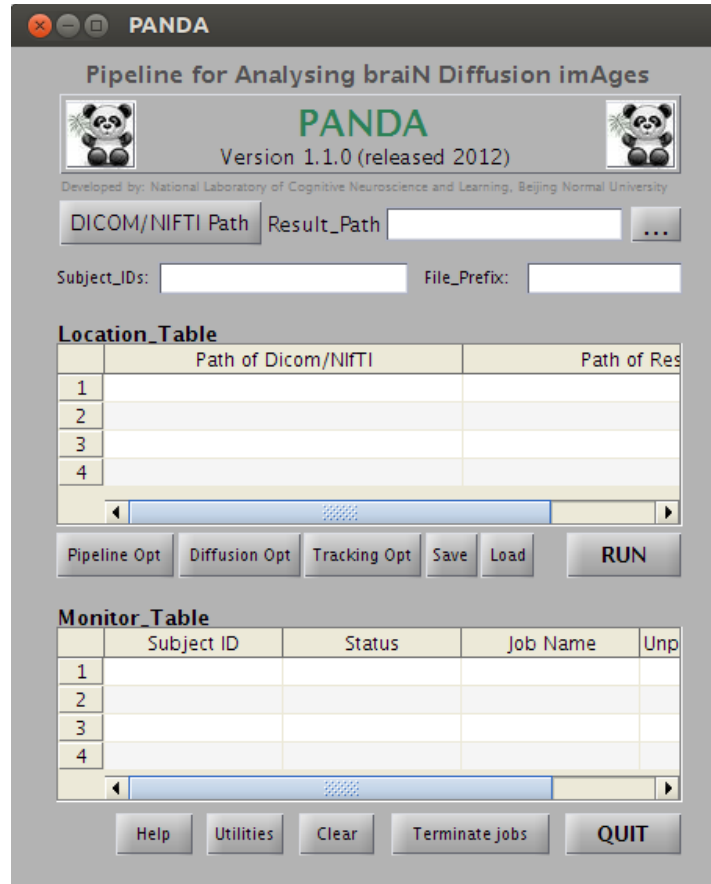


PANDA Manual



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- ➔ • **Overview**
- **Setup**
- **Files/Directories selection**
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- **Understanding resultant files**
- **Utilities**

Overview

Development Environment:

- Linux OS (Ubuntu)
- Matlab (2010b)
- FSL (4.1.6)
- PSOM (0.9)
- Diffusion Toolkit (0.6.2)
- MRICron (dcm2nii)

Overview

Advantage of PANDA


- **Automatic:** Fully-automatic processing from DICOM/NIfTI files to ready-for-statistic data at multiple levels (Atlas-level, Voxel-level, and TBSS-level), brain anatomical networks (deterministic and probabilistic) constructed by using diffusion tractography for any number of subjects.
- **Parallel:** Running jobs in parallel using multiple CPUs of one single computer or within a distributed computing environment.
- **Smart:** If the program terminates mid-way, you can load configuration file and click 'RUN', then PANDA will restart from the terminate point. If you change some options, PANDA will only restart the procedure related to these options.
- **Hidden:** The jobs will be run in background, and PANDA & Matlab can be even closed.

Overview

Processing flow of PANDA

- ✓ **DICOM -> NIFTI:** converting format
- ✓ **Brain extraction:** stripping skull
- ✓ **Cropping the image:** reducing image size
- ✓ **Eddy current correction:** correcting head motion & eddy-current
- ✓ **Calculating DTI parameters:** calculating tensor, FA, MD .etc
- ✓ **Normalizing estimate:** estimating transformation from native to standard space
- ✓ **Normalizing write:** writing images from native to standard space
- ✓ **Smoothing:** gaussian smoothing on the normalized images
- ✓ **WM atlas result:** calculating regional average FA, MD .etc according to the atlas
- ✓ **TBSS:** Tract-Based Spatial Statistic
- ✓ **Deterministic fiber tracking & Network construction**
- ✓ **Probabilistic fiber tracking & Network construction**

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Setup

Requirements :

➤ Linux OS / MAC

PANDA has been tested in Linux (Ubuntu, Centos, Fedora) and MAC

➤ Matlab

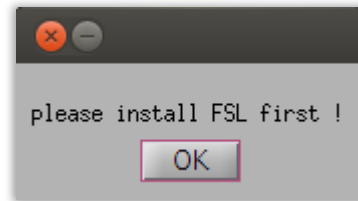
➤ FSL

Now, PANDA is only available for /bin/sh, /bin/bash, /bin/ksh Now.
We will make it available for /bin/tcsh, /bin/csh in next version.

Setup

FSL Setup :

➤ If FSL has not been installed, PANDA can't be opened and a message box will appear.



➤ Download and install FSL:

<http://www.fmrib.ox.ac.uk/fsl/fsl/downloading.html>

Setup

FSL Download :

➤ **Linux OS:**

Please download Linux Centos version FSL in FSL download page, don't download Linux Ubuntu/Debian version FSL.

PANDA will not work well with Ubuntu/Debian version FSL.

➤ **MAC OS:**

Please download MAC version FSL

Setup

PANDA in MAC OS:

Input this command in terminal first:

```
sudo launchctl load -w /System/Library/LaunchDaemons/com.apple.atrun.plist
```

Then, PANDA will work well in MAC.

Setup

Download & Unzip:

- Download PANDA:

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

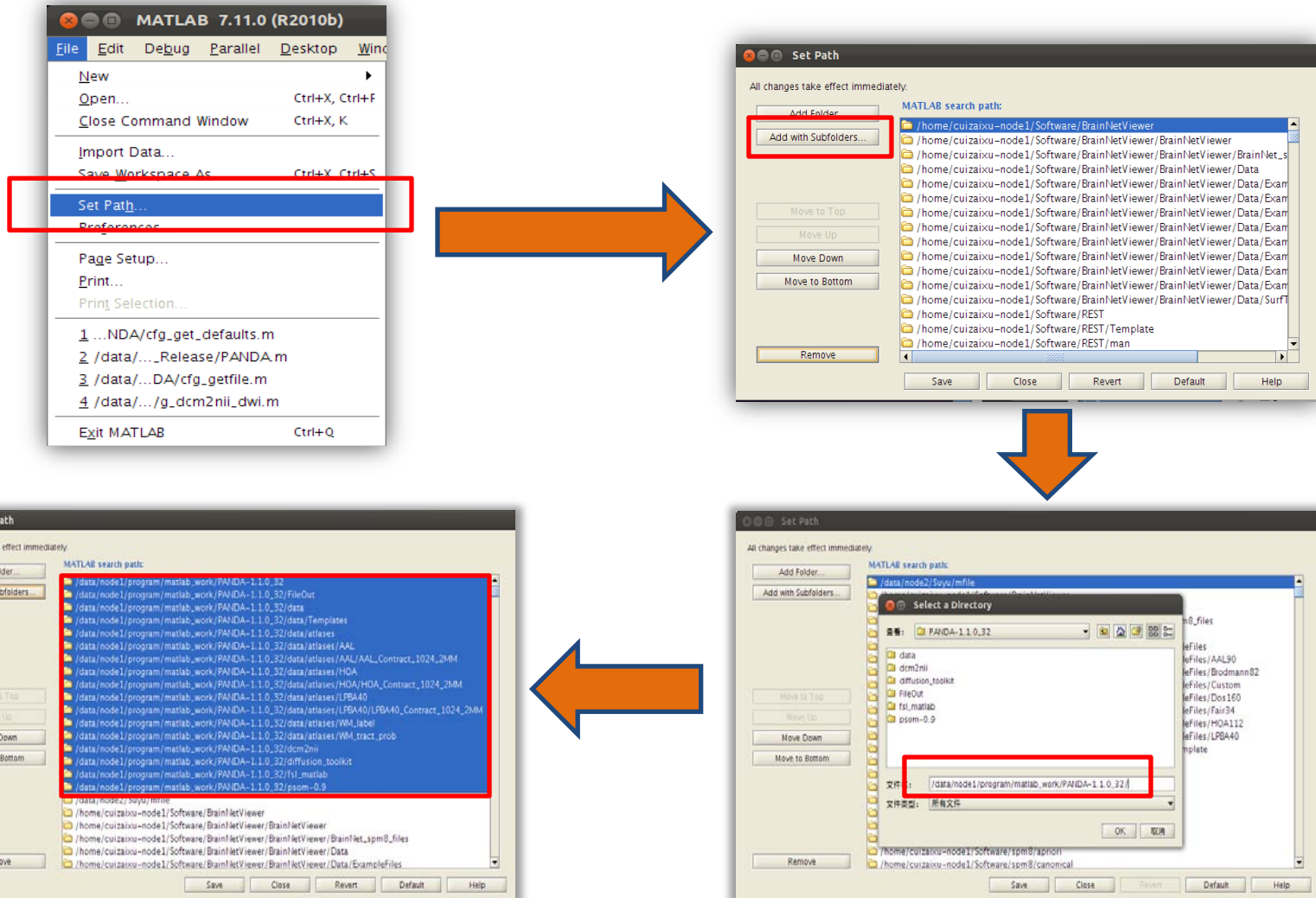
- Unzip:

Example: Unzip PANDA-1.1.0_32.tar.gz

```
tar zxvf PANDA-1.1.0_32.tar.gz
```


Setup

Matlab Search Path



Then, entering 'PANDA' in the MATLAB command window will open PANDA's GUI.¹²

Contents

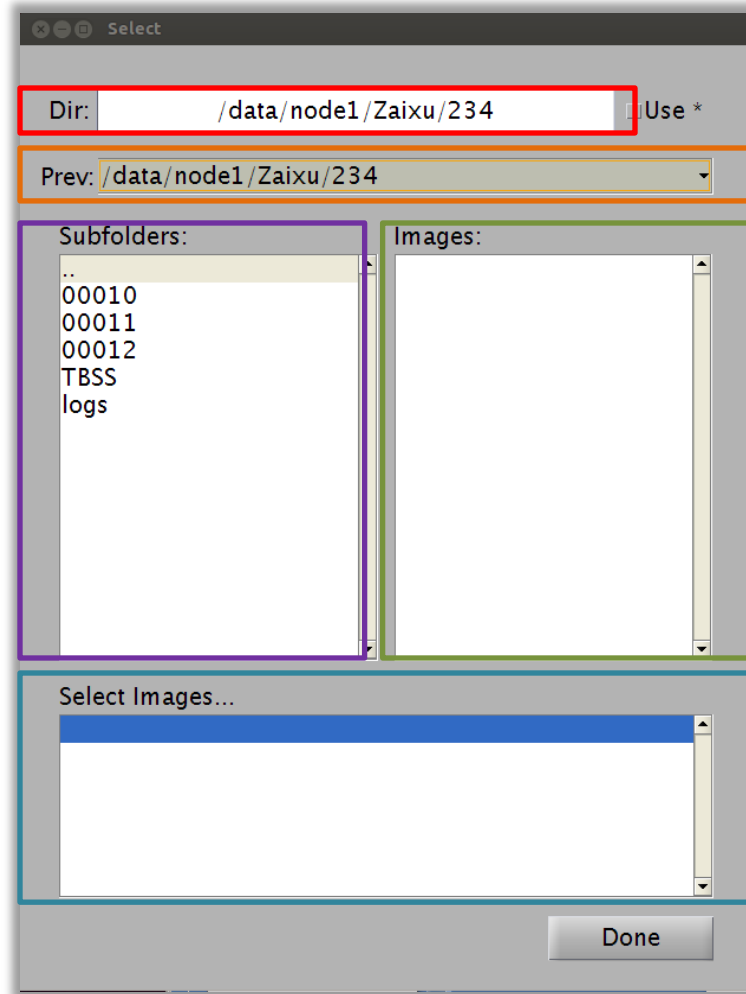
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Files/Directories selection

Dir:
current directory

Prev:
the list of directories
users have selected

Subfolders:
subfolders under
current directory



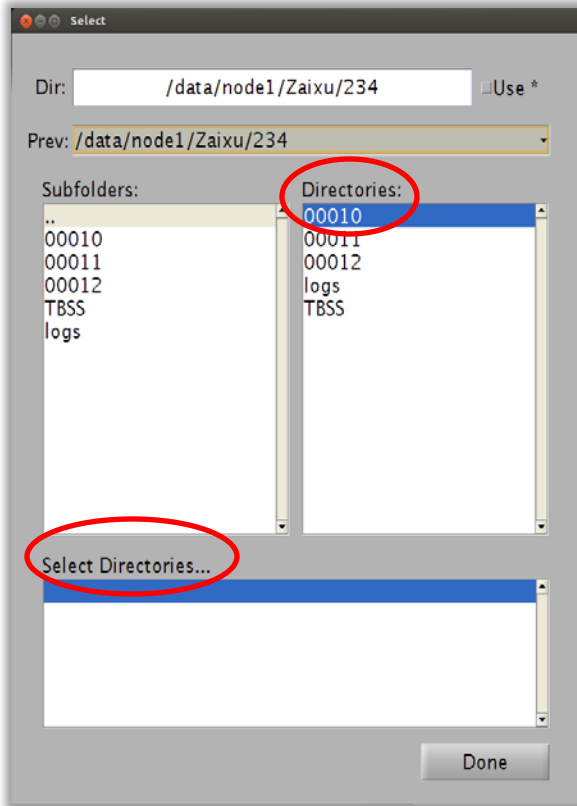
Images/Files/Directories
to be selected,
referring to [next page](#)

Images/Files/Directories
users have selected

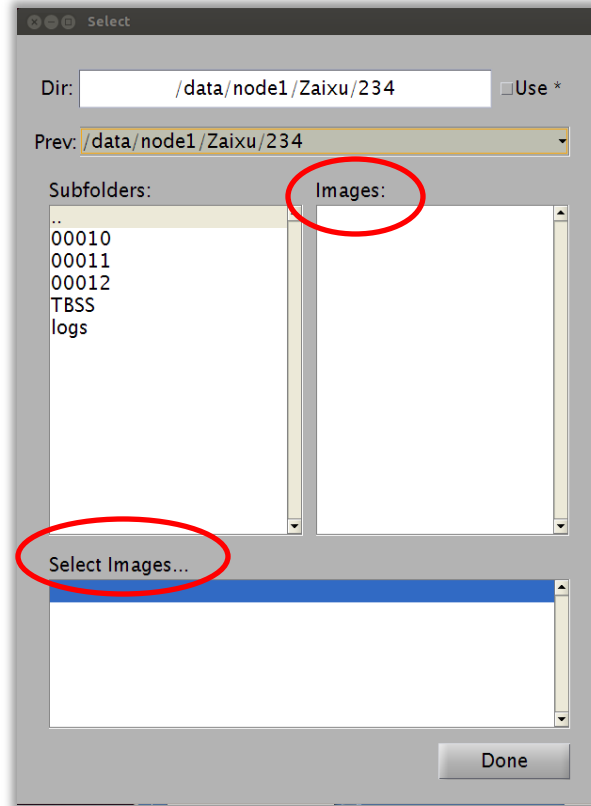
Files/Directories selection

Three situations:

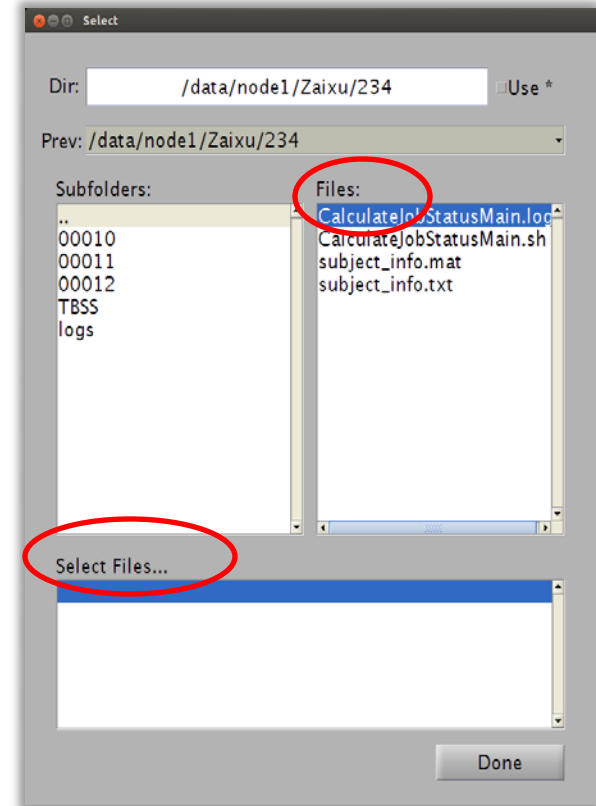
Select **Directories**:



Select **Images (.nii, .nii.gz, .img)**:



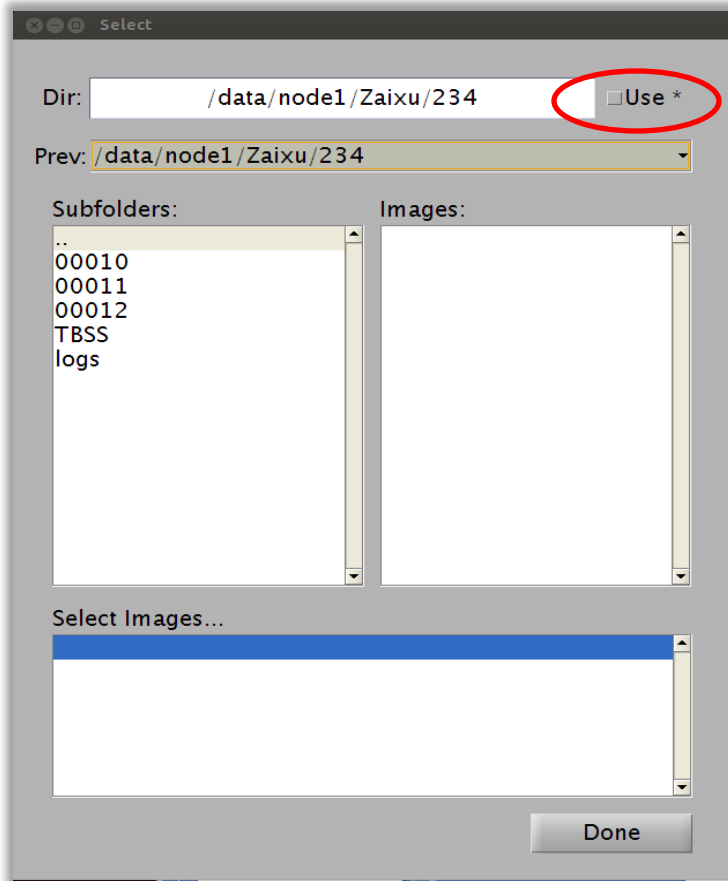
Select **Files**:



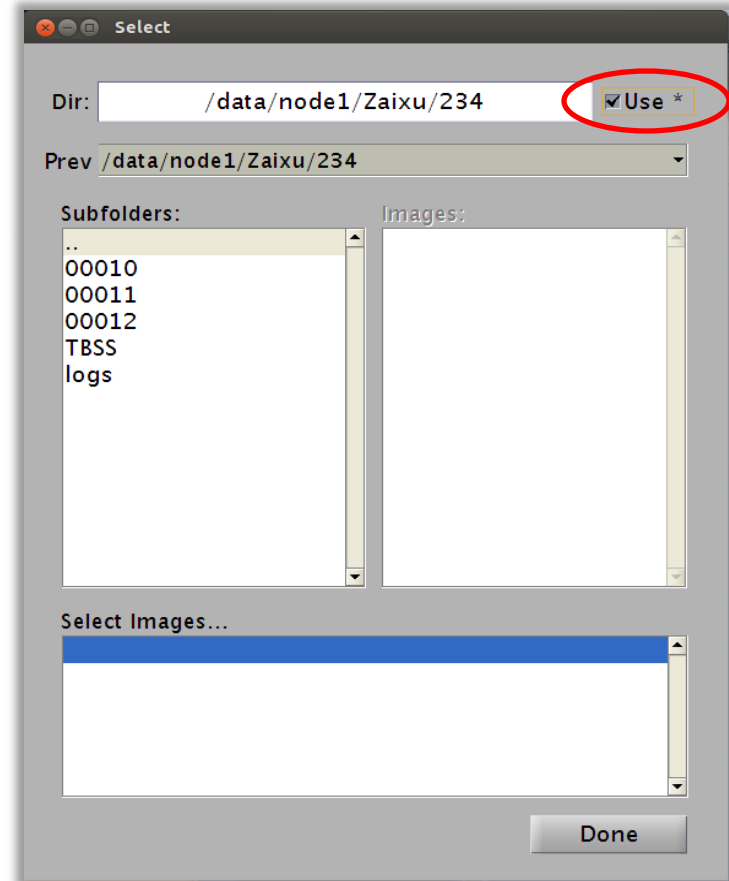
Files/Directories selection

Two methods:

Normal:

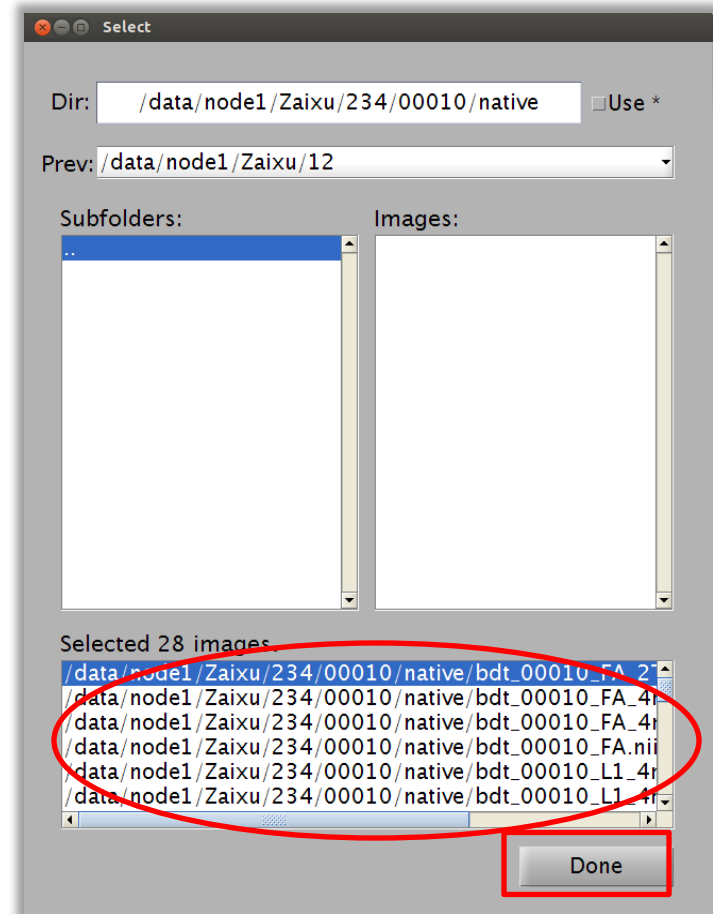
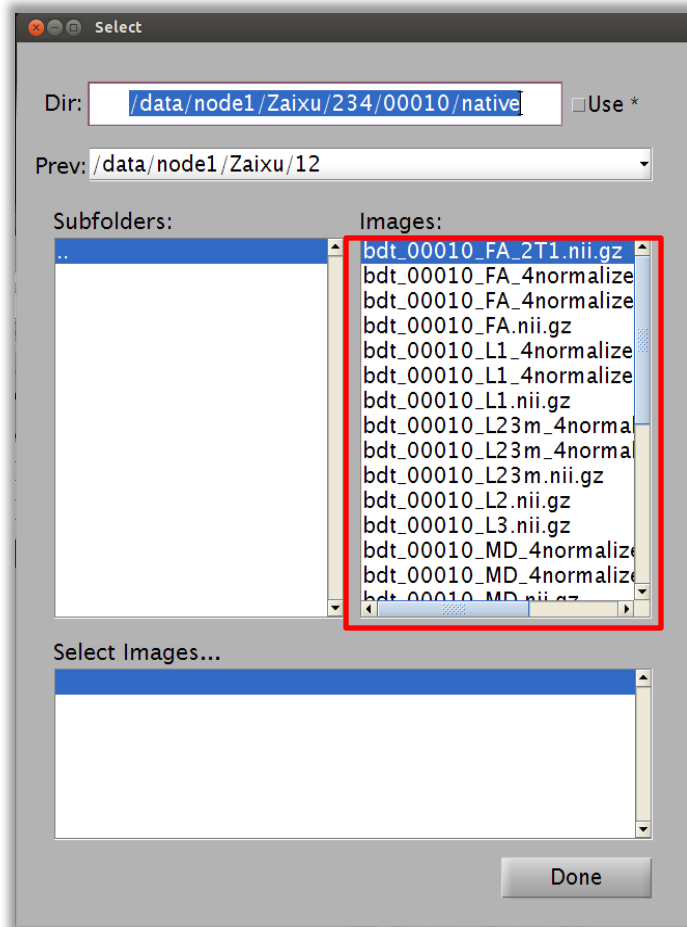


Use *:



Files/Directories selection

Normal:



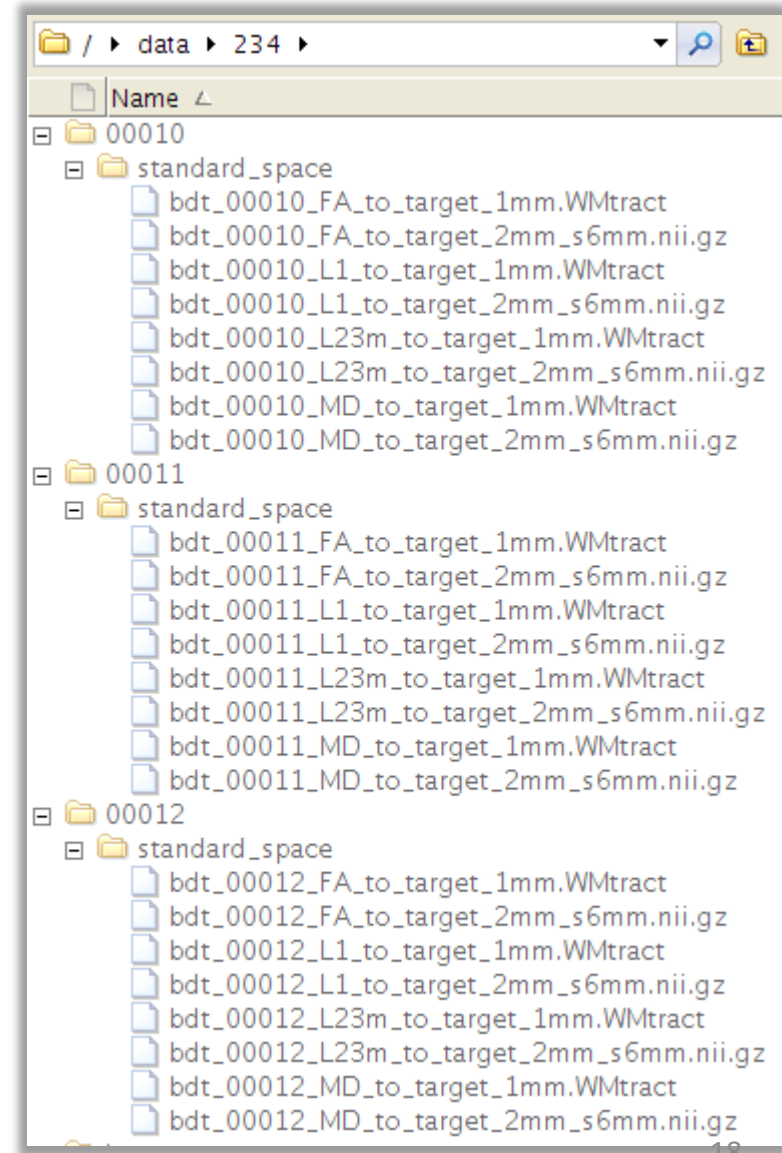
Files/Directories selection

Use *:

Under ‘/data/234’, there are three folders: ‘00010’, ‘00011’, ‘00012’.

Under each folder, there is a subfolder named ‘standard_space’.

