

UKF Tractography Tutorial

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3DSlicer

- The tutorial uses the 3DSlicer software (www.slicer.org)

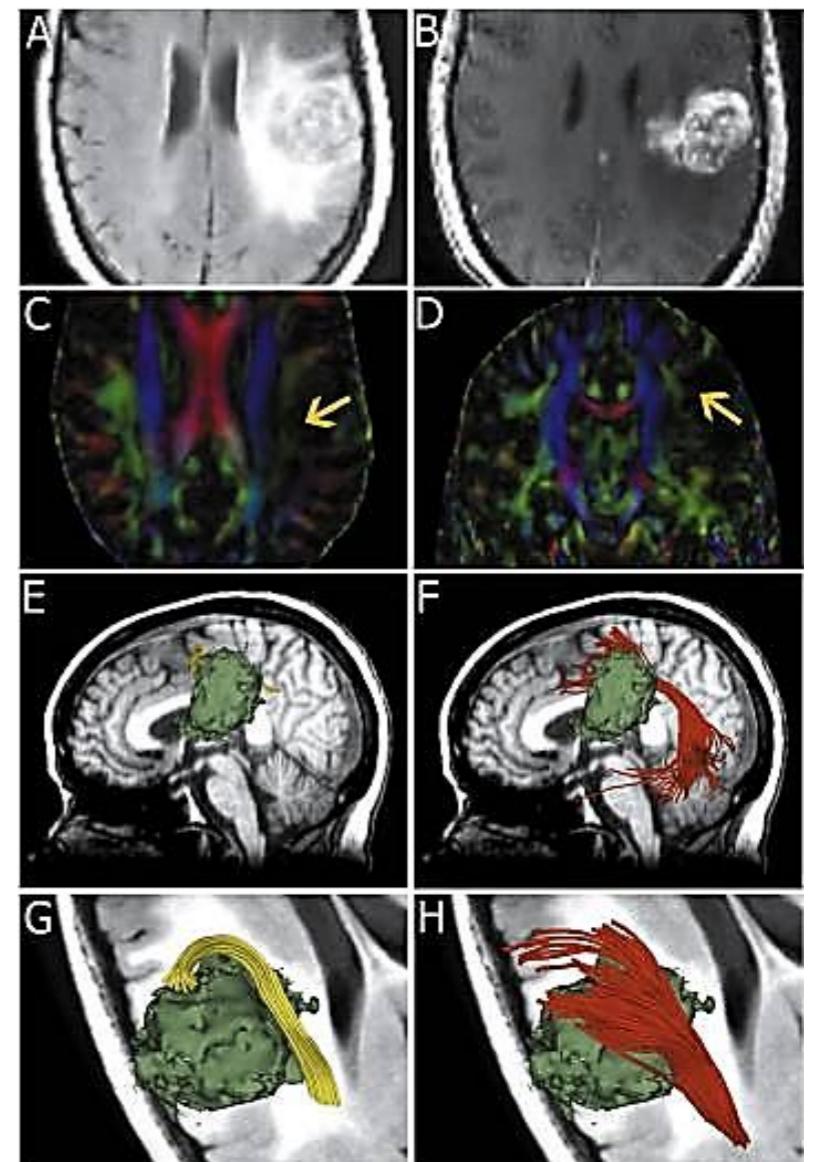
The screenshot shows the official 3DSlicer website. At the top left is the 3DSlicer logo. To its right, the text reads: "A multi-platform, **free and open source** software package for **visualization** and **medical image computing**". Below this are three buttons: "Download", "Slicer Training", and "Feedback". On the left side, there is a sidebar with links: "Download Slicer", "Slicer Wiki", "About Slicer" (with links to Introduction, Acknowledgments, News, Contact Us, Licensing, and Commercial Use), "Publication" (with links to Publication DB, Image Gallery, Slicer Community, and Citing Slicer), "Documentation" (with links to Slicer Training, User Manual, and Developer Manual), and "Help" (with links to Help, User FAQ, Developer FAQ, and Mailing Lists). The main content area features a section titled "Slicer 4.6 released" with a brief description of the software's purpose and recent improvements. It includes a link to "Announcements" and a "download Slicer 4.6" button. Below this, it states that Slicer is made possible through contributions from an international community of scientists. A grid of three images illustrates the software's capabilities: "Powerful processing" (showing medical images and segmentation), "Streamlined interface" (showing a 3D volume rendering of a brain), and "Extensible platform" (showing a complex 3D model of a tissue structure). At the bottom, there is a footer with the 3DSlicer logo and the text "version 4", and the website address "www.slicer.org".

It is the responsibility of the user of 3DSlicer to comply with both the terms of the license and with the applicable laws, regulations and rules. Slicer is a tool for research, and is not FDA approved.

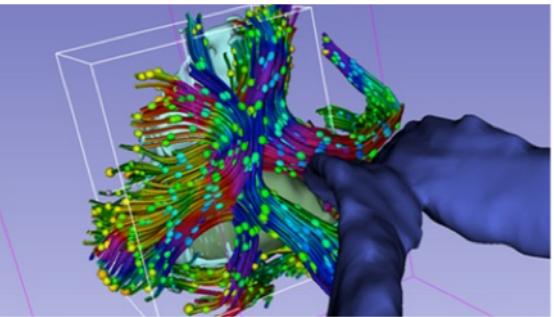


3DSlicer

- An **end-user** application for image analysis
- An **open-source** environment for software development
- A software platform that is both **easy to use** for clinical researchers and **easy to extend** for programmers



[Chen et al, 2015]



Slicer DMRI

An open-source project to improve and extend diffusion magnetic resonance imaging software in 3D Slicer:

<http://slicerdmri.github.io>

Please read the Diffusion MRI Analysis tutorial to install SlicerDMRI:

<https://github.com/SlicerDMRI/slicerdmri.github.io/blob/master/docs/tutorials/DiffusionMRIanalysis.pdf>

UKF Installation

- 3D Slicer now supports plug-ins/extensions that are available for download from an extension server. Extensions allow end-users to selectively install features that are useful for them.
- UKF tractography can be installed on Slicer using “Extension Manager”.
- Instructions for Extension Manager:

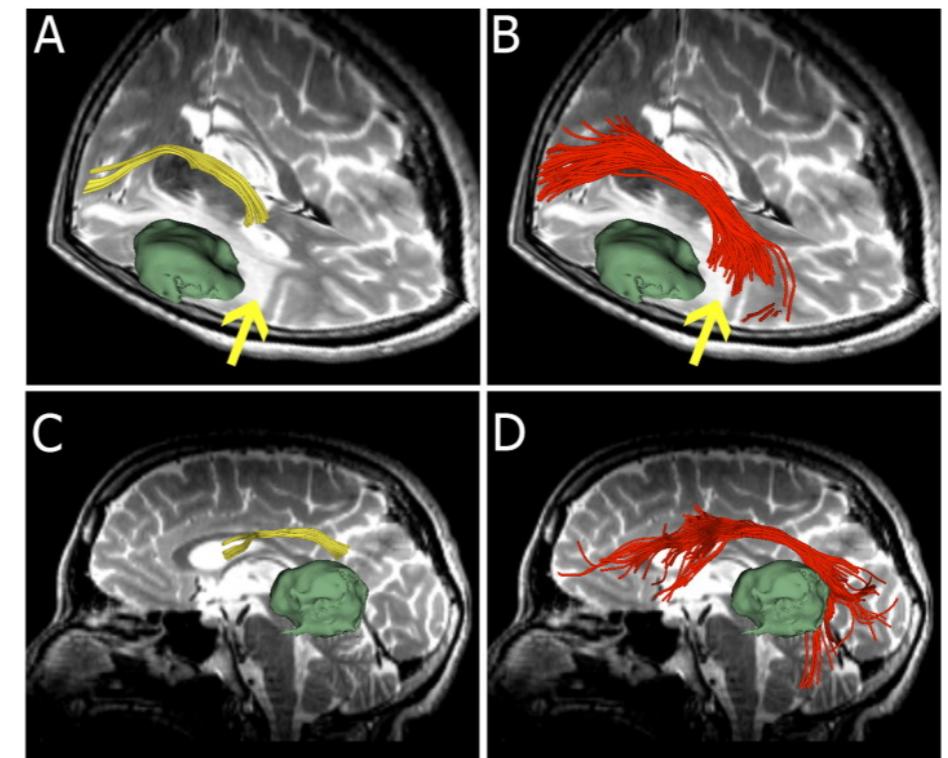
[http://www.slicer.org/wiki/Documentation/4.6/
SlicerApplication/ExtensionsManager](http://www.slicer.org/wiki/Documentation/4.6/SlicerApplication/ExtensionsManager)

UKF Tractography

- Unscented Kalman Filter tractography method:
 - Simultaneous model estimation and tractography
 - The diffusion model is fit to the data during tractography not before.

Why UKF

- UKF tractography may detect more fibers comparing to single-tensor streamline tractography (Slicer default method), especially in edematous areas.
- For example: The UKF two-tensor model traces a larger volume arcuate fasciculus in the setting of edema.



[Chen et al, 2015]

Unscented Kalman Filter Tractography

[Inf Process Med Imaging](#). 2009;21:126-38.

Neural tractography using an unscented Kalman filter.

[Malcolm JG¹](#), [Shenton ME](#), [Rathi Y.](#)

Author information

¹Psychiatry Neuroimaging Laboratory, Harvard Medical School, Boston, MA, USA. malcolm@bwh.harvard.edu

Abstract

We describe a technique to simultaneously estimate a local neural fiber model and trace out its path. Existing techniques estimate the local fiber orientation at each voxel independently so there is no running knowledge of confidence in the estimated fiber model. We formulate fiber tracking as recursive estimation: at each step of tracing the fiber, the current estimate is guided by the previous. To do this we model the signal as a mixture of Gaussian tensors and perform tractography within a filter framework. Starting from a seed point, each fiber is traced to its termination using an unscented Kalman filter to simultaneously fit the local model and propagate in the most consistent direction. Despite the presence of noise and uncertainty, this provides a causal estimate of the local structure at each point along the fiber. Synthetic experiments demonstrate that this approach reduces signal reconstruction error and significantly improves the angular resolution at crossings and branchings. In vivo experiments confirm the ability to trace out fibers in areas known to contain such crossing and branching while providing inherent path regularization.

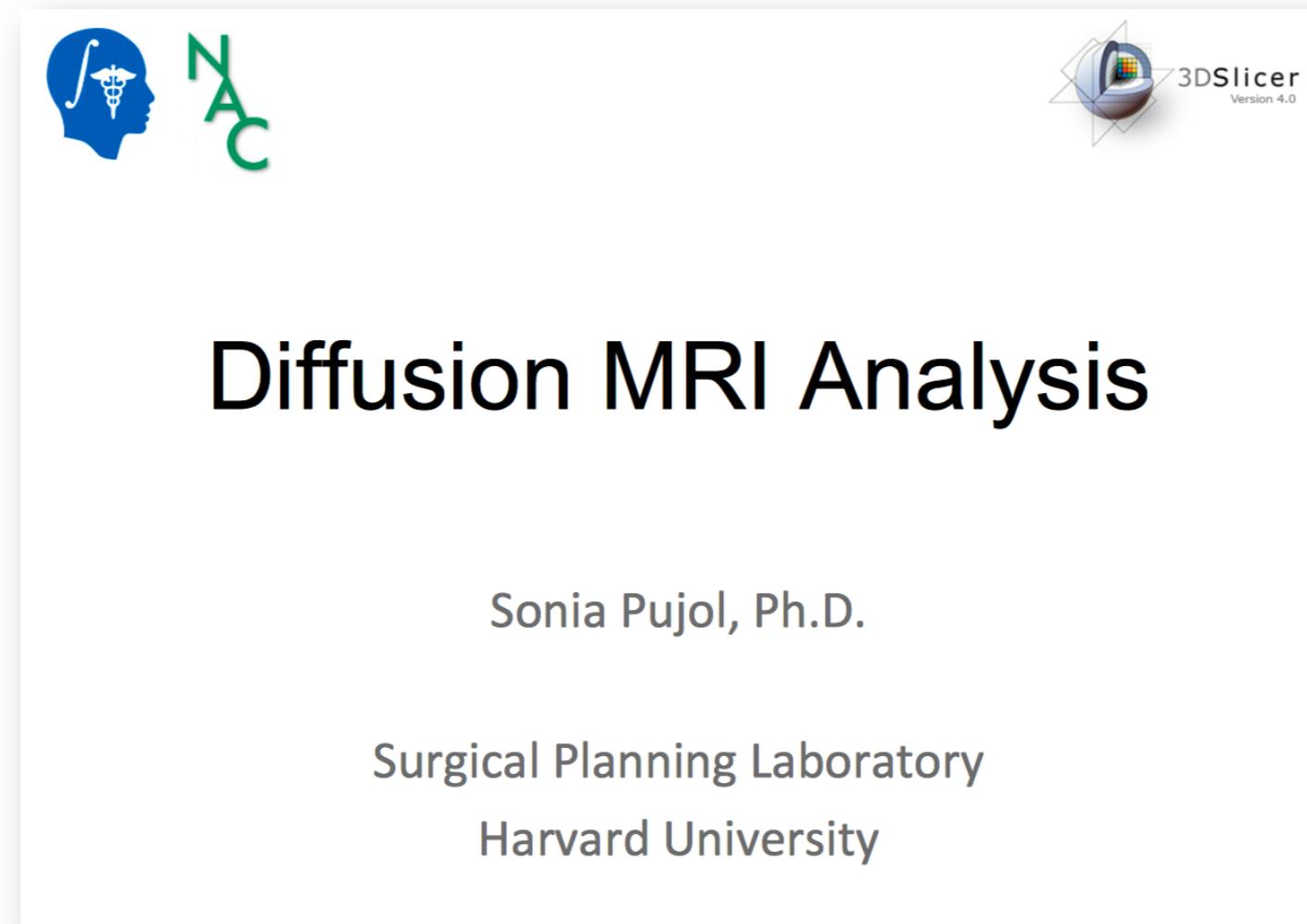
PMID: 19694258 [PubMed - indexed for MEDLINE] PMCID: PMC2768602 [Free PMC Article](#)

[Neural Tractography Using an Unscented Kalman Filter](#)
[Malcom et al., 2009]

Before getting started...

