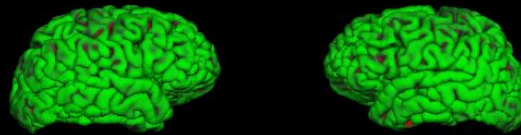
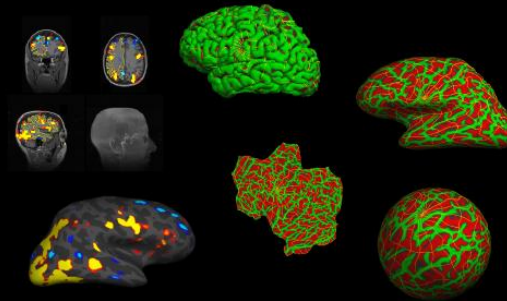


Anatomical Analysis with FreeSurfer

surfer.nmr.mgh.harvard.edu



FreeSurfer



Fully Automated Reconstruction

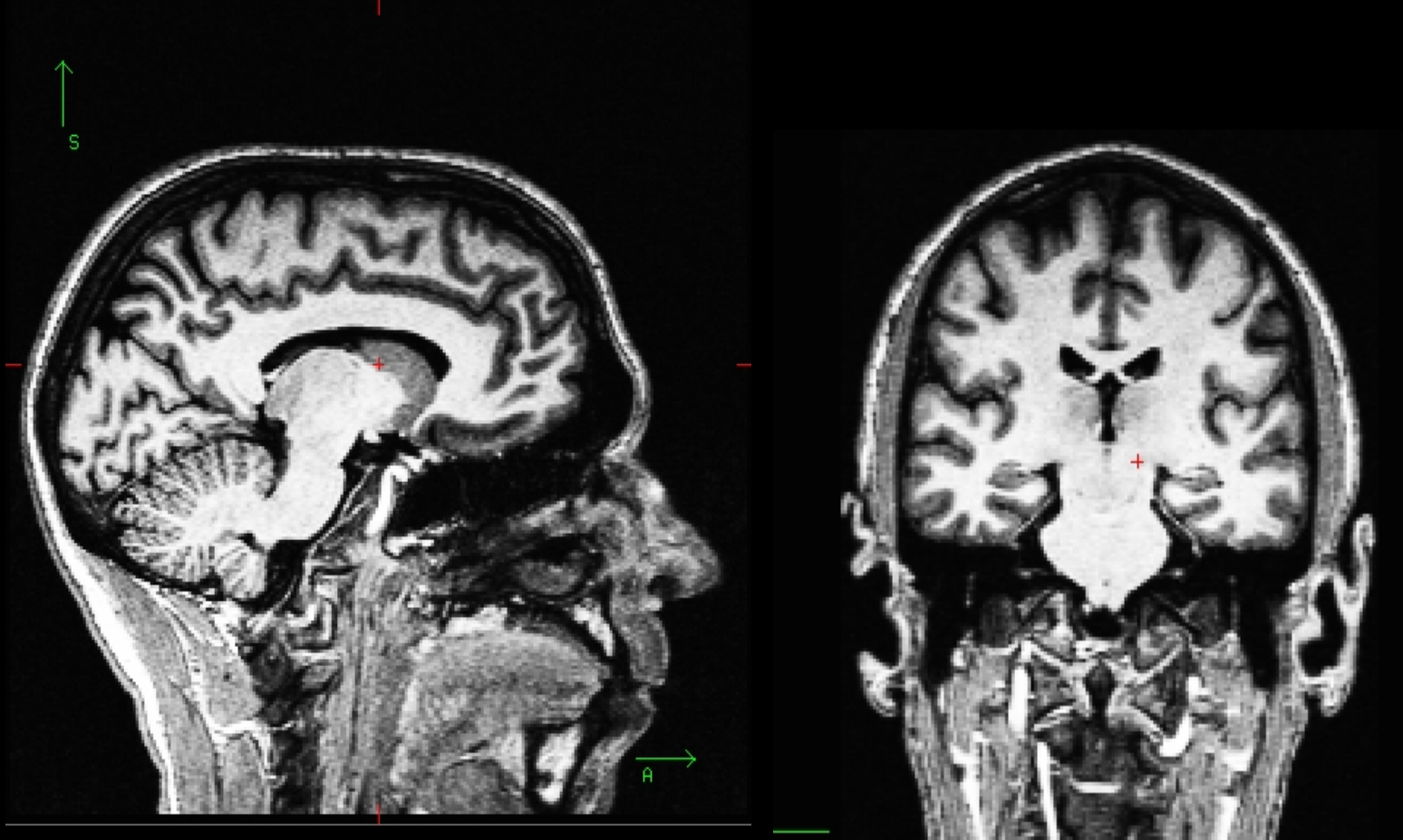
```
recon-all -i file.dcm -subject bert -all
```

Where file.dcm is one file from the correct (T1-weighted) MR series.

Administration

- surfer.nmr.mgh.harvard.edu
 - Register
 - Download
 - Mailing List
- Wiki: surfer.nmr.mgh.harvard.edu/fswiki
- Platforms: Linux, Mac, Windows (VM)
- Bug Reporting
 - Version
 - Command-line
 - Error description
 - [subjid/scripts/recon-all.log](#)
 - freesurfer@nmr.mgh.harvard.edu

Input: T1 Weighted Image

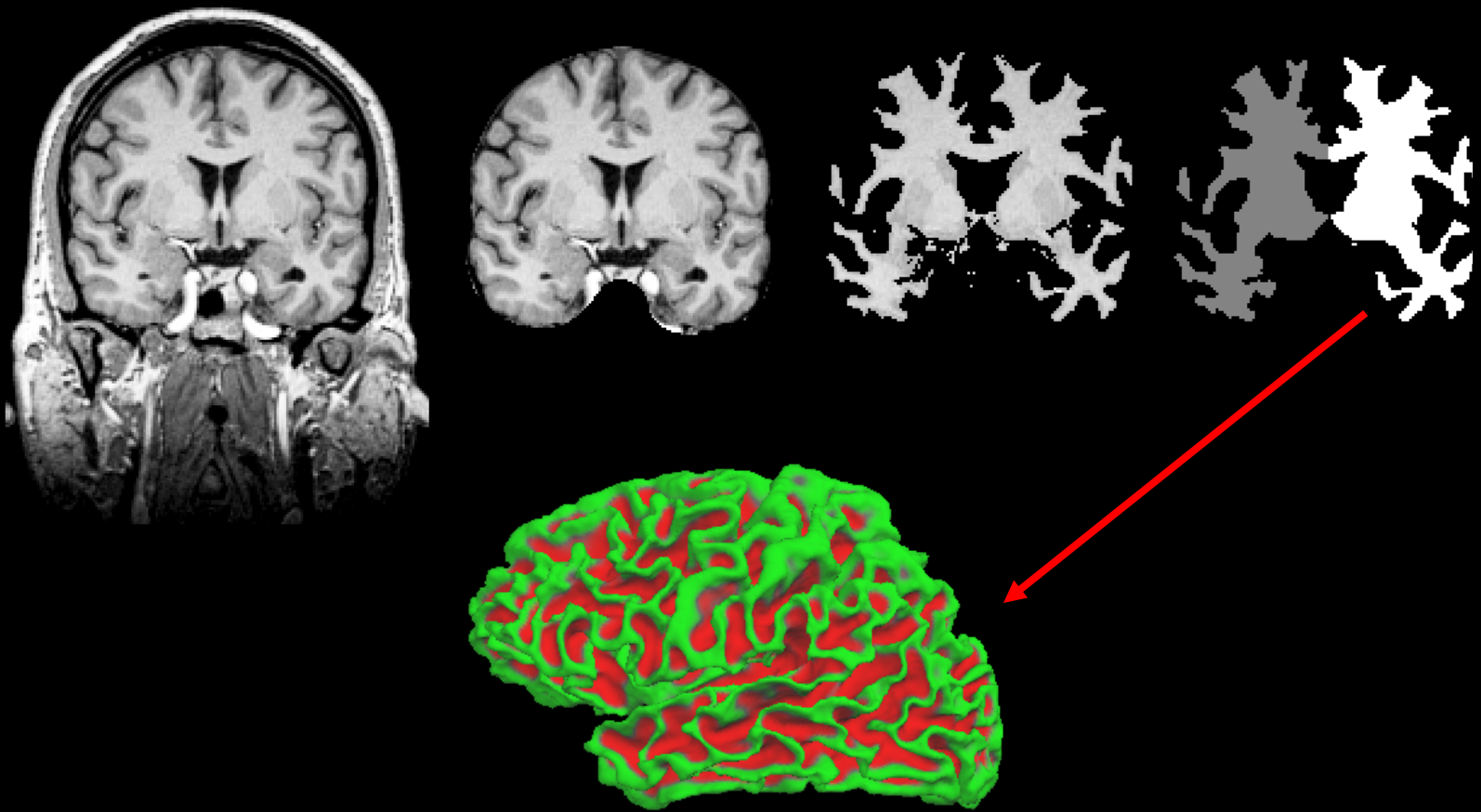


T1 Contrast: White matter brighter than gray matter

Suggested Morphometry Sequences

<http://www.nmr.mgh.harvard.edu/~andre/>

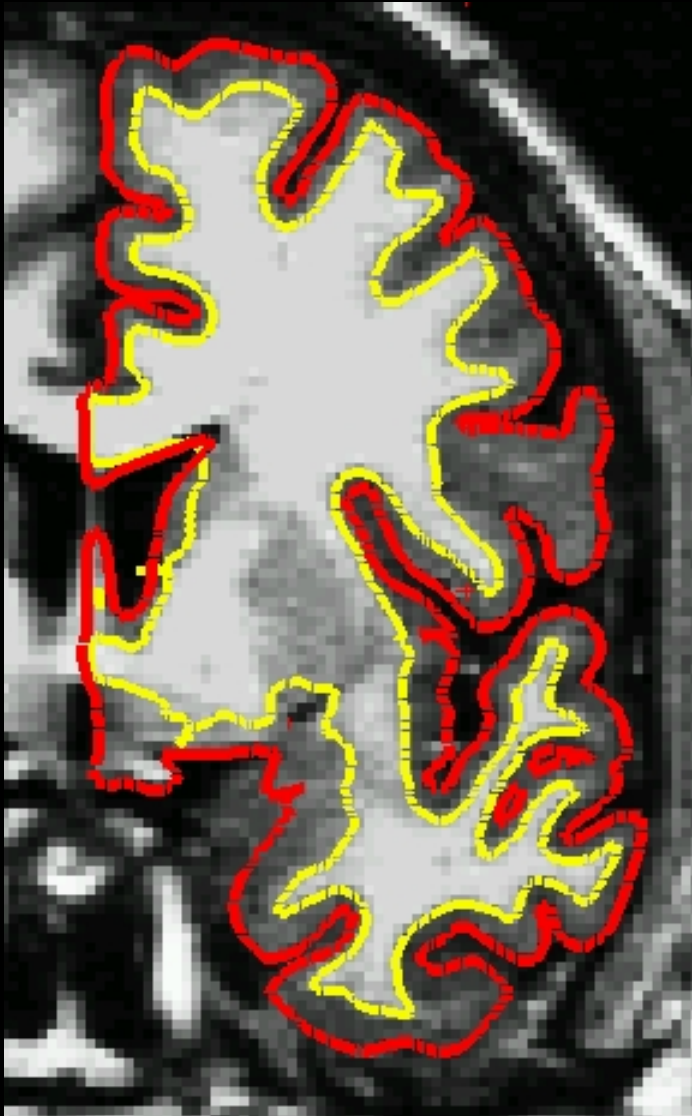
MRI Segmentation and Surface Reconstruction



Surface Reconstruction Overview

- Input: T1-weighted (MPRAGE,SPGR)
- Find white/gray surface
- Find pial surface
- “Find” = create mesh
 - Vertices, neighbors, triangles, coordinates
 - Accurately follows boundaries between tissue types
 - “Topologically Correct”
 - closed surface, no donut holes
 - no self-intersections
- Generate surface-based cross-subject registration
- Label cortical folding patterns
- Subcortical Segmentation along the way

Find “Subcortical Mass”

