**How to Use the DWI Processing Pipeline (Stefan Porier’s)**

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Hello,

This document is going to provide a brief overview of how the processing pipeline script works and how to use it.

**Annotation (if you are only concerned with how to make it work, you can skip this section)**

1. The first segment of 15 lines or so is purely formatting, instructions and claiming authorship
2. Majority of the script is contained within: for subj in (some variable name)
   1. This loop will iterate through patient datasets
   2. Subj is the variable that will be used as a pointer to the current dataset as the for loop progresses through them.
   3. “some variable name” is a folder name to be inserted by the user. You can either make it the name of a particular data set (“patient\_one”) or you can make it the name of a superfolder containing patients two, three etc. I set the variable to a particular dataset because I only have ~10 patients and I wanted to keep it simpler, but if you have many, I can understand the appeal.
   4. The script is designed to start from scratch each time. If it has already been run, it will take the folder it made last time (assuming you haven’t changed the name), delete it and generate a new, empty directory to restart.
   5. It copies the three folders DWI, NODIF\_AP and NODIF\_PA into its new folder. E.g. patient\_one\_preproc
   6. Each of the three folders contains DICOMS, the script uses dcm2nii or the newer (and always preferable) dcm2niix depending on which version of the script you have. This function will convert your many dicoms into 3 niifty files and will store them in your patient directory (i.e. patient\_one\_preproc). **Note that the newer version doesn’t automatically compress anymore. You need to specify that it should compress with -z y**
   7. Using fslmerge, it merges the two phase encoding (AP and PA) images into one file called b0s.nii.gz
   8. Uses a series of fsl operations to preprocess the data (removes motion distortion, field inhomogeneity etc. using functions such as topup and eddy)
   9. using bet2 or dwi2mask, it takes the corrected DWI image and produces a brain mask
   10. using dwi2tensor it fits the diffusion tensor onto the DWI image
   11. using tensor2metric it generates an FA map called dt\_new.nii.gz
   12. dwi2response estimates a single fiber response function.
   13. Using mrresize or the newer mrgrid, the voxel sampling is upsampled using interpolation to make the mask, image etc. have a higher sampling rate (related to resolution)
   14. \*Dwi2fod calculates something called fiber orientation distribution functions (fODFs)
   15. \*Sh2peaks estimates the peak directions
   16. Mrresize or mrgrid Resizes back to the original sampling rate

**How to use the script**

1. Save the script in the folder where your data is contained. I have called this folder “pipeline”. Inside the script, this is referred to as the STUDY\_FOLDER.
2. Put the data for each patient into its own directory, inside the STUDY\_FOLDER. E.g. patient\_one, patient\_two
3. Inside each patient directory, you only need three folders but they must have these names:
   1. DWI – this one will contain your diffusion weighted images
   2. NODIF\_AP and NODIF\_PA – these will contain the respective phase encoded images
4. Go into the script and locate the loop “for subj in (some variable name)”
   1. Change the “some variable name” either to a patient’s folders (recommended unless you have many patients and wish to run the program for days or weeks) or to the STUDY\_FOLDER directory.
5. Open your command terminal (for windows users, the WSL Ubuntu terminal)
   1. Cd to the STUDY\_FOLDER
   2. Type the name of the name of the script (at this time it is “DTI\_preprocess\_MRtrix3”)
   3. If it does not work, try instead

>>bash DTI\_preprocess\_MRtrix3

* 1. If it still does not work and you are a Windows user, try

>> dos2unix DTI\_preprocess\_MRtrix3

The script can take over 24 hours to run, so be patient! It will create a series of files and will save them in the STUDY\_FOLDER. It will have automatically deleted the save\_temp directory, don’t worry about that, it was just intermediate files.

**REMEMBER THAT THE SCRIPT OVERWRITES EVERYTIME YOU RUN IT. IF YOU WANT TO KEEP THE RESULTS OF IT RUNNING, I RECOMMEND YOU RENAME THE FILE AND MOVE IT TO A DIFFERENT DIRECTORY, OUTSIDE OF THE STUDY\_FOLDER.**