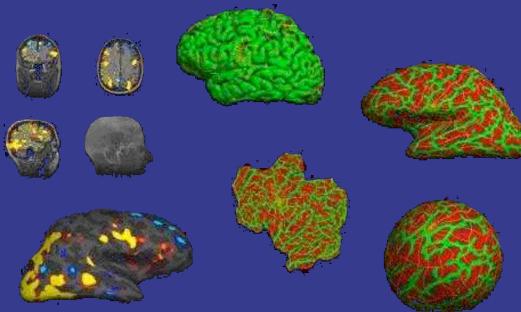


FreeSurfer



FREESURFER: RECONSTRUCTING THE NONHUMAN BRAIN

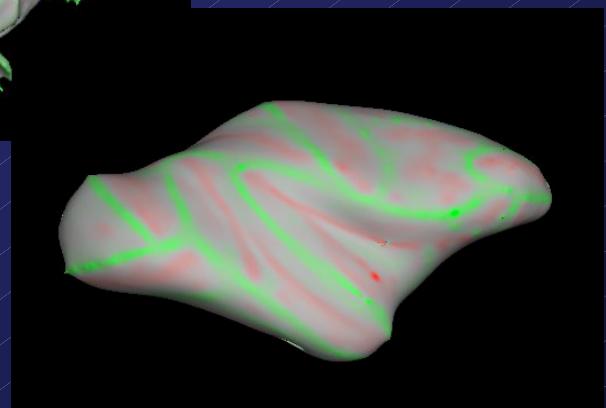
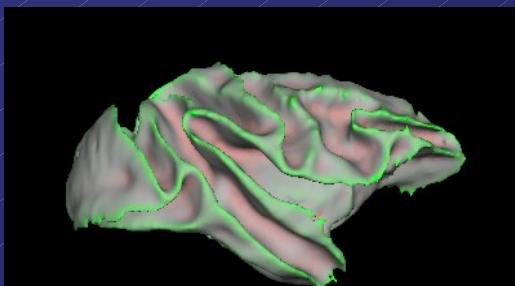
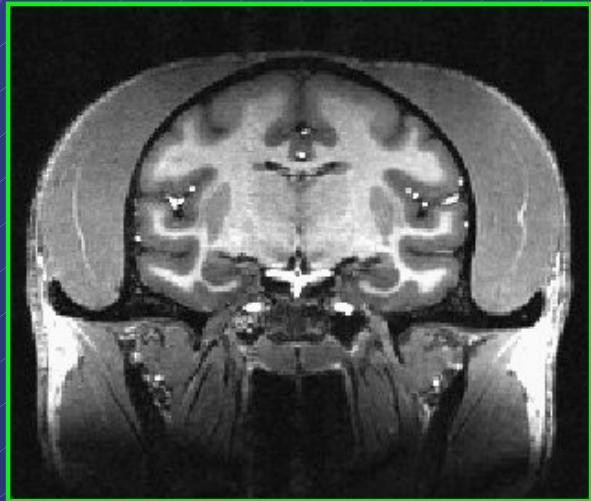
Peggy Christidis

July 14, 2005

National Institutes of Health

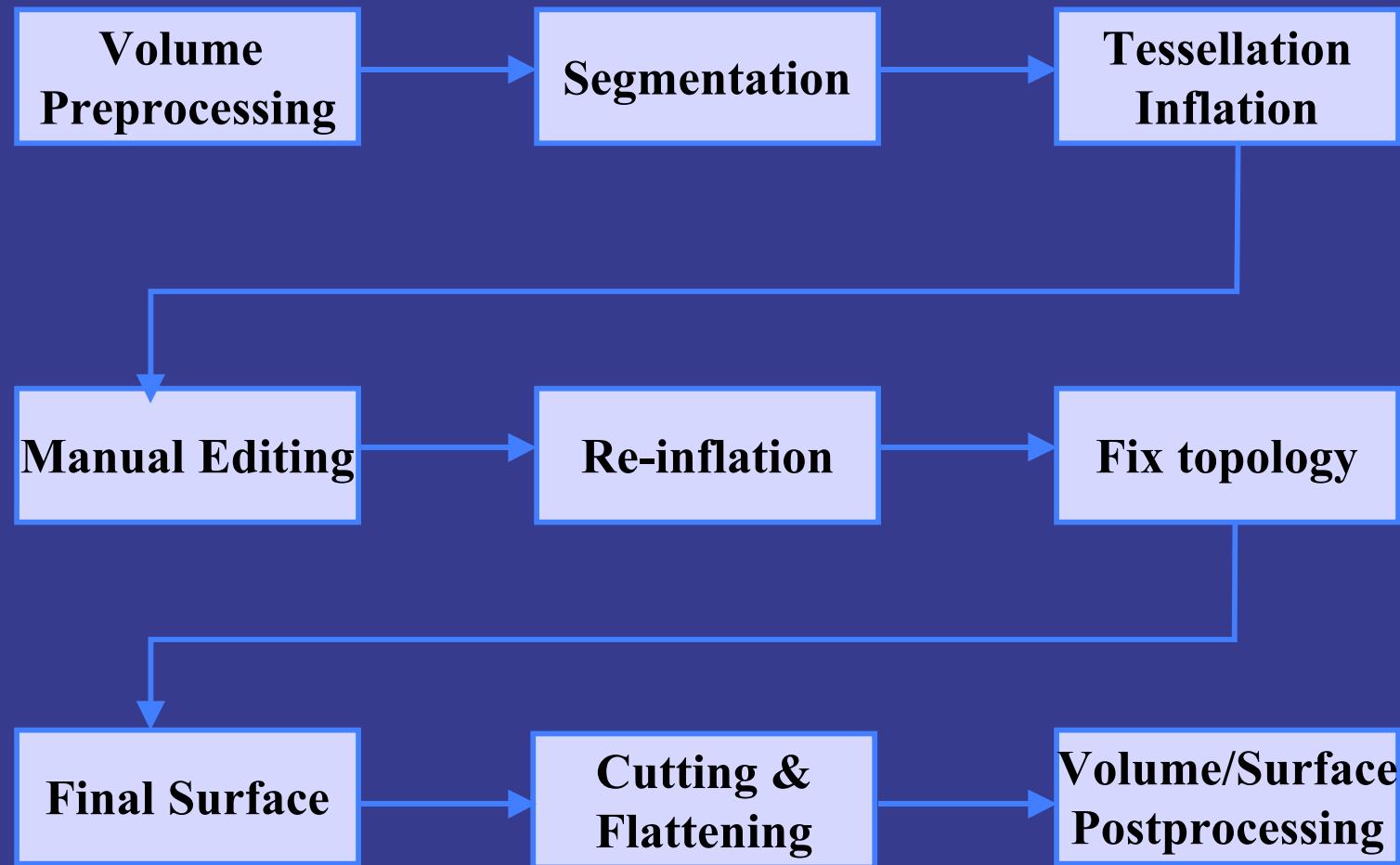
GOAL:

Learn to create monkey surfaces using FreeSurfer

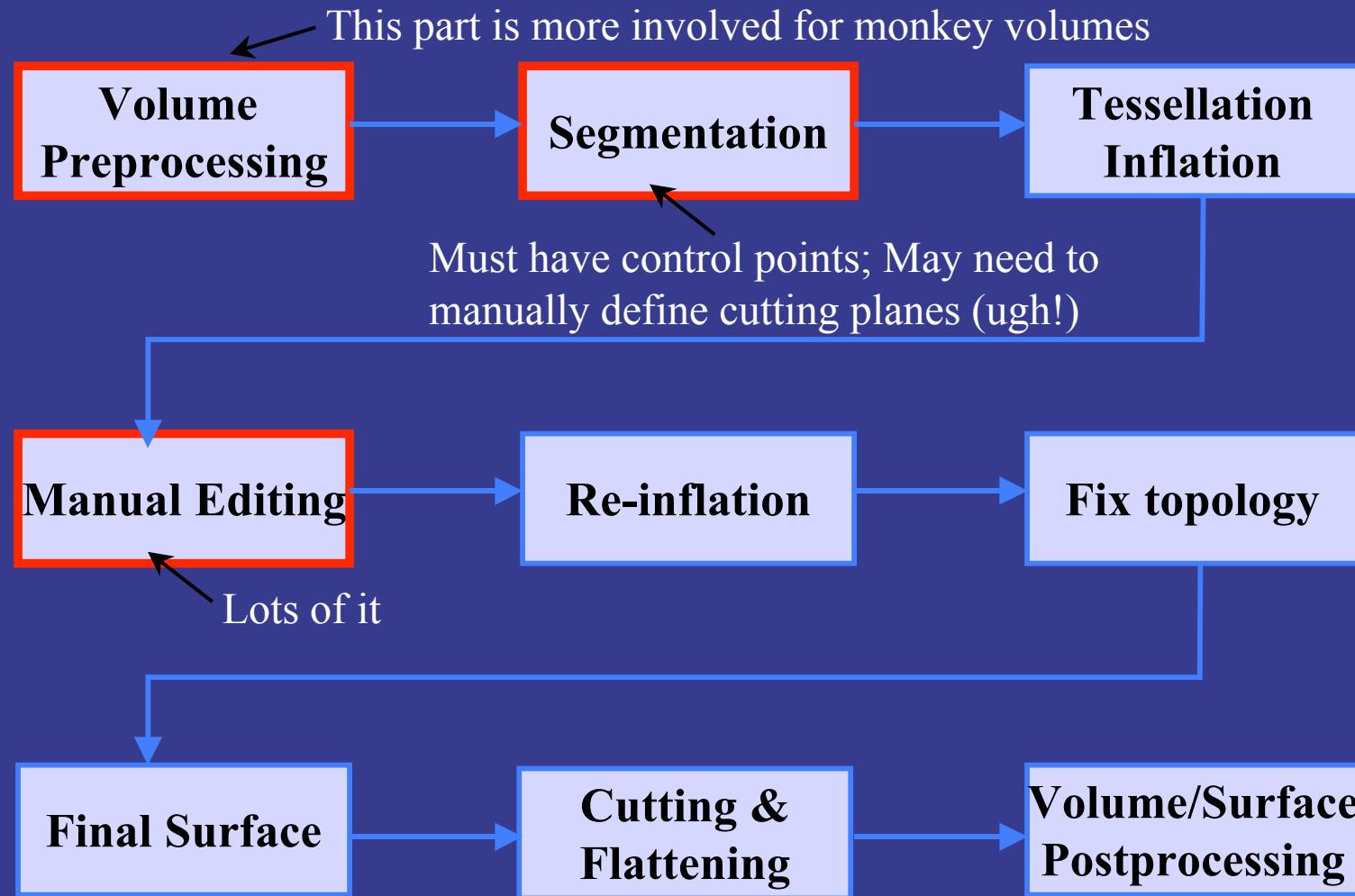


- Primate cortical reconstruction is a more involved and complicated process than human cortical reconstruction
- FreeSurfer manual recommends starting with at least 3 anatomical scans

