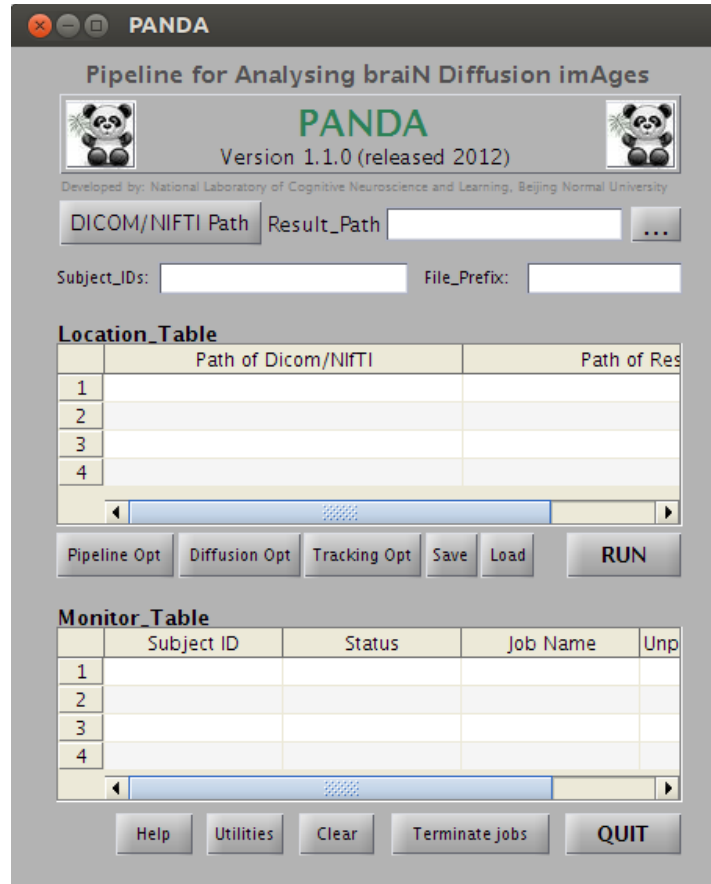# PANDA Manual

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Contents

- **Overview**
- **Setup**
- **Files/Directories selection**
- **Preparing raw data**
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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

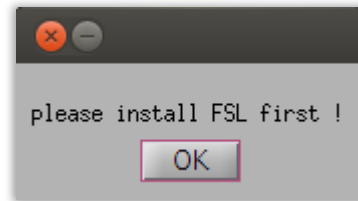PANDA has been tested in Linux (Ubuntu, Centos, Fedora) and MAC

➢ 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.

please install FSL first !

OK

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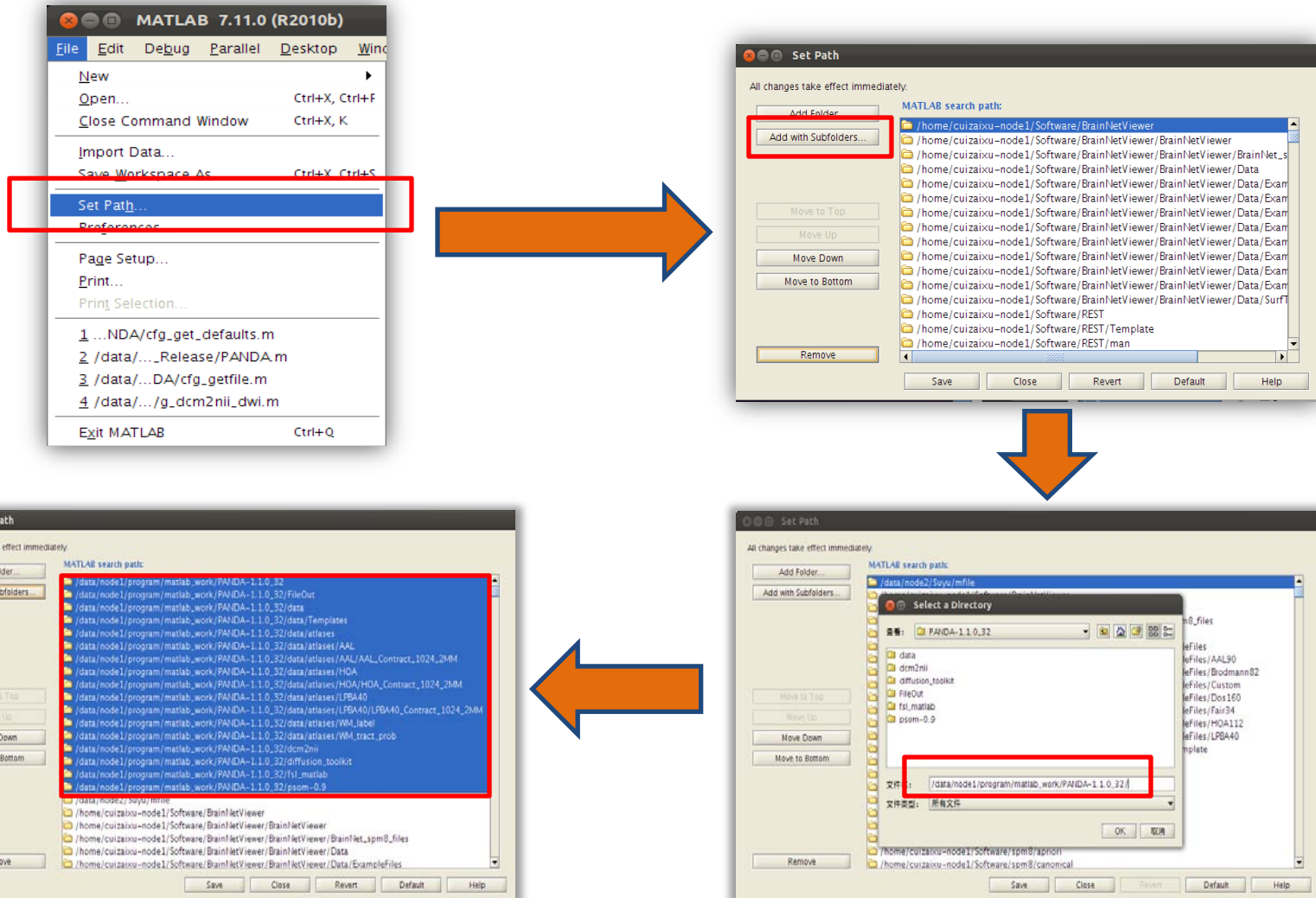
Then, entering 'PANDA' in the MATLAB command window will open PANDA's GUI.

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Files/Directories selection

Dir:
current directory

Prev:
the list of directories
users have selected

Subfolders:
subfolders under
current directory
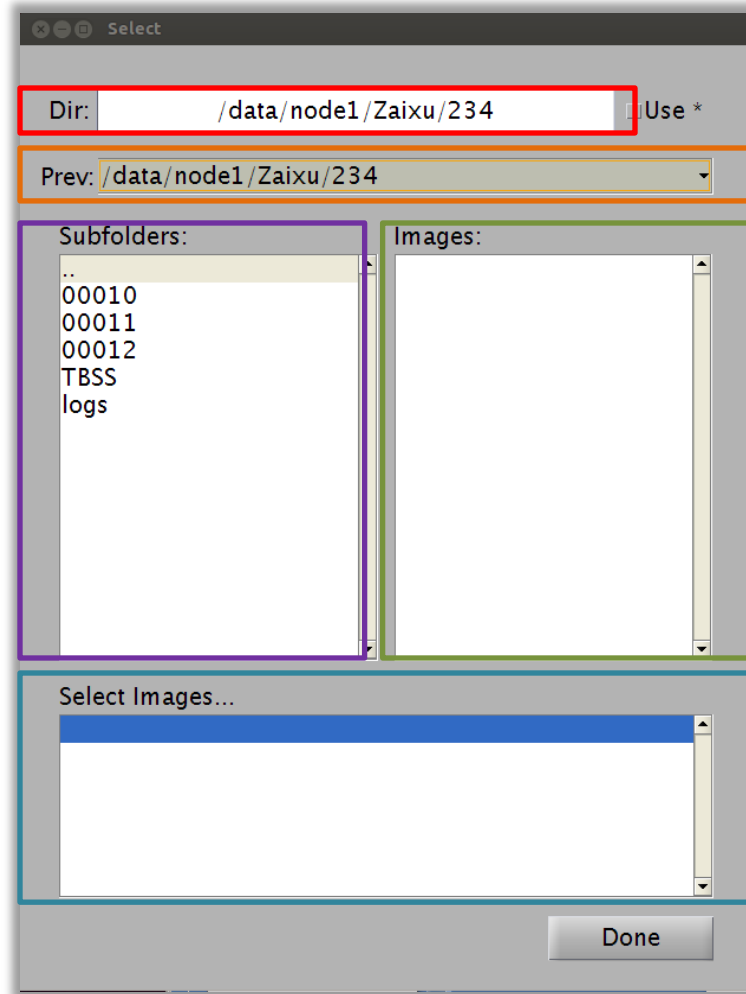
Images/Files/Directories
to be selected,
referring to next page

Images/Files/Directories
users have selected

Select

Dir: /data/node1/Zaixu/234   Use *

Prev: /data/node1/Zaixu/234

Subfolders:
```
..
00010
00011
00012
TBSS
logs
```

Images:

Select Images...

Done

Files/Directories selection

Three situations:

Select **Directories**:
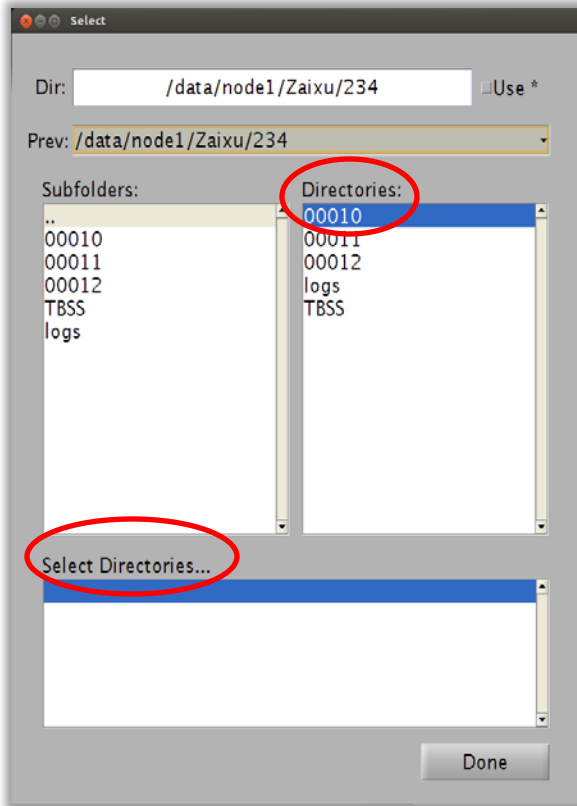
Select **Images (.nii, .nii.gz, .img)**:
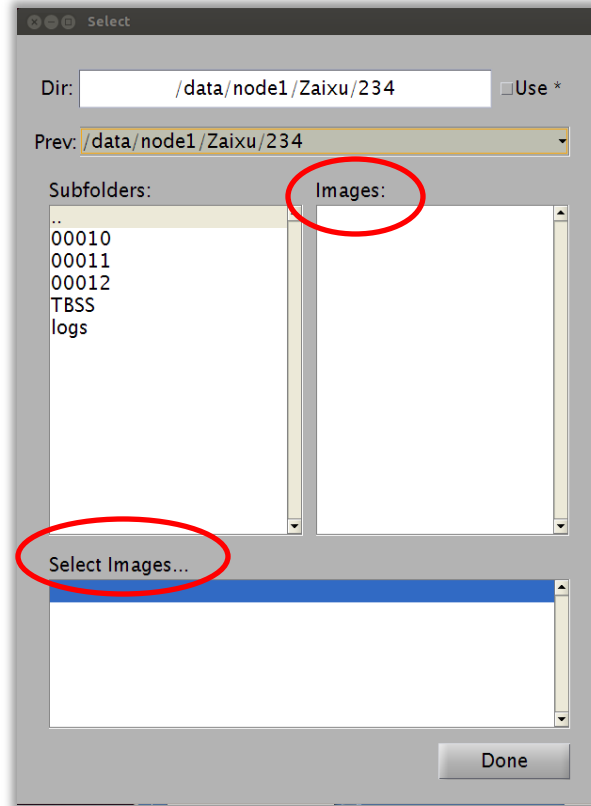
Select **Files**:
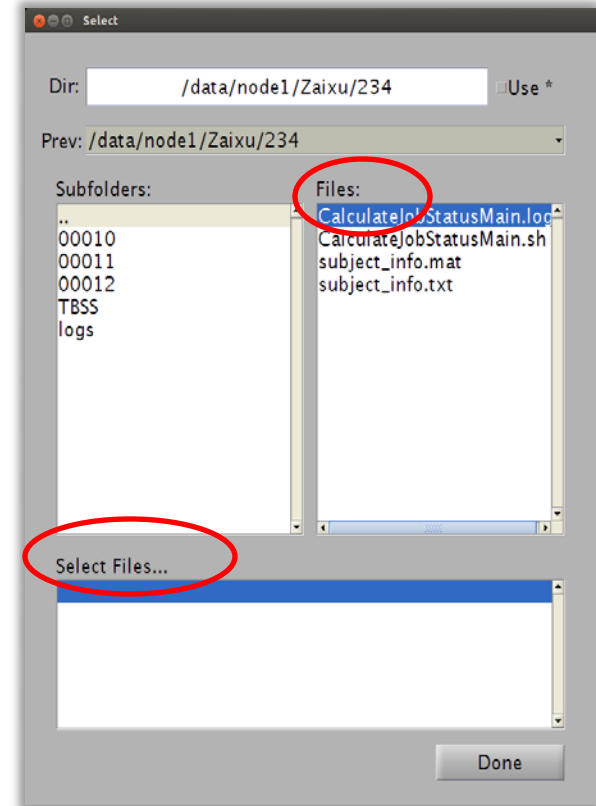
Files/Directories selection

Two methods:
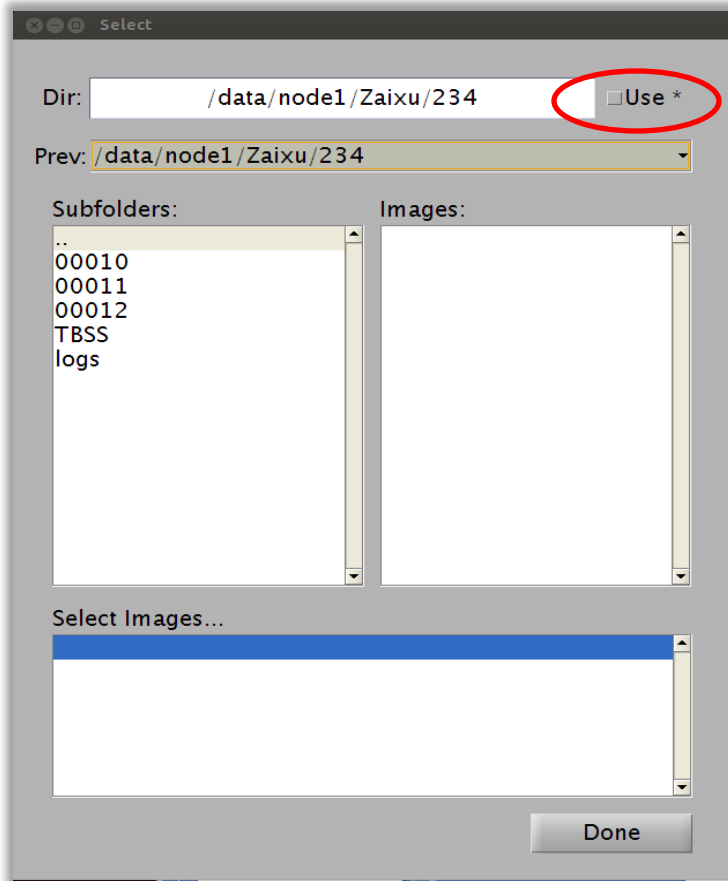
Normal: **Use *:**
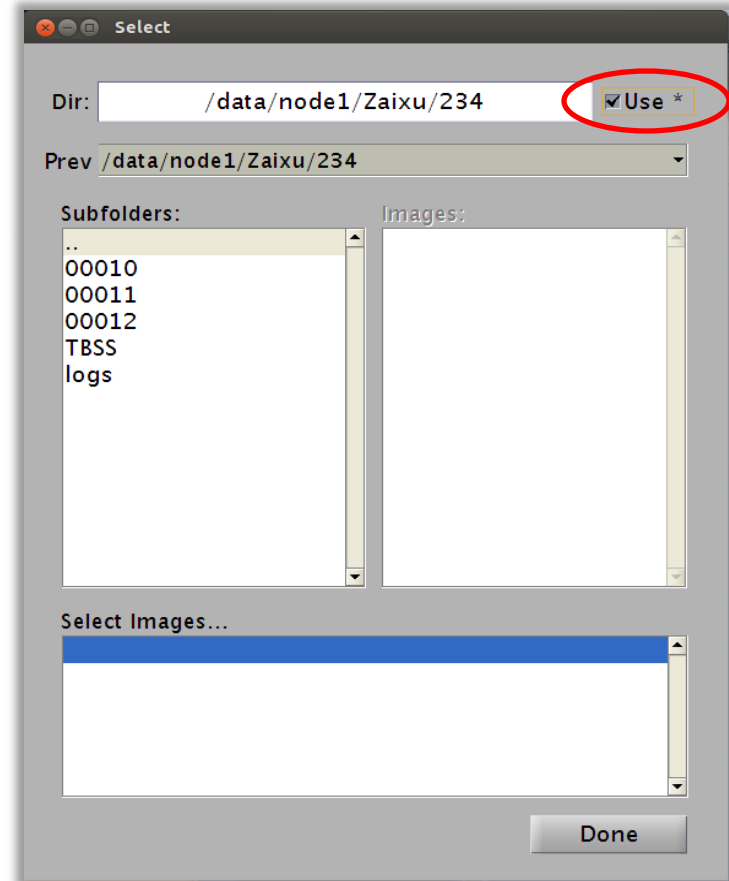
Files/Directories selection

Normal:
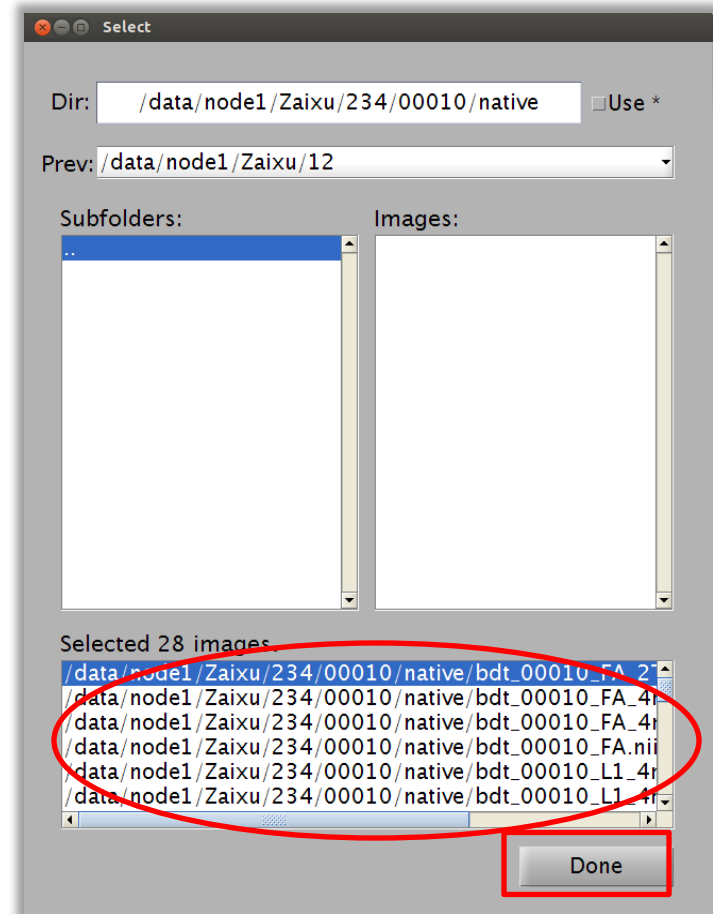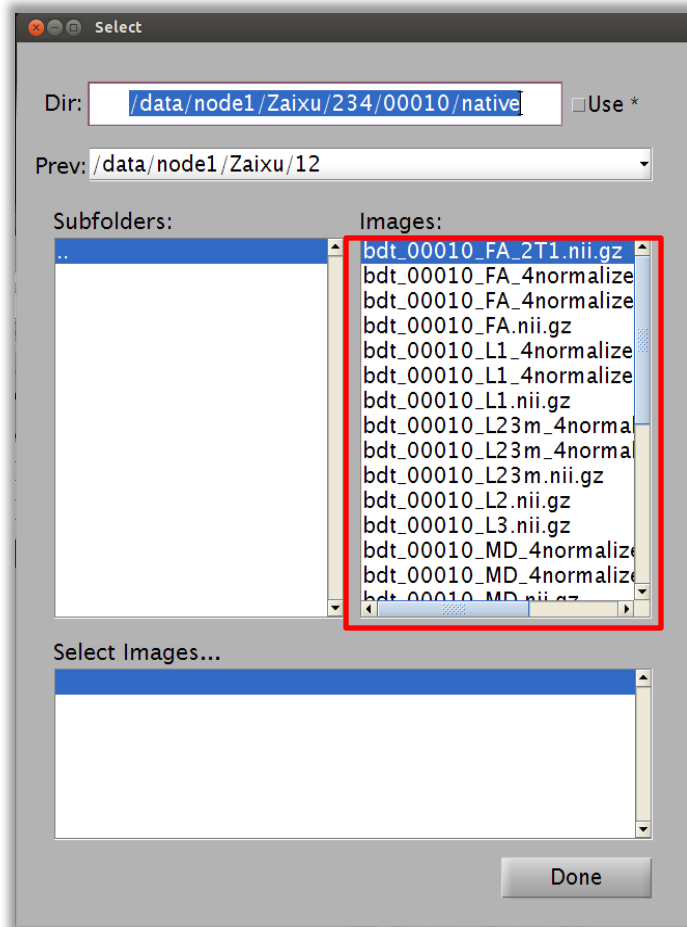
Files/Directories selection

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.


```
/ ▸ data ▸ 234 ▸                                    ▾ 🔍 📁
  Name ∟
☐ 📁 00010
  ☐ 📁 standard_space
      📄 bdt_00010_FA_to_target_1mm.WMtract
      📄 bdt_00010_FA_to_target_2mm_s6mm.nii.gz
      📄 bdt_00010_L1_to_target_1mm.WMtract
      📄 bdt_00010_L1_to_target_2mm_s6mm.nii.gz
      📄 bdt_00010_L23m_to_target_1mm.WMtract
      📄 bdt_00010_L23m_to_target_2mm_s6mm.nii.gz
      📄 bdt_00010_MD_to_target_1mm.WMtract
      📄 bdt_00010_MD_to_target_2mm_s6mm.nii.gz
☐ 📁 00011
  ☐ 📁 standard_space
      📄 bdt_00011_FA_to_target_1mm.WMtract
      📄 bdt_00011_FA_to_target_2mm_s6mm.nii.gz
      📄 bdt_00011_L1_to_target_1mm.WMtract
      📄 bdt_00011_L1_to_target_2mm_s6mm.nii.gz
      📄 bdt_00011_L23m_to_target_1mm.WMtract
      📄 bdt_00011_L23m_to_target_2mm_s6mm.nii.gz
      📄 bdt_00011_MD_to_target_1mm.WMtract
      📄 bdt_00011_MD_to_target_2mm_s6mm.nii.gz
☐ 📁 00012
  ☐ 📁 standard_space
      📄 bdt_00012_FA_to_target_1mm.WMtract
      📄 bdt_00012_FA_to_target_2mm_s6mm.nii.gz
      📄 bdt_00012_L1_to_target_1mm.WMtract
      📄 bdt_00012_L1_to_target_2mm_s6mm.nii.gz
      📄 bdt_00012_L23m_to_target_1mm.WMtract
      📄 bdt_00012_L23m_to_target_2mm_s6mm.nii.gz
      📄 bdt_00012_MD_to_target_1mm.WMtract
      📄 bdt_00012_MD_to_target_2mm_s6mm.nii.gz
```

