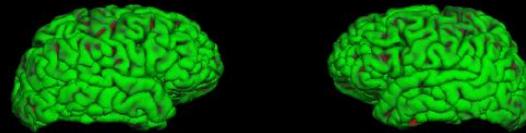
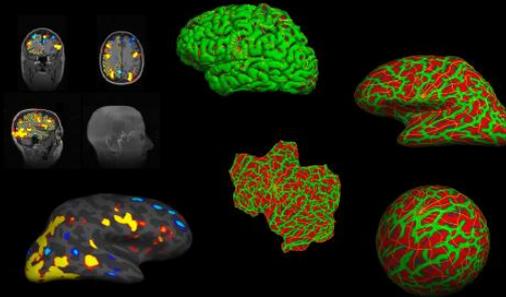


# Anatomical Analysis with FreeSurfer

[surfer.nmr.mgh.harvard.edu](http://surfer.nmr.mgh.harvard.edu)



**FreeSurfer**



# Fully Automated Reconstruction

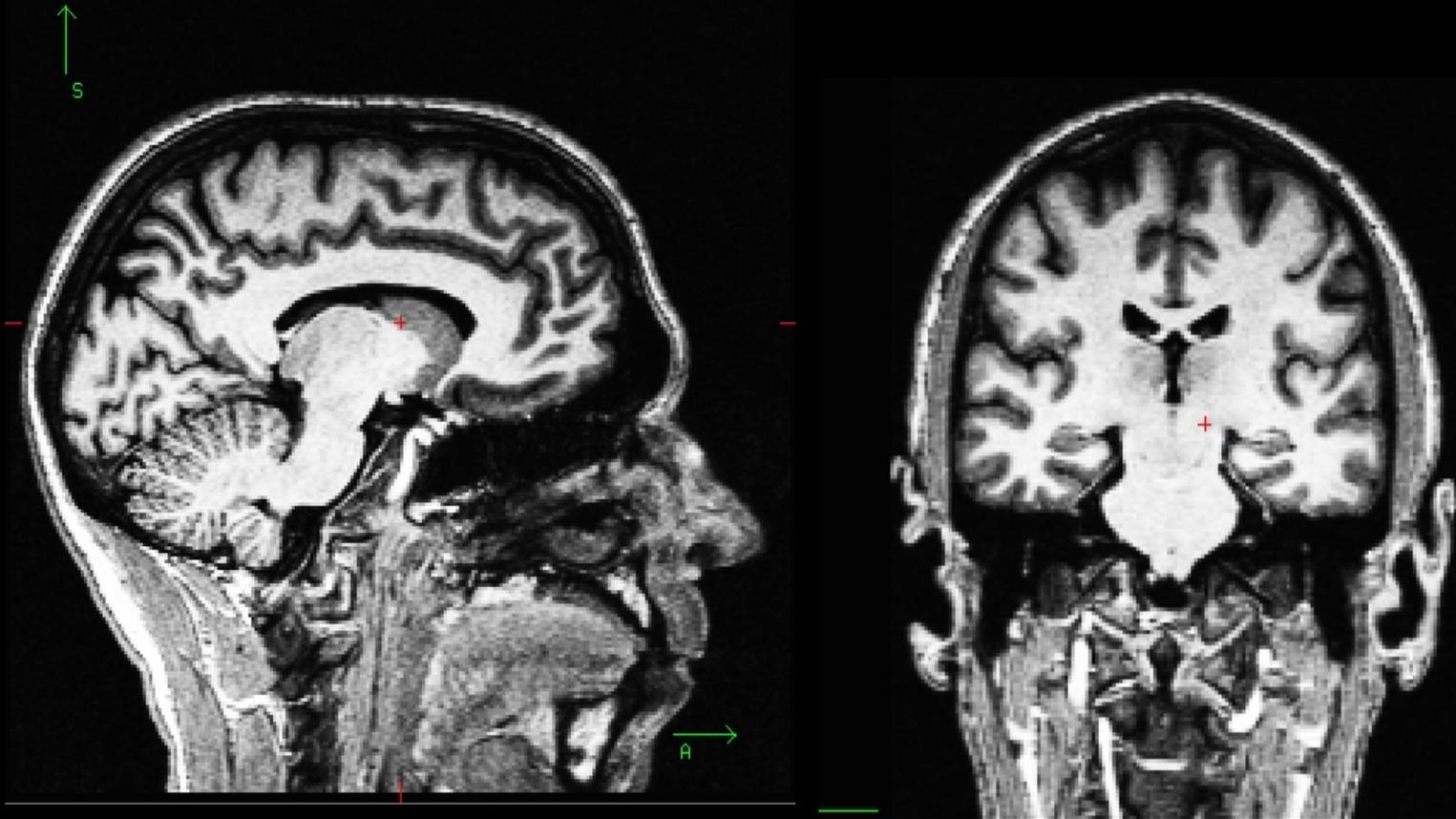
```
recon-all -i file.dcm -subject bert -all
```

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

# Administration

- [surfer.nmr.mgh.harvard.edu](http://surfer.nmr.mgh.harvard.edu)
  - Register
  - Download
  - Mailing List
- Wiki: [surfer.nmr.mgh.harvard.edu/fswiki](http://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](mailto:freesurfer@nmr.mgh.harvard.edu)

# Input: T1 Weighted Image

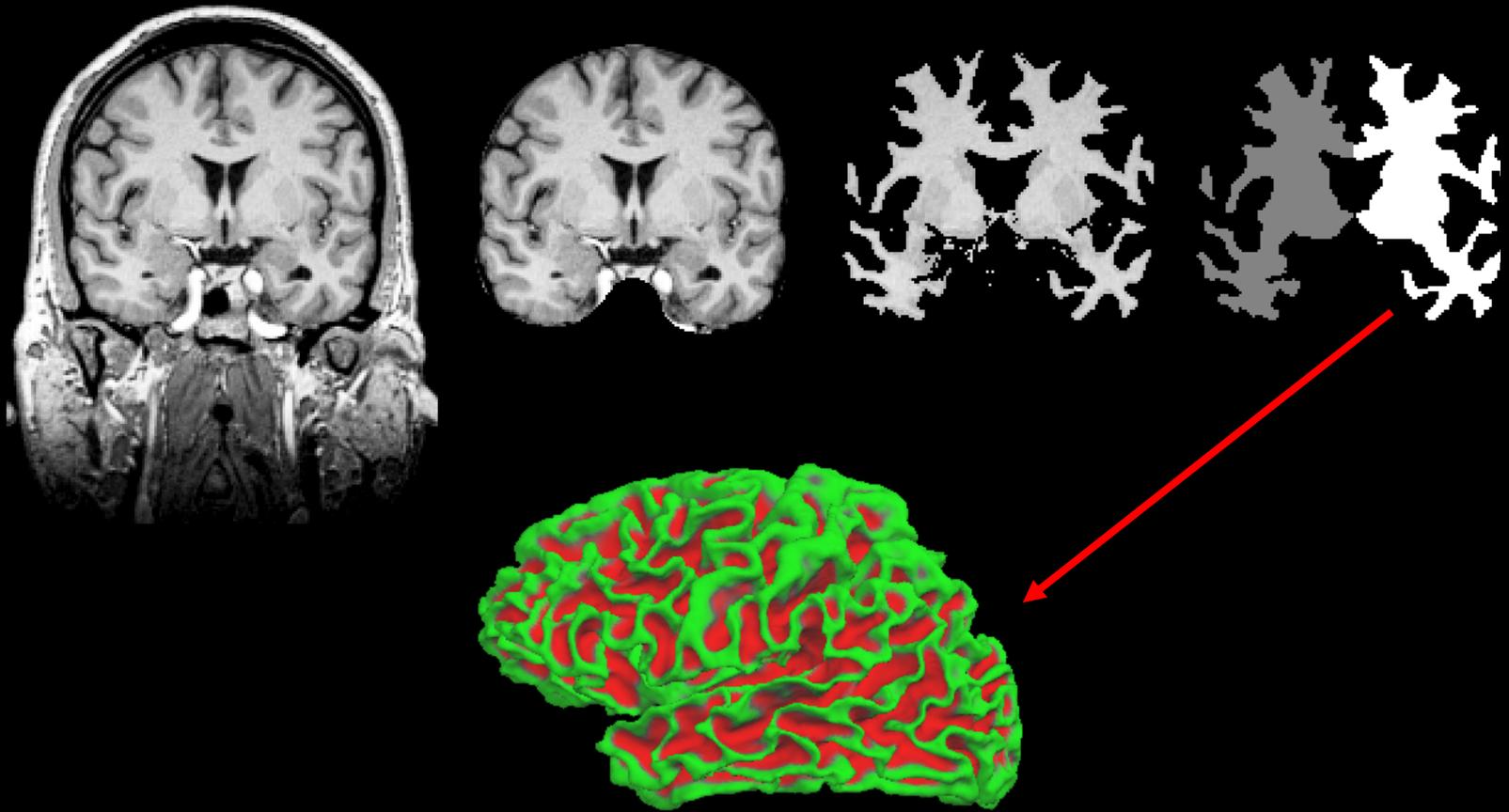


T1 Contrast: White matter brighter than gray matter

# Suggested Morphometry Sequences

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

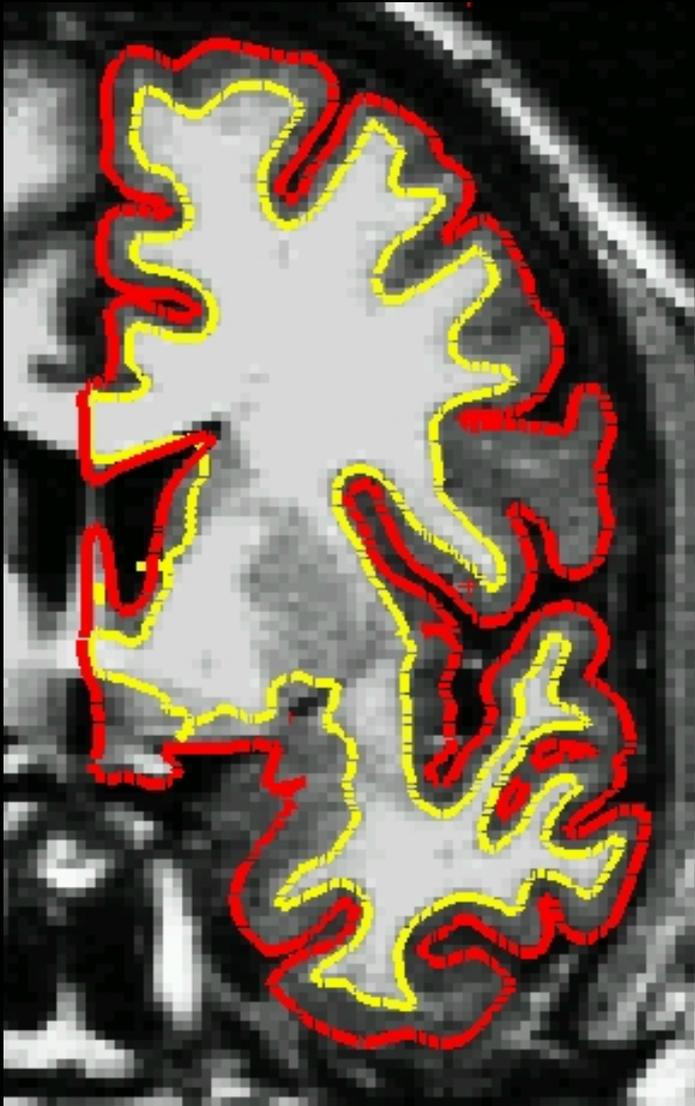
# MRI Segmentation and Surface Reconstruction



