# Pipeline MRtrix3 – DWI

| single tract delineation | data acquisition | registration of diffusion data |
|---|---|---|

| | pre-processing<br>*denoising, Gibbs ringing removal, correction for motion and distortions, …* | group template |
| pre-processing<br>to get anatomical priors | | |

| whole-brain tractography | voxel-level modelling | statistics / GLM |
|---|---|---|

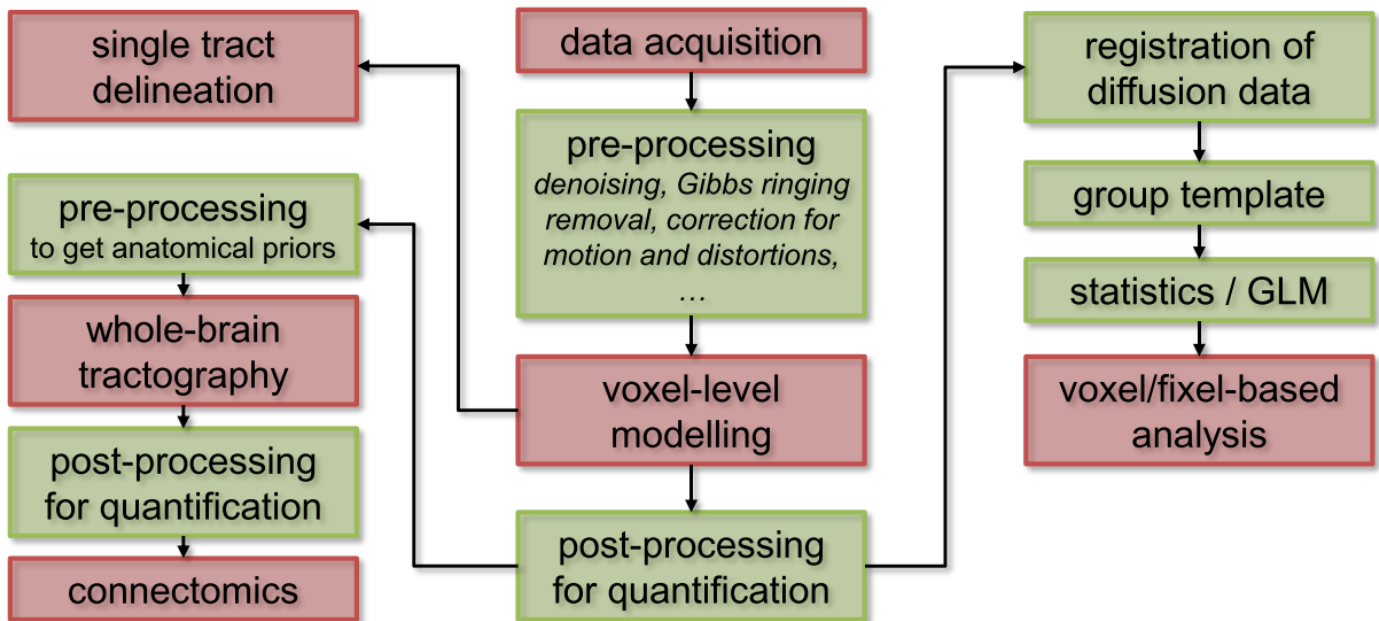| post-processing for quantification | | voxel/fixel-based analysis |

| connectomics | post-processing for quantification | |

Review on simple commands

```
$ ls              #list files in current working directory
$ ls data/        #list files in specific location
$ ls -l           #list files and information's of modifications
$ ls –help        #show how to use some command
$ man ls          #open the help page in a paginator
$cd               #change the directory
$pwd              #print the current working directory
$cp               #copy files
$mv               #move or rename file
$rm               #remove files
$ ls bin/         #show all the available commands
$ … -info         #display information messages, for more details use -info flag
$ … -quiet        #do not show information messages or progress status
$... -debug       #display debugging messages, for more information use -debug flag
$ … -force        #force overwrite of output files
$ … -nthreads number   #use this number of threads in multi-threaded applications
$ … -version      #display the version information
```

Tip 1: press TAB key to complete what you have typed.
Tip 2: press UP/Down to recall commands used previously.
Tip 3: you can load numbered images as a single larger image: $ mrconvert dwi.mif dwi-[].mif

