

# MGH/HST Athinoula A. Martinos Center for Biomedical Imaging

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MASSACHUSETTS  
GENERAL HOSPITAL



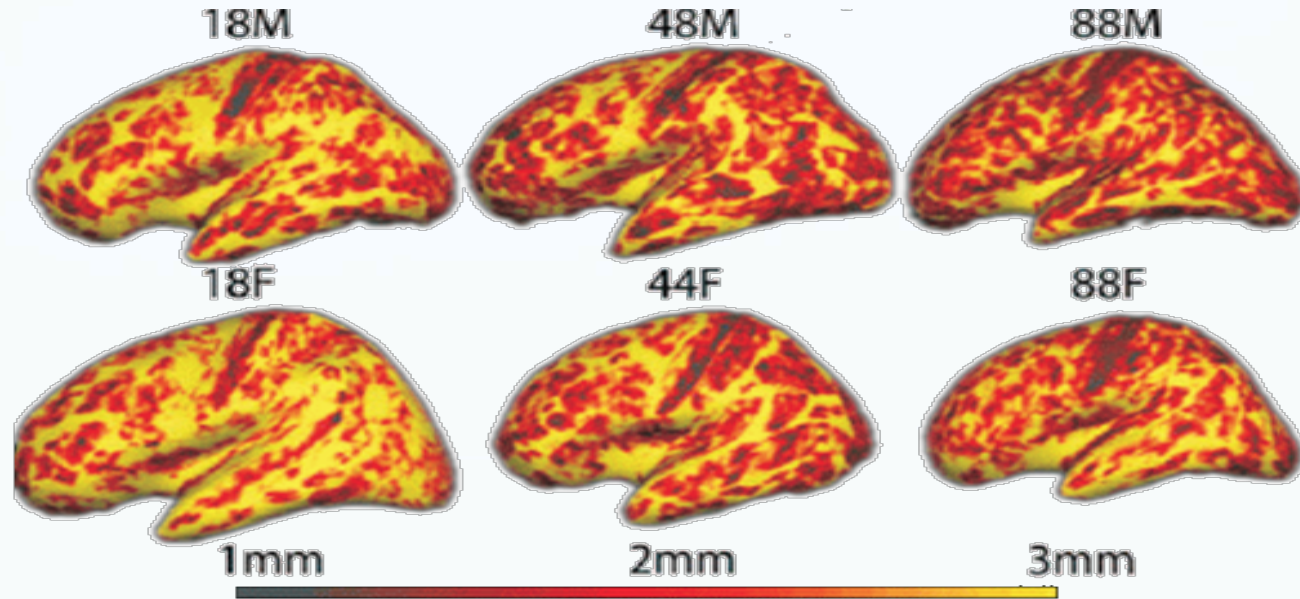
Harvard-MIT  
Health Sciences & Technology

# Surface-based Group Analysis in FreeSurfer

# Outline

- Processing Stages
- Command-line Stream
  - Assemble Data
  - Design/Contrast (GLM Theory)
  - Analyze
  - Visualize
- Interactive/Automated GUI (QDEC)
- Correction for multiple comparisons

# Aging Exploratory Analysis

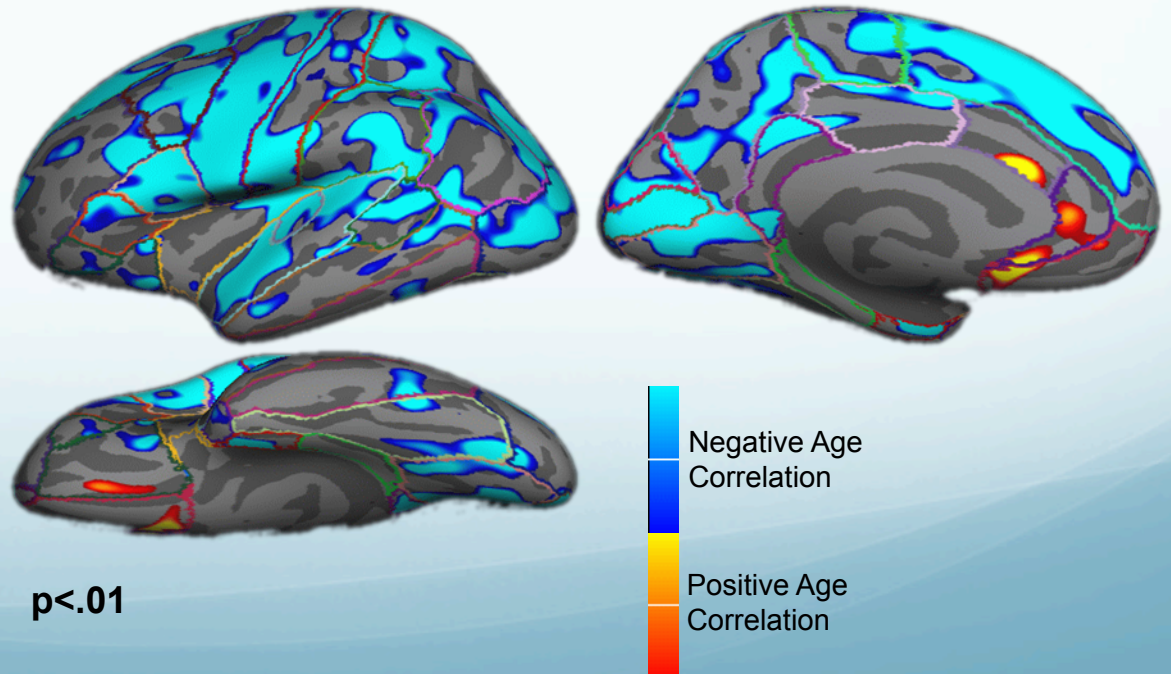
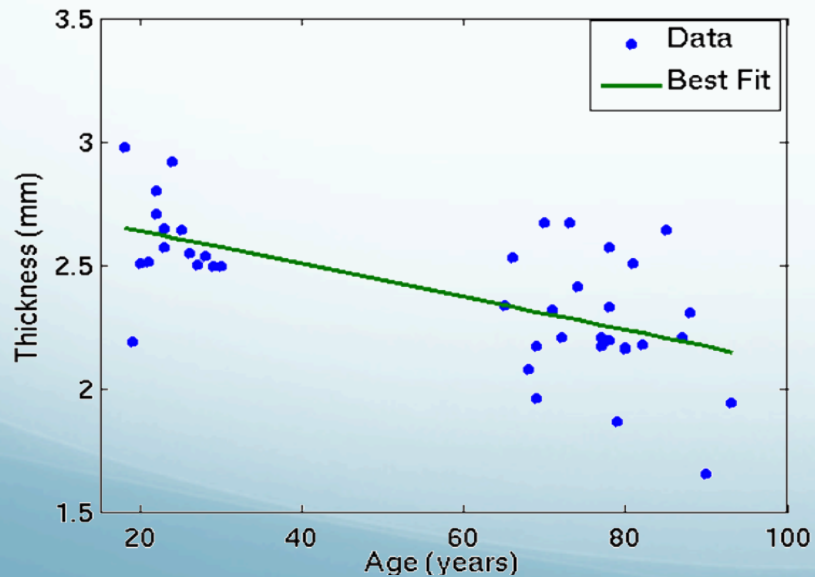
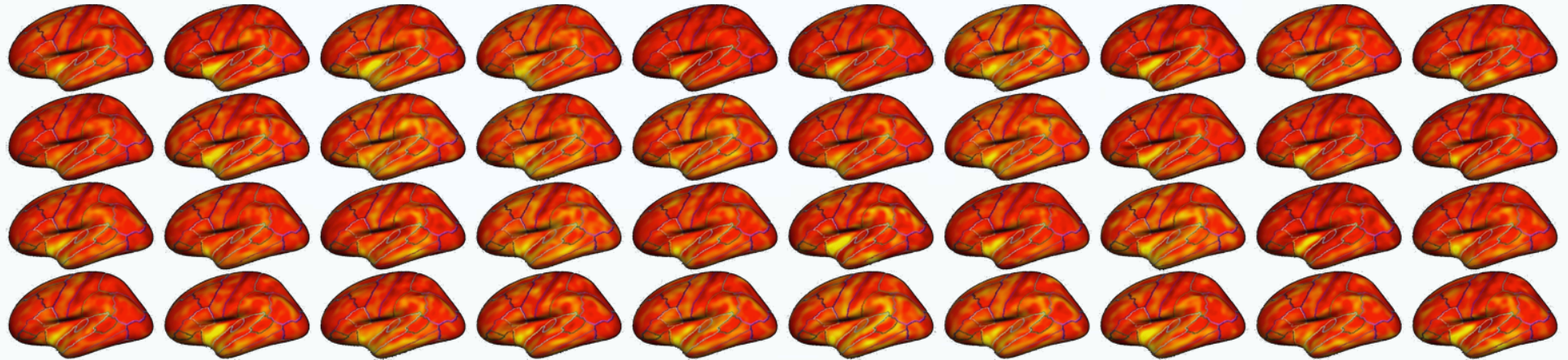


