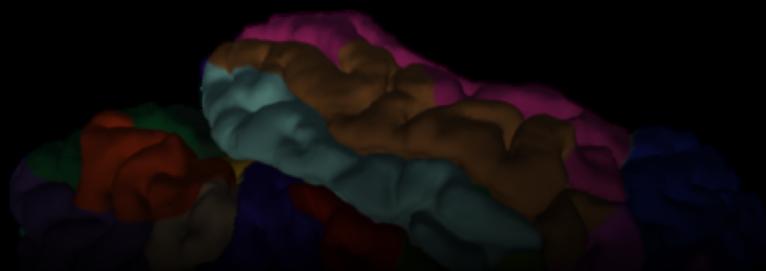


Freesurfer edits



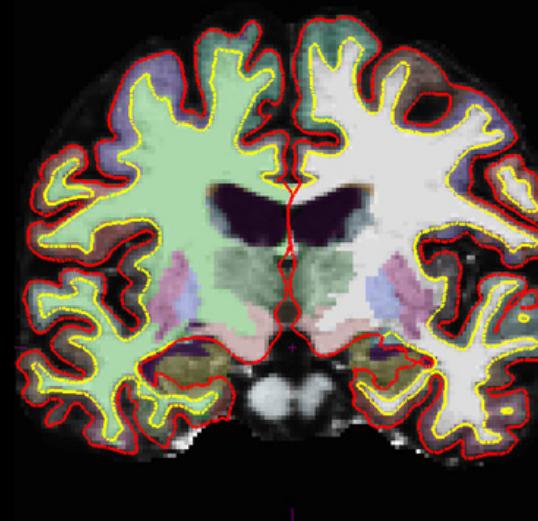
QLAB workshop presentation 5/8/19

What FreeSurfer Does...

FreeSurfer creates computerized models of the brain from MRI data.



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



Output:
Segmented & parcellated conformed
volume
.mgz

After registration

Make sure files are properly reconstructed

- Especially for child populations
 - Children tend to move a lot
 - Their brains are more difficult to model due to high variation between children

Using Qoala-T for QA

- We will use Qoala-T to help us decide which files to include/exclude and/or fix
 - A supervised-learning tool to assess accuracy of manual quality control of automatic segmented MRI data
 - Particularly intended for use in developmental datasets

Using Qoala-T

Predicting scan Qoala-T score by using
Braintime model

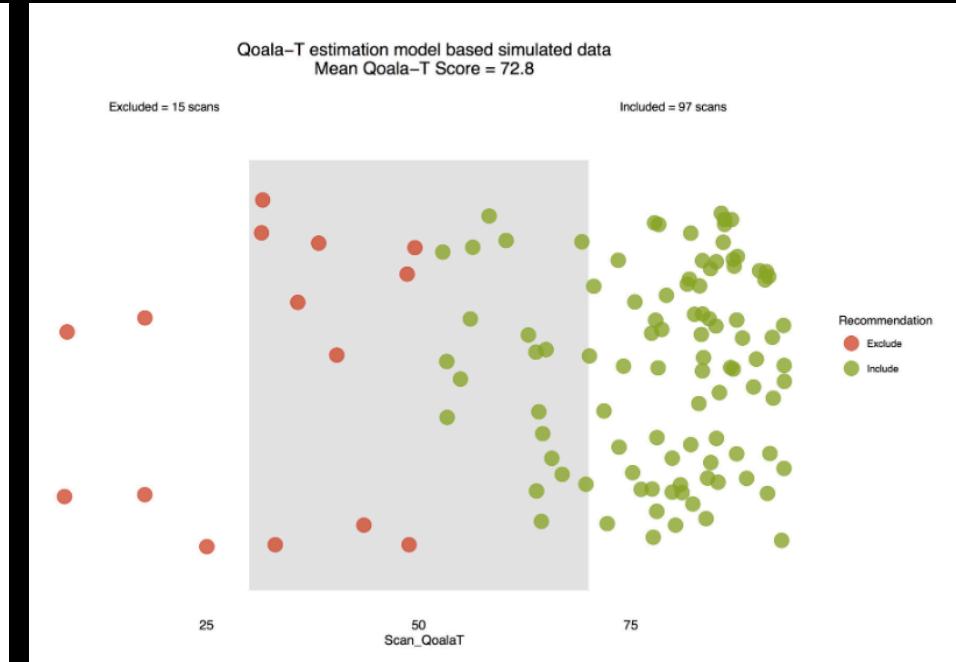
- R script: Qoala-T scores for a dataset are estimated using a supervised- learning model
- Model based on 784 T1-weighted imaging scans of subjects aged between 8 and 25 years old (53% females)
- Only counts errors if they are seen in 3 consecutive slices

Using Qoala-T

Braintime model output

- Provides recommendation for inclusion/exclusion and whether QC is advised

| VisitID | Scan_QoalaT | Recommendation | manual_QC_advised |
|---------------|-------------|----------------|-------------------|
| Simulated_98 | 8 | Exclude | no |
| Simulated_85 | 9 | Exclude | no |
| Simulated_109 | 18 | Exclude | no |
| Simulated_25 | 18 | Exclude | no |
| Simulated_65 | 25 | Exclude | no |
| Simulated_10 | 32 | Exclude | yes |
| Simulated_112 | 32 | Exclude | yes |
| Simulated_22 | 33 | Exclude | yes |
| Simulated_6 | 36 | Exclude | yes |
| Simulated_5 | 38 | Exclude | yes |
| Simulated_51 | 40 | Exclude | yes |



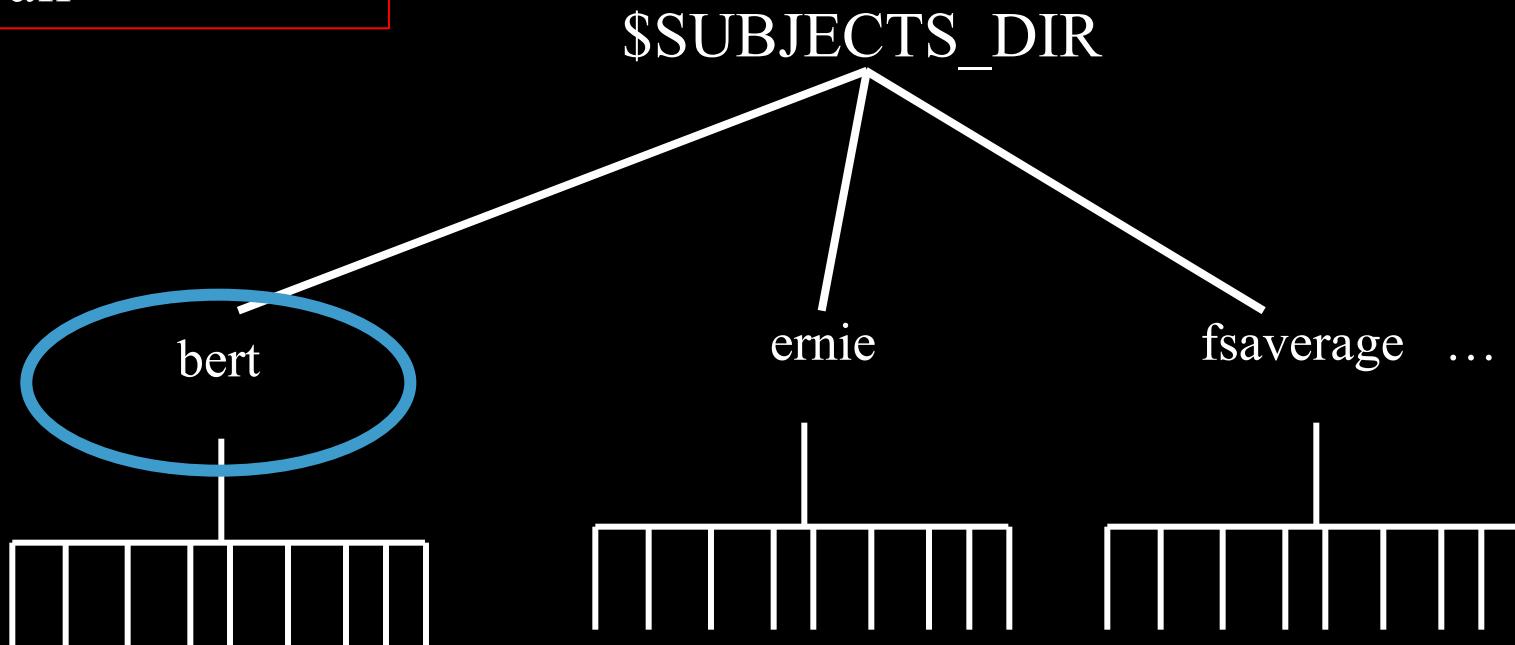
How do we use Qoala-T?

- 1) Extract gray matter volume, cortical thickness, and surface area (SA) for each participant in Freesurfer
- 2) Insert extracted .txt files into Qoala-T app
- 3) Look at output recommendations

Reminder: FS folder structure

```
recon-all  
  -i sMRI.nii  
  -subject bert  
  -all
```

- The first recon-all command creates a subject-specific folder in a structure that Freesurfer can read for all further steps
 - “bert” is the “name” of the subject
 - Creates a folder in \$SUBJECTS_DIR
 - All output goes in this folder (~400MB)
 - Other subjects in \$SUBJECTS_DIR

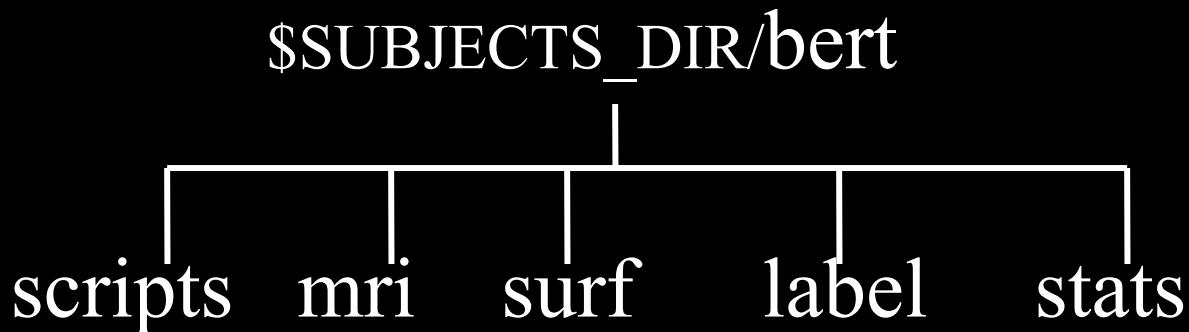


```
export SUBJECTS_DIR /path/to/space
```

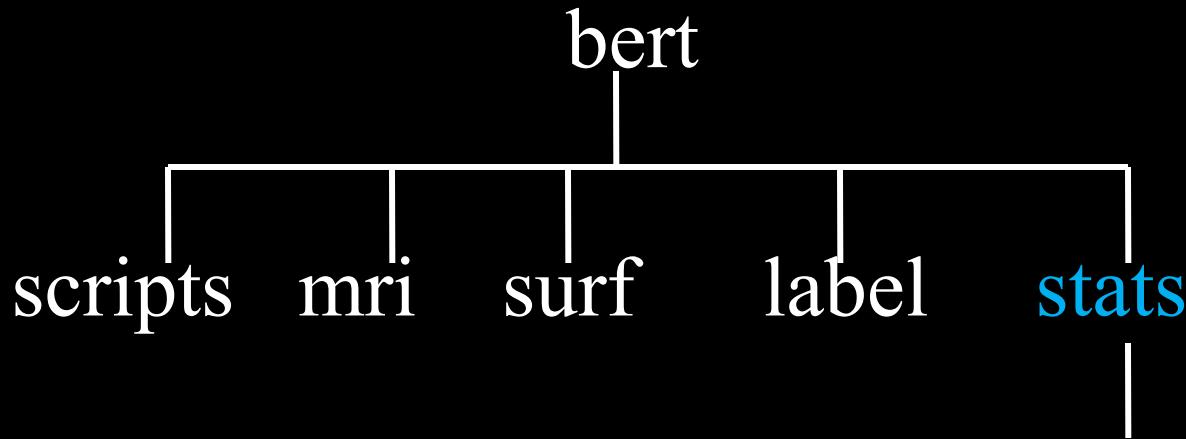
Reminder: FS folder structure

```
recon-all autorecon-all -i sMRI.nii -  
subject bert
```

This does the actual reconstruction



Reminder: FS folder structure



aseg.stats – subcortical volumetric stats

wmparc.stats – white matter segmentation volumetric stats

lh.aparc.stats – left hemi Desikan/Killiany surface stats

rh.aparc.stats – right hemi Desikan/Killiany surface stats

lh.aparc.a2009.stats – left hemi Destrieux

rh.aparc.a2009.stats – right hemi Destrieux

stats files are text files with summary information, eg:

volume of left amygdala

average thickness in superior temporal gyrus

This is where we extract the GM info from

Hands-on activity

Everyone work on extracting GM measures

1. Open a terminal window or PuTTY
2. Log onto sylvian computer:

SSH -XY qigroup@sylvian.ling.udel.edu

Pw: Qi@080117

3. On google drive you can see list of commands
- Qlab > Training > Freesurfer edits training

Extracting GM measures

- 1) Navigate to folder with FS reconstructed data
- 2) Set subject's directory
- 3) Set list of which subjects you want to run the extraction for
- 4) Execute FS commands for GMV, CT, and SA

Extracting GM measures

- 1) Navigate to folder with FS reconstructed data

```
cd /home/qigroup/Documents/Freesurfer_edits_tutorial/
```

- 2) Make your own specific folder where the outputs will go

```
[17:03]qigroup@sylvian:Freesurfer_edits_tutorial$ mkdir Jen  
[17:05]qigroup@sylvian:Freesurfer_edits_tutorial$ ls  
fsaverage Jen sub-blastc019 sub-blastc122
```

Extracting GM measures

1) Set subject's directory

```
[17:07]qigroup@sylvian:Freesurfer_edits_tutorial$ export SUBJECTS_DIR=/home/qigr]
oup/Documents/Freesurfer_edits_tutorial/
[17:08]qigroup@sylvian:Freesurfer_edits_tutorial$ echo $SUBJECTS_DIR
/home/qigroup/Documents/Freesurfer_edits_tutorial/]
```

2) Set list of which subjects you want to run the extraction for

- Set list as every subject in the
directory starting with “sub-blast”

```
list="`ls -d sub-blast*`" ]
```

Extracting GM measures

- 1) First work on extracting GMV (does this for both hemispheres of the brain, includes eTIV)

```
[17:08]qigroup@sylvian:Freesurfer_edits_tutorial$ asegstats2table --subjects $list --meas volume --skip --tablefile /home/qigroup/Documents/Freesurfer_edits_tutorial/Jen/aseg_stats.txt
```

- Make sure instead of /Jen you use your own folder name
- For Qoala-T to work in R, you have to name the files exactly as stated here

