



Diffusion MRI Analysis

Sonia Pujol, Ph.D.

Surgical Planning Laboratory
Harvard University

Brain Anatomy



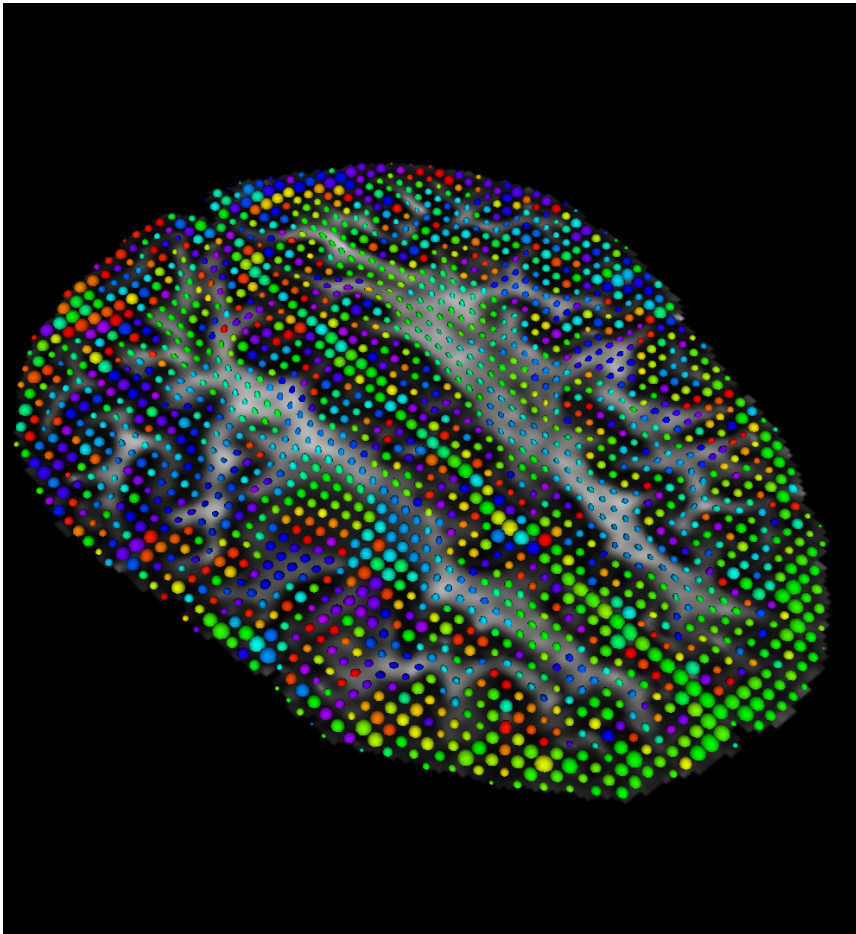
- White matter ~45% of the brain
- Myelinated nerve fibers (~ 10 μm axon diameter)

White Matter Exploration



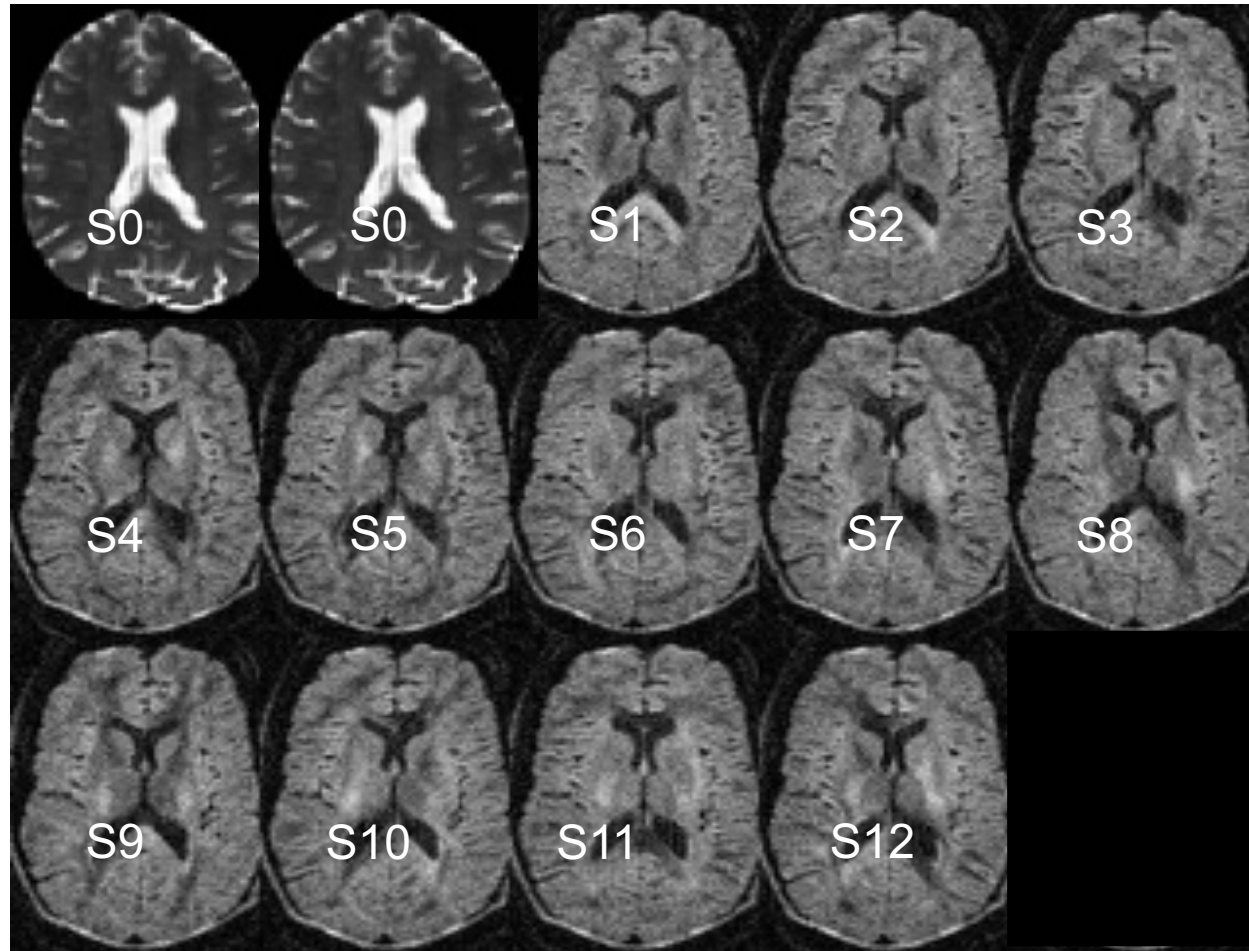
Jules Joseph Dejerine
(*Anatomie des centres
nerveux* (Paris, 1890-1901):
Atlas of Neuroanatomy based
on myelin stained preparation

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

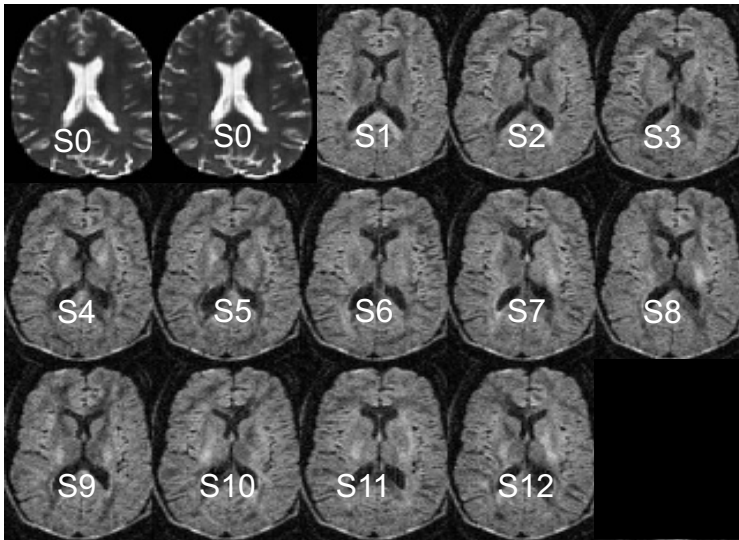
Diffusion Weighted Imaging (DWI)



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

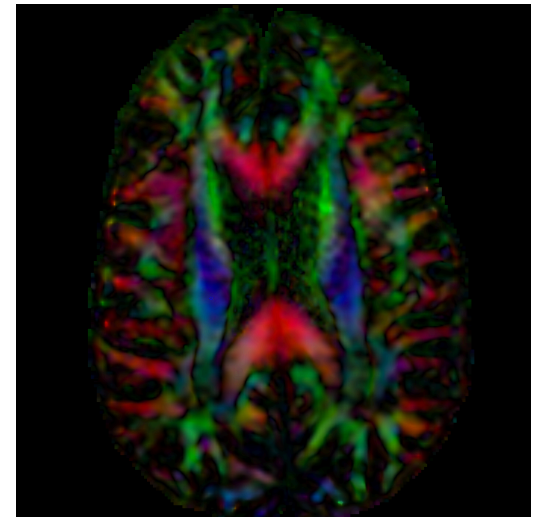
From DWI to DTI

DWI



DWI dataset acquired with 12 gradient and 2 baseline

DTI



DTI dataset

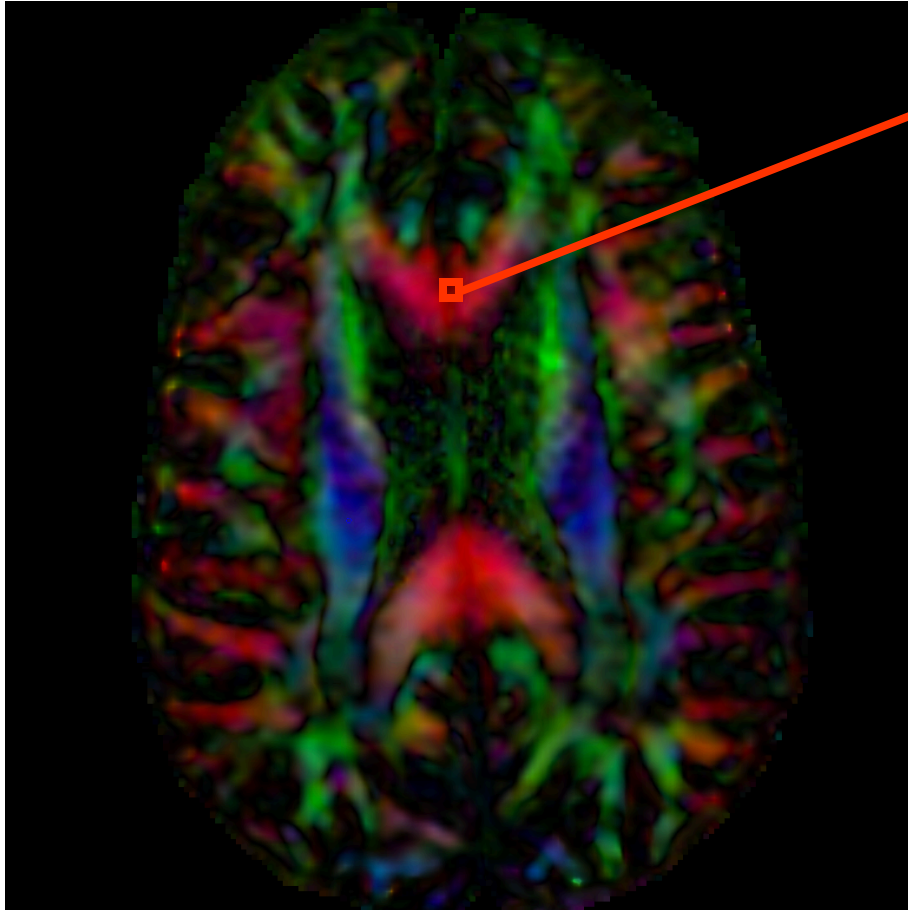
$$S_i = S_0 e^{-b \hat{g}_i^T \underline{D} \hat{g}_i}$$

Stejskal-Tanner (1965)

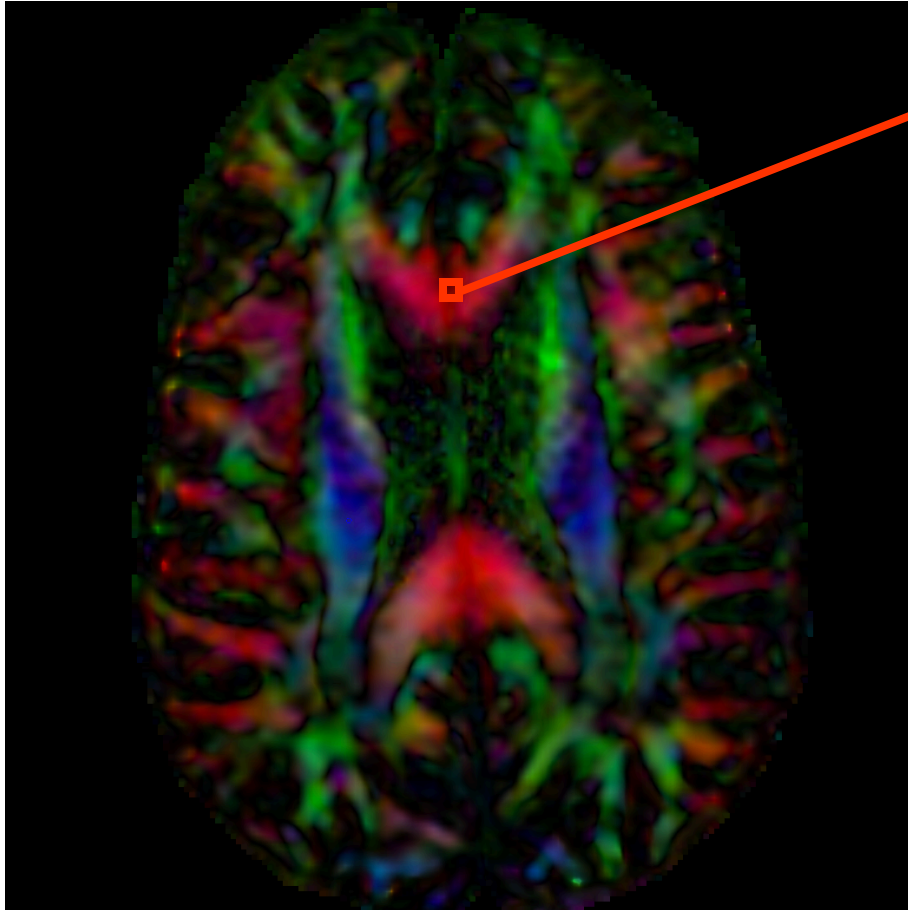
S_i : DWI volume acquired with
 i th gradient
 S_0 : Baseline volume

Diffusion Tensor Imaging

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



Diffusion Tensor Imaging

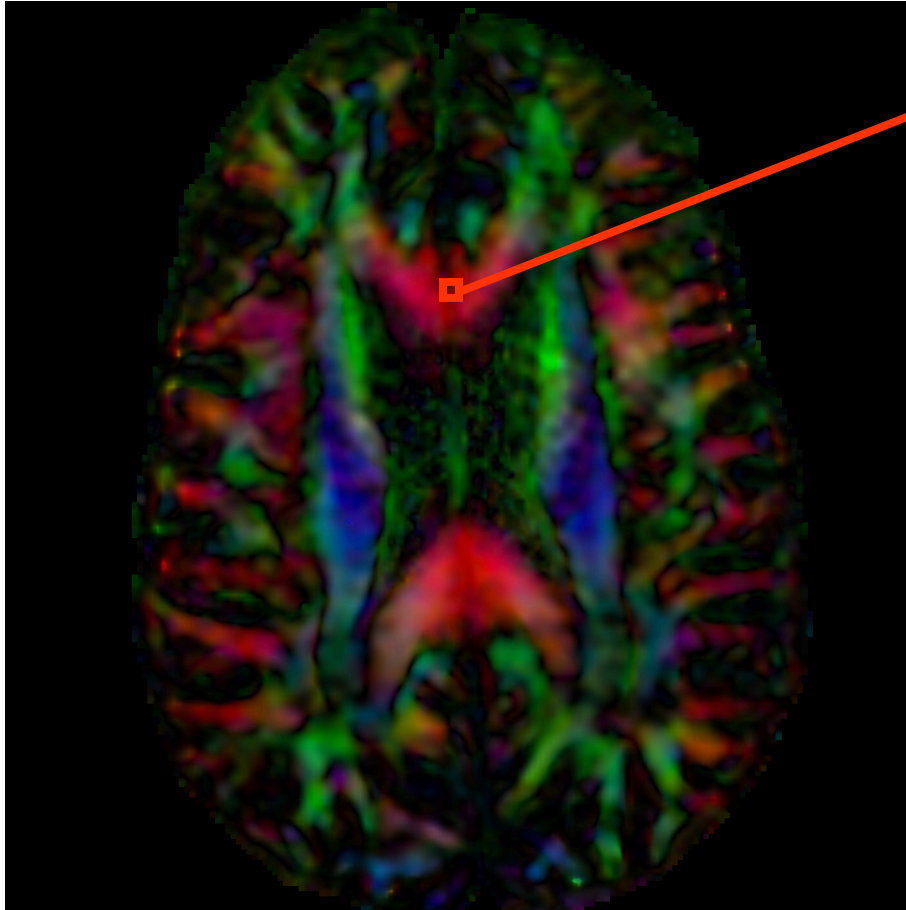


$$S_i = S_0 e^{-b \hat{g}_i^T \underline{D} \hat{g}_i}$$



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

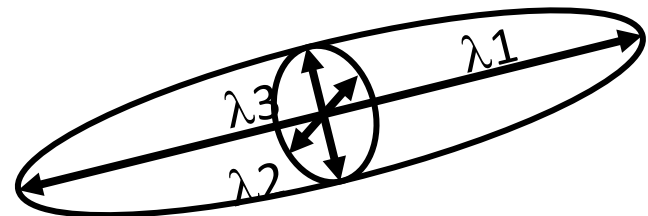
Diffusion Tensor Imaging



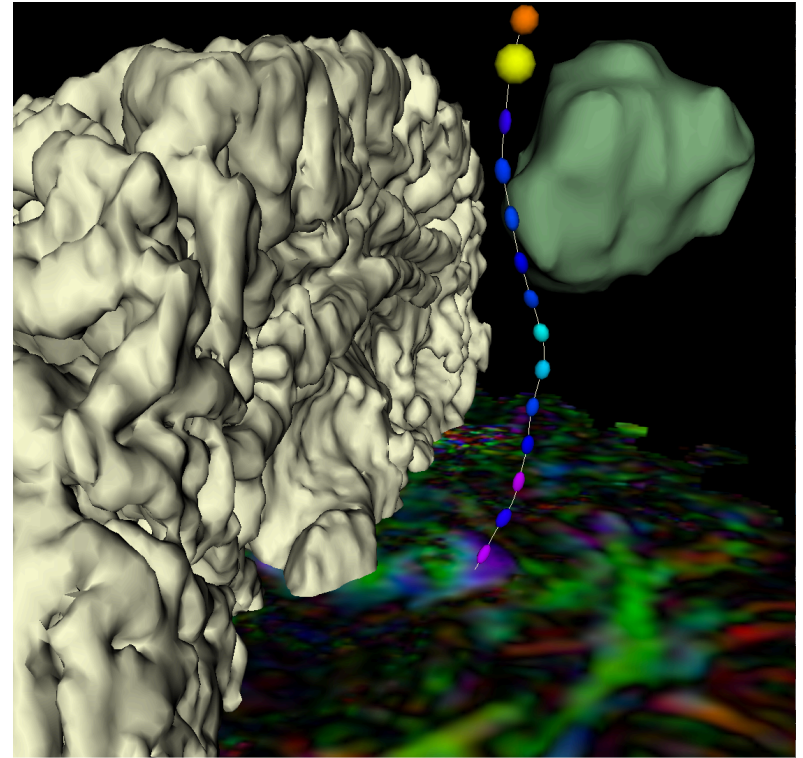
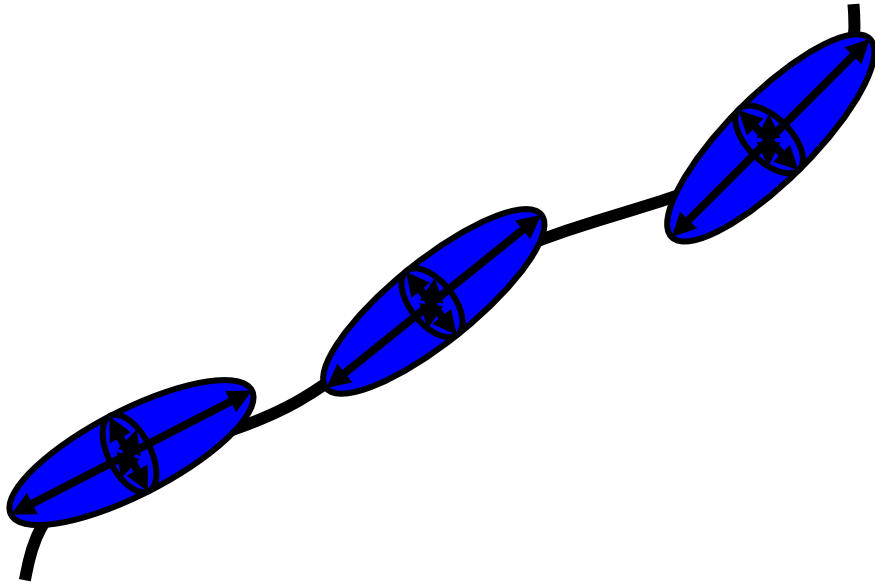
$$S_i = S_0 e^{-b \hat{g}_i^T \underline{D} \hat{g}_i}$$



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



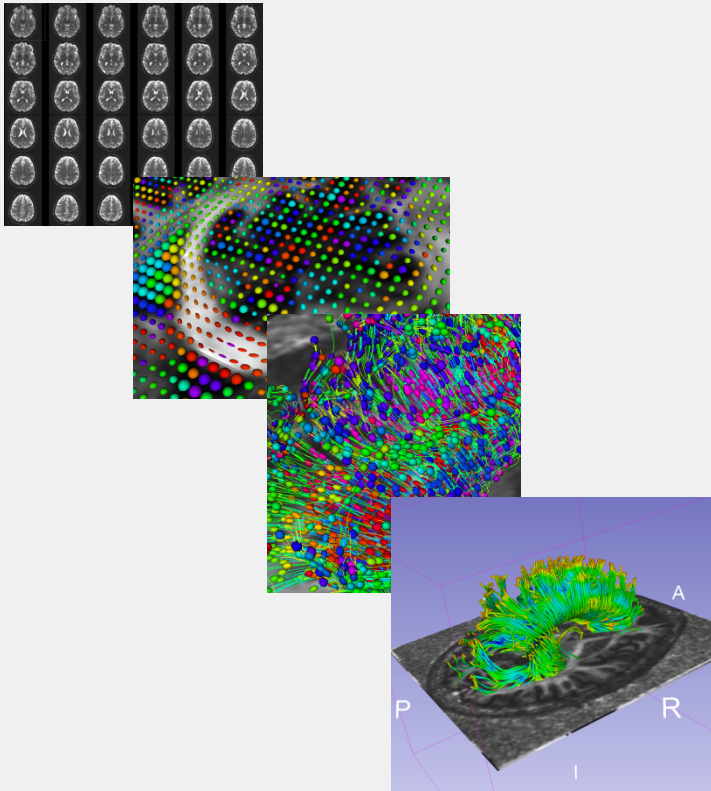
Tractography



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

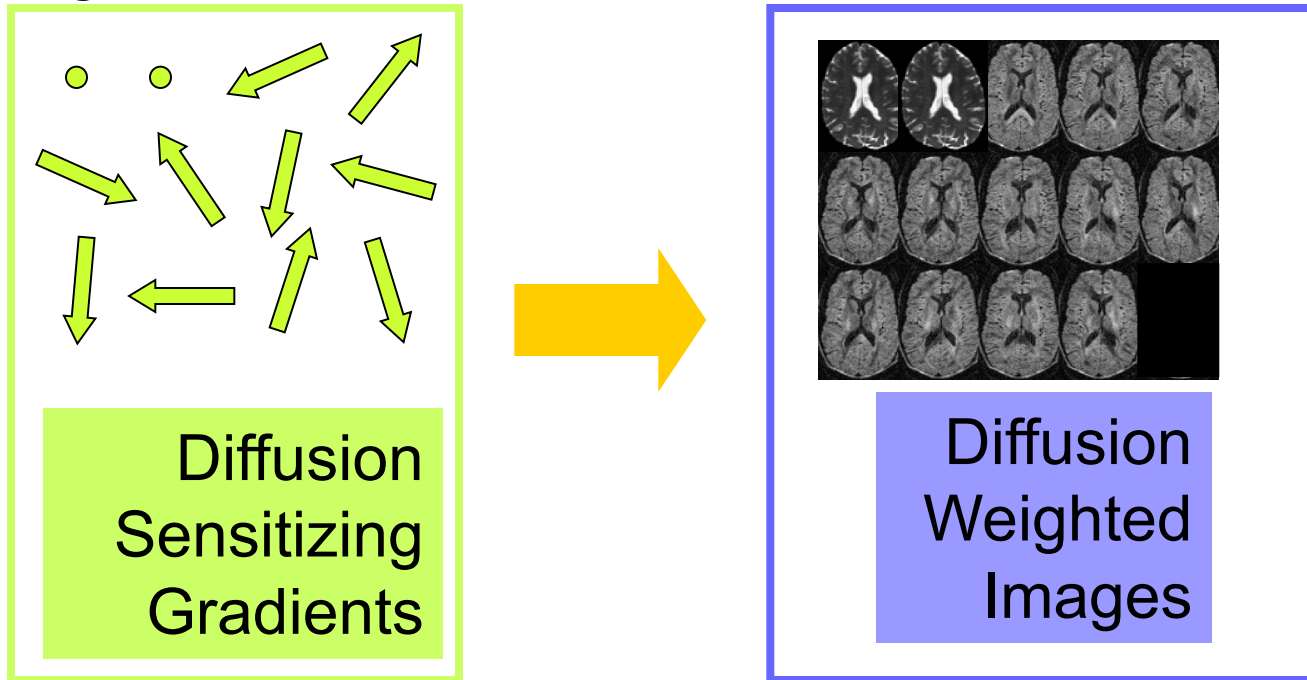
Tutorial Outline

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 DiffusionMRI_tutorialData is a Diffusion Weighted MR scan of the brain acquired with 41 gradient directions and one baseline.



Download the dataset at:

https://www.slicer.org/w/images/e/e6/Dti_tutorial_data.zip

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

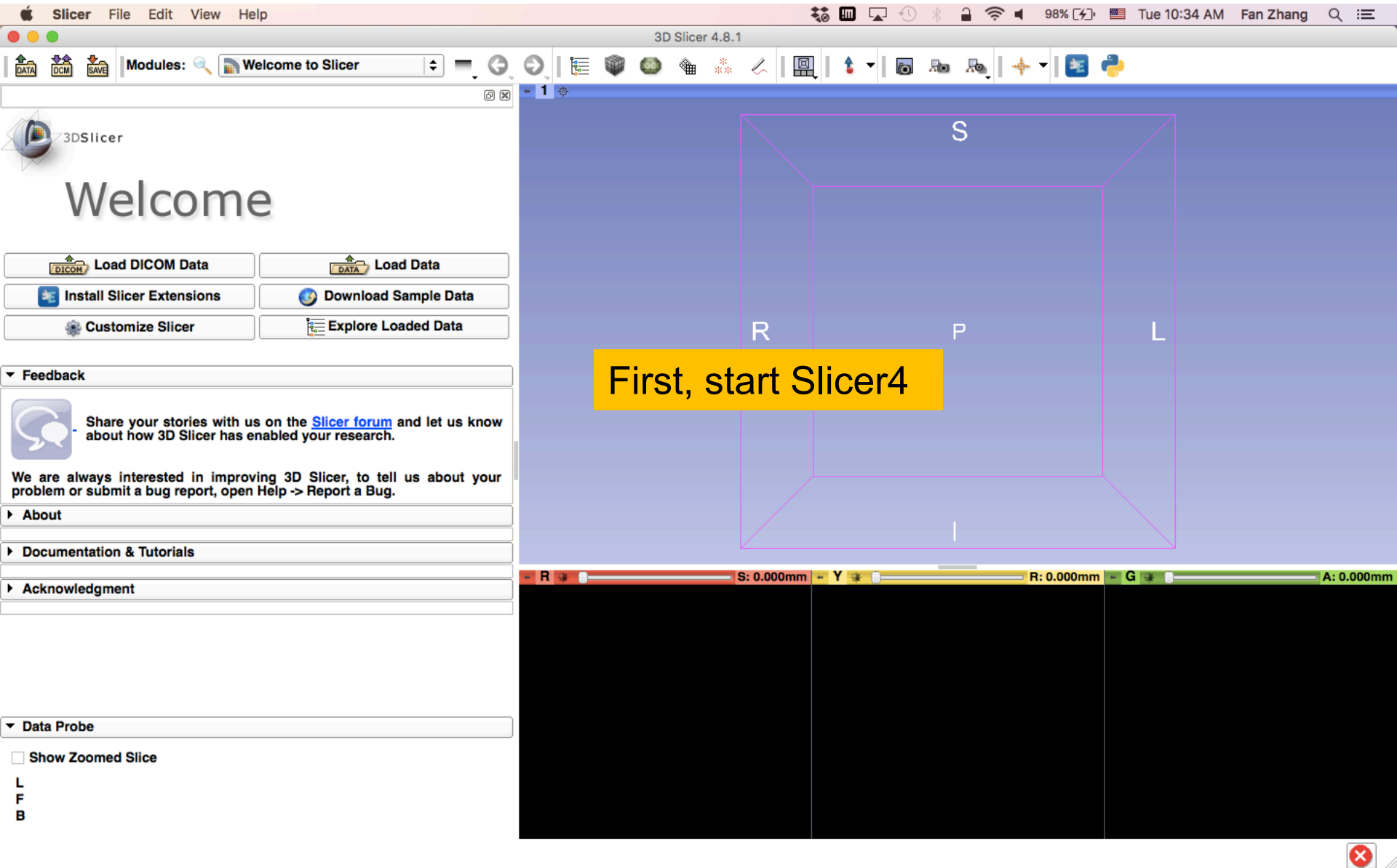
An open-source project to improve and extend diffusion magnetic resonance imaging software in 3D Slicer:

<http://dmri.slicer.org>

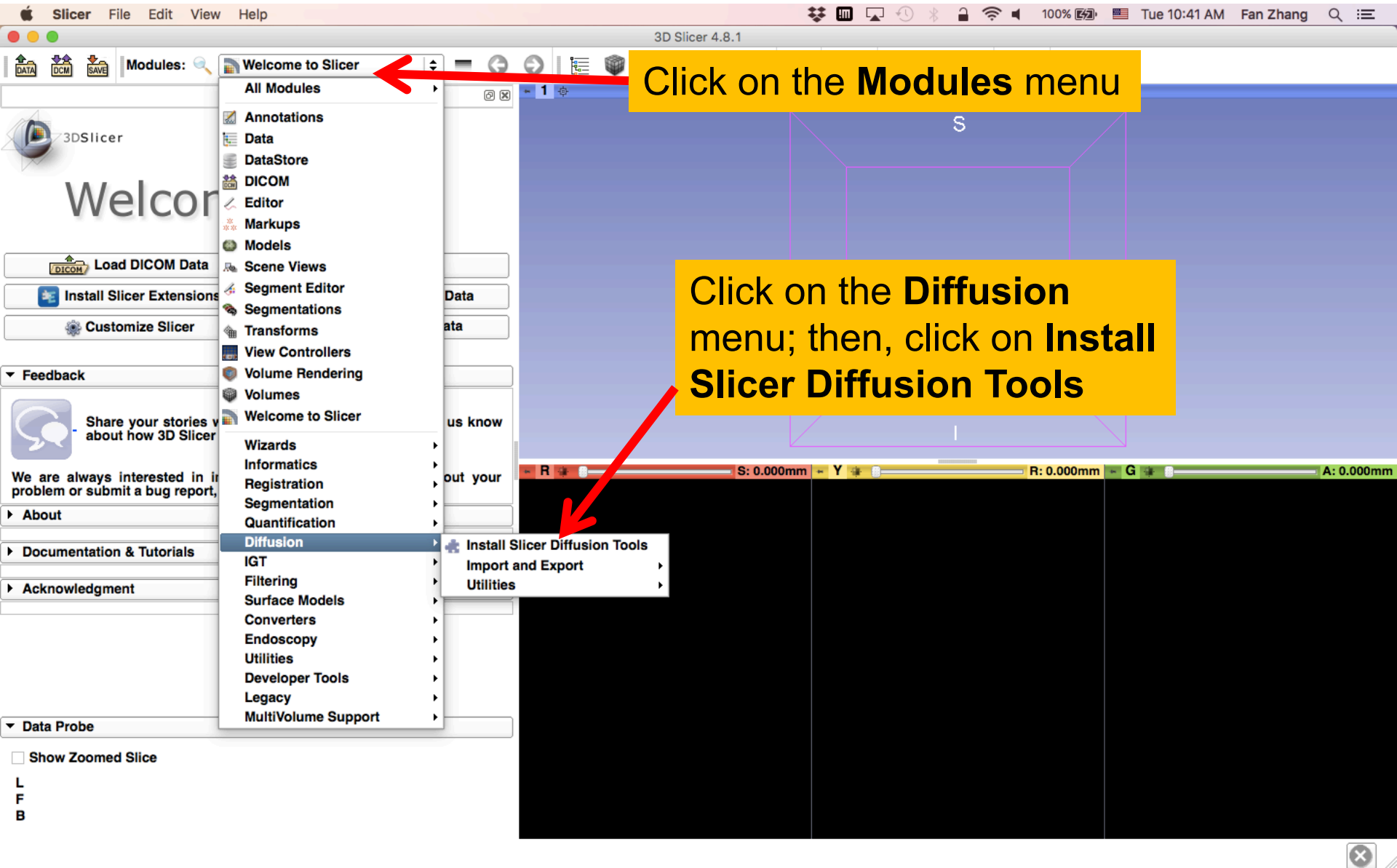
Disclaimer

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.

