

Introduction to FreeSurfer

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Resources

- Make sure you sign-in!
- Tutorial Slides available:
 - <http://rcs.bu.edu/examples/imaging>
- Using FreeSurfer on the SCC Documentation:
 - <http://rcs.bu.edu/examples/imaging/freesurfer/>
- Questions, Problems, Need Help?
 - help@scc.bu.edu
 - mhorn@bu.edu

Outline

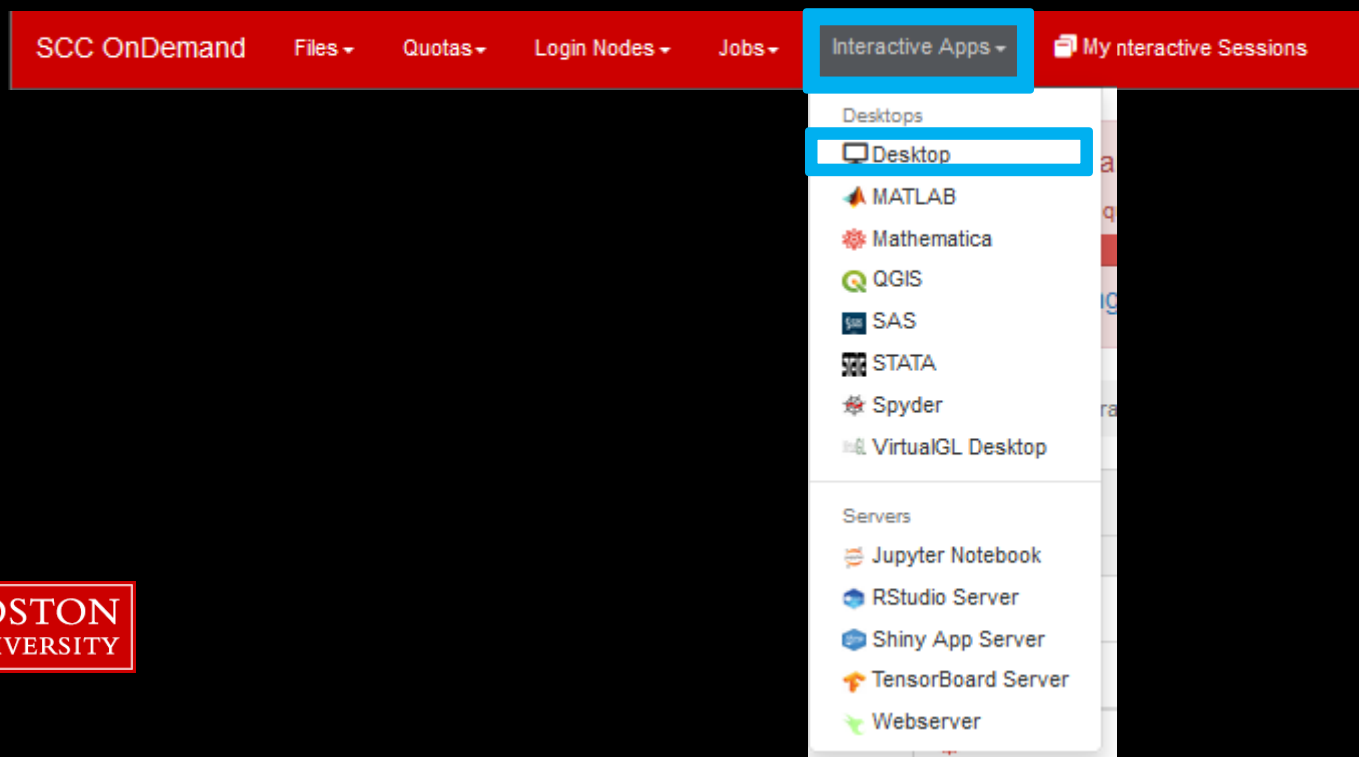
- Tutorial Setup (Hands-On)
- FreeSurfer Terminology/Intro
- Submitting recon-all to the SCC (Hands-On)
- Freeview (Hands-On)
- Review outputs (Hands-On)
- Troubleshooting Data (Hands-On)

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Open an OnDemand session

1. Go to: scc-ondemand.bu.edu
2. Interactive Apps
3. Desktop



Anybody Without an SCC Account?

- `scc-ondemand-tutorial.bu.edu`
- username: `tuta#`
- password:

Open an OnDemand session

Desktop
This app will launch an interactive desktop on a compute node.

List of modules to load (space separated)

Working Directory

The directory to start in. (Defaults to home directory.)

Initial command to run

Number of hours

Number of cores

Number of gpus

Project

Extra qsub options

I would like to receive an email when the session starts

* The Desktop session data for this session can be accessed under the data root directory.

12 hours

1 core

project-ID

click launch!

Open an OnDemand session

Desktop (6994379) 1 core | Running

Host: [>_scc-bb3](#) Delete

Created at: 2022-08-29 11:12:24 EDT

Time Remaining: 19 hours and 53 minutes

Session ID: [afff80fb-ca1f-44fd-a440-0637da849e84](#)

Compression Image Quality

0 (low) to 9 (high) 0 (low) to 9 (high)

[Connect to Desktop](#) View Only (Share-able Link)

click Connect to Desktop!

Tutorial Setup

```
[~]$source /project/scv/examples/imaging/tut_fs_scc/get_data.sh
```

Tutorial Setup

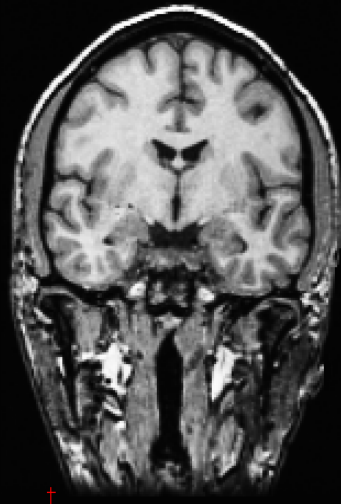
- 1. We copied tutorial data to \$TMPDIR**
- 2. We loaded the FreeSurfer module**
- 3. We copied 2 input images to \$HOME**
- 4. We created an alias for Freeview**
- 5. We switched to the SUBJECTS_DIR**

Questions?

Outline

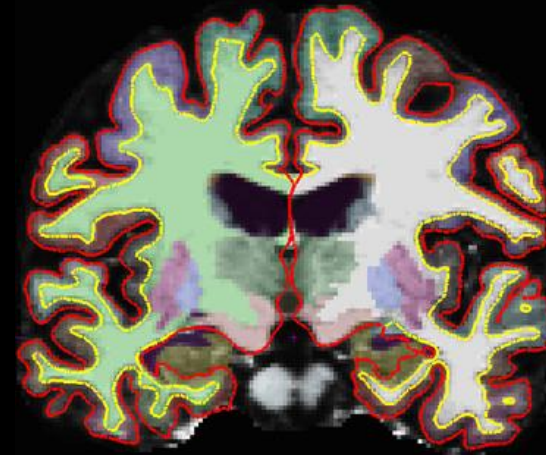
- Tutorial Setup (Hands-On)
- **FreeSurfer Terminology/Intro**
- Submitting recon-all to the SCC (Hands-On)
- Freeview (Hands-On)
- Review outputs (Hands-On)
- Troubleshooting Data (Hands-On)

What FreeSurfer Does



Input:

T1-weighted (MPRAGE)
1mm³ resolution
(.dcm)



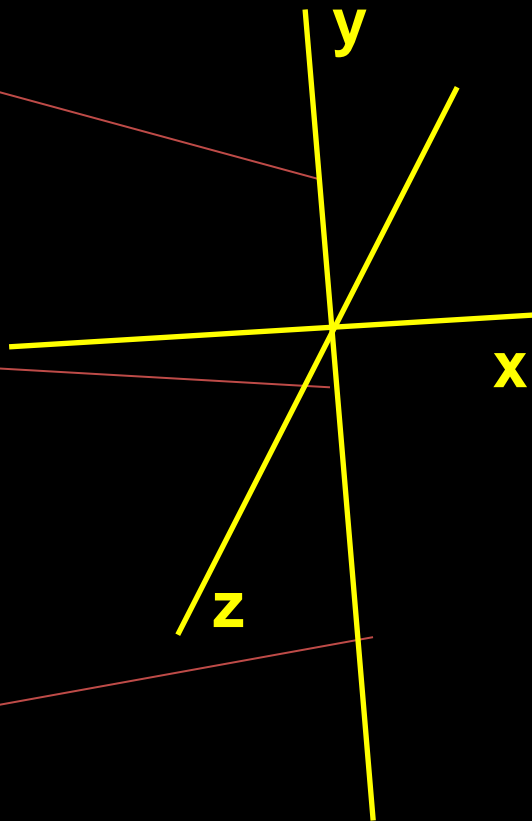
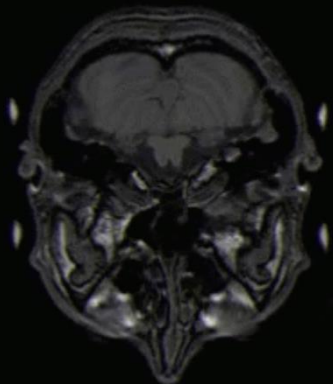
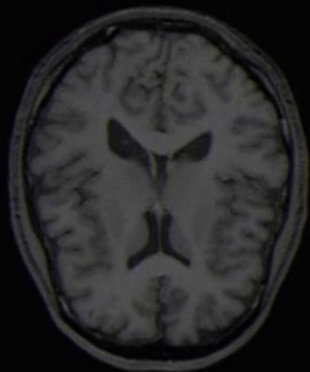
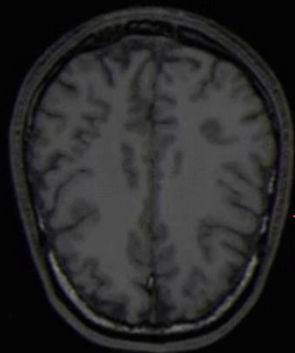
Output:

Segmented & parcellated
conformed volume
(.mgz)

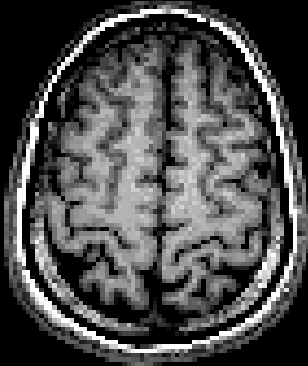
SUBJECTS_DIR

- This is FreeSurfer variable path
- FreeSurfer commands default to this directory for inputs and outputs
- You will find yourself defining and redefining this path variable

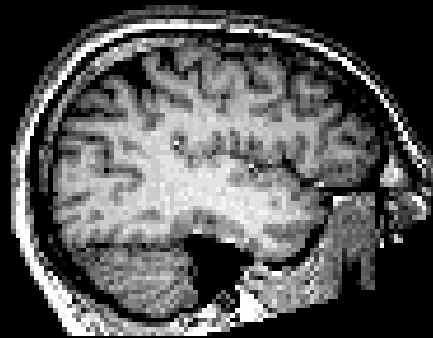
Volumes



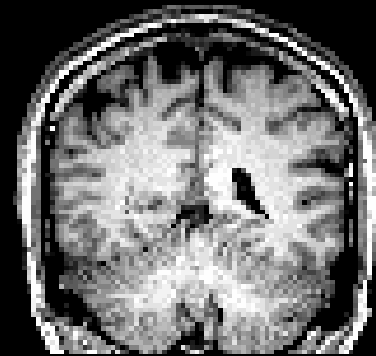
Volumes



axial



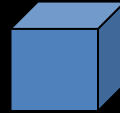
sagittal



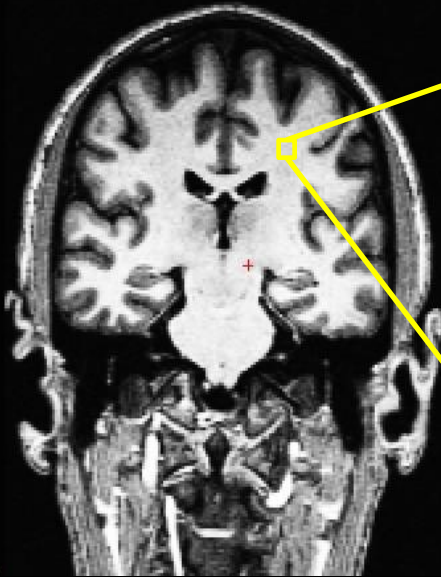
coronal

Voxel

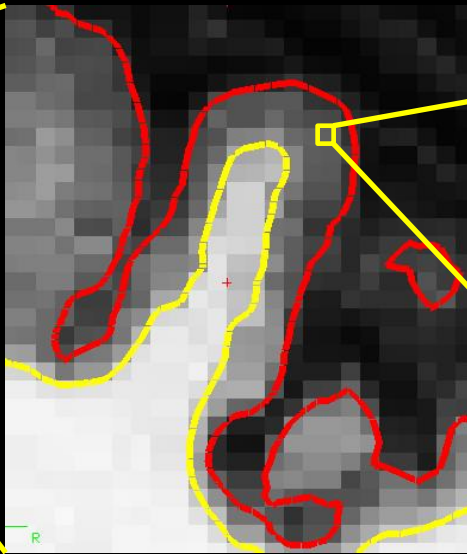
(volume element)



volume



75 voxels

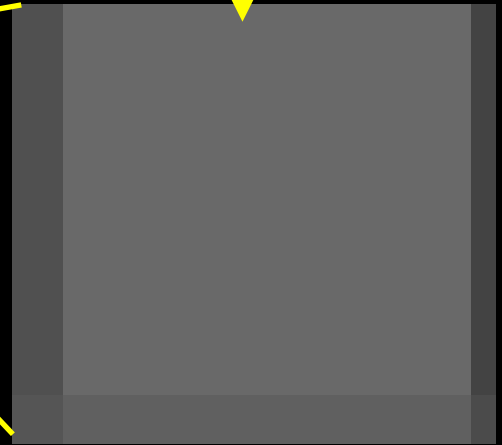


75 voxels

voxel



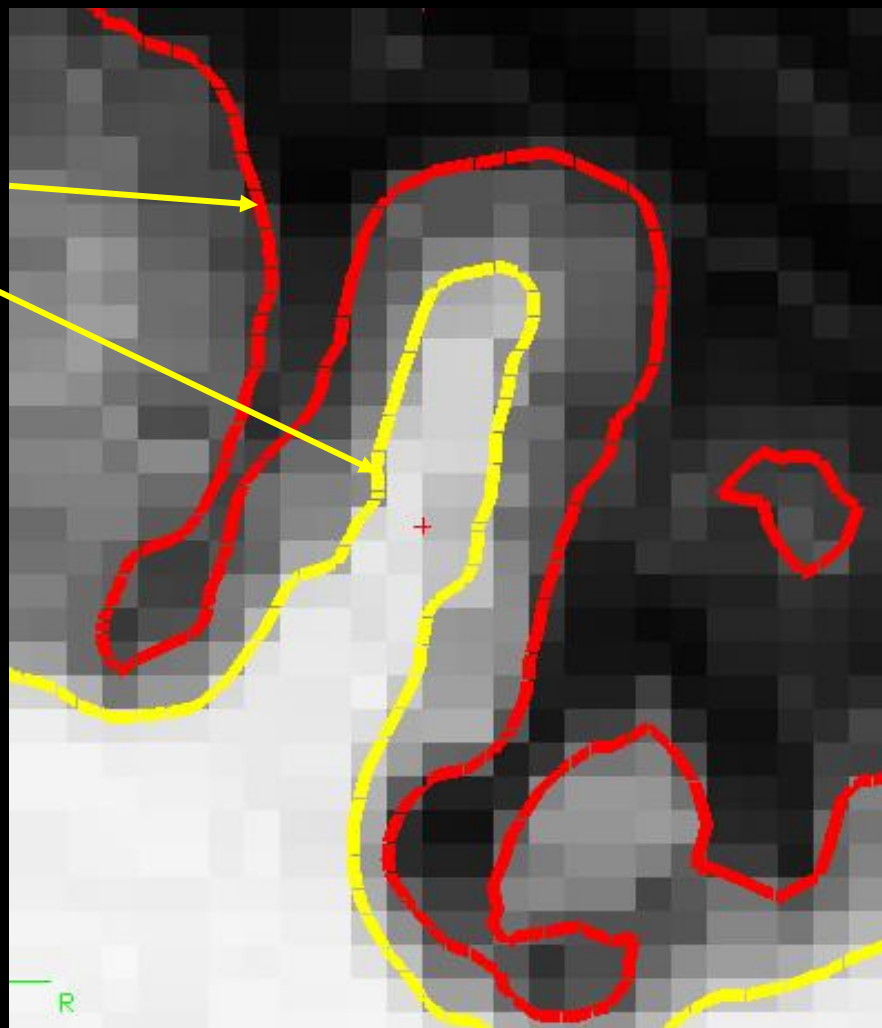
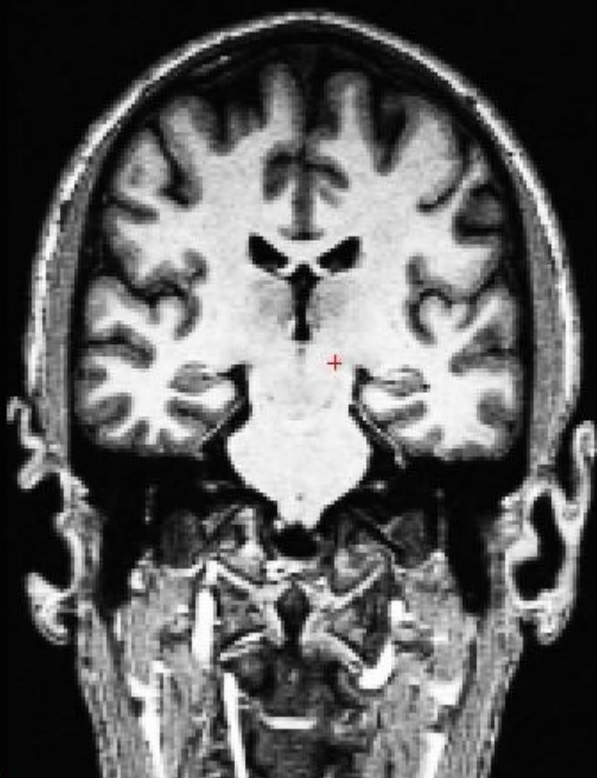
1 voxel



