UKF Tractography Tutorial

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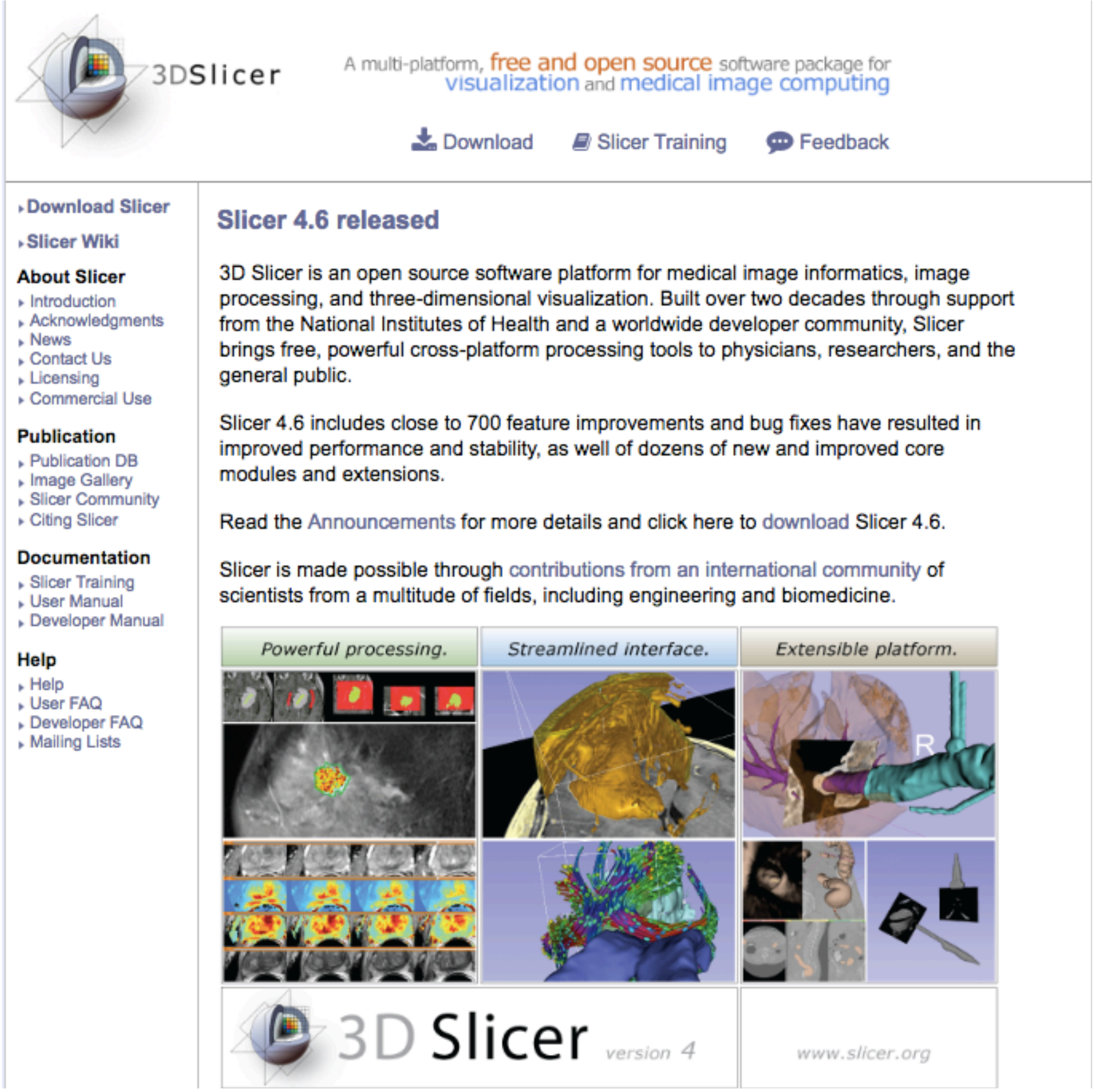
3DSlicer

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



Slicer 4.6 released

3D Slicer is an open source software platform for medical image informatics, image processing, and three-dimensional visualization. Built over two decades through support from the National Institutes of Health and a worldwide developer community, Slicer brings free, powerful cross-platform processing tools to physicians, researchers, and the general public.

Slicer 4.6 includes close to 700 feature improvements and bug fixes have resulted in improved performance and stability, as well of dozens of new and improved core modules and extensions.

Read the Announcements for more details and click here to download Slicer 4.6.

Slicer is made possible through contributions from an international community of scientists from a multitude of fields, including engineering and biomedicine.

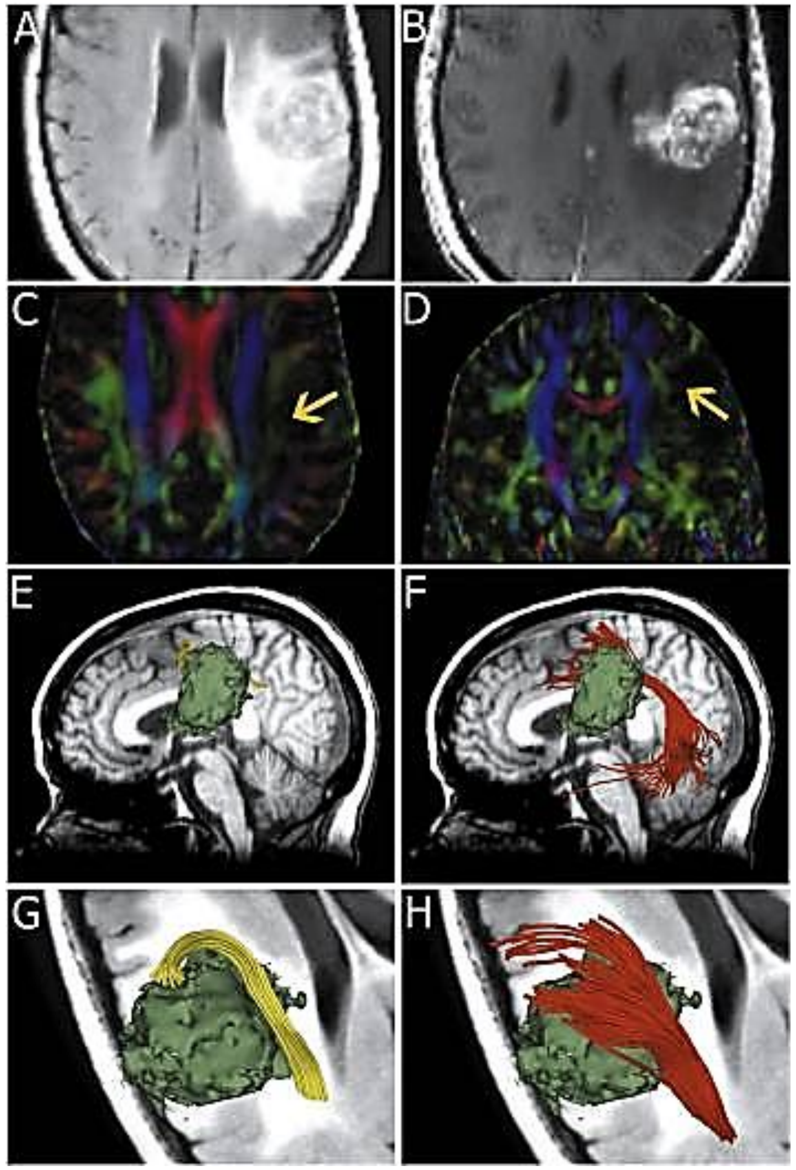
It is the responsibility of the user of 3DSlicer to comply with both the terms of the license and with the applicable laws, regulations and rules. Slicer is a tool for research, and is not FDA approved.

3DSlicer

- An end-user application for image analysis

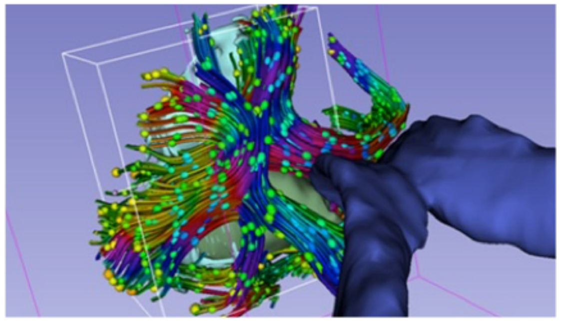
- An open-source environment for software development

- A software platform that is both easy to use for clinical researchers and easy to extend for programmers



[Chen et al, 2015]

3D Slicer is a multi-institution effort supported by the National Institutes of Health.



Slicer DMRI

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

http://dmri.slicer.org

Please read the **Diffusion MRI Analysis** tutorial to install SlicerDMRI:

http://dmri.slicer.org/tutorials/diffusion_mri_analysis

3D Slicer is a multi-institution effort supported by the National Institutes of Health.

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

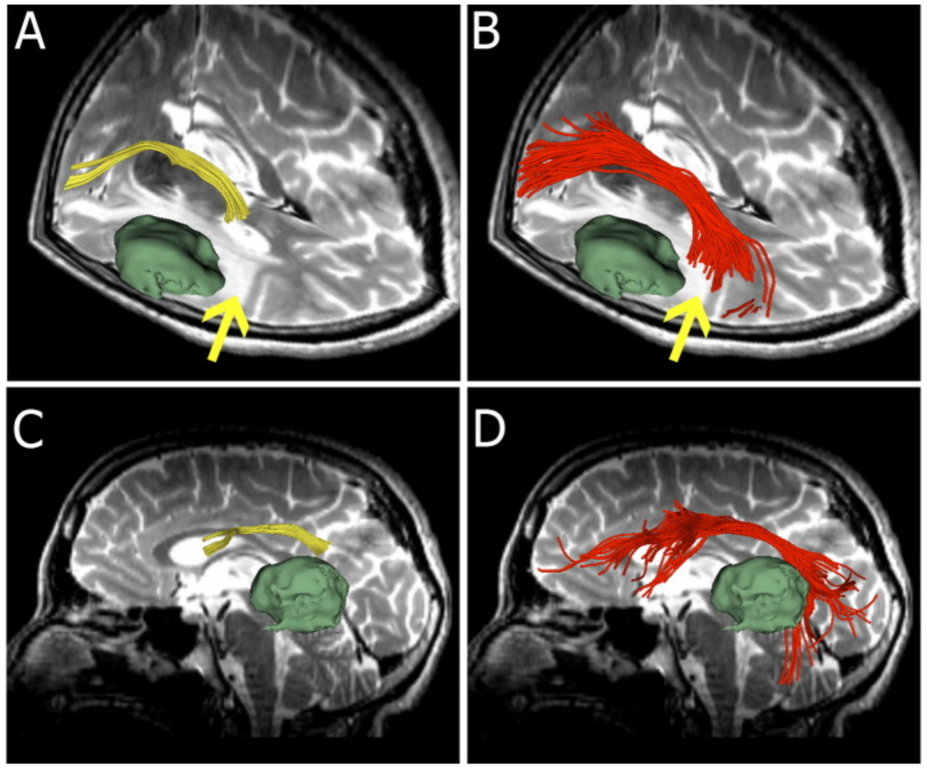
UKF Tractography

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

Why UKF

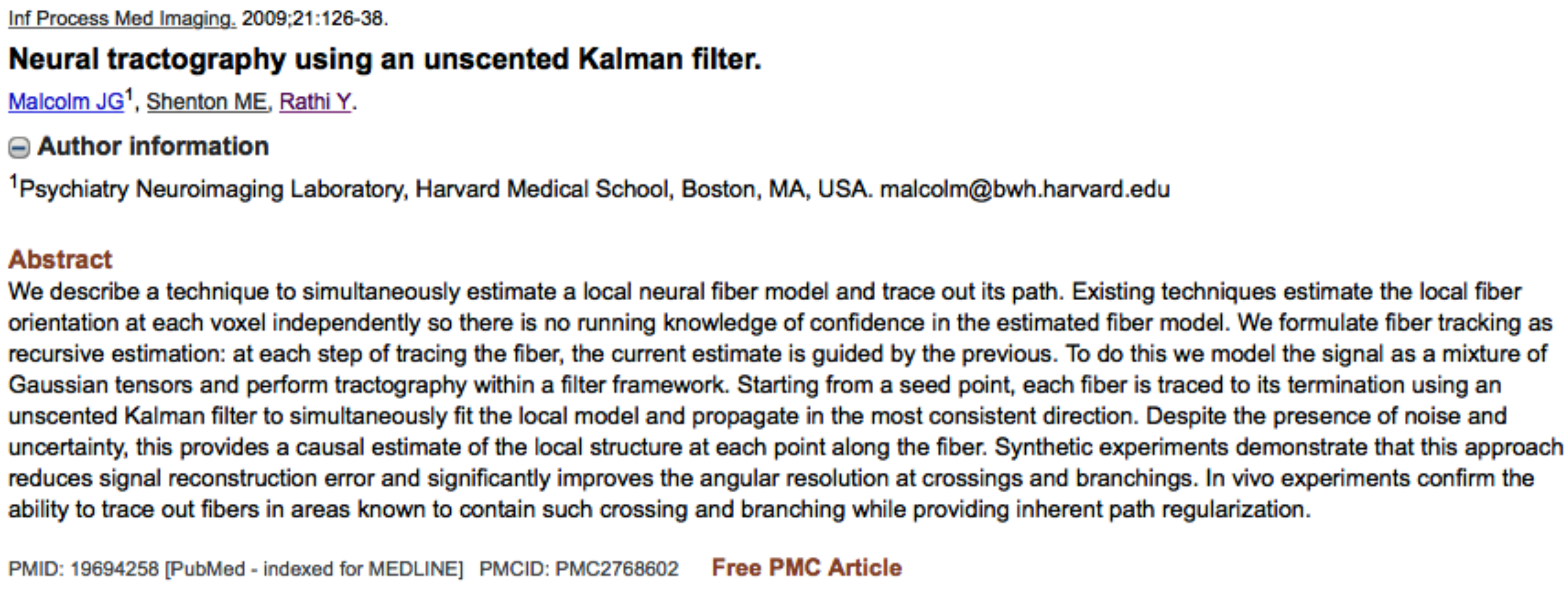
- UKF tractography may detect more fibers comparing to single-tensor streamline tractography (Slicer default method), especially in edematous areas.

- 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 JG[1], Shenton ME, Rathi Y.

Author information

[1]Psychiatry 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.

