

# UFA toolbox tutorial

Gaoxing Zheng

20111210009@fudan.edu.cn

Department of Neurology, Zhongshan Hospital, Fudan University

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# **Part I**

Basic software and hardware installation in Ubuntu system

Table 1 | Software and Hardware configurations required for the accelerate calculation.

Release version	Website	Version number	Categories
Ubuntu	<a href="https://releases.ubuntu.com/20.04/">https://releases.ubuntu.com/20.04/</a>	20.04.4	Operating System
GPU	/	GeForce RTX 3080 Ti	Accelerate hardware
PYTHON	<a href="https://www.python.org/">https://www.python.org/</a>	3.8.12	Programming Platform
MATLAB	<a href="https://matlab.mathworks.com/">https://matlab.mathworks.com/</a>	R2019b	Programming Platform
CUDA	<a href="https://developer.nvidia.com/cuda-downloads">https://developer.nvidia.com/cuda-downloads</a>	v10.2.89	Accelerate module
NVIDIA Driver	<a href="https://www.nvidia.com/Download/index.aspx">https://www.nvidia.com/Download/index.aspx</a>	470.129.06	Accelerate module

## Install NVIDIA driver

### (1) Install NVIDIA Driver

Strategy 1 (failed in my Ubuntu 22.04 computer -- A proprietry driver has private code that ubuntu developers can't review or improve. Security and other updates are dependent on the driver vendor. Error while apply changes: pk-client-error-quark: could not do media change question as no klass support (8)):

Search ‘Software & Updates’ and find the ‘Additional Drivers’

Choose the ‘Using NVIDIA driver metapackage from nvidia-driver-470 (proprietary)’

Apply changes and wait for about half a hour to complete, then reboot the system.

Strategy 2:

```
#sudo add-apt-repository ppa:graphics-drivers/ppa  
#sudo apt update  
#apt list --upgradable  
#sudo apt upgrade  
#ubuntu-drivers devices  
#sudo apt install nvidia-driver-515 (or other version-520)
```

### (2) Check the installation:

```
#sudo nvidia-settings  
#nvidia-smi  
#ls /usr/src | grep nvidia
```

## Install CUDA toolkit

### (1) Install CUDA-Toolkit (CUDA Toolkit 11.7 Update 1 Downloads)

<https://developer.nvidia.com/cuda-toolkit-archive>

```
#wget https://developer.download.nvidia.com/compute/cuda/repos/ubuntu2204/x86_64/cuda-ubuntu2204.pin  
#sudo mv cuda-ubuntu2204.pin /etc/apt/preferences.d/cuda-repository-pin-600  
#wget https://developer.download.nvidia.com/compute/cuda/11.7.1/local_installers/cuda-repo-ubuntu2204-11-7-local_11.7.1-  
515.65.01-1_amd64.deb  
#sudo dpkg -i cuda-repo-ubuntu2204-11-7-local_11.7.1-515.65.01-1_amd64.deb  
#sudo cp /var/cuda-repo-ubuntu2204-11-7-local/cuda-*keyring.gpg /usr/share/keyrings/  
#sudo apt-get update  
#sudo apt-get -y install cuda
```

### (2) Environment configuration (sudo gedit ~/.bashrc)

```
export CUDA_HOME=/usr/local/cuda-11.7  
export LD_LIBRARY_PATH=${CUDA_HOME}/lib64  
export PATH=${CUDA_HOME}/bin:${PATH}
```

source ~/.bashrc

### (3) Check the installation: nvcc -V

(4) Uninstall cuda.

```
#sudo apt-get remove cuda  
#sudo apt autoremove  
#sudo apt-get remove cuda*  
#cd /usr/local/  
#sudo rm -rf cuda-11.7  
  
#sudo dpkg -l | grep cuda  
#sudo dpkg -P cuda-visual-tools-11-7
```

(5) Install cuda 10.2 as eddy\_cuda only support 10.2/9.1/8.0 version.

<https://developer.nvidia.com/cuda-10.2-download-archive>

```
#wget https://developer.download.nvidia.com/compute/cuda/10.2/Prod/local_installers/cuda_10.2.89_440.33.01_linux.run  
#sudo sh cuda_10.2.89_440.33.01_linux.run --override
```

(6) Environment configuration (sudo gedit ~/.bashrc)

```
export CUDA_HOME=/usr/local/cuda-10.2  
export LD_LIBRARY_PATH=${CUDA_HOME}/lib64  
export PATH=${CUDA_HOME}/bin:${PATH}
```

source ~/.bashrc

After installing the NVIDIA driver and CUDA toolkit, you may meet the sereval errors:

(1) ‘Gave up waiting for suspend/resume device’ when you reboot your system.

Solution: Choose a low version kernel to solve it before entering Ubuntu system.

(2) NVIDIA-SMI has failed because it couldn’t communicate with the NVIDIA driver. Make sure that the latest NVIDIA driver is installed and running.

Solution:

```
#sudo apt-get remove --purge nvidia*
#sudo ubuntu-drivers autoinstall
```

or #ubuntu-drivers devices  
and select the recommended nvidia-driver version.  
such as #sudo apt install nvidia-driver-515

Then reboot the system.

If there still exists problems, # ls /usr/src | grep nvidia (it will return 515.65.01)  
# sudo dkms install -m nvidia -v 515.65.01

## **Part II**

A list of neuroimaging toolbox required for successful use of the UFA toolbox

Table 2 | A list of neuroimaging toolbox required for successful use of the UFA toolbox.

Toolbox	Website	Platform	Usage
CNS	<a href="https://github.com/cheba-nil/CNS">https://github.com/cheba-nil/CNS</a>	Matlab	WMH extraction
SPM12	<a href="https://www.fil.ion.ucl.ac.uk/spm/software/spm12/">https://www.fil.ion.ucl.ac.uk/spm/software/spm12/</a>	Matlab	Required by CNS toolbox
FSL (Version 6.0.5)	<a href="https://fsl.fmrib.ox.ac.uk/fsl/fslwi_ki">https://fsl.fmrib.ox.ac.uk/fsl/fslwi_ki</a>	/	Registration module in FSL ‘flirt’
ANTs	<a href="http://stnava.github.io/ANTs/">http://stnava.github.io/ANTs/</a>	/	N4 bias field correction in ANTs are needed
FastSurfer	<a href="https://github.com/Deep-MI/FastSurfer">https://github.com/Deep-MI/FastSurfer</a>	Python	T1 cortical segmentation
WMA	<a href="https://github.com/SlicerDMRI/witematteranalysis">https://github.com/SlicerDMRI/witematteranalysis</a>	Python	White matter fiber clustering
3D Slicer (Version 4.8.1)	<a href="https://www.slicer.org/">https://www.slicer.org/</a>	Linux version	Required by WMA tool
FreeSurfer (Version 7.3.2)	<a href="https://surfer.nmr.mgh.harvard.edu/">https://surfer.nmr.mgh.harvard.edu/</a>	/	T1 cortical segmentation
MRtrix3	<a href="https://www.mrtrix.org/">https://www.mrtrix.org/</a>	Linux version	dMRI tractography

CNS, CHeBA NiL Software ; SPM12, Statistical Parametric Mapping version 12; FSL, FMRIB Software Library; ANTs, Advanced Normalization Tools; WMA, White Matter Analysis.

Before you successfully use our UFA toolbox, you should download the basic neuroimaging toolbox and add the correct path.

## 1. CNS (UBO Detecor)

(1) Download CNS from github : #git clone <https://github.com/cheba-nil/CNS.git>

(2) Add path in the matlab: Set Path --> Add Folder --> (Find where CNS toolbox locates) --> Save and Close

## 2. SPM12

(1) Download SPM12 from gitub: #git clone <https://github.com/spm/spm12.git>

(2) Add path in the matlab: Set Path --> Add Folder --> (Find where SPM12 toolbox locates) --> Save and Close

**Note:** We already put the ‘CNS’ and SPM12 in the folder ‘UFA\_toolbox/plugin’, thus the users don’t need to download and add the path again. In other words, steps 1 and step 2 need to be skipped when you use our UFA\_toolbox.

### 3.1 The first way to install FSL (<https://fsl.fmrib.ox.ac.uk/fsl/fslwiki>)

(1) Download the `fslinstaller.py` from the FSL website (**FSL 6.0.5 is recommended**, the FSL 6.0.6.5 will meet errors when you use the  `${FSLDIR}/bin/cluster` command in the WMH extraction module).

(2) Install python2: # `sudo apt-get install python2`

(3) Install FSL (this step needs long time more than 12 hours, you need to be patient to wait):

```
# python2 fslinstaller.py
```

(4) Set the environment :

(4.1) open the `/etc/profile` and add the below two command: # `sudo gedit /etc/profile`

```
export PATH=$PATH:/usr/local/fsl/bin  
export FSLEDIR=/usr/local/fsl
```

then close the file and `#source /etc/profile`

(4.2) open the `/etc/bash.bashrc` and add the below command: # `sudo gedit /etc/bash.bashrc`

```
FSLEDIR=/usr/local/fsl  
. ${FSLEDIR}/etc/fslconf/fsl.sh  
PATH=${FSLEDIR}/bin:${PATH}  
export FSLEDIR PATH
```

then close the file and `#source /etc/bash.bashrc`

### 3.2 The second way to install FSL (If you encounter errors with the first approach, you can use the second way as an alternative.)

(1) Download the specified version of FSL from the link. ([https://fsl.fmrib.ox.ac.uk/fsldownloads/fsl-6.0.5-centos7\\_64.tar.gz](https://fsl.fmrib.ox.ac.uk/fsldownloads/fsl-6.0.5-centos7_64.tar.gz))

**(FSL 6.0.5 is recommended,** FSL 6.0.6.5 met errors when using the \${FSkdir}/bin/cluster command in the WMH extraction module).

(2) Install FSL: #sudo mkdir /usr/local/fsl (Please check whether there exists the FSL in /usr/local, if exists, please change another path)

```
#cp Your_downloaddir/fsl-6.0.5-centos7_64.tar.gz /usr/local/fsl
```

```
#cd /usr/local/fsl
```

```
#sudo tar -xzvf fsl-6.0.5-centos7_64.tar.gz (then delete *.tar.gz)
```

```
#pip install fsleyes
```

```
#whereis fsleyes (it return the path '/home/gaoxingzheng/anaconda3/bin/fsleyes')
```

```
#ln -s /home/gaoxingzheng/anaconda3/bin/fsleyes /usr/local/fsl/bin/fsleyes
```

(3) Set the environment : (3.1) open the /etc/profile and add the below two command: # sudo gedit /etc/profile

```
export PATH=$PATH:/usr/local/fsl/bin
```

```
export FSkdir=/usr/local/fsl
```

(3.2) open the /etc/bash.bashrc and add the below command: # sudo gedit /etc/bash.bashrc

```
FSkdir=/usr/local/fsl
```

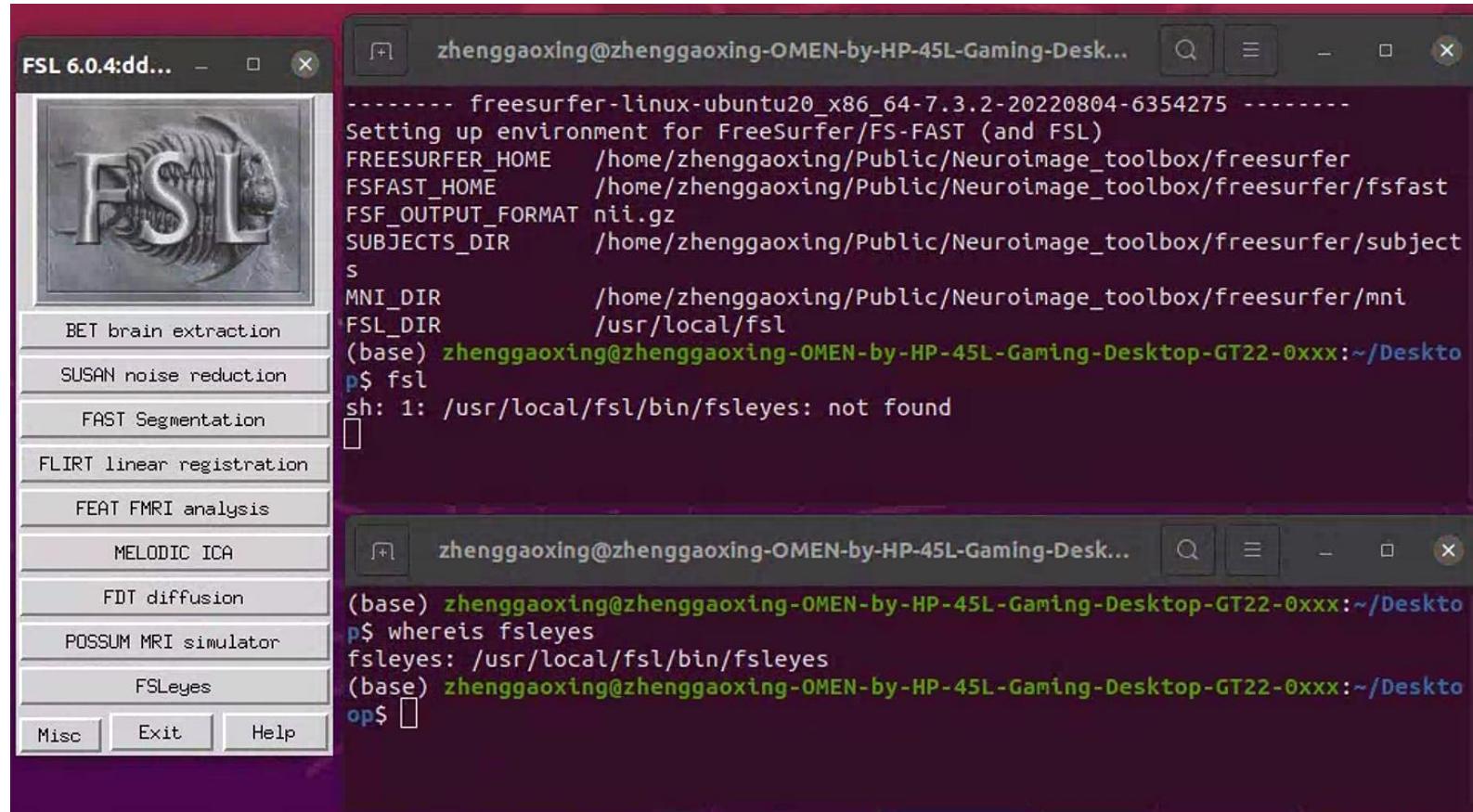
```
. ${FSkdir}/etc/fslconf/fsl.sh
```

```
PATH=${FSkdir}/bin:${PATH}
```

```
export FSkdir PATH
```

then close the file and #source /etc/bash.bashrc #source /etc/profile; Then execute: sudo \$FSkdir/etc/fslconf/post\_install.sh -f \$FSkdir

### 3.3 Solve the problem when using FSL: /usr/local/fsl/bin/fsleyes: not found



Solution:

```
#pip install -f https://extras.wxpython.org/wxPython4/extras/linux/gtk3/ubuntu-20.04 wxpython
#sudo apt-get install git curl libsdl2-mixer-2.0-0 libsdl2-image-2.0-0 libsdl2-2.0-0
#pip install fsleyes
#rm /usr/local/fsl/bin/fsleyes
#ln -s ${Your_Anconda3_Path}/bin/fsleyes /usr/local/fsl/bin/fsleyes
```

### 3.4 Solve the problem when opening fsleyes:

/lib/x86\_64-linux-gnu/libgobject-2.0.so.0: undefined symbol: ffi\_type\_uint32, version LIBFFI\_BSE\_7.0

```
zhenggaoxing@zhenggaoxing-OMEN-by-HP-45L-Gaming-Desktop-GT22-0xxx:~/Downloads$ fsleyes
Traceback (most recent call last):
  File "/home/zhanggaoxing/anaconda3/bin/fsleyes", line 5, in <module>
    from fsleyes.filtermain import main
  File "/home/zhanggaoxing/anaconda3/lib/python3.11/site-packages/fsleyes/__init__.py", line 381, in <module>
    from fsleyes.main import embed, shutdown  # noqa
    ^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^
  File "/home/zhanggaoxing/anaconda3/lib/python3.11/site-packages/fsleyes/main.py", line 35, in <module>
    import wx
  File "/home/zhanggaoxing/anaconda3/lib/python3.11/site-packages/wx/__init__.py", line 17, in <module>
    from wx.core import *
  File "/home/zhanggaoxing/anaconda3/lib/python3.11/site-packages/wx/core.py", line 12, in <module>
    from ._core import *
ImportError: /lib/x86_64-linux-gnu/libgobject-2.0.so.0: undefined symbol: ffi_type_uint32, version LIBFFI_BASE_7.0
(base) zhenggaoxing@zhenggaoxing-OMEN-by-HP-45L-Gaming-Desktop-GT22-0xxx:~/Downloads$
```

Solution:

```
#sudo gedit /etc/bash.bashrc
```

Add the following command in the '/etc/bash.bashrc': export LD\_PRELOAD=/usr/lib/x86\_64-linux-gnu/libffi.so.7

Save and close the /bash.bashrc, and #source /etc/bash.bashrc

## 4. ANTs

(1) Download ANTs from github: #git clone <https://github.com/ANTsX/ANTs.git>

(2) Download cmake(please download the latest cmake version):

```
#wget https://github.com/Kitware/CMake/releases/download/v3.24.1/cmake-3.24.1-linux-x86_64.sh
```

(3) Change the permission: #sudo chmod u+x cmake-3.24.1-linux-x86\_64.sh

(4) Install cmake: #sh cmake-3.24.1-linux-x86\_64.sh

(5) Install cmake GUI: #sudo apt-get install cmake-curses-gui

Install gcc, g++ #sudo apt-get install build-essential

(6) Compiling ANTs with cmake:

```
#cd ANTs
#mkdir build install
#cd build
#ccmake ..
#push c to enter configuration, then enter 'c', and then enter 'g'
#make -j 4
```

During the compiling ANTs, you may meet several errors as follows:

(6.1) No CMAKE\_CXX\_COMPILER could be found. ---> Solution: #sudo apt-get install build-essential

(6.2) Could not find zlib (missing zlib\_library zlib\_include\_dir) linux

Solution: # cd ANTs/

```
#locate libz.so (Note: this command is to find where the libz.so locates, choose the path contains 'zlib-xxx/lib/libz.so')
#cmake -DZLIB_LIBRARY=/usr/local/zlib/lib/libz.so -DZLIB_INCLUDE_DIR=/usr/local/zlib/include $builddir
or #export ZLIB_LIBRARY=/usr/local/zlib/lib
#export ZLIB_INCLUDE_DIR=/usr/local/zlib/include
```

(6.3) Cloning into 'ITKv5'...fatal: unable to connect to github.com:

Solution: <https://github.com/ANTsX/ANTs/issues/621>

Option found.

For the future searches (working behind a proxy or firewall is very common in an academic or corporate and often/always the researcher or local sysadmin cannot modify it):

There is in cmake an option called:

SuperBuild\_ANTS\_USE\_GIT\_PROTOCOL

with description:

SuperBuild\_ANTS\_USE\_GIT\_PROTOCOL: If behind a firewall turn this off to use http instead.

It has to be turned off

The issue is solved. I close it.

(7) After several minutes compile, copy the ANTs scripts into build/bin

```
#cd build  
#mkdir bin  
#cp -r ./ANTS-build/Examples/* ./bin  
#cp -r ./staging/bin/* ./bin  
#cp -r ../Scripts/* ./bin
```

(8) Environment configuration: #sudo gedit /etc/bash.bashrc

add the following commands into the bash.bashrc

```
### Note: ANTs_PATH is your ANTs folder path, such as: /home/zhenggaoxing/Public/NeuroImage_toolbox/ANTs  
export ANTSPATH=${ANTSPATH}/build/bin  
export PATH=$ANTSPATH:$PATH
```

save and close bash.bashrc, and then source it. #source /etc/bash.bashrc

(9) Finally, check if ANTs is installed successfully

```
#which antsRegistration  
it returns : /home/zhenggaoxing/Public/NeuroImage_toolbox/ANTs/build/bin/antsRegistration
```

```
#antsRegistrationSyN.sh  
If it returns instructions for using this command, it means ANTs are installed successfully!
```

## 5. FastSurfer

(1) Download FastSurfer: git clone <http://github.com/Deep-MI/FastSurfer>

(2) #sudo apt install python3-pip  
#sudo apt install python3-setuptools  
#pip install setuptools

(3) Install pip-tools(contains pip-compile): #python -m pip install pip-tools

(4) Install the basic tools in the FastSurfer/requirements.txt.

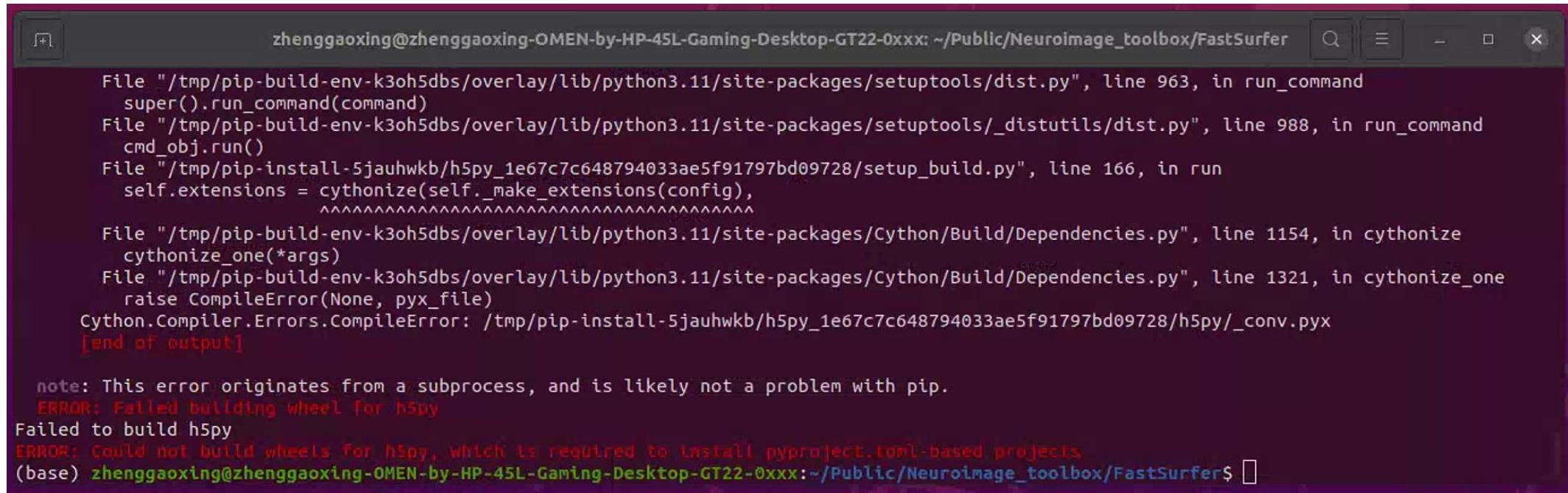
```
#cd FastSurfer/  
#pip install -r requirements.txt  
### if the above command (pip-compile requirements.txt) fails to run, you need to execute 'pip install xxx' for each package in the requirements.txt (xxx is the package name in the requirements.txt).
```

(5) #conda install pytorch==1.11.0 torchvision==0.12.0 torchaudio==0.11.0 cudatoolkit=11.3 -c pytorch  
or #pip install torch==1.11.0+cu113 torchvision==0.12.0+cu113 torchaudio==0.11.0 --extra-index-url https://download.pytorch.org/whl/cu113

(6) Check the pytorch is installed successfully.

```
#python  
#>>>import torch  
#>>>torch.cuda.is_available()  
True
```

(7) You may meet the error when you execute the command: #pip install -r requirements.txt



The screenshot shows a terminal window with the following output:

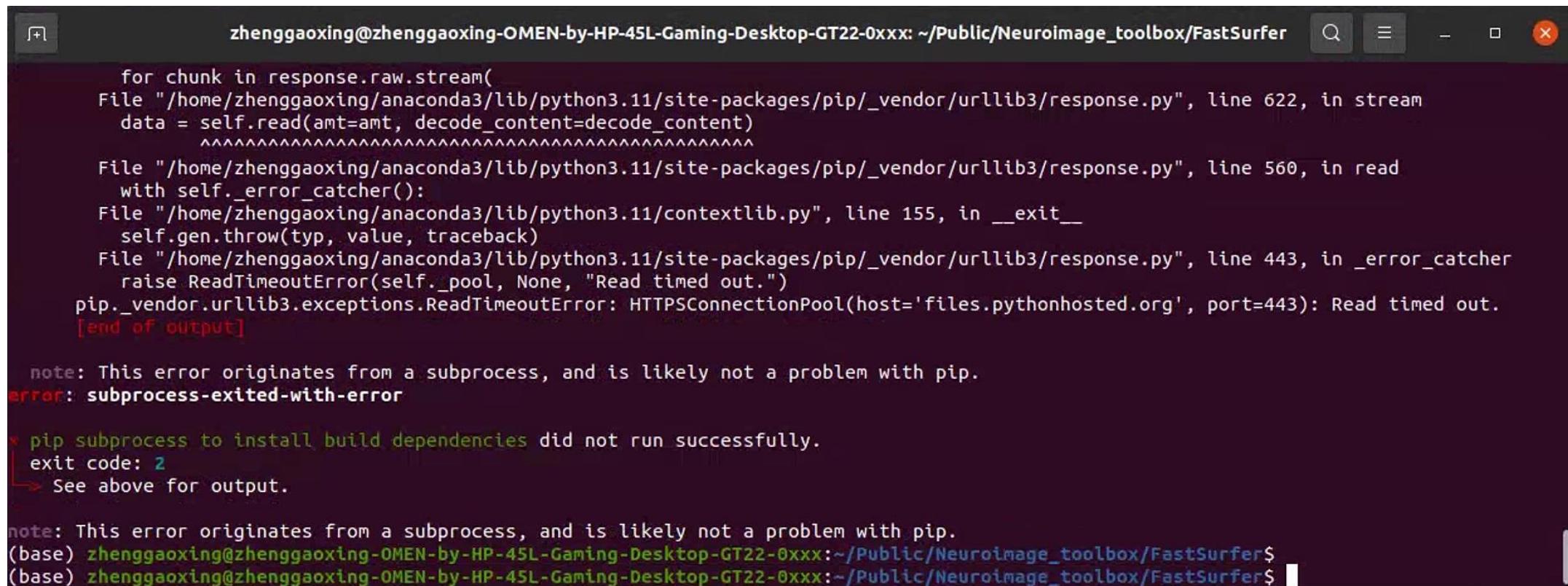
```
zhenggaoxing@zhenggaoxing-OMEN-by-HP-45L-Gaming-Desktop-GT22-0xxx: ~/Public/Neuroimage_toolbox/FastSurfer
File "/tmp/pip-build-env-k3oh5dbs/overlay/lib/python3.11/site-packages/setuptools/dist.py", line 963, in run_command
    super().run_command(command)
File "/tmp/pip-build-env-k3oh5dbs/overlay/lib/python3.11/site-packages/setuptools/_distutils/dist.py", line 988, in run_command
    cmd_obj.run()
File "/tmp/pip-install-5jauhwkb/h5py_1e67c7c648794033ae5f91797bd09728/setup_build.py", line 166, in run
    self.extensions = cythonize(self._make_extensions(config),
                           ^^^^^^^^^^^^^^^^^^^^^^
File "/tmp/pip-build-env-k3oh5dbs/overlay/lib/python3.11/site-packages/Cython/Build/Dependencies.py", line 1154, in cythonize
    cythonize_one(*args)
File "/tmp/pip-build-env-k3oh5dbs/overlay/lib/python3.11/site-packages/Cython/Build/Dependencies.py", line 1321, in cythonize_one
    raise CompileError(None, pyx_file)
Cython.Compiler.Errors.CompileError: /tmp/pip-install-5jauhwkb/h5py_1e67c7c648794033ae5f91797bd09728/h5py/_conv.pyx
[end of output]

note: This error originates from a subprocess, and is likely not a problem with pip.
ERROR: Failed building wheel for h5py
Failed to build h5py
ERROR: Could not build wheels for h5py, which is required to install pyproject.toml-based projects
(base) zhenggaoxing@zhenggaoxing-OMEN-by-HP-45L-Gaming-Desktop-GT22-0xxx:~/Public/Neuroimage_toolbox/FastSurfer$
```

Solution: Before installing the h5py, you should install Cython first.

```
#pip install Cython
#pip install -r requirements.txt
```

(8) You may meet the error when you execute the command: #pip install -r requirements.txt



The screenshot shows a terminal window with the following output:

```
zhenggaoxing@zhenggaoxing-OMEN-by-HP-45L-Gaming-Desktop-GT22-0xxx: ~/Public/Neuroimage_toolbox/FastSurfer
for chunk in response.raw.stream(
File "/home/zhenggaoxing/anaconda3/lib/python3.11/site-packages/pip/_vendor/urllib3/response.py", line 622, in stream
    data = self.read(amt=amt, decode_content=decode_content)
           ^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^
File "/home/zhenggaoxing/anaconda3/lib/python3.11/site-packages/pip/_vendor/urllib3/response.py", line 560, in read
    with self._error_catcher():
File "/home/zhenggaoxing/anaconda3/lib/python3.11/contextlib.py", line 155, in __exit__
    self.gen.throw(typ, value, traceback)
File "/home/zhenggaoxing/anaconda3/lib/python3.11/site-packages/pip/_vendor/urllib3/response.py", line 443, in _error_catcher
    raise ReadTimeoutError(self._pool, None, "Read timed out.")
pip._vendor.urllib3.exceptions.ReadTimeoutError: HTTPSConnectionPool(host='files.pythonhosted.org', port=443): Read timed out.
[end of output]

note: This error originates from a subprocess, and is likely not a problem with pip.
error: subprocess-exited-with-error

× pip subprocess to install build dependencies did not run successfully.
  exit code: 2
  See above for output.

note: This error originates from a subprocess, and is likely not a problem with pip.
(base) zhenggaoxing@zhenggaoxing-OMEN-by-HP-45L-Gaming-Desktop-GT22-0xxx:~/Public/Neuroimage_toolbox/FastSurfer$
```

Solution:

#pip install h5py==

Choose the latest version of h5py and change the corresponding location in requirements.txt

Such as #pip install h5py==3.10.0

You may also adjust different version of packages in ‘requirements.txt’ according to the error information (such as numpy, urllib3).

## 6. White matter tractography clustering package (WMA)

Installation instrument reference : <http://dmri.slicer.org/whitematteranalysis/>

(1) Download and install WMA package by using following command:

```
#pip install git+https://github.com/SlicerDMRI/whitematteranalysis.git
```

During the installation, you may meet the error : command ‘gcc’ failed: No such file or directory.

Soultion: # sudo apt-get install gcc

(2) Run ‘wm\_quality\_control\_tractography.py --help’ in the terminal to test if the installation is successful.

(3) Please see the wiki for usage instructions (<https://github.com/SlicerDMRI/whitematteranalysis/wiki>).

## 7. 3D Slicer (<https://download.slicer.org/>) + SlicerDMRI (<http://dmri.slicer.org/download/>)

(1) Download 3D slicer from the website (<https://download.slicer.org/>).

[https://www.slicer.org/wiki/Documentation/Nightly/FAQ/General#Where\\_can\\_I\\_download\\_Slicer.3F](https://www.slicer.org/wiki/Documentation/Nightly/FAQ/General#Where_can_I_download_Slicer.3F)

<https://slicer-packages.kitware.com/#collection/5f4474d0e1d8c75dfc70547e/folder/5f4474d0e1d8c75dfc705482>

We recommend the version **Slicer-4.8.1-linux-amd64**.

(2) Install Slicer Extensions --> Search SlicerDMRI Extension --> Install  
(Or you can choose to install an extension from file and find slicerDMRI)

However, you may meet the error information as below.



<https://discourse.slicer.org/t/on-ubuntu-22-04-it-is-not-possible-to-install-extensions-using-either-stable-or-preview-build/23819/4>

Solution: you should be able to download the extension archive from <https://extensions.slicer.org/catalog/All/> and install the extension package from file.

**Note (very important!!!):** Since the Slicer 5 version has updated the kernel, the coordinate system changes to RAS, while the coordinate system of the white matter tract is LPS. Thus, we recommended you use Slicer 4.x.x version rather than Slicer 5.x.x. Otherwise, the white matter tractography will not register to T1 images.

Reference: [https://slicer.readthedocs.io/en/latest/user\\_guide/getting\\_started.html](https://slicer.readthedocs.io/en/latest/user_guide/getting_started.html)

## 8. FreeSurfer (We recommend the version 7.3.2 as FastSurfer needs the Freesurfer 7.3.2)

- (1) Download the latest FreeSurfer from the website '<https://www.freesurfer.net>'.
- (2) Apply the license in the website (<https://surfer.nmr.mgh.harvard.edu.cn/registration.html>).

Once you obtain the license.txt key file, copy it to your FreeSurfer installation directory.

