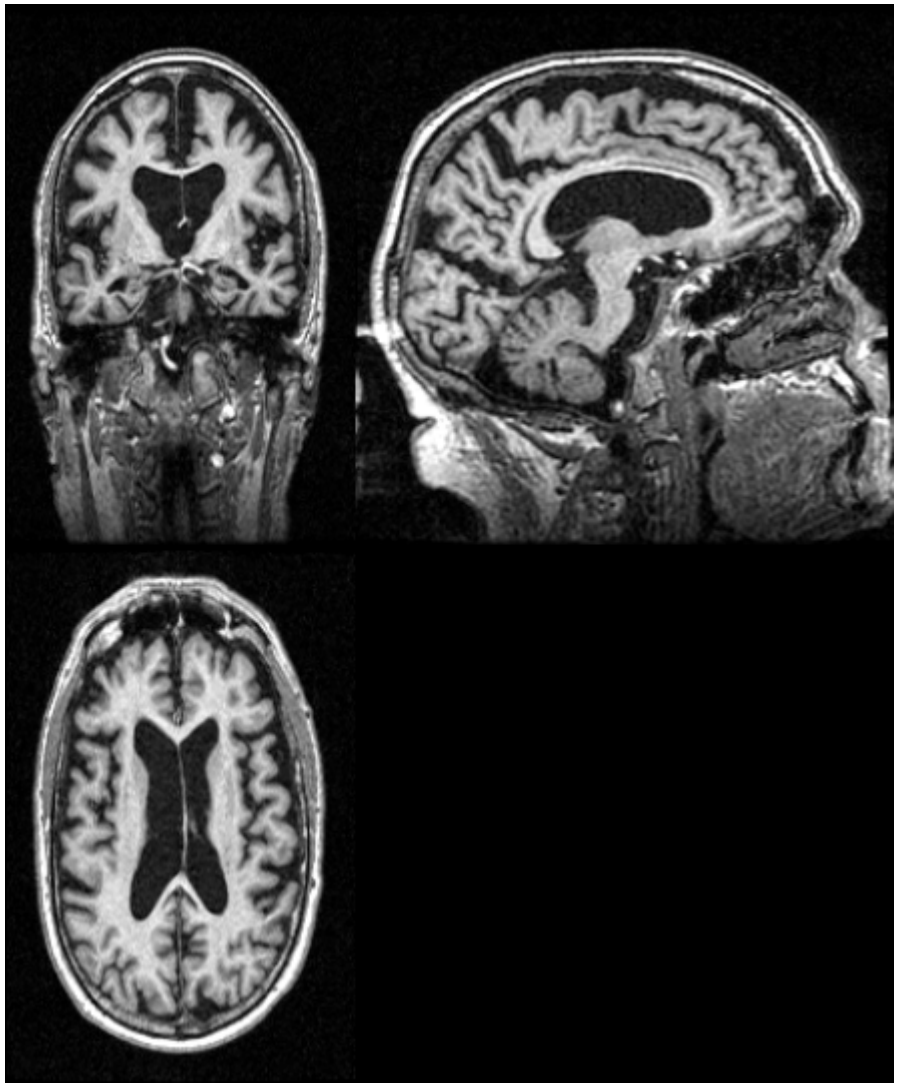
Preprocessing On Brain Volume by FSL and ANTs



sample.nii.gz

Information of Sample Image:

- The image is one of cases in ADNI1 dataset.

- This is an AD sample.

- Volume shape: [166, 256, 256].

- The software used to display image is **MRIcron**.

Steps of Preprocessing

1. Reorientation to Standard Space
2. Registration to Template
3. Skull-skipping
4. Bias Field Correction
5. Tissue Segmentation

Notes

In this document,

1. The source directory of sample is:
   Desktop/BrainPrep/volumes/

   The name of sample file is:
   sample.nii.gz
2. This demo is performed in **Ubuntu** system.

   Commands used to do preprocessing in

   macOS is a bit different with in **Ubuntu**.

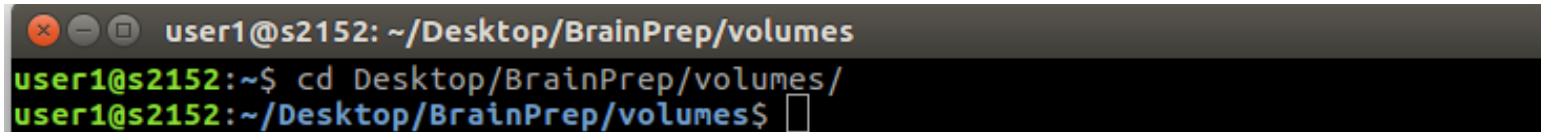
   I will state the difference in some steps

   by the symbol ★.

1. Reorientation to Standard Space

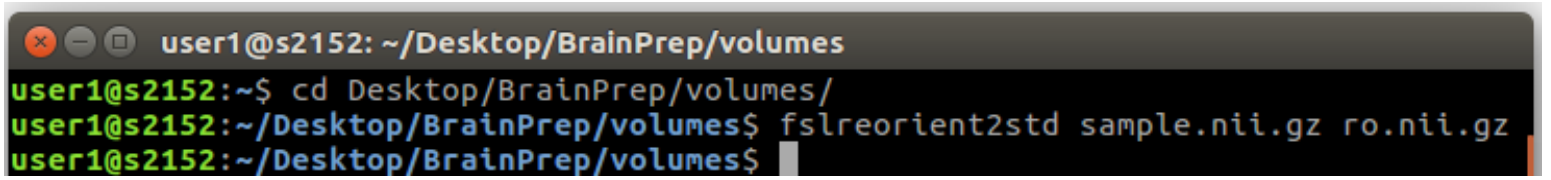
1.1 Change Working Directory to Source Directory

In **terminal**, input command **cd Desktop/BrainPrep/volumes**, click **Enter**.



1.2 Do Reorientation

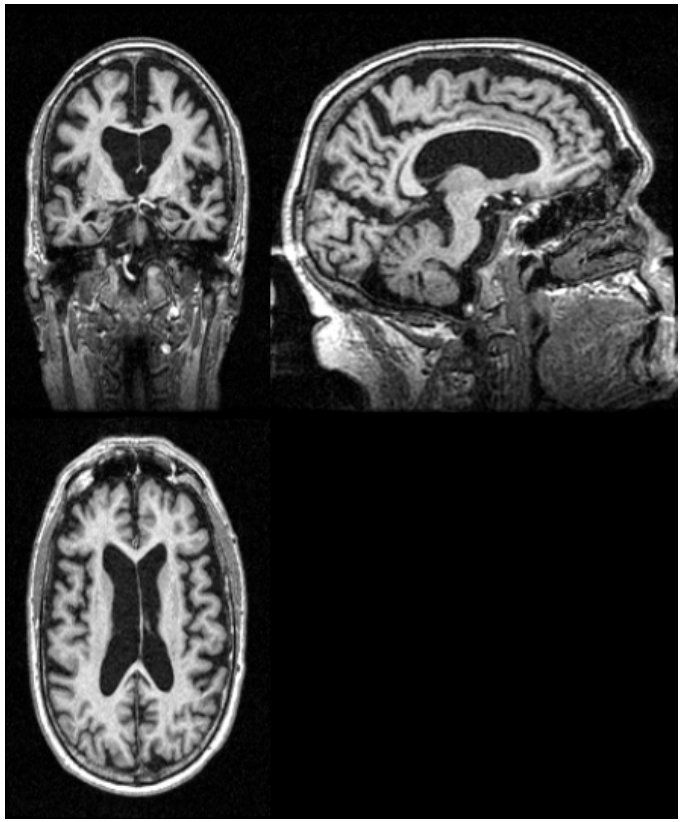
Input command **fslreorient2std sample.nii.gz ro.nii.gz**, click **Enter**.



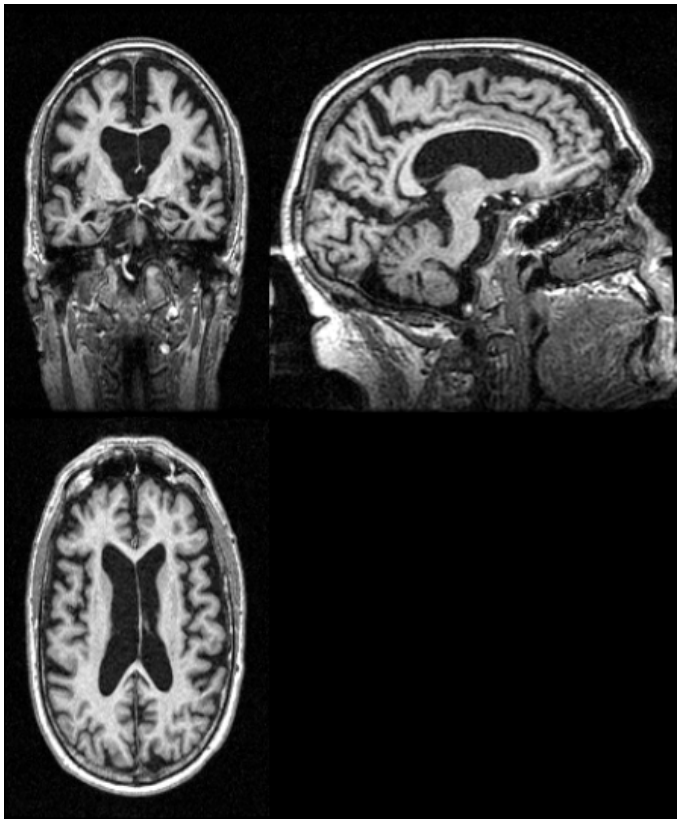
1. Reorientation to Standard Space

1.3 Check Output

You can find the output file in **Desktop/BrainPrep/volumes** with name **ro.nii.gz**. Use **MRIcron** to display the reorientated image. It should look same as the original image. Because **MRIcron** can adjust the input image and display it in standard space.