Obs: MRView handles all display operations in scanner coordinates

**Tractography**

```
$ mrconvert data.nii.gz dwi.mif -fslgrad bvecs bvals -datatype float32 -strides 0,0,0,1    #HCP
$ mrconvert dwi.nii -fslgrad dwi.bvec dwi.bval dwi.mif   #if data is NIFT
$ mrinfo -dwgrad dwi.mif | -norealign dwi.mif | -petable dwi.mif          #check the conversion
$ dwigradcheck        #check orientation in all 3 views, if not right use dwigradcheck
```

```
$ dwi2mask dwi.mif -| maskfilter - dilate preproc_mask.mif -npass 5      #speed improvement of dwidenoised with
dilated brain mask
$ dwidenoise dwi.mif dwi_denoised.mif -noise dwi_noise.mif –mask preproc_mask.mif  #noise correction
$ mrcalc dwi.mif dwi_denoised.mif -subtract dwi_residual.mif    #calculate the noise
$ mrview dwi_residual.mif      #show the noise that has it before the correction

$ mrdegibbs dwi_denoised.mif dwi_degibbs.mif          #gibbs ringing correction
$ mrview dwi_degibbs.mif       #check correction

$ dwifslpreproc -rpe_none -pe_dir AP dwi_degibbs.mif dwi_preproc.mif
#fsl preprocessing (eddy current, subject motion and magnetic field susceptibility induced distortion corrections)
#use the mrinfo to see the PhaseEncodingDirection, I (left-right), j (posterior-anterior), k(inferior-superior), negative
means opposite direction then write j-, for example
#there is the option of TotalRedoutTime
#rpe_none = no reversed phase-encoding data
#correction -eddy_options "—slm=linear" if there is only one asymmetry of sampling number
$ mrview dwi_preproc.mif       #check the preprocessing

$ dwibiascorrect ants -mask dwi_mask.mif dwi_preproc.mif dwi_bias.mif -bias biasfield.mif
$ mrview biasfield.mif   #bias field correction

$ dwinormalise dwi_bias.mif dwi_mask.mif dwi_norm.mif fa_template.mif wm_mask.mif -force #global intensity
normalization across subjects

$ dwiextract dwi.mif -bzero - | mrmath -axis 3 - mean b0.nii       #b0 extraction
$ bet T1.nii T1_bet.nii  -R        #brain extraction of t1 image
$ flirt -dof 6 -cost normmi -in T1.nii -ref b0 -omat T1_fsl.txt       #align diffusion and structural images
$ transformconvert T1_fsl.txt T1w.nii b0.nii flirt_import T1toDWI.txt #transform the flirt matrix to mrtrix format
$ mrtransform -linear T1toDWI.txt T1w.nii T1corregist.nii       #corregistration of T1 image

# mrconvert dwi_b0.mif dwi_b0.nii
# bet T1.nii T1bet.nii -R
# flirt -in dwi_b0.nii -ref T1.nii -dof 6 -omat T12b0.mat
# flirt -in dwi_b0.nii -ref T1.nii -dof 6 -cost bbr -omat b02T1.mat
# transformconvert b02T1.mat dwi_b0.nii T1.nii flirt_import b02T1mrtrix.txt -force
# mrtransform T1.nii -linear b02T1mrtrix.txt T1corregist.nii -inverse -force

$ 5ttgen fsl -nocrop -sgm_amyg_hipp T1corregist.nii 5ttseg.mif -force      #tissue segmentation
$ mrview 5ttseg.mif -mode 4           #check the segmentation
$ 5tt2gmwmi 5tt.mif 5ttgmwm.mif       #white matter and gray matter segmentation
$ 5tt2vis 5ttseg.mif 5ttvis.mif          #visualization
$ mrview 5ttvis.mif
```

FACT algorithm

```
$ dwi2tensor -mask dwi_mask.mif dwi_norm.mif dwi_tensor.mif
#tensor calculation
$ tensor2metric -adc dwi_md.mif -fa dwi_fa.mif -ad dwi_ad.mif -rd dwi_rd.mif -value dwi_values.mif -vector
dwi_vectors.mif -mask dwi_mask.mif dwi_tensor.mif
#extraction of parameters
$ tensor2metric -vec dwi_vec.mif dwi_tensor.mif          #vector file
$ tckgen -algorithm FACT dwi_vec.mif FACT.tck -select 1M -seed_image dwi_mask.mif -act 5ttseg.mif -backtrack -
crop_at_gmwmi -angle 35 -cutoff 0.06   #tractography generation
```