- (3) # sudo cp 'freesurfer package name' /usr/local

```
# cd /usr/local  
# sudo tar -zxf /usr/local/'freesurfer package name'  
# sudo apt-get install tcsh
```

- (4) Environment configuration:
- (4.1) # sudo gedit /etc/profile

add the command in the last line: export FREESURFER\_HOME=/usr/local/freesurfer

- (4.2) # sudo gedit /etc/bash.bashrc

add the command in the last line:

```
export FREESURFER_HOME=/usr/local/freesurfer  
source $FREESURFER_HOME/SetUpFreeSurfer.sh
```

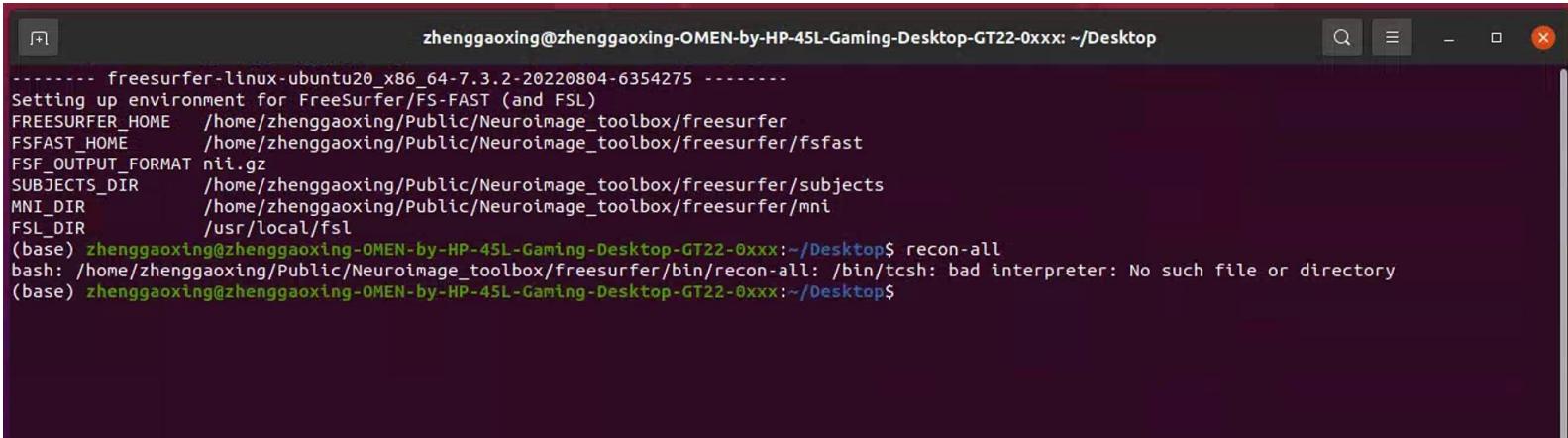
- (5) If FreeSurfer is already installed, please find the installed path : echo \${FREESURFER\_HOME}

- (6) You may meet the error : freeview cannot open normally because no Qt platform plugin could be initialized.

My solution is (**also need by 3DSlicer**) : # sudo apt-get install qtbase5-dev qtchooser qt5-qmake qtbase5-dev-tools qtcreator

## 8.1 Solve the problem when input ‘recon-all’ in the terminal:

Error: [Freesurfer] bad interpreter: No such file or directory



A screenshot of a terminal window titled "zhenggaoxing@zhenggaoxing-OMEN-by-HP-45L-Gaming-Desktop-GT22-0xxx: ~/Desktop". The terminal displays the following text:

```
----- freesurfer-linu... 7.3.2-20220804-6354275 -----
Setting up environment for FreeSurfer/FS-FAST (and FSL)
FREESURFER_HOME    /home/zhanggaoxing/Public/Neuroimage_toolbox/freesurfer
FSFAST_HOME        /home/zhanggaoxing/Public/Neuroimage_toolbox/freesurfer/fsfast
FSF_OUTPUT_FORMAT  nii.gz
SUBJECTS_DIR       /home/zhanggaoxing/Public/Neuroimage_toolbox/freesurfer/subjects
MNI_DIR            /home/zhanggaoxing/Public/Neuroimage_toolbox/freesurfer/mni
FSL_DIR            /usr/local/fsl
(base) zhanggaoxing@zhenggaoxing-OMEN-by-HP-45L-Gaming-Desktop-GT22-0xxx:~/Desktop$ recon-all
bash: /home/zhanggaoxing/Public/Neuroimage_toolbox/freesurfer/bin/recon-all: /bin/tcsh: bad interpreter: No such file or directory
(base) zhanggaoxing@zhenggaoxing-OMEN-by-HP-45L-Gaming-Desktop-GT22-0xxx:~/Desktop$
```

Solution: #sudo apt-get install csh tcsh

## 9. MRtrix3 (<https://www.mrtrix.org/>)

- (1) Download the Anaconda3 from the website '<https://www.anaconda.com>'
- (2) Install Anaconda3: # bash Anaconda3-2022.05-Linux-x86\_64.sh
- (3) Install MRtrix3: # conda install -c mrtrix3 mrtrix3
- (4) Input the command 'mrview' in the terminal to check whether MRtrix3 can be used normally.

When we input the command 'mrview' in the terminal, we meet the error : LibGL error: MESA-LOADER : failed to open swrast: /usr/lib/dri/swrast\_dri.so: cannot open shared object file: No such file or directory.

The solution is here : <https://stackoverflow.com/questions/72110384/libgl-error-mesa-loader-failed-to-open-iris>

To solve this problem, run this in bash:

```
$ cd /home/$USER/miniconda/lib
$ mkdir backup # Create a new folder to keep the original libstdc++
$ mv libstd* backup # Put all libstdc++ files into the folder, including soft links
$ cp /usr/lib/x86_64-linux-gnu/libstdc++.so.6 ./ # Copy the c++ dynamic link library of th
$ ln -s libstdc++.so.6 libstdc++.so
$ ln -s libstdc++.so.6 libstdc++.so.6.0.19
```

where \$USER should be your own username.

# Part III

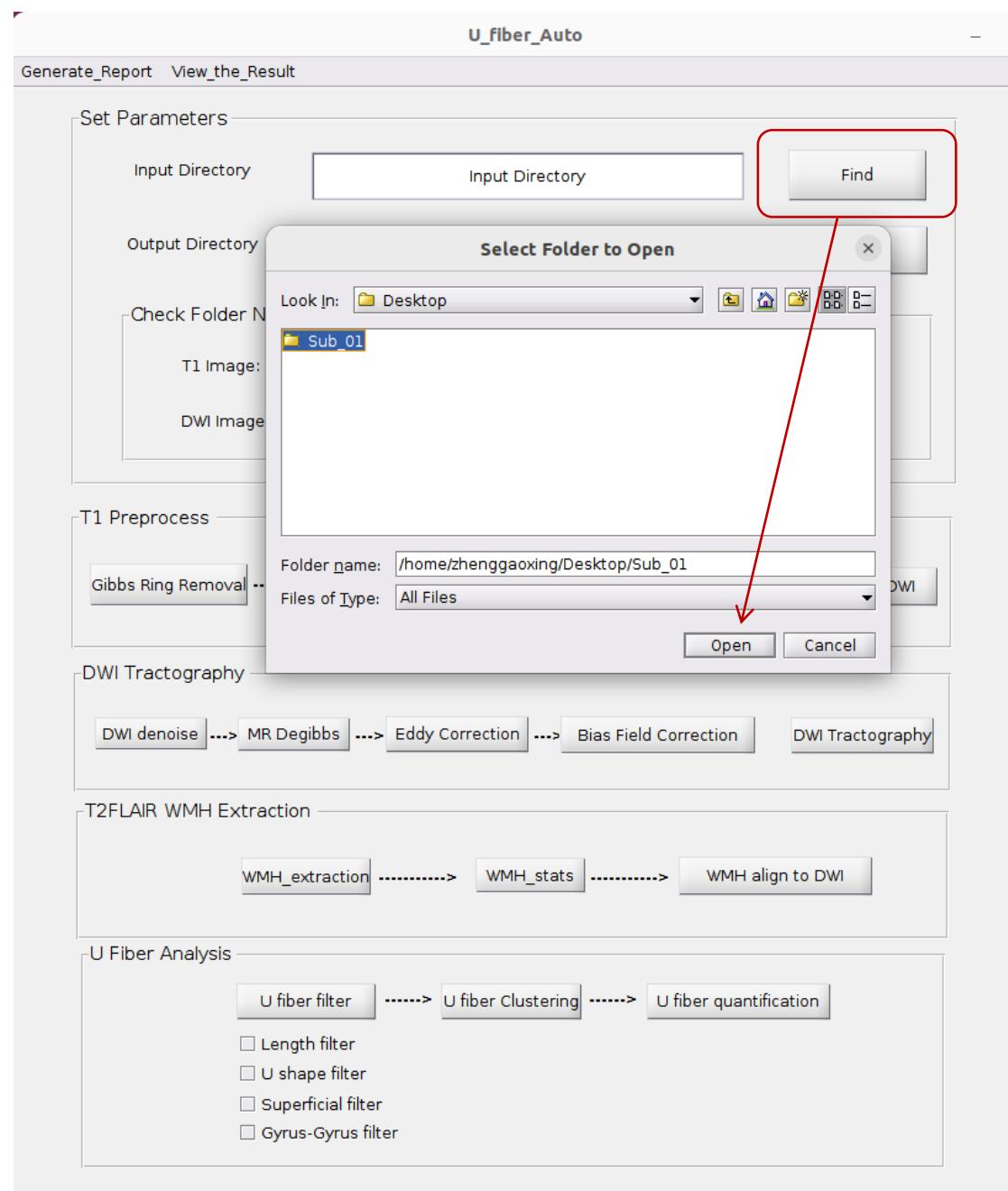
## Tutorial for using the UFA toolbox

Note 1: Before you run the UFA toolbox, please give read and write permissions to all files in the ‘UFA\_toolbox’ folder by using the command ‘sudo chmod 777 -R YourPATH/UFA\_toolbox/’.

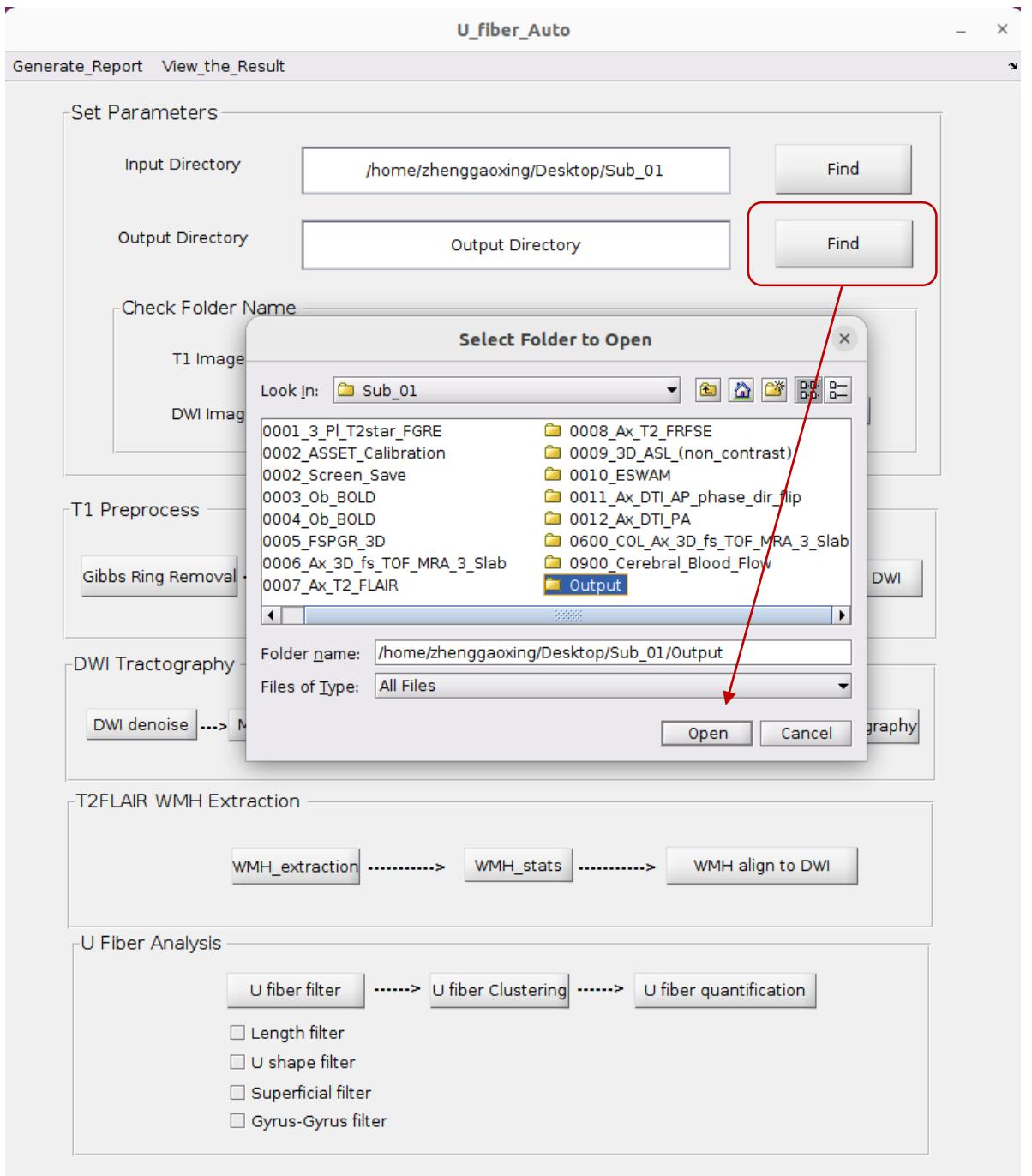
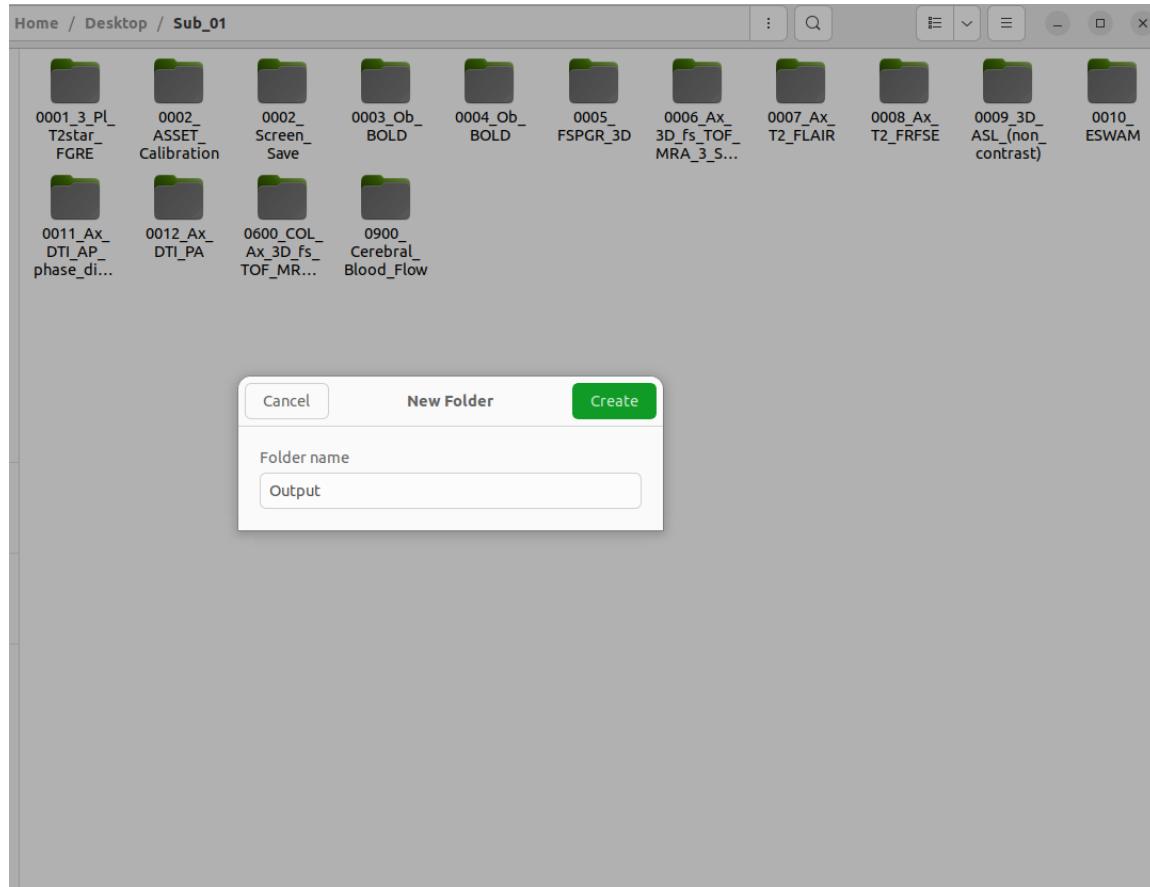
Note 2: Before you run the UFA toolbox, please check whether you install the dcm2niix, you can install it by the command below.

```
#sudo apt install dcm2niix
```

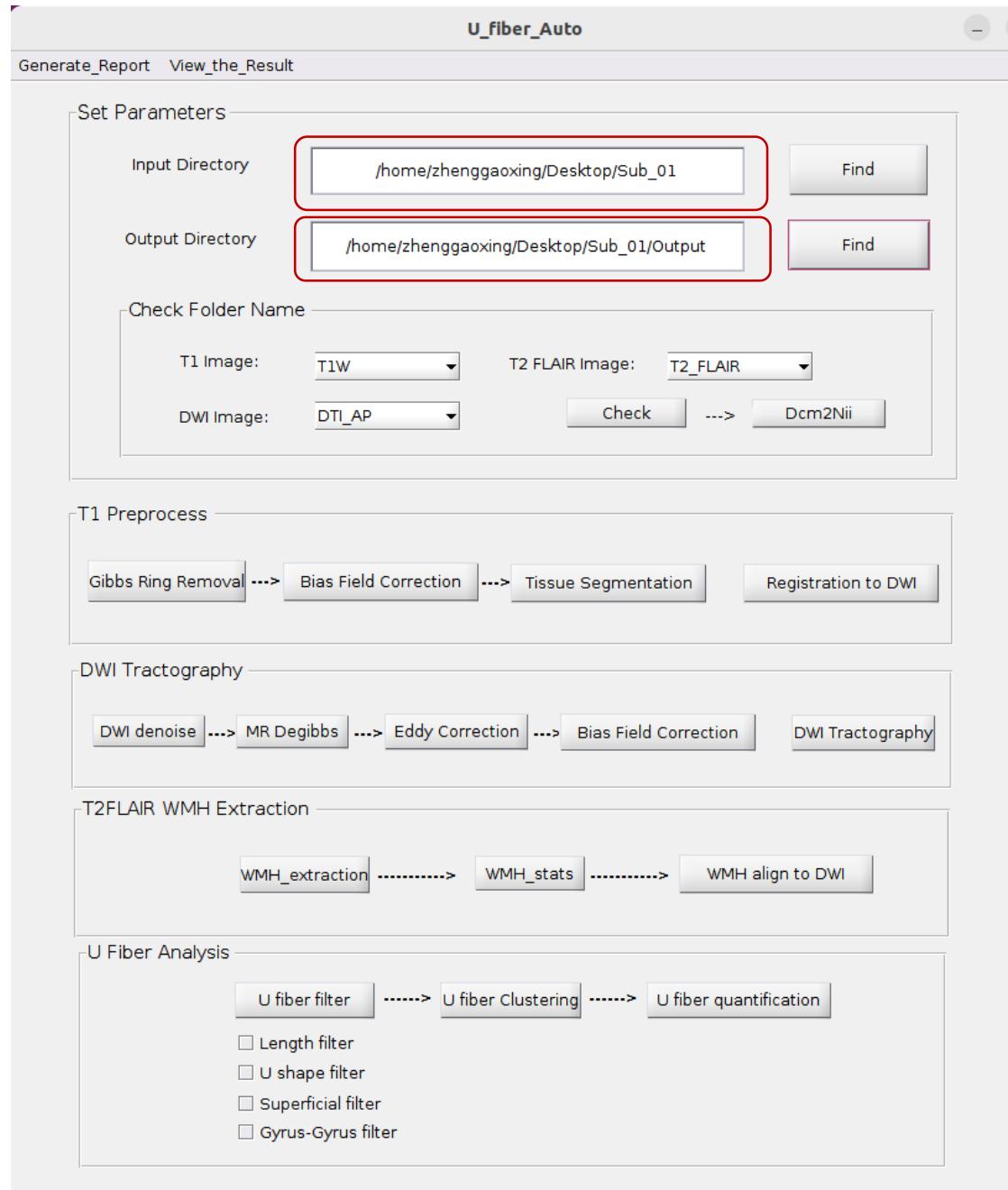
Select the multi-modal neuroimaging folder (contains T1/T2 FLAIR/DWI) of a single participant as the ‘Input Directory’.



Create the ‘Output’ folder in the input folder, and select the ‘Output’ path as the ‘Output Directory’.



The input and output folders are selected as below.



'Check' the key matching fields in the input folder and click "Dcm2nii" to convert the DICOM file to a NIFTI file.

U\_fiber\_Auto

Generate\_Report View\_the\_Result

Set Parameters

Input Directory: /home/zhanggaoxing/Desktop/Sub\_01 Find

Output Directory: /home/zhanggaoxing/Desktop/Sub\_01/Output Find

Choose the key matching fields

Check Folder Name

T1 Image: FSPGR\_3D T2 FLAIR Image: T2\_FLAIR

DWI Image: DTI\_AP, DTI\_PA

Check Dcm2Nii

U\_fiber\_Auto

Generate\_Report View\_the\_Result

Set Parameters

Input Directory: /home/zhanggaoxing/Desktop/Sub\_01 Find

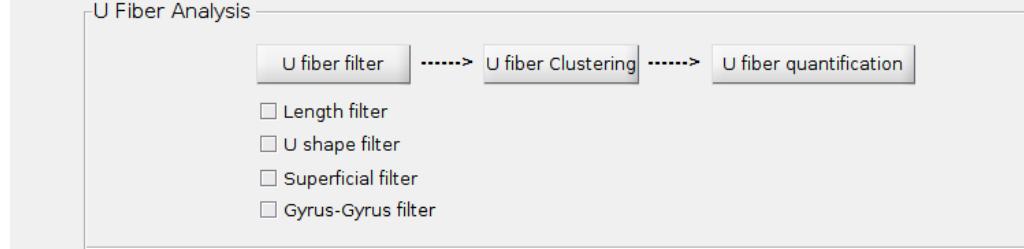
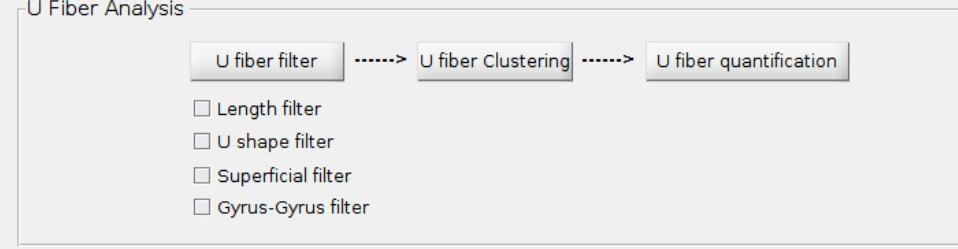
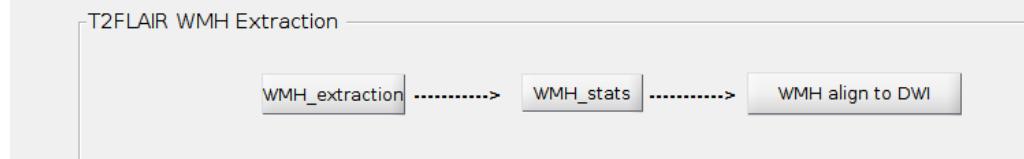
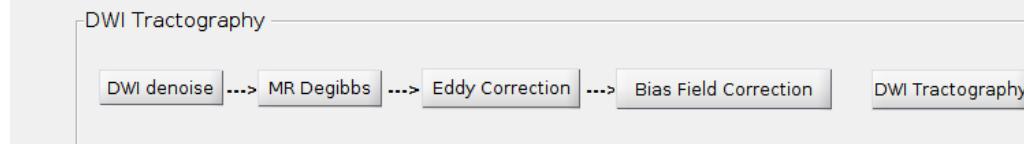
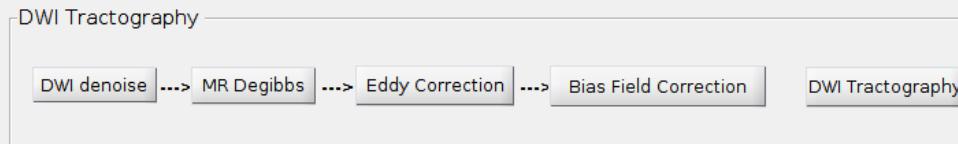
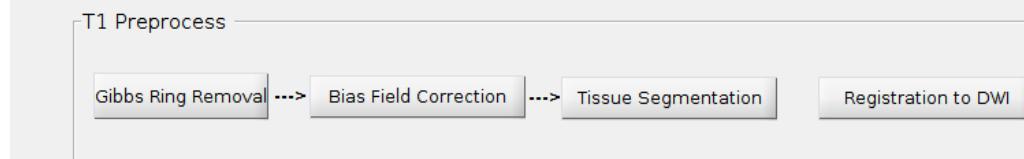
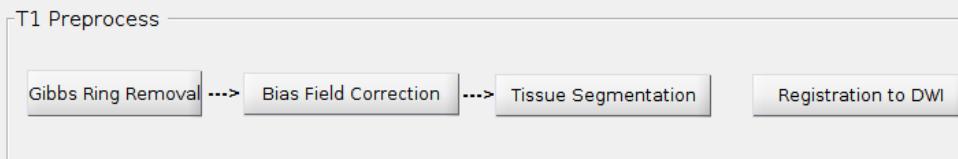
Output Directory: /home/zhanggaoxing/Desktop/Sub\_01/Output Find

Check Folder Name

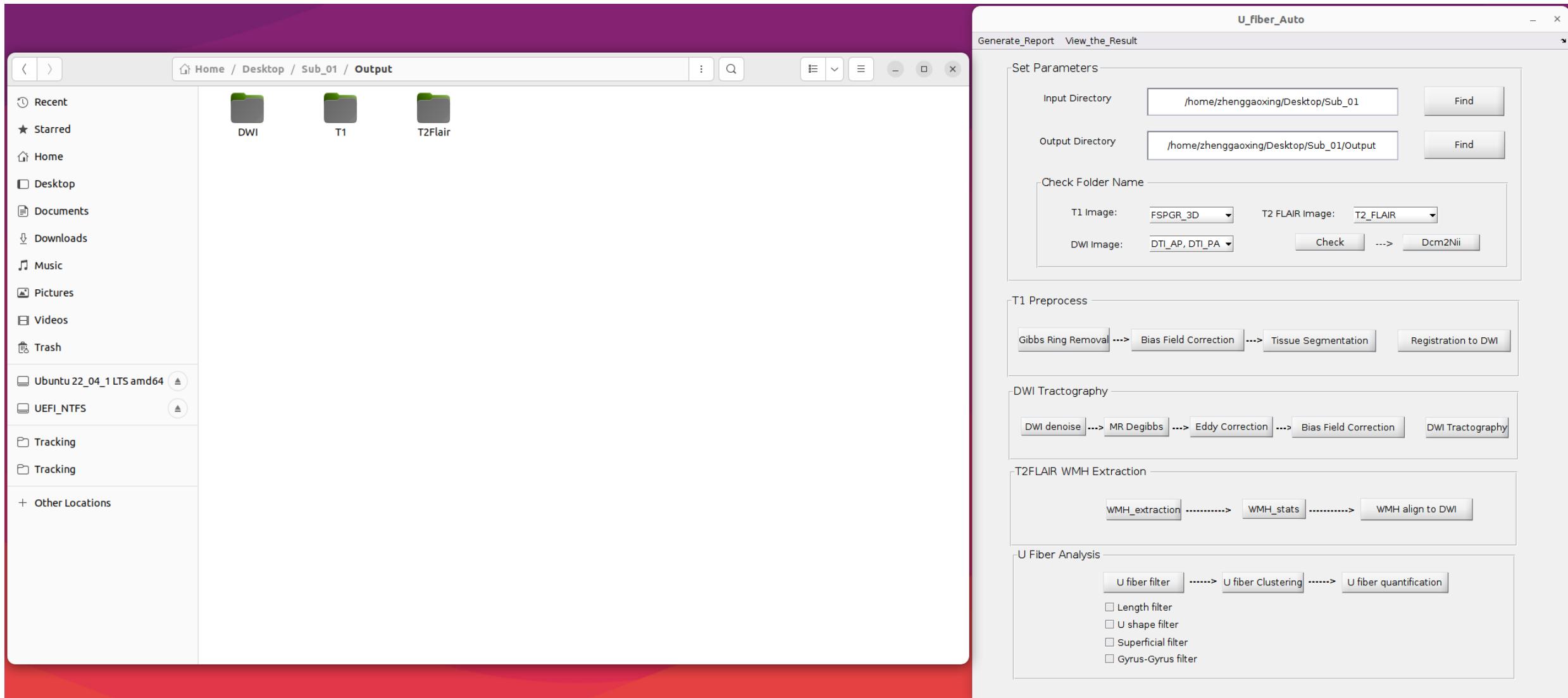
T1 Image: FSPGR\_3D T2 FLAIR Image: T2\_FLAIR

DWI Image: DTI\_AP, DTI\_PA

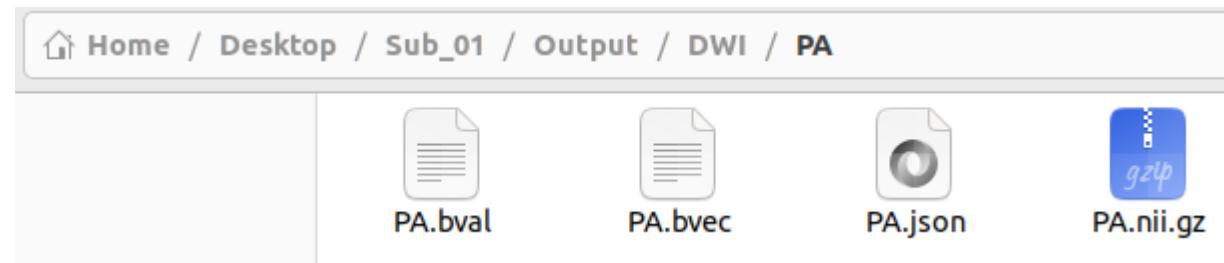
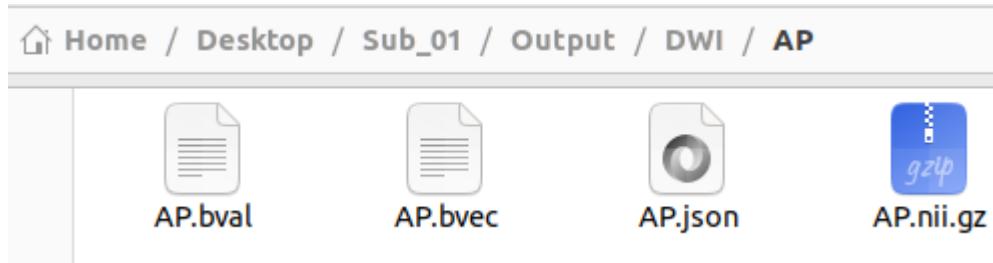
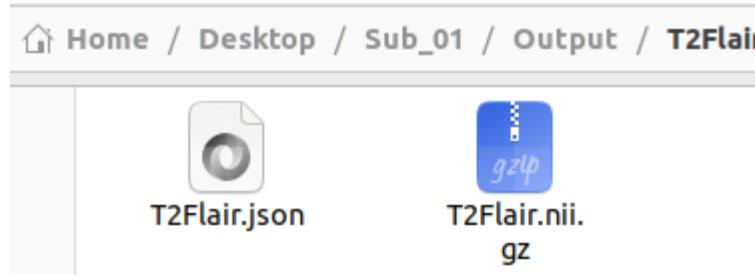
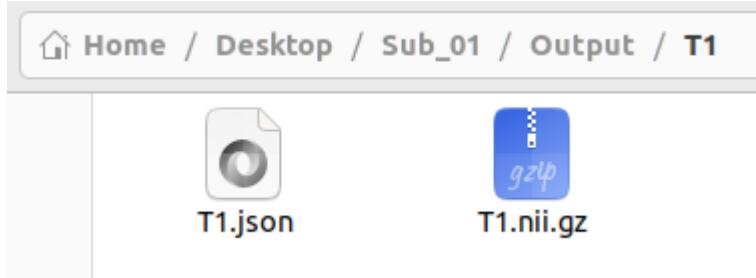
Check Dcm2Nii



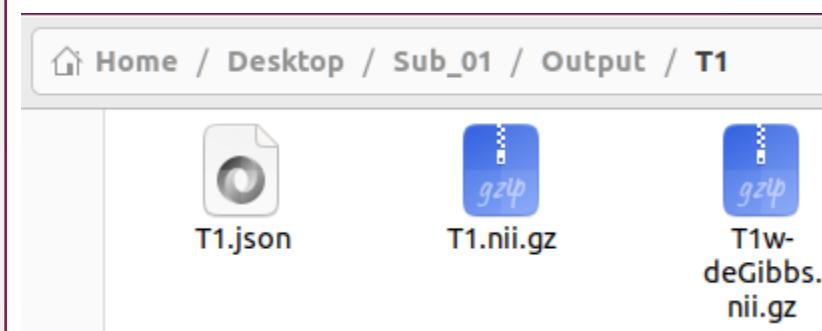
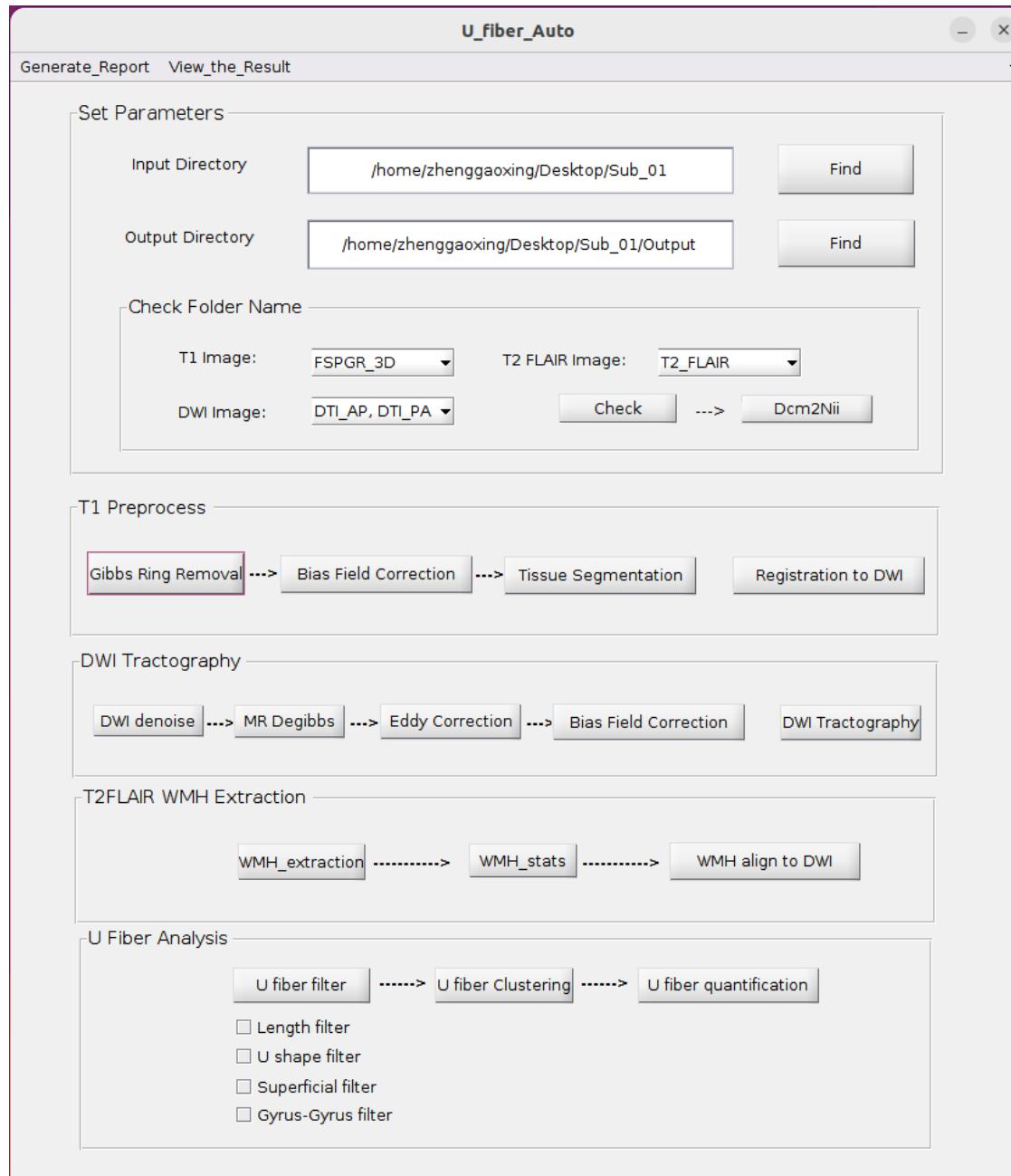
After the ‘Dcm2Nii’, three new folders (DWI/T1/T2Flair) are automatically created in the ‘Output’ folder.



