GUIDE TO

DIFFUSION CONNECTOME PIPELINE (DCP)

MARCH 2023

STATE KEY LABORATORY OF COGNITIVE NEUROSCIENCE AND LEARNING
IDG/MCGOVERN INSTITUTE FOR BRAIN RESEARCH
BEIJING NORMAL UNIVERSITY, BEIJING, CHINA

Table of Contents

1 Installation

- Environment: Matlab R2010b or higher
- Add DCP path to Matlab search path:
  - Click 'Set Path'
  - Click 'Add with Subfolders...' button in the popup dialog
  - Select the 'DCP' folder on the machine
  - Click 'OK' button then Click 'Save' Button
- Add SPM12[1] path to Matlab search path
- Type 'DCP' in the command window of matlab

2 Procedure

2.1 Input Files

The input files must be organized into specified structure (Figure 1). Under the selected folder, each subject has one folder which includes two separate sub-folders for DTI and T1 files separately. In the right of the button 'Select', users can choose to process 'All subjects'(default) or process specified subject by typing the sequence number of the subject(1 or 2 or 3...). If input dMRI data is in NIfTI format, the required files and their

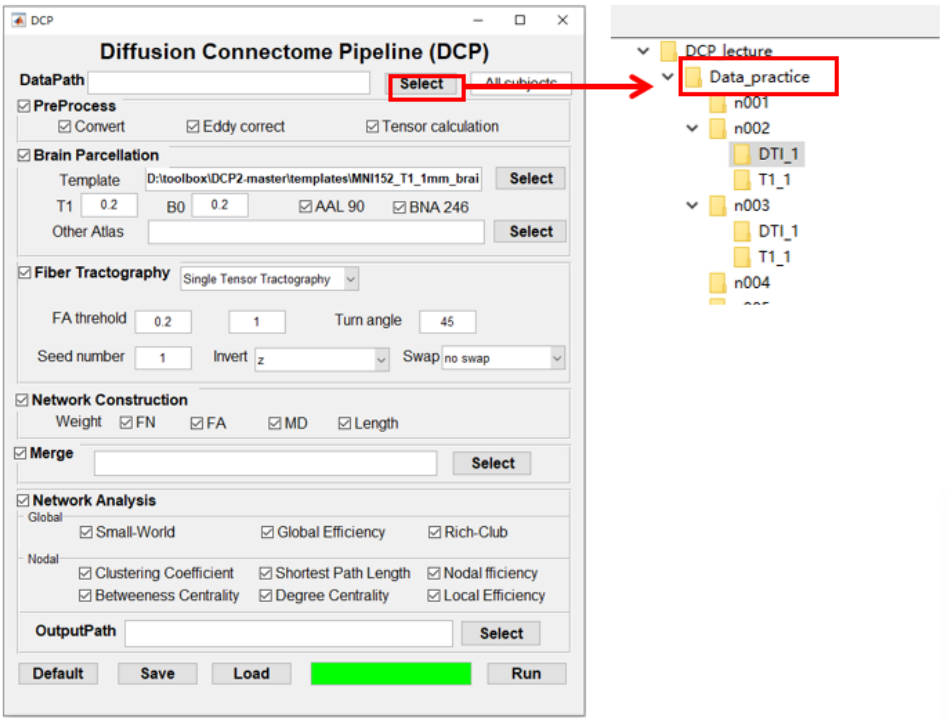

Figure 1: Organization of input files

[1] https://www.fil.ion.ucl.ac.uk/spm/

names should be:

- *.bval, *.bvec, *.nii in DTI folder
- co*.nii in T1 folder

If the files are generated from FSL's bedpost, the '*.bedpostX' folder is needed. It is noted that the name of each subject's folder can't start with digit.

2.2 Preprocess

Preprocessing includes three steps: (1) converting DICOM to NIfTI; (2) eddy-current and head movement correction; and (3) computing diffusion tensor metrics. If users have dMRI data in NIfTI format, the 'convert' step can be skipped.

