

FreeSurfer

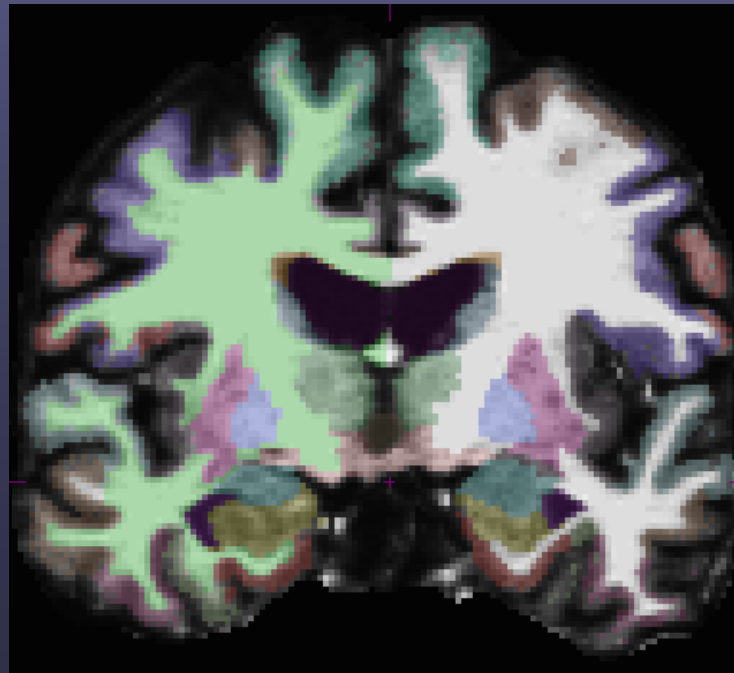
<http://surfer.nmr.mgh.harvard.edu>

Register

Download

Platforms: Linux, Mac, Windows

freesurfer@nmr.mgh.harvard.edu



Analyzing the Individual Subject in FreeSurfer...

What happens?
How do I do that?
Now What?

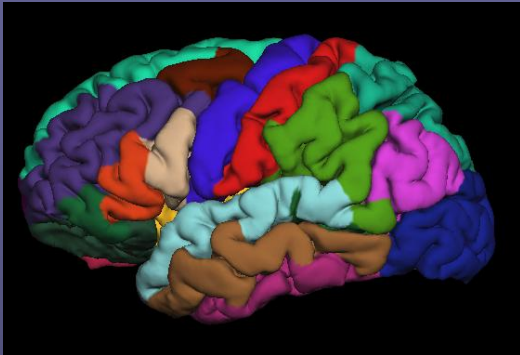
Analyzing the Individual Subject in FreeSurfer...

What happens?

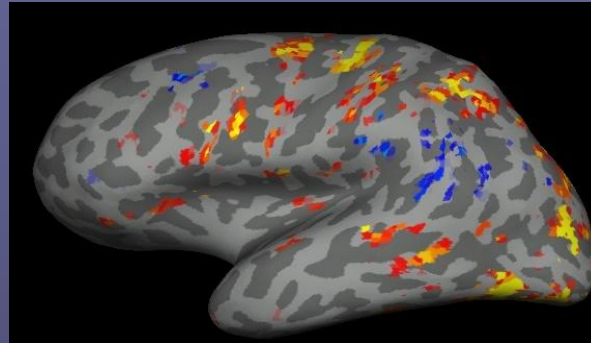
How do I do that?

Now What?

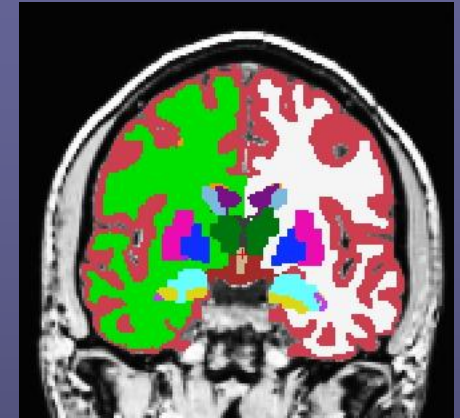
Surface and Volume Analysis



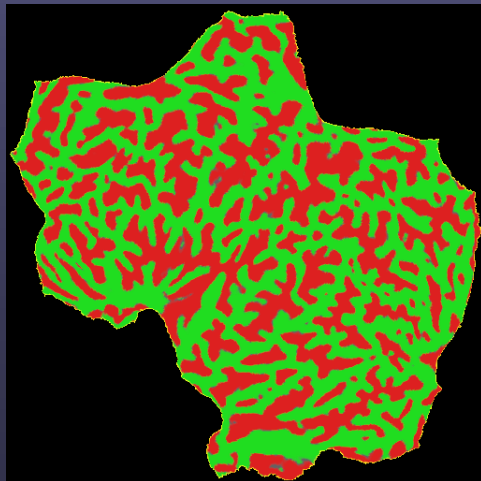
Cortical Reconstruction
and Automatic Labeling



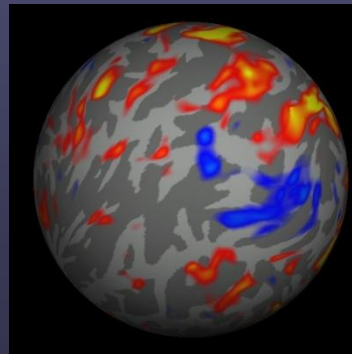
Inflation and Functional
Mapping



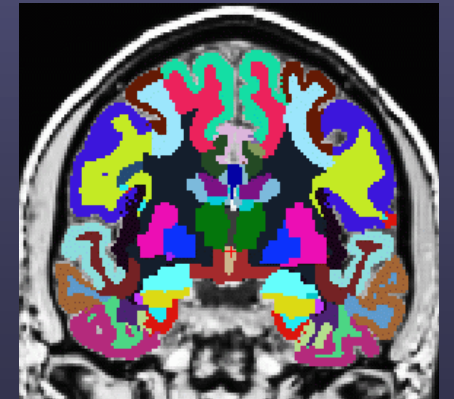
Automatic Subcortical
Gray Matter Labeling



Surface Flattening



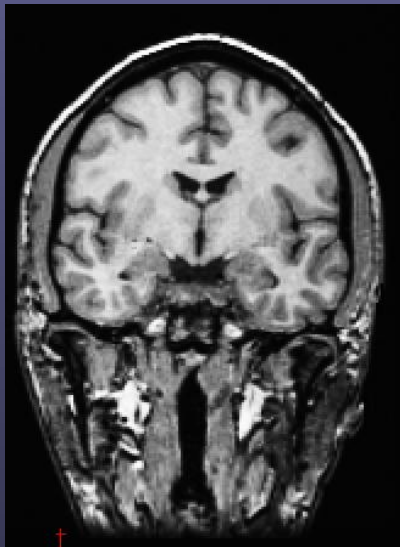
Surface-based Intersubject
Alignment and Statistics



Automatic Gyral White
Matter Labeling

Cortical Surface Reconstruction

FreeSurfer creates computerized models of the brain from MRI data.



Input:
T1-weighted (MPRAGE,SPGR)
1mm³ resolution
(.dcm)

Output:
Segmented & parcellated conformed
volume
(.mgz)

MR Anatomy Caveats

Surfaces are only as good as your scan.

- Dependent on data quality
 - Contrast to noise
 - Signal to noise
 - Voxel resolution
- MR Artifacts
 - MR susceptibility
 - MR distortions
- Variations in MR tissue parameters across regions of the brain are altered in different populations

Suggested Morphometry Sequences

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

Analyzing the Individual Subject in FreeSurfer...

Wait...what happens?

How do I do that?

Now What?

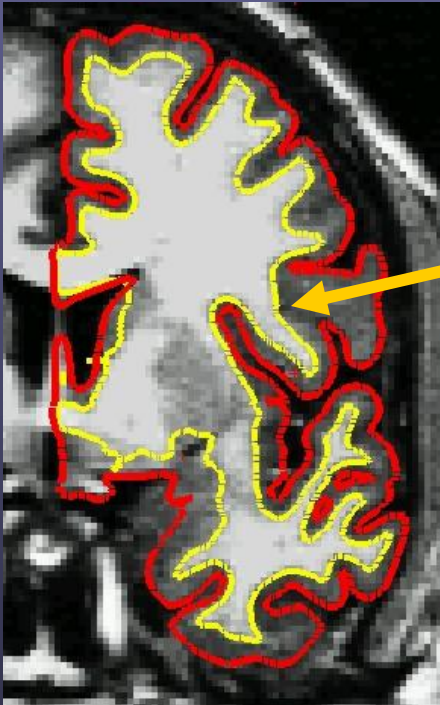
What Happens During Cortical Surface Reconstruction?

- Finds wm/gray boundary – white surface
- Finds gm/CSF boundary – pial surface
- Subcortical Segmentation
- Cortical Parcellation
- Generates surface-based cross-subject registration

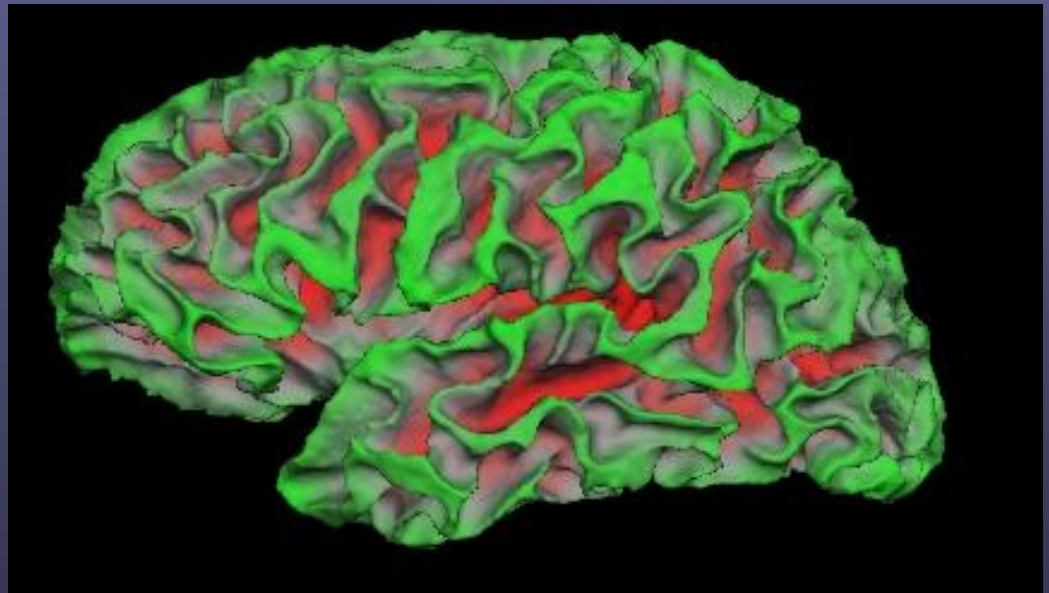
What Happens During Cortical Surface Reconstruction?

- Finds wm/gray boundary – white surface

one slice



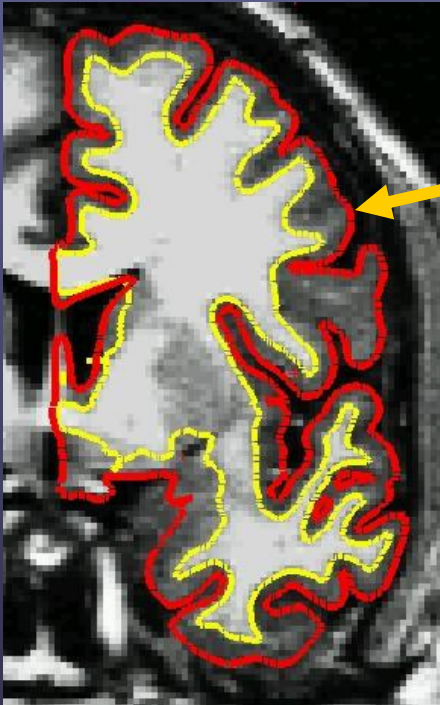
entire brain



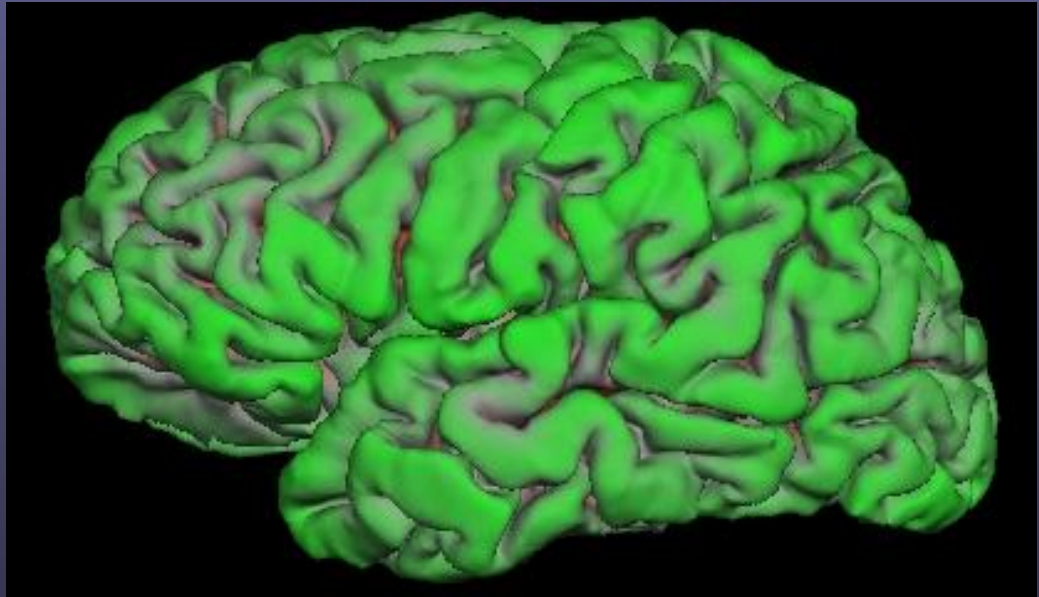
What Happens During Cortical Surface Reconstruction?

- Finds gm/CSF boundary – pial surface

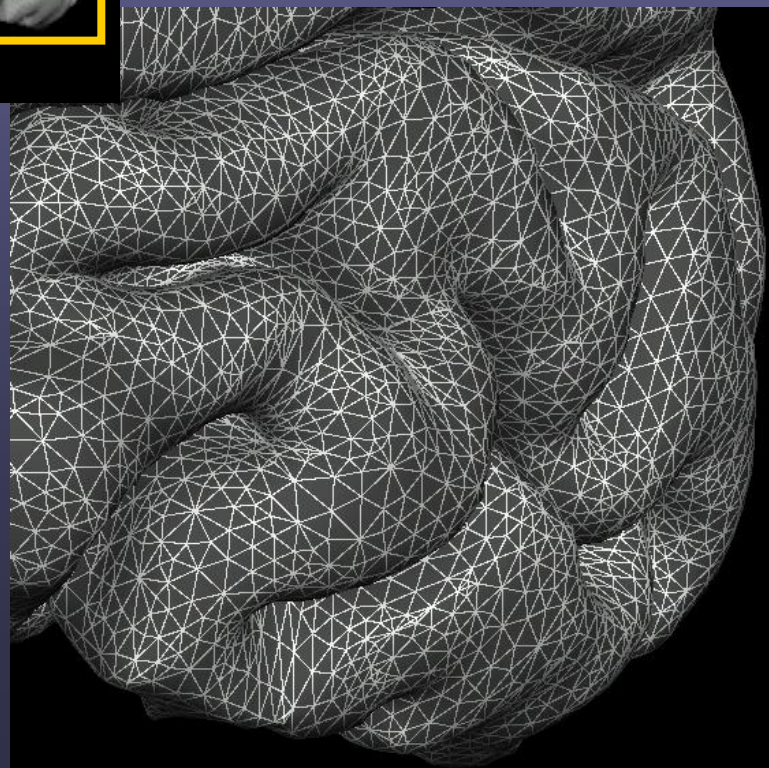
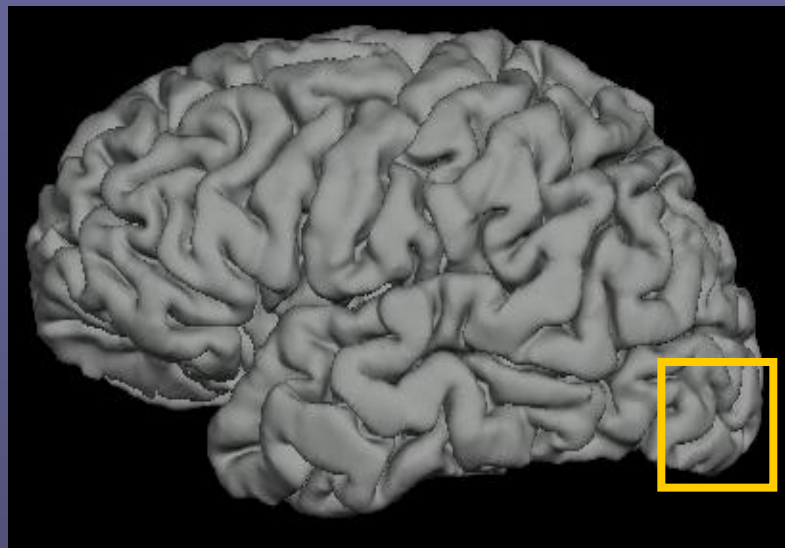
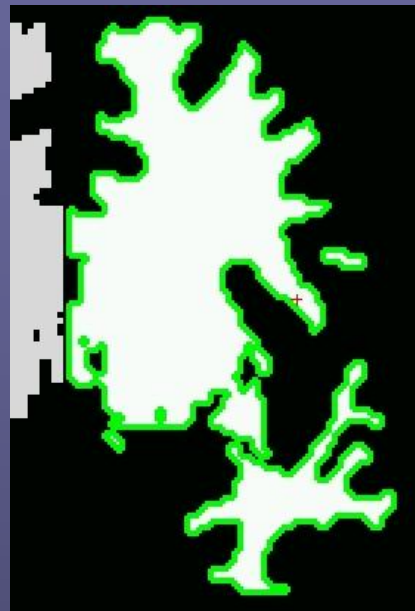
one slice



entire brain

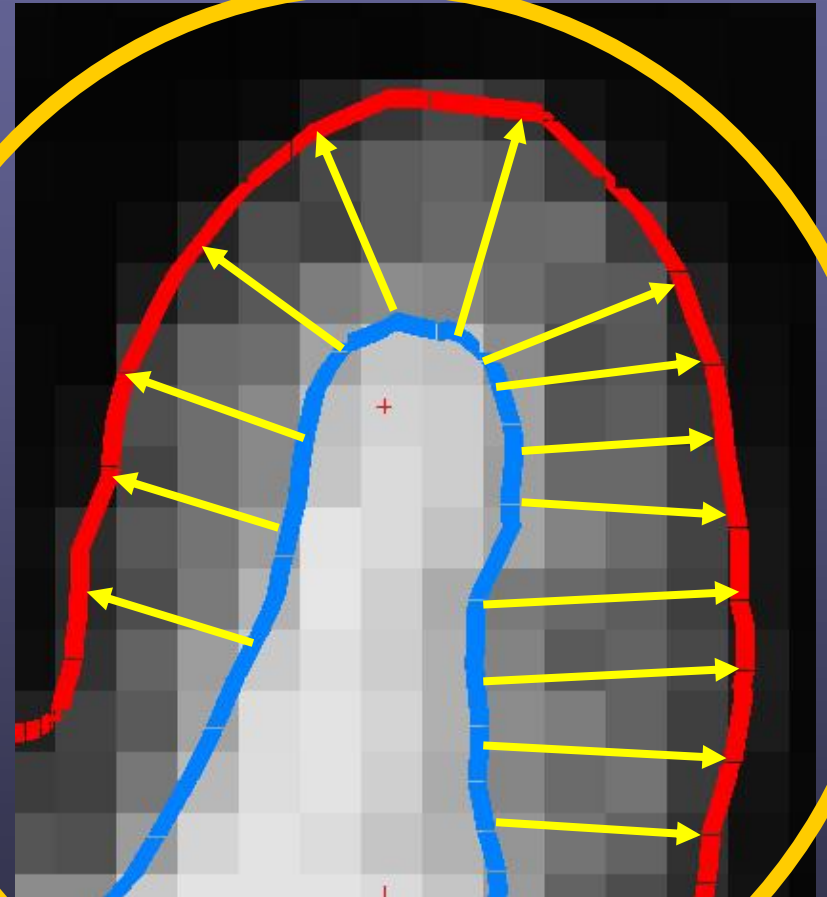
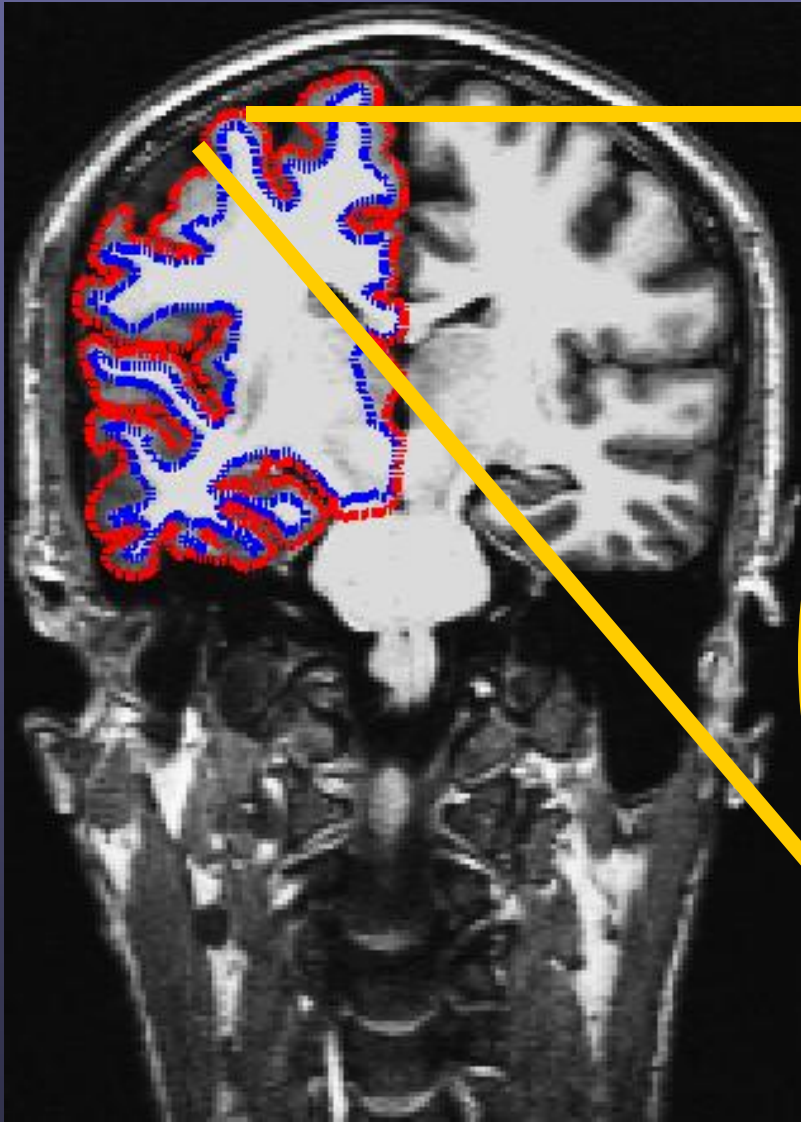


Surface Model



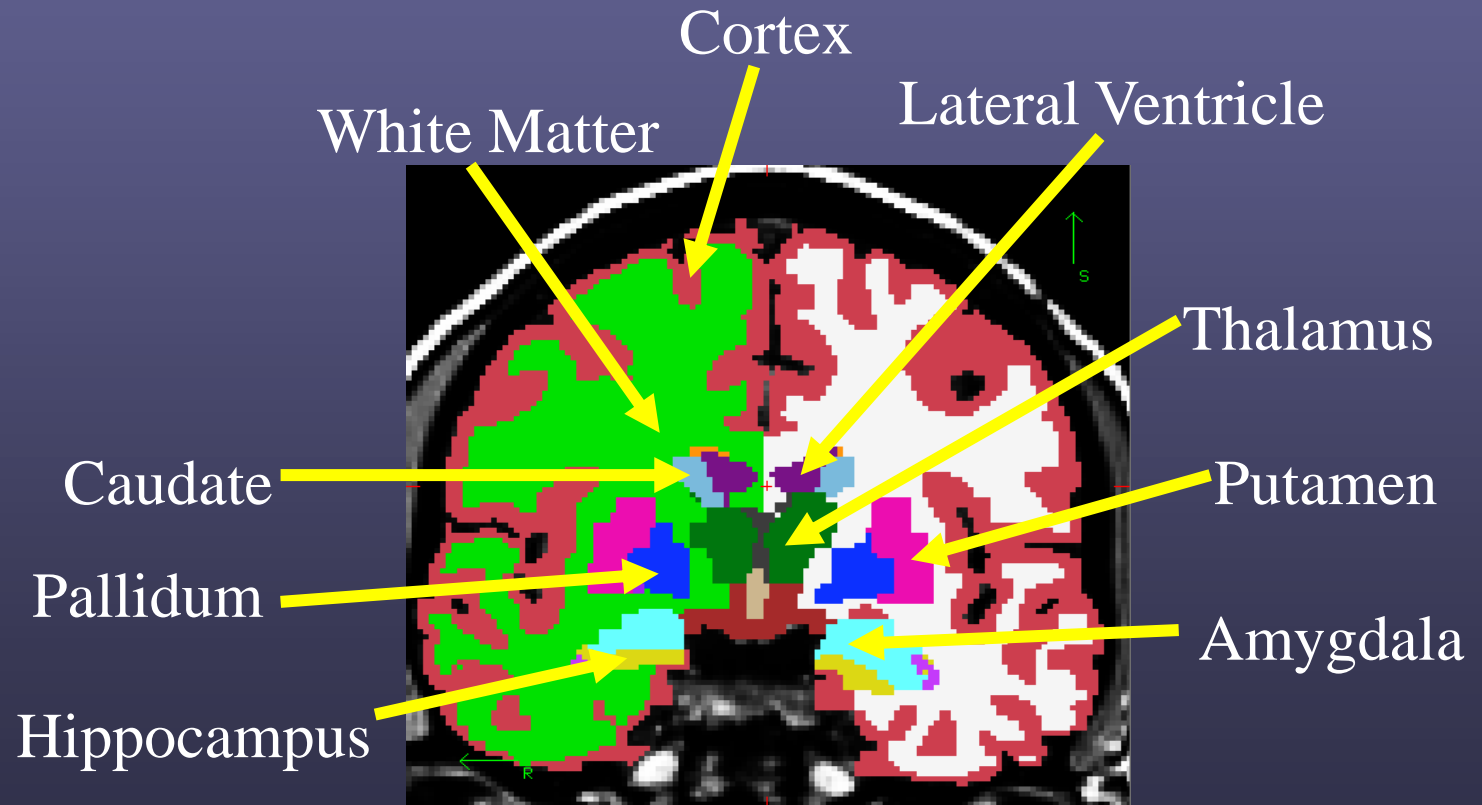
- Mesh of triangles gives a measurable size
- Allows us to measure Area, Curv., Thickness (distance b/w vertices)
- Vertex = point of 6 triangles
- Triangles/Faces ~ 150,000 per hemi
- 1:1 correspondence of vertices
- XYZ at each vertex

Cortical Thickness



What Happens During Cortical Surface Reconstruction?

