best\_method.m is the main program, it uses the other programs to generate all the results and graphs.

To run it, you need a file with all the data named like: LHmat1.mat where LH indicates the hempishere and 1 is the view we used. This is mandatory as the program will have to look back for the original file, extract\_subject.m is doing that, and it should probably be modified if the structure of the directory is different from the one I had.

To add stability: line 137-140 in create\_graph.m, follow instructions and uncomment the line needed.

The label file needs to be called labels.mat and has to be with all the other .mat files in the main directory.