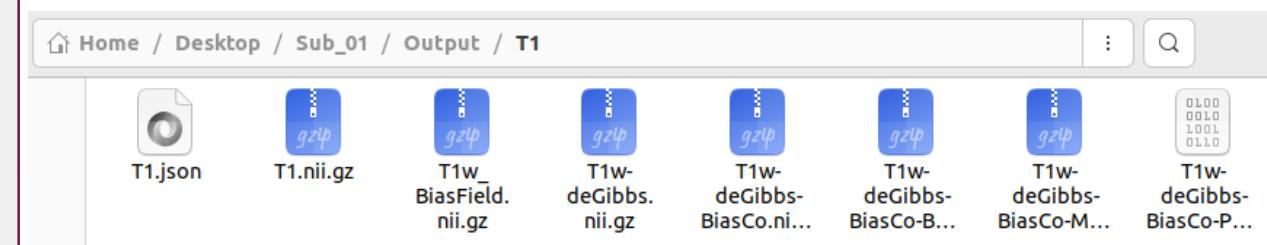
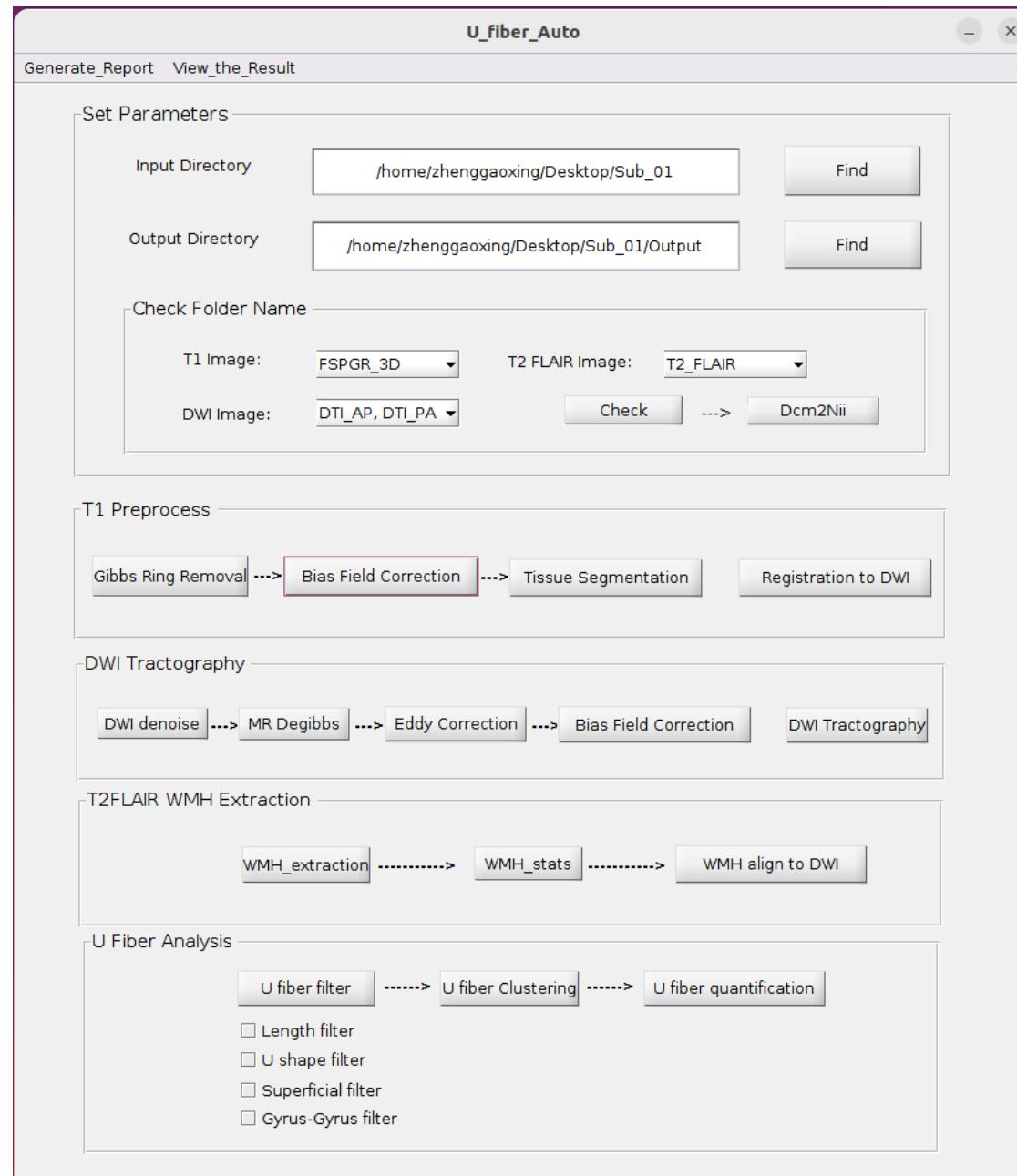
After the ‘Dcm2Nii’, T1/T2FLAIR/DWI image with ‘NIFTI’ format are generated.



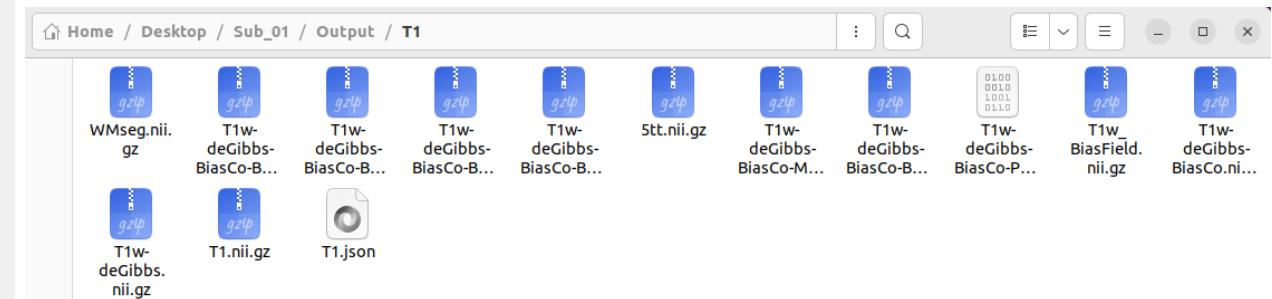
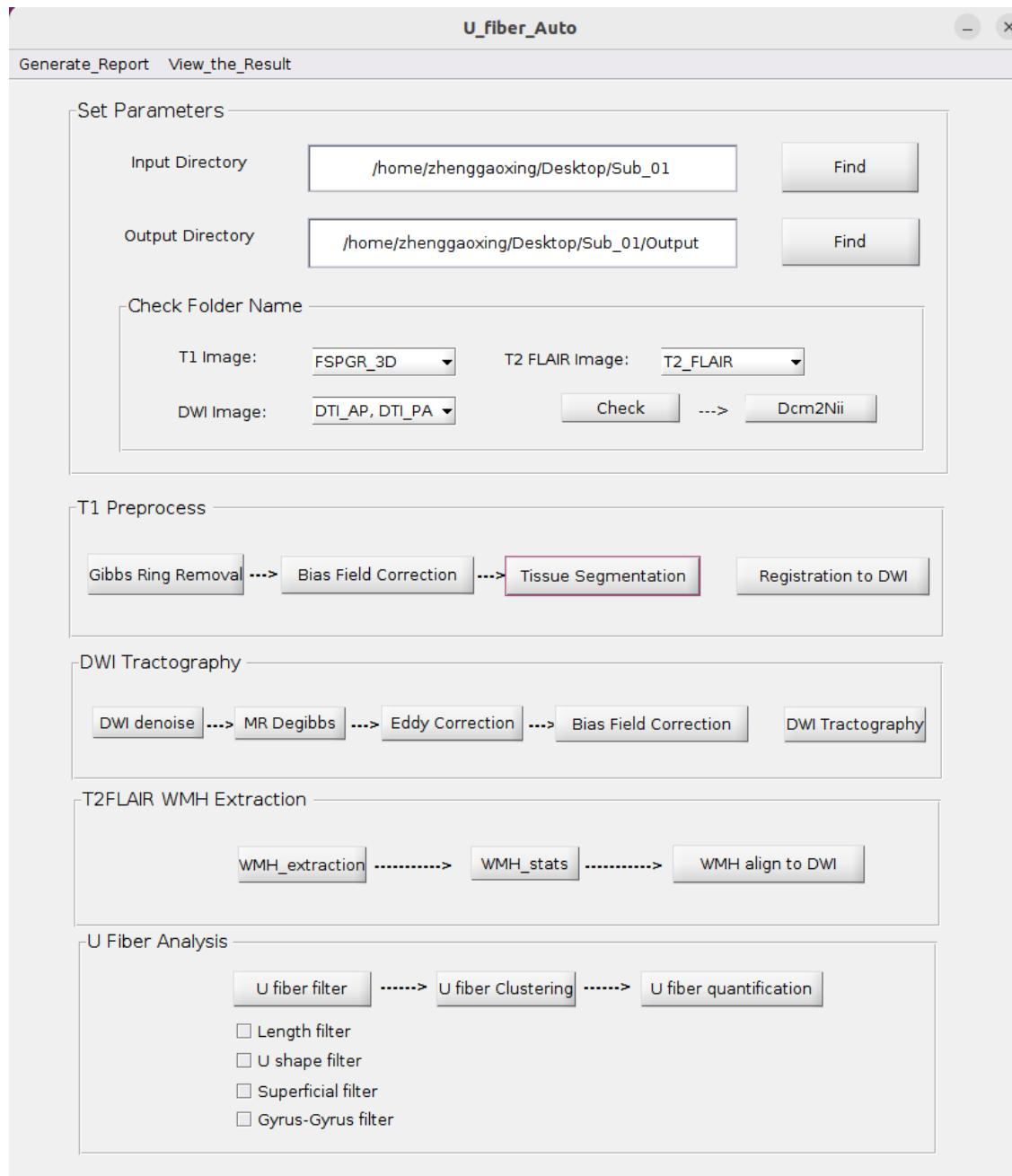
Click the button ‘Gibbs Ring Removal’ to remove the Gibbs artefacts and generate the ‘T1w-deGibbs.nii.gz’ in T1 folder.



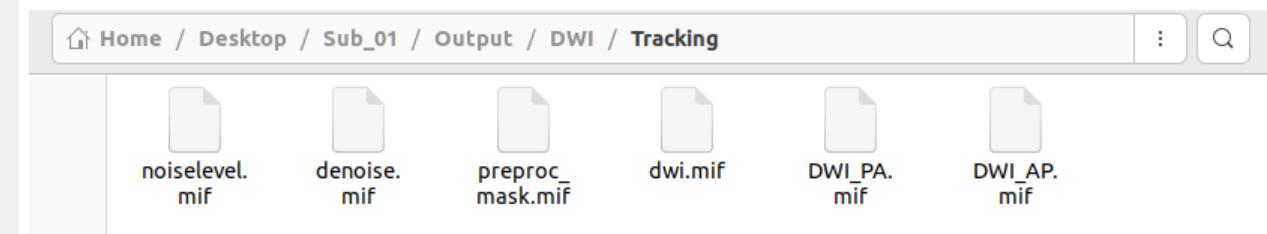
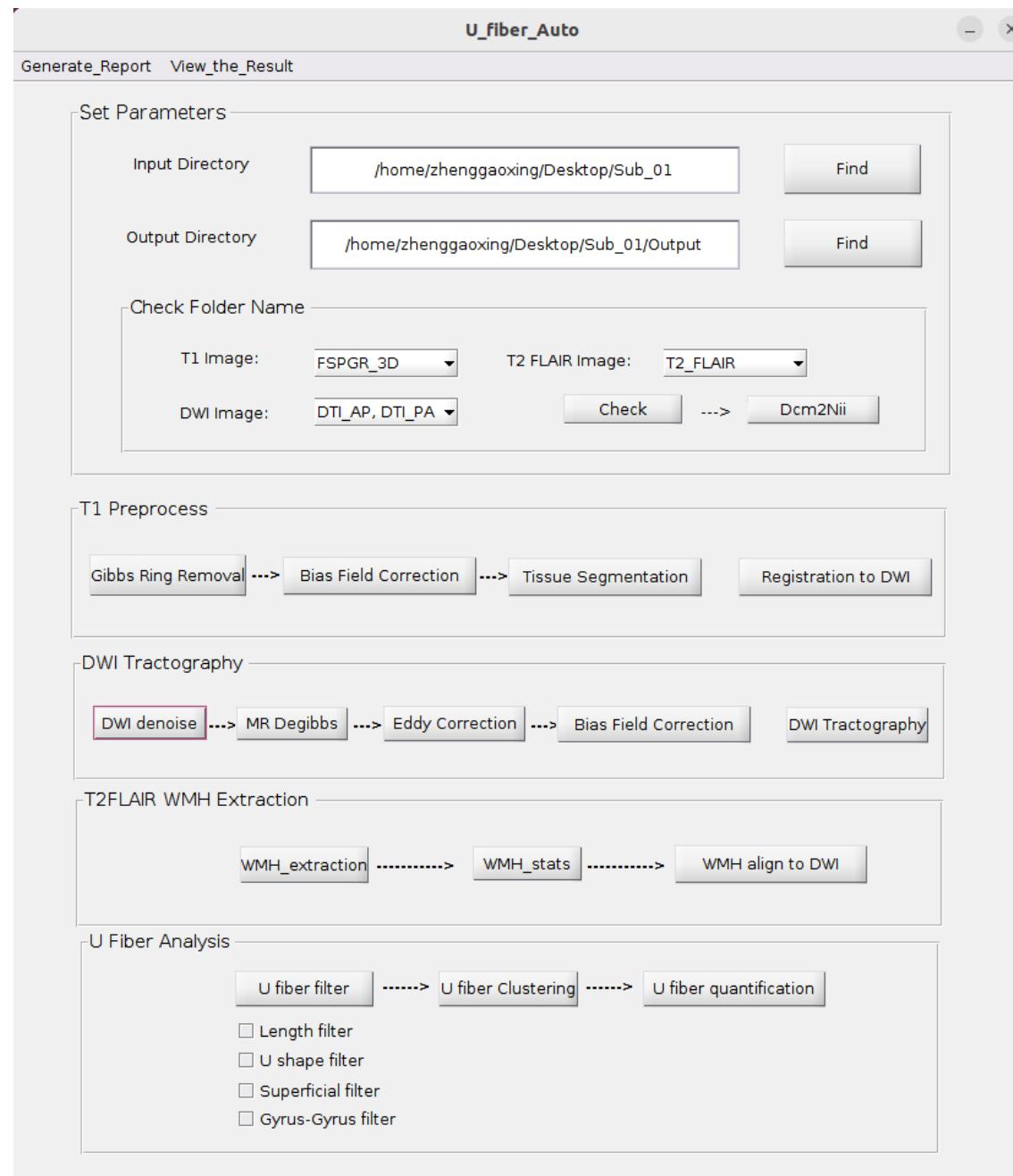
Click the button ‘Bias Field Correction’ to remove the bias field signal and generate the ‘T1w\_BiasField.nii.gz’ and ‘T1w-deGibbs-BiasCo-.nii.gz’ files.



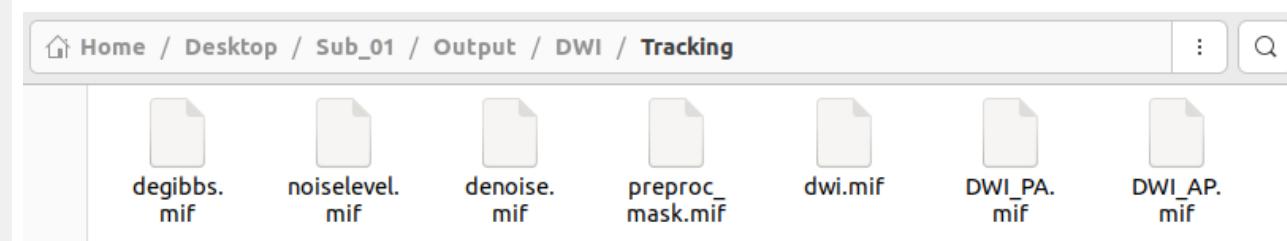
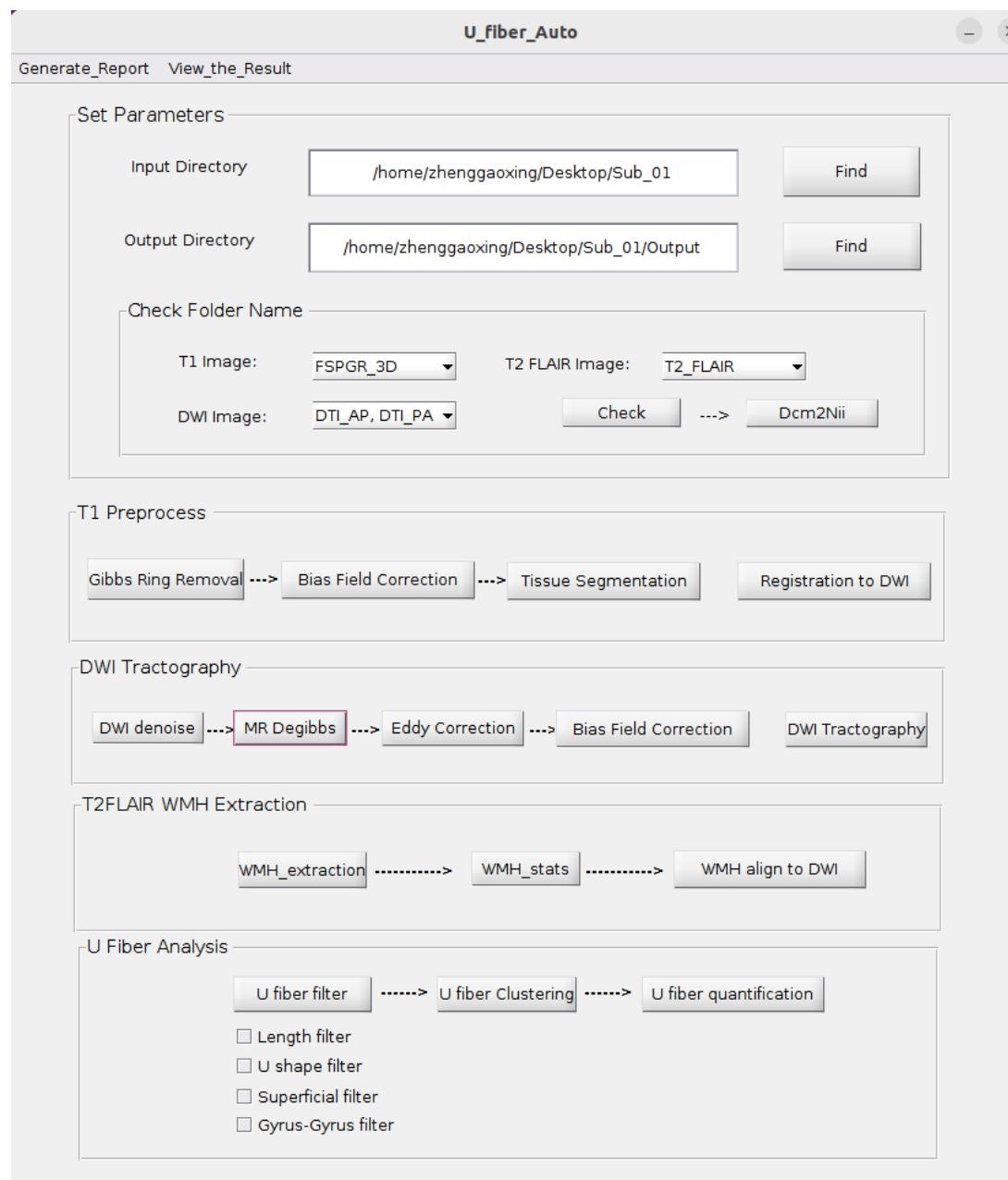
Click the button ‘Tissue Segmentation’ and generate ‘5tt.nii.gz’ and other files (such as WMseg.nii.gz).



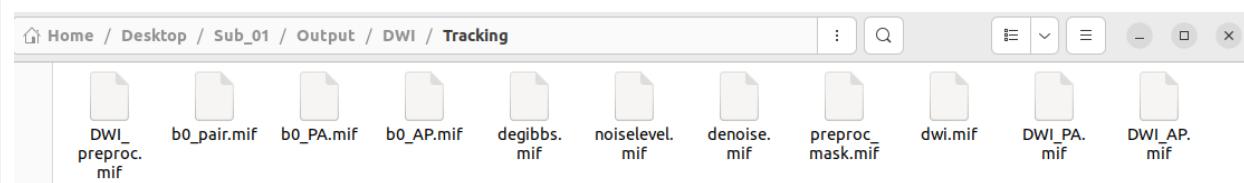
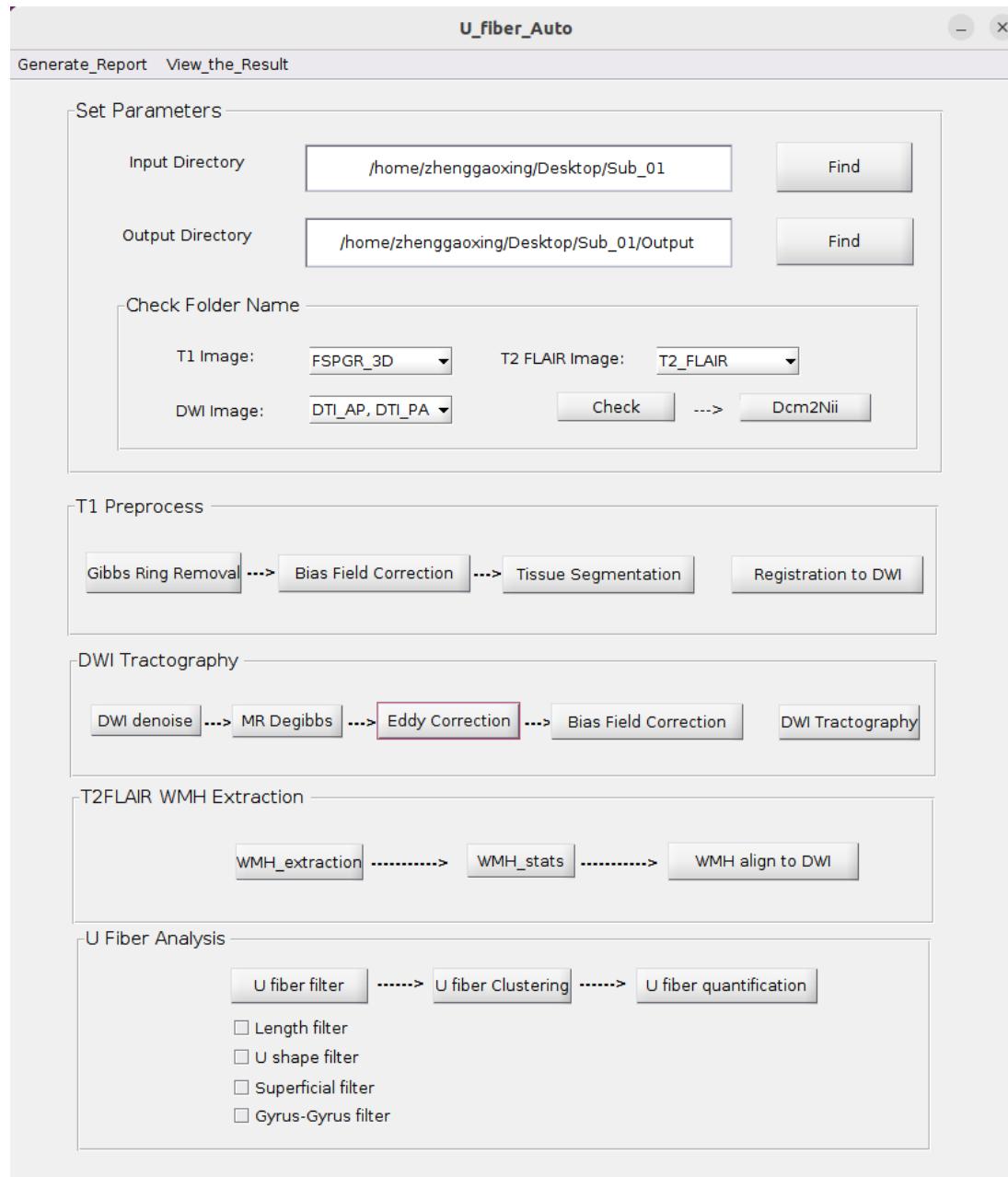
Click the button 'DWI denoise' to remove the noise of DWI image and generate the 'denoise.mif' and 'noiselevel.mif'.



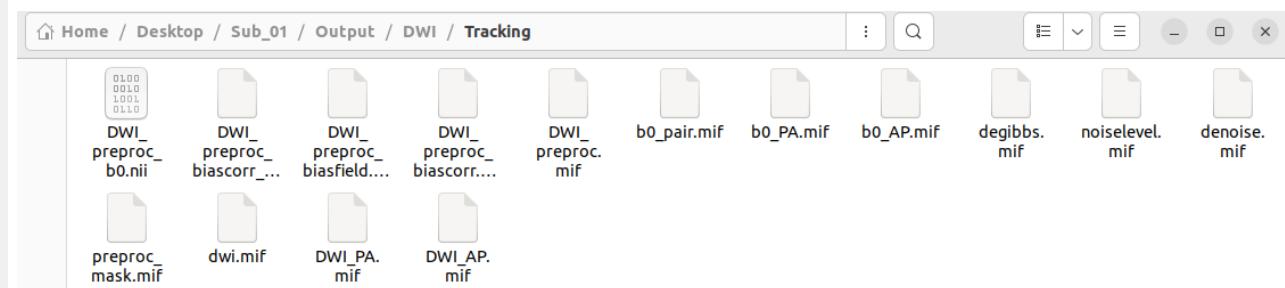
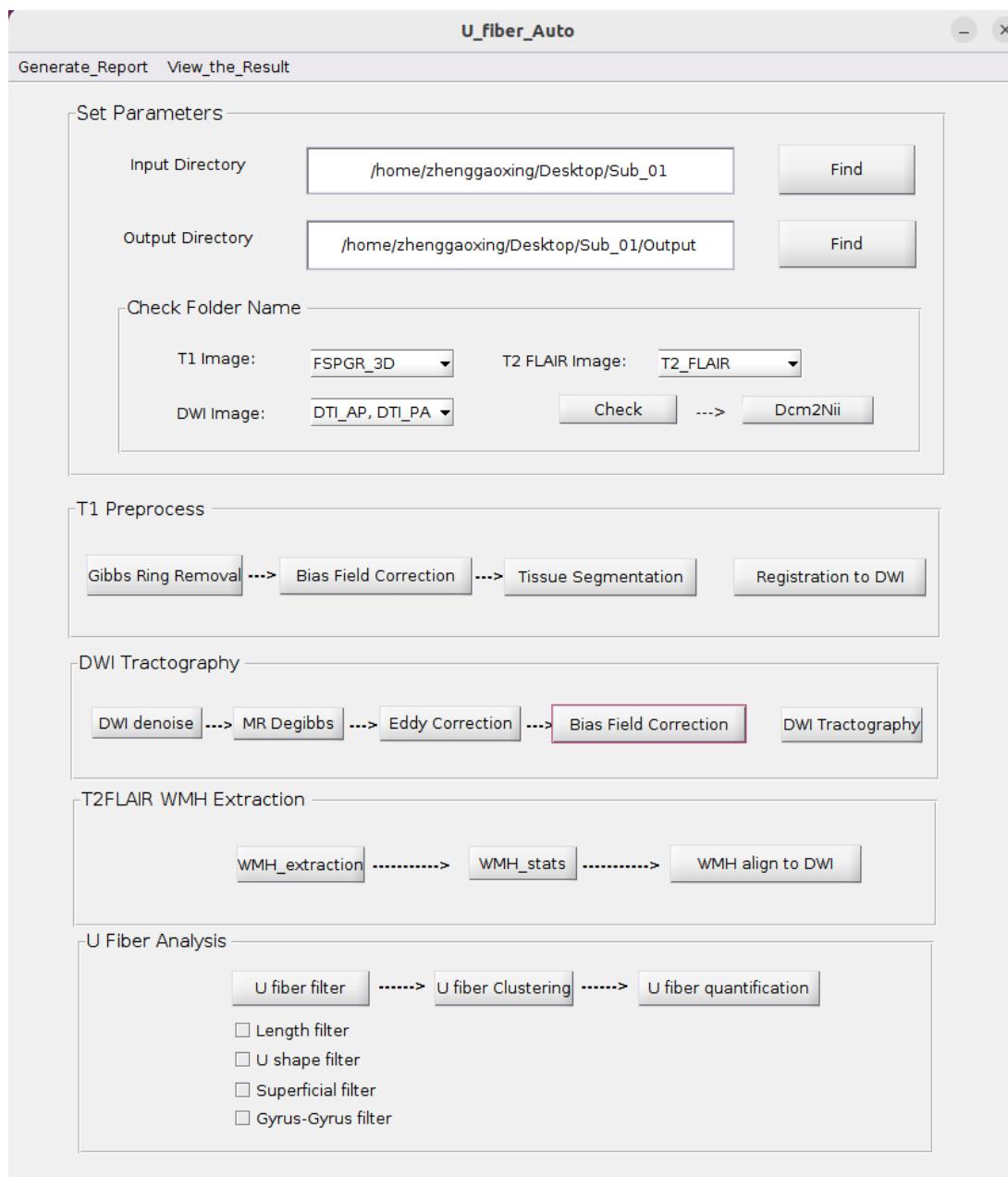
Click the button ‘MR degibbs’ to remove the Gibbs artefacts of DWI image and generate the ‘degibbs.mif’.