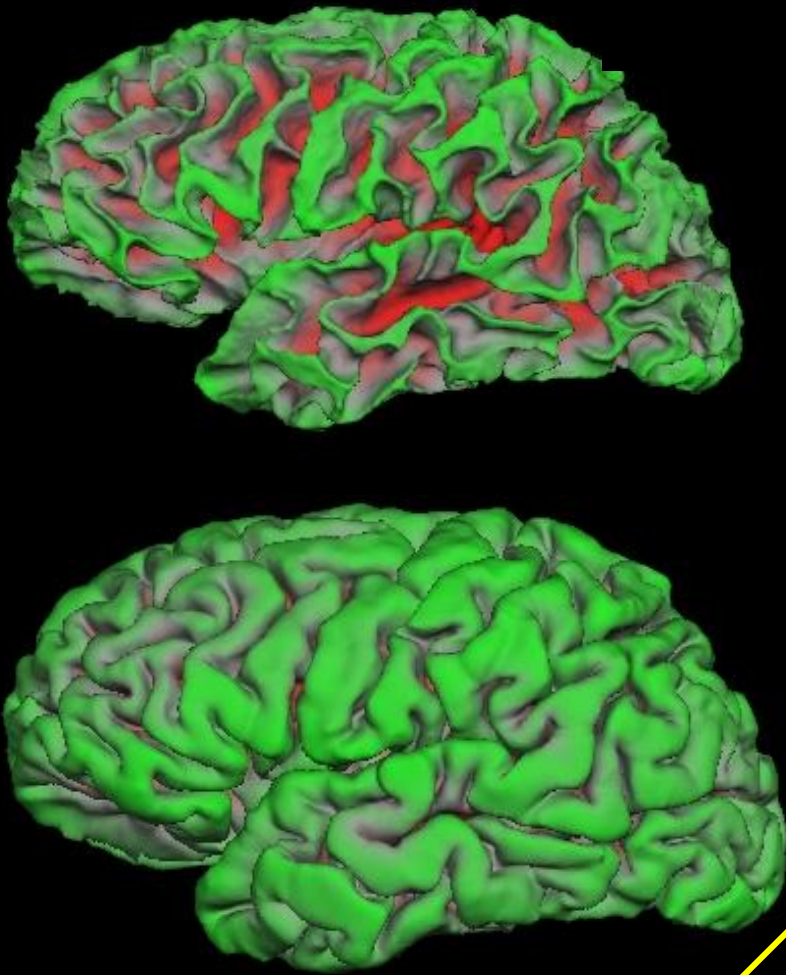
1 voxel

Surface

surfaces



Surface

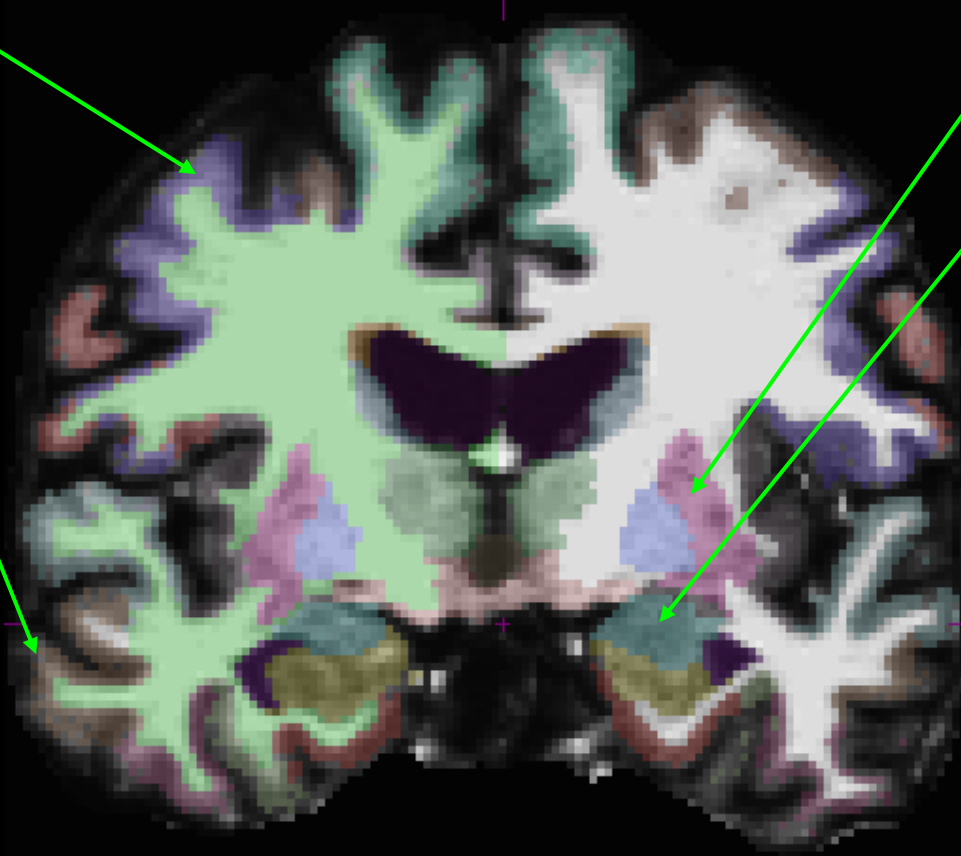


surface

Parcellation vs. Segmentation

(cortical) parcellation

(subcortical) segmentation



A Brief History

- Began as a means for EEG/MEG Analysis
 - Improved localization of cortical activity by combining EEG and MEG with MRI cortical surface reconstruction: a linear approach. AM Dale, MI Sereno. Journal of cognitive neuroscience 5 (2), 162-176, 1994.
 - Dynamic statistical parametric mapping: combining fMRI and MEG for high-resolution imaging of cortical activity. AM Dale, AK Liu, et al, Neuron 26 (1), 55-67, 2000.
- Major unanswered question in the field”
 - How to model the pial surface?
- Idea from 1999 paper:
 - Model the gray/white boundary to infer the pial surface locations

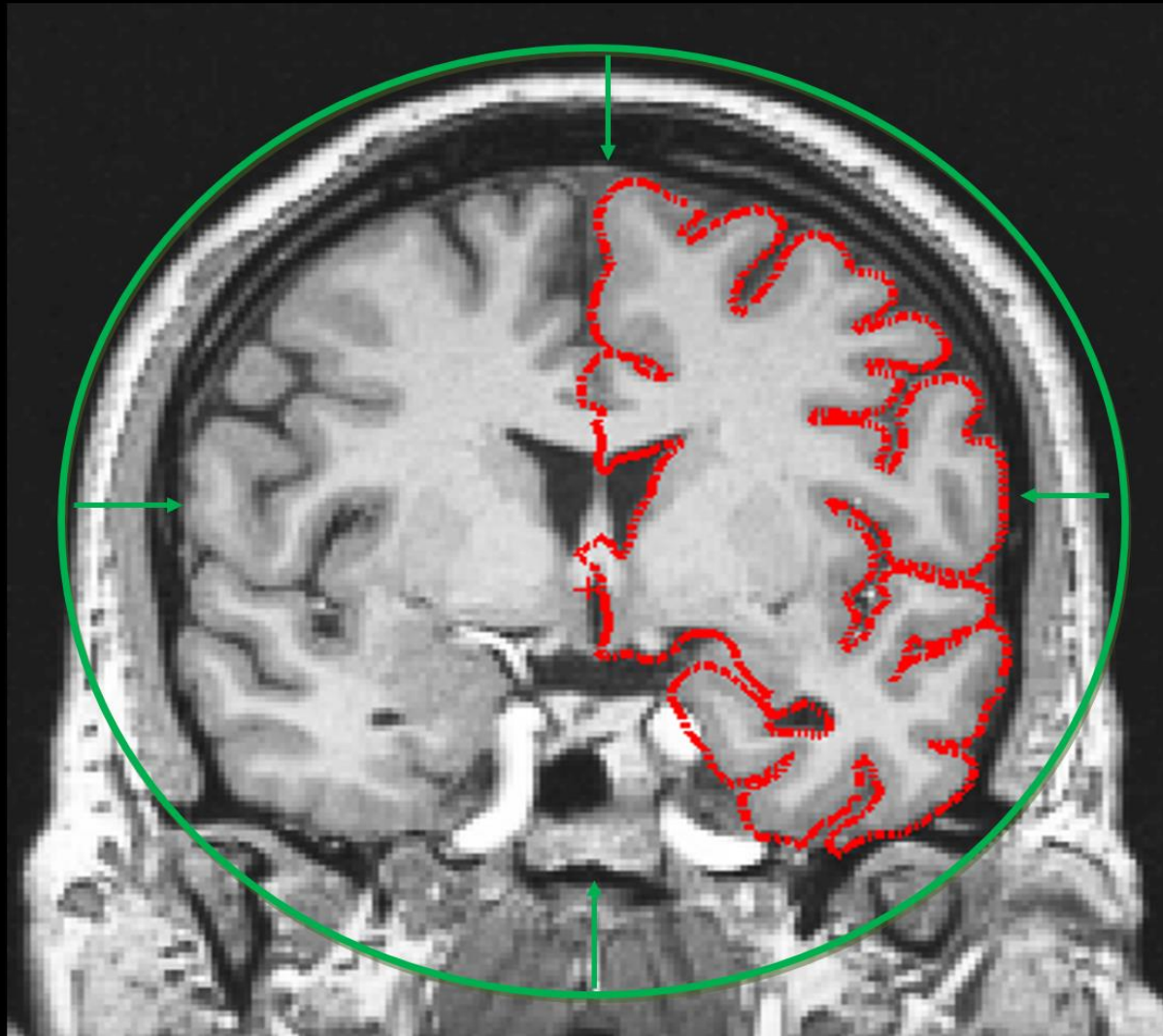


A Brief History

- Goal was to create a topologically correct model (with no handles/holes) so that:
 - 1. distances along the surface aren't dramatically distorted
 - 2. it is possible to establish point-to-point registration across subjects for every point in the cortex.
- Only technique at the time was “shrink wrapping”
 - Start with a surface of the correct topology as a sphere and deform it so that it settle son the true pial surface.
- Problem:
 - Shrink wrapping a highly-folded surface like the brain is **HARD!**

