**Template\_batch\_v1\_5\_all.m**

Summary:

This initial batch script is used to call pipeline scripts to carry out various flags (processing steps).

Structure:

* Setting pipeline paths (does not need to be changed unless receiving path errors).
* Select Subject Directories
  + Set name of directory containing data (generally on the same level as scripts directory).
  + Exclude following subjects
    - Remove subjects from list of those in data directory.
  + Include ONLY following subjects
    - Clear the list and only process the specified subjects.
* Set Up Directory Structure
  + Set names for the sub-directories within each subject directory.
* Select Global Flags
  + Choose which images to process (e.g. T1, fMRI, DWI).
  + The OTHER flags.shen\_org uses the original 278 region shen parcellation. Otherwise a 292 version of shen with updated subcortical regions is used.
* T1\_prepare\_A
  + T1 preprocessing
  + Select T1\_A specific flags:
    - Dcm2nii -> DICOM to nifti format conversion.
    - Denoiser -> denoising of T1
    - Anat -> FSL\_ANAT for bias field correction; field of view crop; subcortical segmentation.
    - Bet -> rain extraction with FSL –R option
      * betF -> fractional intensity threshold (0-1)
      * betG -> vertical gradient in fractional intensity threshold (-1 – 1)
    - re\_extract -> extract brain with bet obtained mask.
* T1\_prepare\_B
  + T1 segmentation and transformation of parcellations into native space.
  + Select T1\_B specific flags:
    - Reg2MNI-> register subject T1 into MNI space and transform parcellations into native space.
    - Seg -> tissue-segmentation; isolation of parcellations to gray matter in native space.
* fMRI\_A
  + Preprocessing of resting state datasets
  + Select fMRI\_A specific flags
    - ReadHeaders -> extract acquisition information from image header.
    - SpinEchoUnwarp -> uses spin echo field maps to perform topup distortion correction.
      * Configs.numMaps -> provide the number of AP/PA pairs of filedmaps
    - SliceTimingCorr -> slice timing correction
      * Configs.UseTcustom -> use header extracted acquisition times (recommended).
    - MotionCorr -> mcflirt motion correction.
    - RegT1 -> linear registration of T1 to epi images.
      * Configs.epi.betf -> fractional intensity threshold for brain extraction (lower values yield a more inclusive mask).
    - RegOthers -> transform parcellations and tissue masks into epi space.
      * Configs.GMprobthr -> FAST –h threshold.
    - Mode1000 -> mormalize data to a mode of 1000.
    - DemeanDetreand -> remove the mean and linear trend of the time-series.
    - MotionRegressors -> regress out motion parameters and estimate scrubbing due to motion.
      * GS -> perform global signal regression = 1; or not =0.
      * Configs.FDth -> frame displacement threshold.
      * Configs.DVARSth -> standardized dvars threshold.
      * Configs.SDth -> standard deviation threshold.
    - Bandpass -> bandpass filtering,
      * Configs.fMin -> minimum
      * Configs.fMax -> maximum
    - TissueRegressors -> regress out tissues from signal.
      * Configs.numCompsPCA -> number of scrubbed components.
    - SpatialSmooth -> spatial smoothing of data.
      * Configs.fwhm -> smoothing kernel size.
    - ROIs -> shen time-series.
* fMRI\_B
  + Generate the figures and correlation matrices of the data.
  + Select fMRI\_B specific flags:
    - FigsMotion -> generate figures of motion estimates,
    - FigsFC -> generate connectivity matrix figures.
    - SaveFigs -> save all figures.
    - SaveMats -> save matrices as .mat files.
* DWI
  + Preprocessing, registration to T1, and tractography of diffusion weighted data.
  + Select DWI specific flags:
    - cleanStart -> removes any existing nifti images in the directory.
    - Dcm2nii -> DICOM to nifti format conversion.
    - topup -> field inhomogeneity distortion correction (requires an opposite phase b0)
    - Bformat -> formatting bvec and bval text files for fsl compatibility.
    - order\_filter -> order the DWI series from lowest to highest b-value.
    - denoiser -> LPCA denoise the DWI data.
    - b0\_proc -> realign and average multiple b0 volumes (single b0 series are renamed as average).
    - bvec\_corr -> motion correction of gradient weighted volumes by rigid body realignment to b0 and updating of bvec.
    - run\_ecc -> eddy current correction with eddy\_correct. Only to be done if topup was not.
    - DWIOutliers -> remove directions that are deemed intensity outliers by fsl criteria (mean values greater than 1.5 times the inter-quartile range above the 75th or below 25th percentiles across all directions.
    - reg2T1 -> combination of dof6 and bbr (white matter boundary based) registrations of b0 to T1\_fov\_denosied, that is then applied to the rest of DWI volumes.
    - tissueMasks -> generation of masks for seeds and fibers and the gray matter/white matter interface mask.
    - Camino.run -> flag for tensor estimation and tractography carried out by Camino. Contains the following subflags:
      * Camino.reset -> removes all files from the Camino directory for the fresh start.
      * Camino.process -> fits a single tensor model to the data and calculates a fractional anisotropy image. Additionally, performs a multitensor voxel classification (isotropic, anisotropic, two-tensor [ansirtropic nongaussian spheric harmonic]) to be used for tractography. Multitensor voxels are filtered to retain only those in clusters >8 voxels (this parameter can be changed).
      * Camino.ProbabilisticSeedBased -> IN PROGRESS
      * Camino.Deterministic -> Performs deterministic 2-tensor whole-brain tractography, seeding the GM/WM interface.
      * Camino.createFiberFiles -> generate .trk tractography files for visualization.
      * Camino.genMatrices -> generate n x n matrices of tract based metrics (e.g. mean and minimum fa, number of fibers, fiber density, mean surface area)
  + DWI parameters:
    - HeapSizeCamino -> memory allocation for Camino
    - bMax -> maximum b-value in the DWI data (set it to slightly above that)
    - file\_bvec and \_bval -> default names for the unprocessed bvec and bval files.
    - rician -> denoising parameter; should be set to zero.
    - schemeOrientation -> orientation transformation for the b-vectors ([1,1,-1] for Siemens data, but is likely dataset dependent)
    - FAthreshold -> minimum FA value for fiber-tracking
    - order2Threshold; order4Threshold; order6Threshold -> F-test cutoffs for voxel classification as isotropic, anisotropic (order2), or multitensor (order4).
    - CURVthreshold -> curve degree threshold over distance of 5mm. Fibers with angles sharper that this threshold will not count.
    - clusterMinSizeMultiTensor -> cluster voxel threshold for a voxel to be considered multitensor.
    - clusterMinSizeTissue -> white matter voxel cluster threshold to be considered white matter.
    - stepSize -> resolution with respect to voxel-size for fiber-tracking.
    - LengthMin and LengthMax -> minimum and maximum fiber length thresholds.