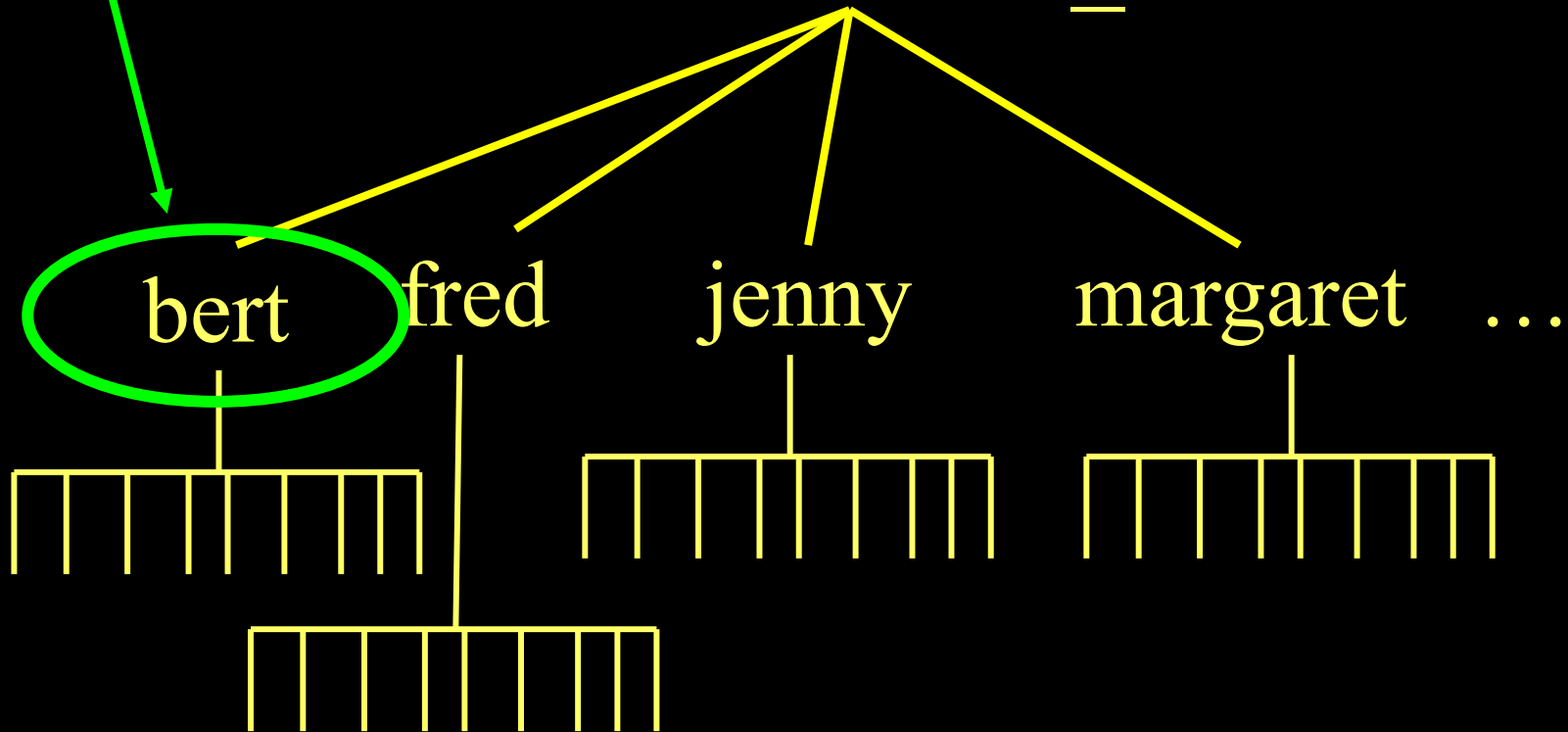


- All White Matter
- All Subcortical Structures
- Ventricles
- Excludes brain stem and cerebellum
- Hemispheres separated
- Connected (no islands)
- Many Stages ... More Later ...

SUBJECTS_DIR Environment Variable

Subject

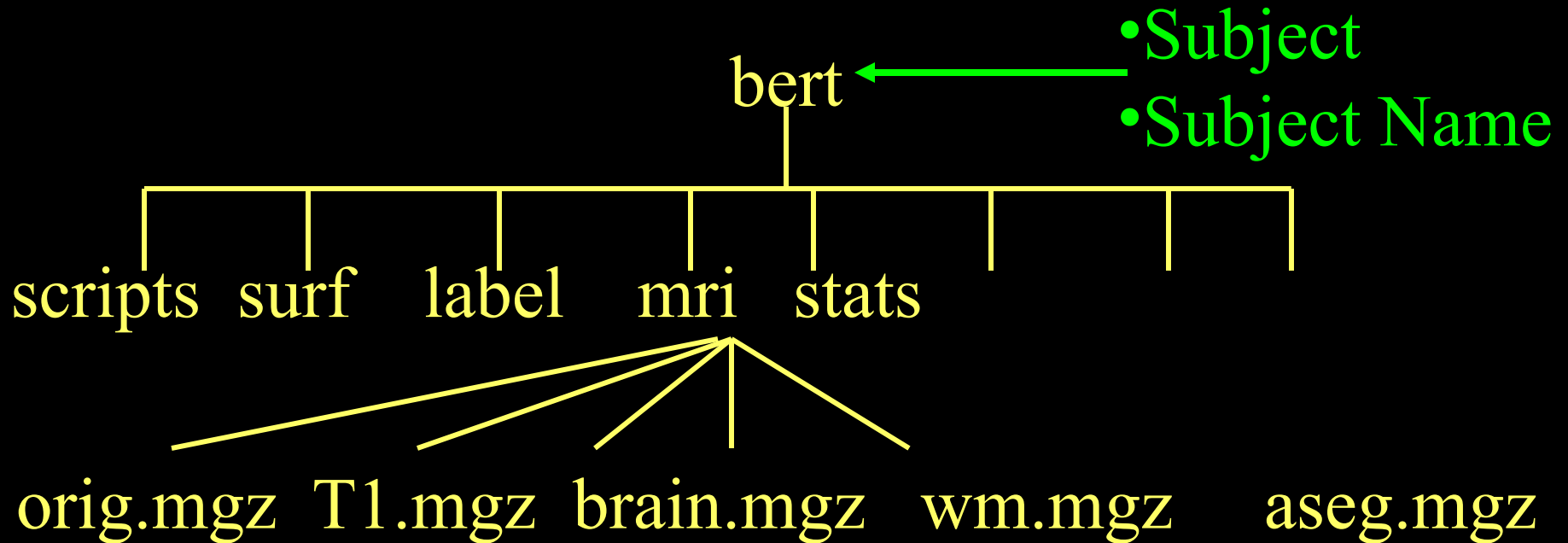
\$SUBJECTS_DIR



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

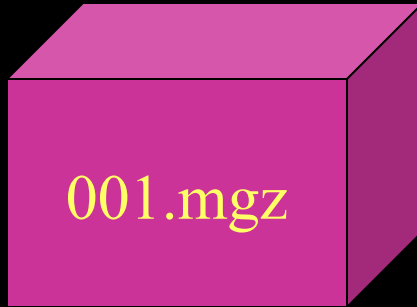
FreeSurfer Directory Tree

Each data set has its own unique SubjectId (eg, bert)



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

MGZ File Format



- mgz = compressed MGH file
- Can store 4D (like NIFTI)
- cols, rows, slices, frames
- Generic: volumes and Surfaces

- Eg, Typical Anatomical volume: 256 x 256 x 128 x 1

“Volume-encoded” Surface Files

A long, thin 3D blue rectangular prism representing a surface file. The text 'lh.thickness.sm10.mgz' is written in black on the top face of the prism.

lh.thickness.sm10.mgz

- nvertices, 1, 1, frames (eg, 163214 x 1 x 1 x 40)
- No geometry information

Other File Formats

- Surface: Vertices, XYZ, neighbors (lh.white)
- Curv: lh.curv, lh.sulc, lh.thickness
- Annotation: lh.aparc.annot
- Label: lh.pericalcarine.label
- Unique to FreeSurfer
- FreeSurfer can read/write:
 - NIFTI, Analyze, MINC
- FreeSurfer can read:
 - DICOM, Siemens IMA, AFNI

Fully Automated Reconstruction

1. Launch reconstruction:

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

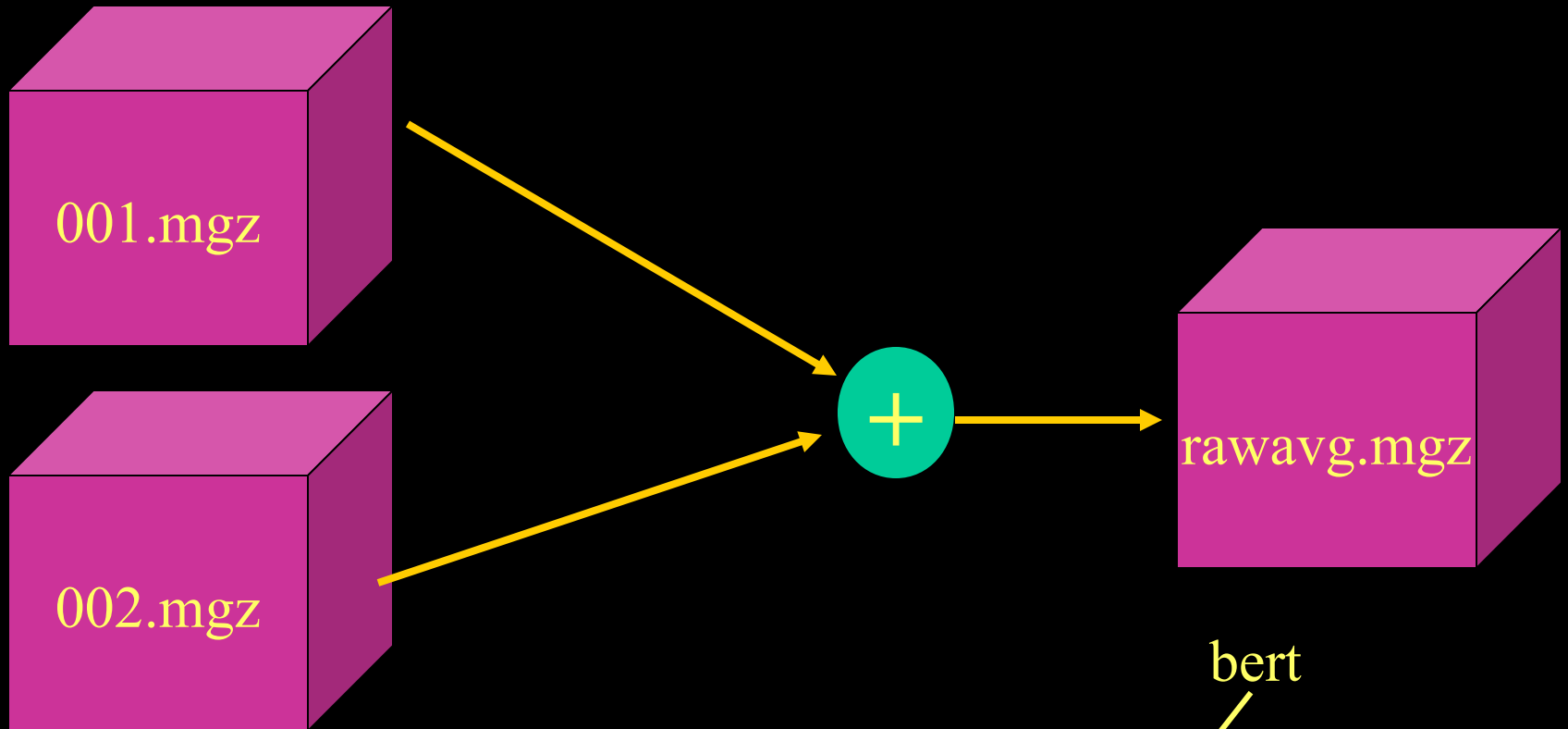
Where file.dcm is one file from the correct (T1-weighted) MR series.

Come back in 20 hours ...

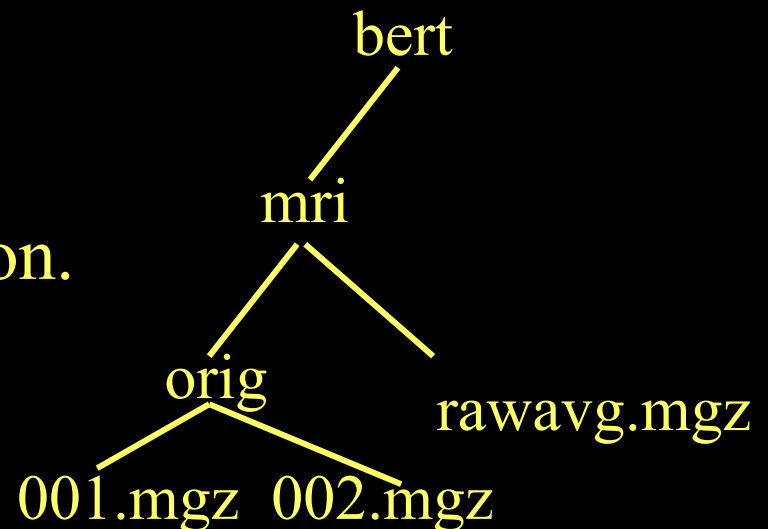
Check your results – do the white and pial surfaces follow the boundaries?