FreeSurfer Flowchart for Human Brains



FreeSurfer Flowchart for Primate Brains

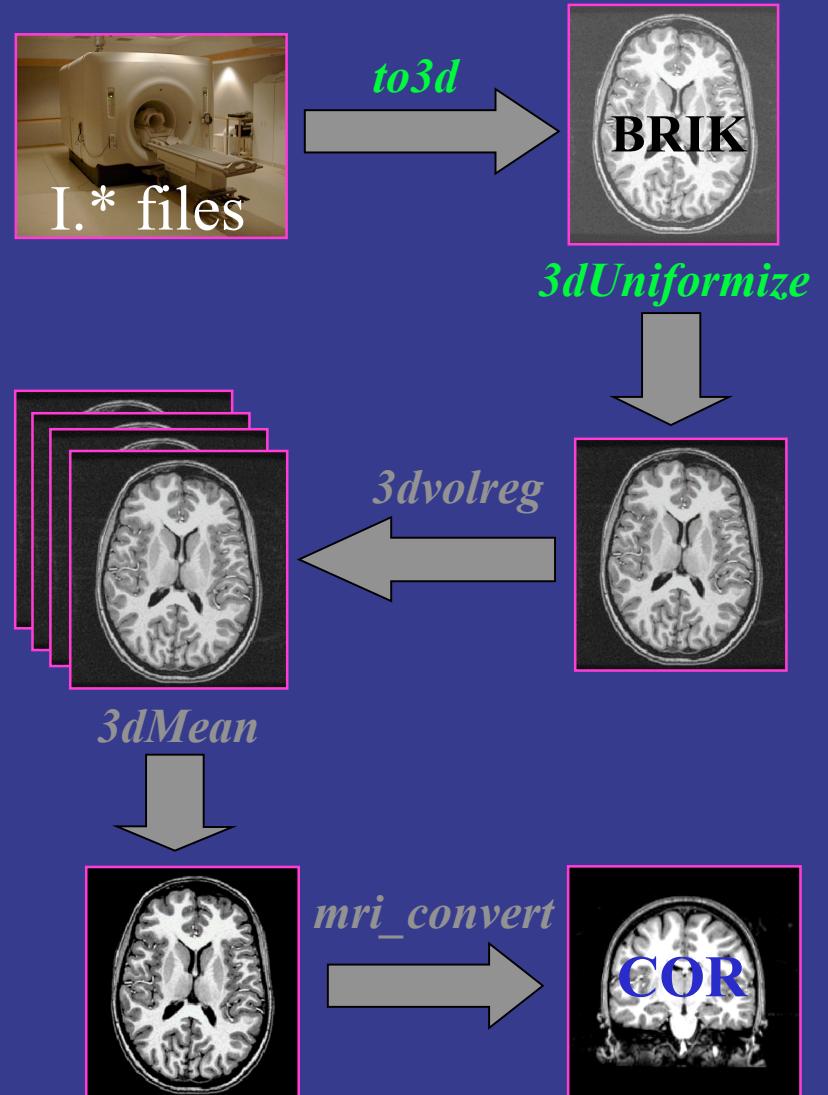


Volume Preprocessing: Humans



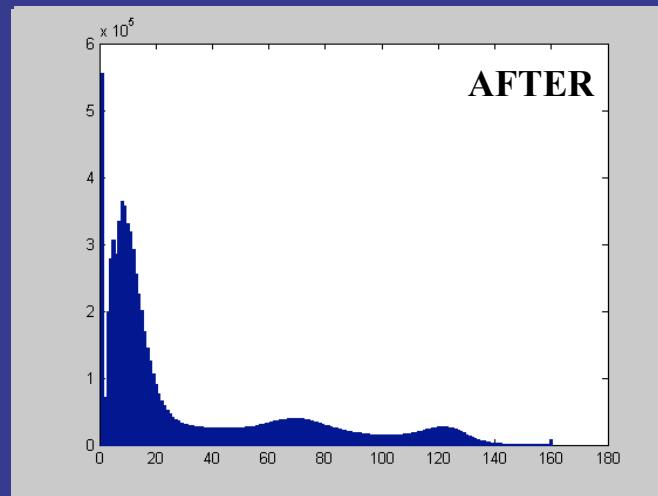
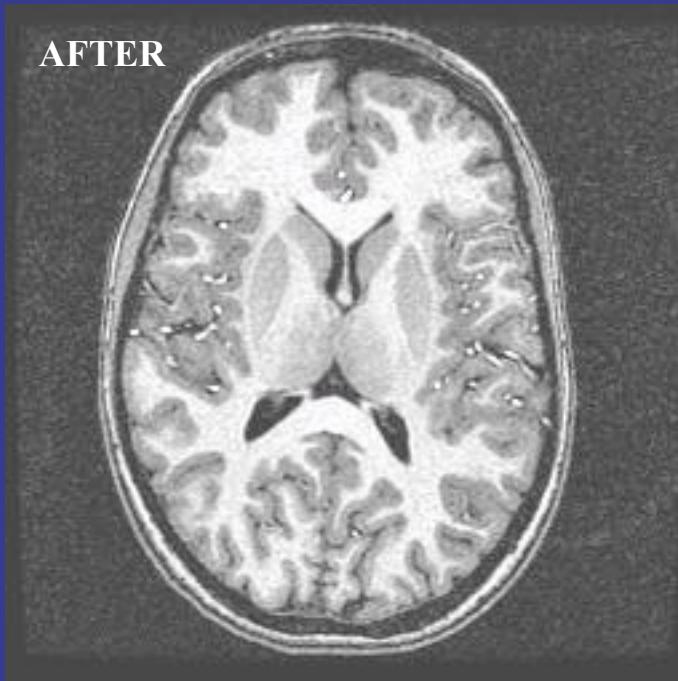
Volume Preprocessing: Humans

- Convert I.* files to BRIK using AFNI *to3d*
- Perform intensity normalization using AFNI *3dUniformize*
- Register multiple volumes using AFNI *3dvolreg*
- Average the registered volumes using AFNI *3dMean*
- Convert to FreeSurfer format using FreeSurfer *mri_convert*



Intensity normalization – critical for segmentation

- Inhomogeneities in scanner fields cause gray and white matter intensities to vary as a function of their spatial location.
- Removes residual non-uniformities in gray and white matter intensity values.

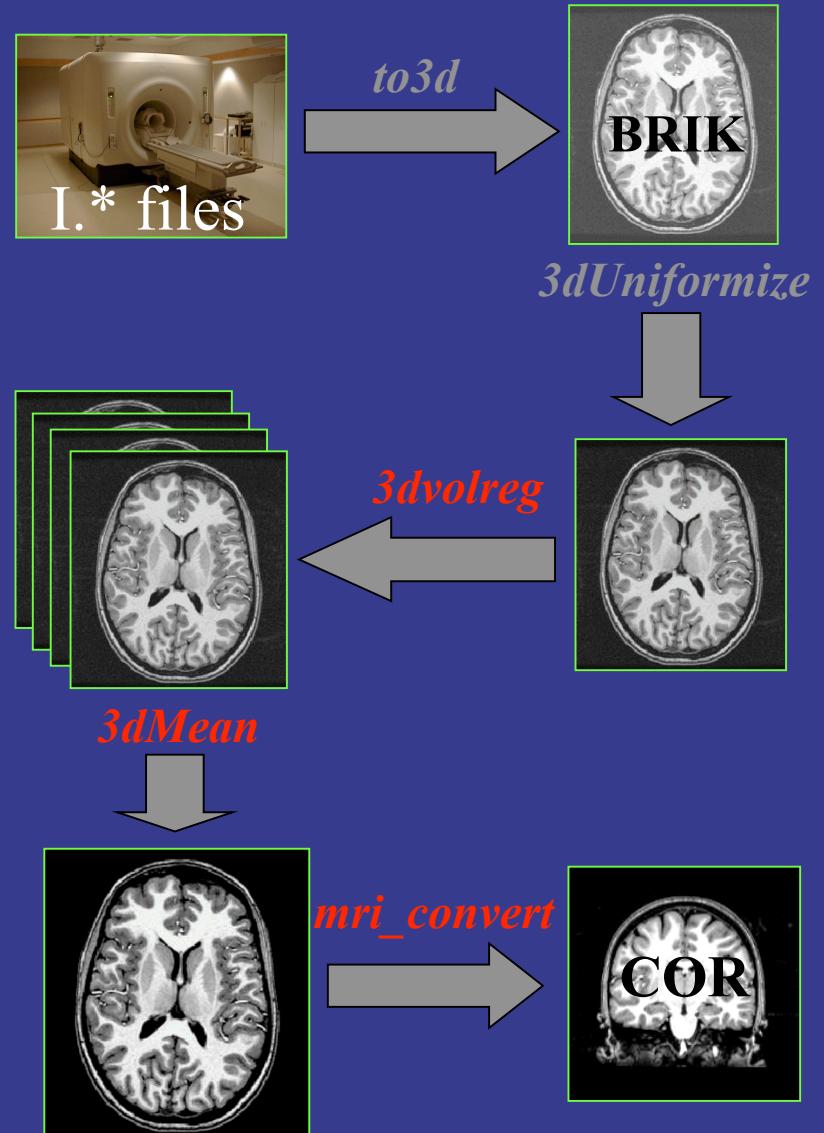


- Increases gray and white matter contrast.
- Sharpens the peaks of the two tissue classes.
- Makes the intensity distribution of gray and white matter spatially uniform.



Volume Preprocessing: Humans

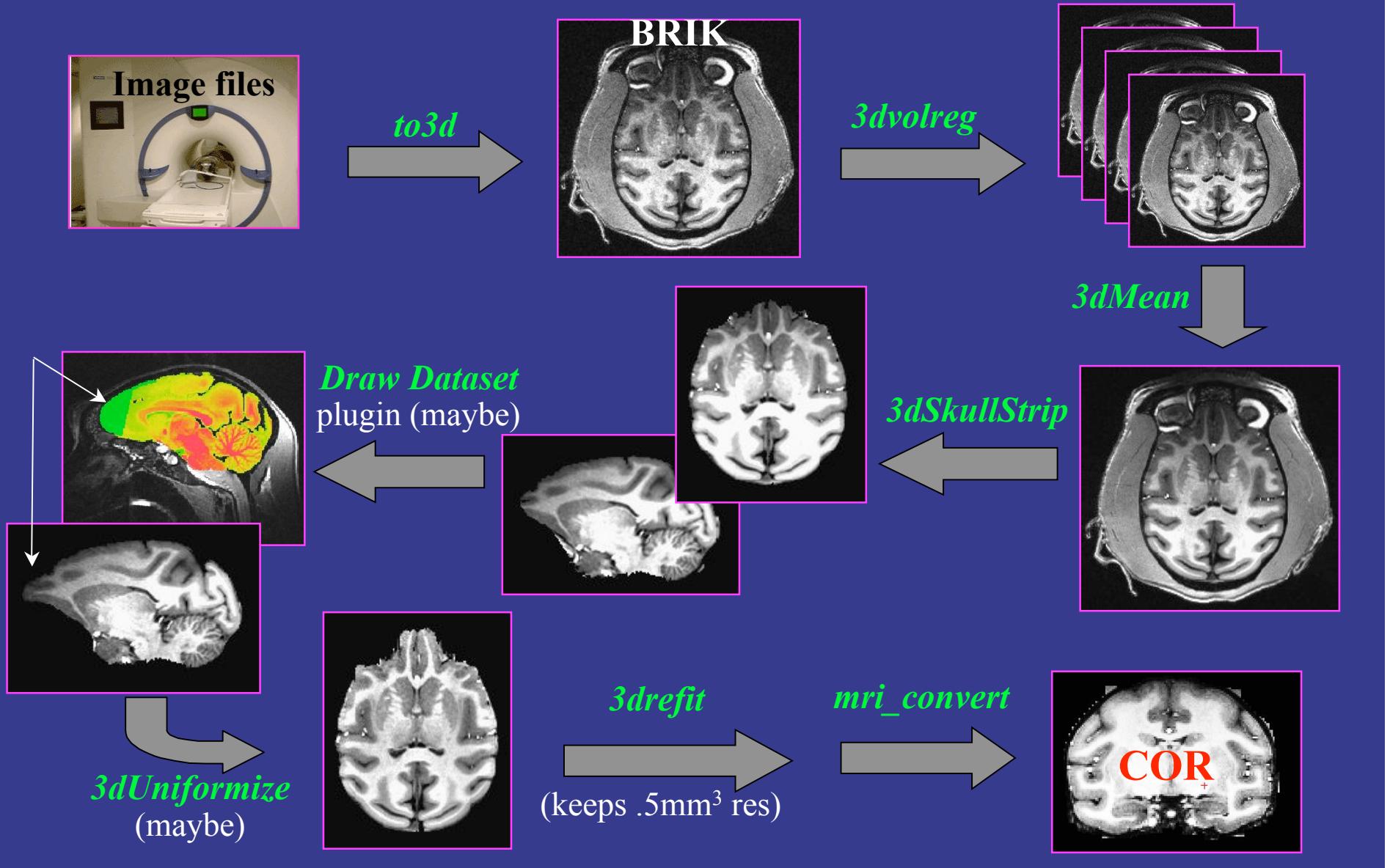
- Convert I.* files to BRIK using AFNI *to3d*
- Perform intensity normalization using AFNI *3dUniformize*
- *Register multiple volumes using AFNI 3dvolreg*
- *Average the registered volumes using AFNI 3dMean*
- *Convert to FreeSurfer format using FreeSurfer mri_convert*



Volume Preprocessing: Monkeys



Volume Preprocessing: Monkeys



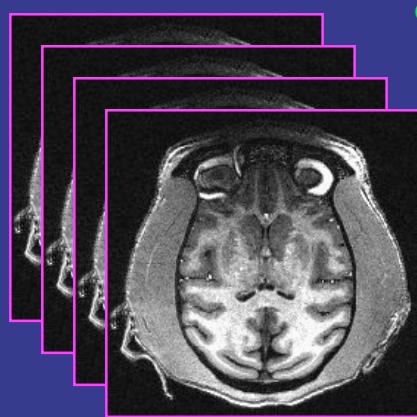
STEP 1: Collect your data

1st_scan+orig.HEAD	1st_scan+orig.BRIK
2nd_scan+orig.HEAD	2nd_scan+orig.BRIK
3rd_scan+orig.HEAD	3rd_scan+orig.BRIK
4th_scan+orig.HEAD	4th_scan+orig.BRIK