Click the button ‘Eddy correction’ to correct eddy currents and movements in diffusion data and generate the ‘DWIpreproc.mif’ file.



Click the button ‘Bias Field Correction’ to correct the bias field noise.



Click the button ‘Registration to DWI’ to align the T1 image to the DWI image.

**U\_fiber\_Auto**

Generate\_Report View\_the\_Result

**Set Parameters**

Input Directory: /home/zhenrgaoxing/Desktop/Sub\_01 Find

Output Directory: /home/zhenrgaoxing/Desktop/Sub\_01/Output Find

**Check Folder Name**

T1 Image: FSPGR\_3D T2 FLAIR Image: T2\_FLAIR

DWI Image: DTI\_AP, DTI\_PA Check ...> Dcm2Nii

**T1 Preprocess**

Gibbs Ring Removal --> Bias Field Correction --> Tissue Segmentation Registration to DWI

**DWI Tractography**

DWI denoise --> MR Degibbs --> Eddy Correction --> Bias Field Correction DWI Tractography

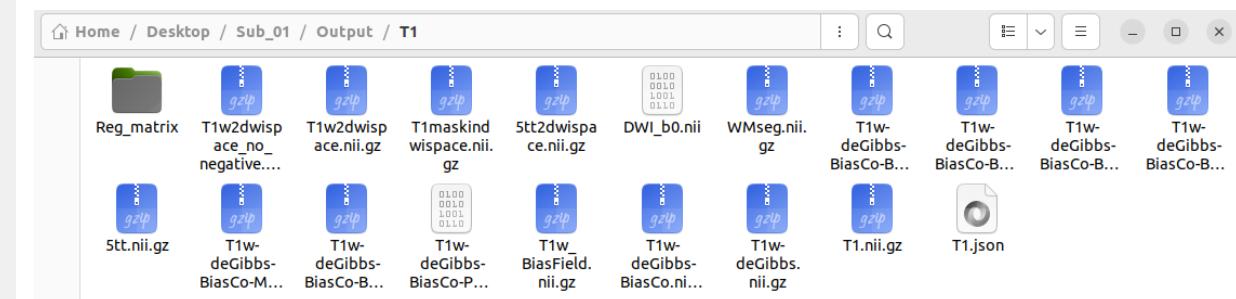
**T2FLAIR WMH Extraction**

WMH\_extraction -----> WMH\_stats -----> WMH align to DWI

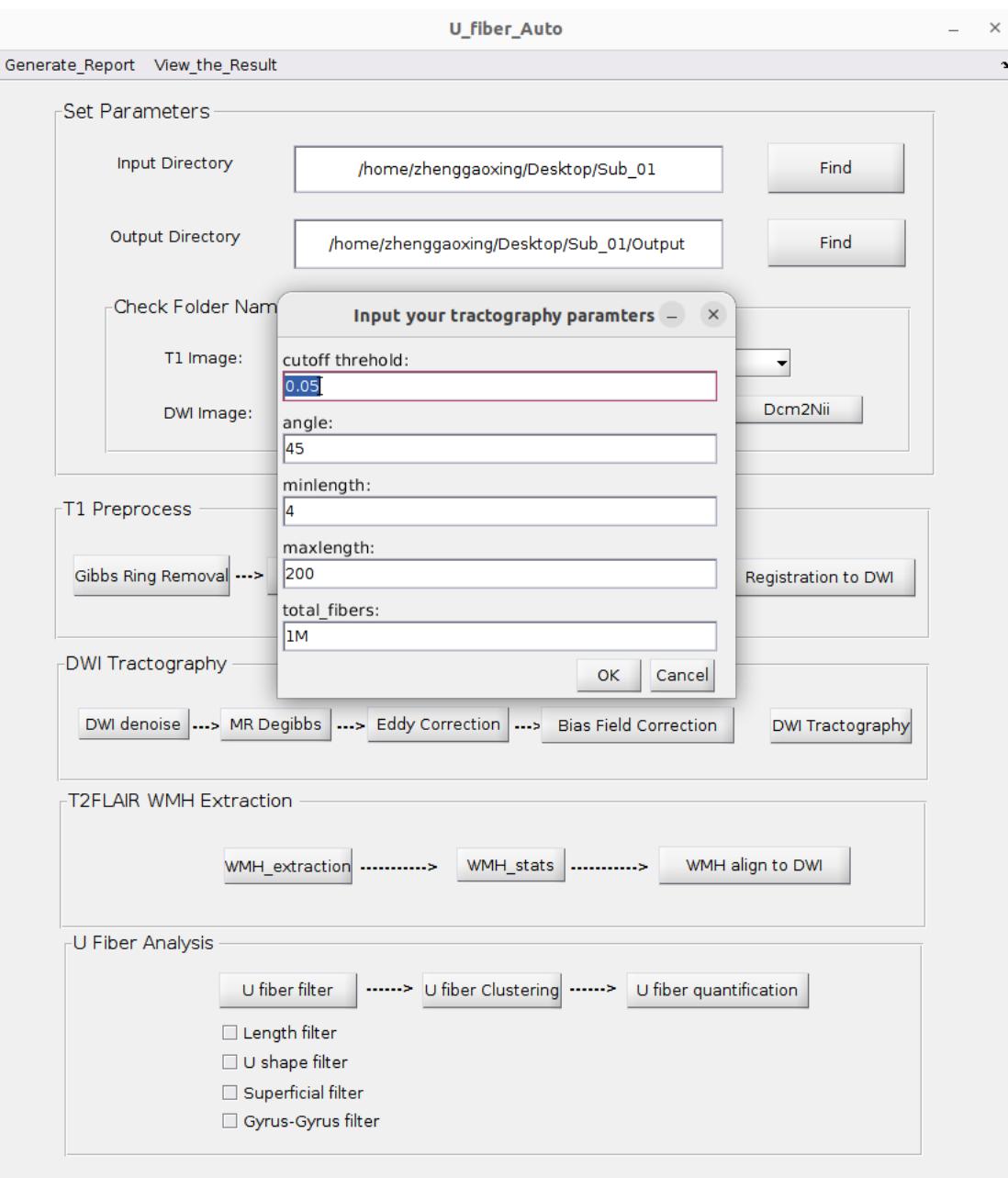
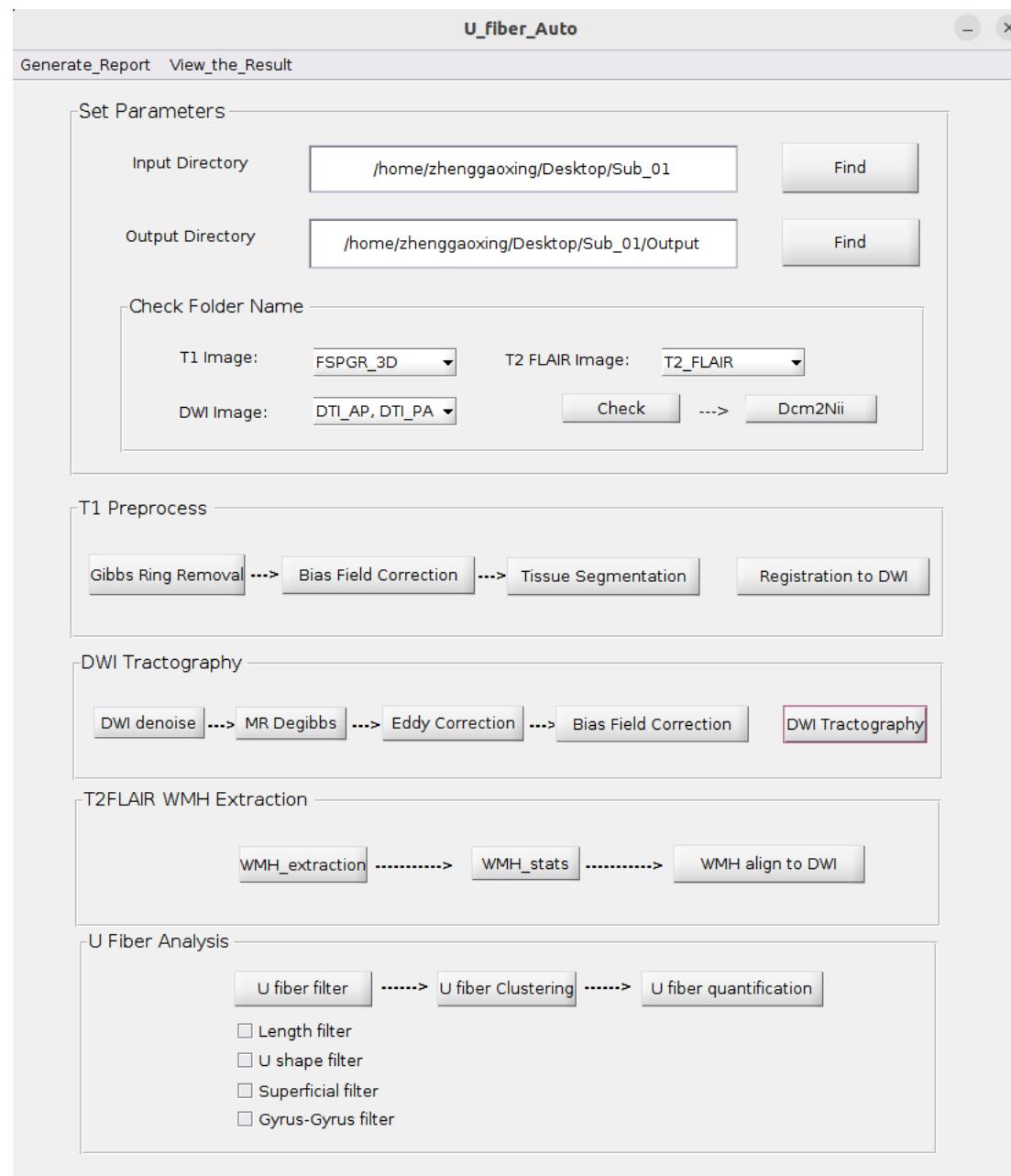
**U Fiber Analysis**

U fiber filter -----> U fiber Clustering -----> U fiber quantification

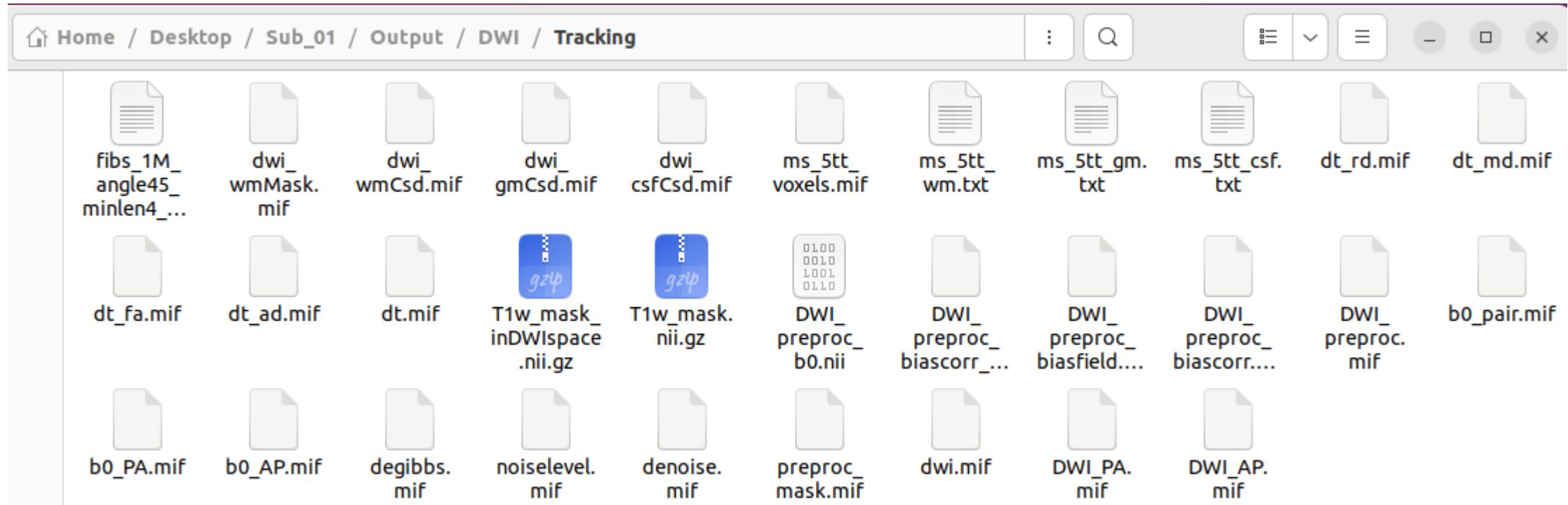
Length filter  
 U shape filter  
 Superficial filter  
 Gyrus-Gyrus filter



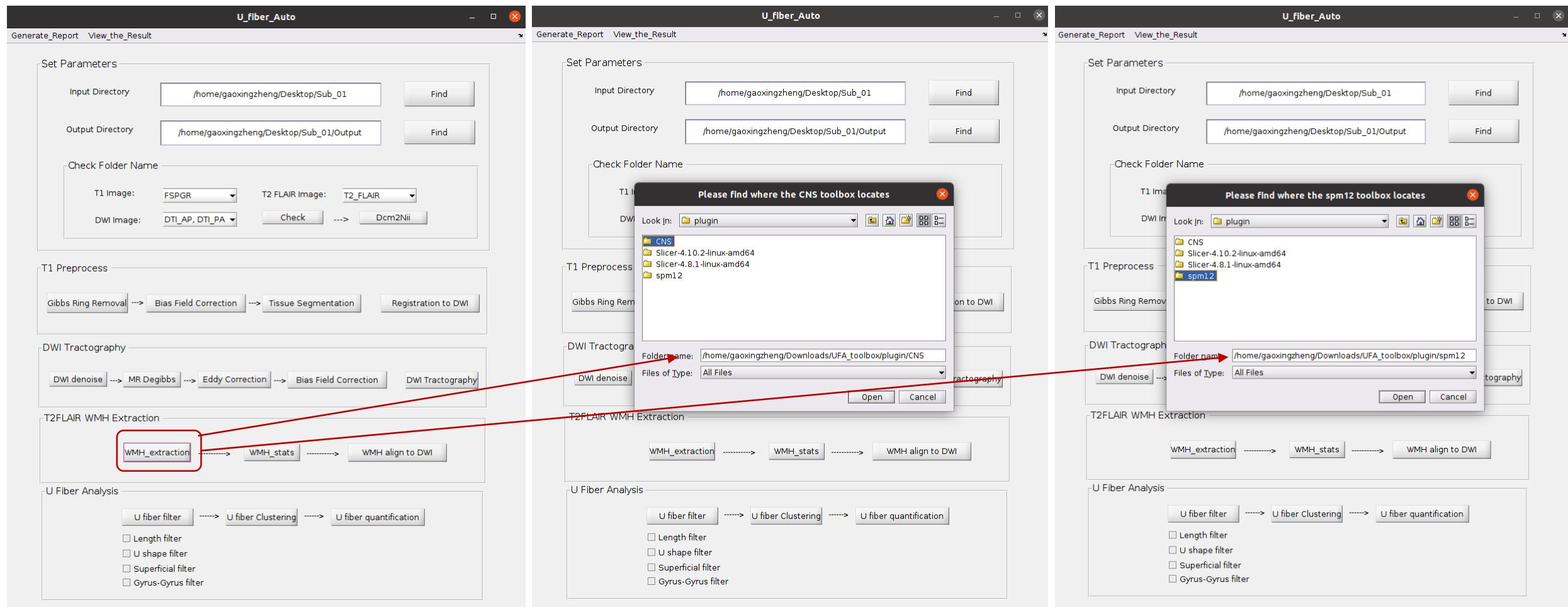
Click the button ‘DWI Tractography’ to generate the white matter tractography. Right panel shows the setting of the tracking parameters.



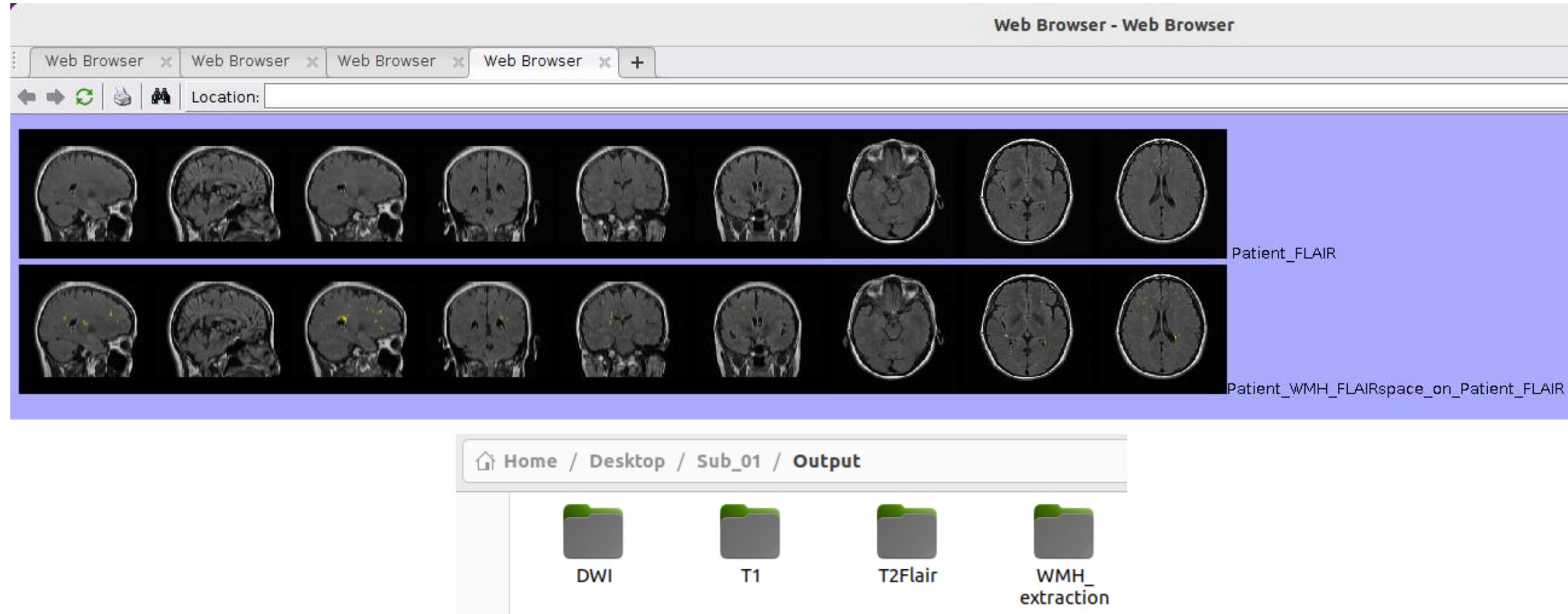
After ‘DWI Tractography’, several files are generated in the ‘Sub\_01/Output/DWI/Tracking’ folder.



Click the button ‘WMH\_extraction’ to call the CNS toolbox (middle panel) and the SPM12 toolbox (right panel) to automatically extract the white matter hyperintensities.



After ‘WMH\_extraction’, it will generate the results as below.



Click the button ‘WMH\_stats’ to visualize the WMH volume and counts in different brain regions.

**U\_fiber\_Auto**

Generate\_Report View\_the\_Result

**Set Parameters**

Input Directory: /home/zhanggaoxiong/Desktop/Sub\_01 Find

Output Directory: /home/zhanggaoxiong/Desktop/Sub\_01/Output Find

Check Folder Name

T1 Image: FSPGR\_3D T2 FLAIR Image: T2\_FLAIR

DWI Image: DTI\_AP, DTI\_PA Check ...> Dcm2Nii

**T1 Preprocess**

Gibbs Ring Removal --> Bias Field Correction --> Tissue Segmentation Registration to DWI

**DWI Tractography**

DWI denoise --> MR Degibbs --> Eddy Correction --> Bias Field Correction DWI Tractography

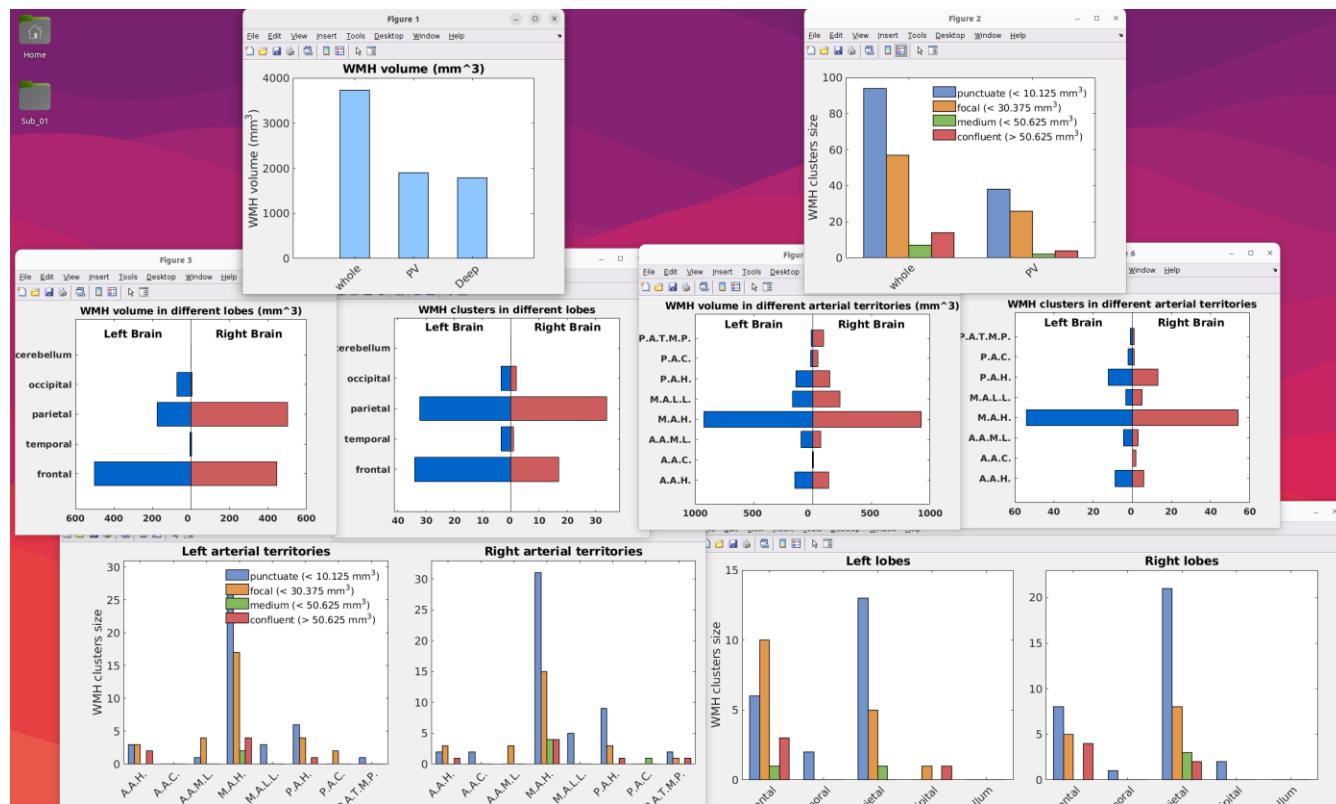
**T2FLAIR WMH Extraction**

WMH\_extraction --> WMH\_stats --> WMH align to DWI

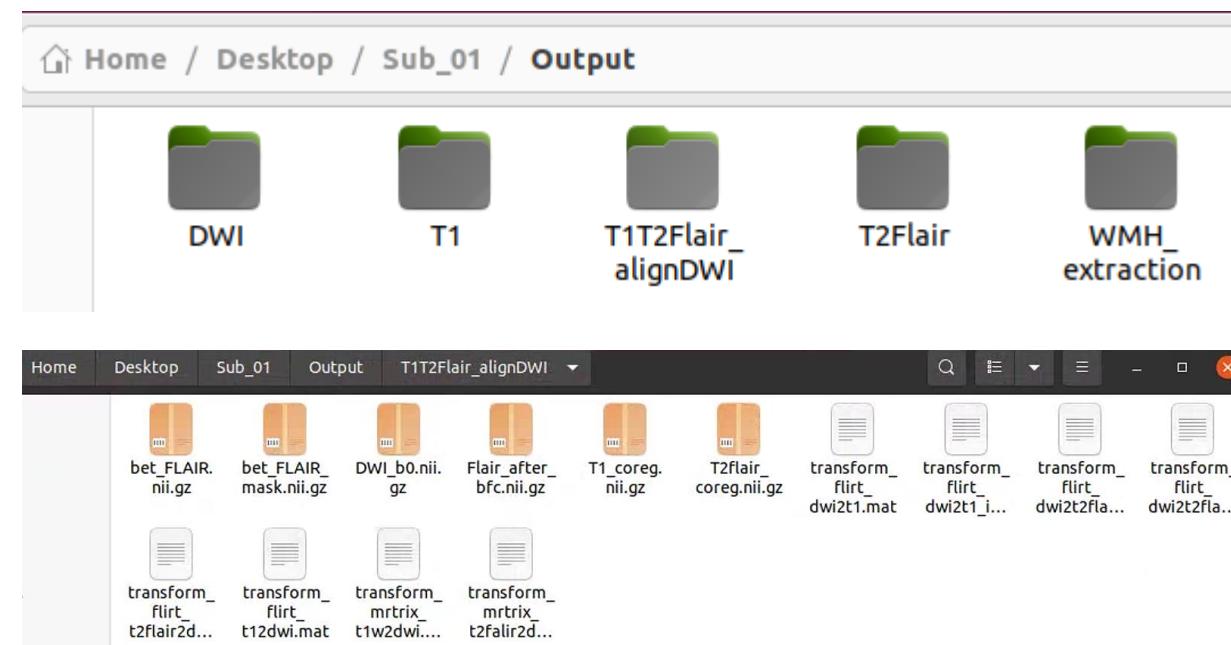
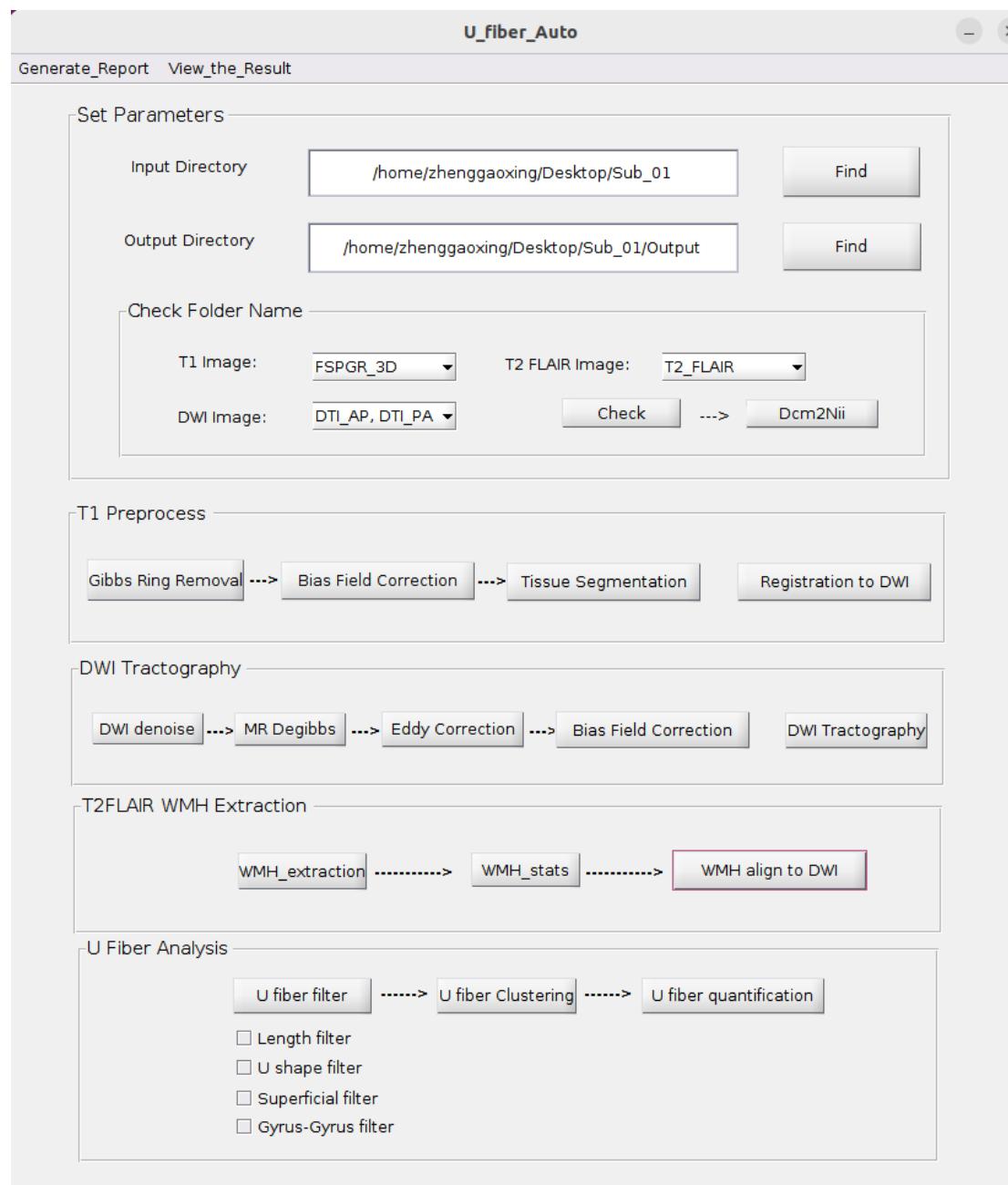
**U Fiber Analysis**

U fiber filter --> U fiber Clustering --> U fiber quantification

Length filter  
 U shape filter  
 Superficial filter  
 Gyrus-Gyrus filter

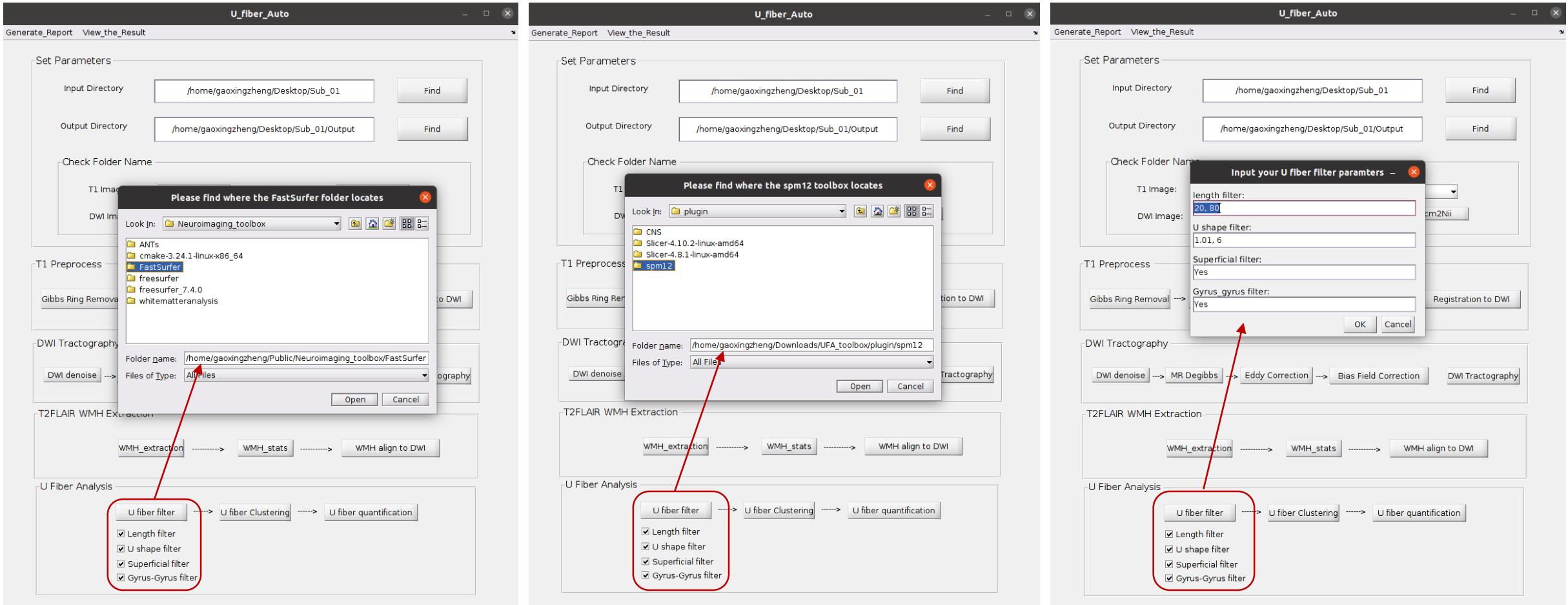


Click the button ‘WMH align to DWI’ to align the WMH (FLAIR Image) to the DWI b0 image.

