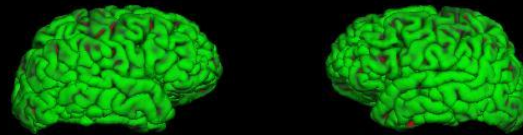
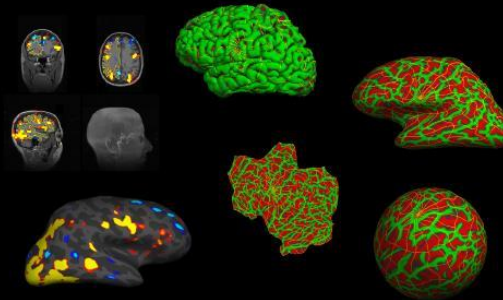


Anatomical Analysis with FreeSurfer

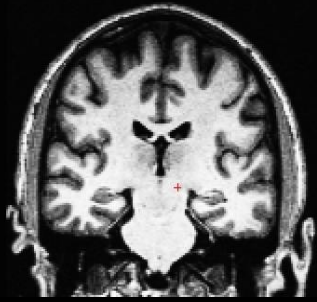
surfer.nmr.mgh.harvard.edu



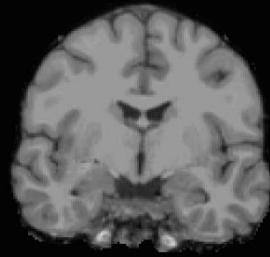
FreeSurfer



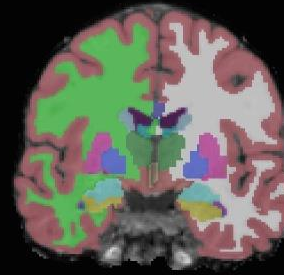
Processing Stream Overview



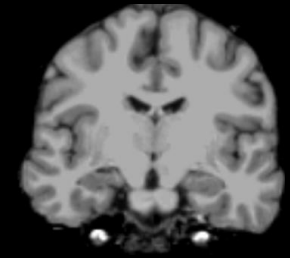
T1 Weighted
Input



Skull Stripping



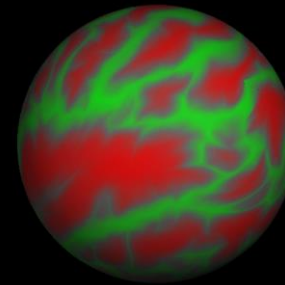
Volumetric Labeling



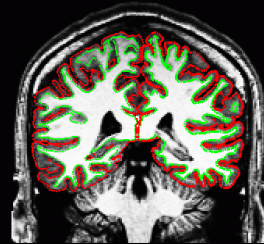
Intensity
Normalization



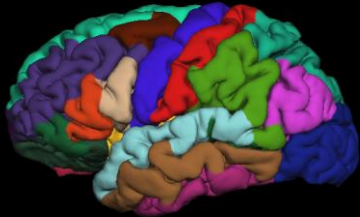
White Matter
Segmentation



Surface Atlas
Registration



Surface Extraction



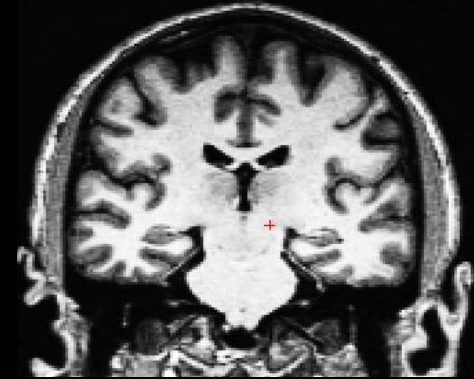
Gyrus Labeling



Stats!

Input: T1 Weighted Image

- T1 Contrast: white matter brighter than gray matter
- $\sim 1\text{mm}^3$ (no more than 1.5mm)
- Higher resolution may be worse!
- Full Brain
- Usually one acquisition is ok
- MPRAGE or SPGR
- 1.5T or 3T
- 7T might have problems
- Subject age > 5 years old
- Brain has no major problems (ie, tumors, parts missing)
- Non-human primates possible

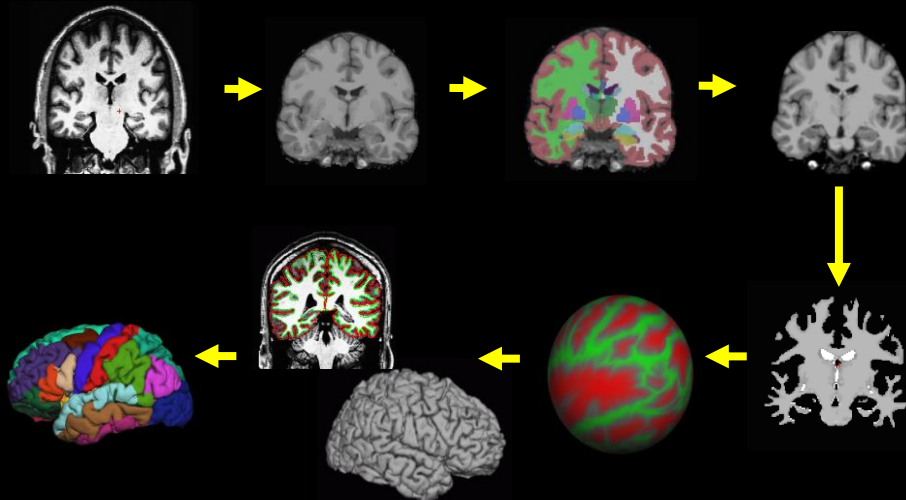


More MRI Pulse Sequence Parameter Details:
<http://www.nmr.mgh.harvard.edu/~andre>

Fully Automated Reconstruction*

```
recon-all -i file.dcm -subject bert -all
```

* “Reconstruction” here refers to cortical reconstruction, not k-space reconstruction.



Fully Automated Reconstruction

```
recon-all
```

```
-i file.dcm
```

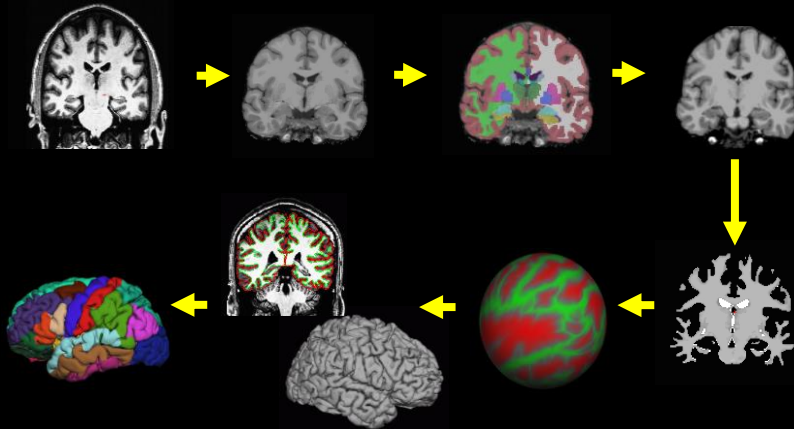
```
-subject bert
```

```
-all
```

file.dcm is a single DICOM file from the T1 MRI series.

If you have more than one T1, then use:

```
-i file1.dcm -i file2.dcm
```



You can use NIFTI as well with

```
-i file.nii
```

To get a list of acquisitions:

```
dcmunpack -src /path/to/dicoms
```

Fully Automated Reconstruction

```
recon-all
```

```
-i file.dcm
```

```
-subject bert
```

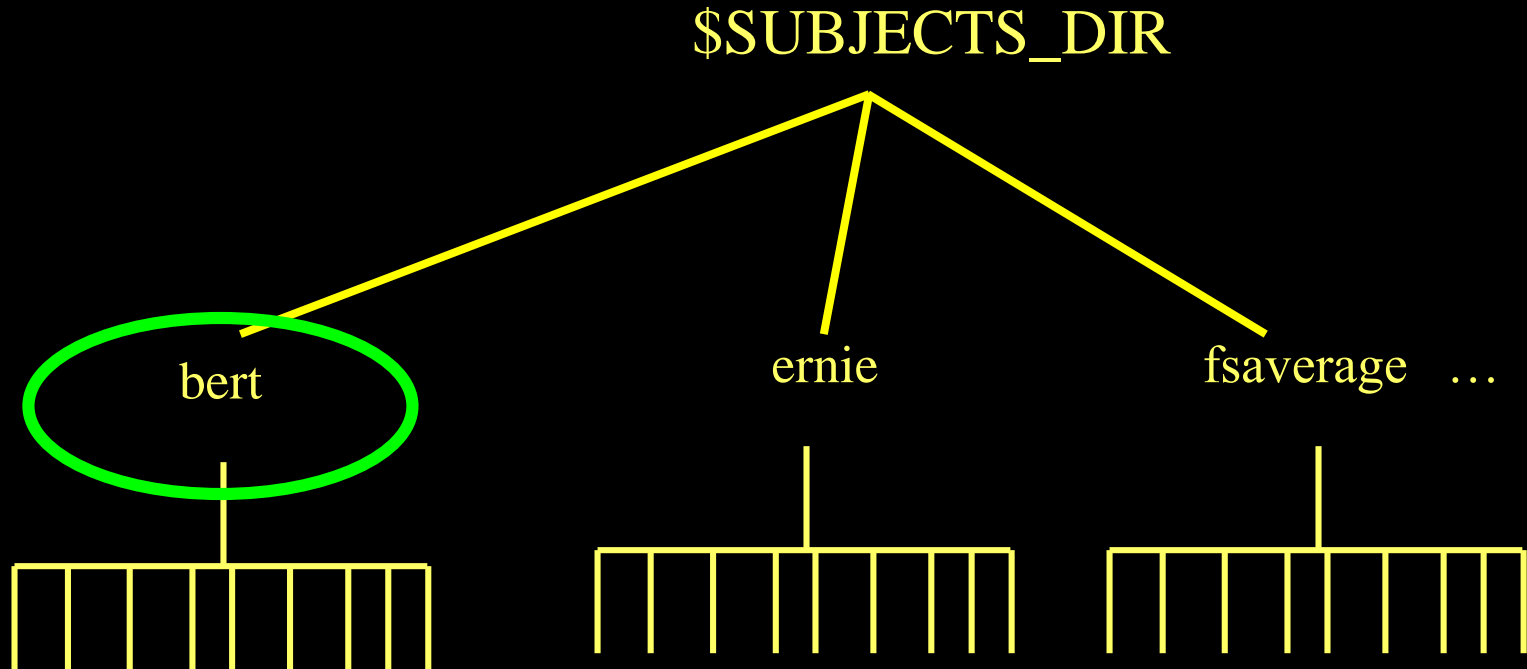
```
-all
```

“bert” is the “name” of the subject

Creates a folder in \$SUBJECTS_DIR

All output goes in this folder (~400MB)

Other subjects in \$SUBJECTS_DIR



```
setenv SUBJECTS_DIR /path/to/space
```

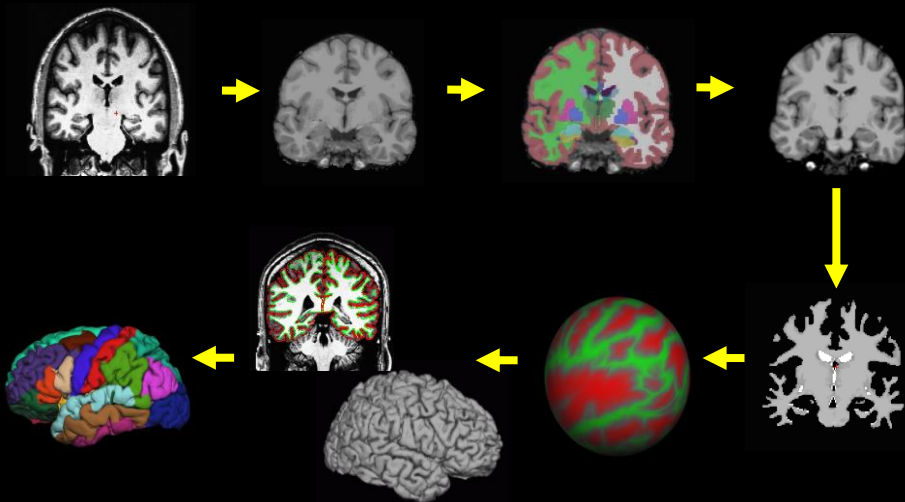
Fully Automated Reconstruction

```
recon-all  
-i file.dcm  
-subject bert  
-all
```

-all means to do everything!

Can take 10-20 hours

Later, we will show you how to run subsets of the processing stream to make it faster when correcting errors.



Individual Steps

Volumetric Processing Stages (subjid/mri):

1. Motion Cor, Avg, Conform (orig.mgz)
2. Non-uniform inorm (nu.mgz)
3. Talairach transform computation
(talairach/talairach.xfm)
4. Intensity Normalization 1 (T1.mgz)
5. Skull Strip (brainmask.mgz)
6. EM Register (linear volumetric registration)
7. CA Intensity Normalization (norm.mgz)
8. CA Non-linear Volumetric Registration
9. CA Label (Volumetric Labeling) (aseg.mgz)
10. Intensity Normalization 2 (T1.mgz)
11. White matter segmentation (wm.mgz)
12. Edit WM With ASeg
13. Fill and cut (filled.mgz)

Surface Processing Stages (subjid/surf):

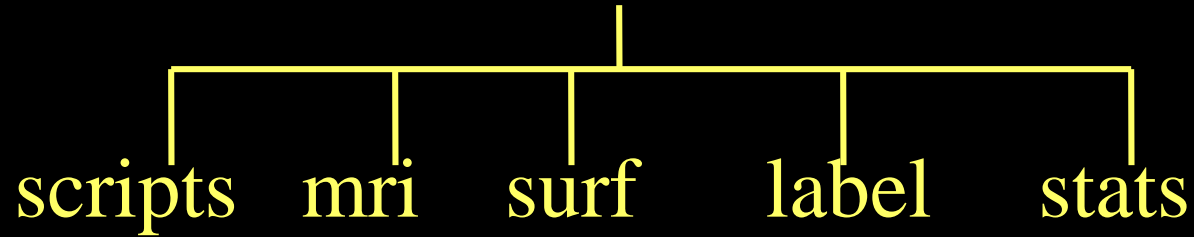
14. Tessellate (?h.orig.nofix)
15. Smooth1
16. Inflate1
17. Sphere (?h.qsphere)
18. Automatic Topology Fixer (?h.orig)
19. Final Surfs (?h.white ?h.pial ?.thickness)
20. Smooth2 (?h.smoothwm)
21. Inflate2 (?h.inflated)
22. Aseg Statistics (stats/aseg.stats)
23. Cortical Ribbon Mask (?h.ribbon.mgz)
24. Spherical Morph
25. Spherical Registration (?h.sphere.reg)
26. Map average curvature to subject
27. Cortical Parcellation (Labeling)
28. Cortical Parcellation Statistics
29. Cortical Parcellation mapped to Aseg
30. White Matter Parcellation (wmparc.mgz)

recon-all -help

Note: ?h.orig means lh.orig or rh.orig

Upon Completion...