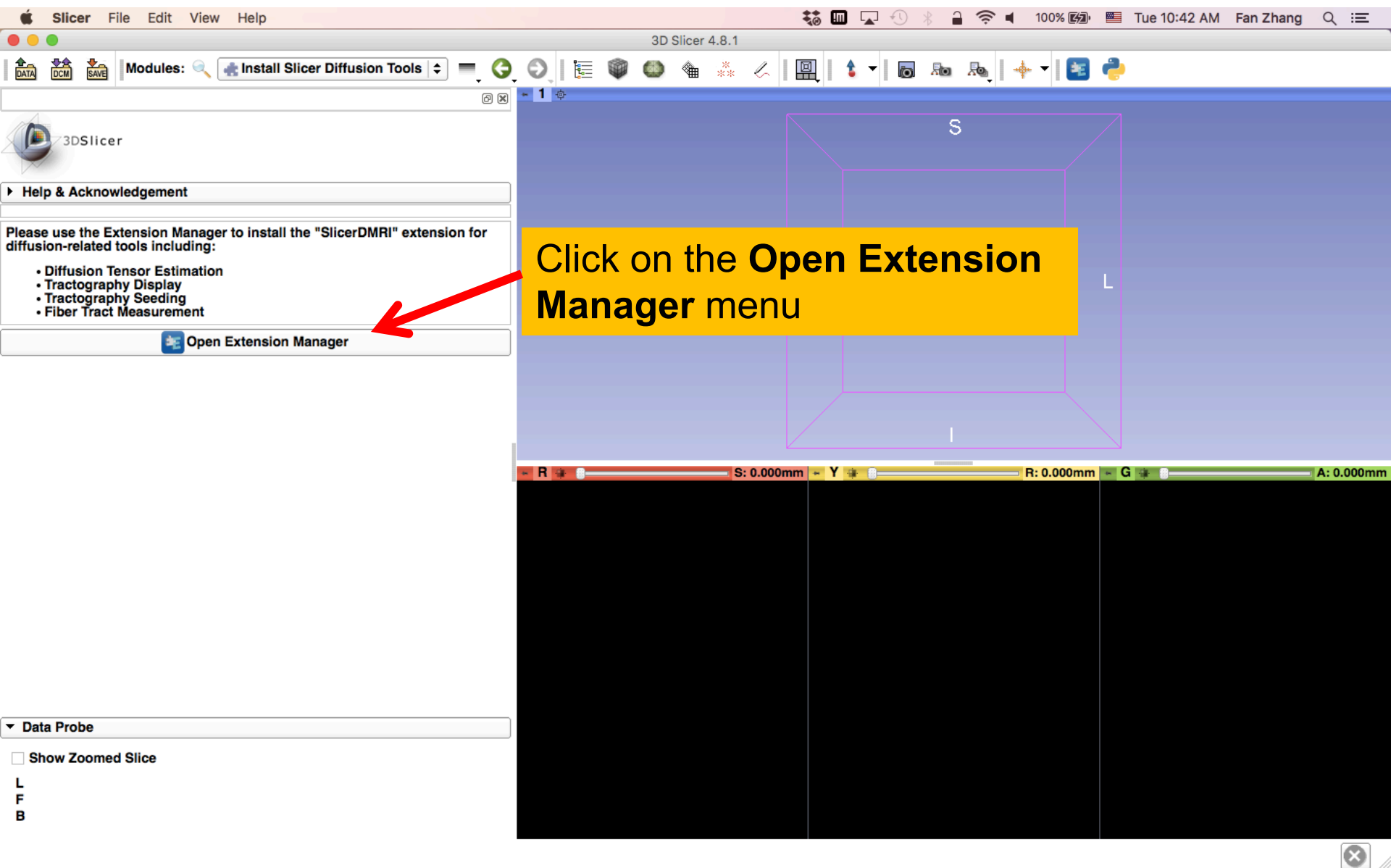
Install SlicerDMRI



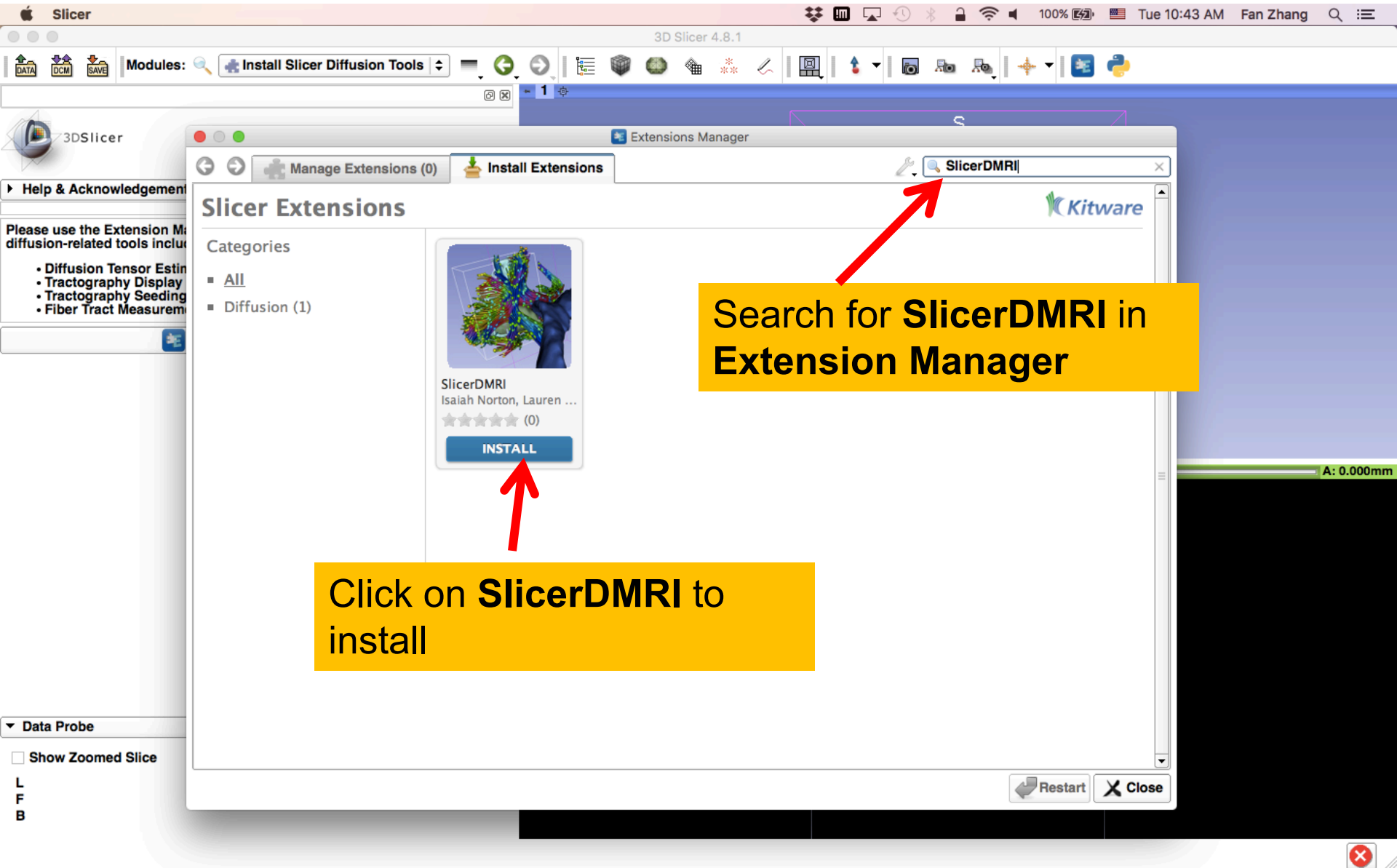
Install SlicerDMRI



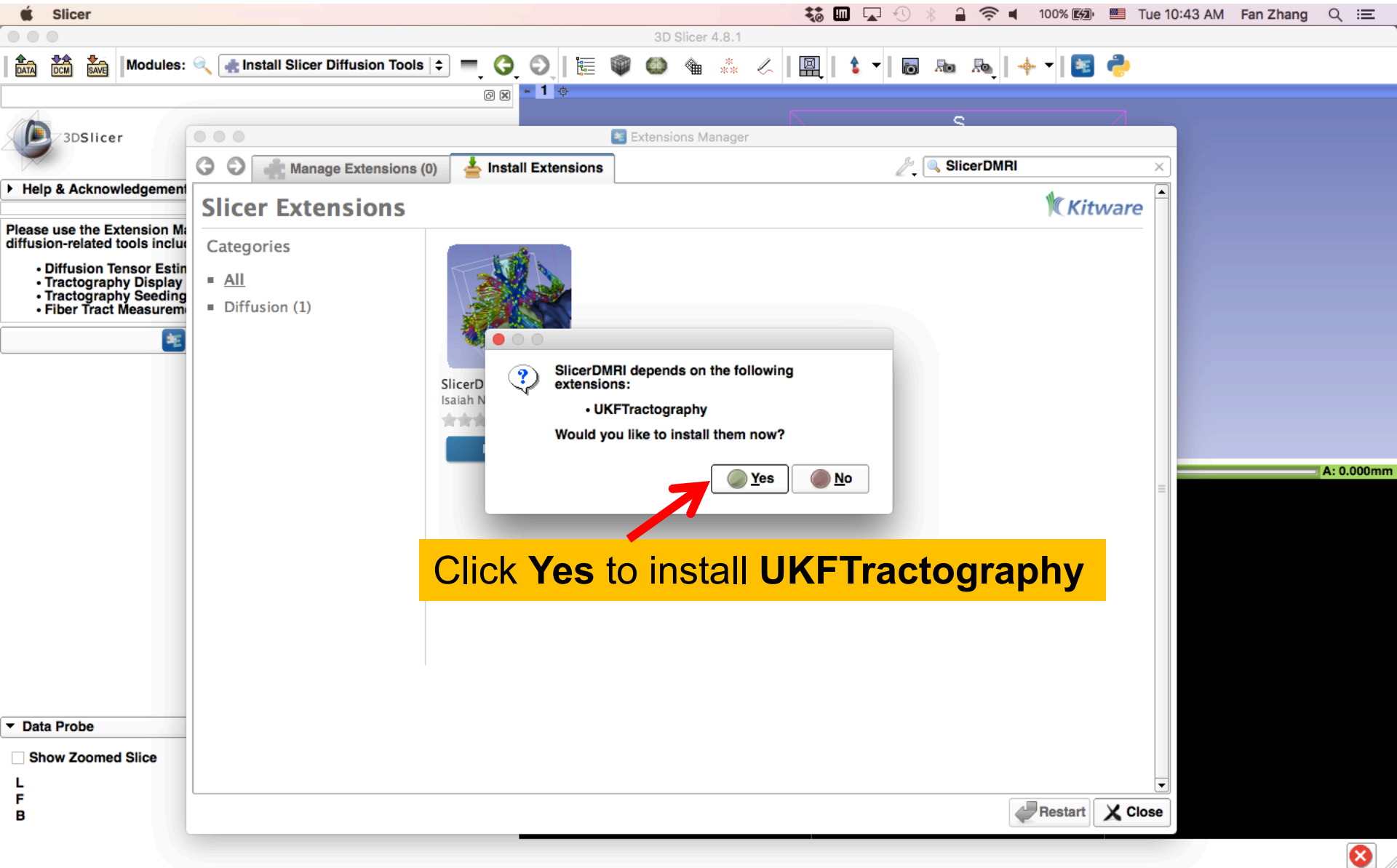
Install SlicerDMRI



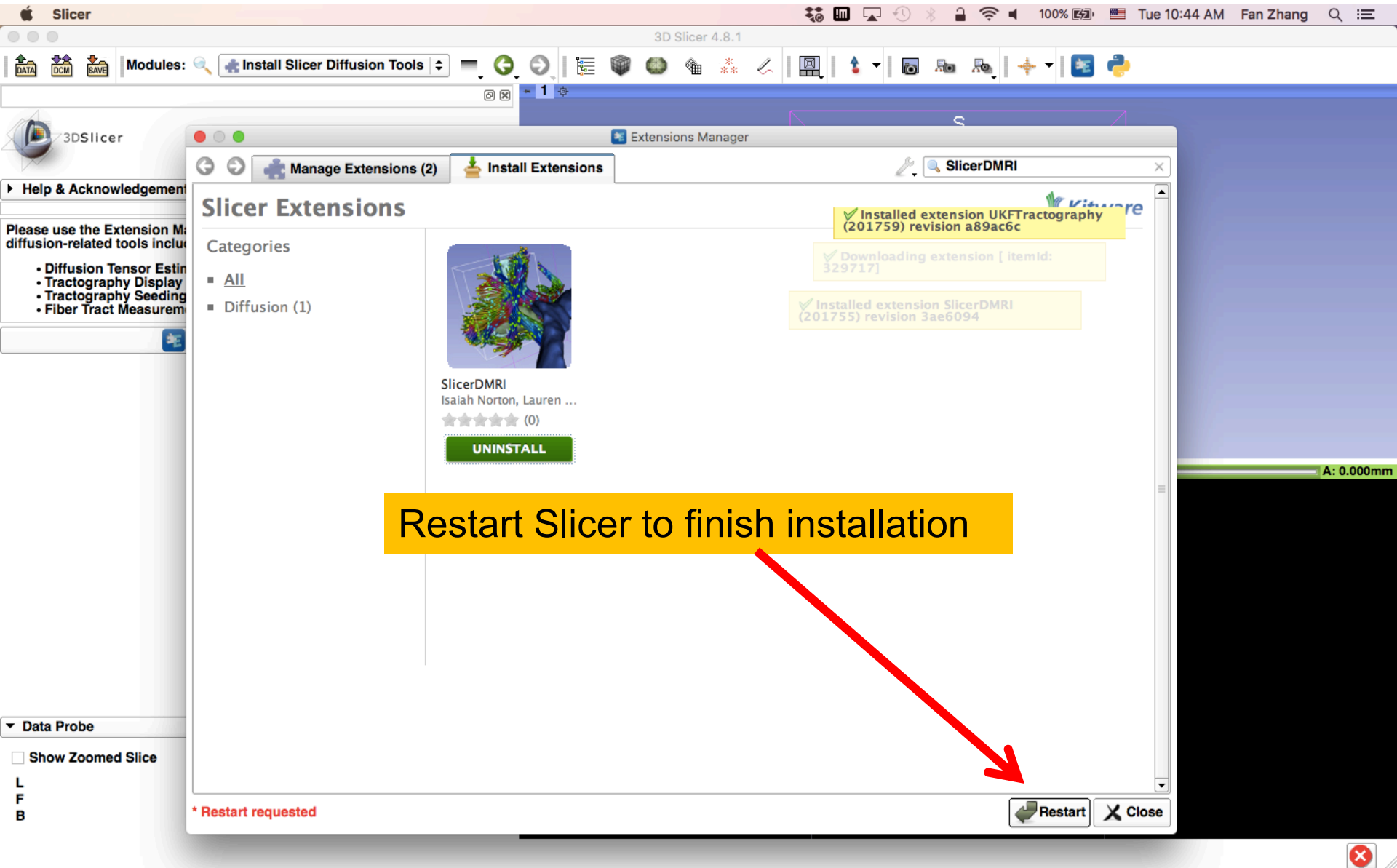
Install SlicerDMRI



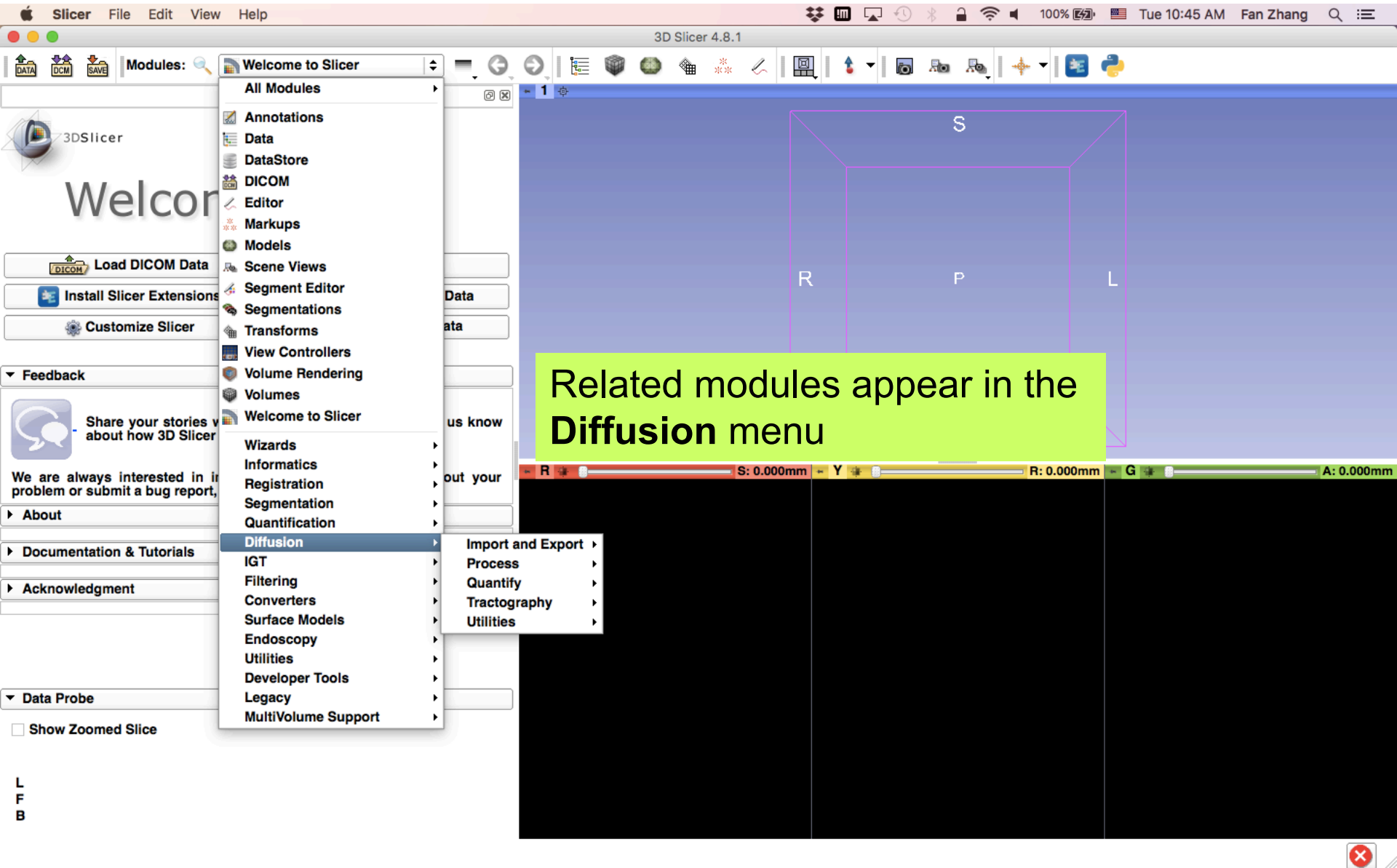
Install SlicerDMRI



Install SlicerDMRI



Install SlicerDMRI

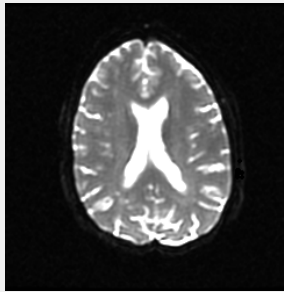


Learning Objectives

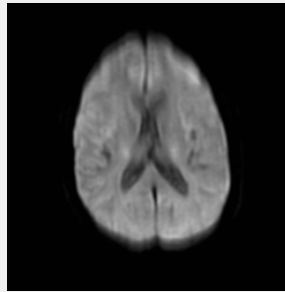
Following this tutorial, you'll be able to