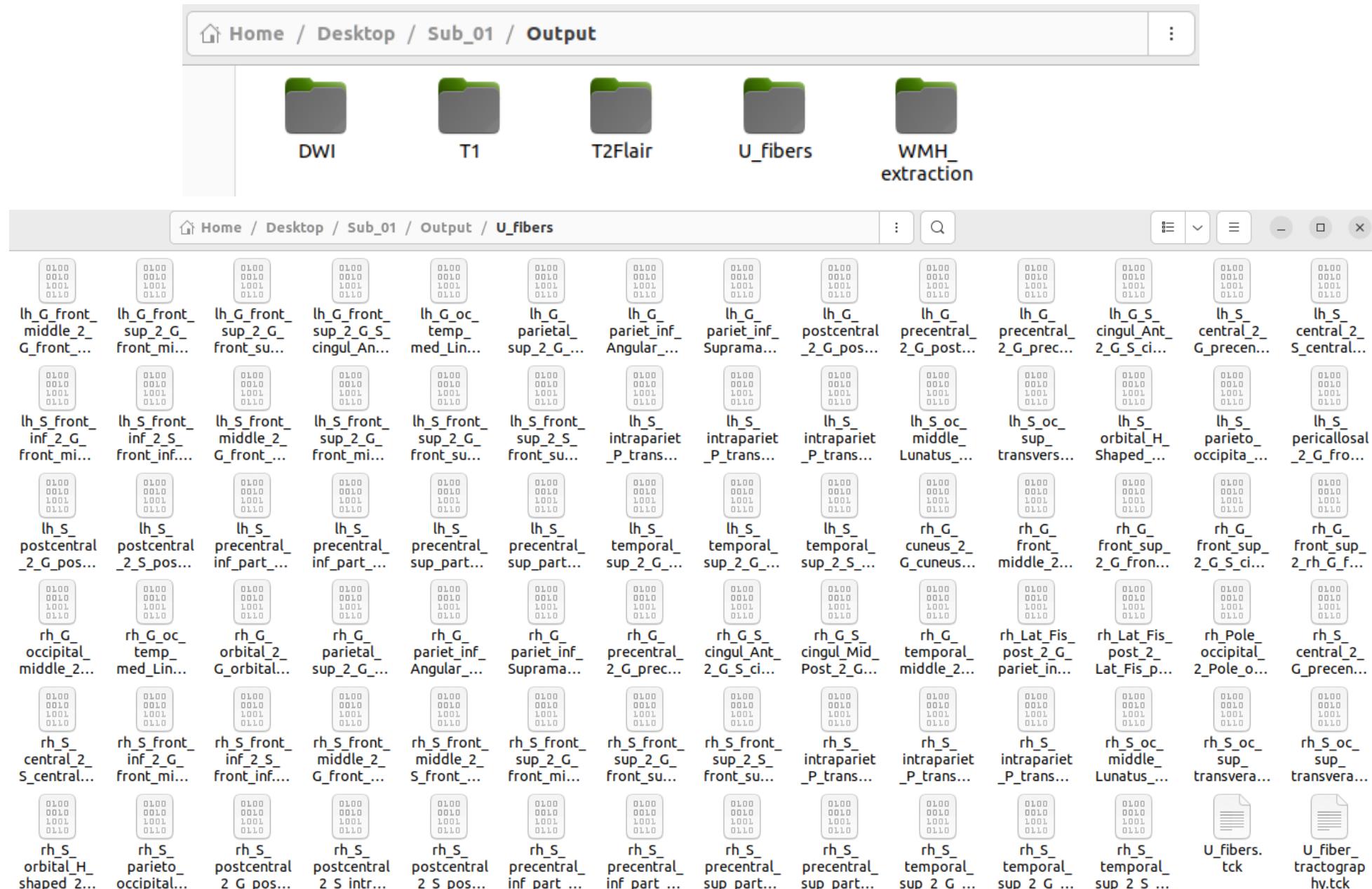


Click the button ‘U fiber filter’ to generate the U fibers tractography from the whole brain white matter tractography.

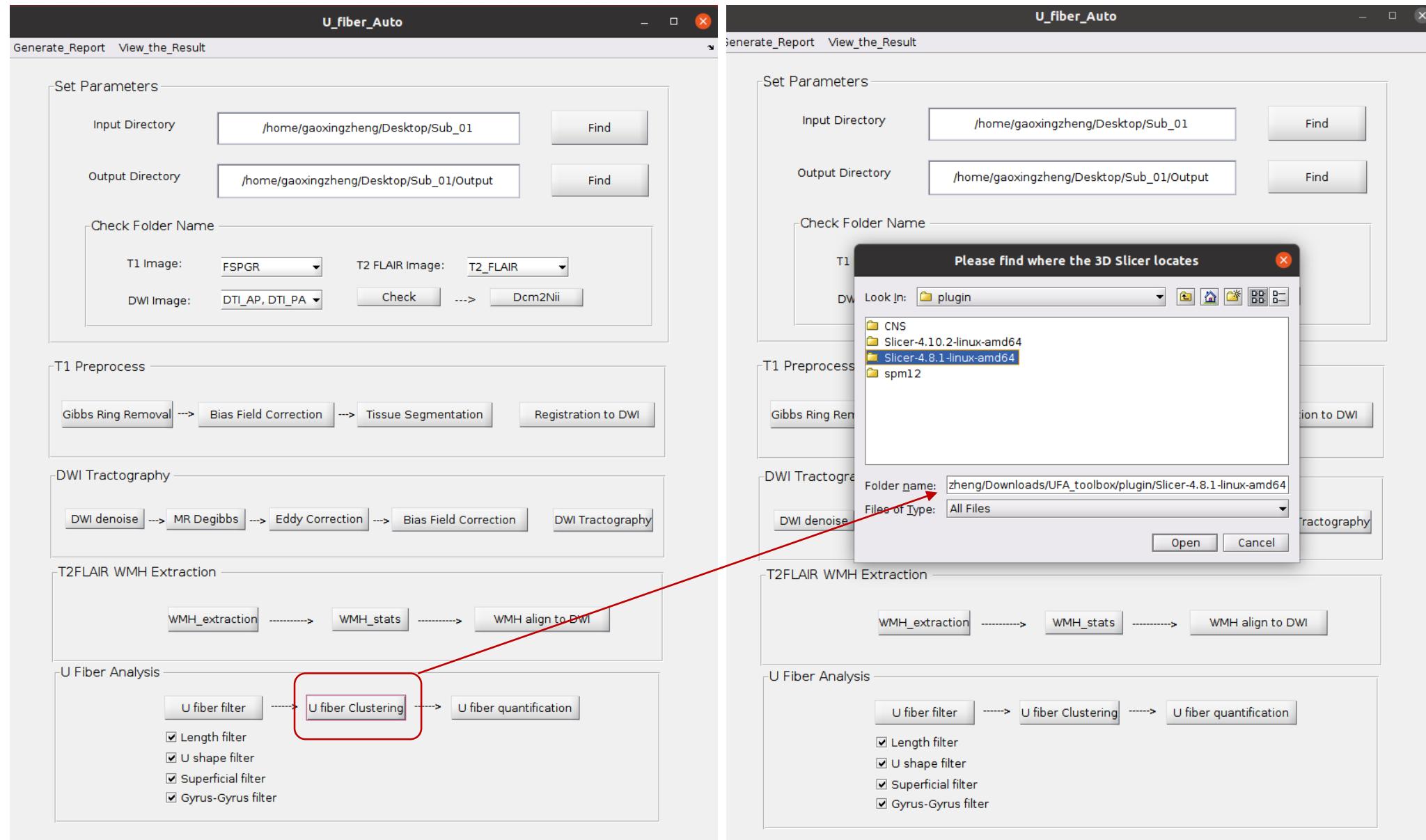
The right panel shows the related parameters settings.



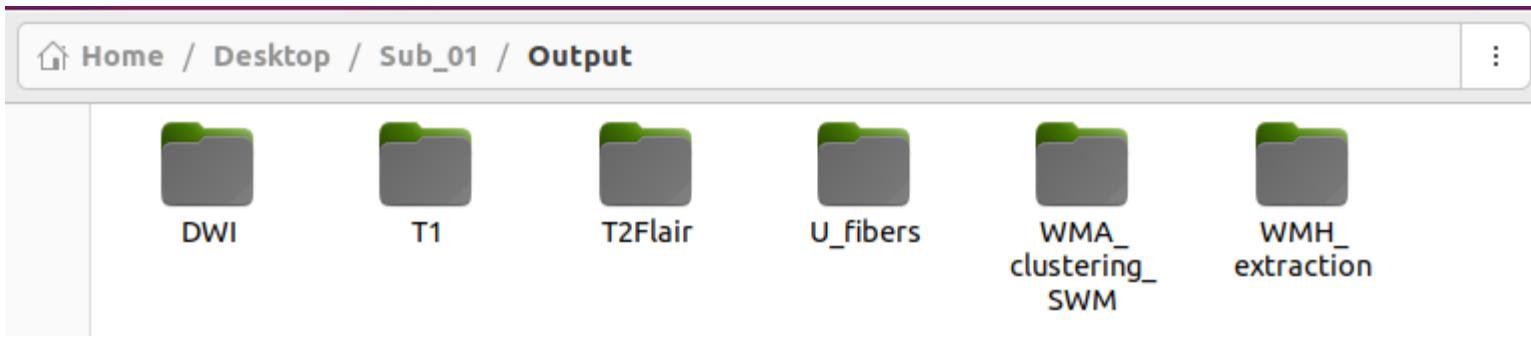
The generated U fibers files are shown below.



Click the button ‘U fiber Clustering’ to generate the superficial U fiber clusters by calling the white matter analysis (WMA) package. The right panel shows how to choose the 3D Slicer path.



The U fiber clustering results are shown below.



DiffusionMeasures	FiberClustering	pycache_-	QC	TractRegistration	T_AF_left.tck	T_AF_left.vtp	T_AF_right.tck	T_AF_right.vtp	T_CB_left.tck	T_CB_left.vtp	T_CB_right.tck	T_CB_right.vtp	T_CC1.tck	T_CC1.vtp	T_CC2.tck	T_CC2.vtp	T_CC3.tck	T_CC3.vtp	T_CC4.tck	T_CC4.vtp	T_CCS.tck	T_CCS.vtp			
0100 0010 1001 0110	</>																								
T_CC6.tck	T_CC6.vtp	T_CC7.tck	T_CC7.vtp	T_CPC_left.tck	T_CPC_left.vtp	T_CPC_right.tck	T_CPC_right.vtp	T_CRF_left.tck	T_CRF_left.vtp	T_CRF_right.tck	T_CRF_right.vtp	T_CRP_left.tck	T_CRP_left.vtp	T_CRP_right.tck	T_CRP_right.vtp	T_CST_left.tck	T_CST_left.vtp	T_CST_right.tck	T_CST_right.vtp	T_EC_left.tck	T_EC_left.vtp	T_EC_right.tck	T_EC_right.vtp		
</>	0100 0010 1001 0110	</>																							
T_EM_right.vtp	T_EM_left.tck	T_EM_left.vtp	T_EM_right.tck	T_ICP_left.tck	T_ICP_left.vtp	T_ICP_right.tck	T_ICP_right.vtp	T_ILF_left.tck	T_ILF_left.vtp	T_ILF_right.tck	T_ILF_right.vtp	T_IntraCBLMI&P_left.tck	T_IntraCBLMI&P_left.vtp	T_IntraCBLMI&P_right.tck	T_IntraCBLMI&P_right.vtp	T_IntraCBLMPaT_left.tck	T_IntraCBLMPaT_left.vtp	T_IntraCBLMPaT_right.tck	T_IntraCBLMPaT_right.vtp	T_IOFF_left.tck	T_IOFF_left.vtp	T_IOFF_right.tck	T_IOFF_right.vtp		
0100 0010 1001 0110	</>																								
T_IOFF_right.tck	T_IOFF_right.vtp	T_MCP.tck	T_MCP.vtp	T_MdLF_left.tck	T_MdLF_left.vtp	T_MdLF_right.tck	T_MdLF_right.vtp	T_PLIC_left.tck	T_PLIC_left.vtp	T_PLIC_right.tck	T_PLIC_right.vtp	T_SF_left.tck	T_SF_left.vtp	T_SF_right.tck	T_SF_right.vtp	T_SLFIII_left.tck	T_SLFIII_left.vtp	T_SLFIII_right.tck	T_SLFIII_right.vtp	T_SLFII_left.tck	T_SLFII_left.vtp	T_SLFII_right.tck	T_SLFII_right.vtp		
</>	0100 0010 1001 0110	</>																							
T_SLFII_right.vtp	T_SLFI_left.tck	T_SLFI_left.vtp	T_SLFI_right.tck	T_SLFI_right.vtp	T_SO_left.tck	T_SO_left.vtp	T_SO_right.tck	T_SO_right.vtp	T_SP_left.tck	T_SP_left.vtp	T_SP_right.tck	T_SP_right.vtp	T_SupF_left.tck	T_SupF_left.vtp	T_SupF_right.tck	T_SupF_right.vtp	T_SupFP_left.tck	T_SupFP_left.vtp	T_SupFP_right.tck	T_SupFP_right.vtp	T_SupF_left.tck	T_SupF_left.vtp	T_SupO_left.tck	T_SupO_left.vtp	
0100 0010 1001 0110	</>	0100 0010 1001 0110	</>																						
T_SupO_right.tck	T_SupO_right.vtp	T_SupOT_left.tck	T_SupOT_left.vtp	T_SupOT_right.tck	T_SupOT_right.vtp	T_SupP_left.tck	T_SupP_left.vtp	T_SupPO_left.tck	T_SupPO_left.vtp	T_SupPO_right.tck	T_SupPO_right.vtp	T_SupP_right.tck	T_SupP_right.vtp	T_SupPT_left.tck	T_SupPT_left.vtp	T_SupPT_right.tck	T_SupPT_right.vtp	T_SupT_left.tck	T_SupT_left.vtp	T_SupT_right.tck	T_SupT_right.vtp	T_SupO_left.tck	T_SupO_left.vtp		
</>	0100 0010 1001 0110	</>																							
T_TF_left.vtp	T_TF_right.tck	T_TF_right.vtp	T_TO_left.tck	T_TO_left.vtp	T_TO_right.tck	T_TO_right.vtp	T_TP_left.tck	T_TP_left.vtp	T_TP_right.tck	T_TP_right.vtp	T_UF_left.tck	T_UF_left.vtp	T_UF_right.tck	T_UF_right.vtp	U_fibers.tck	whole tract.vtk							T_TF_left.tck	T_TF_left.vtp	

Click the button ‘U fiber quantification’ to visualize the numbers and mean length of the U fibers, as well as the diffusion parameters of the 16 superficial U fibers.

**U\_fiber\_Auto**

Generate\_Report View\_the\_Result

**Set Parameters**

Input Directory: /home/zhenggaoxing/Desktop/Sub\_01 Find

Output Directory: /home/zhenggaoxing/Desktop/Sub\_01/Output Find

**Check Folder Name**

T1 Image: FSPGR\_3D T2 FLAIR Image: T2\_FLAIR

DWI Image: DTI\_AP, DTI\_PA Check ...> Dcm2Nii

**T1 Preprocess**

Gibbs Ring Removal ...> Bias Field Correction ...> Tissue Segmentation Registration to DWI

**DWI Tractography**

DWI denoise ...> MR Degibbs ...> Eddy Correction ...> Bias Field Correction DWI Tractography

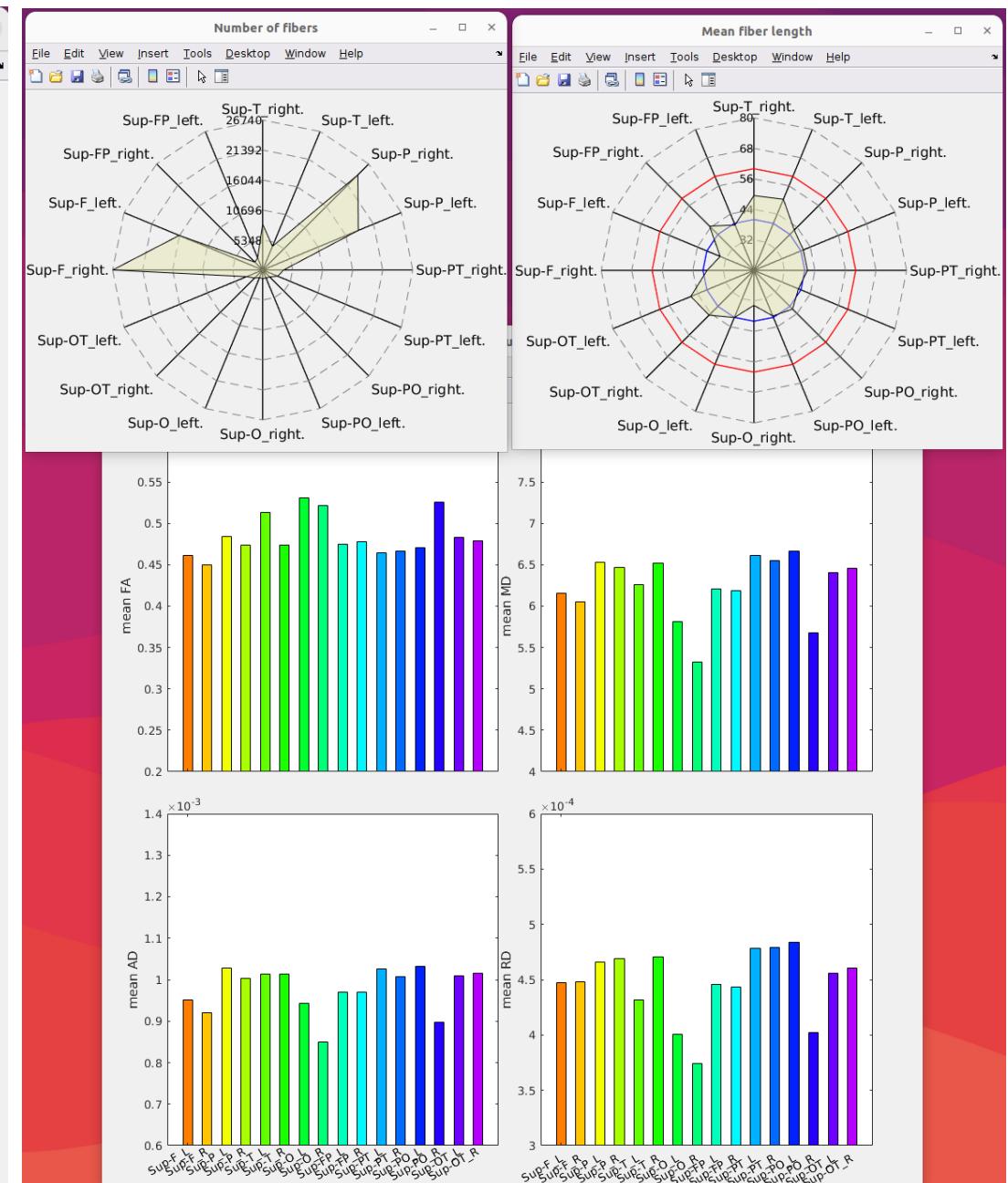
**T2FLAIR WMH Extraction**

WMH\_extraction .....> WMH\_stats .....> WMH align to DWI

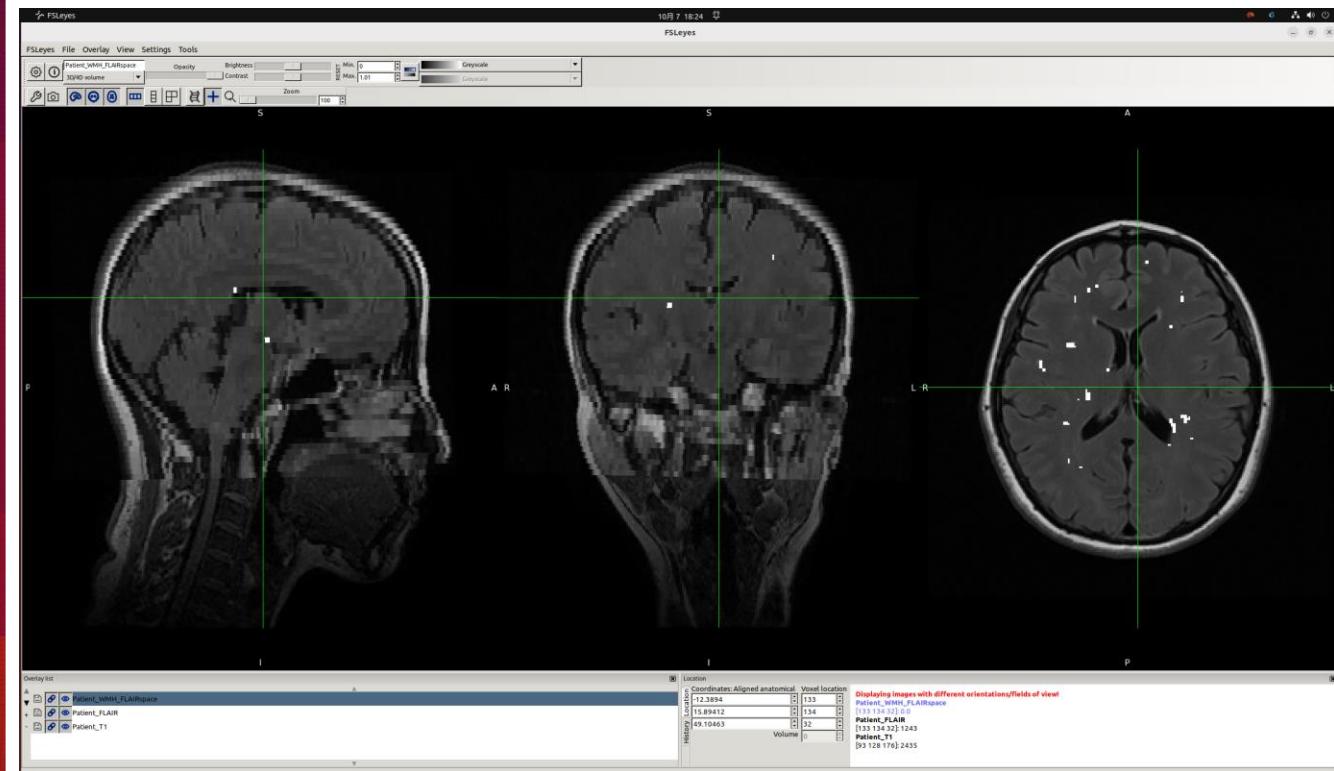
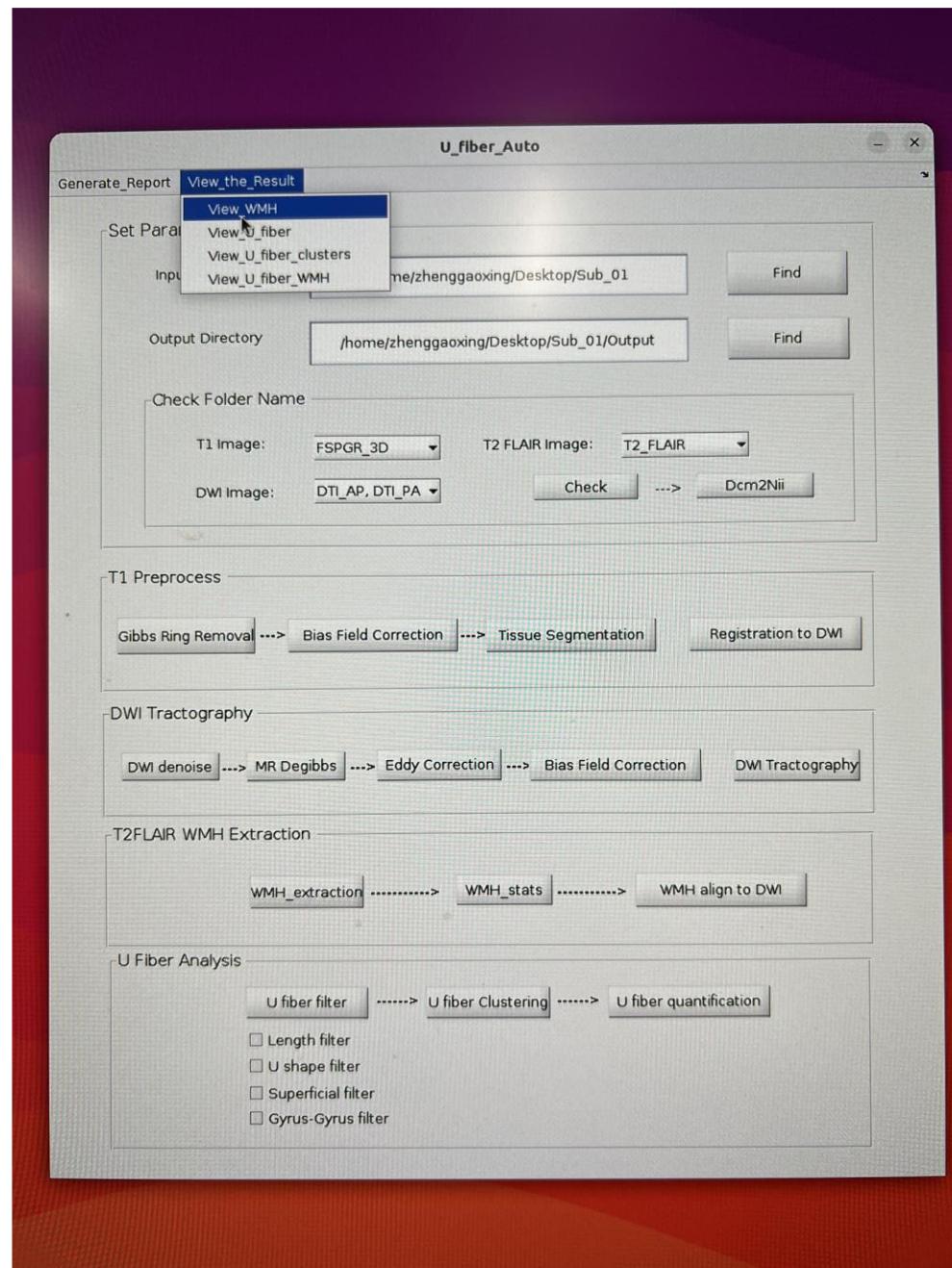
**U Fiber Analysis**

U fiber filter .....> U fiber Clustering .....> U fiber quantification

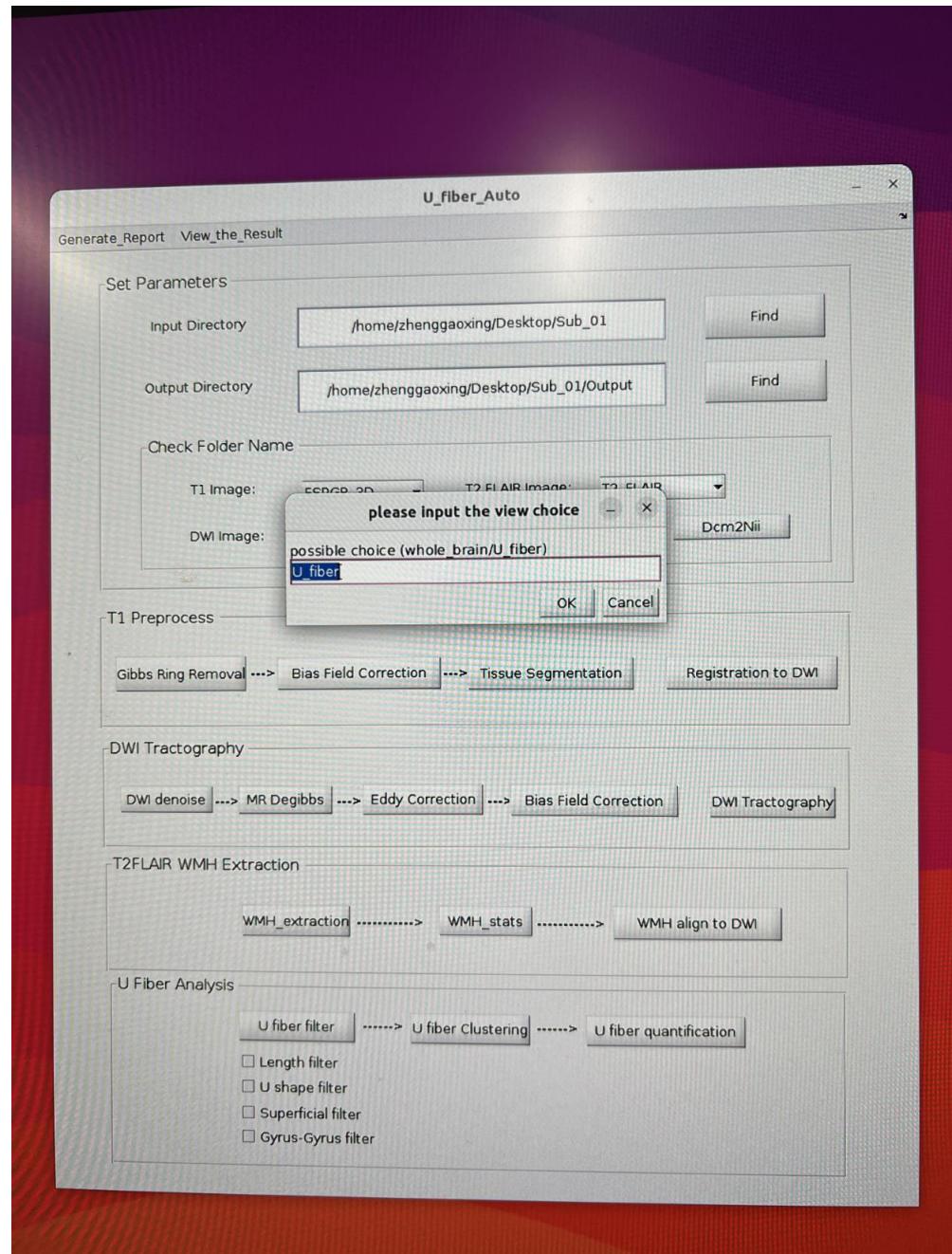
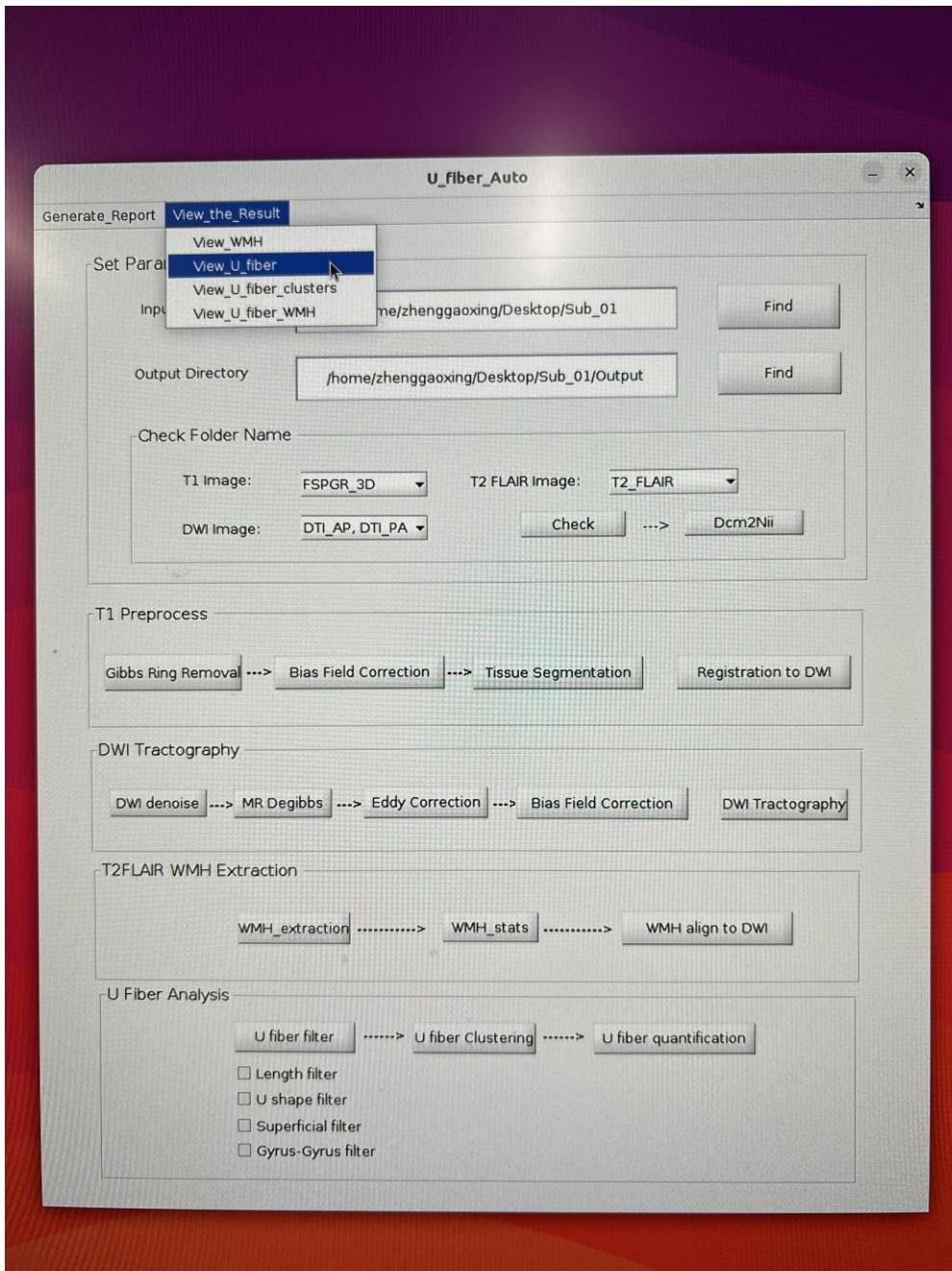
- Length filter
- U shape filter
- Superficial filter
- Gyrus-Gyrus filter