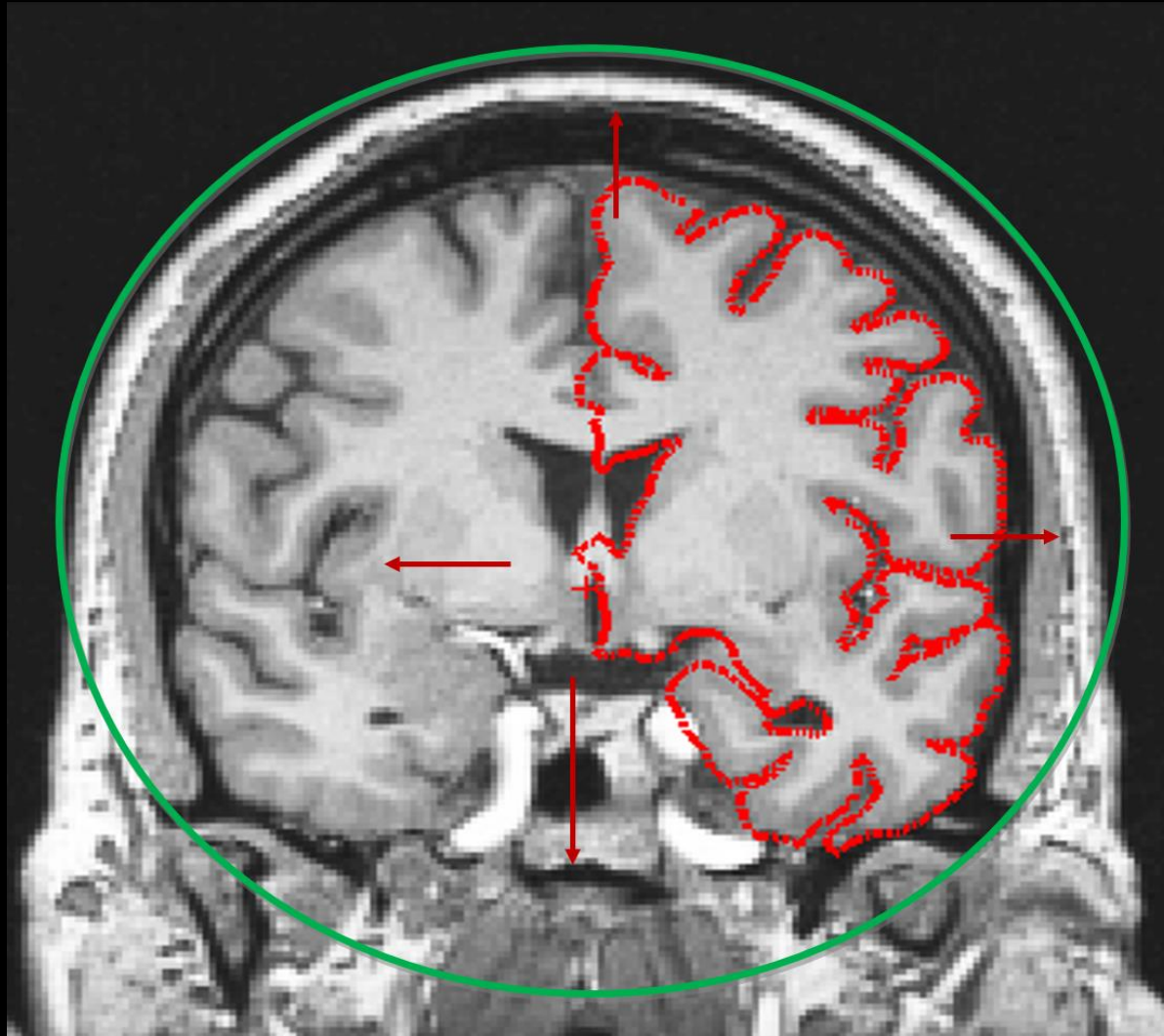
A Brief History: Goal 1

Shrink Wrapping: 1999



A Brief History: Goal 1

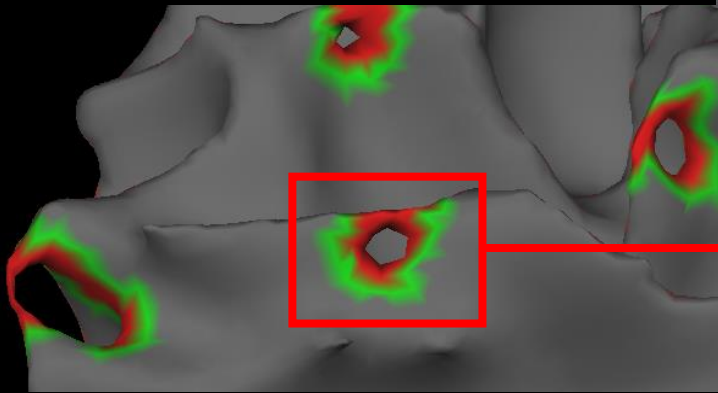
Topology Correction: 1999



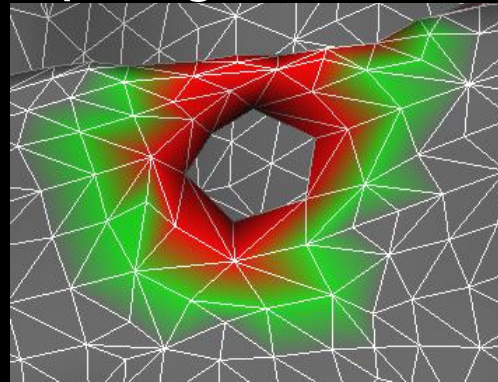
A Brief History: Goal 1

Automatic Defect Correction: 1999

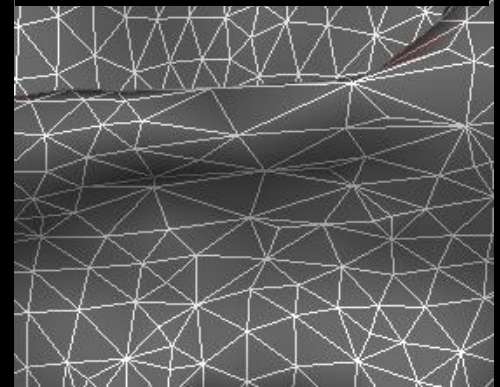
Initial cortical surface



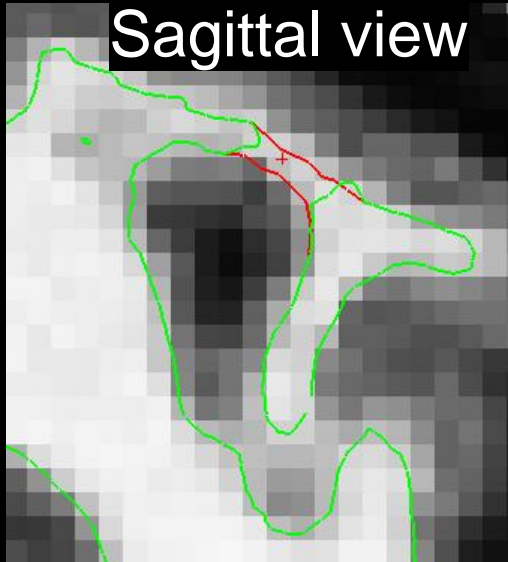
Topological defect



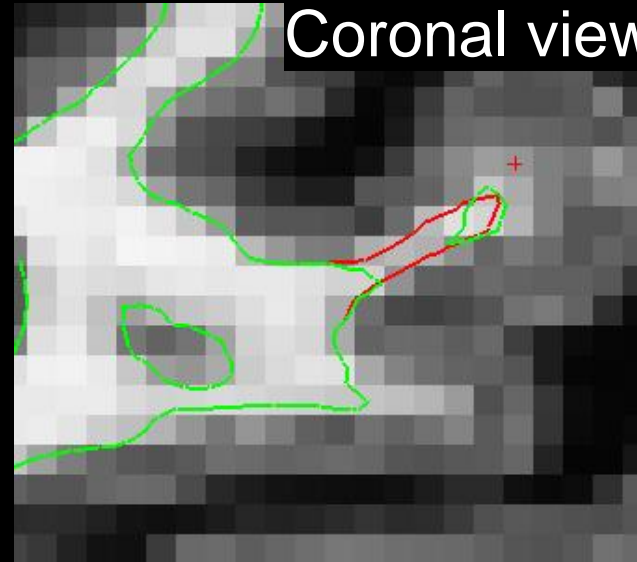
Corrected defect



Sagittal view



Coronal view

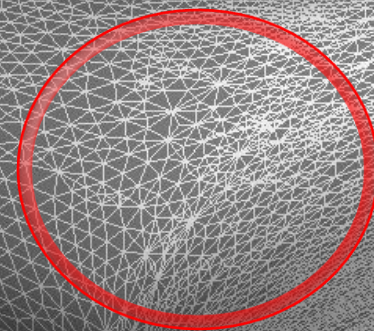
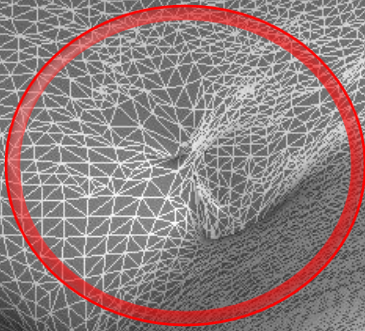


A Brief History: Goal 1

Topology Correction via Manifold Surgery: 2001

Before

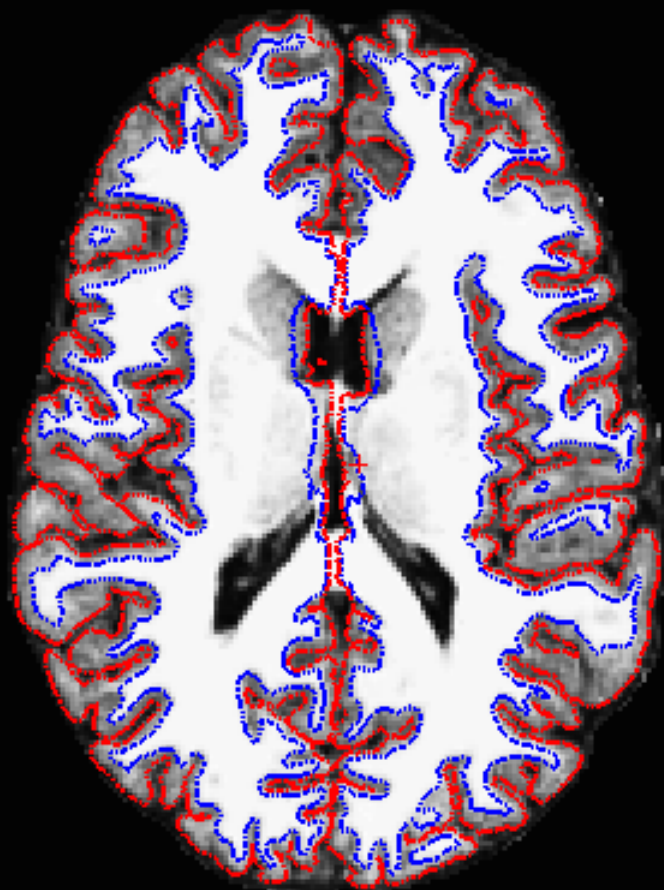
After



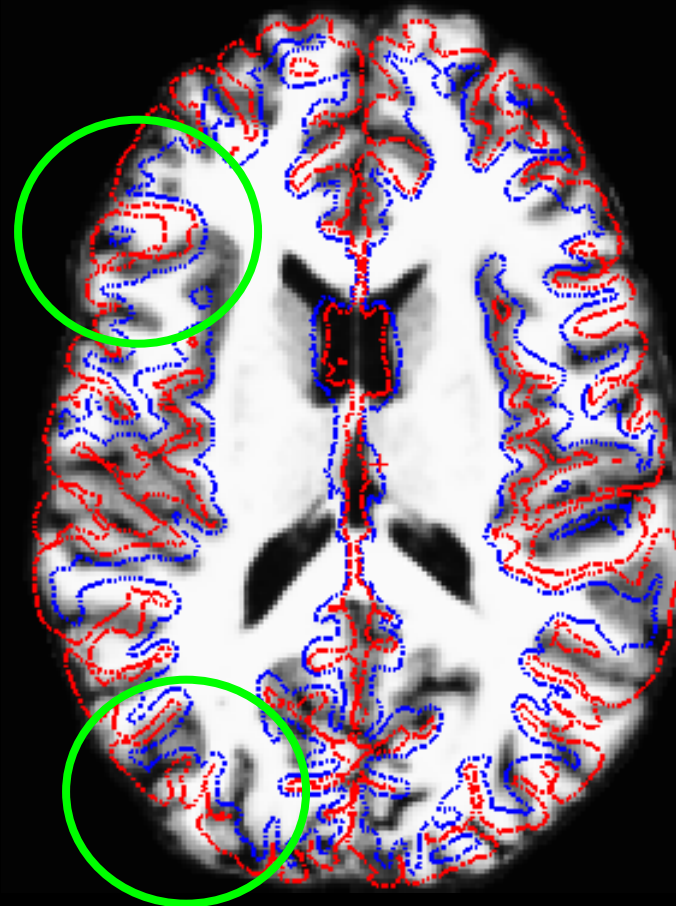
A Brief History: Goal 2

Problems with Affine Registration: 2001

sub-1

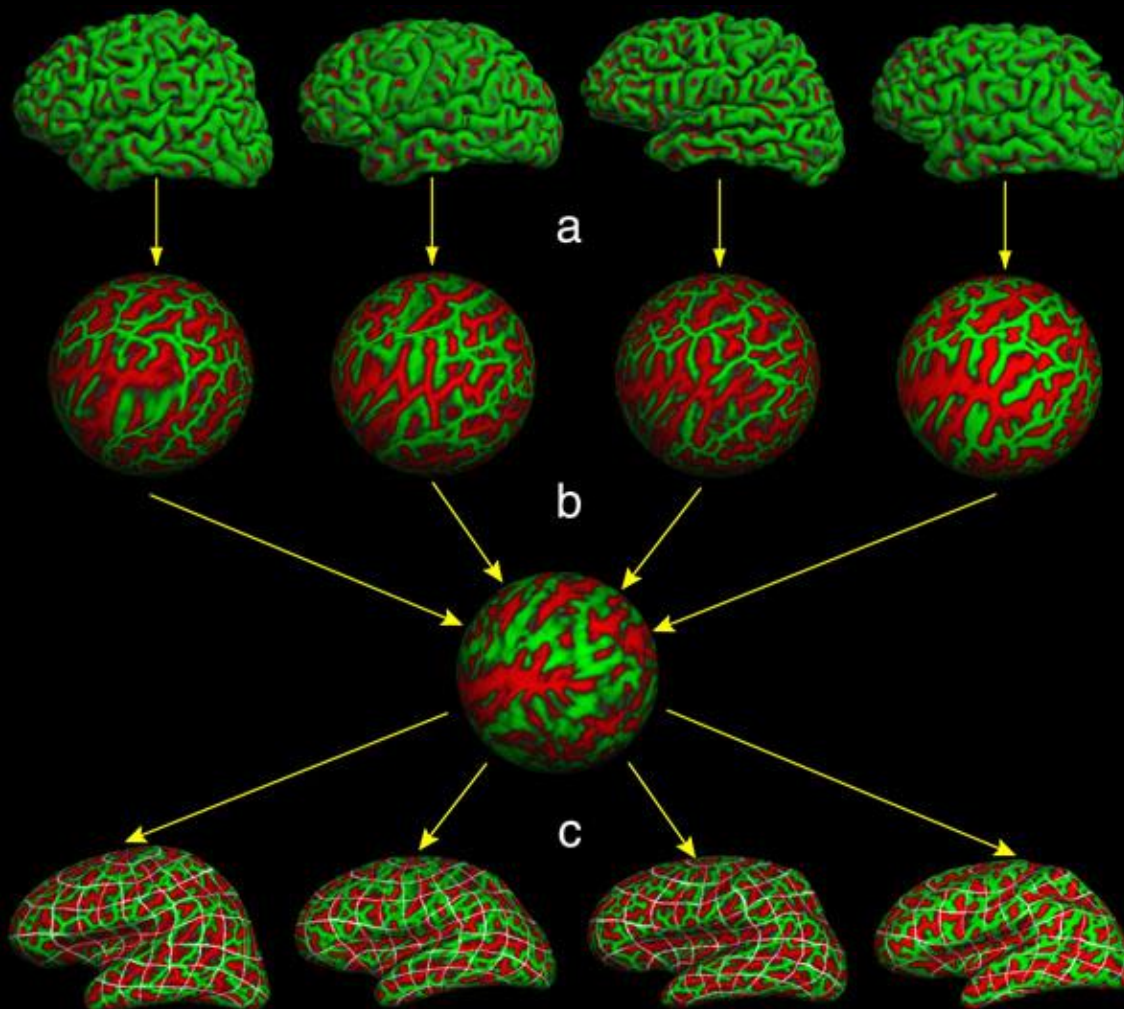


sub-2 aligned with sub-1



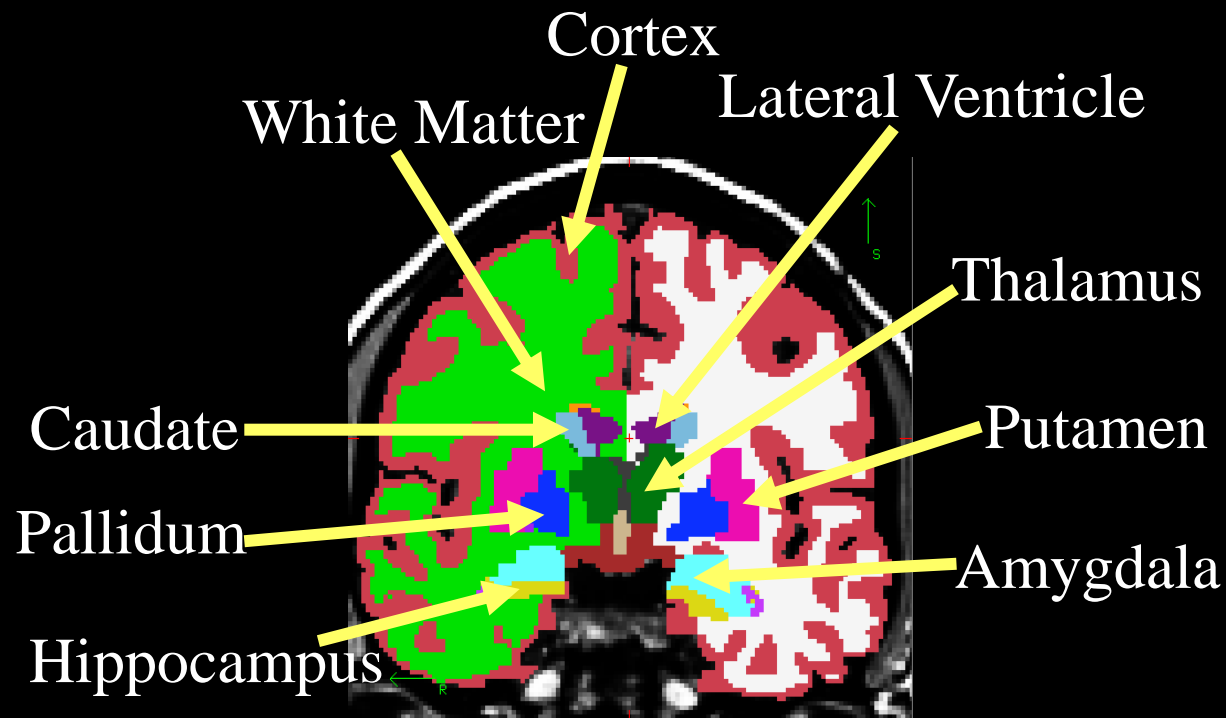
A Brief History: Goal 2

Using a surface-based registration in a common space: 2001



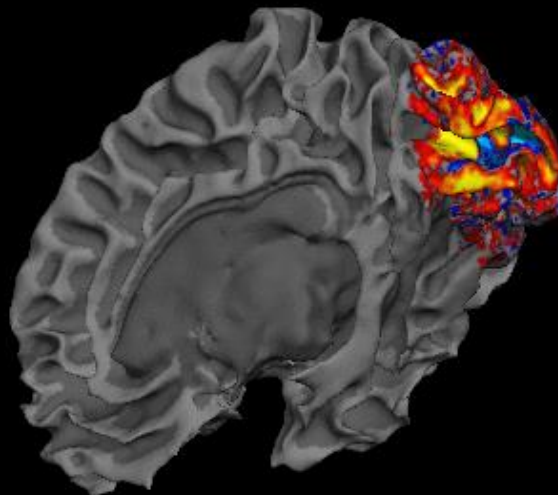
A Brief History: Major Addition

Adding the Aseg: 2002



Why

- What's special about FreeSurfer?:
 - Generates cortical surfaces from grey matter segmentation
 - Fully automated
 - Has surface-base group registration capabilities
 - High accuracy of subcortical structure measurements.