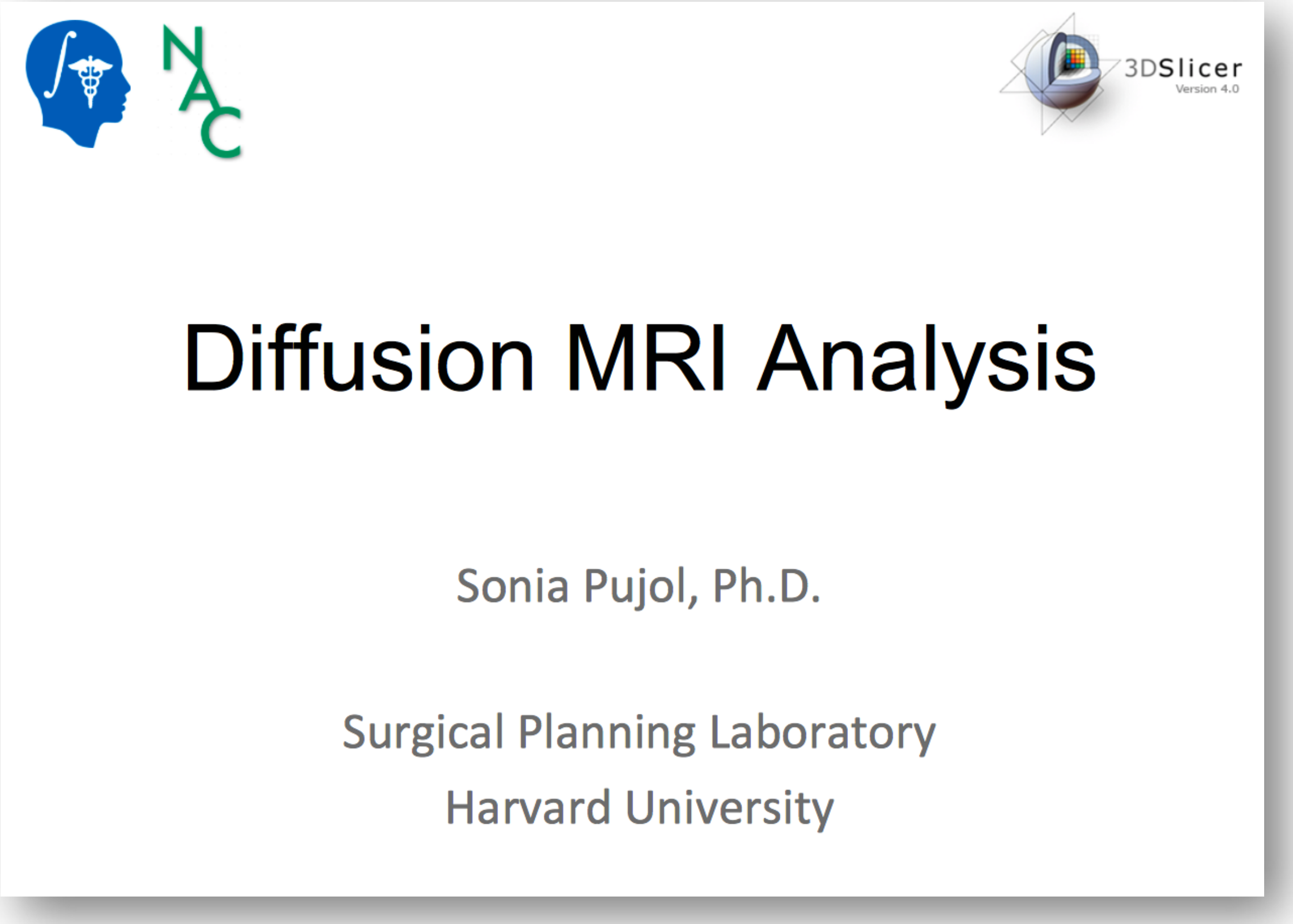
PMID: 19694258 [PubMed - indexed for MEDLINE] PMCID: PMC2768602 **Free PMC Article**

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



Diffusion MRI Analysis

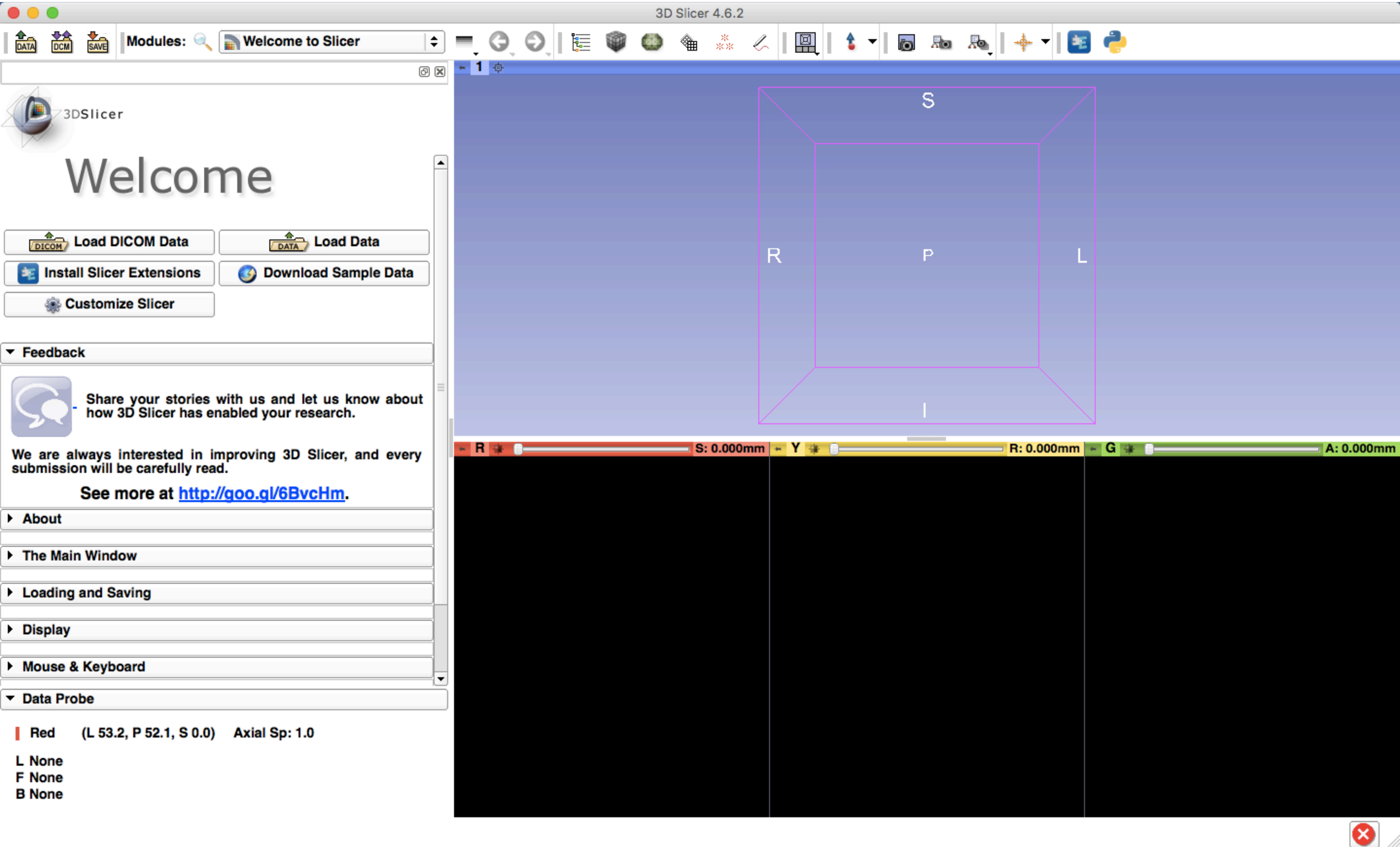
Sonia Pujol, Ph.D.

Surgical Planning Laboratory
Harvard University

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



Share your stories with us and let us know about how 3D Slicer has enabled your research.

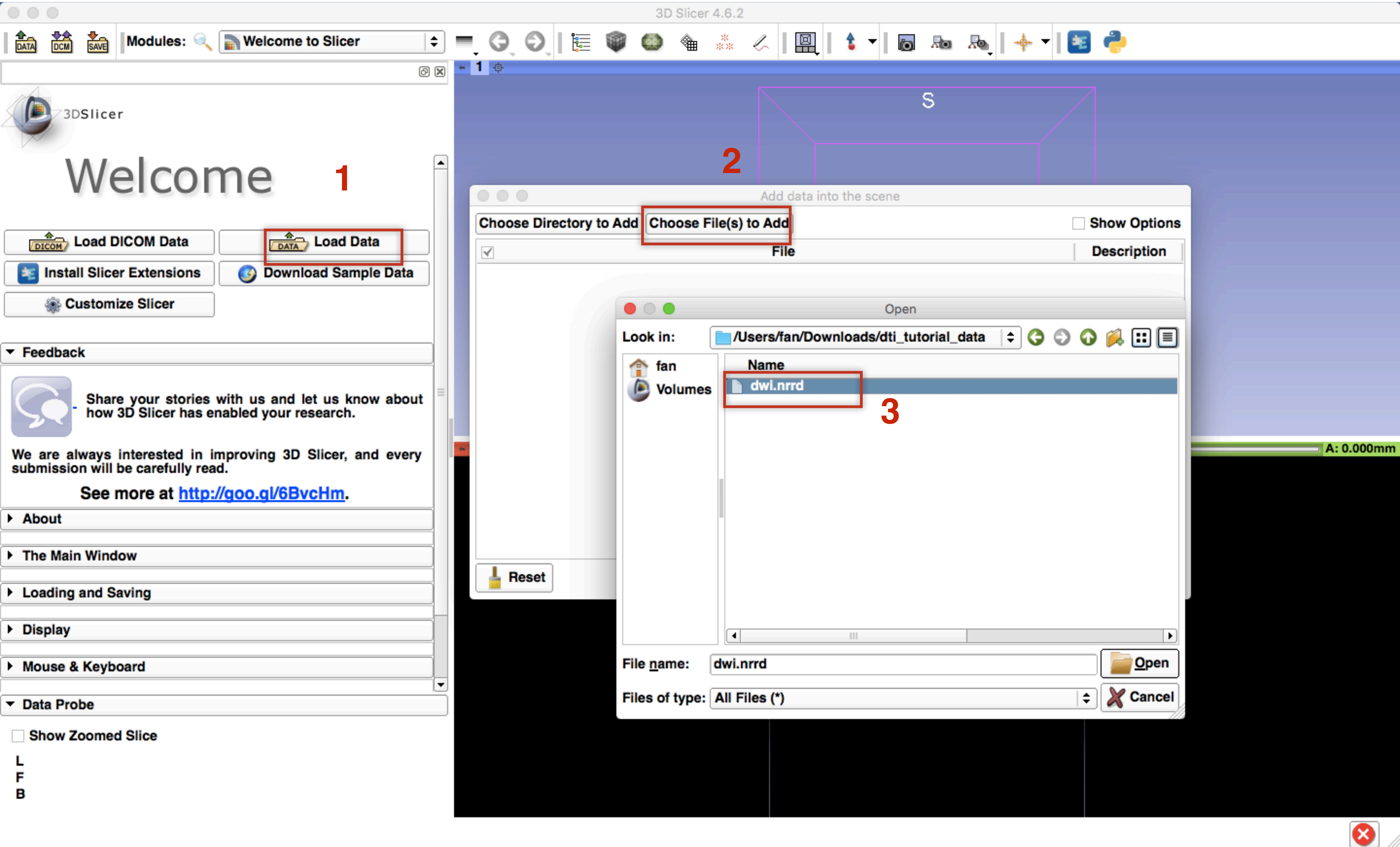
We are always interested in improving 3D Slicer, and every submission will be carefully read.

See more at http://goo.gl/6BvcHm.

Red (L 53.2, P 52.1, S 0.0) Axial Sp: 1.0

L None
F None
B None

Load the data



Share your stories with us and let us know about how 3D Slicer has enabled your research.

We are always interested in improving 3D Slicer, and every submission will be carefully read.

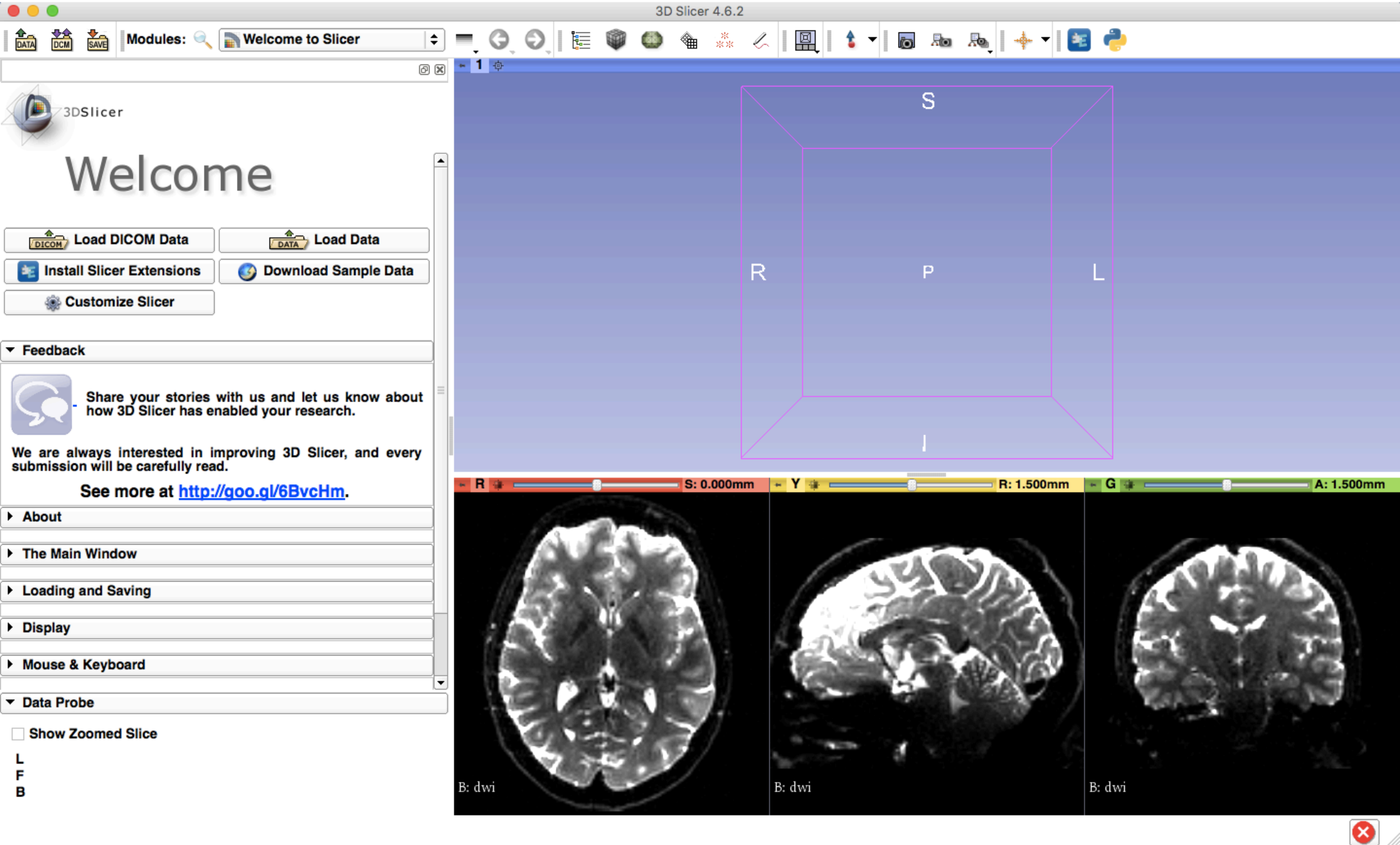
See more at http://goo.gl/6BvcHm.

Look in: /Users/fan/Downloads/dti_tutorial_data

File name: dwi.nrrd

Files of type: All Files (*)

There you go…!



Share your stories with us and let us know about how 3D Slicer has enabled your research.