STEP 2: Volume registration

```
foreach num (1st 2nd 3rd 4th)
    3dvolreg -twopass -cubic -zpad 4 \
              -base 1st_scan+orig \
              -prefix ${num}_scan_vr \
              ${num}_scan+orig
```

end



1st_scan_vr+orig.HEAD	1st_scan_vr+orig.BRIK
2nd_scan_vr+orig.HEAD	2nd_scan_vr+orig.BRIK
3rd_scan_vr+orig.HEAD	3rd_scan_vr+orig.BRIK
4th_scan_vr+orig.HEAD	4th_scan_vr+orig.BRIK

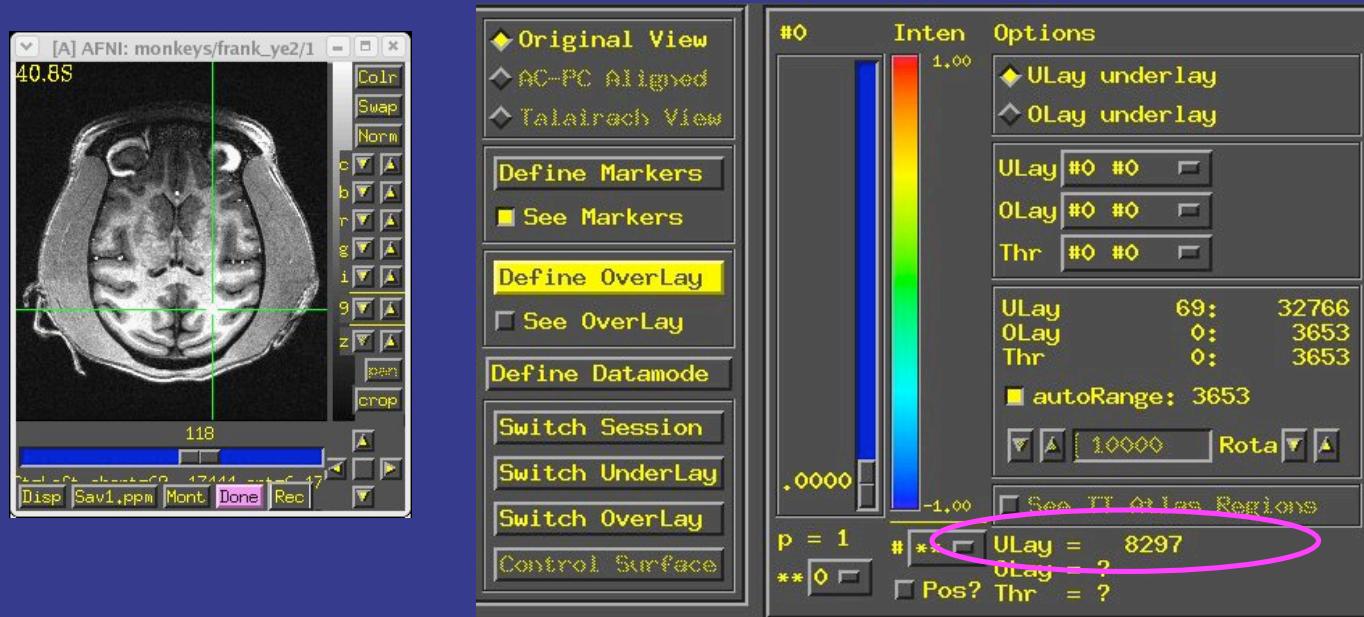
NOTE:

Check your datasets in AFNI or whatever fMRI software package you're comfortable with.

In this case, the datasets had really high intensity values. The nonuniformity correction program in AFNI (**3dUniformize**) has difficulty with high intensity values.

AFNI's **3dcalc** program was used to divide each voxel in each dataset by '20', resulting in smaller intensity values for each volume.

This is a temporary problem with 3dUniformize that will be fixed in the near future.



```

foreach num (1st 2nd 3rd 4th)
    3dcalc -a {$num}_scan_vr+orig -expr 'a/20' \
    -nyscale -prefix {$num}_scan_vr20
end

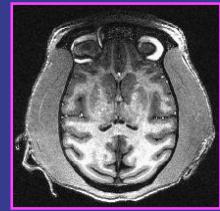
```

1st_scan_vr20+orig.HEAD
 2nd_scan_vr20+orig.HEAD
 3rd_scan_vr20+orig.HEAD
 4th_scan_vr20+orig.HEAD

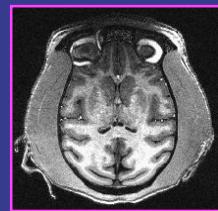
1st_scan_vr20+orig.BRIK
 2nd_scan_vr20+orig.BRIK
 3rd_scan_vr20+orig.BRIK
 4th_scan_vr20+orig.BRIK

STEP 3: Average your volume-registered datasets together

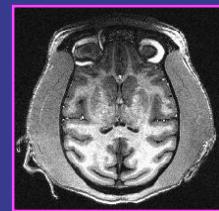
```
3dMean -prefix avg4 \
???_scan_vr+orig.BRIK
```



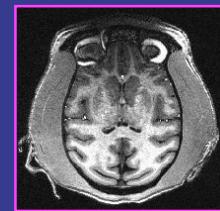
1st_scan_vr



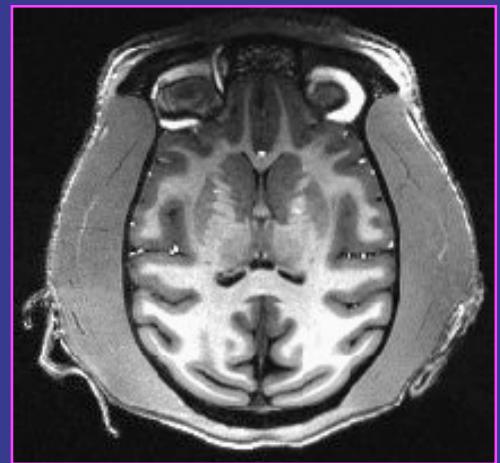
2nd_scan_vr



3rd_scan_vr



4th_scan_vr

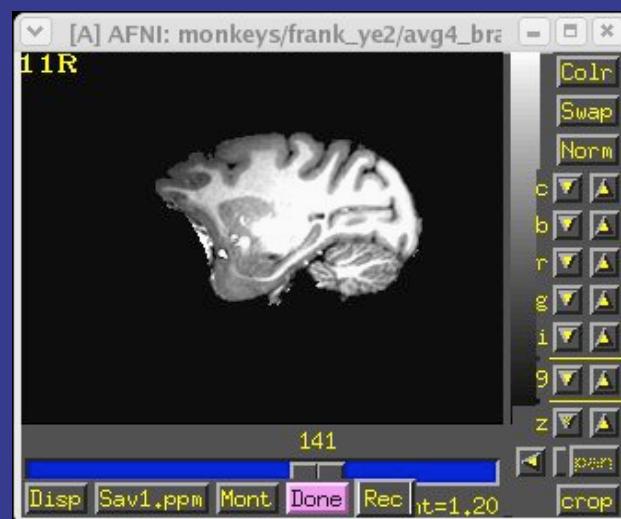
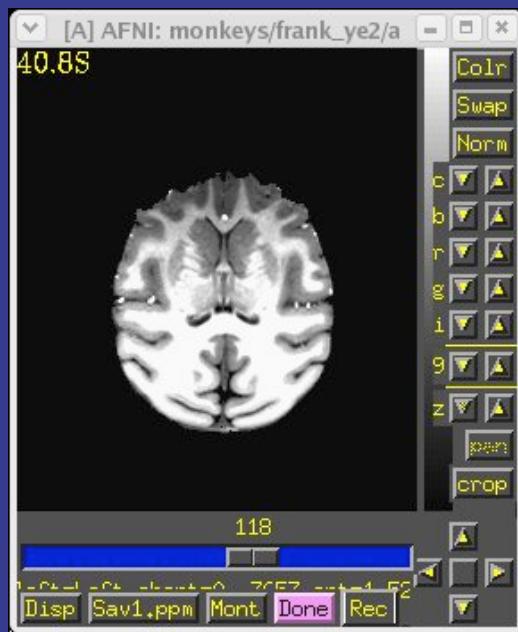


avg4+orig.HEAD
avg4+orig.BRIK

STEP 4: Extract the brain from surrounding tissue and skull

```
3dSkullStrip -prefix avg4_brain \
              -input avg4+orig -no_avoid_eyes
```

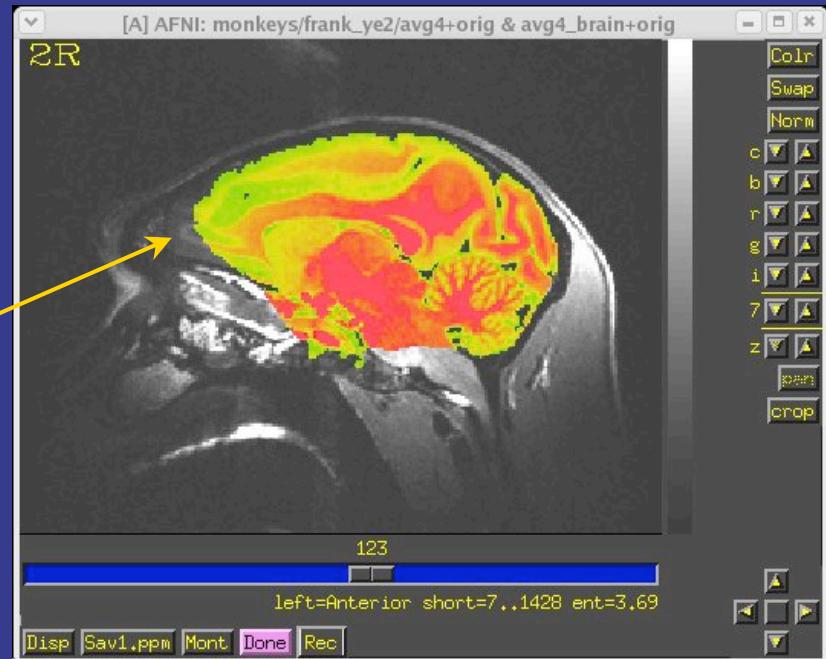
avg4_brain+orig.HEAD
avg4_brain+orig.BRIK



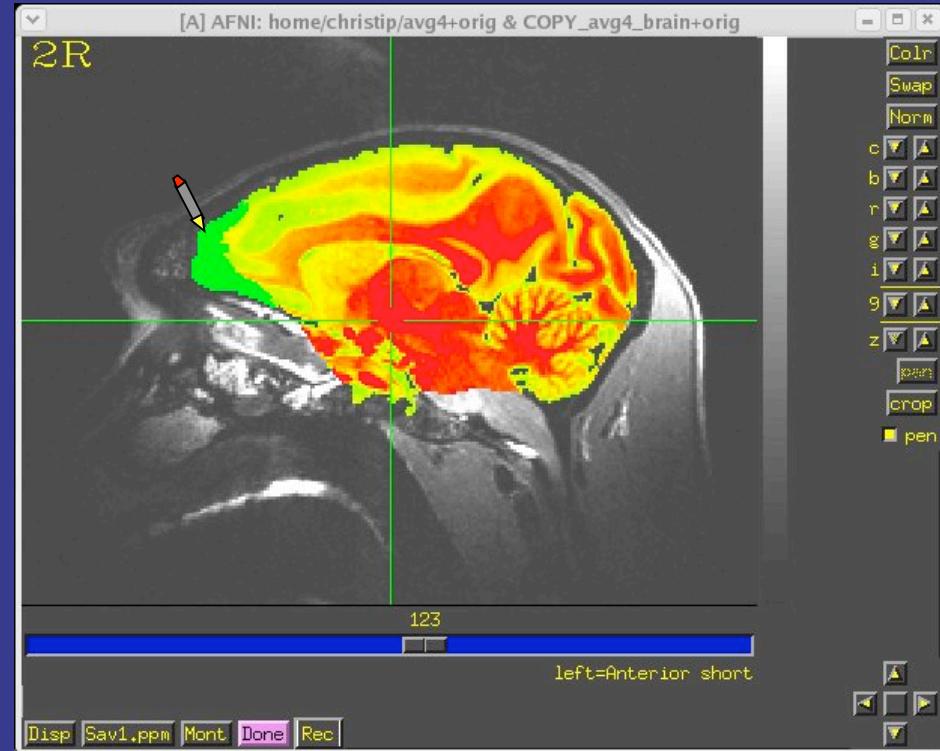
NOTE:

- Check your dataset in AFNI or whatever fMRI software package you're comfortable with.
- In this case, if we overlay the skull-stripped dataset on top of the un-skull-stripped dataset, we can see that a little too much brain was removed from the frontal lobes (that's because these volumes are really dark in the frontal lobe region).
- You may have to manually re-draw it back into the dataset.
- Try the AFNI plugin '**Draw Dataset**'
- Yes, this is labor intensive.
- And yes, you really should do it.