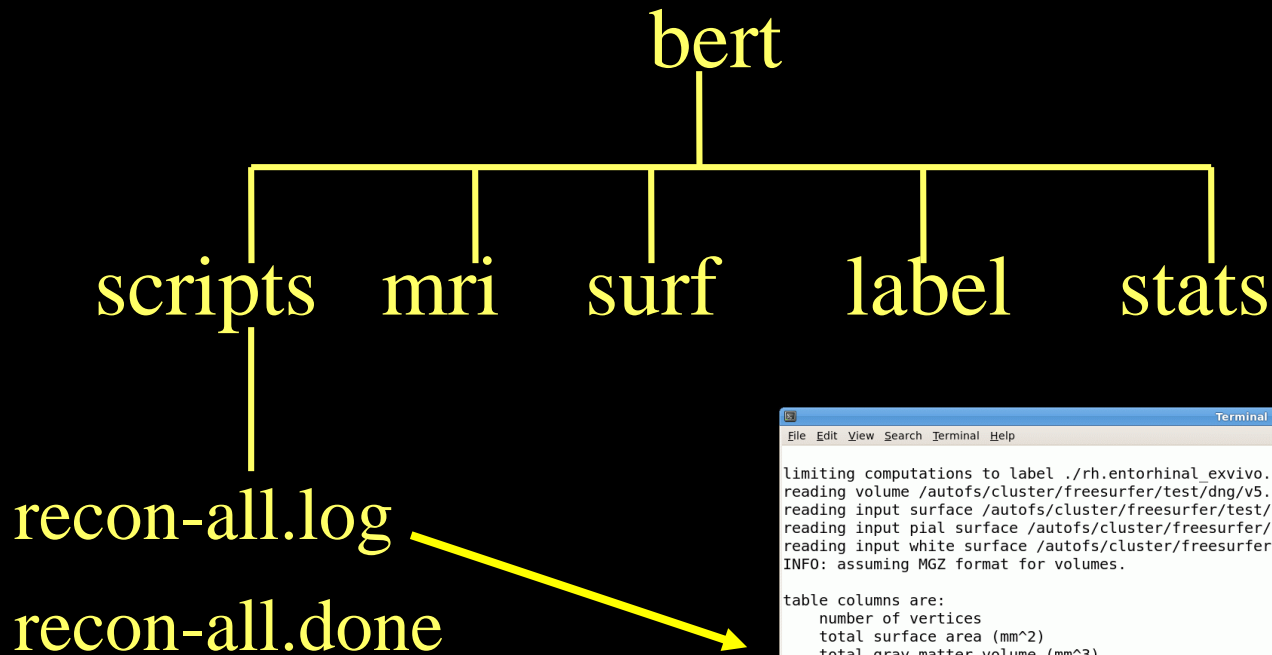
`$SUBJECTS_DIR/bert`



`recon-all -i file.dcm -subject bert -all`

~400MB

Upon Completion...



```
Terminal
File Edit View Search Terminal Help

limiting computations to label ./rh.entorhinal_exvivo.label.
reading volume /autofs/cluster/freesurfer/test/dng/v5.3/b40/045/mri/wm.mgz...
reading input surface /autofs/cluster/freesurfer/test/dng/v5.3/b40/045/surf/rh.white...
reading input pial surface /autofs/cluster/freesurfer/test/dng/v5.3/b40/045/surf/rh.pial...
reading input white surface /autofs/cluster/freesurfer/test/dng/v5.3/b40/045/surf/rh.white...
INFO: assuming MGZ format for volumes.

table columns are:
number of vertices
total surface area (mm^2)
total gray matter volume (mm^3)
average cortical thickness +- standard deviation (mm)
integrated rectified mean curvature
integrated rectified Gaussian curvature
folding index
intrinsic curvature index
structure name

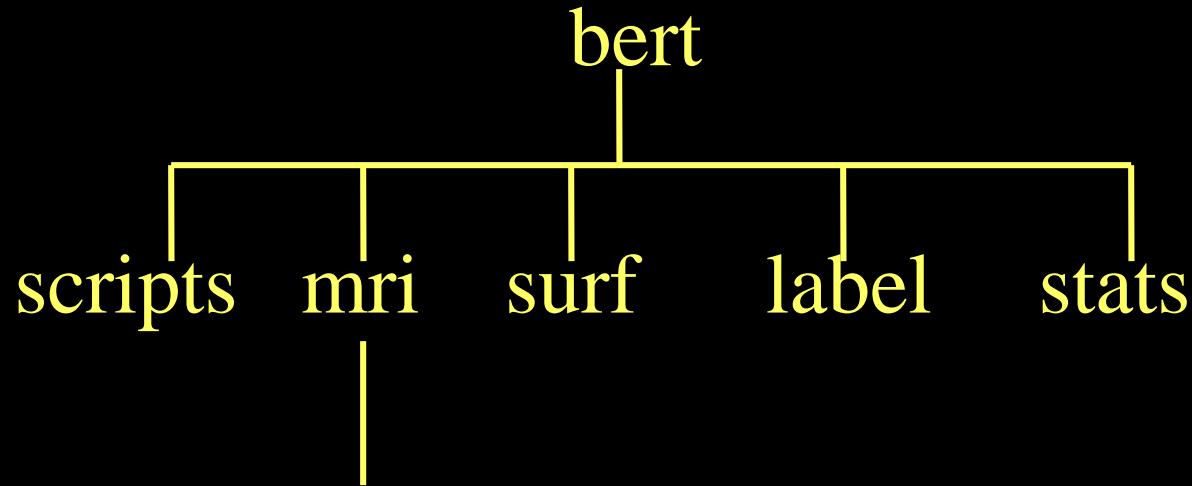
236 152 759 3.117 0.598 0.141 0.035 3 0.4 ./rh.entorhinal_exvivo.label

#-----
Started at Fri Apr 26 19:18:47 EDT 2013
Ended at Sat Apr 27 12:07:26 EDT 2013
#@## recon-all-run-time-hours 16.811
recon-all -s 045 finished without error at Sat Apr 27 12:07:26 EDT 2013
[t:D:-->
```

Just because it finishes
“without error” does not mean
that everything is ok!

Send us recon-all.log when you
have problems!
freesurfer@nmr.mgh.harvard.edu

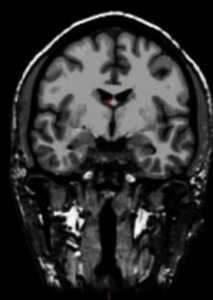
Upon Completion...



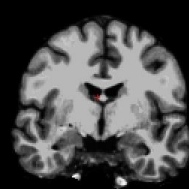
rawavg.mgz



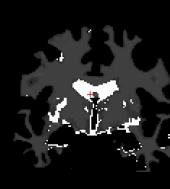
orig.mgz



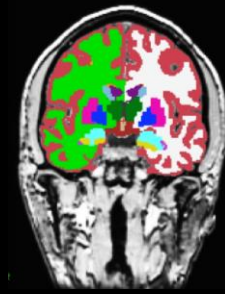
T1.mgz



brainmask.mgz



wm.mgz

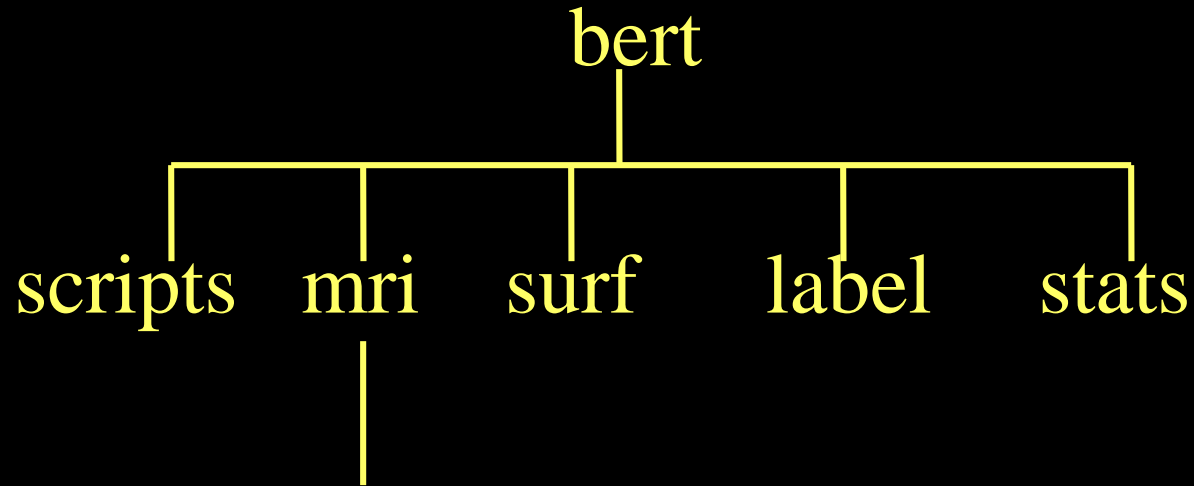


aseg.mgz

others: nu.mgz, norm.mgz, wmparc.mgz, aparc+aseg.mgz, ribbon.mgz

mgz = “compressed mgh” format (like nifti) unique to FreeSurfer

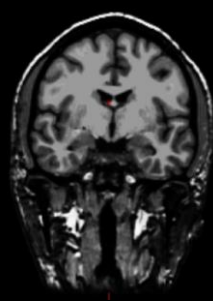
Upon Completion...



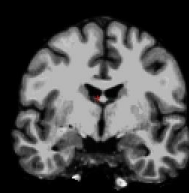
rawavg.mgz



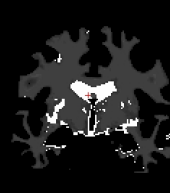
orig.mgz



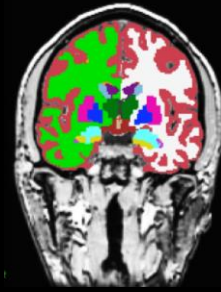
T1.mgz



brainmask.mgz



wm.mgz



aseg.mgz

Native Anatomical Space

eg, $1 \times 1 \times 1.2 \text{mm}^3$, $256 \times 256 \times 128$

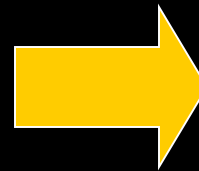
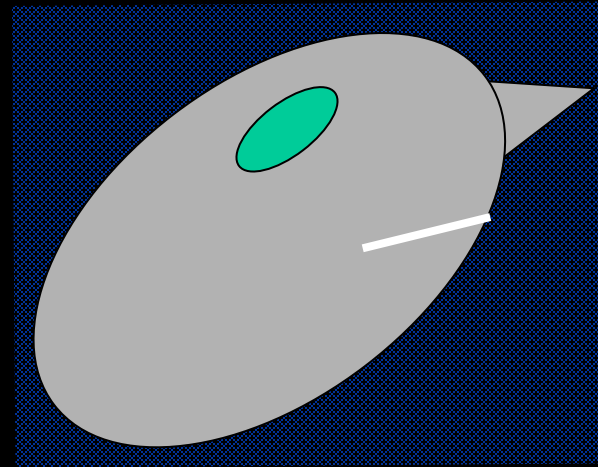
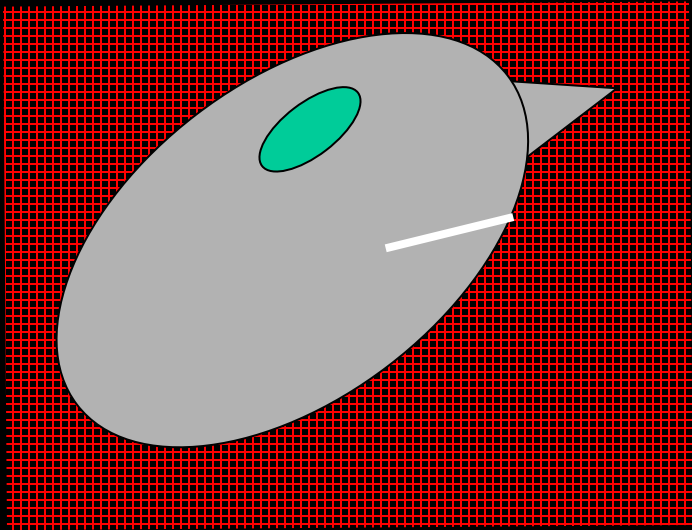
“Conformed” Anatomical Space

$1 \times 1 \times 1 \text{mm}^3$, $256 \times 256 \times 256$

Conform Step

Native Anatomical Space
1x1x1.1mm, 256x256x128, Sag

Conformed Anatomical Space
1x1x1mm, 256x256x256, Cor



rawavg.mgz

bert

mri

rawavg.mgz

orig.mgz

“Anatomical Space”

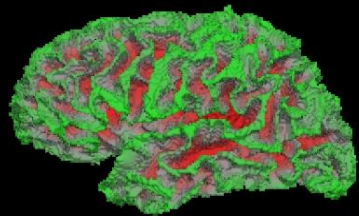
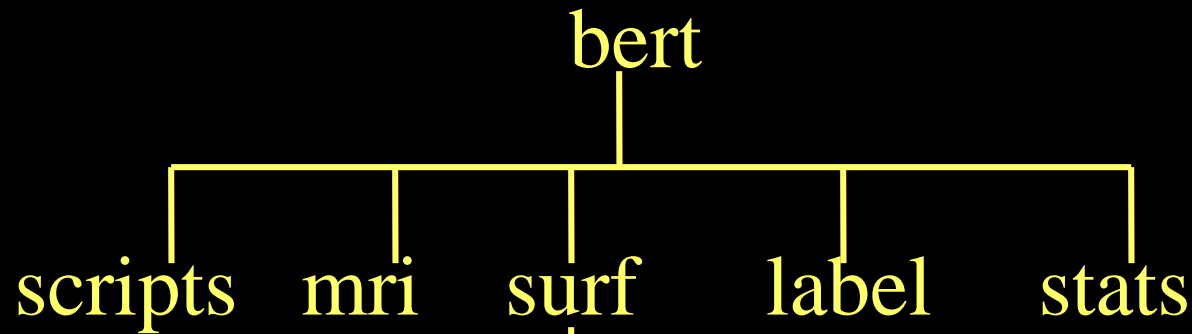
orig.mgz

Surfaces

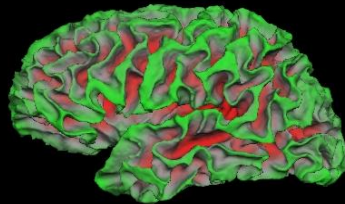
Parcellations

Segmentations

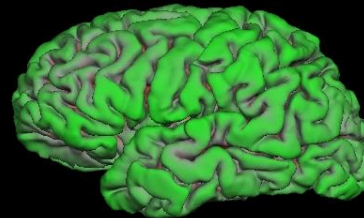
Upon Completion...