2.3 Parcellation

The instructions of parcellation are shown in Figure 2. If custom atlas is used, users should put the '.nii' file of the atlas under the **'templates'** folder which is under DCP folder.

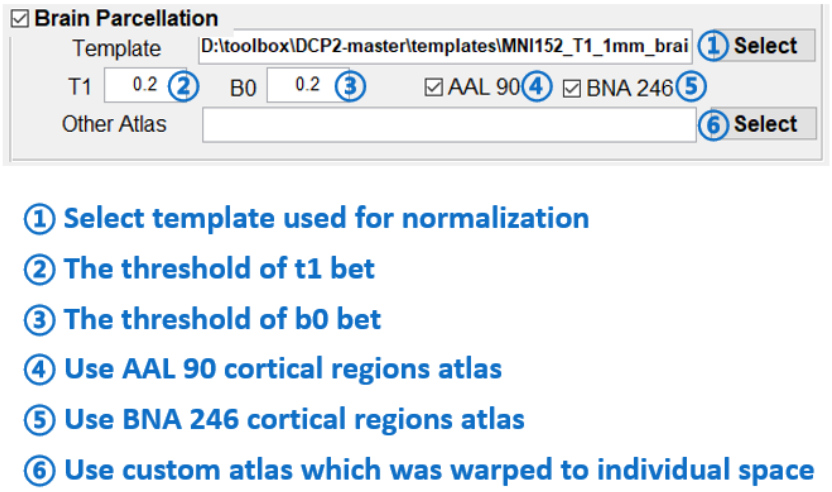

Figure 2: Instructions of parcellation

2.4 Tractography

Deterministic fiber tracking is used to reconstruct all possible fibers. Users can choose single-tensor or multi-tensor fiber tracking algorithm according to acquisition parameter of their data.

2.4.1 Single-tensor fiber tracking

The instructions of single-tensor fiber tracking are shown in Figure 3.

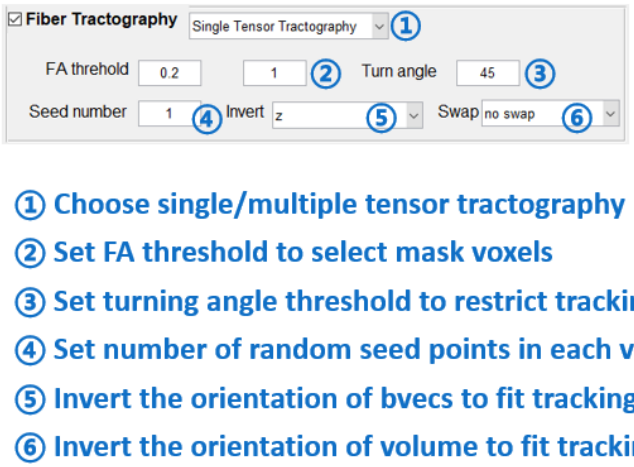

Figure 3: Instructions of single-tensor tracking

2.4.2 Multi-tensor fiber tracking

If the files are generated from FSL's bedpost, multi-tensor fiber tracking should be chosen. Multi-tensor fiber tracking is performed by using *track* and *procstreamlines* command in Camino[2]. Since Camino can only run on Linux OS, users need to call the command by Docker.

- Install **Docker Desktop**[3].
- Pull and run the image by typing the command in cmd:
  `docker pull forsaint/docker_camino`
  `docker run forsaint/docker_camino`

If it succeeds, the 'forsaint/docker_camino' will appear in the local images on Docker Desktop (Figure 4).