# 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”

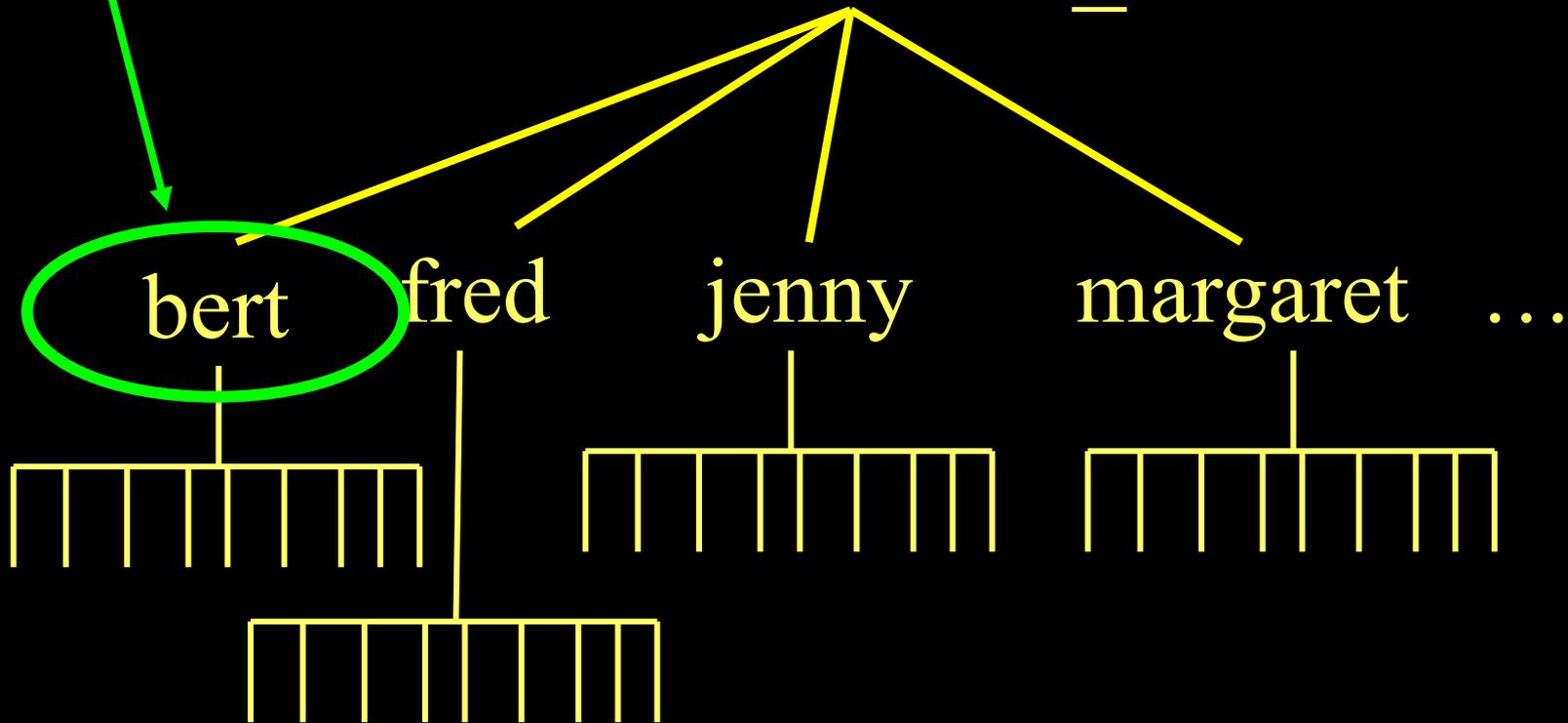


- All White Matter
- All Subcortical Structures
- Ventricles
- Excludes brain stem and cerebellum
- Hemispheres separated
- Connected (no islands)
- Many Stages ... More Later ...