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- **Submitting recon-all to the SCC (Hands-On)**
- Freeview (Hands-On)
- Review outputs (Hands-On)
- Troubleshooting Data (Hands-On)

Submitting a recon

```
recon-all -all -subjid sub-001 -i $SUBJECTS_DIR/sub001.nii.gz
```


Submitting a recon

```
recon-all -all -subjid sub-001 -i $SUBJECTS_DIR/sub001.nii.gz
```



Command for FreeSurfer reconstruction

Submitting a recon

```
recon-all -all -subjid sub-001 -i $SUBJECTS_DIR/sub001.nii.gz
```



flag for which 'recon' processes are to be executed

Submitting a recon

```
recon-all -all -subjid sub-001 -i $SUBJECTS_DIR/sub001.nii.gz
```



flag for instructing next argument is the subject ID

Submitting a recon

```
recon-all -all -subjid sub-001 -i $SUBJECTS_DIR/sub001.nii.gz
```



Subject ID

Submitting a recon

```
recon-all -all -subjid sub-001 -i $SUBJECTS_DIR/sub001.nii.gz
```



flag for next argument is the input MRI image

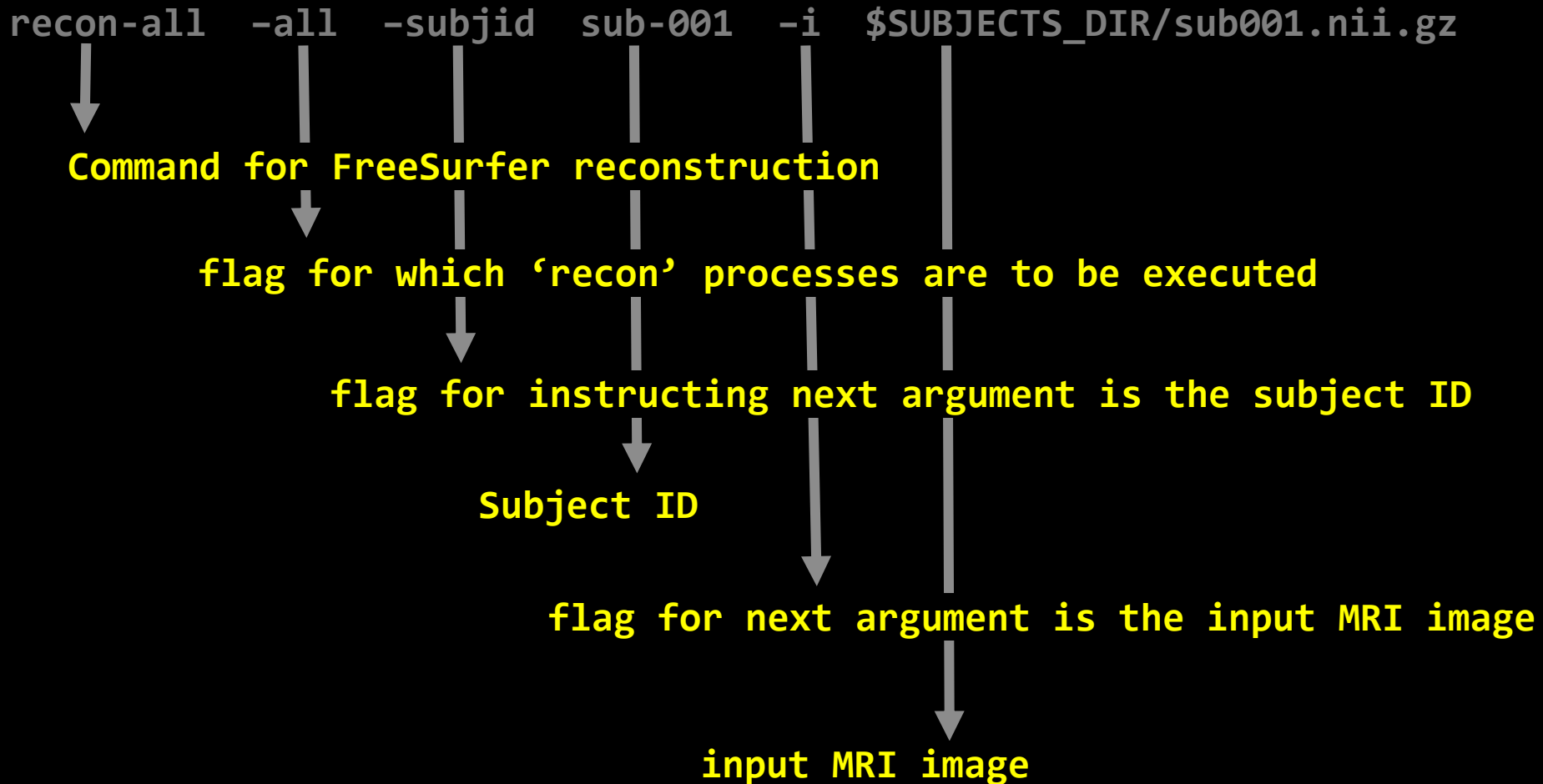
Submitting a recon

```
recon-all -all -subjid sub-001 -i $SUBJECTS_DIR/sub001.nii.gz
```



input MRI image

Submitting a recon



Submitting a recon

```
[tuta0@scc-v01 ~]$ recon-all -help | less
```

ctrl+z

Submitting a recon

```
[tuta0@scc-v01 ~]$ module load sublime
```

Submitting a recon

```
[tuta0@scc-v01 ~]$ sublime recon_SS.qsub
```

Submitting a recon

```
1 #!/bin/bash -l
2
3 # Set SCC project
4 # $ -P my_project
5
6 # Give job a name
7 # $ -N recon-all
8
9 # Combine output and error files into a single file
10 # $ -j y
11
12 # Load desired version of freesurfer
13 module load freesurfer/7.3.2
14
15 # Set environment variables
16 export SUBJECTS_DIR=$HOME/Fall_2022
17
18 # Set recon-all variables
19 recon-all -all -subjid sub-001 -i $SUBJECTS_DIR/sub001.nii.gz
```

Submitting a recon

```
edit line 4: # $ -P my_project
```



use your project!

save

Submitting a recon

```
[tuta0@scc-v01 ~]$ qsub recon_SS.qsub
```

Why Use Batch Processing

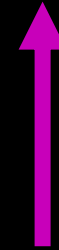
Personal Computer - Non-Parallelized (~40 Hours for 8 Subjects)



SCC - Parallelized (~5 Hours for 8 Subjects)

Submitting a recon

```
[tuta0@scc-v01 ~]$ qstat -u mhorn
```



use your username!

Submitting a recon

1. subject_list.txt

- List of subject ID's and their input T1w

2. recon_MS.qsub

- The submission file containing recon-all

3. recon_bash.sh

- Bash script that loops through each subject and submits

Submitting a recon

```
[tuta0@scc-v01 ~]$ sublime recon_MS.qsub
```

Submitting a recon

```
1 #!/bin/bash -l
2
3 # Set SCC project
4 # $ -P my_project
5
6 # Give job a name
7 # $ -N recon-all|
8
9 # Combine output and error files into a single file
10 # $ -j y
11
12 # Load desired version of freesurfer
13 module load freesurfer/7.3.2
14
15 # Set environment variables
16 export SUBJECTS_DIR=$HOME/Fall_2022
17
18 # Set recon-all variables
19 recon-all -all -subjid $1 -i $2
```

Submitting a recon

```
edit line 4: # $ -P my_project
```



use your project!

save

Submitting a recon

```
[tuta0@scc-v01 ~]$ sublime recon_bash.sh
```

Submitting a recon

```
1 # Set your subject list file
2 subj_list=$HOME/Fall_2022/subj_list.txt
3
4 # Loop and submit to the batch system using the modified recon-all_multi
5 count=$(cat $subj_list | wc -l)
6 for (( i=1; i<=$count; i++ ));
7 do
8     subjid=$(cat $subj_list | head -$i | tail -1 | awk '{print $1}')
9     input=$(cat $subj_list | head -$i | tail -1 | awk '{print $2}')
10    qsub recon_MS.qsub $subjid $input
11 done
```

Submitting a recon

```
[tuta0@scc-v01 ~]$ ./recon_bash.sh
```

Submitting a recon

```
[tuta0@scc-v01 ~]$ qstat -u mhorn
```



use your username!

recon-all

- recon-all with minimal resources
 - 5-8 hours
- Recon-all with parallel pipeline
 - 3-5 hours

Delete recon job(s)

```
[tuta0@scc-v01 ~]$ qstat -u mhorn
```

job-ID	prior	name	user	state	submit/start at	queue	slots	ja-task-ID
7224723	0.11194	recon-all	mhorn	r	09/10/2022 16:18:45	b@scc-bb8.scc.bu.edu		1
7224724	0.11194	recon-all	mhorn	r	09/10/2022 16:18:45	b@scc-bd8.scc.bu.edu		1

```
[tuta0@scc-v01 ~]$ qdel 7334723
```

Questions?

Outline

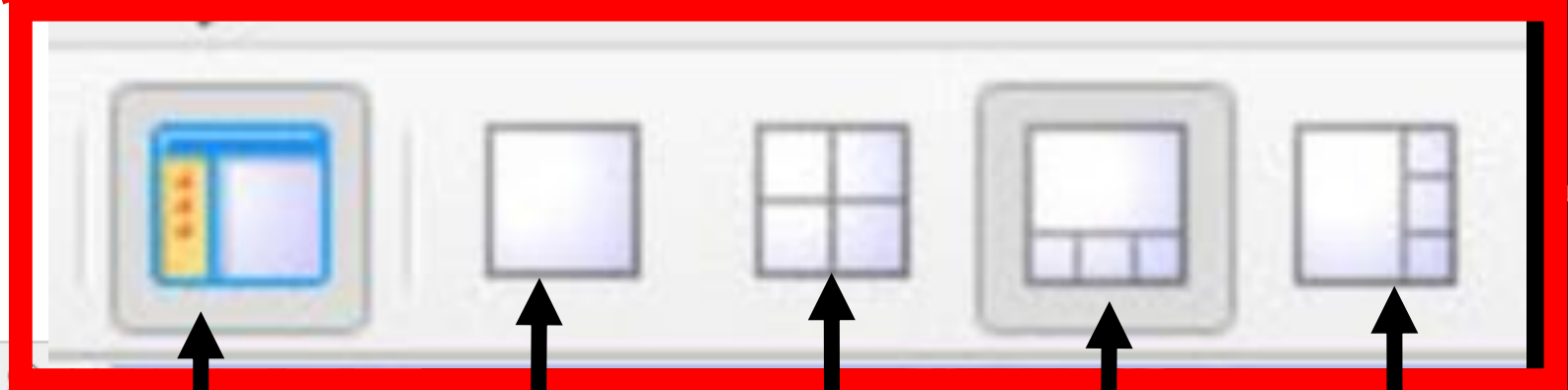
- Tutorial Setup (Hands-On)
- FreeSurfer Terminology/Intro
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- **Freeview (Hands-On)**
- Review outputs (Hands-On)
- Troubleshooting Data (Hands-On)

Freeview

```
[tuta0@scc-v01 ~]$ cd $TMPDIR/Fall_2023/sub-2023/mri
```

Freeview

```
[tuta0@scc-v01 ~]$ freeview T1.mgz
```



side-menu

1-viewport

4-viewport

4-viewport(2)

4-viewport(3)

Opacity 1.00

Smooth display

Color map Grayscale

Window 273.53

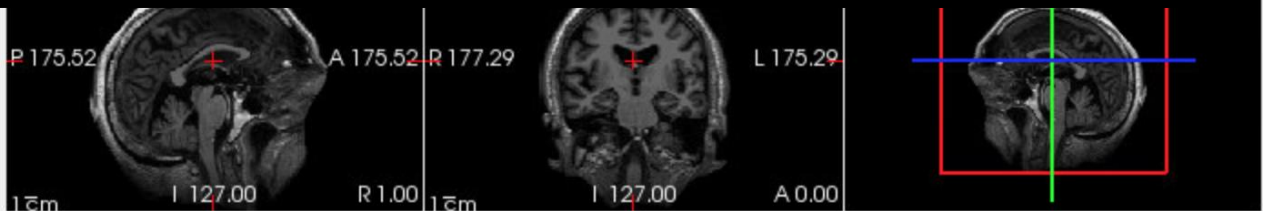
Level 138.81

Min 2.04

Max 275.57

Use percentile

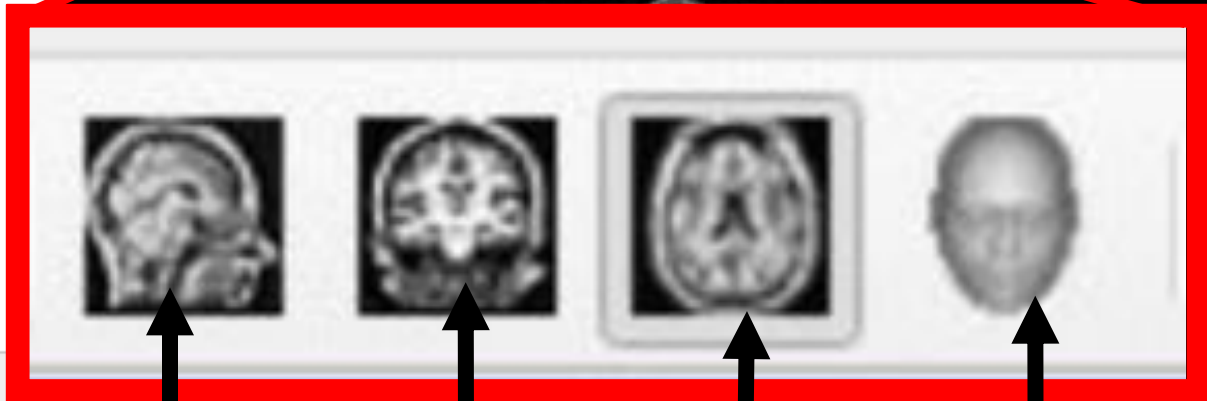
Clear background



Cursor		Mouse	
RAS	1.00, 0.00, 1.00	RAS	432.41, 122.19, 1.00
TkReg RAS (T1)	1.00, 0.00, 1.00	TkReg RAS (T1)	432.41, 122.19, 1.00
MNI305 (T1)	1.39, 0.16, 14.73	MNI305 (T1)	477.95, 137.22, -73.55
T1	23 [127, 127, 128]	T1	0 [-304, 127, 250]



Volumes
✓ T1



sagittal coronal axial 3D

File name /Fall_2022/sub-2022/m

Mask None

Opacity 1.00

Smooth display

Color map Grayscale

Window 273.53

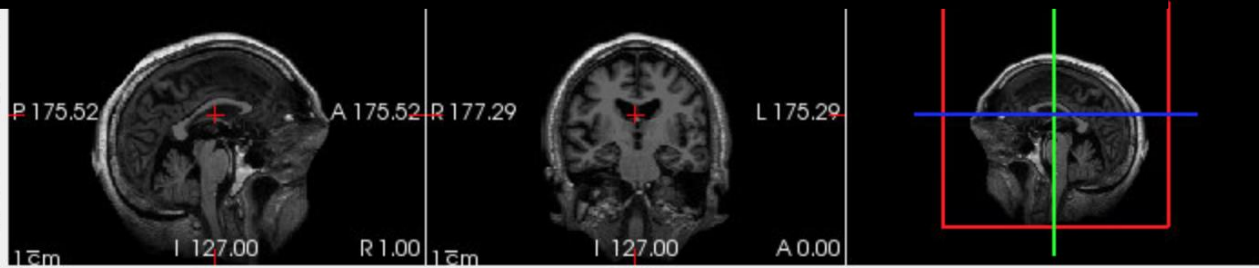
Level 138.81

Min 2.04

Max 275.57

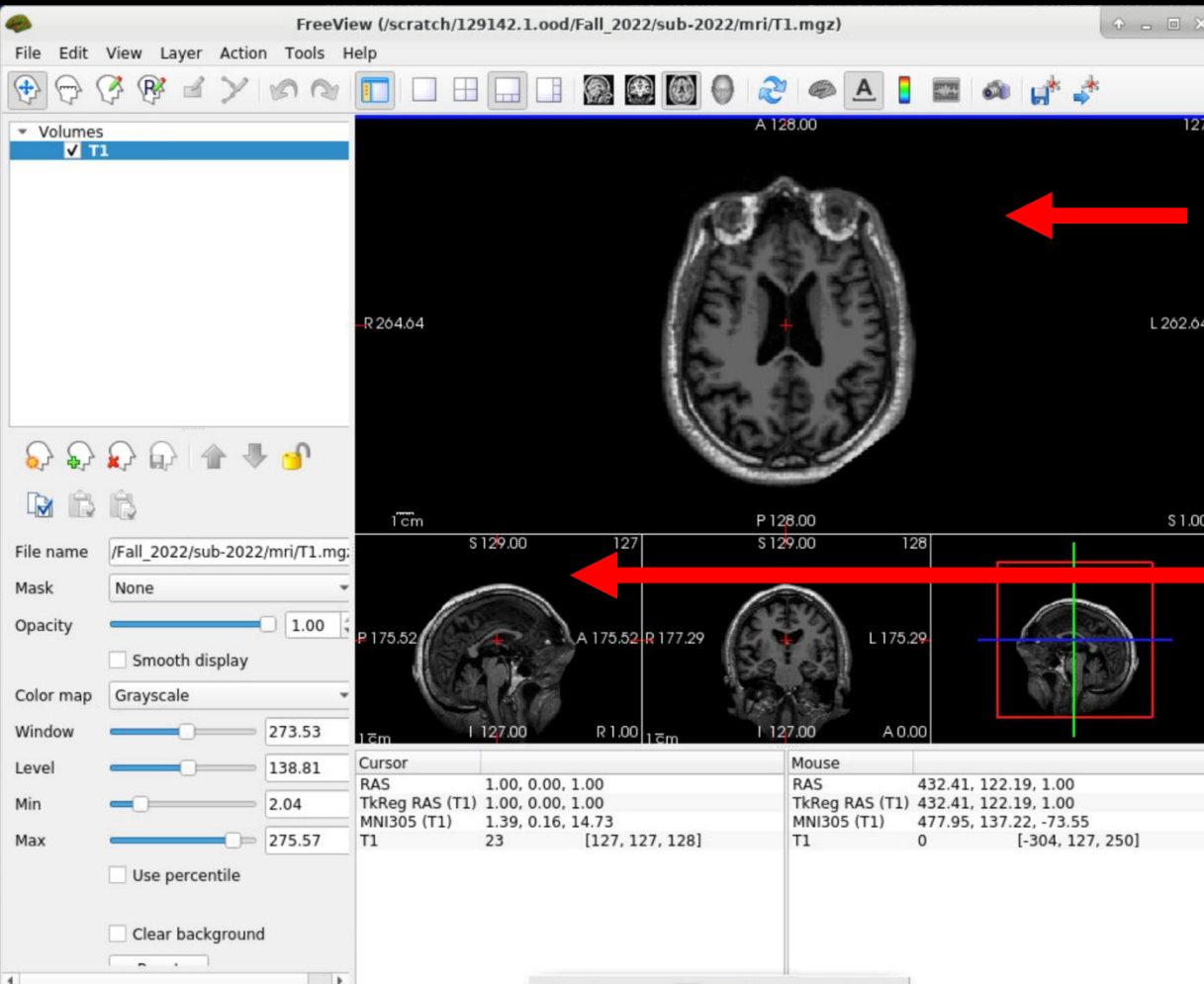
Use percentile

Clear background



Cursor		Mouse	
RAS	1.00, 0.00, 1.00	RAS	432.41, 122.19, 1.00
TkReg RAS (T1)	1.00, 0.00, 1.00	TkReg RAS (T1)	432.41, 122.19, 1.00
MNI305 (T1)	1.39, 0.16, 14.73	MNI305 (T1)	477.95, 137.22, -73.55
T1	23 [127, 127, 128]	T1	0 [-304, 127, 250]

