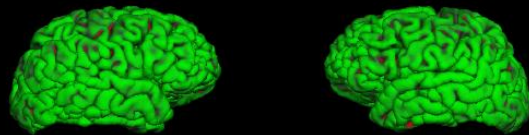
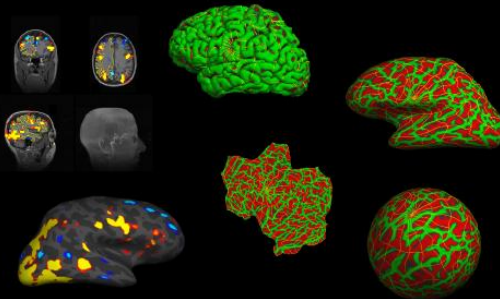


FreeSurfer: Troubleshooting

surfer.nmr.mgh.harvard.edu



FreeSurfer



MASSACHUSETTS
GENERAL HOSPITAL



Hard and Soft Failures

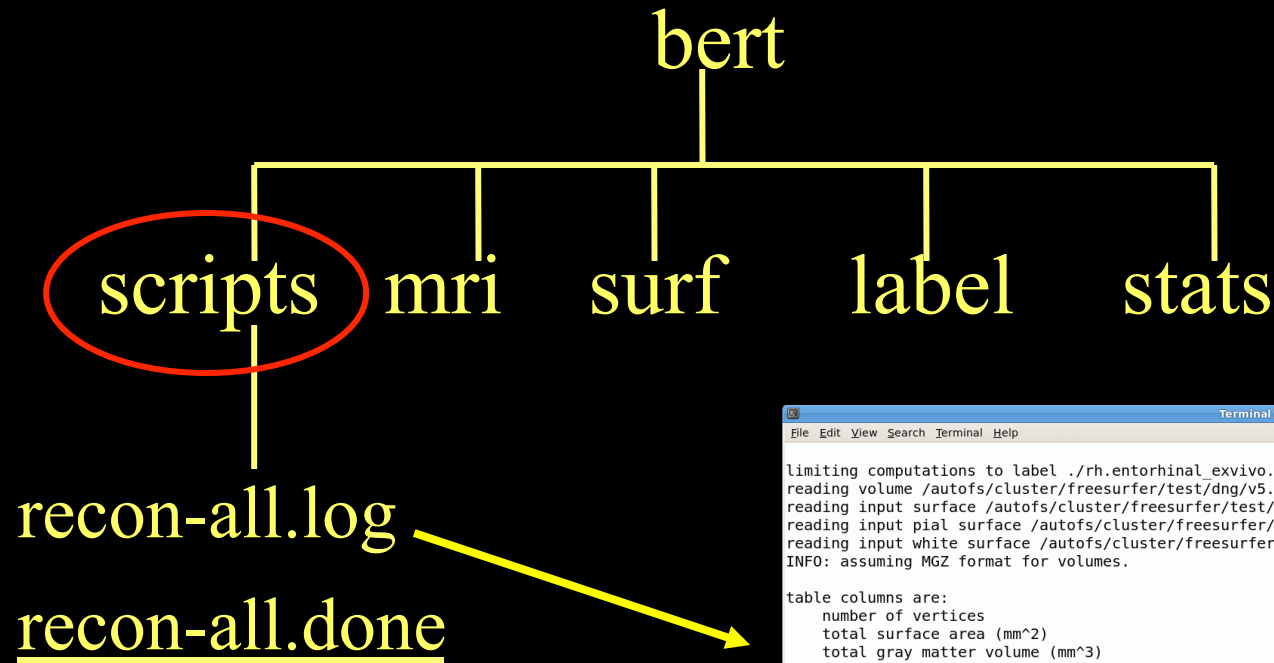
Categories of errors: Hard & Soft Failures

- Hard = recon-all quits before it finishes
- Soft = recon-all finishes but results need modification
 - recon-all takes a long time (10-20 hours) to run & some part of the process may need modification (e.g. cerebellum removed in skull stripping)

Troubleshooting: Soft Failures

- Types of Soft Failures:
 - Skull Strip Errors
 - Segmentation Errors
 - Intensity Normalization Error
 - Pial Surface misplacement
 - Topological Defect

Upon Completion of recon-all...



```
Terminal
File Edit View Search Terminal Help

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

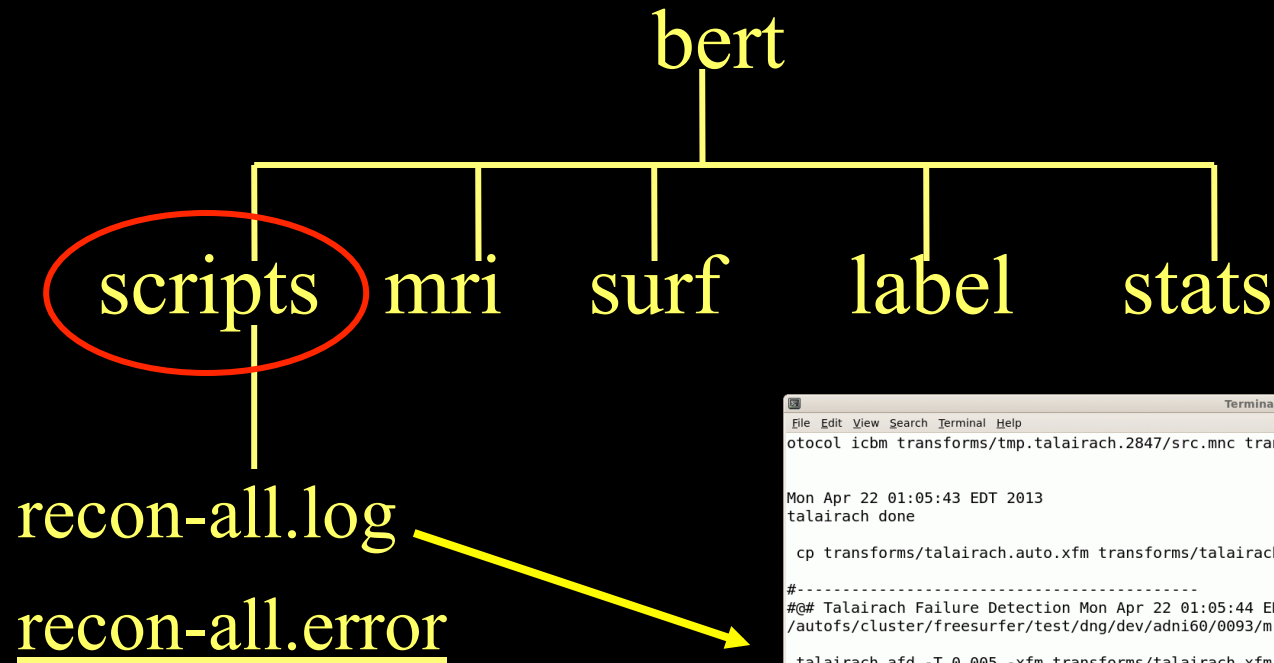
236 152 759 3.117 0.598 0.141 0.035 3 0.4 ./rh.entorhinal_exvivo.label

#-----
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:-->
```

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

Could be a “soft” failure.

Troubleshooting: Hard Failures



```
Terminal
File Edit View Search Terminal Help
otocol icbm transforms/tmp.talairach.2847/src.mnc transforms/talairach.auto.xfm

Mon Apr 22 01:05:43 EDT 2013
talairach done

cp transforms/talairach.auto.xfm transforms/talairach.xfm

#-----
#@# Talairach Failure Detection Mon Apr 22 01:05:44 EDT 2013
/autofs/cluster/freesurfer/test/dng/dev/adni60/0093/mri

talairach_afd -T 0.005 -xfm transforms/talairach.xfm

ERROR: talairach_afd: Talairach Transform: transforms/talairach.xfm ***FAILED*** (p=0.0005, pval=0.0000
< threshold=0.0050)
Manual Talairach alignment may be necessary, or
include the -notal-check flag to skip this test,
making sure the -notal-check flag follows -all
or -autorecon1 in the command string.
See http://surfer.nmr.mgh.harvard.edu/fswiki/FsTutorial/Talairach
Linux compute-0-23 2.6.32-279.22.1.el6.x86_64 #1 SMP Wed Feb 6 03:10:46 UTC 2013 x86_64 x86_64 x86_64 GN
U/Linux

recon-all -s 0093 exited with ERRORS at Mon Apr 22 01:05:44 EDT 2013

To report a problem, see http://surfer.nmr.mgh.harvard.edu/fswiki/BugReporting
[t:D:dng-> ]
```

- Ran out of disk space?
- Ran out of RAM?
- Unix file permissions?
- Pathological conditions (brain, artifact)
- Sunspots??????

Send us recon-all.log
freesurfer@nmr.mgh.harvard.edu

Hard Failure: What to do

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

Hard Failure: Help Us Help You!

- Report version currently using
 - see top of recon-all.log
 - `cat $FREESURFER_HOME/build-stamp.txt`
- Operating System/hardware
- Exact command-line tried to run
- Send recon-all.log
- Output from terminal window if appropriate

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 (manually) change the information in a volume and regenerate the surface.

Check Your Recon for Accuracy

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

Unfortunately we almost never have access to ground truth in imaging.

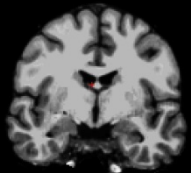
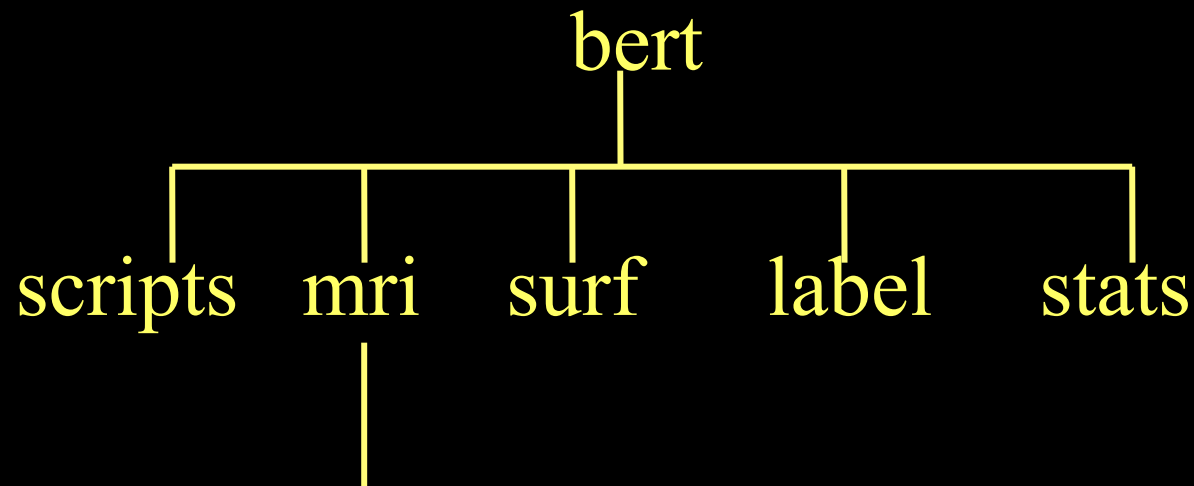
Manual Interventions

1. Erase voxels
2. Fill voxels
3. Clone voxels (ie, copy from one volume to another)
4. Add “Control Points”

Manual interventions should take less than 30min
After manual intervention, re-run parts of recon-all

It is also possible to re-run recon-all with different parameters which is good for systematic or large errors