## CSD algorithm

```
$ dwi2response tournier dwi_norm.mif wm_response.txt
$ shview wm_response.txt        #verify the result
$ dwi2fod csd -mask mask.mif dwi_norm.mif wm_response.txt fod.mif   # CSD
$ mrview fod.mif -odf.load_sh fod.mif           #verify the result
$ tckgen -algorithm iFOD2 fod.mif CSD.tck -select 1M -seed_dynamic fod.mif -act 5ttseg.mif -backtrack -
crop_at_gmwmi -cutoff 0.06      #tractography generation
```

1) SIFT
```
$ tcksift CSD.tck fod.mif CSD_SIFT.tck -act 5TT.mif -term_number 10M
```

2) SIFT2
```
$ tcksift2 CSD.tck fod.mif tck_weights.txt -act 5ttseg.mif -out_mu CSD_SIFT2.txt -out_coeffs csd_tck_coeffs.txt
$ head -c 200 csd_tck_weights.txt
$ cat CSD_SIFT2.txt
$ mrview 5ttvis.mif -plane 2 -tractography.load CSD.tck -tractography.tsf_load csd_tck_coeffs.txt -
tractography.tsf_range -1,1
$ tckmap CSD.tck CSD_SIFT2.mif \ -template mask.mif -precise -tck_weights_in tck_weights.txt   #can use
CSD_SIFT2.tck
$ mrview fod.mif \ CSD_SIFT2.mif CSD_SIFT2.mif
```

## MT-CSD algorithm

```
$ dwi2response dhollander dwi_norm.mif wm_response.txt gm_response.txt csf_response.txt
$ shview wm_response.txt        #verify the result
$ dwi2fod msmt_csd -mask mask.mif dwi_norm.mif wm_response.txt wm_fod.mif gm_response.txt gm_fod.mif
csf_response.txt csf_fod.mif      #multi-tissue CSD
$ mrconvert -coord 3 0 wm_fod.mif - | mrcat csf_fod.mif gm_fod.mif - vf_rgb.mif
$ mrview vf_rgb.mif -odf.load_sh wm_fod.mif    # signal contribution map
$ tckgen -algorithm iFOD2 wm_fod.mif MTCSD.tck -select 1M -seed_dynamic wm_fod.mif -act 5ttseg.mif -backtrack
-crop_at_gmwmi -cutoff 0.06     #tractography generation
```

1) SIFT – filter streamlines densities to match the FOD lobe integrals
```
$ tcksift MTCSD.tck wm_fod.mif SIFT.tck -act 5TT.mif -term_number 10M
```

2) SIFT2 – filter to match the tractography to fixel-wise fibre densities
```
$ tcksift2 MTCSD.tck wm_fod.mif tck_weights.txt -act 5ttseg.mif -out_mu MT_SIFT2.txt -out_coeffs
mt_tck_coeffs.txt
$ head -c 200 tck_weights.txt
$ cat MT_SIFT2.txt
$ mrview 5ttvis.mif -plane 2 -tractography.load MTCSD.tck -tractography.tsf_load mt_tck_coeffs.txt -
tractography.tsf_range -1,1
$ tckmap MTCSD.tck MT_SIFT2.mif \ -template mask.mif -precise -tck_weights_in tck_weights.txt   #can use
MT_SIFT2.tck
$ mrview wm_fod.mif \ MT_SIFT2.mif MT_SIFT2.mif
```

*1)peak extraction and visualization – CSD and MT-CSD*

```
$ sh2peaks ms_wm.mif ms_wm_peaks.mif        # peak amplitude extraction
$ fod2fixel ms_wm.mif ms_wm_fixel -afd afd.mif        #output at fixel format
$ mrview ms_wm.mif -fixel.load ms_wm_peaks.mif -fixel.load ms_wm_fixel/afd.mif
```

*2)to make a better visualization of the tractography*

```
$ tckresample wholebraintractography_FACT.tck -endpoints wholebraintract_FACT _ACT_ ends.tck        #only for
```
*visualization*