# SUBJECTS\_DIR Environment Variable

Subject

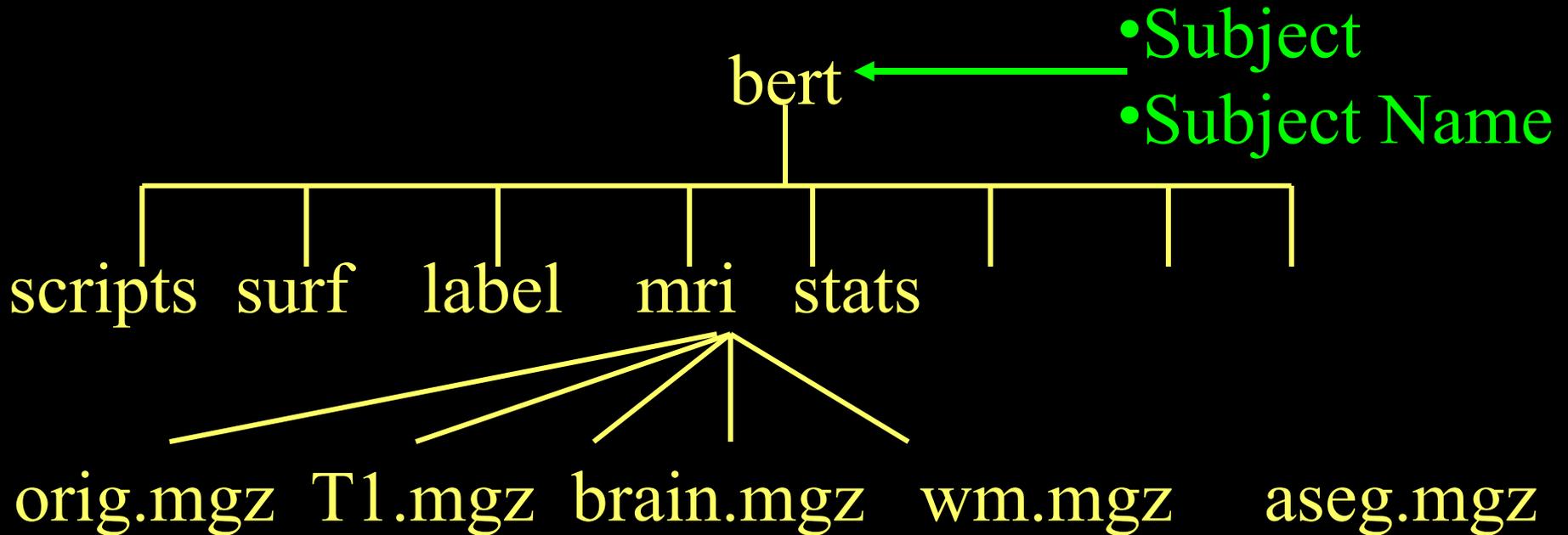
`$$SUBJECTS_DIR`



`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



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
```

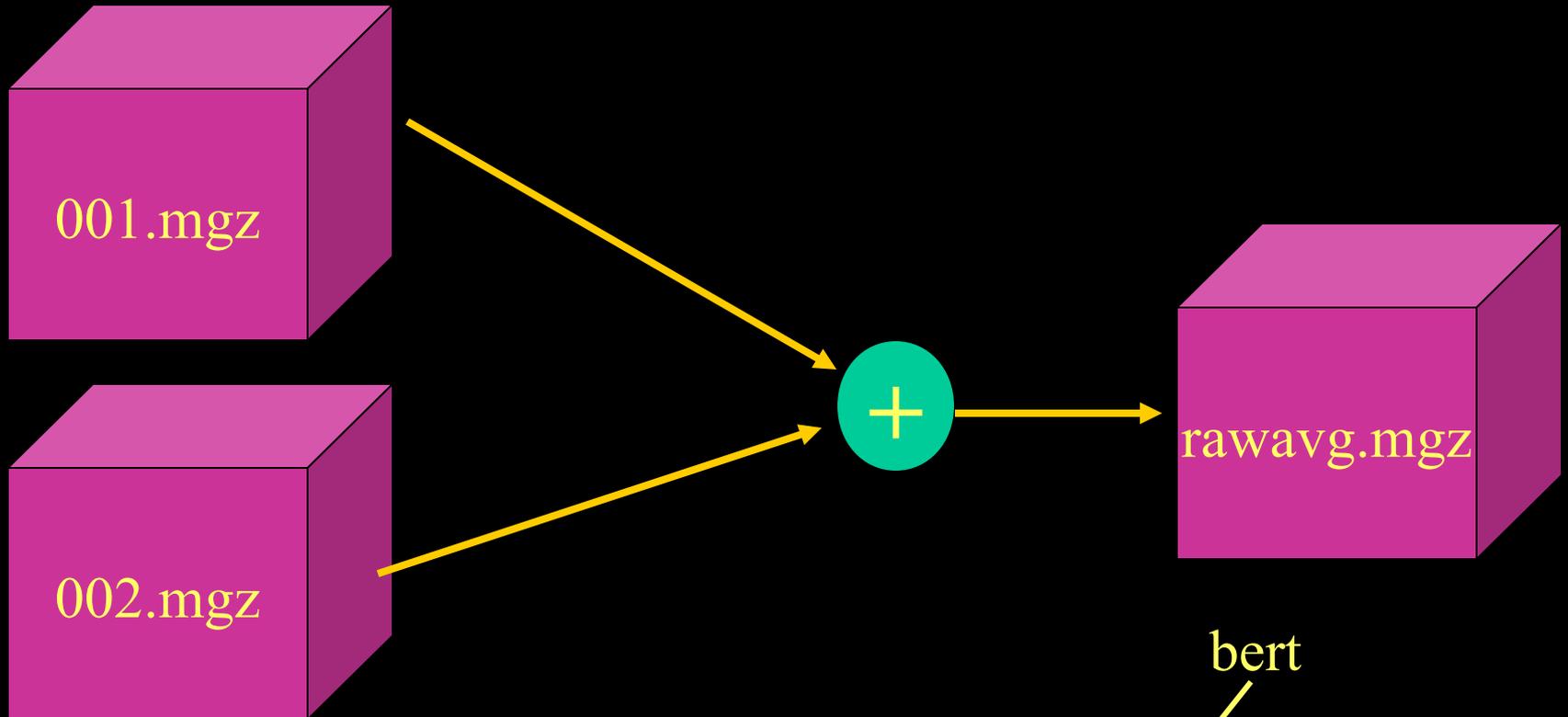
Where file.dcm is one file from the correct (T1-weighted) MR series.

Come back in 20 hours ...

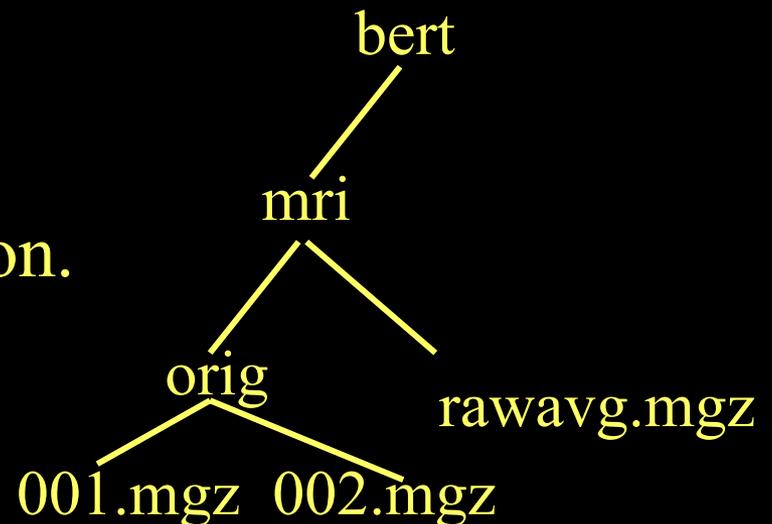
Check your results – do the white and pial surfaces follow the boundaries?

-- Can be broken up

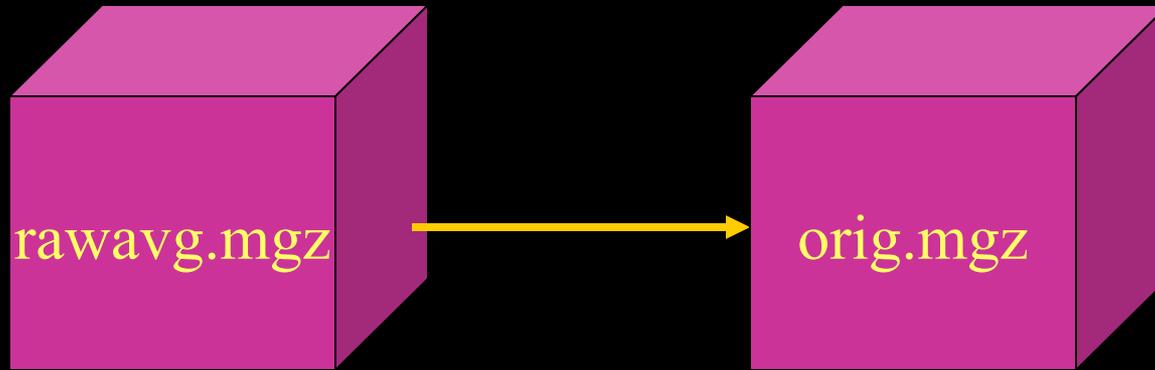
# Motion Correction and Averaging



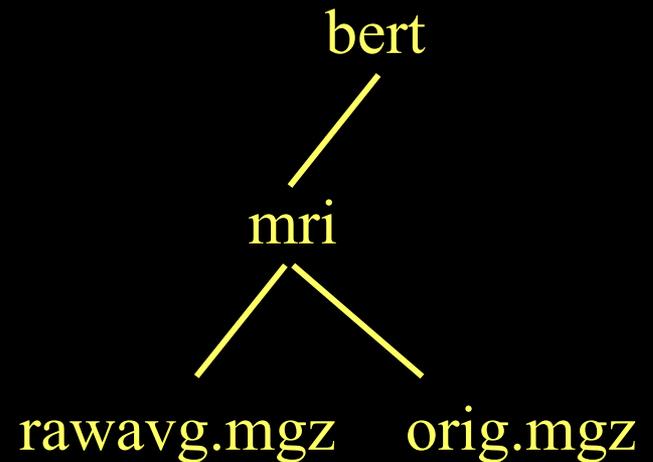
Does not change native resolution.  
Usually only need one.



# Conform

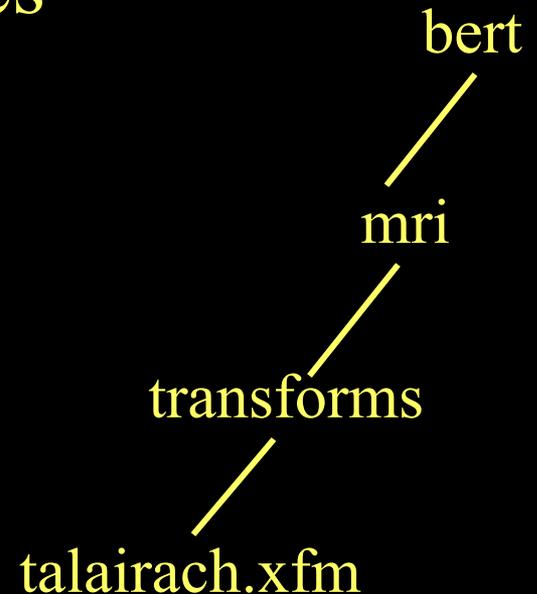


Changes to  $256^3$ ,  $1\text{mm}^3$   
All volumes will be conformed.

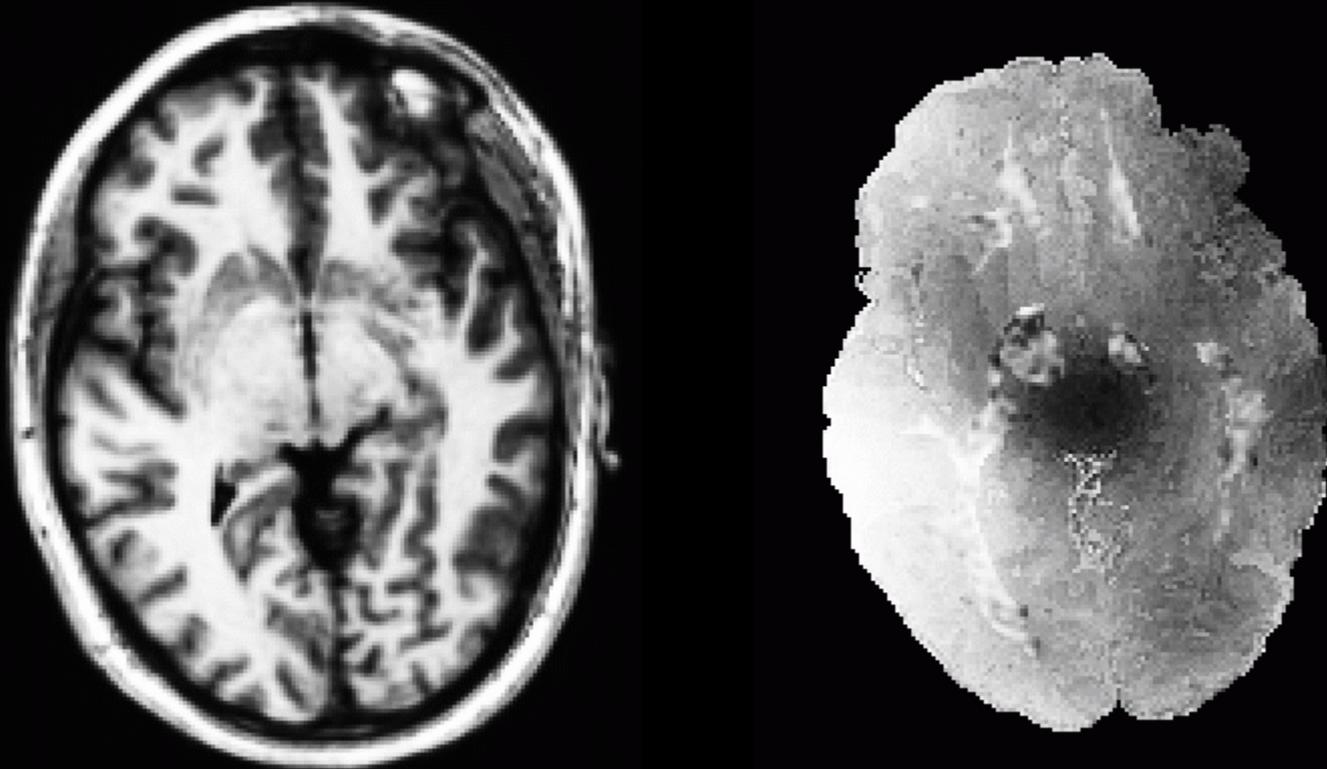


# Talairach Transform

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



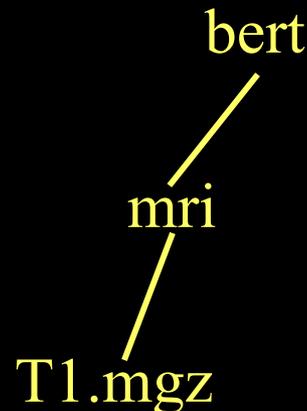
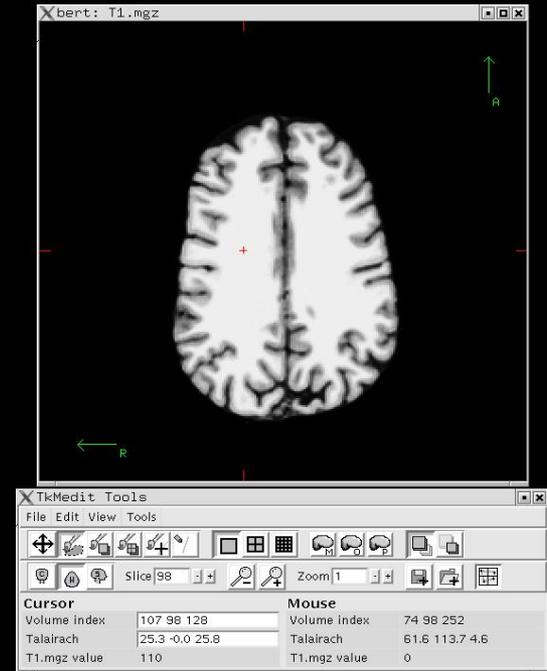
# Intensity Bias



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

