Names:

Main Diffusion scan : DTI\_forward\_nii\_gz

Reverse phase diffusion scan : DTI\_reverse\_phase\_nii\_gz

1. Read bvec and bval files and normalize them. Save them in the "perm" folder.
2. Calculate the norm of each row in bvec and normalize the rows.
3. Multiply each bval by the square of the corresponding row's norm. Perform 3-means clustering to obtain three rounded bvals.
4. Save the normalized bvec and bval paths as:
   * bvec\_path = bvec\_path\_orig
   * bval\_path = bval\_path\_orig
5. Create a "temp" folder. Inside it, create a folder for each subject. Inside each subject folder, create two folders: "timeseries\_input\_fldr" and "timeseries\_coreg\_fldr".
6. Disassemble the time series (DTI\_forward\_nii\_gz) and place the volumes in the "timeseries\_input\_fldr".
7. Identify the b0 volumes (rows with 0 bvals) and store the reference index.
8. Register all volumes of "Main Diffusion scan" to the b0 volume and save the result as DTI\_coreg\_nii\_gz.
9. Read the anatomical image T1\_orig = T1 = T1\_mif.
10. Apply denoising (MP-PCA) to DTI\_coreg\_nii\_gz and save the output as output\_denoise.
11. Generate dt, fa, dk, mk, md, ad, and rd maps.
12. Read the 4D reverse image (PA\_mif) and save the bvec and bval files.
13. Correct distortion by finding the mean b0 of PA\_mif and extracting the b0 from the forward image before taking the average (mean\_b0\_AP\_mif). Unwarp the forward image (b0\_pair\_mif).
14. Use fsldwi to generate den\_preproc\_mif for bias correction.
15. Generate a mask (mask\_mif) using mrtrix.
16. Check if bvec requires transformation using dwigradcheck: bvec\_temp = np.loadtxt(new\_bvec\_path).
17. Estimate basis functions (wm\_txt, gm\_txt, csf\_txt) and voxels\_mif using dhollander. Convert them to the mif version. Create fod using the mask and normalize them: wmfod\_norm\_mif, gmfod\_norm\_mif, csffod\_norm\_mif.
18. Segment the anatomical image (T1\_mif) into 5 different classes using FSL's FAST, and save the result as fivett\_nocoreg\_mif.
19. Extract the b0 volume from den\_unbiased\_mif.
20. Convert the last two files to a format readable by FSL to extract grey and white matter.
21. Coregister the anatomical image to the mean b0 of den\_unbiased\_mif and create a transformation matrix diff2struct\_fsl\_mat.
22. Apply the coregistration transformation to fivett\_nocoreg\_mif and save the result as fivett\_coreg\_mif.
23. Extract the boundary of grey and white matter for seeding purposes and save it as gmwmSeed\_coreg\_mif.
24. Generate 10 million streamlines using fivett\_coreg\_mif and gmwmSeed\_coreg\_mif, with parameters "-maxlength 250 -cutoff 0.06 -select 10000000".
25. Extract a subset of smaller tracks with parameters "-number 2000000 -minlength 0.1".