- take a look at: Diffusion Tensor Imaging Tutorial

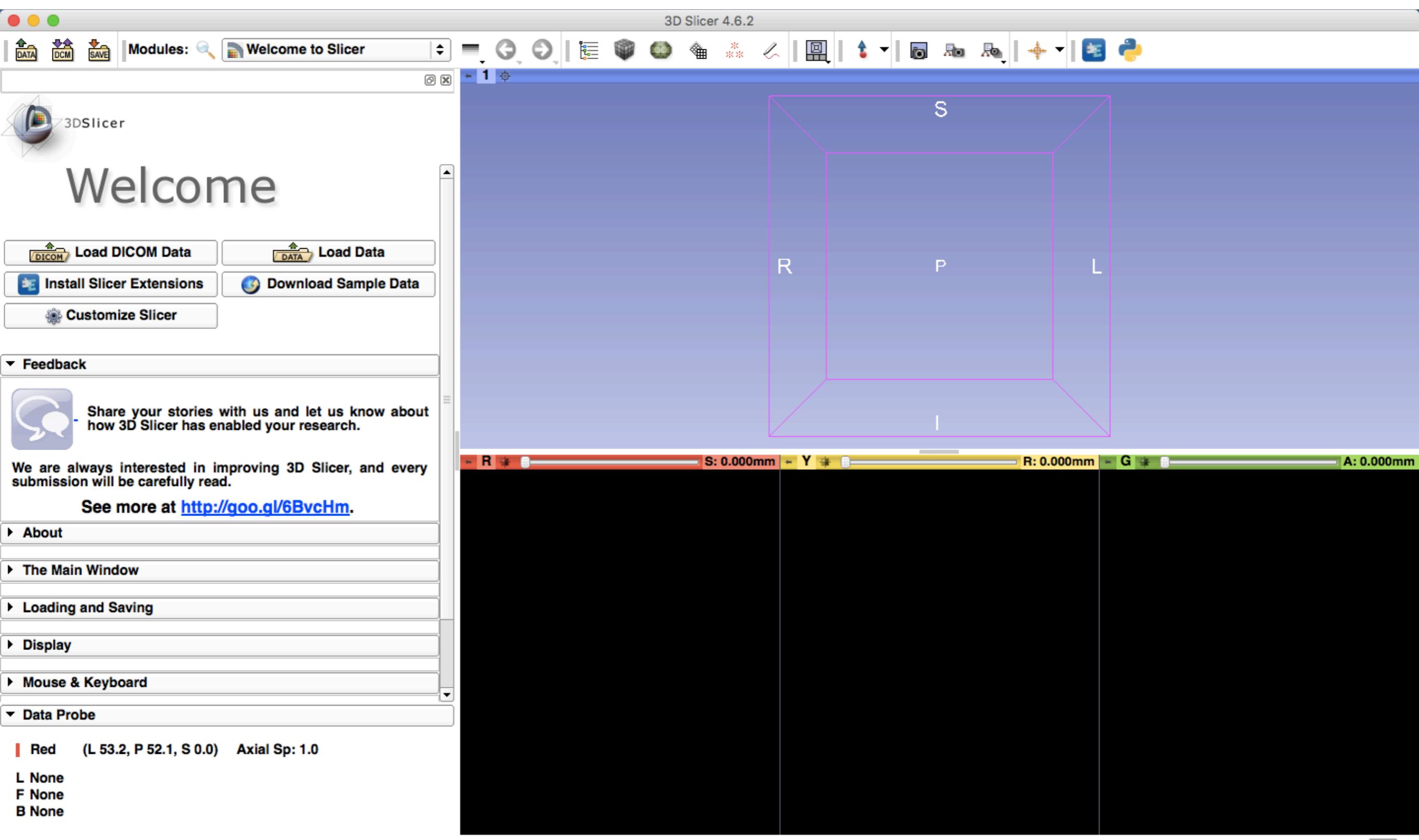
<https://github.com/SlicerDMRI/slicerdmri.github.io/blob/master/docs/tutorials/DiffusionMRIanalysis.pdf>



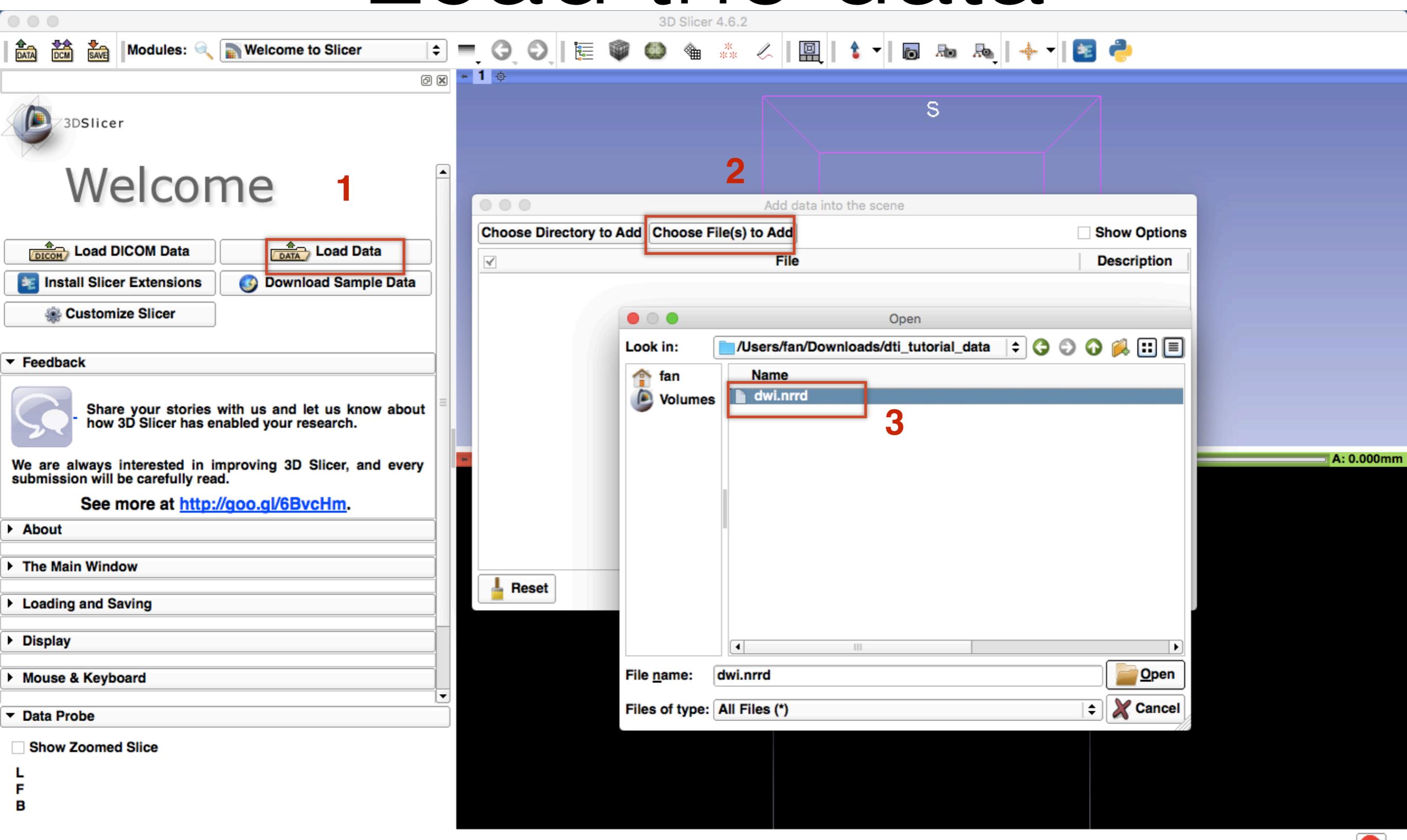
DWI Dataset

- Download the data at:
https://www.slicer.org/w/images/e/e6/Dti_tutorial_data.zip
- The Diffusion Weighted Imaging (DWI) dataset is composed of :
 - 1 volume acquired without diffusion-sensitizing gradient
 - 41 volumes acquired with 41 different diffusion-sensitizing gradient directions