trouble area



STEP 5: If necessary, manually insert “brain” voxels that were removed when you did the skull stripping

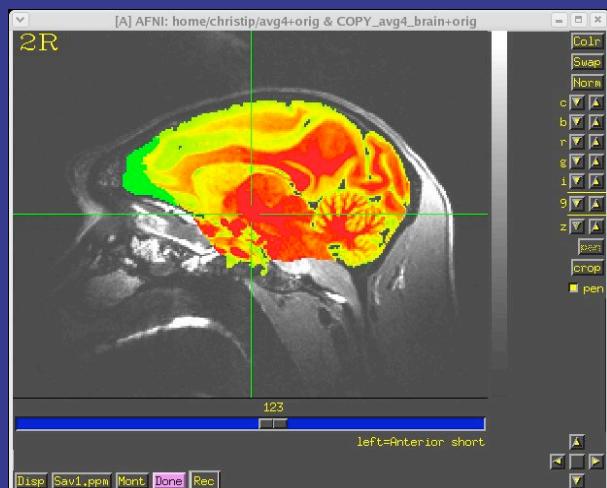


COPY_avg4_brain+orig.HEAD

COPY_avg4_brain+orig.BRIK

STEP 5: continued...

```
3dcalc -a avg4+orig -b COPY_avg4_brain+orig  
-expr 'a*ispositive(b)'  
-prefix avg4_brain_edited
```



COPY_avg4_brain+orig.HEAD
COPY_avg4_brain+orig.BRIK

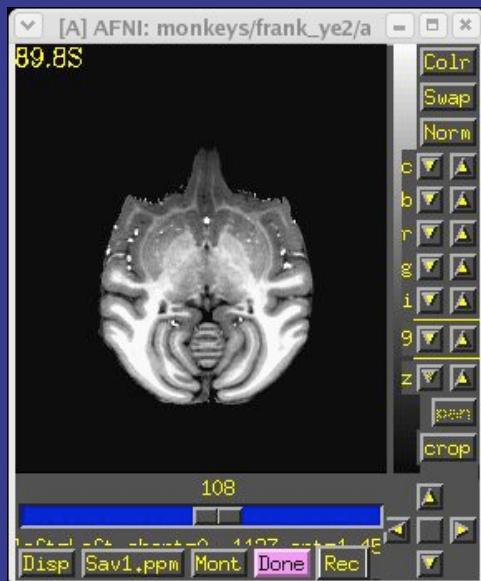


avg4_brain_edited+orig.HEAD
avg4_brain_edited+orig.BRIK

STEP 6: Perform a nonuniformity correction

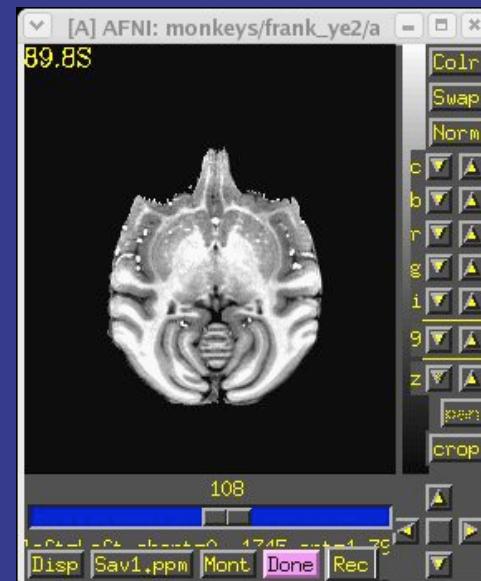
```
3dUniformize -prefix avg4_ready4FS -quiet \
-anat avg4_brain_edited.orig
```

Before 3dUniformize



avg4_brain_edited+orig

After 3dUniformize



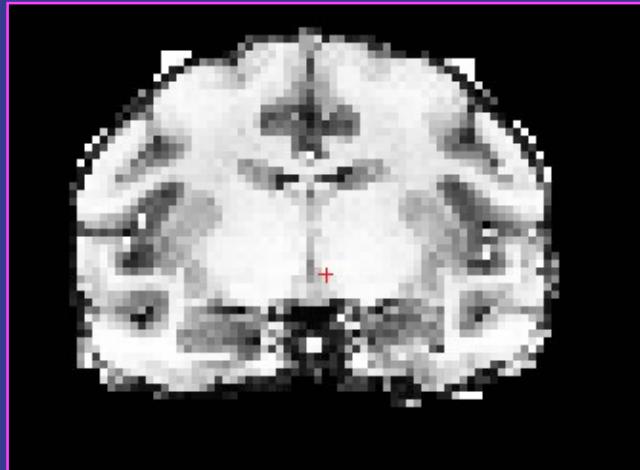
avg4_ready4FS+orig

Note: This may or may not make the data look better. It really depends on the volume. Also, it may look great in AFNI, but not so great in FreeSurfer (I still can't figure that one out)

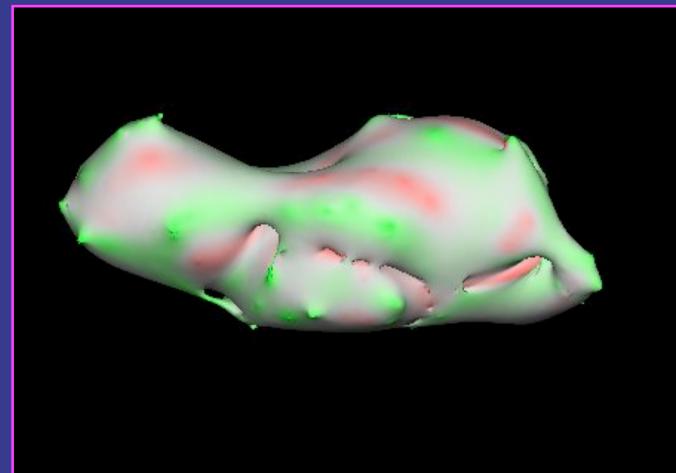
STEP 6: Use 3drefit to make sure FreeSurfer doesn't resample your high-resolution volume to a lower resolution

- When importing your volume into FreeSurfer, the program will resample it to its **COR** format, which is made up of 256 coronal slices, a 256 x 256 in-plane, and a 1mm³ voxel resolution.
- For human volumes, this is okay because a voxel resolution of 1 mm³ is great. For monkey volumes however, the voxel resolution is often better than 1mm³. In our example, the voxel resolution is 0.5mm³.
- If we allowed FreeSurfer to resample our dataset from a 0.5mm³ voxel resolution to a 1mm³ voxel resolution, the COR volume in FreeSurfer would look pixelated.
- Pixelated volume = unsuccessful white matter segmentation

Volume in FreeSurfer if **3drefit** isn't run first:



Segmentation will either fail or give you terrible results:

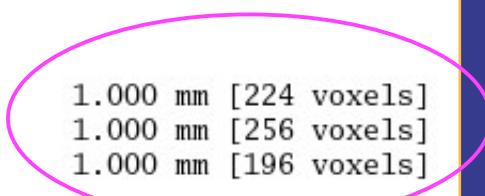


```
3drefit -xdel 1.0 -ydel 1.0 -zdel 1.0 \
avg4_brain_edited+orig
```

3drefit will change the header information in the above dataset, but it won't change the actual data. This way, when FreeSurfer reads the header information of that dataset, it will see the 1mm³ voxel-resolution and won't enlarge the voxels, thinking they're already at the resolution they need to be.

```
3dinfo avg4_brain_edited+orig
```

```
Dataset File: avg4_brain_edited+orig
[dentifier Code: PPC_L05xhKvh_il-vURl88eKYw Creation Date: Fri Jul  8 16:18:17
2005
Dataset Type: Spoiled GRASS (-spgr)
Byte Order: LSB_FIRST [this CPU native = LSB_FIRST]
Storage Mode: BRIK file
Data Axes Orientation:
    first (x) = Right-to-Left
    second (y) = Anterior-to-Posterior
    third (z) = Inferior-to-Superior [-orient RAI]
R-to-L extent: -52.000 [R] -to- 171.000 [L] -step-
A-to-P extent: -83.183 [A] -to- 171.817 [P] -step-
I-to-S extent: -18.199 [I] -to- 176.801 [S] -step-
Number of values stored at each pixel = 1
-- At sub-brick #0 '#0' datum type is short:
```



1.000 mm [224 voxels]
1.000 mm [256 voxels]
1.000 mm [196 voxels]

0 to 1628

STEP 7a: Create FreeSurfer directory tree using `mksubjdirs`

NOTE: Now we're entering FreeSurfer country, so be sure to source your FreeSurfer login file first.

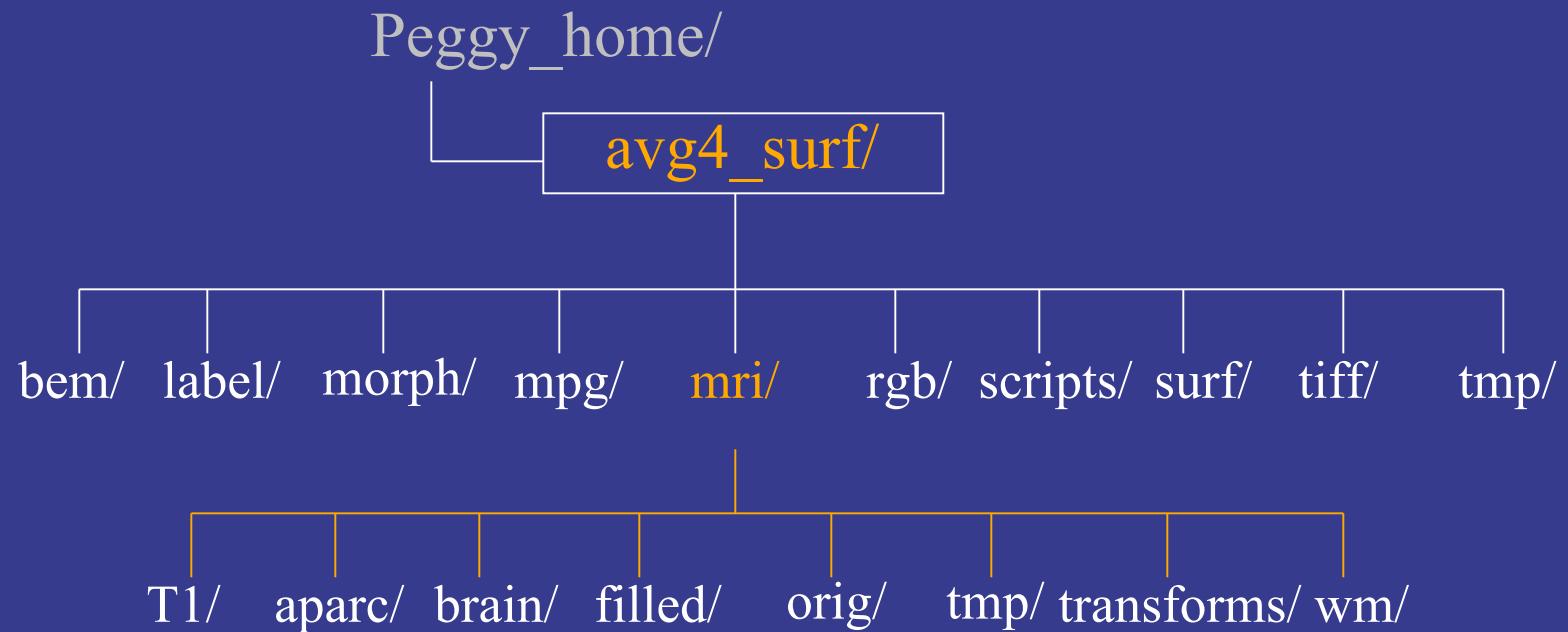
(e.g., my login file is called `.fs_login`)

```
source ~/ .fs_login
```

Usage: `mksubjdirs <subject_name>`

Example: `mksubjdirs avg4_surf`

Result from **`mksubjdirs avg4_surf`**:



STEP 7b: Convert volume dataset into COR format

(i.e., 256 coronal slices, 256 x 256 in-plane, 1mm³ voxel resolution)

Usage: *mri_convert <volume_dataset> <surf_directory/mri/orig>*

Example: (from within **Peggy_home/** directory)

```
mri_convert avg4_brain_edited+orig.BRIK avg4_surf/mri/orig
```

VOLUME PRE-PROCESSING DONE.

NEXT, SEGMENTING THE WHITE MATTER

This step is crucial because the quality of the surface creation is dependent on the quality of the white matter segmentation.