Manual Edits Applied to Volumes not Surfaces



brainmask.mgz

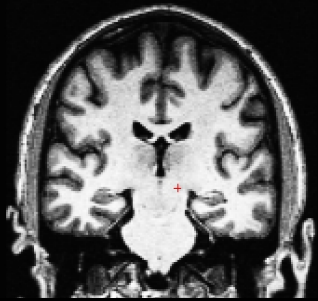


wm.mgz

	Erase	Fill	Clone to	Control Points
brainmask	X		X	X
wm	X	X		

*Other volumes involved in QA: brain.finalsurfs, norm.mgz, T1.mgz

Processing Stream Overview



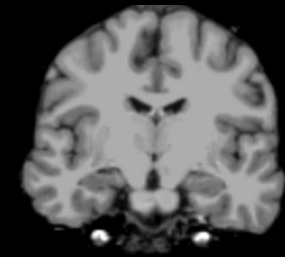
T1 Weighted
Input



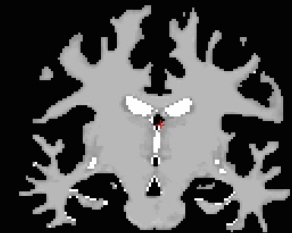
Skull Stripping



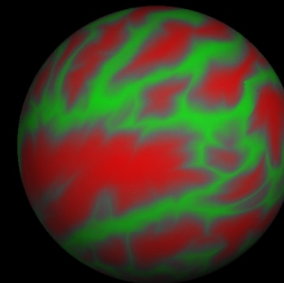
Volumetric Labeling



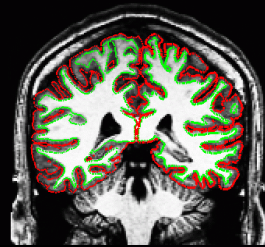
Intensity
Normalization



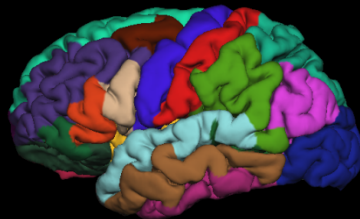
White Matter
Segmentation



Surface Atlas
Registration



Surface Extraction



Gyral Labeling



Stats!

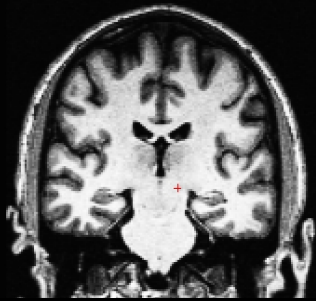
Reconstruction Stages

recon-all is broken into three stages

- autorecon1
- autorecon2
- autorecon3

these 3 stages are equivalent to -all

Processing Stream Overview



T1 Weighted
Input

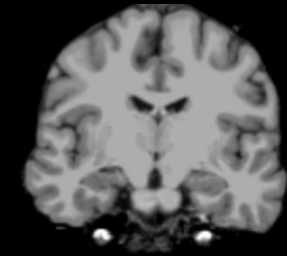


Skull Stripping

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

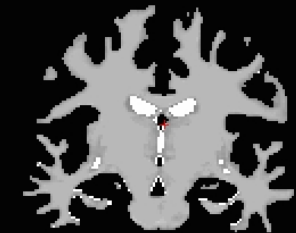


Volumetric Labeling



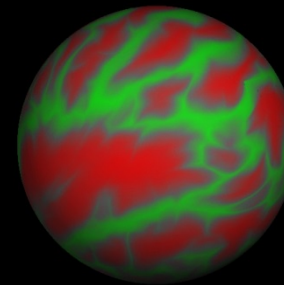
Intensity
Normalization

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



White Matter
Segmentation

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

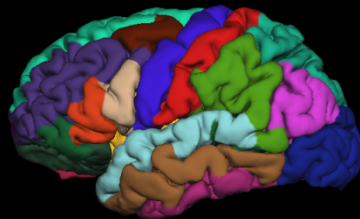


Surface Atlas
Registration



Surface Extraction

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



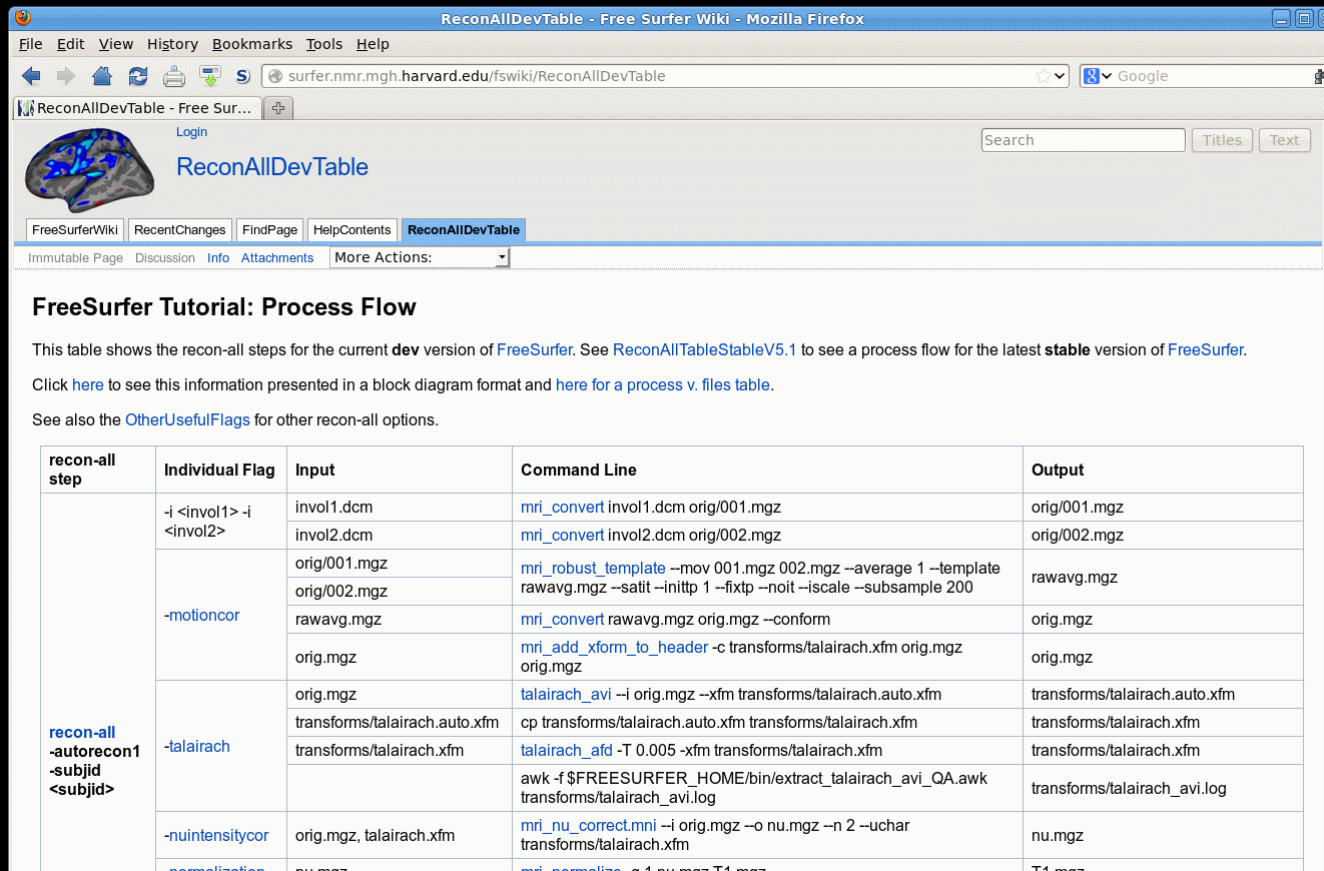
Gyral Labeling



Stats!

Processing Stream Order

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



FreeSurfer Tutorial: Process Flow

This table shows the recon-all steps for the current **dev** version of **FreeSurfer**. See [ReconAllTableStableV5.1](#) to see a process flow for the latest **stable** version of **FreeSurfer**.
Click [here](#) to see this information presented in a block diagram format and [here for a process v. files table](#).
See also the [OtherUsefulFlags](#) for other recon-all options.

recon-all step	Individual Flag	Input	Command Line	Output	
recon-all -autorecon1 -subjid <subjid>	-i <invol1> -i <invol2>	invol1.dcm invol2.dcm	<code>mri_convert invol1.dcm orig/001.mgz</code> <code>mri_convert invol2.dcm orig/002.mgz</code>	orig/001.mgz orig/002.mgz	
	-motioncor	orig/001.mgz orig/002.mgz	rawavg.mgz	<code>mri_robust_template --mov 001.mgz 002.mgz --average 1 --template rawavg.mgz --salit --inittp 1 --fixtp --noit --iscale --subsample 200</code>	rawavg.mgz
		rawavg.mgz	orig.mgz	<code>mri_convert rawavg.mgz orig.mgz --conform</code>	orig.mgz
	-talairach	orig.mgz	orig.mgz	<code>mri_add_xform_to_header -c transforms/talairach.xfm orig.mgz orig.mgz</code>	orig.mgz
		orig.mgz	transforms/talairach.auto.xfm	<code>talairach_avi -i orig.mgz -xfm transforms/talairach.auto.xfm</code>	transforms/talairach.auto.xfm
		transforms/talairach.auto.xfm	transforms/talairach.xfm	<code>cp transforms/talairach.auto.xfm transforms/talairach.xfm</code>	transforms/talairach.xfm
		transforms/talairach.xfm	transforms/talairach.xfm	<code>talairach_afd -T 0.005 -xfm transforms/talairach.xfm</code>	transforms/talairach.xfm
	-nuintensitycor	transforms/talairach.xfm	transforms/talairach_avi.log	<code>awk -f \$FREESURFER_HOME/bin/extract_talairach_avi_QA.awk transforms/talairach_avi.log</code>	transforms/talairach_avi.log
		orig.mgz, talairach.xfm	nu.mgz	<code>mri_nu_correct.mni -i orig.mgz --o nu.mgz --n 2 --uchar transforms/talairach.xfm</code>	nu.mgz
	normalization	sumavg	T1.mgz	<code>mri_normalize -i sumavg T1.mgz</code>	T1.mgz