Files/Directories selection

Use *:

Get all the 'WMlabel' and 'WMtract' file under folder standard_space
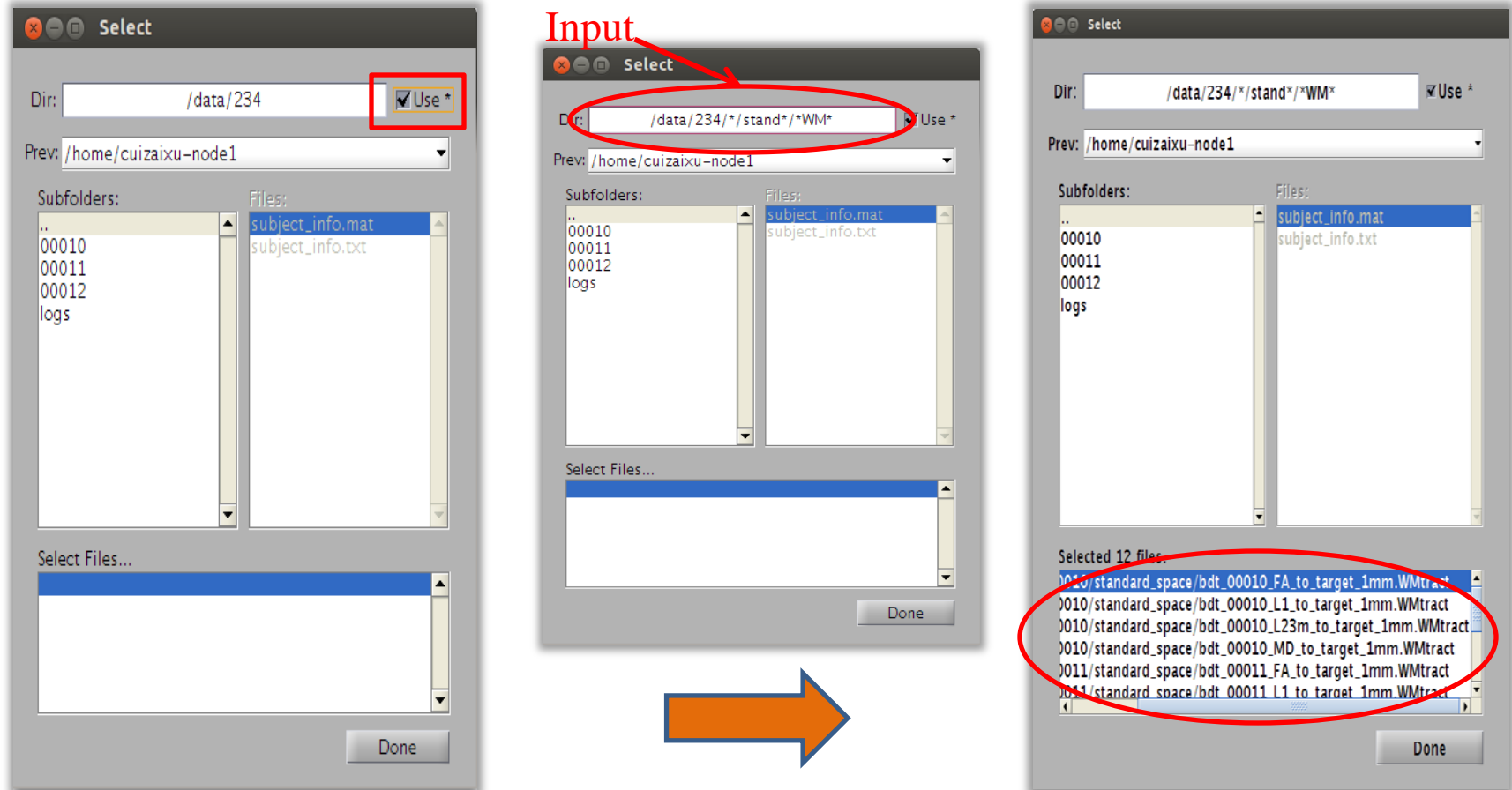
Files/Directories selection

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.
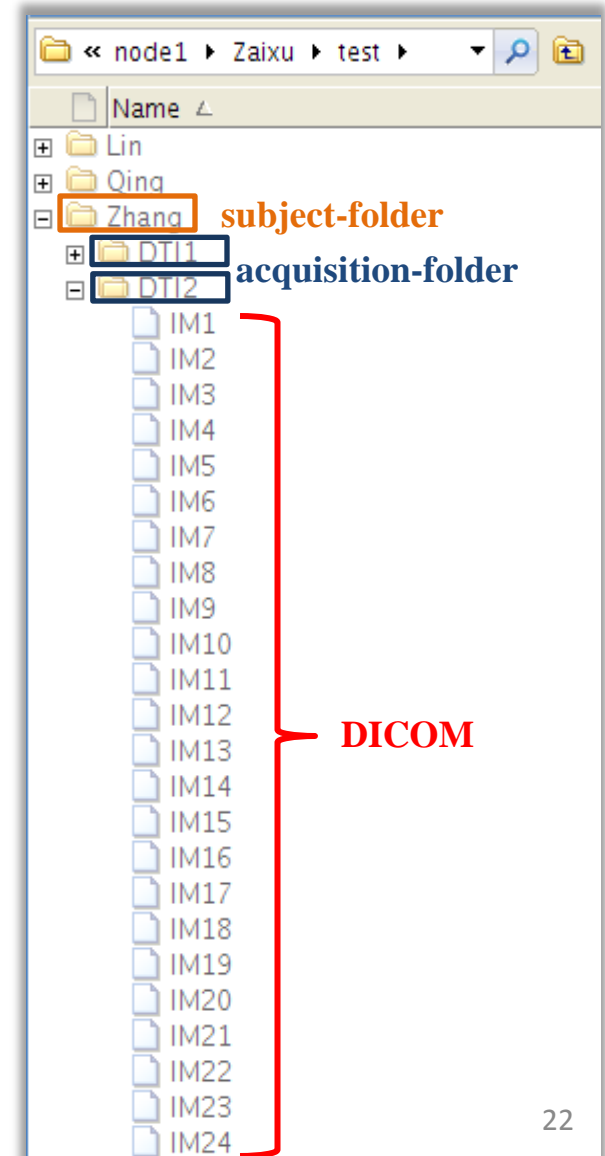
Preparing raw data (NIfTI)

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*'.
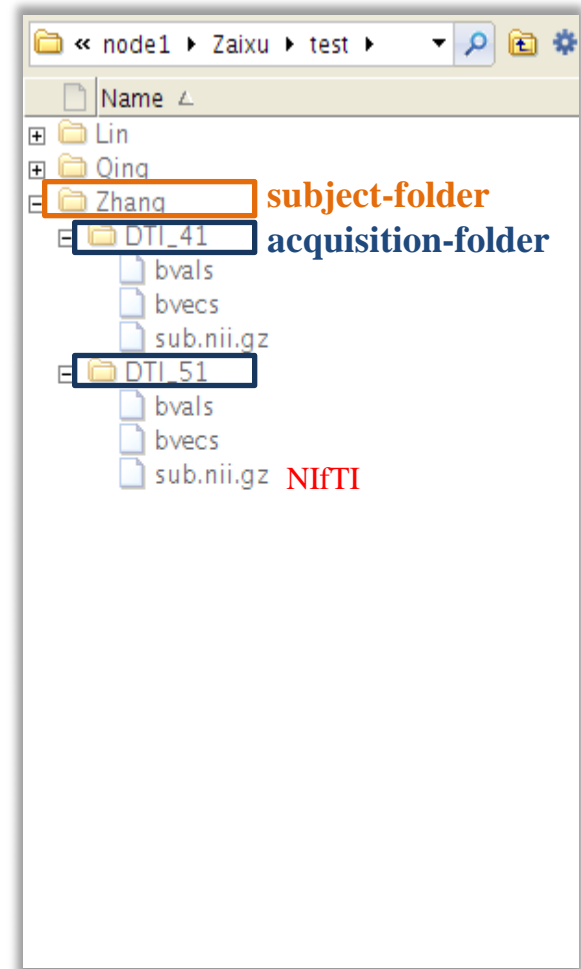
« node1 ▸ Zaixu ▸ test ▸

Name

⊞ Lin
⊞ Qing
⊟ Zhang   **subject-folder**
  ⊟ DTI_41   **acquisition-folder**
      bvals
      bvecs
      sub.nii.gz
  ⊟ DTI_51
      bvals
      bvecs
      sub.nii.gz   NIfTI

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Setting inputs & outputs

Step1: Select subject-folders
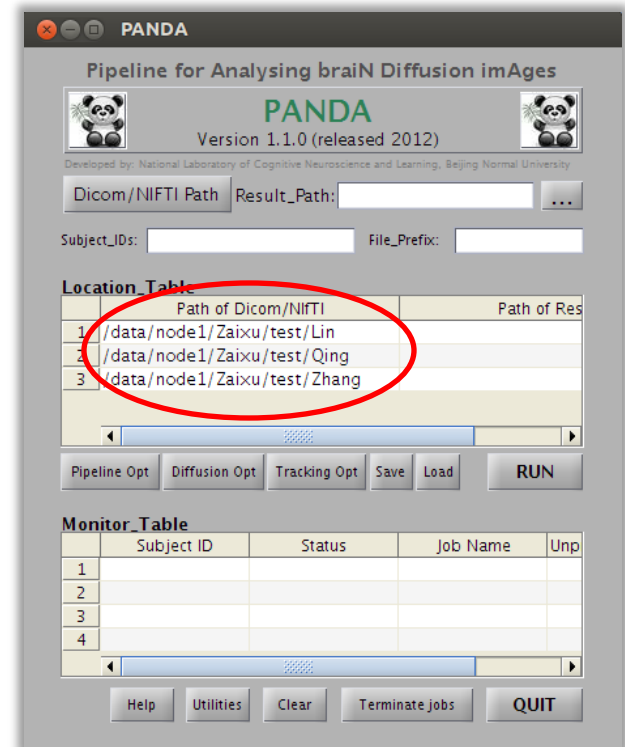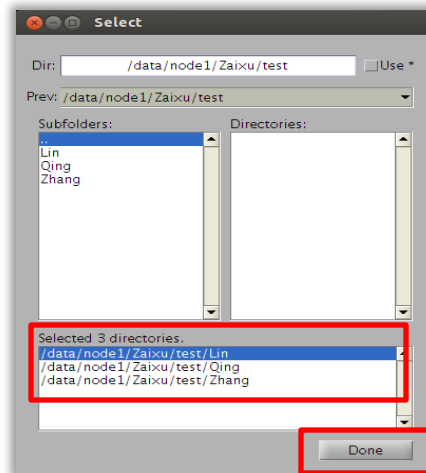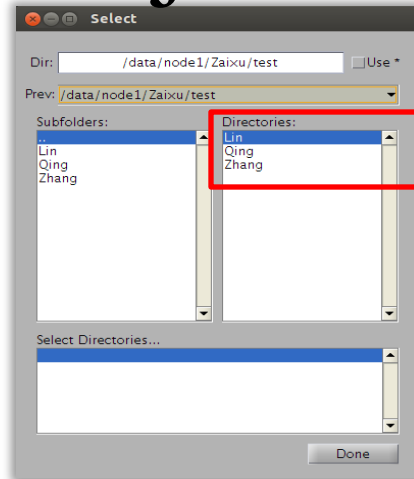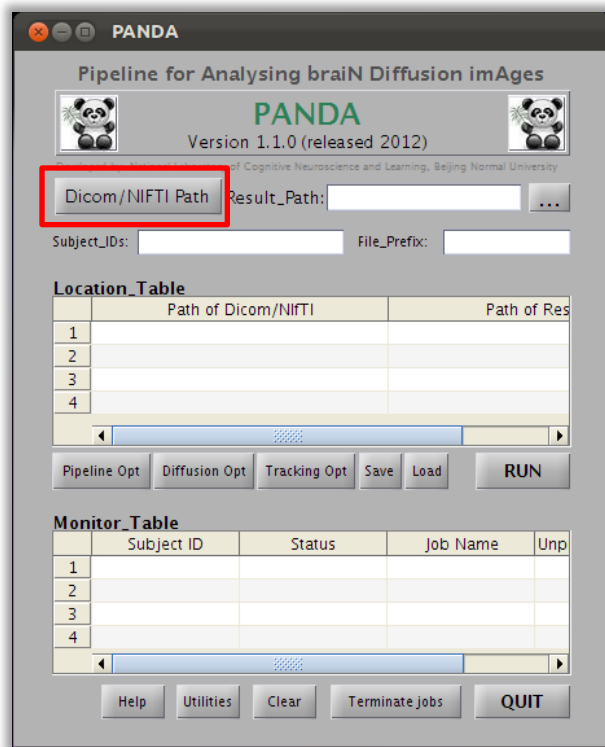
Setting inputs & outputs

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
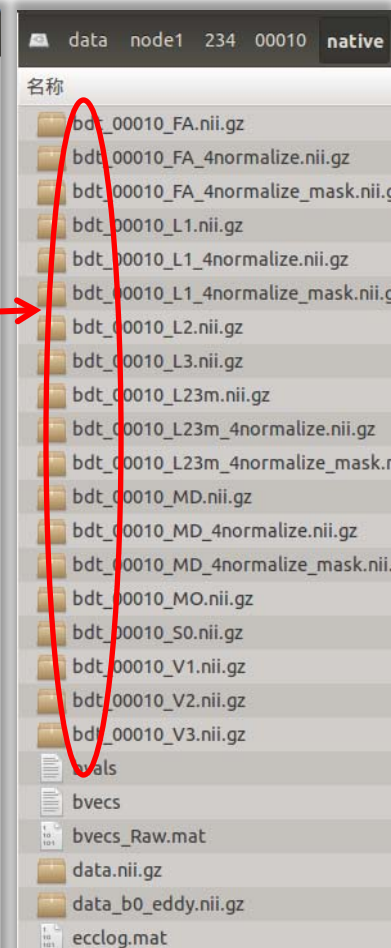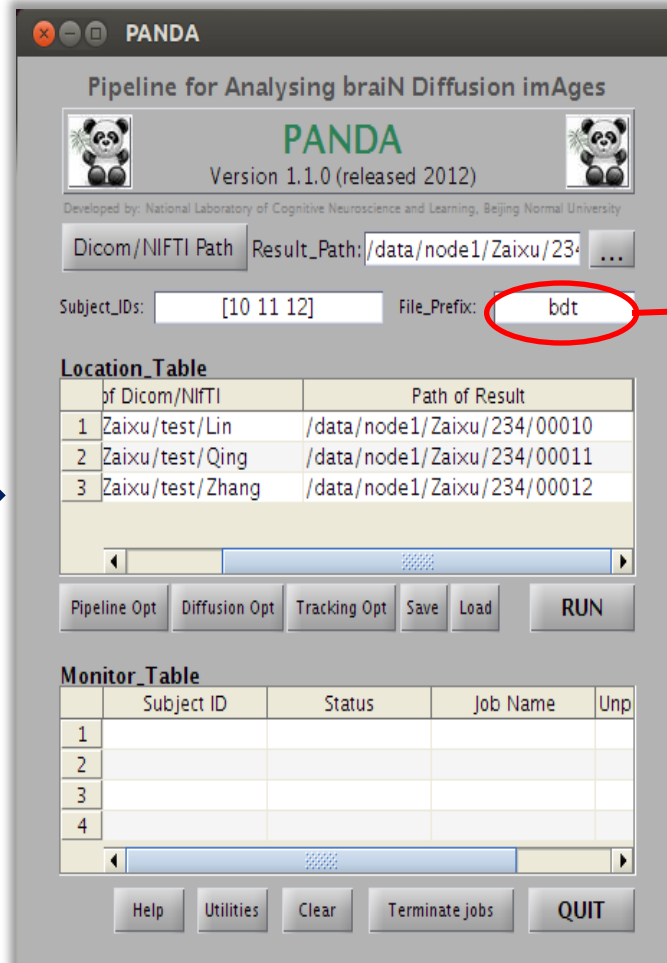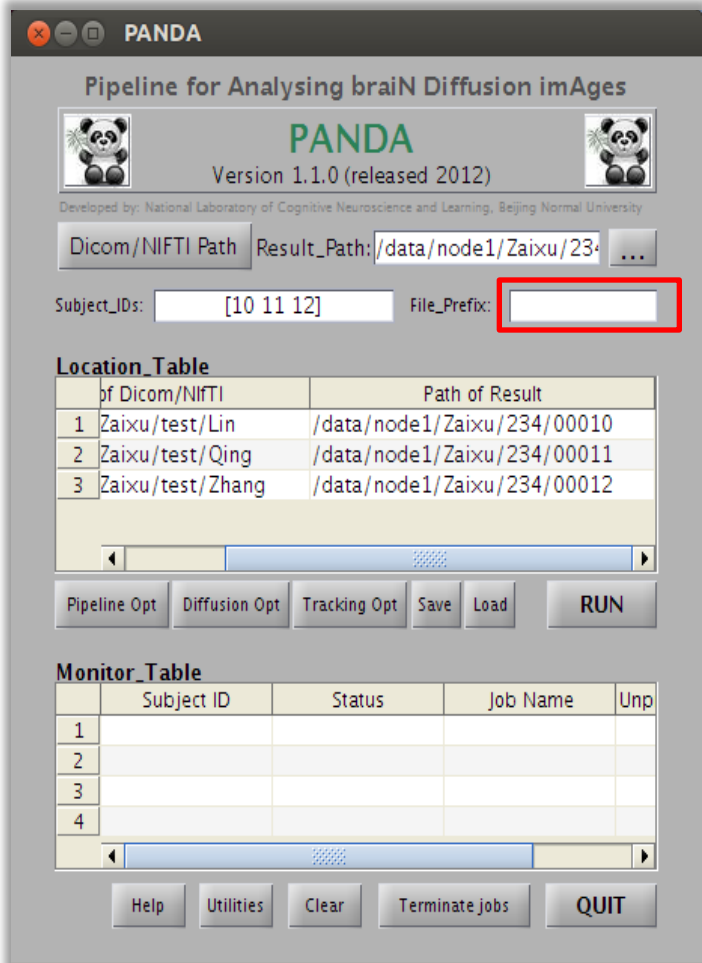
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Changing parameters (optional)
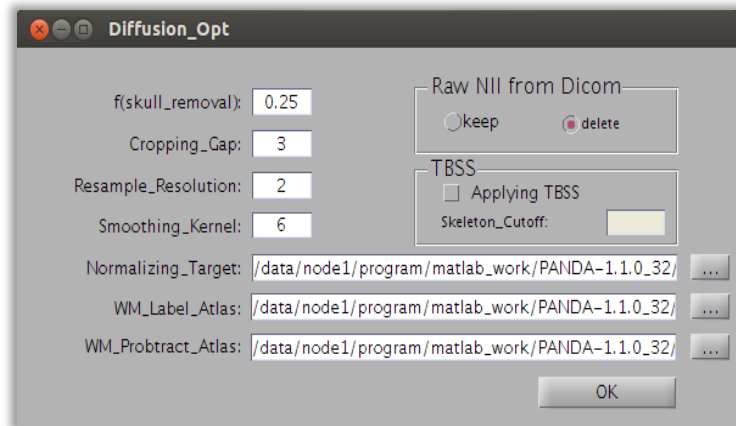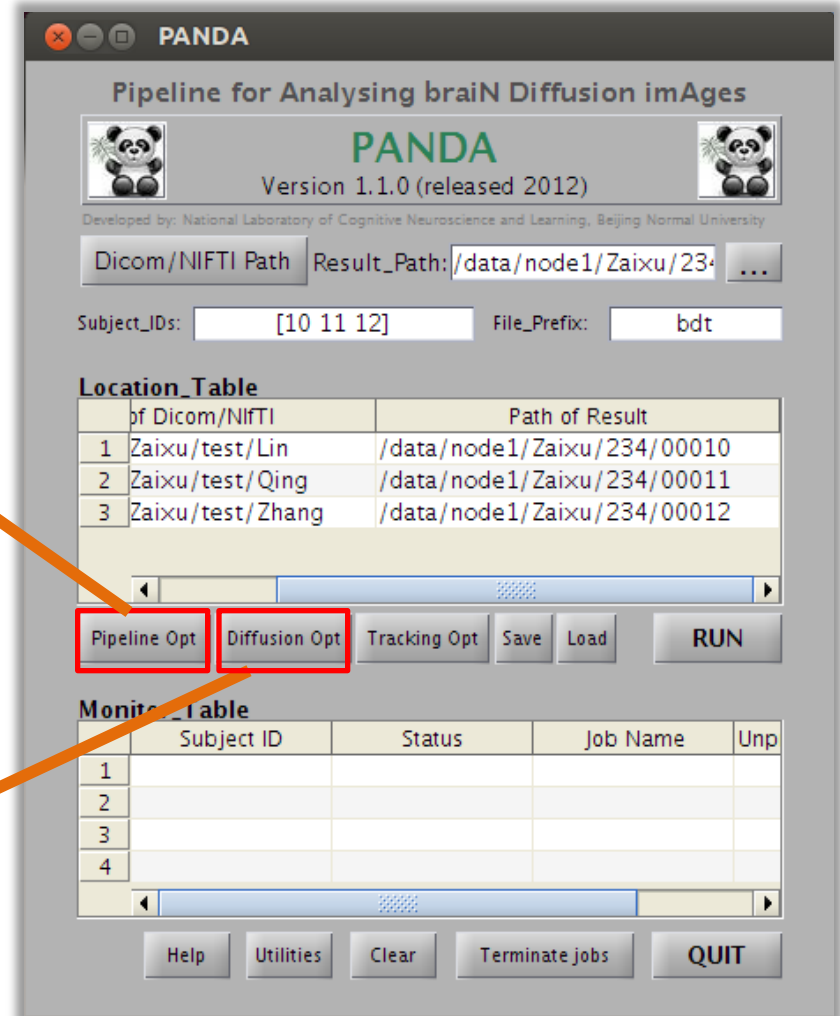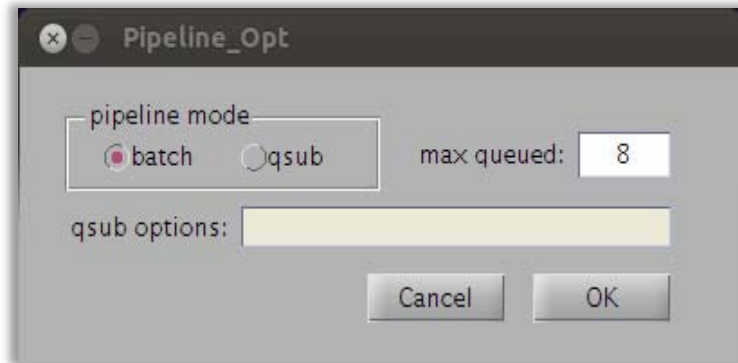
Changing parameters (optional)
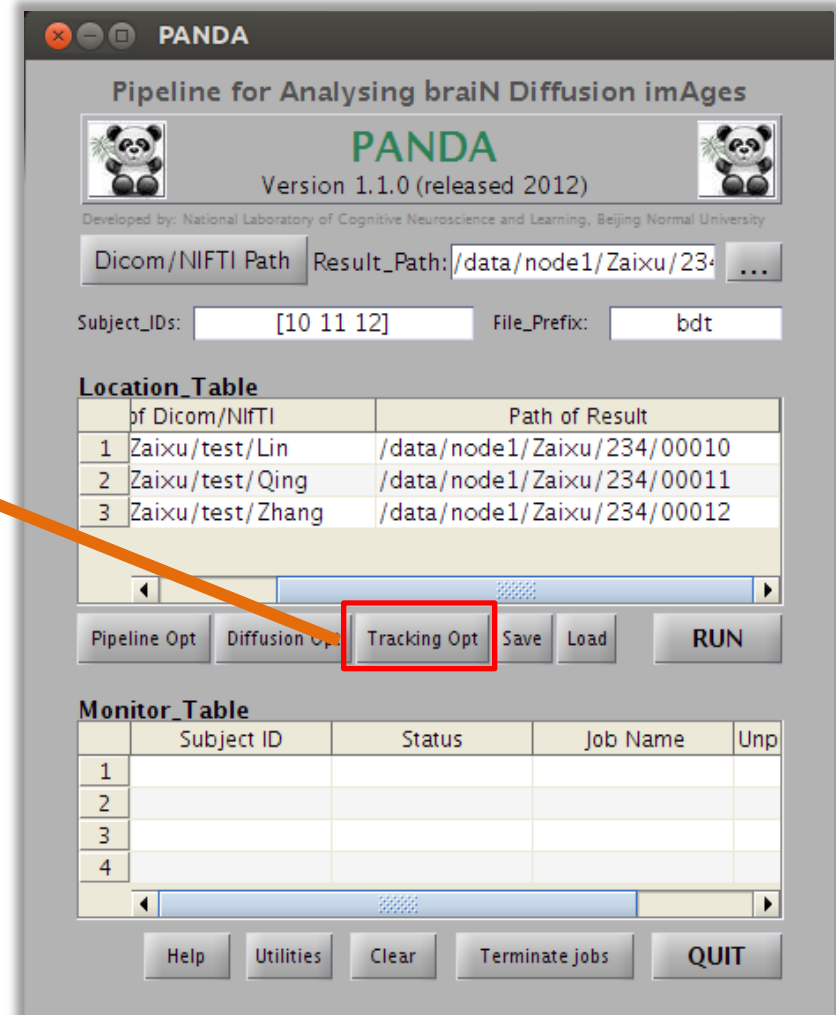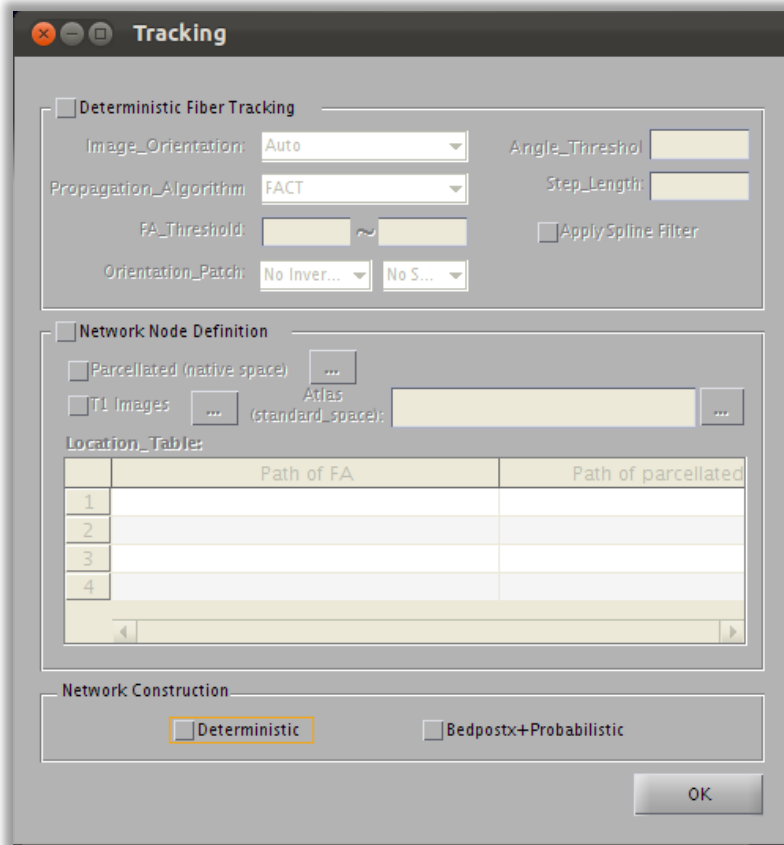
Changing parameters (optional)