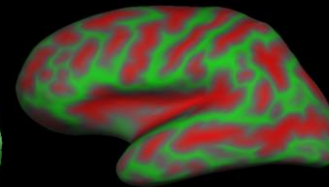
lh.orig



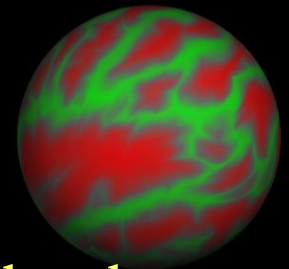
lh.white



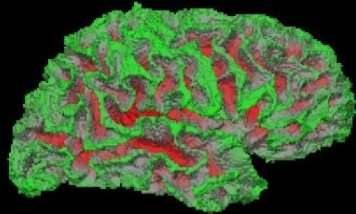
lh.pial



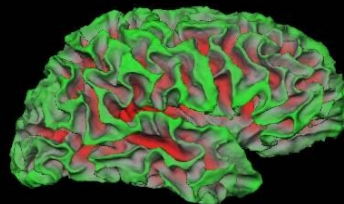
lh.inflated



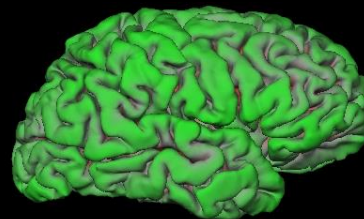
lh.sphere.reg



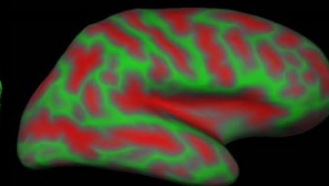
rh.orig



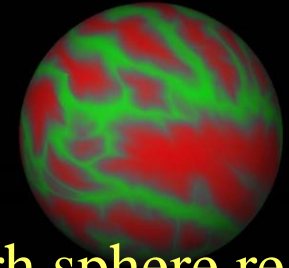
rh.white



rh.pial



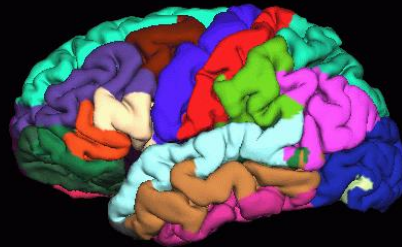
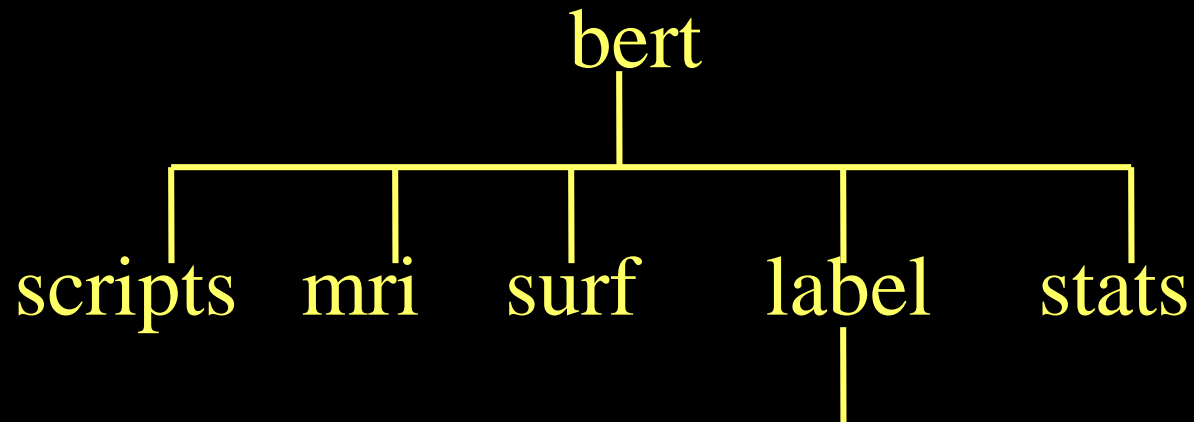
rh.inflated



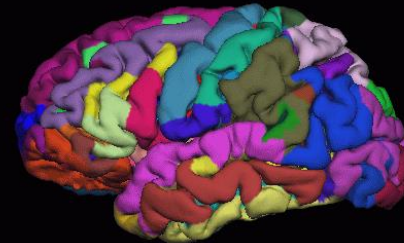
rh.sphere.reg

lh.thickness and rh.thickness, ?h.curv, ?h.sulc

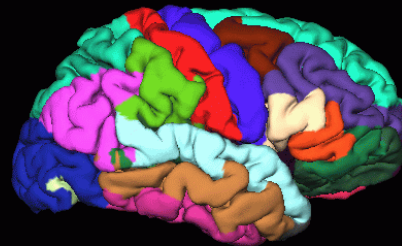
Upon Completion...



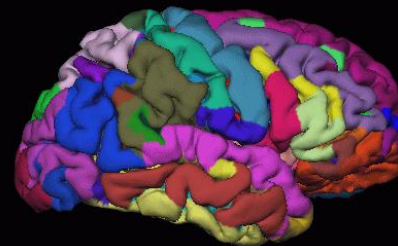
lh.aparc.annot



lh.aparc.a2009s.annot



rh.aparc.annot

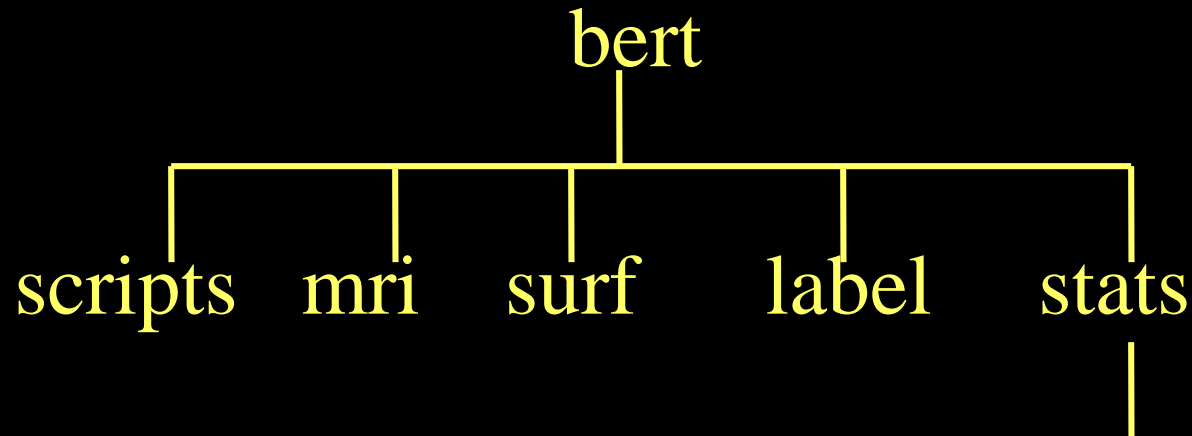


rh.aparc.a2009s.annot

Desikan/Killiany Atlas

Destrieux Atlas

Upon Completion...

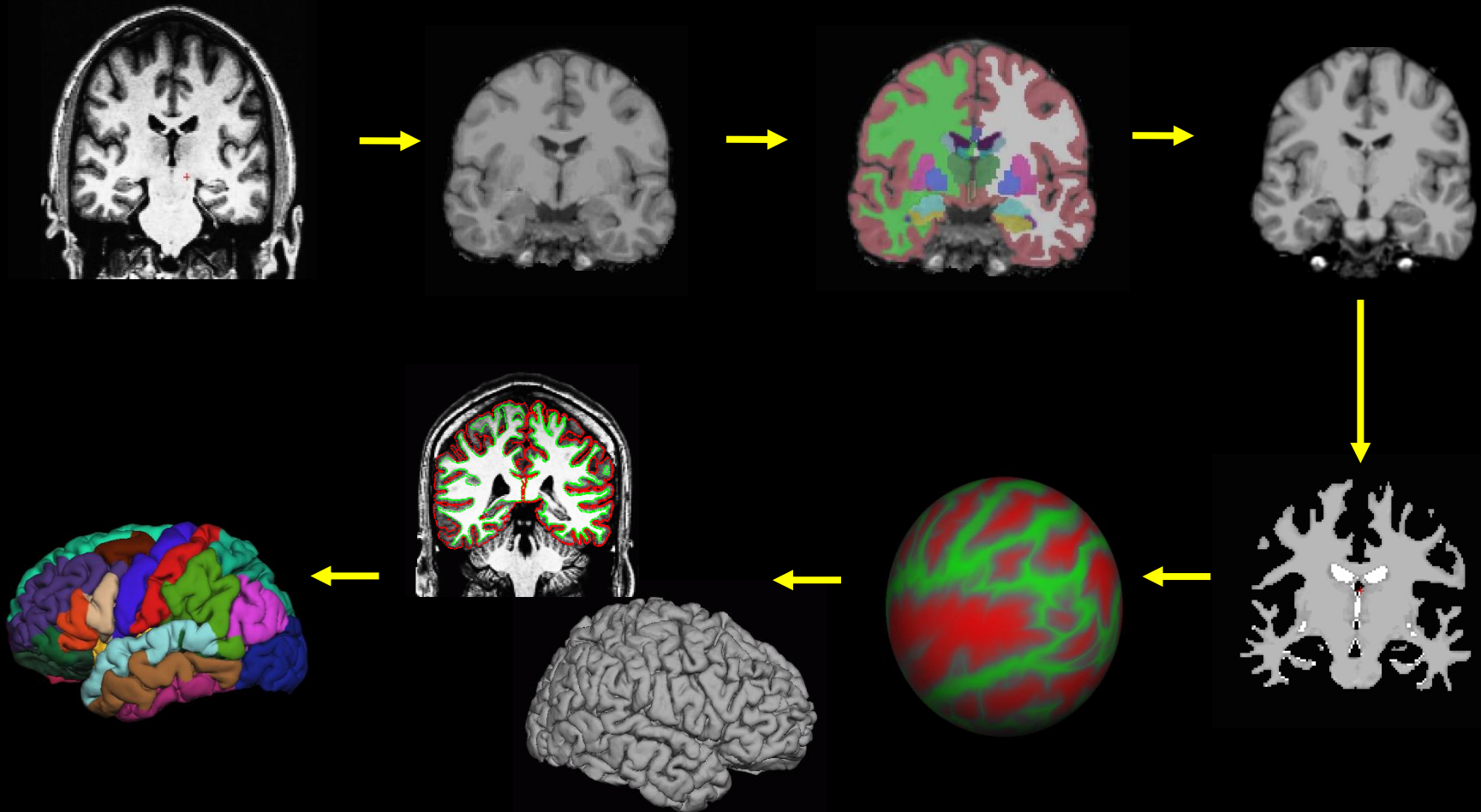


aseg.stats – subcortical volumetric stats
wmparc.stats – white matter segmentation volumetric stats
lh.aparc.stats – left hemi Desikan/Killiany surface stats
rh.aparc.stats – right hemi Desikan/Killiany surface stats
lh.aparc.a2009.stats – left hemi Destrieux
rh.aparc.a2009.stats – right hemi Destrieux

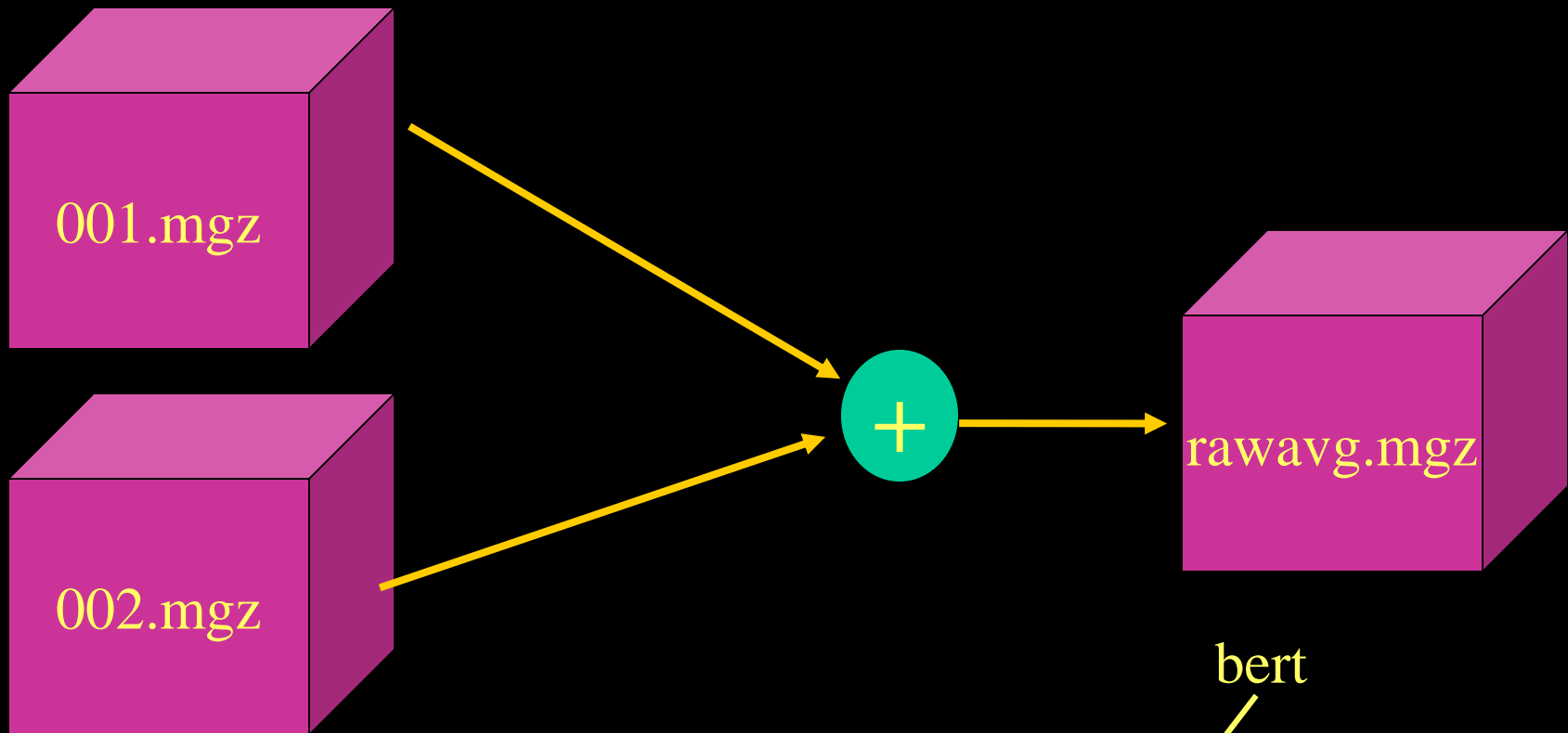
stats files are text files with summary information, eg:
volume of left amygdala
average thickness in superior temporal gyrus



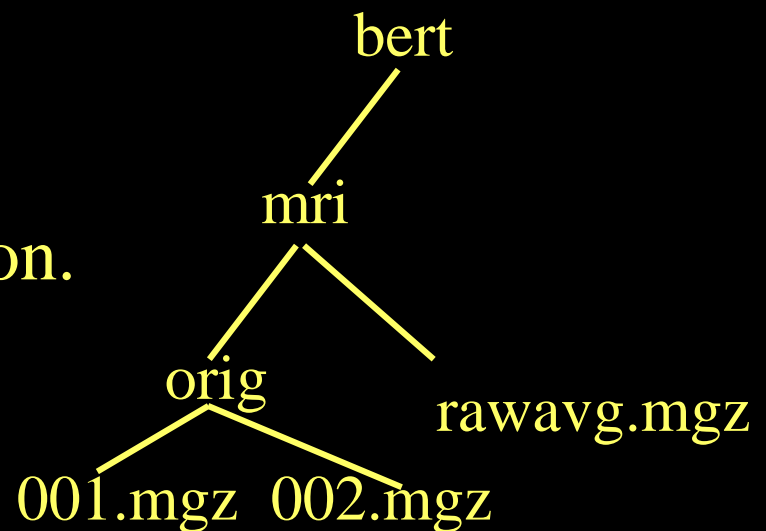
Some of the Processing Steps...



