PANDA Manual

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Citation

We have elaborated the diffusion MRI data processing procedures of PANDA in our recent paper (Cui et al., 2013), which can be a good reference for the users.

If PANDA is used in your work, citing it in your paper will be greatly appreciated, such as 'Processing of the diffusion MRI dataset was implemented using a pipeline toolbox, PANDA (Cui et al., 2013) (http://www.nitrc.org/projects/panda), which is based on …'.

Reference:

Cui Z, Zhong S, Xu P, He Y, Gong G. (2013): PANDA: a pipeline toolbox for analyzing brain diffusion images. Front Hum Neurosci 7:42.

Content

1 Setup

Requirements

Linux/Mac operating system (OS)

Matlab (R2012a version is recommended)

FSL (http://fsl.fmrib.ox.ac.uk/fsldownloads/fsldownloadmain.html)

Please download Centos version for Linux (Ubuntu, Centos, RedHat, Fedora, …)

Download & Unzip

Download PANDA_1.3.0:

http://www.nitrc.org/projects/panda

Example: Unzip PANDA_1.3.0_64.tar.gz

Input the command 'tar zxvf PANDA_1.3.0_64.tar.gz' in the terminal

Start Matlab

Open a terminal

Input 'matlab' in the terminal and click 'Enter'

Note: To use PANDA, users must open Matlab through terminal rather than shortcuts, no matter in Linux or Mac.

Matlab set path

File -> Set path -> Add with Subfolders (select PANDA folder 'PANDA-1.3.0_64') -> Save
Then, entering 'PANDA' in Matlab command window will open PANDA's graphical user interface (GUI).

2 Preparing raw data

The input of PANDA can be either DICOM files or NIfTI images.

2.1 DICOM format

Step 1: Create a separate folder for each subject (subject-folder).

Step 2: For each subject-folder, put all DICOM files of one diffusion weighted imaging (DWI) acquisition into one sub-folder (acquisition-folder).

Note:

1) Only DWI files are allowed to be put in the acquisition-folder.

2) The number of sub-folders should be the same as that of acquisitions for the DWI.

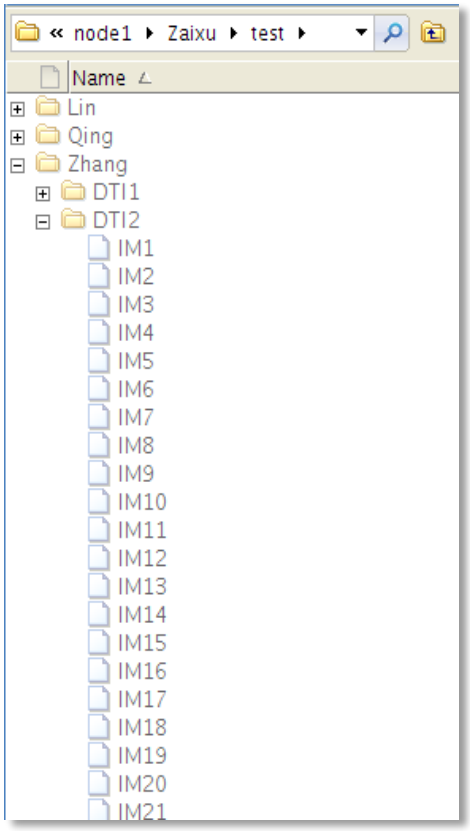

Figure 1. The raw data (DICOM) organization for PANDA input.

For example, in Figure 1, there are three subjects (Lin, Qing, Zhang), each with one folder. Because each subject has two acquisitions in this case, there are two sub-folders under each subject-folder (e.g., DTI1 and DTI2 under folder Zhang). Each sub-folder

contains all the DICOM files of one DWI acquisition. Finally, the subject-folder (e.g., Zhang) is the input of PANDA. PANDA will calculate the quantity of sub-folders under Zhang and be clearly how many acquisitions of this subject. Notably, if this subject has only one acquisition, there should be one sub-folder under Zhang.

2.2 NIfTI format

Step 1: Create a separate folder for each subject (subject-folder).

Step 2: For each subject-folder, put three files (*bval*, *bvec*, and *.nii/*.nii.gz) of one DWI acquisition into one sub-folder (acquisition-folder).

Note:

1) The number of sub-folders should be the same as that of acquisitions for the DWI.
2) Under each sub-folder, there must be only these three files.
3) B value file must be named as *'*bval*'* and b vector file must be named as *'*bvec*'*.
4) The 4D image file supports *.nii* and *.nii.gz* formats.
5) If MRIcron is used to convert DICOM files of DWI data to NIfTI, three files will be created, including a text file containing b values, a text file storing the direction vectors of gradient magnetic field (b vector file) and an 4D image file, which meet PANDA's requirements.

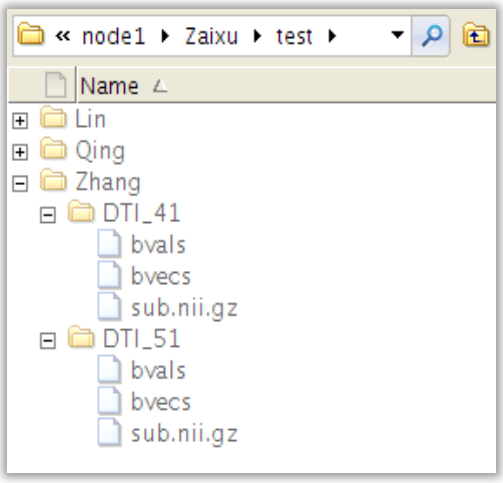

Figure 2. The raw data (NIfTI) organization for PANDA input.

For example, in Figure 2, there are three subjects (Lin, Qing, Zhang), each with one

folder. Two sub-folders are created for Zhang, as there are two acquisitions for this subject. Under each sub-folder, there are three files, named bvals, bvecs, and sub.nii.gz.

3 Full Pipeline

3.1 Basic input

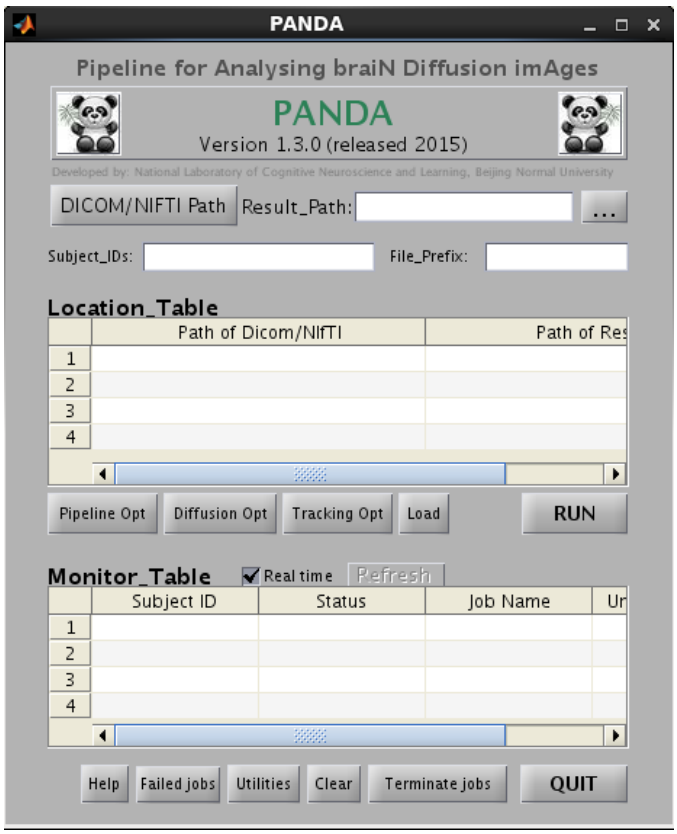

Figure 3. Main GUI for PANDA.

DICOM/NIfTI Path

Input the path of subject-folders prepared in the session **Preparing raw data**, such as folders Lin, Qing and Zhang.

Result Path

Determine resultant folder to store all the results for all subjects.

Subject IDs

Assign a digital ID for each subject. For example, if there are 8 subjects in all, then 8 IDs are needed, such as [1:3 5 7:10].

Note:

1) [] is essential and the digital IDs should be contained in the [].

2) *a:b* means all the IDs between *a* and *b*, such as 7:10 representing 7 8 9 10. Therefore, [1:3 5 7:10] means [1 2 3 5 7 8 9 10].

File Prefix

Determine the prefix for the name of all the resultant files. Leave it empty if you don't need.

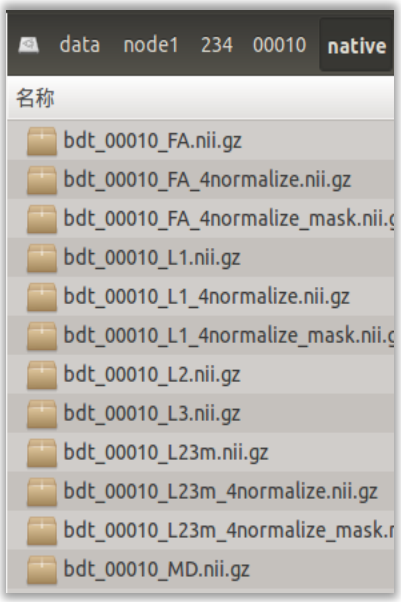

Figure 4. Example for "bdt" as prefix parameter.

For example, in Figure 4, users input 'bdt' in the File Prefix blank, then all the resultant files contain 'bdt' as prefix.

3.2 Parallelization setting

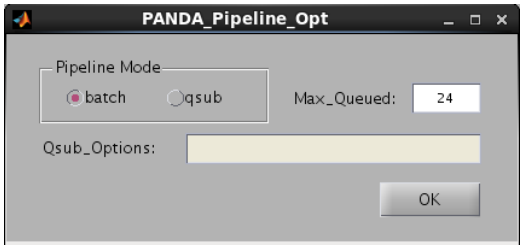

Figure 5. GUI for setting parameters of pipeline environment.

Pipeline Mode

If one single computer is used, please select '*batch*' mode. In this mode, PANDA can call the multi cores in the computer to parallelize multi jobs. The **Max Queued** is for

setting the quantity of jobs running in parallel. If this value is 24, as shown in Figure 5, then 24 jobs can run in parallel, which will largely accelerate data processing speed. Users should set the value of **Max Queued** according to computer performance. Typically, to ensure the normal operation of the computer, this value should not exceed the quantity of cores.

If a distributed computing cluster (e.g., sun grid engine) is used, please select '*qsub*' mode. Also, **Max Queued** is the maximum jobs running in parallel. **Qsub Options** is used to set options for qsub, such as '-q all.q'.

3.3 Diffusion parameters

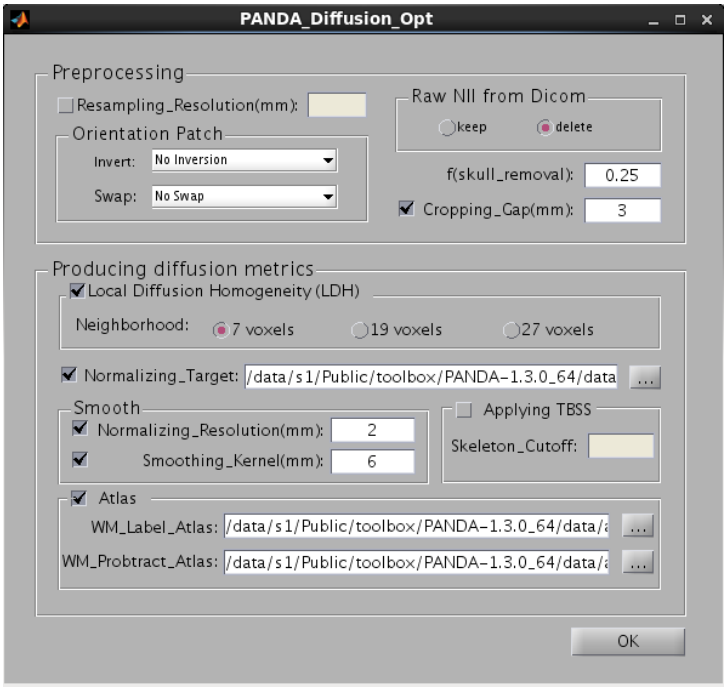

Figure 6. GUI for setting parameters of preprocessing and comparable diffusion metrics calculating.

Resampling resolution

Resample the raw DWI image to a certain voxel size. Generally, the current resolution of DWI image is around 2×2×2 mm^3. However, some MRI scanners up sampled the data to a high resolution (e.g., 0.9×0.9×1 mm^3) when they export the data. This operation adds no information to the raw image but largely increase the data processing

time, especially fiber tracking. Therefore, we recommend users resample the data to $2\times2\times2$ mm^3 in this situation.

Raw NII from Dicom

Users can select 'delete' to delete the raw NIfTI DWI images converted from DICOM files to save the disk space.

f (skull removal)

Parameter for extracting brain tissue of DWI image, smaller values give larger brain outline estimates. Default is 0.25.

Cropping gap (mm)

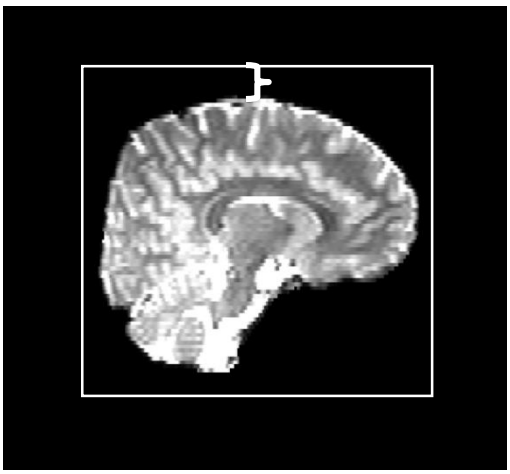

Figure 7. Cropping the original image.

To reduce the memory cost and accelerate the data processing speed, this step will replace the original image with a smaller one, which just contain the brain tissue. As shown in Figure 7, cropping gap is the distance between the border of image we selected and the border of the brain (the default value is 3 mm).

Orientation patch

Please refer to the **Utility Test Bvecs** section.

Neighborhood (local diffusion homogeneity)

Local diffusion homogeneity (LDH) of a given voxel is defined as the overall similarity of the diffusivity series within its nearest neighborhood (Gong, 2013). This parameter is to define the neighborhood, 7 voxels means two voxels are neighborhood if their

surfaces are adjacent, 19 voxels means line adjacent and 27 voxels means dot adjacent.

Normalizing target

Different subjects can be compared only if they are in the same space. Generally, we write different subjects' data into standard space through registering their images into a standardized template. Here, PANDA first register individual fractional anisotropy (FA) images of native space to the FA template in the MNI space and then apply the resultant warping transformations to write the images of the diffusion metrics [i.e., FA, mean diffusivity (MD), axial diffusivity (AD/L1), radial diffusivity (RD/L23m) and LDH] into the MNI space. This parameter is the path of the standardized FA template. Default is the FMRIB58_FA template, which is a high-resolution average of 58 well-aligned good quality FA images from healthy male and female subjects aged between 20 and 50, at 1×1×1mm resolution (http://fsl.fmrib.ox.ac.uk/fsl/fsl-4.1.9/data/FMRIB58_FA.html).

Smooth

The results are used for the whole brain voxel based analysis. To alleviate the registration error and increase the gaussianity of the data, smooth is needed.

Normalizing resolution (mm)

As the original resolution of DWI data is around 2×2×2 mm^3, here we resample the diffusion metrics images into the voxel size of 2×2×2 mm^3.

Smoothing kernel (mm)

Gaussian kernel size for smooth, default is 6.

Atlas

For diffusion metrics (i.e., FA, MD, AD and RD) images with voxel size of 1×1×1 mm^3 in the standard space (the images are *_*1mm.nii.gz* in *standard_space* folder), the regional averages were calculated according to prior WM atlases. The WM atlases in PANDA can be found in the directory *'.../PANDA-1.2.4_64/data/atlases/rICBM_DTI'*.

WM label atlas

This atlas is created by hand segmenting a standard-space average of diffusion MRI

tensor maps from 81 normal subjects according to histology criteria. Atlas *'rICBM_DTI_81_WMPM_FMRIB58.nii.gz'* comprises 50 core regions, which are consistently existed in all these 81 subjects (Mori et al., 2008) (Figure 8). Atlas *'rICBM_DTI_81_WMPM_70p_FMRI58.nii.gz'* comprises 68 regions, which existed in the population with a probability of 70% (Oishi et al., 2008) (Figure 9).