- 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

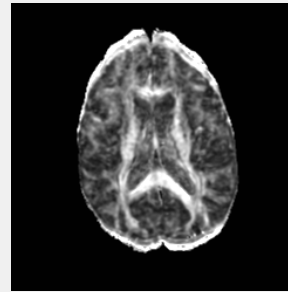
MR Diffusion Analysis Pipeline



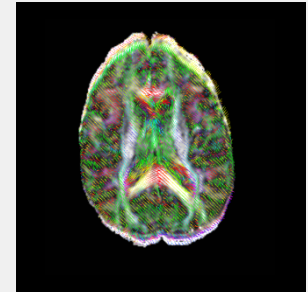
DWI
Acquisition



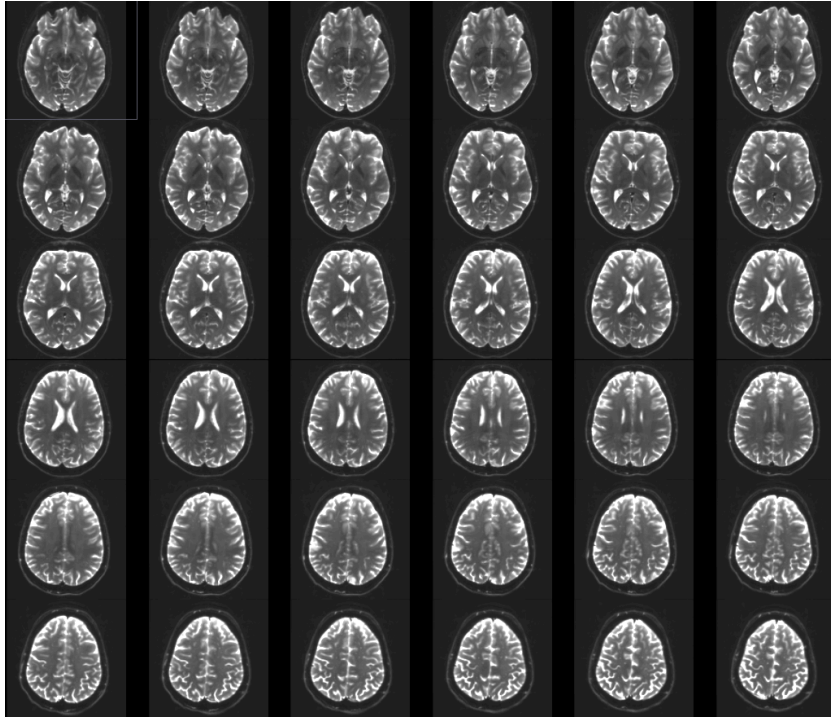
Tensor
Calculation



Scalar
Maps

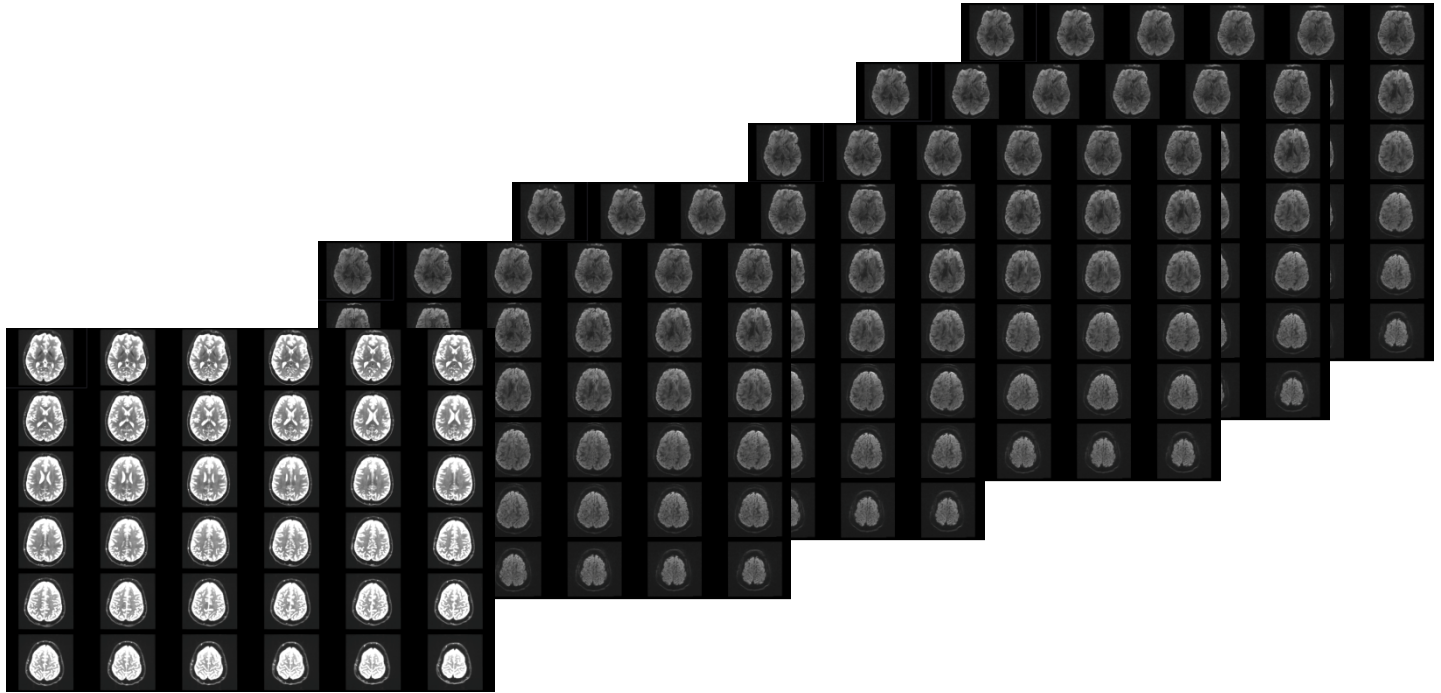


3D
Visualization



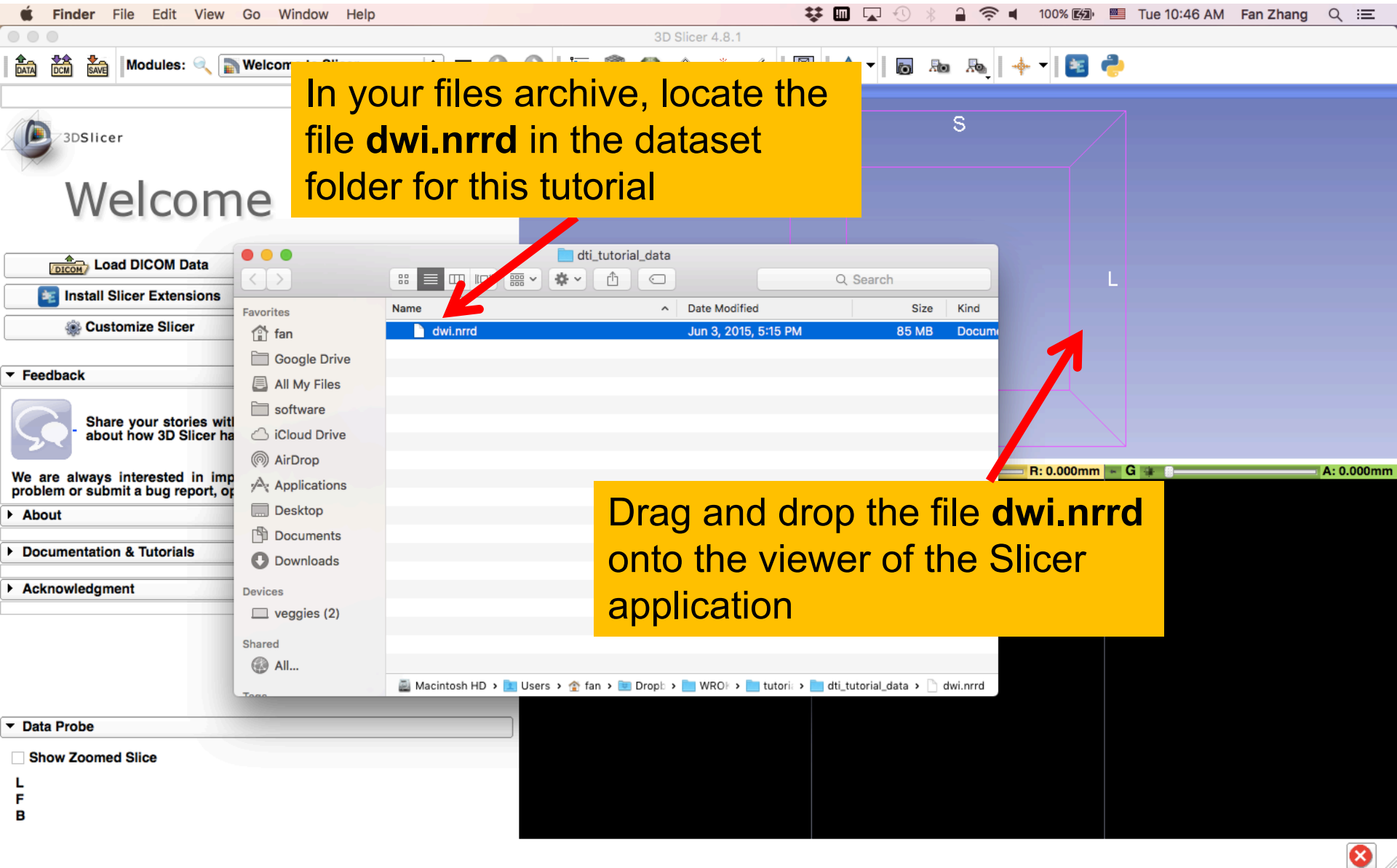
Part 1: From DWI images to Tensors

Understanding the DWI Dataset

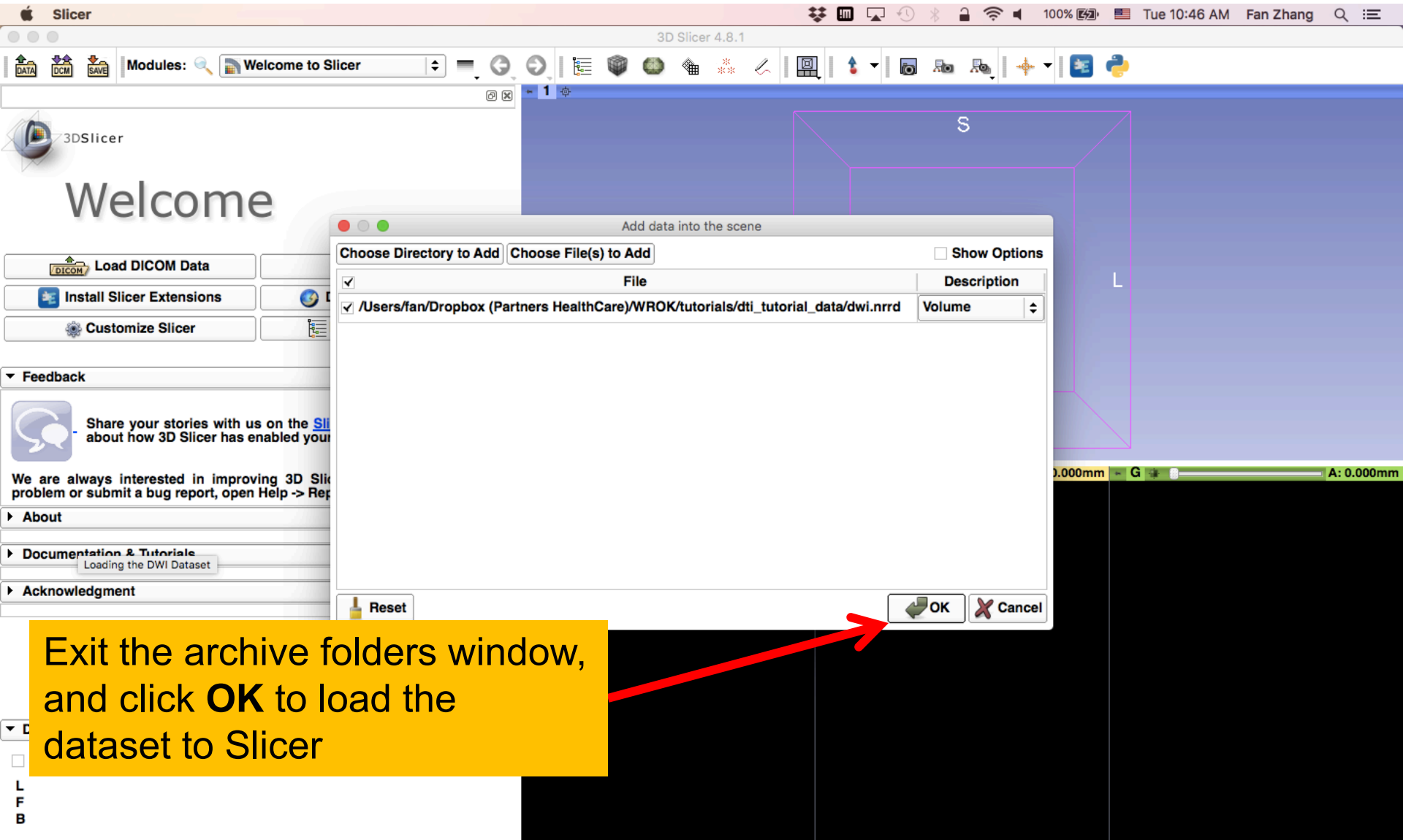


The Diffusion Weighted Imaging (DWI) dataset is composed of 41 volumes acquired with 41 different diffusion-sensitizing gradient directions, and one baseline image acquired without diffusion weighting.

