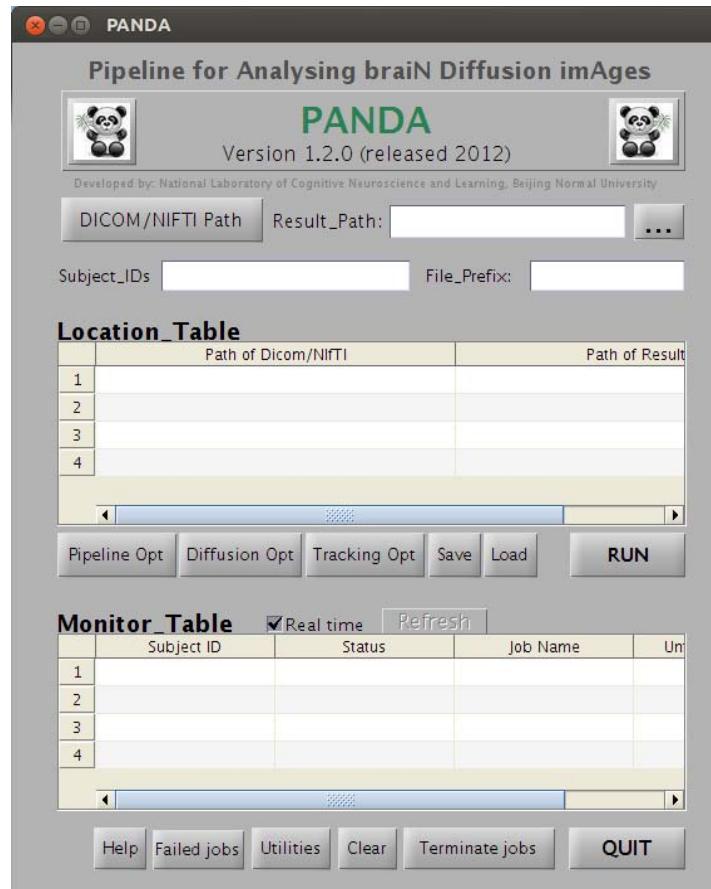


PANDA Manual



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Contents

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

Overview

Associations

➤ FSL

Diffusion data was processed mainly using FSL commands.

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

➤ Diffusion Toolkit

For deterministic fiber tracking.

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

➤ MRIcron (dcm2nii)

For converting DICOM to NIfTI.

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

Overview

Associations

➤ PSOM

The pipeline system for Octave and Matlab (PSOM) is a lightweight library to manage complex multi-stage data processing. 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.

PSOM can automatically offer the following services:

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

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

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Setup

Requirements :

➤ Linux OS / MAC

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

➤ Matlab

➤ FSL

Setup

FSL Installation Guide :

http://hi.baidu.com/heart_eternal/item/3d4049d15a524403e1f46f12

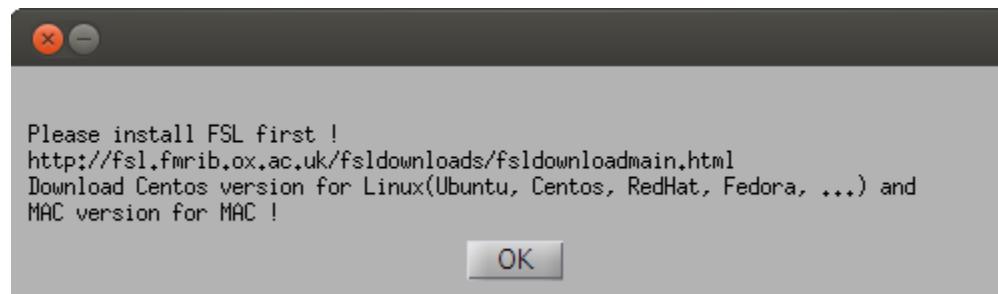
Matlab Installation Guide :

http://hi.baidu.com/heart_eternal/item/355c6327551e13d6ef10f1d7

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://fsl.fmrib.ox.ac.uk/fsldownloads/fsldownloadmain.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-1.2.0_32.tar.gz
`tar zxvf PANDA-1.2.0_32.tar.gz`

Setup

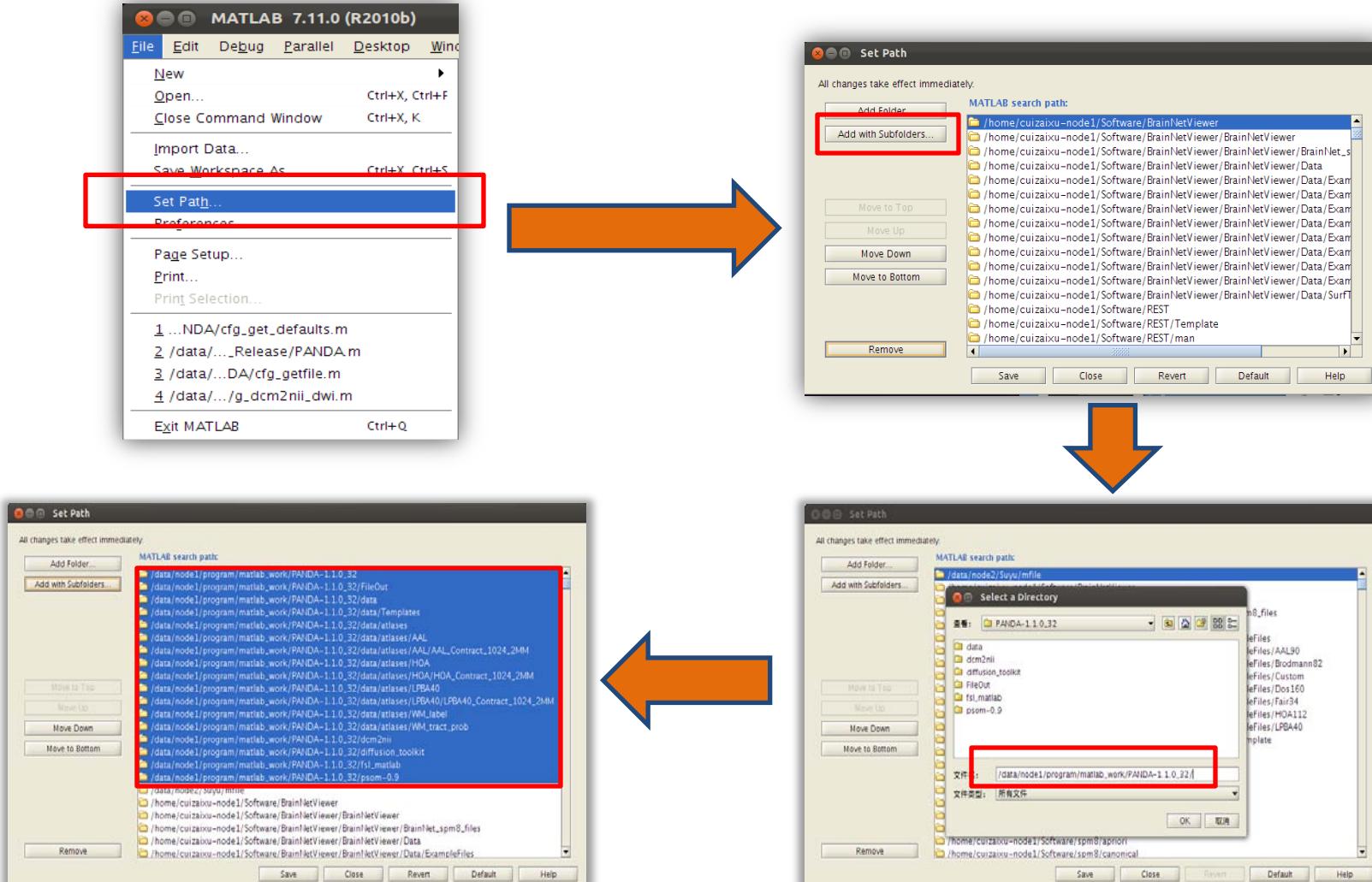
Open Matlab:

- Open a terminal first
- Input ‘matlab’ in terminal, then matlab will be open

To use PANDA, users should not open Matlab through shortcuts and must open Matlab through terminal.

Setup

Matlab Search Path



Then, entering 'PANDA' in the Matlab command window will open PANDA's GUI. 16

Setup

Open PANDA:

- Open a terminal first
- Input ‘matlab’ in terminal, then matlab will be open
- Input ‘PANDA’ in Matlab command window

To use PANDA, users should not open Matlab through shortcuts and must open Matlab through terminal.

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Files/Directories selection

Dir:

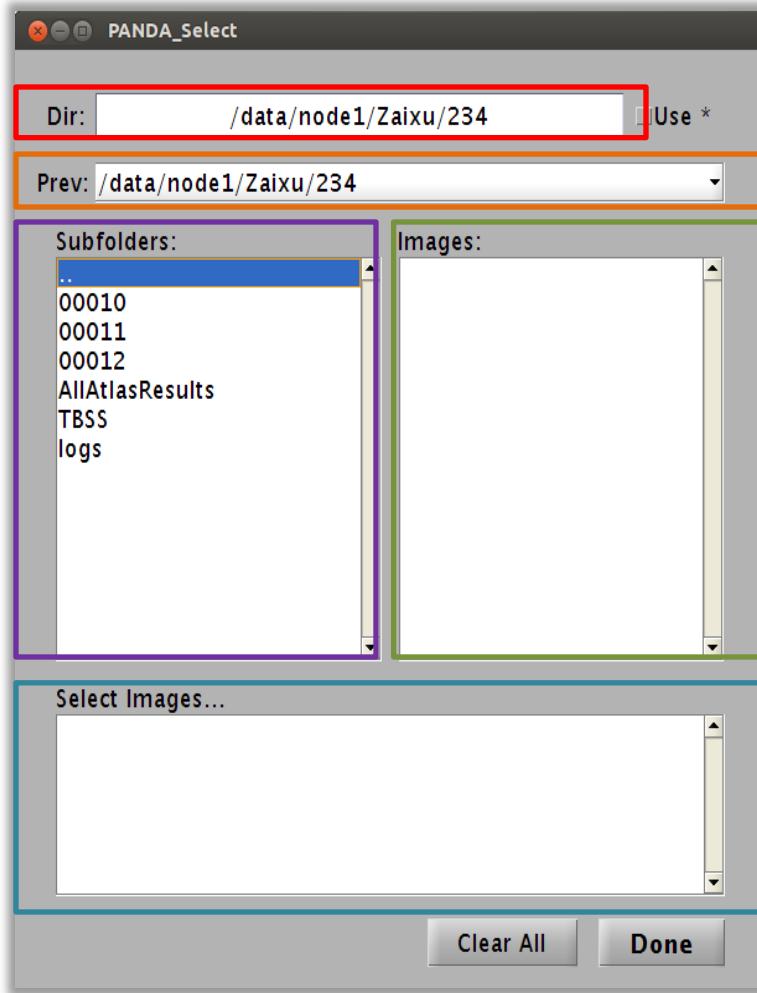
current directory

Prev:

the list of directories users have selected

Subfolders:

subfolders under current directory



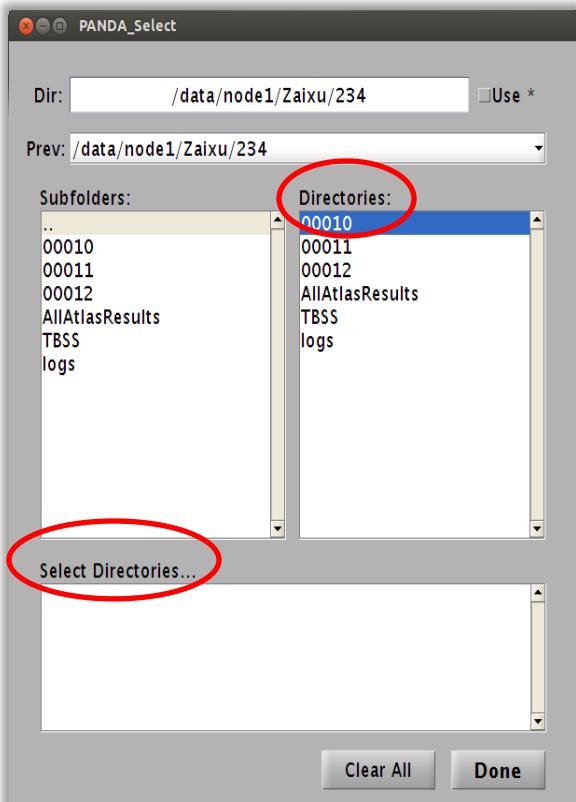
Images/Files/Directories to be selected, referring to [next page](#).

Images/Files/Directories users have selected.

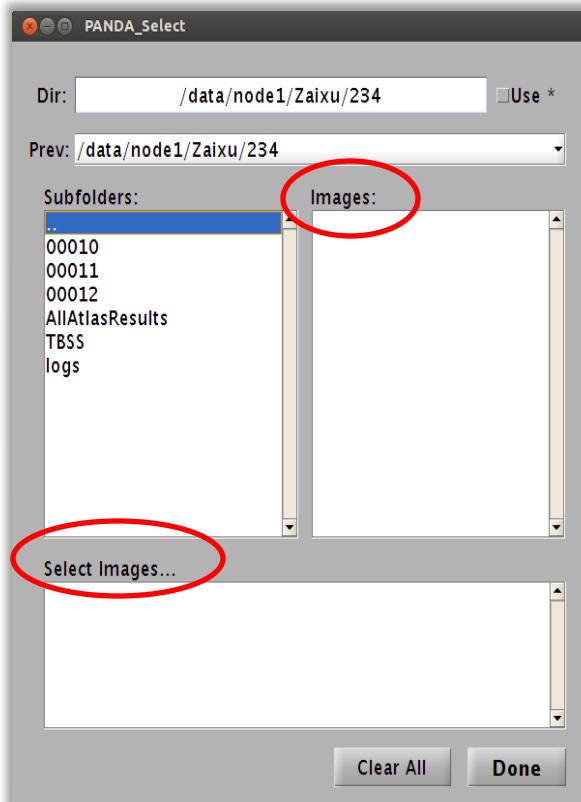
Files/Directories selection

Three situations:

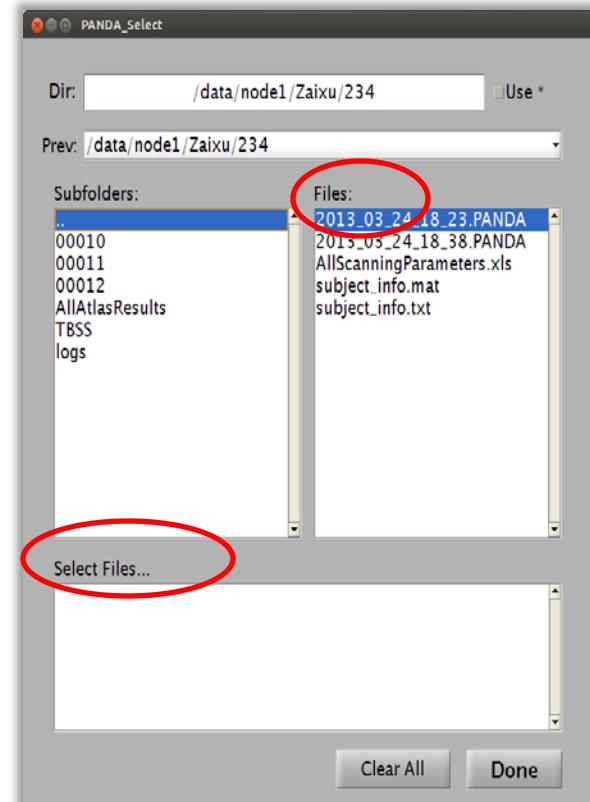
Select **Directories**:



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



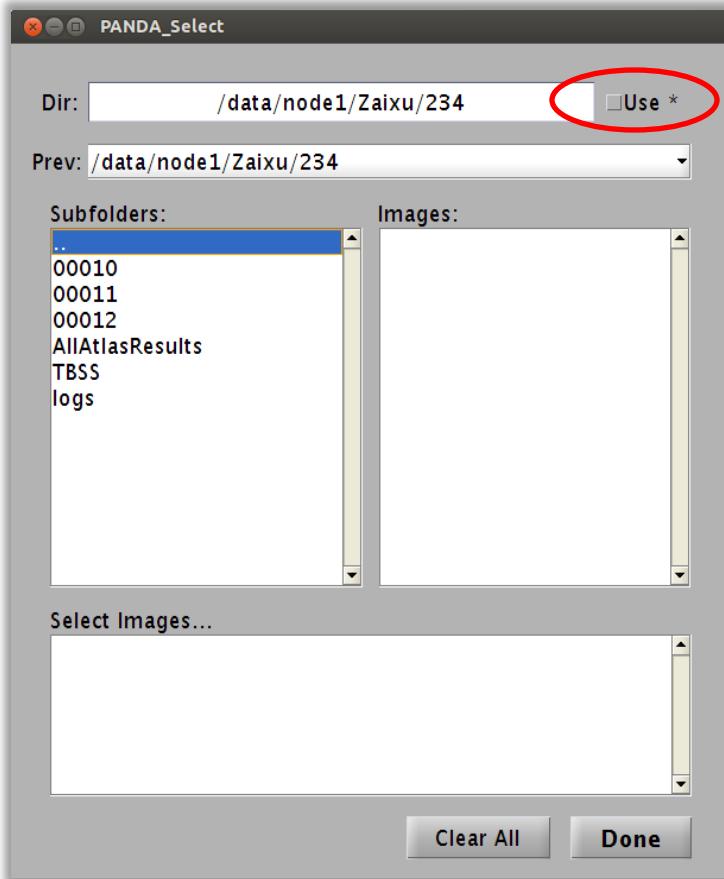
Select **Files**:



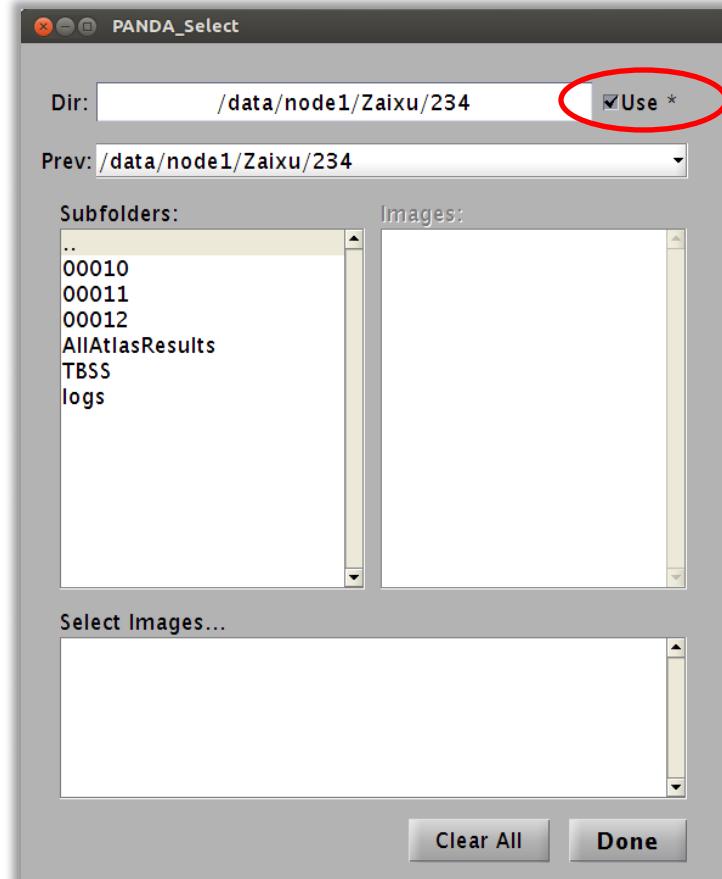
Files/Directories selection

Two methods:

Normal:

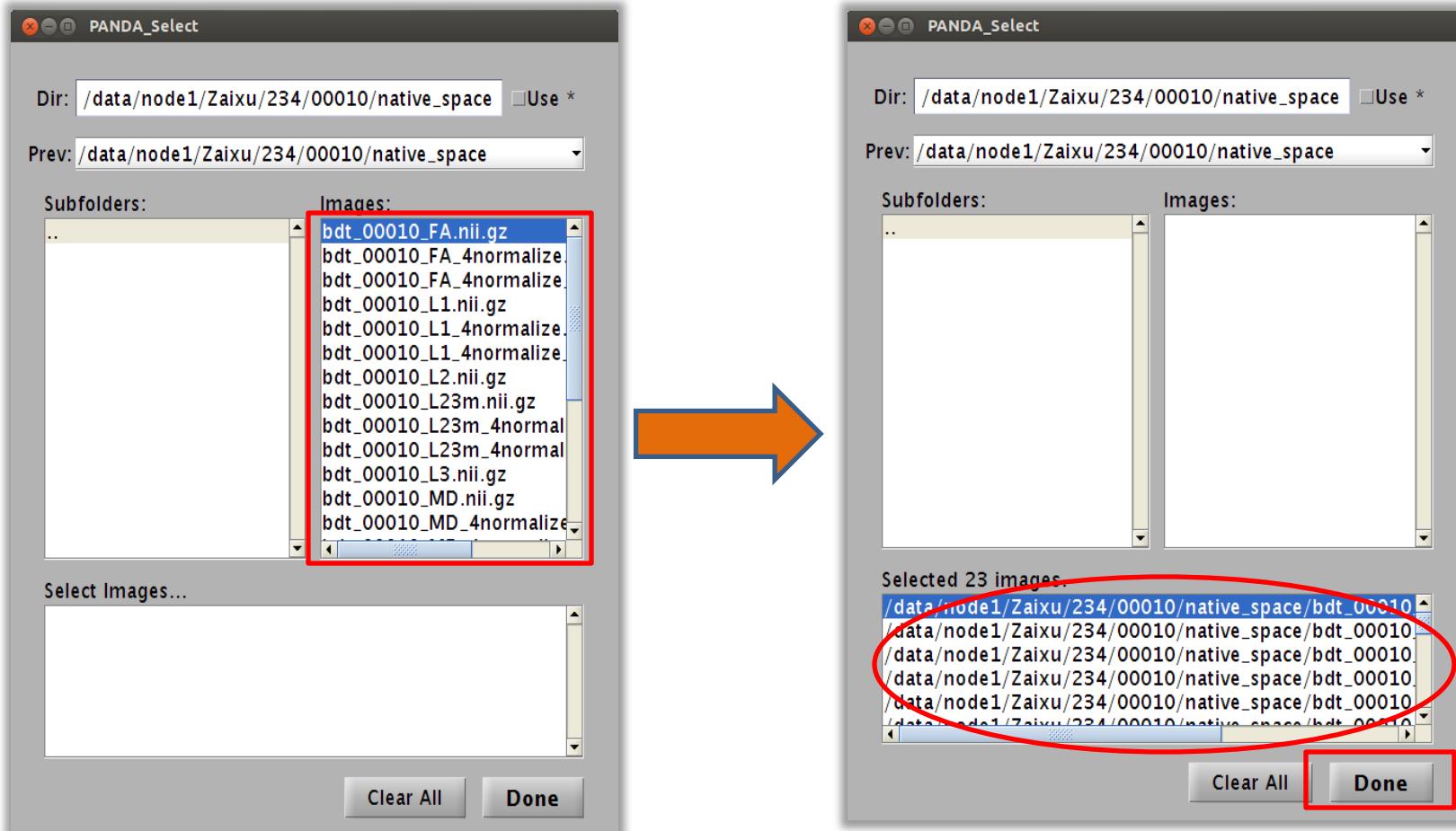


Use *:



Files/Directories selection

Normal:



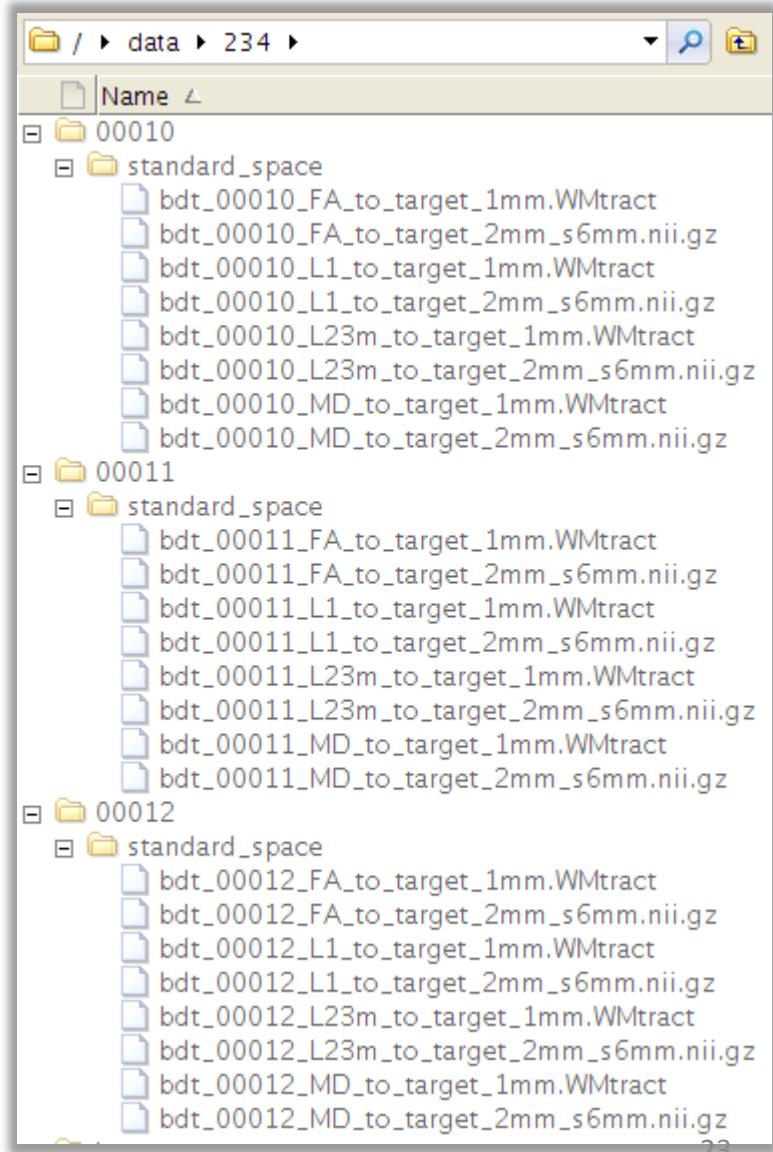
Files/Directories selection

Use *:

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

Under each folder, there is a subfolder named 'standard_space'.

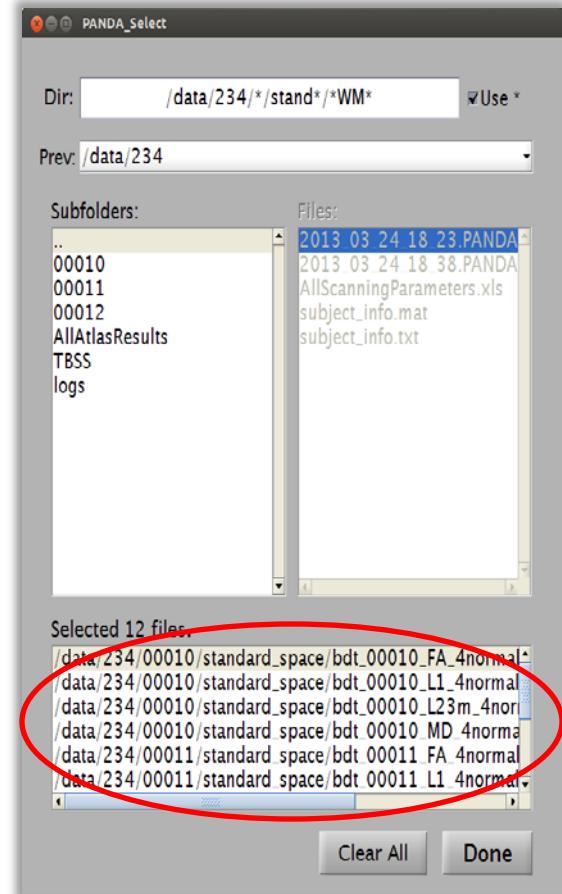
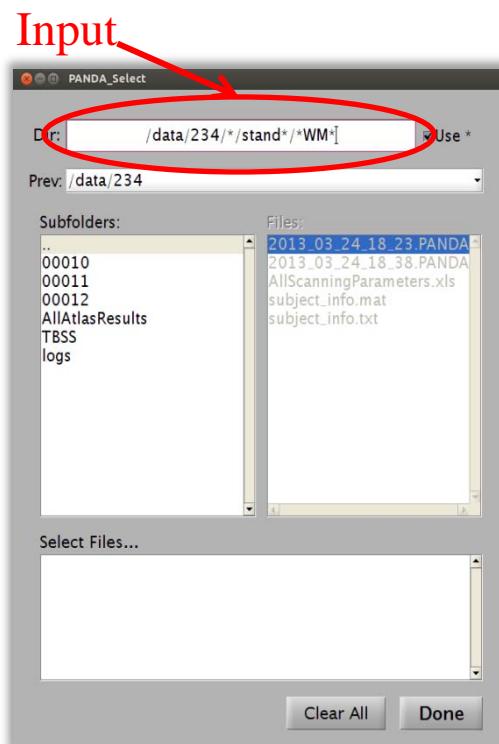
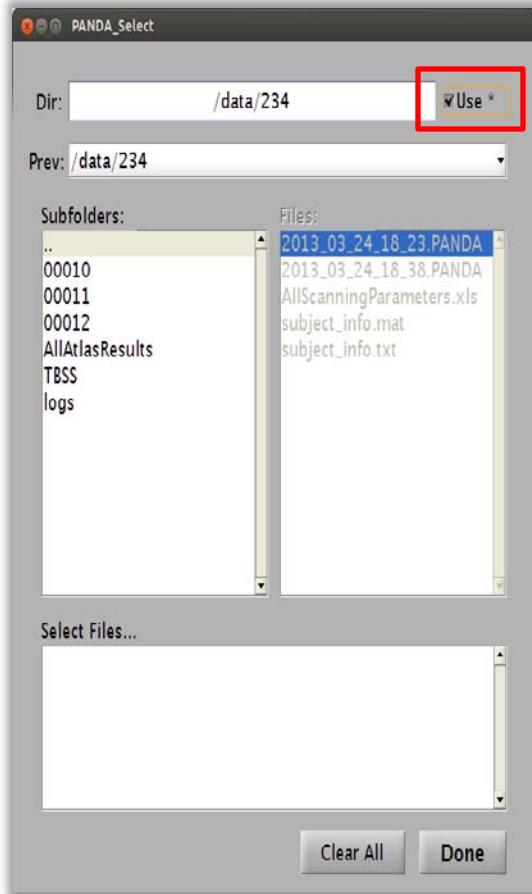
Now, we want to get all the Wmtract file under the folder standard_space.



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 !

Contents

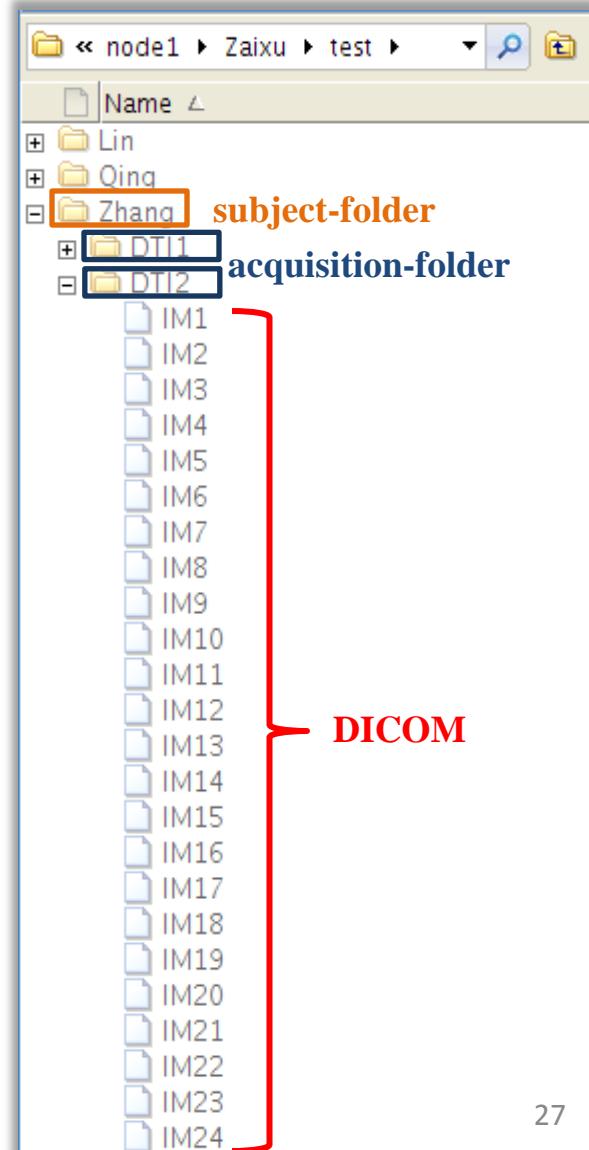
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Preparing raw data (DICOM)

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.

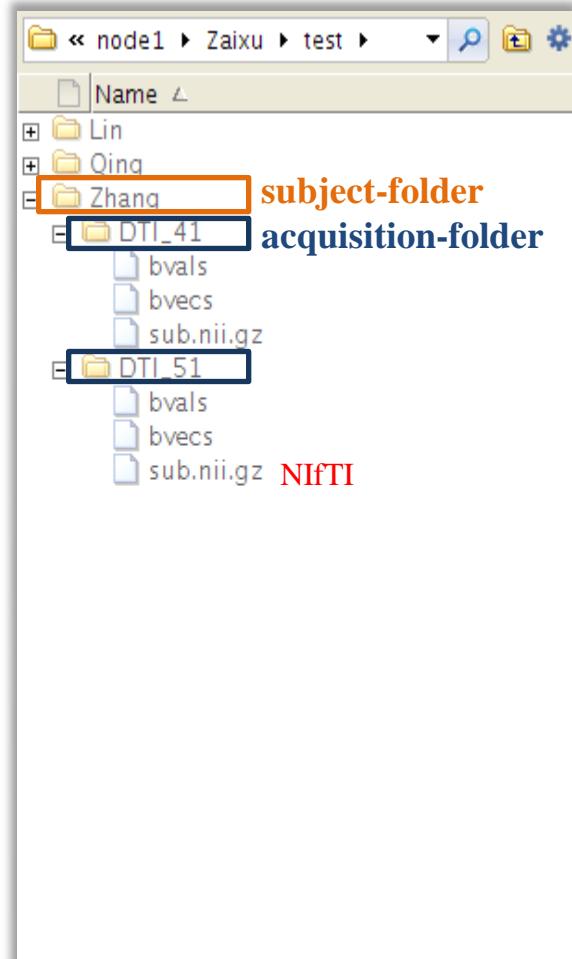


Preparing raw data (NIfTI)

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*’.