-- Can be broken up

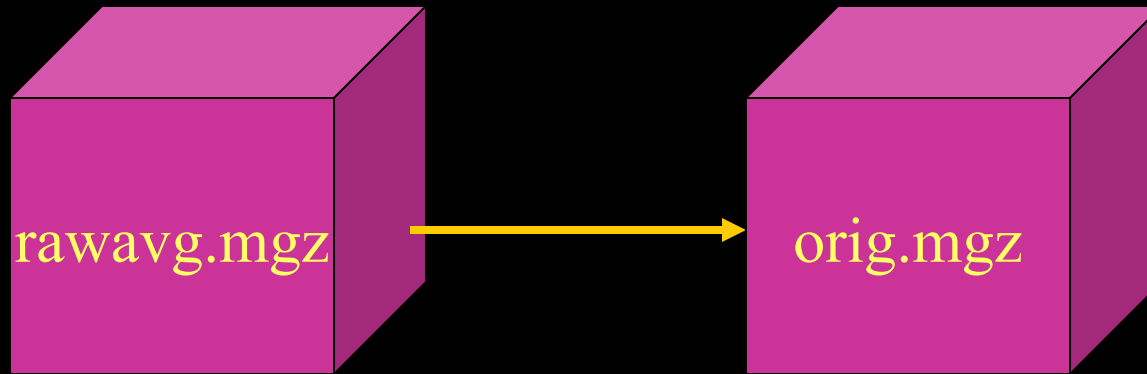
Motion Correction and Averaging



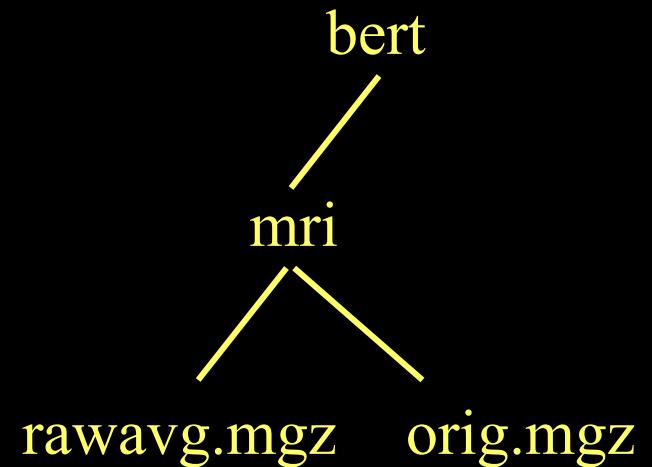
Does not change native resolution.
Usually only need one.



Conform

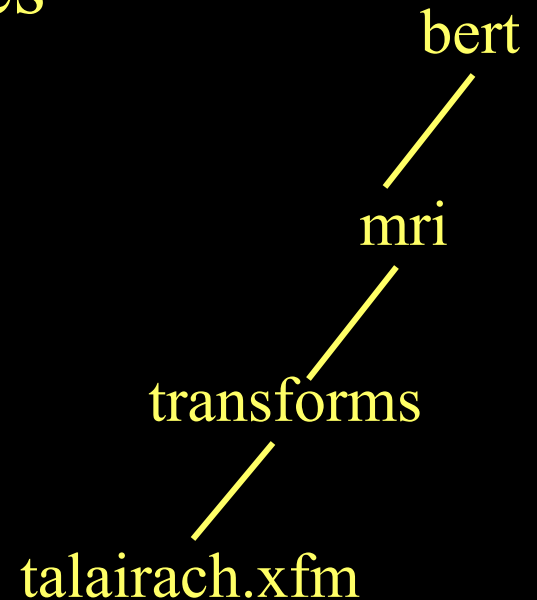


Changes to 256^3 , 1mm^3
All volumes will be conformed.

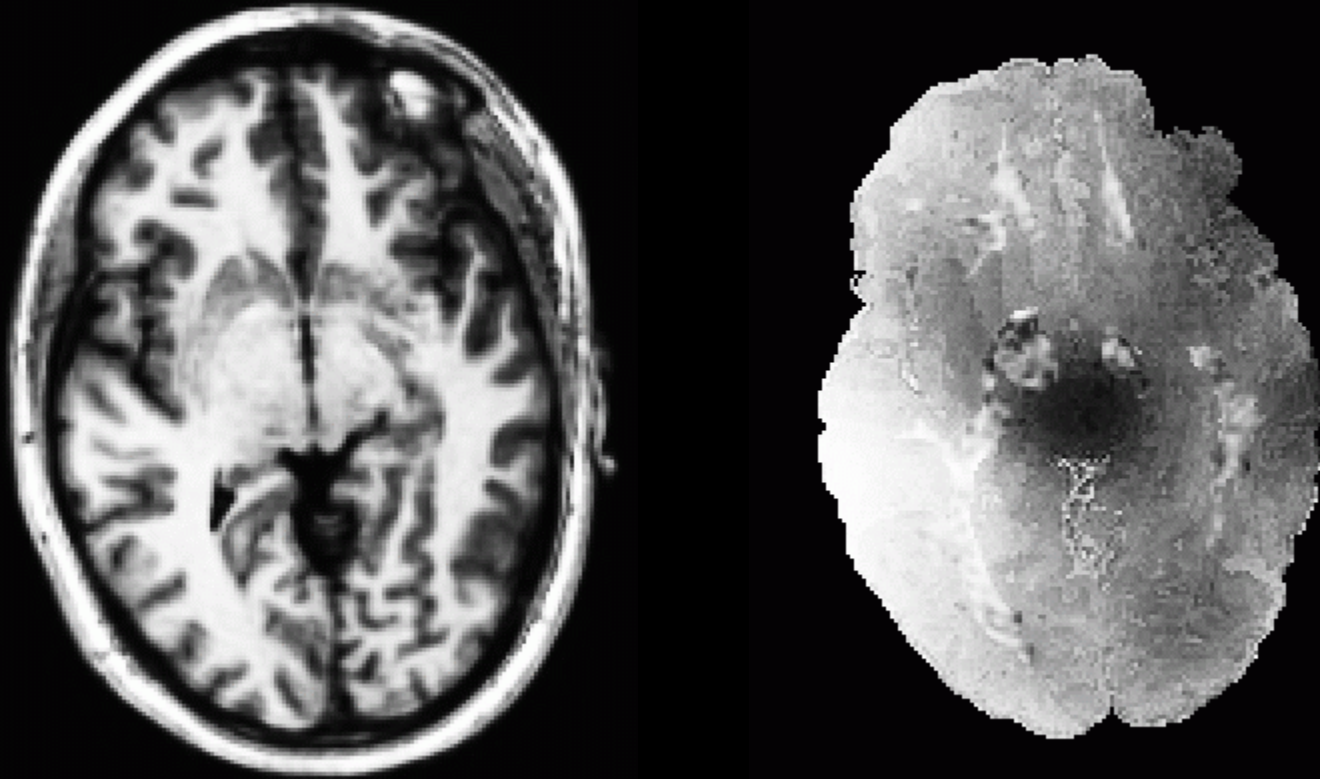


Talairach Transform

- Computes 12 DOF transform matrix
- Does NOT resample
- MNI305 template
- Mostly used to report coordinates
- `mri/transforms/talairach.xfm`



Intensity Bias

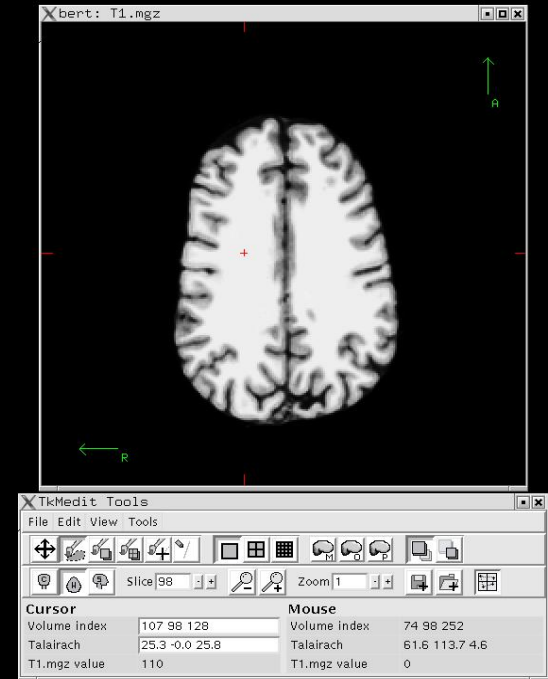


- Left side of the image much brighter than right side
- Worse with many coils
- Makes gray/white segmentation difficult

Intensity Normalization

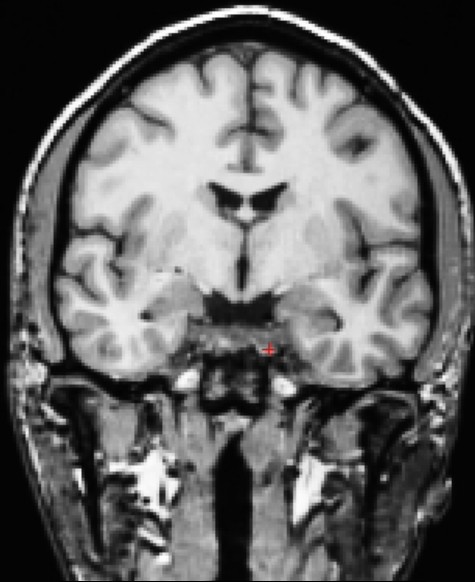
- Removes B1 bias field
- NU (MNI) nu.mgz
- Presegmentation (T1.mgz)
 - Most WM = 110 intensity
 - Pre- and Post-Skull Strip

bert
/ mri
/ T1.mgz



Skull Strip

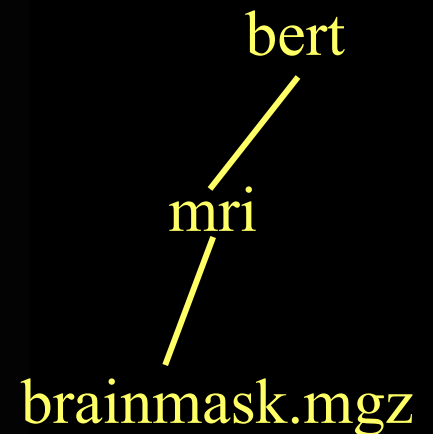
- Removes all non-brain
 - Skull, Eyes, Neck, Dura
- `brainmask.mgz` (cf, `brain.mgz`)



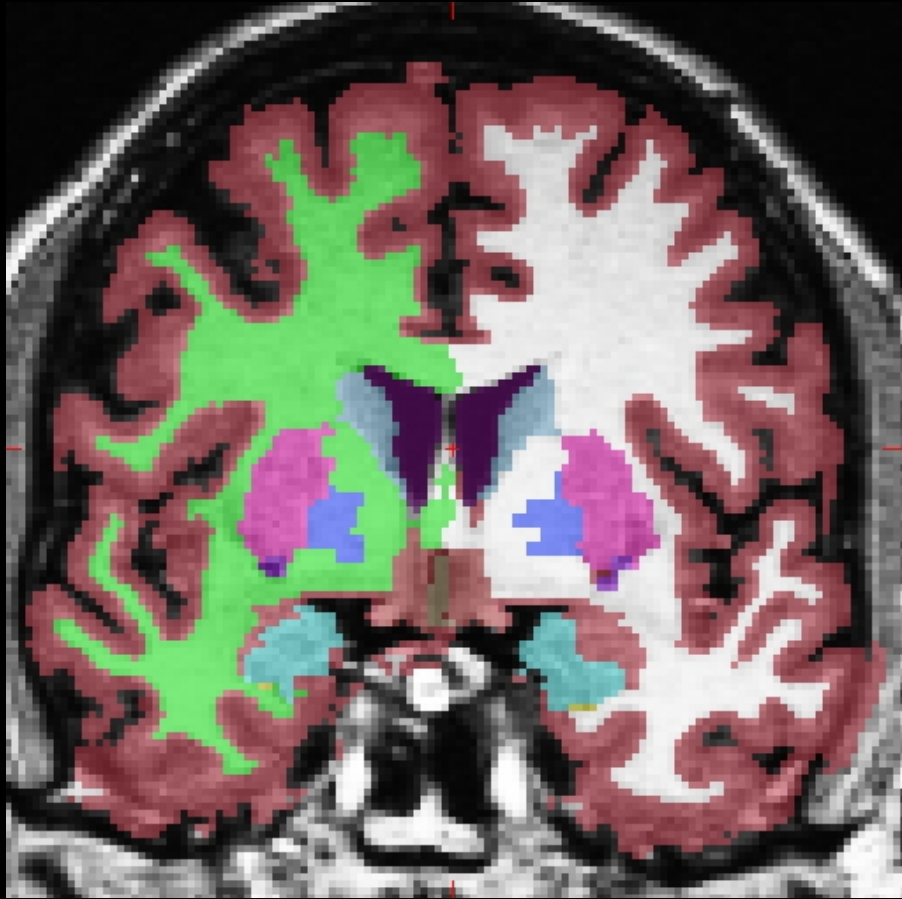
Orig Volume



Brain Volume



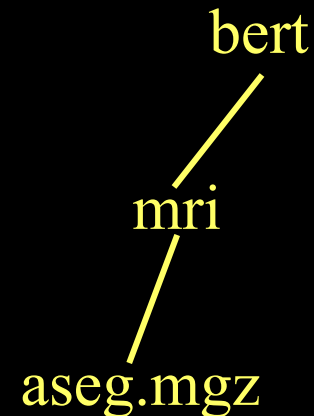
Automatic Volume Labeling



ASeg Volume

Atlas: RB_all_2008-03-26

- 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
- Somewhat redundant with aseg
- wm.mgz