sample.nii.gz



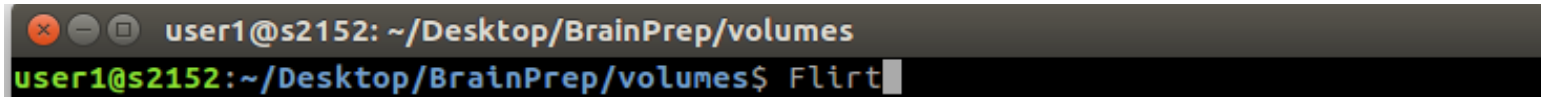
ro.nii.gz

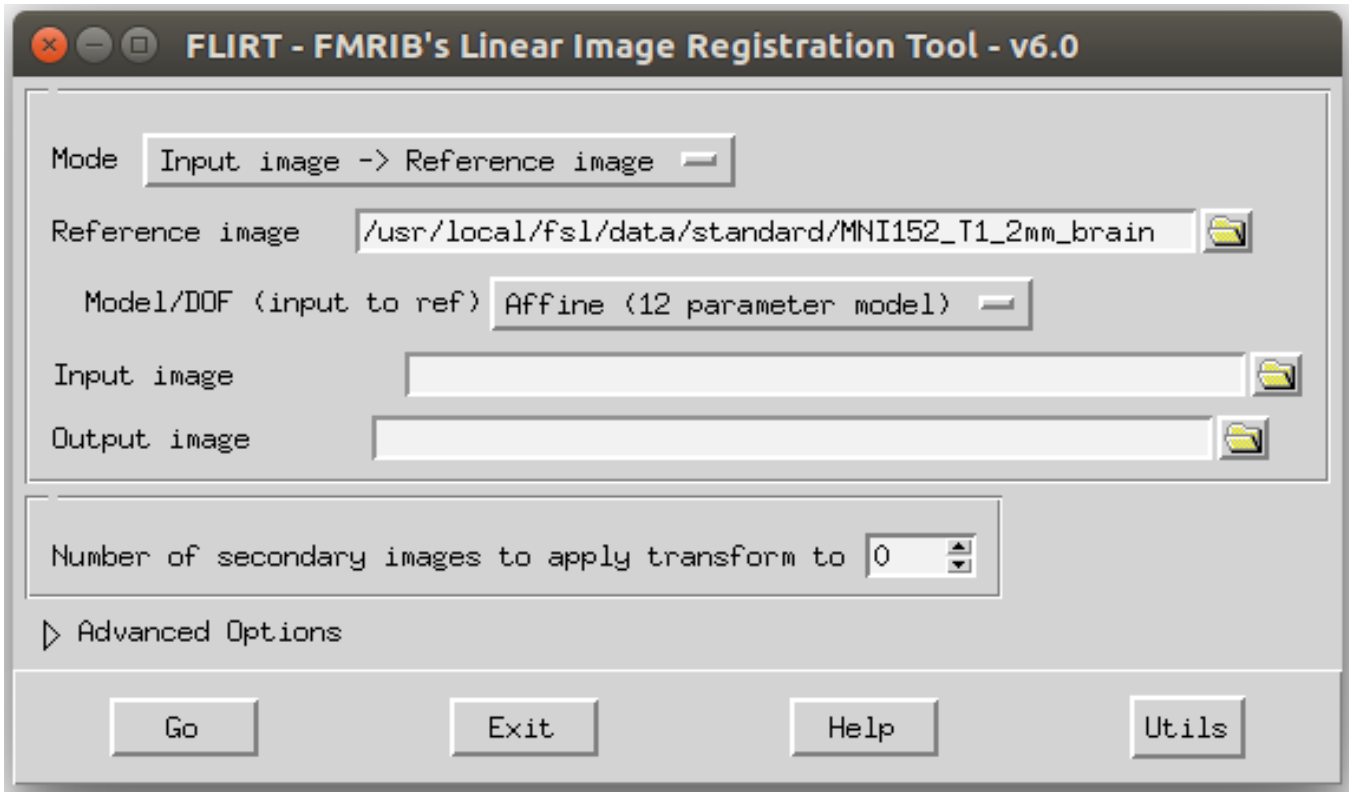
2. Registration to Template

2.1 Start Software

In terminal, input command:

★ for **Ubuntu** is: **Flirt**, for **macOS** is: **Flirt_gui**, click **Enter**.

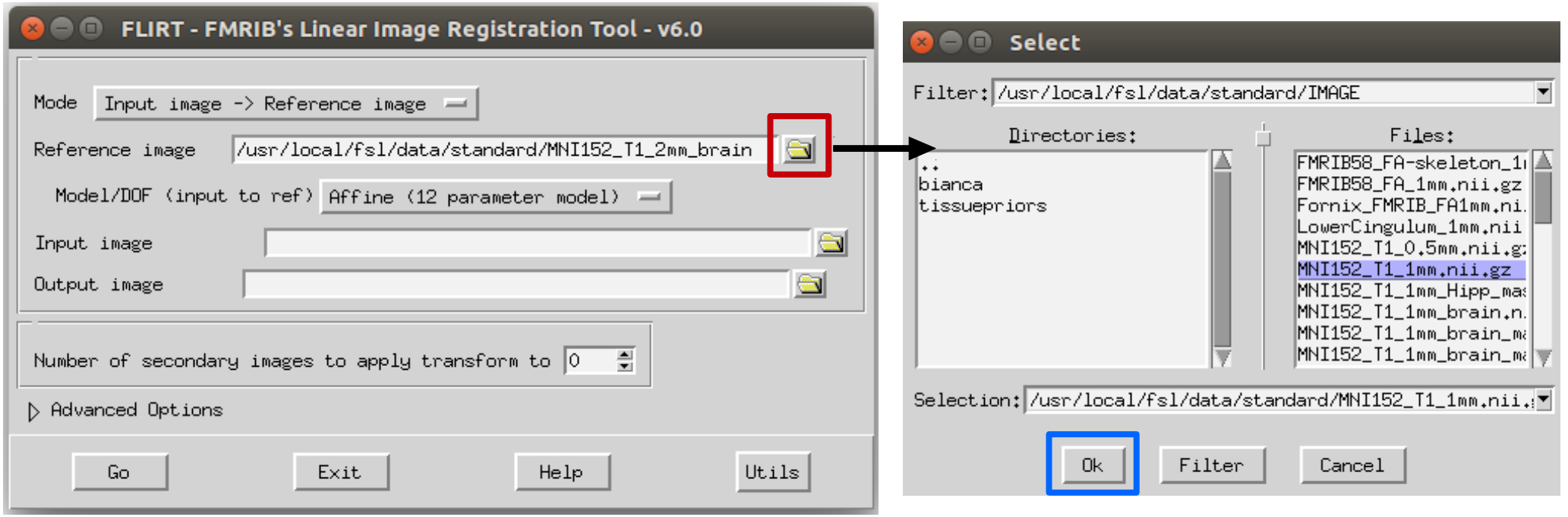




2. Registration to Template

2.2 Select Template

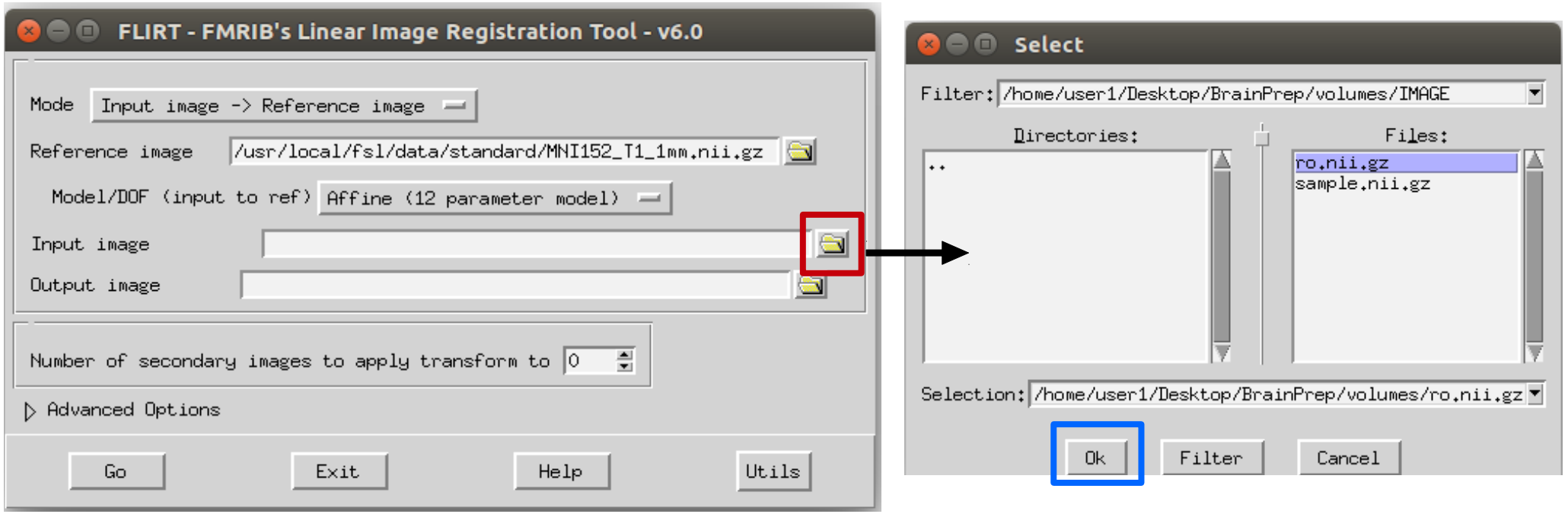
Click button in red box, select **MNI152_T1_1mm.nii.gz**, click **Ok**.



2. Registration to Template

2.3 Set Input Image Path

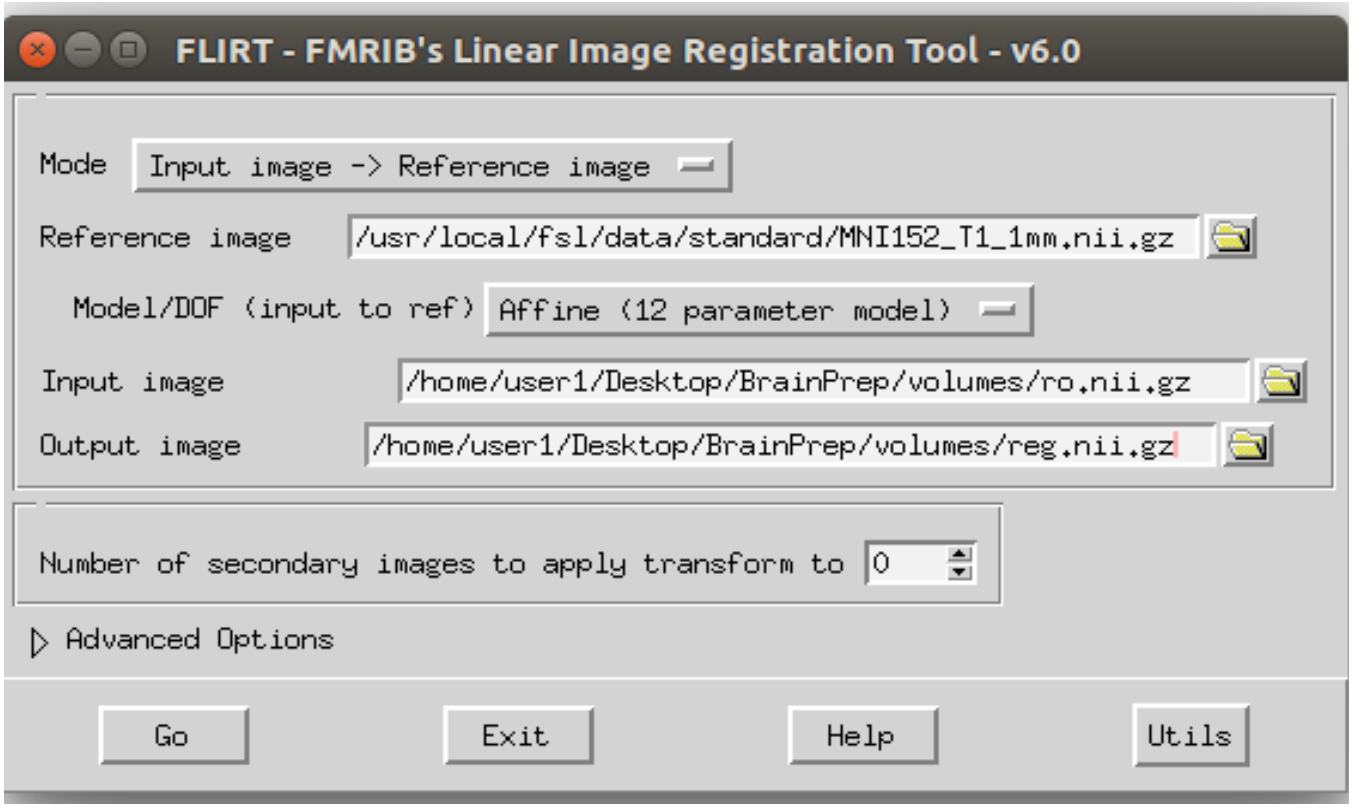
Click button in red box, select **ro.nii.gz** generated in step 1, click **Ok**.