*3) to make in more than one subject – example 1*

```
study/001_patient/dwi.mif
study/002_patient/dwi.mif
study/003_patient/dwi.mif
study/004_control/dwi.mif
study/005_control/dwi.mif
study/006_control/dwi.mif
$ for_each study/* : dwidenoise IN/dwi.mif IN/dwi_denoised.mif
```

*4) to make in more than one subject – example 2*

```
study/dwi/001_patient.mif
study/dwi/002_patient.mif
study/dwi/003_patient.mif
study/dwi/004_control.mif
study/dwi/005_control.mif
study/dwi/006_control.mif
$ mkdir study/dwi_denoised
$ for_each study/dwi/* : dwidenoise IN study/dwi_denoised/NAME
```

*5) to make in more than one subject – example 3*

```
study/dwi/001_patient.mif
study/dwi/002_patient.mif
study/dwi/003_patient.mif
study/dwi/004_control.mif
study/dwi/005_control.mif
study/dwi/006_control.mif
$ mkdir study/dwi_denoised
$ cd study/dwi
$ for_each * : dwidenoise IN ../dwi_denoised/IN
```

*6) use -nthreads to run in parallel*

```
$ for_each study/* -nthreads 2 : two jobs running in parallel
```

# HCP data pipeline

1. Basic preprocessing: Intensity normalization across runs, preparation for later modules.
2. 'TOPUP' algorithm for EPI distortion correction.
3. 'EDDY' algorithm for eddy current and motion correction.
4. Gradient nonlinearity correction, calculation of gradient bvalue/bvector deviation.
5. Registration of mean b0 to native volume T1w with FLIRT BBR+bbregister and transformation of diffusion data, gradient deviation, and gradient directions to 1.25mm structural space. Brain mask based on FreeSurfer segmentation.

$ mrconvert data.nii.gz dwi.mif -fslgrad bvecs bvals -datatype float32 -strides 0,0,0,1
$ dwibiascorrect ants -mask nodif_brain_mask.nii.gz dwi.mif dwi_bias.mif.gz
$ 5ttgen fsl -nocrop -sgm_amyg_hipp T1w_acpc_dc_restore_1.25.nii.gz 5ttseg.mif.gz -mask nodif_brain_mask.nii.gz

## FACT algorithm

$ dwi2tensor -mask nodif_brain_mask.nii.gz dwi_bias.mif.gz dwi_tensor.mif.gz
$ tensor2metric -vec dwi_vec.mif dwi_tensor.mif.gz
$ tckgen -algorithm FACT dwi_vec.mif FACT.tck -select 1M -seed_image nodif_brain_mask.nii.gz -act 5ttseg.mif.gz -crop_at_gmwmi -angle 35 -mask nodif_brain_mask.nii.gz -maxlength 250

## MT-CSD algorithm

$ dwi2response msmt_5tt dwi_bias.mif.gz 5ttseg.mif.gz wm_response.txt gm_response.txt csf_response.txt -voxels RF_voxels.mif -mask nodif_brain_mask.nii.gz
$ dwi2fod msmt_csd -mask nodif_brain_mask.nii.gz dwi_bias.mif.gz wm_response.txt wm_fod.mif gm_response.txt gm_fod.mif.gz csf_response.txt csf_fod.mif.gz
$ tckgen -algorithm iFOD2 wm_fod.mif MTCSD_1M.tck -select 1M -seed_dynamic wm_fod.mif -act 5ttseg.mif.gz -backtrack -crop_at_gmwmi -cutoff 0.06 -maxlength 250 -mask nodif_brain_mask.nii.gz

```
tckgen -algorithm SD_STREAM fod.mif CSD_100k.tck -select 100K -seed_dynamic fod.mif -act
5ttseg.mif.gz -crop_at_gmwmi
```

1) SIFT – filter streamlines densities to match the FOD lobe integrals
$ tcksift MTCSD_1M.tck wm_fod.mif SIFT.tck -act 5TTseg.mif.gz -term_number 500000

Extract peaks -------------------------------------------------------------------------------------------------------------
$sh2peaks FOD2MNI.nii.gz peaks.nii.gz -num 3 -mask MNI_bet_mask.nii.gz