



Diffusion MRI Analysis

Sonia Pujol, Ph.D.

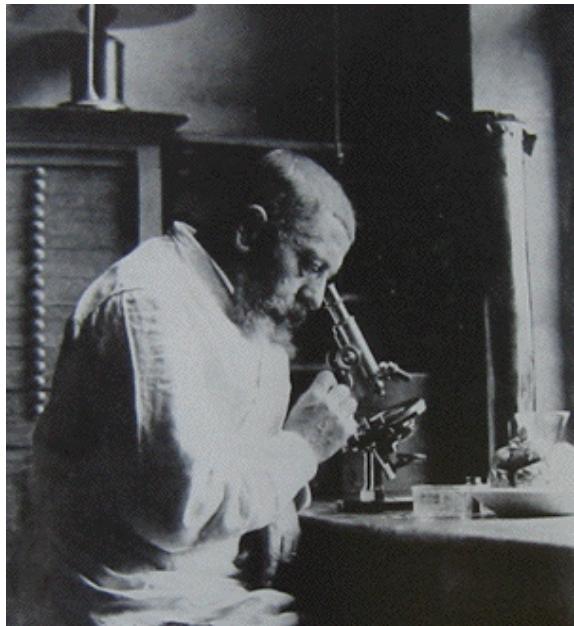
Surgical Planning Laboratory
Harvard University

Brain Anatomy



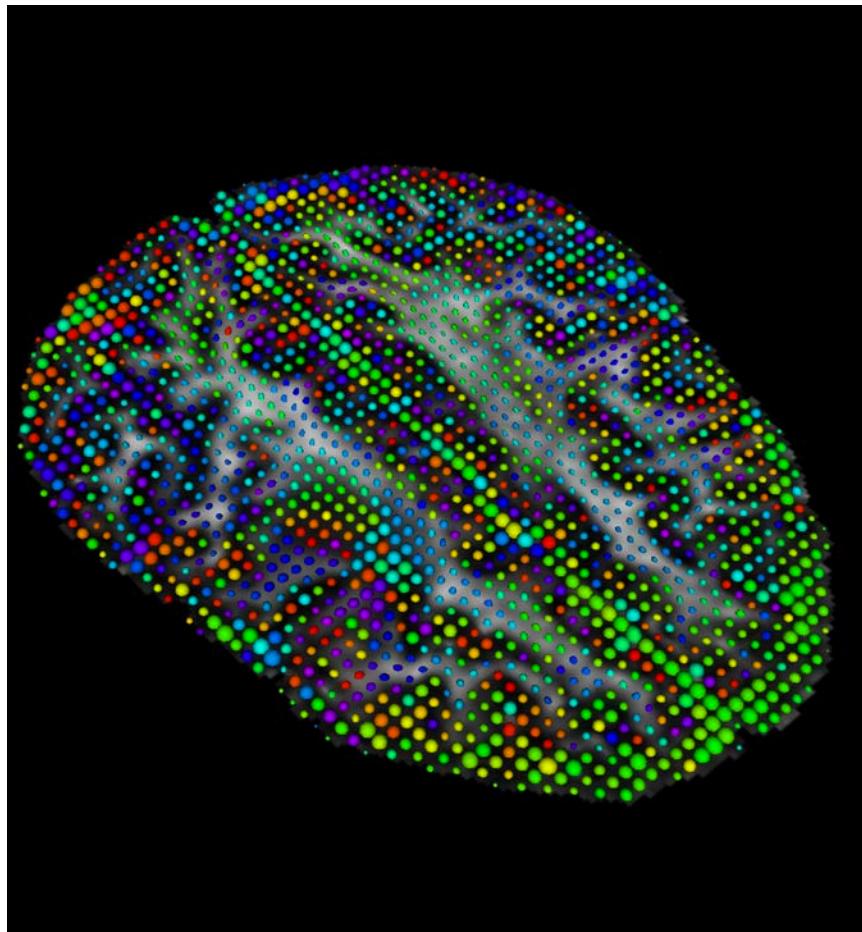
- White matter ~45% of the brain
- Myelinated nerve fibers (~ 10 µm axon diameter)

White Matter Exploration



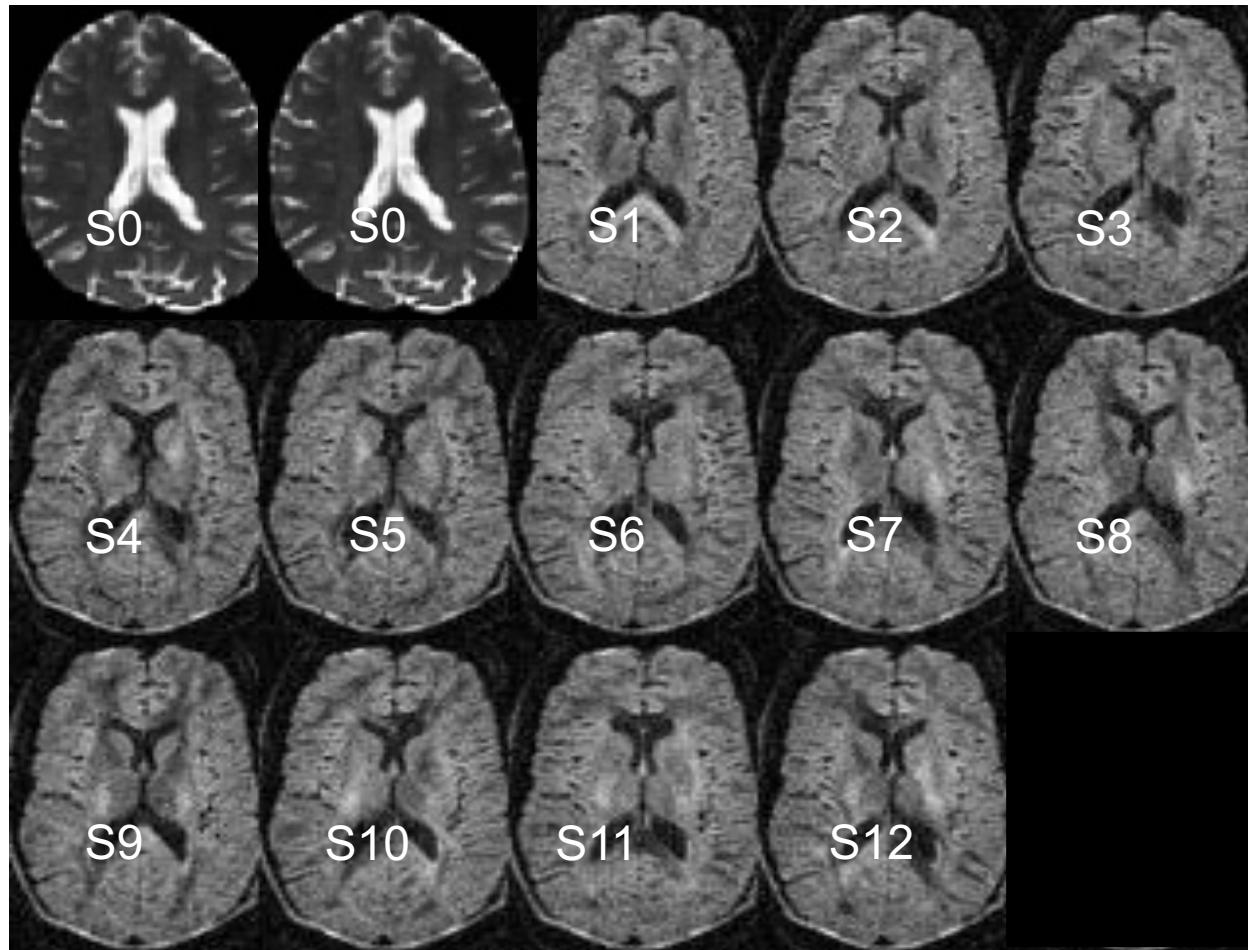
Jules Joseph Dejerine
*(Anatomie des centres
nerveux* (Paris, 1890-1901):
Atlas of Neuroanatomy based
on myelin stained preparation

Diffusion Tensor Imaging (DTI)



- First non-invasive window on white matter anatomy
- Measurement of the motion of water molecules using MRI techniques.
- Three-dimensional reconstruction of the trajectory of white matter bundles

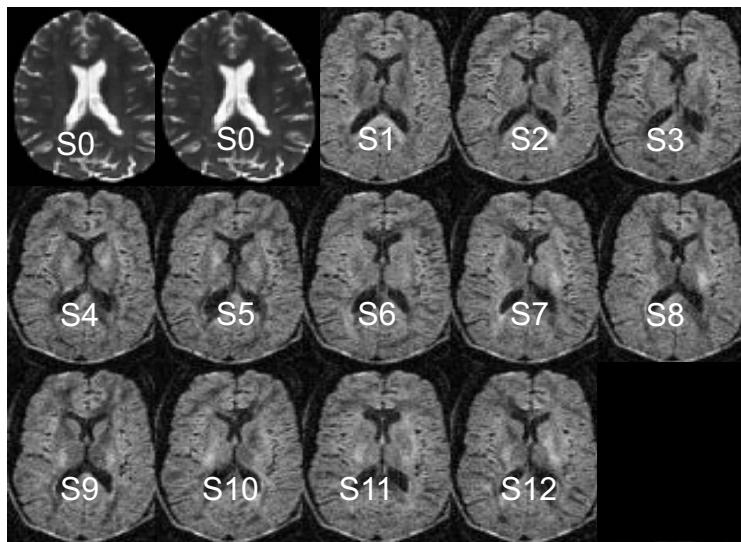
Diffusion Weighted Imaging (DWI)



In this example, the DWI scan was acquired with 12 diffusion sensitizing gradient directions (S1-S12) and 2 non-diffusion sensitizing gradients (S0)

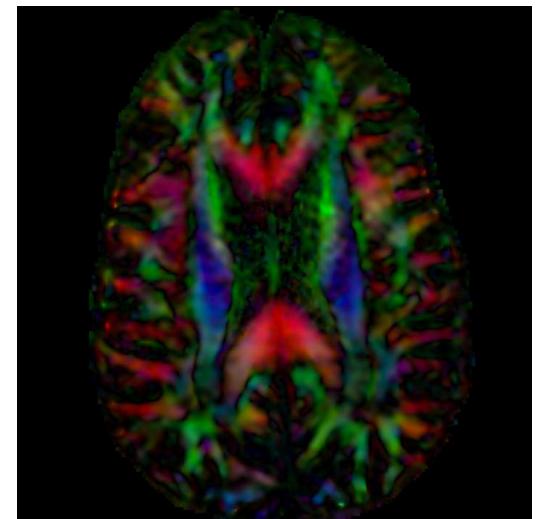
From DWI to DTI

DWI



DWI dataset acquired with
12 gradient and 2 baseline

DTI



DTI dataset

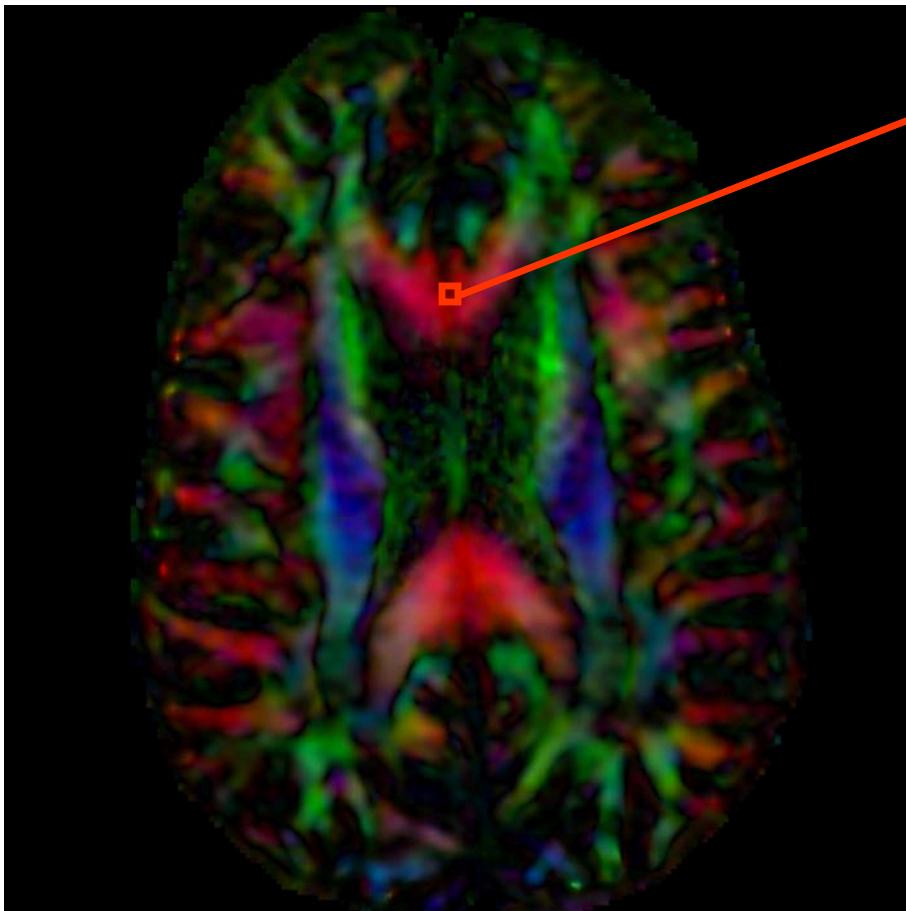


$$S_i = S_0 e^{-b \hat{g}^T \underline{D} \hat{g}_i}$$

Stejskal-Tanner (1965)

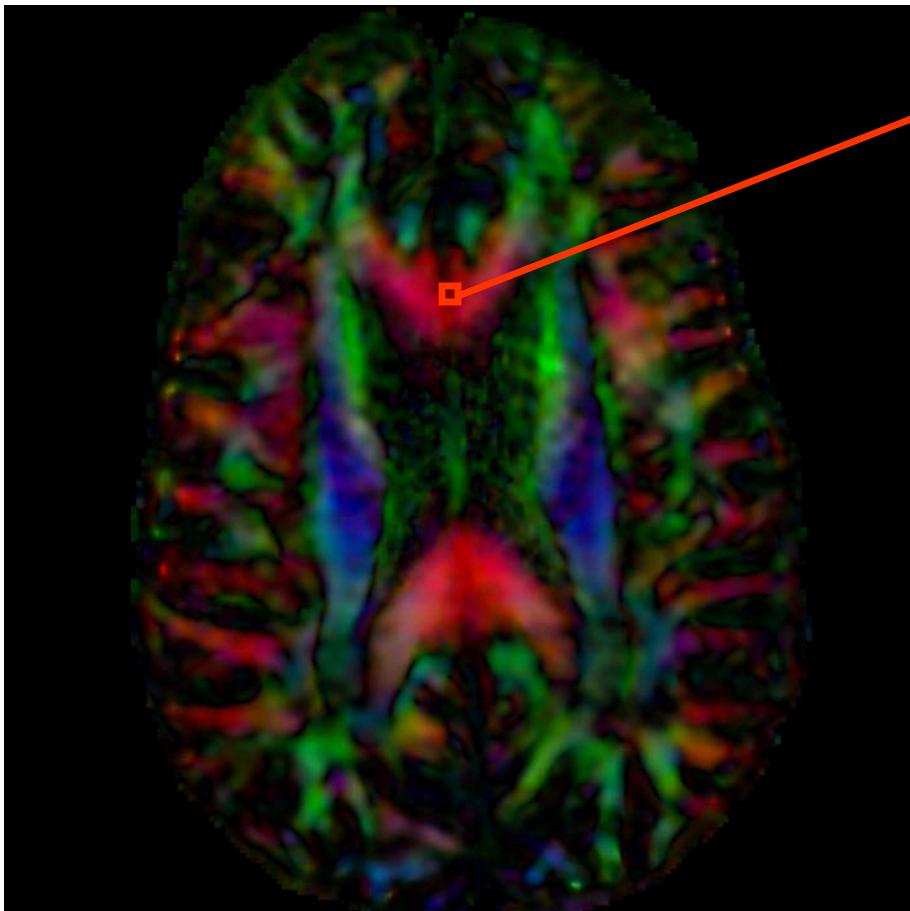
*S_i: DWI volume acquired with
ith gradient
S₀: Baseline volume*

Diffusion Tensor Imaging



$$S_i = S_0 e^{-b \hat{g}_i^T \underline{D} \hat{g}_i}$$

Diffusion Tensor Imaging

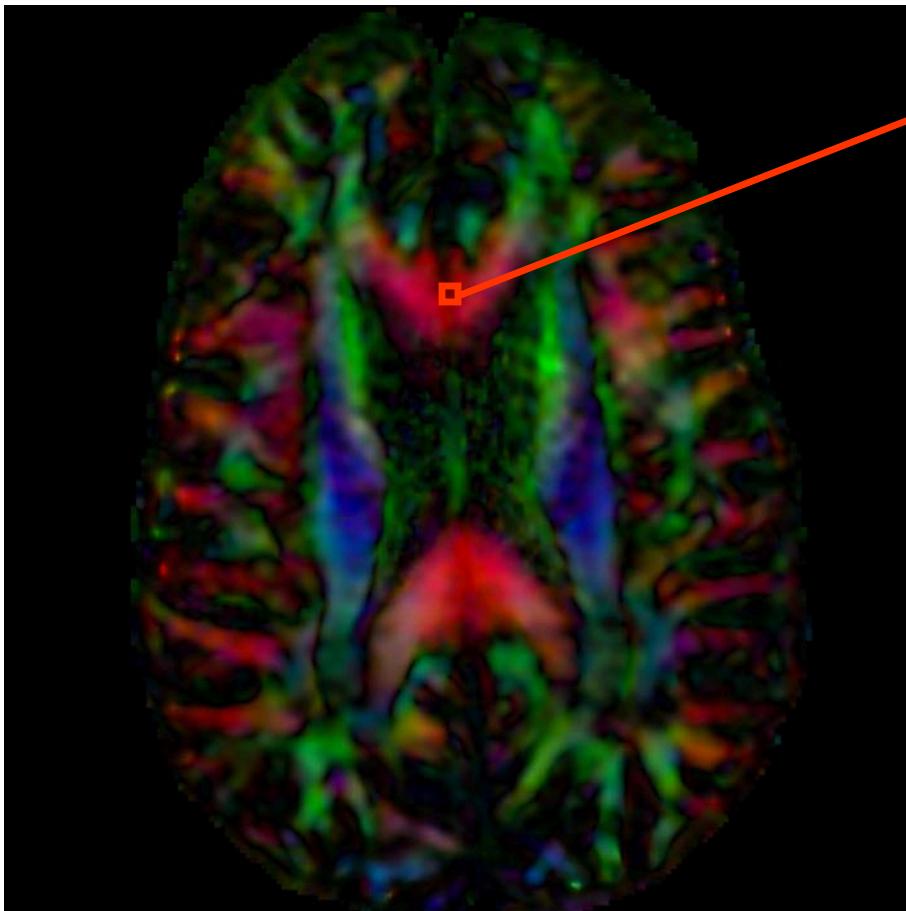


$$S_i = S_0 e^{-b \hat{g}_i^T \underline{D} \hat{g}_i}$$

↓

$$\underline{D} = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{bmatrix}$$

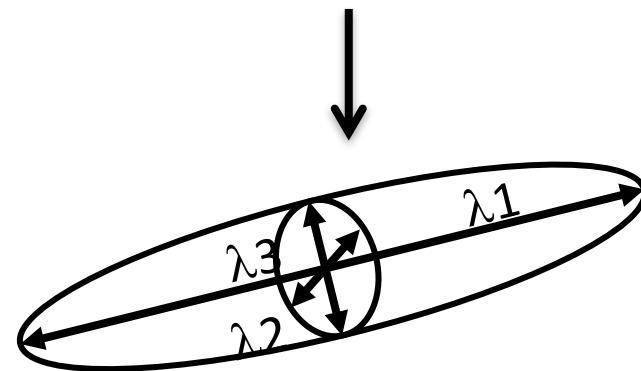
Diffusion Tensor Imaging



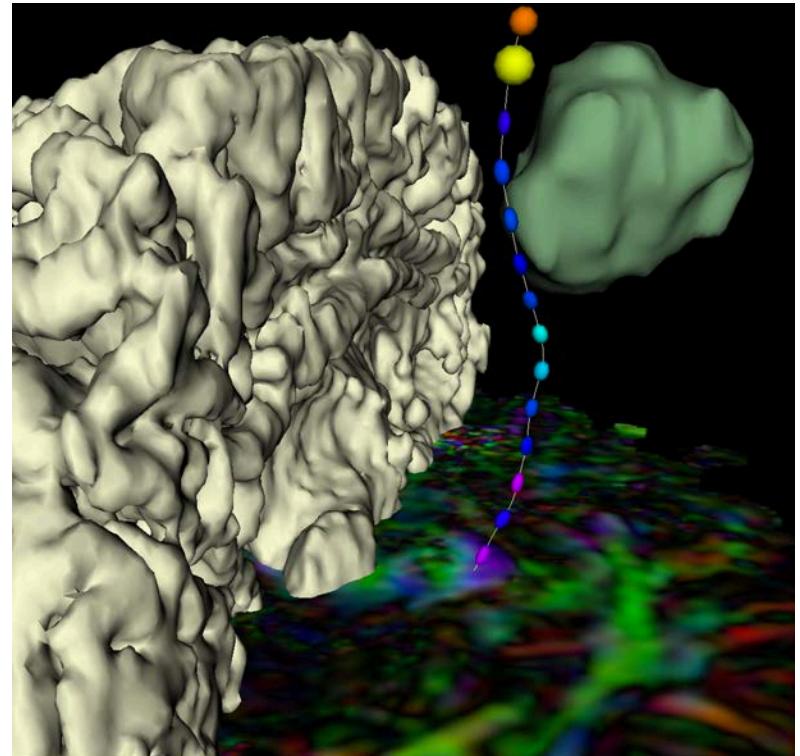
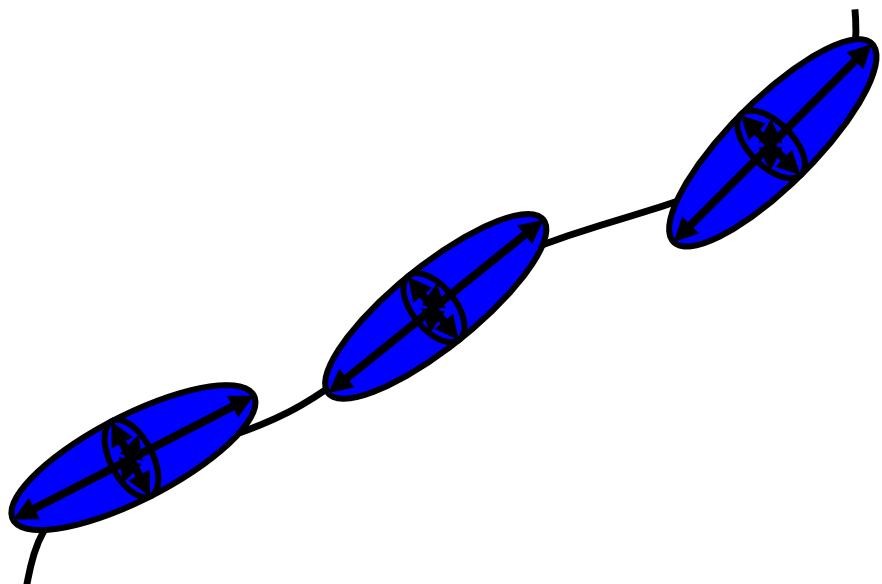
$$S_i = S_0 e^{-b \hat{g}^T \underline{D} \hat{g}_i}$$

↓

$$\underline{D} = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{bmatrix}$$

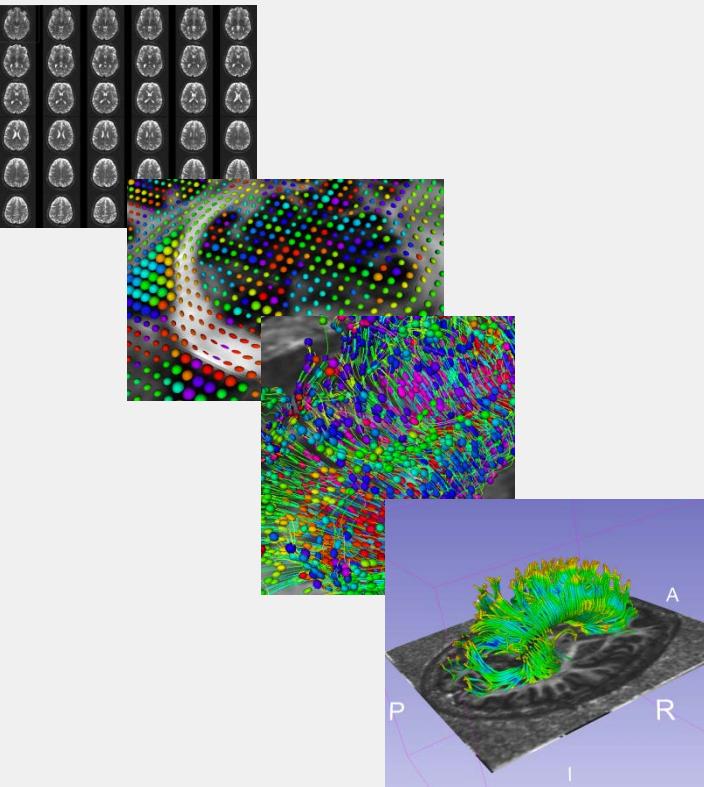


Tractography



DTI tractography provides 3D reconstruction of the trajectory of white matter pathways

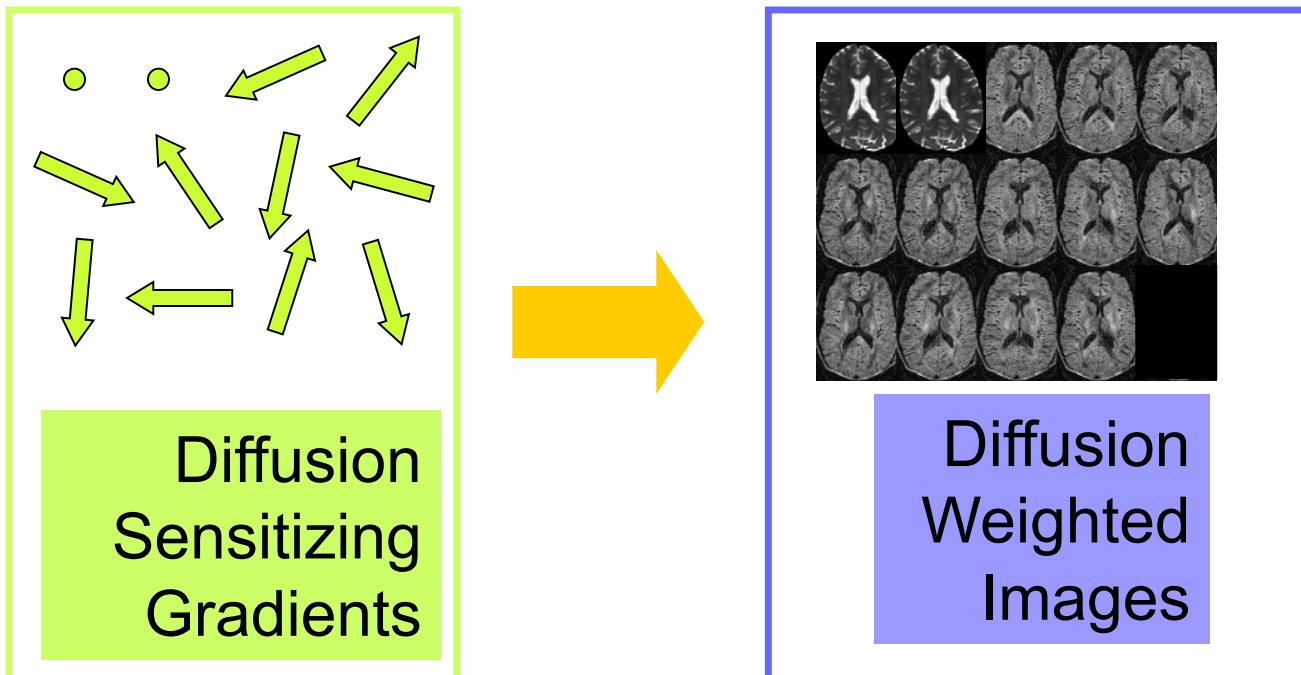
Tutorial Outline



This tutorial is an introduction to the fundamentals of Diffusion MRI analysis, from the estimation of diffusion tensors to the interactive 3D visualization of fiber tracts.

Tutorial Dataset

The tutorial dataset SlicerDiffusionMRITutorialData is a Diffusion Weighted MR scan of the brain acquired with 41 gradient directions and one baseline.



3D Slicer

The tutorial uses the 3D Slicer (Version 4.8.1, revision 26813, Stable Release) software available at:

<http://download.slicer.org>

Disclaimer

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.

SlicerDMRI

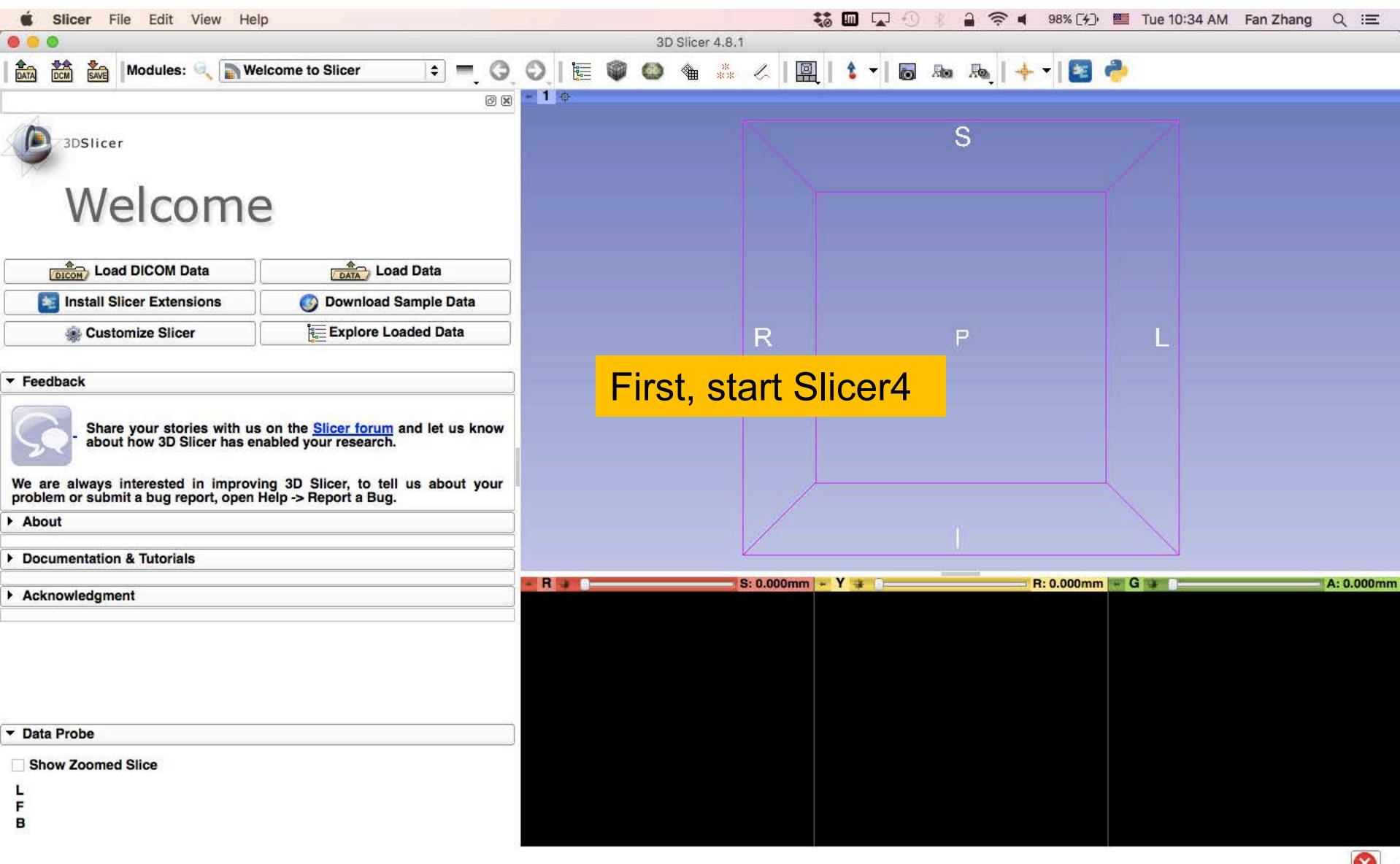
An open-source project to improve and extend diffusion magnetic resonance imaging software in 3D Slicer:

<http://dmri.slicer.org>

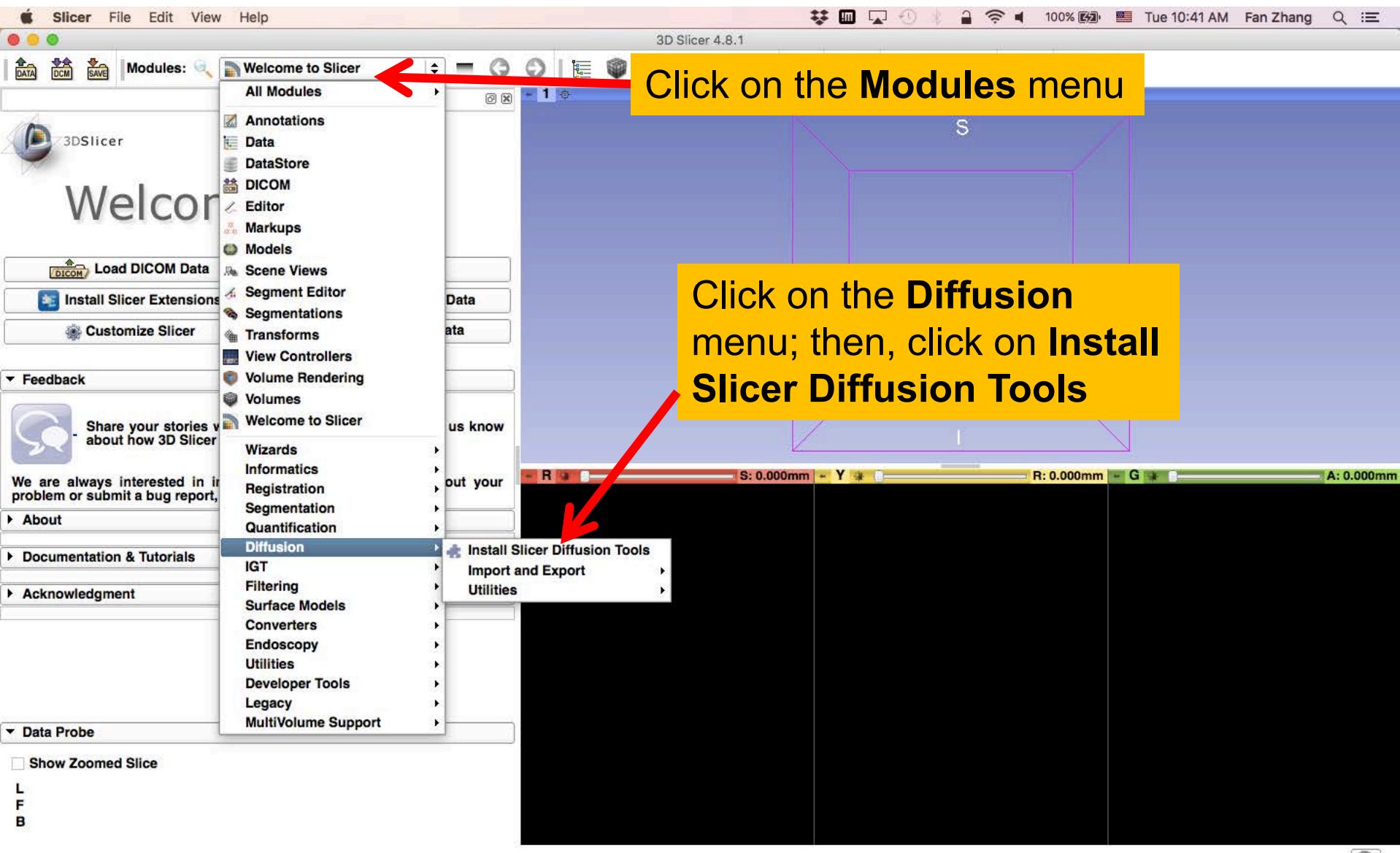
Disclaimer

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.