bert
mri
wm.mgz



WM Volume

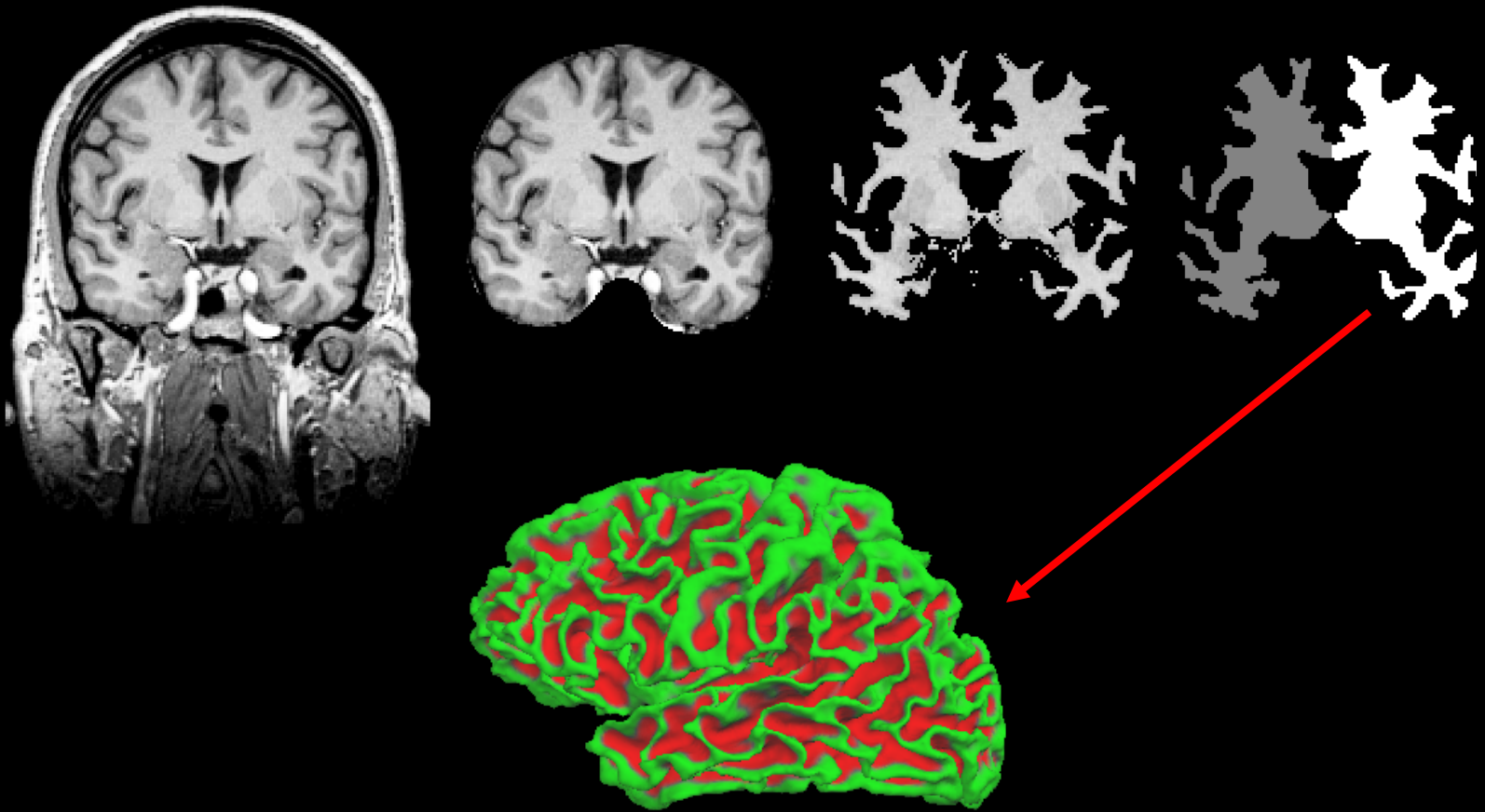
Fill and Cut (Subcortical Mass)

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

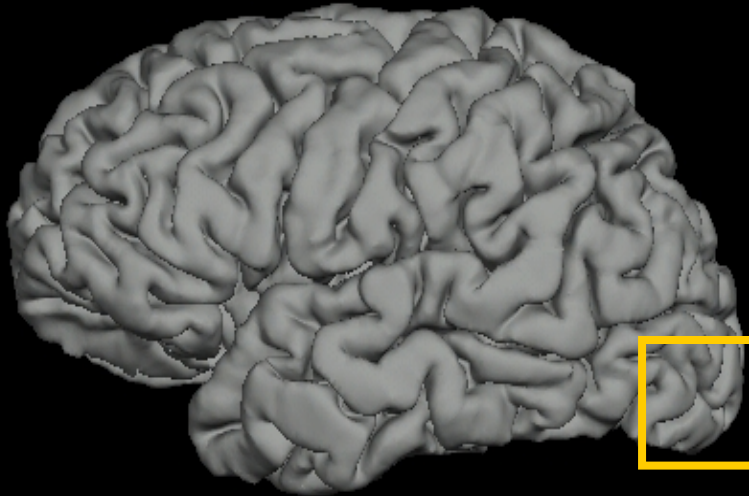


WM Volume (wm.mgz) Filled Volume (filled.mgz)
(Subcortical Mass)

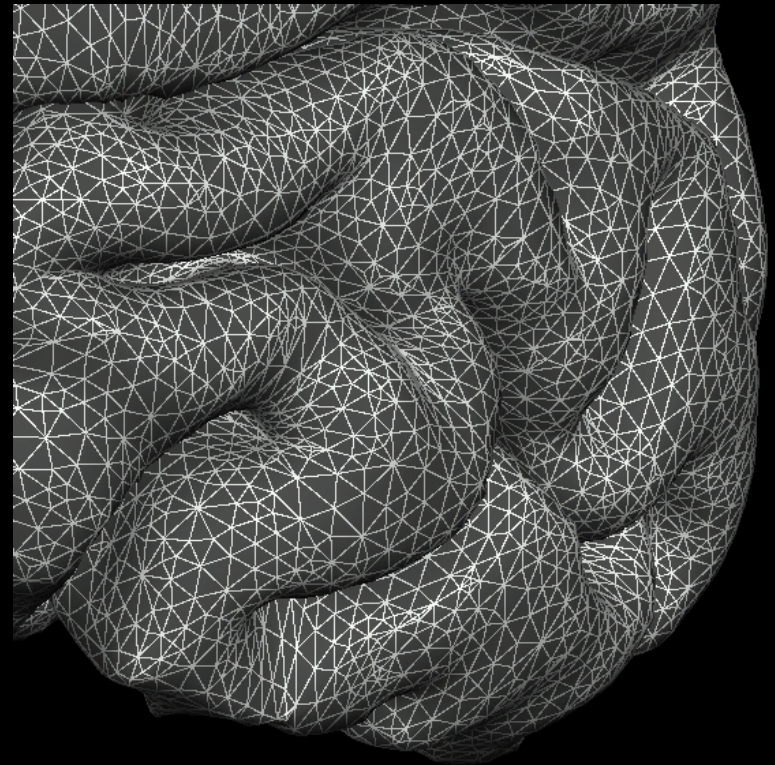
MRI Segmentation and Surface Reconstruction



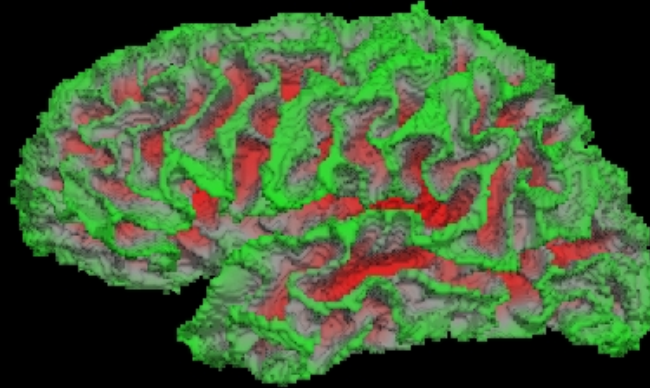
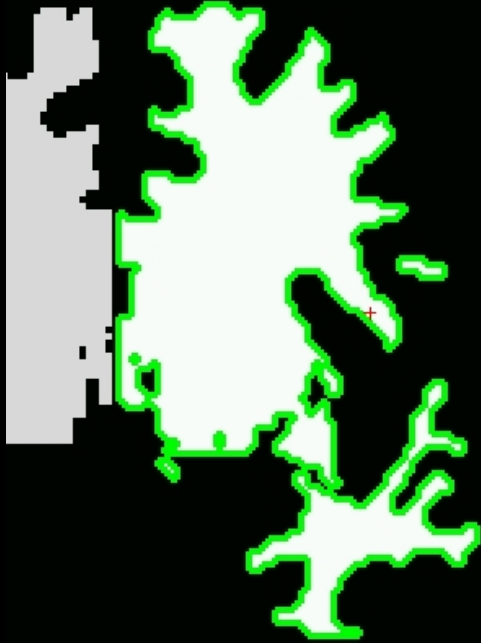
Surface Model