- Subcortical Segmentation

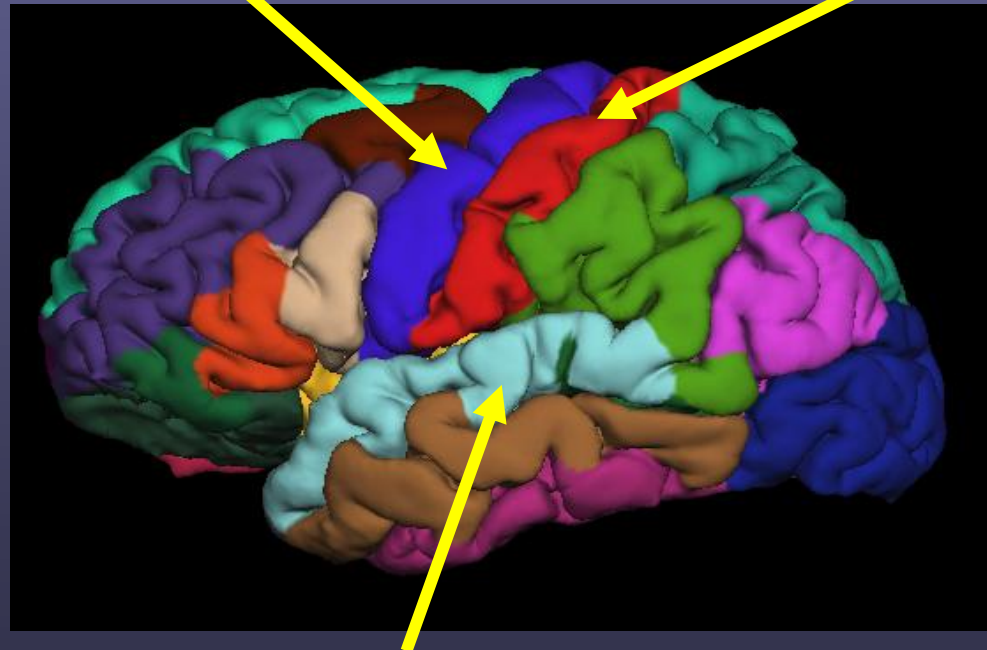


What Happens During Cortical Surface Reconstruction?

- Cortical Parcellation

Precentral Gyrus

Postcentral Gyrus



Superior Temporal Gyrus

What Happens During Cortical Surface Reconstruction?

- Finds white/gray boundary – wm surface
- Finds pial/CSF boundary – pial surface
- Subcortical Segmentation
- Cortical Parcellation
- Generates surface-based cross-subject registration

Analyzing the Individual Subject in FreeSurfer...

Wait...what really happens?

How do I do that?

Now What?

Individual Steps

Volumetric Processing Stages (subjid/mri):

1. Motion Cor, Avg, Conform (orig.mgz)
2. Talairach transform computation
(transforms/talairach.xfm)
3. Non-uniform inorm (nu.mgz)
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. QSphere (?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

Processing Stream Order

NMR FSdev:

<http://surfer.nmr.mgh.harvard.edu/fswiki/ReconAllDevTable>

FSv5.1:

<http://surfer.nmr.mgh.harvard.edu/fswiki/ReconAllTableStableV5.1>

FSv4.5:

<http://surfer.nmr.mgh.harvard.edu/fswiki/ReconAllTableStablev4>

How to Get Started

Use dicoms from scanner as input to Cortical Reconstruction command:

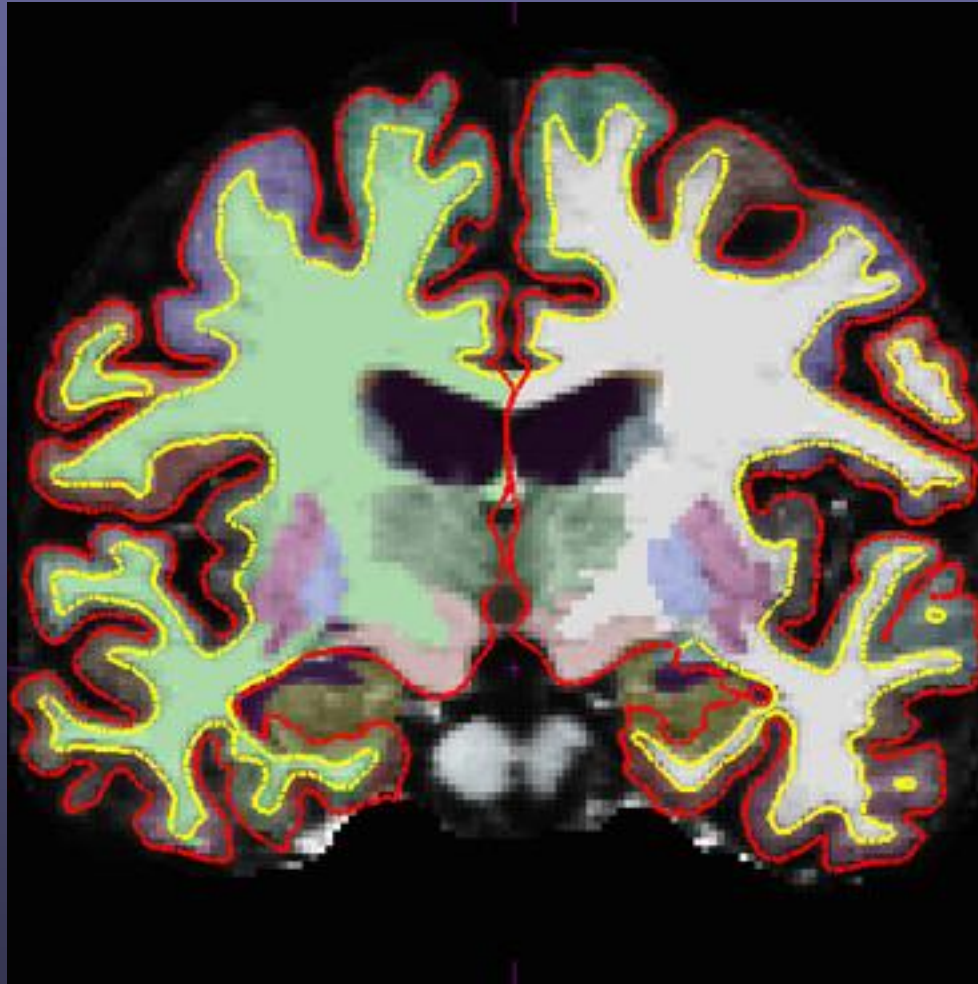
```
recon-all -all -i <input> -s <subject>
```

must do for each subject.

Come back in 15-20 hours ...

Check your results – accurate to the tissue boundaries?

Output of Cortical Surface Reconstruction



Reconstruction Stages

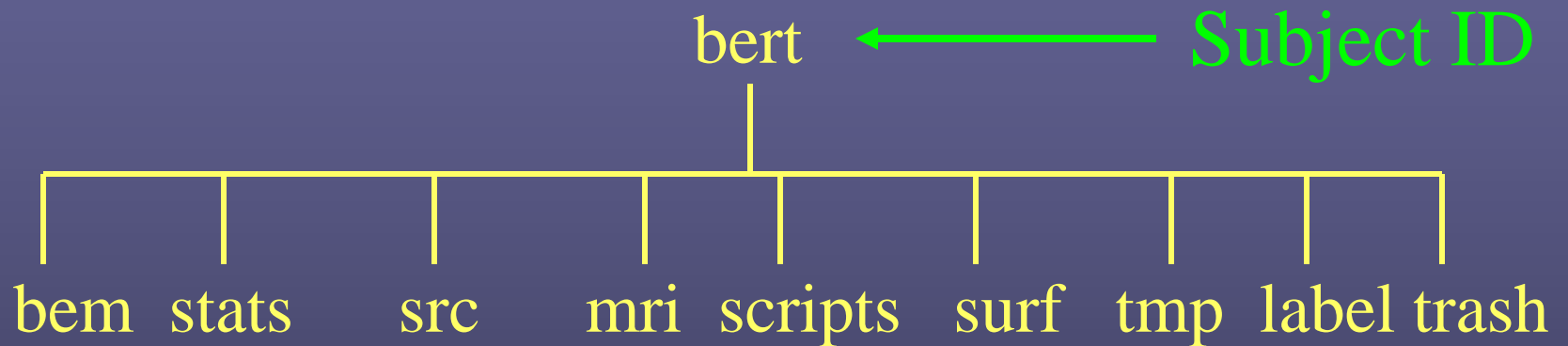
recon-all is broken into three stages

- autorecon1
- autorecon2
- autorecon3

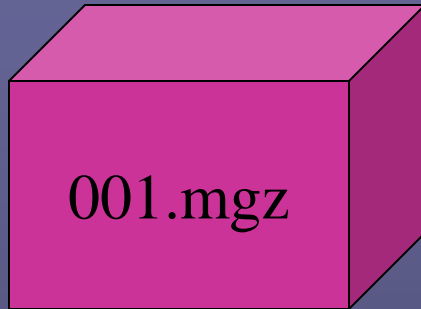
these 3 stages are equivalent to -all

FreeSurfer Directory Tree

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



MGZ File Format



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

• Eg, Typical Anatomical Scan Volume: 256 x 256 x 128 x 1

• *FreeSurfer can read/write:*
NIFTI, Analyze, MINC
Careful with NIFTI! (has
32k column limit; surfaces
could be more)

• *FreeSurfer can read:*
DICOM, Siemens
IMA, AFNI

-autorecon1

Volumetric Processing Stages (subjid/mri):

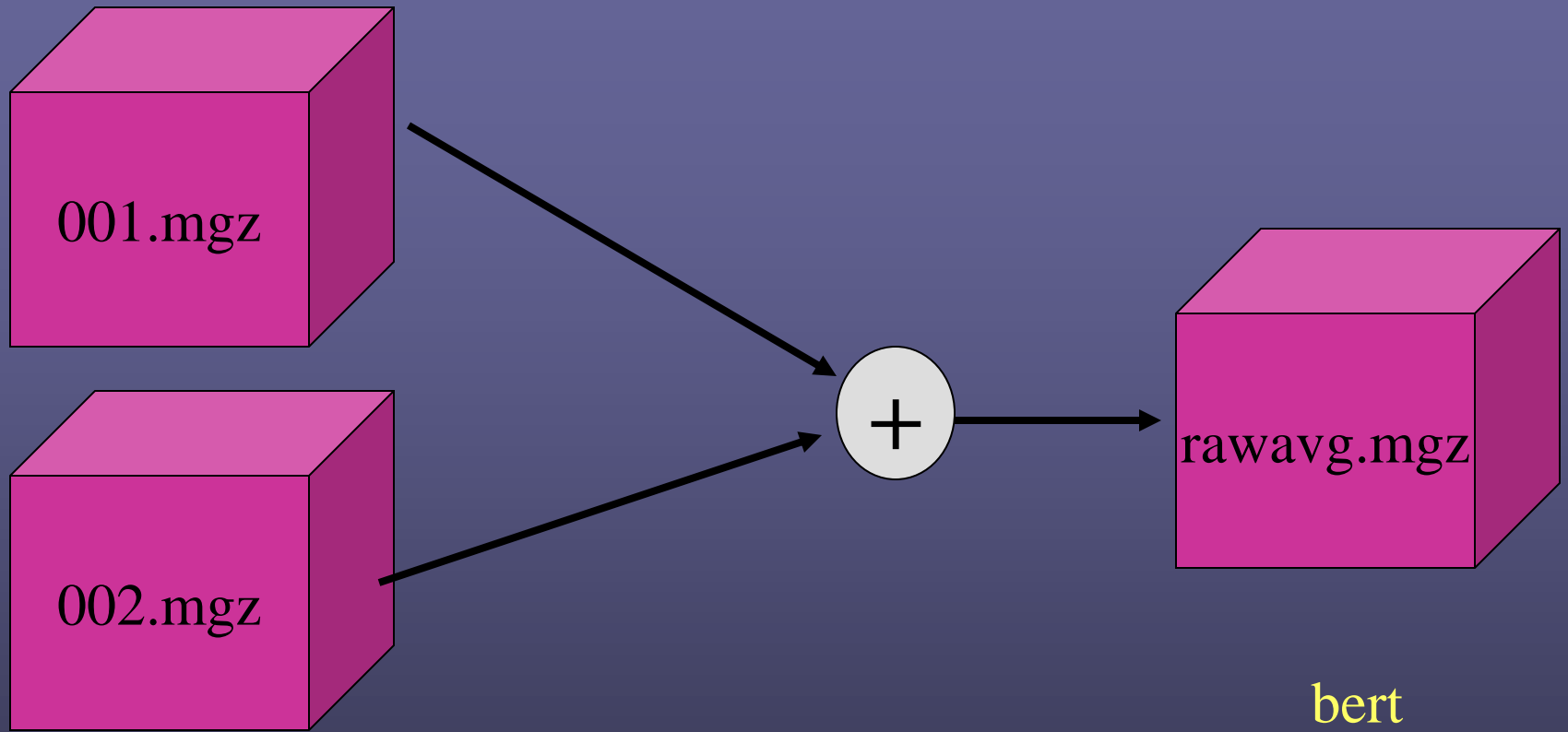
1. Motion Cor, Avg, Conform (orig.mgz)
2. Talairach transform computation
(transforms/talairach.xfm)
3. Non-uniform inorm (nu.mgz)
4. Intensity Normalization 1 (T1.mgz)
5. Skull Strip (brainmask.mgz)
6. EM Register (linear volumetric registration)
7. CA Intensity Normalization (norm.mgz)
8. CA Non-linear 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):

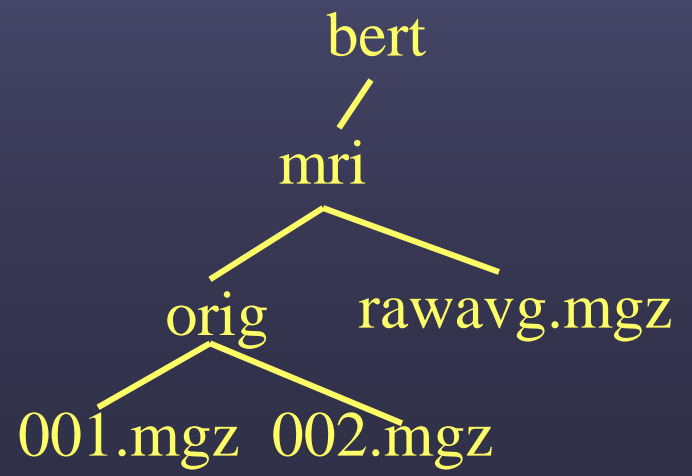
14. Tessellate (?h.orig.nofix)
15. Smooth1
16. Inflate1
17. QSphere (?h.qsphere)
18. Automatic Topology Fixer (?h.orig)
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recon-all -help

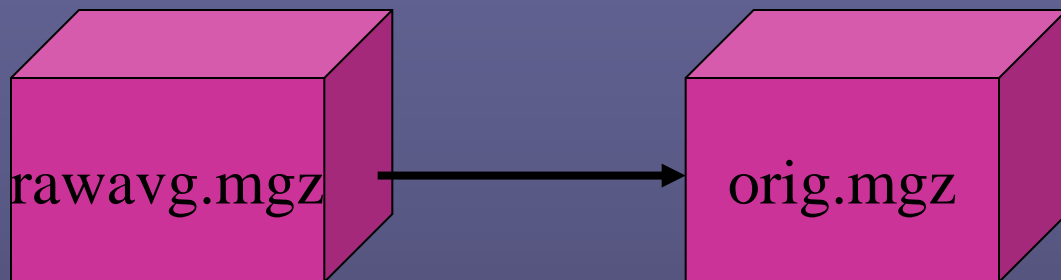
Motion Correction and Averaging



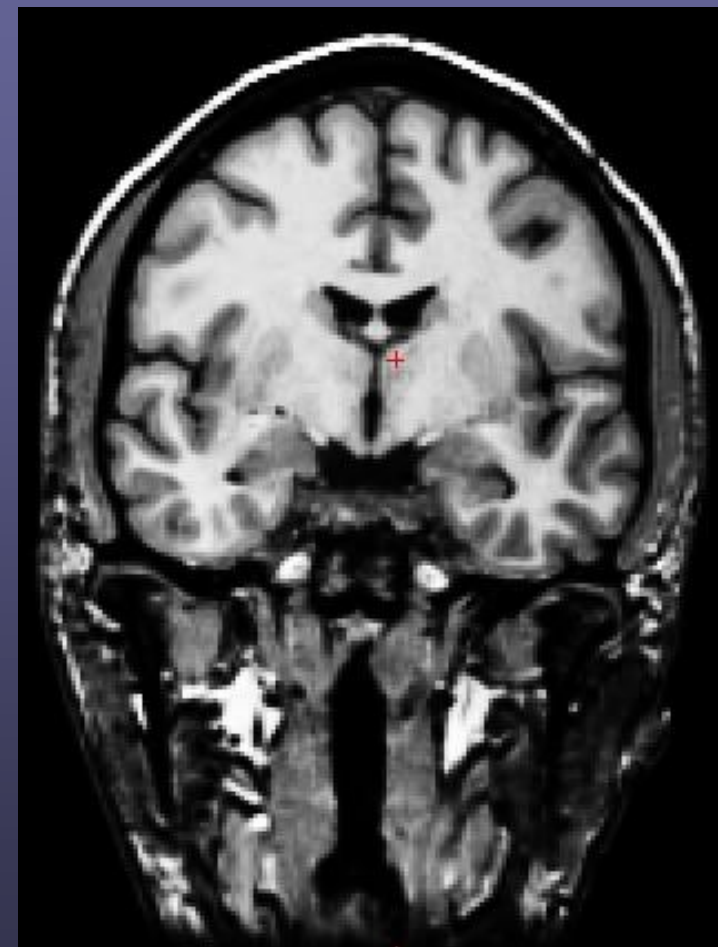
Does not change native resolution.



Conform



Changes to 256^3 , 1mm^3
All volumes will be conformed to
“anatomical space”.



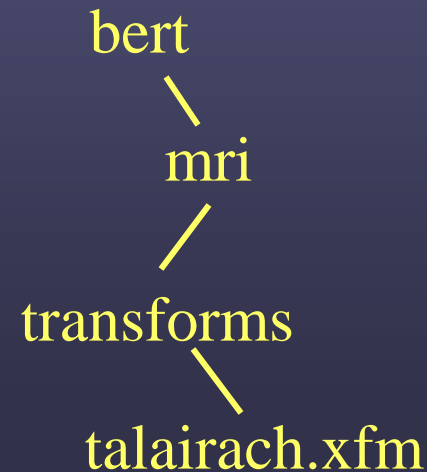
orig Volume

mri_convert -conform

bert
/\
mri
/\
orig.mgz

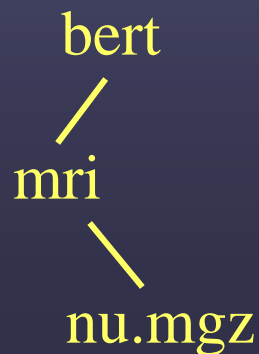
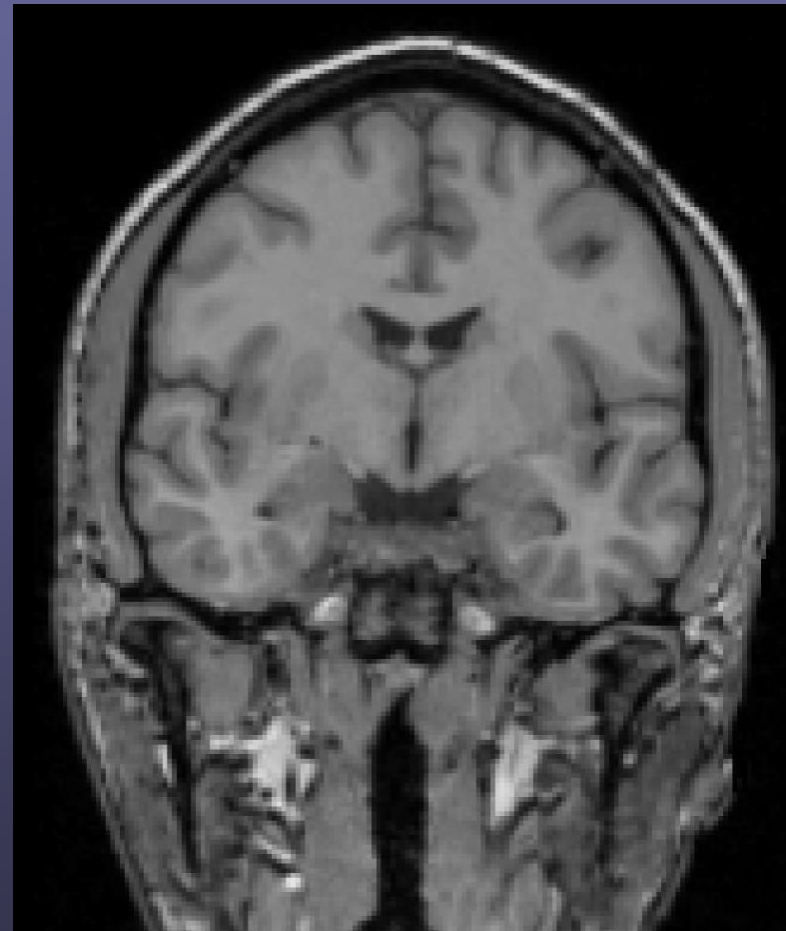
Talairach Transform

- Computes 12 DOF transform matrix
- Does NOT resample
- MNI305 template (compute talairach from this)
- Used to report Talairach coords in papers
- helps with skull strip



Non-Uniform Intensity Correction

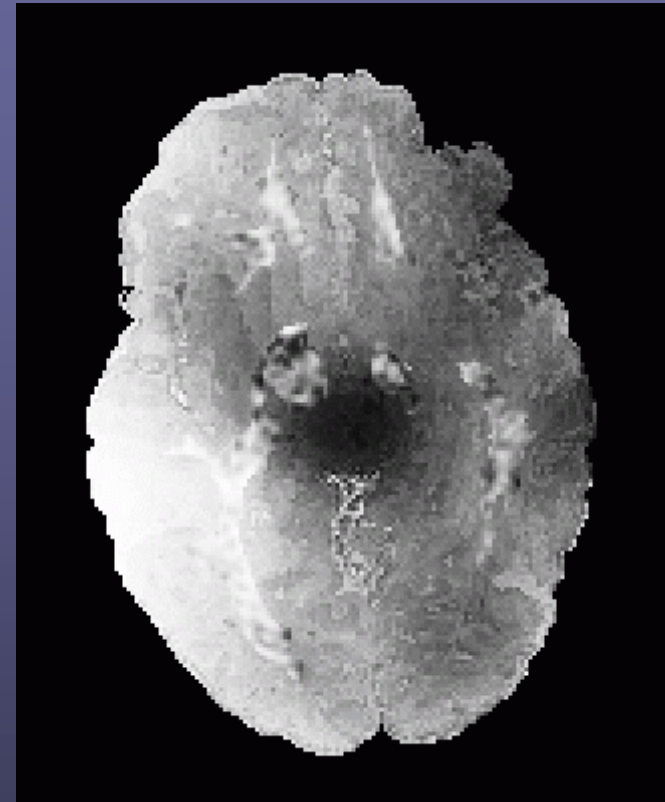
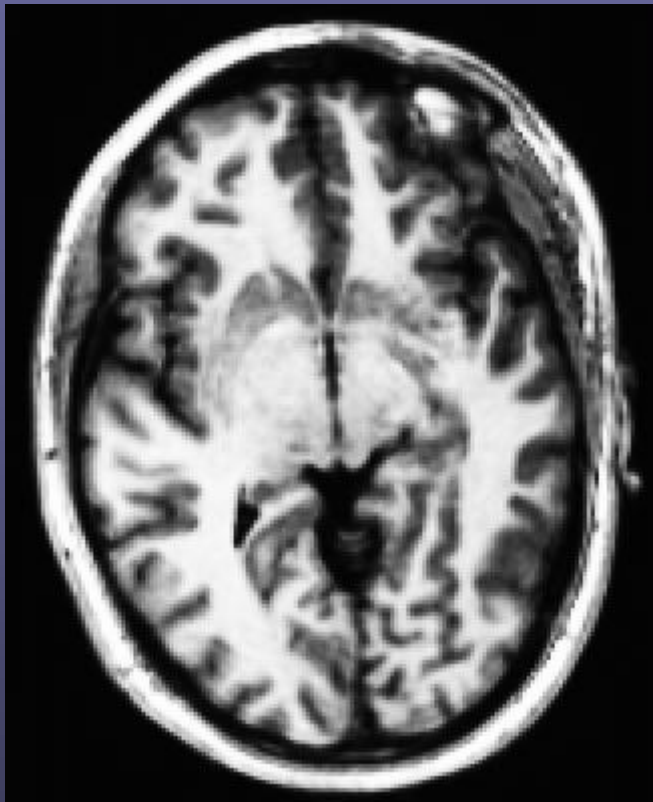
- Uses MNI tool
 - nu_correct
- Corrects intensity non-uniformity (bias fields)



mri_nu_correct.mni

nu Volume

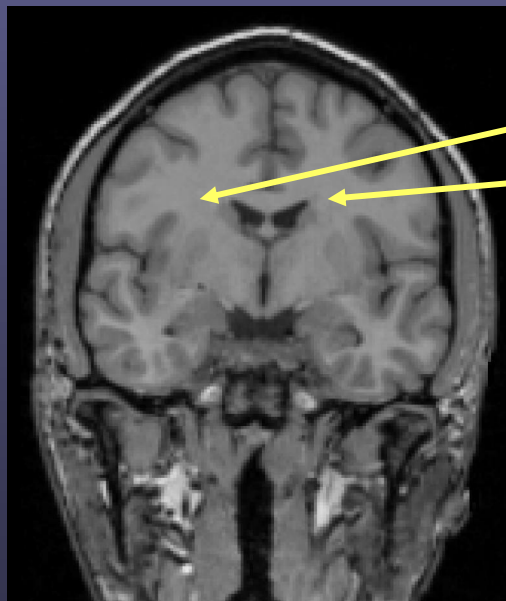
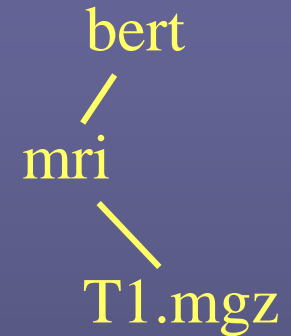
Intensity Bias