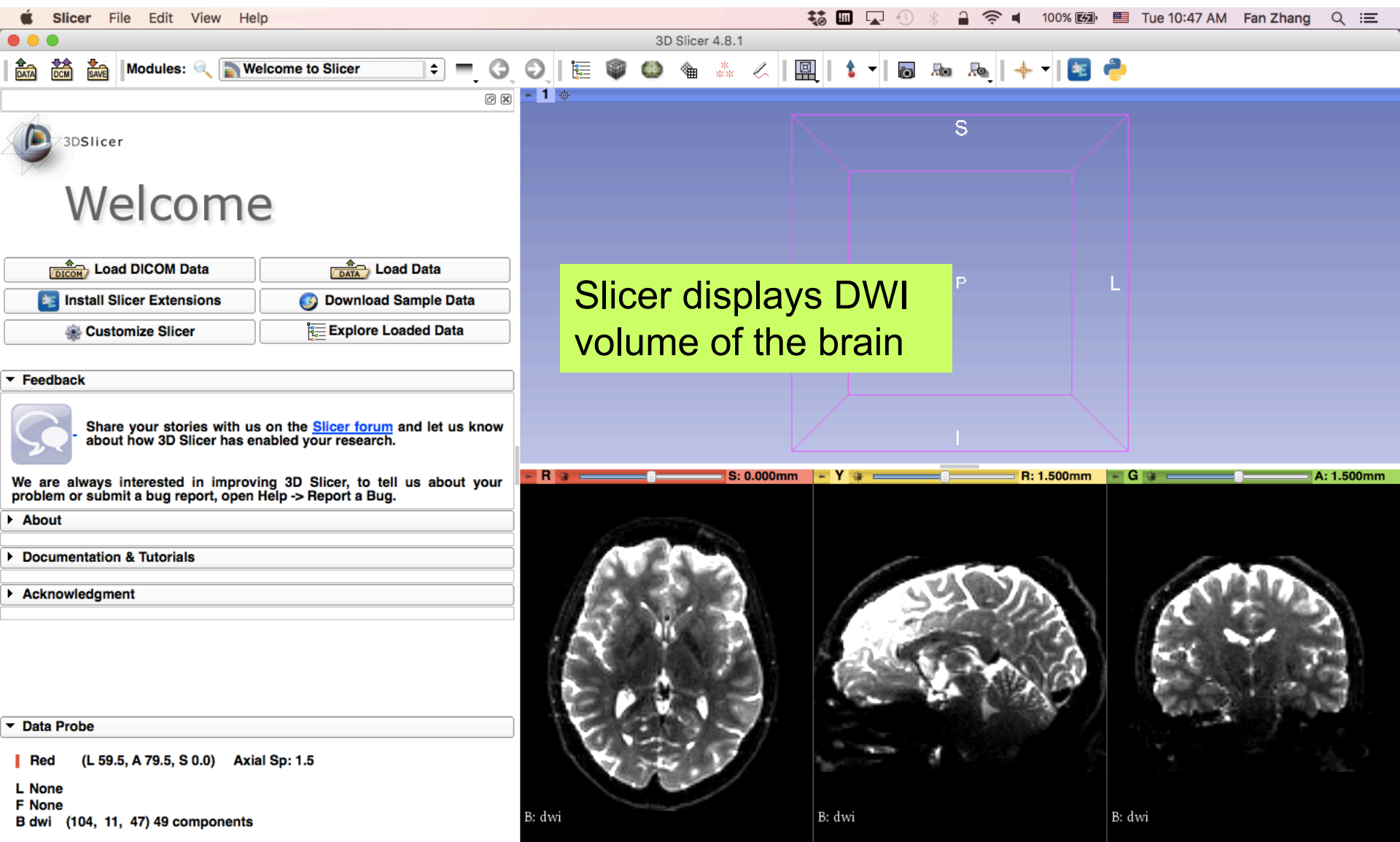
Loading the DWI Dataset



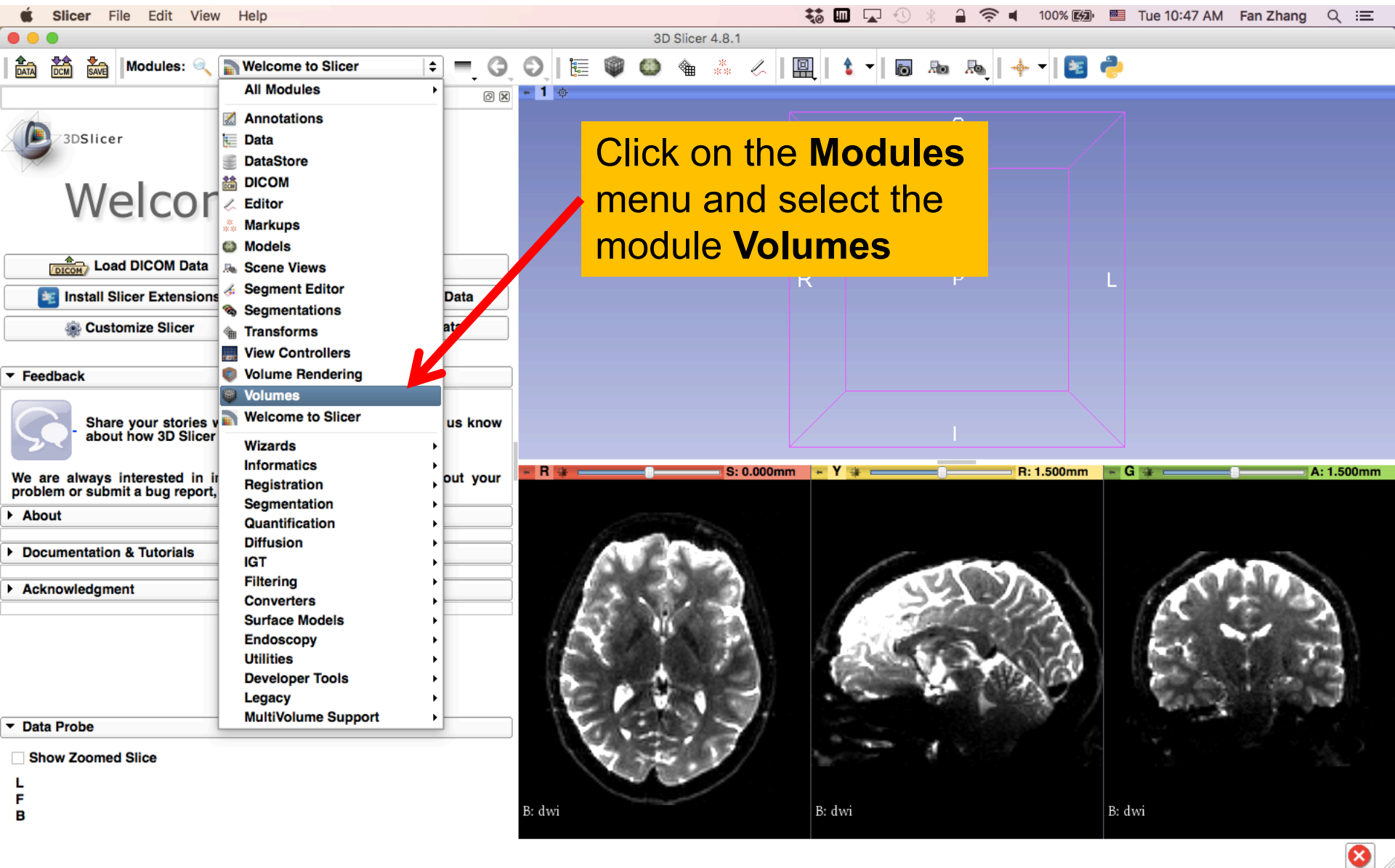
Loading the DWI Dataset



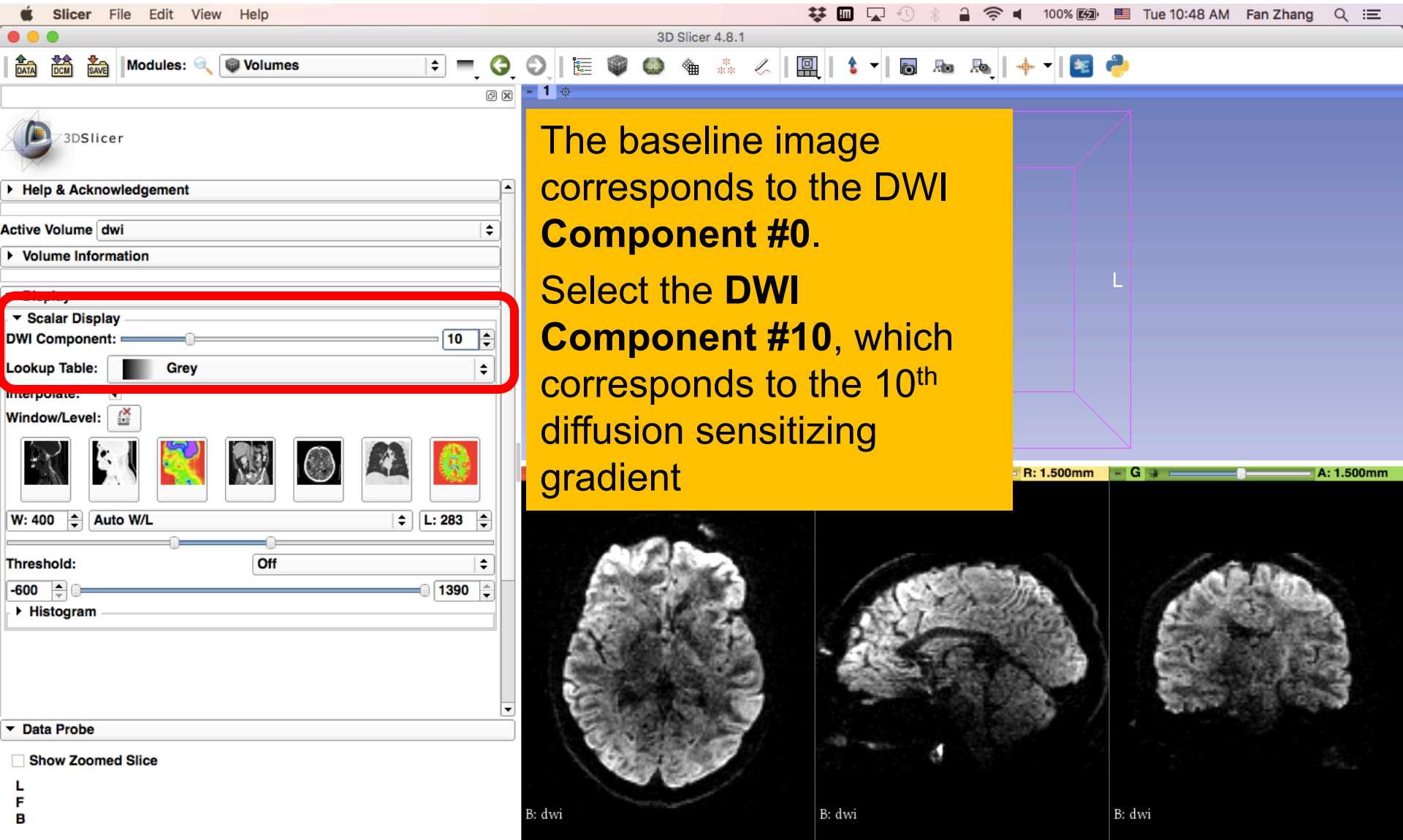
Loading the DWI Dataset



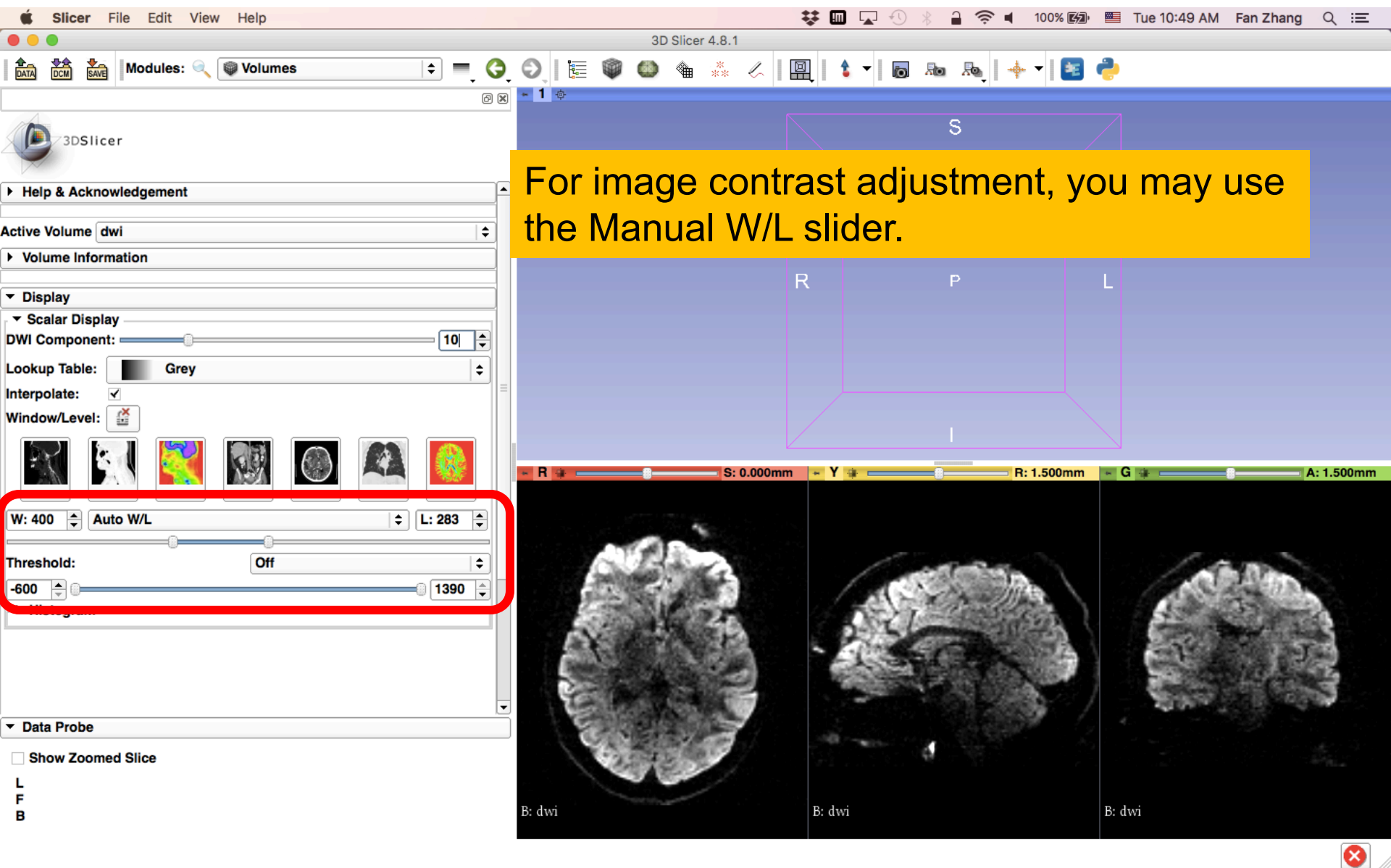
Loading the DWI Dataset



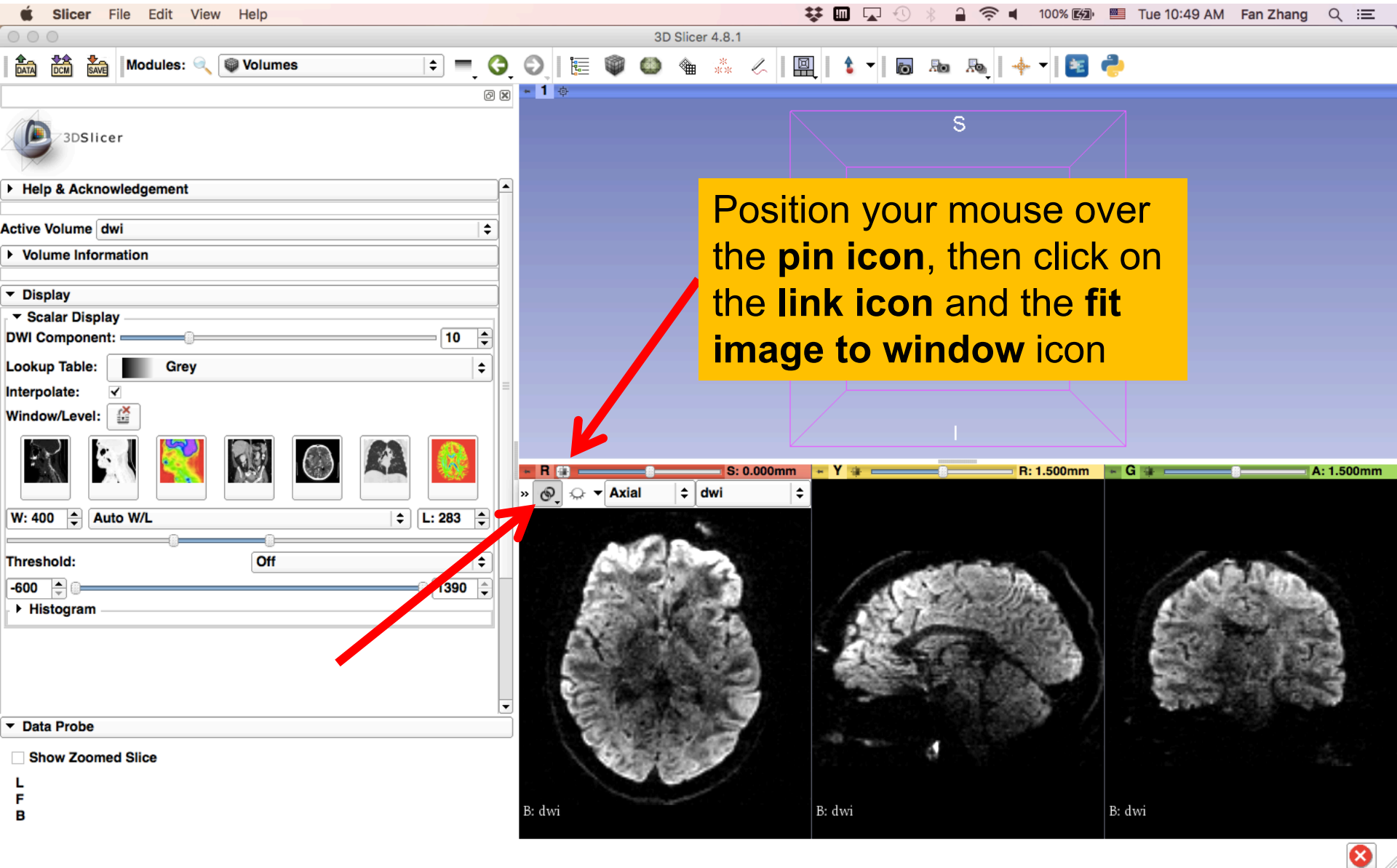
Loading the DWI Dataset



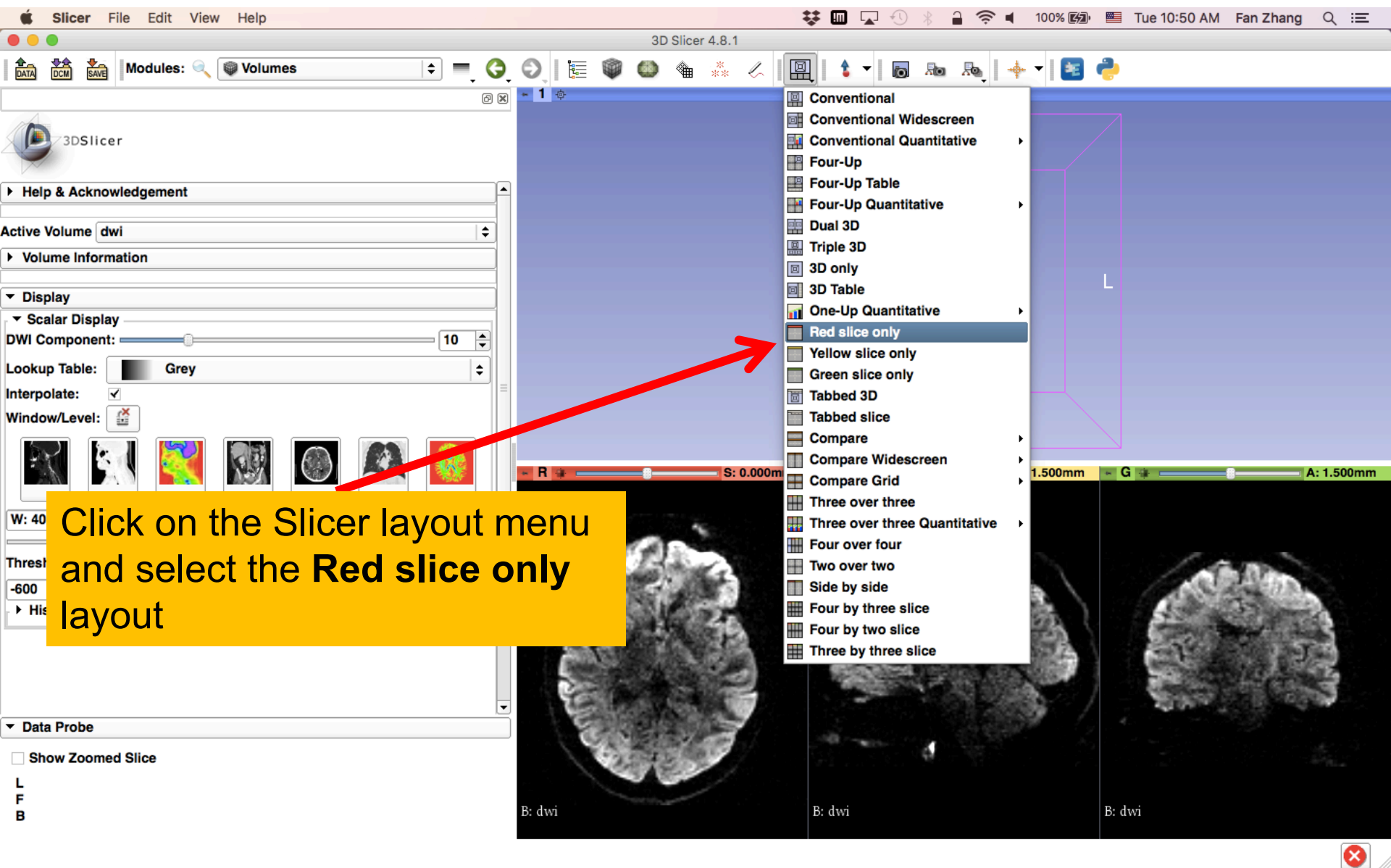
Loading the DWI Dataset



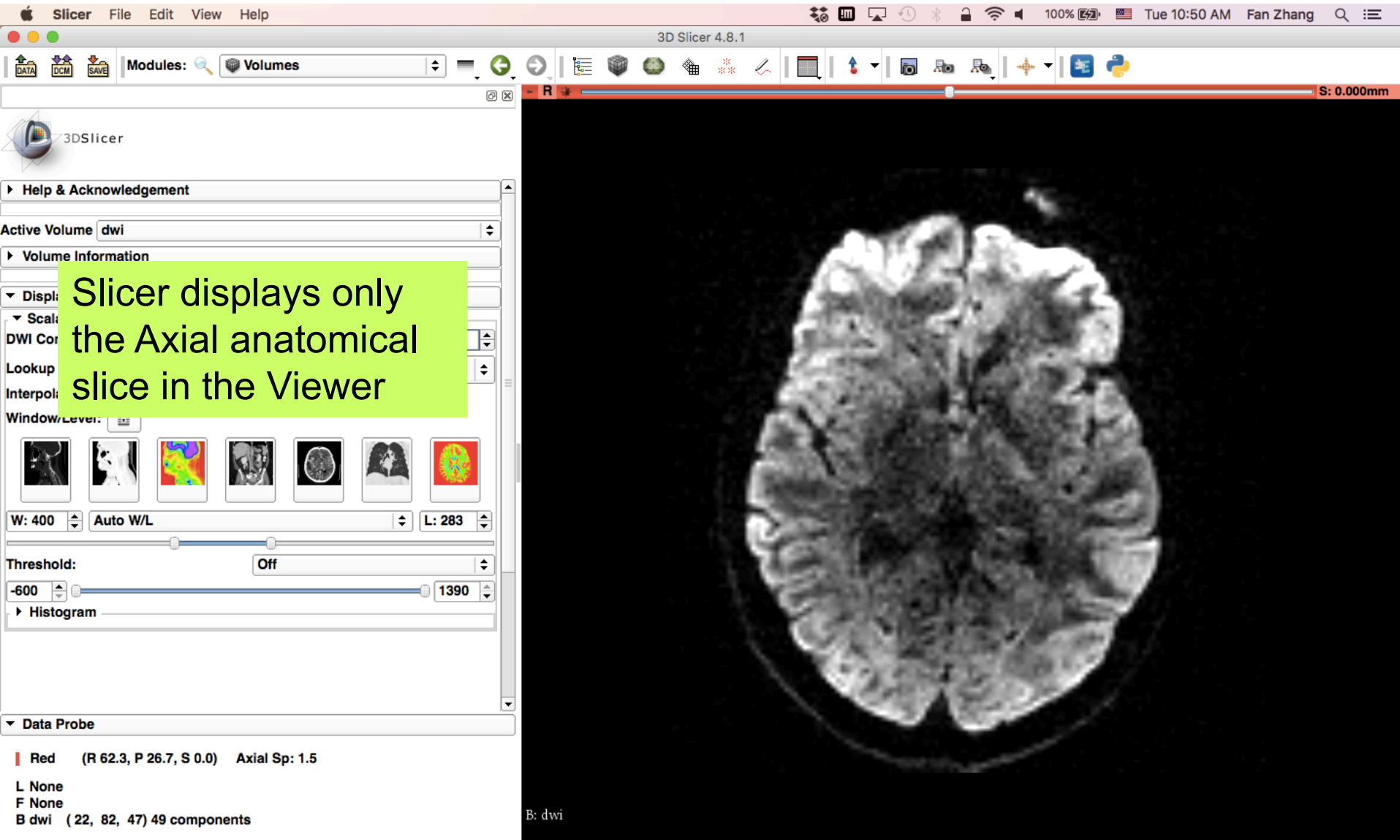
Loading the DWI Dataset



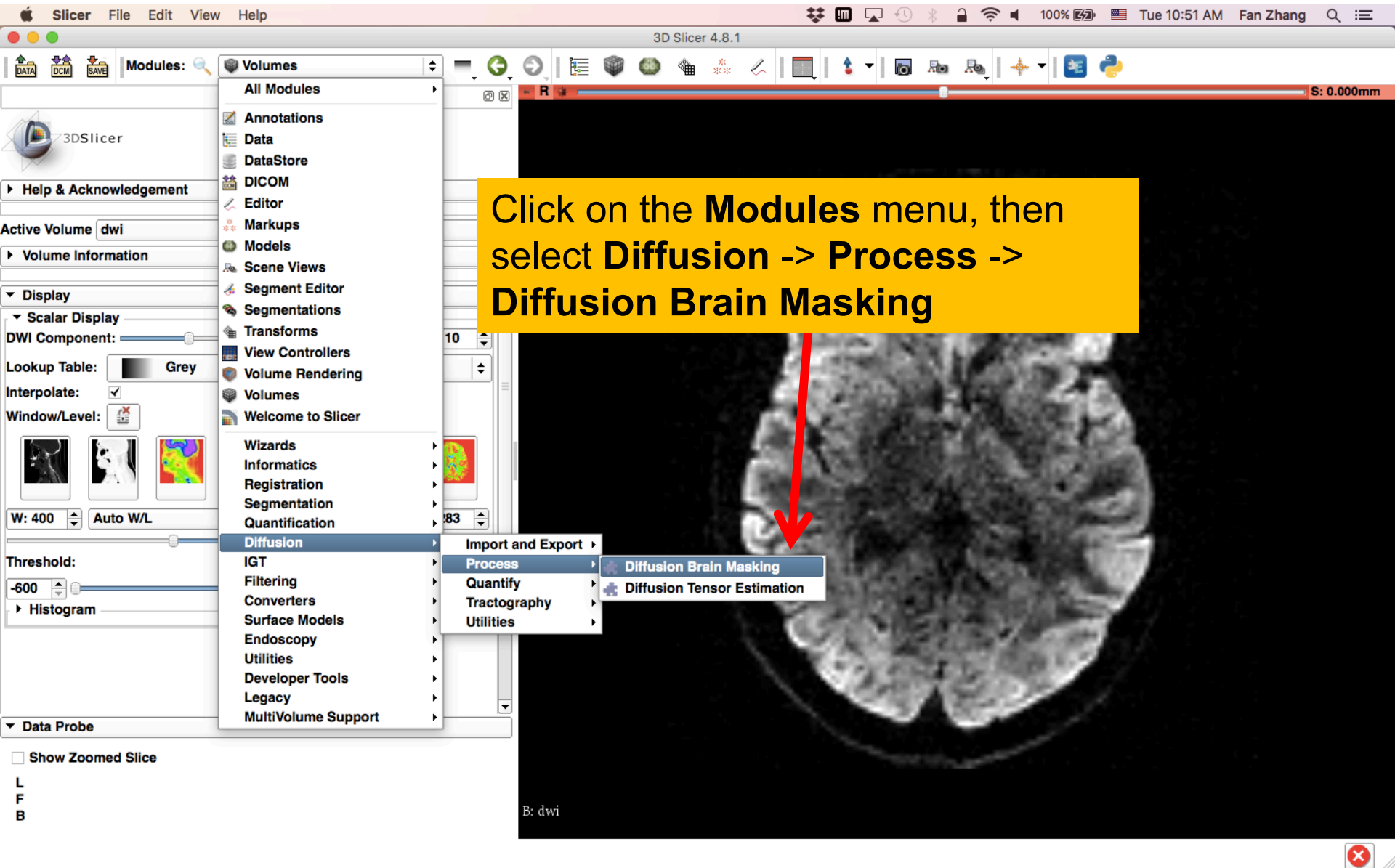
Loading the DWI Dataset



Loading the DWI Dataset



Creating a brain mask



Creating a brain mask

3D Slicer 4.8.1

Modules: **Diffusion Brain Masking**

Parameter set: **Diffusion Brain Masking**

IO

Input DWI Volume: **dwi**

Output Baseline Volume: **baseline**

Output Diffusion Brain Mask: **brain_mask**

Mask Settings

Status: Idle

Restore Defaults AutoRun Cancel **Apply**

Data Probe

☐ Show Zoomed Slice

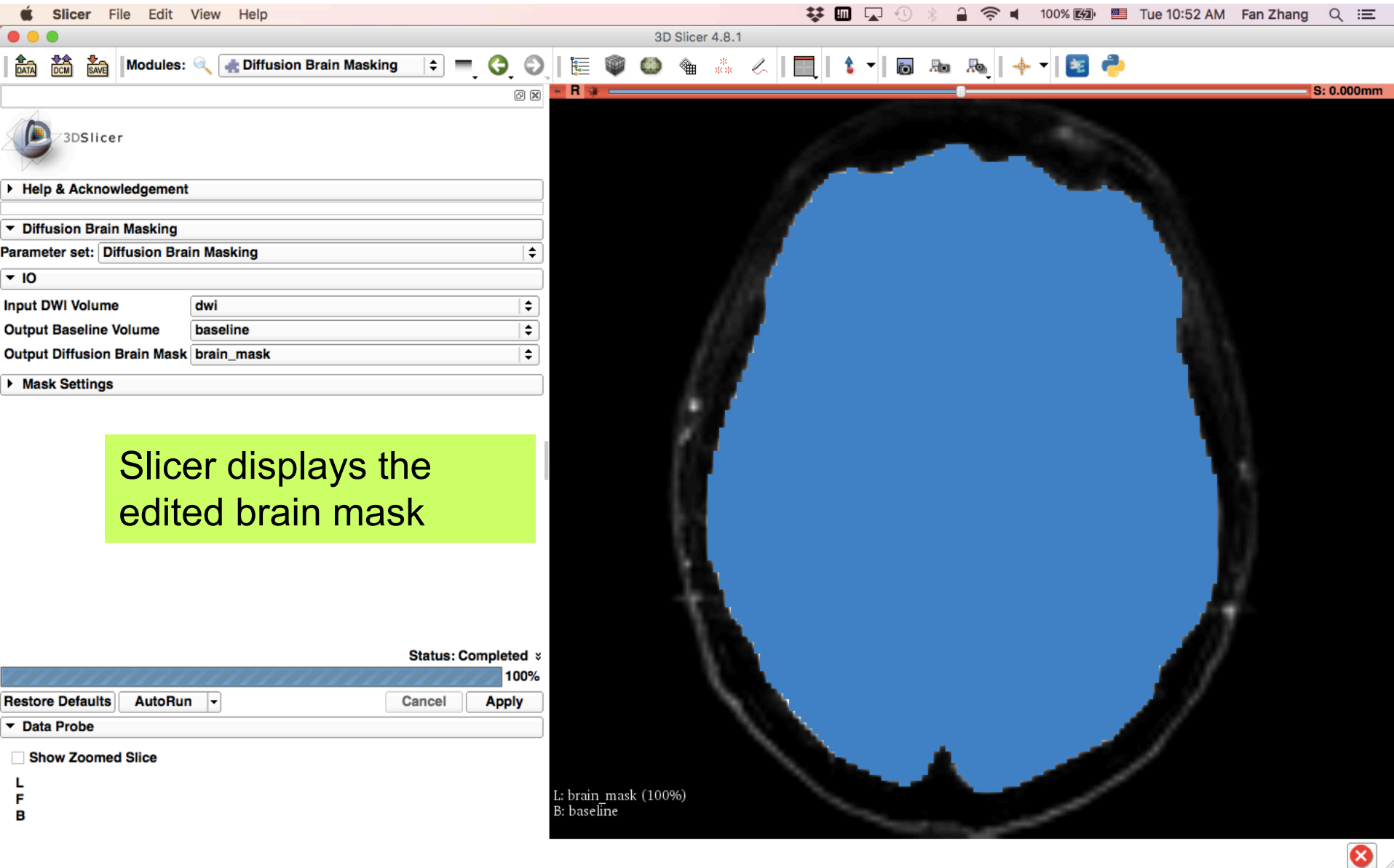
L
F
B

Instructions:

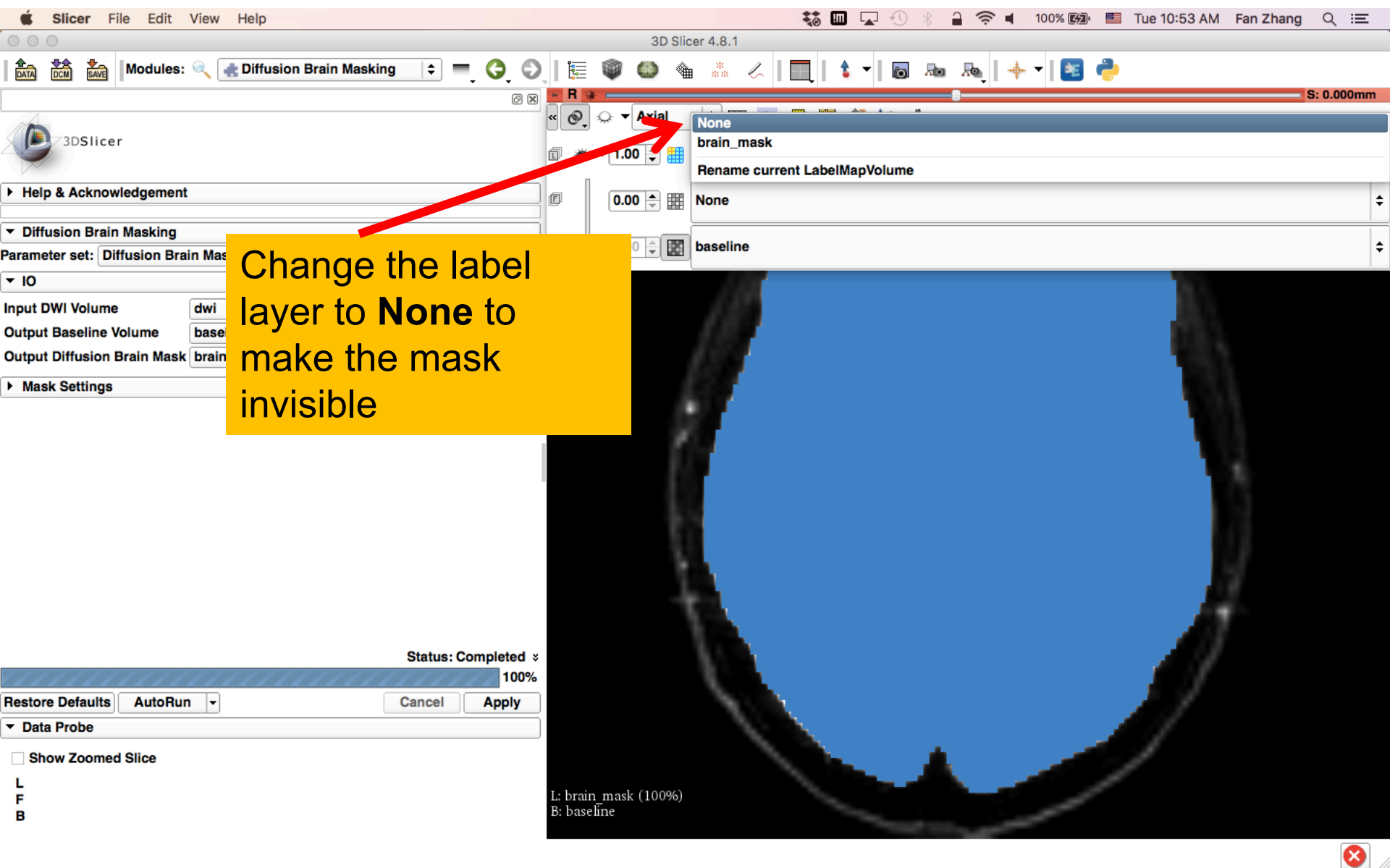
- select the Input DWI volume 'dwi'
- select Output Baseline Volume 'Create new Volume as...', and name it 'baseline'
- select Output Diffusion Brain Mask 'Create new LabelMapVolume as...', and name it 'brain_mask'
- click on **Apply**.

B: dwi

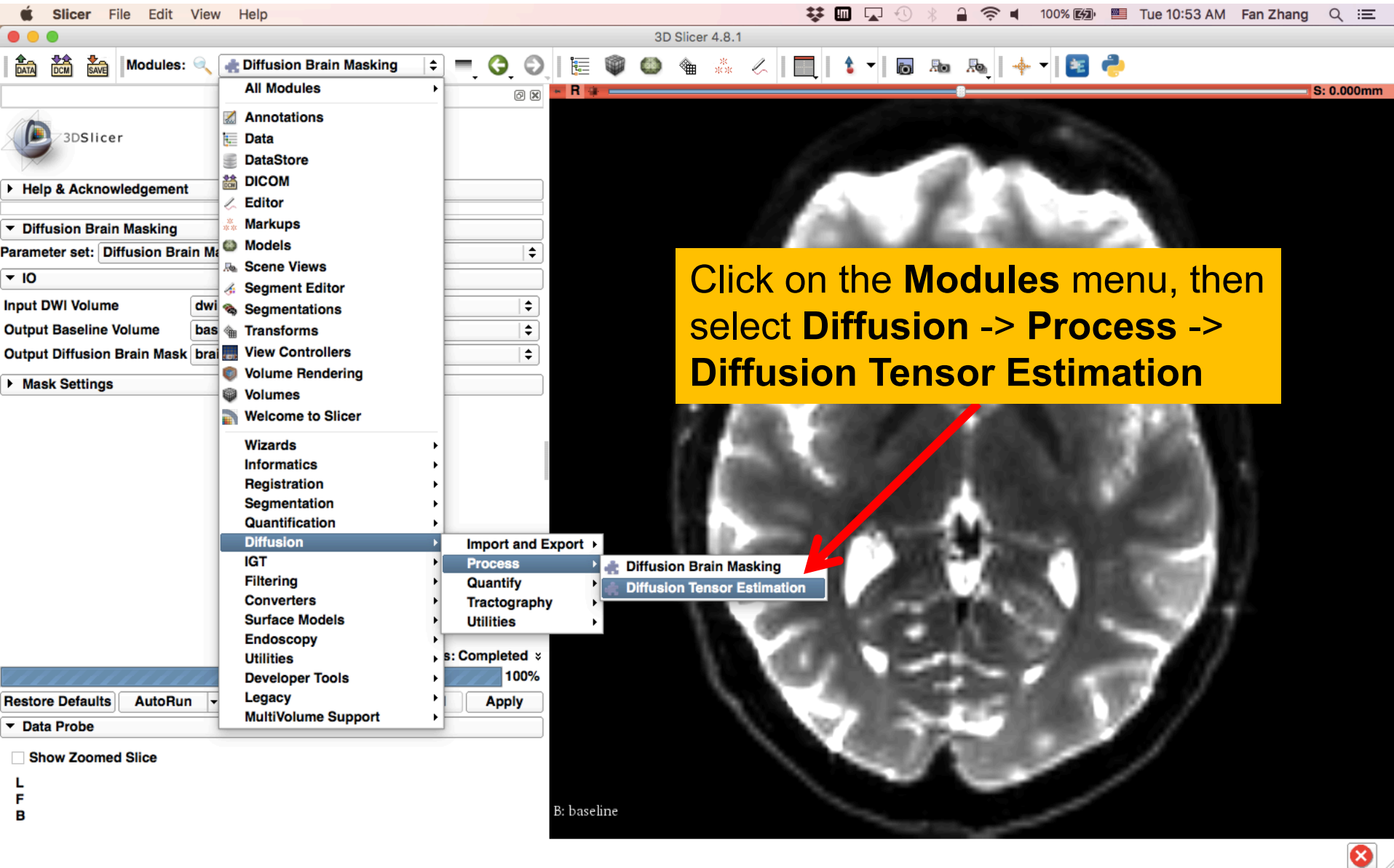
Creating a brain mask



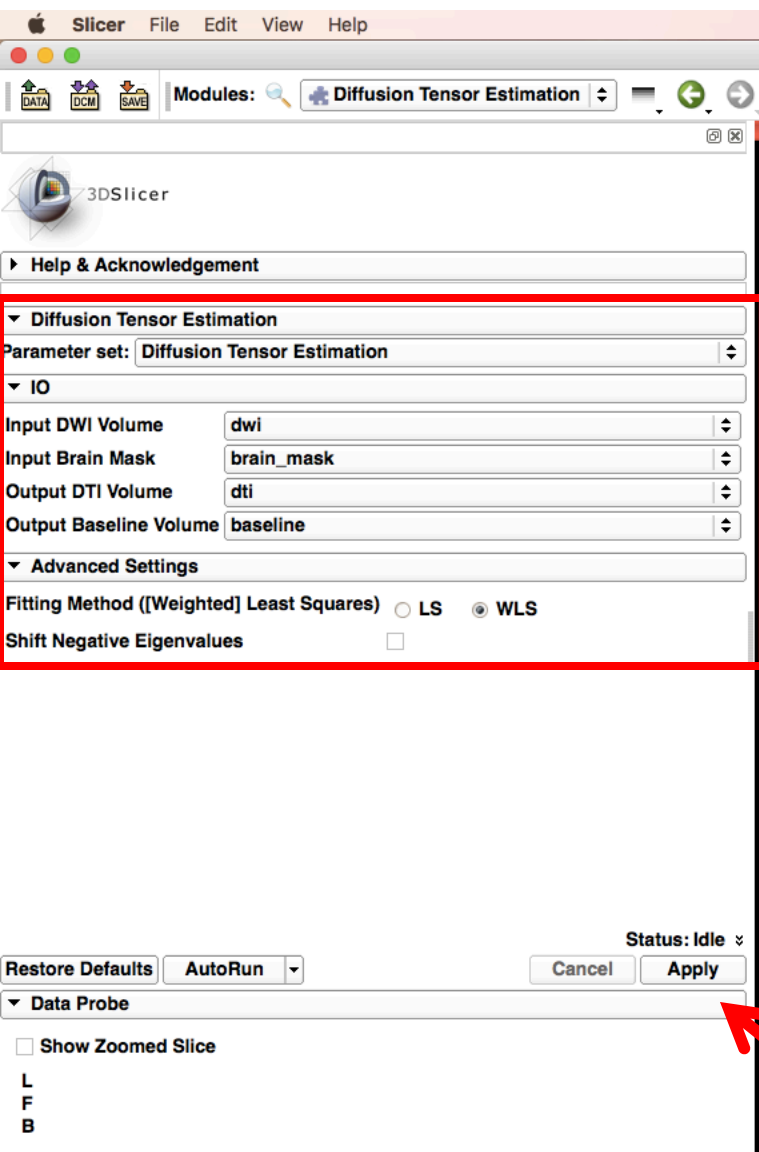
Creating a brain mask



Estimating the tensor



Estimating the tensor



The screenshot shows the 3D Slicer 4.8.1 interface. The 'Diffusion Tensor Estimation' module is selected in the Modules panel. A red box highlights the 'IO' and 'Advanced Settings' sections of the module's parameter set. The 'IO' section contains the following settings:

- Input DWI Volume: dwi
- Input Brain Mask: brain_mask
- Output DTI Volume: dti
- Output Baseline Volume: baseline

The 'Advanced Settings' section contains the following settings:

- Fitting Method ([Weighted] Least Squares): ☐ LS ☒ WLS
- Shift Negative Eigenvalues: ☐

At the bottom of the module panel, there are buttons for 'Restore Defaults', 'AutoRun', 'Cancel', and 'Apply'. A red arrow points to the 'Apply' button. The status bar at the bottom indicates 'Status: Idle'.

Instructions:

- 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

3D Slicer 4.8.1

Modules: Diffusion Tensor Estimation

Parameter set: Diffusion Tensor Estimation

IO

Input DWI Volume: dwi

Input Brain Mask: brain_mask

Output DTI Volume: dti

Output Baseline Volume: baseline

Advanced

Fitting Method: F

Shift Negative: L

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

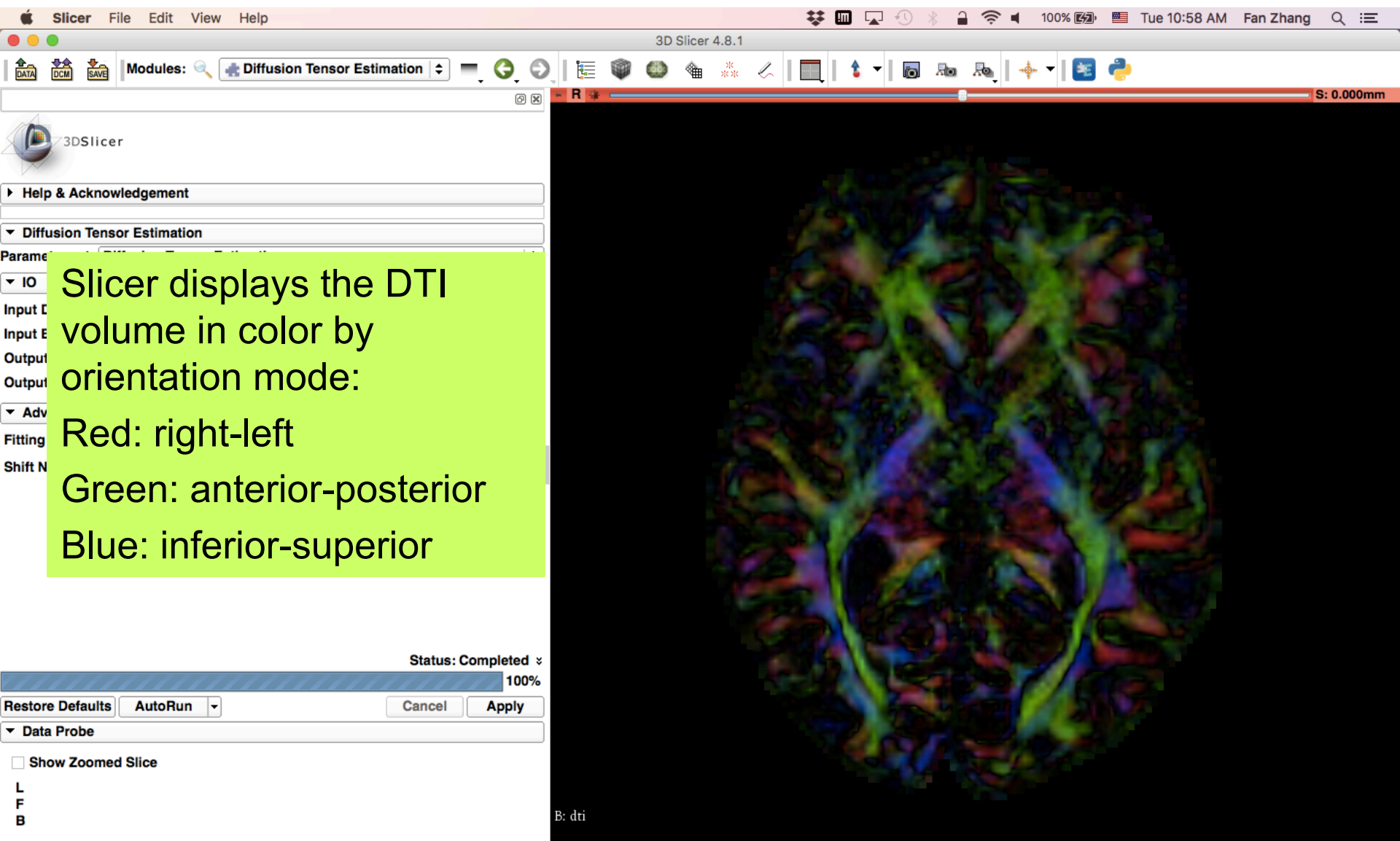
Data Probe

Show Zoomed Slice

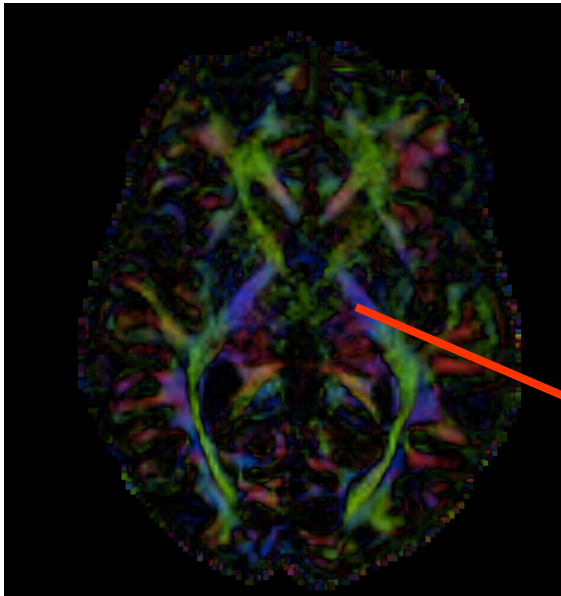
L: brain_mask (100%)
B: dti

Position your mouse over the pin icon, click on the double arrow and select the **dti** in the **B** field, set the **F** and **L** to none.

Exploring the DWI Dataset



Diffusion Tensor Data



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

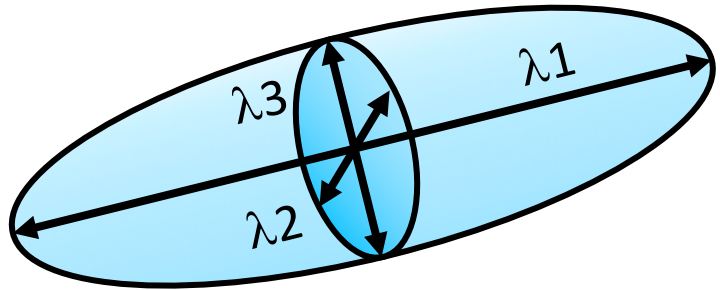
Stejskal-Tanner equation (1965)

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

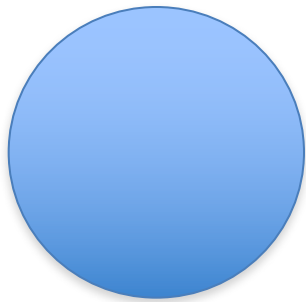
The diffusion tensor $\underline{\mathbf{D}}$ in the voxel (I,J,K) is a 3x3 symmetric matrix.

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 λ_1 , λ_2 , λ_3 to characterize the size and shape of the diffusion tensor.

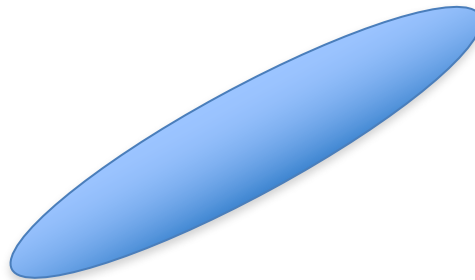


Diffusion Tensor Shape



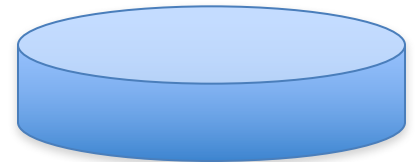
$$\lambda_1 = \lambda_2 = \lambda_3$$

Isotropic media
(Cerebrospinal
Fluid, gray matter)



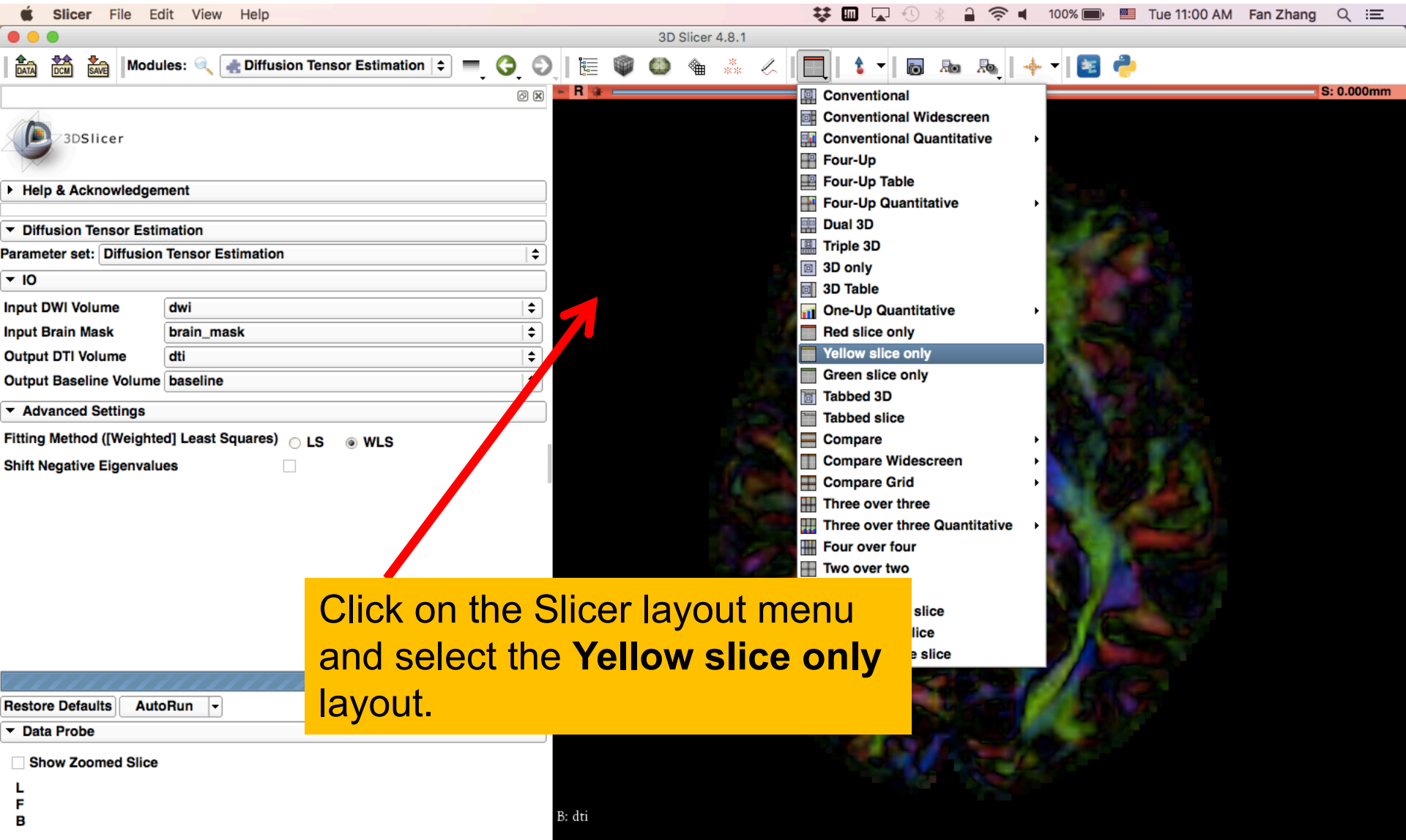
$$\lambda_1 \gg \lambda_2, \lambda_3$$

Anisotropic media
(white matter)

