FreeSurfer Quality Control Protocol

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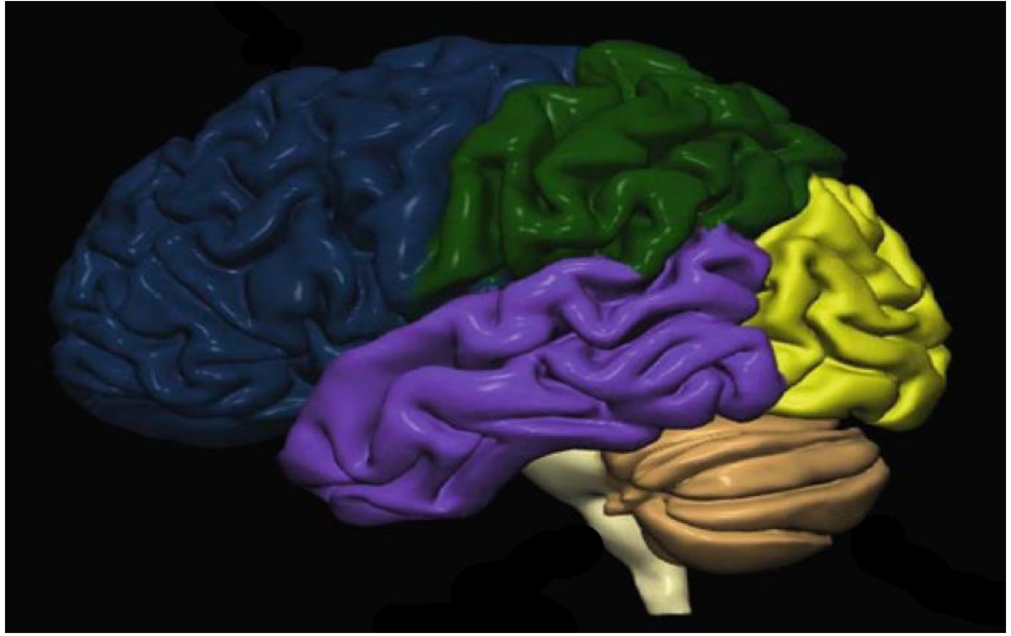
Basic Neuroanatomy

Objective and Brain Orientation

Superior

Anterior



Posterior

Miller, K. (2011). Biomechanics of the Brain edited by Karol Miller. (Biological and Medical Physics, Biomedical Engineering).

Inferior

General objective: To ensure topologic and geometric accuracy of white matter and pial surface models in the FreeSurfer platform.
Specific task: Analyze datasets and perform skull scraping, cortical seeding and white matter correction methods to achieve high quality segmentations.

Basic Neuroanatomy: Major Parcellations and Cerebral Lobes

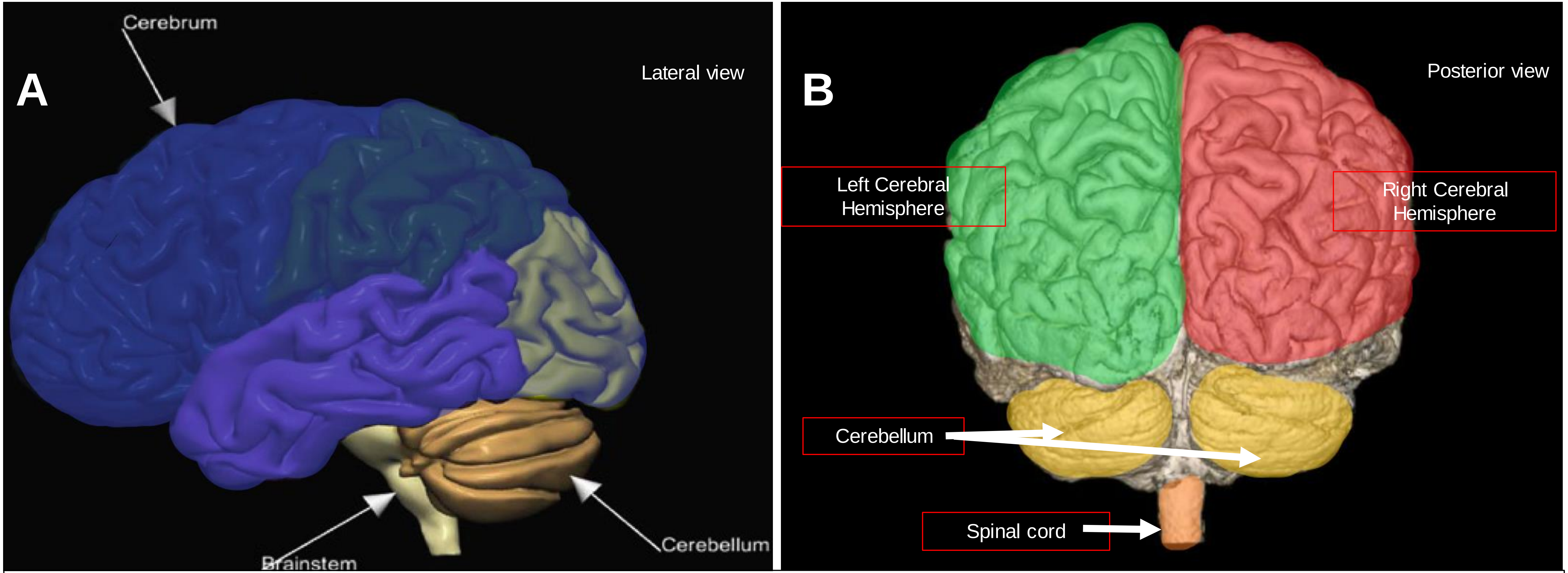
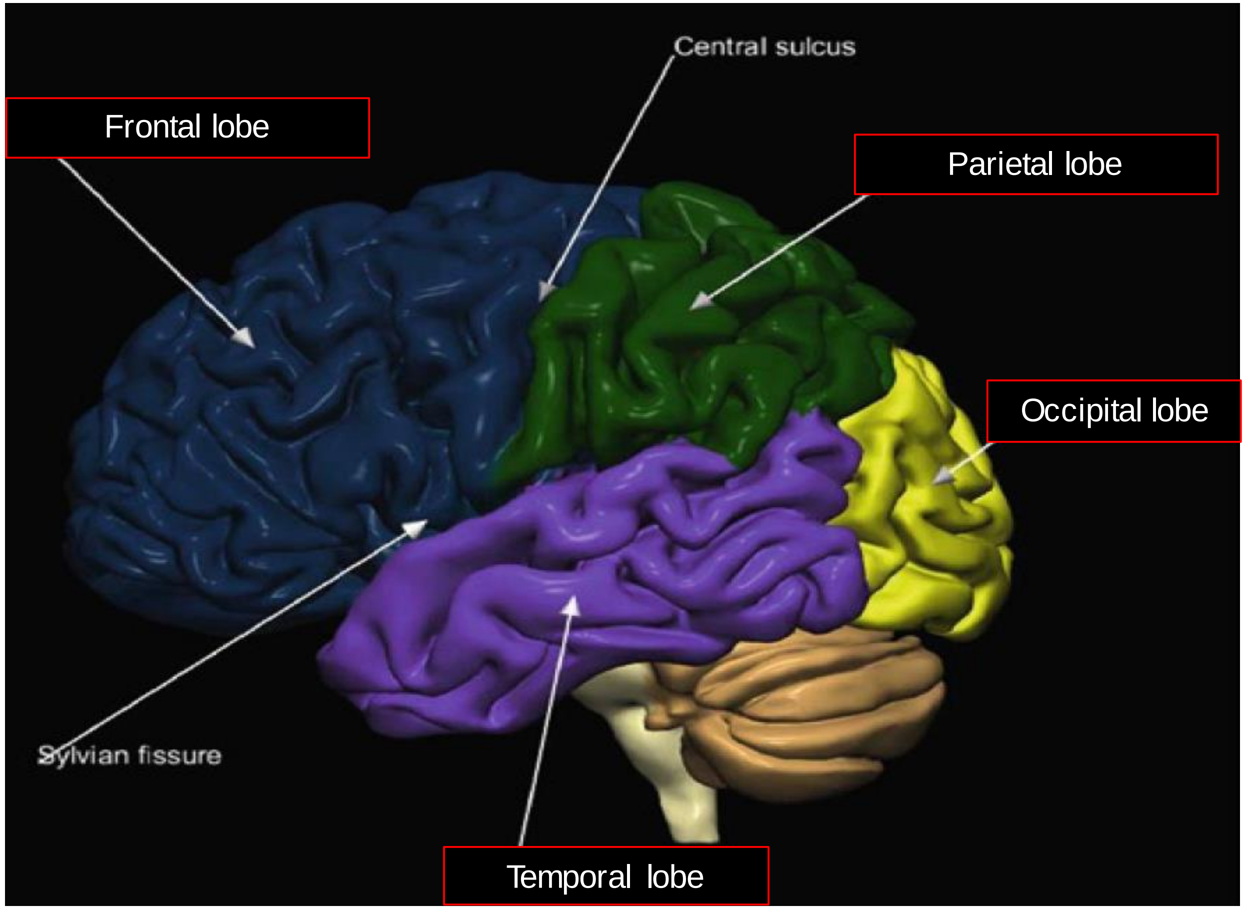
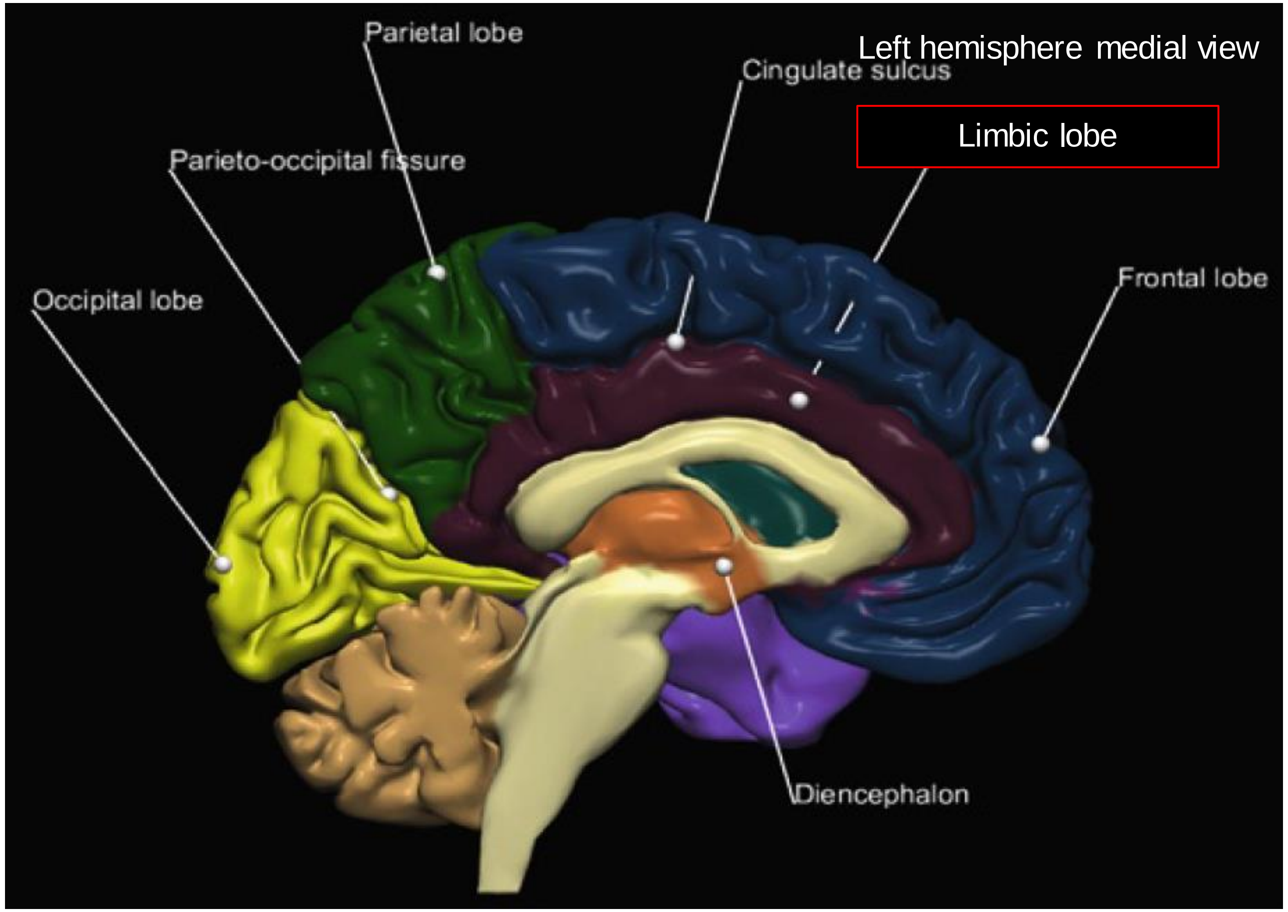


Image A: The three major brain parcellations: **cerebrum** (highlighted in blue), **cerebellum** and **brainstem.**
Image B: The cerebrum consists of two cerebral hemispheres; the **left** (green) **and right** (red) **hemispheres**, and, five cerebral lobes.

Basic Neuroanatomy: Cerebral Lobes

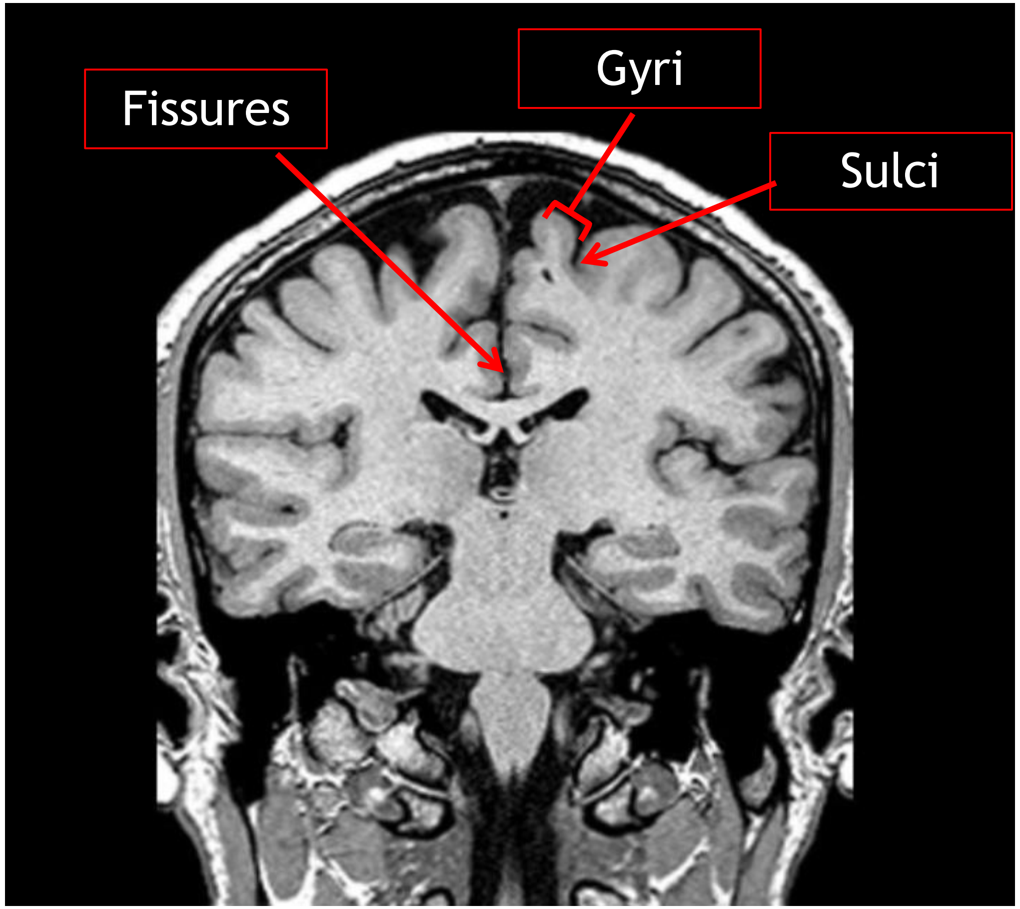


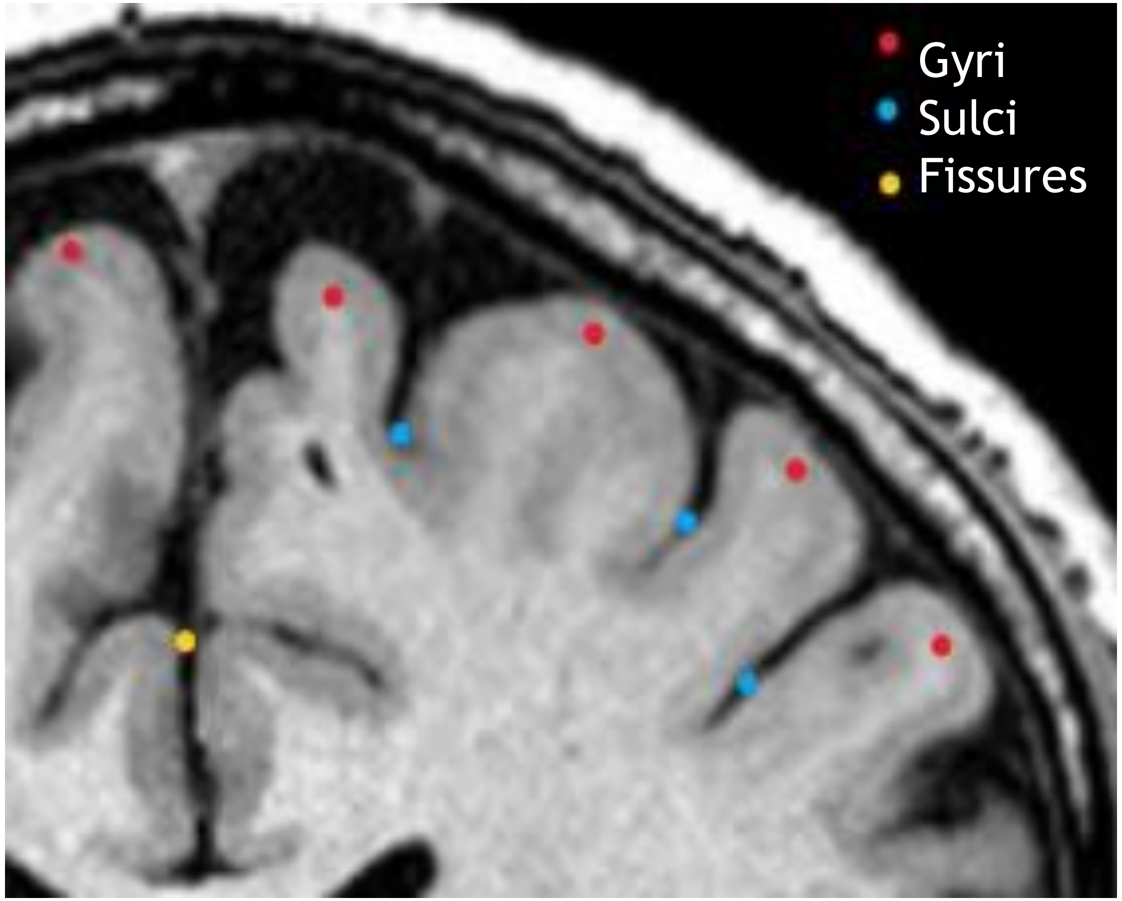


Miller, K. (2011). Biomechanics of the Brain edited by Karol Miller. (Biological and Medical Physics, Biomedical Engineering).

The five cerebral lobes: **frontal** (dark blue), **parietal** (green), **occipital** (yellow), **temporal** (purple) and the internally located **limbic** lobe (dark magenta).

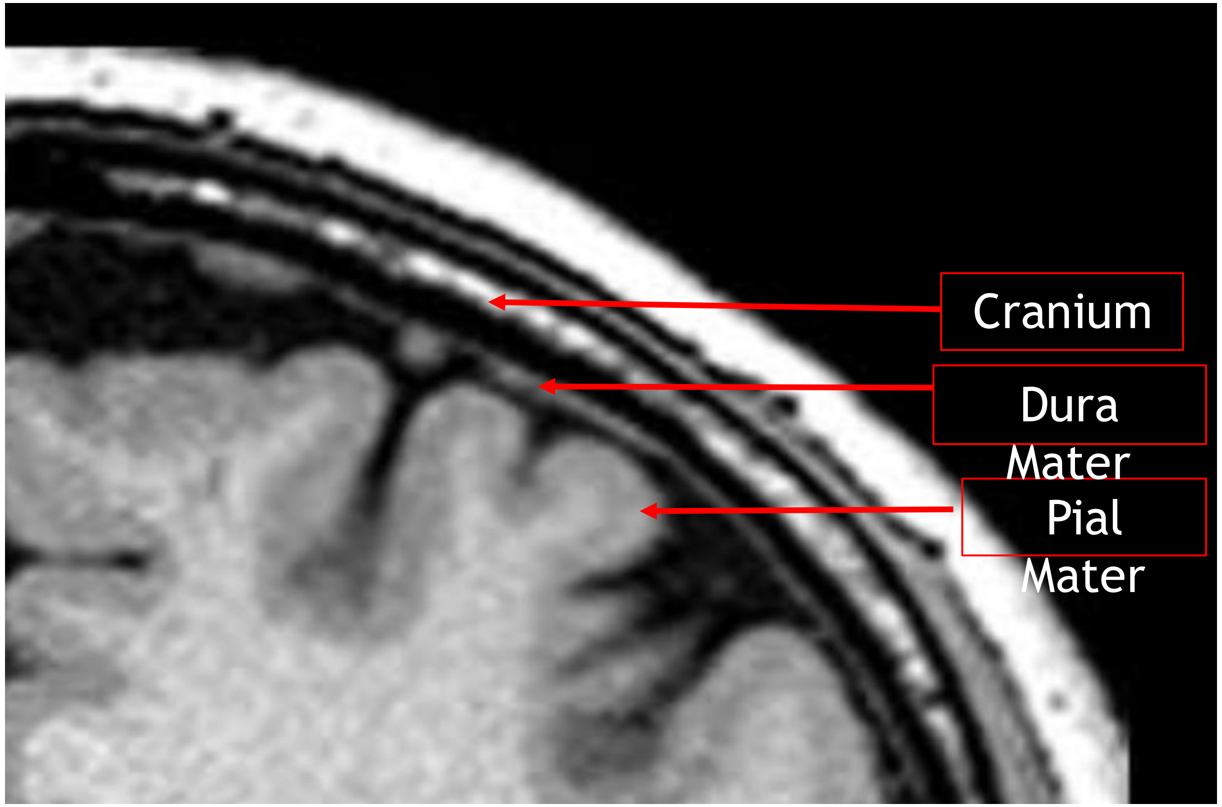
Basic Neuroanatomy: Gyri, Sulci and Fissures





The surface of the brain is highly convoluted and its general anatomical geometry consists of gyri, sulci and fissures. Fissures and sulci may often separate and help with distinguishing different regions of the brain.
Gyri (gyrus): Folds or "ridges". **Sulci (sulcus)**: Grooves or "crevices". **Fissures**: Deep grooves.

Basic Neuroanatomy: Dura Mater, Pia Mater and Cranium



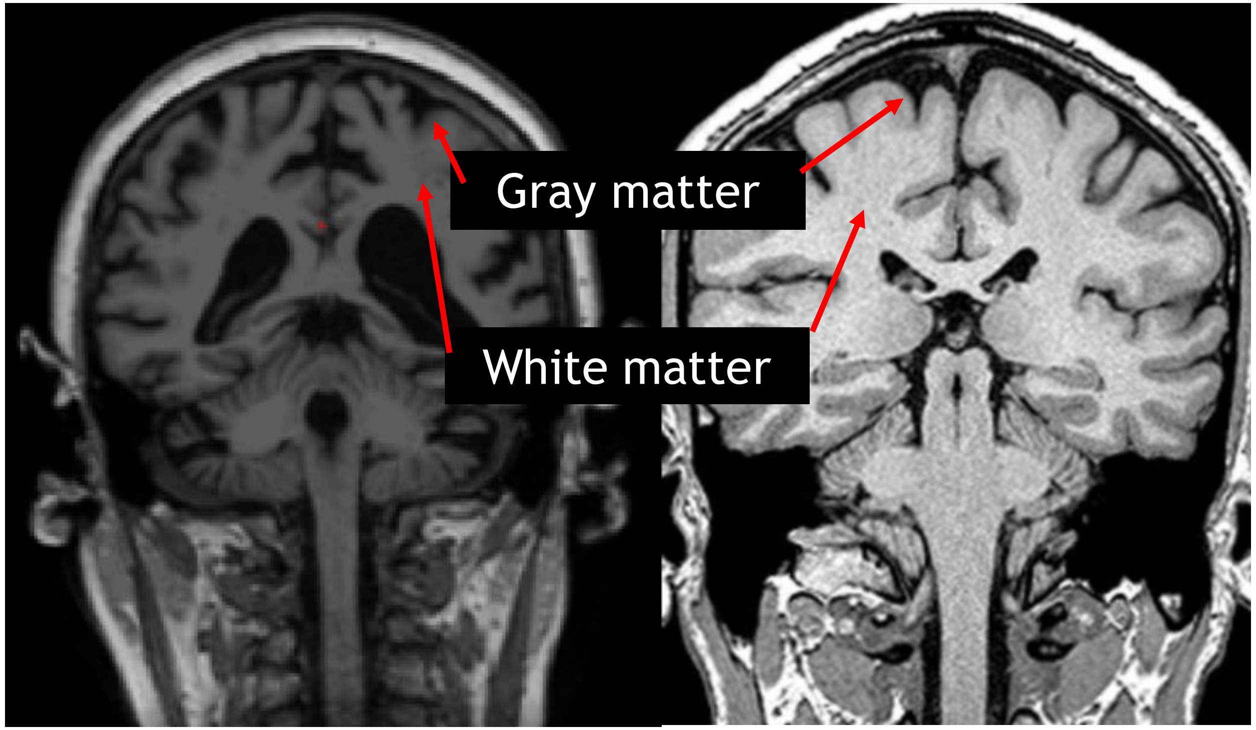
The surface of the brain is highly convoluted and its general anatomical geometry is described with gyri, sulci and fissures. Fissures and sulci may often separate and help with distinguishing different regions of the brain.

Cranium: Part of the skull formed by eight fused bones that act as a hard protective shell for the brain.

Cranial dura mater: A tough fibrous sheet that acts as a supportive capsule for the brain.

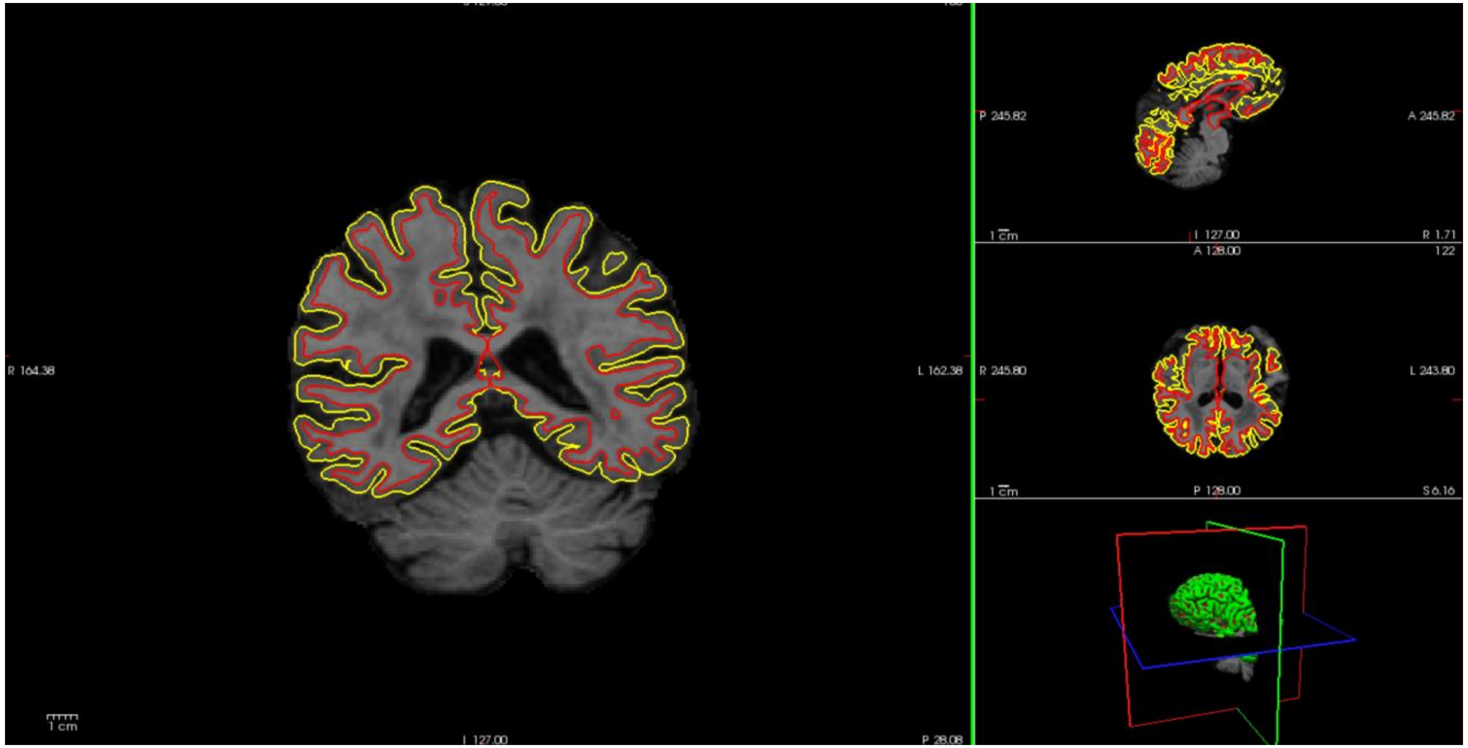
Cranial pia mater: A layer anchored directly to the brain that serves as a cushioning system.

Basic Neuroanatomy: Gray Matter (cerebral cortex) and White Matter



Gray matter is distributed at the surface of the cerebrum. This outer layer of neural tissue is known as the cerebral cortex. The bulk of the inner parts of the brain consist of **white matter.**

FreeSurfer and FreeView

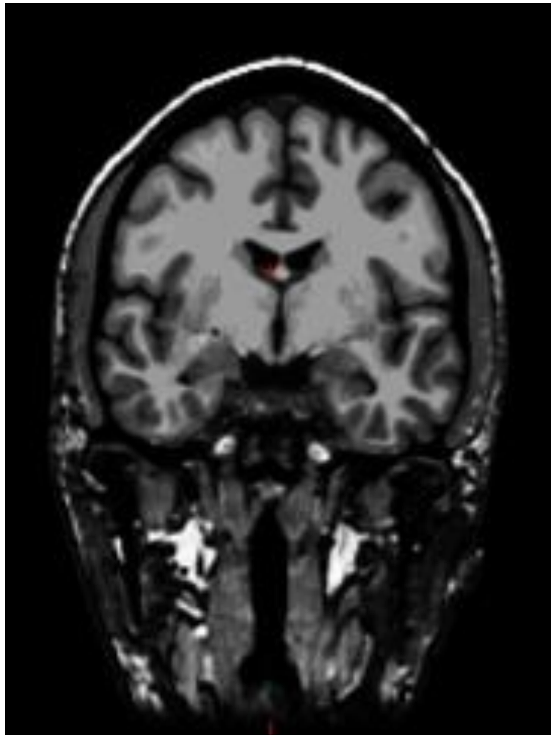


FreeSurfer terms

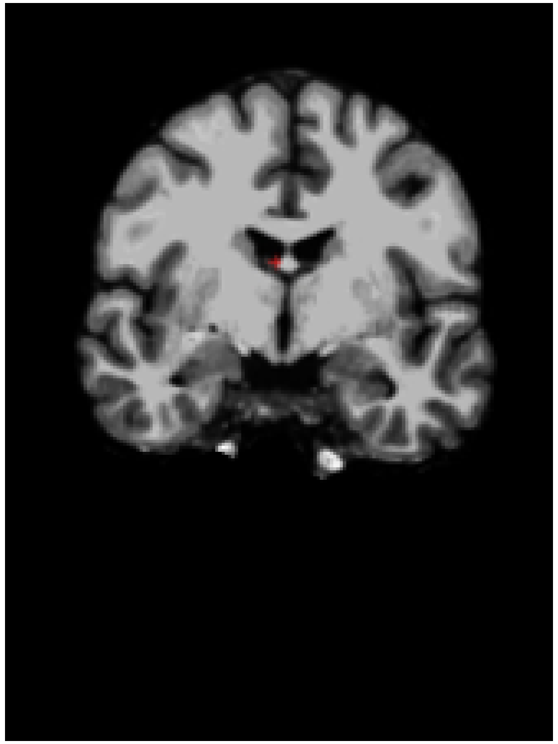
Voxel- A pixel with volume (i.e. a 3D cube)
Surface- Generated boundaries made of vertices between various brain tissues (i.e. white matter surface and pial surface)
Volumes- Files of MRI data
Recon- "Reconstruction" of the cortical surface

FreeSurfer makes an estimation of the surface boundaries between white matter and gray matter and generates output data. The volumetric and surface data may then be viewed and edited in FreeView, FreeSurfer's data viewing program.
In the above image, the boundary between white matter and gray matter is shown in red. The boundary between gray matter and cerebral spinal fluid is the pial surface shown in yellow, which roughly corresponds to the position of the cranial pial mater.

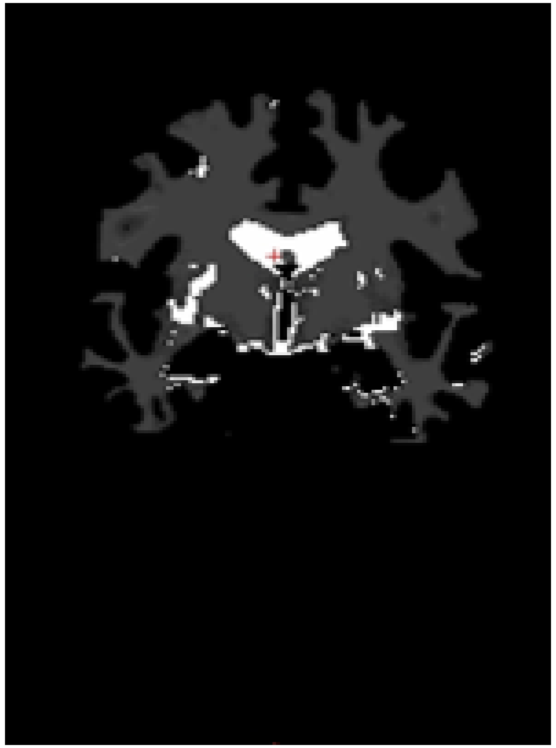
FreeSurfer and FreeView: Volumes - MRI data files



T1.mgz

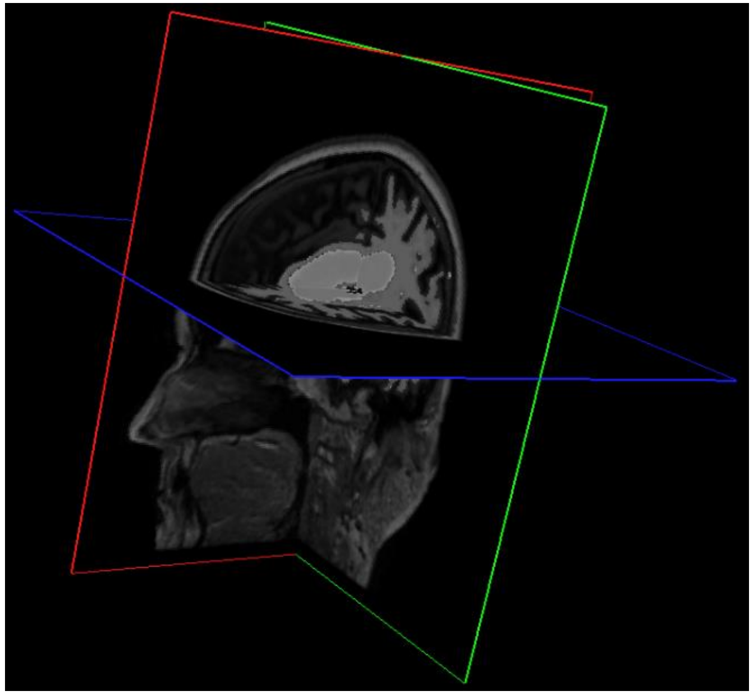


brainmask.mgz

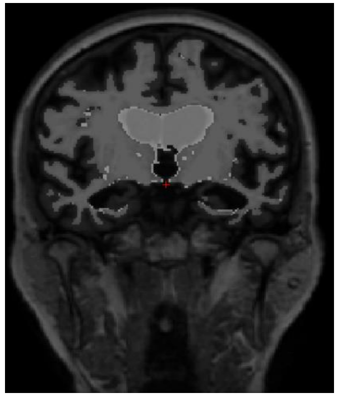


wm.mgz

Axial, Sagittal and Coronal Views

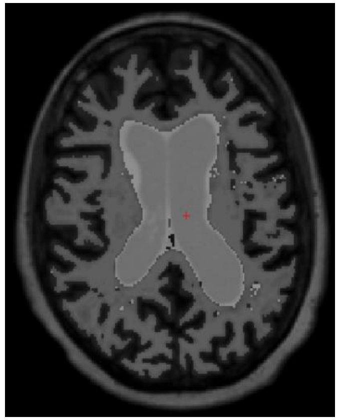


Green: coronal plane
Red: sagittal plane
Blue: axial plane



Coronal view: looking from the front.

Sagittal view: looking from the side.



Axial view: looking from above.

General Workflow

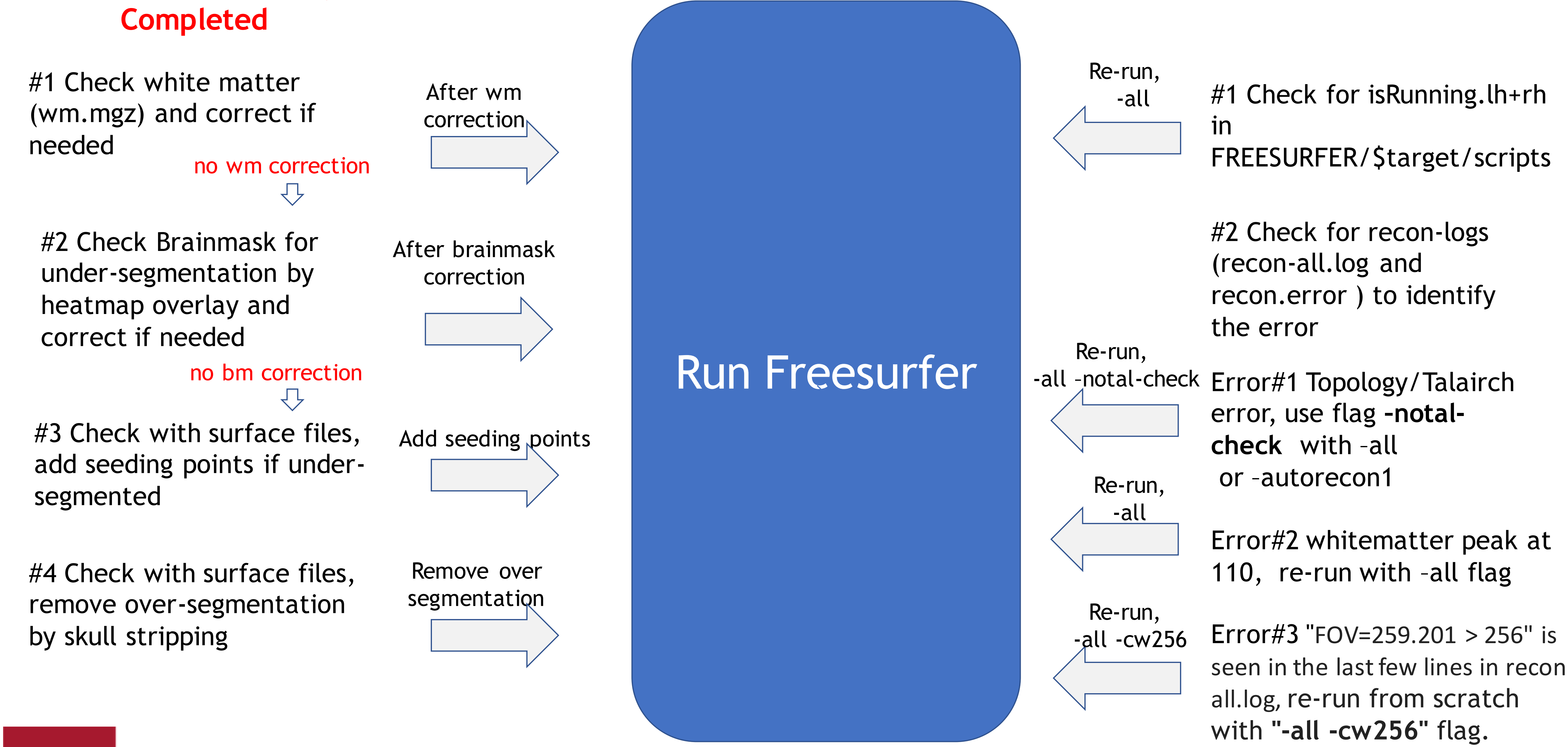
Job submission for processing in FreeSurfer on CERAMICCA

Follow this workflow to upload Freesurfer processing on CERAMICCA

[Instructions to submit freesurfer processing on CERAMICCA]

General Workflow

Quality Control Process



Process Successfully Completed

#1 Check white matter (wm.mgz) and correct if needed

After wm correction

no wm correction

#2 Check Brainmask for under-segmentation by heatmap overlay and correct if needed

After brainmask correction

no bm correction

#3 Check with surface files, add seeding points if under-segmented

Add seeding points

#4 Check with surface files, remove over-segmentation by skull stripping

Remove over segmentation

Run Freesurfer

Process Incomplete

#1 Check for isRunning.lh+rh in FREESURFER/$target/scripts

Re-run, -all

#2 Check for recon-logs (recon-all.log and recon.error) to identify the error

Error#1 Topology/Talairch error, use flag **-notal-check** with –all or –autorecon1

Re-run, -all -notal-check

Error#2 whitematter peak at 110, re-run with –all flag

Re-run, -all

Error#3 "FOV=259.201 > 256" is seen in the last few lines in recon-all.log, re-run from scratch with **"-all -cw256"** flag.