In which areas does thickness  
Change with age?

Cortical Thickness vs Aging  
Salat et al, 2004, Cerebral Cortex

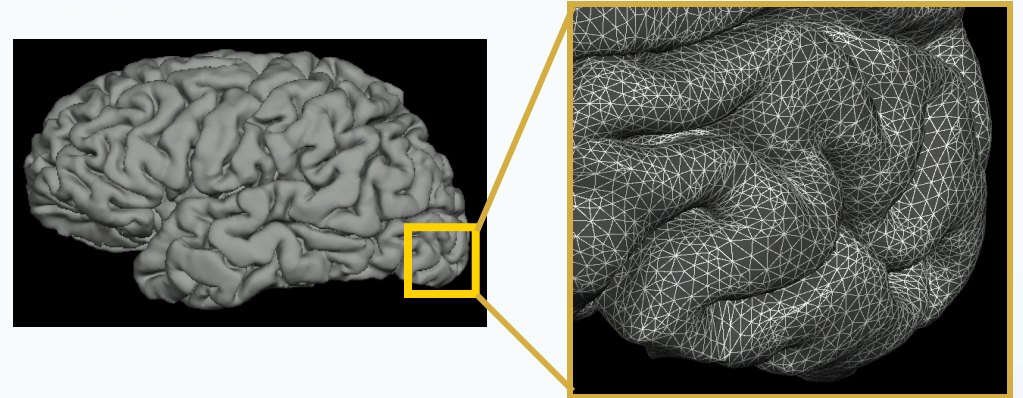
# Aging Thickness Study

N=40 (all in fsaverage space)



# Surface-based Measures

- Morphometric (e.g., thickness)
- Functional
- PET
- MEG/EEG
- Diffusion (?) sampled just under the surface



# Processing Stages

- Specify Subjects and Surface measures
- Assemble Data:
  - Resample into Common Space
  - Smooth
  - Concatenate into one file
- Model and Contrasts (GLM)
- Fit Model (Estimate)
- Correct for multiple comparisons
- Visualize

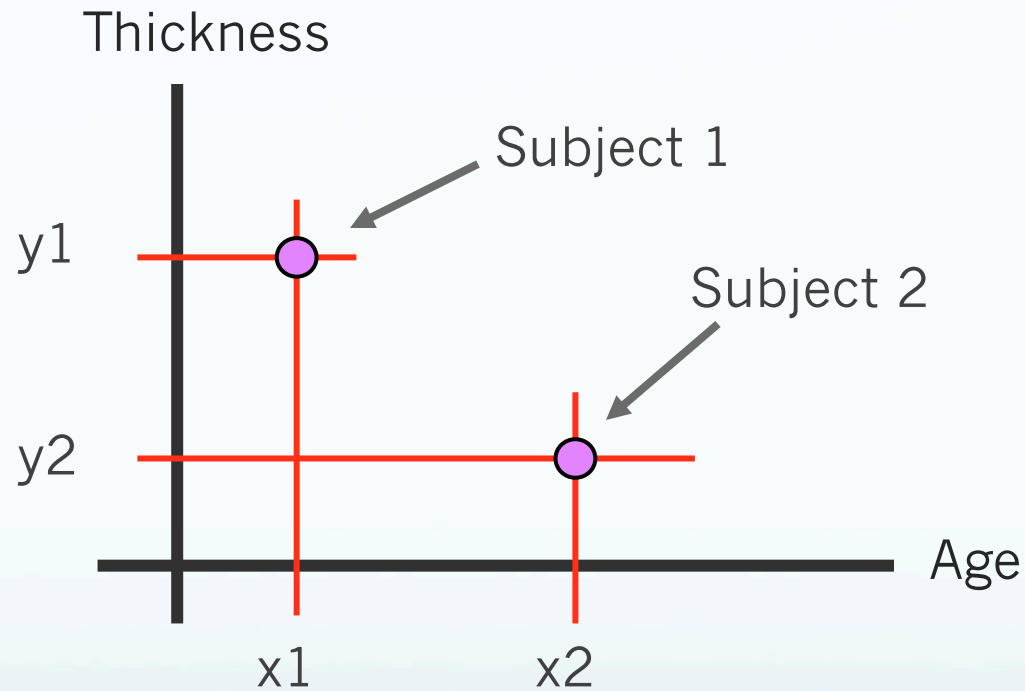
# The General Linear Model (GLM)

