**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 3: Generate Summary Statistics and Histogram Plots**

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 installed:**

* R ([download here](http://cran.r-project.org/))
* Download the automated script for generating the plots (called ENIGMA\_CortexROI\_plots.R) from [**here**](http://enigma.ini.usc.edu/wp-content/uploads/CORTEX/ENIGMA_CortexROI_plots.R).

After having quality checked each of your segmented structures you should have two files called CorticalMeasuresENIGMA\_ThickAvg.csv and CorticalMeasuresENIGMA\_SurfAvg.csv, which are comma separated files with the values of each segmented structure for each subject. **For example, the CorticalMeasuresENIGMA\_ThickAvg.csv file should look like this (note the ... there should be 74 columns) with poorly labeled structures marked with NA:**

SubjID,L\_bankssts\_thickavg,L\_caudalanteriorcingulate\_thickavg, ...

subject1,2.324,2.383, ...

subject2,2.593,NA, ...

subject3,2.77,2.955, ...

subject4,NA,NA, ...

subject5,2.695,3.348, ...

**Generating plots and summary statistics:**

Make a new directory to store all of your summary stats and histogram plots:

mkdir /enigma/figures\_cortical/

Copy your CorticalMeasuresENIGMA\_ThickAvg.csv and CorticalMeasuresENIGMA\_SurfAvg.csv file to your new folder:

cp /enigma/first/data/CorticalMeasuresENIGMA\_ThickAvg.csv /enigma/figures\_cortical/

cp /enigma/first/data/ CorticalMeasuresENIGMA\_SurfAvg.csv /enigma/figures\_cortical/

Move the ENIGMA\_CortexROI\_plots.R script to the same folder:

mv /enigma/downloads/ENIGMA\_CortexROI\_plots.R /enigma/figures\_cortical/

Make sure you are in your new figures folder:

cd /enigma/­­­figures\_cortical

Run the R script to generate the plots:

R --no-save --slave < ENIGMA\_CortexROI\_plots.R

It should only take a minute to generate all of the plots. If you get errors, the script might tell you what things need to be changed in your data file in order to work properly. Just make sure that your input file is in \*.csv format like the example file above.

The output will be a series of PNG image files that you can open in any standard picture viewer. You need to go through each of the PNG files to make sure that your histograms look approximately normal.

**NB: If a subject is an outlier in (one of) your histogram plots, but after inspection you decide the subject is properly segmented, you should KEEP the corresponding value in your CorticalMeasuresENIGMA\_ThickAvg.csv and CorticalMeasuresENIGMA\_SurfAvg.csv files to be used in the analysis.**