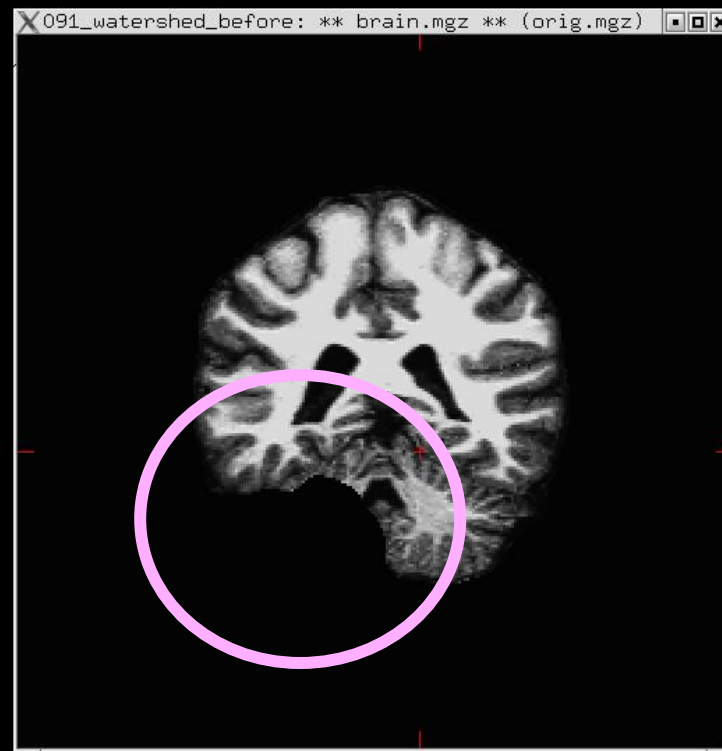
Or Make Life Easier

recon-all -make all -s subjid

Skull Strip Failure: Too Much Removed



T1.mgz



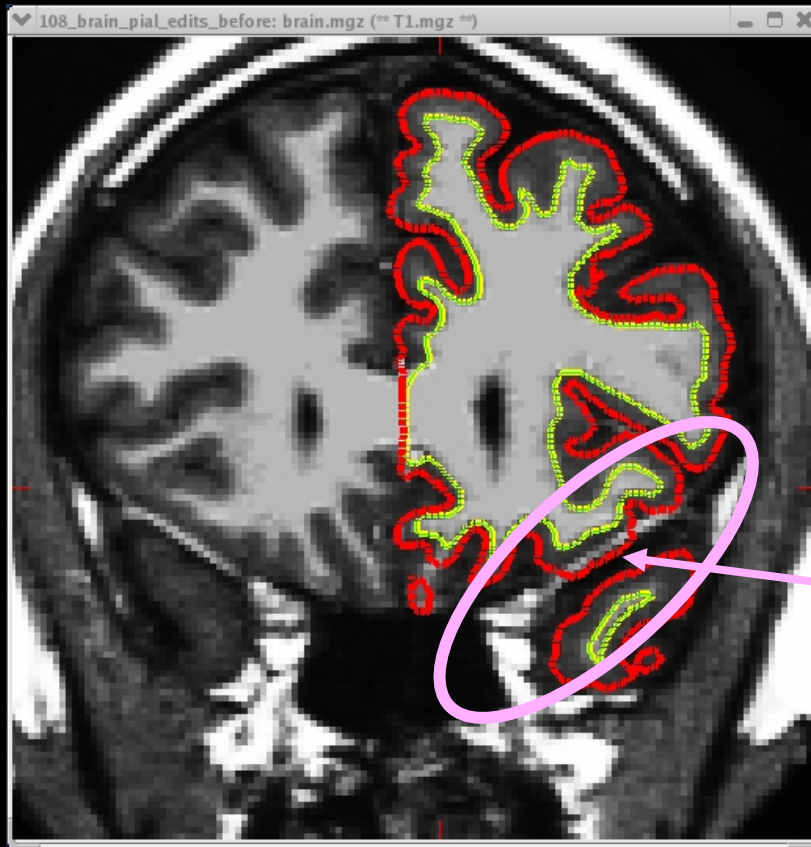
brainmask.mgz

Use “clone” tool to manually correct, or adjust watershed parameters and run (default wsthresh is 25, higher means strip less):

```
recon-all -skullstrip -wsthresh 35 -clean-bm -no-wsgcaatlas -s <subj>
```

```
recon-all -s <subject> -autorecon2 -autorecon3
```

Skull Strip Failure: Not enough Removed

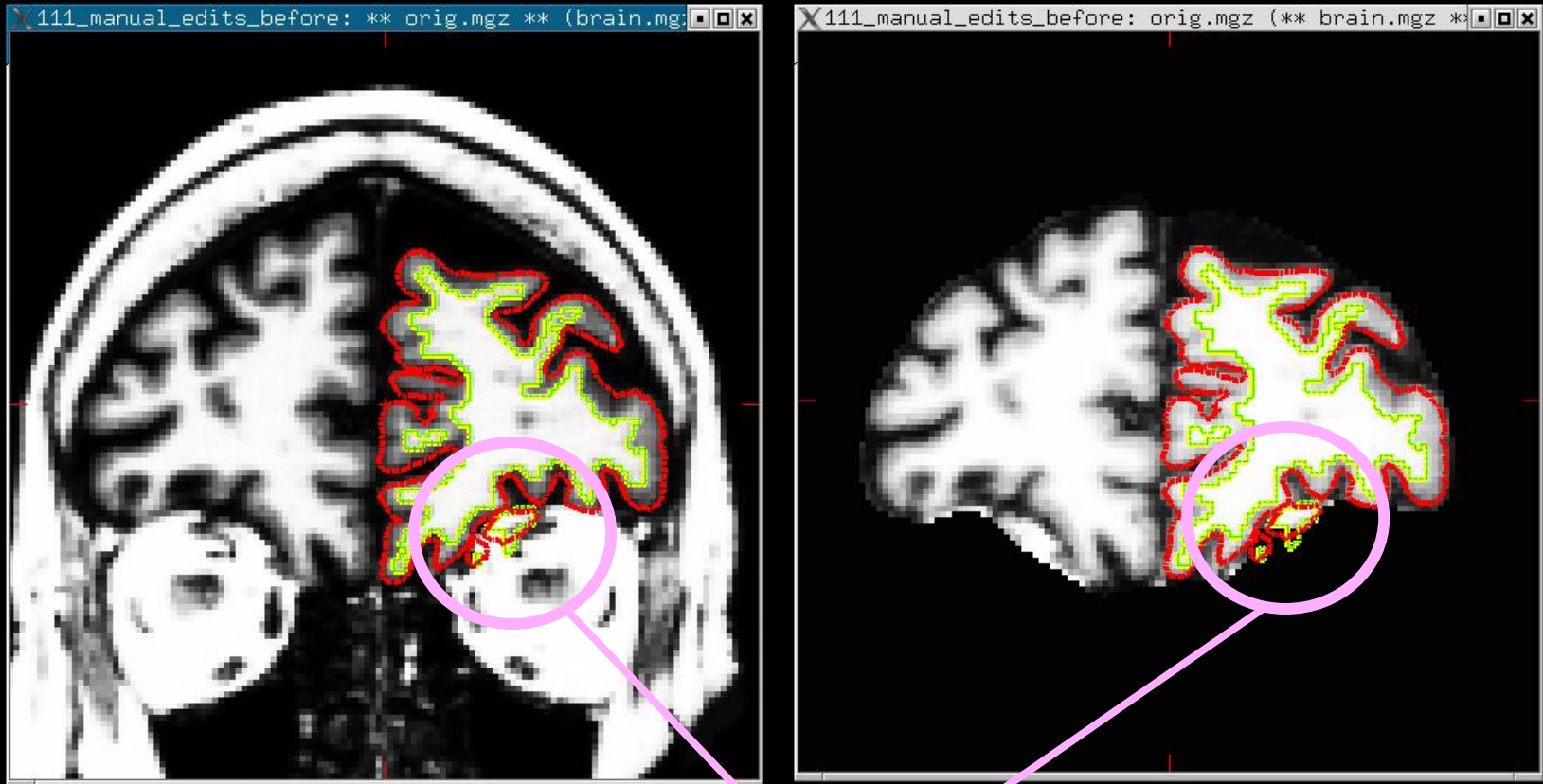


Dura or blood vessel.
the white surface is OK, but
the pial surface is inaccurate

Dura and GM have extremely similar intensity characteristics on most T1-weighted sequences (but different T2*!). Typical fix: edit the brainmask.mgz to erase dura/blood vessels, and run:

```
recon-all -s <subject> -autorecon-pial
```

Skull Strip Failure: Not Enough Removed

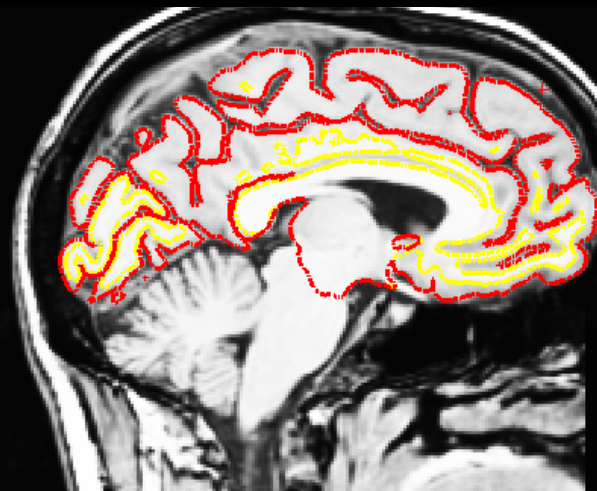
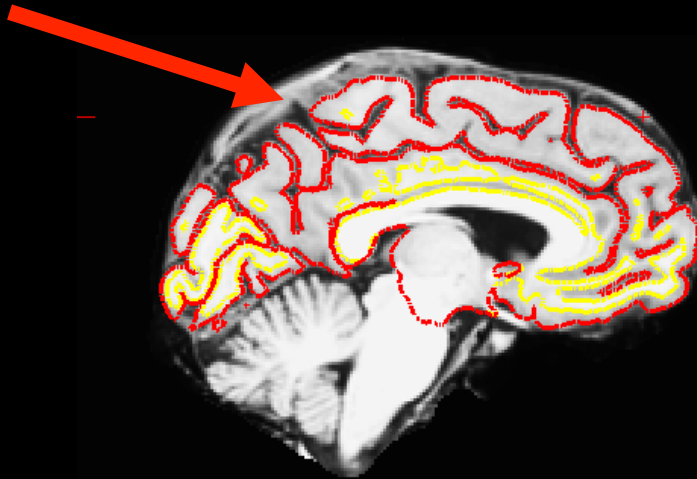


Eye Socket classified as WM due to Skull Strip Failure.
Erase in wm.mgz then run:

```
recon-all -s <subject> -autorecon2-wm -autorecon3
```

This is NOT a Skull Strip Error

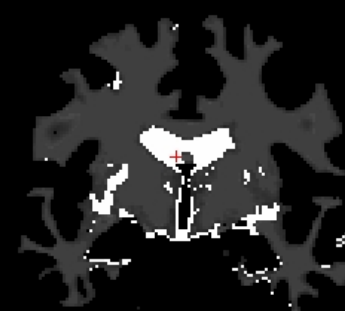
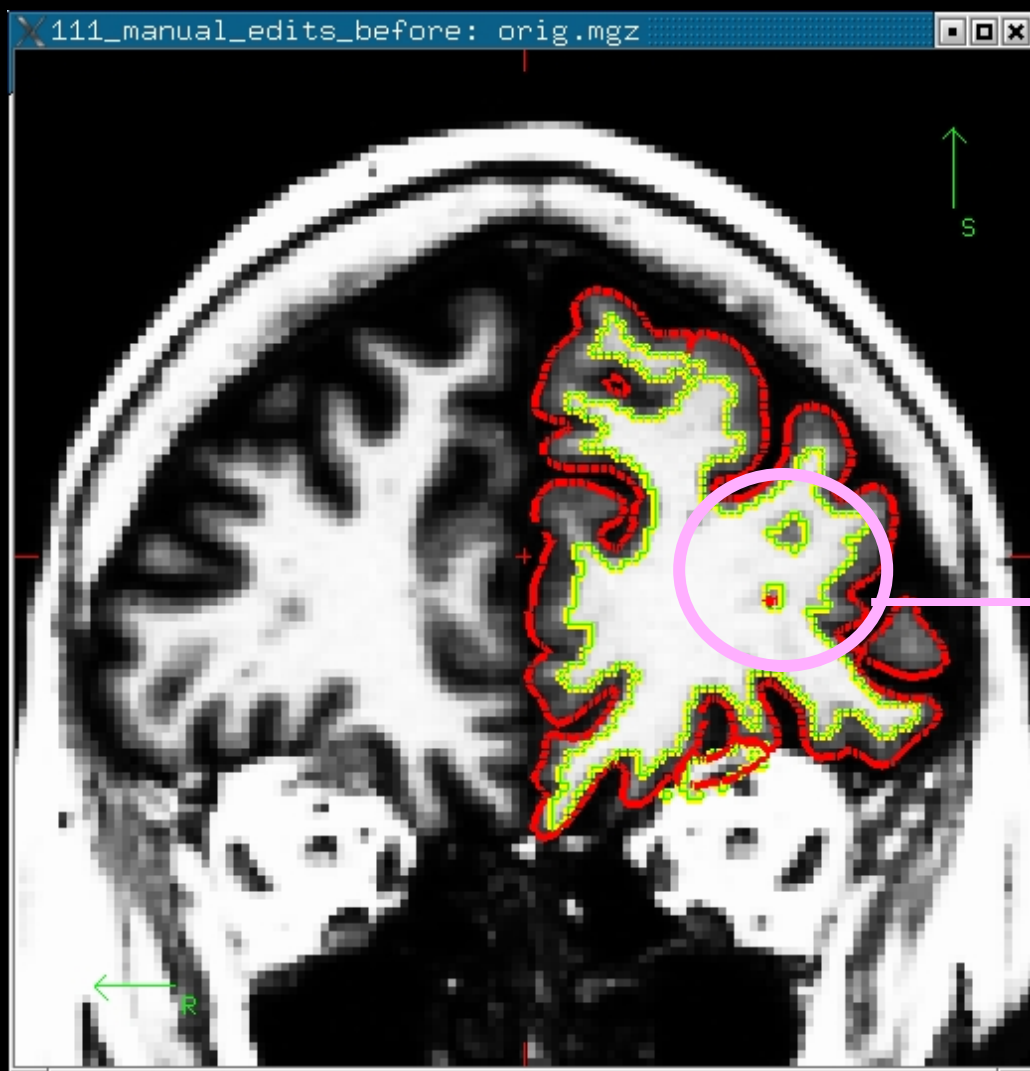
It appears that the skull strip left a lot of dura. It did, but it does not affect the surface, so leave it!