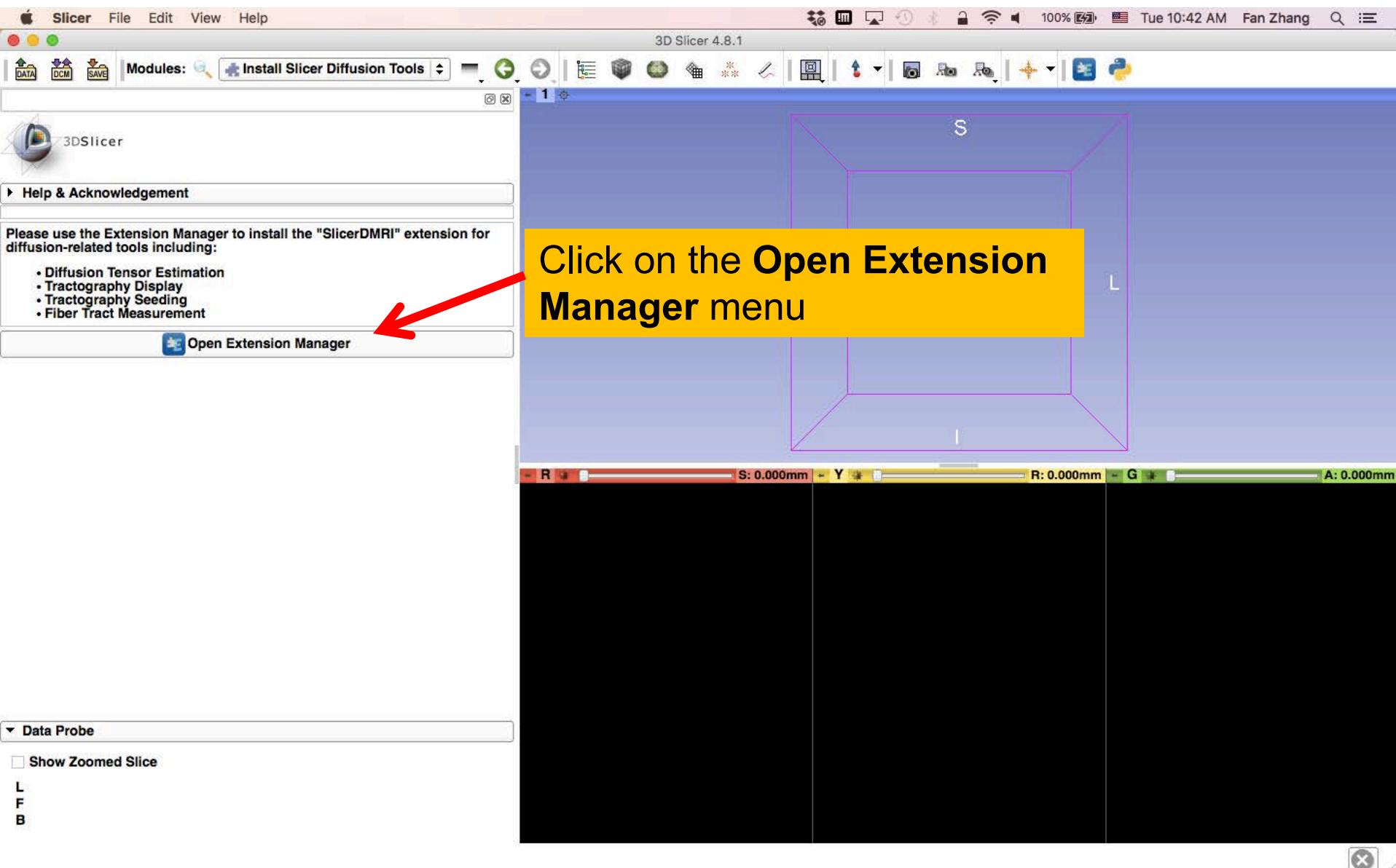
Install SlicerDMRI



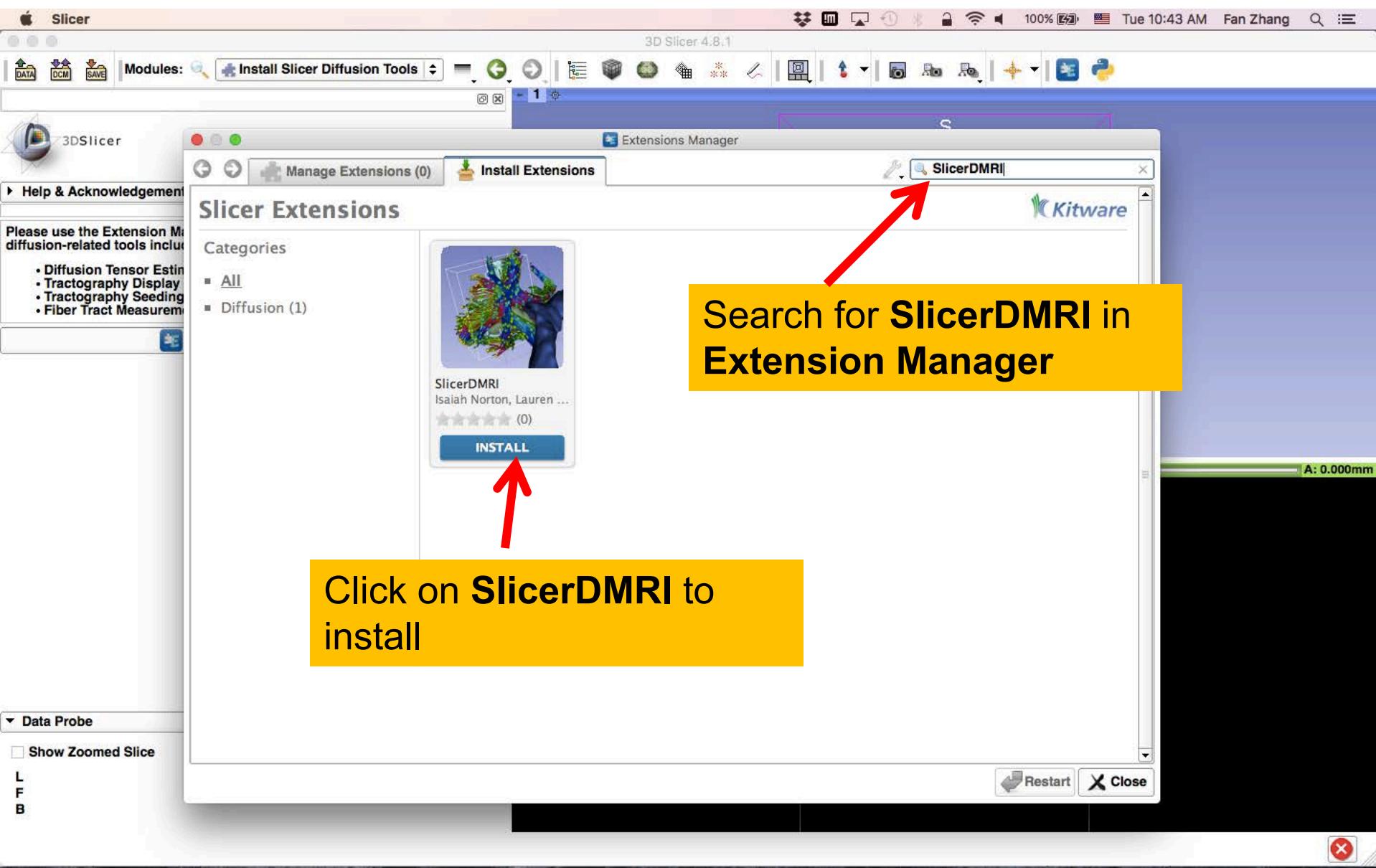
Install SlicerDMRI



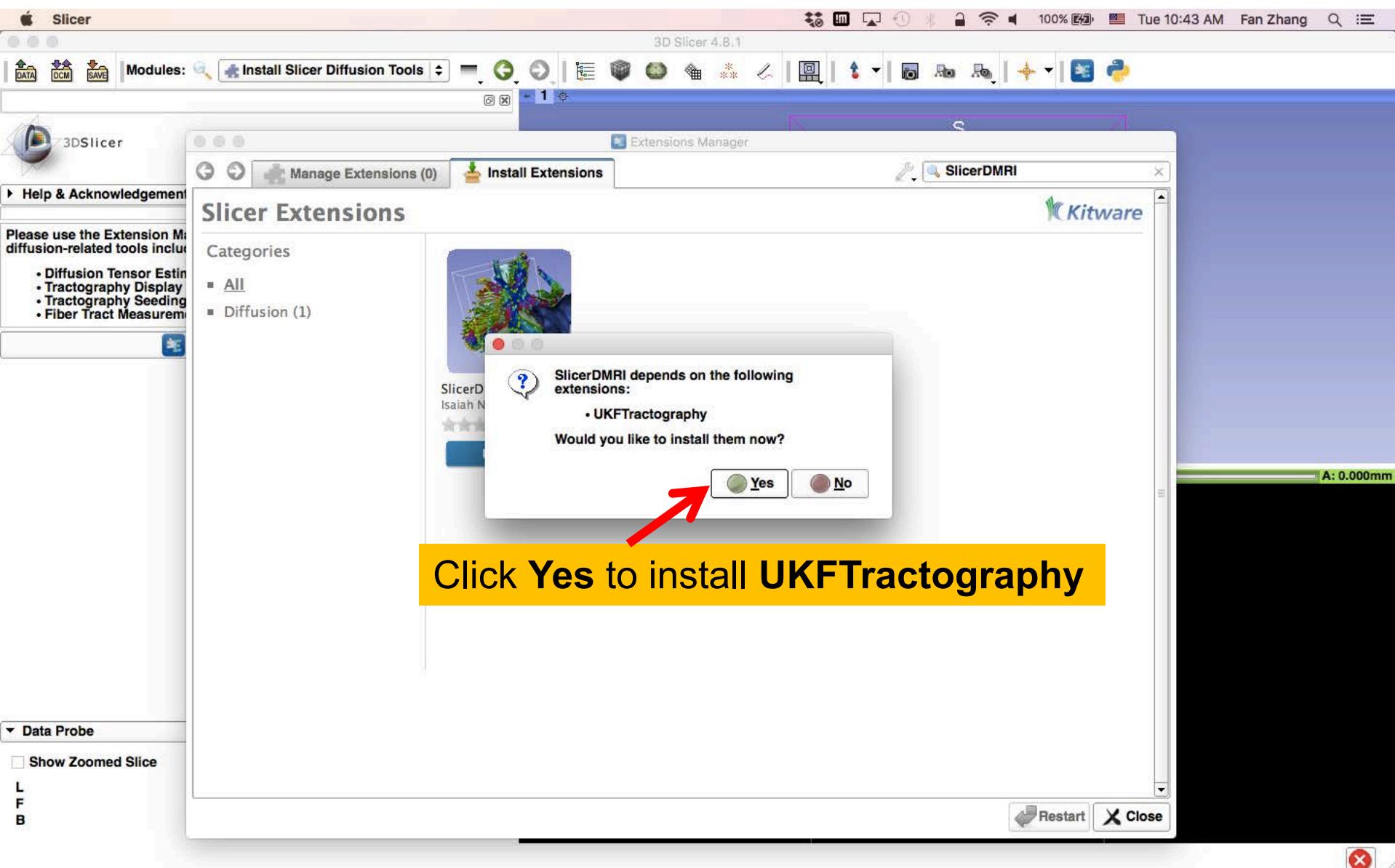
Install SlicerDMRI



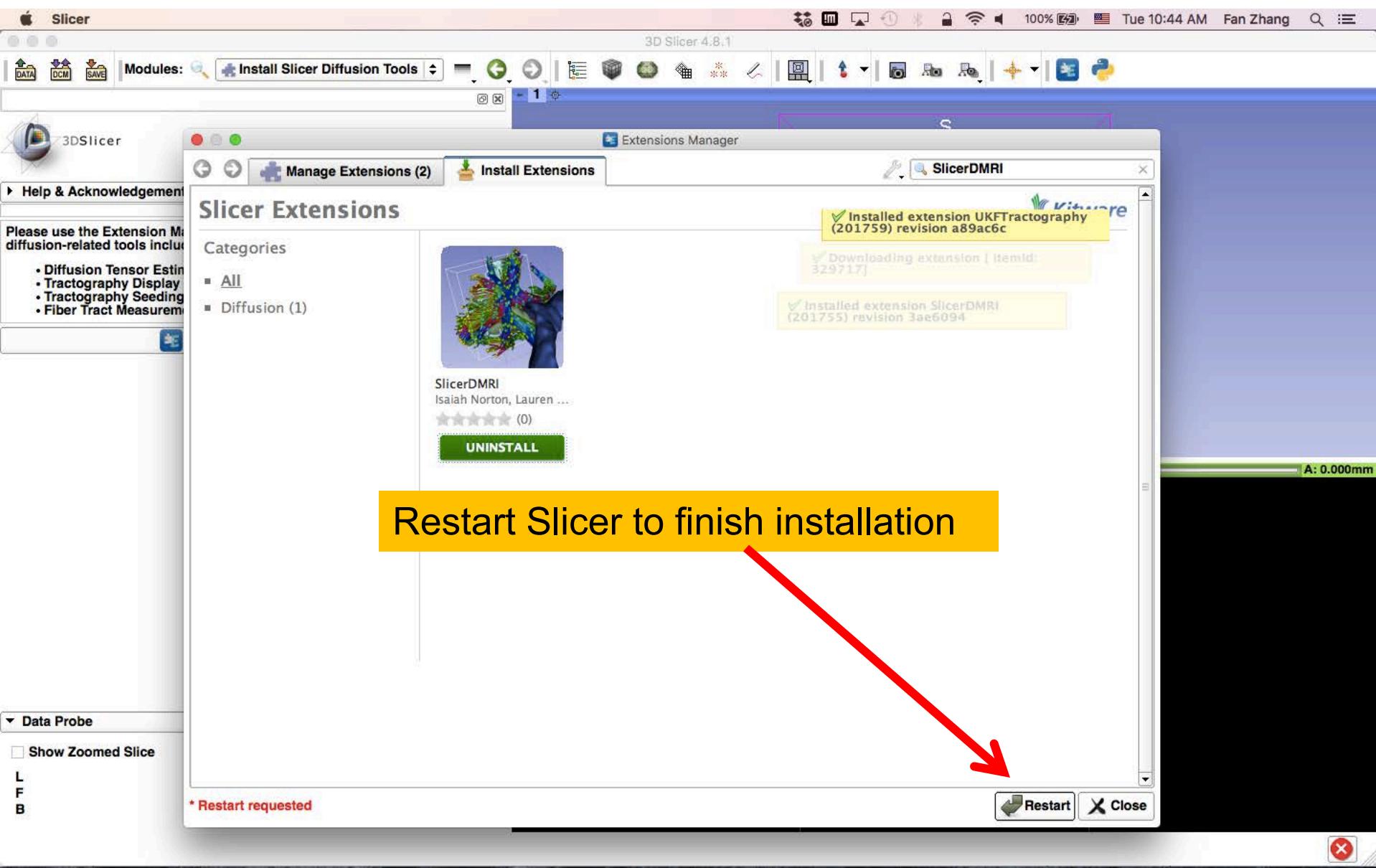
Install SlicerDMRI



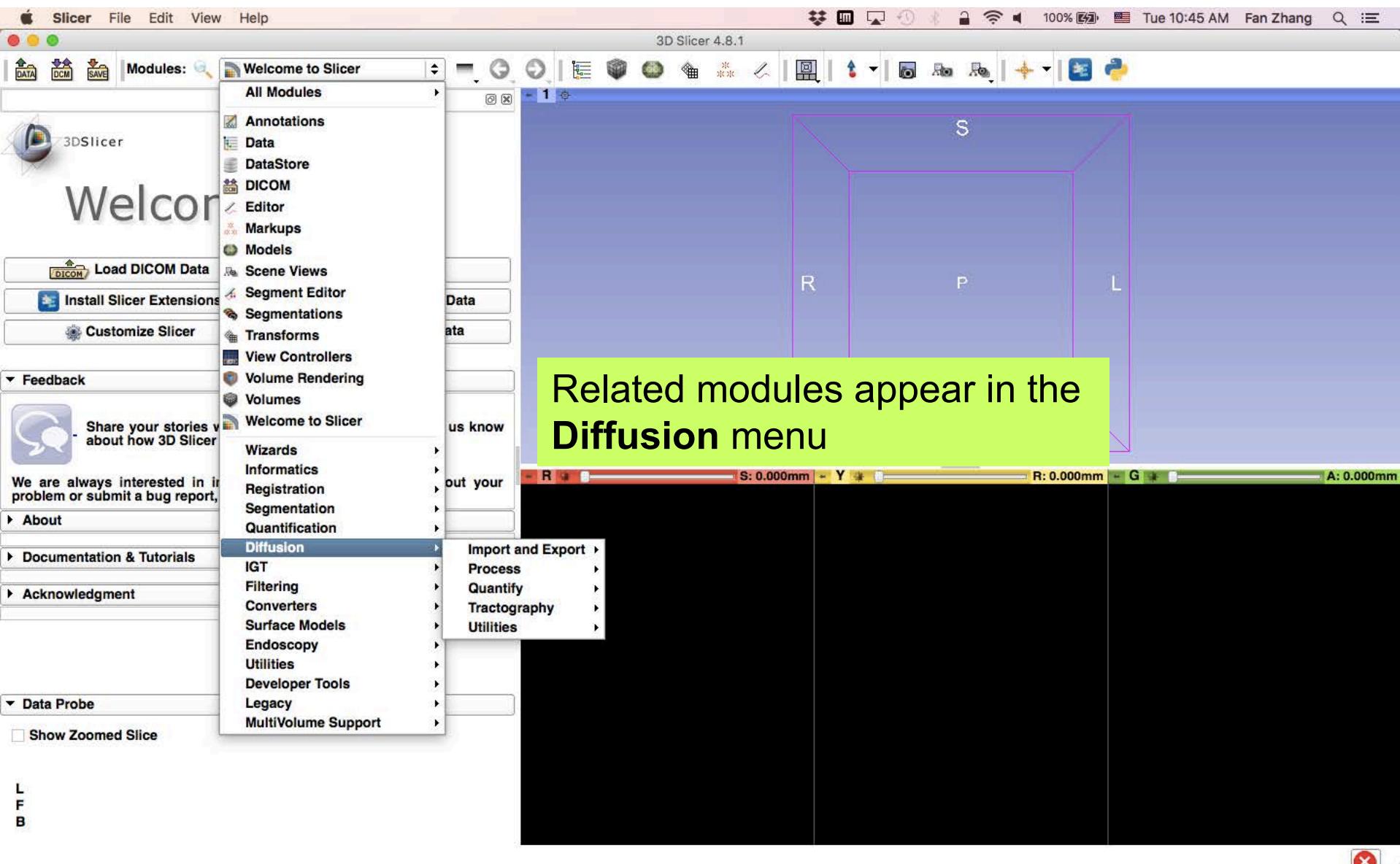
Install SlicerDMRI



Install SlicerDMRI



Install SlicerDMRI

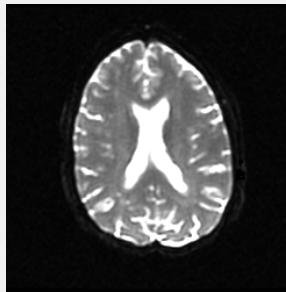


Learning Objectives

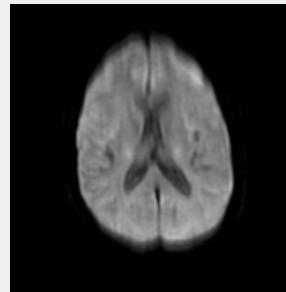
Following this tutorial, you'll be able to

- 1) Estimate a tensor volume from a set of Diffusion Weighted Images
- 2) Understand the shape and size of the diffusion ellipsoid
- 3) Reconstruct DTI tracts from a pre-defined region of interest
- 4) Interactively visualize DTI tracts seeded from a fiducial

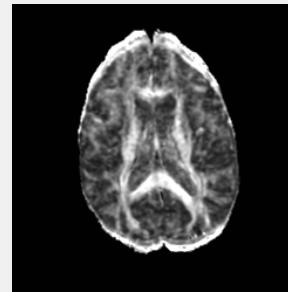
MR Diffusion Analysis Pipeline



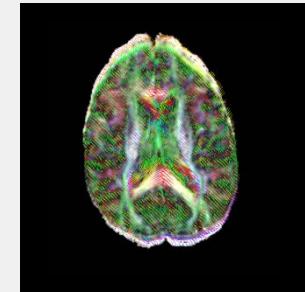
DWI
Acquisition



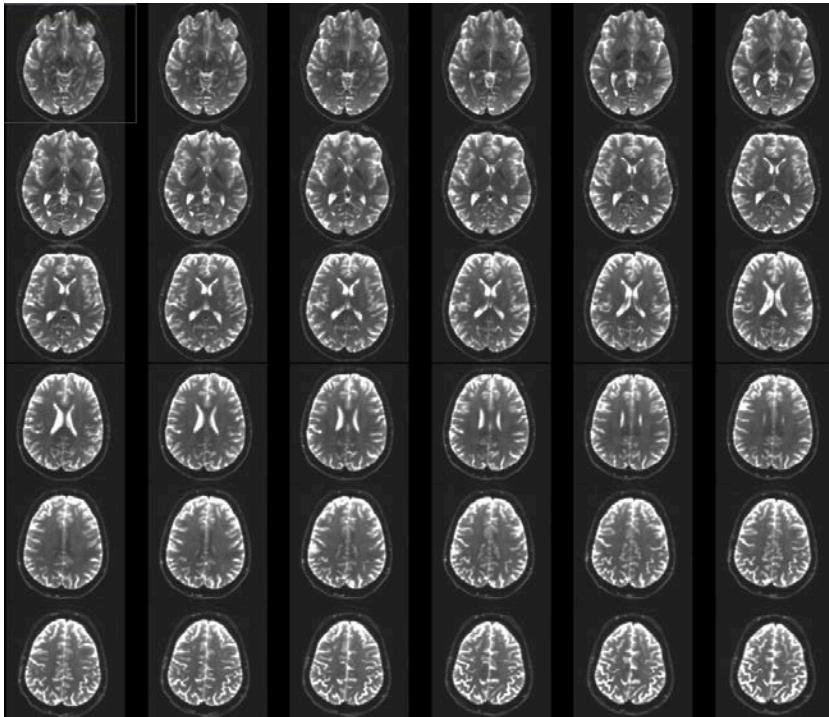
Tensor
Calculation



Scalar
Maps



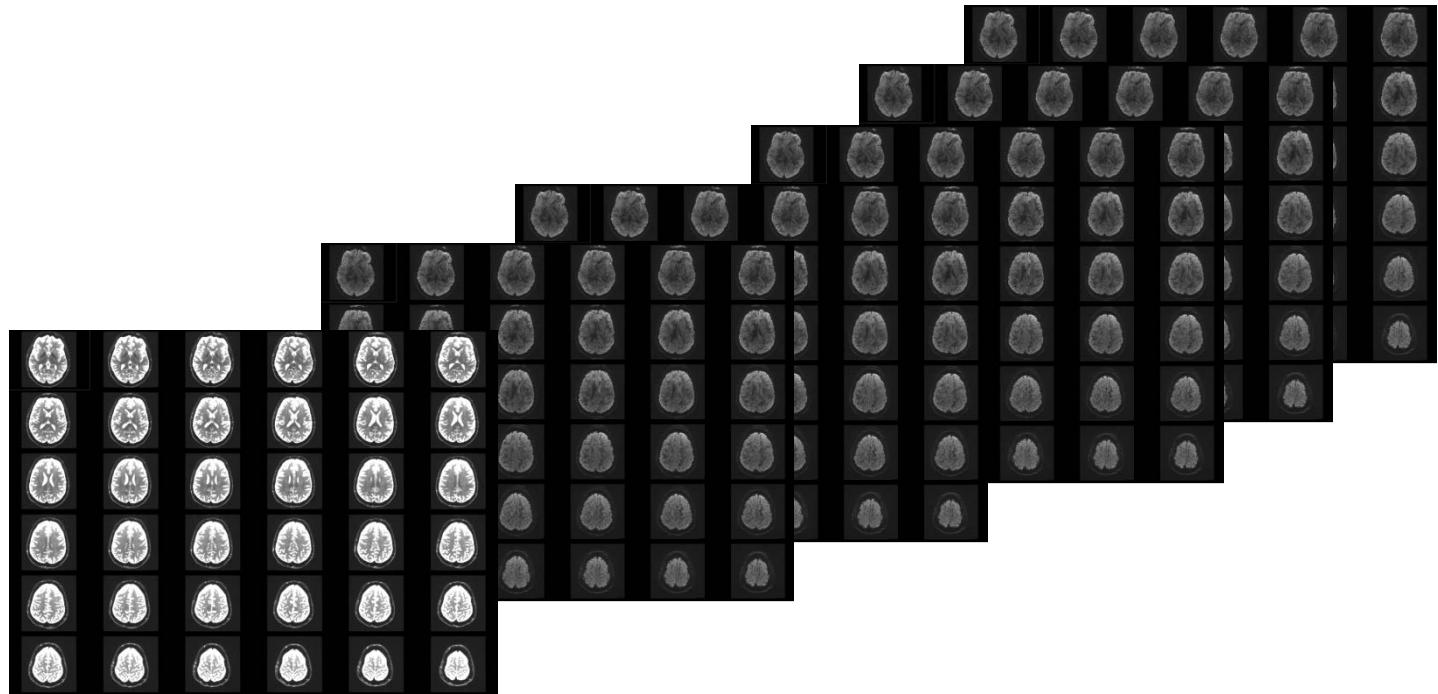
3D
Visualization



Part 1:

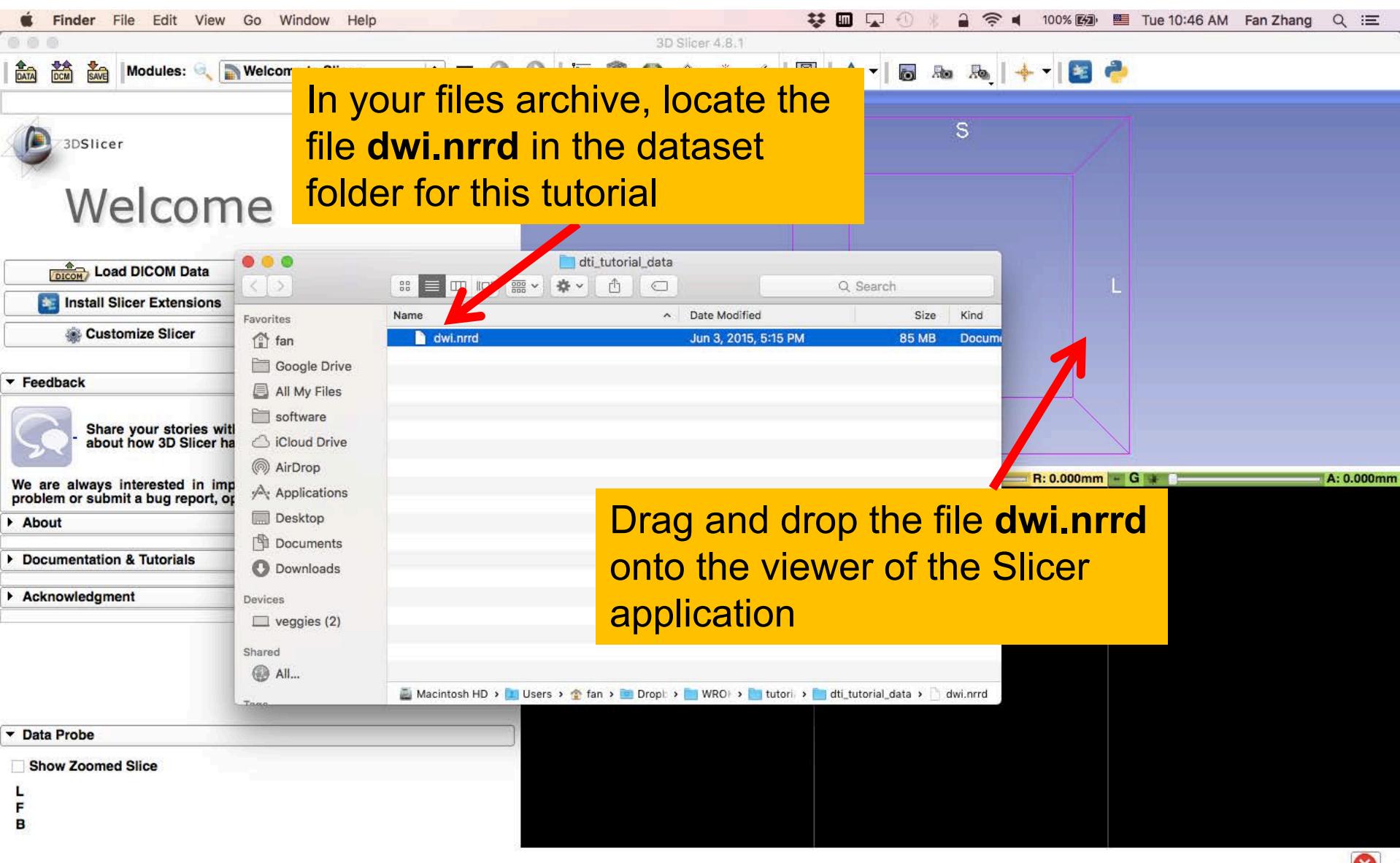
From DWI images to Tensors

Understanding the DWI Dataset

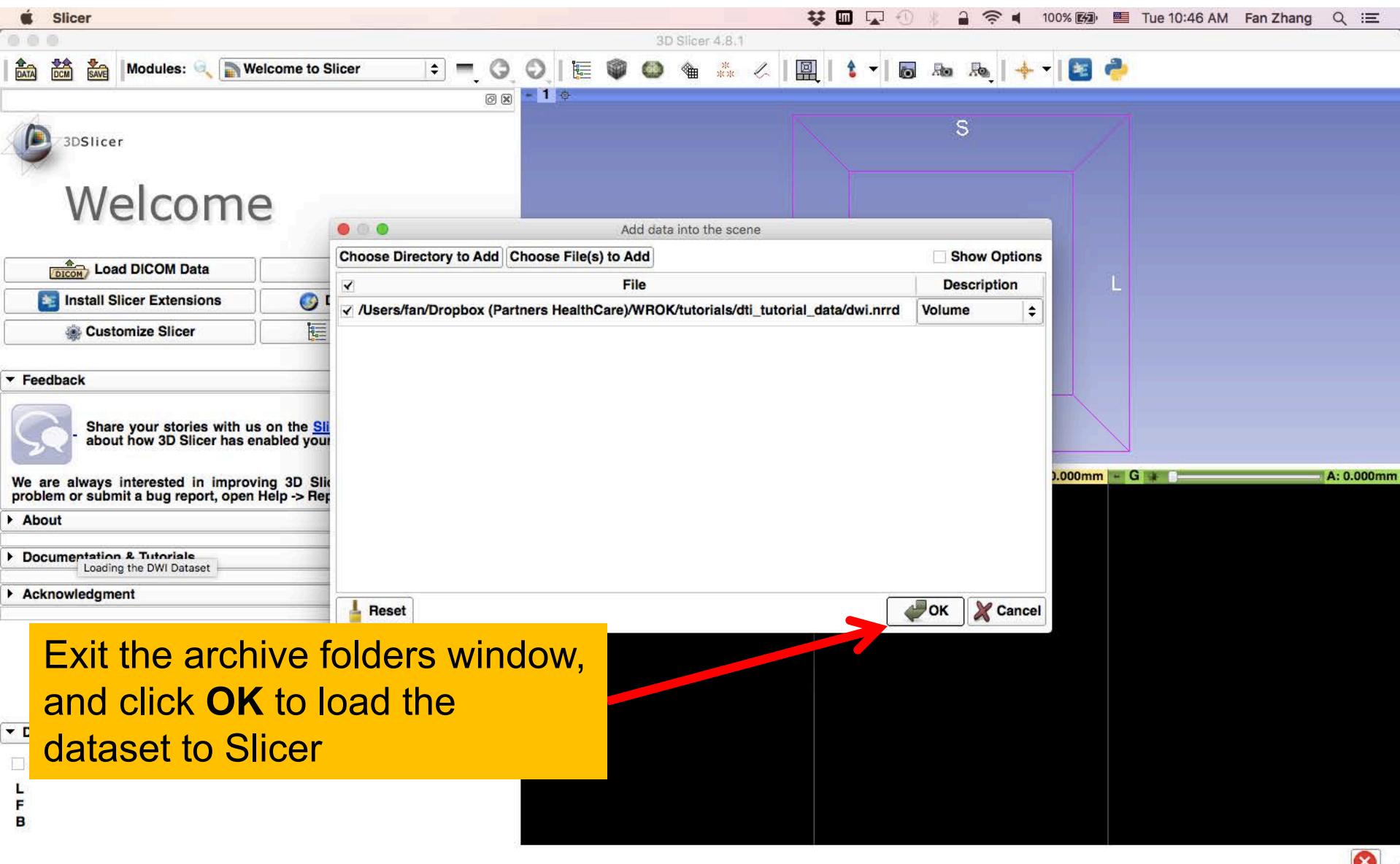


The Diffusion Weighted Imaging (DWI) dataset is composed of 41 volumes acquired with 41 different diffusion-sensitizing gradient directions, and one baseline image acquired without diffusion weighting.