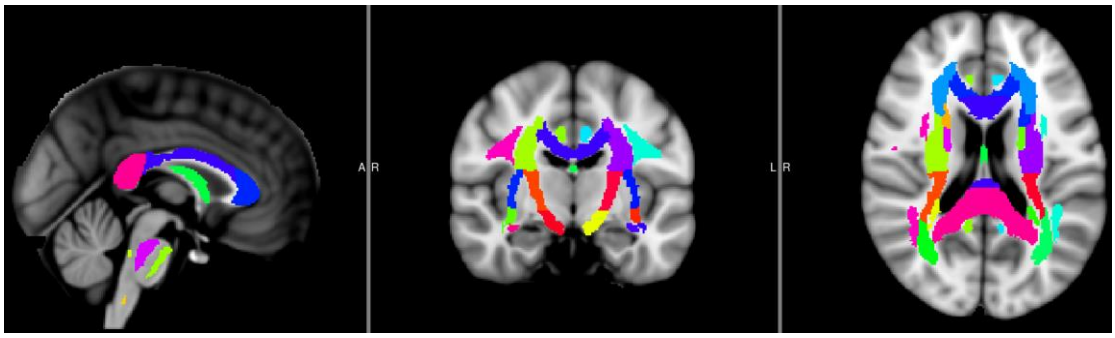

Figure 8. White matter atlas 'rICBM_DTI_81_WMPM_FMRIB58.nii.gz' which comprises 50 core regions.

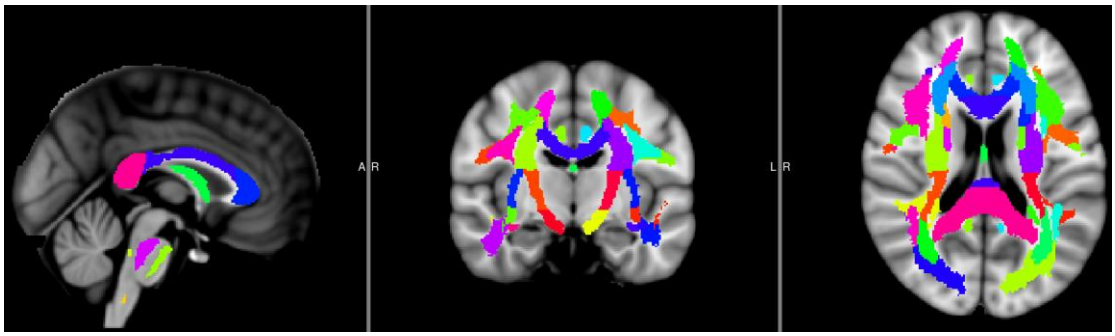

Figure 9. White matter atlas 'rICBM_DTI_81_WMPM_70p _FMRIB58.nii.gz' which comprises 68 regions (70% probability).

WM probtract atlas

This atlas comprises 20 regions, which are identified probabilistically by averaging the results of running deterministic tractography on 28 normal subjects (Hua et al., 2008).

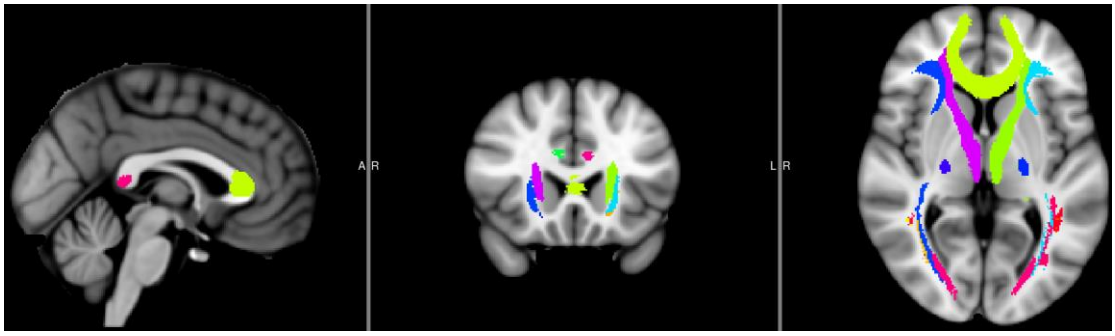

Figure 10. White matter tract probability map, which comprises 20 regions.

Apply TBSS

Executing tract-based spatial statistics (TBSS) procedure and all subjects' skeletons are created for statistics (Smith et al., 2006). Also, the regional average values of skeletonized images are acquired according to WM atlases.

Note:

To do TBSS, the data should be completely collected, as TBSS needs all the subjects' data to generate a group mean FA image. If the data collection is not accomplished, please don't select this option.

Skeleton cutoff

The parameter is used to set the threshold of FA for excluding the voxels in gray matter and CSF during the TBSS processing procedure. Default value is 0.2.

Note:

Correcting for the eddy-current effect

Eddy-current induced distortion of DW images, as well as simple head-motion during scanning, can be corrected by registering the DW images to the b0 image with an affine transformation here. *If multiple b0 images are acquired, the average of these b0 images will be used as reference*. What's more, the gradient direction of each DWI volume was rotated according to the resultant affine transformations (Leemans and Jones, 2009).

3.4 Tracking & Network parameters

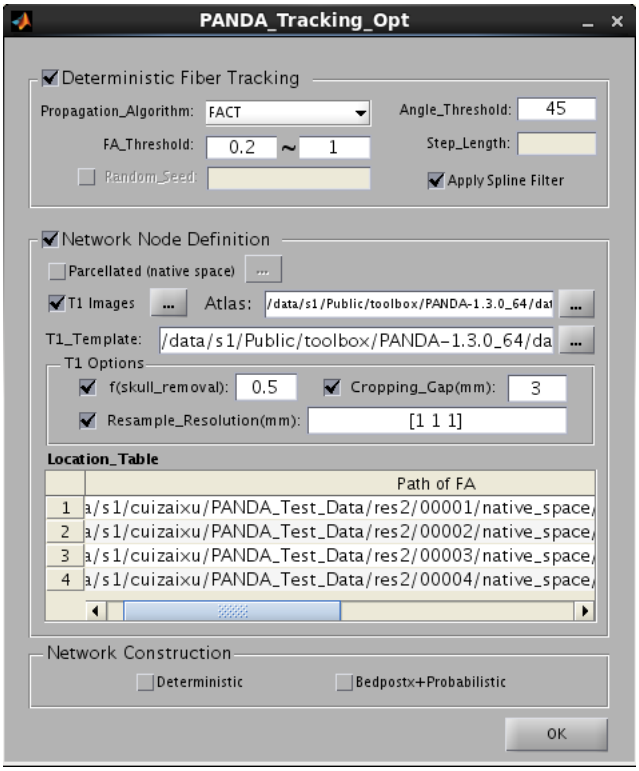

Figure 11. GUI for setting parameters of fiber tracking and network construction (deterministic and probabilistic).

Deterministic fiber tracking

Deterministic fiber tracking is implemented with Diffusion Toolkit (http://trackvis.org/dtk/).

Propagation algorithm

Deterministic fiber tracking algorithms, four selections: Fiber Assignment by Continuous Tracking (FACT), 2nd order runge-kutta; tensorline and interpolated streamline (Mori et al., 1999; Mori and van Zijl, 2002).

Angle threshold

Terminate fiber tracking if two consecutive moving directions have crossing angle above this threshold, default is 45^{o} .

FA threshold

Terminate fiber tracking if the FA is out of the threshold range (default is 0.2~1),

because the tissue with FA outside of this range is thought to be gray matter or CSF.

Step length

Step length means the progressing distance along a certain direction. Here, the unit of step length is the minimum voxel size. Notably, we don't need to set the length for the "FACT" propagation algorithm, while default 0.5 for the interpolated streamline method and default 0.1 for the other two methods

Random seed

Quantity of seeds in each voxel, default is one voxel in the center of the voxel. If the value is bigger than 1, then these seeds will be randomly selected in the voxel.

Apply spline filter

Fiber tracking is a step-by-step procedure, thus will produce many corners. This option is to smooth these corners of the fiber.

Network node definition

The entire brain is divided into multiple regions using a prior gray matter (GM) atlas, where each region represents a network node (Gong et al., 2009b). FA images and structural images (e.g., T1-weighted MP-RAGE image) are needed. If you have not generated the individual parcellated images, you should select *'T1 images'*. After this procedure, a parcellated image in individual space will be created for each subject.

Next time, if you want to rerun deterministic network construction with different options of deterministic fiber tracking, the network node definition doesn't need to run again, you can use the individual parcellated images created before. In this situation, you can select *'Parcellated (native space)'* and input the individual parcellated image of each subject.

T1 image

Path of T1-weighted structural images, which should be in NIfTI format (*.nii or *.nii.gz). The order of T1 images should be in accordance with the FA images. If MRIcron is used to convert T1 DICOM files into T1 NIfTI files. Then, three images will be created, in which the image with *'co'* as prefix in the name is recommended.

Atlas

Path of brain parcellation atlas. Default is AAL atlas (Tzourio-Mazoyer et al., 2002).

T1 template

The T1 template in the standard space. Default is T1 template of ICBM152 in MNI space.

T1 option (skull removal)

Parameter for extracting brain tissue of T1 structural image, smaller values give larger brain outline estimates. Default is 0.5.

T1 option (cropping gap)

Refer to cropping gap parameter in **Diffusion Parameters** section.

T1 option (resample resolution)

Resample T1 image to a certain resolution for accelerating the data processing speed, e.g., 1×1×1 mm^3.

Network construction

Deterministic

Network construction based on deterministic fiber tracking. Based on whole brain fibers, three weighted matrices are created: fiber number matrix, average FA weighted matrix and average fiber length matrix.

Probabilistic

If probabilistic checkbox was checked, the following window will launch.

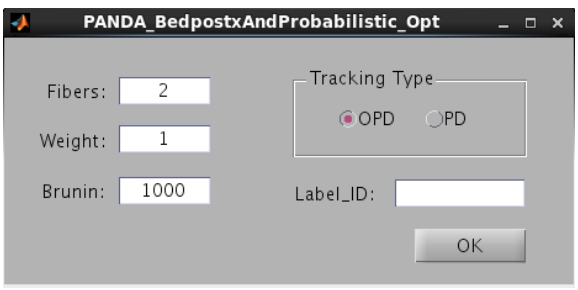

Figure 12. GUI for setting parameters of bedpostX and probabilistic network construction.

Fibers, **weight** and **Burnin** are parameters for BedpostX, please refer to

http://fsl.fmrib.ox.ac.uk/fsl/fsl4.0/fdt/fdt_bedpostx.html. The Default values of these parameters are the ones used in the corresponding paper (Behrens et al., 2007).

Tracking type

OPD: output path distribution directly.

PD: correct path distribution for the length of the pathways and then output path distribution.

Label ID

In the atlas (e.g., AAL atlas), each region was marked with a unique ID (typically an integer). Here, users can input the IDs of the regions they are interested in. For example, if users input [3:5 8], then the program will calculate the connections among any two regions of the 3,4,5,8 regions in the atlas, and then create the network with these four regions as nodes.

3.5 Start running

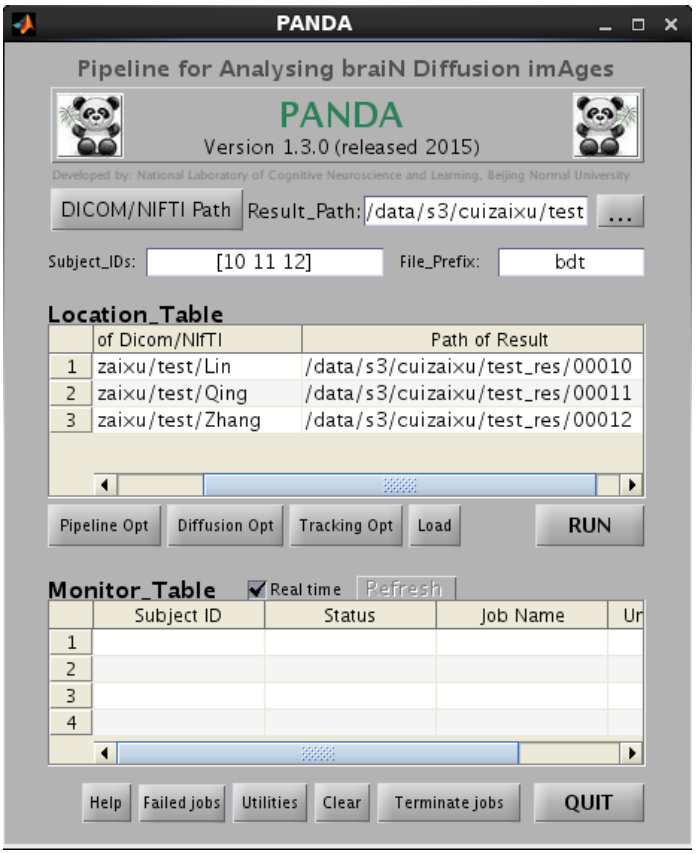

Figure 13. Prepare running after setting the basic inputs and appropriate parameters.

RUN

After the basic inputs and the parameters are set properly, click this button to run the pipeline. A configuration file with ***.PANDA*** as suffix will be created in the result path, which contains all the inputs and parameters.

Load

Once the RUN button is clicked, the data will be running in the background. Even the closing of PANDA's GUI or Matlab will not influence the data processing. If PANDA is closed but the users want to see the status of jobs, they can click this button to load the ****.PANDA*** configuration file in the result path.

Terminate jobs

Click this button to terminate all the jobs if you want to stop data processing. After clicking this button, the status of all the jobs in the status table will be **'Stopped'**.

Clear

Recover the GUI of PANDA back to empty. If you have submitted one dataset and want to run another dataset, you can clear the GUI first and then set the input and parameters for new dataset.

Monitor table

The running status of all the subjects' data.

Subject ID (fixed): ID of each subject.

Status (dynamic): five status in all, including 'wait', 'submitted', 'running', 'finished', 'failed'.

Job Name (dynamic): the whole data processing procedure is split into a number of jobs, each with a name. For example, the name of brain extraction job is 'BET' and that of eddy current job is 'EDDYCURRENT'.

Unfinished Steps (dynamic): the quantity of jobs to be processed

Failed jobs

If the 'status column' in status table represents 'failed', please click this button to check

the reason of the failed jobs. The list box as shown in Figure 14 will open, which displays the name of the failed jobs. Click the particular job name for the reason.

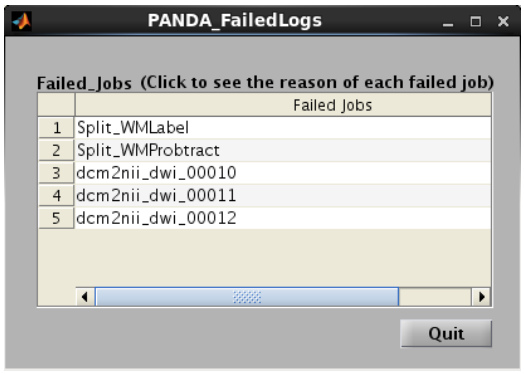

Figure 14. The list of failed jobs.

QUIT

Close the GUI of PANDA.

3.6 Results

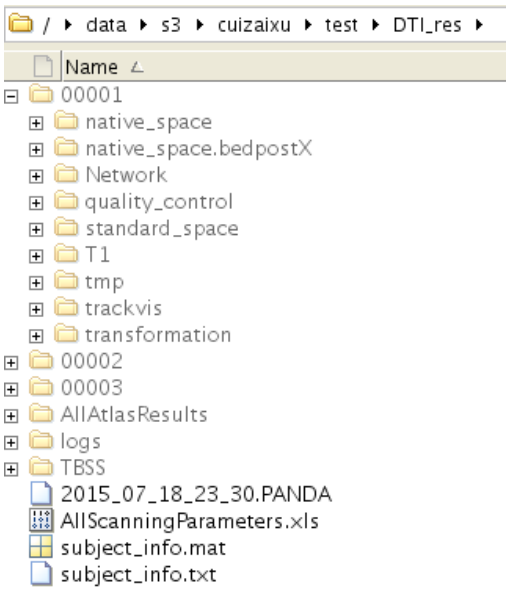

Figure 15. Results of full pipeline.

After the processing, one folder is created for each subject, named by the *Subject ID*. ****.PANDA*** file contains all the inputs and parameters user sets. *AllScanningParameters.xls* is an Excel with scanning parameters for each subject. *Subject_info.txt* contains the correspondence between the input and resultant folder. As

shown in Figure 16, the results of subjects *'Ling'* are stored in the *'00001'* folder.

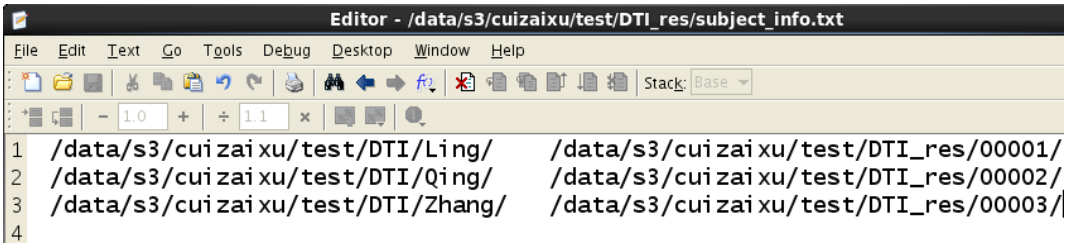

Figure 16. Subject_info.txt in the resultant folder.

