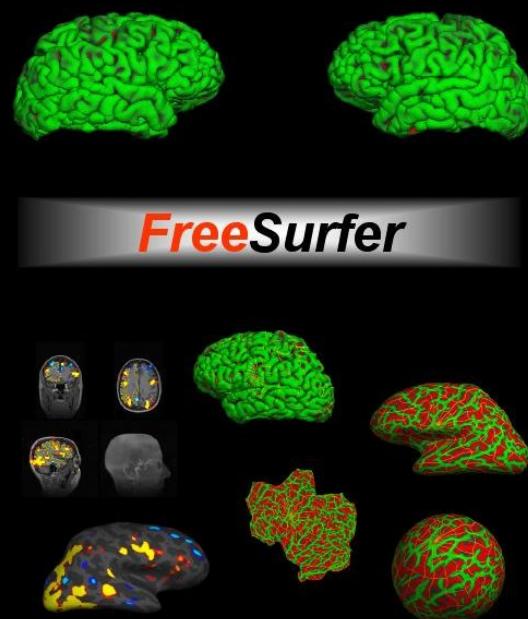


Cortical Reconstruction with FreeSurfer

surfer.nmr.mgh.harvard.edu



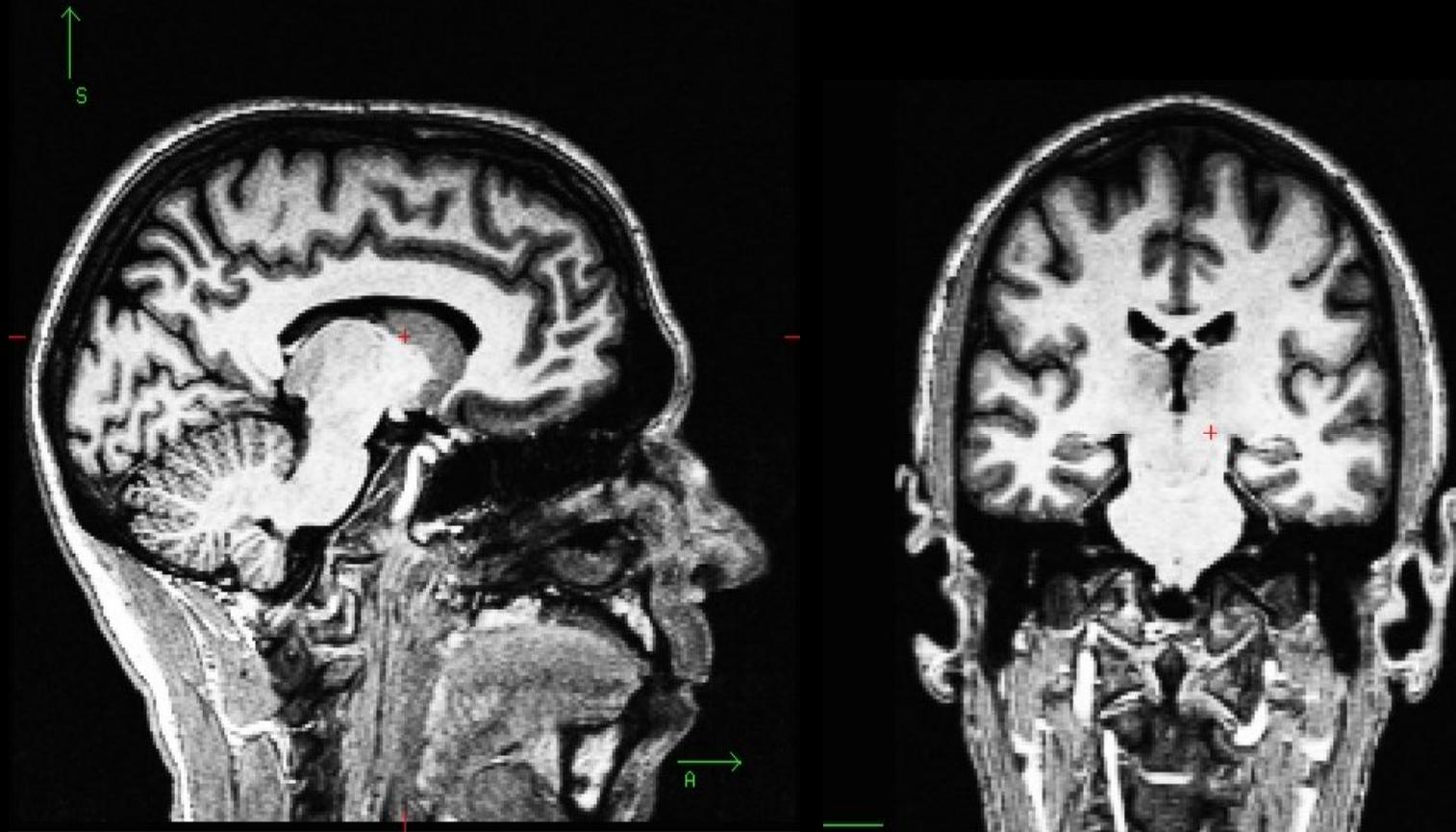
Administratia

- surfer.nmr.mgh.harvard.edu
 - Register
 - Download
 - Mailing List
- Wiki: surfer.nmr.mgh.harvard.edu/fswiki
- Platforms: Linux and Mac
- Important! How to report a bug!
 - Version
 - Command-line
 - Error description
 - subjid/scripts/recon-all.log
 - freesurfer@nmr.mgh.harvard.edu

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

T1 Weighted Image

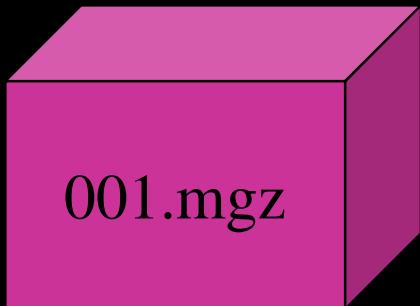


T1 Contrast: White matter brighter than gray matter

Reconstruction Details

- Installation directory:
`$FREESURFER_HOME`
- Unix command-line (Linux, MacOSX)
- File Formats
- Directory structure, naming conventions

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

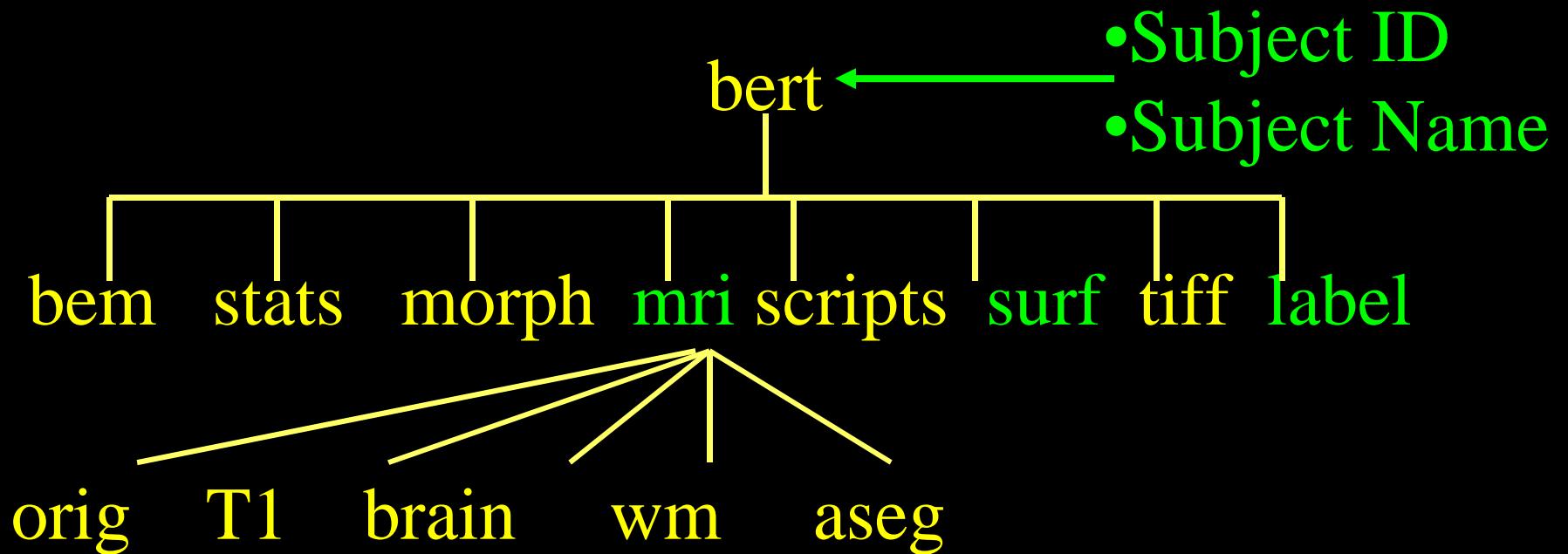
- nvertices, 1, 1, frames (eg, 163214 x 1 x 1 x 40)
- No geometry information

