Introduction to Freesurfer Output, continued - Viewing surfaces:

0. Preparations

Go to: http://vlwp.rug.nl and access your linux digital workspace. Open the terminal.

Run the configuration files for freesurfer with this code (you do this every time you open a new terminal).

```
export FREESURFER_HOME=/opt/netapps/freesurfer_7.4.1
source $FREESURFER_HOME/SetUpFreeSurfer.sh
```

Set the directories for accessing the data

```
export TUTORIAL_DATA=/media/ydrive/staff/let/MRI_tutorials/Freesurfer_tutorials/tutorial_data
export SUBJECTS_DIR=$TUTORIAL_DATA/buckner_data/tutorial_subjs
cd $SUBJECTS_DIR
```

1. Open the surface data

```
freeview -f  good_output/surf/lh.pial:annot=aparc.annot:name=pial_aparc:visible=0 \
good_output/surf/lh.pial:annot=aparc.a2009s.annot:name=pial_aparc_des:visible=0 \
good_output/surf/lh.inflated:overlay=lh.thickness:overlay_threshold=0.1,3::name=inflated_thickness:visible=0 \
good_output/surf/lh.inflated:visible=0 \
good_output/surf/lh.white:visible=0 \
good_output/surf/lh.pial \
--viewport 3d
```

ROI analyses

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export SUBJECTS_DIR=$TUTORIAL_DATA/buckner_data/tutorial_subjs/group_analysis_tutorial
```

1. **Task 1: In the tutorial data we see Freesurfer data which have already been processed. You can then read the data from a single individual. First, we will open the subcortical gray matter statistics file (the aseg.stats file) for subject 004.**

```
cd $SUBJECTS_DIR/004/stats
less aseg.stats #type "q" to quit the 'less' command
```

The top of the output shows information about the command that is ran, the machine running it, and directories. Next we see a list of all the headings of the table presented below. Finally we see a table with metrics for each structure. **Can you tell what is the volume (in mm3) of the left lateral ventricle?**

Next we open the statistics file based on the Destrieux segmentation of cortical data

```
less lh.aparc.a2009s.stats #type "q" to quit the 'less' command
```

2. **Task 2: Normally, we want to extract the data of several subjects and organize that conveniently in a table. Let's do that now. Get the cortical gray matter results organized per region of interest for subjects 004 and 073. Extract specifically cortical thickness measures per ROI for the left hemisphere and save this information in a text file in your desktop.**

Below is the code we need. Before you run it, here is an explanation, for each line.

- The function 'aparcstats2table' summarizes some of the data we specifically ask for. The first line indicates that the participants we want the data from are subjects 073 and 004.
- '--hemi lh' specified that we want the metrics for the left hemisphere
- '--parc aparc.a2009a' specifies that we are using the parcellation from the Destrieux atlas. If we want the Desikan Killiany atlas, we call this as '--parc aparc \'.
- '--meas thickness' specifies that we want the measurements of cortical thickness. You could replace this by area or volume, for example.
- '--tablefile' indicates the location and the name of the output file where the data will be stored. Replace the text in red with your student number,to save the output in your own desktop. You can change the directory behind the file name if you want to save the results in another folder.

```
aparcstats2table --subjects 073 004 \
--hemi lh \
--parc aparc.a2009s \
--meas thickness \
--tablefile /home/p967216/Desktop/aparc_lh_thickness_Destrieux.txt
```

3. **Task 3. Get the left hemisphere volumes for ROIs of the DK parcellation. Do this for subjects 004 021 040 067 080 092. Save the output on your desktop, and name the file according to its content (e.g., aparc_lh_volume_DK.txt).**

```
aparcstats2table --hemi lh \
--subjects 004 021 040 067 080 092 \
--parc aparc \
--meas volume \
--tablefile /home/p967216/Desktop/aparc_lh_volume_DK.txt
```

4. **Task 4: Find out what is the volume of the left IFG pars triangularis of participant 004. The file is a bit difficult to read in this wide format, so we will transpose it by adding the "--transpose" argument.**

```
aparcstats2table --hemi lh \
--subjects 004 \
--parc aparc \
--meas volume \
--transpose \
--tablefile /home/p967216/Desktop/aparc_lh_volume_DK_sub004.txt
```

5. **Task 5: Let's now look at white matter. We now use the function "asegstats2table". We will find out what is the volume of the white matter underlying the left IFG. You can use the same function as above, but the stats come from the wmparc.stats file. We also use the "segno" argument to extract only the regions underlying the IFG.**

```
asegstats2table \
--subjects 004 021 040 067 080 092 \
--segno 3018 3019 3020 \
--stats wmparc.stats \
--tablefile  /home/p967216/Desktop/wmparc_lFG_vol.table
```

Note the "segno" argument. The values 3018, 3019, and 3020 correspond to the index of the left IFG opercularis, left IFG orbitalis, and left IFG triangularis. You can see a full list of structure names and their indices here in the Look Up Table (LUT). If the "segno" option is not included, all ROIs will be included in the output file. Here is an example of each index of the left IFG according to the LUT section which is based on the aparc.a2009s.

Note that you also get extra measures, included the estimated total intracranial volume. This is because for some measures (e.g., volume) it is important to normalize the data to account for the fact that people's heads/brains have different sizes.

Use the command `aparcstats2table --help` and the command `asegstats2table --help` to check all possible ways to access the data by specifying different arguments.

At this point, you can use any statistical software package to run correlations, group comparisons, etc. However, before you trust the data, you also have to have completed the quality control.

GLM tutorial:

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```

1. **set wd**

```
cd $SUBJECTS_DIR/glm
```

2. **You only need to copy this code (all the earlier steps were already computed):**

```
freeview -f
$SUBJECTS_DIR/fsaverage/surf/lh.inflated:annot=aparc.annot:annot_outline=1:overlay=lh.gender_age.glmdir/lh-Avg-thickness-age-Cor/sig.mgh:overlay_threshold=4,5 \
--viewport 3d \
--layout 1
```

(note: this command is very long and extends beyond several lines. If you copy-paste it, make sure that you copy from a word file, not the pdf. The pdf will separate the lines and then the code is not read appropriately in the terminal).

Quality control

The initial segmentation and parcellation produced by Freesurfer can include errors of different types. IIn our tutorials, I wanted to give you an overview of the Freesurfer pipeline and the type of output you get and analyses you can do with the data. But before proceeding to extracting individual or group data, or conducting ROI-based or voxel-based analyses, you need to check the quality of the data.

For those of you who work with Freesurfer in the future, here are some relevant resources.

Here is the link to the Troubleshooting section of the Freesurfer step-by-step tutorial:
https://surfer.nmr.mgh.harvard.edu/fswiki/FsTutorial/TroubleshootingDataV6.0

These two videos that follow are from Freesurfer's YouTube channel:
1) https://www.youtube.com/watch?v=gf0BC0xs0tM&t=1049s
2) https://www.youtube.com/watch?v=AR83_Bt04VQ&t=917s

This video (and the following ones in that series) are also useful. It is from a channel of a researcher called Andrew Jahn.
https://www.youtube.com/watch?v=8n5_XE-OH0E

And also this link from Boston University is helpful:
https://sites.bu.edu/cnrlab/lab-resources/freesurfer-quality-control-guide/