Extracting GM measures

1) Double-check you did this correctly

```
[17:08]qigroup@sylvian:Freesurfer_edits_tutorial$ cd Jen/
[17:09]qigroup@sylvian:Jen$ ls
aseg_stats.txt
[17:09]qigroup@sylvian:Jen$ cat aseg_stats.txt
Measure:volume Left-Lateral-Ventricle Left-Inf-Lat-Vent      Left-Cerebellum-White-Matter   Left-Cerebellum-Cortex]
  Left-Thalamus-Proper   Left-Caudate   Left-Putamen      Left-Pallidum   3rd-Ventricle  4th-Ventricle  Brain-Stem ]
  Left-Hippocampus Left-Amygdala    CSF       Left-Accumbens-area  Left-VentralDC Left-vessel   Left-choroid-plexus
  Right-Lateral-Ventricle Right-Inf-Lat-Vent   Right-Cerebellum-White-Matter Right-Cerebellum-Cortex Right-]
Thalamus-Proper   Right-Caudate   Right-Putamen      Right-Pallidum  Right-Hippocampus Right-Amygdala Right-Accumbens-area
  Right-VentralDC Right-vessel   Right-choroid-plexus 5th-Ventricle WM-hypointensities Left-WM-hypointensitiesRight-WM-hypointensities non-WM-hypointensities Left-non-WM-hypointensities Right-non-WM-hypointensities
Optic-Chiasm    CC_Posterior   CC_Mid_PosteriorCC_Central   CC_Mid_Anterior CC_Anterior   BrainSegVol
  BrainSegVolNotVent  BrainSegVolNotVentSurf lhCortexVol   rhCortexVol   CortexVol    lhCerebralWhiteMat
terVol rhCerebralWhiteMatterVol   CerebralWhiteMatterVol SubCortGrayVol TotalGrayVol  SupraTentorialVol
  SupraTentorialVolNotVenSupraTentorialVolNotVentVox MaskVol BrainSegVol-to-eTIV MaskVol-to-eTIVlhSurfac
eHoles   rhSurfaceHoles SurfaceHoles   EstimatedTotalIntraCranialVol
sub-blastc019/ 7058.0 388.4 11721.3 52777.7 7096.2 3336.0 4548.0 1965.3 901.2 2124.0 15643.1 3733.8 1297.4
  799.1 436.1 3631.8 30.3 474.9 5982.3 874.1 11227.1 50644.2 6498.1 3392.3 4711.7 1612.5 3625.2 1568
  .0 455.3 3645.1 18.8 332.0 0.0 376.3 0.0 0.0 0.0 0.0 0.0 157.9 895.8 339.8 37
  7.2 425.7 904.6 1020839.0 1002319.0 1002791.48444 243642.591178 245312.592207 488955.183385
167014.433407 167879.867651 334894.301058 52836.0 645954.183385 893229.484443 878434.484443 876091.0
  1368600.0 0.75661 1.014358 28.0 30.0 58.0 1349227.9561
sub-blastc122/ 3443.5 389.4 11637.5 56429.9 7624.4 2960.5 5535.8 1862.1 665.6 1425.6 16723.5 3442.2 1284.5
  778.5 630.5 3577.8 40.7 300.4 2416.6 300.2 11659.1 57174.8 7801.6 3482.3 5742.8 1801.5 3697.4 1781
  .0 710.3 3734.8 20.2 362.3 0.0 2462.8 0.0 0.0 0.0 0.0 0.0 112.9 625.2 367.8 43
  9.9 378.7 755.0 1020217.0 1010704.0 1009873.4321 250144.584449 240081.046668 490225.631118
167059.747551 158670.053426 325729.800978 57565.0 661644.631118 882745.432095 875973.432095 874316.0
  1353857.0 0.679579 0.90182 385.0 298.0 683.0 1501249.32584
```

Extracting GM measures

1) Next you can extract CT and SA for right and left hemispheres separately

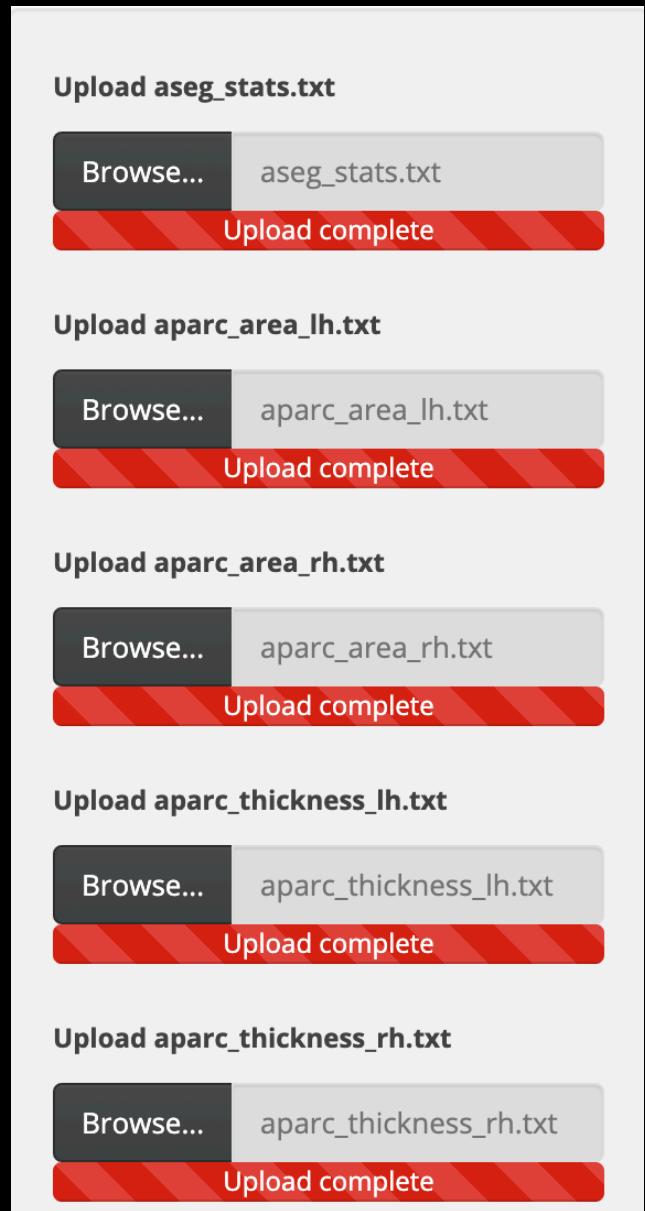
```
[17:09]qigroup@sylvian:Jen$ aparcstats2table --subjects $list --hemi lh --meas thickness --skip --tablefile /home/qigr
oup/Documents/Freesurfer_edits_tutorial/Jen/aparc_thickness_lh.txt
SUBJECTS_DIR : /home/qigroup/Documents/Freesurfer_edits_tutorial/
Parsing the .stats files
Building the table..
Writing the table to /home/qigroup/Documents/Freesurfer_edits_tutorial/Jen/aparc_thickness_lh.txt
[17:11]qigroup@sylvian:Jen$ aparcstats2table --subjects $list --hemi lh --meas area --skip --tablefile /home/qigroup/D
ocuments/Freesurfer_edits_tutorial/Jen/aparc_area_lh.txt
SUBJECTS_DIR : /home/qigroup/Documents/Freesurfer_edits_tutorial/
Parsing the .stats files
Building the table..
Writing the table to /home/qigroup/Documents/Freesurfer_edits_tutorial/Jen/aparc_area_lh.txt
[17:11]qigroup@sylvian:Jen$ aparcstats2table --subjects $list --hemi rh --meas thickness --skip --tablefile /home/qigr
oup/Documents/Freesurfer_edits_tutorial/Jen/aparc_thickness_rh.txt
SUBJECTS_DIR : /home/qigroup/Documents/Freesurfer_edits_tutorial/
Parsing the .stats files
Building the table..
Writing the table to /home/qigroup/Documents/Freesurfer_edits_tutorial/Jen/aparc_thickness_rh.txt
[17:11]qigroup@sylvian:Jen$ aparcstats2table --subjects $list --hemi rh --meas area --skip --tablefile /home/qigroup/D
ocuments/Freesurfer_edits_tutorial/Jen/aparc_area_rh.txt
SUBJECTS_DIR : /home/qigroup/Documents/Freesurfer_edits_tutorial/
Parsing the .stats files
Building the table..
Writing the table to /home/qigroup/Documents/Freesurfer_edits_tutorial/Jen/aparc_area_rh.txt
[17:11]qigroup@sylvian:Jen$ ls
aparc_area_lh.txt  aparc_area_rh.txt  aparc_thickness_lh.txt  aparc_thickness_rh.txt  aseg_stats.txt
```

Extracting GM measures

- 1) Check that your files are in your folder
- 2) Congrats! You extracted Qoala-T ready files!!
 - Note: In regular GM extraction for ROI analyses, you wouldn't use the --skip option

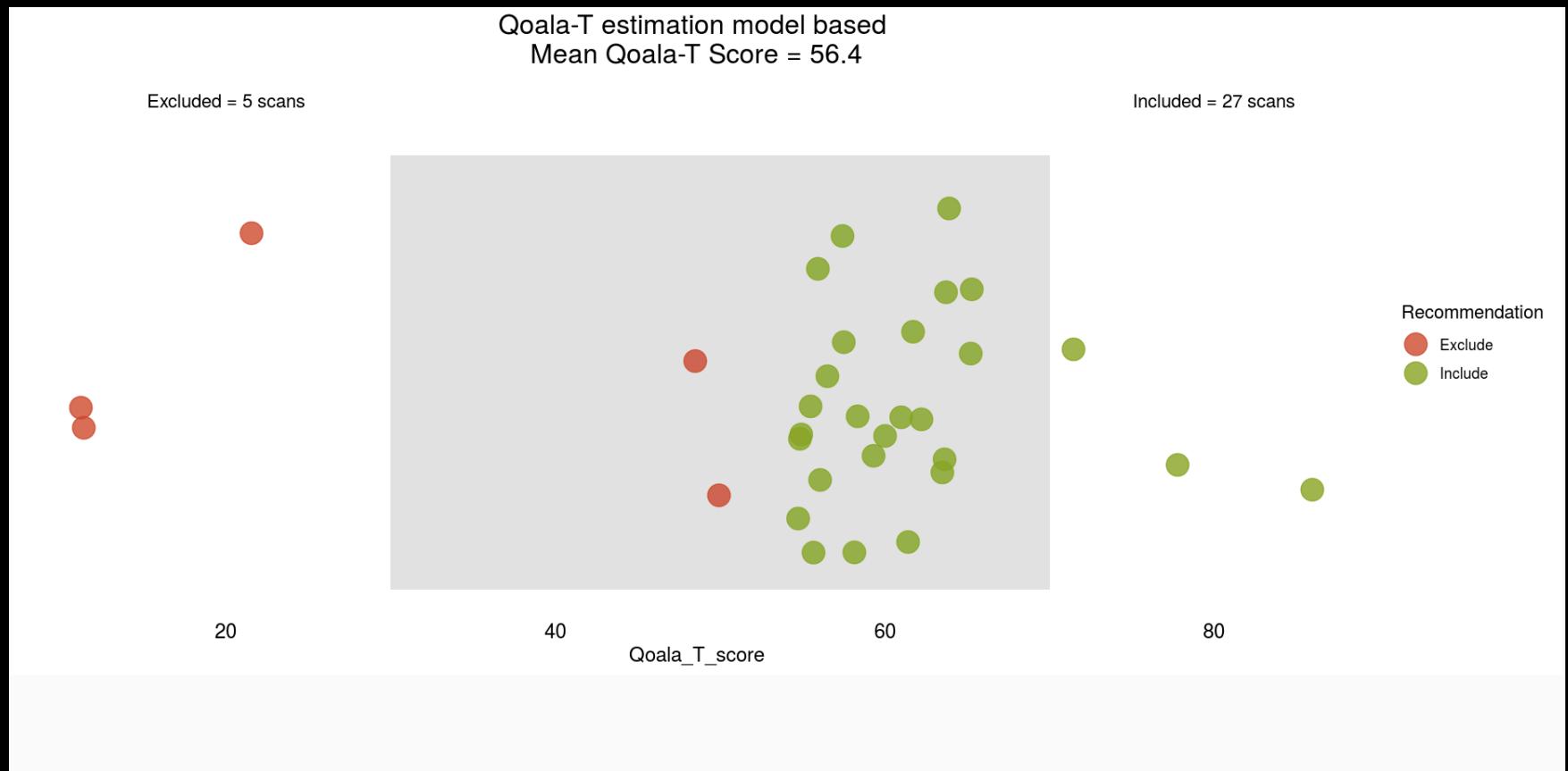
Using Qoala-T

- 1) Go to: https://qoala-t.shinyapps.io/qoala-t_app/
- 2) Insert .txt extracted files in respective locations



Using Qoala-T

1) Look at graph output



Using Qoala-T

1) Look at Table output and download .csv

Graph Table

Once the Qoala-T scores are displayed here, hit 'Download csv' to download a csv file of this table.

[Download csv](#)

| Scan_ID | Qoala_T_score | Recommendation | Manual_QC_advised |
|----------------------|---------------|----------------|-------------------|
| sub-blastc034 | 11.18 | Exclude | no |
| sub-blastc034_Nicolo | 11.38 | Exclude | no |
| sub-blastc122 | 21.56 | Exclude | no |
| sub-blasta013 | 48.50 | Exclude | yes |
| sub-blasta023 | 49.90 | Exclude | yes |
| sub-blasta029 | 54.69 | Include | yes |
| sub-blasta008 | 54.89 | Include | yes |
| sub-blasta021 | 54.89 | Include | yes |
| sub-blastc071 | 55.49 | Include | yes |
| sub-blasta024 | 55.69 | Include | yes |
| sub-blasta012 | 55.89 | Include | yes |
| sub-blasta001 | 71.46 | Include | no |
| sub-blastc019 | 77.84 | Include | no |
| sub-blasta002 | 86.03 | Include | no |

These are probably due to motion in the scanner, which cannot be corrected for if there is too much

These might be reparable with FS edits

These should still be inspected for possible FS edits

These are likely good, but should still be inspected

Next step

- 1) Look at the data and note whether edits are needed
 - Use criterion set in Qoala-T QC manual
- 2) Make Freesurfer edits

How do we make Freesurfer edits?

- 1) Use python script to pull up a graphical user interface (GUI)
 - Select subject
 - Look for brain scan abnormalities
 - Using Qoala-T specifications
 - Correct brain scan abnormalities (if any)

Qoala-T criterion

Four criteria are used to assess scan quality:

- 1) Is the reconstructed image affected by movement?
- 2) Is (part of) the temporal pole missing in the reconstruction?
- 3) Is non-brain tissue (e.g. dura/skull) included in the reconstruction of pial surface (red line)?
- 4) Are parts of the cortex missing in the reconstruction (other than temporal poles)?

Using Qoala-T documentation

Documenting possible errors in data and manually edits

- Quality control file with individual lines with information for each scan
 - .csv file with which types of errors were found

| Subject | Final_Score | Excessive_movement | Temp_pole_miss_LH | Temp_pole_miss_RH | Dura_LH | Dura_RH | Missing_Anterior_LH | Missing_Anterior_RH | Missing_Superior_Medial_LH | Missing_Superior_Medial_RH | Missing_Posterior_LH | Missing_Posterior_RH | Notes |
|------------|-------------|--------------------|-------------------|-------------------|---------|---------|---------------------|---------------------|----------------------------|----------------------------|----------------------|----------------------|--|
| Subject001 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Subject002 | 1 | 0 | 1 | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | 0 Minor parts anterior and temporal lobe missing |