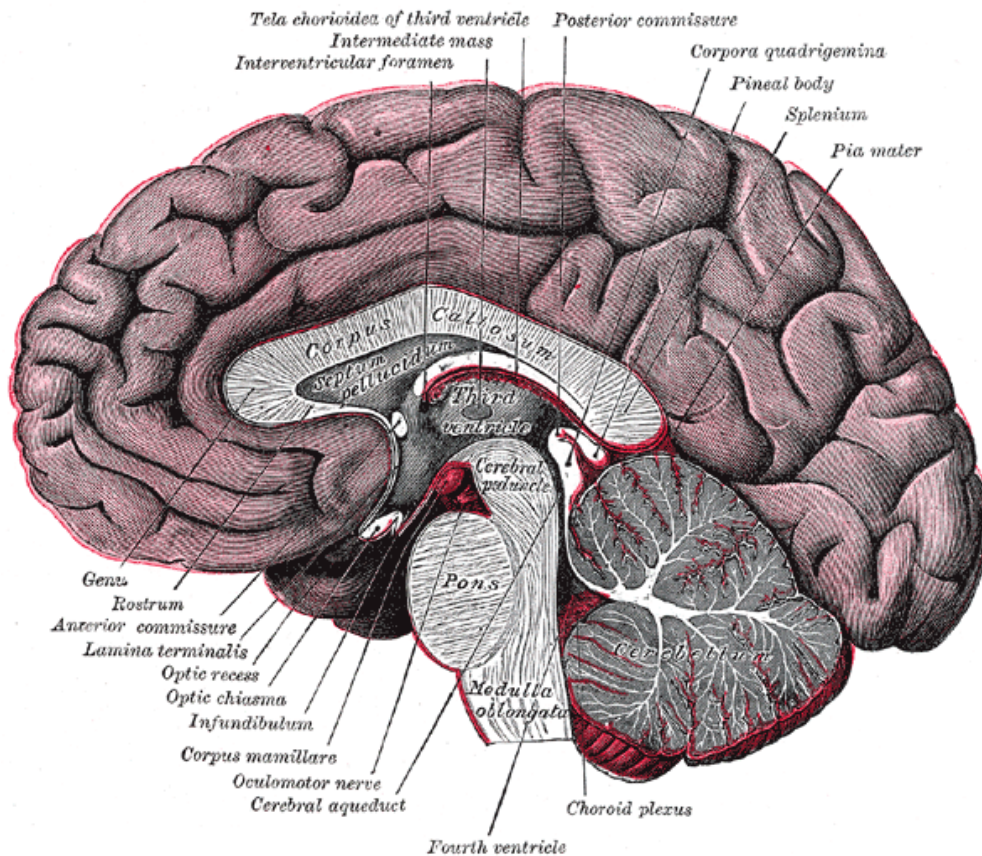


$$\lambda_1 \sim \lambda_2 \gg \lambda_3$$

Exploring the DWI Dataset



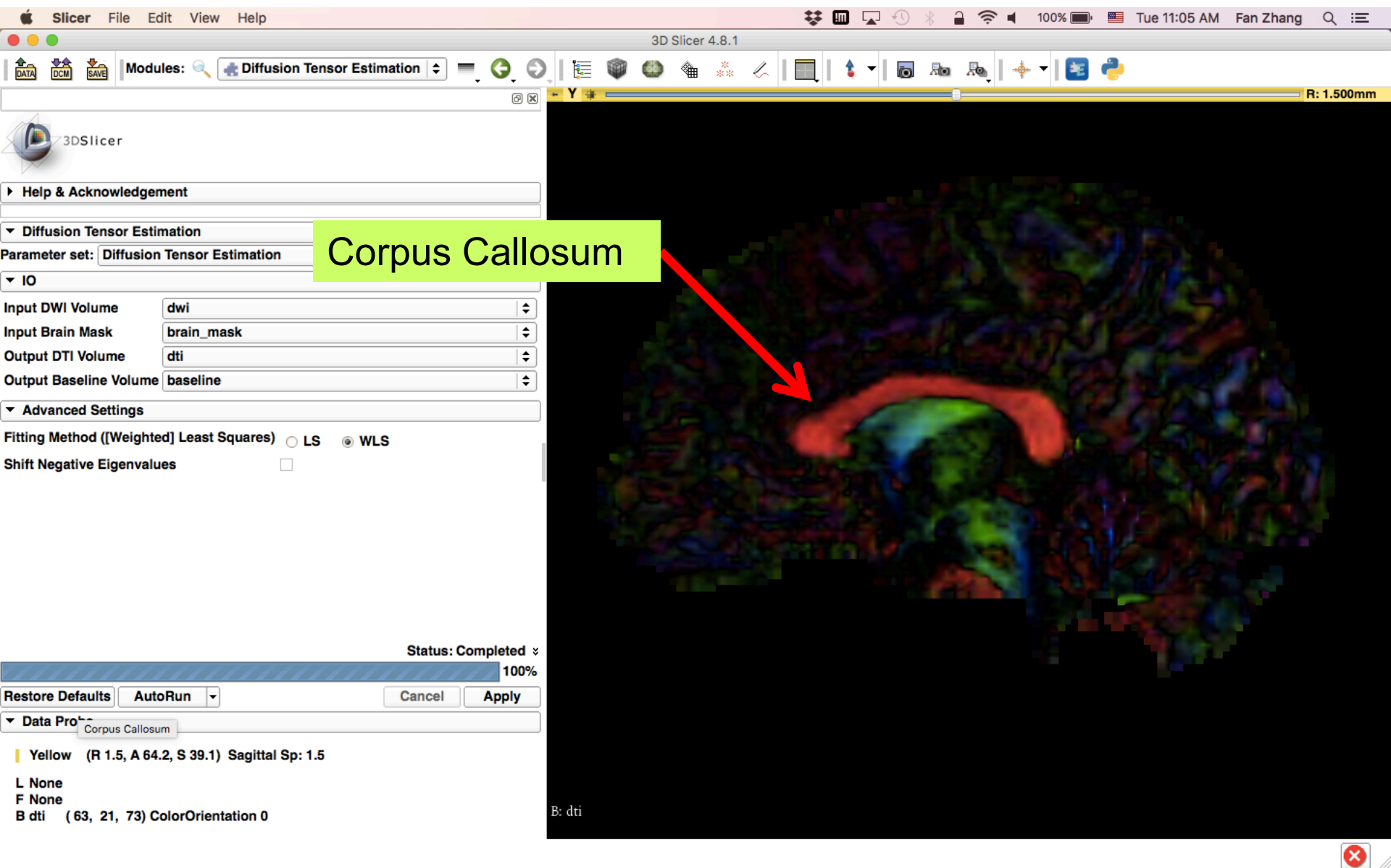
Corpus Callosum



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

Image from Gray's Anatomy

Corpus Callosum

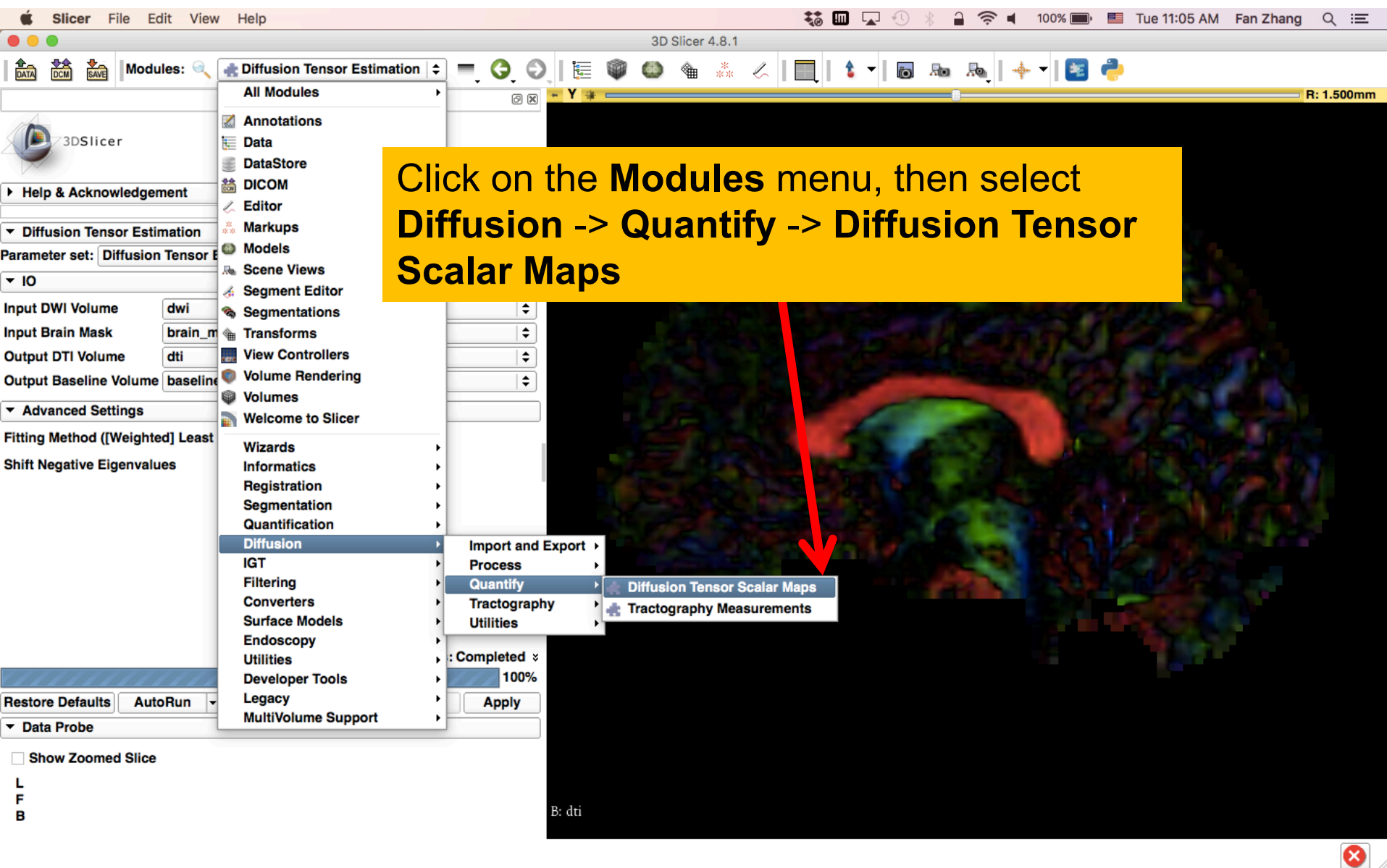


Characterizing the Size of the tensor: Trace

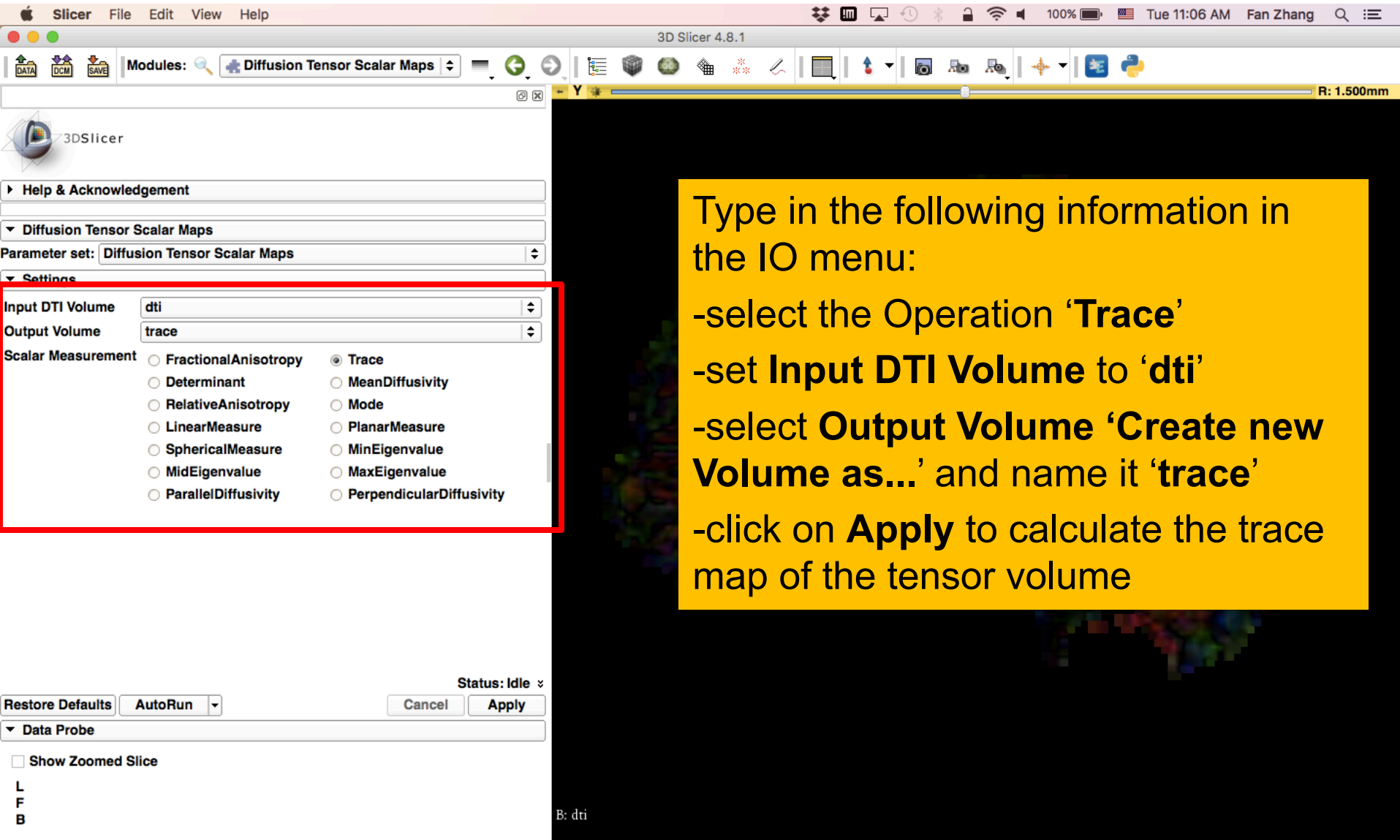
$$\text{Trace}(D) = \lambda_1 + \lambda_2 + \lambda_3$$

- $\text{Trace}(D)$ 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



Trace

3D Slicer 4.8.1

Modules: Diffusion Tensor Scalar Maps

Set L as none.

Help & Acknowledgement

Diffusion Tensor Scalar Maps

Parameter set: Diffusion Tensor Scalar Maps

Settings

Input DTI Volume: dti

Output Volume: trace

Scalar Measurement: ☐ FractionalAnisotropy ☒ Trace ☐ Determinant ☐ MeanDiffusivity

The trace image appears in the yellow viewer

Sagittal

None

0.00

1.00

trace

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

Data Probe

Show Zoomed Slice

L
F
B

B: trace

Trace

3D Slicer 4.8.1

Modules: **Diffusion Tensor Scalar Maps**

Parameter set: **Diffusion Tensor Scalar Maps**

Settings

Input DTI Volume
Output Volume
Scalar Measurement

☐ RelativeAnisotropy ☐ Mode
☐ LinearMeasure ☐ PlanarMeasure
☐ SphericalMeasure ☐ MinEigenvalue
☐ MidEigenvalue ☐ MaxEigenvalue
☐ ParallelDiffusivity ☐ PerpendicularDiffusivity

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

Data Probe

Yellow (L 1.5, A 2.3, I 12.1) Sagittal Sp: 1.5

L None
F None
B trace (65, 62, 39) 0.001984

B: trace

Trace

3DSlicer 4.8.1

Modules: Diffusion Tensor Scalar Maps

Help & Acknowledgement

Diffusion Tensor Scalar Maps

Position your mouse over the **pin icon** and then select the **'>>'** icon to display this table and fill in the following information:

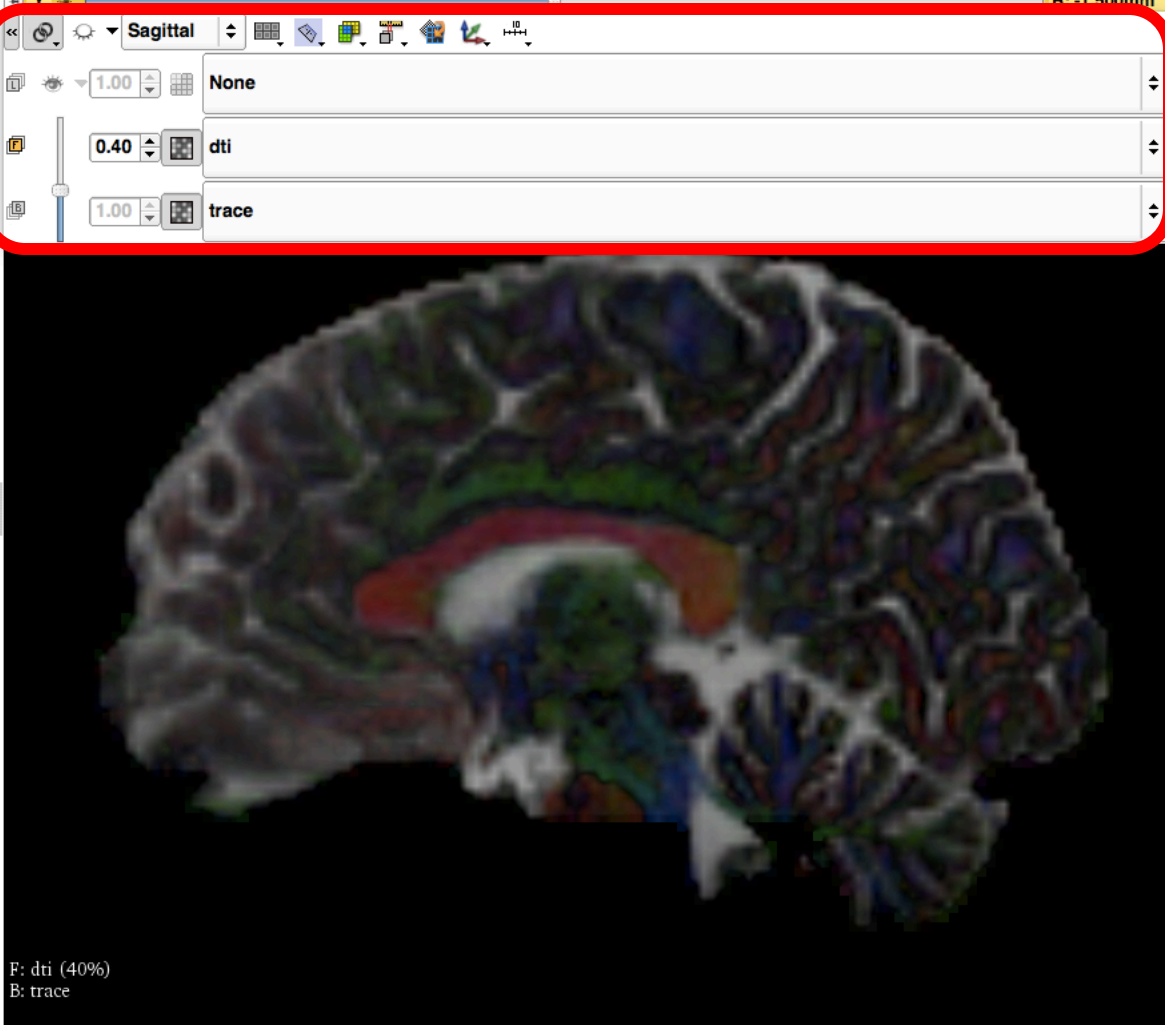
- Select the volume **'trace'** in the Background viewer
- Select the volume **'dti'** in the Foreground viewer

Set the **opacity** of the **dti** volume to **0.40**

Sagittal

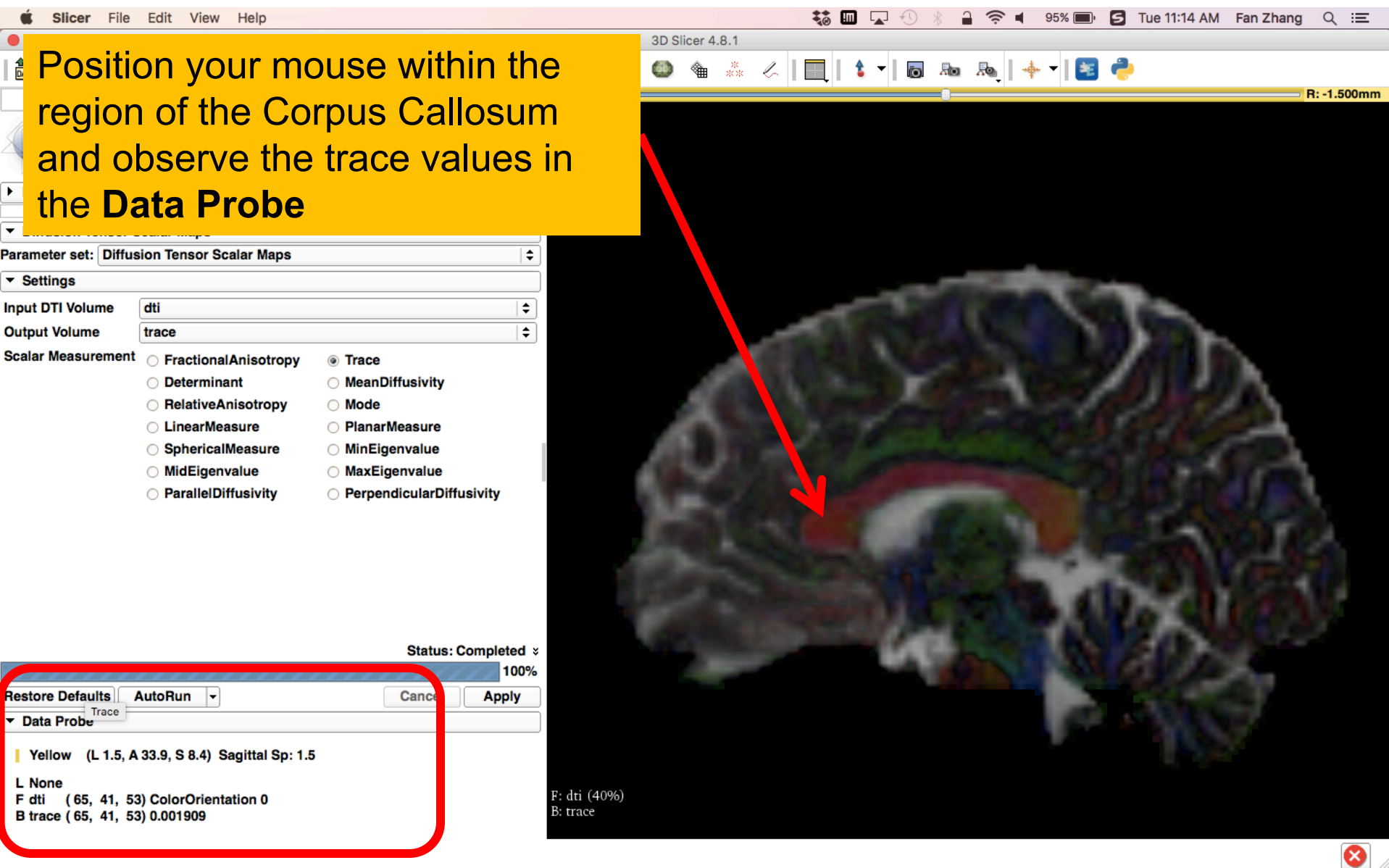
None
0.40 dti
1.00 trace

F: dti (40%)
B: trace



Trace

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



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
- ☐ Determinant
- ☐ RelativeAnisotropy
- ☐ LinearMeasure
- ☐ SphericalMeasure
- ☐ MidEigenvalue
- ☐ ParallelDiffusivity
- ☒ Trace
- ☐ 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

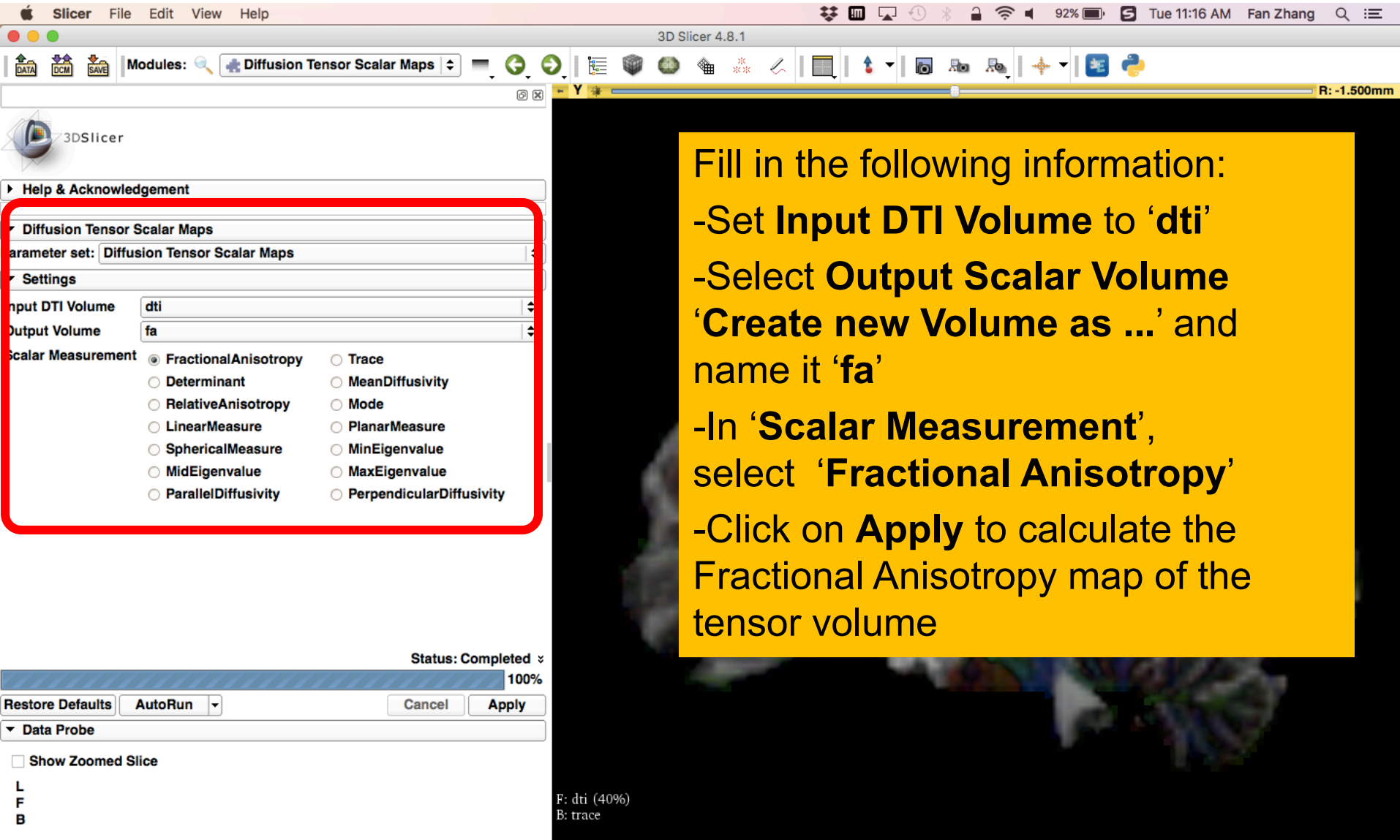
F: dti (40%)
B: trace

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



3D Slicer 4.8.1

Modules: **Diffusion Tensor Scalar Maps**

Help & Acknowledgement

Diffusion Tensor Scalar Maps

Parameter set: Diffusion Tensor Scalar Maps

Settings

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%

Restore Defaults AutoRun Cancel Apply

Data Probe

☐ Show Zoomed Slice

L
F
B

F: dti (40%)
B: trace

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

Fractional Anisotropy

Set L as none.