Re-run, -all -cw256

Freesurfer Run completed

QC image not found

- For "max-resub" error, delete the freesurfer folder, and run from scratch.
- For subjects which do not have a QC image, check FREESURFER/$targetID/scripts/ and look for isRunning.lh+rh or check the recon-logs for errors
- If isRunning.lh+rh is present, delete the FREESURFER FOLDER for that subject (FREESURFER/$targetID) and re-run from scratch, with continued =F
- If there is no IsRunning.lh+rh, then check the recon-logs for errors. Check recon-all.log and the recon.error log to see what the error is. As per the error, re-run the subject again for freesurfer processing by deleting the FREESURFER folder (FREESURFER/$targetID), with-all/-autoreon1 flag and continued =F
- If recon log as topology error, run with –all –notal-check flag from scratch (continued =F)
- If the run is unsuccessful, with errors in recon-log, can also try by running step by step
- For step by step, run for –autorecon1 first, then check the brainmask volume if it is done properly. If it is, run with –autorecon2, check the volumes + surface files again. If they look okay, then go for-autorecon3. If not, then correct the volumes as per the errors, run as per the error flags and then run for -autorecon3

Freesurfer Run completed

QC image generated

- Check if the ventricles have a gap between them, that is, the segmentation boundaries DO NOT cover the ventricles.
- This is white matter error, for this, load white matter and fill in the white matter in the wm.mgz volume
- Upload the scan for freesurfer processing for wm flag
- Next, if wm is okay, check brainmask volume by overlaying the brainmask on T1, with T1 with reduced opacity and brainmask with the heat map instead of grayscale
- Clone the voxels for under-segmented regions
- Upload for processing, with brainmask flags
- If brainmask is okay, check the QC image for under or over segmentation.
- If there is undersegmentation, load the T1, brainmask, and the surface files and add in seeding points and upload the job with cp flag
- If there is oversegmentation, then load T1, brainmask, and the surface files and strip off the oversegmented part from the brainmask and save the brainmask file and upload with pial flag.
- Repeat the corrections until the QC segmentation looks good or the scan no longer accepts any more correction.

- If the freesurfer run finished successfully, and the QC image looks okay, and has no errors, Quality Control is completed.
- If there are errors, correct the subjects till the segmentations look okay, with no errors in the process, or until the time the scan no longer accepts the corrections (This happens only for cortical seeding, after a few rounds).

Error	Flag to use	continued
Under-segmentation (seeding points)	-autorecon2-cp -autorecon3	TRUE
Over-segmentation (skull stripping)	-autorecon-pial -autorecon3	TRUE
Talairch/Topology	-autorecon1 -notal-check or -all -notal-check	FALSE
Brainmask Cloning (under-segmentation)	-autorecon2 -autorecon3	TRUE
White matter errors (under-segmentation)	-autorecon2-wm -autorecon3	TRUE
IsRunning.lh+rh	-all or -autorecon1	FALSE
Whitematter peak at 110	-all	FALSE
FOV > 256	-all -cw256	FALSE

For the re-run from scratch, make sure the $target folder in the FREESURFER directory is deleted first. ONLY then run from scratch again.

For targets with re-run, **continued = FALSE**

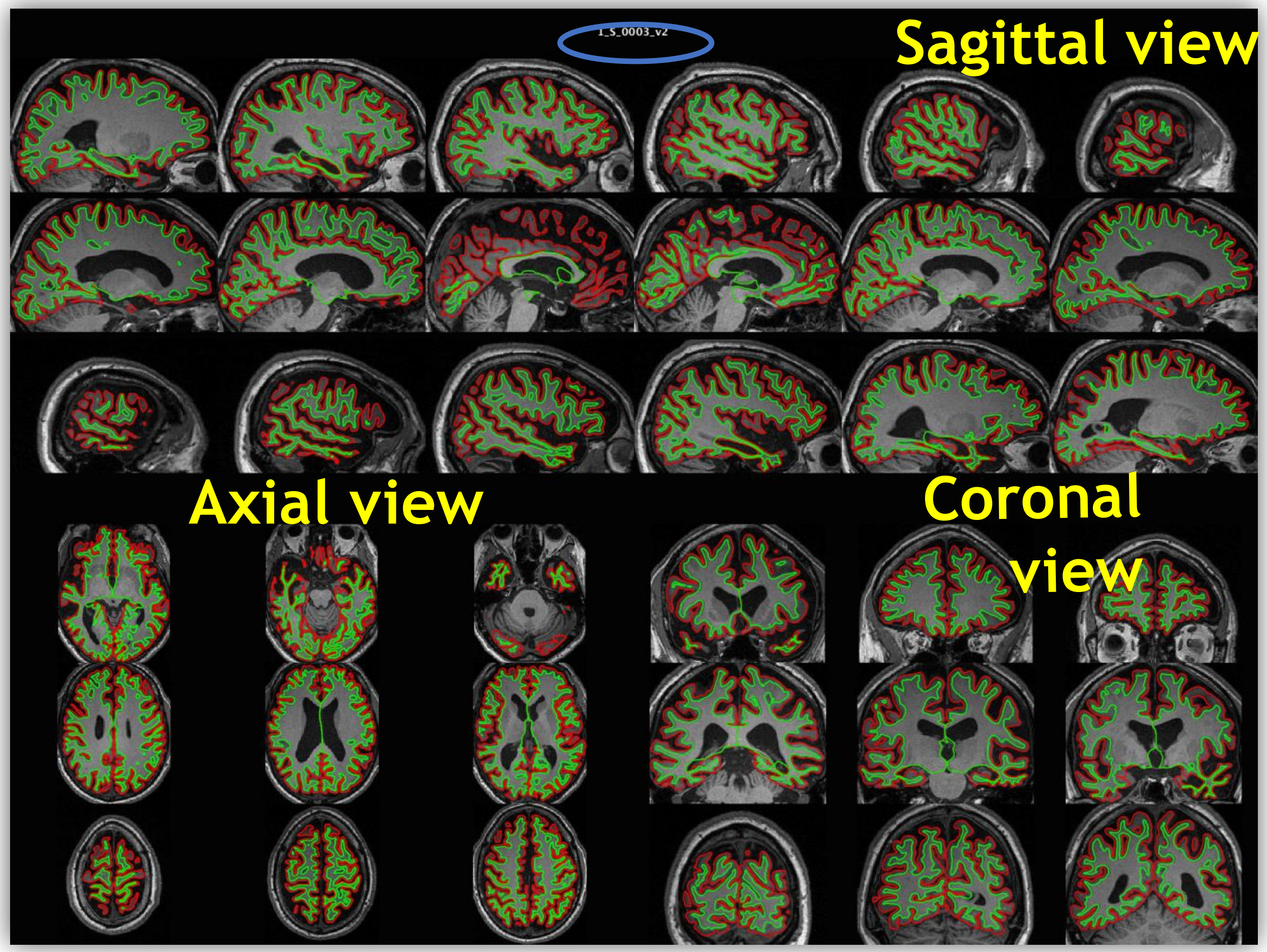
For any other processing, **continued =TRUE**

General Tips

- Generate the QC images using RunQuickchecks script
- Make sure all targets have 2 images – brainmask and Cortical Segmentation (when processing with **-all** flag)
- Once the run is completed, always check the recon-logs. If the run finished successfully, FREESURFER/$targetID/scripts/ would have **recon.done**
- For IsRunning.lh+rh in FREESURFER/$targetID/scripts/ , re-run from scratch
- If not, check the recon-all and recon-error logs to identify the error.
- If the error says, 'white matter peak at 110', it means some seeding points were placed either out of brain or out of the intensity range. So re-run from scratch and correct accordingly.
- On checking/correcting the volumes, follow the order,
  white matter > brainmask > surfaces
  Check white matter first, then brainmask, then for seeding or skull stripping
- Incase there are issues while running with the –all flag, run step by step to see where the issue/error arises.
- For step by step, run for autoreon1, check the brainmask in freeview, then autorecon2, check/correct the brainmask and other volumes/surfaces, then upload the job as per the error correction (with the appropriate flag), then autorecon3.

Error Detection With "Quickchecks"

What is a "Quickcheck" for FreeSurfer?



This is an example of a single .png quickcheck image. The image ID is circled in blue at the top in the center image.

Take note that quickcheck images show the pial surface in red and the white matter surface in green.

The top half of the image consists of sagittal view slices, the bottom right of the image consists of coronal view slices and the bottom left of the image consists of axial view slices.

Because this quickcheck represents a 3D image, it is important to use all views to search and identify errors. However, some views may serve better than other views for identifying specific errors.

Generating QuickCheck Images

Check the FREESURFER/<Subjects folder>/scripts/recon-all.log and .../recon-all.status.log

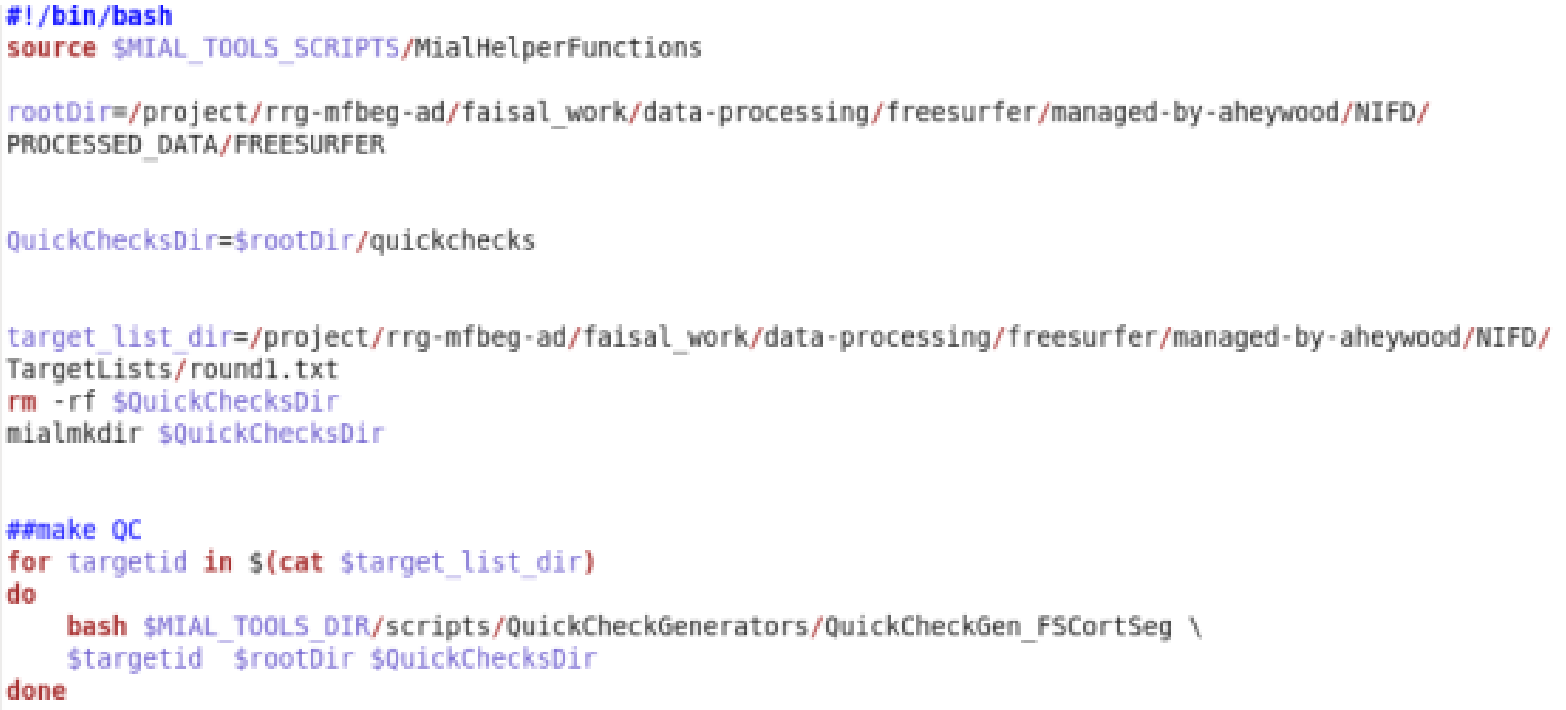
If recon-all finished **without error** > Run the quickcheck generator for the target subjects

> Specify the FreeSurfer Directory and the target list for subjects and run quickcheck generator script

FreeSurfer Directory

QuickCheck Directory

Target List



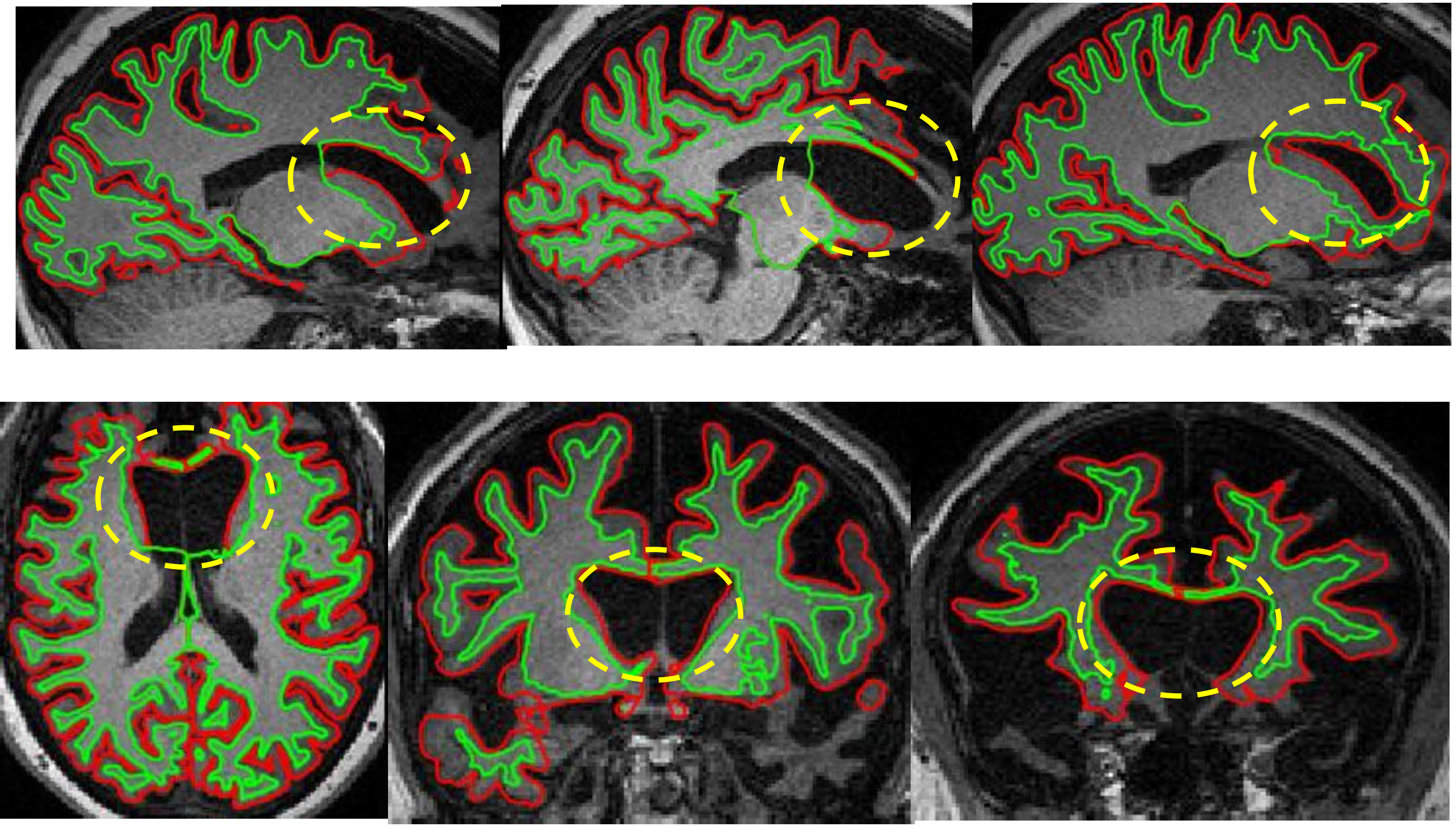
```
#!/bin/bash
source $MIAL_TOOLS_SCRIPTS/MialHelperFunctions

rootDir=/project/rrg-mfbeg-ad/faisal_work/data-processing/freesurfer/managed-by-aheywood/NIFD/
PROCESSED_DATA/FREESURFER


QuickChecksDir=$rootDir/quickchecks


target_list_dir=/project/rrg-mfbeg-ad/faisal_work/data-processing/freesurfer/managed-by-aheywood/NIFD/
TargetLists/round1.txt
rm -rf $QuickChecksDir
mialmkdir $QuickChecksDir


##make QC
for targetid in $(cat $target_list_dir)
do
    bash $MIAL_TOOLS_DIR/scripts/QuickCheckGenerators/QuickCheckGen_FSCortSeg \
    $targetid  $rootDir $QuickChecksDir
done
```

The four types of corrections we are performing:

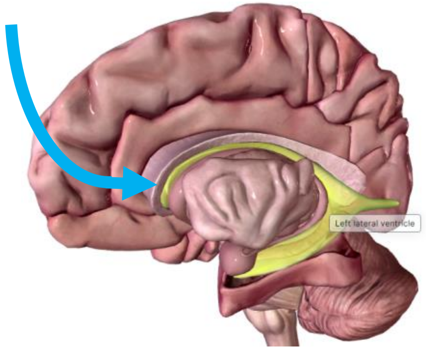
1. **White Matter Corrections:** The white matter has gaps or areas that are missing segmentation.
2. **Brainmask Volume Corrections:**
   - Large area(s) of the brain is excluded in the 'brainmask' volume (under-segmentation due to 'brainmask' volume error, this is the first error that must be corrected, if exists!).
   - Over-segmentation of the pial surface (i.e. the segmentation goes into the skull/dura matter).
3. **Cortical Seeding:** Under-segmentation of the brain volume.
4. **Skull Stripping:** Over-segmentation of the brainmask.

When checking a subject, the corrections should be performed in the order shown above.

White Matter Segmentation Errors



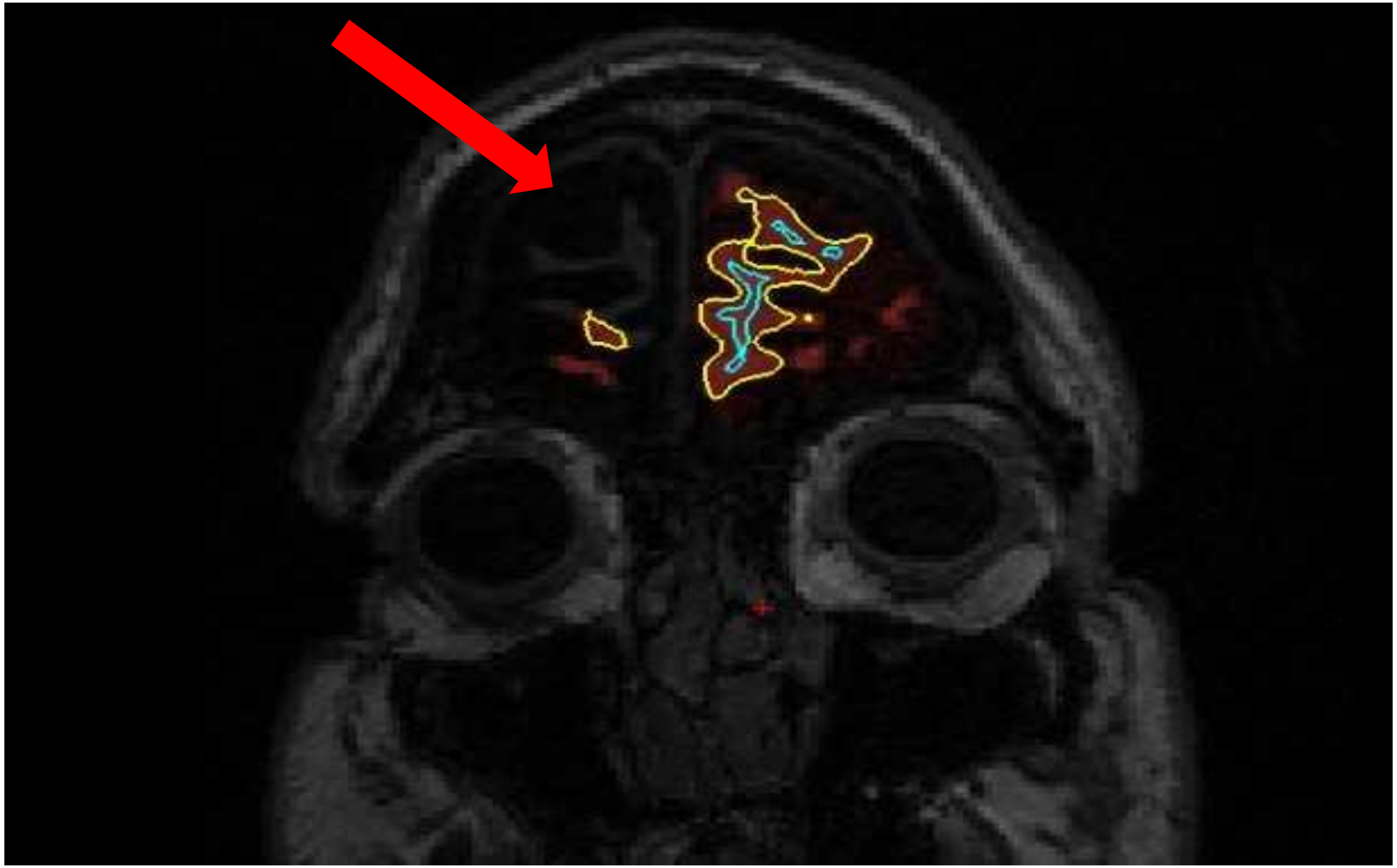
Exclusion of voxels that should be white matter and inclusions of voxels that should not be white matter are examples of white matter errors.
These errors are most often found around the region of brain ventricles (highlighted in yellow below).



https://human.biodigital.com/view?id=production%2FmaleAdult%2Fbrain_v02&type=module

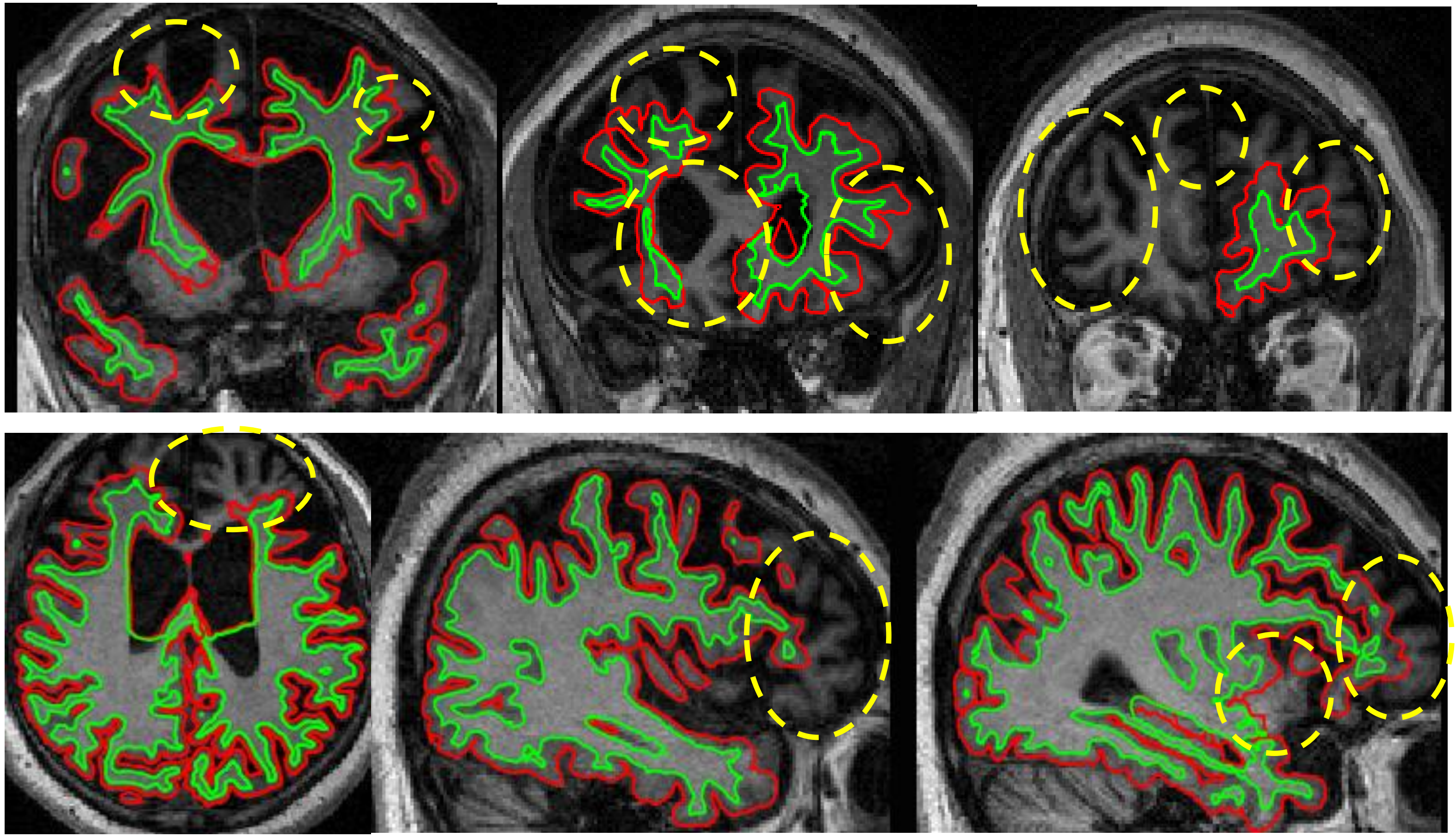
The images to the left are examples of white matter errors found in quickcheck images. Notice areas of brain tissue that are incorrectly segmented (yellow circles). They are viewable in all three view-planes but are easiest to identify in the **coronal plane**.

Brainmask error



This image is an example of 'brainmask' under-segmentation error that requires voxel cloning from the T1 volume to correct. Notice that the "Heat Map" of the 'brainmask' volume has failed to sufficiently cover the all the brain tissue, leaving one hemisphere of the brain unsegmented in this region (i.e. it is not red).

Under-segmentation Errors

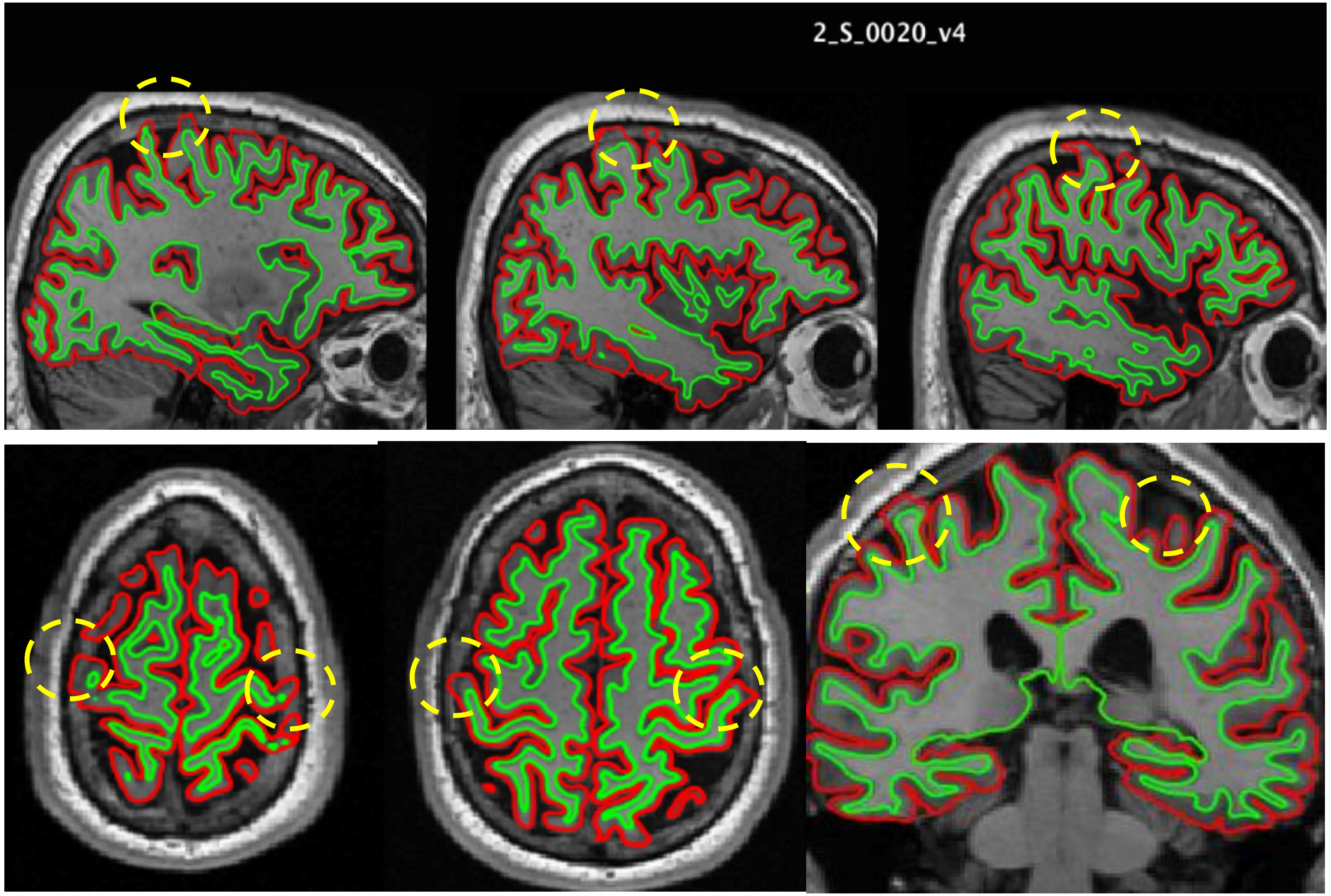


Under-segmentation occurs when FreeSurfer fails to determine the proper intensity for white matter which often affects both the white matter and pial surfaces. This results in areas of brain tissue that should be segmented being left unsegmented. This type of error is less common than over-segmentation errors, but can be more complex to correct.

They must either be corrected by cloning voxels from T1 into the 'brainmask' volume OR by cortical seeding.

The images to the left are examples of under-segmentation found in quickcheck images. Notice areas of brain tissue, including white and gray matter areas, that are not covered by surfaces (yellow circles). They are viewable in all three view-planes but are easiest to identify in the **coronal plane**.

Over-segmentation errors



Skull scraping/over-segmentation is the most common type of error and occurs when the pial surface extends beyond the gray matter-cerebral spinal fluid boundary and crossing into dura mater and the skull.

The images to the left are examples of skull-scraping found in quickcheck images. Notice the over-segmentation of the pial surface (yellow circles) into the dura mater and skull. They are viewable in all three view-planes but are easiest to identify in the **sagittal plane.**

What if there is no quickcheck available?

Check the FREESURFER/<Subjects folder>/scripts/recon-all.log and .../recon-all.status.log

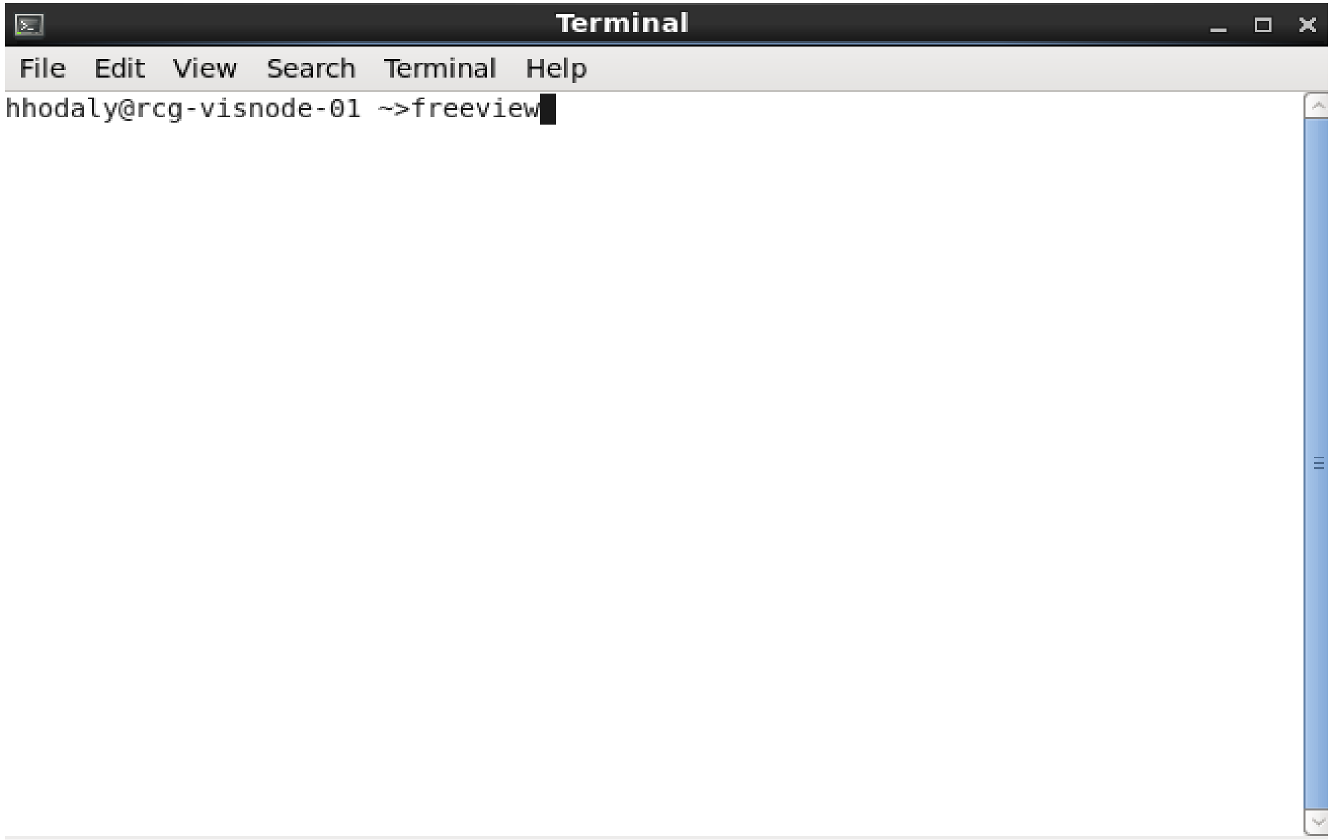
If recon-all finished **without error** > Run the quickcheck generator for that specific subject
> Specify the FreeSurfer Directory and the target list for subjects and run quickcheck generator script

If recon-all finished **with error** > Check the comments in the last few lines of recon-all.log or the last step in recon-all-status.log.

- If the last step is Skull Stripping, it is "skull stripping" error.
- If the last step in recon-all-status.log is "Fix Topology", look for "brainmask undersegmentation", "wm error/ large lateral ventricles" or poor contrast in freeview. If image looks fine in freeview, re-run from scratch.
- If comment "ERROR! FOV=259.201 > 256" is seen in the last few lines in recon-all.log, re-run from scratch with **"-cw256"** flag. The flag causes mri_convert to conform the image to dimensions of 256^3.
- If the last step in recon-all-status.log is "Talairach" or "Talairach Failure Detection", it is the Talairach error.
  - For correcting Talairach error, re-run the process from scratch with **"notal-check".** This flag causes FreeSurfer to skip the automatic failure detection of Talairach alignment. If the error is still occurring, try -notalairach flag. It will perform all the reconstruction steps except talairaching

Freeview Tutorial

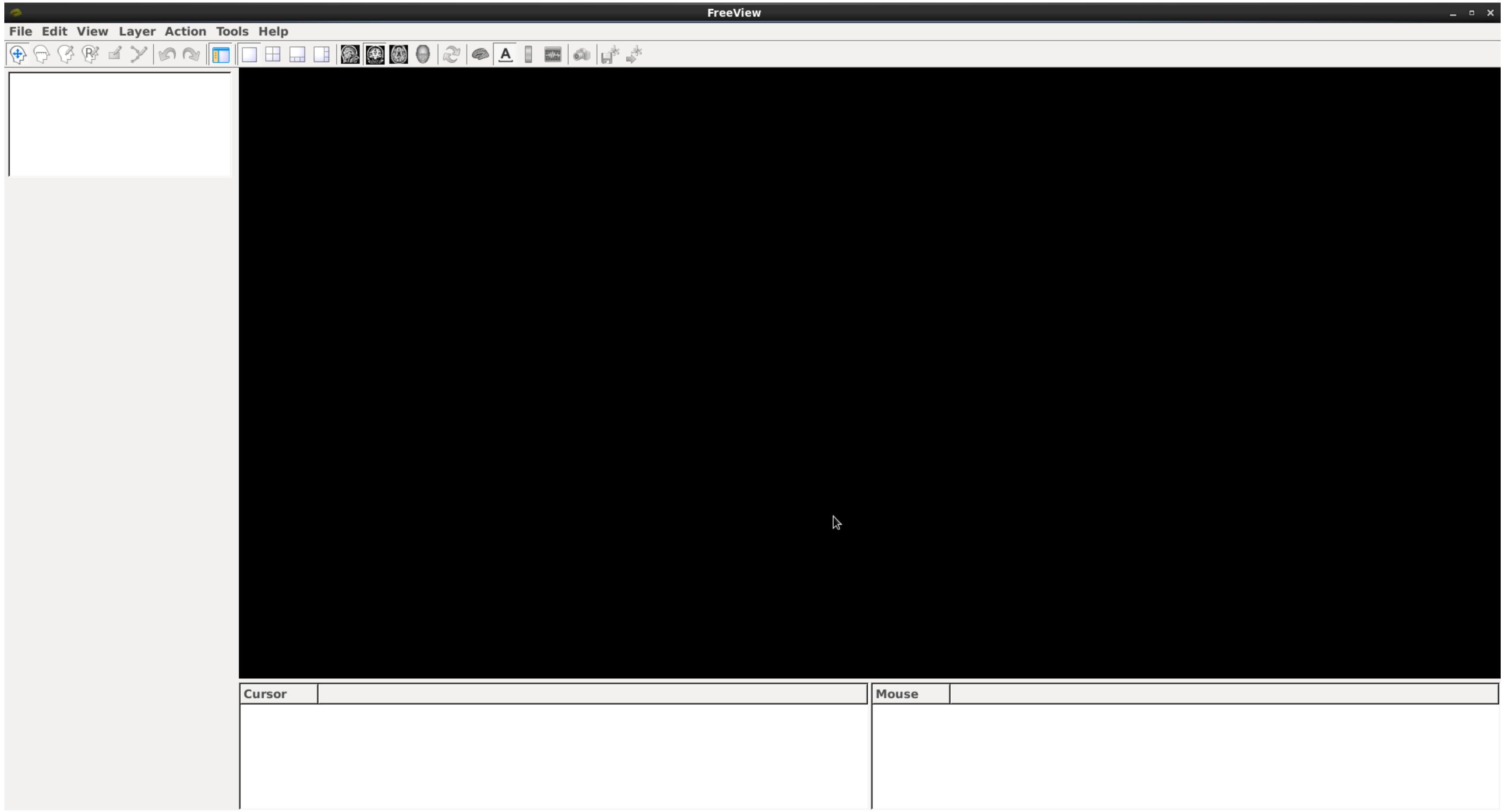
Opening Freeview



```
hhodaly@rcg-visnode-01 ~>freeview
```

Open a terminal and type "freeview" to open FreeView, the program we use to view and edit MRI image segmentations.