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

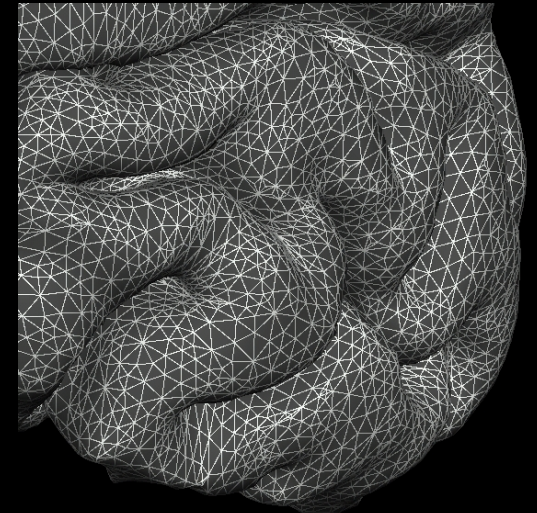


Tessellation and Topology Fixing

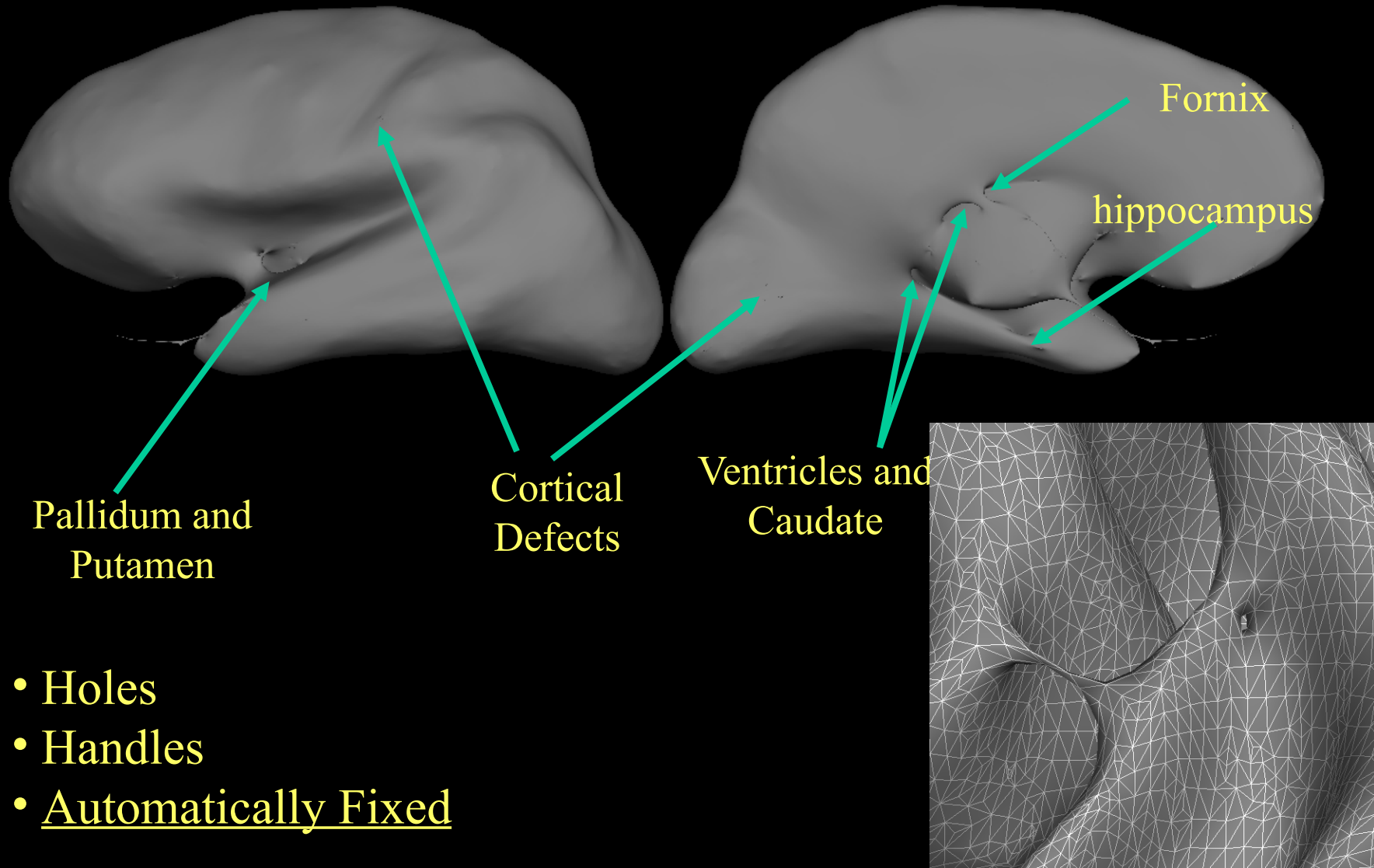


orig surface
surf/lh.orig
surf/rh.orig

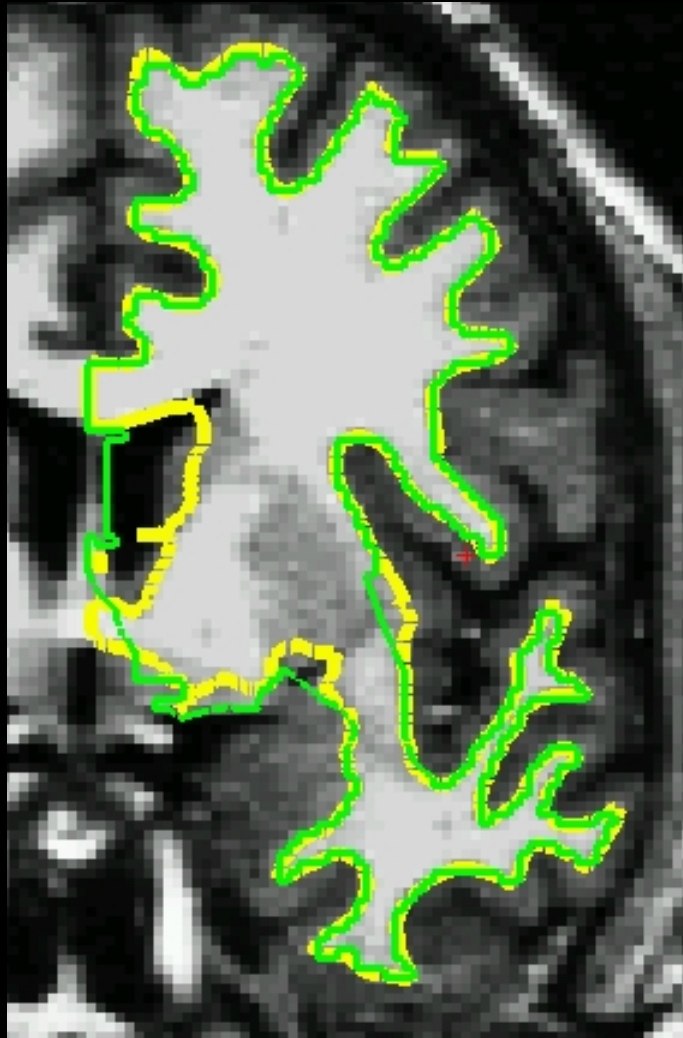
- Mosaic of triangles (“tessellation”)
- Errors: Donut holes, handles
- Automatic topology fixer



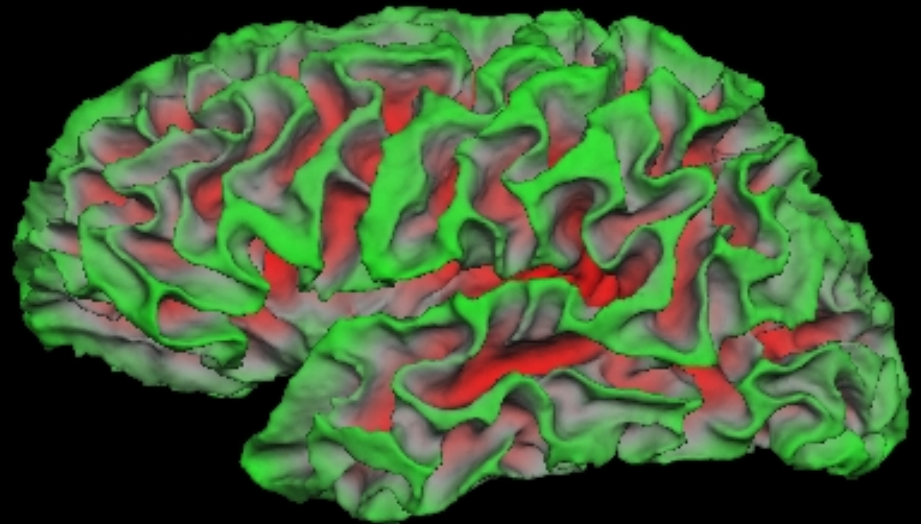
Topological Defects



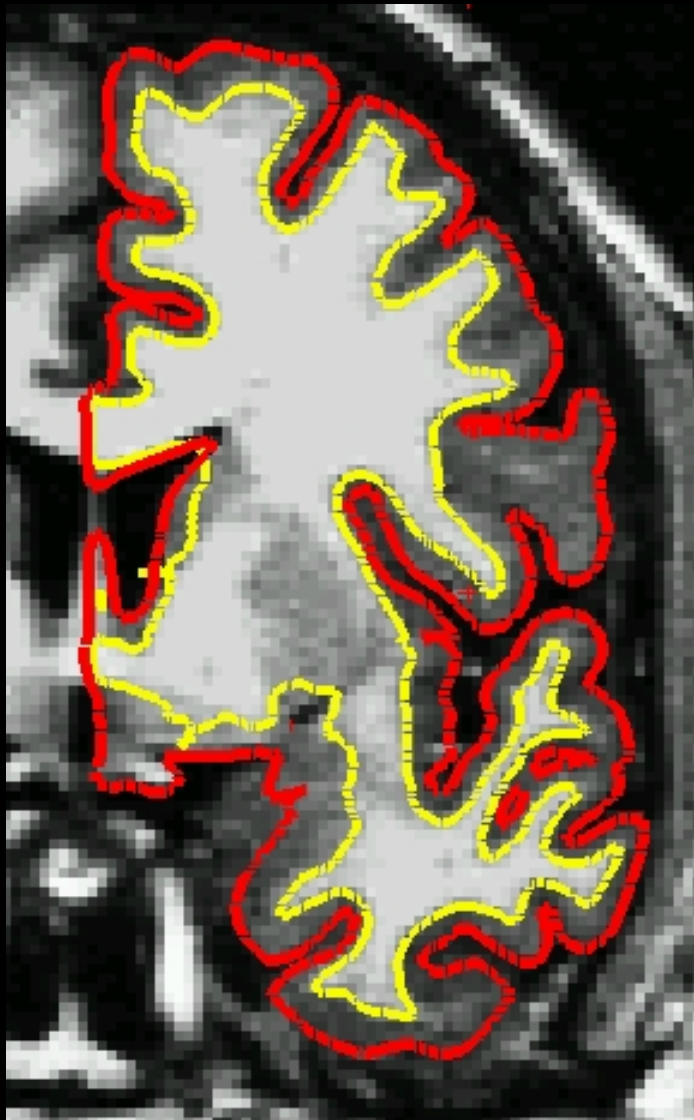
White Matter Surface



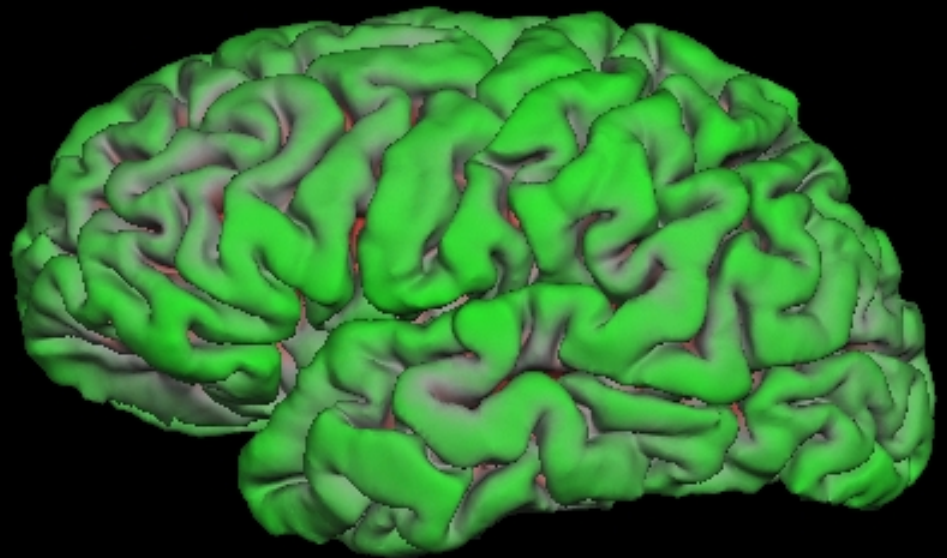
- Nudge orig surface
- Follow T1 intensity gradients
- Smoothness constraint
- Vertex identity preserved



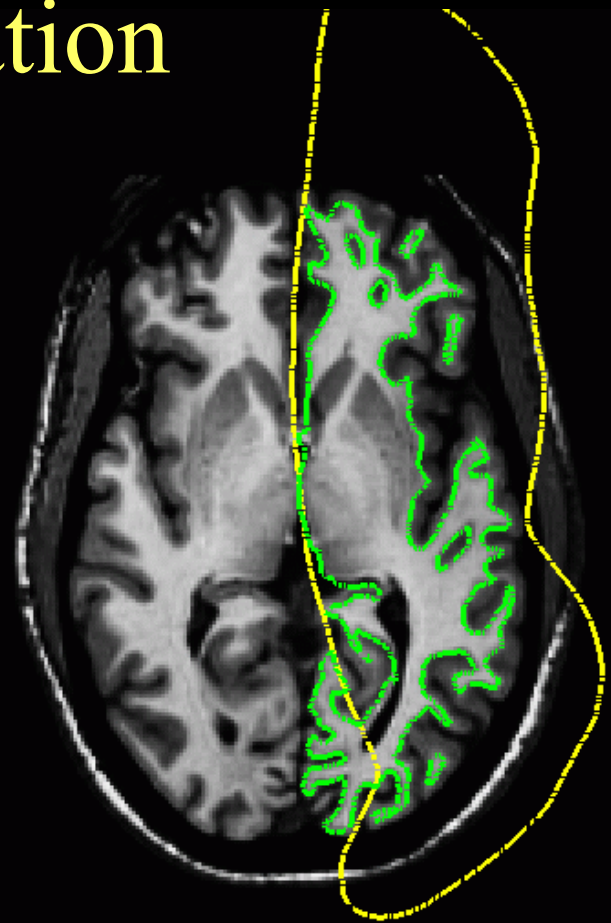
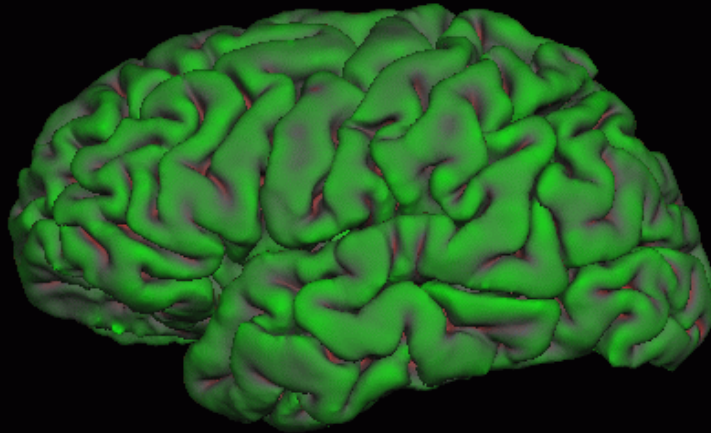
Pial Surface