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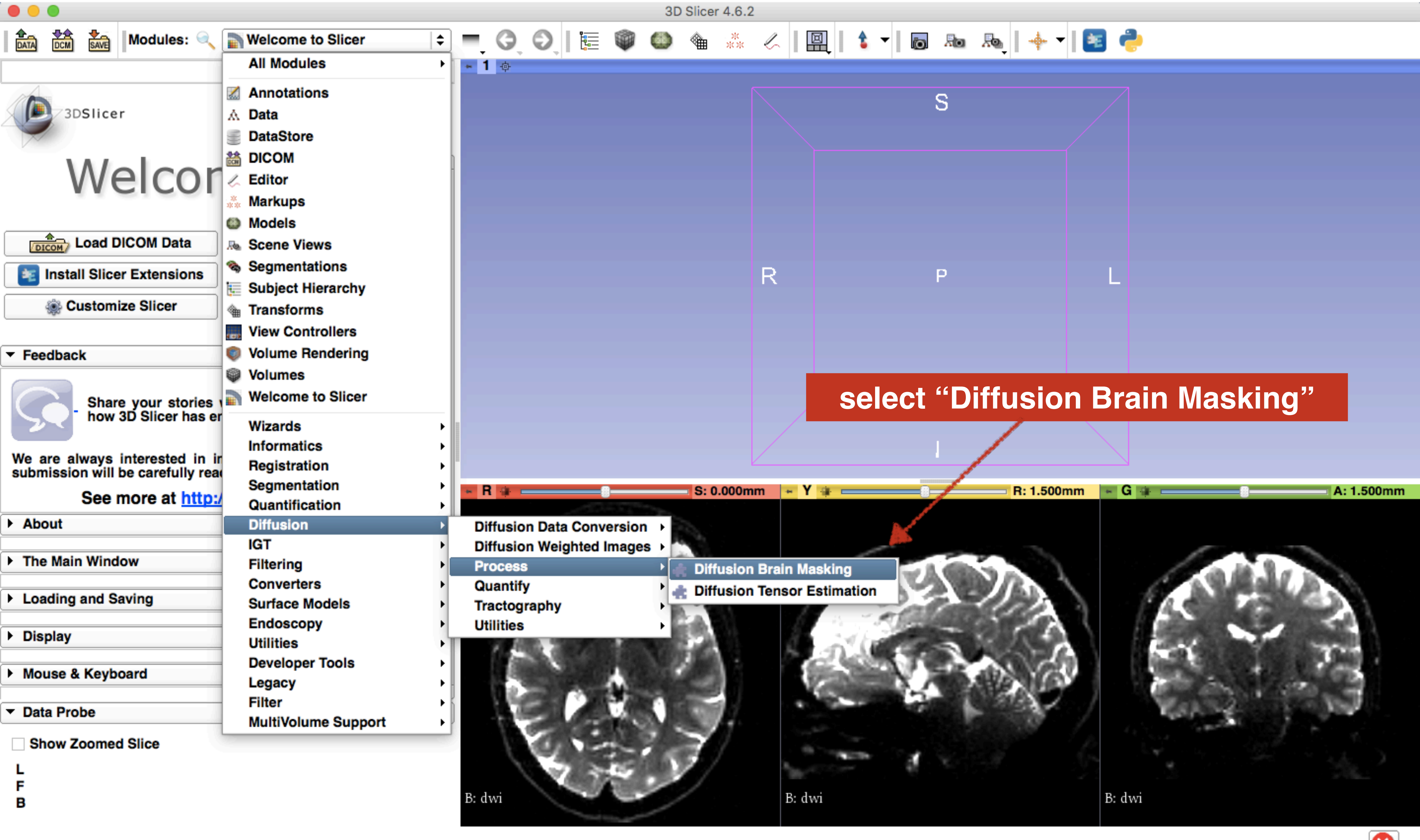
See more at http://goo.gl/6BvcHm.

Main Steps

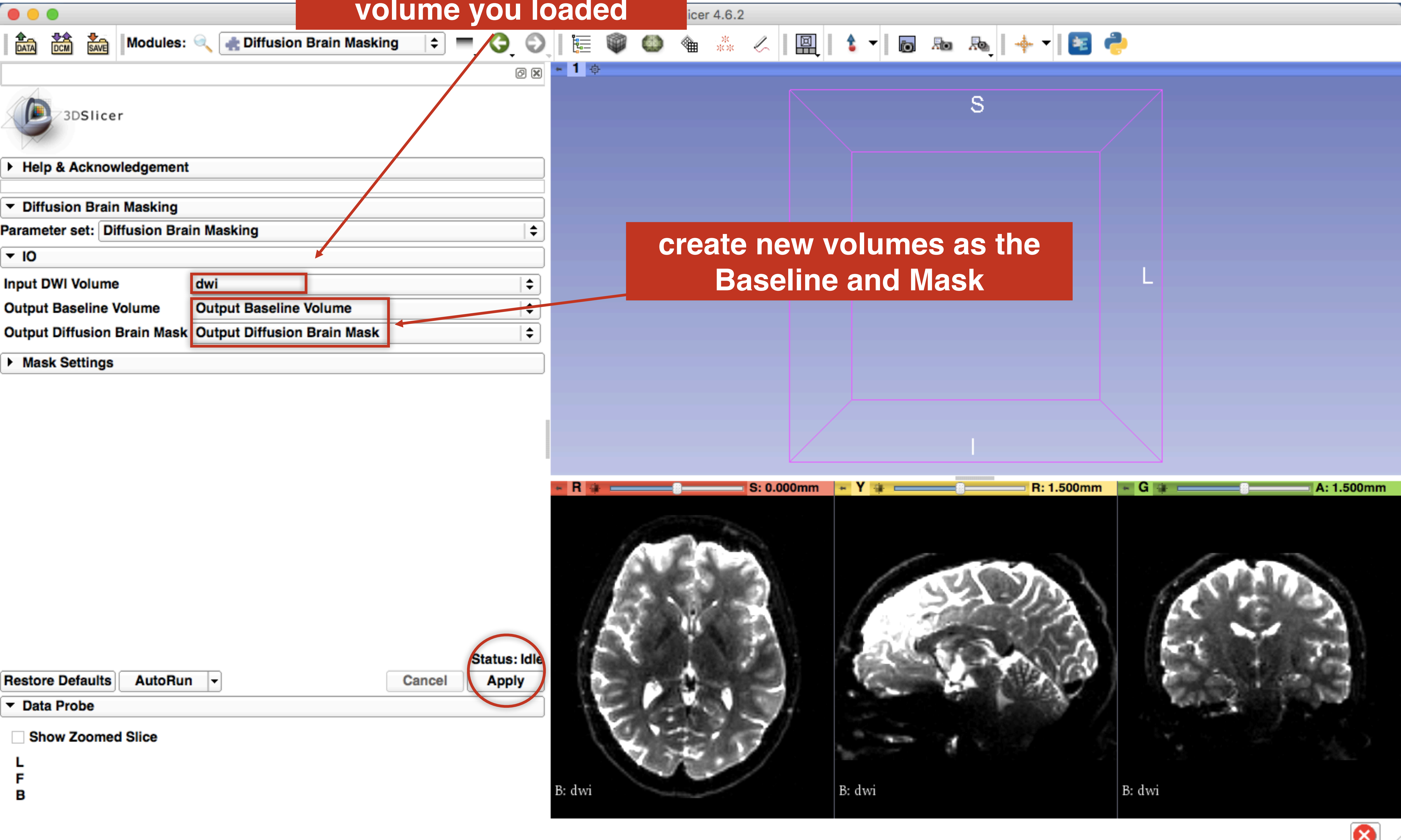
- Creating a brain mask
- Creating FA map
- Creating region of interest for tract seeding
- UKF tractography

Brain Mask Creation



select “Diffusion Brain Masking”

the input is the DWI volume you loaded



Modules: Diffusion Brain Masking

Parameter set: Diffusion Brain Masking

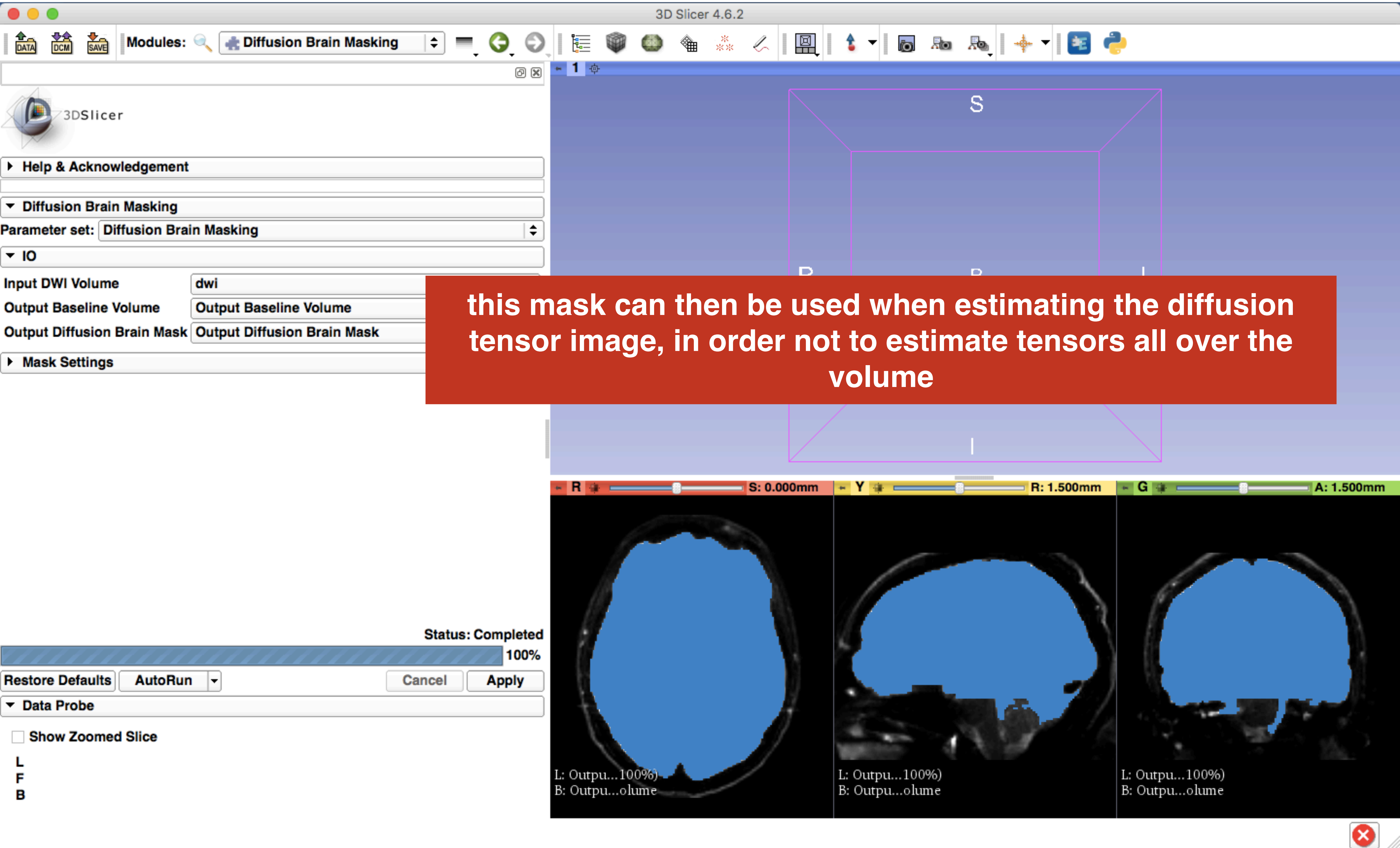
Input DWI Volume: dwi

Output Baseline Volume: Output Baseline Volume

Output Diffusion Brain Mask: Output Diffusion Brain Mask

Status: Idle

create new volumes as the Baseline and Mask



Modules: Diffusion Brain Masking

Diffusion Brain Masking

Parameter set: Diffusion Brain Masking

IO

Input DWI Volume: dwi

Output Baseline Volume: Output Baseline Volume

Output Diffusion Brain Mask: Output Diffusion Brain Mask

Mask Settings

Status: Completed

100%

☐ Show Zoomed Slice

L
F
B

this mask can then be used when estimating the diffusion tensor image, in order not to estimate tensors all over the volume

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

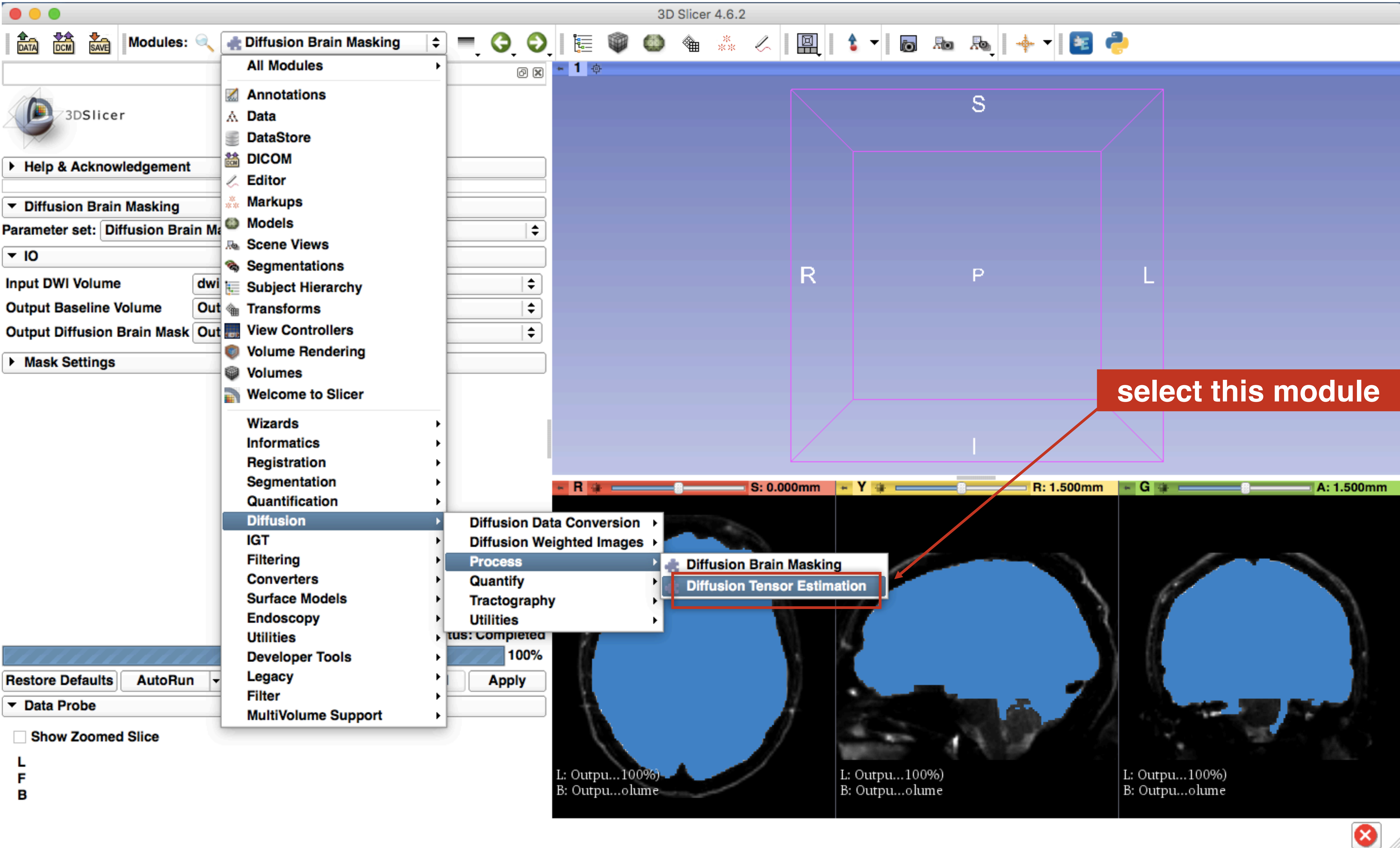
Tract Selection

- Note that FA maps can be more informative for selecting ROIs.