The FA image appears in the yellow viewer

Diffusion Tensor Scalar Maps

Parameter set: Diffusion Tensor Scalar Maps

Settings

- ☐ RelativeAnisotropy
- ☐ LinearMeasure
- ☐ SphericalMeasure
- ☐ MidEigenvalue
- ☐ ParallelDiffusivity
- ☐ Mode
- ☐ PlanarMeasure
- ☐ MinEigenvalue
- ☐ MaxEigenvalue
- ☐ PerpendicularDiffusivity

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

Data Probe

☐ Show Zoomed Slice

L
F
B

Sagittal

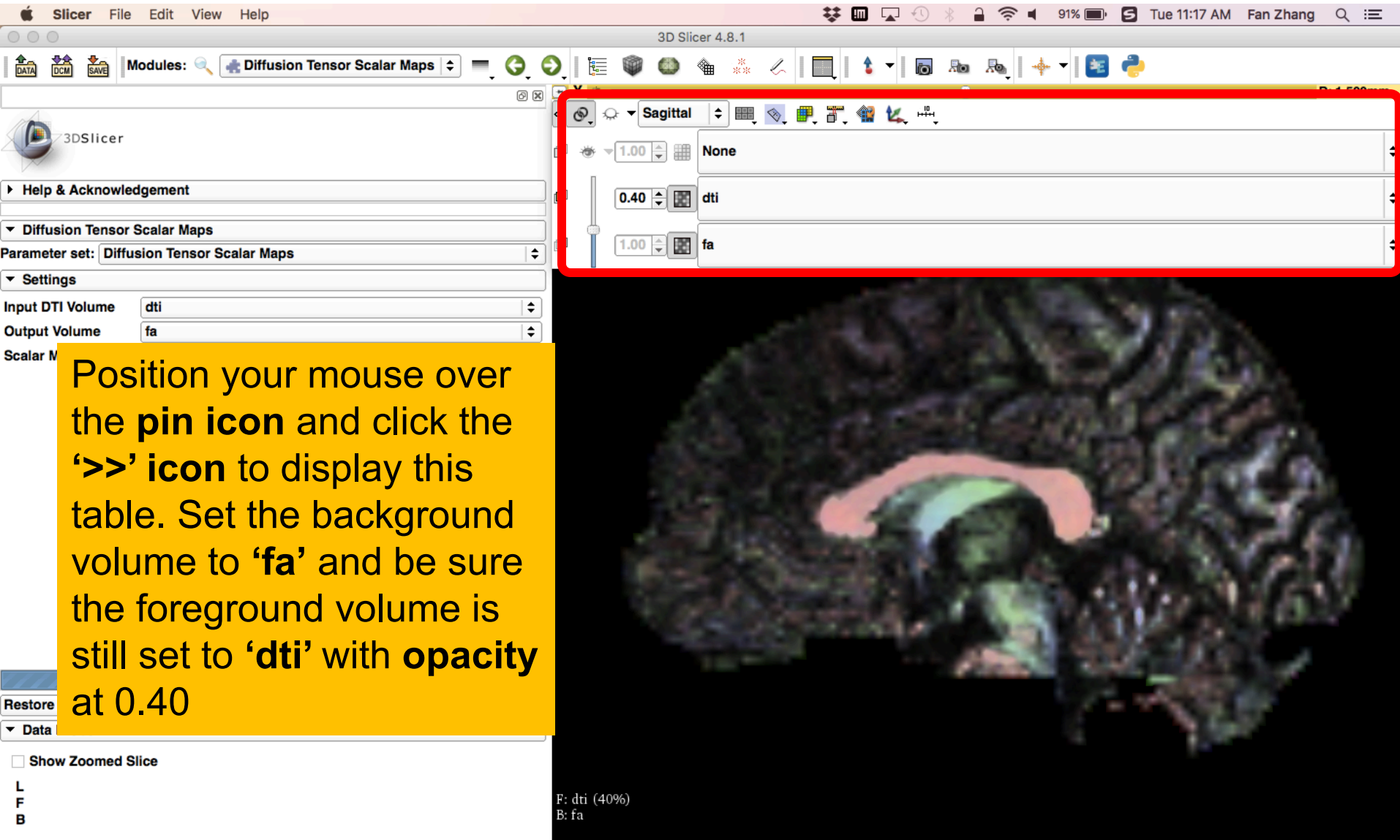
None

None

fa

B: fa

Fractional Anisotropy



3D Slicer 4.8.1

Modules: Diffusion Tensor Scalar Maps

Parameter set: Diffusion Tensor Scalar Maps

Settings

Input DTI Volume: dti

Output Volume: fa

Scalar Map

Position your mouse over the **pin icon** and click the **'>>'** icon to display this table. Set the background volume to **'fa'** and be sure the foreground volume is still set to **'dti'** with **opacity** at 0.40

Restore

Data

Show Zoomed Slice

L
F
B

Sagittal

None

0.40 dti

1.00 fa

F: dti (40%)
B: fa

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

Fractional Anisotropy

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

Data Probe

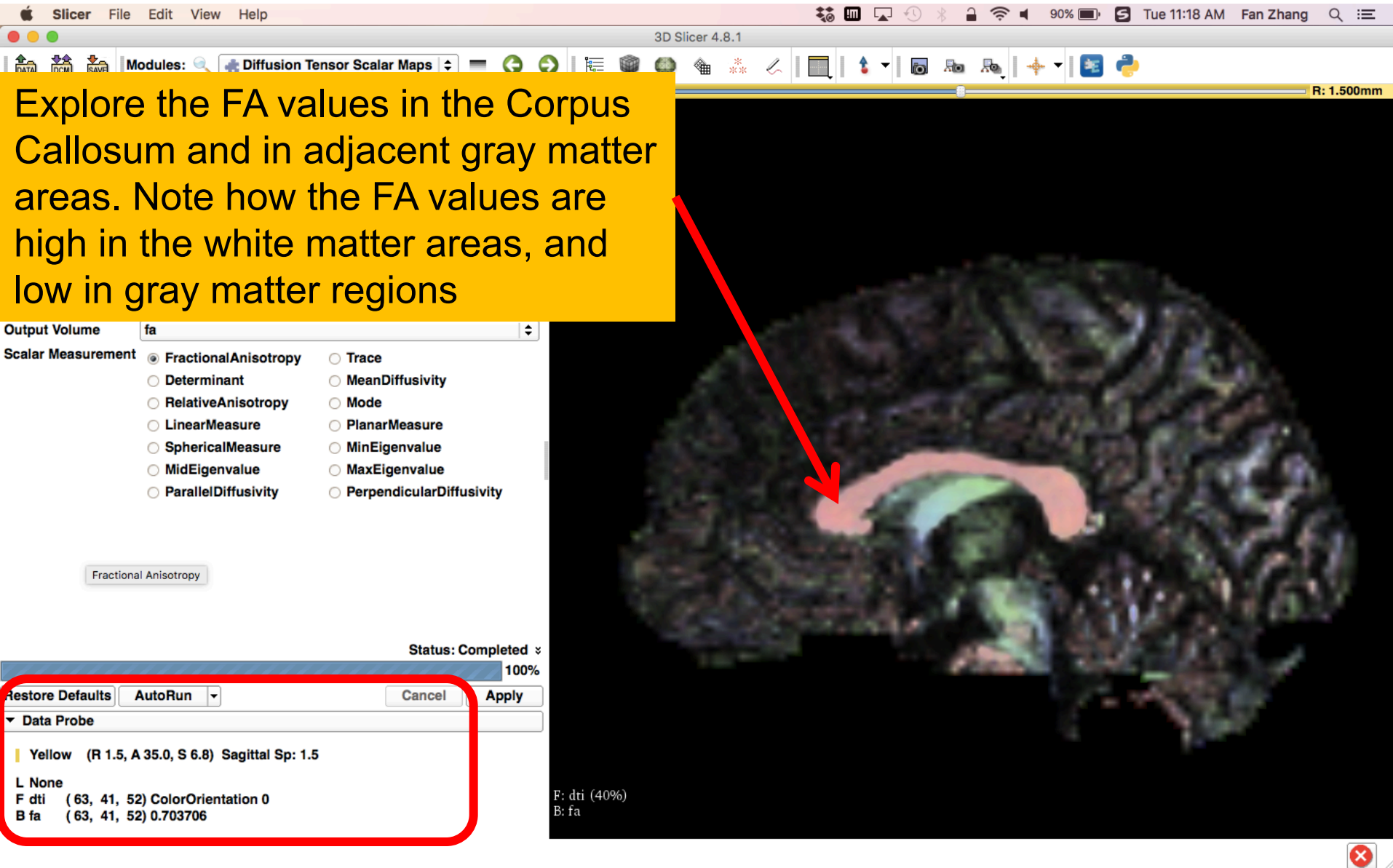
Yellow (R 1.5, A 35.0, S 6.8) Sagittal Sp: 1.5

L None

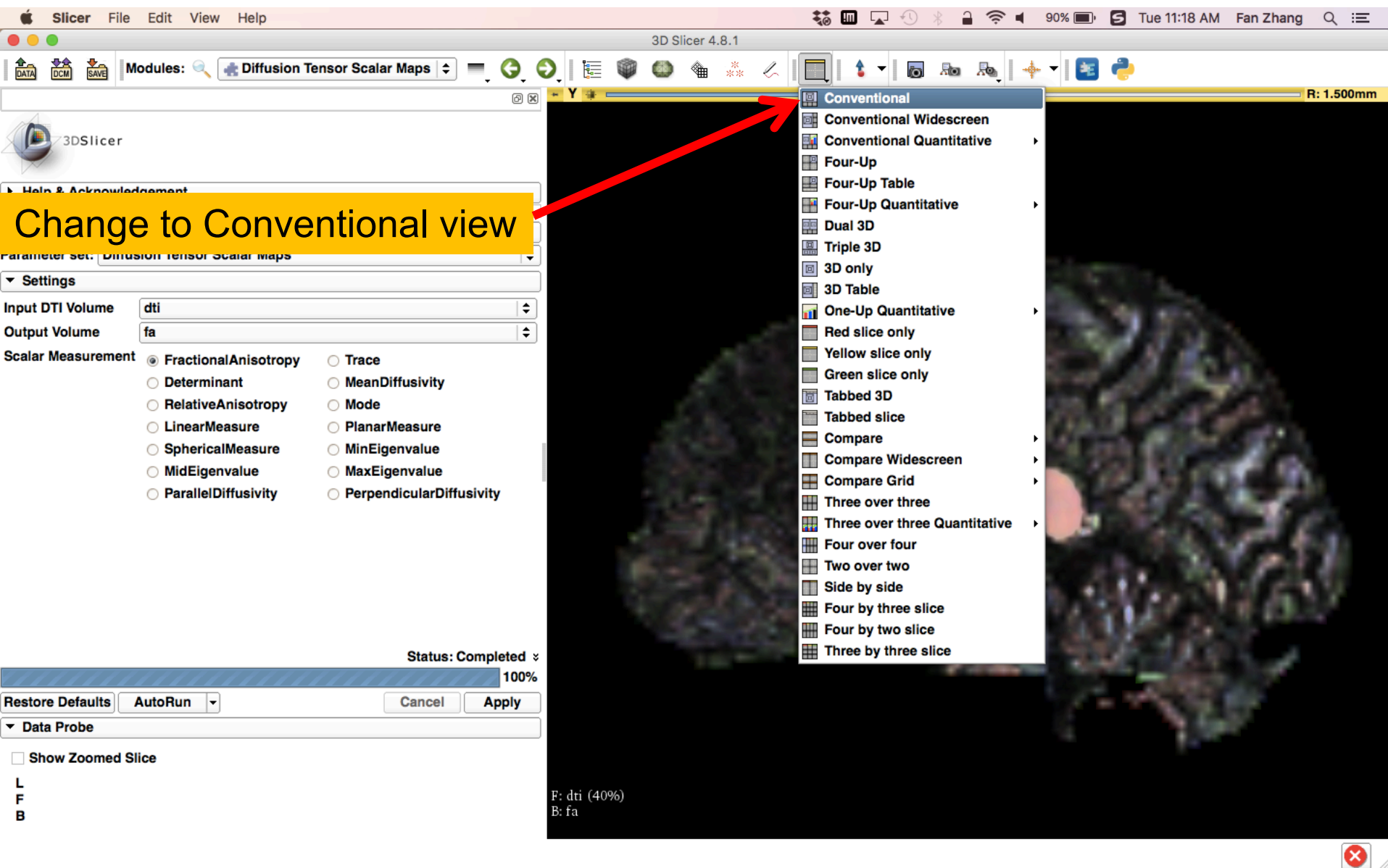
F dti (63, 41, 52) ColorOrientation 0

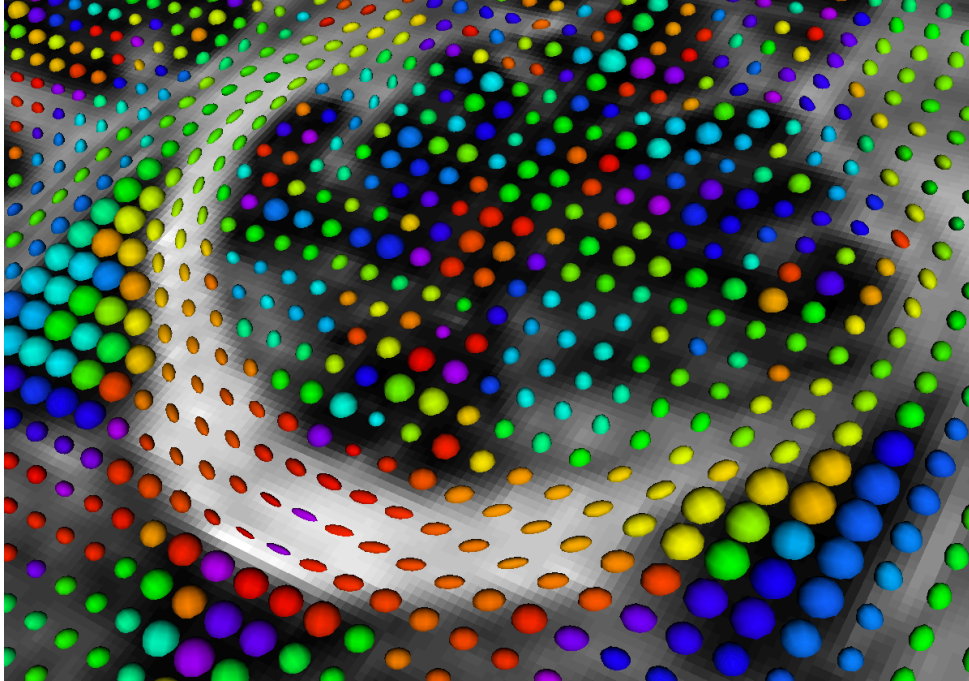
B fa (63, 41, 52) 0.703706

F: dti (40%)
B: fa



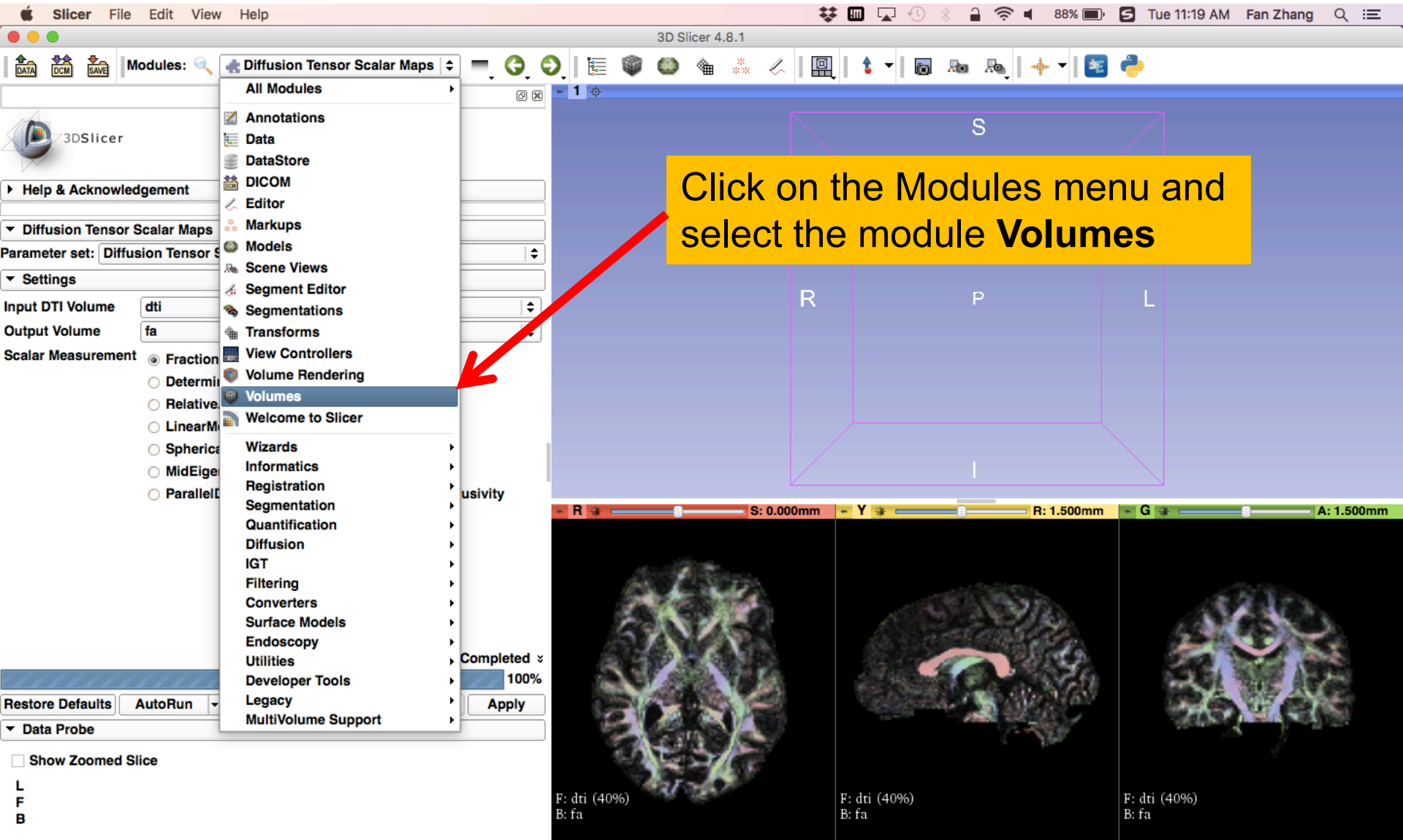
Fractional Anisotropy





Part 2: Visualizing the tensor data

3D Visualization: Glyphs



3D Visualization: Glyphs

The screenshot shows the 3D Slicer 4.8.1 interface. The top menu bar includes Apple logo, Slicer, File, Edit, View, and Help. The top status bar shows system icons, 3D Slicer 4.8.1, and user information (Tue 11:20 AM, Fan Zhang). The left sidebar contains the 'Modules' panel with 'Volumes' selected, and a 'Data Probe' panel with 'Show Zoomed Slice' checked. The main 3D view area displays a brain slice. A yellow text box is overlaid on the 3D view, providing instructions. A red box highlights the 'Glyphs' toolbar in the bottom right corner of the 3D view, which contains three rows of icons for selecting foreground and background colors and opacity.

Position the mouse over the **pin icon** and select the '<<' icon to display the axial slice toolbar. Set the **Foreground** to 'fa' and the **Background** to 'dti', with the **Foreground** opacity set to 1.00

W: 0.0076 Manual W/L L: 0.0050

Threshold: Off

-0.0025 0.0108

Histogram

Data Probe

Show Zoomed Slice

L
F
B

None
fa
dti

F: fa (100%)
B: dti

F: fa (100%)
B: dti

F: fa (100%)
B: dti

3D Visualization: Glyphs

The screenshot displays the 3D Slicer 4.8.1 interface. On the left, the 'Modules' panel shows 'Volumes' selected. Below it, the 'Help & Acknowledgement' section is expanded, and the 'Active Volume' is set to 'dti'. The 'Volume Information' section is also expanded. The 'Display' section is expanded, and the 'Scalar Display' section is expanded, showing 'Scalar Mode: ColorOrientation'. The 'Lookup Table' section is expanded, and the 'Interpolate' checkbox is checked. The 'Window/Level' section is expanded, and the 'W: 255' and 'L: 128' sliders are visible. The 'Threshold' section is expanded, and the 'Off' button is selected. The 'Glyphs on Slices Display' section is expanded, and the 'Slice Visibility' checkboxes for 'Red', 'Yellow', and 'Green' are visible. The 'Opacity' slider is set to 1.00. The 'Scalar ColorMap' is set to 'Rainbow'. The 'Data Probe' section is expanded, and the 'Show Zoomed Slice' checkbox is visible. The main 3D view shows a blue background with a purple wireframe box. A yellow text box in the center of the 3D view contains the text: 'Set the Active Volume to 'dti' and the Scalar Mode to 'ColorOrientation''. Below the 3D view, there are three panels showing the 'dti' volume in different orientations: axial, sagittal, and coronal. Each panel shows the 'F: fa (100%)' and 'B: dti' data. The bottom status bar shows the coordinates: 'R: 1.500mm', 'S: 0.000mm', 'Y: 1.500mm', 'G: 1.500mm', and 'A: 1.500mm'.

3D Slicer 4.8.1

Set the **Active Volume** to 'dti' and the **Scalar Mode** to 'ColorOrientation'

W: 255 Auto W/L L: 128

Threshold: Off

Glyphs on Slices Display

Slice Visibility: ☐ Red ☐ Yellow ☐ Green

Opacity: 1.00

Scalar ColorMap: Rainbow

Data Probe

Show Zoomed Slice

L
F
B

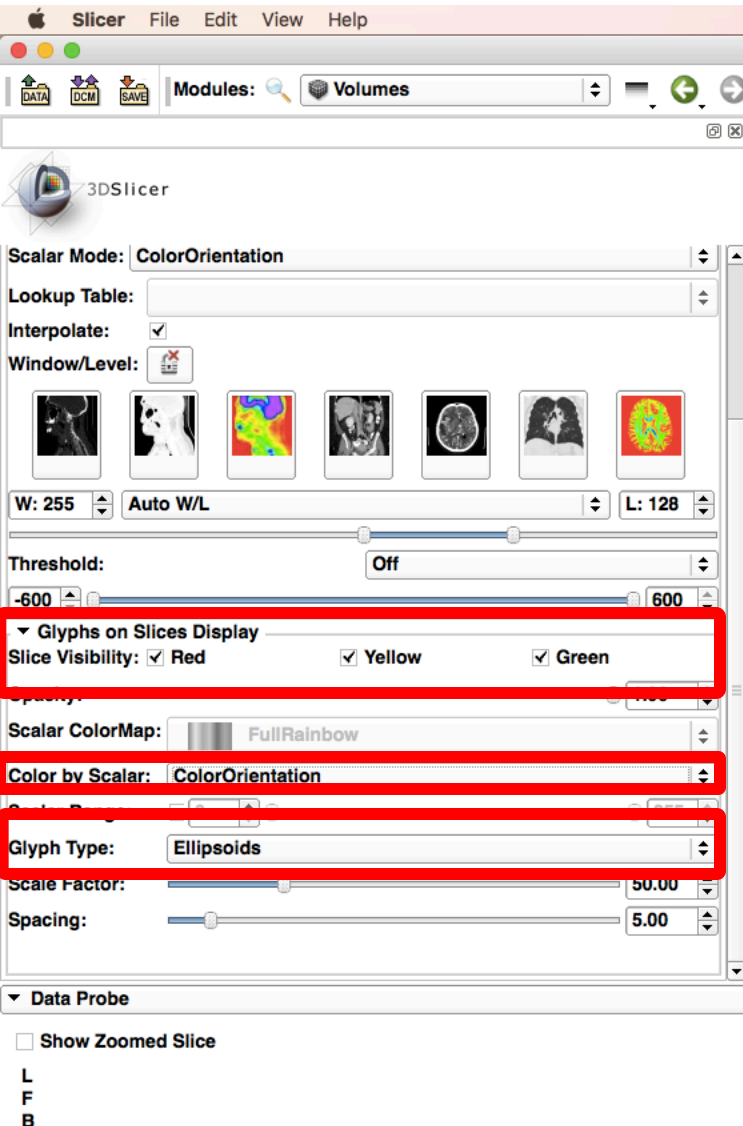
R: 1.500mm S: 0.000mm Y: 1.500mm G: 1.500mm A: 1.500mm

F: fa (100%)
B: dti

F: fa (100%)
B: dti

F: fa (100%)
B: dti

3D Visualization: Glyphs

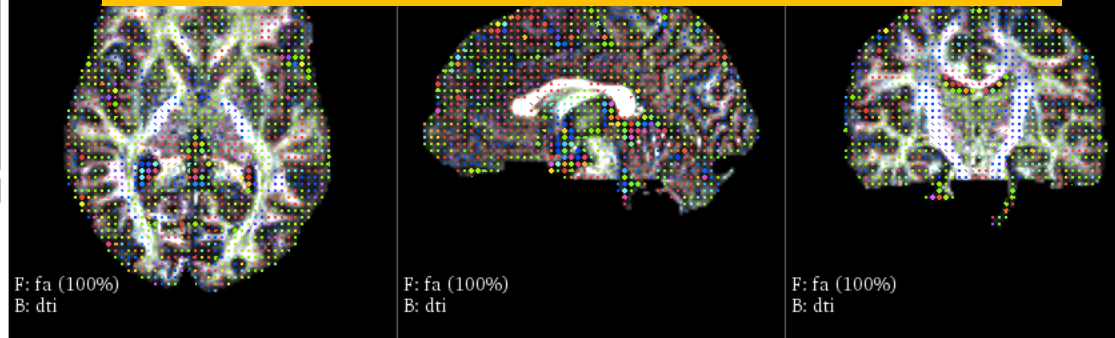


Scroll down the module panel and in the **Glyphs on Slices Display** section:

- 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**'



3D Visualization: Glyphs

The screenshot displays the 3D Slicer 4.8.1 interface. The main 3D view shows a brain model with a grid of colorful glyphs. A yellow text box with a black border is overlaid on the 3D view, containing the text: "The glyphs appear in all 3 slice viewers". The left sidebar contains the "Volumes" module settings. The "Scalar Mode" is set to "ColorOrientation". The "Lookup Table" is set to "FullRainbow". The "Interpolate" checkbox is checked. The "Window/Level" is set to "Auto W/L". The "Threshold" is set to "Off". The "Glyphs on Slices Display" section shows "Slice Visibility" checked for Red, Yellow, and Green. The "Opacity" is set to 1.00. The "Scalar ColorMap" is set to "FullRainbow". The "Color by Scalar" is set to "ColorOrientation". The "Scalar Range" is set to 0 to 255. The "Glyph Type" is set to "Ellipsoids". The "Scale Factor" is set to 50.00. The "Spacing" is set to 5.00. The "Data Probe" section shows the following data: Red (L 37.8, A 56.2, S 0.0) Axial Sp: 1.5, L None, F fa (89, 27, 47) 0.394249, B dti (89, 27, 47) ColorOrientation 0. The bottom right corner shows three slice views: Axial, Sagittal, and Coronal. Each slice view displays the brain model with the glyphs. The slice views are labeled "R" (Right), "L" (Left), and "I" (Inferior). The slice views are also labeled with "F: fa (100%)" and "B: dti".

Scalar Mode: ColorOrientation

Lookup Table: FullRainbow

Interpolate: ☒

Window/Level: Auto W/L

W: 255 L: 128

Threshold: Off

Glyphs on Slices Display

Slice Visibility: ☒ Red ☒ Yellow ☒ Green

Opacity: 1.00

Scalar ColorMap: FullRainbow

Color by Scalar: ColorOrientation

Scalar Range: 0 255

Glyph Type: Ellipsoids

Scale Factor: 50.00

Spacing: 5.00

Data Probe

Red (L 37.8, A 56.2, S 0.0) Axial Sp: 1.5

L None

F fa (89, 27, 47) 0.394249

B dti (89, 27, 47) ColorOrientation 0

The glyphs appear in all 3 slice viewers

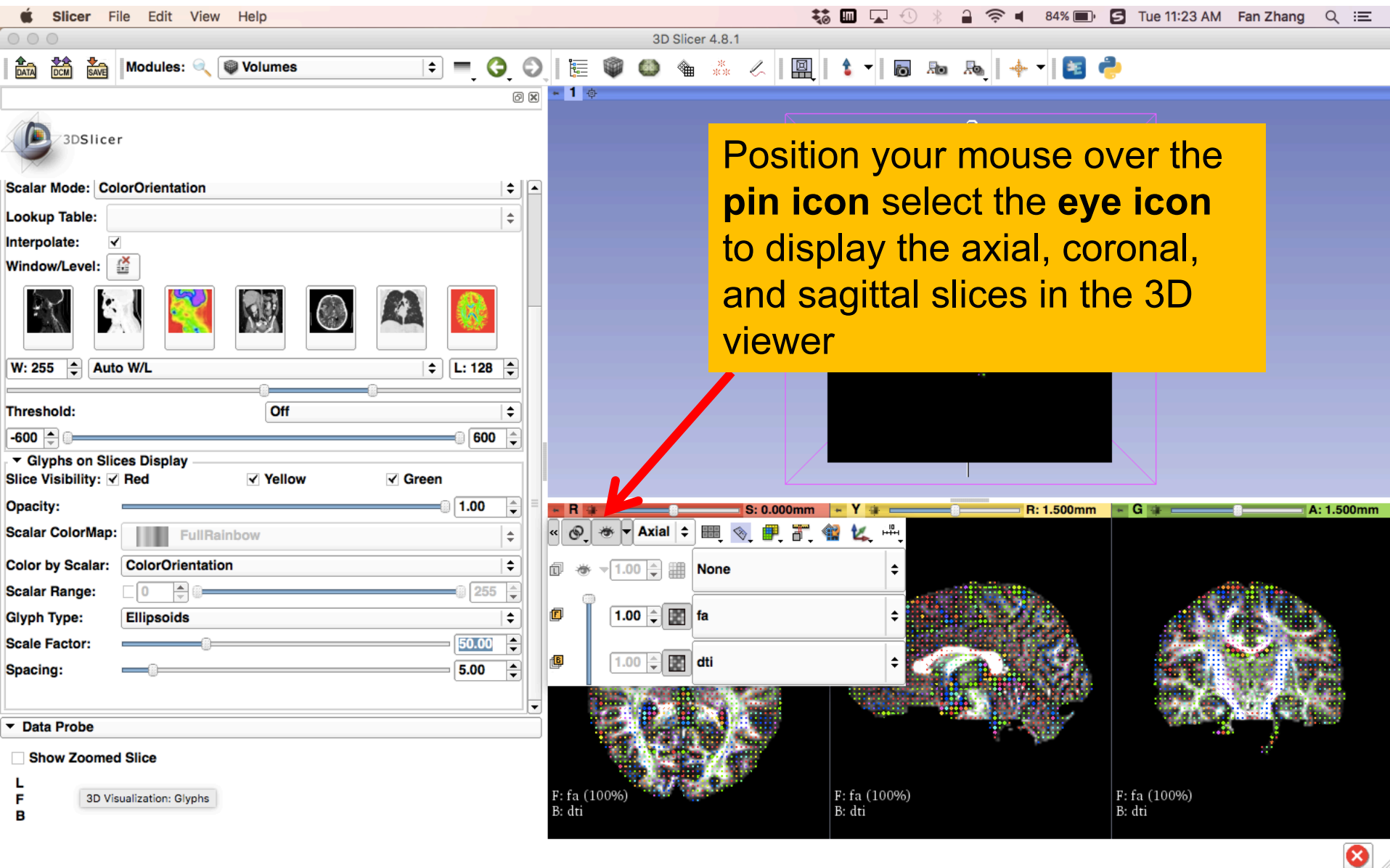
R L I

F: fa (100%) B: dti

F: fa (100%) B: dti

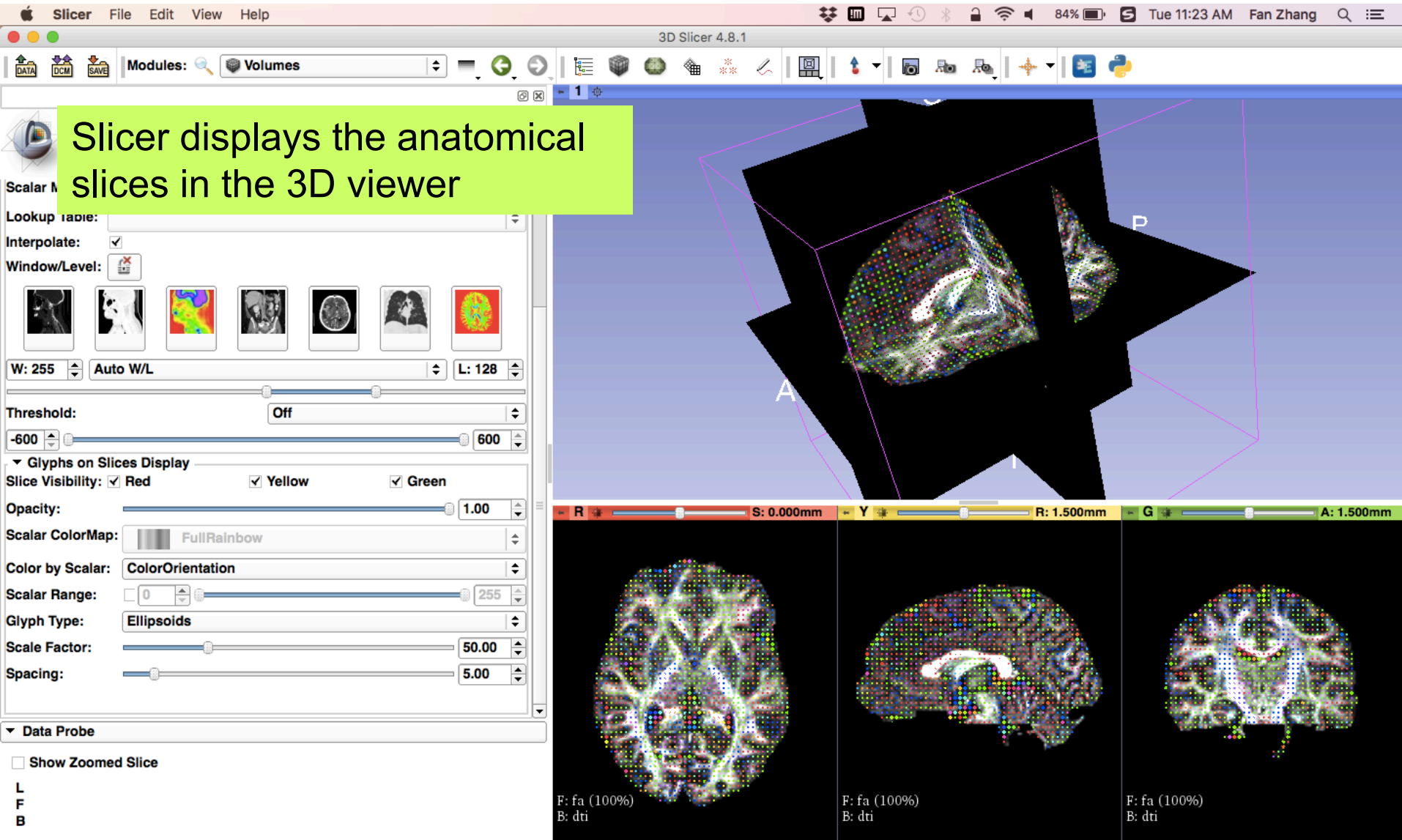
F: fa (100%) B: dti

3D Visualization: Glyphs



3D Visualization: Glyphs

Slicer displays the anatomical slices in the 3D viewer



The screenshot displays the 3D Slicer 4.8.1 interface. The main 3D viewer shows a brain model with glyphs (colored dots) and a black wireframe box. The left sidebar contains the 'Modules' panel with 'Volumes' selected, and the 'Data Probe' panel with 'Show Zoomed Slice' checked. The bottom panel shows three 2D anatomical slices (axial, sagittal, and coronal) with the following labels:

- Left slice: F: fa (100%) B: dti
- Middle slice: F: fa (100%) B: dti
- Right slice: F: fa (100%) B: dti

The bottom panel also includes a color bar with labels: R, S: 0.000mm, Y, R: 1.500mm, G, A: 1.500mm.