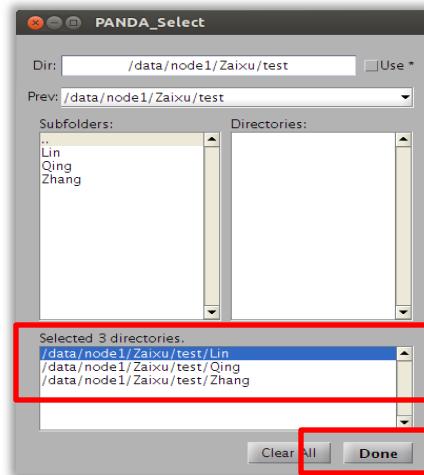
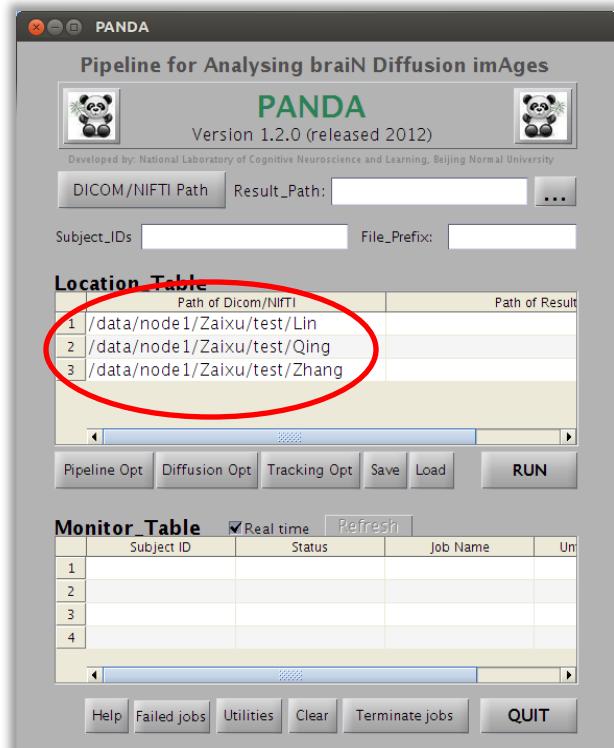
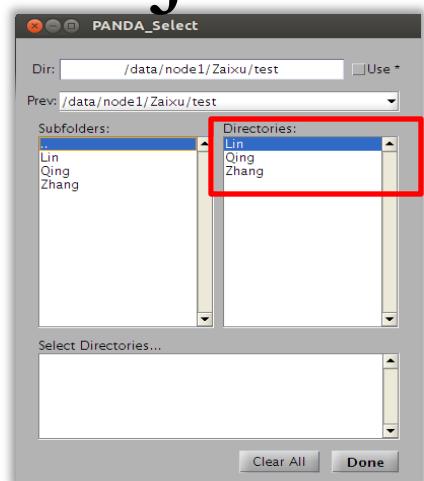
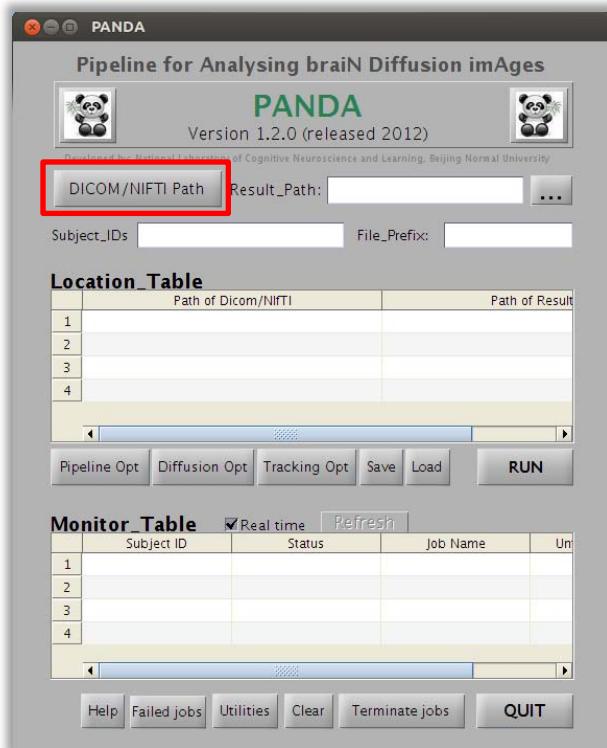


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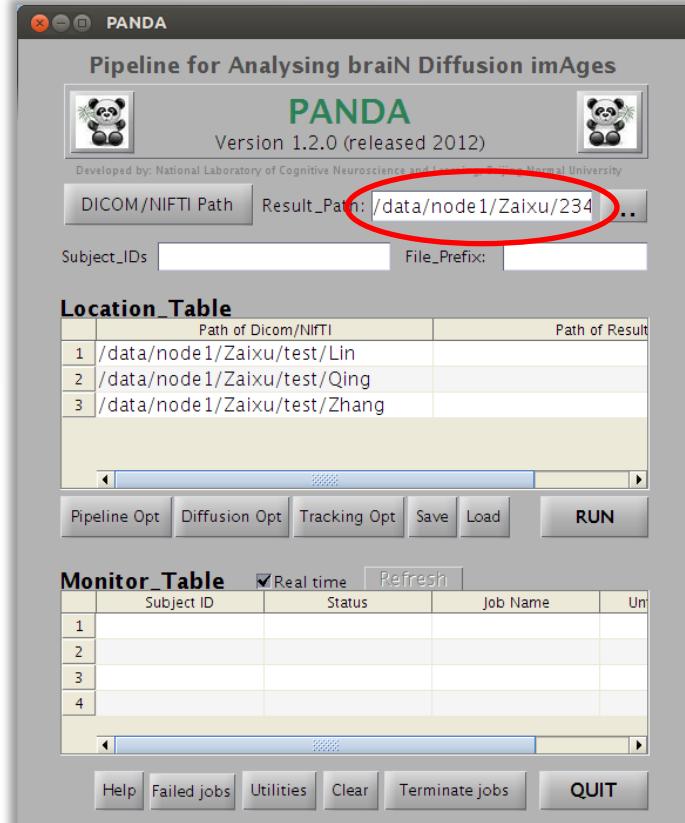
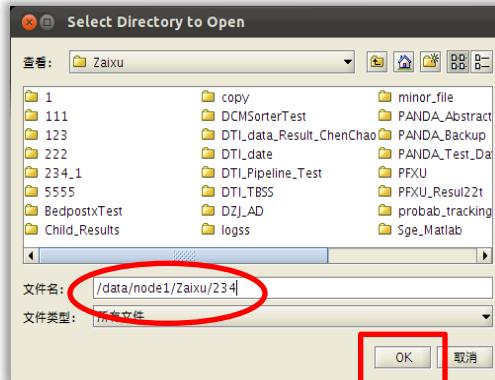
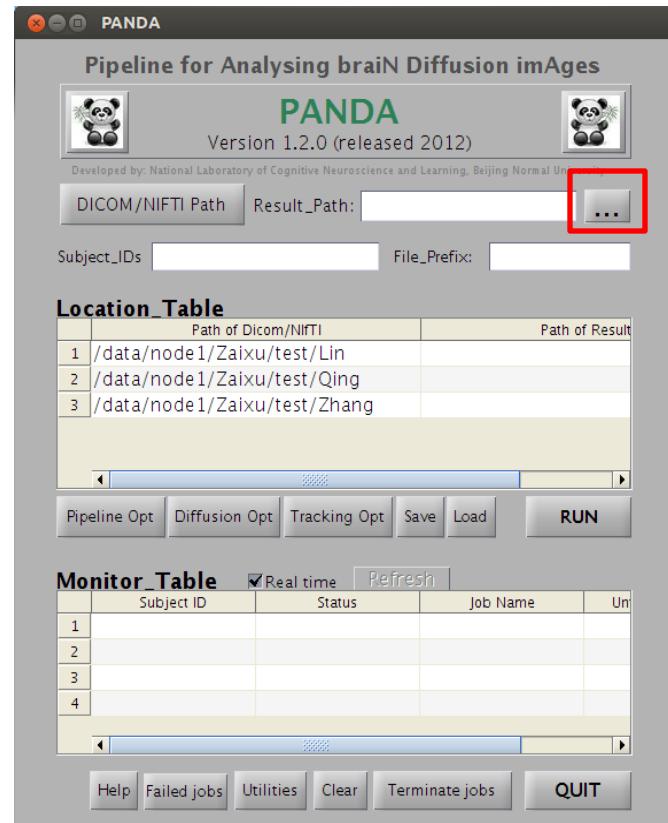
Setting inputs & outputs

Step1: Select subject-folders



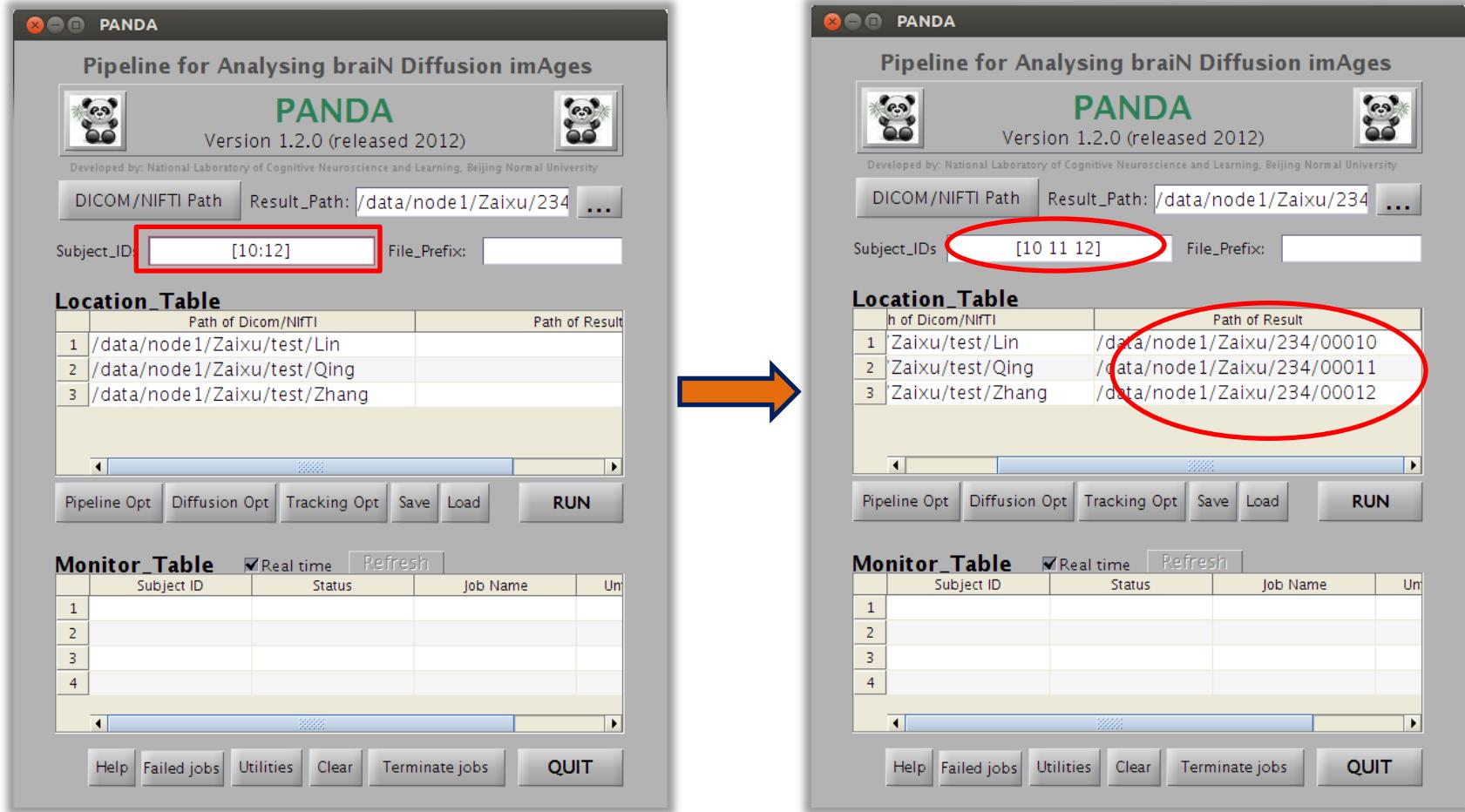
Setting inputs & outputs

Step2: Specify the result-folder



Setting inputs & outputs

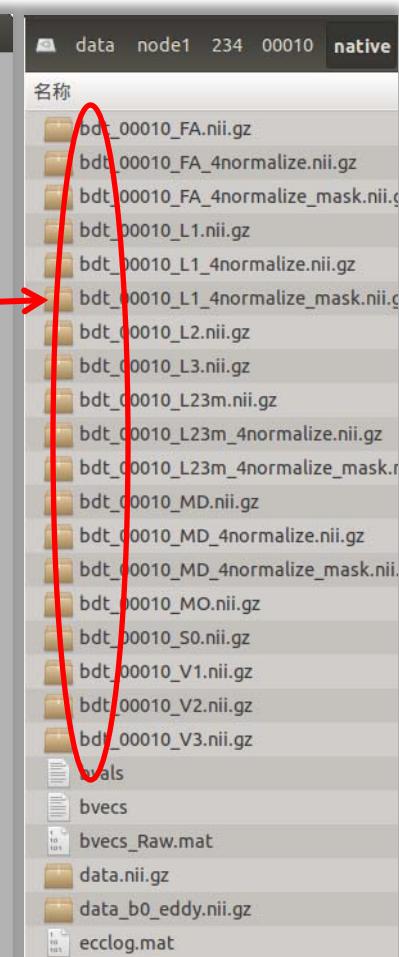
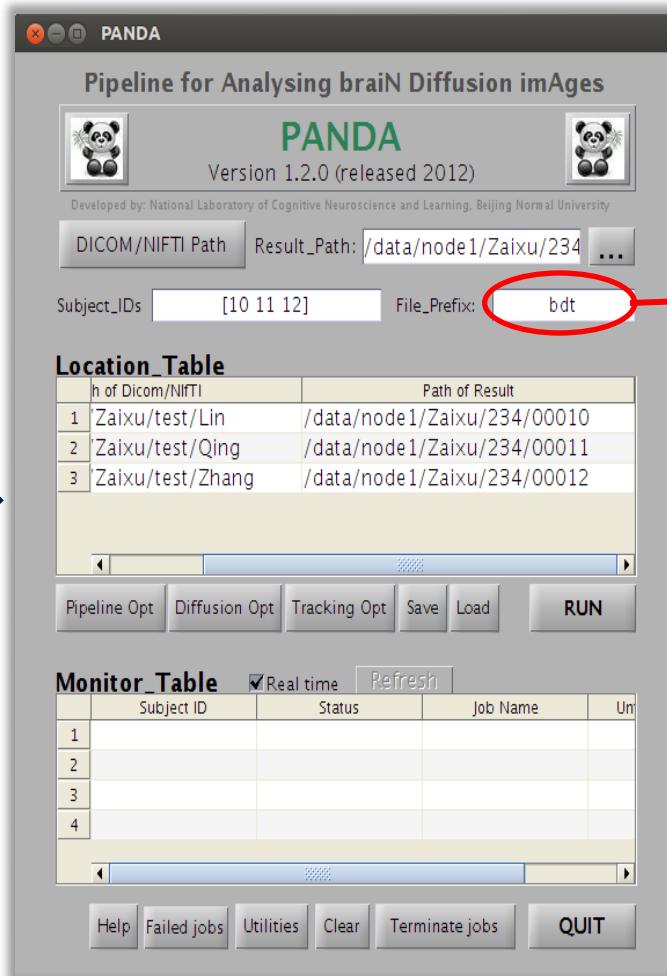
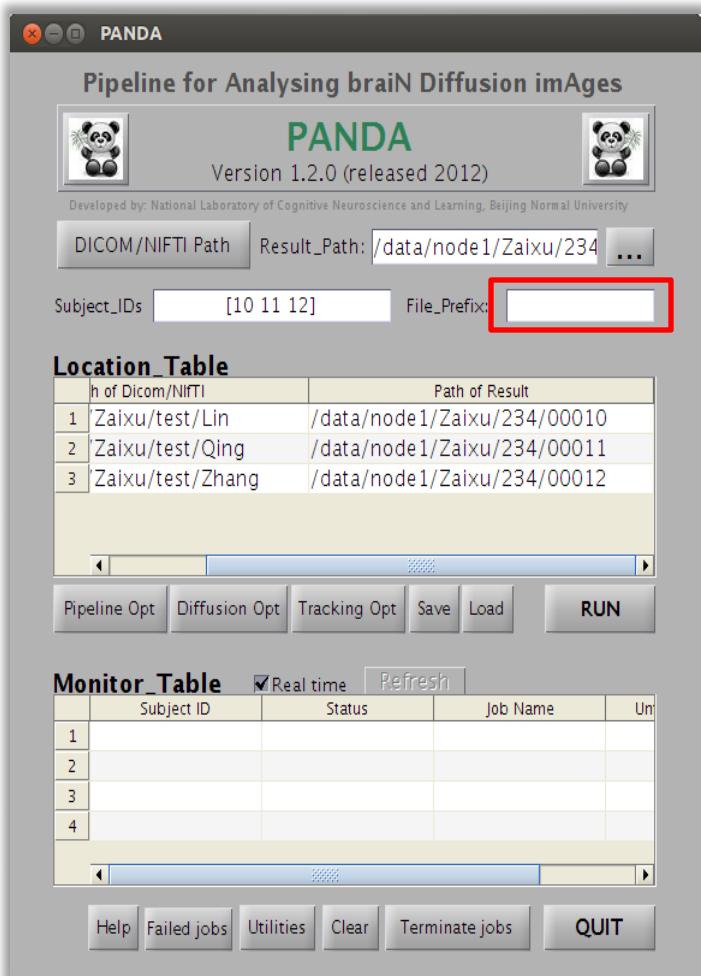
Step3: Assign digital IDs for subjects



- 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

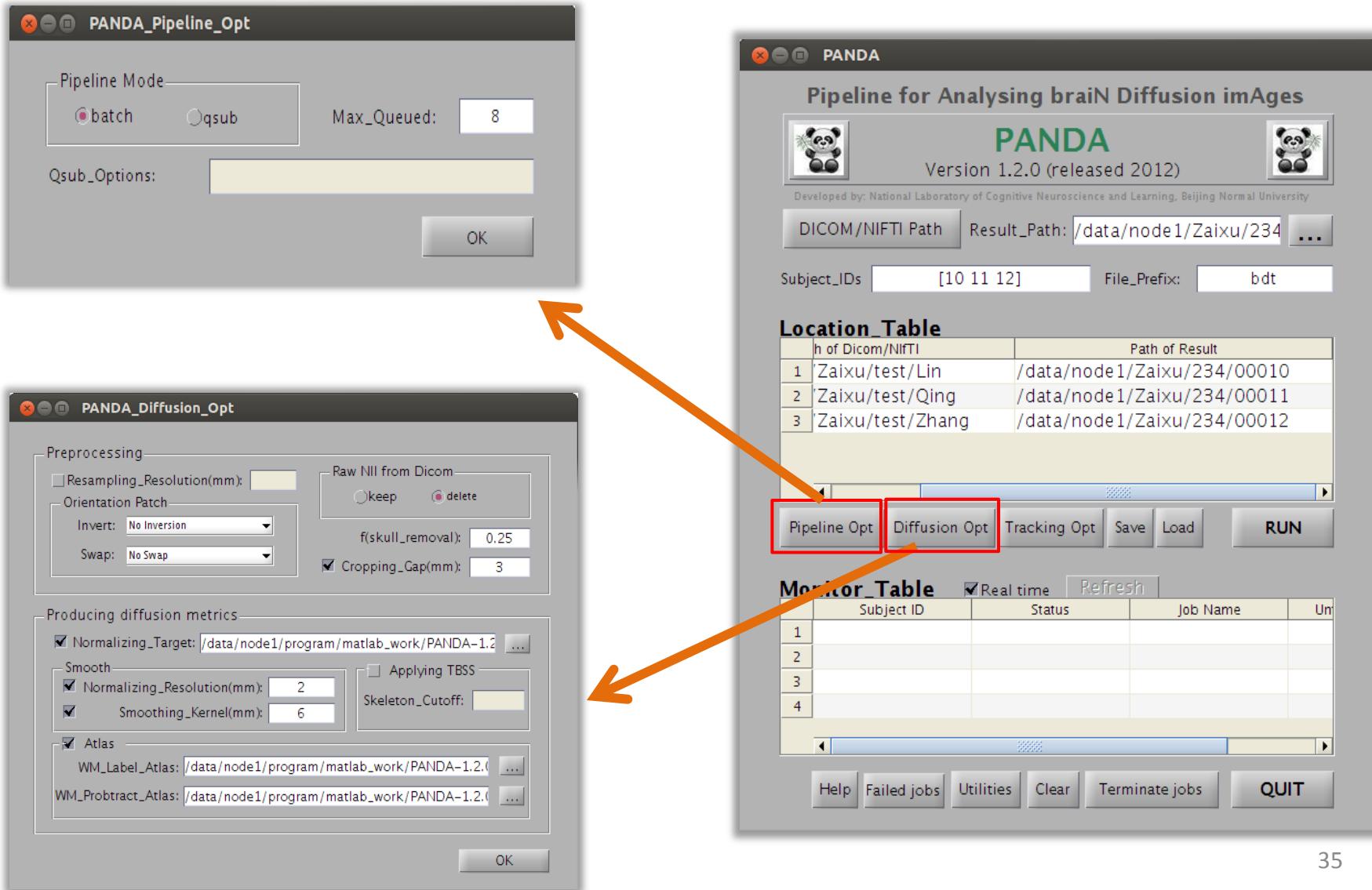
Step4: Input prefix of filenames



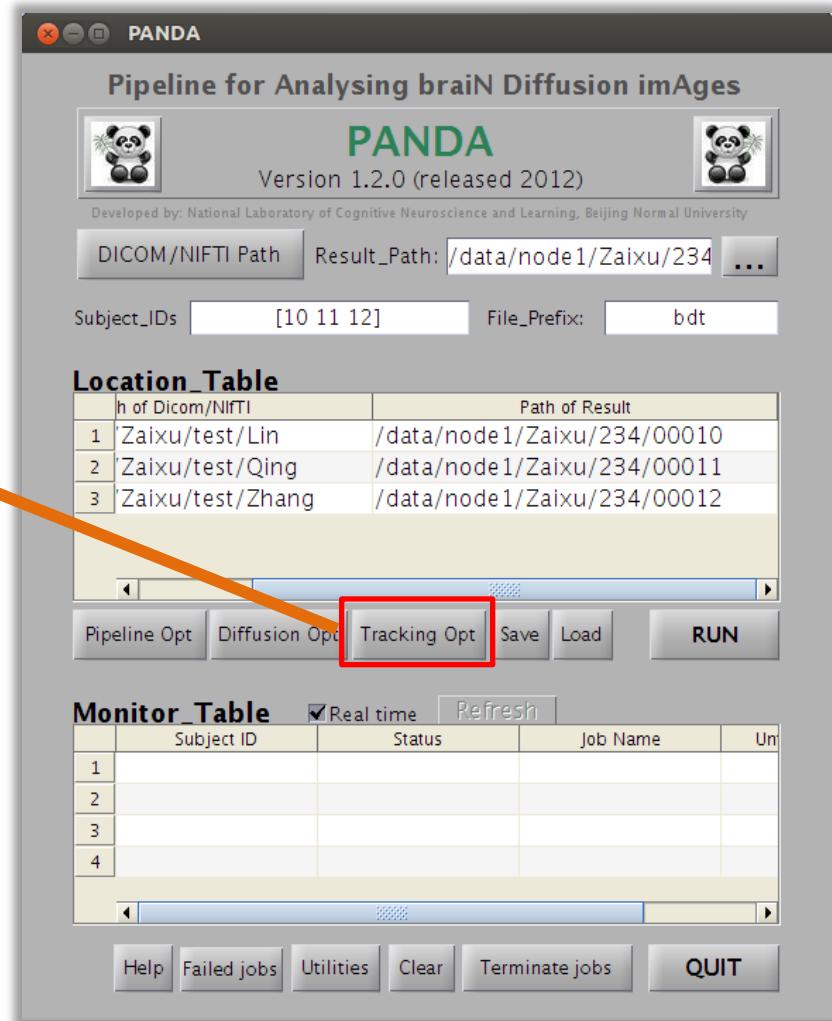
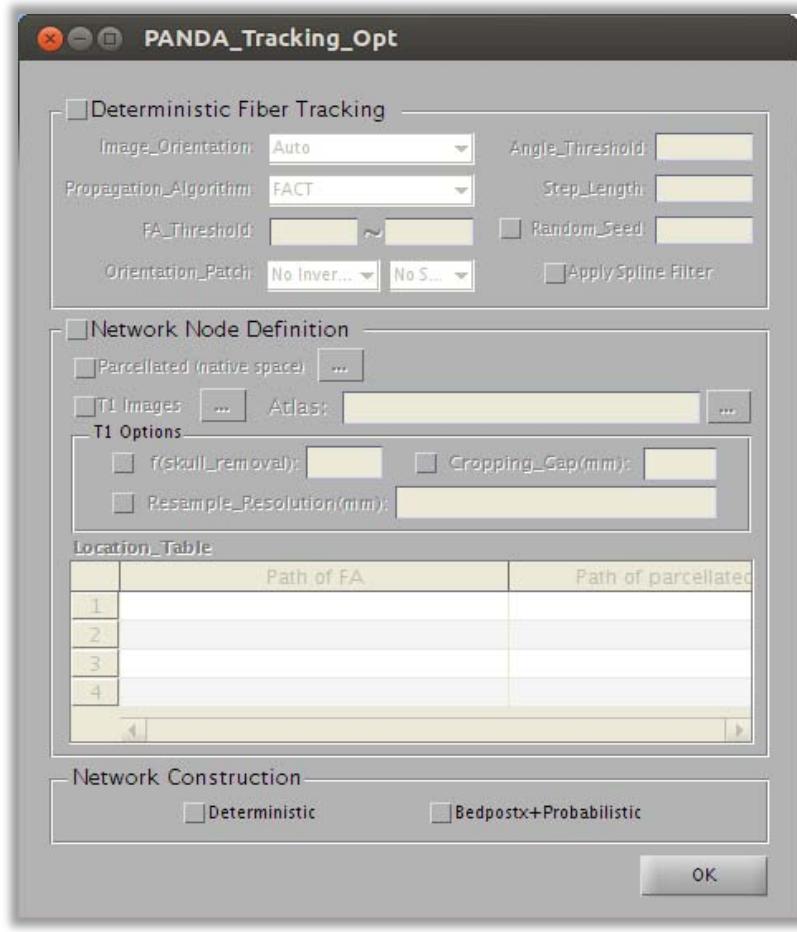
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Changing parameters (optional)

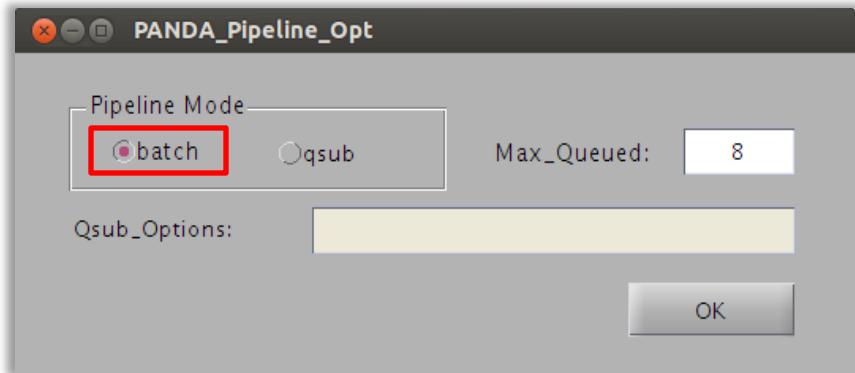


Changing parameters (optional)

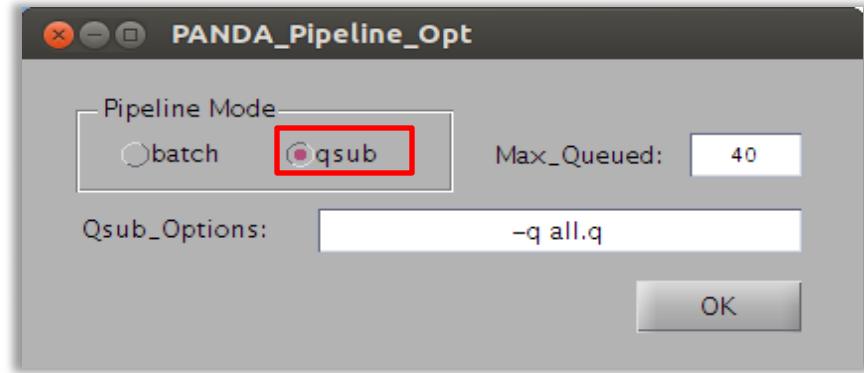


Changing parameters (optional)

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)

Resampling Resolution:

Resolution for resampling raw DWI data.

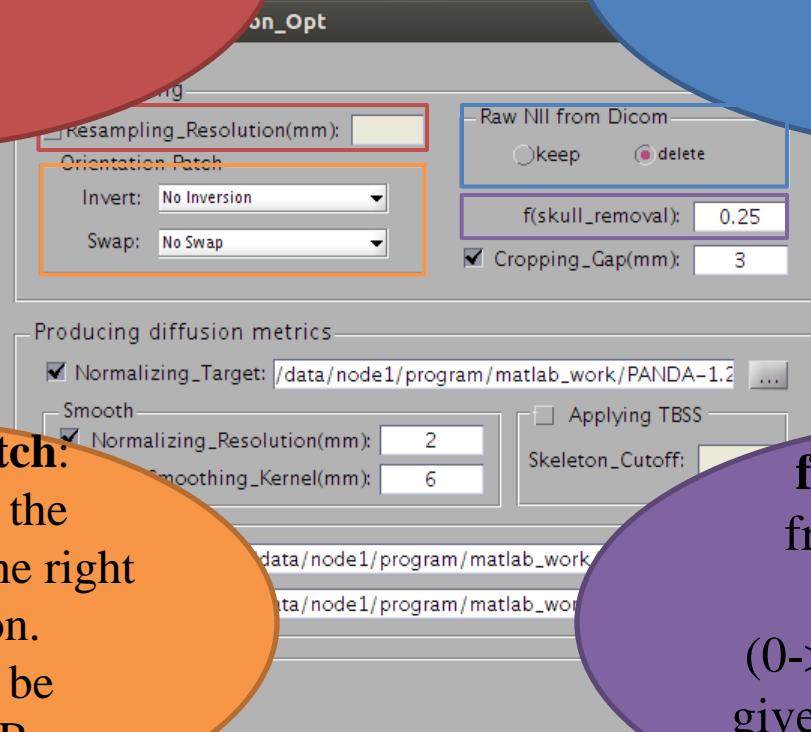
Raw NII from Dicom :

Select whether to delete raw NII converted from DICOM.

Orientation Patch:

Invert and swap the original bvecs for the right fiber orientation.

Parameters can be acquired with TestBvecs Utility.



f(skull removal):

fractional intensity threshold
(0->1); smaller values give larger brain outline estimates.

Changing parameters (optional)

Diffusion_Opt (The default configuration is recommended)

Cropping Gap:

The distance from the selected cube to the border of the brain.

Normalization Target:

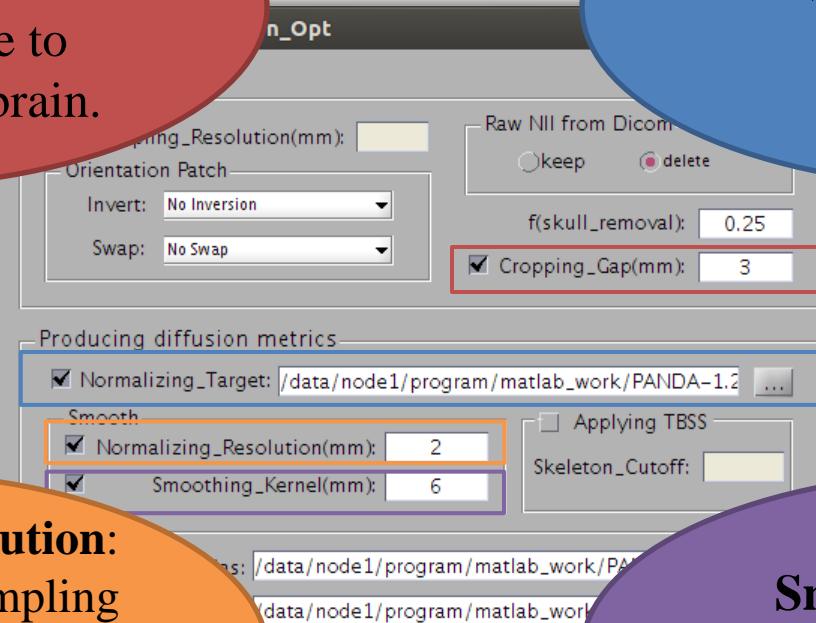
The template for registering.

Normalizing Resolution:

Resolution for resampling metrics in standard space. The resampled data will be smoothed for statistics.

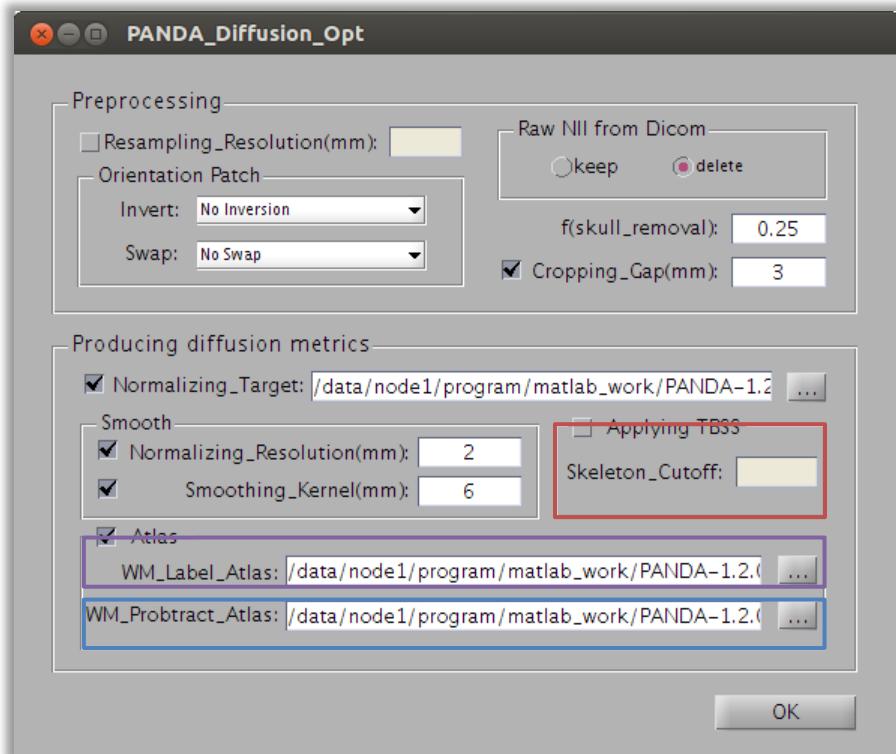
Smoothing Kernel:

Gaussian smoothing kernel size.