- For that purpose you should first estimate DTI and calculate FA map

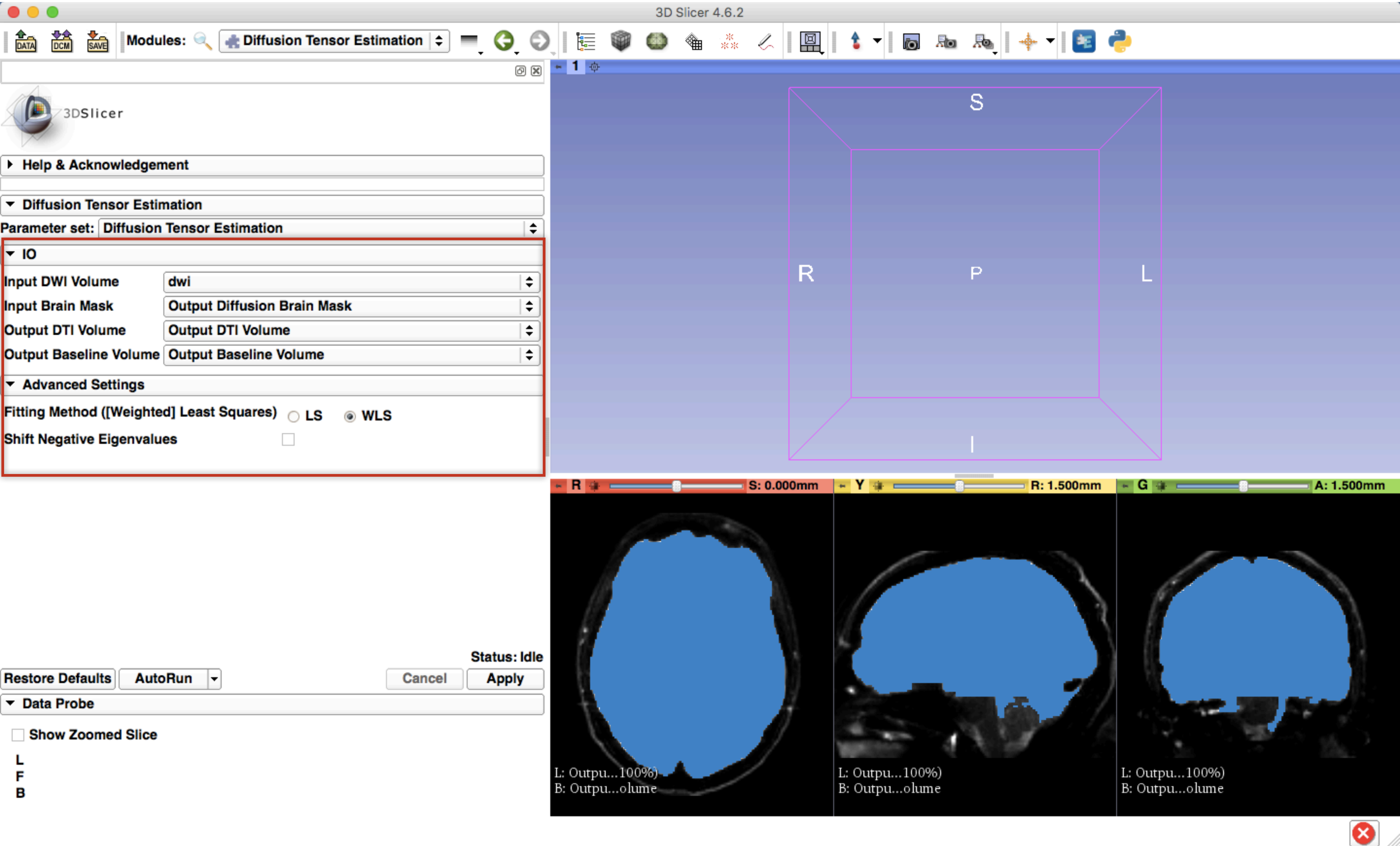
- Although these maps are only used here for ROI selection and the model is again estimated from DWI for UKF tractography.

DWI to DTI Estimation



select this module

Set the Parameters



Help & Acknowledgement

Diffusion Tensor Estimation

Parameter set: Diffusion Tensor Estimation

IO

Input DWI Volume	dwi
Input Brain Mask	Output Diffusion Brain Mask
Output DTI Volume	Output DTI Volume
Output Baseline Volume	Output Baseline Volume

Advanced Settings

Fitting Method ([Weighted] Least Squares) ○ LS ● WLS

Shift Negative Eigenvalues ☐

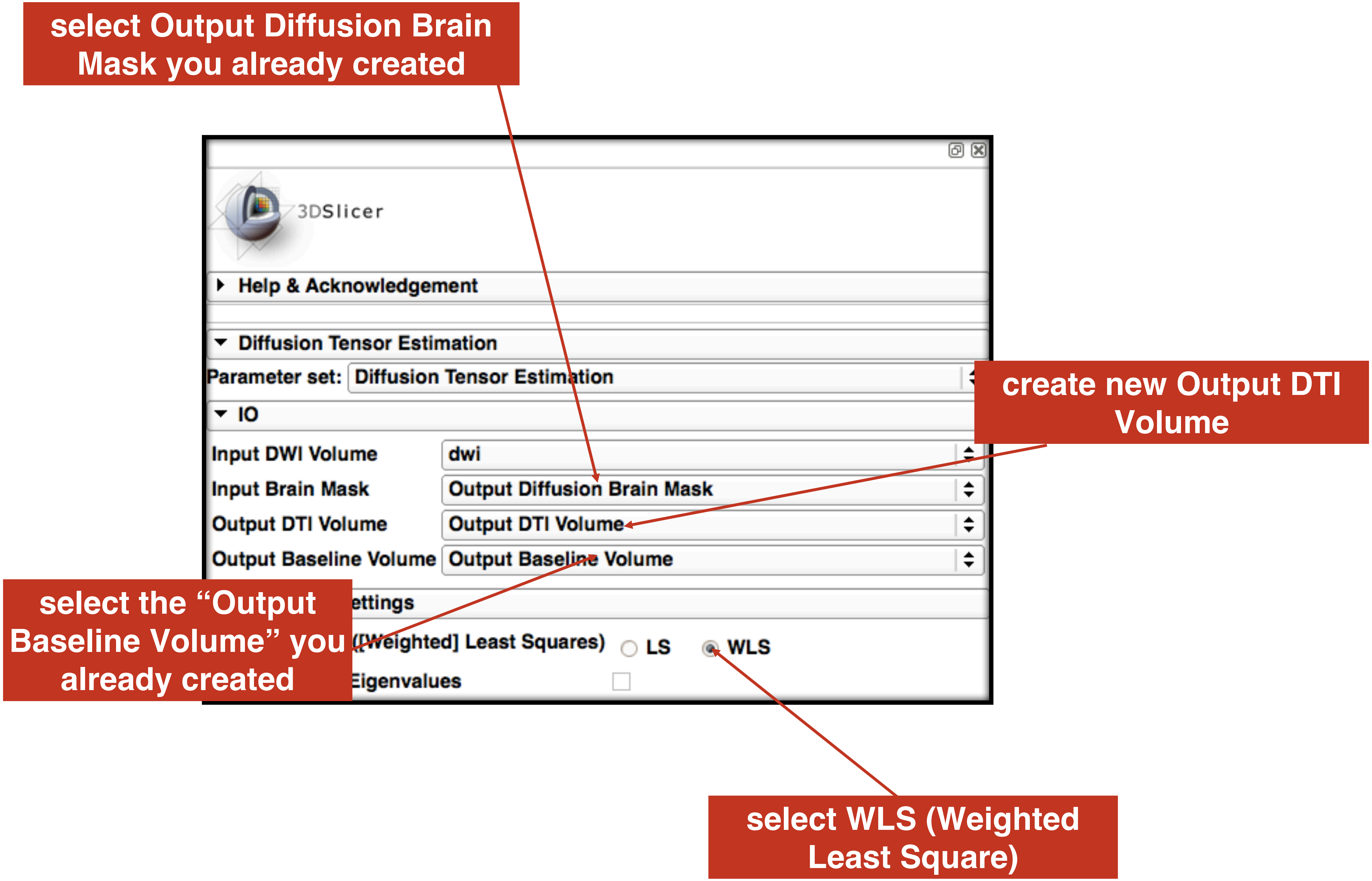
Status: Idle

Restore Defaults | AutoRun | Cancel | Apply

Data Probe

☐ Show Zoomed Slice

L
F
B



select Output Diffusion Brain Mask you already created

create new Output DTI Volume

select the "Output Baseline Volume" you already created

select WLS (Weighted Least Square)

Parameter set: Diffusion Tensor Estimation

IO

Input DWI Volume: dwi

Input Brain Mask: Output Diffusion Brain Mask

Output DTI Volume: Output DTI Volume

Output Baseline Volume: Output Baseline Volume

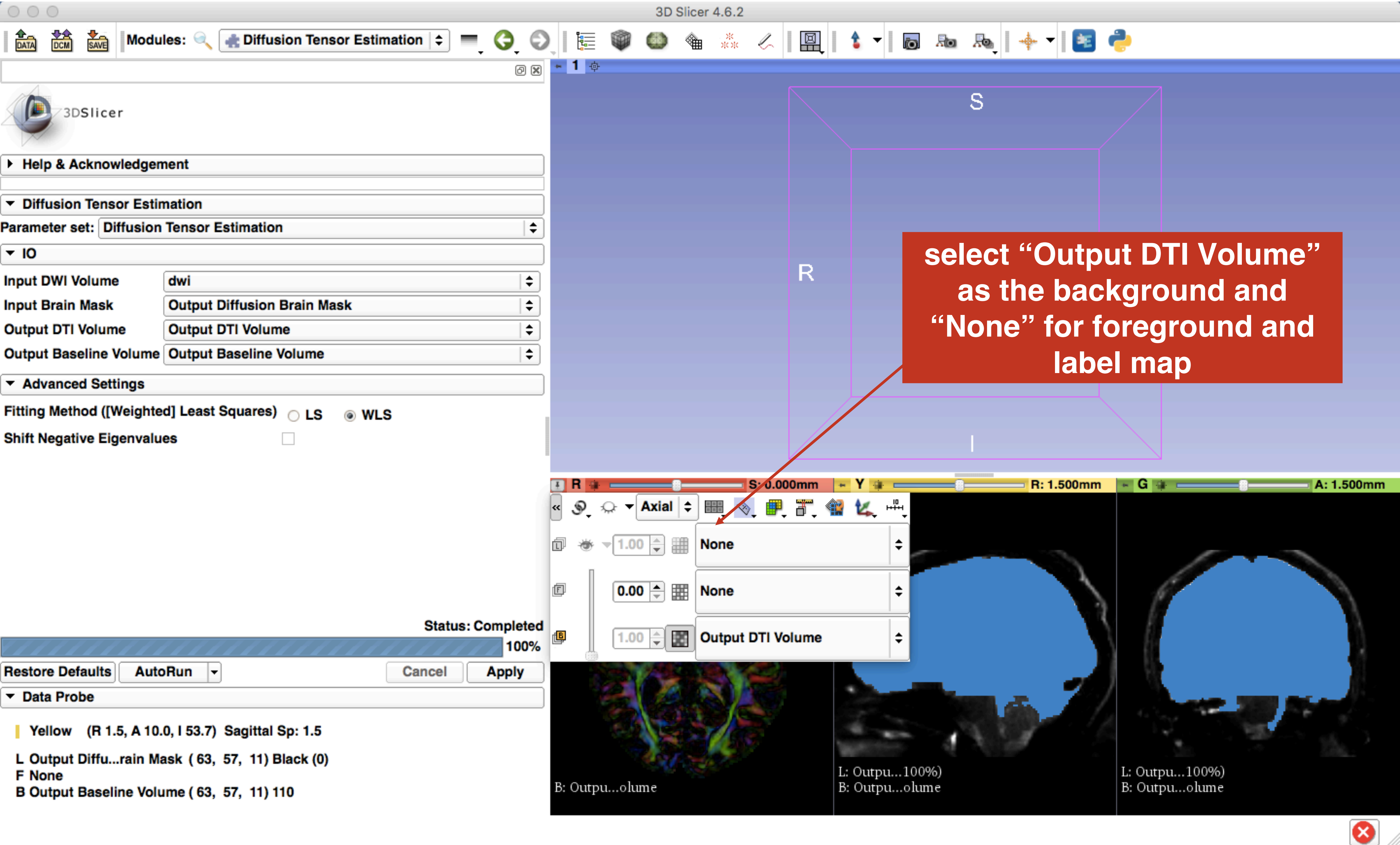
ettings

([Weighted] Least Squares) ○ LS ● WLS

Eigenvalues ☐

Click Apply

Status: Completed! 100%



Modules: Diffusion Tensor Estimation

Diffusion Tensor Estimation

Parameter set: Diffusion Tensor Estimation

IO

Input DWI Volume: dwi
Input Brain Mask: Output Diffusion Brain Mask
Output DTI Volume: Output DTI Volume
Output Baseline Volume: Output Baseline Volume

Advanced Settings

Fitting Method ([Weighted] Least Squares) ○ LS ● WLS
Shift Negative Eigenvalues ☐

Status: Completed
100%

Data Probe

Yellow (R 1.5, A 10.0, I 53.7) Sagittal Sp: 1.5

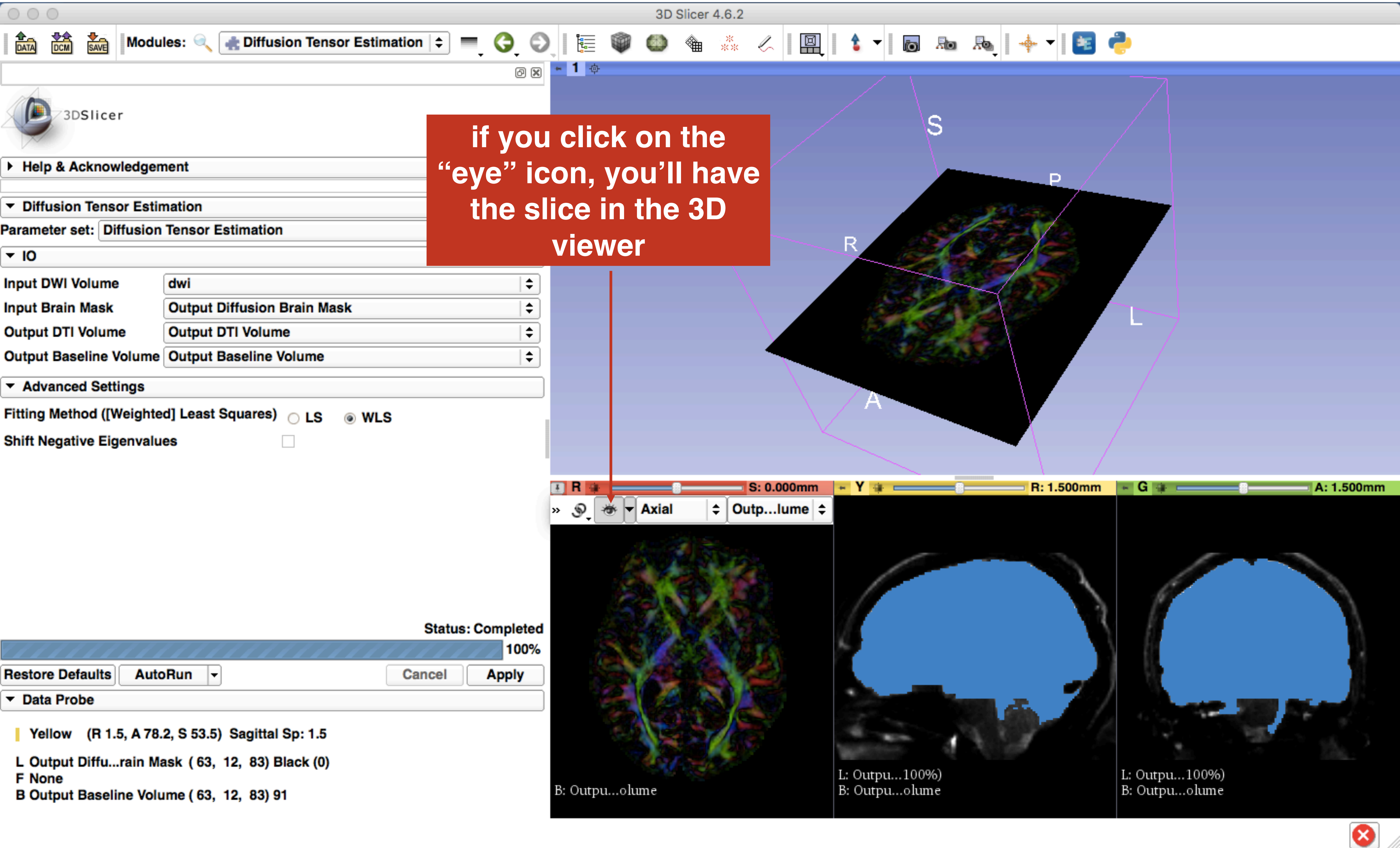
L Output Diffu...rain Mask (63, 57, 11) Black (0)
F None
B Output Baseline Volume (63, 57, 11) 110