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

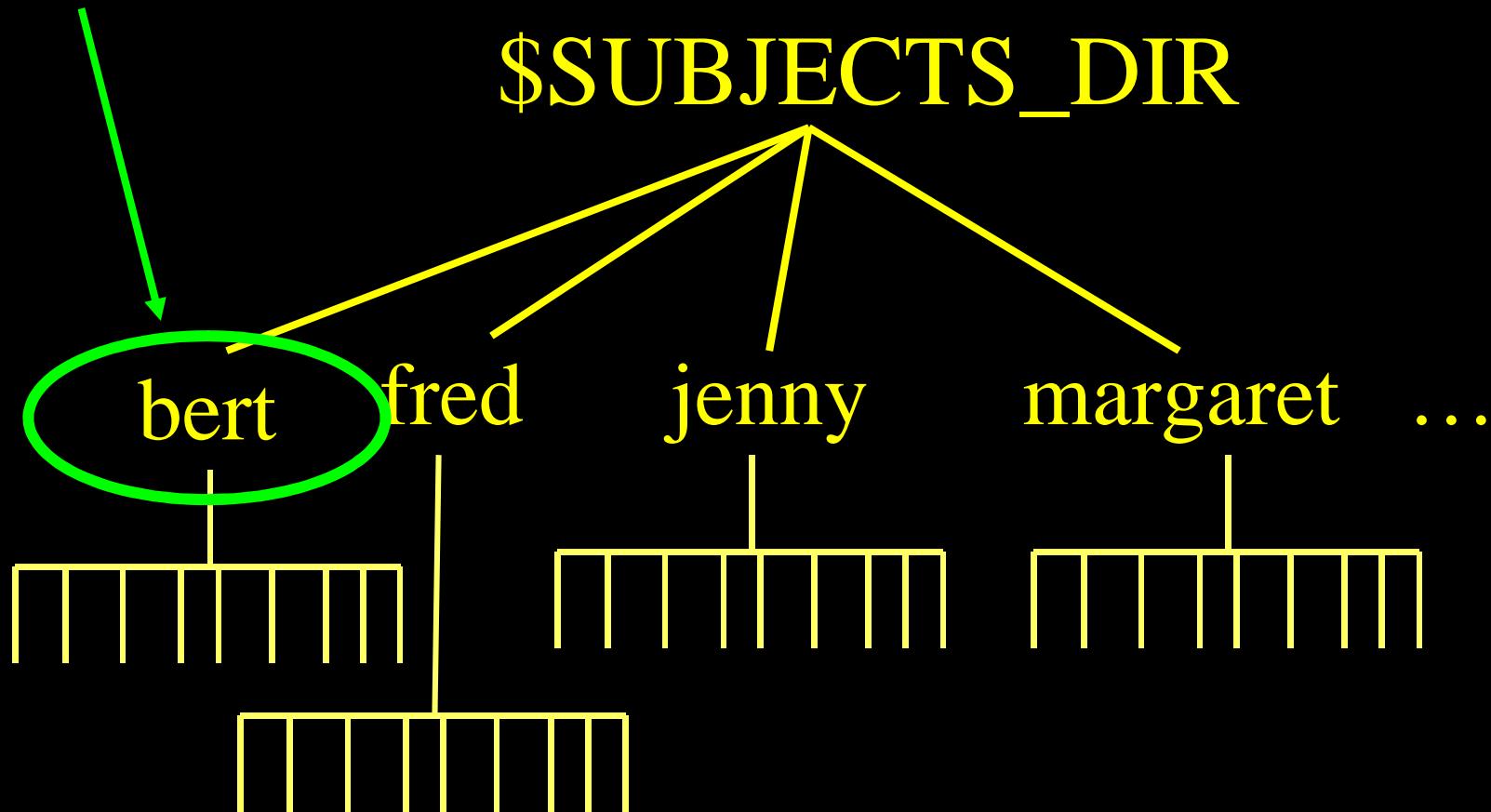
FreeSurfer Directory Tree

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



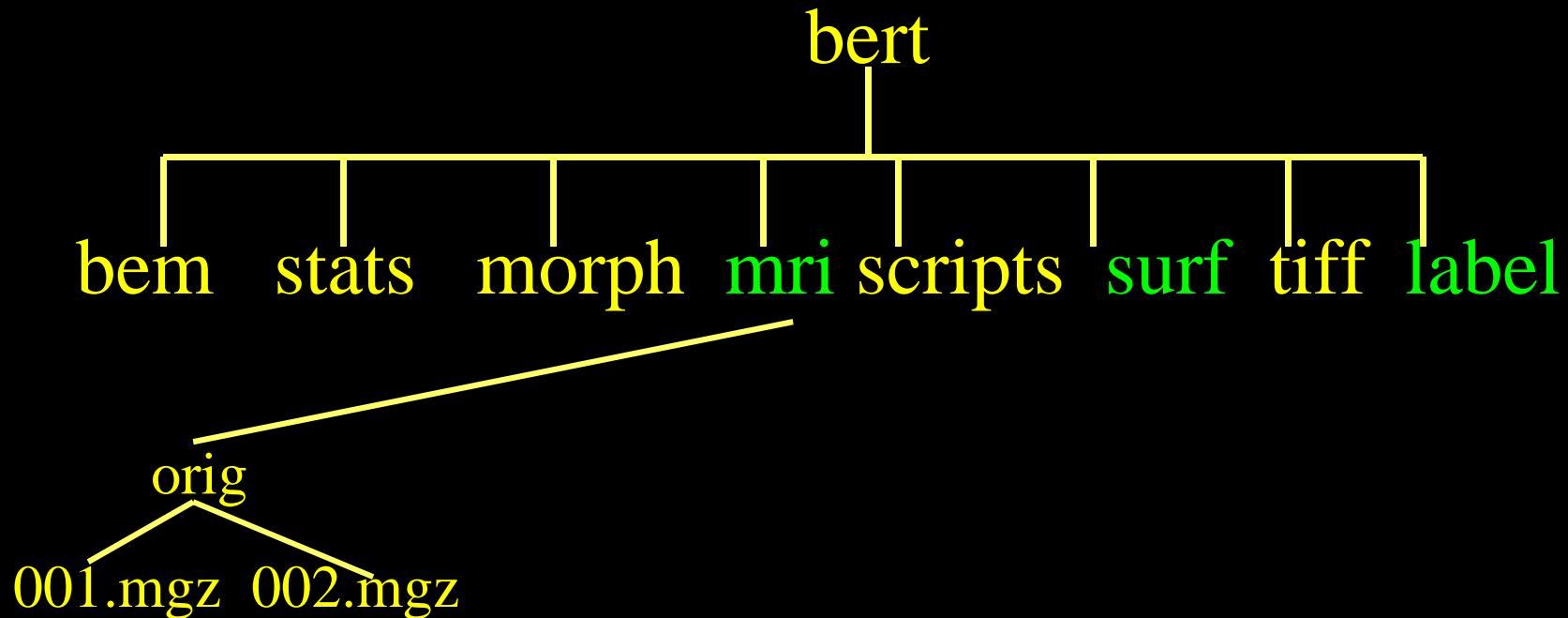
SUBJECTS_DIR Environment Variable

Subject ID



Add Your Data

- cd \$SUBJECTS_DIR
- mkdir -p bert/orig
- mri_convert yourdicom.dcm bert/mri/orig/001.mgz
- mri_convert yourdicom.dcm bert/mri/orig/002.mgz



Fully Automated Reconstruction

1. Create directory for data:

```
mkdir -p $SUBJECTS_DIR/bert/orig
```

2. Copy/Convert data into directory:

```
mri_convert file.dcm $SUBJECTS_DIR/bert/orig/001.mgz
```

3. Launch reconstruction:

```
recon-all -s bert --autorecon-all
```

Come back in 30 hours ...

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

-- Can be broken up

Individual Stages

Volumetric Processing Stages (subjID/mri):

1. Motion Cor, Avg, Conform (`orig.mgz`)
2. Talairach transform computation
3. Non-uniform inorm (`nu.mgz`)
4. Intensity Normalization 1 (`T1.mgz`)
5. Skull Strip (`brain.mgz`)
6. EM Register (linear volumetric registration)
7. CA Intensity Normalization
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`)

Green = Manual Intervention?

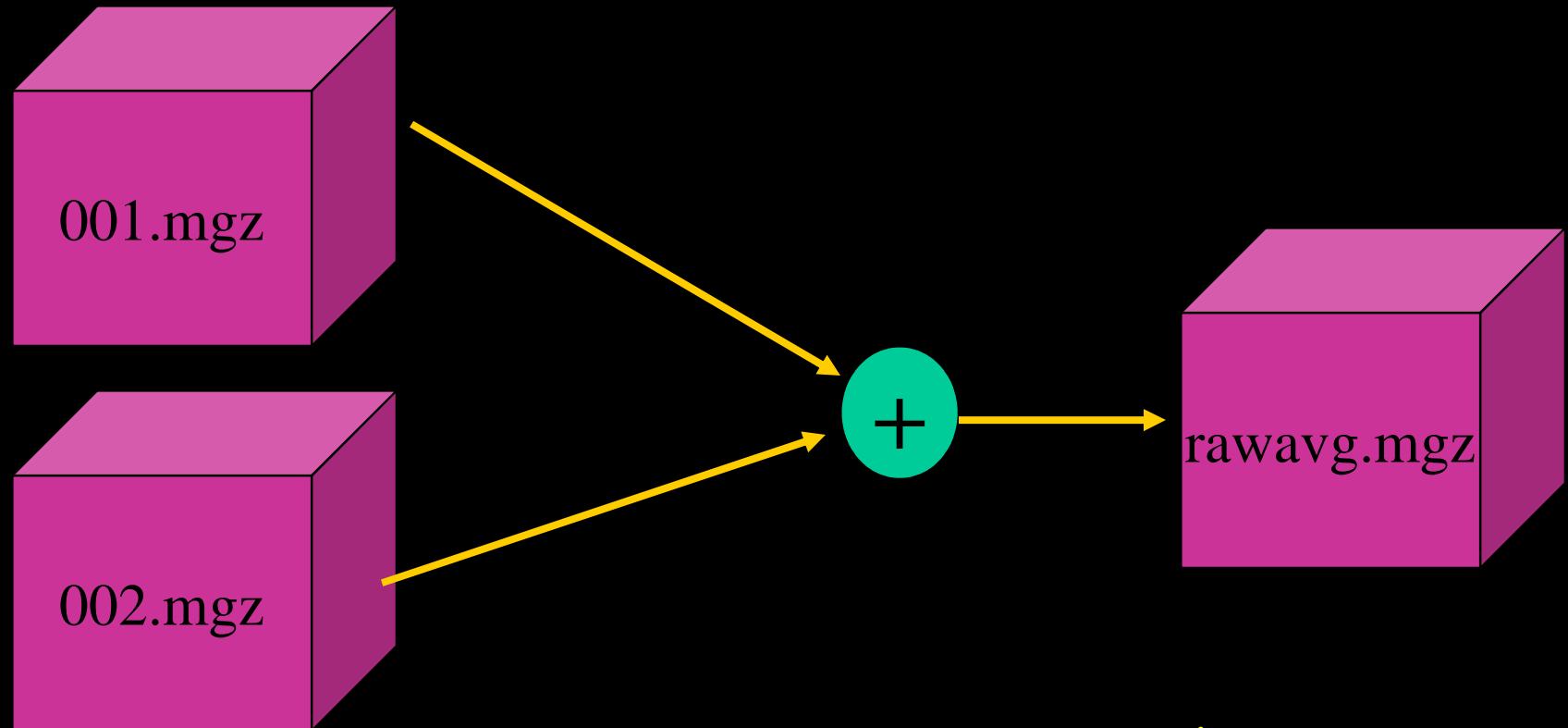
recon-all -help

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

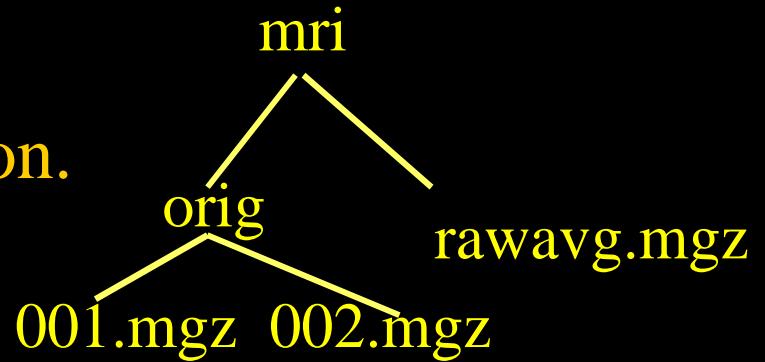
Surface Processing Stages (subjID/surf):

14. Tessellate (?h.orig)
15. Smooth1 (?h.smoothwm)
16. Inflate1 (?h.inflated)
17. QSphere (?h.qsphere)
18. Automatic Topology Fixer (?h.orig)
19. Euler Number
20. Smooth2
21. Inflate2
22. Final Surfs (?h.white,?h.pial)
23. Cortical Ribbon Mask
24. Spherical Morph
25. Spherical Registration
26. Spherical Registration
27. Map average curvature to subject
28. Cortical Parcellation (Labeling)
29. Cortical Parcellation Statistics
30. Cortical Parcellation mapped to ASeg

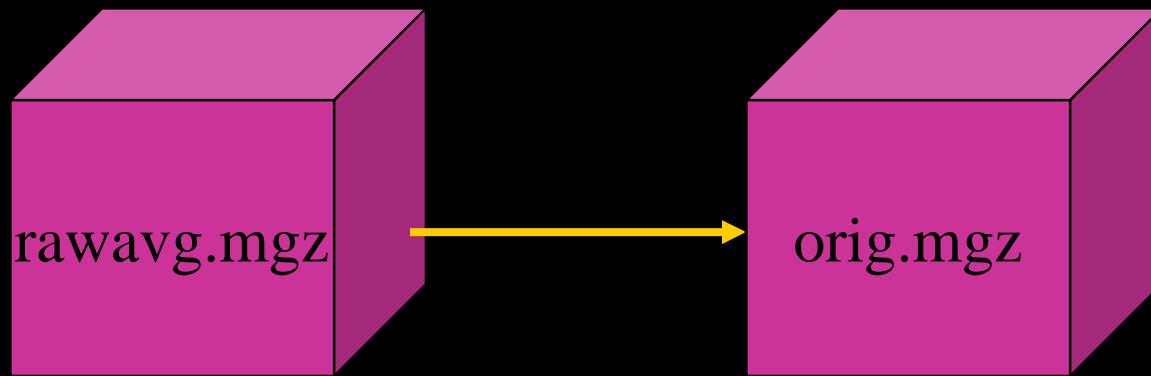
Motion Correction and Averaging



Does not change native resolution.

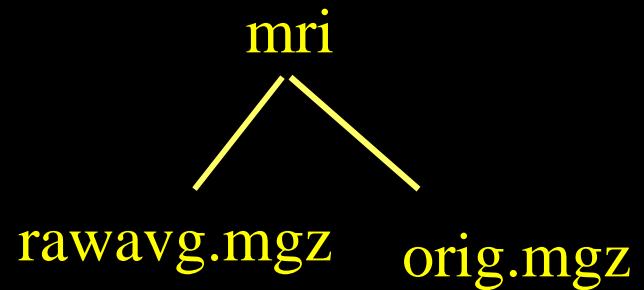


Conform



Changes to 256^3 , 1mm 3

All volumes will be conformed.



