	0.01	0.9000	conditional	

[Save results](#) | [View matrices used for these results](#)

Previous

Next

# Matrix Mode for Complex Designs

31

- Allows direct input of matrices
- Sample size for multilevel and longitudinal designs
- Sample size for reversible mixed models

# Example Autoregressive Covariance

32

Start

Type I Error

Design

Coefficients

Contrasts

Null Hypothesis

**Variability**

Options

Results

Save Design

Help

Cancel

## Covariance of Errors: $\Sigma_e$ Matrix

For each independent sampling unit,  $\Sigma_e$  is the covariance of the random errors. For univariate designs,  $\Sigma_e$  will be a 1x1 matrix containing the variance of the error term. More complex structures may be entered for multivariate or repeated measures designs. Values for  $\Sigma_e$  are typically obtained from pilot data or previous studies.

$\Sigma_e$  is a square, symmetric matrix with dimensions equal to the number of columns in **B**.

Enter values for  $\Sigma_e$  in matrix below.

$\Sigma_e$  Matrix

3 × 3

1	0.5	0.25
0.5	1	0.5
0.25	0.5	1

Previous

Next



# Summary

33

- ❑ GLIMMPSE is an online tool for computing power and sample size for the general linear multivariate model and the mixed model
  - ▣ Power for designs with fixed predictors
  - ▣ Power for designs with a baseline covariate
- ❑ Usable by statisticians and scientists
- ❑ Free, web-based, open-source
- ❑ Version 2, available soon, will have guided mode for repeated measures, and multilevel designs