Segmentation Process in FreeSurfer

**aka “Process Volume” or “segment_subject” or
“recon-all -stage1”**



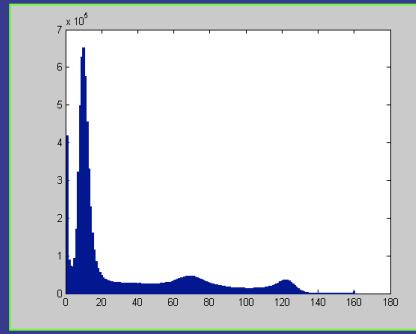
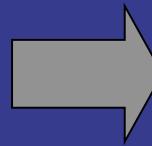
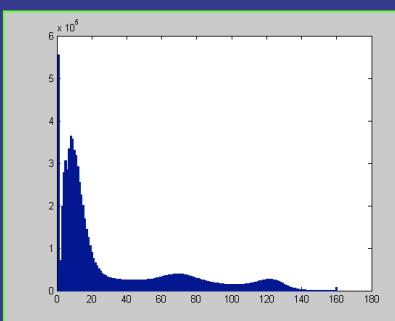
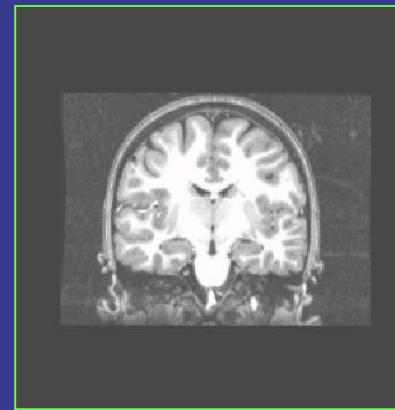
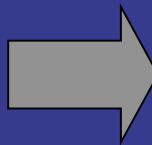
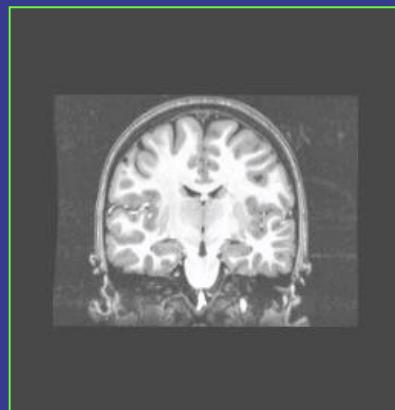
Segmentation

- Intensity normalization
- Skull stripping
- White matter labeling



Segmentation

- Intensity normalization

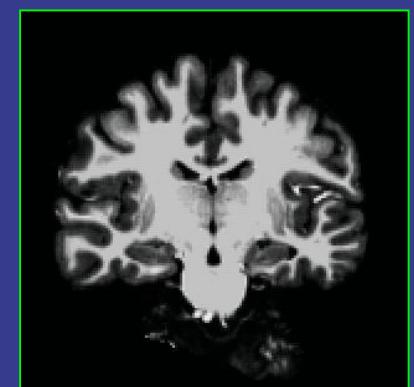
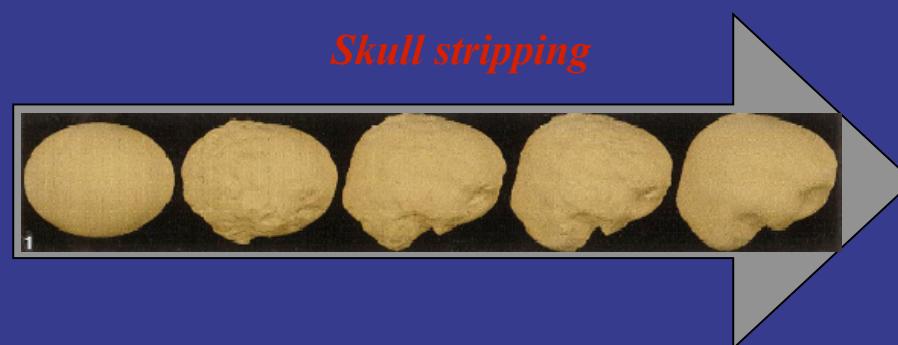
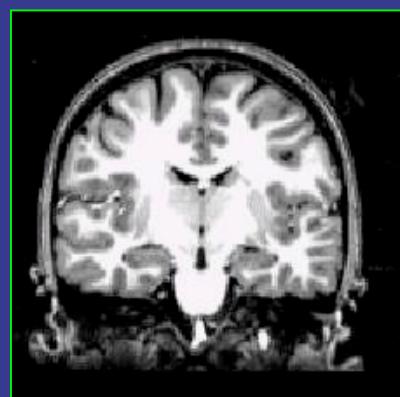


- Skull stripping
- White matter labeling



Segmentation

- Intensity normalization
- Skull stripping
 - Shrink-wrap algorithm
 - Start with ellipsoidal template
 - Minimize brain penetration and curvature



- White matter labeling

Skull Stripping

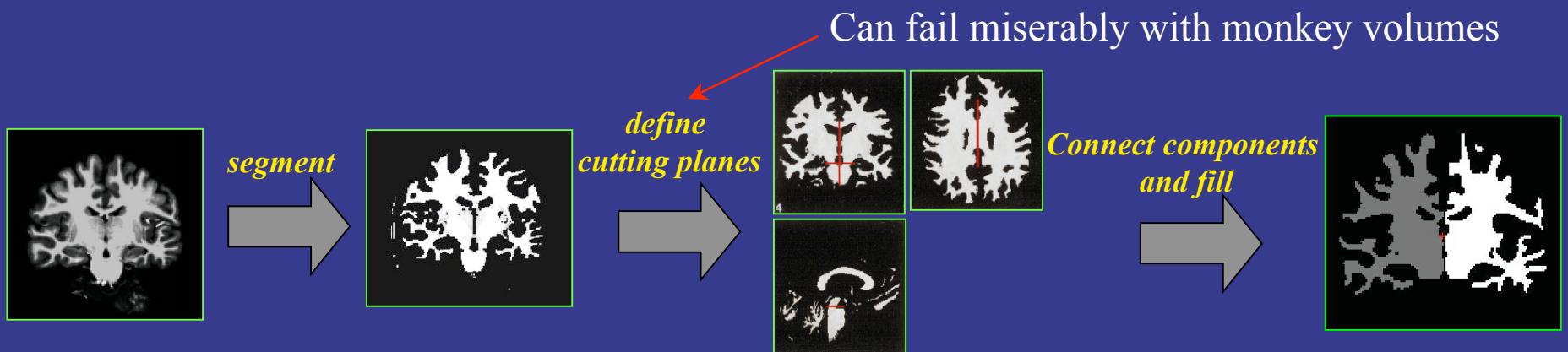


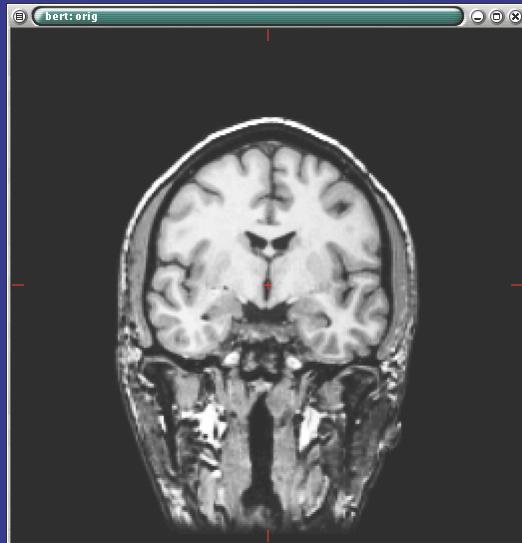
Courtesy: <http://cogsci.ucsd.edu/~sereno/movies.html>



Segmentation

- Intensity normalization
- Skull stripping
- White Matter labeling
 - Preliminary classification solely intensity based
 - Relabeling of mislabeled voxels based on neighborhood information
 - Define cutting planes
 - Find connected components and fill