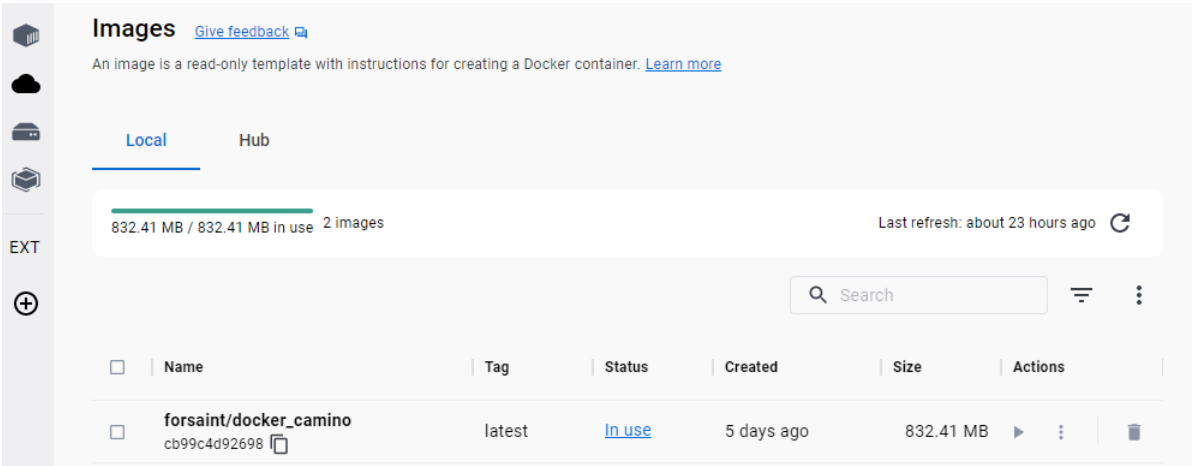

Figure 4: Docker image pulled successfully

[2]http://camino.cs.ucl.ac.uk/
[3]https://docs.docker.com/desktop/

The instructions of multi-tensor fiber tracking are shown in Figure 5.

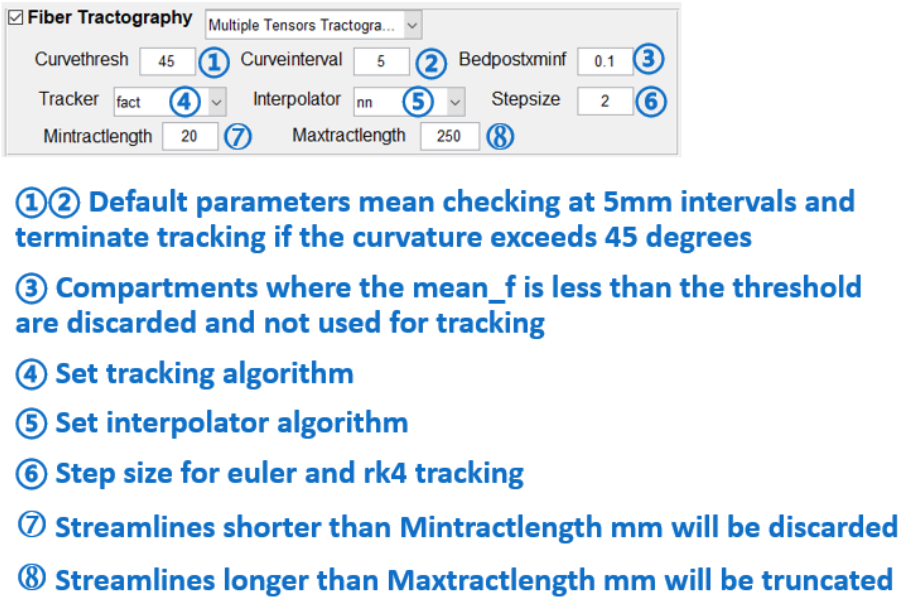

Figure 5: Instructions of multi-tensor tracking

2.5 Network Construction

The instructions of network construction are shown in Figure 6.