# GLM Theory

*Is Thickness correlated with Age?*

Dependent Variable,  
Measurement

HRF Amplitude  
IQ, Height, Weight

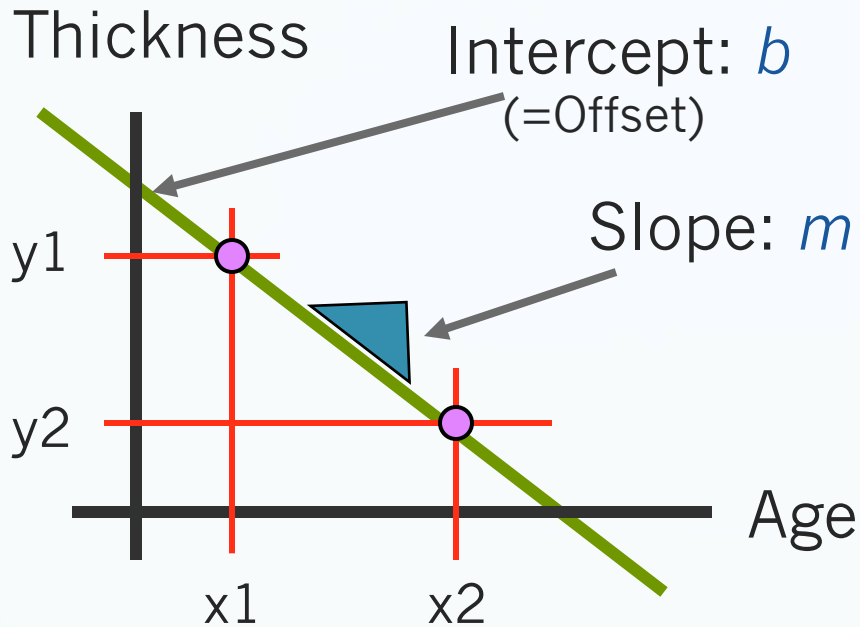


Of course,  
you would  
need more  
than two  
subjects ...

Independent Variable



# Linear Model



System of Linear Equations

$$y_1 = 1*b + x_1*m$$

$$y_2 = 1*b + x_2*m$$

Matrix Formulation

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} 1 & x_1 \\ 1 & x_2 \end{bmatrix} * \begin{bmatrix} b \\ m \end{bmatrix}$$

**X** = Design Matrix

**b** = Regression Coefficients

= Parameter estimates

= “betas”

= beta.mgh (mri\_glmfit output)

$$\mathbf{Y} = \mathbf{X} * \mathbf{b} \quad \mathbf{b} = \begin{bmatrix} b \\ m \end{bmatrix}$$

# Hypotheses and Contrasts

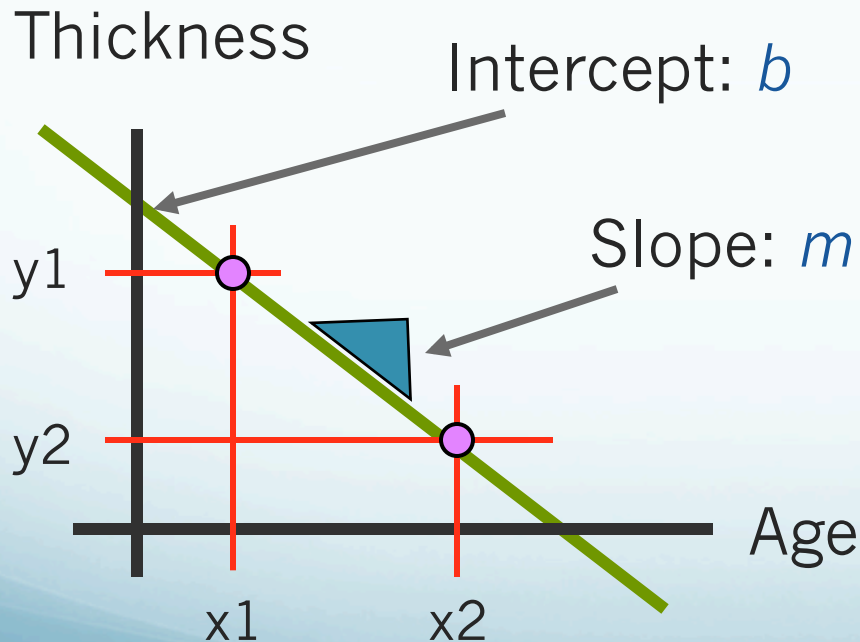
Is Thickness correlated with Age?

Does  $m = 0$ ?

Null Hypothesis:  $H_0: m=0$

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} 1 & x_1 \\ 1 & x_2 \end{bmatrix} * \begin{bmatrix} b \\ m \end{bmatrix}$$

$$m = \begin{bmatrix} 0 & 1 \end{bmatrix} * \begin{bmatrix} b \\ m \end{bmatrix}$$



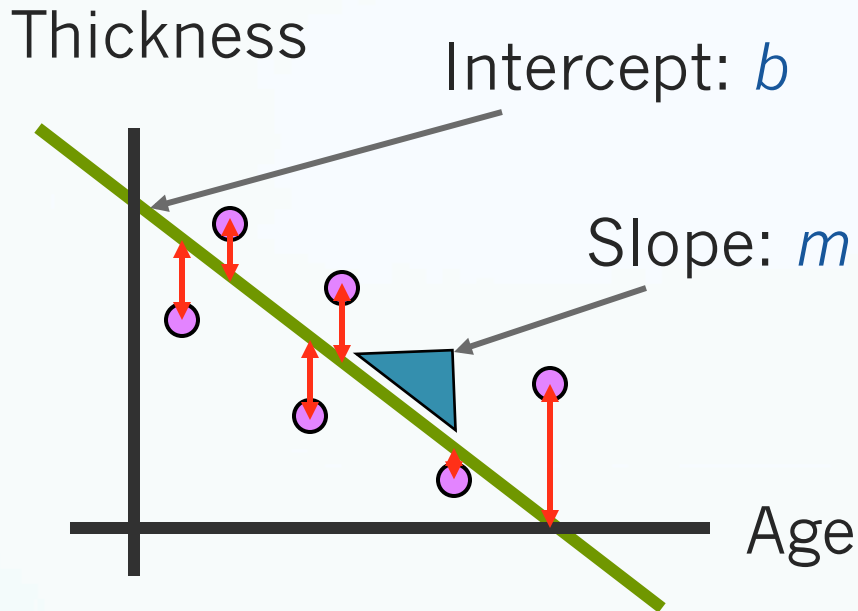
$$\mathbf{b} = \begin{bmatrix} b \\ m \end{bmatrix}$$

$$\mathbf{g} = \mathbf{C} * \mathbf{b} = 0$$

$\mathbf{C} = [0 \ 1]$ : Contrast Matrix

mri\_glmfit output: gamma.mgh

# More than Two Data Points



$$\begin{bmatrix} y1 \\ y2 \\ y3 \\ y4 \end{bmatrix} = \begin{bmatrix} 1 & x1 \\ 1 & x2 \\ 1 & x3 \\ 1 & x4 \end{bmatrix} * \begin{bmatrix} b \\ m \end{bmatrix} + \begin{bmatrix} n1 \\ n2 \\ n3 \\ n4 \end{bmatrix}$$

$$\mathbf{Y} = \mathbf{X} * \mathbf{b} + \mathbf{n}$$

$$\begin{aligned} y1 &= 1 * b + x1 * m + n1 \\ y2 &= 1 * b + x2 * m + n2 \\ y3 &= 1 * b + x3 * m + n3 \\ y4 &= 1 * b + x4 * m + n4 \end{aligned}$$