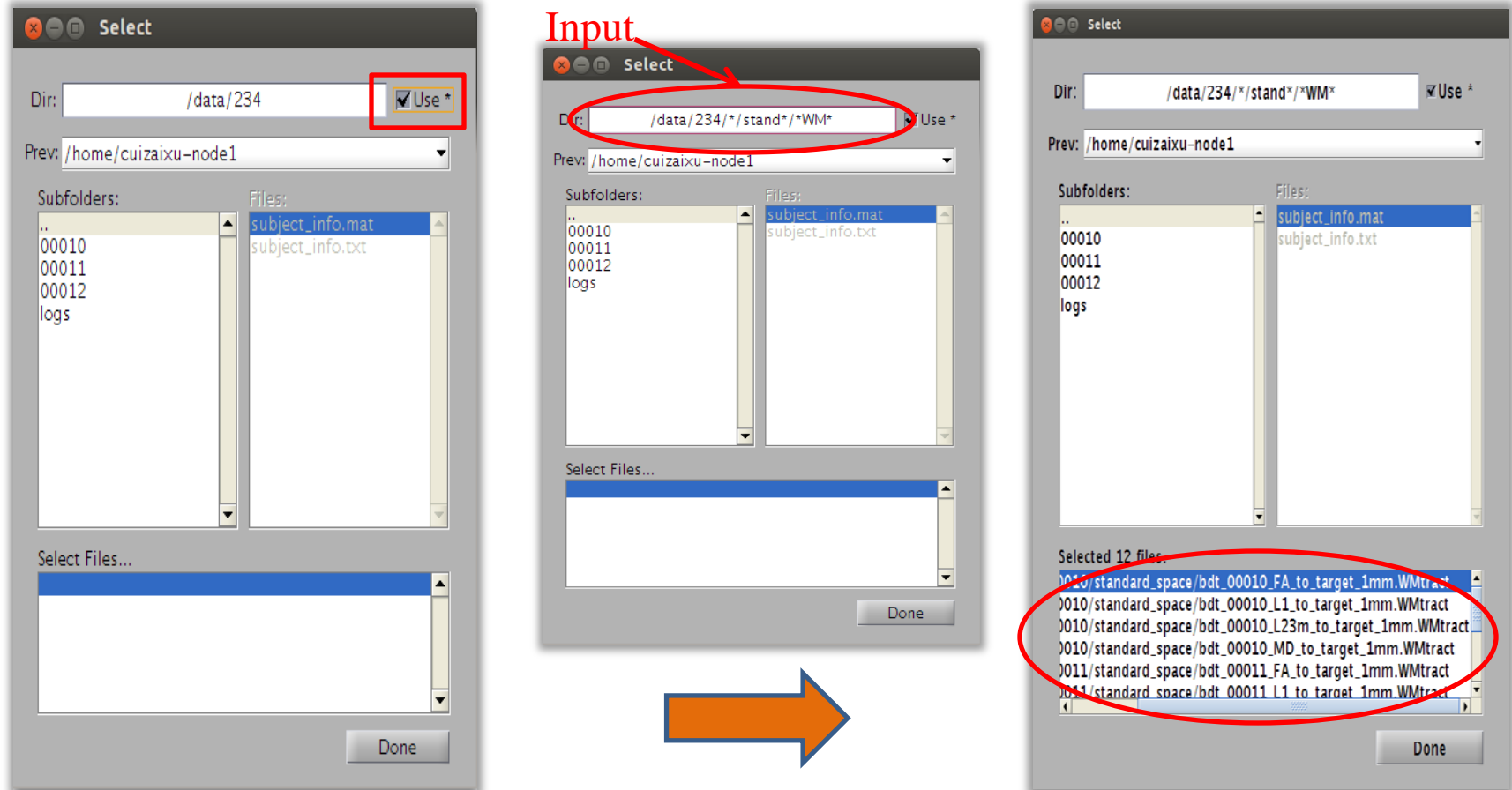
Now, we want to get all the Wmtract file under the folder standard_space.



Files/Directories selection

Use *:

Get all the 'WMlabel' and 'WMtract' file under folder standard_space



Files/Directories selection

Use *:

Explain: `/data/234/*/standard*/*WM*`

First step: `‘/data/234/*’` will get the names of all the subfolders/files under `/data/234`, and the results will be saved in `Path_List1`.

Second step: For each path `A` in `Path_List1`, `‘/data/234/*/standard*’` will get the names of all the subfolders/files whose name has ‘standard’ as prefix in path `A`, and the results will be saved in `Path_List2`.

Third step: For each path `B` in `Path_List2`, `‘/data/234/*/standard*/*WM*’` will get the names of all the subfolders/files whose name contains ‘WM’ in path `B`, and the results will be saved in `Path_List3`.

`Path_List3` is what we want !

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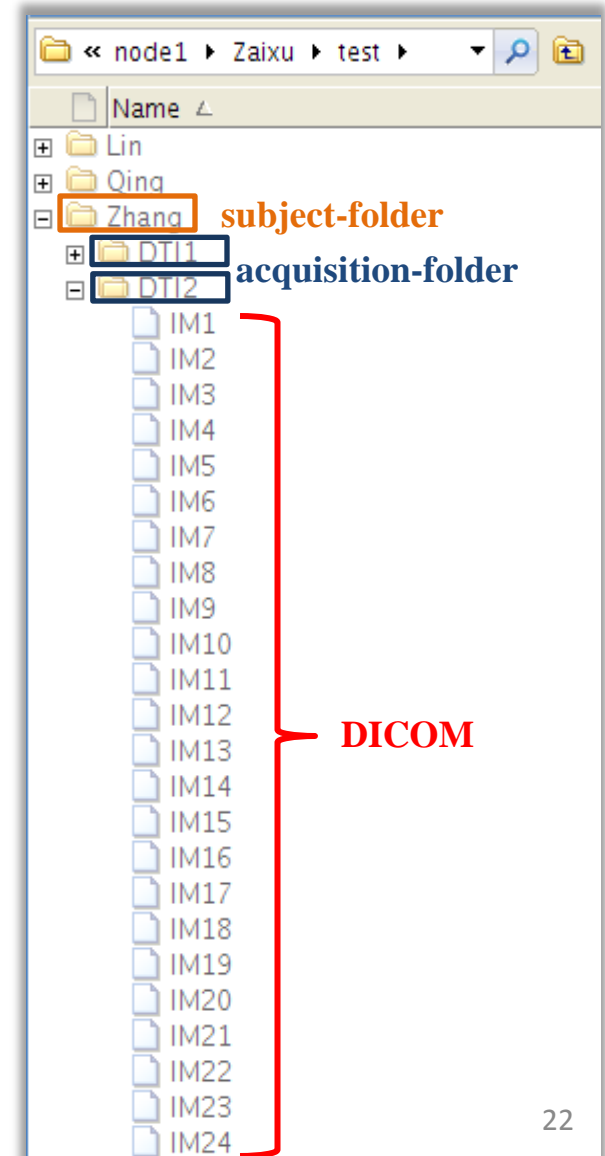
Preparing raw data (DICOM)

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

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

✓ Non-DWI sub-folders under the subject-folder are not allowed.

✓ The number of sub-folders should be the same as the number of acquisition for the DWI.

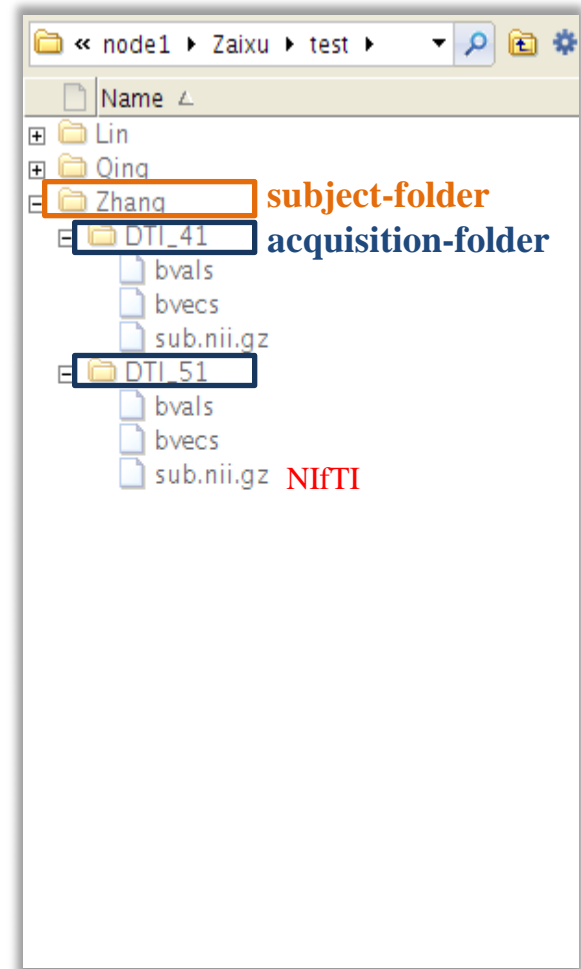


Preparing raw data (NIfTI)


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

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

- ✓ The number of sub-folders should be the same as the number of acquisition for the DWI.
- ✓ Under each sub-folder, there must be three files.
- ✓ B value file must be named as ‘*bval*’ and b vector file must be named as ‘*bvec*’.

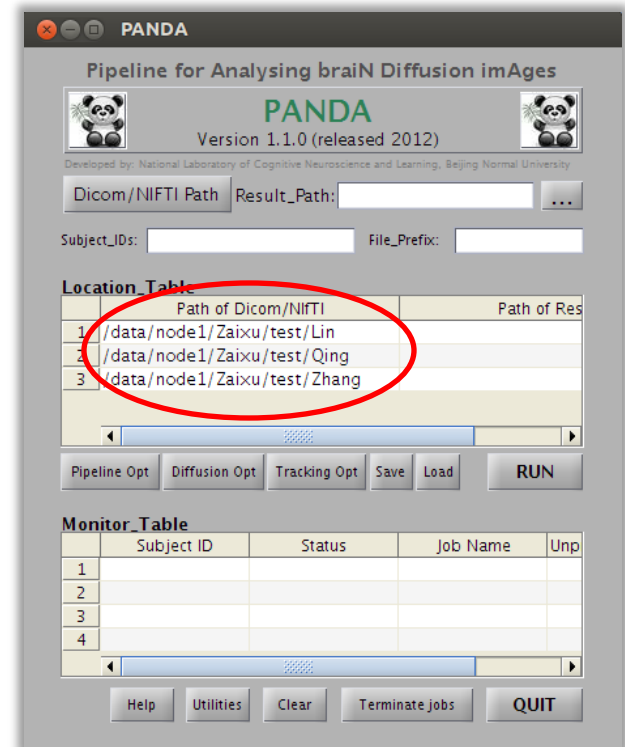
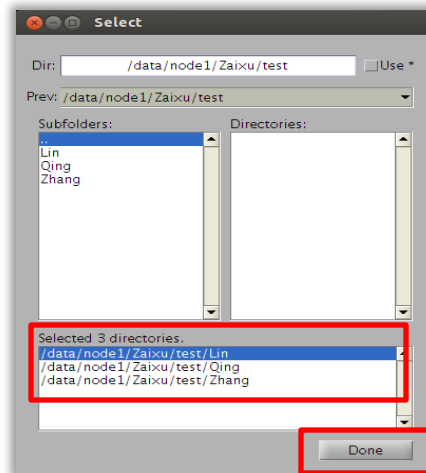
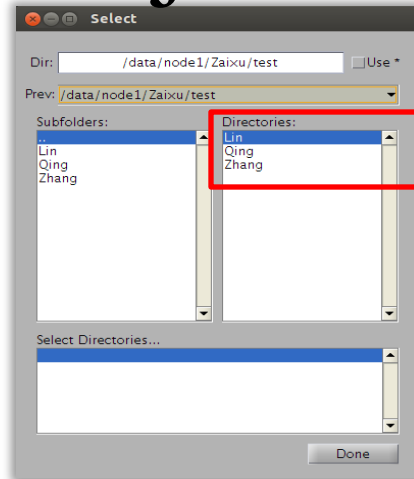
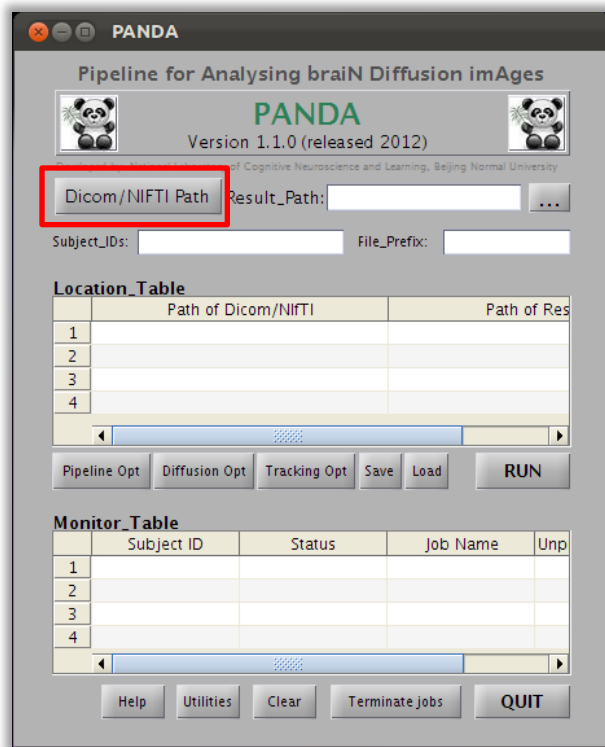


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Setting inputs & outputs

Step1: Select subject-folders



Setting inputs & outputs

Step2: Specify the result-folder

The image illustrates the process of specifying a result folder in the PANDA software. It consists of three screenshots of the PANDA interface, connected by an orange arrow indicating the sequence of steps.

Left Screenshot (Initial State): The PANDA window shows the 'Result_Path' field with an ellipsis button (three dots) highlighted by a red box. Below the field is a 'Location_Table' with three rows of data.

	Path of Dicom/NIFTI	Path of Res
1	/data/node1/Zaixu/test/Lin	
2	/data/node1/Zaixu/test/Qing	
3	/data/node1/Zaixu/test/Zhang	

Middle Screenshot (File Selection): A 'Select Directory to Open' dialog box is shown. The file name field contains '/data/node1/Zaixu/234', which is circled in red. The 'OK' button is also highlighted with a red box.

Right Screenshot (Final State): The PANDA window shows the 'Result_Path' field updated with the path '/data/node1/Zaixu/234', which is circled in red. The 'Location_Table' remains the same.

Bottom Screenshot (Monitor Table): A 'Monitor_Table' is shown with four rows of data.

	Subject ID	Status	Job Name	Unp
1				
2				
3				
4				

Setting inputs & outputs

Step3: Assign digital IDs for subjects

PANDA
Pipeline for Analysing brain Diffusion imAges
Version 1.1.0 (released 2012)
Developed by: National Laboratory of Cognitive Neuroscience and Learning, Beijing Normal University

Dicom/NIFTI Path: Result_Path: ...

Subject_IDs: File_Prefix:

Location_Table

	Path of Dicom/NiftI	Path of Res
1	/data/node1/Zaixu/test/Lin	
2	/data/node1/Zaixu/test/Qing	
3	/data/node1/Zaixu/test/Zhang	

Pipeline Opt Diffusion Opt Tracking Opt Save Load **RUN**

Monitor_Table

	Subject ID	Status	Job Name	Unp
1				
2				
3				
4				

Help Utilities Clear Terminate jobs **QUIT**



PANDA
Pipeline for Analysing brain Diffusion imAges
Version 1.1.0 (released 2012)
Developed by: National Laboratory of Cognitive Neuroscience and Learning, Beijing Normal University

Dicom/NIFTI Path: Result_Path: ...

Subject_IDs: File_Prefix:

Location_Table

	Path of Dicom/NiftI	Path of Result
1	Zaixu/test/Lin	/data/node1/Zaixu/234/00010
2	Zaixu/test/Qing	/data/node1/Zaixu/234/00011
3	Zaixu/test/Zhang	/data/node1/Zaixu/234/00012

Pipeline Opt Diffusion Opt Tracking Opt Save Load **RUN**

Monitor_Table

	Subject ID	Status	Job Name	Unp
1				
2				
3				
4				

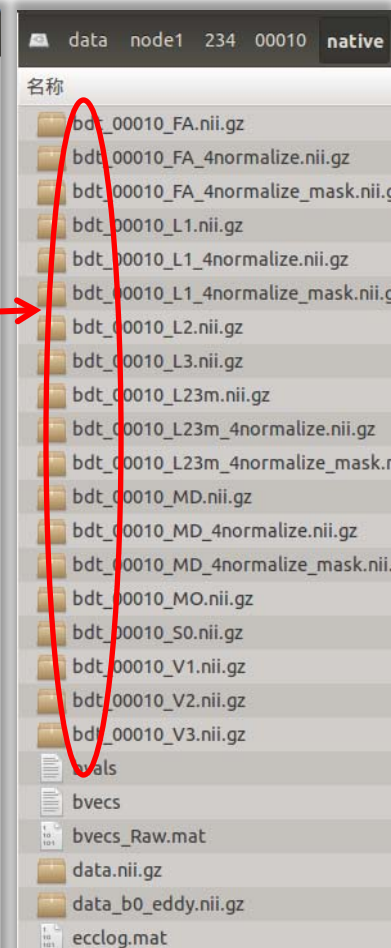
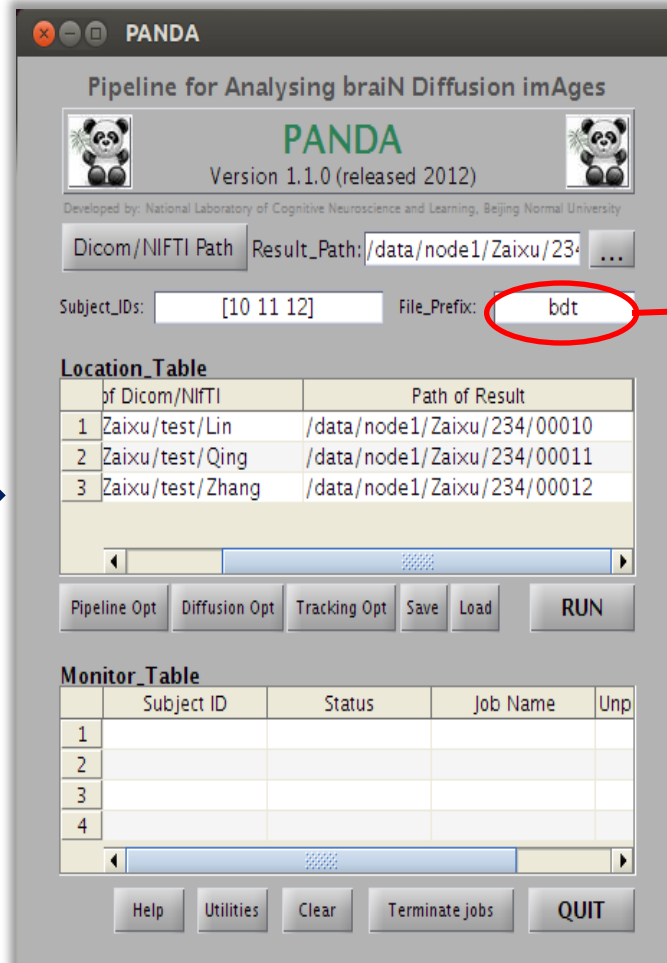
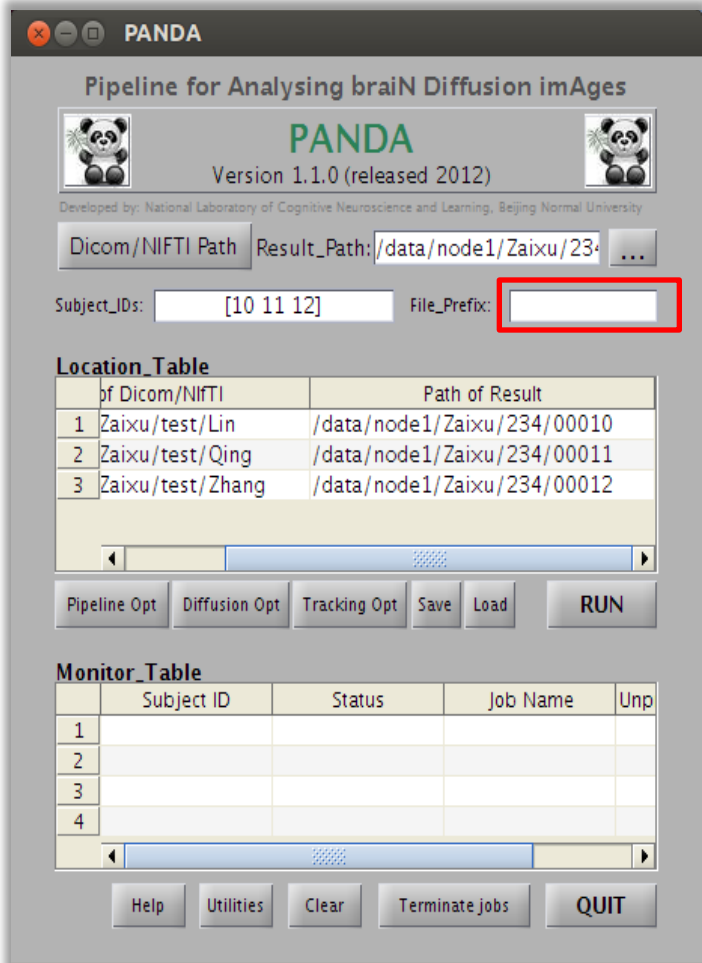
Help Utilities Clear Terminate jobs **QUIT**

- Zero-fill rule if the input digit number is small than 5:


e.g. 1 -> 00001; 10 -> 00010; 100 -> 00100; 1000 -> 01000; 10000 -> 10000

Setting inputs & outputs

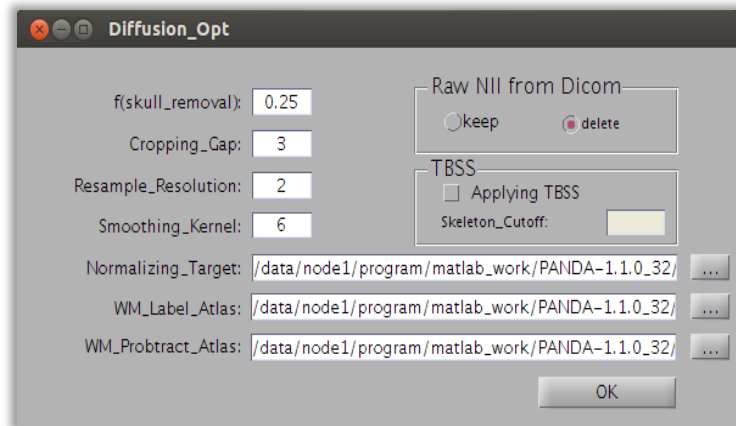
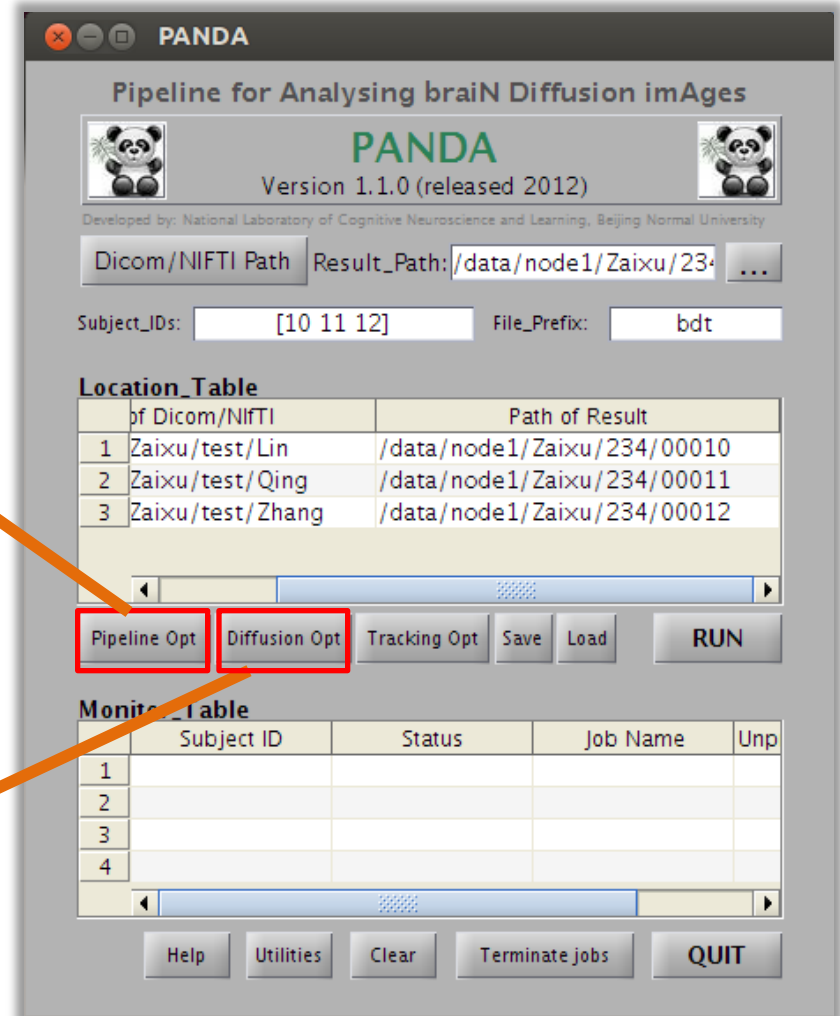
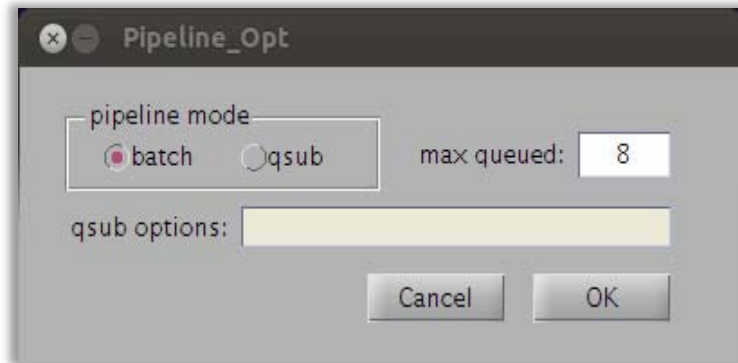
Step4: Input prefix of filenames



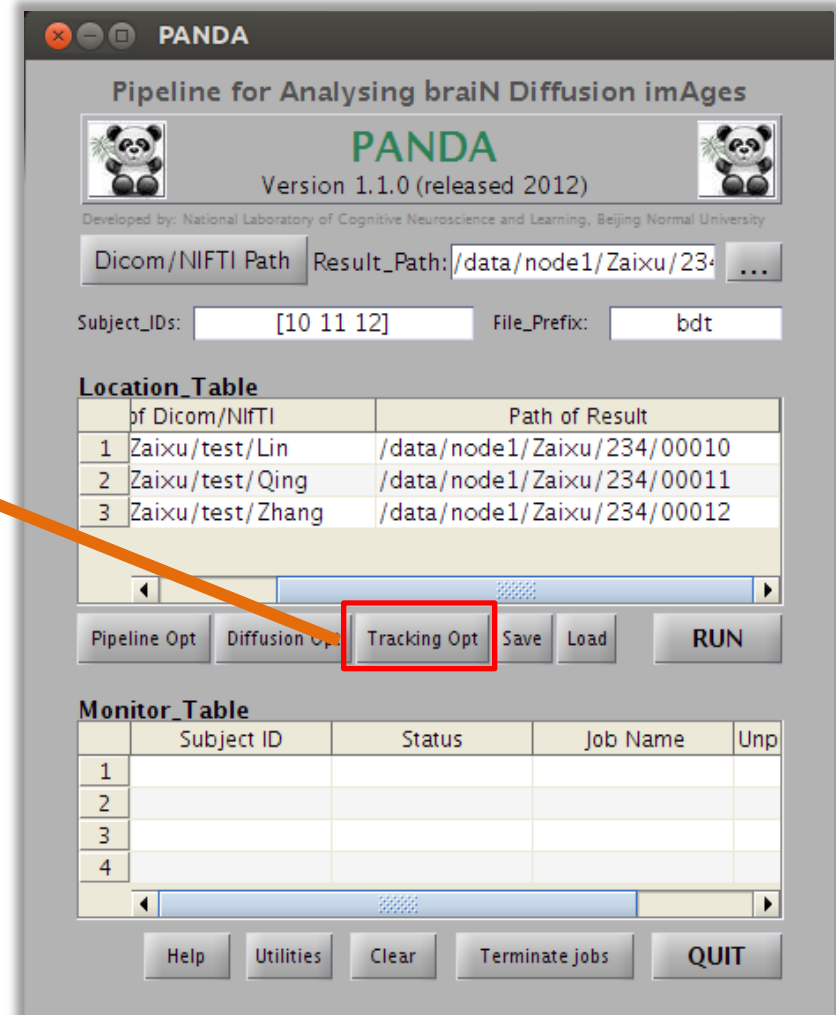
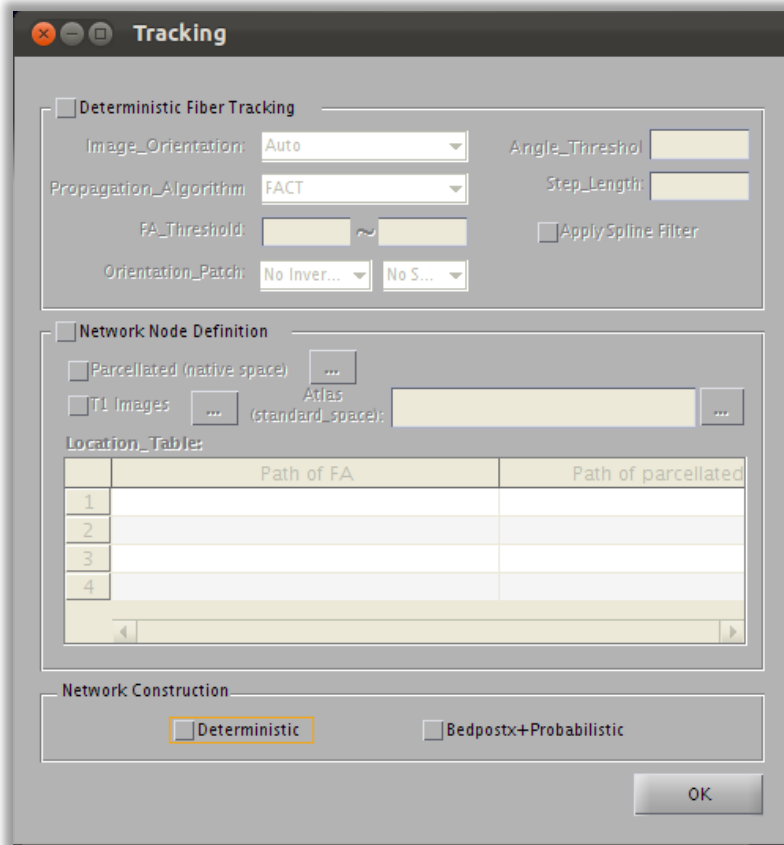
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Changing parameters (optional)

