

Introduction to *FreeSurfer*

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Resources

- Tutorial Slides:
 - https://rcs.bu.edu/examples/imaging/tut_freesurfer/
- Using FreeSurfer on the SCC Documentation:
 - <https://rcs.bu.edu/examples/imaging/freesurfer/getstart/>
- *FreeSurfer* Website
 - <https://surfer.nmr.mgh.harvard.edu>
- Questions? Problems? Help?
 - help@scc.bu.edu
 - kkurkela@bu.edu

Tutorial Feedback

Please open a tab in your web browser and have this page open:

http://scv.bu.edu/survey/tutorial_evaluation.html

Please fill it out at the end of today's tutorial!

Outline

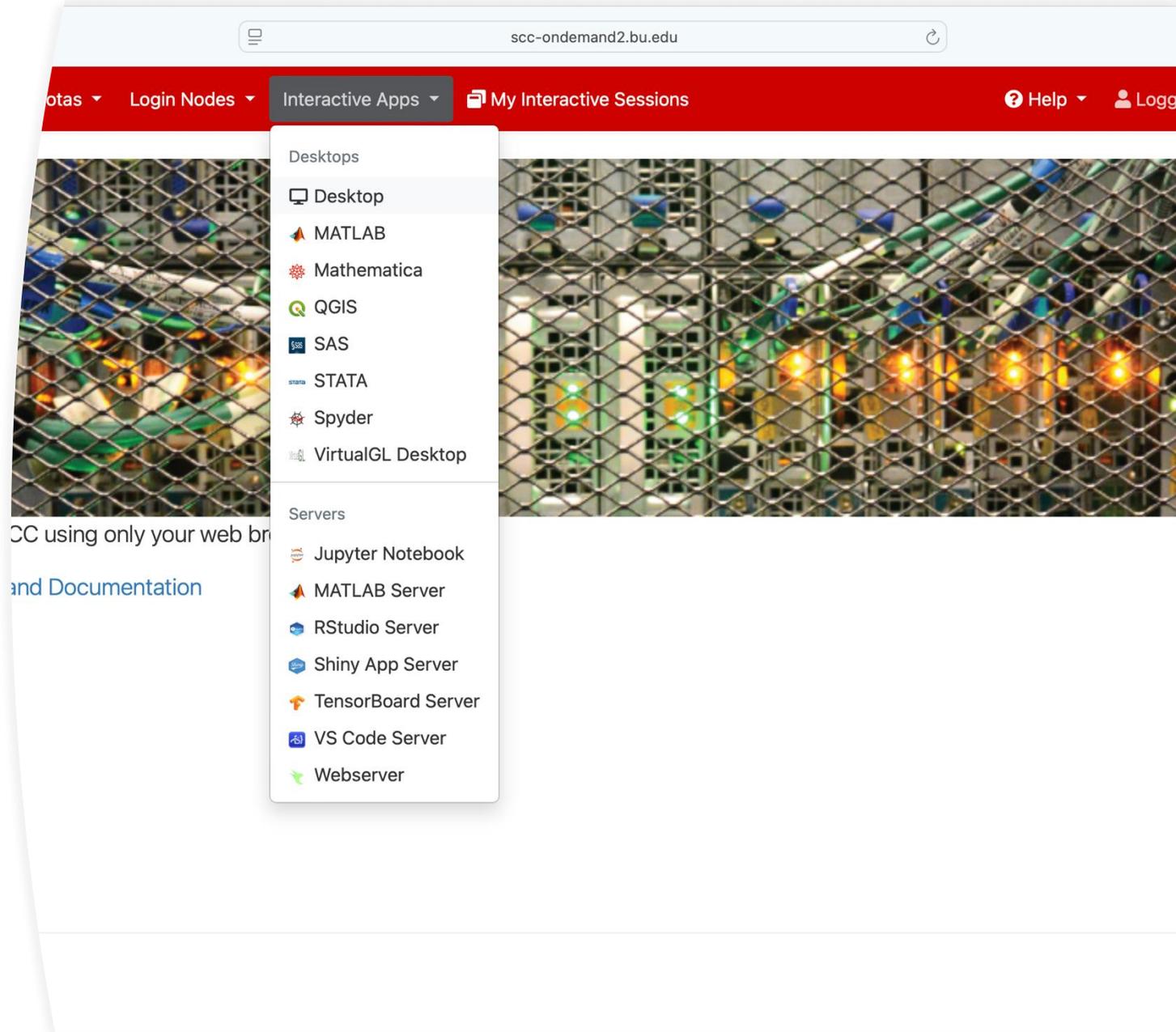
- Tutorial Prep
- FreeSurfer Terminology/Intro
- Submitting recon-all to the SCC
- Freeview
- Review outputs
- Data troubleshooting

Open an OnDemand Session

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

Tutorial Accounts

1. Go to scc-ondemand-tutorial.bu.edu
2. Username and Password will be sent in Zoom chat
3. Go to Interactive Apps
4. Request a Desktop



Desktop

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

List of modules to load (space separated)

Working Directory

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

Initial command to run

Number of hours

Number of cores

Number of gpus

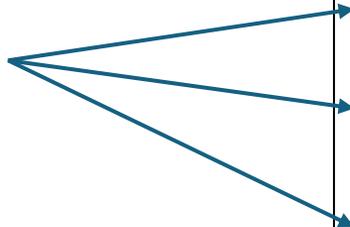
Project

Extra qsub options

I would like to receive an email when the session starts

Save settings

Use these basic options.



Click "Launch"



Pick one of your projects. Mine is "scv".



Desktop (399070)

1 core | Running

Host: >_ scc-wl4

Delete

Created at: 2026-02-10 15:56:15 EST

Time Remaining: 11 hours and 59 minutes

Session ID: b6eb15fc-106e-4cf5-ad84-8b2a53125536

List of modules to load (space separated):

Working Directory:

Number of hours: 12

Number of cores: 1

Number of gpus: 0

GPU compute capability: 3.5

Project: scv

Extra qsub options:

Compression



0 (low) to 9 (high)

Image Quality

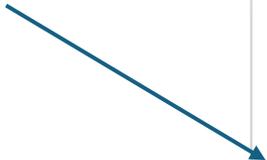


0 (low) to 9 (high)

Connect to Desktop

View Only (Share-able Link)

Click "Connect to Desktop"



Tutorial Setup

```
> mkdir /path/to/a/directory/to/work/outof
```

```
> cd /path/to/a/directory/to/work/outof
```

```
> mkdir output
```

```
> cp -r /project/scv/examples/imaging/tut_freesurfer/* .
```

```
> ls
```

```
ds000174      freesurfer_reconall_array.qsub  output  scan_list.txt  subject_list.txt
```

Outline

- Tutorial Prep
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What is FreeSurfer?

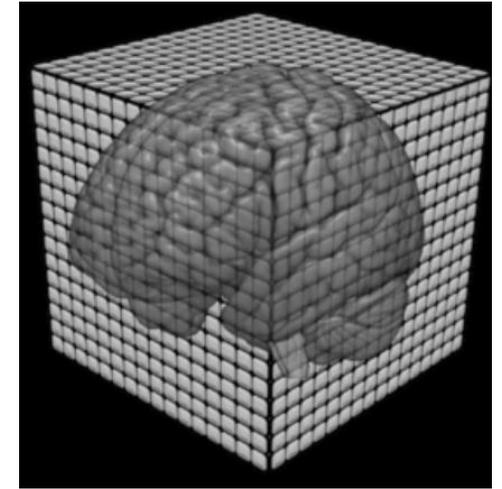
- FreeSurfer is a suite of tools that provide an array of algorithms for the analysis of MRI data of the human brain.
- It is most well known for its routine for generating 3-D surface representations of the cerebral cortex.
- It is very popular.
- It is automated.
- Currently supported by the Laboratory for Computational Neuroimaging at the Martinos Center at MGH right here in Boston!

Volumes vs Surfaces

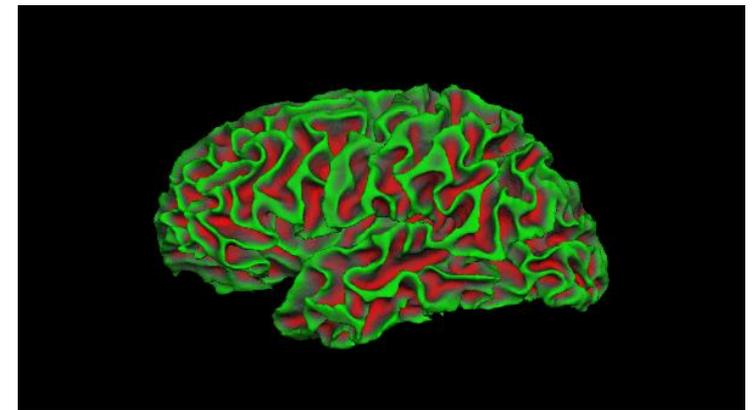
Neuroimaging data is collected as a *volume* – a set of 3-D pixels arranged in a grid.

The cortex, however, is not a volume but a 2-D *surface* that is crammed into a 3-D volume.

In theory, the best way to analyze brain data should be to analyze it as a 2-D surface, not as a 3-D volume.



Volume



Surface

Volumes vs Surfaces

Example: smoothing

Volume Based Smoothing

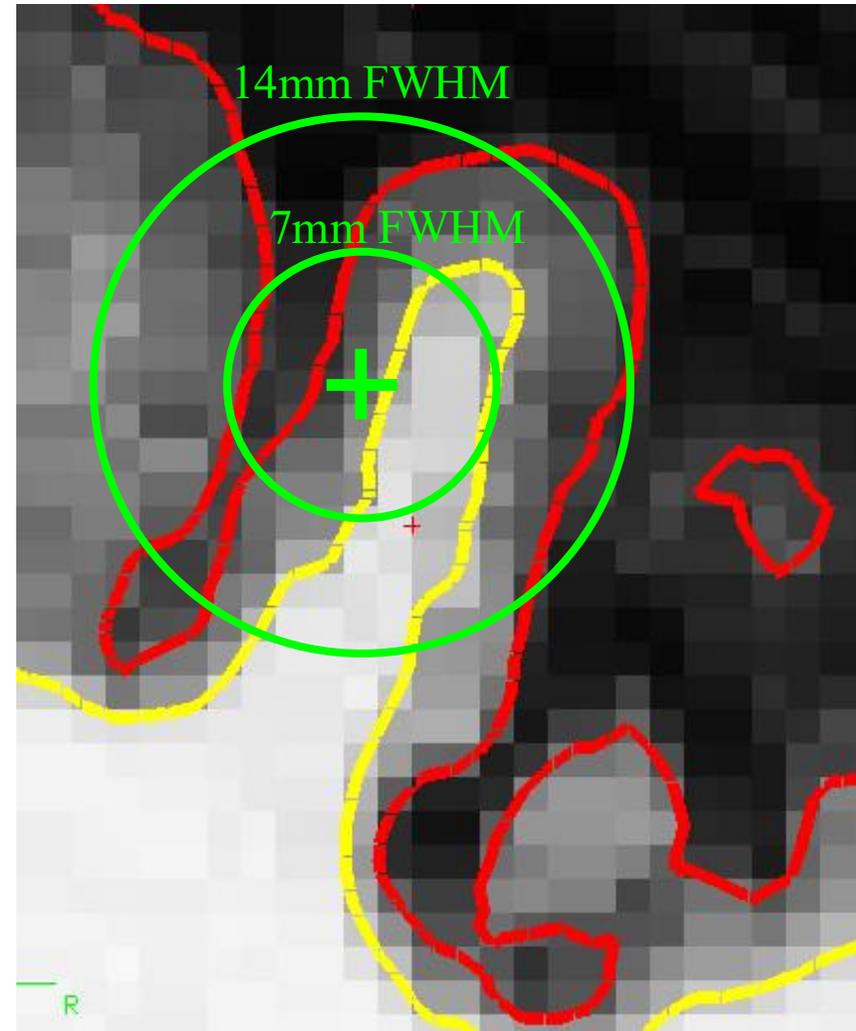


Image Source: FreeSurfer 2026 tutorial

Volumes vs Surfaces

Example: smoothing

Surface Based Smoothing

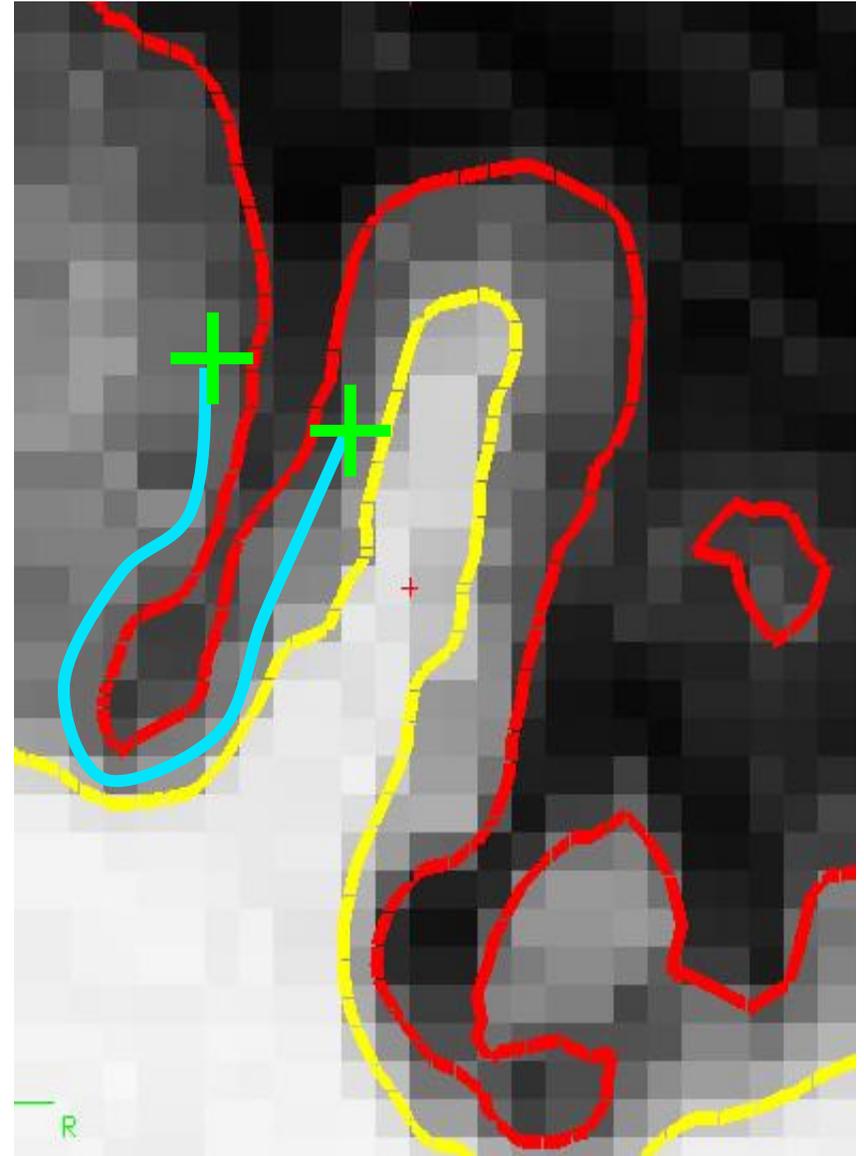
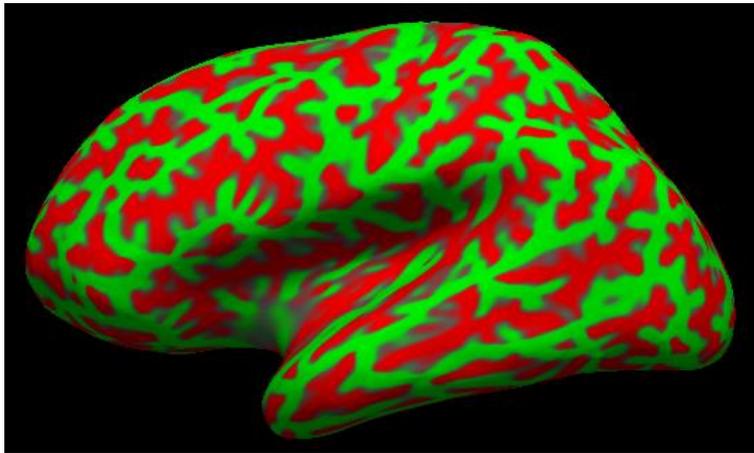
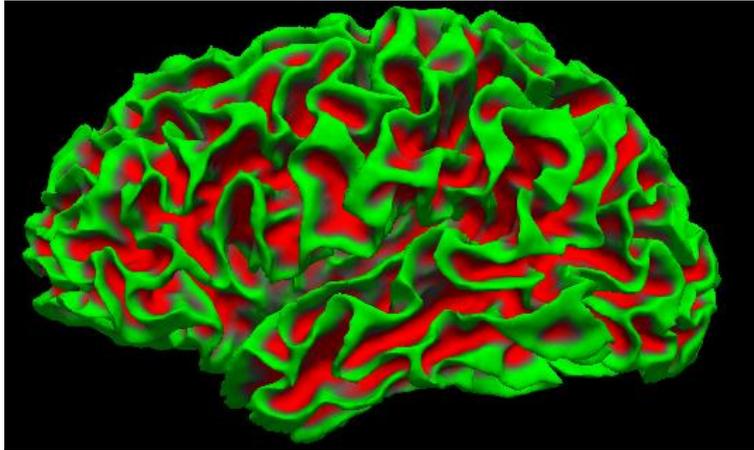