- Model Error
- Noise
- Residuals
- `eres.mgh`

# t-Test and p-values

$$Y = X * b + n$$

$$g = C * b$$

$$t = \frac{C * \beta}{\sqrt{\sigma^2 C * (X^T X)^{-1} C^T}}$$

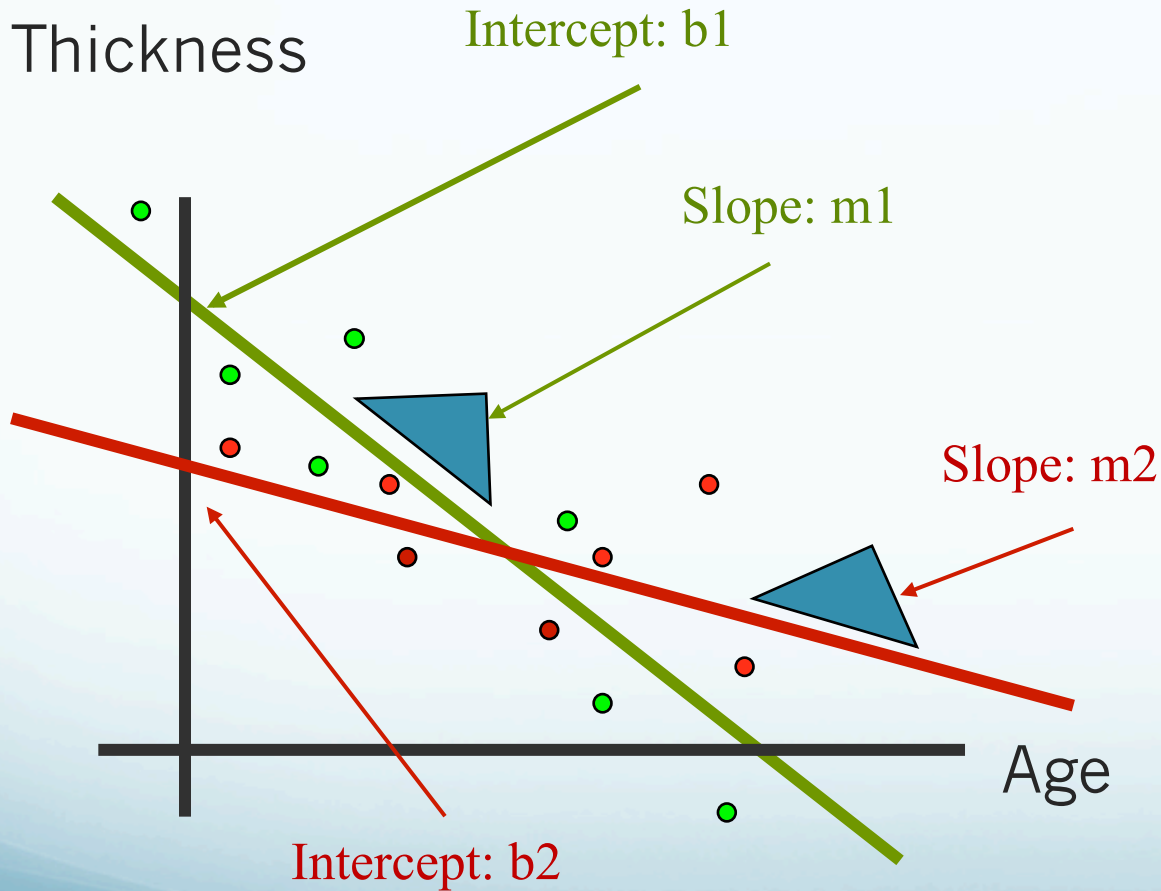
## p-value/significance

- value between 0 and 1
- closer to 0 means more significant

## FreeSurfer stores p-values as $-\log_{10}(p)$ :

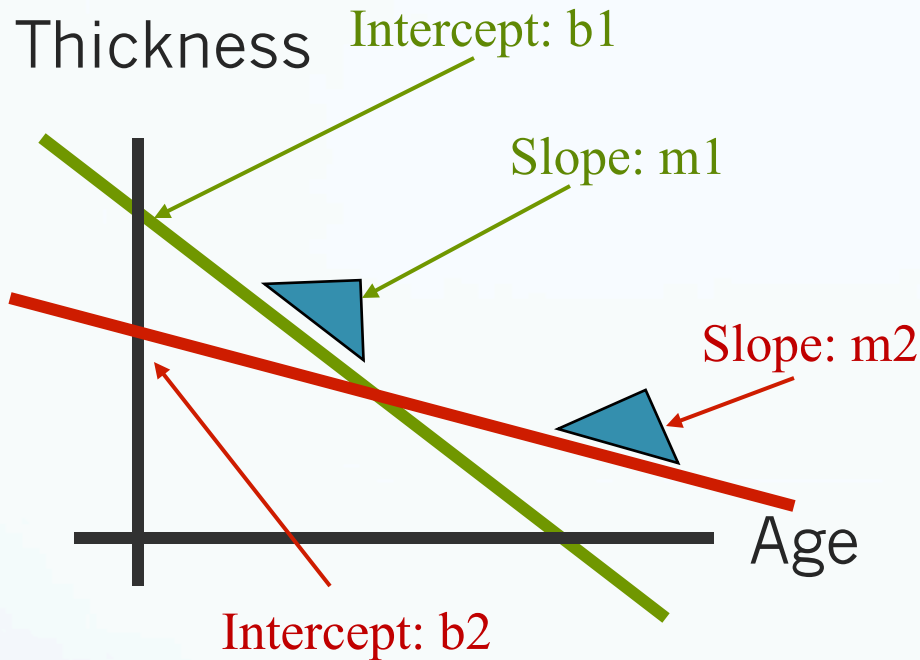
- $0.1 = 10^{-1} \rightarrow \text{sig}=1$ ,  $0.01 = 10^{-2} \rightarrow \text{sig}=2$
- sig.mgh files
- Signed by sign of  $g$
- p-value is for an unsigned test

# Two Groups



- Do groups differ in Intercept?
- Do groups differ in Slope?
- Is average slope different from 0?
- ...

# Two Groups



$$\begin{bmatrix} y_{11} \\ y_{12} \\ y_{21} \\ y_{22} \end{bmatrix} = \begin{bmatrix} 1 & 0 & x_{11} & 0 \\ 1 & 0 & x_{12} & 0 \\ 0 & 1 & 0 & x_{21} \\ 0 & 1 & 0 & x_{22} \end{bmatrix} * \begin{bmatrix} b_1 \\ b_2 \\ m_1 \\ m_2 \end{bmatrix} + n$$

$$\mathbf{Y} = \mathbf{X} * \mathbf{b} + \mathbf{n}$$

$$y_{11} = 1 * b_1 + 0 * b_2 + x_{11} * m_1 + 0 * m_2 + n_{11}$$

$$y_{12} = 1 * b_1 + 0 * b_2 + x_{12} * m_1 + 0 * m_2 + n_{12}$$

$$y_{21} = 0 * b_1 + 1 * b_2 + 0 * m_1 + x_{21} * m_2 + n_{21}$$

$$y_{22} = 0 * b_1 + 1 * b_2 + 0 * m_1 + x_{22} * m_2 + n_{22}$$

# Two Groups

Do groups differ in Intercept?

Does  $b_1 = b_2$ ?

