Newly Preprocessed HCP data release 1.0 – 100 unrelated subjects

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Functional data

General folder structure

SubjID/fMRI _task/Parcellation/TimeSeriesFile

Examples: /100307/rfMRI_REST1_LR/Schaefer100/TS_Schaefer100S_bp_z.mat
/106016/rfMRI_REST1_LR/Schaefer400/TS_Schaefer400S_gsr.mat

Files description

Brain Atlas. We are providing processed HCP time series for 5 different parcellations or brain atlases: Schaefer at 4 different resolutions (100, 200, 400, 800 nodes) and Glasser (360 nodes). To each parcellation we appended 19 subcortical regions at the end. Therefore, the final total number of nodes is Nparcellation + Nsubcortical (e.g., Schaefer100 time series will have 119 brain nodes).

Time Series. Inside each Parcellation named folder (see General Folder structure) we are providing 8 different time series, according to all possible combinations of three different "processing flags". These flags are: Global signal regression (and its derivative) yes/no, Bandpass filter in the range [0.01 0.15] Hz yes/no, z-score yes/no. We added "key strings" to the time series .mat files, accordingly:

- *_bp* = bandpass was performed
- *_gsr* = global signal regression was performed
- *_z* = z-score was performed

and all possible combinations.

Note 1: The S next to the brain atlas keyword (e.g. TS_Schaefer100S) stands for "subcortical regions appended")
Note 2: When there is no "key string" appended to the time series file (e.g., "TS_Schaefer400S.mat") only standard general linear model (GLM) processing was performed. This included: detrending, removal of motion regressors and their first derivatives, removal of WM, CSF signals and their first derivatives.
Note 3: for task time series, it is recommended NOT to use bandpass filtered files.

Fmri_vols. For the GLM-only step, we are also providing the nifti volumes at voxelwise level, in the folder "fMRI_vols_GLMyes" (in case someone wants to play with some CAPs ;)). Outside the folder we are also providing a scrubbing.mat file associated to the fMRI volumes, that is a measurement on how motion-corrupted is each fMRI volume (based on the metrics proposed by Power et al. Neuroimage 2012 and 2014, specifically FD, DVARS and SD).

Scrubbing.mat provides a binary vector of size 1x NfMRIvolumes, where 1=Volume is corrupted.

T1. In this folder you will find all the anatomical files needed to register the parcellations into individual subject space and then fMRI space. The GM, WM and CSF segmentations are also provided.

Misc. In this folder we are providing:

- *Subcortical_labels* subfolder*:* the list of subcortical regions appended in the time series files: "Atlas_ROIs.2_LUT_ordered.txt"

- In the *Cortical_labels* subfolder*:* the label list for all parcellations provided (cortical regions only).

Note1: For Glasser we are appending the (huge) supplementary information from the relevant paper.
Note2: Quite important. Schaefer atlases yeo7 and yeo17, same number of nodes (e.g. Schaefer200_yeo7, Schaefer200_yeo17) DO NOT have the same region assignments. Be careful in case you want to compare them.

- In the *YeoOrder* folder: the yeo_RS7_* files, containing yeoOrder and yeoROIs matlab variables. *yeoROIs*: label assignment of the overlap between a specific Parcellation and Yeo 7 resting state networks (+ an 8th subcortical). *YeoOrder*: in case someone want to visualize functional connectomes ordered according to the "7 Yeo resting-state networks" + 8th subcortical, then she/he should use the yeoOrder variable in these files, as follows (in MATLAB, say A is your functional connectome):

figure, imagesc(A(yeoOrder,yeoOrder)); axis square; colorbar

Structural data

General folder structure

SubjID/MRtrix/Parcellation/SC_File

Examples: /100307/MRtrix/Schaefer100/SC_Schaefer100_mnf_20M.sift2.csv
/106016/MRtrix/Schaefer200/SC_Schaefer100_nof_20M.sift2.csv

Files description

For every subject, we are providing structural connectomes for 5 different brain atlases: Schaefer at 4 different resolutions (100, 200, 400, 800 nodes) and Glasser (360 nodes). To each parcellation we appended 19 subcortical regions at the end. Therefore, the final total number of nodes is Nparcellation + Nsubcortical (e.g., Schaefer100 time series will have 119 brain nodes, see also the *functional data* section). Diffusion data were processed following the main MRtrix guidelines (see the .docx "Processing_DTI" in the Misc folder for details).

Note that two main changes were made with respect to the Processing_DTI.docx guidelines: tract seeding was set to 20 Million tracts, and the “spherical-deconvolution informed filtering of tractograms” 2.0 (SIFT2, Smith et al. NeuroImage 2015) algorithm was used.

For each subject and brain atlas, we are providing 4 different types of structural connectomes or SC, in .csv format. Please note that the SC matrices are not symmetrized (i.e. they are in upper triangular form). There are “key strings” appended to the SC file names, to specify the specific connectome type:

-nof = SC computed as number of streamlines (standard method) between brain region pairs
-mnf = SC computed as number of streamlines normalized by the node volumes between brain region pairs
-mfa = SC computed as average fractional anisotropy (FA) along the fiber tracts between brain region pairs
-mll = SC computed as average fiber length (in millimeters) between brain region pairs

Have fun!

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