Image Source: FreeSurfer 2026 tutorial

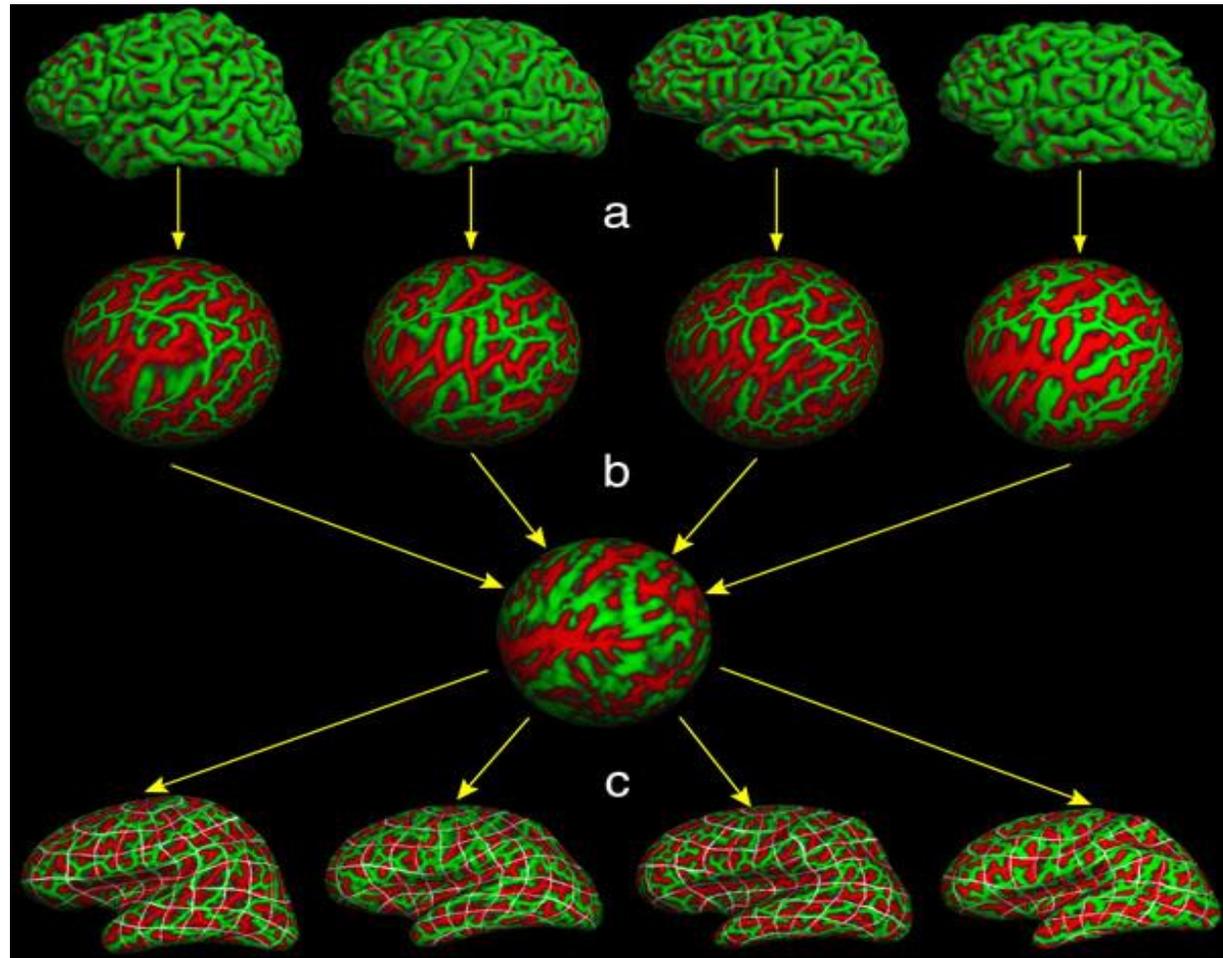
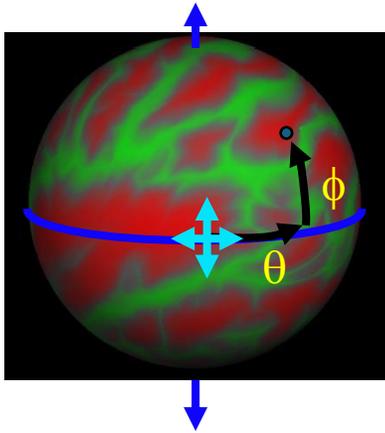
Registration, Segmentation, and Parcellation

- Surface Based Registration – aligning two surfaces to match
- Volumetric Segmentation – what is what in a volume
- Surface Parcellation – what is what on a surface

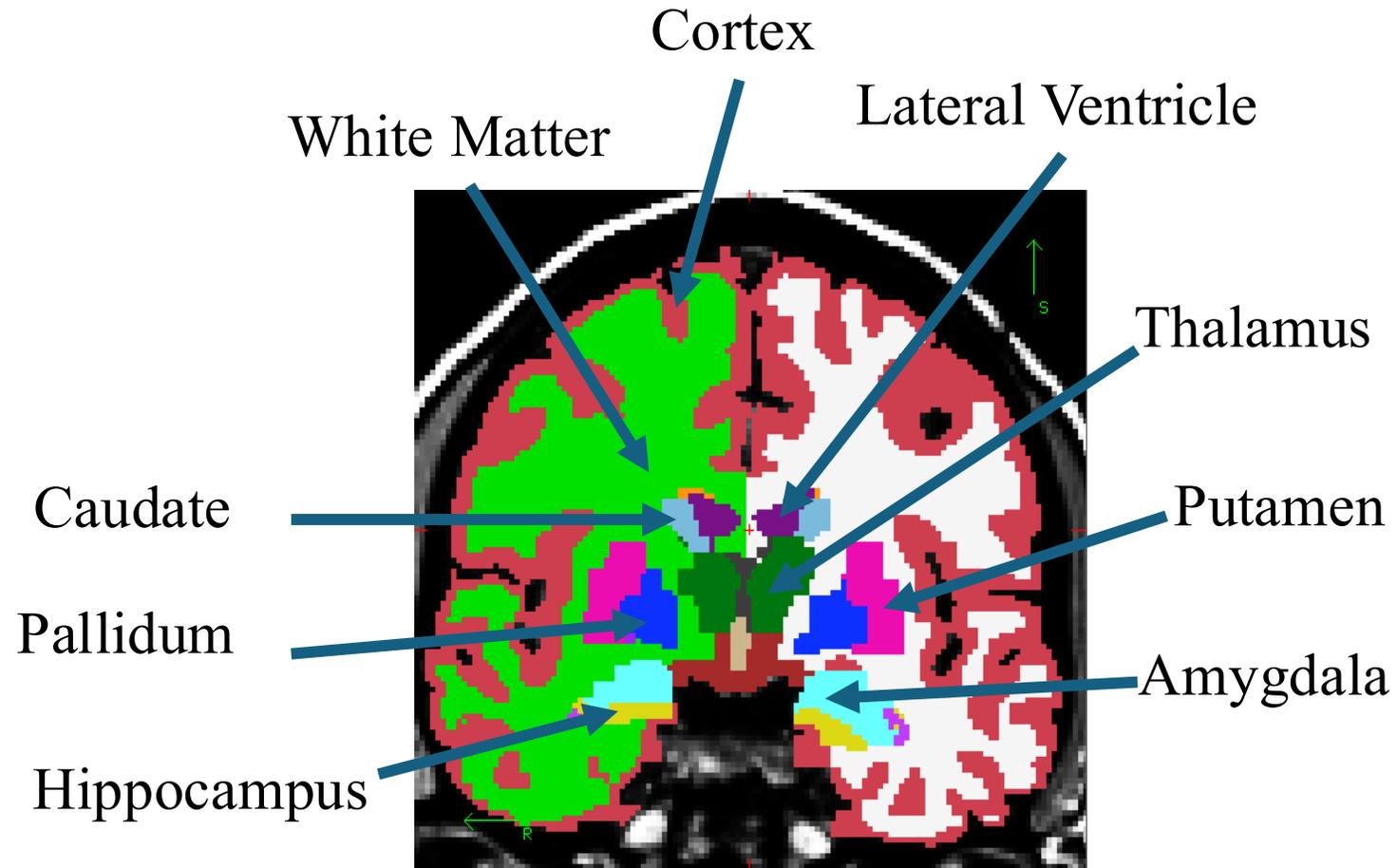
Surface Registration



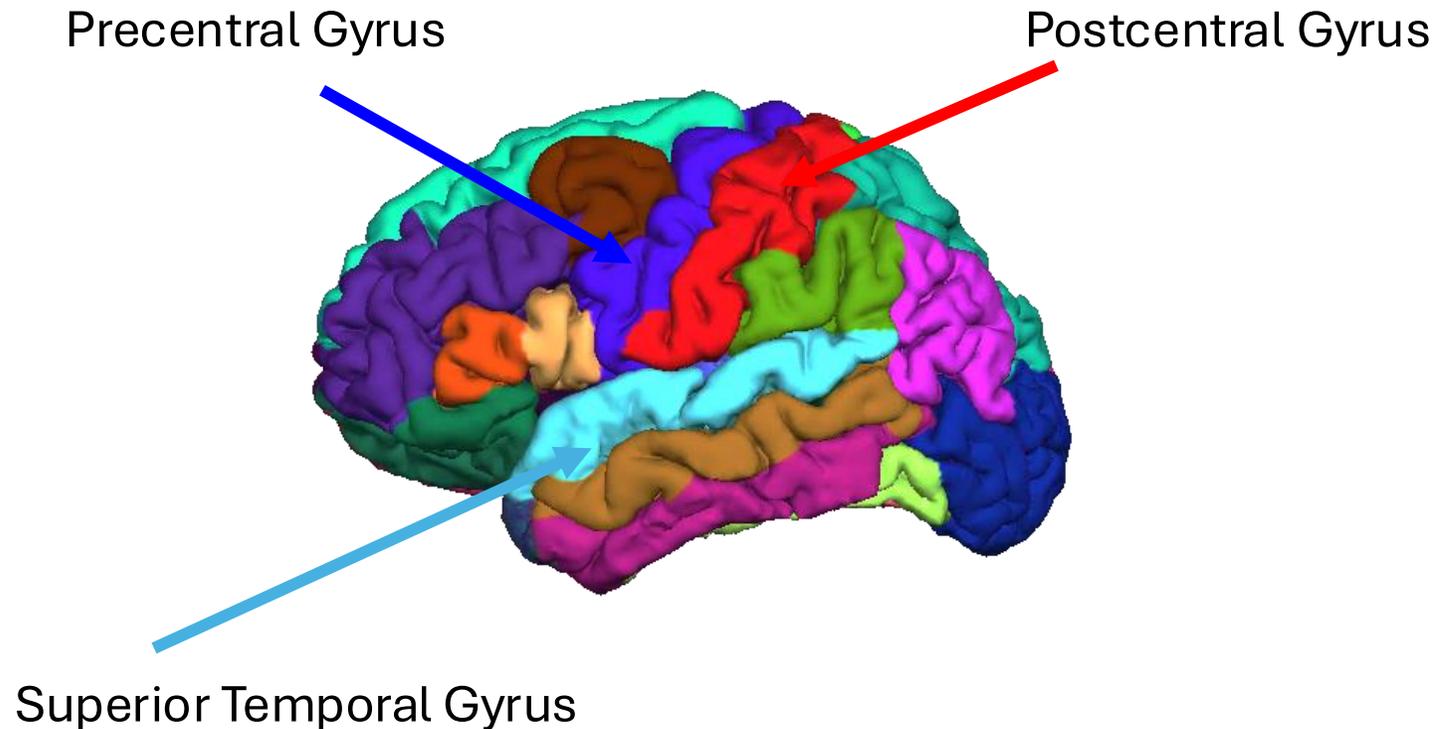
Surface Registration



Automatic Volumetric Segmentation: “aseg”



Automatic Surface Parcellation: Desikan/Killiany Atlas (35 ROI's)