1) Results for atlas-based analysis

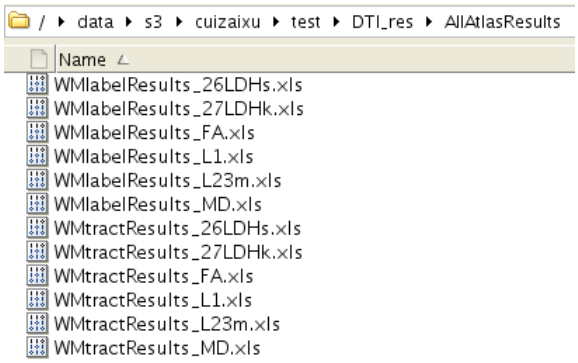

Figure 17. The results for atlas-based analysis.

Under the folder ***'AllAtlasResults'***, twelve Excel files are created, which contain the regional average values for diffusion metrics (i.e., FA, MD, AD and RD) images with voxel size of 1×1×1 mm^3 in the standard space (the image are **_1mm.nii.gz* in *'standard_space'* folder). Users can copy the values in the Excel to Statistical Package for the social Sciences (SPSS) for statistics.

2) Results for TBSS-based analysis

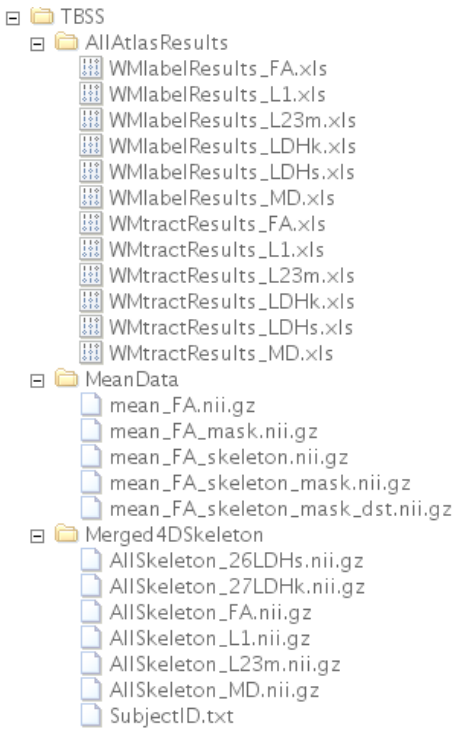

Figure 18. Results of TBSS in full pipeline.

All results of TBSS are located in the ***'TBSS'*** folder. In *'Merged4DSkeleton'*, there are 4D skeletons for all metrics which are the input of randomise statistics. Each 4D skeleton is merge of all subjects' 3D skeletons. The *SubjectID.txt* represents the order of subjects' image in 4D skeleton. In the folder *'MeanData'*, there is a *mean FA skeleton mask* image which is useful for randomise statistics, and also *mean FA* and *mean FA skeleton* which are useful for displaying of the statistical results.

In the folder *'AllAtlasResults'*, twelve Excels are created, which contains the regional average values for the subjects' skeleton images (Huang et al., 2011; Liu et al., 2012).

3) Results for whole-brain voxel-based analysis

Figure 19. Results in standard space of subject 00001.

The files named ***'*_2mm_s6mm.nii.gz'*** in ***standard_space*** folder of each subject can be used for whole-brain voxel-based analysis. These images are in the standard space with voxel size of 2×2×2 mm^3, and have been smoothed with 6mm Gaussian kernel size.

4) Other files in the standard_space folder

(1) *_*1mm.nii.gz*: metric images with voxel size of 1×1×1 mm^3 in the standard space

(2) *_*2mm.nii.gz*: metric images with voxel size of 2×2×2 mm^3 in the standard space.

(3) *_*skeletonised.nii.gz*: the 3D skeleton image for each subject produced by TBSS.The 3D skeletons of all subjects have already been merged into a 4D skeleton in the folder *'TBSS/Merged4DSkeleton'*, which is input of randomise statistics.

(4) *_*1mm.WMlabel & *_1mm.WMtract*: regional average values for diffusion metrics images with voxel size of 1×1×1 mm^3 in the standard space. The average values of all subjects have already been merged into Excels in the folder *'AllAtlasResults'*.

(5) *_*skeletonised*.*WMlabel* & *_*skeletonised*.*WMtract*: regional average values for skeletonized images. The average values of all subjects have already been merged into Excels in the folder *'TBSS/AllAtlasResults'*.

5) Trackvis folder:

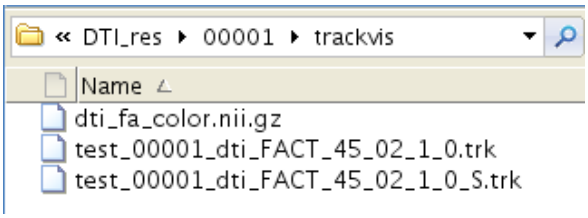

Figure 20. Results in trackvis folder of subject 00001.

As shown in Figure 20, there are whole-brain white matter tract ***(*.trk)*** constructed by deterministic fiber tracking and color FA (dti_fa_color.nii.gz) calculated by diffusion toolkit (http://www.trackvis.org/dtk/). This file (*.trk) can be opened with trackvis (http://www.trackvis.org/). The file named *_S.trk will be created if the **Apply spline filter** is selected in the **Deterministic fiber tracking** options.

6) Results for network analysis

Deterministic

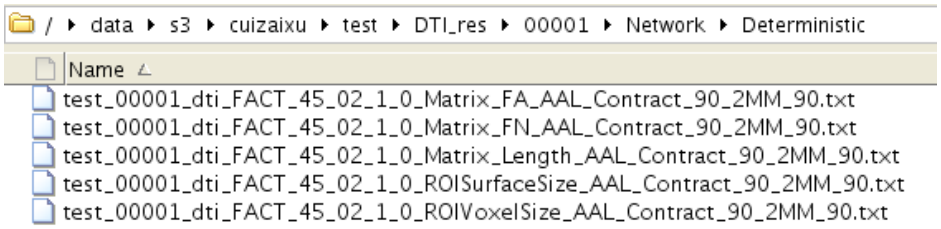

Figure 21. Results of deterministic fiber tracking of subject 00001.

(1) *_*Matrix_FA*_*: matrix with average FA of all the voxels along the fibers between two regions. FA values express the level of anisotropic diffusion of white matter in a brain voxel, which is most commonly used to examine the microstructure aspects of brain connectivity.

(2) *_*Matrix_FN*_*: matrix with total number of fibers between two regions. This matrix provides information on the quantity of white matter connectivity between two regions, which was computed by summing the existing streamlines connections two

regions.

(3) *_Matrix_Length_*: matrix with average length of fibers between two regions. Usually, *_Matrix_FN_* and the *_Matrix_Length_* were combined used to eliminate the bias towards longer fibers introduced by the tractography algorithm (Hagmann et al., 2008).

(4) *_ROISurfaceSize_*: quantity of voxels in which the fibers terminated in each ROI.

(5) *_ROIVoxelSize_*: quantity of voxels in each ROI.

The three matrices (*_Matrix_FA_*, *_Matrix_FN_*, *_Matrix_Length_*) can be used as the input of **GRETNA** ((Wang et al., 2015), http://www.nitrc.org/projects/gretna) for network analysis (Gong et al., 2009b; Zhao et al., 2015).

The ROI size *(*_ROIVoxelSize_*)* and surface size *(*_ROISurfaceSize_*)* can be used for correcting the original matrices (Hagmann et al., 2008).

Probabilistic

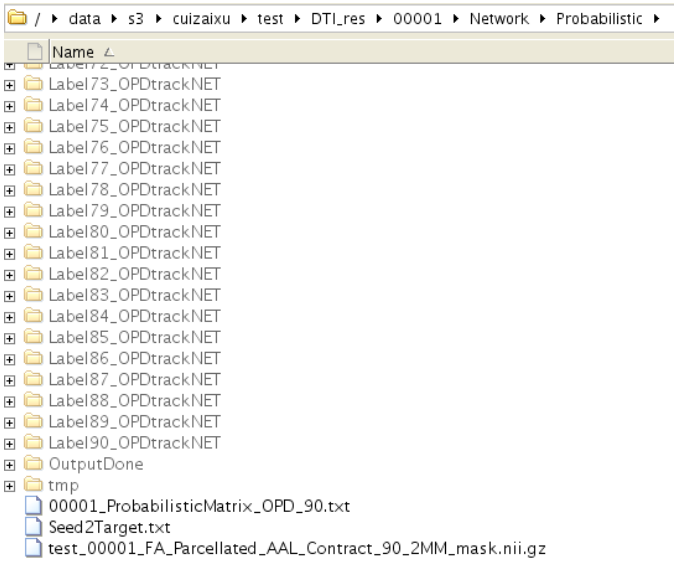

Figure 22. Results of probabilistic fiber tracking of subject 00001.

*_ProbabilisticMatrix_*: matrix with connection probability between two regions. This .txt file can also be used as input of **GRETNA** for network analysis (Cao et al., 2013; Gong et al., 2009a).

Note:

The probability from the *i-th region* to the *j-th region* is not necessarily equivalent to the one from *j* to *i*. However, these two probabilities are highly correlated across the cerebral cortex. Thus, we can average these two probabilities to acquire a unidirectional symmetric matrix for each subject. Then, we can use **GRETNA** to quantify the topological organization of the human brain.

7) Quantity control

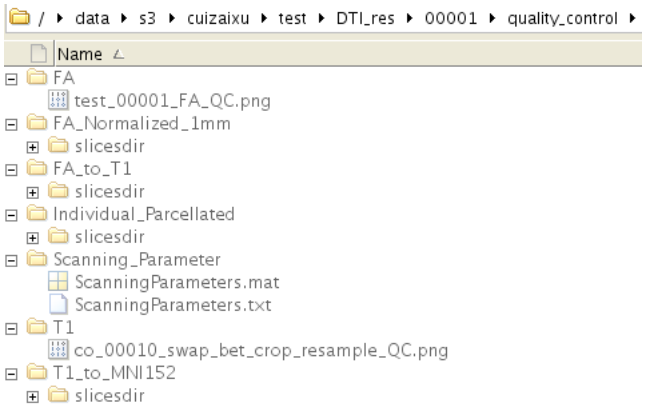

Figure 23. Results probabilistic fiber tracking of subject 00001.

The 2D snapshot pictures of FA, T1, normalized FA to MNI space, normalized FA to T1, normalized T1 to MNI space and individual parcellated image, which can be quickly viewed to check the quality of the data and registrations.

(1) *FA:*

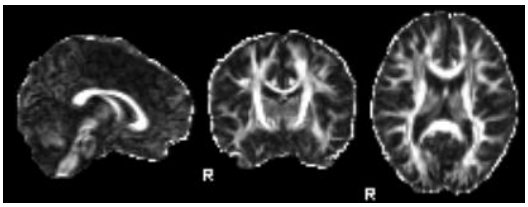

Figure 24. The 2D snapshot pictures of FA (good).

Please check the gray and white matter contrast and the clarity of tissue border, to confirm no obvious error.

(2) *FA_Normalized_1mm:*

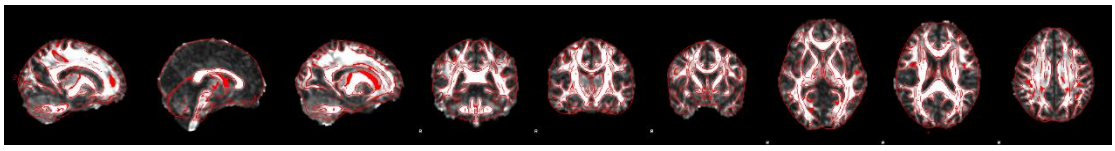

Figure 25. The 2D snapshot pictures of normalized FA to MNI space (good).

The red outline is the border of the template and the background image is the normalized FA in MNI space. Please check whether the tissue border of the background image is in correspondence to the read lines. Figure 25 represents a well registered FA.

(3) *FA_to_T1:*

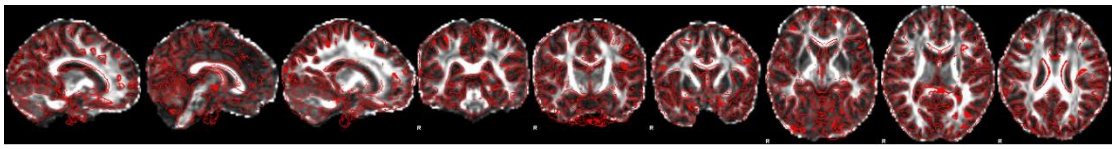

Figure 26. The 2D snapshot pictures of normalized FA to individual T1 (good).

(4) *Individual_Parcellated:*

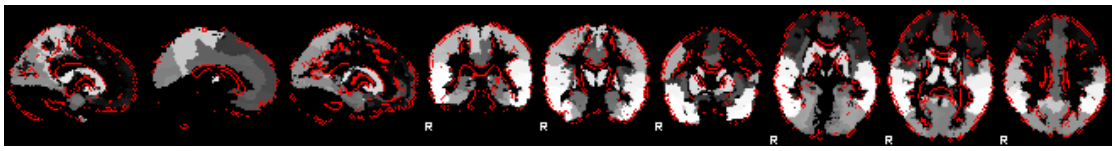

Figure 27. The 2D snapshot pictures of individual parcellated image (good).

(5) *T1_to_MNI152:*

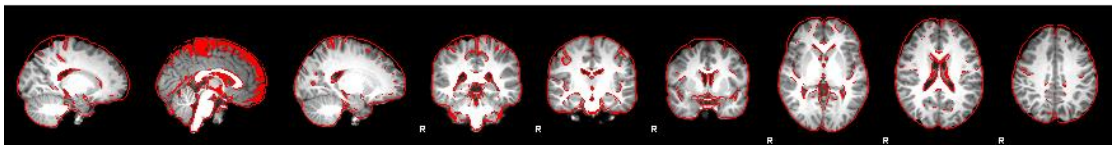

Figure 28. The 2D snapshot pictures of normalized T1 to MNI space (good).

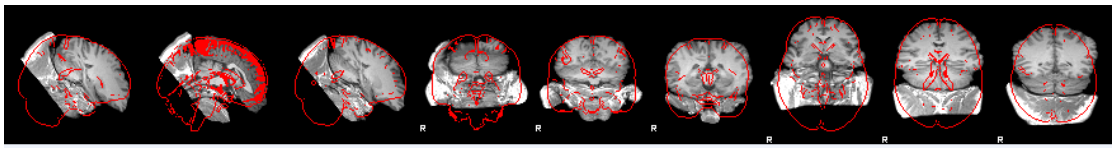

Figure 29. The 2D snapshot pictures of normalized T1 to MNI space (bad).

Figure 28 and Figure 29 represent a good registration of T1 to MNI space and a bad one, respectively. The error in Figure 29 occurred because the brain extraction of T1 image is not successful (the neck is also retained in the image).

8) Results in native_space folder

Figure 30. The resultant files in native space folder.

(1) *bvals*: text file with b values.

(2) *bvecs*: text file containing diffusion weighted directions, after eddycurrent correction.

(3) *data.nii.gz*: 4D DWI image after data preprocessing.

(4) *data_b0_average.nii.gz*: the average of all the b0 images with no diffusion weighting.

(5) *data_b0_average_crop.nii.gz:* the cropped average b0 images, this file will be created if the **Cropping Gap** is selected in the **Diffusion Opt**.

(5) **_S0.nii.gz*: b0 image with no diffusion weighting calculated by dtifit.

(5) **_FA.nii.gz*, **_MD.nii.gz*, **_L1.nii.gz*, **_L2.nii.gz*, **_L3.nii.gz*, **_L23m.nii.gz*, **_26LDHs.nii.gz*, **_27LDHk.nii.gz*: fractional anisotropy, mean diffusivity, 1st eigenvalue (axial diffusivity), 2nd eigenvalue, 3rd eigenvalue, radial diffusivity, local diffusion homogeneity (Spearman) and local diffusion homogeneity (Kendall) images in native space.

(6) *_*V1.nii.gz*, *_*V2.nii.gz*, *_*V3.nii.gz*: 1st eigenvector, 2nd eigenvector and 3rd eigenvector of diffusion tensor model, respectively.

(7) *_*Parcellated*_*: individual brain parcellated image, which can be created when 'Network Node Definition' is checked.