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

Intensity Normalization

- Presegmentation (T1.mgz)
 - Most WM = 110 intensity
 - Pre- and Post-Skull Strip

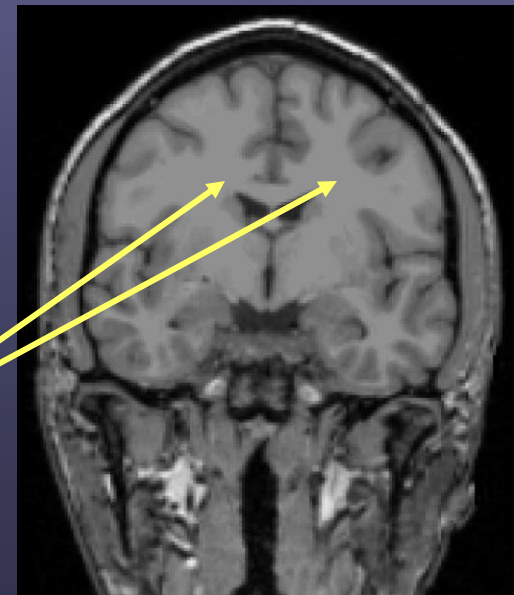


nu Volume

110.9 ± 1.8

108.9 ± 1.5

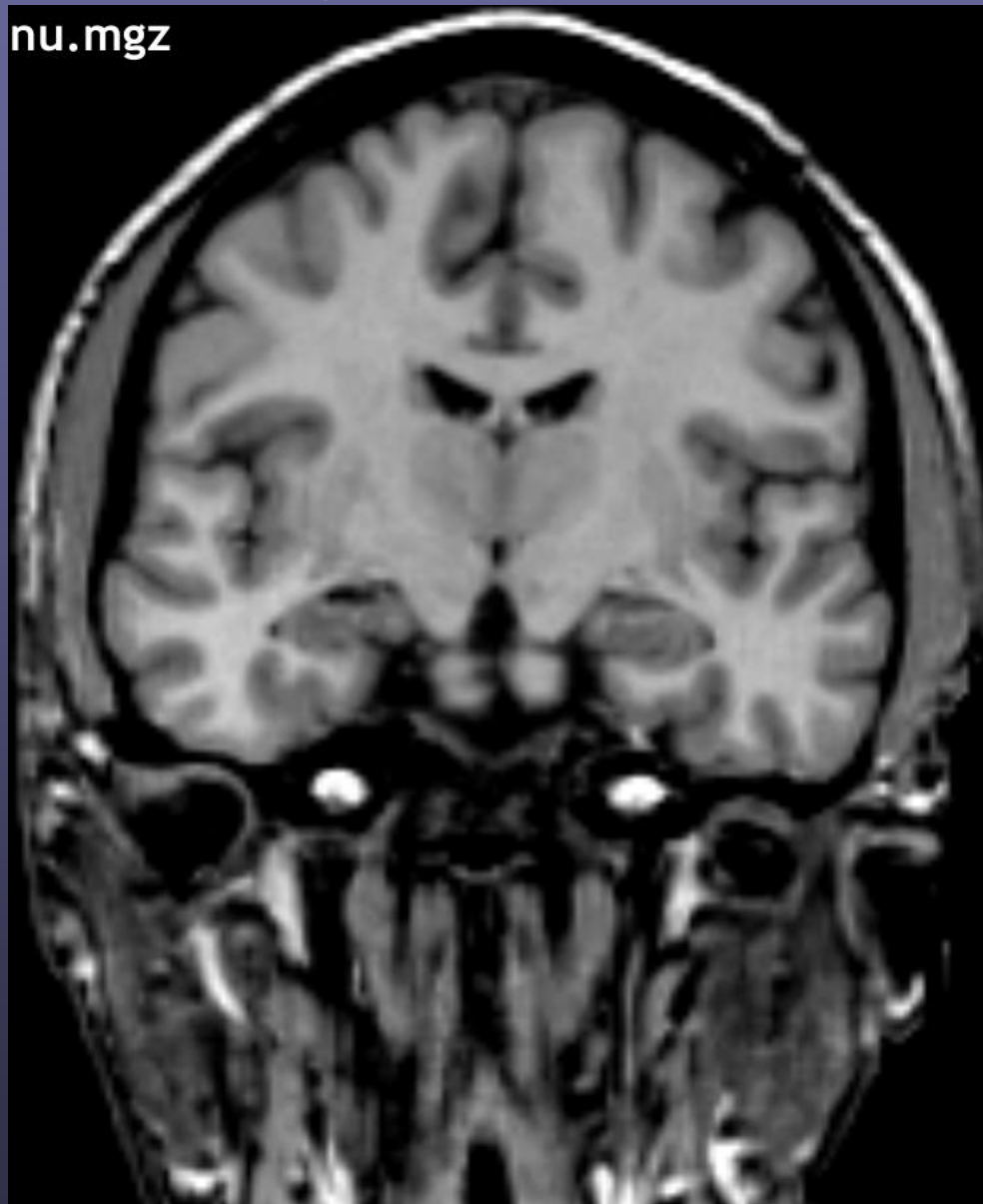
110.0 ± 0.0



T1 Volume

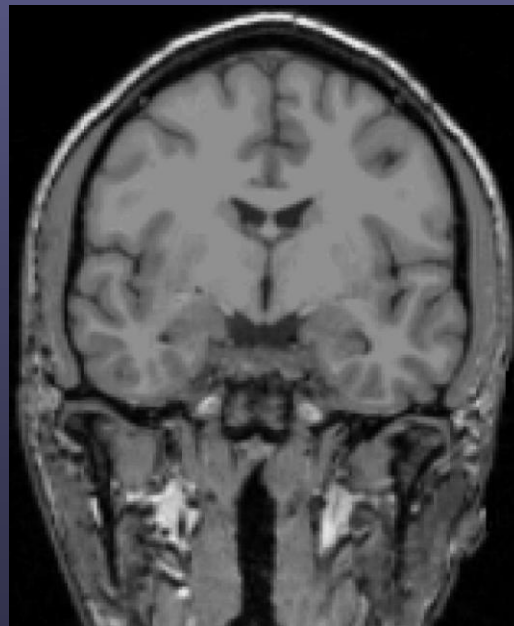
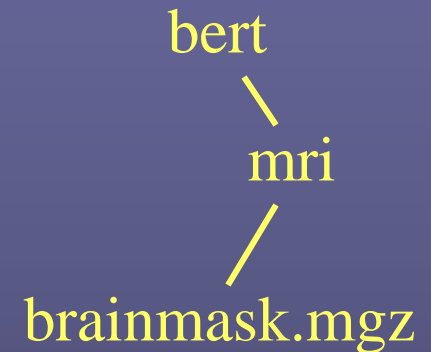
Intensity Normalization

nu.mgz

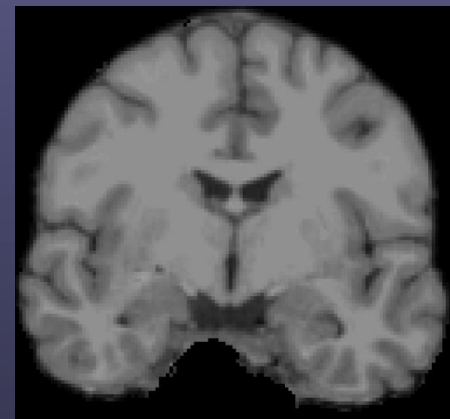


Skull Strip

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



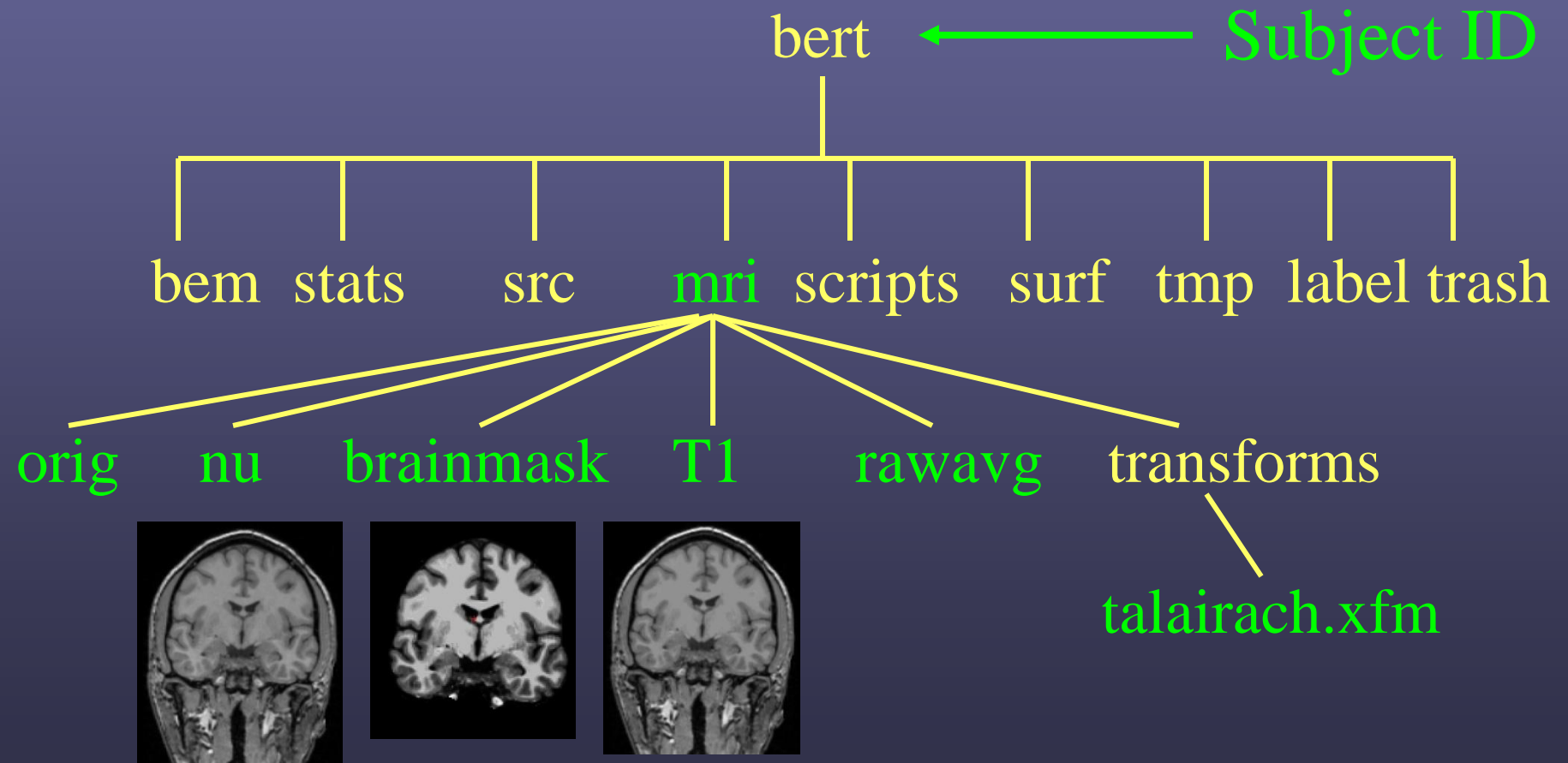
T1 Volume



Brainmask Volume

FreeSurfer Directory Tree

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



-autorecon2

Volumetric Processing Stages (subjid/mri):

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(transforms/talairach.xfm)
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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)

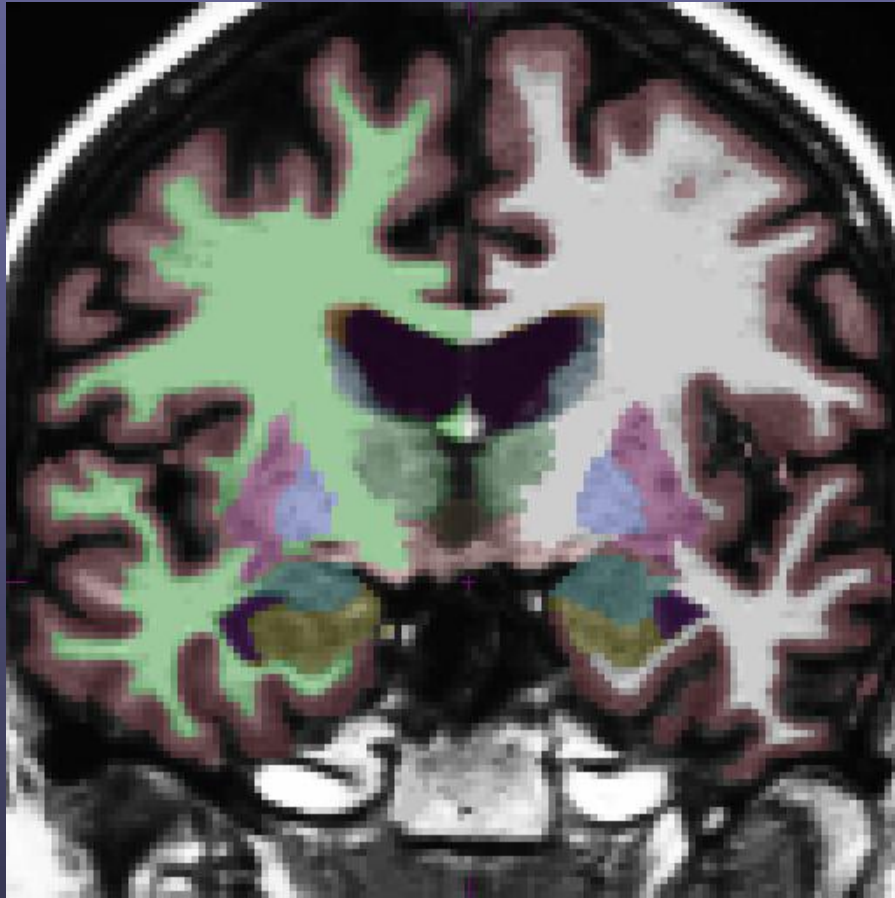
Surface Processing Stages (subjid/surf):

14. Tessellate (?h.orig.nofix)
15. Smooth1
16. Inflate1
17. QSphere (?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: lh processed completely first, then rh.

Automatic Volume Labeling



- Label subcortical structures and wm/gm
- Determine volumes of subcortical structures
- Used to fill in subcortical structures for later steps

aseg.mgz

steps 6-9, 22

(best viewed on norm.mgz)



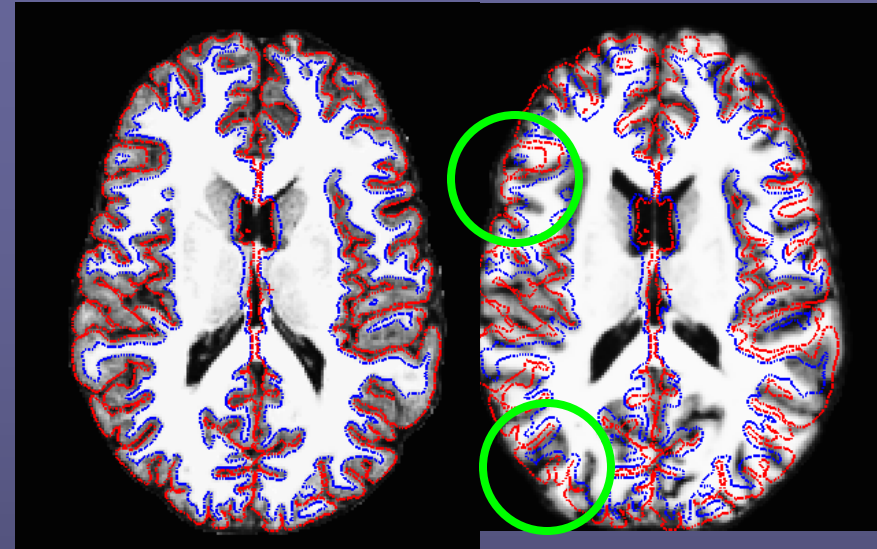
We use atlas + intensity + spatial location + geometric info + neighboring voxels + other info...

Why not just register to an ROI Atlas?



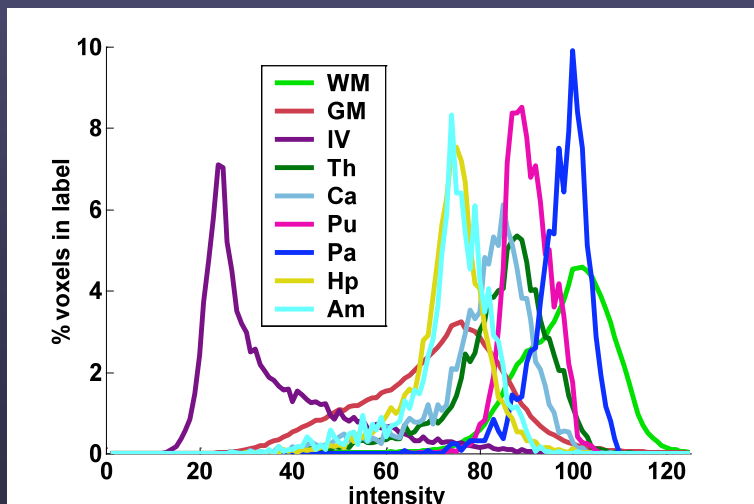
Problems with Affine (12 DOF) Registration

• ROIs need to be individualized.



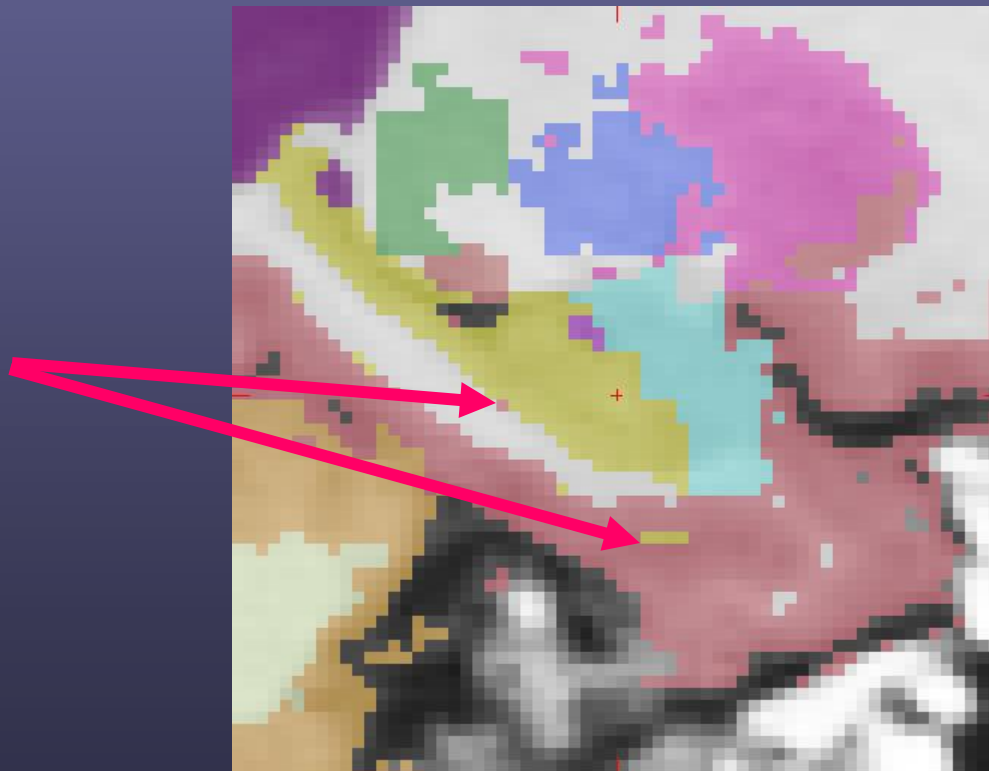
Gaussian classifier array atlas

Can't segment on intensity alone



Markov Random Field: Motivation

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



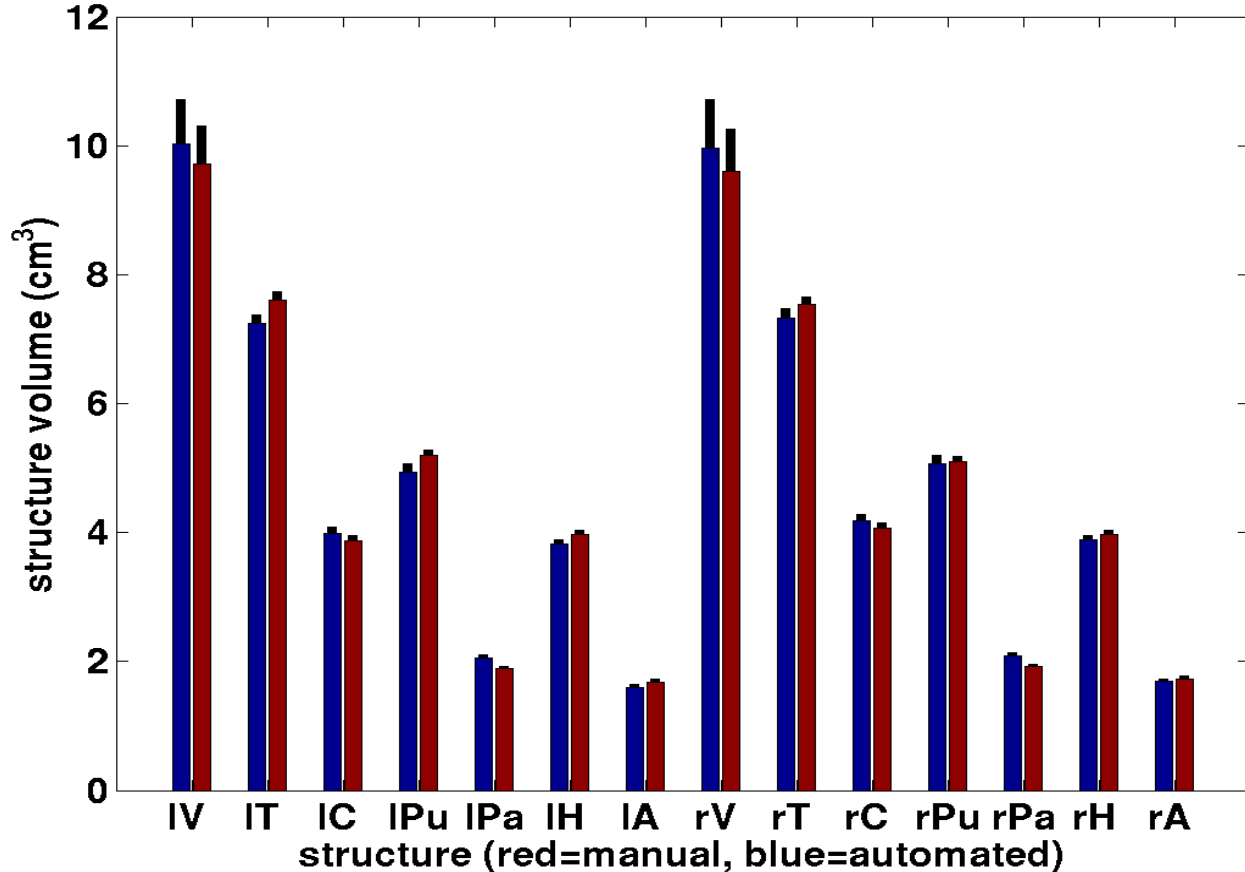
Segmentation: MRF



Prefinal Segmentation

Validation of Volume Labeling *

manual vs. auto structure volumes for normals and schizophrenics (N=59)

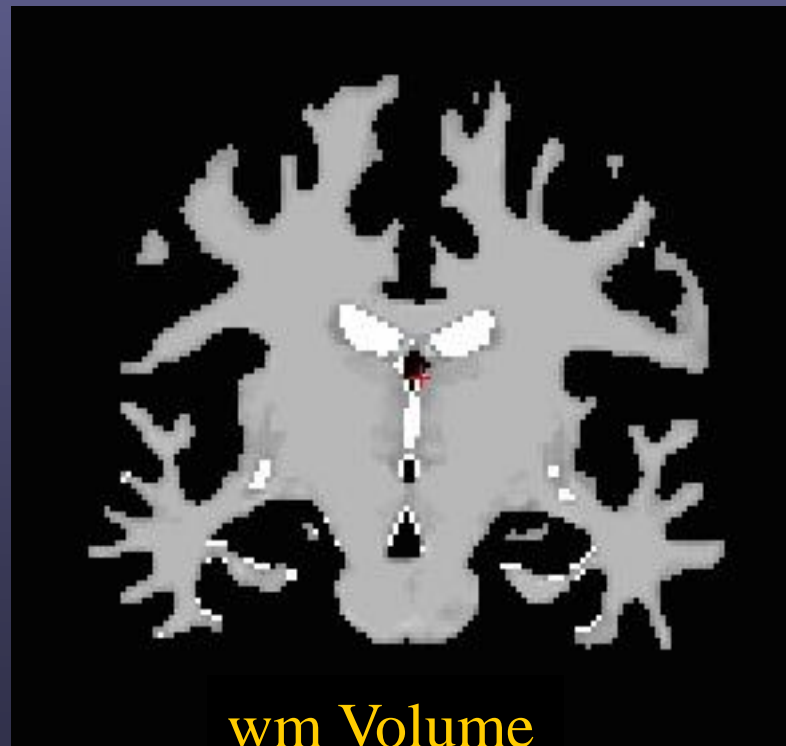


Manual labeling done by Center for Morphometric Analysis (CMA)

*Thanks to Drs Larry Seidman and Jill Goldstein for providing this data.