Pipeline_Opt
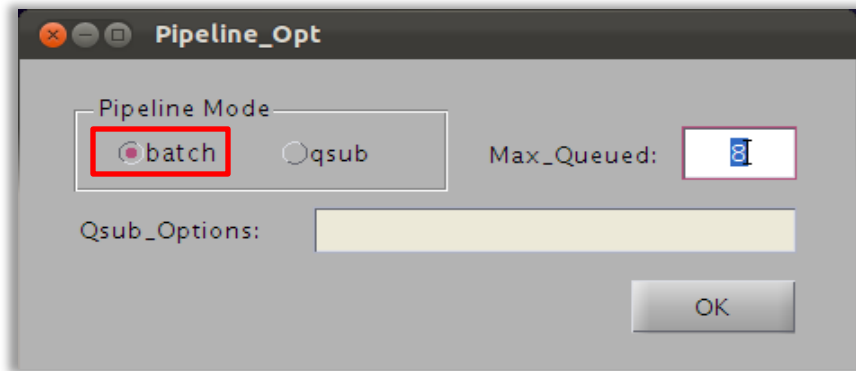
When a single desktop:
Please select 'batch' mode
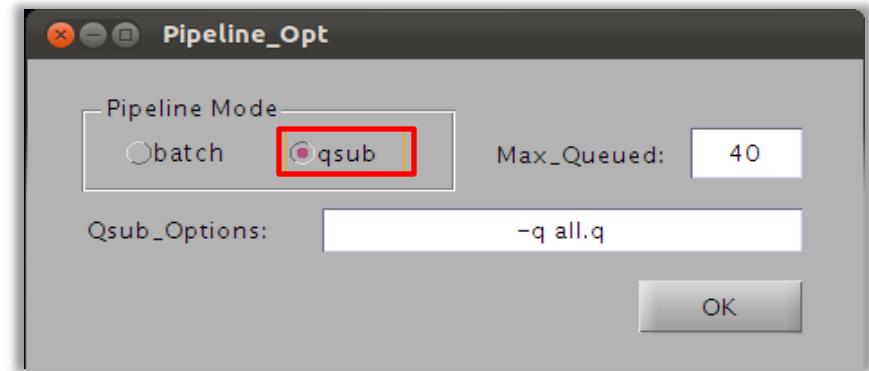
When a SGE environment:
Please select 'qsub' mode
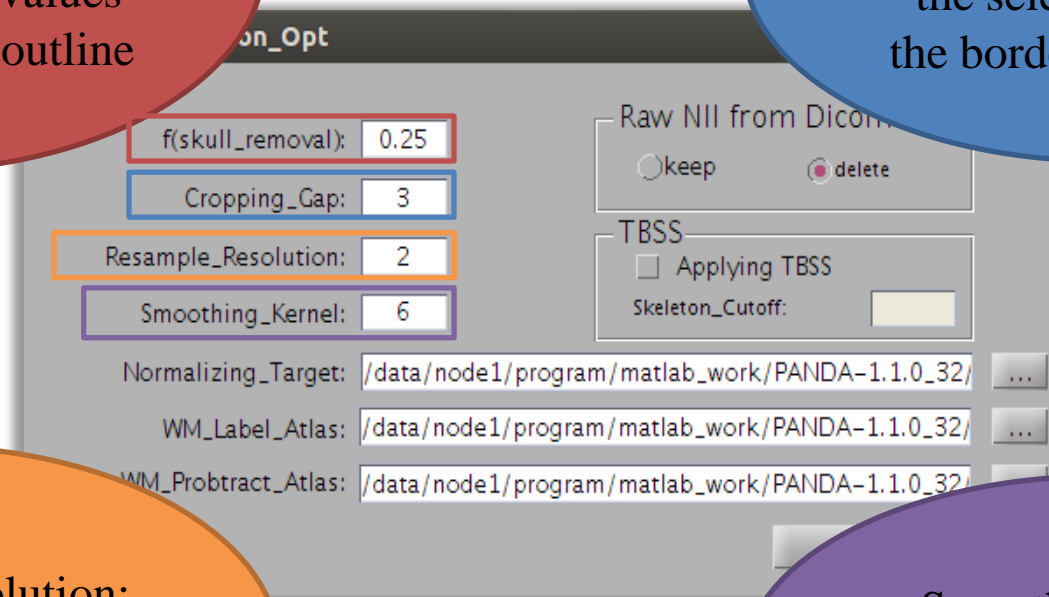
'max queued' is the maximum jobs running in parallel

Changing parameters (optional)

Diffusion_Opt (The default configuration is recommended)

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

			Raw NII from Dicom
f(skull_removal):	0.25		◯keep ◉delete
Cropping_Gap:	3		TBSS
Resample_Resolution:	2		☐ Applying TBSS
Smoothing_Kernel:	6		Skeleton_Cutoff:

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)

Diffusion_Opt

f(skull_removal):	0.25
Cropping_Gap:	3
Resample_Resolution:	2
Smoothing_Kernel:	6
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/ ...

Raw NII from Dicom
○ keep   ● delete

TBSS
☐ Applying TBSS
Skeleton_Cutoff:

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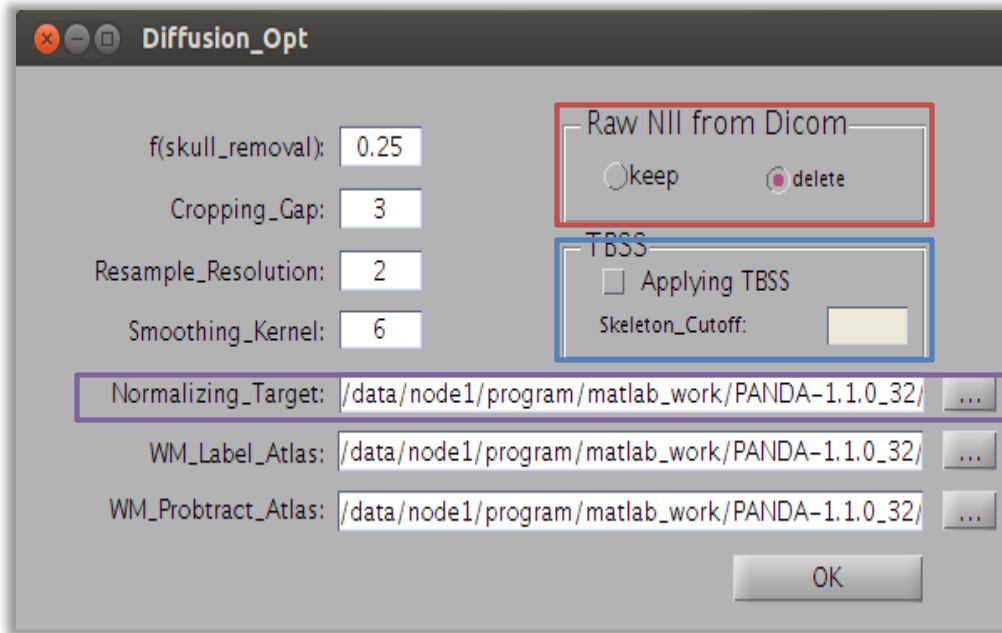
Raw NII from Dicom :
Select whether to delete
raw NII converted from
DICOM

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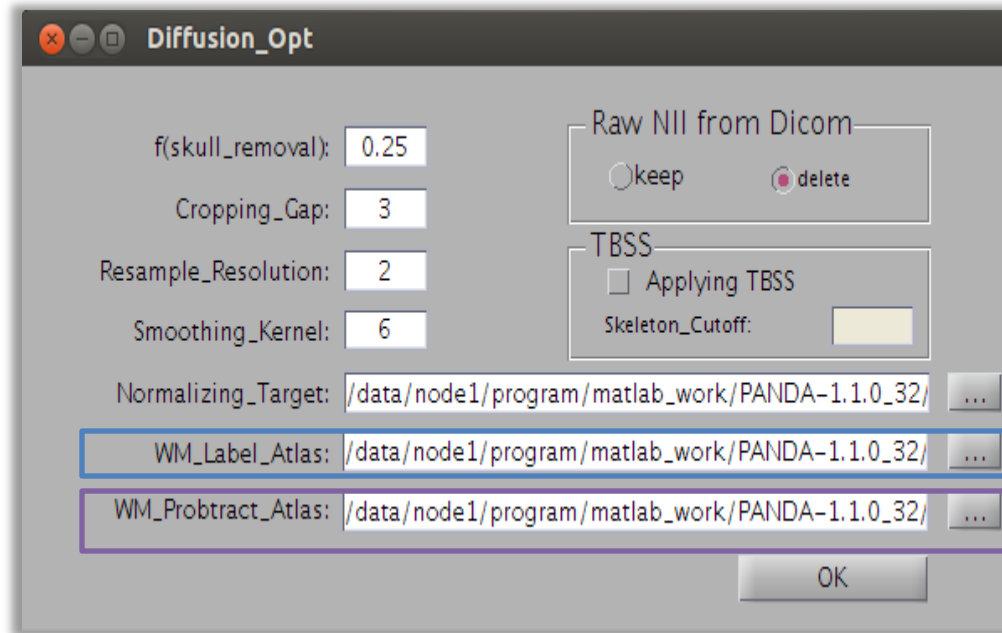
WM_Lable_Atlas:
PANDA will calculate average of FA/MD/λ_1 / λ_{23m} for all the regions in the WM_Lable_Atlas
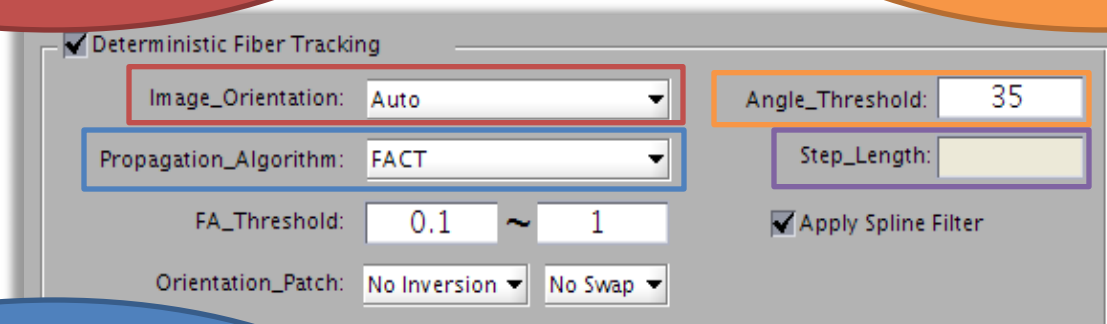
WM_Probtract_Atlas:
PANDA will calculate average of FA/MD/λ_1 /λ_{23m} for all the regions in the WM_Probtract_Atlas

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

☑ Deterministic Fiber Tracking

Image_Orientation:	Auto ▼	Angle_Threshold:	35
Propagation_Algorithm:	FACT ▼	Step_Length:	
FA_Threshold:	0.1 ~ 1	☑ Apply Spline Filter	
Orientation_Patch:	No Inversion ▼ No Swap ▼		

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.

36

Changing parameters (optional)

Deterministic Fiber Tracking

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.

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

Changing parameters (optional)

Network Node Definition
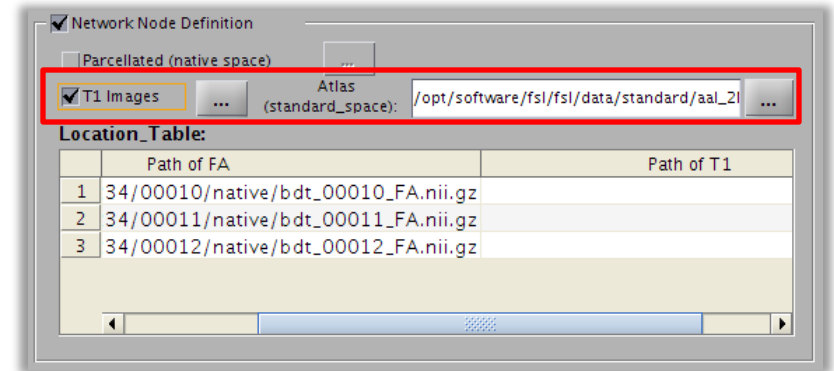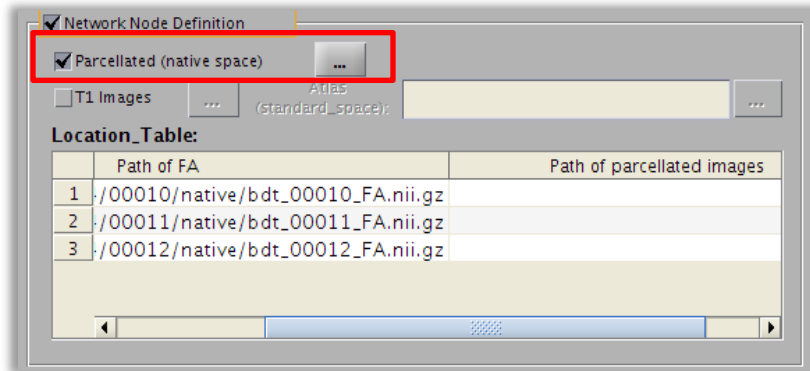
When having parcellated images in native space :
Select 'Parcellated (native space) ' and input these images.

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

Network Construction

☐ Deterministic   ☐ Bedpostx+Probabilistic
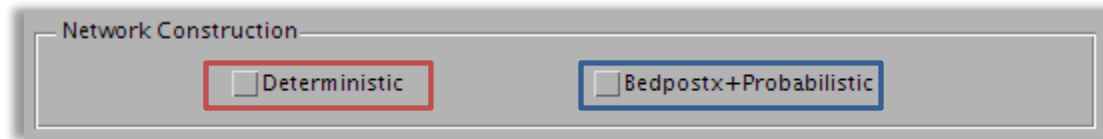
Deterministic Network Construction:
Deterministic Fiber Tracking and
Network Node Definition should be
selected first.

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

Burnin:
Burnin period, default 1000

Label ID:
the ID of brain regions in atlas

Network Construction

☐ Deterministic   ☑ Bedpostx+Probabilistic

BedpostxAndProbabilistic_Opt

Fibers: 2

Weight: 1

Brunin: 1000

Tracking Type
◉ OPD   ○ PD

Label_ID: [1:90]

OK

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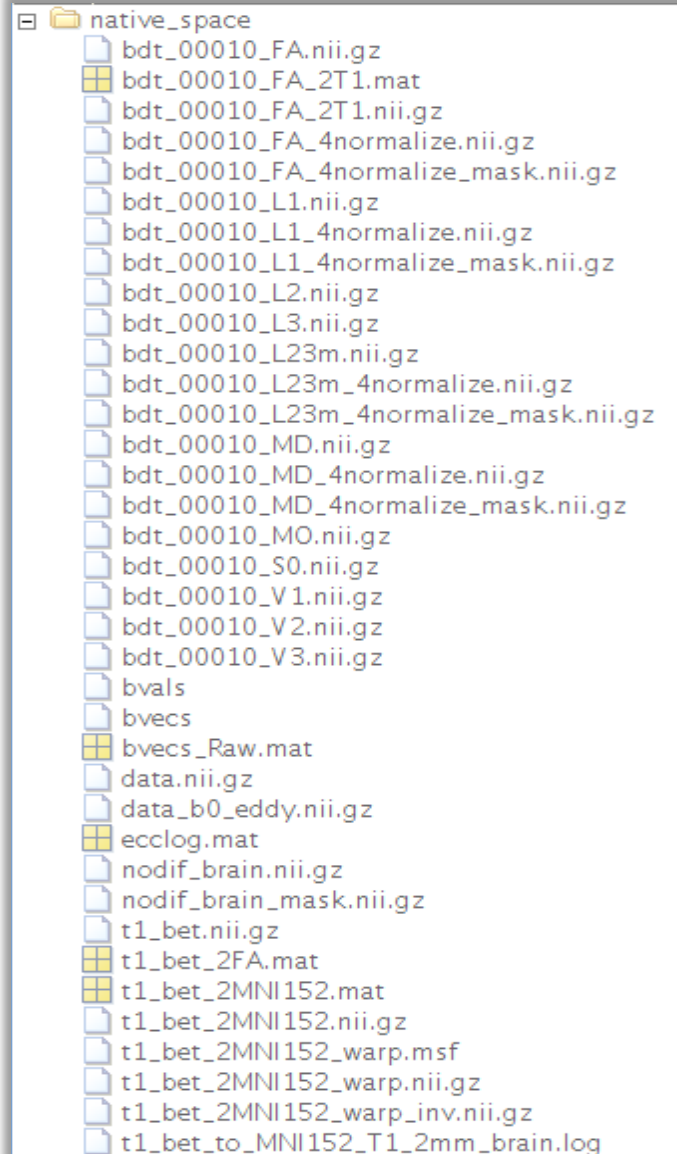
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Initiating process

Start running
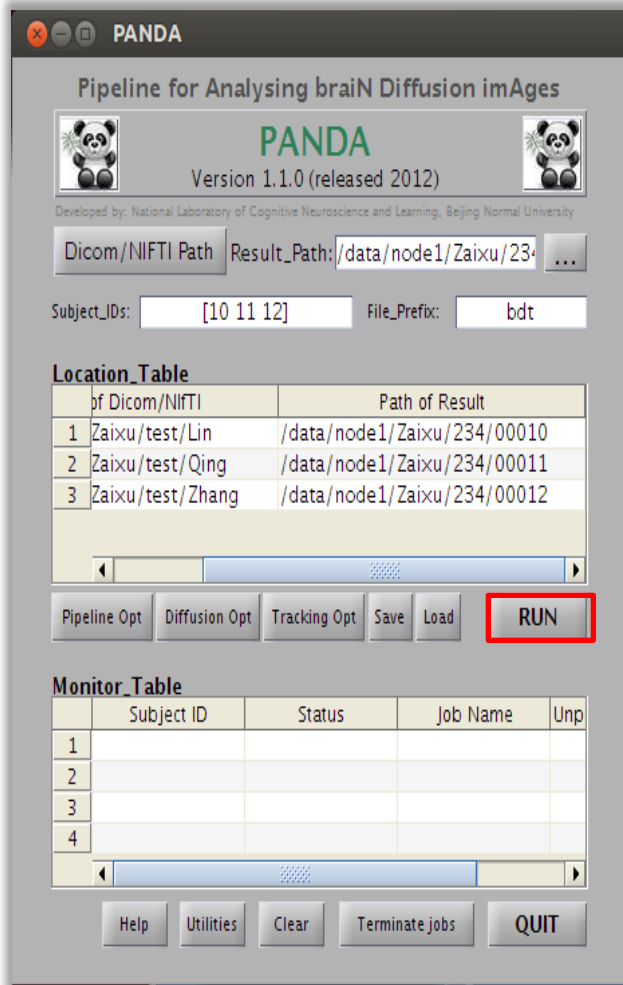
(save configuration)
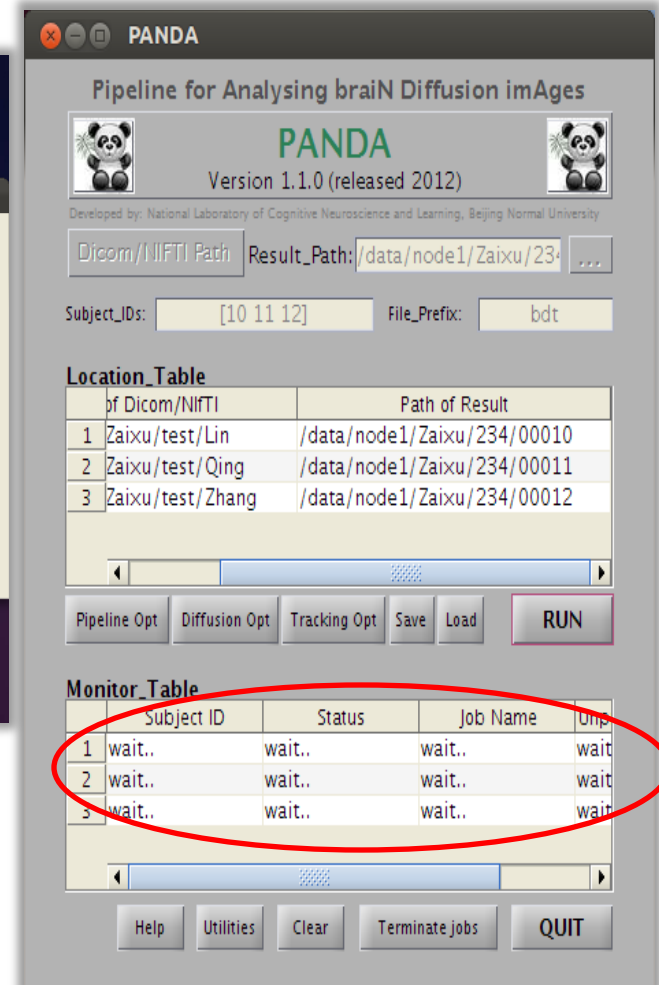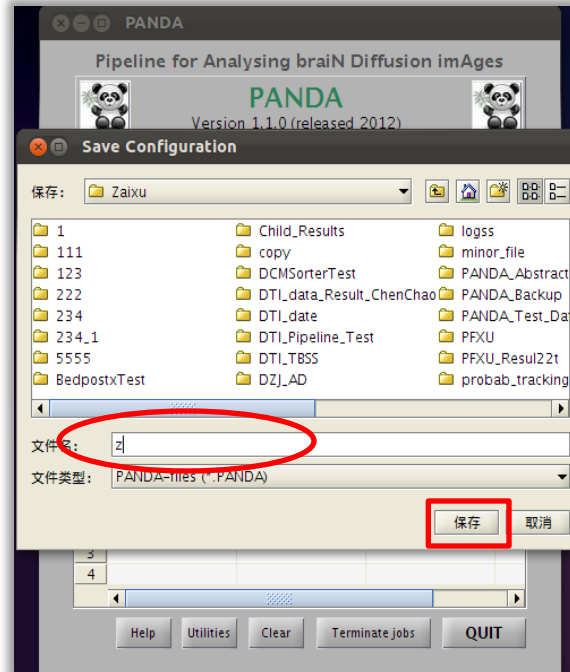
After this, PANDA or even Matlab can be shut down. The jobs will be running in background.