Freeview



Click in a box

Use 

Click another box

Use 



Volumes

- T1



File name: /Fall_2022/sub-2022/mri/T1.mgz

Mask: None

Opacity: 1.00

Smooth display

Color map: Grayscale

Window: 273.53

Level: 138.81

Min: 2.04

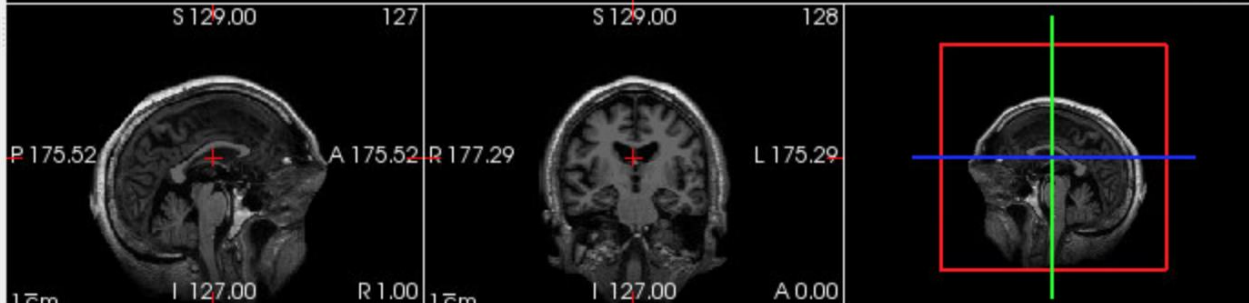
Max: 275.57

Use percentile

Clear background



reset view



Cursor			Mouse		
RAS	1.00, 0.00, 1.00		RAS	432.41, 122.19, 1.00	
TkReg RAS (T1)	1.00, 0.00, 1.00		TkReg RAS (T1)	432.41, 122.19, 1.00	
MNI305 (T1)	1.39, 0.16, 14.73		MNI305 (T1)	477.95, 137.22, -73.55	
T1	23 [127, 127, 128]		T1	0 [-304, 127, 250]	



Volumes

- ✓ T1



File name: /Fall_2022/sub-2022/mri/T1.mgz

Mask: None

Opacity: 1.00

Smooth display

Color map: Grayscale

Window: 273.53

Level: 138.81

Min: 2.04

Max: 275.57

Color map: Grayscale

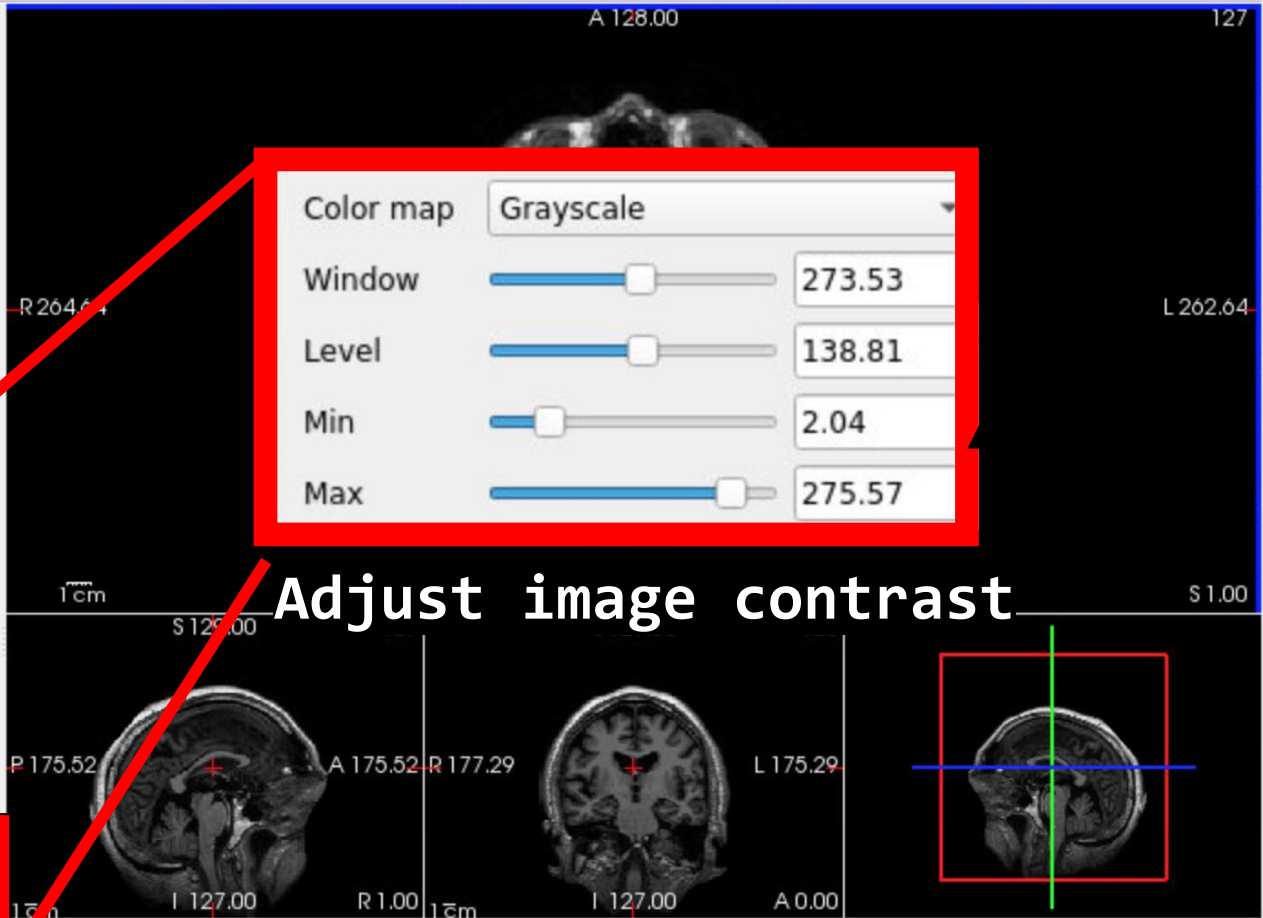
Window: 273.53

Level: 138.81

Min: 2.04

Max: 275.57

Adjust image contrast



Cursor	Mouse
RAS 1.00, 0.00, 1.00	RAS 432.41, 122.19, 1.00
TkReg RAS (T1) 1.00, 0.00, 1.00	TkReg RAS (T1) 432.41, 122.19, 1.00
MNI305 (T1) 1.39, 0.16, 14.73	MNI305 (T1) 477.95, 137.22, -73.55
T1 23 [127, 127, 128]	T1 0 [-304, 127, 250]

Freeview

```
[tuta0@scc-v01 ~]$ ctrl+z
```

```
[tuta0@scc-v01 ~]$ cd ..
```

```
[tuta0@scc-v01 ~]$ fcheck
```

The screenshot displays a neuroimaging software interface with a central 3D brain view and several control panels. The main view shows a brain slice with yellow and blue surface reconstructions. The left panel lists volumes (brainmask, wm, T1) and surfaces (rh.pial, rh.white, lh.pial, lh.white). The bottom-left panel contains settings for file name, opacity, color, render, curvature, and overlay. The bottom-right panel shows coordinate tables for the cursor and mouse.

Volumes

- ✓ brainmask
- ✓ wm
- ✓ T1

Surfaces

- ✓ rh.pial
- ✓ rh.white
- ✓ lh.pial
- ✓ lh.white

File name: /Fall_2022/sub-2022/surf/rh

Opacity: 1.00

Color: Solid Color

Render: Surface

Show vertices

Curvature: Threshold

Mid point: 0

Slope: 10

Overlay: Off

Annotation: Off

Label: New Load Save De

Cursor		Mouse	
RAS	1.00, 0.00, 1.00	RAS	167.12, 38.75, 1.00
TkReg...mask)	1.00, 0.00, 1.00	TkReg...mask)	167.12, 38.75, 1.00
MNI30...mask)	1.39, 0.16, 14.73	MNI30...mask)	185.04, 45.06, -13.98
brainmask	23 [127, 127, 128]	brainmask	0 [-39, 127, 167]
wm	250 [127, 127, 128]	wm	0 [-39, 127, 167]
T1	23 [127, 127, 128]	T1	0 [-39, 127, 167]
rh.pial	SurfaceRAS [1.00, 0.00, 1.00]	rh.pial	SurfaceRAS....75, 1.00]
	Vertex ...5, 0.63]		Vertex N/A
rh.white	SurfaceRAS [1.00, 0.00, 1.00]	rh.white	SurfaceRAS....75, 1.00]
	Vertex ...5, 0.63]		Vertex N/A
lh.pial	SurfaceRAS [1.00, 0.00, 1.00]	lh.pial	SurfaceRAS....75, 1.00]
	Vertex ...5, 0.63]		Vertex N/A

Volumes

- brainmask
- wm
- T1

Surfaces

- rh.pial
- rh.white
- lh.pial
- lh.white

Volumes

- brainmask
- wm
- T1

order matters!

	Cursor	Mouse
RAS	1.00, 0.00, 1.00	167.12, 38.75, 1.00
TkReg...mask)	1.00, 0.00, 1.00	167.12, 38.75, 1.00
MNI30...mask)	1.39, 0.16, 14.73	185.04, 45.06, -13.98
brainmask	23 [127, 127, 128]	0 [-39, 127, 167]
wm	250 [127, 127, 128]	0 [-39, 127, 167]
T1	23 [127, 127, 128]	0 [-39, 127, 167]
rh.pial	SurfaceRAS [1.00, 0.00, 1.00]	rh.pial SurfaceRAS....75, 1.00]
	Vertex ...5, 0.63]	Vertex N/A
rh.white	SurfaceRAS [1.00, 0.00, 1.00]	rh.white SurfaceRAS....75, 1.00]
	Vertex ...5, 0.63]	Vertex N/A
lh.pial	SurfaceRAS [1.00, 0.00, 1.00]	lh.pial SurfaceRAS....75, 1.00]
	Vertex ...5, 0.63]	Vertex N/A

Freeview

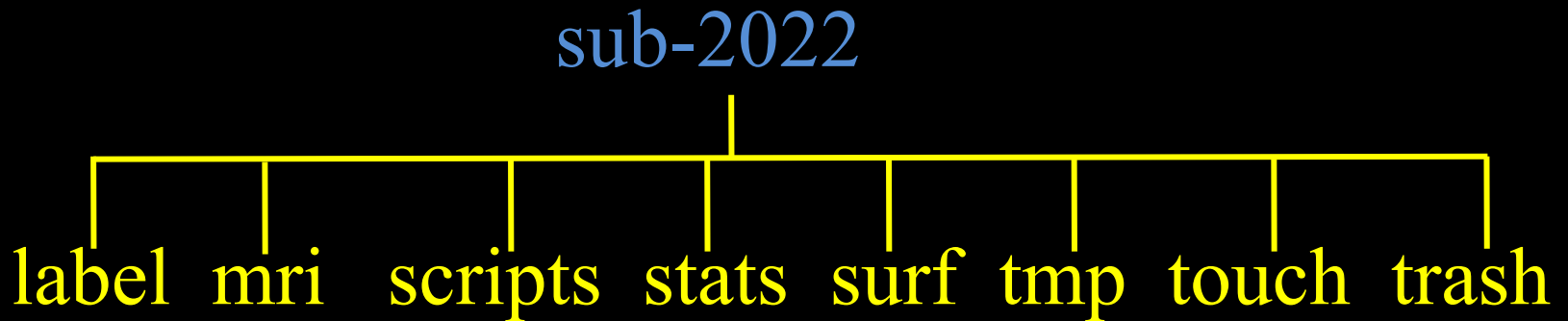
```
[tuta0@scc-v01 ~]$ ctrl+z
```

close freeview

Outline

- Tutorial Setup (Hands-On)
- FreeSurfer Terminology
- Submitting recon-all to the SCC (Hands-On)
- Freeview (Hands-On)
- **Review outputs (Hands-On)**
- Troubleshooting Data (Hands-On)

Outputs

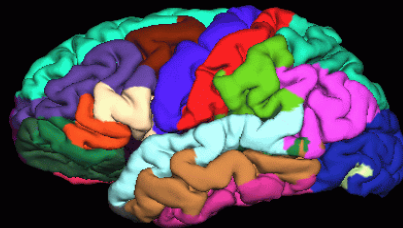


Upon Completion...

sub-2022

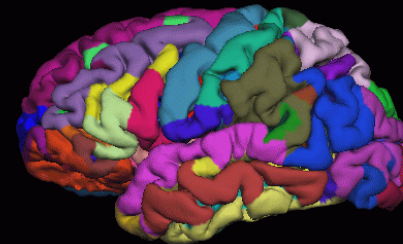
label mri scripts stats surf tmp touch trash