R S: 0.000mm
Y R: 1.500mm
G A: 1.500mm

1.00 None
0.00 None
1.00 Output DTI Volume

select “Output DTI Volume” as the background and “None” for foreground and label map

color-coded DTI volume



if you click on the "eye" icon, you'll have the slice in the 3D viewer

Diffusion Tensor Estimation

Parameter set: Diffusion Tensor Estimation

IO

Input DWI Volume: dwi

Input Brain Mask: Output Diffusion Brain Mask

Output DTI Volume: Output DTI Volume

Output Baseline Volume: Output Baseline Volume

Advanced Settings

Fitting Method ([Weighted] Least Squares) ○ LS ● WLS

Shift Negative Eigenvalues ☐

Status: Completed

100%

S: 0.000mm

R: 1.500mm

A: 1.500mm

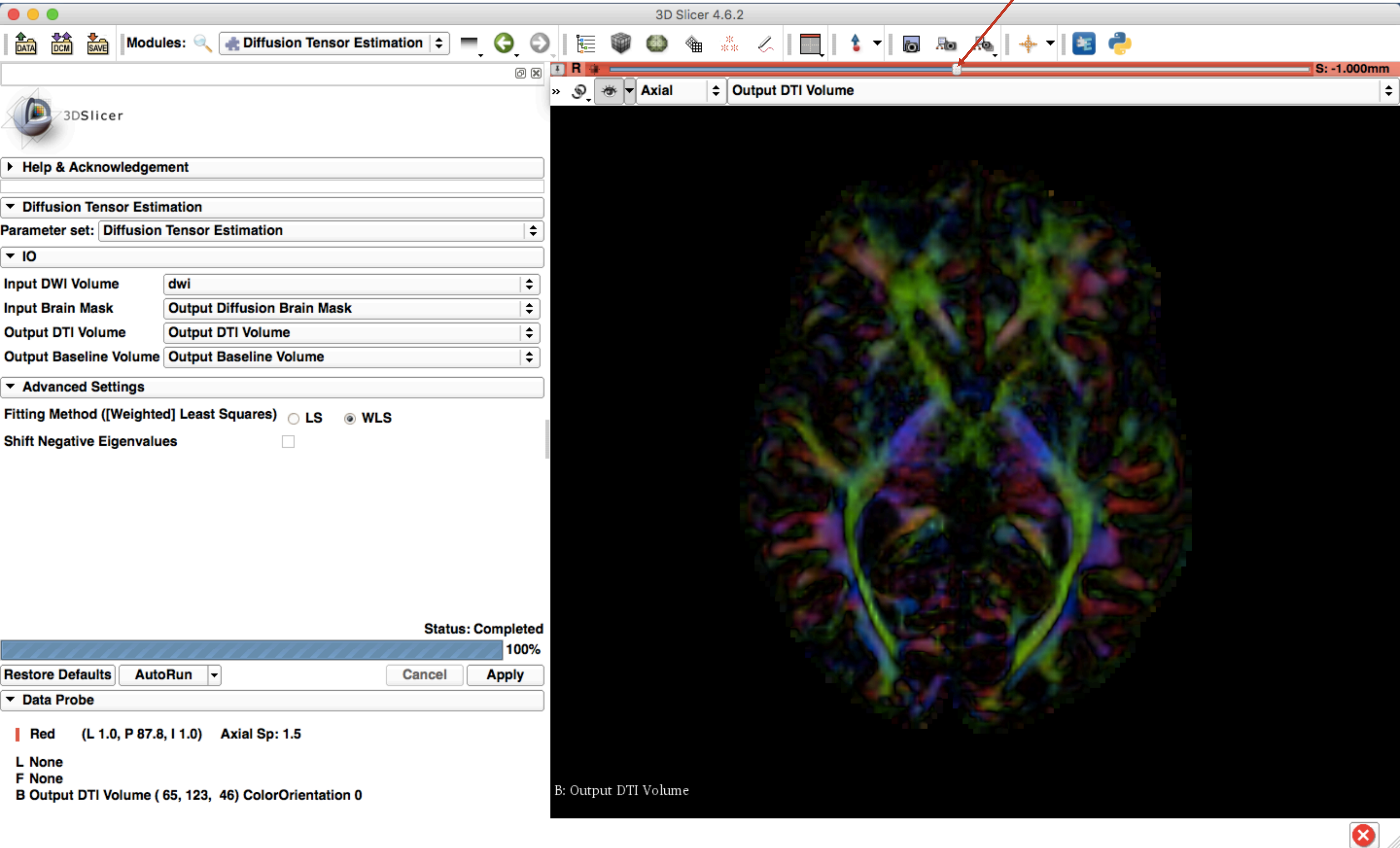
B: Outpu...olume

Data Probe

Yellow (R 1.5, A 78.2, S 53.5) Sagittal Sp: 1.5

L Output Diffu...rain Mask (63, 12, 83) Black (0)
F None
B Output Baseline Volume (63, 12, 83) 91

browse through the DTI volume here



Modules: Diffusion Tensor Estimation

Parameter set: Diffusion Tensor Estimation

Input DWI Volume: dwi
Input Brain Mask: Output Diffusion Brain Mask
Output DTI Volume: Output DTI Volume
Output Baseline Volume: Output Baseline Volume

Fitting Method ([Weighted] Least Squares) ○ LS ● WLS

Shift Negative Eigenvalues ☐

Status: Completed

100%

Red (L 1.0, P 87.8, I 1.0) Axial Sp: 1.5

L None
F None
B Output DTI Volume (65, 123, 46) ColorOrientation 0

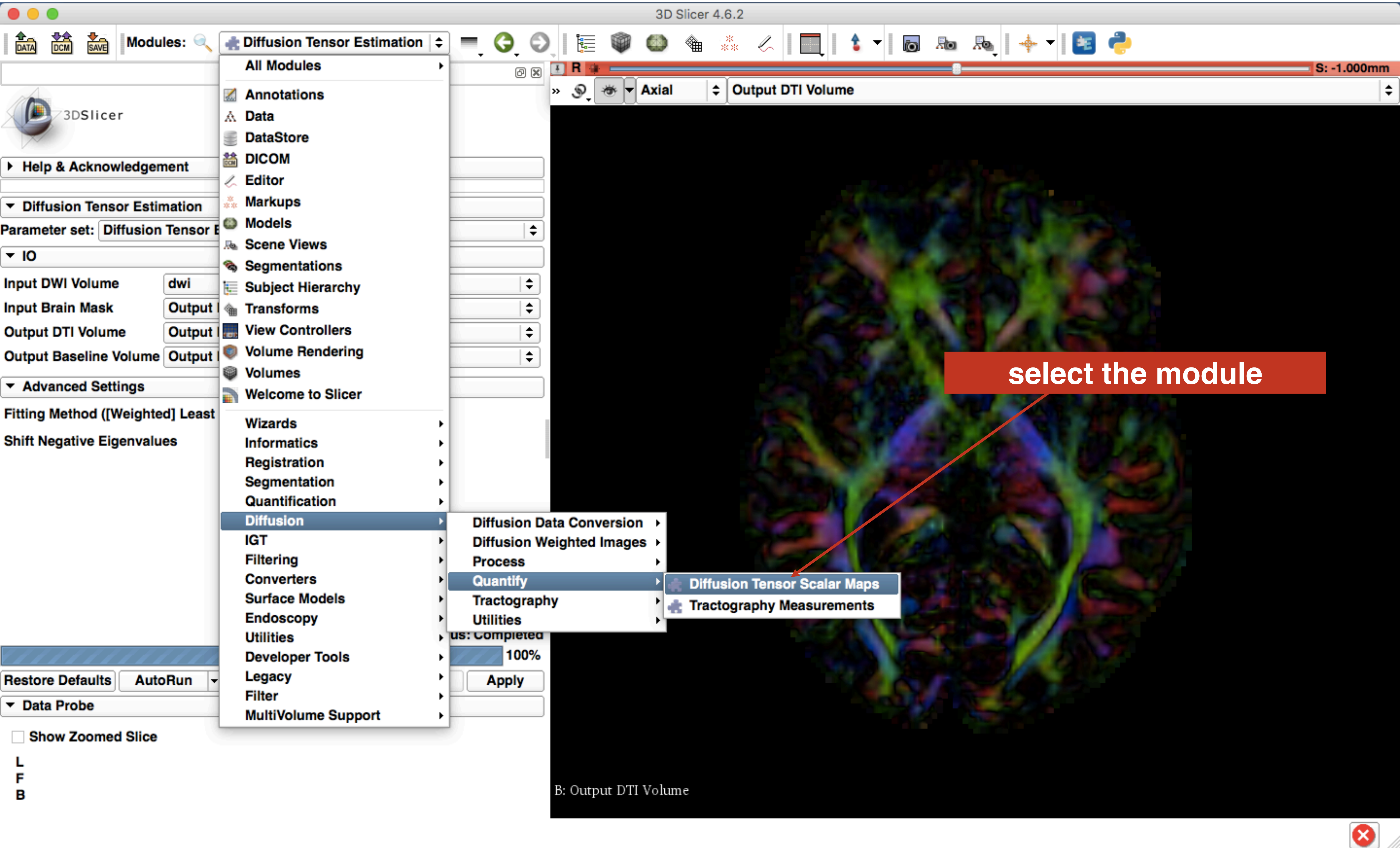
S: -1.000mm

Axial

Output DTI Volume

B: Output DTI Volume

Diffusion Tensor Scalar Measurements; FA



Parameter set: Diffusion Tensor E

Input DWI Volume: dwi

Input Brain Mask: Output

Output DTI Volume: Output

Output Baseline Volume: Output

Fitting Method ([Weighted] Least

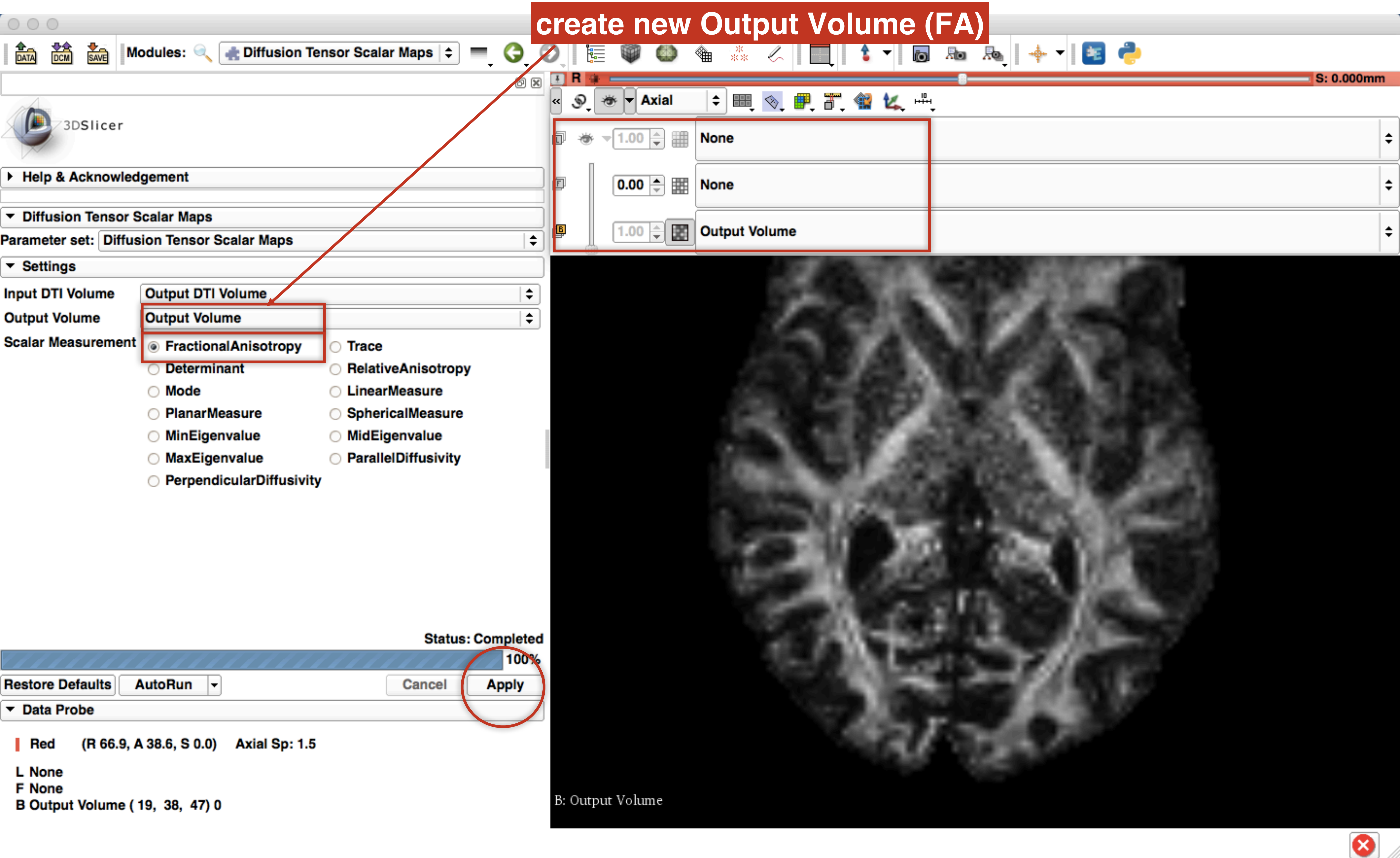
Shift Negative Eigenvalues

us: Completed 100%

Output DTI Volume

select the module

create new Output Volume (FA)



Diffusion Tensor Scalar Maps

Parameter set: Diffusion Tensor Scalar Maps

Settings

Input DTI Volume: Output DTI Volume

Output Volume: Output Volume

Scalar Measurement:
- ● FractionalAnisotropy
- ○ Trace
- ○ Determinant
- ○ RelativeAnisotropy
- ○ Mode
- ○ LinearMeasure
- ○ PlanarMeasure
- ○ SphericalMeasure
- ○ MinEigenvalue
- ○ MidEigenvalue
- ○ MaxEigenvalue
- ○ ParallelDiffusivity
- ○ PerpendicularDiffusivity