2. Registration to Template

2.4 Set Output Image Path

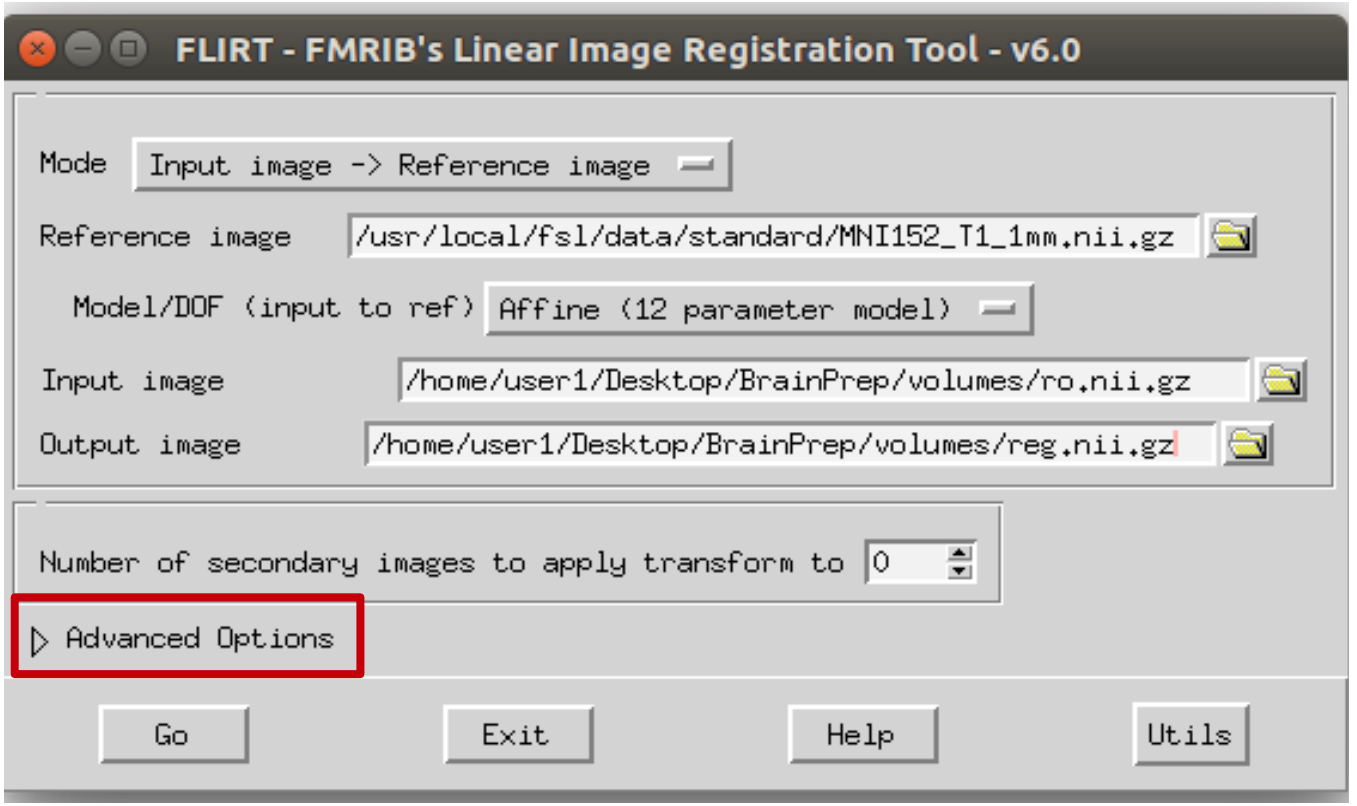
Copy input path to “Output Image” box, change the output file name to **reg.nii.gz**.



2. Registration to Template

2.5 Set Advanced Options

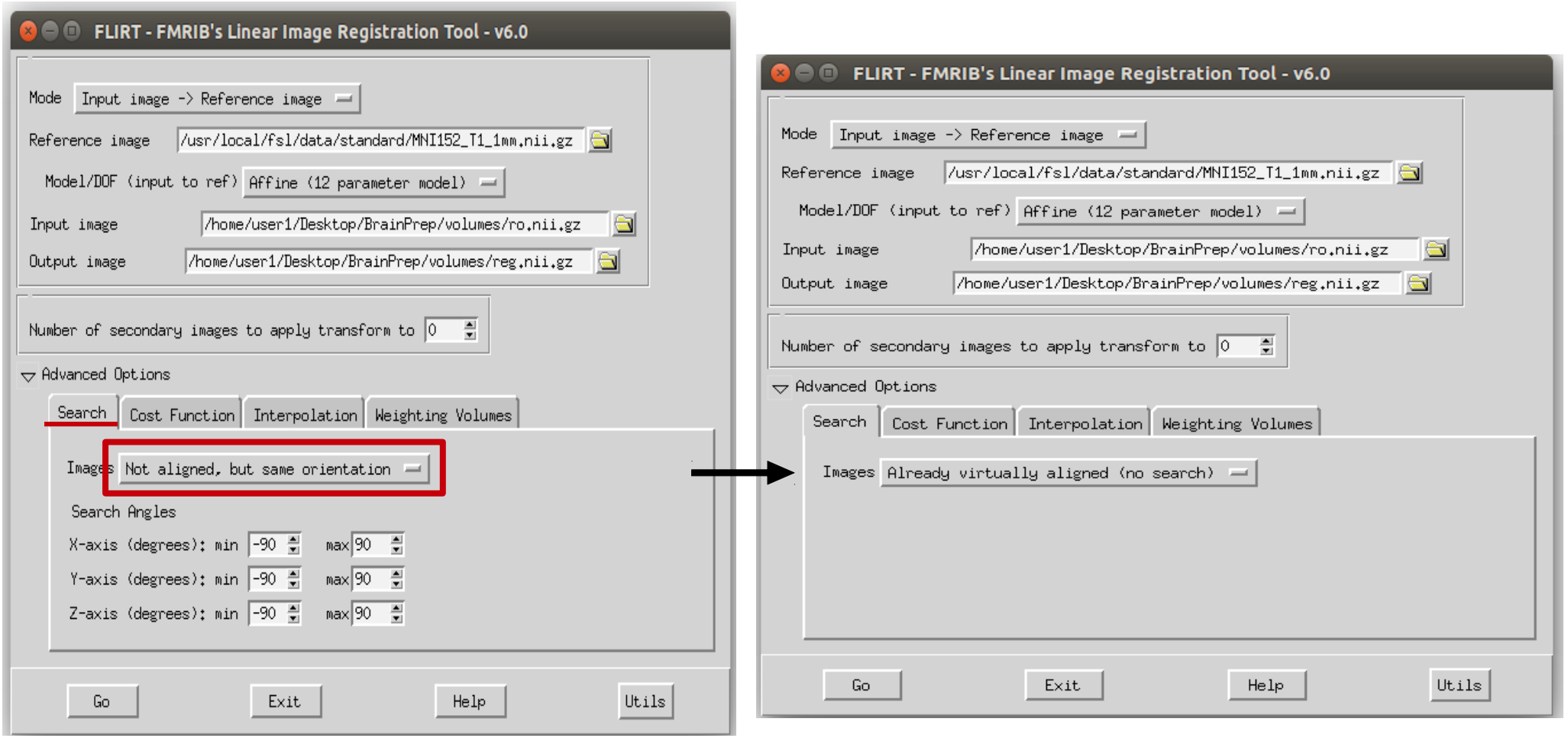
Click the triangle button in red box.



2. Registration to Template

2.5.1 Change Search Option

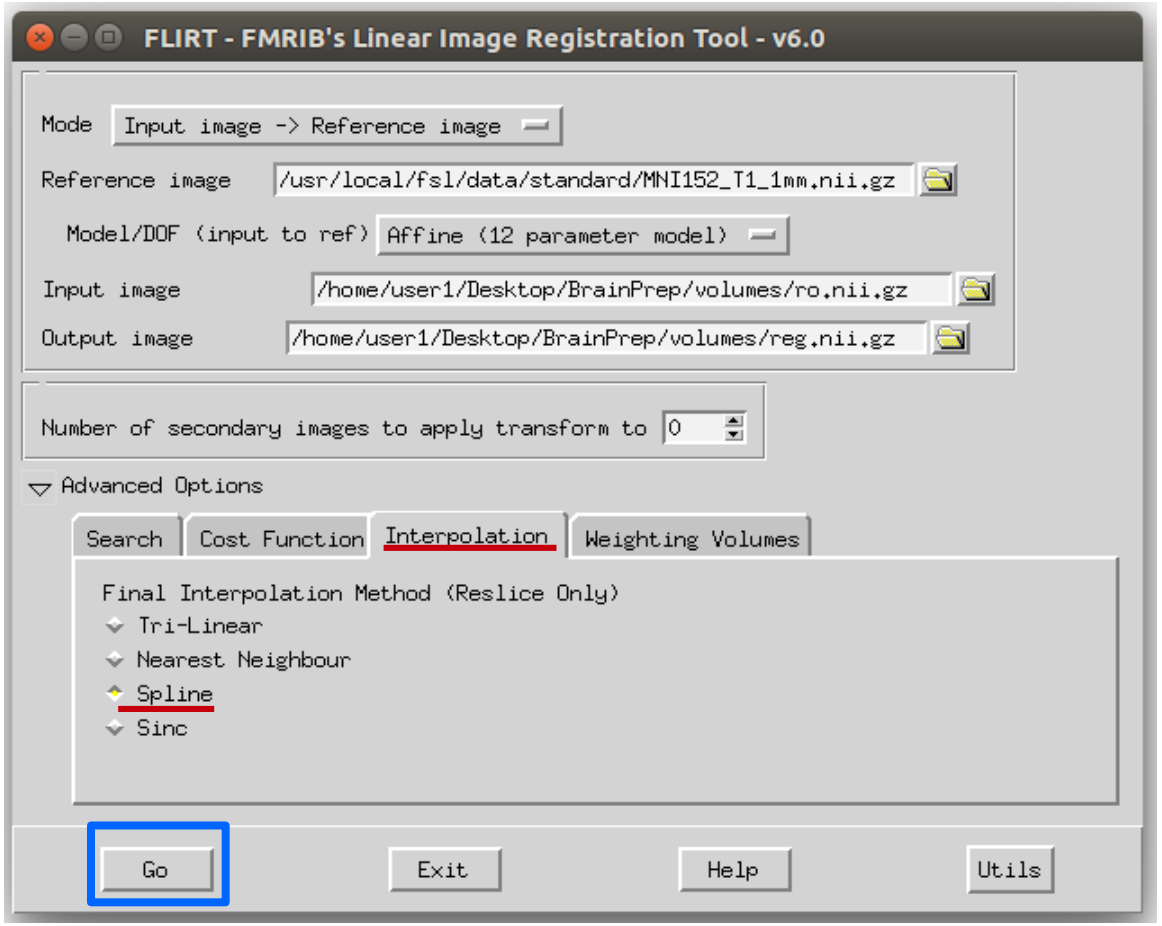
In **Search** tab, click button in red box and select the first option **Already virtually aligned (no search)**.