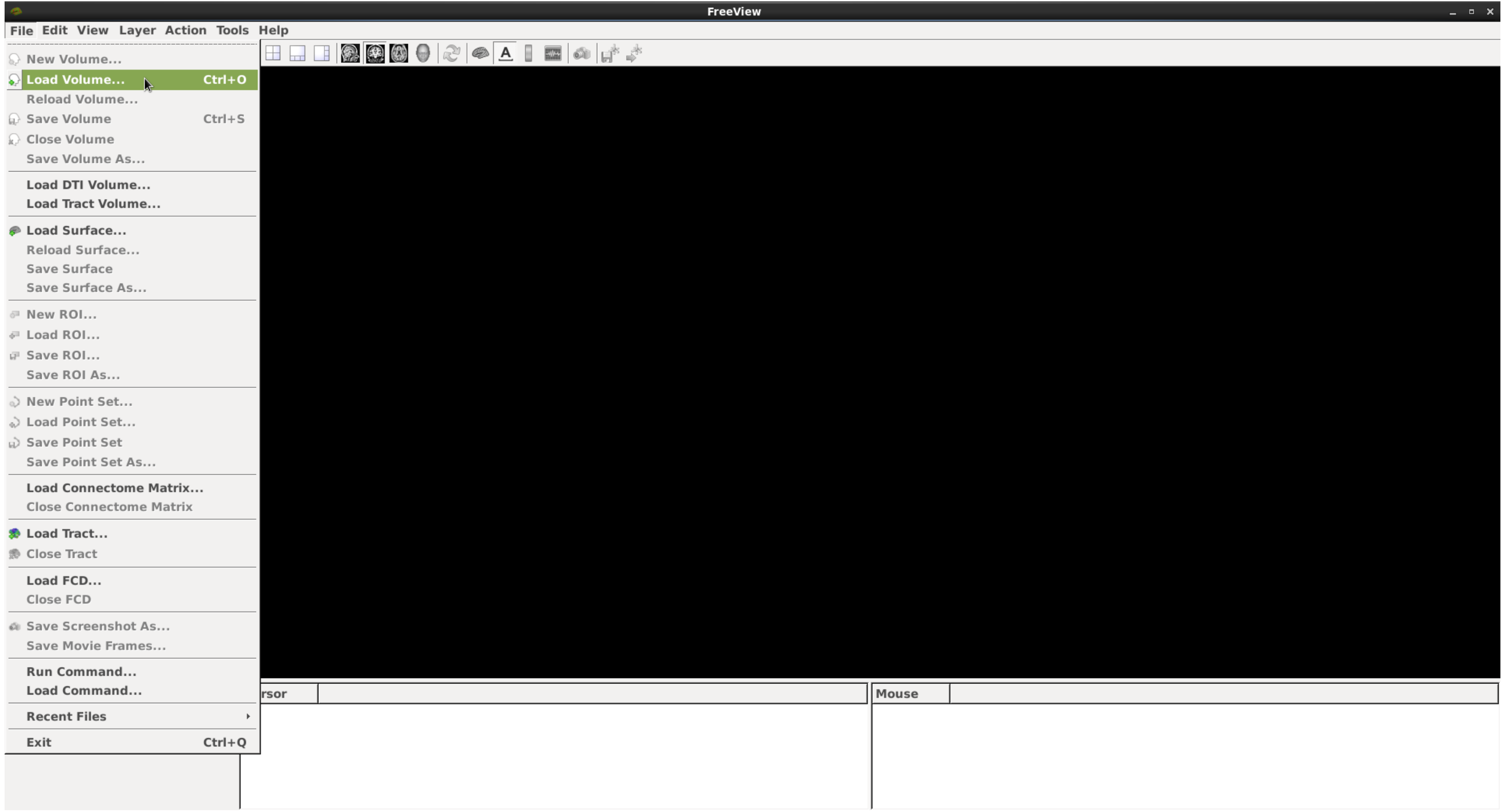
Opening FreeView



This is what FreeView looks like when you first open it and when no images are loaded.

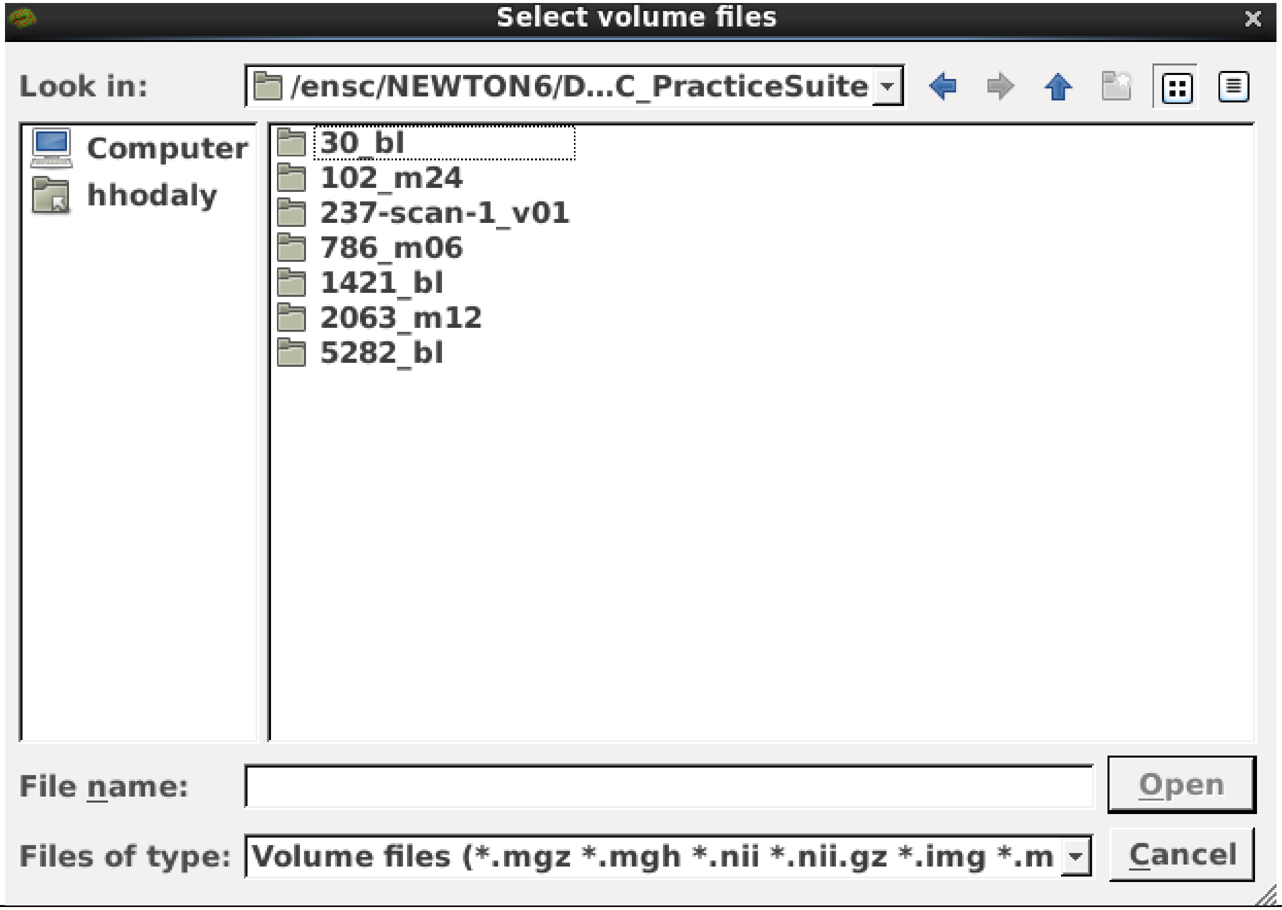
Loading a subject in Freeview

Before we can start correcting an image, we have to load the appropriate files. We first want to load the three volumes required.



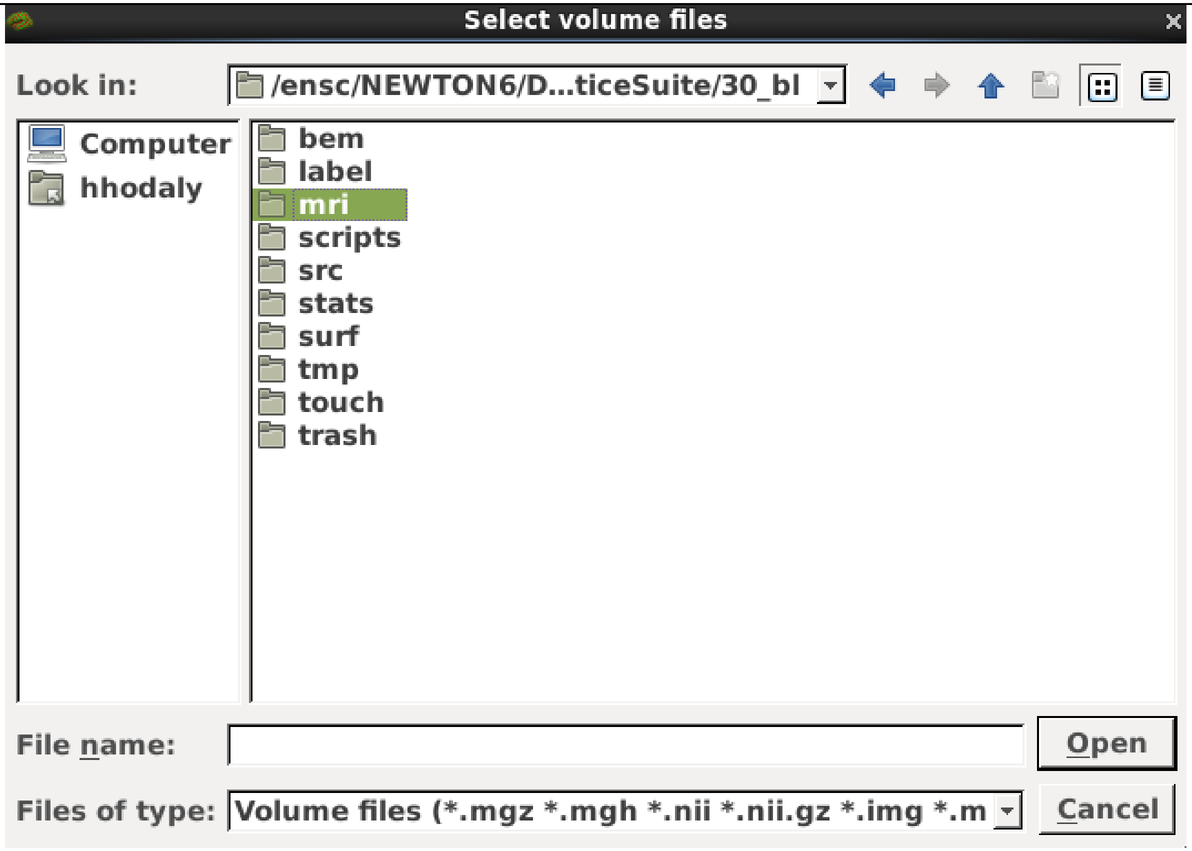
On the top left of FreeView, click "**File**" and then "**Load Volume**"

Now browse to the appropriate image folder.



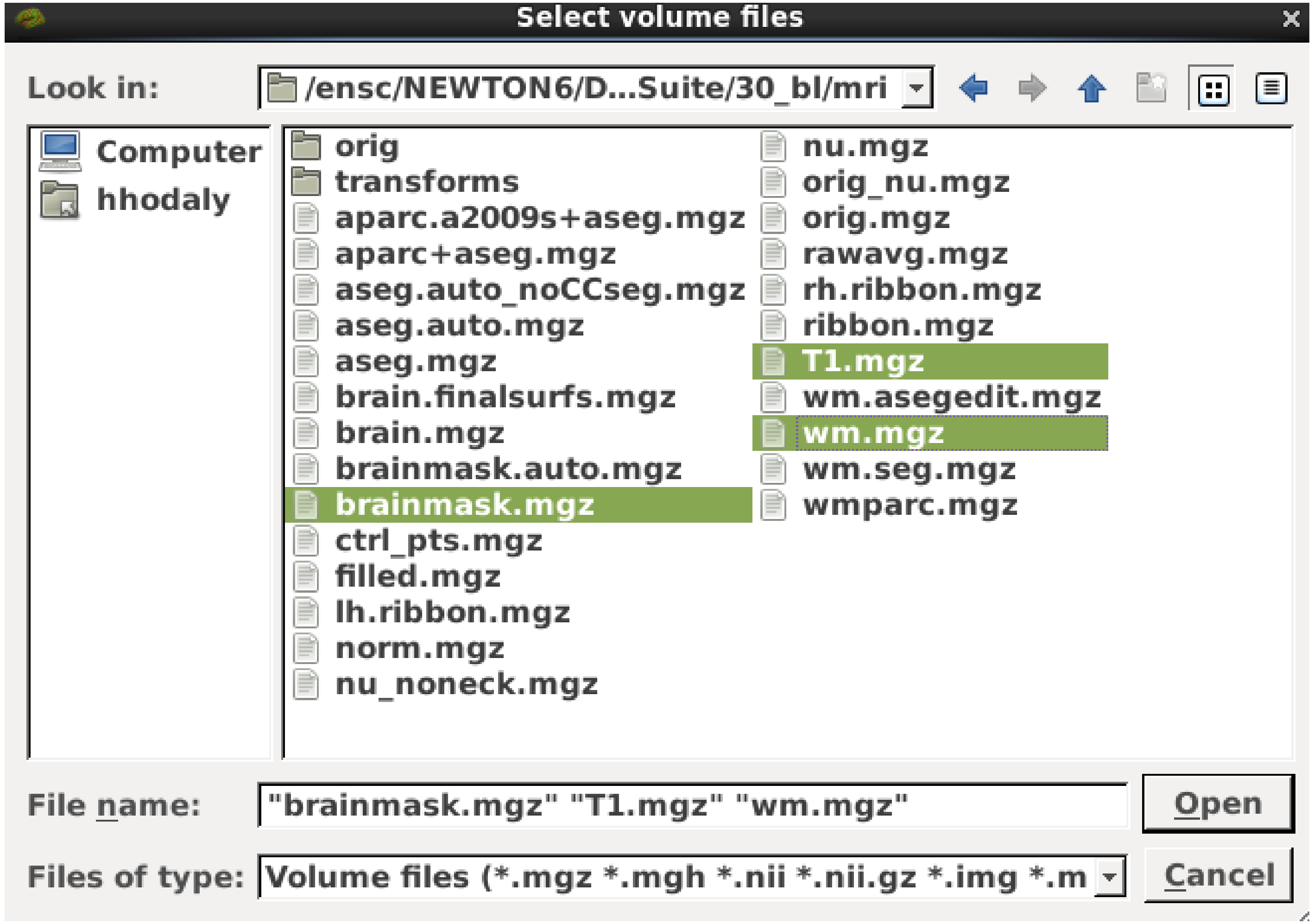
For example, the practice images are located at:
"/ensc/NEWTON6/DOCUMENTATION/FreesurferQC_PracticeSuite"

Select the subject you want to work on and open the folder.



In each folder, there are 10 subfolders. We first want to load the volumes, so select the "**mri**" folder.

The three volumes we want to load are "**brainmask.mgz**", "**T1.mgz**" and "**wm.mgz**".



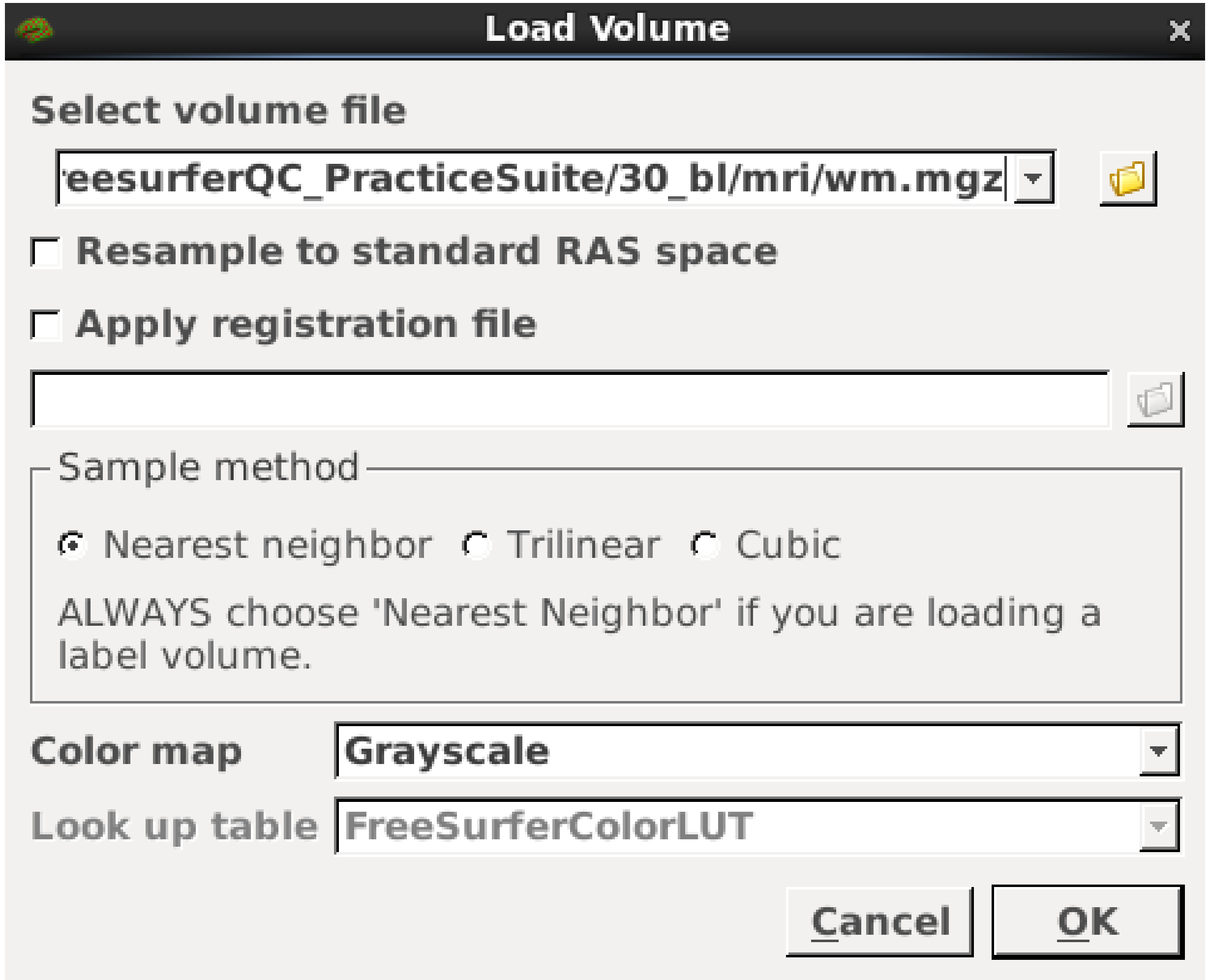
Look in: /ensc/NEWTON6/D...Suite/30_bl/mri

File name: "brainmask.mgz" "T1.mgz" "wm.mgz"

Files of type: Volume files (*.mgz *.mgh *.nii *.nii.gz *.img *.m

Select the three volumes and click "**Open**".

Make sure the next screen looks like this and then click "**OK**".



Select volume file

eesurferQC_PracticeSuite/30_bl/mri/wm.mgz

☐ Resample to standard RAS space

☐ Apply registration file

Sample method

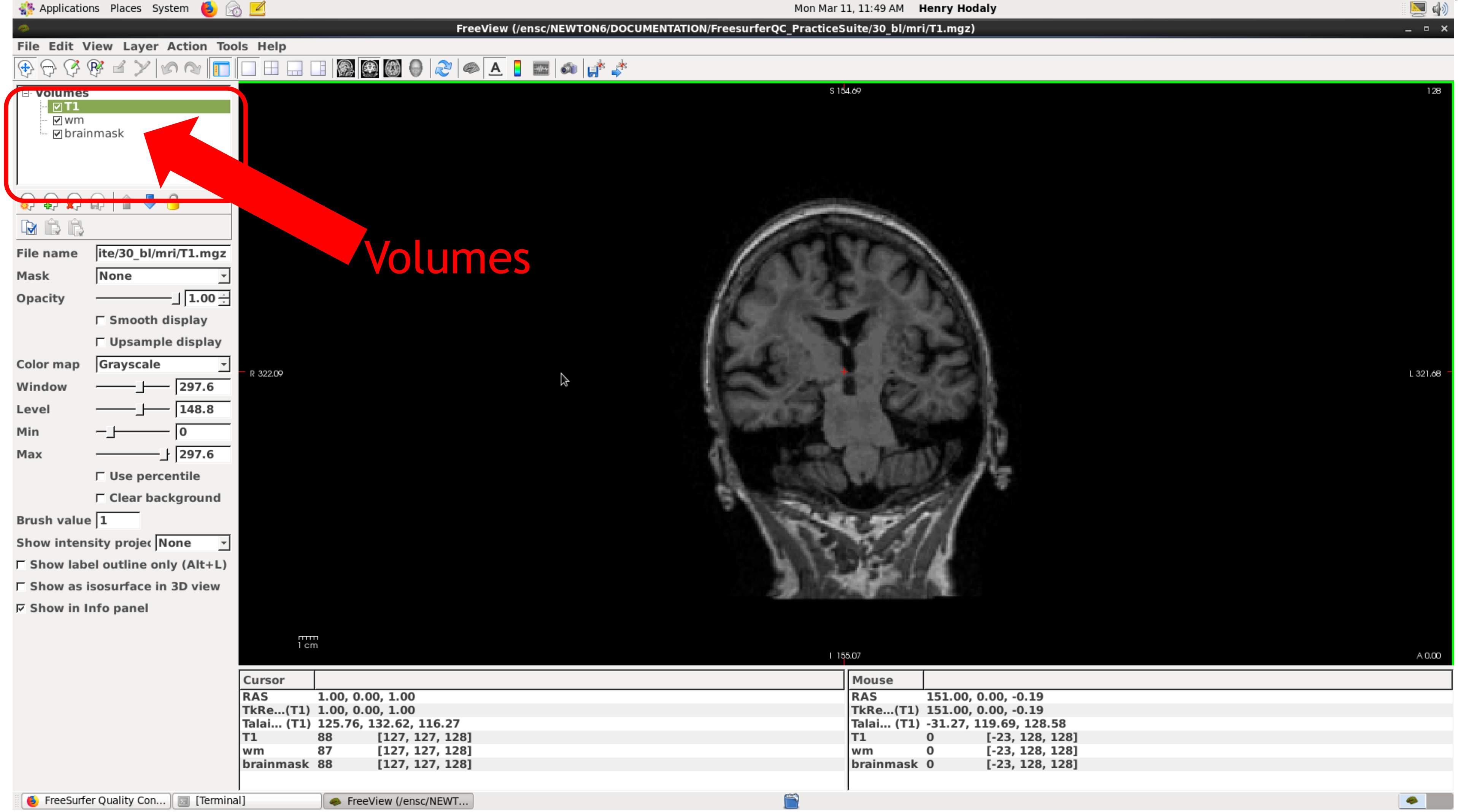
● Nearest neighbor ○ Trilinear ○ Cubic

ALWAYS choose 'Nearest Neighbor' if you are loading a label volume.

Color map: Grayscale

Look up table: FreeSurferColorLUT

If you have loaded the three volumes correctly, you should see them at the top of the side panel. The top volume on the side panel will also be what is visible on the display window.



FreeView (/ensc/NEWTON6/DOCUMENTATION/FreesurferQC_PracticeSuite/30_bl/mri/T1.mgz)

Volumes
- ☑ T1
- ☑ wm
- ☑ brainmask

File name: ite/30_bl/mri/T1.mgz
Mask: None
Opacity: 1.00
☐ Smooth display
☐ Upsample display
Color map: Grayscale
Window: 297.6
Level: 148.8
Min: 0
Max: 297.6
☐ Use percentile
☐ Clear background
Brush value: 1
Show intensity projec: None
☐ Show label outline only (Alt+L)
☐ Show as isosurface in 3D view
☑ Show in Info panel

Cursor		
RAS	1.00, 0.00, 1.00	
TkRe...(T1)	1.00, 0.00, 1.00	
Talai... (T1)	125.76, 132.62, 116.27	
T1	88	[127, 127, 128]
wm	87	[127, 127, 128]
brainmask	88	[127, 127, 128]

Mouse		
RAS	151.00, 0.00, -0.19	
TkRe...(T1)	151.00, 0.00, -0.19	
Talai... (T1)	-31.27, 119.69, 128.58	
T1	0	[-23, 128, 128]
wm	0	[-23, 128, 128]
brainmask	0	[-23, 128, 128]

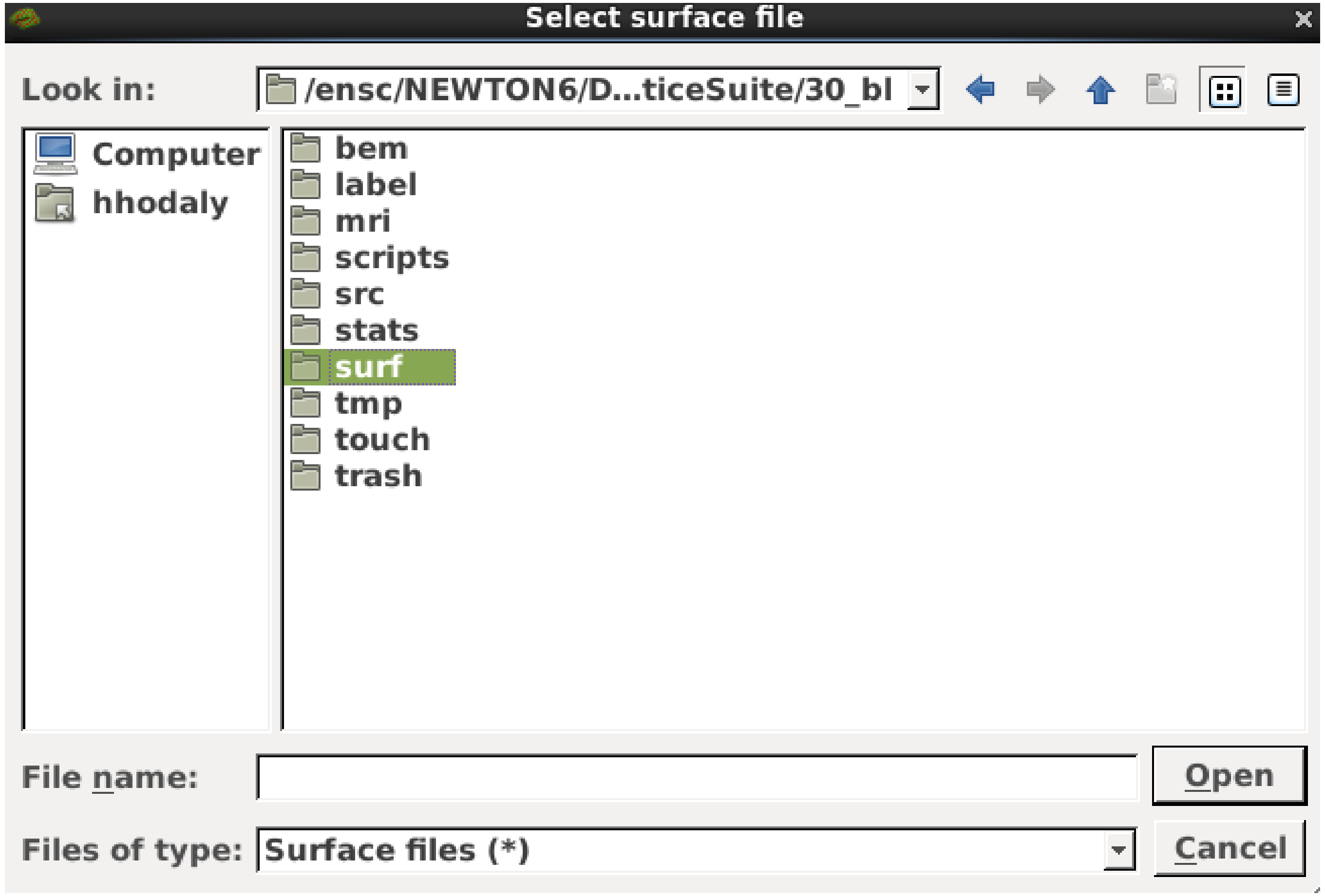
Our next step is to load the segmentation files.

```
rsor
S             1.00, 0.00, 1.00
Re...(T1)     1.00, 0.00, 1.00
ai... (T1)    125.76, 132.62, 116.27
              88          [127, 127, 128]
wm            87          [127, 127, 128]
brainmask     88          [127, 127, 128]
```

```
Mouse
RAS           325.28, 0.00, 115.67
TkRe...(T1)   325.28, 0.00, 115.67
Talai... (T1) -195.52, -3.30, 217.49
T1            0           [-197, 12, 128]
wm            0           [-197, 12, 128]
brainmask     0           [-197, 12, 128]
```

On the top left of FreeView, click "**File**" and then "**Load Surface**"

Now browse to the appropriate image folder. Select the subject you want to work on and open the folder.



Select surface file

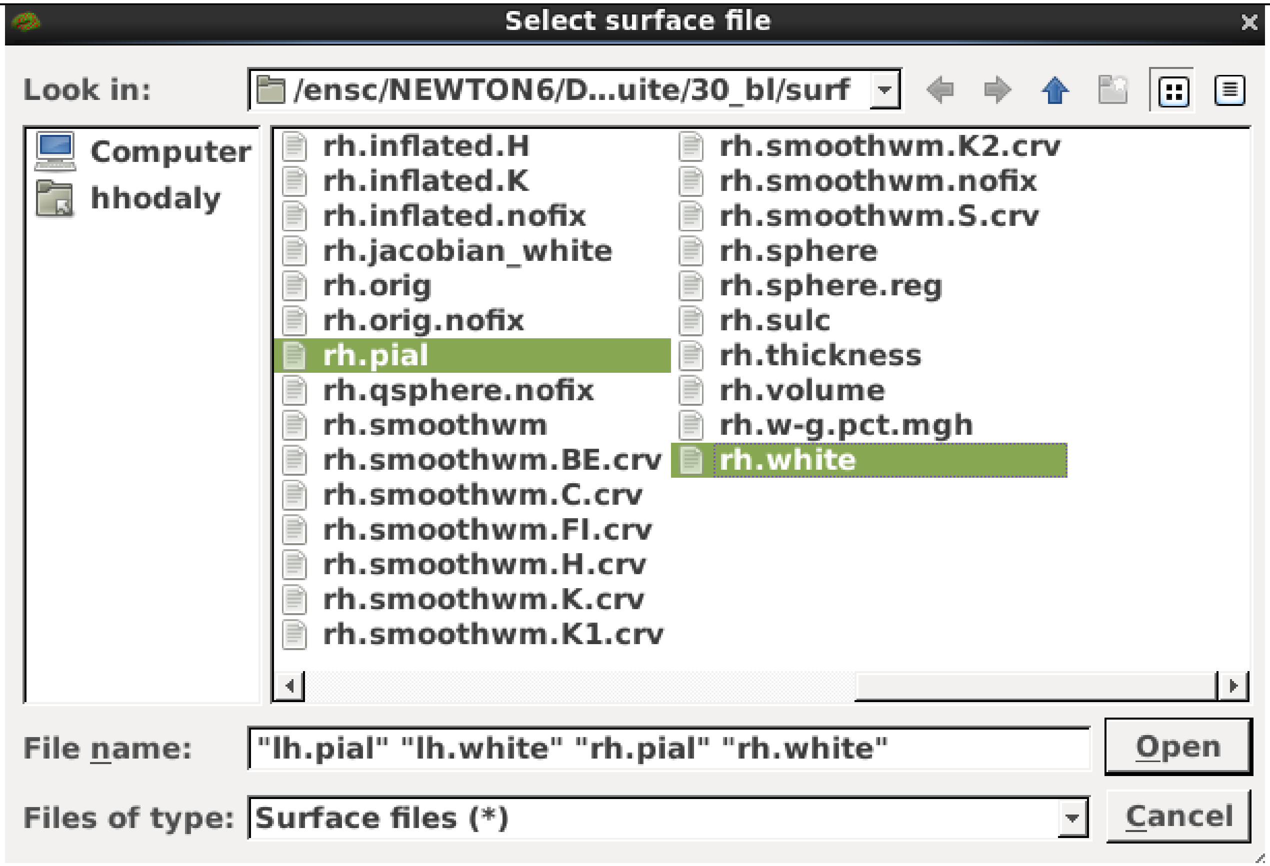
Look in: /ensc/NEWTON6/D...ticeSuite/30_bl

File name:

Files of type: Surface files (*)

Now that we want to load the segmentations, select the "**surf**" folder.

The segmentations we want to load are "**lh.pial**", "**lh.white**", "**rh.pial**" and "**rh.white**".

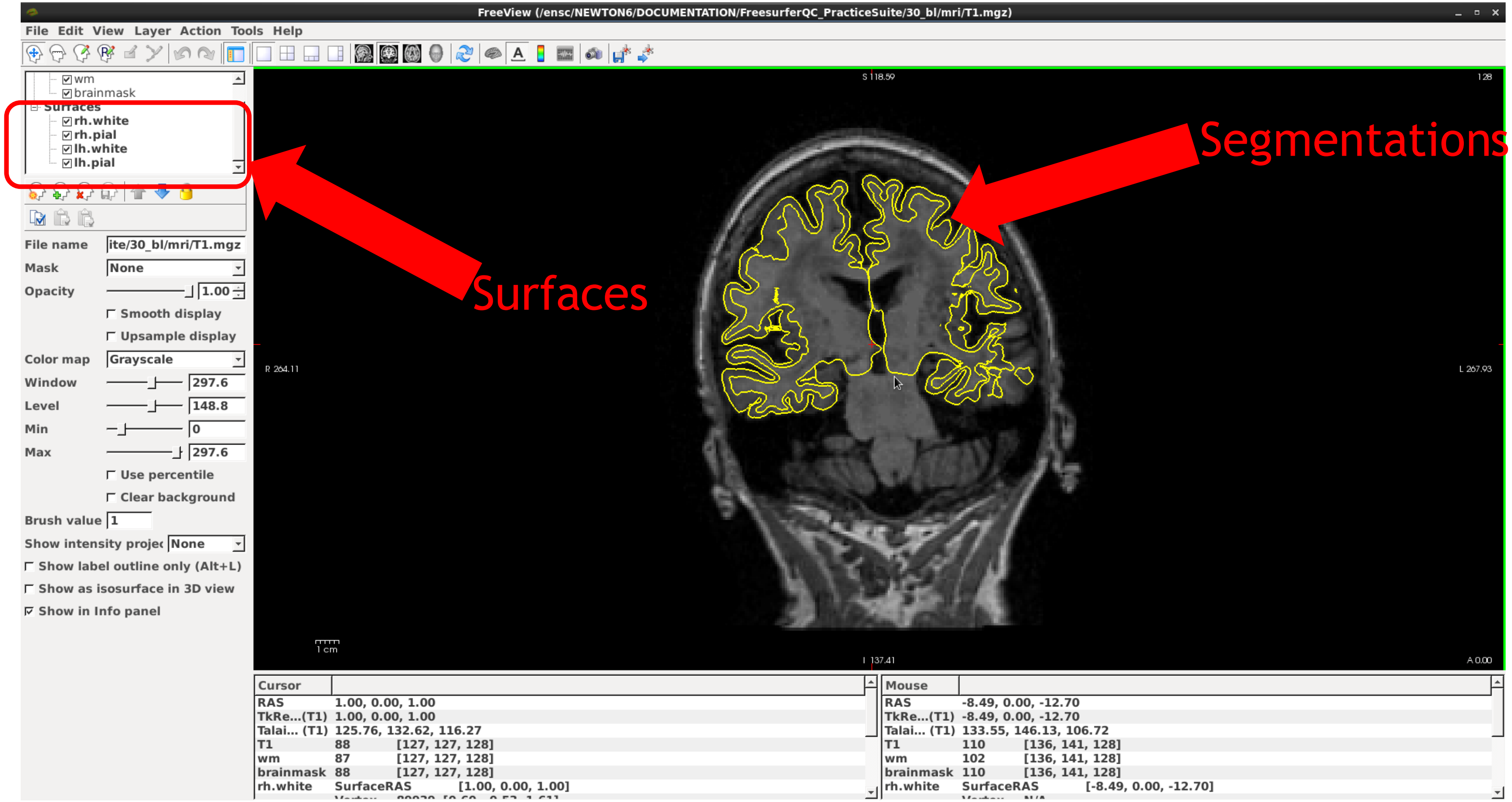


File name: "lh.pial" "lh.white" "rh.pial" "rh.white"

Files of type: Surface files (*)

Select the four surfaces and click "**Open**".

If you have loaded the four surfaces correctly, you should see them at the top of the side panel and the segmentations visible on the volume on the display window.