White Matter Segmentation

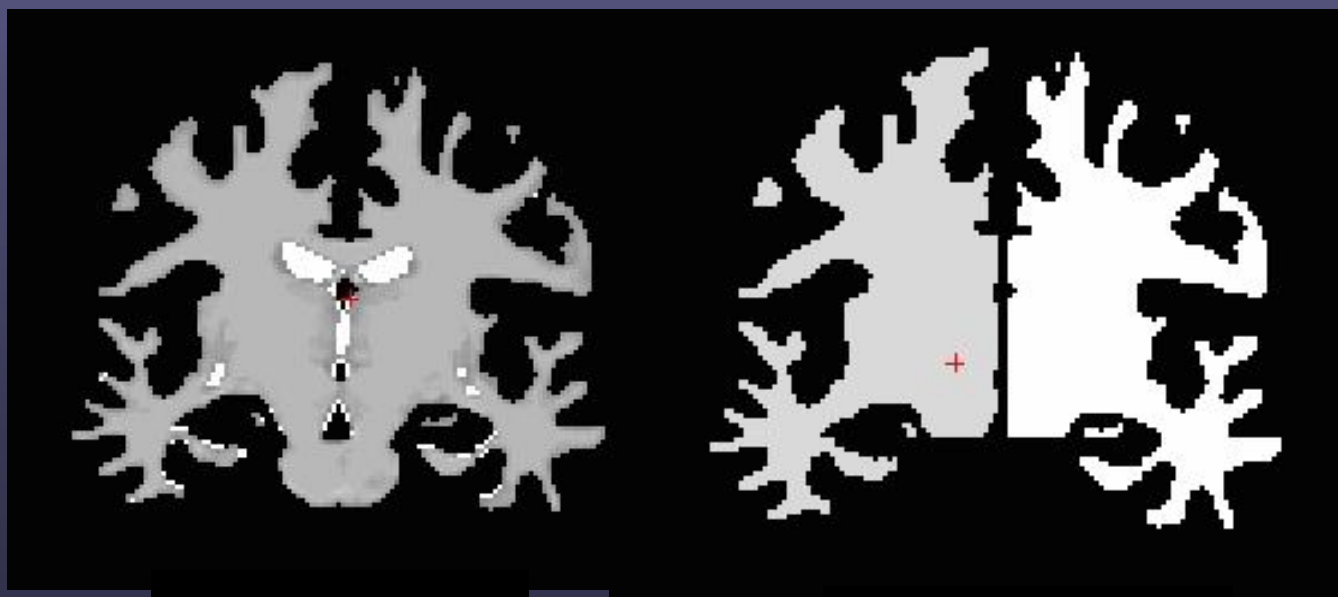
- Separates white matter from everything else
- “Fills in” subcortical structures
- Cerebellum removed, brain stem still there



```
bert  
 \  
  mri  
  /  
wm.mgz
```

Fill and Cut (Subcortical Mass)

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



mri_fill

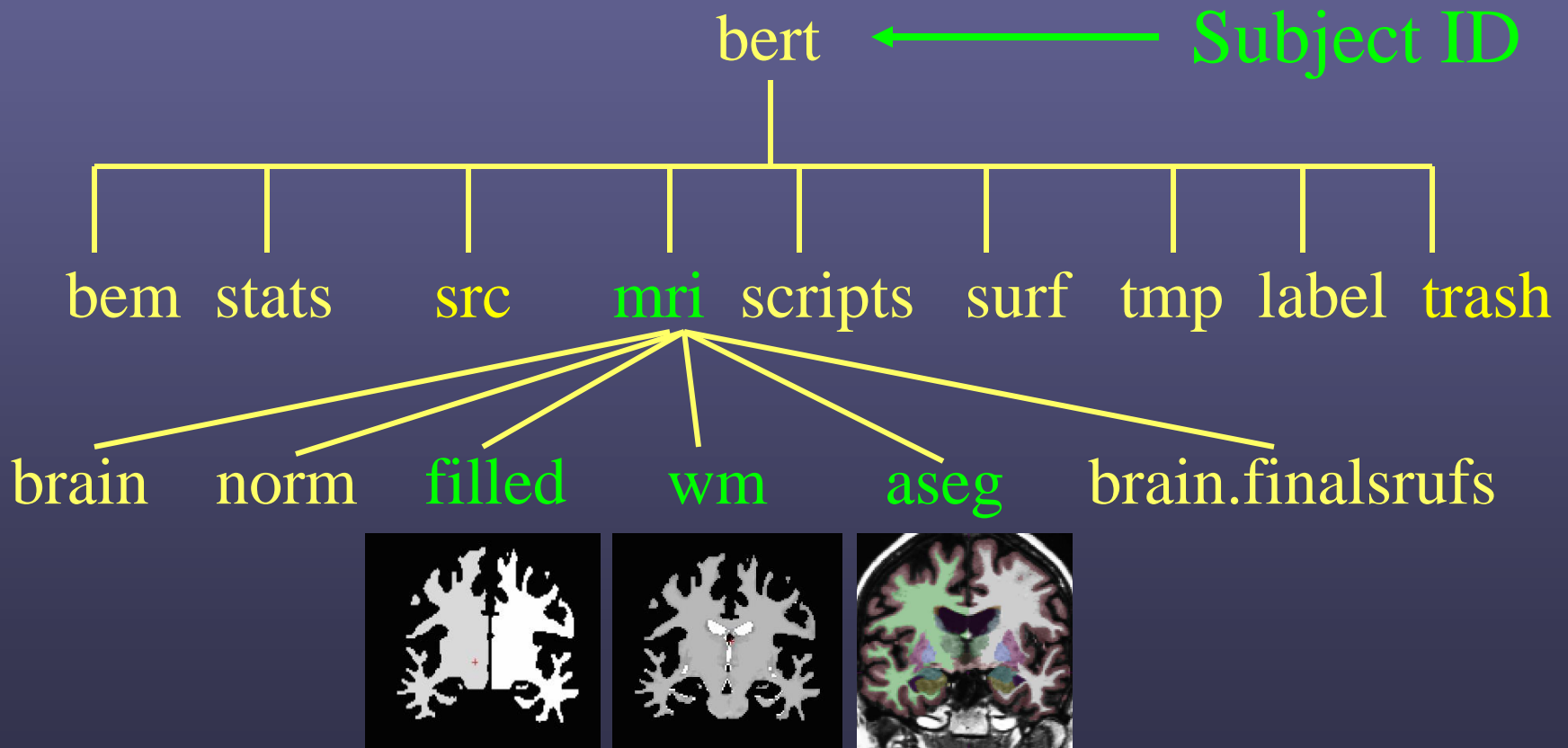
WM Volume

Filled Volume

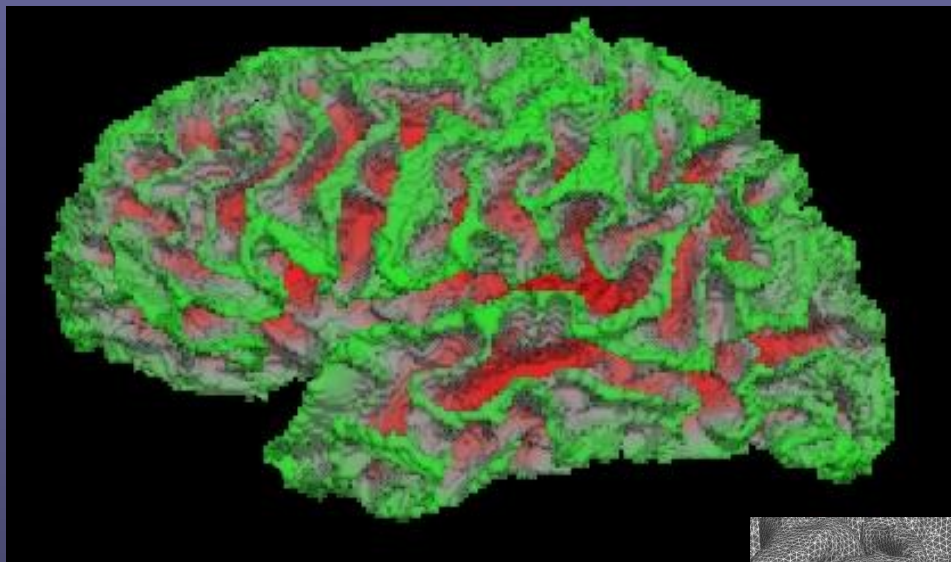
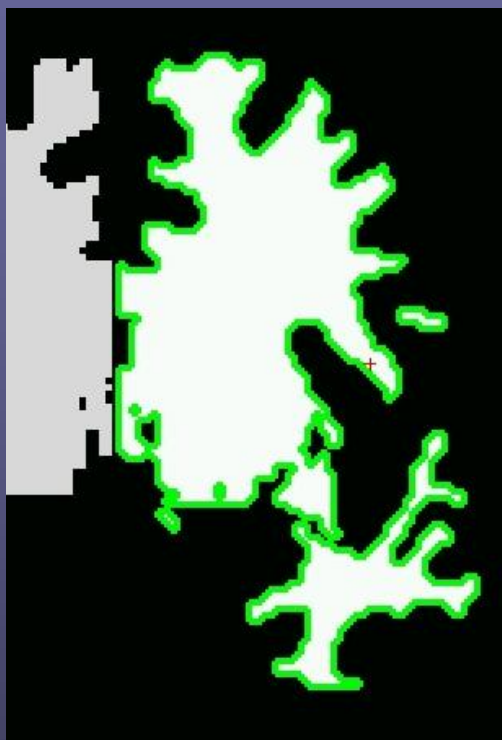
bert
 \
 mri
 /
filled.mgz

FreeSurfer Directory Tree

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

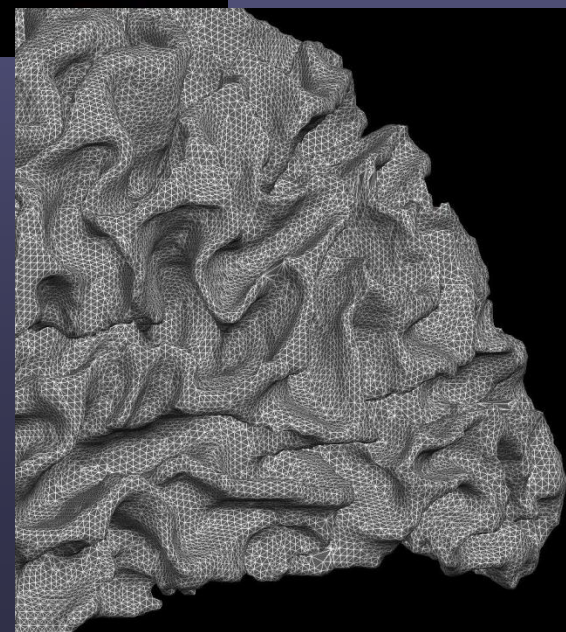


Tessellation

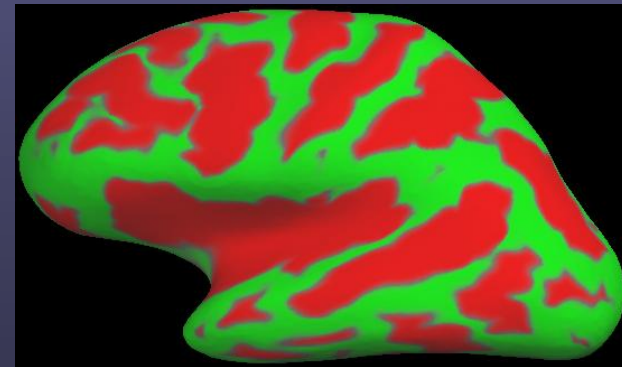
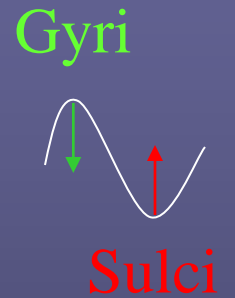
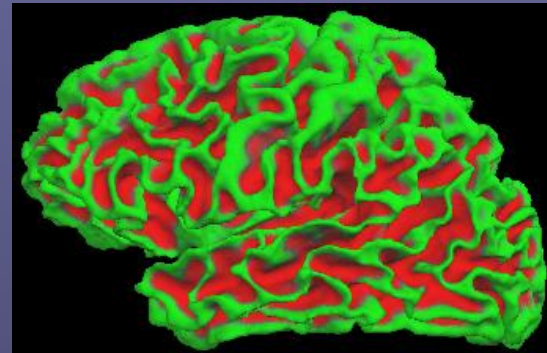
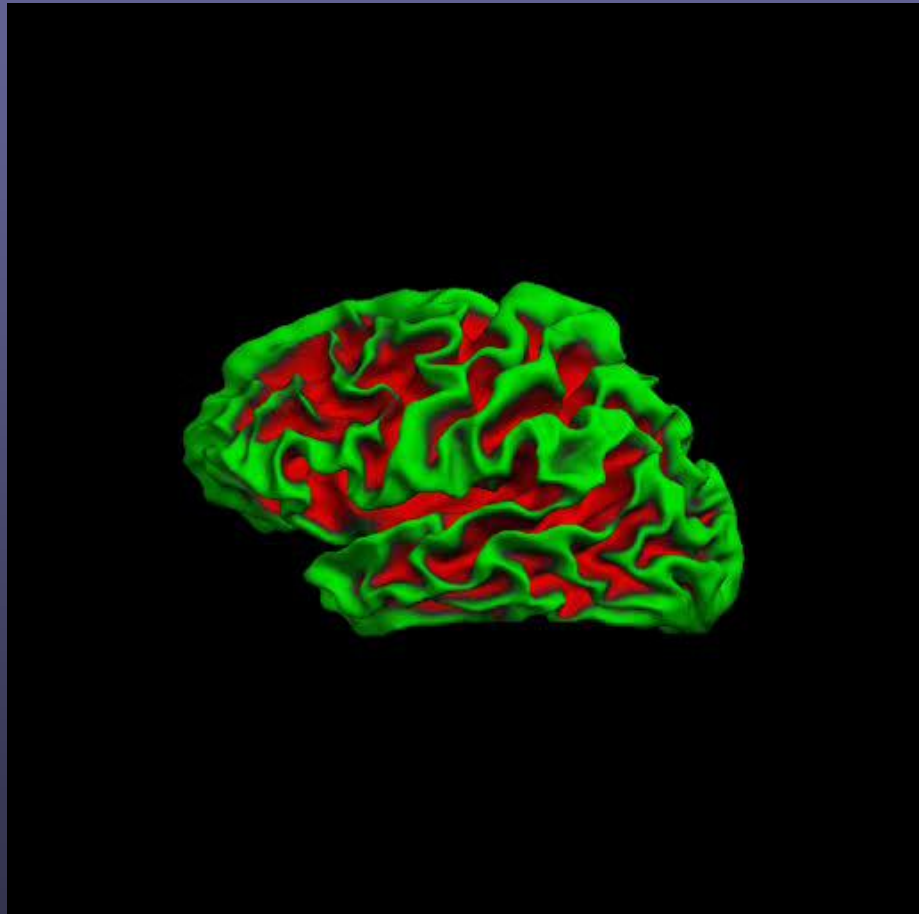


bert
 \
 surf
 /
?h.orig.nofix

- Mosaic of triangles (“tessellation”)
- Errors: Donut holes, handles
 - Subsequently fixed by the automatic topology fixer



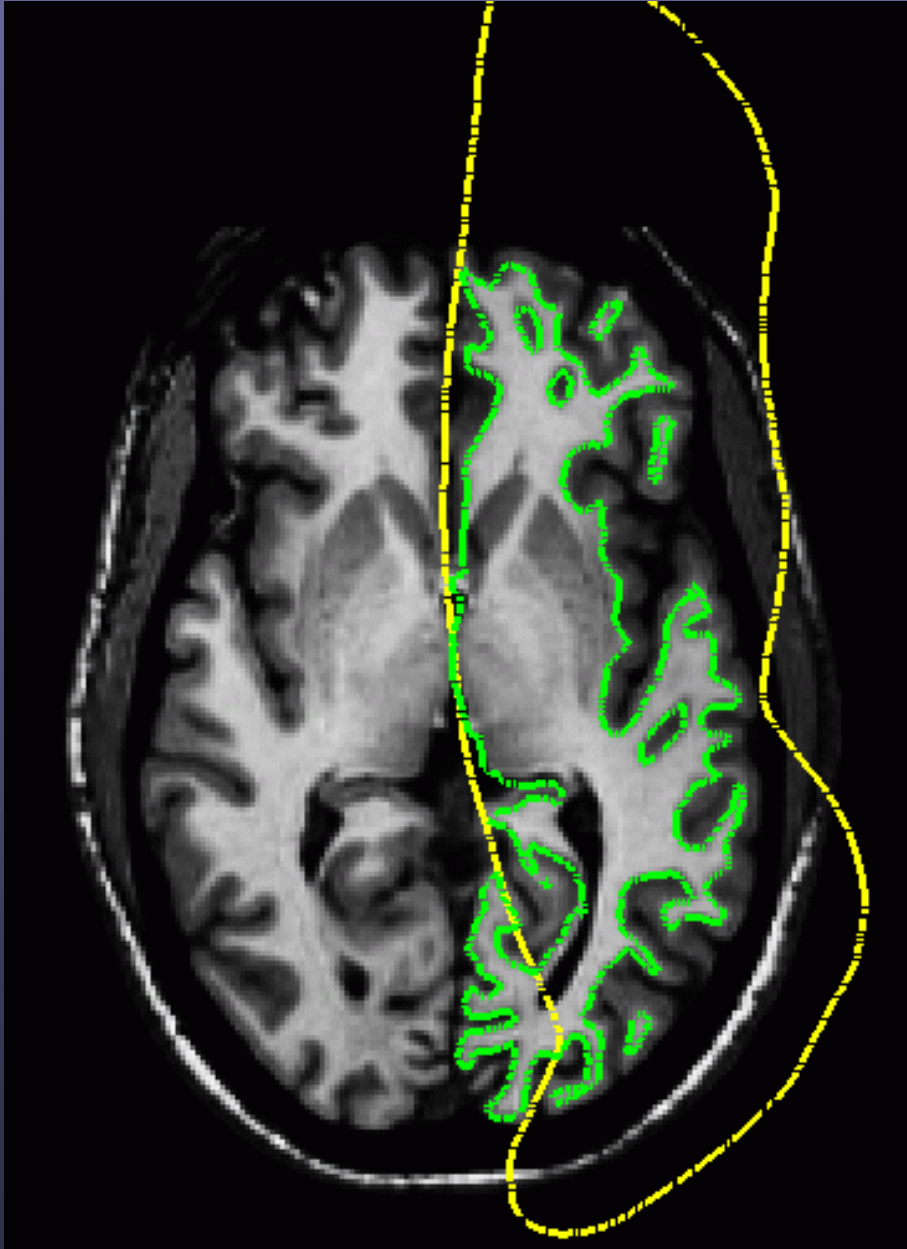
Inflation: Visualization



bert
 \
 surf
 /
?h.inflated.nofix

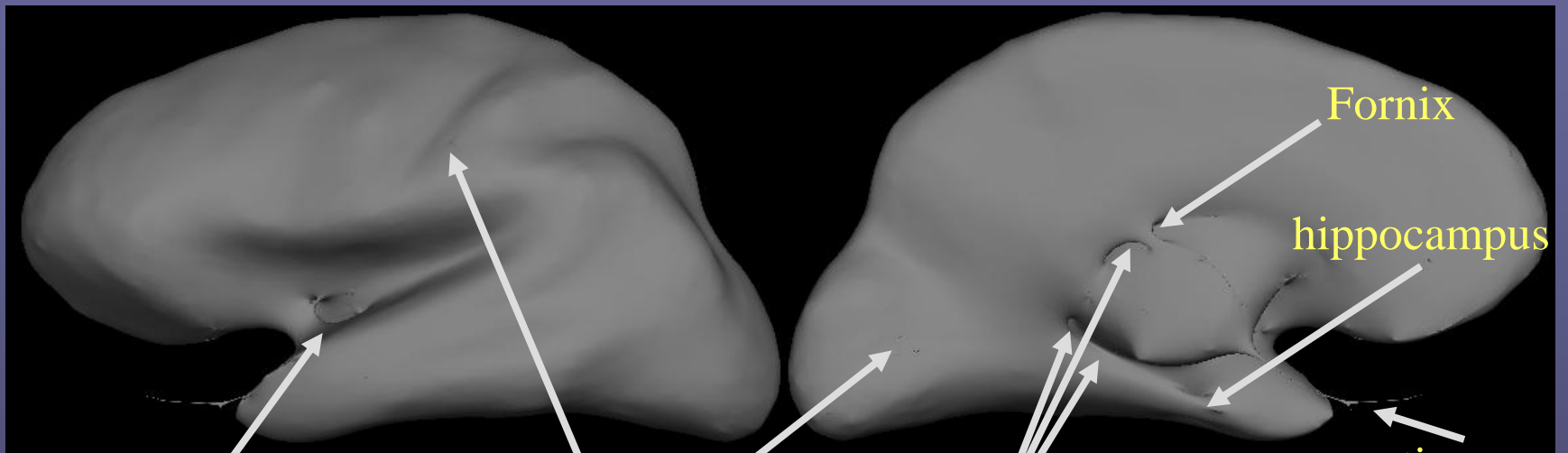
?h.inflated.nofix

Surface Inflation



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

Automatic Topology Fixer



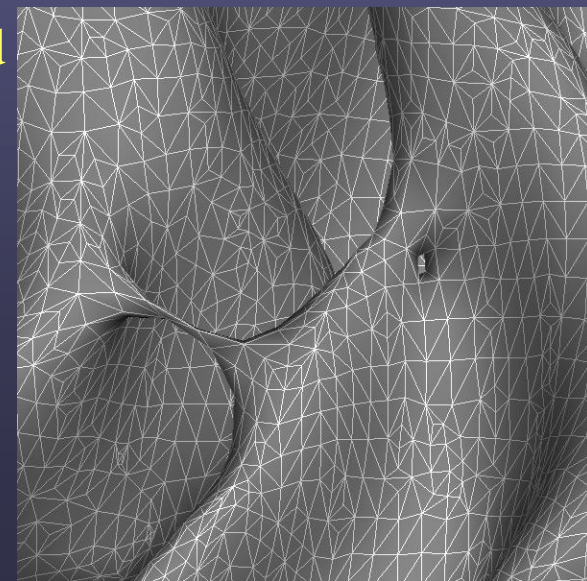
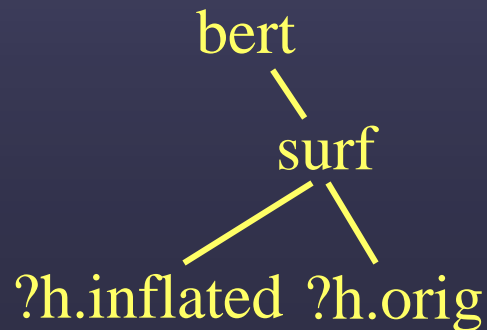
Pallidum and Putamen

Cortical Defects

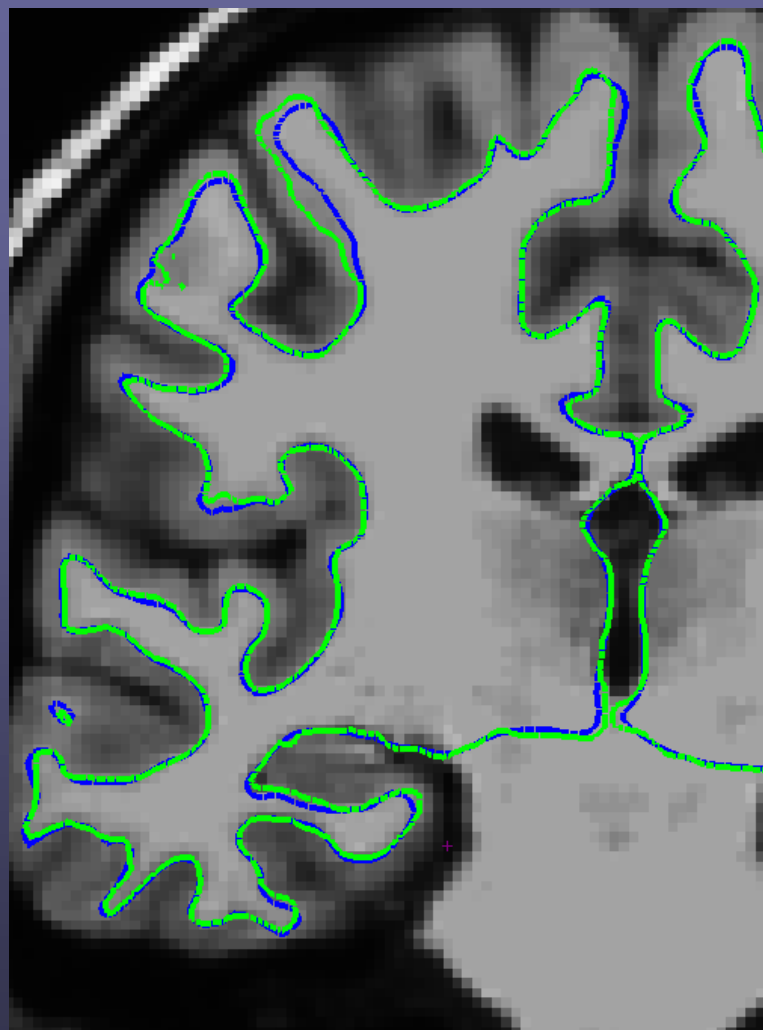
Ventricles and Caudate

optic nerve

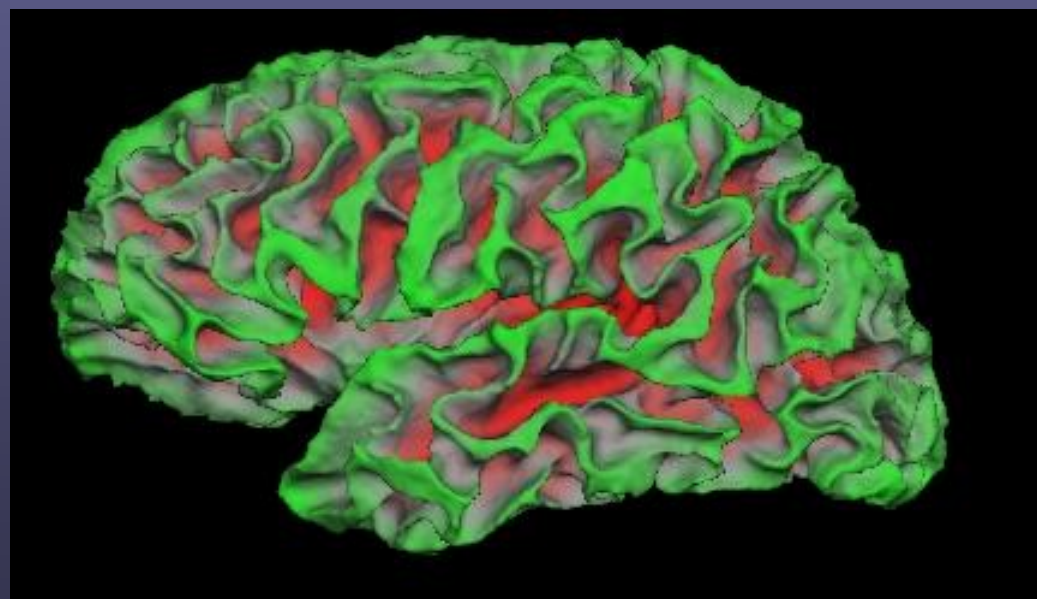
- Holes
- Handles
- Automatically Fixed



White Matter Surface

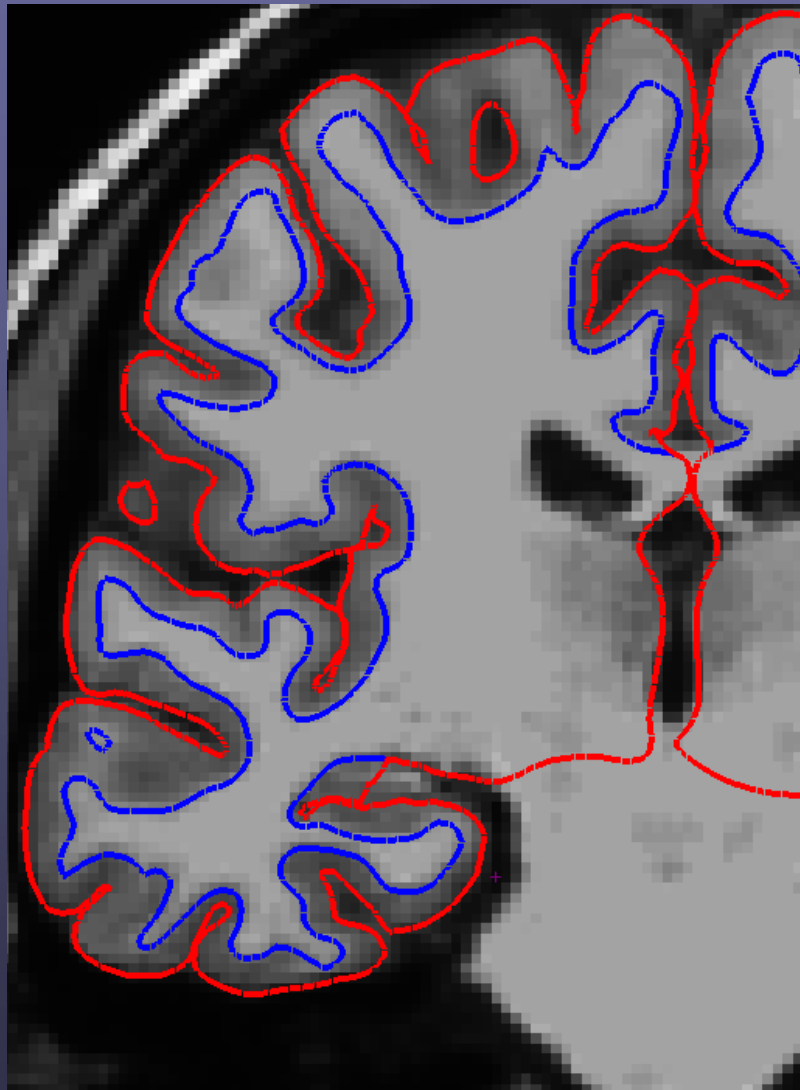


- Nudge orig surface
- Follow T1 intensity gradients
- Smoothness constraint
- Vertex Identity stays constant