2. Registration to Template

2.5.2 Change Interpolation Option

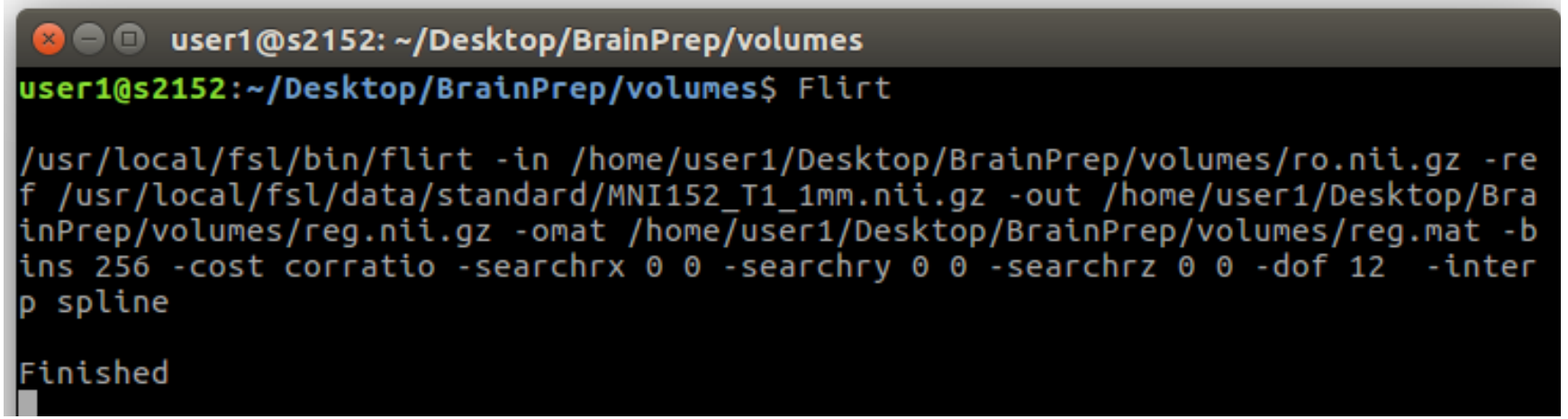
In **Interpolation** tab, select the third option **Spline**. Then, click **Go** to run the program.



2. Registration to Template

2.5.3 Waiting for Program Finished

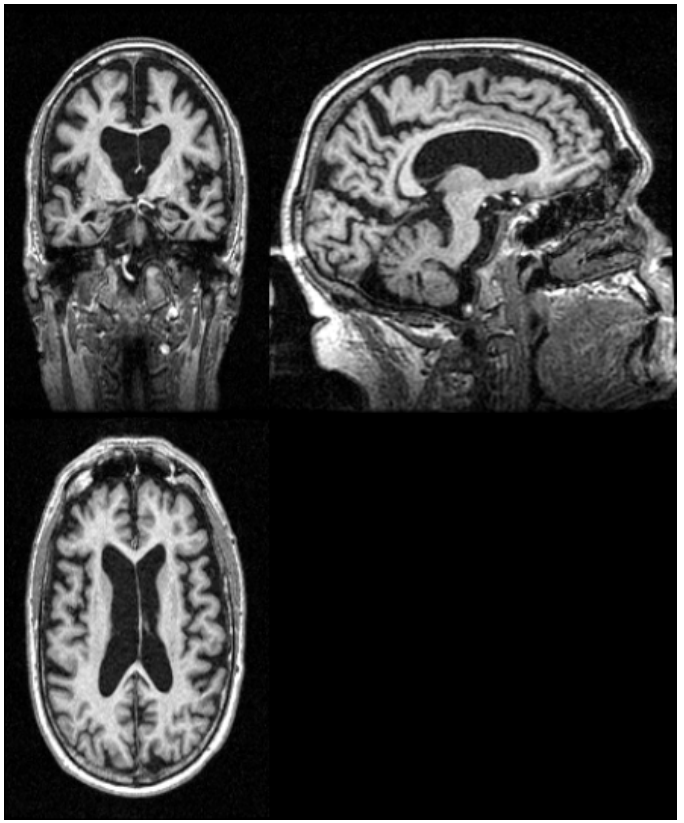
In terminal, the command used to do registration is printed out.



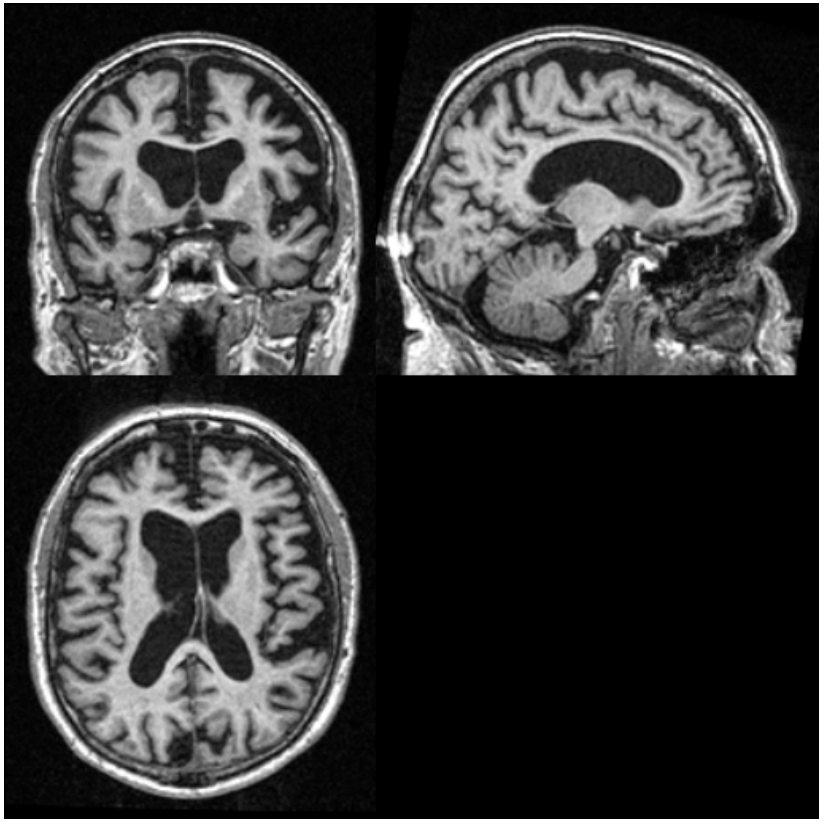
2. Registration to Template

2.5.3 Check Output

You can find the output file in **Desktop/BrainPrep/volumes** with name **reg.nii.gz**. Use **MRIcron** to display the output image. After program finished, close the Flirt window.



ro.nii.gz



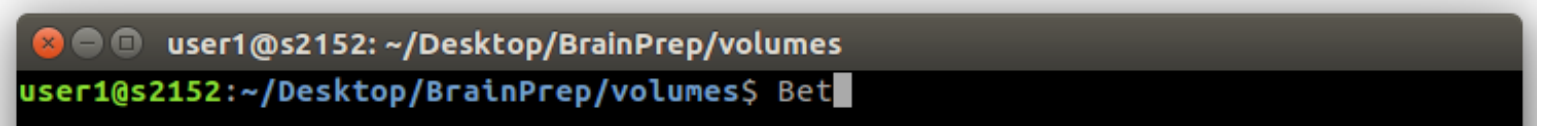
reg.nii.gz

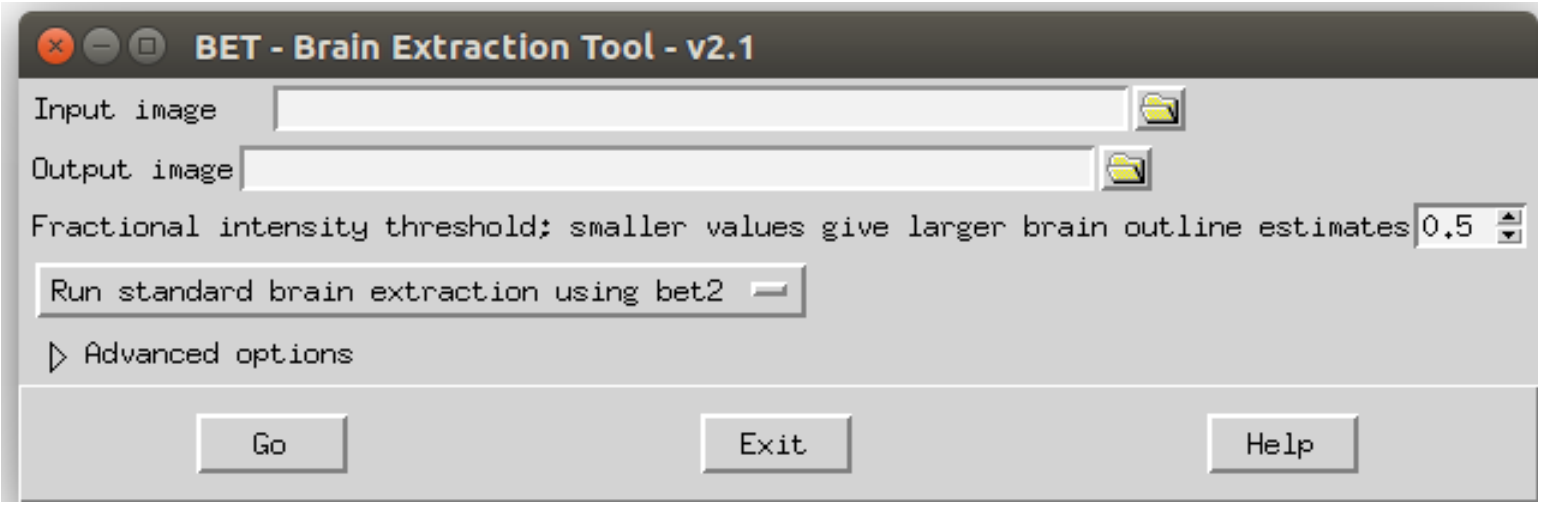
3. Skull Stripping

3.1 Start Software

In terminal, input command:

★ for **Ubuntu** is: **Bet**, for **macOS** is: **Bet_gui**, click **Enter**.