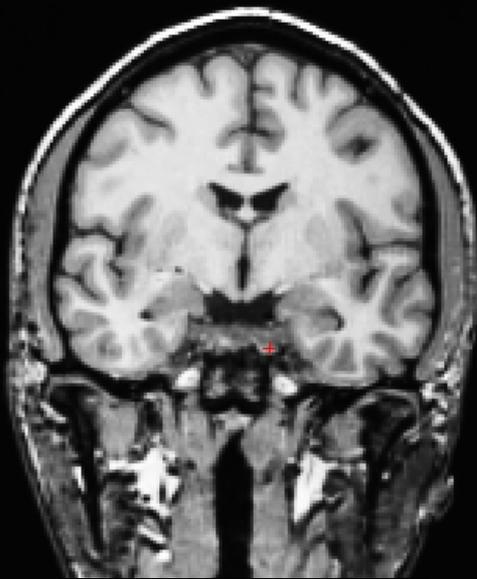
# Intensity Normalization

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



# Skull Strip

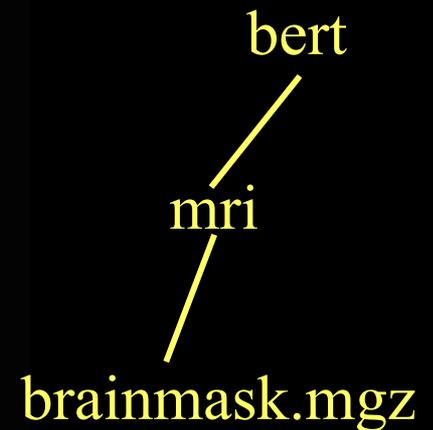
- Removes all non-brain
  - Skull, Eyes, Neck, Dura
- brainmask.mgz (cf, brain.mgz)



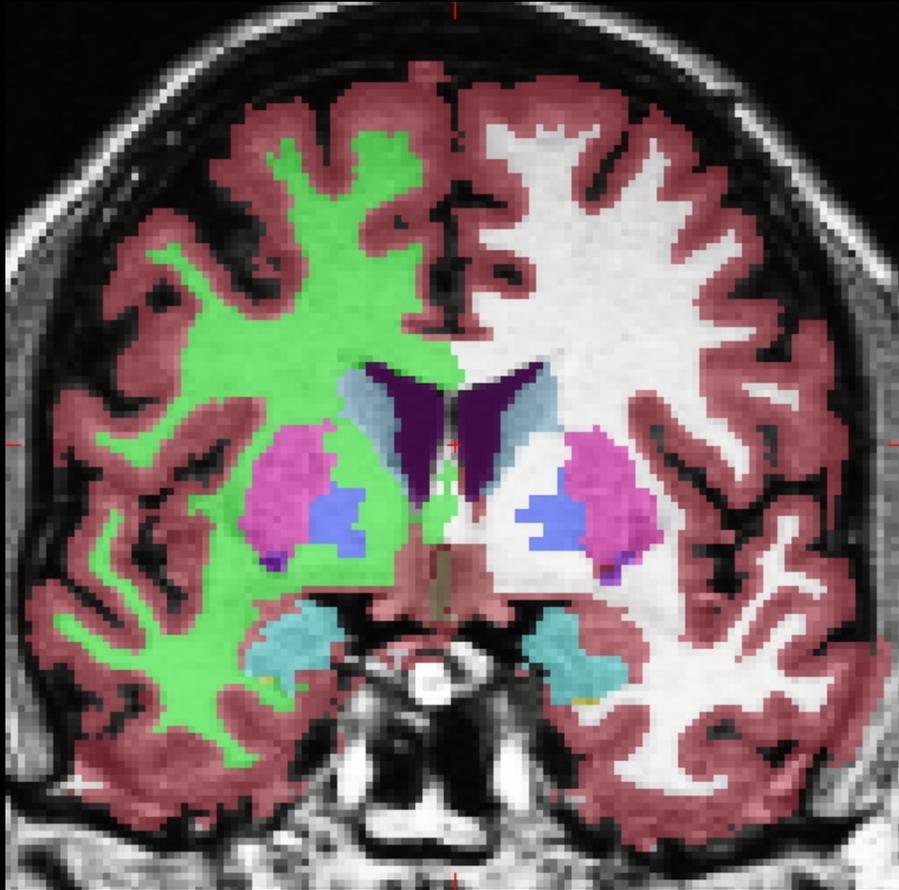
Orig Volume



Brain Volume



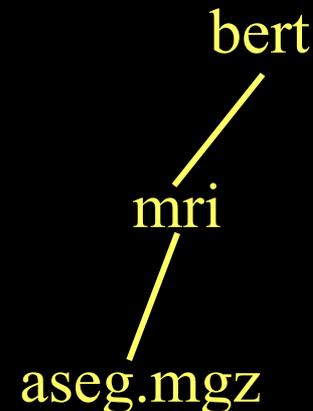
# Automatic Volume Labeling



ASeg Volume

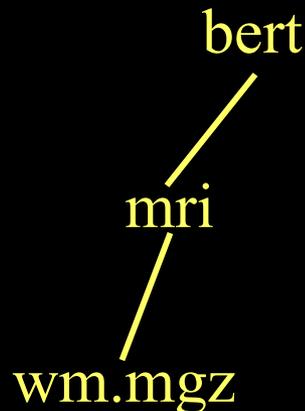
Atlas: RB\_all\_2008-03-26

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



# White Matter Segmentation

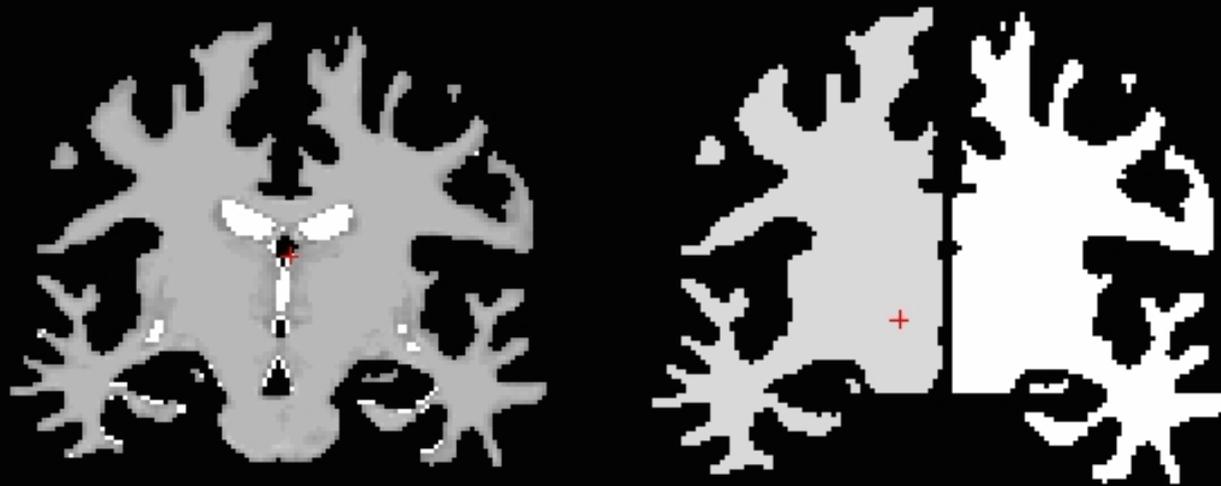
- Separates white matter from everything else
- Uses aseg to “fill in” subcortical structures
- Cerebellum removed, brain stem still there
- Somewhat redundant with aseg
- `wm.mgz`



WM Volume

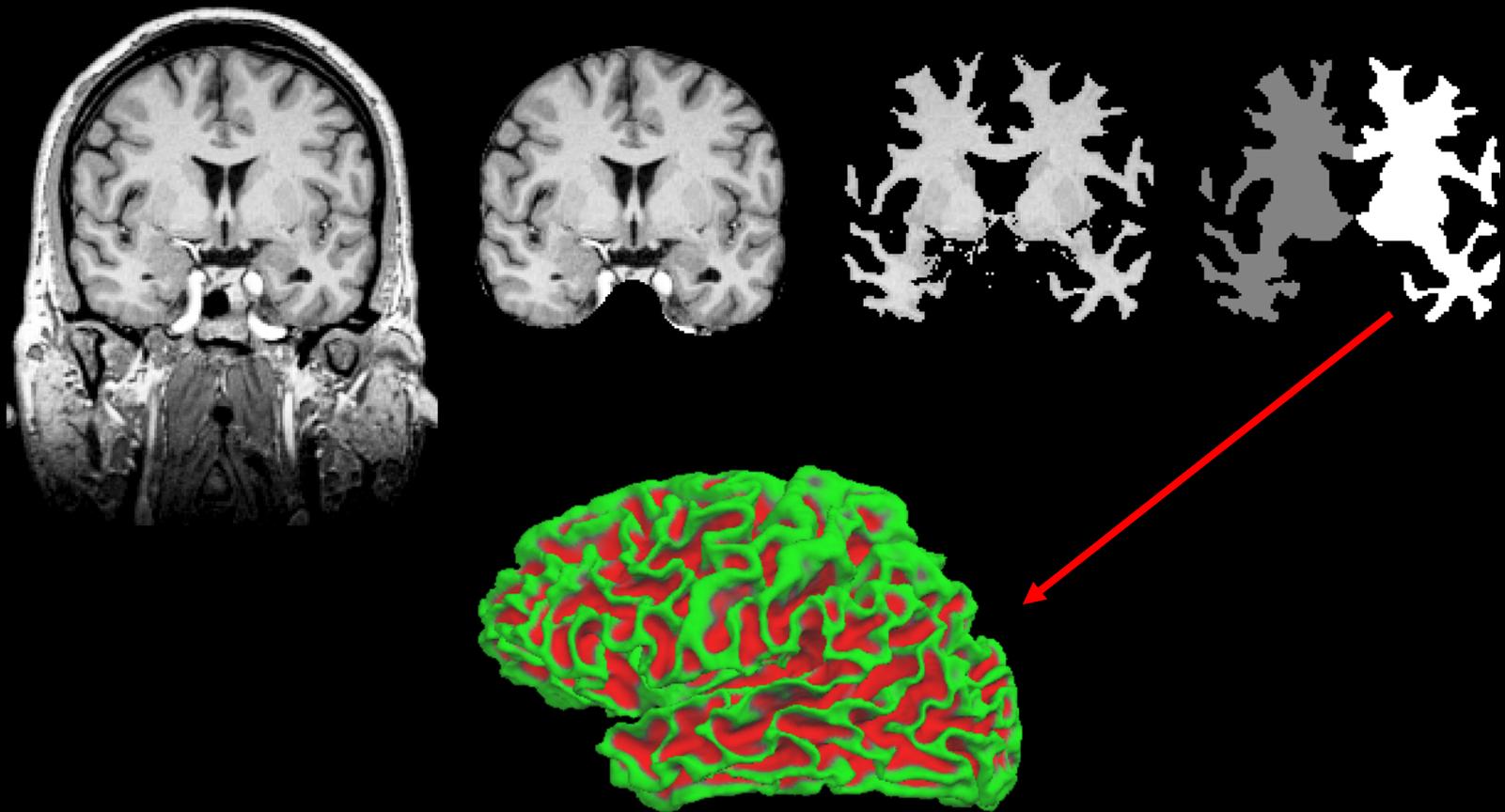
# Fill and Cut (Subcortical Mass)

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

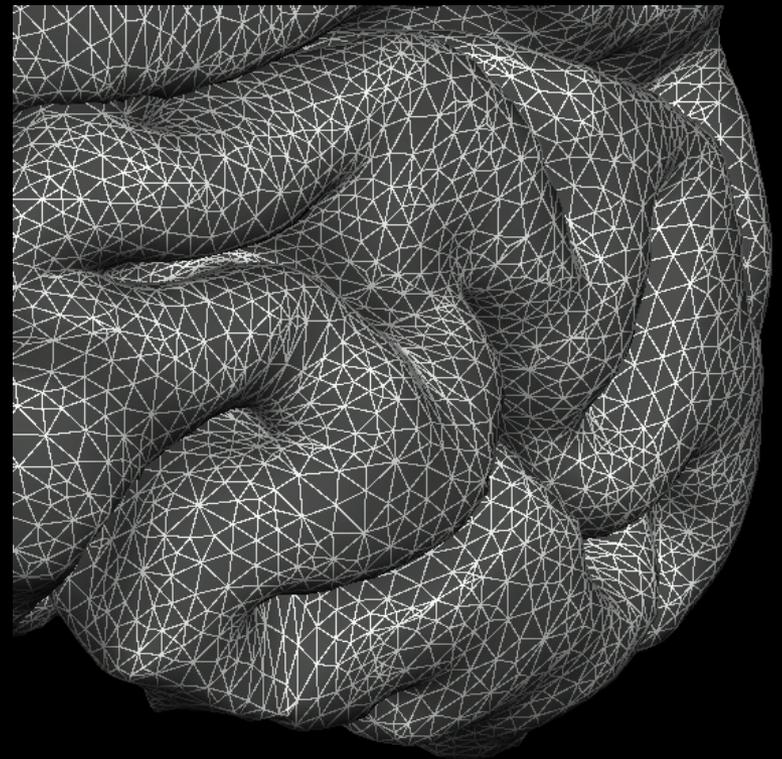
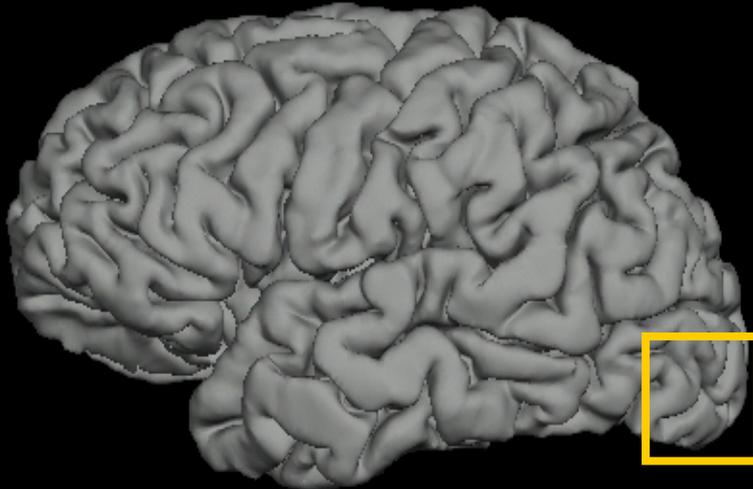