Talairach Transform

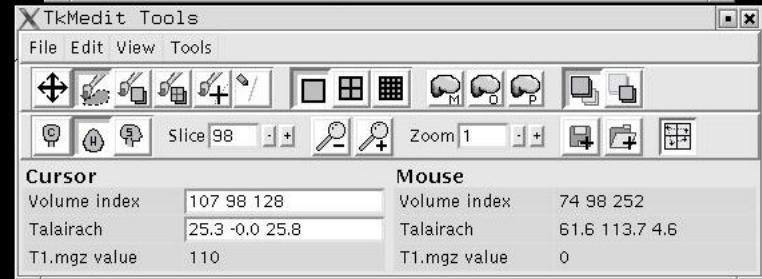
- Computes 12 DOF transform matrix
- Does NOT resample
- MNI305 template
- Mostly used to report coordinates
- mri/transforms/talairach.xfm

```
graph TD; mri[mri] --> transforms[transforms]; transforms --> talairach_xfm[talairach.xfm]
```

mri
 transforms
 talairach.xfm

Intensity Normalization

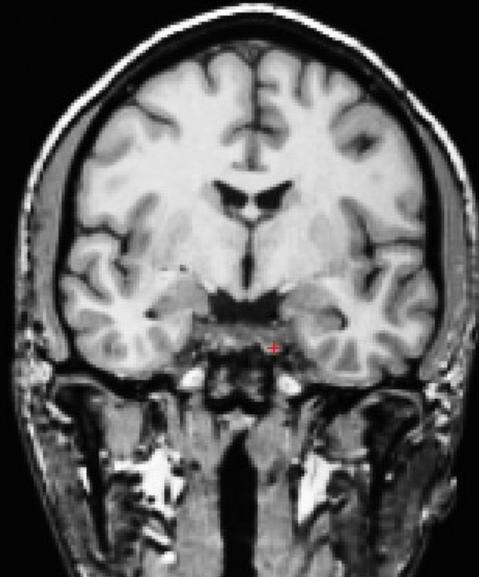
- Removes B1 bias field
- NU (MNI) nu.mgz
- Presegmentation (T1.mgz)
 - Most WM = 110 intensity
 - Pre- and Post-Skull Strip



T1 Volume

Skull Strip

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

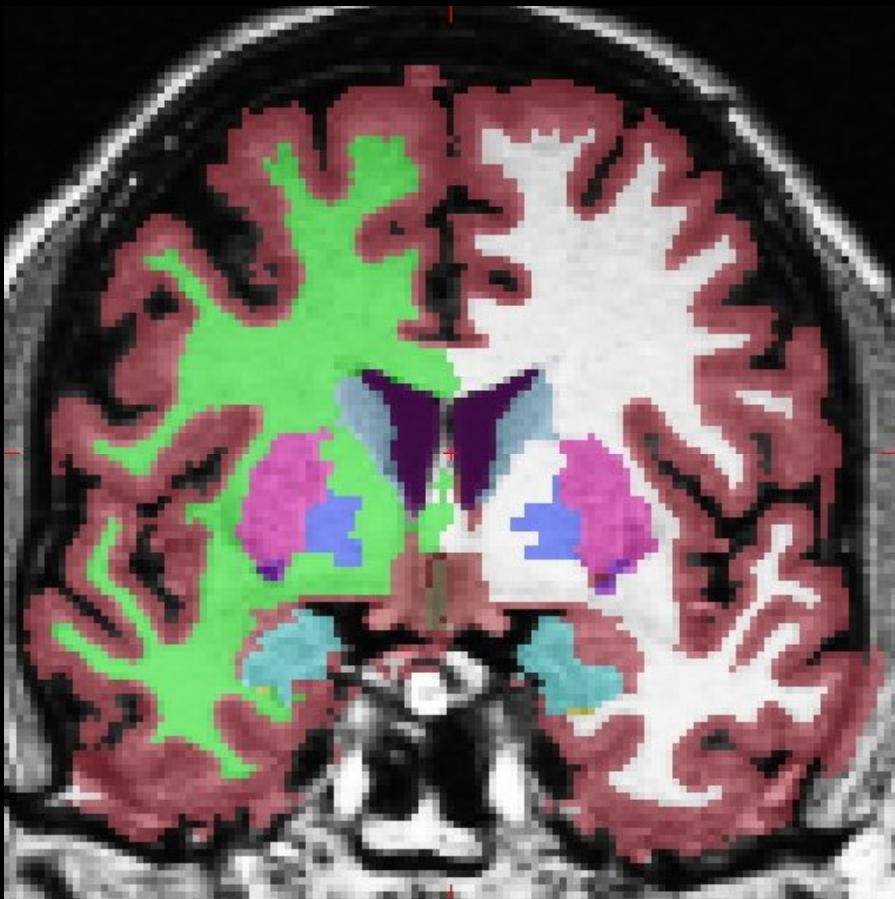


Orig Volume



Brain Volume

Automatic Volume Labeling

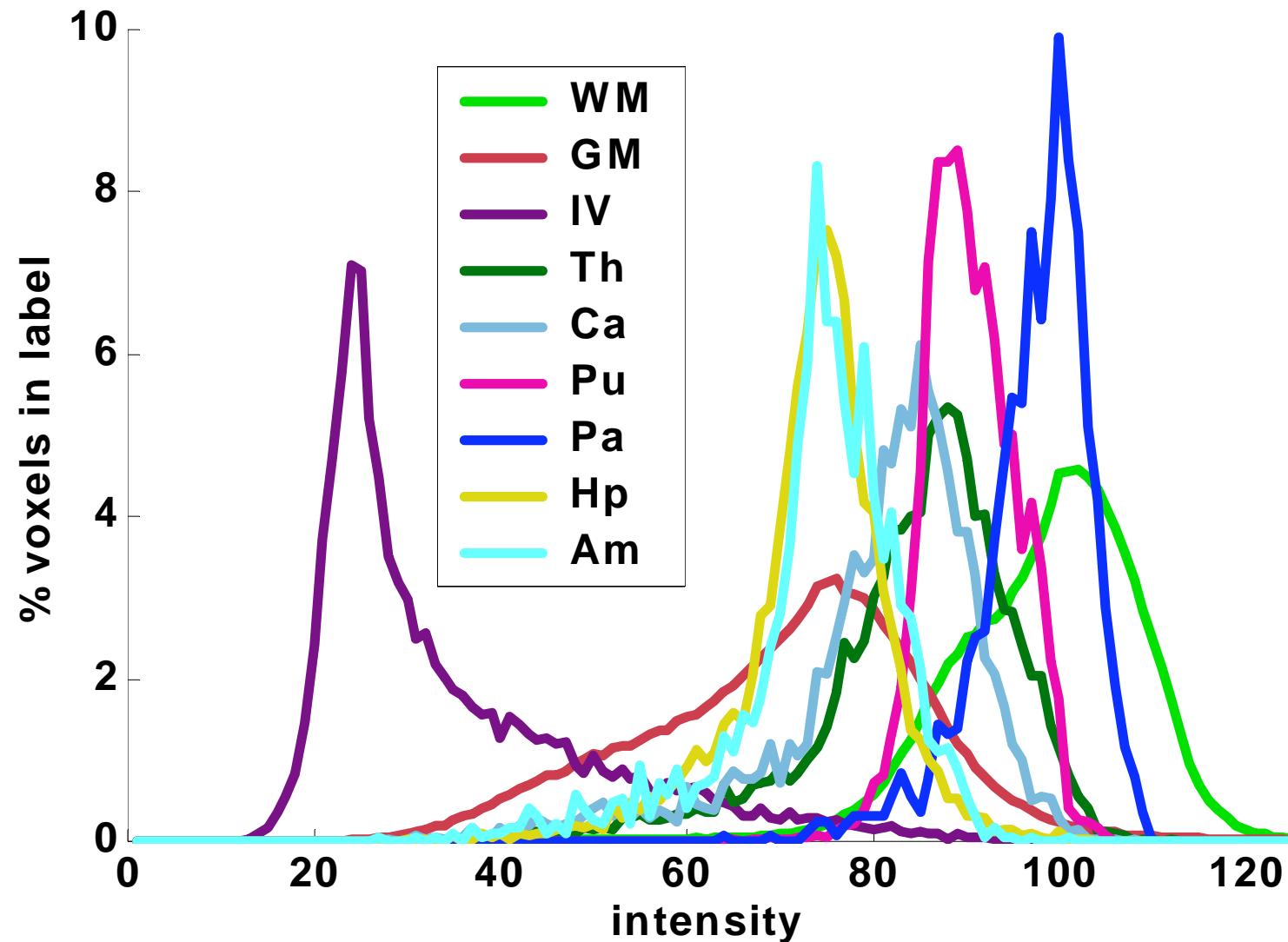


ASeg Volume

Atlas: RB_all_2006-2-15

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

Why Segmentation is Hard!



Inter-subject Registration

Goal: align functionally homologous points across subjects
(e.g. hippocampus with hippocampus, amygdala with amygdala, etc...).

Problem: this information is in general unavailable

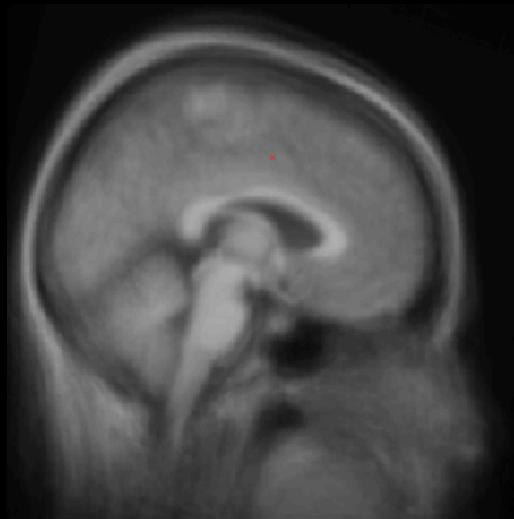
Typical solution: align image intensities and hope this results in alignment of function/structure as well.

Mean-squared Error Registration: Low Quality Data

$I(r)$



$T(r)$



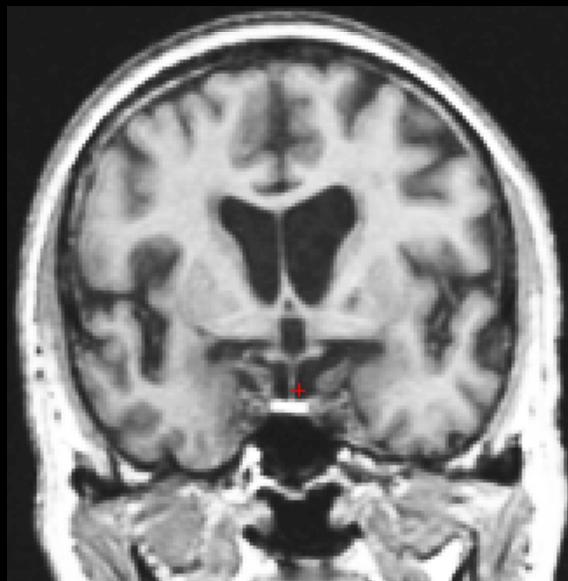
$I(Lr)$



Mean-squared Error Registration

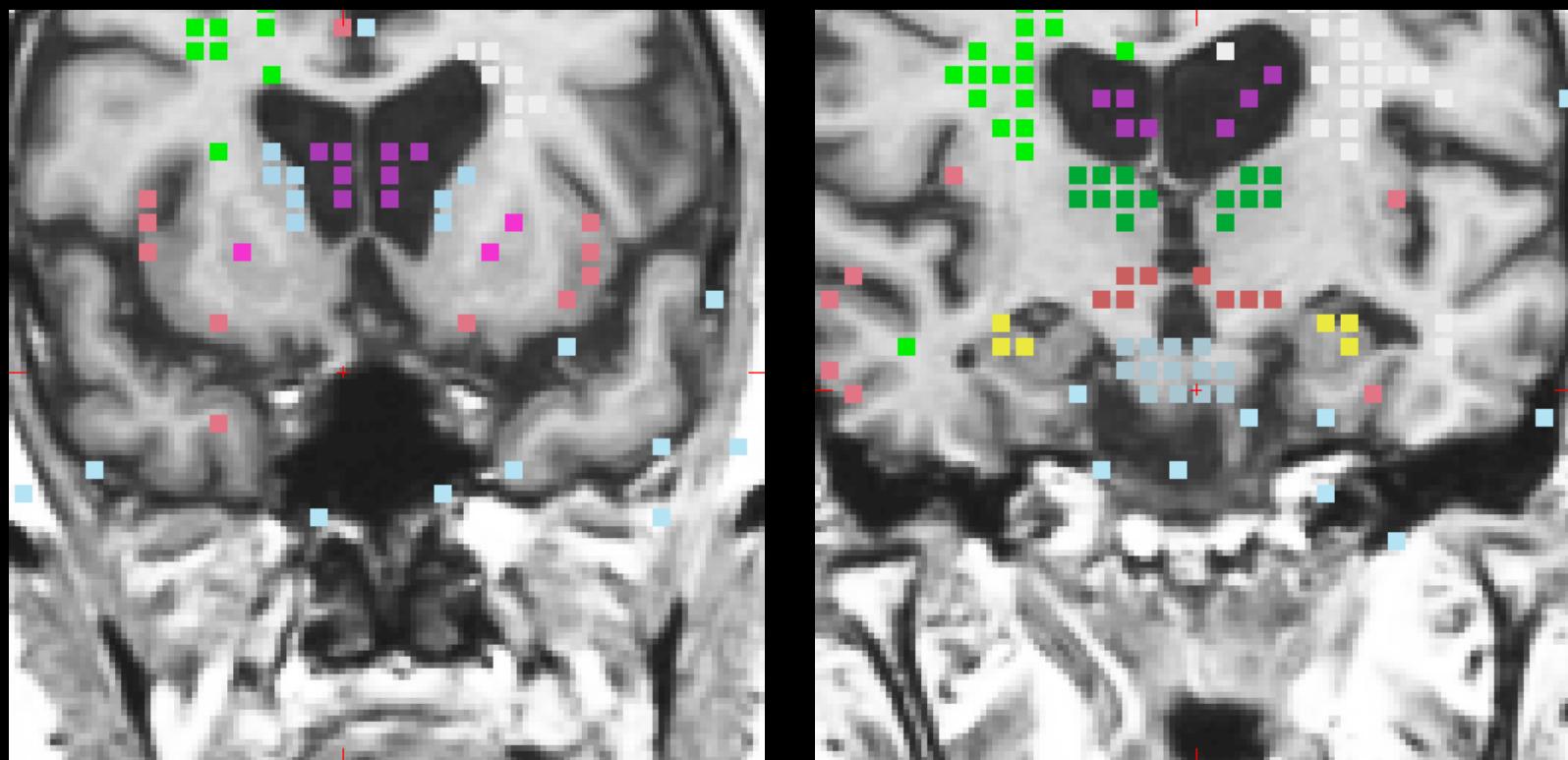
Anatomy is variable, particularly in cases of pathology*

→ *A given spatial location may contain a different tissue class in different types of subjects!*



* Thanks to Marilyn Albert and Ron Killiany for providing this data.