- Add in column with which FS edits were made/any specifications

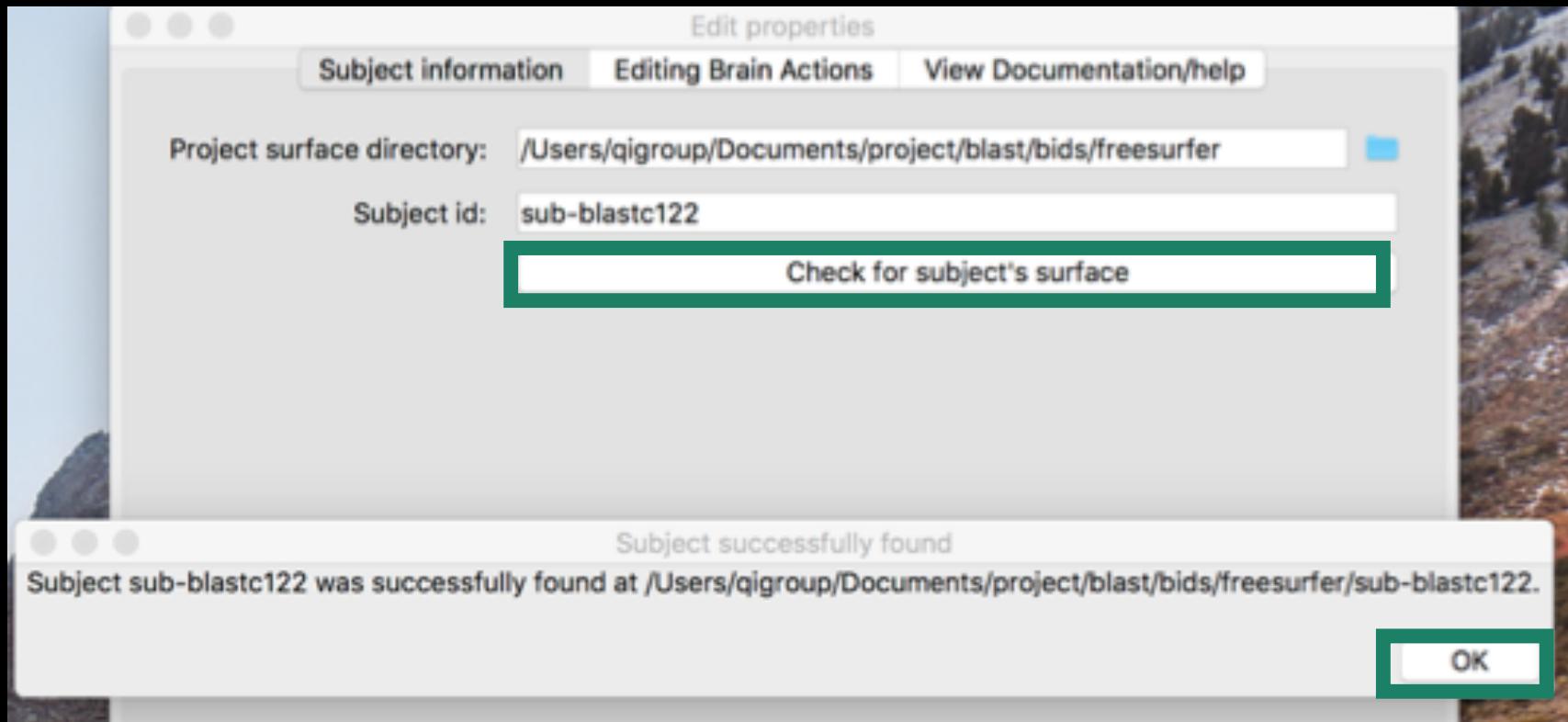
Using the python script

- 1) Use python script to pull up a graphical user interface (GUI)

```
mindhive:~ qigroup$ cd /Users/qigroup/Documents/project/blast/scripts/
mindhive:scripts qigroup$ ls
Higher_Level_reg_rewrite.rtf      recon.sh
dcmnii.sh                          recon_bids.sh
edit_freesurfer_surface.py        surfreg
mindhive:scripts qigroup$ python edit_freesurfer_surface.py
```

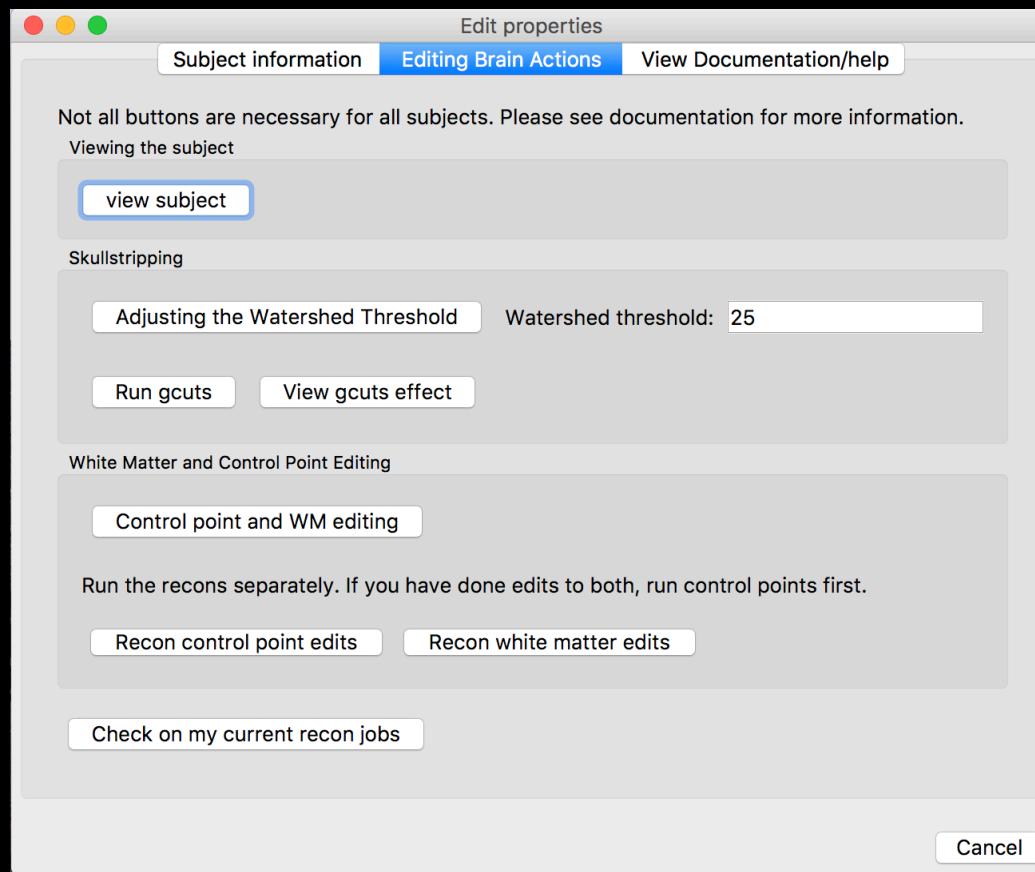
Using the python script

- 1) Designate directory with FS reconstructed data
- 2) Select subject, check for surface, and hit OK



Look for brain scan abnormalities

- 1) Click on Editing Brain Actions tab
 - View subject



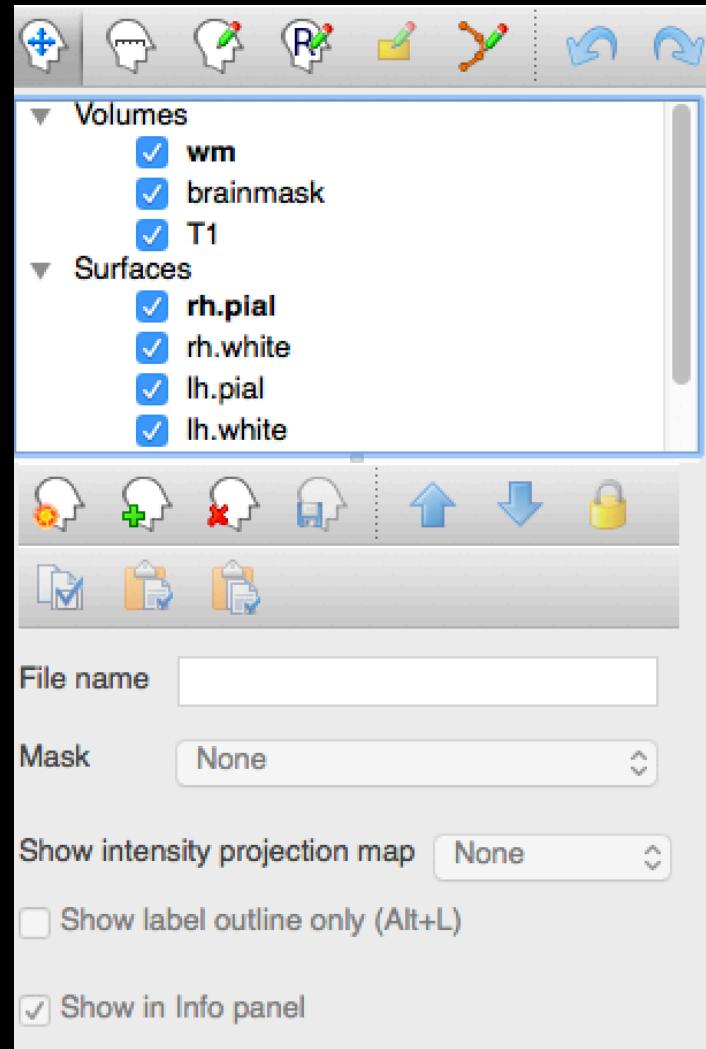
Look for brain scan abnormalities

- 1) This will bring up Freeview - FS visualization software



FS edits: Gray matter

- Freeview default with python code includes most volumes and surfaces you'll need



Check movement

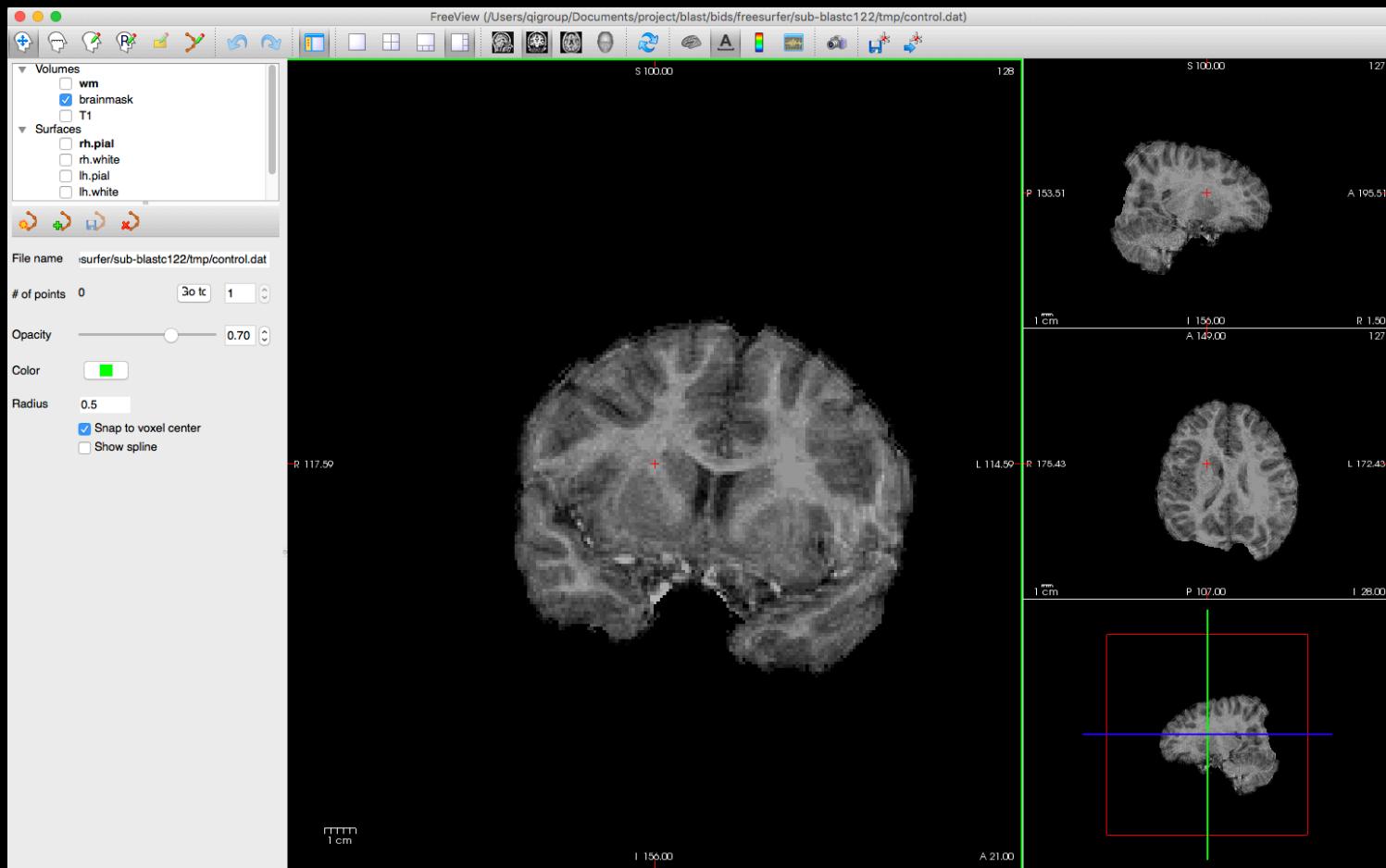
1) Movement assessment

1) If it looks like there are “rings” around the brain, that’s a tell-tale sign of movement



Check movement

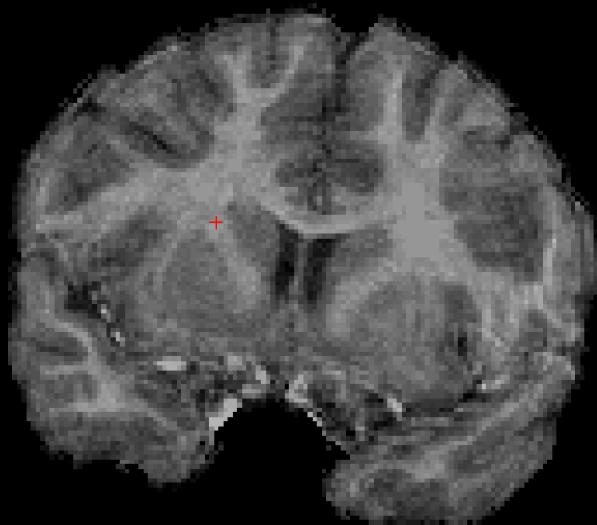
1) Check our data in Freeview: brainmask



Update movement

1) FS edit(s): none

- If there are rings, enter 1 in the .QC_template.xlsx spreadsheet
 - Automatically disqualifies scan
- If there is not a motion artifact, enter 0

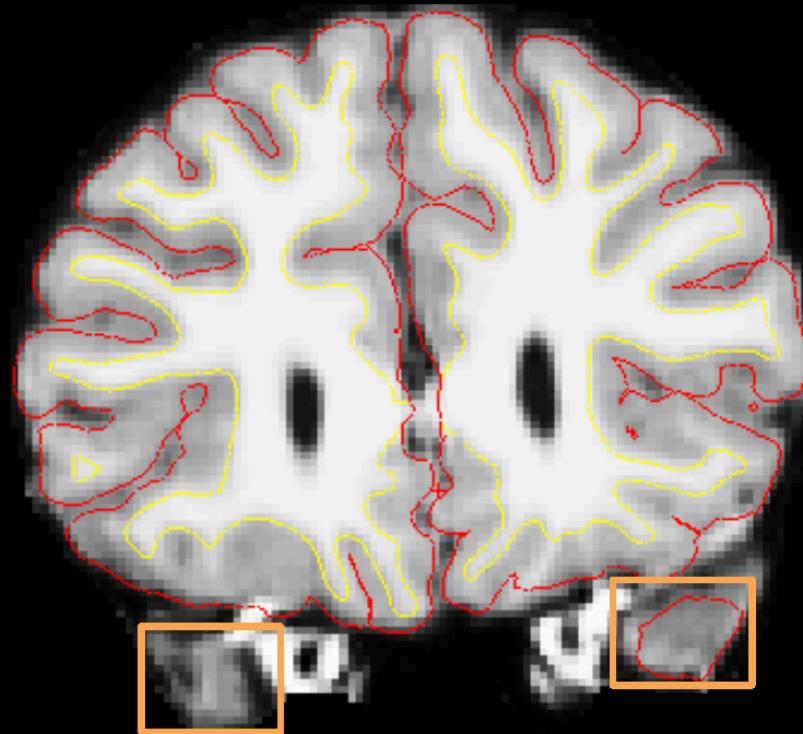


| Subject | Final_Score | Excessive_movement |
|---------------|-------------|--------------------|
| sub-blastc122 | | 1 |

Check Temporal Pole (TP)