Surfaces

Segmentations

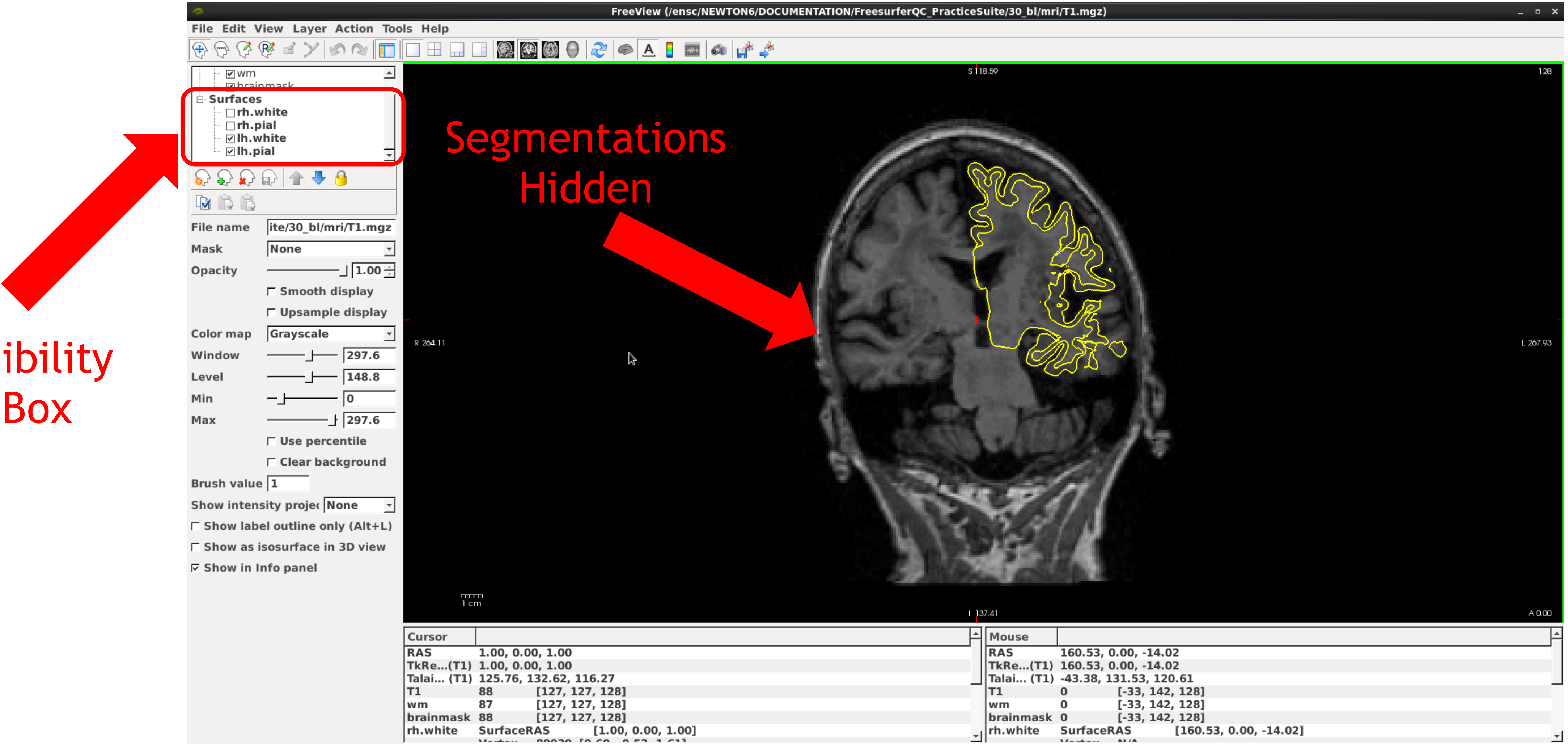
☑ wm
☑ brainmask
Surfaces
☑ rh.white
☑ rh.pial
☑ lh.white
☑ lh.pial

File name: ite/30_bl/mri/T1.mgz
Mask: None
Opacity: 1.00
☐ Smooth display
☐ Upsample display
Color map: Grayscale
Window: 297.6
Level: 148.8
Min: 0
Max: 297.6
☐ Use percentile
☐ Clear background
Brush value: 1
Show intensity projec: None
☐ Show label outline only (Alt+L)
☐ Show as isosurface in 3D view
☑ Show in Info panel

```
Cursor
RAS          1.00, 0.00, 1.00
TkRe...(T1)  1.00, 0.00, 1.00
Talai... (T1) 125.76, 132.62, 116.27
T1           88        [127, 127, 128]
wm           87        [127, 127, 128]
brainmask    88        [127, 127, 128]
rh.white     SurfaceRAS          [1.00, 0.00, 1.00]
```

```
Mouse
RAS          -8.49, 0.00, -12.70
TkRe...(T1)  -8.49, 0.00, -12.70
Talai... (T1) 133.55, 146.13, 106.72
T1           110       [136, 141, 128]
wm           102       [136, 141, 128]
brainmask    110       [136, 141, 128]
rh.white     SurfaceRAS          [-8.49, 0.00, -12.70]
```

You are able to toggle the visibility on and off for both surfaces and volumes by clicking the box next to each one.



File name: ite/30_bl/mri/T1.mgz
Mask: None
Opacity: 1.00
☐ Smooth display
☐ Upsample display
Color map: Grayscale
Window: 297.6
Level: 148.8
Min: 0
Max: 297.6
☐ Use percentile
☐ Clear background
Brush value: 1
Show intensity projec: None
☐ Show label outline only (Alt+L)
☐ Show as isosurface in 3D view
☑ Show in Info panel

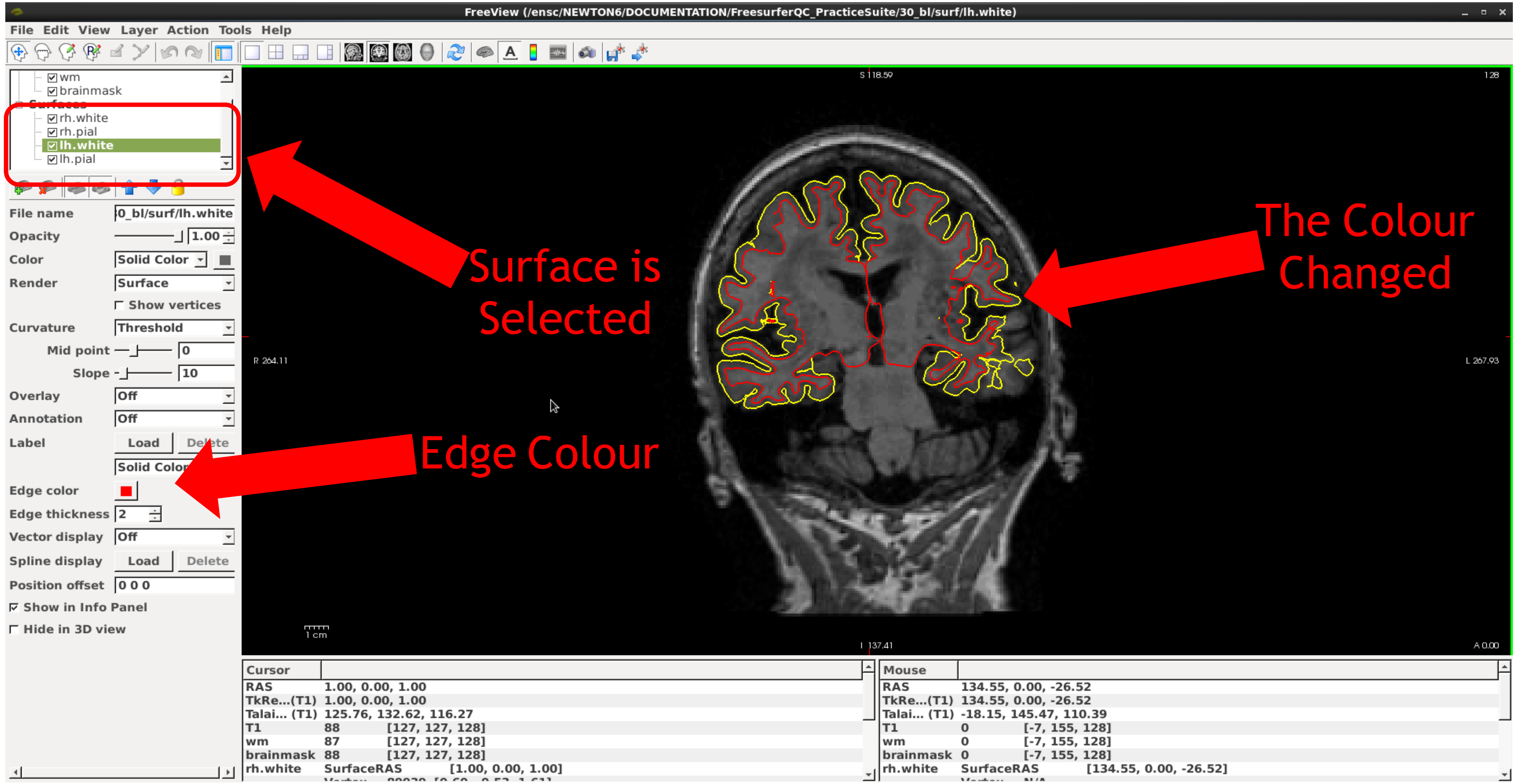
```
Cursor
RAS          1.00, 0.00, 1.00
TkRe...(T1)  1.00, 0.00, 1.00
Talai... (T1) 125.76, 132.62, 116.27
T1           88         [127, 127, 128]
wm           87         [127, 127, 128]
brainmask    88         [127, 127, 128]
rh.white     SurfaceRAS           [1.00, 0.00, 1.00]
```

```
Mouse
RAS          160.53, 0.00, -14.02
TkRe...(T1)  160.53, 0.00, -14.02
Talai... (T1) -43.38, 131.53, 120.61
T1           0          [-33, 142, 128]
wm           0          [-33, 142, 128]
brainmask    0          [-33, 142, 128]
rh.white     SurfaceRAS           [160.53, 0.00, -14.02]
```

Segmentations Hidden

Visibility Box

You can also change the colours of the segmentations. Make sure the surface you want is selected in the side panel and then change the edge colour.



☑ wm
☑ brainmask
Surfaces
☑ rh.white
☑ rh.pial
☑ lh.white
☑ lh.pial

File name: 0_bl/surf/lh.white
Opacity: 1.00
Color: Solid Color
Render: Surface
☐ Show vertices
Curvature: Threshold
Mid point: 0
Slope: 10
Overlay: Off
Annotation: Off
Label: Load Delete
Solid Color
Edge color: 🟥
Edge thickness: 2
Vector display: Off
Spline display: Load Delete
Position offset: 0 0 0
☑ Show in Info Panel
☐ Hide in 3D view

Cursor	
RAS	1.00, 0.00, 1.00
TkRe...(T1)	1.00, 0.00, 1.00
Talai... (T1)	125.76, 132.62, 116.27
T1	88 [127, 127, 128]
wm	87 [127, 127, 128]
brainmask	88 [127, 127, 128]
rh.white	SurfaceRAS [1.00, 0.00, 1.00]

Mouse	
RAS	134.55, 0.00, -26.52
TkRe...(T1)	134.55, 0.00, -26.52
Talai... (T1)	-18.15, 145.47, 110.39
T1	0 [-7, 155, 128]
wm	0 [-7, 155, 128]
brainmask	0 [-7, 155, 128]
rh.white	SurfaceRAS [134.55, 0.00, -26.52]

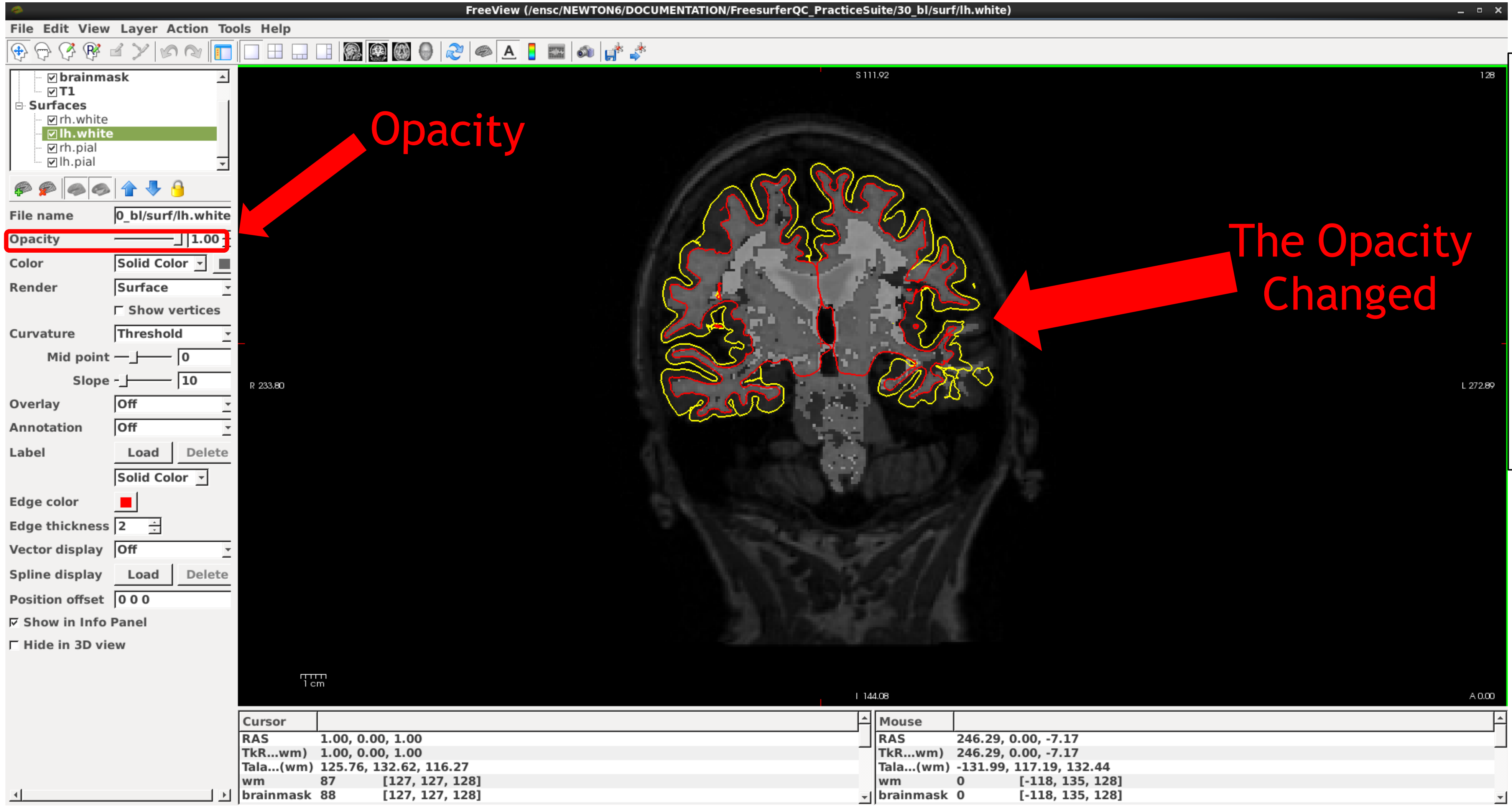
Surface is Selected

The Colour Changed

Edge Colour

Change the colour for "**lh.white**" and "**rh.white**" to red so there is distinction between the white matter and the pial for both hemispheres.

Then you should set the opacity for the volumes so we can see all of them at the same time.



☑ brainmask
☑ T1
Surfaces
☑ rh.white
☑ lh.white
☑ rh.pial
☑ lh.pial

File name: 0_bl/surf/lh.white
Opacity: 1.00
Color: Solid Color
Render: Surface
☐ Show vertices
Curvature: Threshold
Mid point: 0
Slope: 10
Overlay: Off
Annotation: Off
Label: Load Delete
Solid Color
Edge color: 🟥
Edge thickness: 2
Vector display: Off
Spline display: Load Delete
Position offset: 0 0 0
☑ Show in Info Panel
☐ Hide in 3D view

Cursor		
RAS	1.00, 0.00, 1.00	
TkR...wm)	1.00, 0.00, 1.00	
Tala...(wm)	125.76, 132.62, 116.27	
wm	87	[127, 127, 128]
brainmask	88	[127, 127, 128]

Mouse		
RAS	246.29, 0.00, -7.17	
TkR...wm)	246.29, 0.00, -7.17	
Tala...(wm)	-131.99, 117.19, 132.44	
wm	0	[-118, 135, 128]
brainmask	0	[-118, 135, 128]

Opacity

The Opacity Changed

Change the opacity for "**wm**" to be **0.5** and "**brainmask**" to be **0.3**.

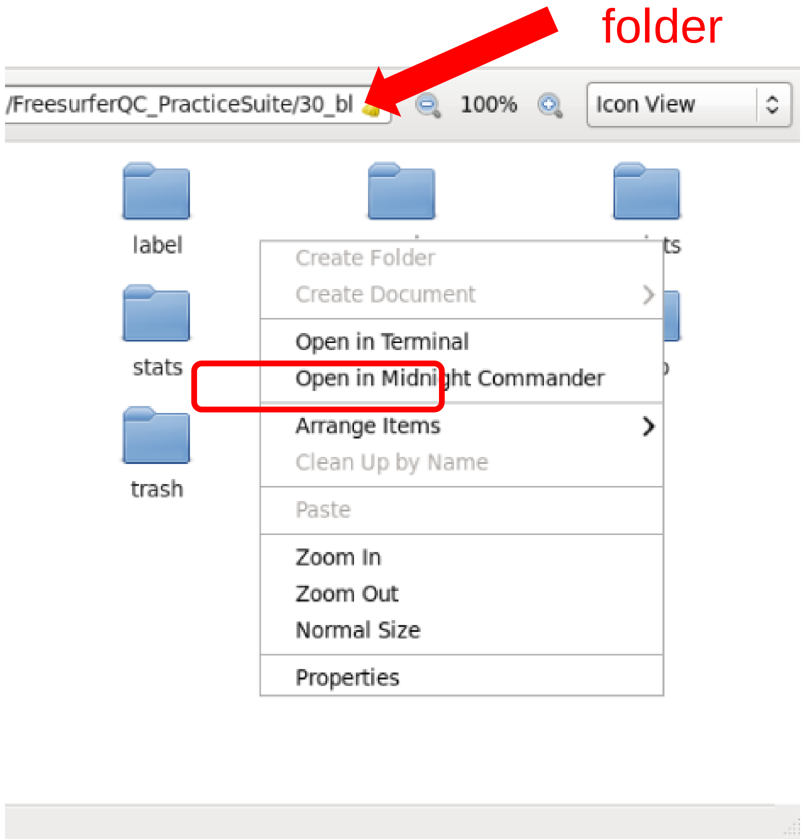
These 8 buttons on the toolbar are quite useful. They allow us to view the sagittal, coronal, axial and 3D views.

When doing the corrections, it is easiest to use the coronal view, but you can use whichever view you prefer!

Coronal View

This link will give a description on what each symbol in the tool bar does and will go in to more description on various aspects of the program.
https://surfer.nmr.mgh.harvard.edu/fswiki/FreeviewGuide/FreeviewGeneralUsage/FreeviewInterface

Another way to load the subject is by entering commands in the terminal opened in the corresponding subject's folder. This way you don't need to open FreeView in advance and adjust different parameters after loading the subject.



Your subject folder

/FreesurferQC_PracticeSuite/30_bl

In the folder of the subject you want to load, open the terminal in the right click menu. Then type in the following commands line by line.

```
freeview -v \
mri/T1.mgz \
mri/brainmask.mgz:opacity=0.3
\
mri/wm.mgz:opacity=0.5 \
-f
surf/lh.white:edgecolor=yellow \
surf/lh.pial:edgecolor=red \
surf/rh.white:edgecolor=yellow \
surf/rh.pial:edgecolor=red
```

The four types of corrections we are performing:

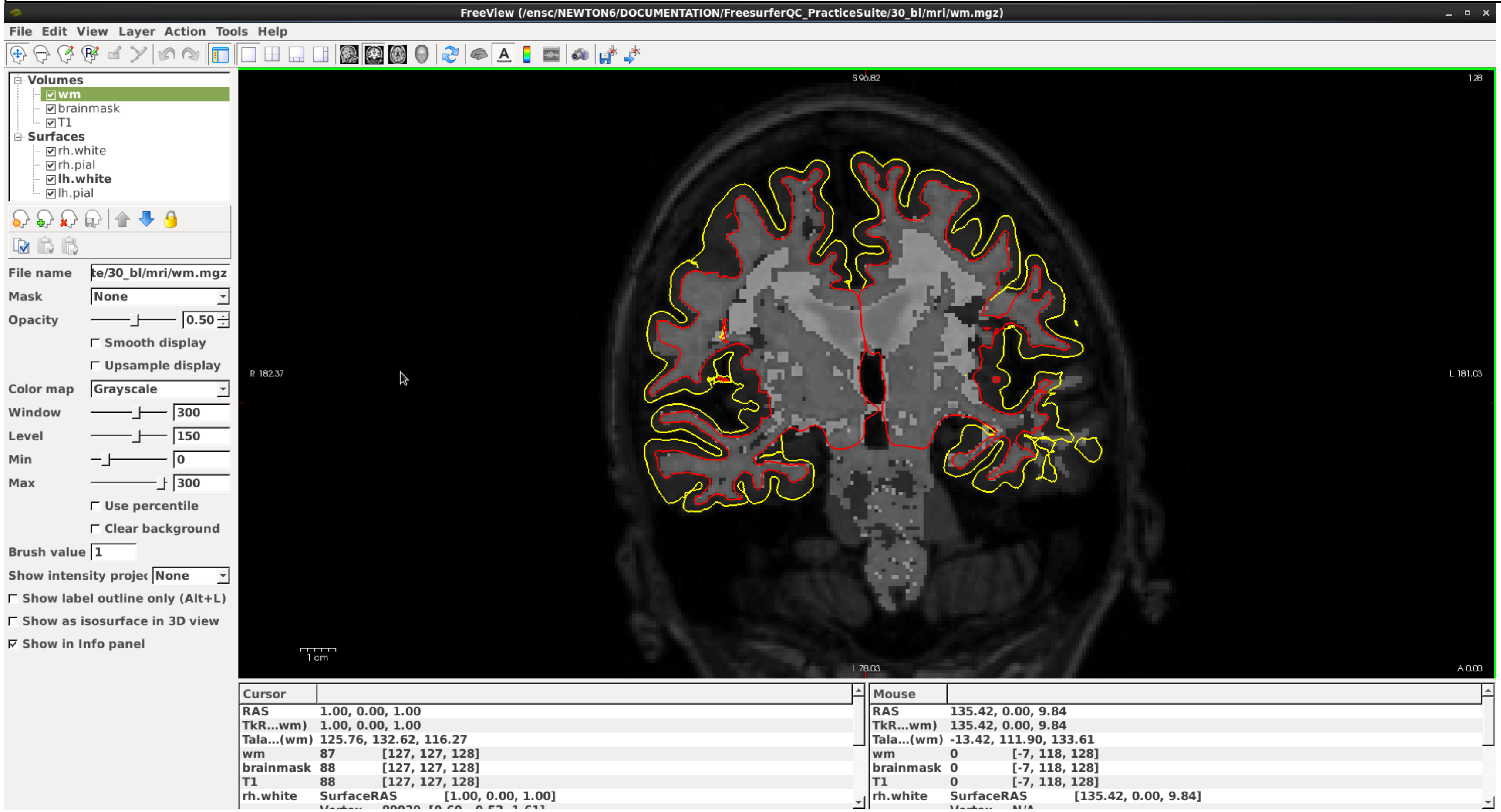
1. **White Matter Corrections:** The white matter has gaps or areas that are missing segmentation.
2. **Brainmask Volume Corrections:**
   - Large area(s) of the brain is excluded in the 'brainmask' volume (under-segmentation due to 'brainmask' volume error, this is the first error that must be corrected, if it exists!).
   - Over-segmentation of the pial surface (i.e. the segmentation goes into the skull/dura matter).
3. **Cortical Seeding:** Under-segmentation of the brain volume.
4. **Skull Stripping:** Over-segmentation of the brainmask.

When checking a subject, the corrections should be performed in the order shown above.

Note that whenever we are making corrections, the volume that we are working on should be highlighted. The only volumes that we actually edit are the 'wm' and the 'brainmask'. The 'T1' will never be edited, it is just there for reference.

White Matter Corrections

On the side panel, double click on "**wm**" to make sure that it is visible. Hide the "**T1**" and "**brainmask**" volumes, as well as the "**rh.pial**" and "**lh.pial**" surfaces.



File name: te/30_bl/mri/wm.mgz
Mask: None
Opacity: 0.50
☐ Smooth display
☐ Upsample display
Color map: Grayscale
Window: 300
Level: 150
Min: 0
Max: 300
☐ Use percentile
☐ Clear background
Brush value: 1
Show intensity projec: None
☐ Show label outline only (Alt+L)
☐ Show as isosurface in 3D view
☑ Show in Info panel

Cursor		
RAS	1.00, 0.00, 1.00	
TkR...wm)	1.00, 0.00, 1.00	
Tala...(wm)	125.76, 132.62, 116.27	
wm	87	[127, 127, 128]
brainmask	88	[127, 127, 128]
T1	88	[127, 127, 128]
rh.white	SurfaceRAS	[1.00, 0.00, 1.00]

Mouse		
RAS	135.42, 0.00, 9.84	
TkR...wm)	135.42, 0.00, 9.84	
Tala...(wm)	-13.42, 111.90, 133.61	
wm	0	[-7, 118, 128]
brainmask	0	[-7, 118, 128]
T1	0	[-7, 118, 128]
rh.white	SurfaceRAS	[135.42, 0.00, 9.84]

This is what your screen should look like before you start making corrections. All of the volumes are visible as well as the segmentations.

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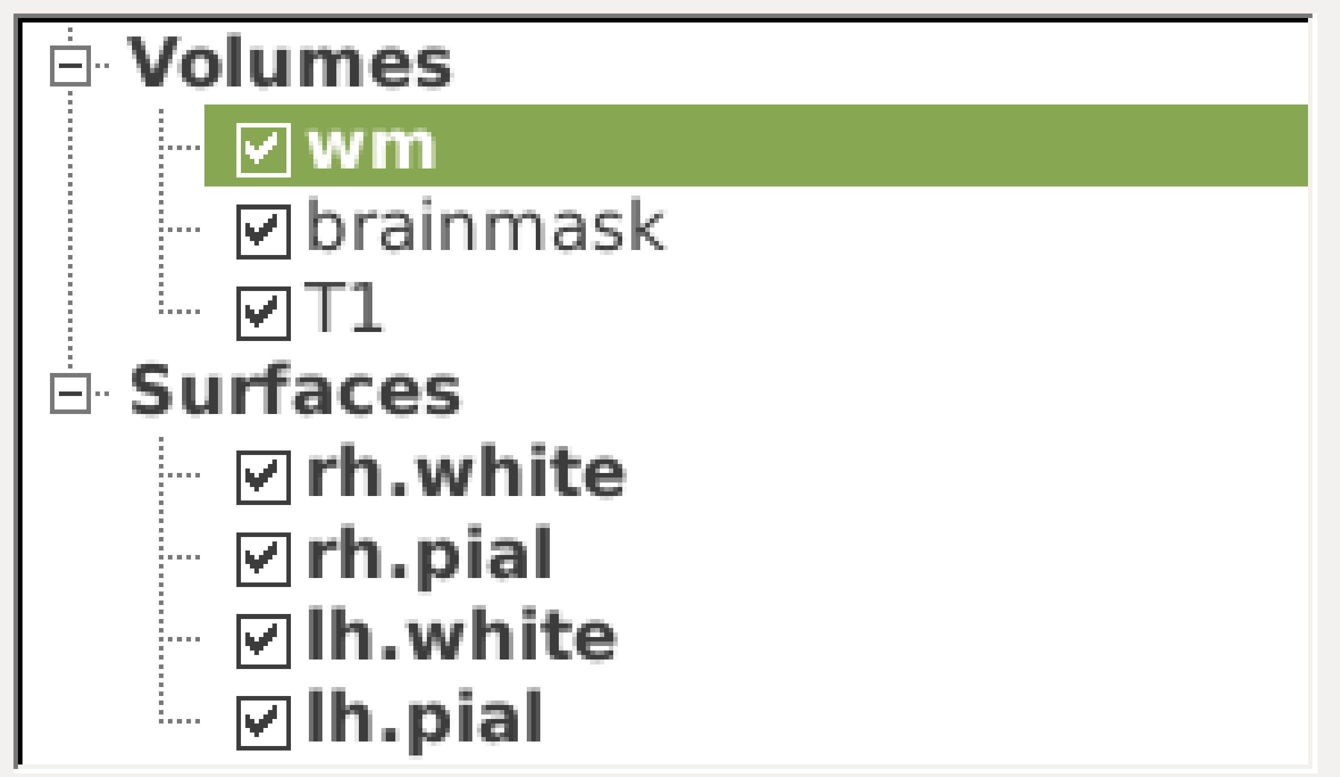
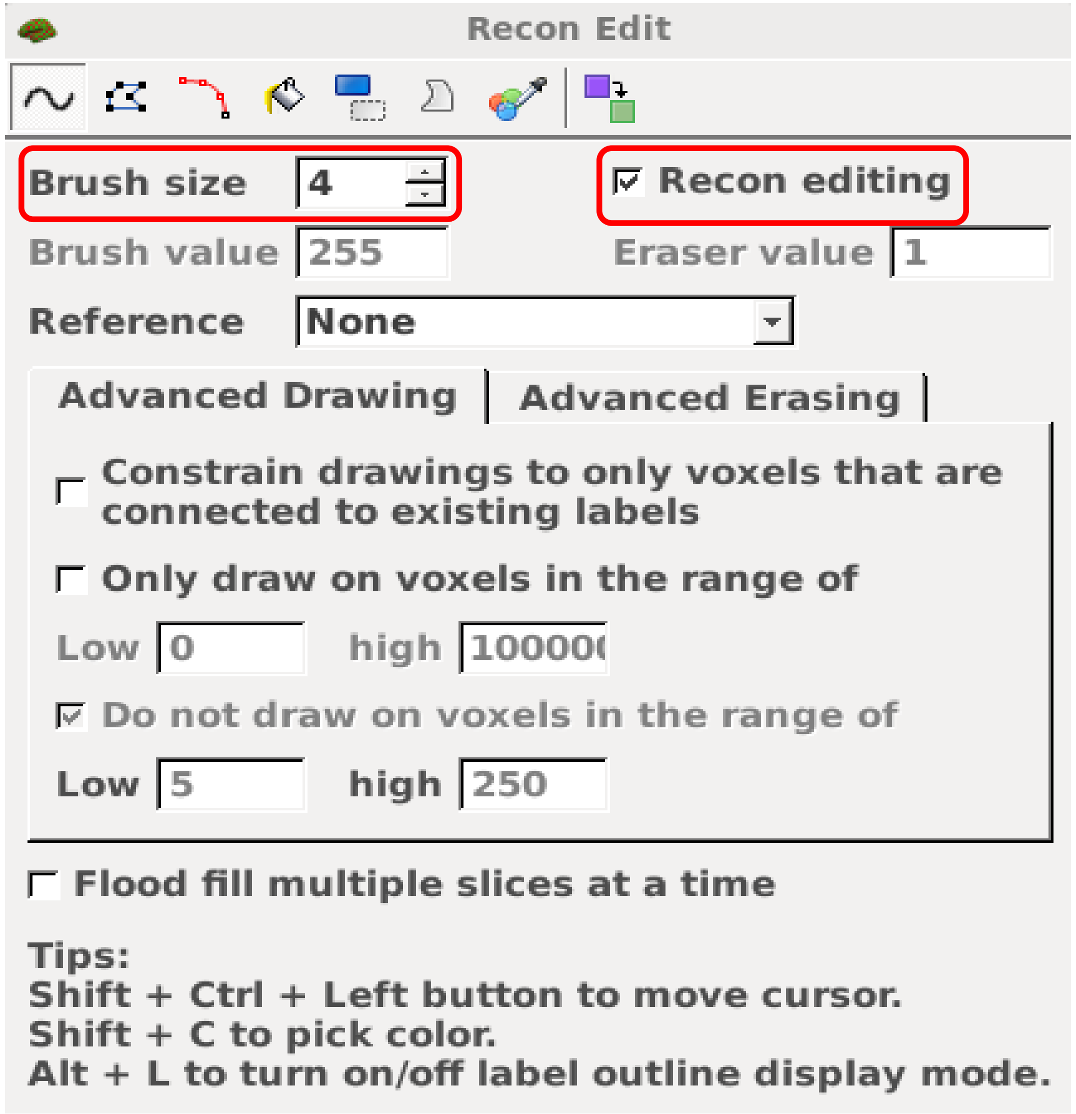
To start correcting the white matter, make sure that "**wm**" is the volume you are working on.





Brush size 4

☑ Recon editing

Brush value 255

Eraser value 1

Reference None

☐ Constrain drawings to only voxels that are connected to existing labels

☐ Only draw on voxels in the range of

Low 0 high 100000

☑ Do not draw on voxels in the range of

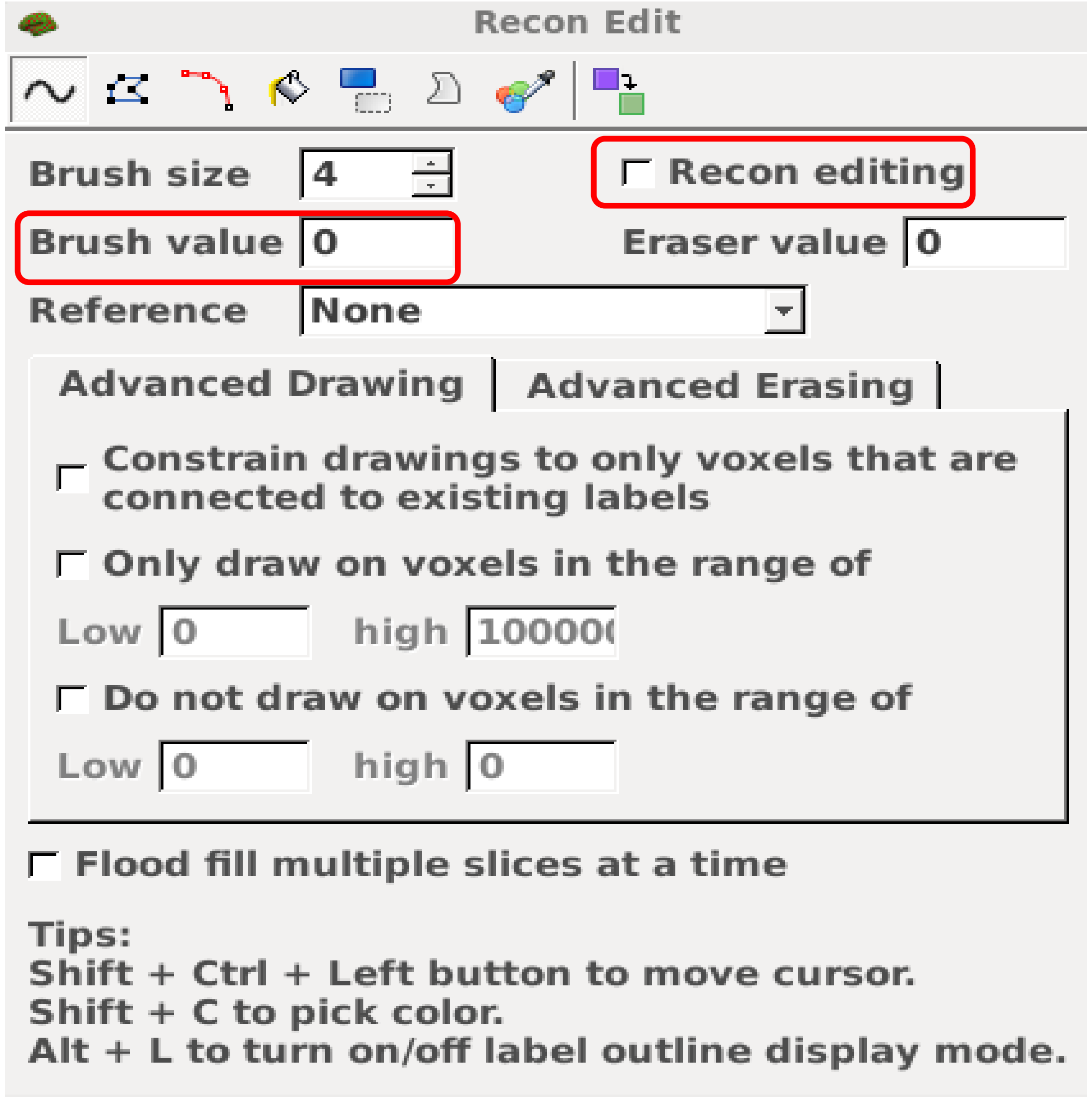
Low 5 high 250

☐ Flood fill multiple slices at a time

Tips:
Shift + Ctrl + Left button to move cursor.
Shift + C to pick color.
Alt + L to turn on/off label outline display mode.

Like in Skull Scaping, select the **Recon Edit** in the toolbar. But this time make sure the box "**Recon editing**" is checked and then click or hold the left mouse button to fill in the areas that need correcting.

You are also able to change the brush size if you want.



Brush size 4

☐ Recon editing

Brush value 0

Eraser value 0

Reference None

☐ Constrain drawings to only voxels that are connected to existing labels

☐ Only draw on voxels in the range of

Low 0 high 100000

☐ Do not draw on voxels in the range of

Low 0 high 0

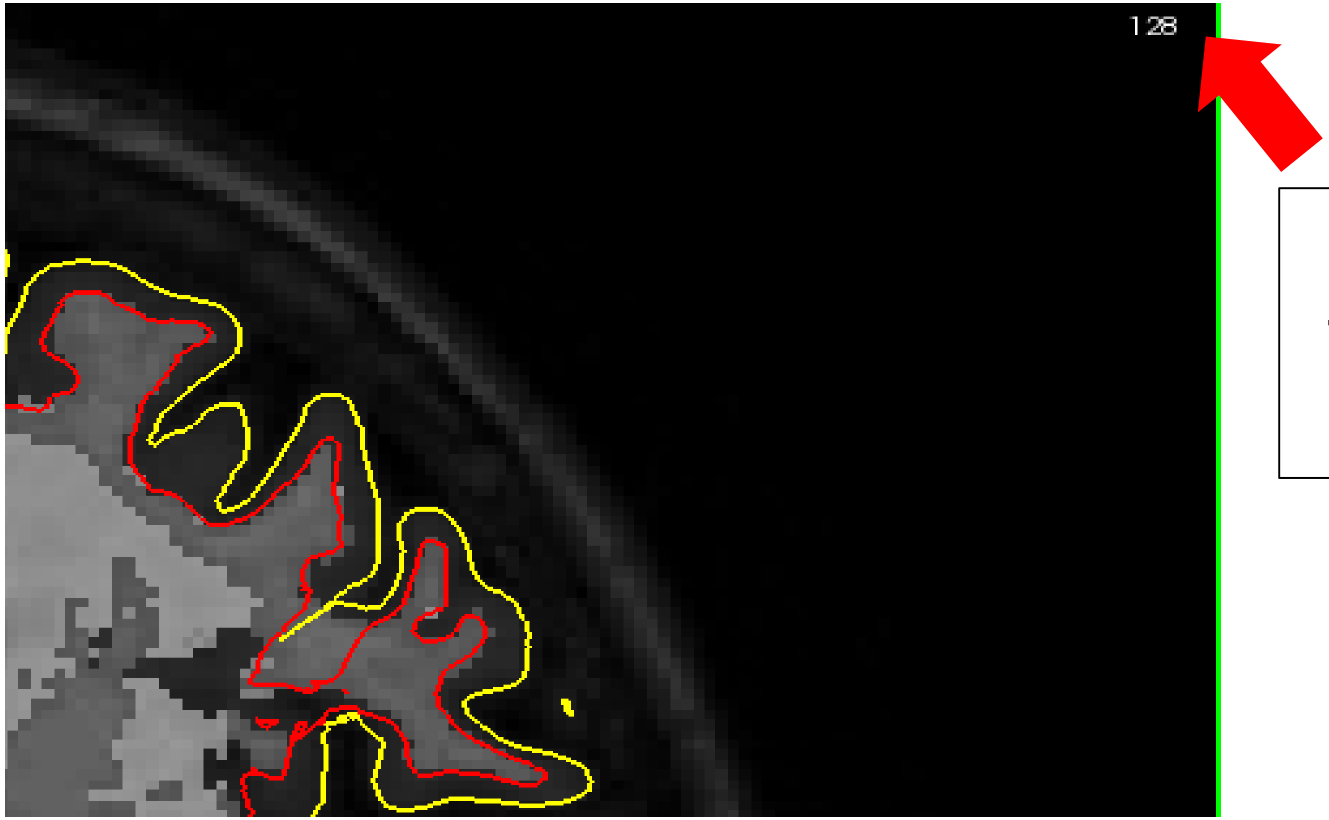
☐ Flood fill multiple slices at a time

Tips:
Shift + Ctrl + Left button to move cursor.
Shift + C to pick color.
Alt + L to turn on/off label outline display mode.

To erase, make sure the box "**Recon editing**" is unchecked and that the "**Brush value**" is set to 0 like in the Skull Scraping part. Then click or hold the left mouse button to erase areas you may have accidentally corrected that didn't need it.

Press Ctrl+z if wish to undo the previous step.