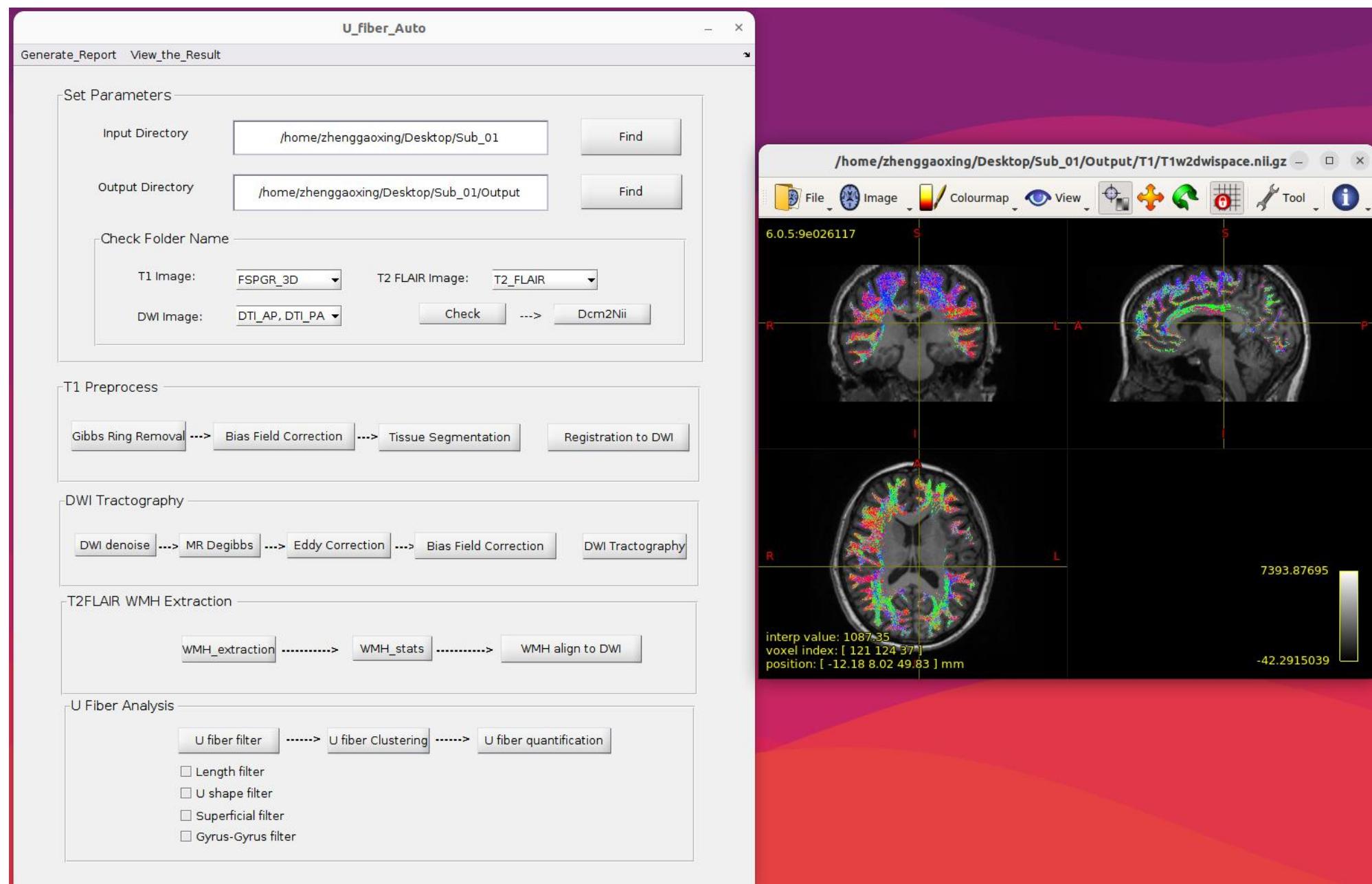
Click the popup-menu ‘View\_WMH’ to visualize the WMH in the T2 FLAIR image by using ‘fsleyes’ in FSL.



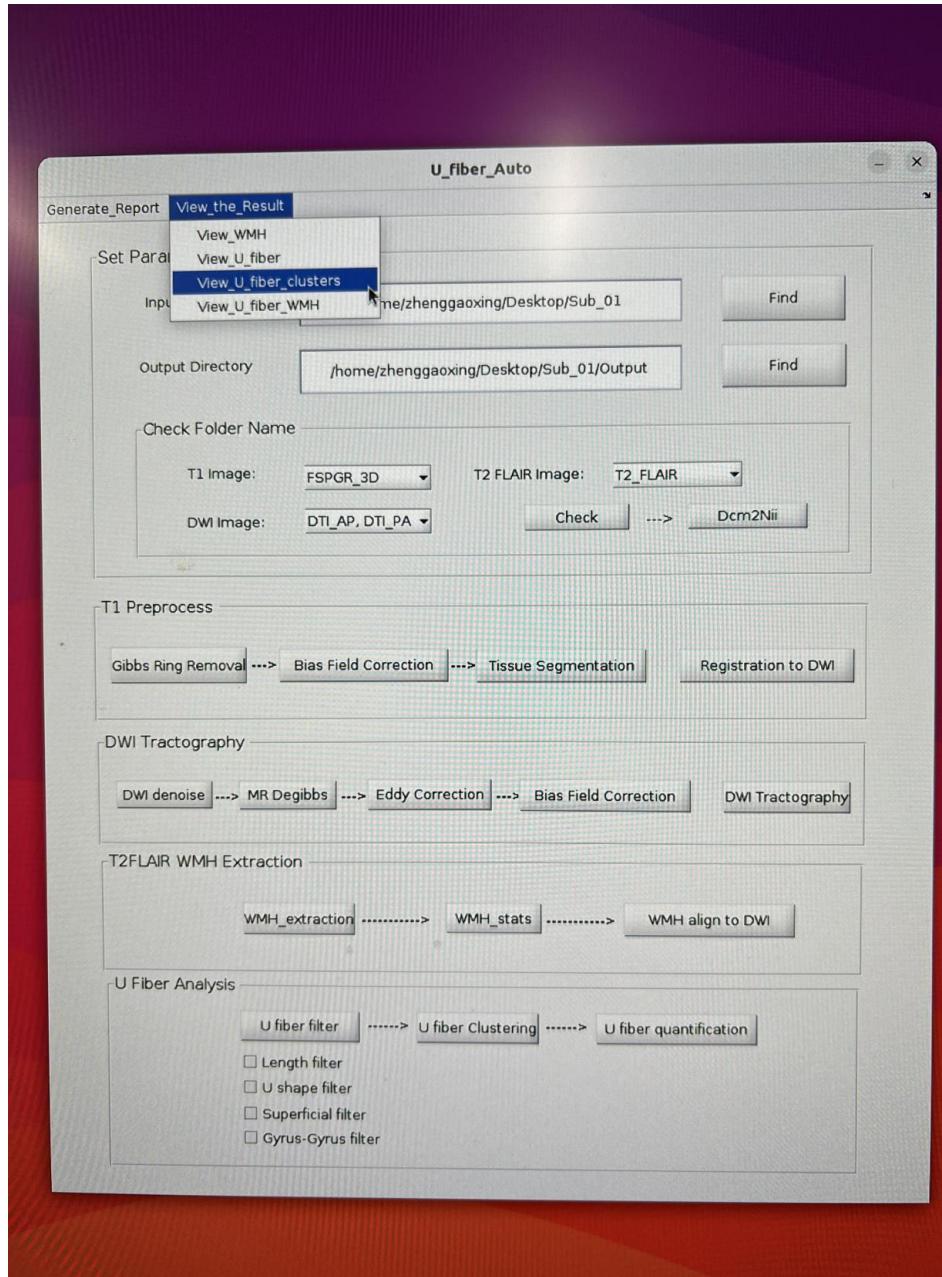
Click the popup-menu ‘View\_U\_fiber’ to visualize the U fibers tractography by using ‘mrview’ in MRtrxi3.



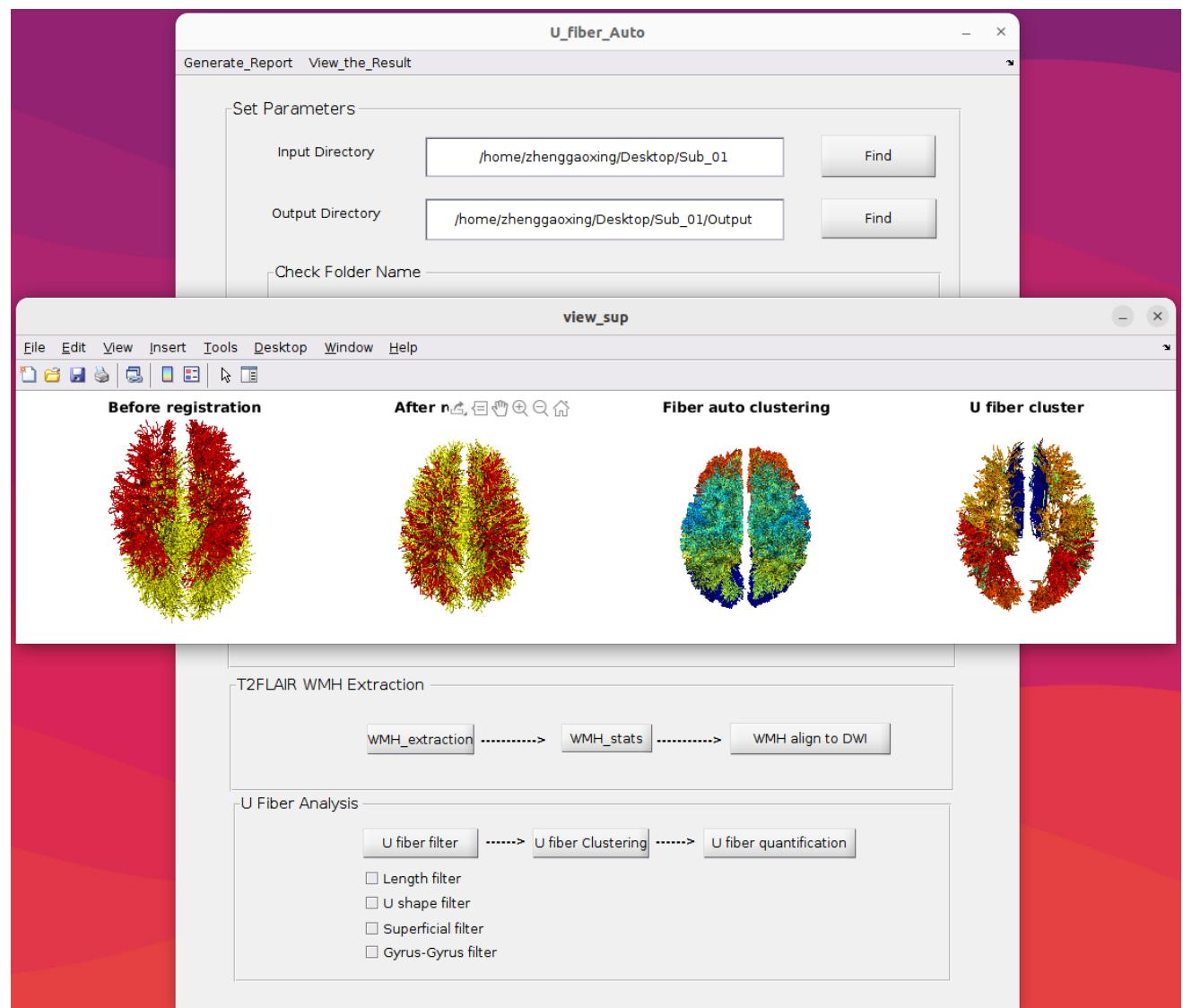
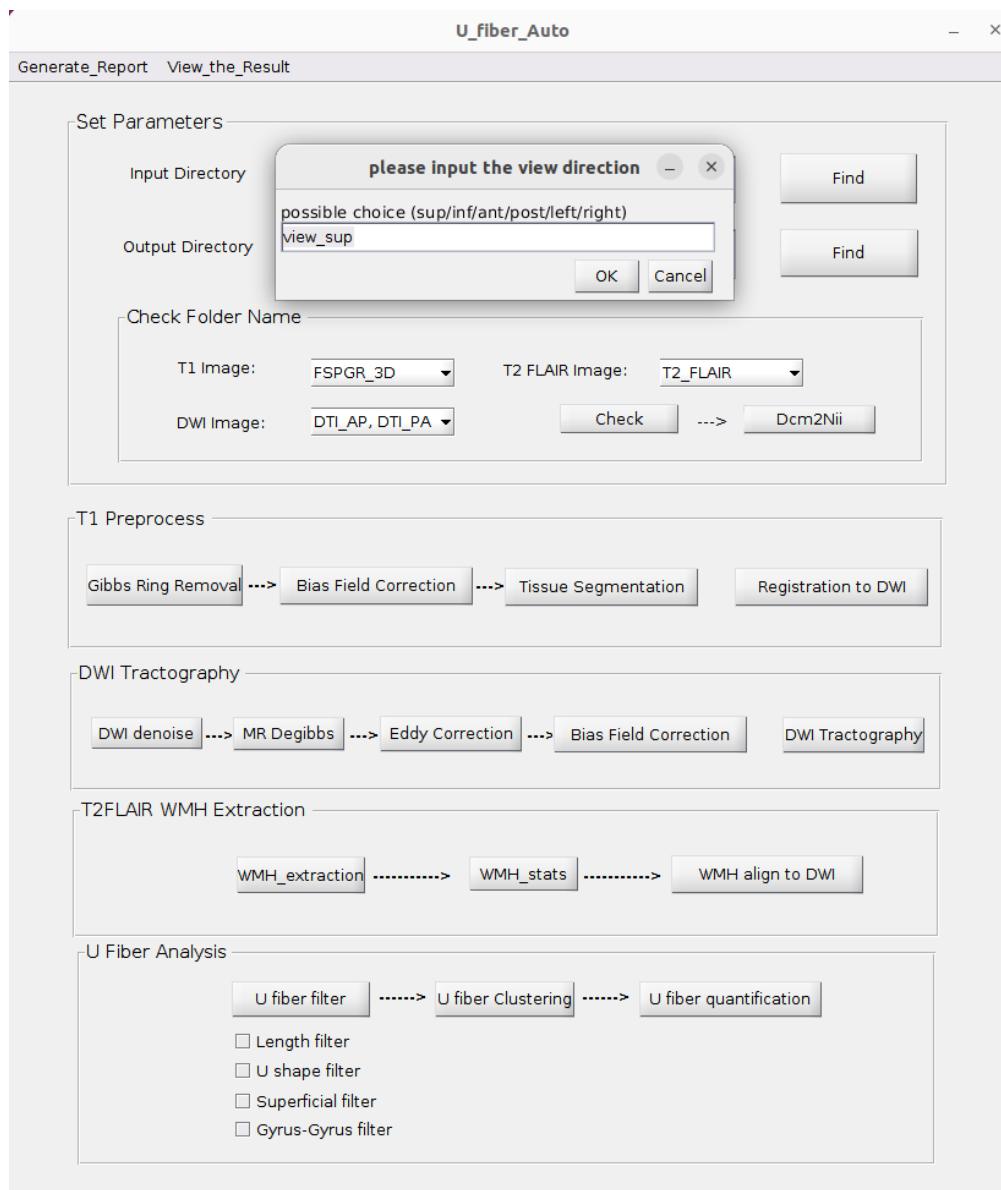
The U fiber tractography is visualized by using ‘mrview’ (right panel).



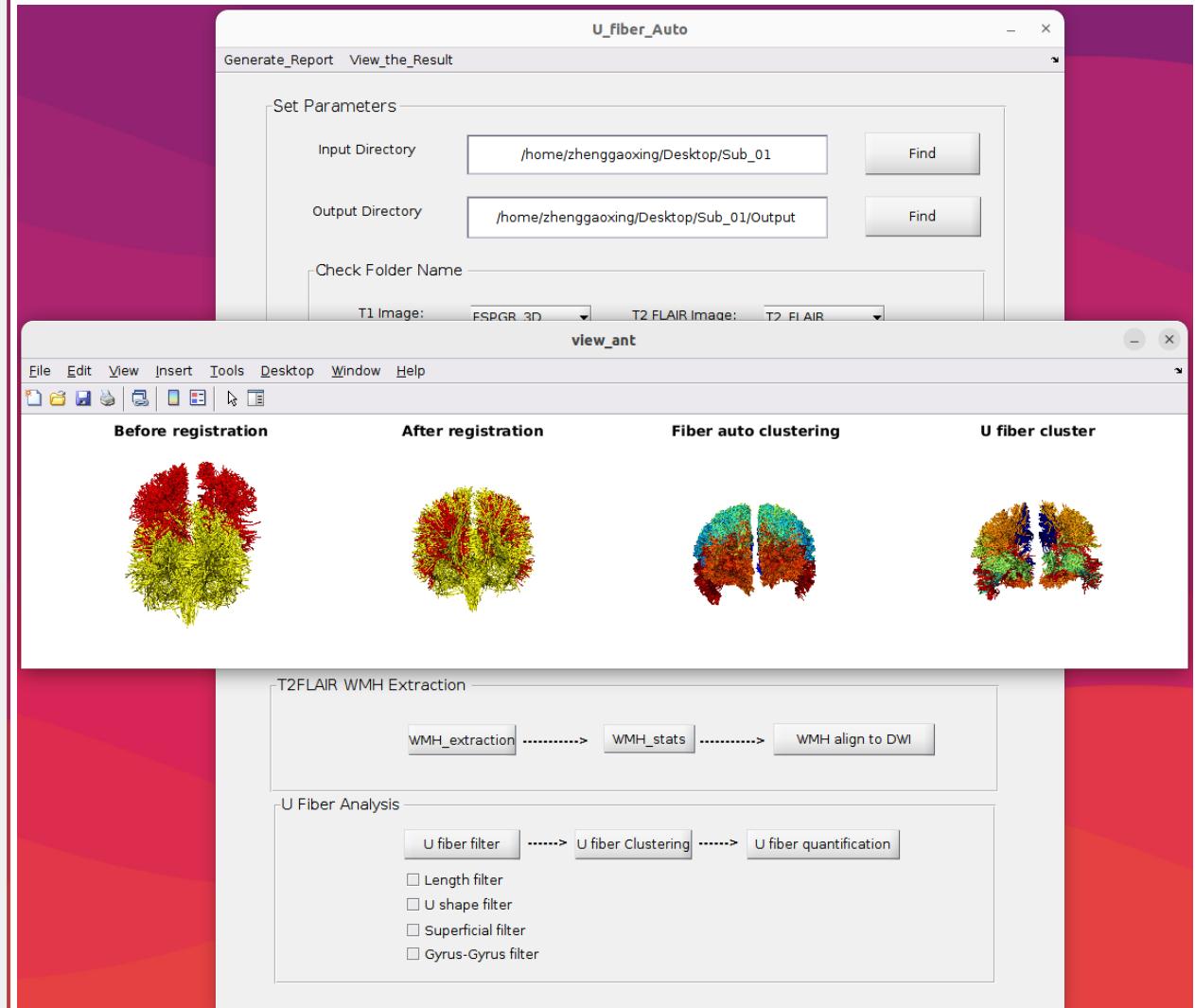
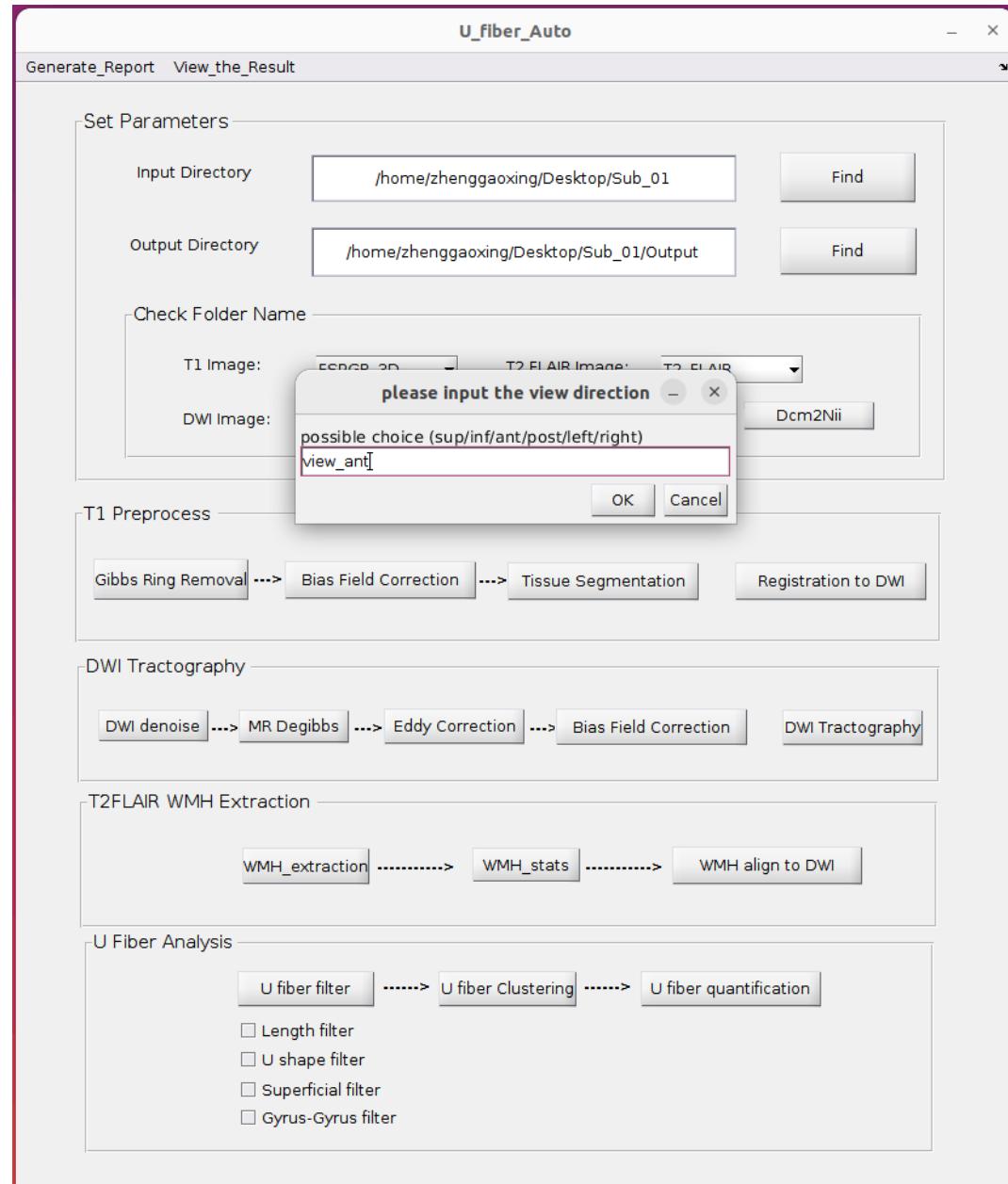
Click the popup-menu ‘View\_U\_fiber\_clusters’ to visualize the U fiber clusters from different view.



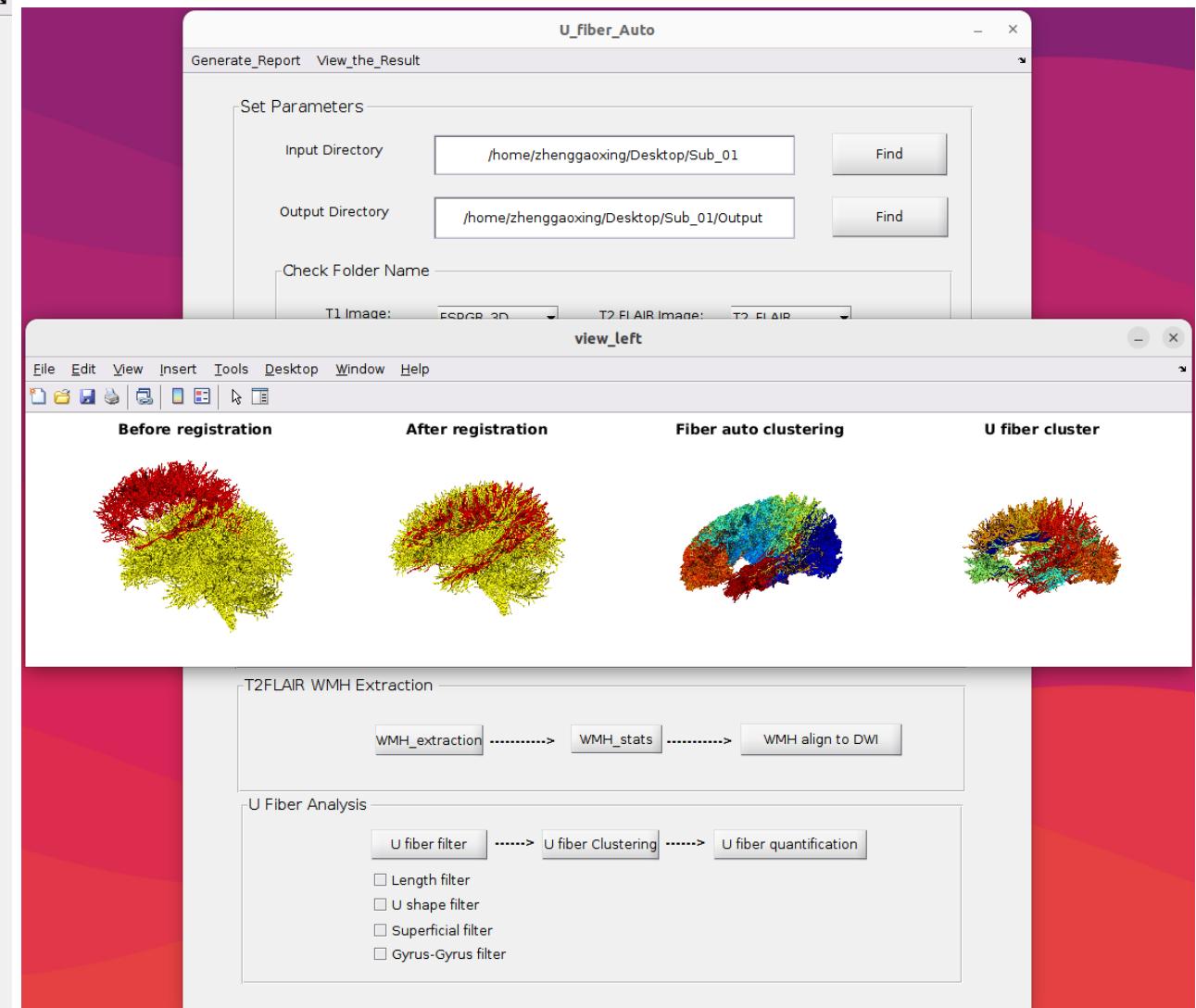
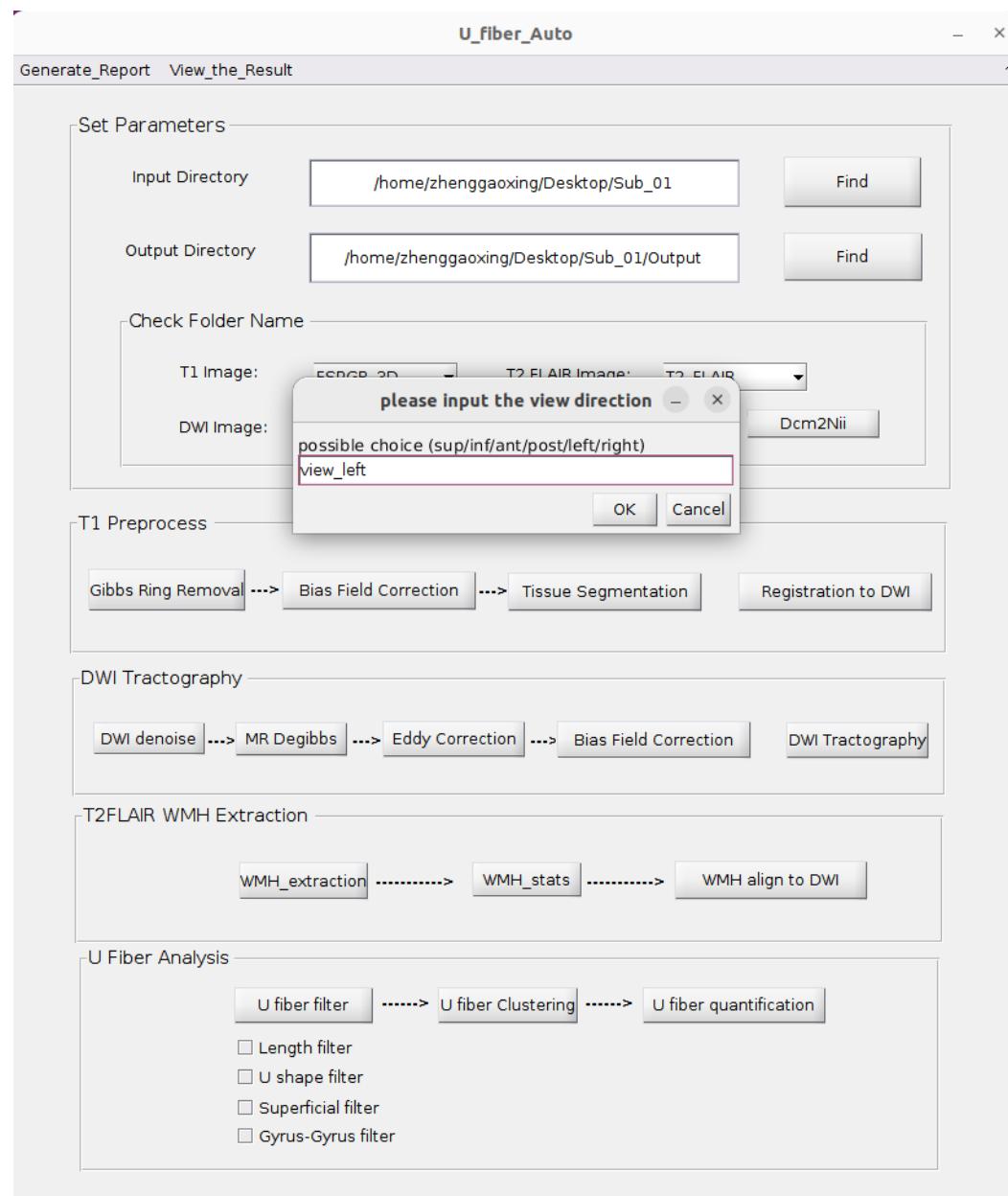
## Visualize the U fiber clusters from the superior view.