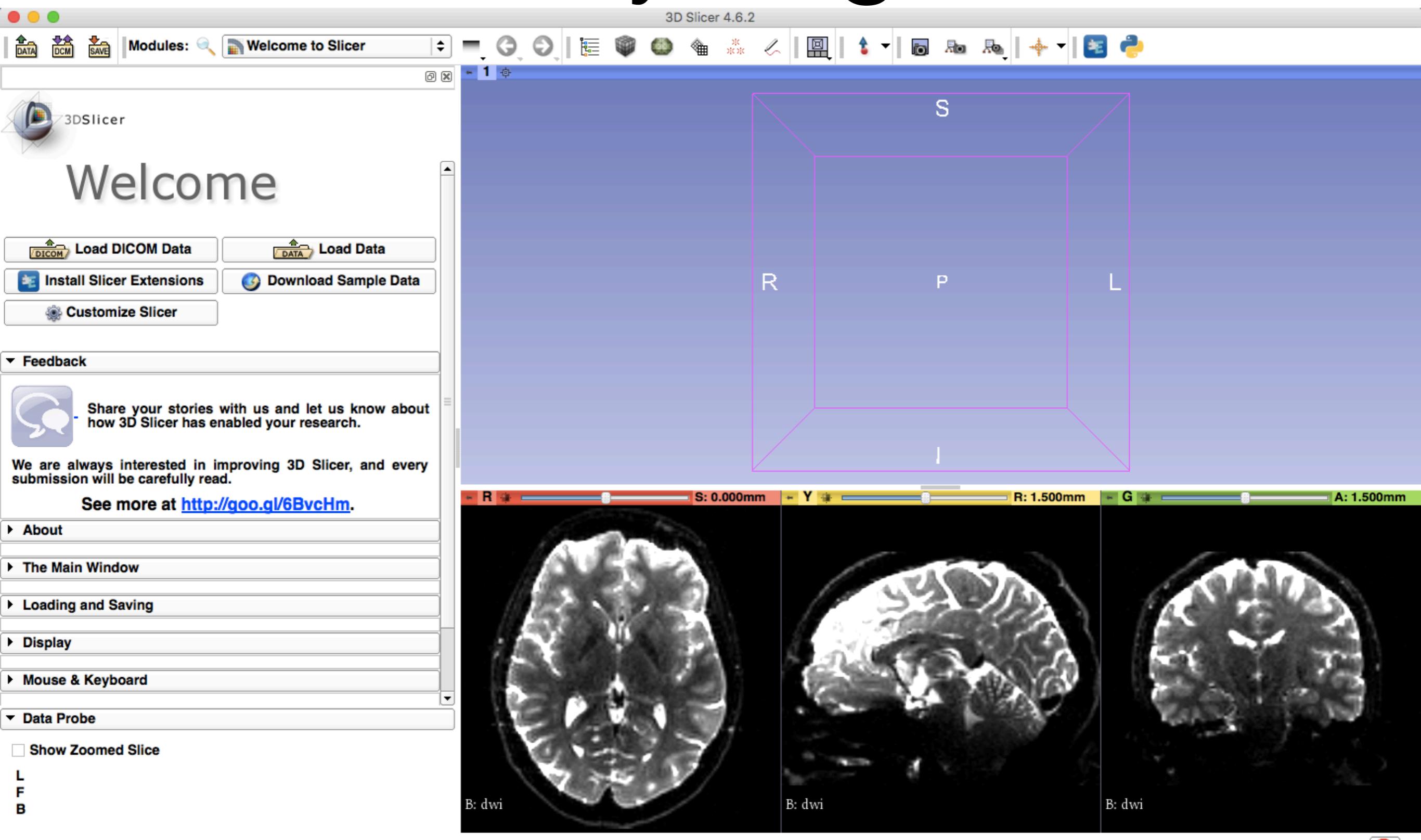
Start Slicer



Load the data



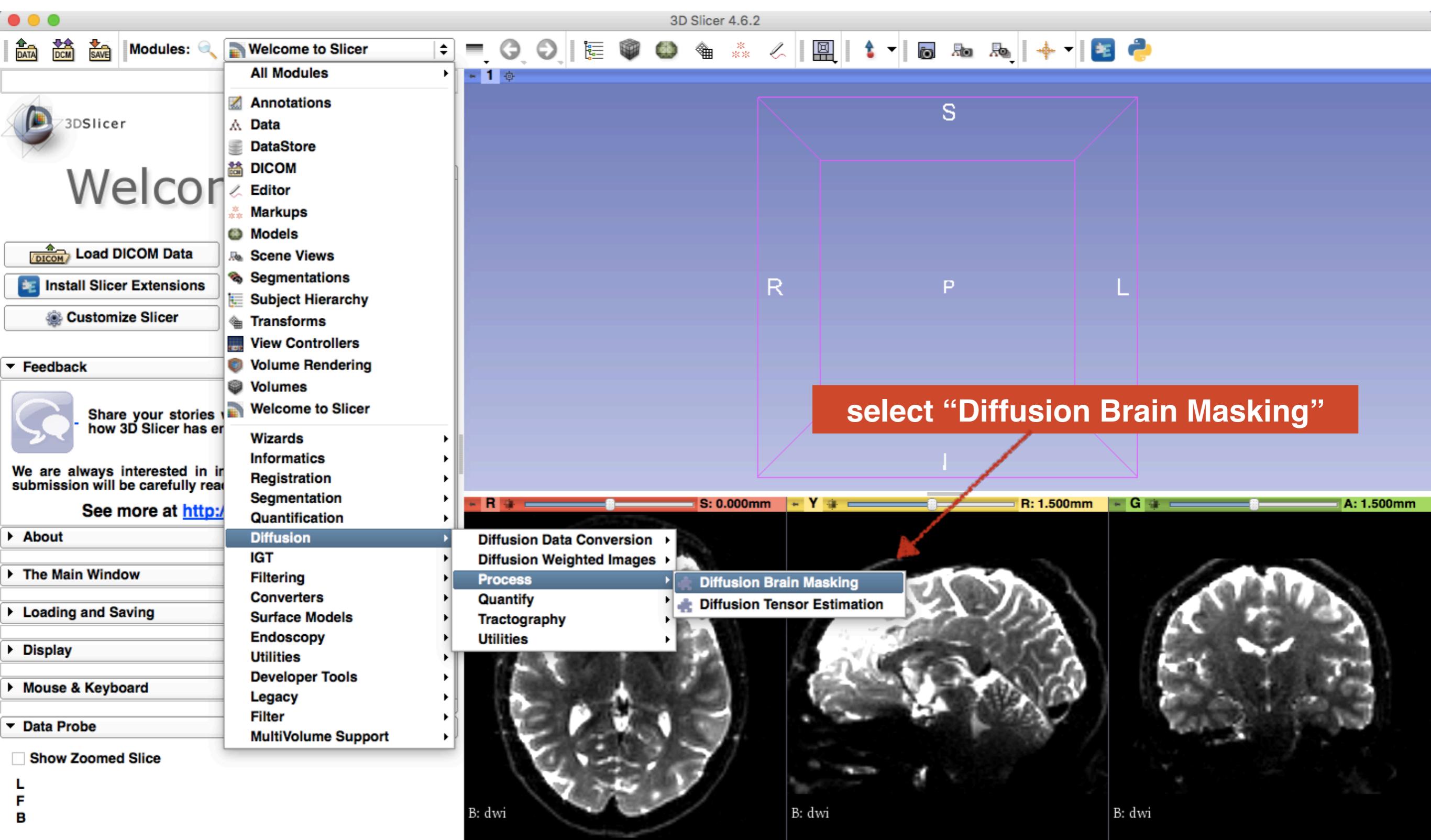
There you go...!



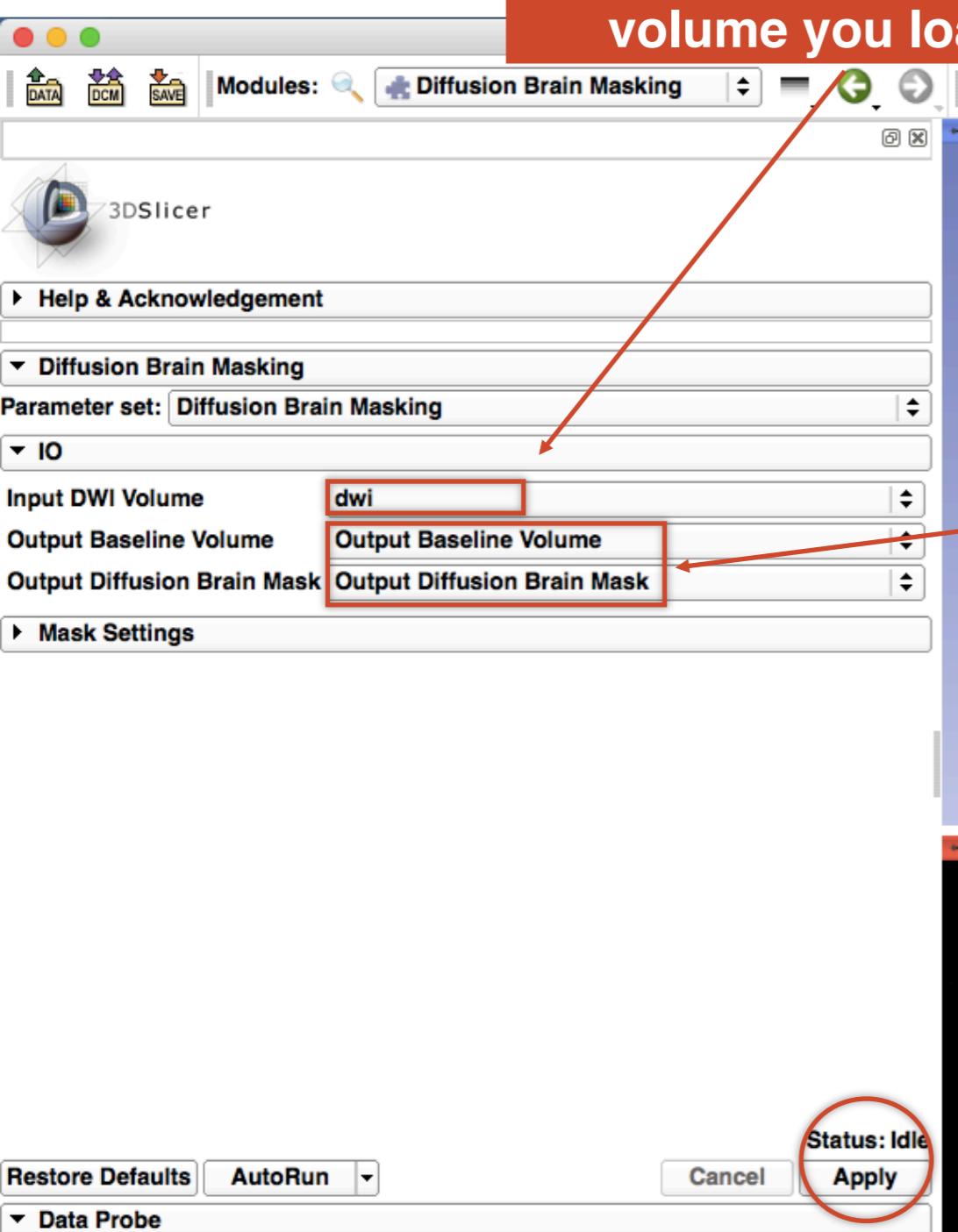
Main Steps

- Creating a brain mask
- Creating FA map
- Creating region of interest for tract seeding
- UKF tractography