4 Utilities

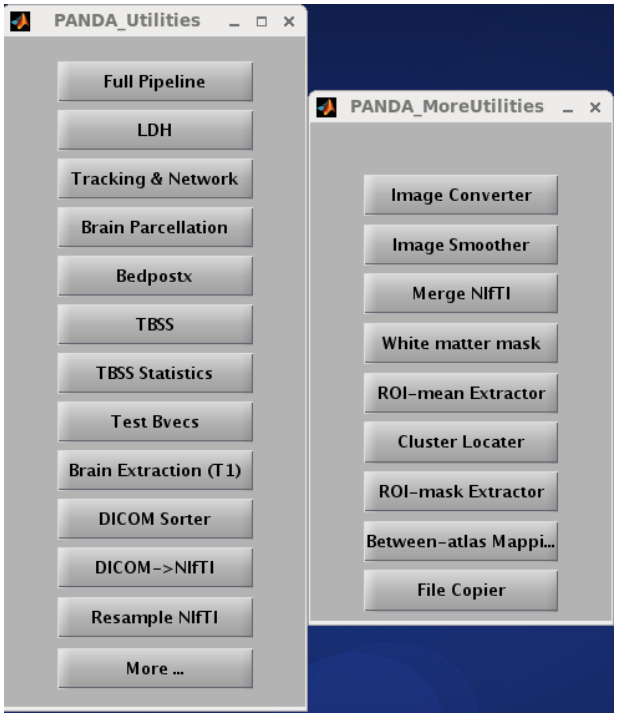

Figure 31. All the utilities in PANDA.

4.1 LDH

Local diffusion homogeneity (LDH) of a given voxel is defined as the overall similarity of the diffusivity series within its nearest neighborhood (Gong, 2013). If you have checked LDH in the **Diffusion Opt** when running full pipeline, then all the LDH images for statistics will be created and this utility is unnecessary.

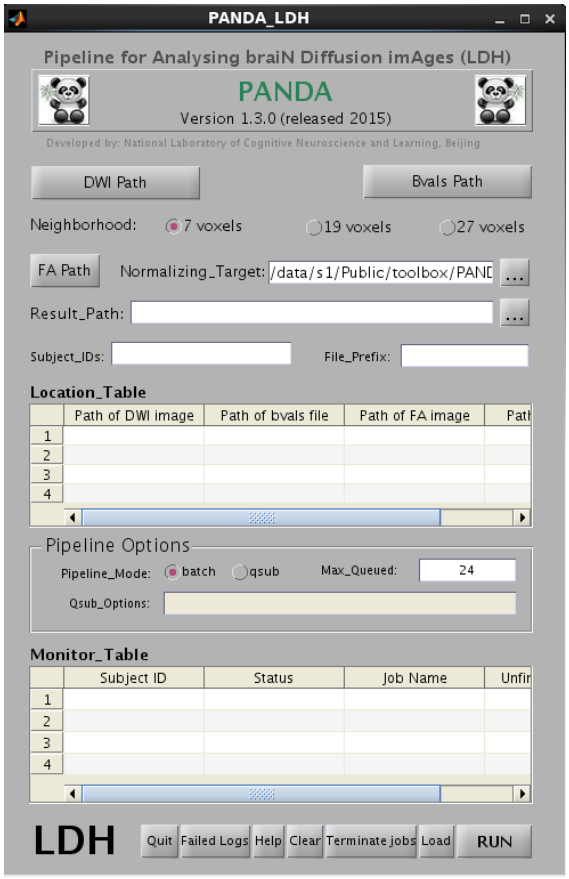

Figure 32. The GUI for the utility of LDH calculation.

DWI path

Path of 4D diffusion weighted images of each subject. NIfTI images with .nii or .nii.gz format are supported. If PANDA is used for preprocessing, this file is *'data.nii.gz'* in the *native_space* folder.

Bvals path

Path of b value files of each subject.

Neighborhood

This parameter is to define the neighborhood, 7 voxels means two voxels are neighborhood if their surfaces are adjacent, 19 voxels means line adjacent and 27 voxels means dot adjacent.

FA path

Path of FA images (native space) of each subject.

Normalizing Target

Path of FA template in standard space. Register the native FA to this template first, and then apply the acquired the resultant warping transformations to write the images of LDH images into the MNI space. Refer to **Diffusion parameters->Normalizing Target**.

Subject IDs

Assign an integer ID for each subject.

File prefix

The prefix for the name of all the resultant files (optional).

Pipeline options

Pipeline mode, **max queued** and **qsub options**, please refer to **Pipeline environment parameters** section.

RUN

Click this button to start running the jobs. A configuration file with suffix of ***.PANDA_LDH*** will be created in the *result path*, and users can load this configuration file to check the job status after close the GUI.

Results

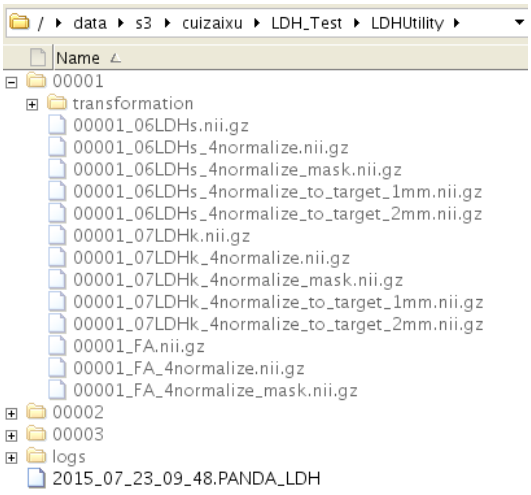

Figure 33. The results of LDH utility.

As shown in Figure 33, in the result path, a folder named with ID is created for each subject. Under each folder, there are LDH (spearman) and LDH (kendall) images in the standard space with voxel size of 1mm (*_1mm.nii.gz) and 2mm (*_2mm.nii.gz). Users

can use **Image Smoother utility** to smooth 2mm images and then do statistics, calculate the regional average of 1mm images according to prior WM atlas using **ROI-mean Extractor utility**, and do TBSS analysis with 1mm images using **TBSS utility**.

4.2 Tracking & Network

This utility is for fiber tracking and network construction (deterministic and probabilistic). As shown in the bottom left of the figure 34, there are three options: deterministic network, probabilistic network and bedpostx + probabilistic network.

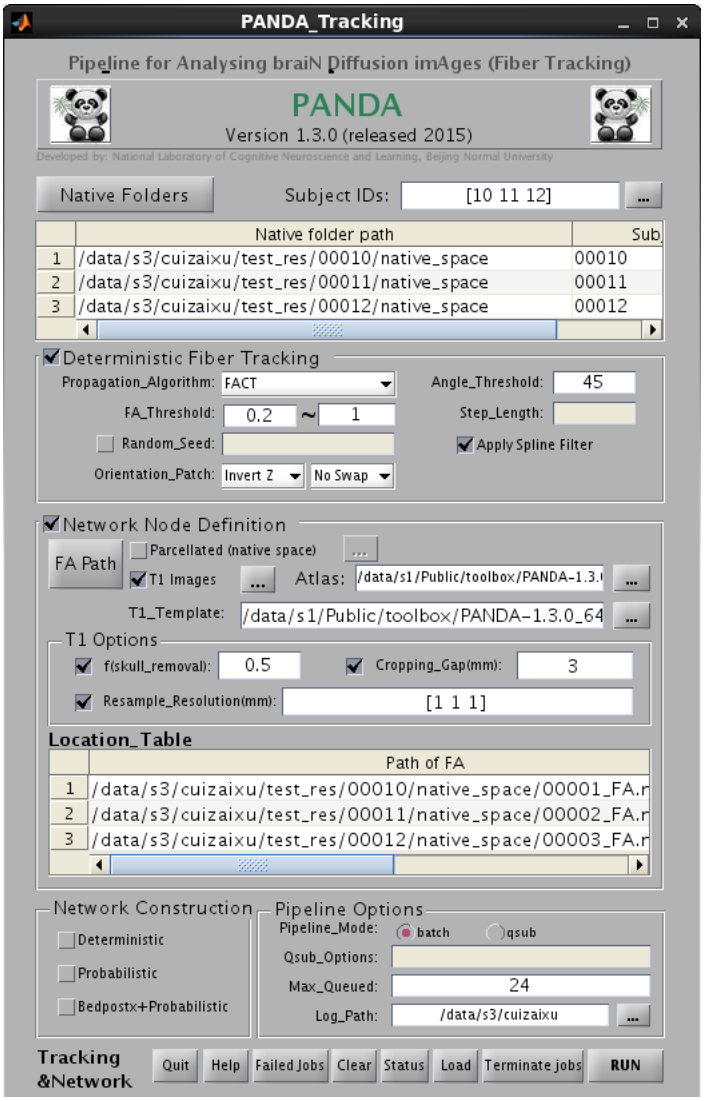

Figure 34. The GUI for the utility of fiber tracking and network construction.

Native folders

1) To do deterministic fiber tracking, deterministic network construction or bedpostx + probabilistic network construction, the full path of a folder containing four files as listed should be entered for each subject:
   (1) a 4D image named *data.nii.gz* containing diffusion-weighted volumes and volumes without diffusion weighting.
   (2) a 3D binary brain mask volume named *nodif_brain_mask.nii.gz*.
   (3) a text file named *bvecs* containing gradient directions for diffusion weighted volumes.
   (4) a text file named *bvals* containing b values applied for each volume acquisition.

   If PANDA is used for data preprocessing, please input the *native_space* folder under each subject's resultant folder.

   Note: Different subjects' native folders should be in different parent folders (e.g., /data/s1/**sub1**/native_folder1, /data/s1/**sub2**/native_folder2 and /data/s1/**sub3**/native_folder3). An error will occur if all the subjects' native folders are in the same parent fold (e.g., /data/s1/native_folder1, /data/s1/native_folder2 and /data/s1/native_folder3).
2) To do probabilistic network, please enter the full path of the resultant folder of bedpostx.

   If PANDA is used for bedpostx, please use the *native_space.bdepostx* folder under each subject's resultant folder.

Subject IDs

Assign an integer ID for each subject. If the data preprocessing was conducted using PANDA and users want to assign the same IDs as before, they can click the button on the right to load the ***.PANDA*** configuration.

Deterministic fiber tracking

Please refer to the **Tracking & Network parameters -> Deterministic fiber tracking** section.

Orientation patch

If data processing was done by PANDA, and you have already used the correct **Invert**

and **Swap** parameters in **Diffusion Opt**, here you should use **Invert Z** and **No Swap**. Otherwise, you should try all the probabilities to find the correct **Invert** and **Swap** parameters. Doing deterministic fiber tracking with a particular **Invert** and **Swap** parameter, and then open the fiber file (*.trk under the 'trackvis' folder) using trackvis (http://www.trackvis.org/). If the parameters are right, the fiber file should be similar to Figure 35, in which you can see the white matter structures (e.g., cingulum, corpus callosum) clearly. Also, an example of "result of wrong parameters" is presenting in Figure 36.

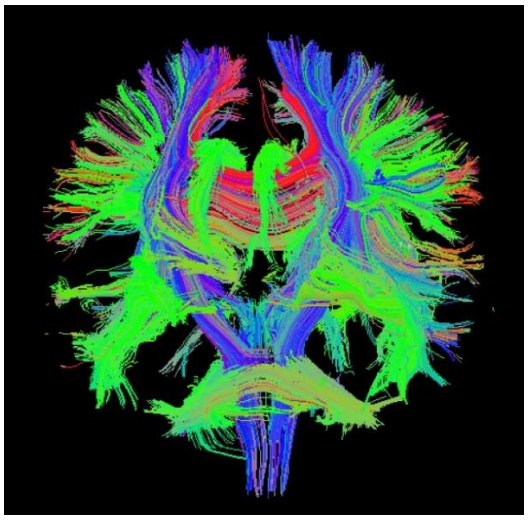

Figure 35. Whole brain white matter connections acquired by deterministic fiber tracking with correct Invert and Swap parameters.

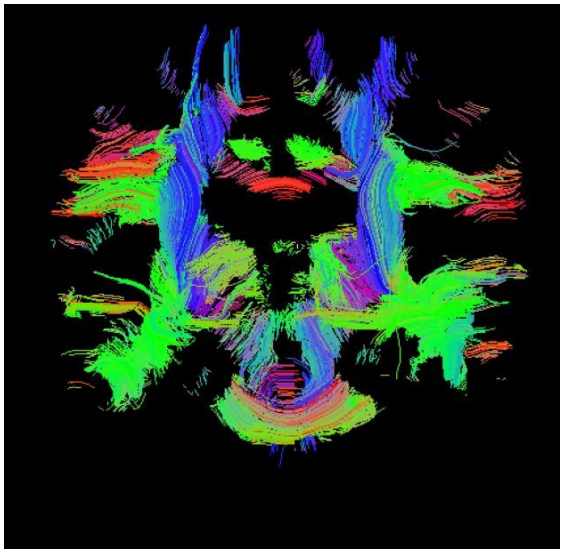

Figure 36. White matter connections acquired by deterministic fiber tracking with wrong Invert and Swap parameters.

Network node definition

FA path

The FA image in the individual space of each subject. If PANDA was used for data preprocessing, this file is stored in the native_space folder and the name is (*Prefix*)_(*SubjectID*)_FA.nii.gz.

Other parameters, please refer to **Tracking & Network parameters -> Network node definition** section.

RUN

Click this button to start the jobs. A folder named ***Tracking_logs*** is created in the *Log path* and a configuration file with suffix of ***.PANDA_Tracking*** is created in this folder, users can load this configuration file to check the job status after closing the GUI.

Status

Click this button, a table with the status of the jobs will show up.

Results

If the **deterministic fiber tracking** is selected, a folder named *trackvis* will be created for each subject. If **deterministic network construction** is selected, a folder named *Network* and a sub-folder named *Deterministic* will be created. If **probabilistic network construction** is selected, a folder named *Network* and a sub-folder named *Probabilistic* (*Network->Probabilistic*) will be created. If **Bedpostx + Probabilistic network construction** is selected, a folder named **.bedpostx* and *Network->Probabilistic* will be created. The folder *trackvis*, **.bedpostx* and *Network* are in the same parent folder of native folder for each subject.

4.3 Brain Parcellation

This utility is for parcellating the brain into multiple regions according to a prior gray matter atlas, where each region represents a network node.

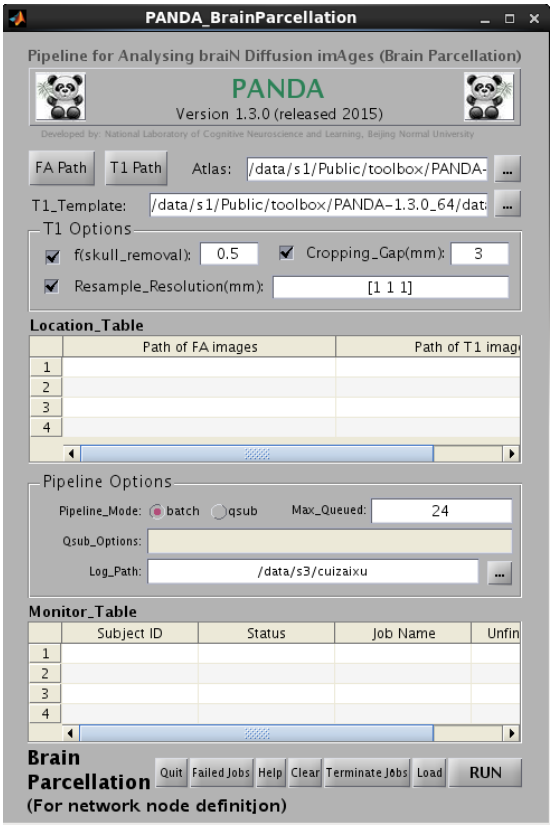

Figure 37. GUI for brain parcellation (network node definition).

FA Path

The FA image in the individual space of each subject. If PANDA was used for data preprocessing, this file is stored in the *native_space* folder and the name is (*Prefix*)_(*SubjectID*)_FA.nii.gz.

T1 Path

Path of T1-weighted structural images, which should be in NIfTI format (*.nii or *.nii.gz). The order of T1 images should be in accordance with the FA images. If MRIcron is used to convert T1 DICOM files into T1 NIfTI files. Then, three images will be created, and the image with *'co'* as prefix in the name is recommended.

Other parameters, please refer to **Tracking & Network parameters -> Network node definition** section.

RUN

Click this button to start running the jobs. A folder named ***BrainParcellation_logs*** will be created in the *Log path* and a configuration file with suffix of ***.PANDA_BrainParcellation*** will be created in this folder, and users can load this configuration file to check the job status after close the GUI.

Results

A file named ****_Parcellated_*.nii.gz*** will be created in the same parent folder of the FA image for each subject.

4.4 BedpostX

GUI for bedpostX, which runs Markov Chain Monte Carlo sampling to build up distributions on diffusion parameters at each voxel and creates all the files necessary for running probabilistic fiber tracking.