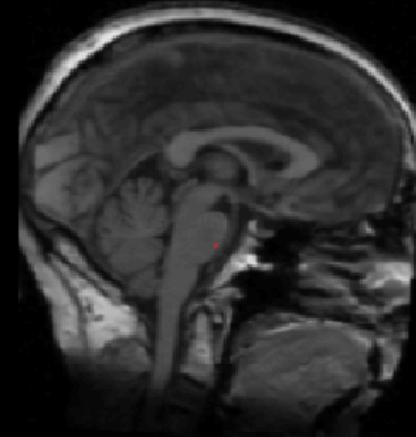
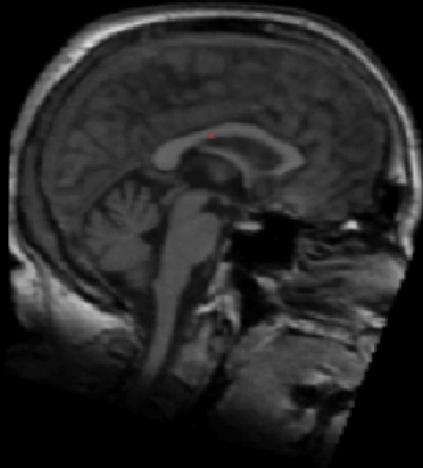
Atlas Points After Registration



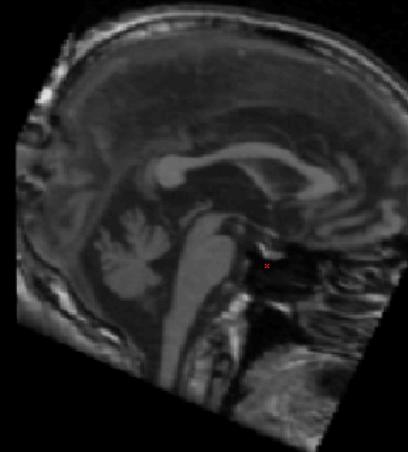
- | | | |
|---------------------|------------------|---------------------|
| ● Cerebellar cortex | ● LH cerebral WM | ● Cerebral cortex |
| ● Cerebellar WM | ● Hippocampus | ● Misc. |
| ● 4th ventricle | ● LH pallidum | ● Lateral ventricle |
| ● RH cerebral WM | ● Thalamus | ● Caudate |

Segmentation-based Registration: Results

Normal

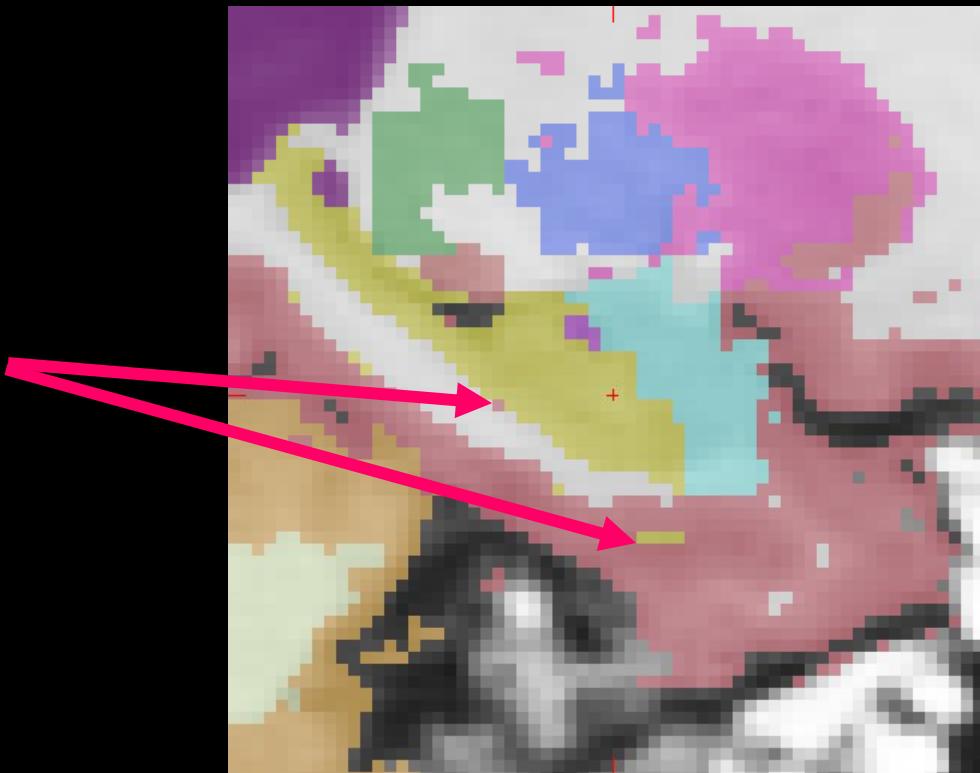


AD



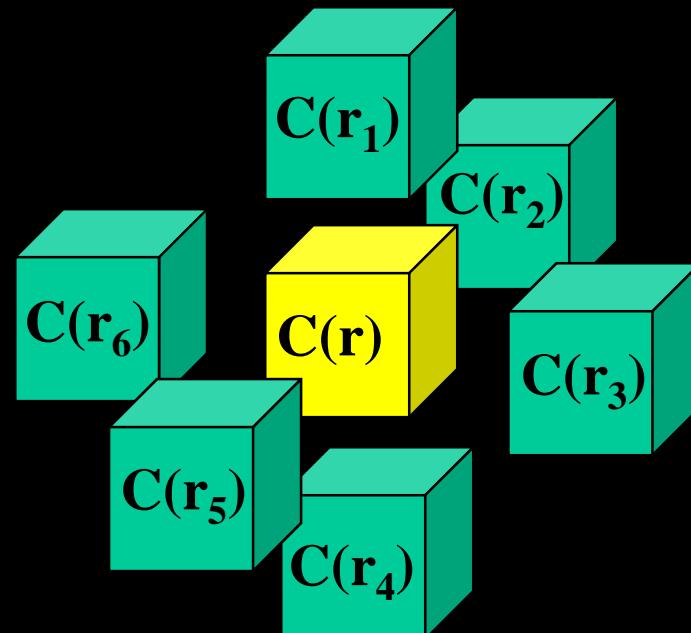
Markov Random Field: Motivation

What is the probability that cortical gray matter occurs inferior to hippocampus?



Segmentation: MRF

$p(C(\mathbf{r}_i)|C(\mathbf{r}), I, \mathbf{r}, \mathbf{r}_i)$ encodes the probability that tissue class $C(\mathbf{r}_i)$ occurs at spatial location \mathbf{r}_i when tissue class $C(\mathbf{r})$ occurred at \mathbf{r} . The segmentation is thus modeled as an *anisotropic* nonstationary *MRF*.

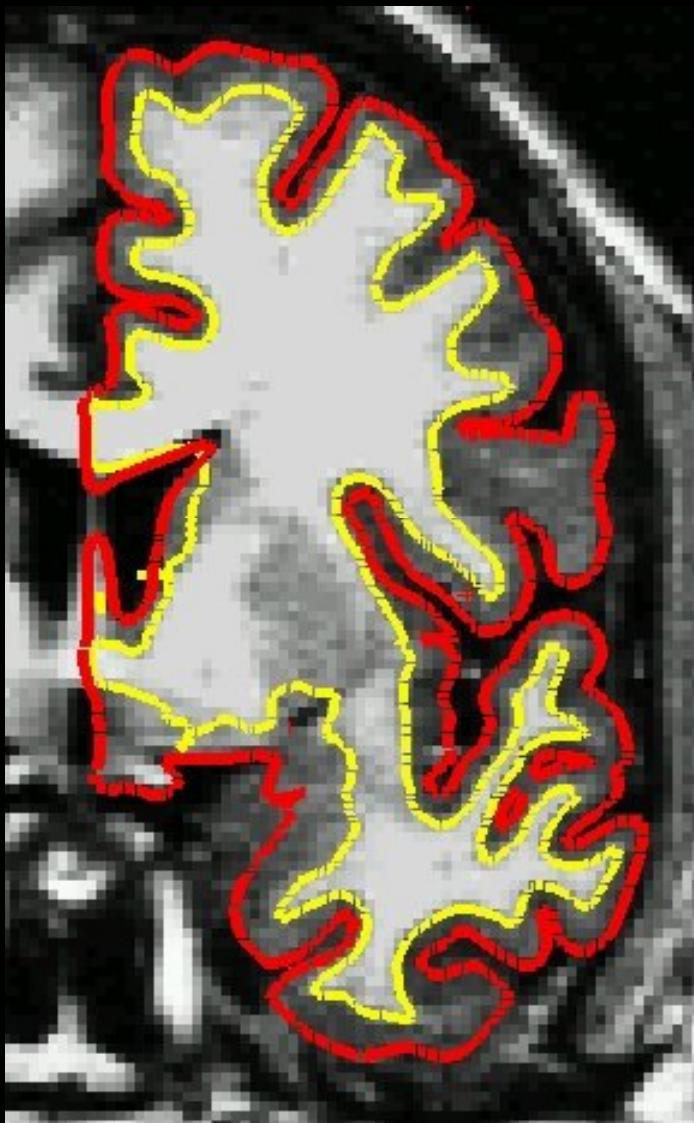


Segmentation: MRF



Preliminary Segmentation

Find “Subcortical Mass”



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

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”