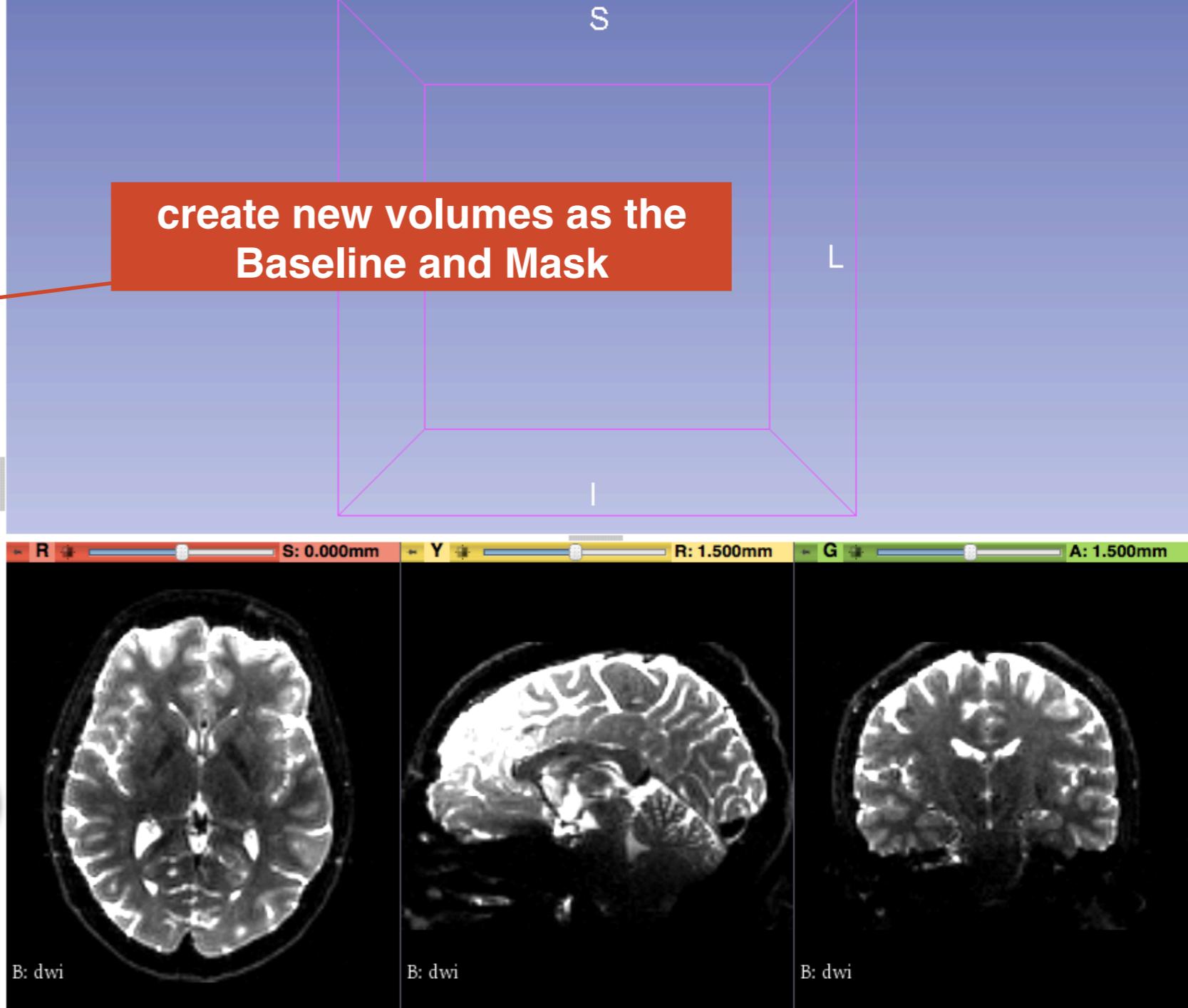
Brain Mask Creation

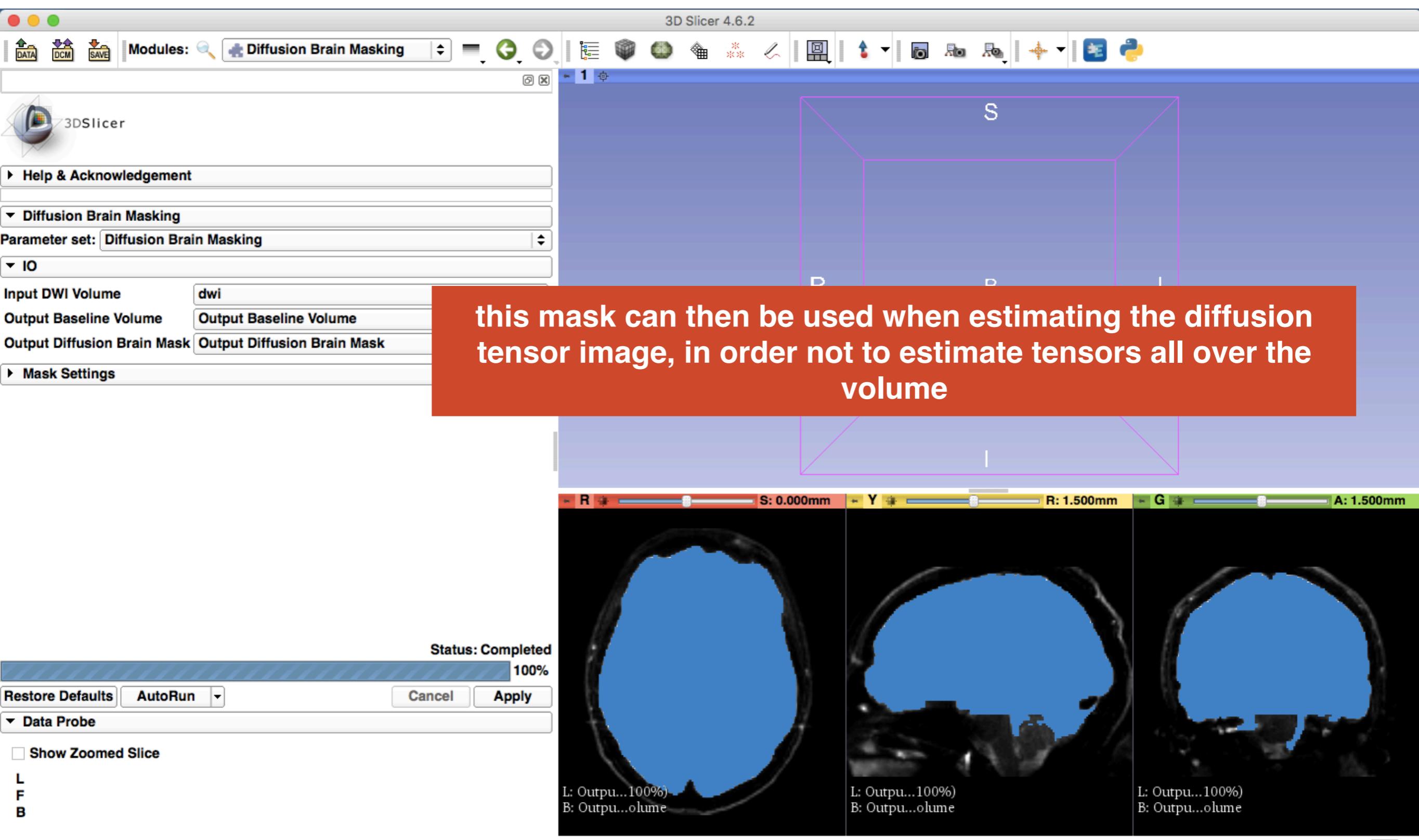


the input is the DWI volume you loaded



create new volumes as the
Baseline and Mask





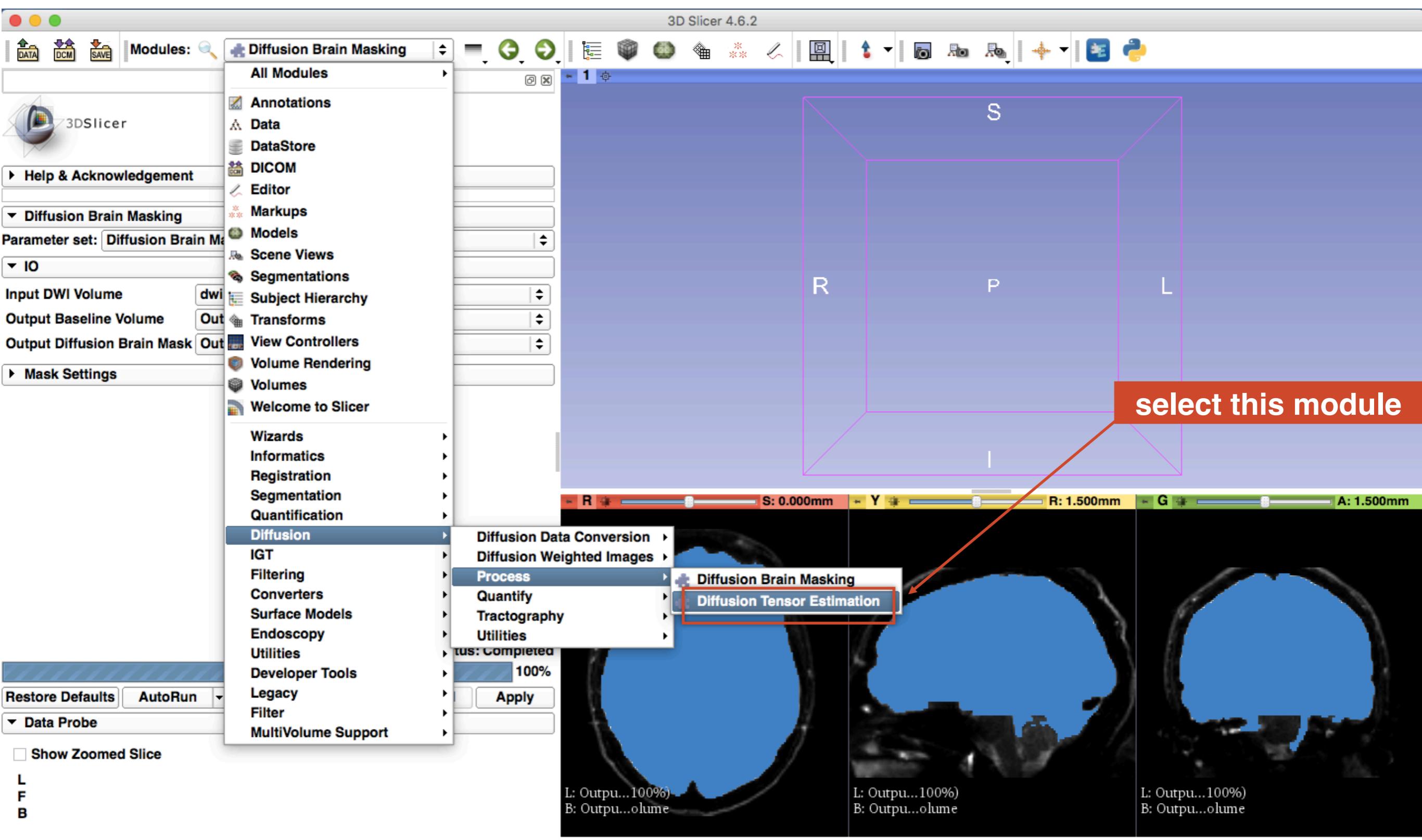
Tract Seeding

- For whole brain tractography with UKF, the Otsu threshold mask is used as the brain mask.
- To seed a specific tract of interest, label maps can be drawn on either:
 - DWI (output baseline volume)
 - FA map

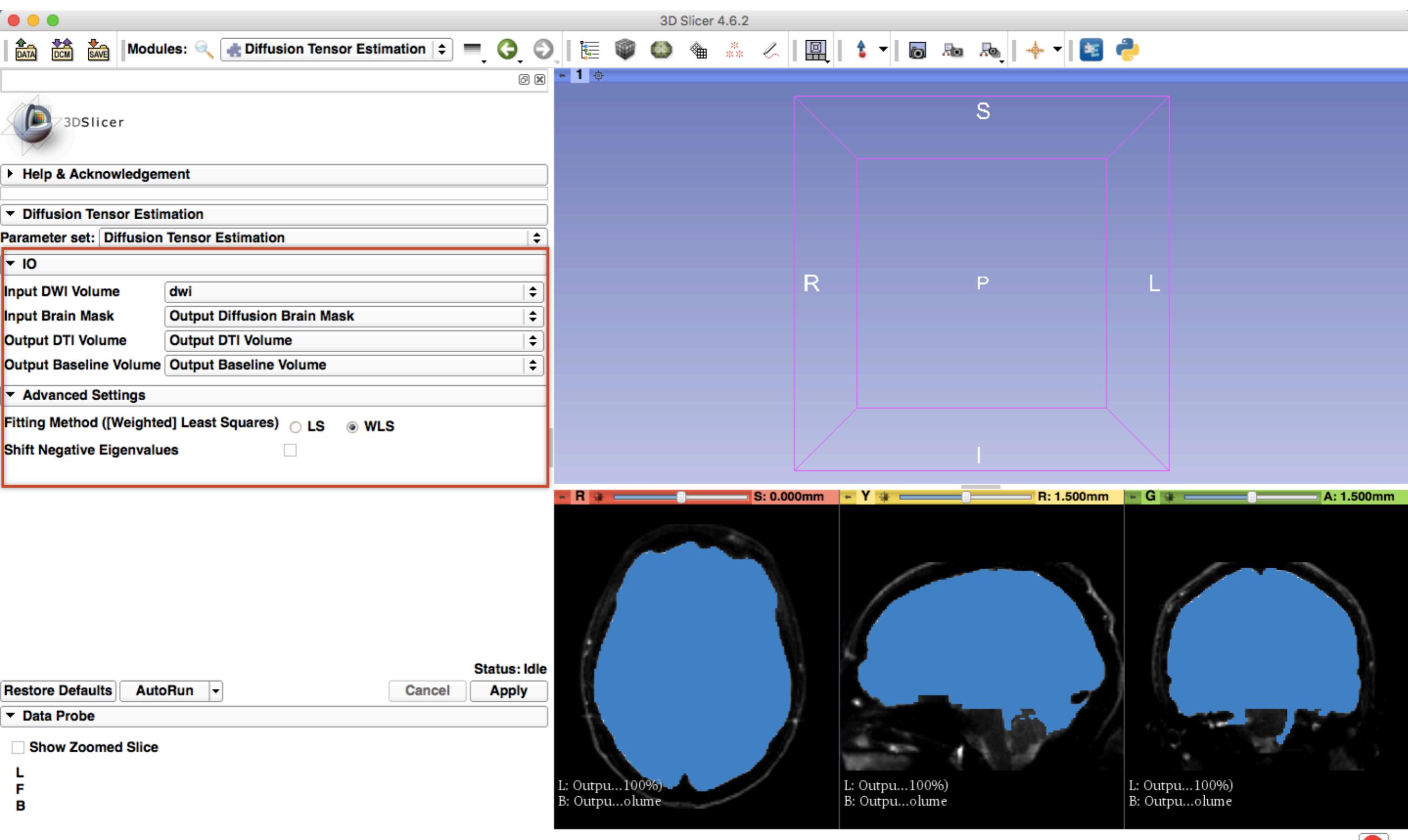
Tract Selection

- Note that FA maps can be more informative for selecting ROIs.
- For that purpose you should first estimate DTI and calculate FA map
- Although these maps are only used here for ROI selection and the model is again estimated from DWI for UKF tractography.