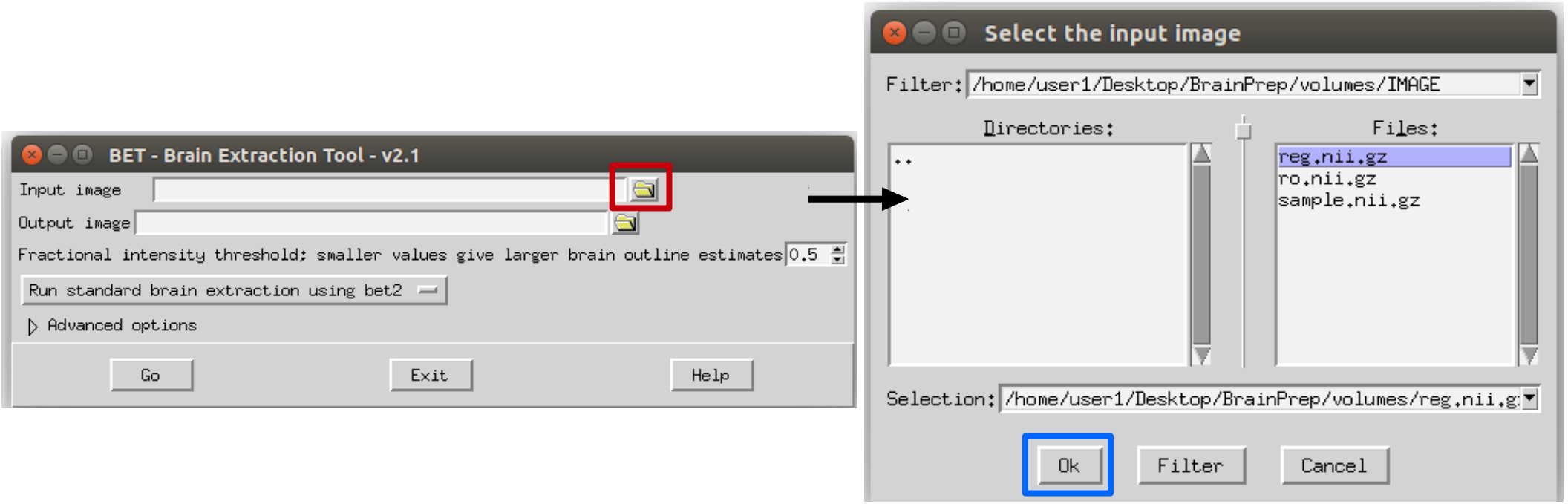




3. Skull Stripping

3.2 Set Path for Input Image

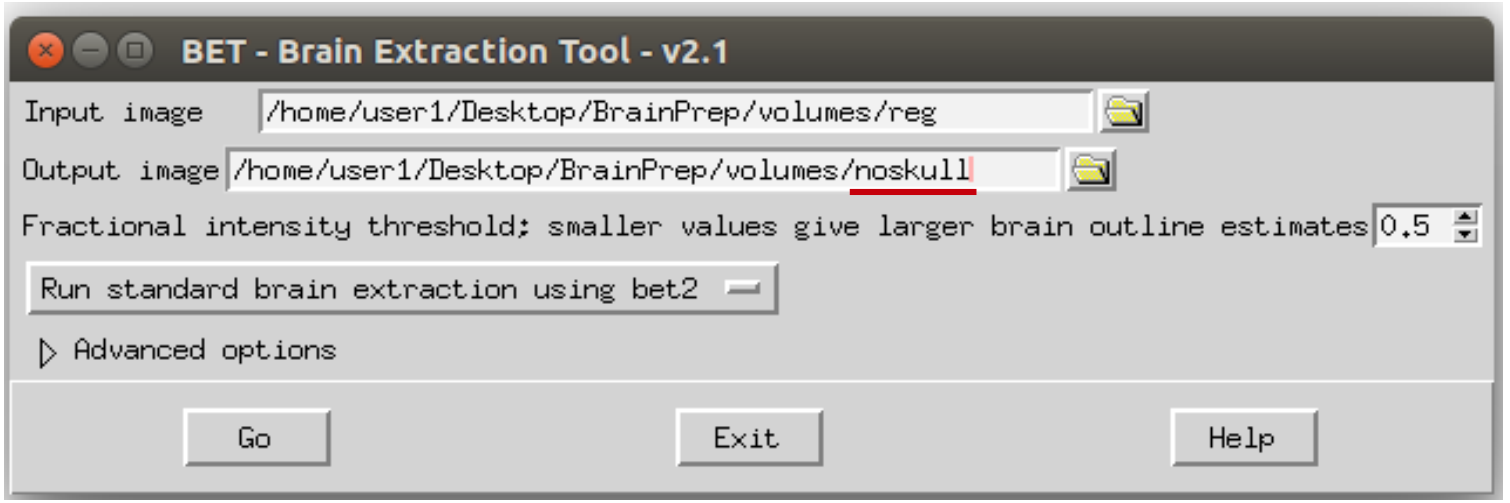
Click the button in red box, select **reg.nii.gz** as input image, click **Ok**.



3. Skull Stripping

3.3 Set Path for Output Image

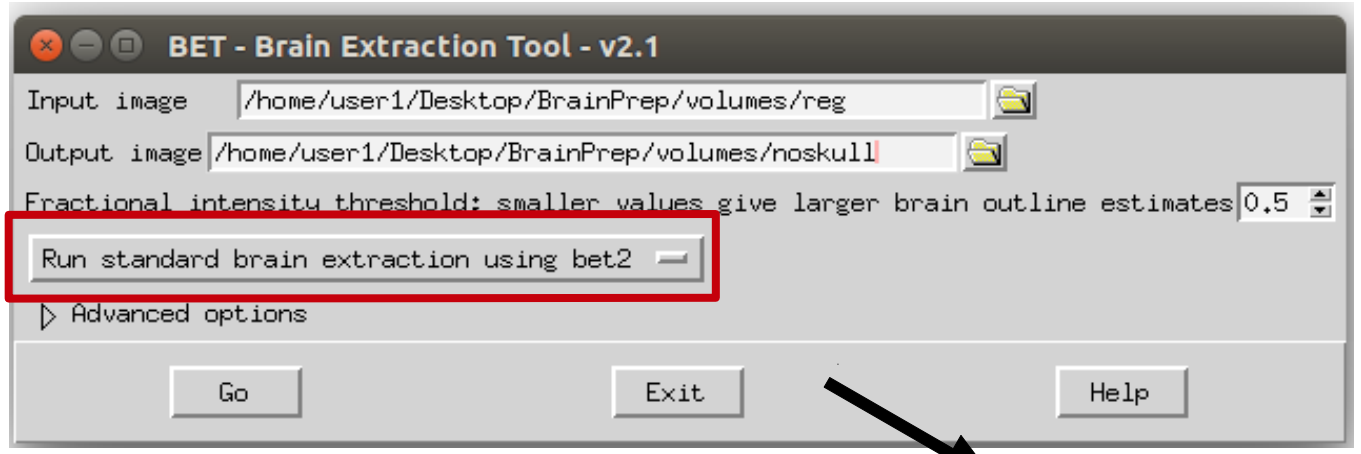
Change the name of output file to **noskull** in “Output Image” box.
The name of output image will be **noskull.nii.gz**.

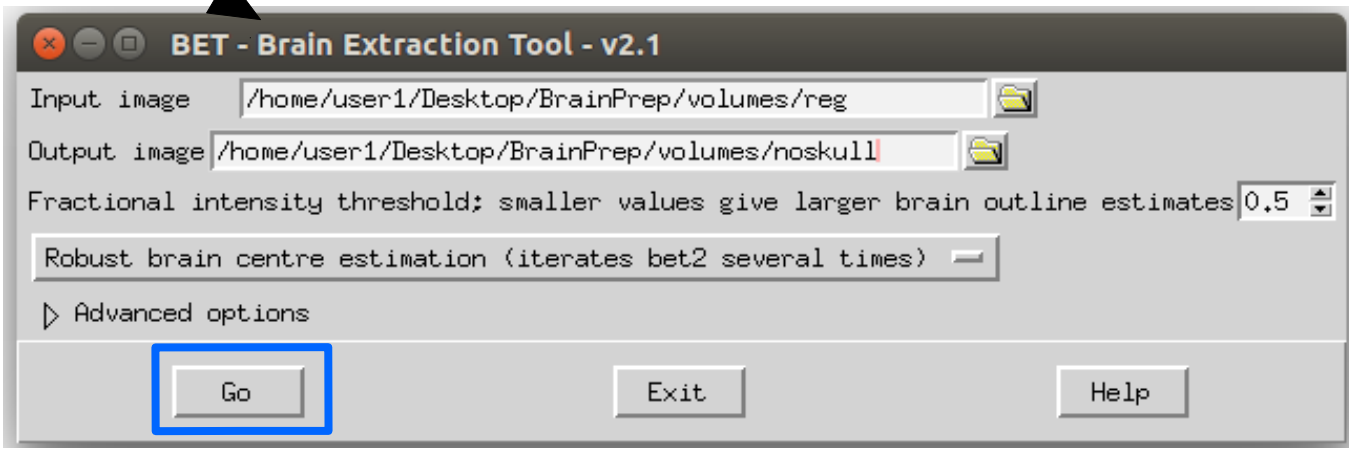


3. Skull Stripping

3.4 Select Method

Click the button in red box and select the second option **Robust brain centre estimation (iterates bet2 several times)**. Click **Go** to run the program.

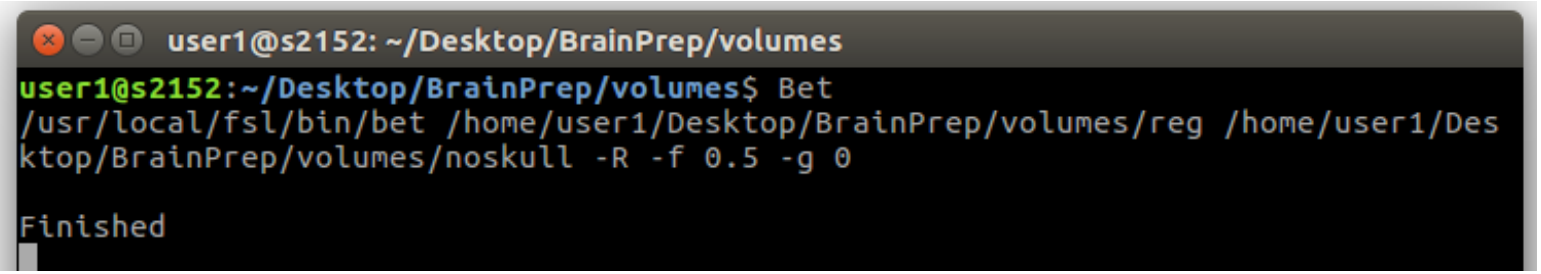




3. Skull Stripping

3.5 Waiting for Program Finished

In terminal, the command used to do skull stripping is printed out.