Does  $b_1 \cdot b_2 = 0$ ?

$$\mathbf{C} = [+1 \ -1 \ 0 \ 0], \quad g = \mathbf{C}^* \mathbf{b}$$

Do groups differ in Slope?

Does  $m_1 = m_2$ ?

Does  $m_1 \cdot m_2 = 0$ ?

$$\mathbf{C} = [0 \ 0 \ +1 \ -1], \quad g = \mathbf{C}^* \mathbf{b}$$

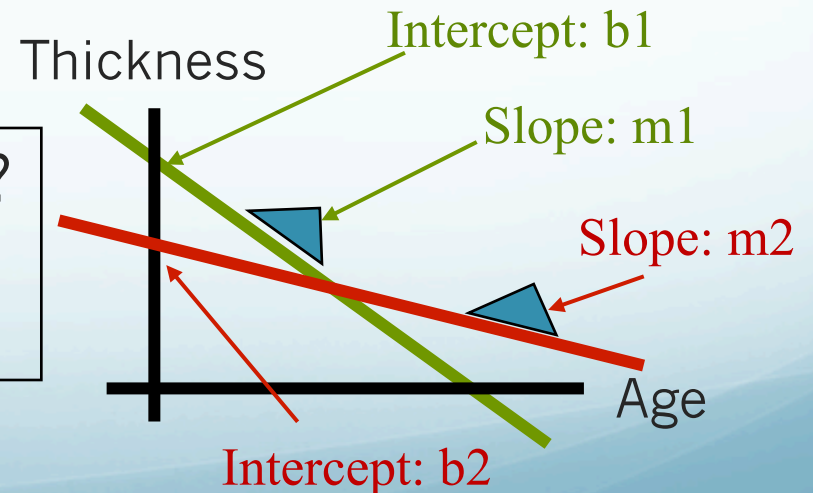
Is average slope different than 0?

Does  $(m_1 + m_2) / 2 = 0$ ?

$$\mathbf{C} = [0 \ 0 \ 0.5 \ 0.5], \quad g = \mathbf{C}^* \mathbf{b}$$

$$\mathbf{Y} = \mathbf{X}^* \mathbf{b} + \mathbf{n}$$

$$\mathbf{b} = \begin{bmatrix} b_1 \\ b_2 \\ m_1 \\ m_2 \end{bmatrix}$$



# Surface-based Group Analysis in FreeSurfer

- Create your own design and contrast matrices
- Create an FSGD File
  - FreeSurfer creates design matrix
  - You still have to specify contrasts
- QDEC
  - Limited to 2 discrete variables, 2 levels max
  - Limited to 2 continuous variables



# Command-line Processing Stages

- Assemble Data (*mris\_preproc*)
  - Resample into Common Space
  - Smooth
  - Concatenate into one file
- Model and Contrasts (GLM) (FSGD)
- Fit Model (Estimate) (*mri\_glmfit*)
- Correct for multiple comparisons
- Visualize (*tksurfer*)

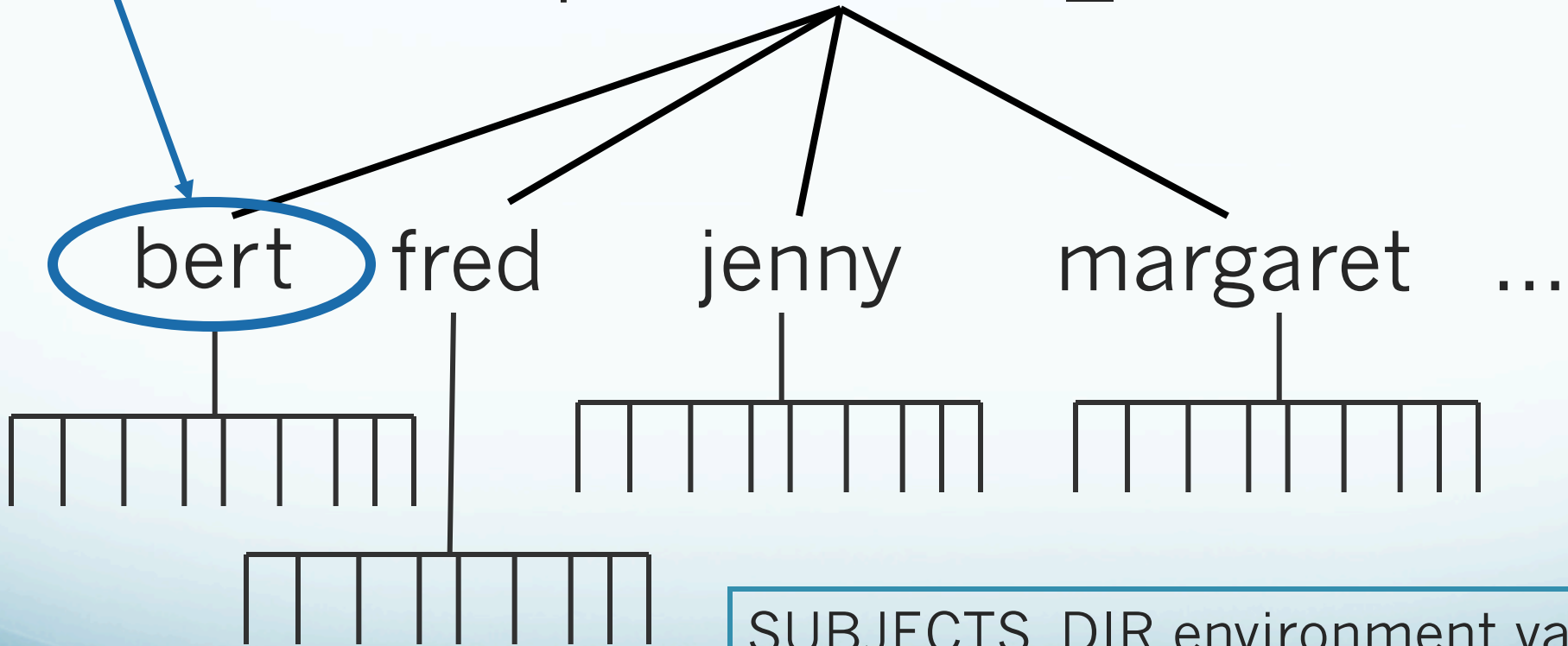
*recon-all -qcache*

Run after all editing is done.