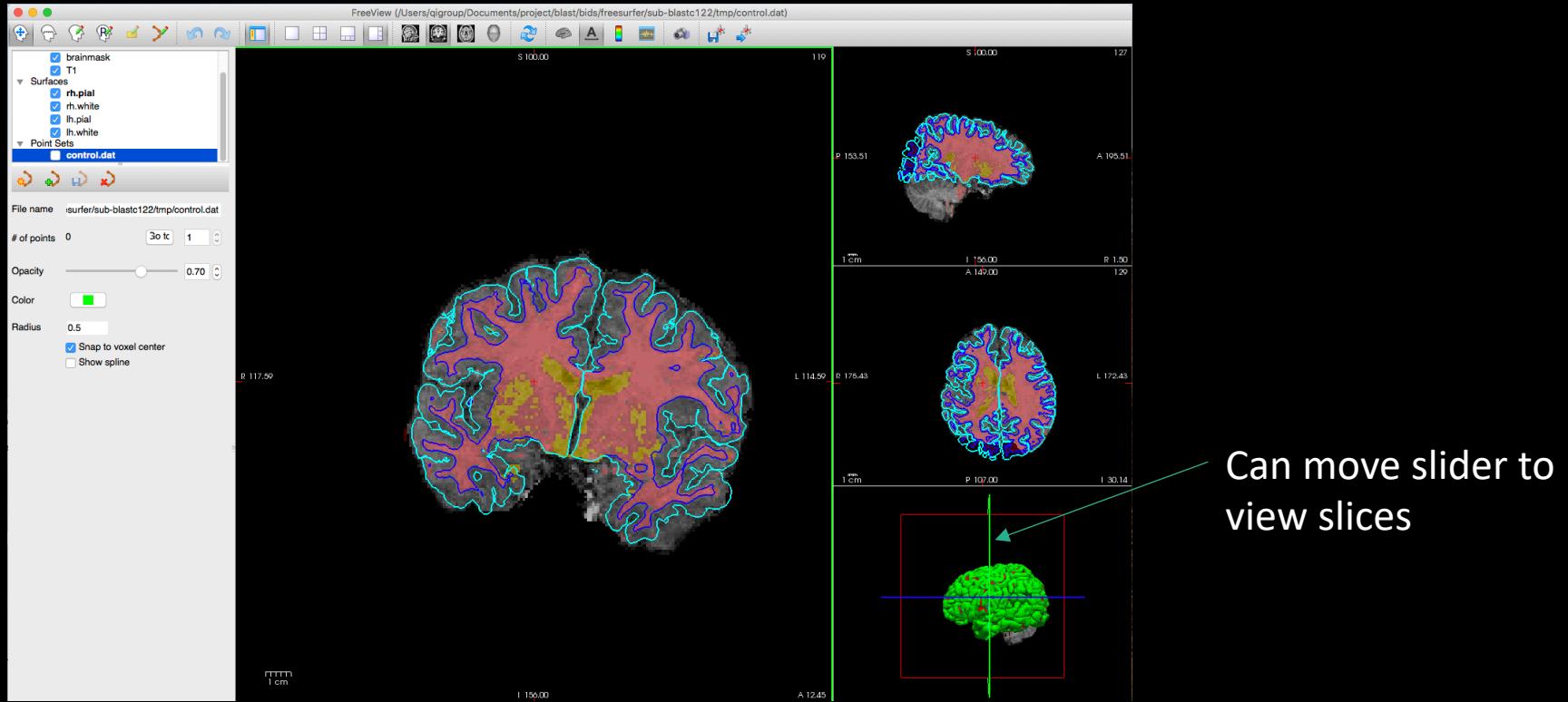
2) Temporal pole assessment

Error: When there is a whole section of temporal lobe not included in red



Check TP

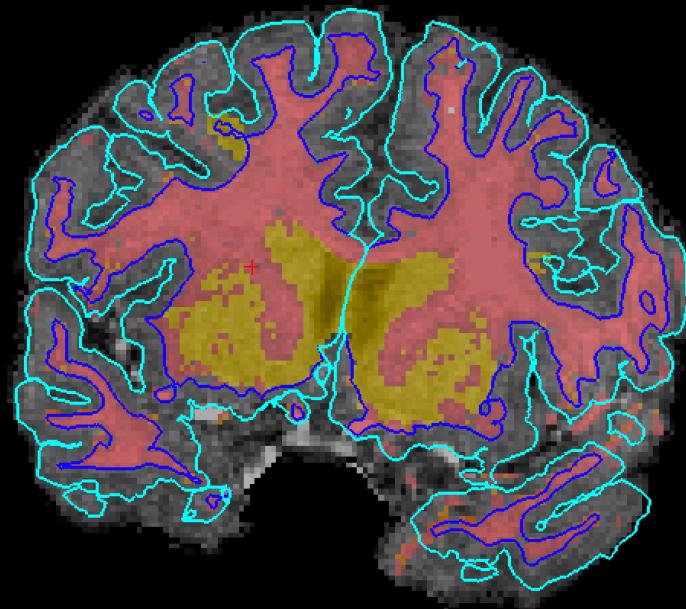
2) Temporal pole assessment in Freeview
Check in at least 3 consecutive slices
-slice 1:



Check TP

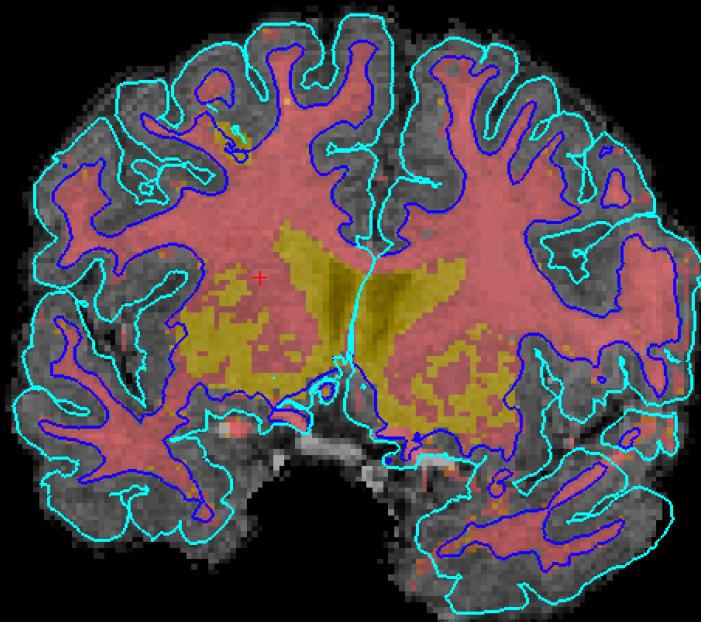
2) Temporal pole assessment in Freeview
Check in at least 3 consecutive slices

-slice 2:



Check TP

- 2) Temporal pole assessment in Freeview
Check in at least 3 consecutive slices
-slice 3:



Update TP

Update .xlsx sheet

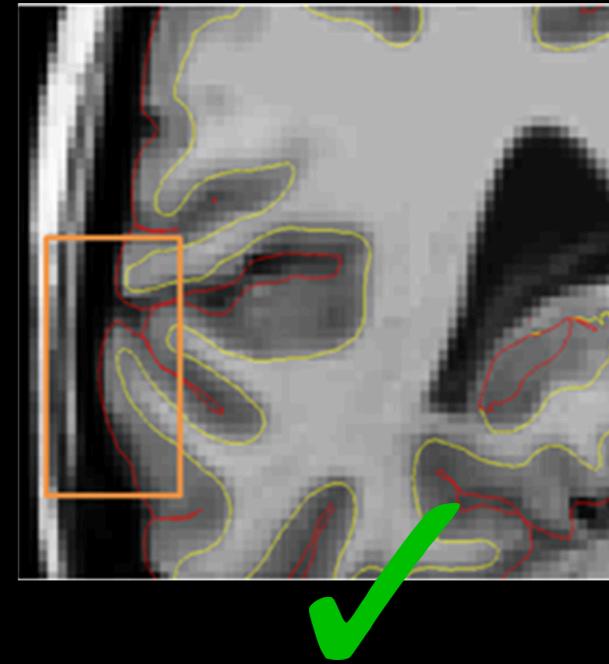
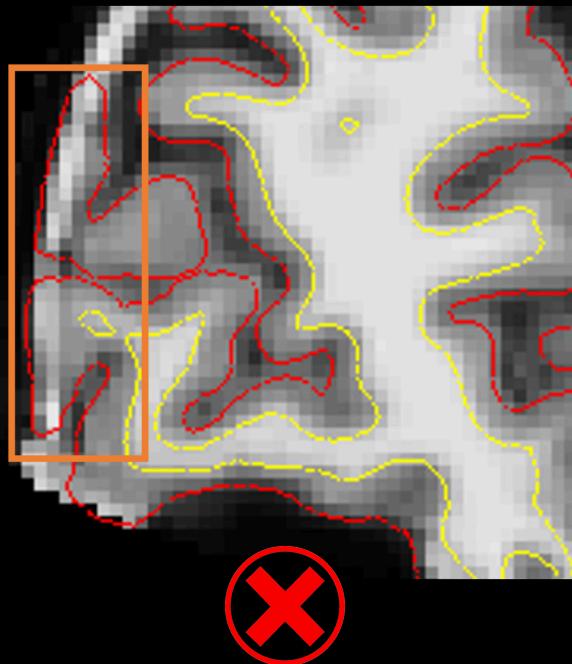
- If there is TP missing, enter 1 in the .QC_template.xlsx spreadsheet
- If there is no missing TP in 3 consecutive slices, enter 0

| Subject | Final_score | Excessive_movement | Temporal_pole_missing_LH | Temporal_pole_missing_RH |
|---------------|-------------|--------------------|--------------------------|--------------------------|
| sub-blastc122 | | 1 | 1 | 1 |

Check Dura

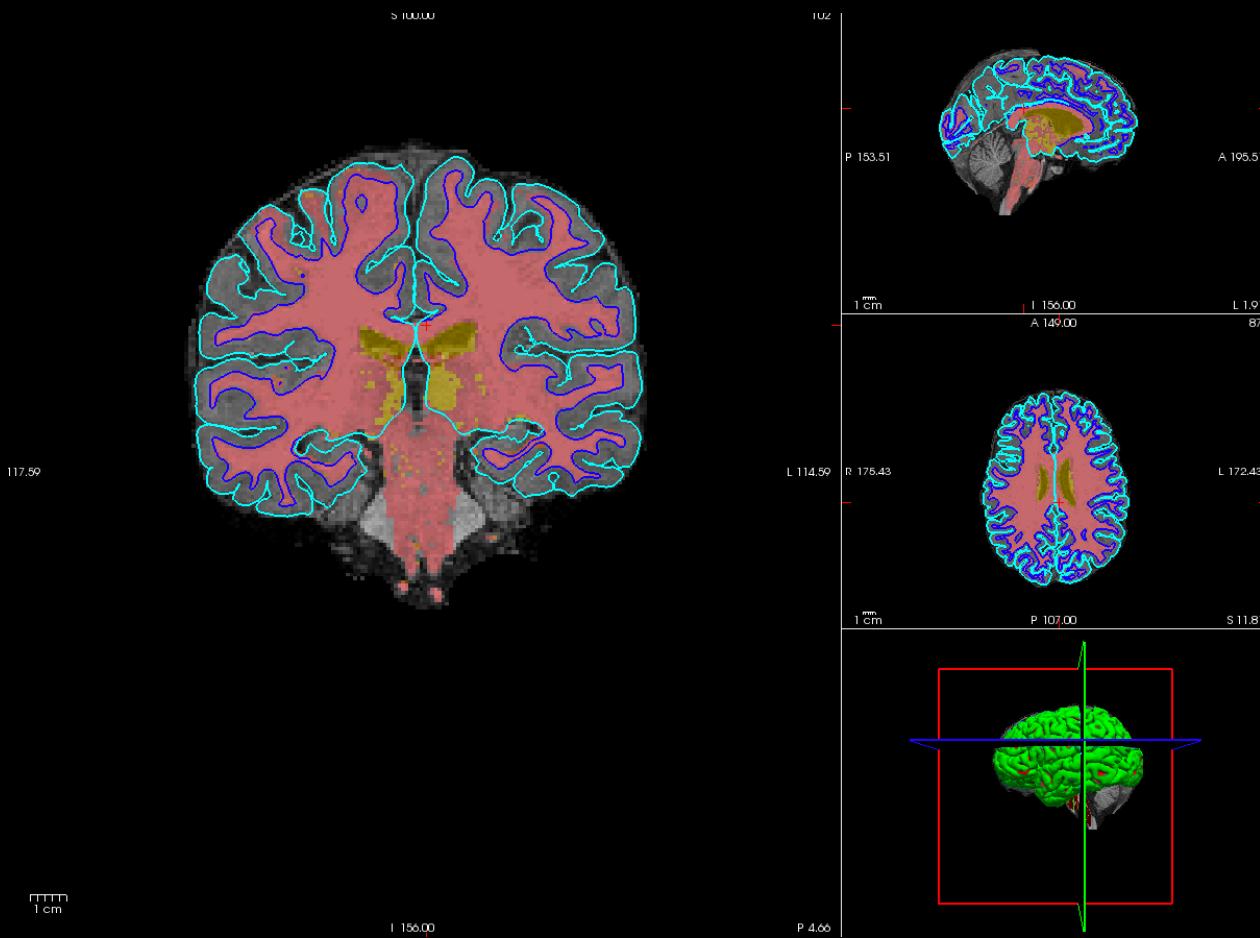
3) Non-brain tissue included in pial surface

Example of dura included (left) and not included (right) in pial surface reconstruction