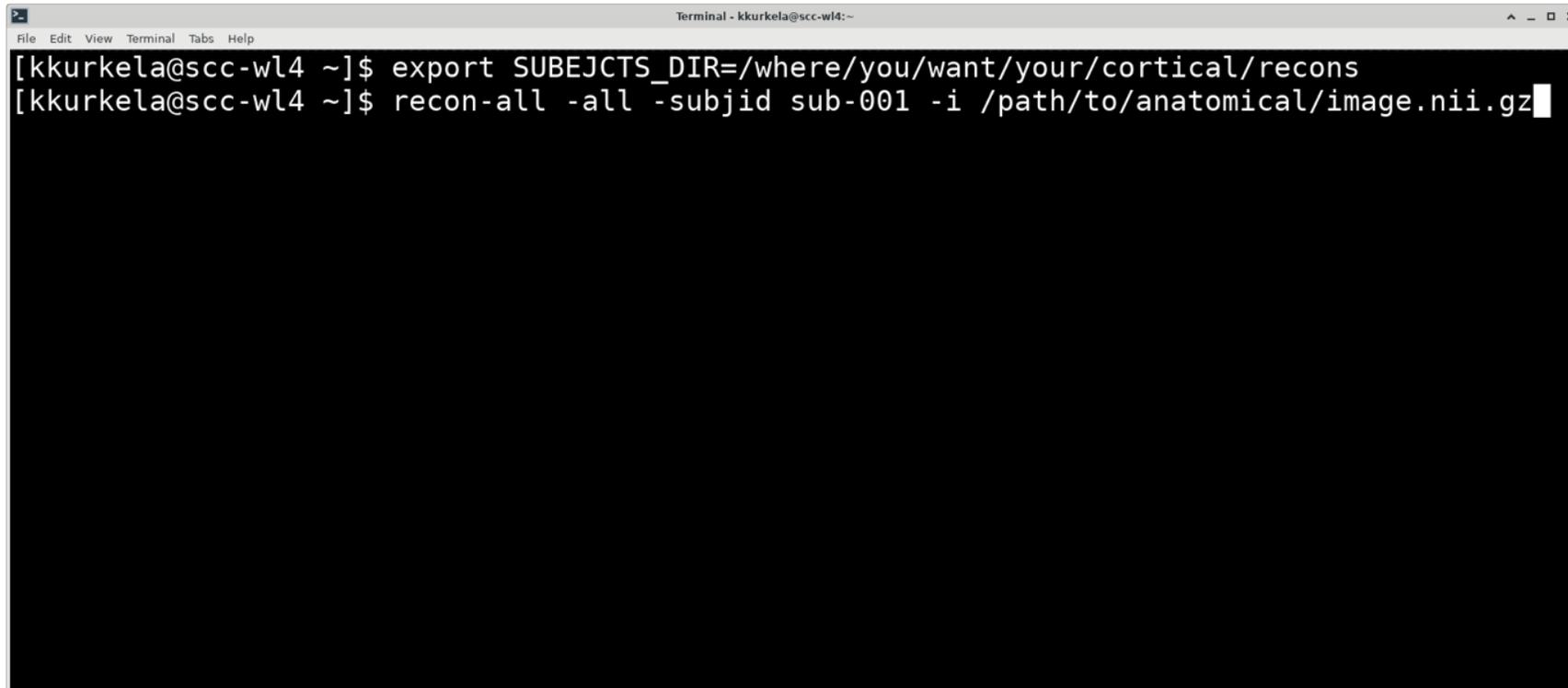


An automated labeling system for subdividing the human cerebral cortex on MRI scans into gyral based regions of interest, Desikan, R.S., F. Segonne, B. Fischl, B.T. Quinn, B.C. Dickerson, D. Blacker, R.L. Buckner, A.M. Dale, R.P. Maguire, B.T. Hyman, M.S. Albert, and R.J. Killiany, (2006). NeuroImage 31(3):968-80.

Outline

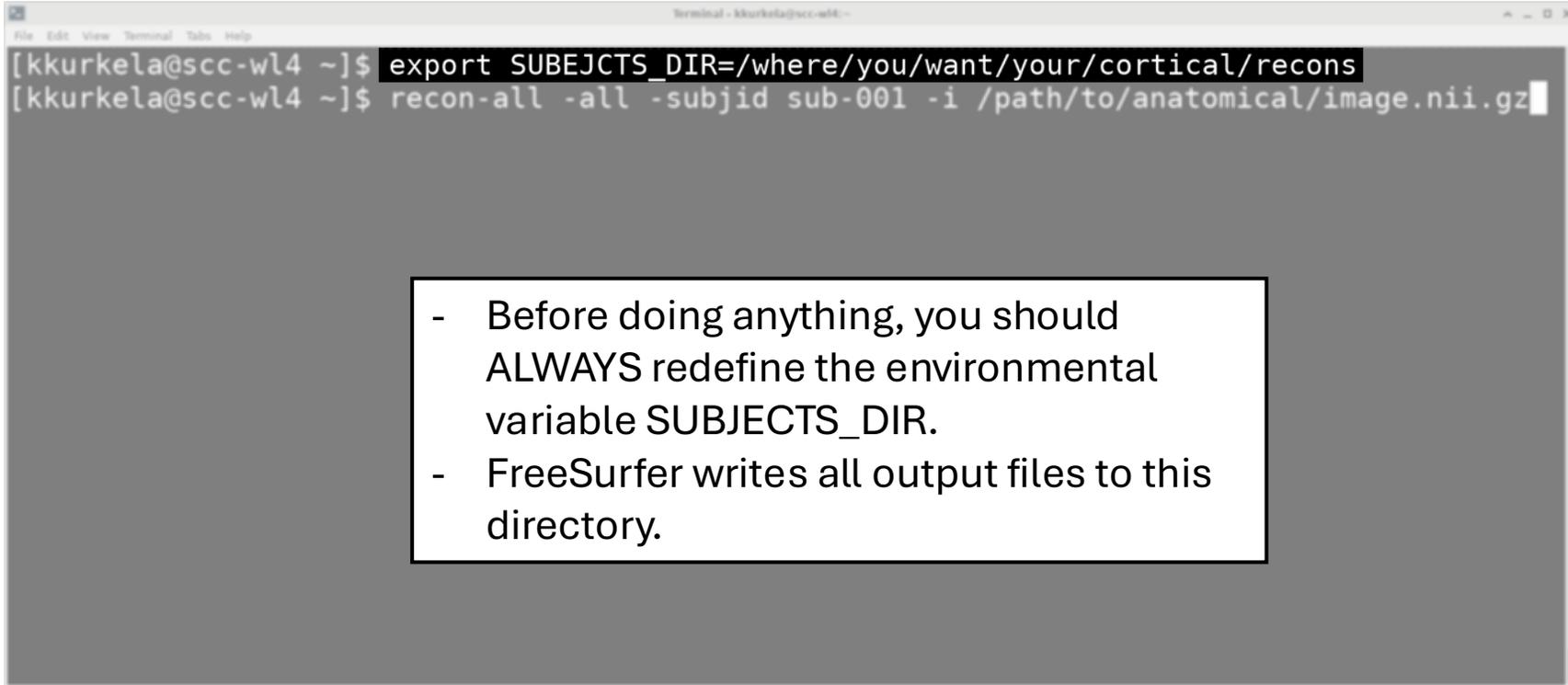
- Tutorial Prep
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- Submitting recon-all to the SCC
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Submitting a Cortical Reconstruction -- Basics



```
Terminal - kkurkela@scc-wl4:~  
File Edit View Terminal Tabs Help  
[kkurkela@scc-wl4 ~]$ export SUBJECTS_DIR=/where/you/want/your/cortical/recons  
[kkurkela@scc-wl4 ~]$ recon-all -all -subjid sub-001 -i /path/to/anatomical/image.nii.gz
```

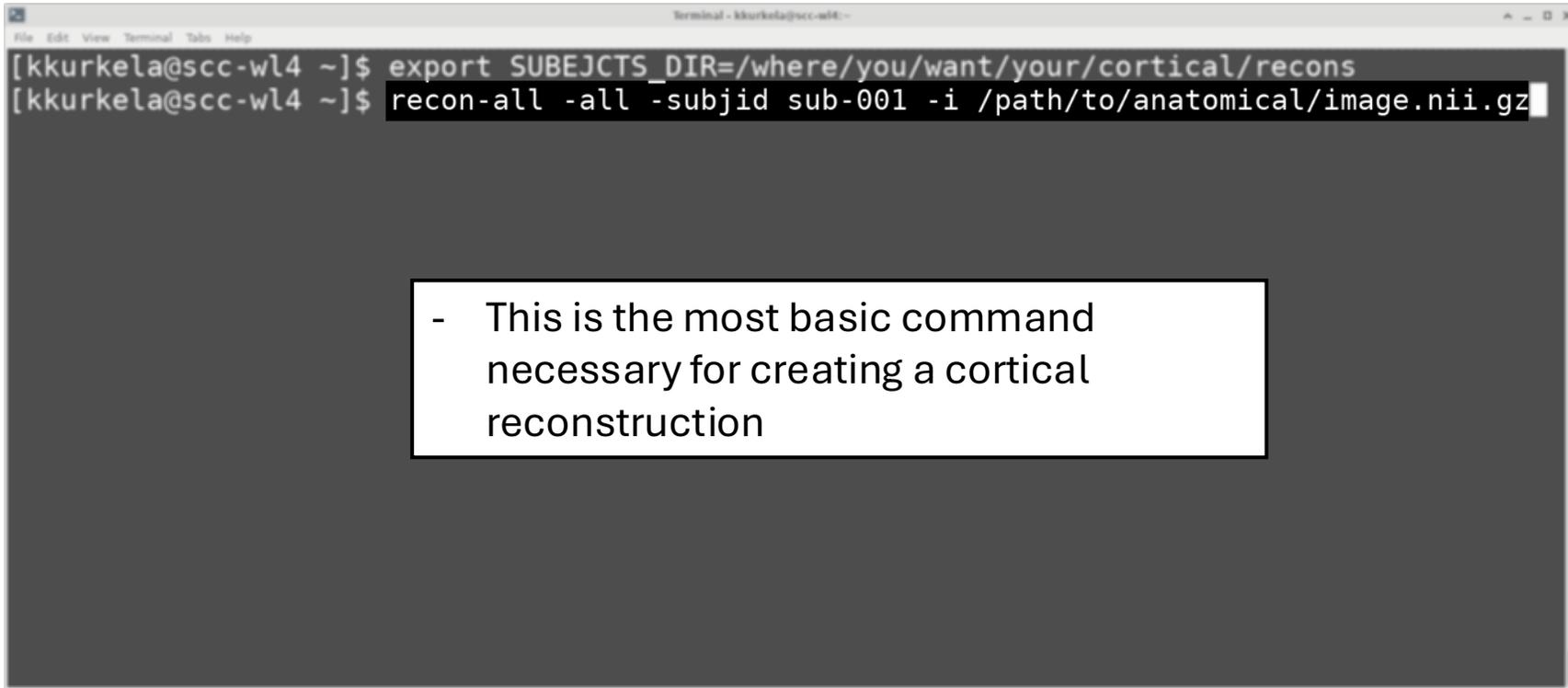
Submitting a Cortical Reconstruction -- Basics



```
Terminal - kkurkela@scc-wl4 -  
File Edit View Terminal Tabs Help  
[kkurkela@scc-wl4 ~]$ export SUBJECTS_DIR=/where/you/want/your/cortical/recons  
[kkurkela@scc-wl4 ~]$ recon-all -all -subjid sub-001 -i /path/to/anatomical/image.nii.gz
```

- Before doing anything, you should ALWAYS redefine the environmental variable SUBJECTS_DIR.
- FreeSurfer writes all output files to this directory.

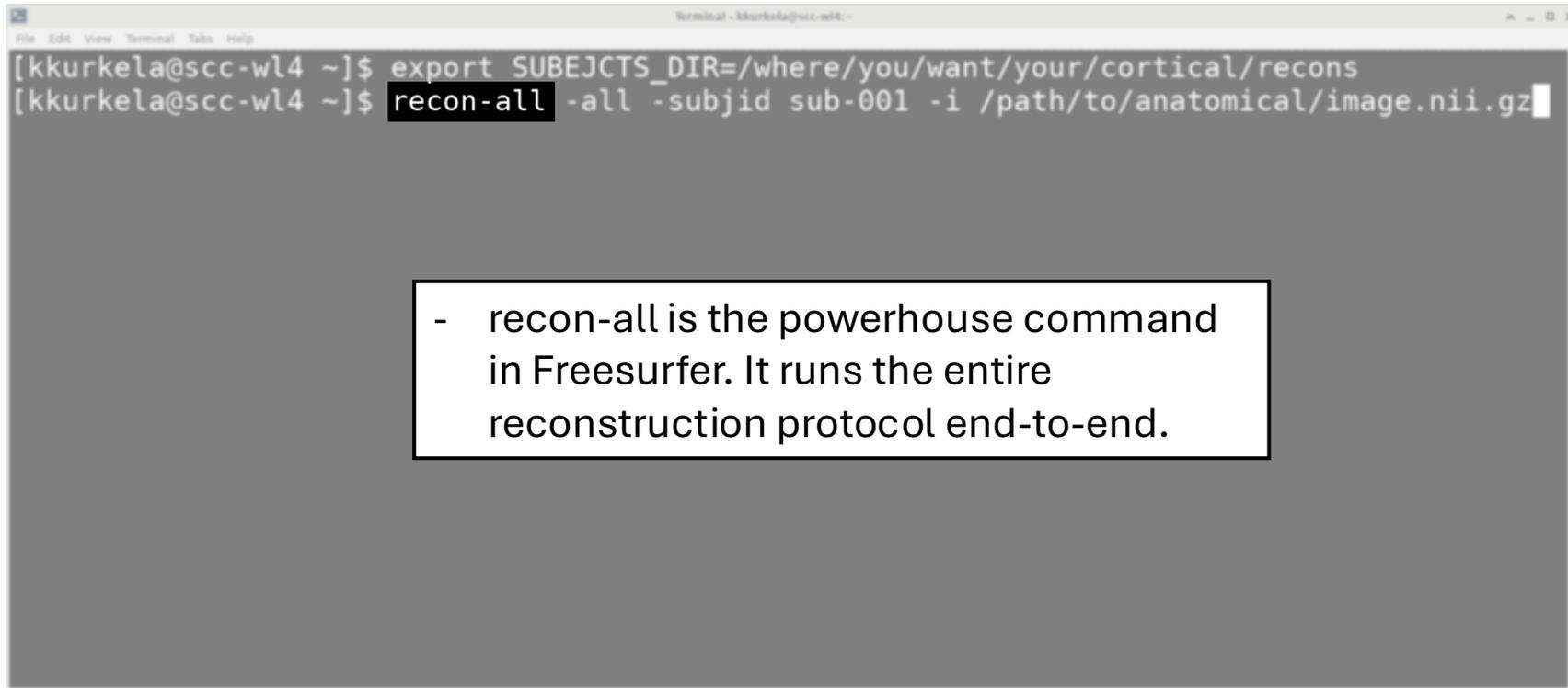
Submitting a Cortical Reconstruction -- Basics

A terminal window titled "Terminal - kkurkela@scc-wl4" showing two commands. The first command is "export SUBJECTS_DIR=/where/you/want/your/cortical/recons" and the second is "recon-all -all -subjid sub-001 -i /path/to/anatomical/image.nii.gz".

```
Terminal - kkurkela@scc-wl4
File Edit View Terminal Tabs Help
[kkurkela@scc-wl4 ~]$ export SUBJECTS_DIR=/where/you/want/your/cortical/recons
[kkurkela@scc-wl4 ~]$ recon-all -all -subjid sub-001 -i /path/to/anatomical/image.nii.gz
```