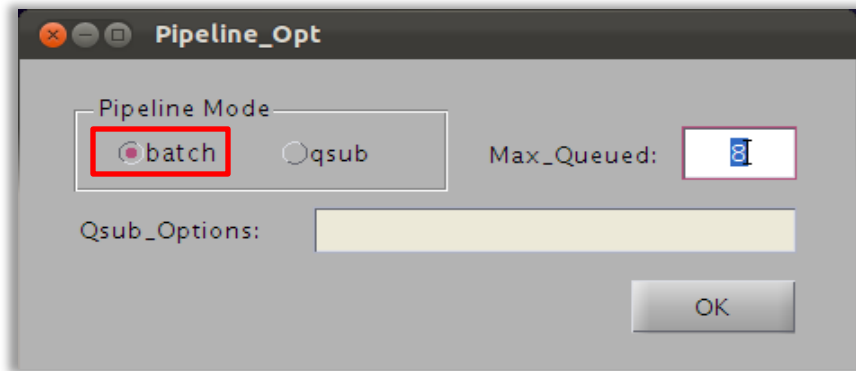


Changing parameters (optional)

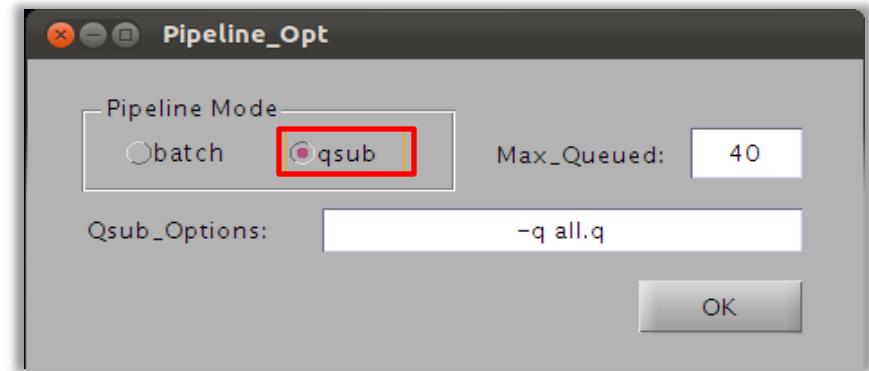


Changing parameters (optional)

Pipeline_Opt



When a single desktop:
Please select 'batch' mode



When a SGE environment:
Please select 'qsub' mode

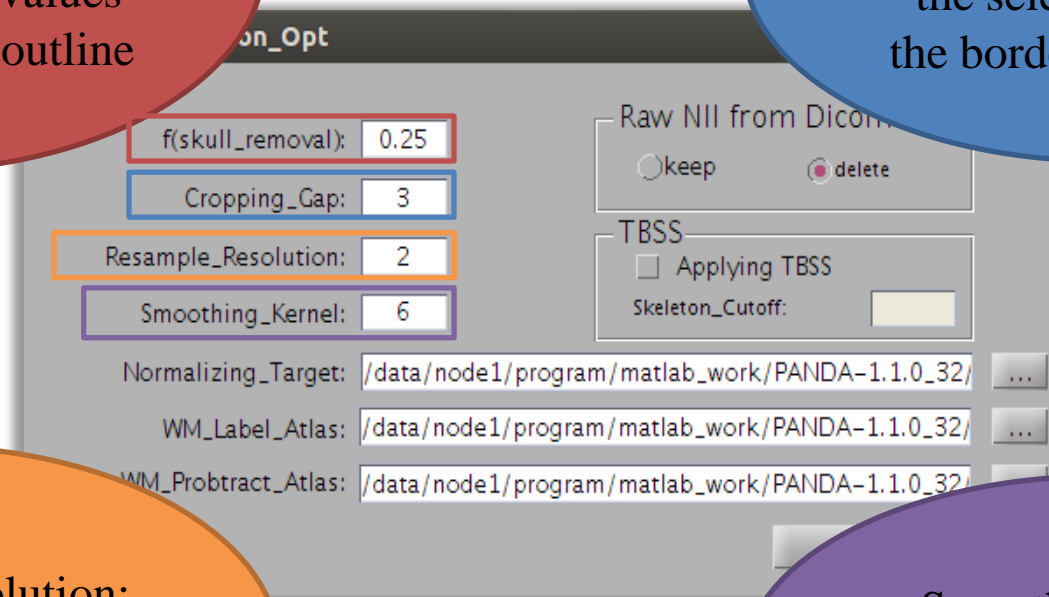
'max queued' is the maximum jobs running in parallel

Changing parameters (optional)

Diffusion_Opt (The default configuration is recommended)

f(skull removal):
fractional intensity
threshold
(0->1); smaller values
give larger brain outline
estimates

Cropping Gap:
The distance from
the selected cube to
the border of the brain



The screenshot shows the 'Diffusion_Opt' window with the following parameters and their values:

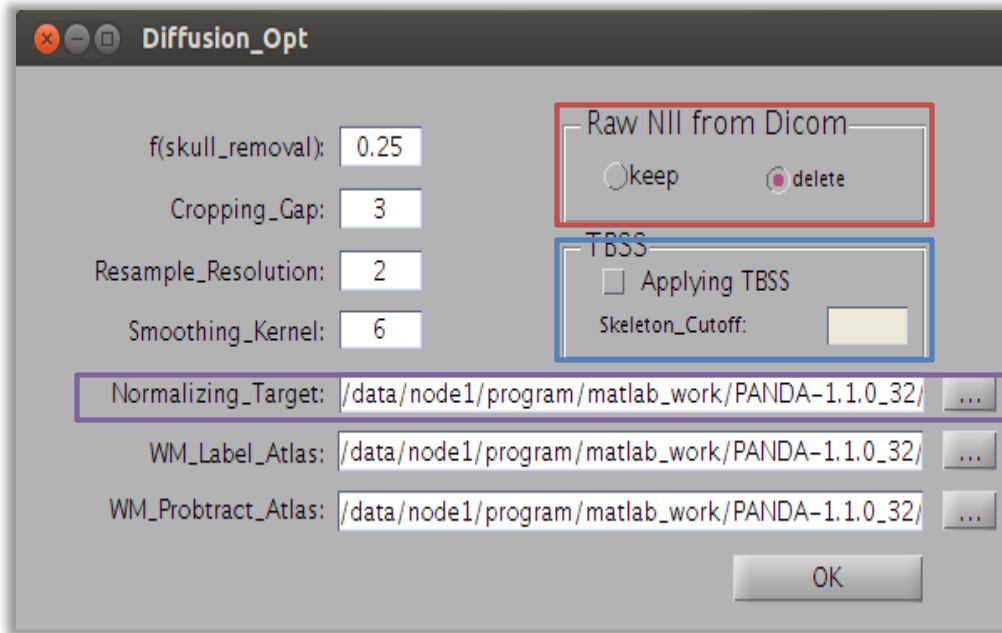
- f(skull_remove): 0.25 (highlighted with a red box)
- Cropping_Gap: 3 (highlighted with a blue box)
- Resample_Resolution: 2 (highlighted with an orange box)
- Smoothing_Kernel: 6 (highlighted with a purple box)
- Raw NII from Dicom: ☐ keep ☒ delete
- TBSS: ☐ Applying TBSS
- Skeleton_Cutoff: (empty text box)
- Normalizing_Target: /data/node1/program/matlab_work/PANDA-1.1.0_32/ ...
- WM_Label_Atlas: /data/node1/program/matlab_work/PANDA-1.1.0_32/ ...
- WM_Probtract_Atlas: /data/node1/program/matlab_work/PANDA-1.1.0_32/ ...

Resample Resolution:
If you input 2, the voxel
size will be 2*2*2.

Smoothing Kernel:
Set Gaussian smoothing
kernel size

Changing parameters (optional)

Diffusion_Opt (The default configuration is recommended)



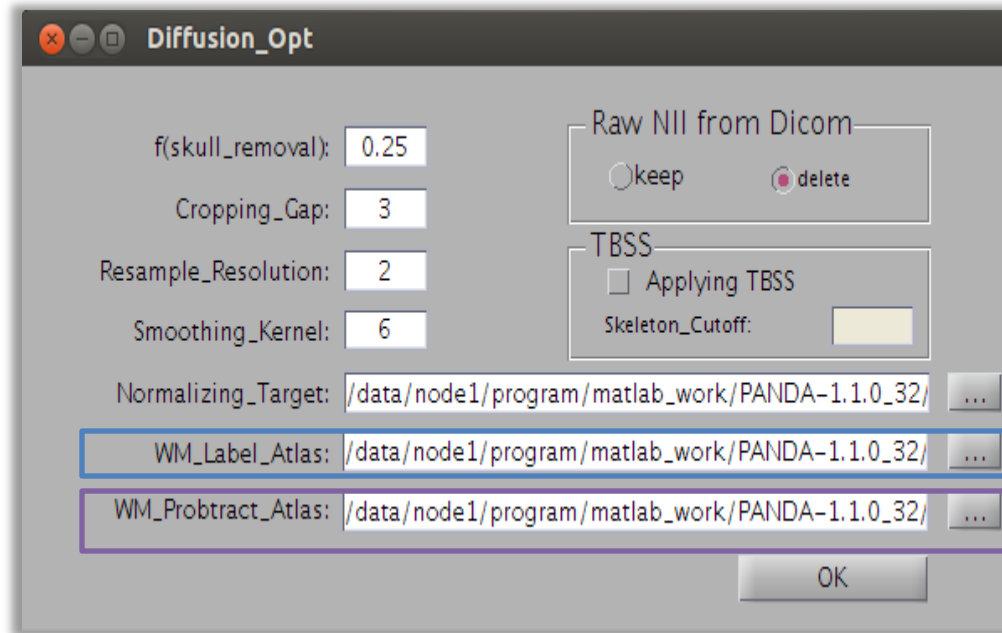
Raw NII from Dicom :
Select whether to delete
raw NII converted from
DICOM

Select whether to do TBSS
Skeleton_Cutoff:
FA threshold to exclude
voxels in the grey matter or
CSF

Normalization Target:
the template for
registering

Changing parameters (optional)

Diffusion_Opt (The default configuration is recommended)



WM_Lable_Atlas:
PANDA will calculate average of
FA/MD/ $\lambda_1 / \lambda_{23m}$ for all the regions in the
WM_Lable_Atlas

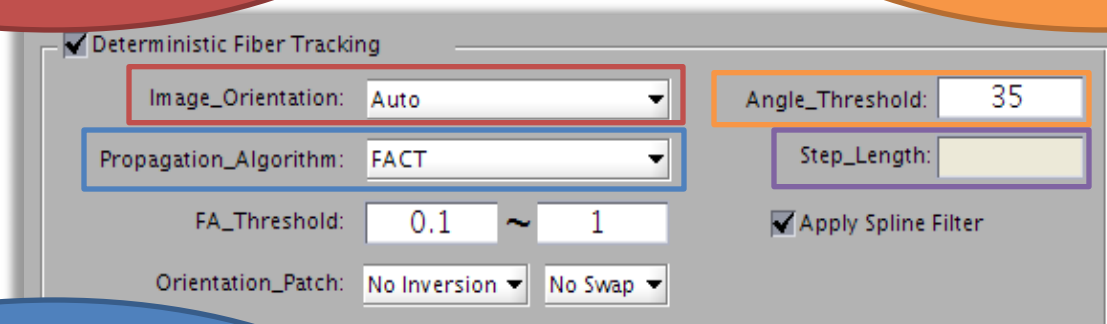
WM_Probtract_Atlas:
PANDA will calculate average of
FA/MD/ $\lambda_1 / \lambda_{23m}$ for all the regions in the
WM_Probtract_Atlas

Changing parameters (optional)

Deterministic Fiber Tracking (The default configuration is recommended)

Image Orientation:
image orientation vector,
'Auto' is recommended

Angle Threshold:
stop tracking when the
angle of the corner is
larger than threshold



The screenshot shows the 'Deterministic Fiber Tracking' window. It contains several controls: a checked checkbox for 'Deterministic Fiber Tracking', a dropdown for 'Image_Orientation' set to 'Auto', a dropdown for 'Propagation_Algorithm' set to 'FACT', a range input for 'FA_Threshold' from 0.1 to 1, a dropdown for 'Orientation_Patch' with 'No Inversion' and 'No Swap' options, a text input for 'Angle_Threshold' set to 35, a text input for 'Step_Length', and a checked checkbox for 'Apply Spline Filter'. Colored boxes highlight these parameters: a red box around 'Image_Orientation', an orange box around 'Angle_Threshold', a blue box around 'Propagation_Algorithm', and a purple box around 'Step_Length'.

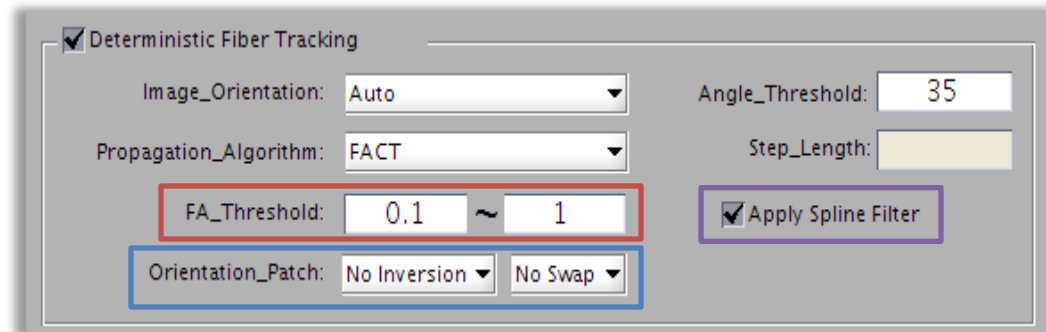
Propagation Algorithm:
four selections (FACT;
2nd order runge-kutta;
tensorline; interpolated
streamline)

Step Length:
set step length
The unit of the step
length is the minimum
voxel size.

Changing parameters (optional)

Deterministic Fiber Tracking

FA Threshold:
stop tracking when FA is
outside of the threshold
range



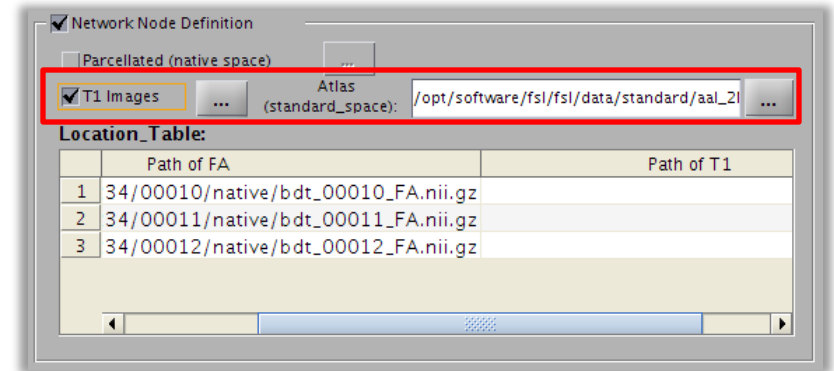
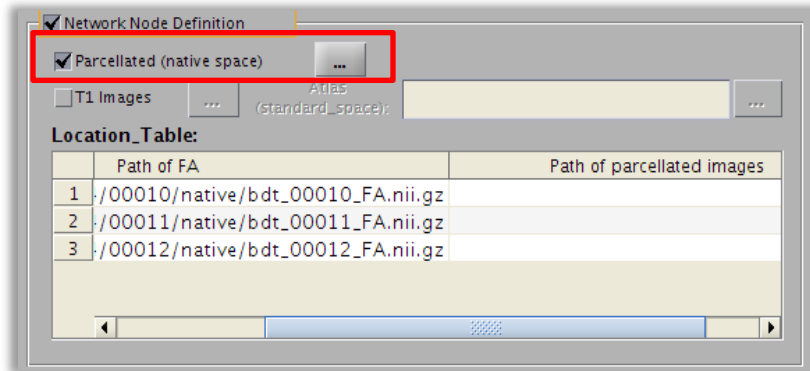
The screenshot shows a software window titled "Deterministic Fiber Tracking". It contains several controls: a checked checkbox at the top left; a dropdown menu for "Image_Orientation" set to "Auto"; a dropdown menu for "Propagation_Algorithm" set to "FACT"; a range input for "FA_Threshold" with values "0.1" and "1" separated by a tilde symbol; a dropdown menu for "Orientation_Patch" with options "No Inversion" and "No Swap"; a text input for "Angle_Threshold" set to "35"; a text input for "Step_Length"; and a checked checkbox for "Apply Spline Filter". The "FA_Threshold" range and the "Orientation_Patch" dropdown are highlighted with colored boxes (red and blue respectively).

Orientation Patch:
invert x, y or z component
of the vector;
swap x & y, y & z or x &
z vectors while tracking.

Apply Spline Filter:
select whether to smooth
& clean up the original
track file

Changing parameters (optional)

Network Node Definition



When having parcellated images in native space :

Select '[Parcellated \(native space\)](#)' and input these images.

When having no parcellated images in native space :

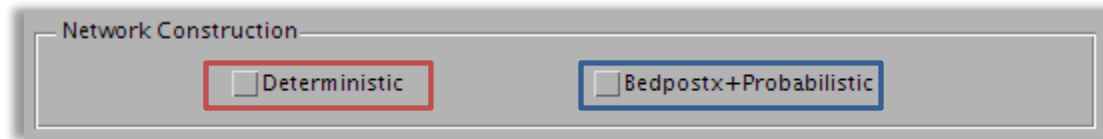
Select '[T1 images](#)' and input T1 images.

[Path of FA](#) is automatically generated.

The order of paths of [parcellated images](#) or [T1 images](#) must be in accordance with the order of the paths of [FA images](#) .

Changing parameters (optional)

Network Construction



Deterministic Network Construction:
Deterministic Fiber Tracking and
Network Node Definition should be
selected first.

Bedpostx & Probabilistic Network
Construction:
Network Node Definition should be
selected first !

Changing parameters (optional)

Network Construction

Fibers:
Number of fibers
per voxel,
default 2

Weight:
ARD weight,
more weight
means less
secondary fibers
per voxel,
default 1


The image shows two overlapping dialog boxes. The top box, titled 'Network Construction', has two radio buttons: 'Deterministic' (unchecked) and 'Bedpostx+Probabilistic' (checked). An orange arrow points from this checked option down to the 'BedpostxAndProbabilistic_Opt' dialog box below. This second dialog box contains several input fields: 'Fibers' with the value '2' (highlighted with a red border), 'Weight' with the value '1' (highlighted with an orange border), 'Brunin' with the value '1000' (highlighted with a blue border), 'Tracking Type' with 'OPD' selected (highlighted with a purple border), and 'Label_ID' with the value '[1:90]' (highlighted with a green border). An 'OK' button is at the bottom right of the second dialog box.

Burnin:
Burnin period,
default 1000

Label ID:
the ID of brain
regions in atlas

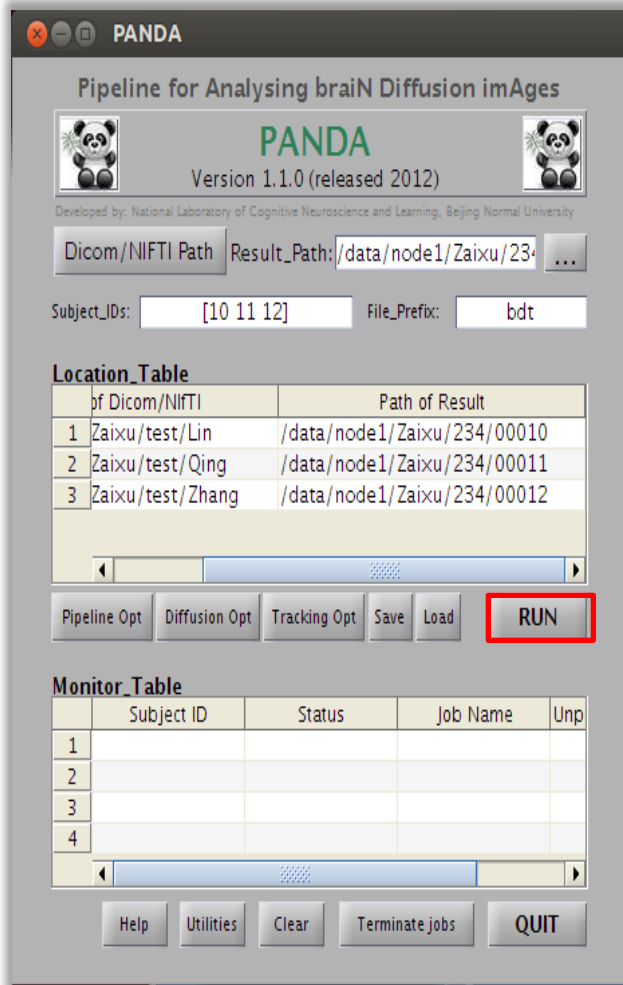
Tracking Type:
OPD(output path distribution);
PD(Correct path distribution for the
length of the pathways and output path
distribution)

Contents

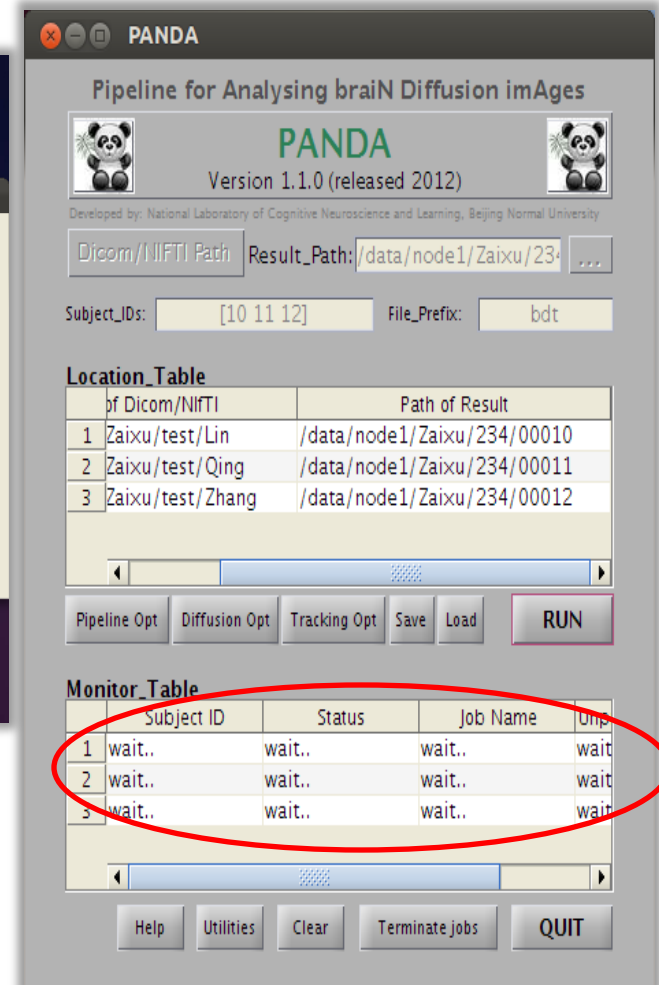
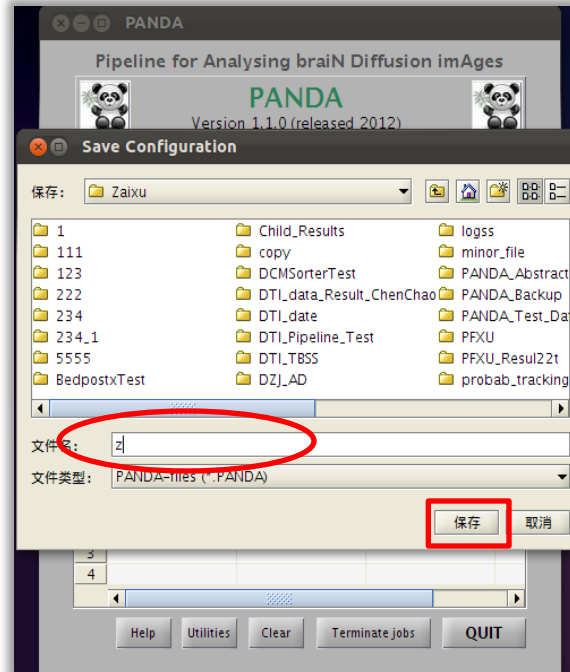
- **Overview**
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- **Changing parameters**
-  • **Initiating process**
- **Monitoring progress**
- **Understanding resultant files**
- **Utilities**

Initiating process

Start running



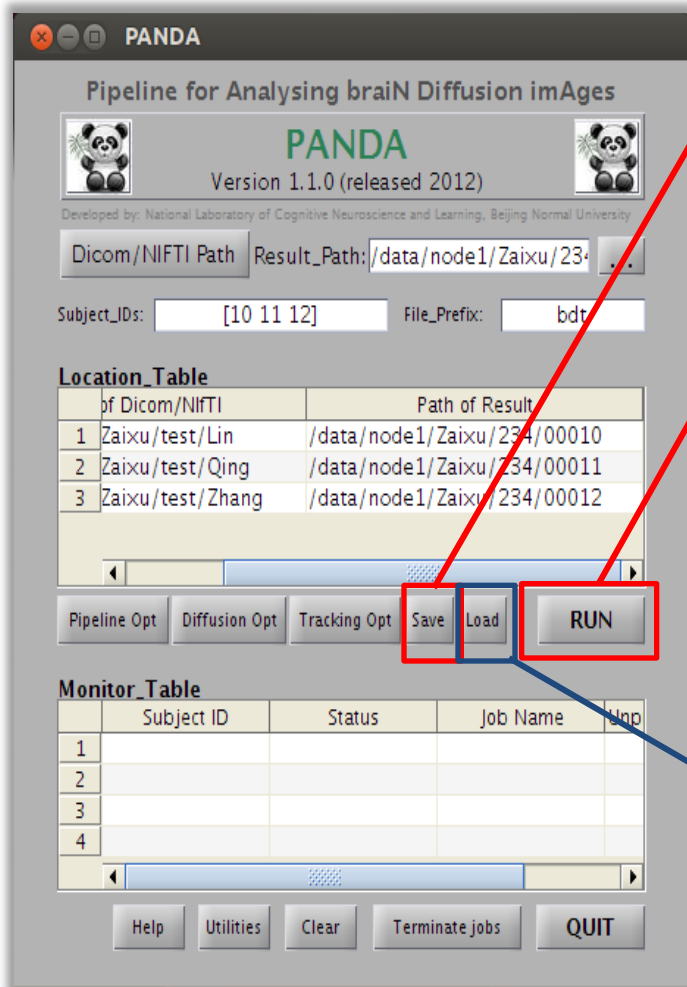
(save configuration)



After this, PANDA or even Matlab can be shut down. The jobs will be running in background.

Initiating process

Save & load configuration




➤ **Save actively**(extension as **.PANDA**) :
Use 'save' button to save current configurations.