Desikan/Killiany Atlas

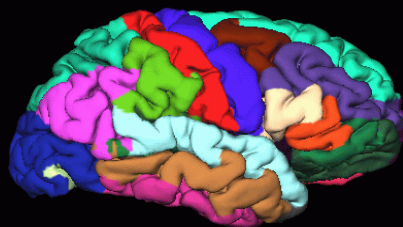


lh.aparc.annot

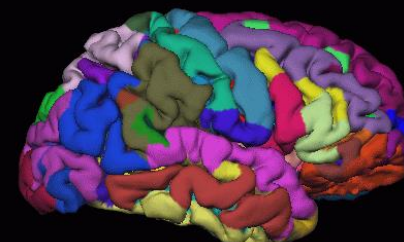
Destrieux Atlas



lh.aparc.a2009s.annot



rh.aparc.annot

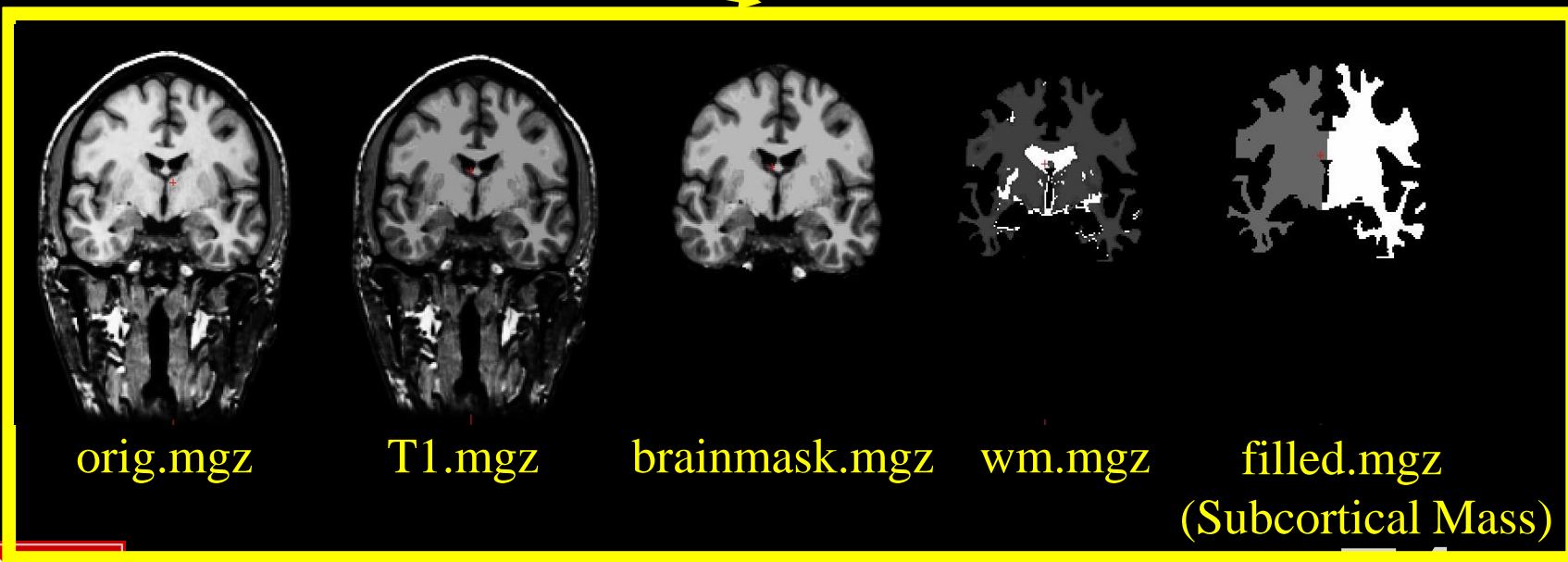


rh.aparc.a2009s.annot

Upon Completion...

sub-2022

label mri scripts stats surf tmp touch trash



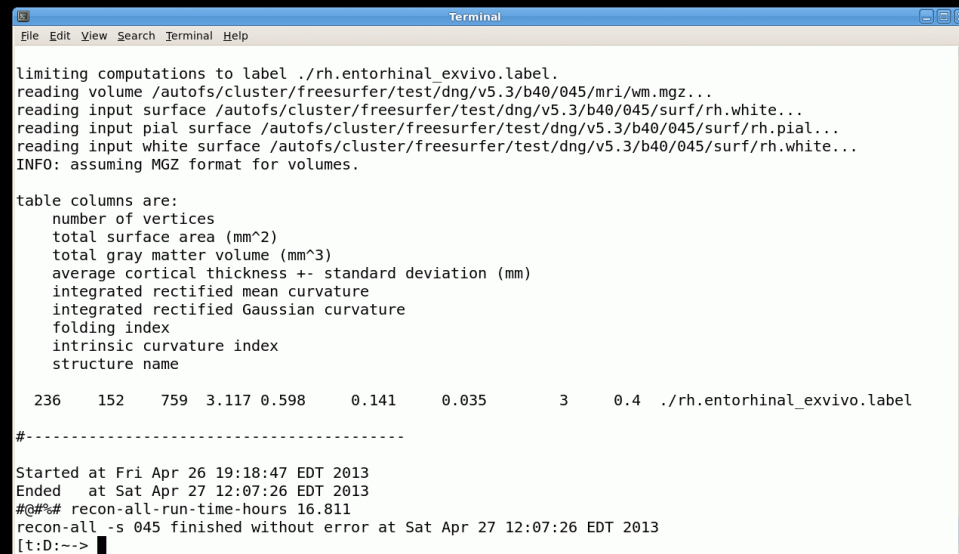
Upon Completion...

sub-2022

label mri scripts stats surf tmp touch trash

recon-all.log
recon-all.done

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



```

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

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

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

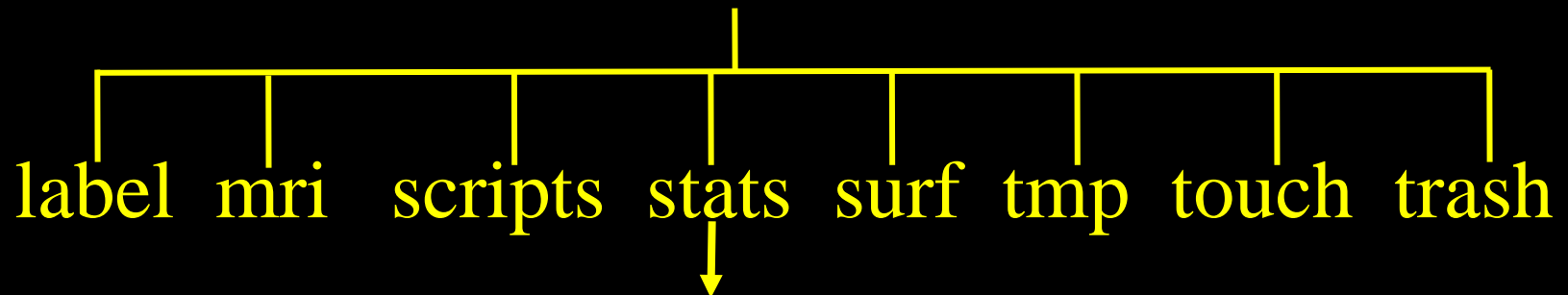
#-----
Started at Fri Apr 26 19:18:47 EDT 2013
Ended at Sat Apr 27 12:07:26 EDT 2013
#@## recon-all-run-time-hours 16.811
recon-all -s 045 finished without error at Sat Apr 27 12:07:26 EDT 2013
[t:D:-->

```

Send us recon-all.log (or path!)
when you have problems! **75**

Upon Completion...

sub-2022



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

stats files are text files with summary information, eg:

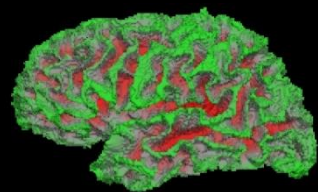
volume of left amygdala

average thickness in superior temporal gyrus

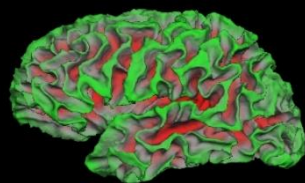
Upon Completion...

sub-2022

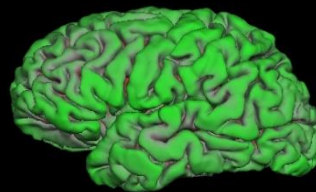
label mri scripts stats surf tmp touch trash



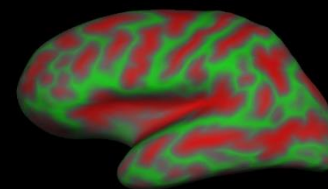
lh.orig



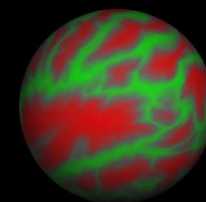
lh.white



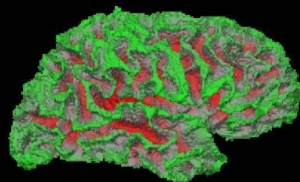
lh.pial



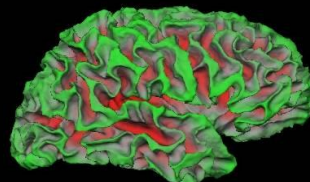
lh.inflated



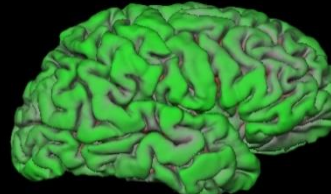
lh.sphere.reg



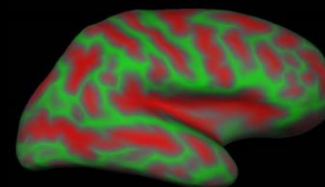
rh.orig



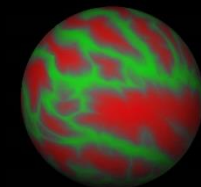
rh.white



rh.pial



rh.inflated

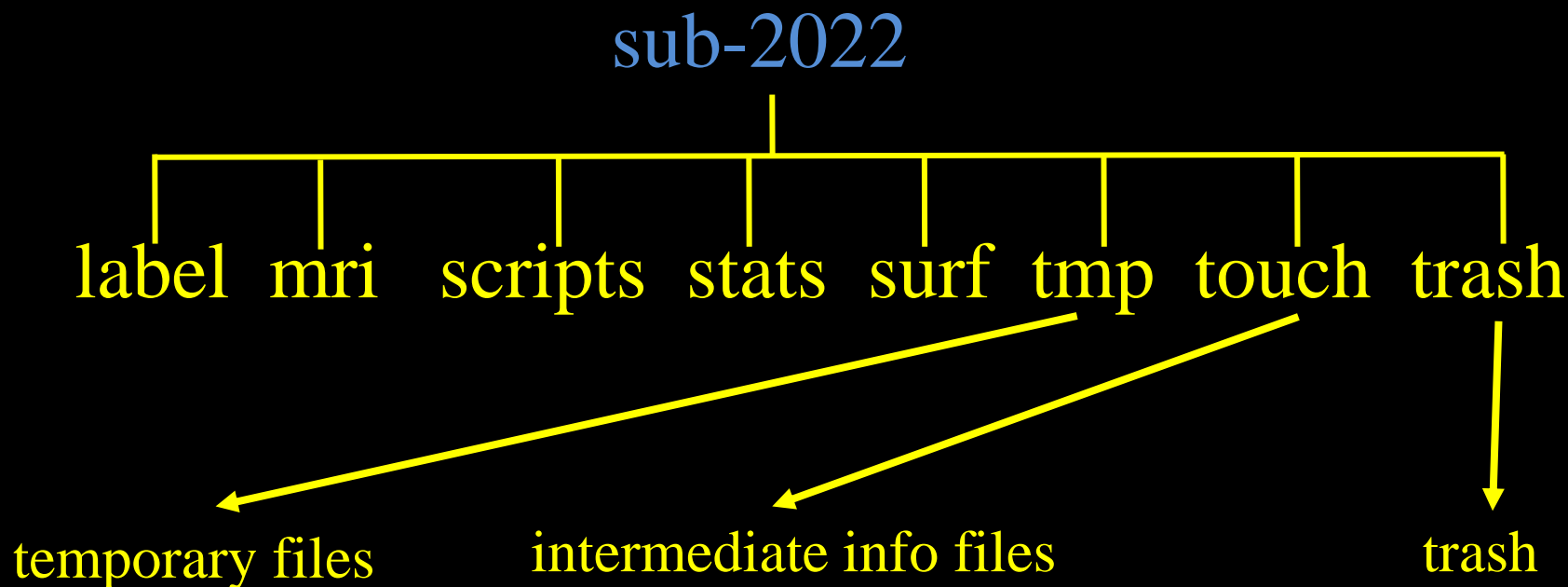


rh.sphere.reg

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

Upon Completion...



- none of these are very useful or need to monitor...

Outline

- Tutorial Setup (Hands-On)
- FreeSurfer Terminology
- Submitting recon-all to the SCC (Hands-On)
- Freeview (Hands-On)
- Review outputs (Hands-On)
- Troubleshooting Data (Hands-On)

Hard Failure: What to do?

Common Issues....

- Ran out of disk (home/project) space
- Ran out of RAM (what image type? What resources?)
- Unix file permissions (accidentally unwritable folders)
- Pathological conditions (brain artifact)
- **SUBJECTS_DIR** not correctly defined
- `/scripts/IsRunning.lh+rh` not deleted before re-run

Hard Failure: What to do?

When recon-all quits before it finishes....

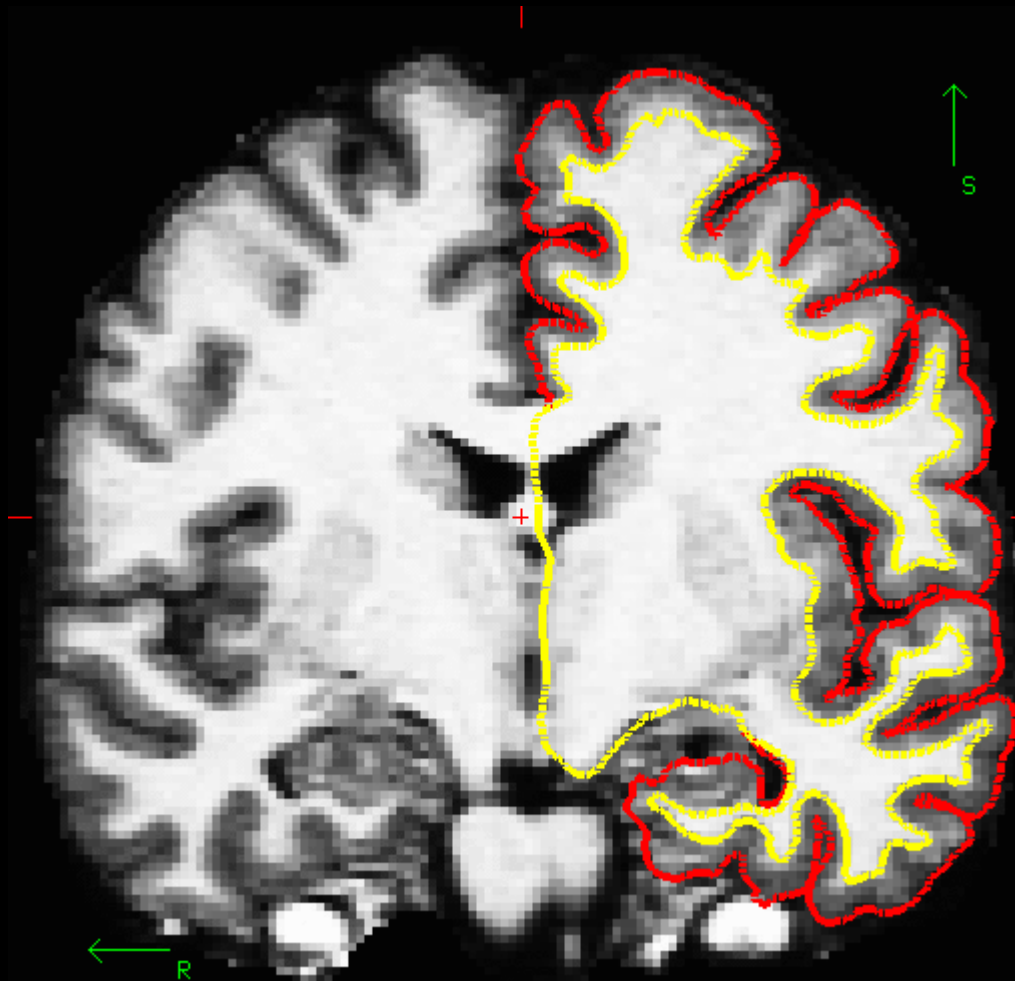
- Check recon-all.log for error message
- Examine data quality
- Rerun step that failed
- Verify output from last successful step
- Contact me! help@scc.bu.edu
- Search FreeSurfer mailing list for this problem
- Run modified version of command if needed
- Email the FreeSurfer mailing list

Soft Failures

- recon-all finishes but surfaces or aseg not accurate
- It is not possible to directly edit the location of a surface.
- When the surfaces are inaccurate, you have to change the information in a volume and regenerate the surface.

Soft Failures

- It is not possible to directly edit the location of a surface.