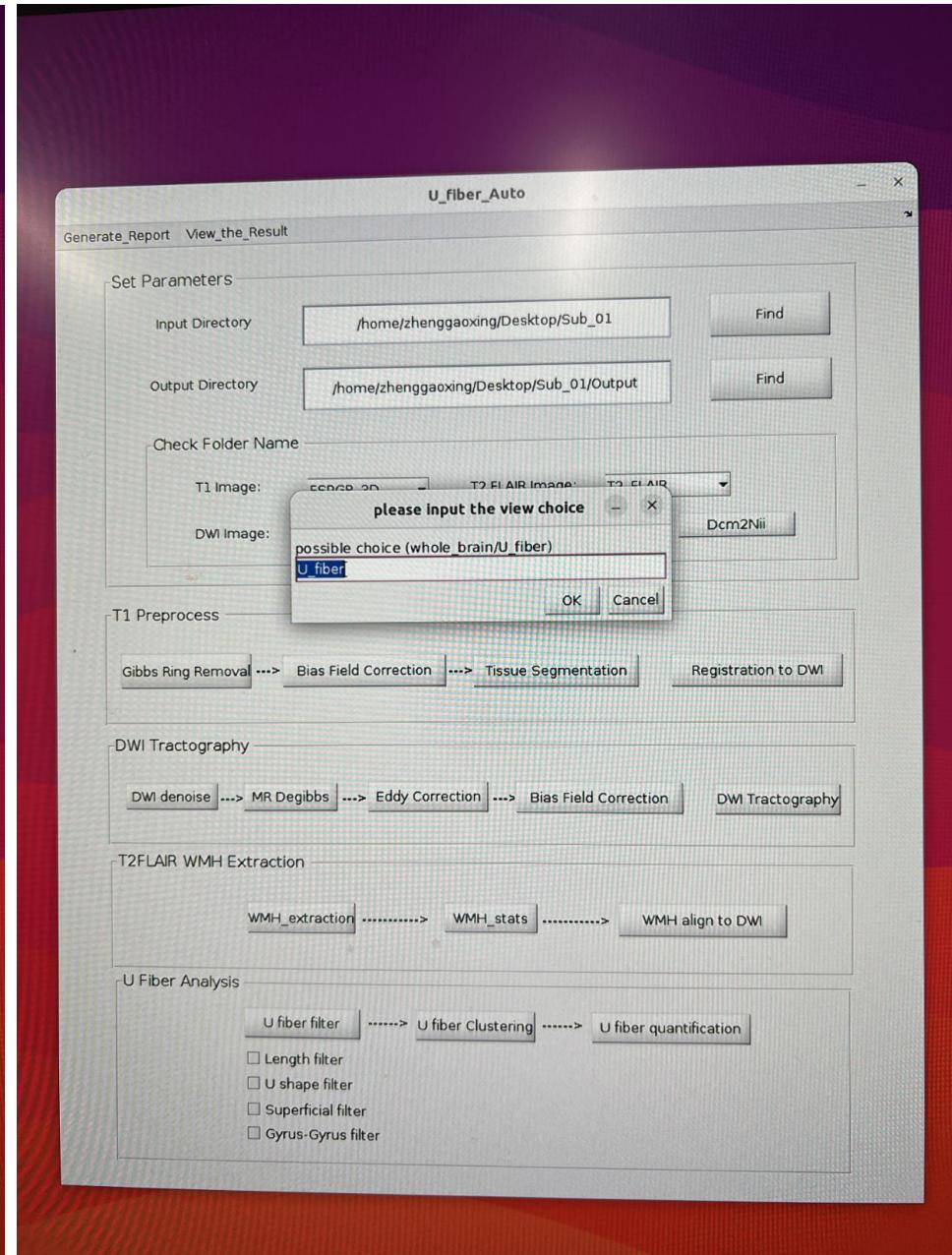
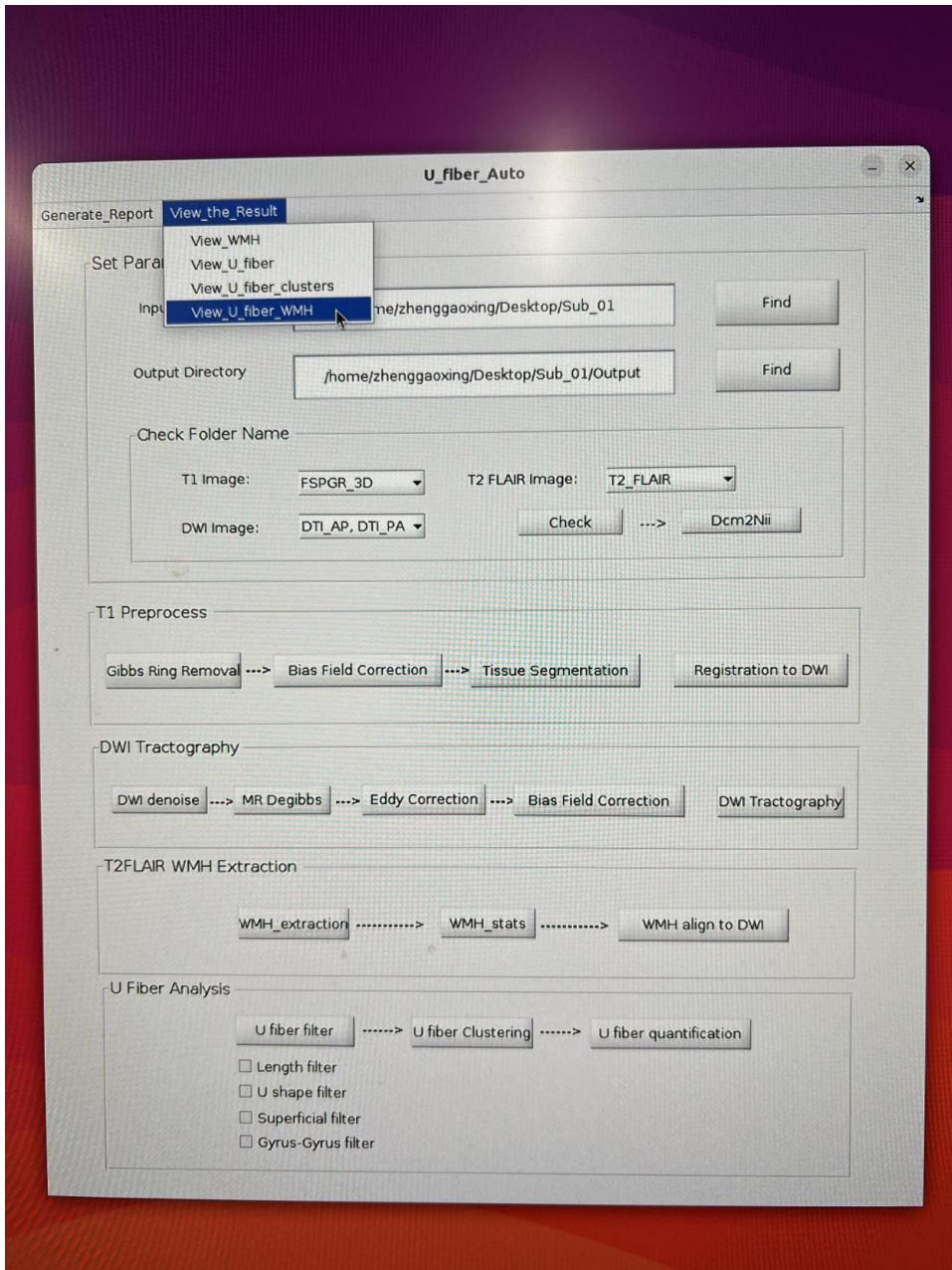
## Visualize the U fiber clusters from the anterior view.



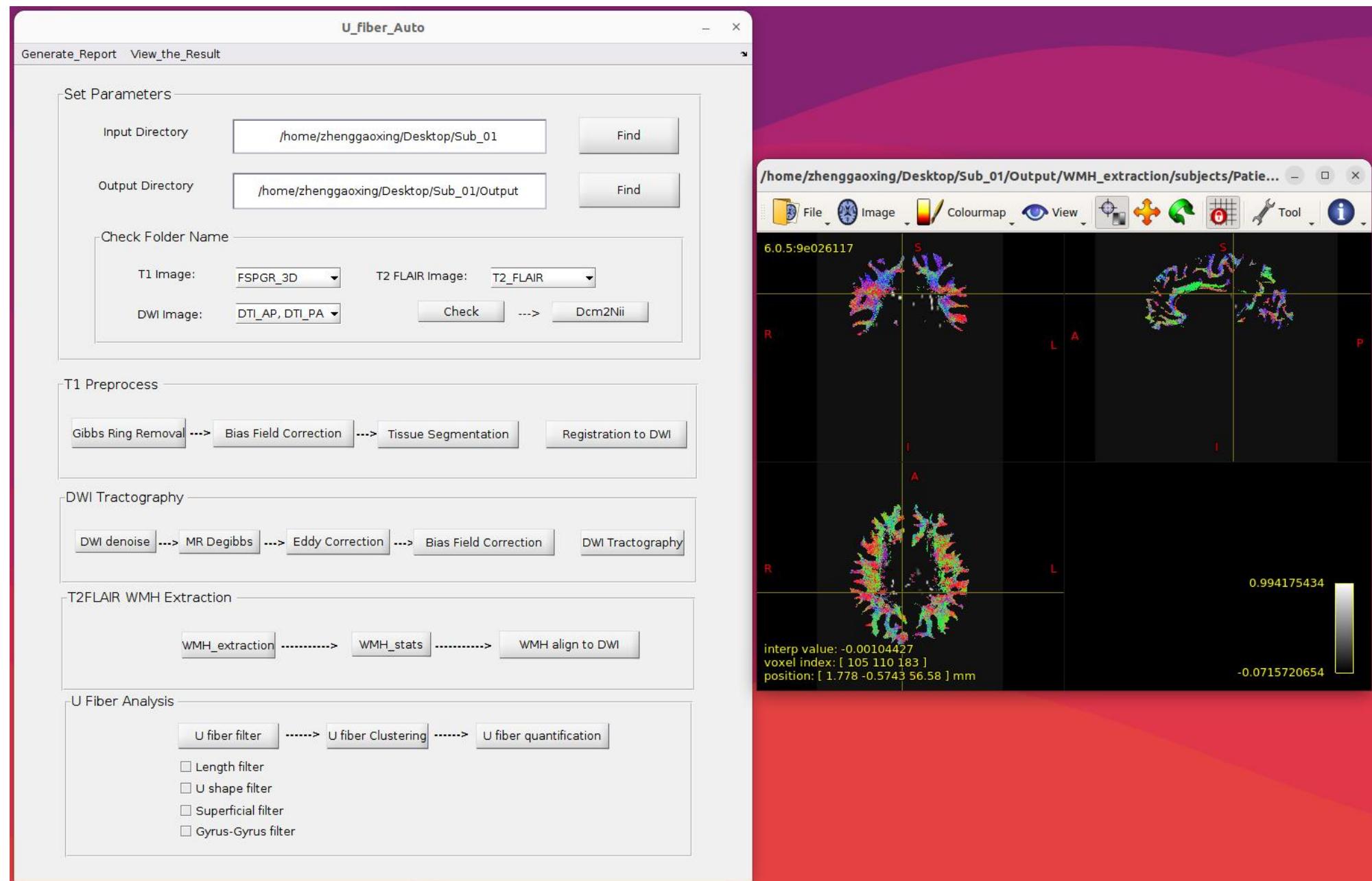
## Visualize the U fiber clusters from the left view.



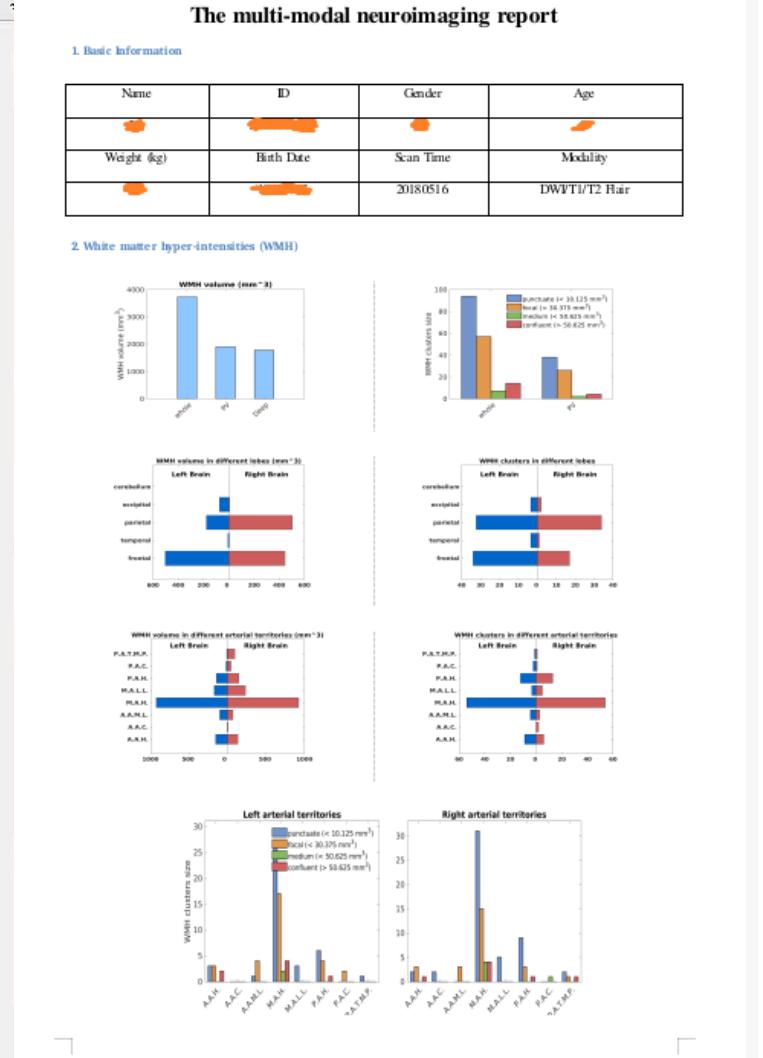
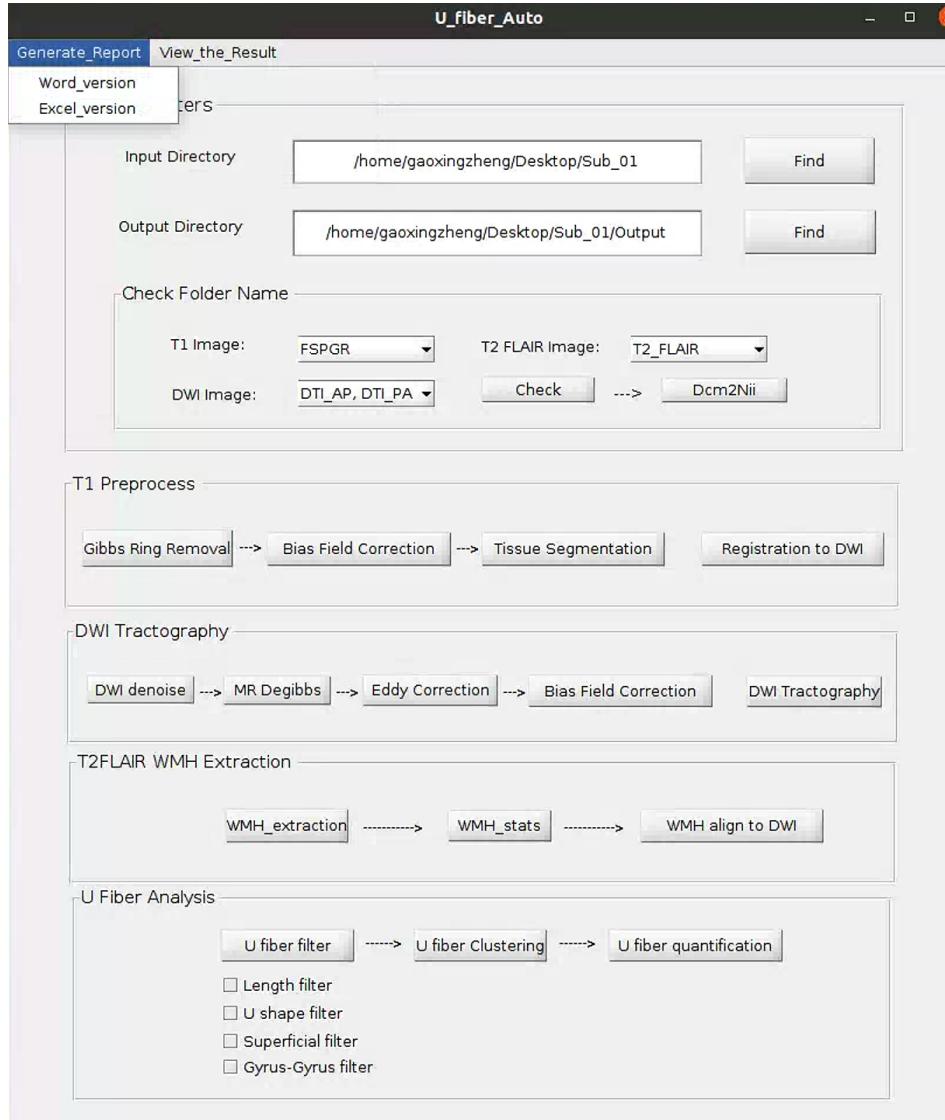
Click the popup-menu ‘View\_U\_fiber\_WMH’ to visualize the U fibers and WMH in one map.



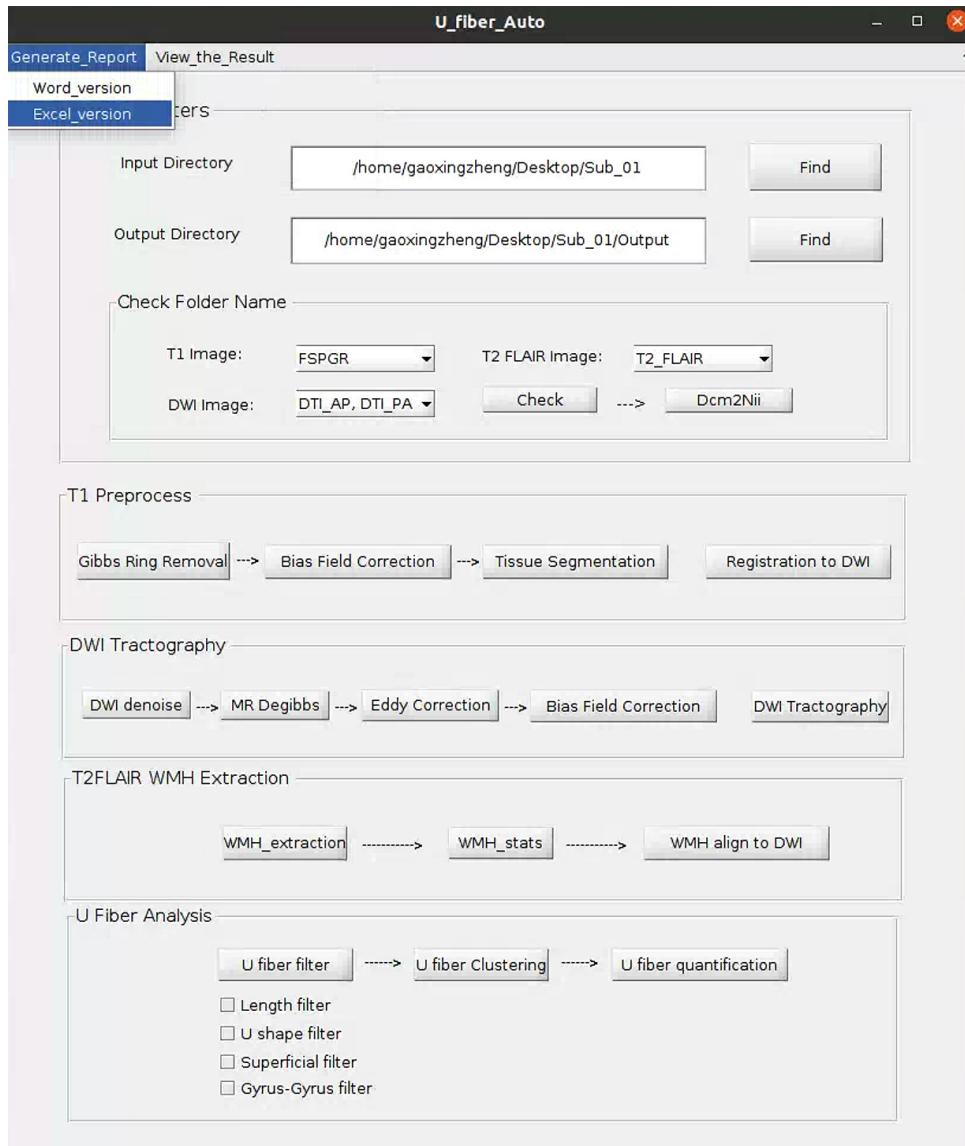
Visualize the U fibers and WMH in one map by using ‘mrview’.



Click the popup-menu ‘Generate\_Report/Word\_version’ to generate the neuroimaging analysis report.



Click the popup-menu ‘Generate\_Report/Excel\_version’ to generate the quantitative analysis results.



Three screenshots of LibreOffice Calc windows showing the contents of 'Sub\_01\_Results.xlsx' on three different sheets:

- Sheet1:** Subject\_Name\_and\_ID, wholeBrainWMVol\_mm3, PVWMVol\_mm3, DWIMVol\_mm3, Lfrontal\_WMVol\_mm3, Rfrontal\_WMVol\_mm3, Ltemporal\_WMVol\_mm3, Rtemporal\_WMVol\_mm3, Lparietal\_WMVol\_mm3, Rparietal\_WMVol\_mm3. Data for Sub\_01: 44158.5, 25734.375, 18059.625, 1900.125, 2706.75, 617.625, 182.25, 4795.875, 4836.375.
- Sheet2:** Subject\_Name\_and\_ID, T\_SupFP\_left\_FA, T\_SupFP\_right\_FA, T\_SupF\_left\_FA, T\_SupF\_right\_FA, T\_SupOT\_left\_FA, T\_SupOT\_right\_FA, T\_SupC\_left\_FA, T\_SupO\_right\_FA, T\_SupPO\_left\_FA, T\_SupO\_right\_FA, T\_SupPT\_left\_FA, T\_SupPT\_right\_FA. Data for Sub\_01: 0.4235824702854, 0.43342181878983, 0.398263526456, 0.4013368968741, 0.4076408228393, 0.422754265325, 0.411467692944, 0.4026906073731, 0.42364043596894, 0.42682071707623, 0.4327137947705, 0.399950.
- Sheet3:** Subject\_Name\_and\_ID, lh\_G\_S\_cingul\_Ant\_2\_G\_S\_cingul\_Ant\_FA, lh\_G\_front\_middle\_2\_G\_front\_middle\_FA, lh\_G\_front\_sup\_2\_G\_cingul\_Ant\_FA, lh\_G\_front\_sup\_2\_G\_front\_middle\_FA, lh\_G\_front\_sup\_2\_G\_front\_sup\_FA, lh\_G\_front\_sup\_2\_G\_cingul\_Ant\_FA. Data for Sub\_01: 0.466934861085128, 0.385788981997943, 0.421877254355661, 0.391337981264879, 0.37753425470907.

## **Part IV**

Error information you may meet when you use UFA toolbox

Error information you may meet when you use our UFA toolbox.

(1) When you click the ‘Bias Field Correction’ in the ‘T1 Preprocess’ panel of the UFA toolbox, you may meet the error below.

```
Matlab/sys/glnxa64/libstdc++.so.6: version 'GLIBCXX_3.4.26' not found (required by N4BiasFieldCorrection)
Matlab/sys/glnxa64/libstdc++.so.6: version 'GLIBCXX_3.4.29' not found (required by N4BiasFieldCorrection)
Matlab/sys/glnxa64/libstdc++.so.6: version 'GLIBCXX_3.4.30' not found (required by N4BiasFieldCorrection)
Matlab/sys/glnxa64/libstdc++.so.6: version 'CXXABI_1.3.11' not found (required by N4BiasFieldCorrection)
Matlab/sys/glnxa64/libstdc++.so.6: version 'CXXABI_1.3.13' not found (required by N4BiasFieldCorrection)
```

Solution: Check the GLIBCXX version and CXXABI version by using the commands below.

```
#strings /usr/lib/x86_64-linux-gnu/libstdc++.so.6 | grep GLIBCXX
#strings /usr/lib/x86_64-linux-gnu/libstdc++.so.6 | grep CXXABI
```

```
#sudo rm -rf Your_matlab_path/sys/os/glnxa64/libstdc++.so.6
#sudo gedit ~/.bashrc (not the #sudo gedit /etc/profile)
```

Add the command below:

```
#export LD_LIBRARY_PATH=$LD_LIBRARY_PATH:/usr/lib/x86_64-linux-gnu/libstdc++.so.6
```

```
#source ~/.bashrc (not the #source /etc/profile)
#reboot
```

If there didn't exist the GLIBCXX\_3.24.26/29/30 and CXXABI\_1.3.11/13 version.

```
#sudo add-apt-repository ppa:ubuntu-toolchain-r/test  
#sudo apt update  
#sudo apt install gcc-'version number'  
#sudo apt install libstdc++6
```

And then repeat the operator to check the libstdc++.so.6 contains the latest GLIBCXX and CXXABI version.

```
#strings /usr/lib/x86_64-linux-gnu/libstdc++.so.6 | grep GLIBCXX  
#strings /usr/lib/x86_64-linux-gnu/libstdc++.so.6 | grep CXXABI  
  
#sudo rm -rf Your_matlab_path/sys/os/glnxa64/libstdc++.so.6  
#sudo gedit ~/.bashrc (not the #sudo gedit /etc/profile)
```

Add the command below:

```
#export LD_LIBRARY_PATH=$LD_LIBRARY_PATH:/usr/lib/x86_64-linux-gnu/libstdc++.so.6  
  
#source ~/.bashrc (not the #source /etc/profile)  
#reboot
```

Error information you may meet when you use our UFA toolbox.

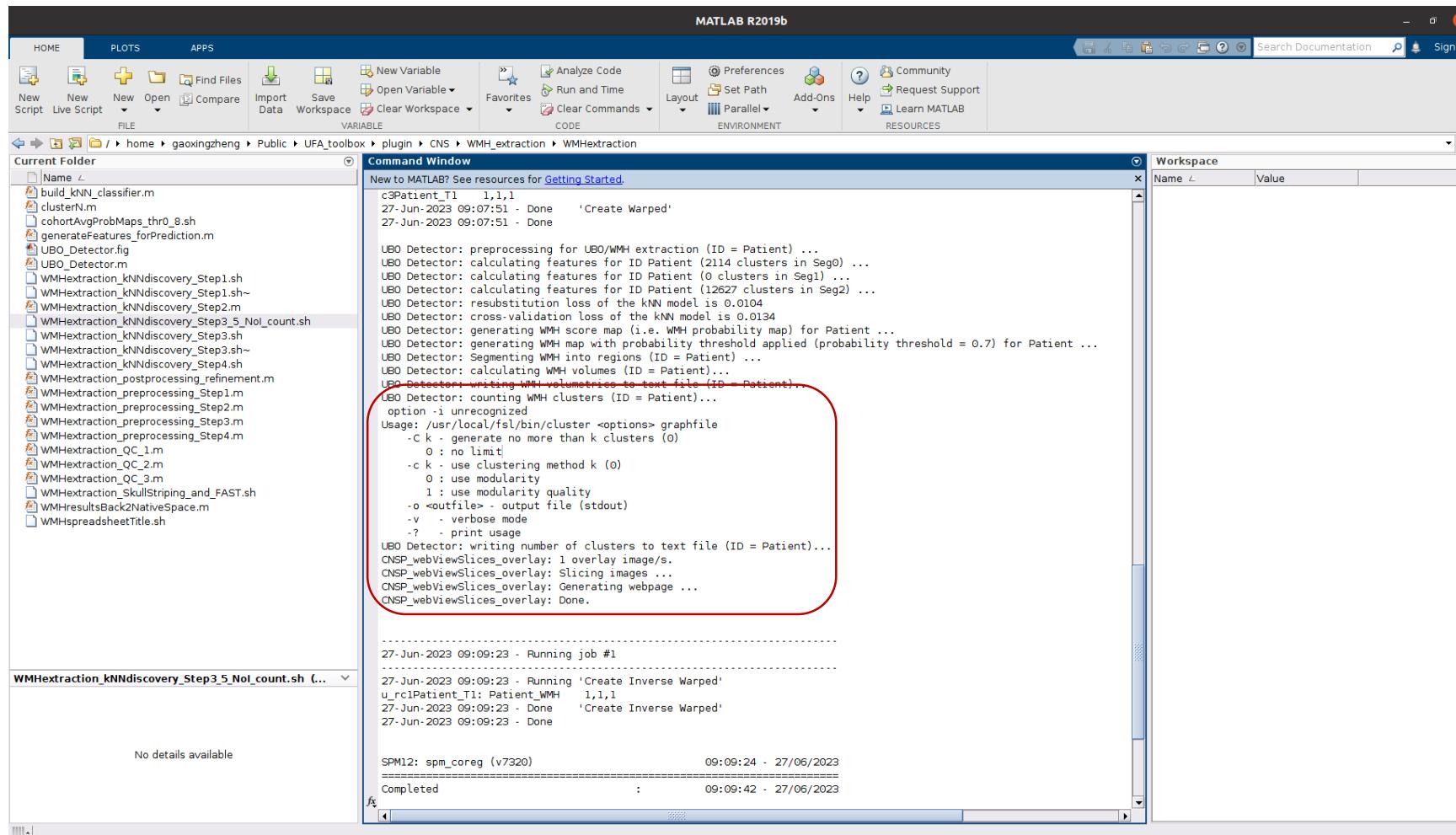
(2) When you click the ‘Eddy Correction’ in the ‘DWI Tractography’ panel of the UFA toolbox, you may meet the error below.

```
dwifslpreproc: [ERROR] dwi2mask dwi_pad2_pe_0_applytopup.mif - | maskfilter - | mrconvert - eddy_mask.nii -datatype float32 -strides -1,+2,+3
dwi2mask : preloading data for dwi_pad2_pe_0_applytopup.mif
dwi2mask : [Error] no valid diffusion gradient table found
dwi2mask: [Error] error importing diffusion gradient table for image dwi_pad2_pe_0_applytopup.mif
maskfilter: [Error] no filename supplied to standard input (broken pipe?)
maskfilter: [Error] error open image
```

Solution: <https://community.mrtrix.org/t/the-command-dwifslpreproc-error-in-mrtrix3-version-3-0-3-while-correctly-run-in-the-version-3-0-2/5841>

Error information you may meet when you use our UFA toolbox.

(3) When you click the ‘WMH\_extraction’ in the ‘T2FLAIR WMH Extraction’ panel of the UFA toolbox, you may meet the error below (The error results in all the WMH cluster sizes are zero).

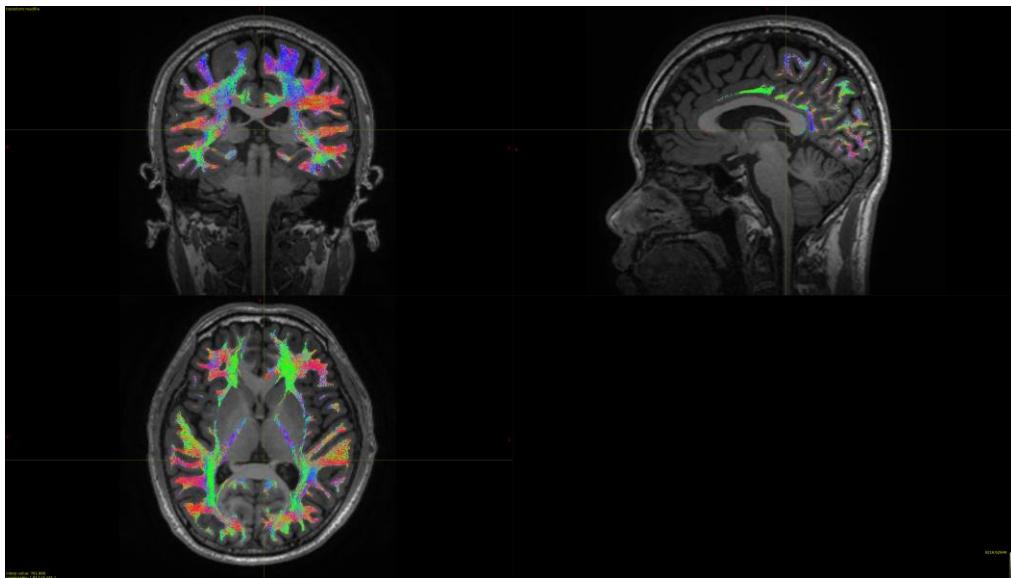


Solution: It seems the new version of FSL (6.0.6.5) changed the ‘cluster’ command. **We recommended the user install the old FSL (such as version 6.0.5) rather than the latest version.** Or you can replace \${FSLDIR} with /path/to/old/FSL in line 47 of WMHextraction\_kNNdiscovery\_Step3\_5\_Nol\_count.sh, to force using the old ‘cluster’ command.