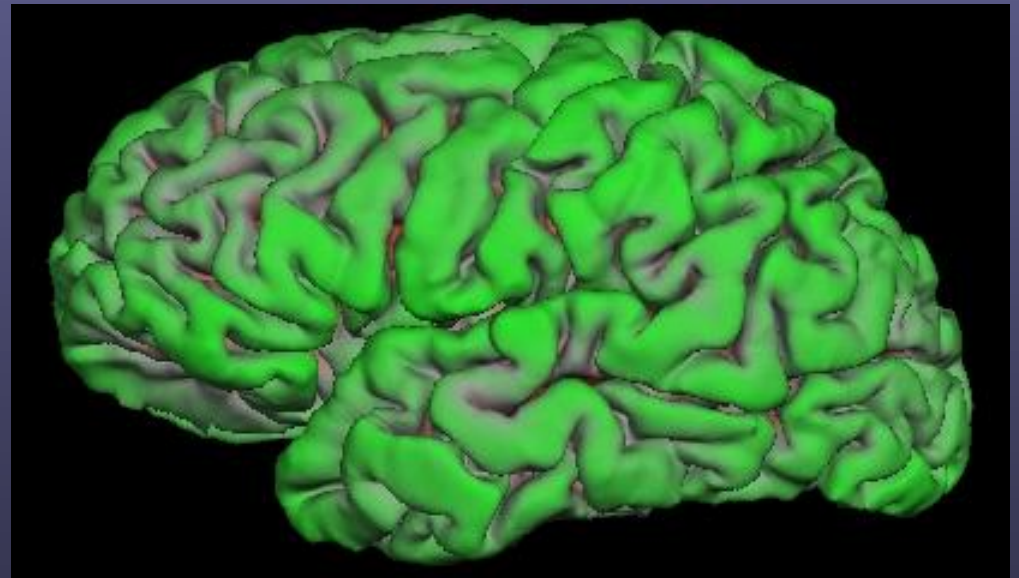


bert
 \
 surf
 \
 ?h.white

Pial Surface

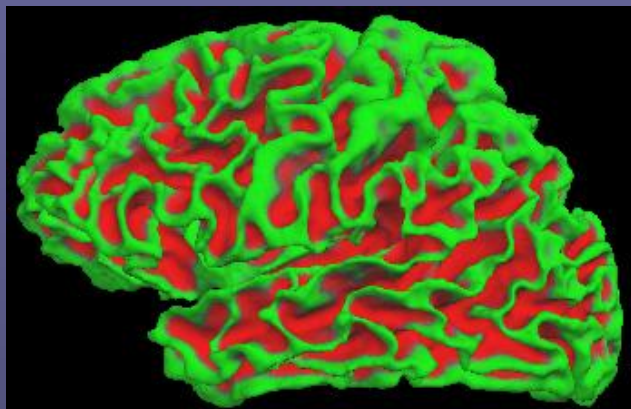


- Nudge white surface
- Follow T1 intensity gradients
- Vertex Identity Stays

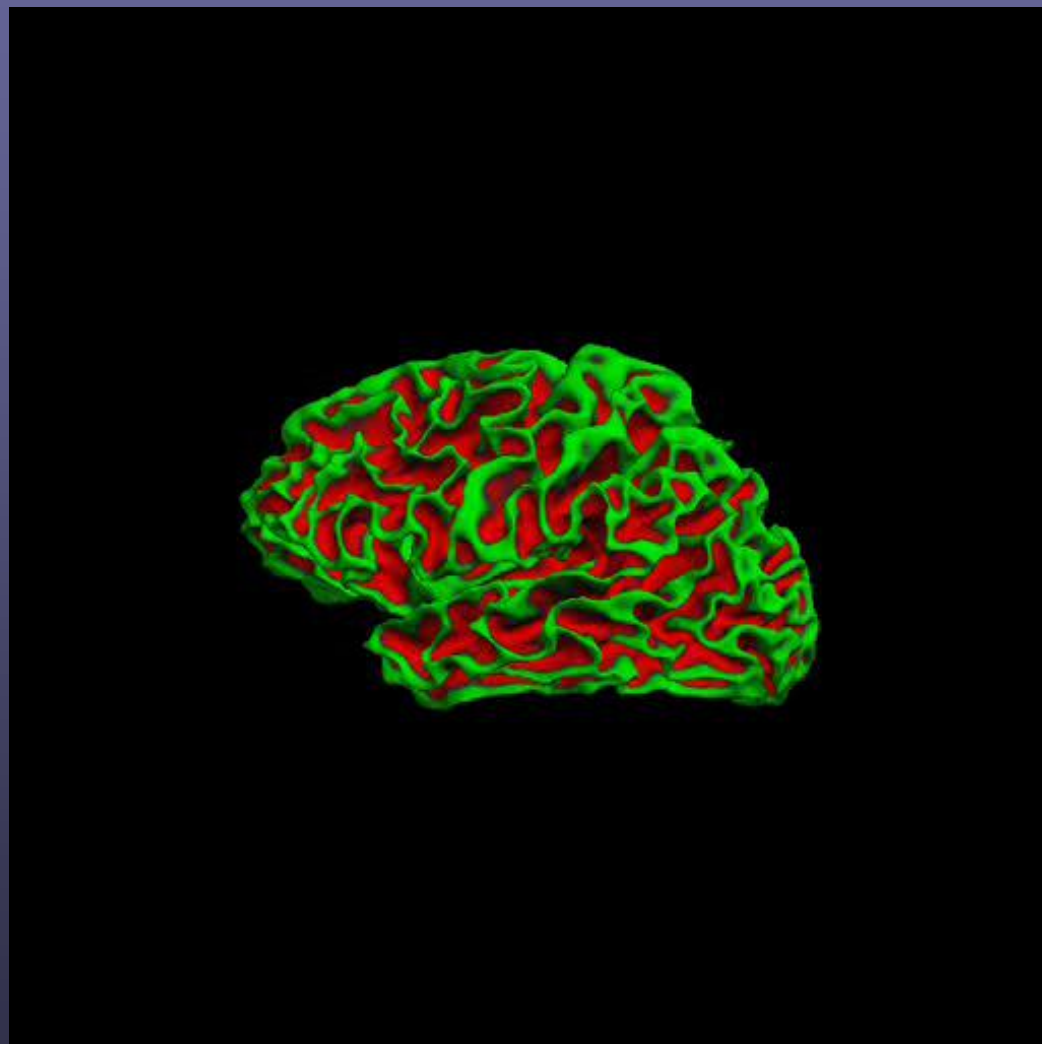
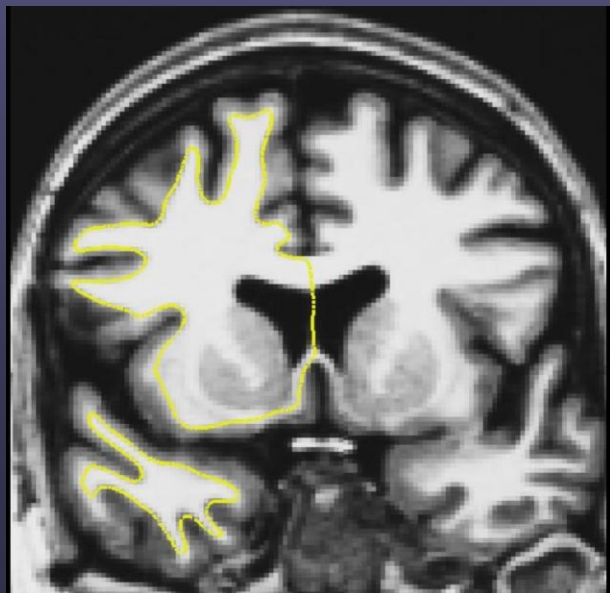


bert
 \
 surf
 \
 ?h.pial

Optimal Surface Placement



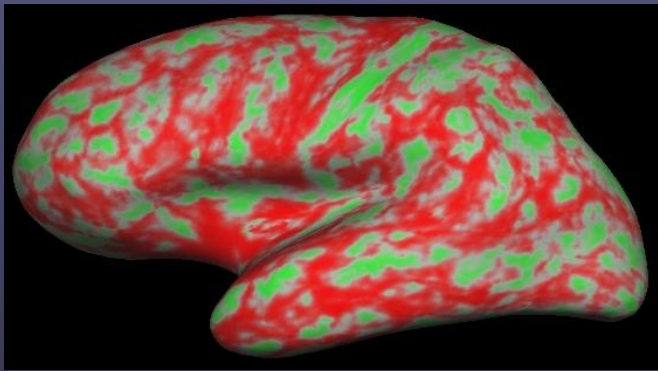
Gray-White Boundary



Outer Cortical Surface

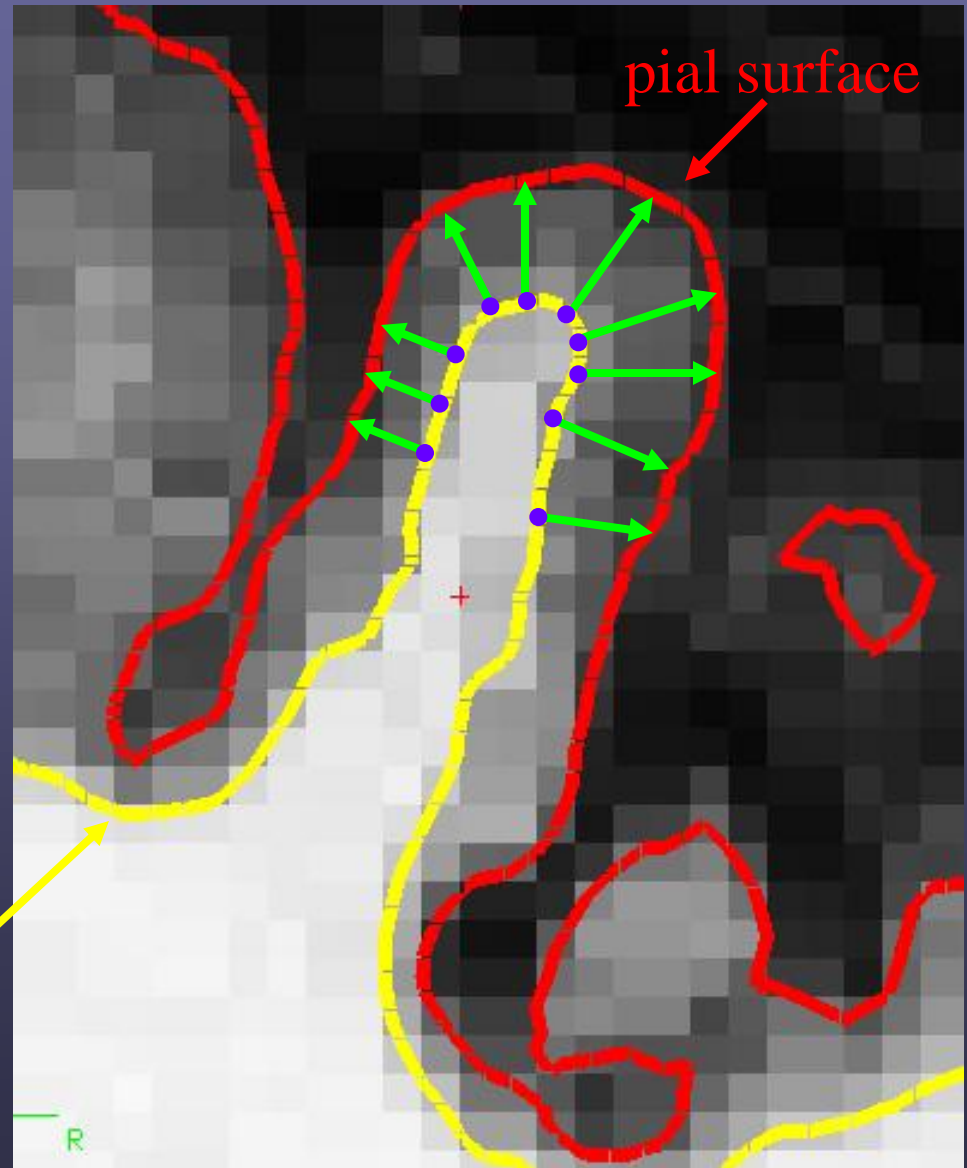
Cortical Thickness

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



white surface

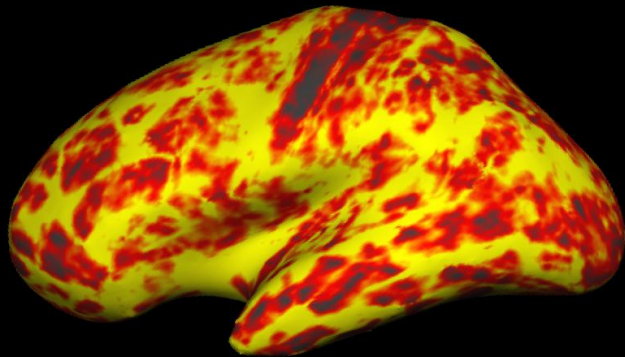
lh.thickness, rh.thickness



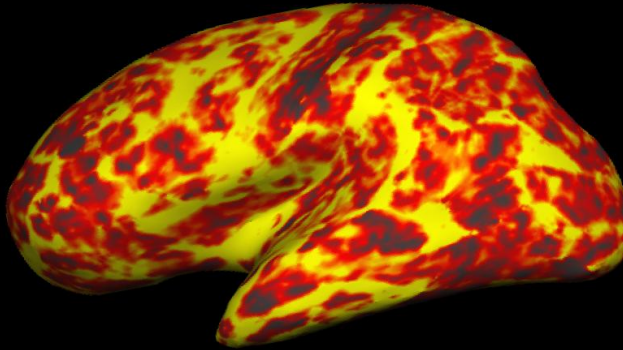
Thickness Maps

- Red regions are thinner
- Yellow regions are thicker

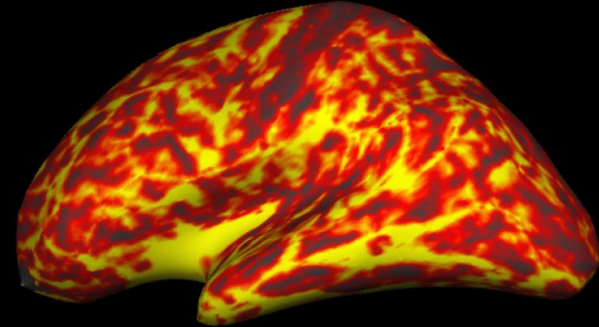
18M



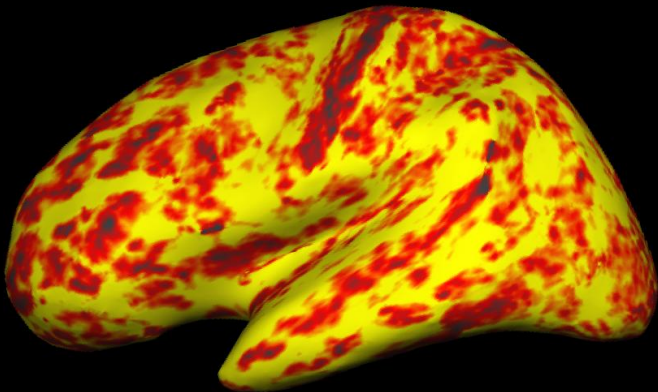
48M



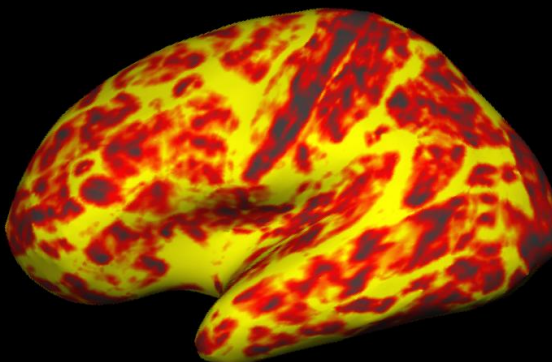
88M



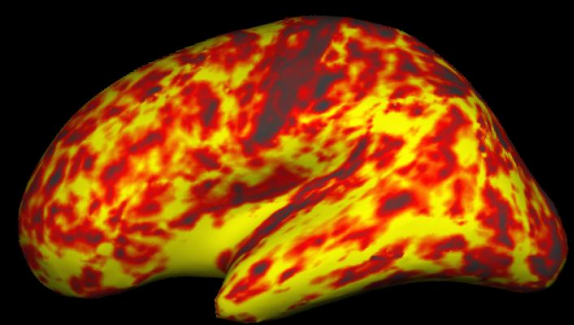
18F



44F



88F



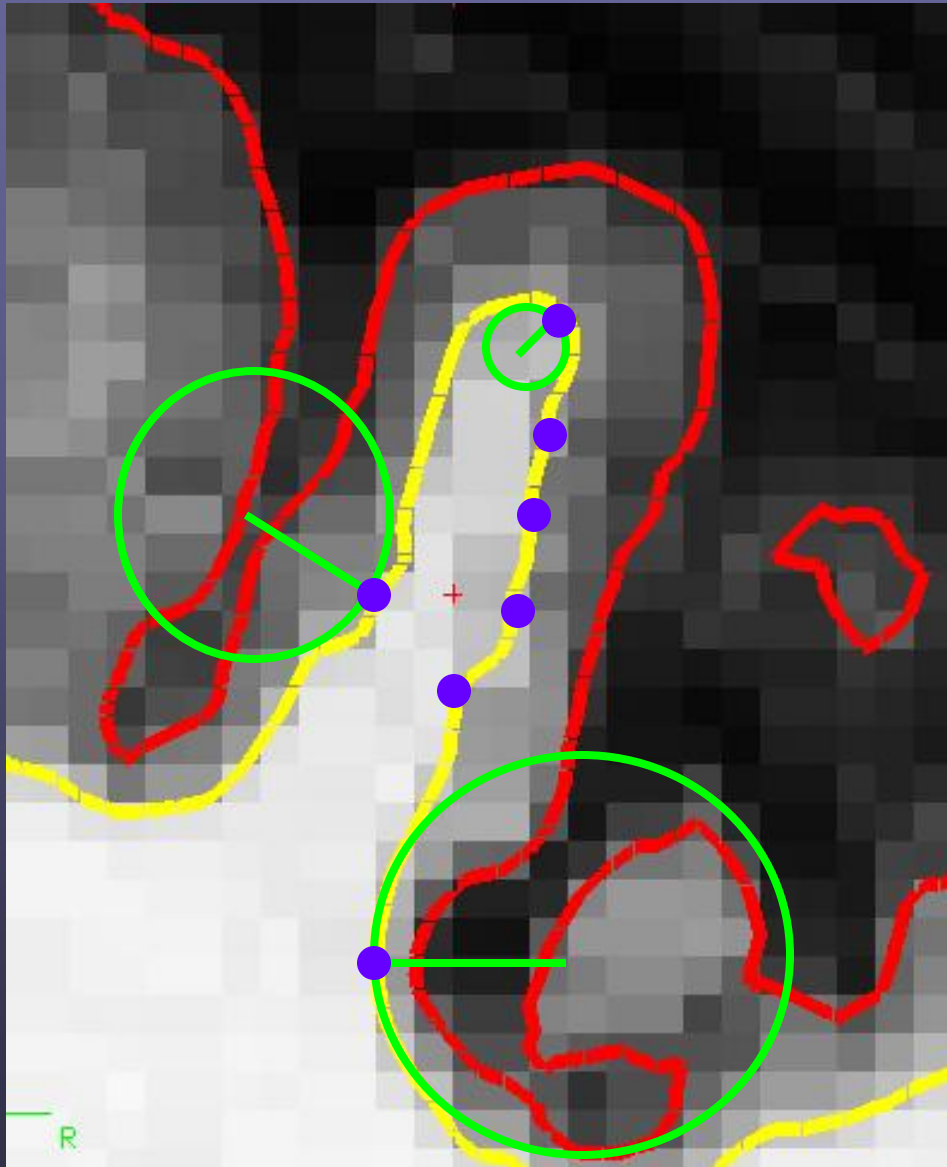
1mm

2mm

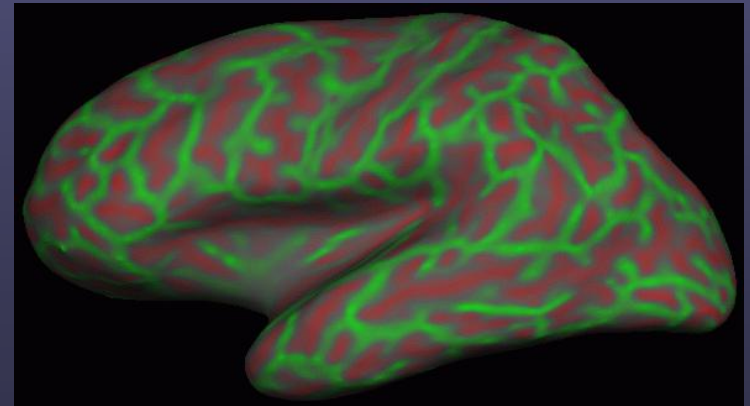
3mm



Curvature (Radial)

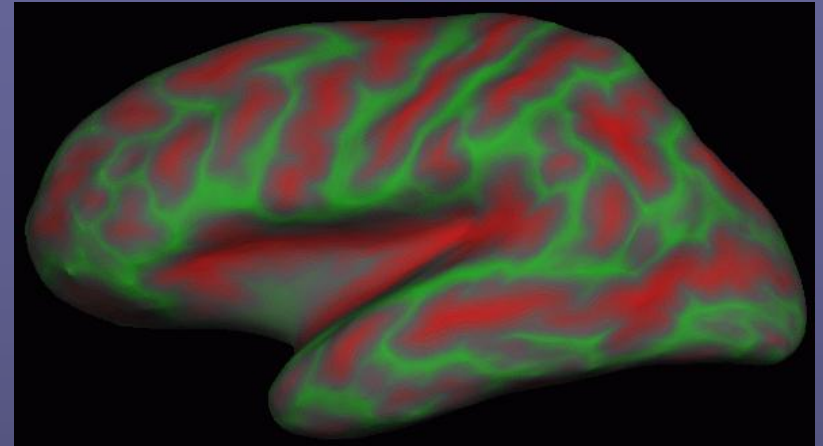
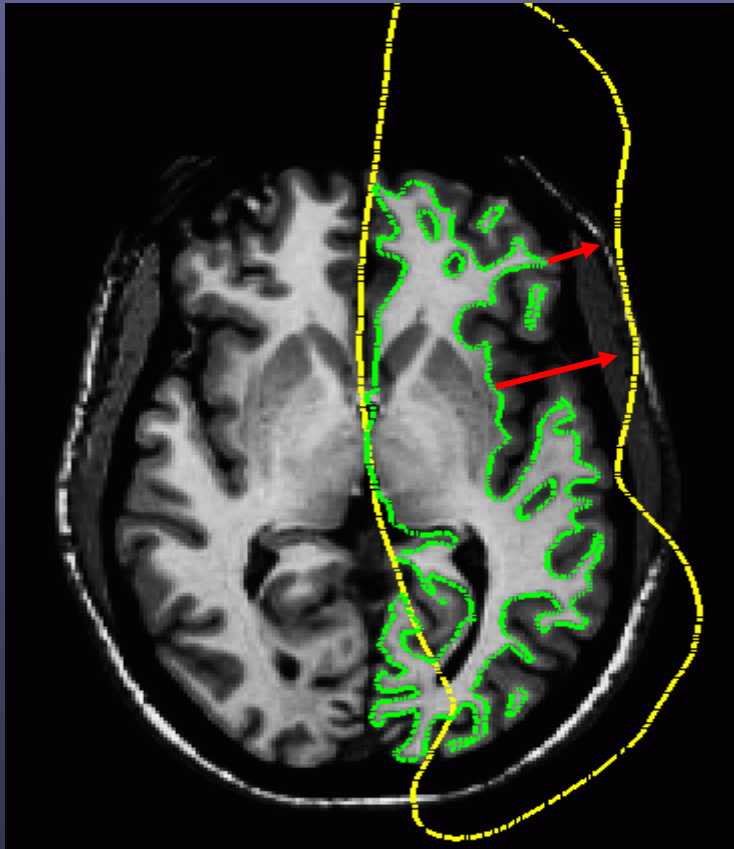