Changing parameters (optional)

Diffusion_Opt (The default configuration is recommended)



Select whether to do TBSS.

Skeleton_Cutoff:

FA threshold to exclude voxels in the grey matter or CSF.

WM_Label_Atlas:

PANDA will calculate average of FA/MD/ λ_1/λ_{23m} for all the regions in the WM_Label_Atlas.

WM_Probtract_Atlas:

PANDA will calculate average of FA/MD/ λ_1/λ_{23m} for all the regions in the WM_Probtract_Atlas.

Changing parameters (optional)

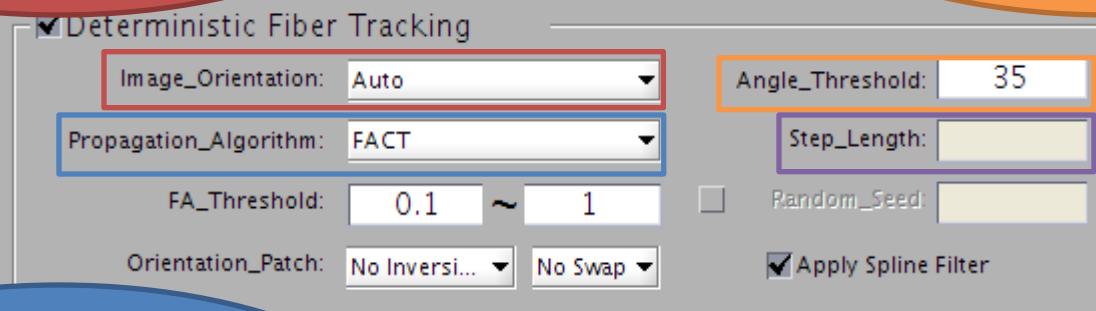
Deterministic Fiber Tracking (The default configuration is recommended)

Image Orientation:

image orientation vector,
'Auto' is recommended.

Angle Threshold:

stop tracking when the
angle of the corner is
larger than threshold.



Propagation Algorithm:

four selections (FACT;
2nd order runge-kutta;
tensorline; interpolated
streamline).

Step Length:

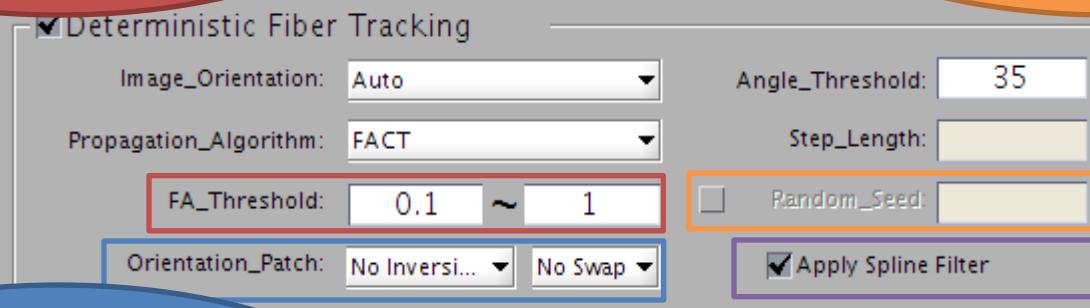
set step length
The unit of the step
length is the minimum
voxel size.

Changing parameters (optional)

Deterministic Fiber Tracking (The default configuration is recommended)

FA Threshold:

stop tracking when FA
is outside of the
threshold range.



Orientation Patch:

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

Random Seed:

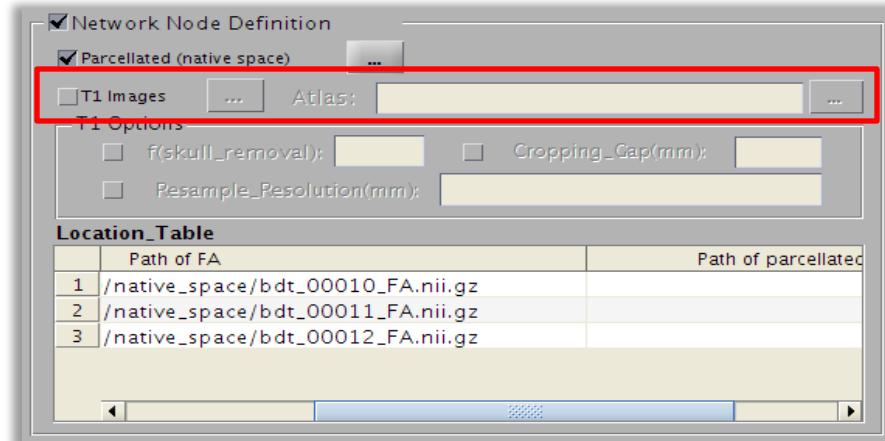
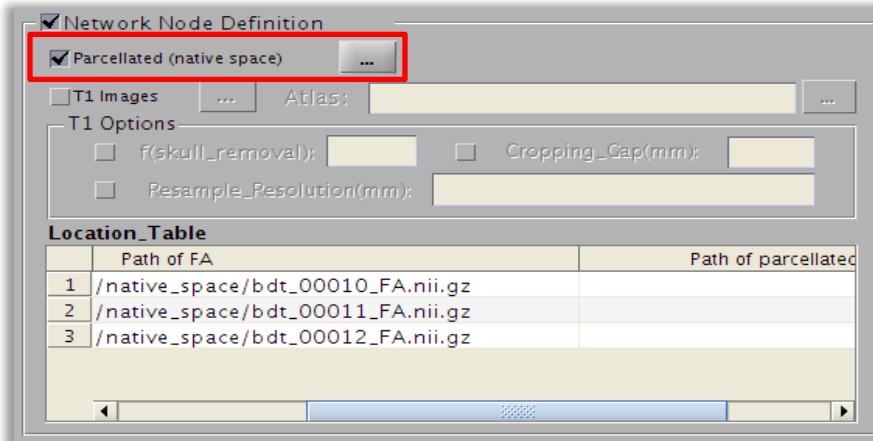
quantity of seeds of each
voxel.

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 :

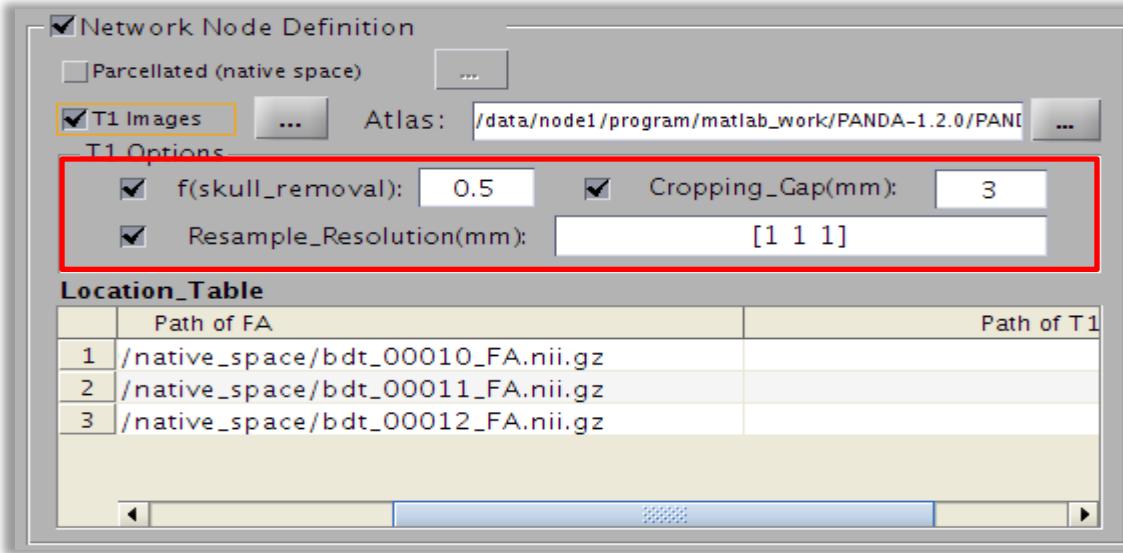
Select 'T1 images' and input T1 images.

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 Node Definition



Options when 'T1 images' was selected :

f (skull removal): fractional intensity threshold (0->1); smaller values give larger brain outline estimates. For extracting the brain of T1 image.

Cropping Gap (mm): The distance from the selected cube to the border of the brain. For cropping T1 image.

Resample Resolution (mm): Voxel size for resampling T1 image.

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)

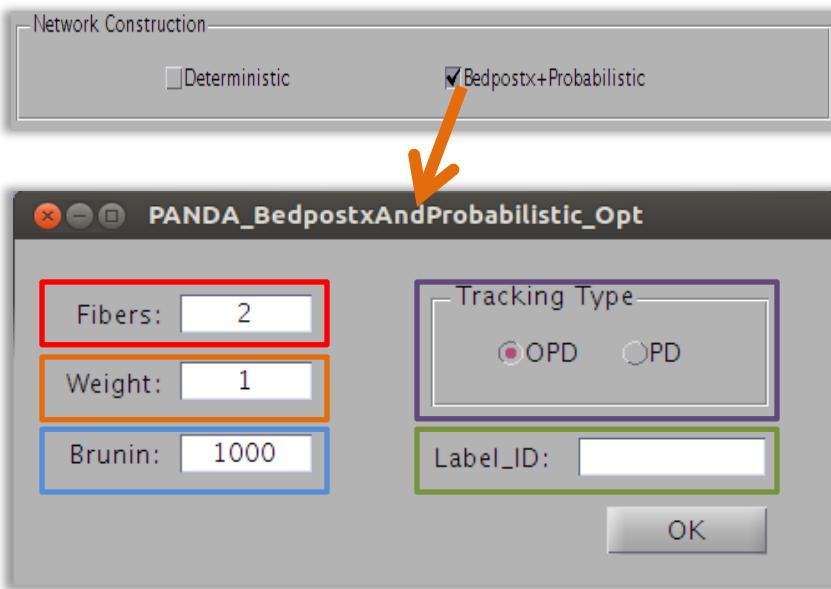
Network Construction

Fibers:

Number of fibers per voxel, default 2.

Weight:

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



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

Burnin:

Burnin period, default 1000.

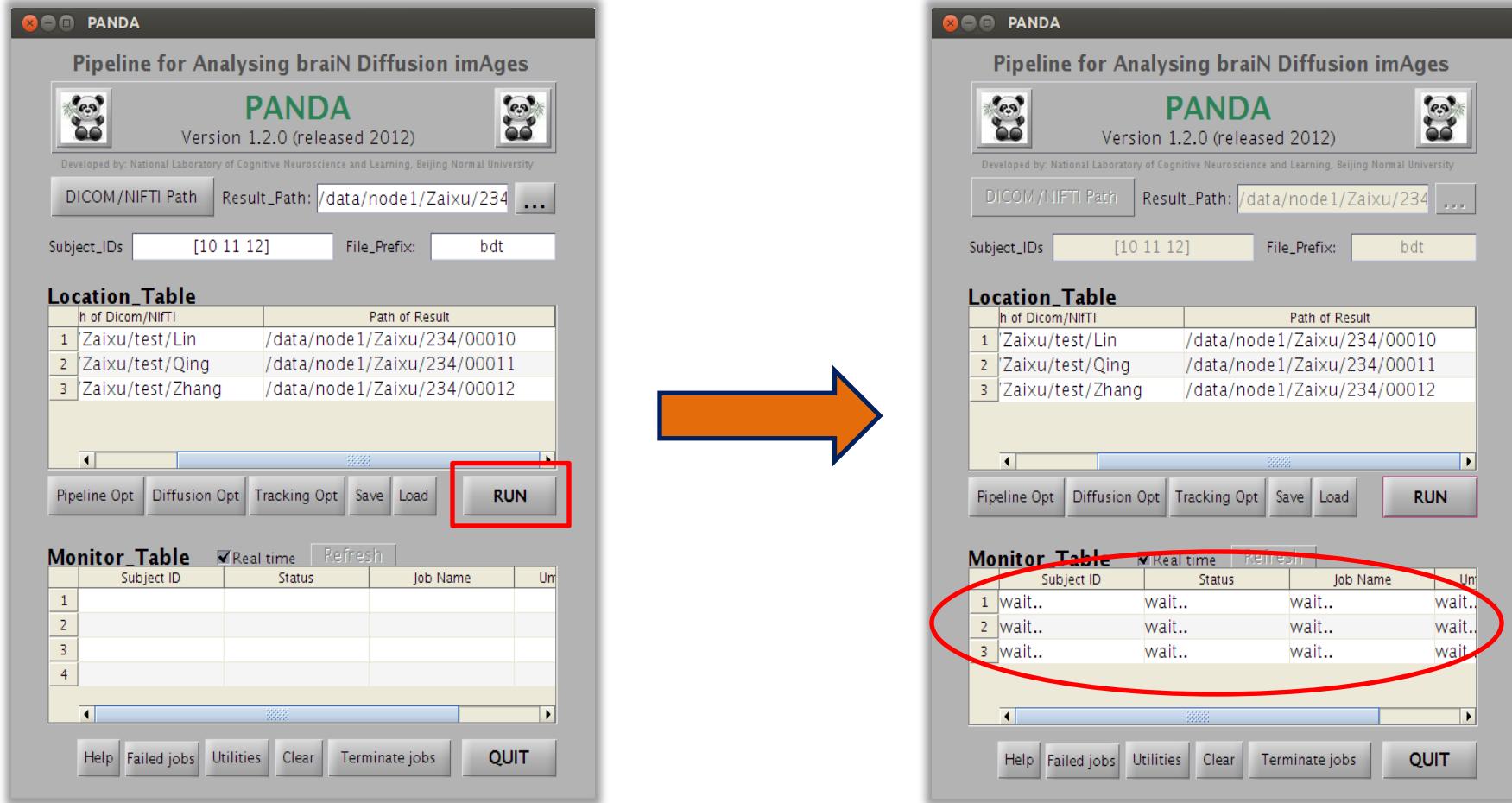
Label ID:
the ID of brain regions in atlas.

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Initiating process

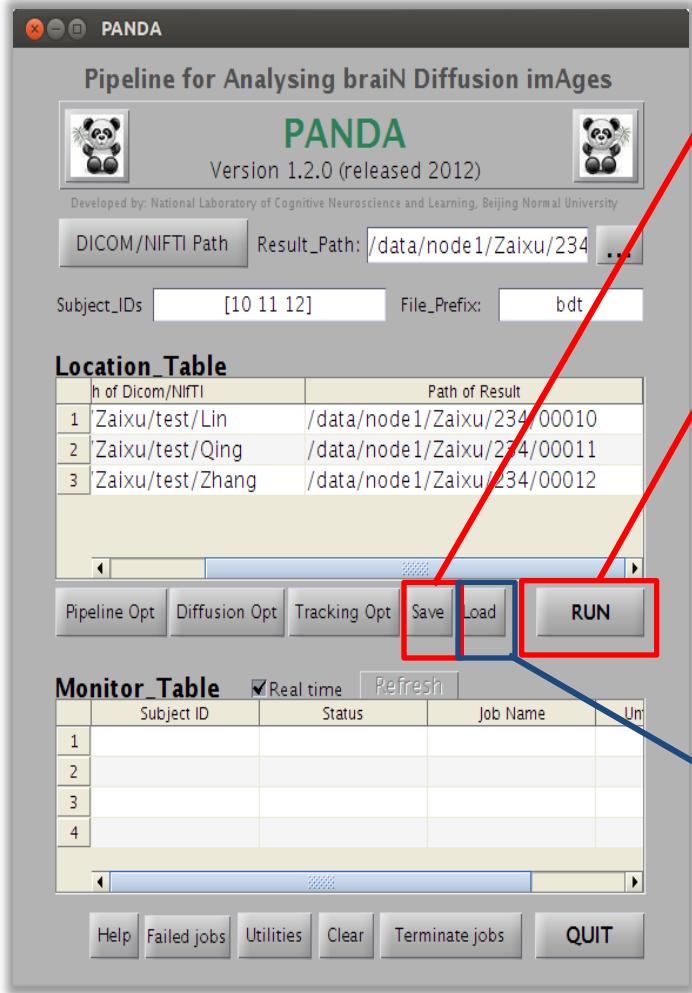
Start running



■ 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):

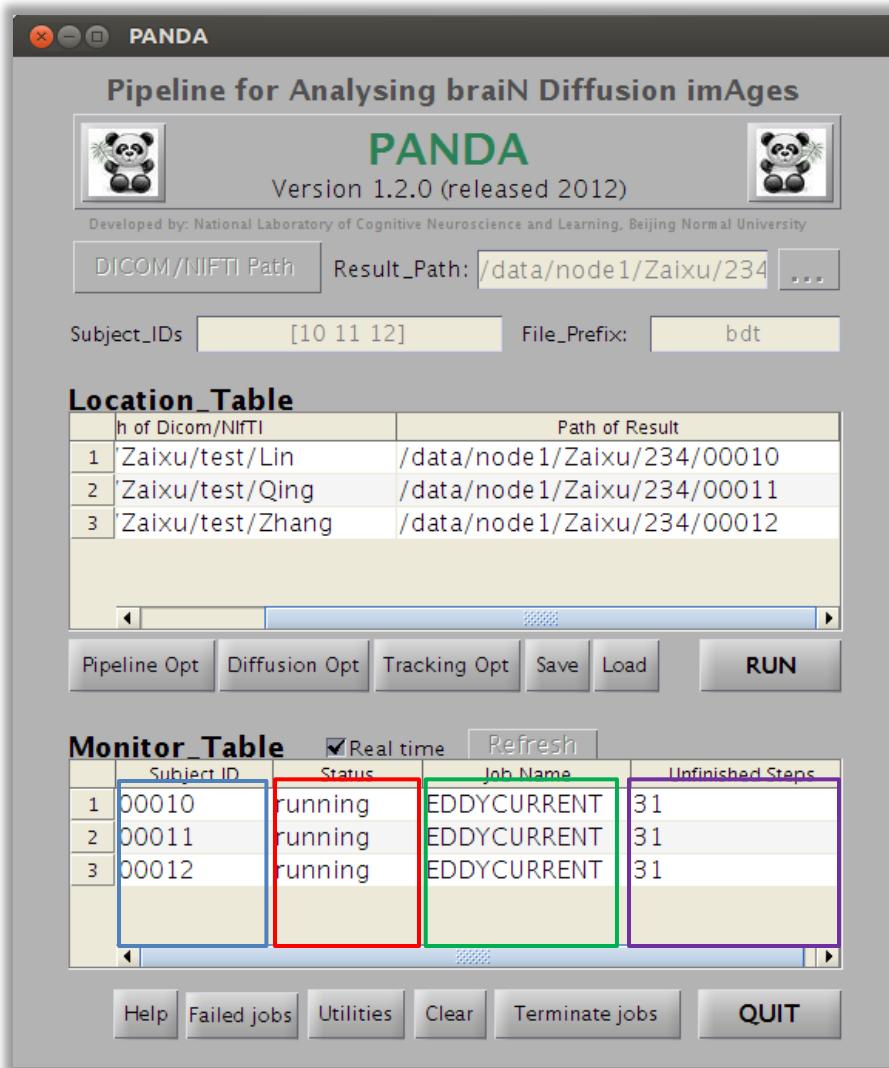
Current configuration will be saved in the 'Result Path' automatically after clicking ‘RUN’ button.

➤ Loading the *.PANDA file.

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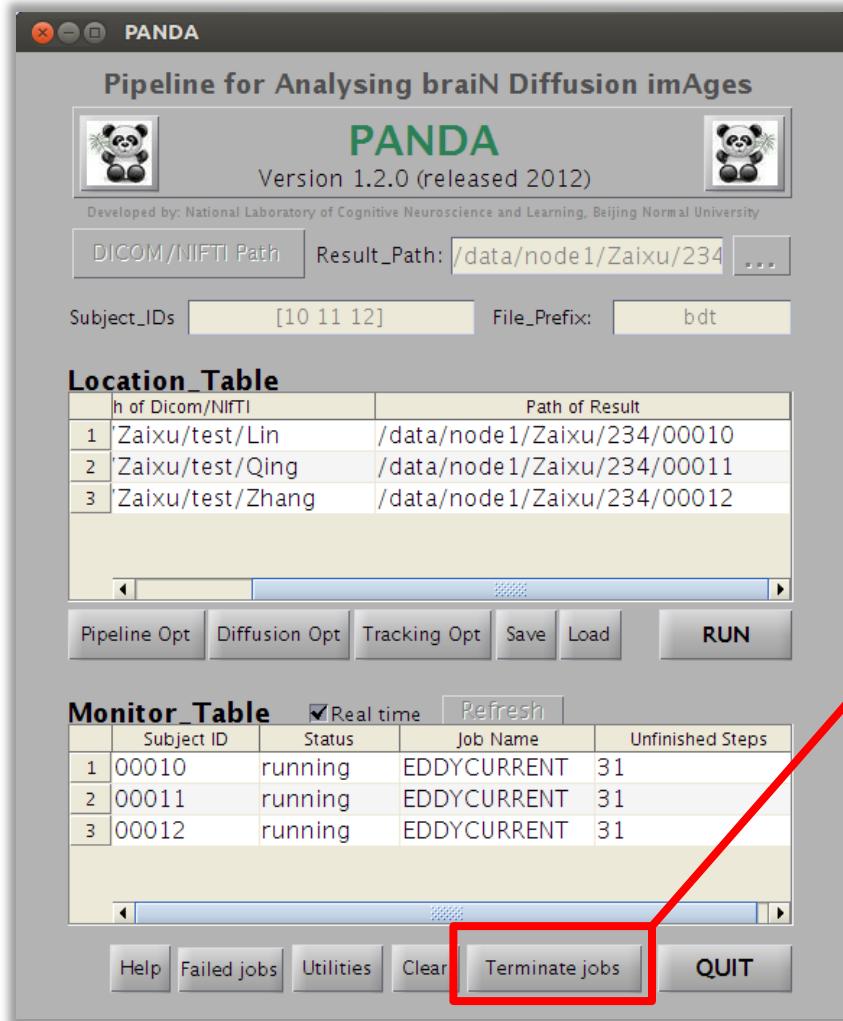
Monitoring progress



- **Subject ID**(fixed)
- **Status**(dynamic)
 - wait
 - submitted
 - running
 - finished
 - failed
- **Job Name**(dynamic)
- **Unprocessed Step**(dynamic)

Monitoring progress

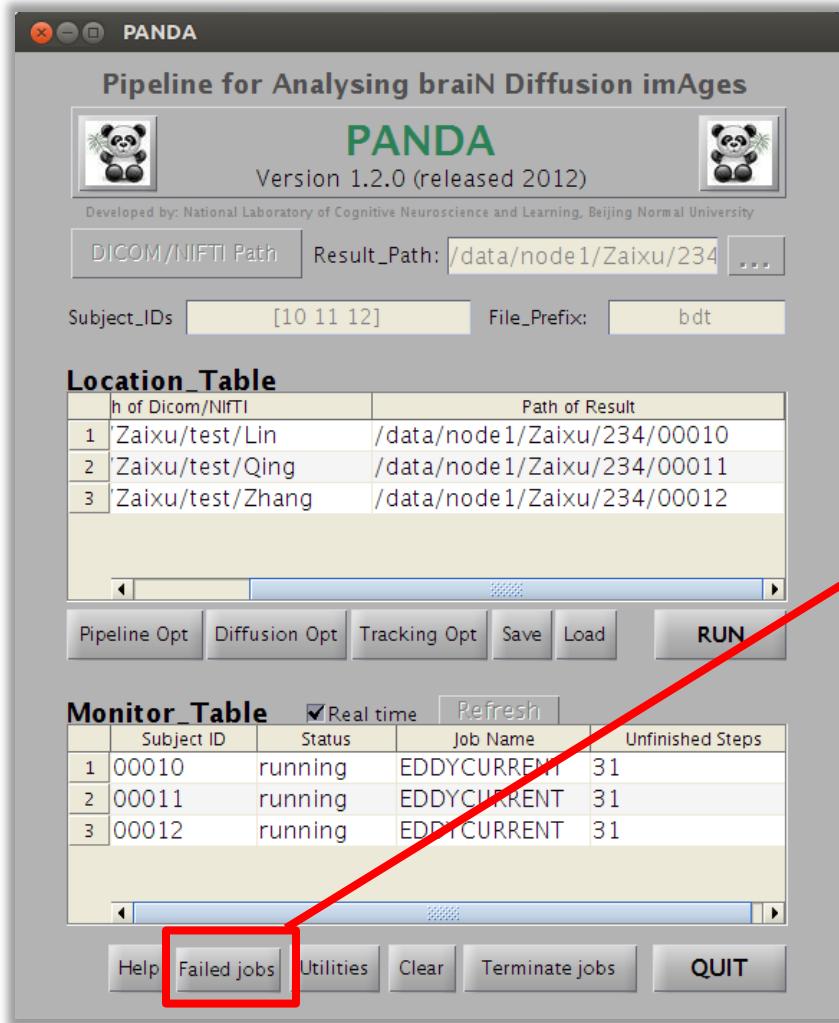
Terminate jobs



Terminate all the jobs running in background.

Monitoring progress

Failed jobs

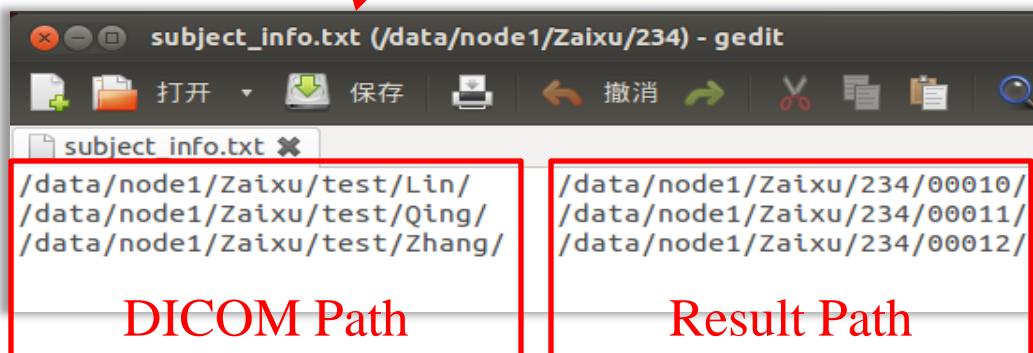
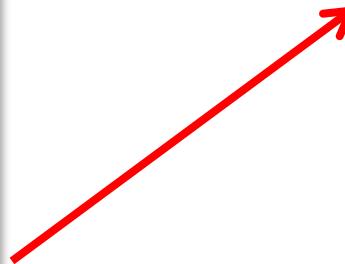
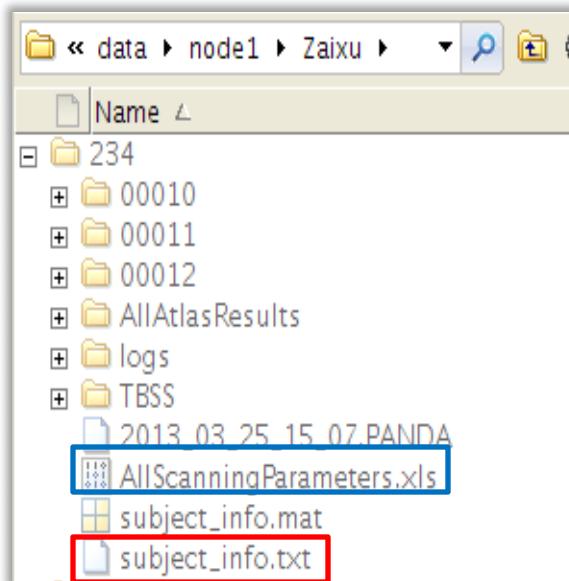


When some jobs failed,
click this button to see the
reasons of jobs' failing.

Contents

- Overview
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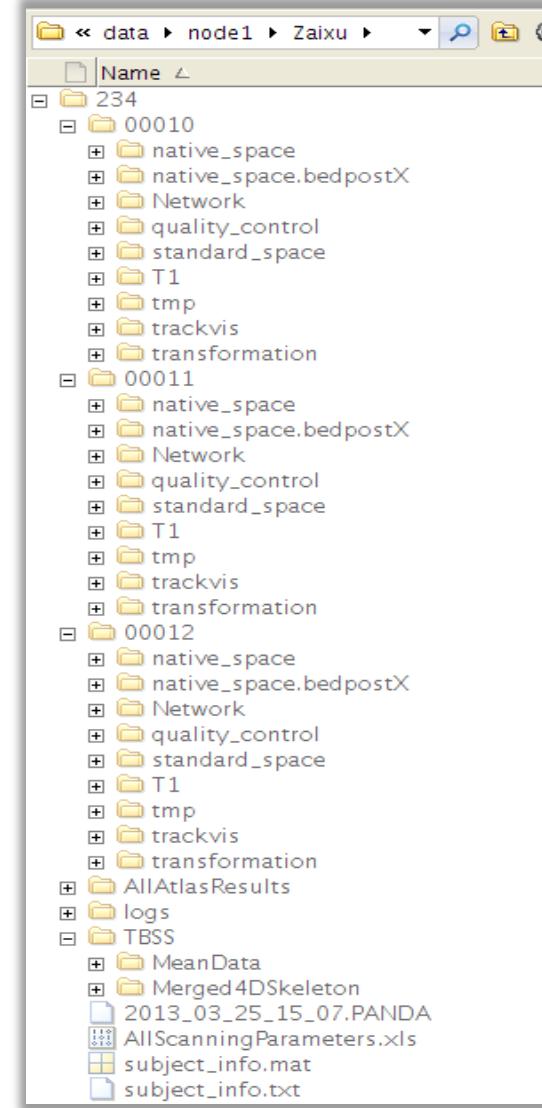
Understanding resultant files



DICOM Path

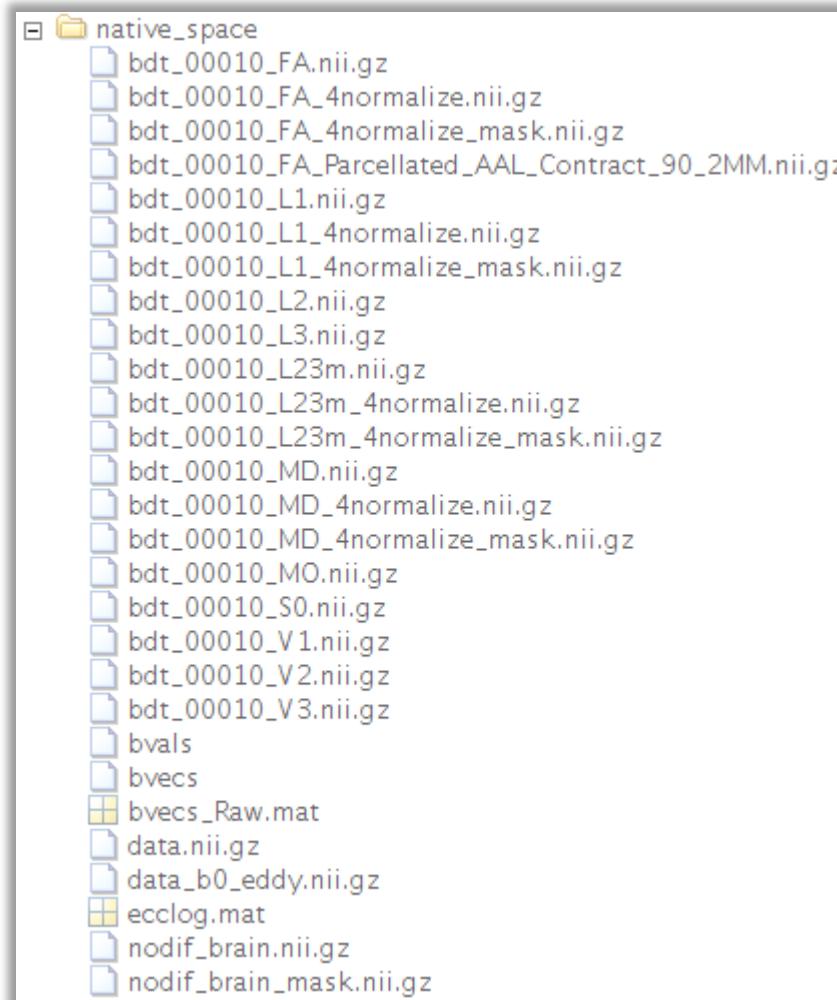
/data/node1/Zaixu/234/00010/
/data/node1/Zaixu/234/00011/
/data/node1/Zaixu/234/00012/

Result Path



Understanding resultant files

Folder `native_space`:



Understanding resultant files

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

In the folder named ‘native_space’