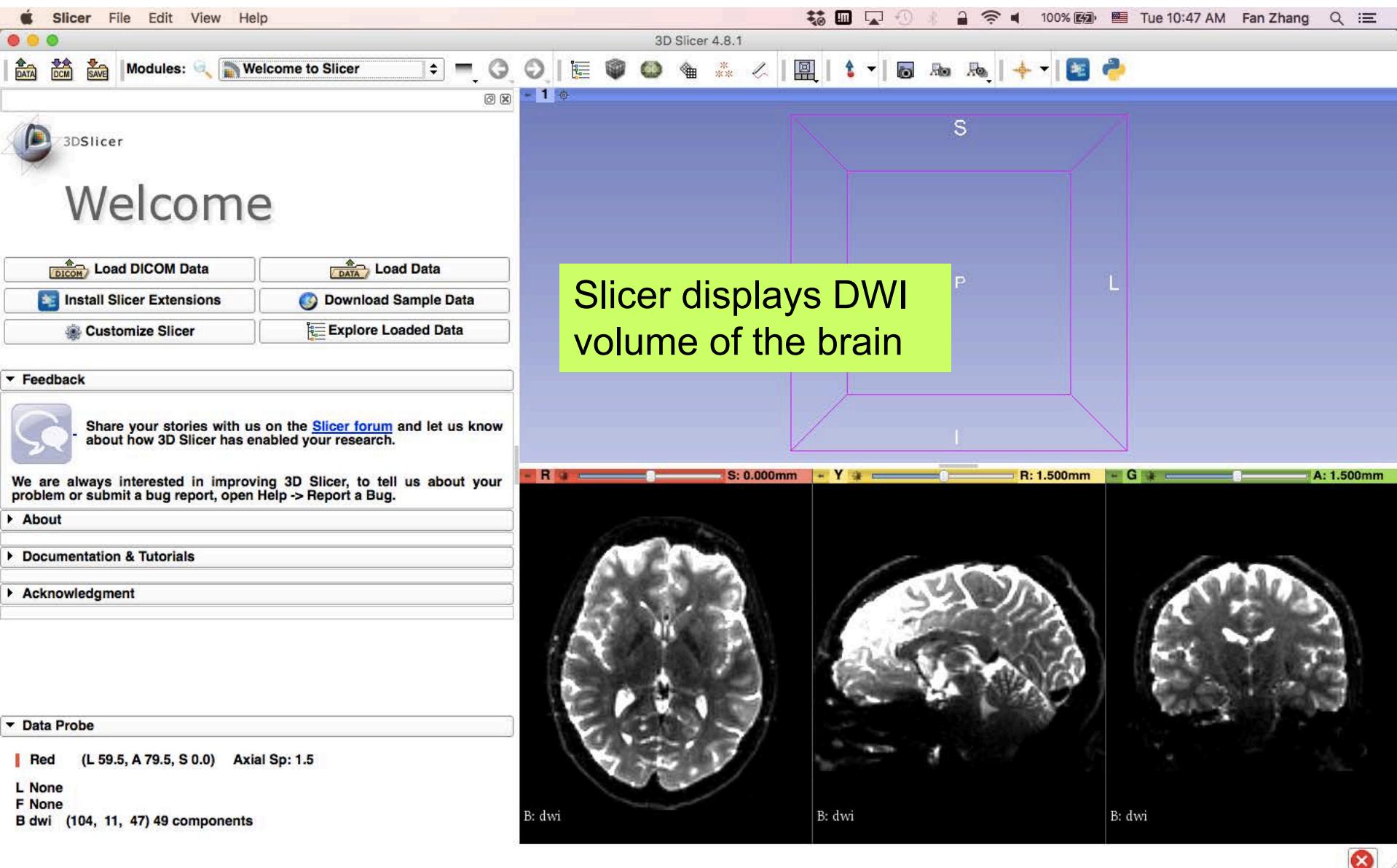
Loading the DWI Dataset



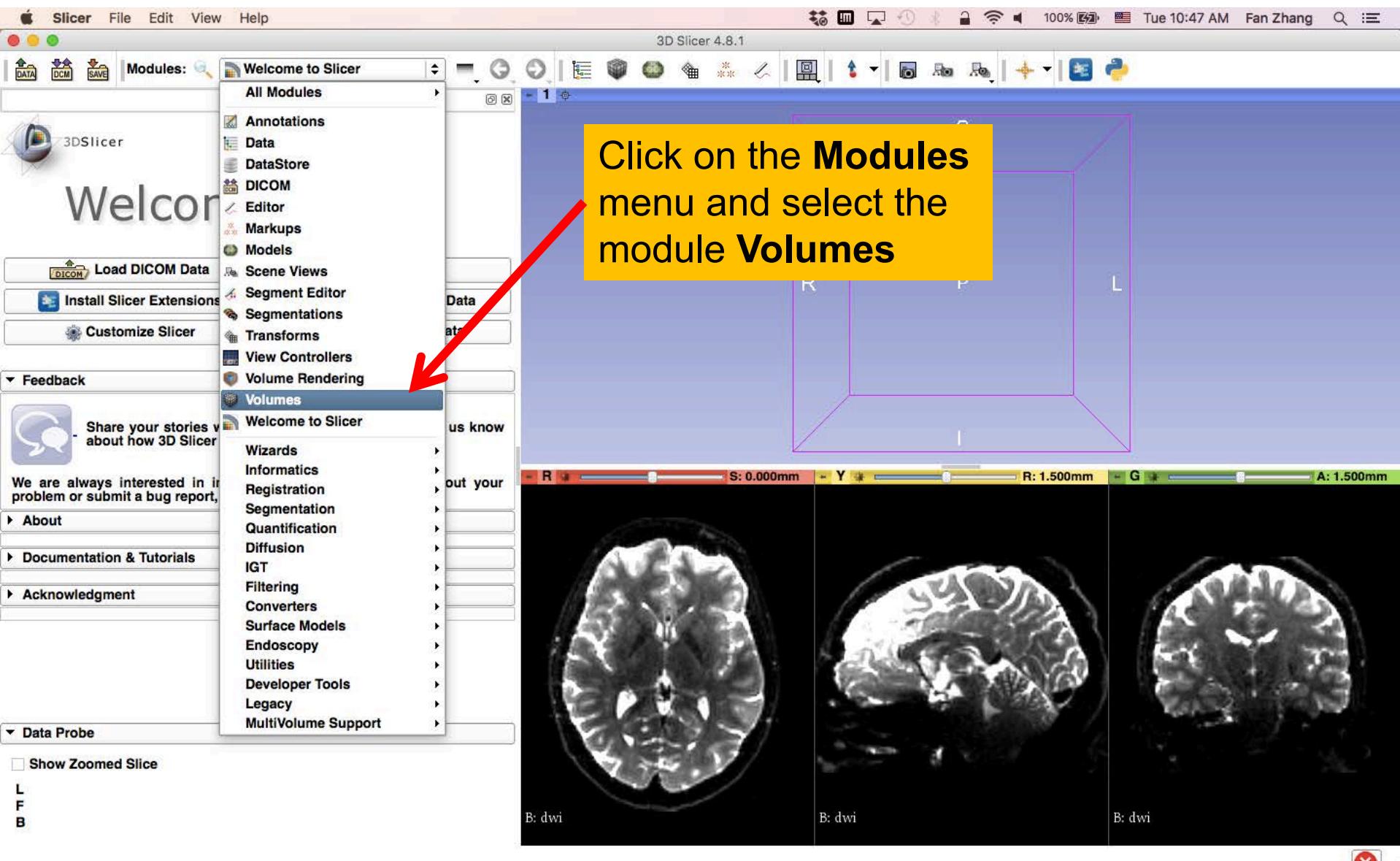
Loading the DWI Dataset



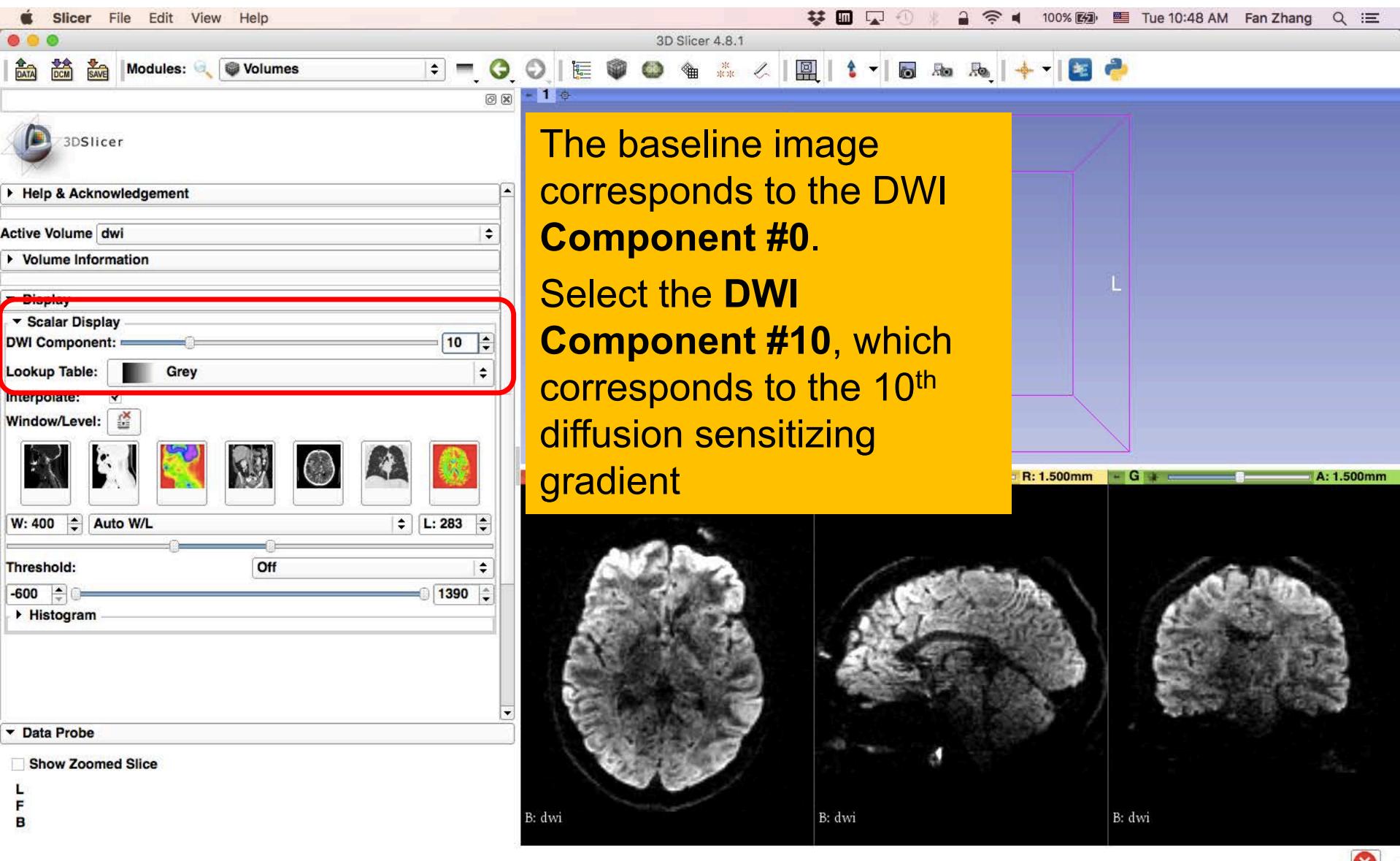
Loading the DWI Dataset



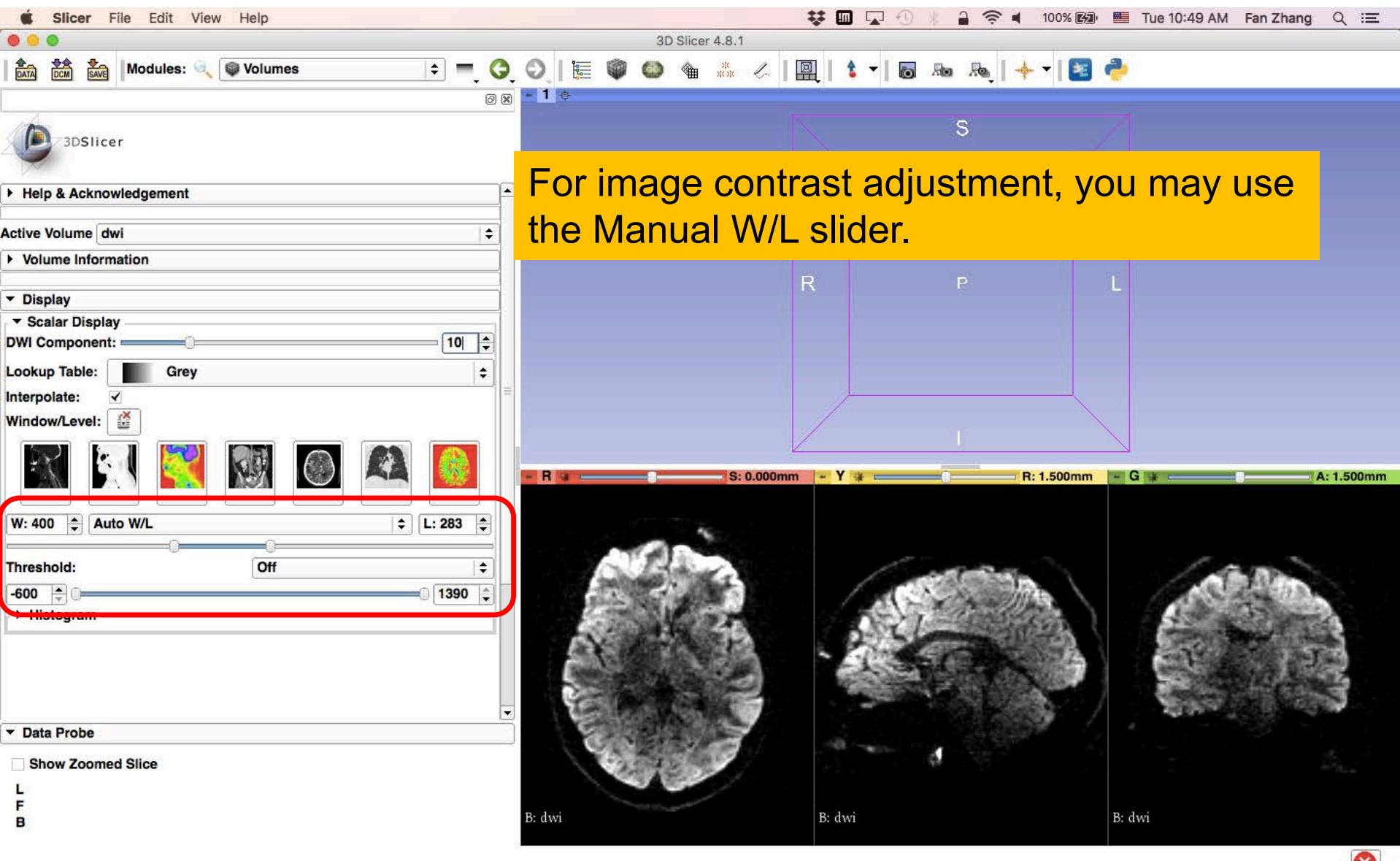
Loading the DWI Dataset



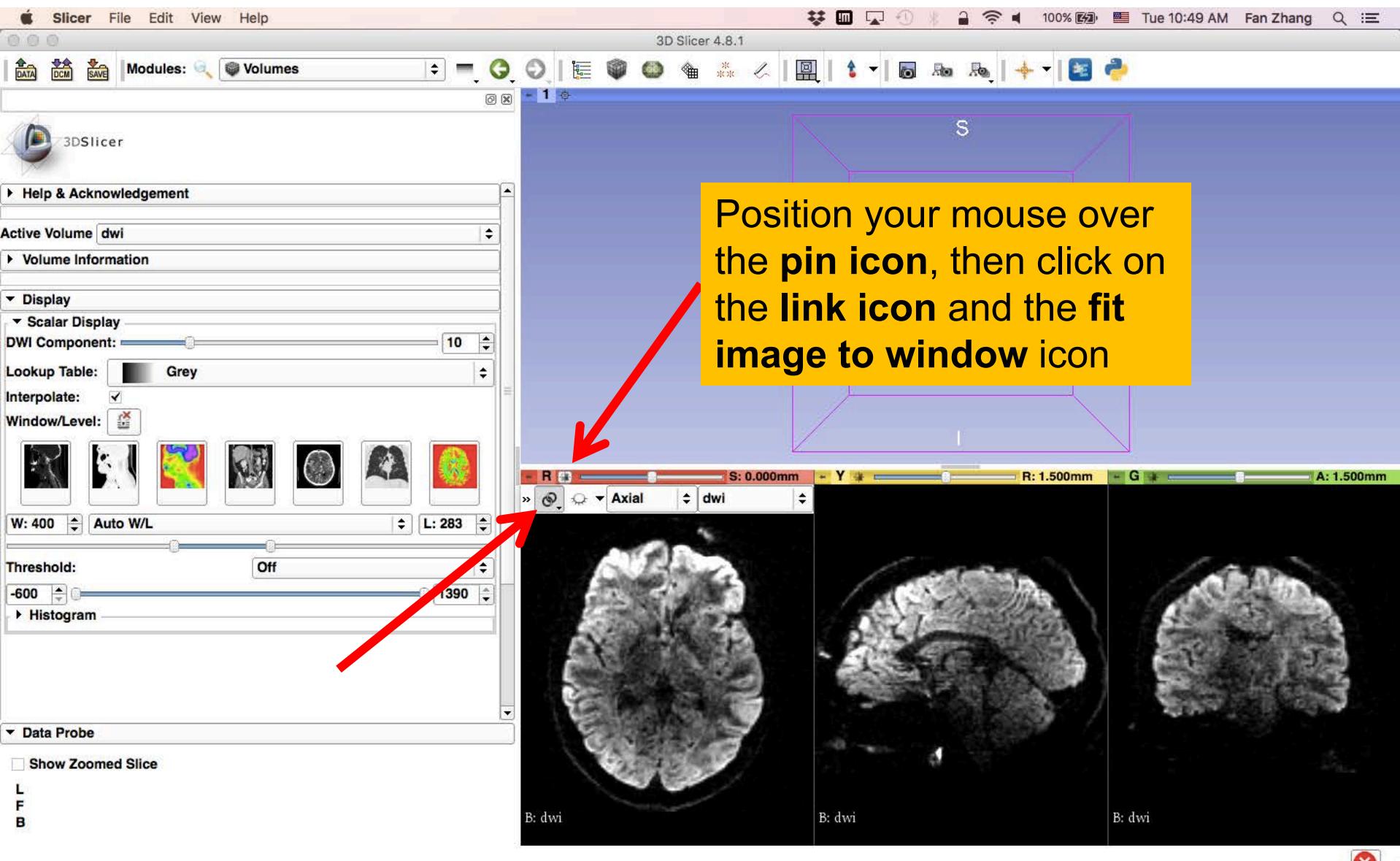
Loading the DWI Dataset



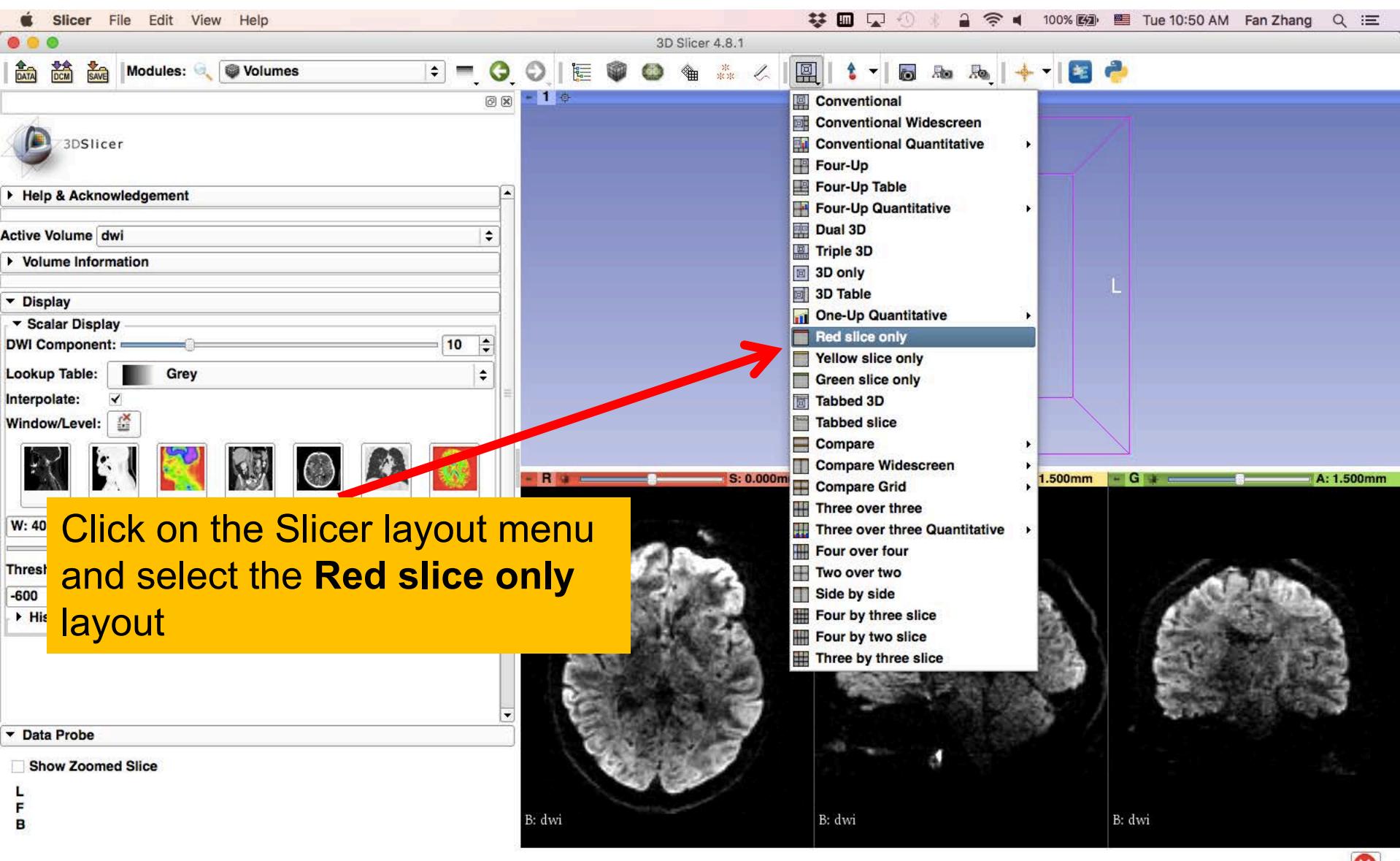
Loading the DWI Dataset



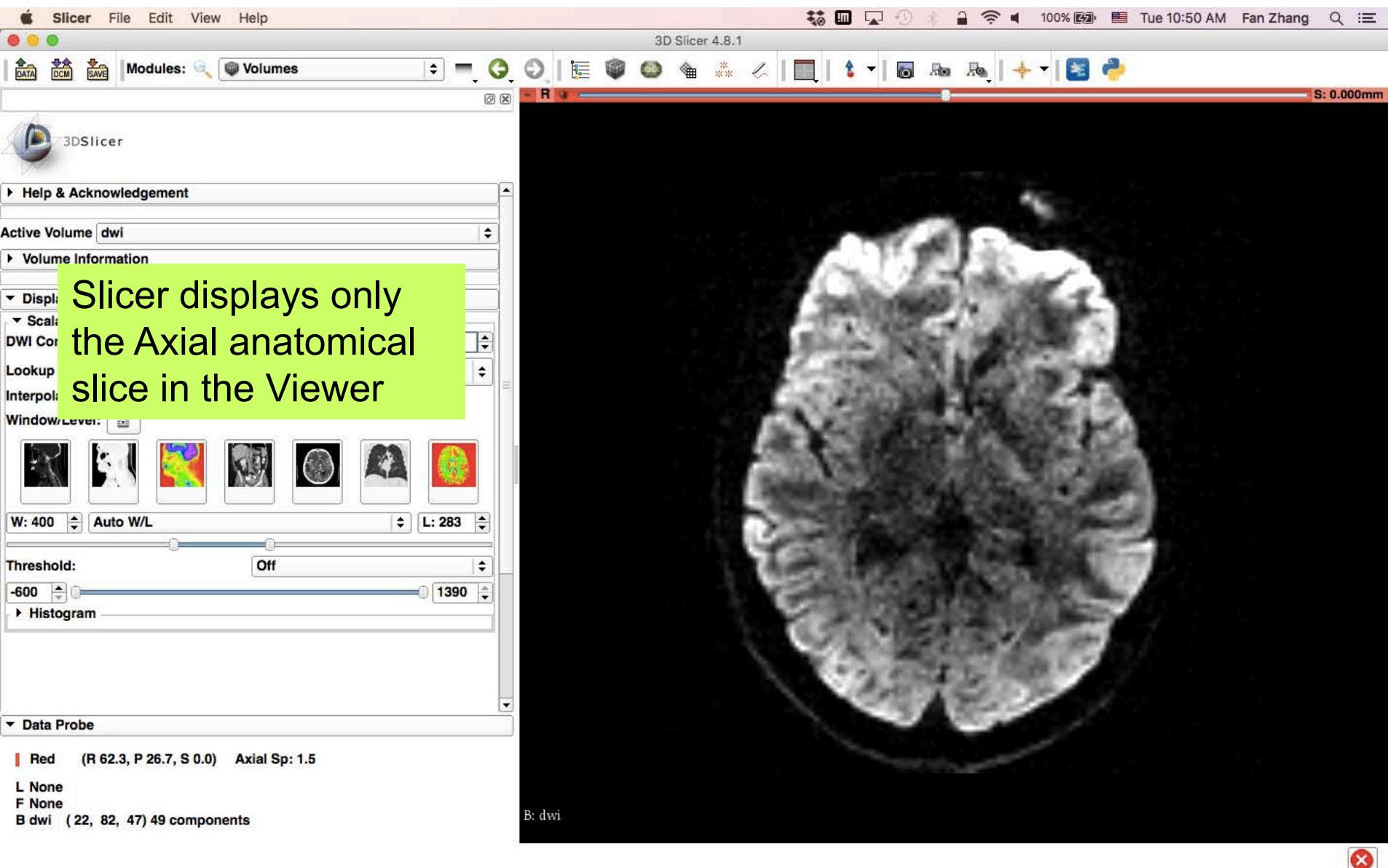
Loading the DWI Dataset



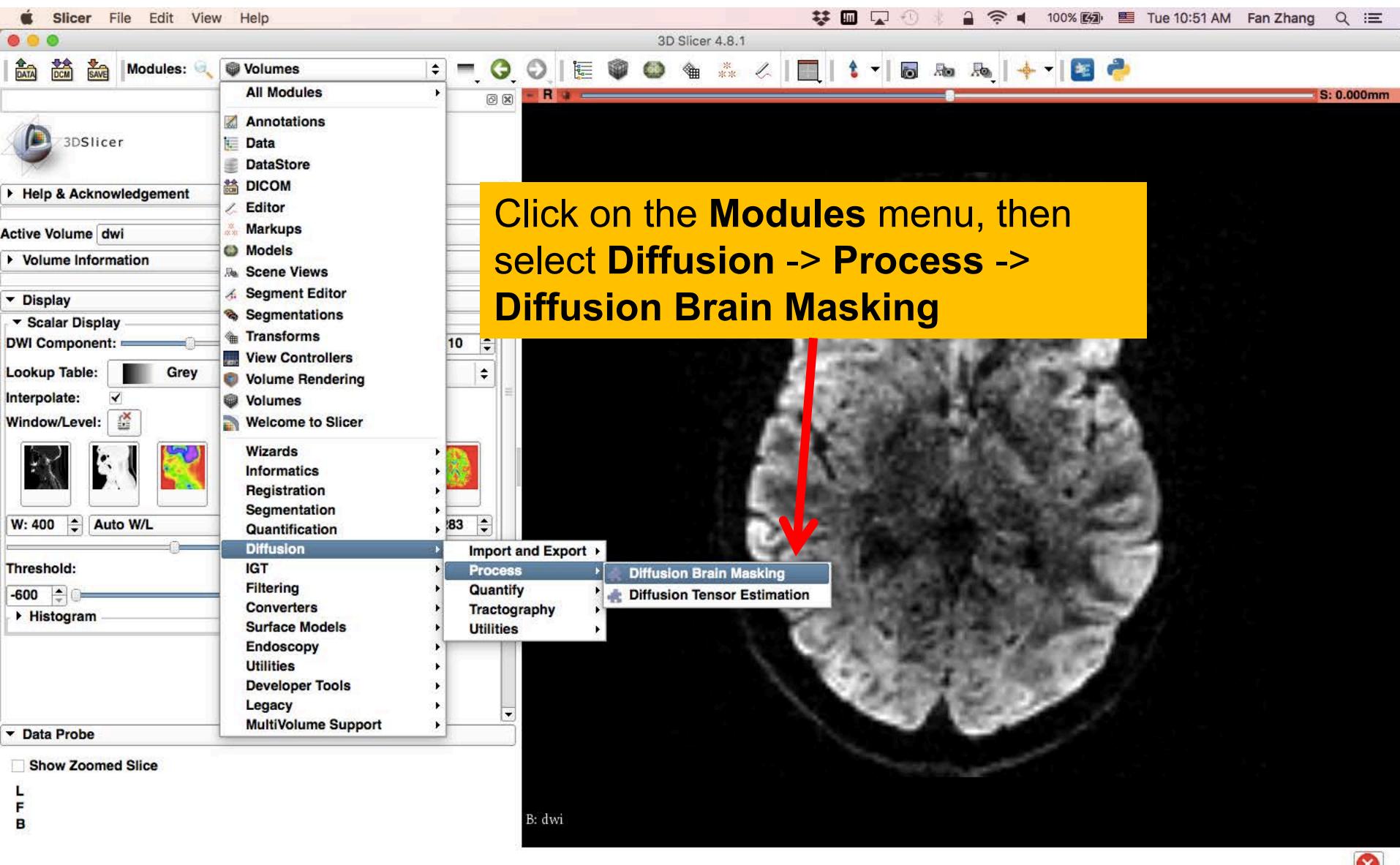
Loading the DWI Dataset



Loading the DWI Dataset



Creating a brain mask



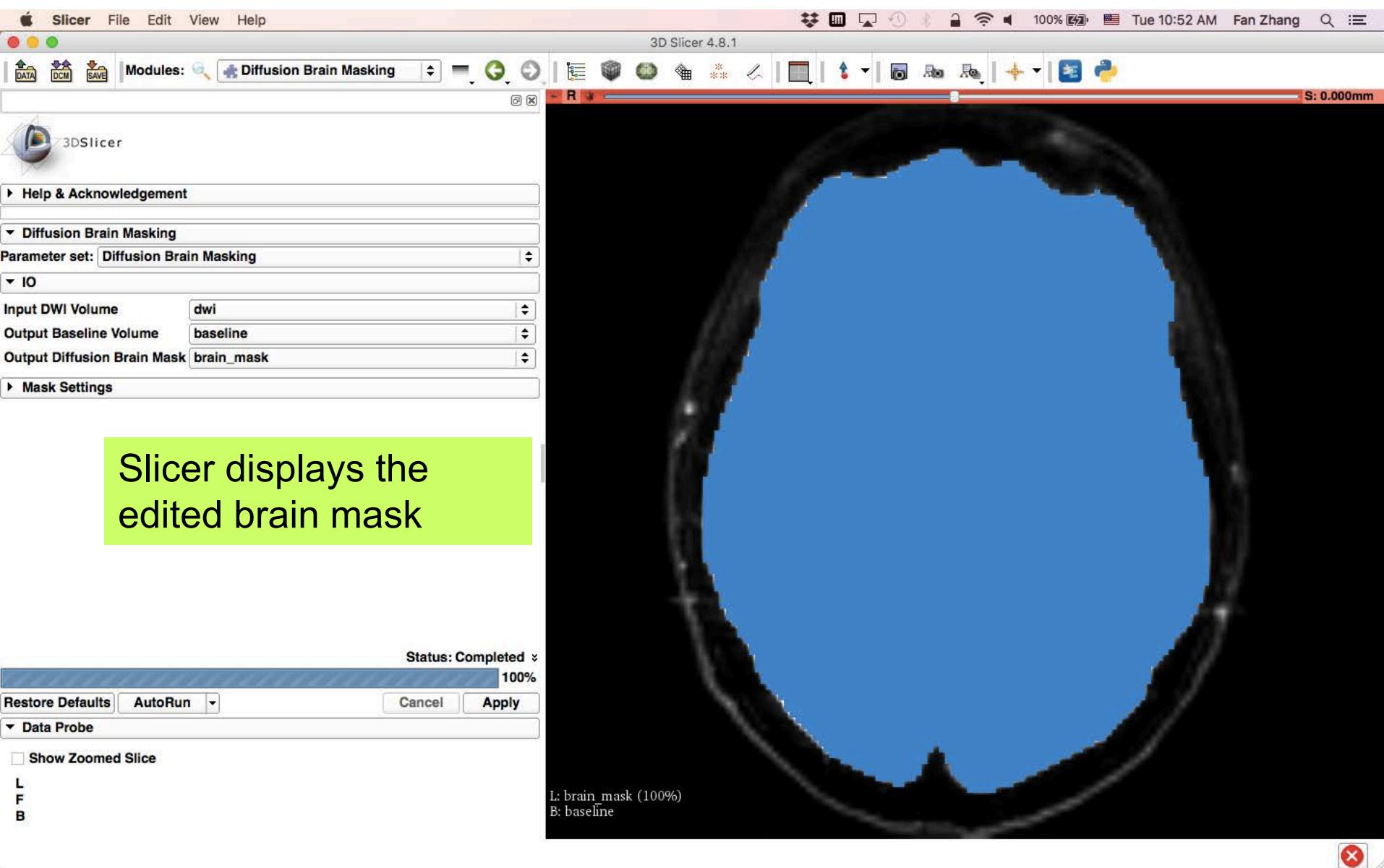
Creating a brain mask

The screenshot shows the 3D Slicer 4.8.1 interface with the 'Diffusion Brain Masking' module selected. A red box highlights the 'IO' parameters section, which includes fields for 'Input DWI Volume' (set to 'dwi'), 'Output Baseline Volume' (set to 'baseline'), and 'Output Diffusion Brain Mask' (set to 'brain_mask'). Below this, a yellow box contains step-by-step instructions for creating a brain mask:

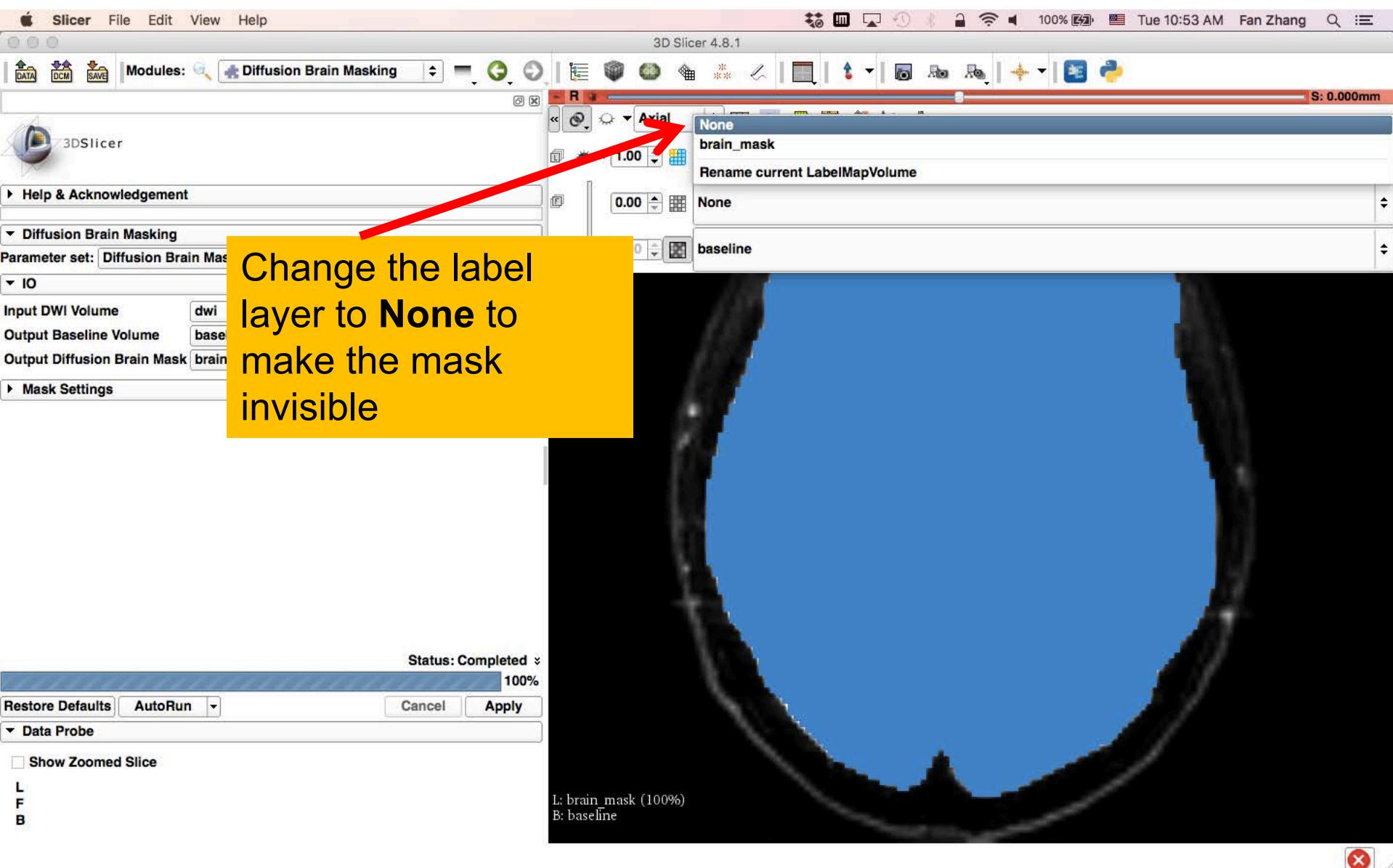
- select the **Input DWI volume 'dwi'**
- select **Output Baseline Volume 'Create new Volume as...', and name it 'baseline'**
- select **Output Diffusion Brain Mask 'Create new LabelMapVolume as...', and name it 'brain_mask'**
- click on **Apply**.

At the bottom of the interface, there are buttons for 'Status: Idle', 'Cancel', and 'Apply'. A red arrow points to the 'Apply' button. The status bar at the bottom shows 'B: dwi'.

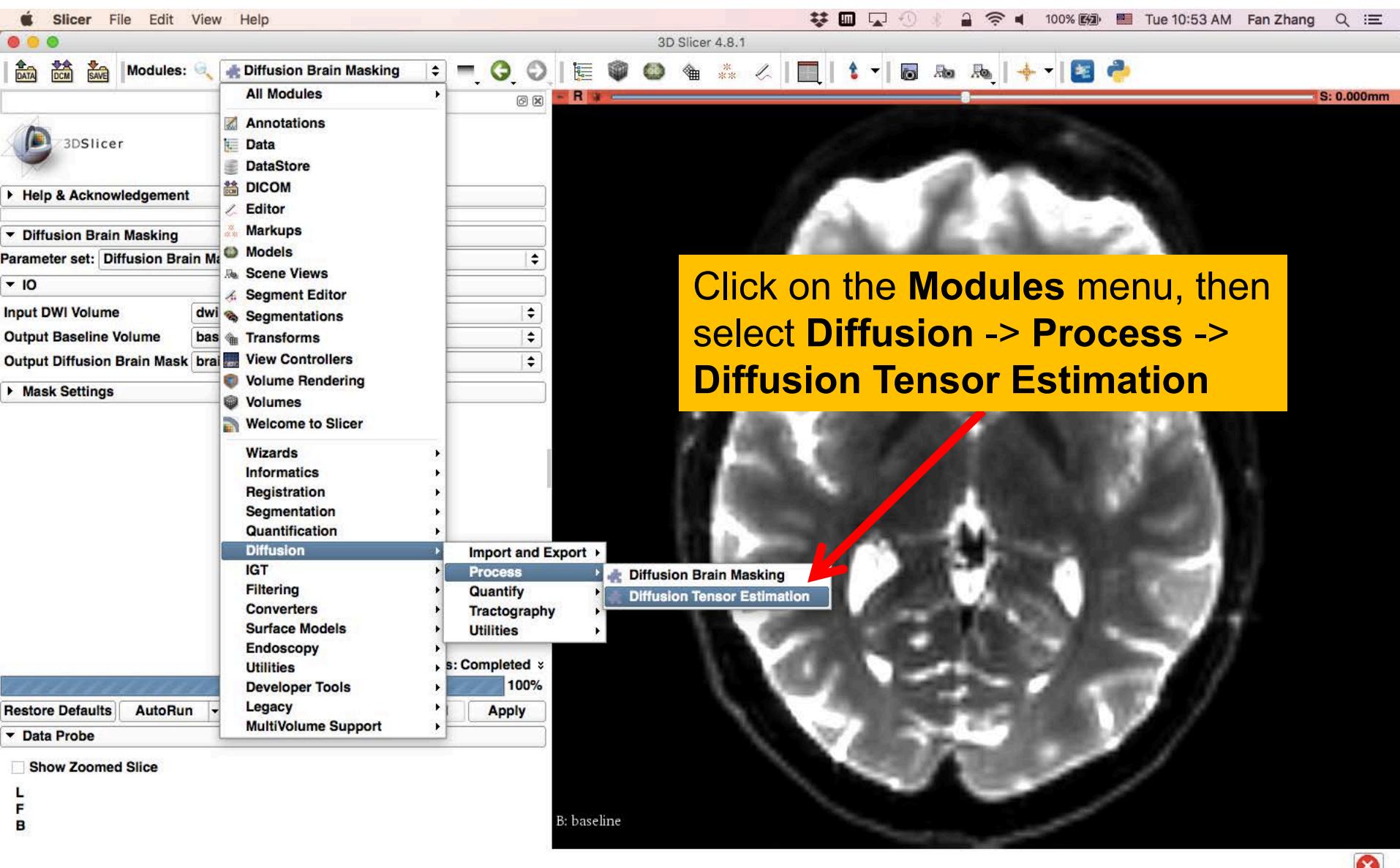
Creating a brain mask



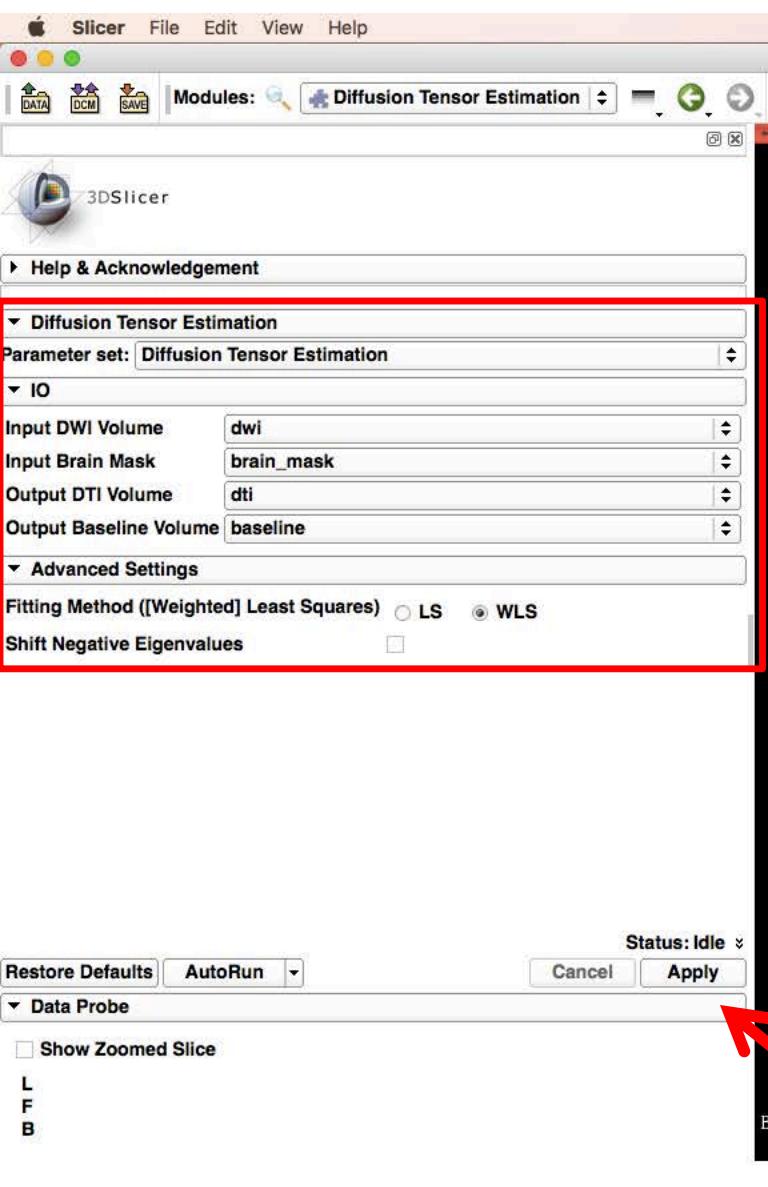
Creating a brain mask



Estimating the tensor



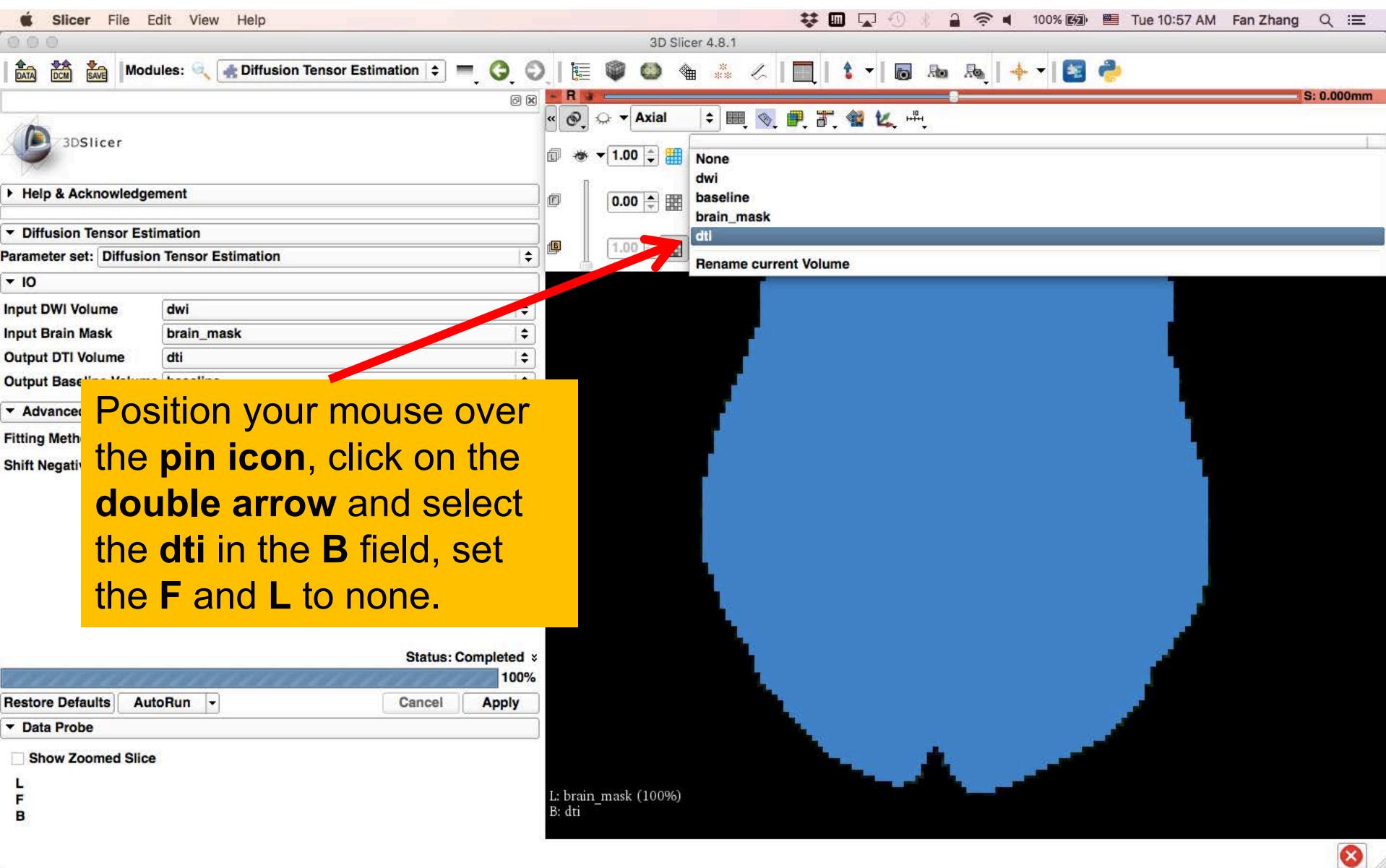
Estimating the tensor



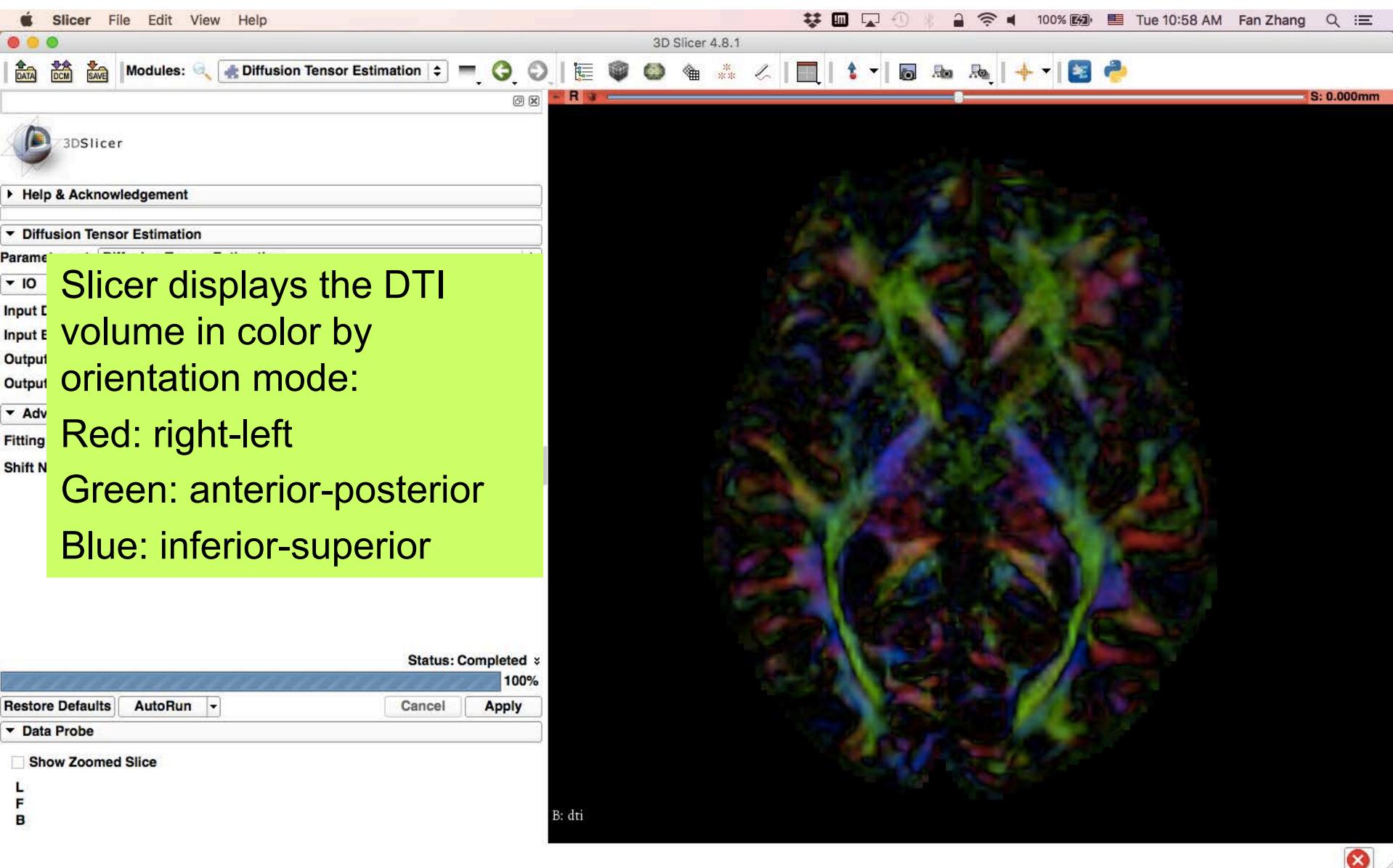
The screenshot shows the 3D Slicer 4.8.1 interface with the 'Diffusion Tensor Estimation' module selected. A red box highlights the 'IO' parameters section, which includes fields for 'Input DWI Volume' (set to 'dwi'), 'Input Brain Mask' (set to 'brain_mask'), 'Output DTI Volume' (set to 'dti'), and 'Output Baseline Volume' (set to 'baseline'). Below this, under 'Advanced Settings', the 'Fitting Method' is set to 'WLS' (Weighted Least Squares). At the bottom right of the module panel, there are 'Status: Idle' and 'Apply' buttons, with a red arrow pointing to the 'Apply' button.