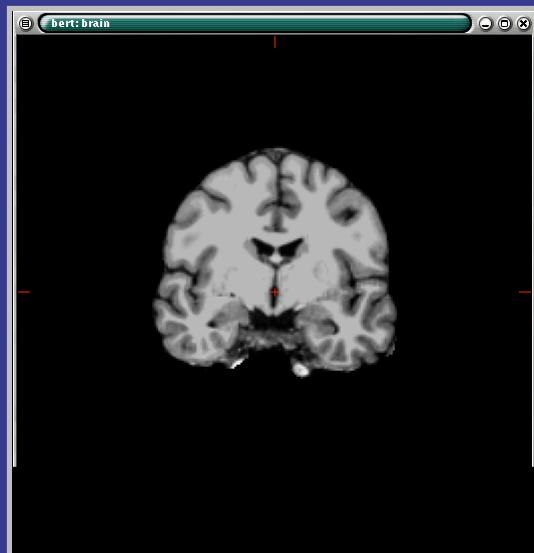


mri/orig

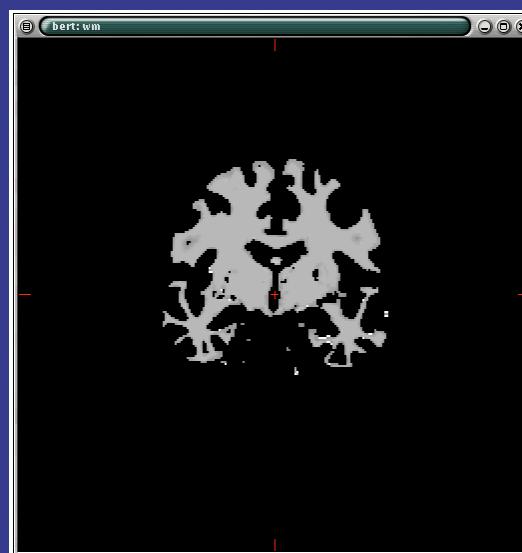
HUMANS



mri/T1

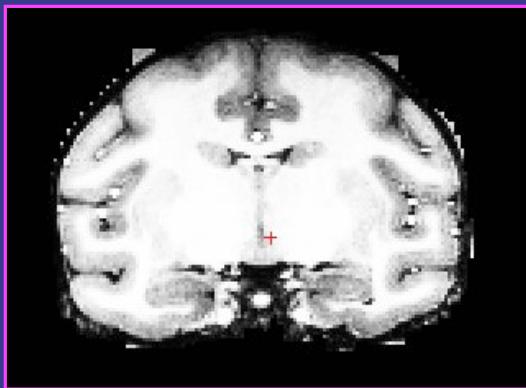


mri/brain



mri/wm

MONKEYS



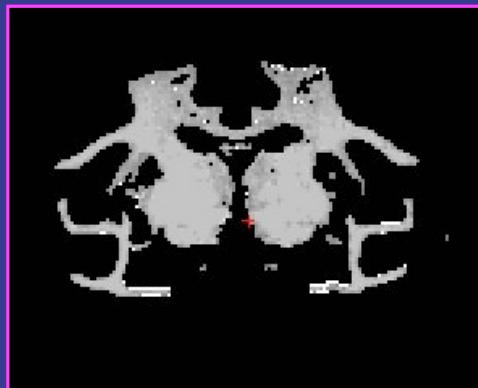
mri/orig



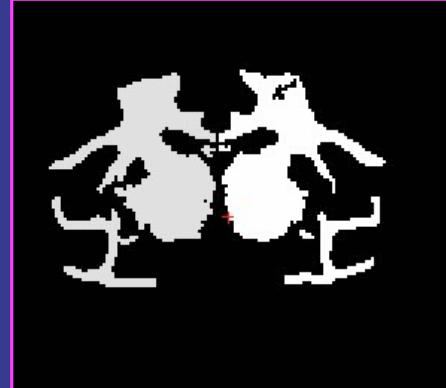
mri/T1



mri/brain



mri/wm

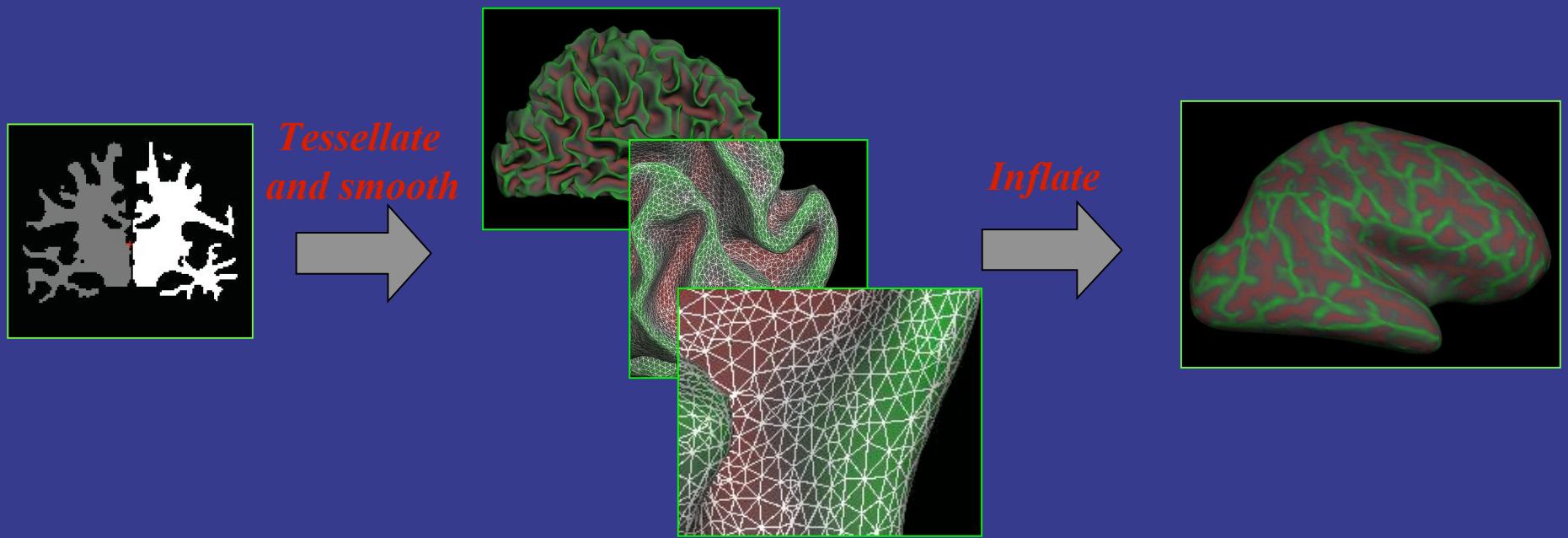


mri/filled

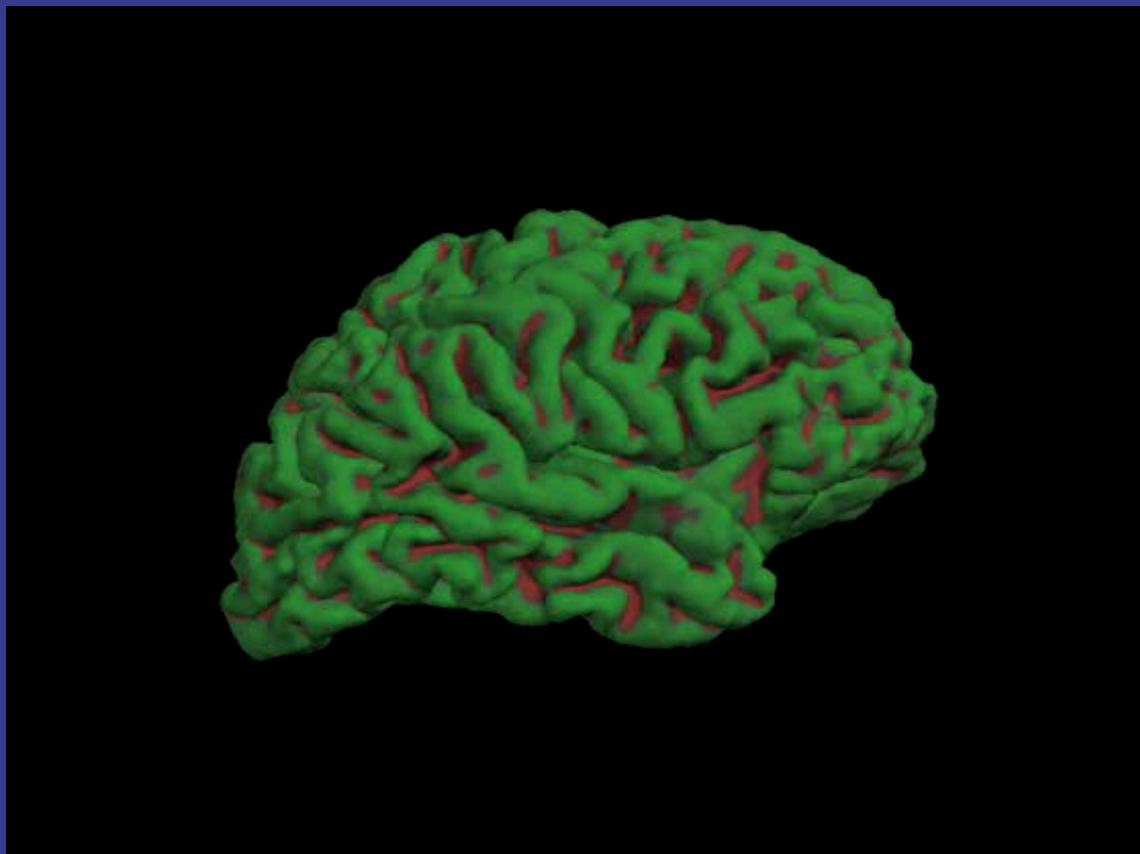


Tessellation and Inflation

- Surface Tessellation
 - Use two triangles to represent each face separating white matter voxels from other voxels
 - Smooth initial tessellation with a deformable surface algorithm
- Surface Inflation
 - Retain shape and metrics while making the interior of sulci visible



Inflation

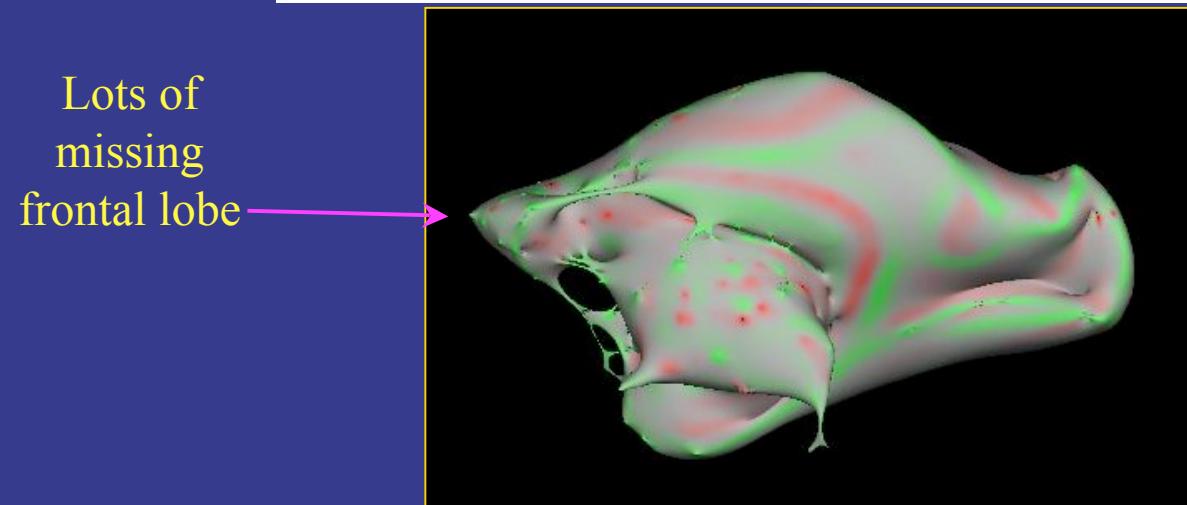
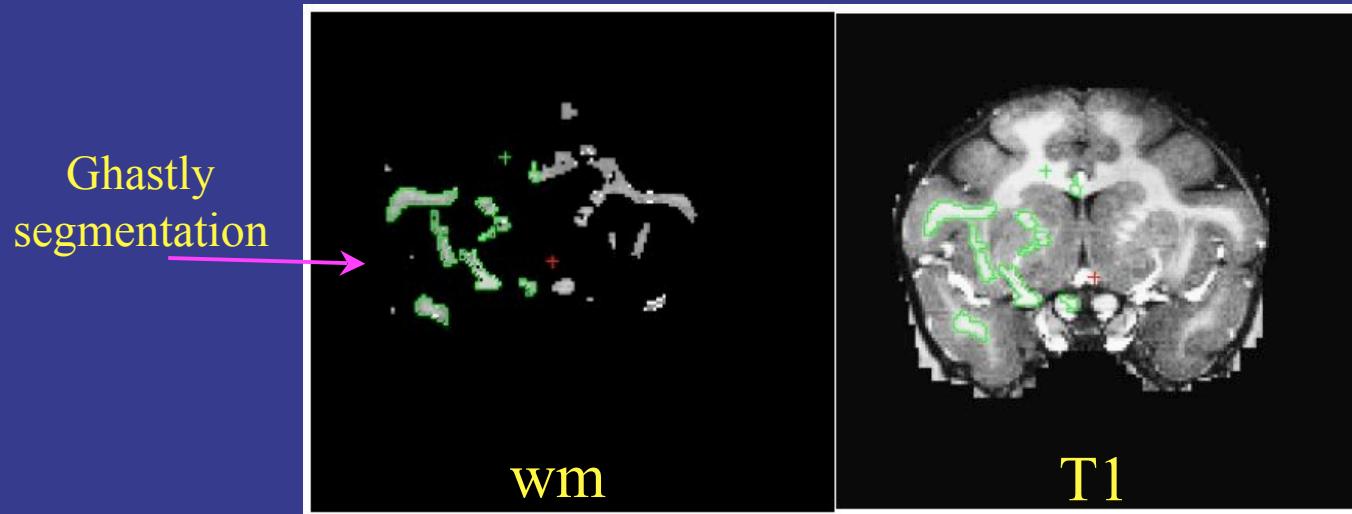


Courtesy: <http://cogsci.ucsd.edu/~sereno/movies.html>

Troubleshooting

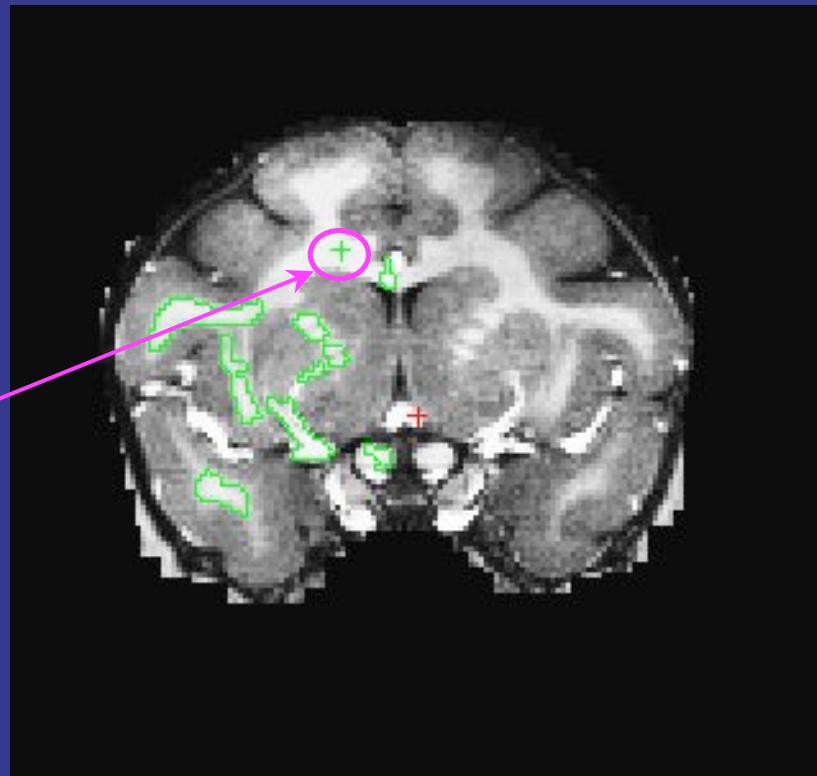
- **OFTEN, things can go terribly wrong when dealing with monkey volumes/surfaces.**
- **Be prepared for this!!!**
- **Luckily, with some patience and skill, you can fix these problems.**
- **If you still can't fix the problem, join the FreeSurfer mailing list and ask for help!**

Troubleshooting: When segmentation fails

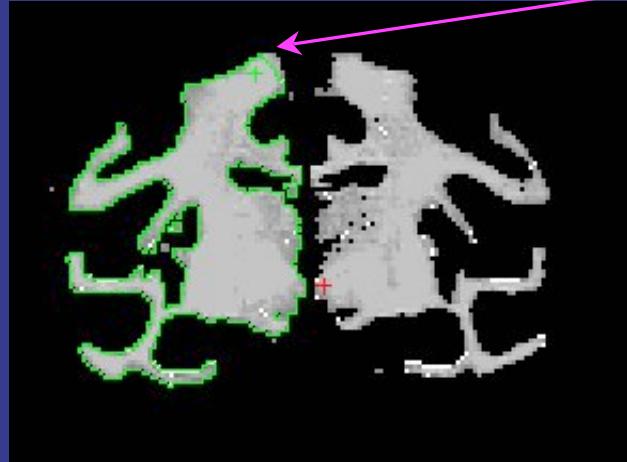


- Monkey brains have very fine lines of white matter that are difficult to segment.
- With monkey volumes, you must always add control points to the T1 volume (inside a clearly white matter area), then re-run the white matter segmentation.
- The FreeSurfer manual recommends using about 20 control points max.