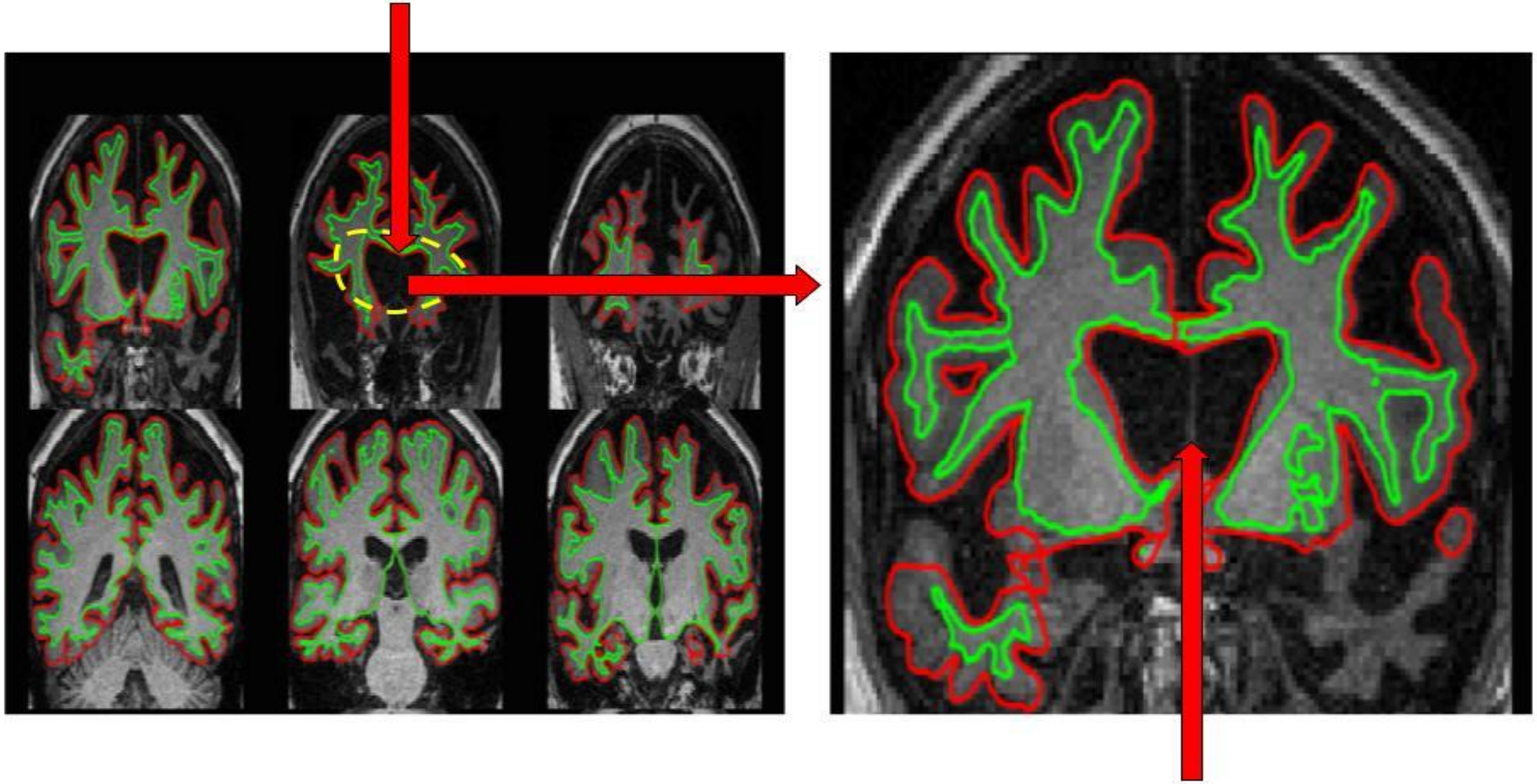
Using the up and down arrow keys, scroll to the end of one view (where you see the last/first slice developing) and from there scroll in the opposite direction, one slice at a time and see/correct the possible errors.



Your current frame is displayed in the top right corner of the display window.

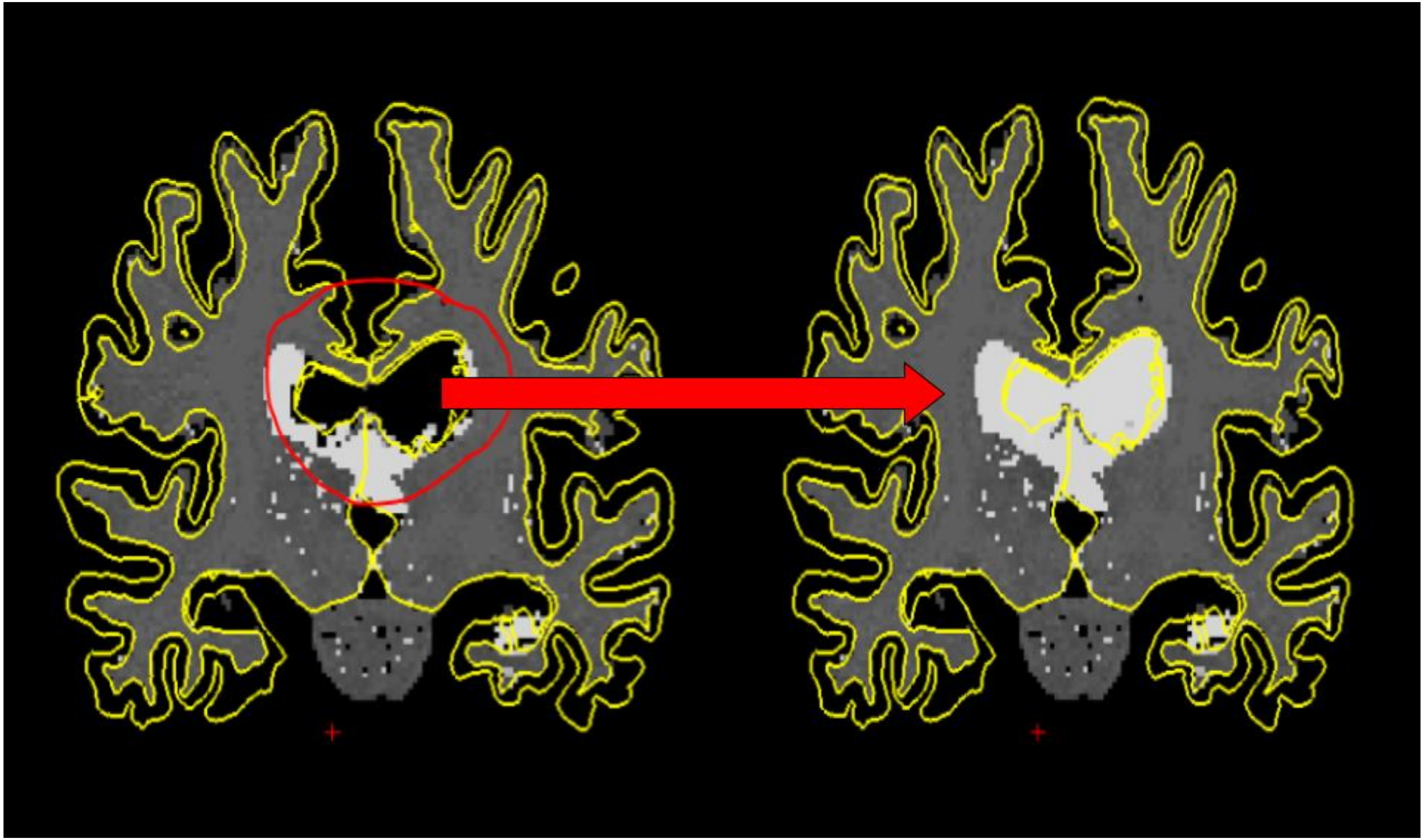
The following slides contain some examples on correcting the White Matter.

White Matter Corrections



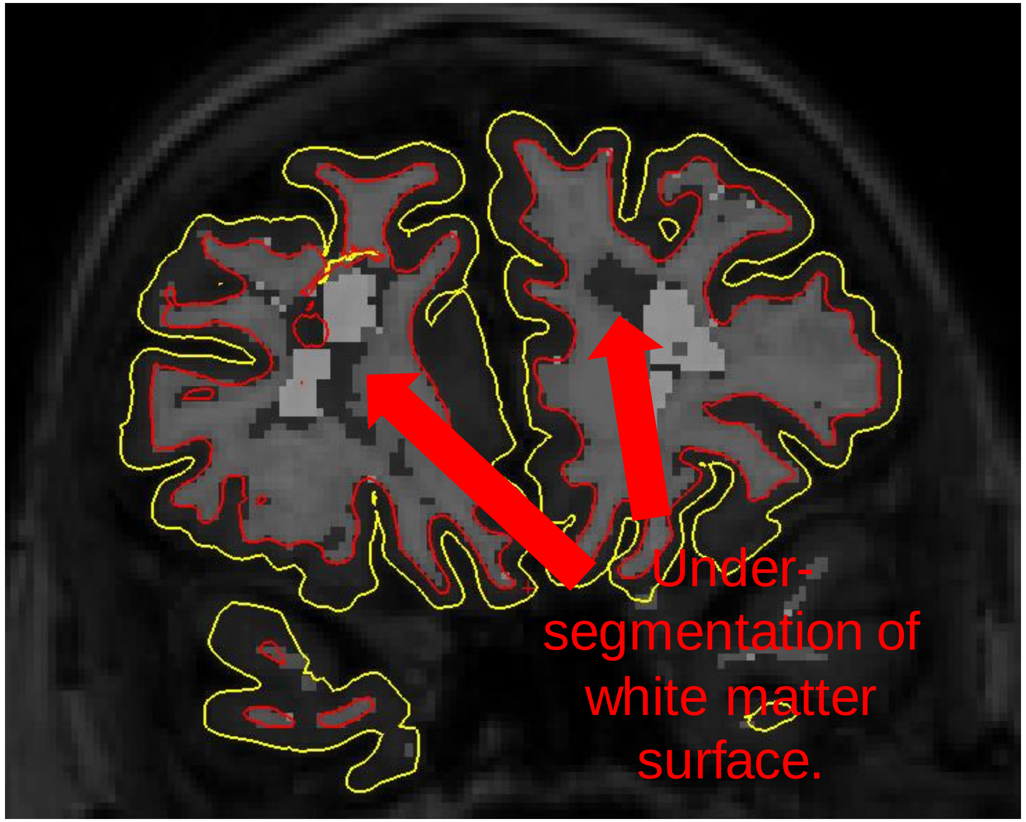
White matter segmentation error

Missing white matter



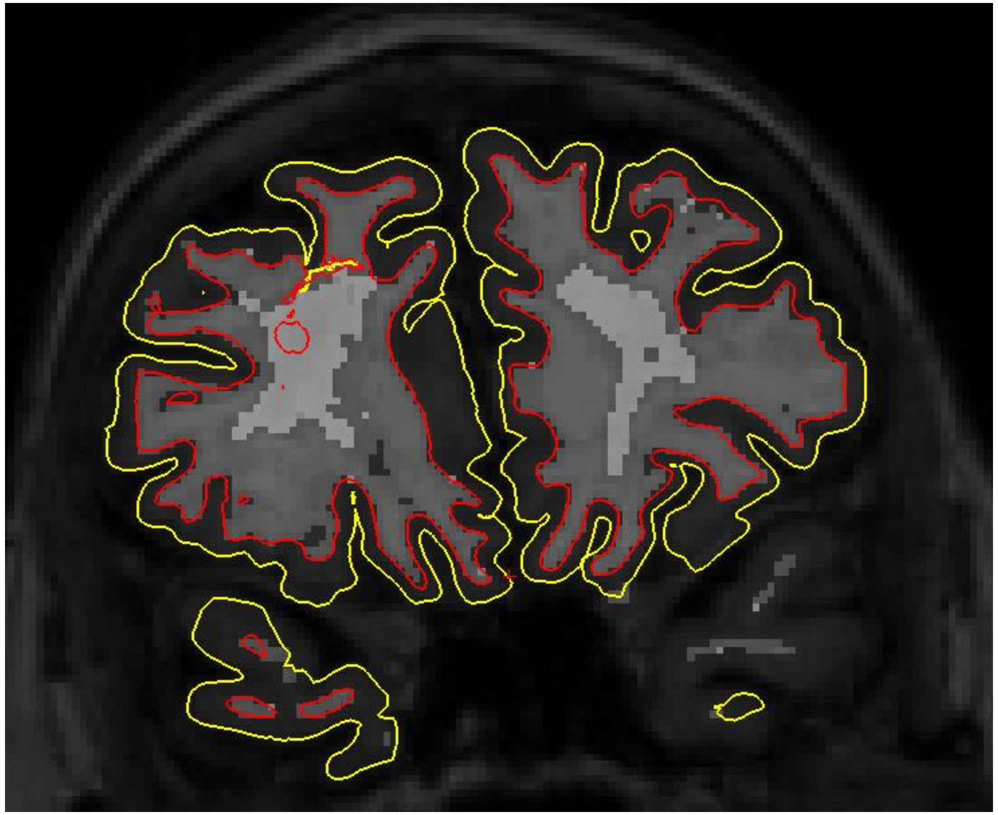
When correcting the White Matter, we usually want to fill in any spaces that are connected to large areas of already segmented white matter.

Before Corrections:



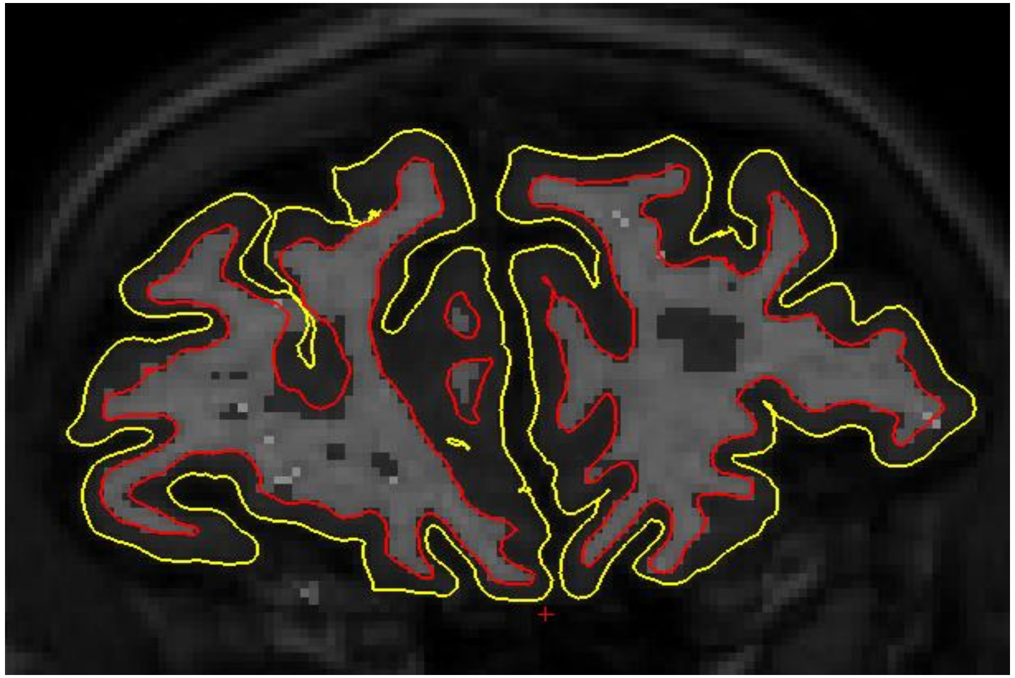
Under-segmentation of white matter surface.

After Corrections:

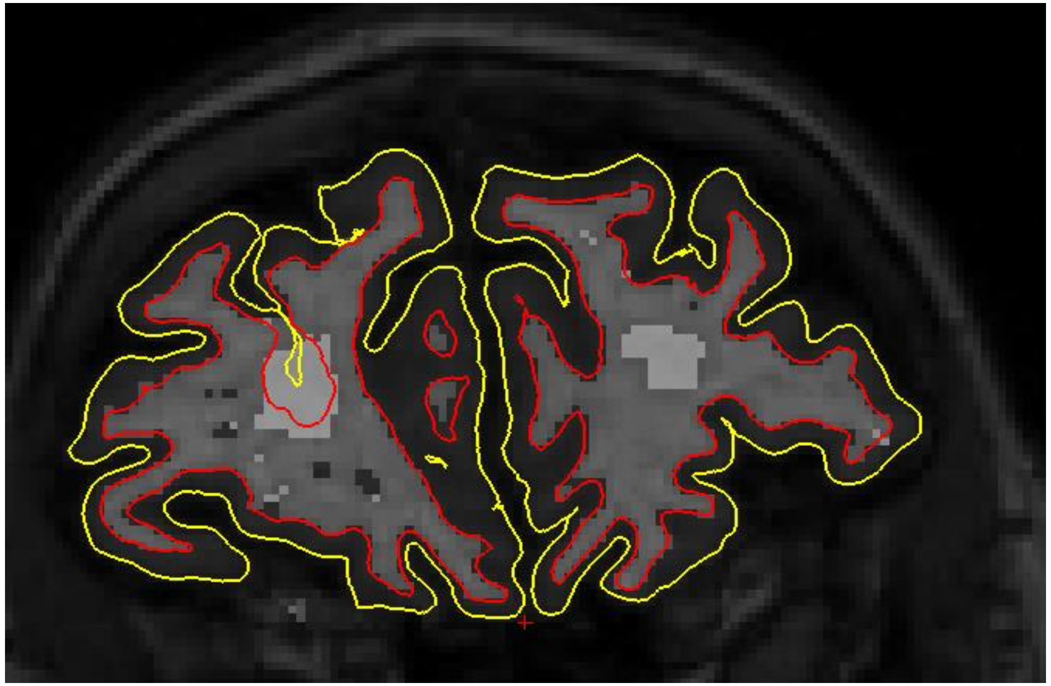


Sometimes, some areas will not have any white matter segmentation so it is your job to figure out if an area requires it. You can scroll through the frames to get a general idea of the structure as well as looking at the T1 volume to help in these cases. If you are ever unsure of anything, don't hesitate to ask someone for help!

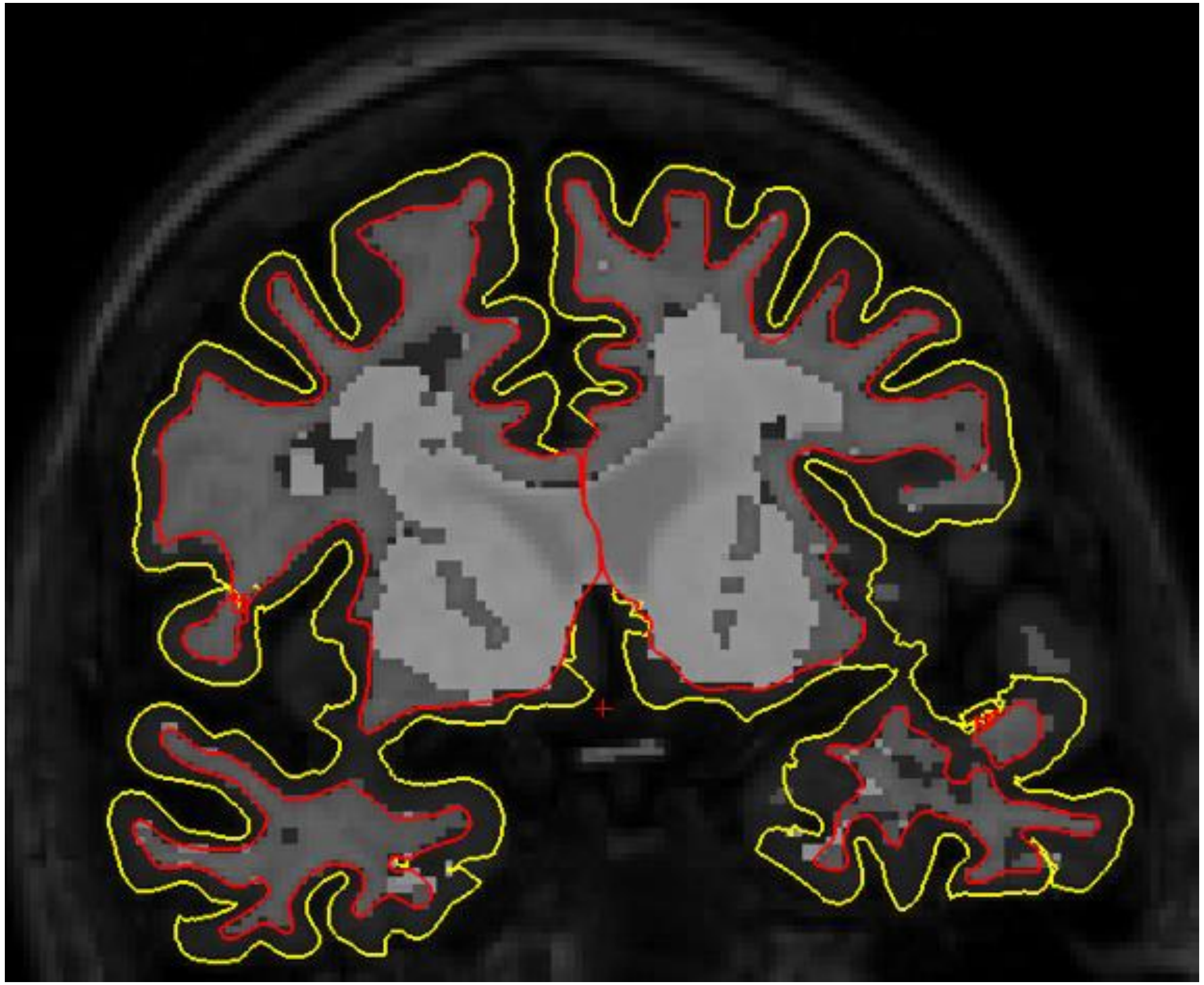
Before Corrections:



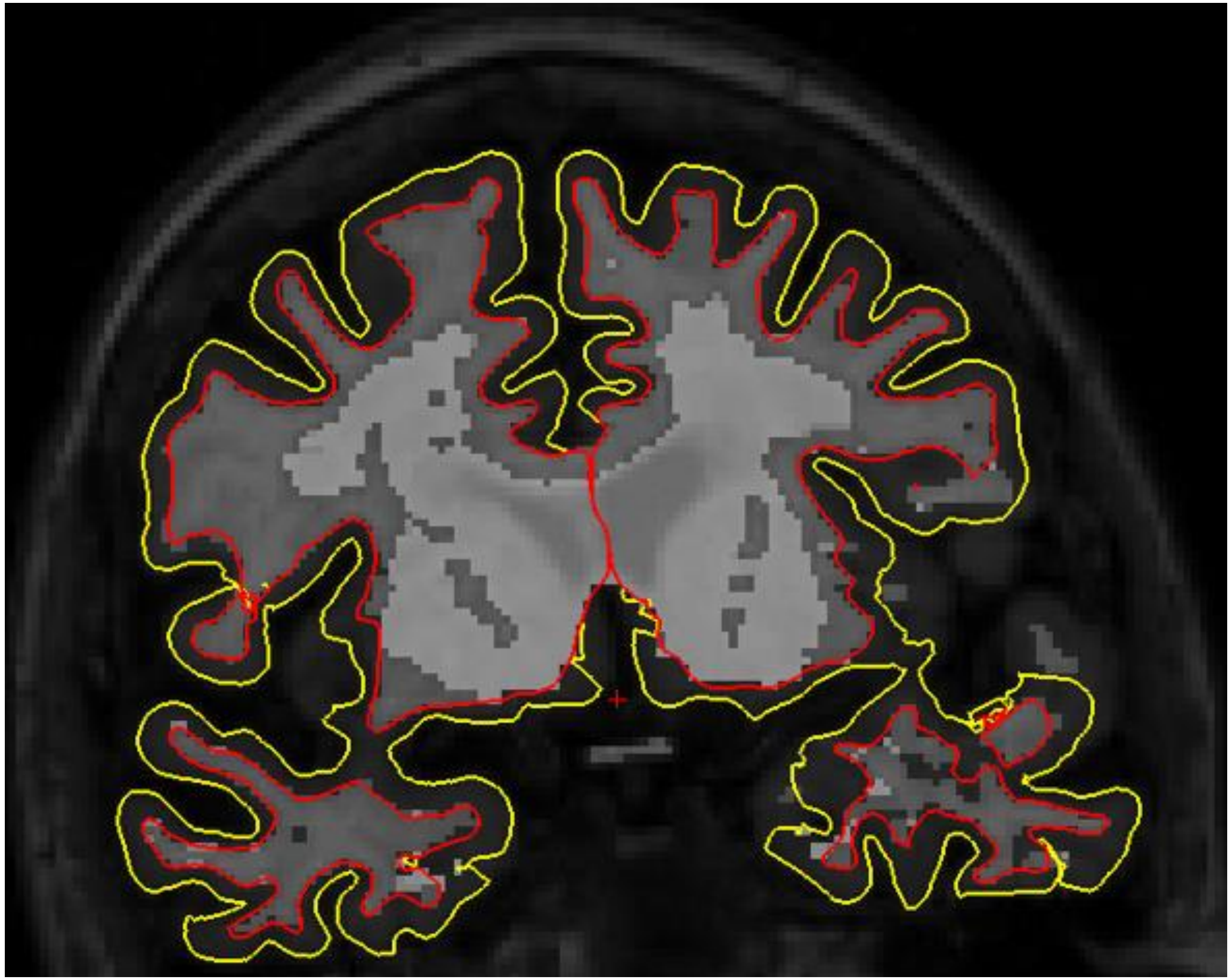
After Corrections:



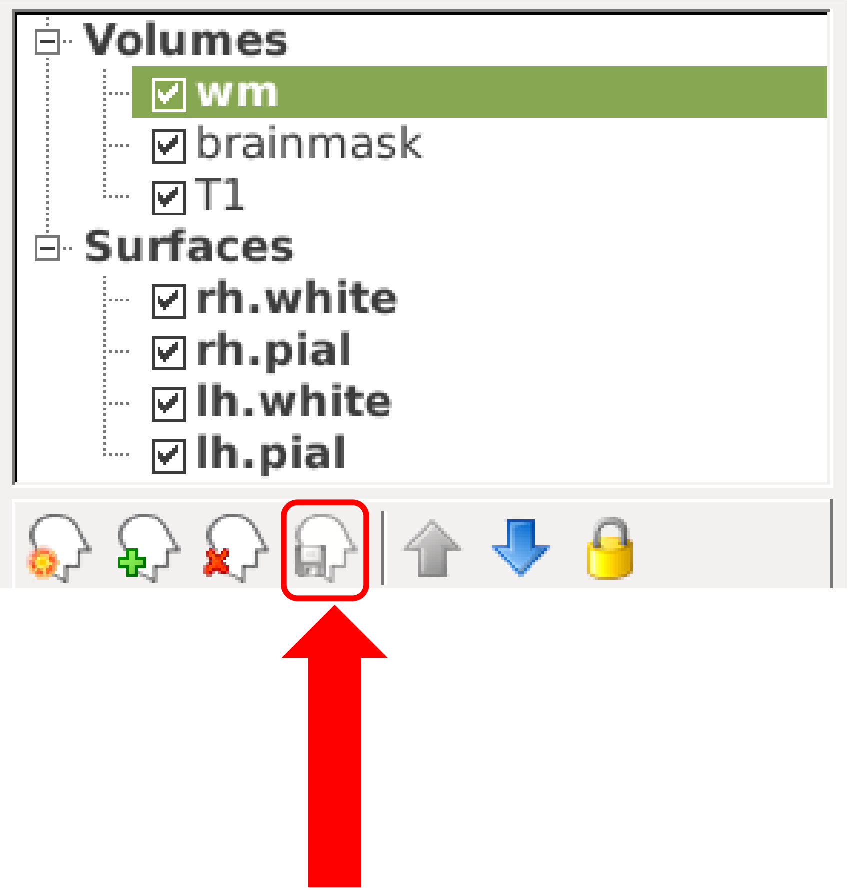
Before Corrections:



After Corrections:



At last, remember saving your wm volume through and at the end of the correction.



Save Volume

For white matter editing, it is not needed to have T1, brainmask, and surface files opened. We can use these for reference viewing with the white matter but for white matter correction, we need not open them in freeview while we correct white matter. This reduces confusion and also lowers chances of mistakes.

Brainmask Volume Corrections

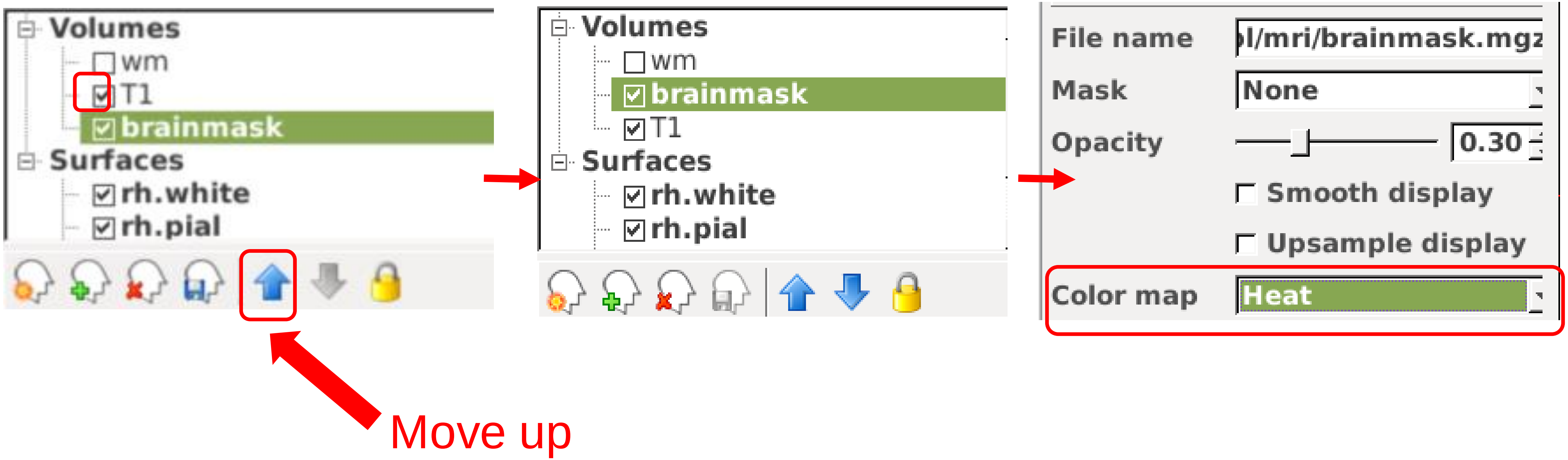
'Brainmask' corrections can be applied to:

Under-segmentation due to 'brainmask' volume error(s) (if this error is present, it must be corrected first before seeding/skull stripping).

White Matter Corrections

Note that whenever we are making corrections, the volume that we are working on should be highlighted. The only volumes that we actually edit are the 'wm' and the 'brainmask'. The 'T1' will never be edited, it is just there for reference.

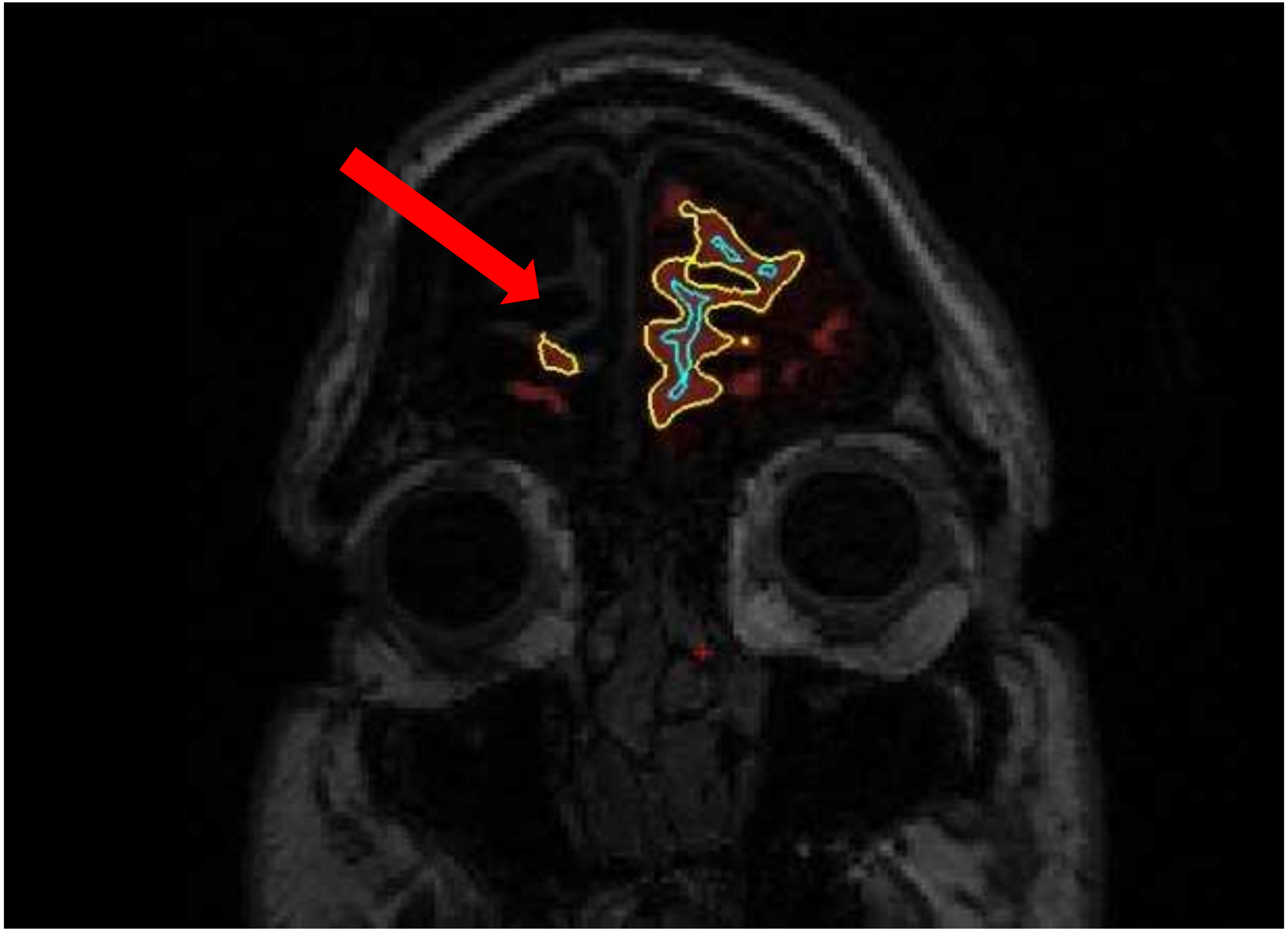
Load the subject volumes and surfaces in FreeView. These types of errors require editing the 'brainmask.mgz' volume. To have a better view of the volume, uncheck the box of "**wm**", move "**brainmask**" up if it is not already above "**T1**". Then, change its **Color map** to "**Heat**" (remember to recheck "**wm**" and switch back to "**Gray scale**" after finishing the skull stripping).



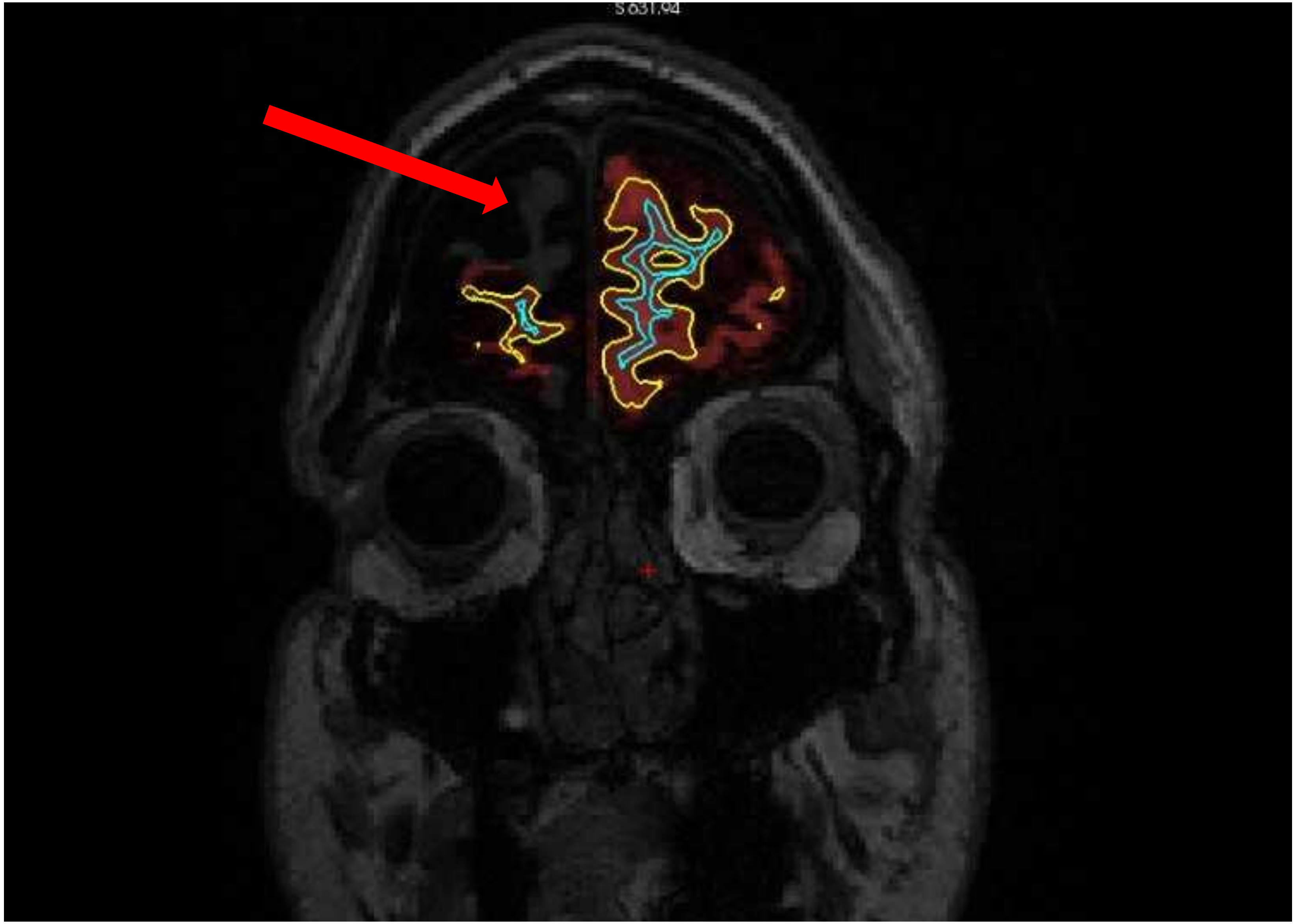
File name: l/mri/brainmask.mgz
Mask: None
Opacity: 0.30
☐ Smooth display
☐ Upsample display
Color map: Heat

Look at the viewing planes. Subjects that have 'brainmask' volume errors will show insufficient coverage of brain matter. The "Heat Map" function will show regions of brain tissue not covered by the colour map if there is a 'brainmask' volume error. This image is an example of 'brainmask' under-segmentation error that requires voxel cloning from the T1 volume to correct. Notice that the "Heat Map" of the 'brainmask' volume has failed to sufficiently cover the all the brain tissue, leaving one hemisphere of the brain unsegmented in this region (i.e. it is not red).

See the following slides for more examples.