- 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

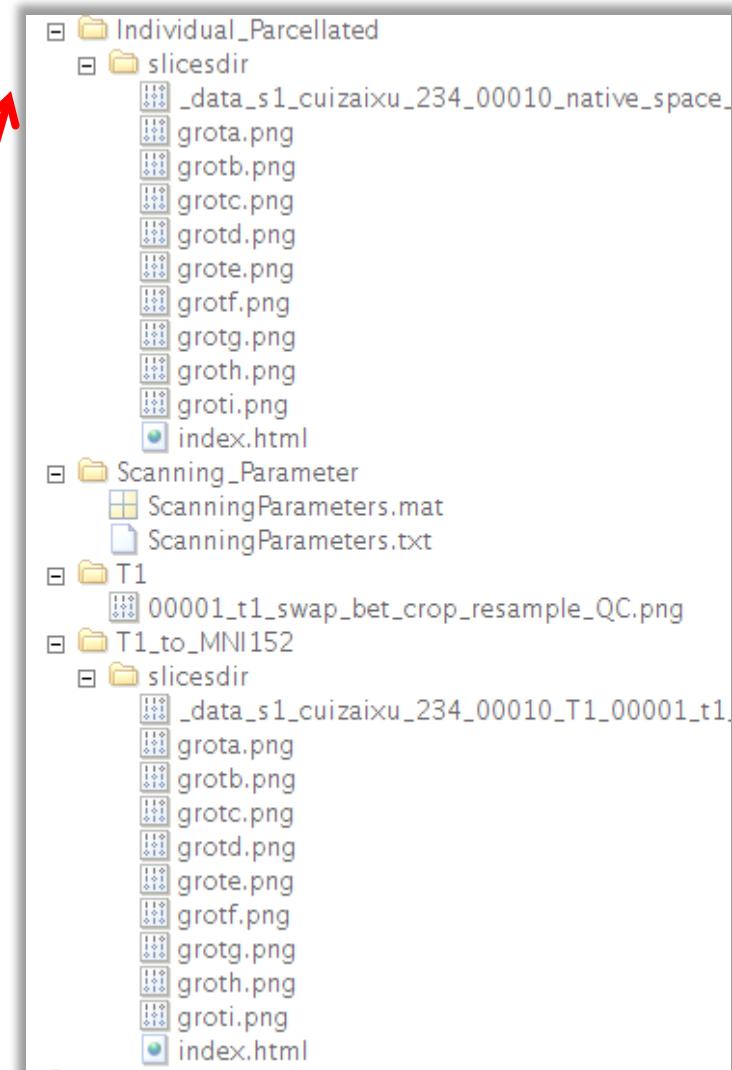
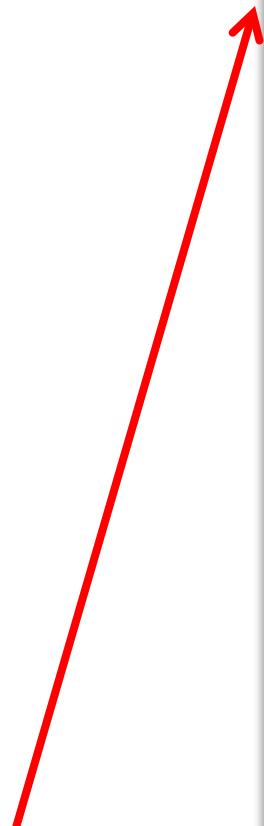
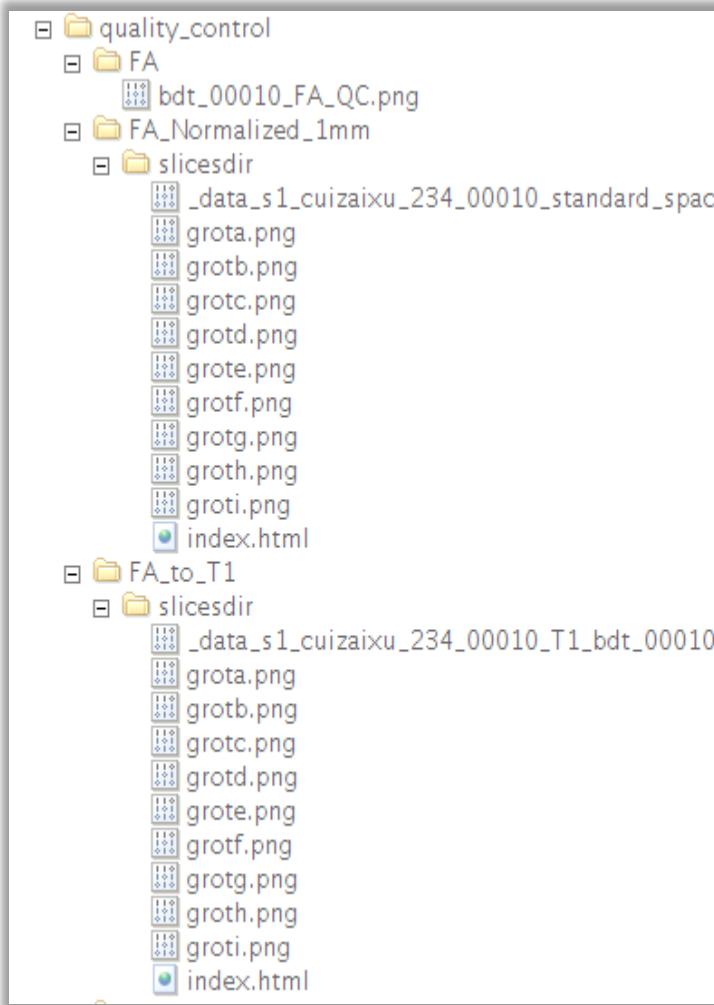
Native space

In the folder named ‘native_space’

- b value file:
bvals
- b vector file:
bvecs
- brain mask:
nodif_brain_mask
- 4D image data after preprocessing:
data.nii.gz
- parcellated image (native space):
Parcellated (produced when network node definition is selected)

Understanding resultant files

Folder `quality_control`:



Understanding resultant files

Check Quality

In the folder named ‘quality_control’

- Check quality of FA:

FA -> *_FA_QC.png

- Check quality of FA normalization to Template:

FA_Normalized_1mm -> slicesdir -> *

- Check quality of FA normalization to T1:

FA_Normalized_1mm -> slicesdir -> *

- Check quality of parcellated image in native space:

Individual_Parcellated -> slicesdir -> *

- Check the scanning parameters:

Scanning_Parameter -> *

Understanding resultant files

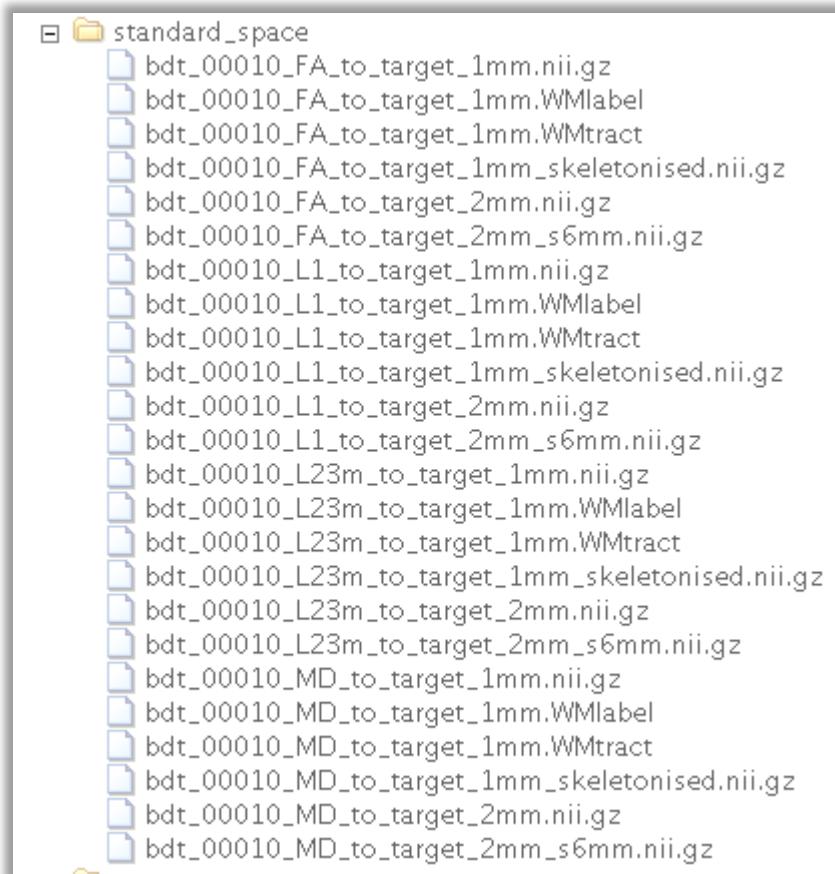
Check Quality

In the folder named ‘quality_control’

- Check quality of T1:
T1 -> *_QC.png
- Check quality of T1 normalization to MNI152 space:
T1_to_MNI152 -> slicesdir -> *

Understanding resultant files

Folder **standard_space**:



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

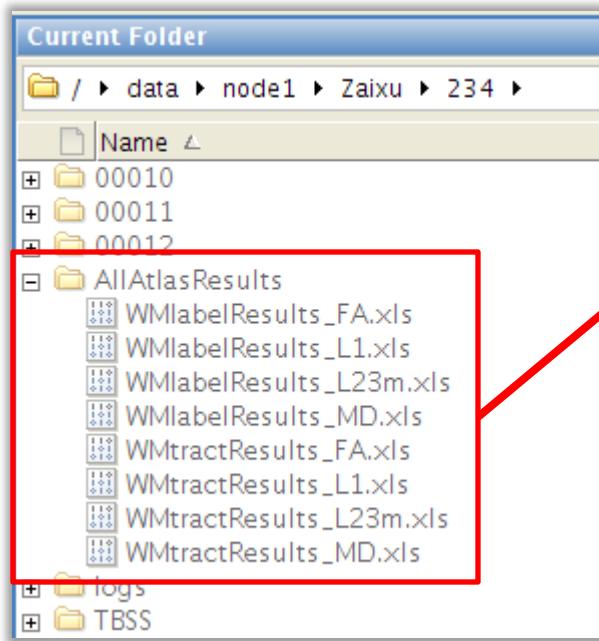
In the folder named ‘standard_space’

- 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

Regional-level results

In the folder named ‘AllAtlasResults’



- All subjects regional average values, can be directly used for statistics with SPSS.
- WMlabelResults_FA.xls:
All subjects regional FA average based on WMlabel-atlas
- WMtractResults_FA.xls:
All subjects regional FA average based on WMtract-atlas

Understanding resultant files

TBSS results

In the folder named ‘standard_space’

- 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

TBSS results

- 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

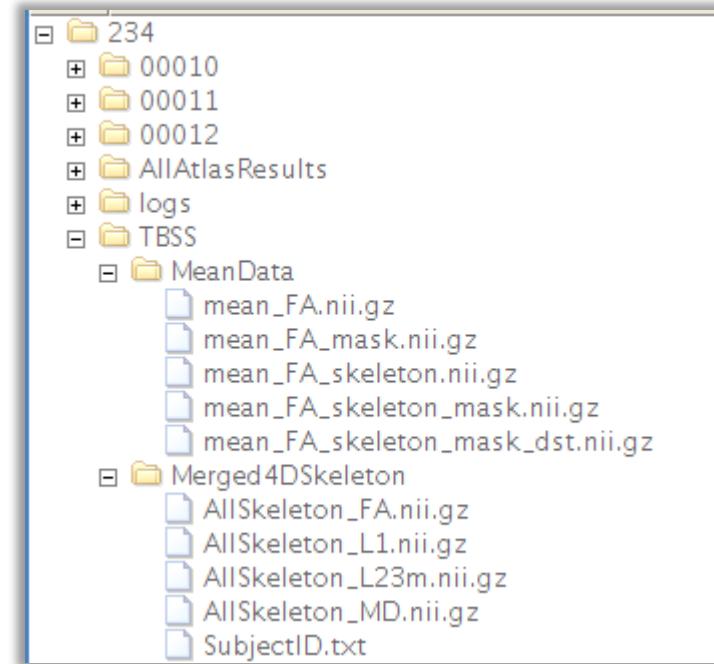
mean_FA_skeleton.nii.gz :

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



- Merged skeletons which can be used for statistics with [randomise](#) command

AllSkeleton_FA.nii.gz : merged FA skeleton for all subjects

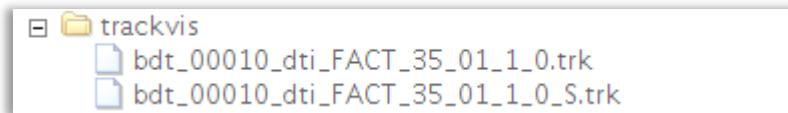
AllSkeleton_MD.nii.gz : merged MD skeleton for all subjects

AllSkeleton_L1.nii.gz : merged λ_1 skeleton for all subjects

AllSkeleton_L23m.nii.gz: merged λ_{23m} skeleton for all subjects

Understanding resultant files

Folder **trackvis**:

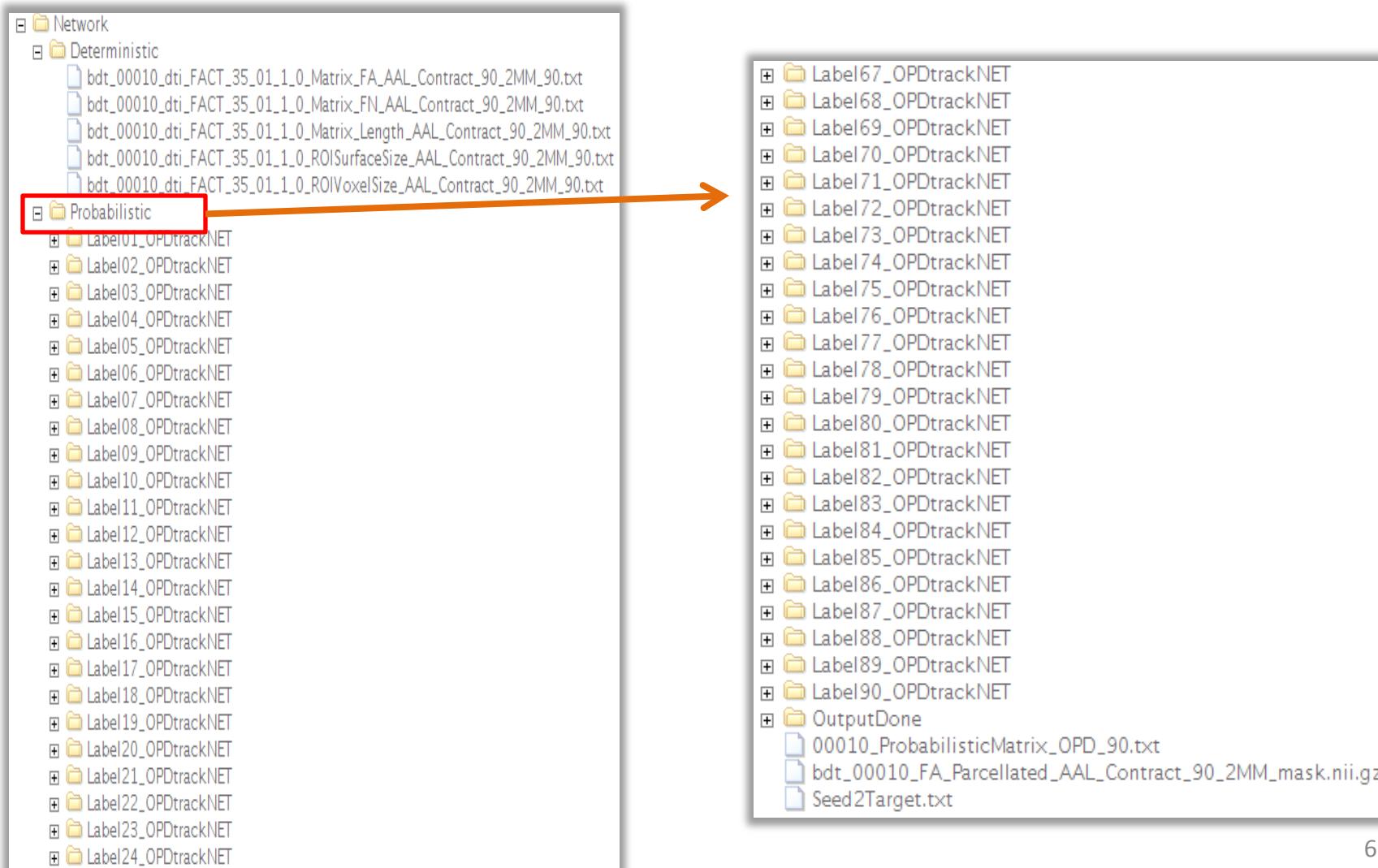


Deterministic Fiber Tracking

- 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

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
- *_ROIVoxelSize_*: quantity of voxels in each ROI
- *_ROISurfaceSize_*: quantity of voxels in which the fibers terminated in each ROI

Understanding resultant files

Probabilistic Network

In the folder named ‘Network/Probabilistic’

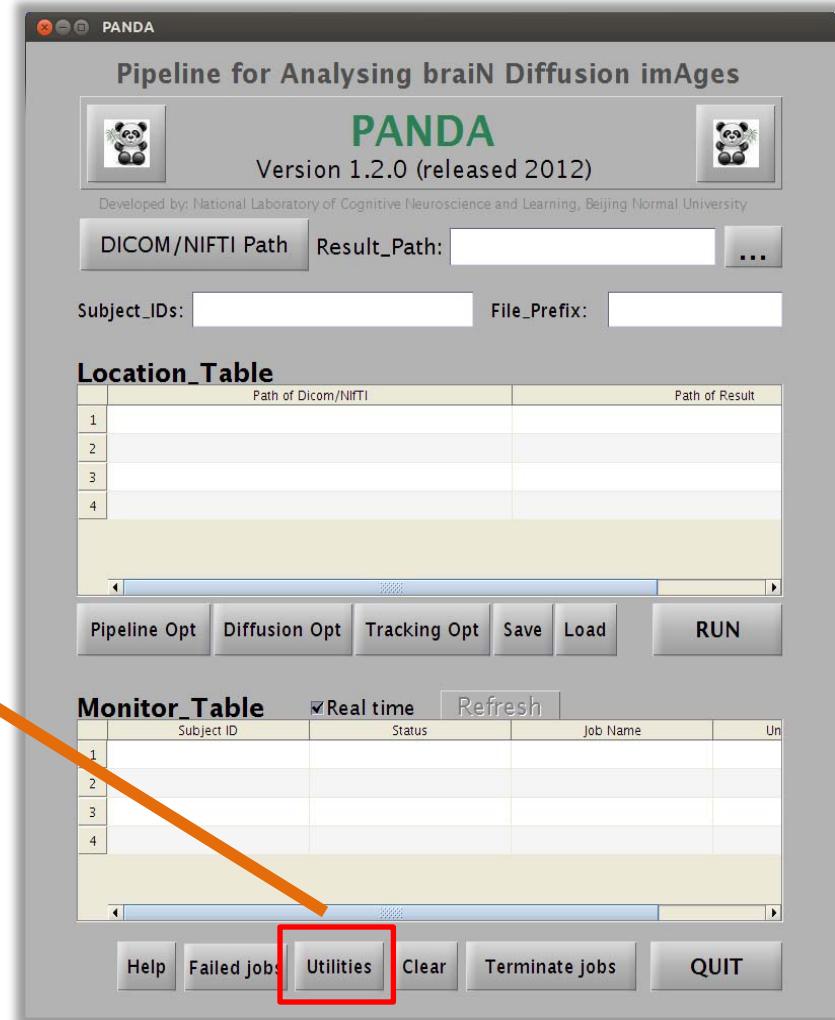
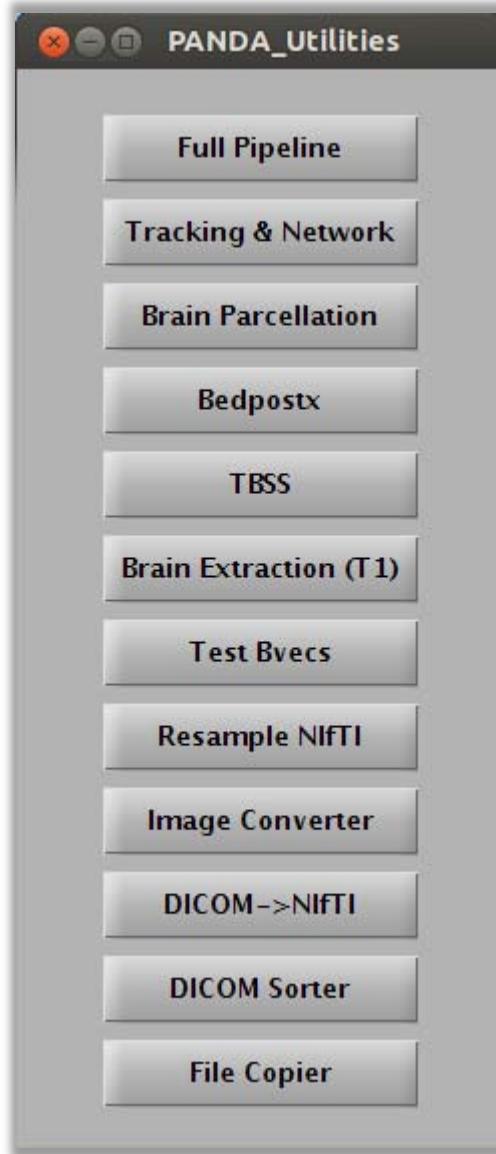
➤ * _ProbabilisticMatrix_ *

connection probability between two regions

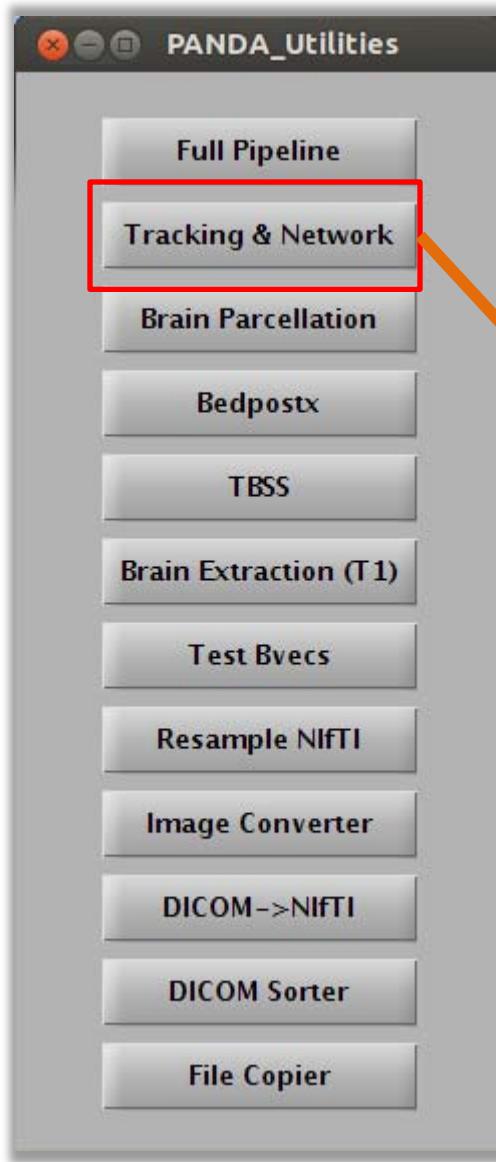
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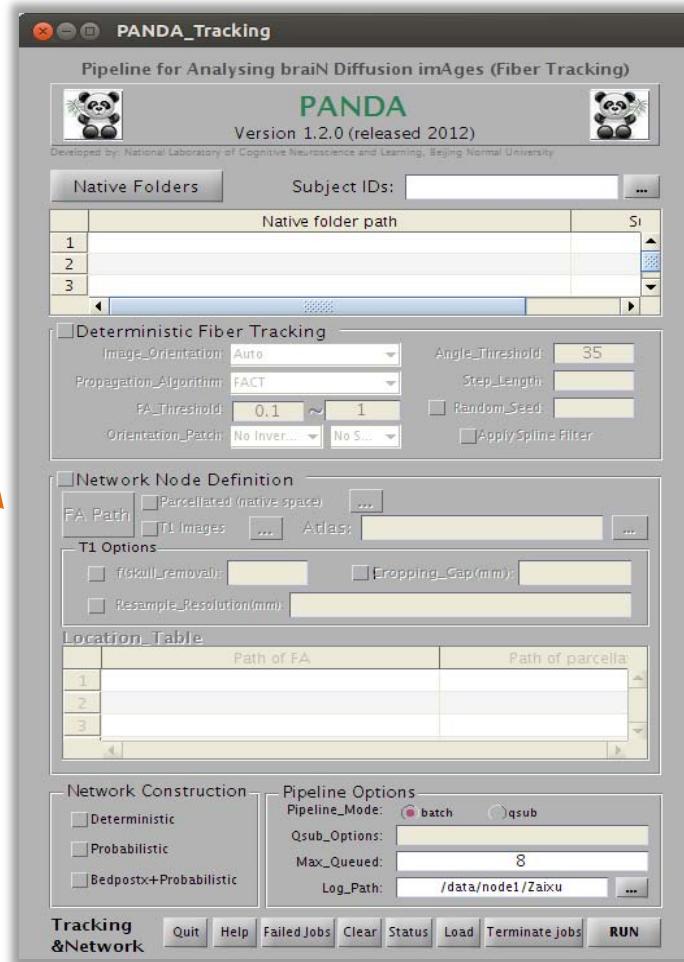
Utilities



Utilities (Tracking & Network)



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



Utilities (Tracking & Network)

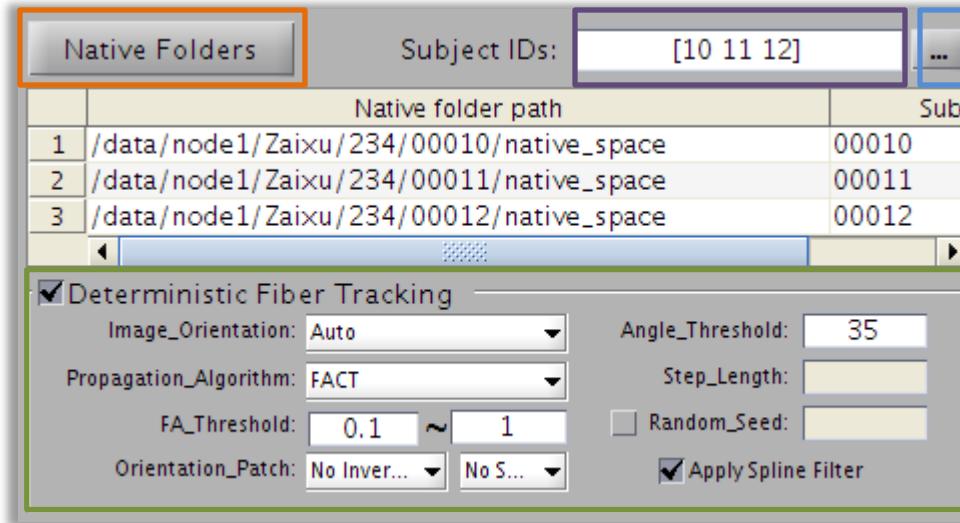
With PANDA_Tracking GUI, you can do:

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

Utilities (Tracking & Network)

Deterministic Fiber Tracking

Native Folders:
Subjects' folders which contain bvcx, bvals, mask and 4D data.



Select Deterministic Fiber Tracking.
Reference to:
[Deterministic Fiber Tracking](#)

Subject IDs:
Input IDs for subjects.

Subject IDs :
Select *.PANDA file to import IDs
user set in Main GUI.

Utilities (Tracking & Network)

Deterministic Network Construction

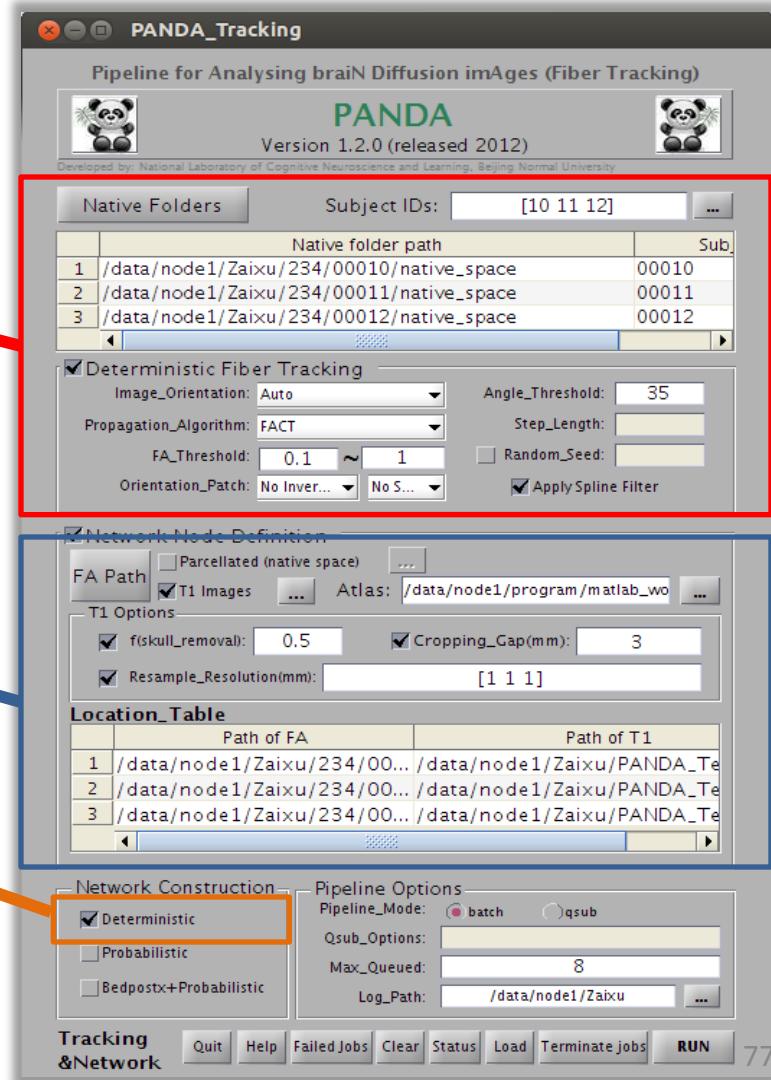
First step: select Deterministic Fiber Tracking

Referring to: [Deterministic Fiber Tracking](#)

Second step: select Network Node Definition

Referring to: [Next Page](#)

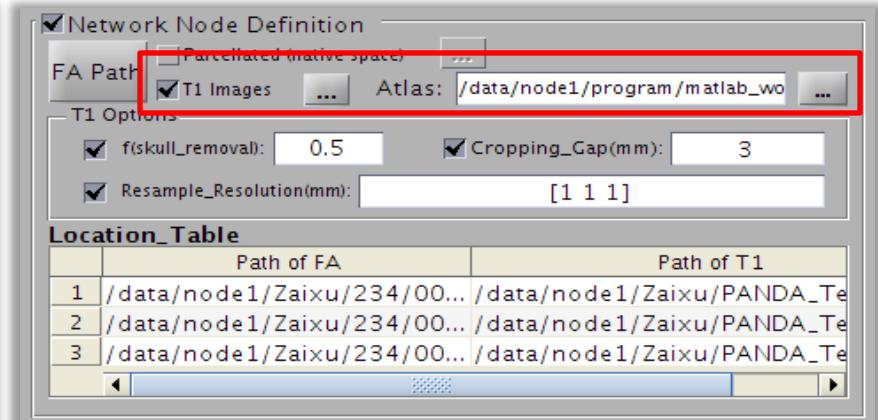
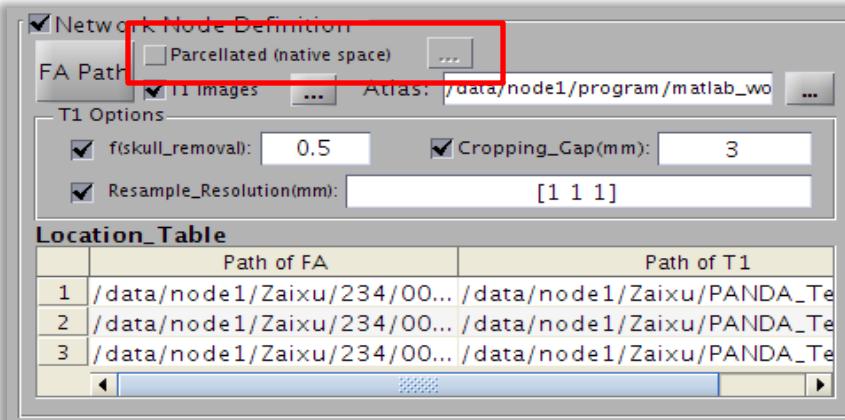
Third step: select Deterministic Network Construction



Utilities (Tracking & Network)

Network Node Definition

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



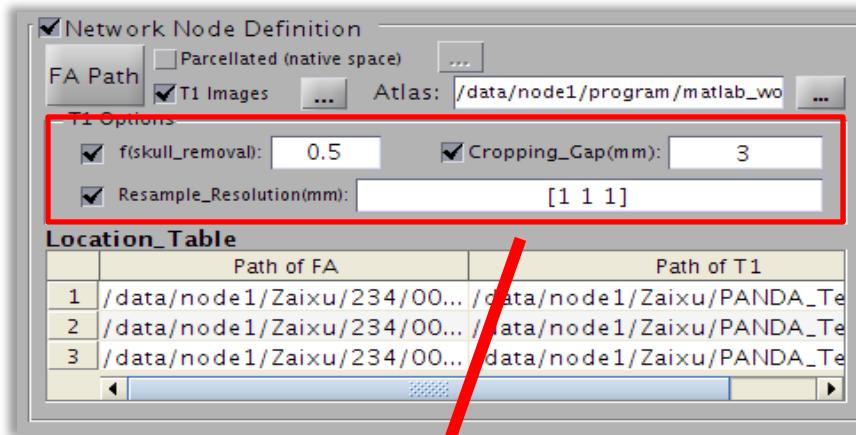
When you have parcellated images in native space :
Please select '[Parcellated \(native space\)](#)' and input these images.

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)

Network Node Definition



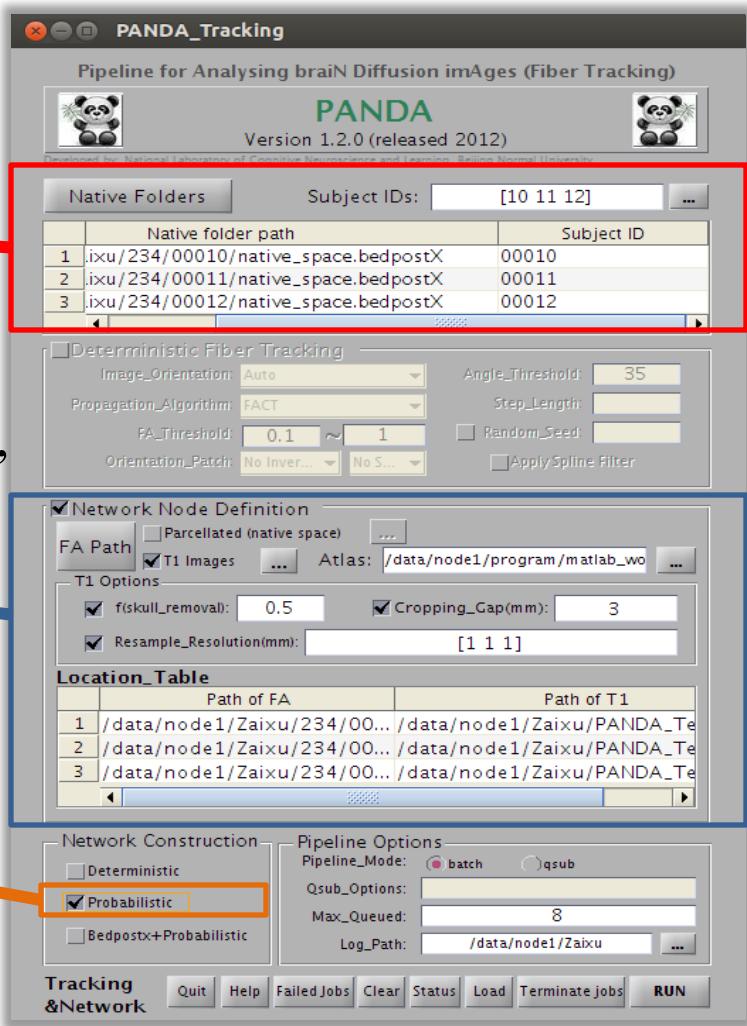
Options for '[T1 images](#)'.

Reference: [Network Node Definition](#).

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](#).