- Set the **Input DWI volume** to 'dwi'
- Set the **Input Brain Mask** to 'brain_mask'
 - Select **Output DTI Volume** 'Create DiffusionTensorVolume as ...', and name it 'dti'
- Set **Output Baseline Volume** to 'baseline'
- Under '**Advanced Settings**', set **Fitting Methods** to 'WLS' (Weighted Least Squares)
- Click on **Apply**.

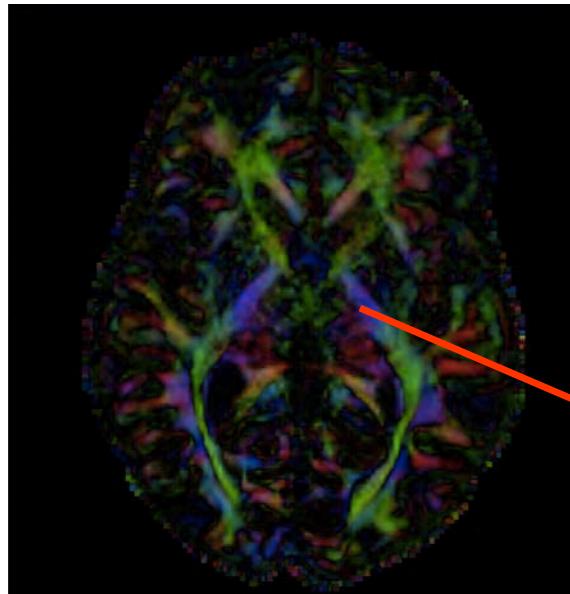
Estimating the tensor



Exploring the DWI Dataset



Diffusion Tensor Data



$$S_i = S_0 e^{-b \hat{g}^T \underline{D} \hat{g}_i}$$

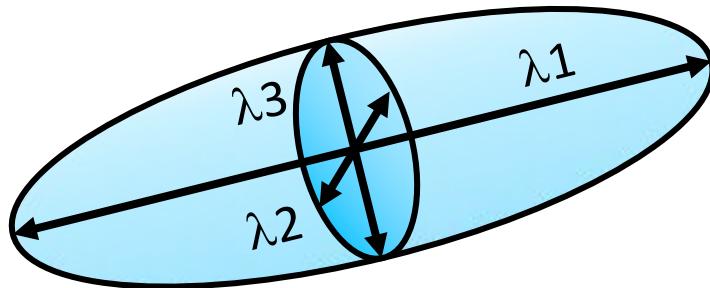
Stejskal-Tanner equation (1965)

$$\underline{D} = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{bmatrix}$$

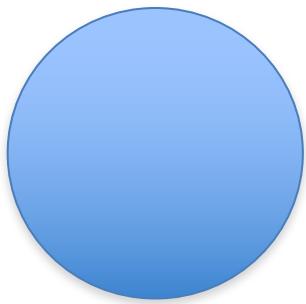
The diffusion tensor \underline{D} in the voxel (I,J,K) is a 3x3 symmetric matrix.

Diffusion Tensor

- The diffusion tensor \underline{D} in each voxel can be visualized as a diffusion ellipsoid, with the eigenvectors indicating the directions of the principal axes, and the ellipsoidal proportional to the square root of the eigenvalues defining the
- Scalar maps can be derived from the rotationally invariant eigenvalues $\lambda_1, \lambda_2, \lambda_3$ to characterize the size and shape of the diffusion tensor.

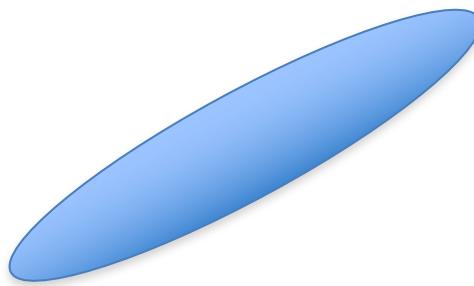


Diffusion Tensor Shape



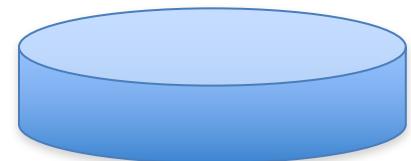
$$\lambda_1 = \lambda_2 = \lambda_3$$

Isotropic media
(Cerebrospinal
Fluid, gray matter)



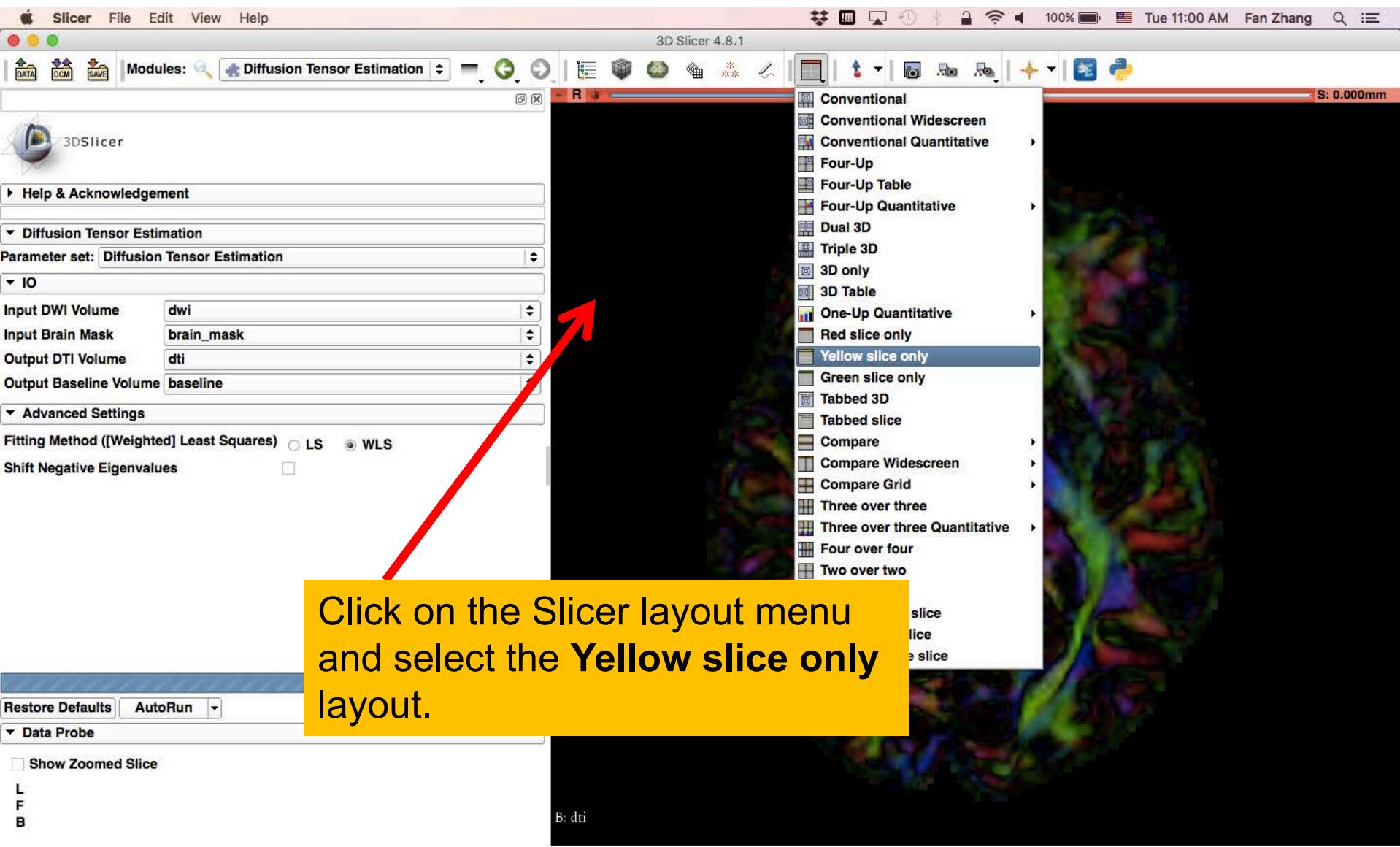
$$\lambda_1 >> \lambda_2, \lambda_3$$

Anisotropic media
(white matter)



$$\lambda_1 \sim \lambda_2 >> \lambda_3$$

Exploring the DWI Dataset



Corpus Callosum

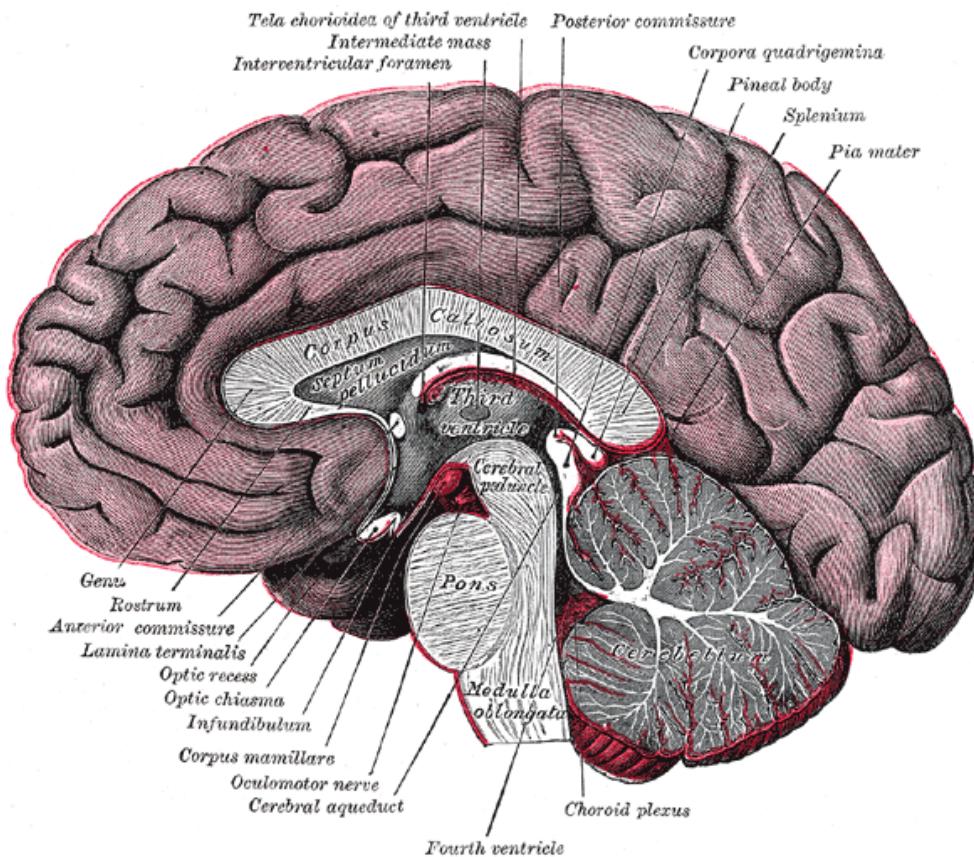
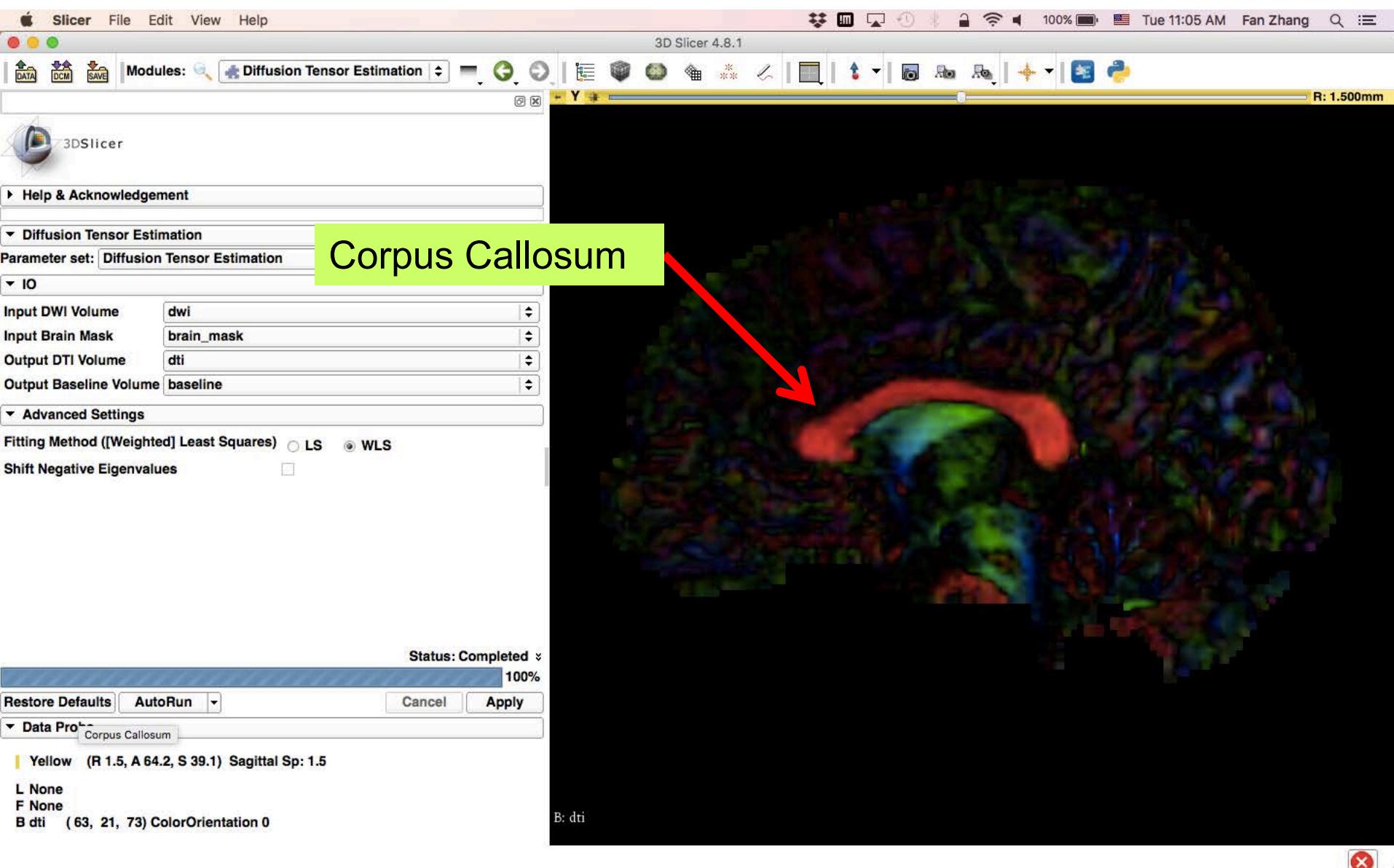


Image from Gray's Anatomy

The corpus callosum is a broad thick bundle of dense myelinated fibers that connect the left and right hemisphere. It is the largest white matter structure in the brain.

Corpus Callosum

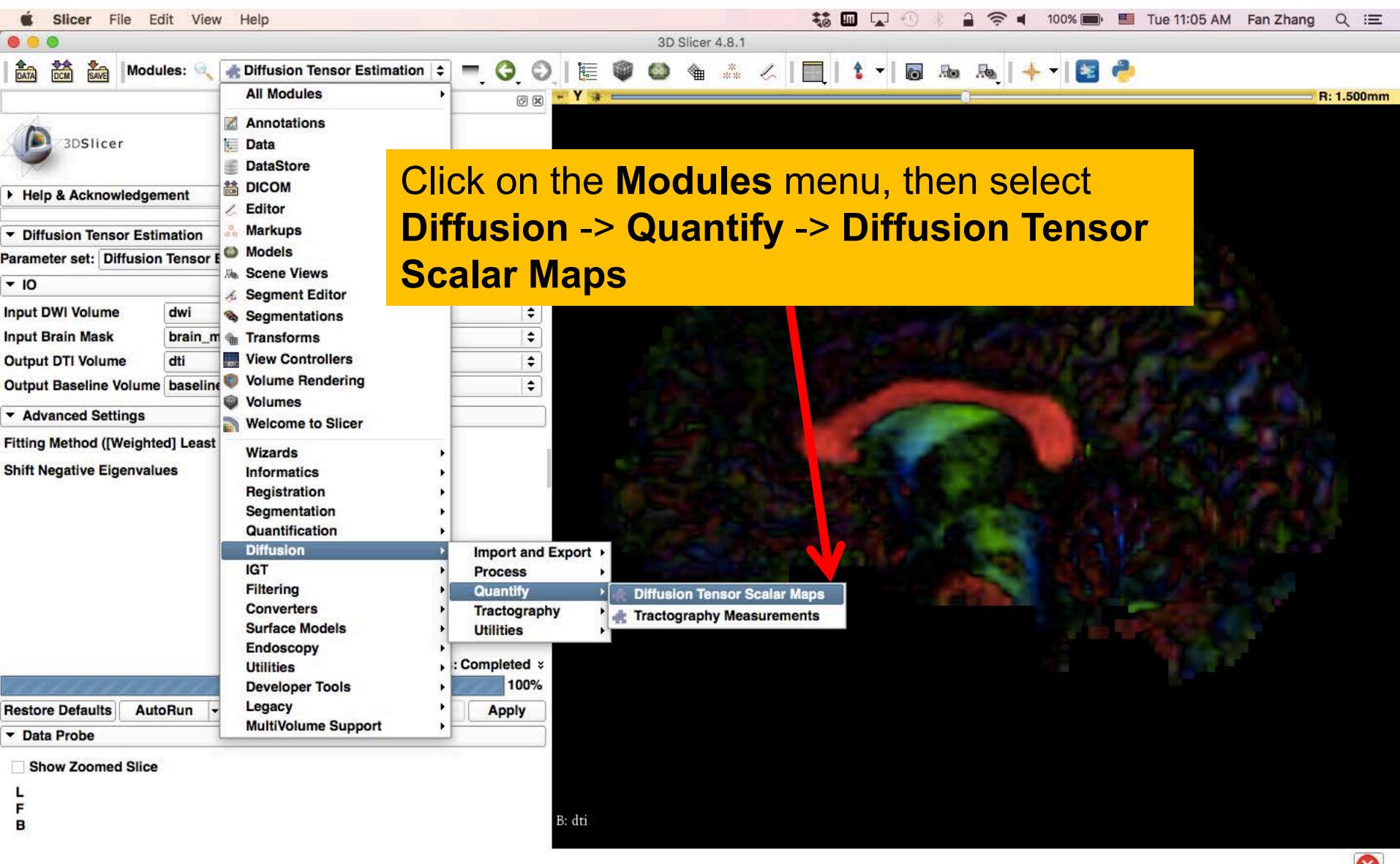


Characterizing the Size of the tensor: Trace

$$\text{Trace}(D) = \lambda_1 + \lambda_2 + \lambda_3$$

- $\text{Trace}(D)$ is intrinsic to the tissue and is independent of fiber orientation, and diffusion sensitizing gradient directions
- $\text{Trace}(D)$ is a clinically relevant parameter for monitoring stroke and neurological condition (degree of structural coherence in tissue)
- $\text{Trace}(D)$ is useful to characterize the size of the diffusion ellipsoid

Trace



Trace

The screenshot shows the 3D Slicer 4.8.1 interface. The top menu bar includes Slicer, File, Edit, View, Help, and a status bar showing Tue 11:06 AM, Fan Zhang, and R: 1.500mm. The toolbar has various icons for file operations and modules. The main window displays a 3D volume rendering of a brain with colored fibers. On the left, the 'Diffusion Tensor Scalar Maps' module is selected in the 'Modules' list. The parameter set is set to 'Diffusion Tensor Scalar Maps'. A red box highlights the 'Scalar Measurement' section, which contains the following configuration:

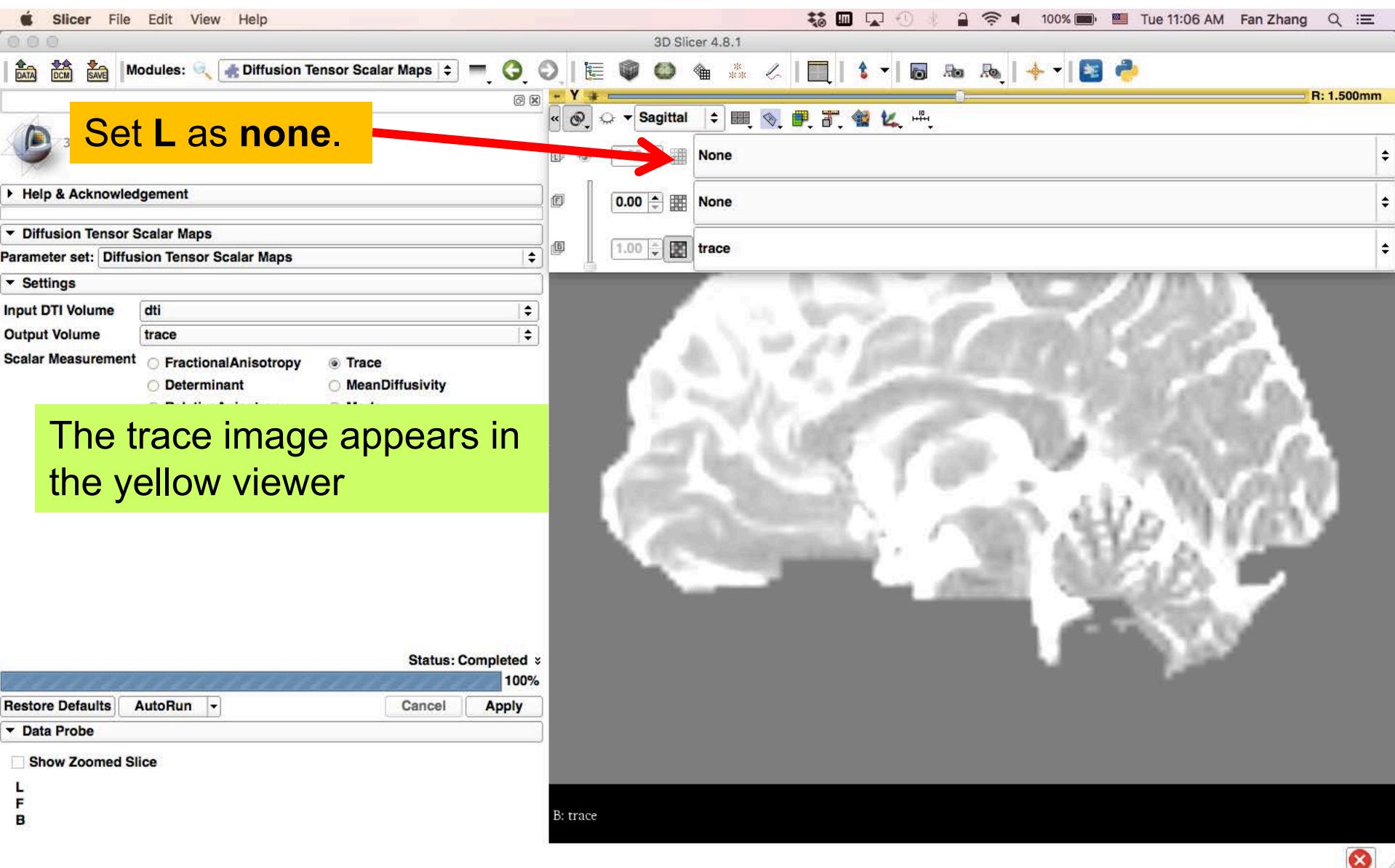
Input DTI Volume	dti
Output Volume	trace
Scalar Measurement	<input checked="" type="radio"/> Trace <input type="radio"/> FractionalAnisotropy <input type="radio"/> Determinant <input type="radio"/> RelativeAnisotropy <input type="radio"/> LinearMeasure <input type="radio"/> SphericalMeasure <input type="radio"/> MidEigenvalue <input type="radio"/> ParallelDiffusivity <input type="radio"/> MeanDiffusivity <input type="radio"/> Mode <input type="radio"/> PlanarMeasure <input type="radio"/> MinEigenvalue <input type="radio"/> MaxEigenvalue <input type="radio"/> PerpendicularDiffusivity

Below the module settings, there are buttons for Restore Defaults, AutoRun, Status: Idle, Cancel, Apply, and Data Probe. A checkbox for Show Zoomed Slice is also present. The bottom status bar shows L, F, B and B: dti.

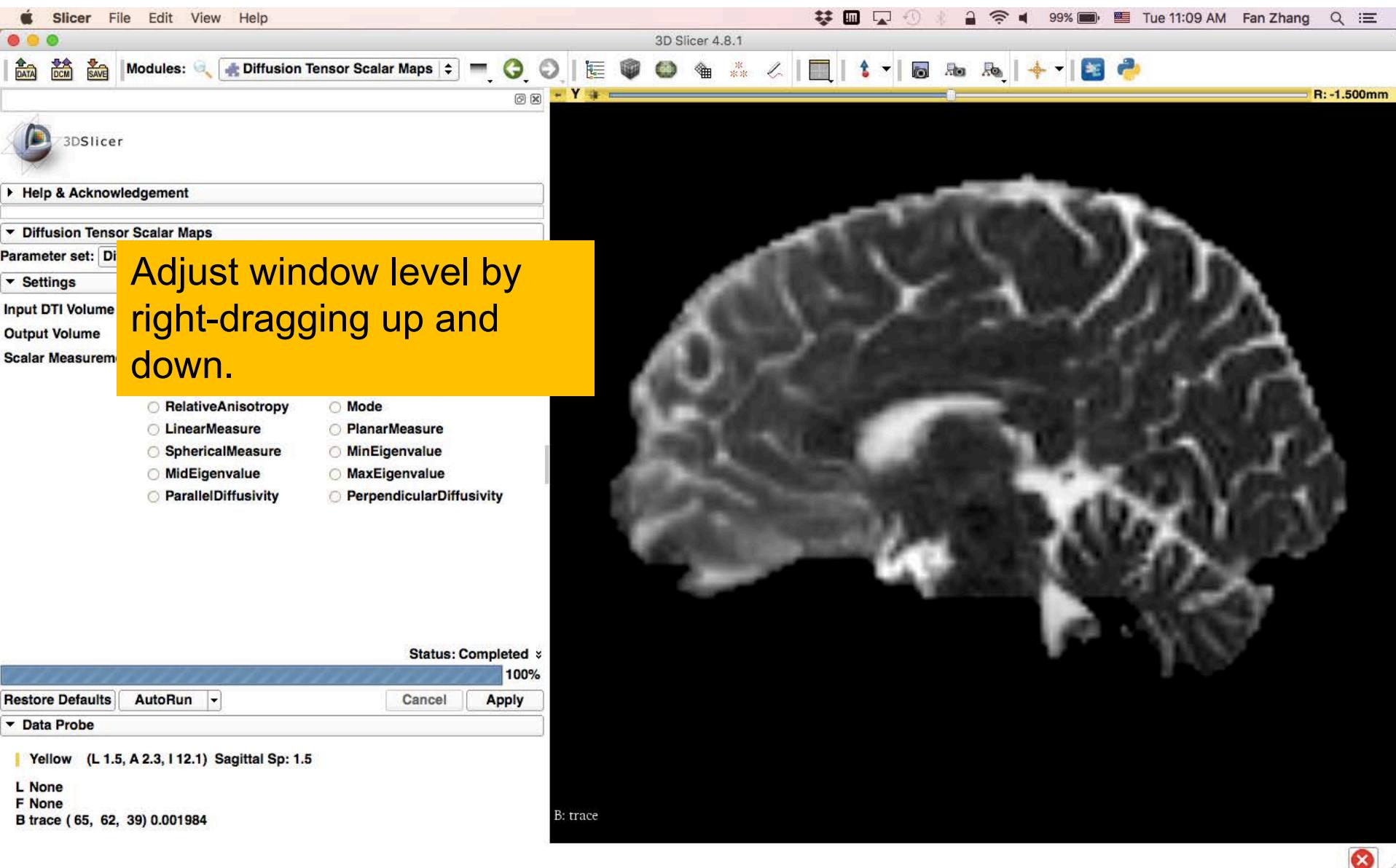
Type in the following information in the IO menu:

- select the Operation '**Trace**'
- set **Input DTI Volume** to '**dti**'
- select **Output Volume 'Create new Volume as...'** and name it '**trace**'
- click on **Apply** to calculate the trace map of the tensor volume

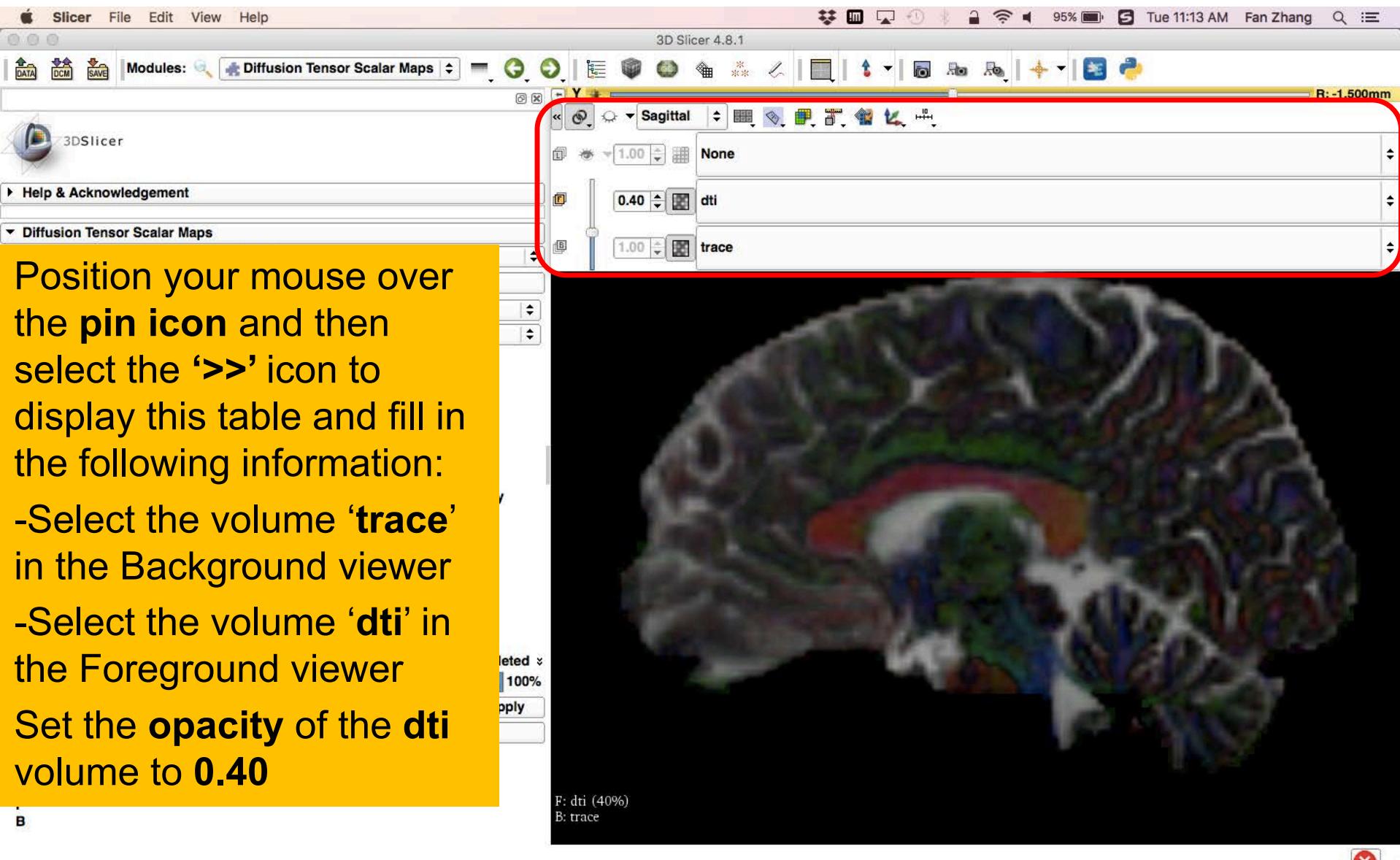
Trace



Trace



Trace



Trace

Position your mouse within the region of the Corpus Callosum and observe the trace values in the Data Probe

Parameter set: Diffusion Tensor Scalar Maps

Input DTI Volume: dti

Output Volume: trace

Scalar Measurement: Trace

FractionalAnisotropy

Determinant

RelativeAnisotropy

LinearMeasure

SphericalMeasure

MidEigenvalue

ParallelDiffusivity

MeanDiffusivity

Mode

PlanarMeasure

MinEigenvalue

MaxEigenvalue

PerpendicularDiffusivity

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

Trace

Data Probe

Yellow (L 1.5, A 33.9, S 8.4) Sagittal Sp: 1.5

L None

F dti (65, 41, 53) ColorOrientation 0

B trace (65, 41, 53) 0.001909

R: -1.500mm

Tue 11:14 AM Fan Zhang

F: dti (40%)

B: trace

Trace

Note how the Trace values are fairly uniform in both white and gray matter, even if the tissues are different in structure.