Segmentation Errors

- White Matter classified as non-White Matter
- Gray Matter classified as White Matter
- Causes:
 - Intensity Normalization Failures
 - Partial voluming

Segmentation Error



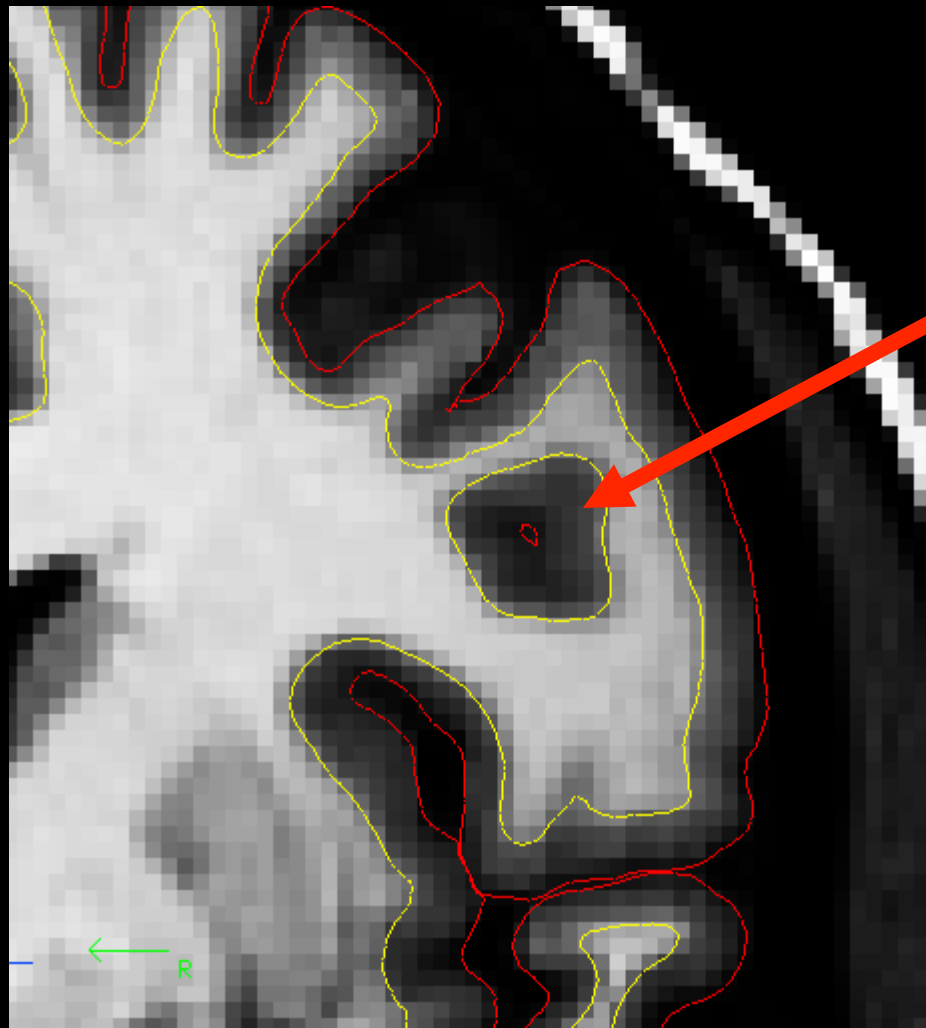
wm.mgz

“Hypo-Intensities”
White Matter Lesions
Misclassified as gray
matter

Fill in wm.mgz then run:

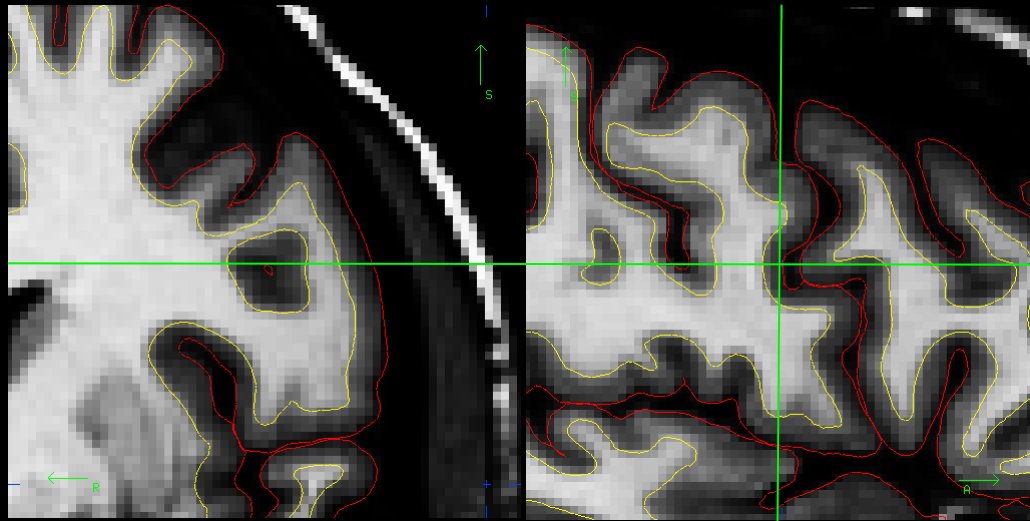
```
recon-all -s <subject> -autorecon2-wm -autorecon3
```

Is this a segmentation error?



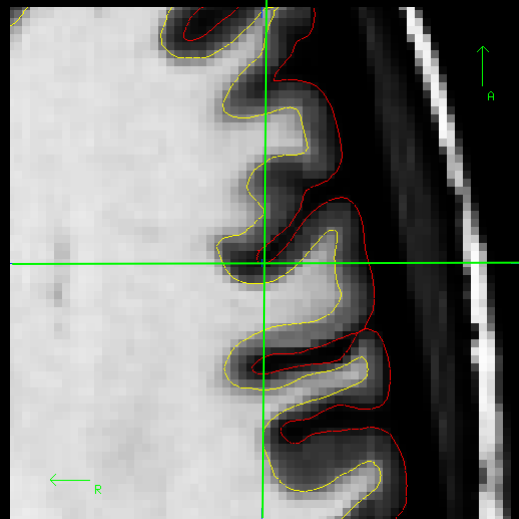
Coronal View

This is NOT an an error.



Coronal View

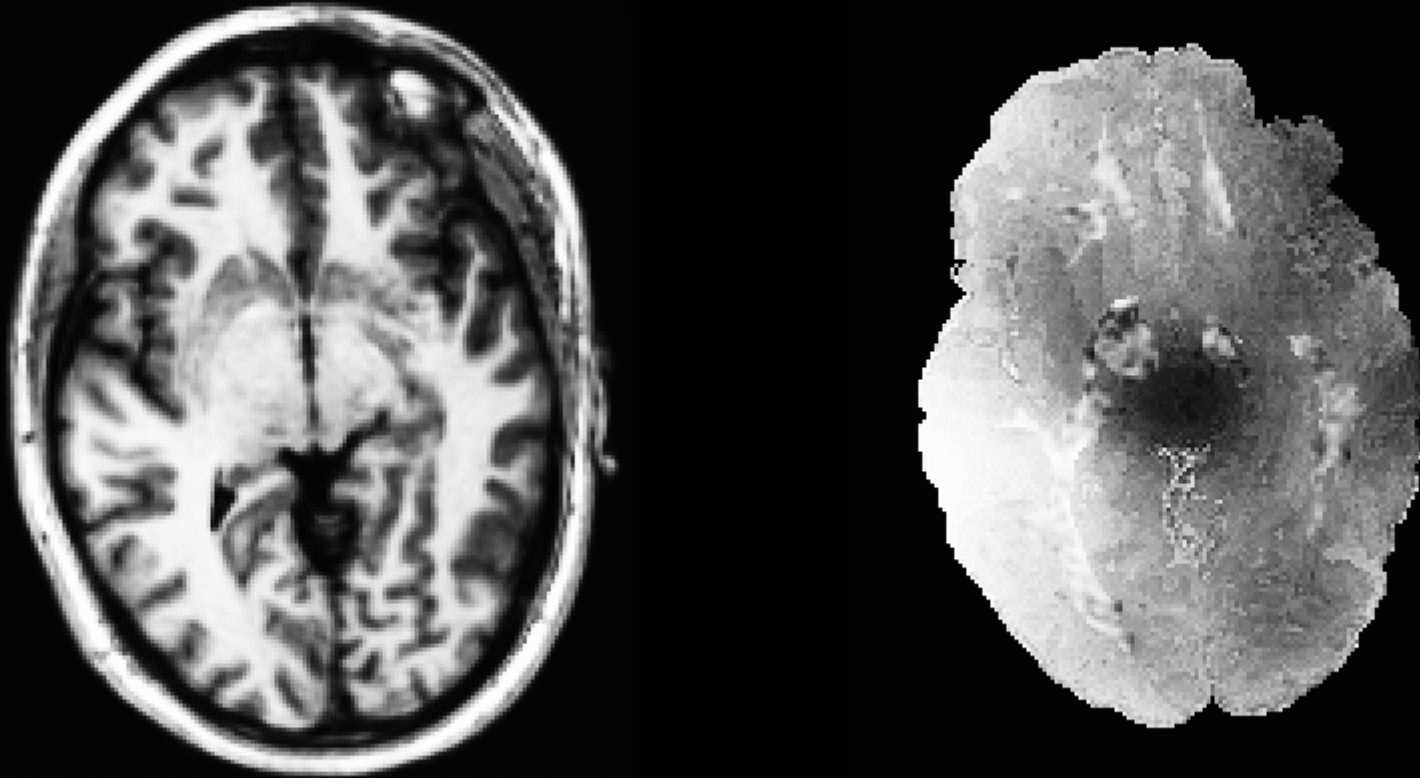
Sagittal View



Axial View

Make sure to look at all 3 views before deciding!