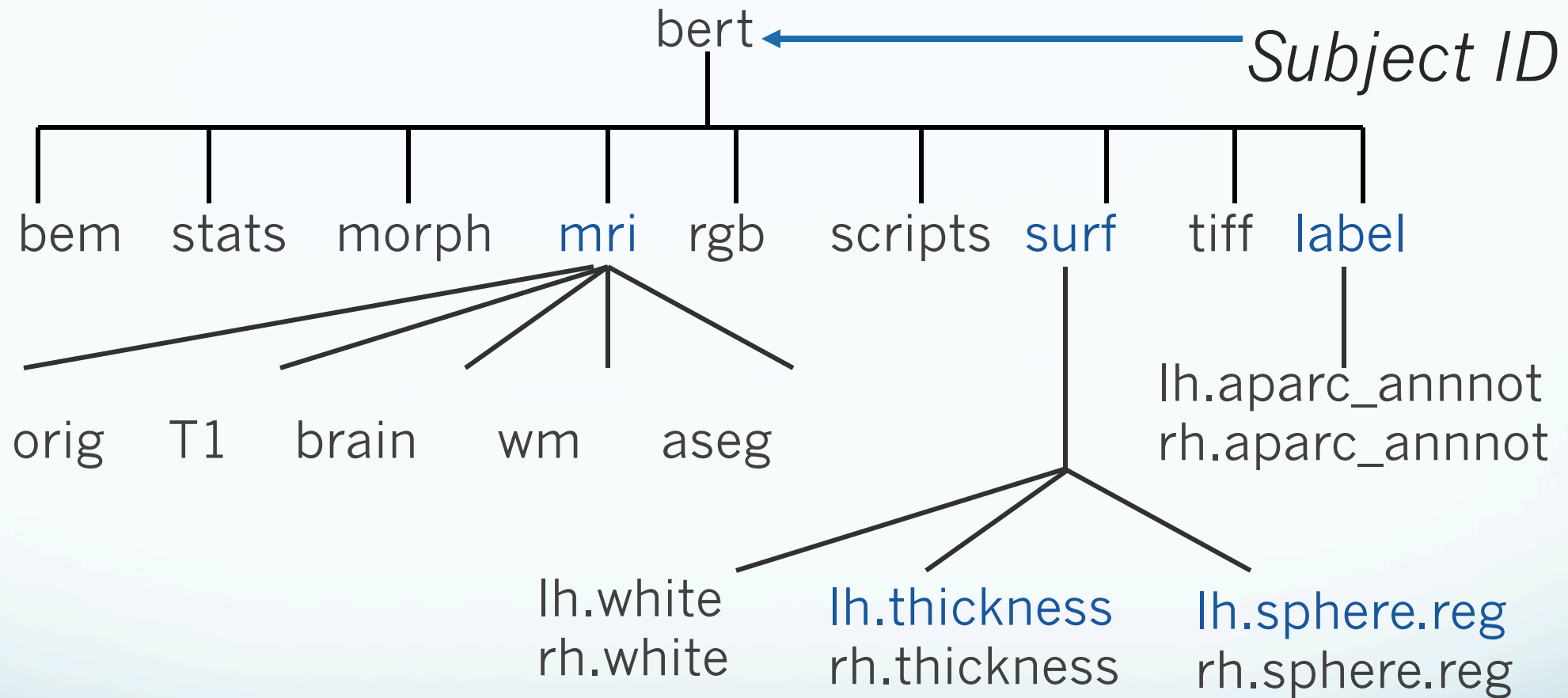
# Specifying Subjects

*Subject ID*

\$SUBJECTS\_DIR



# FreeSurfer Directory Tree



SUBJECTS\_DIR environment variable

# Example: Thickness Study

1. `$SUBJECTS_DIR/bert/surf/lh.thickness`
2. `$SUBJECTS_DIR/fred/surf/lh.thickness`
3. `$SUBJECTS_DIR/jenny/surf/lh.thickness`
4. `$SUBJECTS_DIR/margaret/surf/lh.thickness`
5. ....

# FreeSurfer Group Descriptor (FSGD) File

- Simple text file
- List of all subjects in the study
- Accompanying demographics
- Automatic design matrix creation
- You must still specify the contrast matrices
- Integrated with tksurfer

Note: *Can* specify design matrix explicitly with `--design`

# FSGD Format

```
GroupDescriptorFile 1
Class Male
Class Female
Variables                Age    Weight    IQ
Input bert               Male    10    100    1000
Input fred               Male    15    150    1500
Input jenny              Female  20    200    2000
Input margaret           Female  25    250    2500
```

- One Discrete Factor (Gender) with Two Levels (M&F)
- Three Continuous Variables: Age, Weight, IQ

Class = Group

Note: Can *specify* design matrix explicitly with --design

# FSGDF $\rightarrow$ X (Automatic)

Female Group  
Male Group

Male Age  
Female Age

$$X = \begin{bmatrix} 1 & 0 & 10 & 0 & 100 & 0 & 1000 & 0 \\ 1 & 0 & 15 & 0 & 150 & 0 & 1500 & 0 \\ 0 & 1 & 0 & 20 & 0 & 200 & 0 & 2000 \\ 0 & 1 & 0 & 25 & 0 & 250 & 0 & 2500 \end{bmatrix}$$

Age                  Weight                  IQ

$$C = \begin{bmatrix} -1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Tests for the difference in intercept/offset between groups

$$C = \begin{bmatrix} 0 & 0 & -1 & 1 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Tests for the difference in age slope between groups

# Another FSGD Example

- Two Discrete Factors
  - Gender: Two Levels (M&F)
  - Handedness: Two Levels (L&R)
- One Continuous Variable: Age

GroupDescriptorFile 1

Class MaleRight

Class MaleLeft

Class FemaleRight

Class FemaleLeft

Variables

Input bert

MaleLeft

Age

10

Input fred

MaleRight

15

Input jenny

FemaleRight

20

Input margaret

FemaleLeft

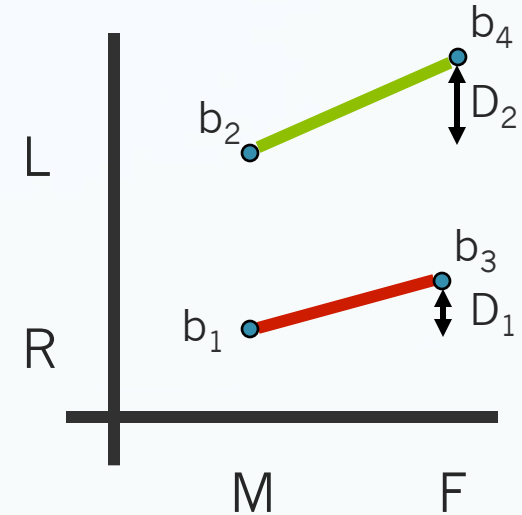
25

Class = Group



# Interaction Contrast

- Two Discrete Factors (no continuous, for now)
  - Gender: Two Levels (M&F)
  - Handedness: Two Levels (L&R)
- Four Regressors (Offsets)
  - MR ( $b_1$ ), ML ( $b_2$ ), FR ( $b_3$ ), FL ( $b_4$ )



```

GroupDescriptorFile 1
Class MaleRight
Class MaleLeft
Class FemaleRight
Class FemaleLeft
Input bert           MaleLeft
Input fred           MaleRight
Input jenny          FemaleRight
Input margaret       FemaleLeft
    
```

$$\begin{aligned}
 g &= D_1 - D_2 \stackrel{?}{=} 0 \\
 g &= (b_3 - b_1) - (b_4 - b_2) \\
 &= -b_1 + b_2 + b_3 - b_4 \\
 C &= [-1 \quad +1 \quad +1 \quad -1]
 \end{aligned}$$

# Factors, Levels, Groups

Usually each Group/Class:

- Has its own Intercept
- Has its own Slope (for each continuous variable)
- $N\text{Regressors} = N\text{Classes} * (N\text{Variables} + 1)$

# Factors, Levels, Groups, Classes

Continuous Variables/Factors: Age, IQ, Volume, etc.