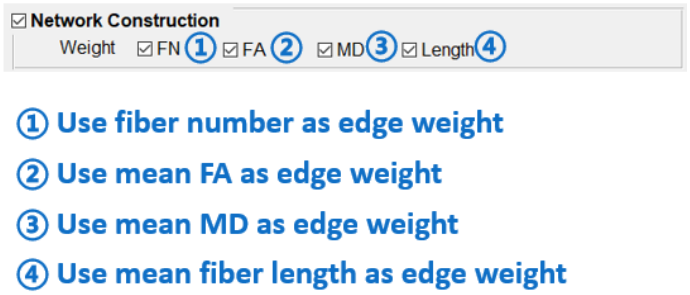

Figure 6: Instructions of network construction

2.6 Matrix Merge

In this step, the matrixs of all subjects will be merged into one single .mat file. The instructions of matrix merge are shown in Figure 7. The 'merge' step can't be executed alone without the boxes selected in 'network construction' step.

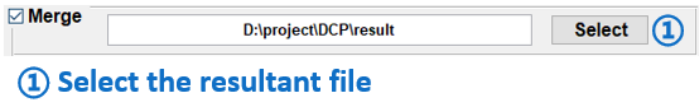

Figure 7: Instructions of merge

2.7 Network Analysis

The instructions of network analysis are shown in Figure 8. The 'network analysis' step can't be executed alone without the path selected in merge step.

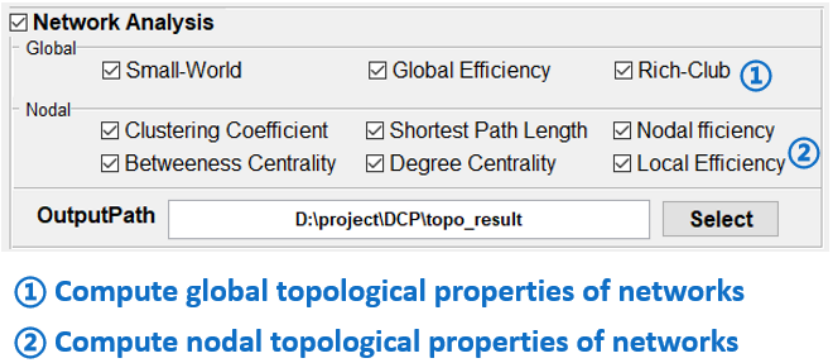

Figure 8: Instructions of network analysis

2.8 General Setting

The functions of buttons at bottom are shown in Figure 9. The subject names and status are shown in the green box. When 'finished' shows up, it means the pipeline finishes.

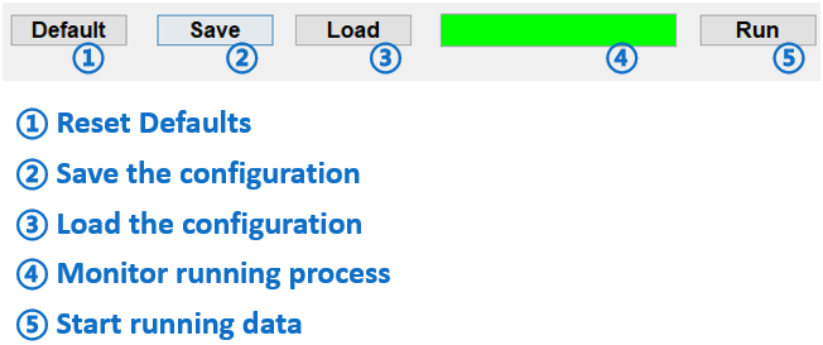

Figure 9: Instructions of buttons at bottom

3 Output Files

Under each subject's folder, three output folders named 'DCP_' are generated (Figure 10).