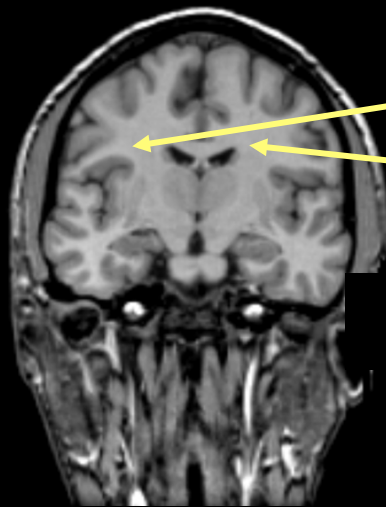
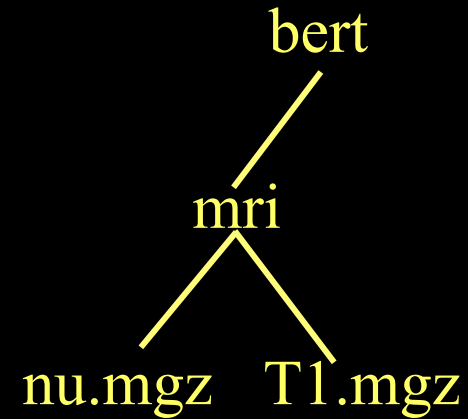
Intensity Bias



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

Intensity Normalization

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

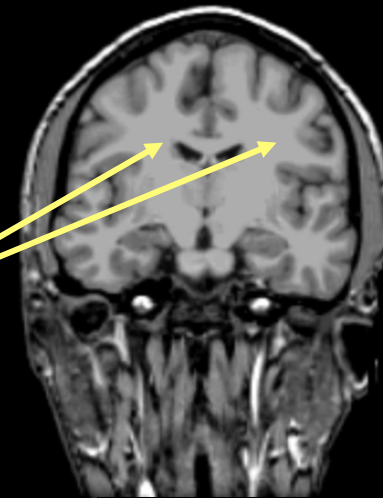


nu.mgz

110.9 ± 1.8

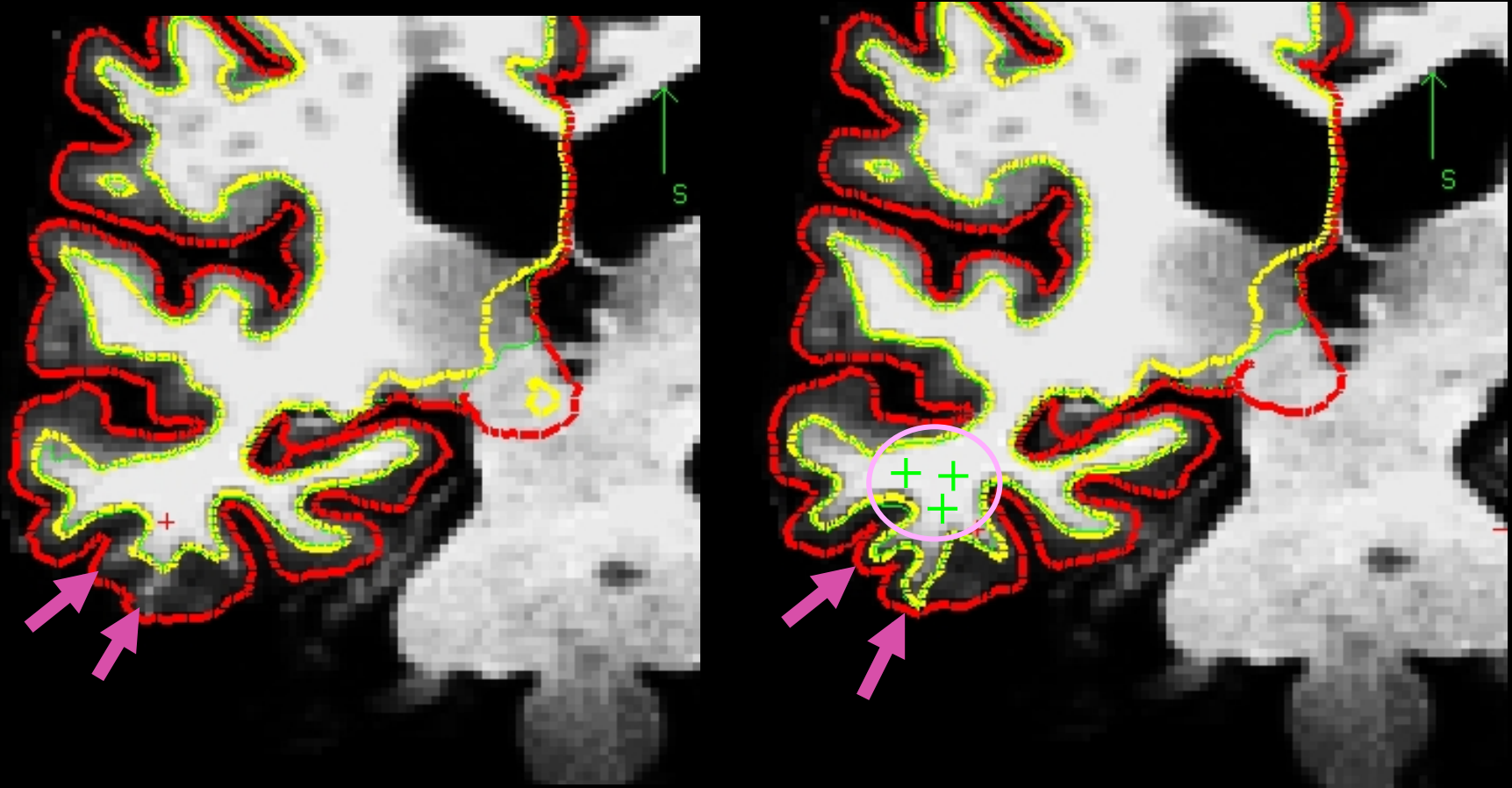
108.9 ± 1.5

110.0 ± 0.0



T1.mgz

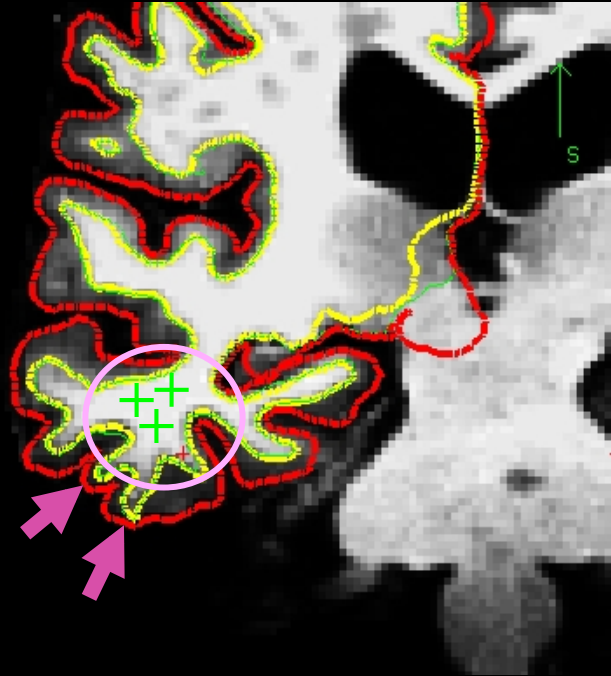
Troubleshooting: Intensity Normalization



Intensity Normalization Failure. Most WM in T1 volume (T1.mgz) should be close to 110. Can fix by editing wm.mgz or adding **“Control Points”** (+). Beware partial voluming!

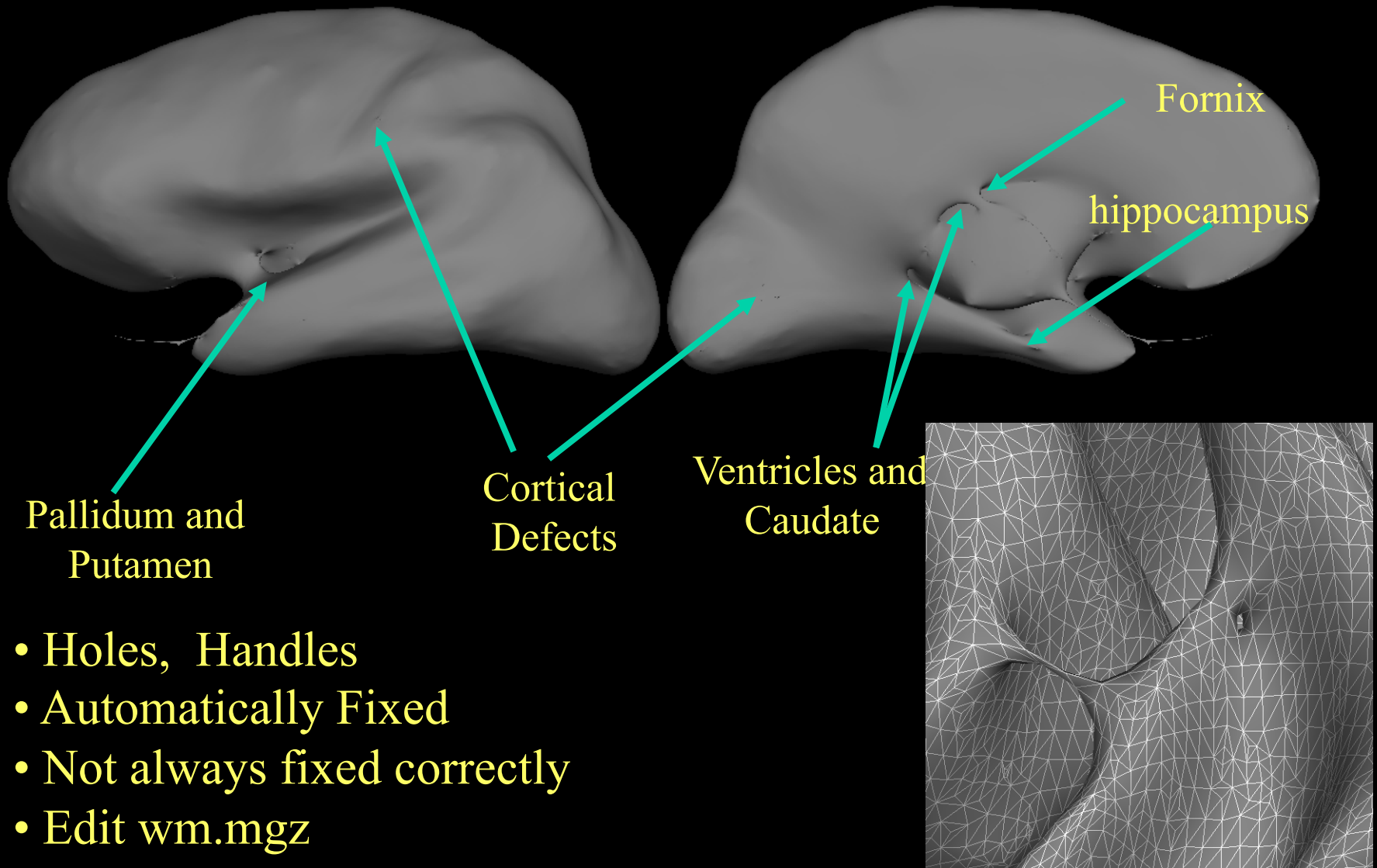
```
recon-all -s <subject> -autorecon2-cp -autorecon3
```

