**Use this protocol for the analysis of mean cortical thickness and surface area data within FreeSurfer ROI's for the ENIGMA Bipolar, Schizophrenia, Major Depressive Disorder, ADHD, Addiction and Anxiety working groups.**

**These protocols are offered with an unlimited license and without warranty. However, if you find these protocols useful in your research, please provide a link to the ENIGMA website in your work: www.enigma.ini.usc.edu**

**Step 1: Extract and Organize Cortical Measures (FreeSurfer)**

Highlighted portions of the instructions may require you to make changes so that the commands work on your system and data.

**This section assumes that you have downloaded:**

* Download the script for extracting SurfaceArea and Thickness Values: [extract.sh](http://enigma.ini.usc.edu/wp-content/uploads/CORTEX/extract.sh)

**---------------------------------------------**

We want to get the Surface Area and Thickness of each ROI for each subject from FreeSurfer.

The extract.sh script will extract and organize each of the values for each FreeSurfer ROI. The script assumes that your FreeSurfer output are organized in a standard way:

{Parent Folder} 🡪 {Subject1} 🡪 {FreeSurfer Output Folders}

🡪 {Subject2} 🡪 {FreeSurfer Output Folders}

…

cd /enigma/Parent\_Folder/

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Save the **extract.sh** script in the Parent Folder with your FreeSurfer output. Open the **extract.sh** and edit the for loop (line 6) so that the *ls* command selects the subject folder naming scheme used in your study:

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for subj\_id in $(ls -d Subj\*); do #may need to change this so that it selects subjects with FS output

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Save the extract.sh script after editing. On the command line, you can run the script directly by running:

sh extract.sh

The result of this step will be two comma-separated (CSV) files that can be opened in your favorite spreadsheet application (i.e. Excel). The first row is a header describing the extracted regions and data type for each column. Each row after the first gives the cortical thickness or surface area measures for each subject found in your FreeSurfer directory. In the next step, you will do a QC of the segmentation quality.

**Note 1:** After running the extract.sh script, open both of the CSV files (CorticalMeasuresENIGMA\_ThickAvg.csv and CorticalMeasuresENIGMA\_SurfAvg.csv) and make sure that only subjects are listed in the rows of the file. Sometimes if there are other folders in your parent directory those folders can become included in your final files. If that happens just delete those from your CSV files and save.

**Note 2:** When you edit the files in Excel, be sure to keep them in CSV format when you save!