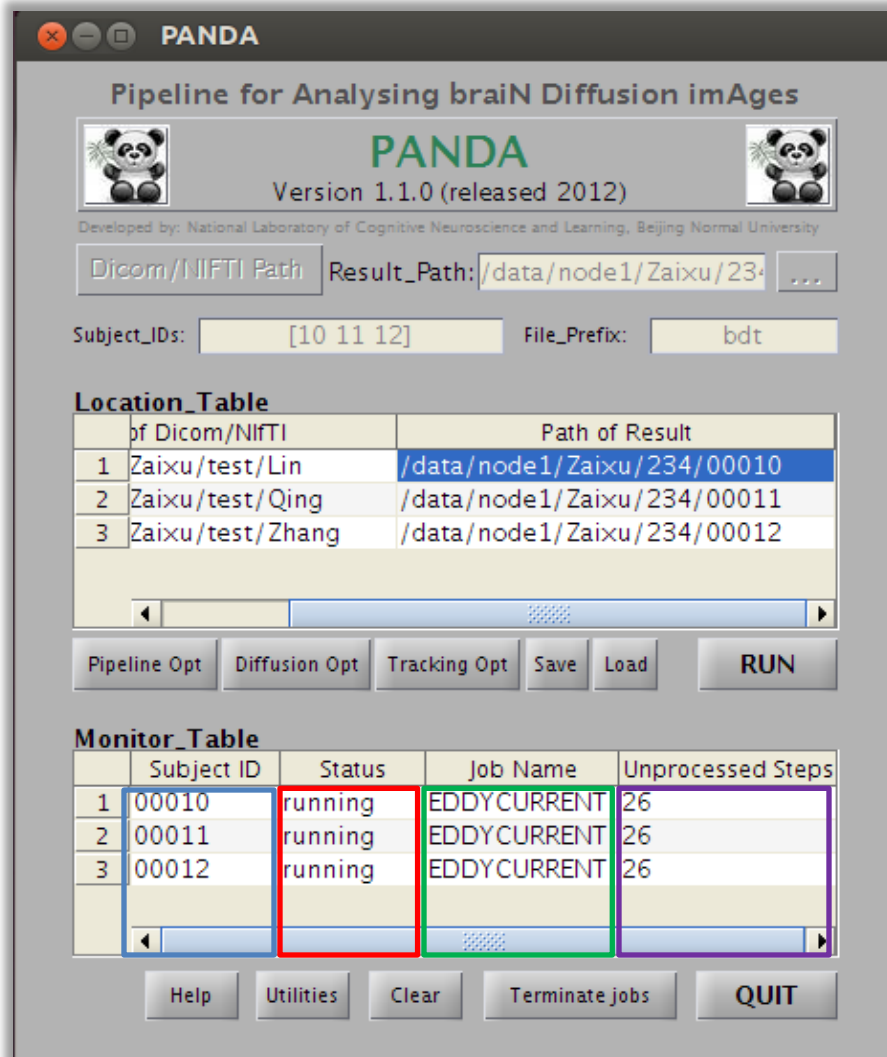
➤ **Save passively**(extension as **.PANDA**):
Current configuration will be forced to save after clicking 'RUN' button.

➤ Loading the ***.PANDA** file

Contents

- **Overview**
- **Setup**
- **Files/Directories selection**
- **Preparing raw data**
- **Setting inputs & outputs**
- **Changing parameters**
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- **Utilities**

Monitoring progress



➤ **Subject ID**(fixed)

➤ **Status**(dynamic)

wait

submitted

running

finished

failed

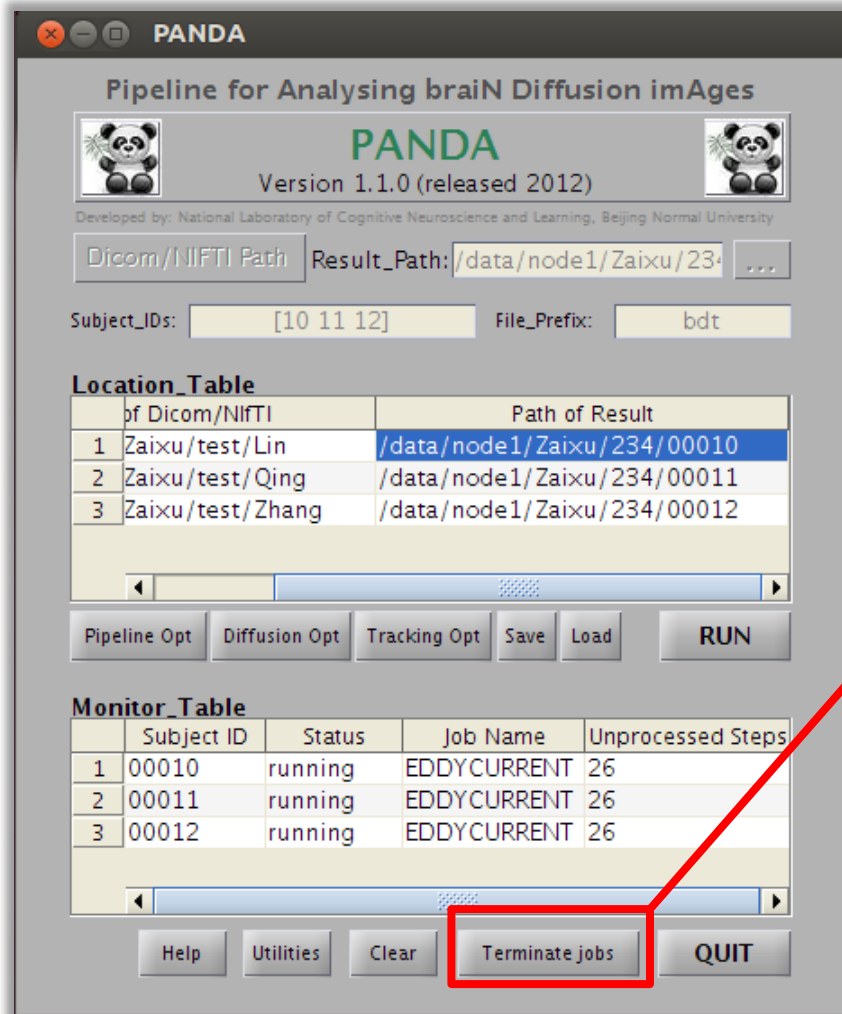
➤ **Job Name**(dynamic)

➤ **Unprocessed Step**(dynamic)

■ You can load the *.PANDA file to re-monitor the progress anytime, after shutting down PANDA or even Matlab


Monitoring progress

Terminate jobs

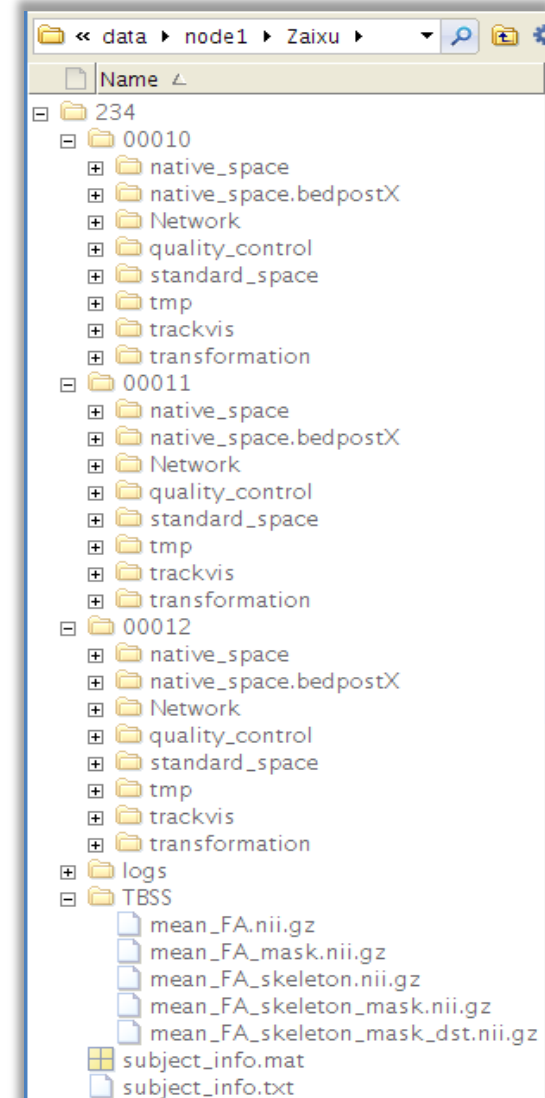
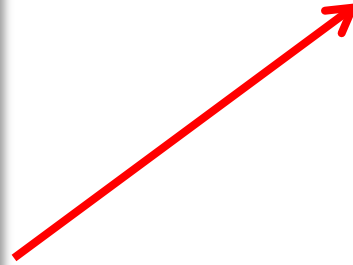
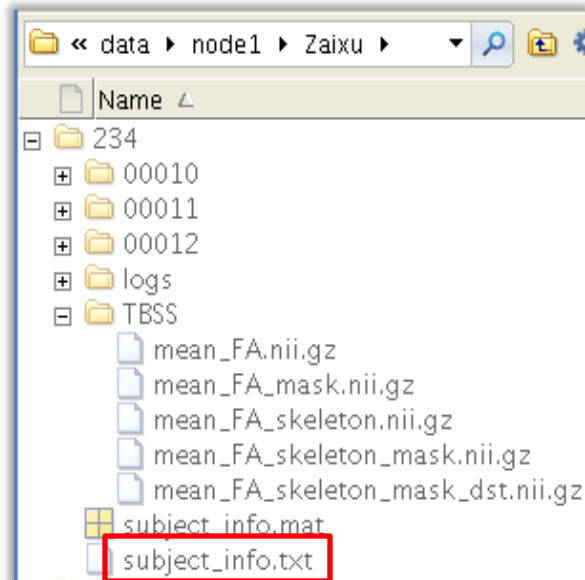


Terminate all the jobs running in background.

Contents

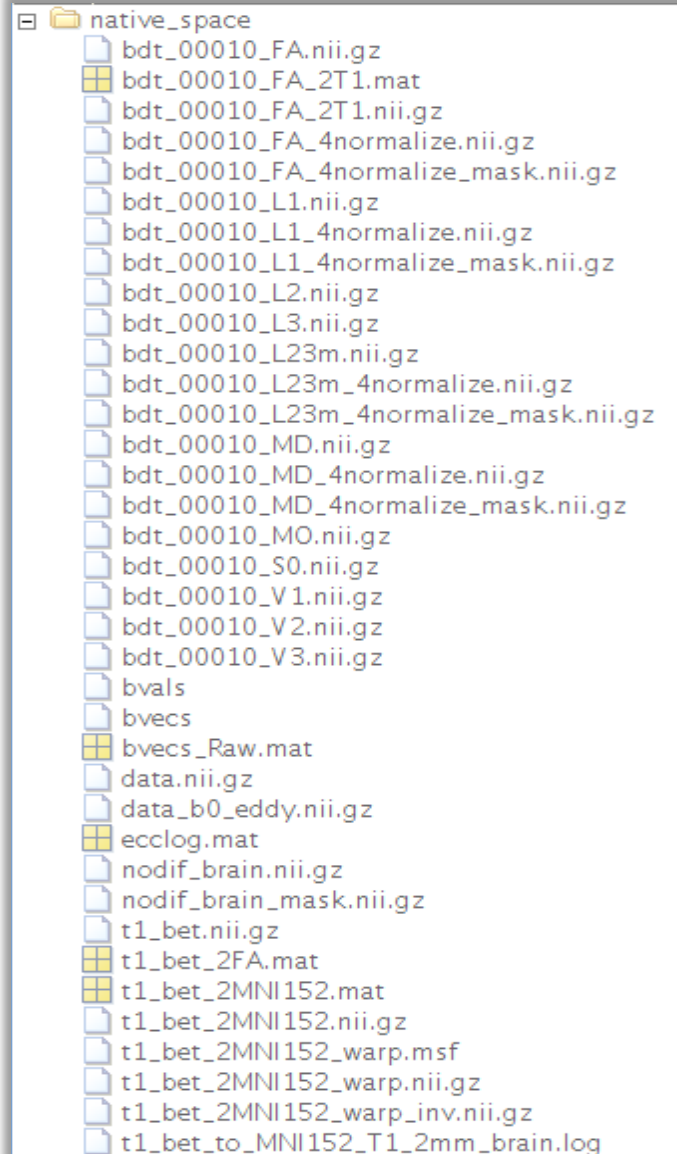
- **Overview**
- **Setup**
- **Files/Directories selection**
- **Preparing raw data**
- **Setting inputs & outputs**
- **Changing parameters**
- **Initiating process**
- **Monitoring progress**
-  • **Understanding resultant files**
- **Utilities**

Understanding resultant files



Understanding resultant files

Folder `native_space`:



Understanding resultant files

Native space

In the folder named 'native_space'

- Origin FA (Fractional Anisotropy):

*_FA.nii.gz

- Origin MD (Mean Diffusivity):

*_MD.nii.gz

- 1st eigenvalue (Axial Diffusivity):

*_L1.nii.gz

- 2nd eigenvalue:

*_L2.nii.gz

- 3rd eigenvalue:

*_L3.nii.gz

- Radial Diffusivity:

*_L23m.nii.gz

- b0:

*_S0.nii.gz, data_b0_eddy.nii.gz

- 1st eigenvector:

*_V1.nii.gz

- 2nd eigenvector:

*_V2.nii.gz

- 3rd eigenvector:

*_V3.nii.gz

Understanding resultant files

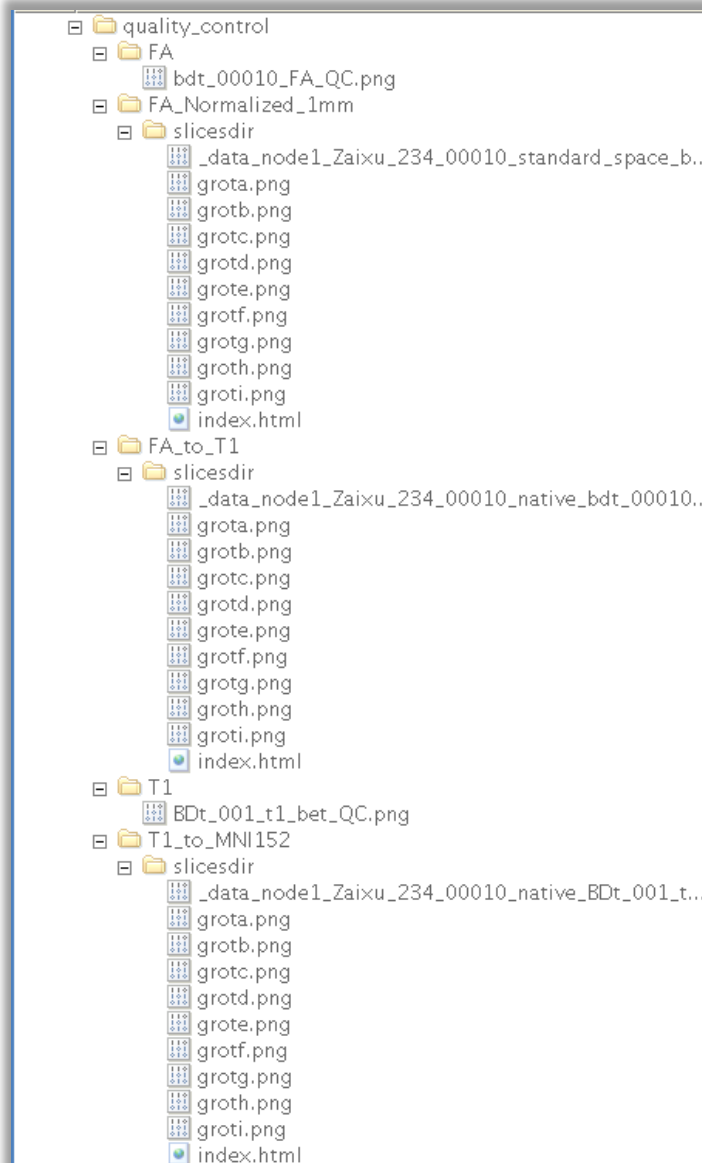
Native space

In the folder named `'native_space'`

- b value file:
bvals
- b vector file:
bvecs
- brain mask:
nodif_brain_mask
- 4D image data:
data.nii.gz
- T1 normalization to MNI152 space:
*_2MNI152.nii.gz
- FA normalization to T1 image:
*_T1.nii.gz
- parcellated image (native space):
Parcellated

Understanding resultant files

Folder `quality_control`:



Understanding resultant files

Check Quantity

In the folder named 'quantity_control'

- Check quantity of FA:

FA -> *_FA_QC.png

- Check quantity of FA normalization to Template:

FA_Normalized_1mm -> slicesdir -> *

- Check quantity of FA normalization to T1:

FA_Normalized_1mm -> slicesdir -> *

- Check quantity of T1:

T1 -> *_QC.png

- Check quantity of T1:

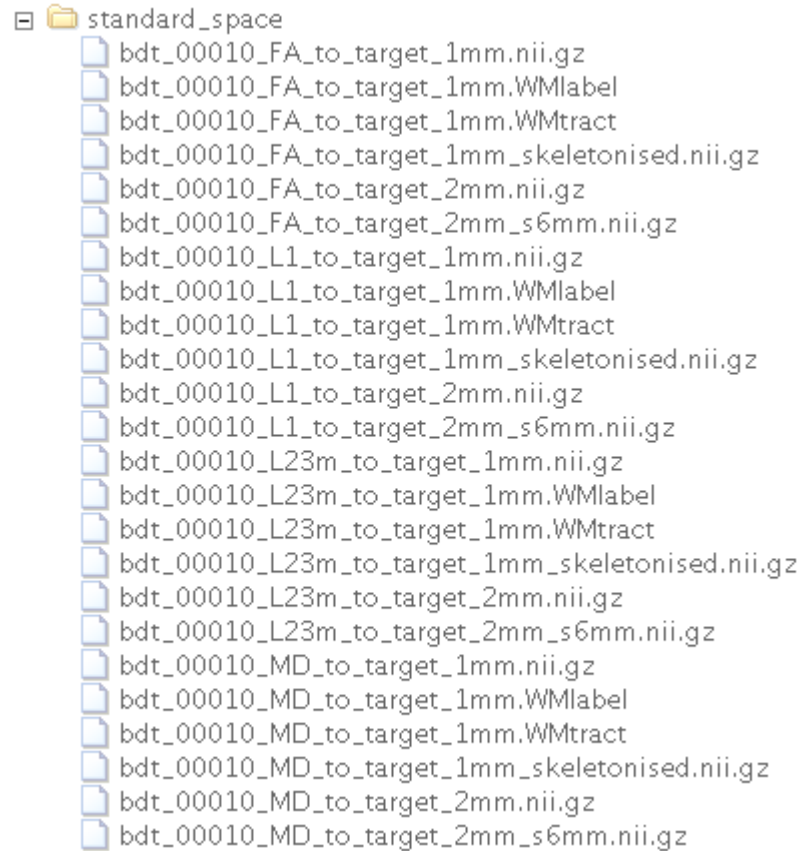
T1 -> *_QC.png

- Check quantity of T1 normalization to MNI152 space:

T1_to_MNI152 -> slicesdir -> *

Understanding resultant files

Folder `standard_space`:



A screenshot of a file explorer window showing the contents of a folder named 'standard_space'. The folder contains 24 files, all with '.nii.gz' or '.WMlabel' or '.WMtract' extensions. The files are organized into groups based on their naming convention, which includes a subject ID (bdt_00010), a source type (FA, L1, L23m, MD), a target resolution (1mm, 2mm), and a processing step (skeletonised, s6mm). The files are listed in a single column, with a small folder icon to the left of the folder name and a document icon to the left of each file name.

- standard_space
 - bdt_00010_FA_to_target_1mm.nii.gz
 - bdt_00010_FA_to_target_1mm.WMlabel
 - bdt_00010_FA_to_target_1mm.WMtract
 - bdt_00010_FA_to_target_1mm_skeletonised.nii.gz
 - bdt_00010_FA_to_target_2mm.nii.gz
 - bdt_00010_FA_to_target_2mm_s6mm.nii.gz
 - bdt_00010_L1_to_target_1mm.nii.gz
 - bdt_00010_L1_to_target_1mm.WMlabel
 - bdt_00010_L1_to_target_1mm.WMtract
 - bdt_00010_L1_to_target_1mm_skeletonised.nii.gz
 - bdt_00010_L1_to_target_2mm.nii.gz
 - bdt_00010_L1_to_target_2mm_s6mm.nii.gz
 - bdt_00010_L23m_to_target_1mm.nii.gz
 - bdt_00010_L23m_to_target_1mm.WMlabel
 - bdt_00010_L23m_to_target_1mm.WMtract
 - bdt_00010_L23m_to_target_1mm_skeletonised.nii.gz
 - bdt_00010_L23m_to_target_2mm.nii.gz
 - bdt_00010_L23m_to_target_2mm_s6mm.nii.gz
 - bdt_00010_MD_to_target_1mm.nii.gz
 - bdt_00010_MD_to_target_1mm.WMlabel
 - bdt_00010_MD_to_target_1mm.WMtract
 - bdt_00010_MD_to_target_1mm_skeletonised.nii.gz
 - bdt_00010_MD_to_target_2mm.nii.gz
 - bdt_00010_MD_to_target_2mm_s6mm.nii.gz

Understanding resultant files

Voxel-level results

In the folder named 'standard_space'

- Resultant images in MNI space with $1\text{mm} \times 1\text{mm} \times 1\text{mm}$ resolution
 - *_FA_4normalize_to_target_1mm.nii.gz : FA image
 - *_MD_4normalize_to_target_1mm.nii.gz : MD image
 - *_L1_4normalize_to_target_1mm.nii.gz : λ_1 image
 - *_L23m_4normalize_to_target_1mm.nii.gz : λ_{23m} image
- Resultant images in MNI space with $2\text{mm} \times 2\text{mm} \times 2\text{mm}$ resolution
 - *_FA_4normalize_to_target_2mm.nii.gz : FA image in $2 \times 2 \times 2$ standard space
 - *_MD_4normalize_to_target_2mm.nii.gz : MD image in $2 \times 2 \times 2$ standard space
 - *_L1_4normalize_to_target_2mm.nii.gz : λ_1 image in $2 \times 2 \times 2$ standard space
 - *_L23m_4normalize_to_target_2mm.nii.gz : λ_{23m} image in $2 \times 2 \times 2$ standard space
- Resultant images after Gaussian smoothing
 - *_FA_4normalize_to_target_2mm_s6mm.nii.gz : smoothing images of $2 \times 2 \times 2$ FA image
 - *_MD_4normalize_to_target_2mm_s6mm.nii.gz : smoothing images of $2 \times 2 \times 2$ MD image
 - *_L1_4normalize_to_target_2mm_s6mm.nii.gz : smoothing images of $2 \times 2 \times 2$ λ_1 image
 - *_L23m_4normalize_to_target_2mm_s6mm.nii.gz :
smoothing images of $2 \times 2 \times 2$ λ_{23m} image
(s6mm means that smoothing kernel size is 6mm)

Understanding resultant files

Regional-level results In the folder named 'standard_space'

- Regional results based on atlas
 - *_FA_4normalize_to_target_1mm.WMlabel :
regional FA average based on WMlabel-atlas
 - *_FA_4normalize_to_target_1mm.WMtract :
regional FA average based on WMtract-atlas
 - *_MD_4normalize_to_target_1mm.WMlabel :
regional MD average based on WMlabel-atlas
 - *_MD_4normalize_to_target_1mm.WMtract :
regional MD average based on WMtract-atlas
 - *_L1_4normalize_to_target_1mm.WMlabel :
regional λ_1 average based on WMlabel-atlas
 - *_L1_4normalize_to_target_1mm.WMtract :
regional λ_1 average based on WMtract-atlas
 - *_L23m_4normalize_to_target_1mm.WMlabel :
regional λ_{23m} average based on WMlabel-atlas
 - *_L23m_4normalize_to_target_1mm.WMtract :
regional λ_{23m} average based on WMtract-atlas

Understanding resultant files

TBSS results

In the folder named 'standard_space'

- Mean FA from TBSS

mean_FA.nii.gz : mean of all subjects' FA image

mean_FA_mask.nii.gz : mask of mean_FA.nii.gz

mean_FA_skeleton.nii.gz : mean FA skeleton of all subjects

mean_FA_skeleton_mask.nii.gz : the mask of mean FA skeleton

mean_FA_skeleton_mask_dst.nii.gz : distance map

- FA&MD& λ_1 & λ_{23m} skeleton from TBSS

*_FA_4normalize_to_target_1mm_skeletonised.nii.gz : FA skeleton

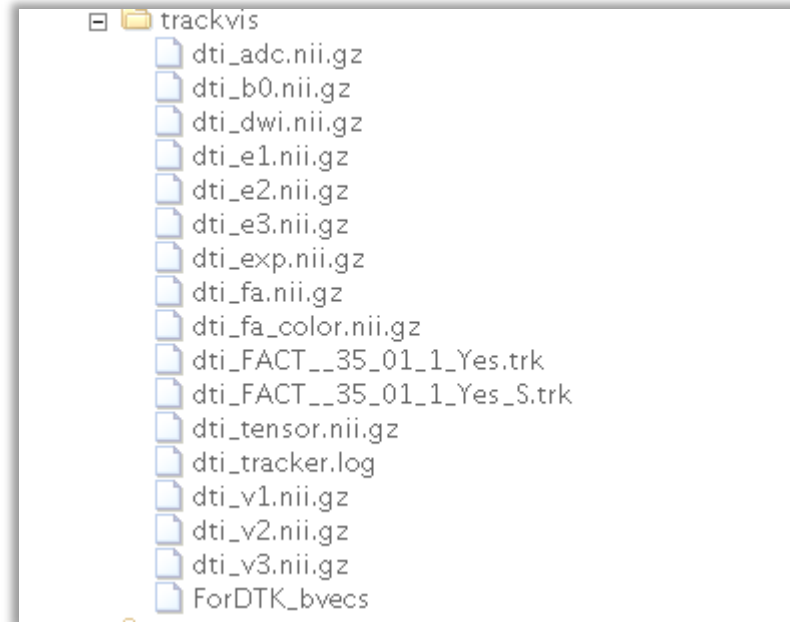
*_MD_4normalize_to_target_1mm_skeletonised.nii.gz : MD skeleton

*_L1_4normalize_to_target_1mm_skeletonised.nii.gz : λ_1 skeleton

*_L23m_4normalize_to_target_1mm_skeletonised.nii.gz : λ_{23m} skeleton

Understanding resultant files

Folder `trackvis`:



Understanding resultant files

Deterministic Fiber Tracking In the folder named 'trackvis'

- track file :
dti_*.trk
- track file after applying spline filter:
dti_*_S.trk
- You can open .trk file with **Trackvis Software**
(<http://www.trackvis.org/>) to draw ROI and do statistical analysis.