Control Points: Summary



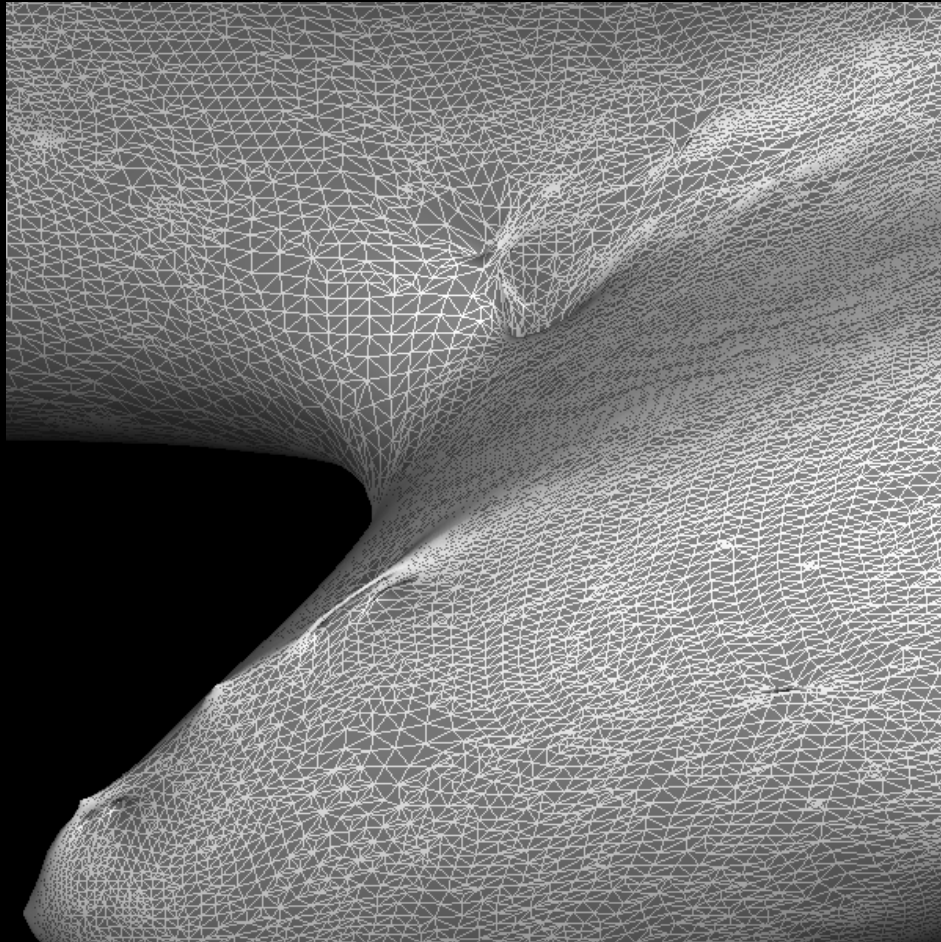
- Used to rescale intensity near the control point
- Must go in voxels that are fully WM but not 110 !!!
- Use sparingly
- Can be created viewing any volume
- Saved in a separate text file (e.g., bert/tmp/control.dat)

Segmentation Errors: Topological Defects

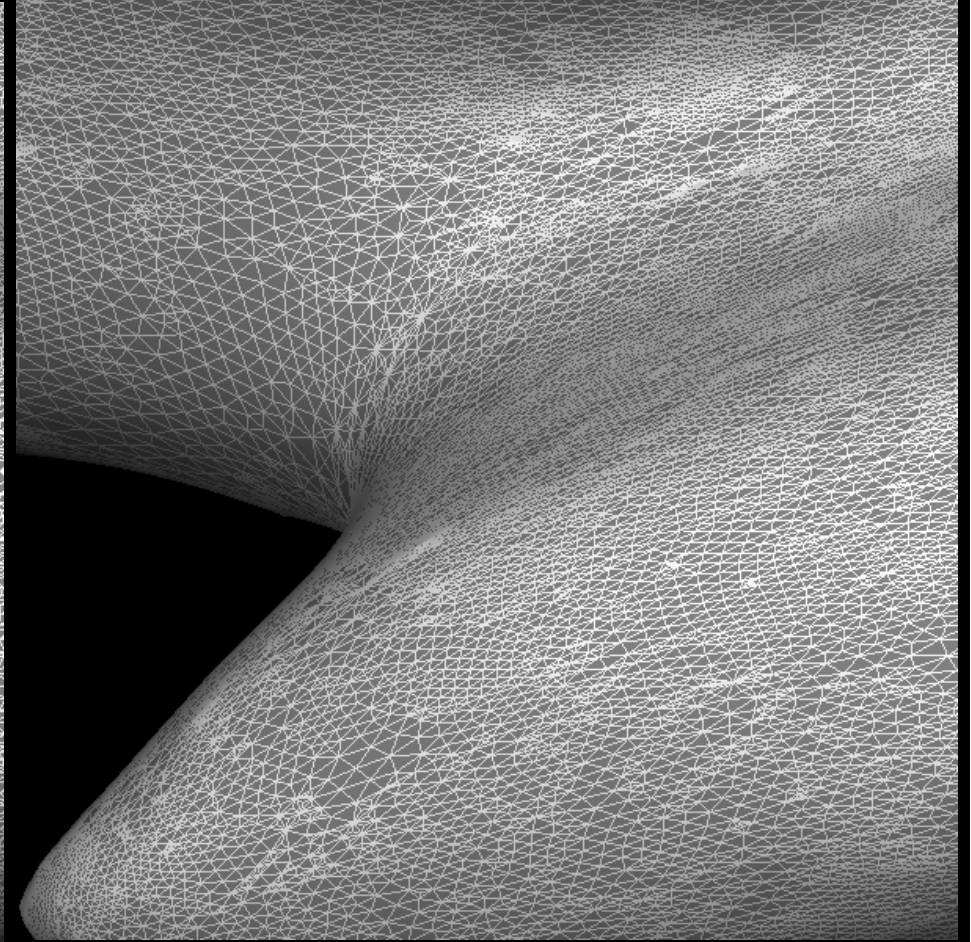


- Holes, Handles
- Automatically Fixed
- Not always fixed correctly
- Edit `wm.mgz`

Topology Correction

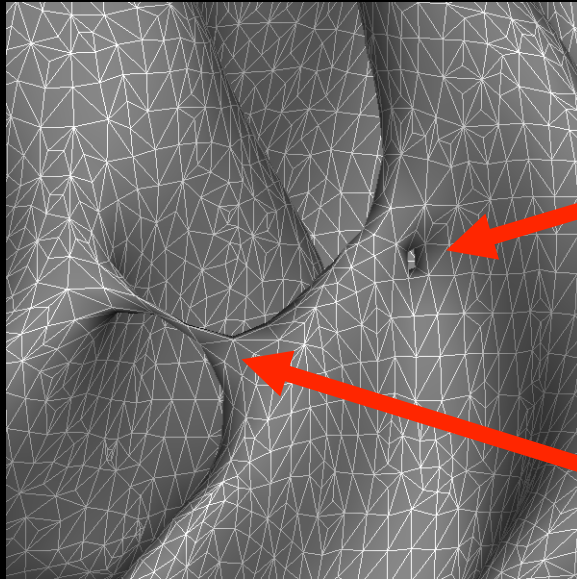


BEFORE



AFTER

Segmentation Errors: Topological Defects

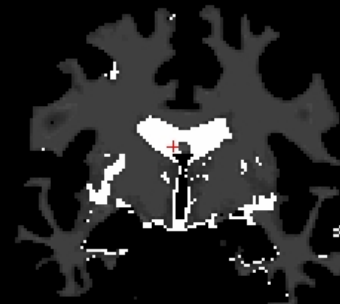


Hole: Partial Voluming: WM + GM looks like non-WM, it is segmented as non-WM and creates a hole

Handle: Something bright in a sulcus that gets classified as WM.