Status: Completed

100%

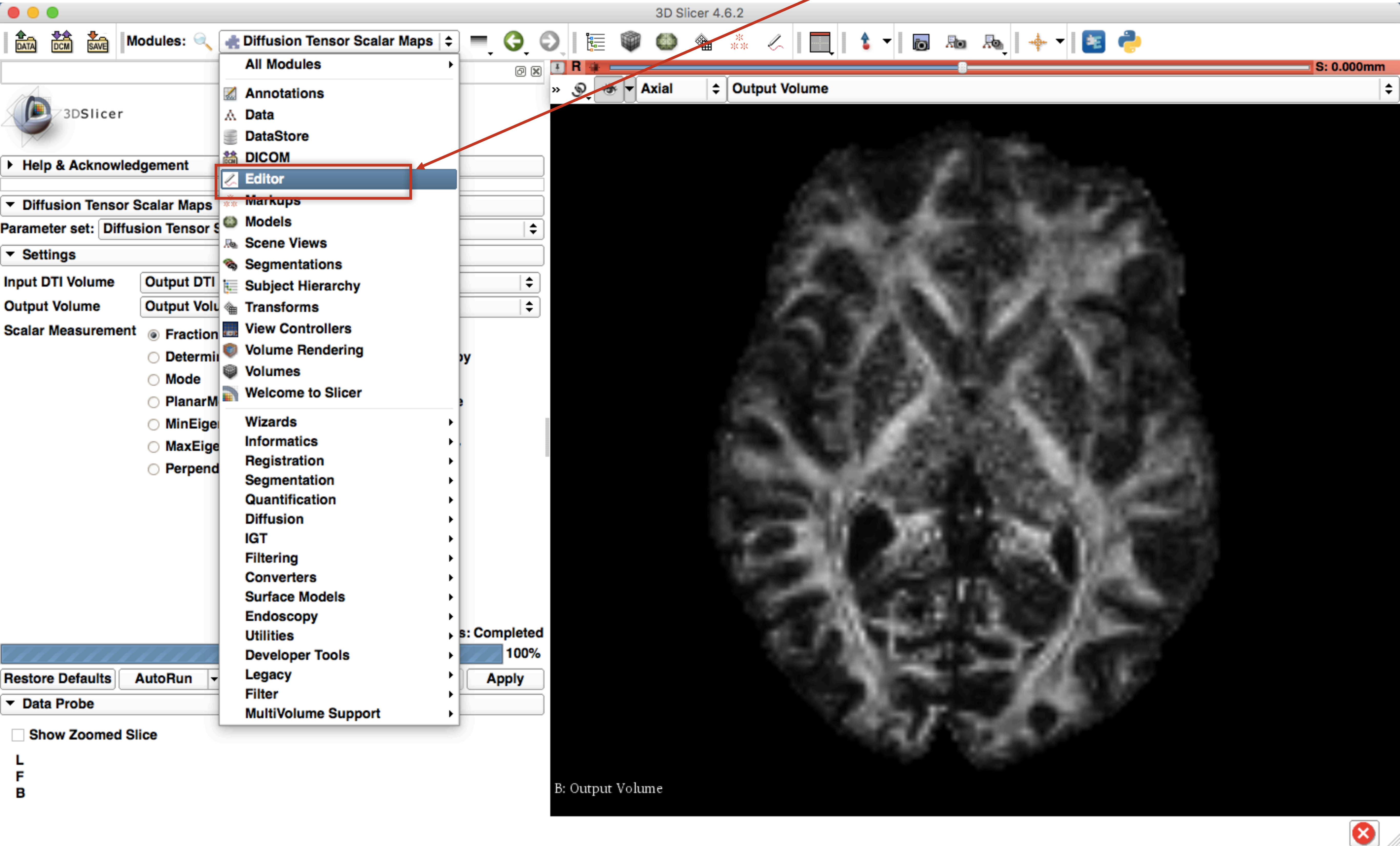
Data Probe

Red (R 66.9, A 38.6, S 0.0) Axial Sp: 1.5

L None
F None
B Output Volume (19, 38, 47) 0

1.00	None
0.00	None
1.00	Output Volume

Select the Editor Module



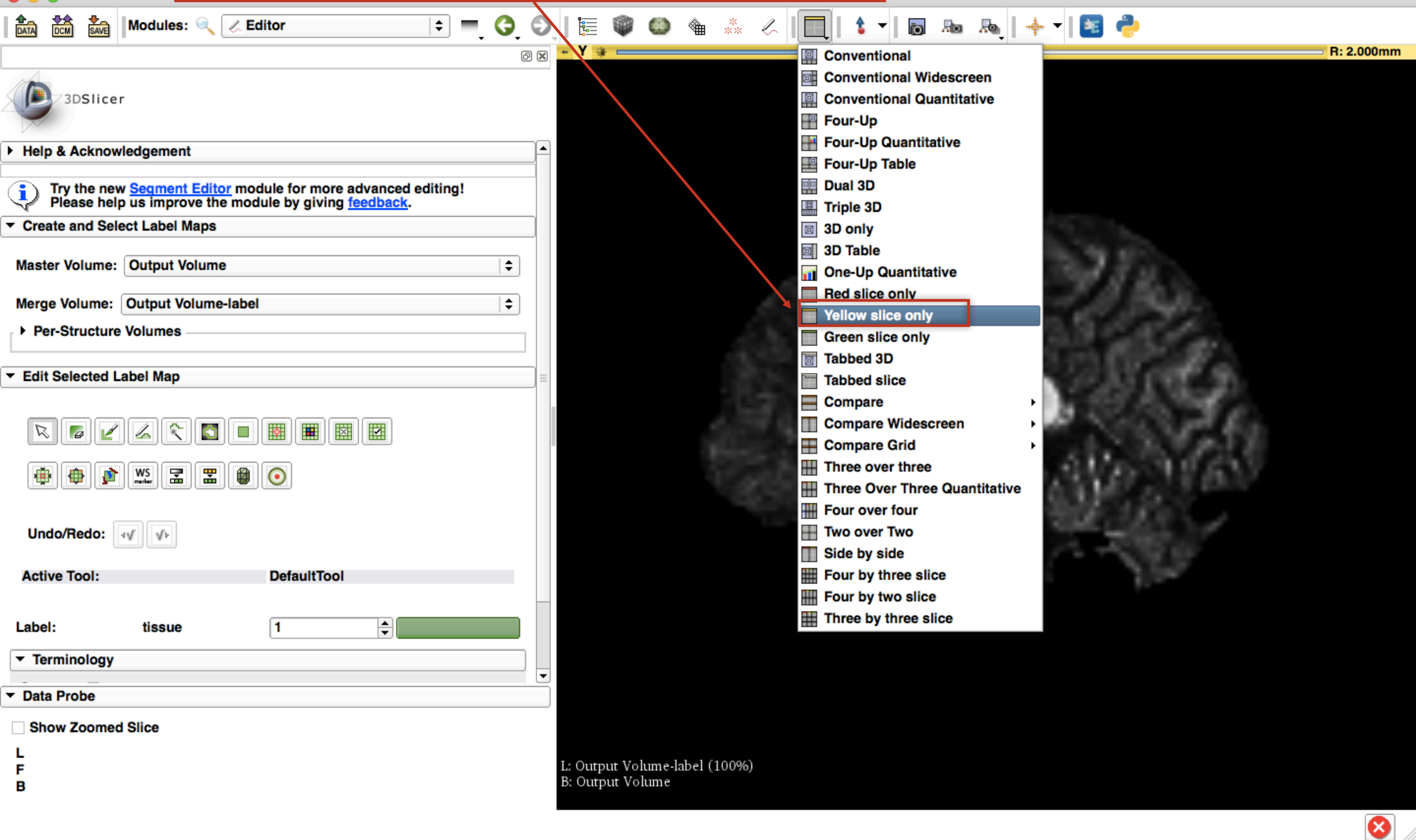
Modules: Diffusion Tensor Scalar Maps

Parameter set: Diffusion Tensor S

Input DTI Volume: Output DTI

Output Volume: Output Volu

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



Modules: Editor

Help & Acknowledgement

Try the new Segment Editor module for more advanced editing!
Please help us improve the module by giving feedback.

Create and Select Label Maps

Master Volume: Output Volume

Merge Volume: Output Volume-label

Per-Structure Volumes

Edit Selected Label Map

Undo/Redo:

Active Tool: DefaultTool

Label: tissue 1

Terminology

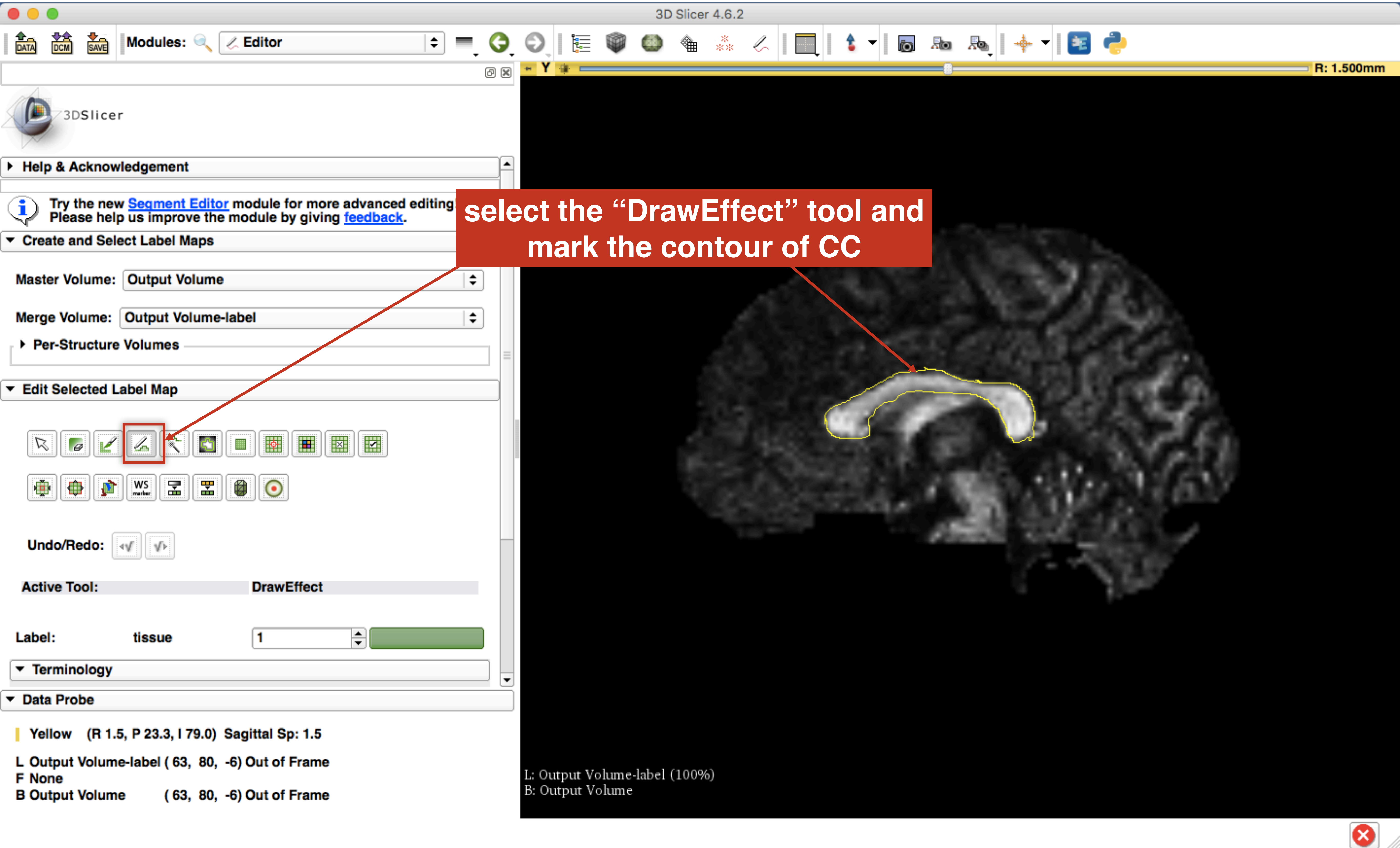
Data Probe

☐ Show Zoomed Slice

L
F
B

L: Output Volume-label (100%)
B: Output Volume

ROI Definiton



Modules: Editor

Try the new Segment Editor module for more advanced editing!
Please help us improve the module by giving feedback.

Master Volume: Output Volume

Merge Volume: Output Volume-label

Active Tool: DrawEffect

Label: tissue 1

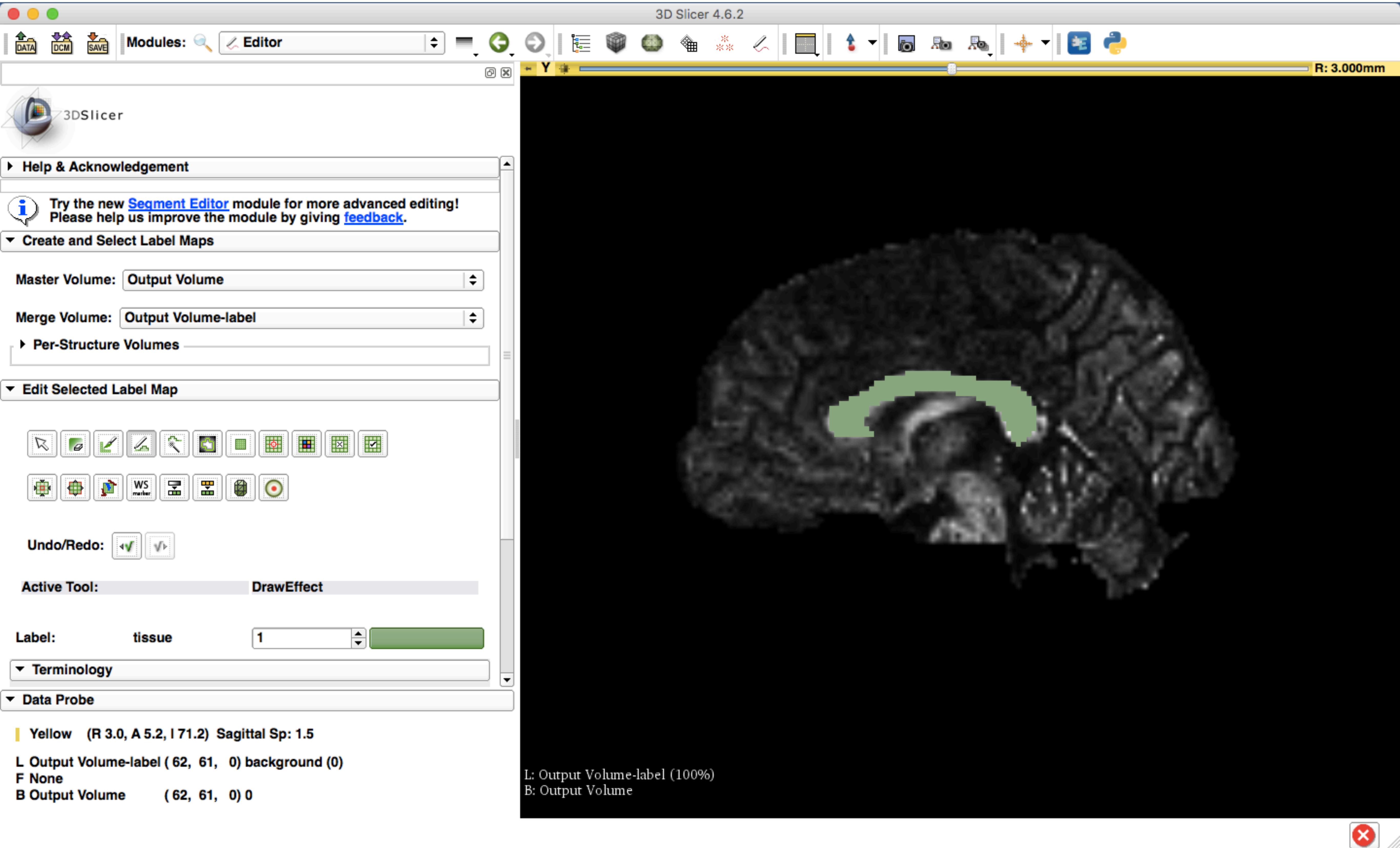
Yellow (R 1.5, P 23.3, I 79.0) Sagittal Sp: 1.5

L Output Volume-label (63, 80, -6) Out of Frame
F None
B Output Volume (63, 80, -6) Out of Frame

L: Output Volume-label (100%)
B: Output Volume

select the “DrawEffect” tool and mark the contour of CC

press enter
repeat this for 3 adjacent slices



Modules: Editor

Try the new Segment Editor module for more advanced editing!
Please help us improve the module by giving feedback.