- This is the most basic command necessary for creating a cortical reconstruction

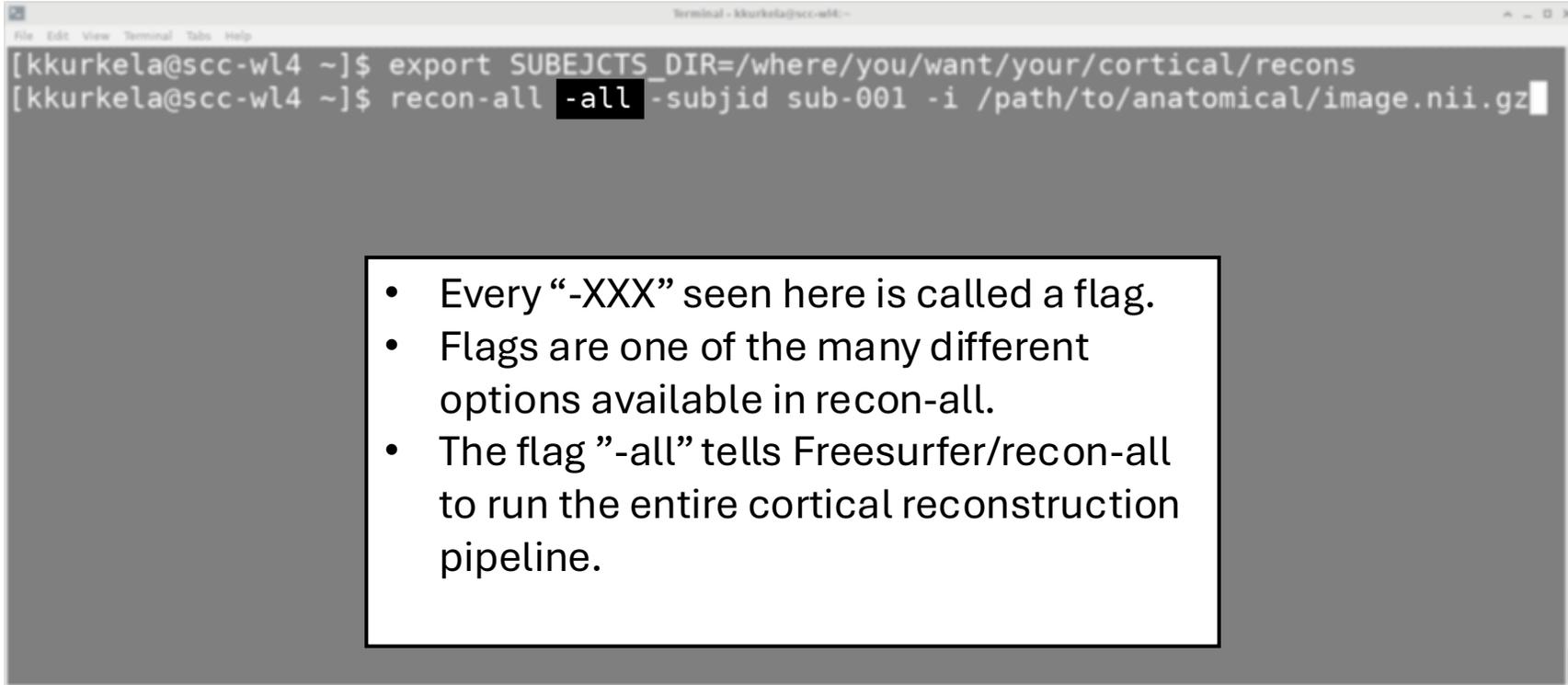
Submitting a Cortical Reconstruction -- Basics



```
Terminal - kkurkela@scc-wl4 -  
File Edit View Terminal Tabs Help  
[kkurkela@scc-wl4 ~]$ export SUBJECTS_DIR=/where/you/want/your/cortical/recons  
[kkurkela@scc-wl4 ~]$ recon-all -all -subjid sub-001 -i /path/to/anatomical/image.nii.gz
```

- recon-all is the powerhouse command in Freesurfer. It runs the entire reconstruction protocol end-to-end.

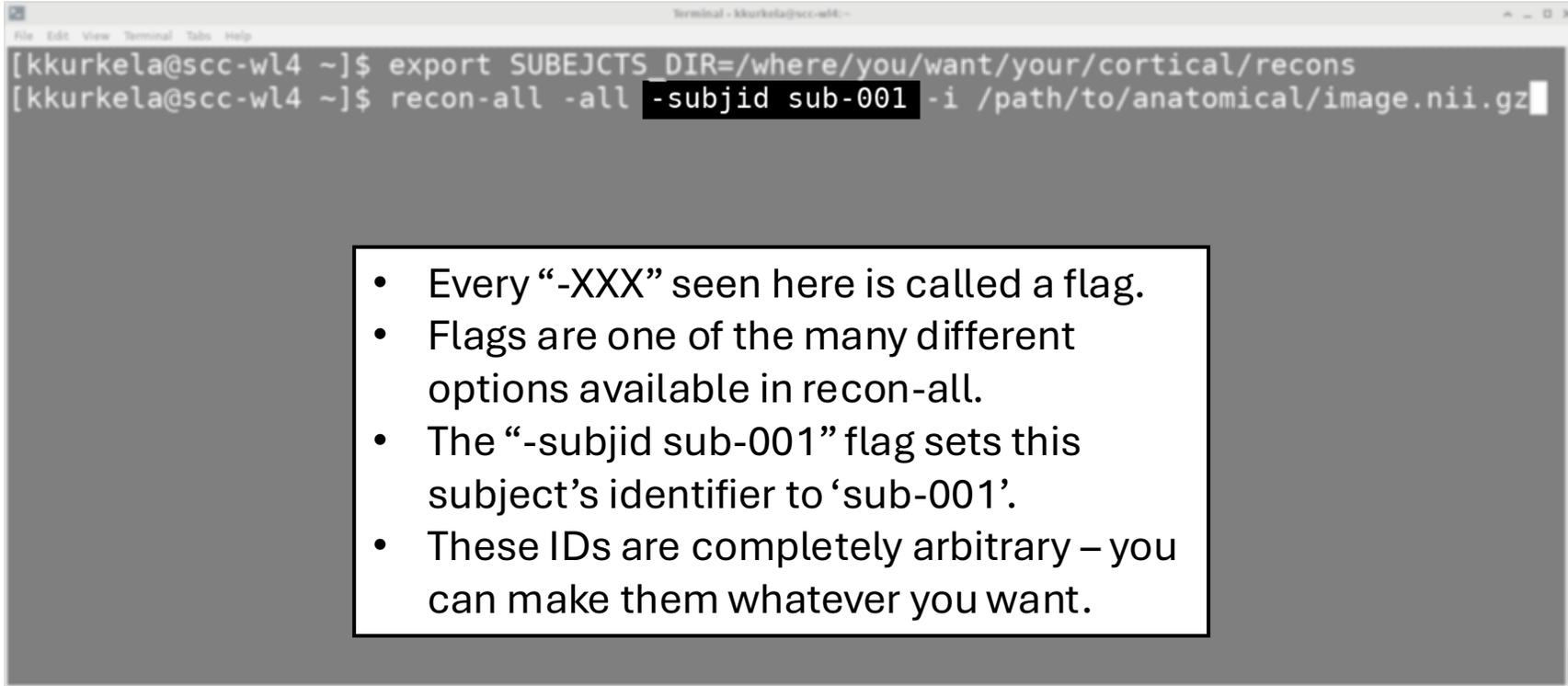
Submitting a Cortical Reconstruction -- Basics



```
Terminal - kkurkela@scc-wl4 -  
File Edit View Terminal Tabs Help  
[kkurkela@scc-wl4 ~]$ export SUBJECTS_DIR=/where/you/want/your/cortical/recons  
[kkurkela@scc-wl4 ~]$ recon-all -all -subjid sub-001 -i /path/to/anatomical/image.nii.gz
```

- Every “-XXX” seen here is called a flag.
- Flags are one of the many different options available in recon-all.
- The flag “-all” tells Freesurfer/recon-all to run the entire cortical reconstruction pipeline.

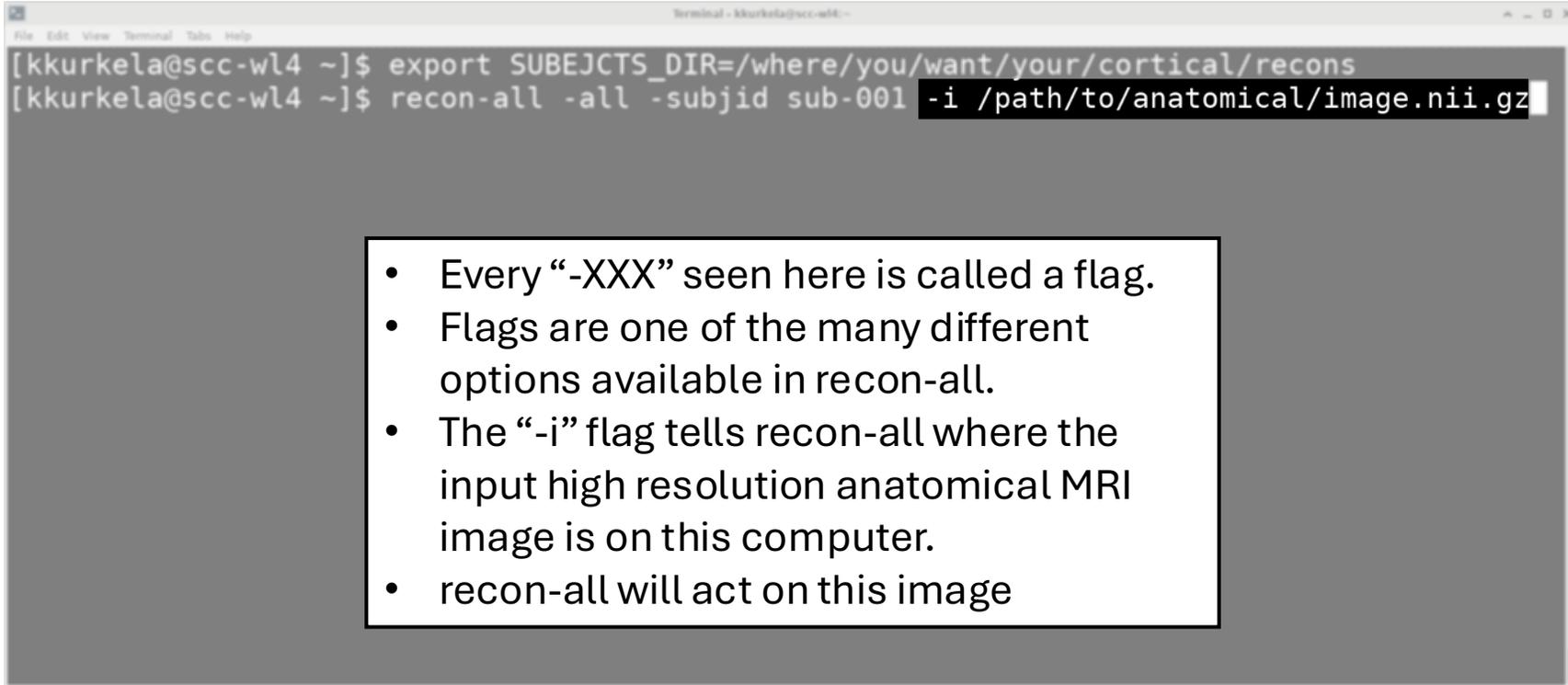
Submitting a Cortical Reconstruction -- Basics

A terminal window titled "Terminal - kkurkela@scc-wl4" showing two lines of command execution. The first line is `[kkurkela@scc-wl4 ~]$ export SUBJECTS_DIR=/where/you/want/your/cortical/recons`. The second line is `[kkurkela@scc-wl4 ~]$ recon-all -all -subjid sub-001 -i /path/to/anatomical/image.nii.gz`. The flag `-subjid sub-001` is highlighted with a black background.

```
[kkurkela@scc-wl4 ~]$ export SUBJECTS_DIR=/where/you/want/your/cortical/recons
[kkurkela@scc-wl4 ~]$ recon-all -all -subjid sub-001 -i /path/to/anatomical/image.nii.gz
```

- Every “-XXX” seen here is called a flag.
- Flags are one of the many different options available in recon-all.
- The “-subjid sub-001” flag sets this subject’s identifier to ‘sub-001’.
- These IDs are completely arbitrary – you can make them whatever you want.

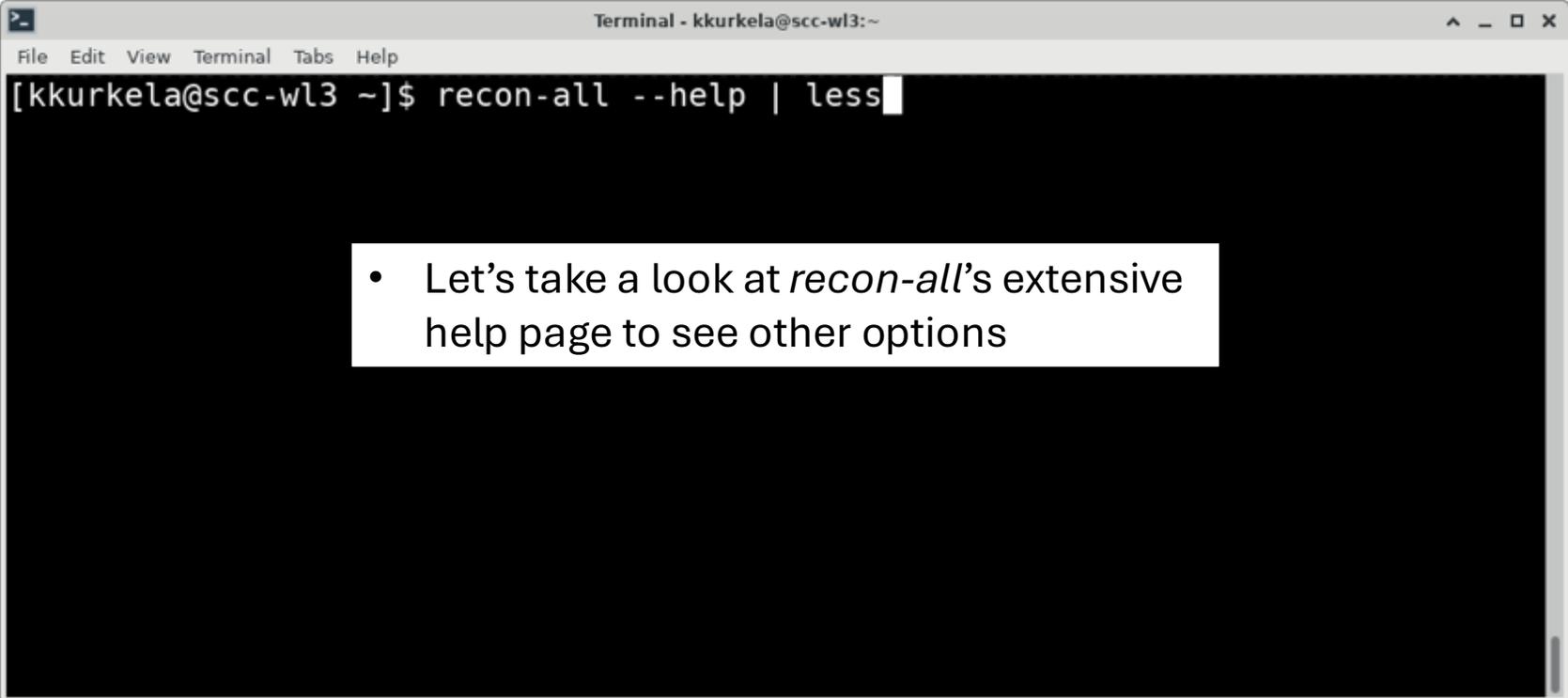
Submitting a Cortical Reconstruction -- Basics