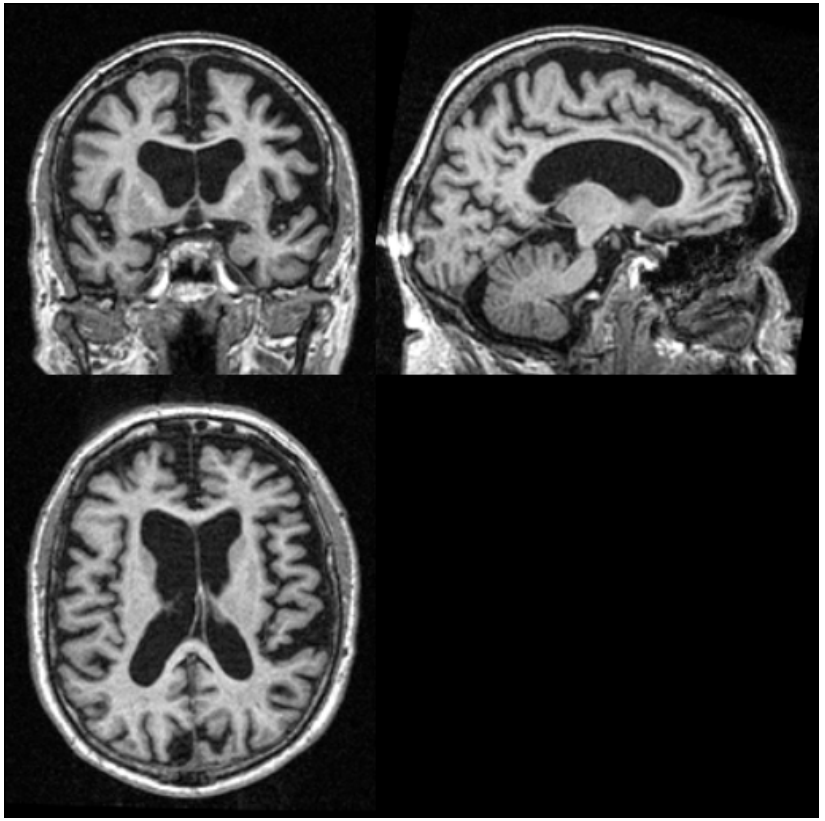


3. Skull Stripping

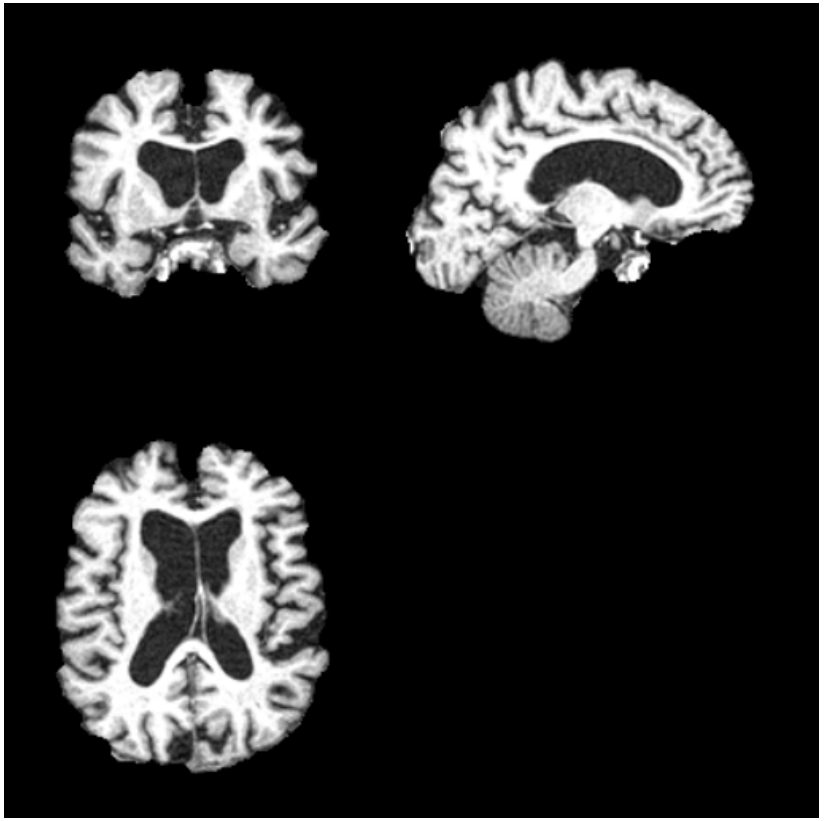
3.6 Check Output

You can find the output file in **Desktop/BrainPrep/volumes** with name **noskull.nii.gz**. Use **MRIcron** to display the output image.

After program finished, close the Bet window.



reg.nii.gz



noskull.nii.gz

4. Bias Field Correction

4.1 Run Program

This step is performed by ANTs.

I only did the test in **Ubuntu** system.

The command should also work in **macOS**.

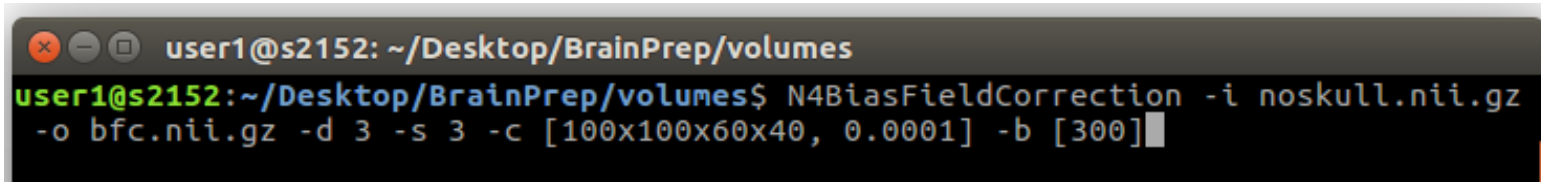
If not, you may skip this step.

In terminal, input command: **N4BiasFieldCorrection -i noskull.nii.gz -o bfc.nii.gz -d 3 -s 3 -c [100x100x60x40, 0.0001] -b [300]**,

click **Enter**.

-i: input file name

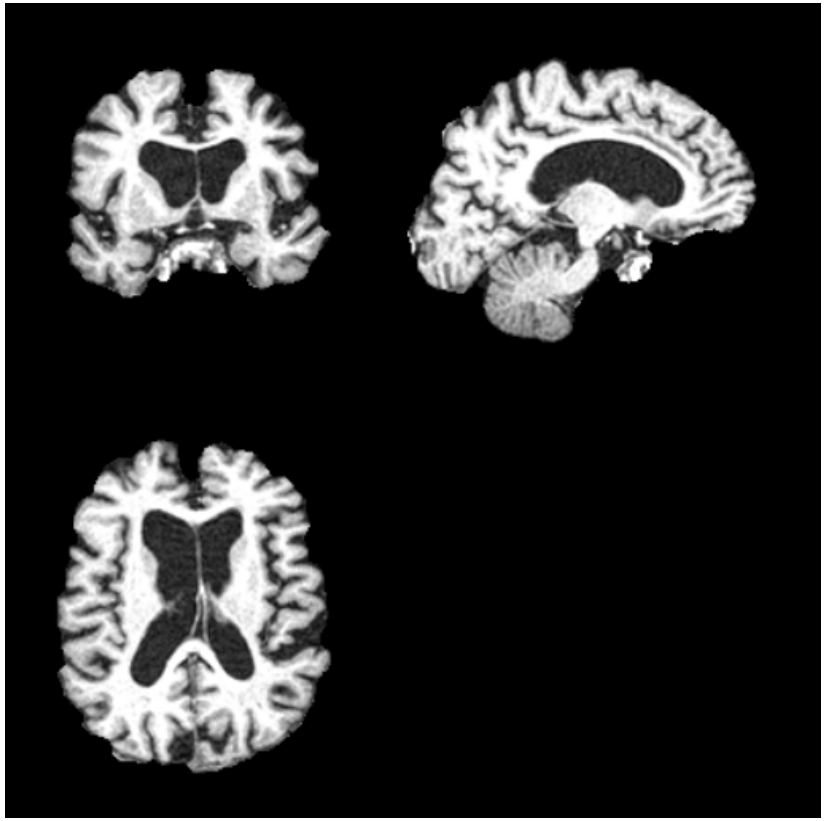
-o: output file name



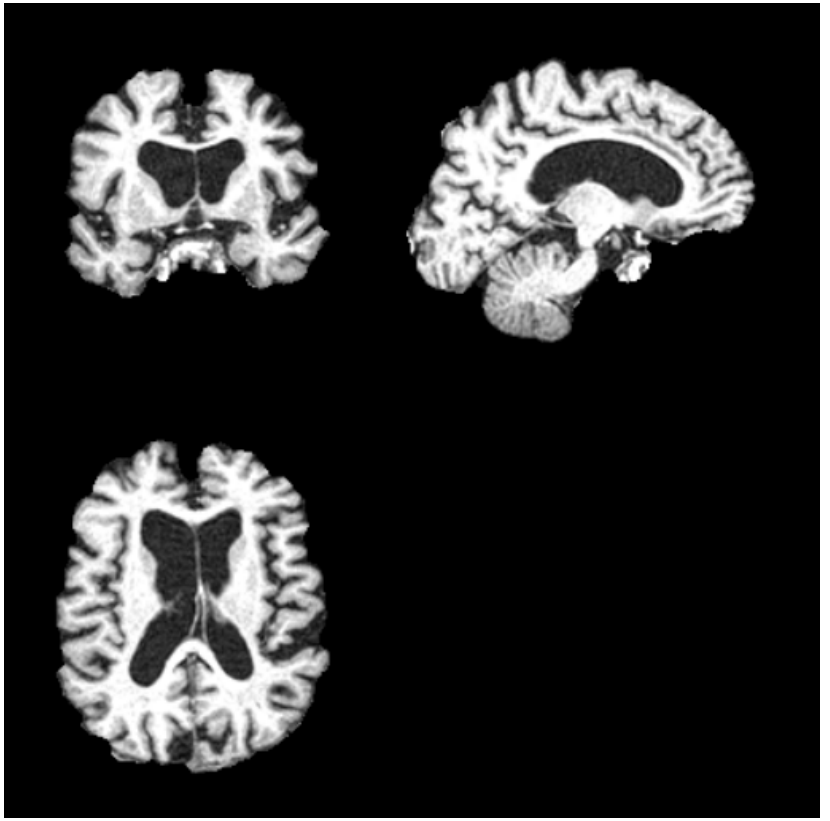
4. Bias Field Correction

4.2 Check Output

You can find the output file in **Desktop/BrainPrep/volumes** with name **bfc.nii.gz**. Use **MRIcron** to display the output image.



noskull.nii.gz



bfc.nii.gz

4. Bias Field Correction

Notes:

Two disadvantages of using command line in terminal to do bias field correction:

- It can only process one input image at every run.