Discrete Variables/Factors:

Gender, Handedness, Diagnosis

Levels of Discrete Variables:

- Handedness: *Left and Right*
- Gender: *Male and Female*
- Diagnosis: *Normal, MCI, AD*

Group or Class: Specification of All Discrete Factors

- Left-handed Male MCI
- Right-handed Female Normal

# Assemble Data: mris\_preproc

## mris\_preproc --help

--fsgd FSGDFile : Specify subjects thru FSGD File  
--hemi lh : Process left hemisphere  
--meas thickness : subjectid/surf/hemi.thickness  
--target fsaverage : common space is subject fsaverage  
--o lh.thickness.mgh : output “volume-encoded surface file”

Lots of other options!

- Output: lh.thickness.mgh – file with stacked thickness maps for all subjects
- Input to Smoother or GLM

# Surface Smoothing

- `mri_surf2surf --help`
- Loads stacked lh.thickness.mgh
- 2D surface-based smoothing
- Specify FWHM (eg, `fwhm = 10 mm`)
- Saves stacked lh.thickness.sm10.mgh
- Can be slow (~10-60min)
- `recon-all -qcache` (computes for each subject, run after you are finished editing subject)

# mri\_glmfit

- Reads in FSGD File and constructs **X**
- Reads in your contrasts (**C1**, **C2**, etc.)
- Loads data (lh.thickness.sm10.mgh)
- Fits GLM (ie, computes **b**)
- Computes contrasts ( $g = \mathbf{C} * \mathbf{b}$ )
- t or F ratios, significances
- Significance  $-\log_{10}(p)$  (.01  $\rightarrow$  2, .001  $\rightarrow$  3)

# mri\_glmfit

mri\_glmfit

--y lh.thickness.sm10.mgh

--fsgd gender\_age.txt

--C age.mtx --C gender.mtx

--surf fsaverage lh

--cortex

--glmdir lh.gender\_age.glmdir

mri\_glmfit --help

# mri\_glmfit

mri\_glmfit

```
--y lh.thickness.sm10.mgh  
--fsgd gender_age.txt  
--C age.mtx -C gender.mtx  
--surf fsaverage lh  
--cortex  
--glmdir lh.gender_age.glmdir
```

- Input file (output from smoothing).
- Stack of subjects, one frame per subject.



# mri\_glmfit

```
mri_glmfit  
--y lh.thickness.sm10.mgh  
--fsgd gender_age.txt  
--C age.mtx -C gender.mtx  
--surf fsaverage lh  
--cortex  
--glmdir lh.gender_age.glmdir
```

- FreeSurfer Group Descriptor File (FSGD)
- Group membership
- Covariates

# mri\_glmfit

mri\_glmfit

--y lh.thickness.sm10.mgh

--fsgd gender\_age.txt

--C age.mtx --C gender.mtx

--surf fsaverage lh

--cortex

--glmdir lh.gender\_age.glmdir

- Contrast Matrices
- Simple text/ASCII files
- Test hypotheses

# mri\_glmfit

mri\_glmfit

--y lh.thickness.sm10.mgh

--fsgd gender\_age.txt

--C age.mtx --C gender.mtx

--surf fsaverage lh

--cortex

--glmdir lh.gender\_age.glmdir

- Perform analysis on left hemisphere of fsaverage subject
- Masks by fsaverage cortex.label
- Computes FWHM in 2D

# mri\_glmfit

```
mri_glmfit
--y lh.thickness.sm10.mgh
--fsgd gender_age.txt
--C age.mtx -C gender.mtx
--surf fsaverage lh
--cortex
--glmdir lh.gender_age.glmdir
```

Output directory:

lh.gender\_age.glmdir/

beta.mgh – parameter estimates  
rvar.mgh – residual error variance  
etc ...