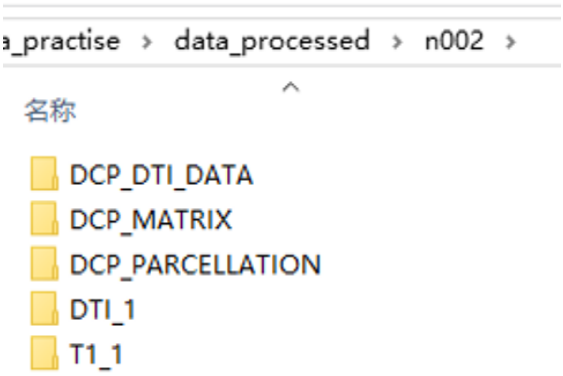

Figure 10: output folders

- DCP_DTI_DATA

If inputs are raw images in DICOM or NIfTI format, the files generated under DCP_DTI_DATA folder are shown in figure 11.

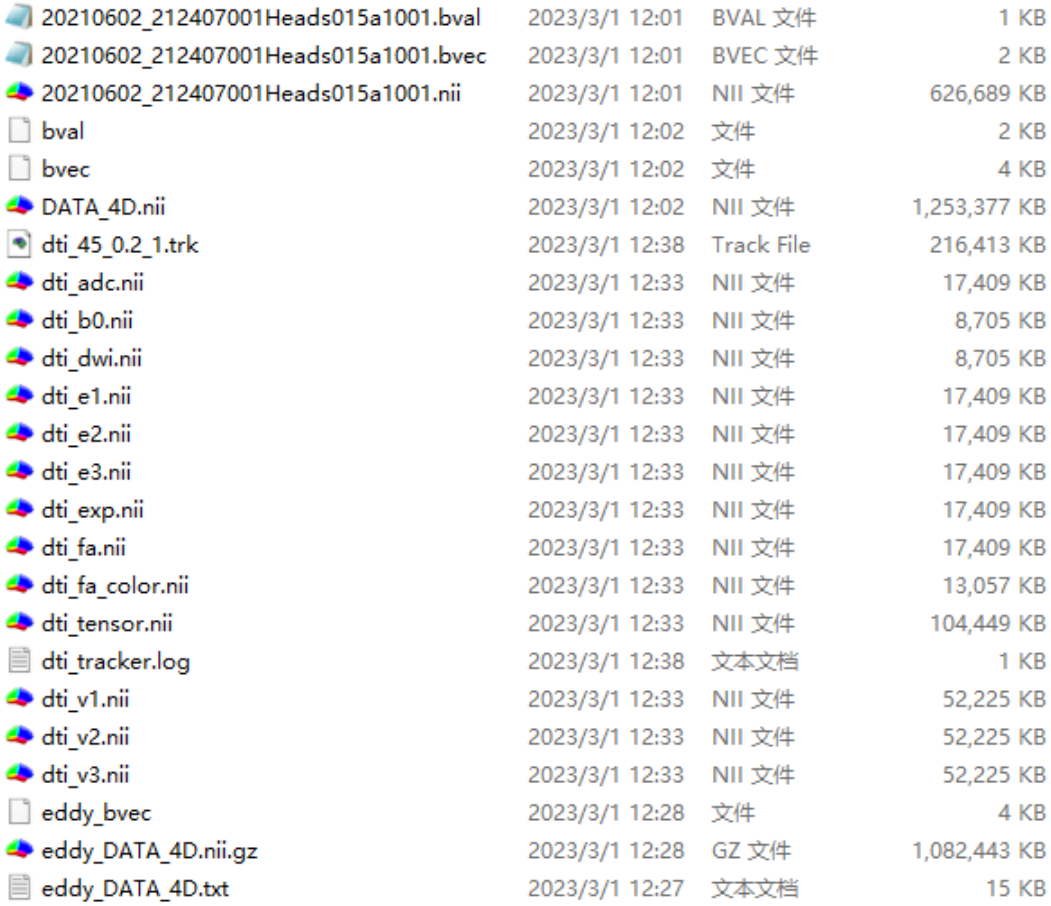

Figure 11: Files in folder 'DCP_DTI_DATA'

20xxxHeadxxx.bval, .bvec, .nii: Converted files from DICOM images.
bval, bvec, DATA_4D.nii: b-value table and gradient direction table, 4D DWI volume series.
.trk: Result of single-tensor fiber tracking.
dti_xxx.nii: Results of diffusion tensor metrics calculation.

eddy_xxx: Results of eddy-current and head motion.