- Circle tangent to surface at each vertex
- Curvature measure is $1/\text{radius of circle}$
- One value per vertex
- Signed (sulcus/gyrus)
- Actually use gaussian curvature

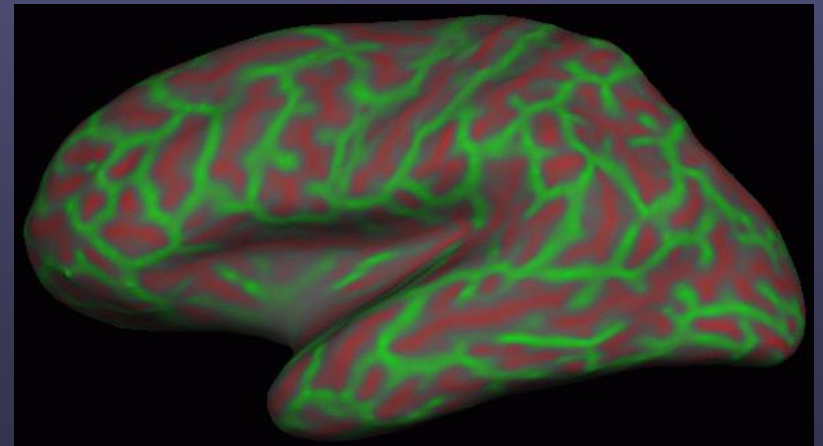


lh.curv, rh.curv

Sulcal Depth



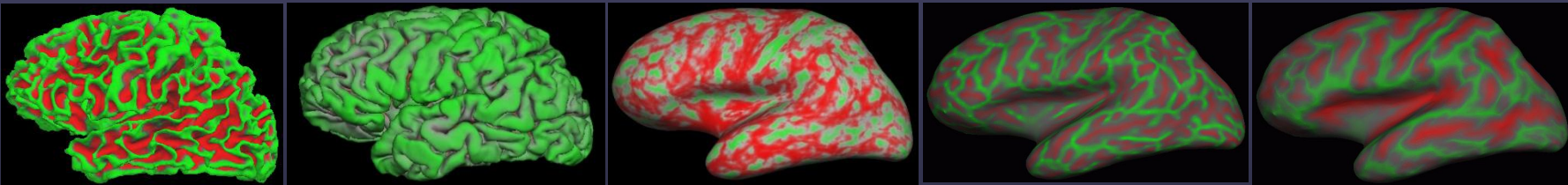
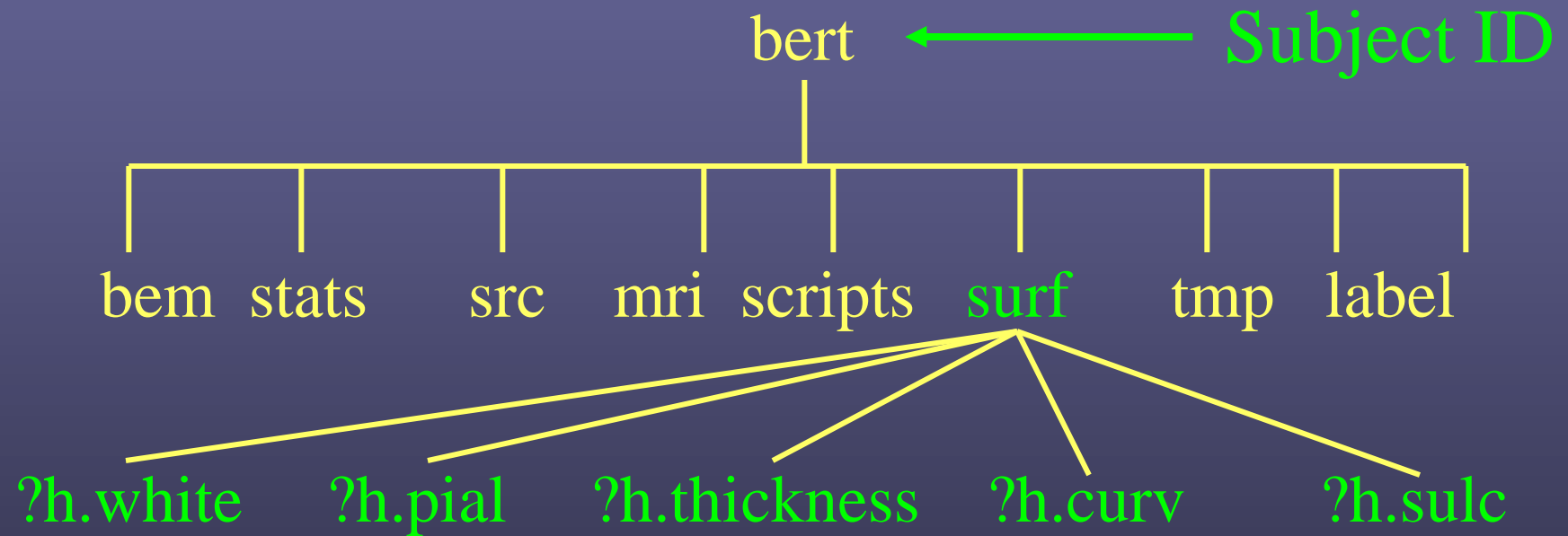
lh.sulc, rh.sulc



lh.curv, rh.curv

FreeSurfer Directory Tree

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



-autorecon3

Volumetric Processing Stages (subjid/mri):

1. Motion Cor, Avg, Conform (orig.mgz)
2. Talairach transform computation
(transforms/talairach.xfm)
3. Non-uniform inorm (nu.mgz)
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)

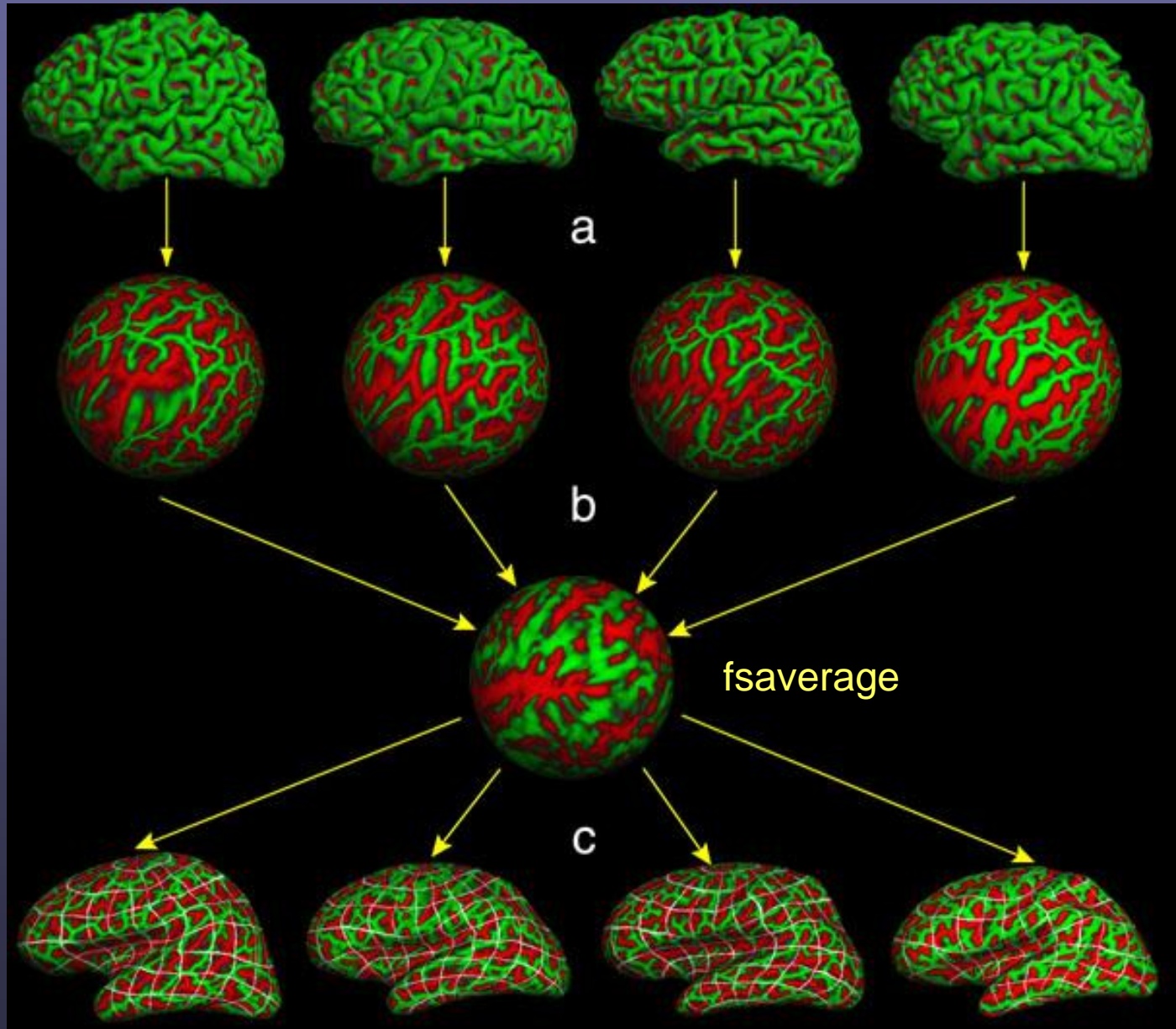
Surface Processing Stages (subjid/surf):

14. Tessellate (?h.orig.nofix)
15. Smooth1
16. Inflate1
17. QSphere (?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: lh processed completely first, then rh.

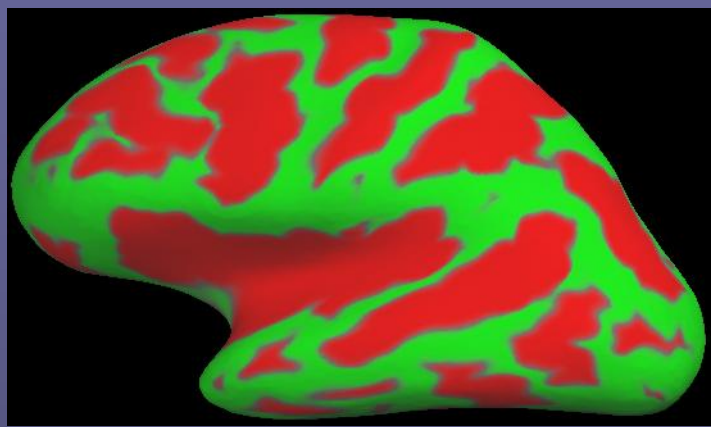
Surface-Based Spherical Coord System



-sphere
-surfreg

-autorecon3

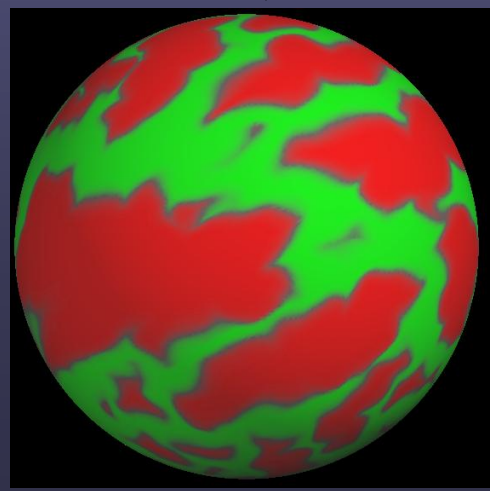
“Spherical” Registration



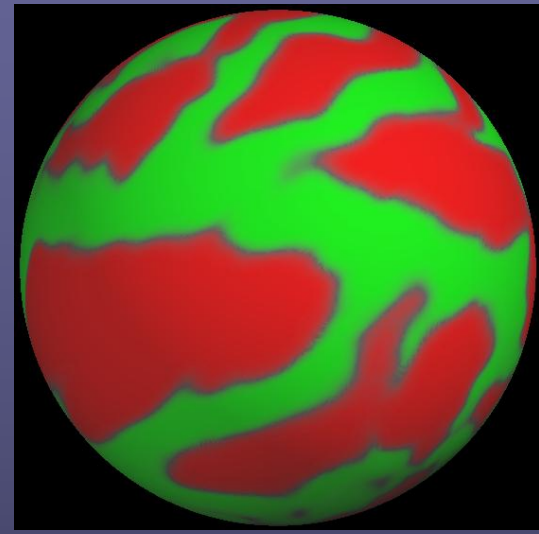
Inflated Surface (Sulcal Map)



Spherical Inflation



Individual Subject



Atlas (Target)



High-Dimensional Registration
to Spherical Template

bert

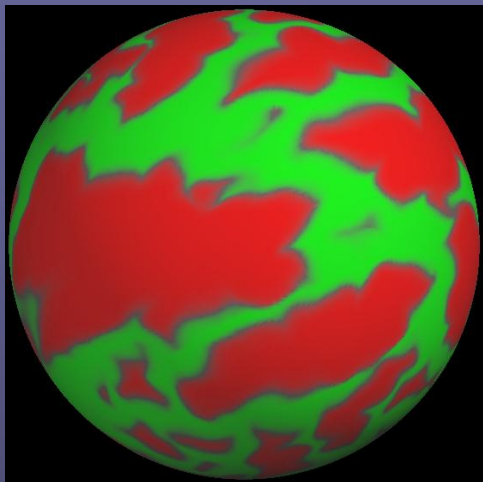
surf

?h.sphere

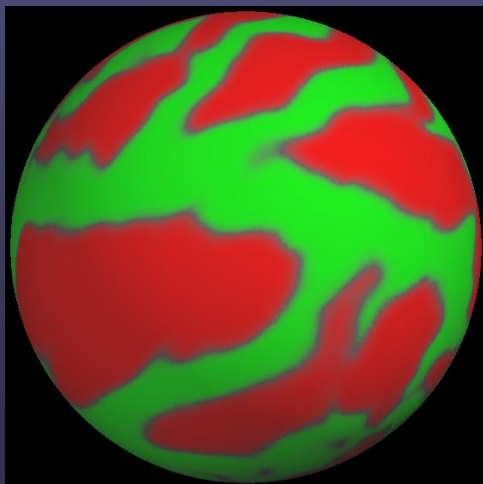
-sphere
-surfreg

-autorecon3

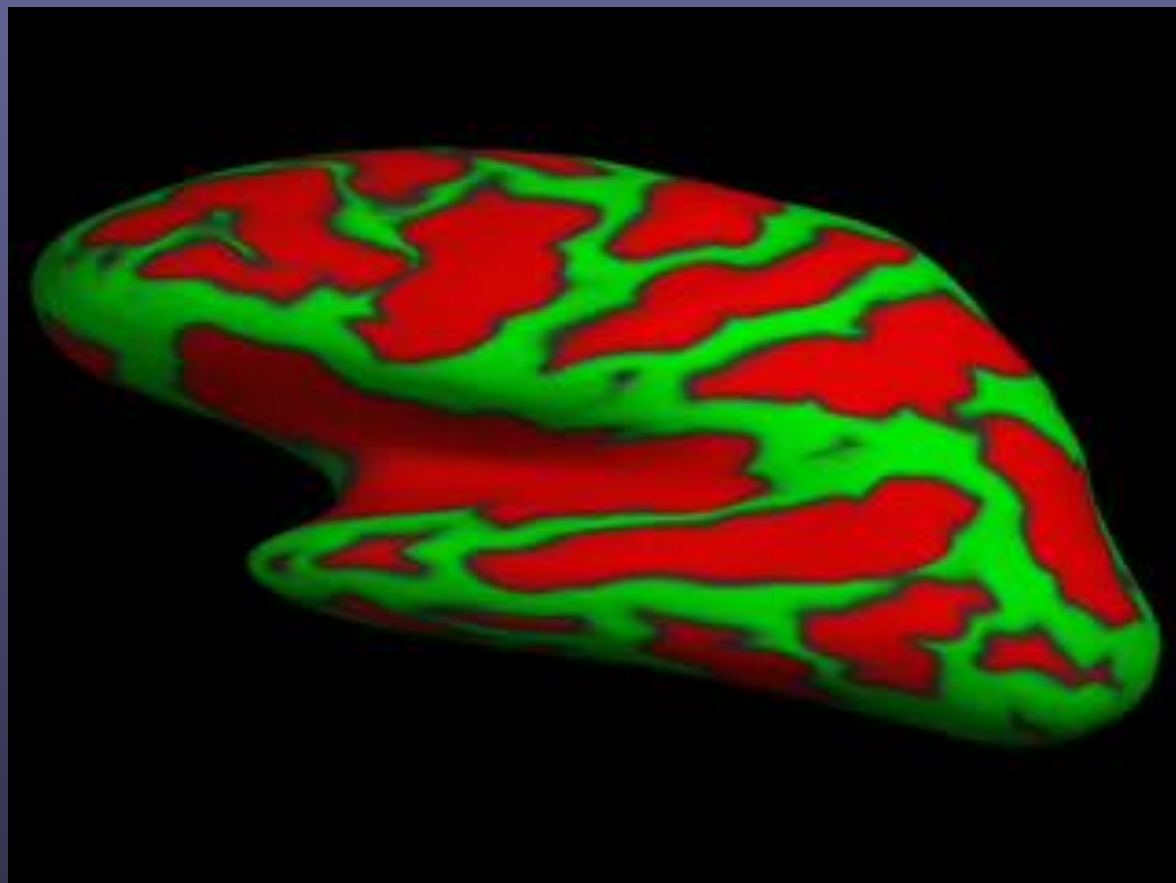
Spherical Inflation Registration to Atlas



Individual Subject



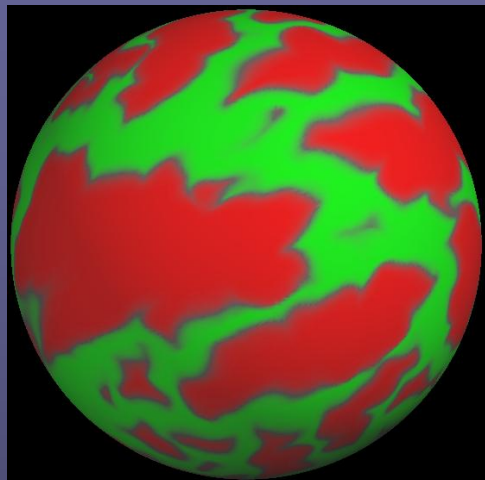
Atlas (Target)



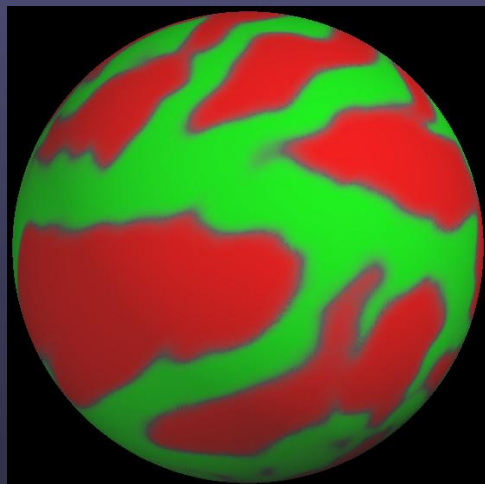
-sphere
-surfreg

-autorecon3

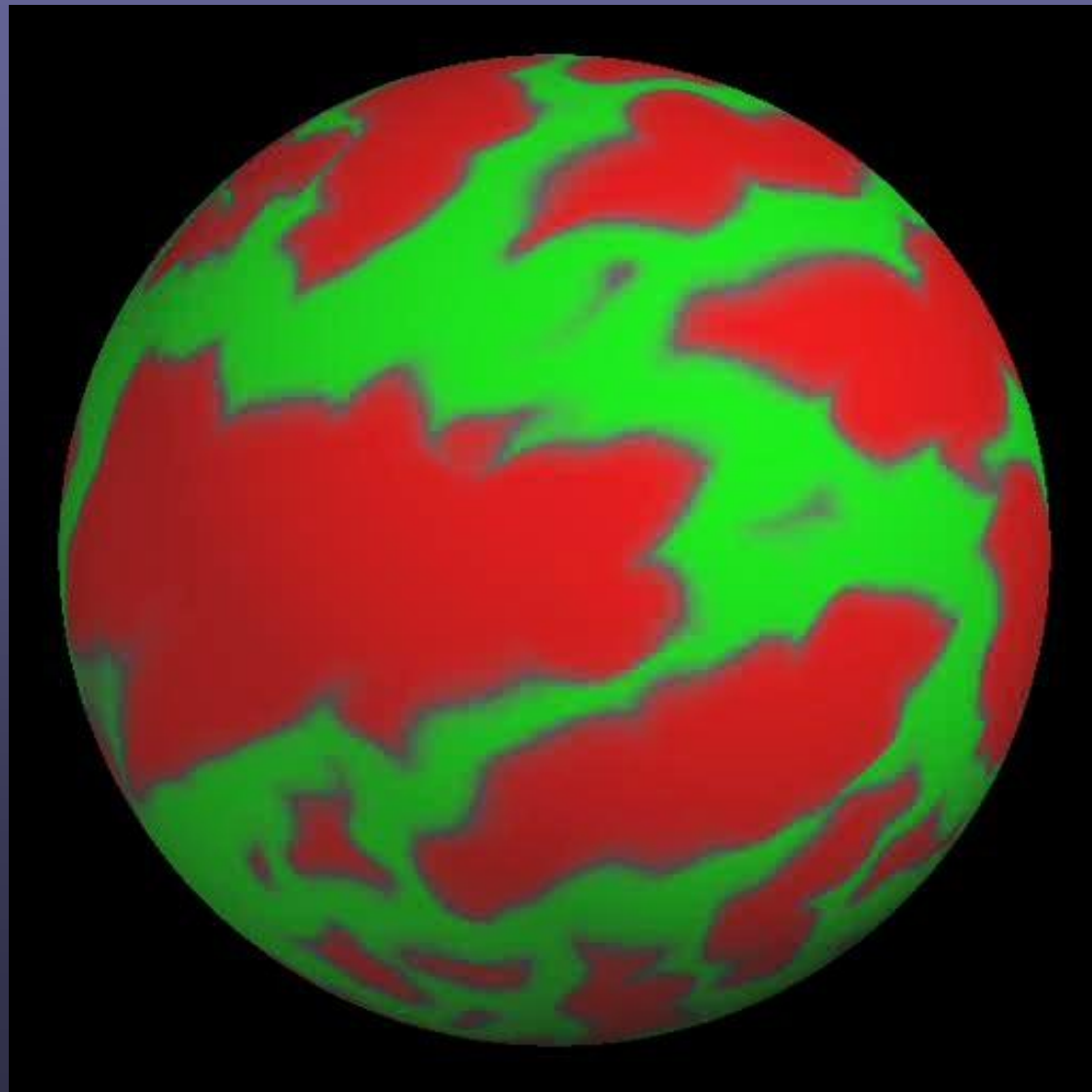
Spherical Inflation Registration to Atlas



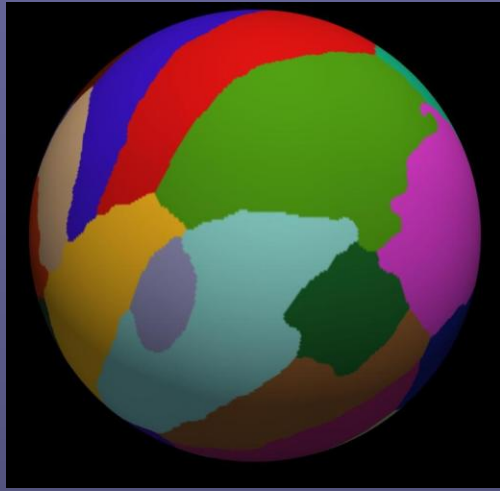
Individual Subject



Atlas (Target)

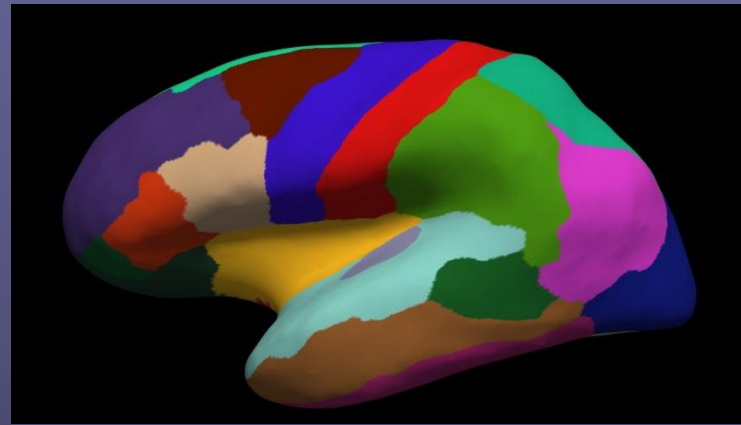


Cortical Parcellation

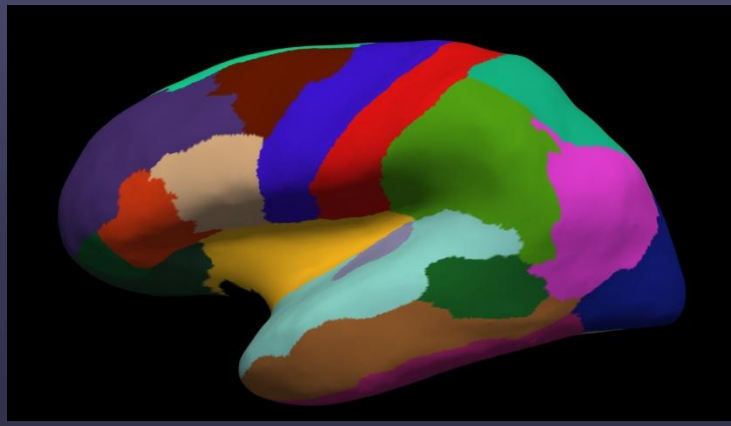


Spherical Template based on Manual Parcellation

Map to Individual Thru Spherical Reg

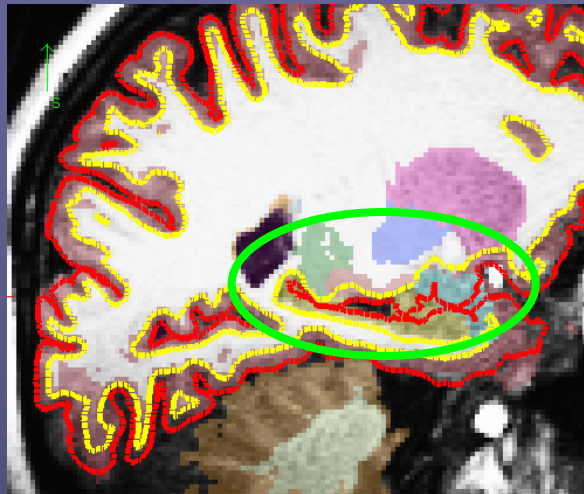
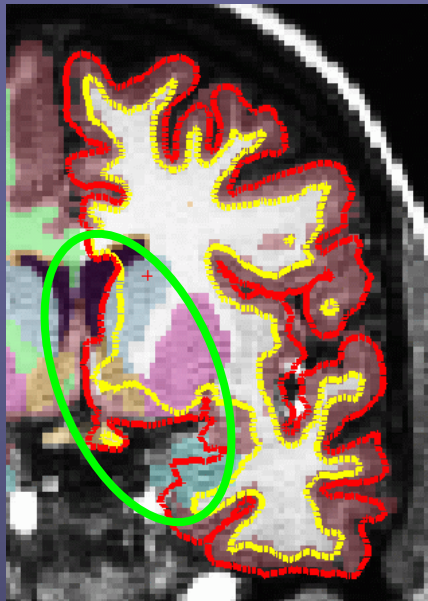