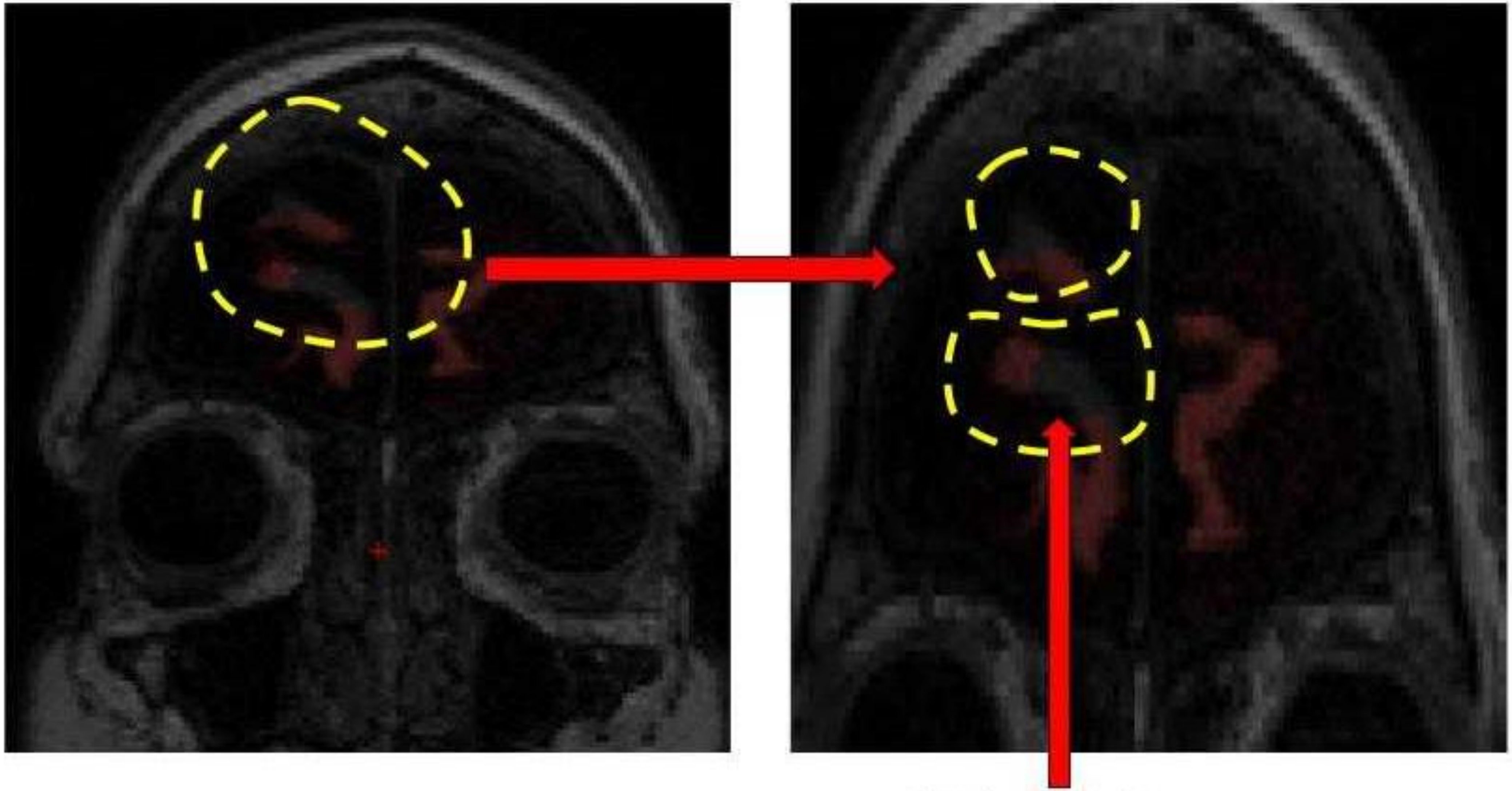
'Brainmask' corrections



Brainmask under-segmentation error requiring voxel cloning.

Brainmask under-segmentation error requiring voxel cloning.

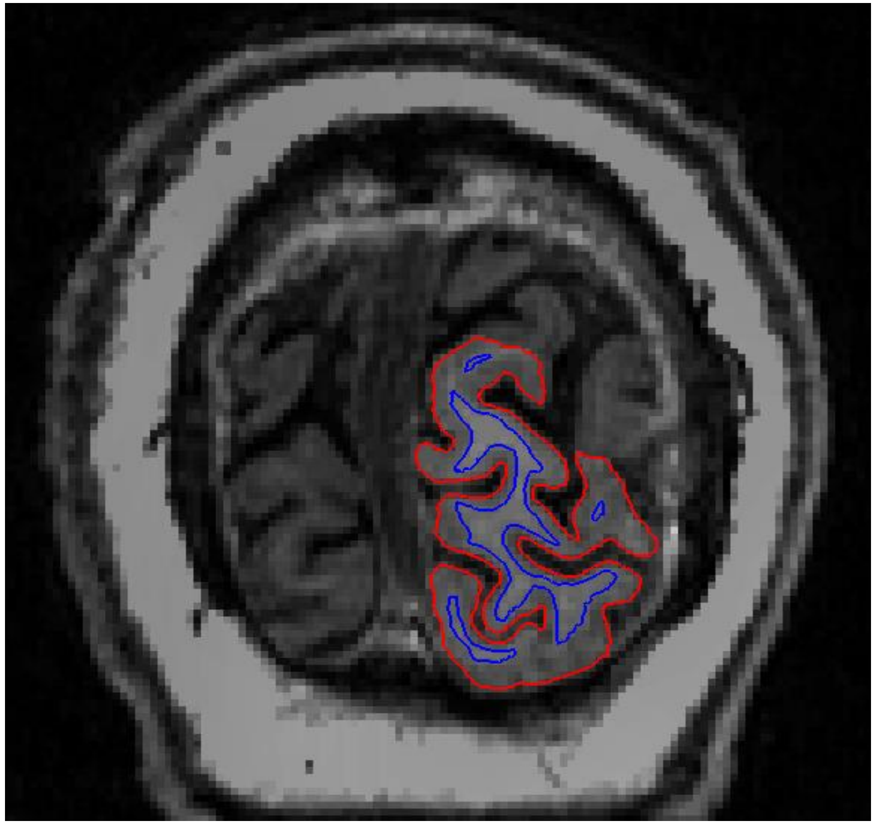
'Brainmask' corrections



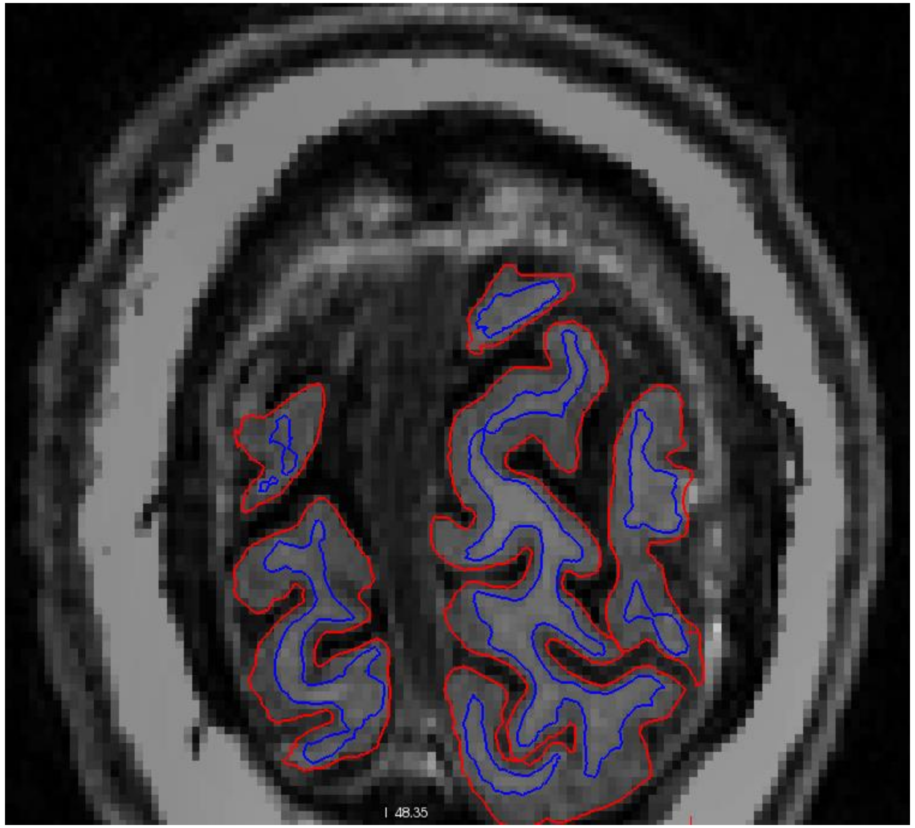
Missing brain tissue

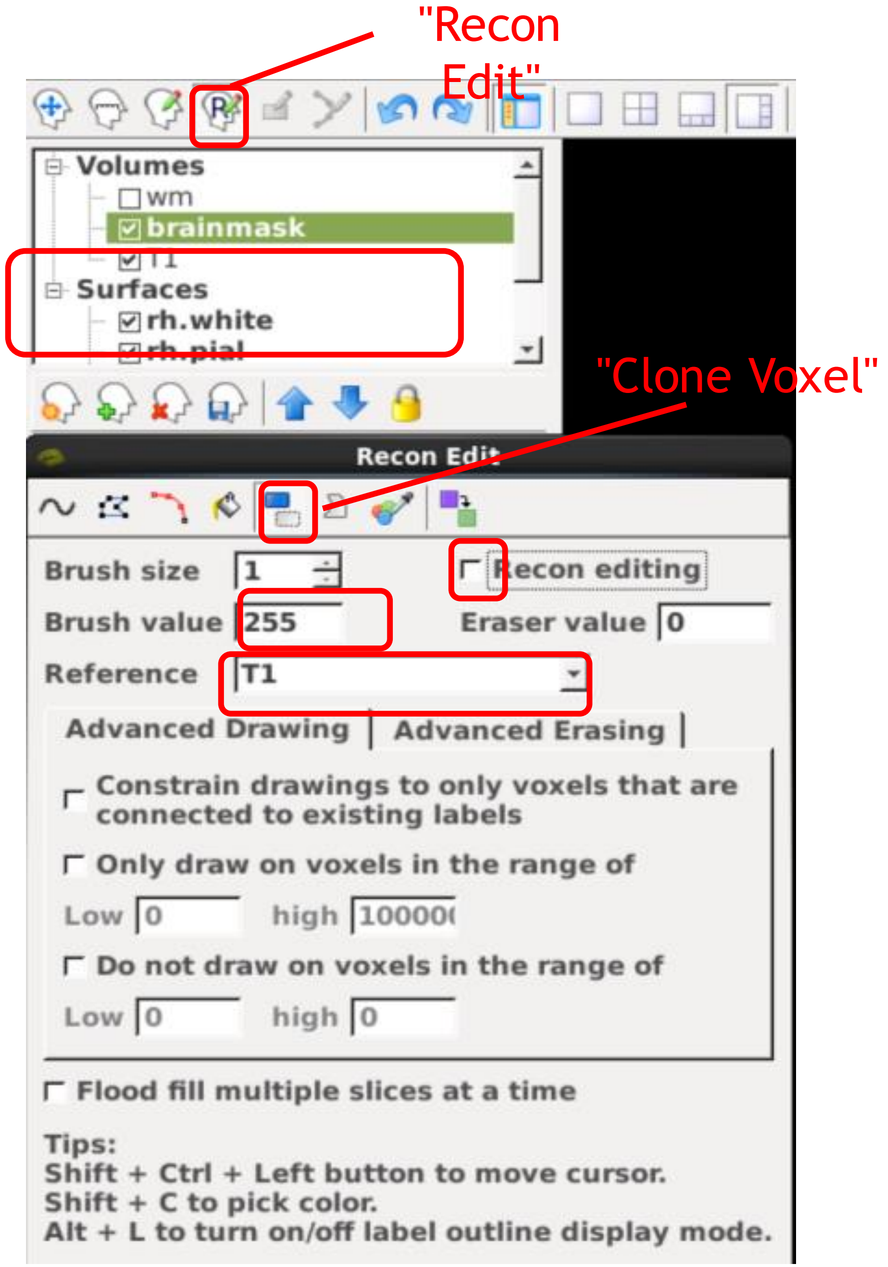
Brainmask Volume Errors: Correcting 'brainmask' under-segmentation errors by cloning voxels from the T1 volume

Before Corrections:



After Corrections:





Volumes
☐ wm
☑ brainmask
☑ T1
Surfaces
☑ rh.white
☑ rh.pial

Brush size 1
☐ Recon editing
Brush value 255
Eraser value 0
Reference T1

Advanced Drawing | Advanced Erasing

☐ Constrain drawings to only voxels that are connected to existing labels
☐ Only draw on voxels in the range of
Low 0 high 10000
☐ Do not draw on voxels in the range of
Low 0 high 0

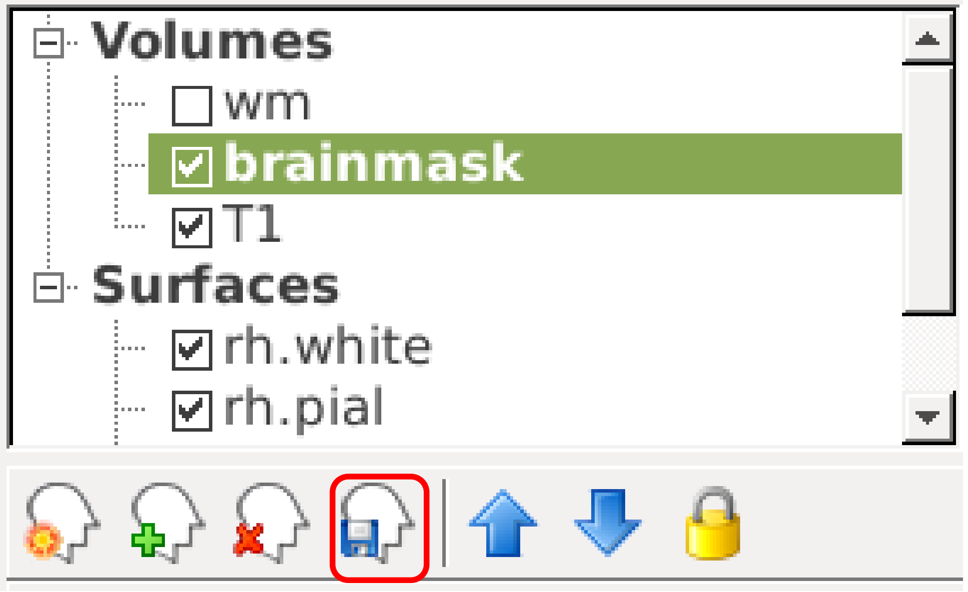
☐ Flood fill multiple slices at a time

Tips:
Shift + Ctrl + Left button to move cursor.
Shift + C to pick color.
Alt + L to turn on/off label outline display mode.

To edit 'brainmask' under-segmentation, select "**Recon Edit**". In the pop-up Recon Edit window, ensure that you have "**Clone voxel**" selected. Uncheck the "**Recon editing**" option, change the "**Brush value**" to **255**, and set the "**Reference**" to **T1.** We are ready to fill in the missing voxels in the 'brainmask' volume.

Click on regions of brain tissue not covered by the Heat Map.

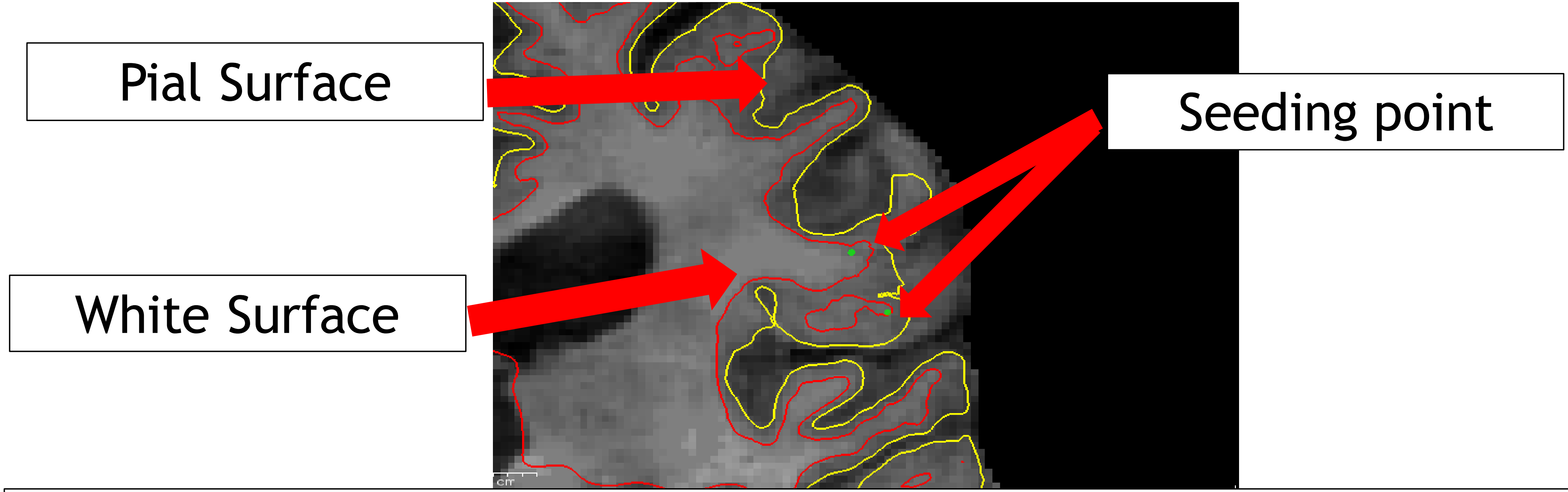
Finally, remember to save your brainmask volume constantly and when you have finished. You don't want to do the whole process again just because the program crashes before you could have saved!



Save Volume

Cortical Seeding

Cortical seeding is required when we find an area is under segmented, which means the pial surface fails to include some of the brain tissues.

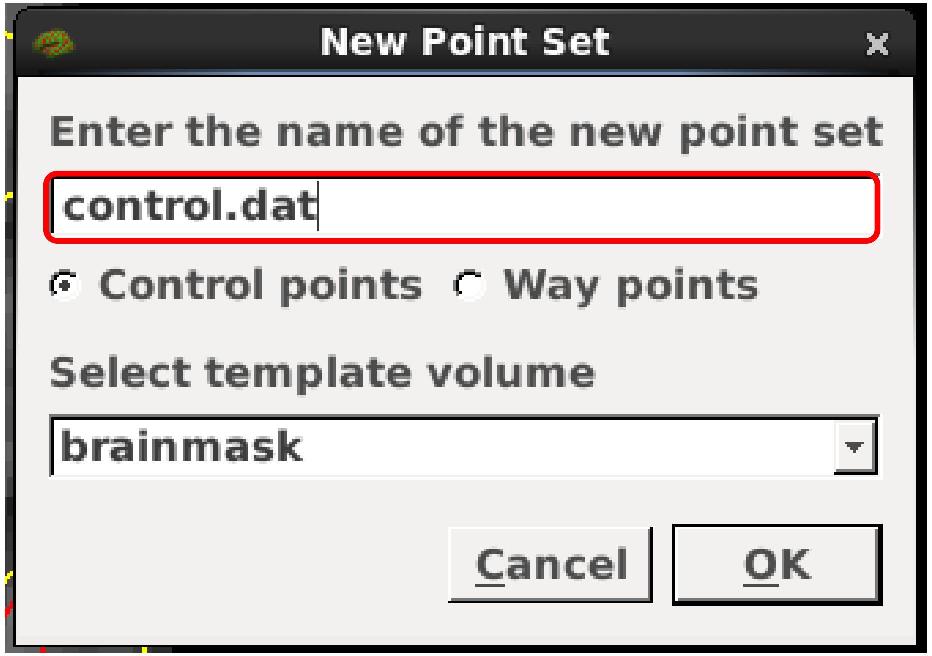


Pial Surface

Seeding point

White Surface

What seeding is doing is that it tells the processing program to "push out" the white surface, and eventually "push" the pial surface to include the desired brain tissue.



New Point Set

Enter the name of the new point set

control.dat

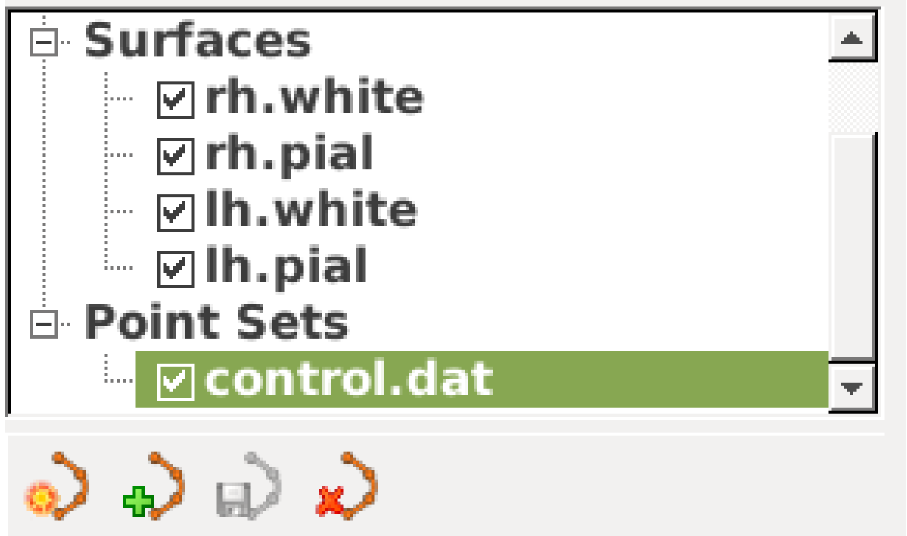
● Control points ○ Way points

Select template volume

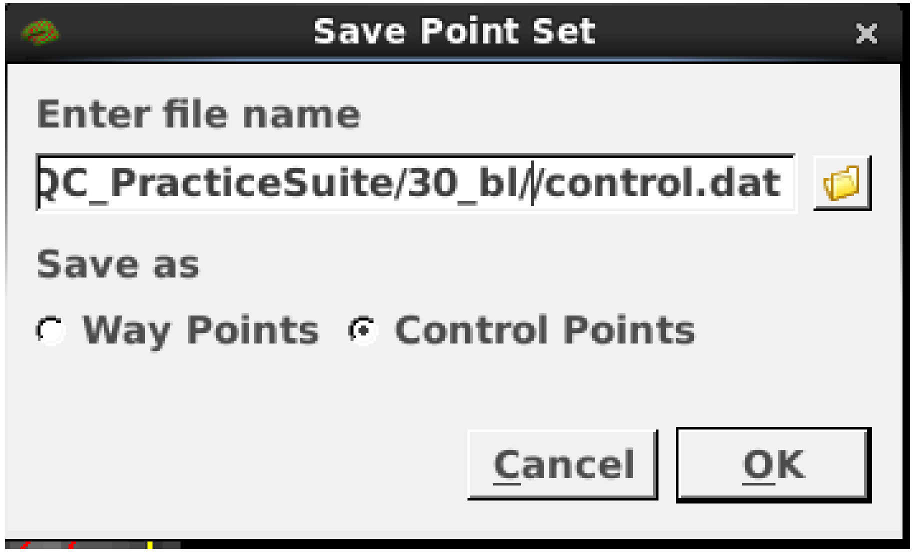
brainmask

First, click "**File**" and select "**New Point Set**", so this window pops up.

Name the point set as "**control.dat**" and make sure that the "**Control points**" option is selected. Finally, set its template volume to be "**brainmask**", then press "**OK**" to add it.



Confirm that the "**control.dat**" has appeared under the "**Point Sets**" column on the side bar.



Enter file name

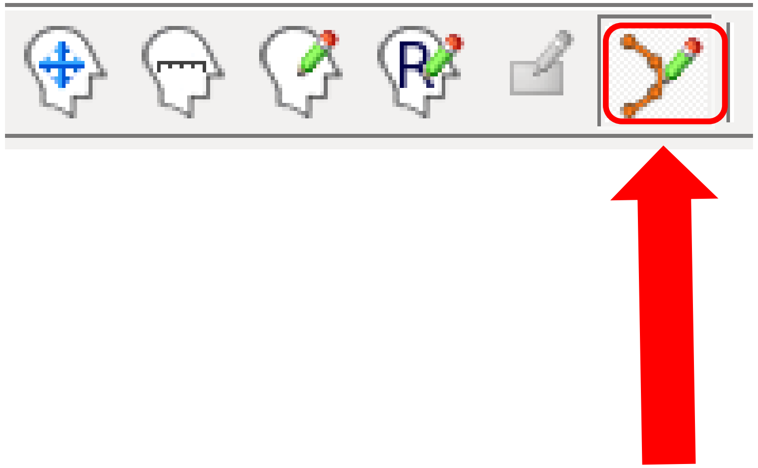
QC_PracticeSuite/30_bl//control.dat

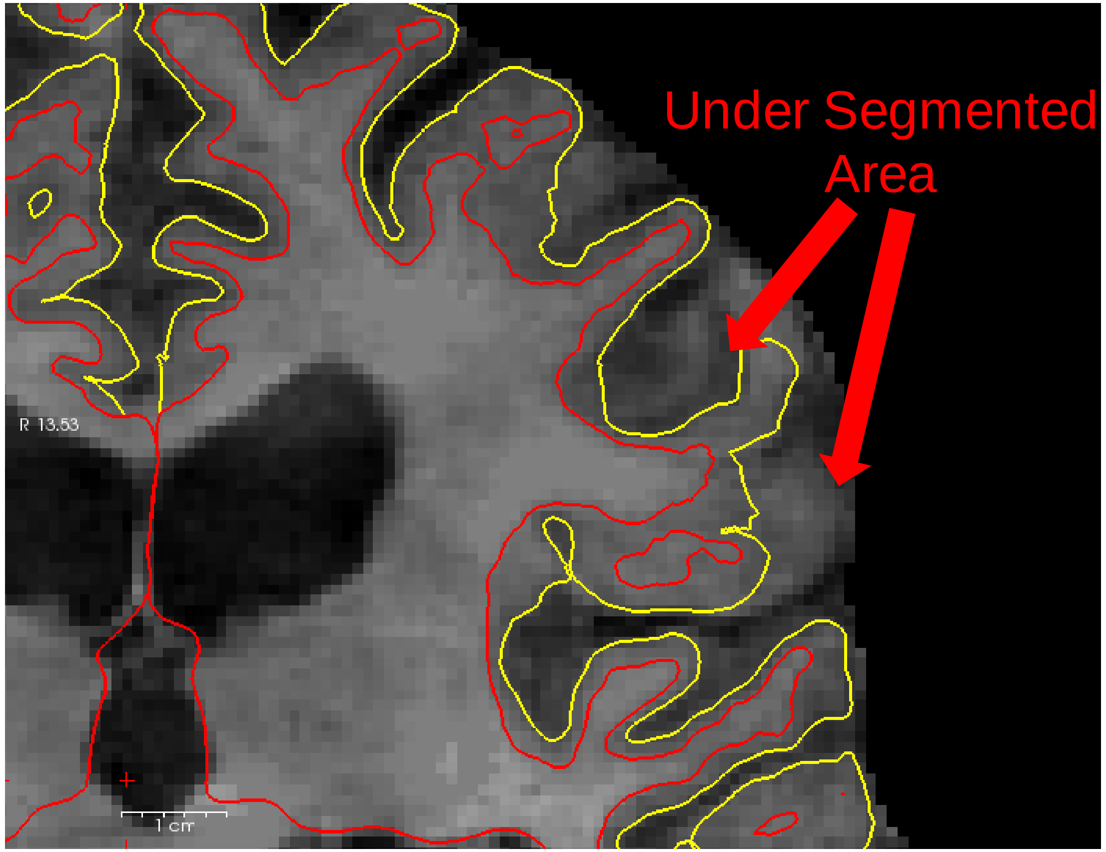
Save as

○ Way Points ● Control Points

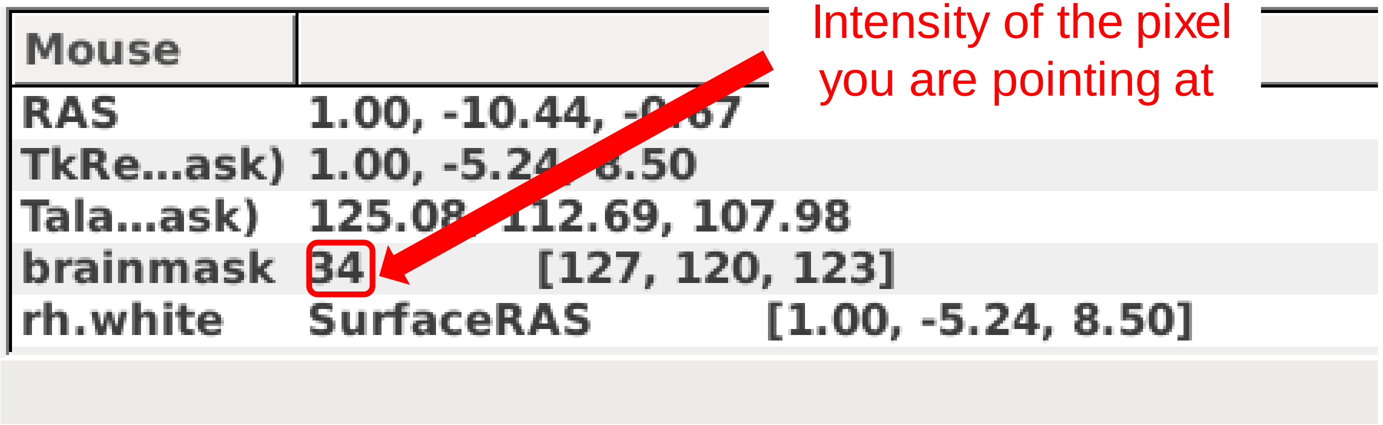
Now go to "**File**" and click on "**Save Point Set As**", choose $targetID/tmp/control.dat to save Control Points.

After checking that the "**brainmask**" volume is selected on the side bar, and that "**Point Set Edit"** is selected on the toolbar, identify the under segmented area and left click to place a seeding point. To remove a seed that you have placed, you can press shift on your keyboard and then click the point again.





Watch out for the intensity, which is shown in the lower right on the screen of the pixel you are putting a seed at, it should always be from **80 to 110**, both ends **inclusive**.



Mouse		
RAS	1.00, -10.44, -0.67	
TkRe...ask)	1.00, -5.24, 8.50	
Tala...ask)	125.08, 112.69, 107.98	
brainmask	34	[127, 120, 123]
rh.white	SurfaceRAS	[1.00, -5.24, 8.50]

Intensity of the pixel you are pointing at

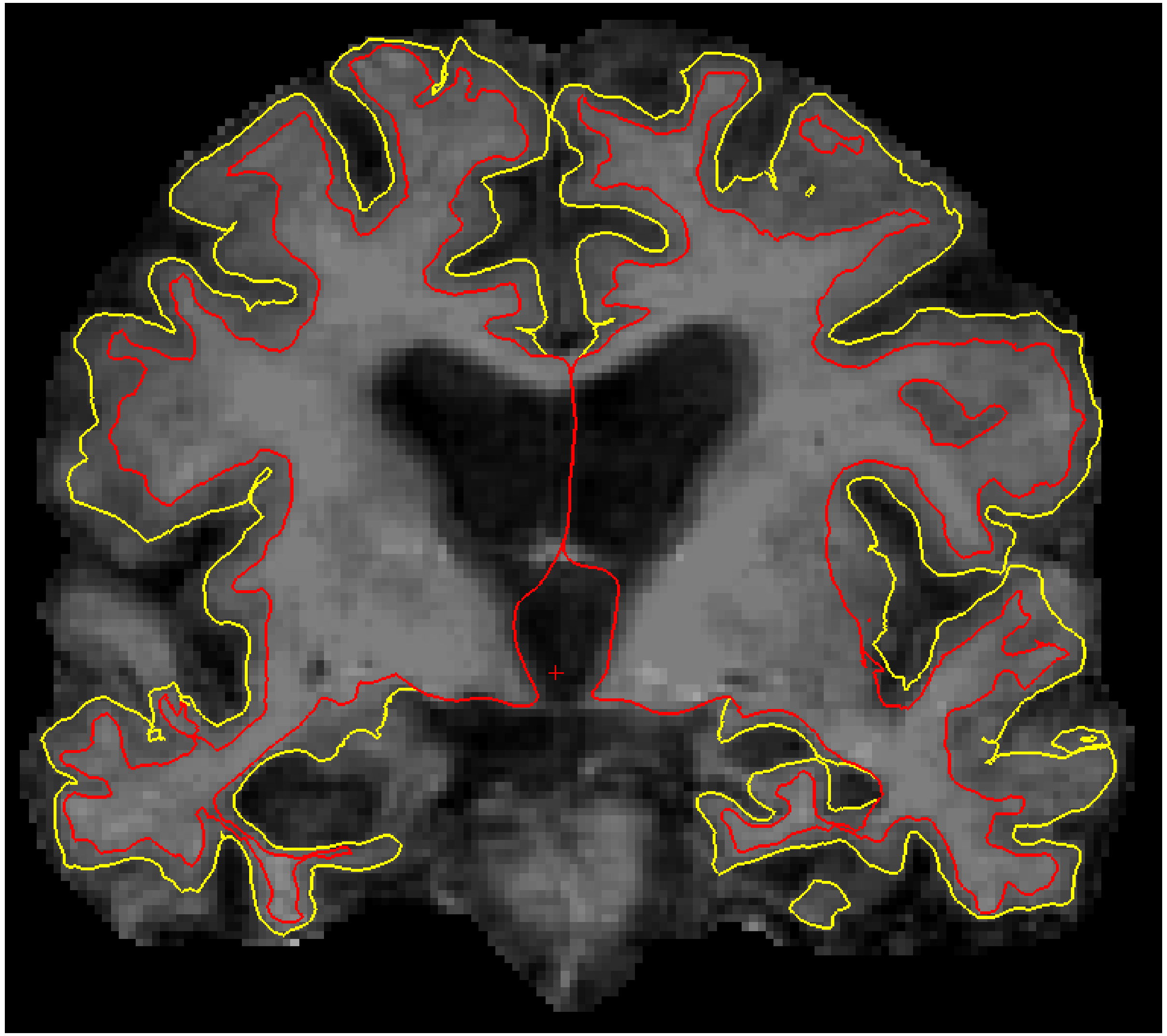
Also, try to put the seed within the white matter segmentation if possible. In some cases, you can only seed outside the white matter boundary since there is no segmentation at all. That is ok to do, but only seeds at the pixel within the intensity range 80 to 110, with both ends inclusive.

Again, remember to save from time to time and after you have inspected through the entire volume.

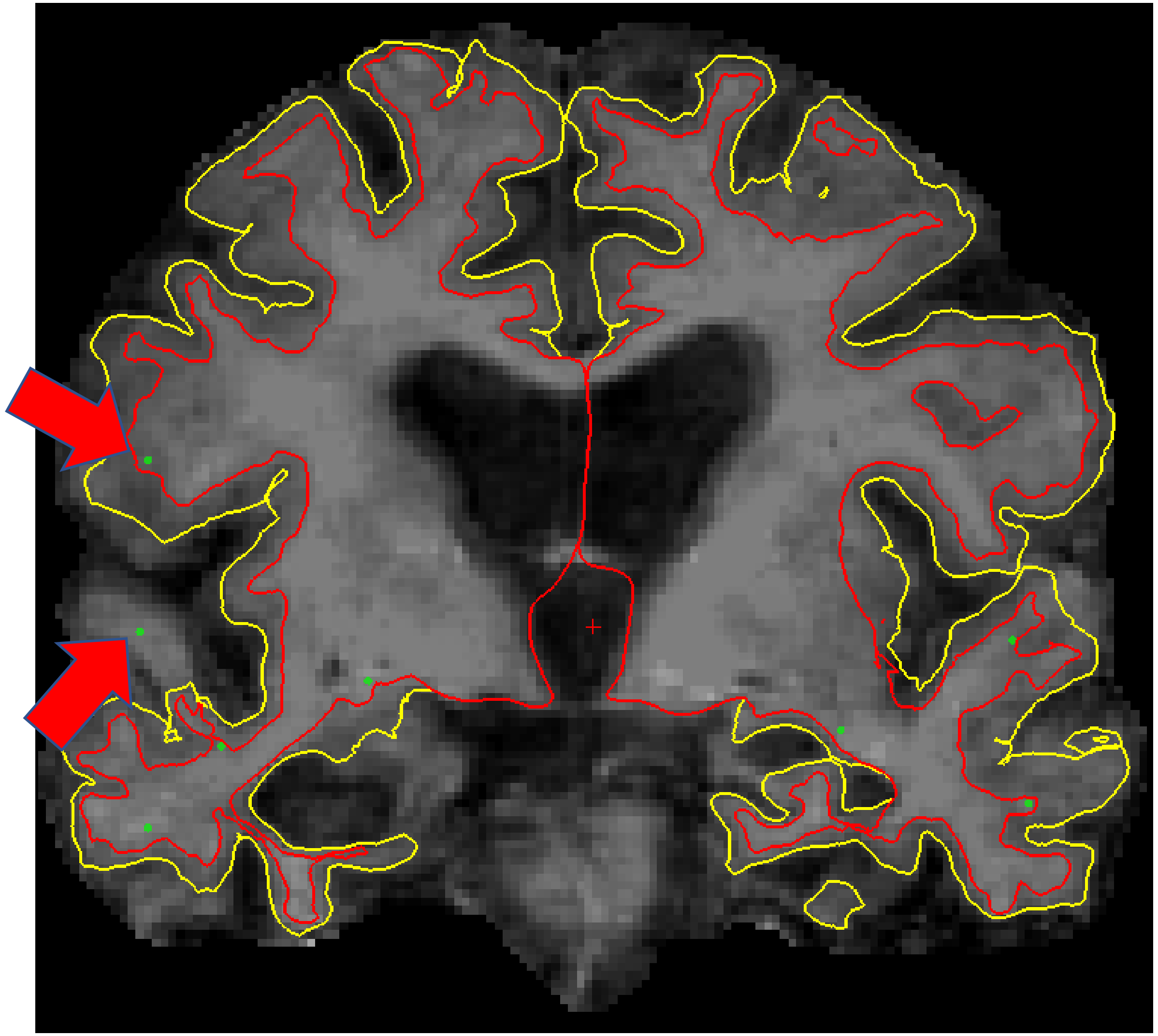
Save Point Set

The following slides contain examples on Cortical Seeding.

