**DTI-Pipeline**

mrconvert EP2D\_DIFF\_MDDW\_64\_P2\_B3000\_0016 DWI.mif -strides +1,2,3,4

mrconvert DWI\_REVPE\_P\_A\_B3000\_0023 PA.mif -strides +1,2,3,4

mrdegibbs DWI.mif DWI-unringed.mif

mrdegibbs PA.mif PA-unringed.mif

dwidenoise DWI-unringed.mif DWI-unringed-denoised.mif

dwidenoise PA-unringed.mif PA-unringed-denoised.mif

dwiextract DWI-unringed-denoised.mif AP-b0s.mif -bzero

mrcat AP-b0s.mif PA-unringed-denoised.mif allb0s.mif -axis 3

dwifslpreproc -rpe\_pair -se\_epi allb0s.mif -pe\_dir AP DWI-unringed-denoised.mif DWI-unringed-denoised-undistorted-noeddycurr.mif -eddy\_options " --repol --data\_is\_shelled --slm=linear "

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| --- |
| dwiextract DWI-unringed-denoised-undistorted-noeddycurr.mif -bzero - | mrmath -axis 3 - mean DWI-unringed-denoised-undistorted-noeddycurr-b0.nii |

bet2 DWI-unringed-denoised-undistorted-noeddycurr-b0.nii DWI-unringed-denoised-undistorted-noeddycurr-brain -m -f 0.15

Mask file will be called x\_mask.nii.gz where x is DWI-unringed-denoised-undistorted-noeddycurr-brain

 mask file: DWI-unringed-denoised-undistorted-noeddycurr-brain\_mask.nii.gz

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| Dwibiascorrect ants -mask DWI-unringed-denoised-undistorted-noeddycurr-brain\_mask.nii.gz DWI-unringed-denoised-undistorted-noeddycurr.mif DWI-preprocessed.mif |
| dwi2tensor DWI-preprocessed.mif dwitensor.nii -mask DWI-unringed-denoised-undistorted-noeddycurr-brain\_mask.nii.gz |

tensor2metric dwitensor.nii -fa fa.nii -adc md.nii -rd rd.nii -ad ad.nii -mask DWI-unringed-denoised-undistorted-noeddycurr-brain\_mask.nii.gz

mrconvert T1\_MPRAGE\_SAG\_P2\_1\_0\_ISO\_0005 T1.nii -strides +1,2,3

SUBJECTS\_DIR=/Volumes/entities/institute/MSRG-HMRI/HMRI/FINCOG-DICOMS/F03-TC/BL/BL-DTI/FS

mkdir -p ${SUBJECTS\_DIR}

recon-all -all -i T1.nii -subjid F03-TC -sd $SUBJECTS\_DIR -no-isrunning -mprage

mrconvert $SUBJECTS\_DIR/$subj/mri/brain.mgz brainFS.nii -strides +1,2,3

bet T1.nii T1brain -B

flirt -ref T1brain.nii.gz -in brainFS.nii -dof 6 -omat FS2FSL.mat

flirt -ref DWI-unringed-denoised-undistorted-noeddycurr-brain.nii.gz -in T1brain.nii.gz -dof 12 -omat FSL2diff.mat

5ttgen freesurfer $SUBJECTS\_DIR/F03-TC/mri/aparc.a2009s+aseg.mgz 5TT.nii -sgm\_amyg\_hipp -nocrop

flirt -ref T1brain.nii.gz -in 5TT.nii -applyxfm -init FS2FSL.mat -cost normmi -out 5TTfsl.nii -interp nearestneighbour

flirt -ref DWI-unringed-denoised-undistorted-noeddycurr-brain.nii.gz -in 5TTfsl.nii -applyxfm -init FSL2diff.mat -cost normmi -out 5TTdiff.nii -interp nearestneighbour

#normal appearing WM

mrconvert 5TTdiff.nii wm.nii -coord 3 2

#pathological tissue

mrconvert 5TTdiff.nii lesions.nii -coord 3 4

# get mean DTI metrics in NAWM

fslmeants fa.nii wm.nii > fa\_nawm.txt

fslmeants md.nii wm.nii > md\_nawm.txt

fslmeants ad.nii wm.nii > ad\_nawm.txt

fslmeants rd.nii wm.nii > rd\_nawm.txt

#mean metrics in lesion

fslmeants fa.nii lesions.nii > fa\_lesions.txt

fslmeants md.nii lesions.nii > md\_lesions.txt

fslmeants ad.nii lesions.nii > ad\_lesions.txt

fslmeants rd.nii lesions.nii > rd\_lesions.txt

#FOD calc can be done after DWI preprocessing

dwi2response dhollander DWI-preprocessed.mif wm.txt gm.txt csf.txt -mask DWI-unringed-denoised-undistorted-noeddycurr-brain\_mask.nii.gz

dwi2fod msmt\_csd DWI-preprocessed.mif wm.txt wm.mif gm.txt gm.mif csf.txt csf.mif -mask DWI-unringed-denoised-undistorted-noeddycurr-brain\_mask.nii.gz

#tractography

tckgen wm.mif 25Mstreamlines.tck -act 5TTdiff.nii -backtrack -crop\_at\_gmwmi -seed\_dynamic wm.mif -minlength 10 -maxlength 250 -select 25M -mask DWI-unringed-denoised-undistorted-noeddycurr-brain\_mask.nii.gz