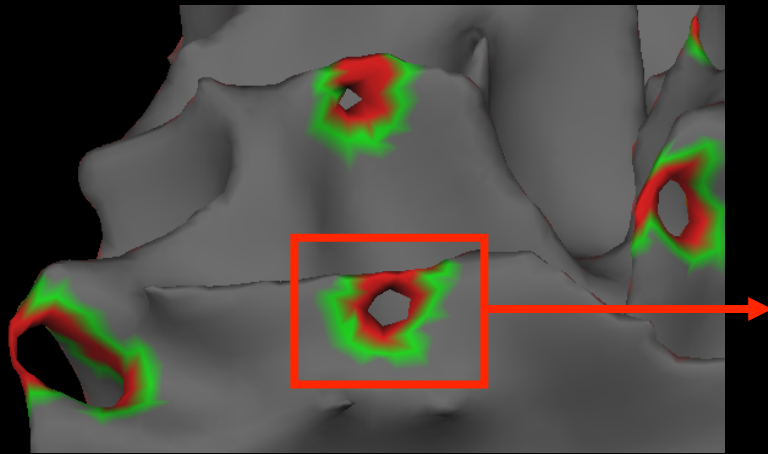
Holes: fill voxels in the wm.mgz

Handles: erase voxels in the wm.mgz

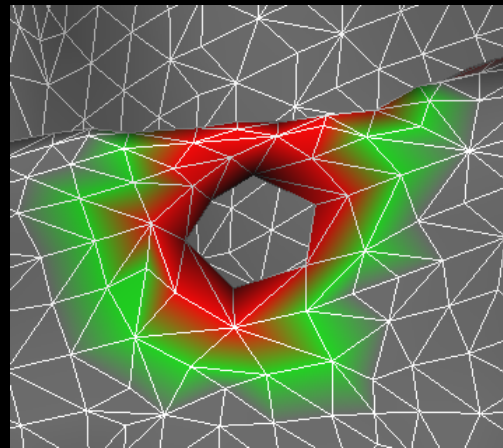


wm.mgz

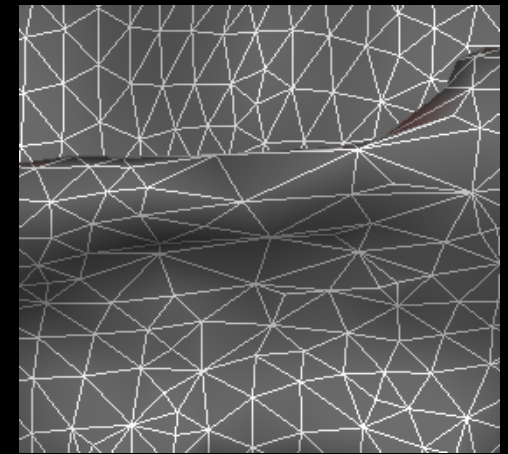
Automatic Defect Correction



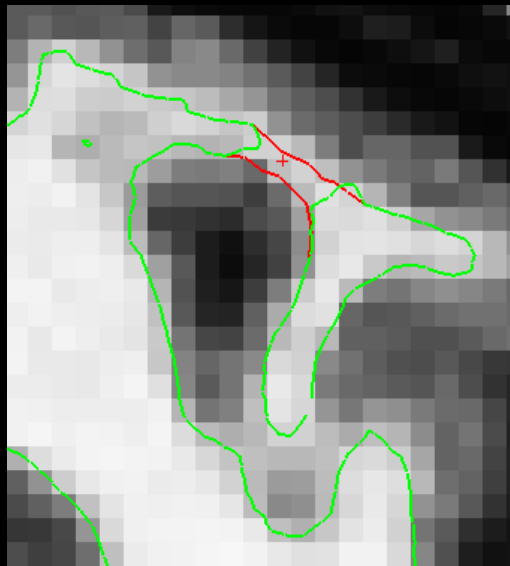
Initial cortical surface



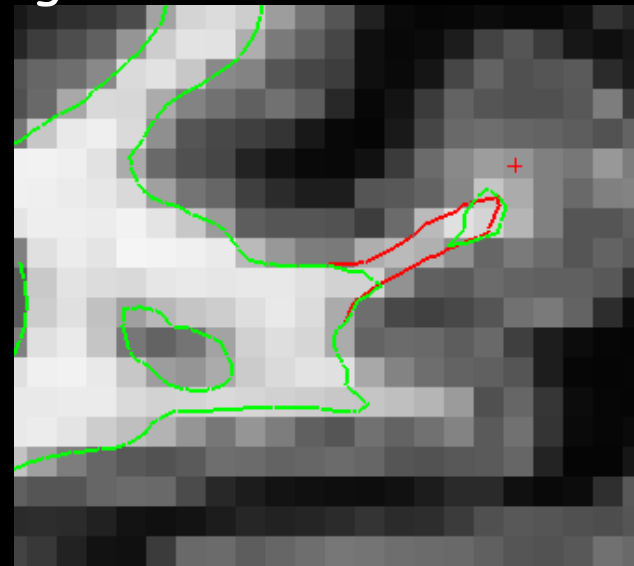
Topological defect



Corrected defect

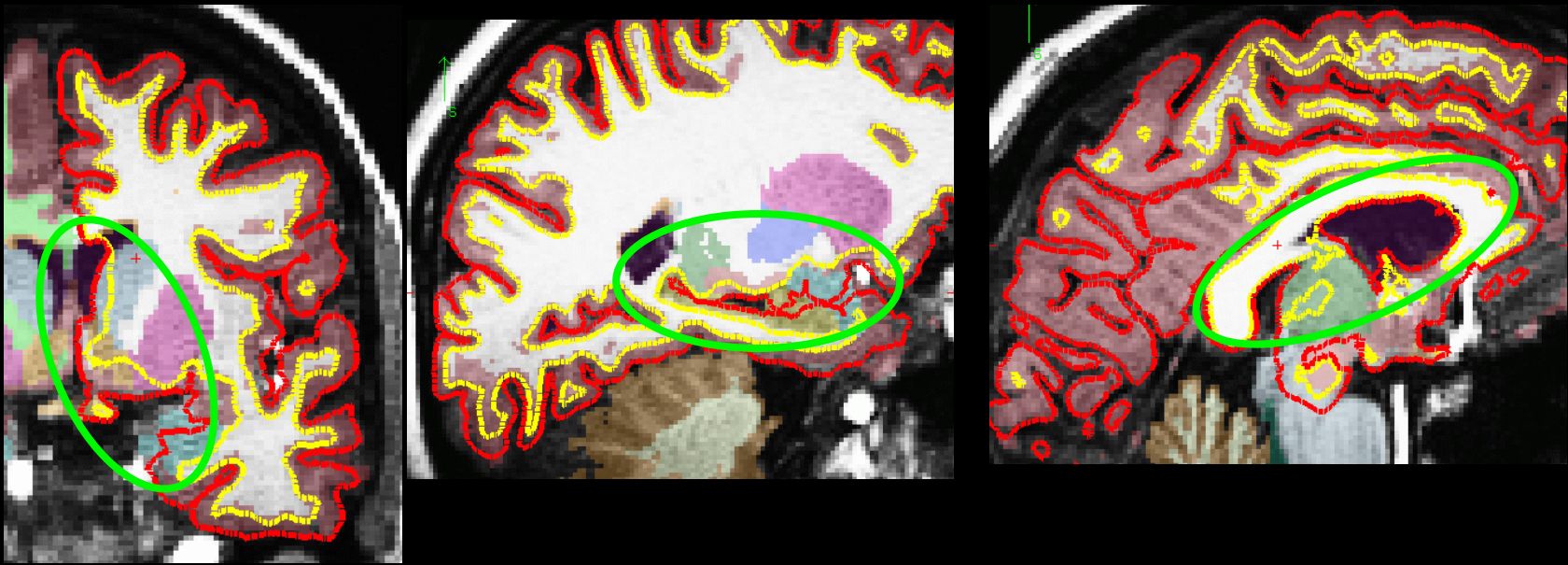


Sagittal view

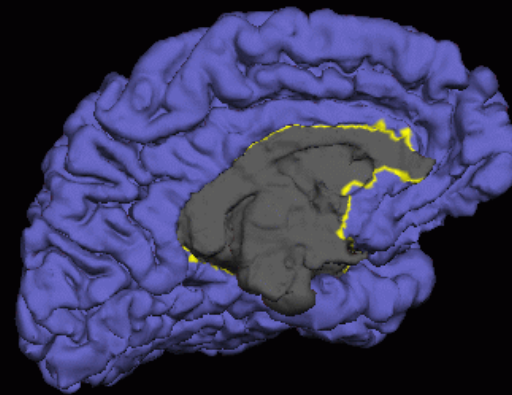
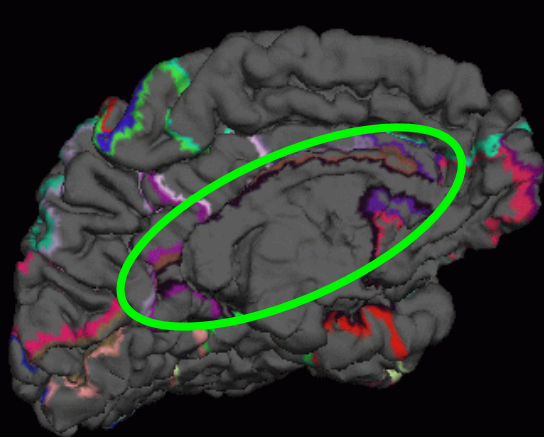


Coronal view

Noncortical Regions: These are not errors



Amygdala, Putamen, Hippocampus, Caudate, Ventricles, CC



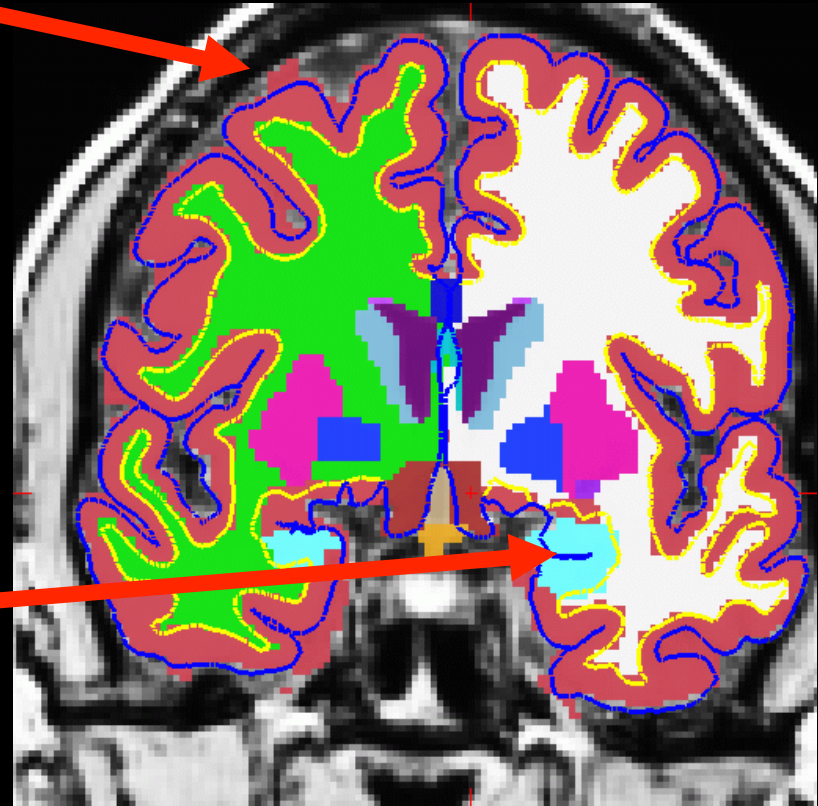
?h.cortex.label

These are NOT errors

It appears that the aseg cortical ribbon is inaccurate. It is, but the aseg cortical ribbon is not used for anything!

Surfaces are not valid in subcortical regions along the medial wall.

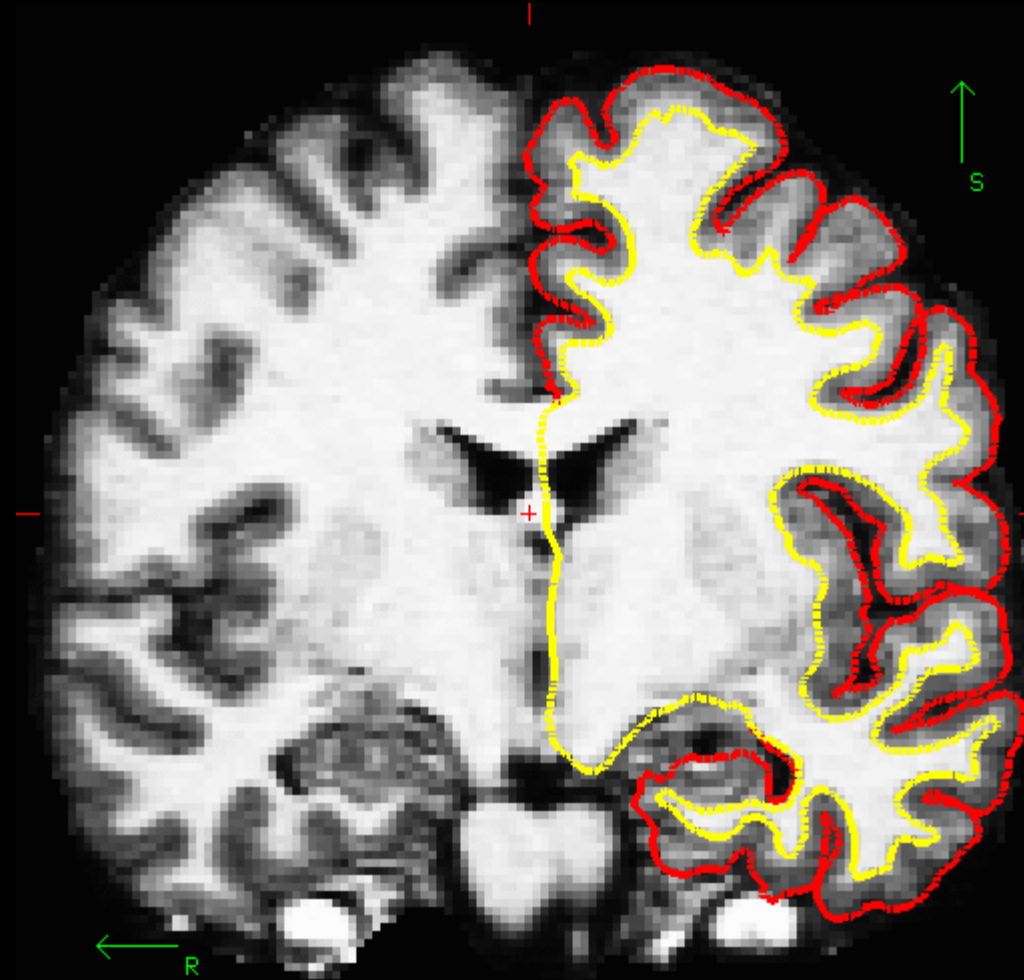
It is possible to edit the segmentation.



How Do You Know What to Edit?

- If **pial surface** includes too much:
 - edit brainmask.mgz
- If it affects the **white surface** (too much/little) or If **pial surface** includes too little:
 - edit the wm.mgz (*if segmentation error*)
 - add control points (*if normalization error*)

Pial surf grows from white surf



Errors in pial surface placement are typically caused by underlying errors in the white surface placement, and can be corrected by interventions that fix the white surface.

Which Volumes to Edit & When...

	Non-gm in pial surf	Non-wm in white surf	wm excluded from surf & intensity = 110	wm excluded from surf & intensity < 110	Cerebellum in pial surf
brainmask.mgz	X				
brain.finalsurfs.mgz	X				X
wm.mgz		X	X		
add control points				X	

FreeSurfer Remembers!

- When edits are made, the changes are saved in a way that indicates manual changes were made (e.g. voxels that are erased are set to 1, not 0, so we can detect them)
- Re-running with a new version preserves these changes.
- To rerun without edits, use `–clean` flags or start from scratch

Summary

- Hard Errors (recon-all.log file)
 - Soft Errors – surfaces not accurate
 - Change volumes, regenerate surfaces
 - Manual touch ups (erase, fill, clone, control points)
 - Volumes: brainmask.mgz, wm.mgz
 - Skull strip: too much, not enough
 - Segmentation: WM classified as non-WM, or reverse
 - FreeSurfer keeps track of edits
 - Look at all 3 views and scroll back and forth a few slices
-
- Should take less than 30 min (or even 15min)
 - If you don't know, leave it alone

Troubleshooting – Advice (Bruce)

- Always look at the data in multiple views and scroll back and forth a few slices – 3D structure is difficult to discern!
- If large regions of white matter are significantly darker than 110 (the target white matter intensity for normalization) then try adding control points, but make sure they are in the interior of the white matter.
- If the ?h.orig surface misses white matter that is accurately labeled in the wm.mgz or extends into regions where there is no wm in the wm.mgz, then there is an incorrectly fixed topological defect.
- Even one or two missing voxels can cause large-scale defects, so very minor editing (e.g. filling in white matter voxels that are holes, or erasing handles) may fix the problem.
- Don't edit too much! This will reduce reliability and is almost never needed. Usually this means you need to start over as you've done something wrong (e.g. put control points in the wrong place).