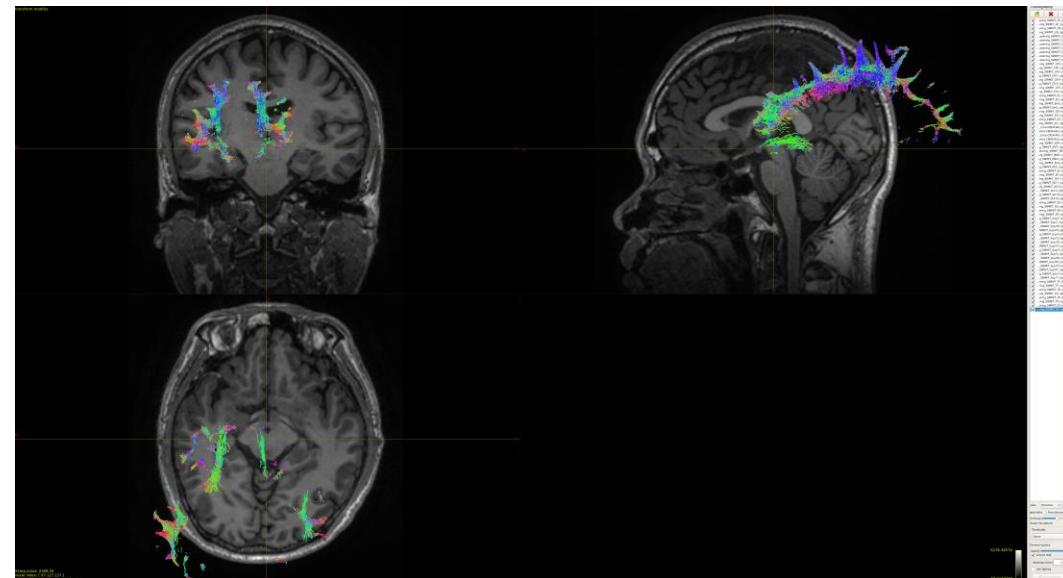
Error information you may meet when you use our UFA toolbox.

(4) When you click the ‘U fiber clustering’ in the ‘U Fiber Analysis’ panel of the UFA toolbox, you may meet the error below.

If you call the 3D Slicer version 5 (such as 5.0.3), the fiber tractography will not match well with the T1 image. However, the situation when using Slicer 4.8.1 is okay!



(U fiber clustering by Slicer 4.8.1)



(U fiber clustering by Slicer 5.0.3)

**Note (very important!):** Since the Slicer 5 version has updated the kernel, the coordinate system changes to RAS, while the coordinate system of the white matter tract is LPS. Thus, we recommended you use Slicer 4.x.x version rather than Slicer 5.x.x. Otherwise, the white matter tractography will not registered to T1 images.

We recommend the version **Slicer-4.8.1-linux-amd64**.

Error information you may meet when you use our UFA toolbox.

(5) Executing unix commands set in PATH in matlab does not work with unix command.

For example, when matlab call the .sh script, it returns the error ‘mrconvert command not found’.

Solution: add the below commands in the matlab function or execute in matlab command window.

```
PATH = getenv('PATH');  
setenv('PATH', [PATH ':/home/zhenggaoxing/anaconda3/bin/']);
```

Reference: <https://ww2.mathworks.cn/matlabcentral/answers/27762-executing-unix-commands-set-in-path-in-matlab-does-not-work-with-unix-command>

Error information you may meet when you use our UFA toolbox.

(6) Fail to generate the white matter clusters when using white matter analysis package.

such as when you execute the command : `wm_register_to_atlas_new.py -h`, you may get the warning information.

```
<frozen importlib._bootstrap>:219: RuntimeWarning: scipy._lib.messagestream.MessageStream size changed, may indicate binary incompatibility. Expected 56 from C header, got 64 from PyObject.
```

Solution: Try to update or downdate the scipy:

```
# pip uninstall scipy  
# pip uninstall numpy  
# pip install scipy  
# pip install numpy  
# pip install --upgrade pip
```

(7) When you start MATLAB, it output the error information: MATLAB is crashing by low-level graphics error.

Solution: Type `opengl('save','software')` at the MATLAB command prompt. Then, restart MATLAB.

Reference: [https://www.mathworks.com/help/matlab/creating\\_plots/resolving-low-level-graphics-issues.html](https://www.mathworks.com/help/matlab/creating_plots/resolving-low-level-graphics-issues.html)

Error information you may meet when you use our UFA toolbox.

(8) Failed to load module "canberra-gtk-module", MATLAB is existing because of fatal error.

```
MATLAB is exiting because of fatal error
Killed
(base) zhenggaoxing@zhenggaoxing-OMEN-by-HP-45L-Gaming-Desktop-GT22-0xxx:~/Public/NeuroImage_toolbox$ matlab
[0203/183505.190389:INFO:context.cpp(159)] Using multi-threaded message loop for Linux
/home/zhen.../NeuroImage_toolbox/Matlab_R2019b/bin/glnxa64/jcef_helper: symbol lookup error: /lib/x86_64-linux-gnu/libpango-1.0.so.0: undefined symbol: g_mendup2
/home/zhen.../NeuroImage_toolbox/Matlab_R2019b/bin/glnxa64/jcef_helper: symbol lookup error: /lib/x86_64-linux-gnu/libpango-1.0.so.0: undefined symbol: g_mendup2
.....
Segmentation violation detected at 五月 03 18:37:11 2023 +0800

Configuration:
Crash Decoding : Disabled - No sandbox or build area path
Crash Mode : continue (default)
Default Encoding : UTF-8
Deployed : false
Deployment Environment : ubuntu:GNOME
GNU C Library : 2.35 stable
Graphics Driver : NVIDIA Corporation NVIDIA GeForce RTX 3080/PCIE/SSE2 Version 4.6.0 NVIDIA 515.86.01
Graphics card 1 : 0x10de (0x10de ) 0x2216 Version 515.86.1.0 (0-0-0)
Java Version : Java 1.8.0_202-b08 with Oracle Corporation Java HotSpot(TM) 64-Bit Server VM mixed mode
MATLAB Architecture : glnxa64
MATLAB Entitlement ID : 6257793
MATLAB Root : /home/zhen.../NeuroImage_toolbox/Matlab_R2019b
MATLAB Version : v9.1.1199202 (R2019b)
Operating System : Linux 5.15.0-43-generic #46-Ubuntu SMP Tue Jul 12 10:30:17 UTC 2022 x86_64
Process ID : 7083
Processor ID : x86 Family 6 Model 151 Stepping 2, GenuineIntel
Session Key : c9733af-5508-42a8-acd0-0dffffdf2e8
Static TLS mitigation : Enabled: Full
Window System : The X.Org Foundation (12101003), display :1

Fault Count: 1

Abnormal termination: Segmentation violation

Register State (from fault):
RAX = 00000007fabcabbd RBX = 00007fa0e2fcf3c
RCX = 0000000000000000 RDX = 00007fa0e2fcfcd8
RSP = 00007fa0e2fcfcd8 RBP = 00007fa0ca0bd210
RSI = 00007fa0ca0cf73950 RDI = 00007fa0ca0bd210

RB = 00007fabcd1efca0 R9 = 000000000fd234250
R10 = 0000000000000000780 R11 = 00007fab11ccf3c
R12 = 00007fab2fefc5e0 R13 = 00007fa0ca0f71030
R14 = 00007fab23c7e1c0 R15 = 0000000000000000

RIP = 00007fabf0cac64e EFL = 00000000000010202
CS = 0033 FS = 0000 GS = 0000

Stack Trace (from fault):
[ 0] 0x00007fabf0cac64e /lib/x86_64-linux-gnu/libX11.so.6-6.0-0+00321102 XSetICValues+00000270
[ 1] 0x00007fab0ad008309 /home/zhen.../Public/NeuroImage_toolbox/Matlab_R2019b/sys/java/jre/glnxa64/jre/lib/amd64/libawt_xawt.so+00225103 Java_sun.awt.X11_XInputMethod_setXICFocusNative+00000143
[ 2] 0x00007fab0ad008307 <unknow>.modul+>+00000000
[ 3] 0x00007fab0ad0082bd <unknow>.modul+>+00000000
[ 4] 0x00007fab0ad0082bd <unknow>.modul+>+00000000
[ 5] 0x00007fab0ad008302 <unknow>.modul+>+00000000
[ 6] 0x00007fab0ad0082bd <unknow>.modul+>+00000000
[ 7] 0x00007fab0ff3064 <unknow>.modul+>+00000000

** This crash report has been saved to disk as /home/zhen.../matlab_crash_dump.7083-1 **

MATLAB is exiting because of fatal error
Killed
(base) zhenggaoxing@zhenggaoxing-OMEN-by-HP-45L-Gaming-Desktop-GT22-0xxx:~/Public/NeuroImage_toolbox$
```

Solution:

```
# sudo gedit ~/.bashrc
```

add the following commands in the file `~/.bashrc`

```
#export MATLAB_JAVA=/usr/lib/jvm/java-1.8.0-openjdk-amd64/jre
#export LD_LIBRARY_PATH=/usr/lib/x86_64-linux-gnu/gtk-2.0/modules
```

then save and close the file `~/.bashrc`

```
#source ~/.bashrc
```

Reference:

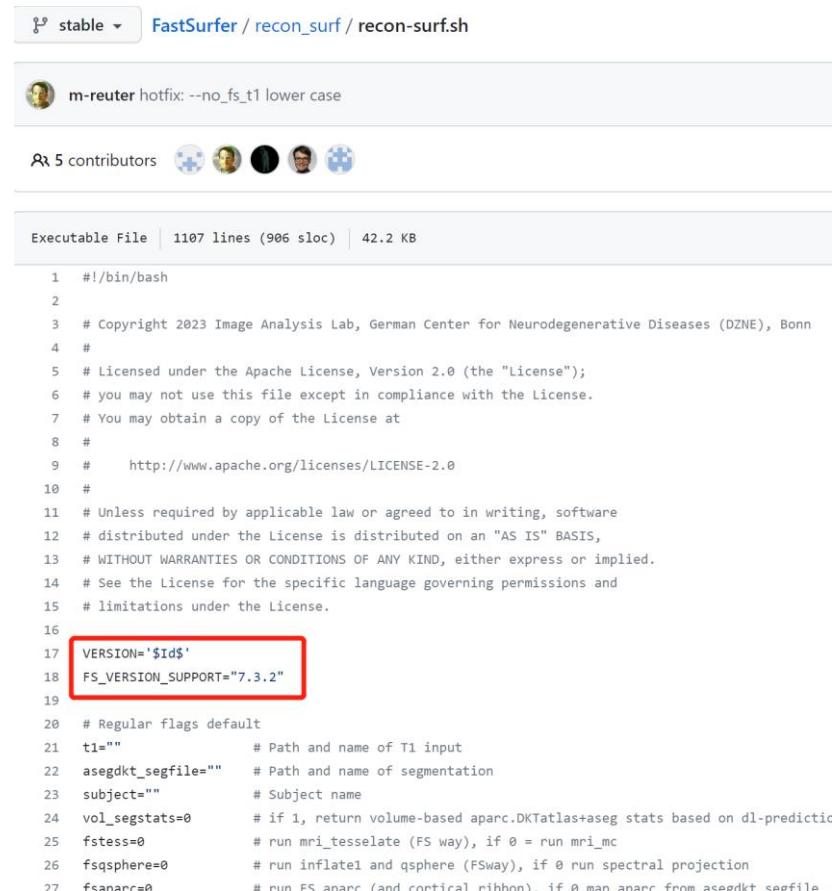
[https://bugzilla.redhat.com/show\\_bug.cgi?id=1775764](https://bugzilla.redhat.com/show_bug.cgi?id=1775764)

Error information you may meet when you use our UFA toolbox.

(9) You may meet the following errors when you click the button “U fiber filter” in the “U Fiber Analysis” module of the UFA toolbox.

mris\_info xxx/T1/surf/lh.orig.nofix | grep -q ‘vertex locs : surfaceRAS’file xxx/T1/mri/filled-pretess255.mgz Incorrect header information detected in xxx/T1/surf/lh.orig.nofix: vertex locs is not set to surfaceras. Exiting... Command exited with non-zero status 1.

Solution: I guess you used the new version of Freesurfer (such as 7.4.0). We recommend the user install the Freesurfer 7.3.2 and the “U Fiber Analysis” process will run without error.



```
stable ▾ FastSurfer / recon_surf / recon-surf.sh

m-reuter hotfix: --no_fs_t1 lower case

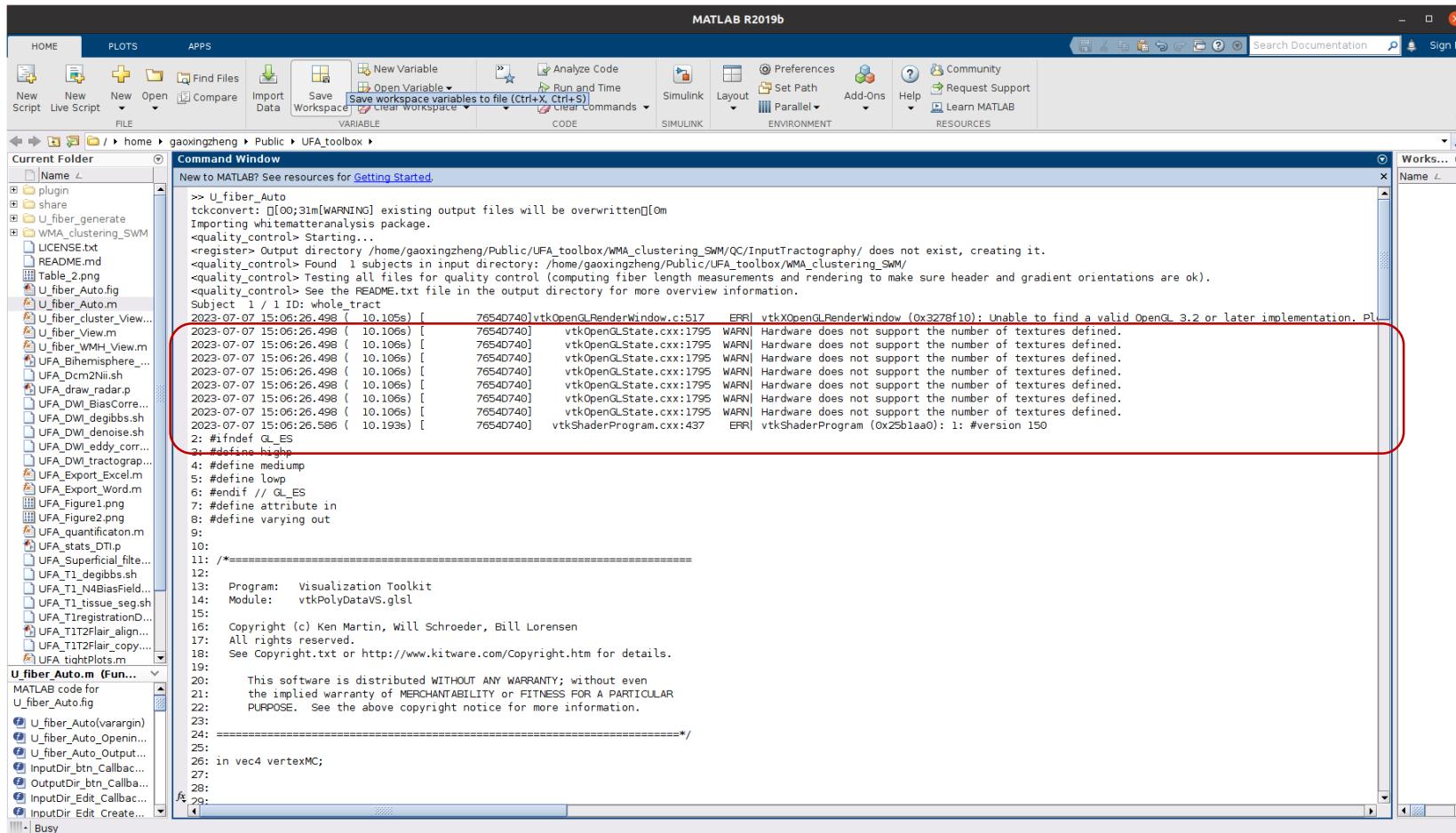
5 contributors

Executable File | 1107 lines (906 sloc) | 42.2 KB

1  #!/bin/bash
2
3  # Copyright 2023 Image Analysis Lab, German Center for Neurodegenerative Diseases (DZNE), Bonn
4  #
5  # Licensed under the Apache License, Version 2.0 (the "License");
6  # you may not use this file except in compliance with the License.
7  # You may obtain a copy of the License at
8  #
9  #     http://www.apache.org/licenses/LICENSE-2.0
10 #
11 # Unless required by applicable law or agreed to in writing, software
12 # distributed under the License is distributed on an "AS IS" BASIS,
13 # WITHOUT WARRANTIES OR CONDITIONS OF ANY KIND, either express or implied.
14 # See the License for the specific language governing permissions and
15 # limitations under the License.
16
17 VERSION='$Id$'
18 FS_VERSION_SUPPORT="7.3.2"
19
20 # Regular flags default
21 t1=""          # Path and name of T1 input
22 asegdkt_segfile="" # Path and name of segmentation
23 subject=""      # Subject name
24 vol_segstats=0 # if 1, return volume-based aparc.DKTatlas+aseg stats based on dl-prediction
25 fstess=0        # run mri_tesselate (FS way), if 0 = run mri_mc
26 fsqsphere=0     # run inflate1 and qsphere (FSway), if 0 run spectral projection
27 fsaparc=0       # run FS aparc (and cortical ribbon). if 0 mao aparc from asegdkt seefile
```

Error information you may meet when you use our UFA toolbox.

(10) You may meet the following errors when you click the button “U fiber Clustering” in the “U Fiber Analysis” module of the UFA toolbox.

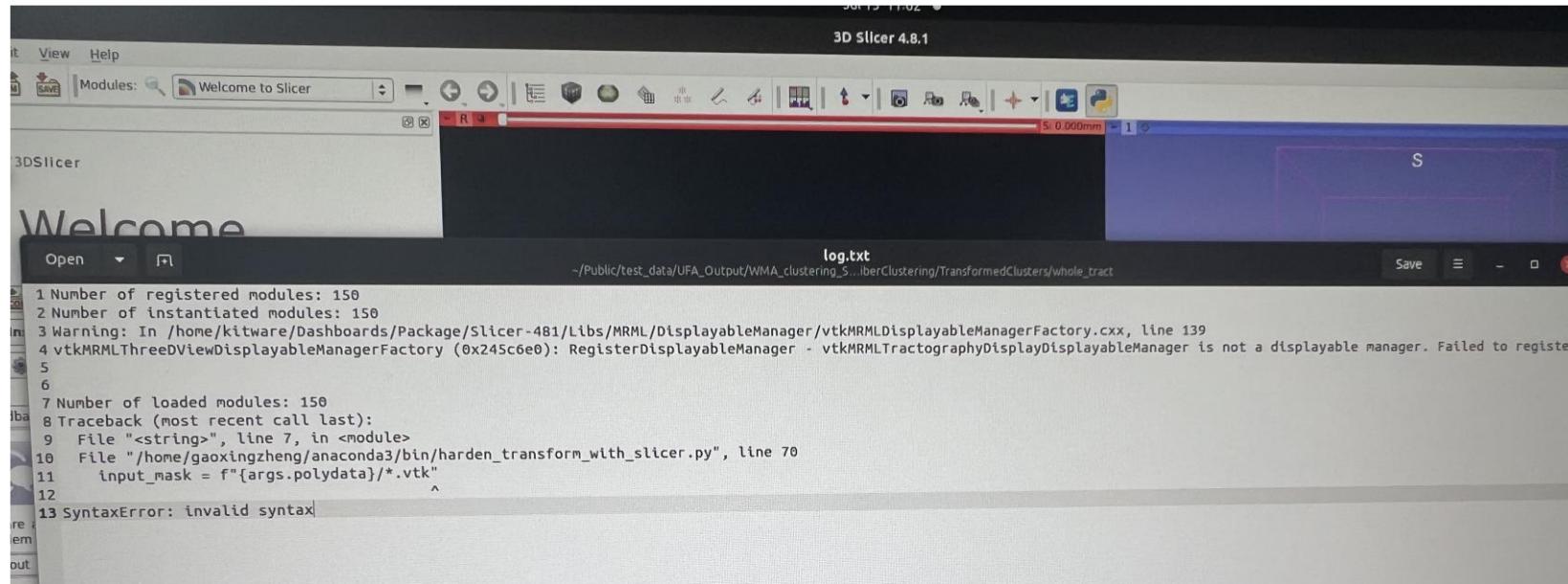


Reason: It may be that the software OpenGL of Matlab is different from the version of system hardware OpenGL.

Solution: You can set the Matlab OpenGL startup method to hardware OpenGL by Matlab command (`opengl('save','hardware')`) and then restart Matlab, the U-fiber clustering step will run without error. However, using hardware OpenGL may prevent Matlab from calling the graphical interface normally, and the drawing will not be displayed. You can wait until the U-fiber clustering is finished, then switch back to software OpenGL by Matlab command (`opengl('save','software')`), and then restart Matlab to draw the graph normally.

Error information you may meet when you use our UFA toolbox.

(11) You may meet the following errors when you run the “U fiber Clustering” in the “U Fiber Analysis” module of the UFA toolbox.



Reason: This is due to a Python version issue.

Solution: #sudo gedit Your\_anaconda3\_PATH/bin/harden\_transform\_with\_slicer.py  
such as #sudo gedit /home/gaoxingzheng/anaconda3/bin/harden\_transform\_with\_slicer.py

and change the lines 70 and 71 as follows:

```
input_mask = "{}".format(args.polydata)+"/*.vtk"
input_mask2 = "{}".format(args.polydata)+"/*.vtpl"
```

## Error information you may meet when you use our UFA toolbox.

(12) You may meet the following errors when you run the “U fiber Clustering” in the “U Fiber Analysis” module of the UFA toolbox.

The screenshot shows a MATLAB R2019b interface with the Command Window active. The workspace contains several files related to the UFA toolbox, including U\_fiber\_Auto.m, U\_fiber\_Cluster\_View.m, and various DWI processing scripts. The Command Window displays a series of command-line outputs and errors. A red box highlights the following error message:

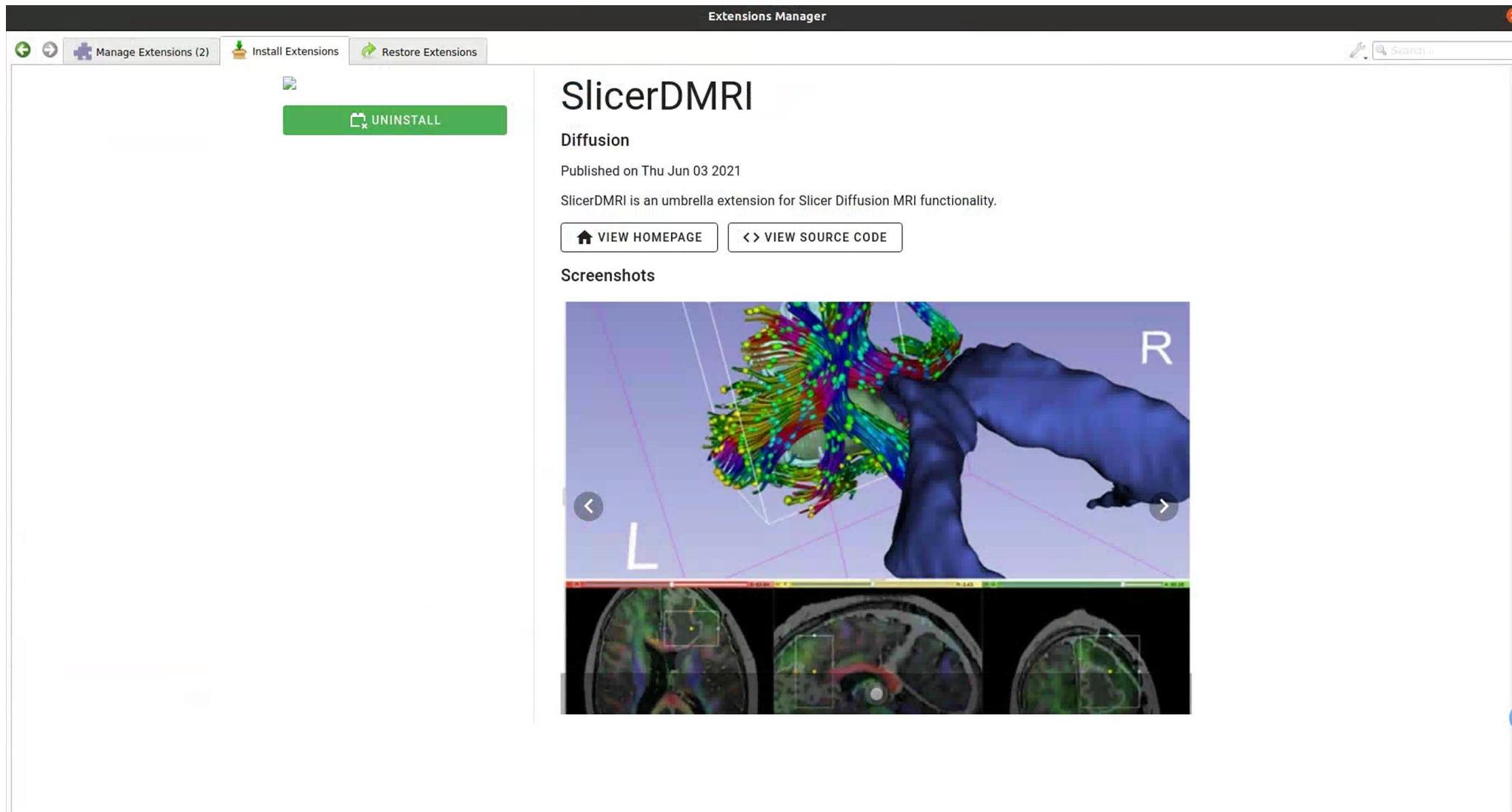
```
<wm_harden_transform.py> Transform were conducted for 0 subjects.  
Error: The numbers of inputs and outputs are different. Check log file for errors.
```

This error indicates that the script was unable to process the input data correctly due to a mismatch between the number of inputs and outputs.

```
====output directory====  
/media/zhenggaoxing/ZhengGaoxing/UFA_toolbox/WMA_clustering_SWM/FiberClustering/TransformedClusters/whole_tract  
====3D Slicer====  
/media/zhenggaoxing/ZhengGaoxing/UFA_toolbox/plugin/Slicer-4.10.2-linux-amd64/Slicer  
====Way of transform====  
individual  
=====Inverse? ====  
True  
=====Transform file(s) path====  
/media/zhenggaoxing/ZhengGaoxing/UFA_toolbox/WMA_clustering_SWM/TractRegistration/whole_tract/output_tractography/itk_txform_whole_tract.tfm  
=====Number of jobs====  
1  
===== /media/zhenggaoxing/ZhengGaoxing/UFA_toolbox/WMA_clustering_SWM/TractRegistration/whole_tract/output_tractography/itk_txform_whole_tract.tfm will be applied to all inputs.  
<wm_harden_transform.py> Transforming: /media/zhenggaoxing/ZhengGaoxing/UFA_toolbox/WMA_clustering_SWM/FiberClustering/OutlierRemovedClusters/whole_tract_reg_outlier_removed  
<wm_harden_transform.py> Transform were conducted for 0 subjects.  
Error: The numbers of inputs and outputs are different. Check log file for errors.  
Importing whitematteranalysis package.  
<wm_separate_clusters_by_hemisphere.py> Output directory /media/zhenggaoxing/ZhengGaoxing/UFA_toolbox/WMA_clustering_SWM/FiberClustering/SeparatedClusters/ does not exist, creating it.  
<wm_separate_clusters_by_hemisphere.py> Starting computation.  
  
====input directory====  
/media/zhenggaoxing/ZhengGaoxing/UFA_toolbox/WMA_clustering_SWM/FiberClustering/TransformedClusters/whole_tract/  
====output directory====  
/media/zhenggaoxing/ZhengGaoxing/UFA_toolbox/WMA_clustering_SWM/FiberClustering/SeparatedClusters/  
====  
  
<wm_separate_clusters_by_hemisphere.py> Input number of vtk/vtp files: 0  
  
<wm_separate_clusters_by_hemisphere.py> Done!!!  
Importing whitematteranalysis package.  
<wm_append_clusters_to_anatomical_tracts.py> 41 mrml files are detected.  
<wm_append_clusters_to_anatomical_tracts.py> Output directory /media/zhenggaoxing/ZhengGaoxing/UFA_toolbox/WMA_clustering_SWM/AnatomicalTracts/ does not exist, creating it.  
Traceback (most recent call last):  
File "/home/zhenggaoxing/anaconda3/bin/wm_append_clusters_to_anatomical_tracts.py", line 224, in <module>  
    main()  
File "/home/zhenggaoxing/anaconda3/bin/wm_append_clusters_to_anatomical_tracts.py", line 185, in main  
    fname = get_local_atlas_bundle_fname(ORGAtlasVersion(args.version))  
    ~~~~~~  
File "/home/zhenggaoxing/anaconda3/lib/python3.11/site-packages/whitematteranalysis/data/atlas/utils.py", line 27, in get_local_atlas_bundle_fname  
    with path.open() as f:  
        ~~~~~~  
FileNotFoundError: [Errno 2] No such file or directory: '/home/zhenggaoxing/anaconda3/lib/python3.11/site-packages/whitematteranalysis/data/atlas/org_atlas_version.json'  
Importing whitematteranalysis package.  
<wm_quality_control_tractography.py> Starting...  
<wm_quality_control_tractography.py> Output directory /media/zhenggaoxing/ZhengGaoxing/UFA_toolbox/WMA_clustering_SWM/QC/AnatomicalTracts/ does not exist, creating it.  
<wm_quality_control_tractography.py> Found 0 subjects in input directory: /media/zhenggaoxing/ZhengGaoxing/UFA_toolbox/WMA_clustering_SWM/AnatomicalTracts/  
  
<quality_control> Error: No .vtk or .vtp files were found in the input directory.  
  
Elapsed time is 4249.646800 seconds.  
fx >>
```

Possible cause: You may have forgotten to install the SlicerDMRI extension in 3D Slicer.

Solution: Open 3D Slicer and Install Slicer Extensions --> Search SlicerDMRI Extension --> Install  
(Or you can choose to install an extension from file and find slicerDMRI)



Error information you may meet when you use our UFA toolbox.

(13) You may meet the following errors when you launch 3D Slicer:

```
(base) zhenggaoxing@zhenggaoxing-OMEN-by-HP-45L-Gaming-Desktop-GT22-0xxx:/media/zhanggaoxing/ZhengGaoxing/UFA_toolbox/plugin/Slicer-4.10.2-linux-amd64$ sudo ./Slicer
X Error: BadAccess (attempt to access private resource denied) 10
  Extension:    130 (MIT-SHM)
  Minor opcode: 1 (X_ShmAttach)
  Resource id: 0x14b
X Error: BadShmSeg (invalid shared segment parameter) 128
  Extension:    130 (MIT-SHM)
  Minor opcode: 3 (X_ShmPutImage)
  Resource id: 0x460000c
QStandardPaths: XDG_RUNTIME_DIR not set, defaulting to '/tmp/runtime-root'
error: [/media/zhanggaoxing/ZhengGaoxing/UFA_toolbox/plugin/Slicer-4.10.2-linux-amd64/bin/SlicerApp-real] exit abnormally - Report the problem.
X Error: BadShmSeg (invalid shared segment parameter) 128
  Extension:    130 (MIT-SHM)
  Minor opcode: 2 (X_ShmDetach)
  Resource id: 0x460000c
```

Solution: #sudo vi /etc/environment

Add the following command in the /etc/environment:

QT\_X11\_NO\_MITSHM=1

And close the /etc/environment and # source /etc/environment

If you still encounter the following error, it means your Linux system has a conflict with 3D Slicer, we suggest you use Ubuntu 18.04 or 20.04 rather than 22.04, and we suggest you use 3D Slicer-4.8.1.

```
(base) zhenggaoxing@zhenggaoxing-OMEN-by-HP-45L-Gaming-Desktop-GT22-0xxx:/media/zhanggaoxing/ZhengGaoxing/UFA_toolbox/plugin/Slicer-4.10.2-linux-amd64$ sudo ./Slicer
QStandardPaths: XDG_RUNTIME_DIR not set, defaulting to '/tmp/runtime-root'
error: [/media/zhanggaoxing/ZhengGaoxing/UFA_toolbox/plugin/Slicer-4.10.2-linux-amd64/bin/SlicerApp-real] exit abnormally - Report the problem.
(base) zhenggaoxing@zhenggaoxing-OMEN-by-HP-45L-Gaming-Desktop-GT22-0xxx:/media/zhanggaoxing/ZhengGaoxing/UFA_toolbox/plugin/Slicer-4.10.2-linux-amd64$
```

## **Part V**

Some commands you may need

## Some commands you may need:

1. sudo apt-get update

    sudo apt-get upgrade

    sudo apt install git

2. sudo apt install dcm2niix

3. #top

    #gnome-system-monitor

4. The command below maybe need by fsleyes

#sudo apt-get install libsd12-2.0-0

#strings /usr/lib/x86\_64-linux-gnu/libstdc++.so.6 | grep GLIBCXX

#sudo add-apt-repository ppa:ubuntu-toolchain-r/test

#sudo apt update

#sudo apt install libstdc++6

#whereis fsleyes (it returns fsleyes:/home/gaoxingzheng/anaconda3/bin/fsleyes)

#ln -s /home/gaoxingzheng/anaconda3/bin/fsleyes /usr/local/fsl/bin/fsleyes

5. #locate lib\*\*\*.so.0 (it will return where the lib\*\*\*.so.0 locates)

    #sudo ln -s ‘wherelib\*\*.so.0 locates’ /usr/lib