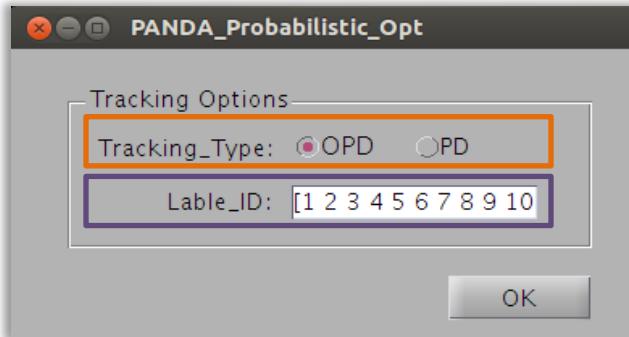
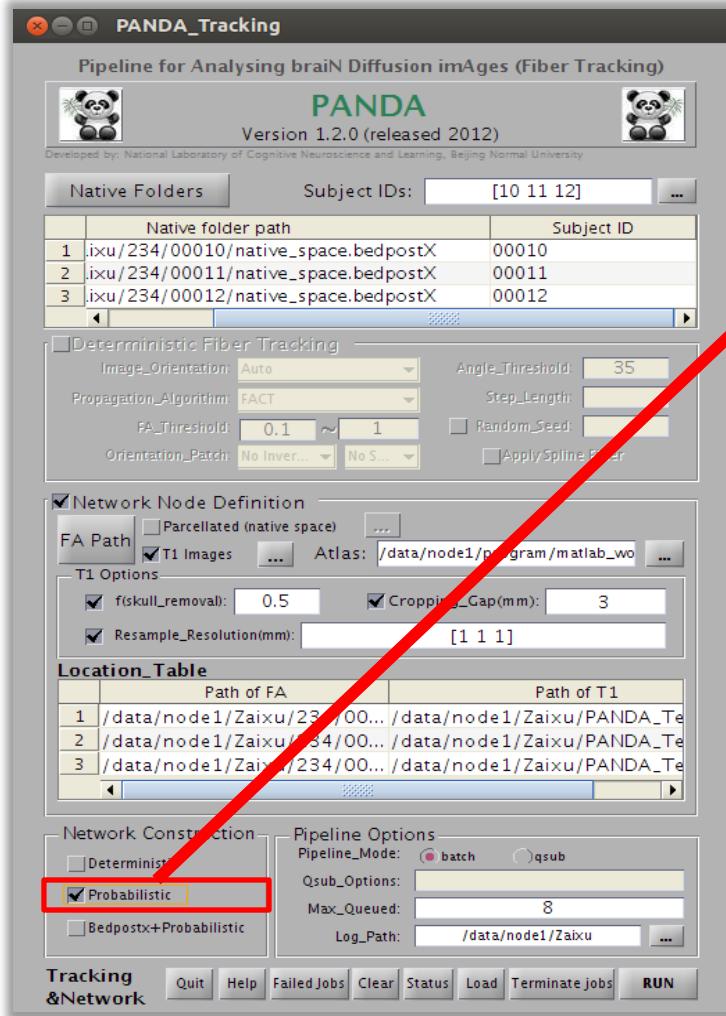


Third step: select Probabilistic Network
Construction
Referring to [Next Page](#).



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).

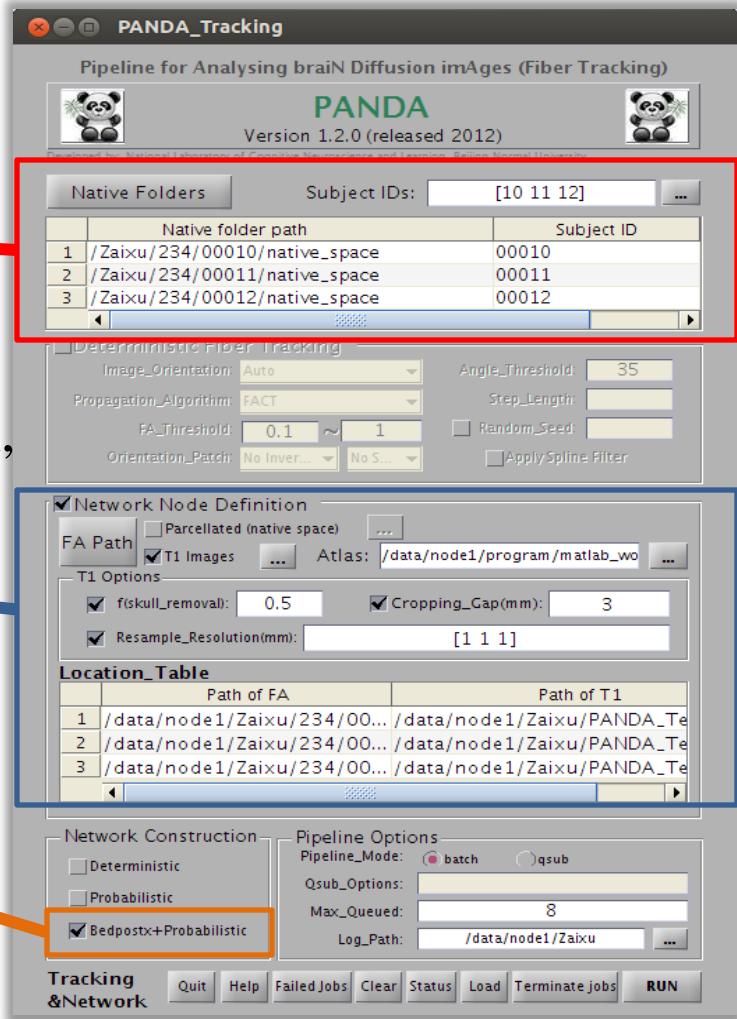
Label ID:

The IDs of brain region in atlas.

Utilities (Tracking & Network)

BedpoxT+Probabilistic Fiber Tracking & Network Construction

First step: input subjects' folder which contain bvecs, bvals, mask, 4D data.



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

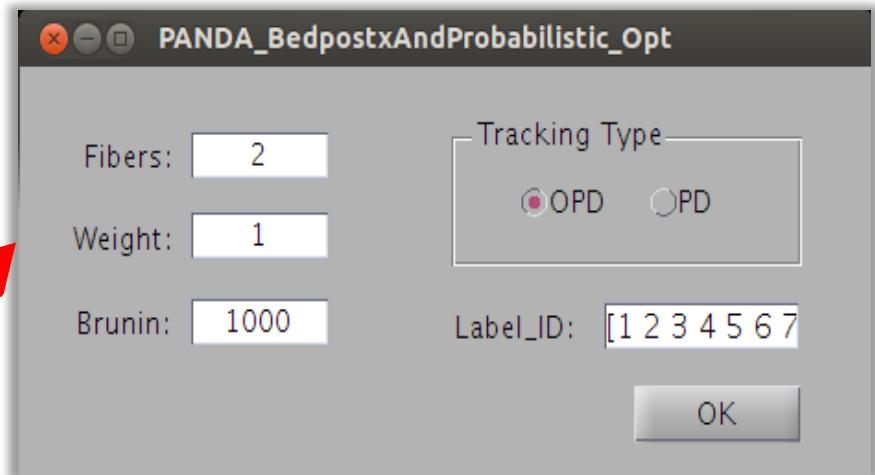
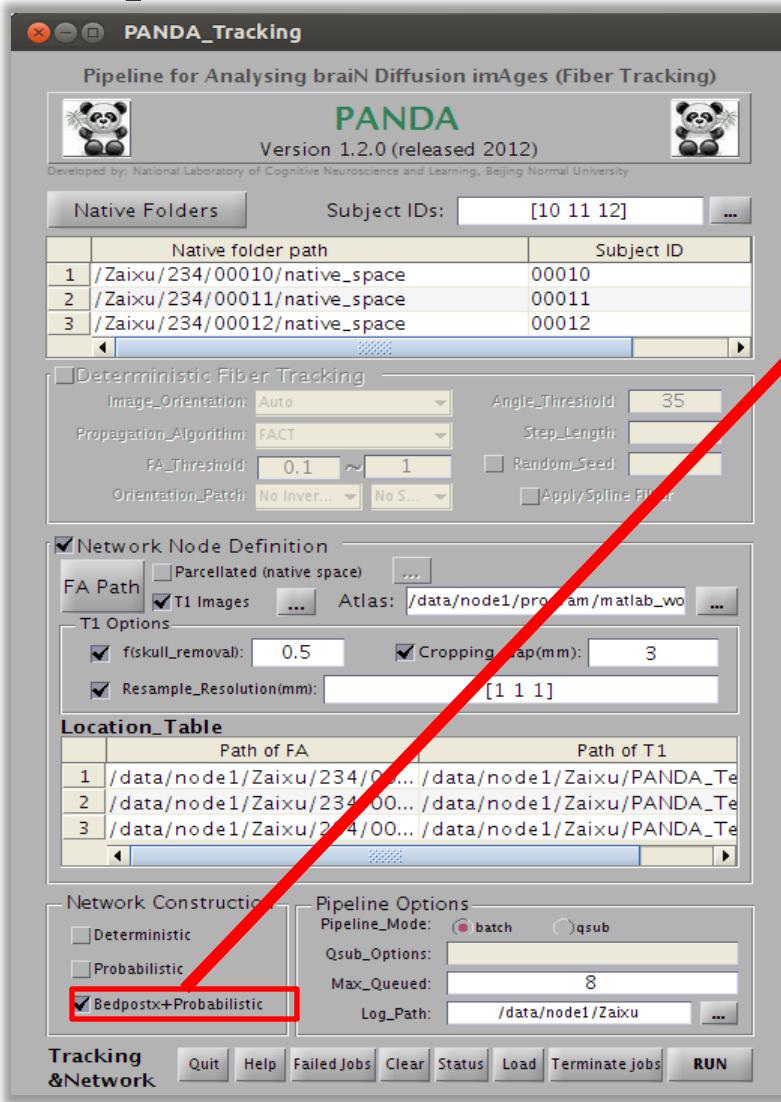


Third step: select Bedpostx+Probabilistic
Network Construction
Referring to [Next Page](#).



Utilities (Tracking & Network)

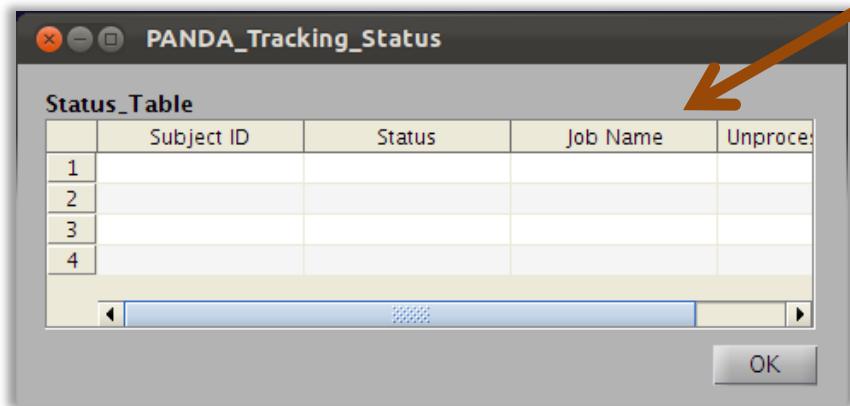
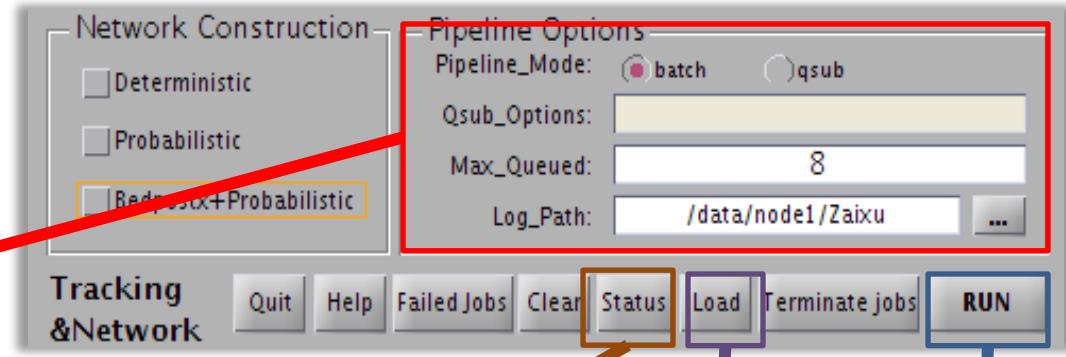
BedpoxT+Probabilistic Fiber Tracking & Network Construction



Referring to: [Network Node Definition](#).

Utilities (Tracking & Network)

Referring to: Pipeline Opt



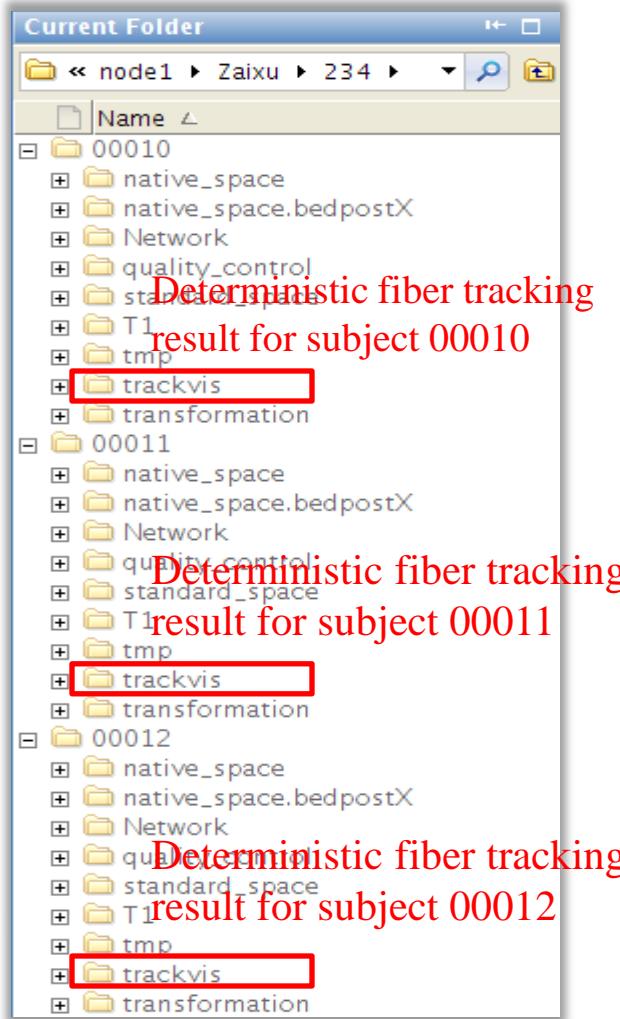
Referring to: Monitoring Progress

Loading the
*.PANDA_Tracking file.

Current configuration will be
saved in 'Log Path'
automatically after
clicking 'RUN' button.
(extension as .PANDA_Tracking).

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_space
/data/node1/Zaixu/234/00011/native_space
/data/node1/Zaixu/234/00012/native_space

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 Network Construction):

➤ 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_space  
/data/node1/Zaixu/234/00011/native_space  
/data/node1/Zaixu/234/00012/native_space
```

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 Network Construction):

➤ 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:

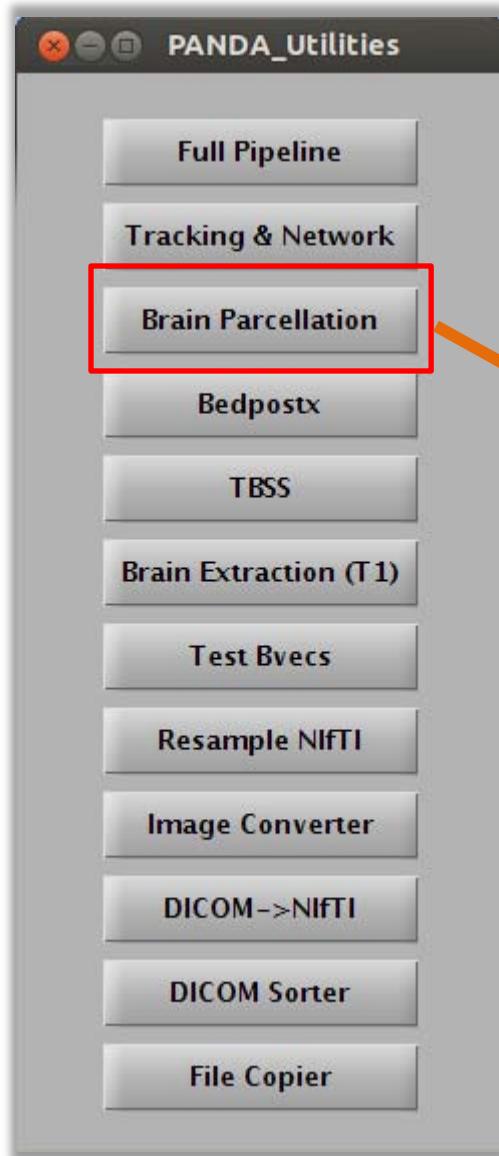
Inputs are

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

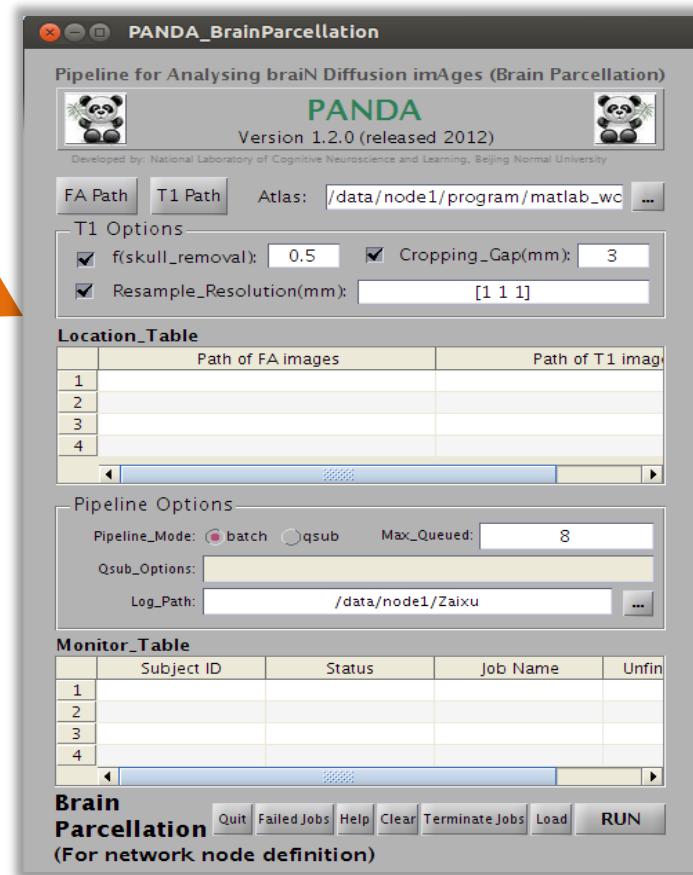
Outputs are