WM Volume (wm.mgz) Filled Volume (filled.mgz)  
(Subcortical Mass)

# MRI Segmentation and Surface Reconstruction

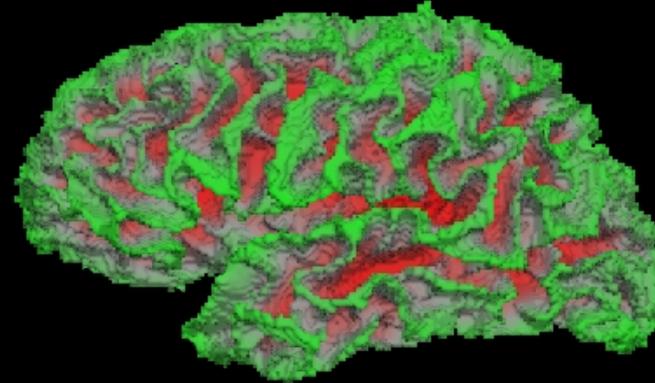
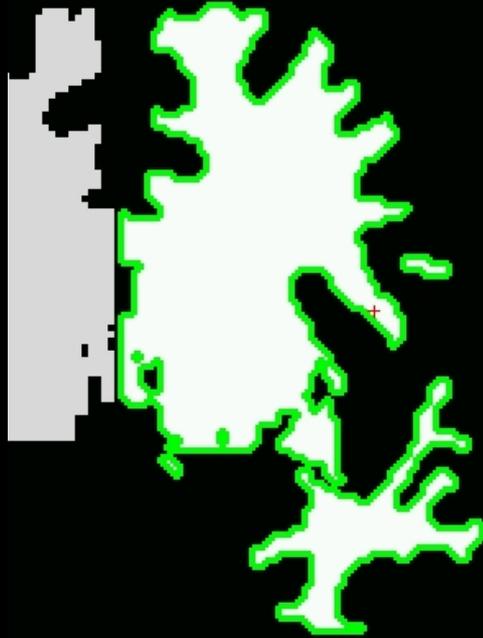


# Surface Model

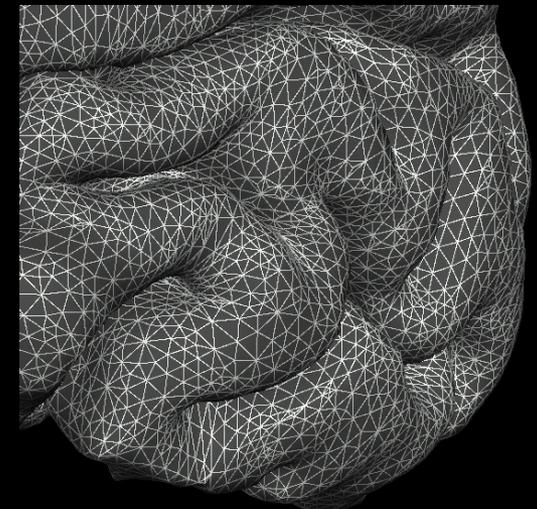


- Mesh (“Finite Element”)
- Vertex = point of triangles
- Neighborhood
- XYZ at each vertex
- Triangles/Faces ~ 300,000
- Area, Distance
- Curvature, Thickness
- Movable

# Tessellation and Topology Fixing

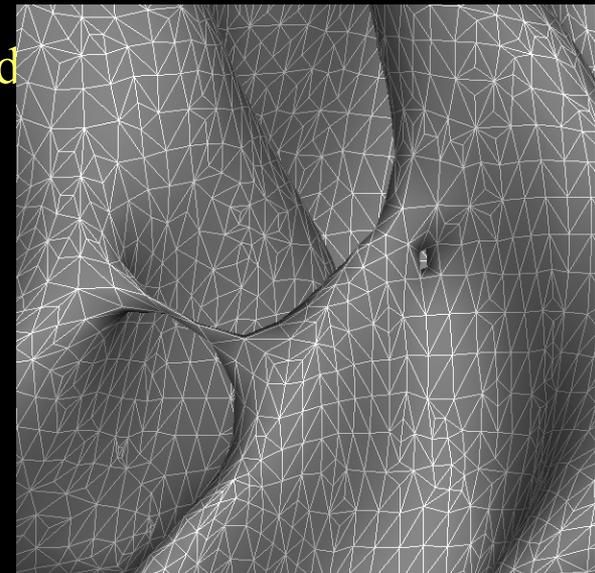
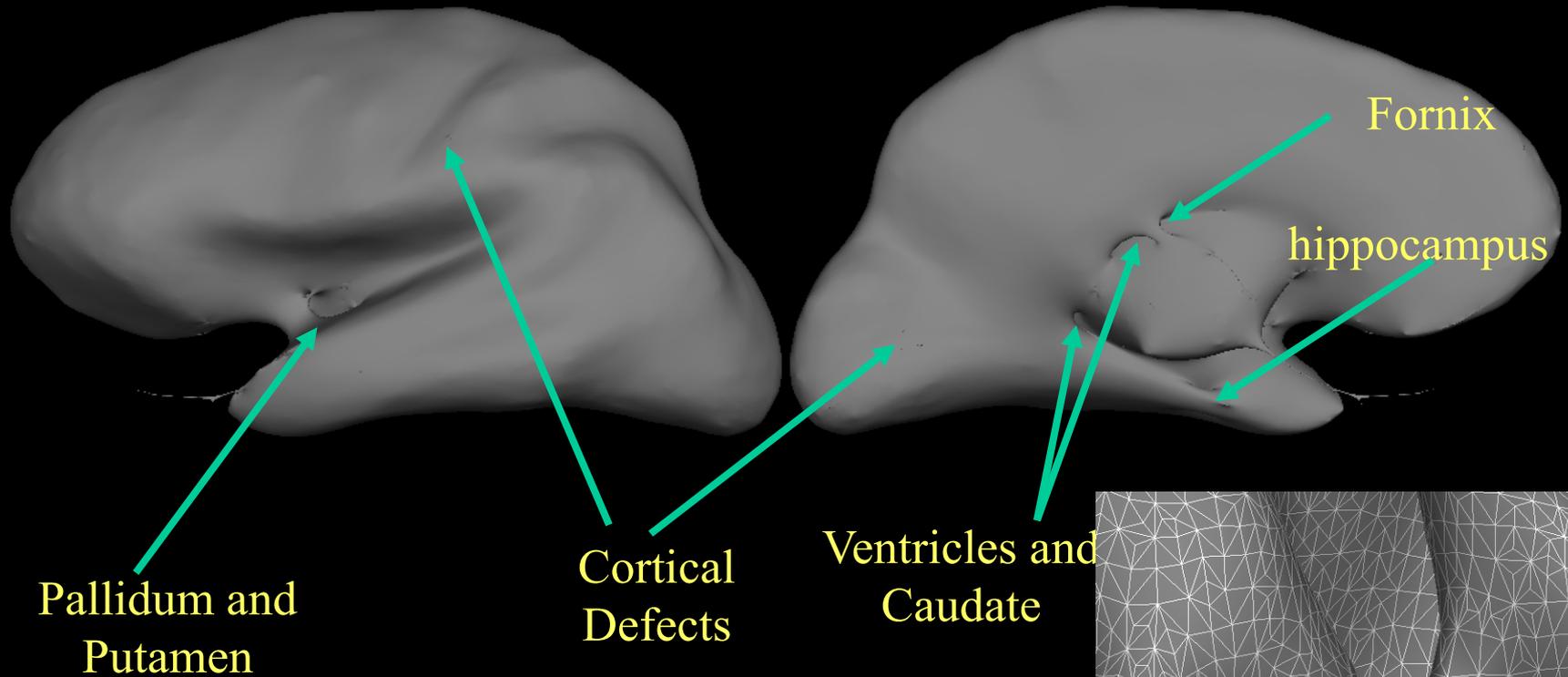


orig surface  
surf/lh.orig  
surf/rh.orig



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

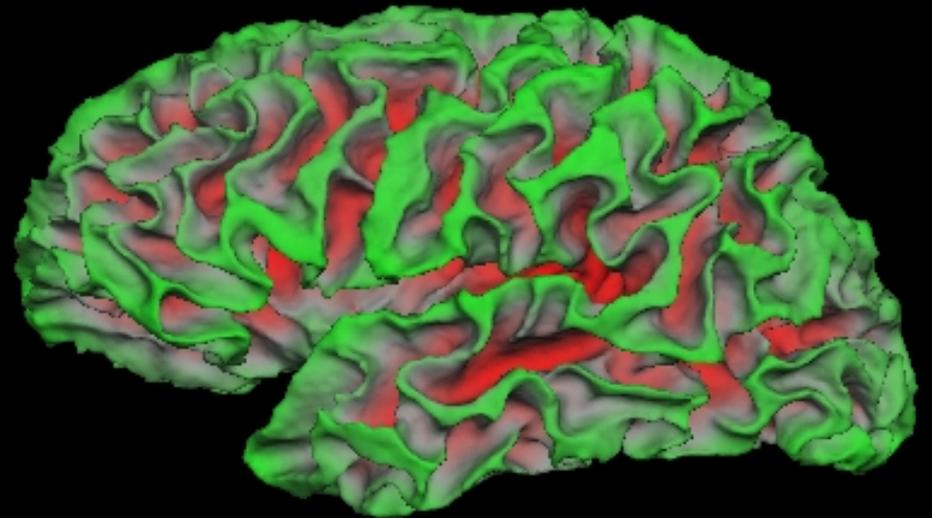
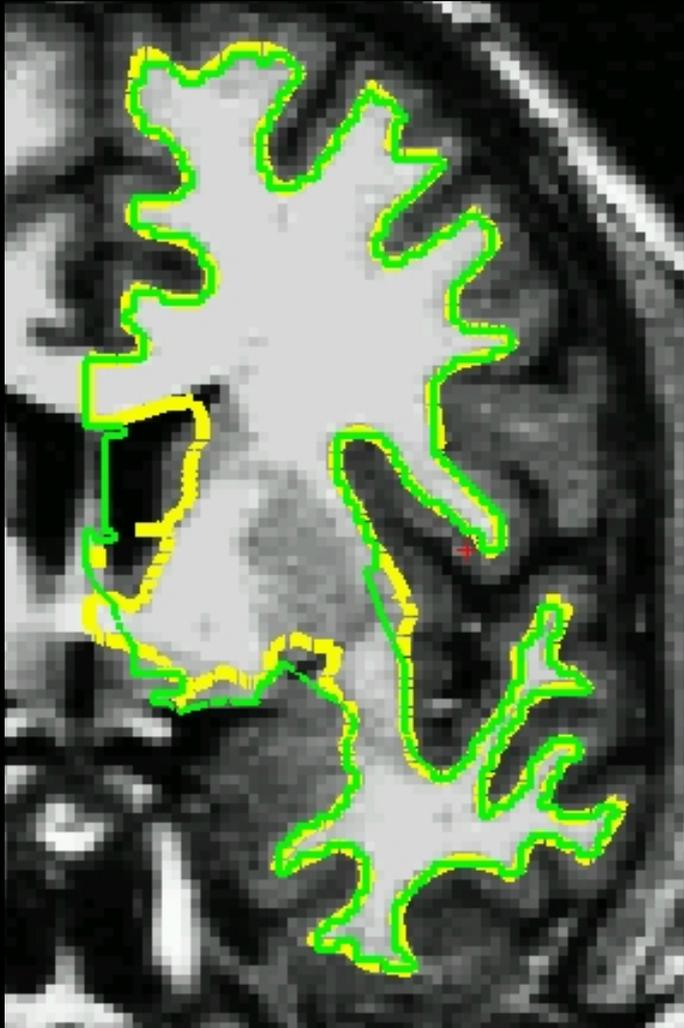
# Topological Defects



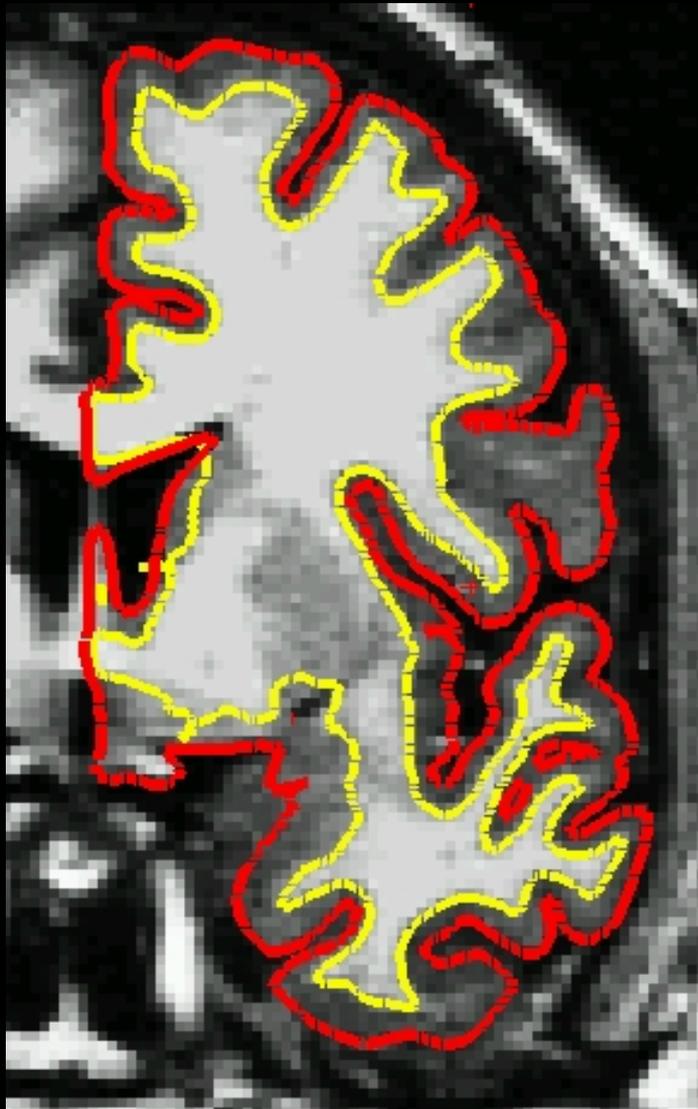
- Holes
- Handles
- Automatically Fixed

# White Matter Surface

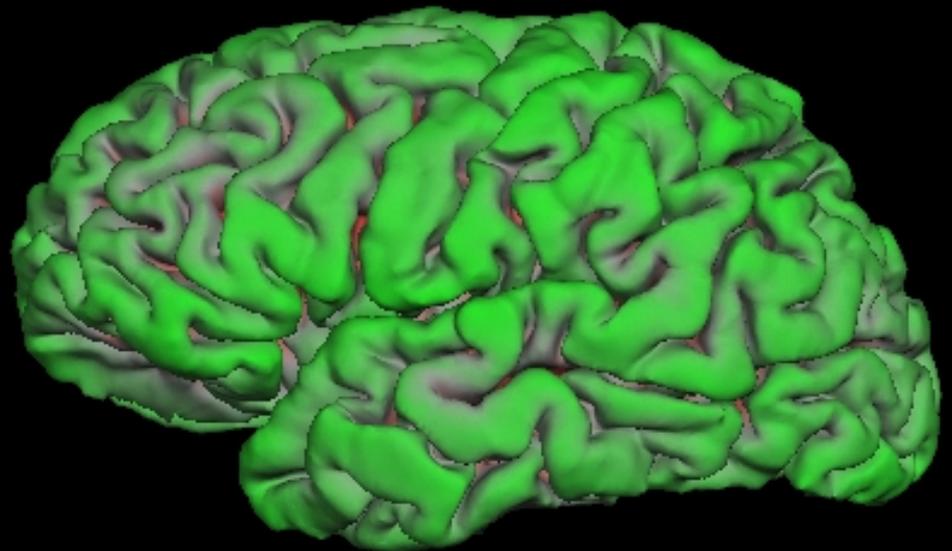
- Nudge orig surface
- Follow T1 intensity gradients
- Smoothness constraint
- Vertex identity preserved



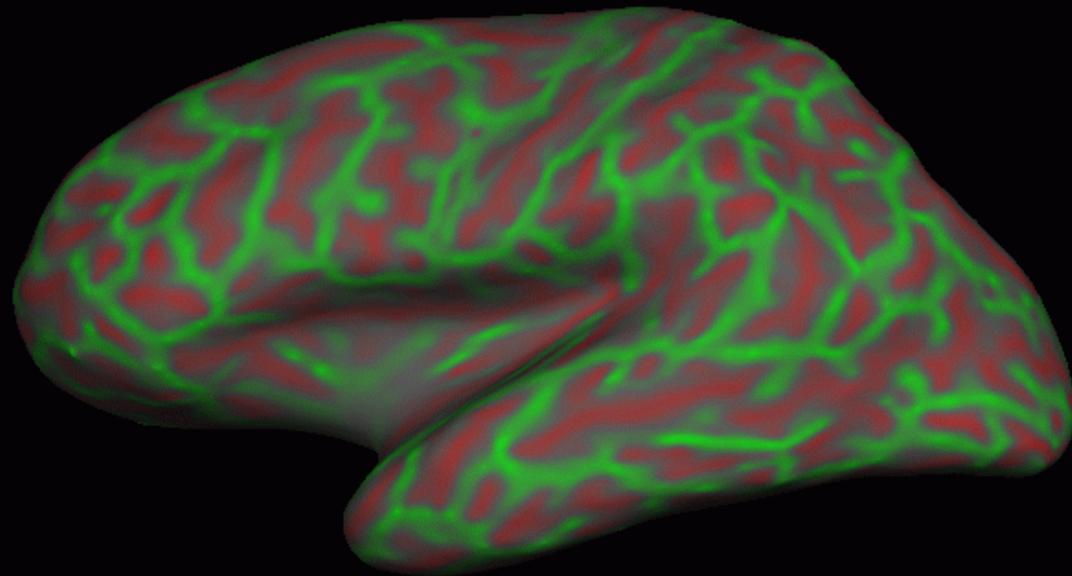
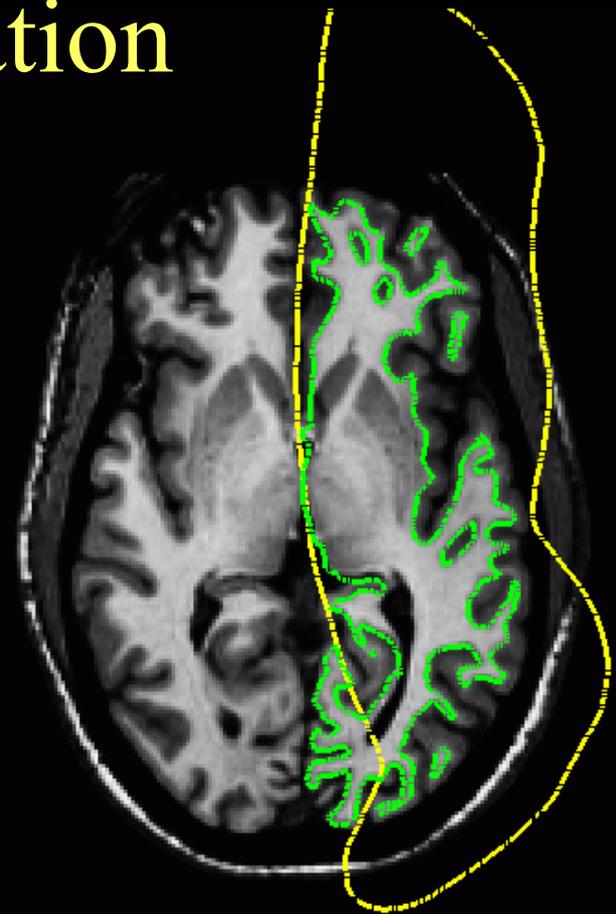