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



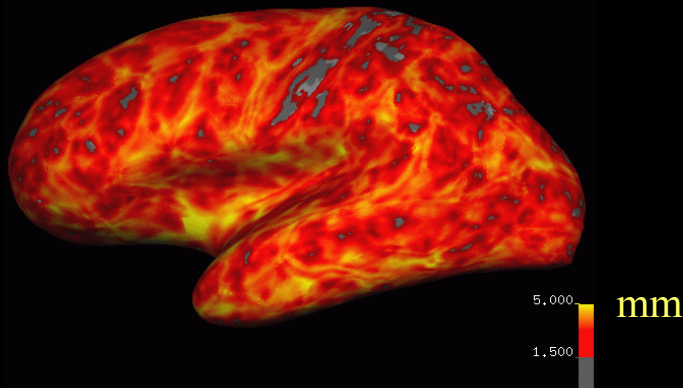
Surface Inflation



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

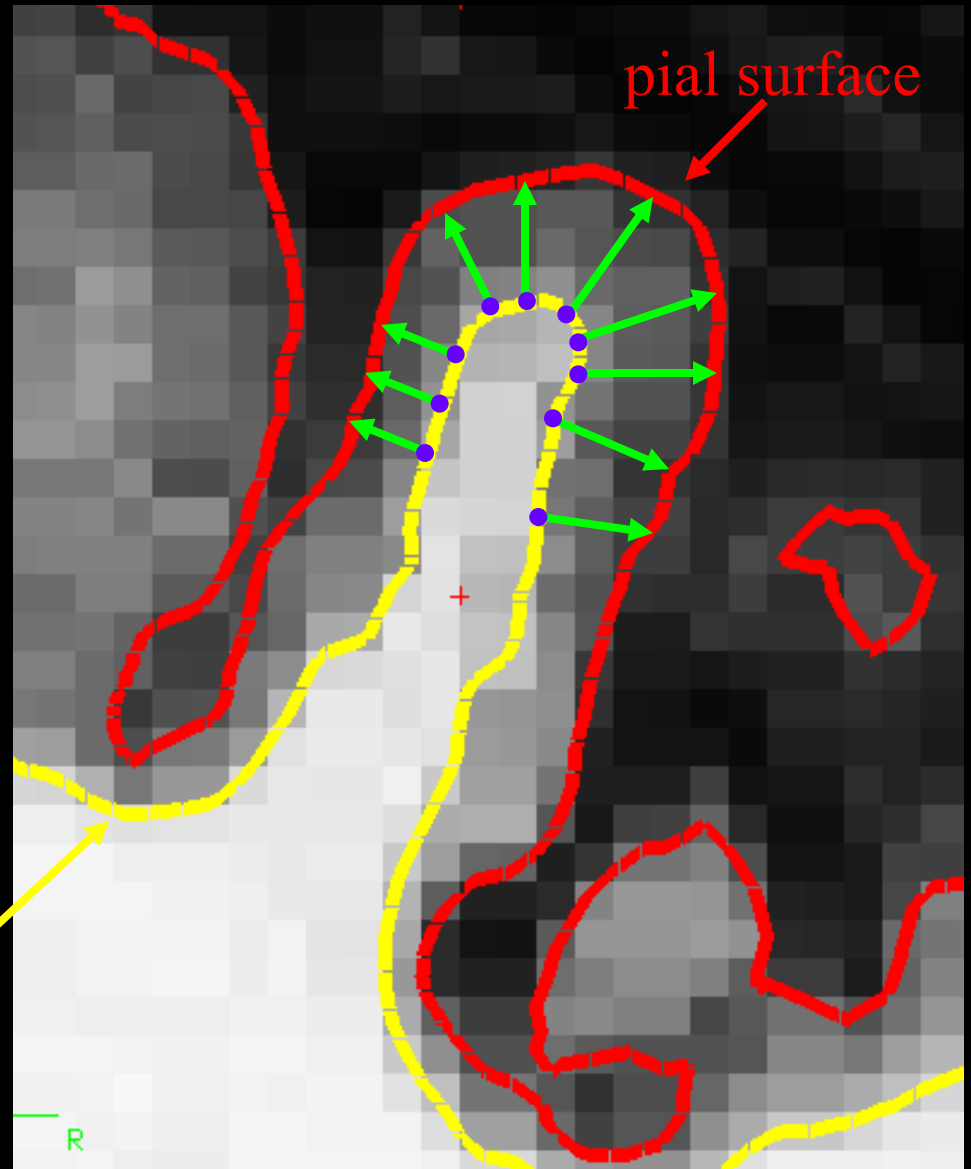
Cortical Thickness

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

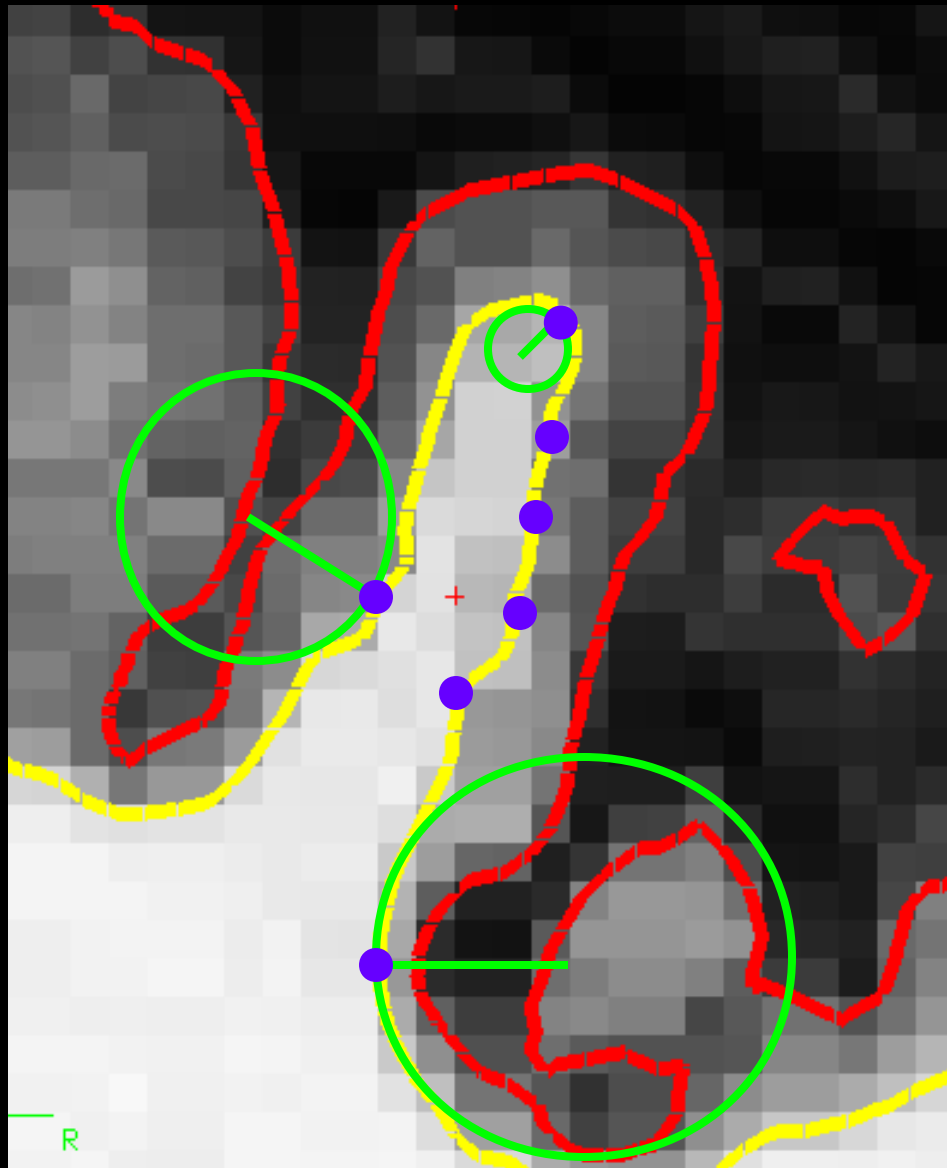


white/gray surface

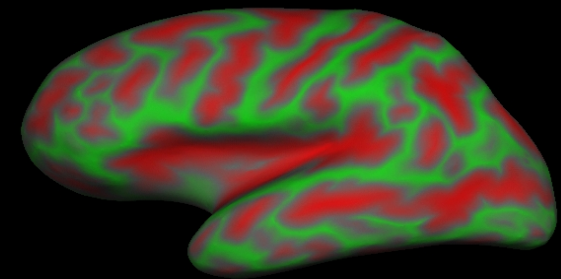
lh.thickness, rh.thickness



Curvature (Radial)

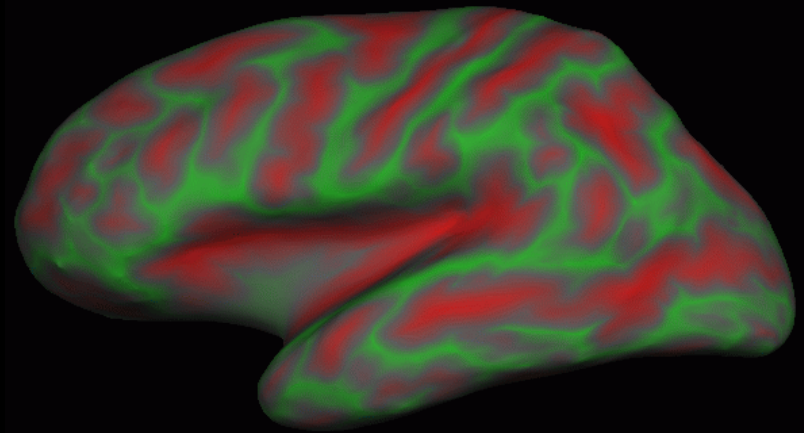
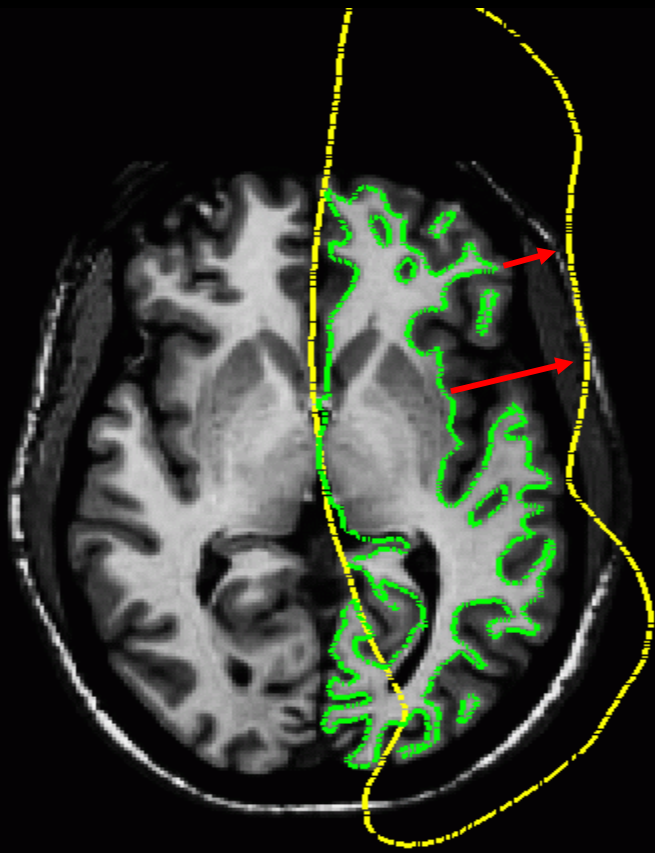


- Circle tangent to surface at each vertex
- Curvature measure is $1/\text{radius of circle}$
- One value per vertex
- Signed (sulcus/gyrus)
- Actually use gaussian curvature