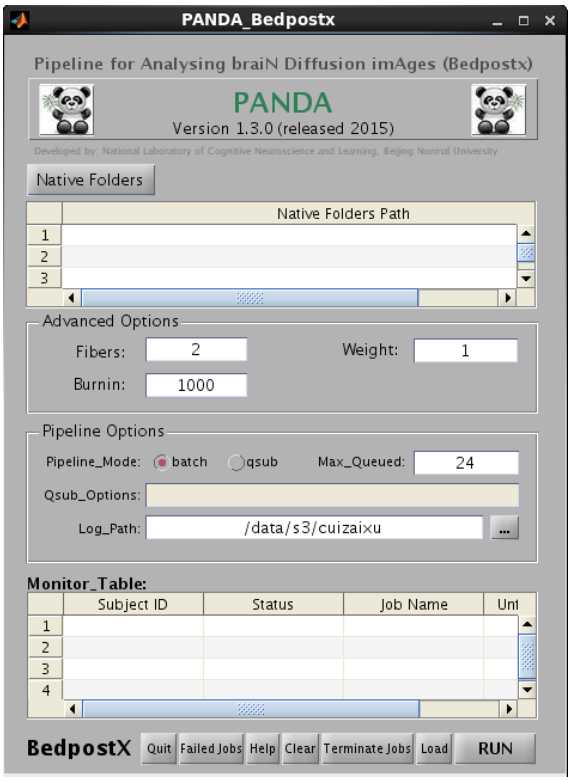

Figure 38. GUI for bedpostX.

Native folders

The full path of a folder containing four files as listed should be entered for each subject:

1) A 4D image named *data.nii.gz* containing diffusion-weighted volumes and volumes

without diffusion weighting.

2) A 3D binary brain mask volume named *nodif_brain_mask.nii.gz*.
3) A text file named *bvecs* containing gradient directions for diffusion weighted volumes.
4) A text file named *bvals* containing b values applied for each volume acquisition.

Also, if all the subjects' native folders are in the same parent fold, error will occur. Refer to **Utility Tracking & Network -> Native folder**.

Other parameters, refer to **Tracking & Network parameters -> Network construction -> Probabilistic**.

RUN

Click this button to start running the jobs. A folder named ***Bedpostx_logs*** will be created in the *Log path* and a configuration file with suffix of ***.PANDA_Bedpostx*** will be created in this folder, and users can load this configuration file to check the job status after close the GUI.

4.5 Tract-based Spatial Statistics (TBSS)

If you use full pipeline of PANDA and have selected the 'Apply TBSS' in the Diffusion Opt, all the TBSS procedure will be accomplished. In this situation, this utility is unnecessary and users can go to TBSS Randomise section. Otherwise, you can use this utility to do TBSS with the diffusion metric images ($1\times1\times1mm^3$ voxel size) in the standard space (Smith et al., 2006).

TBSS first averages all the subjects' FA images and acquires a skeletonized image from this average FA. Then, this skeletonized image was projected to each subject's standardized image (e.g., FA, MD, AD, RD and LDH).

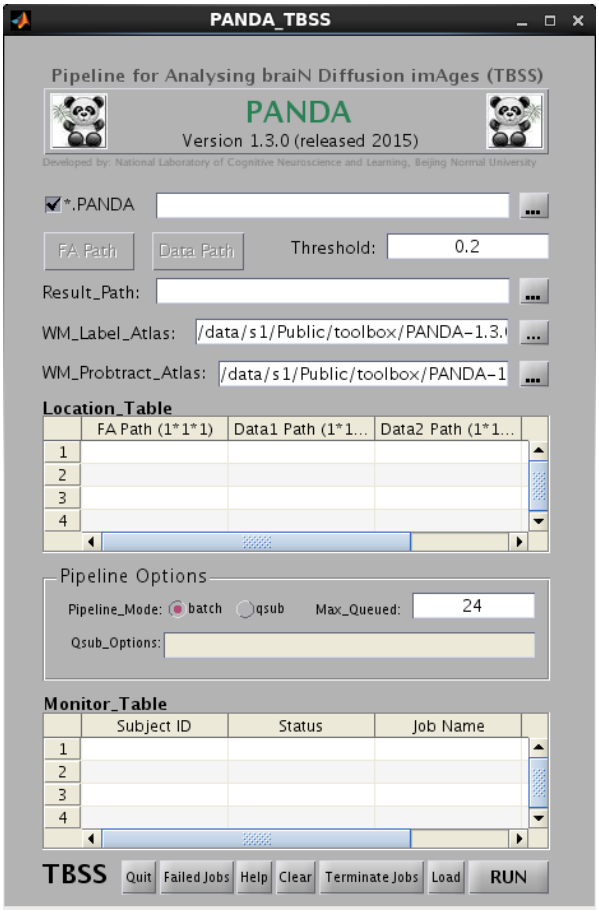

Figure 39. GUI for TBSS.

*.PANDA

If you use PANDA for data processing, please select ***.PANDA** configuration file and the appropriate input will be imported. The skeletons of FA, MD, AD, RD and LDH for each subject will be calculated.

FA Path

The full path of FA images with $1\times1\times1mm^3$ voxel size in the standard space. If the full pipeline of PANDA was used for process the data, this file is located in the *standard_space* folder, named (*Prefix*)_(*SubjectID*)_FA_4normalize_to_target_1mm.nii.gz.

Data Path

Input the diffusion image you want to project the mean skeleton to. The FA images are added by default. If you want to add MD, AD, RD, or LDH, please input these diffusion images with $1\times1\times1mm^3$ voxel size in the standard space. Click this button one time to

add one kind of images. For example, click this button to import all the MD images and then click this button again to import all the AD images. If the full pipeline of PANDA was used for process the data, the files needed can be found in the *standard_space* folder, named (*Prefix*)_(*SubjectID*)_MD_4normalize_to_target_1mm.nii.gz and (*Prefix*)_(*SubjectID*)_AD_4normalize_to_target_1mm.nii.gz.

Threshold

FA threshold is used to exclude the voxels in gray matter and CSF during the TBSS processing procedure. Default value is 0.2.

Result path

Path of folder storing the resultant files.

WM label atlas & WM Probtract atlas

Refer to **Diffusion parameters -> atlas**. Calculating regional average of each subject's skeleton according to prior white matter atlases.

RUN

Click this button to start the jobs. A configuration file with suffix of ***.PANDA_TBSS*** will be created in the *result path*, and users can load this configuration file to check the job status after close the GUI.

Results

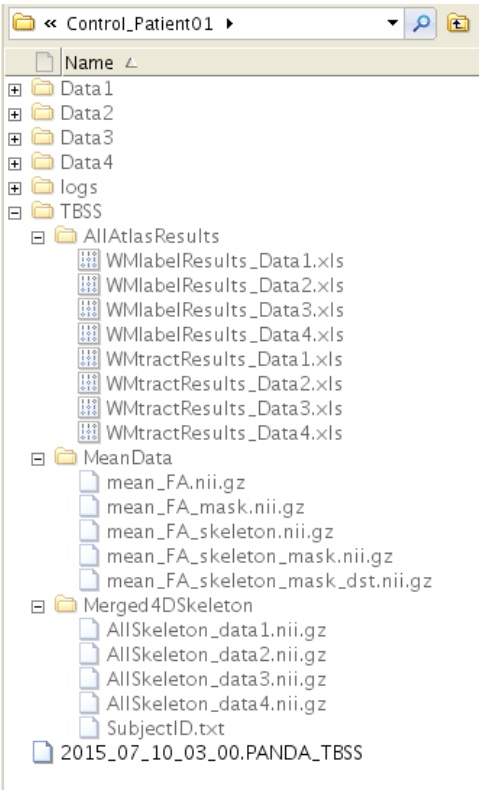

Figure 40. Results of TBSS preprocessing.

As shown in Figure 40, the 4D skeletons(i.e.AllSkeleton_data1.nii.gz) are located in the folder 'Merged4DSkeleton', which are the input of randomise statistics. In the folder 'MeanData', there is a mean FA skeleton mask image which is useful for randomise statistics, and also mean FA and mean FA skeleton which are useful for displaying of the statistical results.

In the folder 'AllAtlasResults', there are two Excel spredsheets for each metric. The Excel stored the regional average values of the subjects' skeletons according to the prior white matter atlas.

4.6 TBSS Randomise

Statistical analysis for 4D skeleton outputted from TBSS procedure. Please refer to http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/TBSS/UserGuide, http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/Randomise/UserGuide and http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FEAT/UserGuide.

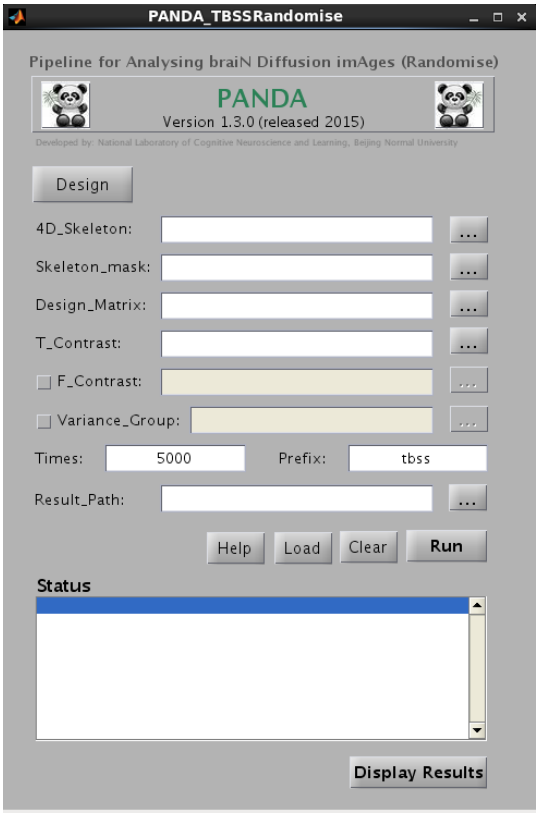

Figure 41. GUI for TBSS randomise.

Design

Design matrix is needed for randomise statistics. Open FSL, click Misc -> GLM Setup, then select 'Higher-level / non-timeseries design' to make the design matrix. For more information, please refer to http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FEAT/UserGuide.

4D skeleton

The 4D skeleton produced in the TBSS processing procedure. If PANDA is used for data processing, this file was in the folder '…/TBSS/MergedSkeleton'.

Skeleton mask

The mask of the skeleton. If PANDA is used for data processing, this file was located at '…/TBSS/MeanData/mean_FA_skeleton_mask.nii.gz'.

Design matrix

A text file containing the design matrix which contains all the predictors in the general linear model (GLM) that corresponds the experimental design and other effects to be

modeled. The filename should be with .mat suffix.

T contrast

A text file with a list of T-test contrast. The filename should be with .con as suffix.

F contrast

A text file contatining F-test constrast which combines individual T-tests contrasts. The filename should be with .fts as suffix.

Variance group

A text file offers variance group or so called exchangeability-block information which can be entered via the "Group" column in the GLM Setup GUI. The values is used to specify which data can be exchanged, that is, only data within the same block. The filename should be with .grp as suffix.

Times

The times of permutation.

Prefix

The prefix of the resultant files.

Result Path

The path of the folder storing all the resultant files.

RUN

Click this button to start the jobs. A configuration file with the suffix of ***.PANDA_TBSSRandomise*** will be created in the *result path*, and users can load this configuration file to check the job status after close the GUI.

Status

The running status will be displayed real time in the status box in the GUI. Also, a file named **'tbss.log'** is created, which update the running progress real time.

Note: Once the randomise statistics starts running here, it will not stop unless the computer is closed or it is finished. If the status table is stopped (may be due to the bugs in GUI), users can look up the **'tbss.log'** file in the resultant folder for the real-time

running status.

Results

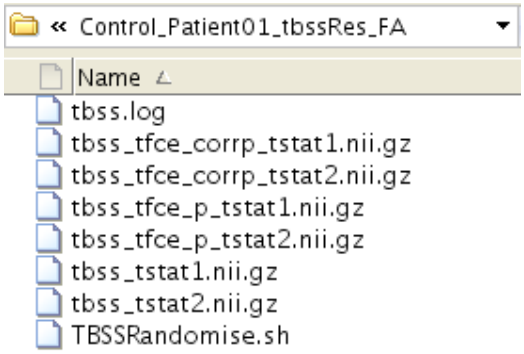

Figure 42. Results of TBSS randomise statistics (two-sample t-test).

The raw (unthresholded) tstat images are *tbss_tstat1* and *tbss_tstat2*. The uncorrected p images are *tbss_tfce_p_tstat1* and *tbss_tfce_p_tstat2*. The TFCE p-value images (fully corrected for multiple comparisons across space) are *tbss_tfce_corrp_tstat1* and *tbss_tfce_corrp_tstat2*. In the *p* map, the value is 1-p, so thresholding at .95 gives significant clusters.

Display Results

Click this button to show the statistical results of TBSS, a GUI as shown in Figure 43 will be open.

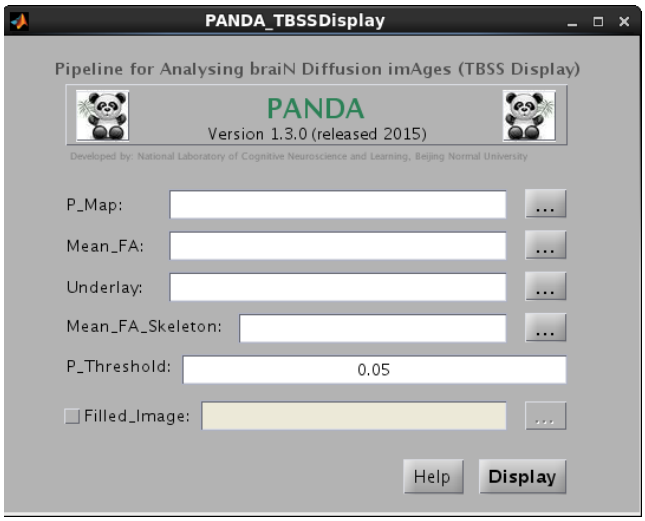

Figure 43. GUI for display TBSS statistics results.

P map

The p-value images (e.g., *tbss_tfce_corrp_tstat1.nii.gz*) acquired.

Mean FA

Located in the *'.../TBSS/MeanData/mean_FA.nii.gz'*.

Underlay

Mean FA image or T1 structural image.

Mean FA skeleton

Located in the *'.../TBSS/MeanData/mean_FA_skeleton.nii.gz'*.

Display

Firstly, the skeletonized results is 'thickened' using tbss_fill command and a file named ***_tbssfill.nii.gz*** is created (Figure 44). Then, FSLView is used to open the filled image, the mean FA skeleton and the mean FA.

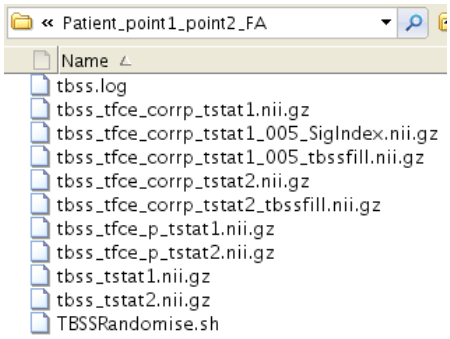

Figure 44. File **_tbssfill.nii.gz* is created for better visualization.

Results

The filled image *(*_tbssfill.nii.gz)* for better visualization is created. In addition, a file named **_SigIndex.nii.gz* is also created. It is a mask for significant regions. Users can use the **ROI-mean Extractor utility** with this mask and the original 3D skeleton images for each subject as input to extract the average value of this significant regions. May be you want to calculate the correlation between this average value and the behavioral scores.

Filled image

Calculating the filled image is time consuming. So if you have already acquired the tbss

filled image *(*_tbssfill.nii.gz)*, please check this checkbox and input the full path of the filled image.

As shown in Figure 45, input underlay image (T1 structural image or *mean FA image*), mean FA skeleton image (*.../TBSS/MeanData/mean_FA_skeleton.nii.gz*) and tbss filled image *(*_tbssfill.nii.gz)* and then click Display button, the statistical image will be displayed as Figure 46.

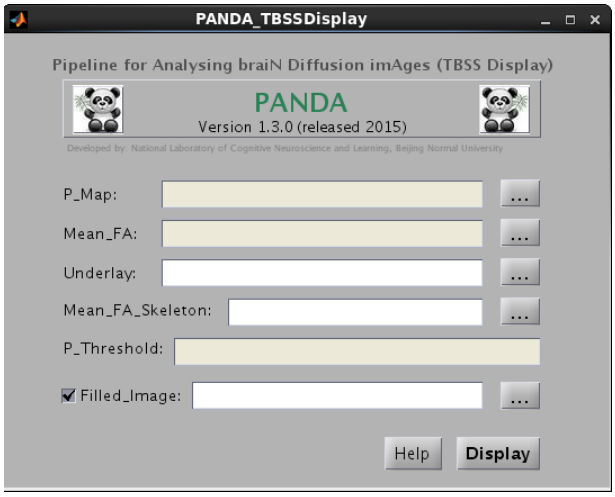

Figure 45. GUI for display TBSS statistics results (when filled image is selected).