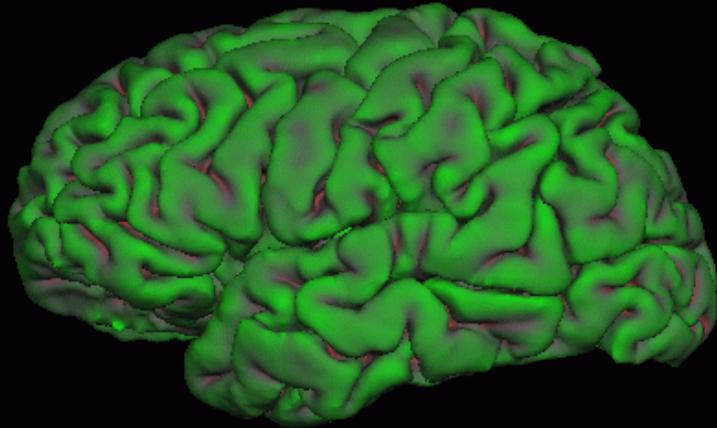
# Pial Surface



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



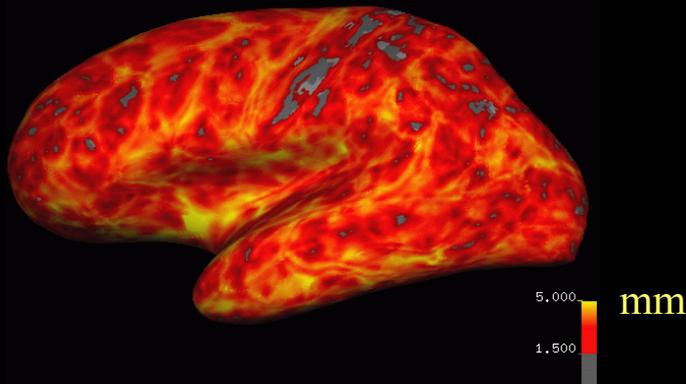
# Surface Inflation



- 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

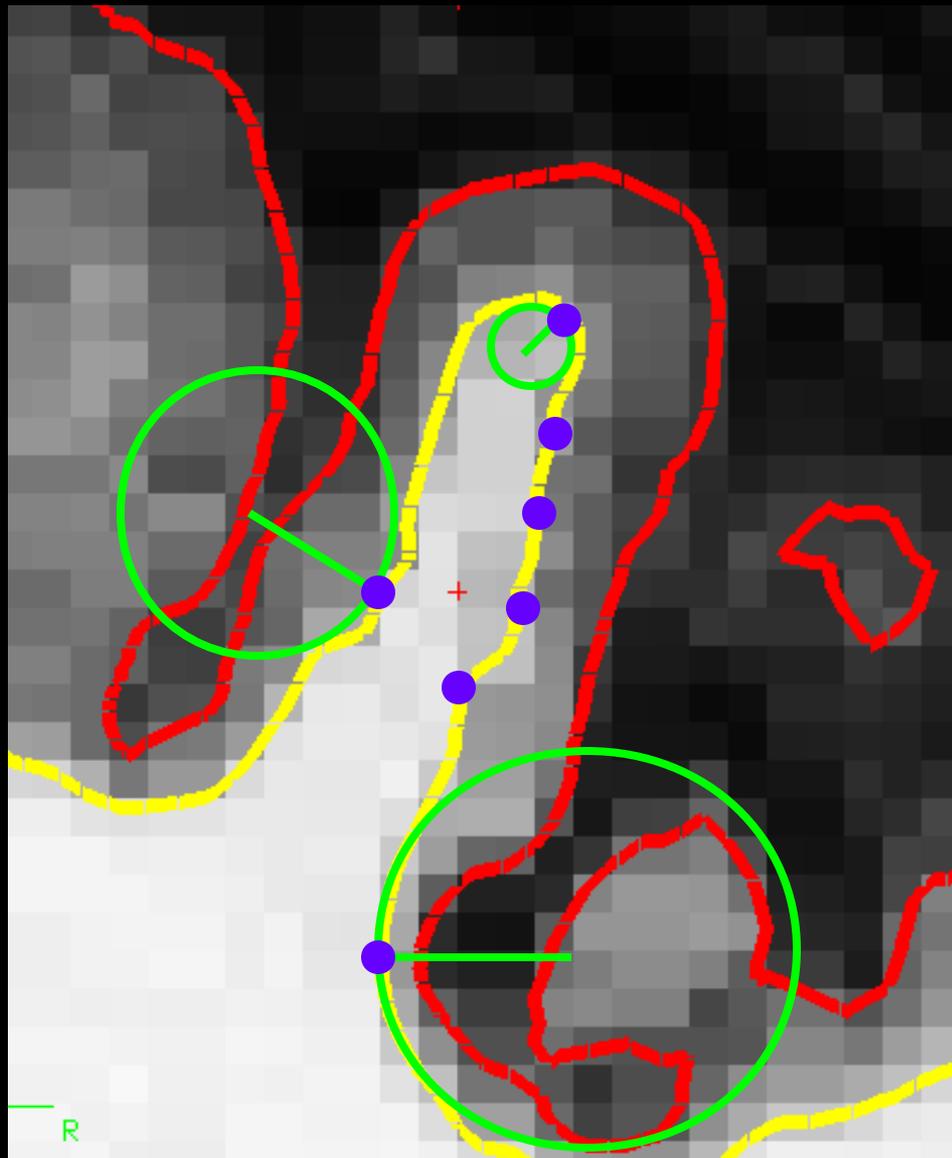


white/gray surface

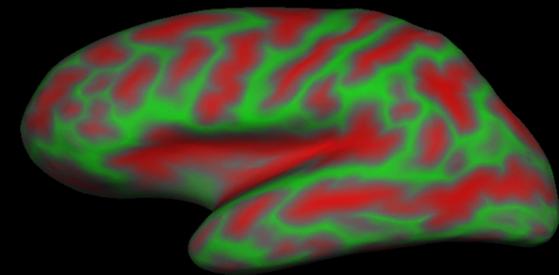
lh.thickness, rh.thickness



# Curvature (Radial)

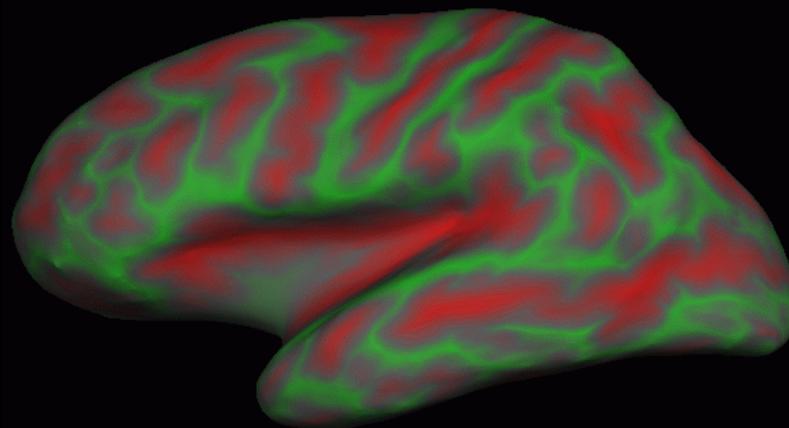
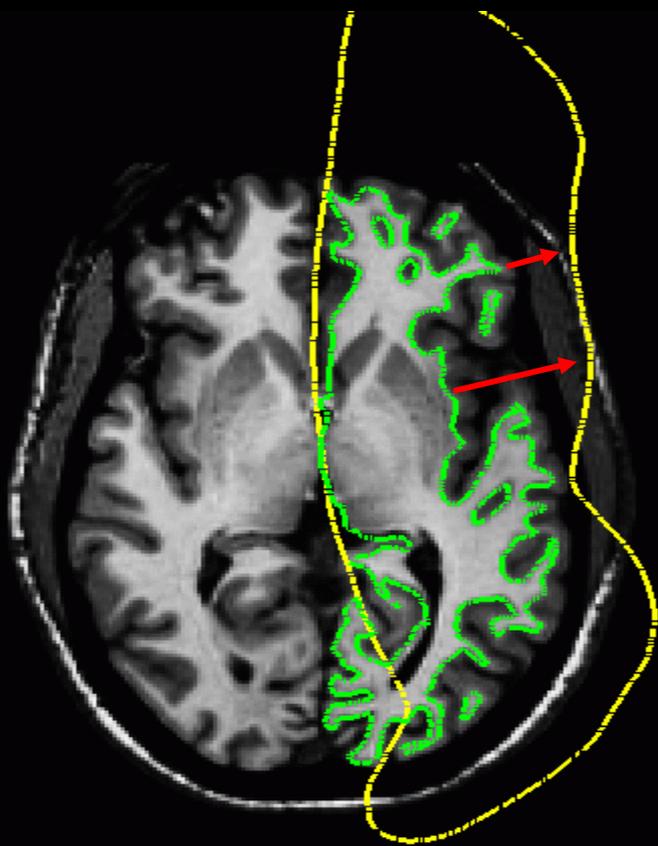


- Circle tangent to surface at each vertex
- Curvature measure is  $1/\text{radius of circle}$
- One value per vertex
- Signed (sulcus/gyrus)
- Actually use gaussian curvature

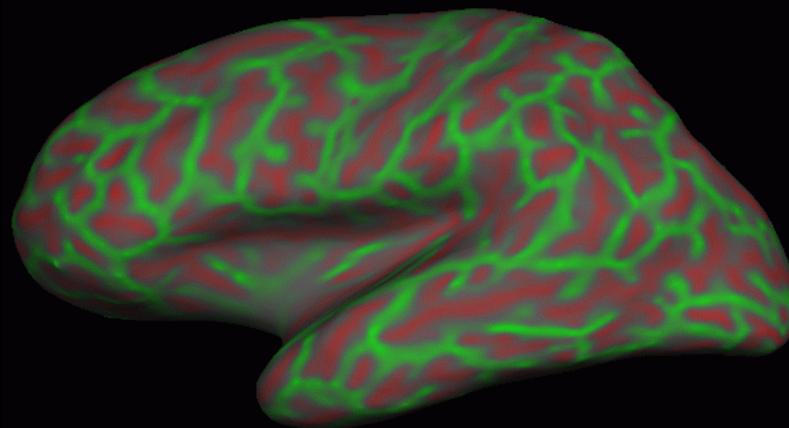


lh.curv, rh.curv

# Sulcal Depth

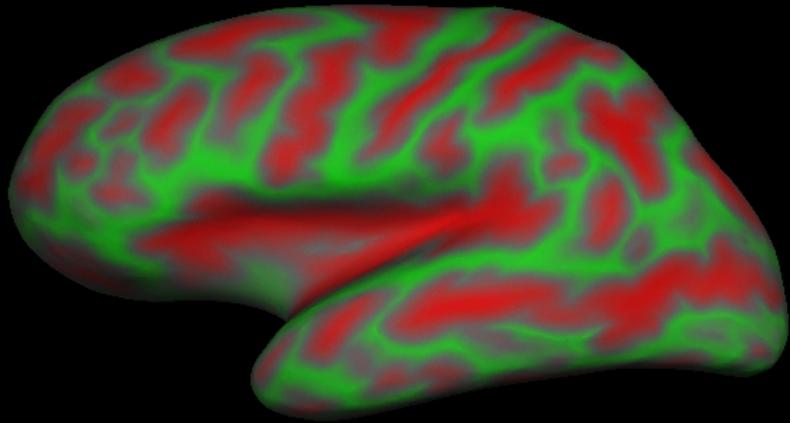


lh.sulc, rh.sulc



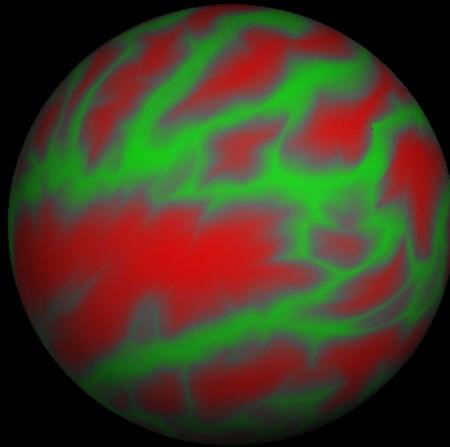
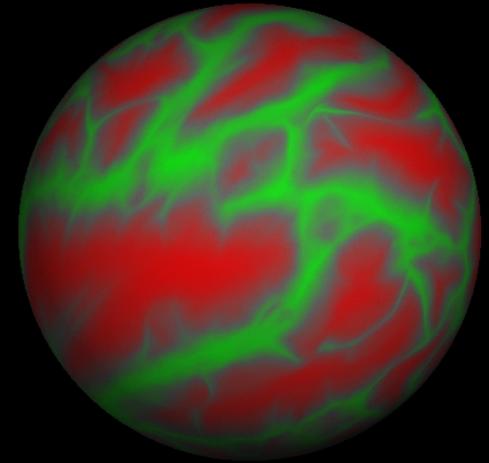
lh.curv, rh.curv

# Spherical Registration



Sulcal Map

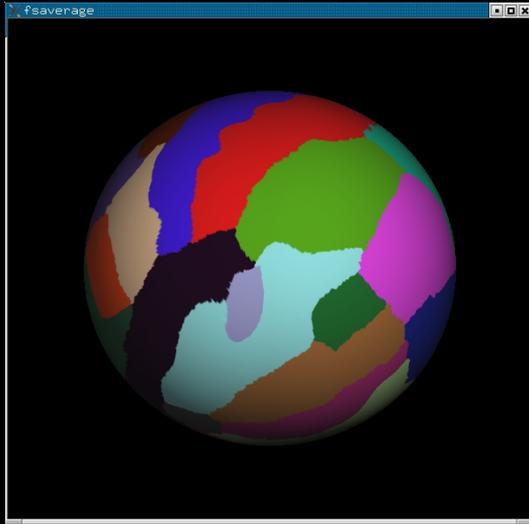
Spherical Inflation



High-Dimensional  
Registration to  
Spherical Template