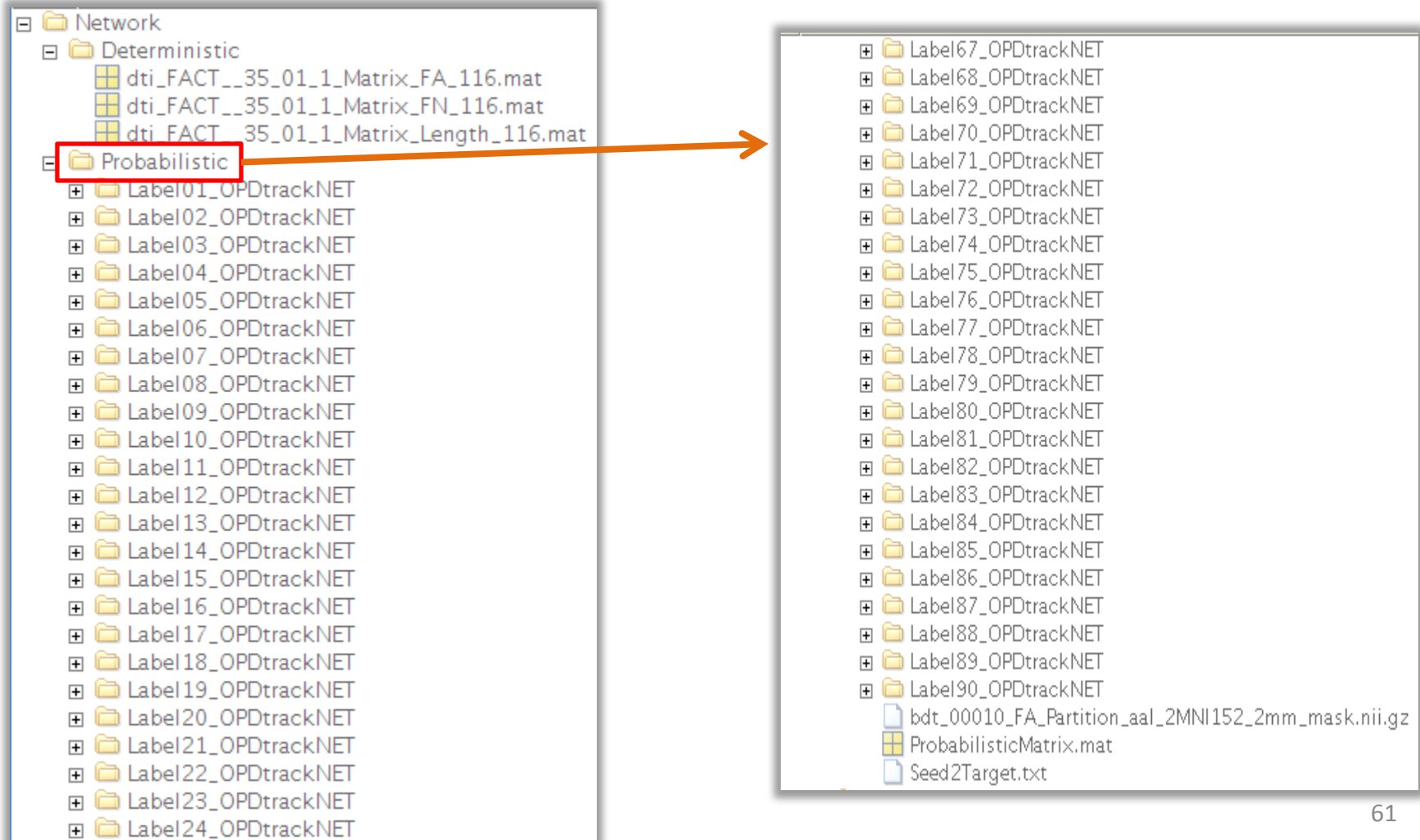
Understanding resultant files

Deterministic Fiber Tracking In the folder named 'trackvis'

- FA:
dti_fa.nii.gz
- color FA:
dti_fa_color.nii.gz
- MD:
dti_adc.nii.gz
- b0:
dti_b0.nii.gz
- 1st eigenvector:
dti_v1.nii.gz
- 2nd eigenvector:
dti_v2.nii.gz
- 3rd eigenvector:
dti_v3.nii.gz
- 1st eigenvalue:
dti_e1.nii.gz
- 2nd eigenvalue:
dti_e2.nii.gz
- 3rd eigenvalue:
dti_e3.nii.gz
- 4D data:
dti_dwi.nii.gz
- b vector file:
ForDTK_bvecs

Understanding resultant files

Folder Network:



Understanding resultant files

Deterministic Network In the folder named 'Network/Deterministic'

- *_Matrix_FA_*: average FA of all the voxels along the fibers between two regions
- *_Matrix_FN_*: fiber number between two regions
- *_Matrix_Length_*: average length of fibers between two regions

Understanding resultant files

Probabilistic Network

In the folder named 'Network/Probabilistic'

➤ ProbabilisticMatrix.mat:

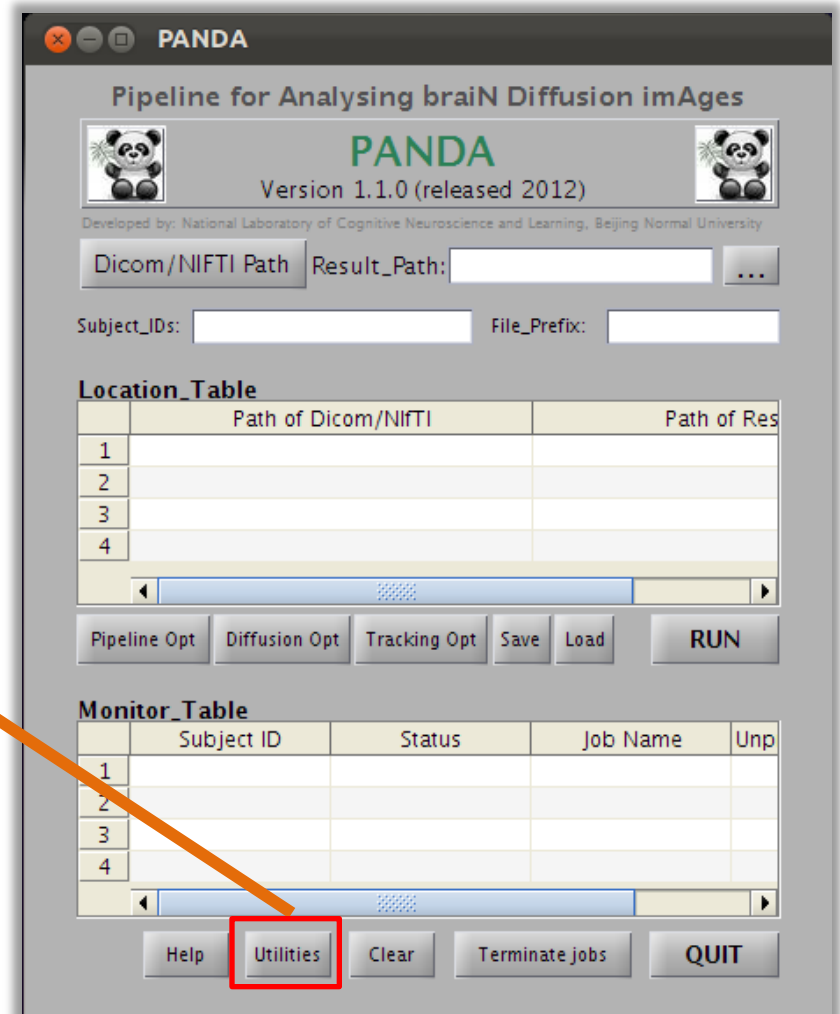
connection probability between two regions

Contents

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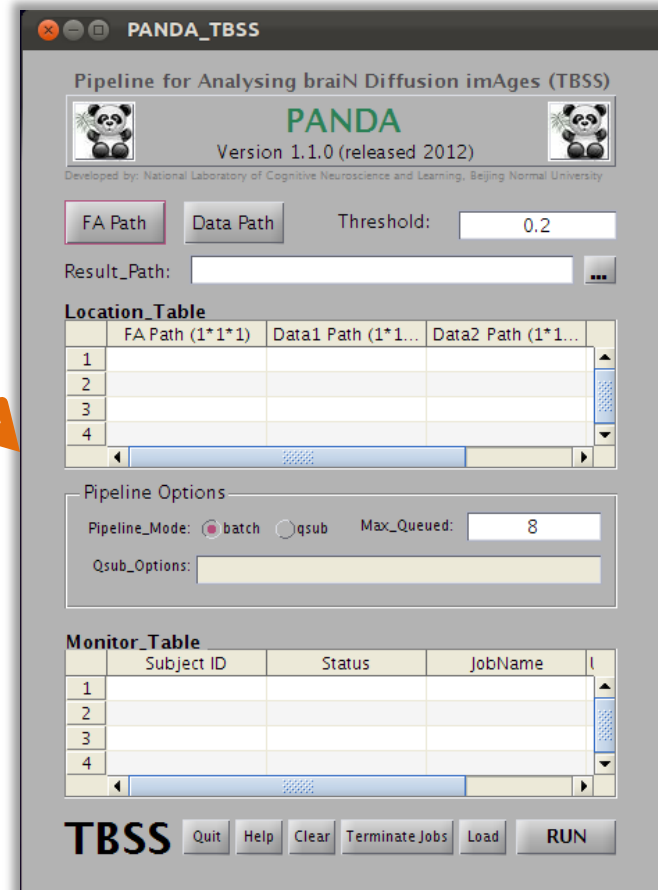
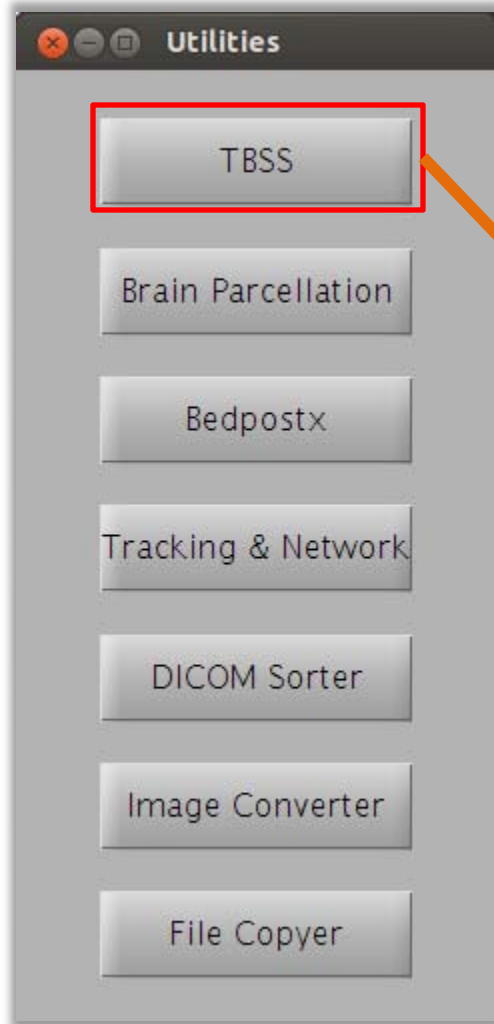


Utilities



Utilities (TBSS)

➤ Run TBSS for a group of subjects in parallel



Utilities (TBSS)

FA Path:
full path of subjects'
1*1*1 FA image

Data Path:
full path of 1*1*1 data to
be projected to the
average skeleton, such as
FA, MD, λ_1 , λ_{23m}

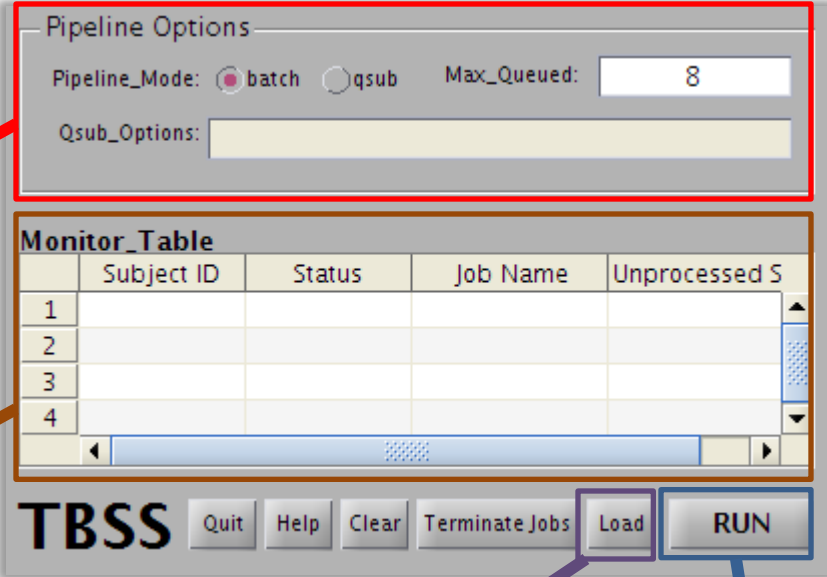
Threshold:
FA threshold to exclude
voxels in the grey matter
or CSF

Location_Table			
	FA Path (1*1*1)	Data1 Path (1*1...	Data2 Path (1*1...
1			
2			
3			
4			

Result Path:
full path of TBSS results

- 'Data Path' button can be clicked several times.
- Click 'Data Path' button once, user can add one type of data.
- The order of the [Data path](#) must be in accordance with [FA path](#).

Utilities (TBSS)



The screenshot shows the TBSS utility window. The 'Pipeline Options' section at the top is highlighted with a red box. It contains 'Pipeline_Mode' with radio buttons for 'batch' (selected) and 'qsub', a 'Max_Queued' text box with the value '8', and a 'Qsub_Options' text box. Below this is a 'Monitor_Table' with columns 'Subject ID', 'Status', 'Job Name', and 'Unprocessed S'. The table has four rows numbered 1 to 4. At the bottom, there are buttons: 'Quit', 'Help', 'Clear', 'Terminate Jobs', 'Load', and 'RUN'. The 'Load' button is highlighted with a purple box, and the 'RUN' button is highlighted with a blue box. Arrows point from text labels to these elements: a red arrow from 'Referring to: Pipeline Opt' to the 'Pipeline Options' box; a brown arrow from 'Referring to: Monitoring Progress' to the 'Monitor_Table'; a purple arrow from 'Loading the *.PANDA_TBSS file' to the 'Load' button; and a blue arrow from 'Current configuration will be forced to save after clicking 'RUN' button. (extension as .PANDA_TBSS)' to the 'RUN' button.

Referring to: Pipeline Opt

Referring to: Monitoring Progress

Loading the *.PANDA_TBSS file

Current configuration will be forced to save after clicking 'RUN' button.
(extension as .PANDA_TBSS)

Utilities (TBSS)

Set FA Path:

The image illustrates the process of setting the FA Path in the PANDA_TBSS software. It consists of three screenshots showing the software's interface and a selection dialog.

Screenshot 1: PANDA_TBSS Main Window

The main window displays the 'Pipeline for Analysing brain Diffusion imAges (TBSS)' interface. The 'FA Path' button is highlighted with a red box. The 'Data Path' and 'Threshold' (0.2) fields are also visible. The 'Result_Path' field is empty. Below the 'Location_Table' is the 'Pipeline Options' section, which includes 'Pipeline_Mode' (batch) and 'Max_Queued' (8). The 'Monitor_Table' is at the bottom.

Screenshot 2: Select Dialog Box

The 'Select' dialog box shows the directory '/data/node1/Zaixu/234'. The 'Subfolders' list includes '00010', '00011', '00012', 'TBSS', and 'logs'. The 'Images' list is empty. A red circle highlights the 'Selected 3 images' section, which contains the following files:

- pace/bdt_00010_FA_4normalize_to_target_1mm.nii.gz
- pace/bdt_00011_FA_4normalize_to_target_1mm.nii.gz
- pace/bdt_00012_FA_4normalize_to_target_1mm.nii.gz

Screenshot 3: PANDA_TBSS Main Window (After Selection)

The main window shows the 'Location_Table' with the selected files listed. A red circle highlights the 'Location_Table' content:

FA Path (1*1*1)
pace/bdt_00010_FA_4normalize_to_target_1mm.nii.gz
pace/bdt_00011_FA_4normalize_to_target_1mm.nii.gz
pace/bdt_00012_FA_4normalize_to_target_1mm.nii.gz

The 'Pipeline Options' and 'Monitor_Table' sections remain the same as in the first screenshot.

Utilities (TBSS)

Set Data1 Path:

The image illustrates the process of setting the Data1 Path in the PANDA_TBSS software. It consists of three screenshots showing the software's interface and a file selection dialog.

First Screenshot (Left): The PANDA_TBSS main window is shown. The 'Data Path' tab is selected. The 'Threshold' is set to 0.2. The 'Result_Path' is empty. The 'Location_Table' shows three entries for FA Path (1*1*1).

Location_Table	
FA Path (1*1*1)	
1	pace/bdt_00010_FA_4normalize_to_target_1mm.nii.gz
2	pace/bdt_00011_FA_4normalize_to_target_1mm.nii.gz
3	pace/bdt_00012_FA_4normalize_to_target_1mm.nii.gz

Second Screenshot (Middle): A 'Select' dialog box is open, showing the directory '/data/node1/Zaixu/234'. The 'Subfolders' list contains '00010', '00011', '00012', 'TBSS', and 'logs'. The 'Images' list is empty. The 'Selected 3 images' section shows three files: 'pace/bdt_00010_FA_4normalize_to_target_1mm.nii.gz', 'pace/bdt_00011_FA_4normalize_to_target_1mm.nii.gz', and 'pace/bdt_00012_FA_4normalize_to_target_1mm.nii.gz'.

Third Screenshot (Right): The PANDA_TBSS main window is shown again. The 'Data Path' tab is selected. The 'Result_Path' is now '/data/node1/Zaixu/234_tbss'. The 'Location_Table' shows three entries for Data1 Path (1*1*1), which are the paths of the three selected images from the previous screenshot.

Location_Table	
Path (1*1*1)	Data1 Path (1*1*1)
1	aiXu/234/00010/... /data/node1/Zaixu/234/00010/s...
2	aiXu/234/00011/s... /data/node1/Zaixu/234/00011/s...
3	aiXu/234/00012/s... /data/node1/Zaixu/234/00012/s...

An orange arrow points from the first screenshot to the third, indicating the sequence of steps.

Utilities (TBSS)

Set Data2 Path:

The image shows three screenshots of the PANDA_TBSS software interface, illustrating the process of setting the Data2 Path.

Screenshot 1: PANDA_TBSS Main Window

The main window displays the 'Pipeline for Analysing brain Diffusion imAges (TBSS)' interface. The 'Data Path' button is highlighted with a red box. The 'Threshold' is set to 0.2. The 'Result_Path' is set to /data/node1/Zaixu/234_tbss. The 'Location_Table' shows the following data:

	Path (1*1*1)	Data1 Path (1*1*1)
1	/data/node1/Zaixu/234/00010/s...	/data/node1/Zaixu/234/00010/s...
2	/data/node1/Zaixu/234/00011/s...	/data/node1/Zaixu/234/00011/s...
3	/data/node1/Zaixu/234/00012/s...	/data/node1/Zaixu/234/00012/s...

Screenshot 2: Select Dialog Box

The 'Select' dialog box shows the 'Dir' field set to /data/node1/Zaixu/234/*/*MD*1mm.nii.gz. The 'Prev' field is set to /data/node1/Zaixu/234. The 'Subfolders' list includes 00010, 00011, 00012, TBSS, and logs. The 'Images' list shows three selected images, which are circled in red:

- ce/bdt_00010_MD_4normalize_to_target_1mm.nii.gz
- ce/bdt_00011_MD_4normalize_to_target_1mm.nii.gz
- ce/bdt_00012_MD_4normalize_to_target_1mm.nii.gz

Screenshot 3: PANDA_TBSS Main Window (After Selection)

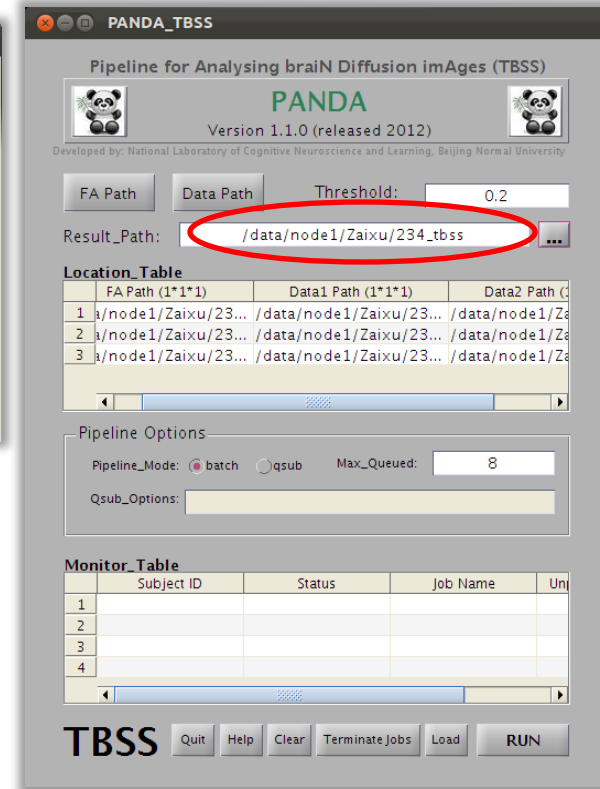
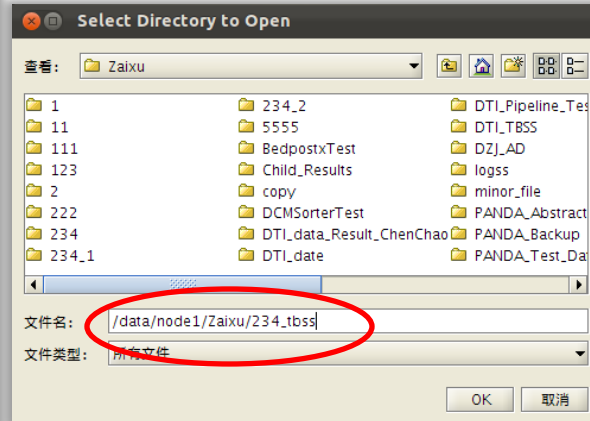
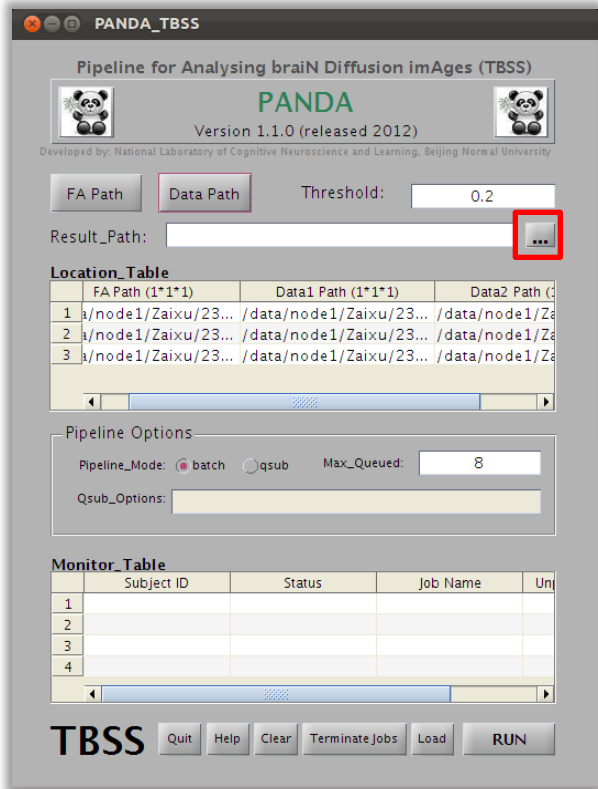
The main window displays the 'Pipeline for Analysing brain Diffusion imAges (TBSS)' interface. The 'Data Path' button is highlighted with a red box. The 'Threshold' is set to 0.2. The 'Result_Path' is set to /data/node1/Zaixu/234_tbss. The 'Location_Table' shows the following data:

	1*1	Data1 Path (1*1*1)	Data2 Path (1*1*1)
1	/data/node1/Zaixu/2...	/data/node1/Zaixu/2...	/data/node1/Zaixu/2...
2	/data/node1/Zaixu/2...	/data/node1/Zaixu/2...	/data/node1/Zaixu/2...
3	/data/node1/Zaixu/2...	/data/node1/Zaixu/2...	/data/node1/Zaixu/2...

An orange arrow points from the 'Select' dialog box to the third screenshot, indicating the flow of the process.

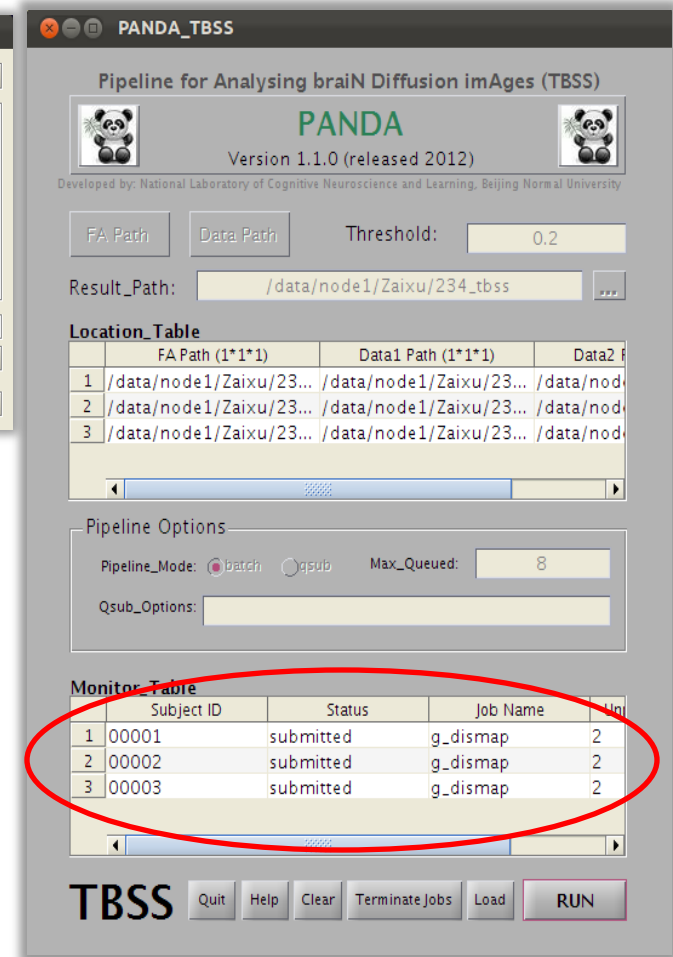
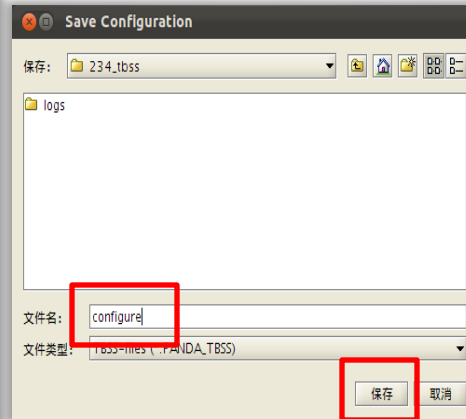
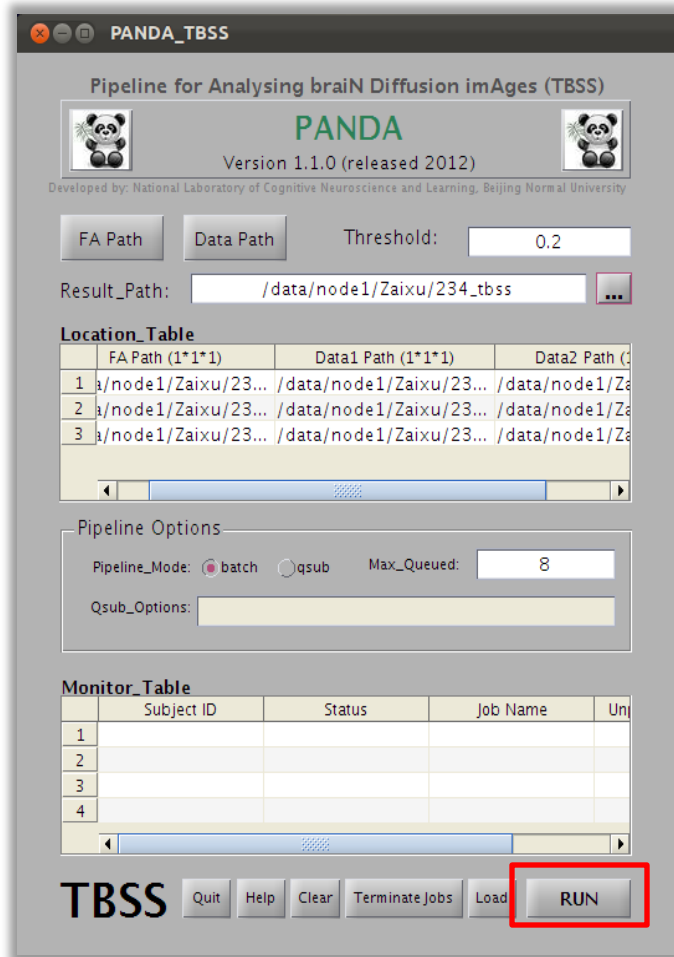
Utilities (TBSS)

Set Result Path:



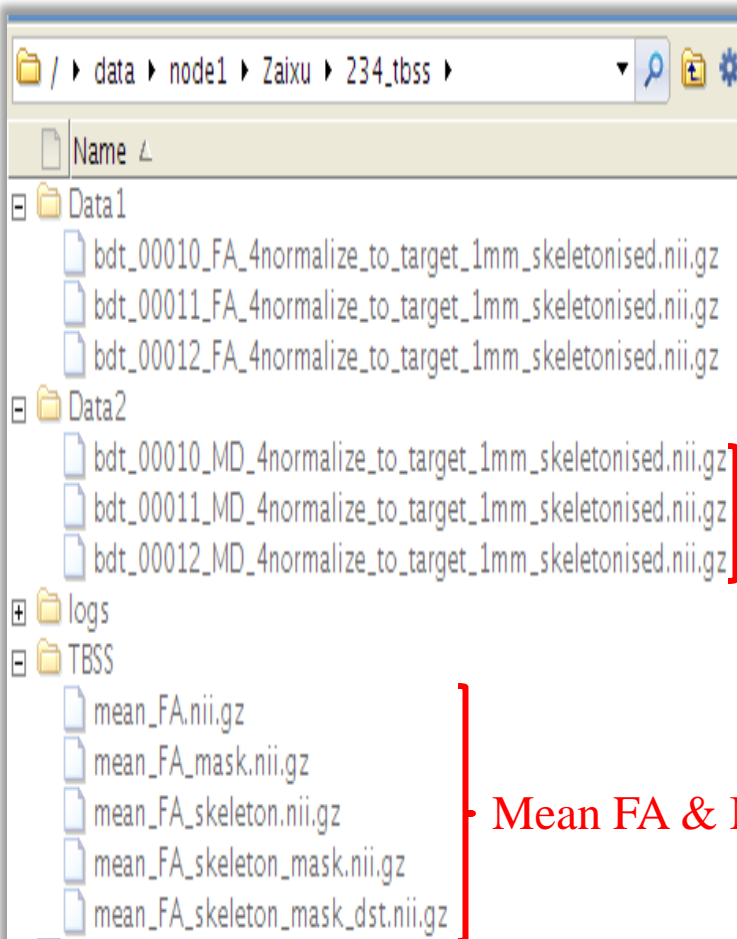
Utilities (TBSS)

Initiating Process:



Utilities (TBSS)

Resultant Files:



➤ First: mean FA and mean FA skeleton will be produced in 'TBSS' folder .