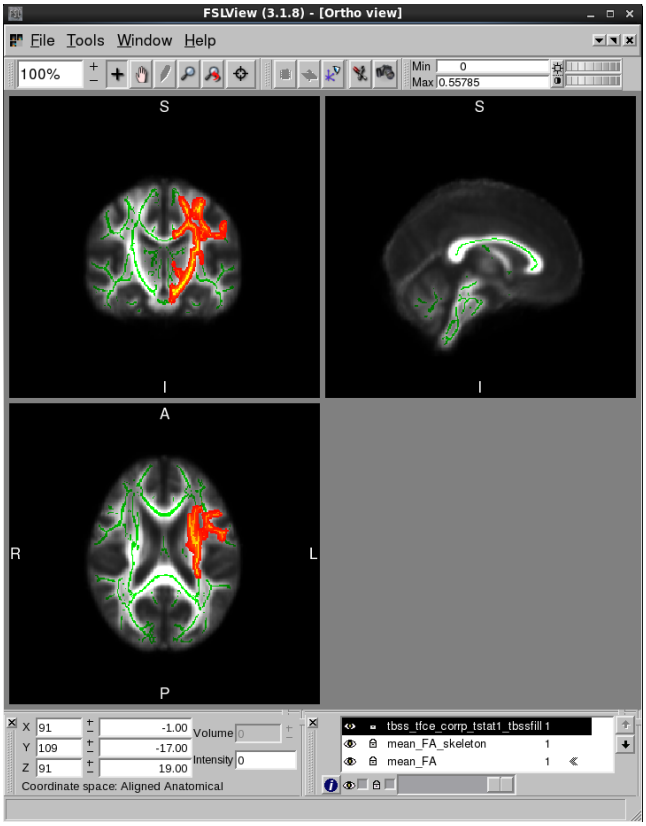

Figure 46. TBSS results displayed using FSLView. Here, mean FA was used as underlay, also mean FA skeleton also used as background, tbss filled image was visualized.

4.7 Test Bvecs

Diffusion weighted images are typically scanned with different gradient magnetic fields. The directions of these gradient magnetic fields are stored in the bvecs file and crucial for fiber tracking. However, the directions are in the coordinate of the scanner, and tensor calculating and probabilistic tracking in PANDA are implemented using FSL. The coordinate of the scanner and that of FSL may be different, thus we should modify the directions according to the coordinate of FSL. This utility is used to find the correct Invert and Swap parameter to adjust the bvecs. All the subjects with same scanning parameters should use the same Invert and Swap parameters. Therefore, we only need to test one subject.

Figure 47. GUI for test the correctness of bvecs.

DICOM/NIfTI path, **Result path**, **Subjects IDs** and **File prefix**, please refer to the **Basic input** of **full pipeline** of PANDA.

Orientation Patch

Invert means flipping the original value, e.g. Invert x means replacing the value of x direction with -x. Swap means exchanging the values of the two directions, e.g., Swap x/y means exchange the value of x direction and that of y direction. Generally, Swap is 'No Swap' but users should try to find the correct Invert parameter.

Try different Invert and Swap parameters, and click RUN. Open the subject's V1 image, which is *{Result_Path}/{Subject_ID}/*_V1.nii.gz*. As shown in Figure 48, open V1 image with FSLView. Click the 'i' button in the middle bottom of the FSLView to open the 'overlay information dialog'. Set *Lookup table options* as *'Random-Rainbow'* and *Display as option* with *'Lines (RGB)'*. If you can find some white matter anatomical structure (e.g., cingulum and corpus callosum) clearly, then your current Invert and Swap parameters are correct.

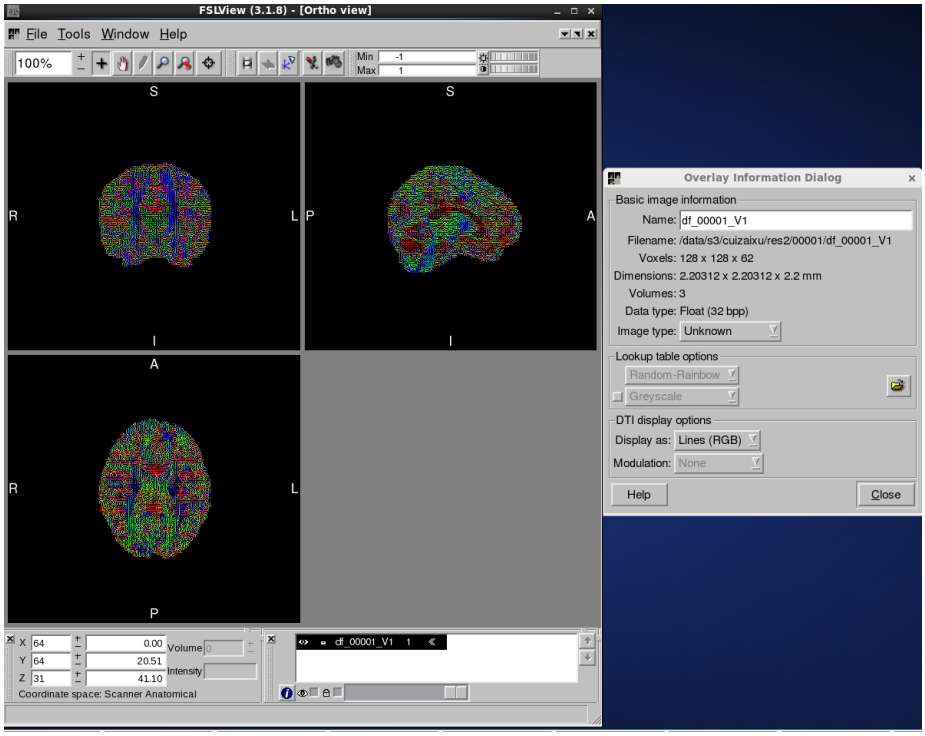

Figure 48. The principle direction (V1) image.

4.8 Brain Extraction (T1)

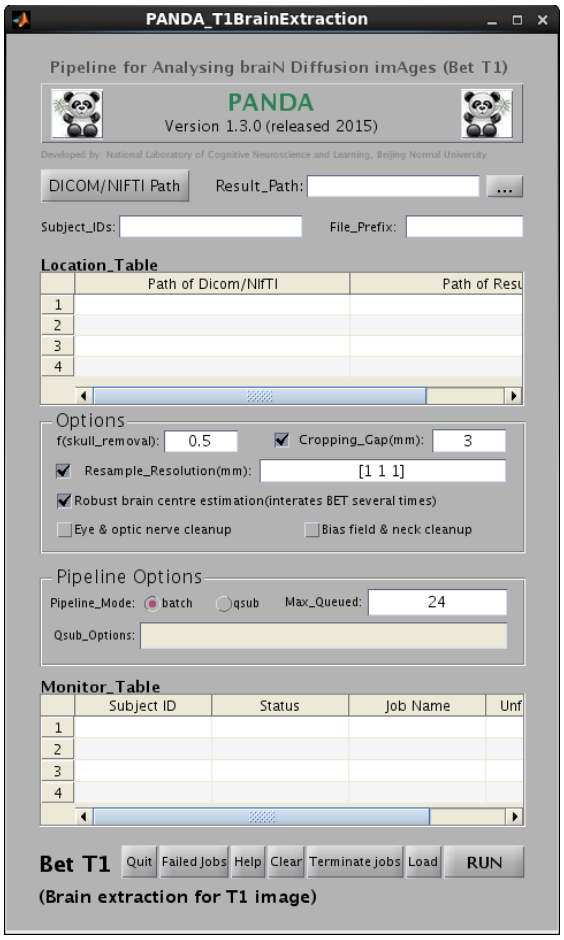

Figure 49. GUI for brain extraction of T1 images.

DICOM/NIFTI path

Full path of the Subjects' folders, under each folder there should be DICOM or NIFTI files. If NIFTI image is used, there should be only one file under the folder, which is converted from DICOM files.

Result path, **Subjects IDs** and **File prefix**, refer to **Basic input** of the **Full Pipeline**.

f (skull_removal), **Cropping gap** and **Resample resolution**, refer to **Tracking & Network parameters -> Network node definition**.

Robust brain centre estimation

By iterating brain extraction many times, the center-of-gravity should move up each time towards the true center, resulting in a better final estimate.

Eye & optic nerve cleanup

This option attempts to cleanup residual eye and optic nerve voxels, can produce better results but run much slower.

Bias field & neck cleanup

This attempts to reduce image bias and residual neck voxels, can produce better results but run much slower.

RUN

Click this button to start running the jobs. A configuration file with suffix of ***.PANDA_BetT1*** will be created in the *result path*, and users can load this configuration file to check the job status after close the GUI.

Results

A folder named *'T1'* will be created in the resultant folder. If *Cropping* and *Resample* are not selected, the final images is *'*_t1_swap_bet.nii.gz'*. If *Cropping* is selected, the final image is *'*_t1_swap_bet_crop.nii.gz'*. If the *Resample* is selected, the final image is *'*_t1_swap_bet…_resample.nii.gz'*.

4.9 DICOM Sorter

Typically, various series data (e.g., T1 structural, diffusion, functional) are mixed in one folder when they are exported from the MRI scanner. Before analyzing one particular modality, we should separate different modalities/sequences. This utility is used for separate files of various modalities into different folders.

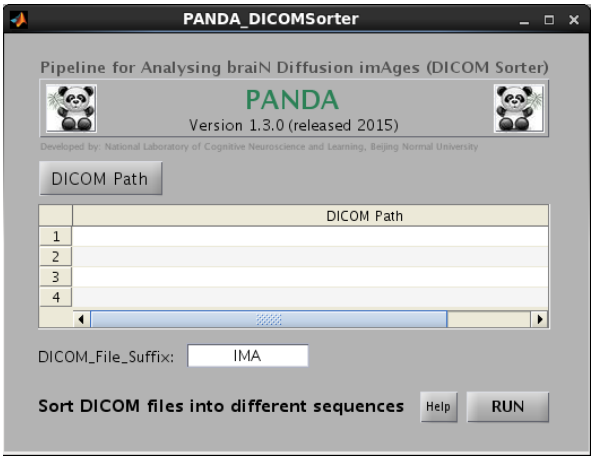

Figure 50. The GUI of the utility for sorting DICOM files into various series.

DICOM path

The path of subjects' folders containing all the DICOM files.

DICOM file suffix

The suffix of the DICOM files (e.g., IMA, dcm, etc.). If no suffix, here should be left empty.

RUN

After clicking this button, sub-folders will be created in the folder users defined as the input path, each storing one modality.

4.10 DICOM->NIfTI

Convert DICOM files into NIfTI images.

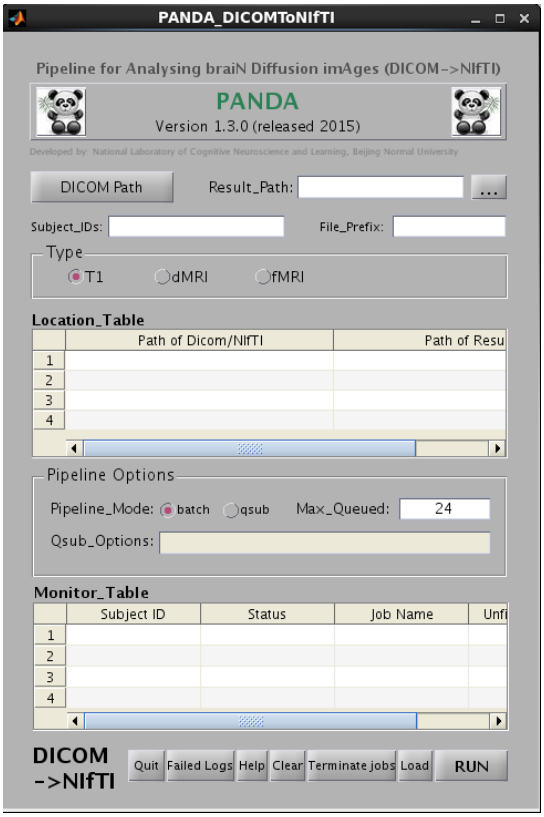

Figure 51. The GUI of the utility for converting DICOM files to NIfTI images.

DICOM path

T1 or fMRI: Full path of subjects' folders, under which there should be DICOM files.

dMRI: Make a separate folder for each subject (subject-folder) first. Then, for each folder, put all DICOM files of one DWI acquisition into one sub-folder of subject-folder. Here, the full path of subject-folder should be the input. Refer to **Preparing raw data (for Full Pipeline) -> DICOM format**.

Type

Support T1 structural MRI, diffusion MRI and functional MRI data.

RUN

Click this button to start running the jobs. A configuration file with suffix of ***.PANDA_DICOMNIfTI*** will be created in the *result path*, and users can load this configuration file to check the job status after closing the GUI.

Results

Figure 52 represents the resultant files organization of this utility.

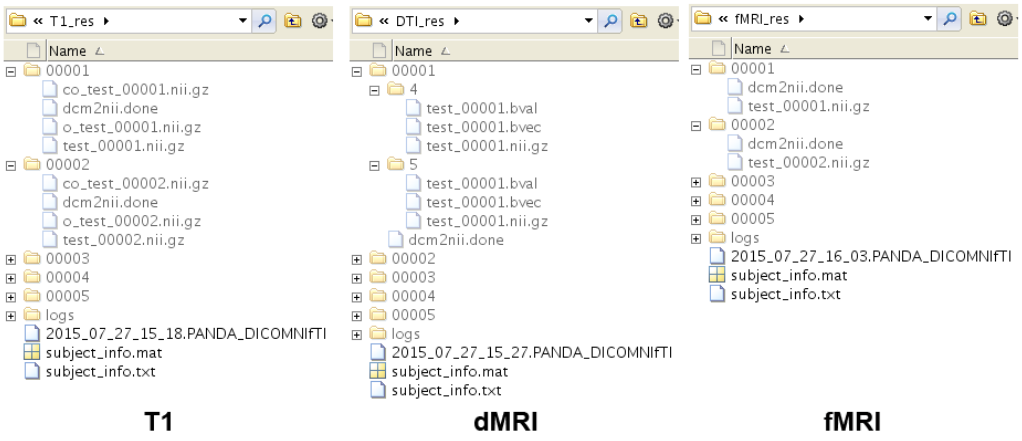

Figure 52. The results of utility of DICOM -> NIfTI.

T1: Three NIfTI images will be created for each subject. *{Prefix}_{Subject_ID}.nii.gz* is the NIfTI directly converted from DICOM files. *o_{Prefix}_{Subject_ID}.nii.gz* means reorienting the image *{Prefix}_{Subject_ID}.nii.gz* to the nearest orthogonal plane, *co* means cropping the neck in the image *o_{Prefix}_{Subject_ID}.nii.gz*.

dMRI: One folder and several sub-folders (the quantity of sub-folders is the same as the acquisitions) will be created for each subject. Under each sub-folder, there are three files: *{Prefix}_{Subject_ID}.nii.gz* is the 4D NIfTI image, *{Prefix}_{Subject_ID}.bval* contains b values and *{Prefix}_{Subject_ID}.bvec* file contains diffusion weighted directions

fMRI: A 4D NIfTI image (*{Prefix}_{Subject_ID}.nii.gz*) is created for each subject.

4.11 Resample NIfTI

Resample NIfTI images to a certain voxel size.

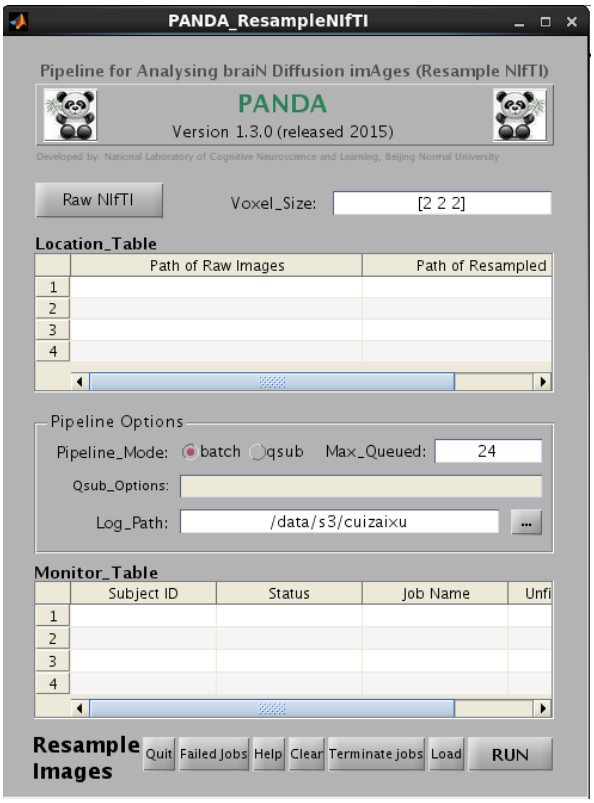

Figure 53. GUI for resampling NIfTI images.