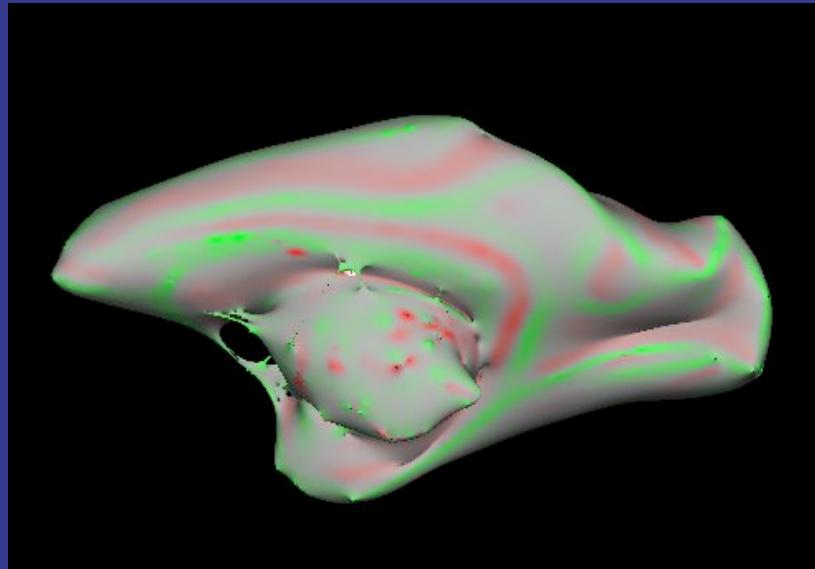
Add ctrl pts like this one throughout T1 volume and re-run the wm segmentation



After adding control points:



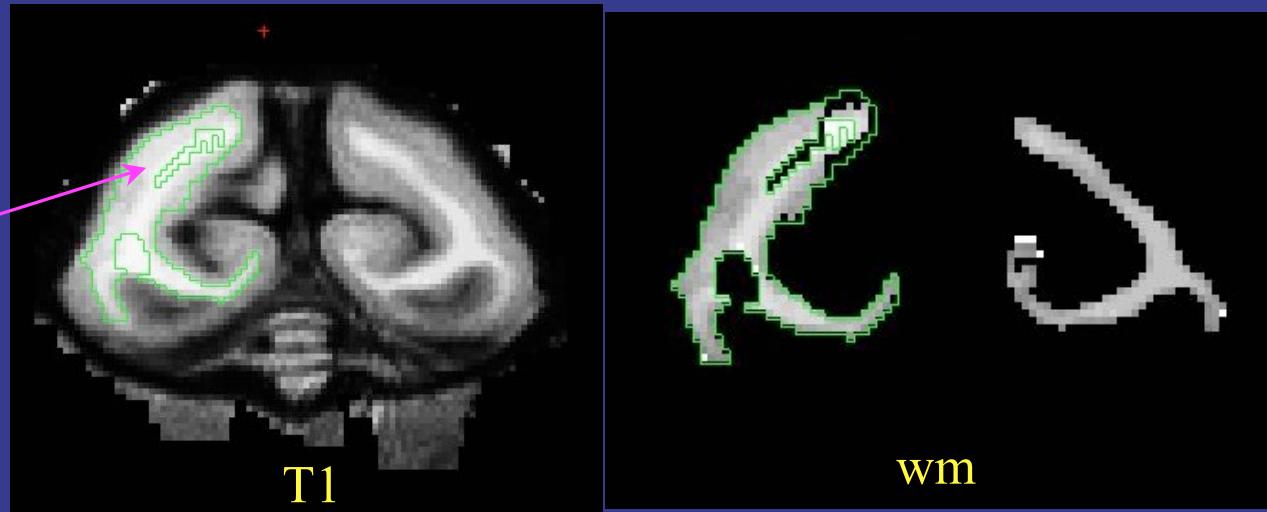
You may still have to hand draw
the wm areas that the control
points did not pick up



Much better surface

Occipital area also a little problematic. Some gray matter has been included in the white matter segmentation. You may have to manually remove it.

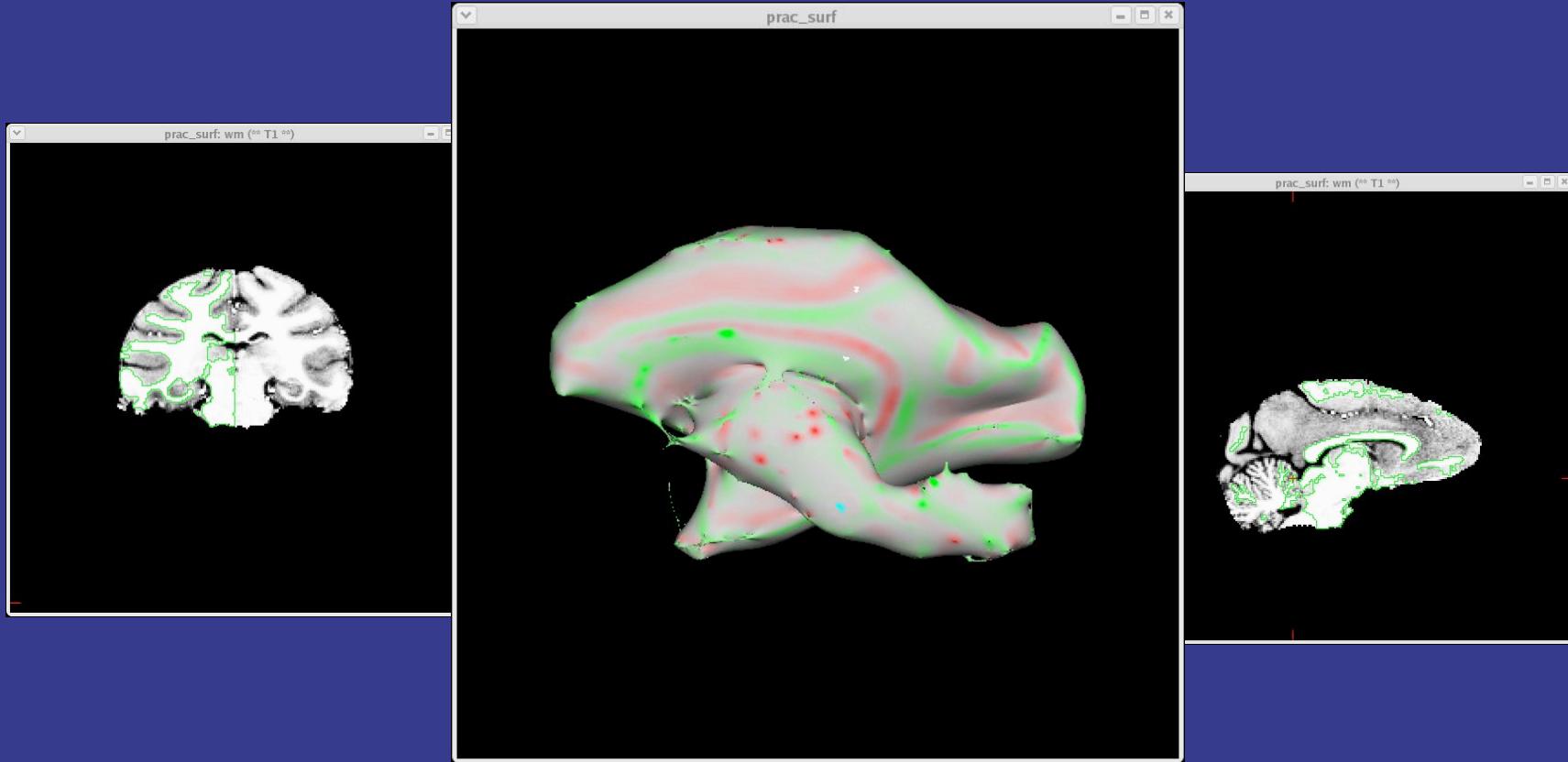
Gray matter in the
wm segmentation.
Must be manually
removed.



After manual
editing. Much
better



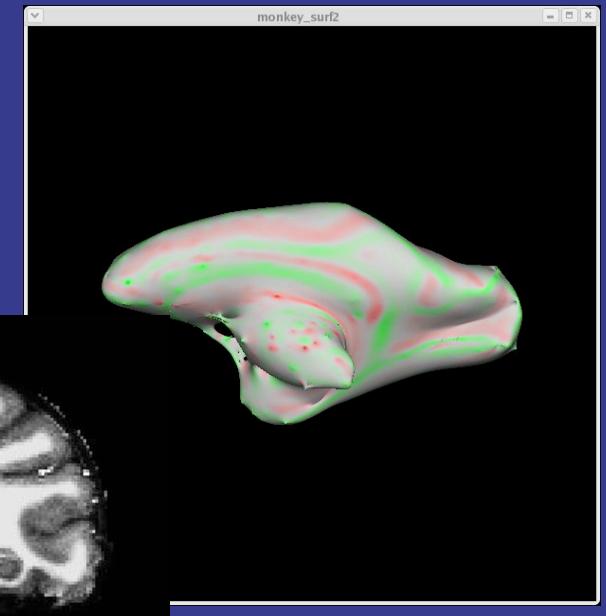
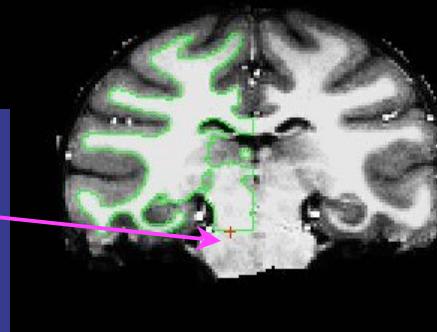
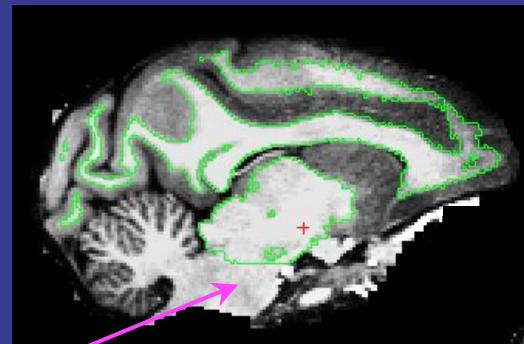
Troubleshooting: When cutting planes fail



- According to FreeSurfer manual:

“All nonhuman cortices need to have their cutting planes defined manually after the initial segmentation.”
- This is a royal pain. Not always the easiest thing to do.
- Manually defining the cutting planes must be done via the FreeSurfer interface. Select “Expert Preferences”.
- Follow instructions in the manual.

Example of
properly
defined
cutting planes

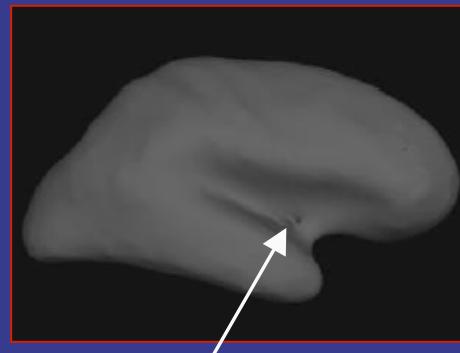


- Good news: FreeSurfer often defines the cutting planes of monkey volumes pretty well without any manual intervention.