Fine-tune based on individual anatomy

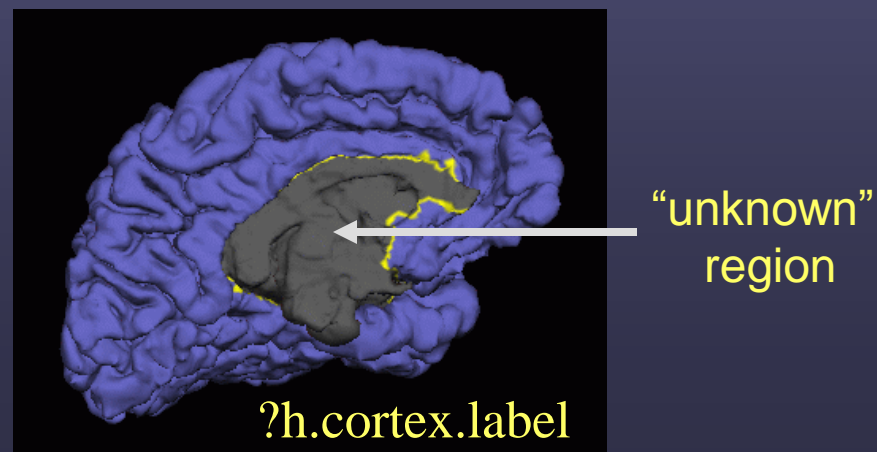
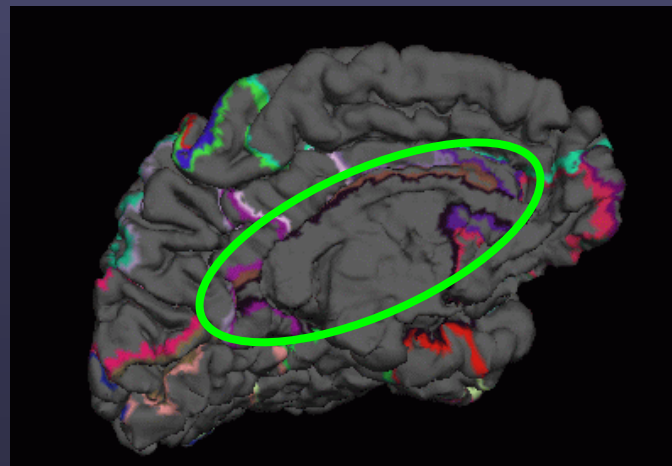


bert
└─ label ─┘
 ?h.aparc.annot

Non-Cortical Areas of Surface



Amygdala, Putamen, Hippocampus, Caudate, Ventricles, CC

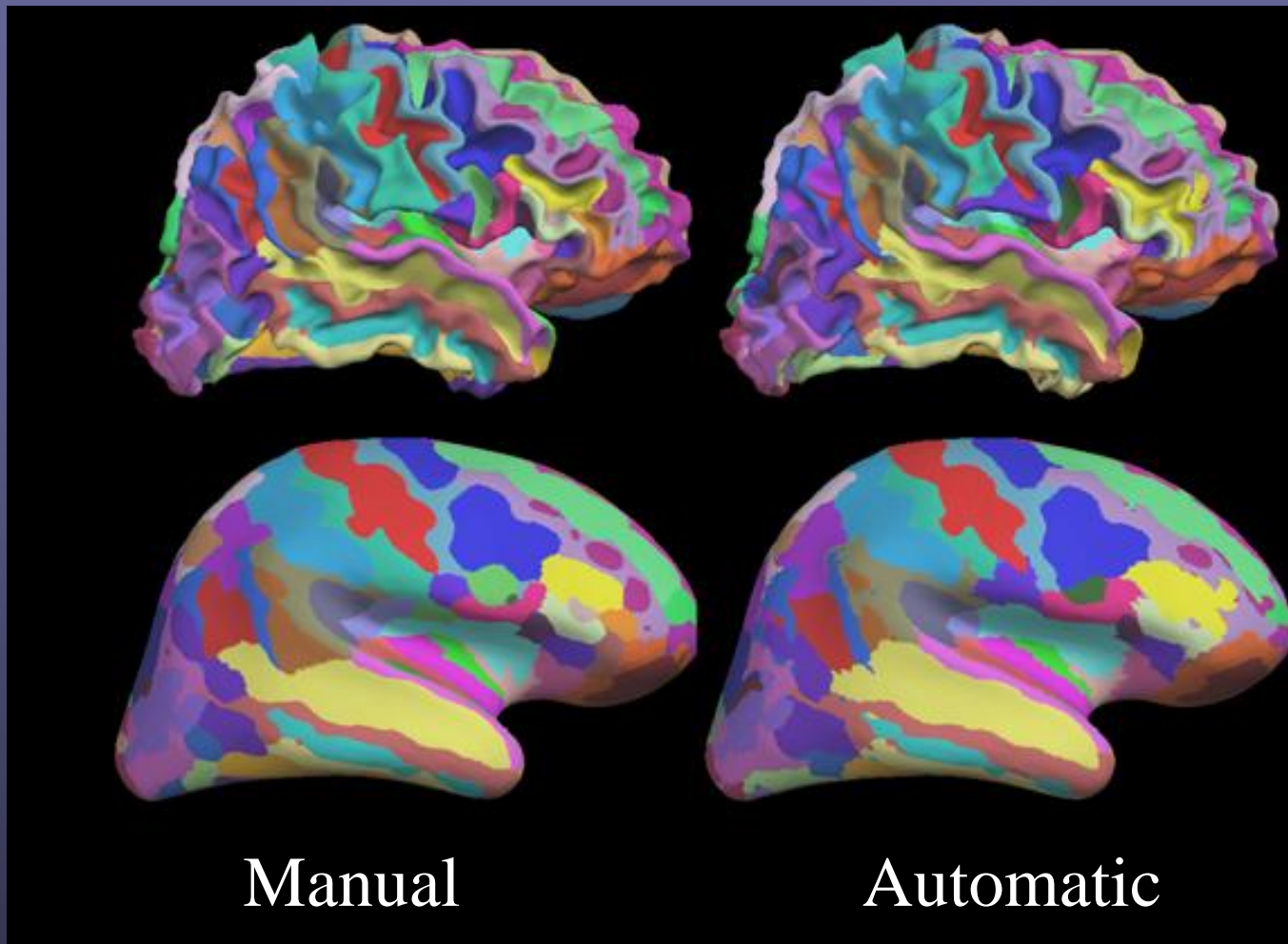


Output of Cortical Surface Reconstruction



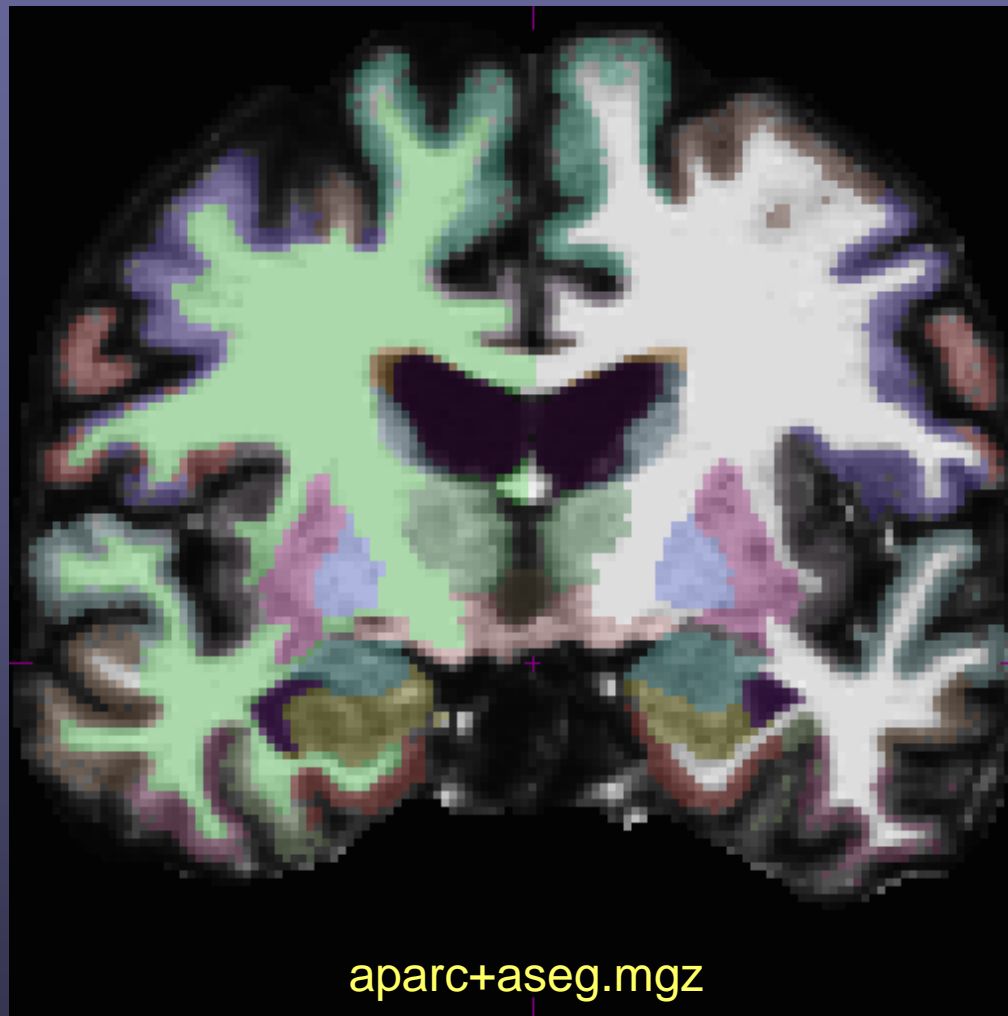
Amygdala, Hippocampus

Cortical Parcellation: 2



Thanks to Christophe Destrieux for this slide.

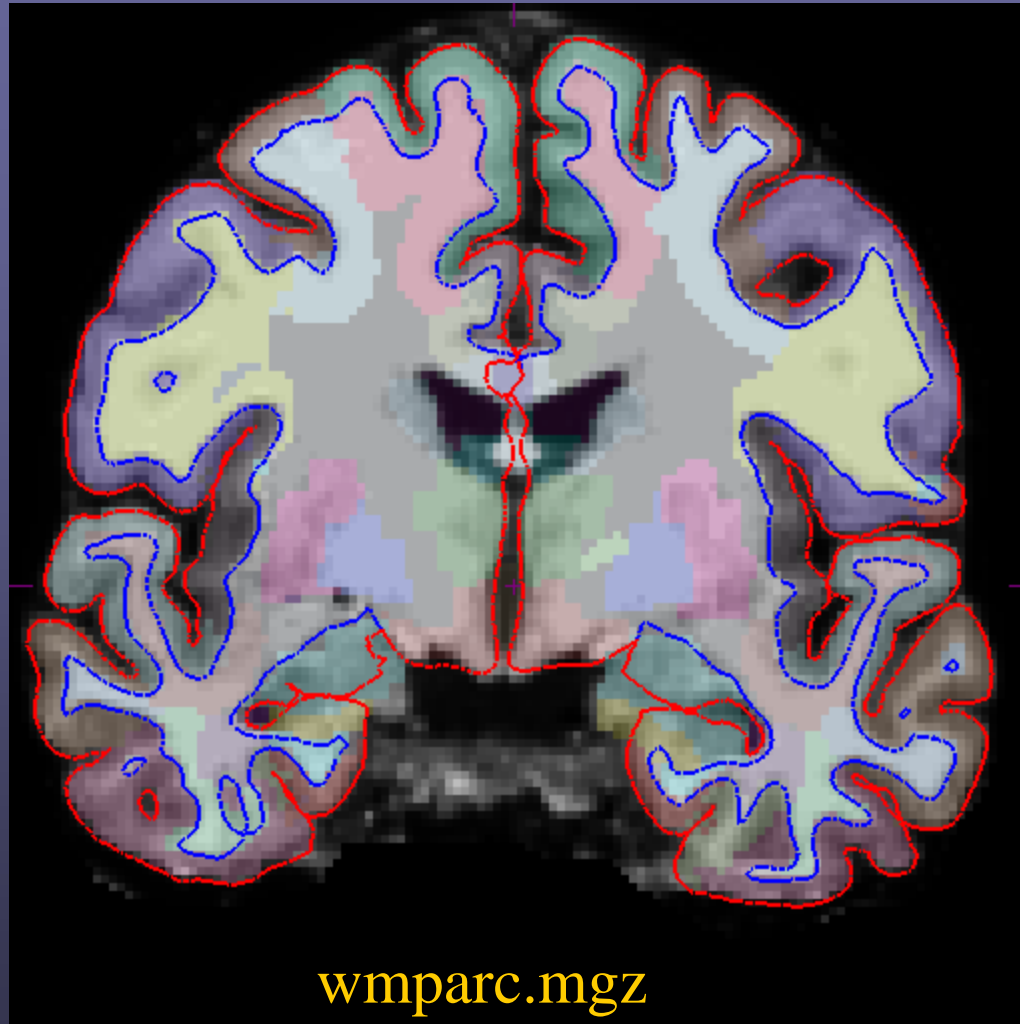
Aparc+Aseg



There is also `aparc.a2009s+aseg.mgz` for Destrieux atlas

White Matter Parcellation

Nearest Cortical
Label to point in
White Matter

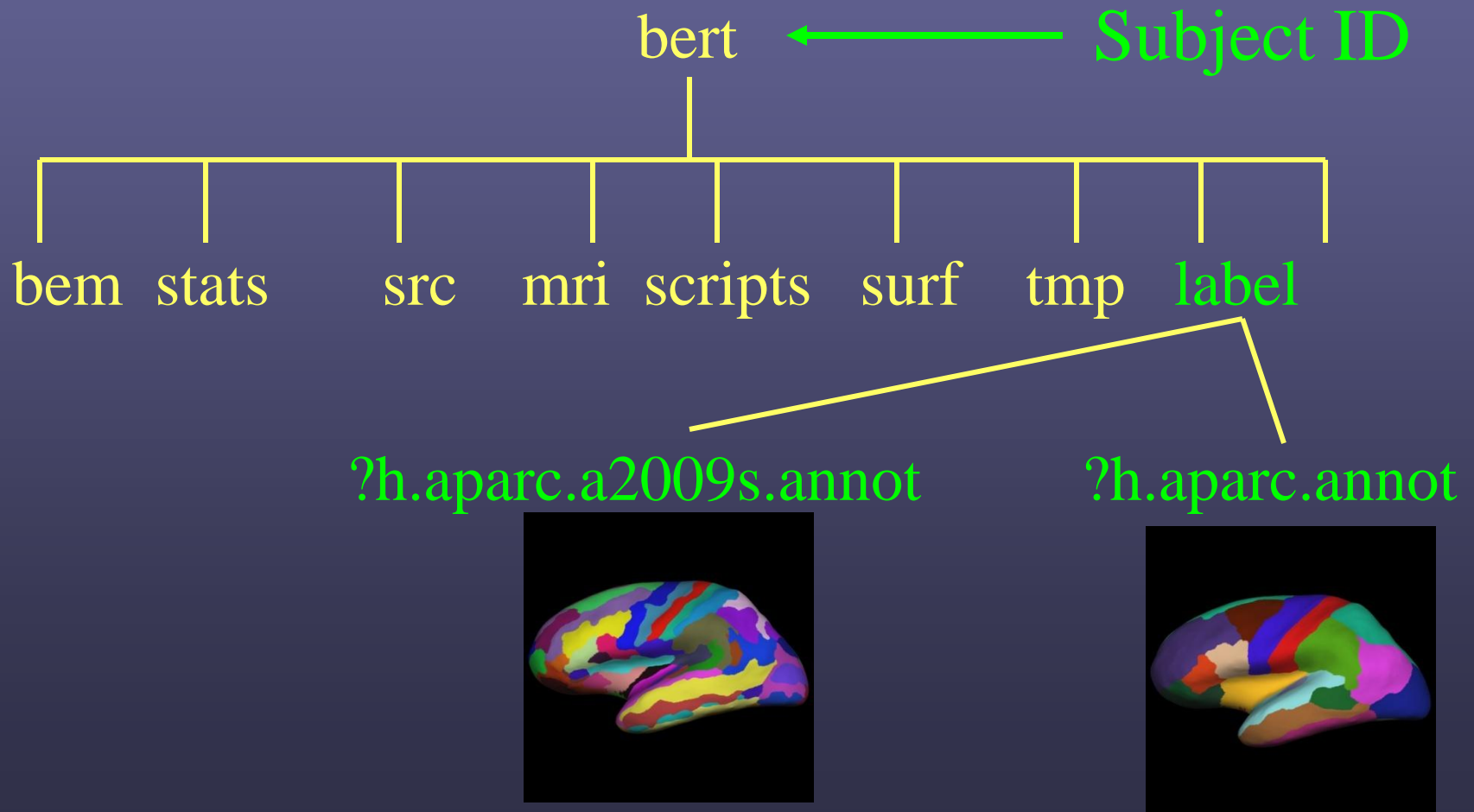


bert
 \
 label
 /
wmparc.mgz

Salat DH, Greve DN, Pacheco JL, Quinn BT, Helmer KG, Buckner RL, Fischl B. Regional white matter volume differences in nondemented aging and Alzheimer's disease. Neuroimage. 2008 Nov 5.

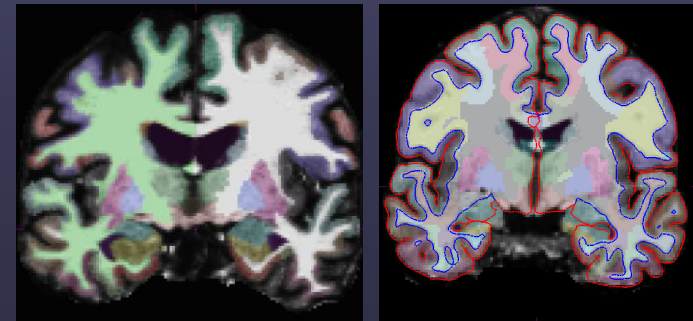
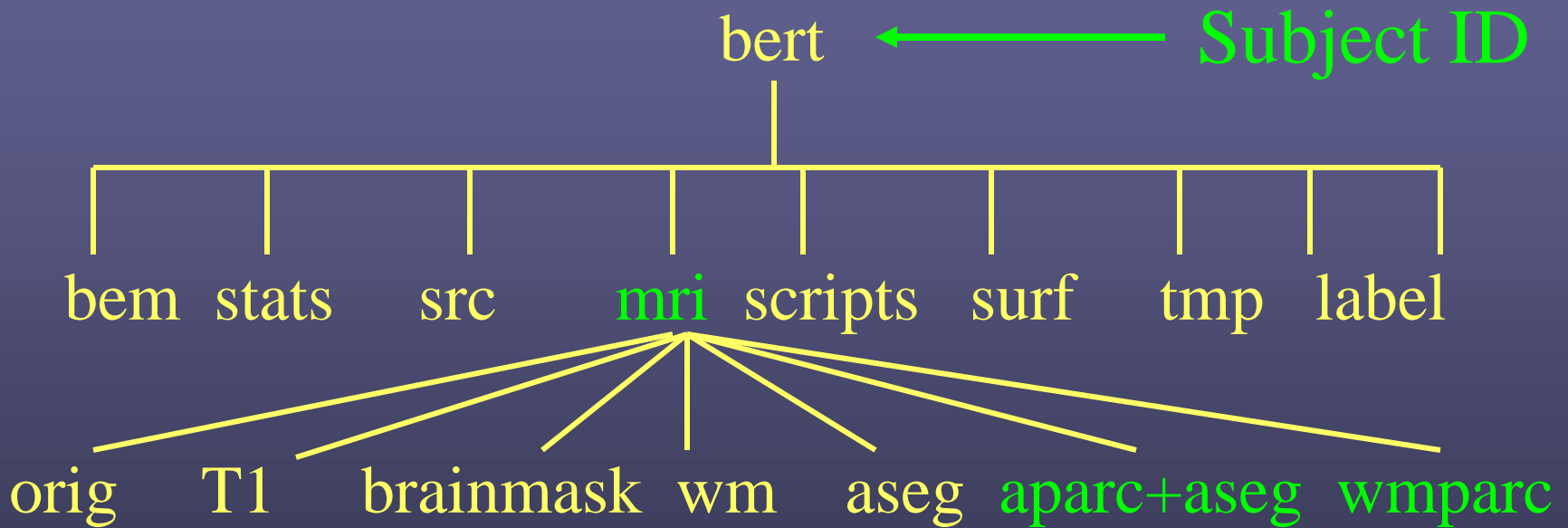
FreeSurfer Directory Tree

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



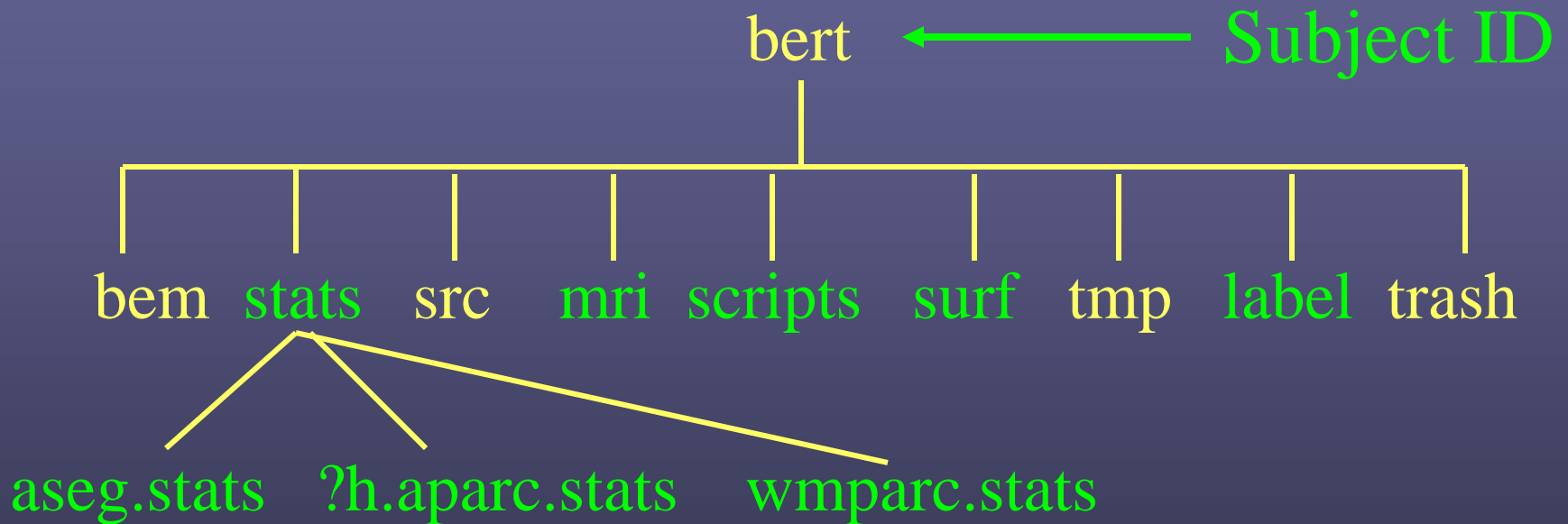
FreeSurfer Directory Tree

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



FreeSurfer Directory Tree

Directories used often are in green.



Why use FreeSurfer?

What happens?

How do I do that?

Now What?