A terminal window titled "Terminal - kkurkela@scc-wl4" showing two lines of command execution. The first line is "export SUBJECTS_DIR=/where/you/want/your/cortical/recons" and the second line is "recon-all -all -subjid sub-001 -i /path/to/anatomical/image.nii.gz". The second line is highlighted with a black background and white text.

```
[kkurkela@scc-wl4 ~]$ export SUBJECTS_DIR=/where/you/want/your/cortical/recons
[kkurkela@scc-wl4 ~]$ recon-all -all -subjid sub-001 -i /path/to/anatomical/image.nii.gz
```

- Every “-XXX” seen here is called a flag.
- Flags are one of the many different options available in recon-all.
- The “-i” flag tells recon-all where the input high resolution anatomical MRI image is on this computer.
- recon-all will act on this image

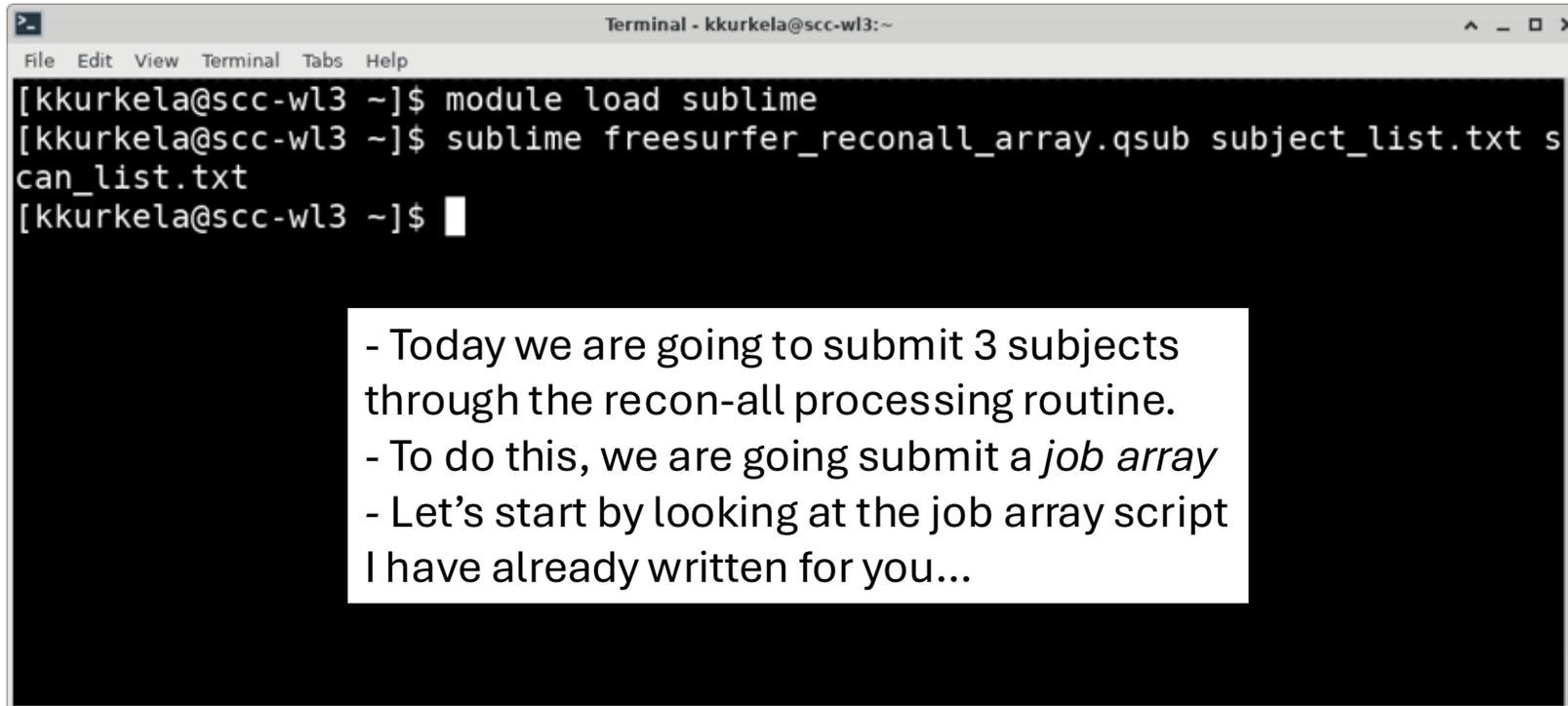
Submitting a Cortical Reconstruction -- Basics



A terminal window titled "Terminal - kkurkela@scc-wl3:~" with a menu bar containing "File", "Edit", "View", "Terminal", "Tabs", and "Help". The terminal prompt is "[kkurkela@scc-wl3 ~]\$ recon-all --help | less". A white box with a black border is overlaid on the terminal, containing a bullet point.

- Let's take a look at *recon-all*'s extensive help page to see other options

Submitting a Cortical Reconstruction – Job Array



```
Terminal - kkurkela@scc-wl3:~  
File Edit View Terminal Tabs Help  
[kkurkela@scc-wl3 ~]$ module load sublime  
[kkurkela@scc-wl3 ~]$ sublime freesurfer_reconall_array.qsub subject_list.txt s  
can_list.txt  
[kkurkela@scc-wl3 ~]$ █
```

- Today we are going to submit 3 subjects through the recon-all processing routine.
- To do this, we are going submit a *job array*
- Let's start by looking at the job array script I have already written for you...

Submitting a Cortical Reconstruction – Job Array

Change this to your SCC project

```
~/freesurfer_reconall_array.qsub - Sublime Text (UNREGISTERED)
File Edit Selection Find View Goto Tools Project Preferences Help
freesurfer_reconall_array.qsub x subject_list.txt x scan_list.txt x
1 #!/bin/bash -l
2
3 # Set SCC project
4 # $ -P PROJECT_NAME
5
6 # Give this job a name
7 # $ -N JOB_NAME
8
9 # Combine output and error files into a single file
10 # $ -j y
11
12 # Send an email when the job finishes or if it is aborted (by default no email is sent)
13 # $ -m ae
14
15 # Request 4 cores for the -parallel flag.
16 # $ -pe omp 4
17
18 # Defaults to fair-share mem_per_core, which is at minimum 4GB.
19 # $ -l mem_per_core=4G
20
21 # Submit N jobs. Gives access to the environmental variable $SGE_TASK_ID,
22 # which is equal to the current job number
23 # This example creates 3 jobs
24 # $ -t 1-3
25
26 # Load desired version of freesurfer
27 module load freesurfer/8.0.0
28
29 # create a list of inputs from the text files "subject_list.txt" and "scan_list.txt".
30 # These text files must be in the same directory as this file
```

Change this to "freesurfer_job"



The screenshot shows the Sublime Text editor with the file `scan_list.txt` open. The text in the editor is as follows:

```
1 /projectnb/scv/kkurkela/fsl_test/ds000102-00001/sub-01/anat/sub-01_T1w.nii.gz
2 /projectnb/scv/kkurkela/fsl_test/ds000102-00001/sub-02/anat/sub-02_T1w.nii.gz
3 /projectnb/scv/kkurkela/fsl_test/ds000102-00001/sub-03/anat/sub-03_T1w.nii.gz
4
```

A callout box with a green arrow pointing to the first line contains the text: "Change these lines to be full path to your data."

The screenshot shows the Sublime Text editor with the file `subject_list.txt` open. The text in the editor is as follows:

```
1 sub-01
2 sub-02
3 sub-03
4
```

A callout box with a green arrow pointing to the first line contains the text: "Change these lines to be your desired subject ids. For this tutorial, we will use sub-101, sub-103, and sub-104."

What resources should I request?

Running recon-all on the SCC

The more specific your request of resources, the shorter the list of possible nodes that can accept your batch job. Therefore, if you are in a rush or have 100s of subjects to recon, you are best off requesting resources that can successfully perform recon-all and can be fulfilled by the most nodes (i.e. reducing queue time). Freesurfer recommends a minimum of 1-core and 4GB of memory for an absolute minimum of success.

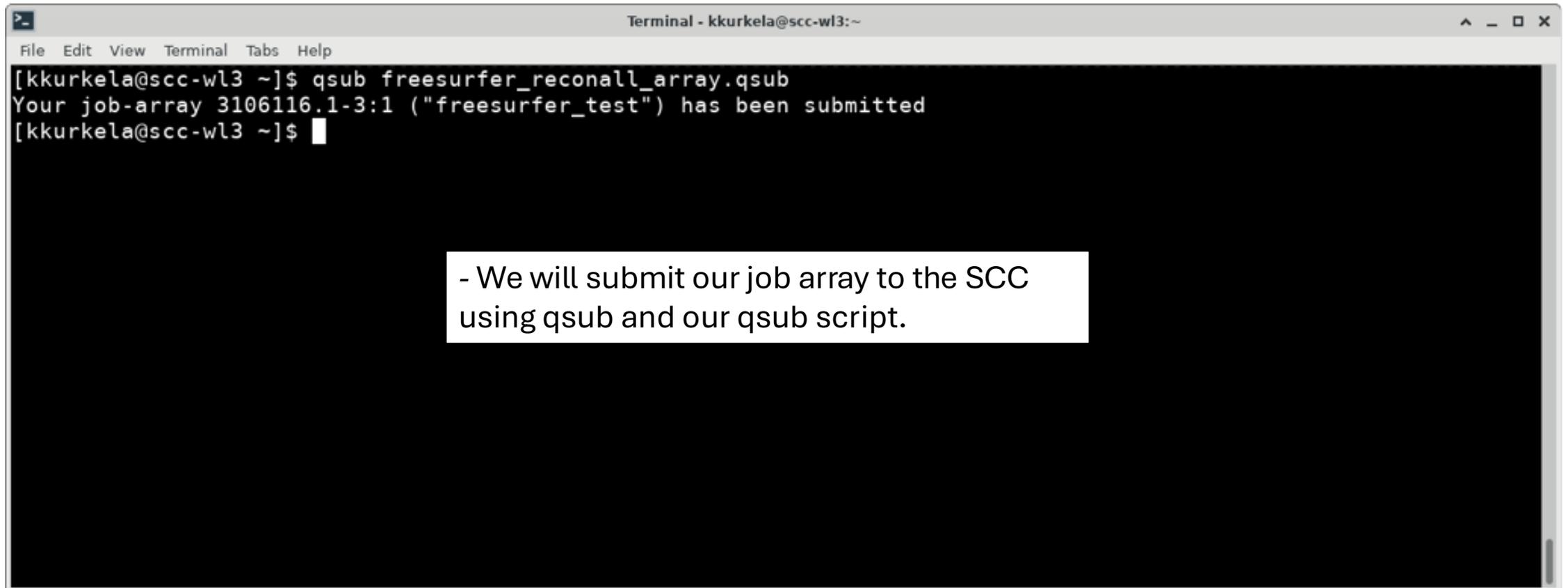
We've found that the trade off between queue time and processing time peaks at 8-cores. Requesting more than 8-cores will not yield significant speed improvements but will significantly increase the time before your job lands on a node.

Depending on how many subjects you need to process and your time constraints confer with the table below for choosing the appropriate resources:

# of Subjects	# of Cores (Recommended)
<10	8
<100	4
>100	1

See: for detailed benchmarking:
<https://rcs.bu.edu/examples/imaging/freesurfer/appendix/>

Submitting a Cortical Reconstruction – Job Array

A terminal window titled "Terminal - kkurkela@scc-wl3:~" with a menu bar containing "File", "Edit", "View", "Terminal", "Tabs", and "Help". The terminal output shows the command `qsub freesurfer_reconall_array.qsub` being executed, followed by the message "Your job-array 3106116.1-3:1 ('freesurfer_test') has been submitted" and the prompt `[kkurkela@scc-wl3 ~]$` with a cursor.

```
[kkurkela@scc-wl3 ~]$ qsub freesurfer_reconall_array.qsub
Your job-array 3106116.1-3:1 ("freesurfer_test") has been submitted
[kkurkela@scc-wl3 ~]$
```

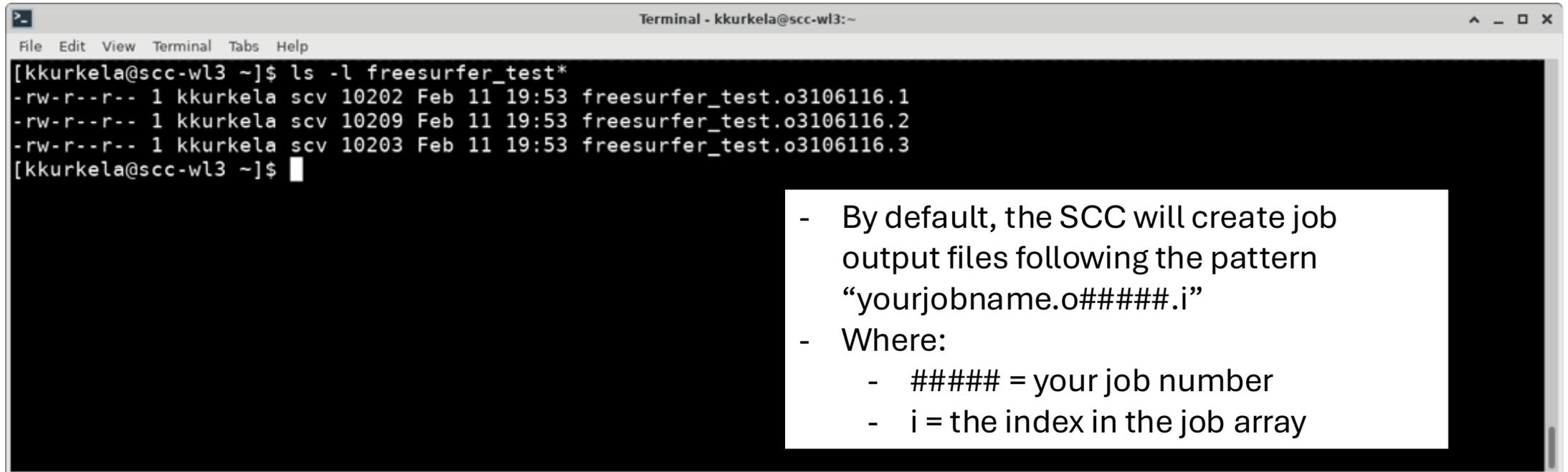
- We will submit our job array to the SCC using qsub and our qsub script.