Input DTI Volume: dti
Output Volume: trace

Scalar Measurement:

- FractionalAnisotropy
- Trace
- Determinant
- RelativeAnisotropy
- LinearMeasure
- SphericalMeasure
- MidEigenvalue
- ParallelDiffusivity
- MeanDiffusivity
- Mode
- PlanarMeasure
- MinEigenvalue
- MaxEigenvalue
- PerpendicularDiffusivity

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

▼ Data Probe

Yellow (L 1.5, A 31.3, S 19.1) Sagittal Sp: 1.5

L None
F dti (65, 43, 60) ColorOrientation 0
B trace (65, 43, 60) 0.002775

F: dti (40%)
B: trace

Scalar Maps: Fractional Anisotropy

$$FA(D) = \frac{\sqrt{(\lambda_1 - \lambda_2)^2 + (\lambda_1 - \lambda_3)^2 + (\lambda_2 - \lambda_3)^2}}{\sqrt{2} \sqrt{\lambda_1^2 + \lambda_2^2 + \lambda_3^2}}$$

- FA(D) is intrinsic to the tissue and is independent of fiber orientation, and diffusion sensitizing gradient directions
- FA(D) is useful to characterize the shape (degree of ‘out-of-roundness’) of the diffusion ellipsoid
- Low FA:  → High FA: 

Fractional Anisotropy

The screenshot shows the 3D Slicer 4.8.1 interface. The top menu bar includes Apple, Slicer, File, Edit, View, Help, and a status bar showing Tue 11:16 AM, Fan Zhang, and battery level. The toolbar has icons for DATA, DCM, and SAVE. The Modules panel shows 'Diffusion Tensor Scalar Maps' is selected. The main window displays a 3D brain volume with fiber tracts. On the left, the 'Diffusion Tensor Scalar Maps' module parameters are shown:

- Parameter set: Diffusion Tensor Scalar Maps
- Input DTI Volume: dti
- Output Volume: fa
- Scalar Measurement:
 - FractionalAnisotropy
 - Determinant
 - RelativeAnisotropy
 - LinearMeasure
 - SphericalMeasure
 - MidEigenvalue
 - ParallelDiffusivity
 - Trace
 - MeanDiffusivity
 - Mode
 - PlanarMeasure
 - MinEigenvalue
 - MaxEigenvalue
 - PerpendicularDiffusivity

Status: Completed 100%

Buttons: Restore Defaults, AutoRun, Cancel, Apply

Data Probe: L, F, B

Show Zoomed Slice

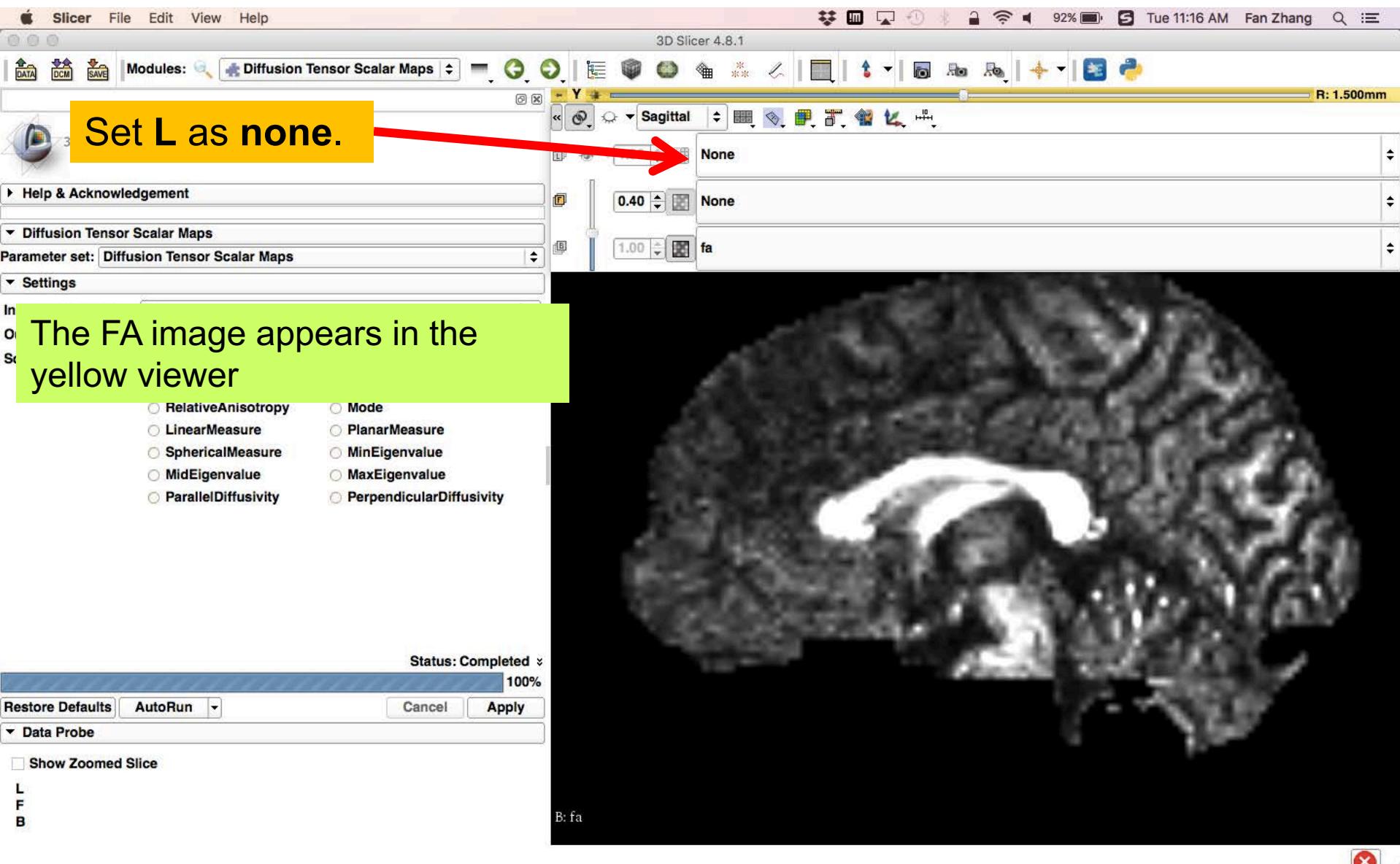
A yellow callout box on the right contains the following instructions:

Fill in the following information:

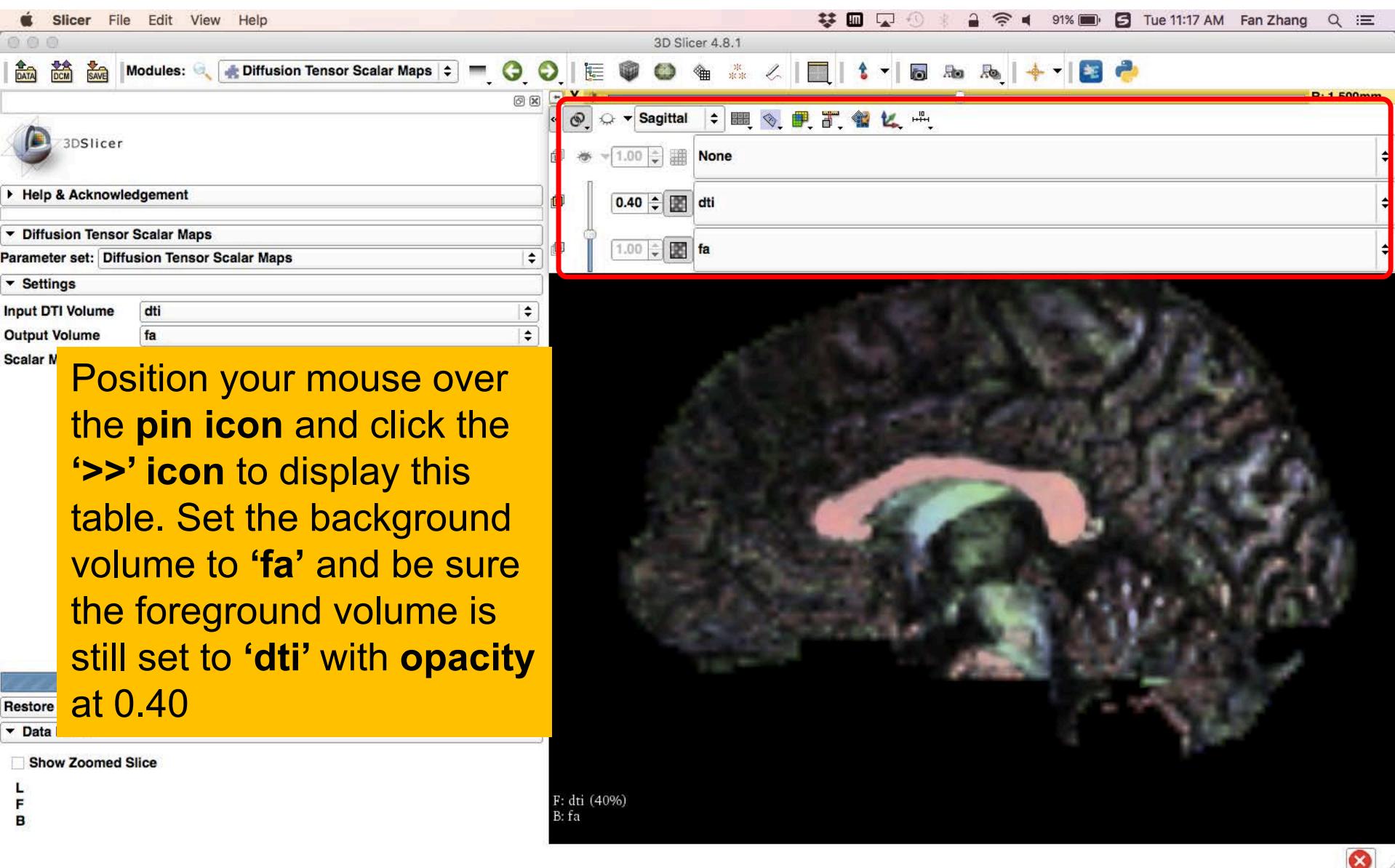
- Set **Input DTI Volume** to 'dti'
- Select **Output Scalar Volume** 'Create new Volume as ...' and name it 'fa'
- In '**Scalar Measurement**', select '**Fractional Anisotropy**'
- Click on **Apply** to calculate the Fractional Anisotropy map of the tensor volume

F: dti (40%)
B: trace

Fractional Anisotropy



Fractional Anisotropy



Fractional Anisotropy

Explore the FA values in the Corpus Callosum and in adjacent gray matter areas. Note how the FA values are high in the white matter areas, and low in gray matter regions

Output Volume fa

Scalar Measurement FractionalAnisotropy Trace
 Determinant MeanDiffusivity
 RelativeAnisotropy Mode
 LinearMeasure PlanarMeasure
 SphericalMeasure MinEigenvalue
 MidEigenvalue MaxEigenvalue
 ParallelDiffusivity PerpendicularDiffusivity

Fractional Anisotropy

Status: Completed 100%

Restore Defaults AutoRun

▼ Data Probe

Yellow (R 1.5, A 35.0, S 6.8) Sagittal Sp: 1.5

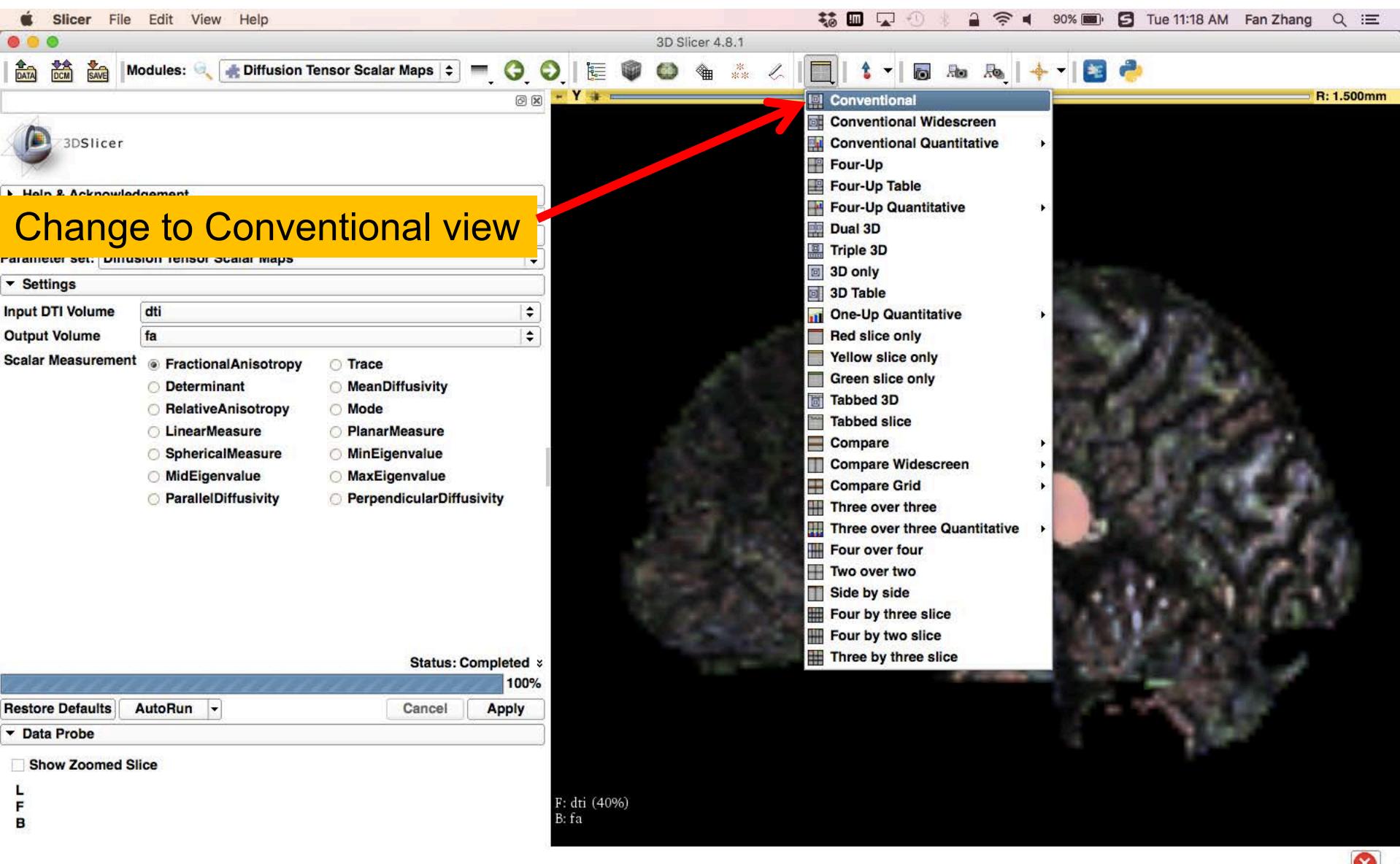
L None
F dti (63, 41, 52) ColorOrientation 0
B fa (63, 41, 52) 0.703706

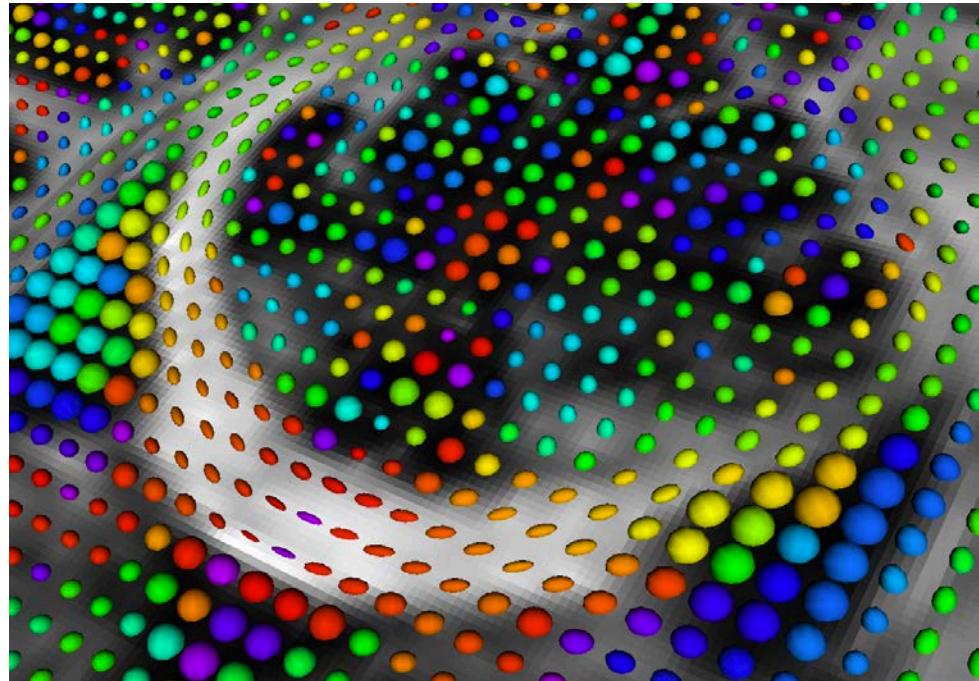


R: 1.500mm

F: dti (40%)
B: fa

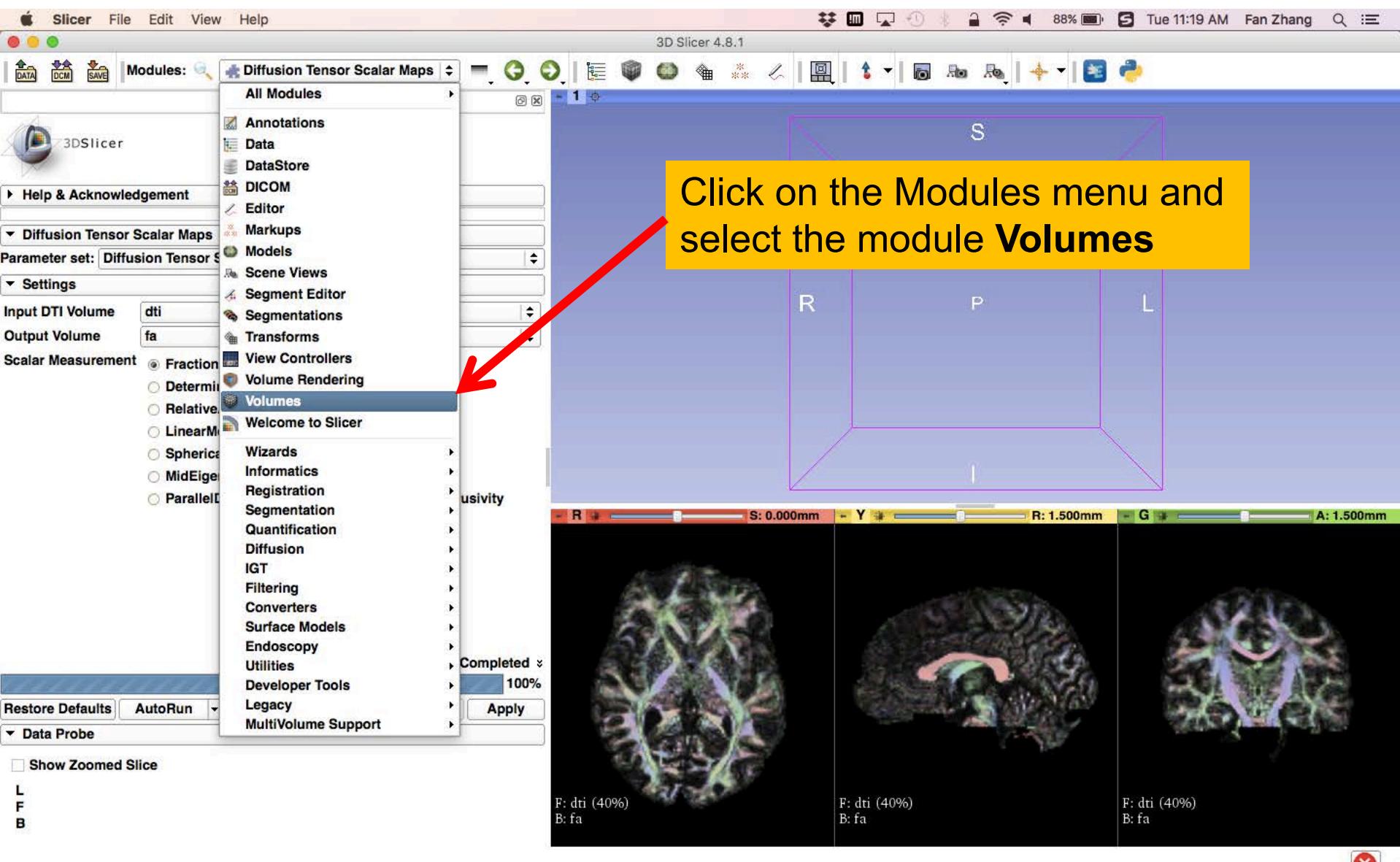
Fractional Anisotropy



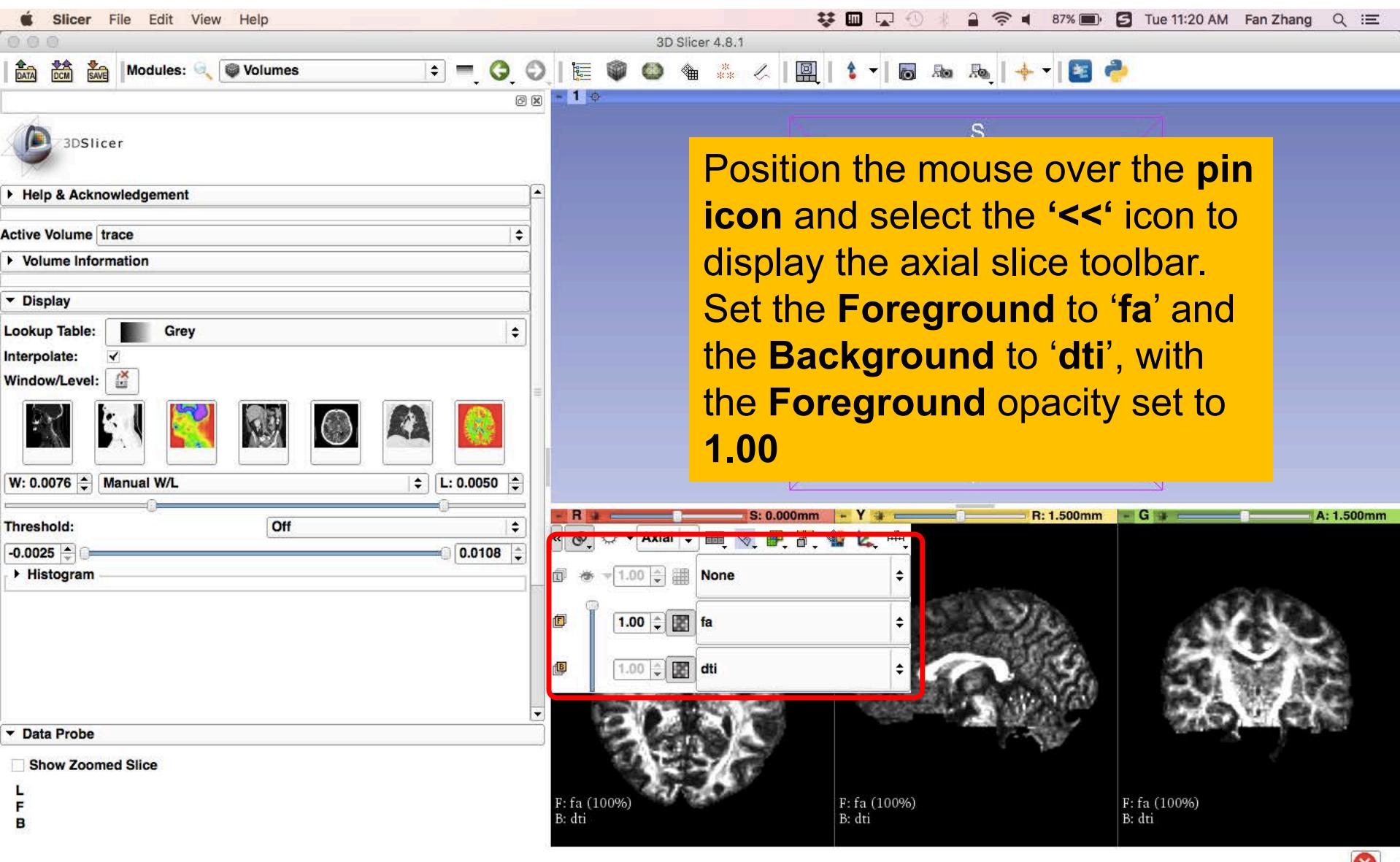


Part 2: Visualizing the tensor data

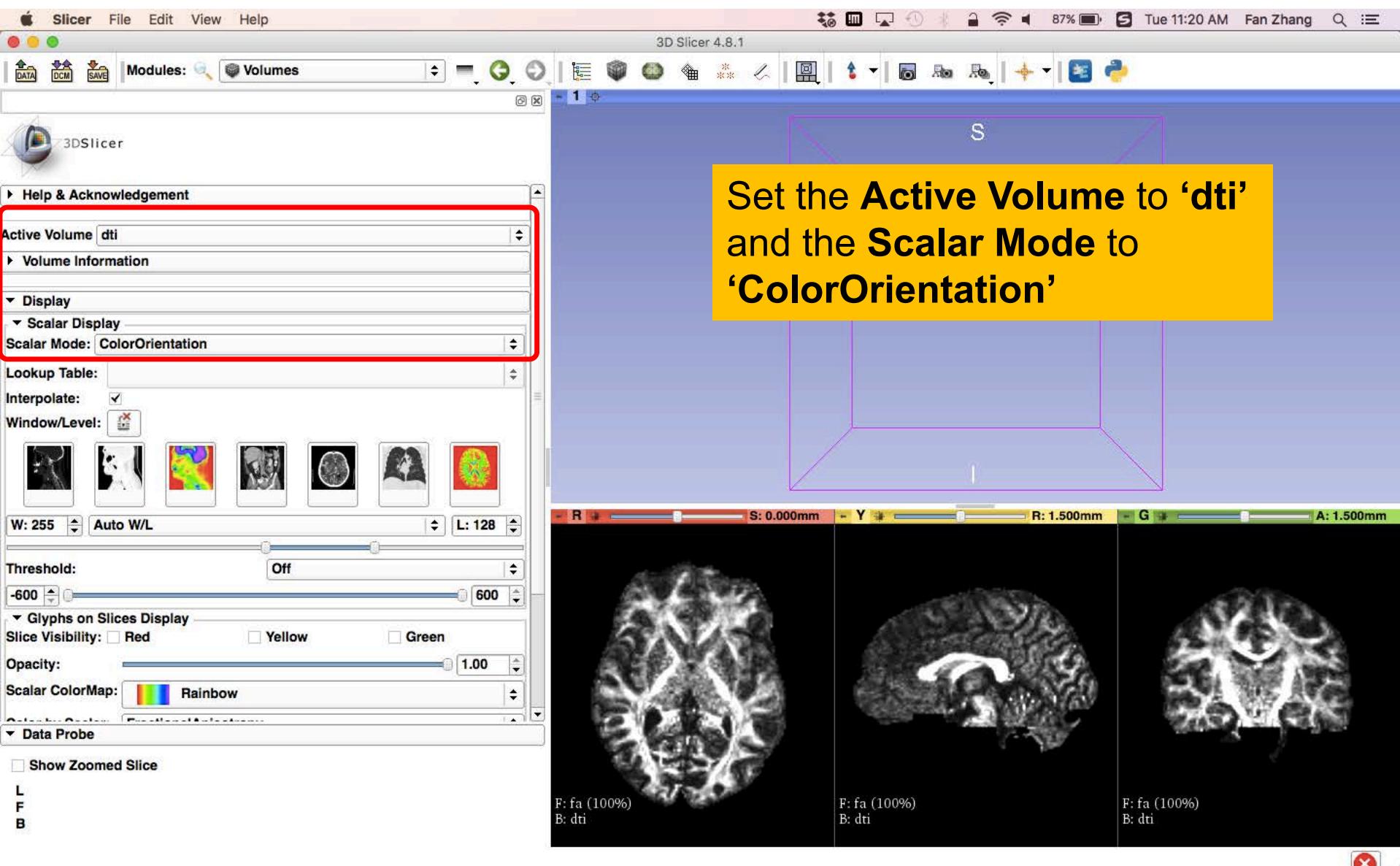
3D Visualization: Glyphs



3D Visualization: Glyphs



3D Visualization: Glyphs



3D Visualization: Glyphs

Slicer File Edit View Help

3D Slicer 4.8.1

Scalar Mode: ColorOrientation
Lookup Table:
Interpolate:
Window/Level: W: 255 Auto W/L L: 128
Threshold: Off -600 600
Glyphs on Slices Display
Slice Visibility: Red Yellow Green
Opacity: 1.00
Scalar ColorMap: FullRainbow
Color by Scalar: ColorOrientation
Scalar Range: OFF
Glyph Type: Ellipsoids
Scale Factor: 50.00
Spacing: 5.00
Data Probe
Show Zoomed Slice
L F B

Scroll down the module panel and in the **Glyphs on Slices Display** section:

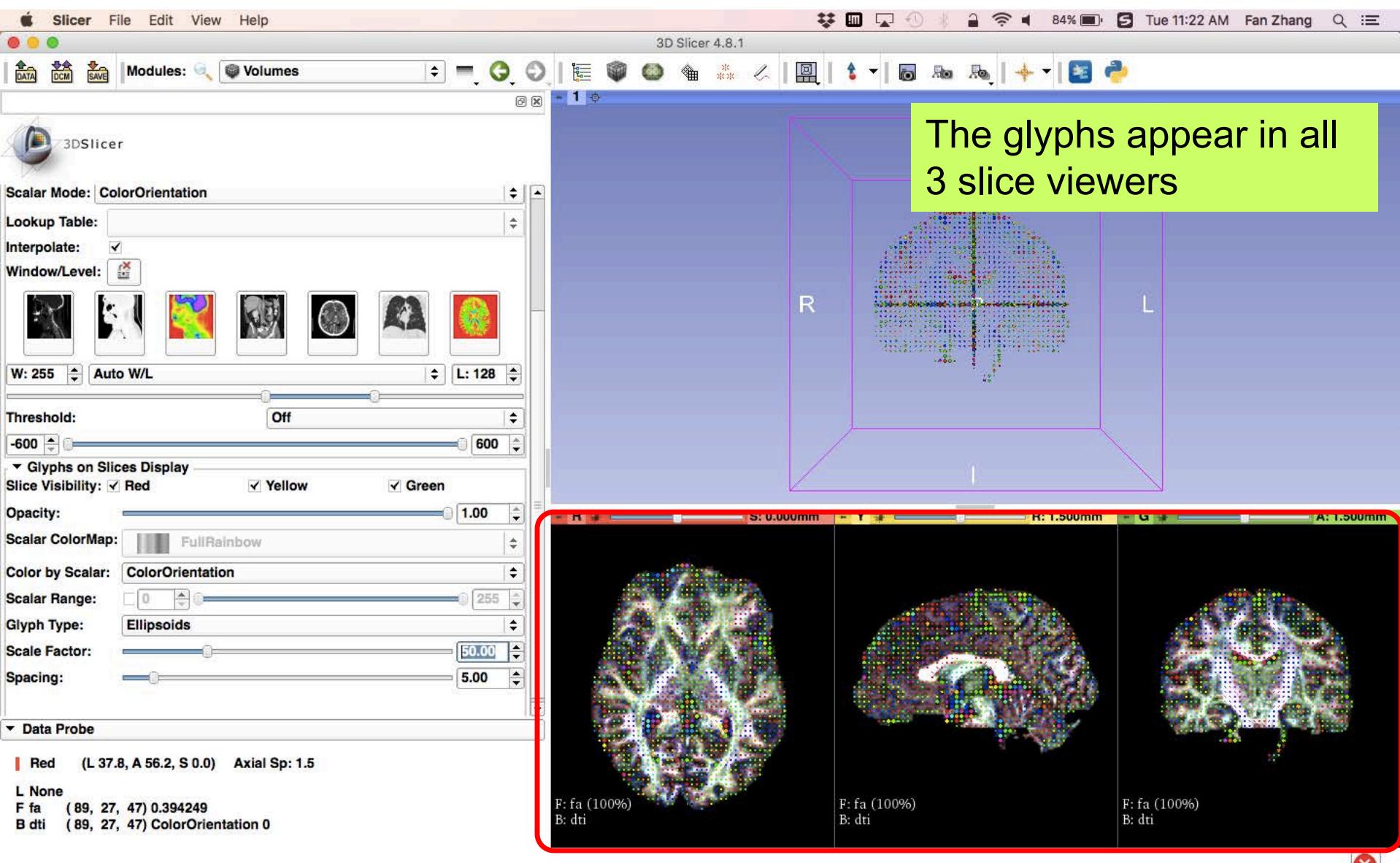
- Check off the option for **Red, Yellow, and Green Slice Visibility**
- Set the **Color by Scalar** parameter to '**ColorOrientation**'
- Set the **Glyph Type** to '**Ellipsoids**'