Initiating process

Save & load configuration
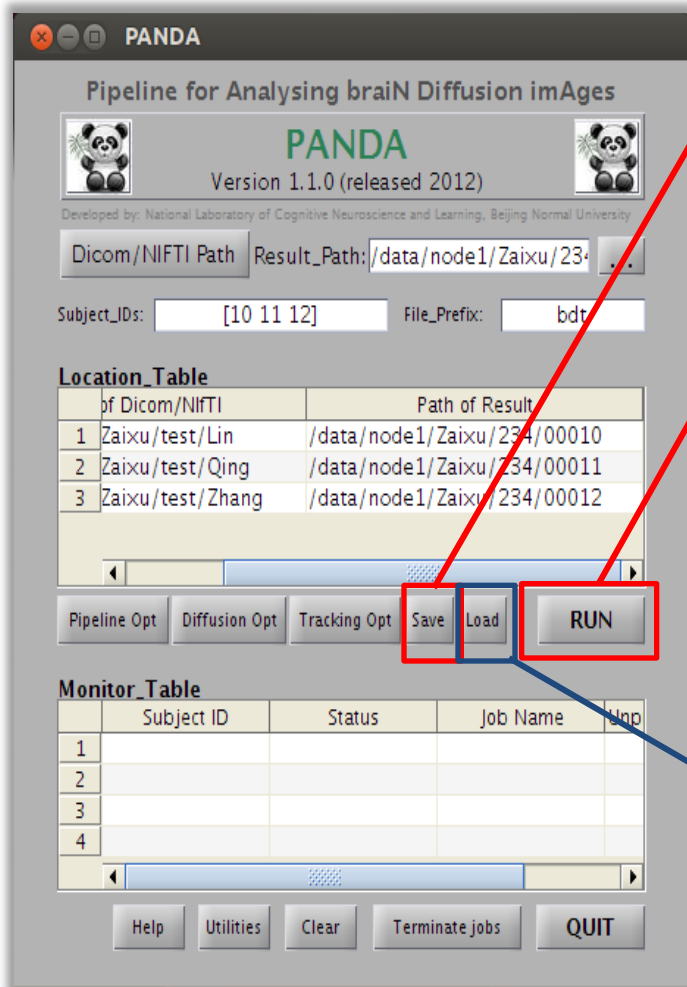
➢ **Save actively**(extension as **.PANDA**) :
Use 'save' button to save current configurations.

➢ **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**
- **Initiating process**
- ➡ **Monitoring progress**
- **Understanding resultant files**
- **Utilities**

Monitoring progress
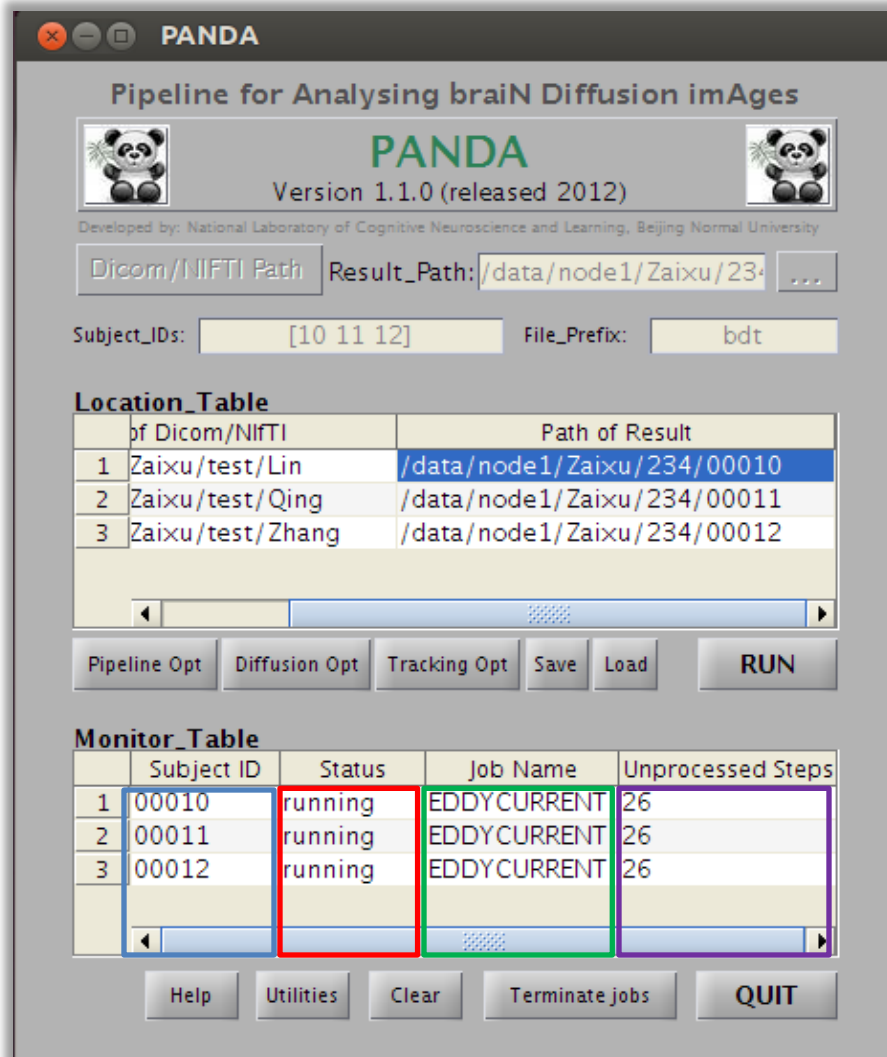
> ➢ **Subject ID**(fixed)
>
> ➢ **Status**(dynamic)
> > **wait**
> > **submitted**
> > **running**
> > **finished**
> > **failed**
>
> ➢ **Job Name**(dynamic)
>
> ➢ **Unprocessed Step**(dynamic)

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

Monitoring progress

Terminate jobs
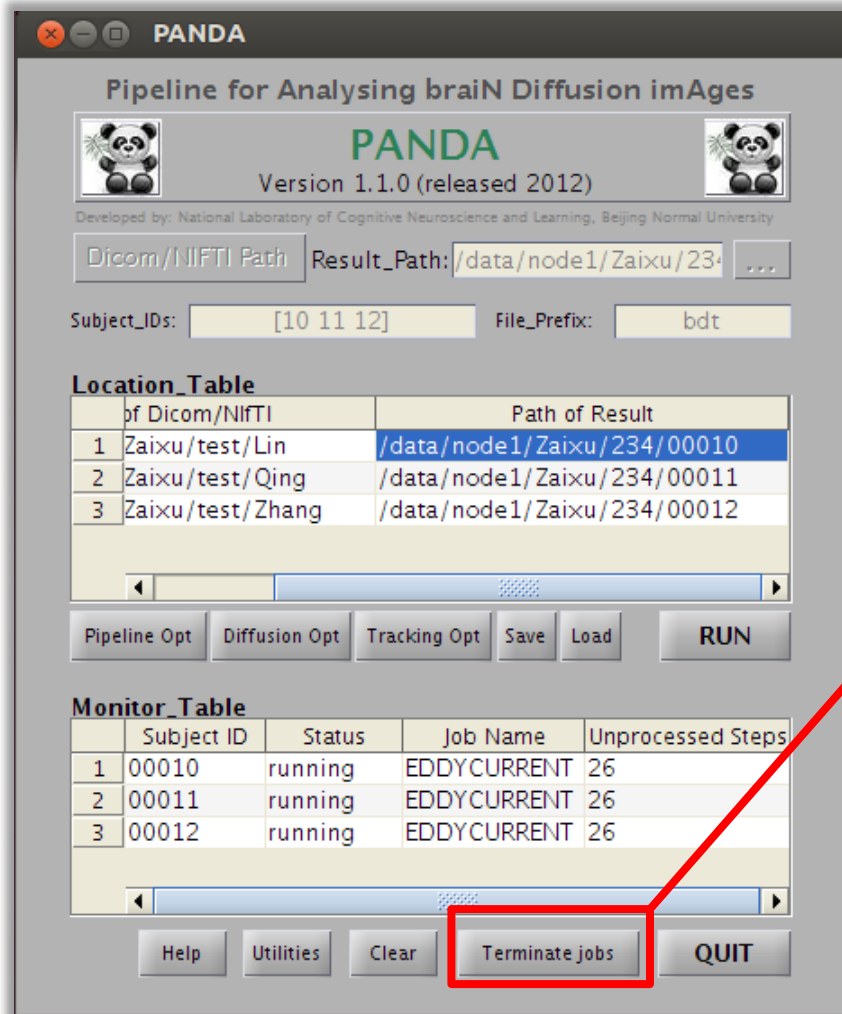
Terminate all the jobs running in background.

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

DICOM Path

Result Path
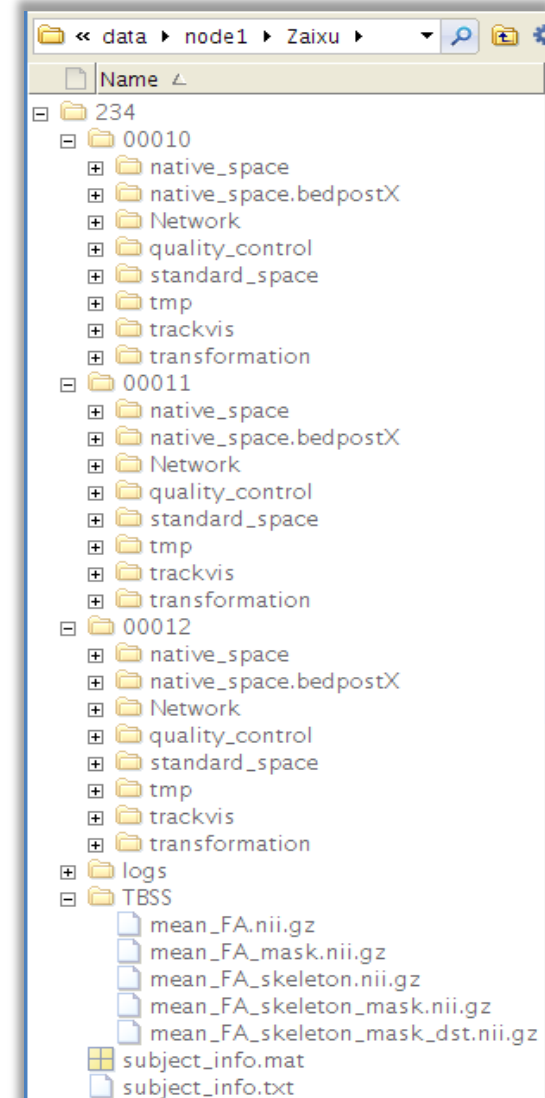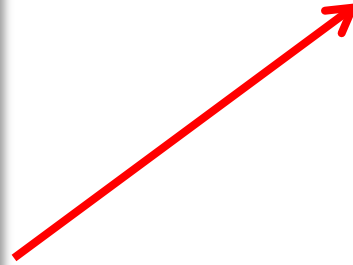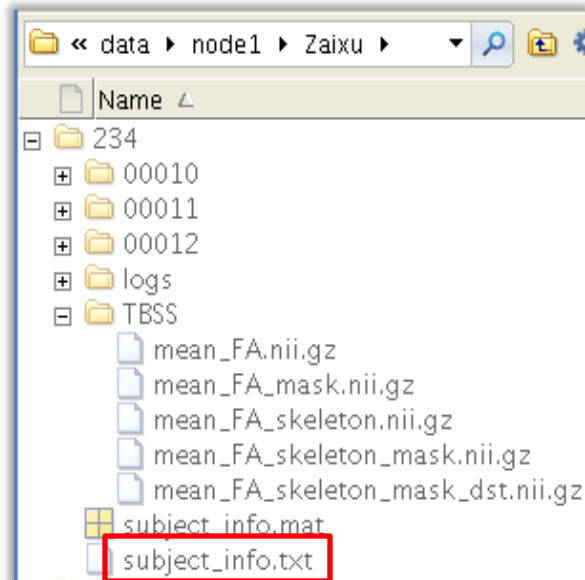
Understanding resultant files

Folder native_space:

```
native_space
    bdt_00010_FA.nii.gz
    bdt_00010_FA_2T1.mat
    bdt_00010_FA_2T1.nii.gz
    bdt_00010_FA_4normalize.nii.gz
    bdt_00010_FA_4normalize_mask.nii.gz
    bdt_00010_L1.nii.gz
    bdt_00010_L1_4normalize.nii.gz
    bdt_00010_L1_4normalize_mask.nii.gz
    bdt_00010_L2.nii.gz
    bdt_00010_L3.nii.gz
    bdt_00010_L23m.nii.gz
    bdt_00010_L23m_4normalize.nii.gz
    bdt_00010_L23m_4normalize_mask.nii.gz
    bdt_00010_MD.nii.gz
    bdt_00010_MD_4normalize.nii.gz
    bdt_00010_MD_4normalize_mask.nii.gz
    bdt_00010_MO.nii.gz
    bdt_00010_S0.nii.gz
    bdt_00010_V1.nii.gz
    bdt_00010_V2.nii.gz
    bdt_00010_V3.nii.gz
    bvals
    bvecs
    bvecs_Raw.mat
    data.nii.gz
    data_b0_eddy.nii.gz
    ecclog.mat
    nodif_brain.nii.gz
    nodif_brain_mask.nii.gz
    t1_bet.nii.gz
    t1_bet_2FA.mat
    t1_bet_2MNI152.mat
    t1_bet_2MNI152.nii.gz
    t1_bet_2MNI152_warp.msf
    t1_bet_2MNI152_warp.nii.gz
    t1_bet_2MNI152_warp_inv.nii.gz
    t1_bet_to_MNI152_T1_2mm_brain.log
```

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:
  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:
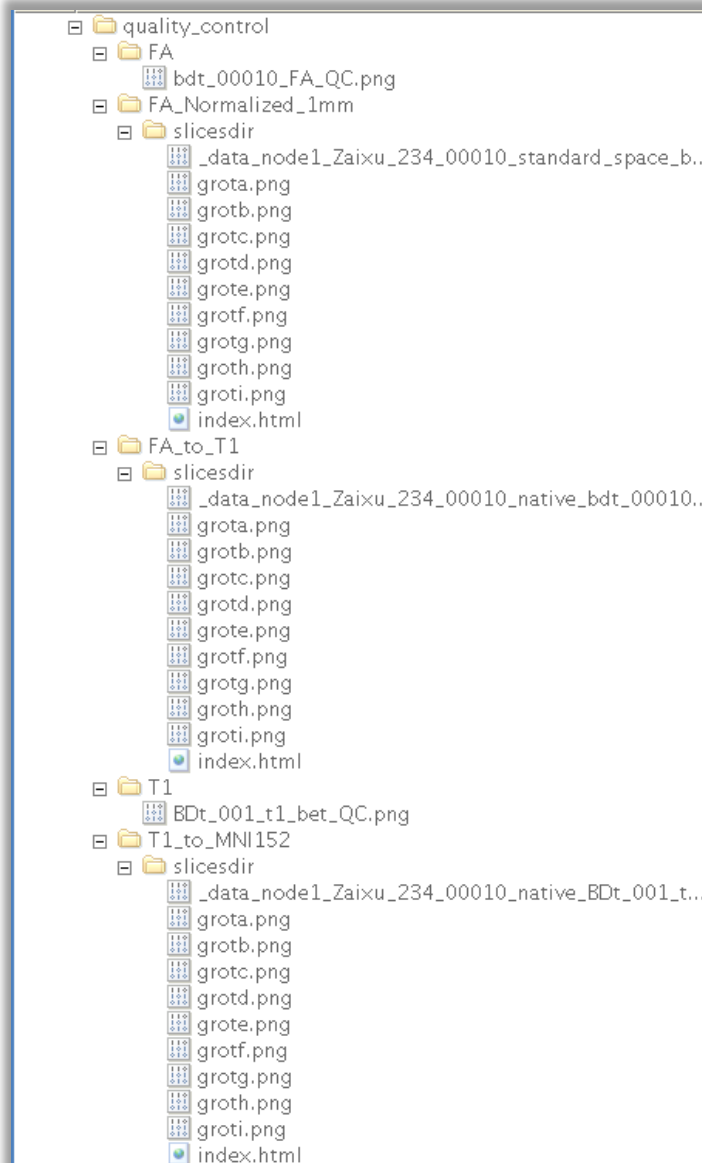
Understanding resultant files

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
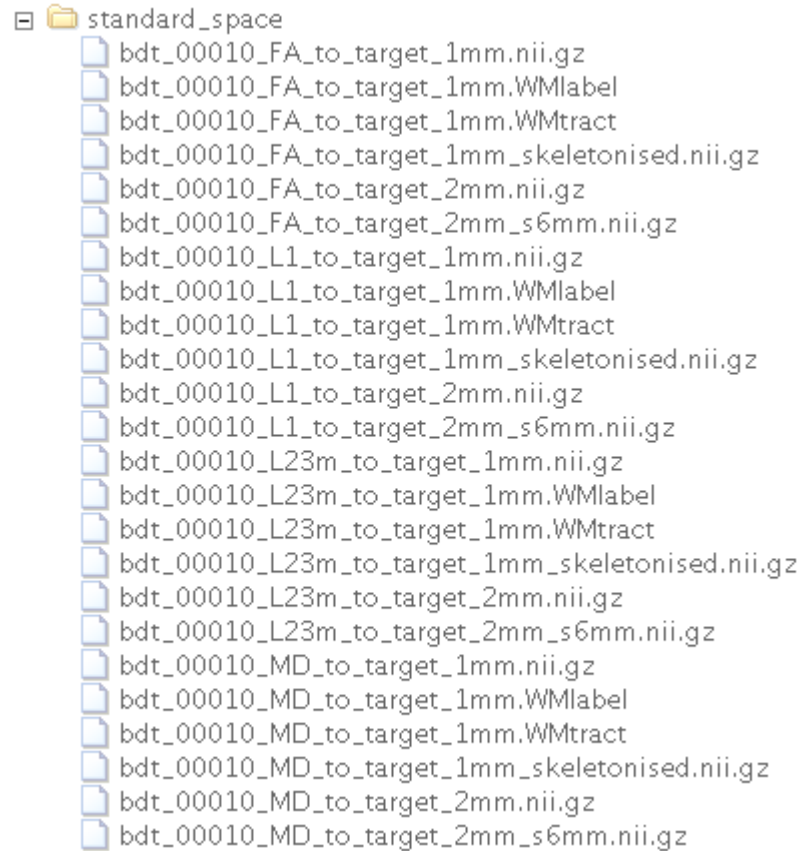
➢ Check quantity of T1 normalization to MNI152 space:
   T1_to_MNI152 -> slicesdir -> *

Understanding resultant files

Folder standard_space:

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 $2\times2\times2$ standard space
  - *_MD_4normalize_to_target_2mm.nii.gz :MD image in $2\times2\times2$ standard space
  - *_L1_4normalize_to_target_2mm.nii.gz : λ_1 image in $2\times2\times2$ standard space
  - *_L23m_4normalize_to_target_2mm.nii.gz : λ_{23m} image in $2\times2\times2$ standard space

- Resultant images after Gaussian smoothing
  - *_FA_4normalize_to_target_2mm_s6mm.nii.gz : smoothing images of $2\times2\times2$ FA image
  - *_MD_4normalize_to_target_2mm_s6mm.nii.gz : smoothing images of $2\times2\times2$ MD image
  - *_L1_4normalize_to_target_2mm_s6mm.nii.gz : smoothing images of $2\times2\times2$ λ_1 image
  - *_L23m_4normalize_to_target_2mm_s6mm.nii.gz :
    smoothing images of $2\times2\times2$ 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:
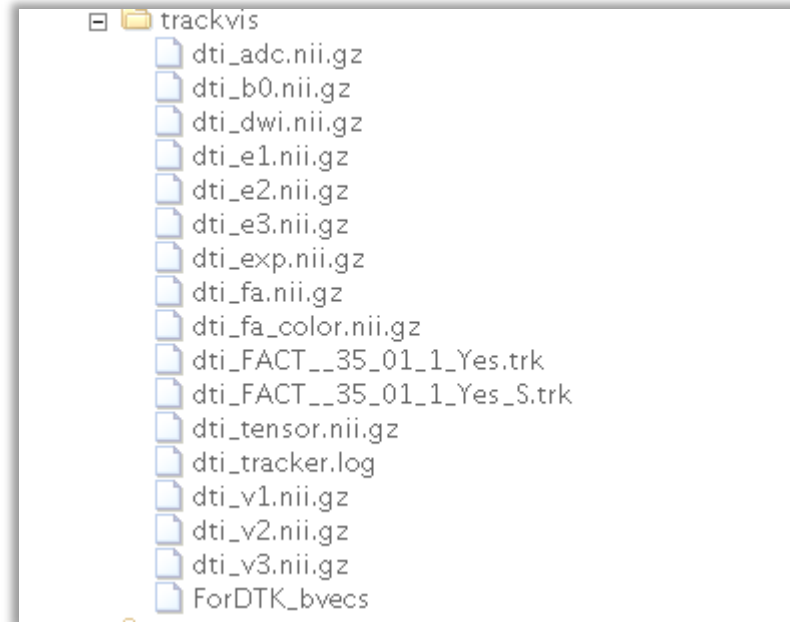

```
⊟ 📁 trackvis
    📄 dti_adc.nii.gz
    📄 dti_b0.nii.gz
    📄 dti_dwi.nii.gz
    📄 dti_e1.nii.gz
    📄 dti_e2.nii.gz
    📄 dti_e3.nii.gz
    📄 dti_exp.nii.gz
    📄 dti_fa.nii.gz
    📄 dti_fa_color.nii.gz
    📄 dti_FACT__35_01_1_Yes.trk
    📄 dti_FACT__35_01_1_Yes_S.trk
    📄 dti_tensor.nii.gz
    📄 dti_tracker.log
    📄 dti_v1.nii.gz
    📄 dti_v2.nii.gz
    📄 dti_v3.nii.gz
    📄 ForDTK_bvecs
```