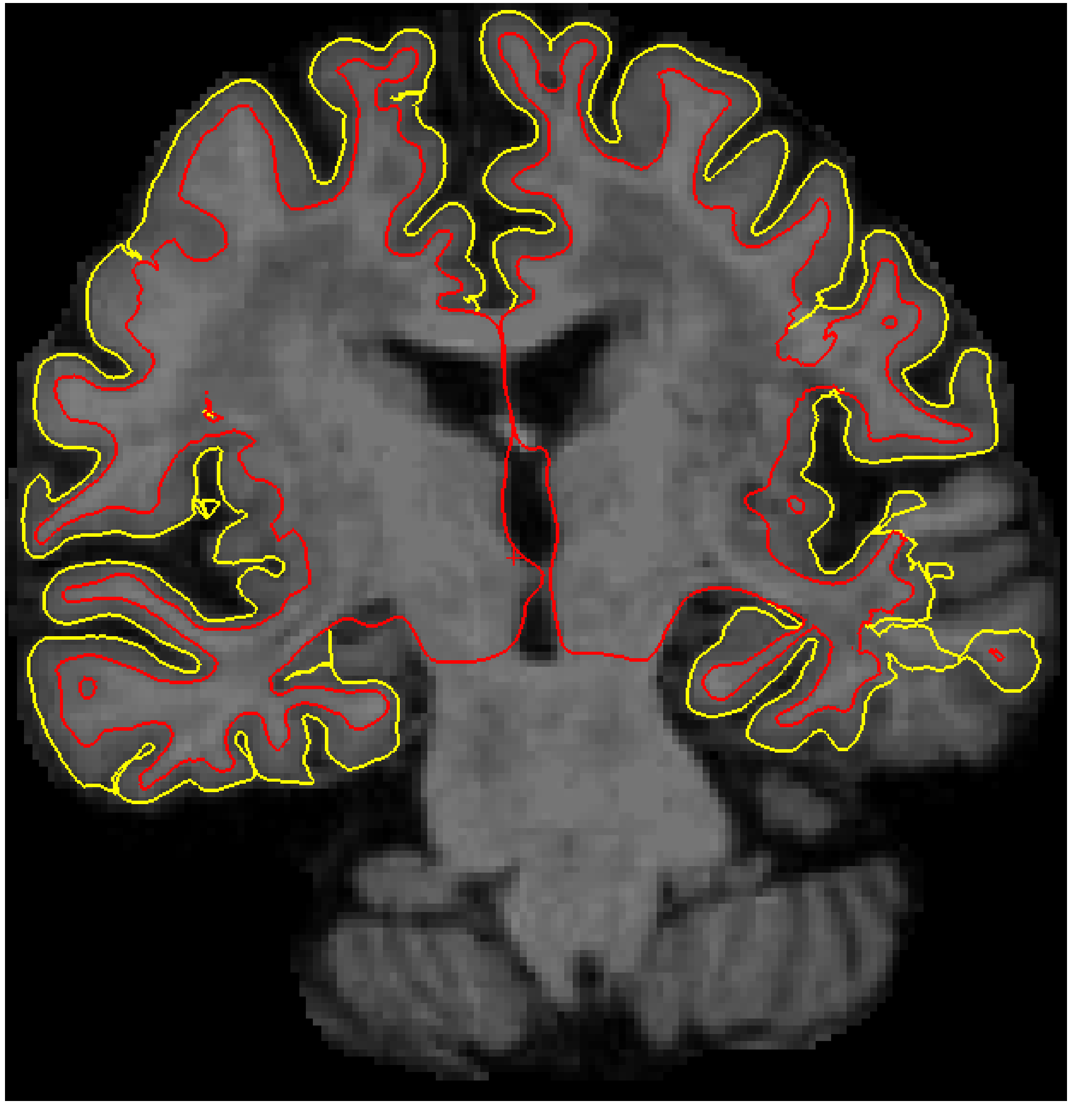
Before Adding Seeding Points:



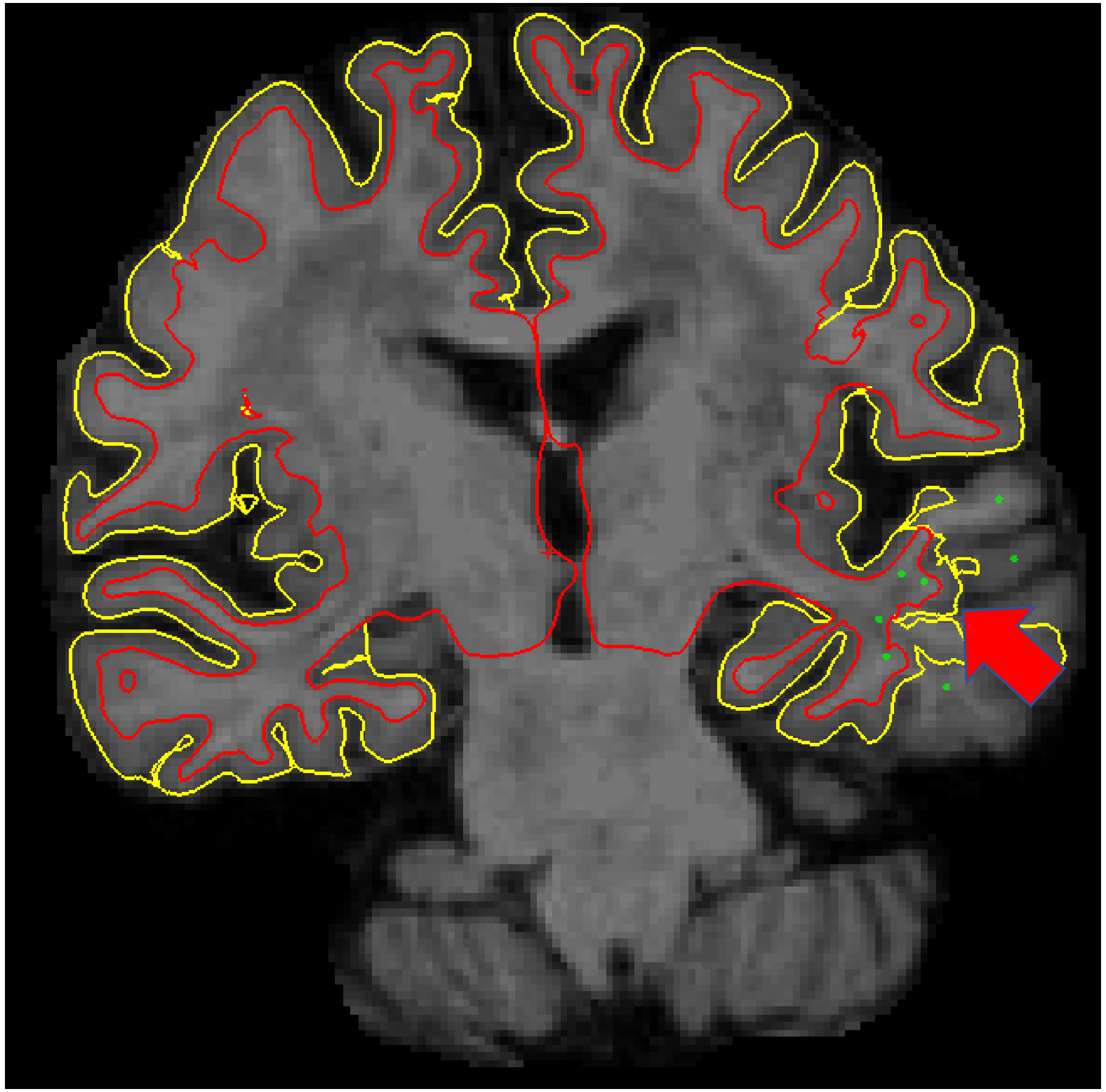
After Adding Seeding Points:



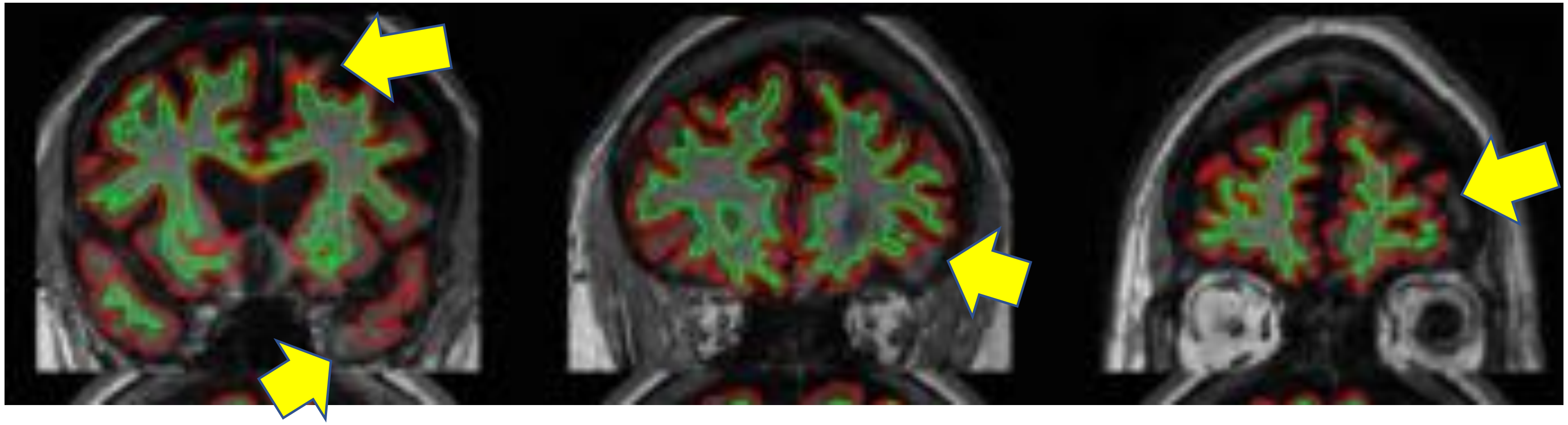
Before Adding Seeding Points:



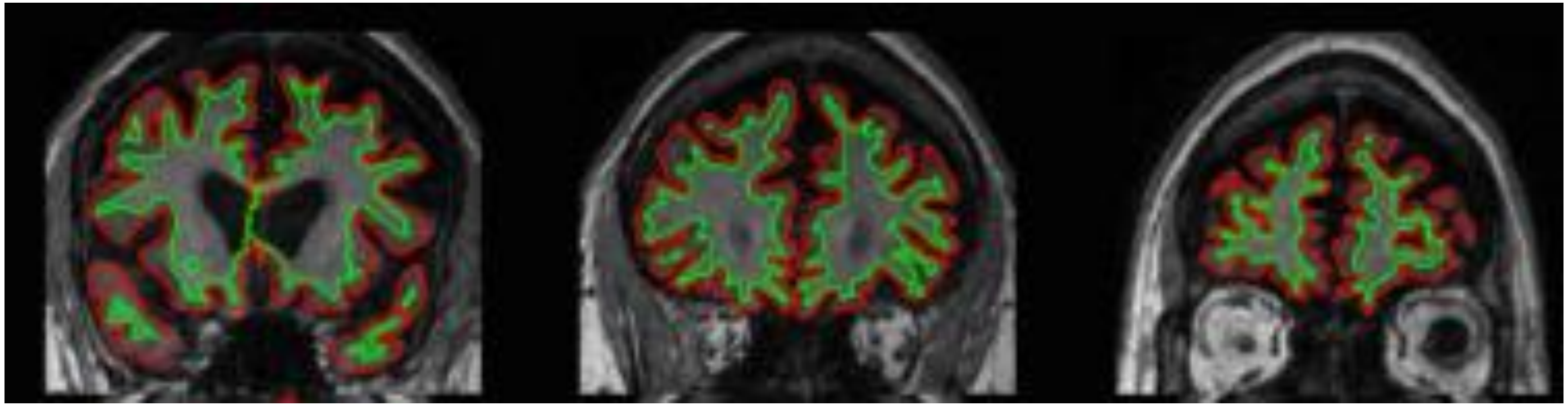
After Adding Seeding Points:



Before Correction

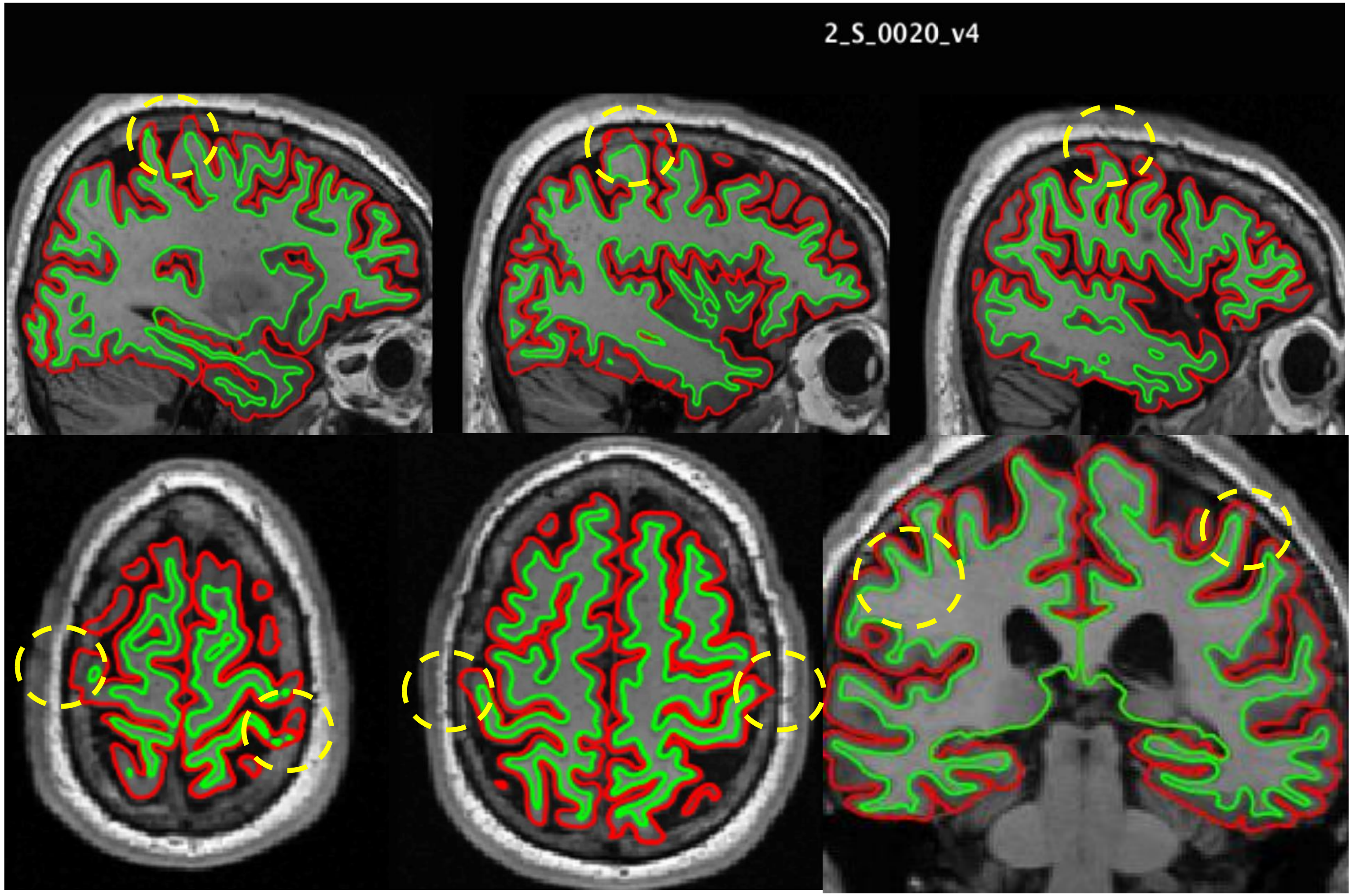


After Correction

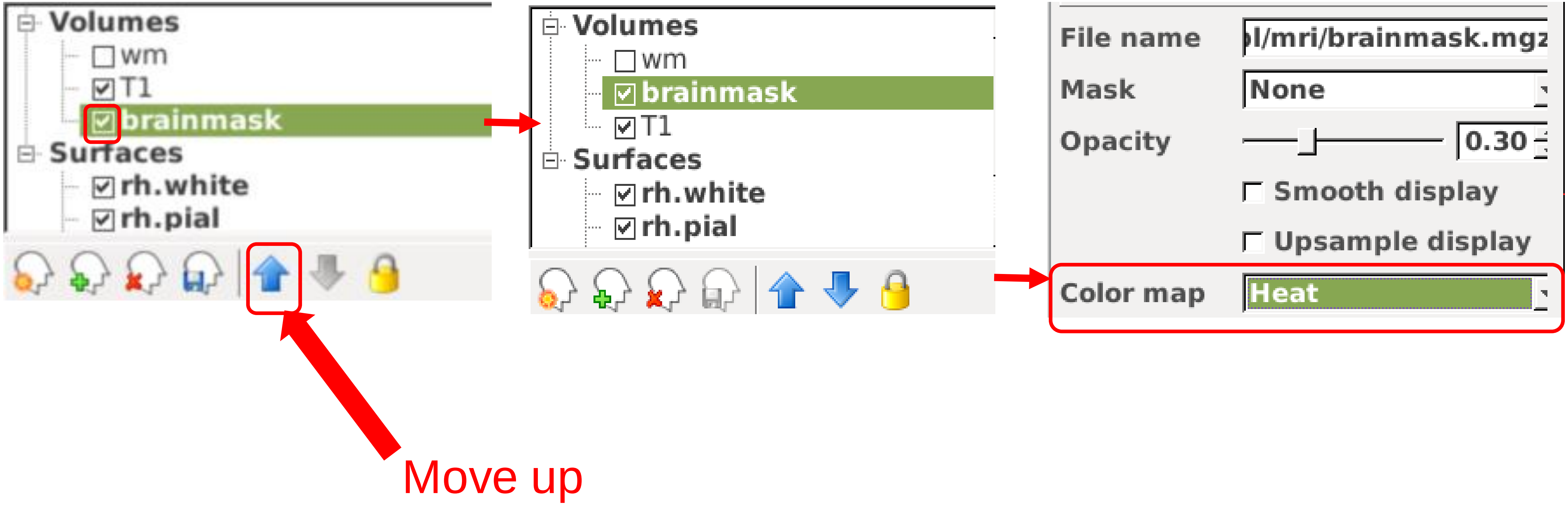


Skull Stripping

Correcting over-segmentation (in yellow circles) of the pial surface with freehand voxel erasing (skull stripping)



Skull stripping errors require editing the 'brainmask.mgz' volume. To have a better view of the volume, uncheck the box of "**wm**", move "**brainmask**" up if it is not already above "**T1**". Then, change its **Color map** to "**Heat**" (remember to recheck "**wm**" and switch back to "**Gray scale**" after finishing the Skull stripping).



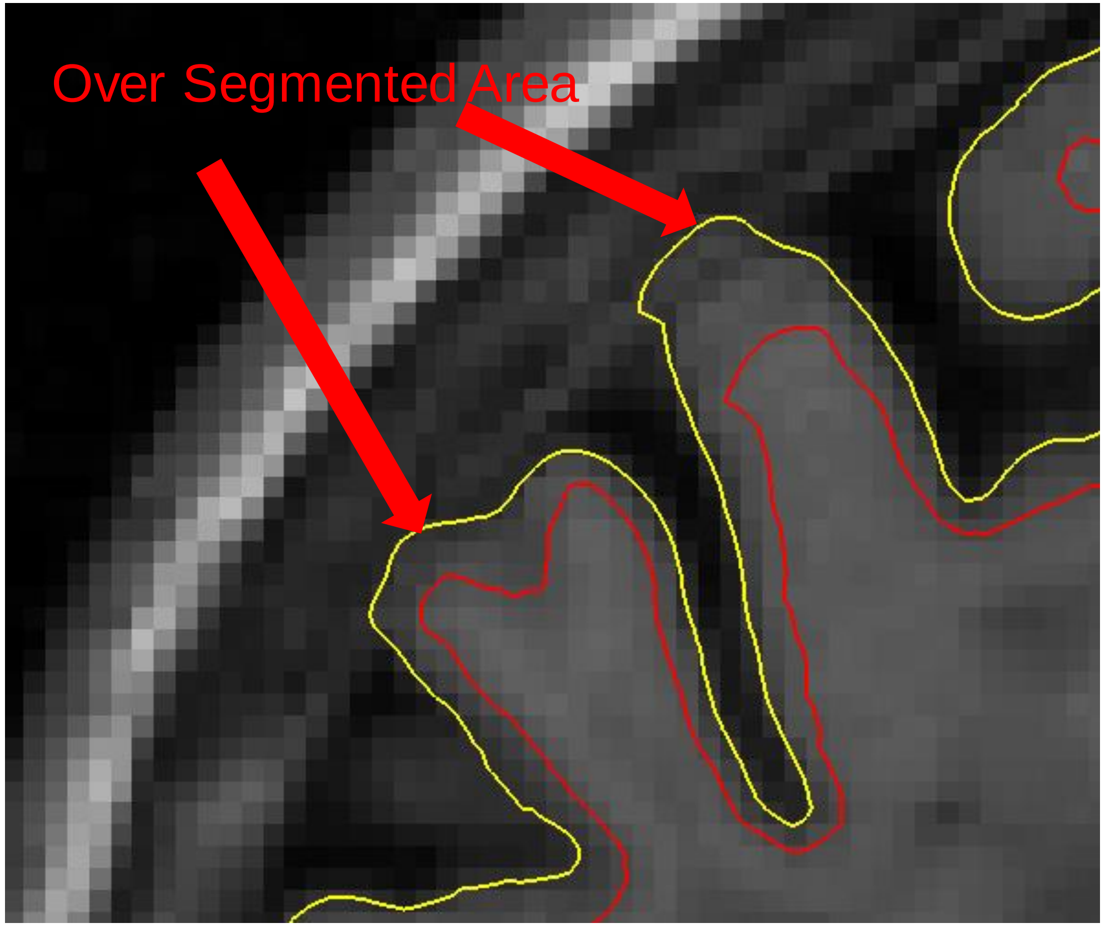
File name: l/mri/brainmask.mgz

Mask: None

Opacity: 0.30

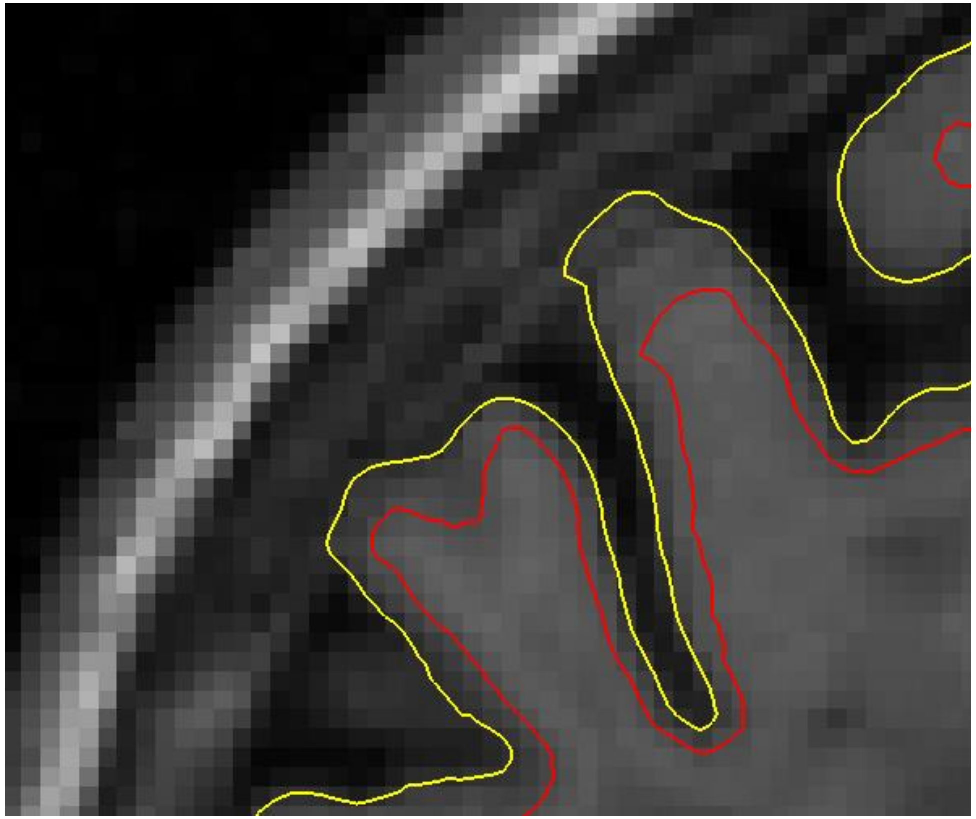
Color map: Heat

Skull stripping is required when the pial surface includes the skull area. To resolve this error, we will **freehand erase** the over-segmented area from the brainmask volume to remove unwanted areas from our segmentation.

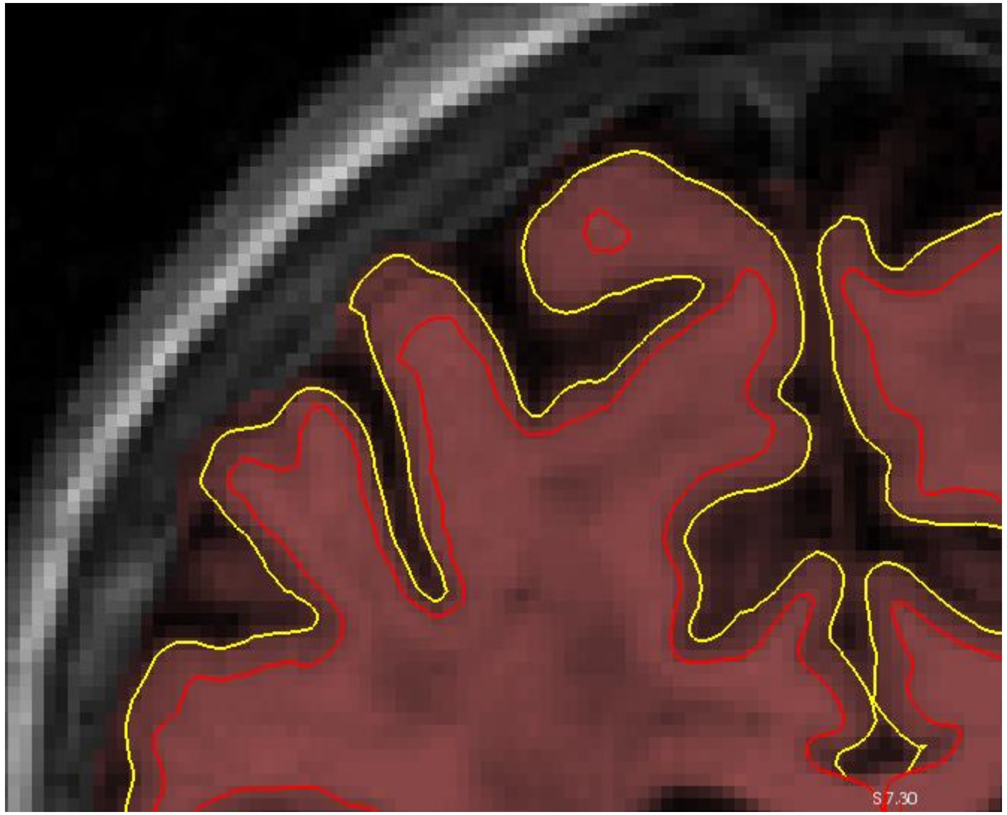


You should find it easier and quicker to identify the over segmented area.

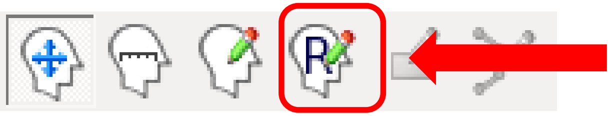
Before



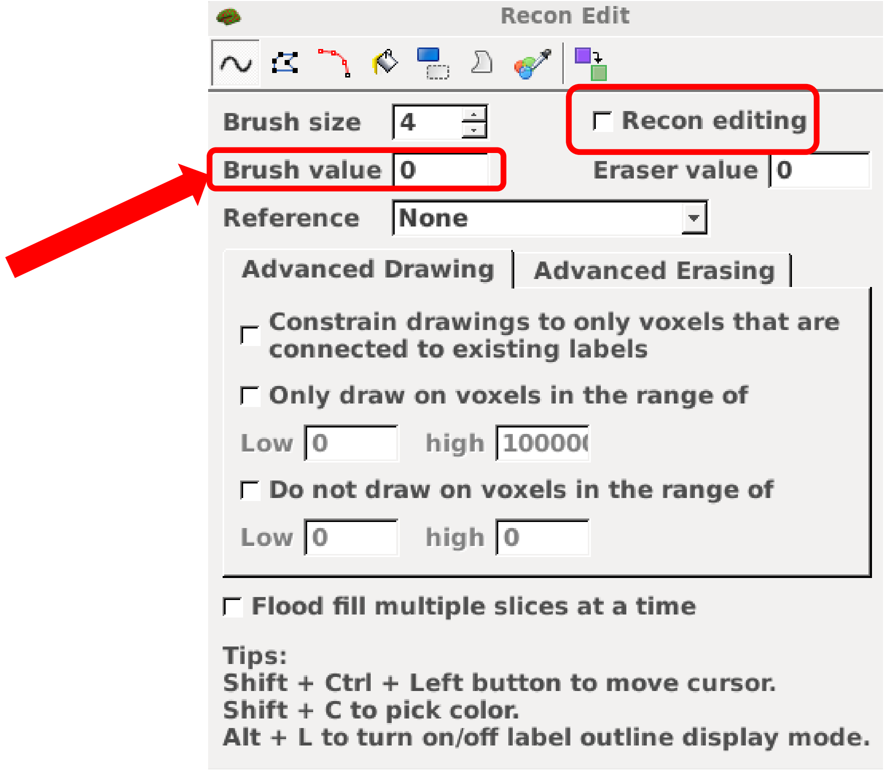
After



Confirm that you are working with the brainmask volume highlighted, select the "**Recon Edit**" option in the toolbar



Recon Edit



Recon Edit

Brush size 4

☐ Recon editing

Brush value 0

Eraser value 0

Reference None

Advanced Drawing | Advanced Erasing

☐ Constrain drawings to only voxels that are connected to existing labels

☐ Only draw on voxels in the range of

Low 0 high 100000

☐ Do not draw on voxels in the range of

Low 0 high 0

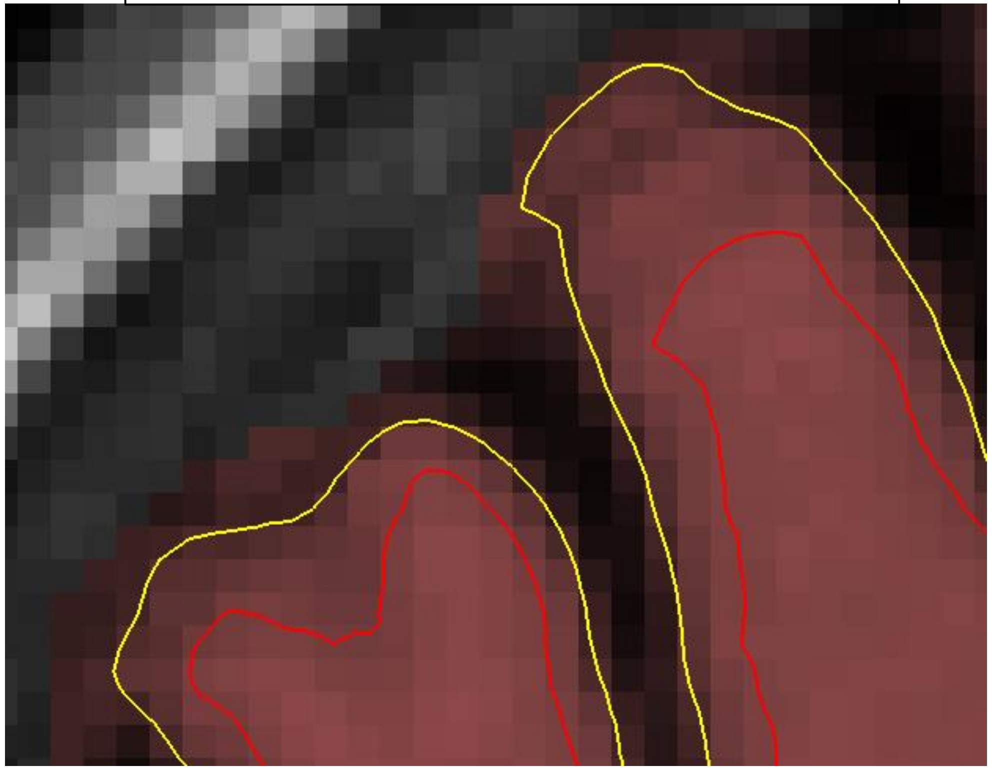
☐ Flood fill multiple slices at a time

Tips:
Shift + Ctrl + Left button to move cursor.
Shift + C to pick color.
Alt + L to turn on/off label outline display mode.

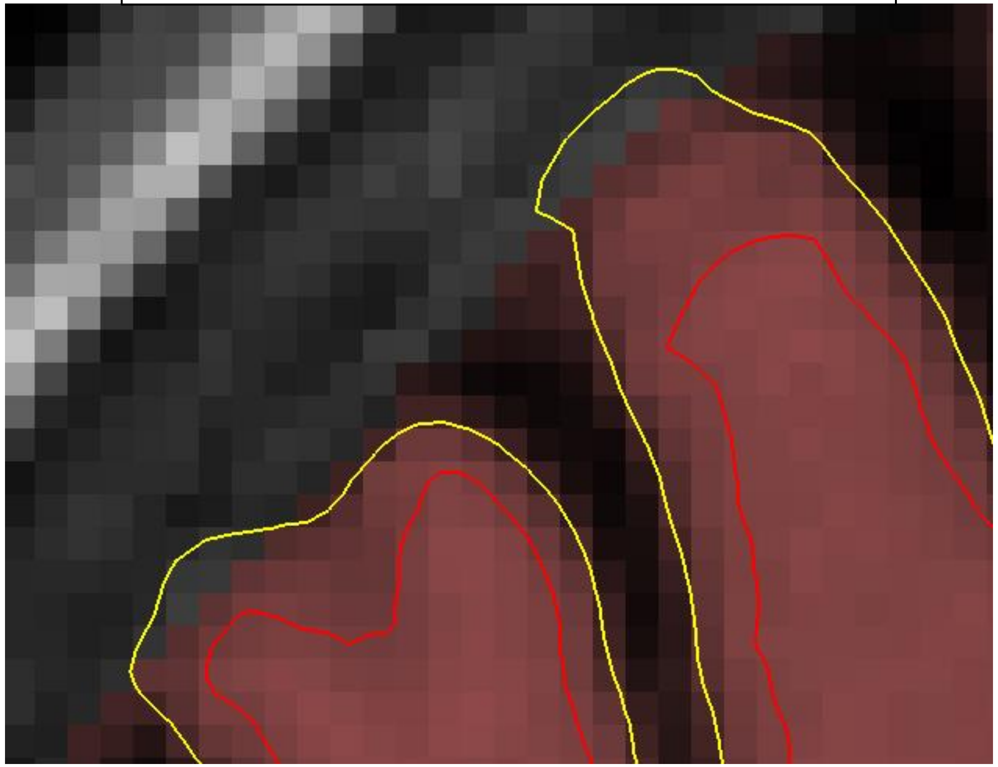
In the pop-up Recon Edit window, ensure that you have "**Freehand voxel edit**" ∿ selected. Uncheck the "**Recon editing**" option and change the "**Brush value**" to 0. You can change the "**Brush size**" if you want.

Identify the areas that are over segmented and the boundary between skull tissue and brain tissue, then carefully erase the unwanted region without overdoing it.

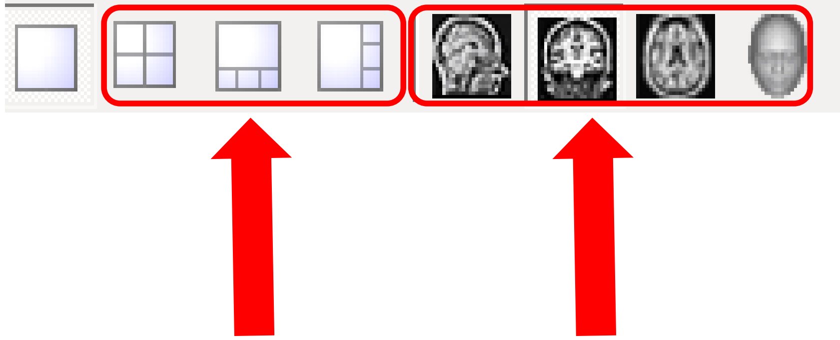
Before Corrections:



After Corrections:

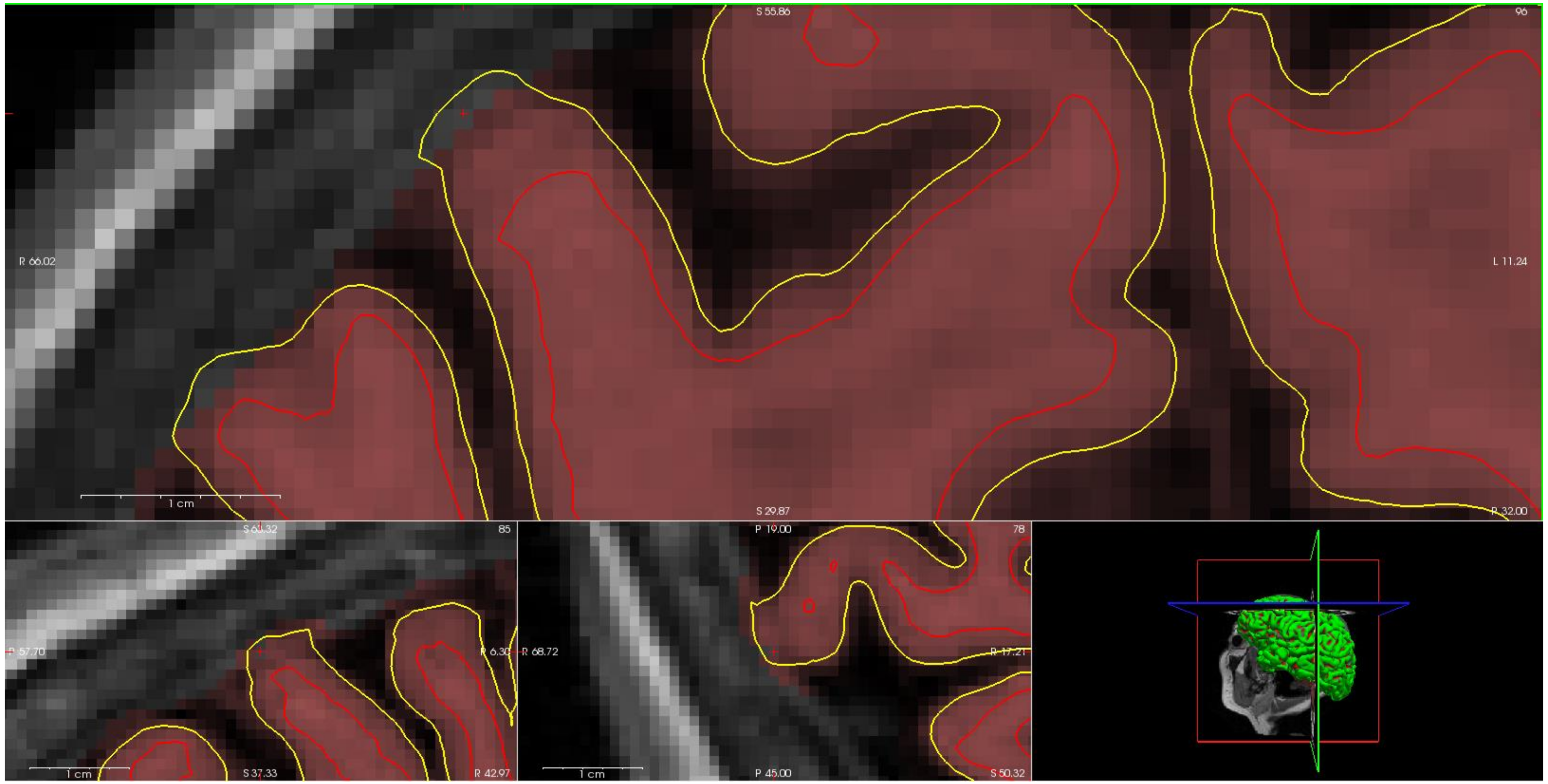


If you are not sure about whether to erase an area or not, you can move your cursor by holding ctrl and shift, or just exit the recon edit. You can then inspect that area from different views, which could give you a better idea.

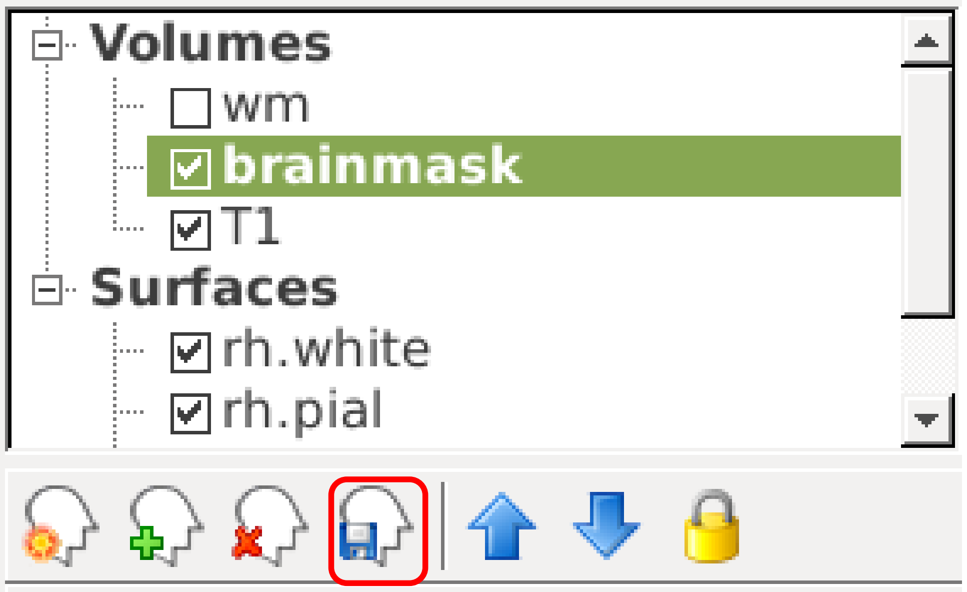


Multiview Option

Main view Option



Finally, remember to save your brainmask volume constantly and when you have finished. You don't want to do the whole process again just because the program crashes before you could have saved!