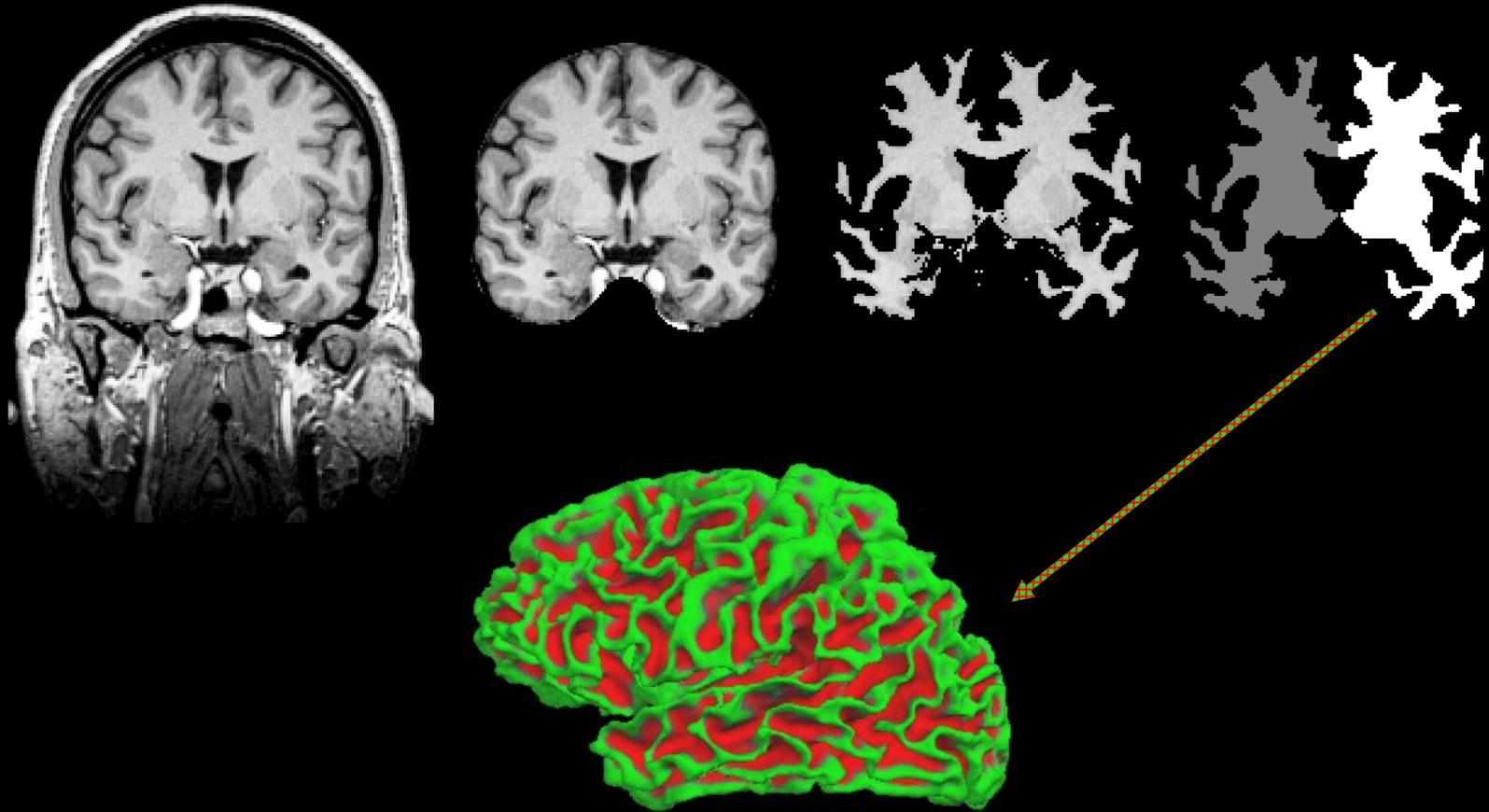


WM Volume

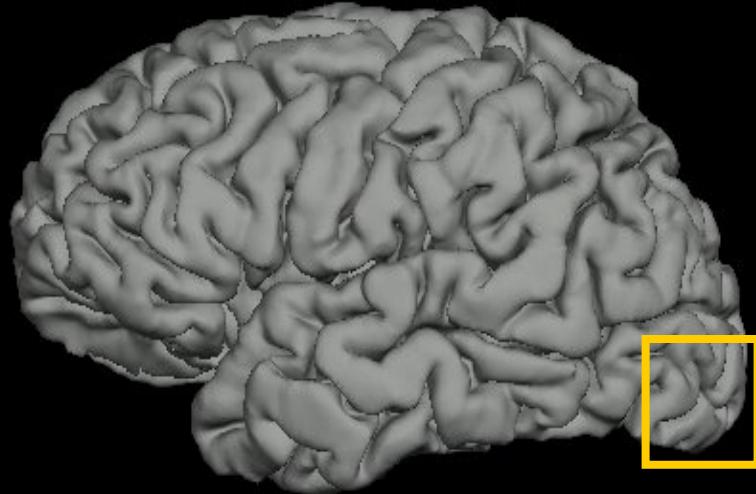


Filled Volume

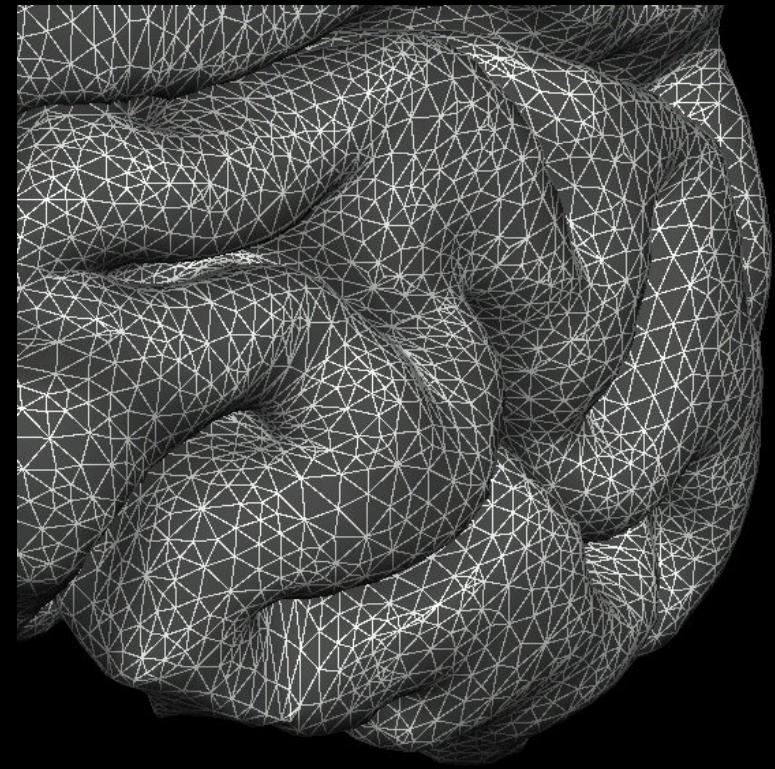
MRI Segmentation and Surface Reconstruction



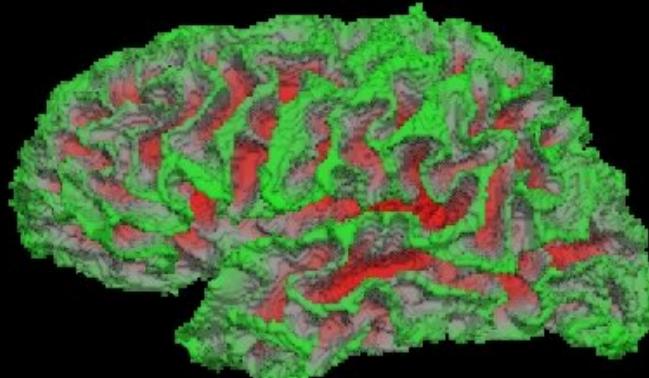
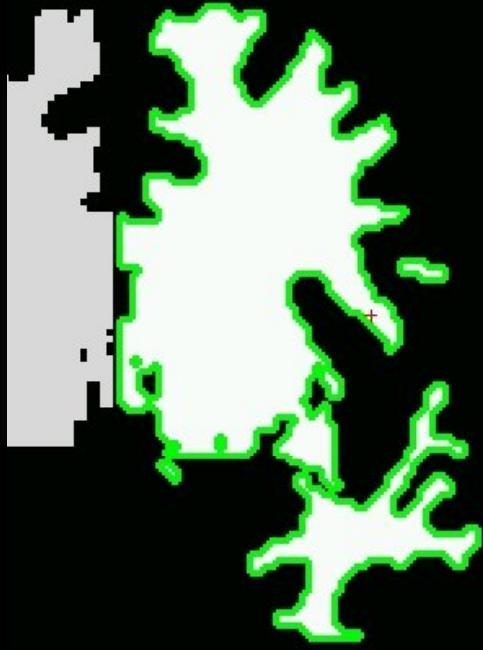
Surface Model



- Mesh (“Finite Element”)
- Vertex = point of 6 triangles
- Neighborhood
- XYZ at each vertex
- Triangles/Faces $\sim 150,000$
- Area, Distance
- Curvature, Thickness
- Moveable

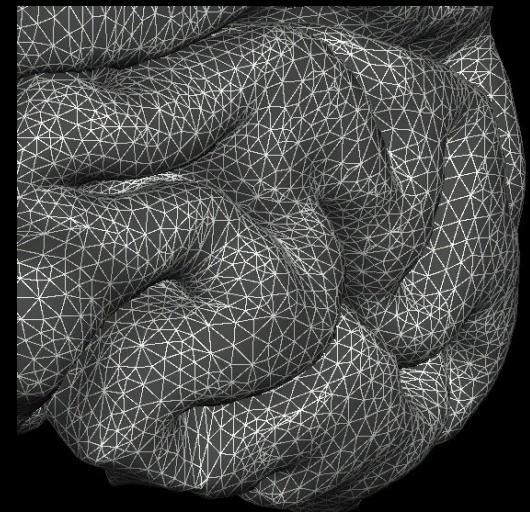


Tessellation and Topology Fixing

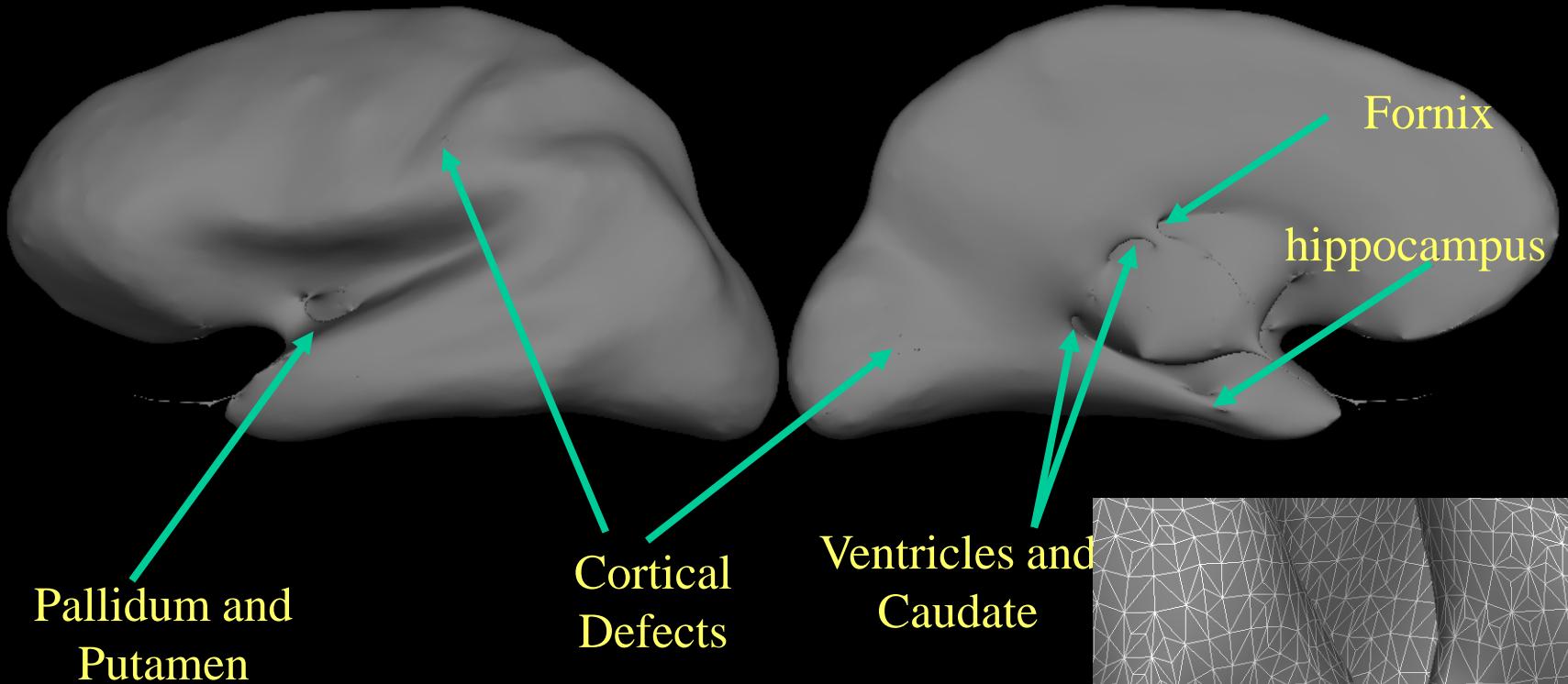


orig surface
surf/lh.orig
surf/rh.orig

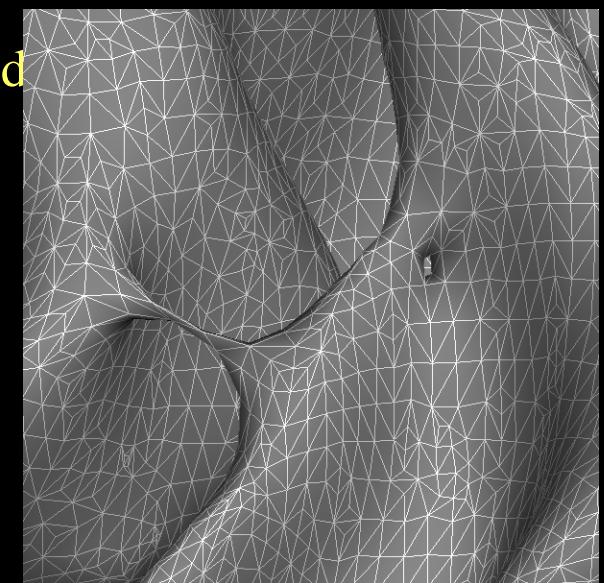
- Mosaic of triangles (“tessellation”)
- Errors: Donut holes, handles
- Automatic topology fixer