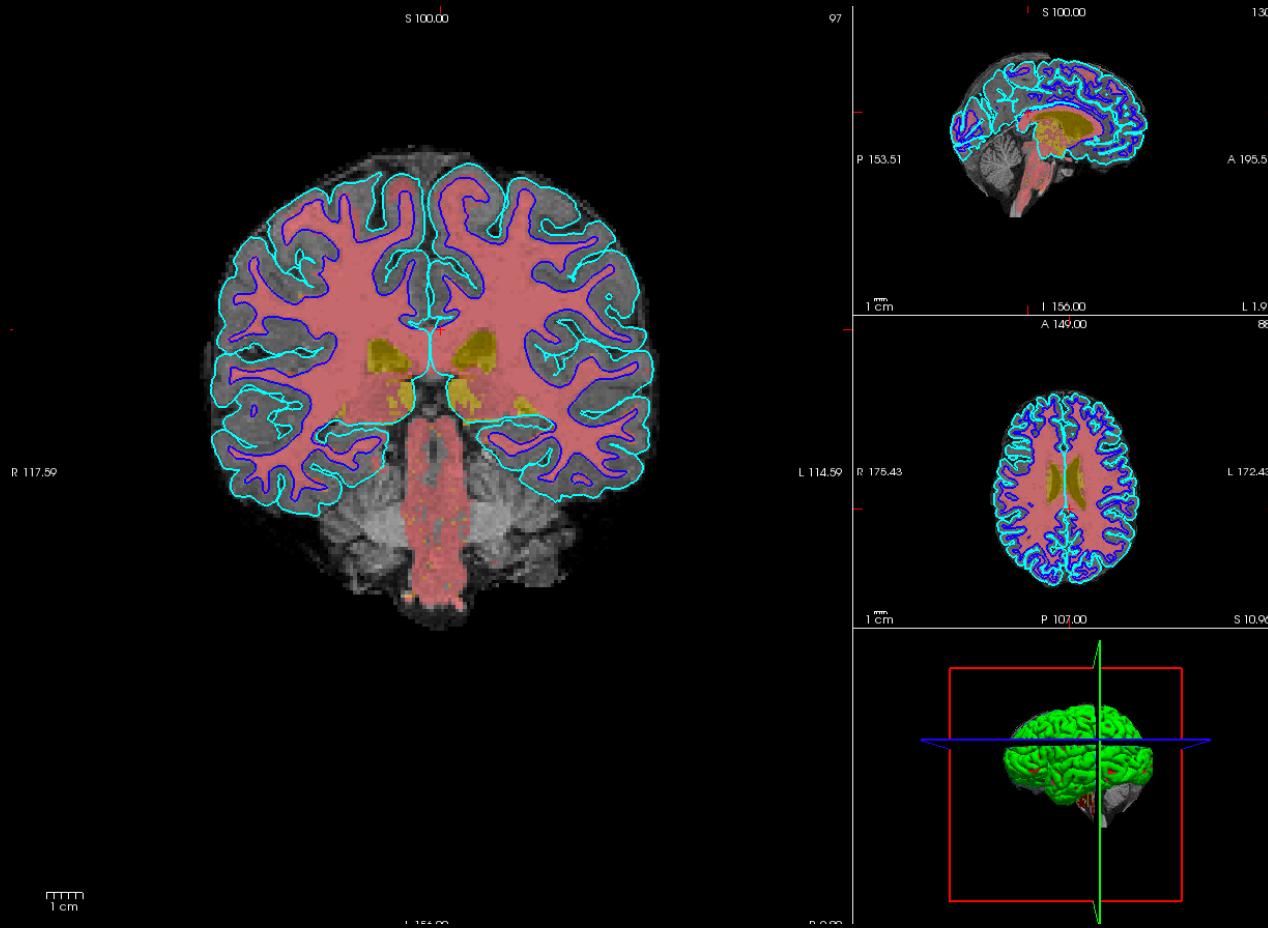
Check Dura

3) Check 3 consecutive slices



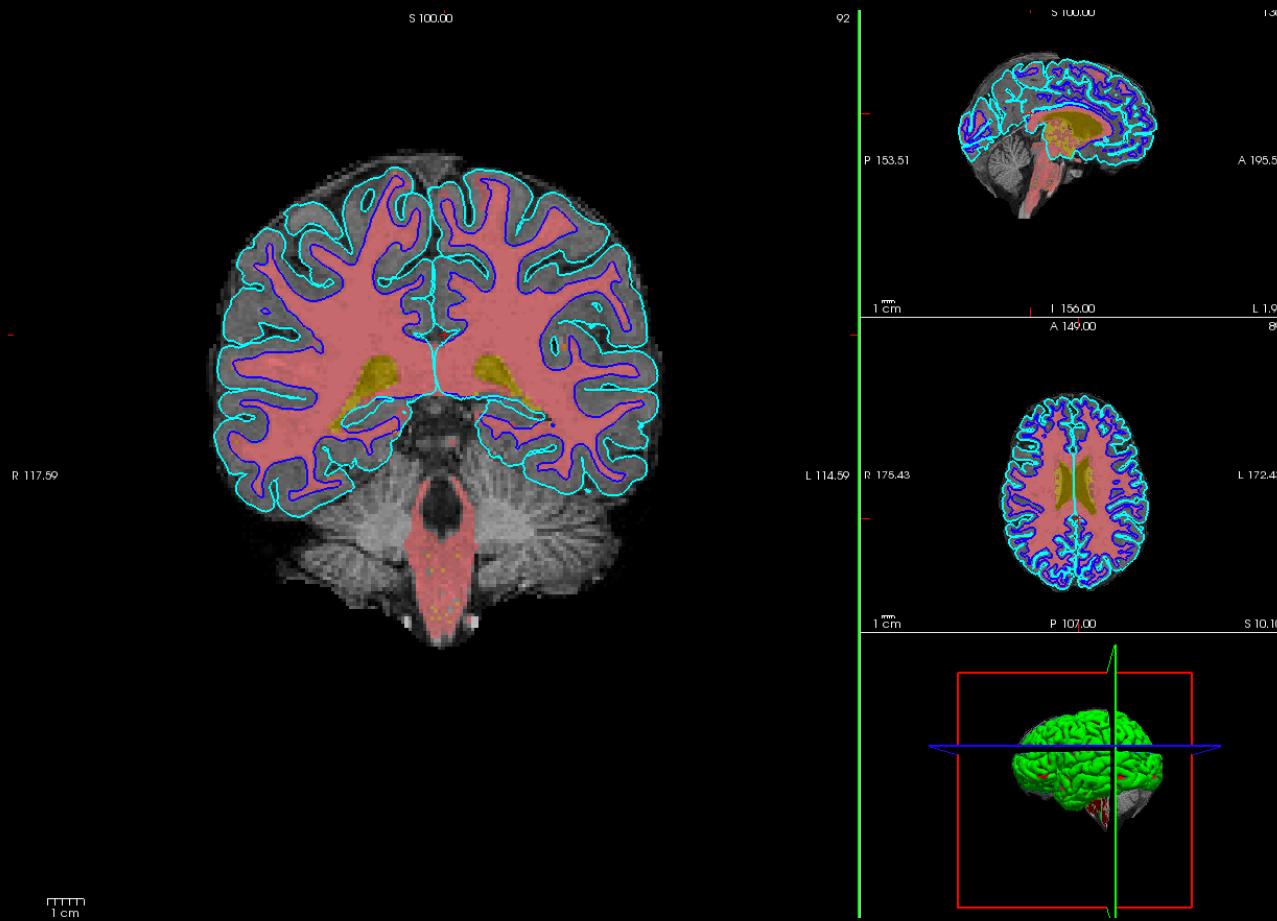
Check Dura

3) Check 3 consecutive slices



Check Dura

3) Check 3 consecutive slices



Update Dura

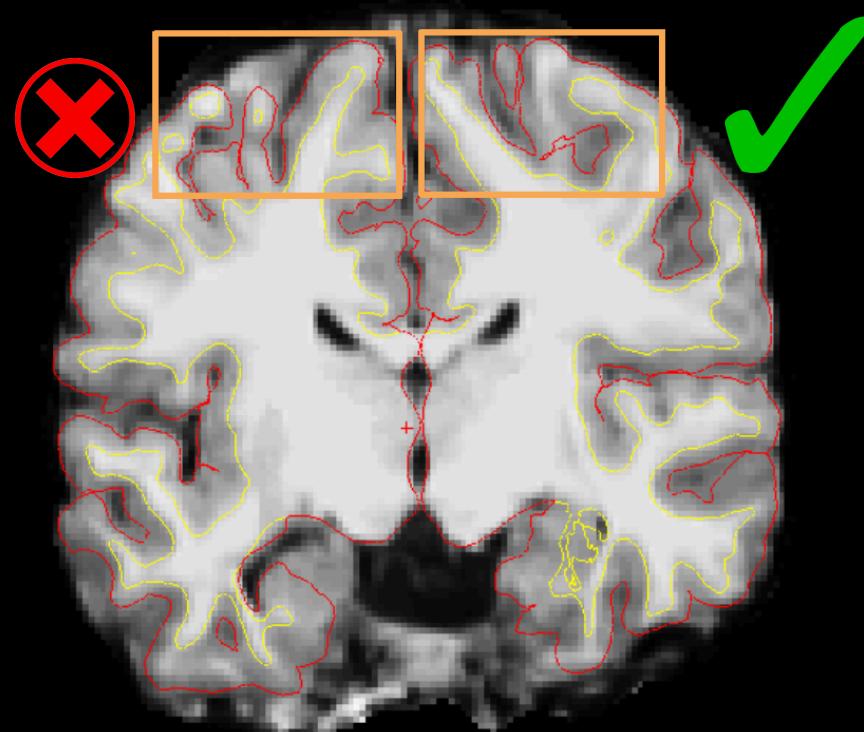
Update .xlsx sheet

| Subject | Final_score | Excessive_movement | Temporal_pole_missing_LH | Temporal_pole_missing_RH | Dura_LH | Dura_RH |
|---------------|-------------|--------------------|--------------------------|--------------------------|---------|---------|
| sub-blastc122 | | 1 | 1 | 1 | 0 | 0 |

Check omission of other regions

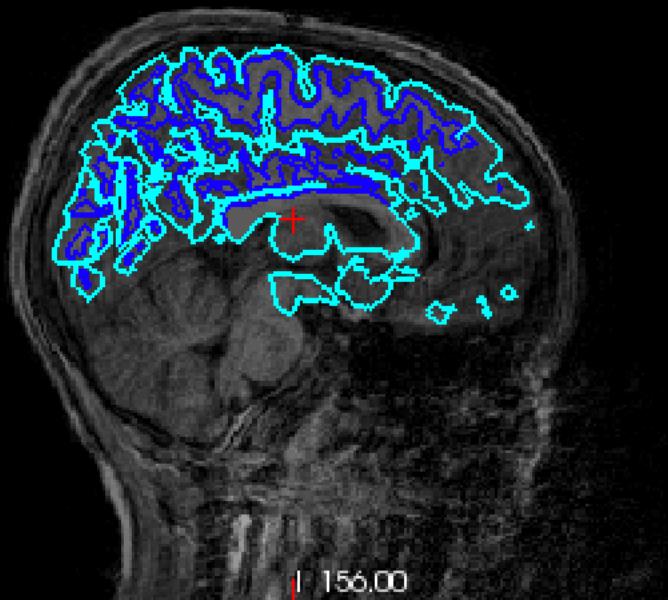
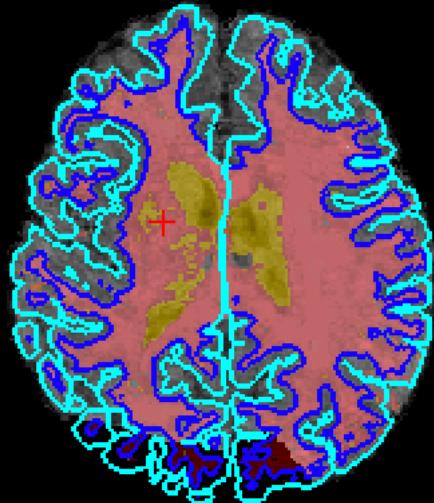
4) Other parts of brain not included

Where there is a whole section of temporal lobe not included in red



Check omission of other regions

E.g. Checking anterior brain regions



Update other areas in spreadsheet

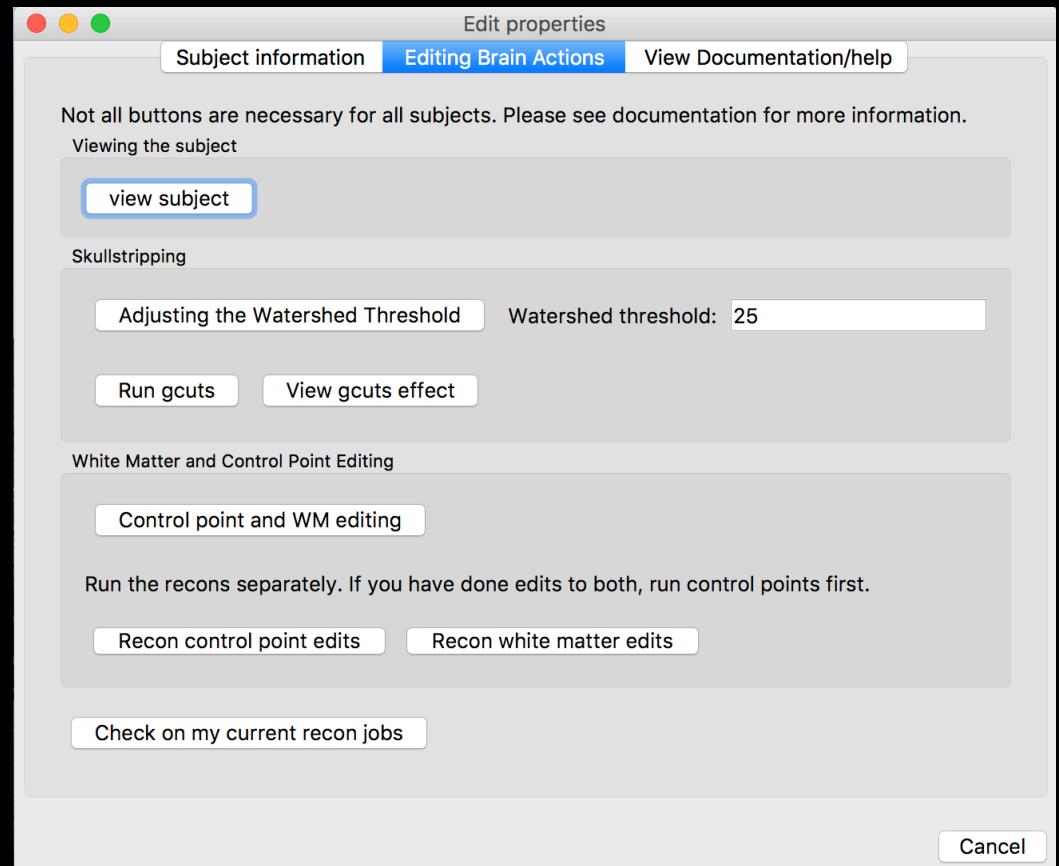
In .xlsx sheet

| A | B | C | D | E | F | G | H | I | J | K | L | M |
|---------------|-------------|--------------------|--------------------------|--------------------------|---------|---------|---------------------|---------------------|----------------------------|----------------------------|----------------------|----------------------|
| Subject | Final_score | Excessive_movement | Temporal_pole_missing_LH | Temporal_pole_missing_RH | Dura_LH | Dura_RH | Missing_anterior_LH | Missing_anterior_RH | Missing_Superior_Medial_LH | Missing_Superior_Medial_RH | Missing_Posterior_LH | Missing_Posterior_RH |
| sub-blastc122 | 5 | 1 | 1 | 1 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 0 |

FS edits: Gray matter

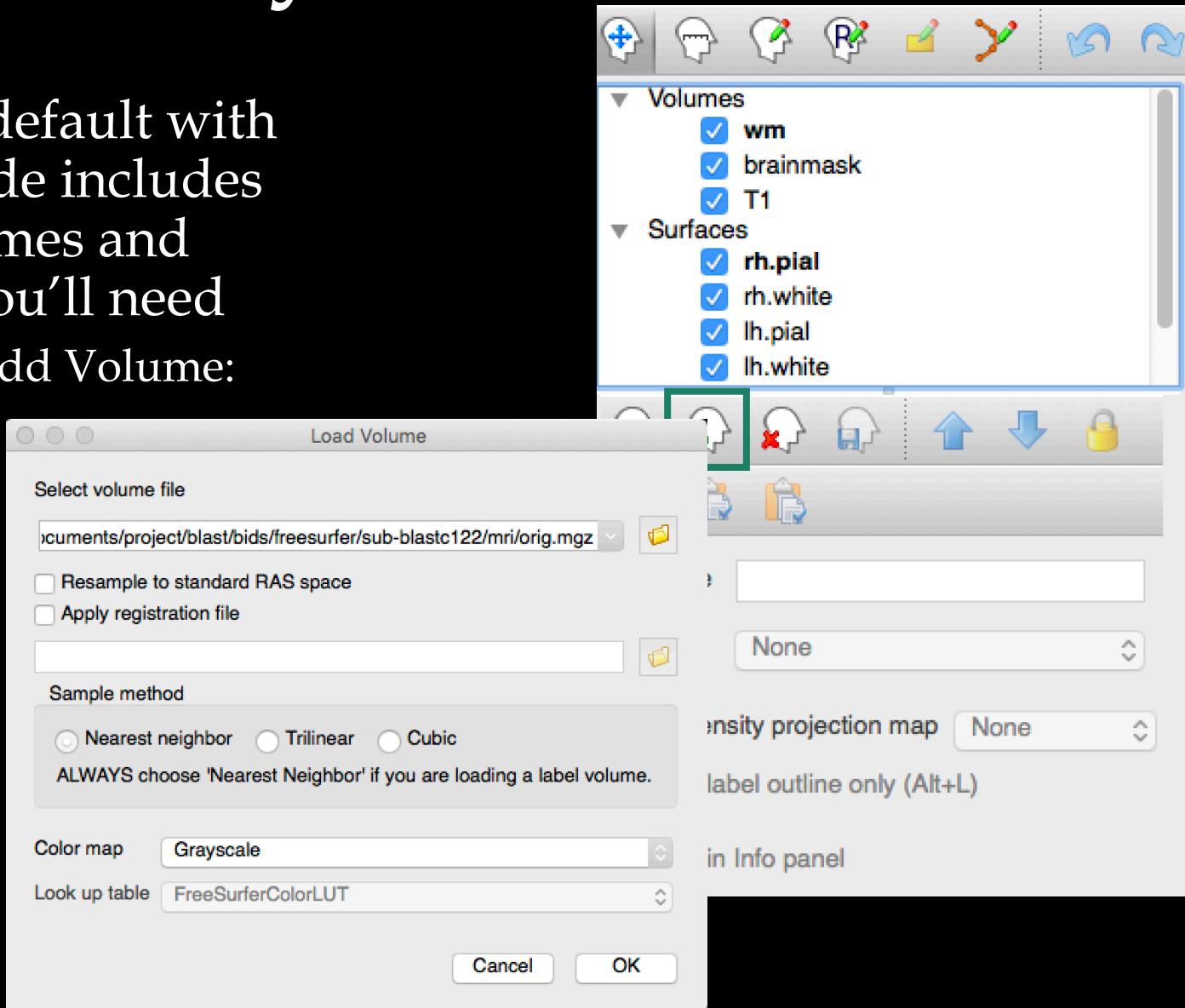
FS Edits:

- Make sure you're viewing a subject



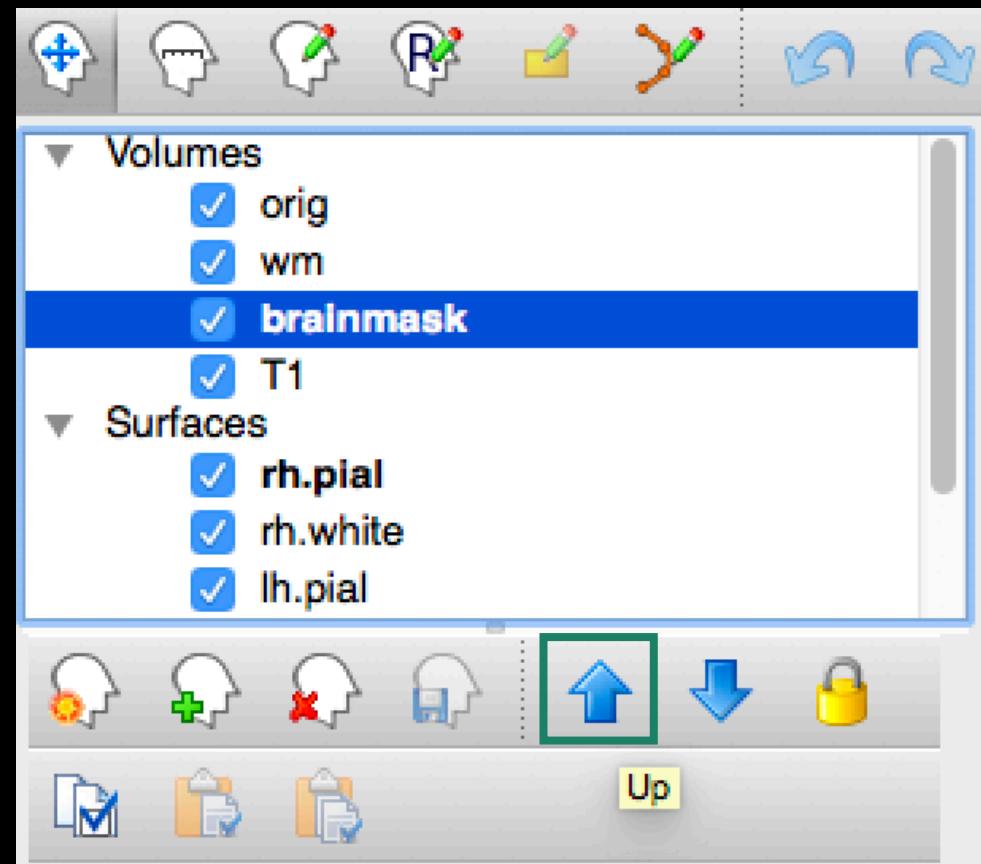
FS edits: Gray matter

- Freeview default with python code includes most volumes and surfaces you'll need
- GM edits: add Volume: orig.mgz



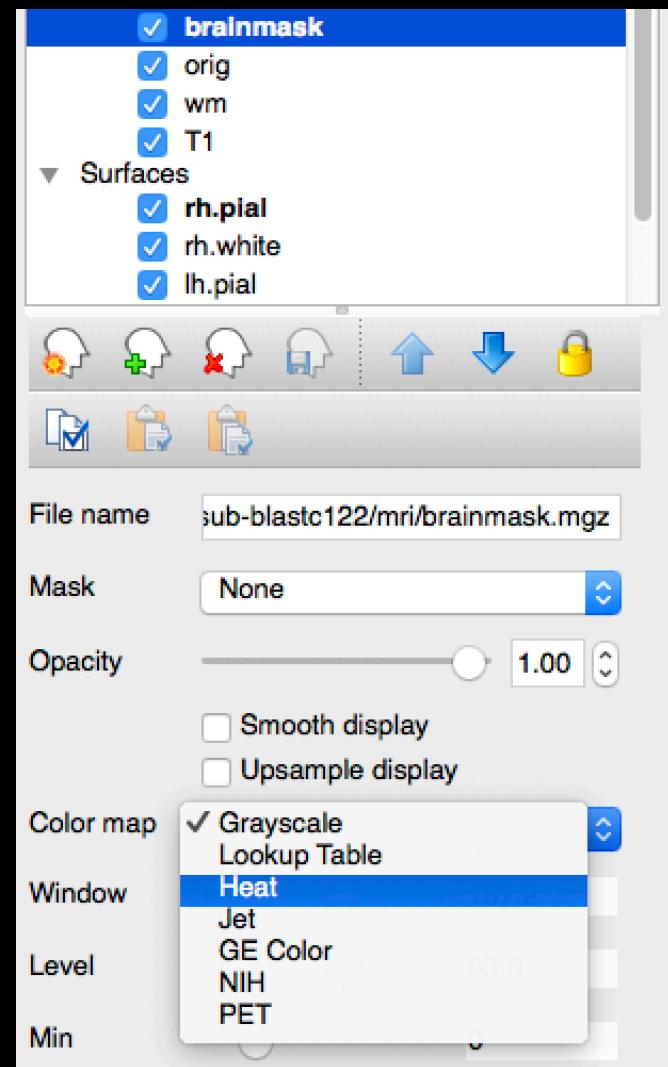
FS edits: Gray matter

- Make sure brainmask is above orig.mgz



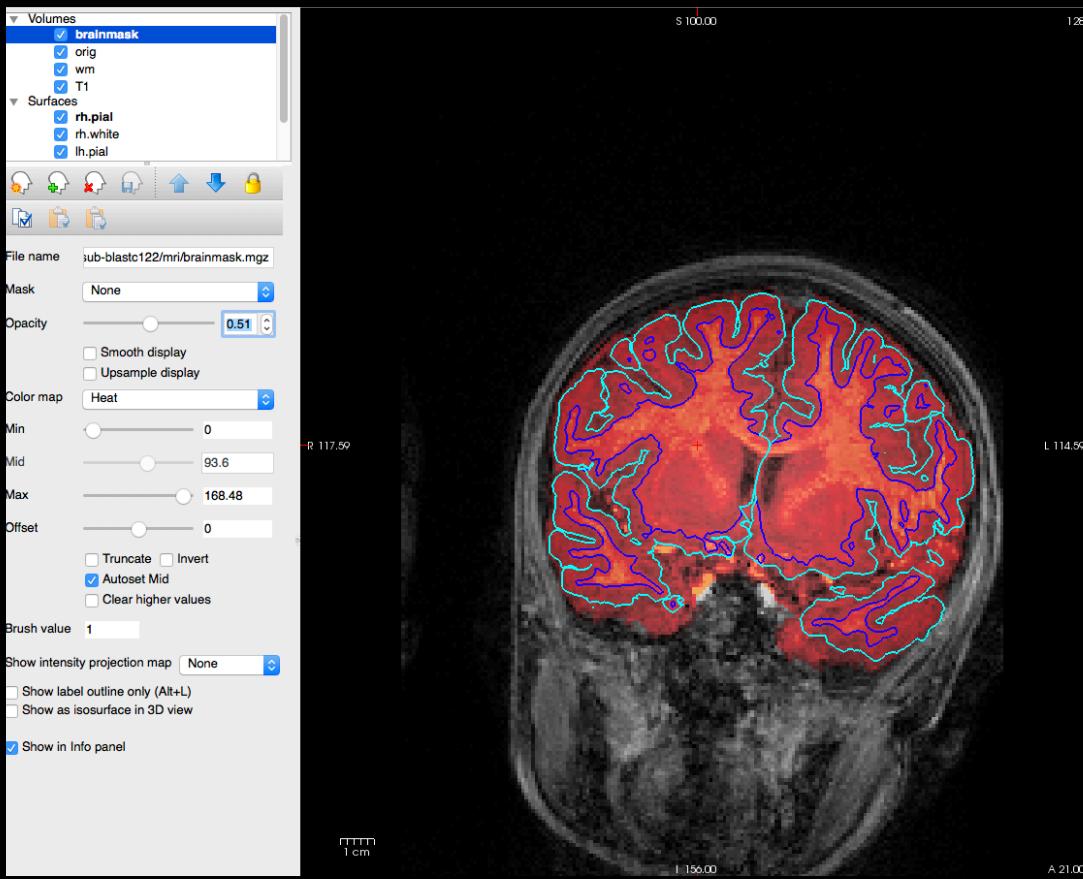
FS edits: Gray matter skullstripping

- Make sure brainmask is above orig.mgz
 - Change brainmask colormap to Heat



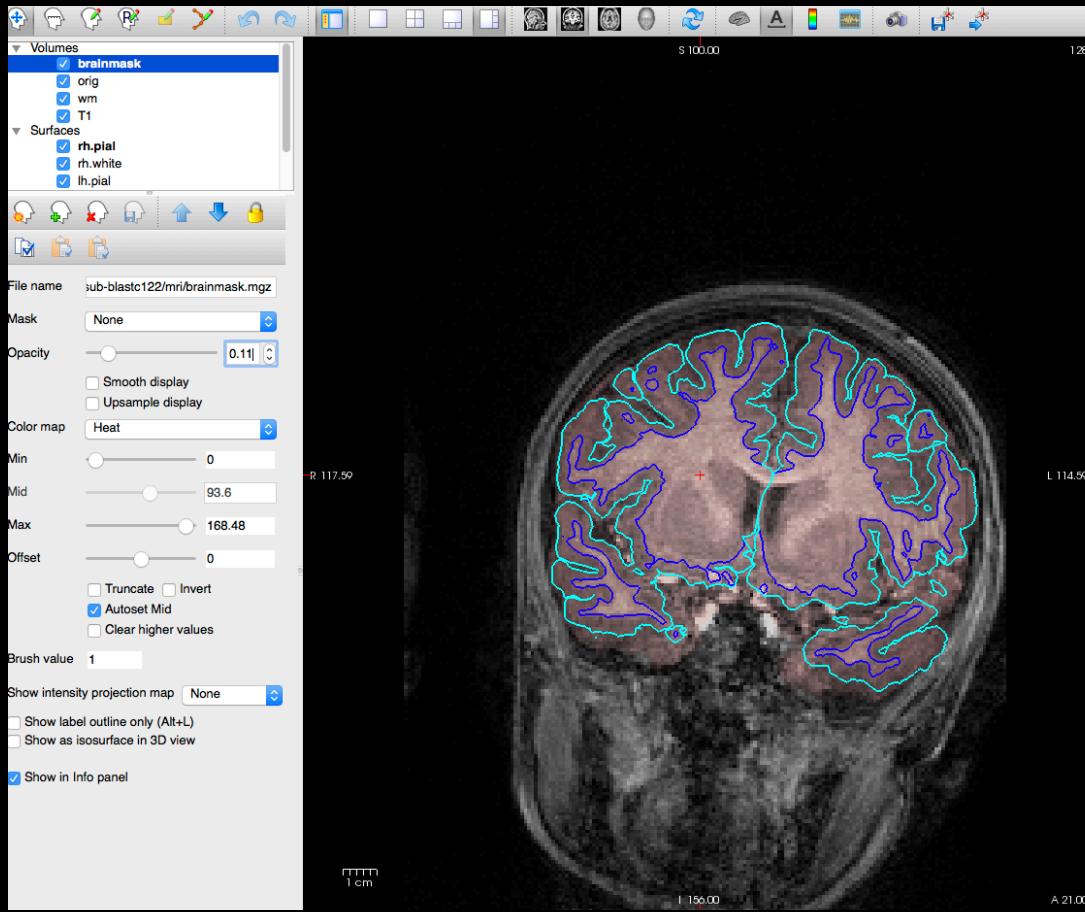
FS edits: Gray matter skullstripping

- Change opacity



FS edits: Gray matter skullstripping

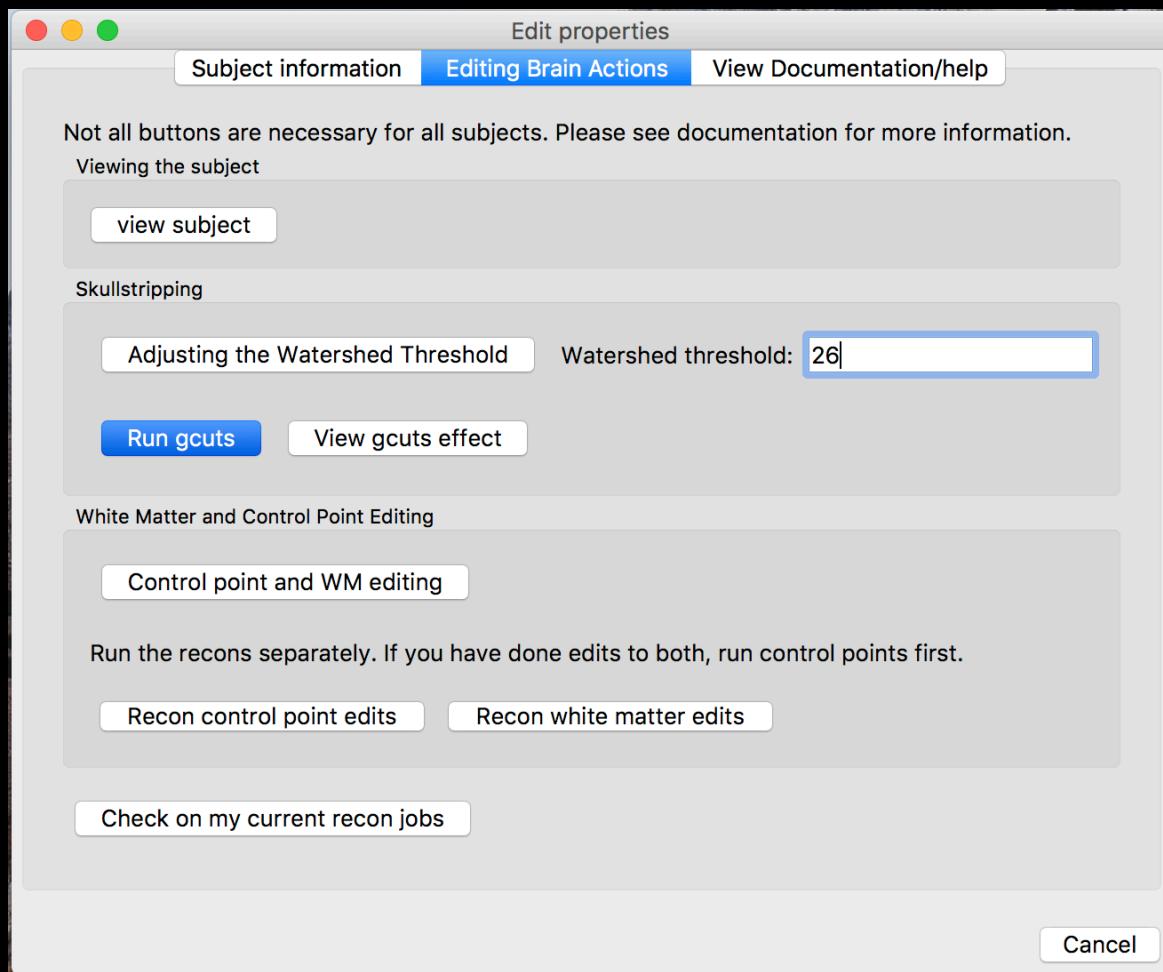
- Change opacity (~.11 seems to work decently)



FS edits: Gray matter skullstripping

FS Edits:

- If not enough brain is included, you can increase the watershed threshold from 25 to 26
- If too much included, decrease watershed threshold
- Run gcuts