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:
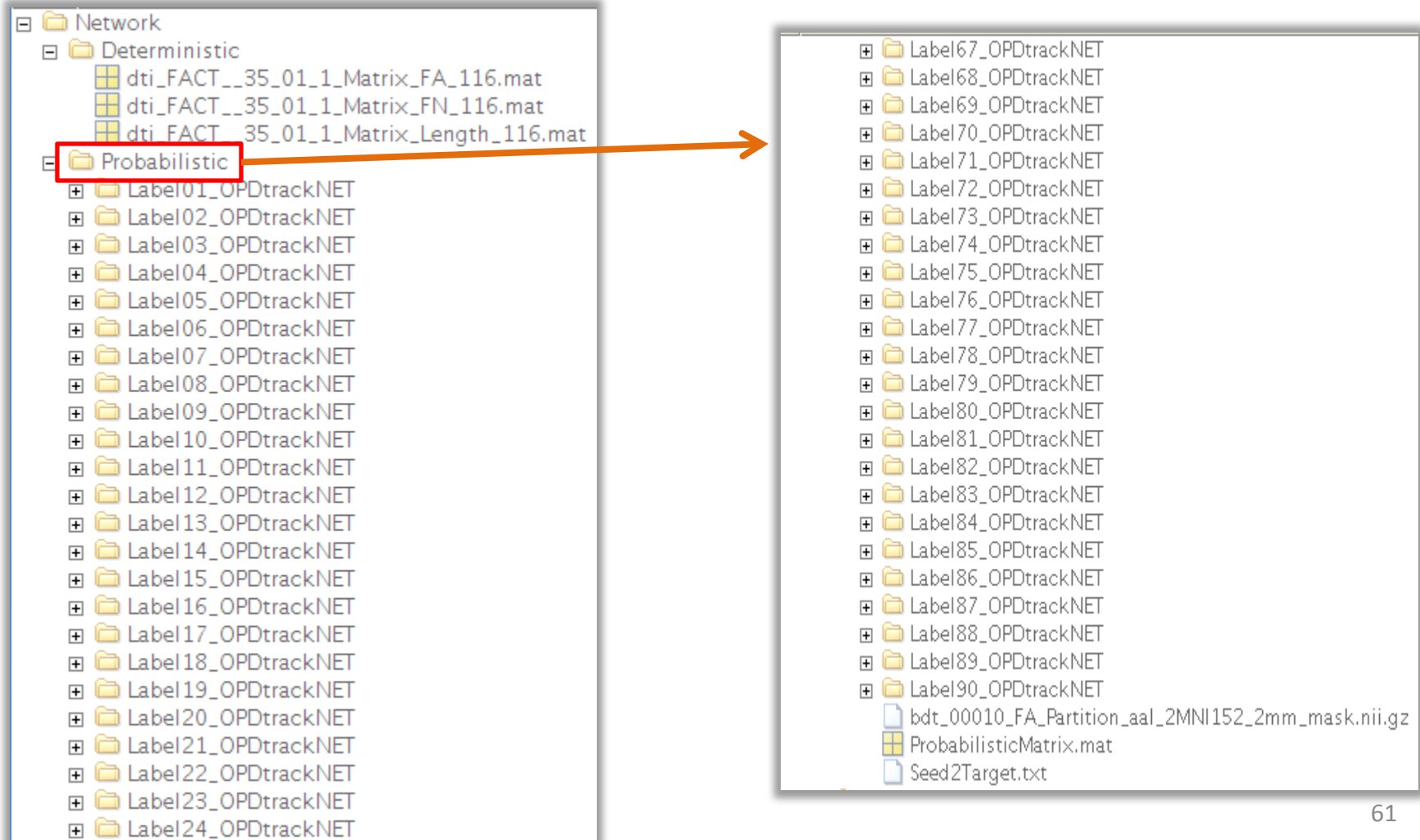
Understanding resultant files

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

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

Utilities
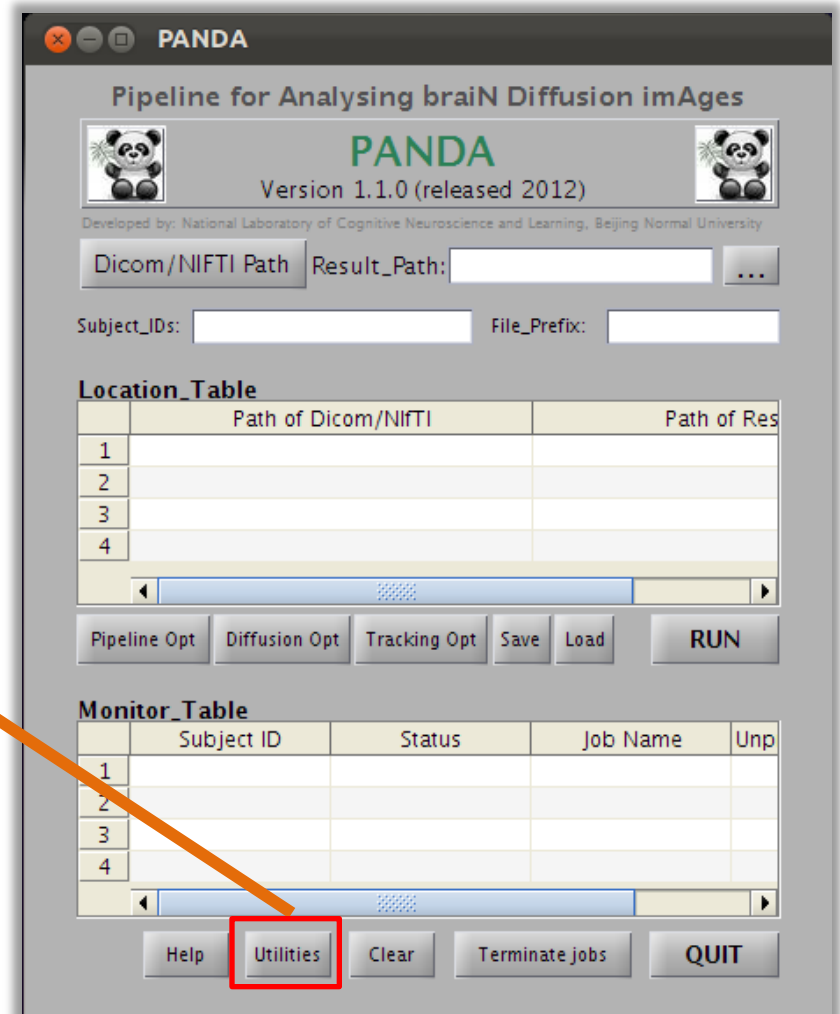
Utilities (TBSS)

➢Run TBSS for a group of subjects in parallel
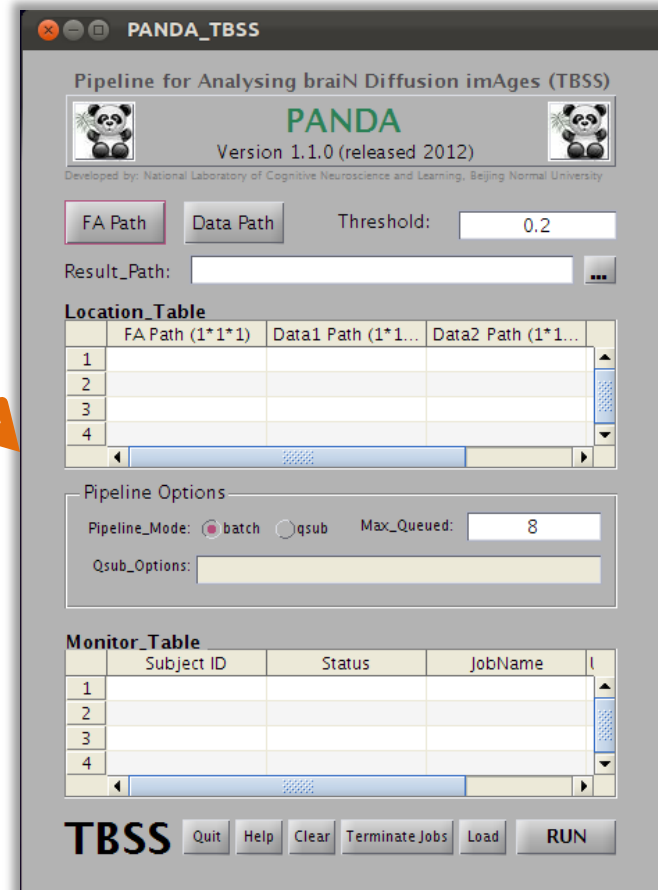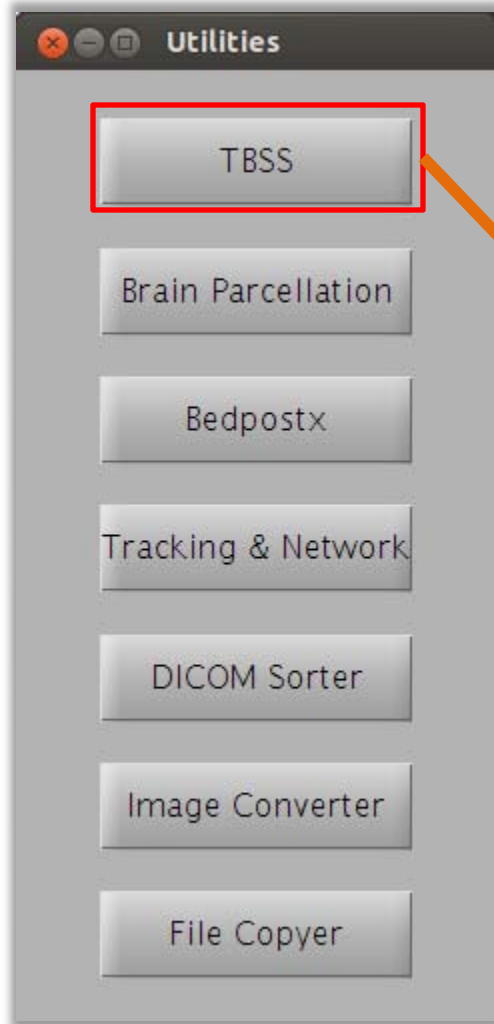
Utilities (TBSS)

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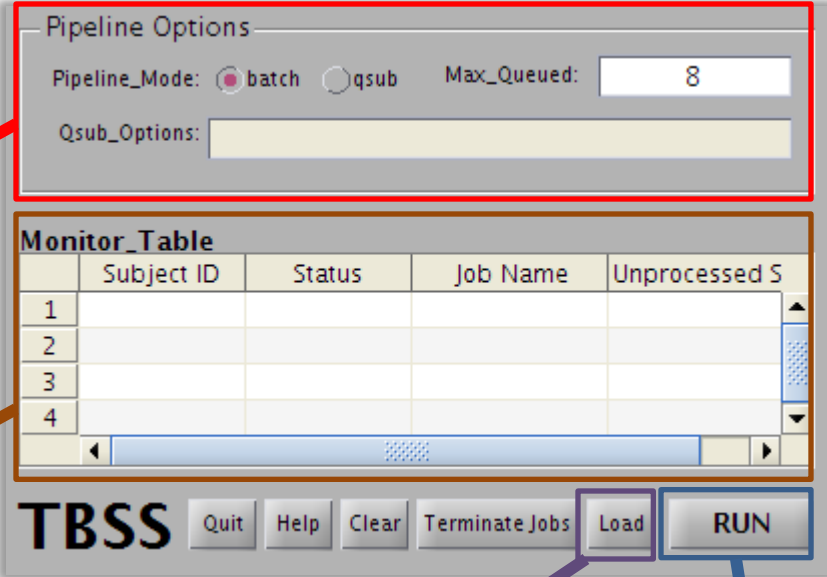
Threshold:
FA threshold to exclude
voxels in the grey matter
or CSF

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 forced to save after clicking 'RUN' button. (extension as **.PANDA_TBSS**)

Utilities (TBSS)

Set FA Path:

Utilities (TBSS)

Set Data1 Path:

Utilities (TBSS)

Set Data2 Path:

Utilities (TBSS)

Set Result Path:
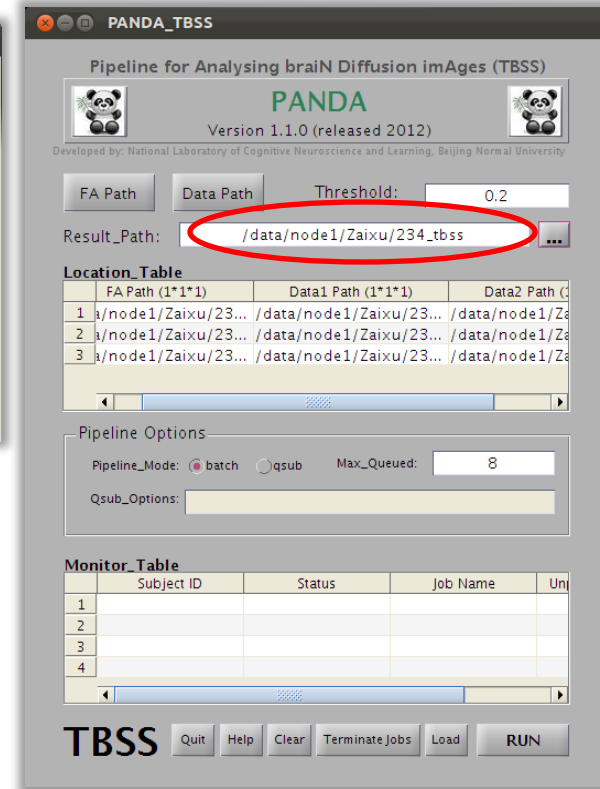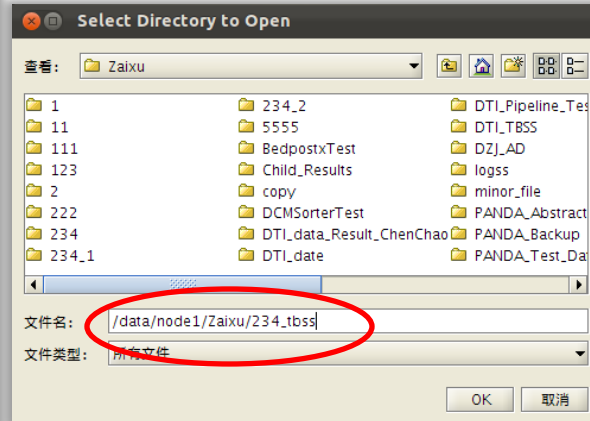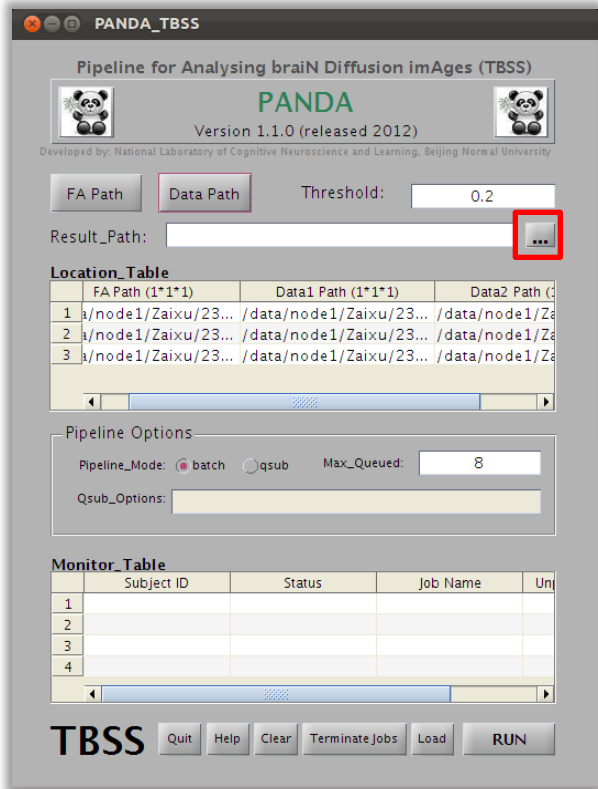
Utilities (TBSS)

Initiating Process:
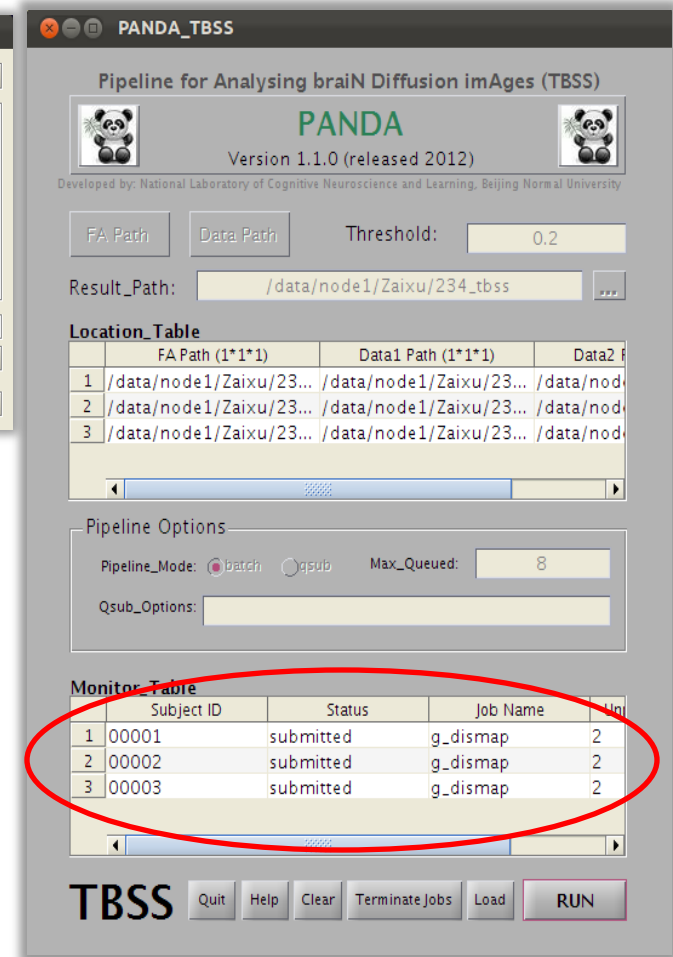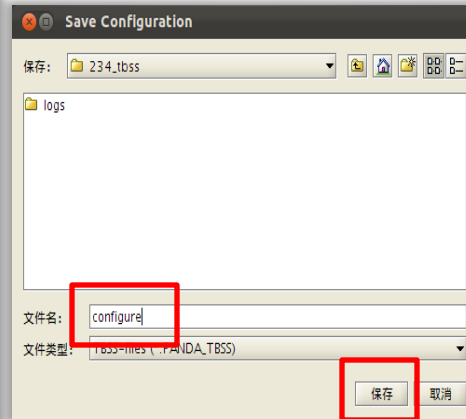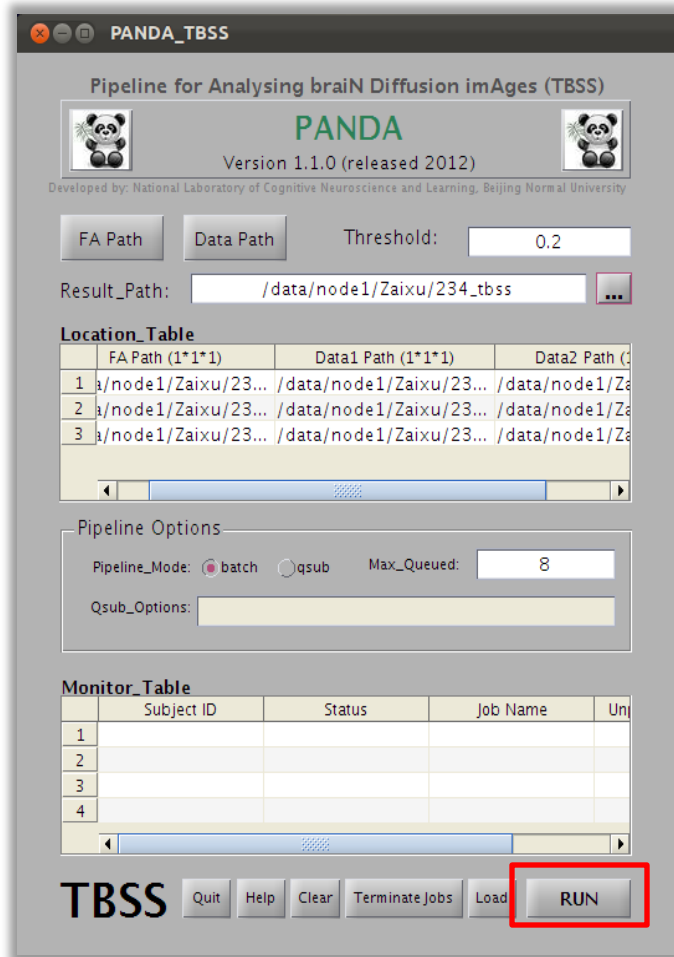
Utilities (TBSS)

Resultant Files:
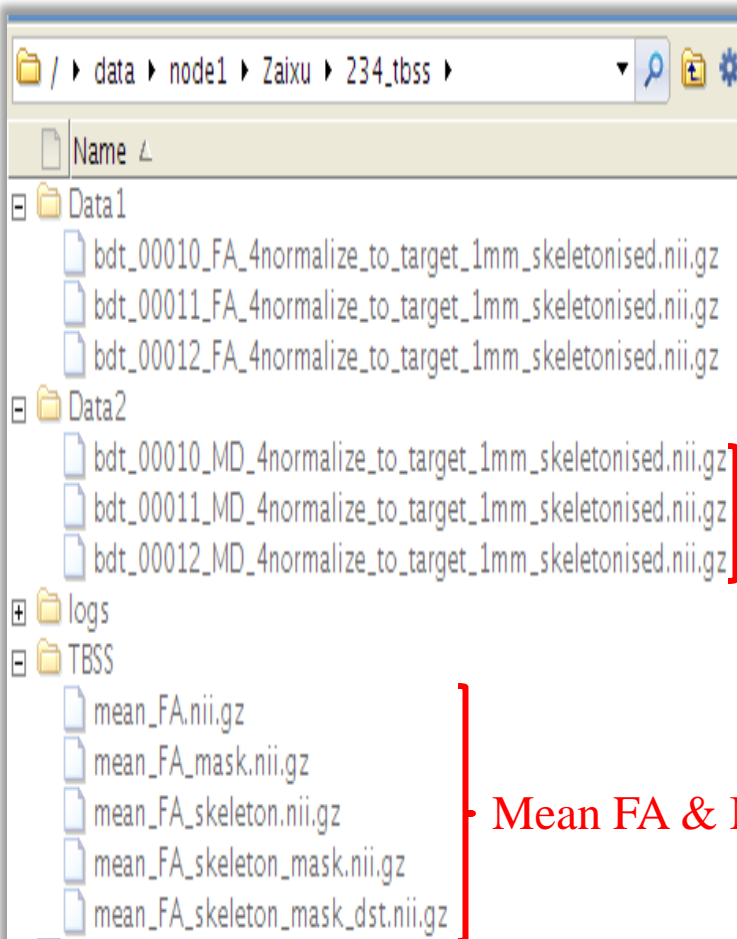
➢ First: mean FA and mean FA skeleton will be produced in 'TBSS' folder .