Topological Defects



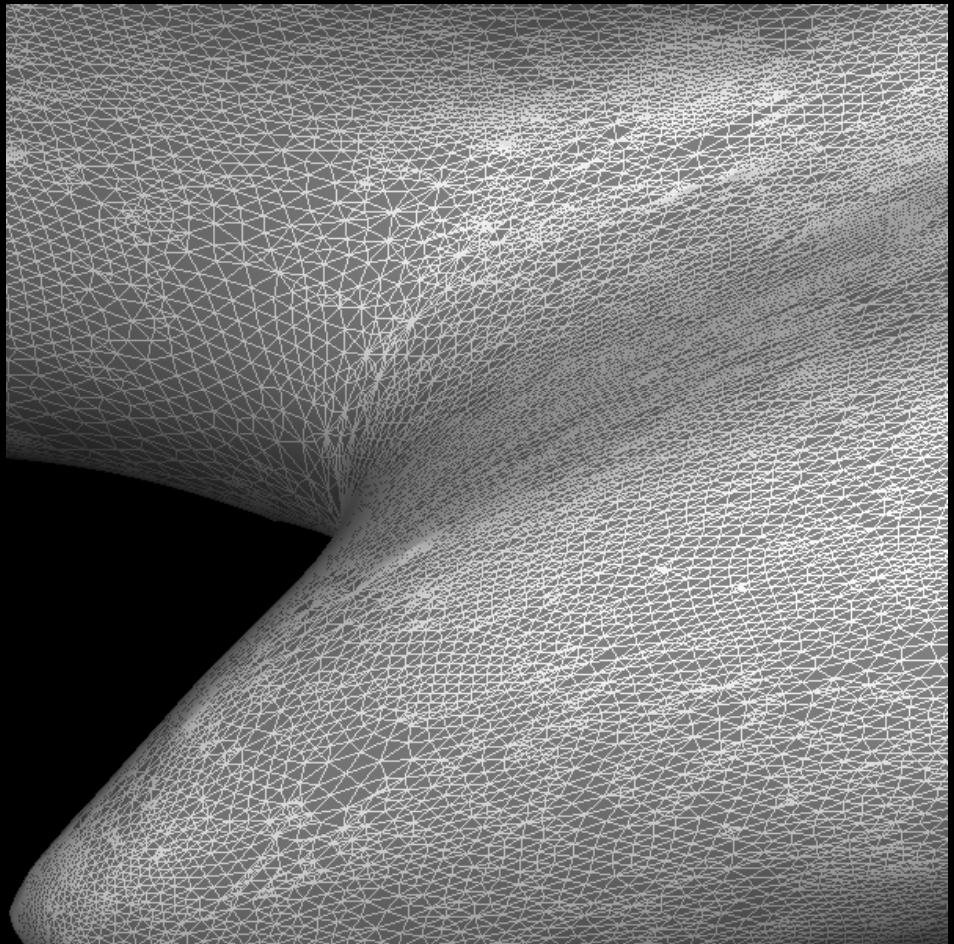
- Holes
- Handles
- Automatically Fixed



Manifold Surgery

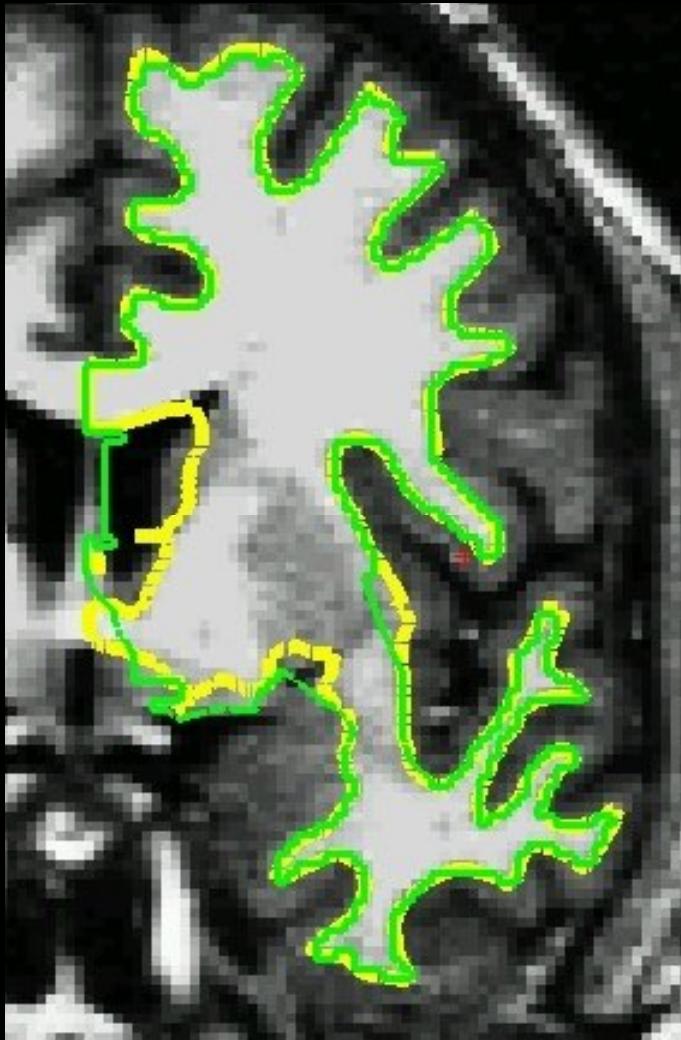


BEFORE

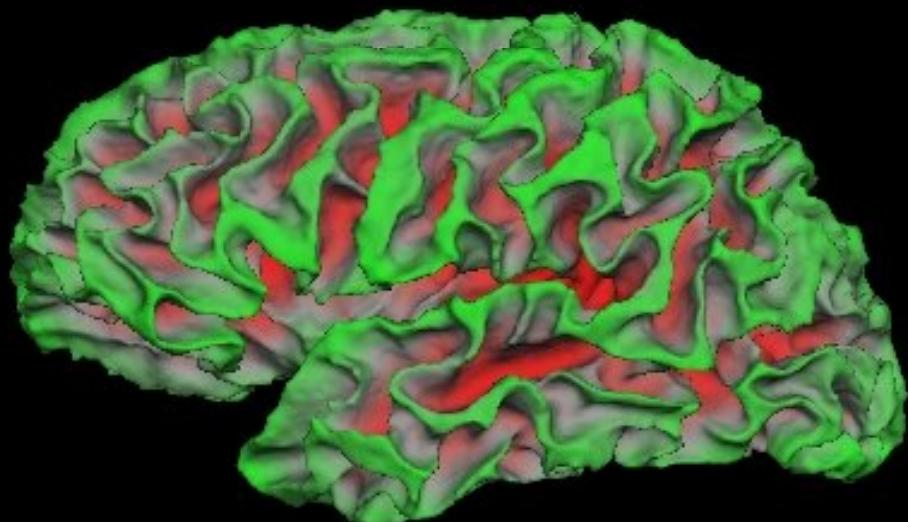


AFTER

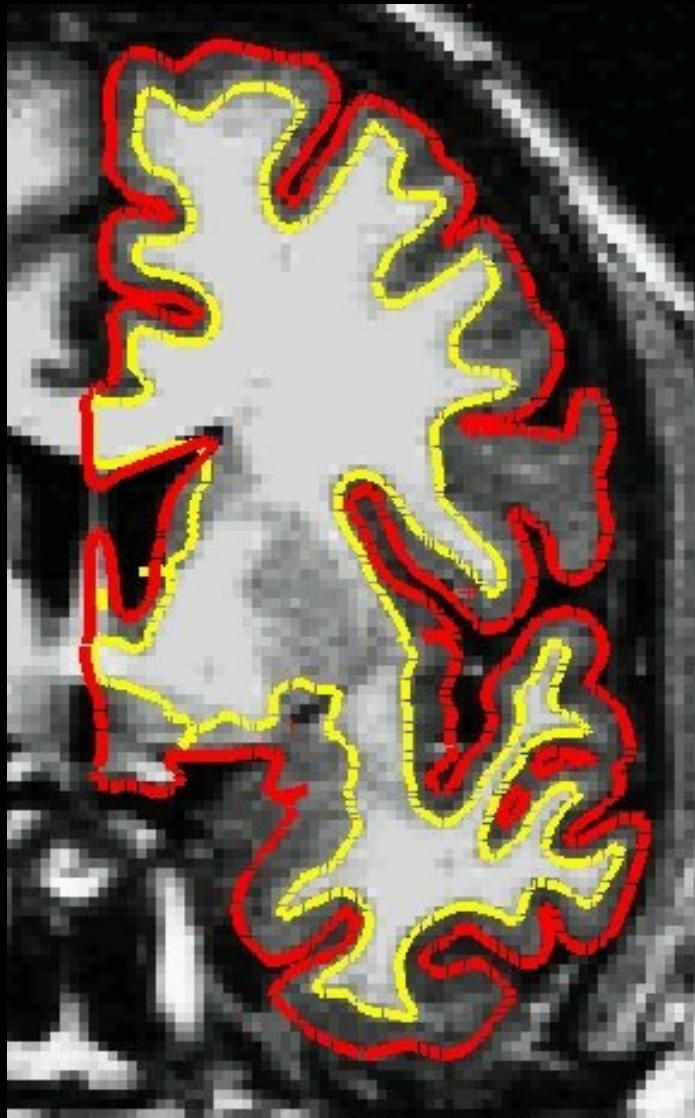
White Matter Surface



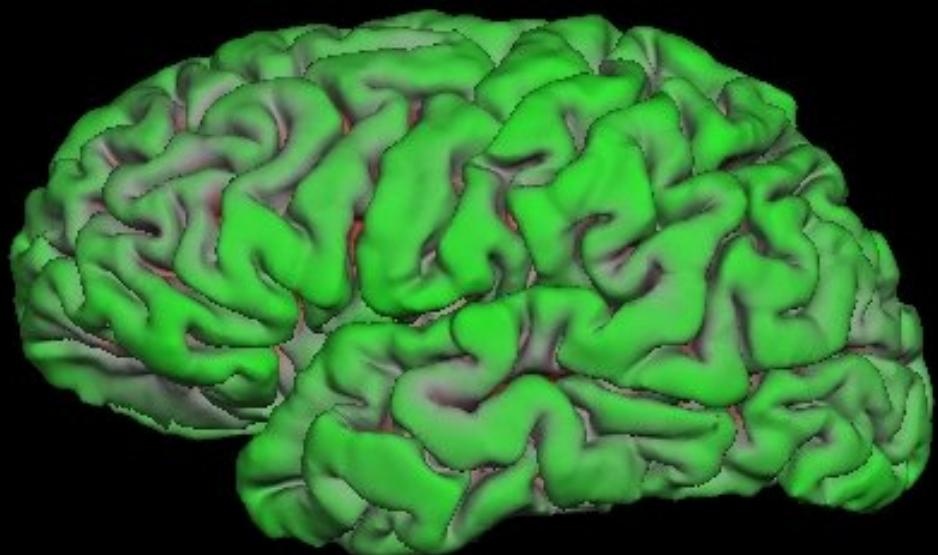
- Nudge orig surface
- Follow T1 intensity gradients
- Smoothness constraint
- Vertex identity preserved



Pial Surface

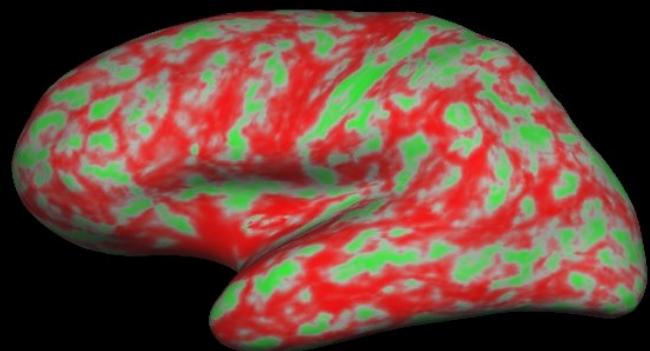


- Nudge white surface
- Follow T1 intensity gradients
- Vertex identity preserved