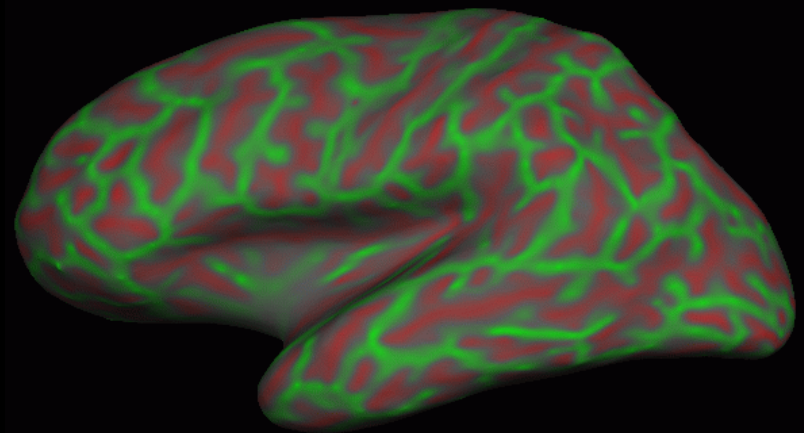


lh.curv, rh.curv

Sulcal Depth

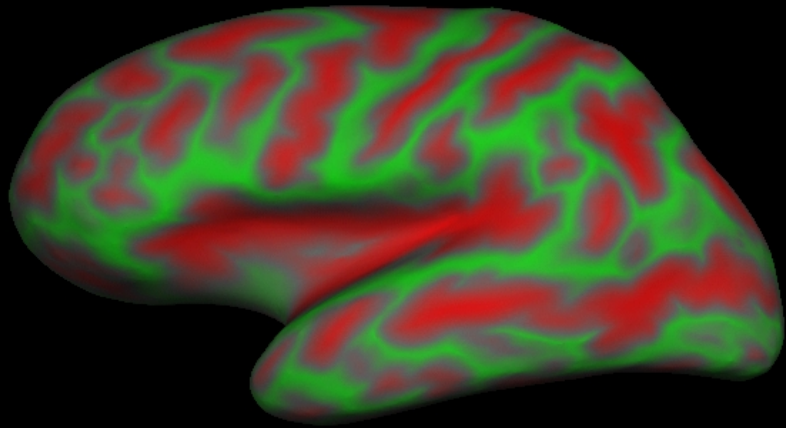


lh.sulc, rh.sulc



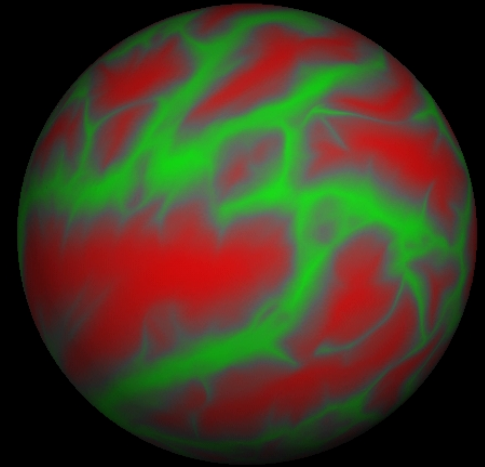
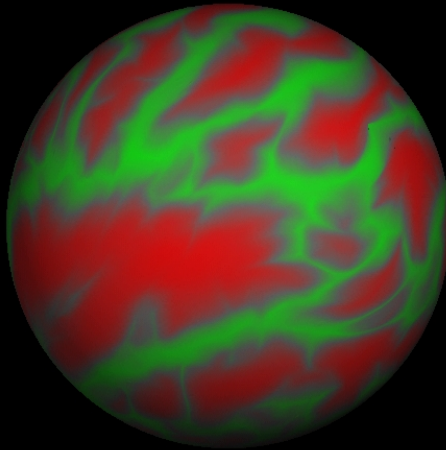
lh.curv, rh.curv

Spherical Registration



Sulcal Map

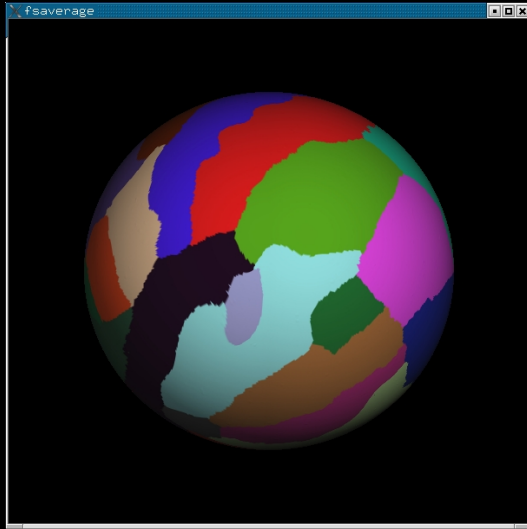
Spherical Inflation



High-Dimensional
Registration to
Spherical Template

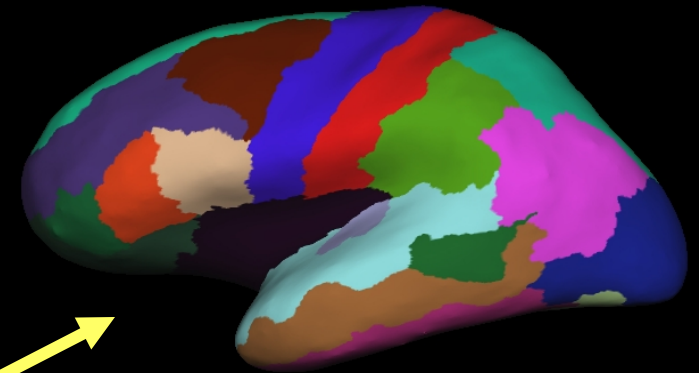
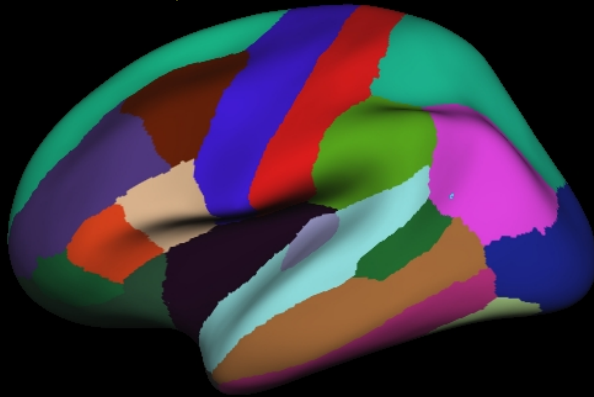
Uses population means *and* variances (more on this in the group analysis talk)

Automatic Cortical Parcellation



Spherical Atlas based on Manual
Parcellations (40 of them)

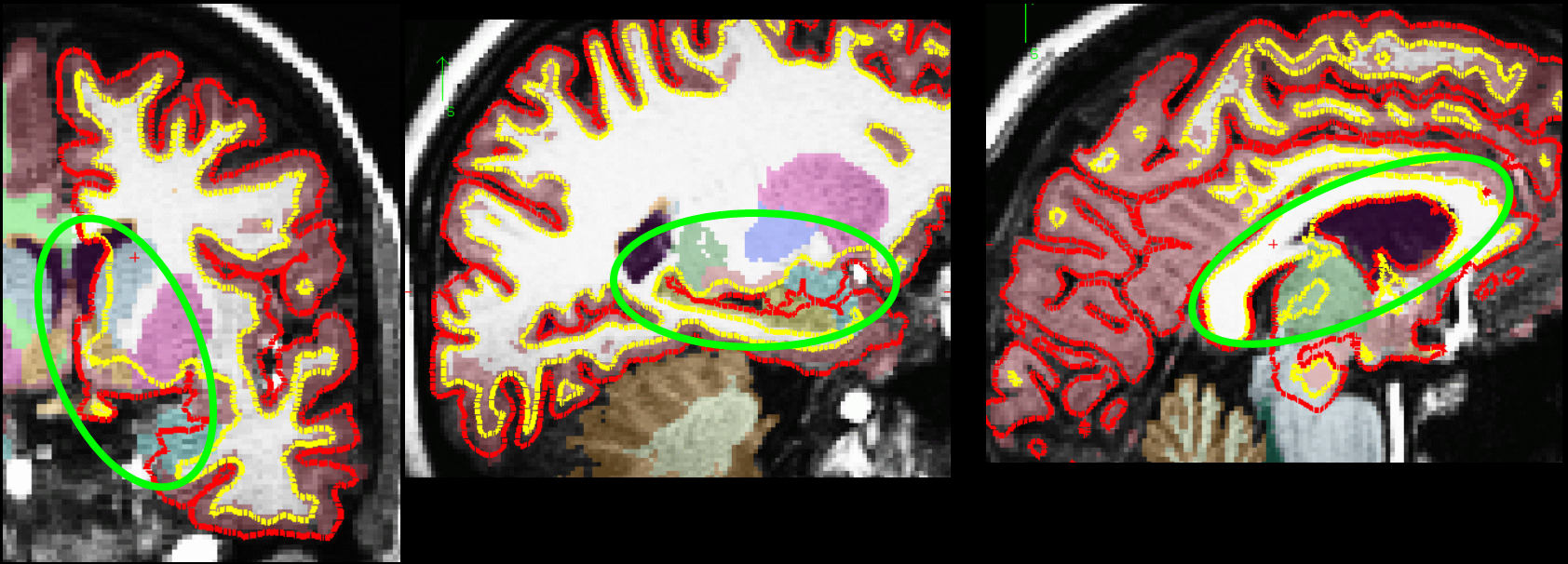
Map to Individual
Thru Spherical Reg



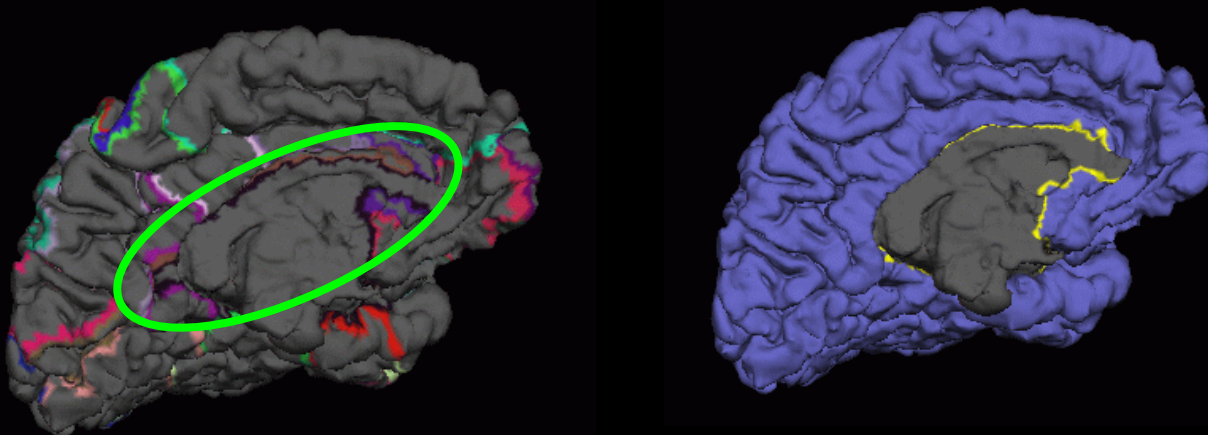
Fine-tune based on
individual anatomy

Note: Similar methodology
to volume labeling

Non-Cortical Areas of Surface



Amygdala, Putamen, Hippocampus, Caudate, Ventricles, CC



?h.cortex.label

Workflow in Stages

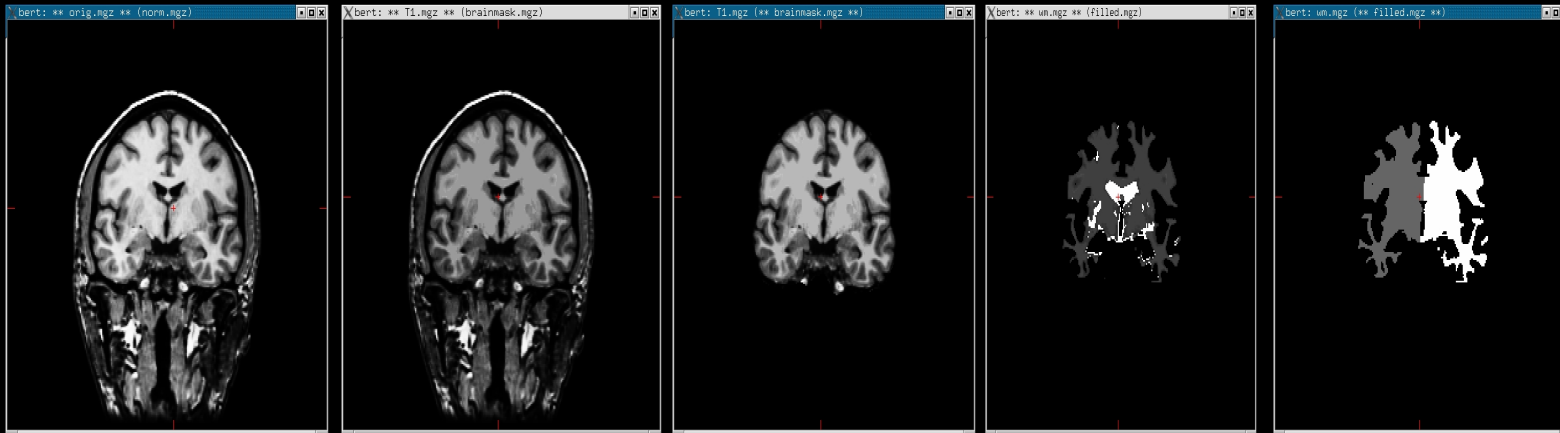
1. `recon-all --autorecon1` (Stages 1-5)
2. Check talairach transform, skull strip, normalization (?)
3. `recon-all --autorecon2` (Stages 6-23)
 1. Add control points: `recon-all --autorecon2` (Stages 10-23)
 2. Edit wm.mgz: `recon-all --autorecon2-wm` (Stages 13-23)
 3. Edit brainmask.mgz: `recon-all --autorecon-pial` (Stage 23)
5. `recon-all --autorecon3` (Stages 24-30)