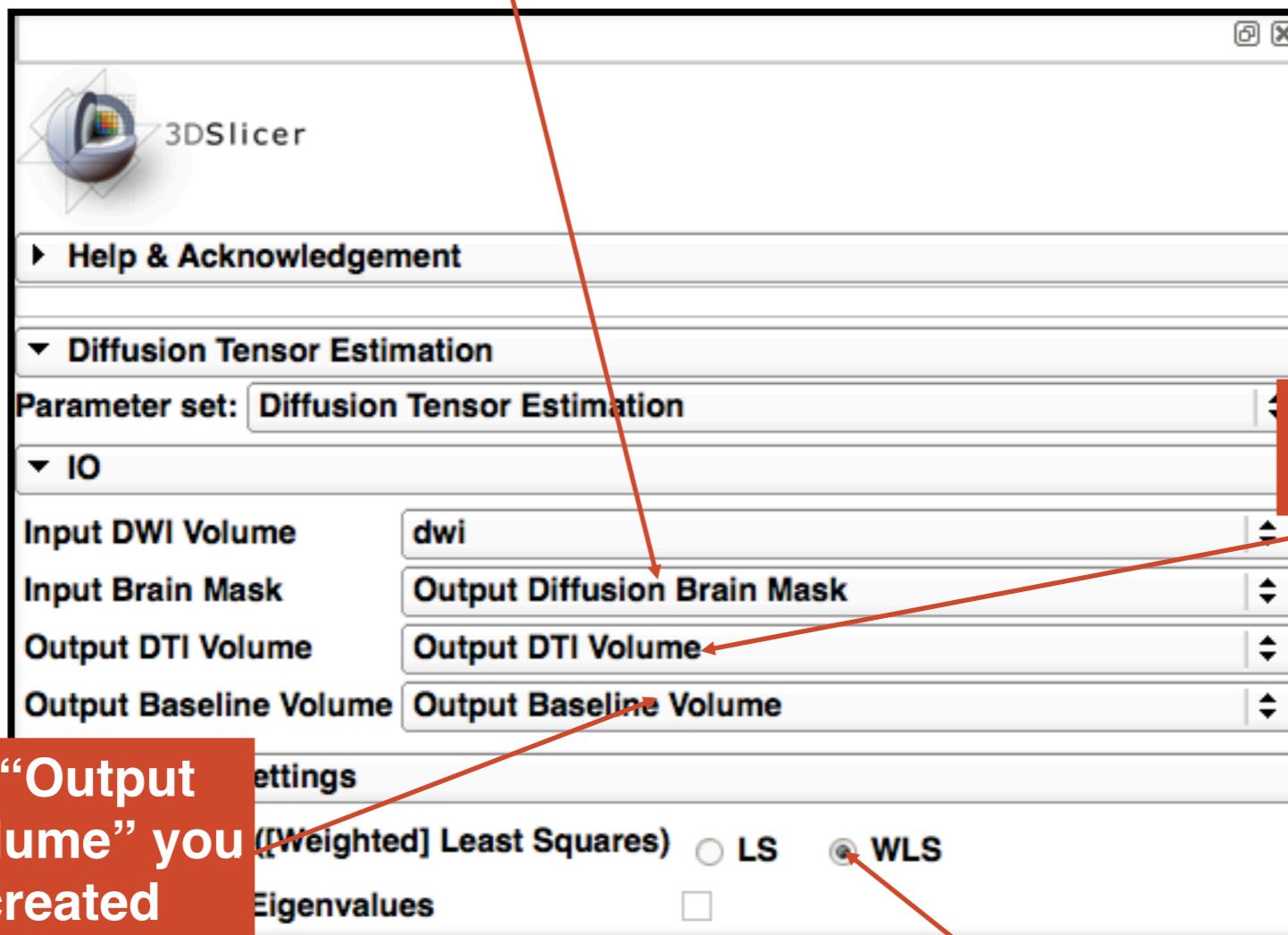
DWI to DTI Estimation



Set the Parameters



select Output Diffusion Brain Mask you already created



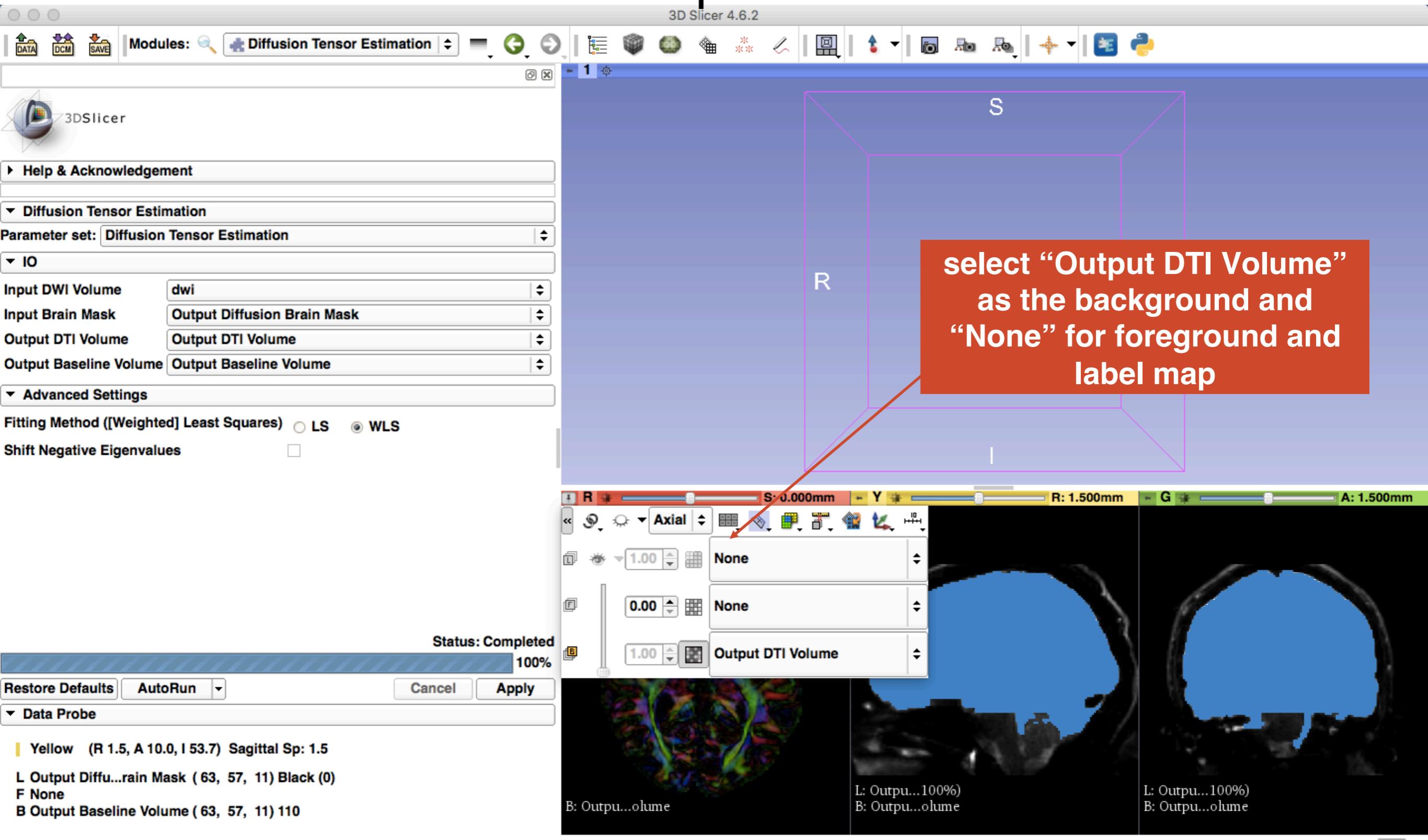
select the “Output Baseline Volume” you already created

create new Output DTI Volume

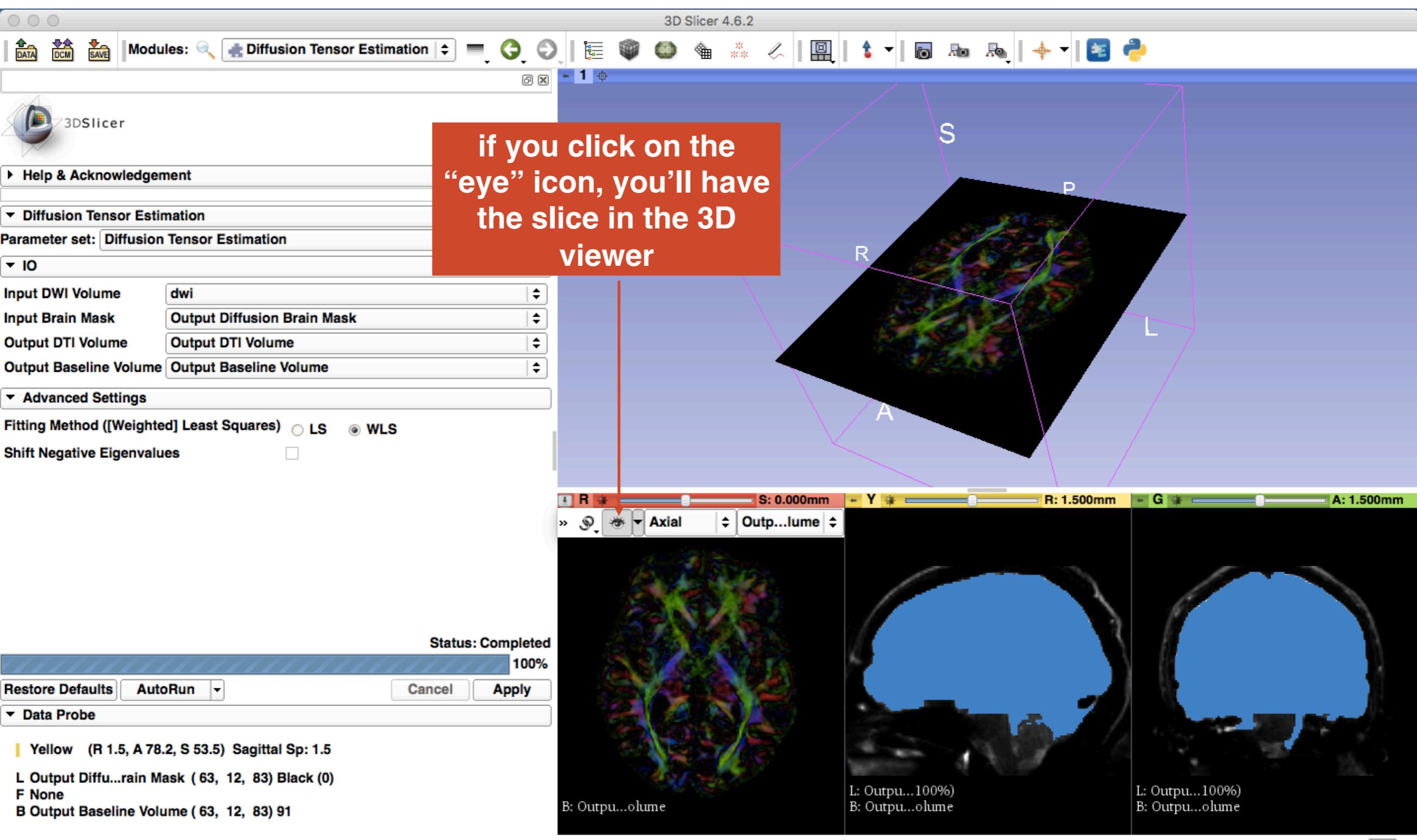
select WLS (Weighted Least Square)