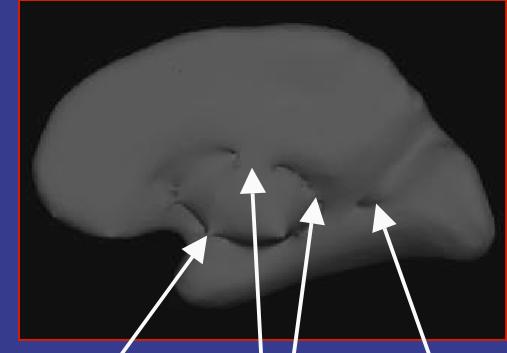


Manual editing

- Examine surface for defects
 - manually reclassify voxels in the following areas:
 - Lateral ventricle
 - Fornix
 - Optic nerve
 - Basal ganglia
 - Other defect areas



Basal Ganglia

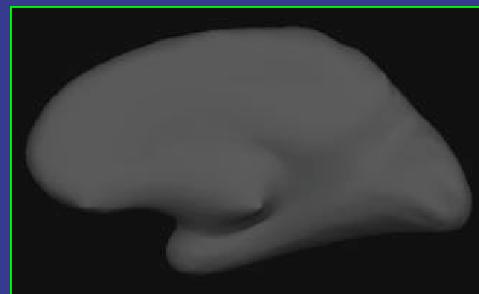


Optic Nerve

Fornix

Lateral Ventricle

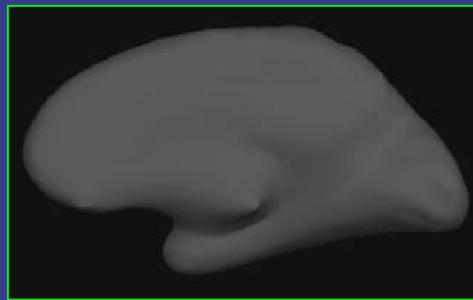
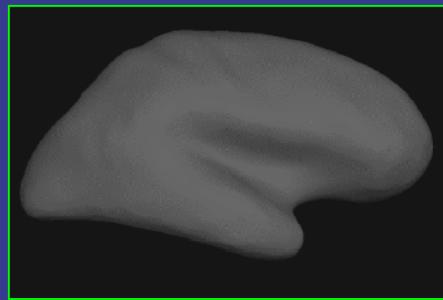
Re-inflation





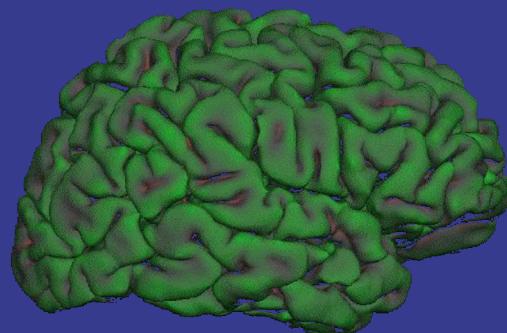
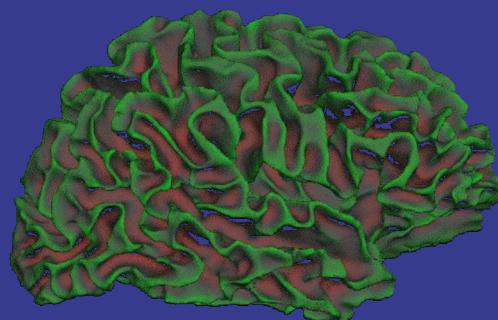
Fix topology

- Automatic defect removal algorithm that removes minor defects ensuring that the surface is topologically correct.



Make final surface

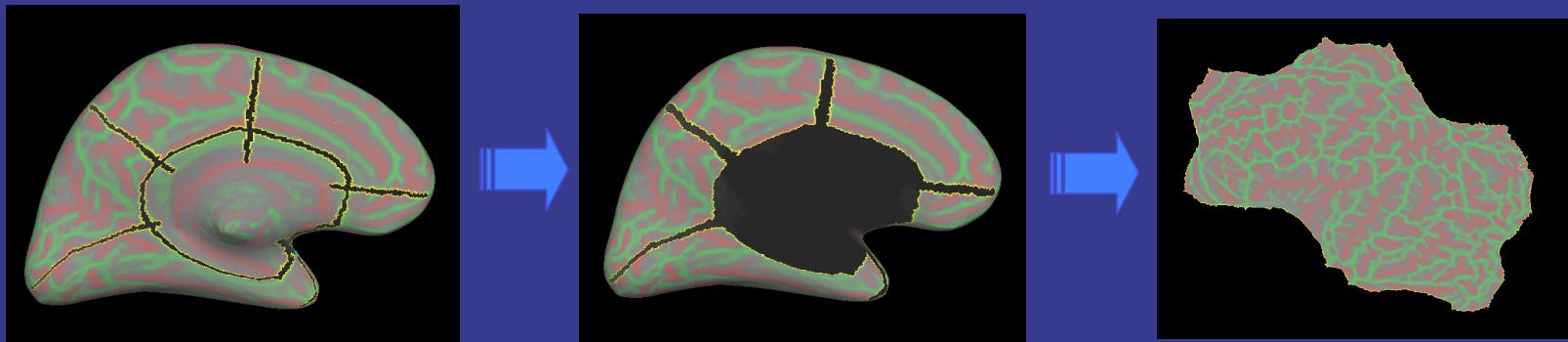
- Final gray/white boundary (white)
- Final gray/csf boundary (pial)



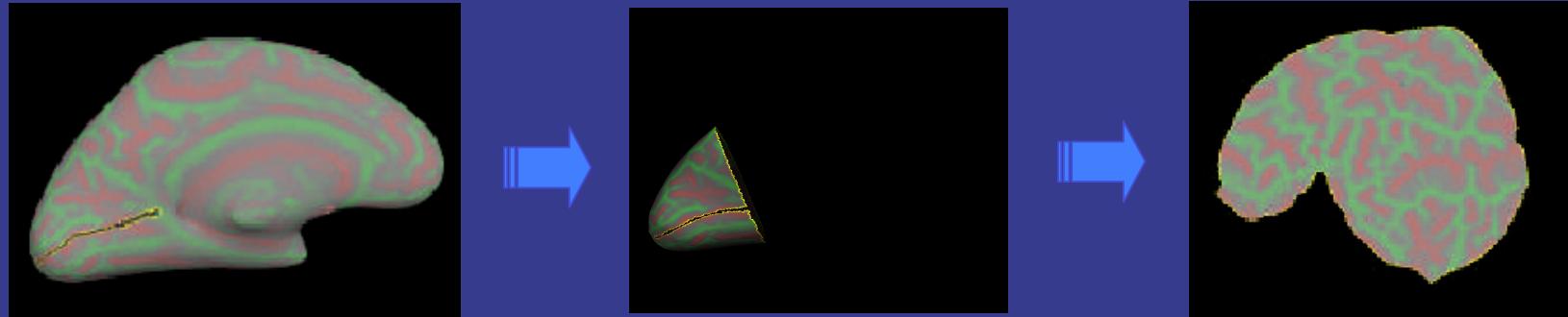


Cutting and flattening

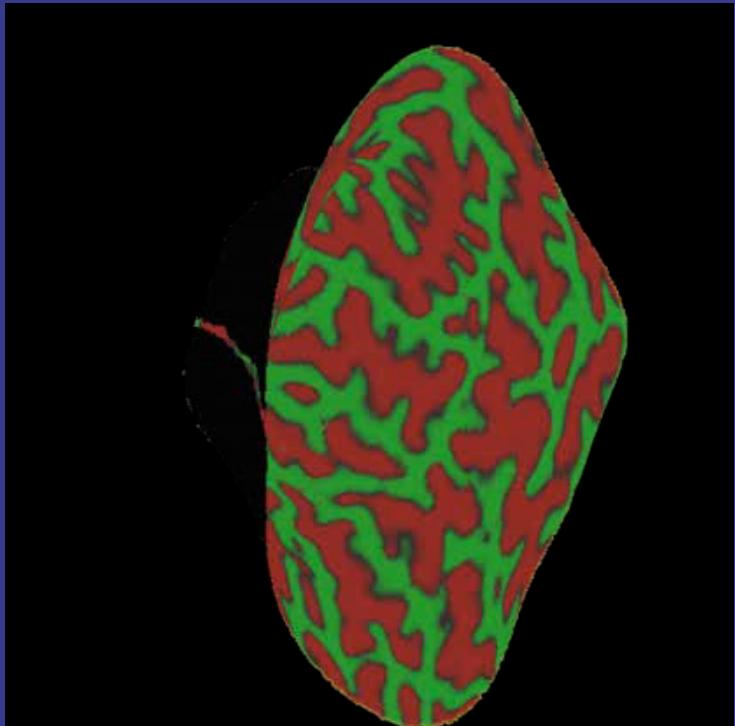
- For a full surface patch



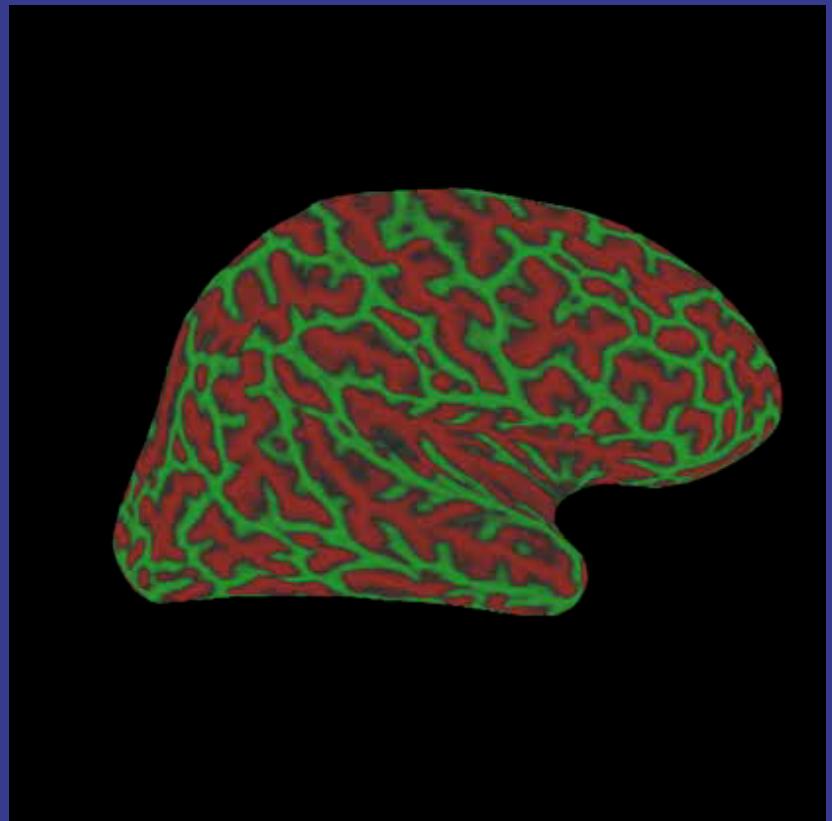
- For occipital patch



Flattening of occipital patch



Flattening of full surface

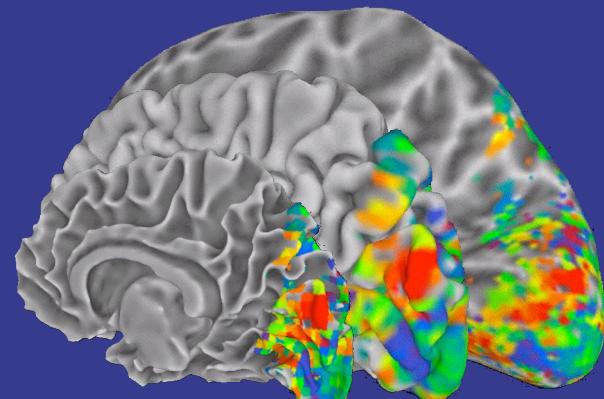
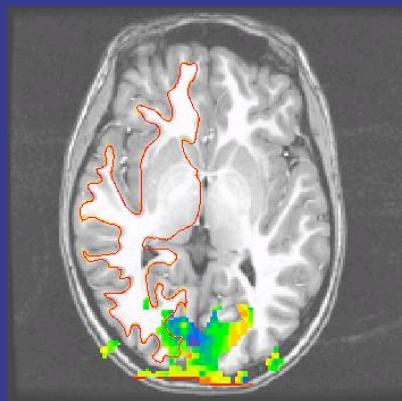
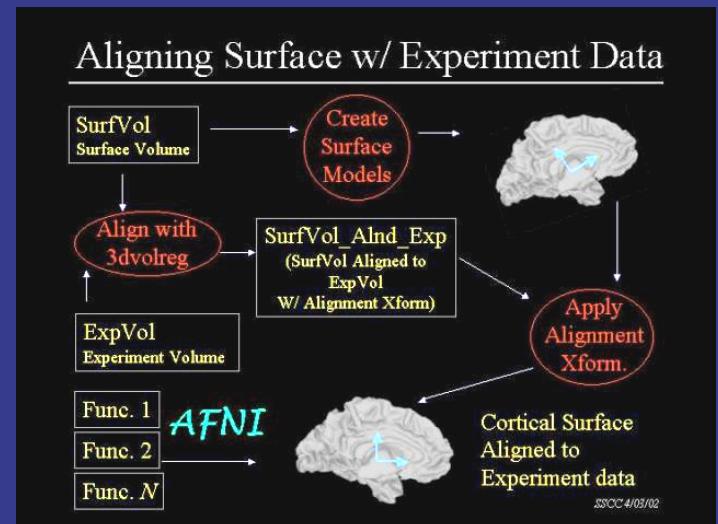


Courtesy: <http://cogsci.ucsd.edu/~sereno/movies.html>



SUMA

- Convert surfaces to ASCII format
- Align surface volume to experiment volume
- Overlay functional data onto surface
- Create link between AFNI and SUMA
- View function on volume and surface simultaneously
- Visit SUMA website for details:
 - <http://afni.nimh.nih.gov/ssc/ziad/SUMA/>



AFNI

SUMA

FreeSurfer Links

FreeSurfer Website (articles, download, docs, FAQ):

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

Mail Archives:

www.mail-archive.com/freesurfer@mail.nmr.mgh.harvard.edu