Raw NIfTI

Path of NIfTI images (.nii or .nii.gz) to be resampled.

Voxel size

The final resolution you want, e.g., [2 2 2] means 2×2×2 mm^3.

RUN

Click this button to start running the jobs. A configuration file with suffix of ***.PANDA_Resample*** will be created in the *log path*, and users can load this configuration file to check the job status after closing the GUI.

Results

Resultant files are in the same folder of the original files, with *'r'* in the prefix of the file name.

4.12 Image Converter

There are three NIfTI formats (i.e., .hdr/img, .nii, .nii.gz).

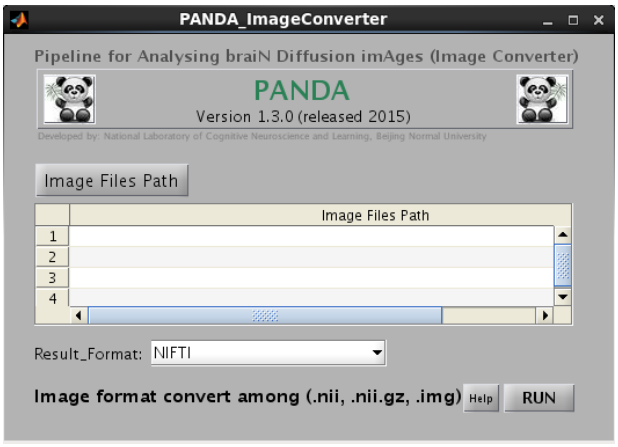

Figure 54. The GUI of the utility for converting among three NIfTI formats (.hdr/.img, .nii, .nii.gz).

Image files path

The full path of NIfTI images to be converted.

Result format

Three options, *NIFTI* means .nii format, *NIFTI_GZ* means .nii.gz format and *NIFTI_PAIR* means .hdr/.img format.

Results

The resultant images will **replace** the original images.

4.13 Image Smoother

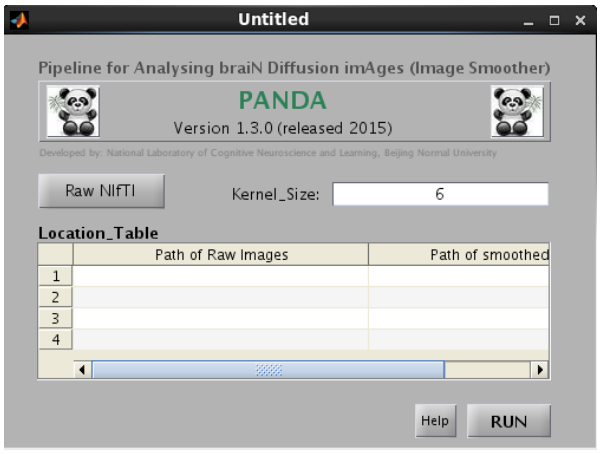

Figure 55. The GUI of the utility for smoothing NIfTI images.

Raw NIfTI

The full path of NIfTI images (.nii or .nii.gz) to be smoothed.

Kernel Size

Gaussian kernel size for smooth, default is 6 mm.

4.14 Merge NIfTI

This utility is for merging a series of 3D NIfTI images into a 4D images.

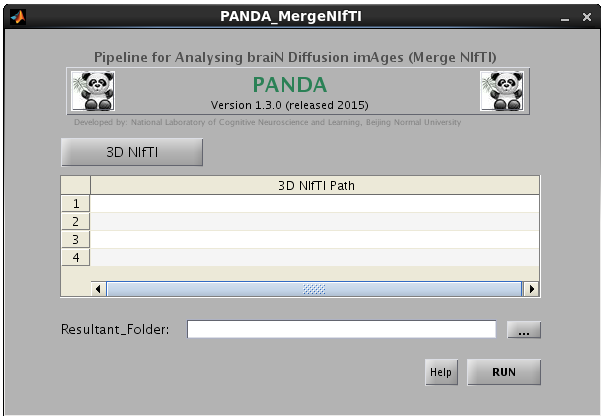

Figure 56. The GUI of the utility for merging 3D NIfTI images to a 4D NIfTI image.

3D NIfTI

The path of all 3D NIfTI images to merge (.nii or .nii.gz format).

Note: The resolution of all 3D NIfTI images should be the same.

Results

A file named *Merged4DData.nii.gz* will be created in the resultant folder. Also, a *subjectID.txt* represents the order of subjects' images in the 4D skeleton is created.

4.15 White Matter Mask

White matter mask can be used to restrict the statistical analysis in white matter. It can be acquired through thresholding the FA images. Typically, we average all subjects' normalized FA images and then thresholding the average FA image.

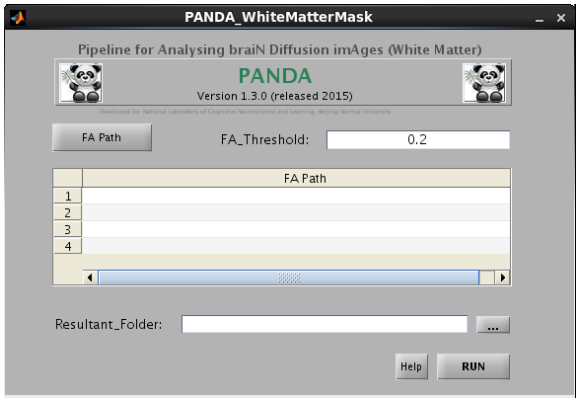

Figure 57. The GUI of the utility for calculating white matter mask.

FA Path

The full path of all subjects' FA images.

Note: the FA images should be in the standard space.

FA threshold

Typically, the tissue with small FA are thought to be gray matter or CSF. The tissue with FA smaller than this threshold will be excluded from the white matter mask.

Results

A file named '*WM_mask.nii.gz*' is created in the resultant folder, which is the white matter mask.

4.16 ROI-mean Extractor

Calculating the regional average value of the images for each ROI in the index mask image.

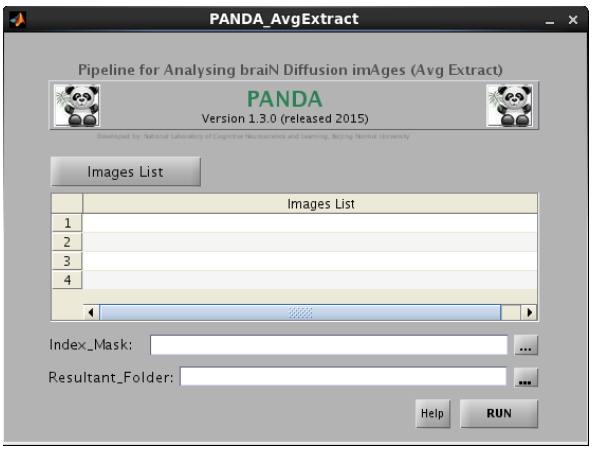

Figure 58. The GUI of the utility for calculating regional average according to index mask image.

Images list

Full path of NIfTI images (.nii, .nii.gz).

Index mask

A NIfTI image (.nii, .nii.gz) with several ROIs, each with a unique integer ID.

Note: the resolution of the *index mask* image should be the same with that of the *image list* users input.

Results

For example, an index mask image with two regions was input, the values of which are 3, 5, respectively. Then, the regional average of these two regions are calculated and an Excel named *AvgExtract.xls* is created in the resultant folder. As shown in Figure 59, row is subject's image and column is the region index, the value is the regional average.

A	B	C
	Cluster.index=3	Cluster.index=5
/data/s3/cuizaixu/PANDA_DTI_res/0	0.556938	0.614073
/data/s3/cuizaixu/PANDA_DTI_res/0	0.583939	0.629578
/data/s3/cuizaixu/PANDA_DTI_res/0	0.59103	0.617493
/data/s3/cuizaixu/PANDA_DTI_res/0	0.545624	0.597588
/data/s3/cuizaixu/PANDA_DTI_res/0	0.521454	0.558232
/data/s3/cuizaixu/PANDA_DTI_res/0	0.550224	0.622303
/data/s3/cuizaixu/PANDA_DTI_res/0	0.552647	0.600508
/data/s3/cuizaixu/PANDA_DTI_res/0	0.559051	0.587487
/data/s3/cuizaixu/PANDA_DTI_res/0	0.592552	0.63458
/data/s3/cuizaixu/PANDA_DTI_res/0	0.545168	0.582283
/data/s3/cuizaixu/PANDA_DTI_res/0	0.559373	0.588507
/data/s3/cuizaixu/PANDA_DTI_res/0	0.554699	0.599163
/data/s3/cuizaixu/PANDA_DTI_res/0	0.589742	0.637091
/data/s3/cuizaixu/PANDA_DTI_res/0	0.556226	0.589136

Figure 59. The regional average values calculated according to the index mask.

4.17 Cluster Locater

After statistical comparisons, locating the statistical significant clusters is essential. This utility is used to locate the cluster image according to prior white matter or gray matter atlas.

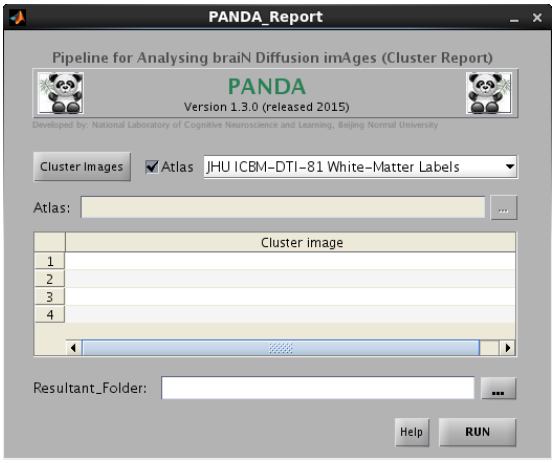

Figure 60. The GUI of the utility for report clusters.

Cluster images

The statistical image after thresholding (.nii or .nii.gz format).

Atlas

Here, we provide five selections:

1) *JHU ICBM-DTI-81 White-Matter Labels*: the image located in the {PANDAPath}/data/atlases/rICBM_DTI/rICBM_DTI_81_WMPM_FMRIB58.nii.gz.

2) *JHU White-Matter Tractography Atlas*: the image located in the {PANDAPath}/data/atlases/rICBM_DTI/JHU_ICBM_tracts_maxprob_thr25_1mm.nii.gz.

3) *Automated Anatomical Labeling Atlas*: the image located in the {PANDAPath}/data/atlases/ForReport/AAL_1mm.nii.gz.

4) *Harvard-Oxford Atlas*: the image located in the {PANDAPath}/data/atlases/ForReport/HOA_112_1mm.nii.gz.

5) *Brodman Atlas*: the image located in the {PANDAPath}/data/atlases/ForReport/brodmann.nii.gz.

Also, users can input any atlas they need.

Results

A folder named **'Report'** with an Excel will be created in the resultant folder. As shown in Figure 61, there are four columns: the index of the cluster, the quantity of voxels in the cluster, the atlas regions this cluster involves and the quantity of voxels in this

cluster overlapped with each atlas region.

A	B	C	D
Index	voxel size in total	region name	voxel size
1	1834	Splenium.of.corpus.callosum	345
		Cingulum.(hippocampus).L	44
		Cingulum.(cingulate.gyrus).L	40
		Posterior.thalamic.radiation.(include.optic.radiation).L	36
		Fornix.(cres)./.Stria.terminalis.(can.not.be.resolved.with.current.resolution).L	35
		Cingulum.(cingulate.gyrus).R	16
		Sagittal.stratum.(include.inferior.longitidinal.fasciculus.and.inferior.fronto-occipital.fasciculus).L	13
		Uncinate.fasciculus.L	11
		Superior.longitudinal.fasciculus.L	3
		Posterior.corona.radiata.L	2
		Body.of.corpus.callosum	1
		Inferior.fronto-occipital.fasciculus.L	1
2	1805	Body.of.corpus.callosum	400
		Genu.of.corpus.callosum	300
		Superior.corona.radiata.L	64
		Cingulum.(cingulate.gyrus).L	53
		Anterior.corona.radiata.L	23
		Anterior.corona.radiata.R	19
3	1197	Superior.longitudinal.fasciculus.R	84
		Anterior.corona.radiata.R	2
4	738	Posterior.thalamic.radiation.(include.optic.radiation).R	135
		Splenium.of.corpus.callosum	124
		Tapetum.R	65
		Posterior.corona.radiata.R	24
		Cingulum.(hippocampus).R	10

Figure 61. The results of cluster locater.

4.18 ROI-mask Extractor

Extract particular ROIs from a prior atlas and assign these ROI with particular labels. For example, if we want to construct brain network with several particular ROIs of AAL atlas rather than all 116 regions, we can use this utility to extract the ROIs we care about. Additionally, this utility is useful for visualize the atlas-based statistical results. After statistical analysis of the data in the Excel under *{Result_Path}/AllAtlasResults*, may be several regions are significant, then we can extract these regions from the white matter atlas (e.g., WM label atlas, WM protract atlas, etc.) using this utility. Moreover, we can assign some values to the ROI we extract, which is useful to display the statistical results. *For example, we compared the mean FA of 50 regions in WM label atlas between two groups and found three tracts (ROIs) represented significant differences. We can use this utility to display the statistical map of this comparison. We can extract the three tracts (ROIs) from the atlas, assign the t-value to this three tracts (ROIs) and displayed it with FSLView.*

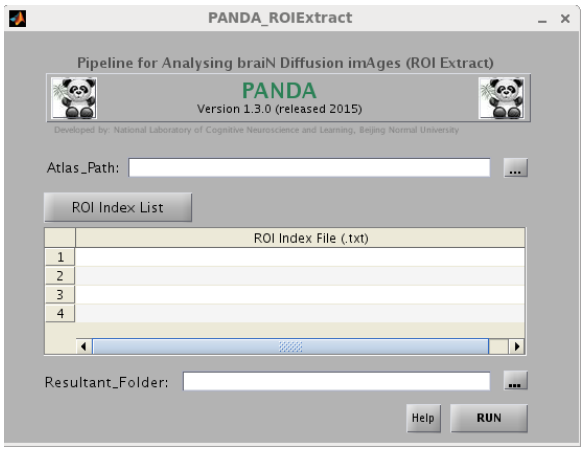

Figure 62. The GUI of the utility for extracting ROIs from the prior atlas.

Atlas path

The full path of atlas (e.g., white matter atlas, AAL atlas, etc.).

ROI index list

List of .txt files, which have one or two columns. The first column is the index of ROIs to be extracted and the second column (optional) represents values to be assigned to these ROIs. As shown in Figure 63, the left .txt means we extracting the ROIs with IDs of 6, 8, 9, 23 and 45 from the atlas, the right .txt means extracting 3, 5, 6, 7, 8 th regions in the atlas and assign these regions with values of 3.4, 5.6, 2.4, 1.6 and 7.8.

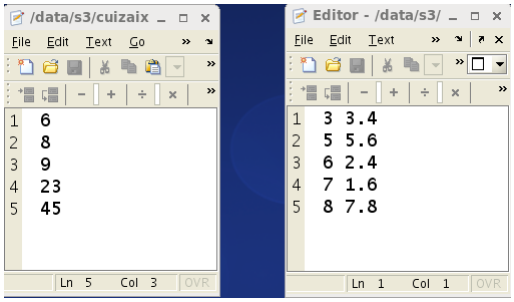

Figure 63.Two examples of the ROI index files (.txt format).

Results

A NIfTI image named *'*_Extract.nii.gz'* is created in the resultant folder.

4.19 Between-atlas mapping

This utility is for mapping high-resolution atlas (e.g., random 1024 atlas) or functional

atlas (e.g., Craddock atlas) to anatomical atlas (e.g., AAL 116 atlas). Typically, there is no exact name for the regions of the high-resolution and functional atlases. However, sometimes we need to locate these regions. To this end, we can map high-resolution and functional atlas to prior anatomical atlas (e.g., AAL atlas).

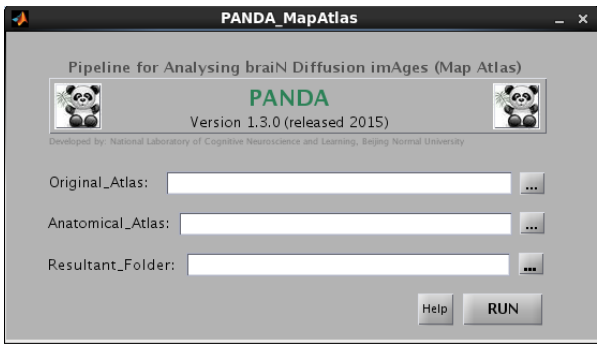

Figure 64. The GUI of the utility for mapping atlas.

