BuSA project summary

Paths Outputs:

Munin:

/Volumes/Data/Badea/Lab/AD\_Decode/TRK\_bundle\_splitter/

Code:

<https://github.com/JacquesStout/DTC_private/tree/main/AD_Decode>

We have N subjects, that are defined as APOE3, APOE4 (other genotypes), with {percentage} of them with standard cognition, {percentage} with MCI, {percentage} with AD. Their age range is {min-age}-{max-age}.

We generate 2 million streamlines using mrtrix

(codepath: https://github.com/JacquesStout/DTC\_private/blob/main/AD\_Decode/AD\_Decode\_trc\_generation.py)

(command line:

os.system('tckgen -backtrack -seed\_image '+ gmwmSeed\_coreg\_mif + ' -maxlength 410 -cutoff 0.05 -select 10000000 ' + wmfod\_norm\_mif + ' ' + tracks\_10M\_tck + ' -force')

smallerTracks = path\_perm+subj+'\_smallerTracks2mill.tck'

os.system('echo tckedit '+ tracks\_10M\_tck + ' -number 2000000 -minlength 0.1 ' + smallerTracks + ' -force') )

The AD\_Decode files generated with mrtrix are converted to trk files using tcktotrk function (<https://github.com/JacquesStout/DTC_private/blob/main/DTC/tract_manager/tract_handler.py>), then transferred to MDT space based on the SAMBA registration files already established by SAMBA (<https://github.com/JacquesStout/DTC_private/blob/main/AD_Decode/AD_Decode_subj_to_MDT_clustered.py> ), specifically the rigid, affine, and warp deformations as applied to streamlines.

This is done on all subjects.

At this point, I recommend either looking up the configuration files already created for the BuSA project (found at ‘/Volumes/Data/Badea/Lab/jacques/BuSA\_headfiles/’) or to use the python file used to generate these configuration files. <https://github.com/JacquesStout/DTC_private/blob/main/AD_Decode/00_config_filemaker.py>

The configuration files are used to keep consistent parameters throughout a specified run.

Such configuration files are set up like this:

[parameters]

project = AD\_Decode (For now, always AD\_Decode)

streamline\_type = mrtrix (For now, always mrtrix, possible values would be dipy, dsi-studio, etc)

test = True (special parameter that creates additional figures during analysis, such as centroid figures)

streamline\_lr\_inclusion = only\_mask (this parameter has three parameters, all, only\_mask, and clip. The one that was used until December was ‘only\_mask’, which means that when splitting streamlines by left or right, we only ever included those streamlines that were entirely in mask left or right, ‘all’ would mean that we would include any streamlines that have even a single point in the left side or right side, and ‘clip’ includes the only the part of the streamline that is in the left side or the right side, and not anything else)

ratio = 1000 (The ratio of streamlines compared to original size, for example if ratio=1000, trk goes from 2 million to 2 000 )

stepsize = 2 (stepsize of streamlines, deprecated)

bundle\_points = 50 (The number of points is used as the input for the ResampleFeature when defining bundles: feature2 = ResampleFeature(nb\_points=num\_points) )

(It is also used to resample the points if setpoints is on,

distance = 50 (defines the threshold distance for inclusion in a bundle)

num\_bundles = 6 (defines the total number of bundles generated)

verbose = True (whether the output is more verbose or silent, not fully implemented)

setpoints = True (whether we should resample the streamlines or not)

points\_resample = 50 (to how many points the streamlines should be resampled)

saveflip = False

figures\_outpath = /home/jas297/linux/jacques/Figures\_ADDecode

template\_subjects = [list of ten subjects used for template]

added\_subjects = [list of included subjects not found in template] ([S02373, S02386, etc])

removed\_list = [list of subjects to ignore from the added\_subjects list, used to keep track of which subjects from initial analysis should not be included]

references = [fa,ln] (list of references to get point per point information on, ln stands for length and is a streamline based metric rather than a point metric)

The BuSA process first step is found in

<https://github.com/JacquesStout/DTC_private/blob/main/AD_Decode/01_split_streams_left_right.py>

It iterates through each template subjects and isolates the streams on whether they are on the left side or the right side, based on the masks identified as:

/Volumes/Data/Badea/Lab/mouse/VBM\_21ADDecode03\_IITmean\_RPI\_fullrun-results/atlas\_to\_MDT/IITmean\_RPI\_MDT\_mask\_right.nii.gz  
which are isolated through the function  
filter\_streamlines(roi\_mask\_right, streamlines, world\_coords = True, include=streamline\_lr\_inclusion)   
and saves them to ‘trk\_roi\_{ratio}”.