➢ 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)
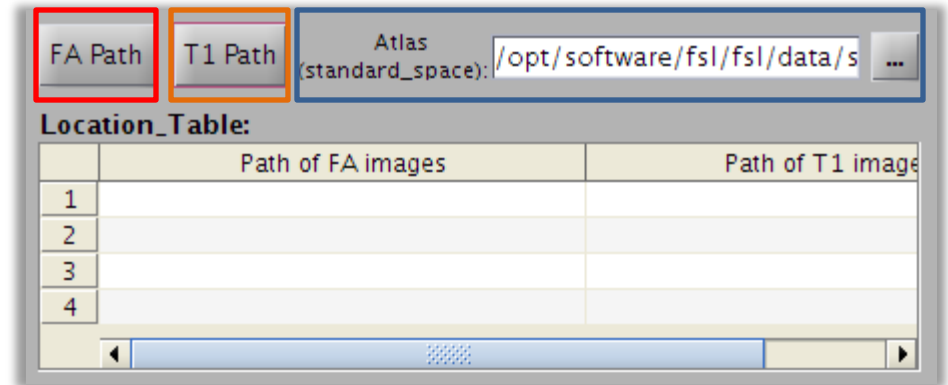
➢Run brain parcellation according to atlas for any number of subjects in parallel
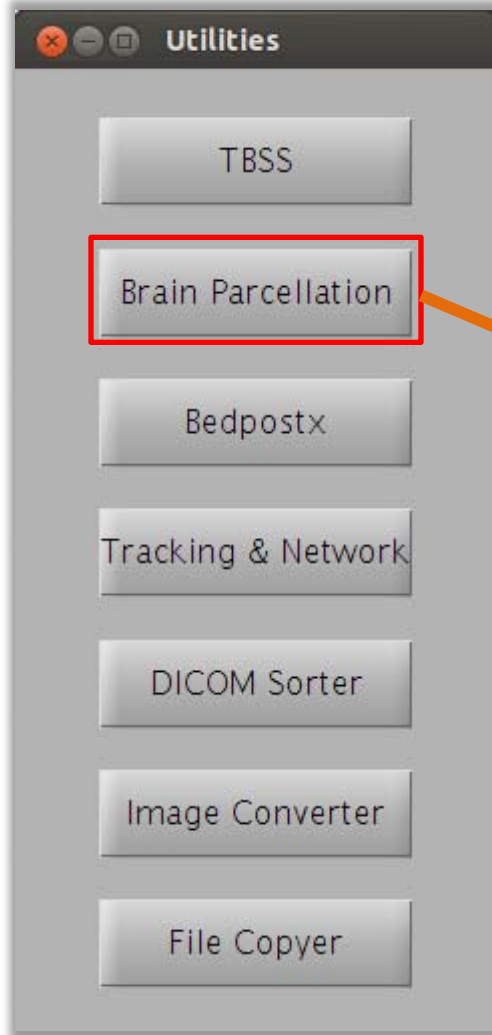
Utilities (Brain Parcellation)

FA Path:
full path of subjects' FA images

T1 Path:
full path of subjects' T1 images

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)

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:

Utilities (Brain Parcellation)

Set T1 Path:

Utilities (Brain Parcellation)

Initiating Process:
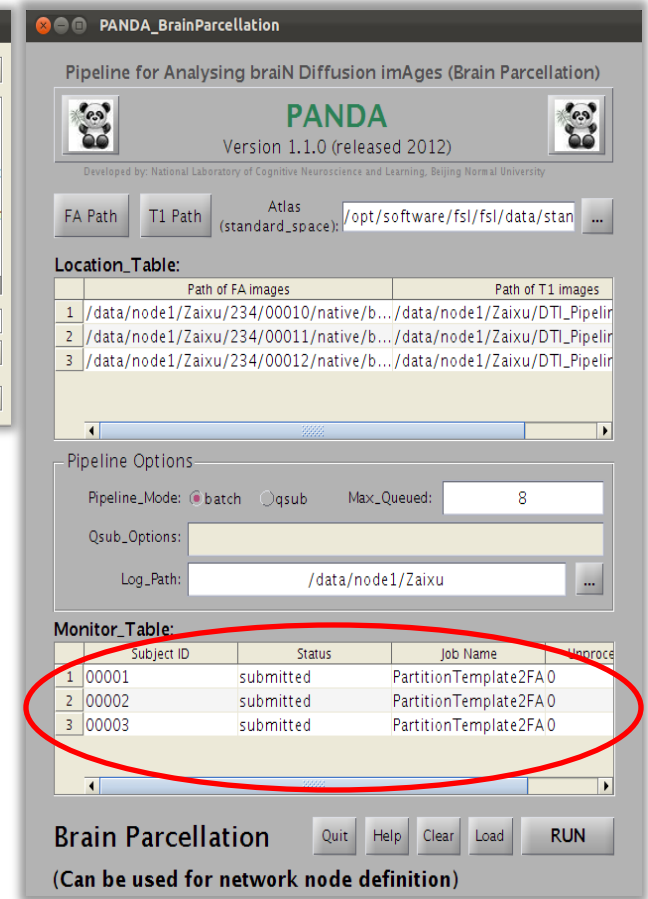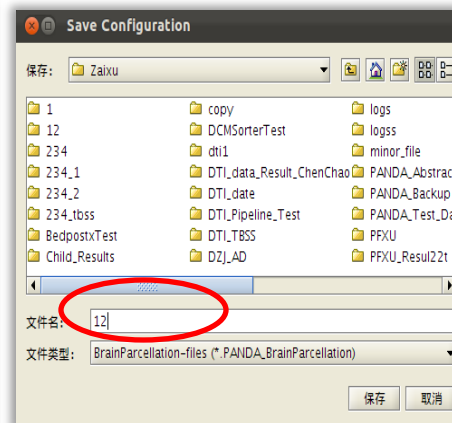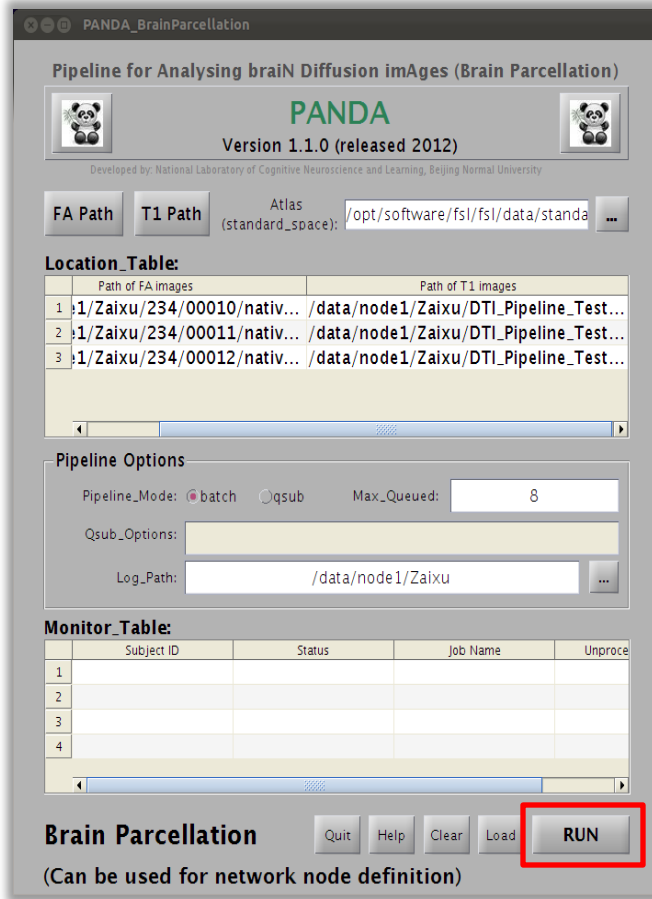
Utilities (Brain Parcellation)

Resultant Files:

Parcellated image for subject 00010
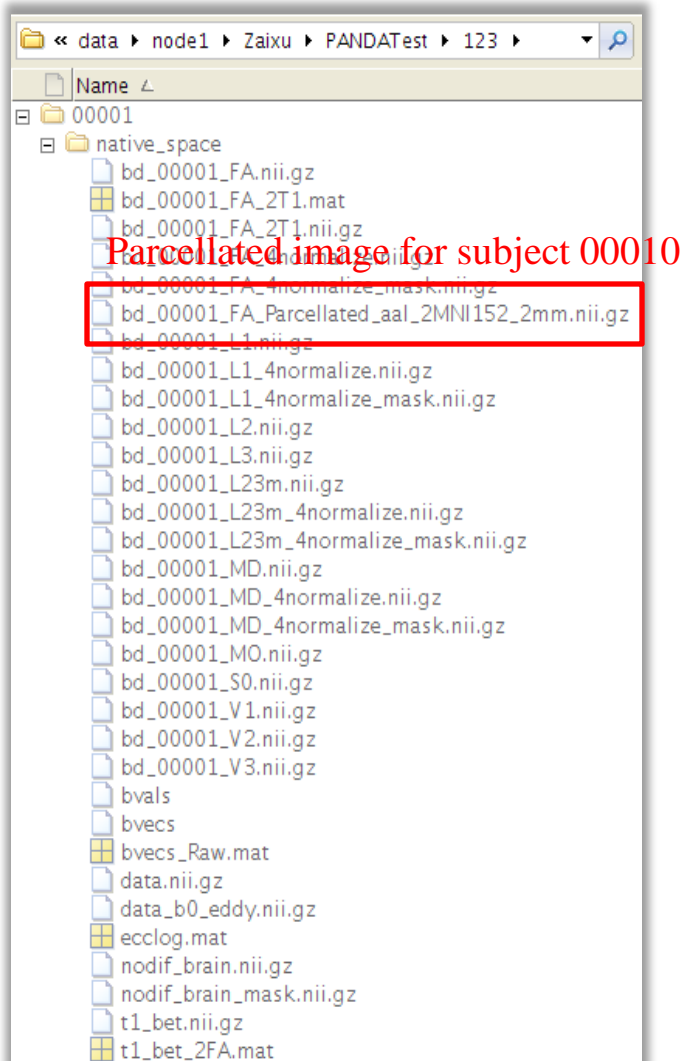
> A file named '*_Parcellated_*.nii.gz ' will be produced in the same folder of FA.

> 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
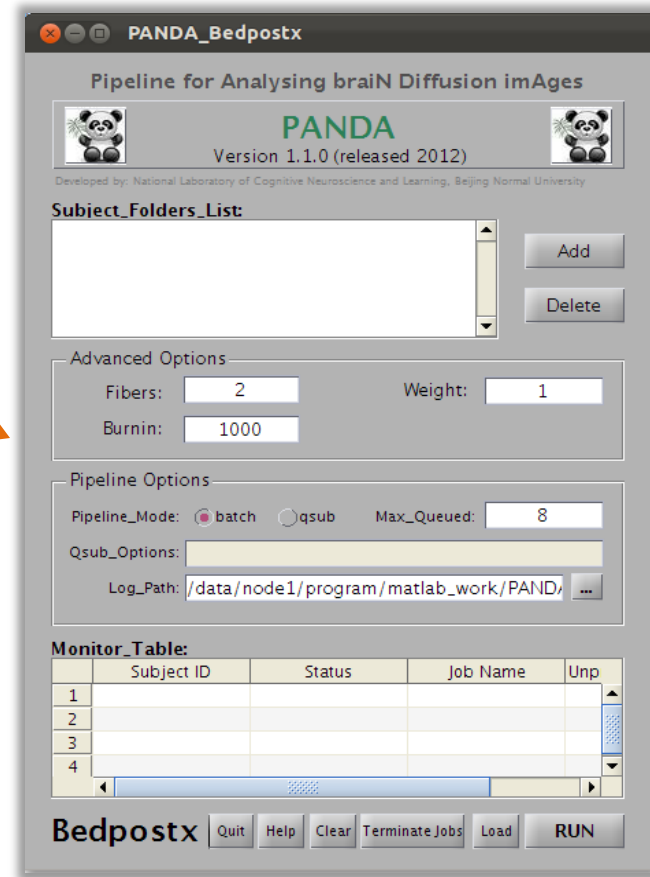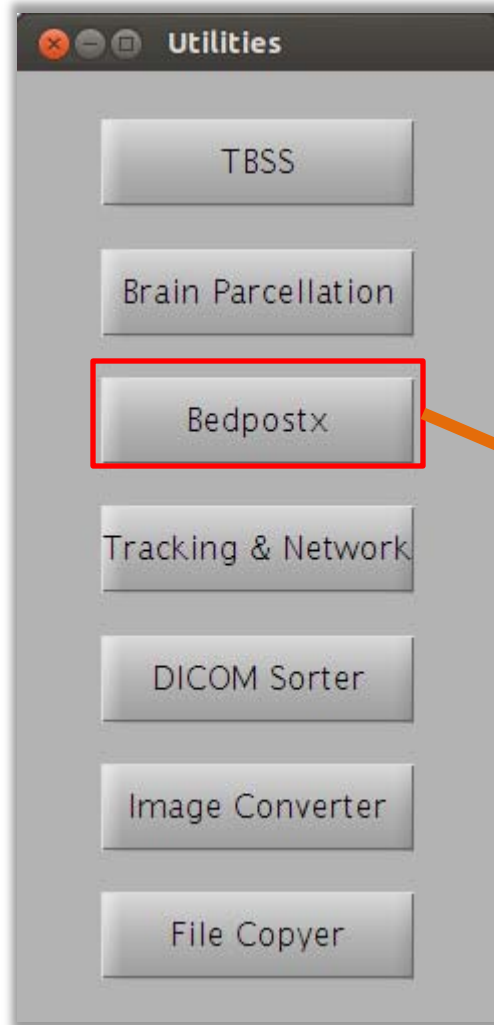　　　　/data/node1/Zaixu/234/00011/native/
bd_00011_FA_Parcellated_*.nii.gz
　　　　/data/node1/Zaixu/234/00012/native/
bd_00012_FA_Parcellated_*.nii.gz

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

Burnin:
Burnin period, default 1000

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

Subject_Folders_List:

Add

Delete

Advanced Options
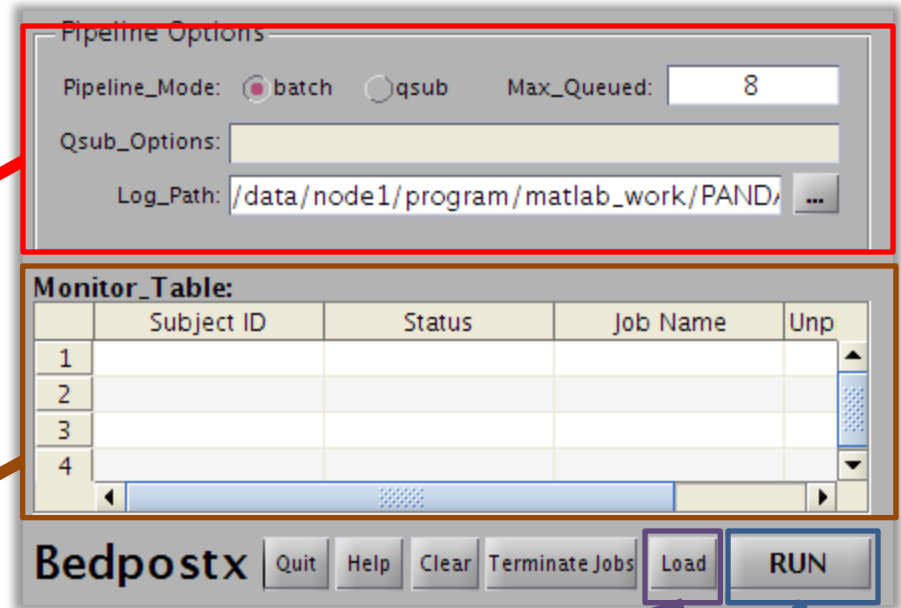
Fibers: 2

Weight: 1

Burnin: 1000

Utilities (BedpostX)
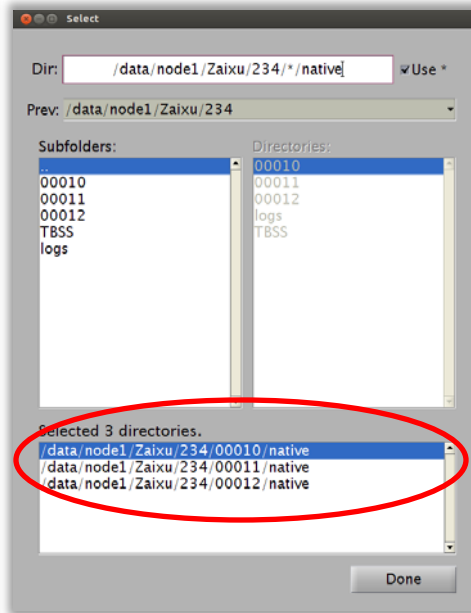

Referring to: <u>Pipeline_Opt</u>

Referring to: <u>Monitoring Progress</u>

Loading the ***.PANDA _BedpostX** file

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

Utilities (BedpostX)

Input subjects' folder:

Utilities (BedpostX)

Initiating Process:

Utilities (BedpostX)

Resultant Files:
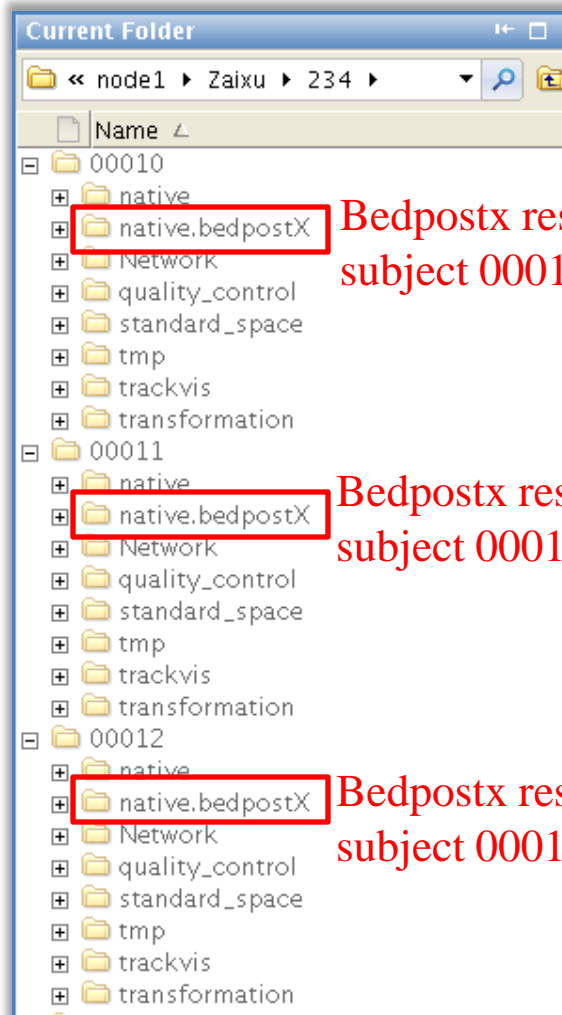
Bedpostx result for subject 00010

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
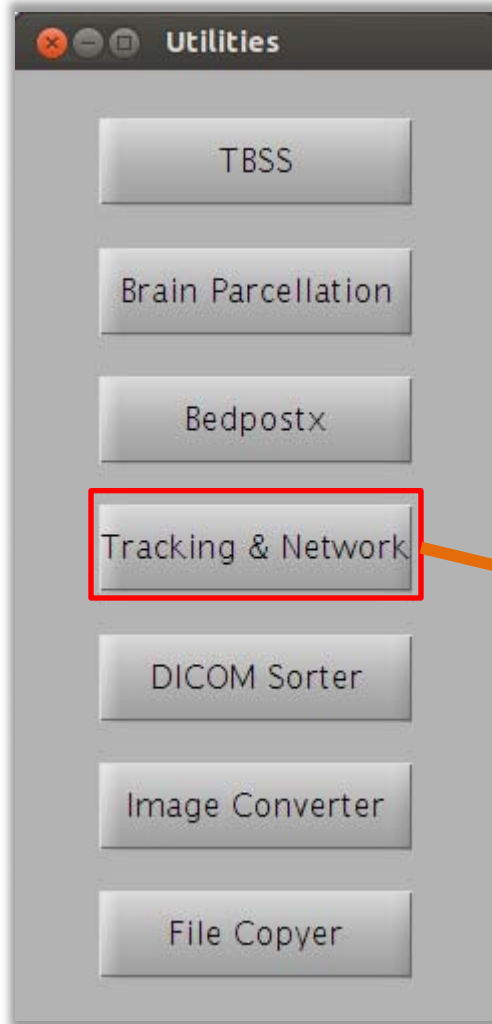
Utilities (Tracking & Network)

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, bvals, mask and 4D data

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
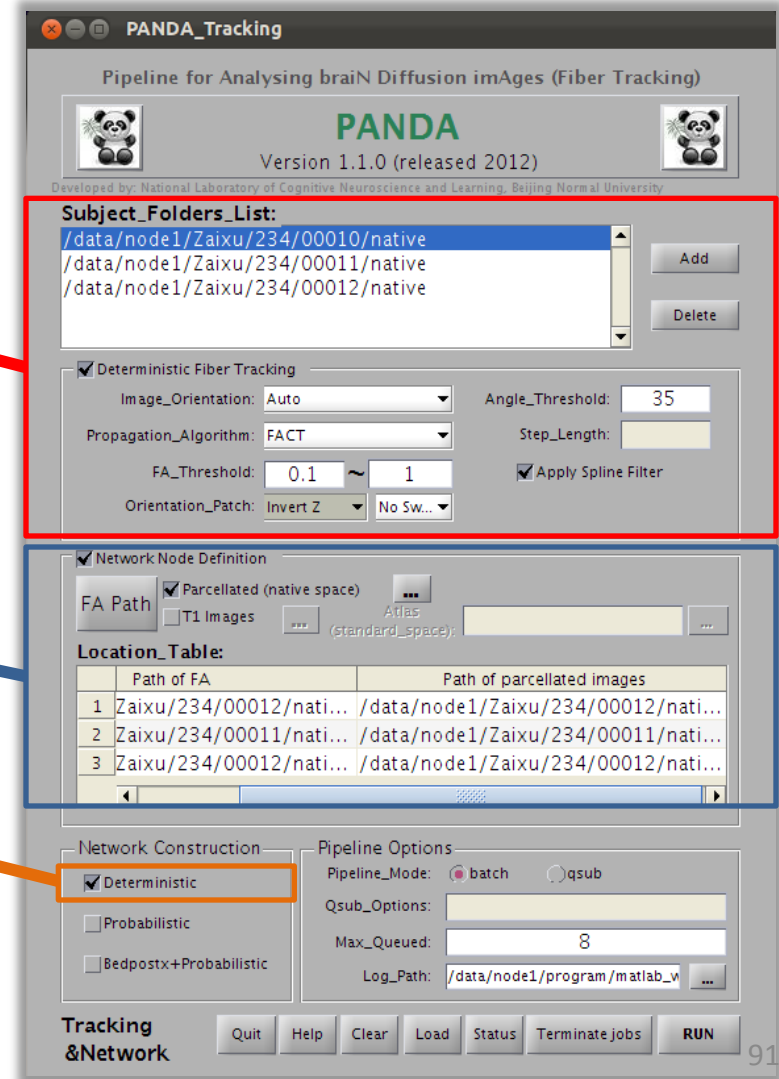
Utilities (Tracking & Network)

Network Node Definition

First, please click 'FA Path' button to input subjects' FA paths
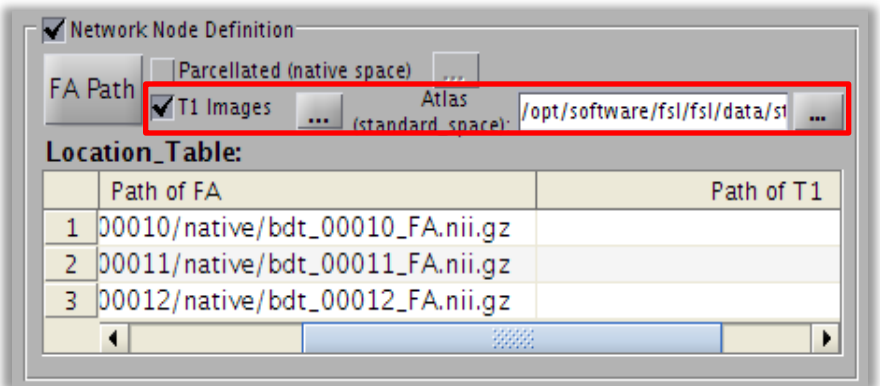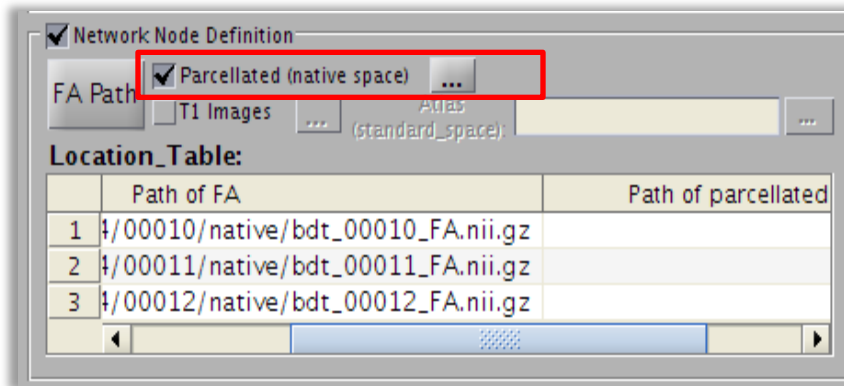
When you have parcellated images in native space :
Please select 'Parcellated (native space) ' and input these images