Check Your Recon for Accuracy

Step 1: brainmask.mgz

- Objective 1a: looking for gm/wm missing from brainmask.mgz volume

Check for Accuracy

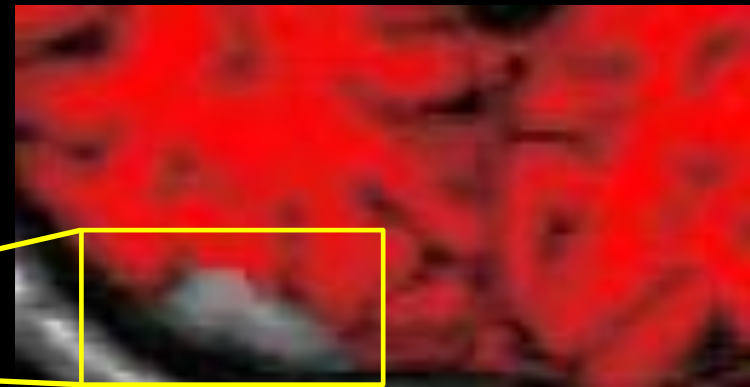
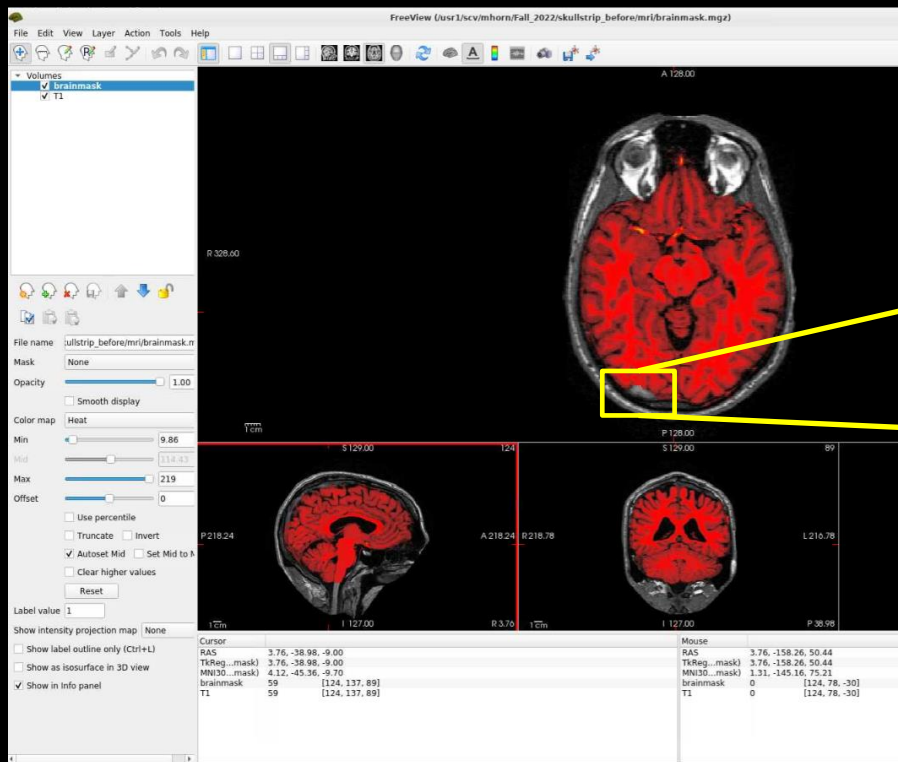
```
[tuta0@scc-v01 ~]$ cd ../skullstrip_before
```

```
[tuta0@scc-v01 ~]$ fcheck
```

Check Your Recon for Accuracy

Step 1: brainmask.mgz

- Objective 1a: looking for gm/wm missing from brainmask.mgz volume
- How: view T1.mgz volume with the brainmask.mgz overlayed in “heat”



Check Your Recon for Accuracy

Step 1: brainmask.mgz

- Objective 1b: looking for non-gm/wm included in the pial/wm surfaces

Check for Accuracy

```
[tuta0@scc-v01 ~]$ cd ../pial_edits_before
```

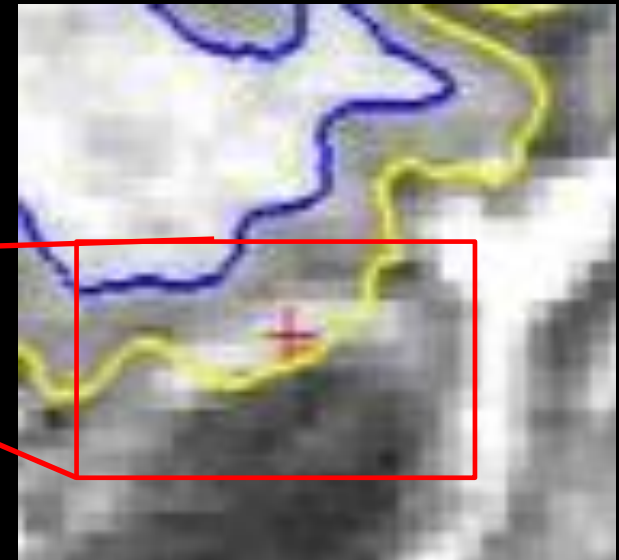
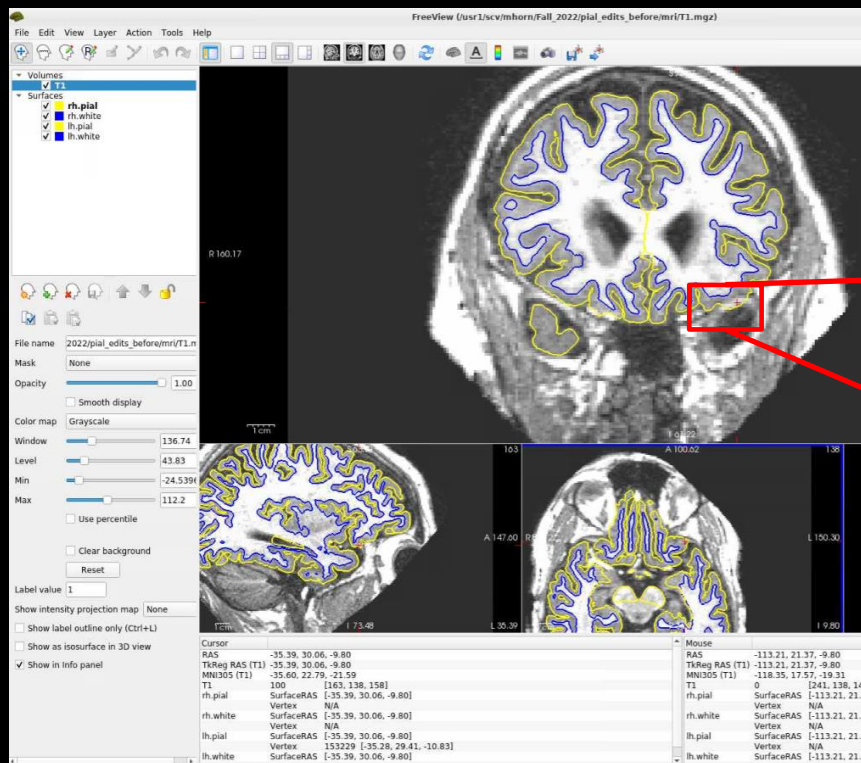
```
[tuta0@scc-v01 ~]$ fcheck
```


Check Your Recon for Accuracy

Step 1: brainmask.mgz

Objective 1b: looking for non-gm/wm included in the pial/wm surfaces

How: view T1.mgz volume with the pial/wm surfaces overlaid



Check Your Recon for Accuracy

Step 1: brainmask.mgz

The fix? : depends on the size of the affect

Large Areas & Many Slices: watershed preflooding height

- crude mean of adjusting brainmask threshold
- default = 25, increase to cut less / decrease to cut more

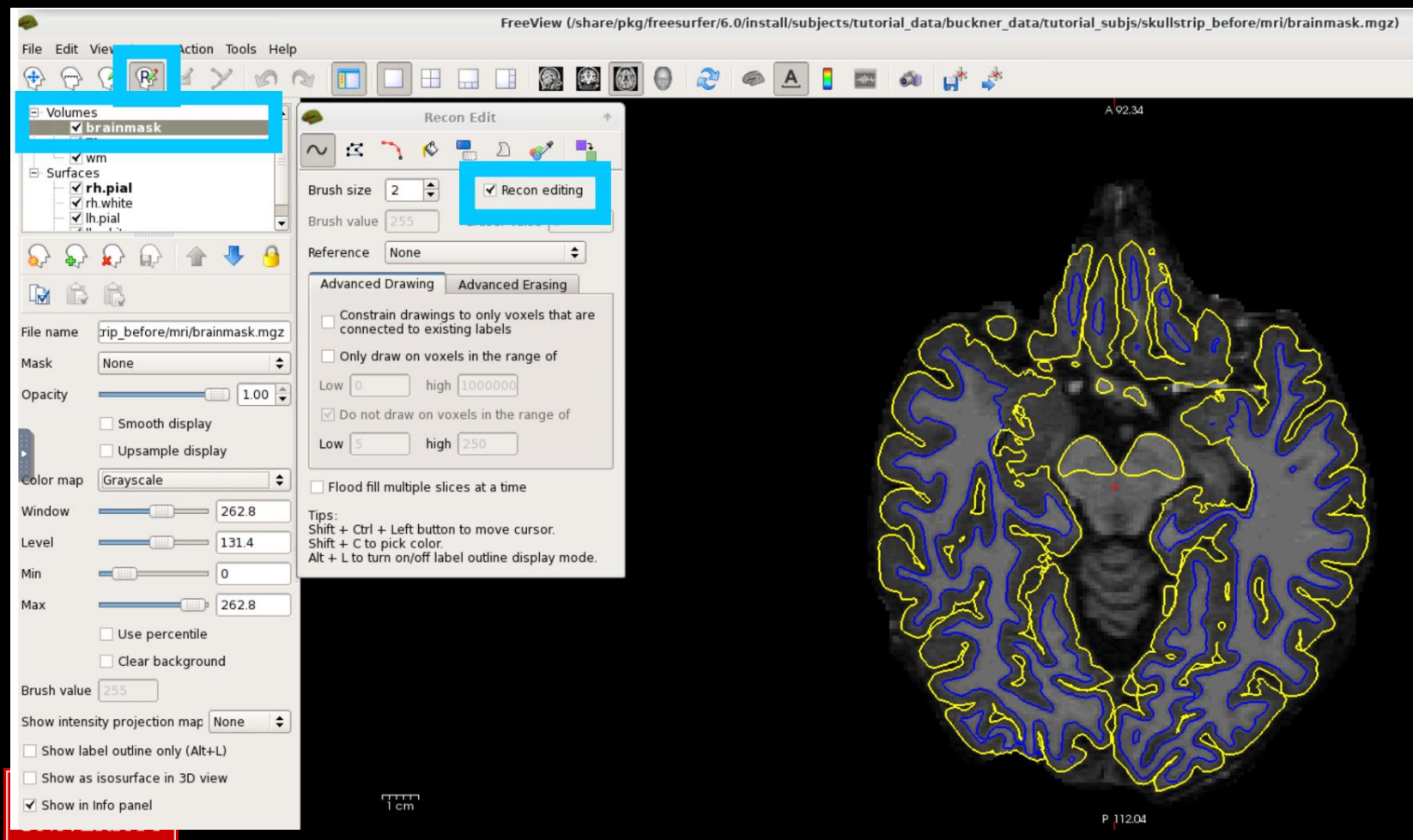
Small Area & Few Slices: manual edits

- precise mean of editing at the voxel level
- done by hand, like using photoshop

Check Your Recon for Accuracy

Step 1: brainmask.mgz

Manual Edits



Check Your Recon for Accuracy

Step 2: wm.mgz

- Objective 2a: looking for non-wm within/below the wm surface

Check for Accuracy

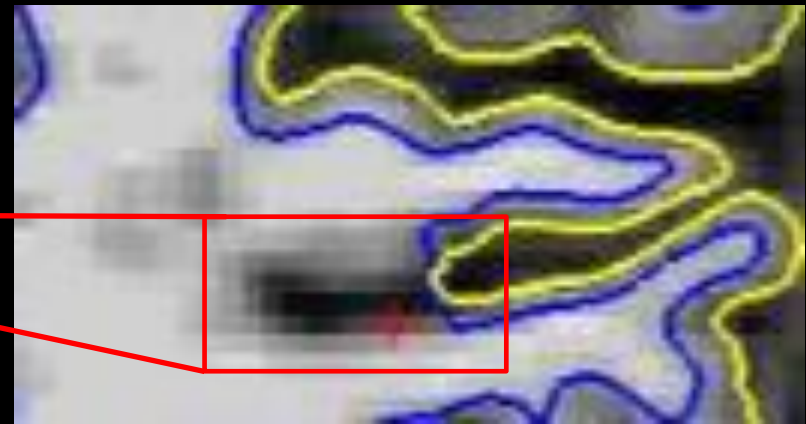
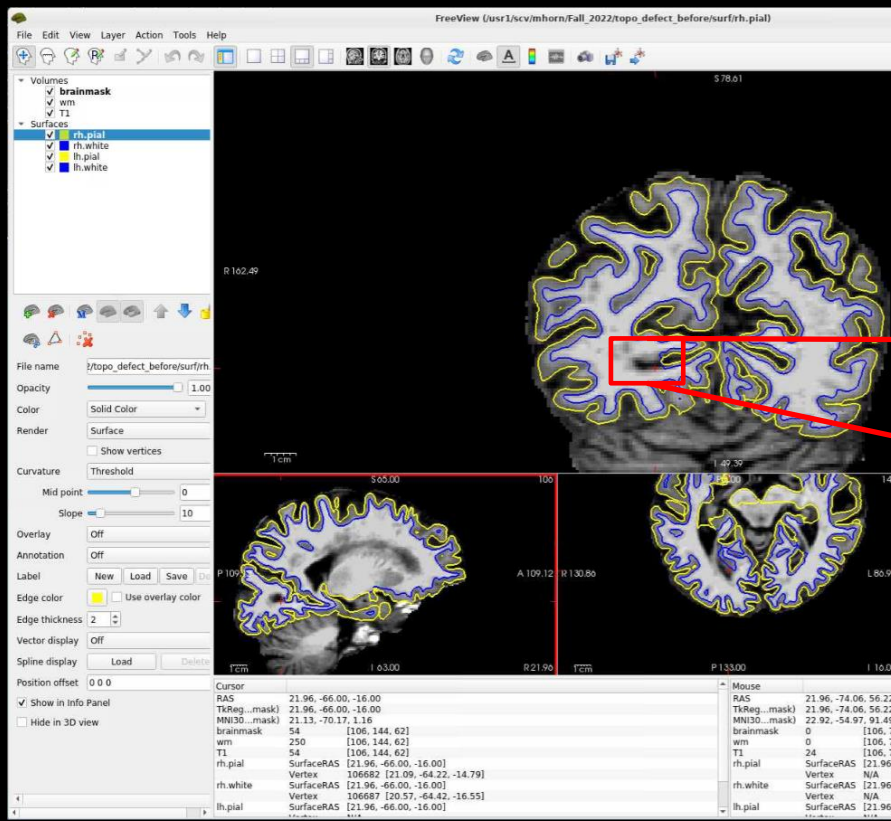
```
[tuta0@scc-v01 ~]$ cd ../topo_defect_before
```

```
[tuta0@scc-v01 ~]$ fcheck
```

Check Your Recon for Accuracy

Step 2: wm.mgz

- Objective 2a: looking for gm/wm missing from brainmask.mgz volume
- How: view T1.mgz volume with the brainmask.mgz overlaid in “heat”



Check Your Recon for Accuracy

Step 2: wm.mgz

- Objective 2b: looking for wm excluded from in the wm surface

Check for Accuracy

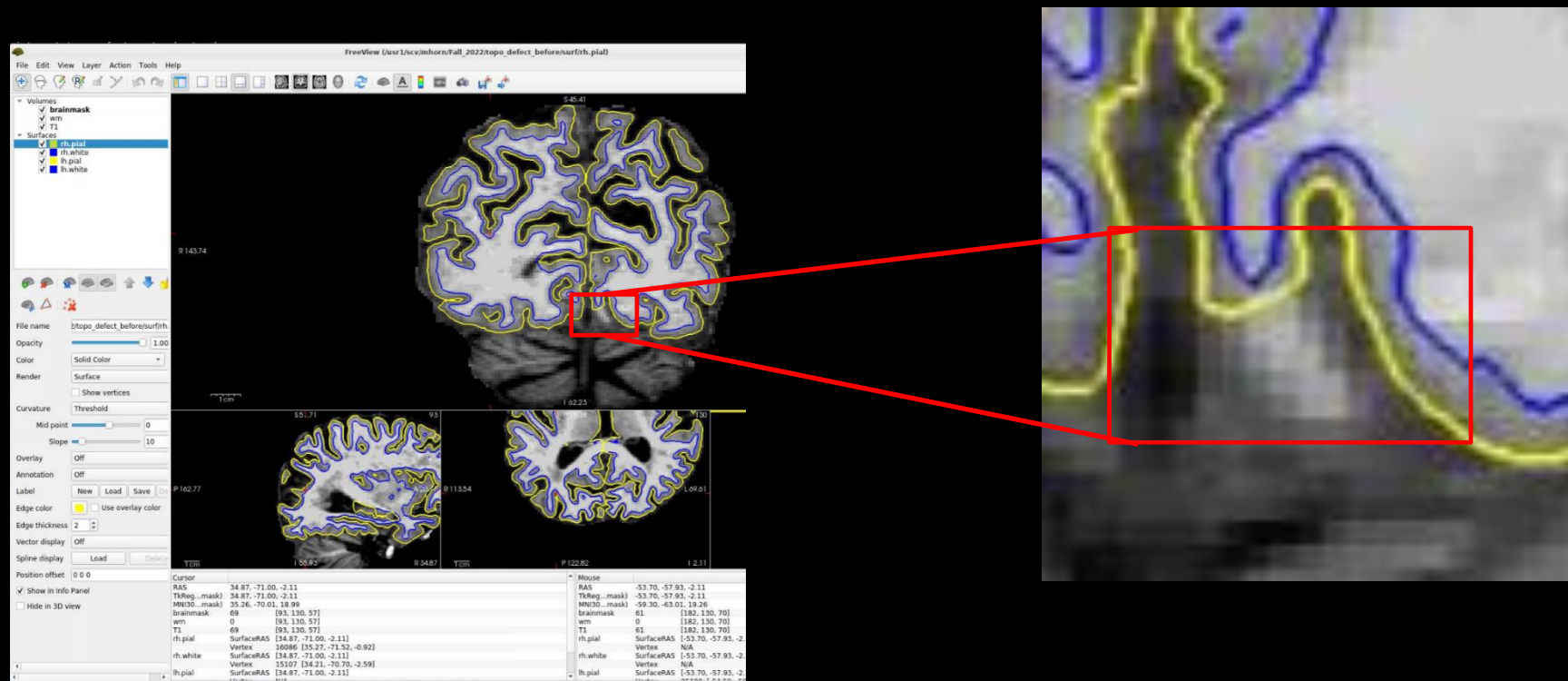
```
[tuta0@scc-v01 ~]$ cd ../pial_edits_before
```

```
[tuta0@scc-v01 ~]$ fcheck
```


Check Your Recon for Accuracy

Step 2: wm.mgz

- Objective 2b: looking for wm excluded from in the wm surface
- How: view brainmask.mgz volume with the wm.mgz volume in heat and pial/wm surfaces overlaid



Check Your Recon for Accuracy

Step 2: wm.mgz

The fix? : depends on the error

wm outside the surface & < 110: control points

- specific wm error, means of normalizing voxels
- use sparingly!