3D Visualization: Glyphs

Zoom in to observe the glyphs.
The ellipsoids represent the principal direction of diffusion (main eigenvector)

3D Slicer 4.8.1

Modules: Volumes

W: 255 Auto W/L L: 128

Threshold: Off

Glyphs on Slices Display

Slice Visibility: ☒ Red ☒ Yellow ☒ Green

Opacity: 1.00

Scalar ColorMap: FullRainbow

Color by Scalar: ColorOrientation

Scalar Range: 0 255

Glyph Type: Ellipsoids

Scale Factor: 50

Spacing: 5.00

Data Probe

☐ Show Zoomed Slice

L F B

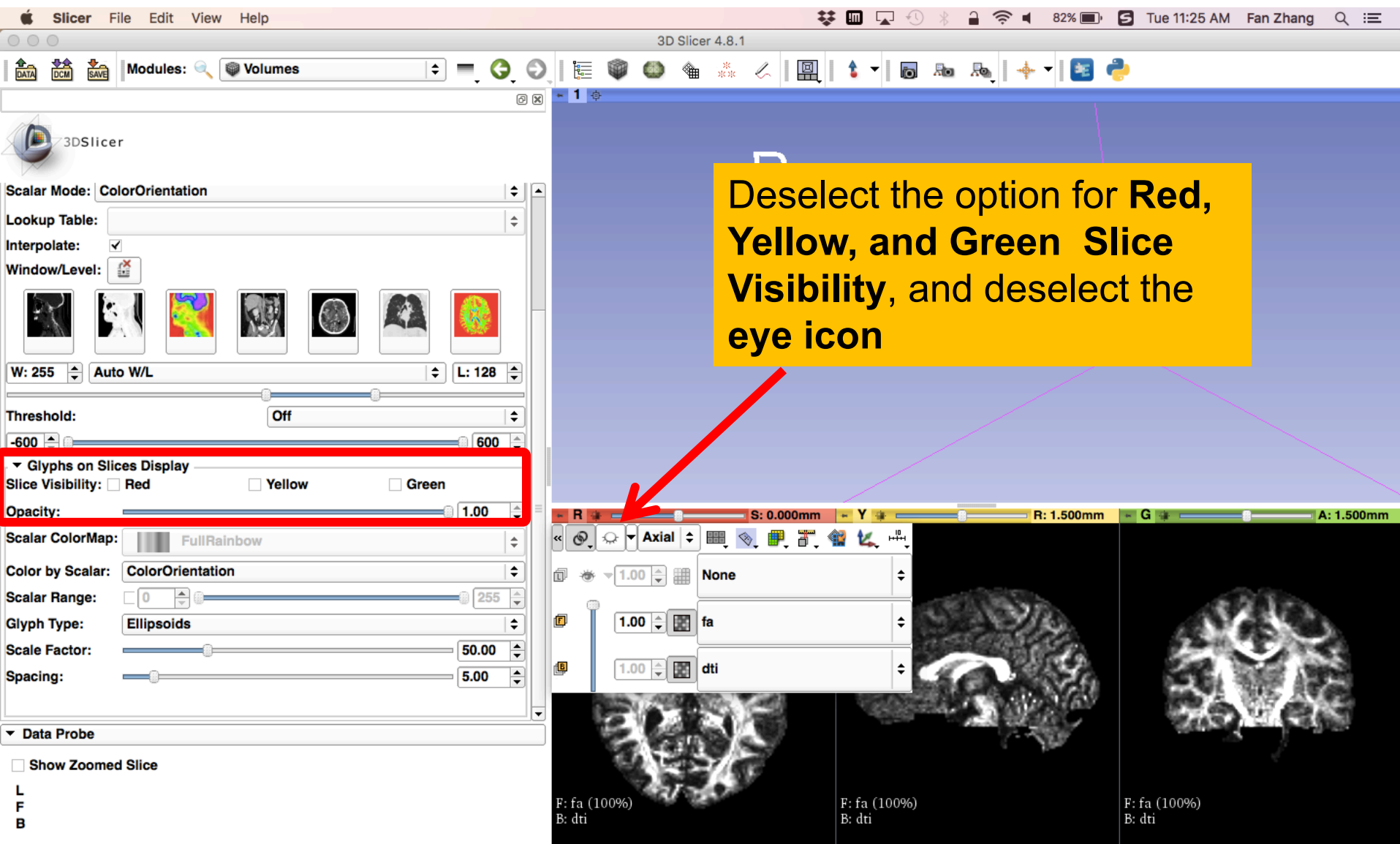
R S: 0.000mm Y R: 1.500mm G A: 1.500mm

F: fa (100%)
B: dti

F: fa (100%)
B: dti

F: fa (100%)
B: dti

Diffusion MRI tractography



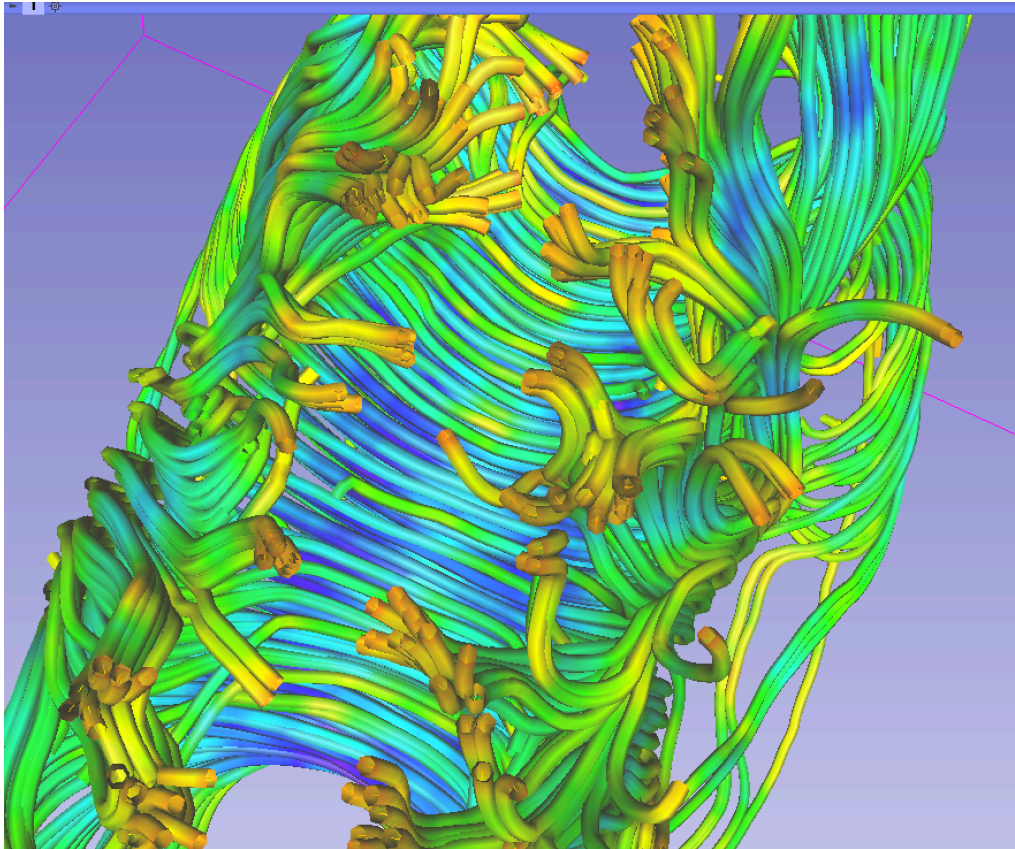
Diffusion MRI tractography

The screenshot displays the 3D Slicer 4.8.1 interface. The top menu bar includes 'Slicer', 'File', 'Edit', 'View', and 'Help'. The main window is divided into several panels:

- Left Panel (Modules):** Shows the 'Volumes' module. Below it, the 'Scalar Mode' is set to 'ColorOrientation'. The 'Lookup Table' is set to 'FullRainbow'. The 'Interpolate' checkbox is checked. The 'Window/Level' section shows 'W: 255' and 'L: 128'. The 'Threshold' is set to 'Off'. The 'Glyphs on Slices Display' section has 'Slice Visibility' set to 'Red', 'Yellow', and 'Green'. The 'Opacity' is set to '1.00'. The 'Scalar ColorMap' is set to 'FullRainbow'. The 'Color by Scalar' is set to 'ColorOrientation'. The 'Scalar Range' is set to '0' to '255'. The 'Glyph Type' is set to 'Ellipsoids'. The 'Scale Factor' is set to '50.00'. The 'Spacing' is set to '5.00'. The 'Data Probe' section has 'Show Zoomed Slice' checked.
- Top Center Panel (3D View):** Shows a 3D view of a brain slice. A red arrow points to the 'L' button in the '3D View' toolbar, which is used to reset the 3D view to left.
- Bottom Panel (Slices):** Shows three orthogonal slices (Axial, Sagittal, Coronal). The 'Axial' slice is highlighted. The 'Sagittal' slice is labeled 'B: fa'. The 'Coronal' slice is labeled 'B: fa'.

Two yellow callout boxes provide instructions:

- Click L to reset the 3D view to left** (pointing to the 'L' button in the 3D View toolbar).
- Position your mouse over the pin icon and change the Foreground to 'None' and the background to 'fa'** (pointing to the 'pin' icon in the 'Slices' panel).

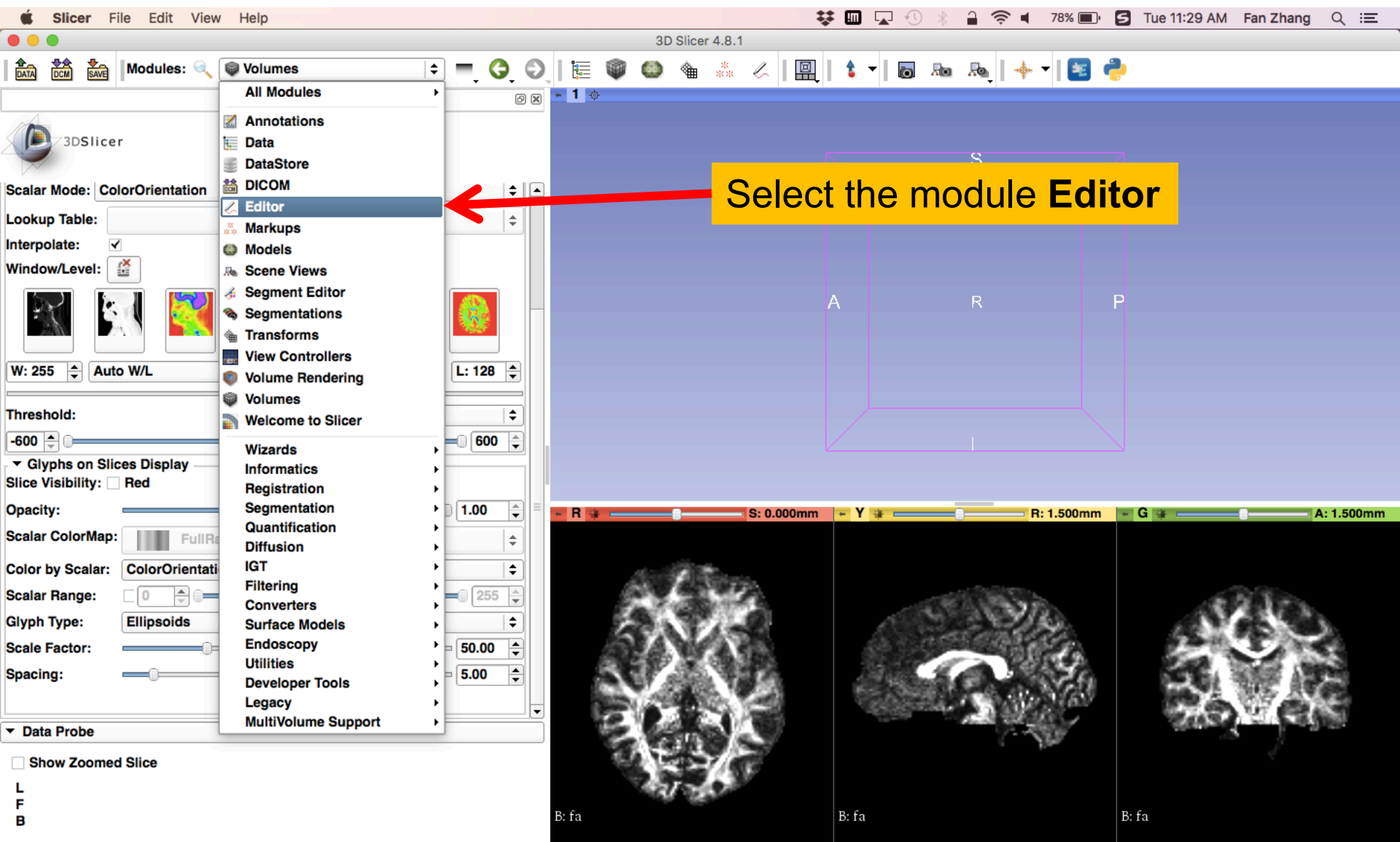


Part 3: From tensors to tracts

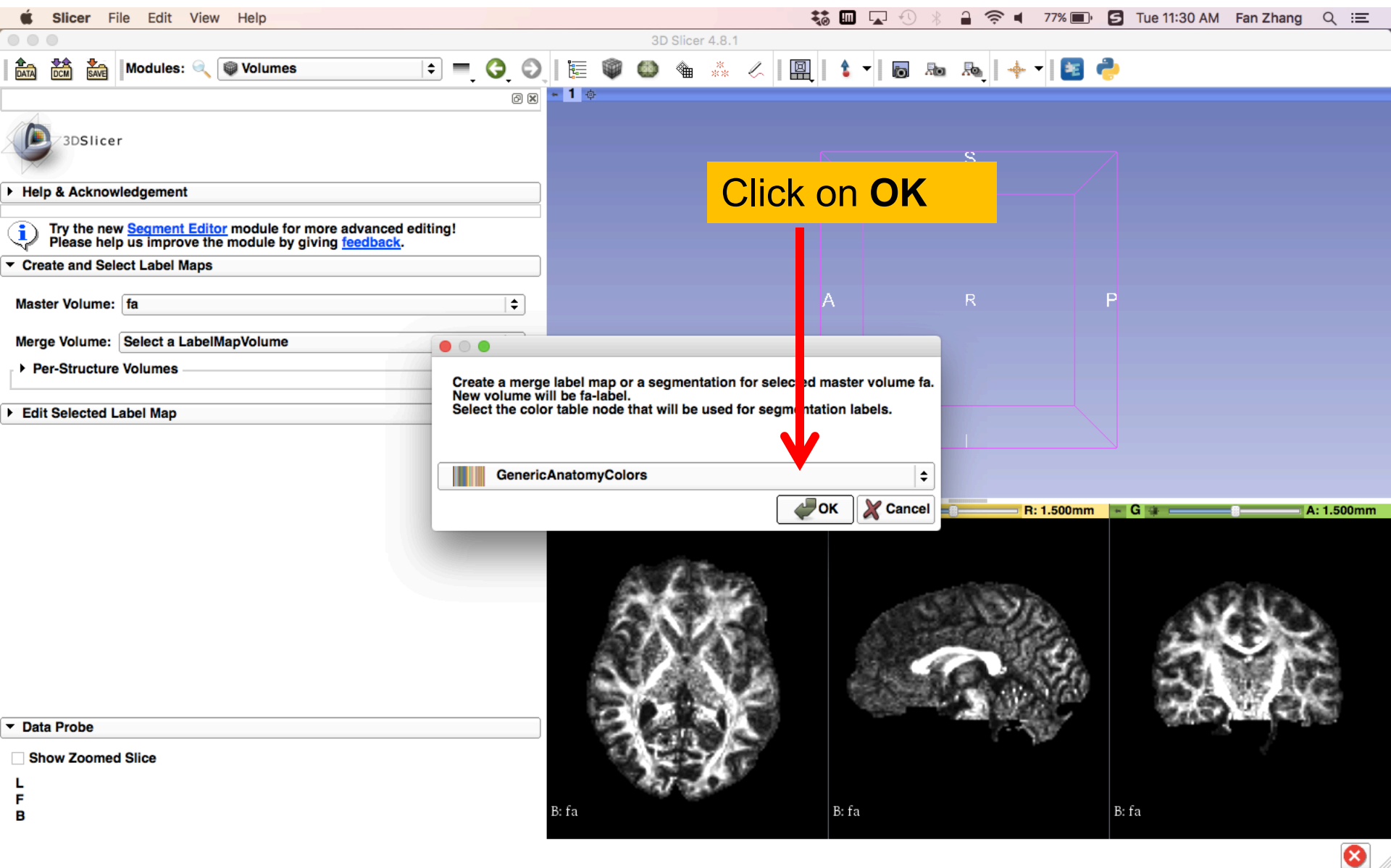
DTI tractography

- 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)

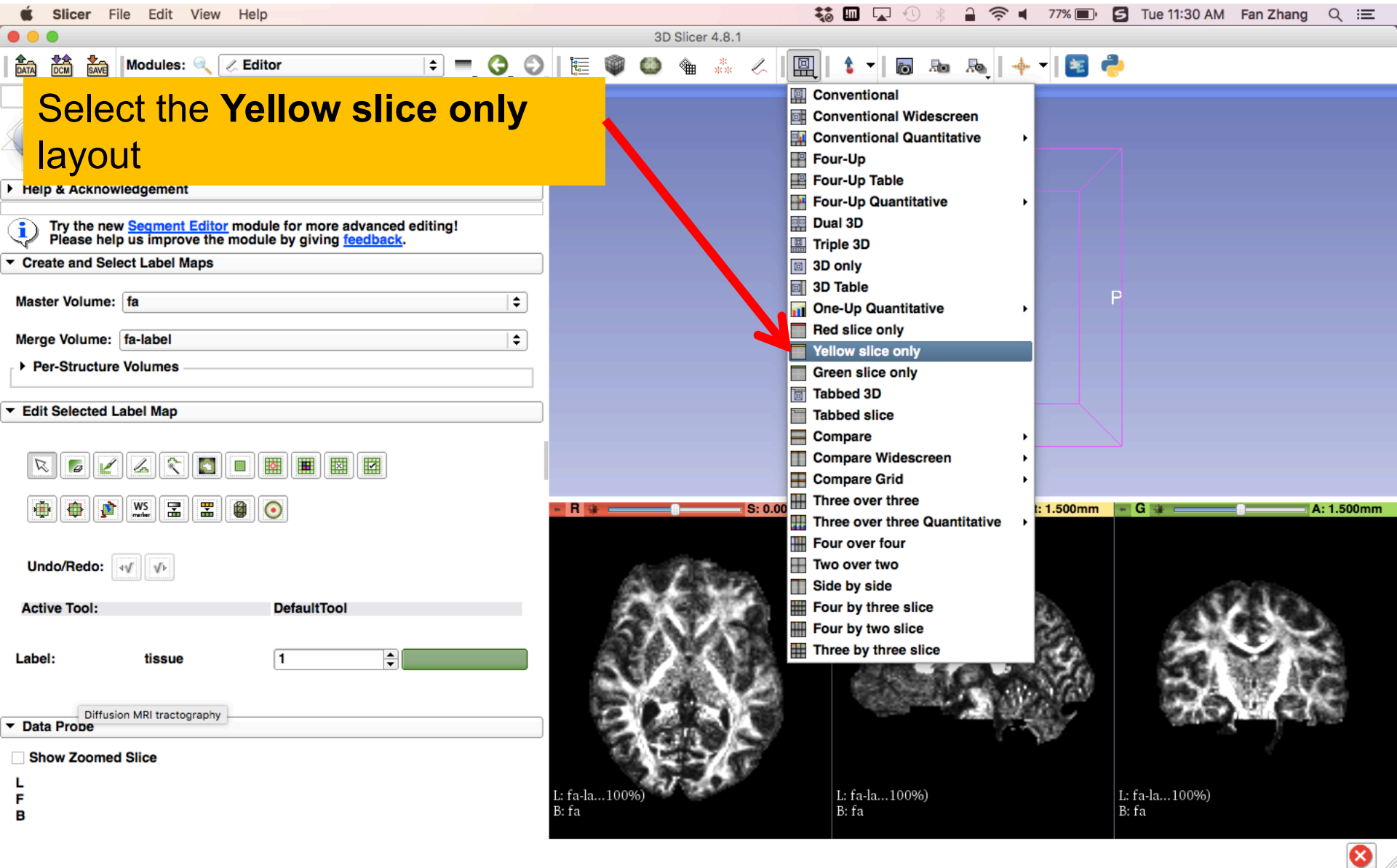
Diffusion MRI tractography



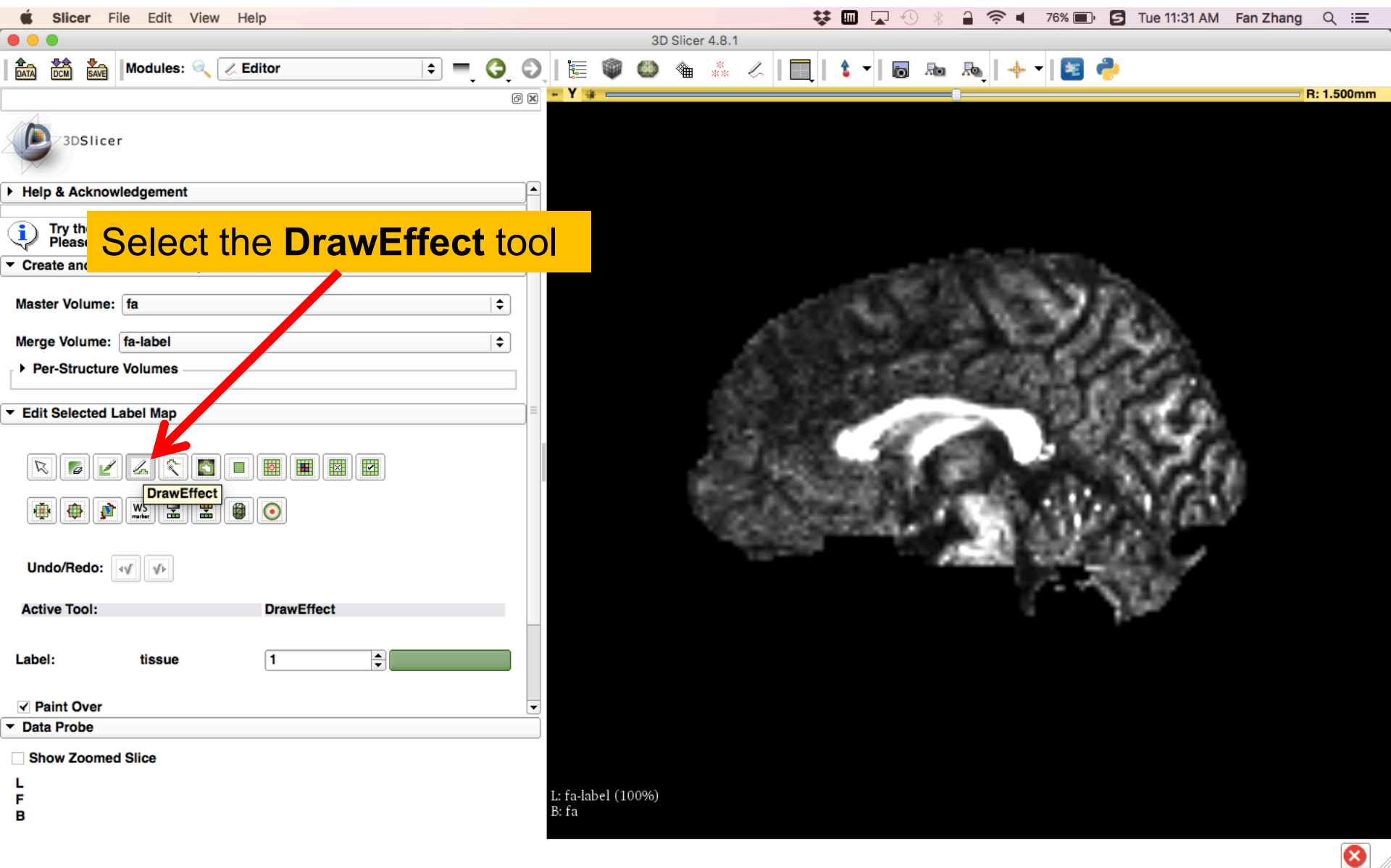
Diffusion MRI tractography



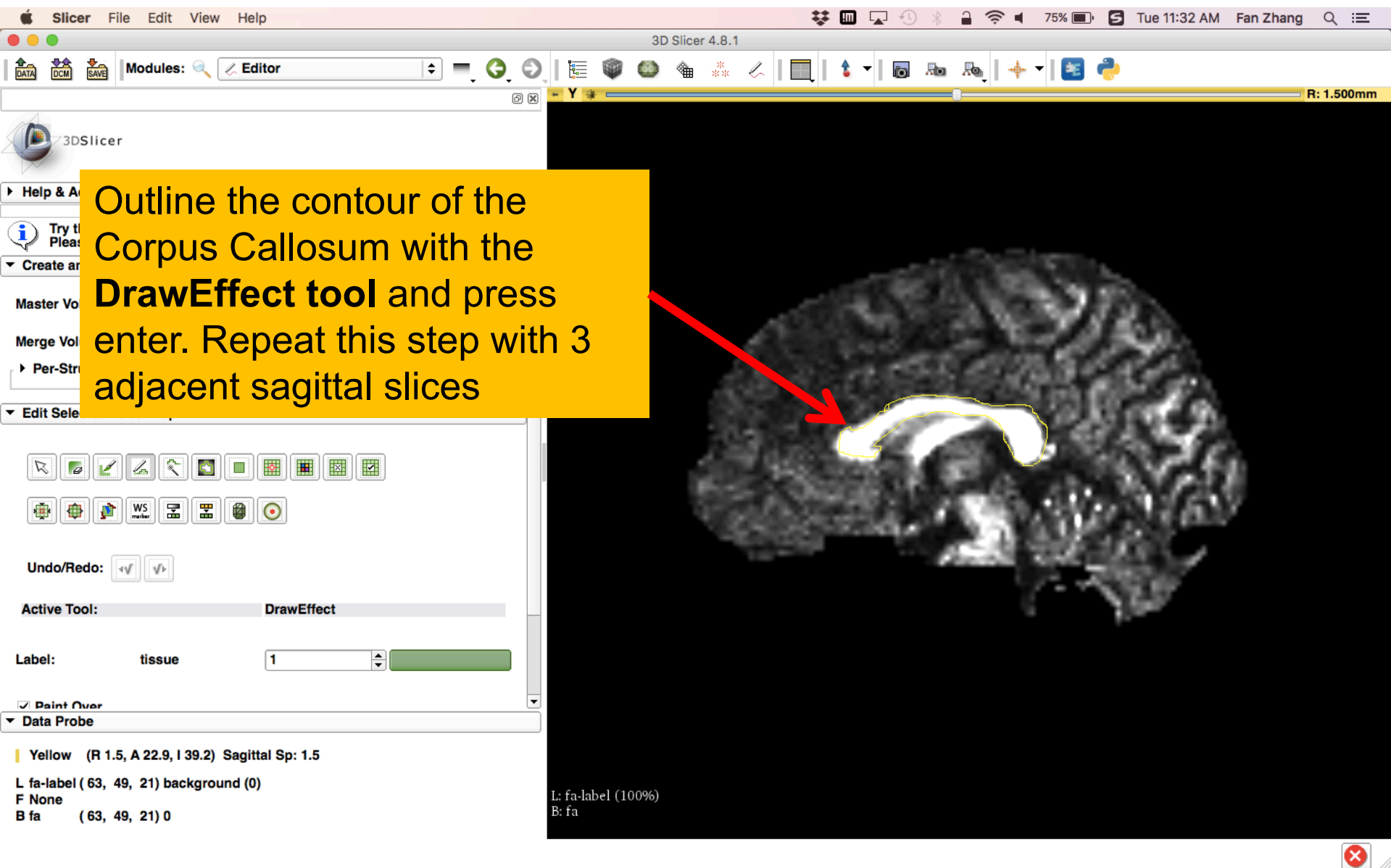
Diffusion MRI tractography



Diffusion MRI tractography



Diffusion MRI tractography



Outline the contour of the Corpus Callosum with the **DrawEffect** tool and press enter. Repeat this step with 3 adjacent sagittal slices

Active Tool: DrawEffect

Label: tissue 1

Yellow (R 1.5, A 22.9, I 39.2) Sagittal Sp: 1.5

L: fa-label (63, 49, 21) background (0)