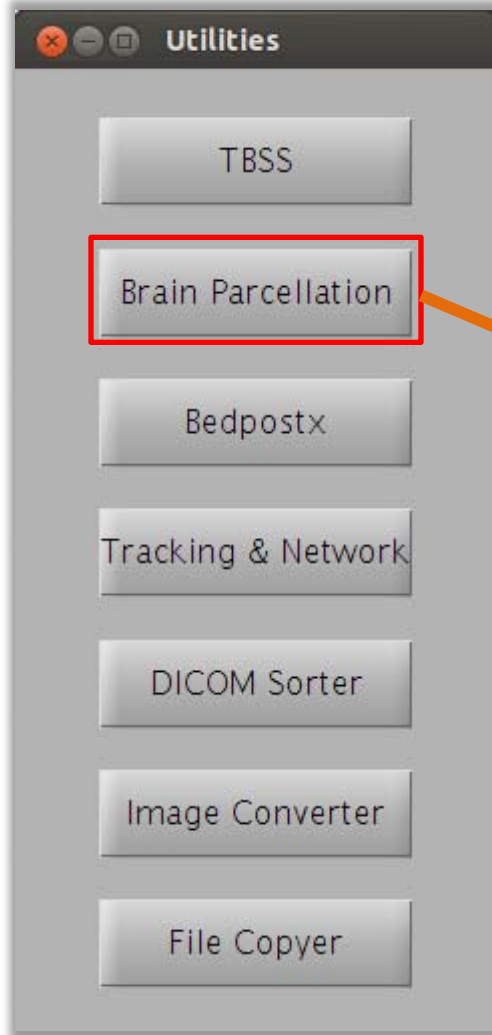
➤ Next: map mean FA skeleton to native data (FA, MD, λ_1 , λ_{23m} .etc), resulting in native skeleton.

Native MD skeleton

Mean FA & Mean FA skeleton

Utilities (Brain Parcellation)

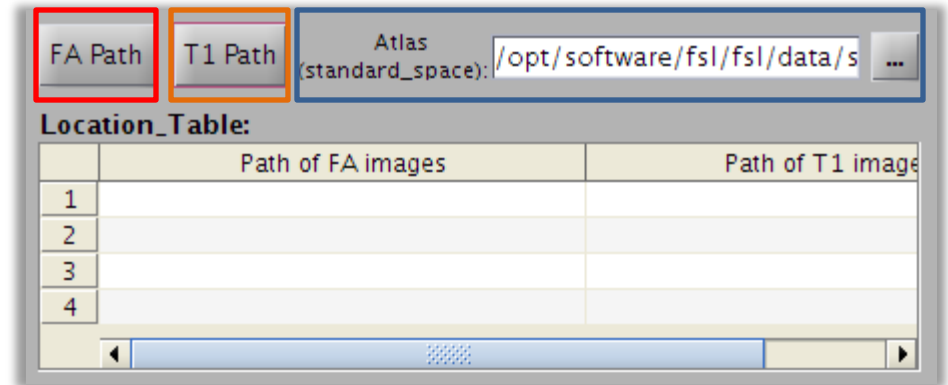
- Run brain parcellation according to atlas for any number of subjects in parallel



Utilities (Brain Parcellation)

FA Path:
full path of subjects' FA
images

T1 Path:
full path of subjects' T1
images



FA Path T1 Path Atlas (standard_space): /opt/software/fsl/fsl/data/s ...

Location_Table:

	Path of FA images	Path of T1 image
1		
2		
3		
4		

Atlas (standard space):
full path of atlas in the
standard space, such as
AAL atlas

➤ The order of T1 path must be in accordance with the order of FA path

Utilities (Brain Parcellation)

The screenshot shows the 'Brain Parcellation' utility window. The 'Pipeline Options' section at the top includes a 'Pipeline_Mode' with radio buttons for 'batch' (selected) and 'qsub', a 'Max_Queued' input field set to '8', a 'Qsub_Options' text field, and a 'Log_Path' field with the value '/data/node1/program/matlab_work/PANDA_Private'. Below this is a 'Monitor_Table' with columns 'Subject ID', 'Status', 'Job Name', and 'Unproc'. The table has four rows numbered 1 to 4. At the bottom, there are buttons for 'Quit', 'Help', 'Clear', 'Load', and 'RUN'. The 'Load' button is highlighted with a purple box, and the 'RUN' button is highlighted with a blue box. Arrows point from text labels to these elements: a red arrow from 'Referring to: Pipeline Opt' to the Pipeline Options section; a brown arrow from 'Referring to: Monitoring Progress' to the Monitor_Table; a purple arrow from 'Loading the *.PANDA_BrainParcellation file' to the Load button; and a blue arrow from 'Current configuration will be forced to save after clicking 'RUN' button. (extension as .PANDA_BrainParcellation)' to the RUN button.

Referring to: [Pipeline Opt](#)

Referring to: [Monitoring Progress](#)

Loading the ***.PANDA_BrainParcellation** file

Current configuration will be forced to save after clicking 'RUN' button. (extension as **.PANDA_BrainParcellation**)

Utilities (Brain Parcellation)

Set FA Path:

The image shows three screenshots of the PANDA Brain Parcellation software interface, illustrating the process of setting FA paths.

Screenshot 1: PANDA Brain Parcellation (Initial State)

The interface shows the 'FA Path' button highlighted with a red box. The 'Location Table' is empty.

	Path of FA Images	Path of T1 Images
1		
2		
3		
4		

Screenshot 2: Select Dialog Box

The 'Select' dialog box shows the 'Dir' field set to `/data/node1/Zaixu/234/*/*FA.nii.gz` and the 'Prev' field set to `/data/node1/Zaixu/234`. The 'Subfolders' list contains `00010`, `00011`, `00012`, `TBSS`, and `logs`. The 'Images' list is empty. The 'Selected 3 Images' list contains:

- `Zaixu/234/00010/native_space/bdt_00010_FA.nii.gz`
- `Zaixu/234/00011/native_space/bdt_00011_FA.nii.gz`
- `Zaixu/234/00012/native_space/bdt_00012_FA.nii.gz`

Screenshot 3: PANDA Brain Parcellation (After Selection)

The 'Location Table' is updated with the selected files, highlighted with a red circle:

	Path of FA Images	Path of T1 Images
1	<code>/00010/native/bdt_00010_FA.nii.gz</code>	
2	<code>/00011/native/bdt_00011_FA.nii.gz</code>	
3	<code>/00012/native/bdt_00012_FA.nii.gz</code>	
4		

A large orange arrow points from the first screenshot to the third, indicating the sequence of steps.

Utilities (Brain Parcellation)

Set T1 Path:

PANDA_BrainParcellation

Pipeline for Analysing brain Diffusion imAges (Brain Parcellation)

PANDA
Version 1.1.0 (released 2012)
Developed by: National Laboratory of Cognitive Neuroscience and Learning, Beijing Normal University

FA Path T1 Path Atlas (standard_space): /opt/software/fsl/fsl/data/s ...

Location_Table:

	Path of FA images	Path of T1 images
1	/00010/native/bdt_00010_FA.nii.gz	
2	/00011/native/bdt_00011_FA.nii.gz	
3	/00012/native/bdt_00012_FA.nii.gz	

Pipeline Options

Pipeline_Mode: ☒ batch ☐ qsub Max_Queue:

Qsub_Options:

Log_Path: /data/node1/Zaixu/234_tbss ...

Monitor_Table:

	Subject ID	Status	Job Name	Unproc
1				
2				
3				
4				

Brain Parcellation Quit Help Clear Load **RUN**
(Can be used for network node definition)

Select

Dir: /data/node1/Zaixu/DTI_Pipeline_Test/BDt_T1_Pipeline/003 ☐ Use

Prev: /data/node1/Zaixu/DTI_Pipeline_Test/BDt/BDt...

Subfolders: .. 003

Images: BDt_003_t1_bet.nii.gz BDt_003_t1.nii.gz

Selected 3 images:

- /data/node1/Zaixu/DTI_Pipeline_Test/BDt_T1_Pipeline/001/BDt_001_t1_bet.nii.gz
- /data/node1/Zaixu/DTI_Pipeline_Test/BDt_T1_Pipeline/002/BDt_002_t1_bet.nii.gz
- /data/node1/Zaixu/DTI_Pipeline_Test/BDt_T1_Pipeline/003/BDt_003_t1_bet.nii.gz

Done



PANDA_BrainParcellation

Pipeline for Analysing brain Diffusion imAges (Brain Parcellation)

PANDA
Version 1.1.0 (released 2012)
Developed by: National Laboratory of Cognitive Neuroscience and Learning, Beijing Normal University

FA Path T1 Path Atlas (standard_space): /opt/software/fsl/fsl/data/standa ...

Location_Table:

	Path of FA images	Path of T1 images
1	/1/Zaixu/234/00010/nativ...	/data/node1/Zaixu/DTI_Pipeline_Test...
2	/1/Zaixu/234/00011/nativ...	/data/node1/Zaixu/DTI_Pipeline_Test...
3	/1/Zaixu/234/00012/nativ...	/data/node1/Zaixu/DTI_Pipeline_Test...

Pipeline Options

Pipeline_Mode: ☒ batch ☐ qsub Max_Queue: 8

Qsub_Options:

Log_Path: /data/node1/Zaixu ...

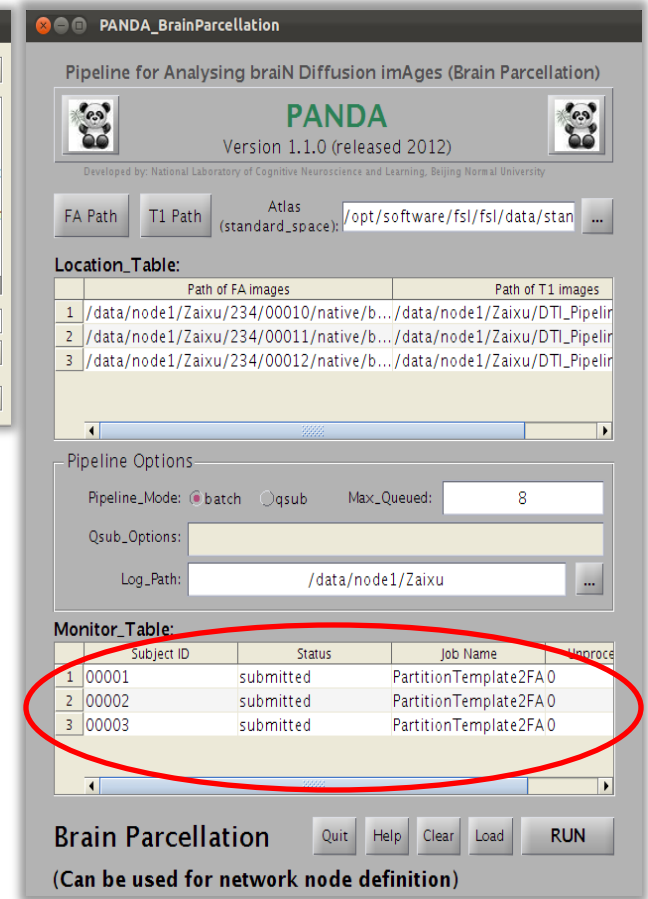
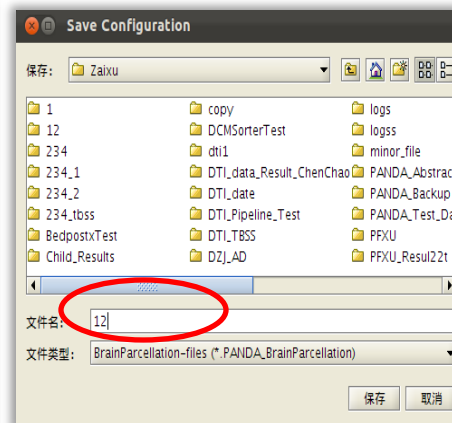
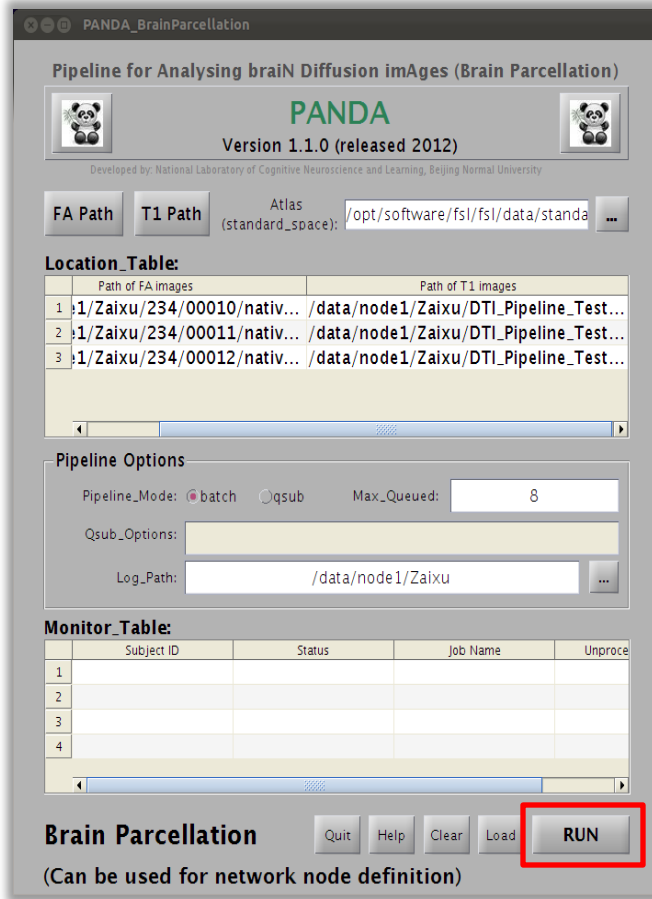
Monitor_Table:

	Subject ID	Status	Job Name	Unproc
1				
2				
3				
4				

Brain Parcellation Quit Help Clear Load **RUN**
(Can be used for network node definition)

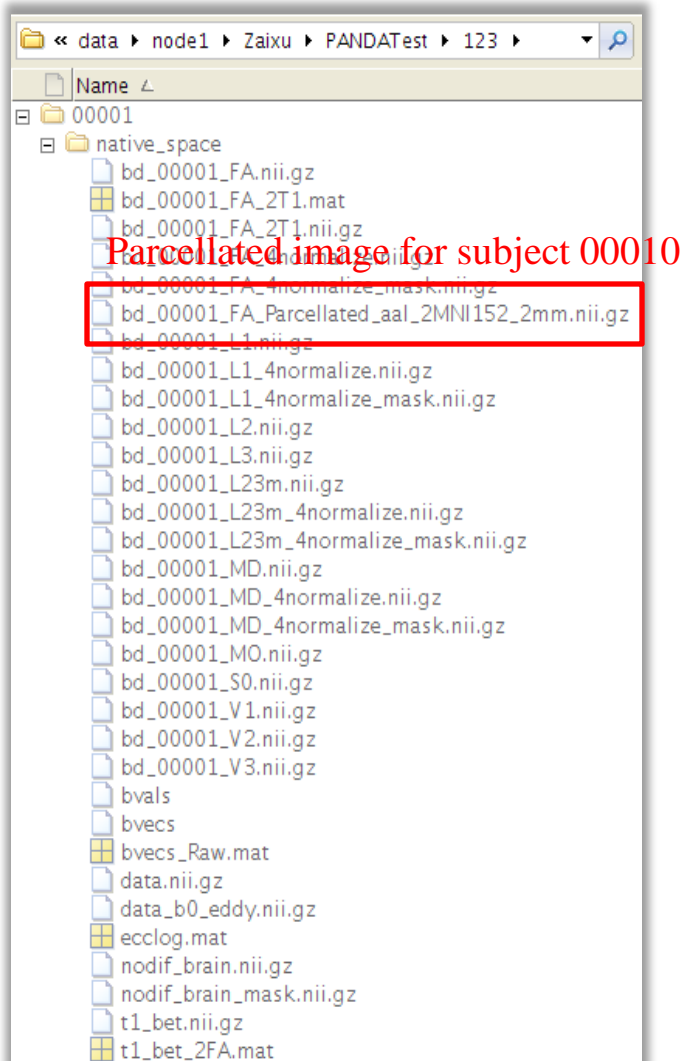
Utilities (Brain Parcellation)

Initiating Process:



Utilities (Brain Parcellation)

Resultant Files:



➤ A file named ‘*_Parcellated_*.nii.gz’ will be produced in the same folder of FA.

➤ In this example:

Path of FA images are

/data/node1/Zaixu/234/00010/native/

bd_00010_FA.nii.gz

/data/node1/Zaixu/234/00011/native/

bd_00011_FA.nii.gz

/data/node1/Zaixu/234/00012/native/

bd_00012_FA.nii.gz

Outputs are

/data/node1/Zaixu/234/00010/native/

bd_00010_FA_Parcellated_*.nii.gz

/data/node1/Zaixu/234/00011/native/

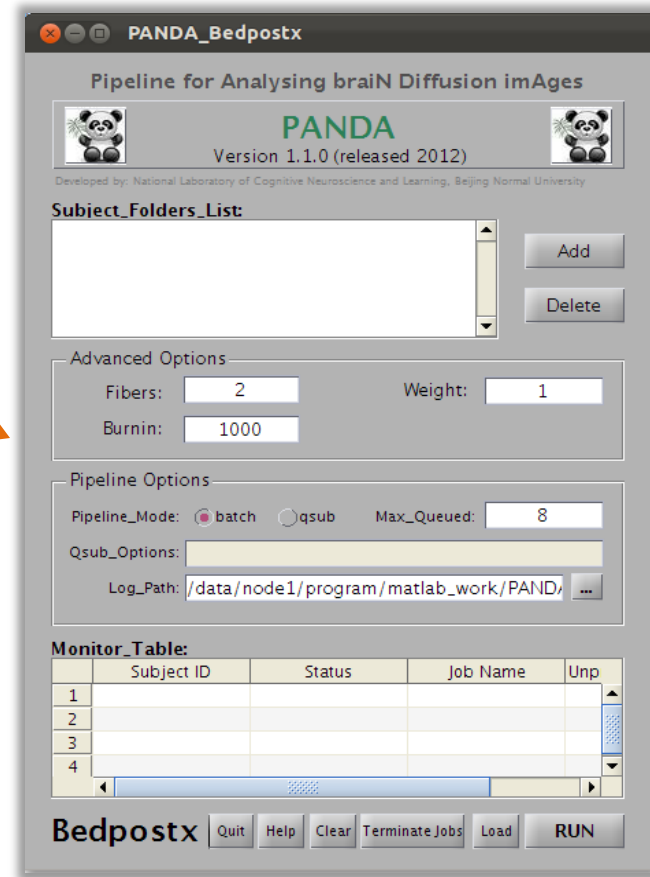
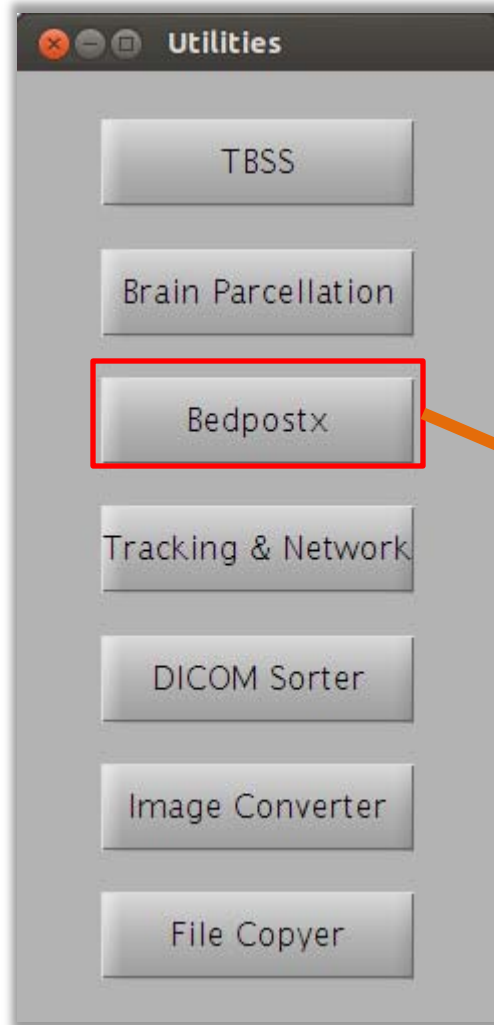
bd_00011_FA_Parcellated_*.nii.gz

/data/node1/Zaixu/234/00012/native/

bd_00012_FA_Parcellated_*.nii.gz

Utilities (BedpostX)

- Run bedpostX for any number of subjects in parallel



Utilities (BedpostX)

Subject Folders List:
full path of subjects'
folders which contain
mask, bvecs, bvals and 4D
data

Fibers:
Number of fibers per
voxel, default 2

The screenshot shows a window titled "Subject_Folders_List" with a list box and "Add" and "Delete" buttons. Below this is an "Advanced Options" section with three input fields: "Fibers" (value 2), "Burnin" (value 1000), and "Weight" (value 1). The "Fibers" field is highlighted with an orange border, and the "Weight" field is highlighted with a blue border.

Burnin:
Burnin period, default
1000

Weight:
ARD weight, more weight
means less secondary
fibers per voxel, default 1

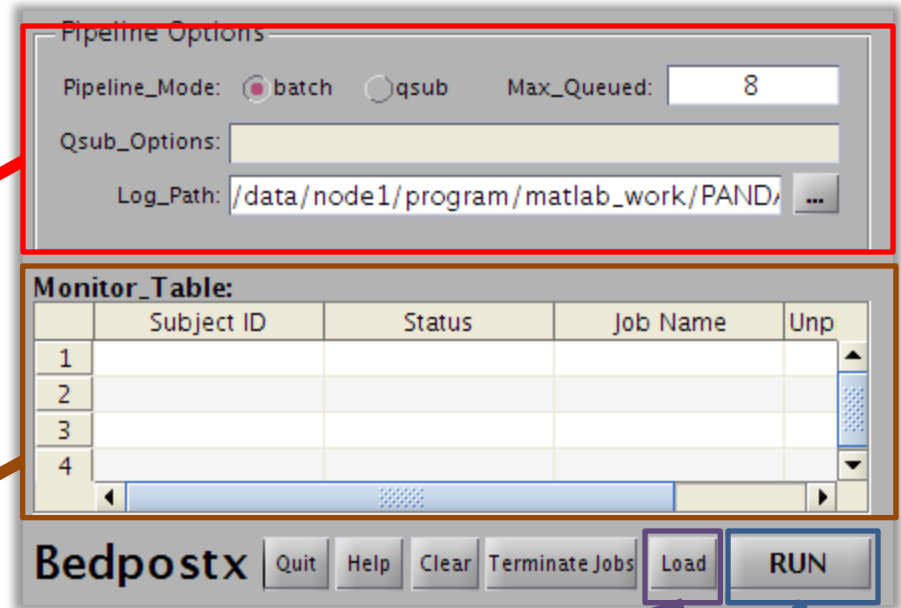
Utilities (BedpostX)

Referring to: [Pipeline Opt](#)

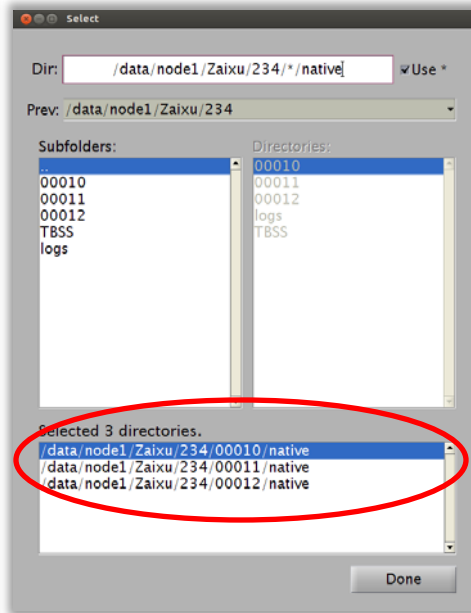
Referring to: [Monitoring Progress](#)

Loading the *.PANDA_BedpostX file

Current configuration will be forced to save after clicking 'RUN' button.
(extension as .PANDA_BedpostX)



Input subjects' folder:



Utilities (BedpostX)

Initiating Process:

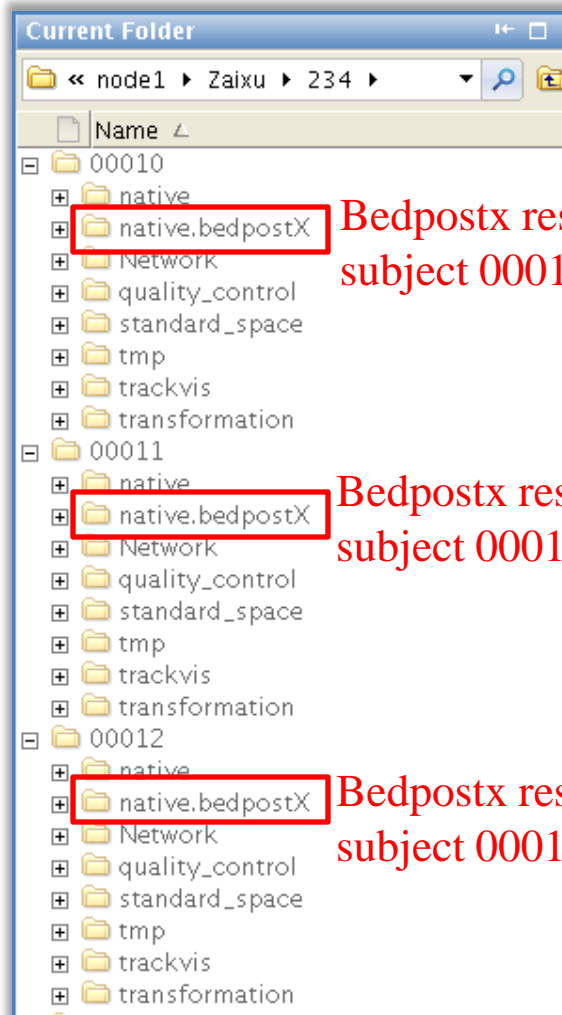
The image illustrates the process of initiating the BedpostX utility within the PANDA software. It consists of three sequential screenshots:

- Initial State:** The PANDA_Bedpostx window is open, showing the 'Pipeline for Analysing brain Diffusion images (Bedpostx)'. The 'Subject_Folders_List' contains three entries. The 'Advanced Options' section shows 'Fibers' set to 2 and 'Weight' set to 1. The 'Pipeline Options' section shows 'Pipeline_Mode' set to 'batch' and 'Max_Queued' set to 2. The 'Monitor_Table' is empty. The 'RUN' button is highlighted with a red box.
- Save Configuration:** A 'Save Configuration' dialog box is open, showing the file name '12' circled in red. The file type is 'Bedpostx-files (*.PANDA_Bedpostx)'. The '保存' (Save) button is visible.
- Monitoring:** The PANDA_Bedpostx window is shown again, with the 'Monitor_Table' circled in red. The table contains three rows of data, indicating the start of the process.

	Subject ID	Status	Job Name	Unproc
1	00001	wait	Bedpostx	1
2	00002	wait	Bedpostx	1
3	00003	wait	Bedpostx	1

Utilities (BedpostX)

Resultant Files:



Bedpostx result for
subject 00010

Bedpostx result for
subject 00011

Bedpostx result for
subject 00012

➤ A folder named `*.bedpostX` will be produced for each subject.

➤ In this example:
Inputs are

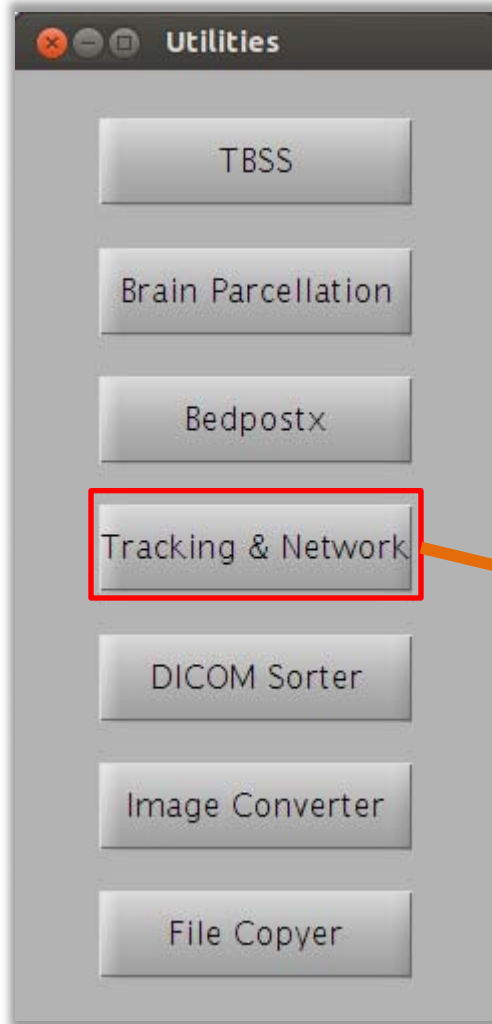
`/data/node1/Zaixu/234/00010/native`
`/data/node1/Zaixu/234/00011/native`
`/data/node1/Zaixu/234/00012/native`

Outputs are

`/data/node1/Zaixu/234/00010/native.bedpostX`
`/data/node1/Zaixu/234/00011/native.bedpostX`
`/data/node1/Zaixu/234/00012/native.bedpostX`

Utilities (Tracking & Network)

- Run Tracking & Network Construction for any number of subjects in parallel



Utilities (Tracking & Network)

With PANDA_Tracking GUI, you can do:

- Deterministic Fiber Tracking
- Deterministic Network Construction
- Probabilistic Fiber Tracking & Network Construction
- BedpostX & Probabilistic Fiber Tracking & Network Construction

Utilities (Tracking & Network)

Deterministic Fiber Tracking

First step: input subjects' folders which contain bvces, bvvals, mask and 4D data

Subject_Folders_List:

- /data/node1/Zaixu/234/00010/native
- /data/node1/Zaixu/234/00011/native
- /data/node1/Zaixu/234/00012/native

Add

Delete

☒ Deterministic Fiber Tracking

Image_Orientation: Auto

Propagation_Algorithm: FACT

FA_Threshold: 0.1 ~ 1

Orientation_Patch: Invert Z No Sw...