Motion Correction and Averaging

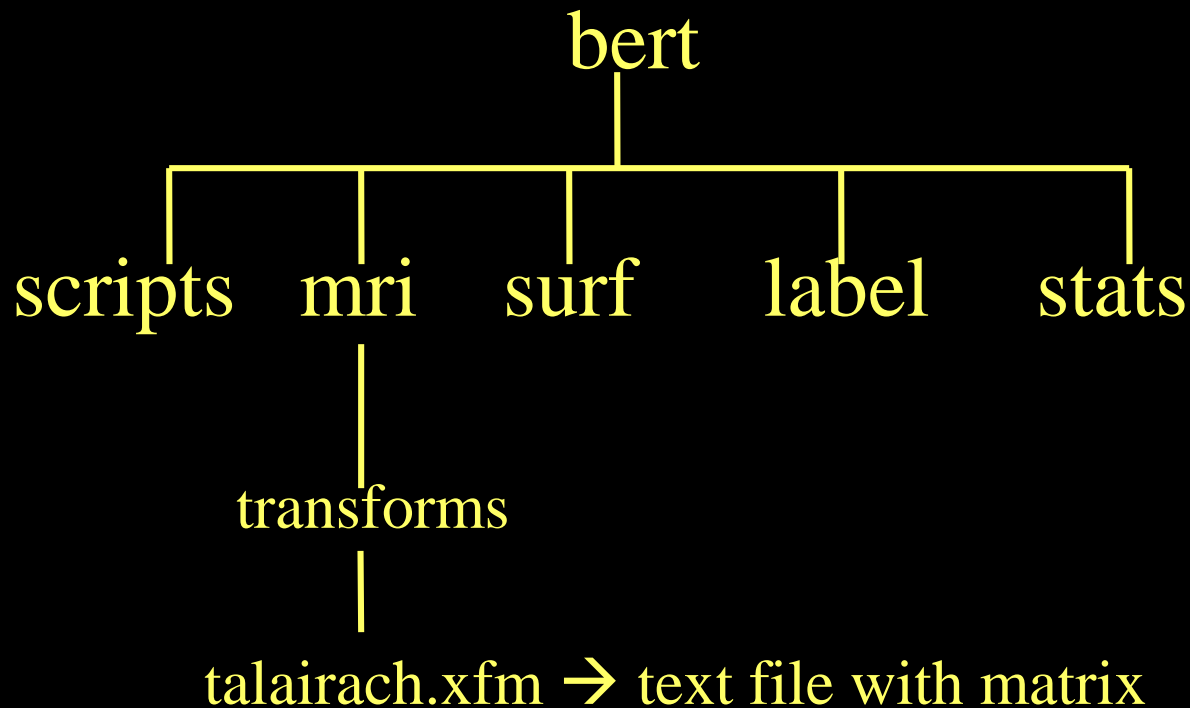


Does not change native resolution.
Usually only need one.

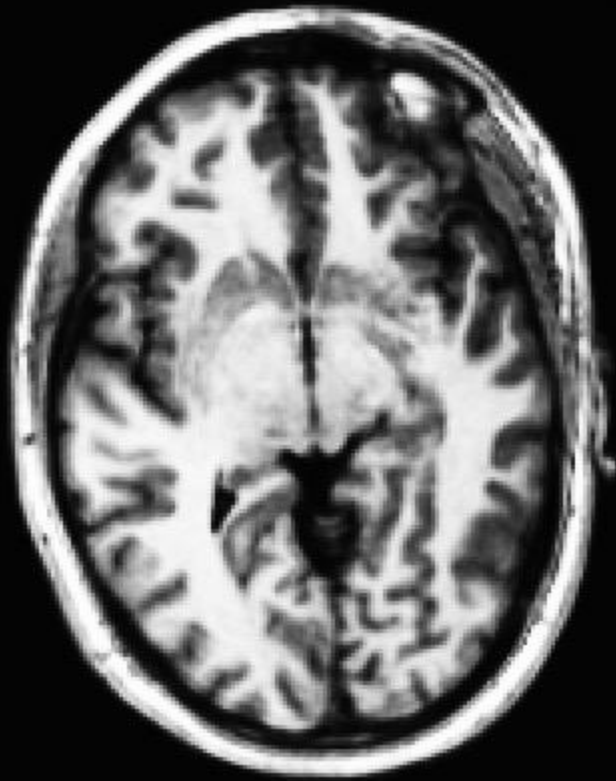


Talairach Transform

- Computes 12 DOF transform matrix
- Does NOT resample
- MNI305 template
- Mostly used to report coordinates



Intensity Bias

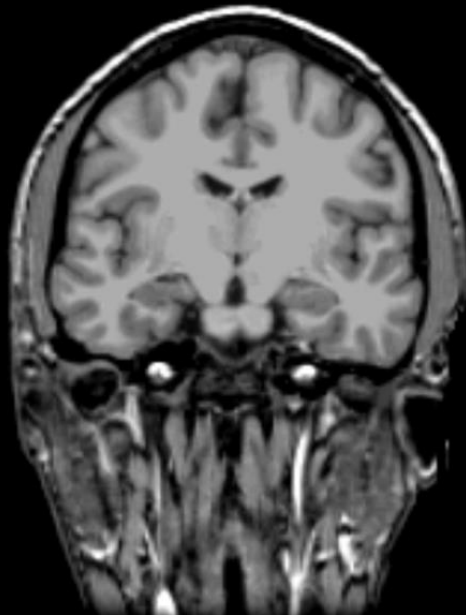


bert
|
mri
|
T1.mgz

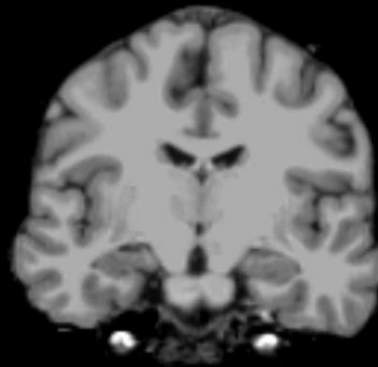
- Left side of the image much brighter than right side
- Worse with many coils
- Makes gray/white segmentation difficult

Skull Strip

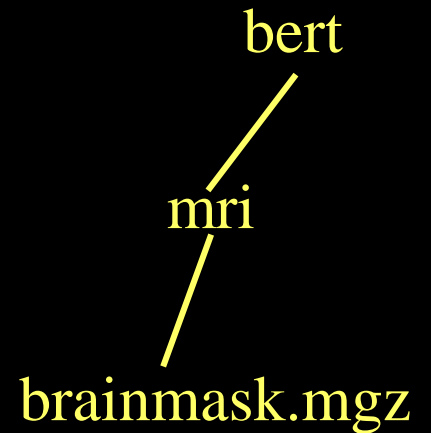
- Removes all non-brain
 - Skull, Eyes, Neck, Dura
- brainmask.mgz (cf, brain.mgz)



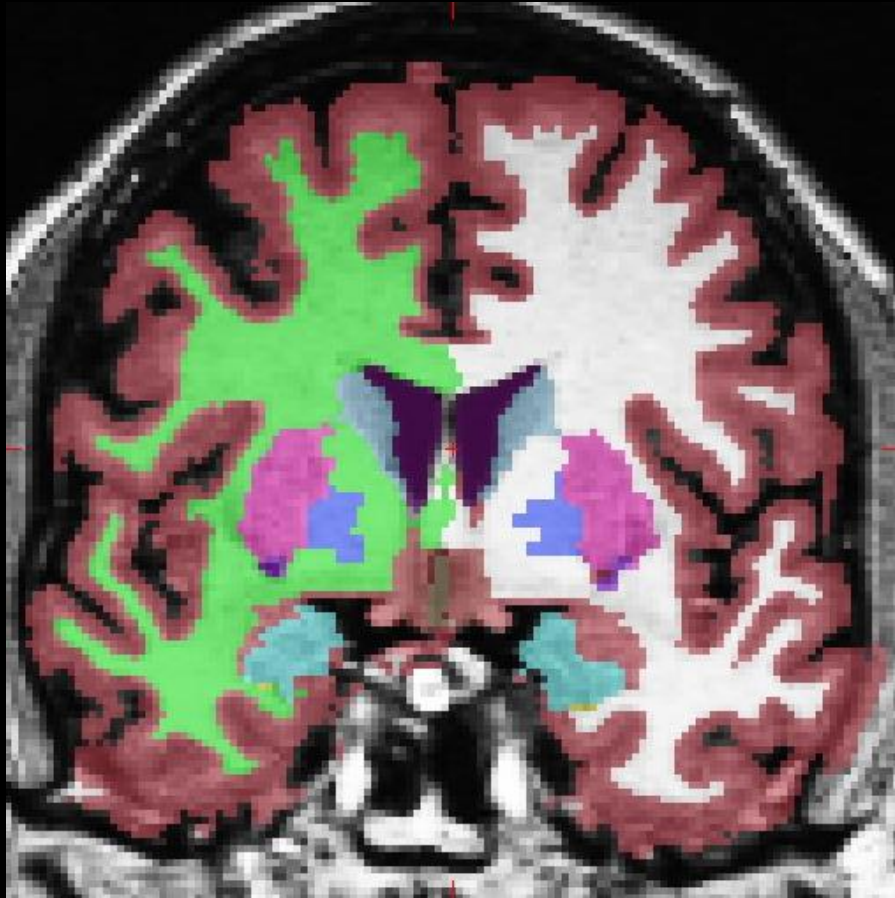
T1.mgz



brainmask.mgz

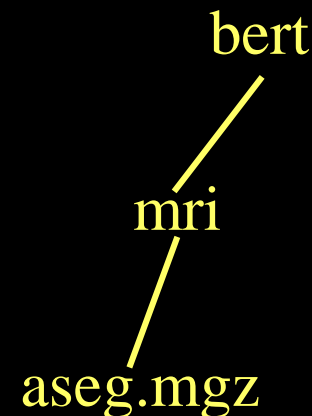


Automatic Volume Labeling



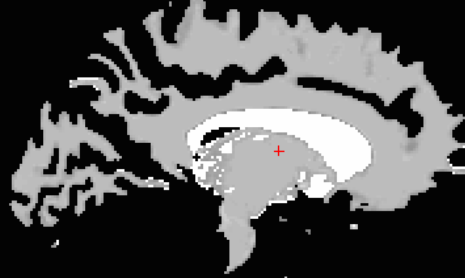
ASeg Volume

- Used to fill in subcortical structures for creating subcortical mass
- Useful in its own right
- aseg.mgz
- More in ROI Talk



“White Matter” Segmentation

- Separates white matter from everything else
- Uses aseg to “fill in” subcortical structures
- Cerebellum removed, brain stem still there
- wm.mgz -- “wm” not a very good name!



bert

mri

wm.mgz

Fill and Cut (Subcortical Mass)

- Fills in any holes.
- Removes any islands
- Removes brain stem
- Separates hemispheres (each hemi has different value)
- filled.mgz = “Subcortical Mass”



WM Volume (wm.mgz)



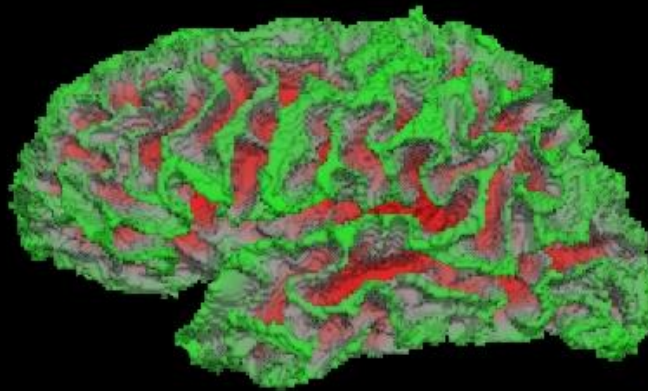
Filled Volume (filled.mgz)
(Subcortical Mass)