F: fa (100%)
B: dti

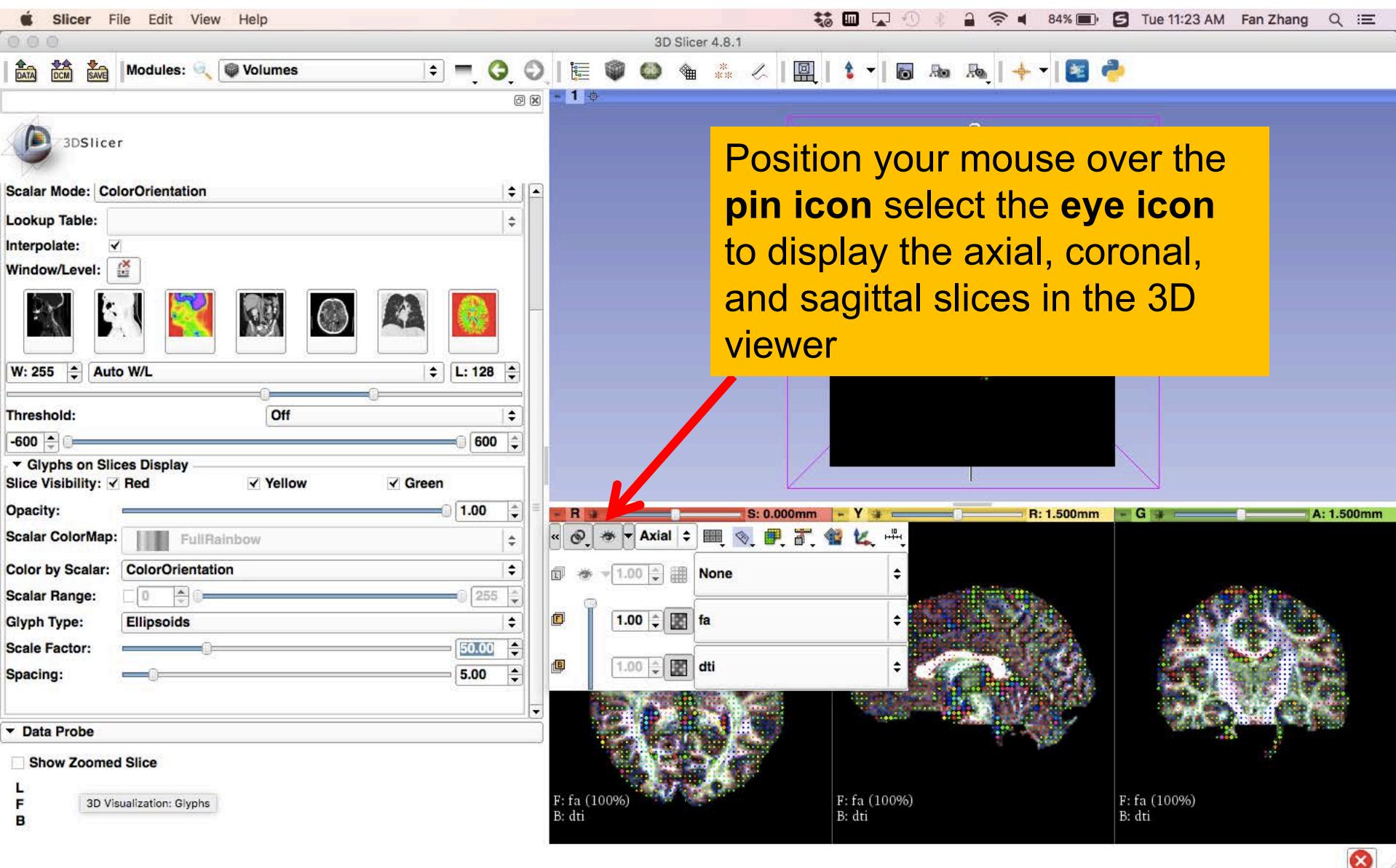
S

A: 1.500mm

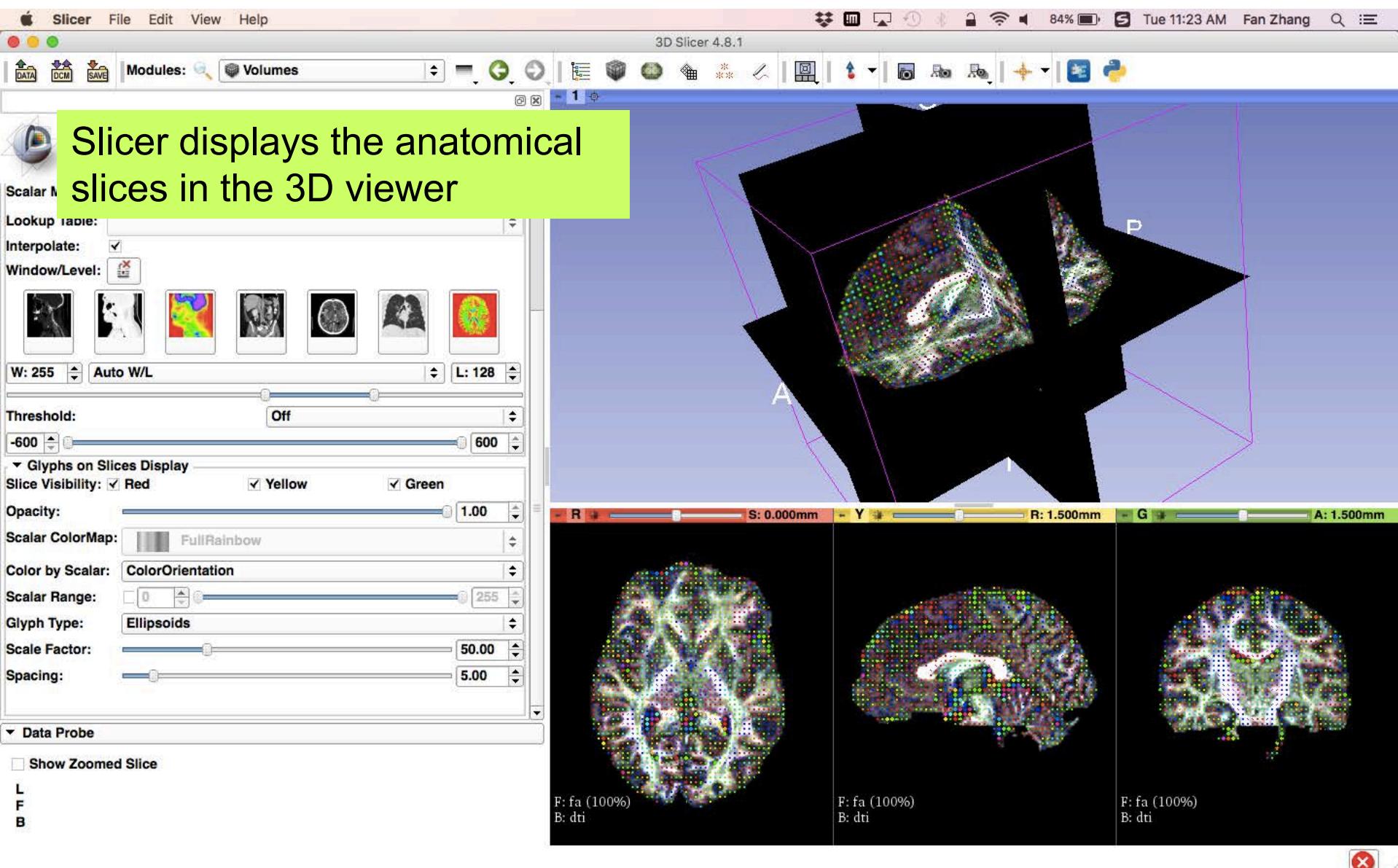
3D Visualization: Glyphs



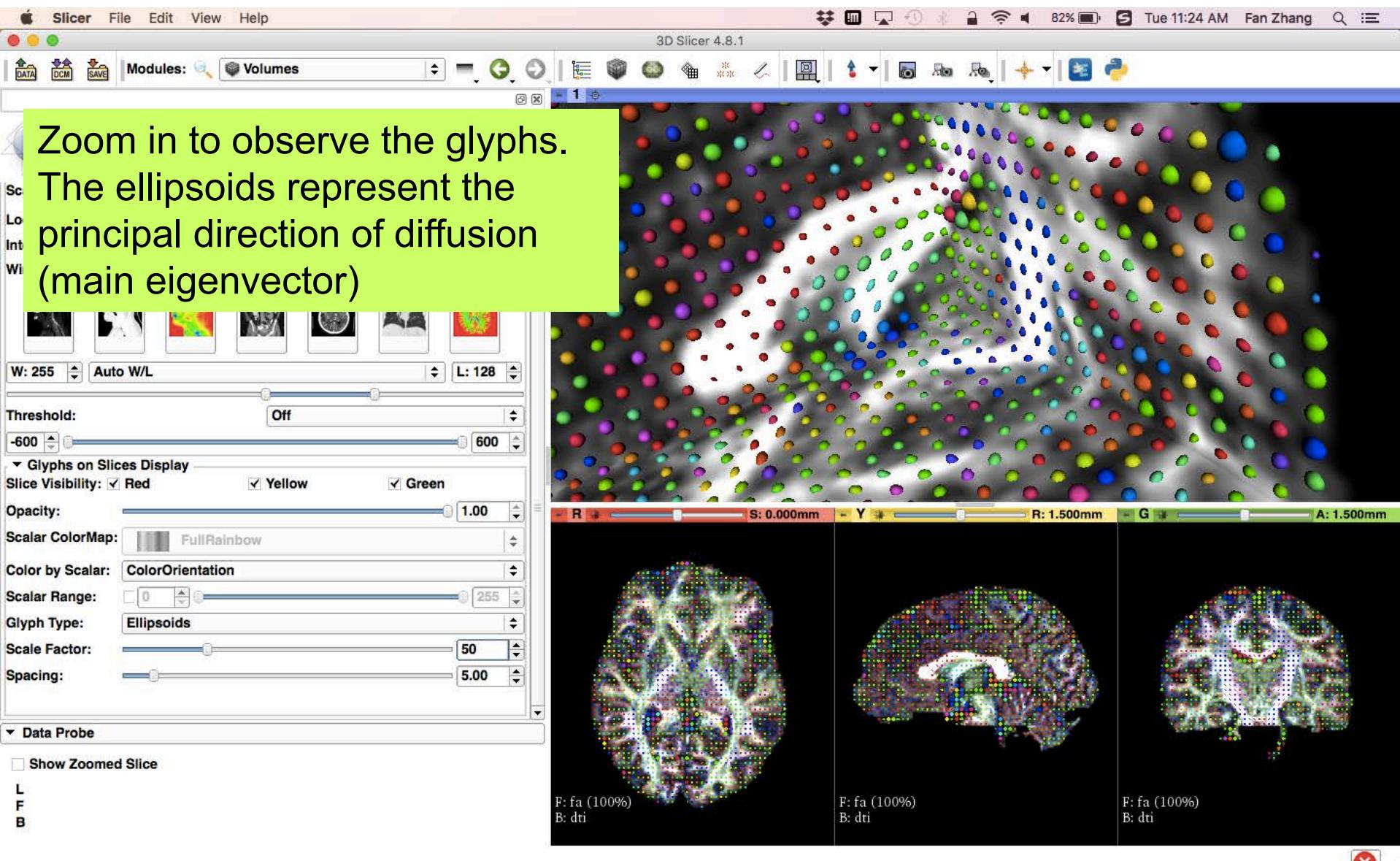
3D Visualization: Glyphs



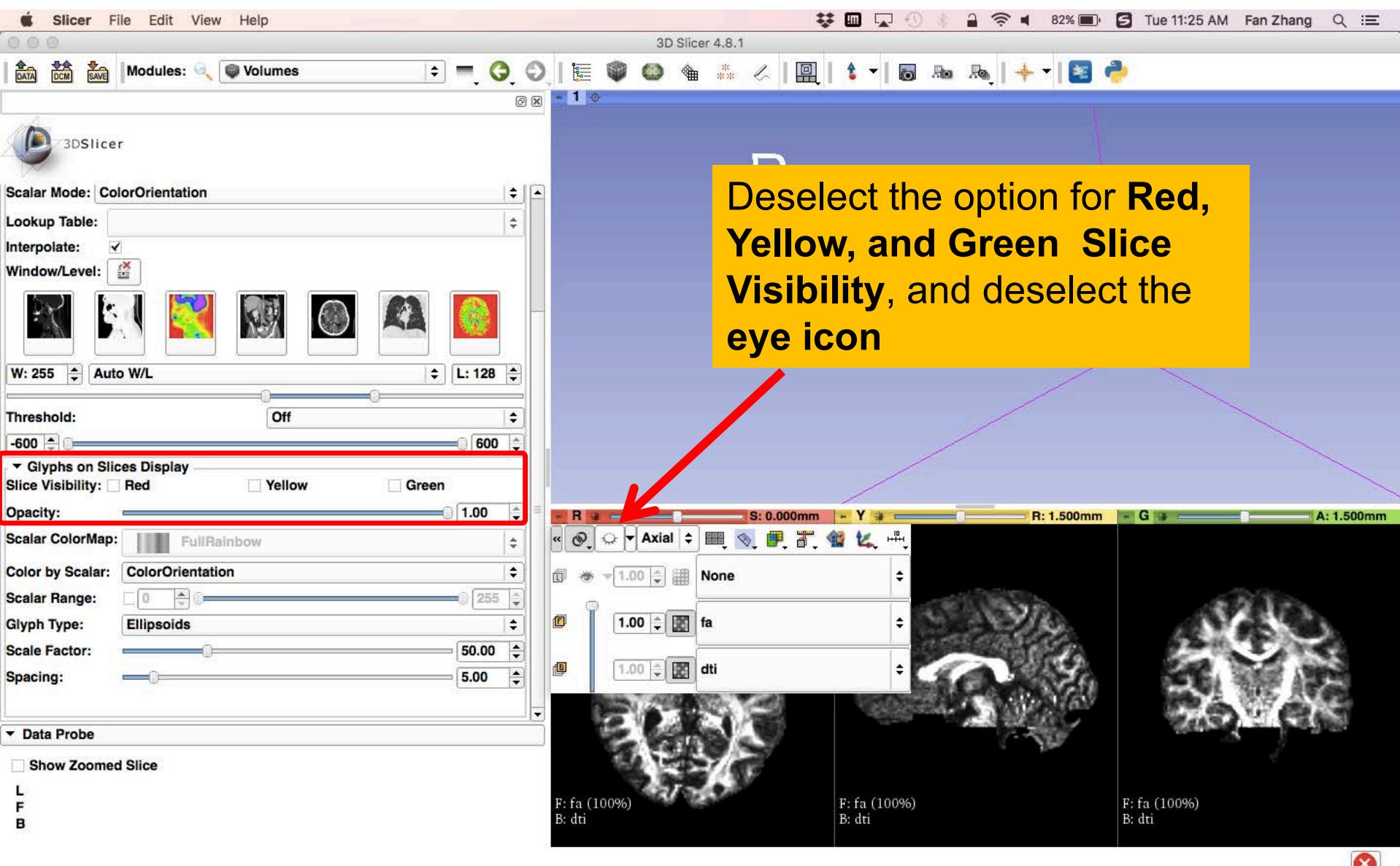
3D Visualization: Glyphs



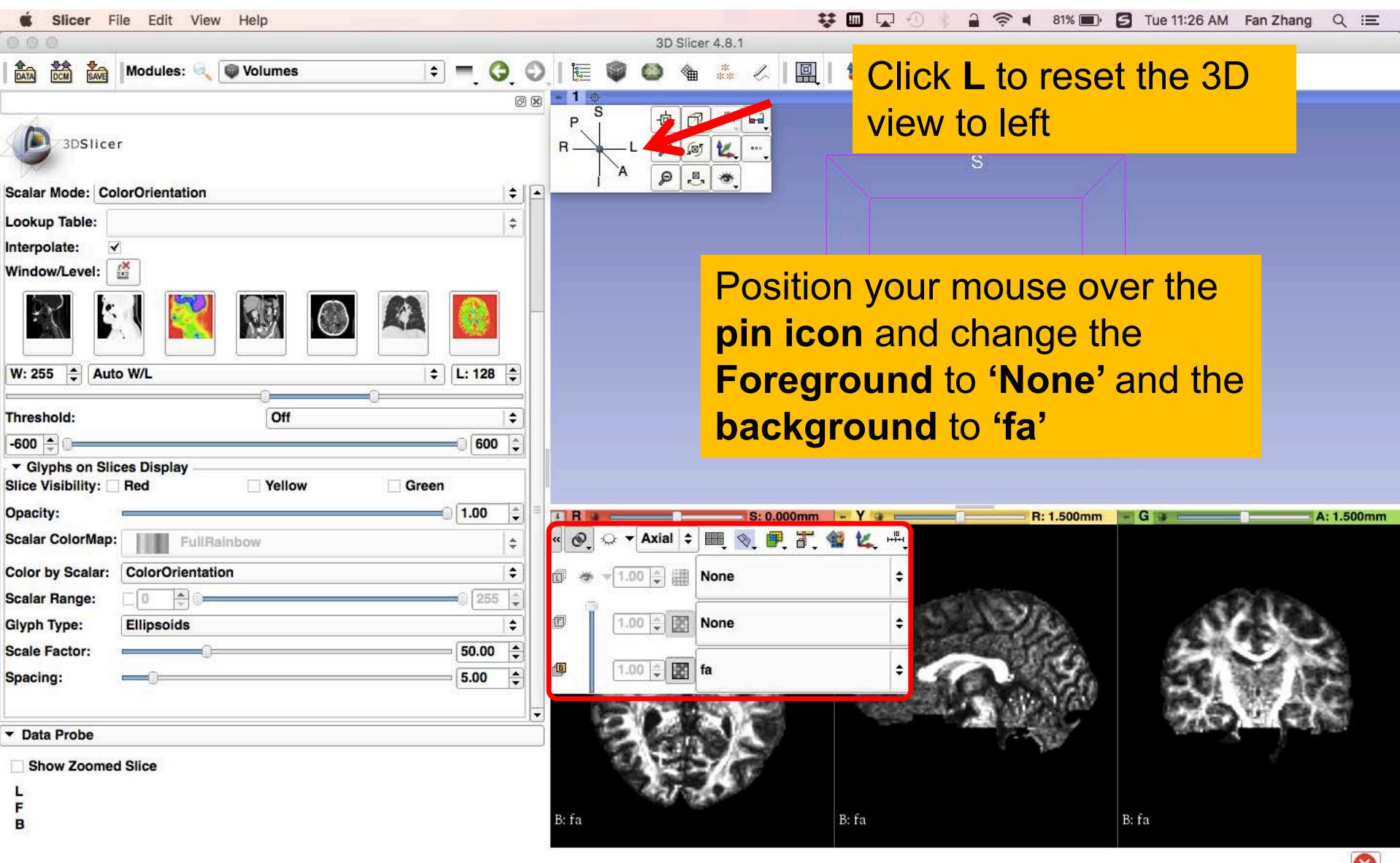
3D Visualization: Glyphs

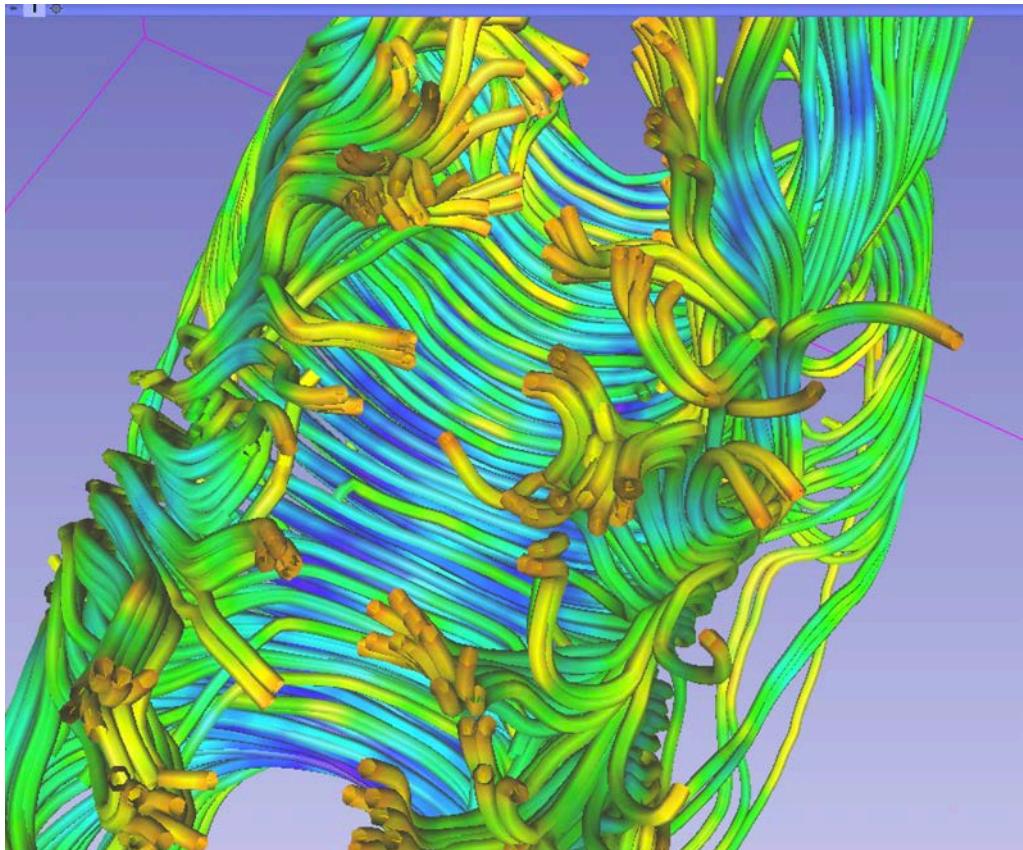


Diffusion MRI tractography



Diffusion MRI tractography



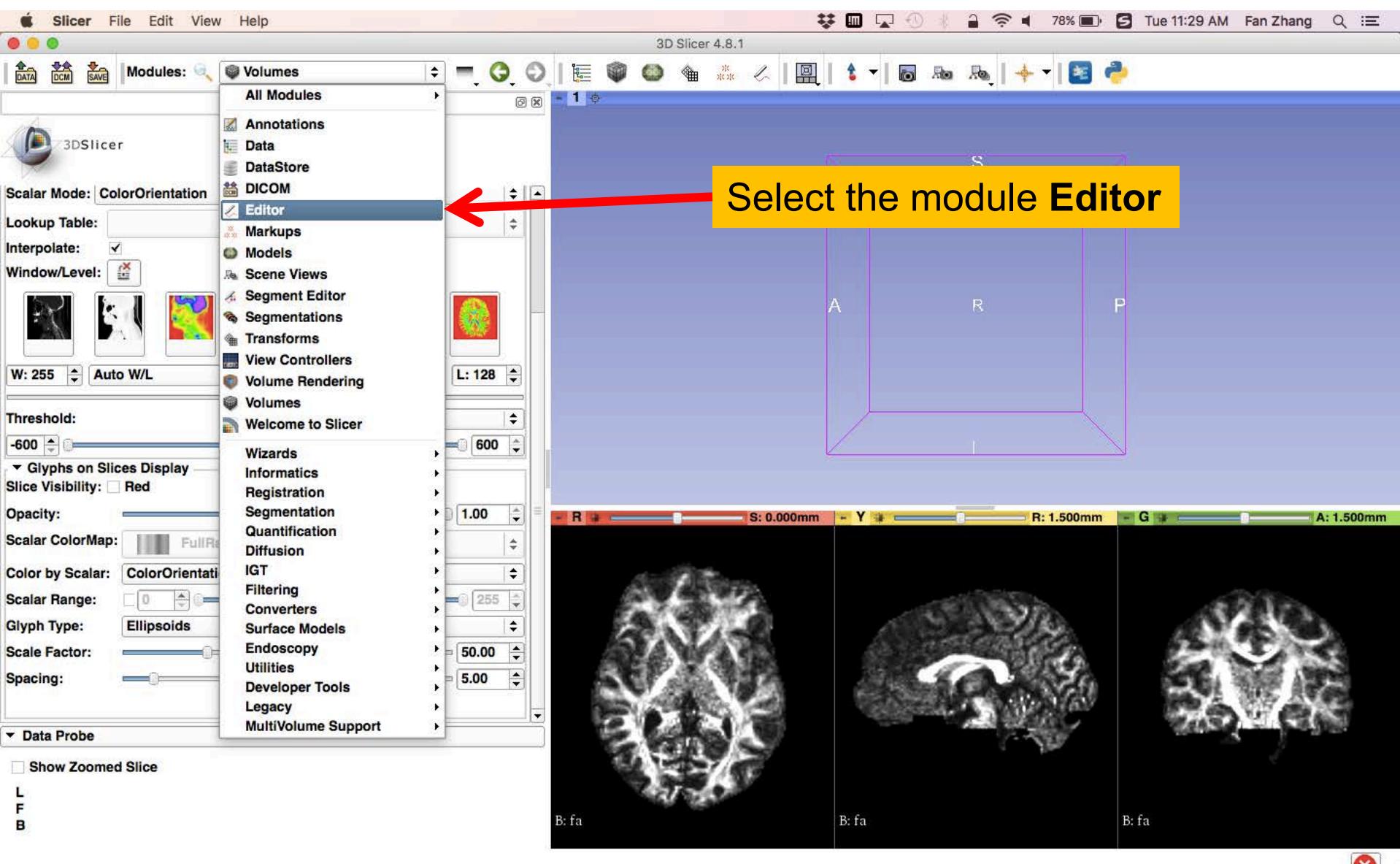


Part 3: From tensors to tracts

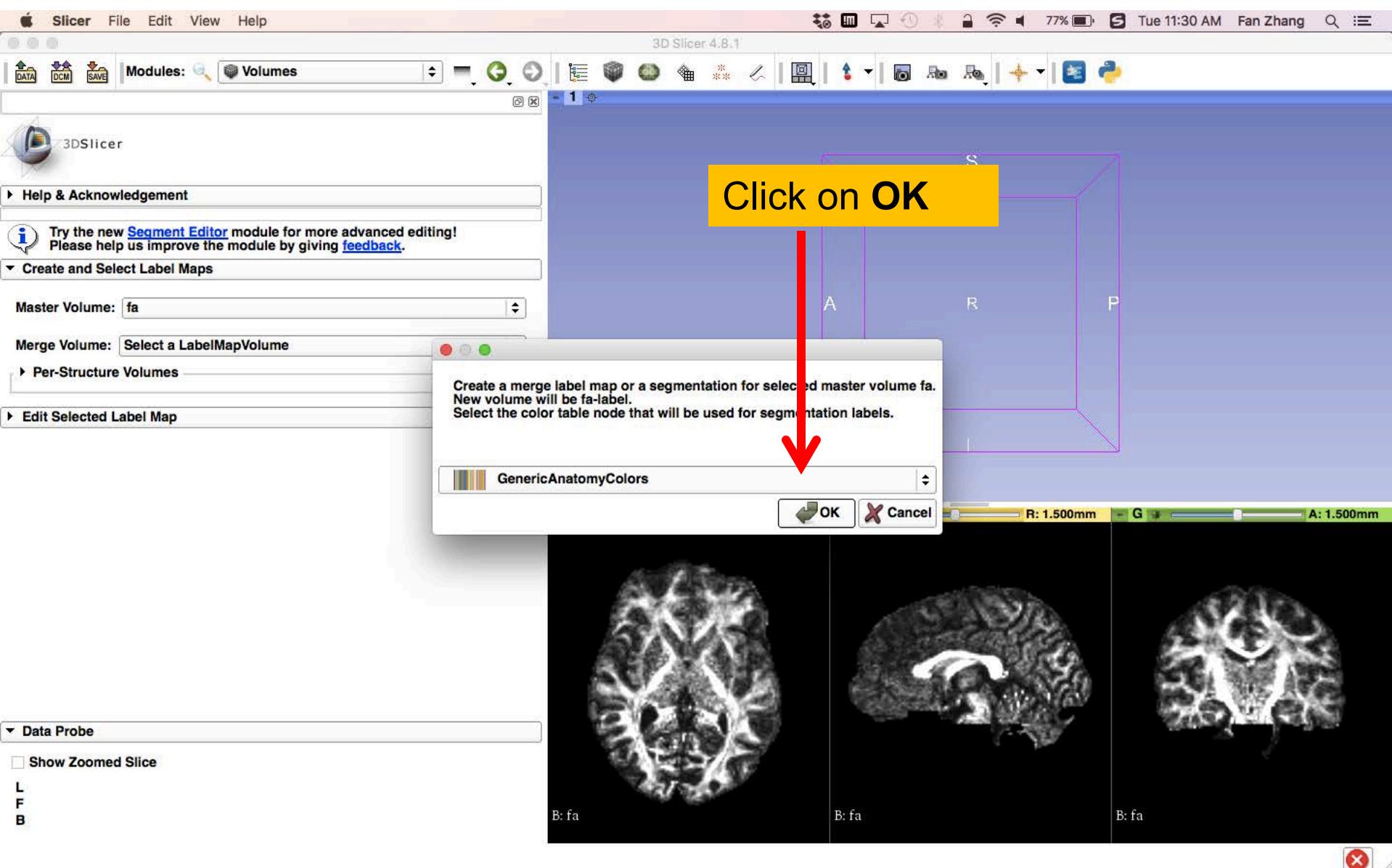
DTI tractography

- Definition of a region of interest (ROI) for seeding tract in an FA map (Editor module)
- Single-tensor tractography (Tractography Interactive Seeding module)
- Fiducial-seeding tractography (Tractography Interactive Seeding module)

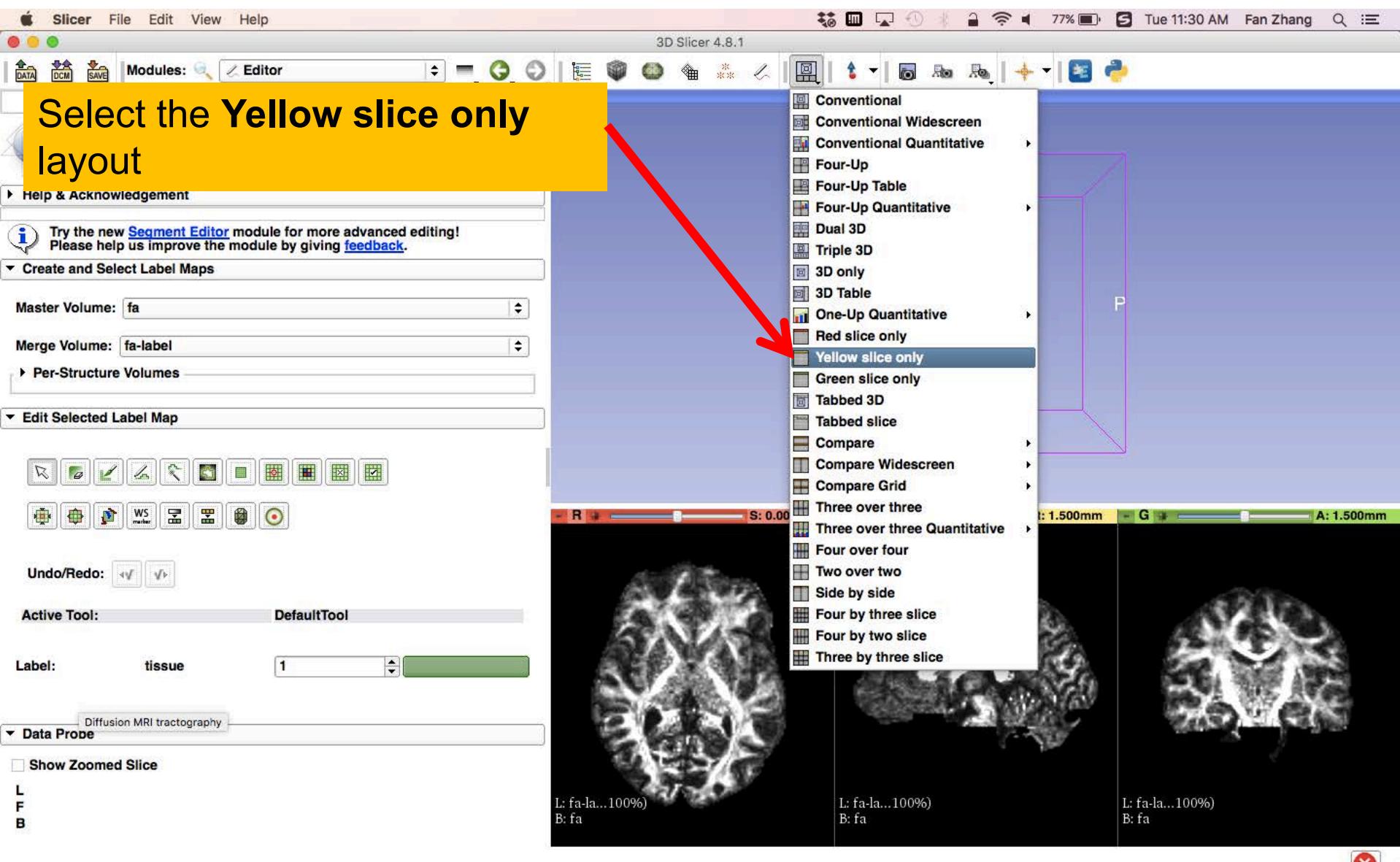
Diffusion MRI tractography



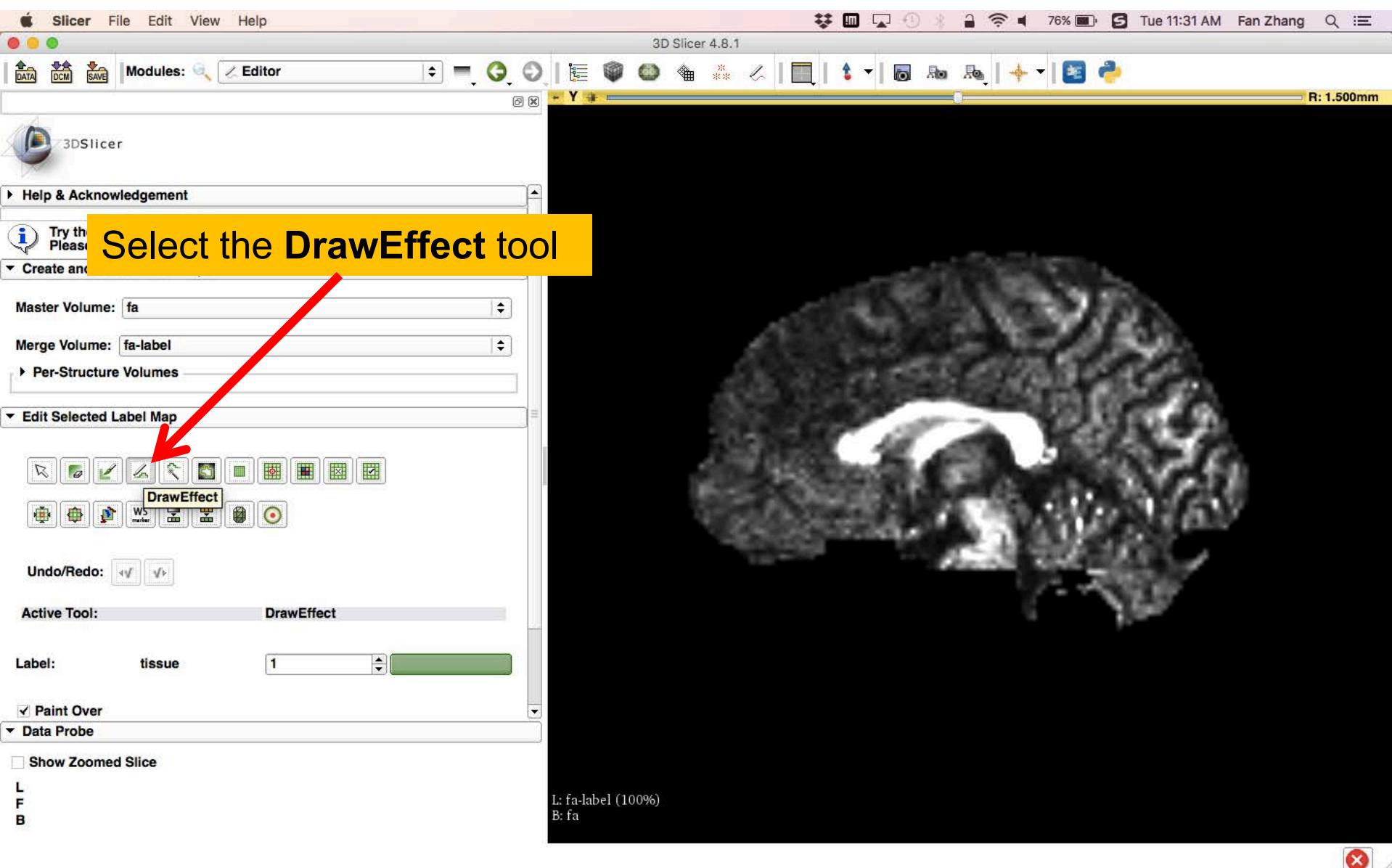
Diffusion MRI tractography



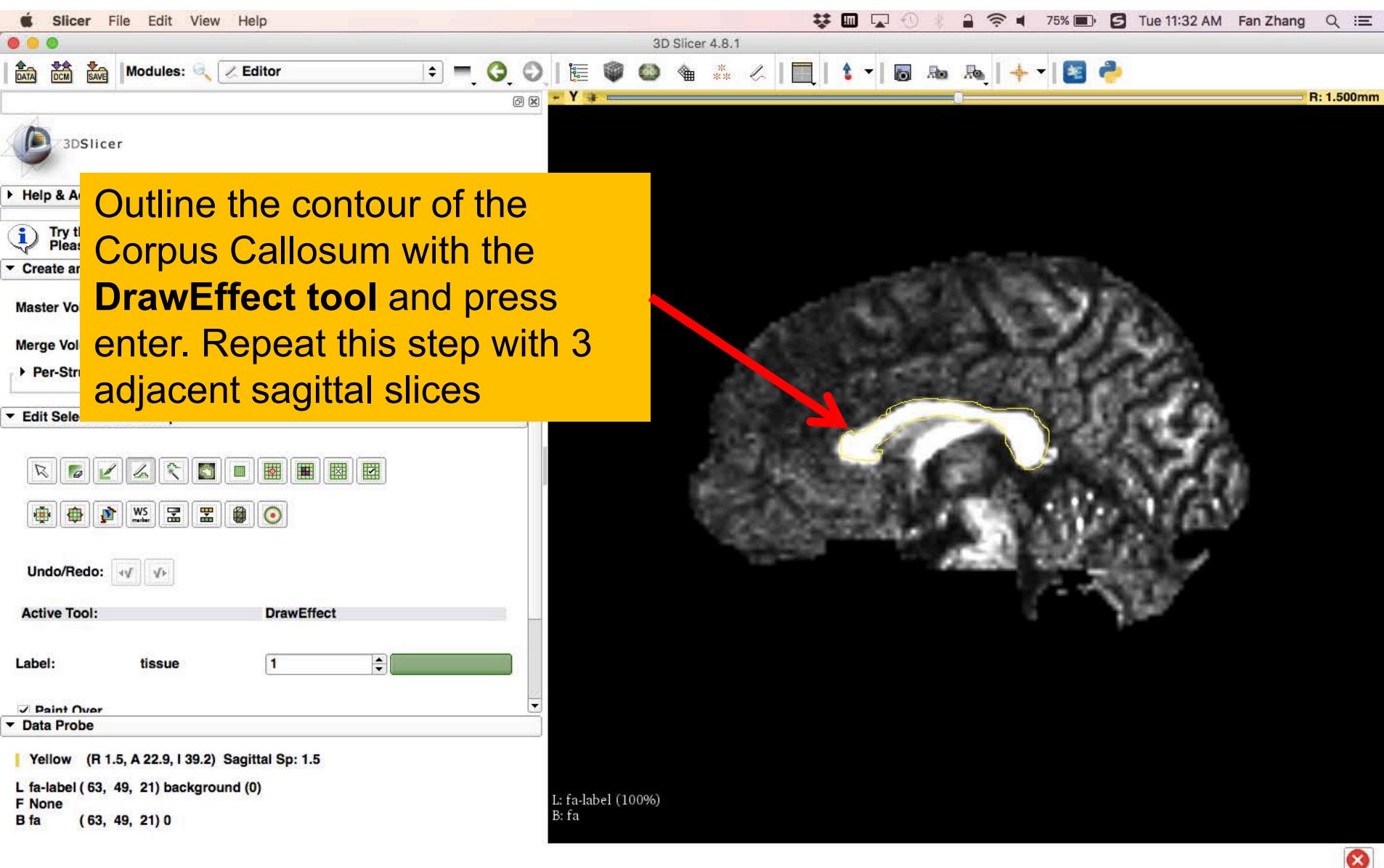
Diffusion MRI tractography



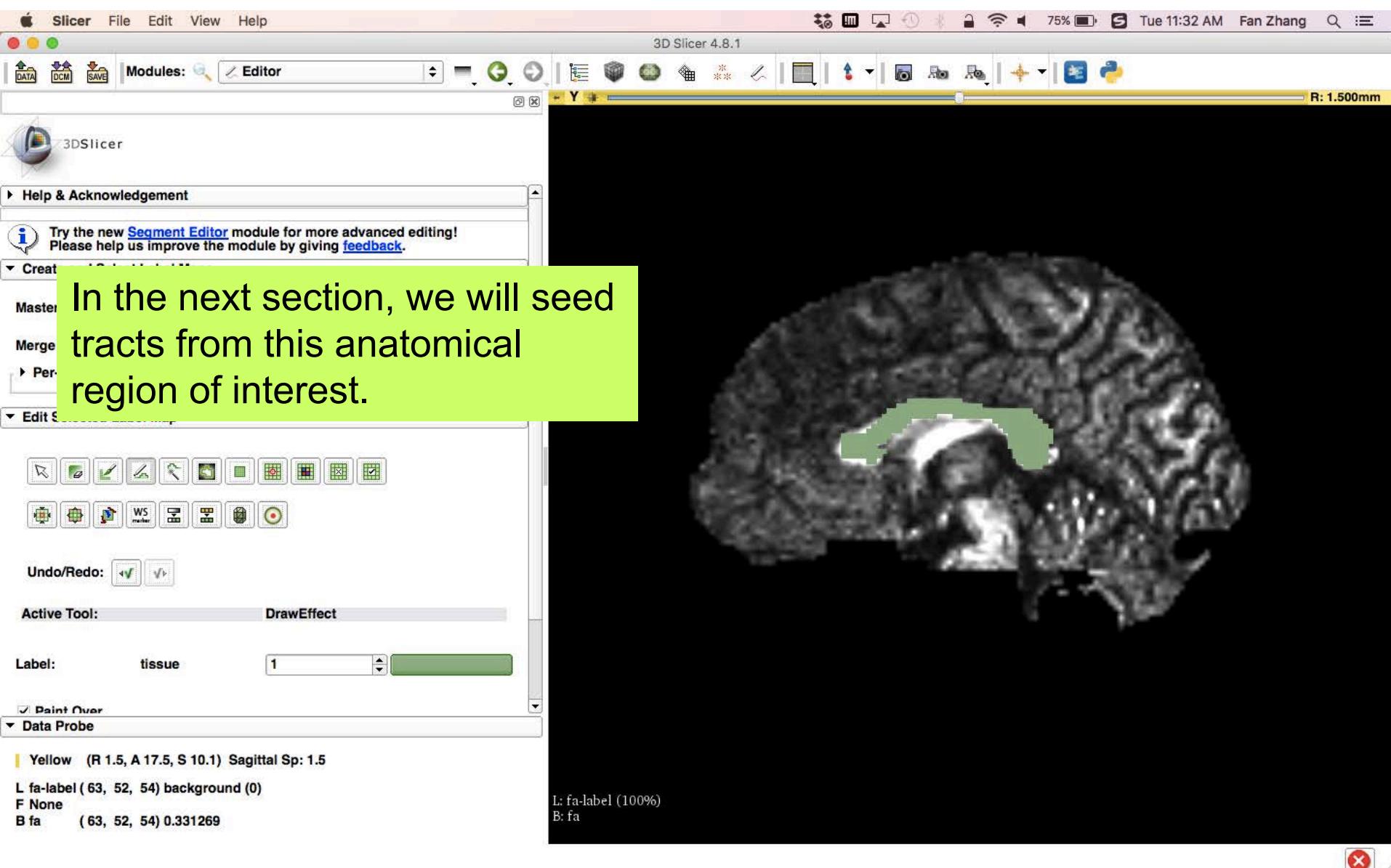
Diffusion MRI tractography



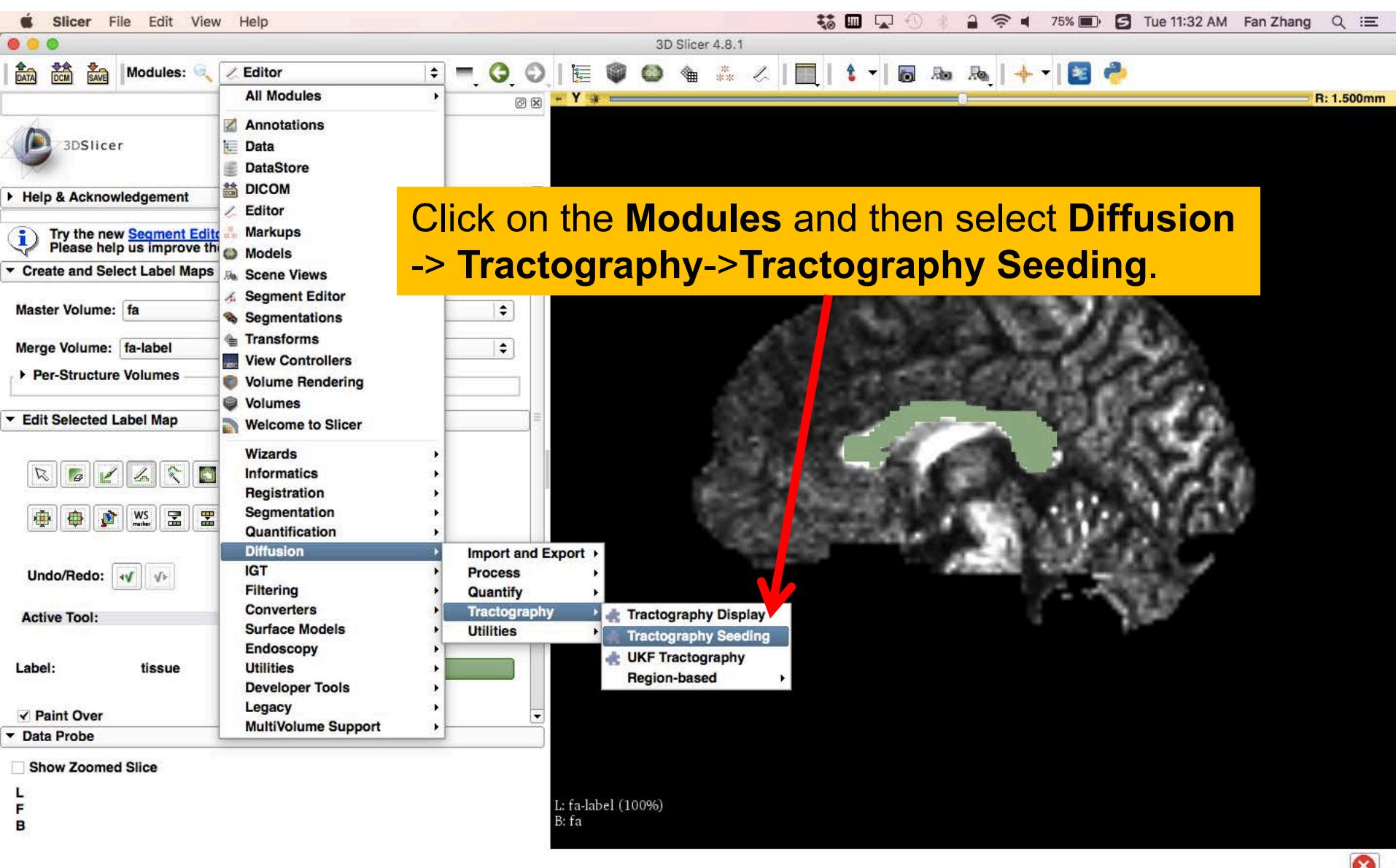
Diffusion MRI tractography



Diffusion MRI tractography



Diffusion MRI tractography



Step1: I/O

Change to **Conventional** view

The screenshot shows the 3D Slicer 4.8.1 interface. A red arrow points from the text "Change to Conventional view" to the top of the interface, specifically the toolbar area. A yellow box highlights the "Tractography Seeding" module parameters in the left panel. The "IO" section is expanded, showing:

- Input DTI Volume: dti
- Output Fiber Bundle: corpusCallosum
- Seeding
- Input Fiducials, Model or Label Map: fa-label

Below these, there are fields for "Seeding Label Value" (set to 1), "Seed Spacing (mm)" (set to 2.00), and checkboxes for "Use Index Space" and "Random Grid".