```
/data/node1/Zaixu/234/00010/Network/Probabilistic  
/data/node1/Zaixu/234/00011/Network/Probabilistic  
/data/node1/Zaixu/234/00012/Network/Probabilistic
```

Utilities (Brain Parcellation)



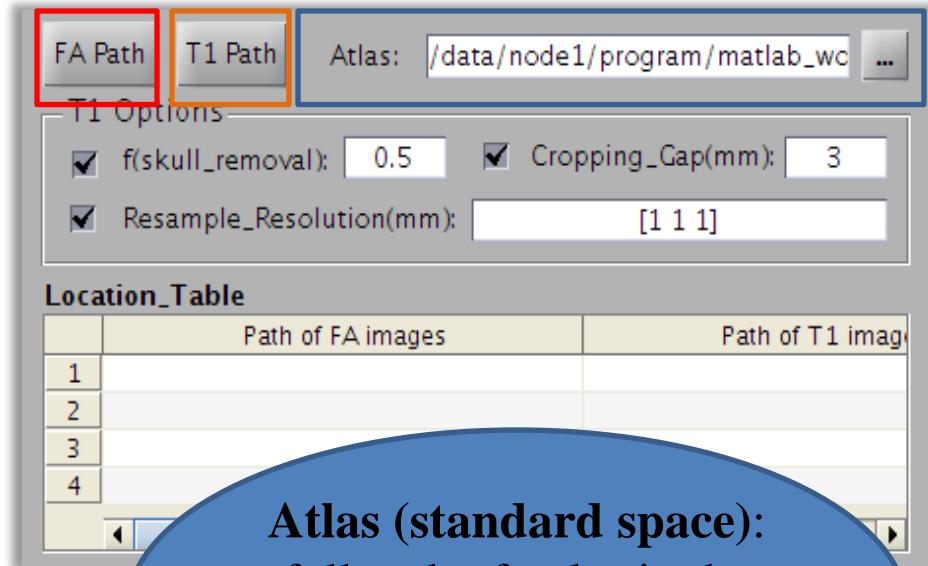
➤ Run brain parcellation according to atlas for any number of subjects in parallel.



Utilities (Brain Parcellation)

FA Path:
full path of subjects' FA images.

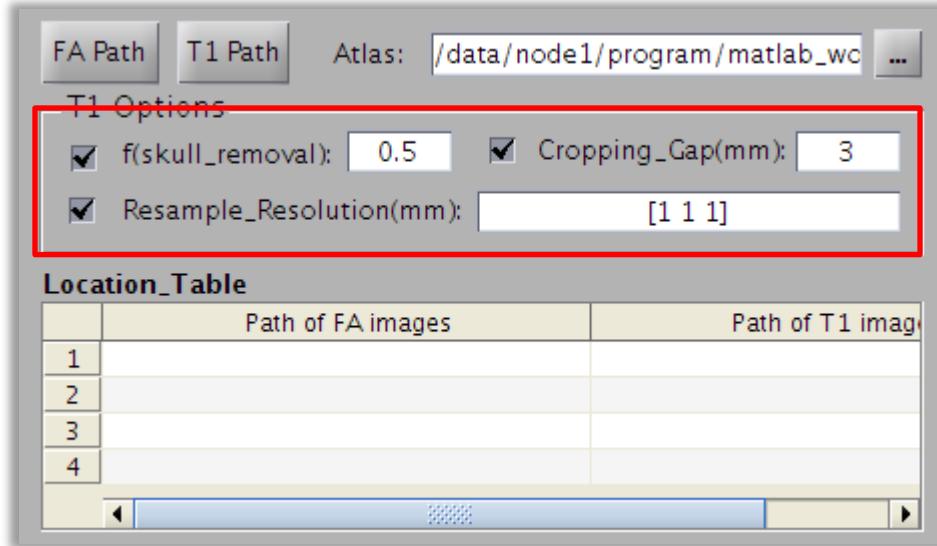
T1 Path:
full path of subjects' T1 images.



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)



Options for T1 images :

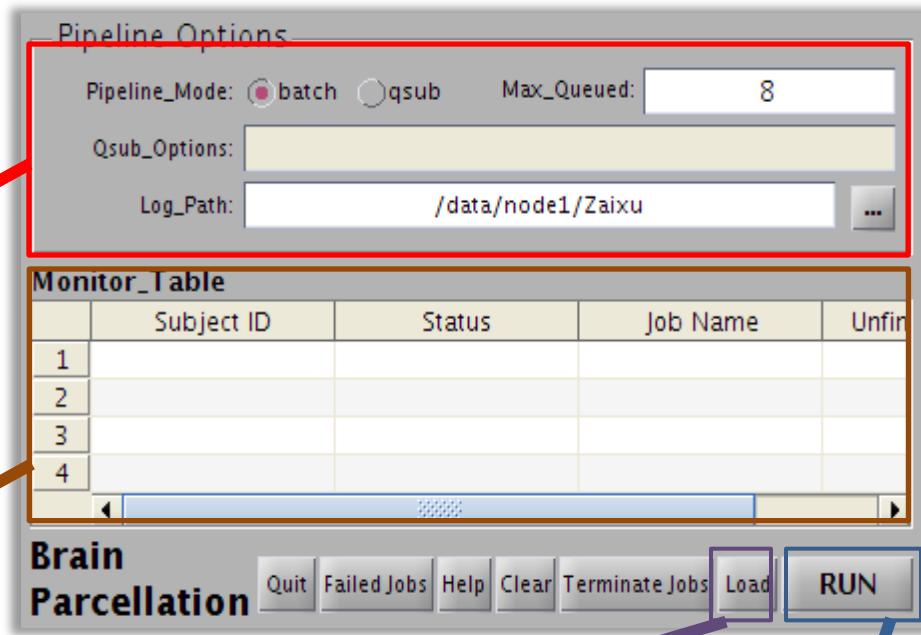
f (skull removal): fractional intensity threshold (0->1); smaller values give larger brain outline estimates. For extracting the brain of T1 image.

Cropping Gap (mm): The distance from the selected cube to the border of the brain. For cropping T1 image.

Resample Resolution (mm): Voxel size for resampling T1 image.

Utilities (Brain Parcellation)

Referring to: [Pipeline Opt](#)



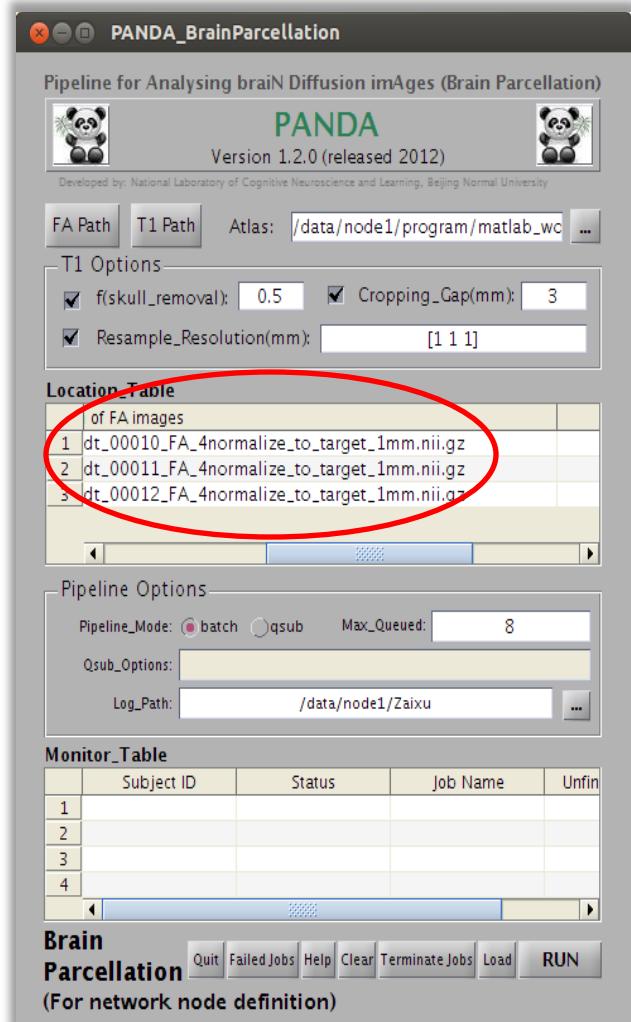
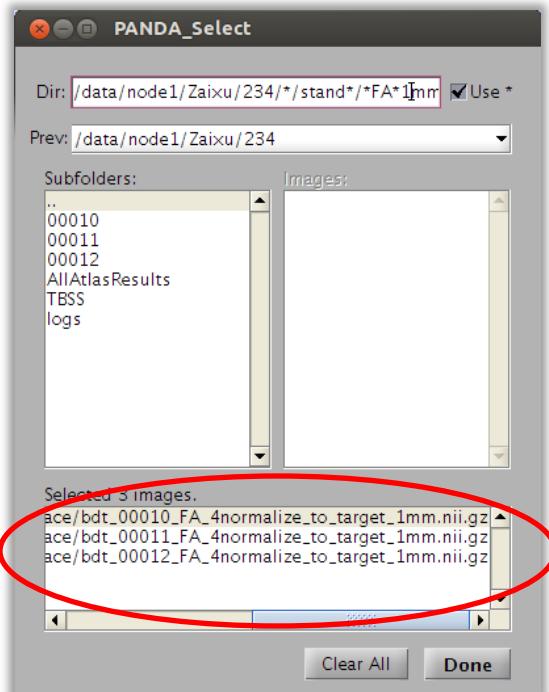
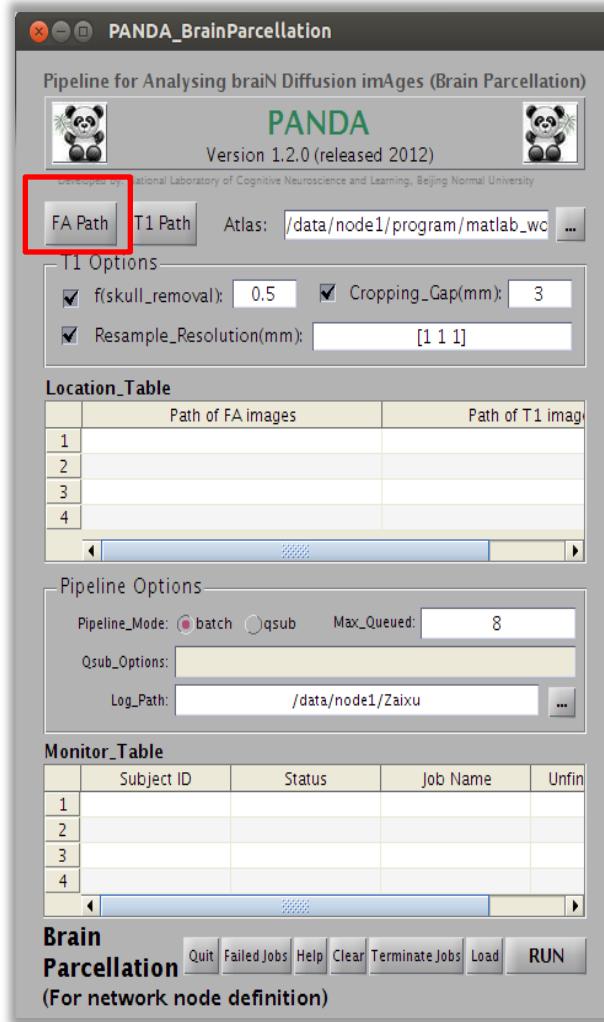
Referring to: [Monitoring Progress](#)

Loading the *.PANDA_BrainParcellation file.

Current configuration will be saved in '[Log Path](#)' automatically after clicking 'RUN' button. (extension as **.PANDA_BrainParcellation**).

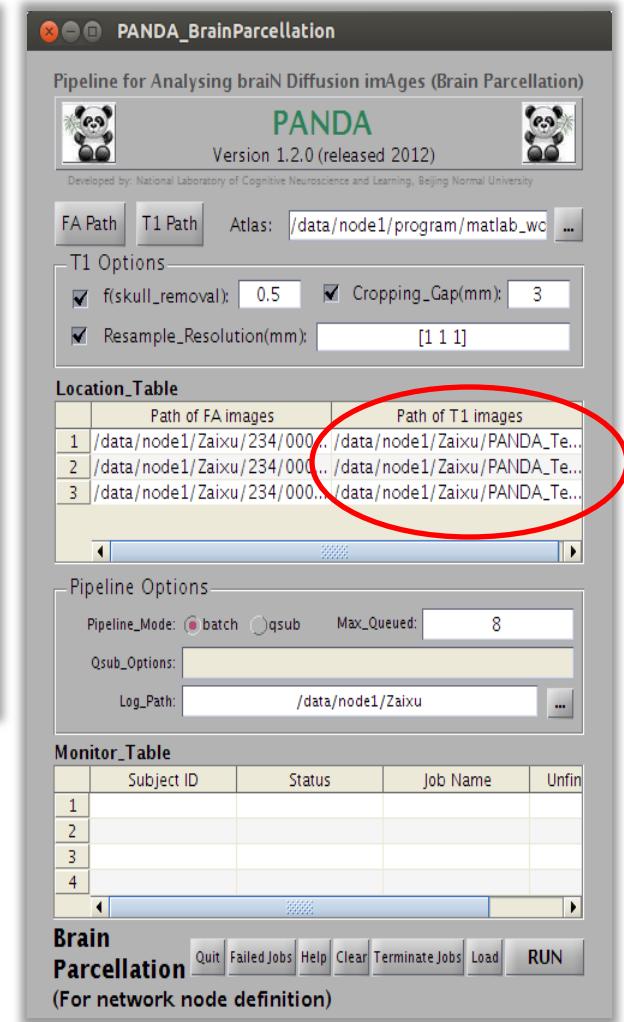
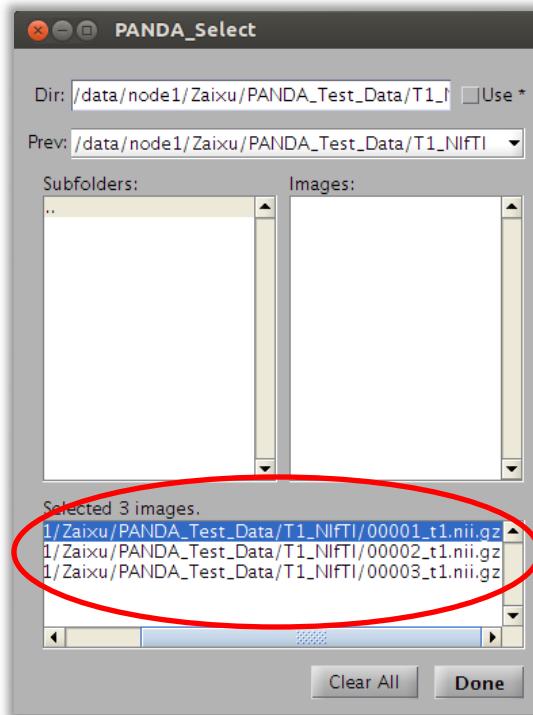
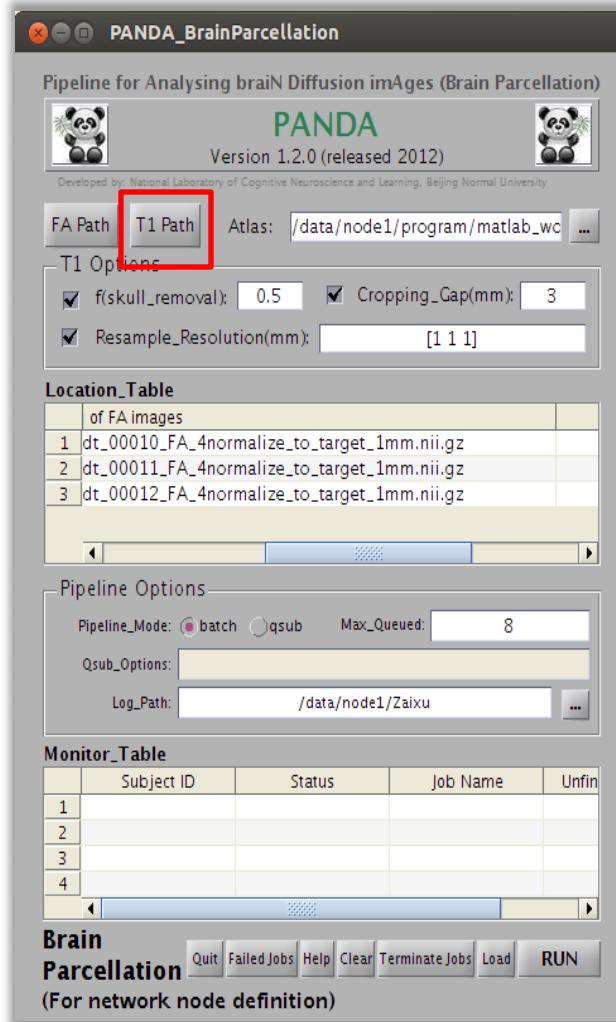
Utilities (Brain Parcellation)

Set FA Path:



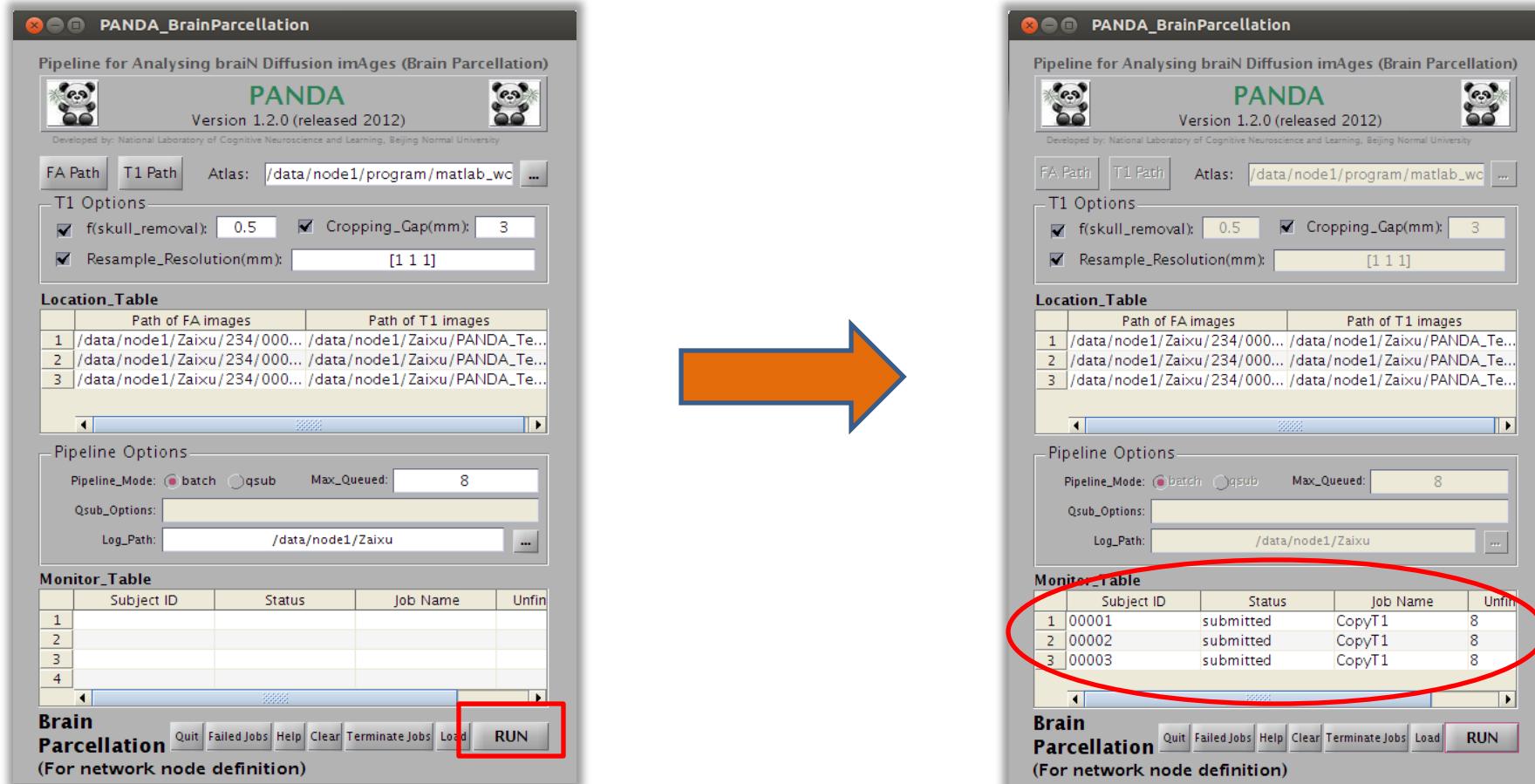
Utilities (Brain Parcellation)

Set T1 Path:



Utilities (Brain Parcellation)

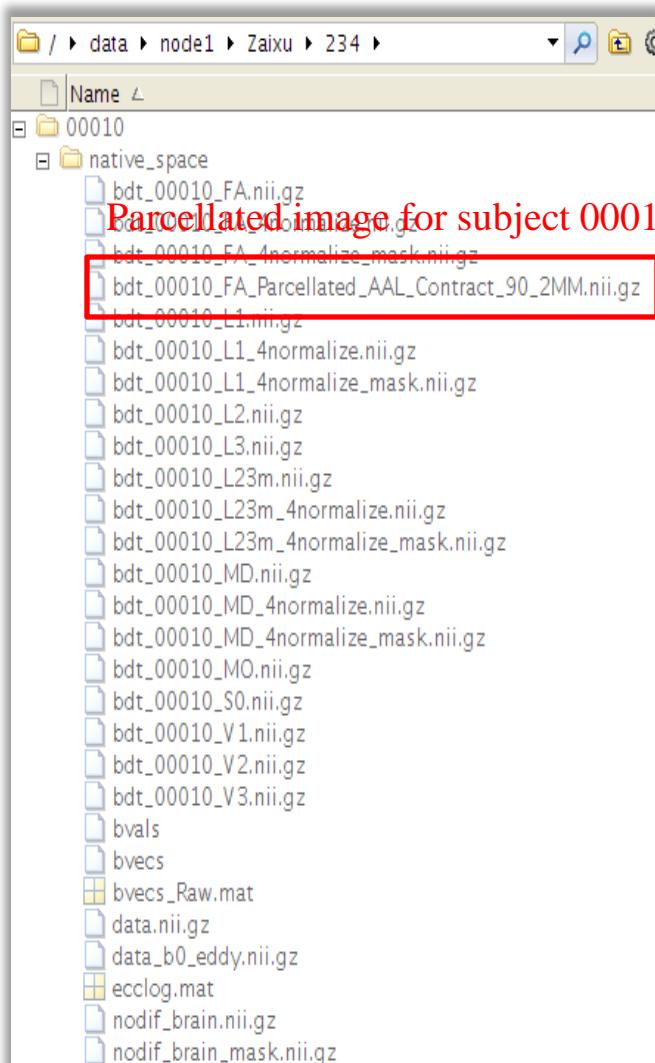
Initiating Process:



- Current configuration was saved in '[Log Path](#)' automatically after clicking 'RUN' button.
(extension as .PANDA_BrainParcellation)

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_space/

bd_00010_FA.nii.gz

/data/node1/Zaixu/234/00011/native_space/

bd_00011_FA.nii.gz

/data/node1/Zaixu/234/00012/native_space/

bd_00012_FA.nii.gz

[Outputs](#) are

/data/node1/Zaixu/234/00010/native_space/

bd_00010_FA_Parcellated_*.nii.gz

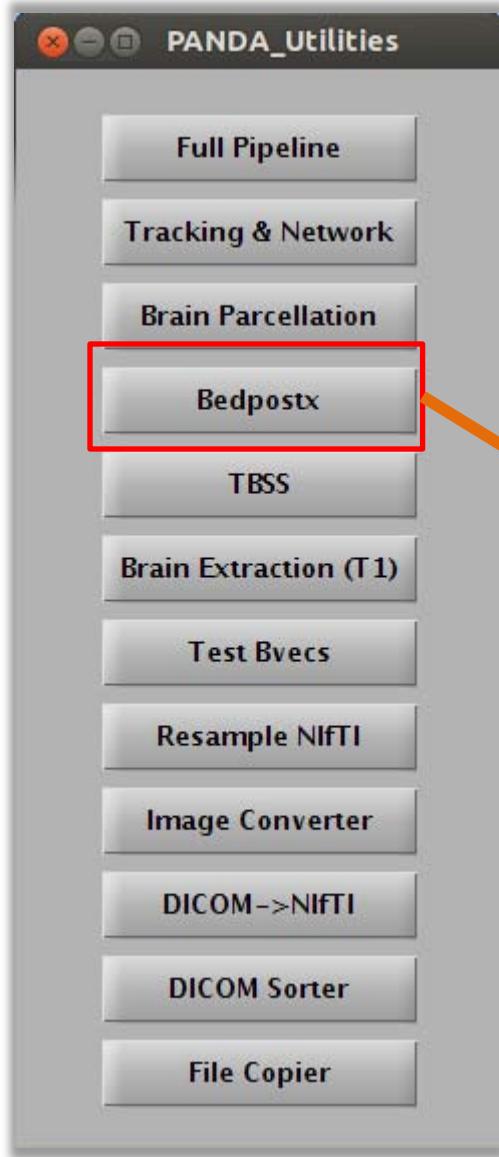
/data/node1/Zaixu/234/00011/native_space/

bd_00011_FA_Parcellated_*.nii.gz

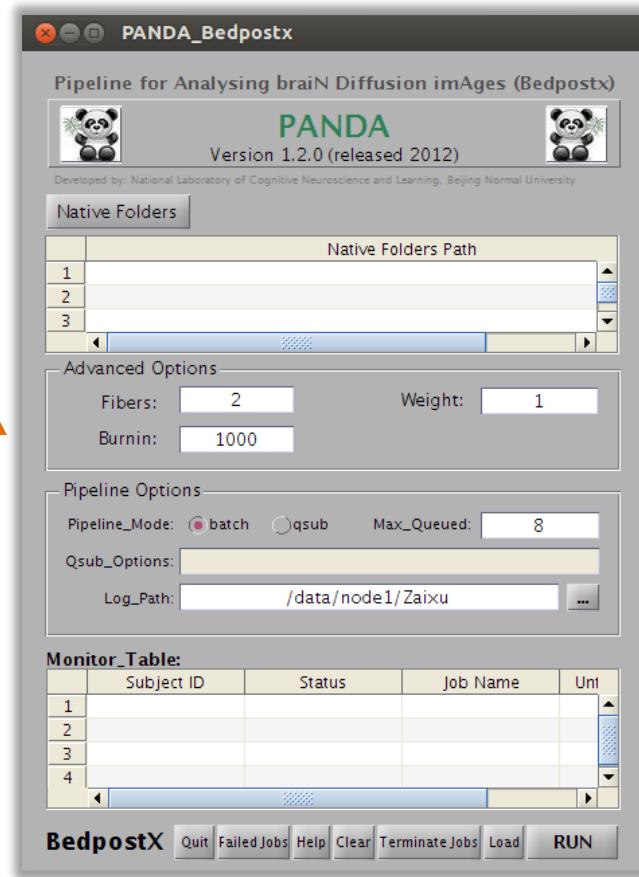
/data/node1/Zaixu/234/00012/native_space/

bd_00012_FA_Parcellated_*.nii.gz

Utilities (BedpostX)



➤ Run bedpostX for any number of subjects in parallel.



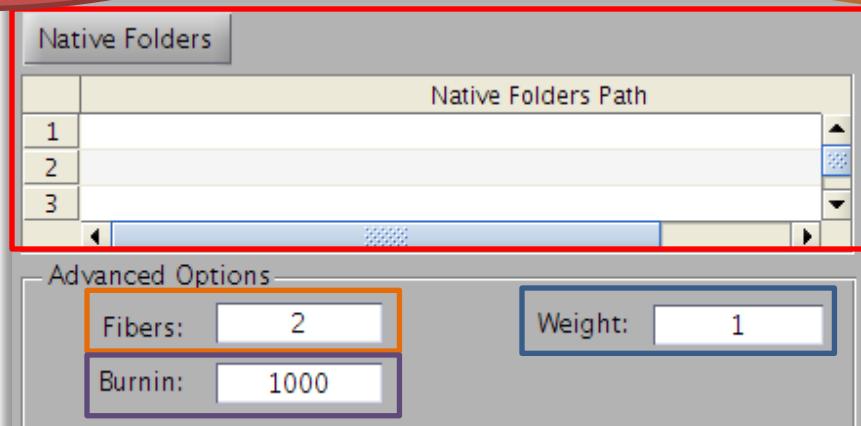
Utilities (BedpostX)

Native Folders:

full path of subjects' folders which contain mask, bvecs, bvals and 4D data.

Fibers:

Number of fibers per voxel, default 2.



Burnin:

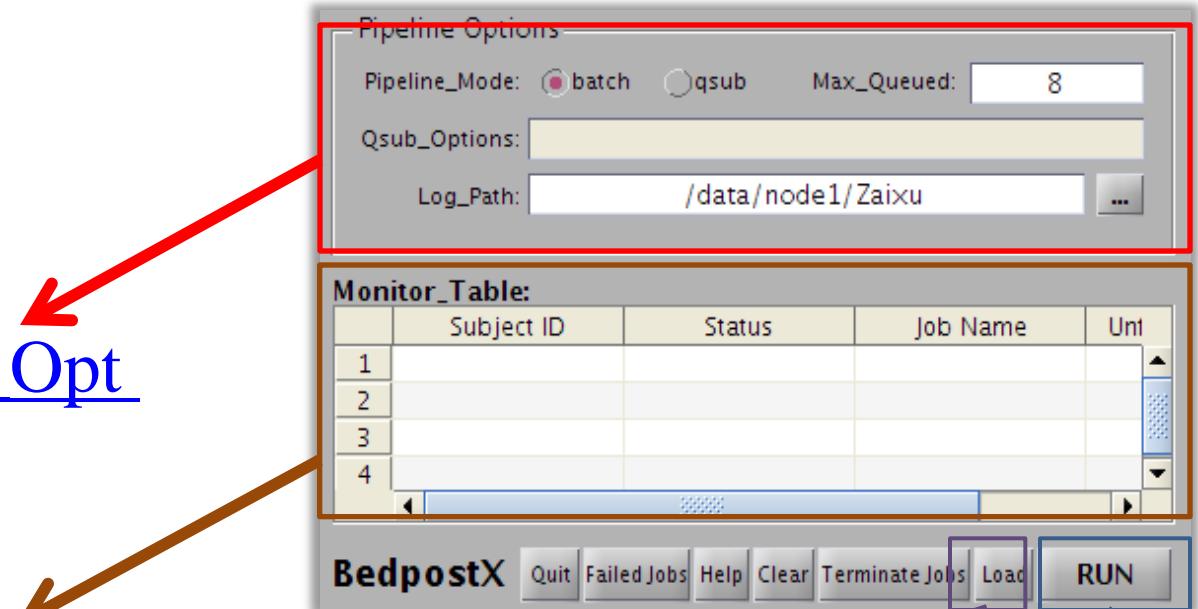
Burnin period, default 1000.

Weight:

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

Utilities (BedpostX)

Referring to: Pipeline Opt



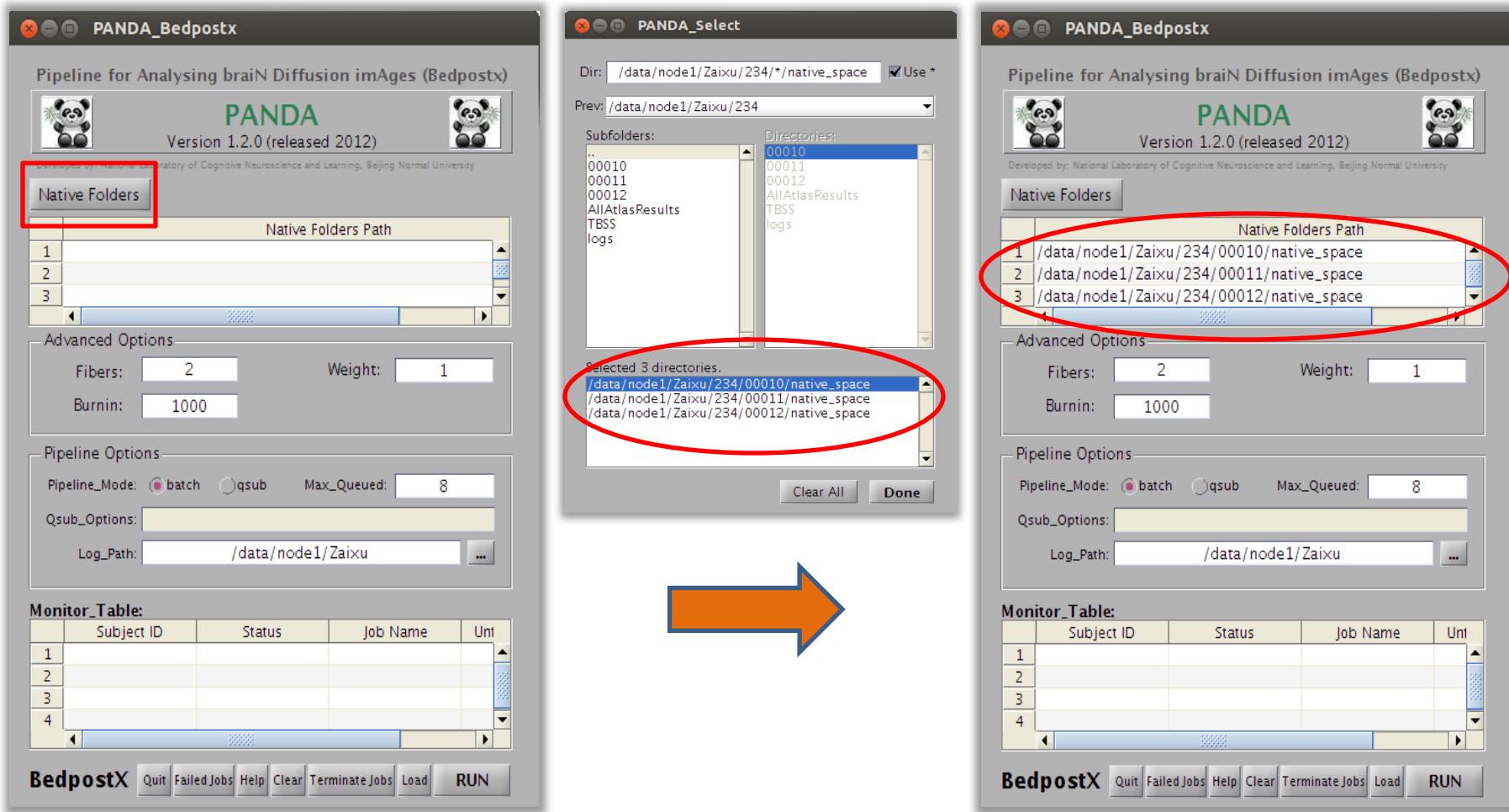
Referring to: Monitoring Progress

Loading the *.PANDA_BedpostX file.

Current configuration will be saved in 'Log Path' automatically after clicking 'RUN' button. (extension as .PANDA_BedpostX).⁹⁸

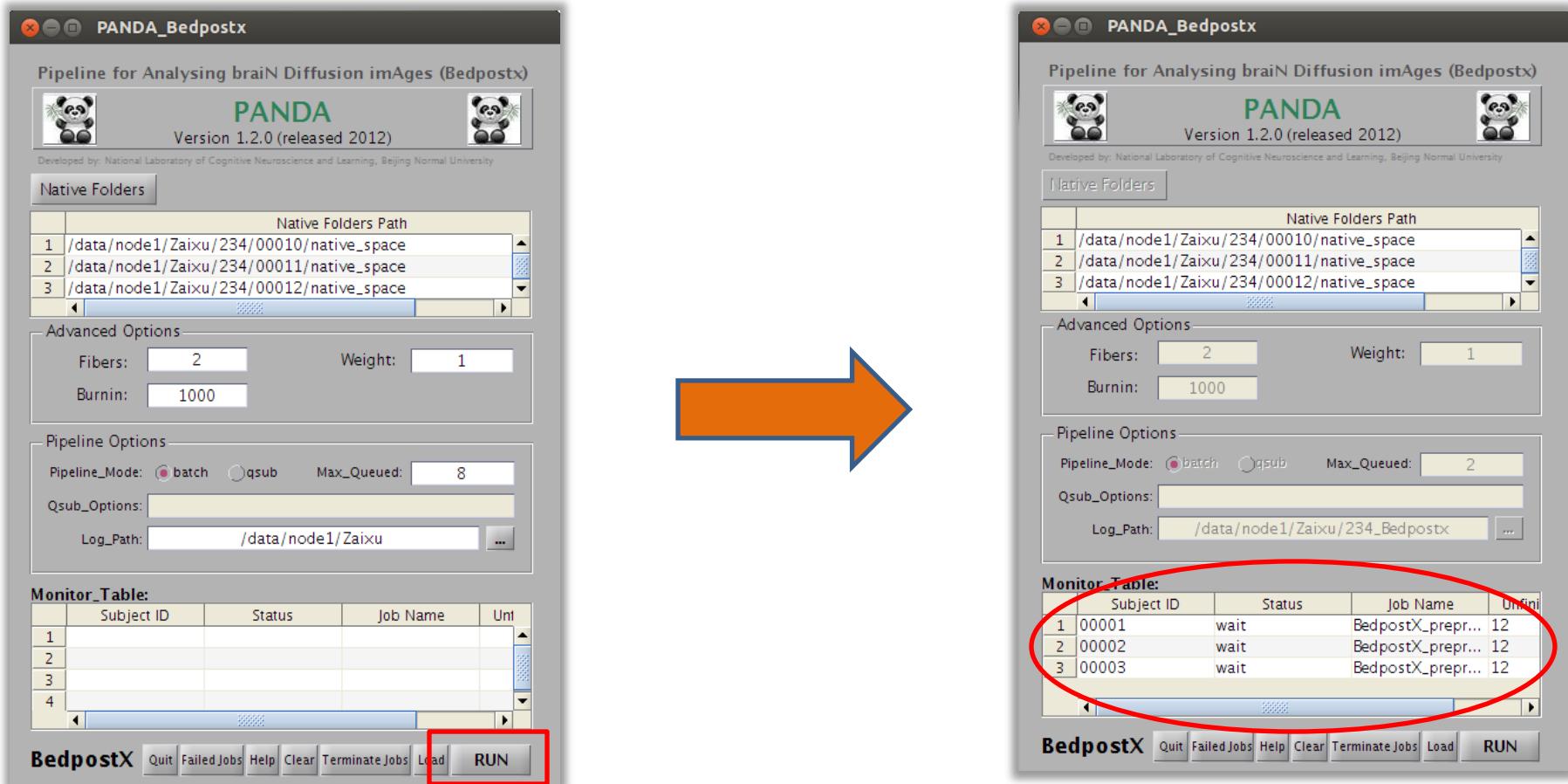
Utilities (BedpostX)

Input subjects' folder:



Utilities (BedpostX)

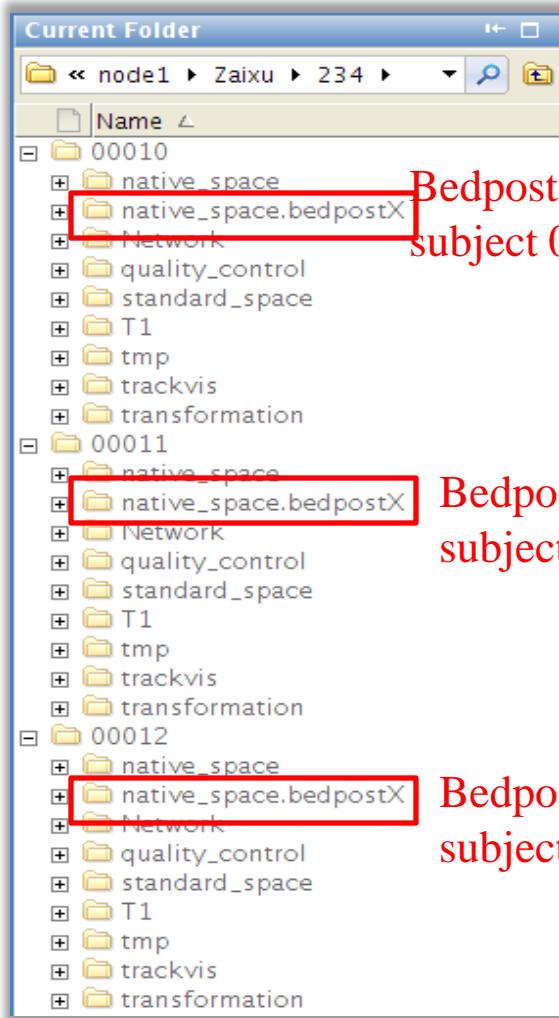
Initiating Process:



- Current configuration was saved in '[Log Path](#)' automatically after clicking 'RUN' button.
(extension as .PANDA_BedpostX).

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.