Submitting a Cortical Reconstruction – Job Array

```
Terminal - kkurkela@scc-wl3:~
File Edit View Terminal Tabs Help
[kkurkela@scc-wl3 ~]$ qstat -u kkurkela
job-ID  prior   name       user          state submit/start at   queue                                slots ja-task-ID
-----  -
3106116 0.12678 freesurfer kkurkela      r       02/11/2026 19:52:50 p-int@scc-pi2.scc.bu.edu             4 1
3106116 0.12678 freesurfer kkurkela      r       02/11/2026 19:52:50 w@scc-wg4.scc.bu.edu                 4 2
3106116 0.12678 freesurfer kkurkela      r       02/11/2026 19:52:50 w@scc-wg4.scc.bu.edu                 4 3
[kkurkela@scc-wl3 ~]$
```

- We can check on our jobs using the qstat command.
- They should take about 1.5 hours to run.

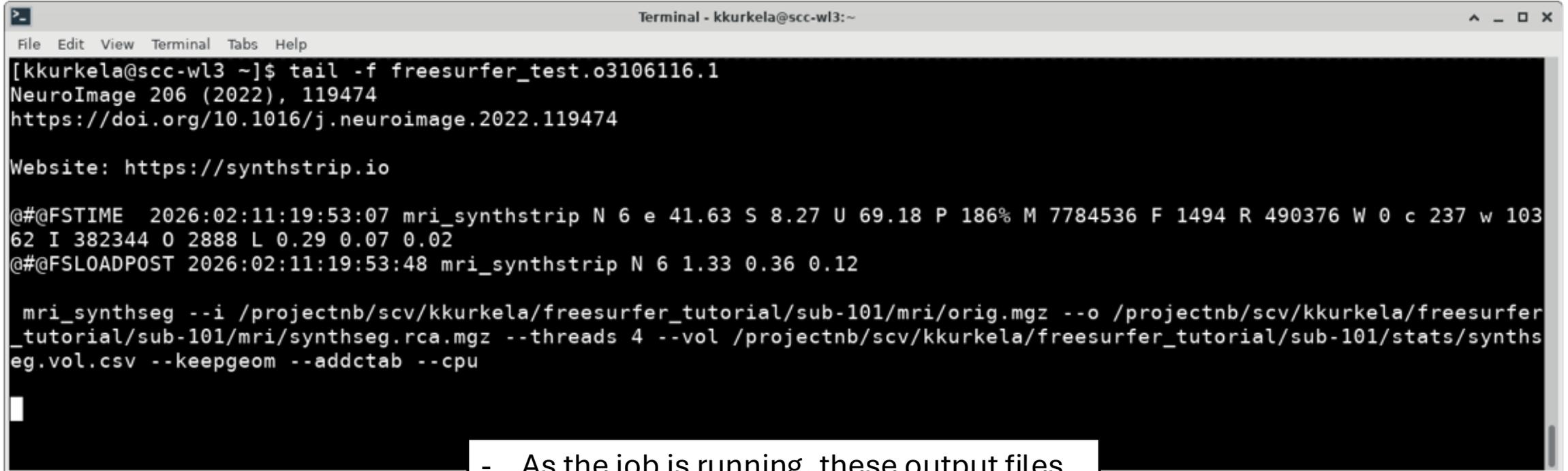
Submitting a Cortical Reconstruction – Job Array



```
Terminal - kkurkela@scc-wl3:~  
File Edit View Terminal Tabs Help  
[kkurkela@scc-wl3 ~]$ ls -l freesurfer_test*  
-rw-r--r-- 1 kkurkela scv 10202 Feb 11 19:53 freesurfer_test.o3106116.1  
-rw-r--r-- 1 kkurkela scv 10209 Feb 11 19:53 freesurfer_test.o3106116.2  
-rw-r--r-- 1 kkurkela scv 10203 Feb 11 19:53 freesurfer_test.o3106116.3  
[kkurkela@scc-wl3 ~]$
```

- By default, the SCC will create job output files following the pattern “yourjobname.o#####.i”
- Where:
 - ##### = your job number
 - i = the index in the job array

Submitting a Cortical Reconstruction – Job Array



```
Terminal - kkurkela@scc-wl3:~
File Edit View Terminal Tabs Help
[kkurkela@scc-wl3 ~]$ tail -f freesurfer_test.o3106116.1
NeuroImage 206 (2022), 119474
https://doi.org/10.1016/j.neuroimage.2022.119474

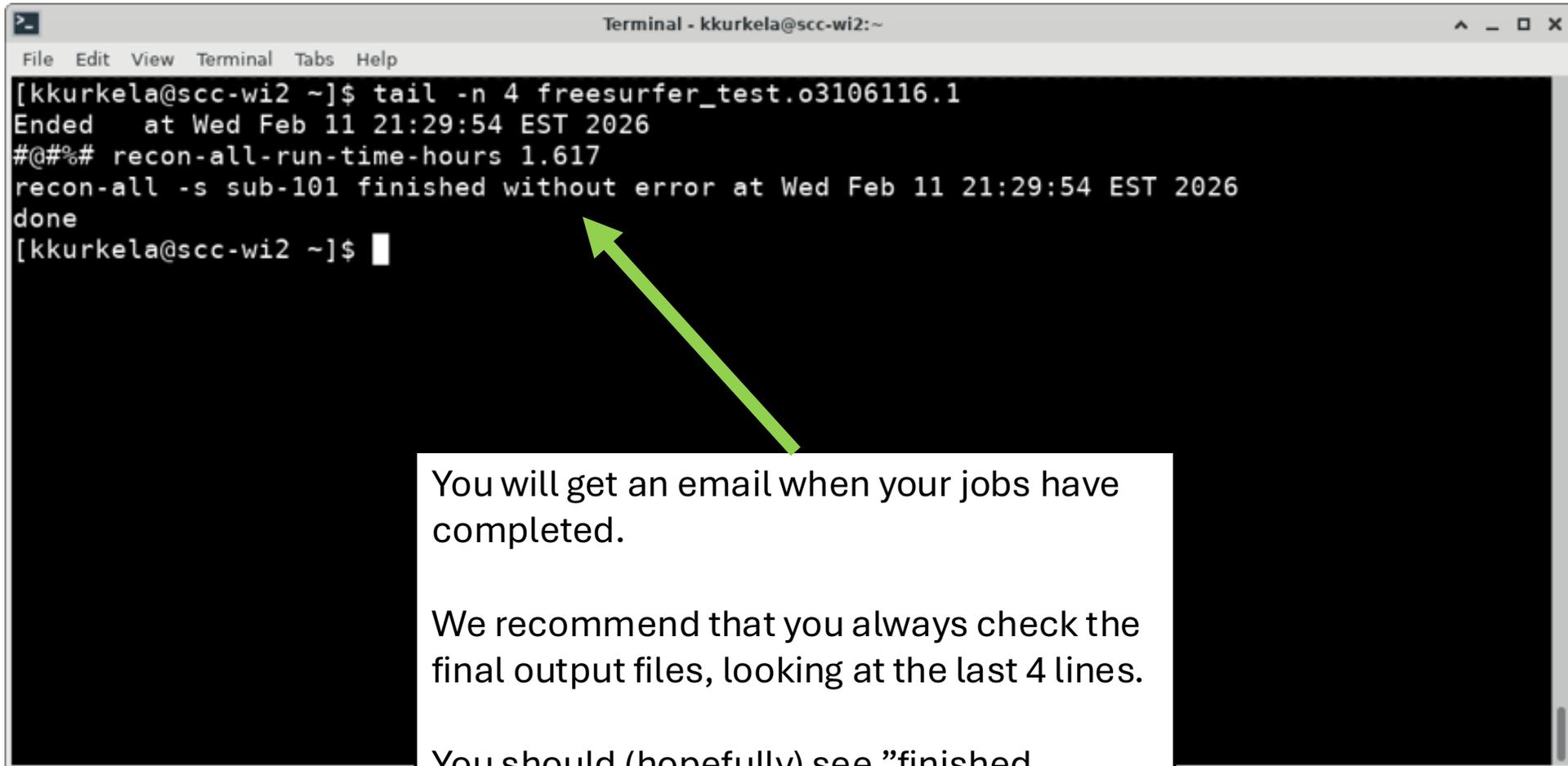
Website: https://synthstrip.io

@@@FSTIME 2026:02:11:19:53:07 mri_synthstrip N 6 e 41.63 S 8.27 U 69.18 P 186% M 7784536 F 1494 R 490376 W 0 c 237 w 103
62 I 382344 O 2888 L 0.29 0.07 0.02
@@@FSLOADPOST 2026:02:11:19:53:48 mri_synthstrip N 6 1.33 0.36 0.12

mri_synthseg --i /projectnb/scv/kkurkela/freesurfer_tutorial/sub-101/mri/orig.mgz --o /projectnb/scv/kkurkela/freesurfer
_tutorial/sub-101/mri/synthseg.rca.mgz --threads 4 --vol /projectnb/scv/kkurkela/freesurfer_tutorial/sub-101/stats/synths
eg.vol.csv --keepgeom --addctab --cpu
```

- As the job is running, these output files will be continually updated with the text output of recon-all.
- You can track these files using the “tail -f” command

Submitting a Cortical Reconstruction – Job Array



```
Terminal - kkurkela@scc-wi2:~
File Edit View Terminal Tabs Help
[kkurkela@scc-wi2 ~]$ tail -n 4 freesurfer_test.o3106116.1
Ended at Wed Feb 11 21:29:54 EST 2026
#@#%# recon-all-run-time-hours 1.617
recon-all -s sub-101 finished without error at Wed Feb 11 21:29:54 EST 2026
done
[kkurkela@scc-wi2 ~]$
```

You will get an email when your jobs have completed.

We recommend that you always check the final output files, looking at the last 4 lines.

You should (hopefully) see "finished without errors"

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- Tutorial Prep
- FreeSurfer Terminology/Intro
- Submitting recon-all to the SCC
- Freeview
- Review outputs
- Data troubleshooting

A Note on Using Freeview on the SCC

- Freeview is a 3-D rendering program that can take advantage of the Graphical Processing Units (GPUs) we have on the SCC
- Having a GPU available greatly increases the frame rate and the quality of life when working with surfaces within Freeview
- You can request a Desktop session with a GPU by using the “VirtualGL Desktop”
- Once in a VirtualGL Desktop session, start up freeview using:

```
> module load freesurfer/8.0.0  
> vglrun freeview
```

This will ensure the freeview uses the GPU when rendering surfaces.

Freeview – Tour Around the User Interface

Change the Viewport

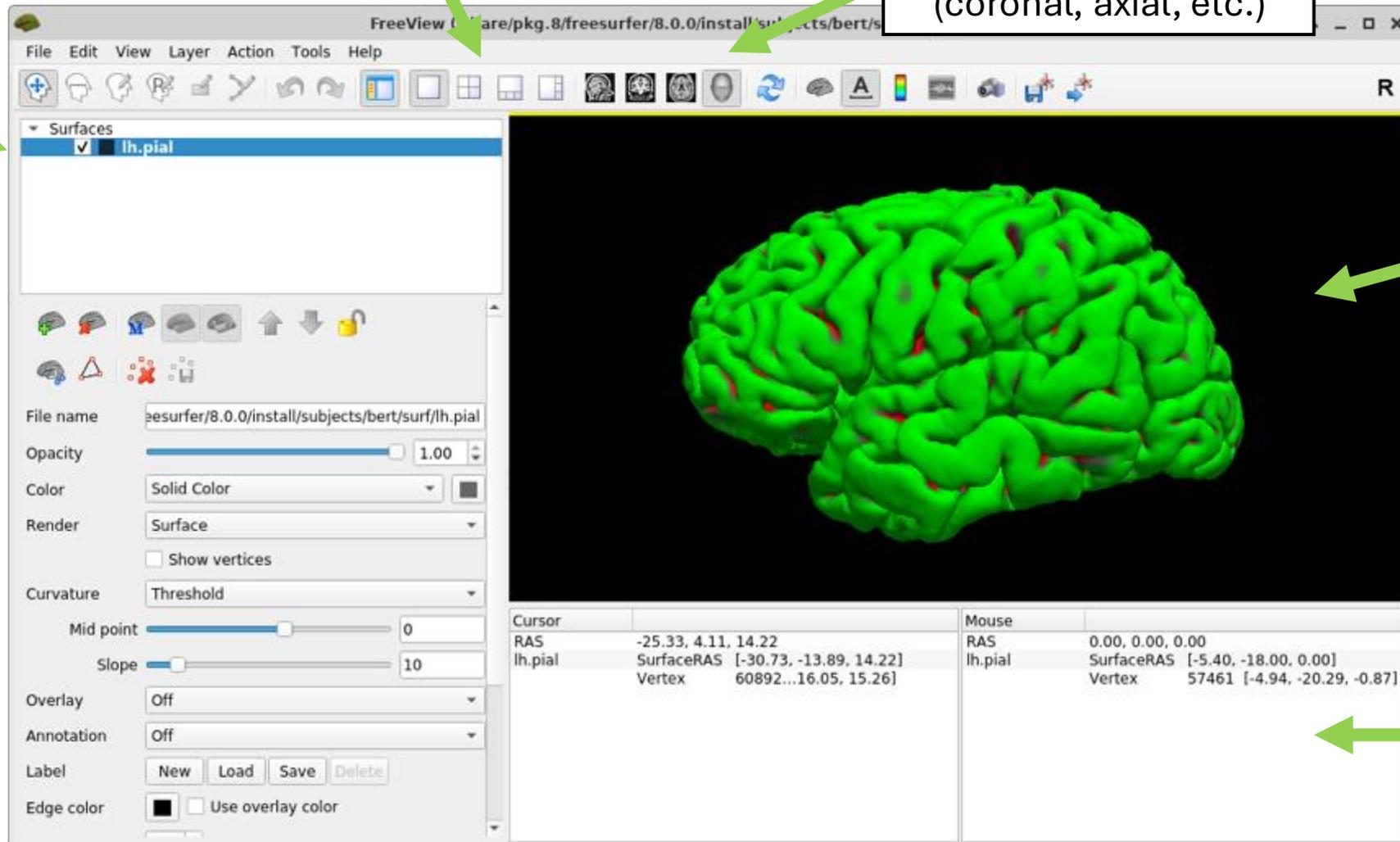
View to Focus On
(coronal, axial, etc.)