Original atlas

The atlas users want to locate region names (e.g., random 1024 atlas).

Anatomical atlas

The path of the anatomical atlas (e.g., AAL).

Results

A file named *MapAtlas.txt* is created in the resultant folder (Figure 64). For example, if the original atlas is a random 1024 atlas, then there will be 1024 lines in this .txt file. As shown in Figure 65, the second line

0002 01 0.291 57 0.709

means that 29.1% of the 2th region in the random 1024 atlas locates in the 1th region in AAL atlas (the *anatomical atlas* is set AAL atlas), while 70.9% locates in the 57th region in AAL atlas.

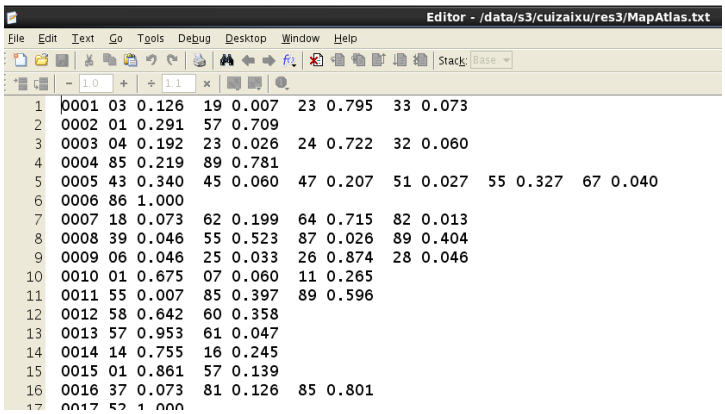

Figure 65. Results of mapping a random 1024 atlas to AAL 90 atlas.

4.20 File Copyer

This utility is for copying plenty of files into a particular folder. For example, the results PANDA produced are under each subject's personal folder. However, to do statistical analysis, we always need to move one particular file (e.g., the *_s6mm.nii.gz in *standard_space* folder of each subject's folder) of all subjects into the same folder.

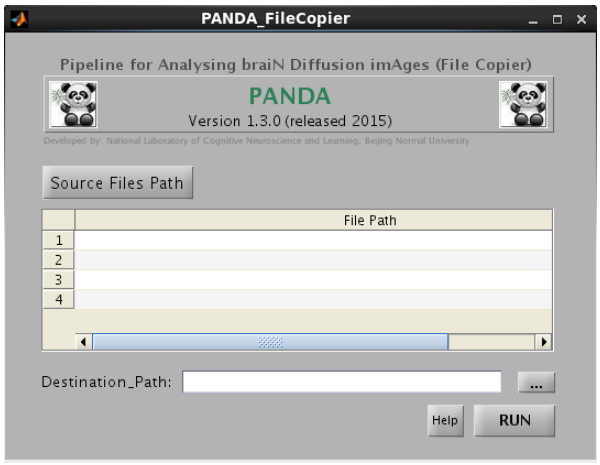

Figure 66. The GUI of the utility for copying files into one particular folder.

Source files path

Select all the files to copy.

Destination path

The path of the folder users want to move the files to.

5 Files/Directories selection

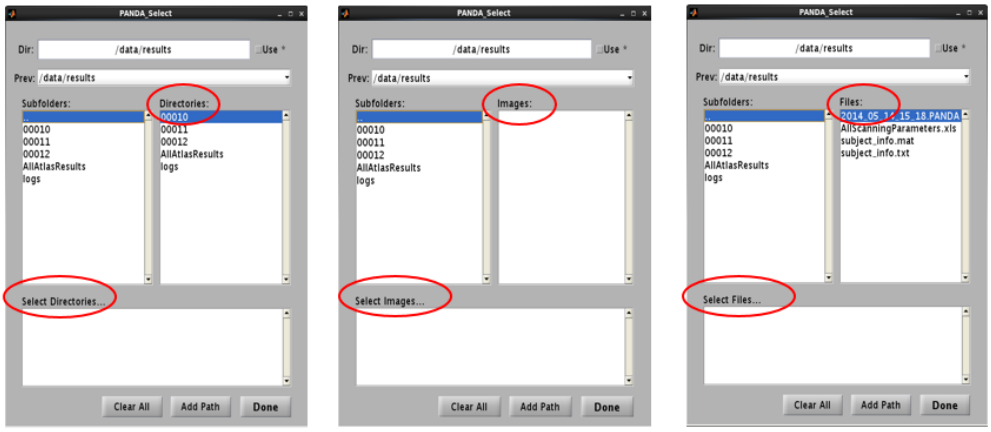

Figure 67. The GUI for selecting files, images or directories.

Dir

Current directory.

Prev

The list of directories users have selected.

Subfolders

Subfolders under current directory. Users can click the folder name here to change the current directory.

Directories/Images/Files

Directories, images or files to be selected.

Selected Directories/Images/Files

The Directories, images or files users selected.

Add Path

If users have already stored all the paths elsewhere (e.g., Excel), then they can click this button. A box will be opened (Figure 68), users can copy all the paths in Excel to the box and click ‘OK’ button.

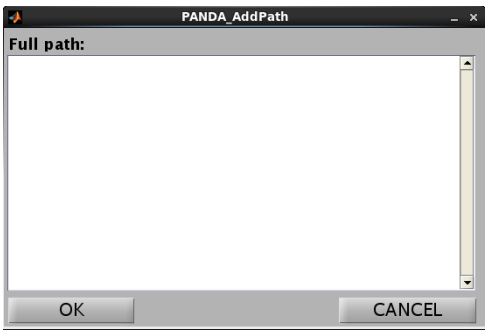

Figure 68. The box for pasting the paths.

Use *

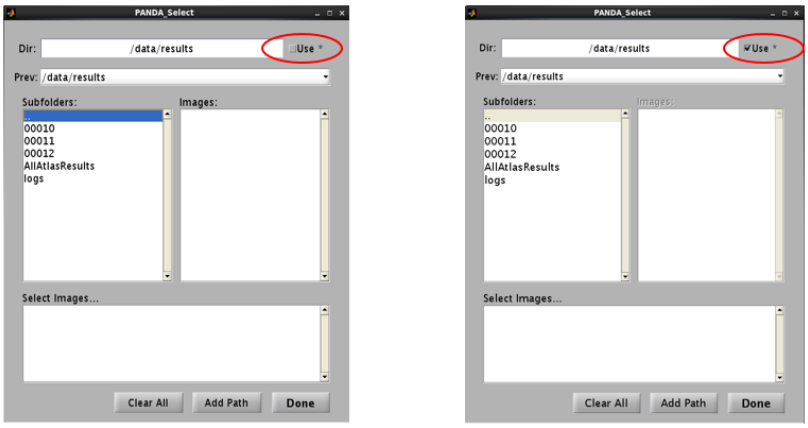

Figure 69. Two modes of using Files/Directories selection.

As shown in Figure 70, there are three folders under /data/s3/cuizaixu/LDHUtility, named *00001*, *00002* and *00003*. Under each folder, there are a folder 'transformation' and may files/images. Now, we want to select all the files with path like '*06LDHs*1mm.nii.gz' under the three folder. If 'Use *' is used (Figure 69), then we can select the files we need in one time.

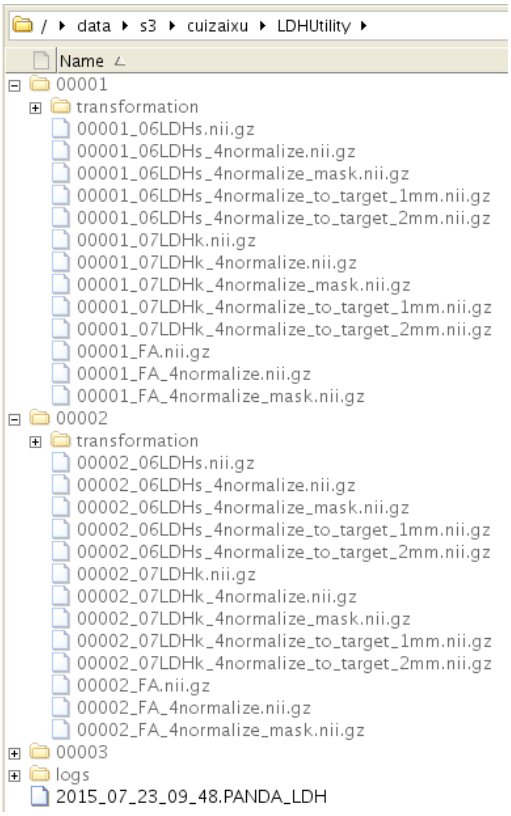

Figure 70. An example for using ‘Use *’.

As shown in Figure 70, select ‘Use *’ first. Then, input an expression (/data/s3/cuizaixu/LDHUtility/*/*06LDHs*1mm*) in the Dir box and click Enter. Then, all the three files with path like ‘*06LDHs*1mm.nii.gz’ are selected.

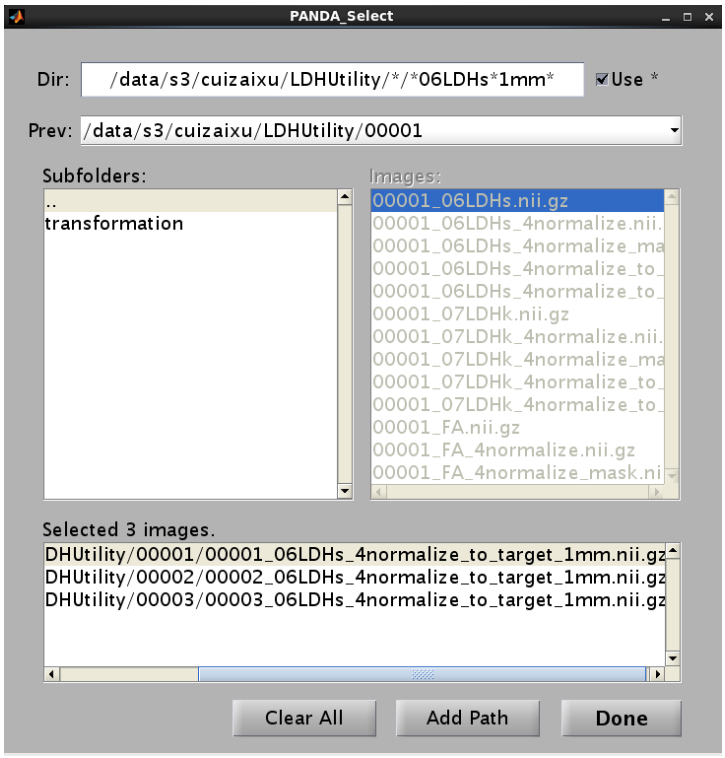

Figure 71. Select all the files with path like '*06LDHs*1mm.nii.gz' in Figure 70.

In this simplified example, there are only three folders. If there are hundreds of folders, users can also select all the files with path like '*06LDHs*1mm.nii.gz' in one time and the time is saved significantly.

Also, if we input '/data/s3/cuizaixu/LDHUtility/*/transformation', then all the folders named 'transformation' in Figure 68 are selected. If we input '/data/s3/cuizaixu/LDHUtility/*/*FA.nii.gz', then all the three images named *FA.nii.gz are selected.

6 Appendix

6.1 FSL Installation Guide

Note:

1) If you use fsl for PANDA, please download Linux centos version for Linux OS (Centos, RedHat, Ubuntu, Fedora, etc.) and MAC version of MAC OS in the website: http://fsl.fmrib.ox.ac.uk/fsldownloads/fsldownloadmain.html.
2) Don't use Ubuntu/Debian version FSL, PANDA will not work with it.

Installation in Linux (Ubuntu, Centos, etc.)

Copy fsl to /home/username

Open a terminal (Ctrl + Alt + T)

Step 1: Switch to root user

sudo su

Step 2: Create a folder named 'Software' under /opt

mkdir /opt/software

Step 3: Copy fsl to /opt/Software

For example, the path of fsl is /home/username/fsl-5.0.0-centos5_64.tar.gz

cp /home/username/fsl-5.0.0-centos5_64.tar.gz /opt/software

Step 4: Go to /opt/Software directory

cd /opt/software

Step 5: Extract the package

tar zxvf fsl-5.0.0-centos5_64.tar.gz

Step 6: Write the environment variables to system file

(Copy the commands below to terminal)

(This step is quite important)

(Note: There is a space after the first '.' in the second command)

```
echo "FSLDIR=/opt/software/fsl" >> /etc/profile
echo ". \${FSLDIR}/etc/fslconf/fsl.sh" >> /etc/profile
```

echo "PATH=\${FSLDIR}/bin:\${PATH}" >> /etc/profile

echo "export FSLDIR PATH" >> /etc/profile

Step 7: Reboot the computer

Open a terminal and input fsl, FSL GUI will open.

And PANDA will work well.

Installation in MAC

Open a terminal

Step 1: Copy fsl..tar.gz to /Applications folder

Step 2: double click this package to extract it

Step 3: Go to personal directory, input following command to the terminal

cd

Step 6: Write the environment variables to .bash_profile

(Copy the commands below to terminal)

(This step is quite important)

(Note: There is a space after the first '.' in the second command)

echo "FSLDIR=/Applications/fsl" >> .bash_profile

echo ". \${FSLDIR}/etc/fslconf/fsl.sh" >> .bash_profile

echo "PATH=\${FSLDIR}/bin: \${PATH}" >> .bash_profile

echo "export FSLDIR PATH" >> .bash_profile

Open a new terminal and input fsl, FSL GUI will open.

And PANDA will work well.

6.2 Matlab Installation Guide

Installation in Linux (Ubuntu, Centos, etc.)

Suppose the installation file is named 'MatlabR2012a.ISO'.

Step 1: Put it under the path '/home/username'.

So, the path of matlab package is '/home/username/MatlabR2012a.ISO'

Step 2: Switch to root user, open a terminal and input the following command into the terminal

sudo su

(input password of the user and click enter, the password will not display)

Step 3: Mount matlab package into path '/mnt'

mount -o loop /home/username/MatlabR2012a.ISO /mnt

Step 4: Enter path '/mnt'

cd /mnt

Step 5: Install

./install

A GUI for installation will open, and please install Matlab in the directory '/opt/Matlab'.

Step 6: Add the path of Matlab to the Linux environment variable 'PATH' **(This step is quite important)**

echo "PATH=/opt/Matlab/bin:\${PATH}" >> /etc/profile

echo "export PATH" >> /etc/profile

Reboot the computer.

Enter 'matlab' in the terminal, and then matlab will open.

Installation in MAC

Install Matlab to /Applications directory, such as /Applications/MATLAB_R2012a.app. Then, we should write the environment variables to .bash_profile.

Open a terminal

Step 1: Go to personal directory, input following command to the terminal

cd

Step 2: Copy the commands below to terminal

(This step is quite important)

echo " PATH=/Applications/MATLAB_R2012a.app /bin: \${PATH}" >> .bash_profile

echo "export PATH" >> .bash_profile

Open a new terminal and input 'matlab', Matlab GUI will open.

Note:

Users should open Matlab through terminal to make PANDA work well.

6.3 PSOM

The pipeline system for Octave and Matlab (PSOM) is a lightweight library to manage complex multi-stage data processing under Linux, Windows and Mac OSX. A pipeline is a collection of jobs, i.e., Matlab or Octave codes with a well identified set of options that are using files for inputs and outputs (Bellec et al., 2012). PSOM can handle smoothly pipelines with thousands of jobs involving tens of thousands of files, and distribute those amongst hundreds of processors.

PSOM can automatically offer the following services:

1) Run jobs in parallel using multiple CPUs or within a distributed computing environment.
2) Generate log files and keep track of the pipeline execution. These logs are detailed enough to fully reproduce the analysis.
3) Handle job failures: successful completion of jobs is checked and failed jobs can be restarted.
4) Handle updates of the pipeline: change options or add jobs and let PSOM figure out what to reprocess.

Download:

http://psom.simexp-lab.org/

7 References

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8 Publication Guidelines

Relevant references for the dMRI data processing pipeline in PANDA are listed below:

1) Regarding the PANDA package.

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Core regions

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Peripheral regions

Oishi K, Zilles K, Amunts K, Faria A, Jiang H, Li X, Akhter K, Hua K, Woods R, Toga AW and others. (2008): Human brain white matter atlas: identification and assignment of common anatomical structures in superficial white matter. Neuroimage 43(3):447-57.

11) Regarding the JHU white-matter tractography atlas.

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13) Regarding the brain parcellation (network node definition).

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http://psom.simexp-lab.org/

9 Help

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