Master Volume: Output Volume

Merge Volume: Output Volume-label

Undo/Redo:

Active Tool: DrawEffect

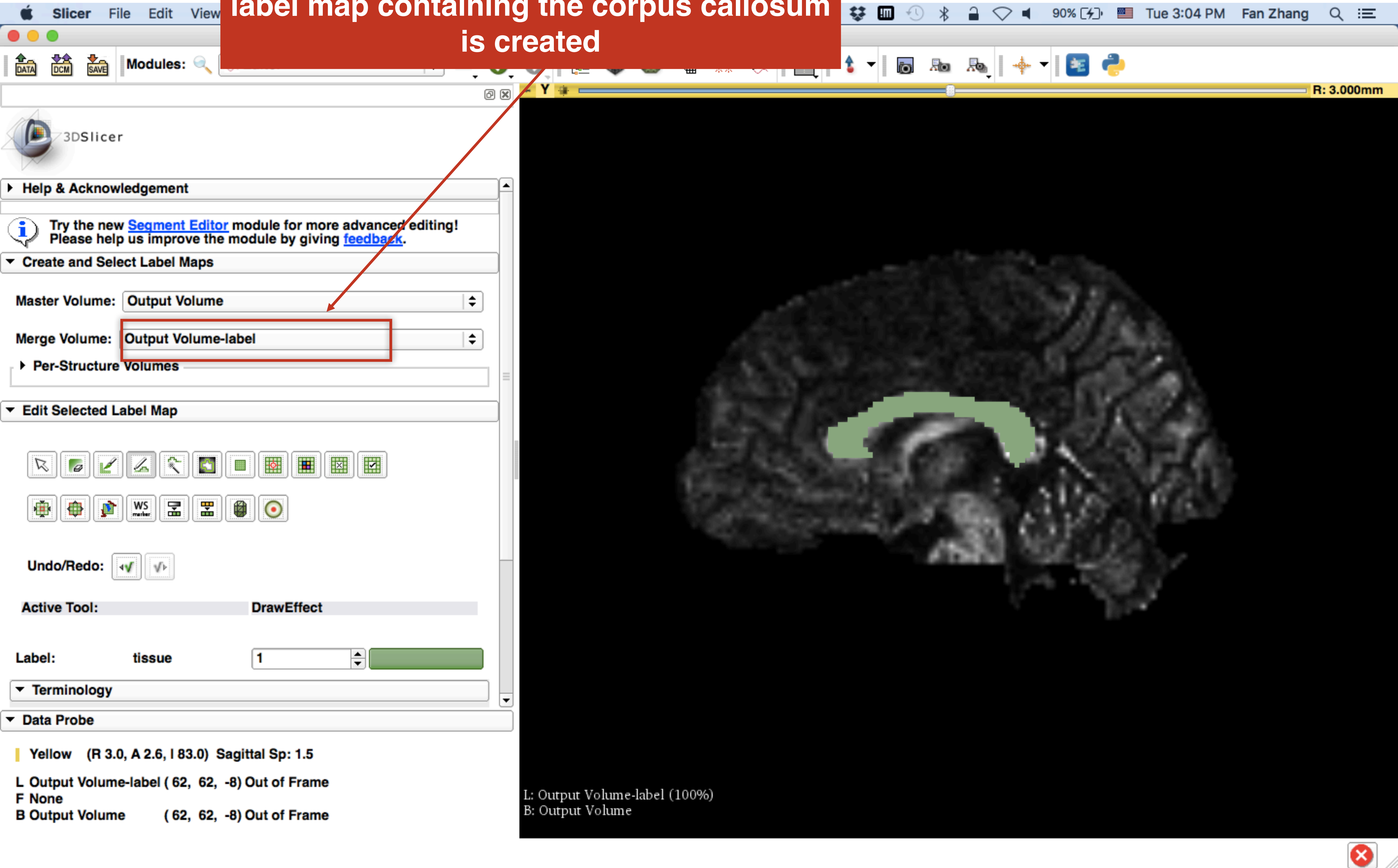
Label: tissue 1

Yellow (R 3.0, A 5.2, I 71.2) Sagittal Sp: 1.5

L Output Volume-label (62, 61, 0) background (0)
F None
B Output Volume (62, 61, 0) 0

L: Output Volume-label (100%)
B: Output Volume

label map containing the corpus callosum is created



Try the new Segment Editor module for more advanced editing!
Please help us improve the module by giving feedback.

Master Volume: Output Volume

Merge Volume: Output Volume-label

Undo/Redo:

Active Tool: DrawEffect

Label: tissue 1

Yellow (R 3.0, A 2.6, I 83.0) Sagittal Sp: 1.5

L Output Volume-label (62, 62, -8) Out of Frame
F None
B Output Volume (62, 62, -8) Out of Frame

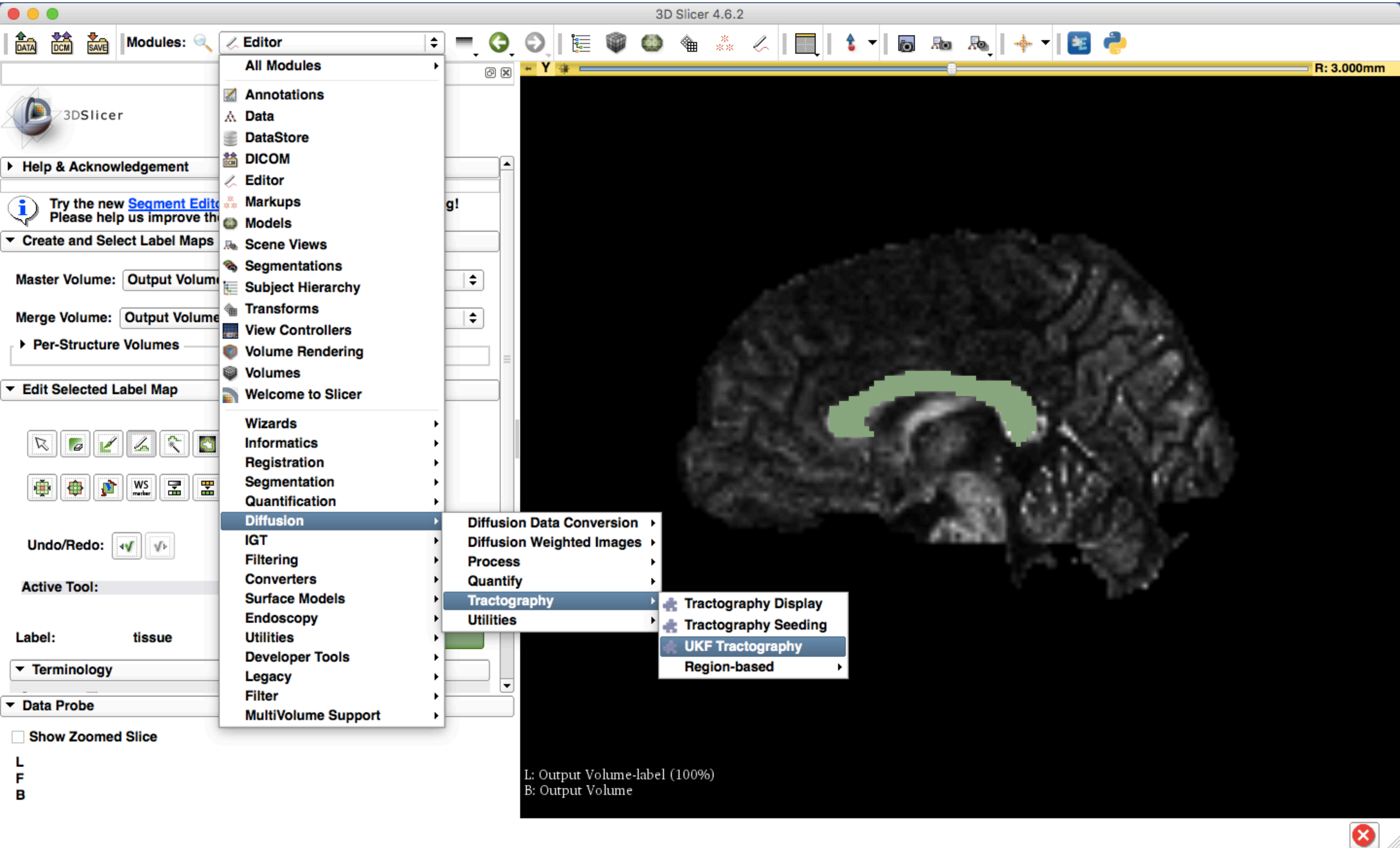
L: Output Volume-label (100%)
B: Output Volume

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)

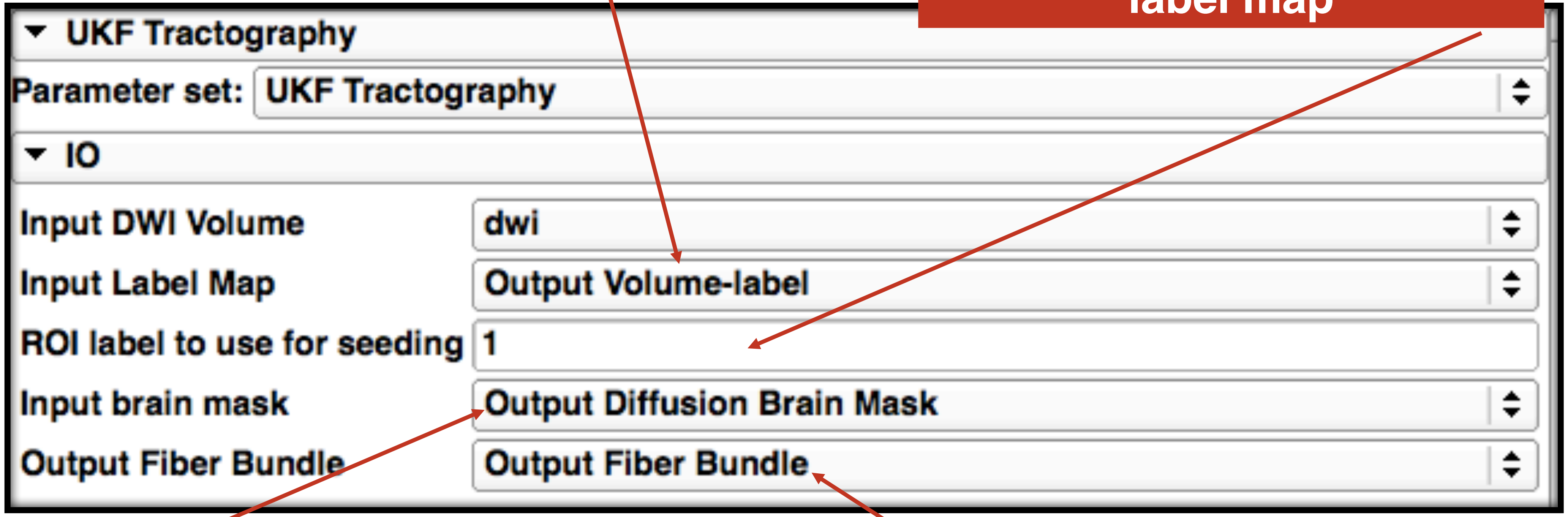
❖ The module can add a term for the free water model. This model tries to separate the signal from partial voluming with cerebrospinal fluid.

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

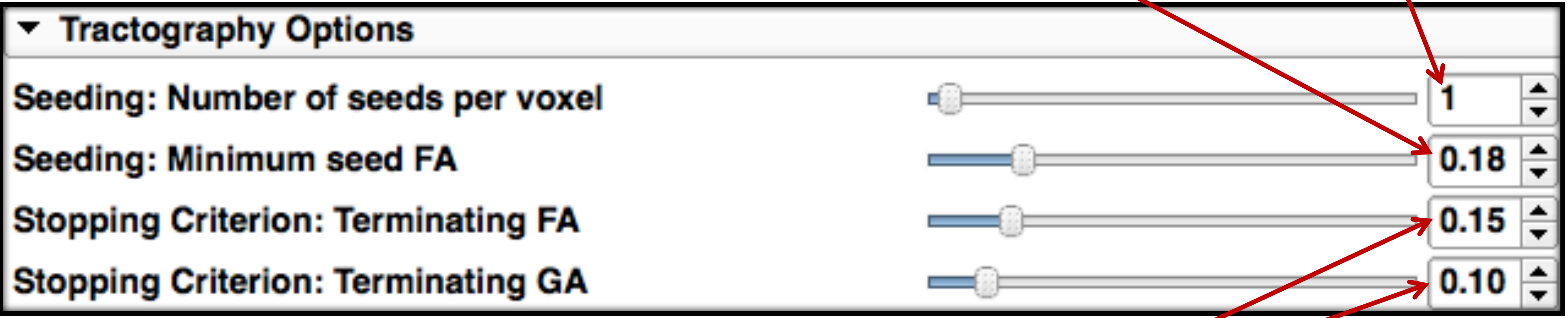
Output Fiber Bundle: Output Fiber Bundle

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)



Tractography Options

Seeding: Number of seeds per voxel 1

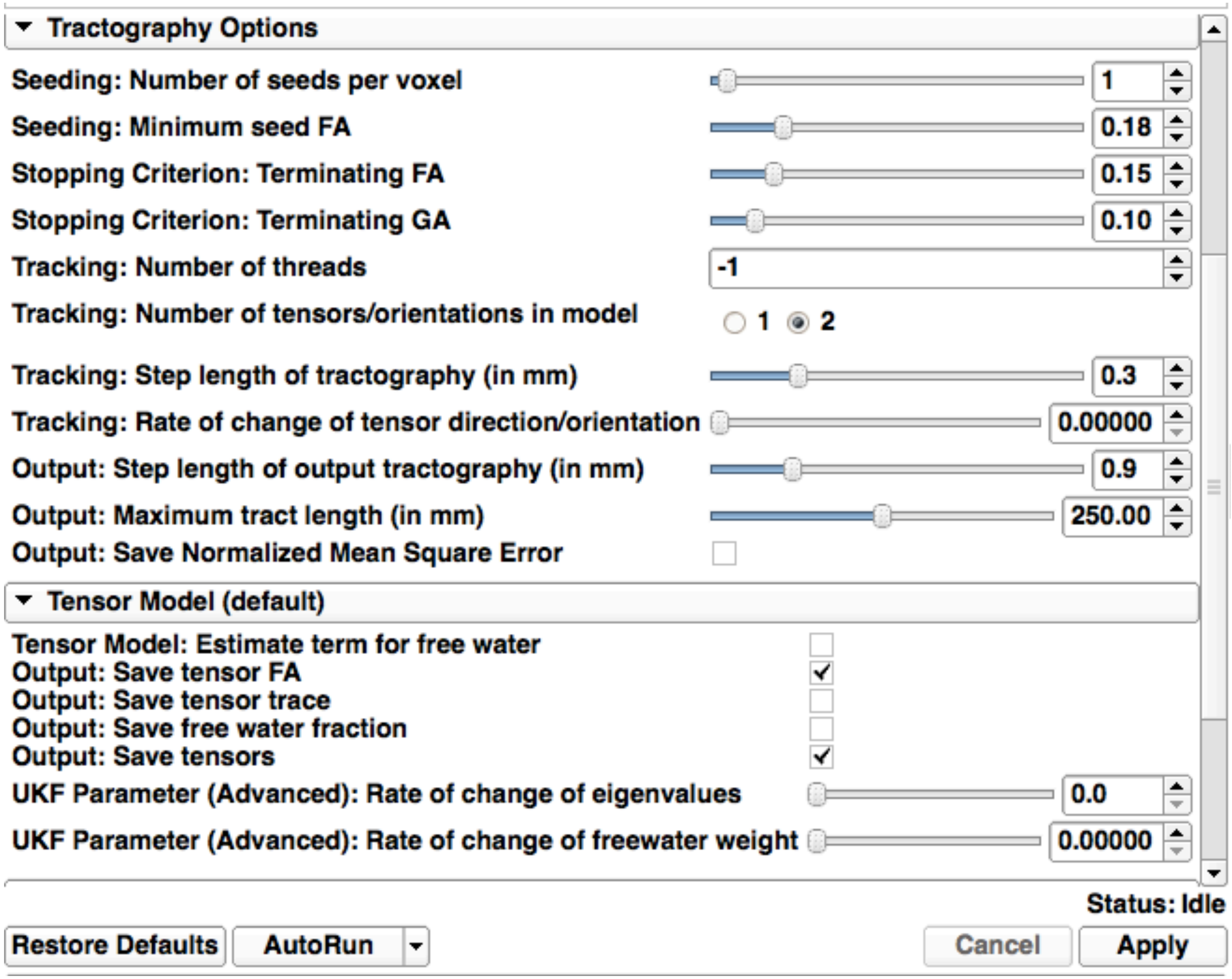
Seeding: Minimum seed FA 0.18

Stopping Criterion: Terminating FA 0.15

Stopping Criterion: Terminating GA 0.10

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

Set other parameters here:



Tractography Options

Seeding: Number of seeds per voxel 1

Seeding: Minimum seed FA 0.18

Stopping Criterion: Terminating FA 0.15

Stopping Criterion: Terminating GA 0.10

Tracking: Number of threads -1

Tracking: Number of tensors/orientations in model ○ 1 ● 2

Tracking: Step length of tractography (in mm) 0.3

Tracking: Rate of change of tensor direction/orientation 0.00000

Output: Step length of output tractography (in mm) 0.9

Output: Maximum tract length (in mm) 250.00

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 0.0

UKF Parameter (Advanced): Rate of change of freewater weight 0.00000

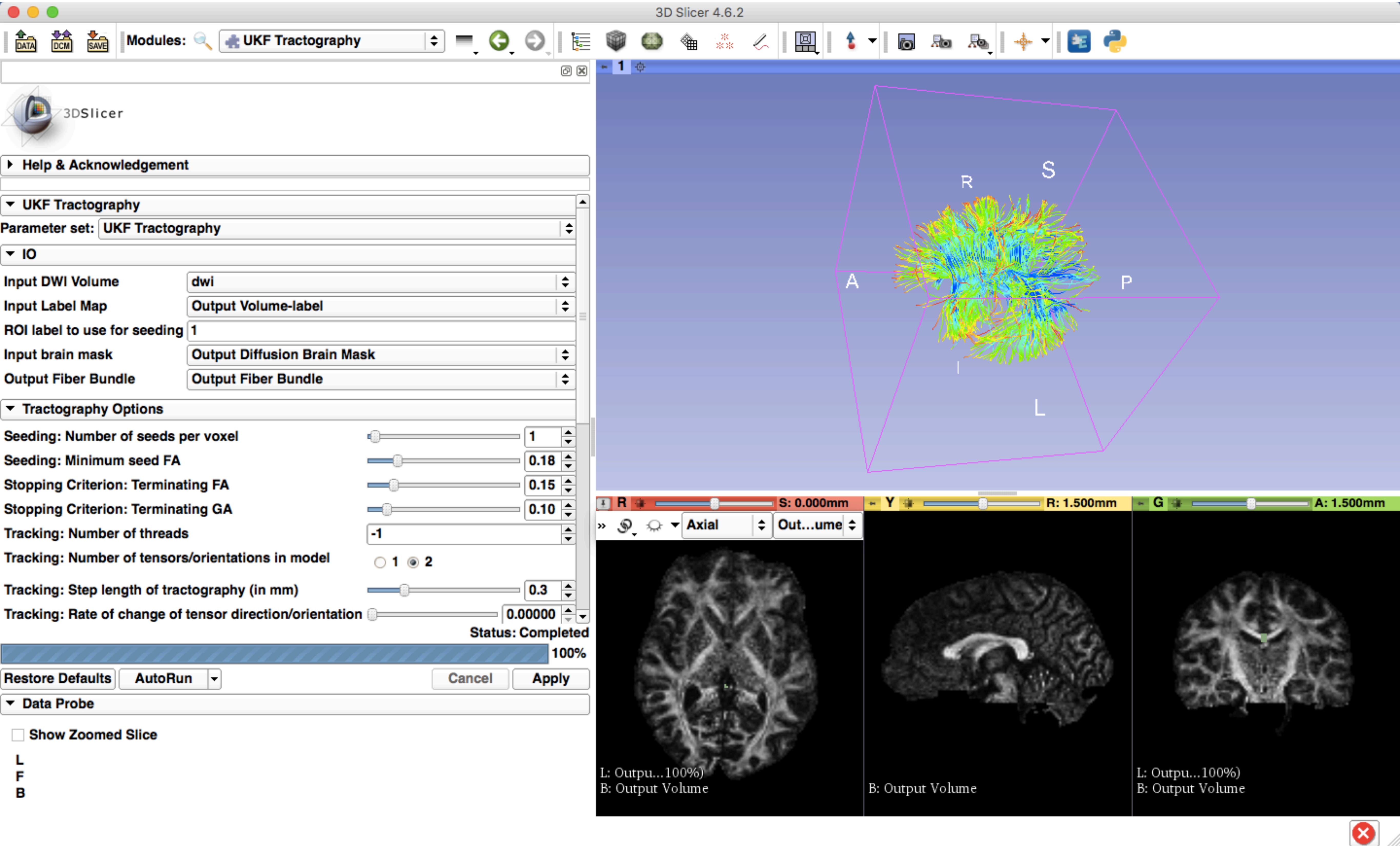
Status: Idle

find out more details at:

Documentation/Nightly/Modules/UKFTractography

Click Apply

Corpus Callosum



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

Tractography Options

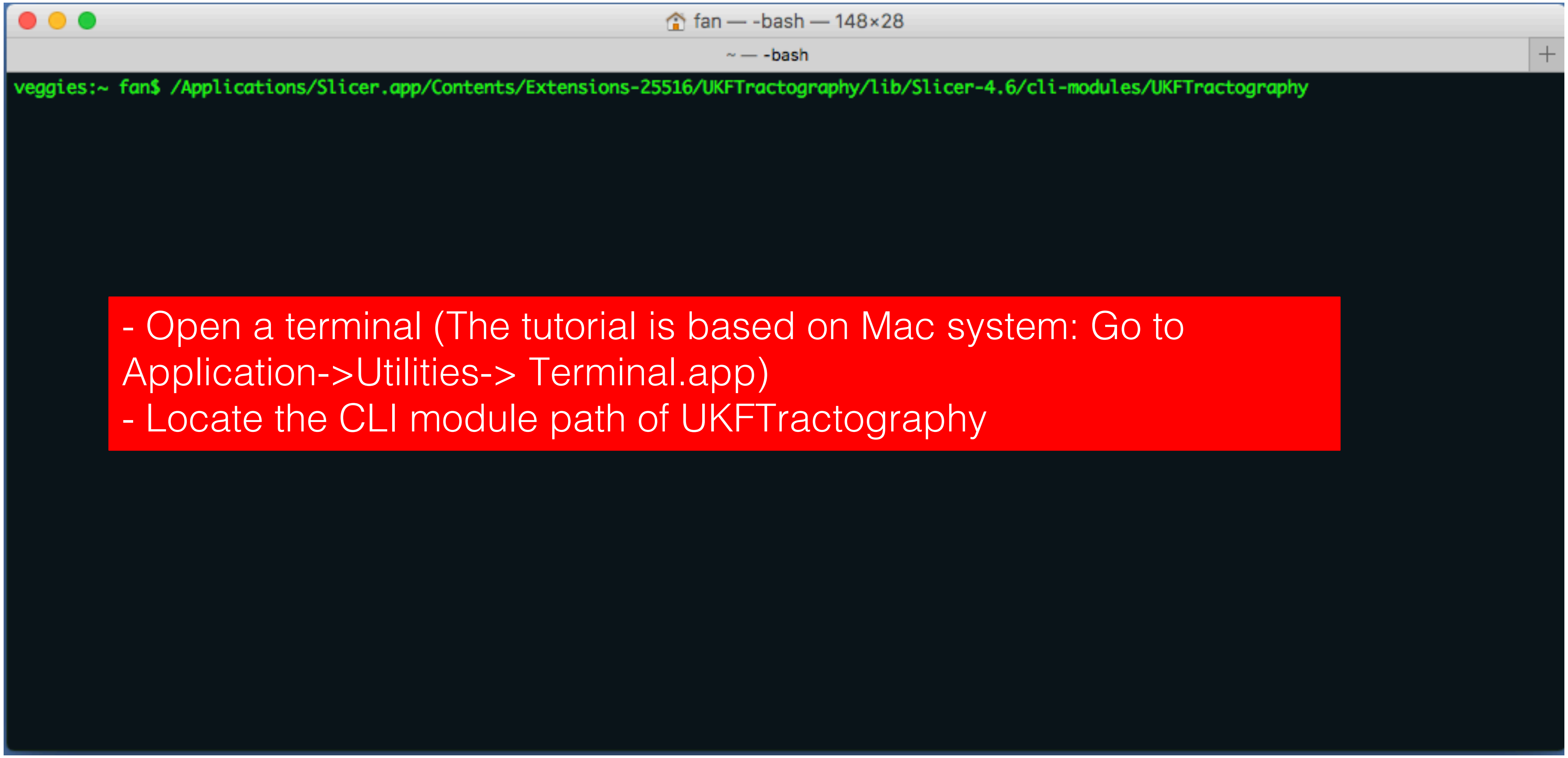
Seeding: Number of seeds per voxel	1
Seeding: Minimum seed FA	0.18
Stopping Criterion: Terminating FA	0.15
Stopping Criterion: Terminating GA	0.10
Tracking: Number of threads	-1
Tracking: Number of tensors/orientations in model	○ 1 ● 2
Tracking: Step length of tractography (in mm)	0.3
Tracking: Rate of change of tensor direction/orientation	0.00000

Status: Completed

100%

☐ Show Zoomed Slice

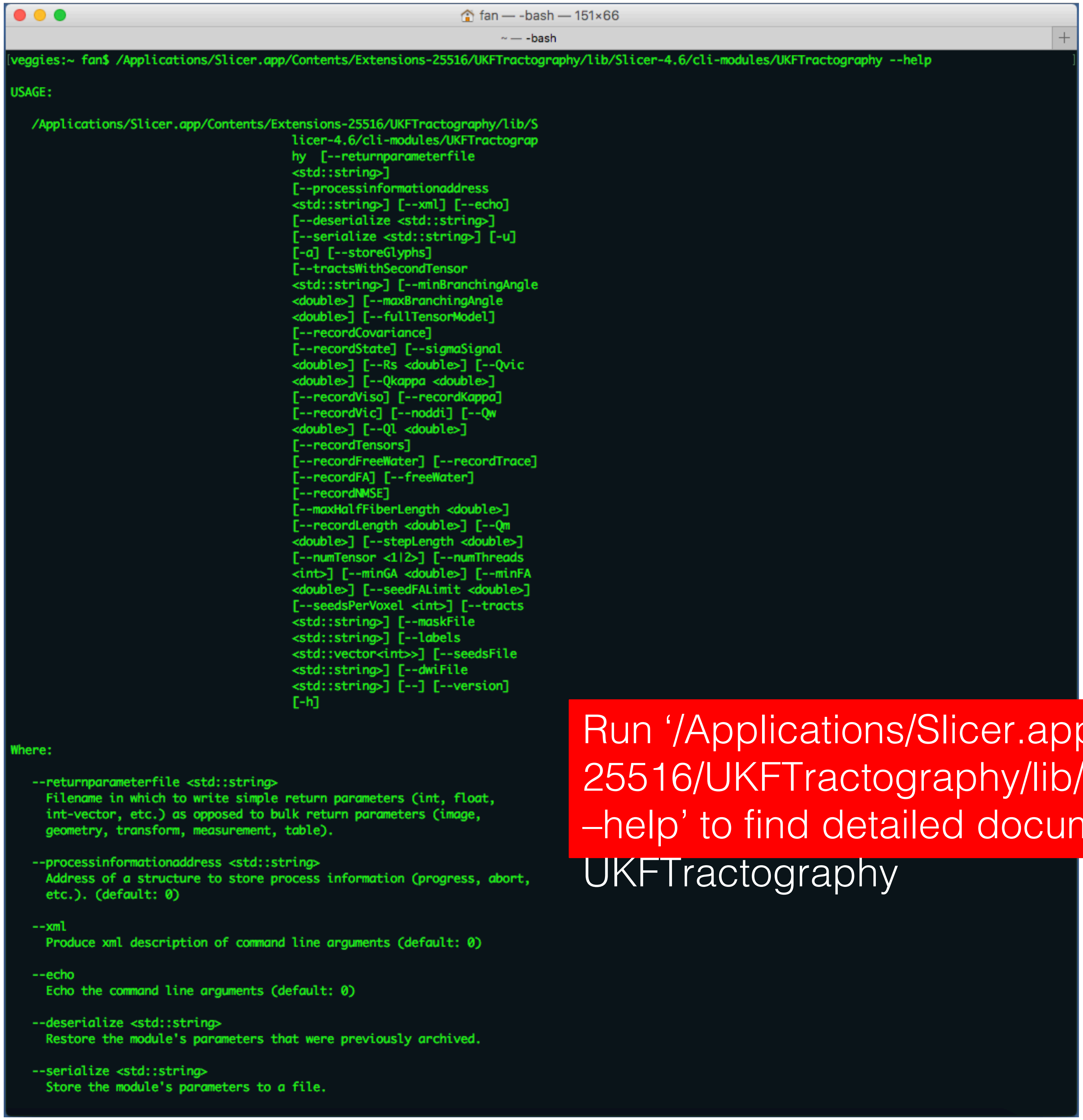
Run UKF Tractography in CLI



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

- Open a terminal (The tutorial is based on Mac system: Go to Application->Utilities-> Terminal.app)
- Locate the CLI module path of UKFTractography

Run UKF Tractography in CLI



```
[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/S
                                        licer-4.6/cli-modules/UKFTractograp
                                        hy  [--returnparameterfile
                                        <std::string>]
                                        [--processinformationaddress
                                        <std::string>] [--xml] [--echo]
                                        [--deserialize <std::string>]
                                        [--serialize <std::string>] [-u]
                                        [-a] [--storeGlyphs]
                                        [--tractsWithSecondTensor
                                        <std::string>] [--minBranchingAngle
                                        <double>] [--maxBranchingAngle
                                        <double>] [--fullTensorModel]
                                        [--recordCovariance]
                                        [--recordState] [--sigmaSignal
                                        <double>] [--Rs <double>] [--Qvic
                                        <double>] [--Qkappa <double>]
                                        [--recordViso] [--recordKappa]
                                        [--recordVic] [--noddi] [--Qw
                                        <double>] [--Ql <double>]
                                        [--recordTensors]
                                        [--recordFreeWater] [--recordTrace]
                                        [--recordFA] [--freeWater]
                                        [--recordNMSE]
                                        [--maxHalfFiberLength <double>]
                                        [--recordLength <double>] [--Qm
                                        <double>] [--stepLength <double>]
                                        [--numTensor <1|2>] [--numThreads
                                        <int>] [--minGA <double>] [--minFA
                                        <double>] [--seedFALimit <double>]
                                        [--seedsPerVoxel <int>] [--tracts
                                        <std::string>] [--maskFile
                                        <std::string>] [--labels
                                        <std::vector<int>>] [--seedsFile
                                        <std::string>] [--dwiFile
                                        <std::string>] [--] [--version]
                                        [-h]


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

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

Neuroimage Analysis Center (NAC)
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Surgical Planning laboratory (SPL)
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Psychiatry Neuroimaging Laboratory (PNL)
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