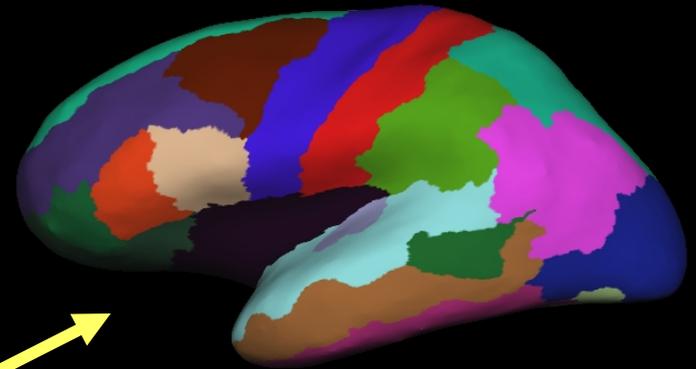
Uses population means *and* variances (more on this in the group analysis talk)

# Automatic Cortical Parcellation



Spherical Atlas based on Manual Parcellations (40 of them)

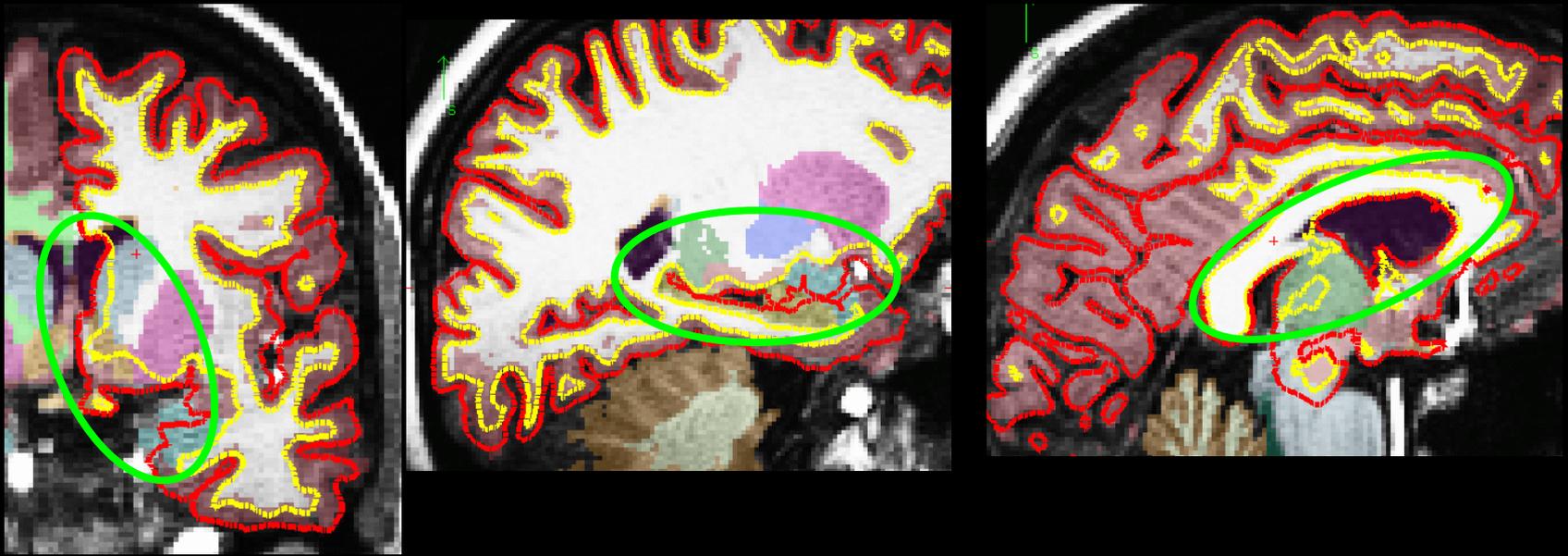
Map to Individual  
Thru Spherical Reg



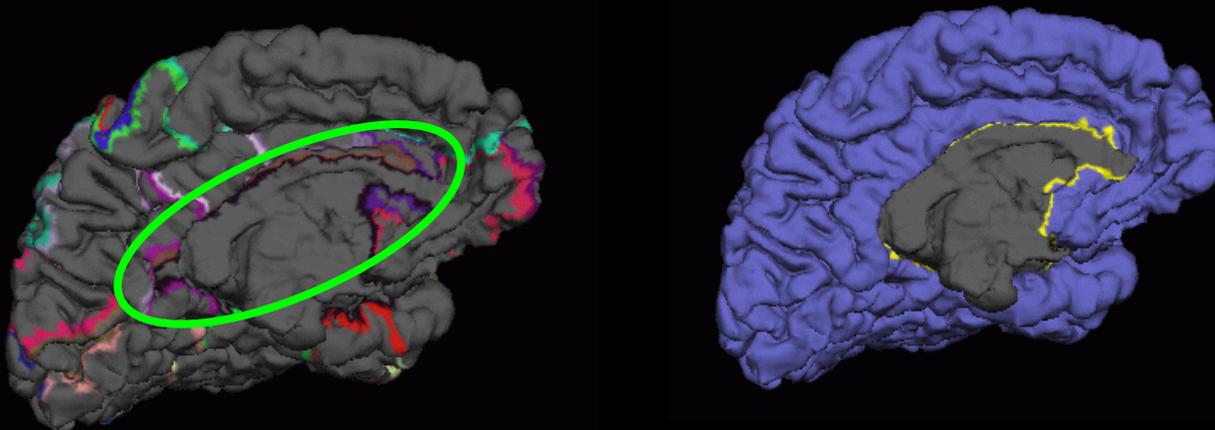
Fine-tune based on  
individual anatomy

Note: Similar methodology  
to volume labeling

# Non-Cortical Areas of Surface



Amygdala, Putamen, Hippocampus, Caudate, Ventricles, CC



?h.cortex.label

# Workflow in Stages

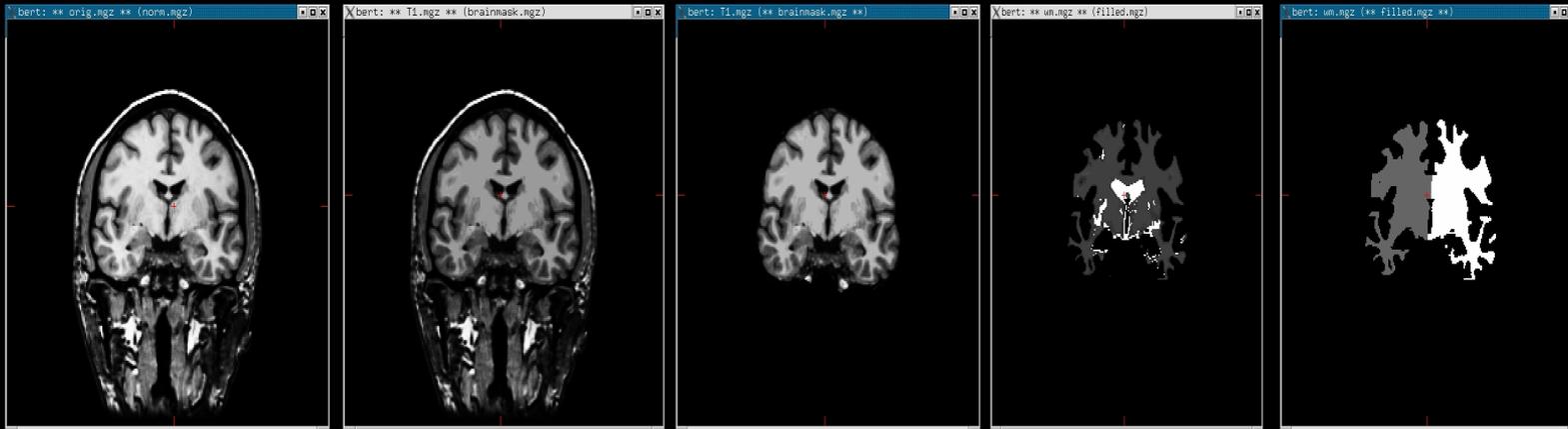
1. `recon-all -autorecon1` (Stages 1-5)
2. Check talairach transform, skull strip, normalization (?)
3. `recon-all -autorecon2` (Stages 6-23)
  1. Add control points: `recon-all -autorecon2` (Stages 10-23)
  2. Edit `wm.mgz`: `recon-all -autorecon2-wm` (Stages 13-23)
  3. Edit `brainmask.mgz`: `recon-all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



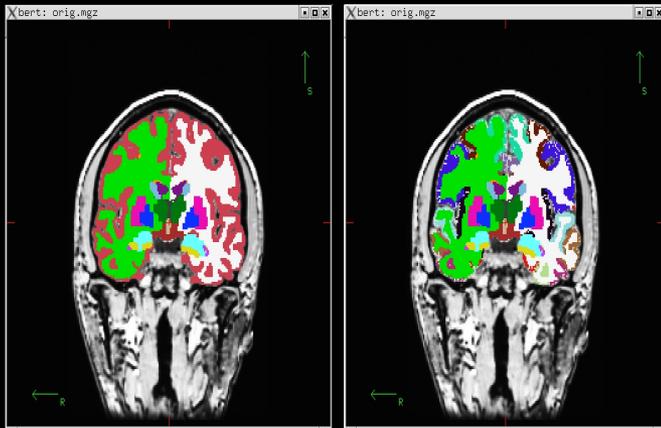
orig.mgz

T1.mgz brainmask.mgz

wm.mgz

filled.mgz

Subcortical Mass