Surface Extraction

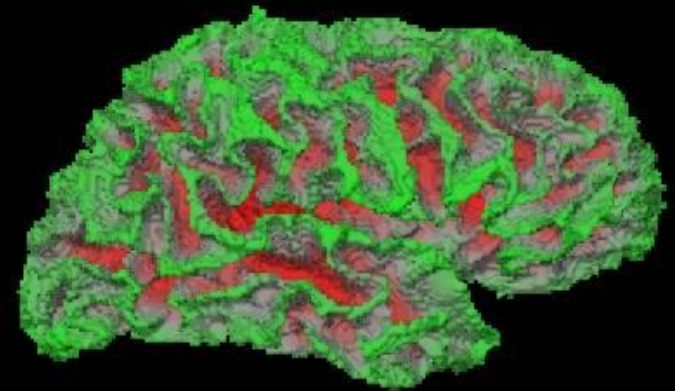
- Hemispheres separated
- Fit to wm.mgz
- 1mm resolution
- Rough, jagged



bert
|
surf
|
lh.orig
rh.orig

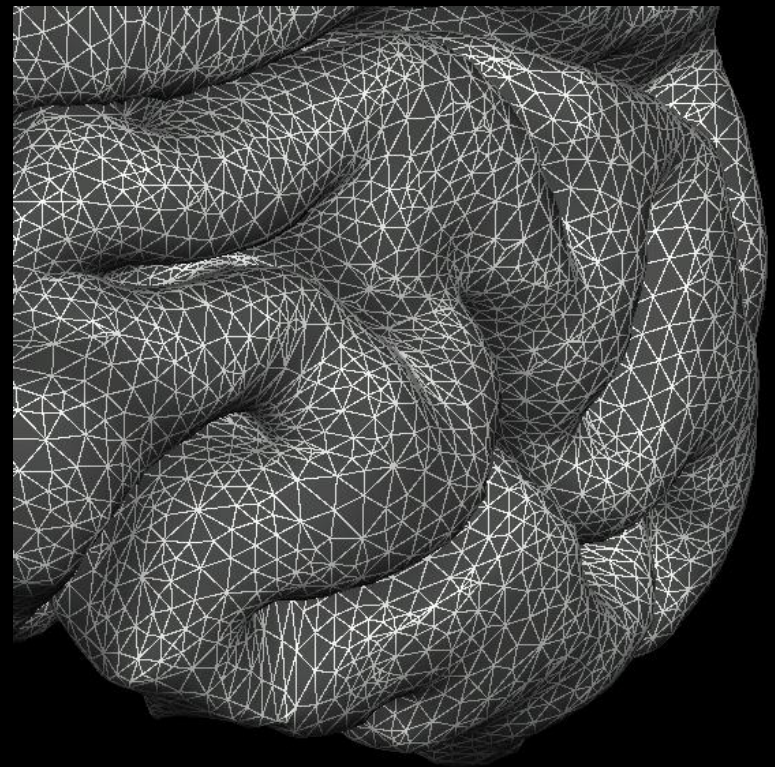
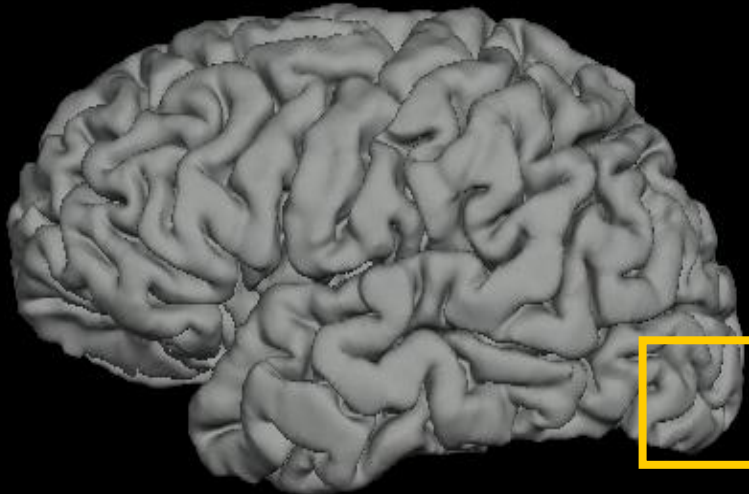


lh.orig



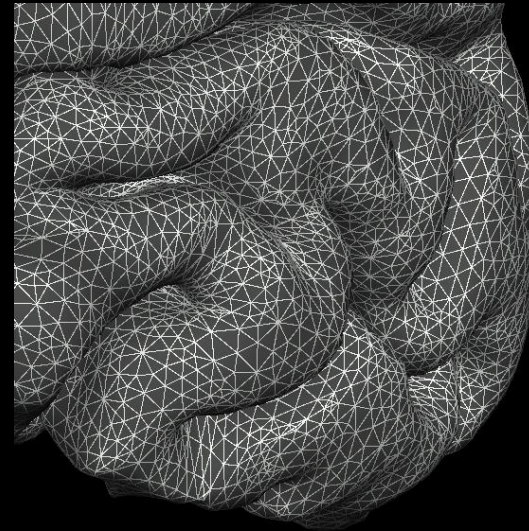
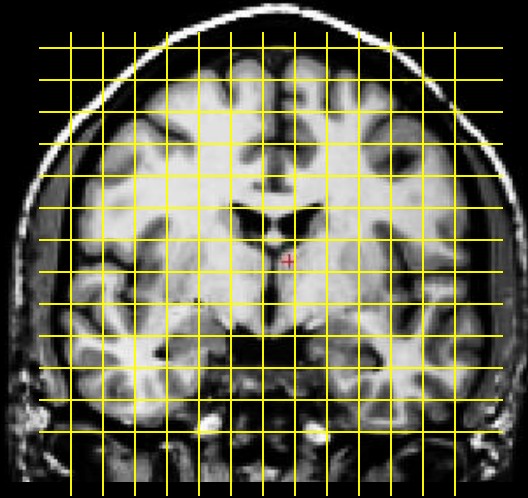
rh.orig

Surface Model



- Mesh (“Finite Element”)
- Vertex = point of triangles
- Neighborhood
- XYZ at each vertex
- Triangles/Faces ~ 300,000
- Vertices ~ 140,000
- Area, Distance
- Curvature, Thickness

Volume vs Surface Model



Volume

- uniform grid
- voxel is an intersection of grid lines
- columns, rows, slices
- voxel size/distance
- voxel assigned a value
- XYZ

Surface

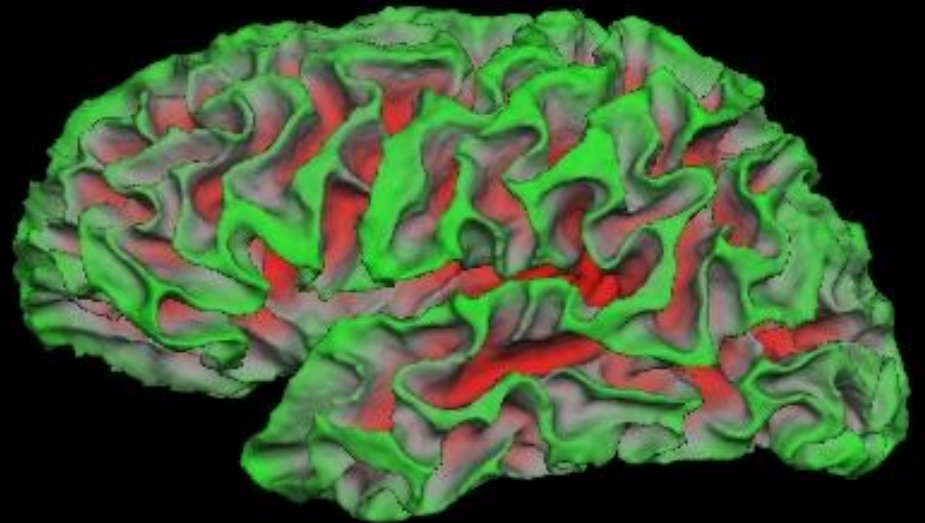
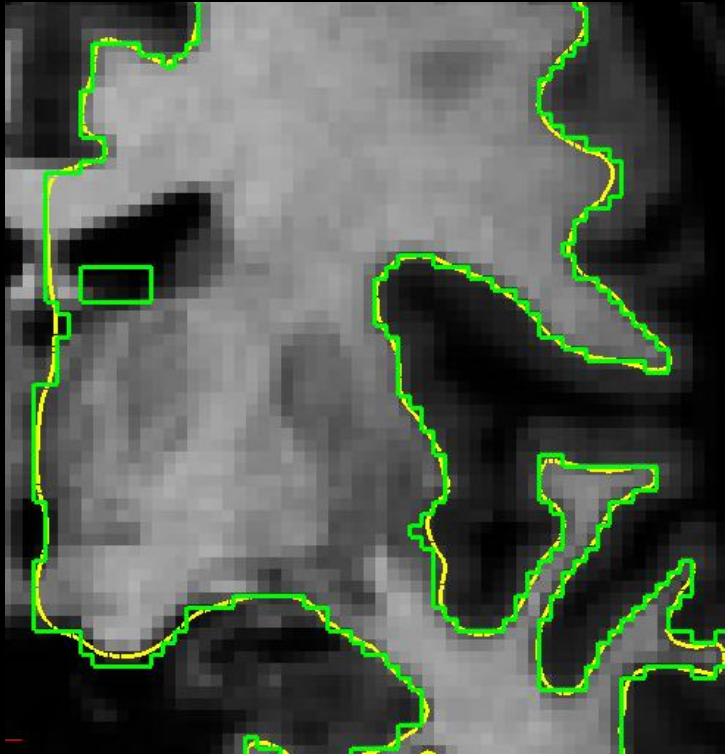
- NON-uniform grid
- vertex is an intersection of triangles
- each vertex has an index
- distance between vertices ~1mm
- vertex assigned a value
- XYZ

Vector of vertex values (~140,000)



White Matter Surface

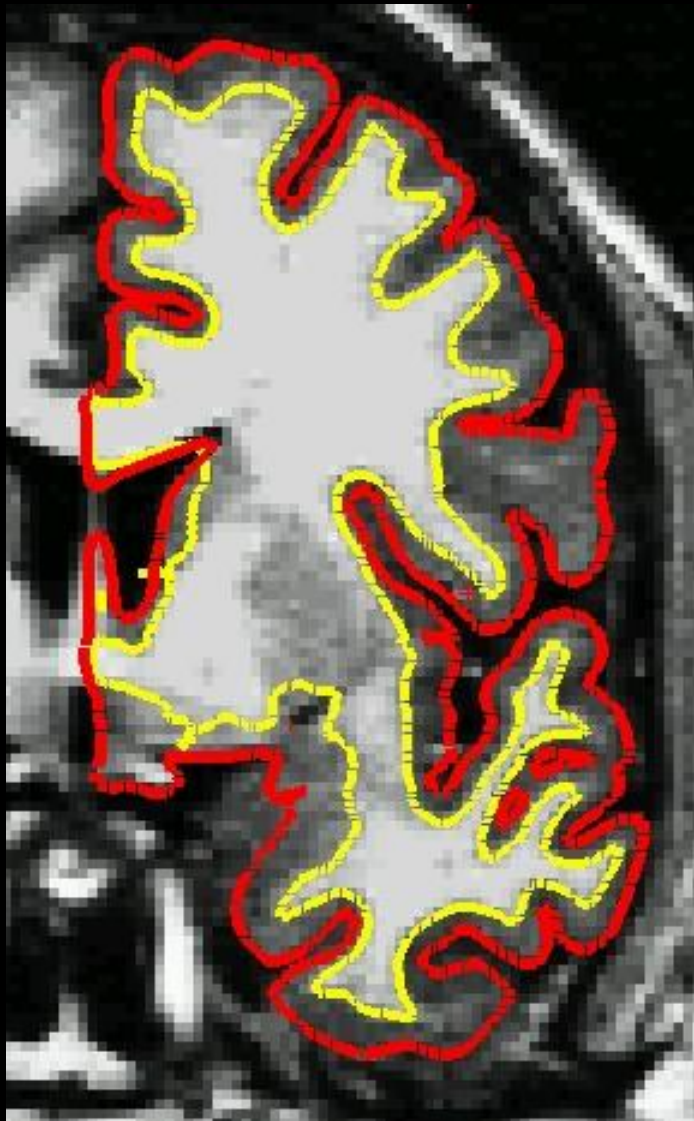
- Nudge orig surface
- Follow T1 intensity gradients
- Smoothness constraint
- Vertex identity preserved



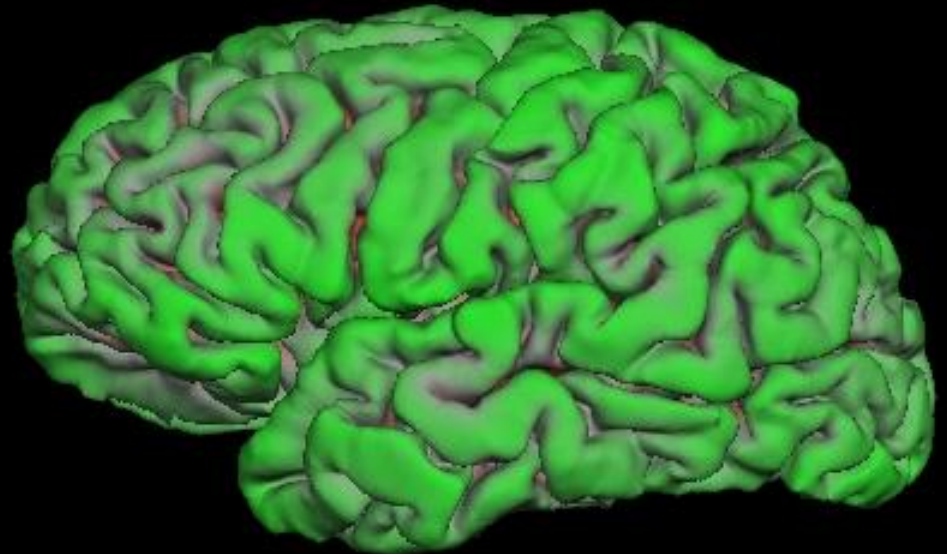
— orig surface
— white surface

lh.white
rh.white

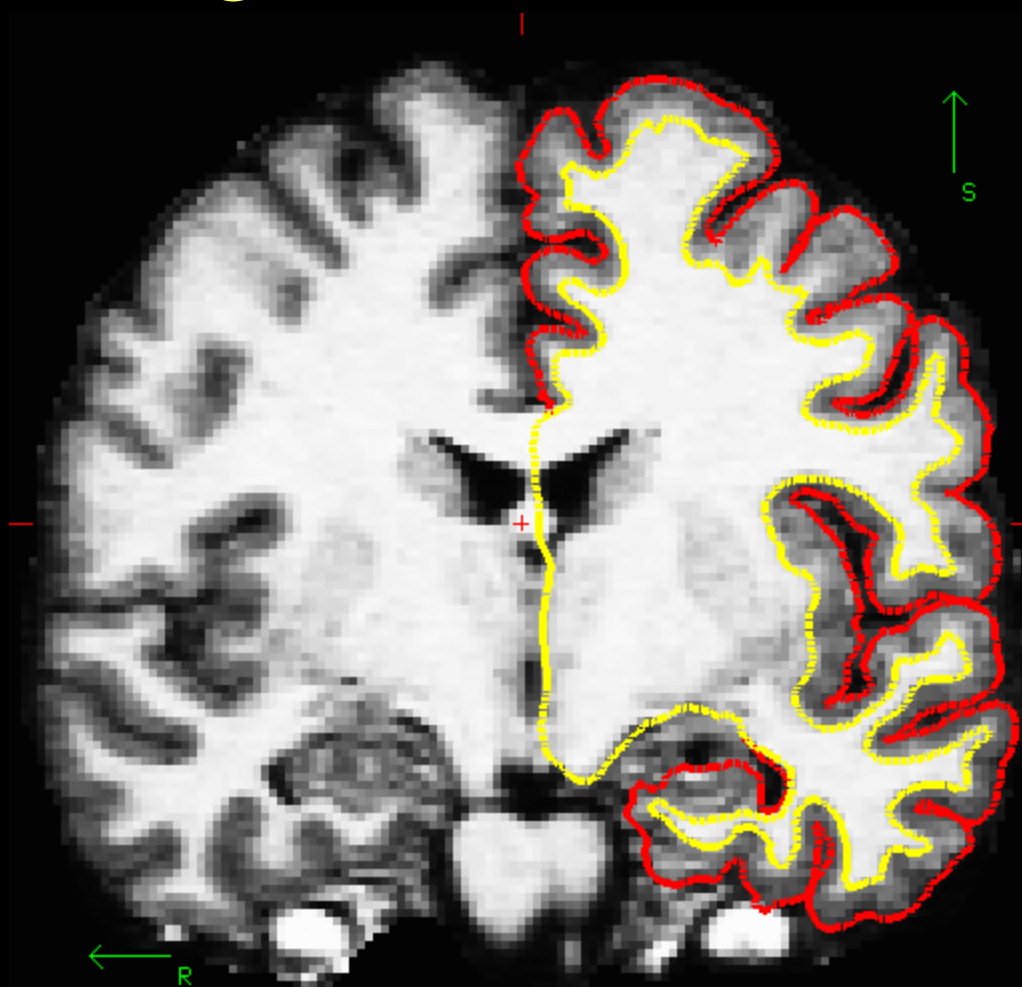
Pial Surface



- Nudge white surface
- Follow T1 intensity gradients
- Vertex identity preserved