FS edits: Gray matter skullstripping

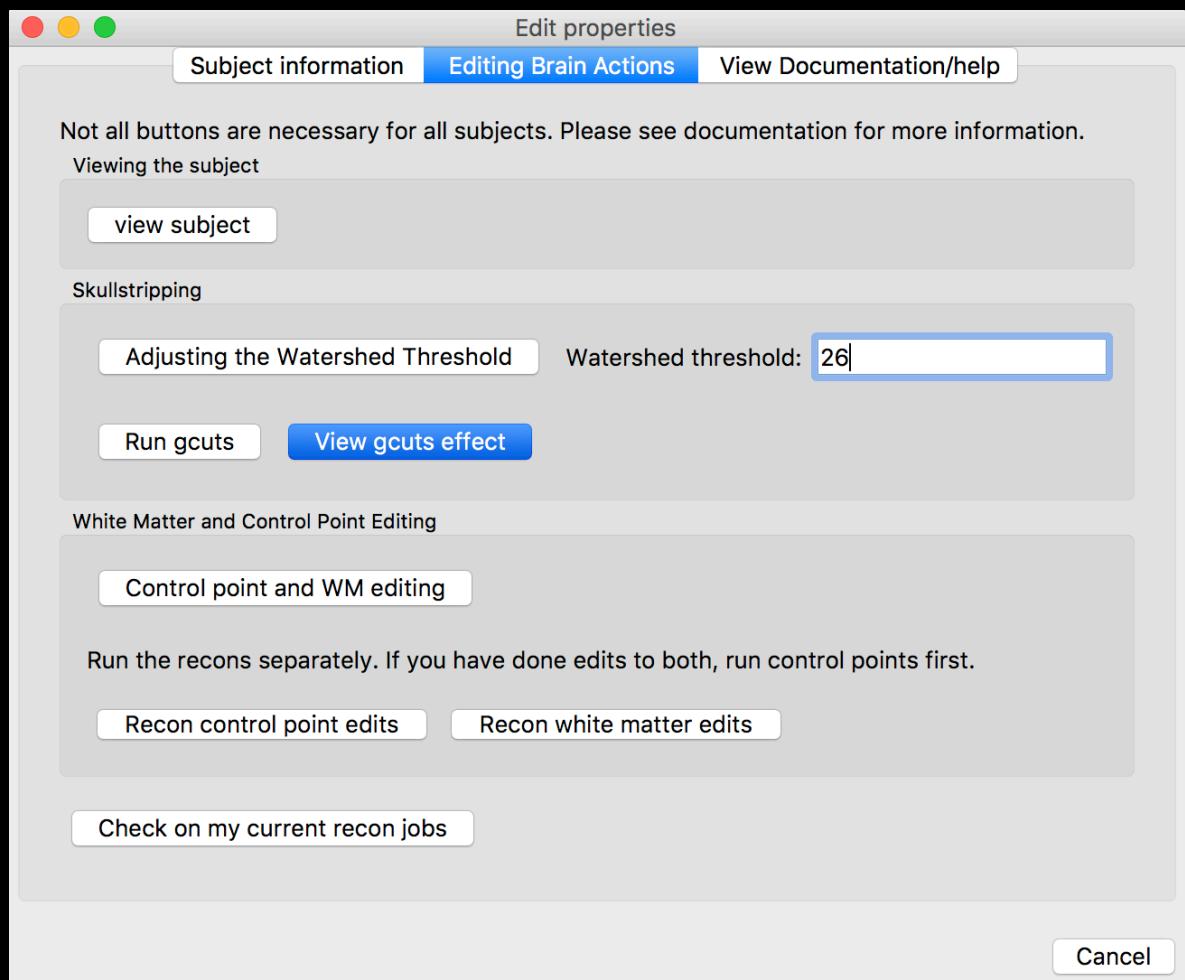
FS Edits:

- Check to make sure the gcuts finished without error in Terminal window

```
Started at Mon May 6 16:53:37 EDT 2019
Ended   at Mon May 6 16:54:18 EDT 2019
#@## recon-all-run-time-hours 0.011
recon-all -s sub-blastc122 finished without error at Mon May 6 16:54:18 EDT 201
9
done
[]
```

FS edits: Gray matter skullstripping

Check gcuts effects

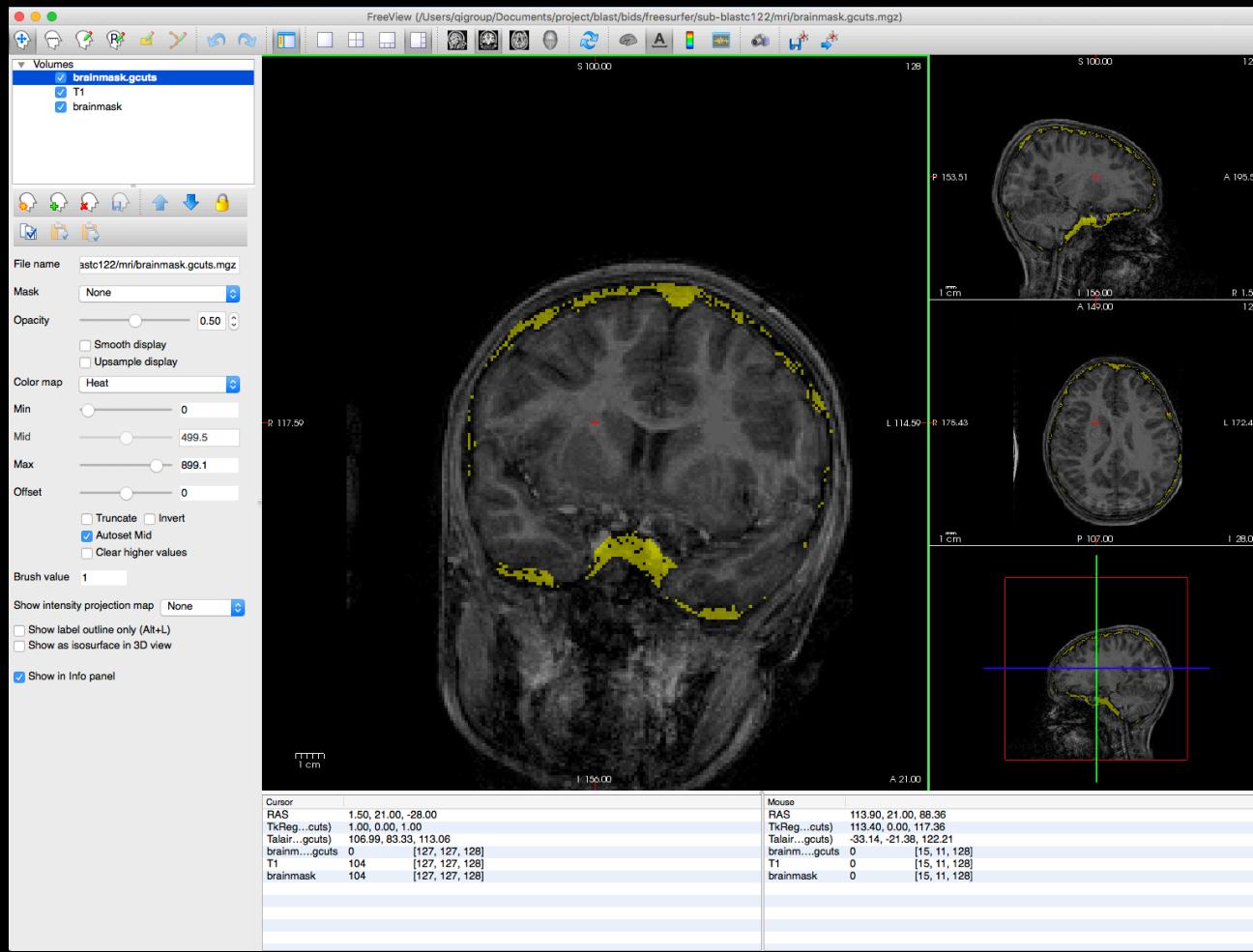


FS edits: Gray matter skullstripping

Check gcuts effects

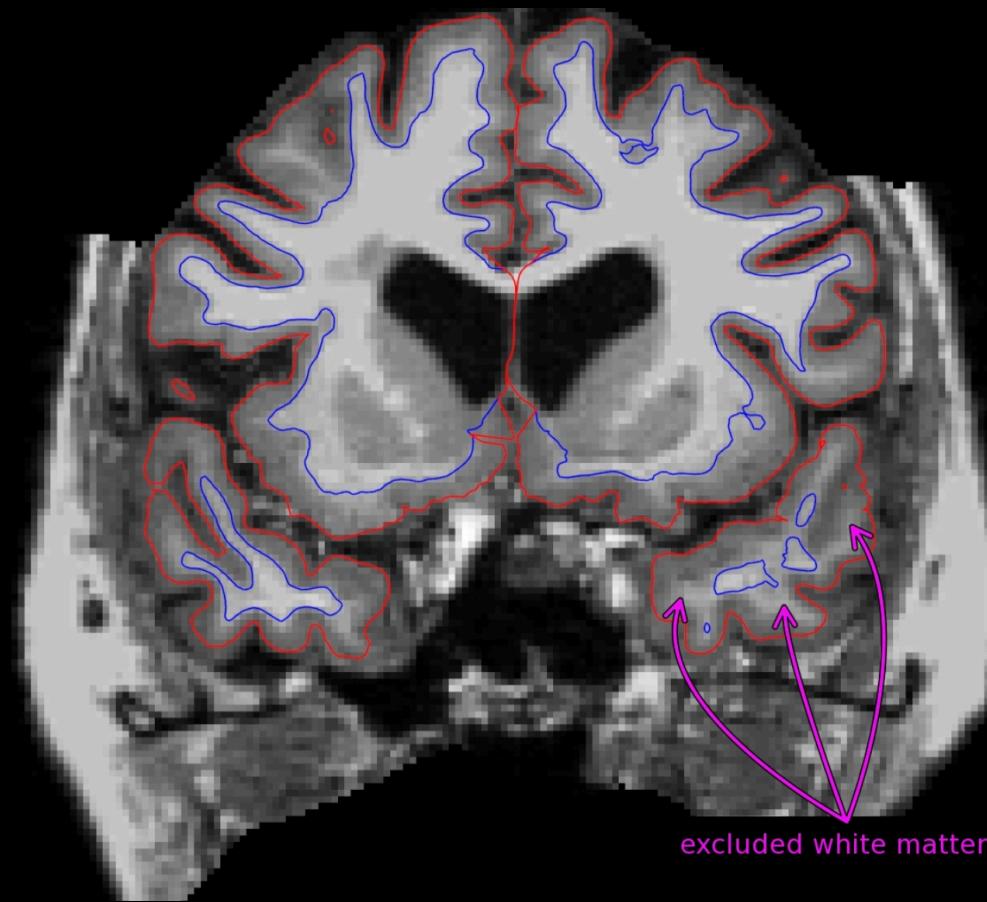
Yellow: regions that have been removed

-make sure this doesn't include gray matter, otherwise, go up in watershed parameters



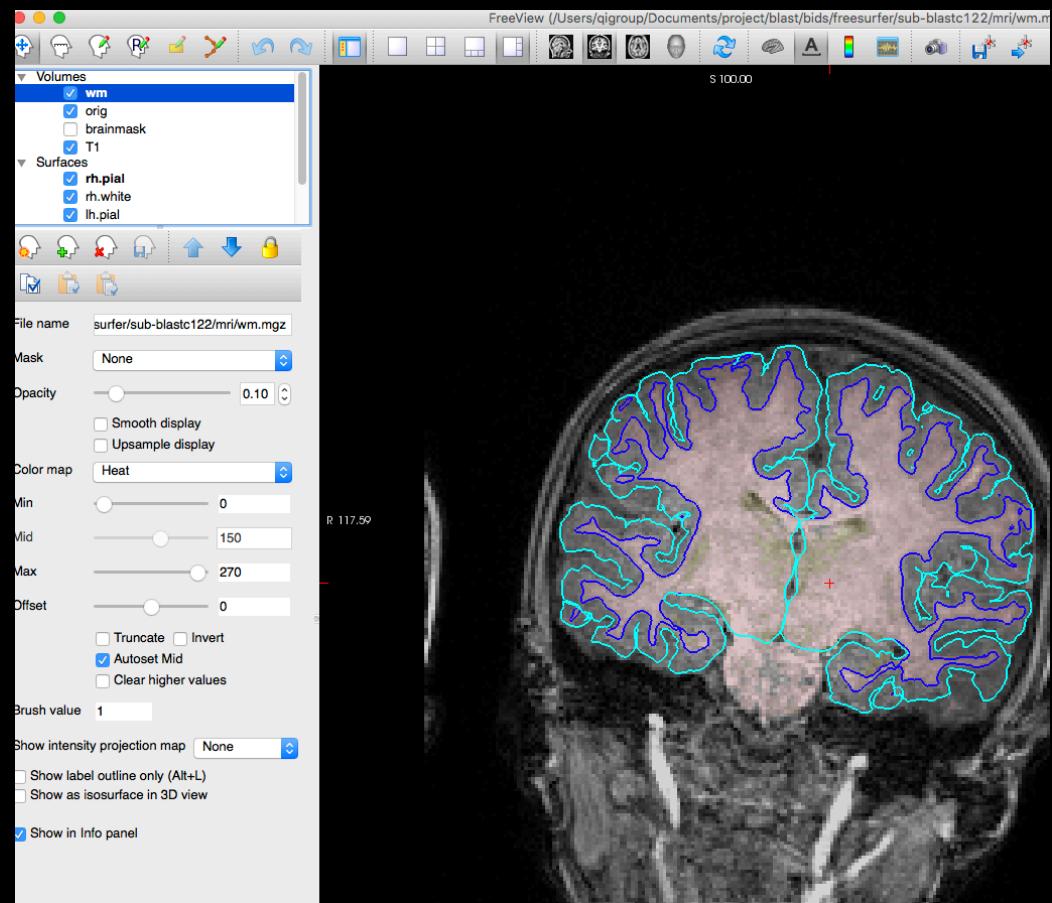
FS WM edits: Control points

- Control points are used to include white matter that is not inside the surface



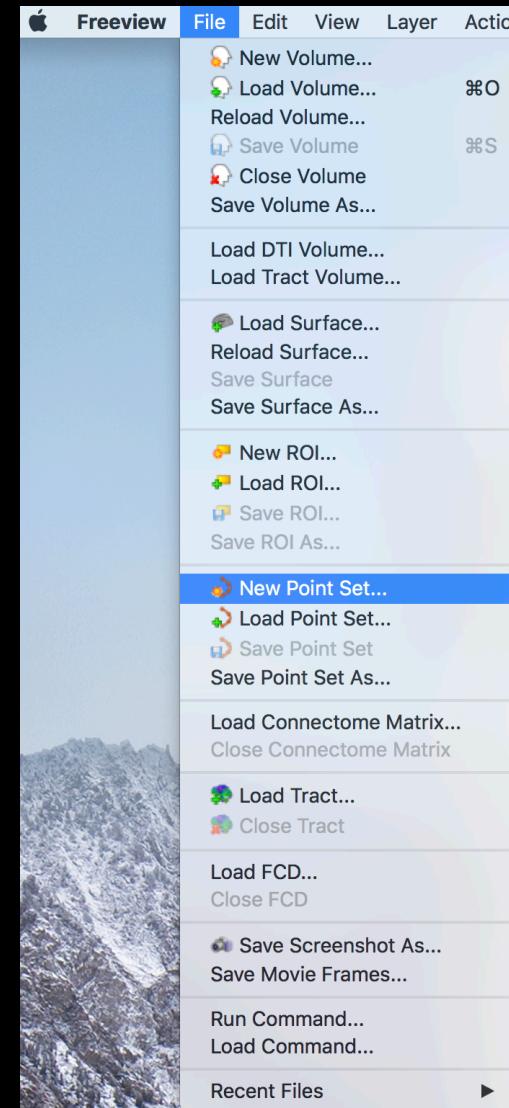
FS WM edits: Control points

- In Freeview: Make sure wm is above orig.mgz
 - Change wm colormap to Heat
 - Lower opacity