If inputs are bedpost files, the files generated under DCP_DTI_DATA folder are shown in figure 12.

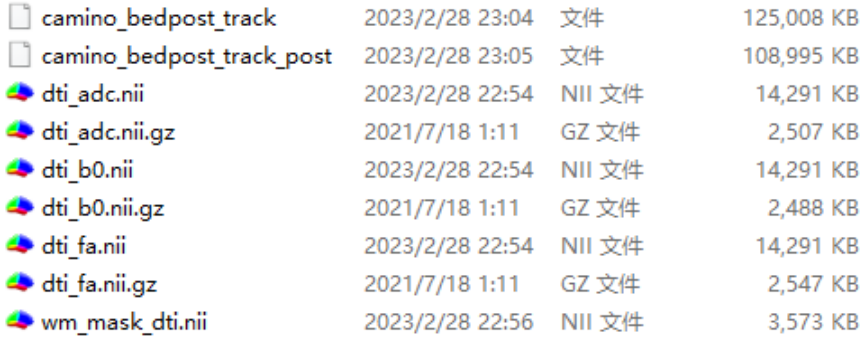

Figure 12: Files in folder 'DCP_DTI_DATA' for bedpost

camino_bedpost_track: Result of multi-tensor fiber tracking.
camino_bedpost_track_post: Post-processing of the tracts.