A brain scan is displayed on the right, with a green highlighted region indicating the tractography results.

-Set the Input DTI Volume to 'dti'

-Set Output Fiber Bundle to 'corpusCallosum' by renaming the default parameter 'Fiber Bundle'

-Set the Input Fiducials, Model or Label Map to 'fa-label'

Step 2: Seeding parameters

Slicer File Edit View Help

3D Slicer 4.8.1

DATA DCM SAVE Modules: Tractography Seeding

R: 1.500mm

3DSlicer

Help & Acknowledgement

Parameters Node

IO

Input DTI Volume: dti

Output Fiber Bundle: corpusCallosum

Seeding

Input Fiducials, Model or Label Map: fa-label

Seeding Label Value: 1

Seed Spacing (mm):

Use Index Space Random Grid

Update

Tractography Parameters

- Threshold Type: Fractional Anisotropy
- Seeding Threshold: 0.30
- Stopping Threshold: 0.25
- Integration Step Length (mm): 0.500mm

Advanced Options

Data Probe

Show Zoomed Slice

L F B

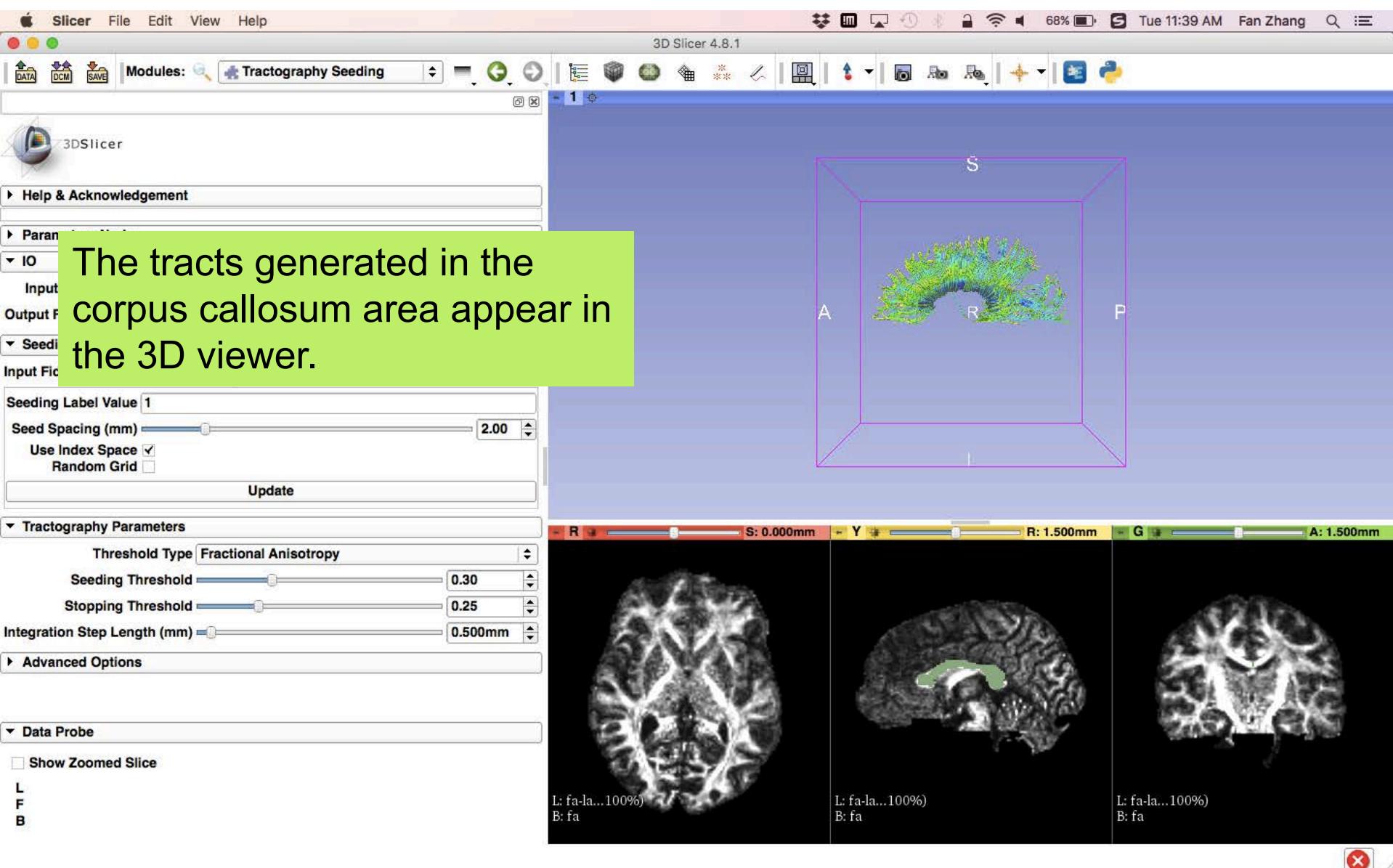
Select the default Tractography Seeding parameters:

- Threshold Type: FractionalAnistropy
- Seeding Threshold:0.30
- Stopping Threshold: 0.25

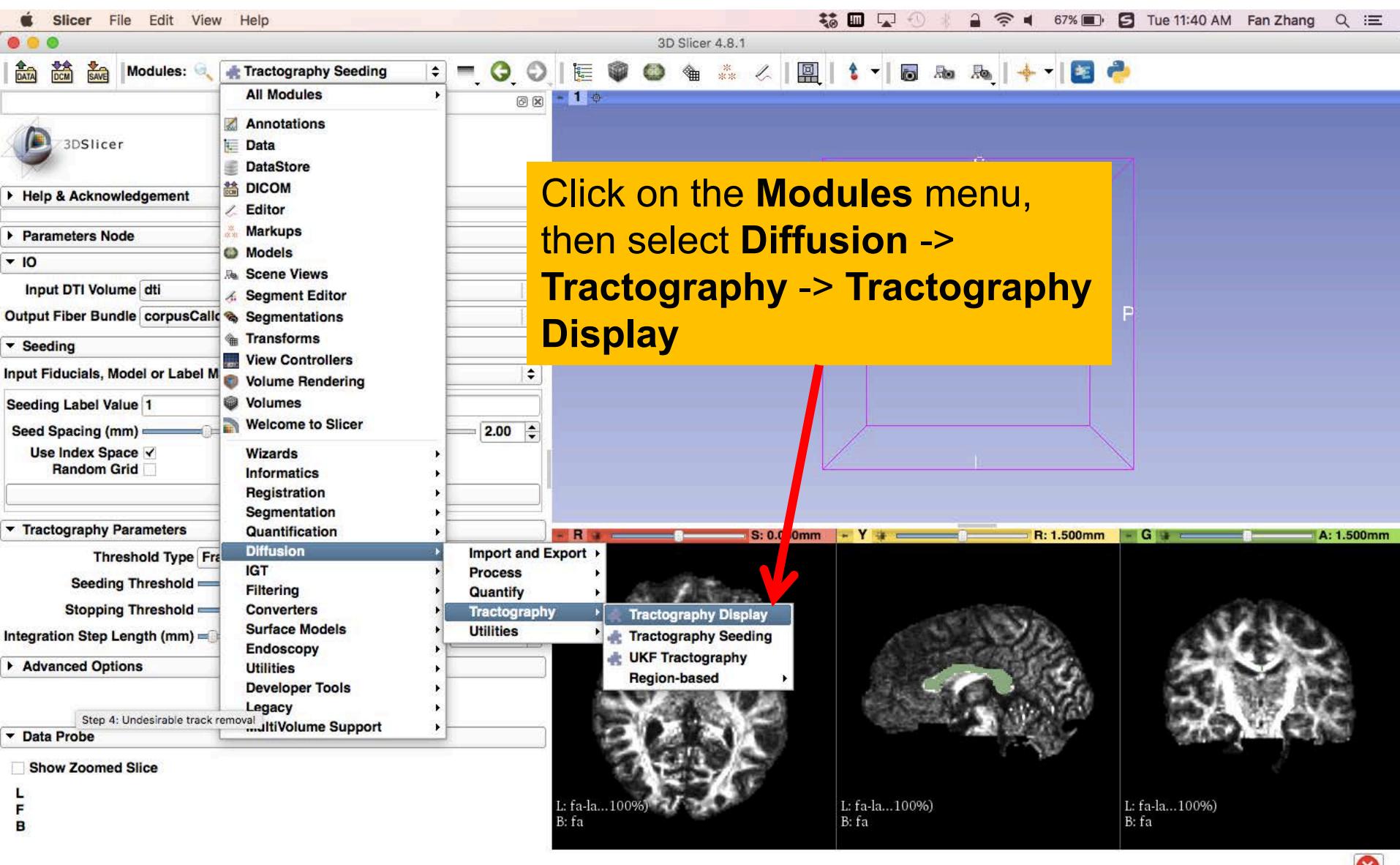
Click **Update** to generate tractography

L: fa-label (100%)
B: fa

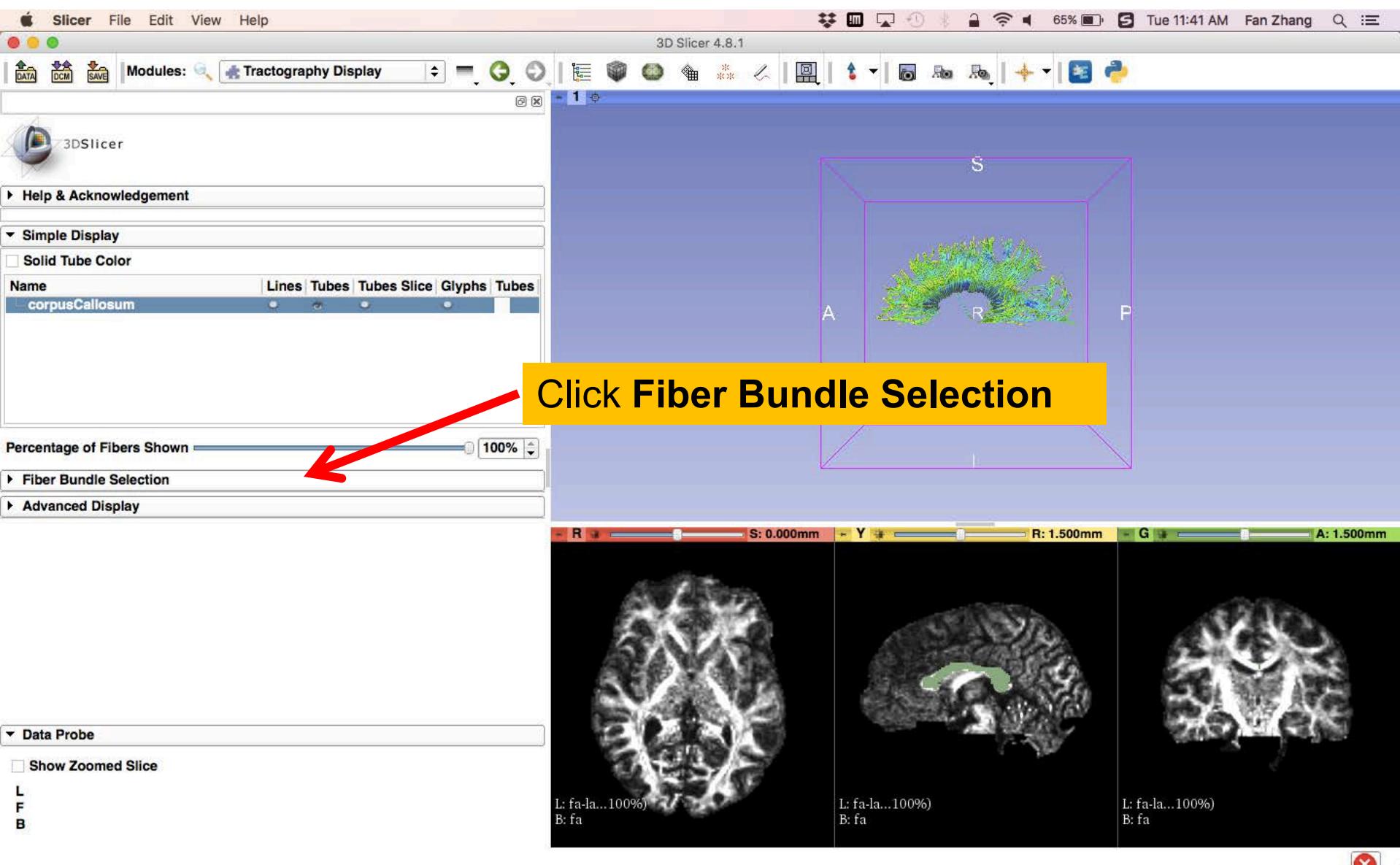
Step 3: Generate Tracts



Step 4: Undesirable track removal



Step 4: Undesirable track removal



Step 4: Undesirable track removal

Slicer File Edit View Help

3D Slicer 4.8.1

DATA DCM SAVE Modules: Tractography Display

3DSlicer

Help & Acknowledgement

Simple Display

Solid Tube Color

Name corpusCallosum Lines Tubes Tubes Slice Glyphs Tubes

Percentage of Fibers Shown 100%

Fiber Bundle Selection

ROI for Fiber Selection ROI Node

Disable ROI Positive ROI Negative ROI

Interactive ROI Updates ROI Visibility

Extract Bundle From ROI None

Update corpusCallosum From ROI Confirm update

Enable Interactive Edit

Advanced Display Step 4: Undesirable track removal

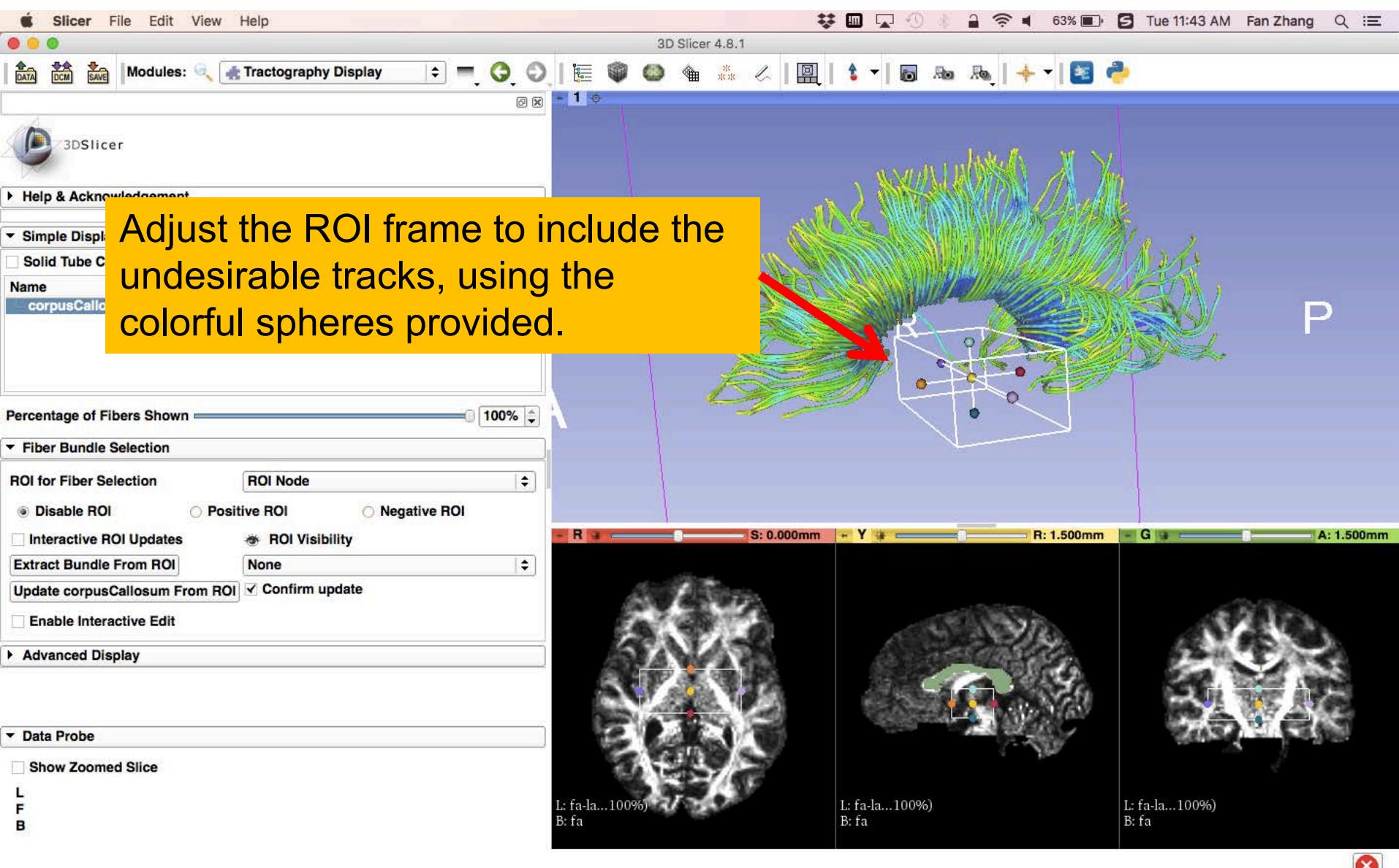
Show Zoomed Slice L F B

In 'Fiber Bundle Selection', under **ROI for Fiber Select**, create a new **AnnotationROI** as 'ROI node' and select **Disable ROI**.

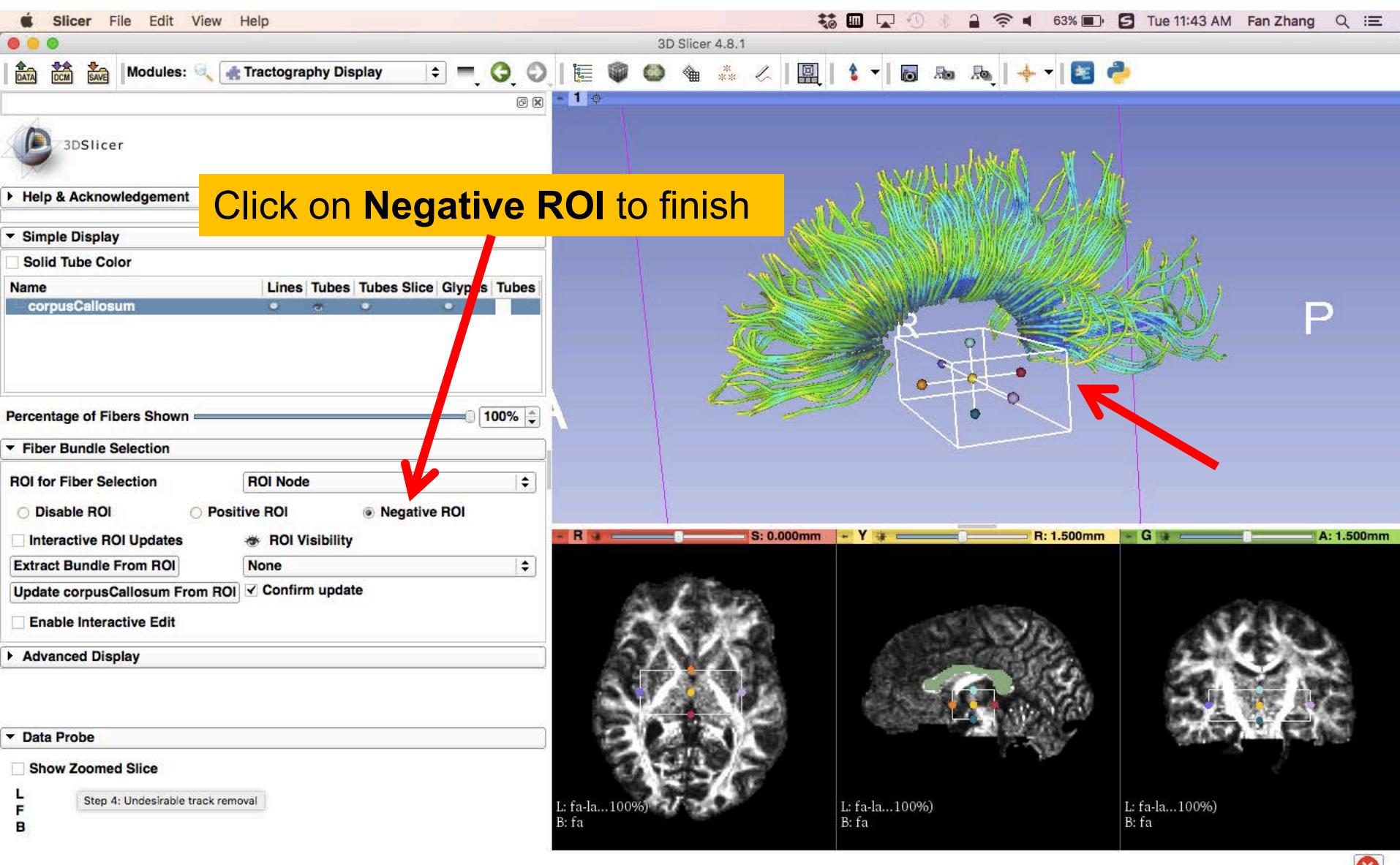
A: 1.500mm

The screenshot shows the 3D Slicer interface. On the left, the 'Tractography Display' module is active. The 'Fiber Bundle Selection' panel is open, with a red arrow pointing to the 'ROI for Fiber Selection' dropdown set to 'ROI Node'. Below it, the 'Disable ROI' radio button is selected. The main window displays a 3D brain model with a green fiber bundle highlighted. A yellow callout box contains the instructions. At the bottom, three 2D brain slices show the fiber bundle's path through different planes.