FS WM edits: Control points

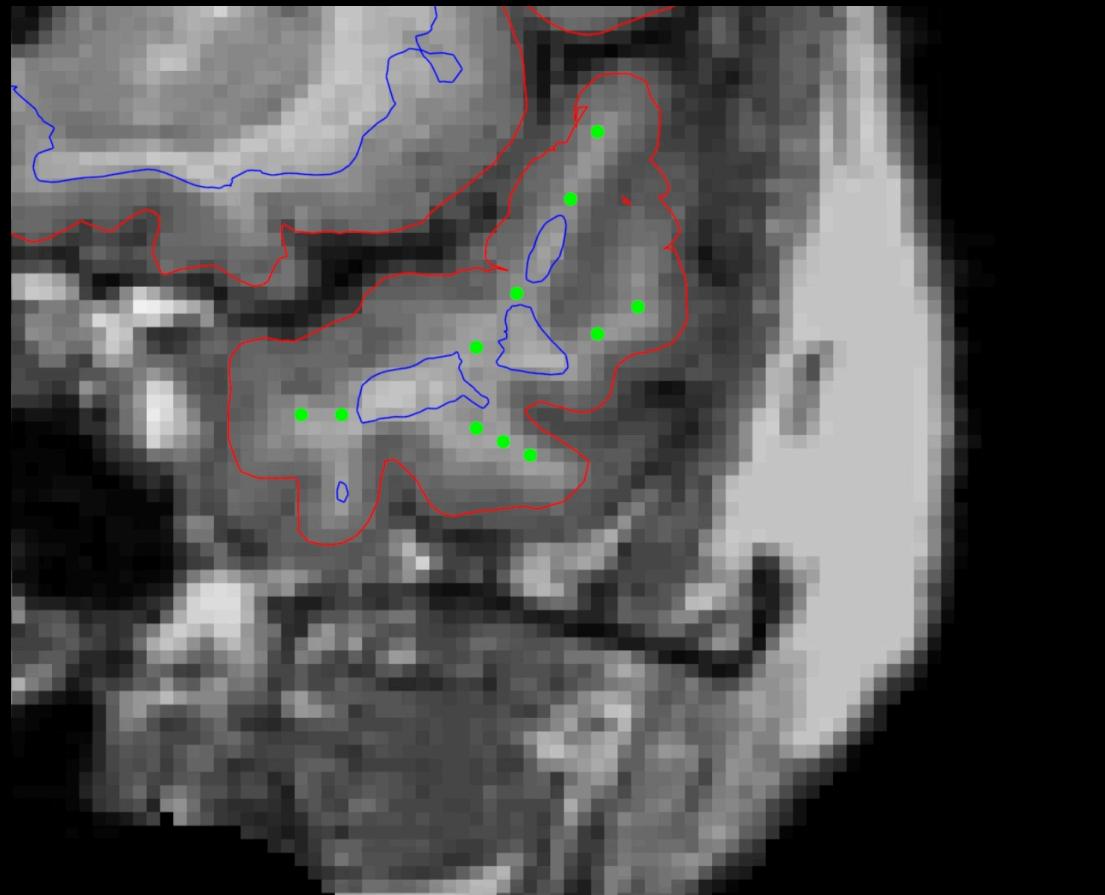
- Control points are used to include white matter that is not inside the surface
 - File>New point Set
 - If there's a large area, just put a lot of control points there
 - If you previously created a control point, you can Load Point Set



FS WM edits: Control points

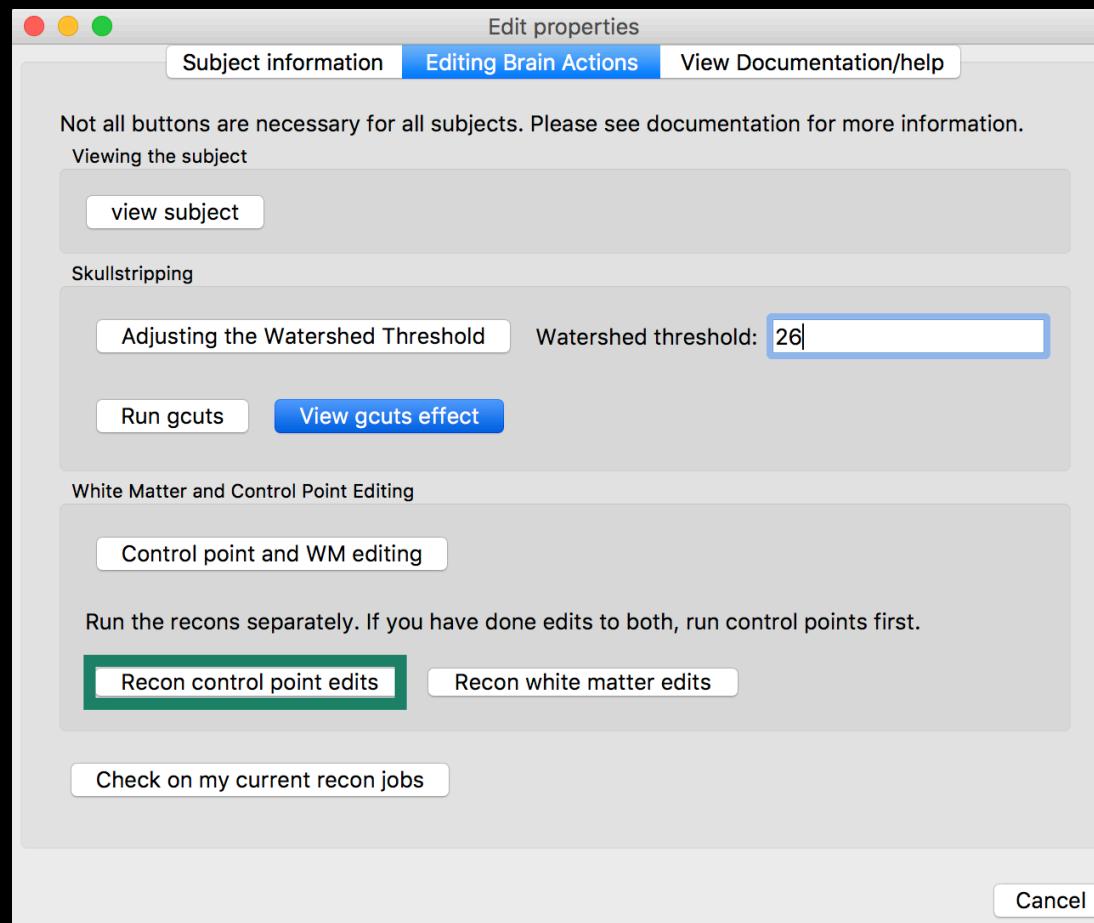
- Make sure you select "control points" instead of "way points", assign template volume to wm, then click "OK".

Control
points added
in green



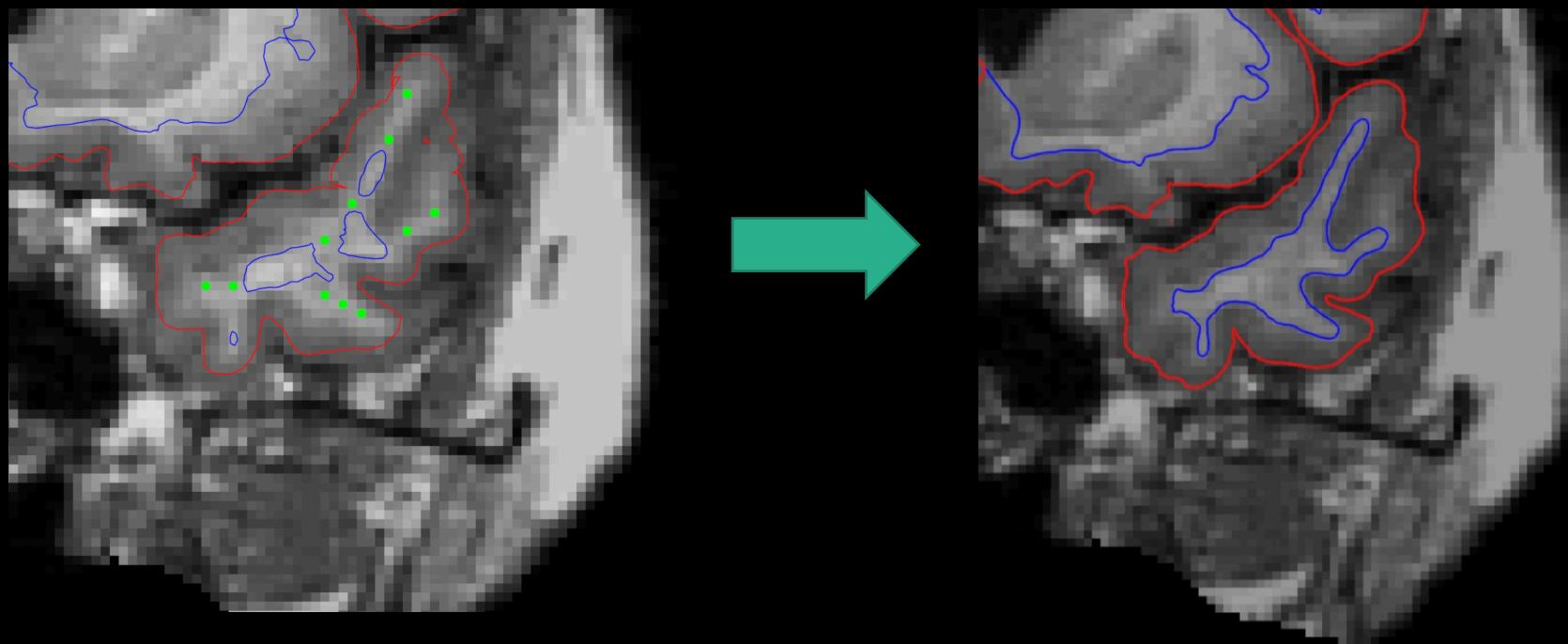
FS WM edits: Control points

- Run control point edits: This will take ~10 hours, leave it on the queue overnight.



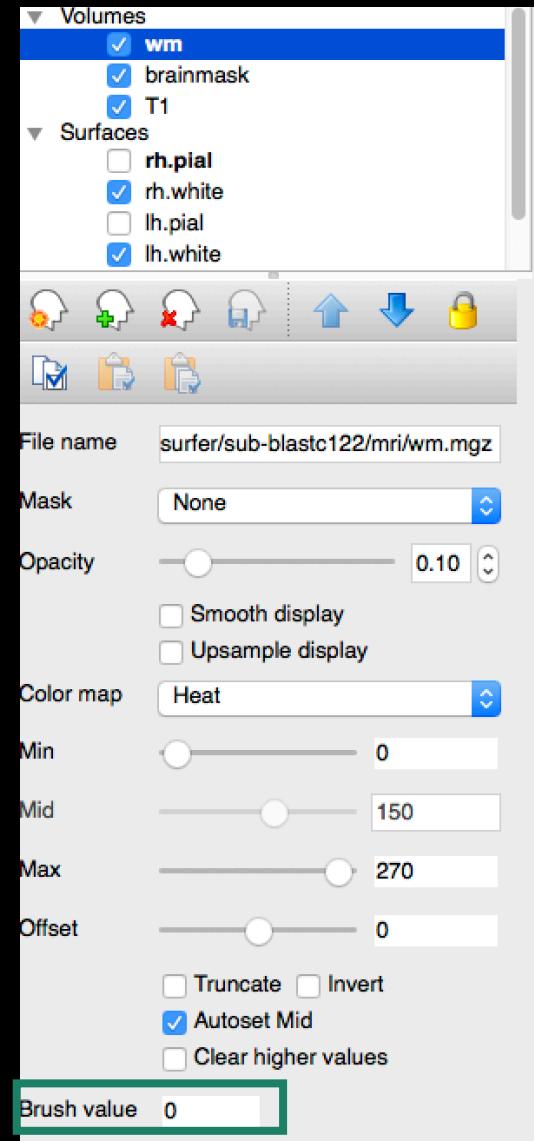
FS WM edits: Control points

- Check output to make sure WM is now improved



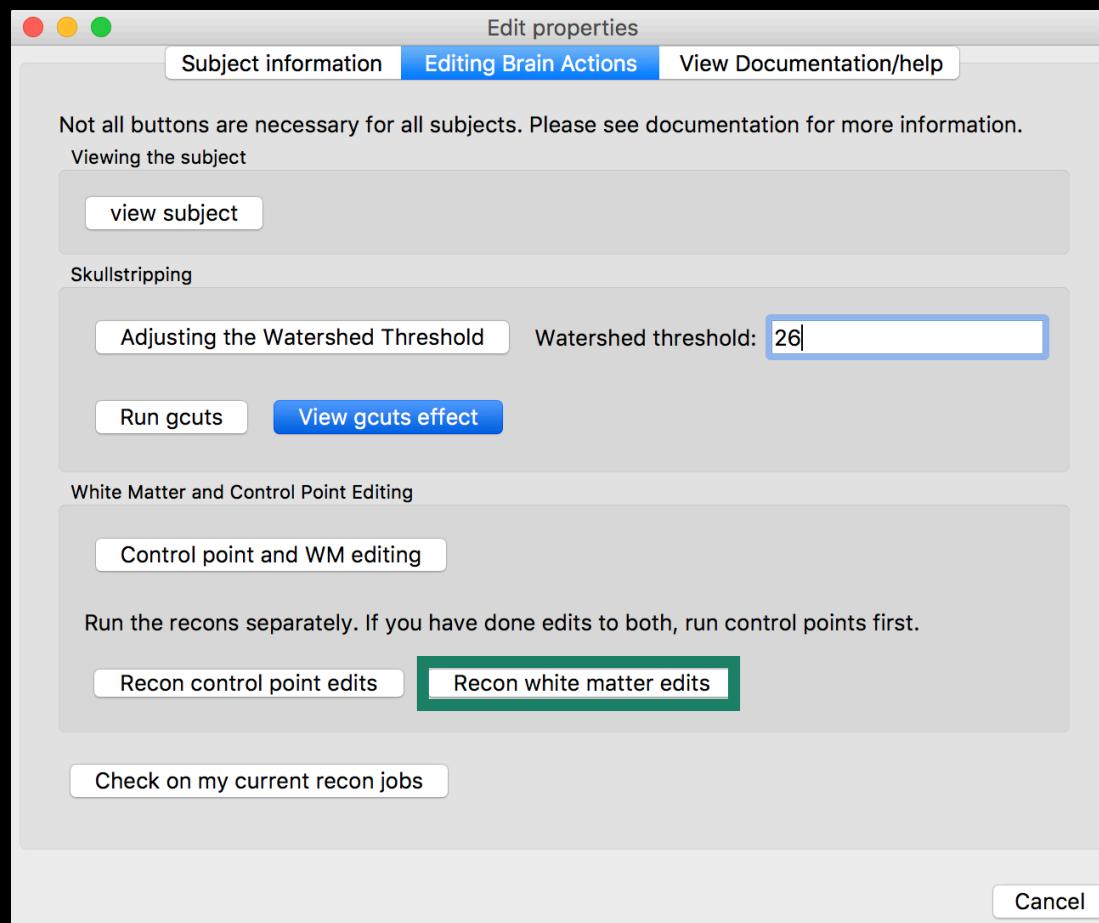
FS WM edits: White matter edits

- Edit the white matter volume to get rid of gray matter that is inside the surface boundary
- Again: Make sure wm is above orig.mgz
 - Change wm colormap to Heat
 - Lower opacity
- For any GM regions that were categorized as WM, use brush value = 0 and erase GM



FS WM edits: Control points

- Run white matter edits



Update QC spreadsheet

- Make notes of any edits made

| A | B | C | D | E | F | G | H | I |
|---------------|-------------|--------------------|--------------------------|--------------------------|---------|---------|---------------------|---------------------|
| Subject | Final_score | Excessive_movement | Temporal_pole_missing_LH | Temporal_pole_missing_RH | Dura_LH | Dura_RH | Missing_anterior_LH | Missing_anterior_RH |
| sub-blastc122 | 5 | 1 | 1 | 1 | 0 | 0 | 1 | 1 |

| J | K | L | M | N | O |
|--|---|---|---|---|---|
| Notes | FS edits | | | | |
| Missing_Superior_Medial_LH Missing_Superior_Medial_RH Missing_Posterior_LH Missing_Posterior_RH | Movement artifact; bilateral temporal and anterior frontal lobes had missing GM increased/decreased watershed parameters to ____; note all other FS edits here | | | | |