Note: all stages can be run individually

Results

- Volumes
- Surfaces
- Surface Overlays
- ROI Summaries

Volumes



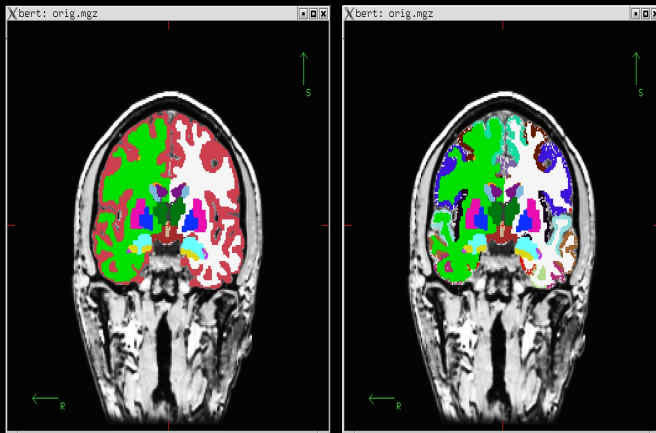
orig.mgz

T1.mgz brainmask.mgz

wm.mgz

filled.mgz

Subcortical Mass



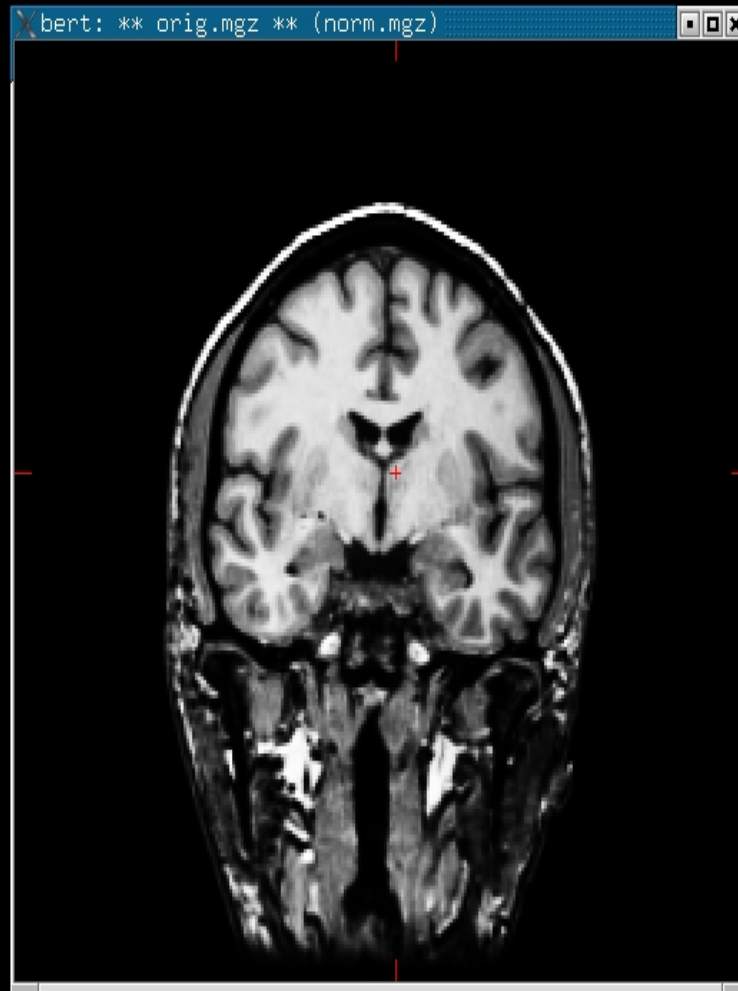
aseg.mgz

- `$$SUBJECTS_DIR/bert/mri`
- All “Conformed” 256^3 , 1mm^3
- Many more ...

Volume Viewer:
tkmedit

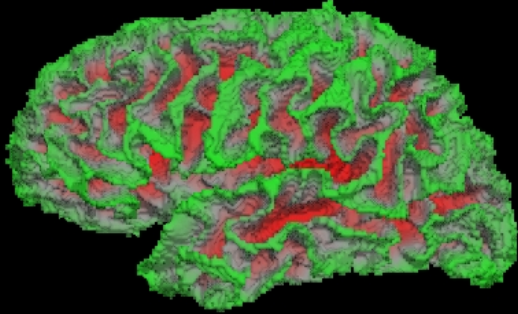
Volume Viewer (tkmedit)

Right

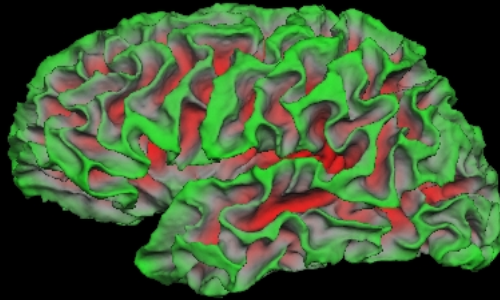


Left

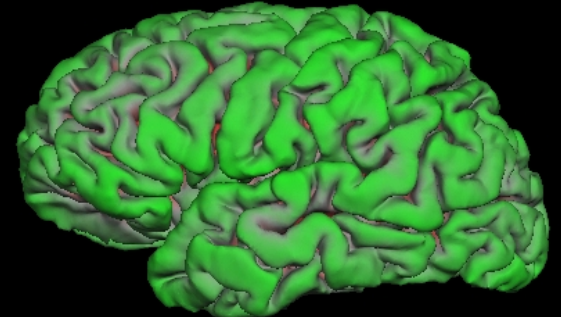
Surfaces



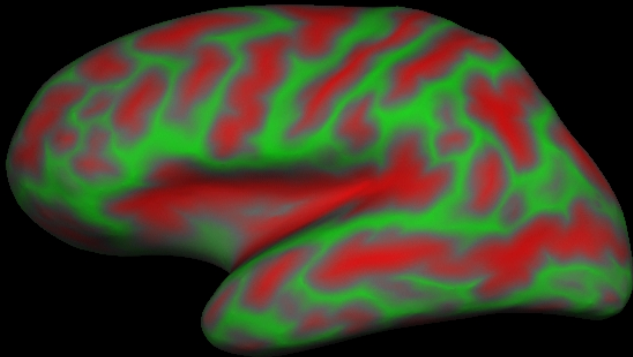
orig



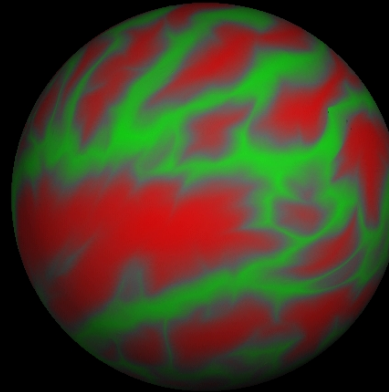
white



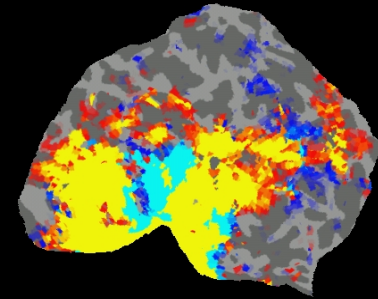
pial



inflated



sphere,sphere.reg



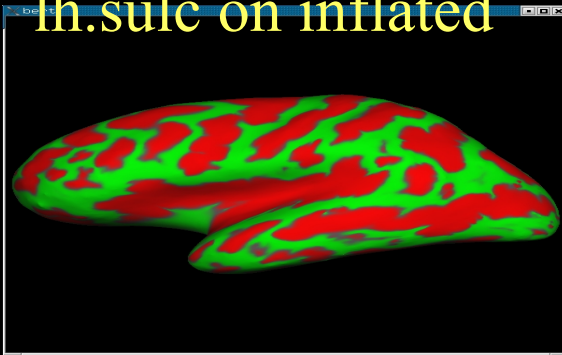
patch (flattened)

- `$SUBJECTS_DIR/bert/surf`
- Number/Identity of vertices stays the same (except patches)
- XYZ Location Changes
- Flattening not done as part of standard reconstruction

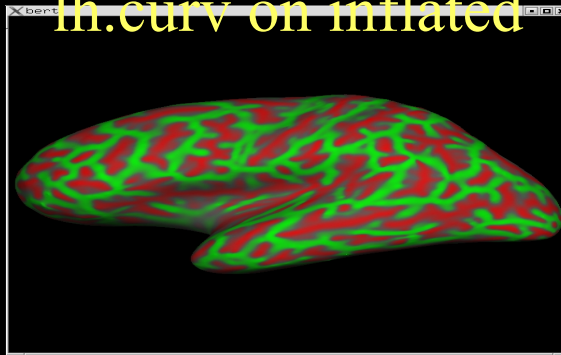
Surface Viewer:
tksurfer

Surface Overlays

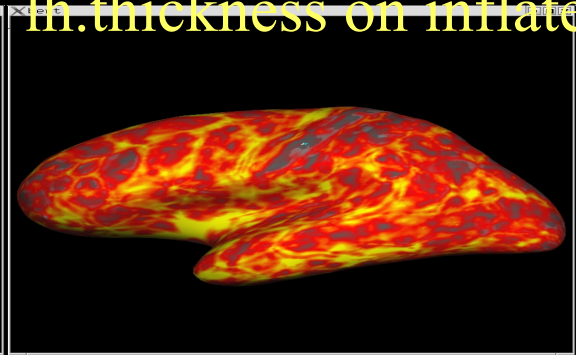
lh.sulc on inflated



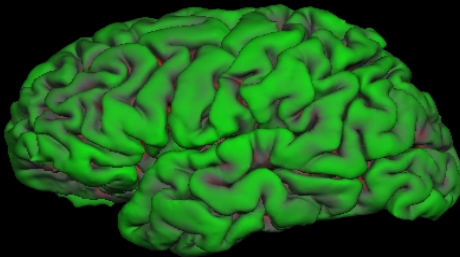
lh.curv on inflated



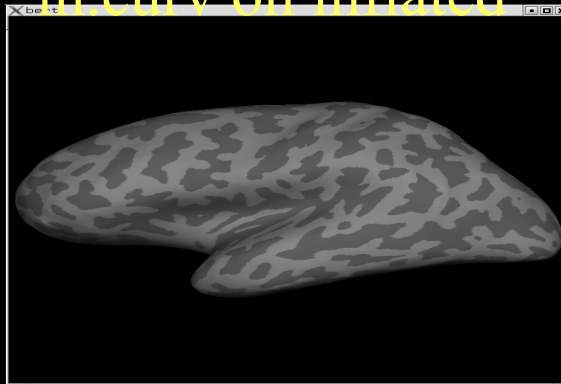
lh.thickness on inflated



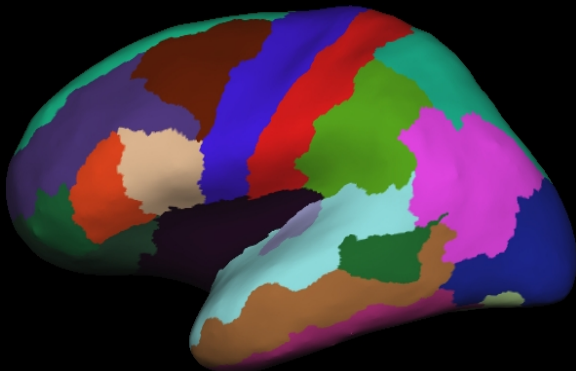
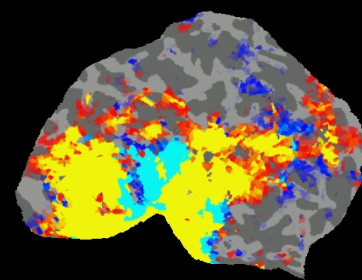
lh.sulc on pial



lh.curv on inflated



fMRI on flat



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.

Overview

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

- Command-line (not GUI)
- \$SUBJECTS_DIR
- Subject Directory Tree
- MGZ File (orig.mgz)
- Subcortical Mass
- Intensity Bias
- Skull Stripping
- Surface Model
- white, pial, and inflated surfaces
- curvature vs. sulcal depth
- Automatic Segmentation

Tutorial Tips

- DO NOT open tkmedit & tksurfer from the same terminal window. (Use two terminal windows)
- You CANNOT type commands in a terminal window if you are running tkmedit or tksurfer from it. (Open a new terminal window to do this.)