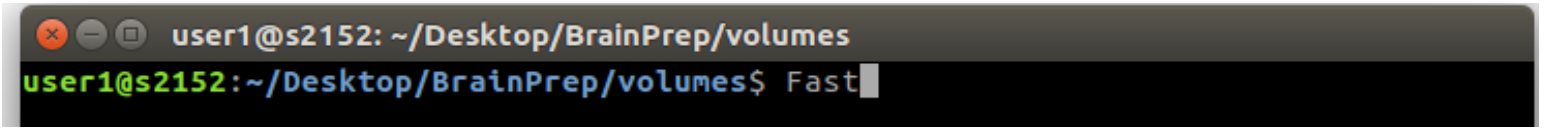
- It is a bit difficult to change parameters, since it does not has a friendly user interface.

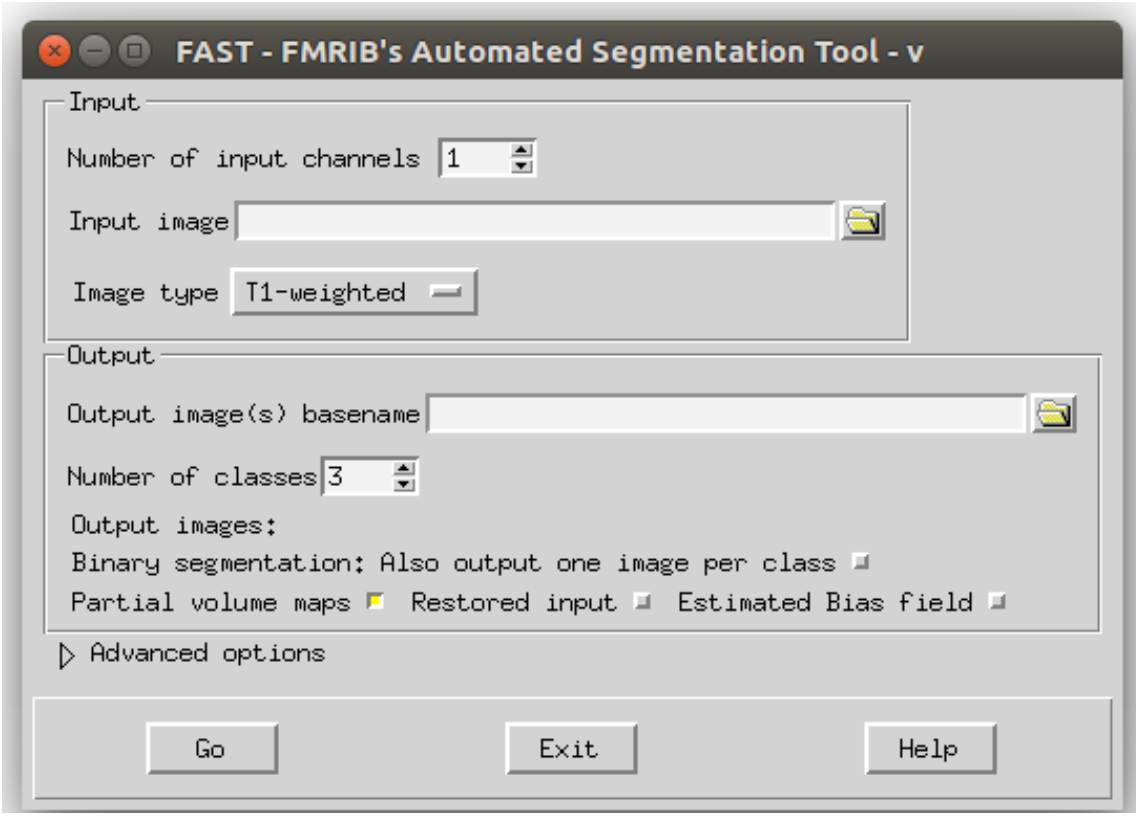
5. Tissue Segmentation

5.1 Start Software

In terminal, input command:

★ for **Ubuntu** is: **Fast**, for **macOS** is: **Fast_gui**, click **Enter.**

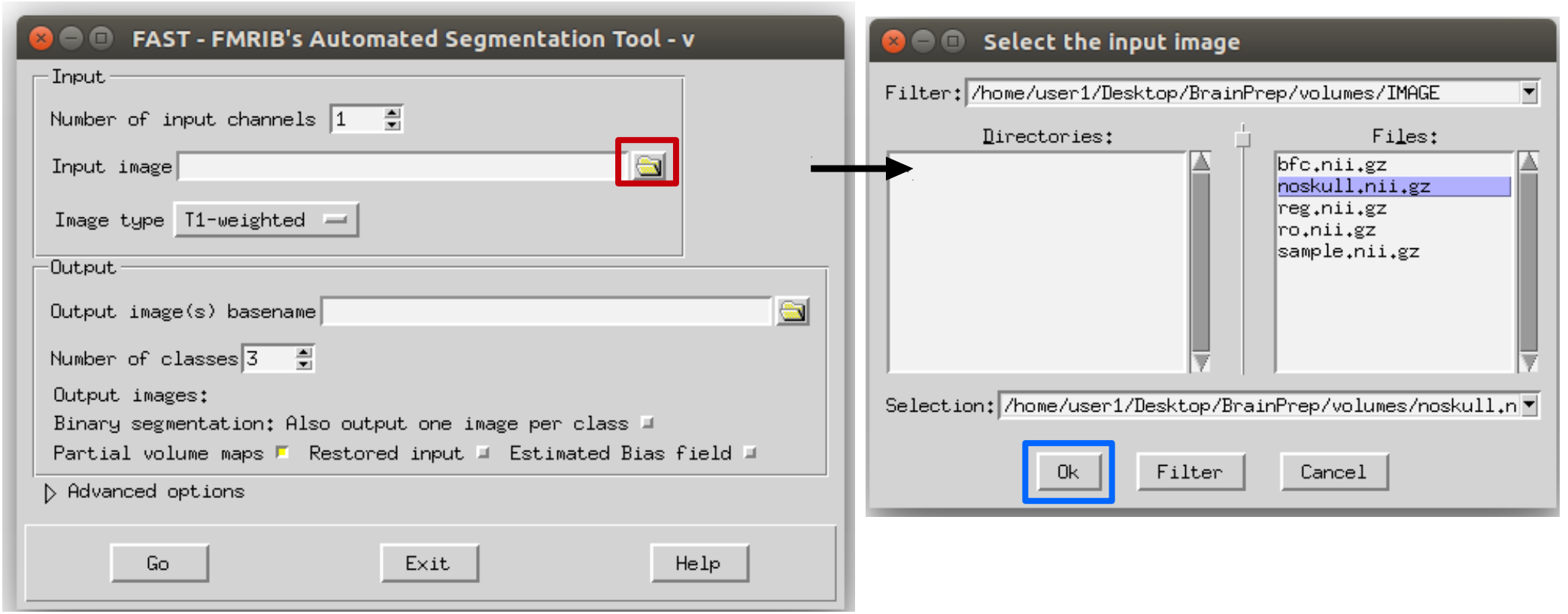




5. Tissue Segmentation

5.2 Set Path for Input Image

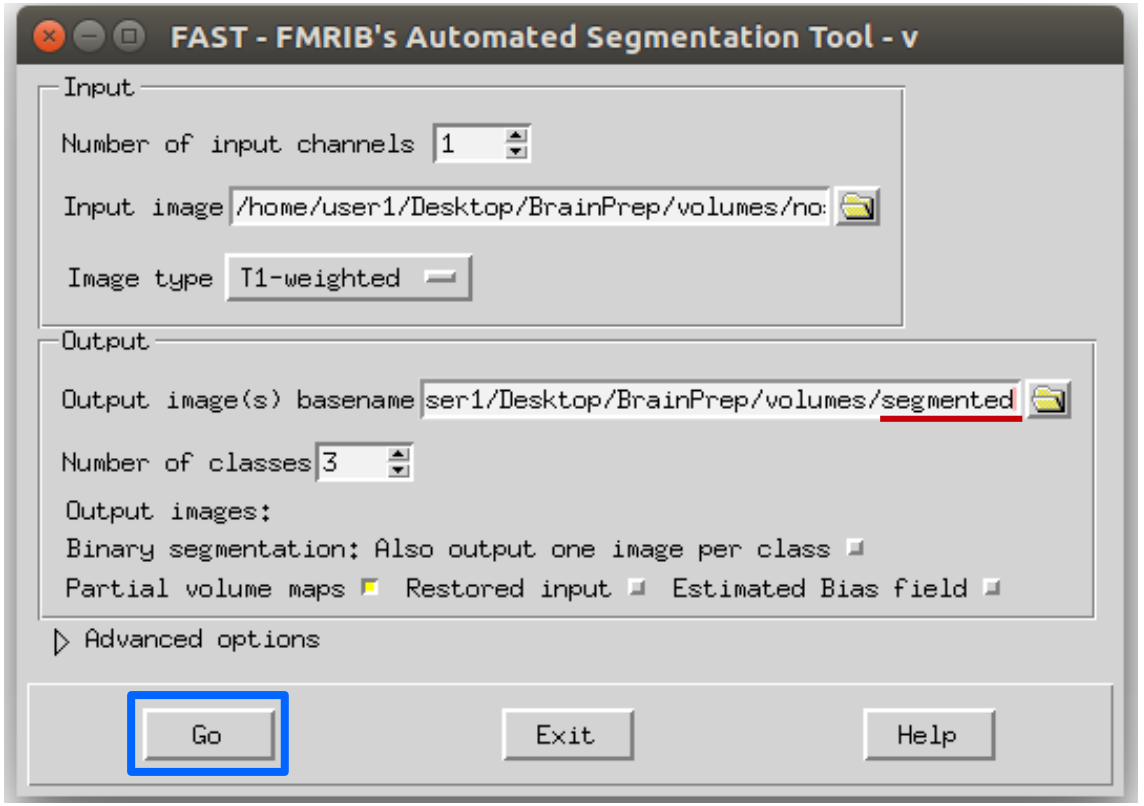
Click the button in red box, select **noskull.nii.gz** as input image. Because **Fast** will do bias field correction before doing segmentation. Click **Ok**.



5. Tissue Segmentation

5.3 Set Basename for Output Image

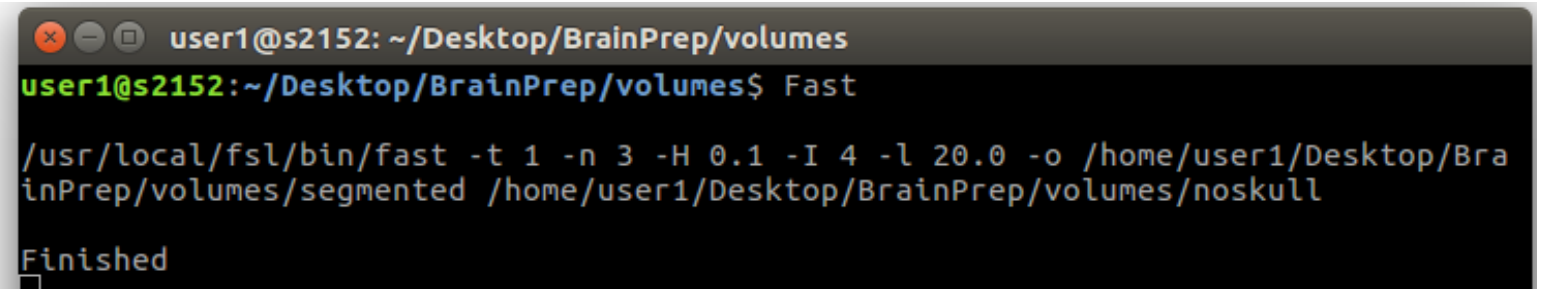
Change the basename of output file to **segmented** in “Output Image(s) basename” box. The names of output images will be started with **segmented**. Click **Go** to run program.