Angle_Threshold: 35

Step_Length: [empty]

☒ Apply Spline Filter

Second step: select Deterministic Fiber Tracking
Referring to: [Deterministic Fiber Tracking](#)

Utilities (Tracking & Network)

Deterministic Network Construction

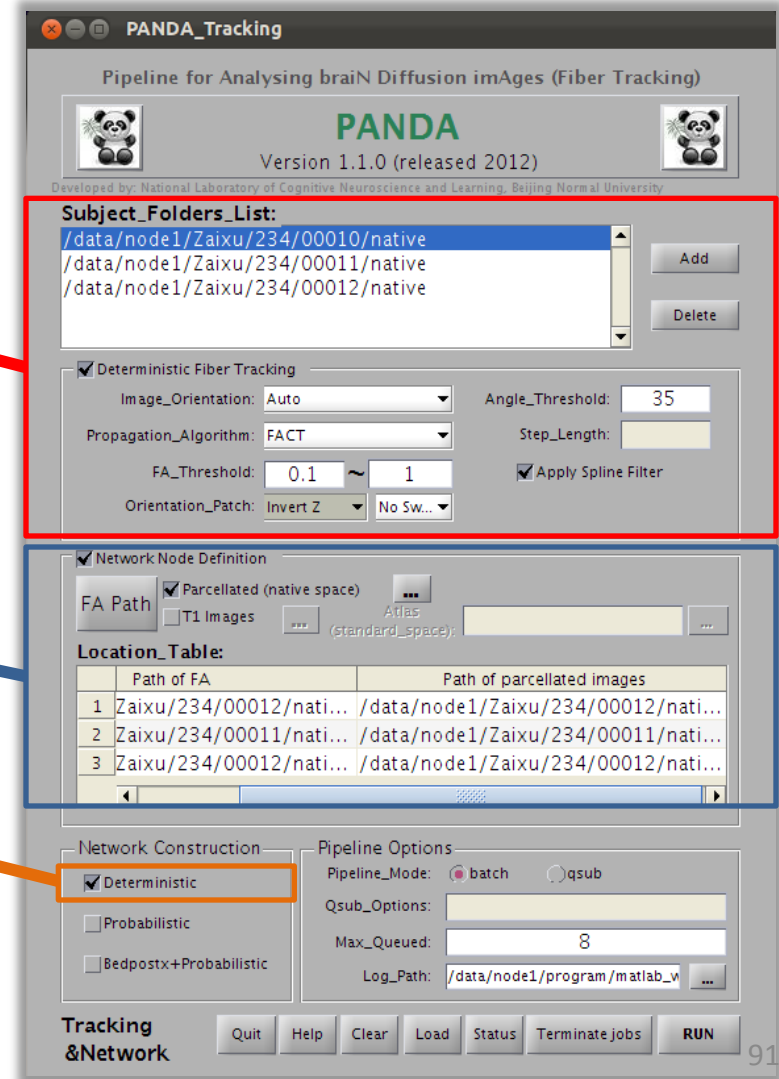
First step: select Deterministic Fiber Tracking

Referring to: [Deterministic Fiber Tracking](#)

Second step: select Network Node Definition

Referring to: [Next Page](#)

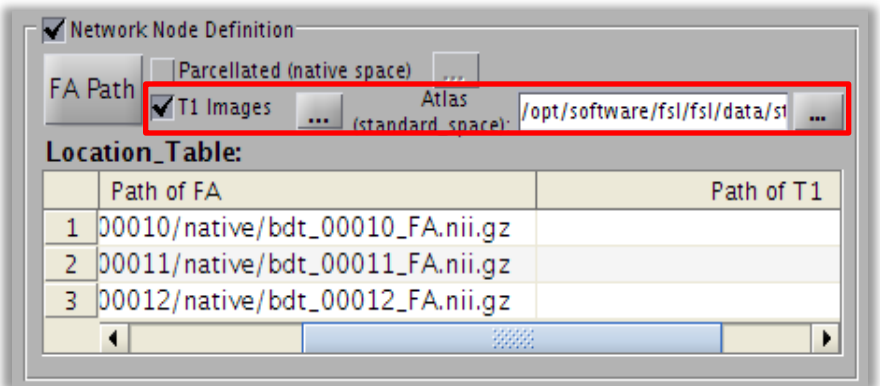
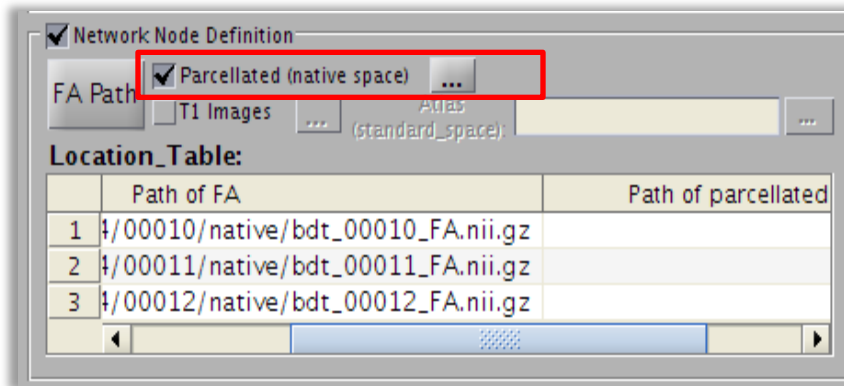
Third step: select Deterministic
Network Construction



Utilities (Tracking & Network)

Network Node Definition

First, please click '[FA Path](#)' button to input subjects' FA paths



When you have parcellated images in native space :

Please select '[Parcellated \(native space\)](#)' and input these images

When you don't have parcellated images in native space :

Please select '[T1 images](#)' and input these images

The order of paths of [parcellated images](#) or [T1 images](#) must be in accordance with the order of the paths of [FA images](#) .

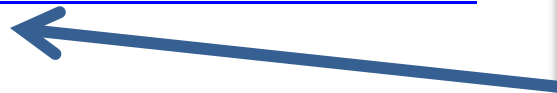
Utilities (Tracking & Network)

Probabilistic Fiber Tracking & Network Construction

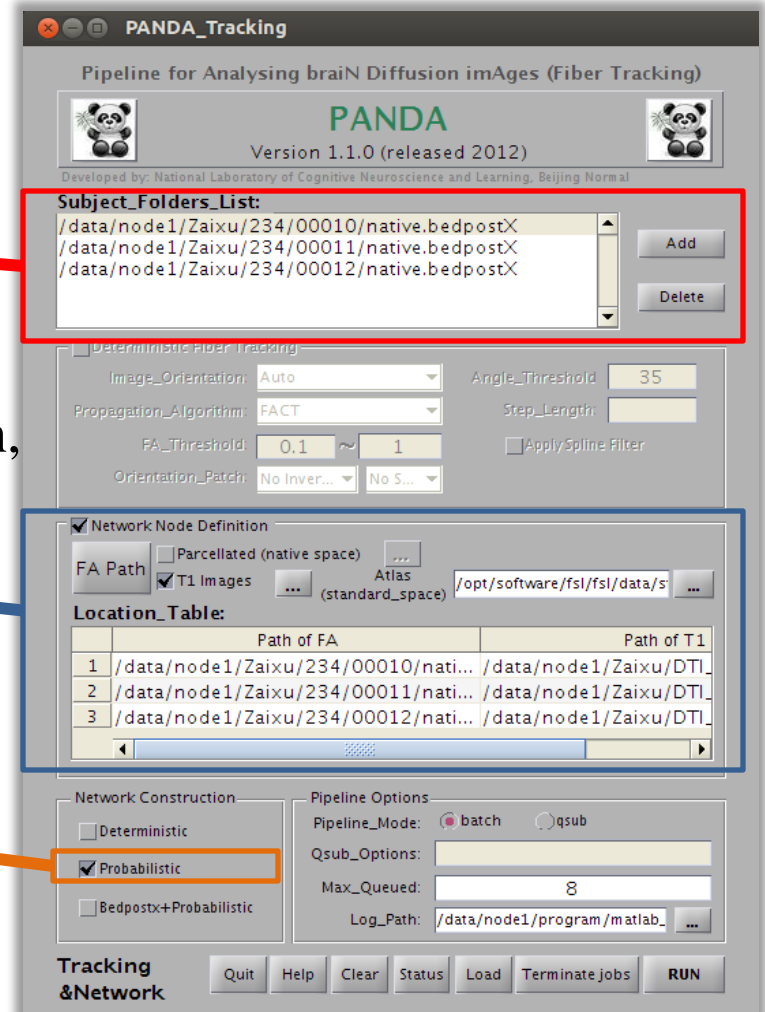
First step: input subjects' bedpostX
result folder



Second step: select Network Node Definition,
Referring to: [Network Node Definition](#)

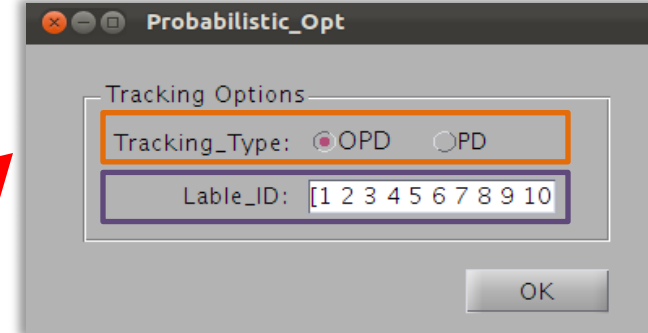
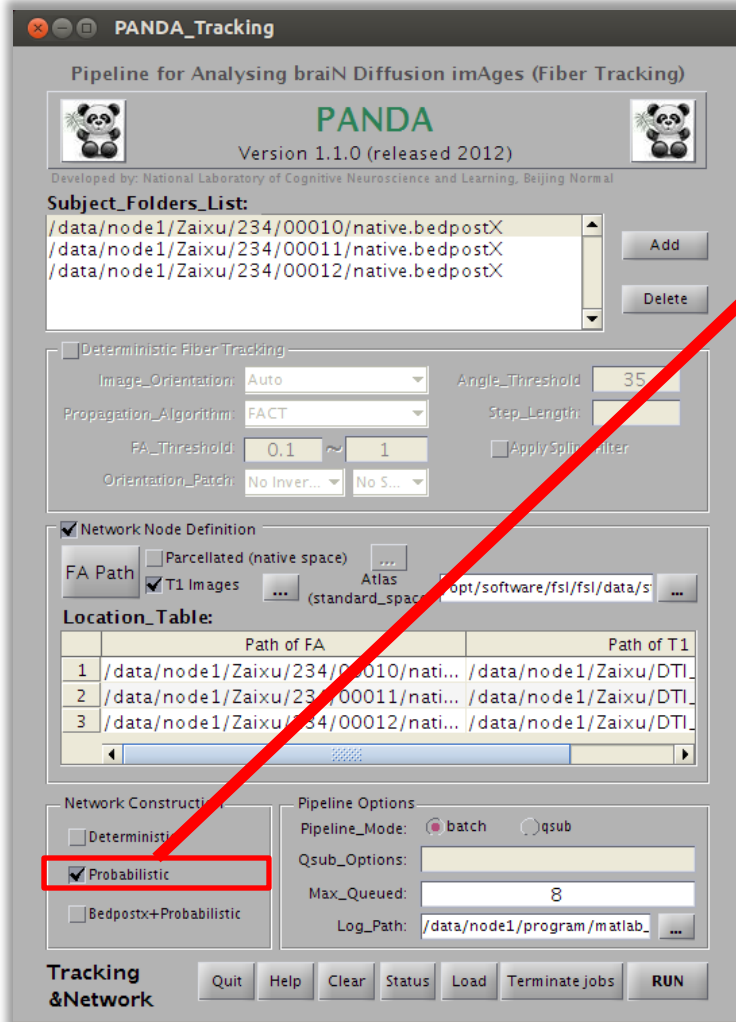


Third step: select Probabilistic Network
Construction
Referring to [Next Page](#)



Utilities (Tracking & Network)

Probabilistic Fiber Tracking & Network Construction



Tracking Type:
OPD(output path distribution);
PD(Correct path distribution for
the length of the pathways and
output path distribution)

Label ID:
the id of brain region in atlas

Utilities (Tracking & Network)

BedpostX+Probabilistic Fiber Tracking & Network Construction

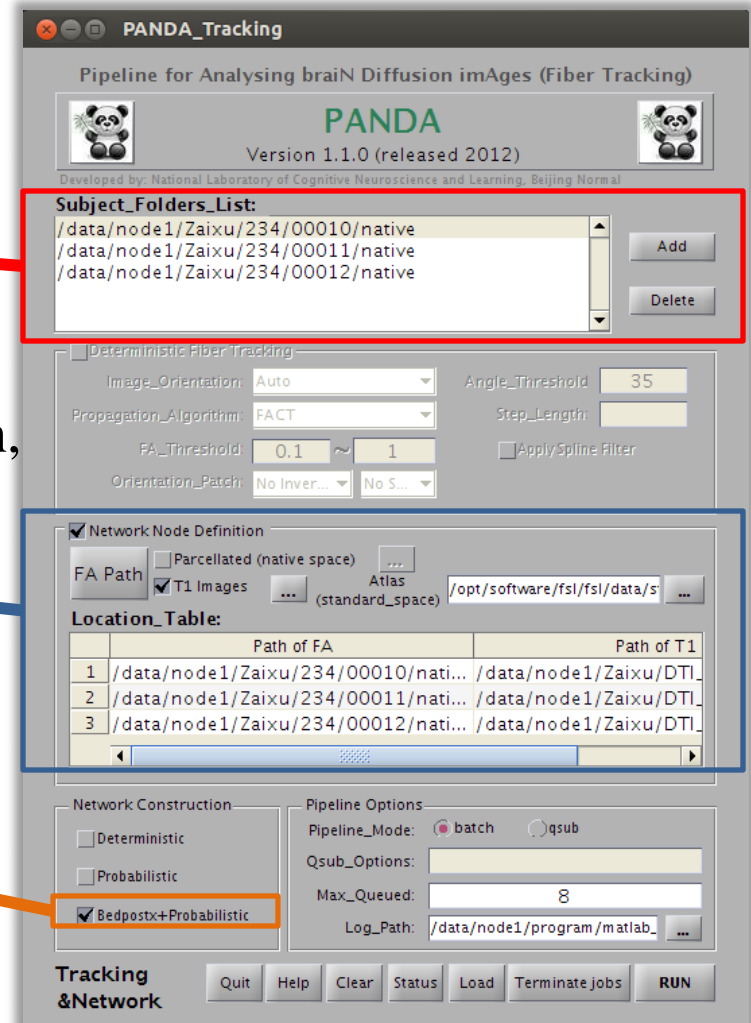
First step: input subjects' folder which contain bvces, bvvals, mask, 4D data



Second step: select Network Node Definition,
Referring to: [Network Node Definition](#)

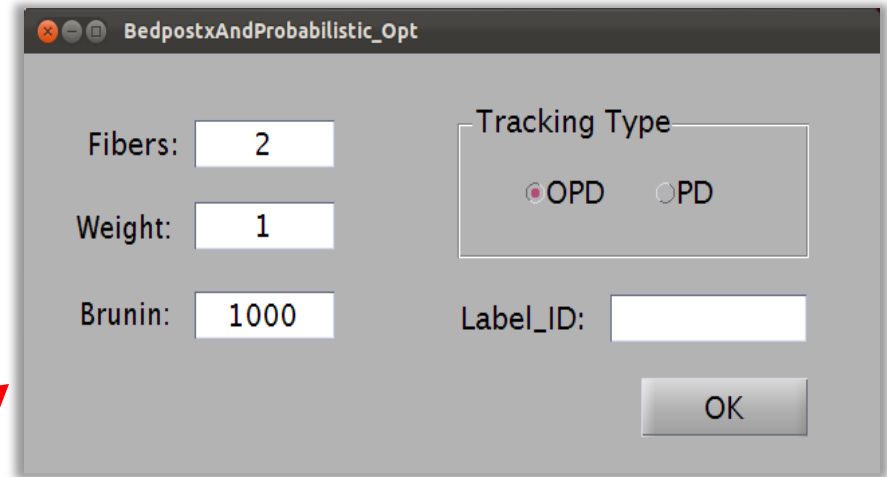
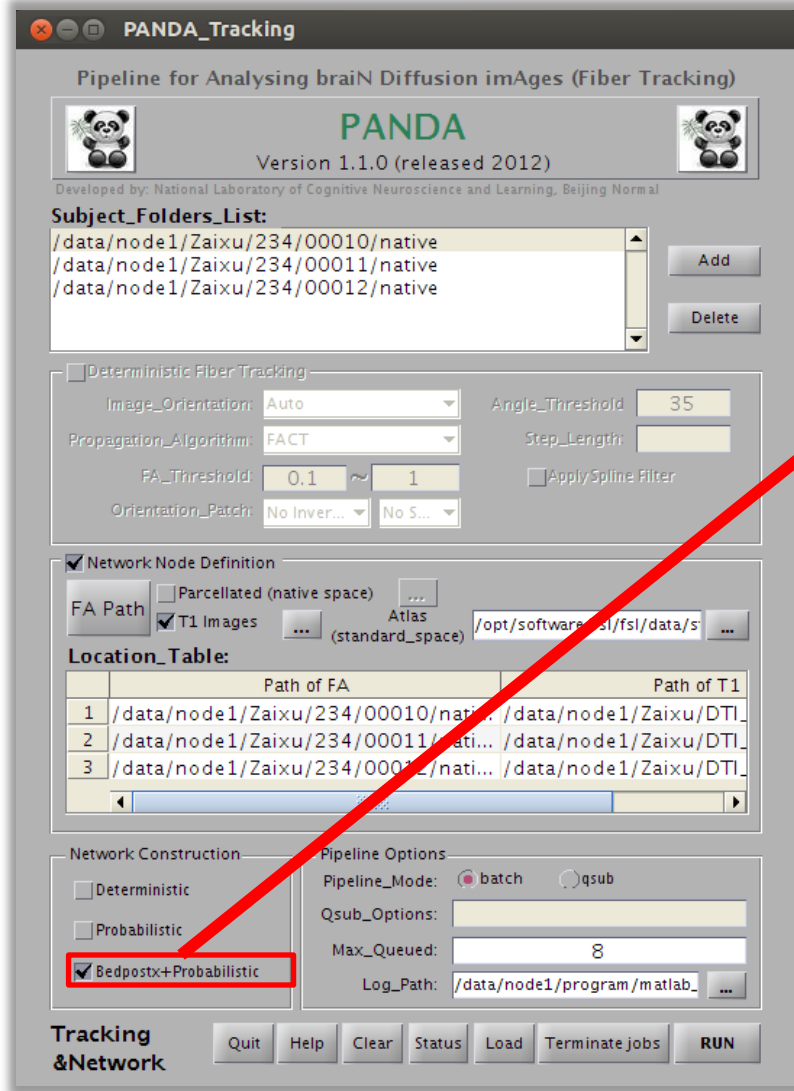


Third step: select Bedpostx+Probabilistic
Network Construction
Referring to [Next Page](#)



Utilities (Tracking & Network)

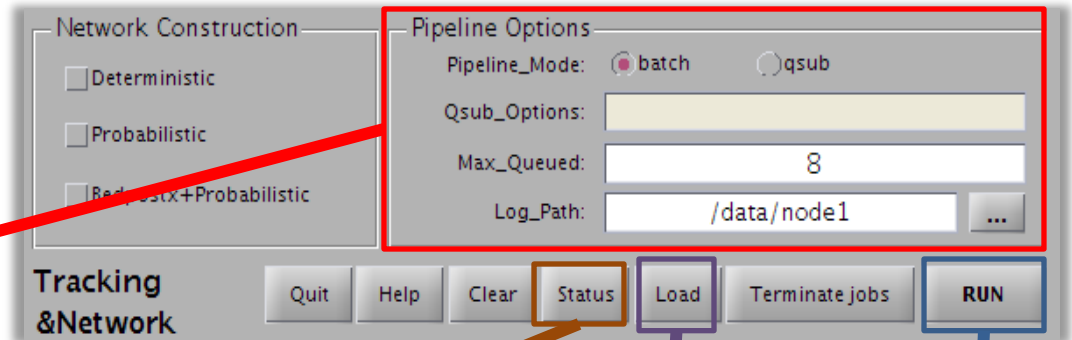
BedpostX+Probabilistic Fiber Tracking & Network Construction



Referring to: [Network Node Definition](#)

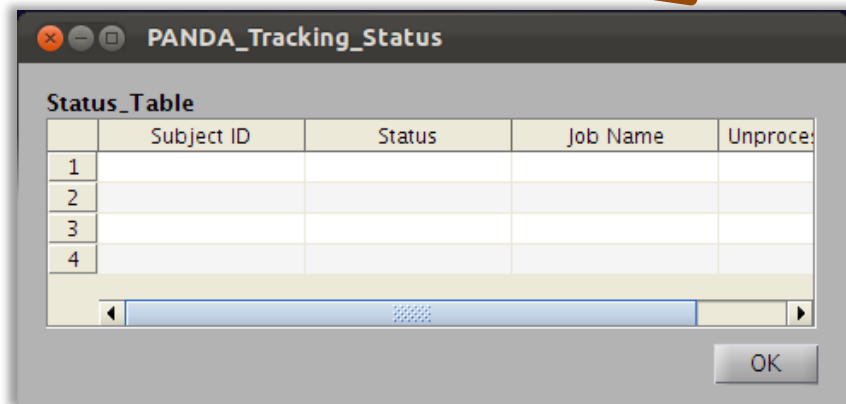
Utilities (Tracking & Network)

Referring to: [Pipeline Opt](#)



Loading the
*.PANDA_Tracking file

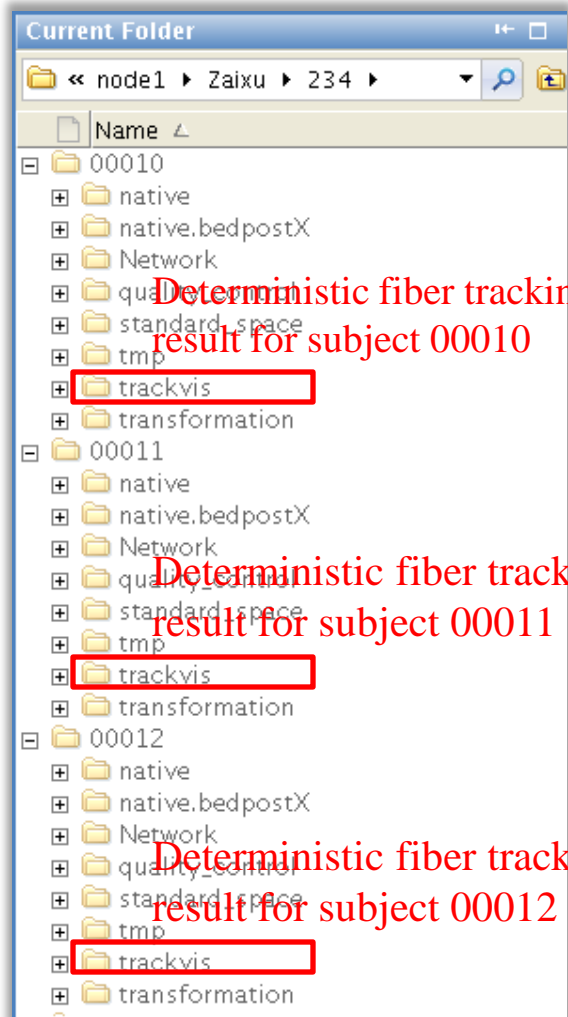
Current configuration will be
forced to save after
clicking 'RUN' button.
(extension as .PANDA_Tracking)



Referring to: [Monitoring Progress](#)

Utilities (Tracking & Network)

Resultant Files (Deterministic Fiber Tracking):



➤ A folder named **'trackvis'** will be produced for each subject.

➤ In this example:

Inputs are

/data/node1/Zaixu/234/00010/native
/data/node1/Zaixu/234/00011/native
/data/node1/Zaixu/234/00012/native

Outputs are

/data/node1/Zaixu/234/00010/trackvis
/data/node1/Zaixu/234/00011/trackvis
/data/node1/Zaixu/234/00012/trackvis

Utilities (Tracking & Network)

Resultant Files :

➤Deterministic Fiber Tracking:

➤A folder named 'Network' will be produced for each subject, then a folder named 'Deterministic' will be produced in the folder 'Network'.

➤In this example:

Inputs are

/data/node1/Zaixu/234/00010/native

/data/node1/Zaixu/234/00011/native

/data/node1/Zaixu/234/00012/native

Outputs are

/data/node1/Zaixu/234/00010/Network/Deterministic

/data/node1/Zaixu/234/00011/Network/Deterministic

/data/node1/Zaixu/234/00012/Network/Deterministic

Utilities (Tracking & Network)

Resultant Files (Probabilistic Fiber Tracking):

➤ A folder named 'Network' will be produced for each subject, then a folder named 'Probabilistic' will be produced in the folder 'Network'.