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
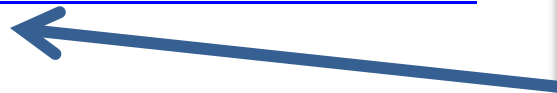
Third step: select Probabilistic Network
Construction
Referring to Next Page
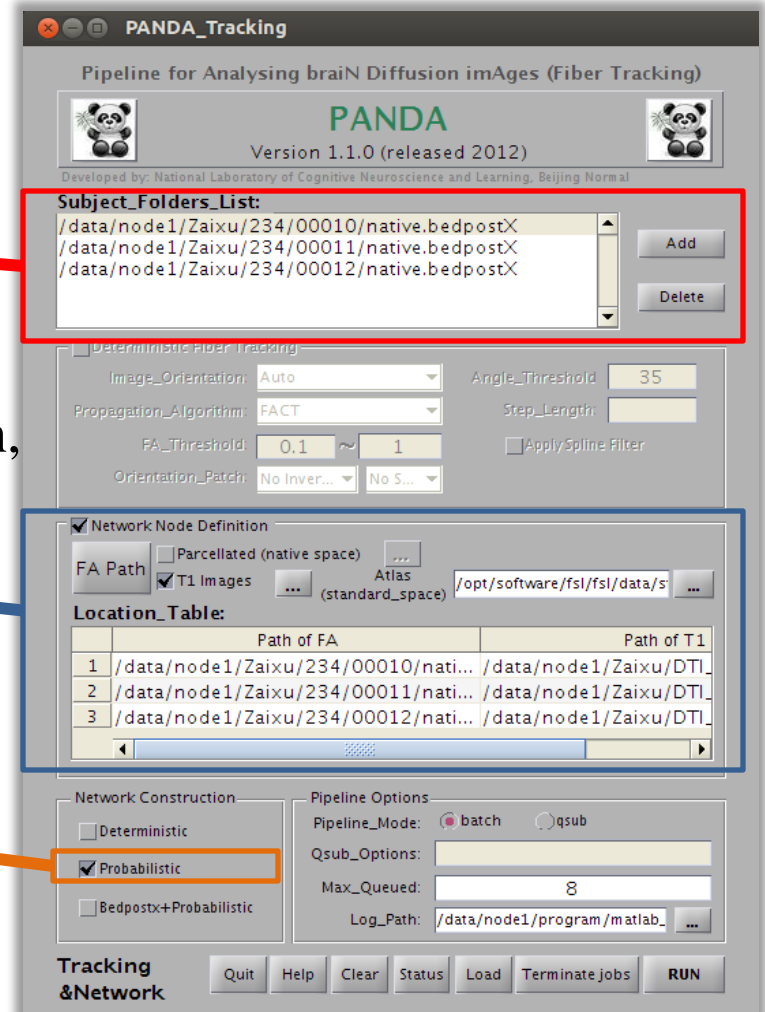
Utilities (Tracking & Network)

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)

BedpoxtX+Probabilistic Fiber Tracking & Network Construction

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

Second step: select Network Node Definition,
  Referring to: Network Node Definition
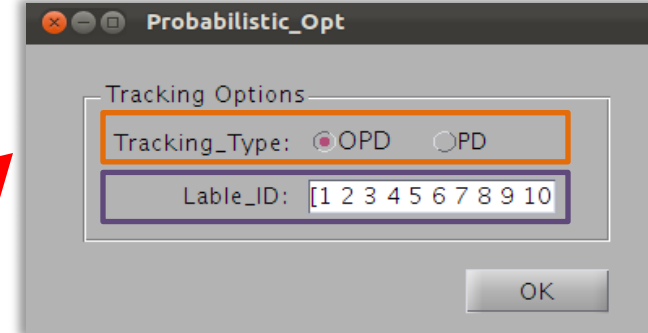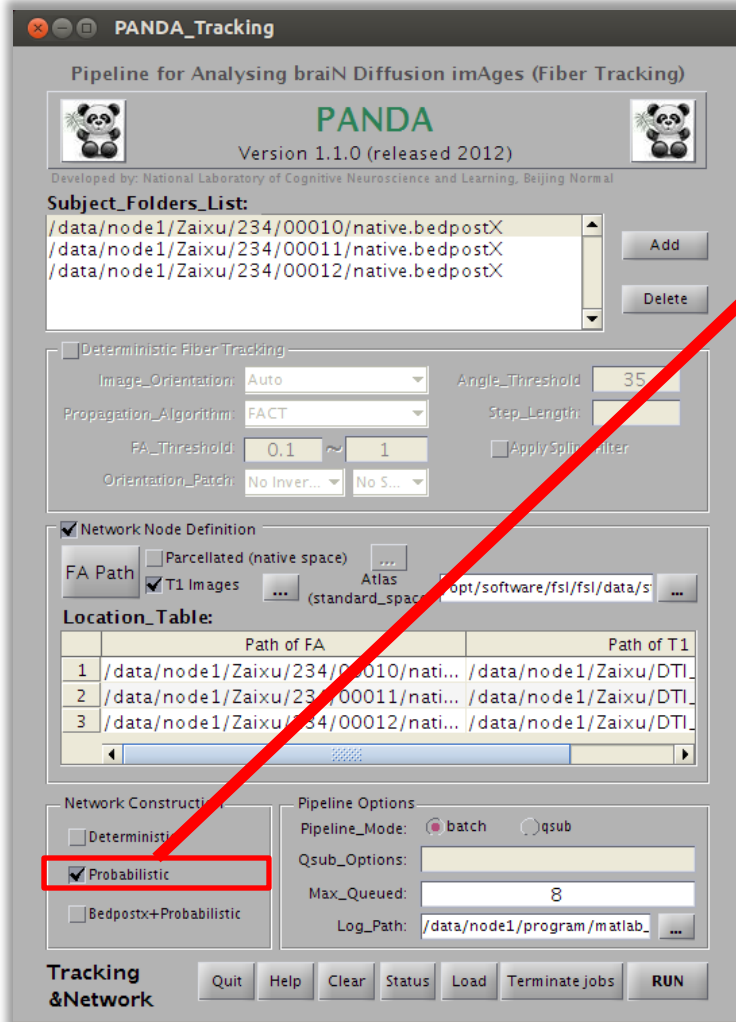
Third step: select Bedpostx+Probabilistic
  Network Construction
  Referring to Next Page
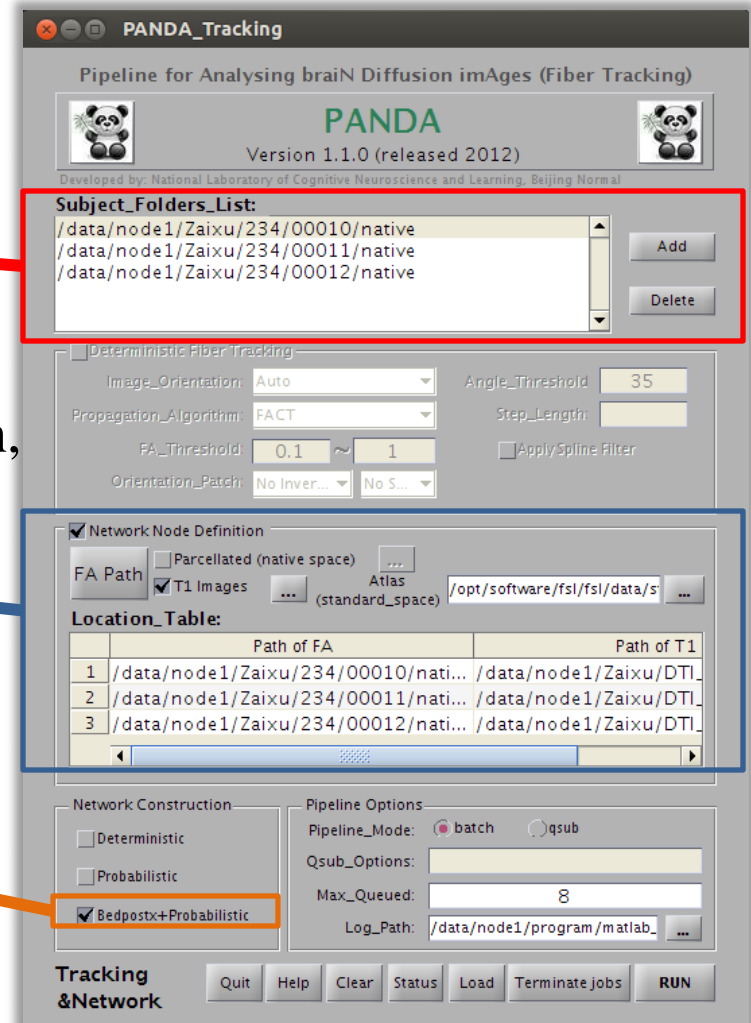
Utilities (Tracking & Network)

BedpoxtX+Probabilistic Fiber Tracking & Network Construction
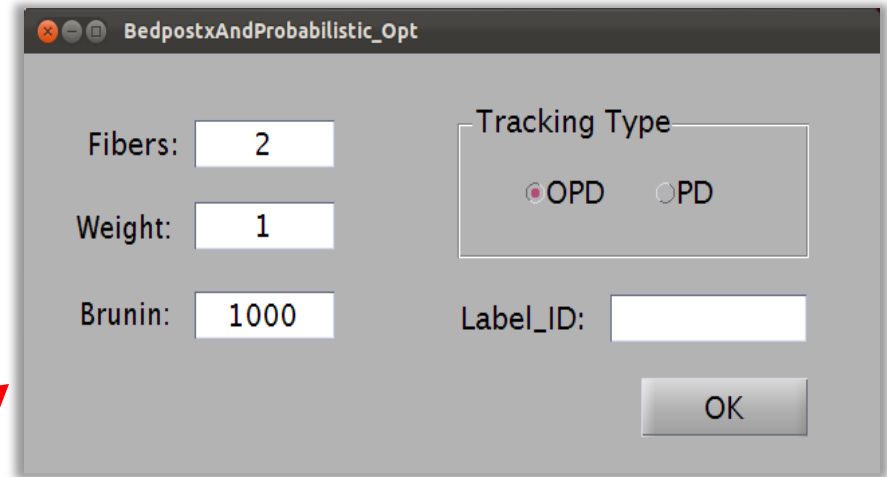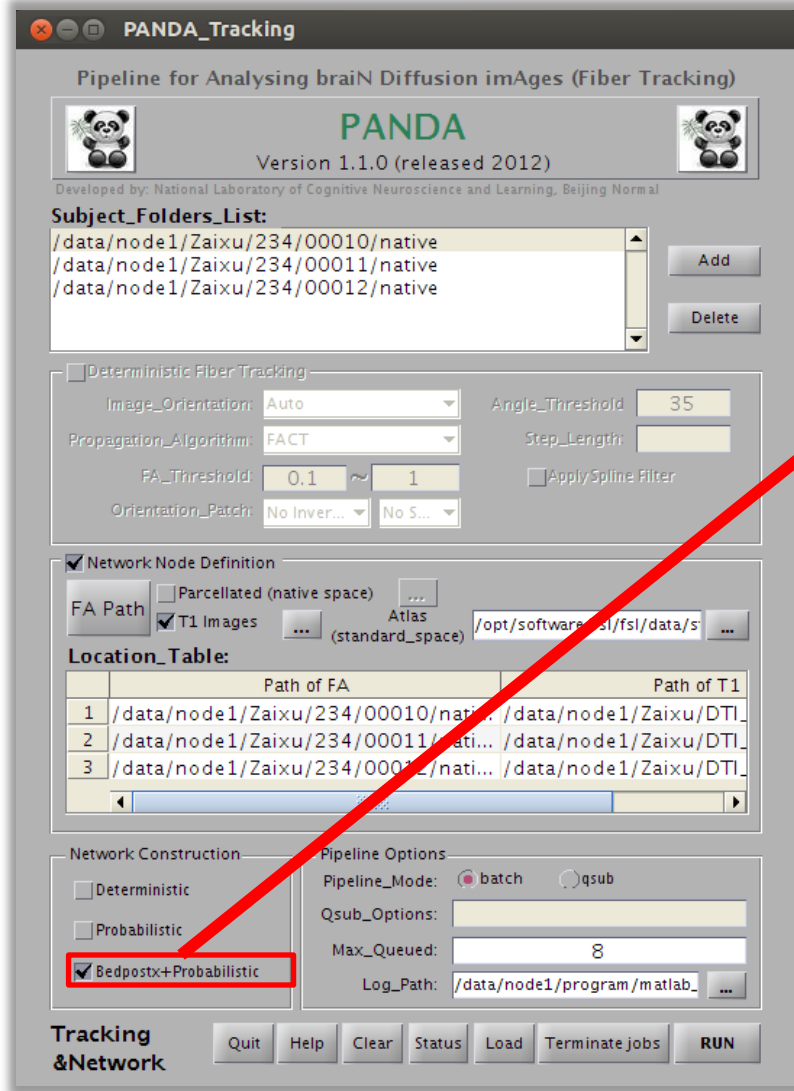
Referring to: Network Node Definition

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):

Current Folder

« node1 ▸ Zaixu ▸ 234 ▸

Name

- 00010
  - native
  - native.bedpostX
  - Network
  - quality_control — *Deterministic fiber tracking result for subject 00010*
  - standard_space
  - tmp
  - trackvis
  - transformation
- 00011
  - native
  - native.bedpostX
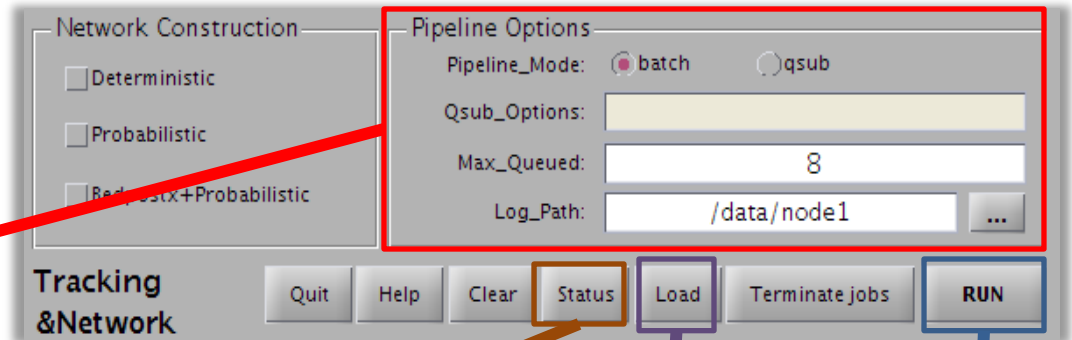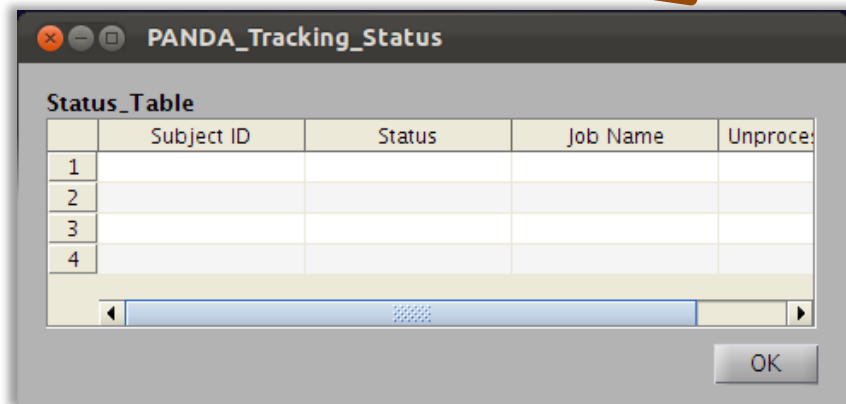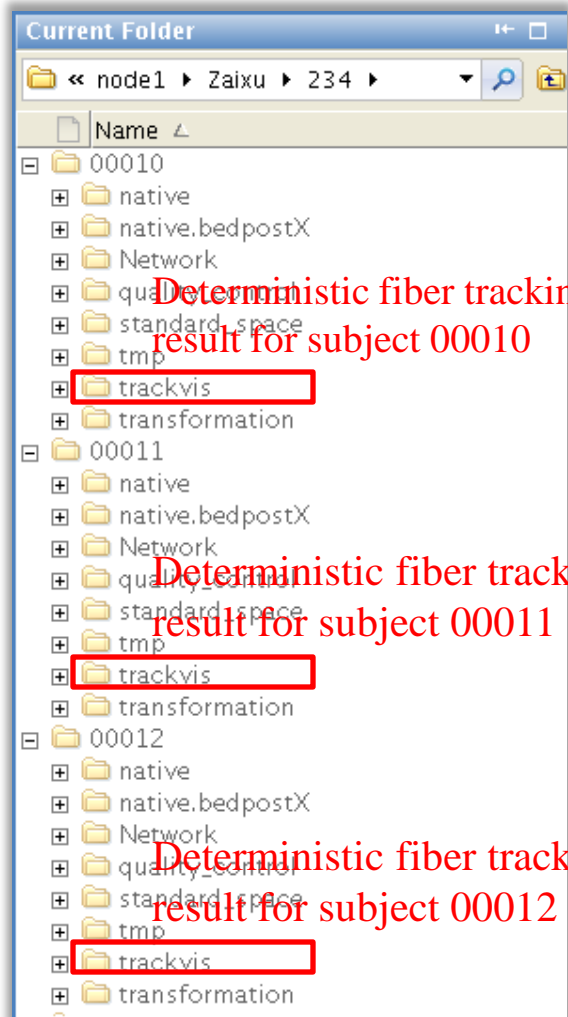 - Network
  - quality_control — *Deterministic fiber tracking result for subject 00011*
  - standard_space
  - tmp
  - trackvis
  - transformation
- 00012
  - native
  - native.bedpostX
  - Network
  - quality_control — *Deterministic fiber tracking result for subject 00012*
  - standard_space
  - tmp
  - trackvis
  - transformation

➢ 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
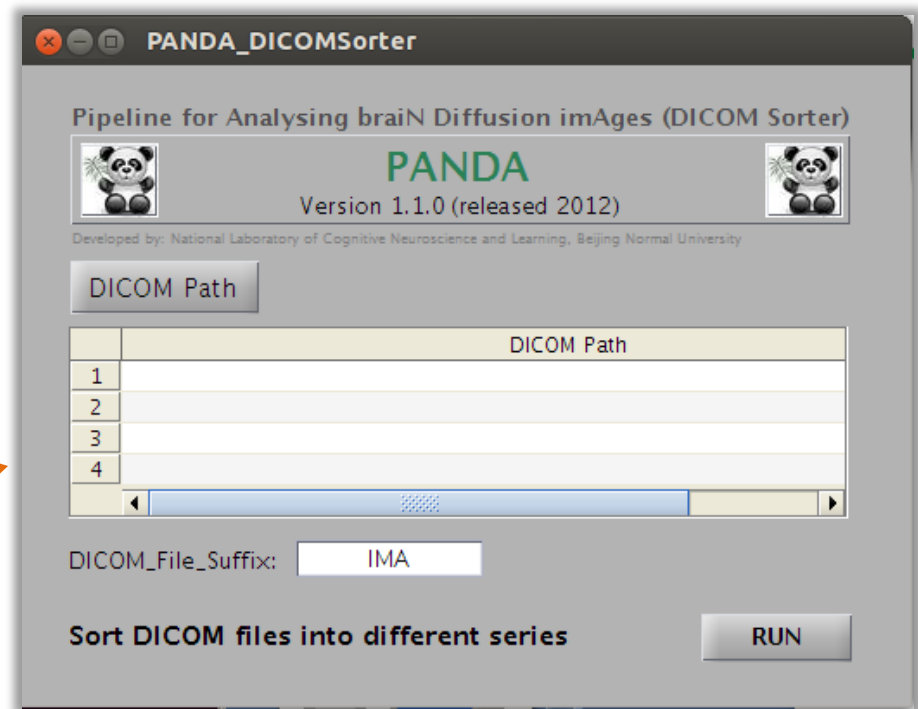/data/node1/Zaixu/234/00012/native

Outputs are

/data/node1/Zaixu/234/00010/Network/Probabilistic
/data/node1/Zaixu/234/00011/Network/Probabilistic
/data/node1/Zaixu/234/00012/Network/Probabilistic
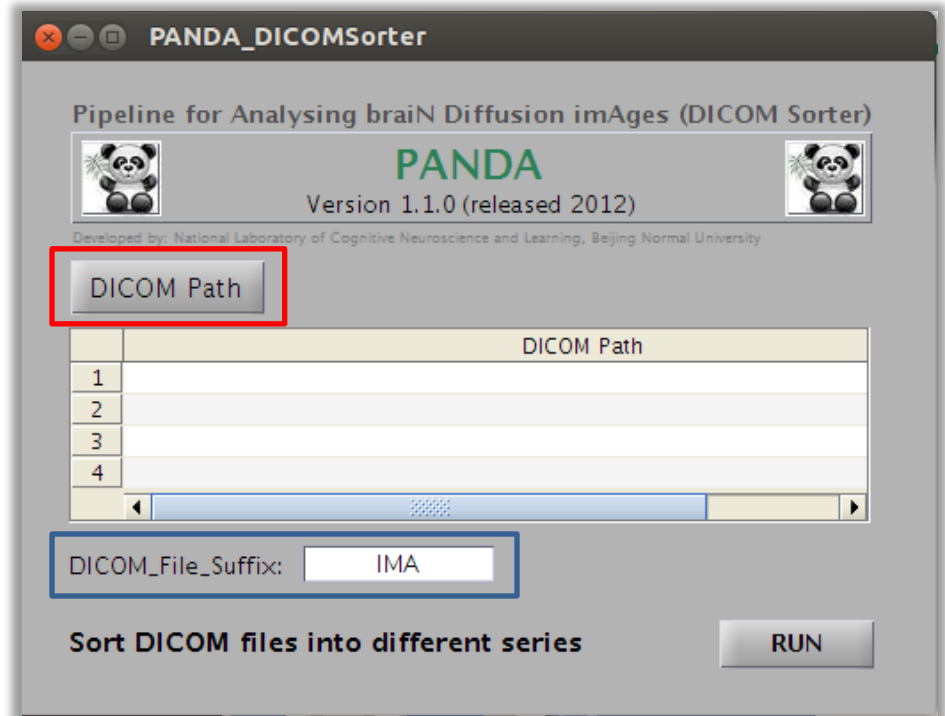
Utilities (DICOM Sorter)

➢ 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

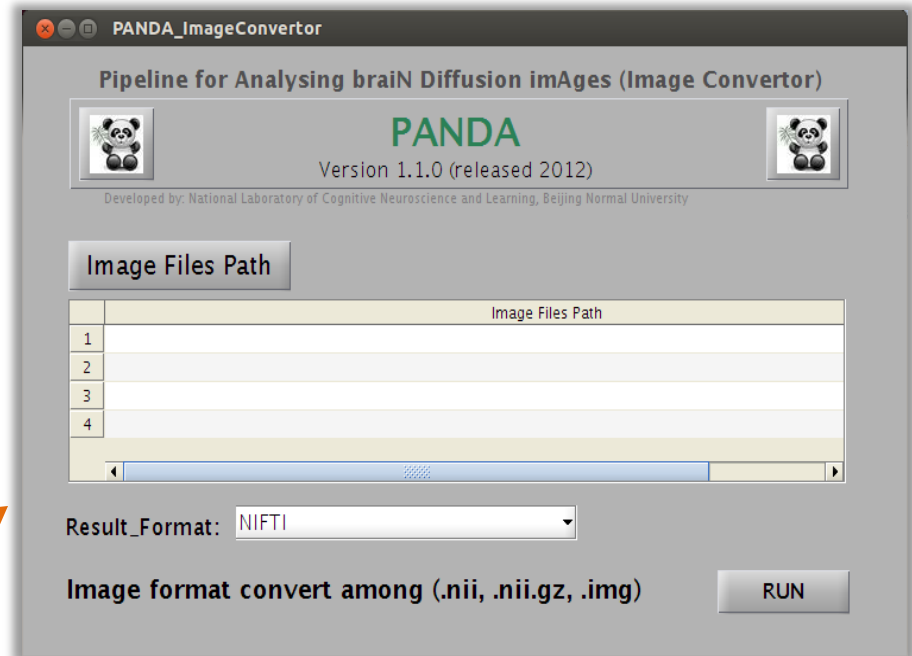DICOM File Suffix:
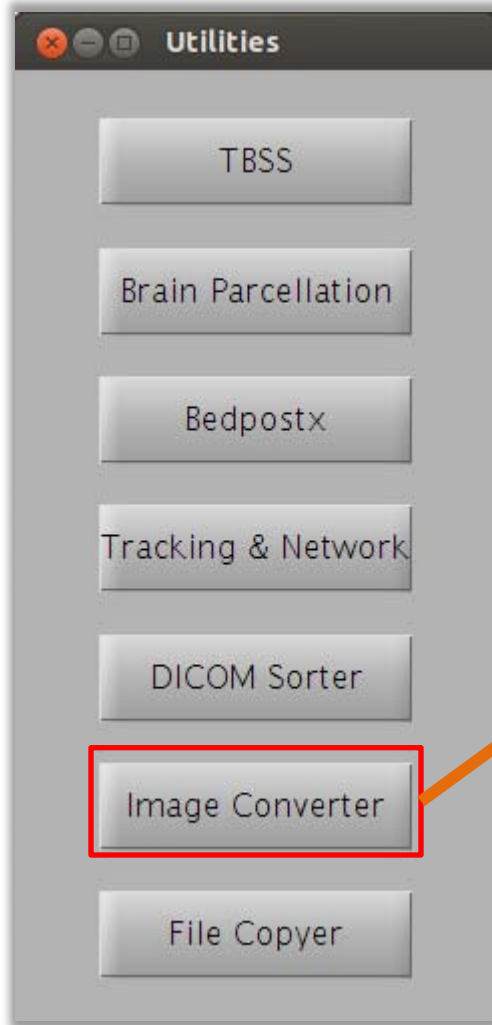The extension of DICOM file name

➢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.