Using FreeSurfer

With FreeSurfer, certain variables must be set in order to use it correctly:

FREESURFER_HOME

tell Operating System where FreeSurfer is

SUBJECTS_DIR

tell FreeSurfer where data is

Within NMR/Martinos

Stable version:

```
source /usr/local/freesurfer/nmr-stable-env
```

Development version:

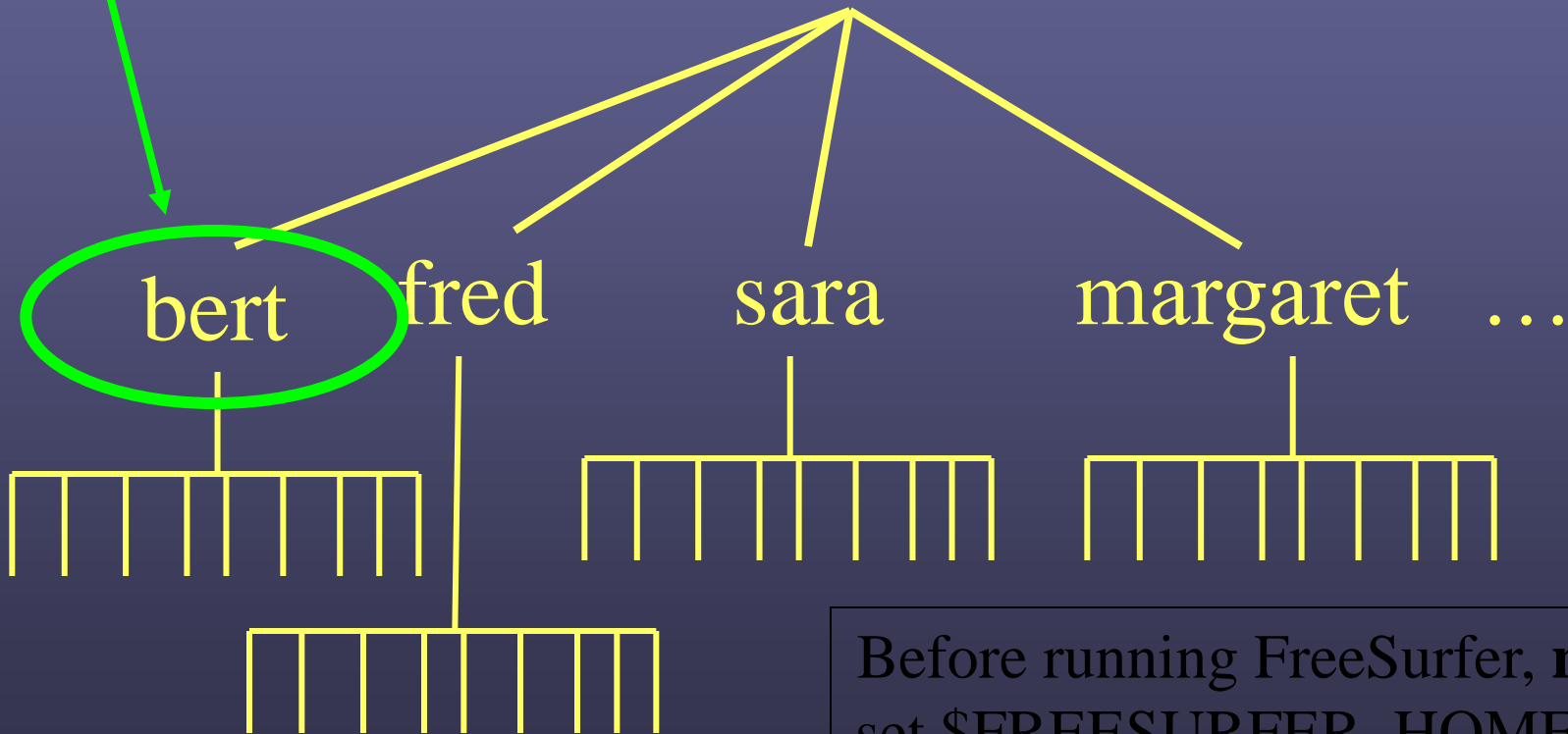
```
source /usr/local/freesurfer/nmr-dev-env
```

<http://surfer.nmr.mgh.harvard.edu/fswiki/InternalFreeSurferDistributions>

Set-up Environmental Variables

Subject ID

`$$SUBJECTS_DIR`



Before running FreeSurfer, **must** set `$$FREESURFER_HOME` and `$$SUBJECTS_DIR`

Starting the Reconstruction Process

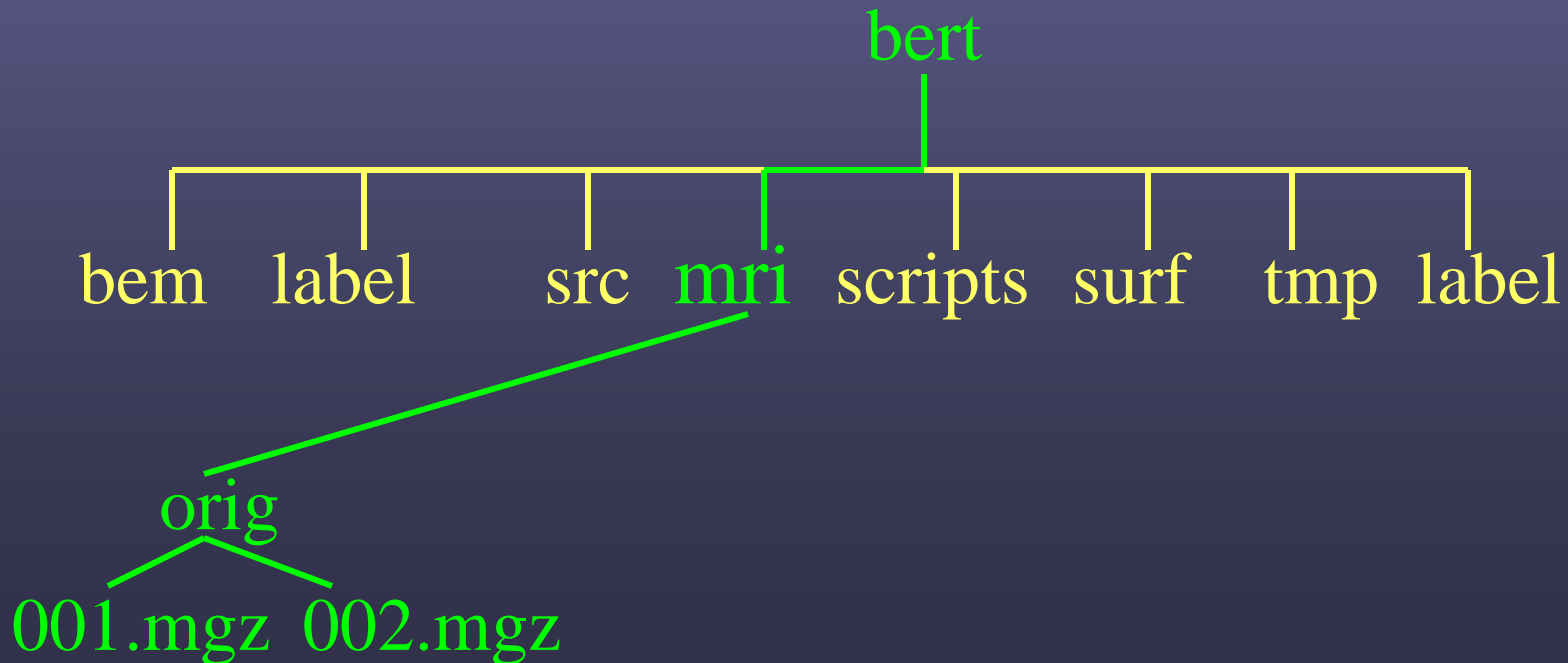
Before running FreeSurfer, **must** set
\$FREESURFER_HOME and \$SUBJECTS_DIR

```
recon-all \
-i /path/to/your/raw/data1 \
-i /path/to/your/raw/data2 \
-all -s subject_id
```

- This will create the subject directory ‘subject_id’ in your \$SUBJECTS_DIR and convert your 2 raw acquisitions to mgz and use them as input for the ‘-all’ command.

Alternative: Add Your Data

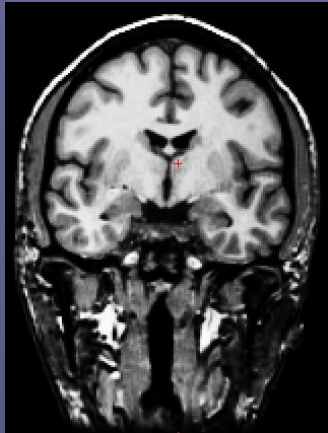
- `cd $SUBJECTS_DIR`
- `mkdir -p bert/mri/orig`
- `mri_convert rawdata.nii bert/mri/orig/001.mgz`
- `mri_convert rawdata.nii bert/mri/orig/002.mgz`
- `recon-all -all -s bert`



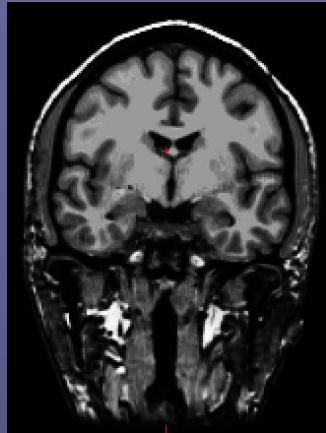
FreeSurfer Output

- Volumes
- Surfaces
- Surface Overlays
- ROI Summaries

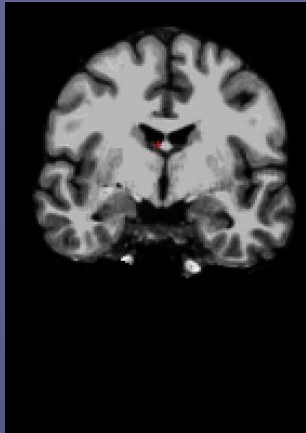
Volumes



orig.mgz



T1.mgz



brainmask.mgz

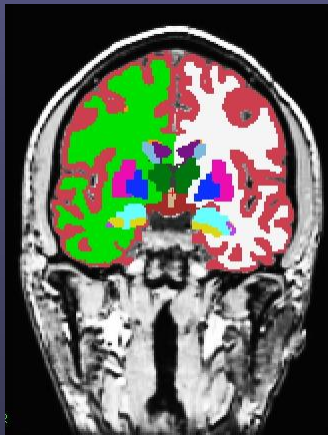


wm.mgz

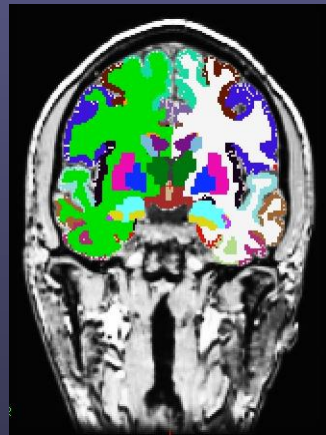


filled.mgz

Subcortical Mass



aseg.mgz

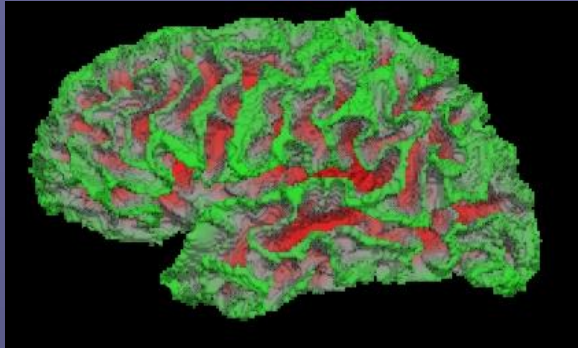


aparc+aseg.mgz

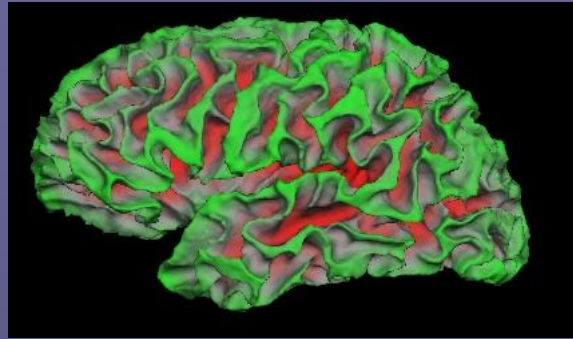
- `$$SUBJECTS_DIR/bert/mri`
- All “Conformed” 256^3 , 1mm
- File format: .mgz

Volume Viewer:
tkmedit

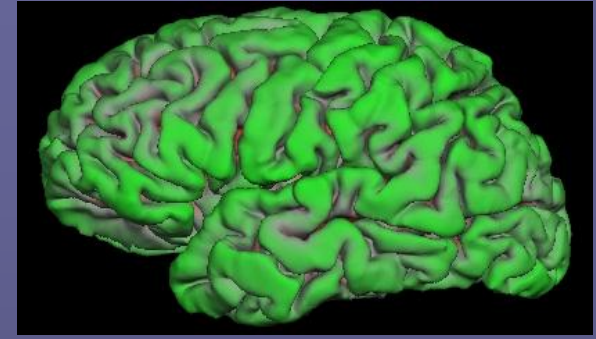
Surfaces



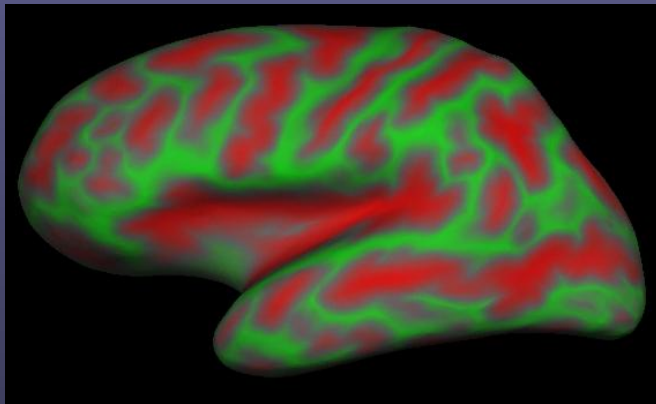
.orig



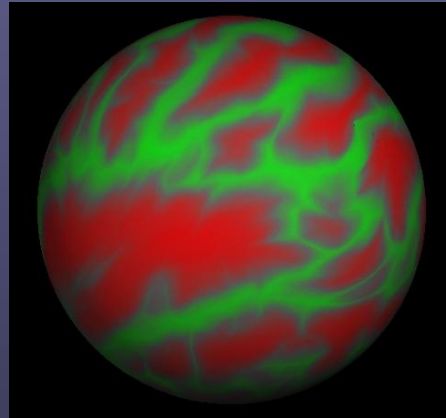
.white



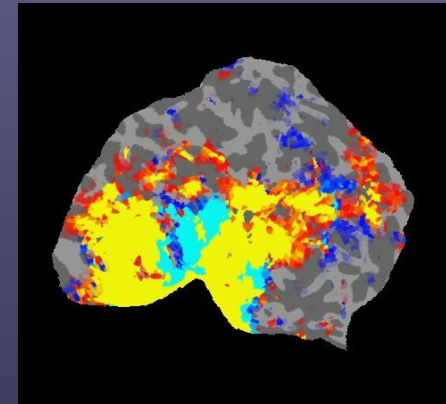
.pial



.inflated



sphere, sphere.reg



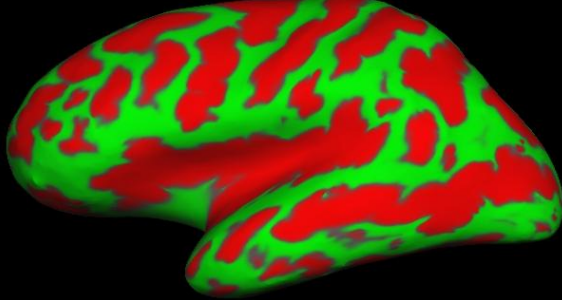
flat

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

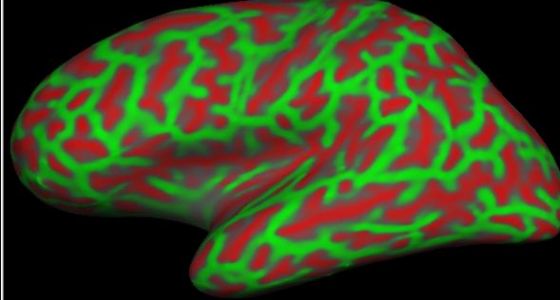
Surface Viewer:
tksurfer

Surface Overlays

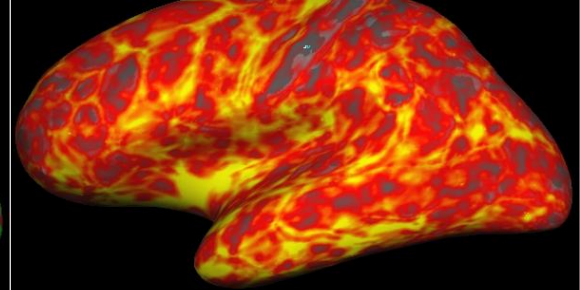
lh.sulc on inflated



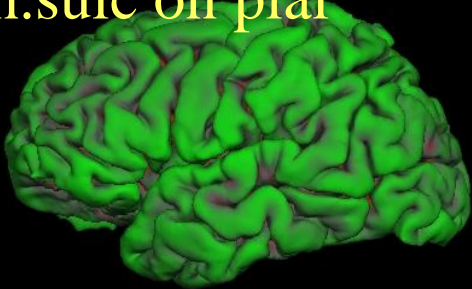
lh.curv on inflated



lh.thickness on inflated



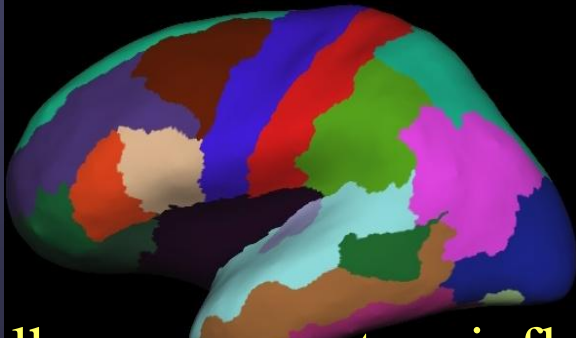
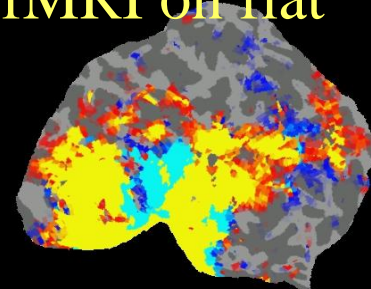
lh.sulc on pial



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

Other FreeSurfer File Formats

Unique to FreeSurfer

- Surface: lh.white, lh.pial, lh.orig
- Curv: lh.curv, lh.sulc, lh.thickness
- Annotation: lh.aparc.annot
- Label: lh.pericalcarine.label

Why use FreeSurfer?

What happens?

How do I do that?

Now What?

Quality Check Your Recon

- Do your surfaces follow gm/wm borders?
- Does the subcortical segmentation follow intensity boundaries?

Troubleshooting

recon-all fails

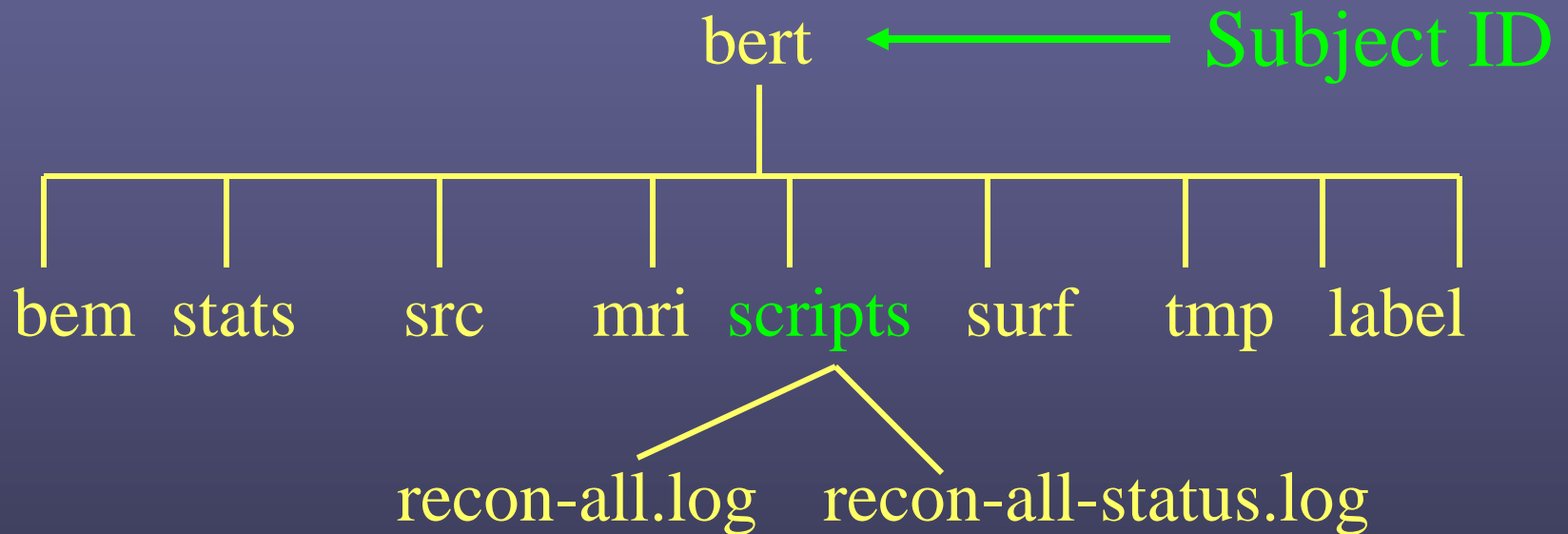
- check recon-all.log
- try to rerun step that failed
- look at volume from last successful step
- examine data quality to see what might cause error
- if it fails again, attempt to run modified version of command if possible
- search FreeSurfer mailing list for other instances of this problem:

<http://www.mail-archive.com/freesurfer@nmr.mgh.harvard.edu/>

- email the mailing list if still need help

FreeSurfer Directory Tree

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

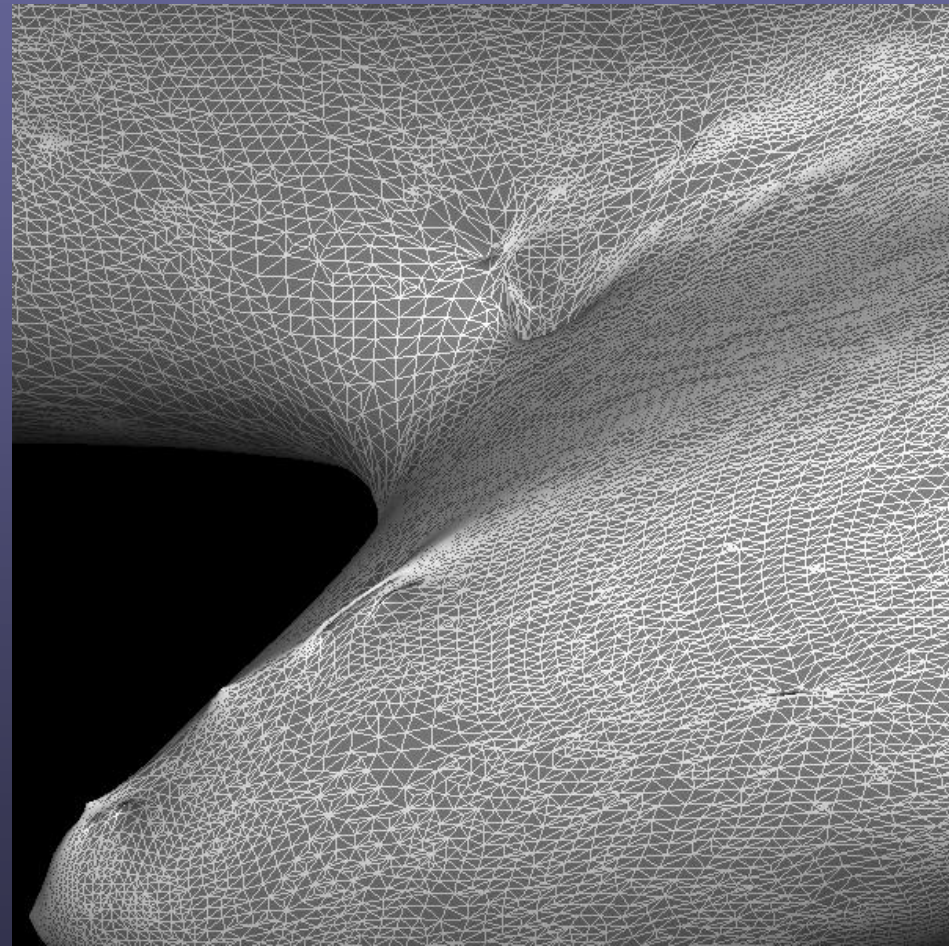


Bug Reporting

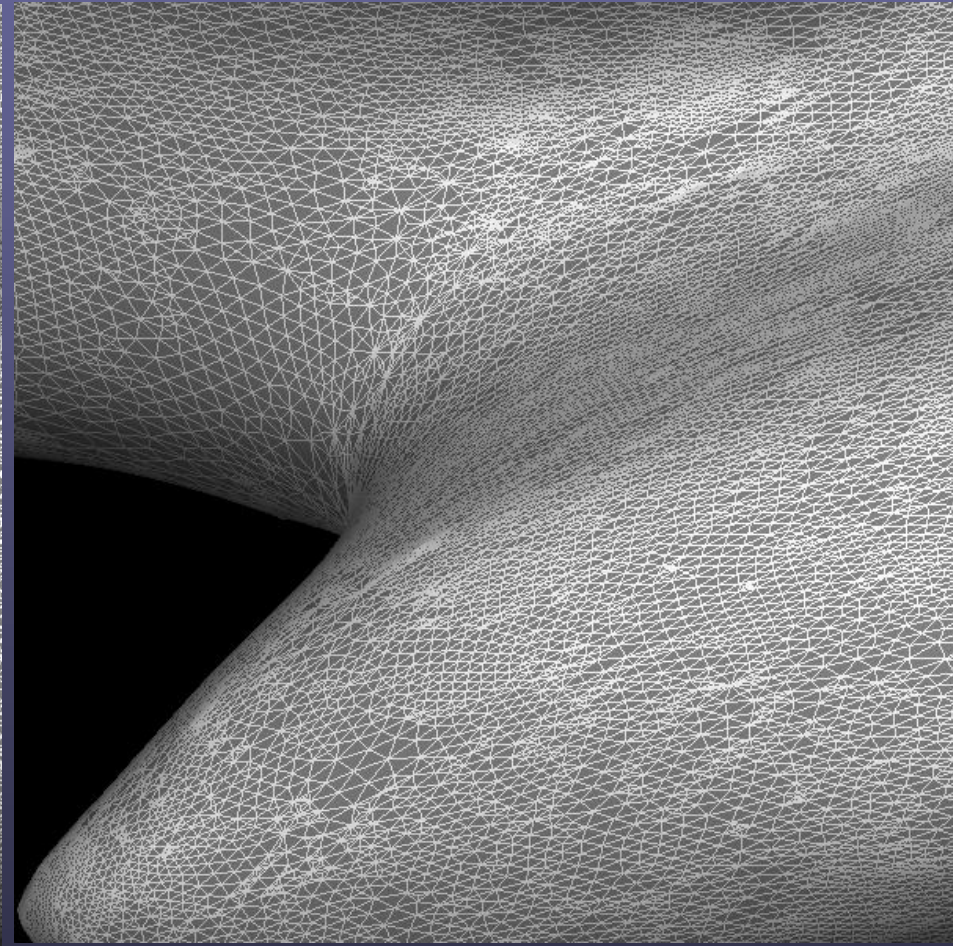
- Report version currently using
 - see top of recon-all.log
 - more `$FREESURFER_HOME/build-stamp.txt`
- command line tried to run
- attach recon-all.log
- Output in terminal window if appropriate
- Operating System

The End

Manifold Surgery



BEFORE



AFTER

Problems with Affine (12 DOF) Registration

- ROIs need to be individualized.