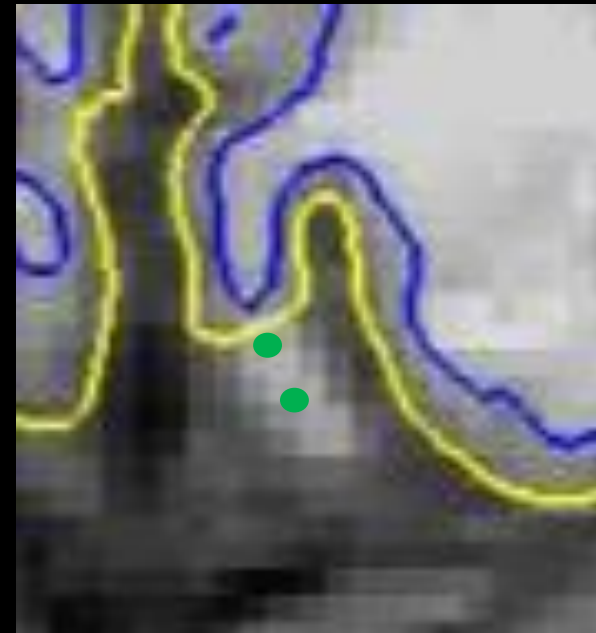
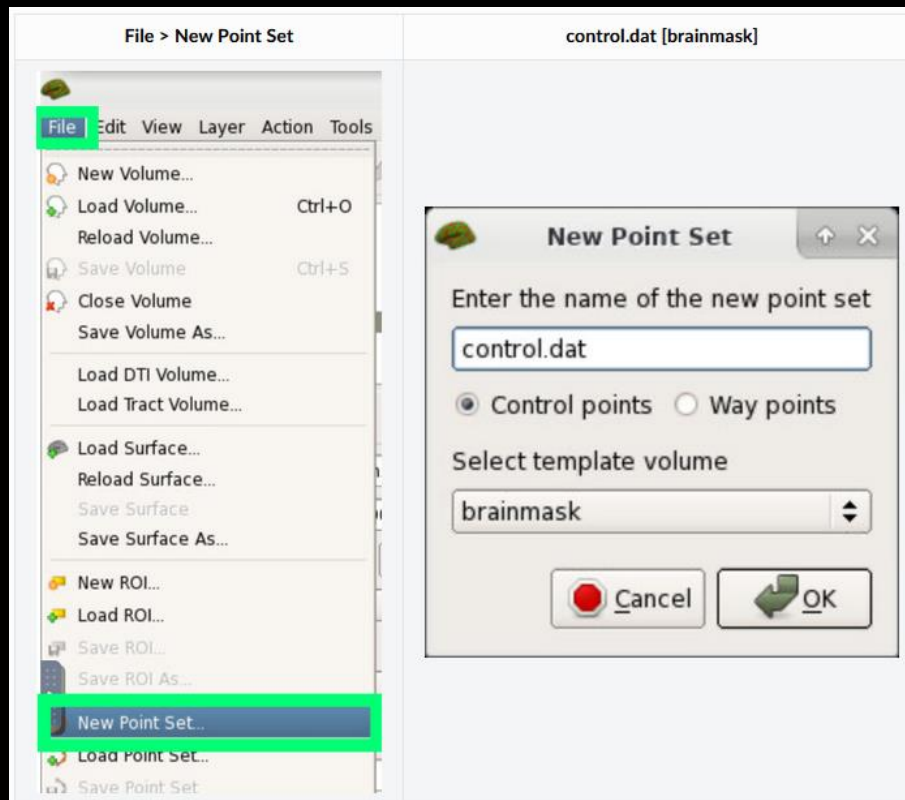
all other wm errors: manual edits

- precise mean of editing at the voxel level
- done by hand, like using photoshop

Check Your Recon for Accuracy

Step 2: wm.mgz

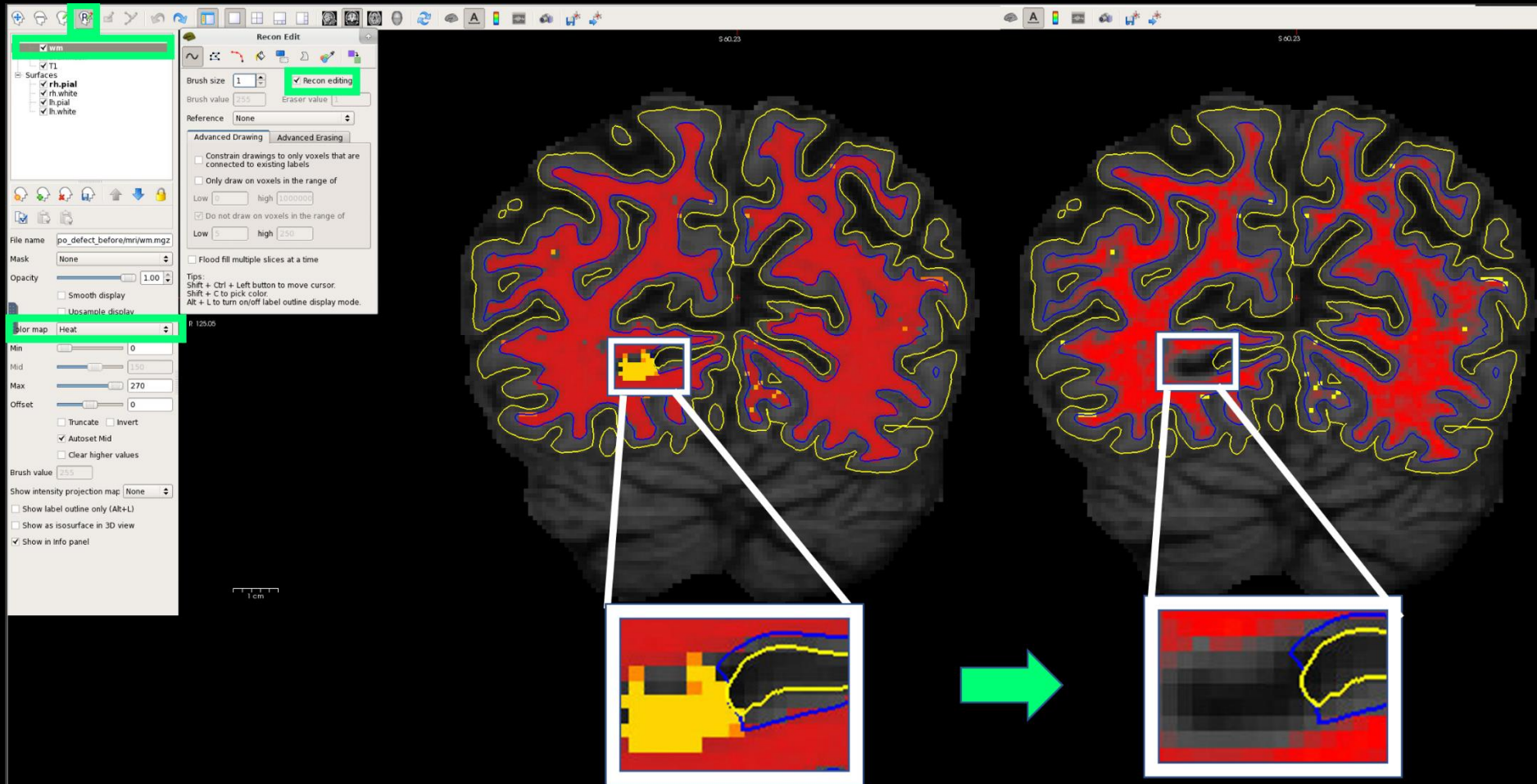
Control Points



Check Your Recon for Accuracy

Step 2: wm.mgz

Manual Edits



Less common errors

You don't like how something is labelled in the aseg.mgz...

- Generally, **NOT** recommended unless absolute necessary
- Editing the aseg will add more variance to your data
- First, try to use the expert options flag in recon-all
 - <https://freesurfer.net/fswiki/recon-all#ExpertOptionsFile>

How: view aseg.presurf.mgz volume and manually edit voxels

Making Edits to aseq

How: view [aseg.presurf.mgz](#) volume and manually edit voxels



Check Your Recon for Accuracy

Step 3: resubmit!

A. Made ANY changes to the brainmask.mgz

- `recon-all -autorecon2 -autorecon3 -subjid $SUBJECTS_DIR/$subject`

B. Made changes to the wm.mgz with control points

- `recon-all -autorecon2-cp -autorecon3 -subjid $SUBJECTS_DIR/$subject`

C. Made changes to the wm.mgz via manual edits

- `recon-all -autorecon2-wm -autorecon3 -subjid $SUBJECTS_DIR/$subject`

D. Made changes to the aseg.presurf.mgz via manual edits

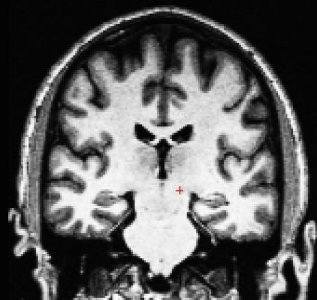
- `recon-all -autorecon2-noaseg -autorecon3 -subjid $SUBJECTS_DIR/$subject`

Check Your Recon for Accuracy

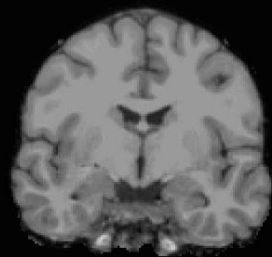
When to leave errors alone?

- you should not be spending more than 30 minutes troubleshooting and correcting a full-brain recon
- if the white matter error is only in a handful of voxels across 1-2 slices you can leave the recon as-is

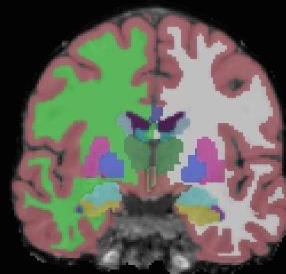
Processing Stream Overview



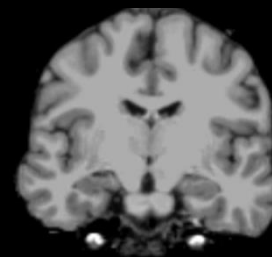
T1 Weighted
Input



Skull Stripping



Volumetric Labeling



Intensity
Normalization

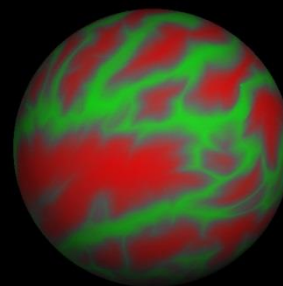
Adjust skull strip algorithm:
`recon-all -autorecon2`

Add control points:
`recon-all -autorecon2-cp`

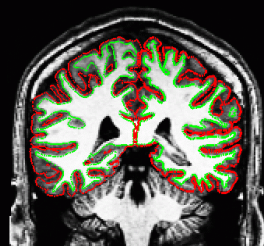


White Matter
Segmentation

Fix white surf:
`recon-all -autorecon2-wm`

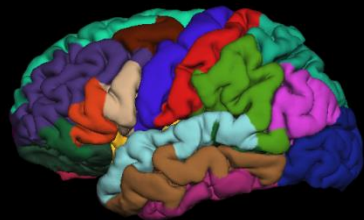


Surface Atlas
Registration



Surface Extraction

Fix pial surf:
`recon-all -autorecon3-pial`



Gyrus Labeling

Stats!

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ROI summaries

aseg.stats – volume summaries

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

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

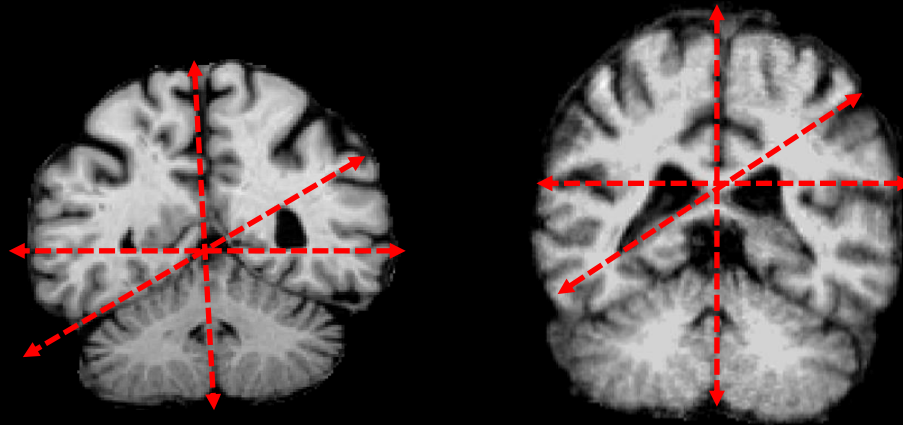
wmparc.stats – white matter parcellation

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

- Generating spreadsheets of group data
 - `asegstats2table --help`
 - `aparcstats2table --help`
- More info in ROI tutorial on fswiki

Subject Normalization

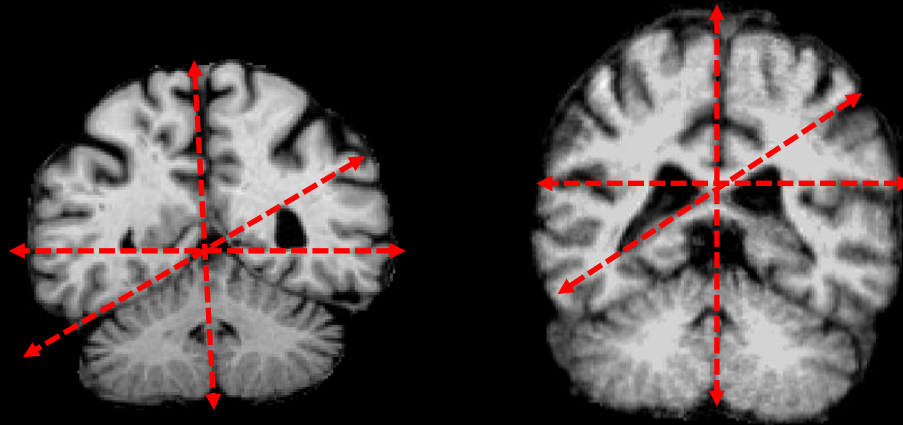
- FreeSurfer measures statistics in subject-space



- How can we account for variability in head size?
- Couple of options: brainseg, brainsegnotvent, etiv, supratentorial, etc.

eTIV

- **Estimated Total Intracranial Volume**



- **Can represent volumes as % of eTIV**
- **White Matter Volume = 643178 mm³**
- **White Matter Volume = 42.09 % of eTIV**

Additional BU RCS Web Resources

- Research Computing Support Pages
<http://www.bu.edu/tech/support/research/>
- Technical Summary of SCC Resources
<http://www.bu.edu/tech/support/research/computing-resources/tech-summary/>
- SCC Updates – Latest SCC News
<http://www.bu.edu/tech/support/research/whats-happening/updates/>
- Code Examples for Popular Software Packages
<http://scv.bu.edu/examples/>

1. Please open a web browser and:
2. Google “rsc tutorial evaluation”
3. Click 1st link
http://scv.bu.edu/survey/tutorial_evaluation.html
4. Fill out the survey!