Cortical Thickness

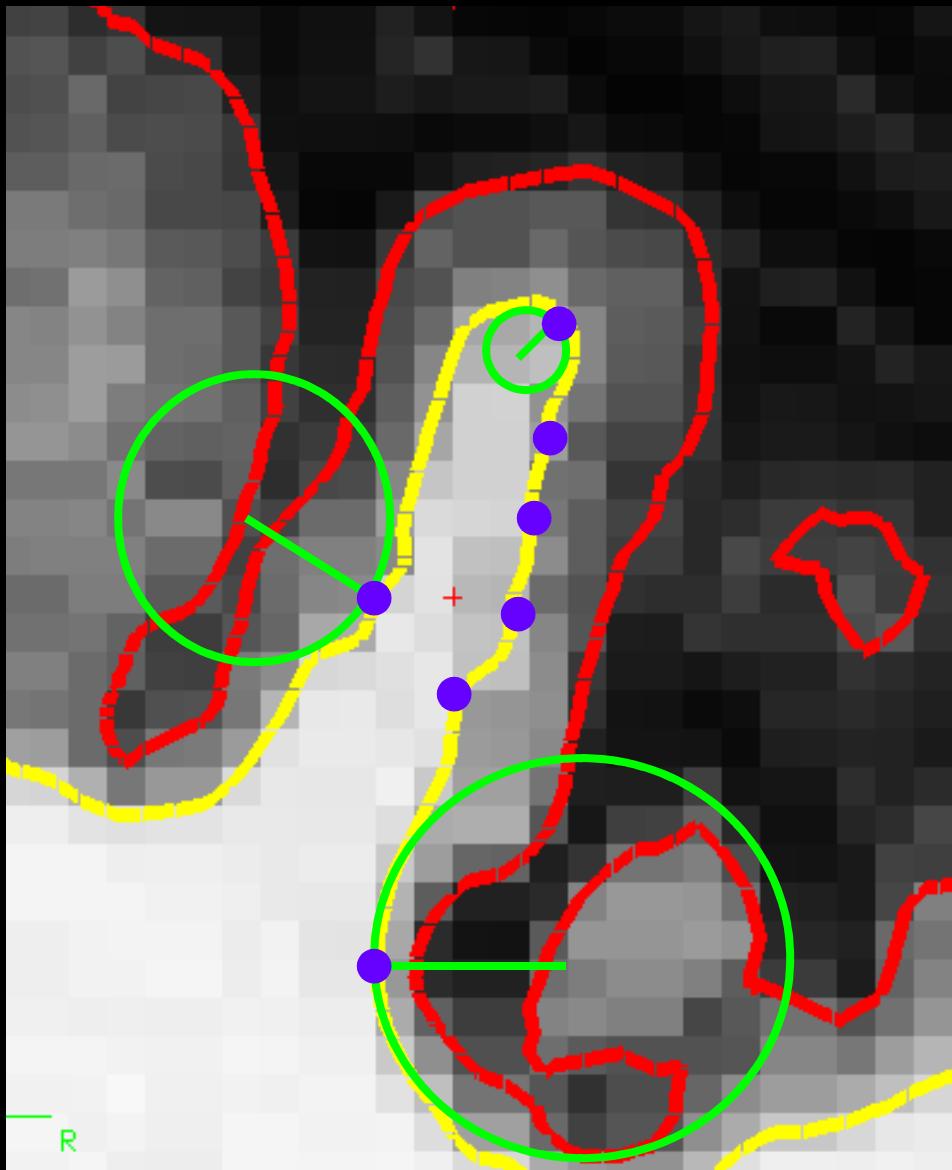
- Distance between white and pial surfaces
- One value per vertex
- Surface-based more accurate than volume-based



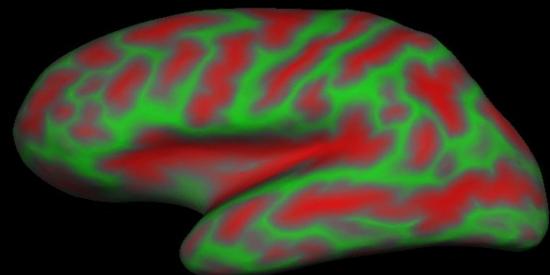
white/gray surface
lh.thickness, rh.thickness



Curvature (Radial)

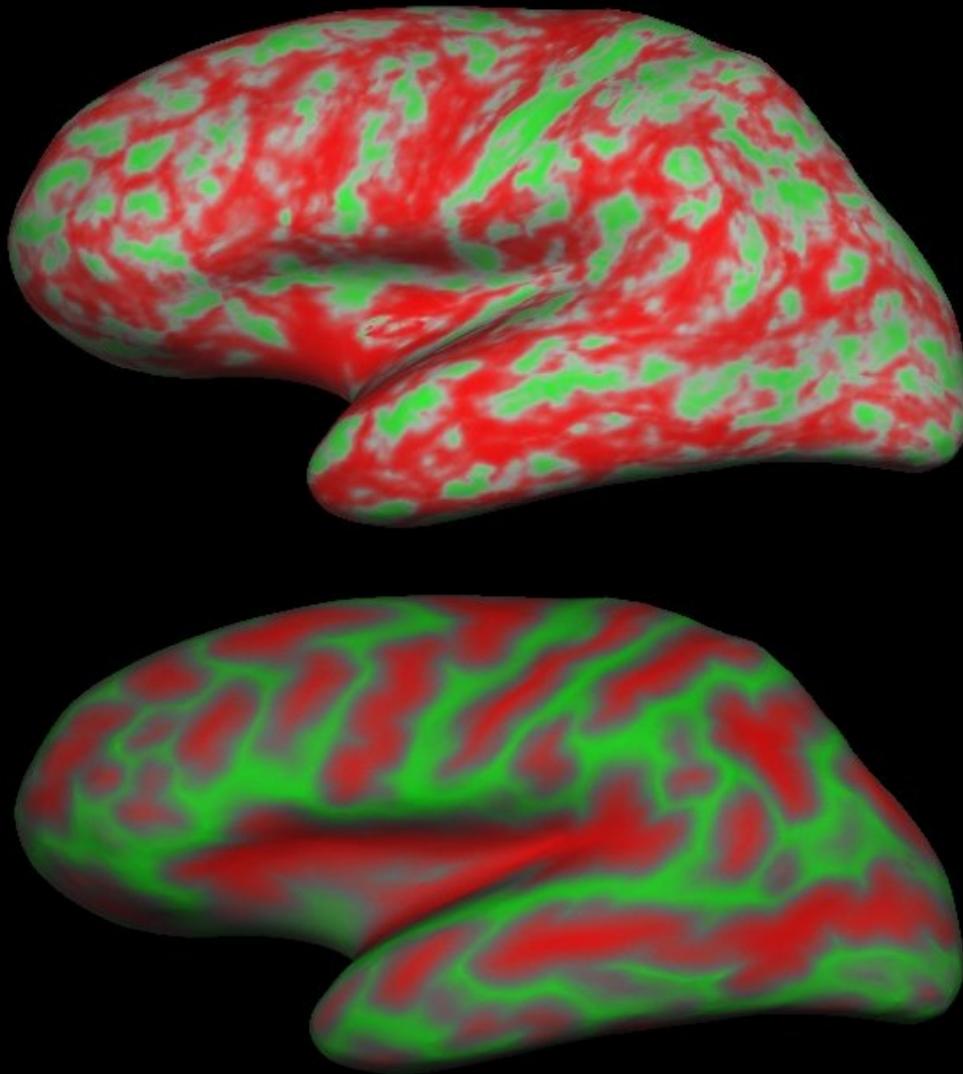


- Circle tangent to surface at each vertex
- Curvature measure is $1/\text{radius}$ of circle
- One value per vertex
- Signed (sulcus/gyrus)
- Actually use gaussian curvature

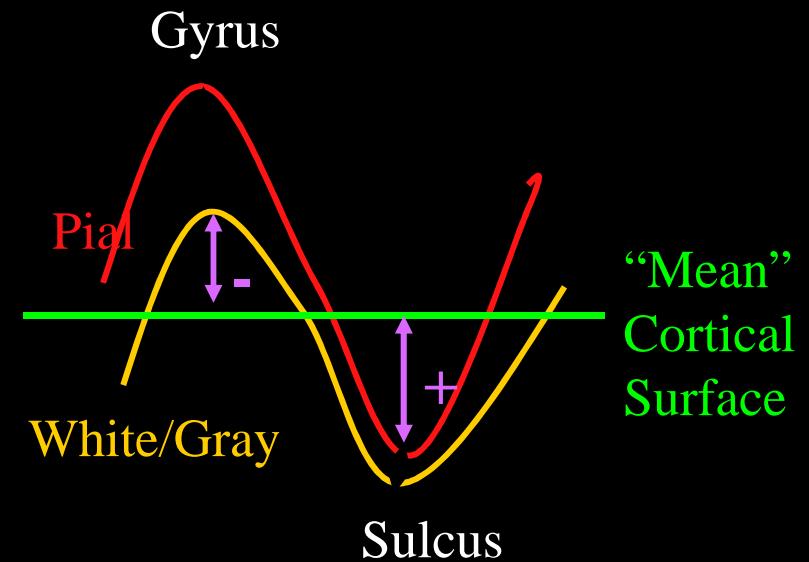


lh.curv, rh.curv

Cortical Morphometry

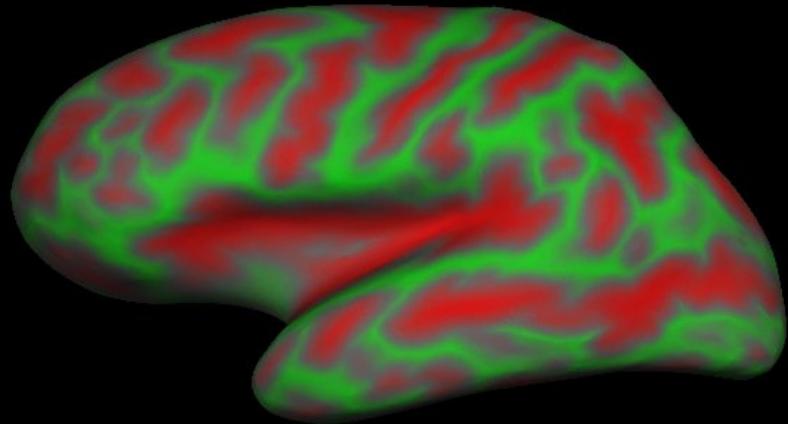


Thickness



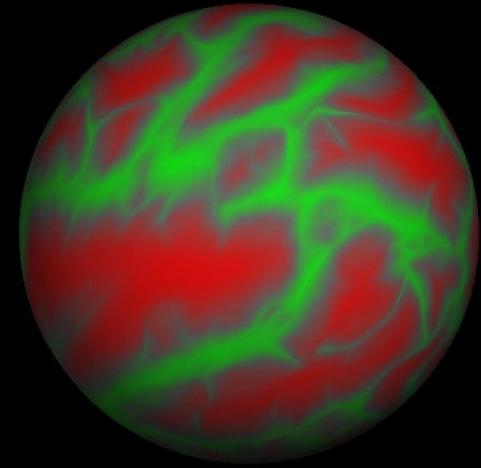
Sulcal Curvature

“Spherical” Registration

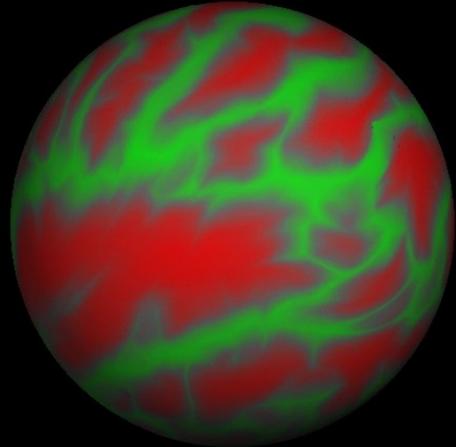


Sulcal Map

Spherical Inflation



High-Dimensional
Registration to
Spherical Template



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

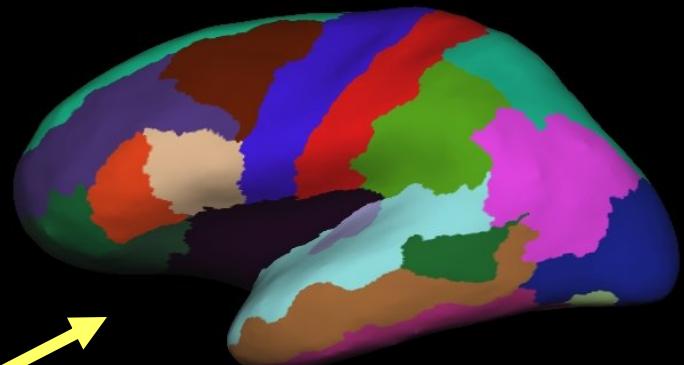
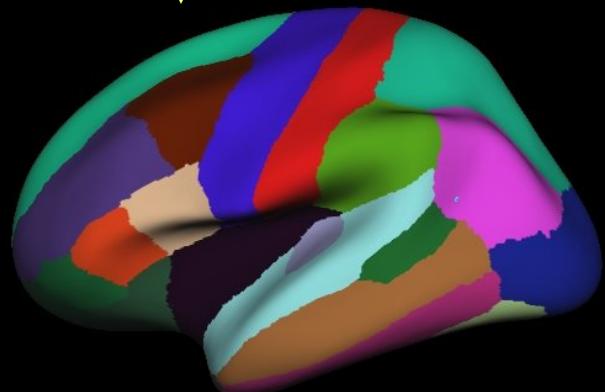
Automatic Cortical Parcellation



Spherical Atlas based on Manual
Parcellations (40 of them)



