DTI processing for structural cortical networks analysis

\# First use MRIConvert on dicoms to create *.nii, bvals* and *bvecs*.

\# pre-process with eddy-correct which produces data.nii.gz
eddy_correct <dti_scan.nii.gz> data 0

\# use brain extraction tool (bet) to extract brain from image and add < -m > to automatically
\# create binary brain mask
bet data.nii.gz nodif_brain -m

\# run dtifit with Fdt
Fdt
        - in GUI select dtifit

\# this should output the following files
\# dti_V1 - *1st eigenvector*
\# dti_V2 - *2nd eigenvector*
\# dti_V3 - *3rd eigenvector*
\# dti_L1 - *1st eigenvalue*
\# dti_L2 - *2nd eigenvalue*
\# dti_L3 - *3rd eigenvalue*
\# dti_MD - *mean diffusivity*
\# dti_FA - *fractional anisotropy*
\# dti_MO - *mode of the anisotropy (oblate ~ -1; isotropic ~ 0; prolate ~ 1)*
\# dti_S0 - *raw T2 signal with no diffusion weighting*

\# check results, e.g. and change DTI display to RGB and modulate with FA map
fslview dti_V1 dti_FA

\# create forbedpost directory and copy data, nodif_brain_mask, nodif_brain, bvals, bvecs
mkdir forbedpost
cp –av bvals bvecs nodif_brain* data.nii.gz forbedpost/

\# run bedpostX and use forbedpost dir as input directory in GUI. This will create
\# forbedpost.bedpostX directory. This will take approx 20 hours (up to a day).
Fdt
        - Select BEDPOSTX
        - input dir <forbedpost>

\# this should create the following outputs in forbedpost.bedpostX
\# <i> indicates the i-th fibre. It ranges from 1 to the maximum number of fibres set in the
\# advanced options.):
\# merged_th<i>samples - *4D volume - Samples from the distribution on theta*
\# merged_ph<i>samples - *Samples from the distribution on phi*
\# theta and phi together represent the principal diffusion direction in spherical polar
\# coordinates
\# merged_f<i>samples - *4D volume - Samples from the distribution on anisotropic volume*
\# fraction (see technical report).
\# mean_th<i>samples - *3D Volume - Mean of distribution on theta*

mean_ph<i>samples - *3D Volume - Mean of distribution on phi*
mean_f<i>samples - *3D Volume - Mean of distribution on f anisotropy*
Note that in each voxel, fibres are ordered according to a decreasing mean f-value
mean_dsamples - *3D Volume - Mean of distribution on diffusivity d*
mean_S0samples - *3D Volume - Mean of distribution on S0 intensity*
dyads<i> - *Mean of PDD distribution in vector form. Note that this file can be loaded into*
fslview for easy viewing of diffusion directions
dyads<i>_dispersion - *3D Volume - Uncertainty on the estimated fibre orientation.*
Characterizes how wide the orientation distribution is around the respective dyad.
nodif_brain - *brain extracted version of nodif - copied from input directory*
nodif_brain_mask - *binary mask created from nodif_brain - copied from input directory*

change dir into forbedpost.bedpostX/
        # copy perl scripts to home/abcd1234/bin/ and add dir_path (only first time)
        # aal_images.pl generate_matrix.pl calc_total_matrix.pl calculate_vector.pl
        # calculate_matrix.pl

use flirt for getting nodif_brain into standard space.
this will also create a nodif2std.mat file
Flirt
in GUI use following
        - ref is standard set to T1_2mm_mni brain.
        - in nodif_brain.nii.gz
        - out nodif2std

invert the nodif2std.mat file
InvertXFM
in GUI use following
        - in nodif2std.mat
        - out std2nodif.mat

Apply inverse mat-file on aal.nii.gz to create aal image in dti space
ApplyXFM
in GUI use following
        - mat std2nodif.mat
        - in /home/psyc0613/aal.nii.gz
        - ref nodif_brain.nii.gz
        - out aal2nodif.nii.gz

Use nearest neighbour !

Perform visual check on *data.nii.gz* and *aal2nodif.nii.gz*

run first perl script to create 90 masks (only cortical areas from aal space).
this will also create a directory aal_im where all 90 masks will be stored in the following
format: aal2nodif_xx.nii.gz, furthermore a file called target_list.txt will be created, which is
where the 90 masks are listed (check aal_im dir for all 90 masks).
run the script from the forbedpost.bedpostX folder.
aal_images.pl aal2nodif.nii.gz

generate connections with perl script. This will create 90 directories, 1 for each mask/region
with all other regions in the form of XX_all
this step will take several days
the following files from bedpostX will be used:
 # merged_th\<i\>samples
 # merged_ph\<i\>samples
 # merged_f\<i\>samples
 # nodif_brain_mask
generate_matrix.pl

check if *_all dirs all have 90 seeds_to_aal2nodif_XX.nii.gz, fdt_paths.nii.gz,
probtrackx.log and waytotal,

now run the ROI vector perl script. This will create a ROI_XX_probmatrix.txt in every
XX_all dir. Output: Calculates the sizes of seed ROIs (number of voxels for each XX_all
dir.)
calculate_vector.pl

Now generate a connectivity matrix, this will create a 90x90 matrix
calc_new_total_matrix.pl

Now generate a probability matrix, this will create a different 90x90 matrix
calc_total_prob_matrix.pl