Click Apply

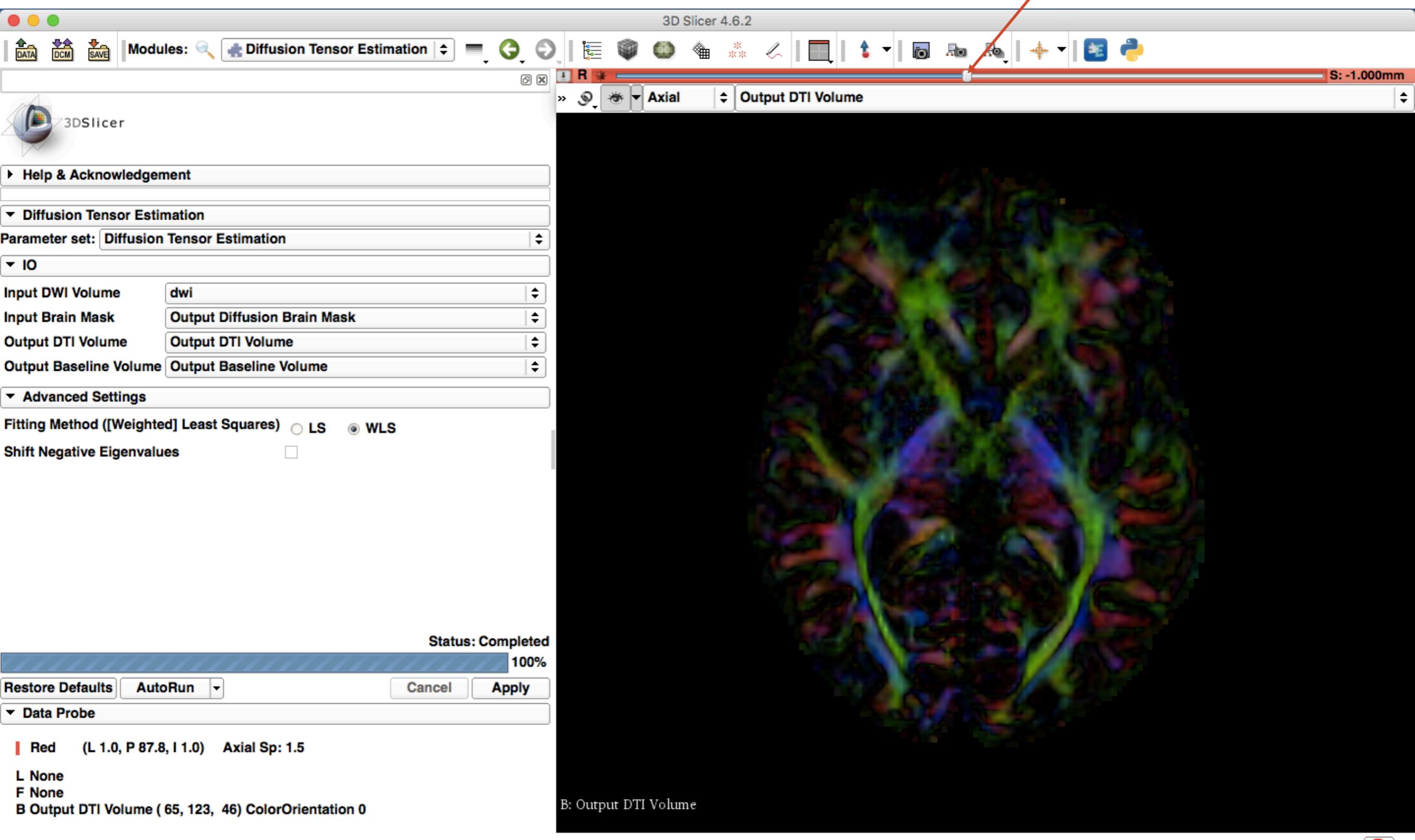
Status: Completed! 100%



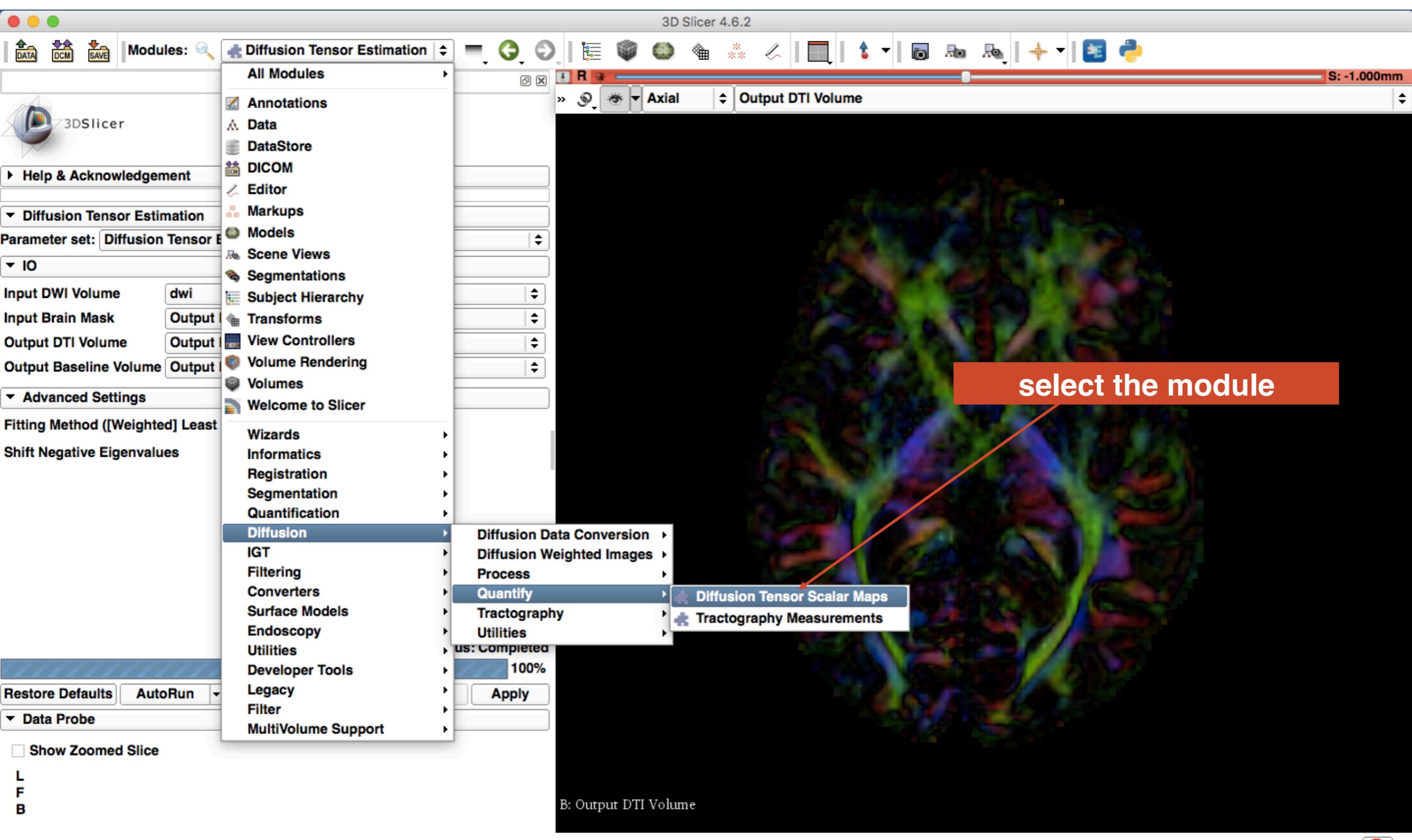
color-coded DTI volume



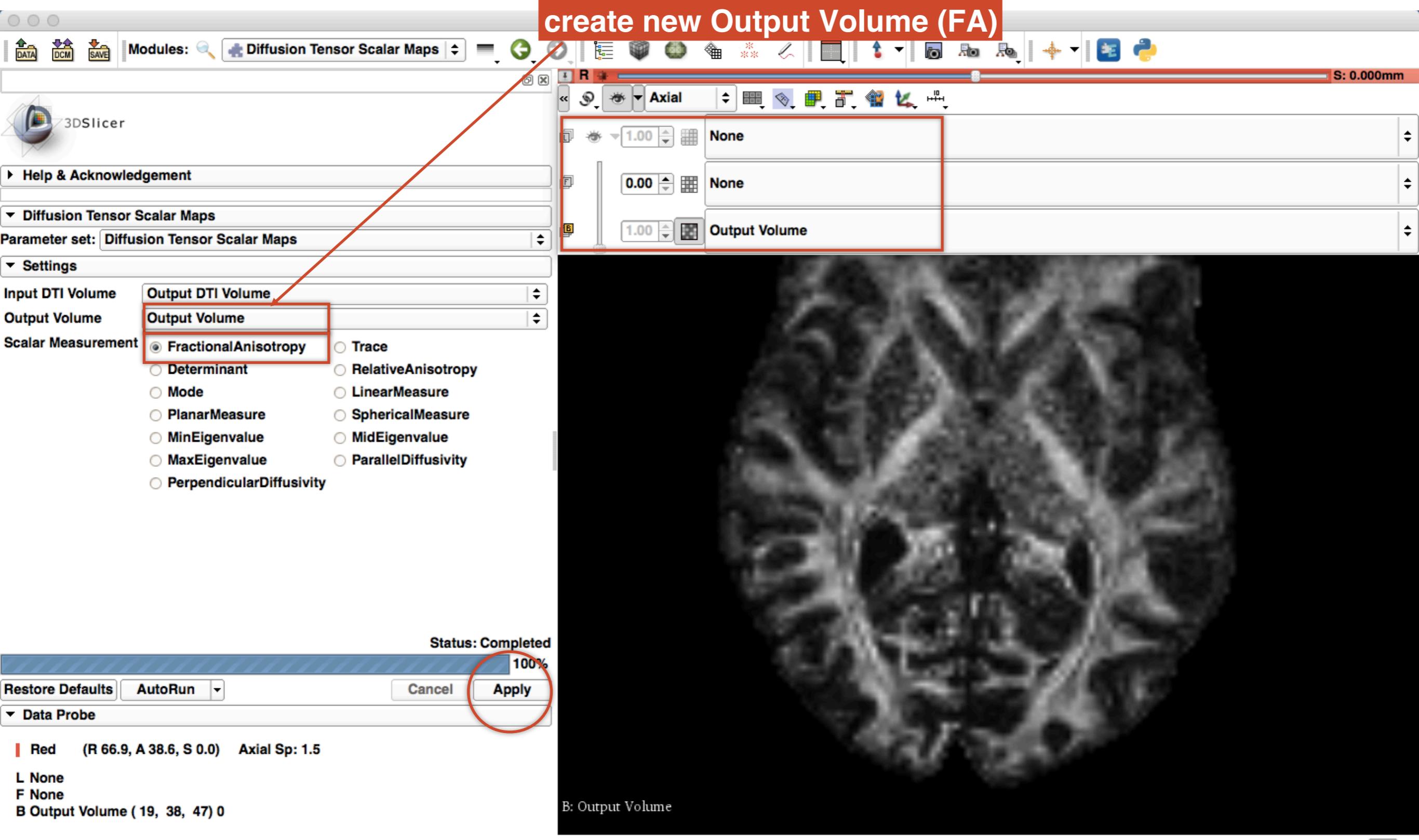
browse through the DTI volume here



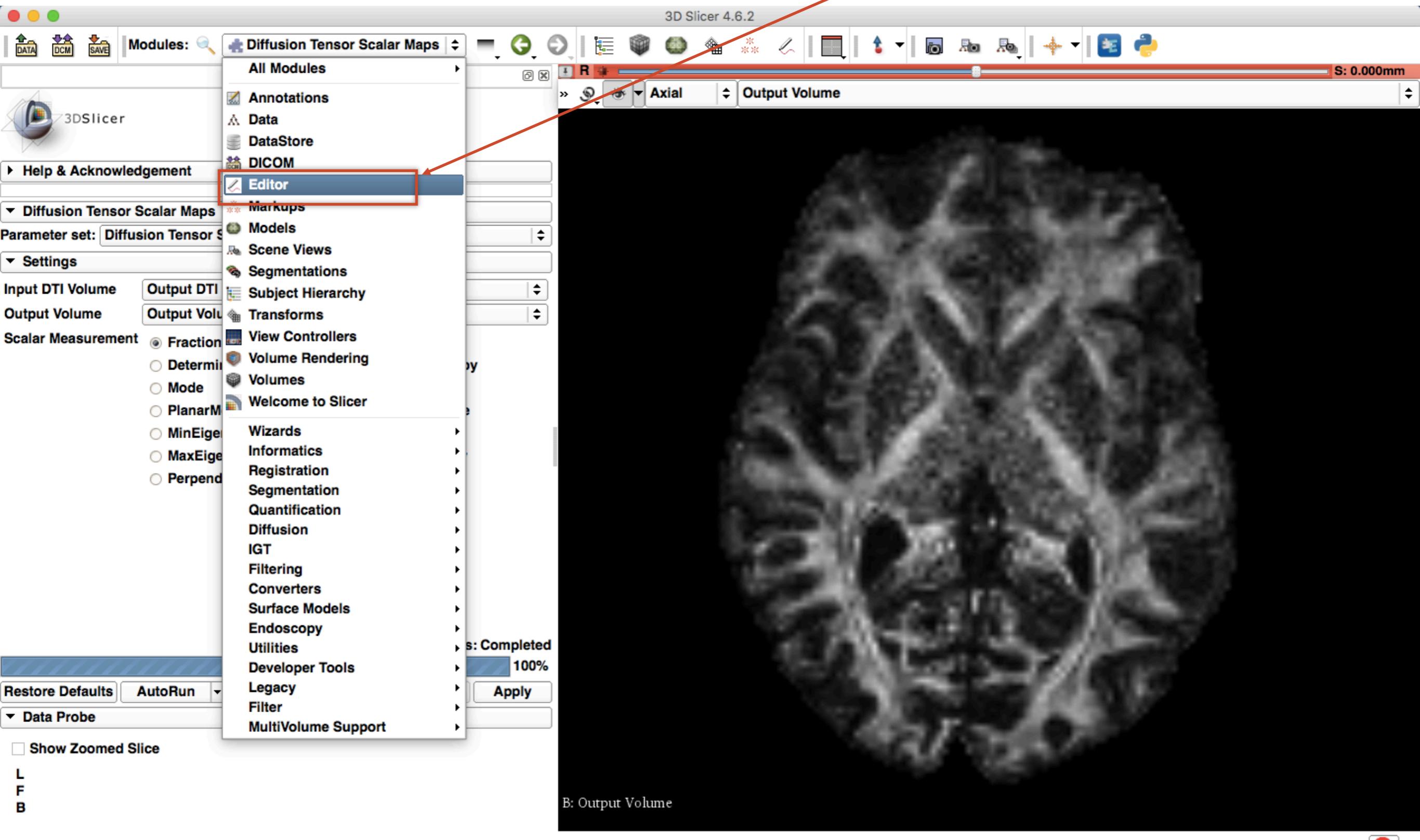
Diffusion Tensor Scalar Measurements; FA



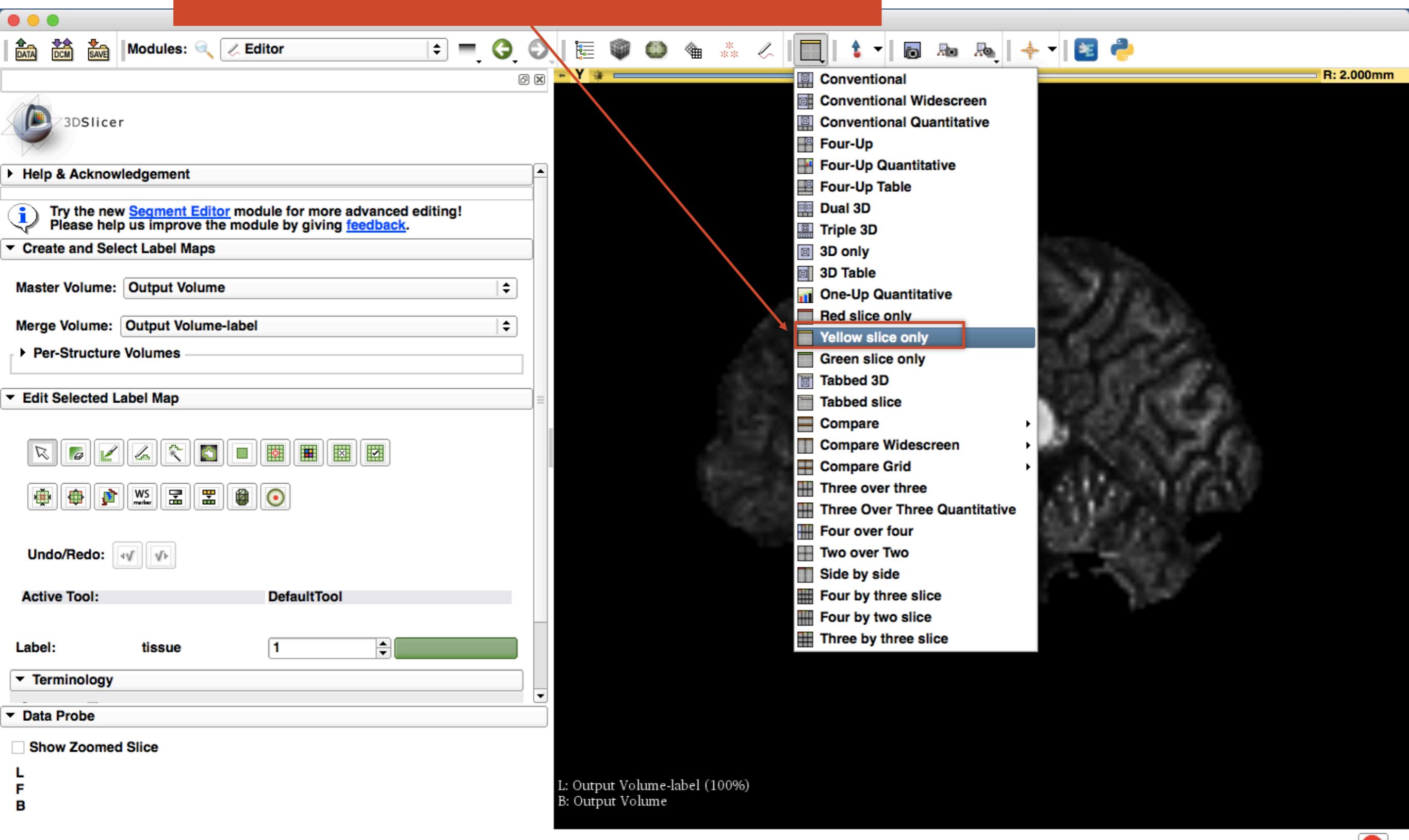
create new Output Volume (FA)