Map to Individual
Thru Spherical Reg



Fine-tune based on
individual anatomy

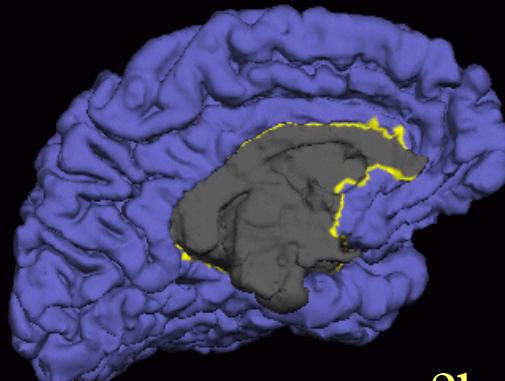
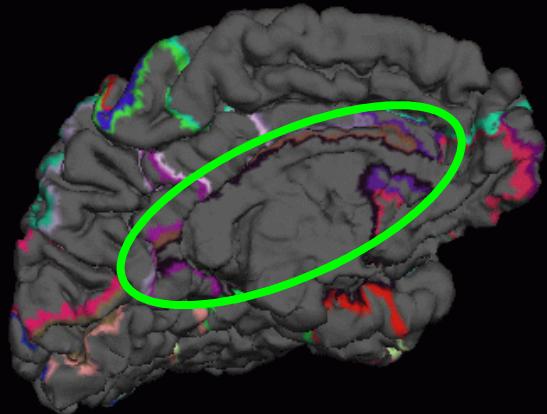
Note: Similar methodology
to volume labeling

More in the Anatomical ROI talk

Non-Cortical Areas of Surface



Amygdala, Putamen, Hippocampus, Caudate, Ventricles, CC



?h.cortex.label

Individual Stages

Volumetric Processing Stages (subjID/mri):

1. Motion Cor, Avg, Conform (`orig.mgz`)
2. Talairach transform computation
3. Non-uniform inorm (`nu.mgz`)
4. Intensity Normalization 1 (`T1.mgz`)
5. Skull Strip (`brain.mgz`)
6. EM Register (linear volumetric registration)
7. CA Intensity Normalization
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`)

Green = Manual Intervention?

recon-all -help

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

Surface Processing Stages (subjID/surf):

14. Tessellate (?h.orig)
15. Smooth1 (?h.smoothwm)
16. Inflate1 (?h.inflated)
17. QSphere (?h.qsphere)
18. Automatic Topology Fixer (?h.orig)
19. Euler Number
20. Smooth2
21. Inflate2
22. Final Surfs (?h.white,?h.pial)
23. Cortical Ribbon Mask
24. Spherical Morph
25. Spherical Registration
26. Spherical Registration
27. Map average curvature to subject
28. Cortical Parcellation (Labeling)
29. Cortical Parcellation Statistics
30. Cortical Parcellation mapped to ASeg

Workflow in Stages

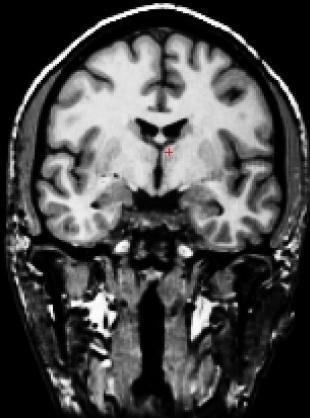
1. `recon-all -autorecon1` (Stages 1-5)
2. Check talairach transform, skull strip, normalization (?)
3. `recon-all -autorecon2` (Stages 6-23)
 4. Check surfaces
 1. Add control points: `recon-all -autorecon2-cp` (Stages 10-23)
 2. Edit `wm.mgz`: `recon-all -autorecon2-wm` (Stages 13-23)
 3. Edit `brain.mgz`: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

Note: all stages can be run individually

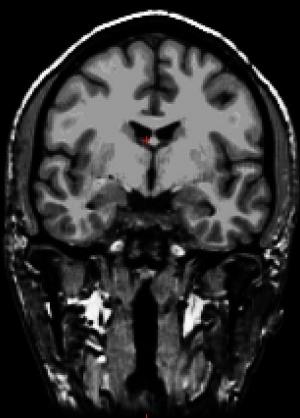
Results

- Volumes
- Surfaces
- Surface Overlays
- ROI Summaries

Volumes



orig.mgz



T1.mgz



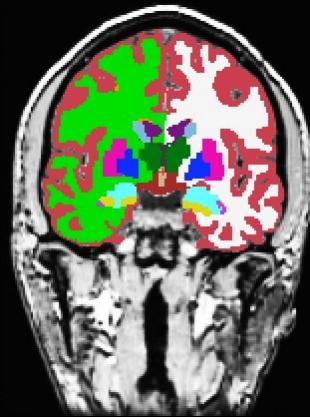
brainmask.mgz



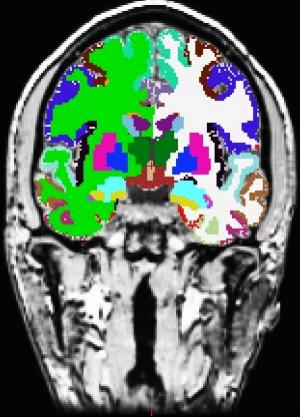
wm.mgz



filled.mgz
Subcortical Mass



aseg.mgz



aparc+aseg.mgz

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

Volume Viewer:
tkmedit

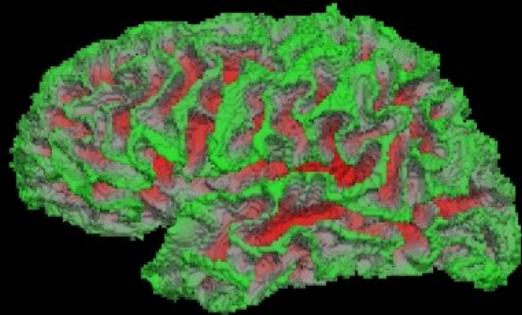
Volume Viewer (tkmedit)

Right

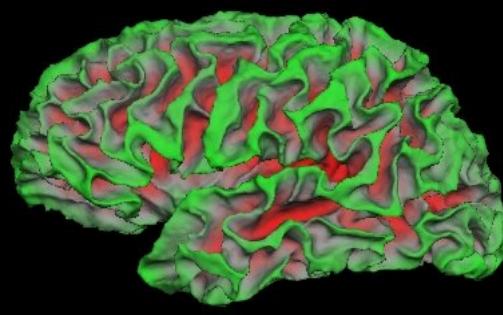
Left



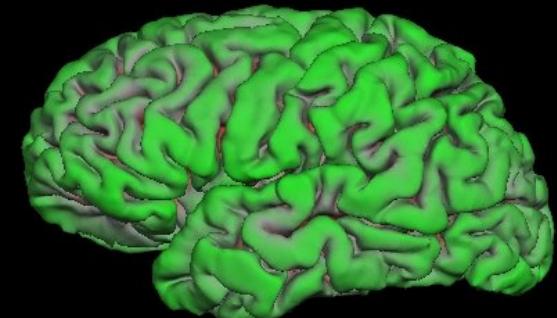
Surfaces



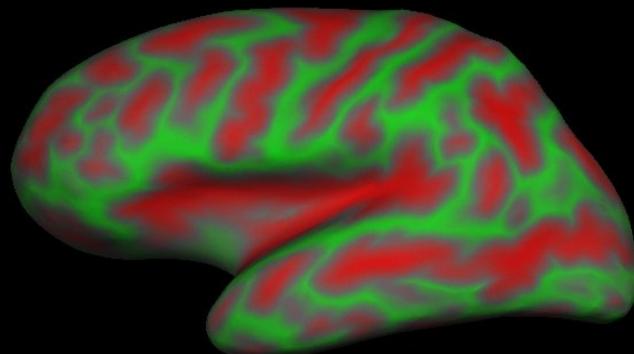
orig



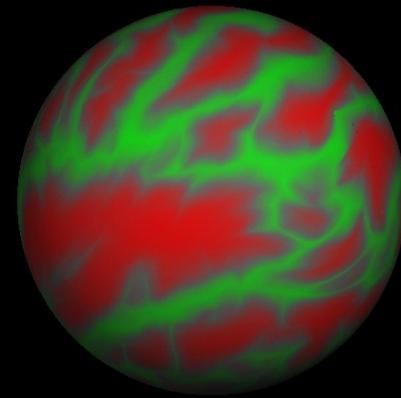
white



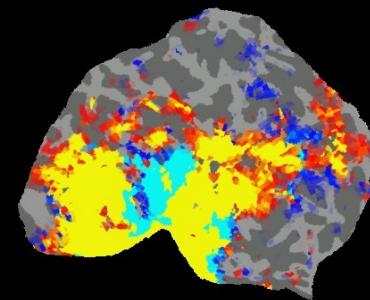
pial



inflated



sphere,sphere.reg



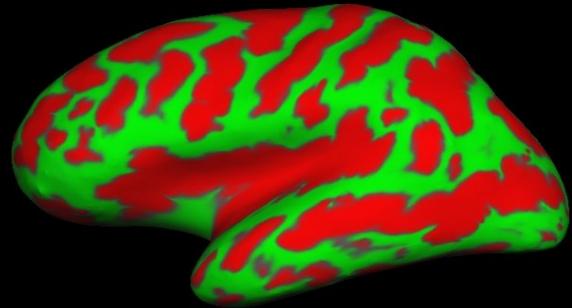
patch (flattened)

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

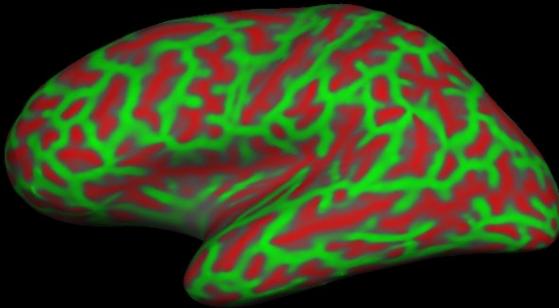
Surface Viewer:
tksurfer

Surface Overlays

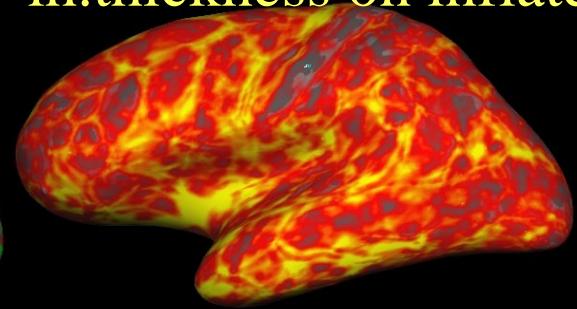
lh.sulc on inflated



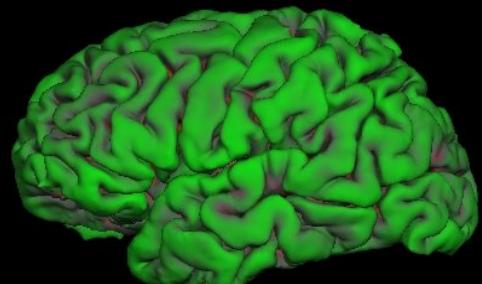
lh.curv on inflated



lh.thickness on inflated



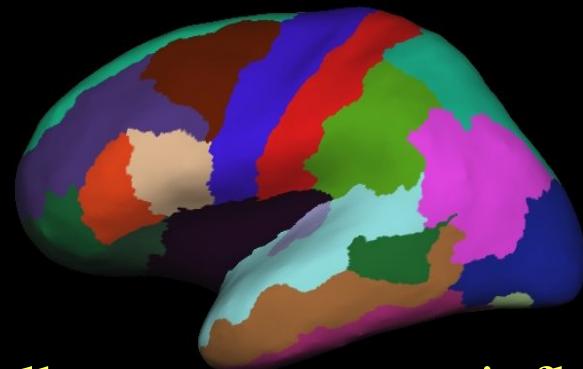
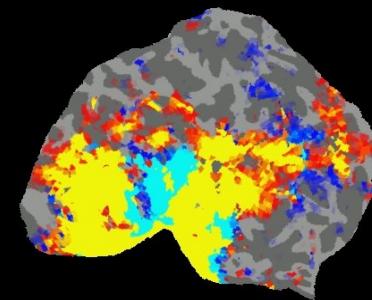
lh.sulc on pial



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.2005.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

- asegestats2table --help
- aparcstats2table --help

More info in Anatomical ROI talk.

Concepts, Ideas, Terms

Bug Report	Sulc	Manual Edit
Reconstruction	Curv	Segmentation
Surface Mesh	Thickness	Parcellation
Subcortical Mass	Atlas	tkregister2
\$SUBJECTS_DIR	Sphere	register.dat
Subject Id	tkmedit	--help
\$FREESURFER_HOME	tksurfer	Vertex
MGZ File	aseg	FSGD
Conformed	aparc	Painting
Control Point	aparc+aseg	Skull Strip
Topological Defect	aparc.a2005s	wmparc
Intensity Normalization	White surface	
Volume-encoded Surface	Pial surface	