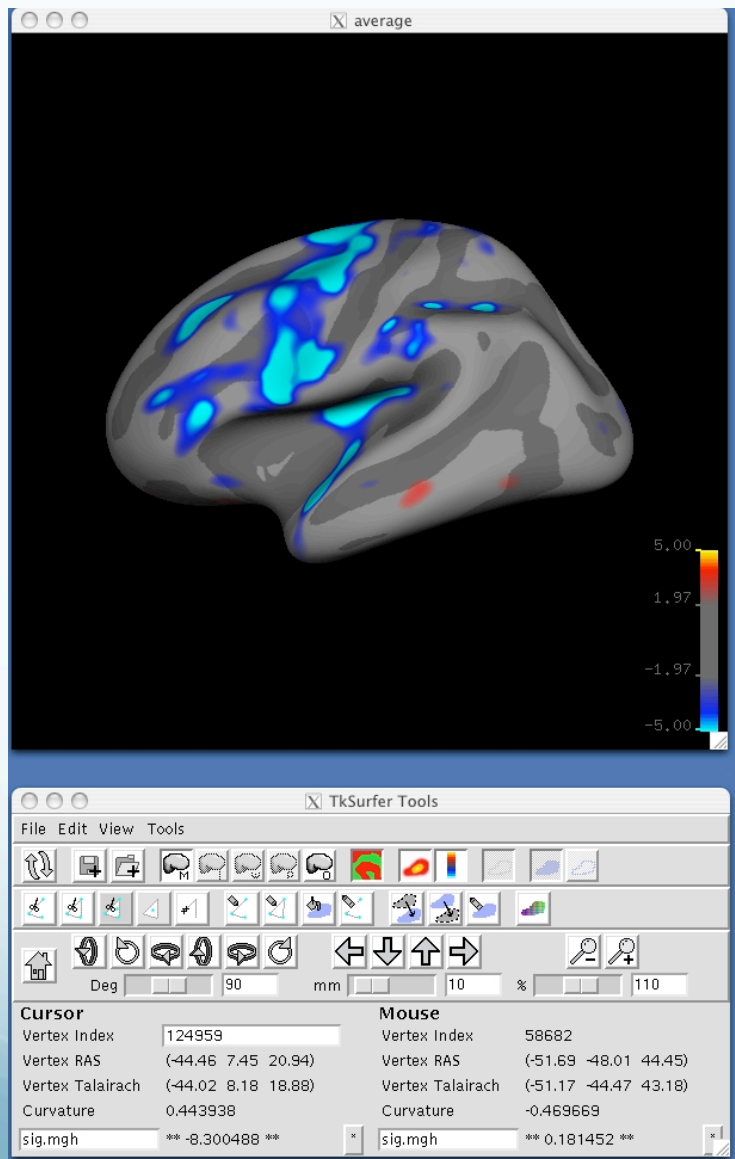
age/

sig.mgh –  $-\log_{10}(p)$ , uncorrected  
gamma.mgh, F.mgh

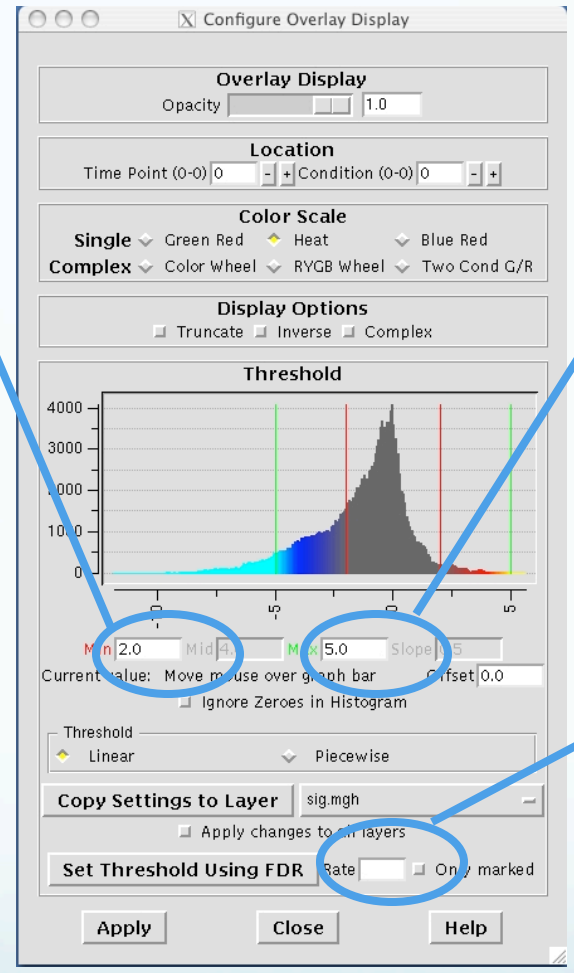
gender/

sig.mgh –  $-\log_{10}(p)$ , uncorrected  
gamma.mgh, F.mgh

# Visualization with tk-surfer



Threshold:  
-log<sub>10</sub>(p),  
Eg, 2=.01



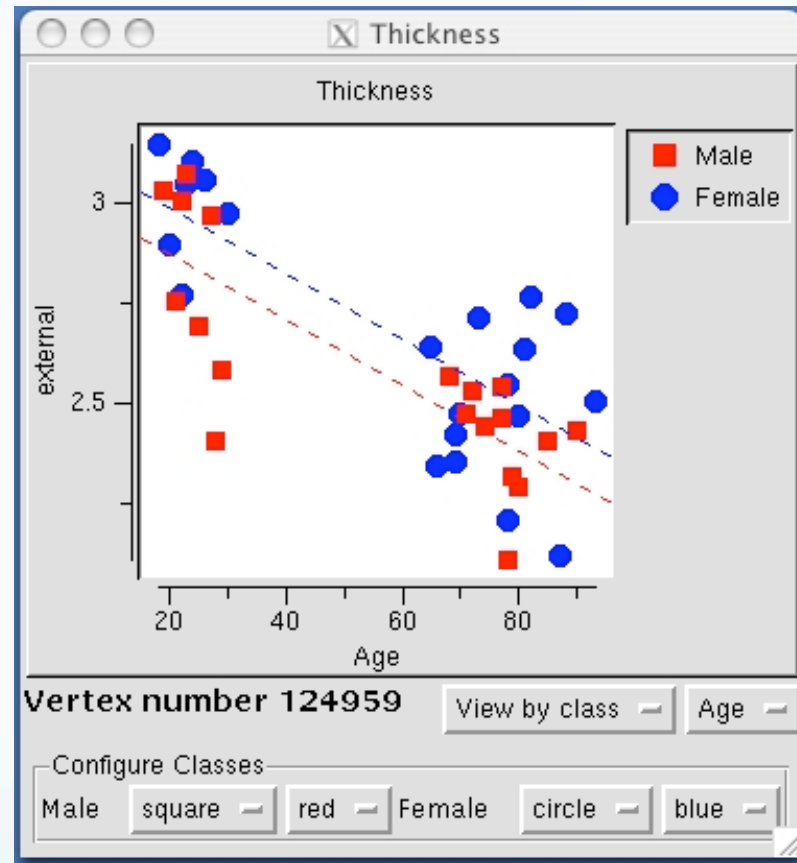
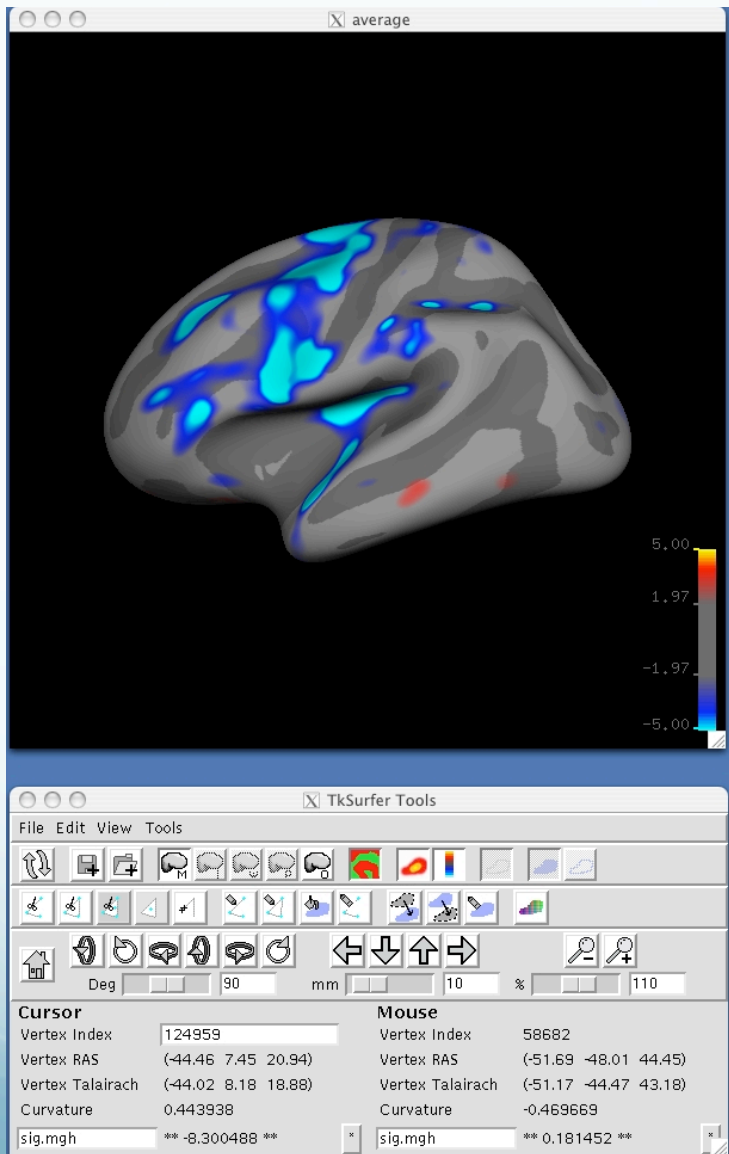
Saturation:  
-log<sub>10</sub>(p),  
Eg, 5=.00001

False  
Discovery  
Rate  
Eg, .01

View->Configure->Overlay

File->LoadOverlay

# Visualization with tksurfer



File->  
Load Group Descriptor File ...

# Tutorial

## Command-line Stream

- Create an FSGD File for a thickness study
- Age and Gender
- Run
  - `mris_preproc`
  - `mri_surf2surf`
  - `mri_glmfit`