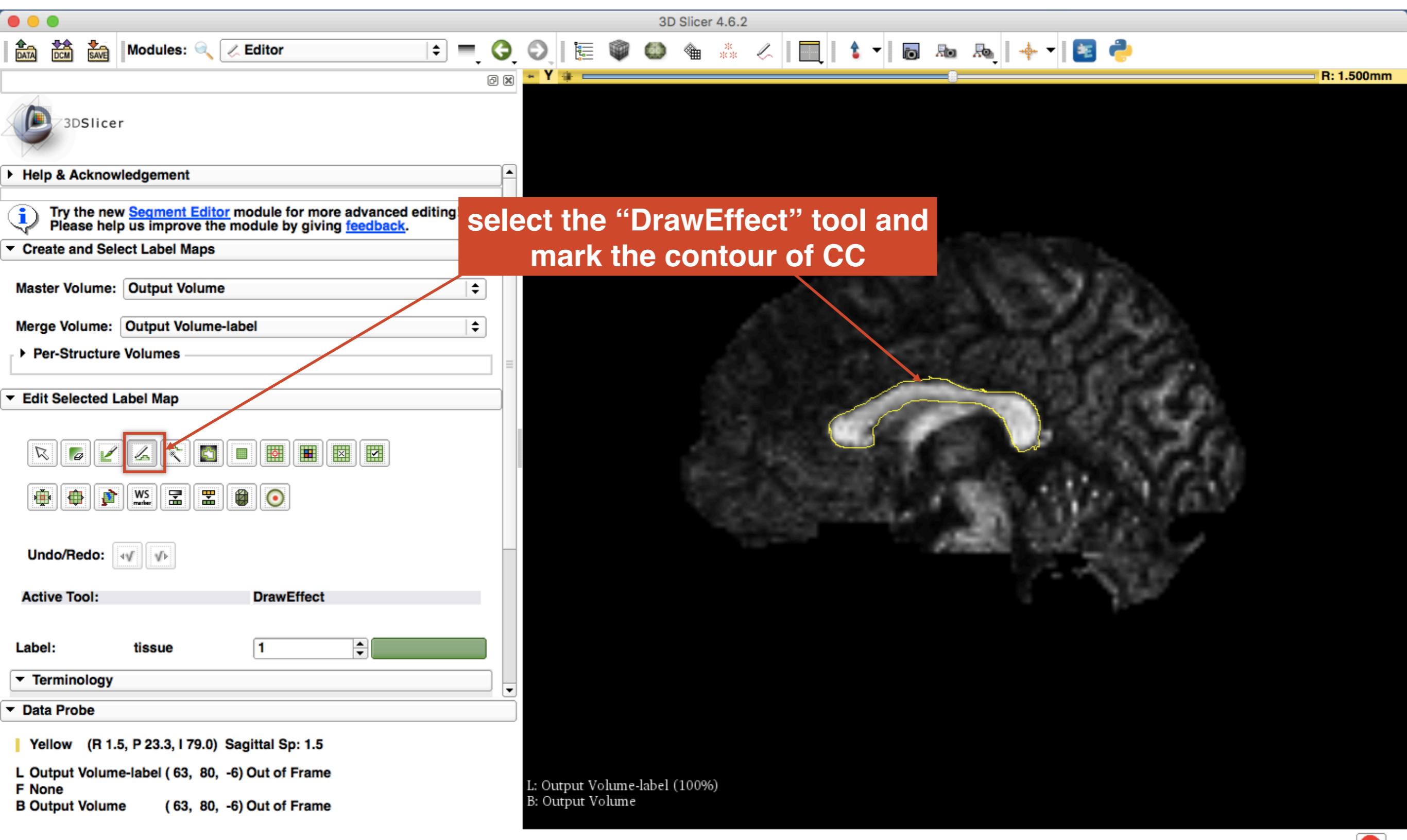
Select the Editor Module



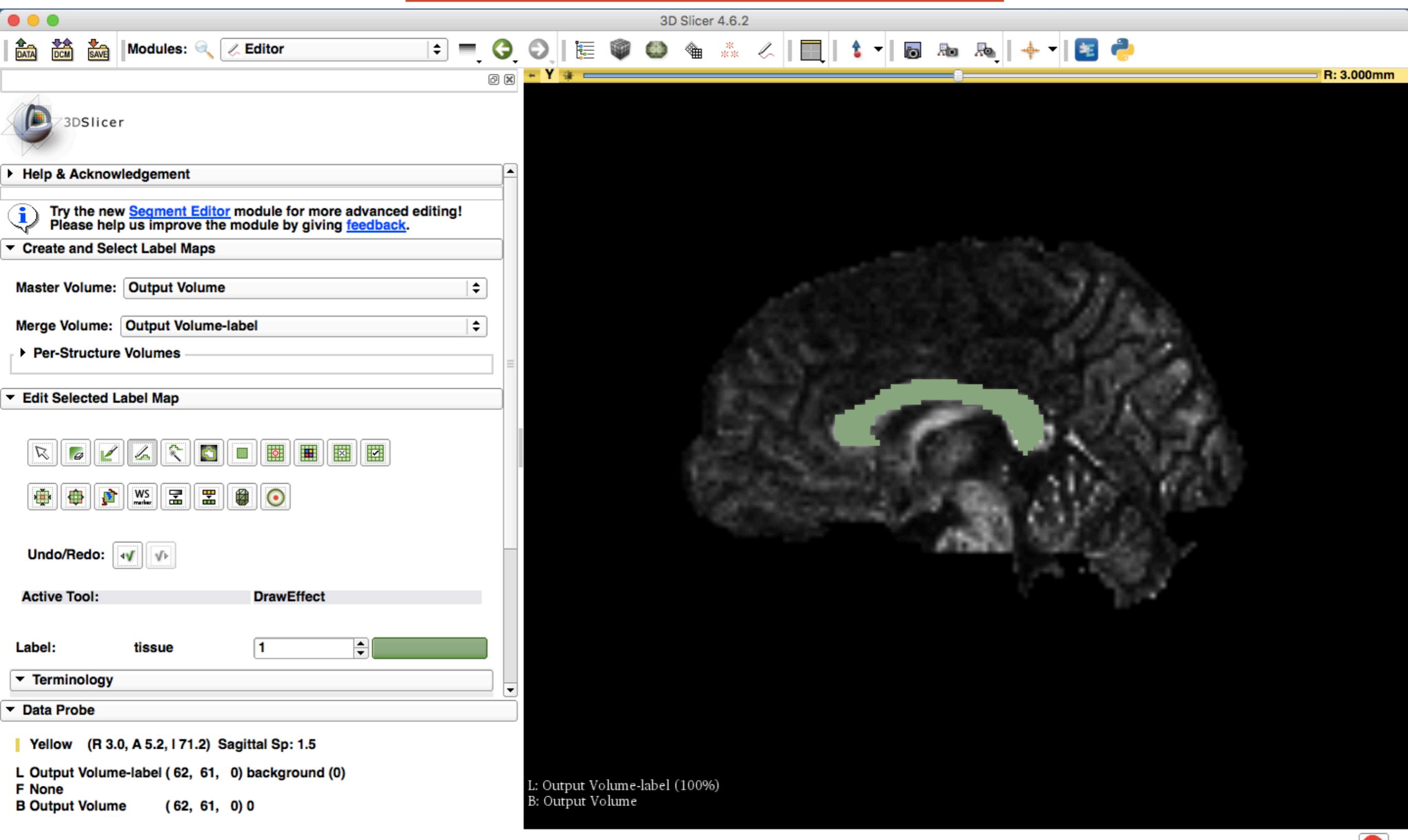
to be able to select ROI for CC as an example,
select sagittal view (yellow slice only)



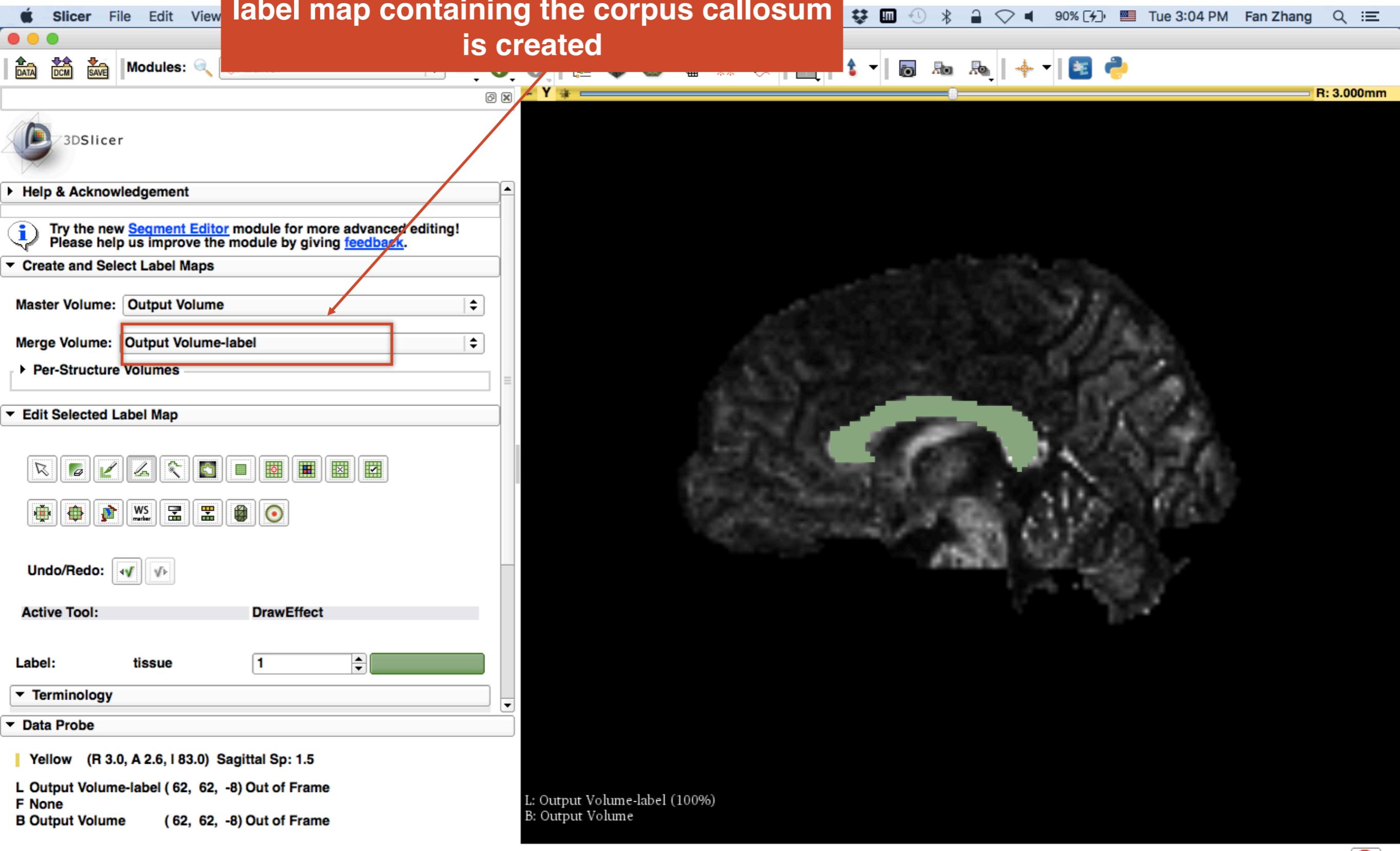
ROI Definition



press enter
repeat this for 3 adjacent slices



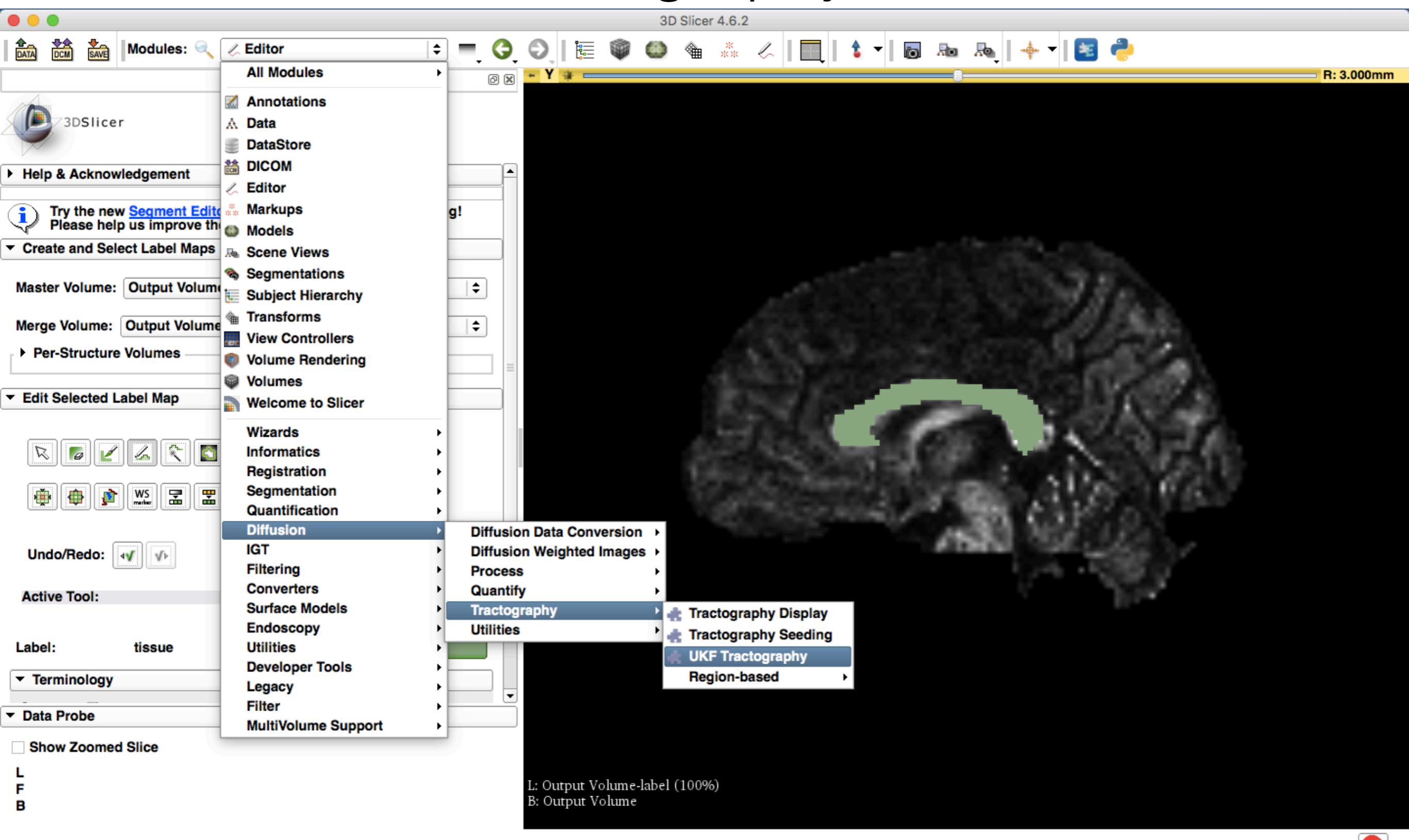
label map containing the corpus callosum
is created



UKF Tractography

- The module can use different methods:
 - 1-Tensor tractography (single fiber model)
 - 2-Tensor tractography (crossing fiber model)
 - NODDI (estimates microstructural complexity of dendrites and axons)
- ❖ The module can add a term for the free water model. This model tries to separate the signal from partial voluming with cerebrospinal fluid.