Loaded Files

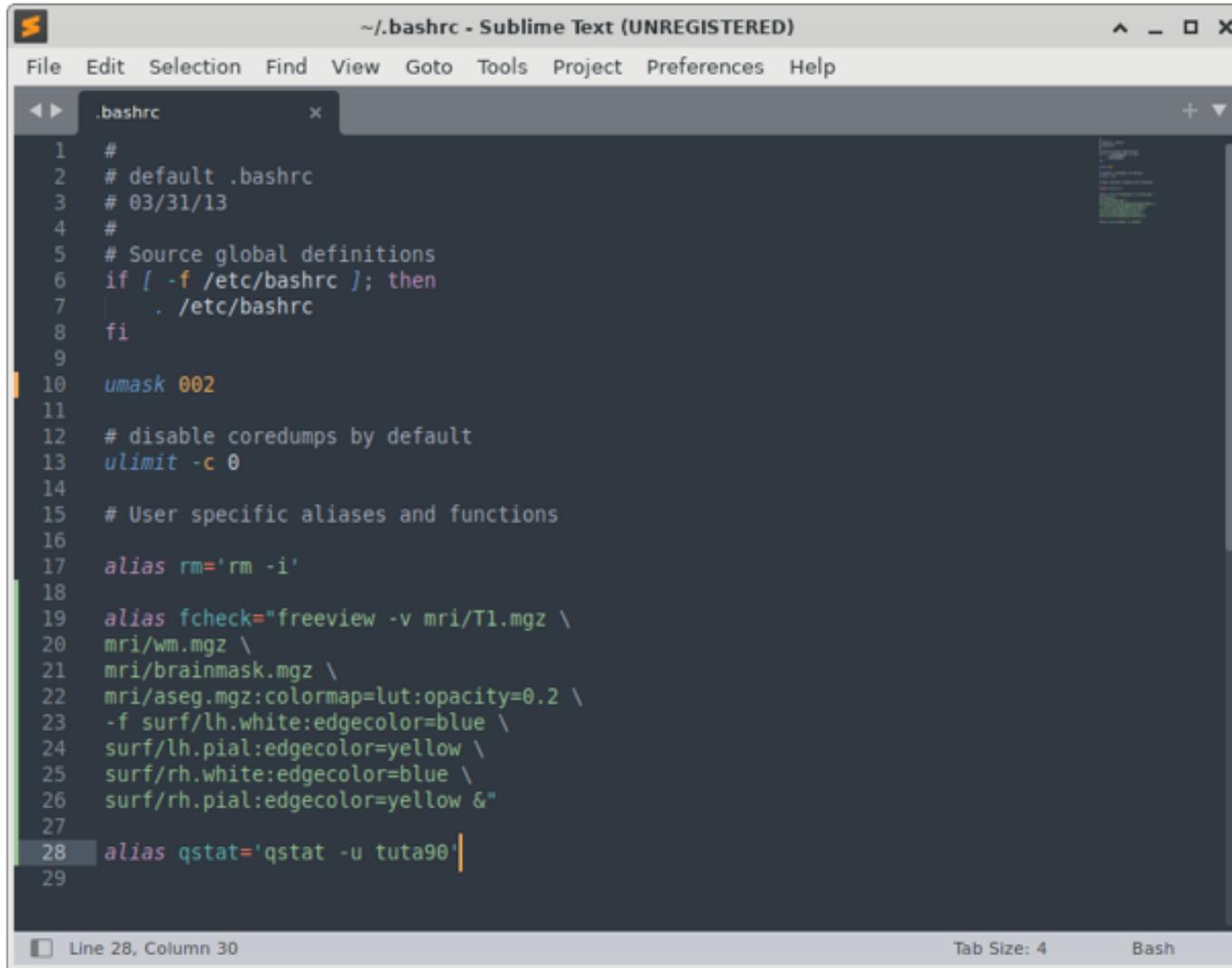
Main Viewport

Options for
highlighted file
above “lh.pial”

Information
about the point
where your
cursor/mouse
are



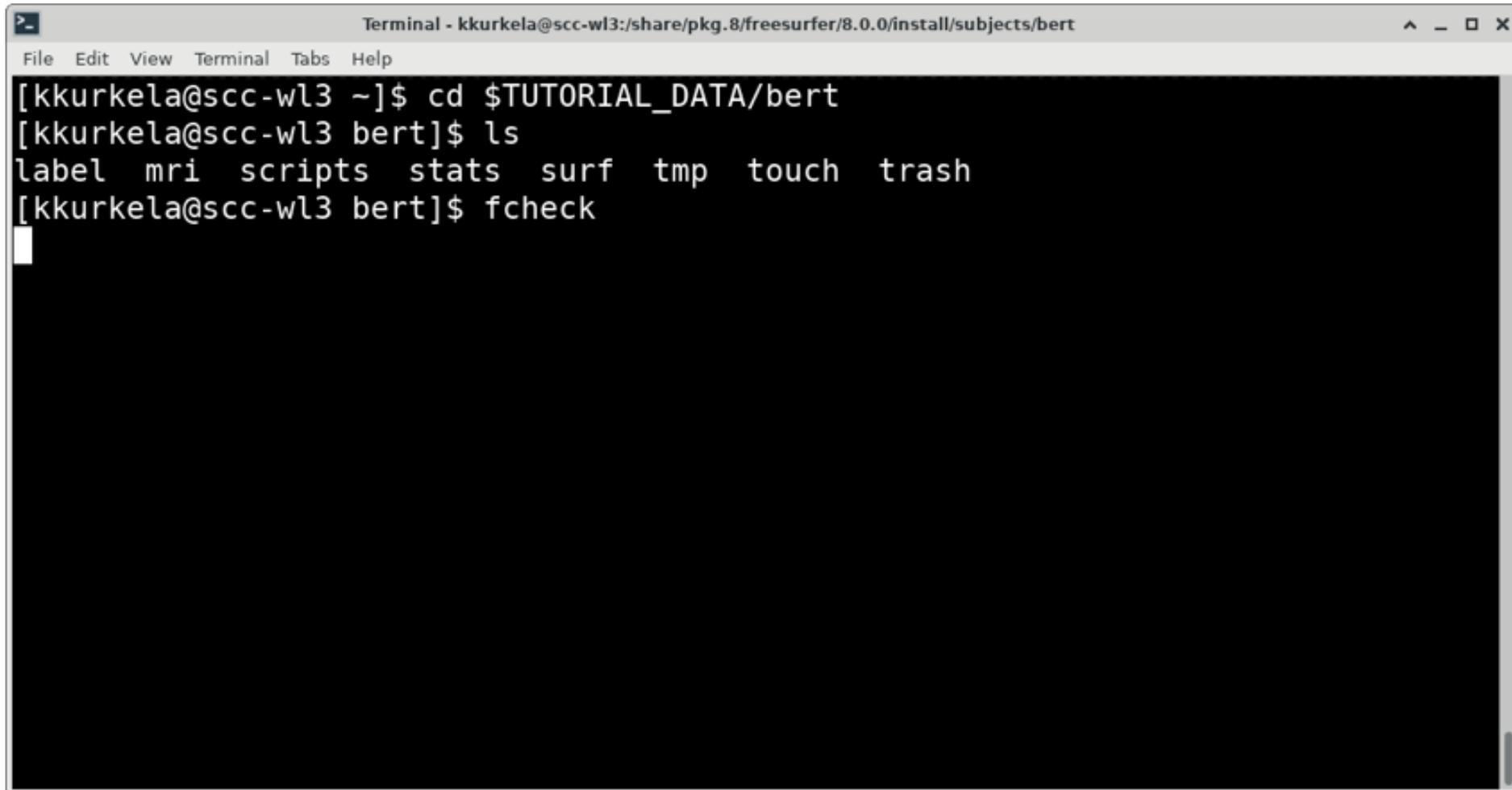
Freeview – adding fcheck to our .bashrc



```
~/bashrc - Sublime Text (UNREGISTERED)
File Edit Selection Find View Goto Tools Project Preferences Help
.bashrc
1 #
2 # default .bashrc
3 # 03/31/13
4 #
5 # Source global definitions
6 if [ -f /etc/bashrc ]; then
7     . /etc/bashrc
8 fi
9
10 umask 002
11
12 # disable coredumps by default
13 ulimit -c 0
14
15 # User specific aliases and functions
16
17 alias rm='rm -i'
18
19 alias fcheck="freeview -v mri/T1.mgz \
20 mri/wm.mgz \
21 mri/brainmask.mgz \
22 mri/aseg.mgz:colormap=lut:opacity=0.2 \
23 -f surf/lh.white:edgecolor=blue \
24 surf/lh.pial:edgecolor=yellow \
25 surf/rh.white:edgecolor=blue \
26 surf/rh.pial:edgecolor=yellow &"
27
28 alias qstat='qstat -u tuta90'
29

Line 28, Column 30 Tab Size: 4 Bash
```

Freeview – Let's use fcheck



```
Terminal - kkurkela@scc-wl3:/share/pkg.8/freesurfer/8.0.0/install/subjects/bert
File Edit View Terminal Tabs Help
[kkurkela@scc-wl3 ~]$ cd $TUTORIAL_DATA/bert
[kkurkela@scc-wl3 bert]$ ls
label mri scripts stats surf tmp touch trash
[kkurkela@scc-wl3 bert]$ fcheck
```

Freeview – Let's use fcheck

The screenshot displays the FreeView application window. The title bar reads "FreeView (/share/pkg.8/freesurfer/8.0.0/install/subjects/bert/surf/rh.pial)". The interface includes a menu bar (File, Edit, View, Layer, Action, Tools, Help) and a toolbar with various icons. On the left, a "Volumes" and "Surfaces" tree view shows loaded data, with "rh.pial" selected. Below this is a control panel with settings for file name, opacity, color, render mode, curvature, mid point, slope, overlay, annotation, label, and edge color. The main window is divided into four quadrants showing different views of the brain surface. The top-left view is a coronal slice with a green border. The top-right view is a sagittal slice. The bottom-left view is an axial slice. The bottom-right view shows a 3D brain model with a red bounding box and intersecting axes. At the bottom, two data tables are visible: "Cursor" and "Mouse".

Cursor			
RAS	6.40, 18.00, 1.00		
TkReg...mask)	1.00, 0.00, 1.00		
MNI30...mask)	0.40, -4.28, -4.77		
brainmask	26	[127, 127, 128]	
wm	0	[127, 127, 128]	
T1	26	[127, 127, 128]	
rh.pial	SurfaceRAS	[1.00, 0.00, 1.00]	
	Vertex	74225 [2.01, -0.56, 1.24]	
rh.white	SurfaceRAS	[1.00, 0.00, 1.00]	
	Vertex	74225 [2.01, -0.56, 1.24]	
lh.pial	SurfaceRAS	[1.00, 0.00, 1.00]	
	Vertex	73553 [-0.78, -0.51, 1.24]	

Mouse			
RAS	238.07, 18.00, 35.09		
TkReg...mask)	232.67, 0.00, 35.09		
MNI30...mask)	254.08, 6.41, 21.47		
brainmask	0	[-105, 93, 128]	
wm	0	[-105, 93, 128]	
T1	0	[-105, 93, 128]	
rh.pial	SurfaceRAS	[232.67, 0.00, 35.09]	
	Vertex	N/A	
rh.white	SurfaceRAS	[232.67, 0.00, 35.09]	
	Vertex	N/A	
lh.pial	SurfaceRAS	[232.67, 0.00, 35.09]	
	Vertex	N/A	

Outline

- Tutorial Prep
- FreeSurfer Terminology/Intro
- Submitting recon-all to the SCC
- Freeview
- Review outputs
- Data troubleshooting

FreeSurfer's Outputs

```
[username@scc ~] cd $SUBJECTS_DIR/bert
```

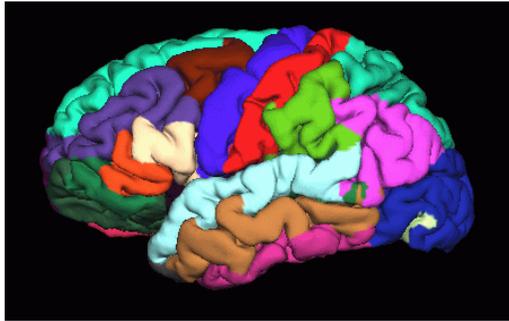
```
[username@scc bert] ls
```

```
label    mri      scripts  stats    surf     tmp      touch    trash
```

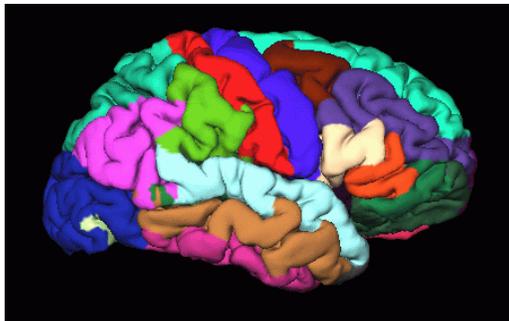
```
[username@scc ~] cd $SUBJECTS_DIR/bert
[username@scc bert] ls
```

```
label  mri  scripts  stats  surf  tmp  touch  trash
```

Desiken/Killiany Atlas

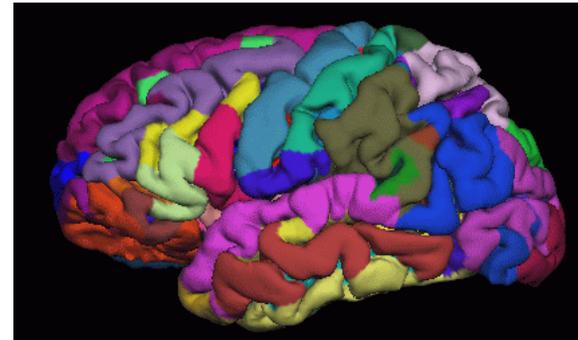


lh.aparc.annot

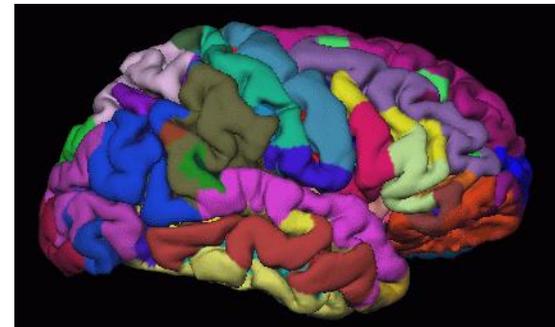


rh.aparc.annot

Destrieux Atlas



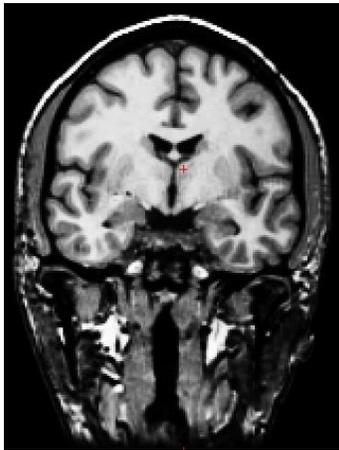
lh.aparc.a2009s.annot



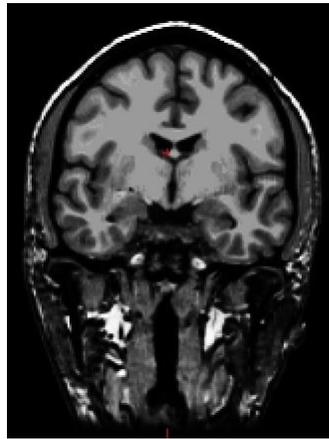
rh.aparc.a2009s.annot

```
[username@scc ~] cd $SUBJECTS_DIR/bert  
[username@scc bert] ls
```