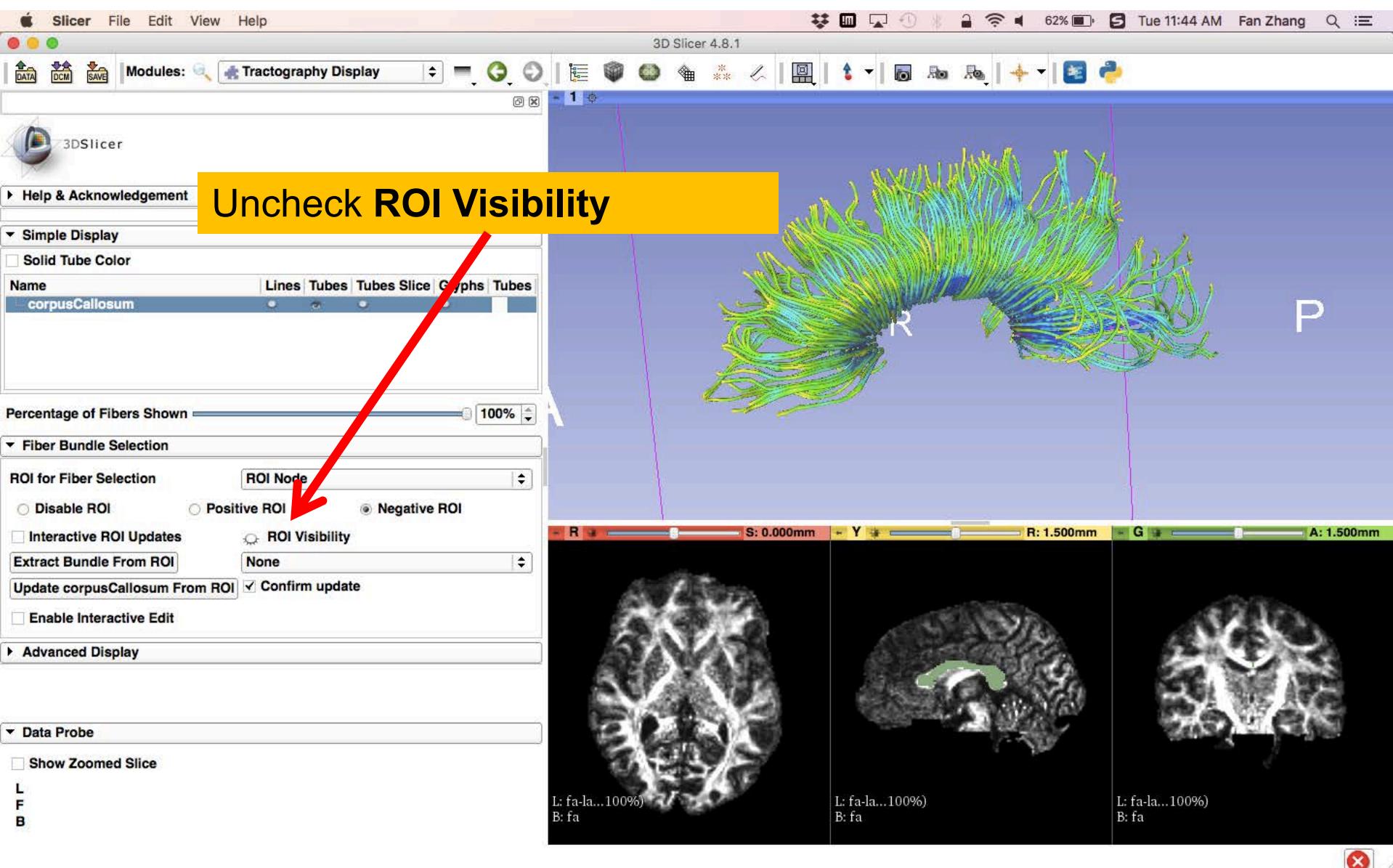
Step 4: Undesirable track removal



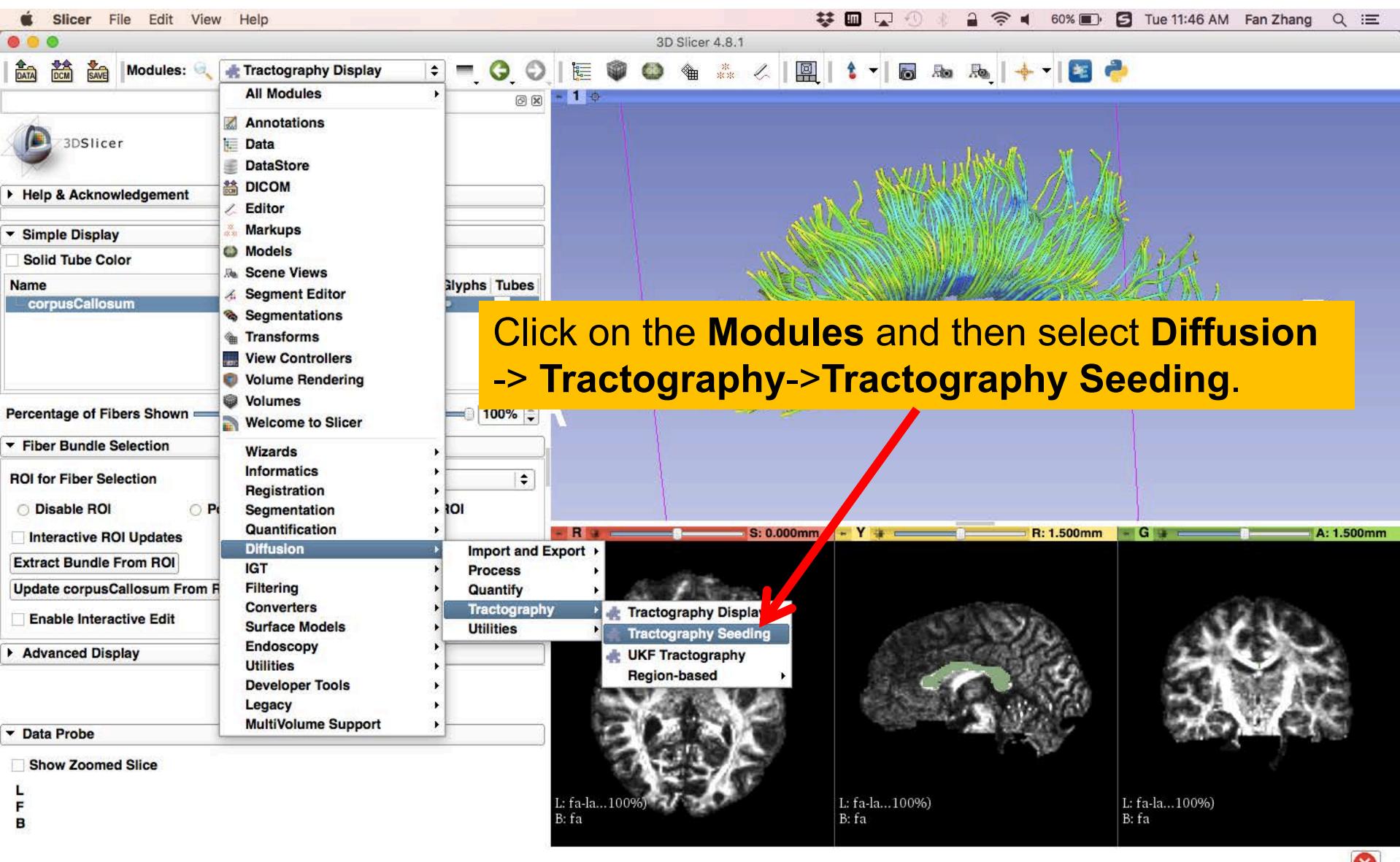
Step 4: Undesirable track removal



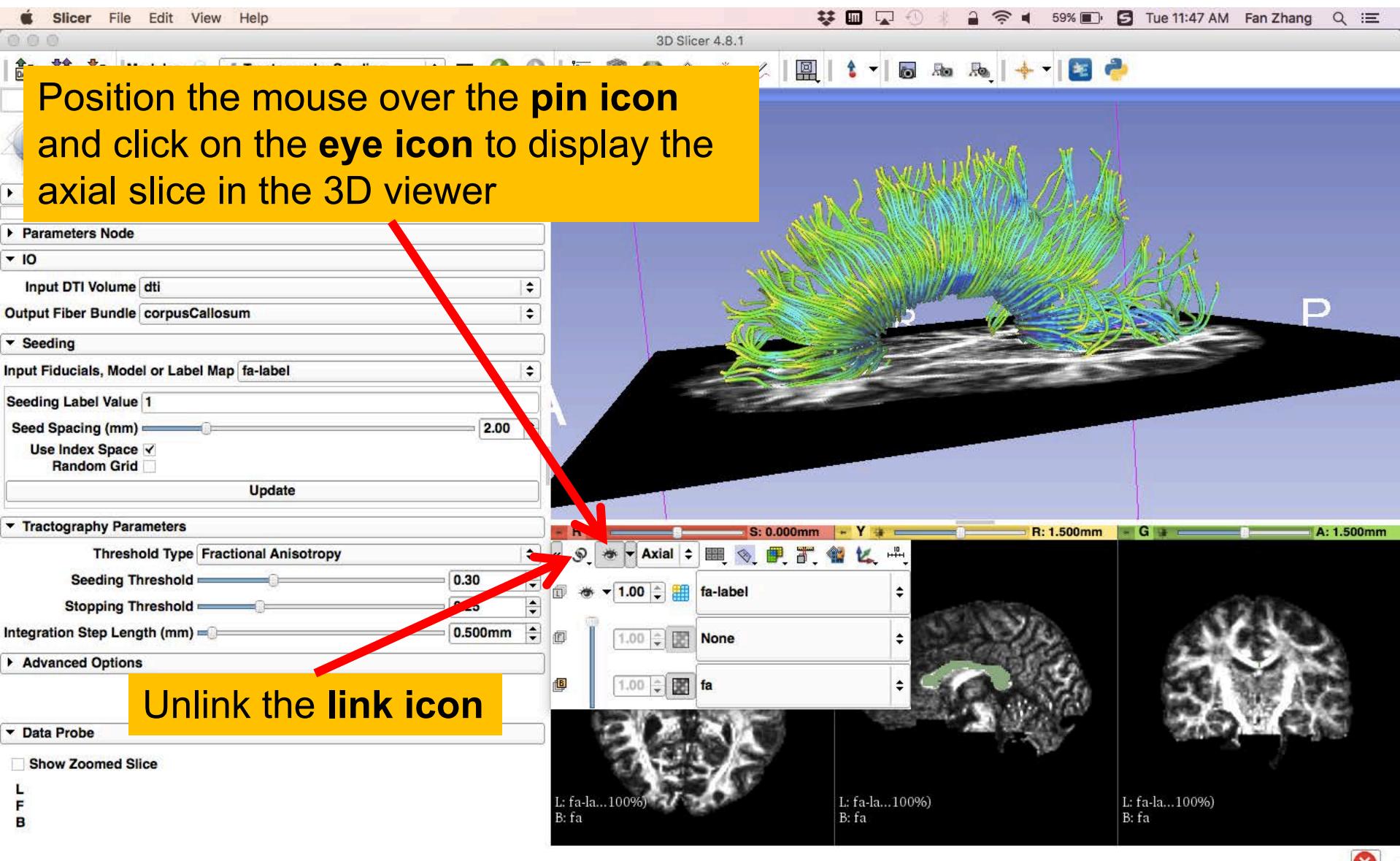
Step 4: Undesirable track removal



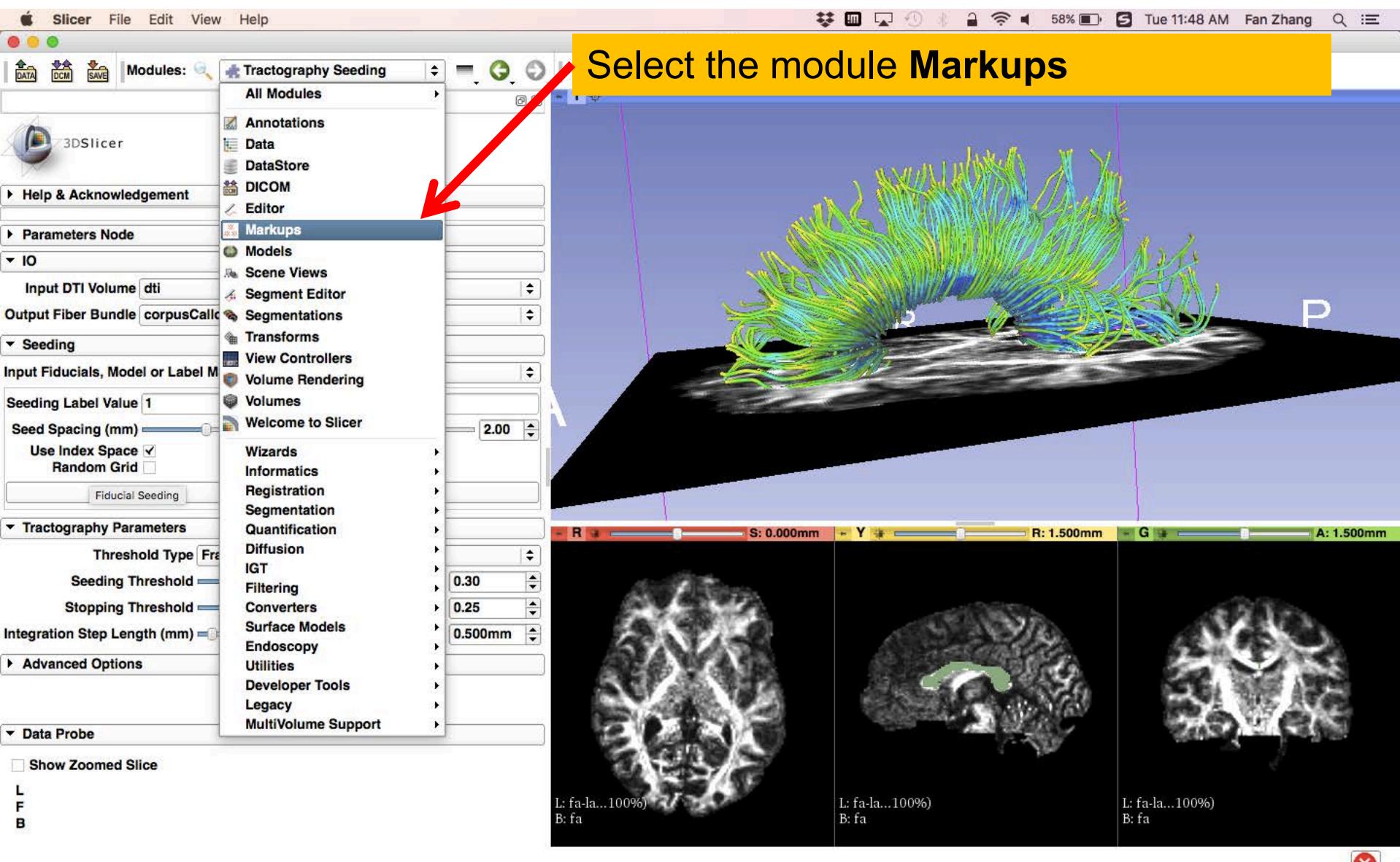
Fiducial Seeding



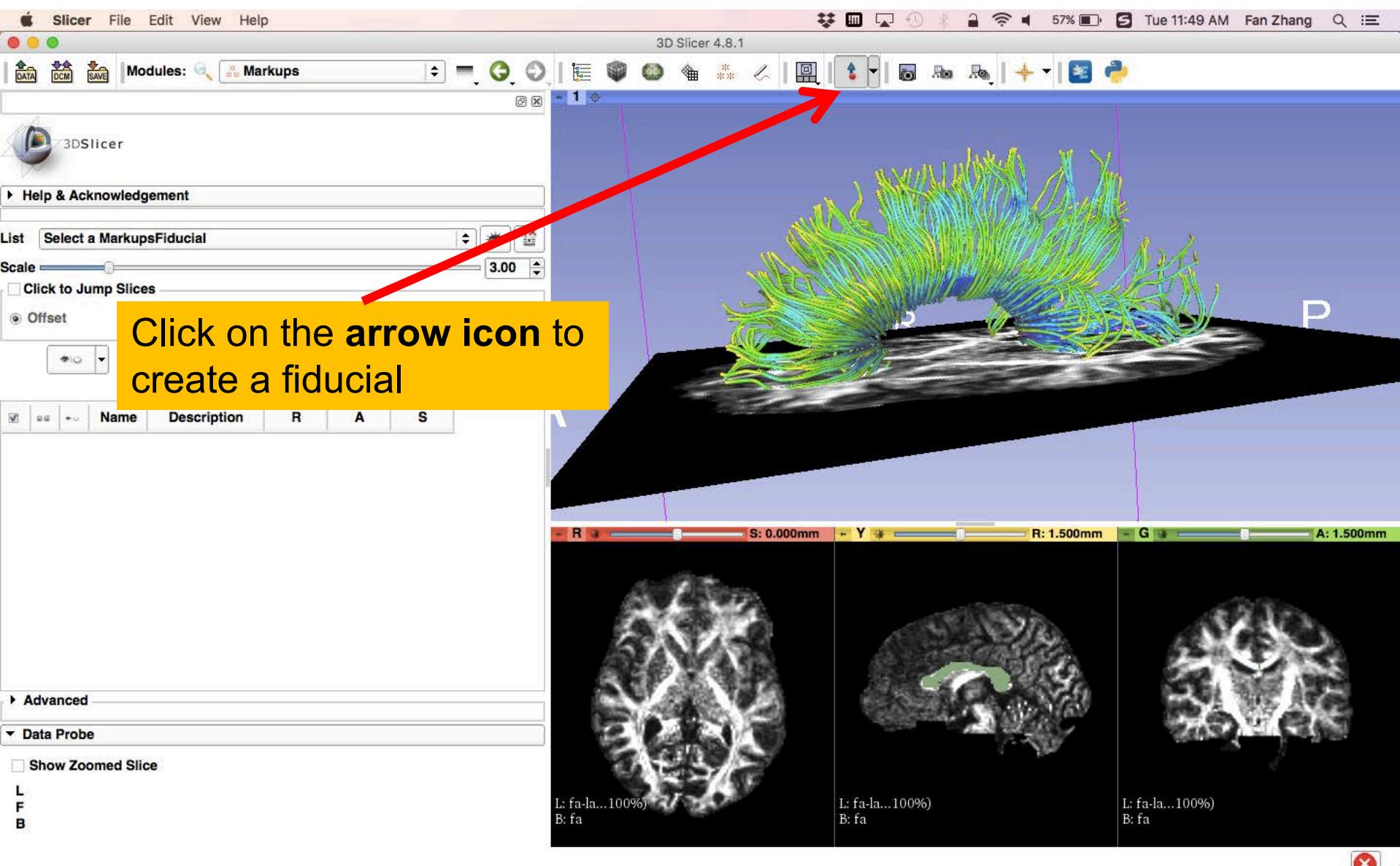
Fiducial Seeding



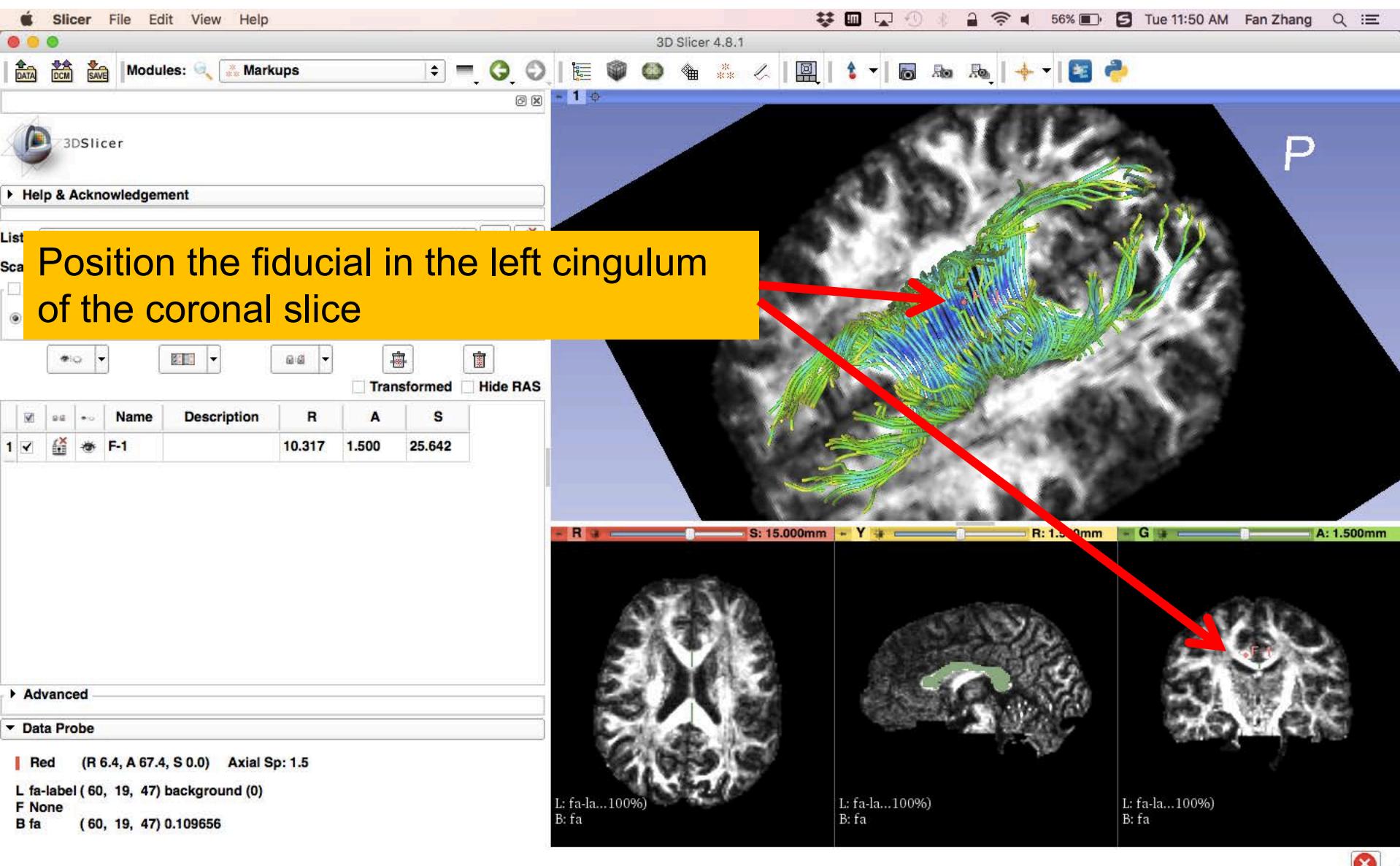
Fiducial Seeding



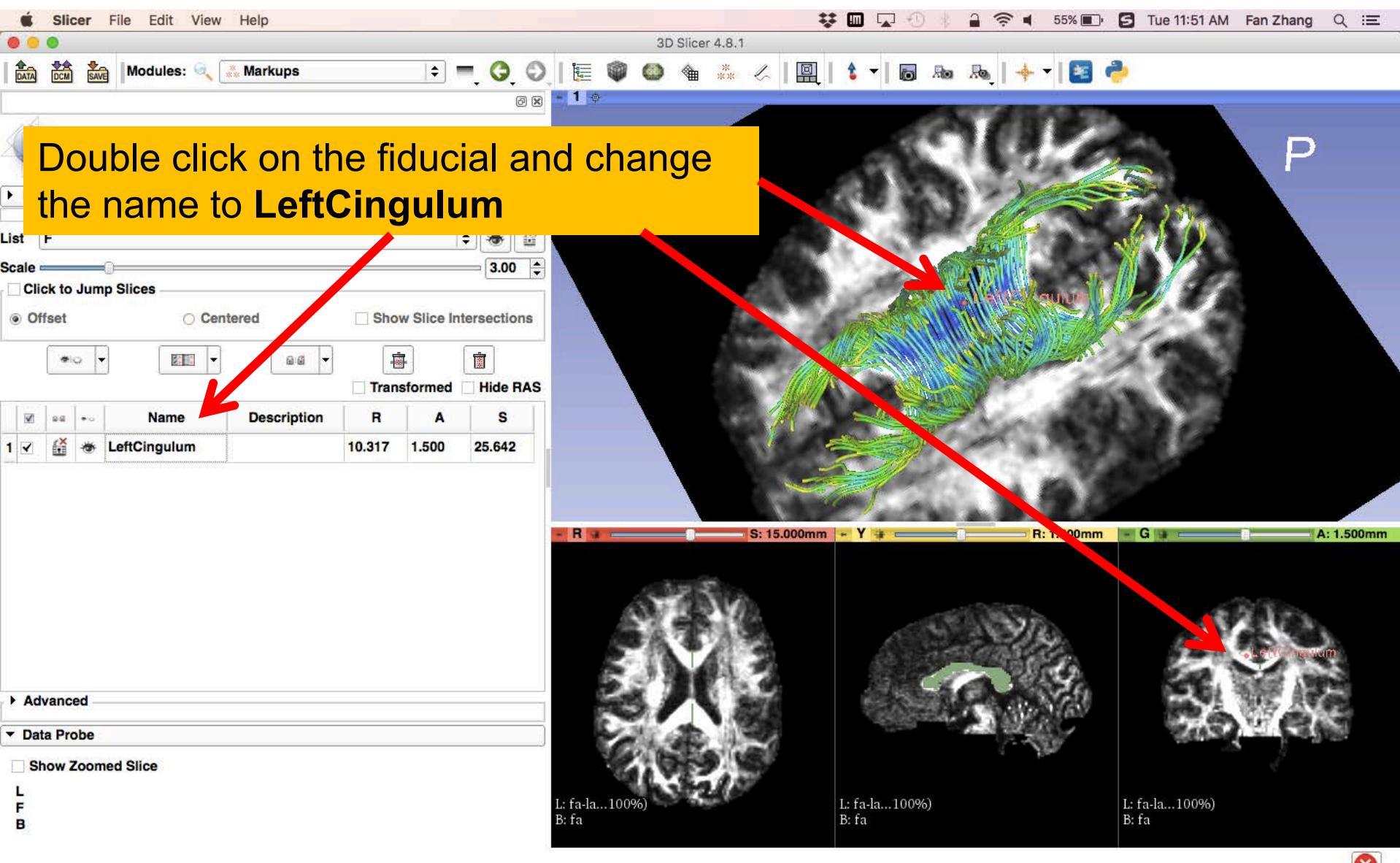
Fiducial Seeding



Fiducial Seeding



Fiducial Seeding



Fiducial Seeding

The screenshot shows the 3D Slicer 4.8.1 interface. A red box highlights the 'Modules' dropdown menu at the top, which is set to 'Tractography Seeding'. Another red box highlights the 'Input DTI Volume' field in the 'IO' panel, which is set to 'dti'. A red arrow points from the text 'Click Update' in the yellow box below to the 'Update (check for interactive)' button in the 'Seeding' section of the 'Tractography Seeding' module settings.

Click on the **Modules** and then select **Diffusion -> Tractography->Tractography Seeding**.

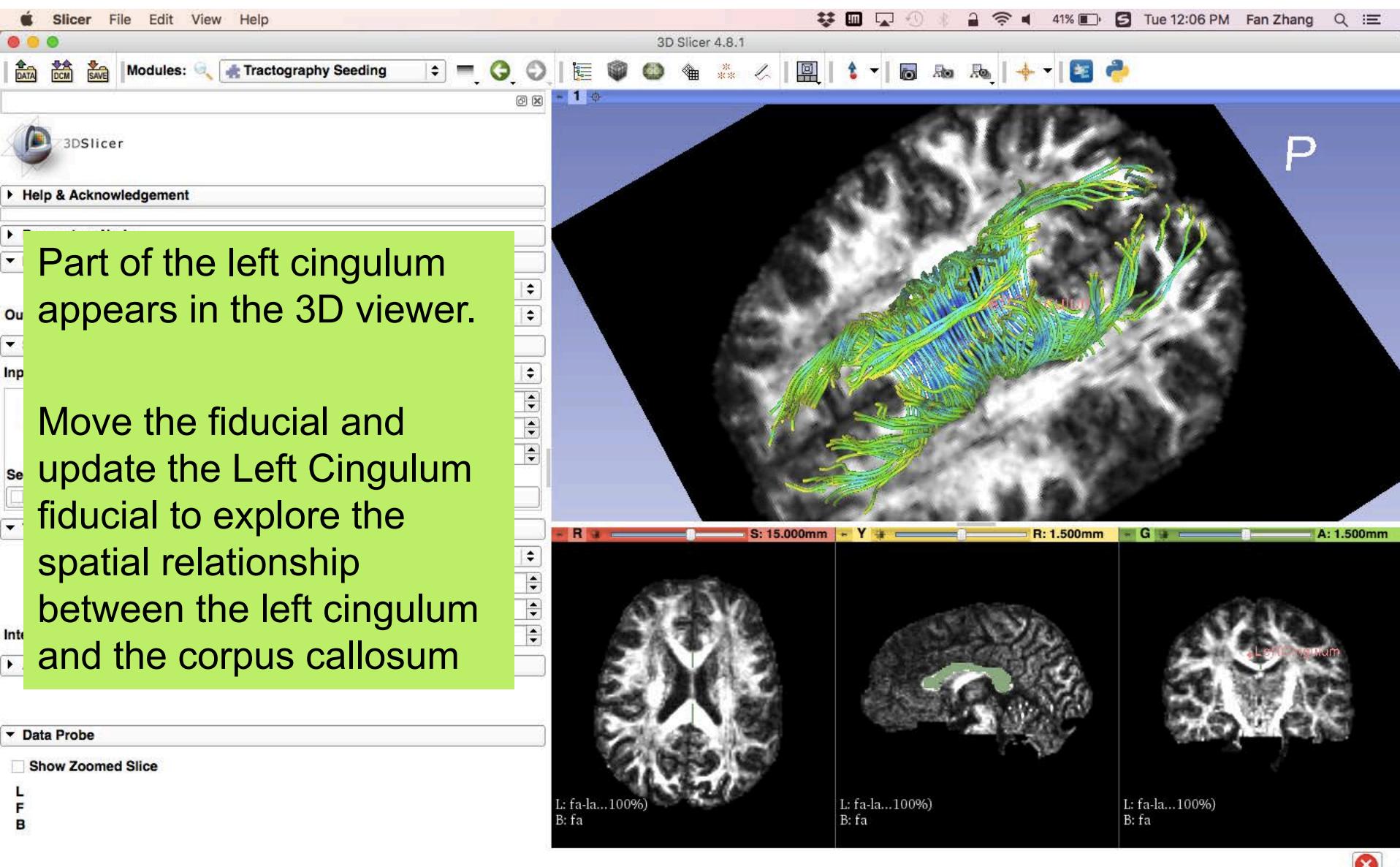
Set the Input DTI volume to '**dti**'

Set the Input **Fiducials, Model or Label Map** to '**F**'

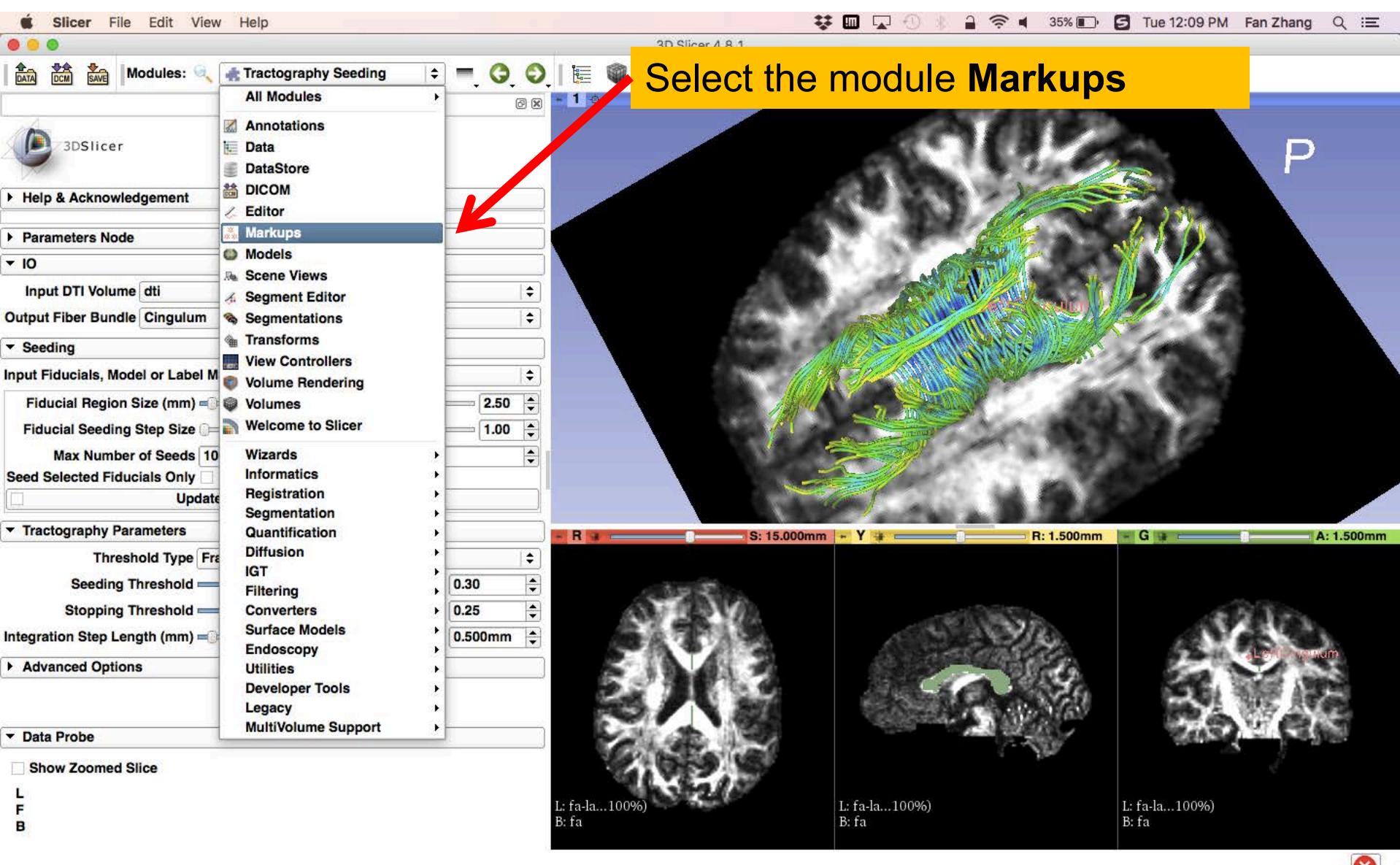
Select the Output Fiber Bundle 'Create New Fiber Bundle as ...' and name it '**Cingulum**'

Click **Update**

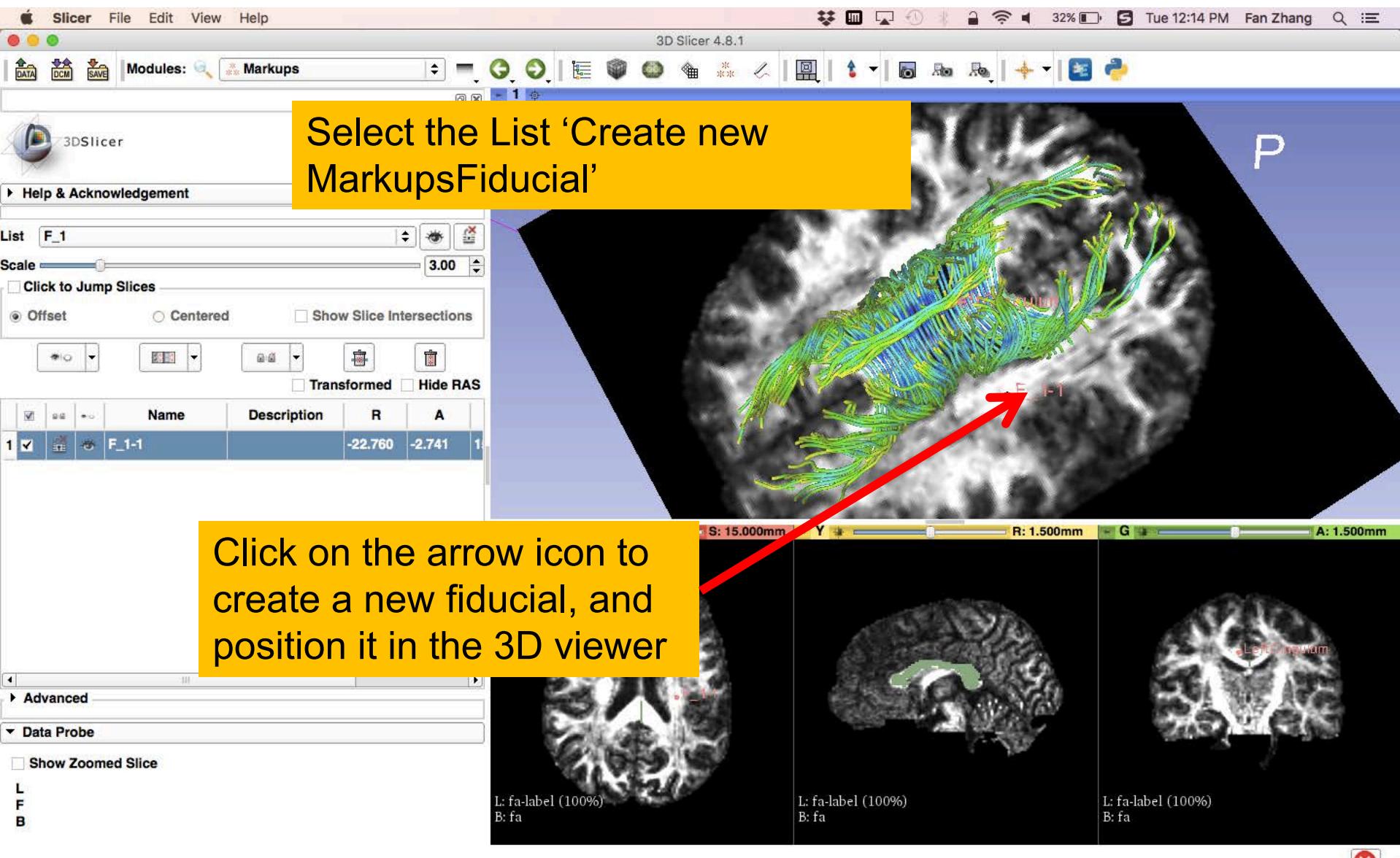
Fiducial Seeding



Tractography ‘on-the-fly’



Tractography ‘on-the-fly’



Tractography ‘on-the-fly’

The screenshot shows the 3D Slicer 4.8.1 interface. At the top, the title bar reads "3D Slicer 4.8.1". Below it is a toolbar with various icons. The "Modules" dropdown menu is highlighted with a red box and contains the option "Tractography Seeding". The main window displays a 3D brain scan with numerous colored fibers representing tractography results. On the left, the "Parameters Node" panel is open, showing the "Tractography Seeding" module configuration. A yellow box highlights the "Input DTI Volume" field set to "dti" and the "Output Fiber Bundle" field set to "TractOnTheFly". Another yellow box highlights the "Input Fiducials, Model or Label Map" field set to "F_1". A red arrow points from this field to the text "Set the Input DTI volume to 'dti'". A red box also surrounds the "Seeding" section of the parameters. A red arrow points from the "Update (check for interactive)" checkbox in this section to the text "Check Update (check for interactive)". The bottom of the screen shows a control bar with sliders for "S: 15.000mm", "R: 1.500mm", "G: 1.500mm", and "A: 1.500mm".

Click on the **Modules** and then select **Diffusion -> Tractography->Tractography Seeding**.

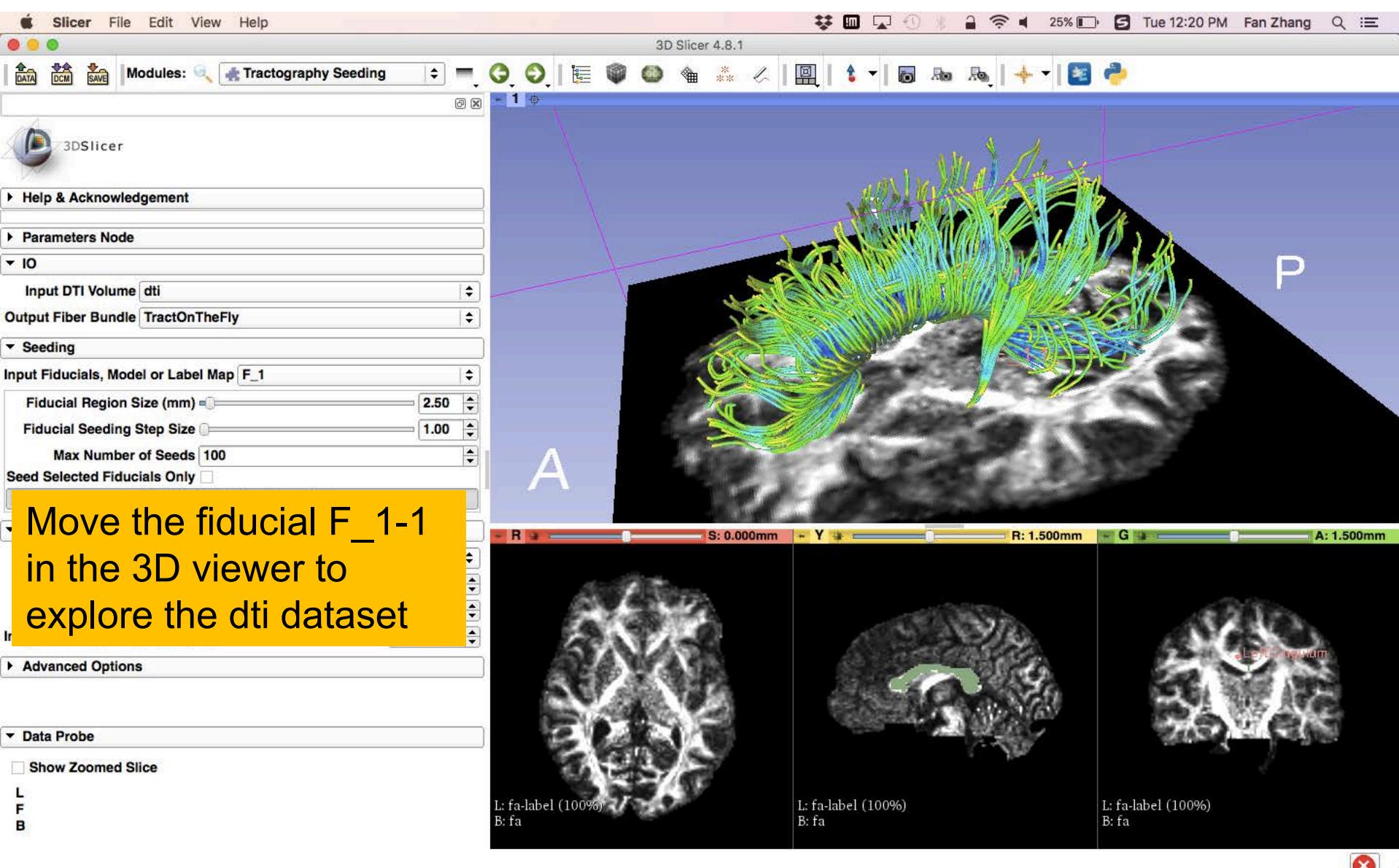
Set the Input DTI volume to '**dti**'

Set the Input **Fiducials, Model or Label Map** to '**F_1**'

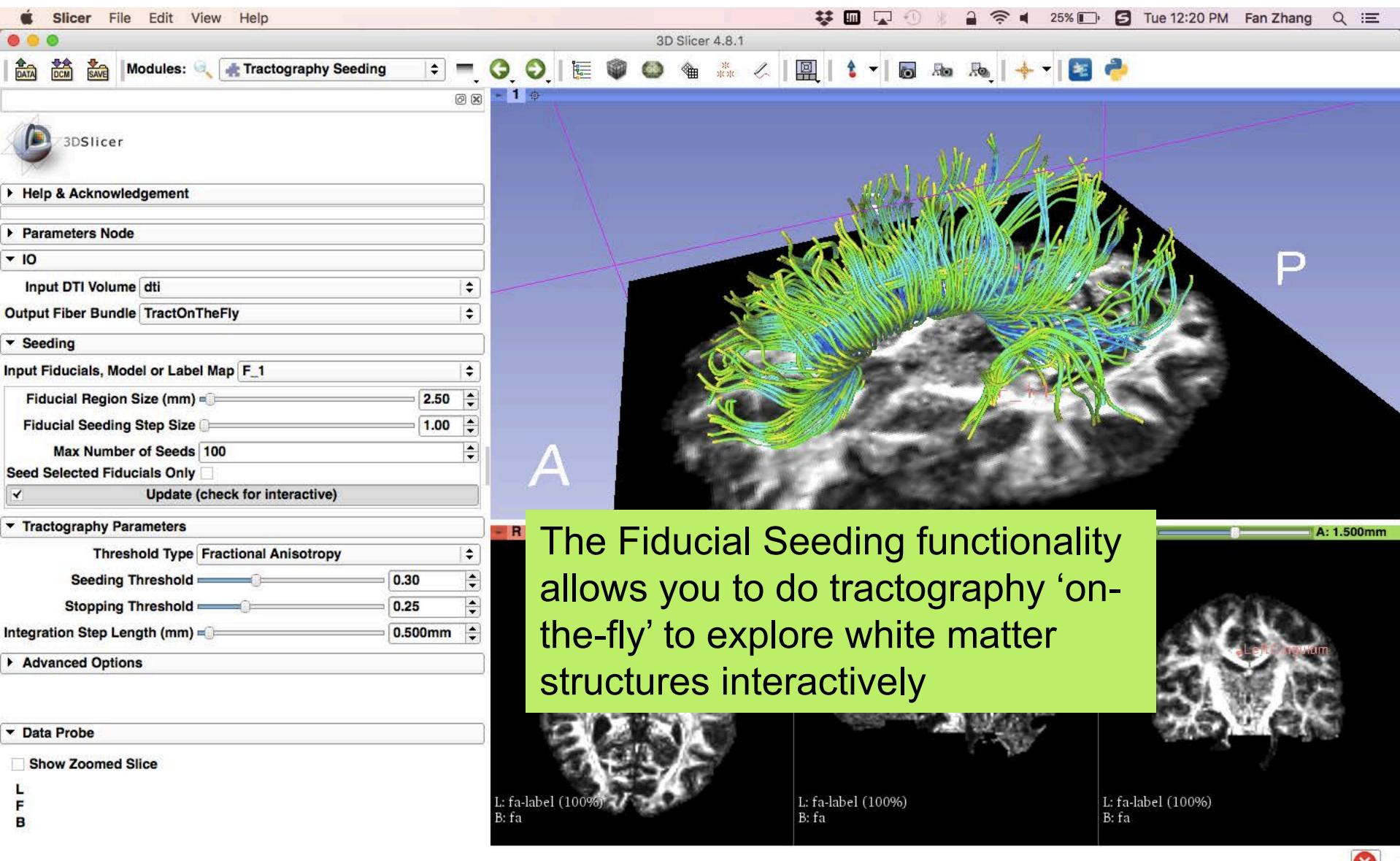
Select the Output Fiber Bundle 'Create New Fiber Bundle as ...' and name it '**TractOnTheFly**'

Check **Update (check for interactive)**

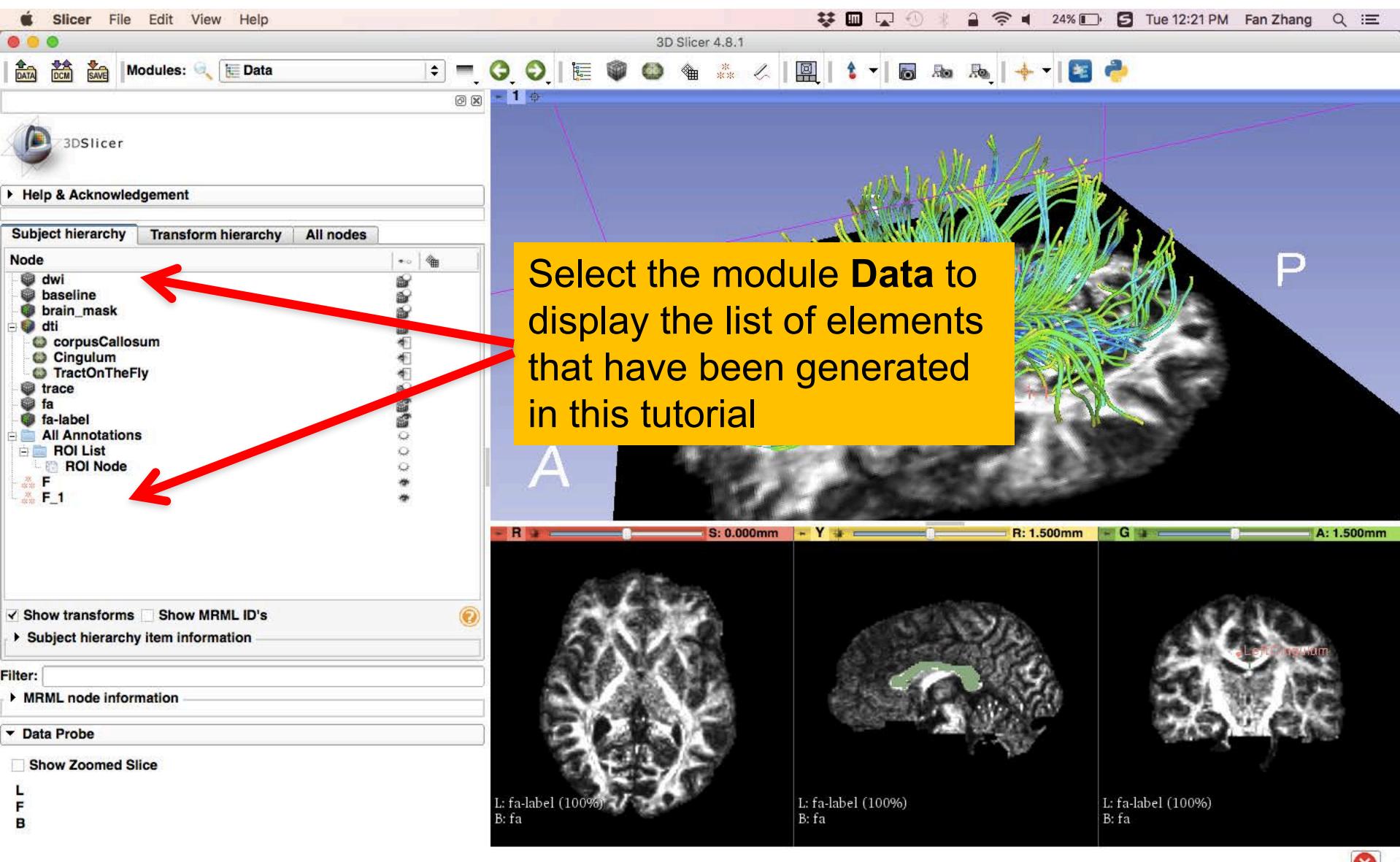
Tractography ‘on-the-fly’



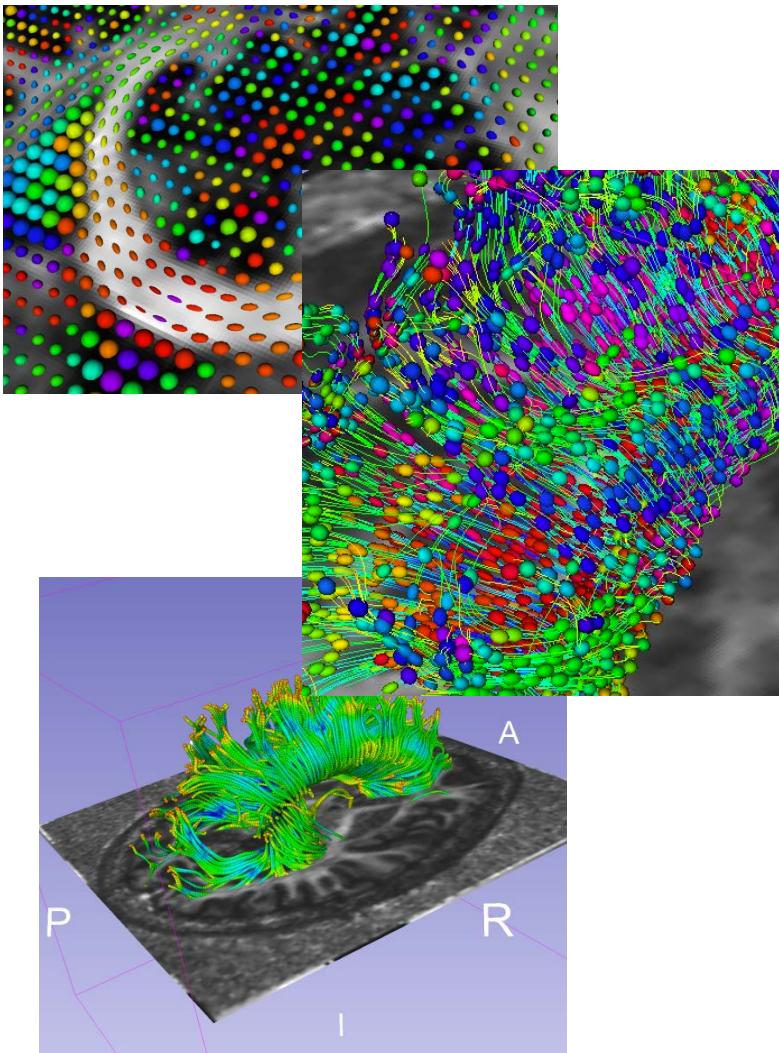
Tractography ‘on-the-fly’



DTI Analysis



Conclusion



This tutorial guided you through the different steps of a Diffusion MR analysis pipeline, from tensor estimation to 3D tracts visualization, for exploring and studying the 3D architecture of the brain white matter.

Acknowledgments



- **Open Source Diffusion MRI Technology For Brain Cancer Research** NIH U01CA199459
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Brigham and Women's Hospital, Harvard Medical School