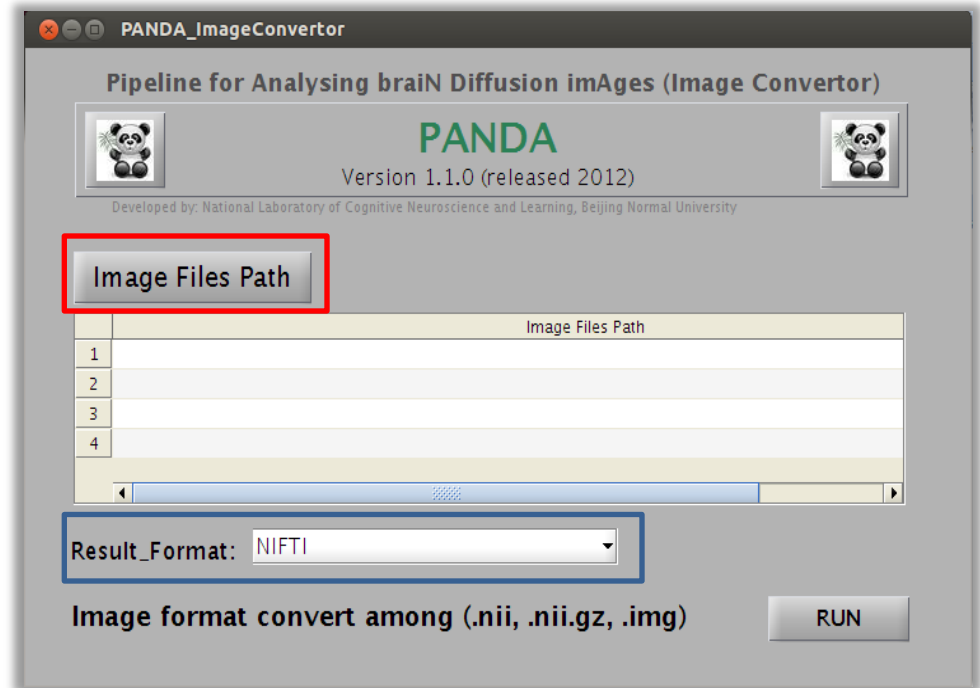# Utilities (DICOM Sorter)
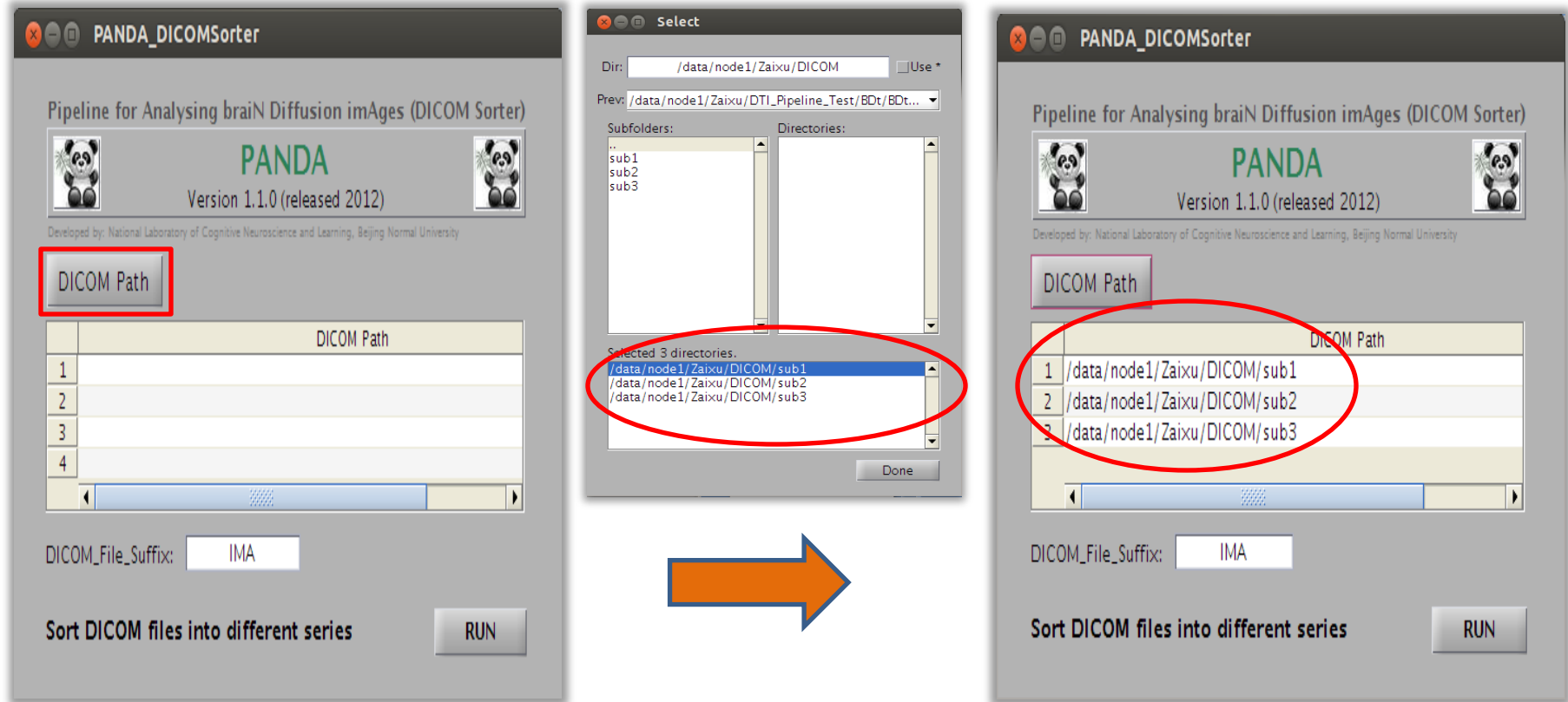
Utilities (Image Converter)

➢ Convert image format among (.nii, .nii.gz, .img)
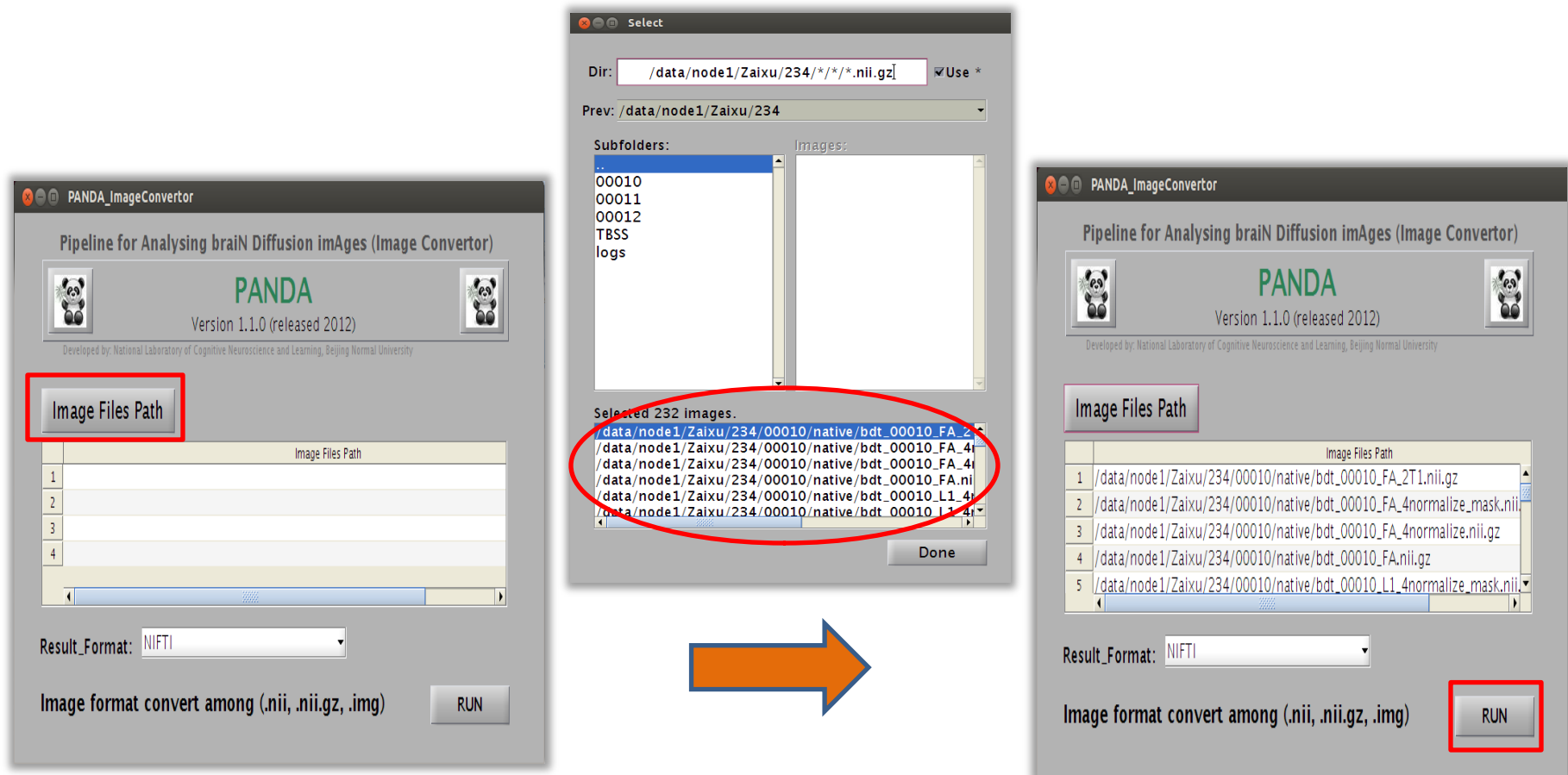
Utilities (Image Converter)

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

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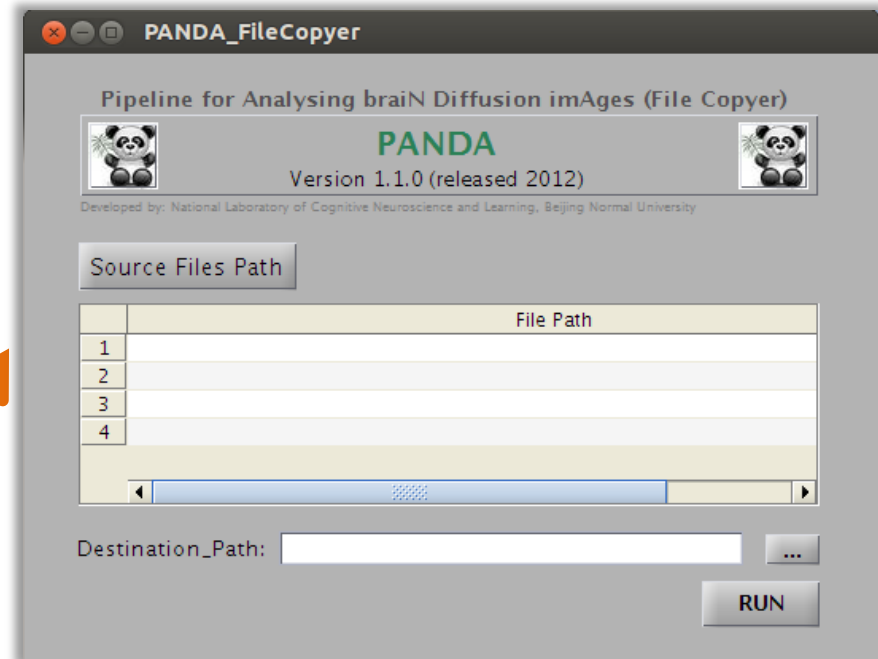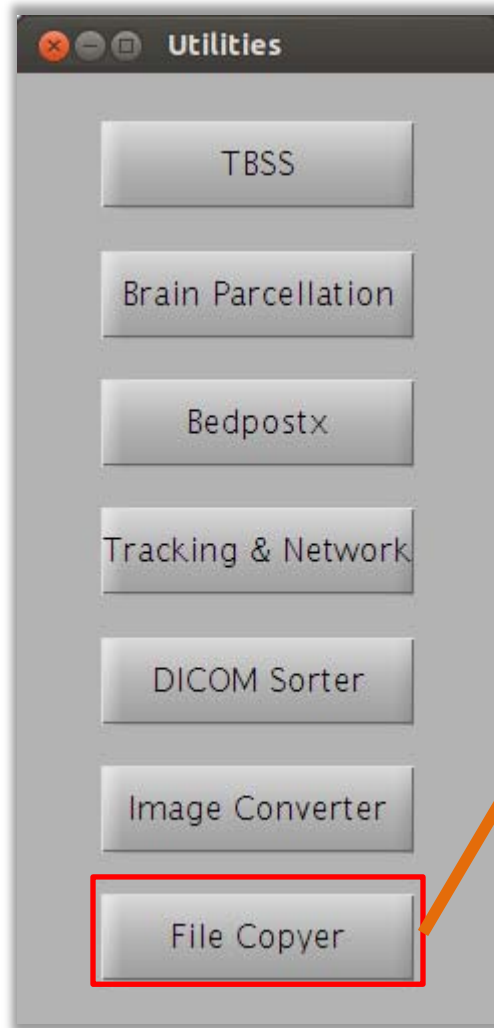NIFTI_GZ, NIFTI_PAIR)

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

Utilities (Image Converter)
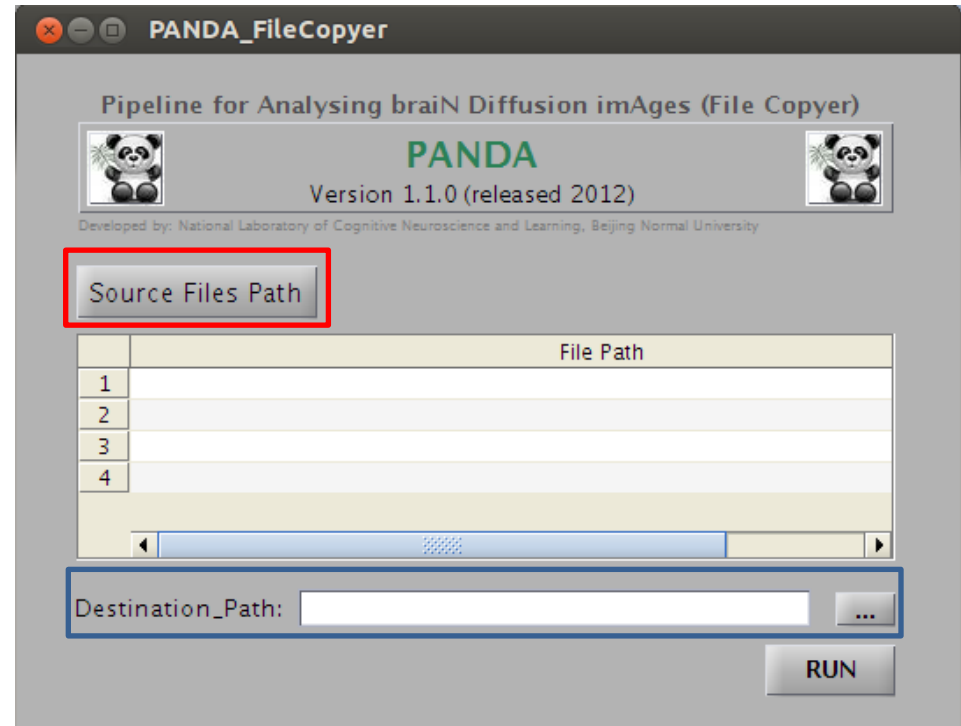
Utilities (File Copyer)
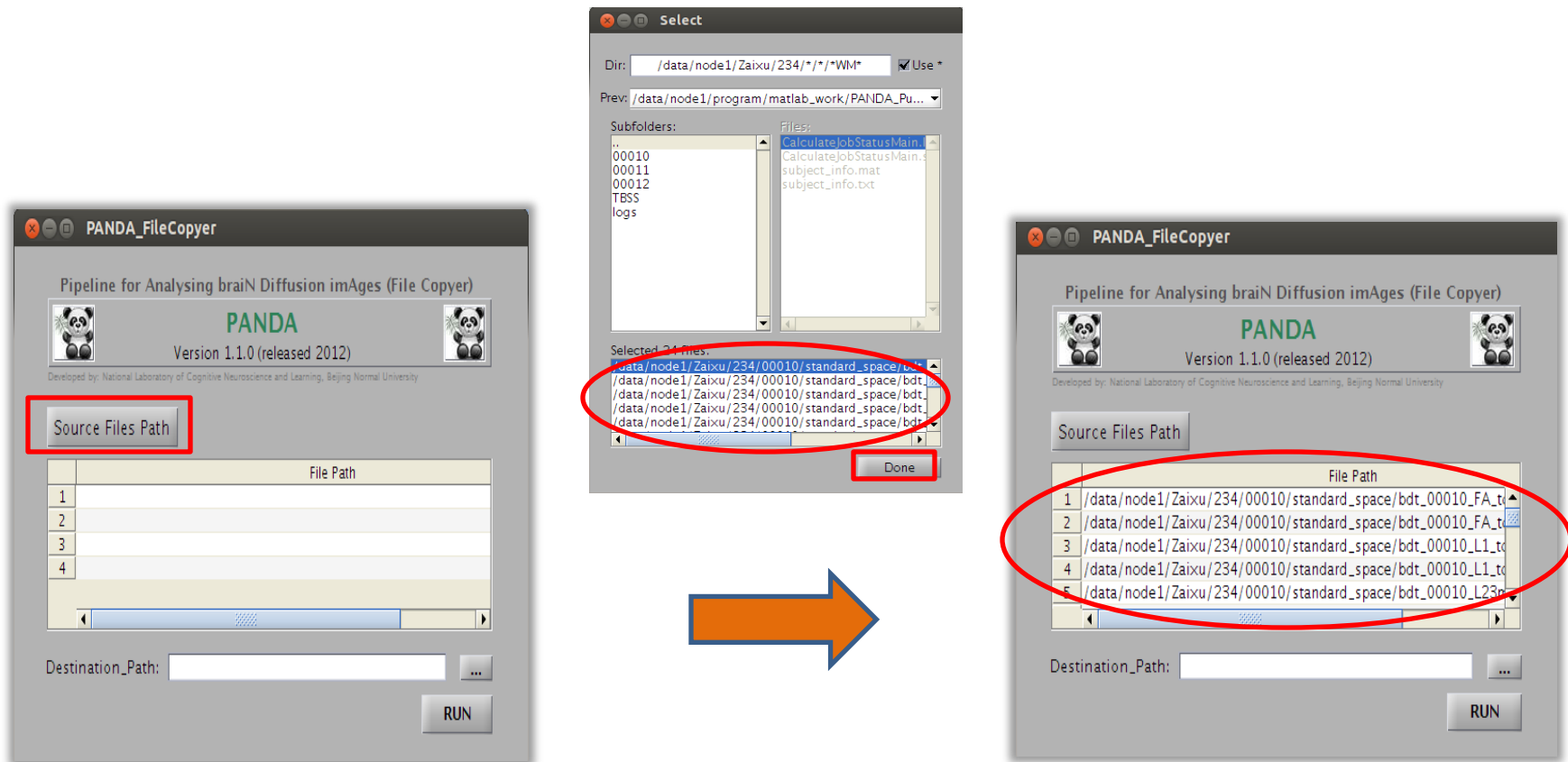
➢ Copy files to the destination path

Utilities (File Copyer)

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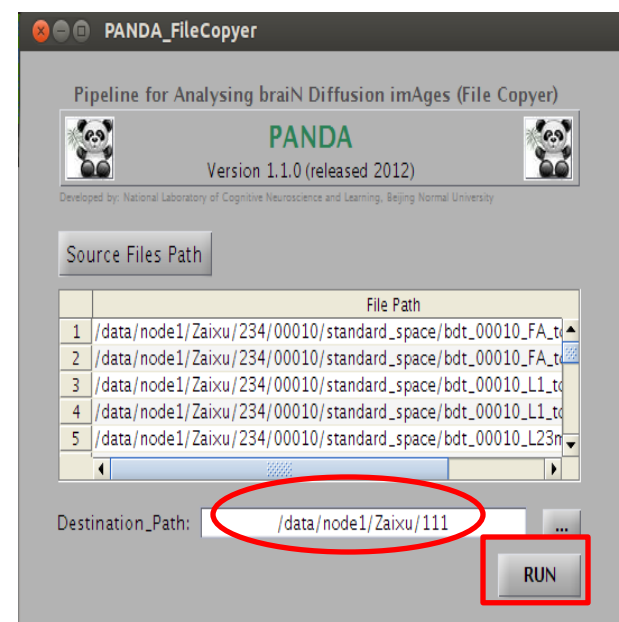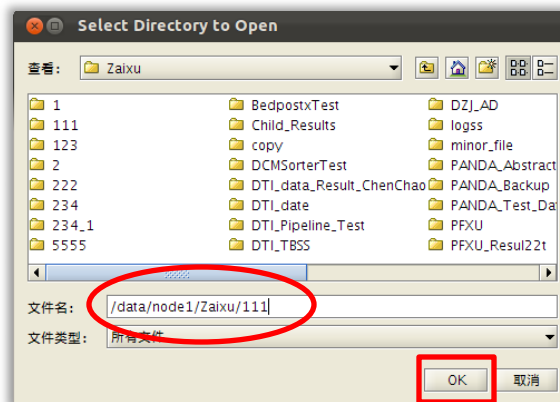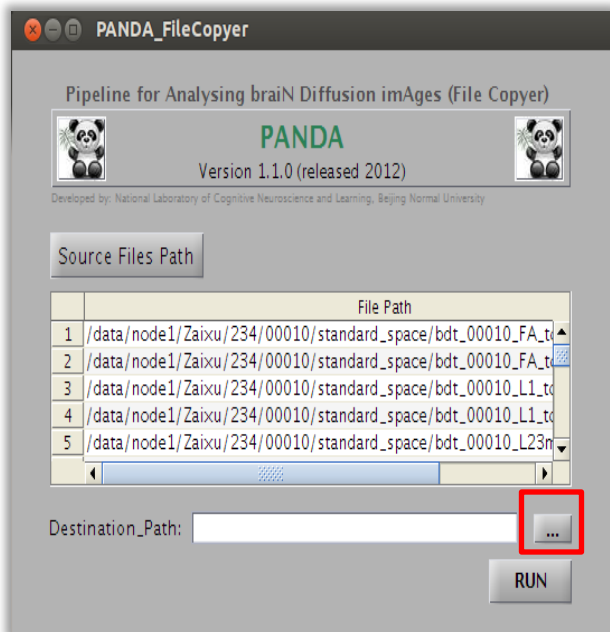full path of files users
want to copy

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:

Zaixu Cui: zaixucui@gmail.com

Suyu Zhong: suyu.zhong@gmail.com

Gaolang Gong (PI): gaolang.gong@gmail.com

Thanks !