UKF Tractography Module



select the label map as seeds for tractography

select the number of the label map

▼ UKF Tractography

Parameter set: UKF Tractography

▼ IO

Input DWI Volume	dwi
Input Label Map	Output Volume-label
ROI label to use for seeding	1
Input brain mask	Output Diffusion Brain Mask
Output Fiber Bundle	Output Fiber Bundle

select the Mask to confine the tractography

create new FiberBundle

for bigger voxels, use higher number of seeds per voxel

To increase seeding sensitivity, lower seed FA (0.15)



To track further, lower terminating FA (0.1) and GA (0.075)

Set other parameters here:

Tractography Options

Seeding: Number of seeds per voxel

Seeding: Minimum seed FA

Stopping Criterion: Terminating FA

Stopping Criterion: Terminating GA

Tracking: Number of threads

Tracking: Number of tensors/orientations in model 1 2

Tracking: Step length of tractography (in mm)

Tracking: Rate of change of tensor direction/orientation

Output: Step length of output tractography (in mm)

Output: Maximum tract length (in mm)

Output: Save Normalized Mean Square Error

Tensor Model (default)

Tensor Model: Estimate term for free water

Output: Save tensor FA

Output: Save tensor trace

Output: Save free water fraction

Output: Save tensors

UKF Parameter (Advanced): Rate of change of eigenvalues

UKF Parameter (Advanced): Rate of change of freewater weight

Status: Idle

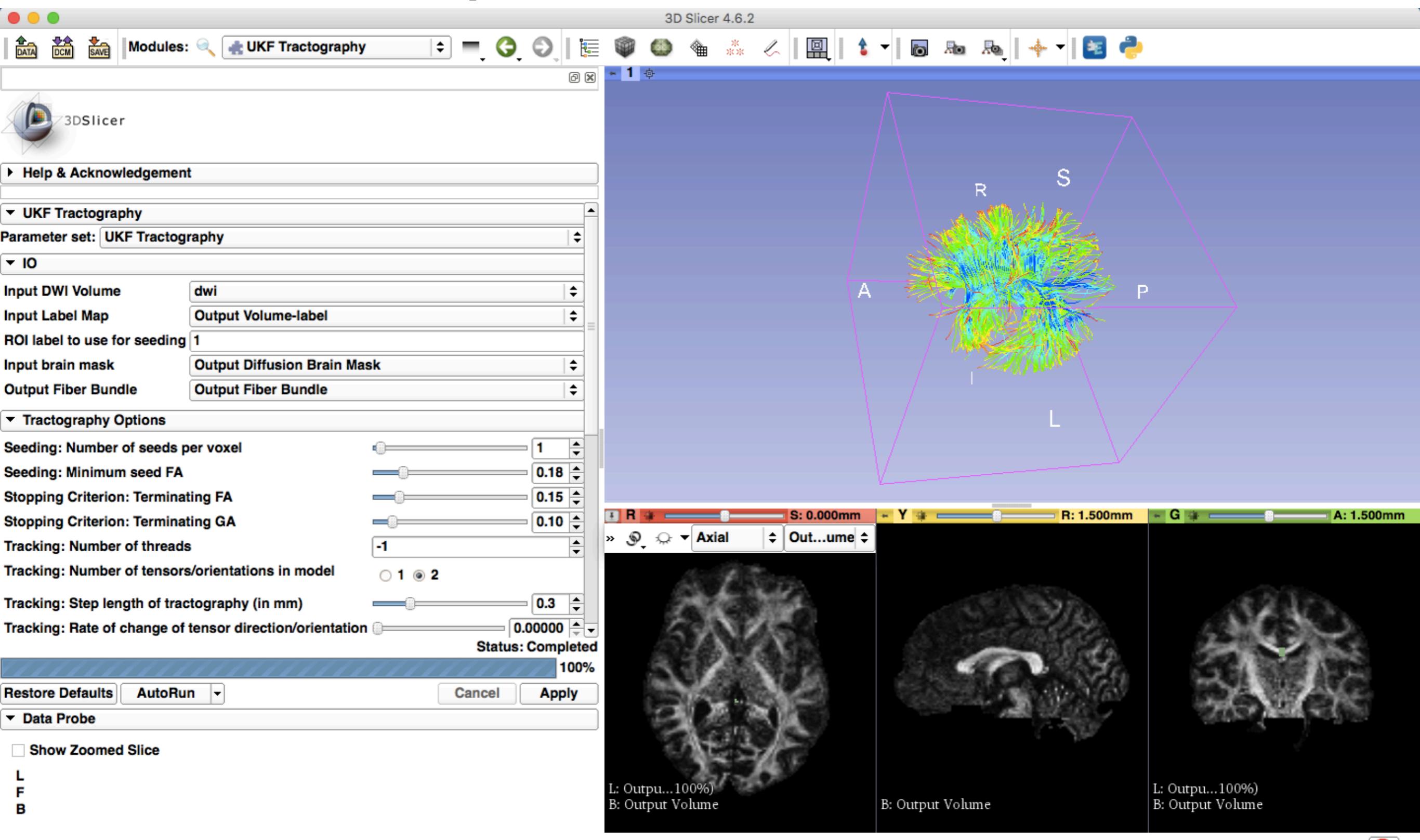
Buttons:

find out more details at:

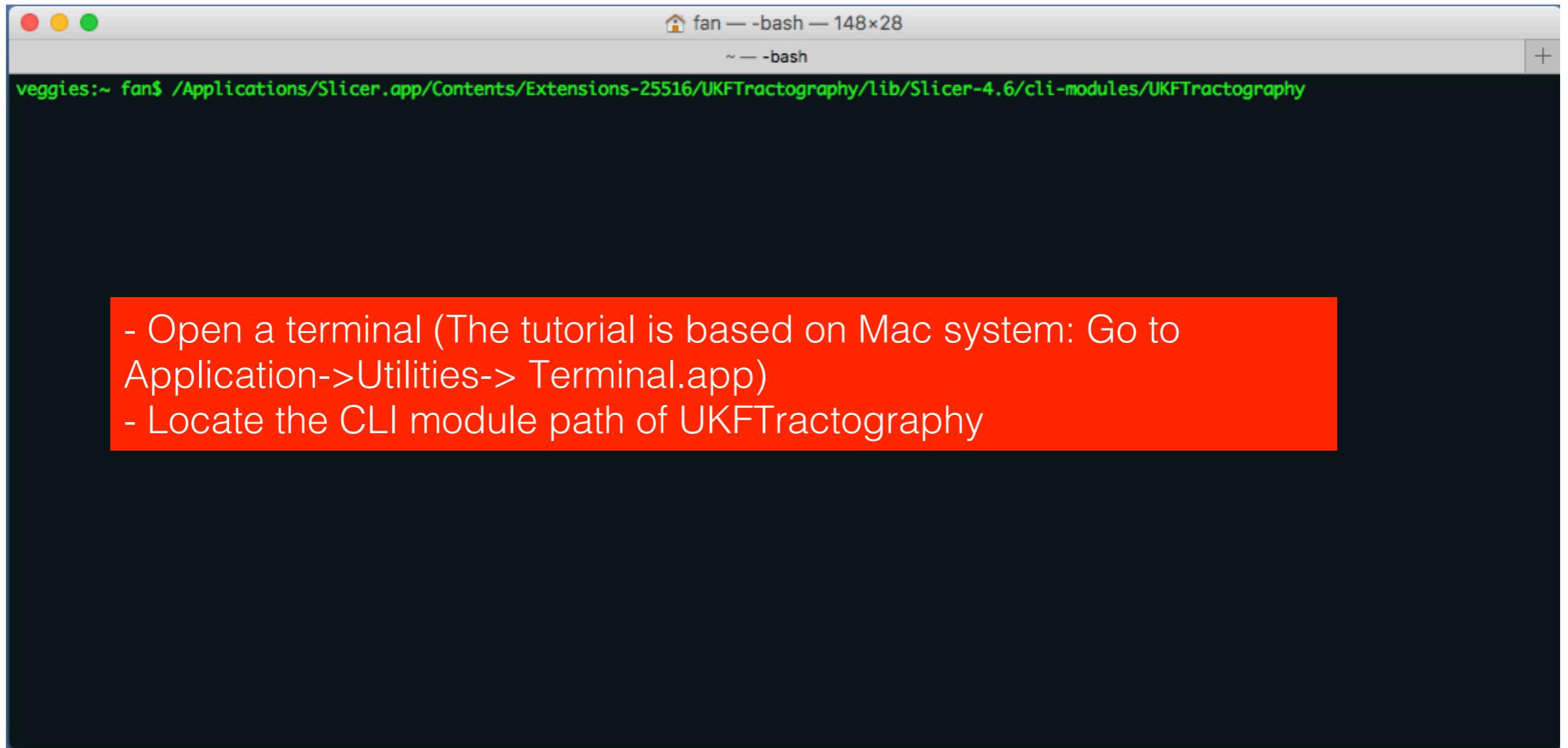
[Documentation/Nightly/Modules/UKFTractography](#)

Click Apply

Corpus Callosum



Run UKF Tractography in CLI



Run UKF Tractography in CLI

```
fan — -bash — 151x66
~ -- -bash

[veggies:~ fan$ /Applications/Slicer.app/Contents/Extensions-25516/UKFTractography/lib/Slicer-4.6/cli-modules/UKFTractography --help

USAGE:

/Applications/Slicer.app/Contents/Extensions-25516/UKFTractography/lib/Slicer-4.6/cli-modules/UKFTractography [options] [args]
  --returnparameterfile <std::string>
    Filename in which to write simple return parameters (int, float, int-vector, etc.) as opposed to bulk return parameters (image, geometry, transform, measurement, table).
  --processinformationaddress <std::string>
    Address of a structure to store process information (progress, abort, etc.). (default: 0)
  --xml
    Produce xml description of command line arguments (default: 0)
  --echo
    Echo the command line arguments (default: 0)
  --deserialize <std::string>
    Restore the module's parameters that were previously archived.
  --serialize <std::string>
    Store the module's parameters to a file.

Where:

--returnparameterfile <std::string>
  Filename in which to write simple return parameters (int, float, int-vector, etc.) as opposed to bulk return parameters (image, geometry, transform, measurement, table).

--processinformationaddress <std::string>
  Address of a structure to store process information (progress, abort, etc.). (default: 0)

--xml
  Produce xml description of command line arguments (default: 0)

--echo
  Echo the command line arguments (default: 0)

--deserialize <std::string>
  Restore the module's parameters that were previously archived.

--serialize <std::string>
  Store the module's parameters to a file.
```

Run '/Applications/Slicer.app/Contents/Extensions-25516/UKFTractography/lib/Slicer-4.6/cli-modules/UKFTractography –help' to find detailed documentation of the usage of UKFTractography

Conclusion

- This tutorial, helps you to load diffusion data, run the tensor estimation, calculate scalar measurements, and define ROIs to finally be able to run UKF tractography.
- contact: yogesh@bwh.harvard.edu

Acknowledgments

U01CA199459, Open Source Diffusion MRI
Technology For Brain Cancer Research



National Alliance for Medical Image Computing (NA-MIC)
namic.org



National Center for Image Guided Therapy (NCIGT)
ncigt.org



Neuroimage Analysis Center (NAC)
nac.spl.harvard.edu



Surgical Planning laboratory (SPL)
spl.harvard.edu



Psychiatry Neuroimaging Laboratory (PNL)
pnl.bwh.harvard.edu