5. Tissue Segmentation

5.4 Waiting for Program Finished

In terminal, the command used to do tissue segmentation is printed out.



5. Tissue Segmentation

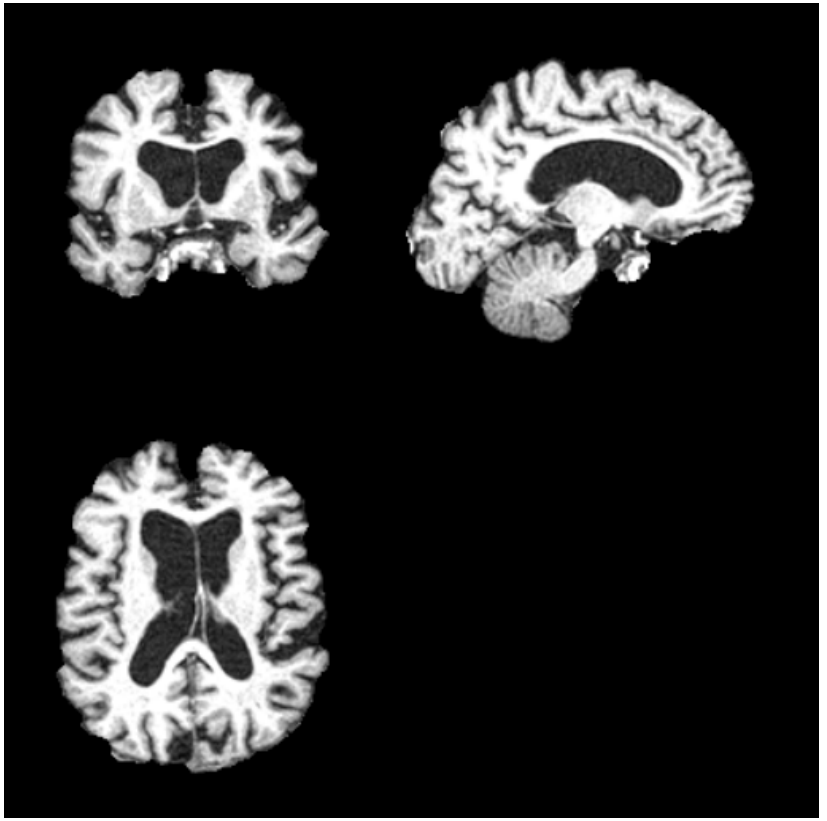
5.5 Check Outputs

You can find the output files in **Desktop/BrainPrep/volumes** whose name is started with **segmented**. Use **MRIcron** to display the output images. After program finished, close the Fast window.

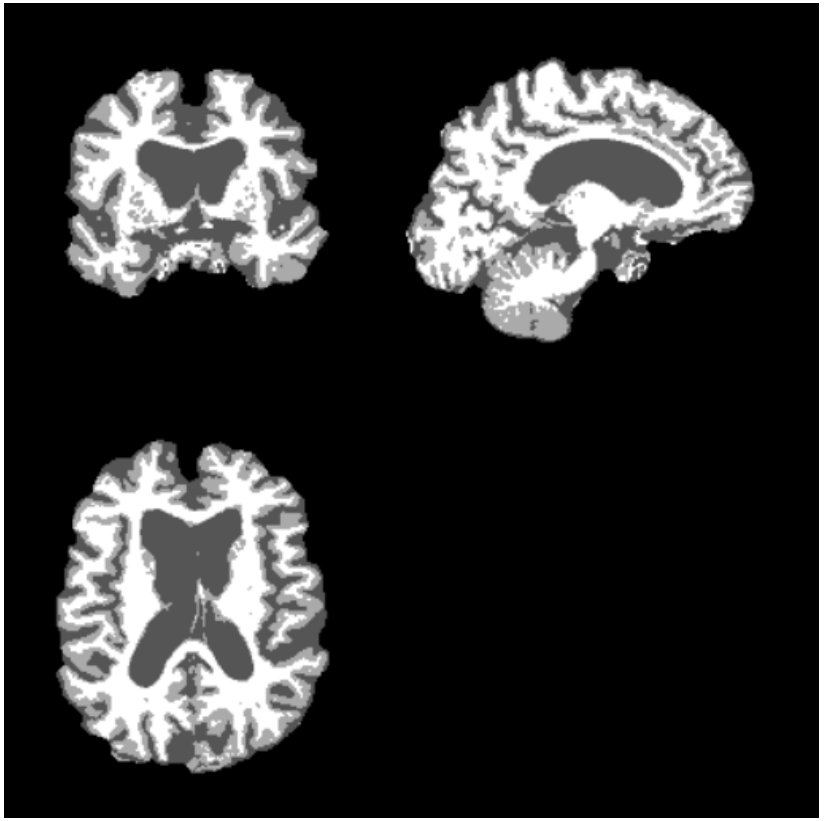
Output images:

- **segmented_seg.nii.gz**: contains three labels, 1 for CSF, 2 for gray matter and 3 for white matter.
- **segmented_pve_0.nii.gz**: segmentation of CSF.
- **segmented_pve_1.nii.gz**: segmentation of gray matter.
- **segmented_pve_2.nii.gz**: segmentation of white matter.

5. Tissue Segmentation

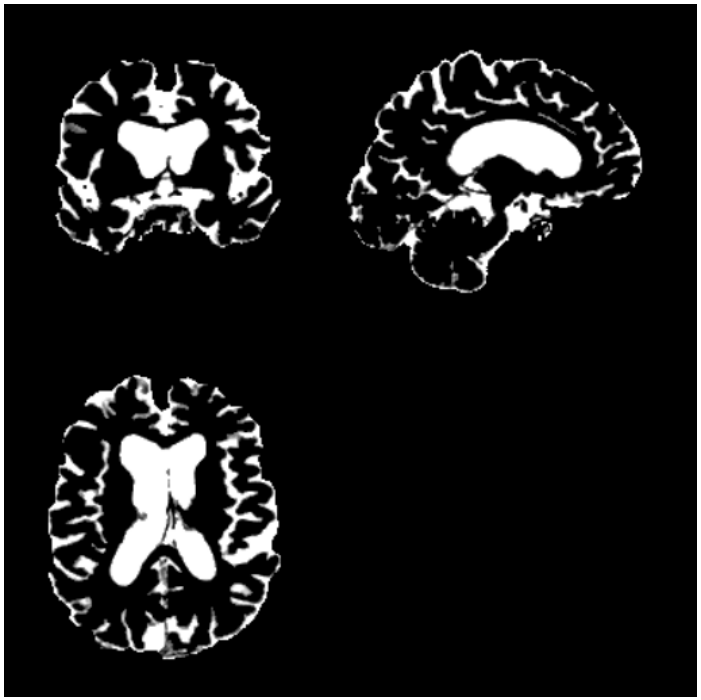


noskull.nii.gz

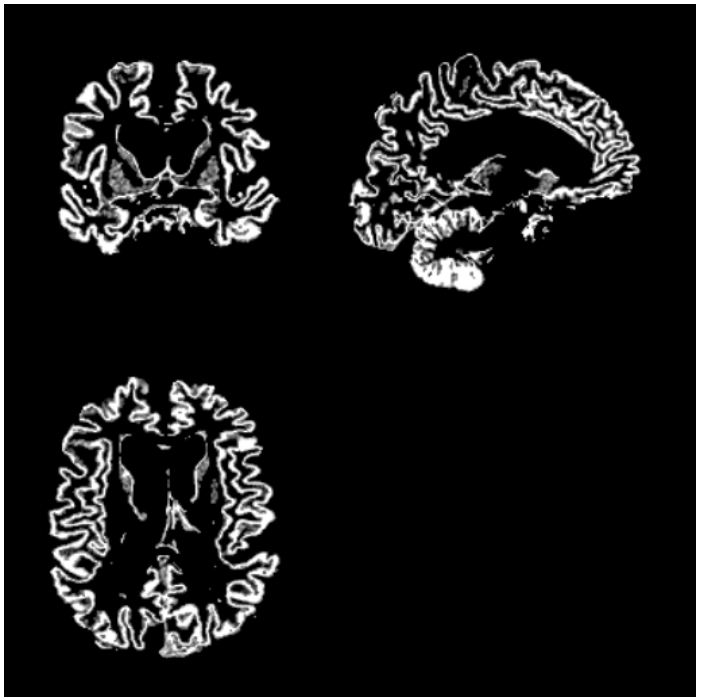


segmented_seg.nii.gz

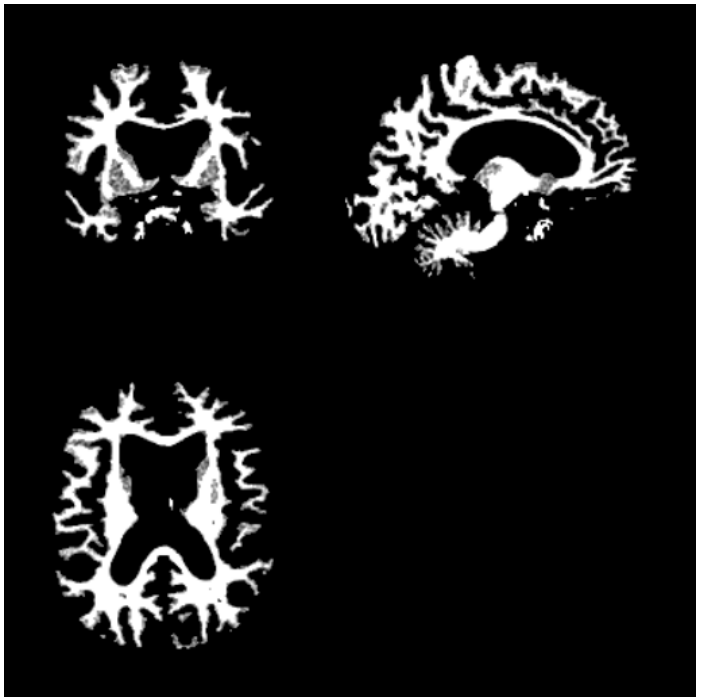
5. Tissue Segmentation



segmented_pve_0.nii.gz
(CSF)



segmented_pve_1.nii.gz
(Gray Matter)



segmented_pve_2.nii.gz
(White Matter)

Resources

1. FSL

- Official website: https://fsl.fmrib.ox.ac.uk/fsl/fslwiki
- List of all programs: https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FslOverview
- FSL courses: http://fsl.fmrib.ox.ac.uk/fslcourse/

2. ANTs

- Source code: https://github.com/ANTsX/ANTs
- Wiki page: https://github.com/ANTsX/ANTs/wiki