Troubleshooting – Advice (Allison)

FLOW

AMBIGUITY

CONSISTENCY

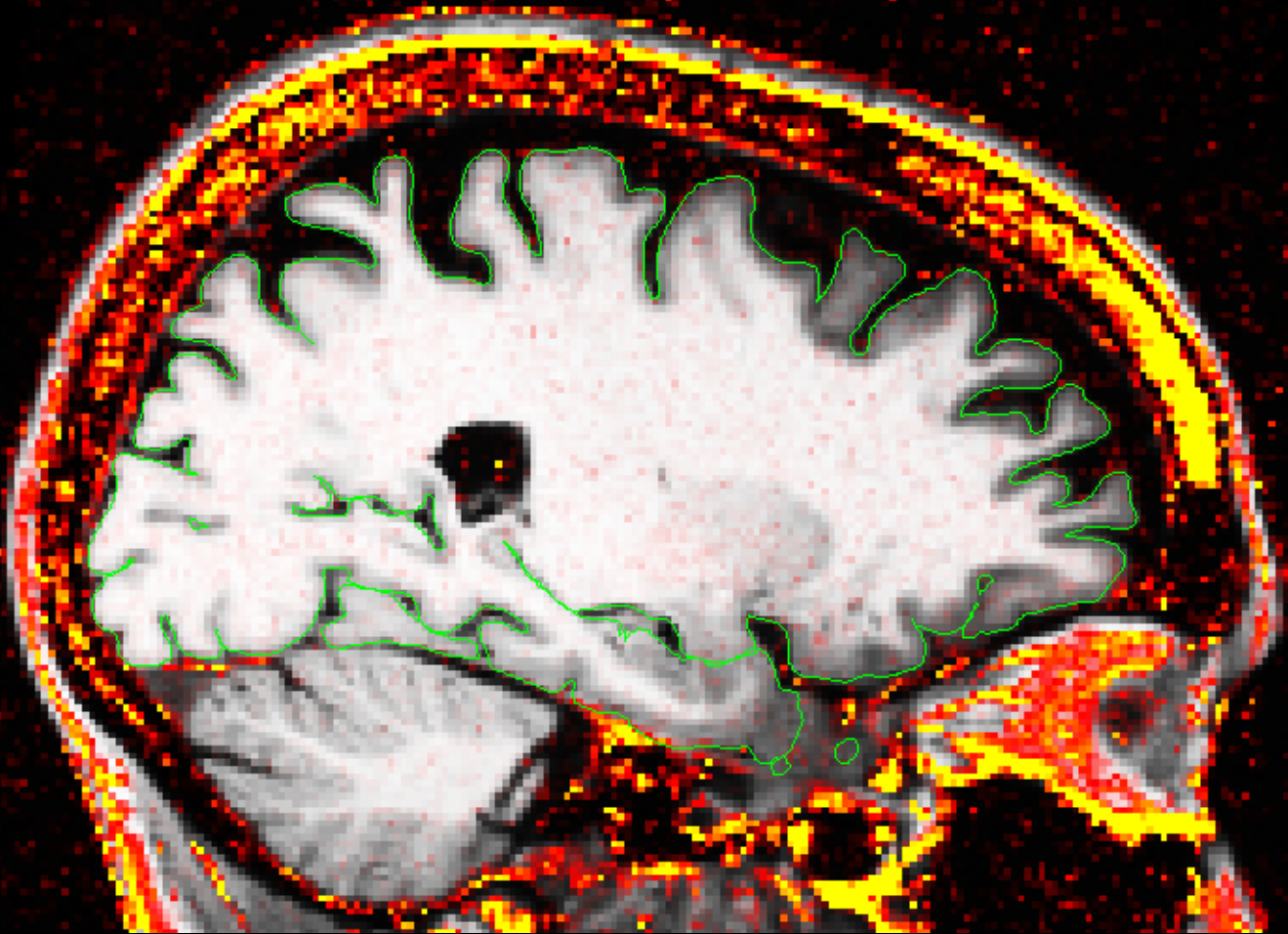
- Edit consistently within and across subjects.

SPEED

- You will get faster with time; certain sections go faster.

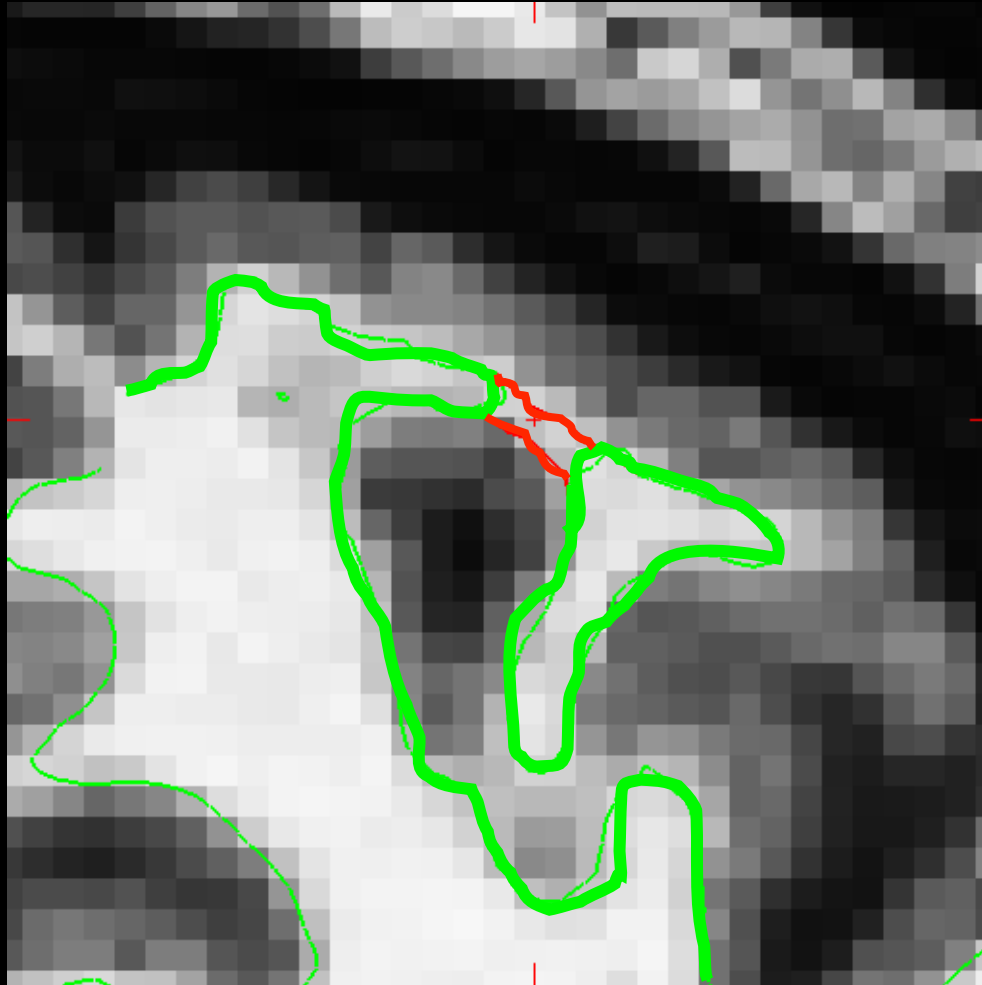
End of Presentation

New Morphometry Protocol: Identifying Dura with Multi-echo MP-RAGE



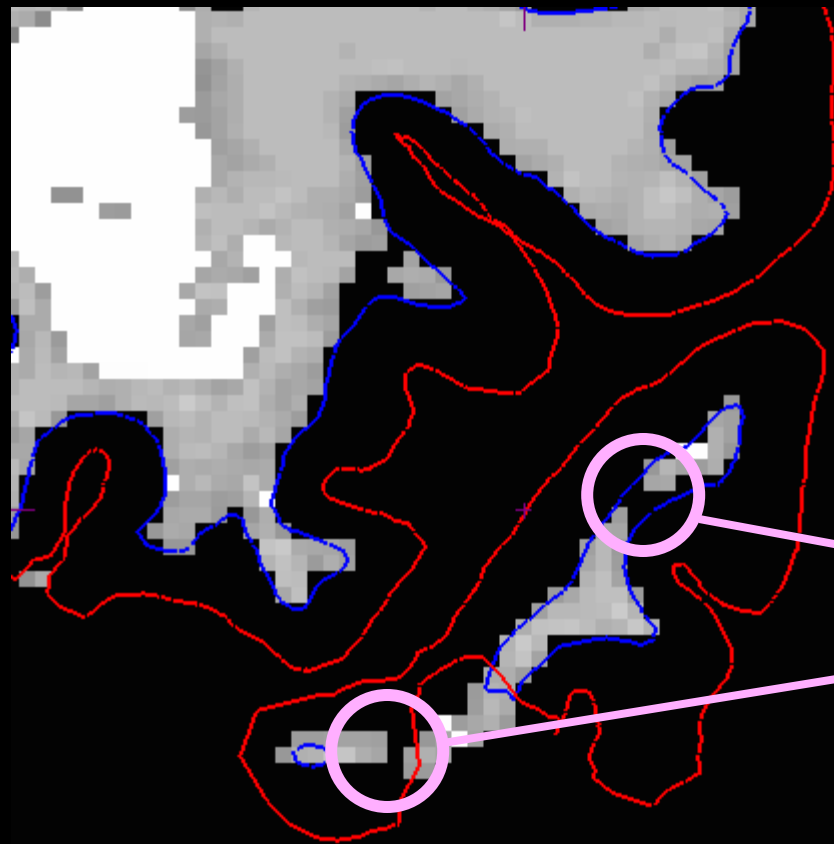
*joint work with Andre van der Kouwe

Automatic Defect Correction



Difference between uncorrected (green) and corrected (red)

Troubleshooting: Topology Fixer Error



White Matter
“disconnects”

orig.nofix will be
accurate

What are the Common Interventions?

- Manually edit the `wm.mgz` to change incorrectly labeled voxels (only for small errors).
- Manually edit the `brainmask.mgz` to erase dura/vasculature.
- Adjust watershed parameters or use `-gcut` to fix large-scale skull-strip errors.
- Manually erase/clone regions of skull strip failure.
- Control Points – add locations that are in the interior of the white matter and `<110` to bring regional wm intensity up.
- Use `tkregister2` to fix incorrect `talairach.xfm`

Troubleshooting – Common Cases

($\approx 98\%$ of surface accurate in about 98% of cases for good data [1])

- **Symptom:** white matter not accurate in `wm.mgz`
- **Interventions**
 - add control points (if `wm` \ll 110).
 - Expert opts to set intensity thresholds in segmentation (almost never).
 - Manually erase/draw `wm` in `wm.mgz`
- **Symptom:** skull strip not accurate
- **Interventions**
 - Adjust `mri_watershed` parameters or try `-gcut`
 - Manually erase skull/clone `T1.mgz` to recover brain
- **Symptom:** surfaces are not accurate.
- **Interventions:**
 - Add control points (if white matter \ll 110).
 - Erase dura/blood vessels
 - Check topology on `?h.inflated.nofix` (if `?h.orig` surface doesn't follow `wm.mgz`)