- Volumes
  - ☐ wm
  - ☑ brainmask
  - ☑ T1
- Surfaces
  - ☑ rh.white
  - ☑ rh.pial

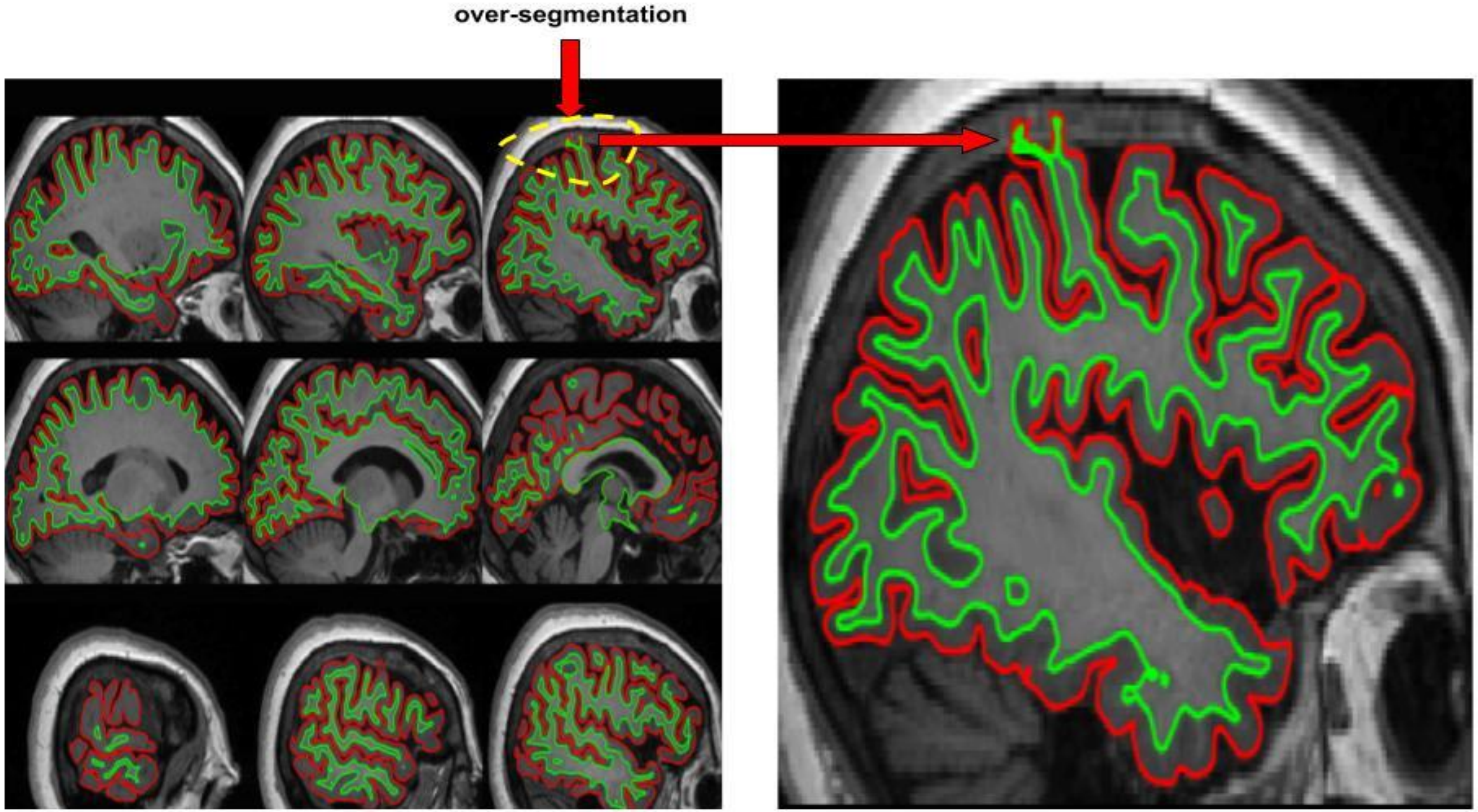
Save Volume

Volume Editing tips

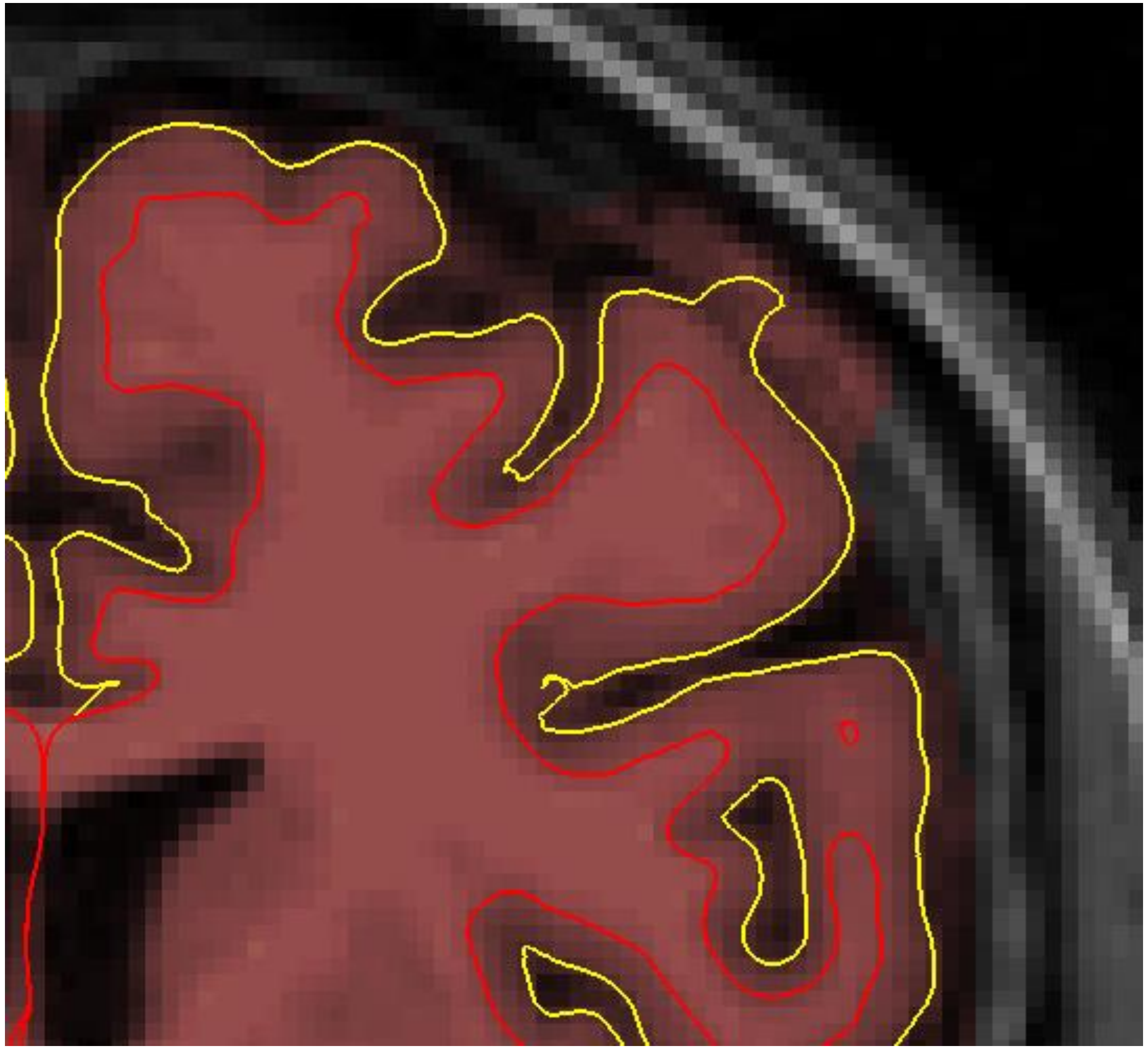
- **For brainmask editing;** you need not have wm open in freeview. You can use it as a reference to view the scan but it is not needed during the brainmask edits. Only T1 (for actual reference), and brainmask are needed during brainmask editing.
- **For wm editing;** T1, brainmask, and surface files can be referenced to view the scan all together but they need not be open in freeview during the editing process.

The following slides contain examples on Skull Stripping

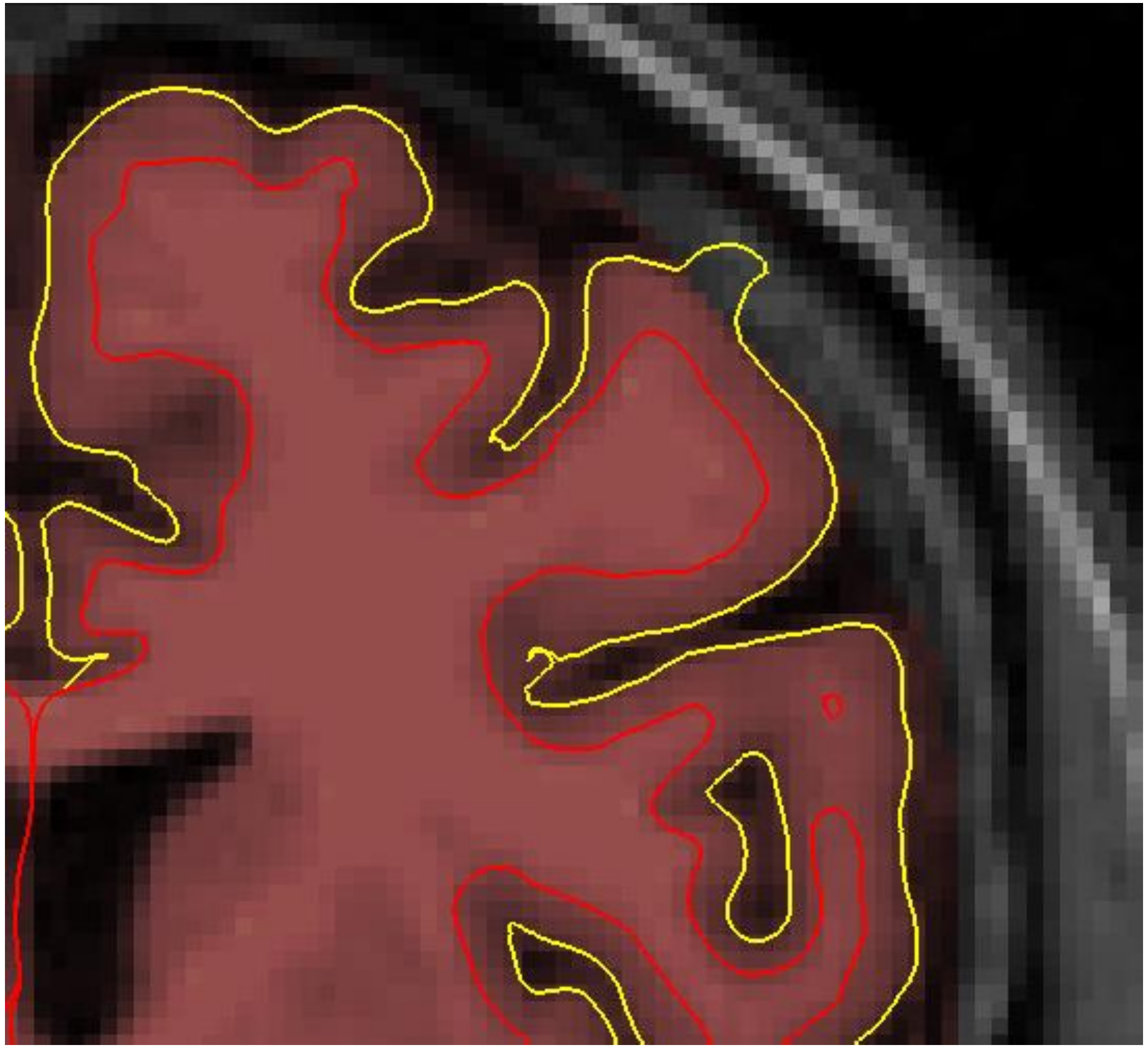
Skull Stripping



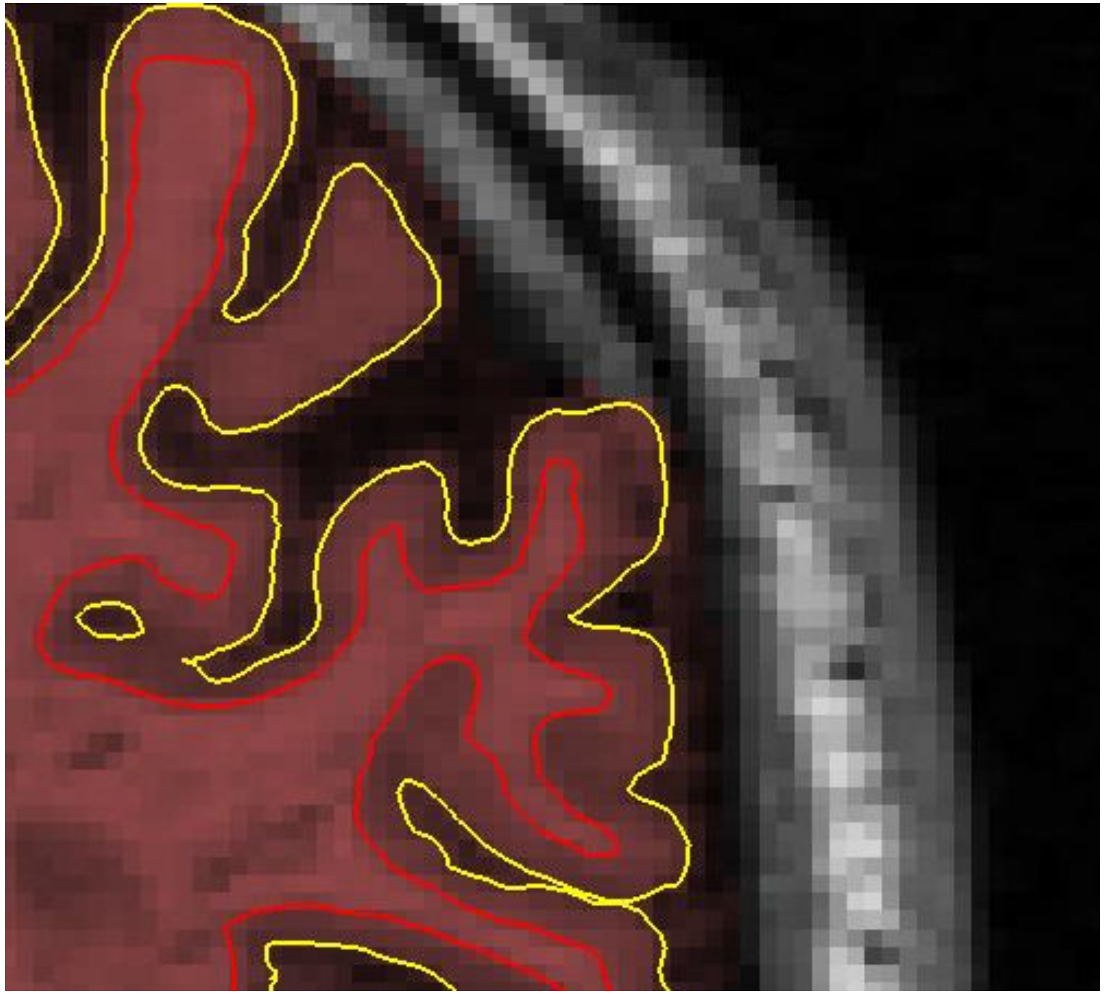
Before Corrections:



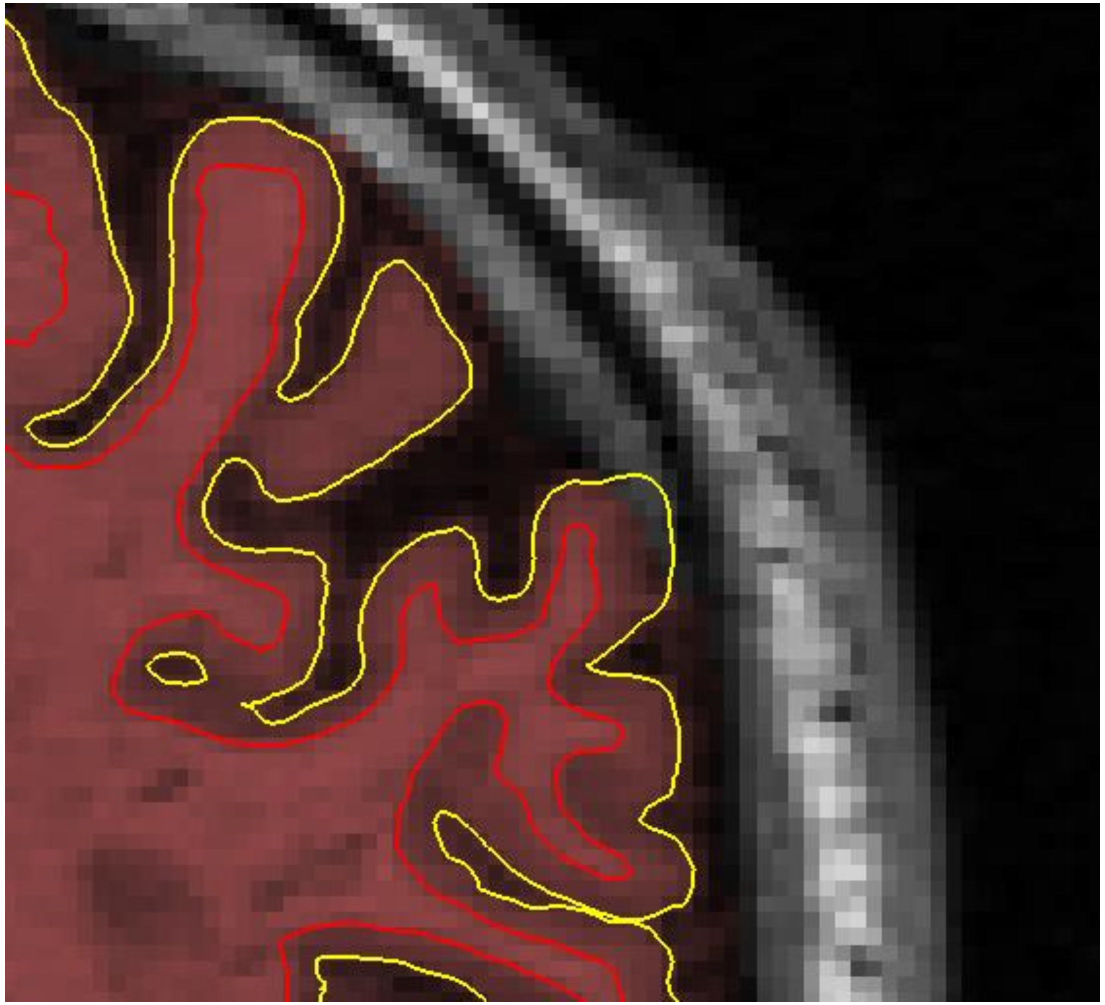
After Corrections:



Before Corrections:

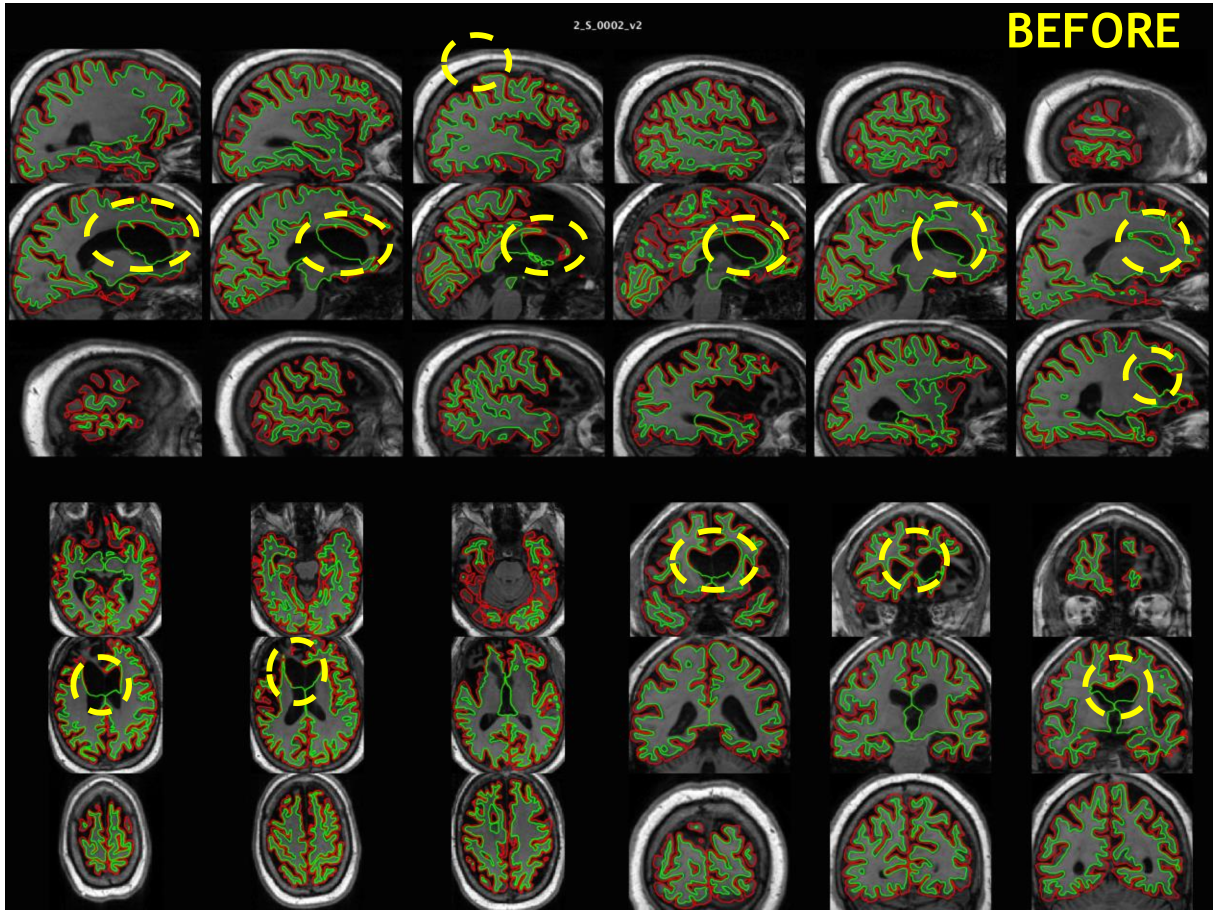


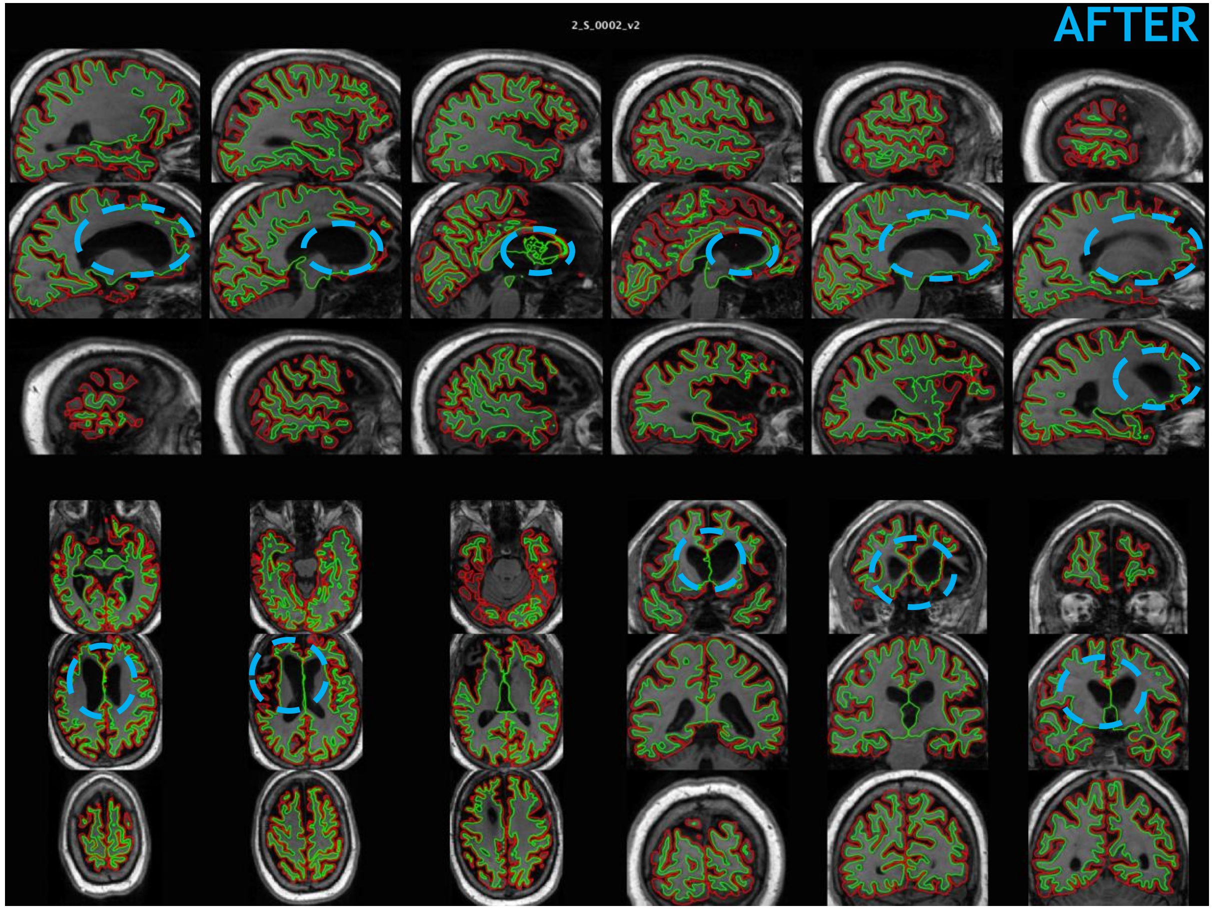
After Corrections:



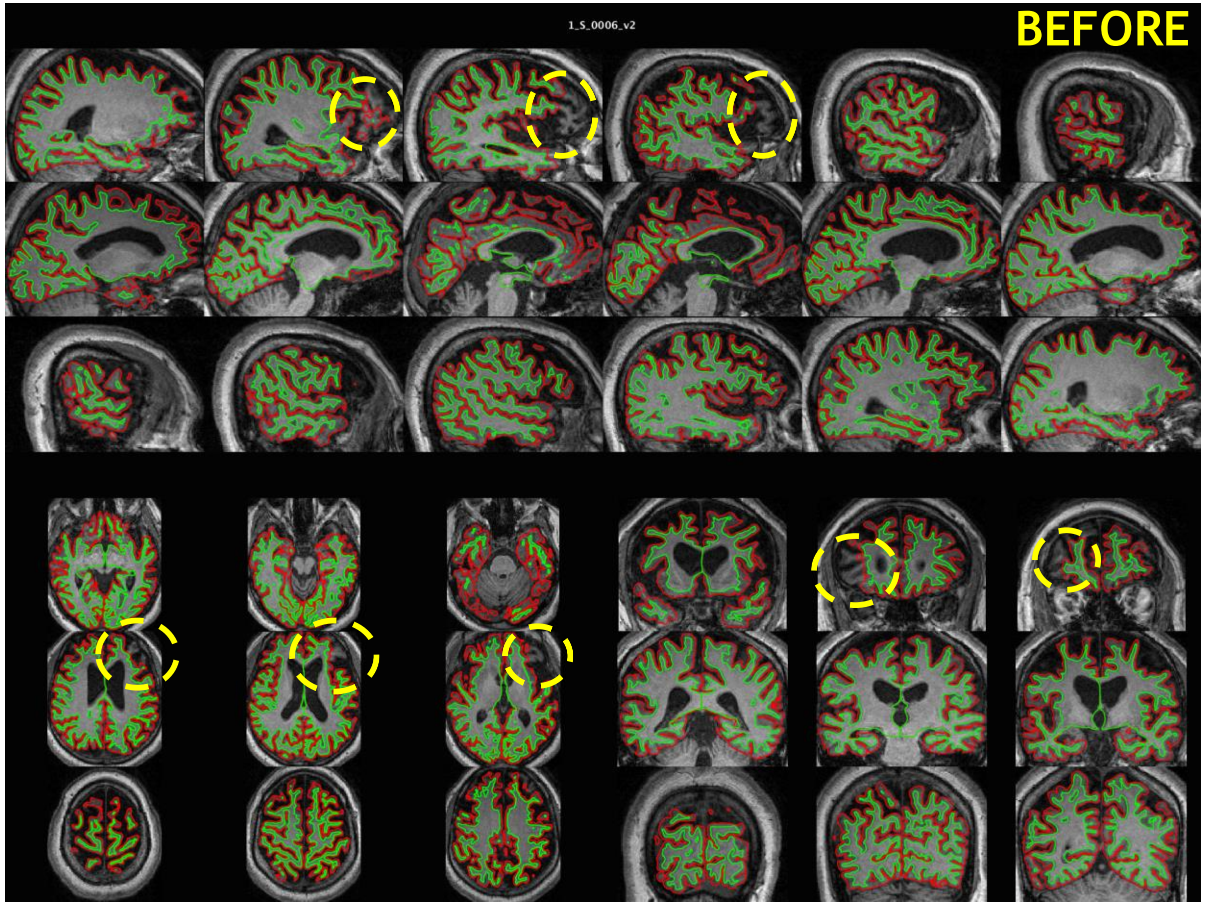
Confirming Corrections with "Quickchecks"

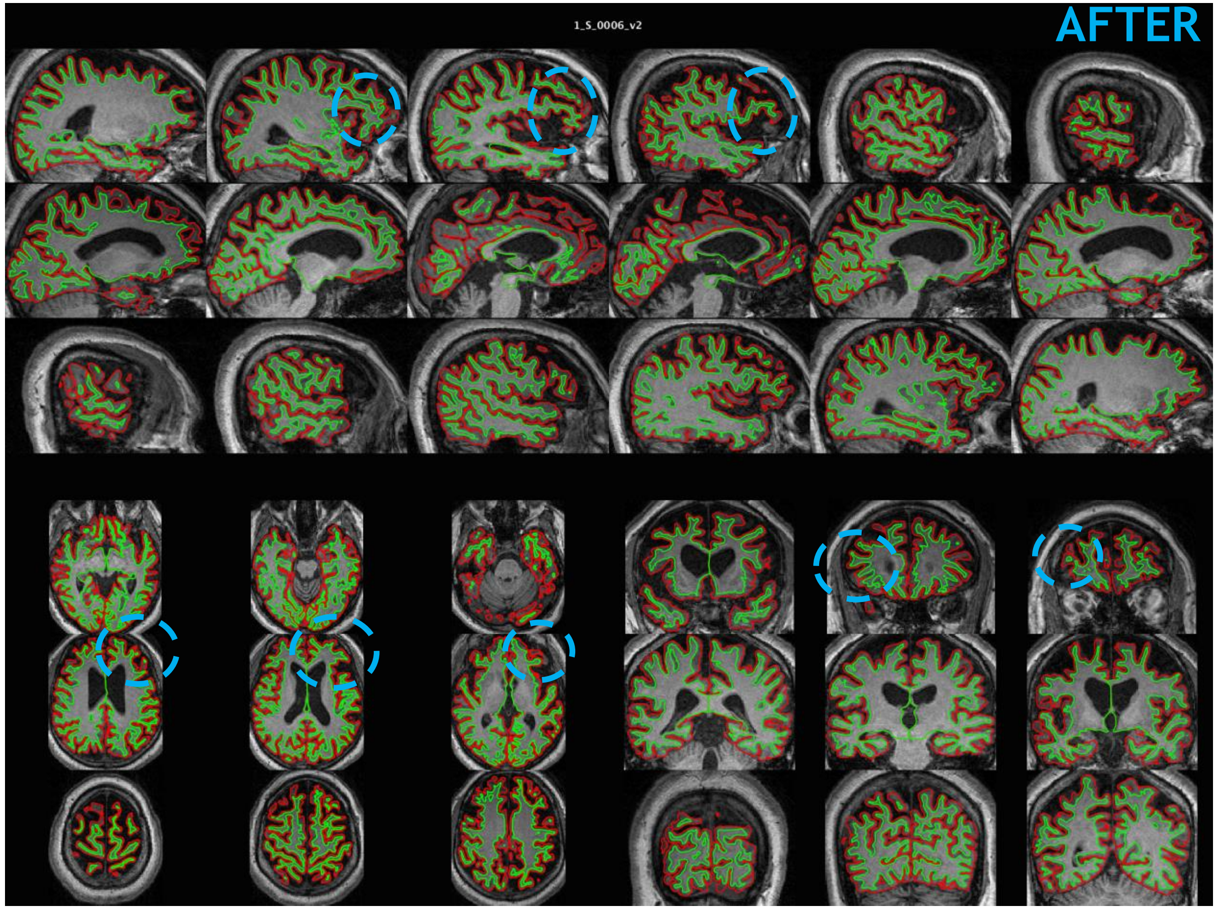
Quickchecks: 'Before' and 'After' White Matter Corrections



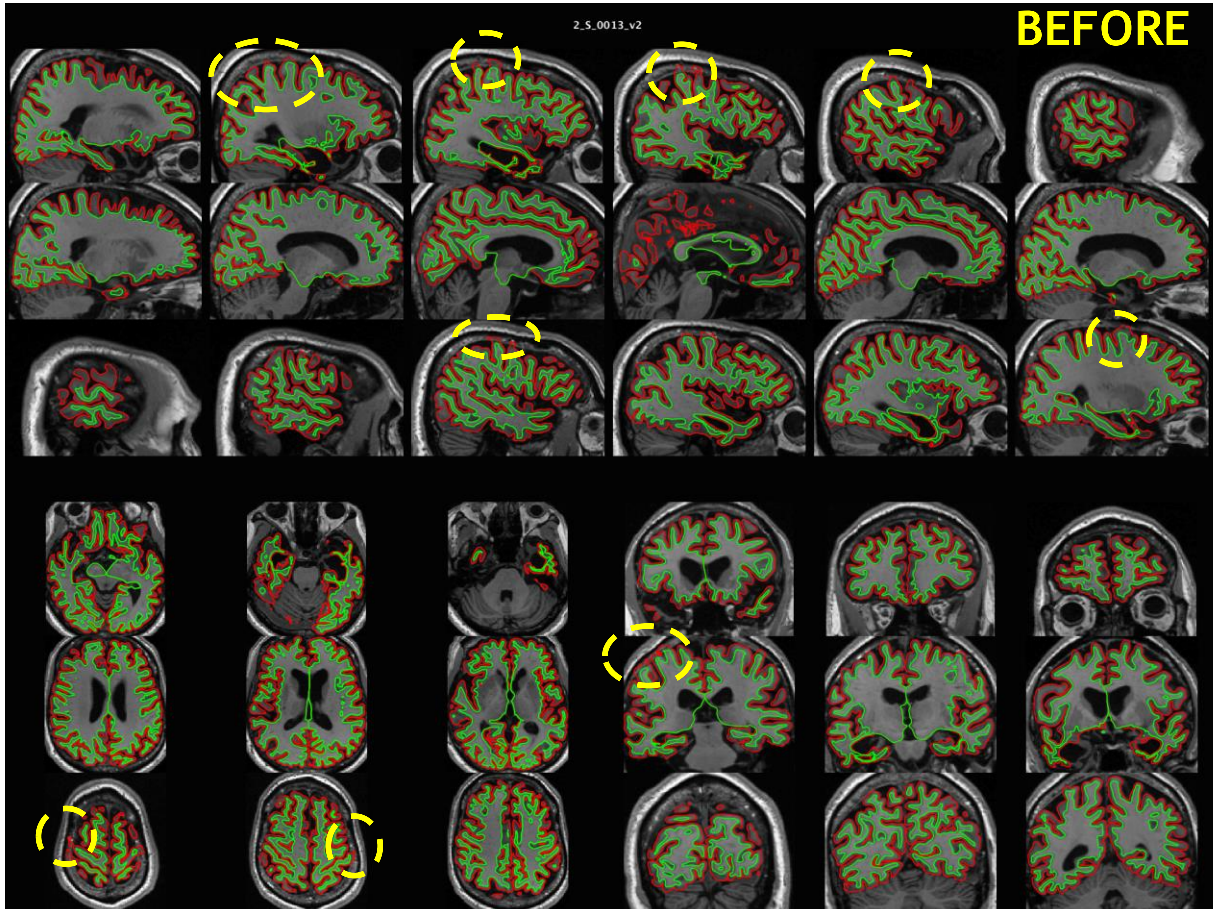


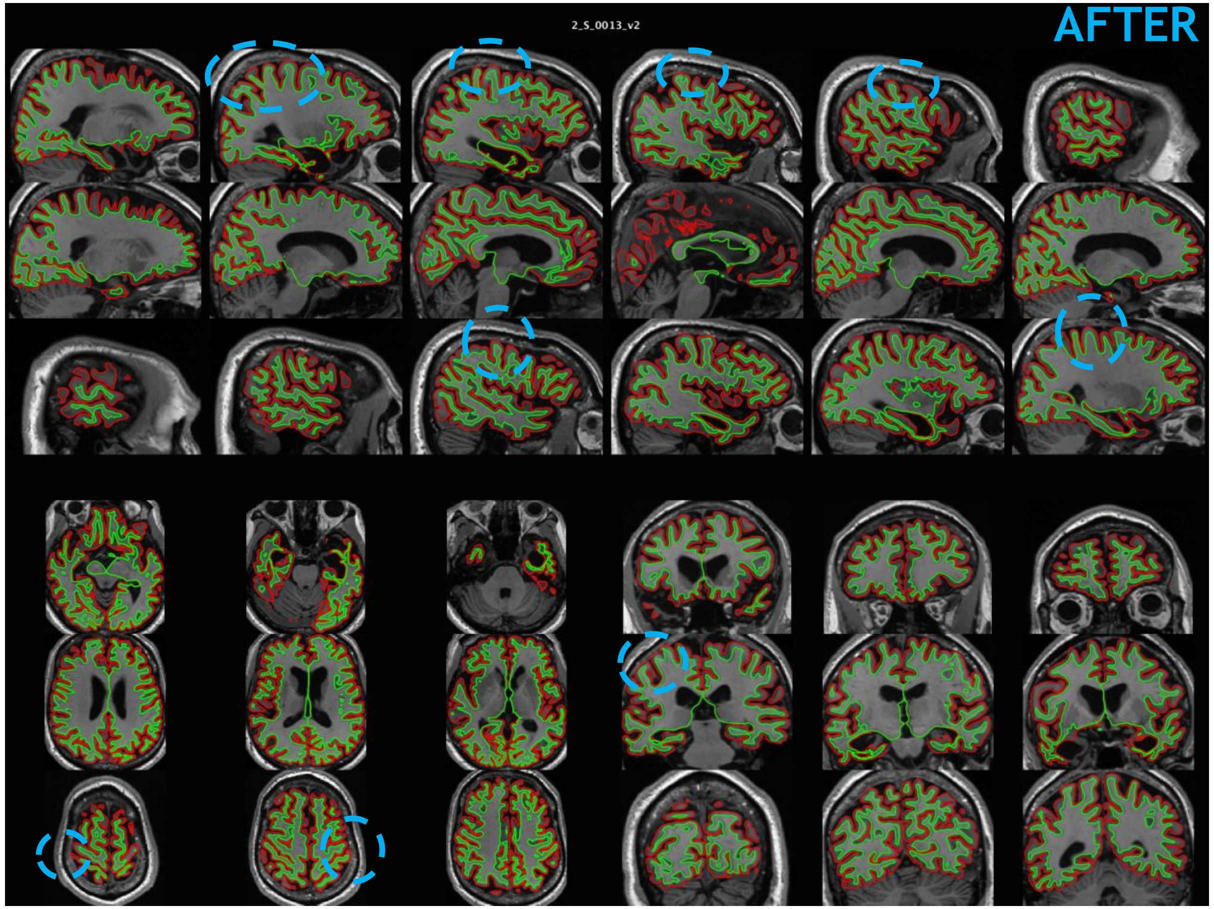
Quickchecks: 'Before' and 'After' Cortical Seeding Corrections





Quickchecks: 'Before' and 'After' Skull Stripping Corrections





After Quality Control

Once the segmentations are corrected (to the best that they can be corrected, until the scan stops accepting any more corrections)

- If the segmentations look good, check the **Freesurfer/$targetID/scripts** once again to make sure there are no IsRunning.lh+rh or recon-all.error log
- If IsRunning.lh+rh and/or recon-all.error log are not there, FreeSurfer folders are ready to be imported. Contact the repo-manager and request an import.

[Discuss with repo-manager for this part below]

- If the segementations no longer improve and there are still massive errors, try to find a new scan for that subject, at the same time point and process that. If no other scan is available, discuss with repo-manager and maybe discard the scan from analysis.