- DCP_PARCELLATION

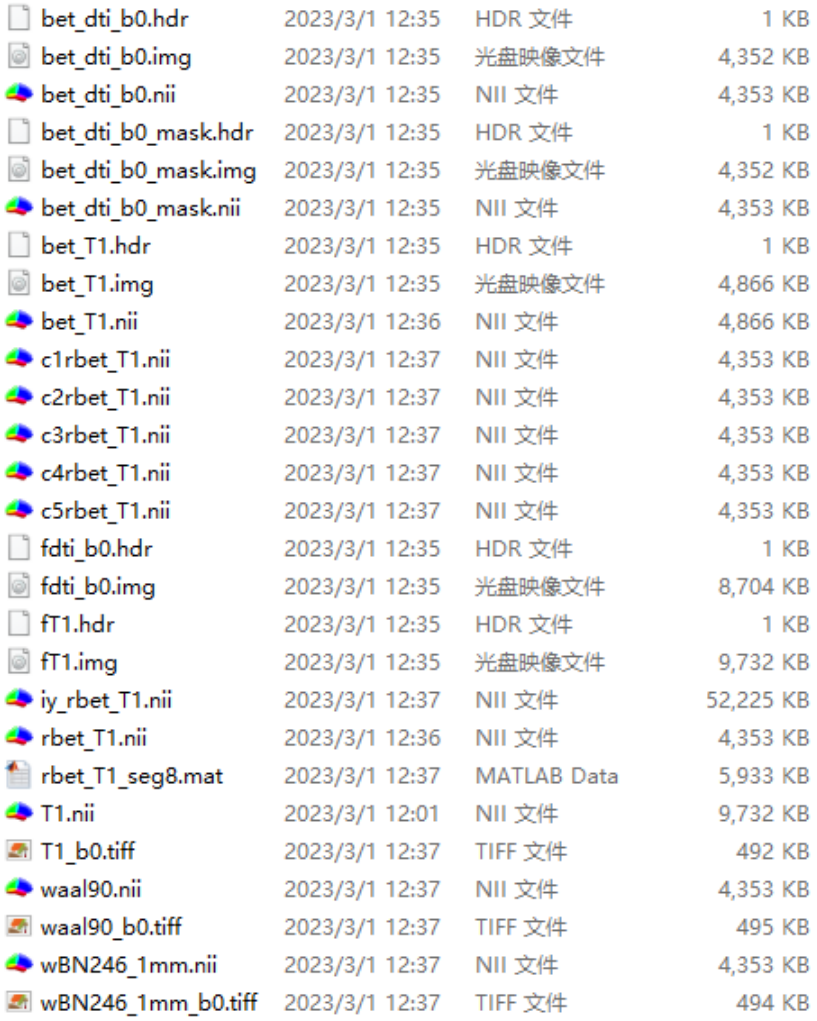

Figure 13: Files in folder 'DCP_PARCELLATION'

bet_dti_b0*: Individual T1 image is coregistered to its corresponding individual b0 image and brain mask generates.
***bet_T1*:** Individual T1 image that is coregistered to the b0 image space is mapped into ICBM152 template, generating a nonlinear transformation matrix.
T1_b0.tiff, waal90*, wBN246*: Prior atlases in the standard space are warped to individual native dMRI space.

- DCP_MATRIX

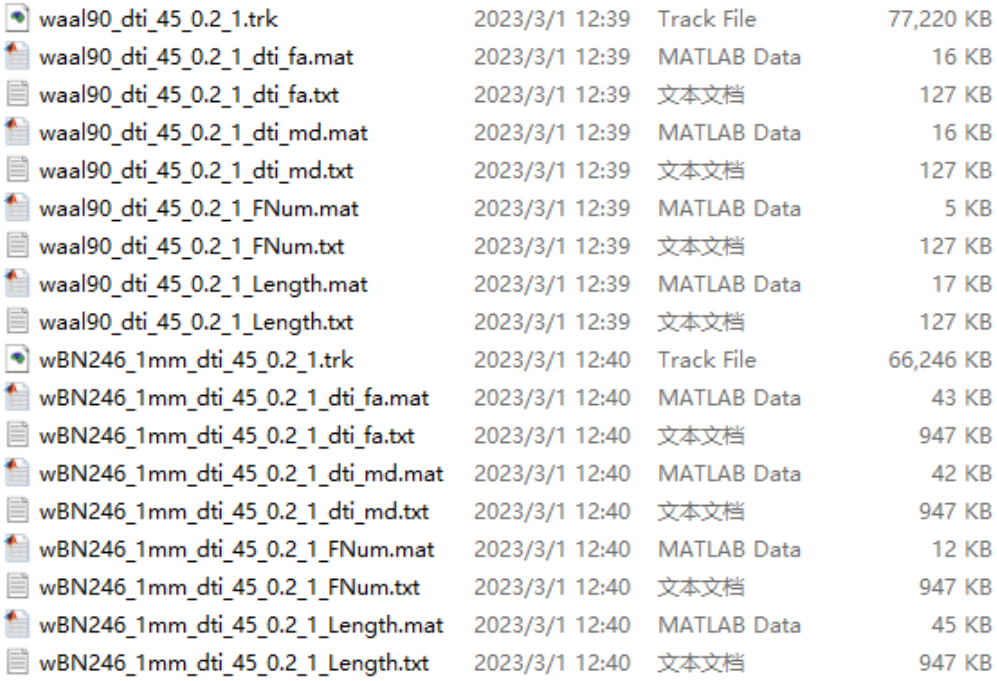

Figure 14: Files in folder 'DCP_MATRIX'

waal90xxx_fa: Matrix constructed with aal90 atlas and using FA as edge weight.
waal90xxx_md: Matrix constructed with aal90 atlas and using MD as edge weight.
waal90xxx_FNum: Matrix constructed with aal90 atlas and using fiber number as edge weight.
waal90xxx_Length: Matrix constructed with aal90 atlas and using fiber length as edge weight.
wBN246xxx: Matrix constructed with BN246 atlas, same as aal90 atlas.