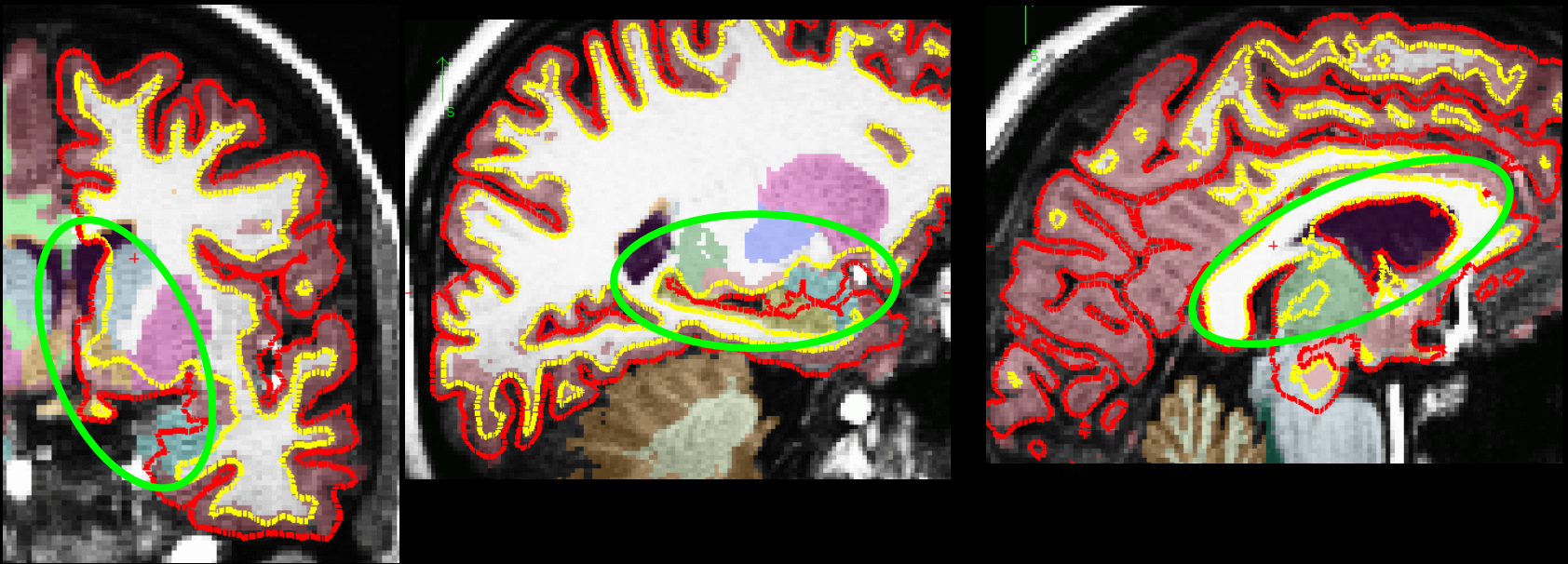


Pial surf grows from white surf

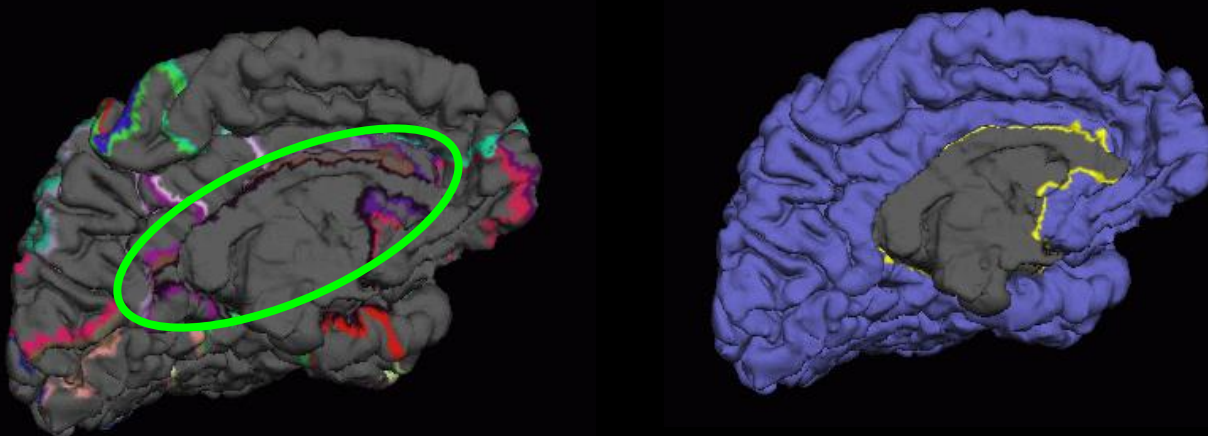


Errors in pial surface placement are typically caused by underlying errors in the white matter placement, and can be corrected by interventions such as white matter control points.

Non-Cortical Areas of Surface

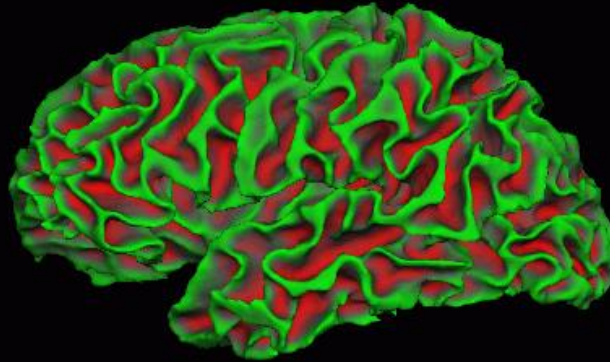
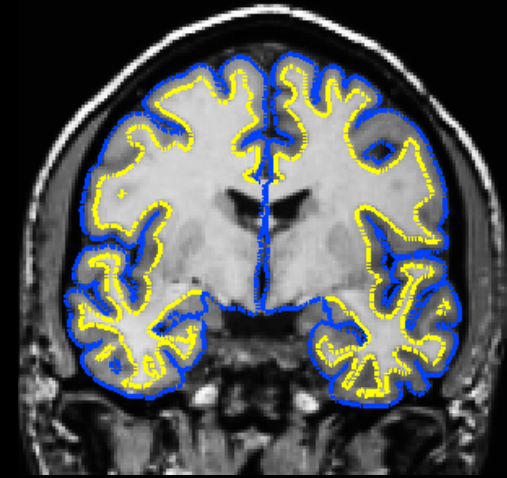


Amygdala, Putamen, Hippocampus, Caudate, Ventricles, CC

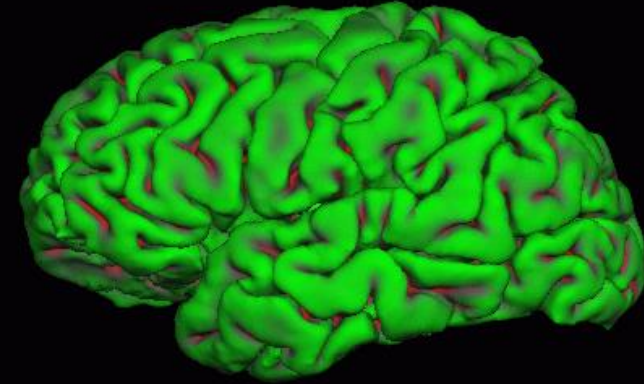


?h.cortex.label

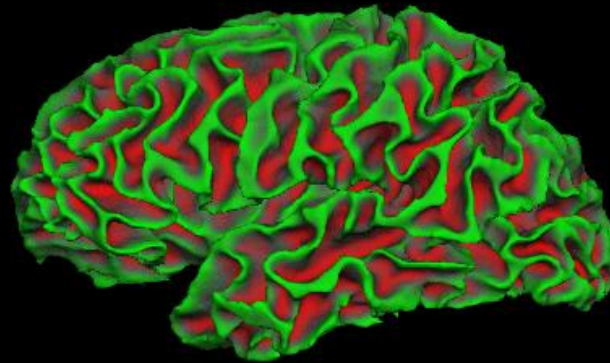
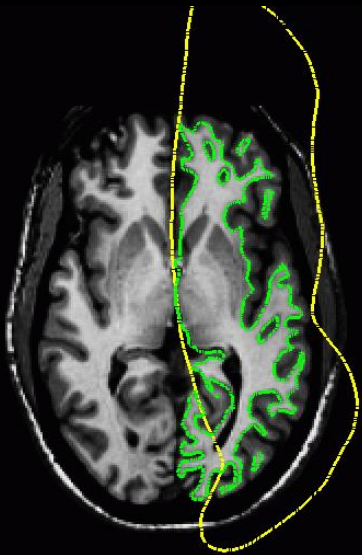
Inflation: 2D Surface in 3D Space



White Surface



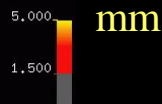
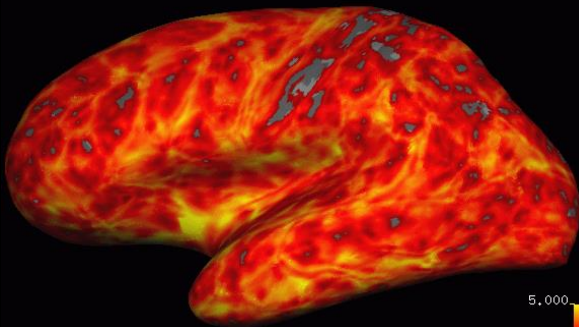
Pial Surface



- Nudge vertices
- No intensity constraint
- See inside sulci
- Used for sphere

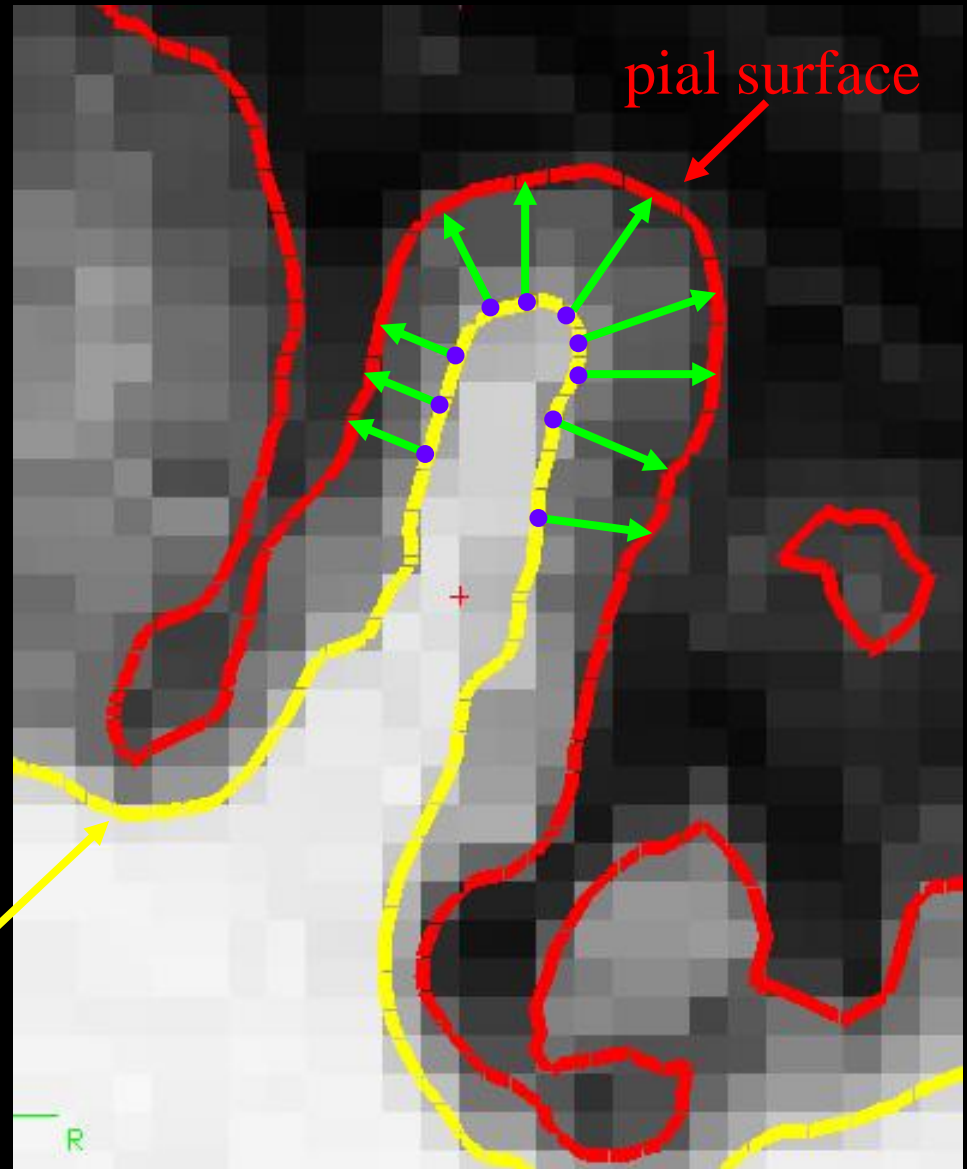
Cortical Thickness

- Distance between white and pial surfaces
- One value per vertex
- Surface-based more accurate than volume-based