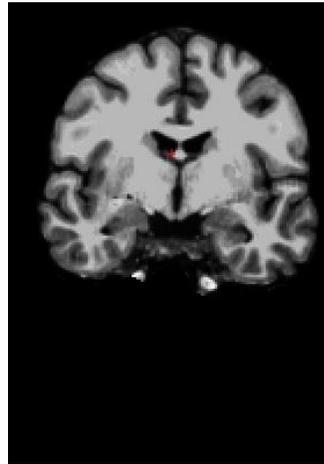
```
label  mri  scripts  stats  surf  tmp  touch  trash
```



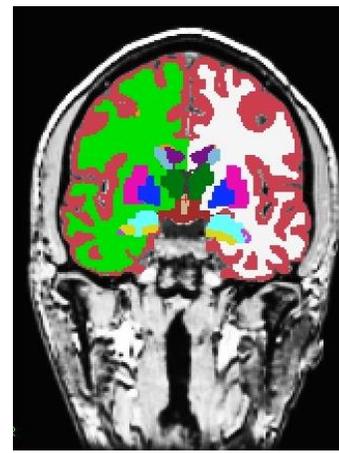
orig.mgz



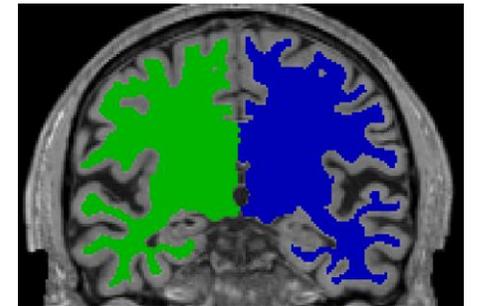
T1.mgz



brainmask.mgz



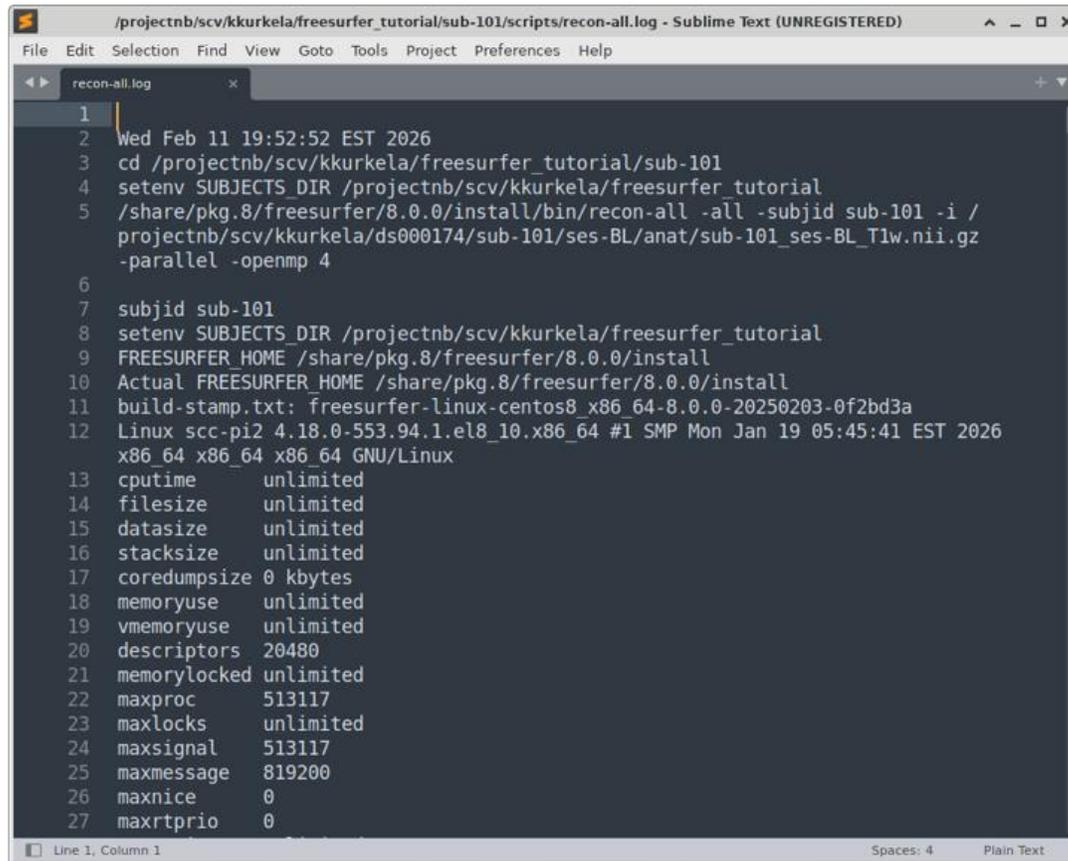
aseg.mgz



filled.mgz

```
[username@scc ~] cd $SUBJECTS_DIR/bert  
[username@scc bert] ls
```

label mri **scripts** stats surf tmp touch trash



```
/projectnb/scv/kkurkela/freesurfer_tutorial/sub-101/scripts/recon-all.log - Sublime Text (UNREGISTERED)  
File Edit Selection Find View Goto Tools Project Preferences Help  
recon-all.log x  
1  
2 Wed Feb 11 19:52:52 EST 2026  
3 cd /projectnb/scv/kkurkela/freesurfer_tutorial/sub-101  
4 setenv SUBJECTS_DIR /projectnb/scv/kkurkela/freesurfer_tutorial  
5 /share/pkg.8/freesurfer/8.0.0/install/bin/recon-all -all -subjid sub-101 -i /  
projectnb/scv/kkurkela/ds000174/sub-101/ses-BL/anat/sub-101_ses-BL_T1w.nii.gz  
-parallel -openmp 4  
6  
7 subjid sub-101  
8 setenv SUBJECTS_DIR /projectnb/scv/kkurkela/freesurfer_tutorial  
9 FREESURFER_HOME /share/pkg.8/freesurfer/8.0.0/install  
10 Actual FREESURFER_HOME /share/pkg.8/freesurfer/8.0.0/install  
11 build-stamp.txt: freesurfer-linux-centos8_x86_64-8.0.0-20250203-0f2bd3a  
12 Linux scc-pi2 4.18.0-553.94.1.el8_10.x86_64 #1 SMP Mon Jan 19 05:45:41 EST 2026  
x86_64 x86_64 x86_64 GNU/Linux  
13 cputime unlimited  
14 filesize unlimited  
15 datasize unlimited  
16 stacksize unlimited  
17 coredumpsize 0 kbytes  
18 memoryuse unlimited  
19 vmemoryuse unlimited  
20 descriptors 20480  
21 memorylocked unlimited  
22 maxproc 513117  
23 maxlocks unlimited  
24 maxsignal 513117  
25 maxmessage 819200  
26 maxnice 0  
27 maxrtprio 0  
Line 1, Column 1      Spaces: 4      Plain Text
```

recon-all.log

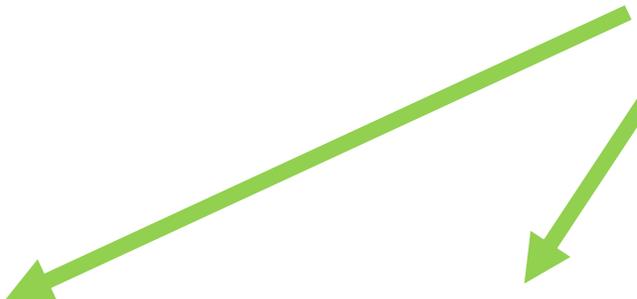
This is the most important log file.

If something goes wrong with your recon, the error will be recorded here.

Send this file to me if you run have problems.

```
[username@scc ~] cd $SUBJECTS_DIR/bert  
[username@scc bert] ls
```

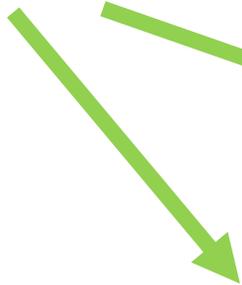
```
label  mri  scripts  stats  surf  tmp  touch  trash
```



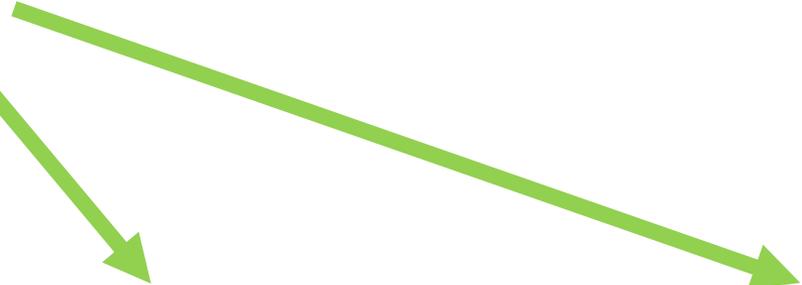
aseg.stats



wmparc.stats



lh/rh.aparc.stats



lh/rh.aparc.a2009.stats

Let's look at some of the stats files.

```
[username@scc ~] sublime stats/aseg.stats
```

```
[username@scc ~] sublime stats/wmparc.stats
```

```
[username@scc ~] sublime stats/lh.aparc.stats
```

How do we aggregate the stats for further analysis?

```
# command for aggregating the aseg.stats files:
```

```
> asegstats2table --subjects sub-101 sub-103 sub-104 -t my_seg_table.tsv
```

```
# command for aggregating the parc.stats files:
```

```
> aparstats2table --subjects sub-101 sub-103 sub-104 -t my_parc_table.tsv
```

mytable.tsv - LibreOffice Calc

File Edit View Insert Format Styles Sheet Data Tools Window Help

Liberation Sa 10 B I U A % 7.4 00 00

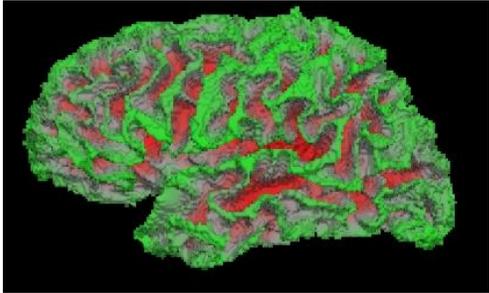
E11 fx Σ =

	A	B	C	D	E	F	G	H	I
1	Measure:volume	Left-Lateral-Ventricle	Left-Inf-Lat-Vent	Left-Cerebellum-White-Matter	Left-Cerebellum-Cortex	Left-Thalamus	Left-Caudate	Left-Putamen	L
2	sub-101	5920.9	534.6	15866.1	50958.8	6846.9	3478.6	4986.4	
3	sub-103	7516.1	491.5	15656.1	59771	6924.6	4085.2	6231.7	
4	sub-104	6796.3	504.3	15646.6	53111.2	6122.1	3528.7	5709.8	
5									
6									
7									
8									
9									
10									
11									
12									
13									
14									
15									
16									
17									
18									
19									
20									
21									
22									

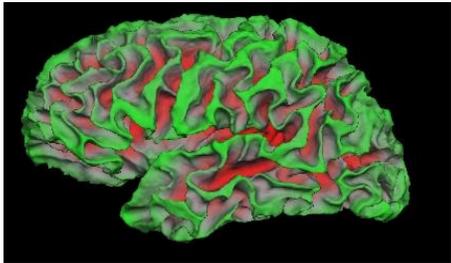
Sheet 1 of 1 | Default | English (USA) | Average: ; Sum: 0 | 150%

```
[username@scc ~] cd $SUBJECTS_DIR/bert
[username@scc bert] ls
```

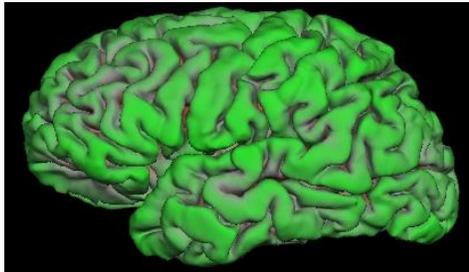
```
label  mri  scripts  stats  surf  tmp  touch  trash
```



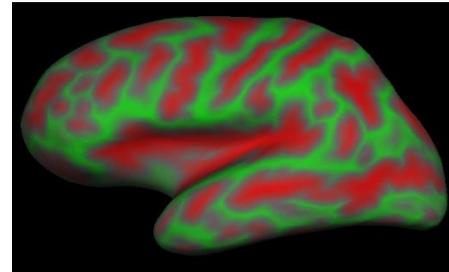
lh/rh.orig



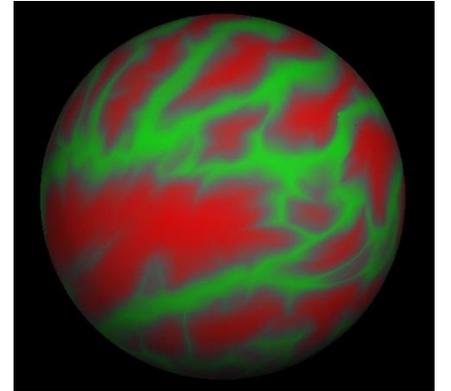
lh/rh.white



lh/rh.pial



lh/rh.inflated



lh/rh.sphere.reg

```
[username@scc ~] cd $SUBJECTS_DIR/bert  
[username@scc bert] ls
```

label mri scripts stats surf **tmp** **touch** **trash**

As the name implies, temporary files.
Used when setting control points (we
will return to this).

These are files that keep track of which
steps have been run

None of the files in these directories
are very useful to monitor...



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What do “bad” recons look like? How do we fix them?

- Let's go through our QA guide found here:

<https://rcs.bu.edu/examples/imaging/freesurfer/qa/>

Example 1: Fixing a bad skull strip

- Copy the tutorial subject to your working space
- ```
> cp -r $TUTORIAL_DATA/skullstrip_before ./
```
- ```
> cp -r $TUTORIAL_DATA/skullstrip_after ./
```

We are going to follow the FreeSurfer Tutorial here:

<https://surfer.nmr.mgh.harvard.edu/fswiki/FsTutorial/SkullStripFixV6.0>

Example 2: Correcting the Pial Surface

- Copy the tutorial subject to your working space
- ```
> cp -r $TUTORIAL_DATA/pial_edits_before ./
```
- ```
> cp -r $TUTORIAL_DATA/pial_edits_after ./
```

We are going to follow the FreeSurfer Tutorial here:

<https://surfer.nmr.mgh.harvard.edu/fswiki/FsTutorial/PialEditsV6.0>

Example 3: Using Control Points

- Copy the tutorial subject to your working space

```
> cp -r $TUTORIAL_DATA/cp_before ./
```

```
> cp -r $TUTORIAL_DATA/cp_after ./
```

We are going to follow the FreeSurfer Tutorial here:

<https://surfer.nmr.mgh.harvard.edu/fswiki/FsTutorial/ControlPointsV6.0>

Questions? Comments? Concerns?

Please Give Tutorial Feedback!!

http://scv.bu.edu/survey/tutorial_evaluation.html

Please fill it out at the end of today's tutorial!