FCPROCESS README

4/12/13 JDP

These are the new scripts for processing functional connectivity data, and they’re the last ones I’ll write before leaving the Petersen/Schlaggar lab. They are completely rewritten and are a departure from the previous set of scripts (v2). The input data (datalist) and output data formats (corrfile, 4dfps) are essentially unchanged, but intermediate steps are changed. Some extra inputs are needed, mainly related to nuisance seed definition.

Previously, in v2, there was an initial processing script, a cohort selection script, and a (re)processing script. The initial processing script was actually a wrapper for the (re)processing script, and many options were available for the cohort selection script. The cohort selection script depended largely on a set of assumed file names and such. The approach now is somewhat different.

There is a single processing script, no more wrapper for initial processing. The script will process the data mainly in MATLAB. At the end of processing the usual 4dfps and some associated files will be present, but most of the data relevant to QC and reprocessing the data will be in a large MATLAB file called QC.mat. For 160 subjects, this file is about 4.5GB. This file is what the cohortselector script now takes for generating temporal masks, prmfiles, etc. The QC.mat contains a large structure, named QC, which has an element for each subject. In this structure are many variables, such as FD or FDbar or MPRAGE or CSFseed, etc. The data in this QC.mat file is actually sufficient for a great many types of analysis, such as all of the analyses on motion that you’ve seen in 2012 and 2013. If you want to do seed maps or some voxel-based analysis you will of course need the 4dfps, which are generated.

The processing script is flexible, allowing you to turn various steps on and off, and the most relevant parameters prompt you for their setting, with default suggestions. The cohort selection script does not have all of the bells and whistles of the previous versions, largely because we’ve settled on a way to process the data. The cohortselector script will output temporal masks, modified prmfiles, and new datalists, so that reprocessing is relatively easy. Reprocessing uses the same script that you use to first process the data.

**To best suppress motion artifact, our default recommendations are:**

- global signal regression

- nuisance seeds defined by Freesurfer

- the 24-parameter expansion of realignment estimates (not the old 12-parameter lab standard)

- excluding FD > 0.2 mm on the 3T Trio data

- reprocessing with interpolation

**Changes:**

1. The classic fixed nuisance seeds are no longer operational. You need to use Freesurfer seeds, defined on each subject. The script MAKE\_FS\_SEEDS.csh does this for you once you have segmented a subject’s MPRAGE and you will need to provide a list of where each subject’s seeds are located.

2. Some output files are no longer made; almost always the files now omitted were things like total\_FD.txt, which is now the variable FD in the QC structure.

SCRIPTS:

MAKE\_FS\_MASKS.csh: a cshell script that takes a Freesurfer segmentation for a subject and creates eroded nuisance seed masks of the ventricles and white matter, and also defines gray matter and whole-brain masks for the subject. Usage is:

MAKE\_FS\_MASKS.csh subjected voxeldimension segmentationdirectory

e.g.: MAKS\_FS\_MASKS.csh vc12232 333 /data/cn4/freesurfer/

FCPROCESS.m: a MATLAB script that processes functional connectivity data. See its help file for details

FCPROCESS(datalist,targetdir,tmasktype,cleanup,roilist,freesurferlist);

COHORTSELECTOR.m: a MATLAB script that makes temporal masks and prmfiles and datalists

COHORTSELECTOR(QCmat,datalist,vcidfile);