➤ In this example:

Inputs are

/data/node1/Zaixu/234/00010/native

/data/node1/Zaixu/234/00011/native

/data/node1/Zaixu/234/00012/native

Outputs are

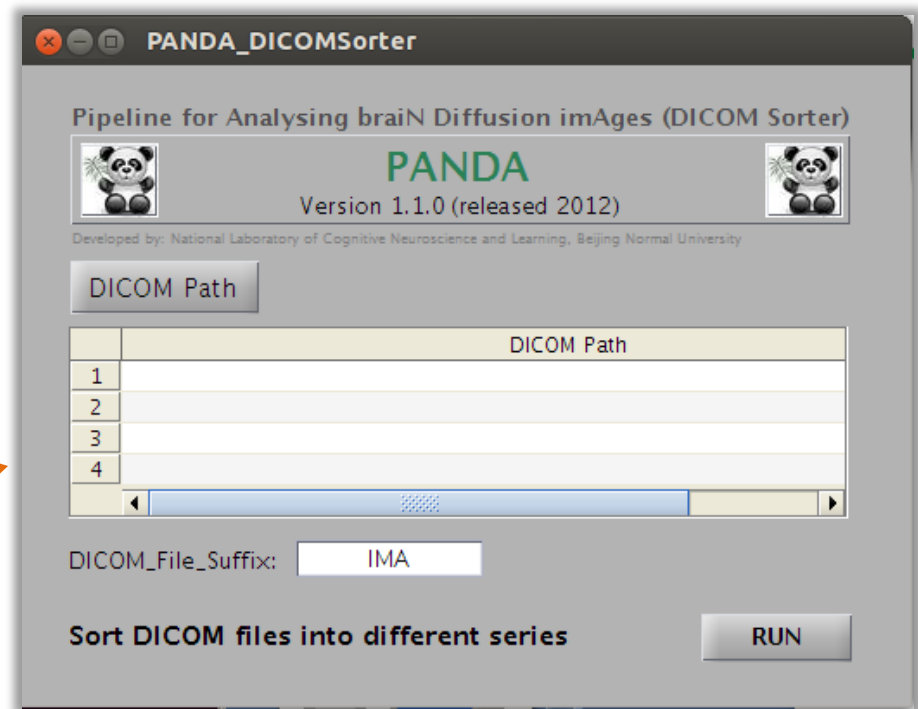
/data/node1/Zaixu/234/00010/Network/Probabilistic

/data/node1/Zaixu/234/00011/Network/Probabilistic

/data/node1/Zaixu/234/00012/Network/Probabilistic

Utilities (DICOM Sorter)

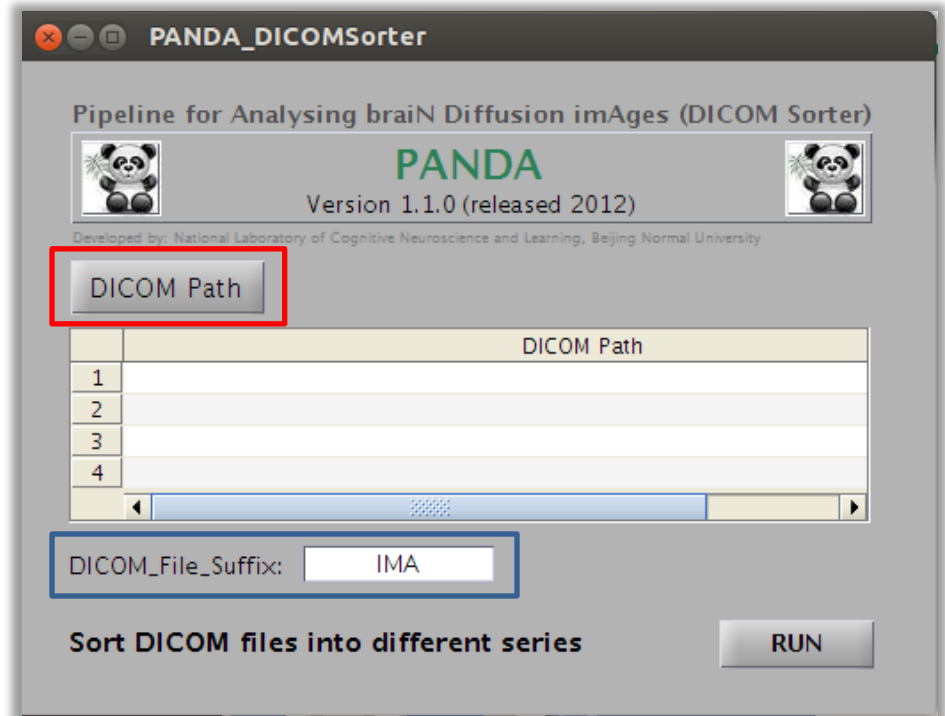
➤ Sort DICOM files into different series



Utilities (DICOM Sorter)

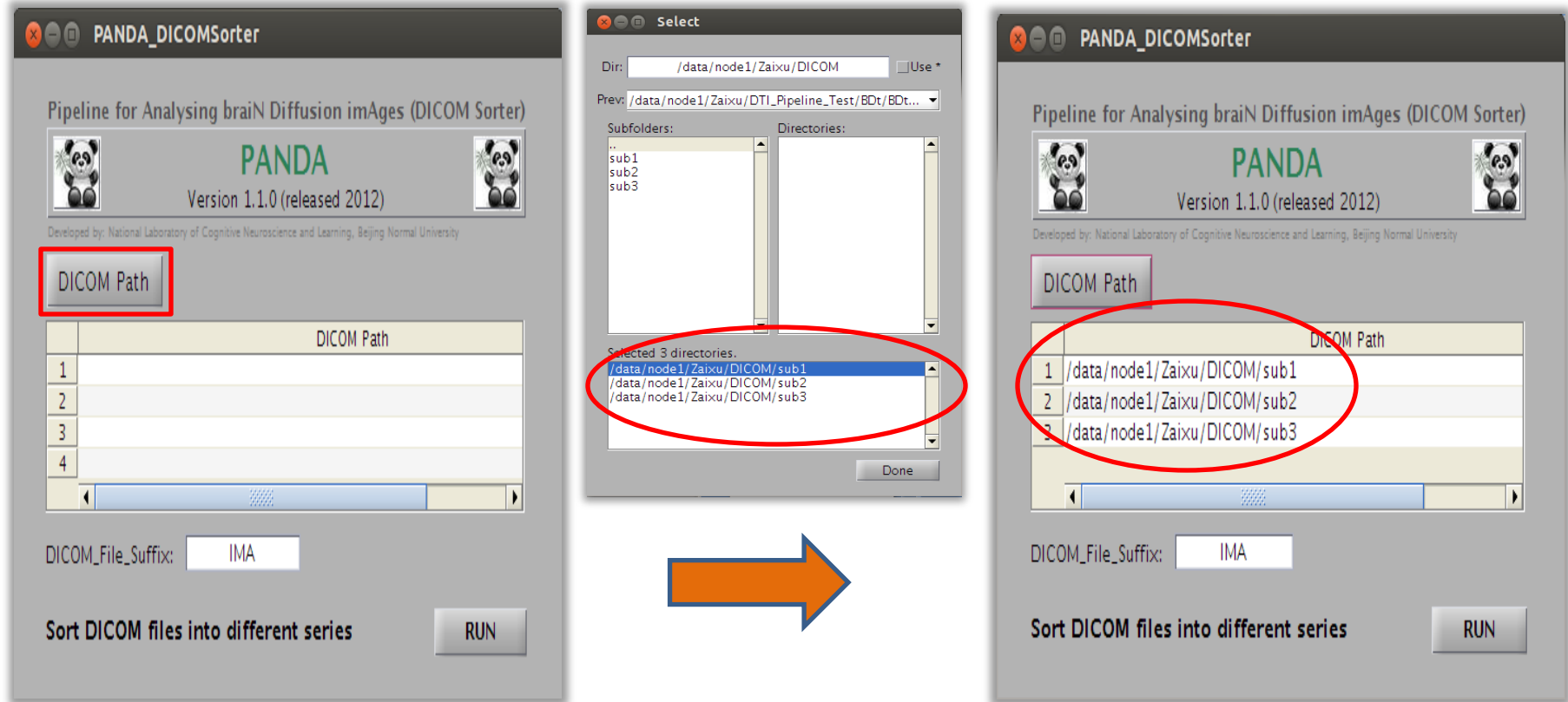
DICOM Path:
the full path of subjects' folders which contain all the DICOM files to be sorted

DICOM File Suffix:
The extension of DICOM file name



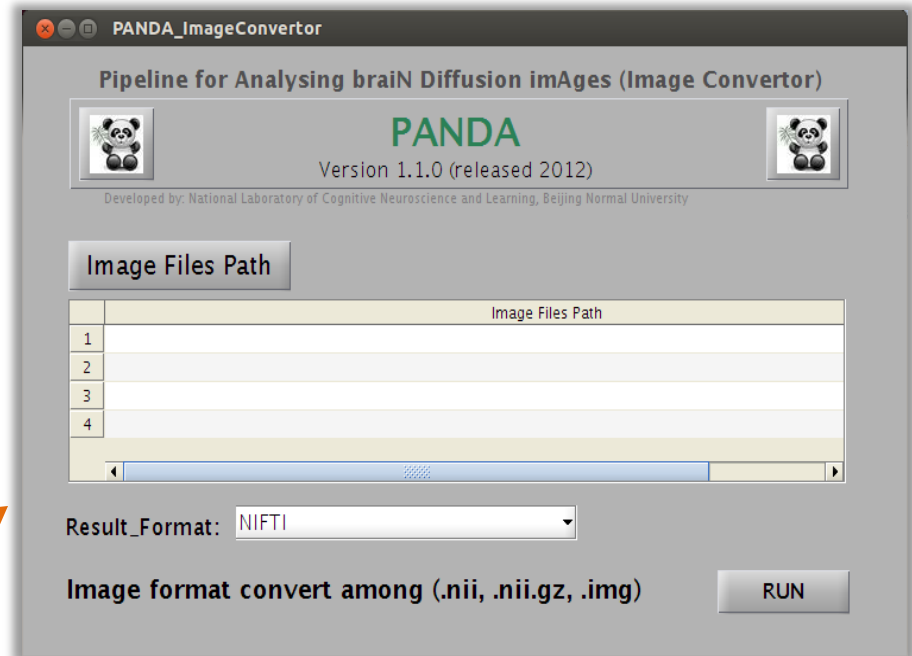
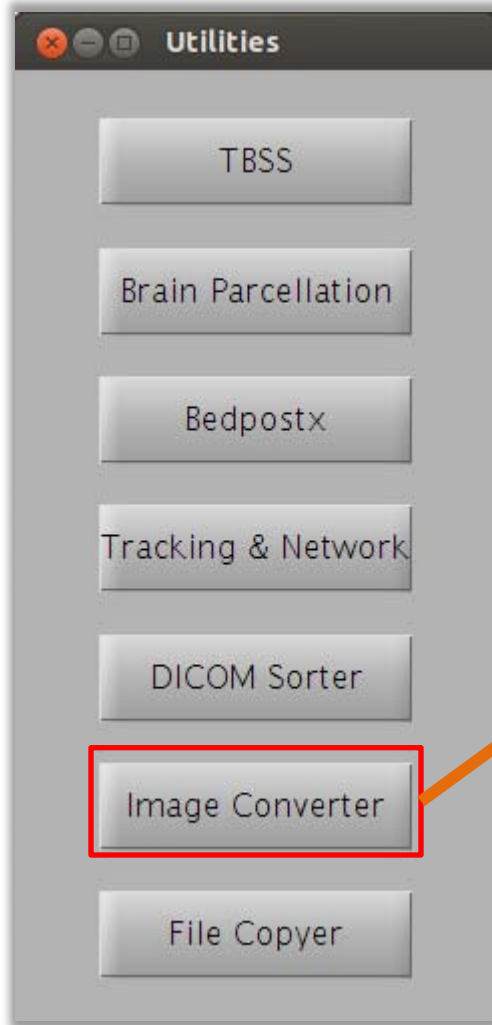
- If you input the DICOM file suffix, it will sort all the files with the extension as the suffix under subjects' DICOM folders.
- If the DICOM_File_Suffix is empty, it will sort all the files under subjects' DICOM folders.

Utilities (DICOM Sorter)



Utilities (Image Converter)

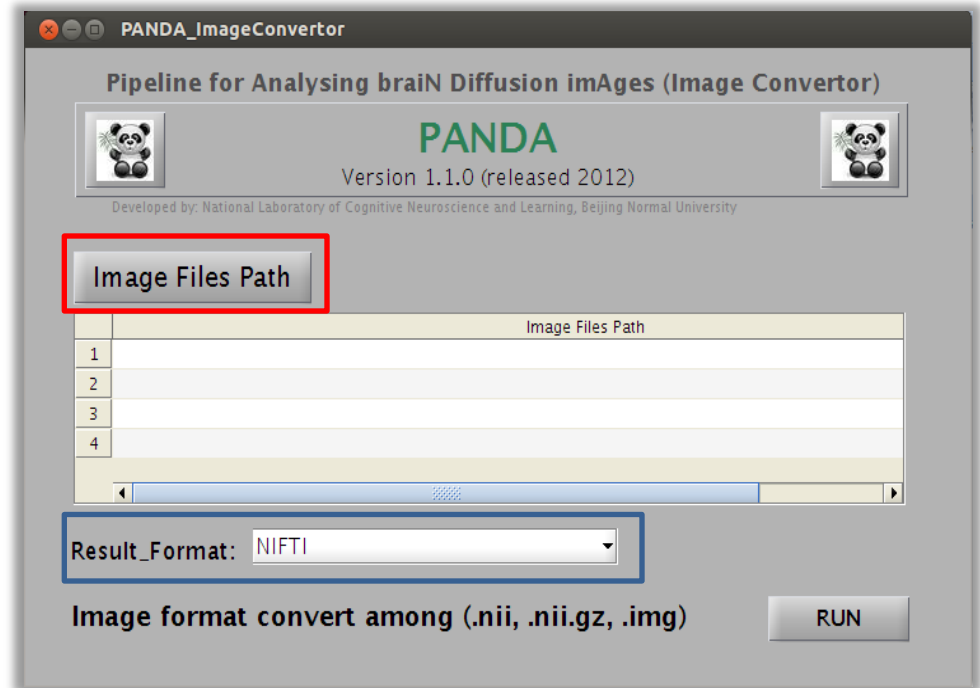
- Convert image format among (.nii, .nii.gz, .img)



Utilities (Image Converter)

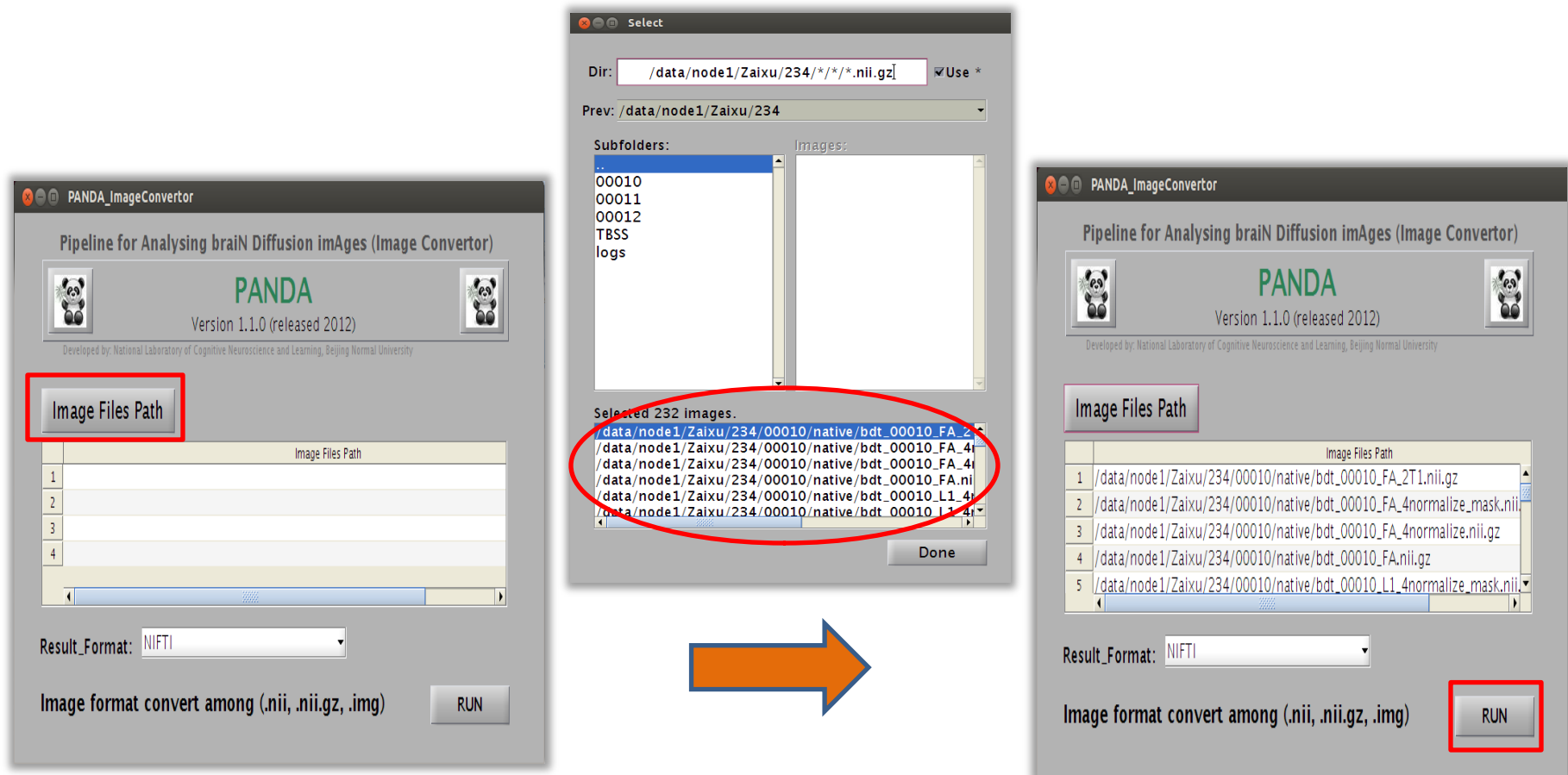
Image Files Path:
the full path of image files
(.nii, .nii.gz, .img) to be
converted

Result Format:
3 choices (NIFTI,
NIFTI_GZ, NIFTI_PAIR)



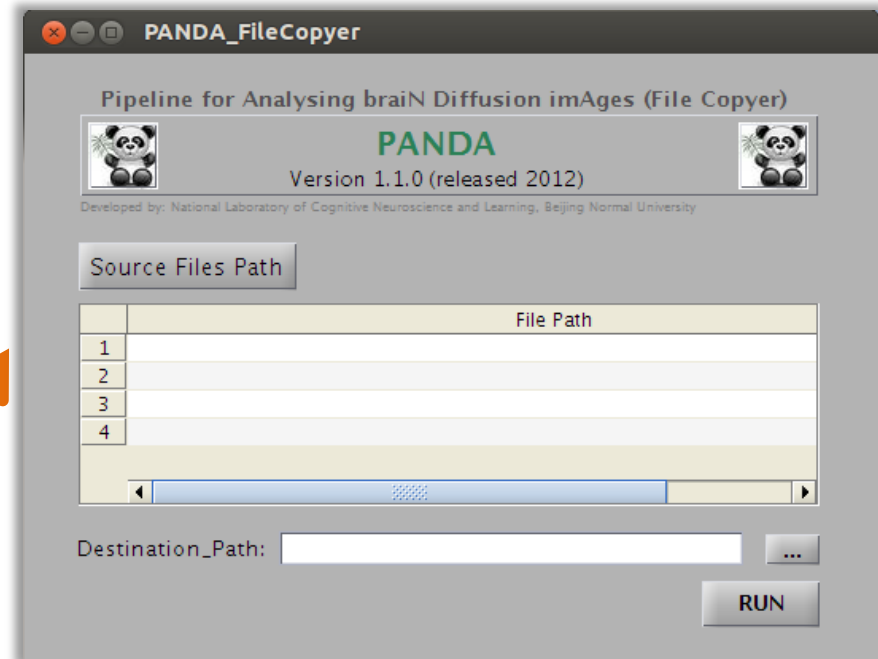
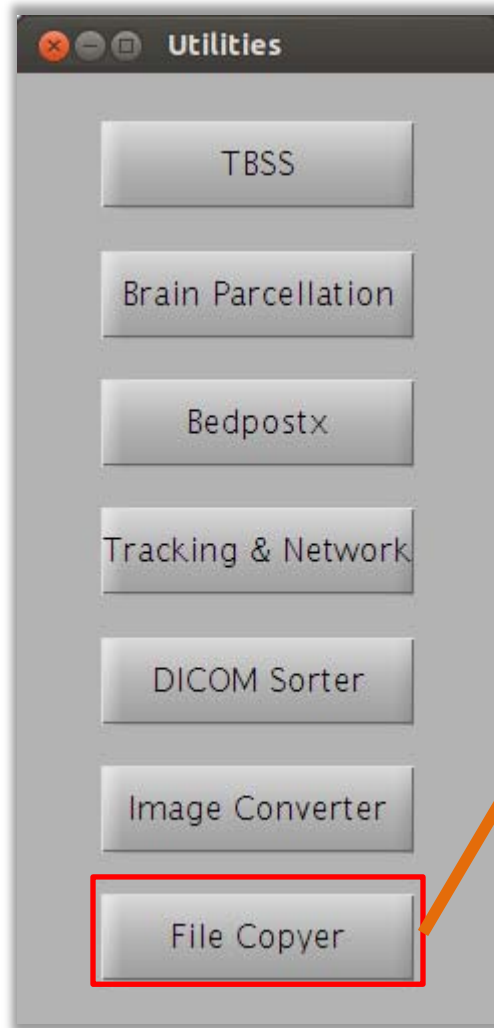
➤ After the conversion, new image files will replace the origin image files.

Utilities (Image Converter)



Utilities (File Copyer)

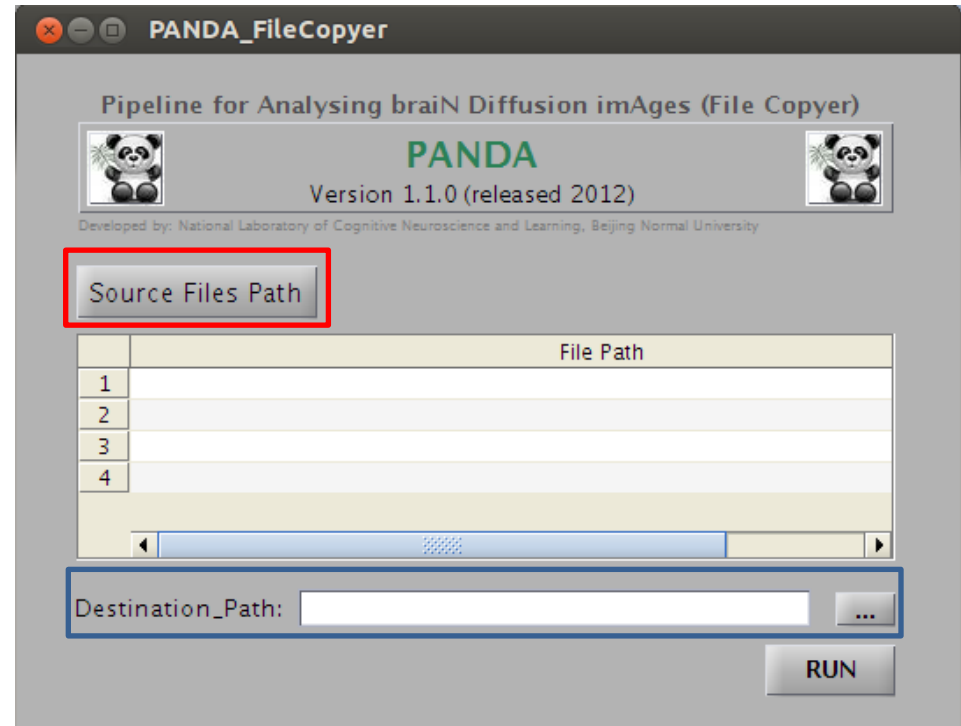
➤ Copy files to the destination path



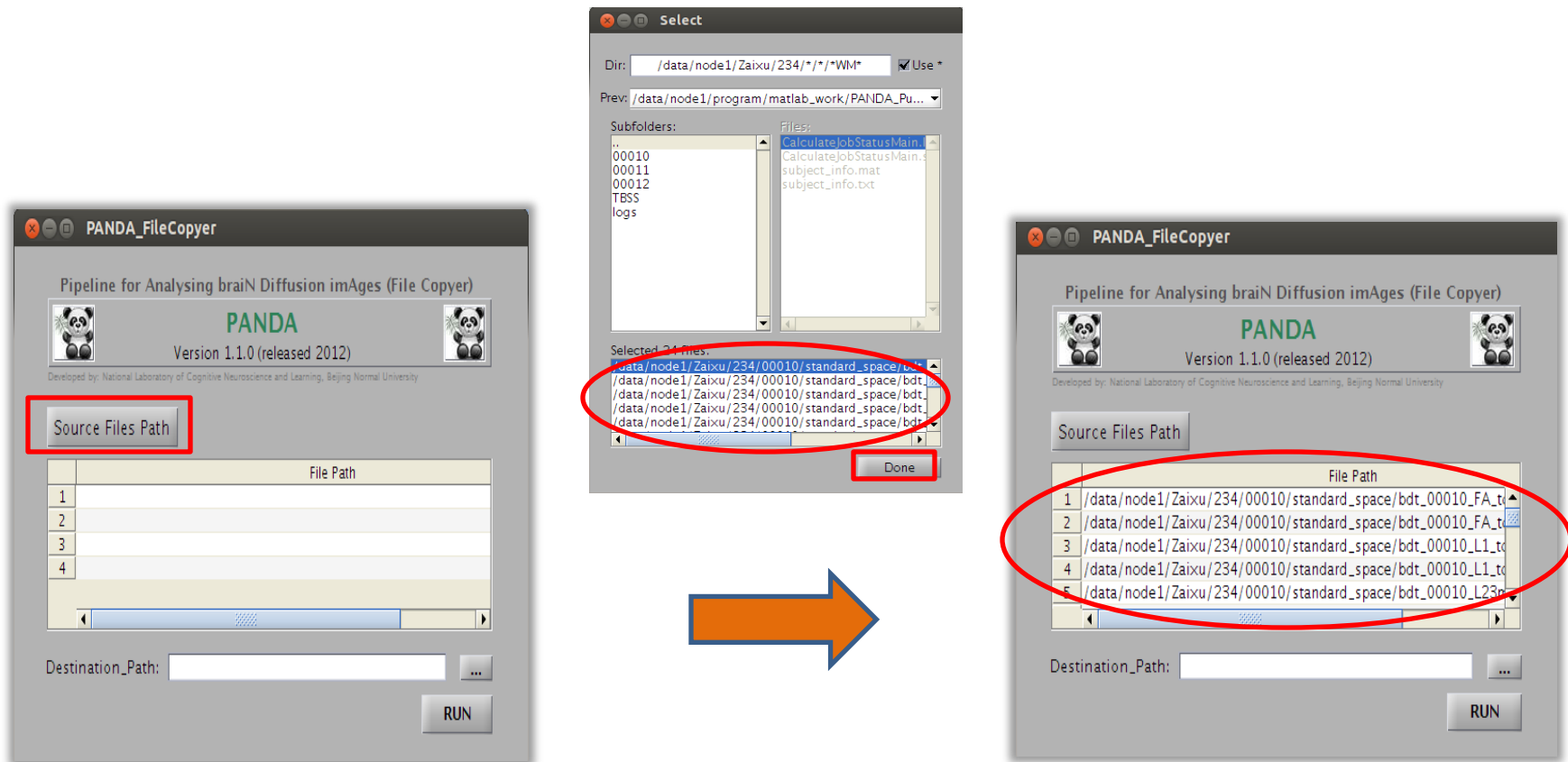
Utilities (File Copyer)

Source Files Path:
full path of files users
want to copy

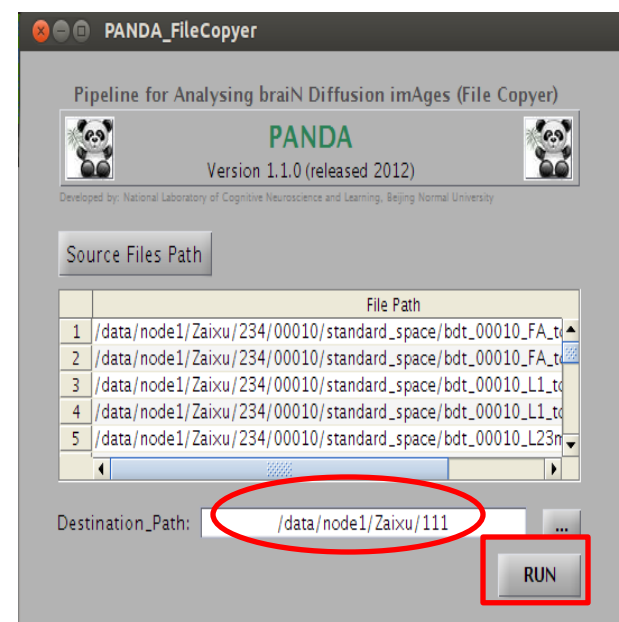
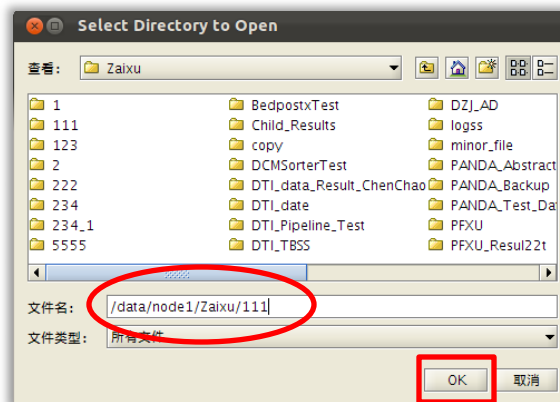
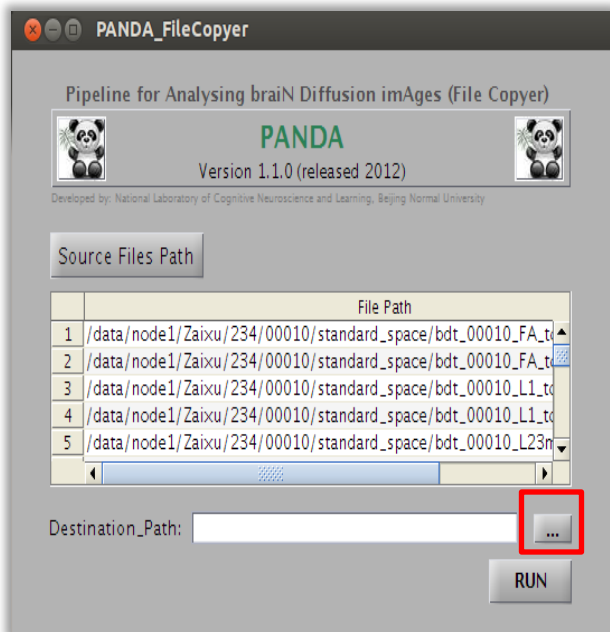
Destination Path:
the path user wants to
save these files



Utilities (File Copyer)



Utilities (File Copyer)



Acknowledgement

➤ FSL

<http://www.fmrib.ox.ac.uk/fsl/>

➤ PSOM

<http://code.google.com/p/psom/>

➤ Diffusion Toolkit

<http://www.trackvis.org/dtk/>

➤ MRICRON

<http://www.mccauslandcenter.sc.edu/mricro/mricron>

Help

Please report bugs or requests to:

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Thanks !