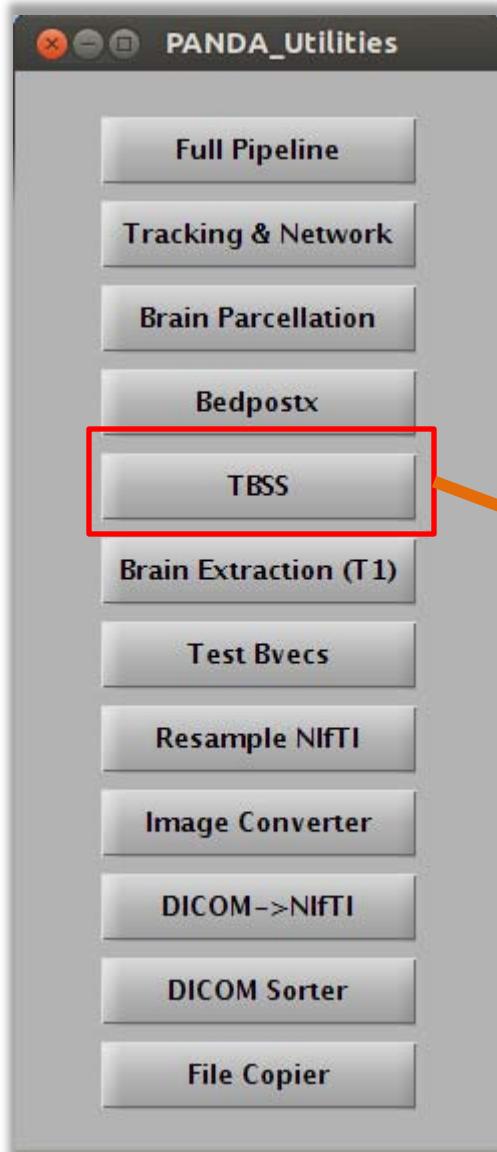
➤ In this example:
Inputs are

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

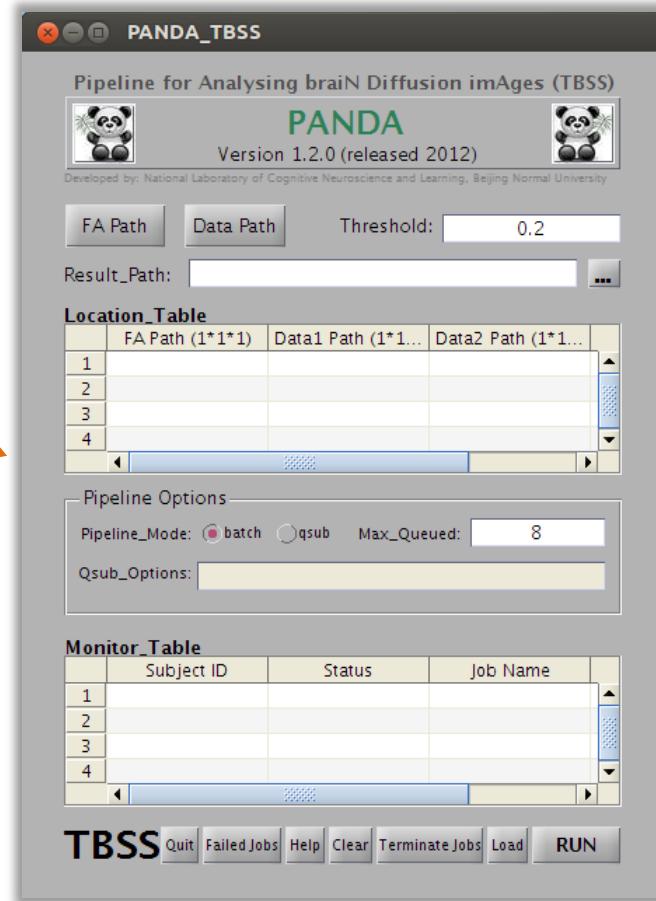
Outputs are

/data/node1/Zaixu/234/00010/native_space.bedpostX
/data/node1/Zaixu/234/00011/native_space.bedpostX
/data/node1/Zaixu/234/00012/native_space.bedpostX

Utilities (TBSS)



➤ Run TBSS for a group of subjects in parallel.



Utilities (TBSS)

FA Path:

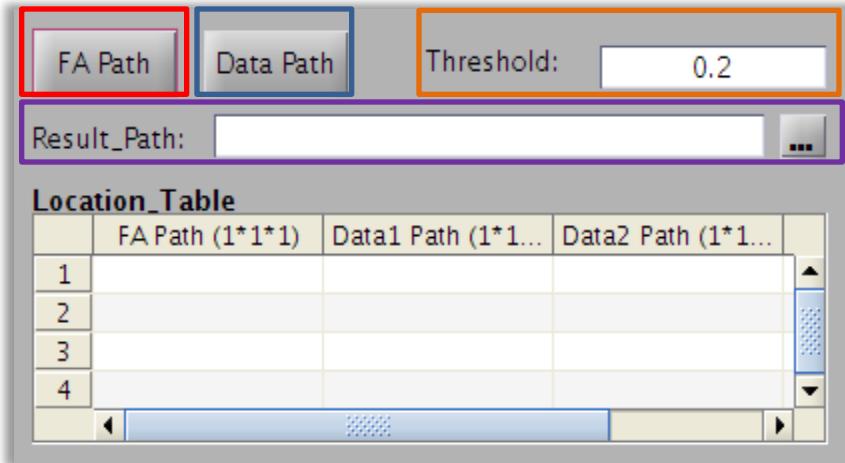
full path of subjects' 1*1*1 FA image.

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.



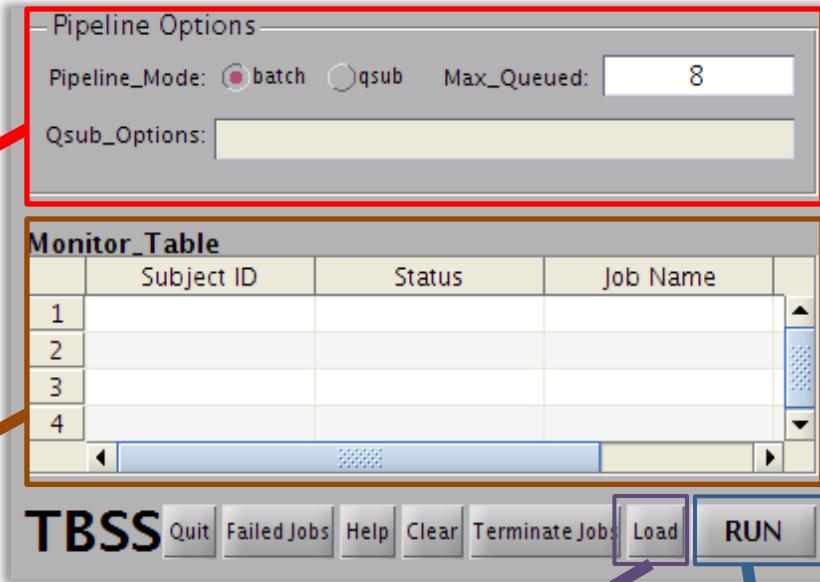
Result Path:

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)

Referring to: Pipeline Opt



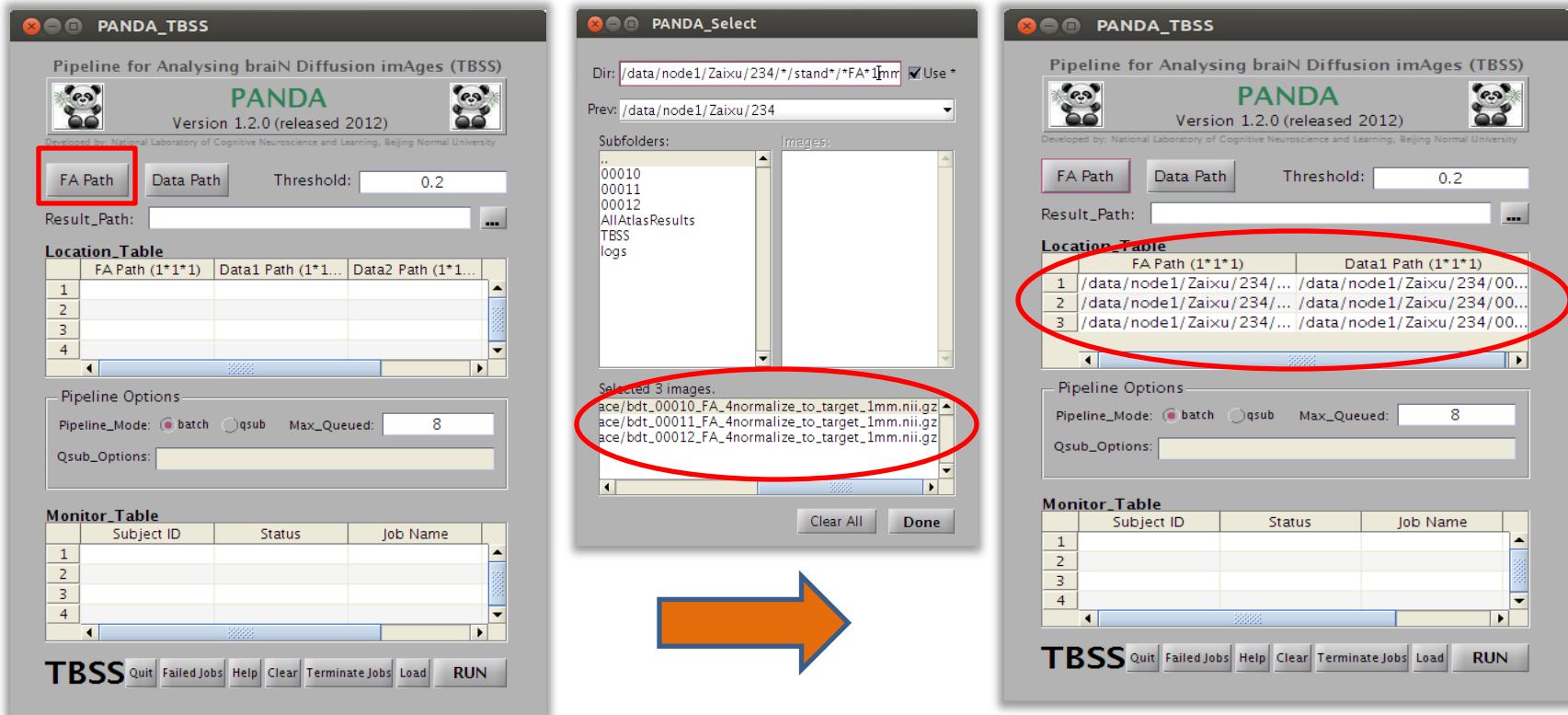
Referring to: Monitoring Progress

Loading the *.PANDA_TBSS file.

Current configuration will be saved in 'Result Path' automatically after clicking 'RUN' button. (extension as .PANDA_TBSS).

Utilities (TBSS)

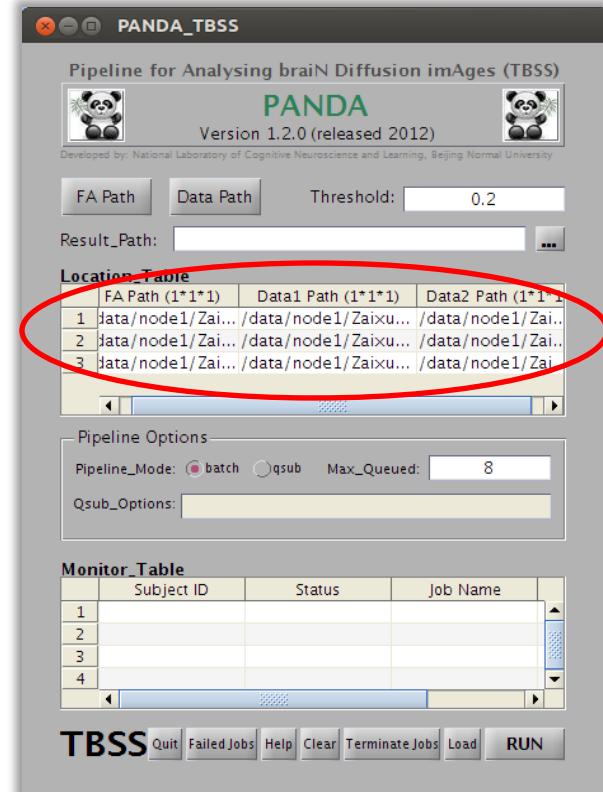
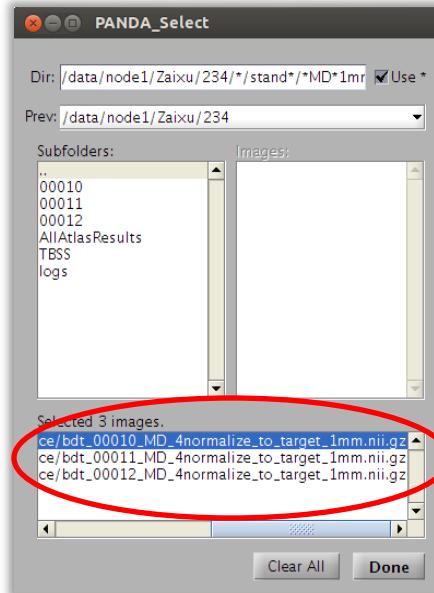
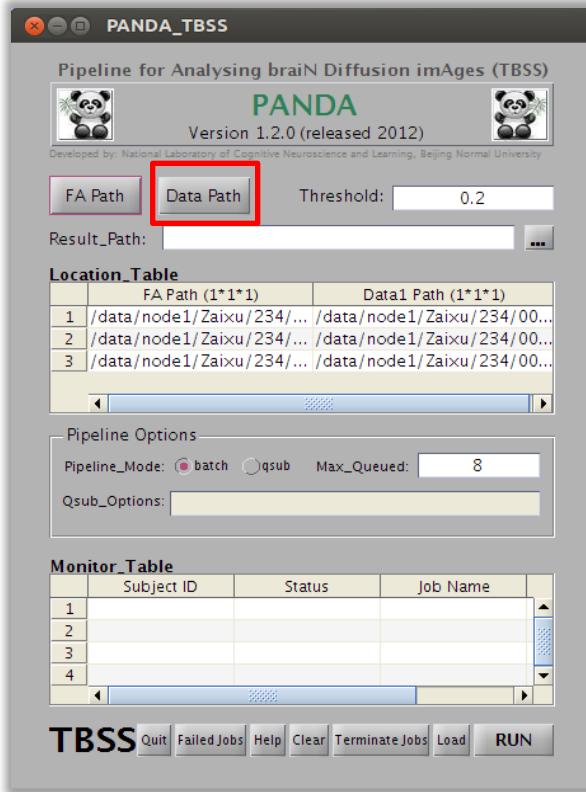
Set FA Path:



FA was set as Data1 by default.

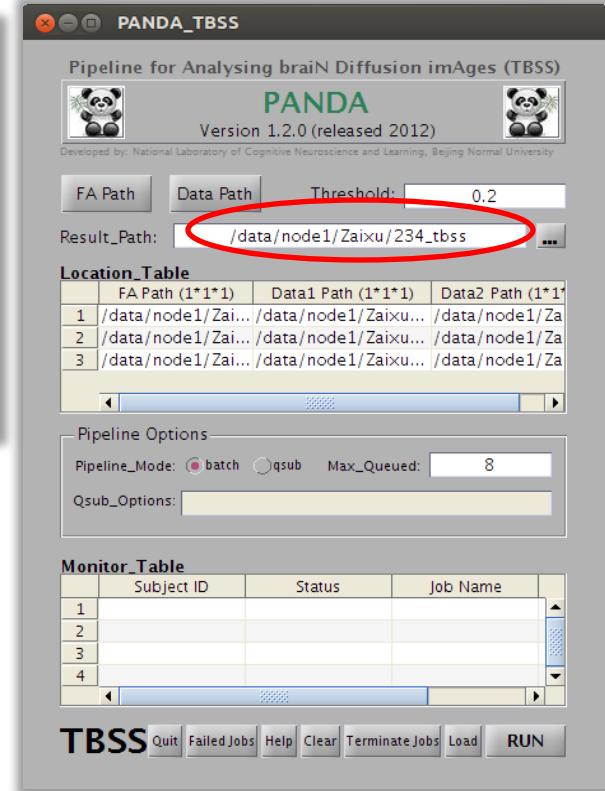
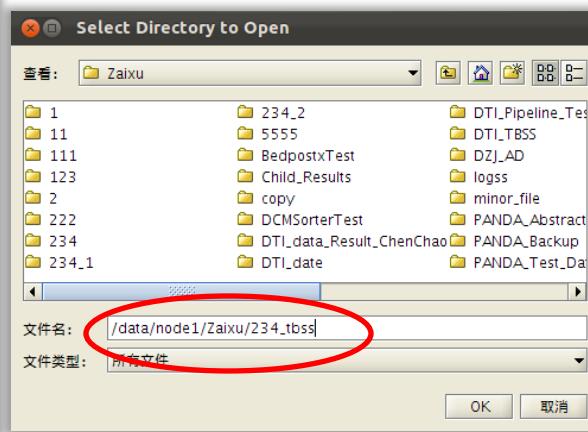
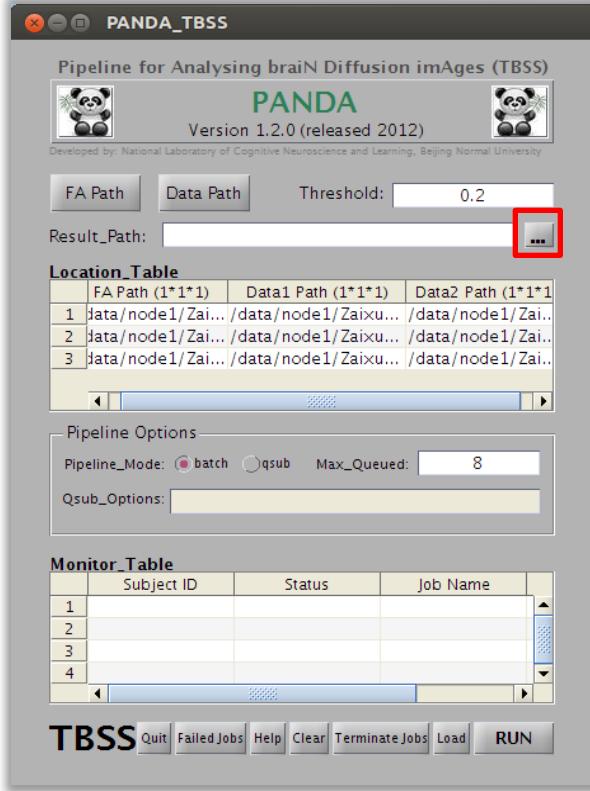
Utilities (TBSS)

Set Data2 Path:



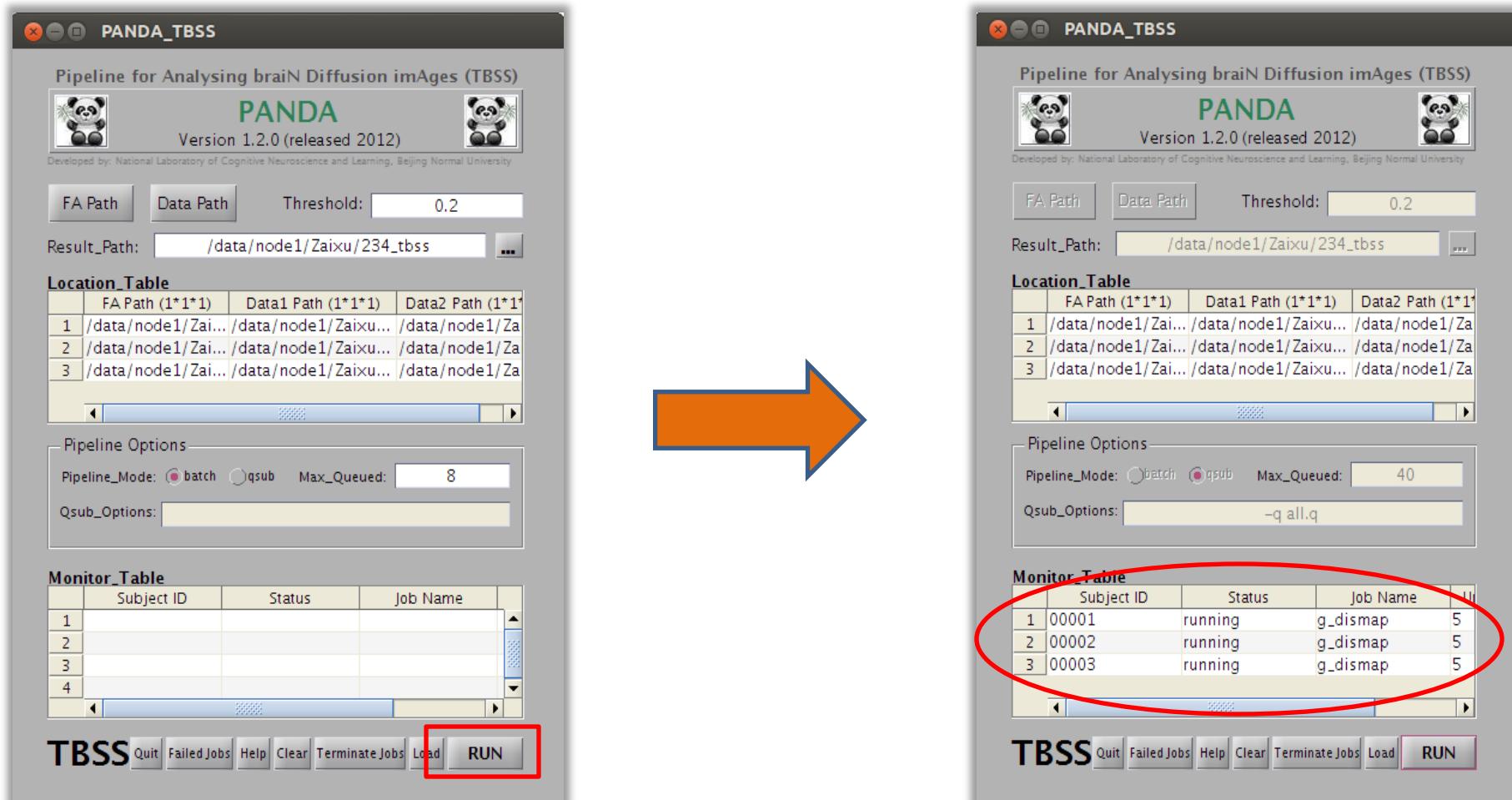
Utilities (TBSS)

Set Result Path:



Utilities (TBSS)

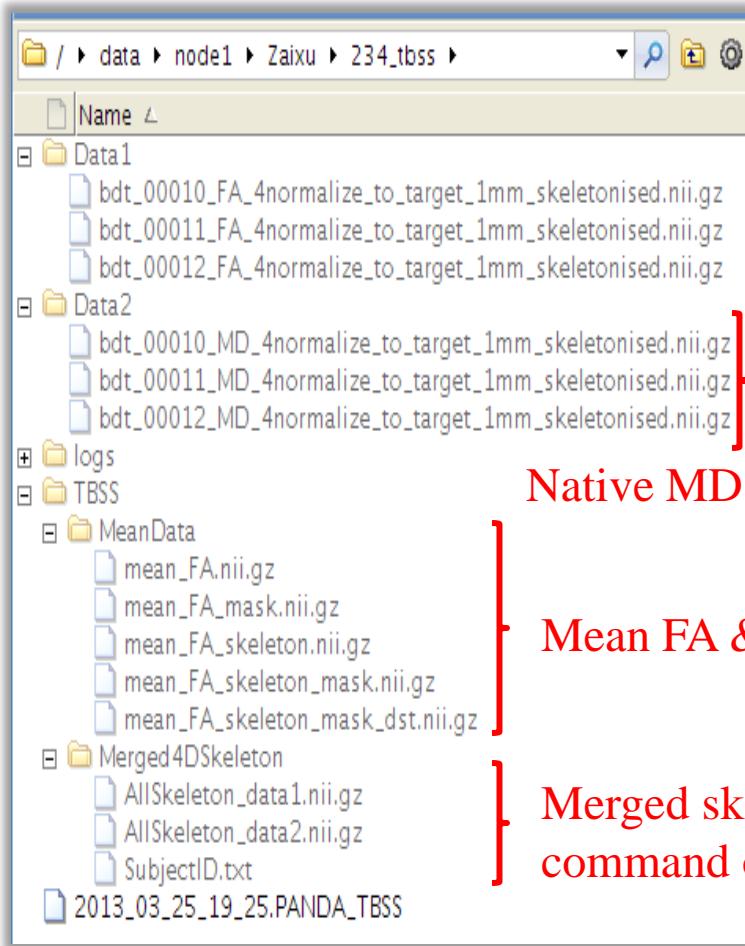
Initiating Process:



- Current configuration will be saved in '[Result Path](#)' automatically after clicking 'RUN' button.

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.

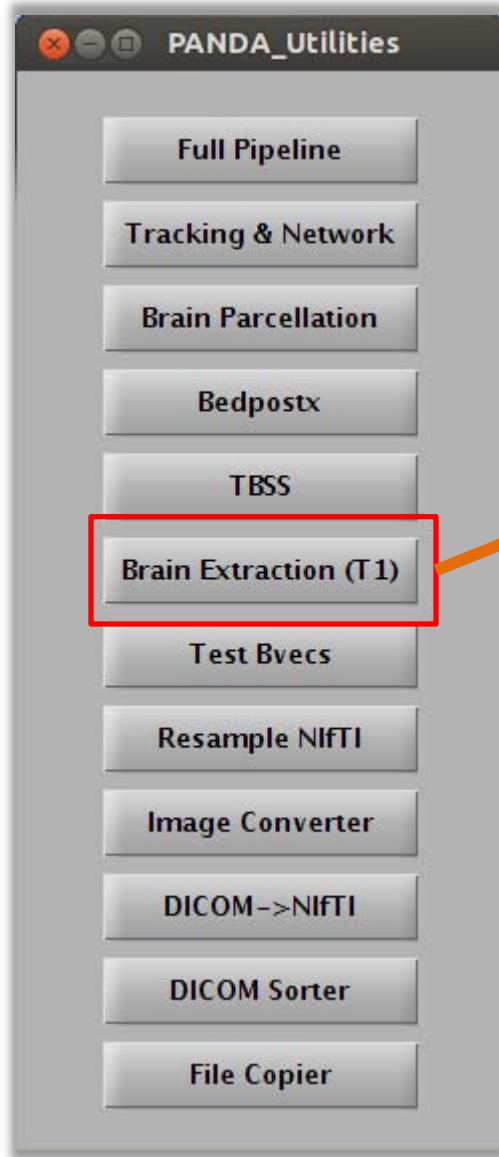
➤ Then: all native skeletons will be merged to a 4D skeleton for statistics.

Native MD skeleton

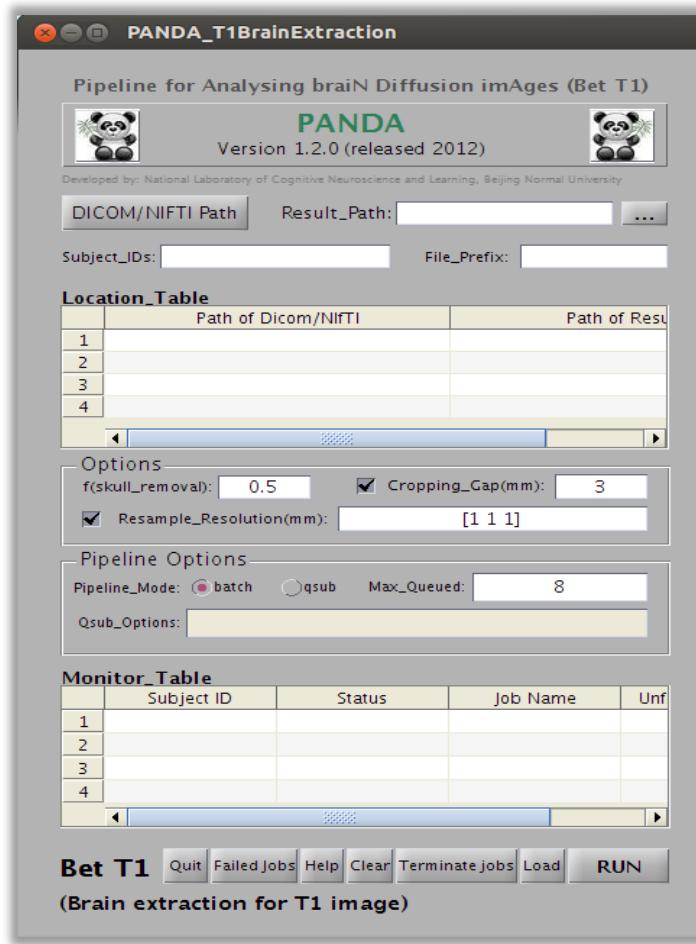
Mean FA & Mean FA skeleton

Merged skeleton (directly used for statistics with ‘randomise’ command of FSL)

Utilities (Brain Extraction (T1))



➤ Extract brain for T1 image for any subjects in parallel.



Utilities (Brain Extraction (T1))

DICOM/NIfTI Path:

Input subjects' folders, each of which contains DICOM or NIfTI. If input is NIfTI, there should be only one NIfTI image in the subject' folder.

DICOM/NIFTI Path	Result_Path: <input type="text"/>	
Subject_IDs: <input type="text"/>	File_Prefix: <input type="text"/>	
Location_Table		
	Path of Dicom/NifTI	Path of Resu
1		
2		
3		
4		

Result Path:

Reference: [Specify the result-folder.](#)

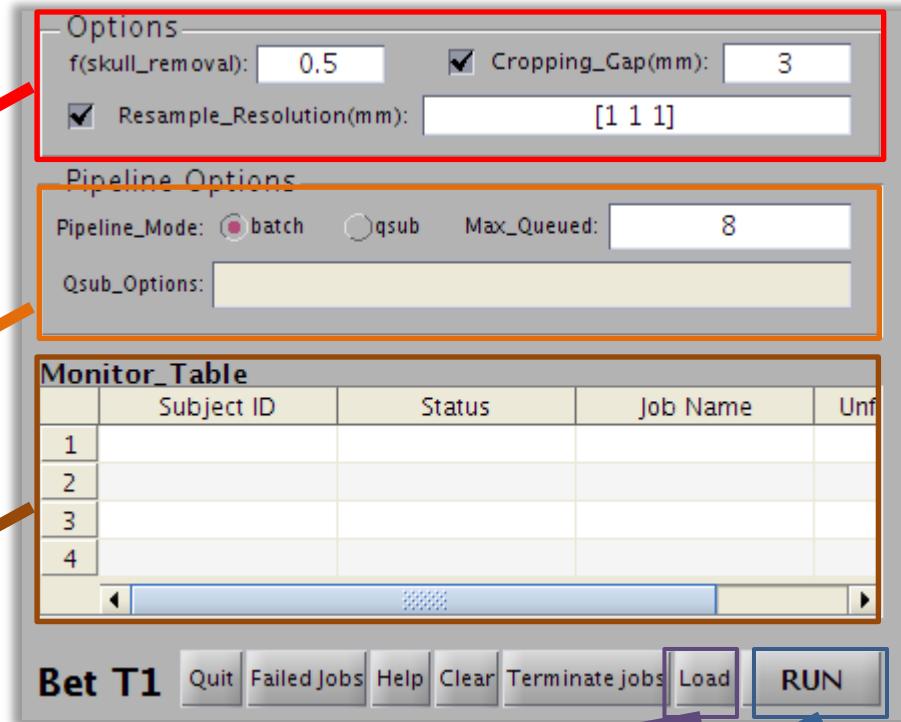
Subject IDs:

Reference: [Assign digital IDs for subjects.](#)

File Prefix:

Reference: [Input prefix of filenames.](#)

Utilities (Brain Extraction (T1))



Referring to: [T1 Options](#)

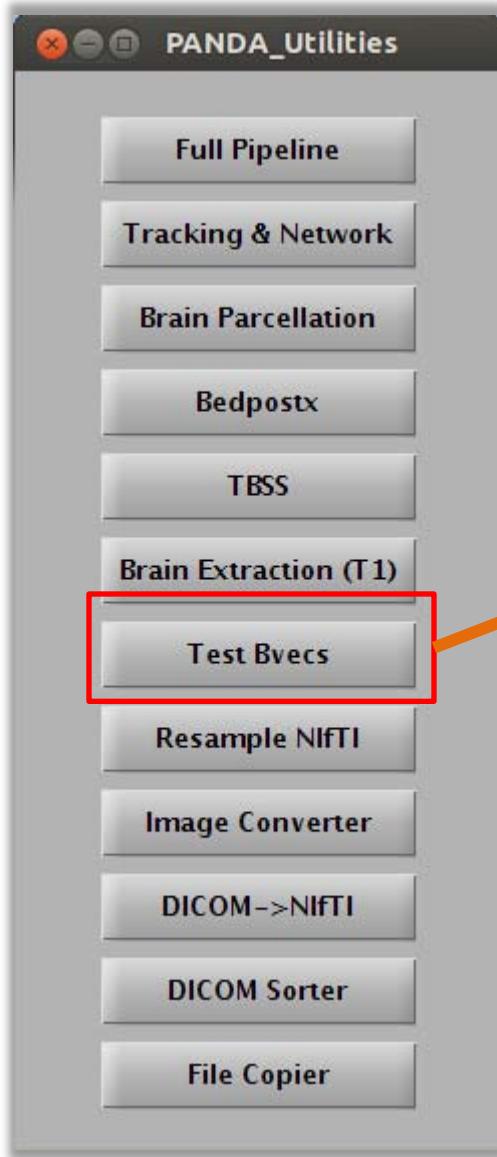
Referring to: [Pipeline Opt](#)

Referring to: [Monitoring Progress](#)

Loading the *.PANDA_BetT1 file.

Current configuration will be saved in '[Result Path](#)' automatically after clicking 'RUN' button. (extension as .PANDA_BetT1).

Utilities (Test Bvecs)



- Examine whether the direction of the tensor is right.



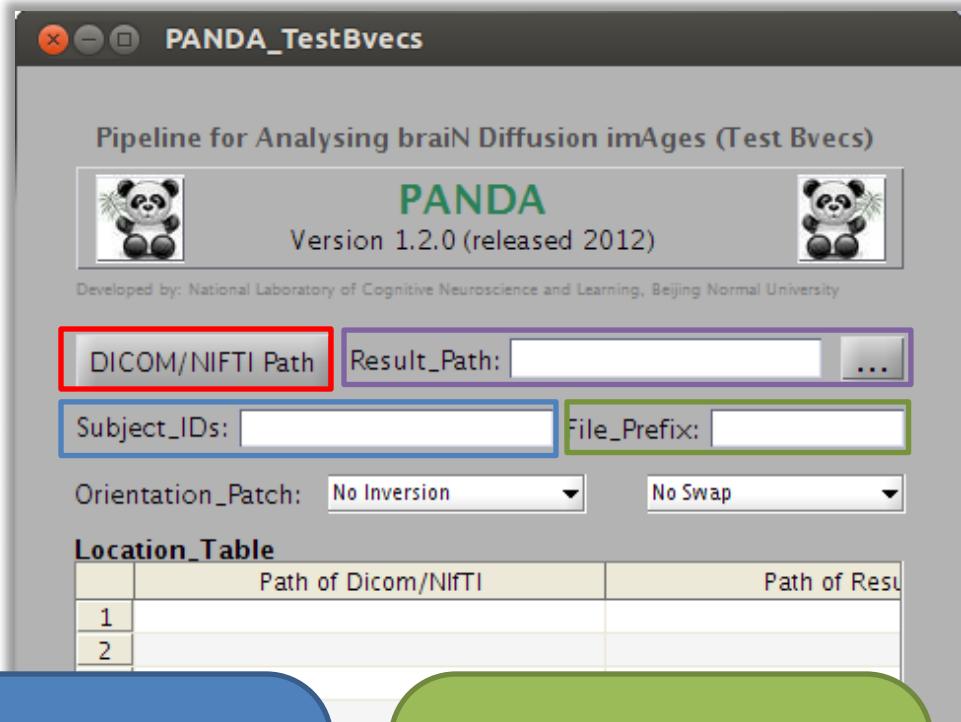
Utilities (Test Bvecs)

DICOM/NIfTI Path:
Reference: [Select subject-folders.](#)

Result Path:
Reference: [Specify the result-folder.](#)

Subject IDs:
Reference: [Assign digital IDs for subjects.](#)

File Prefix:
Reference: [Input prefix of filenames.](#)



Utilities (Test Bvecs)

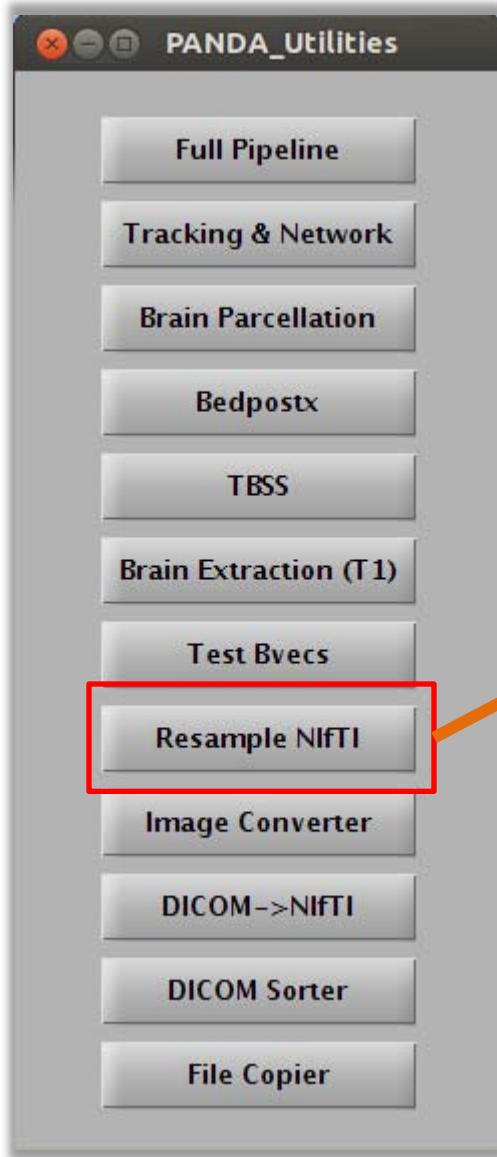