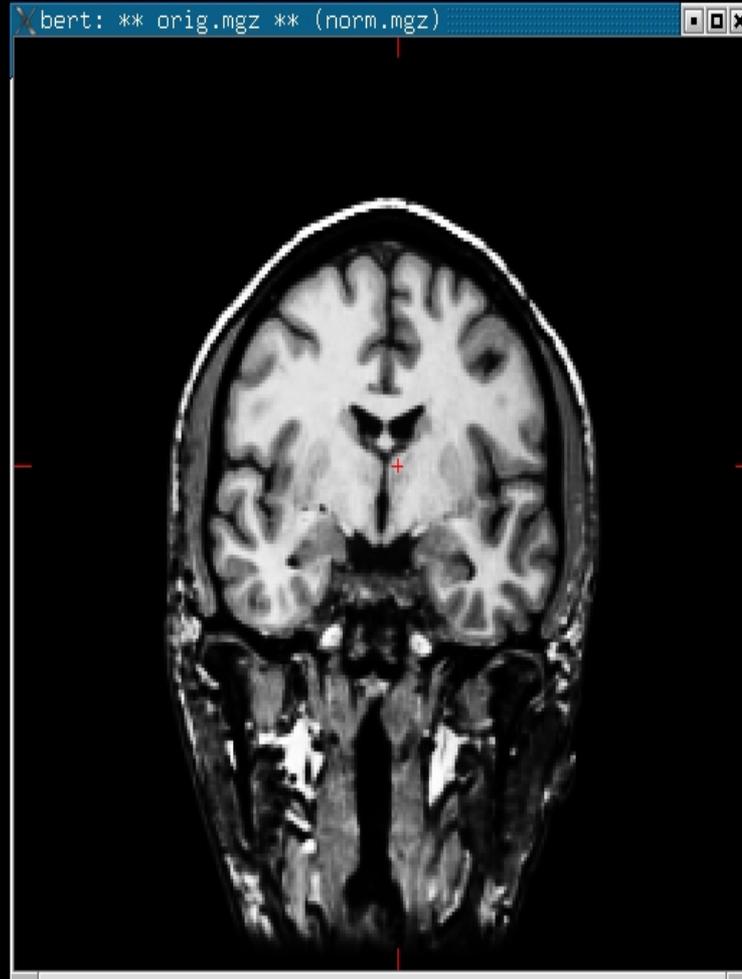
aseg.mgz parc+aseg.mgz

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

Volume Viewer:  
tkmedit

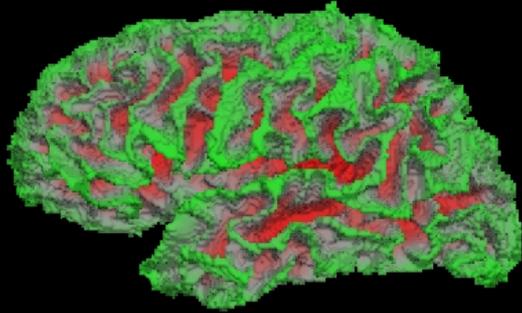
# Volume Viewer (tkmedit)

Right

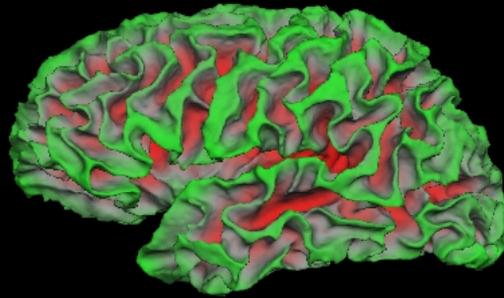


Left

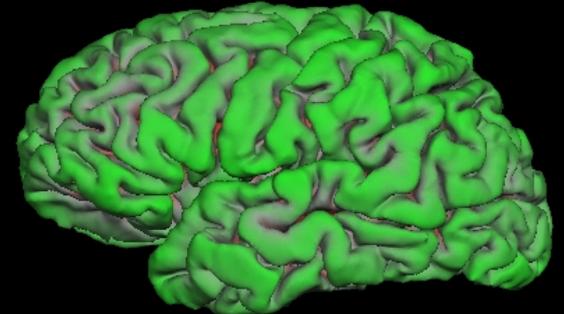
# Surfaces



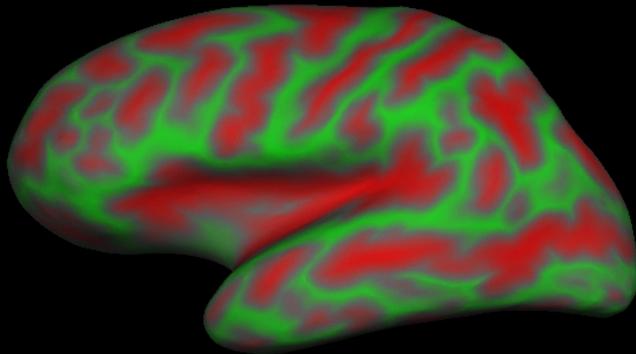
orig



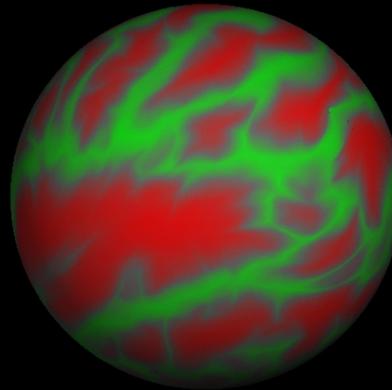
white



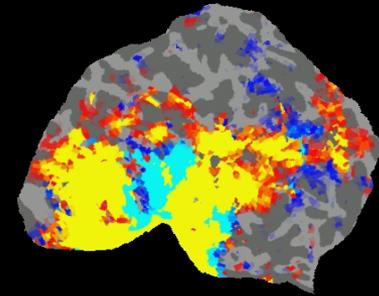
pial



inflated



sphere,sphere.reg



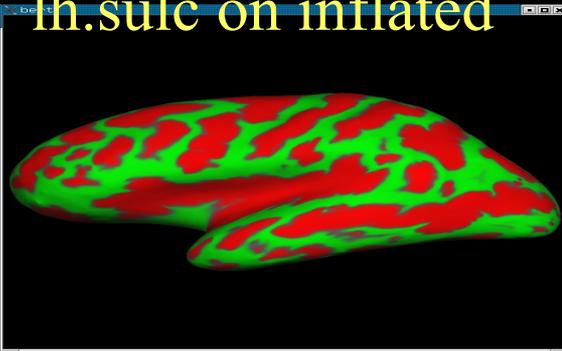
patch (flattened)

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

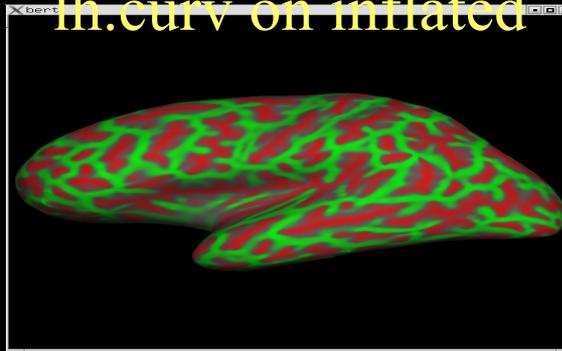
Surface Viewer:  
tksurfer

# Surface Overlays

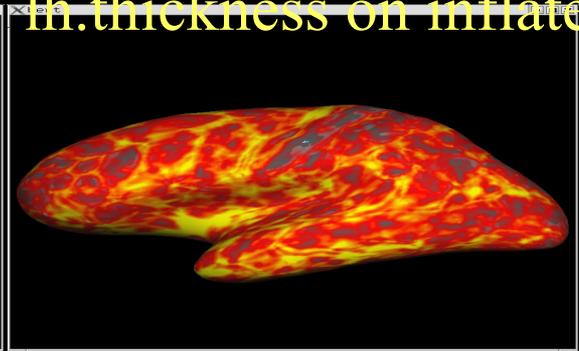
lh.sulc on inflated



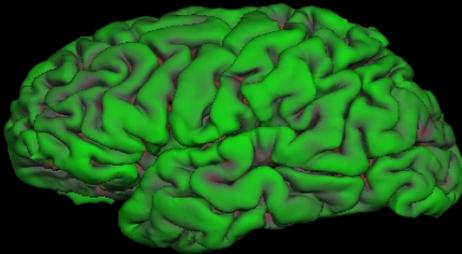
lh.curv on inflated



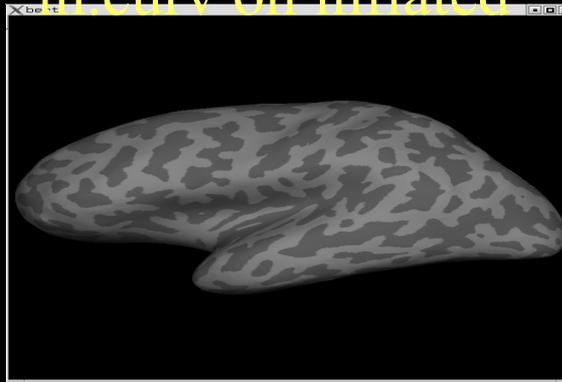
lh.thickness on inflated



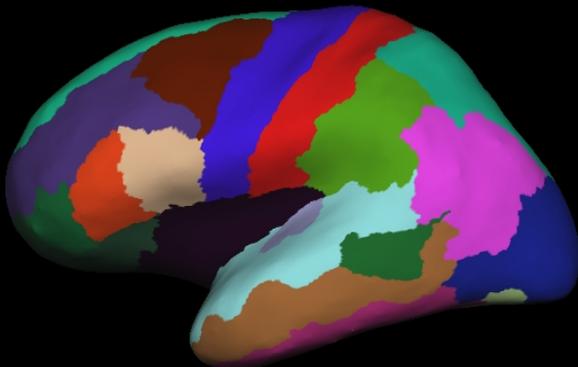
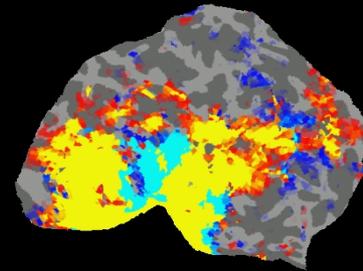
lh.sulc on pial



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.)