**TASH: Toolbox for the Automated Segmentation of Heschl’s gyrus** **USER MANUAL**

**TASH Installation Setup** (Perform it just once, when installing the toolbox)

1. Have MATLAB (preferred version R2012a) installed on your linux platform.
2. Have Freesurfer (preferred version 5.3) installed on your linux platform.
3. On the OS X terminal Tcsh Shell, set in the folder where the file TASH\_complete.csh is.
4. On the OS X terminal Tcsh Shell, type: chmod +x TASH\_complete.csh

**Preparing for processing the data** (Adjust it every time you need to process a new data)

1. Perform Freesurfer recon-all command on each of the T1 MR images.

recon-all -subject Your\_Subject -i Your\_Subject\_T1\_image\_file -all -qcache

1. On the terminal Tcsh Shell, set in the folder where the TASH tcsh files are.
2. Open the file TASH\_DefineSubjects and define your subjects on the line 2, as:

set SUBJECTS = (Your\_Subject\_1 Your\_Subjetct\_2 All\_Other\_Subjects)

1. Open the file TASH\_DefineSubjects.m
   1. On the line 2, define your subjects, enveloped by apostrophes, as:

sub = {'Your\_Subject\_1' 'Your\_Subjetct\_2 ' 'All\_Other\_Subjects'};

* 1. On the line 3, define the folder where freesurfer subjects are:

Dload = '/…/freesurfer/subjects';

* 1. On the line 4, define the folder where TASH output images should be saved:

Dsave = '/…/…/…';

**Processing the data**

On the terminal Tcsh Shell, type: ./TASH\_complete.csh → For Freesurfer 7 run TASH\_completev7

**Data output**

1. Two matlab files contains the numerical output of TASH (actual values for anatomical measures).
   1. 'TASH\_measures\_complete.mat' stores two matlab structs ('lh' and 'rh'), each one contains the anatomical measures (volume, suface area, mean thickness, etc...) considering all gyri of the hemisphere together. In this way, each matrix inside the struct (for example 'lh.volume') contains one value per line, while each line is each different inputted T1 image.
   2. 'TASH\_measures\_complete\_individual.mat' file has the same structure of the file mentioned above. However, in this case it stores the anatomical measures considering each gyrus individually. In this way, each matrix inside the struct (for example 'lh.volume') contains N values per line, where N is the number of transverse temporal gyri for each hemisphere. Then, the first column stores results for the first gyrus and so on (from anterior to posterior).
2. About the images, the ones in the main folder displays all temporal transverse gyri per hemisphere, while the images in the subfolder 'individual' displays each gyrus individually per image.

**Extra steps**

1. qdec:

aparcstats2table --subjectsfile=subjectlist.txt --skip --parc aparc.a2009s --hemi lh --meas area -t qdec\_DestrieuxAtlas\_area\_lh.txt

aparcstats2table --subjectsfile=subjectlist.txt --skip --parc aparc.a2009s --hemi rh --meas area -t qdec\_DestrieuxAtlas\_area\_rh.txt

aparcstats2table --subjectsfile=subjectlist.txt --skip --parc aparc.a2009s --hemi lh --meas volume -t qdec\_DestrieuxAtlas\_vol\_lh.txt

aparcstats2table --subjectsfile=subjectlist.txt --skip --parc aparc.a2009s --hemi rh --meas volume -t qdec\_DestrieuxAtlas\_vol\_rh.txt

aparcstats2table --subjectsfile=subjectlist.txt --skip --parc aparc.a2009s --hemi lh --meas thickness -t qdec\_DestrieuxAtlas\_th\_lh.txt

aparcstats2table --subjectsfile=subjectlist.txt --skip --parc aparc.a2009s --hemi rh --meas thickness -t qdec\_DestrieuxAtlas\_th\_rh.txt

aparcstats2table --subjectsfile=subjectlist.txt --skip --parc aparc.a2009s --hemi lh --meas meancurv -t qdec\_DestrieuxAtlas\_mc\_lh.txt

aparcstats2table --subjectsfile=subjectlist.txt --skip --parc aparc.a2009s --hemi rh --meas meancurv -t qdec\_DestrieuxAtlas\_mc\_rh.txt

asegstats2table --subjectsfile=subjectlist.txt --skip --meas volume -t qdec\_subcort\_vol.txt

1. MCAI: MCAI=MCAI\_TASH(Dir)
2. Comprehensive Excel table: Excel\_Output.m