Users can regulate the direction of the tensor, through modifying the parameters "Invert" and "Swap".

Whether the direction of the tensor is right determines whether the fiber tracking result is right.

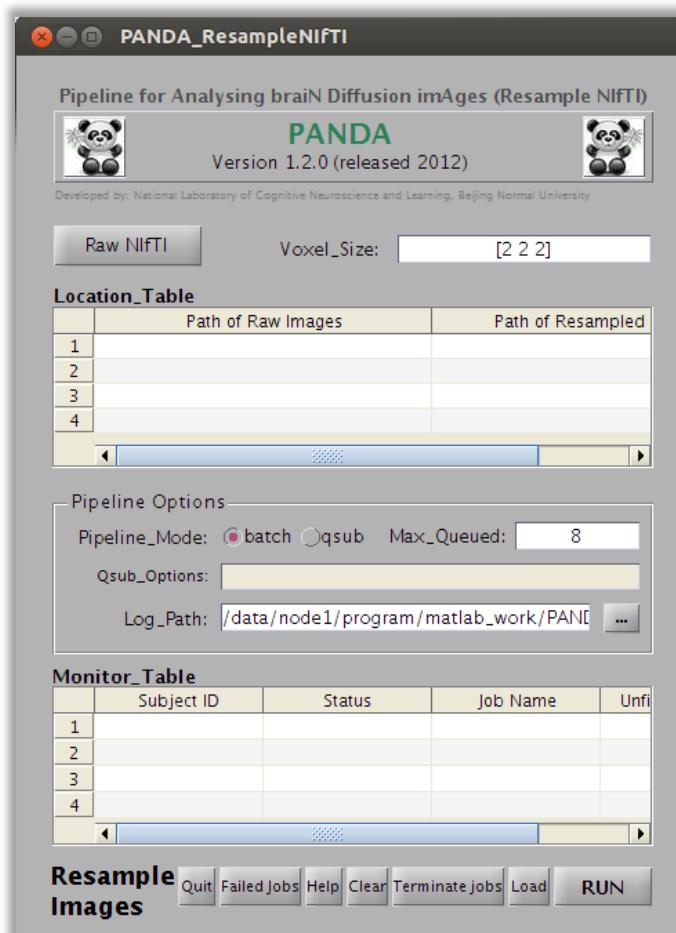
It is recommended using this utility to check the direction of the tensor before data analysis, when doing fiber tracking.



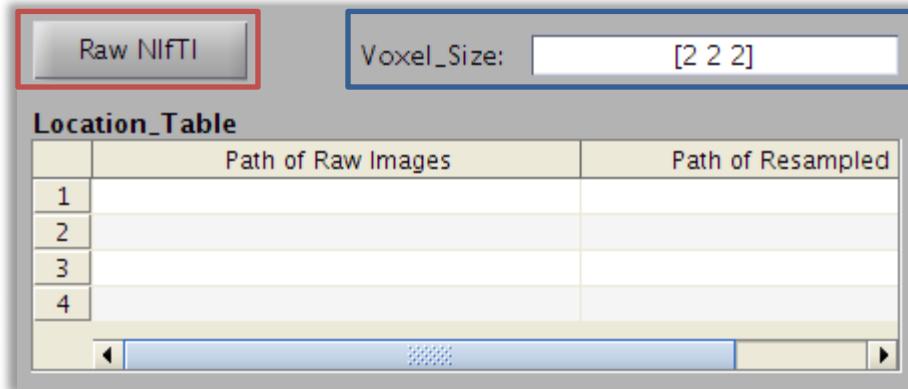
Utilities (Resample NIfTI)



➤ Resample NIfTI to voxel size user inputs for any number of subjects in parallel.



Utilities (Resample NIfTI)



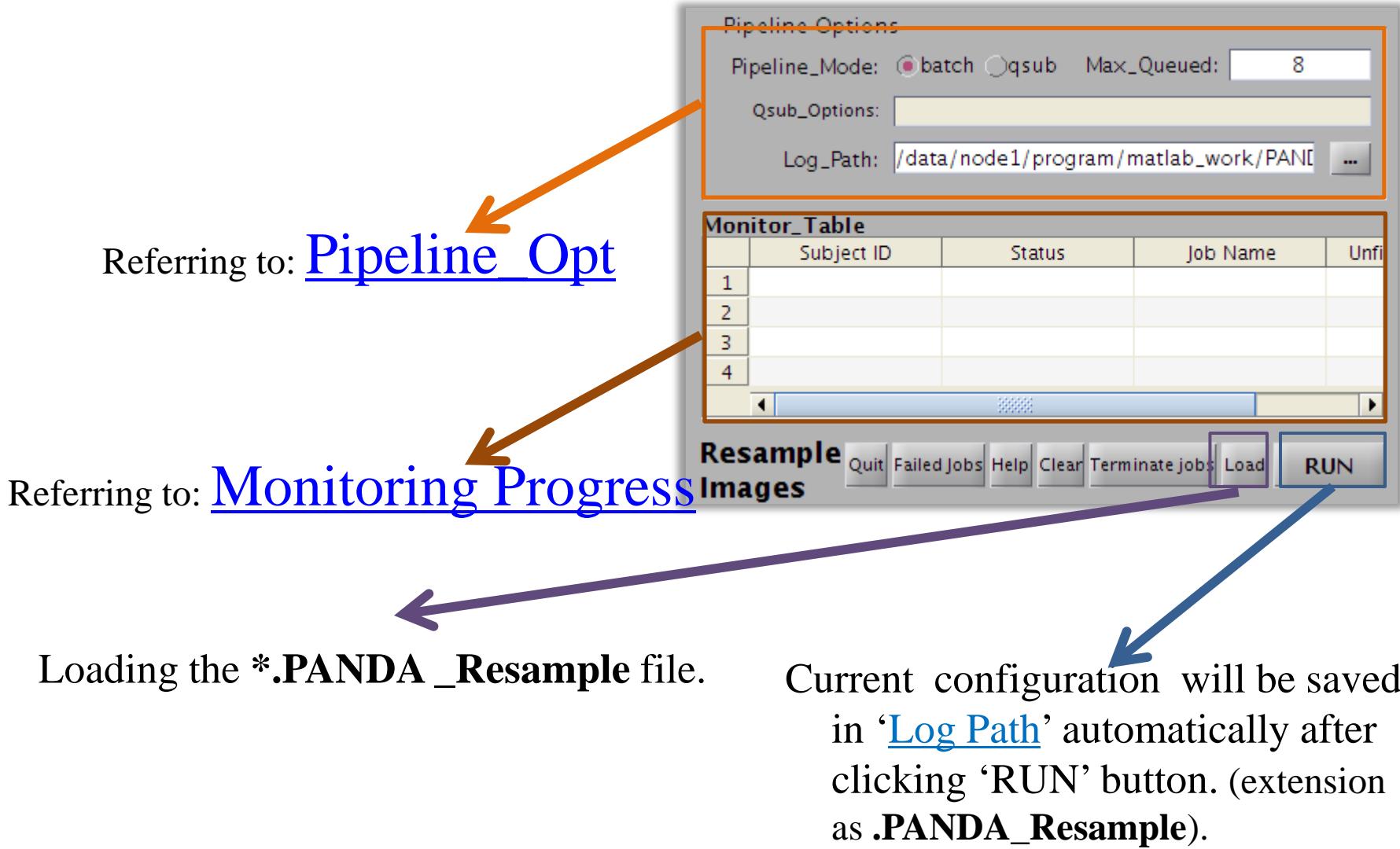
Raw NIfTI :

Select NIfTI images to be resampled.

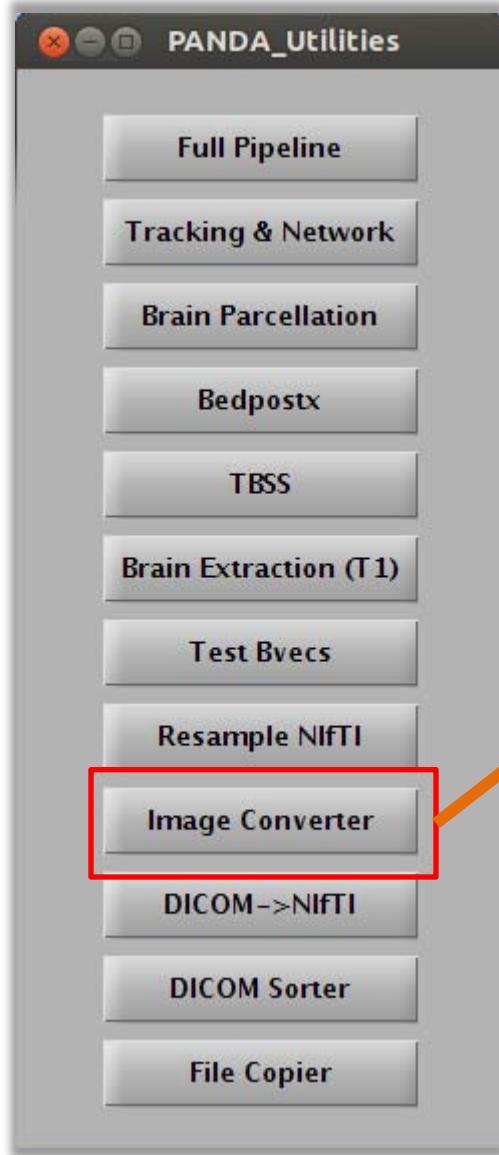
Voxel Size:

Final voxel size after resampling.

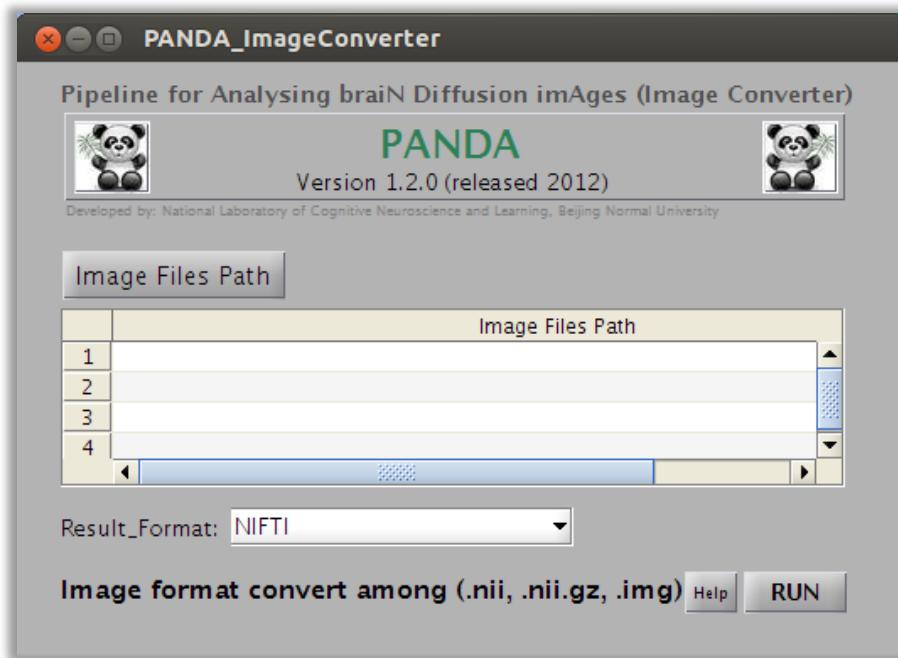
Utilities (Resample NIfTI)



Utilities (Image Converter)



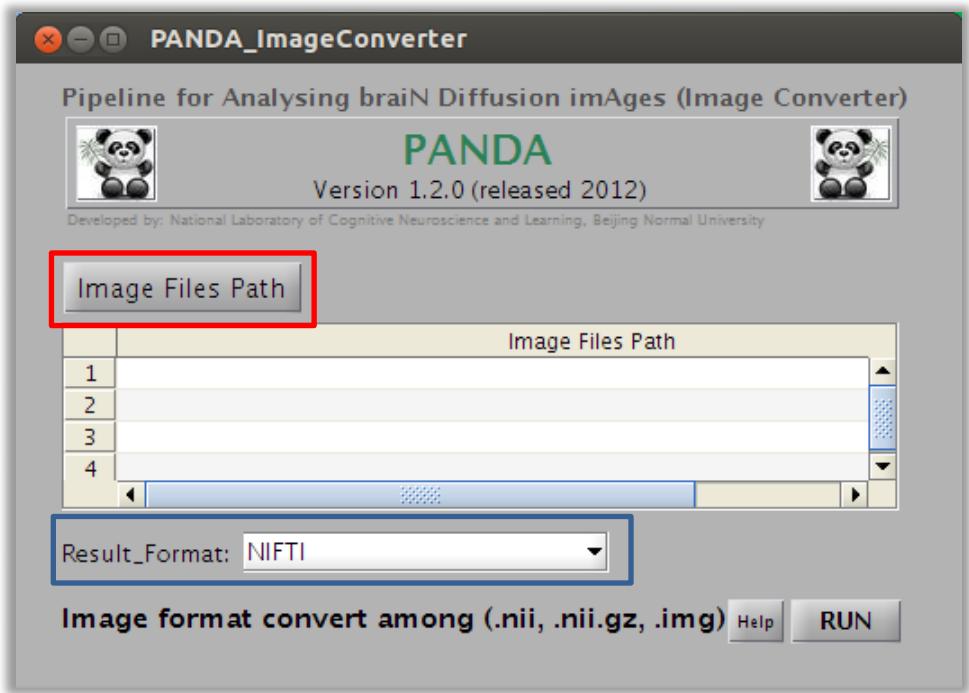
- Convert image format among (.nii, .nii.gz, .img).



Utilities (Image Converter)

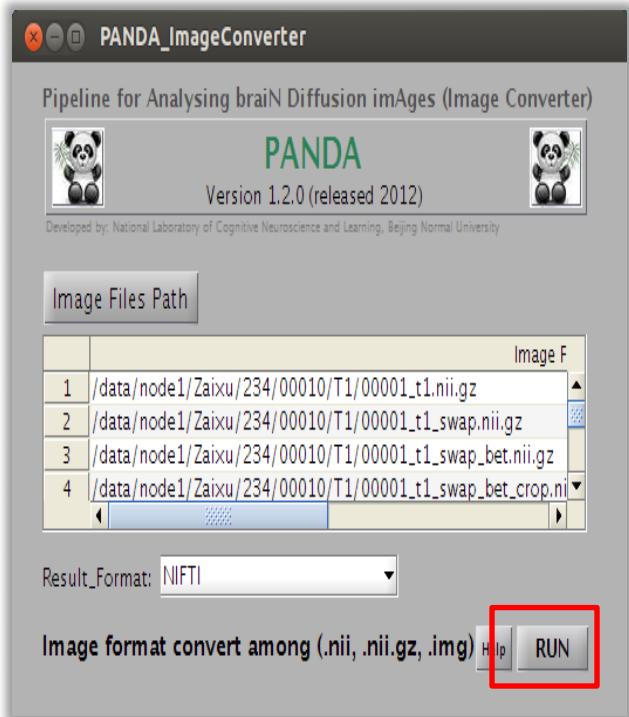
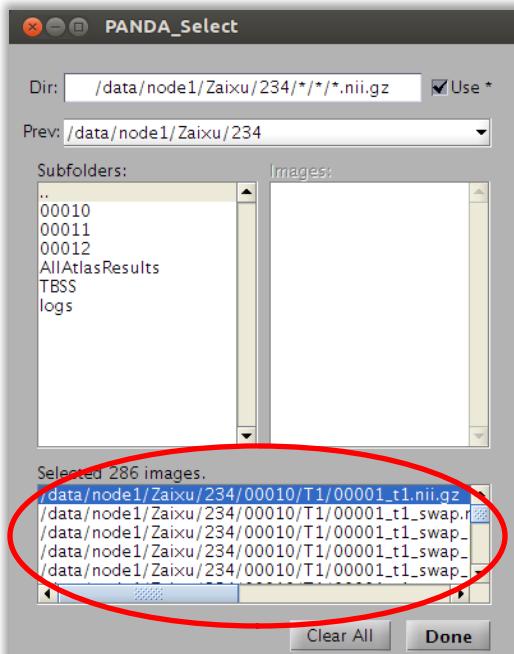
Image Files Path:
the full path of image files
(.nii, .nii.gz, .img) to be
converted

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

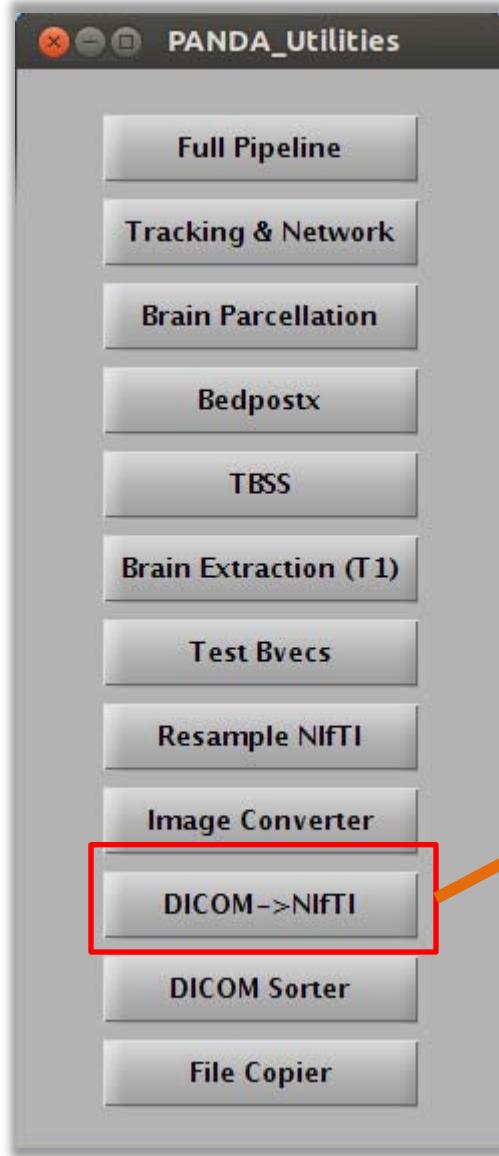


➤ After the conversion, new image files will replace the origin image files.

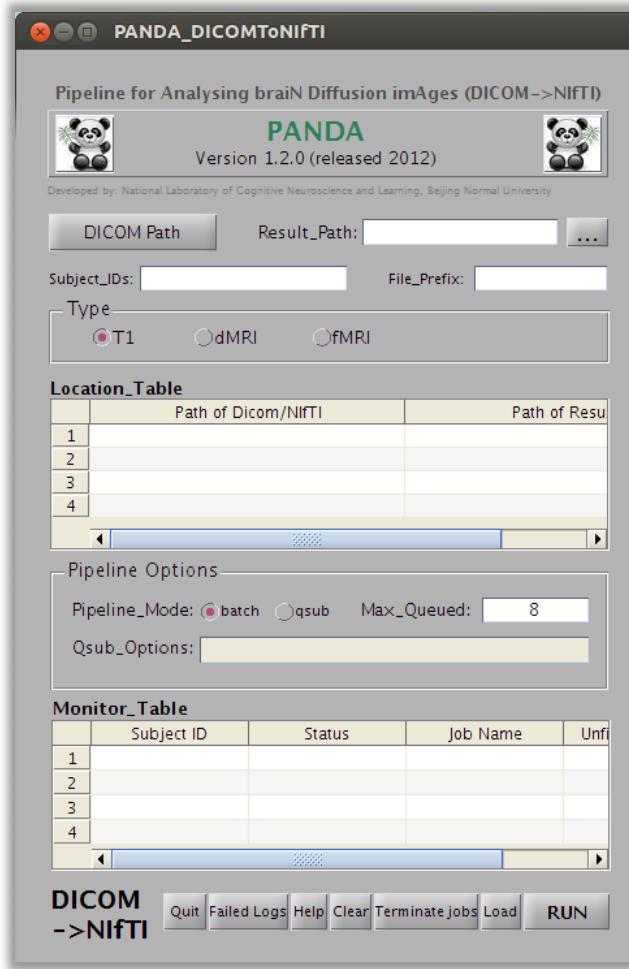
Utilities (Image Converter)



Utilities (DICOM -> NIfTI)



- Convert DICOM to NIfTI for any number of subjects in parallel.



Utilities (DICOM -> NIfTI)

DICOM Path:

Input subjects' folders, each of which contains DICOM files.

	Path of Dicom/NIfTI	Path of Resu
1		
2		
3		
4		

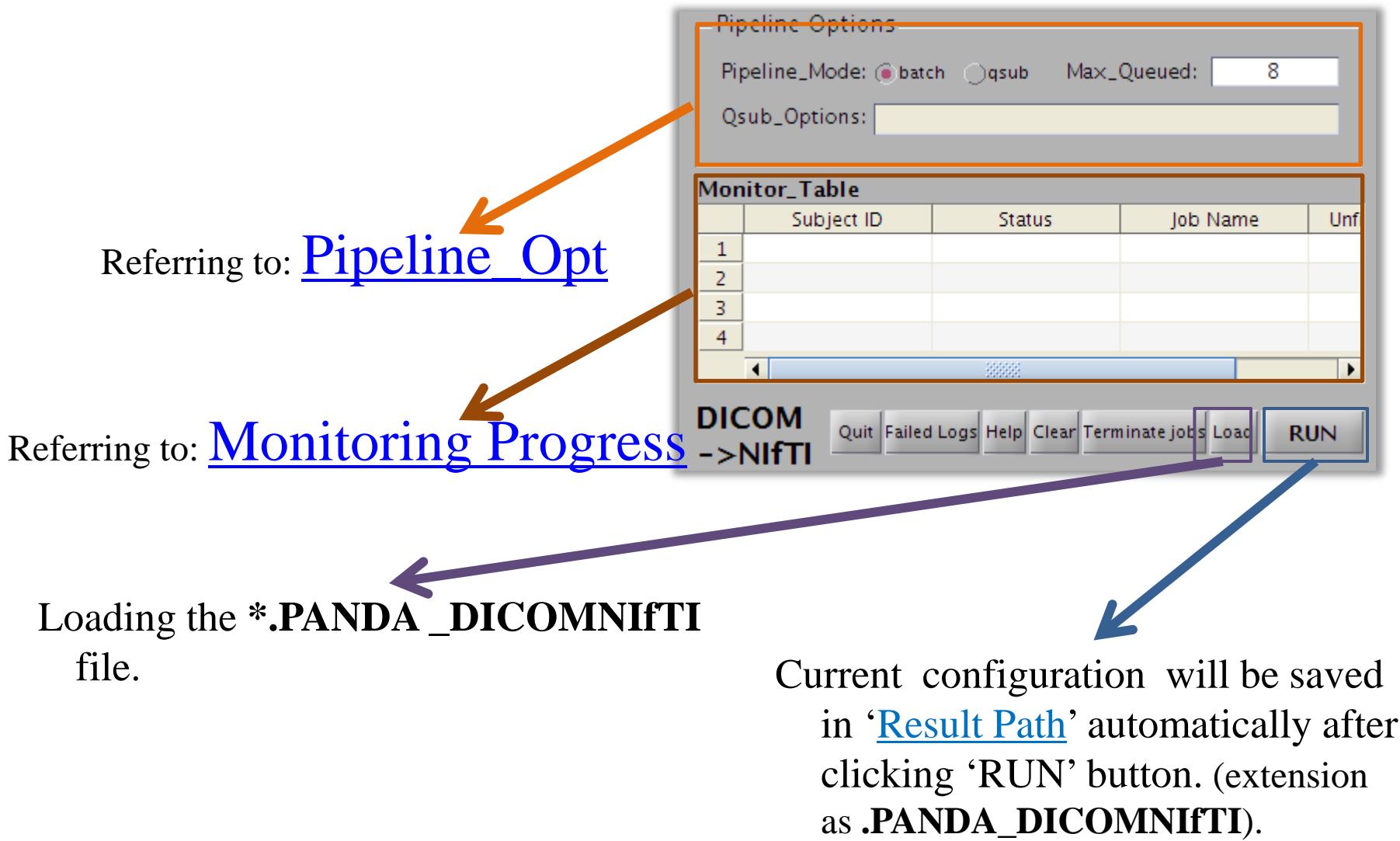
Result Path:
Reference:
Specify the result-folder.

Subject IDs:
Reference:
Assign digital IDs for subjects.

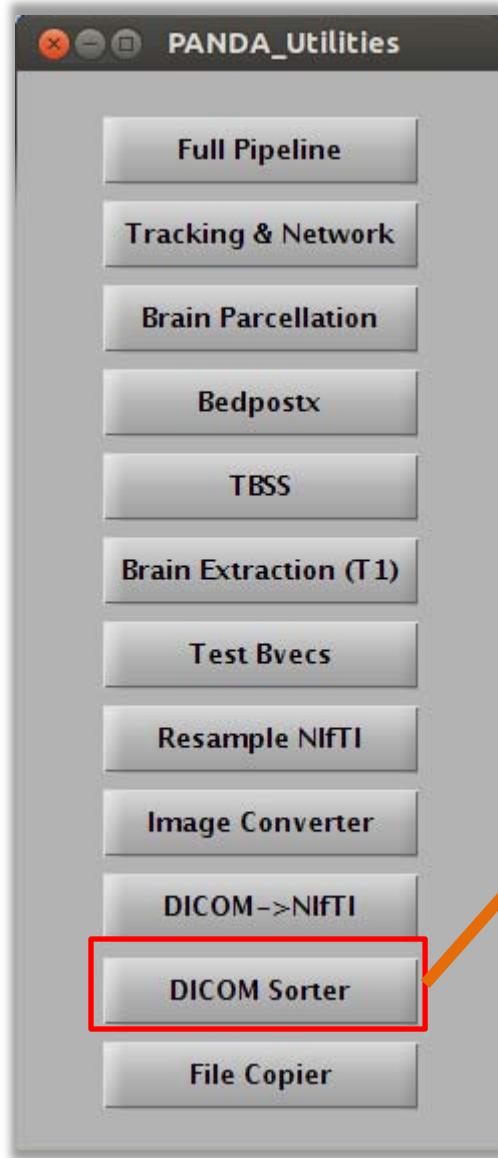
File Prefix:
Reference:
Input prefix of filenames.

Type:
Select which type of images to convert.

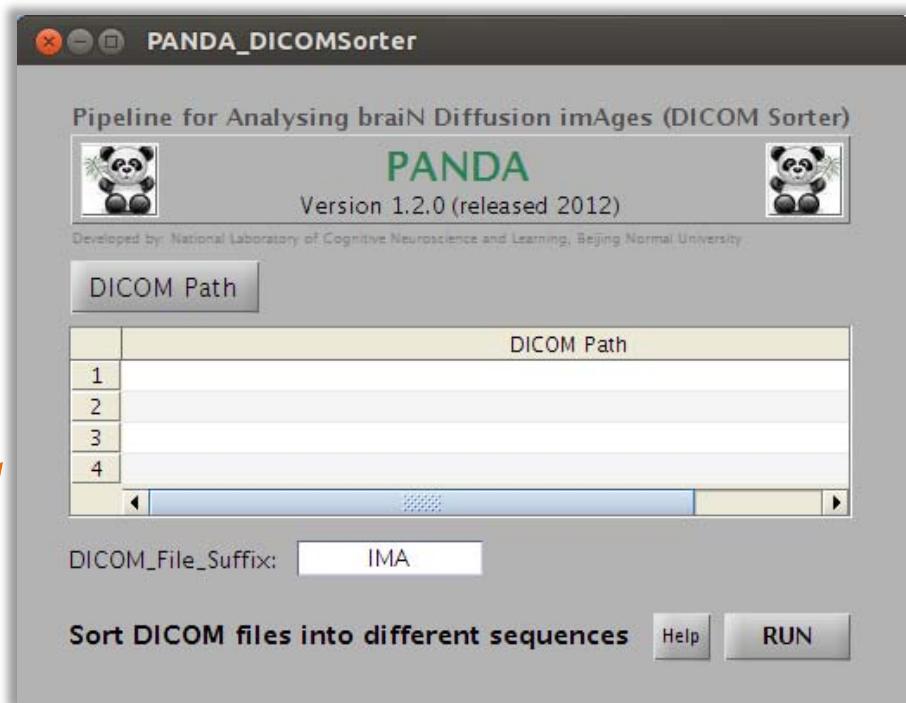
Utilities (DICOM -> NIfTI)



Utilities (DICOM Sorter)



➤ Sort DICOM files into different series.



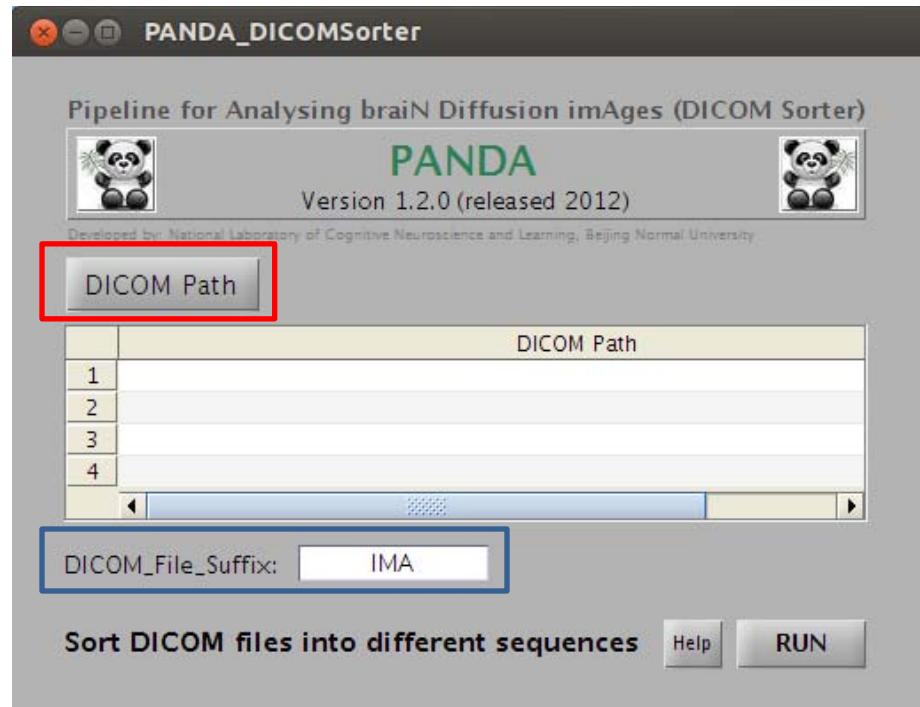
Utilities (DICOM Sorter)

DICOM Path:

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

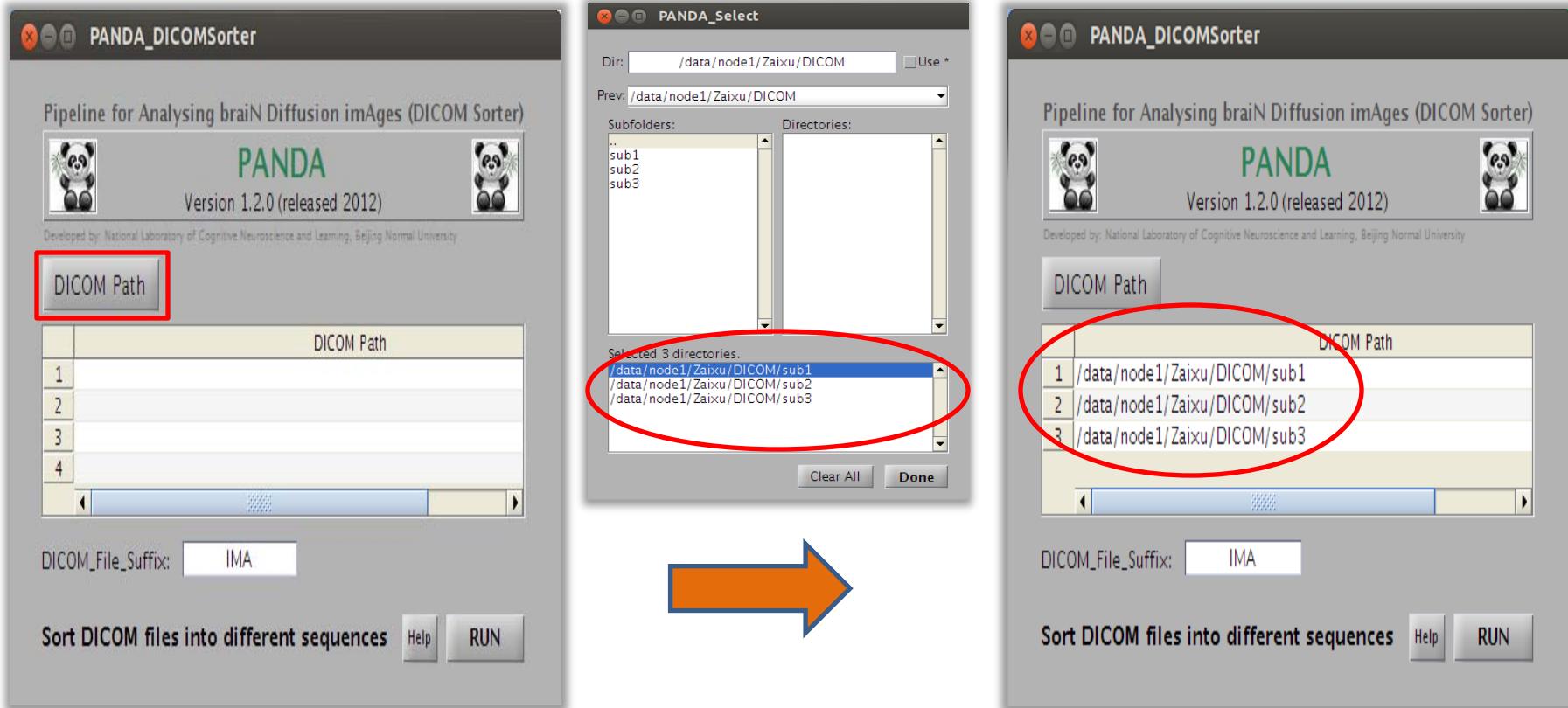
DICOM File Suffix:

The extension of DICOM file name.

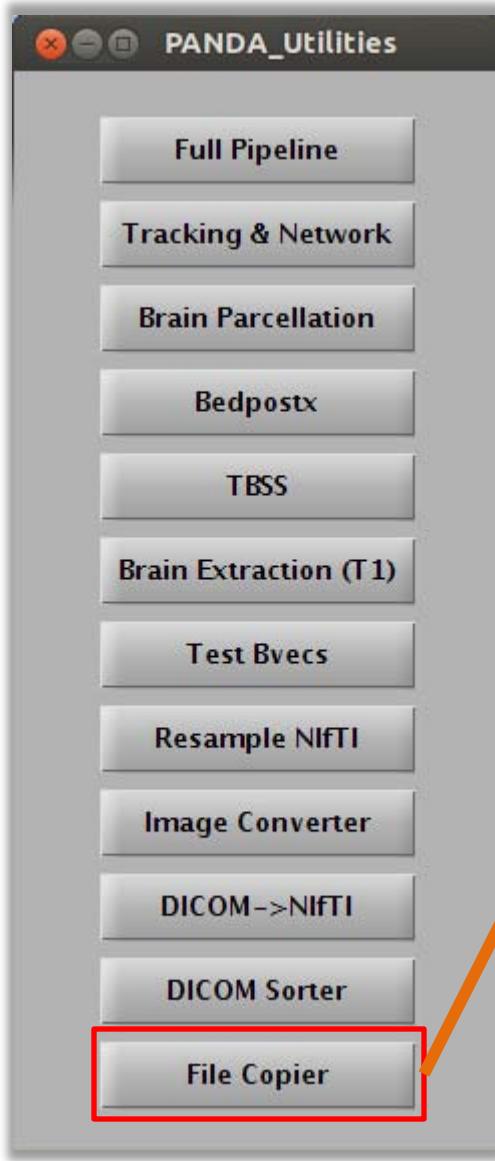


- If you input the DICOM file suffix, it will sort all the files with the extension as the suffix under subjects' DICOM folders.
- If the DICOM_File_Suffix is empty, it will sort all the files under subjects' DICOM folders.

Utilities (DICOM Sorter)



Utilities (File Copier)



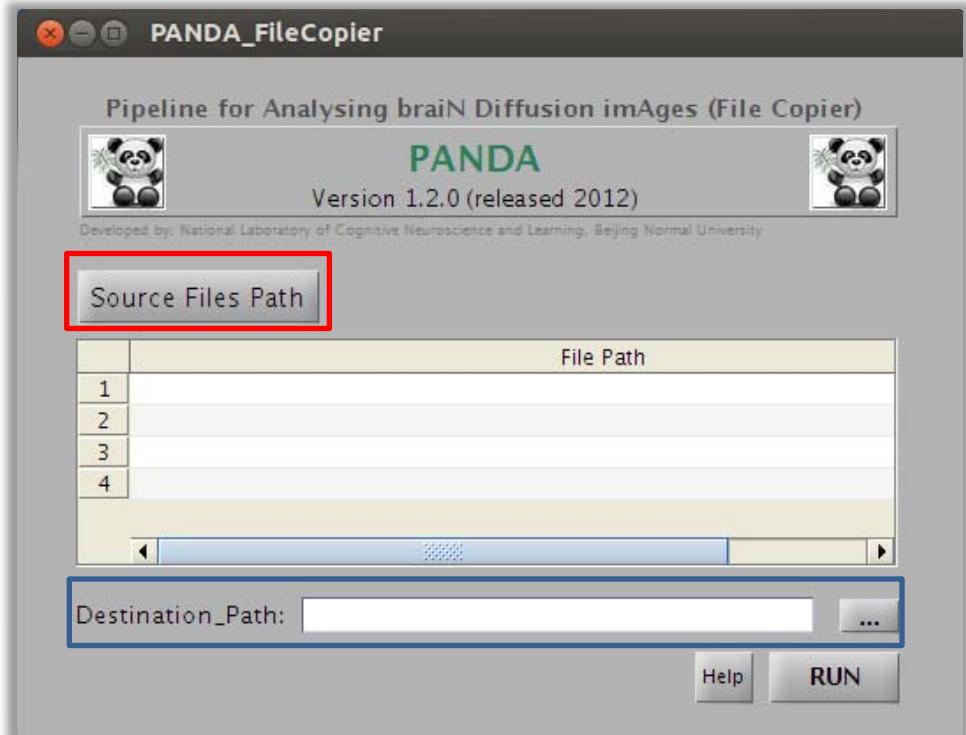
➤ Copy files to the destination path.



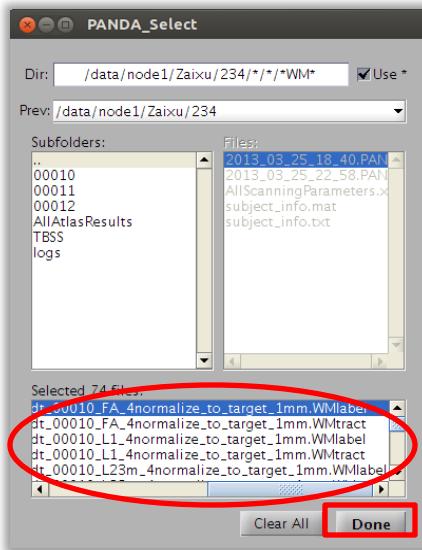
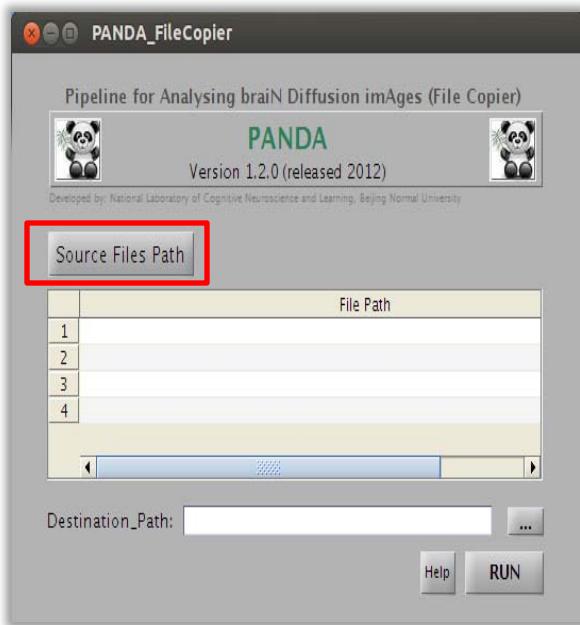
Utilities (File Copier)

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

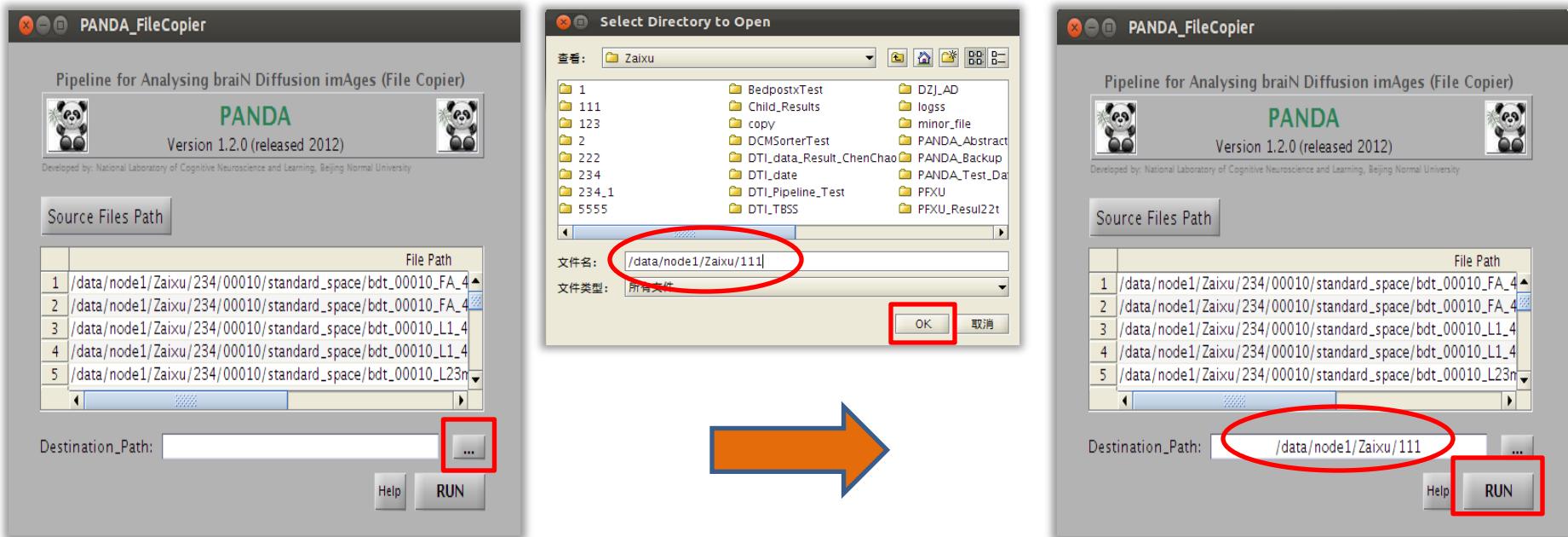
Destination Path:
the path user wants to
save these files.



Utilities (File Copyer)



Utilities (File Copier)



Acknowledgement

➤ FSL (see page 6)

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

➤ PSOM (manage pipelines, see page 7)

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

➤ Diffusion Toolkit (see page 6)

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

➤ MRICRON (see page 6)

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

Help

Please report bugs or requests to:

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Thanks !