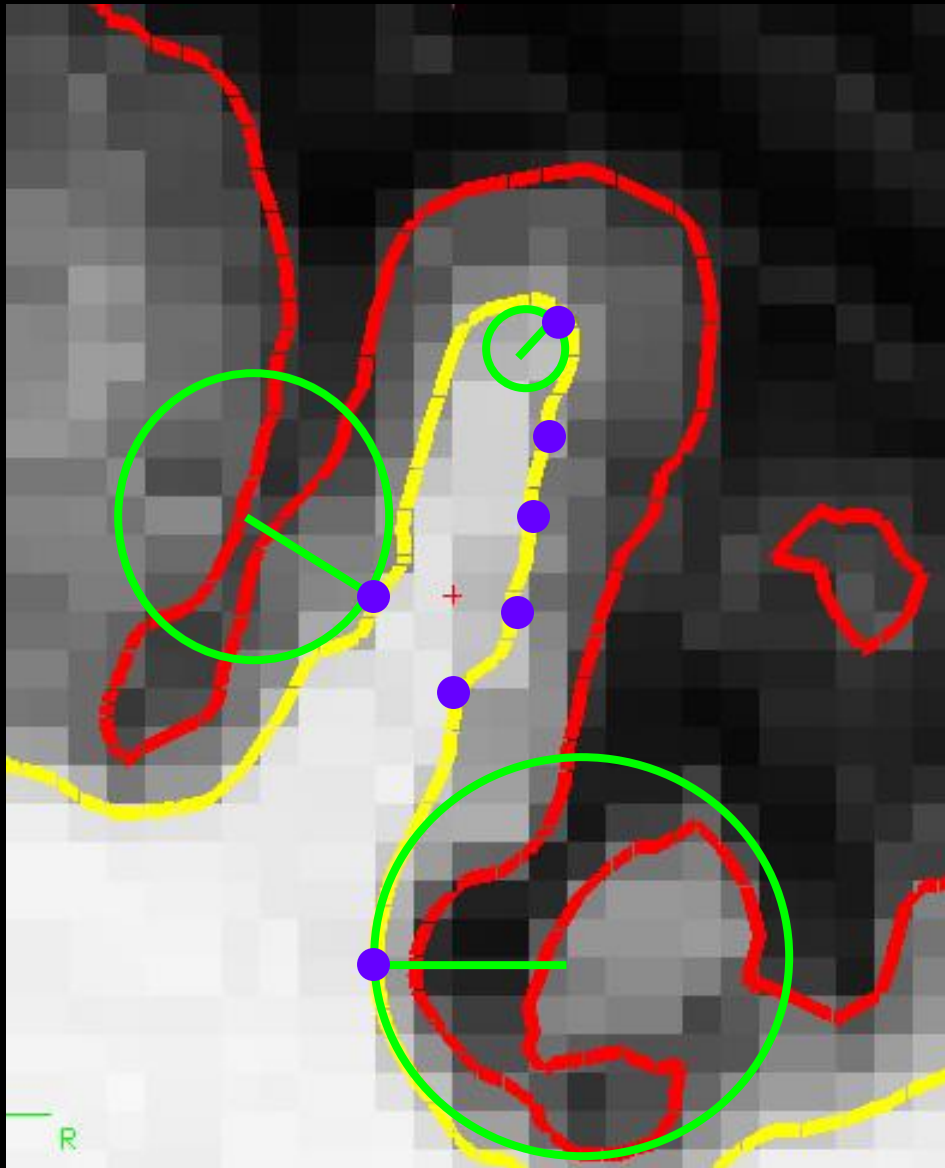


white/gray surface

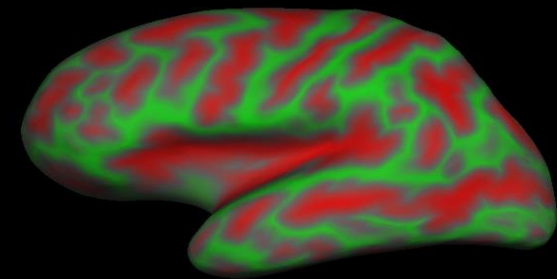
lh.thickness, rh.thickness



Curvature (Radial)

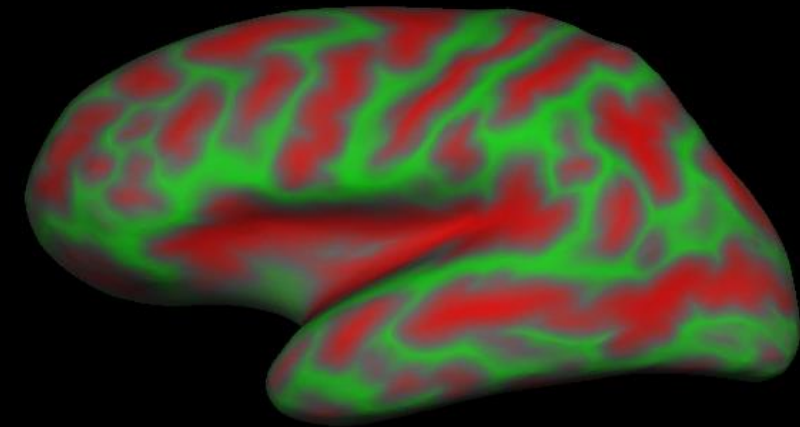


- Circle tangent to surface at each vertex
- Curvature measure is $1/\text{radius of circle}$
- One value per vertex
- Signed (sulcus/gyrus)



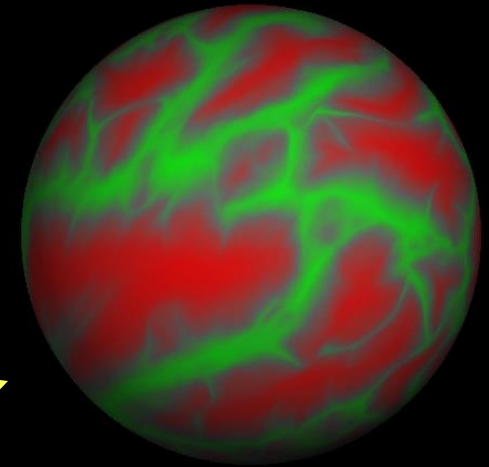
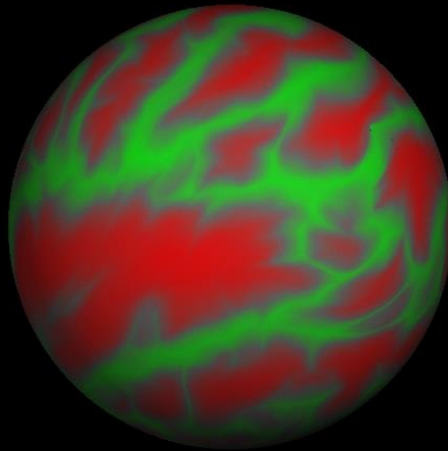
lh.curv, rh.curv

Spherical Registration



Sulcal Map

Spherical Inflation



High-Dimensional
Non-linear
Registration to
Spherical Template

Atlas template is called “fsaverage”

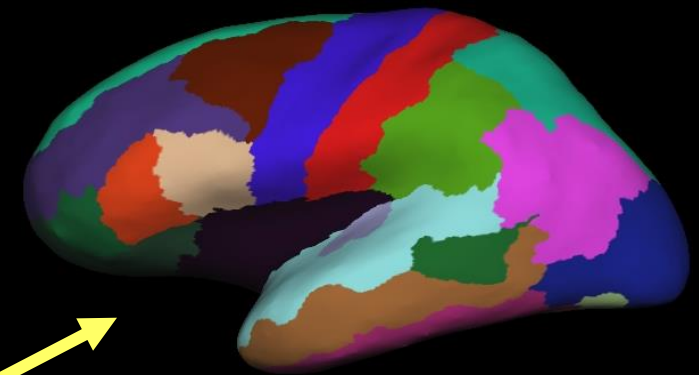
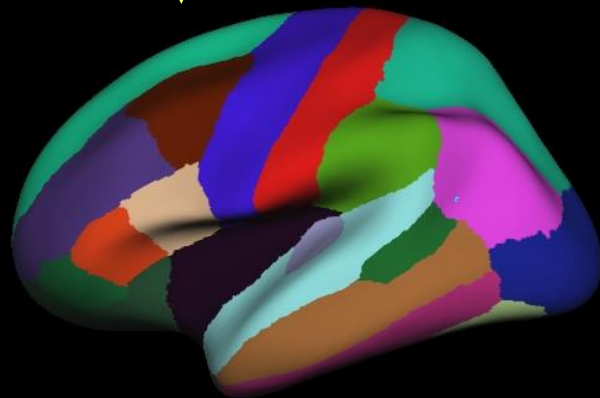
More in surface-based analysis talk.

Automatic Cortical Parcellation

Spherical Atlas based on Manual Labeling



Map to Individual
Thru Spherical Reg

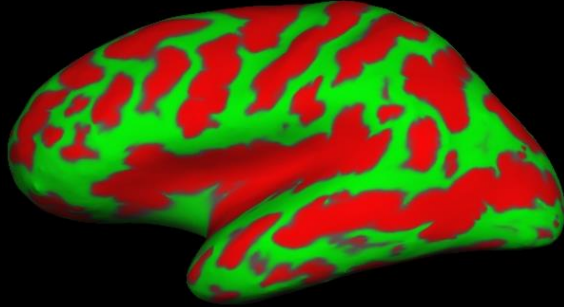


Fine-tune based on
individual anatomy

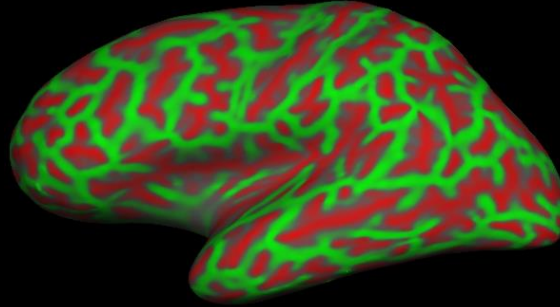
Note: Similar methodology
to volume labeling

Surface Overlays

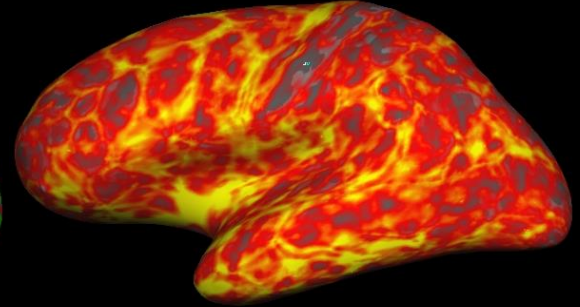
lh.sulc on inflated



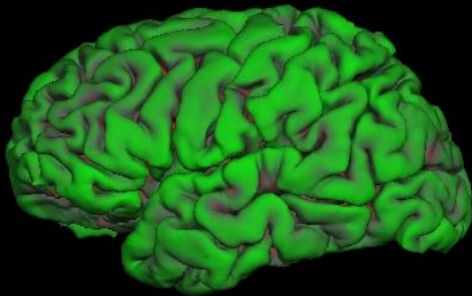
lh.curv on inflated



lh.thickness on inflated



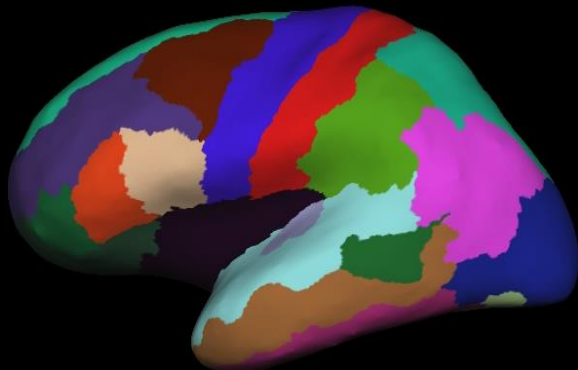
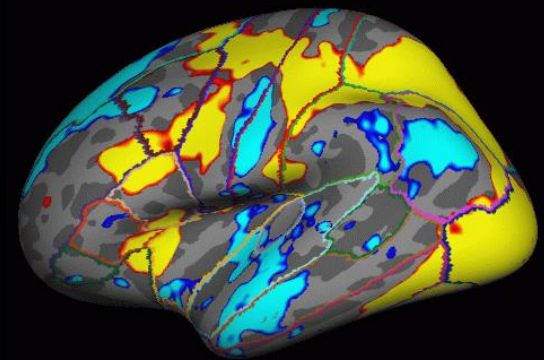
lh.sulc on pial



lh.curv on inflated



fMRI on inflated



lh.aparc.annot on inflated

- Value for each vertex
- Color indicates value
- Color: gray, red/green, heat, color table
- Rendered on any surface
- fMRI/Stat Maps too

ROI Summaries:

`$SUBJECTS_DIR/bert/stats`

`aseg.stats` – volume summaries

`?h.aparc.stats` – desikan/killiany surface summaries

`?h.aparc.a2009s.stats` – destrieux surface summaries

`wmparc.stats` – white matter parcellation

Index	SegId	NVoxels	Volume_mm3	StructName	normMean	normStdDev	normMin	normMax	normRange
1	1	0	0.0	Left-Cerebral-Exterior	0.0000	0.0000	0.0000	0.0000	0.0000
2	2	265295	265295.0	Left-Cerebral-White-Matter	106.6763	8.3842	35.0000	169.0000	134.0000
3	3	251540	251540.0	Left-Cerebral-Cortex	81.8395	10.2448	29.0000	170.0000	141.0000
4	4	7347	7347.0	Left-Lateral-Ventricle	42.5800	12.7435	21.0000	90.0000	69.0000
5	5	431	431.0	Left-Inf-Lat-Vent	66.2805	11.4191	30.0000	95.0000	65.0000
6	6	0	0.0	Left-Cerebellum-Exterior	0.0000	0.0000	0.0000	0.0000	0.0000
....									

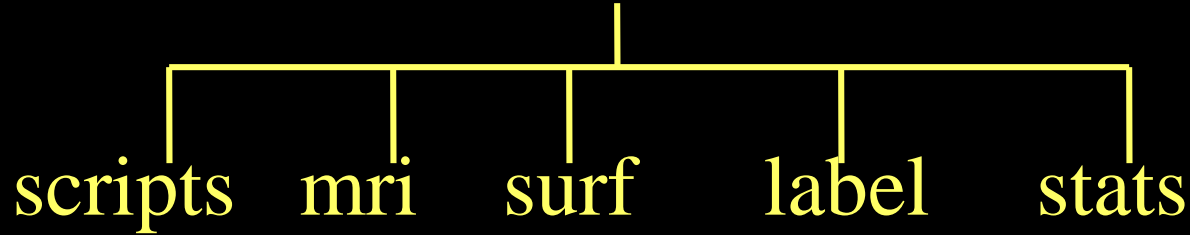
Routines to generate spread sheets of group data

- `asegstats2table --help`
- `aparcstats2table --help`

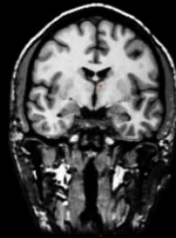
More info in Anatomical ROI talk.

Upon Completion of recon-all

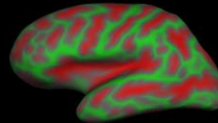
`$SUBJECTS_DIR bert`



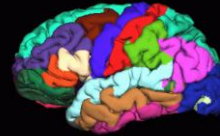
`recon-all.log`



`orig.mgz`



`lh.inflated`



`lh.aparc.annot`

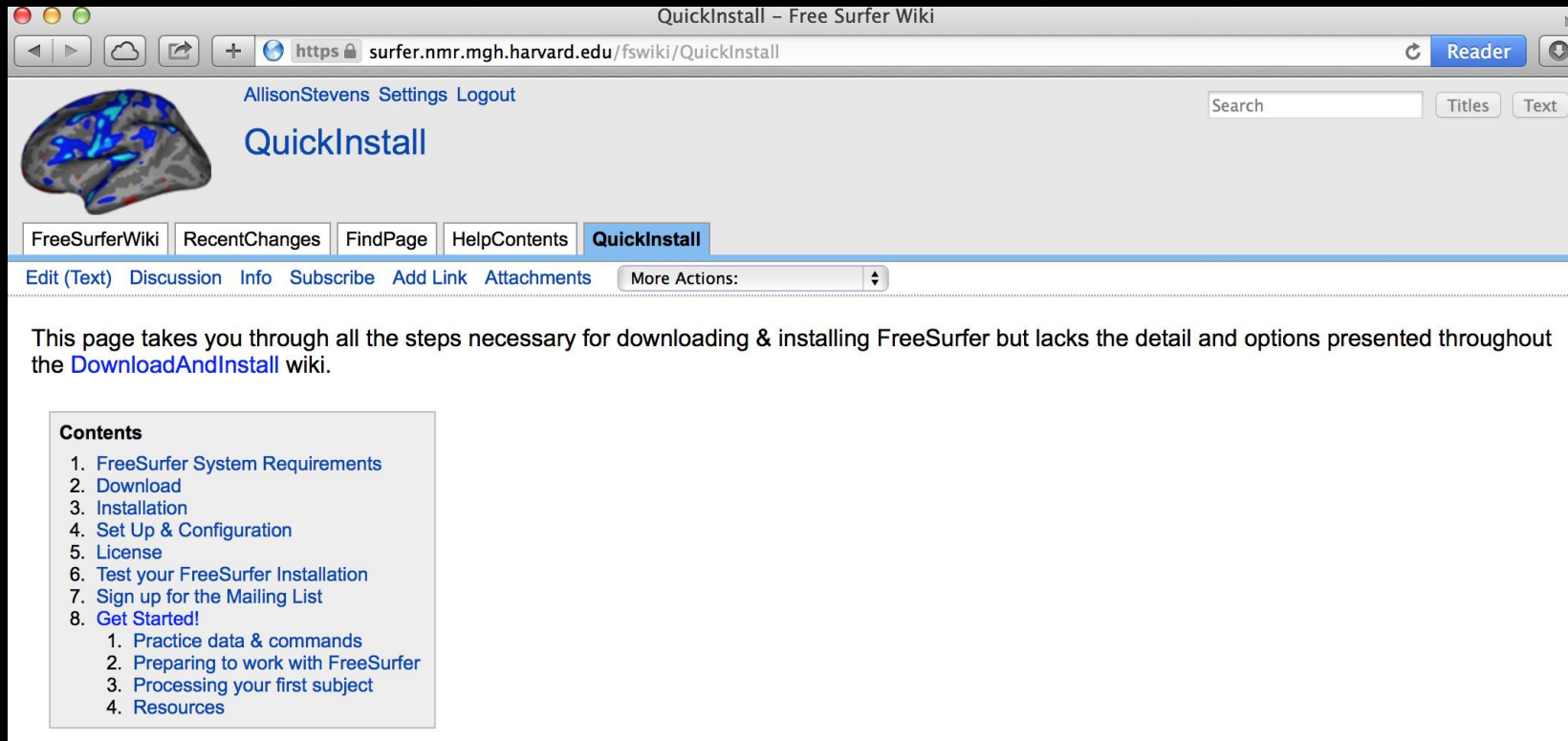
`aseg.stats`

`recon-all -i file.dcm -subject bert -all`

Getting FreeSurfer

- surfer.nmr.mgh.harvard.edu
 - Register
 - Download
 - Mailing List
- Wiki: surfer.nmr.mgh.harvard.edu/fswiki
- Platforms:
 - Linux
 - Mac
 - Windows (VirtualBox)
- Installed in `$FREESURFER_HOME`

Download & Install



QuickInstall - Free Surfer Wiki

https://surfer.nmr.mgh.harvard.edu/fswiki/QuickInstall

AllisonStevens Settings Logout

QuickInstall

FreeSurferWiki RecentChanges FindPage HelpContents **QuickInstall**

Edit (Text) Discussion Info Subscribe Add Link Attachments More Actions:

This page takes you through all the steps necessary for downloading & installing FreeSurfer but lacks the detail and options presented throughout the [DownloadAndInstall](#) wiki.

Contents

1. [FreeSurfer System Requirements](#)
2. [Download](#)
3. [Installation](#)
4. [Set Up & Configuration](#)
5. [License](#)
6. [Test your FreeSurfer Installation](#)
7. [Sign up for the Mailing List](#)
8. [Get Started!](#)
 1. [Practice data & commands](#)
 2. [Preparing to work with FreeSurfer](#)
 3. [Processing your first subject](#)
 4. [Resources](#)

What to do next

Get Started!

Practice data & commands

We highly recommend downloading the [tutorial dataset](#) and learning FreeSurfer with our guided tutorials. You can find the list of tutorials on our course wiki, under the [Course Schedule](#) section. Here, you will also find slides from our most recent lecture series with videos of the lectures [here](#).

Preparing to work with FreeSurfer

Whenever you want to work with FreeSurfer, you must make sure three things have happened:

1. The variable `FREESURFER_HOME` is set (so your computer knows where FreeSurfer is installed):

```
setenv FREESURFER_HOME <freesurfer_installation_directory>/freesurfer
```
2. The FreeSurfer set up script must be sourced (so FreeSurfer knows the location of everything it needs):

```
source $FREESURFER_HOME/SetupFreeSurfer.csh
```
3. FreeSurfer has been pointed to a directory of subjects to work on:

```
setenv SUBJECTS_DIR /location/of/subjects
```

If you followed all the Quick Install instructions on this page, you have set it up so all 3 of these things happen automatically when you open a terminal window. However, when working on the tutorial data or on your own data, keep in mind that you may need to redo #3 in order to specify a different set of subjects for FreeSurfer to work with. You can change the location the `SUBJECTS_DIR` variable is set to in the `$FREESURFER_HOME/SetupFreeSurfer.csh` file or you can run the command listed in step #3 every time you open a new terminal window.

Processing your first subject

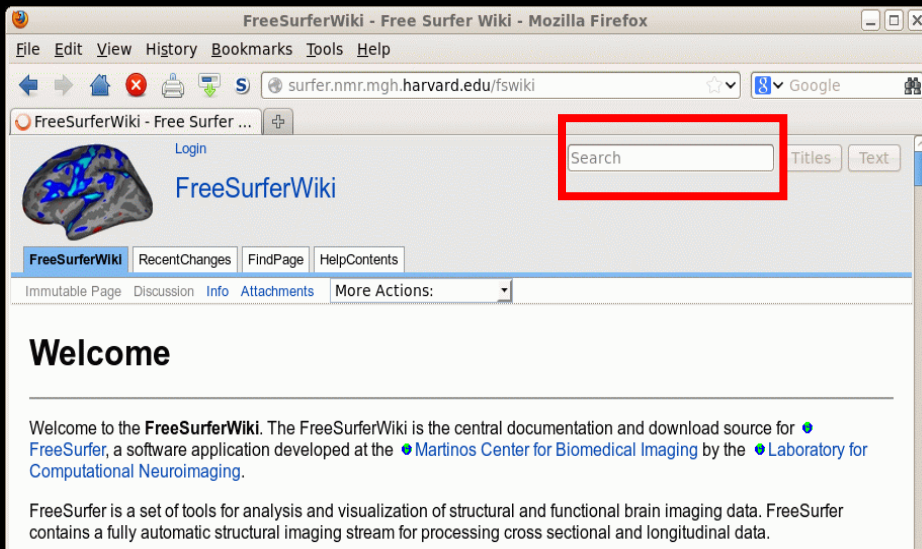
If you have data you would like to process with FreeSurfer, you can do so using the command `recon-all`. An example of how to run this command is below:

```
recon-all \  
-all \  
-i <one slice in the anatomical dicom series> \  
-s <subject id that you make up> \  

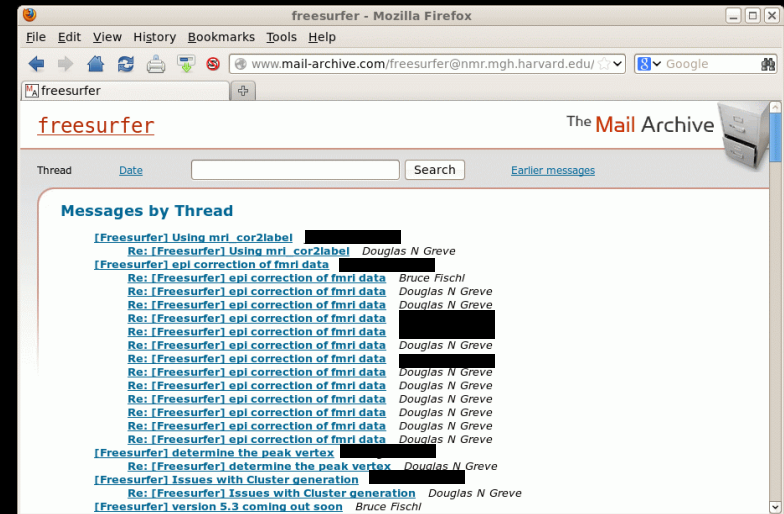
```

Getting Answers

Wiki



Mail Archive



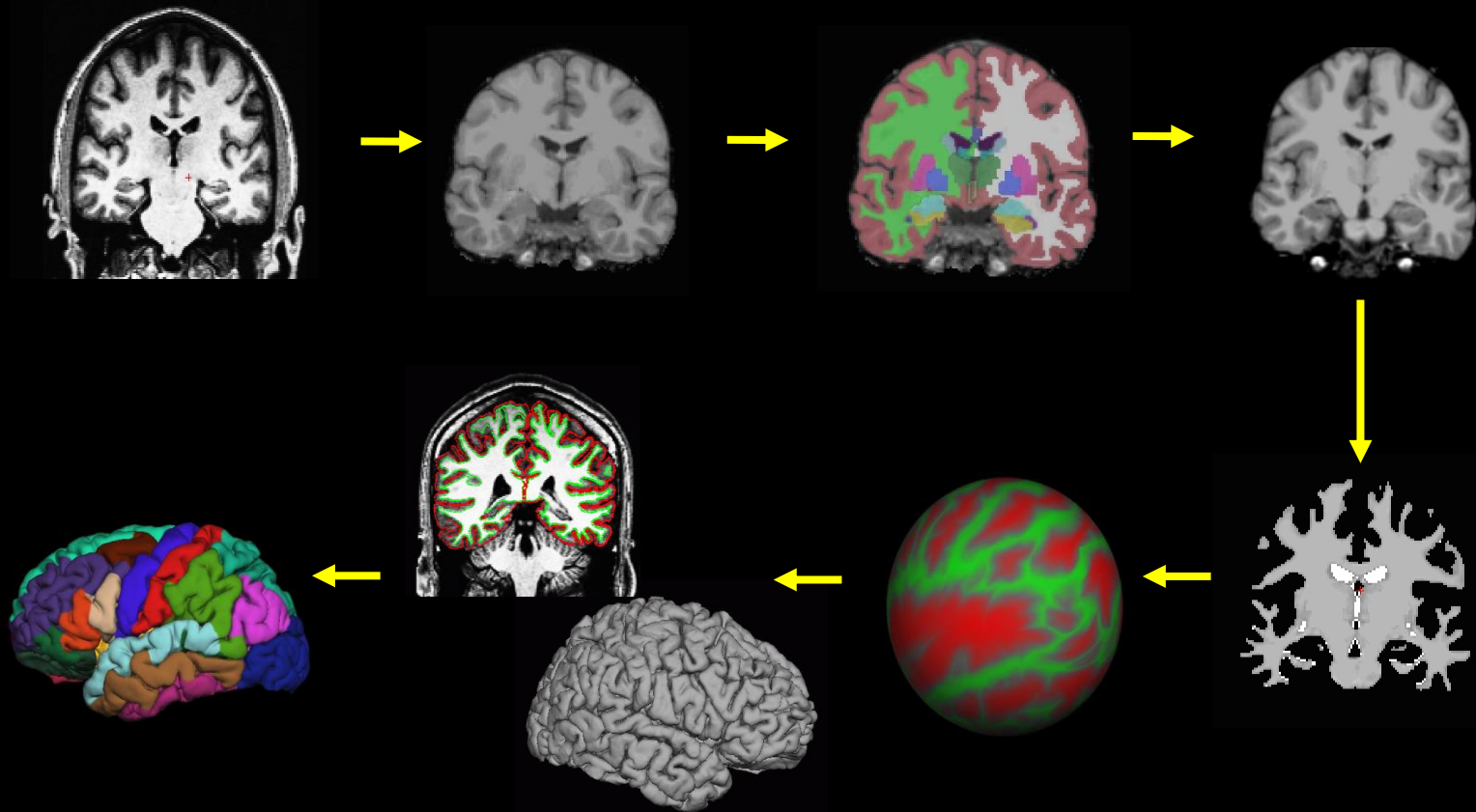
recon-all -help
mri_convert -help

\$FREESURFER_HOME/docs

Send questions to:
freesurfer@nmr.mgh.harvard.edu

Overview

```
recon-all -i file.dcm -subject bert -all
```



Tutorial Tips

- Best not to run multiple instances of Freeview at the same time unless you have > 8GB RAM.
- If you are running a command in the foreground, you should not type additional commands in that terminal (command prompt will be missing)

Volume Viewer (Freeview) Radiological Orientation