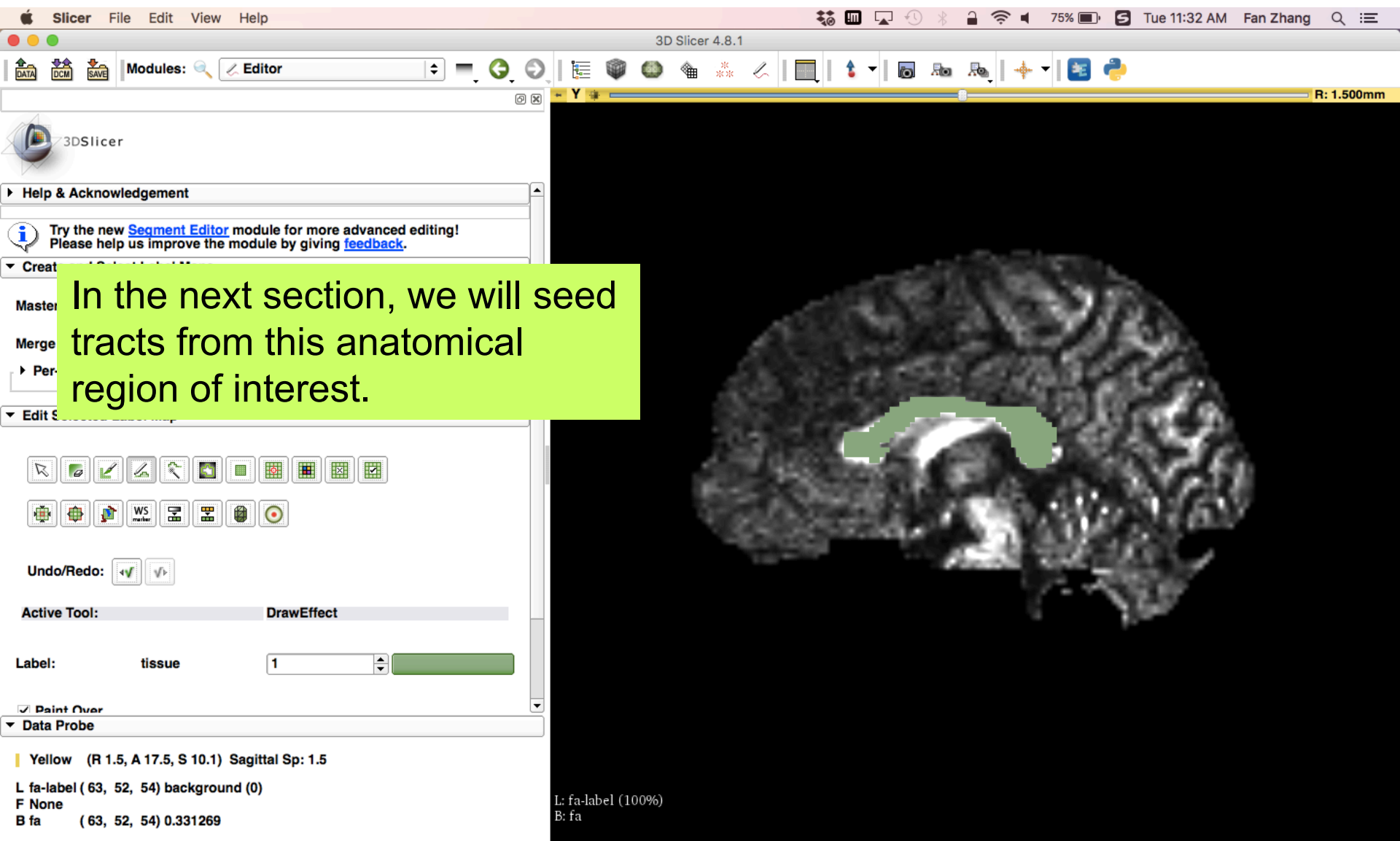
F None

B fa (63, 49, 21) 0

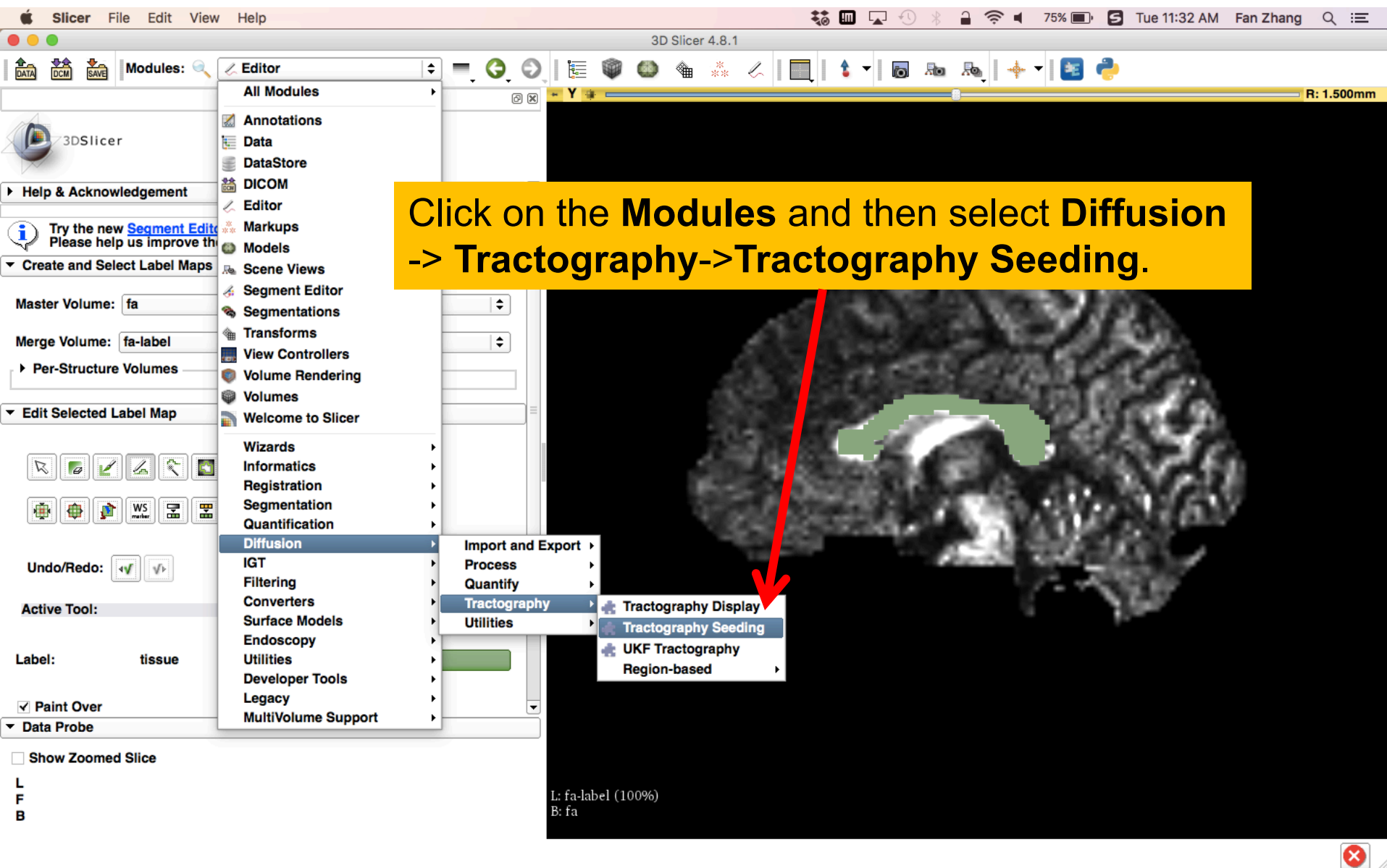
L: fa-label (100%)

B: fa

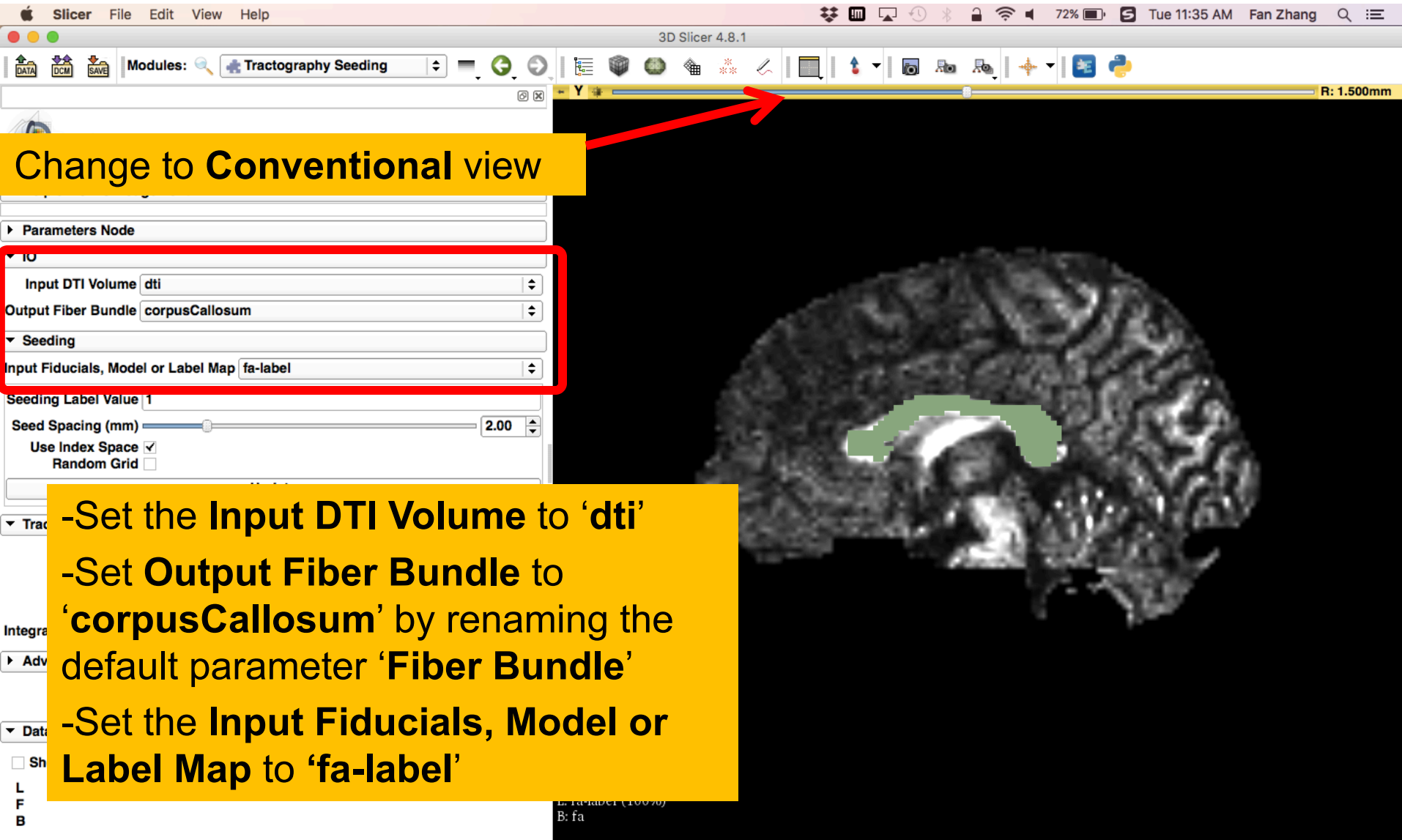
Diffusion MRI tractography



Diffusion MRI tractography



Step1: I/O



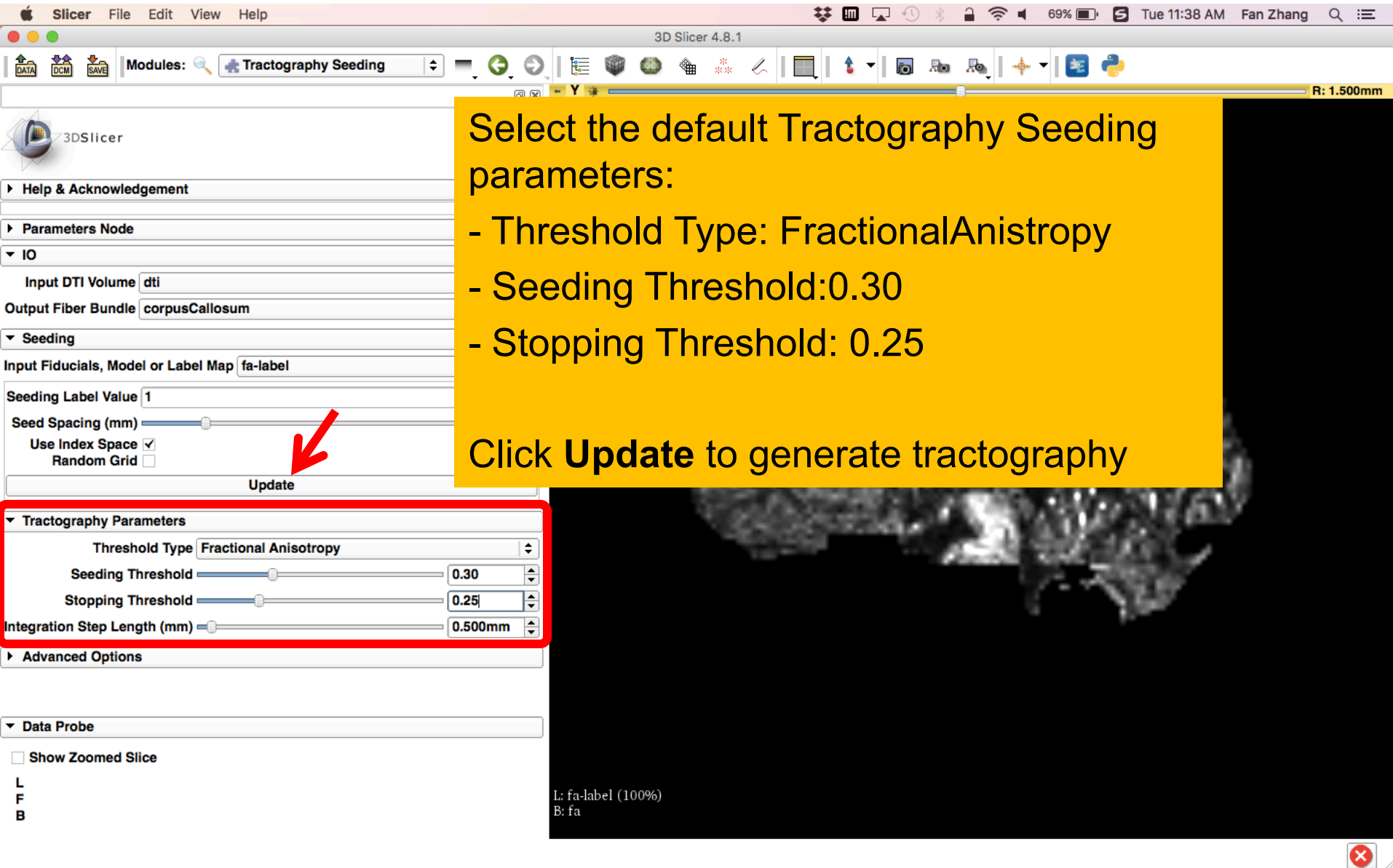
Change to **Conventional** view

Parameters Node

- Input DTI Volume: **dti**
- Output Fiber Bundle: **corpusCallosum**
- Seeding
 - Input Fiducials, Model or Label Map: **fa-label**
 - Seeding Label Value: 1
 - Seed Spacing (mm): 2.00
 - Use Index Space: ☒
 - Random Grid: ☐

- 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



3D Slicer 4.8.1

Modules: Tractography Seeding

Input DTI Volume: dti

Output Fiber Bundle: corpusCallosum

Seeding

Input Fiducials, Model or Label Map: fa-label

Seeding Label Value: 1

Seed Spacing (mm): [Slider]

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: fa-label (100%)
B: fa

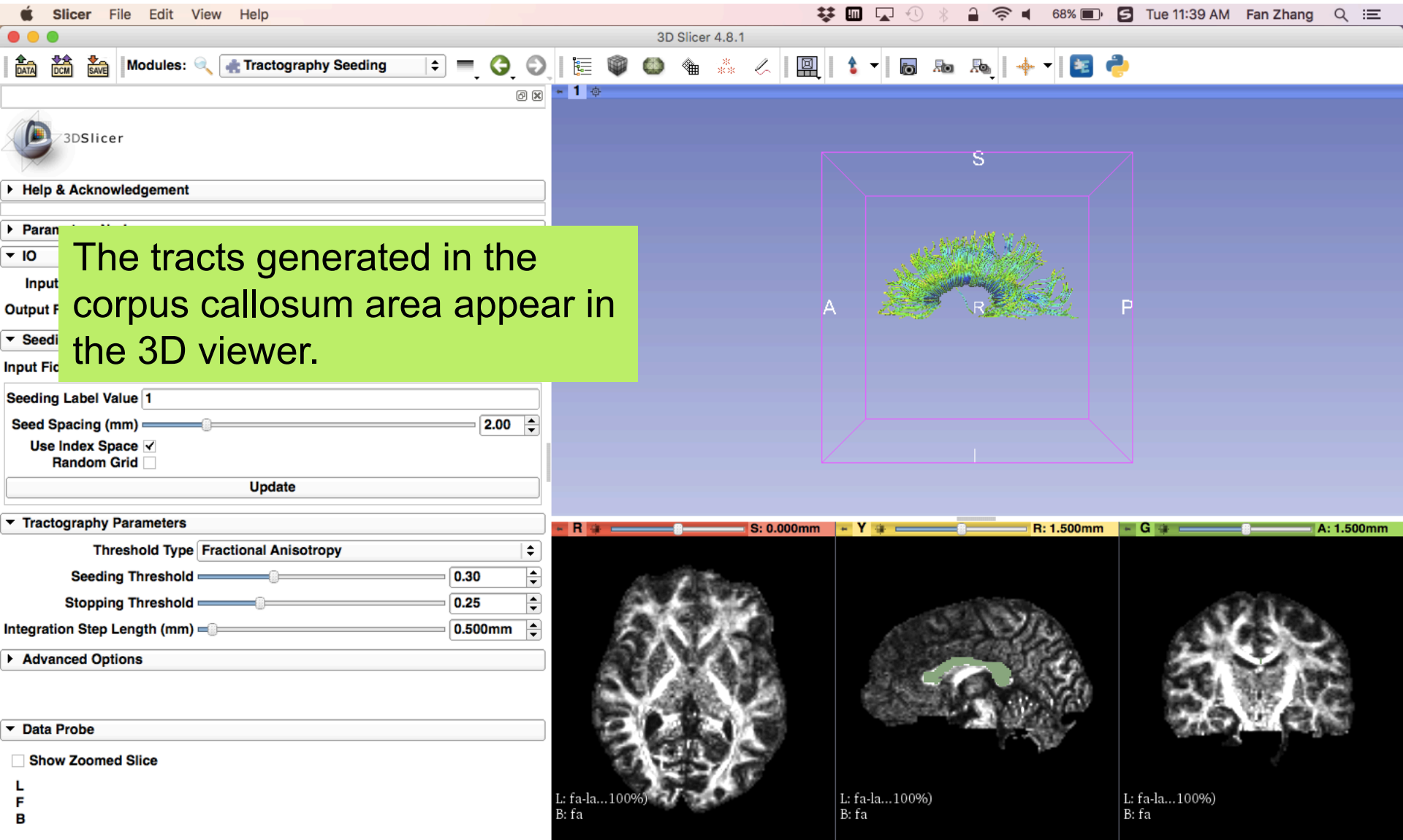
R: 1.500mm

Select the default Tractography Seeding parameters:

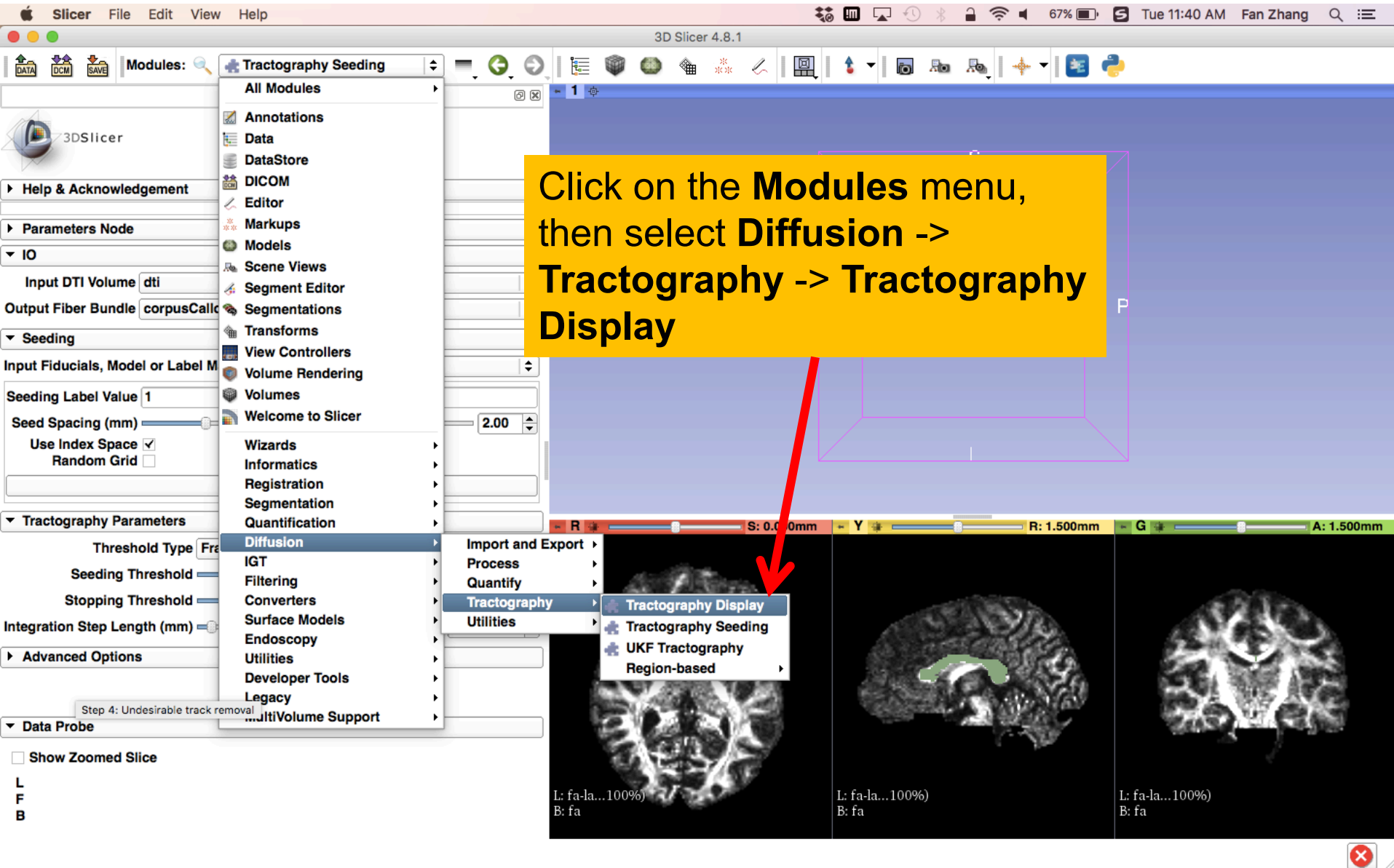
- Threshold Type: FractionalAnisotropy
- Seeding Threshold: 0.30
- Stopping Threshold: 0.25

Click **Update** to generate tractography

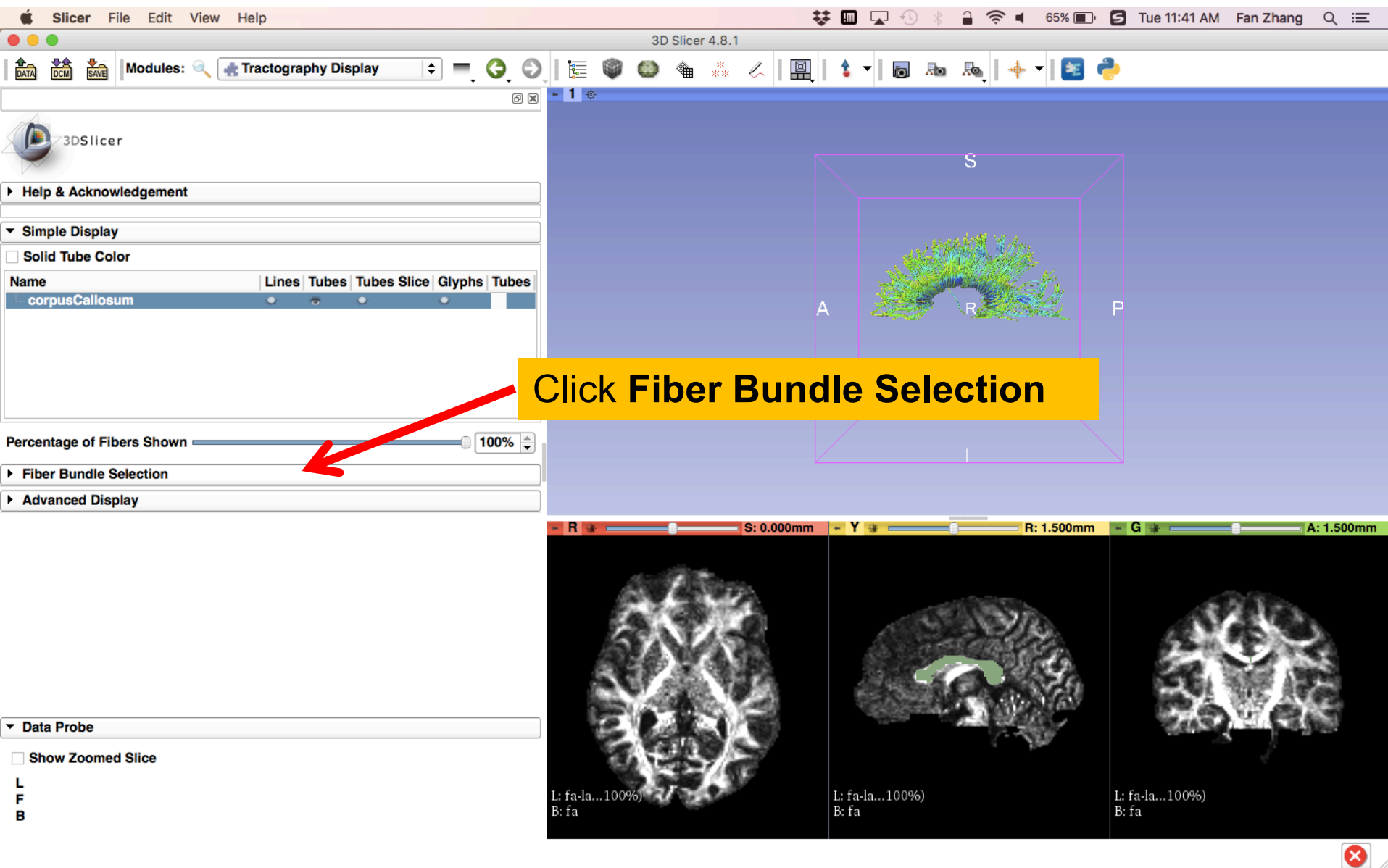
Step 3: Generate Tracts



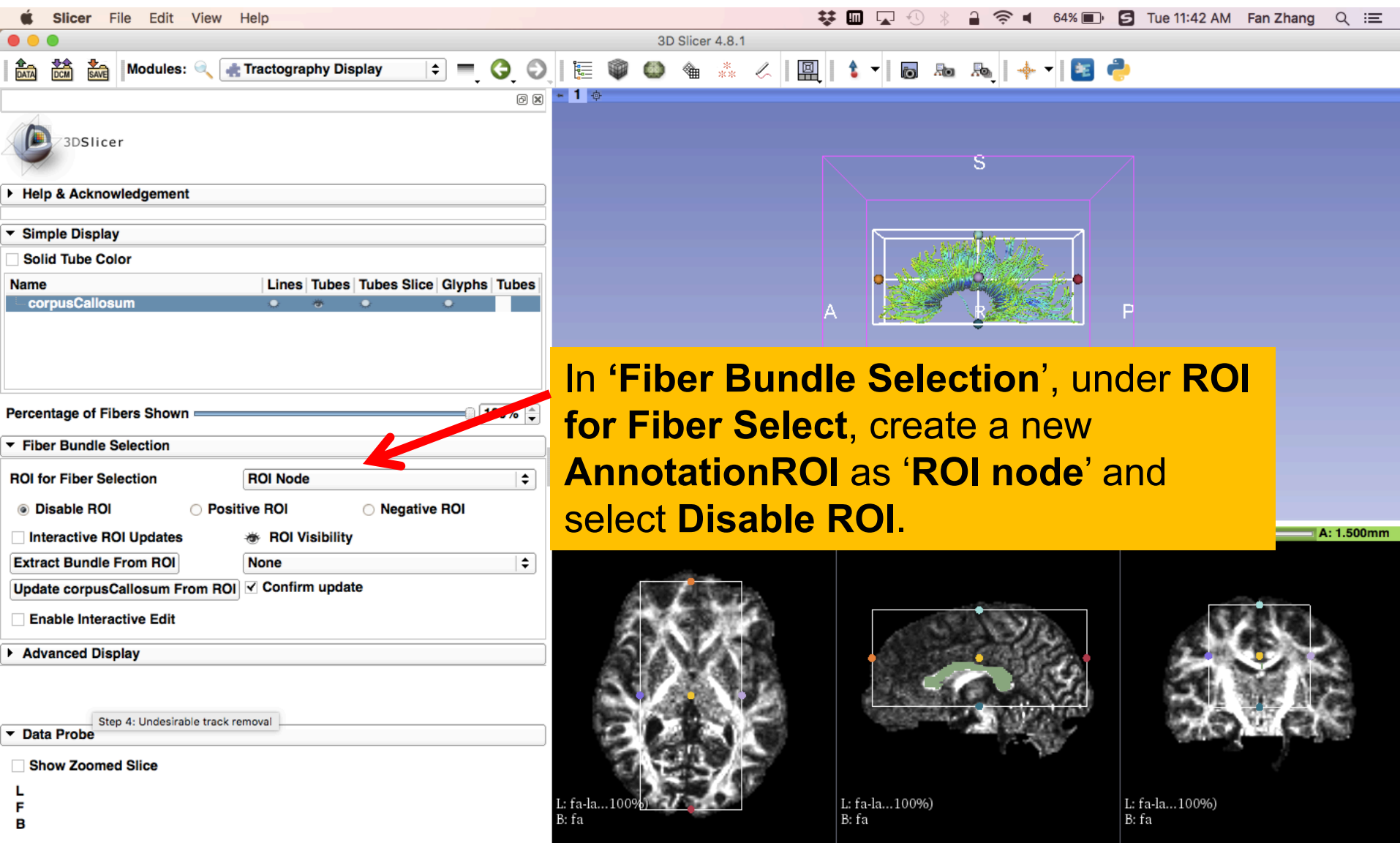
Step 4: Undesirable track removal



Step 4: Undesirable track removal



Step 4: Undesirable track removal



3D Slicer 4.8.1

Modules: **Tractography Display**

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

Data Probe

☐ 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

L: fa-la...100%)
B: fa

L: fa-la...100%)
B: fa

L: fa-la...100%)
B: fa

Step 4: Undesirable track removal

Adjust the ROI frame to include the undesirable tracks, using the colorful spheres provided.

The screenshot displays the 3D Slicer 4.8.1 interface. The main 3D view shows a bundle of fiber tracts in green and blue. A white wireframe box (ROI) is positioned around a section of these tracts, with a red arrow pointing to it. Inside the box are several small, colorful spheres (purple, orange, green, red, blue) used for selecting specific fibers. The left sidebar contains the 'Modules' panel with 'Tractography Display' selected, and the 'Fiber Bundle Selection' panel with 'ROI for Fiber Selection' set to 'ROI Node'. The 'Percentage of Fibers Shown' is set to 100%. The bottom panel shows three orthogonal views (axial, sagittal, and coronal) of the brain data, with the ROI box visible in each. The status bar at the bottom indicates the current slice position: S: 0.000mm, R: 1.500mm, A: 1.500mm.

Step 4: Undesirable track removal

The screenshot displays the 3D Slicer 4.8.1 interface. The main 3D view shows a bundle of fiber tracts in green and blue, with a white wireframe box highlighting a specific region. A red arrow points from the 'Negative ROI' option in the 'Fiber Bundle Selection' panel to this box. Another red arrow points from a yellow text box to the 'Negative ROI' option. The 'Fiber Bundle Selection' panel includes options for 'ROI for Fiber Selection' (set to 'ROI Node'), 'Disable ROI', 'Positive ROI', and 'Negative ROI' (selected). It also has checkboxes for 'Interactive ROI Updates', 'ROI Visibility', and 'Enable Interactive Edit'. The 'Advanced Display' panel is visible below. The 'Data Probe' panel shows 'Show Zoomed Slice' and a status bar indicating 'Step 4: Undesirable track removal'. The bottom of the interface features three orthogonal views (axial, sagittal, and coronal) of the brain data, each with a red box indicating the current slice position. The status bar at the bottom right shows 'L: fa-la...100%) B: fa'.

Click on **Negative ROI** to finish

3DSlicer

Help & Acknowledgement

Simple Display

☐ Solid Tube Color

Name: corpusCallosum

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

Data Probe

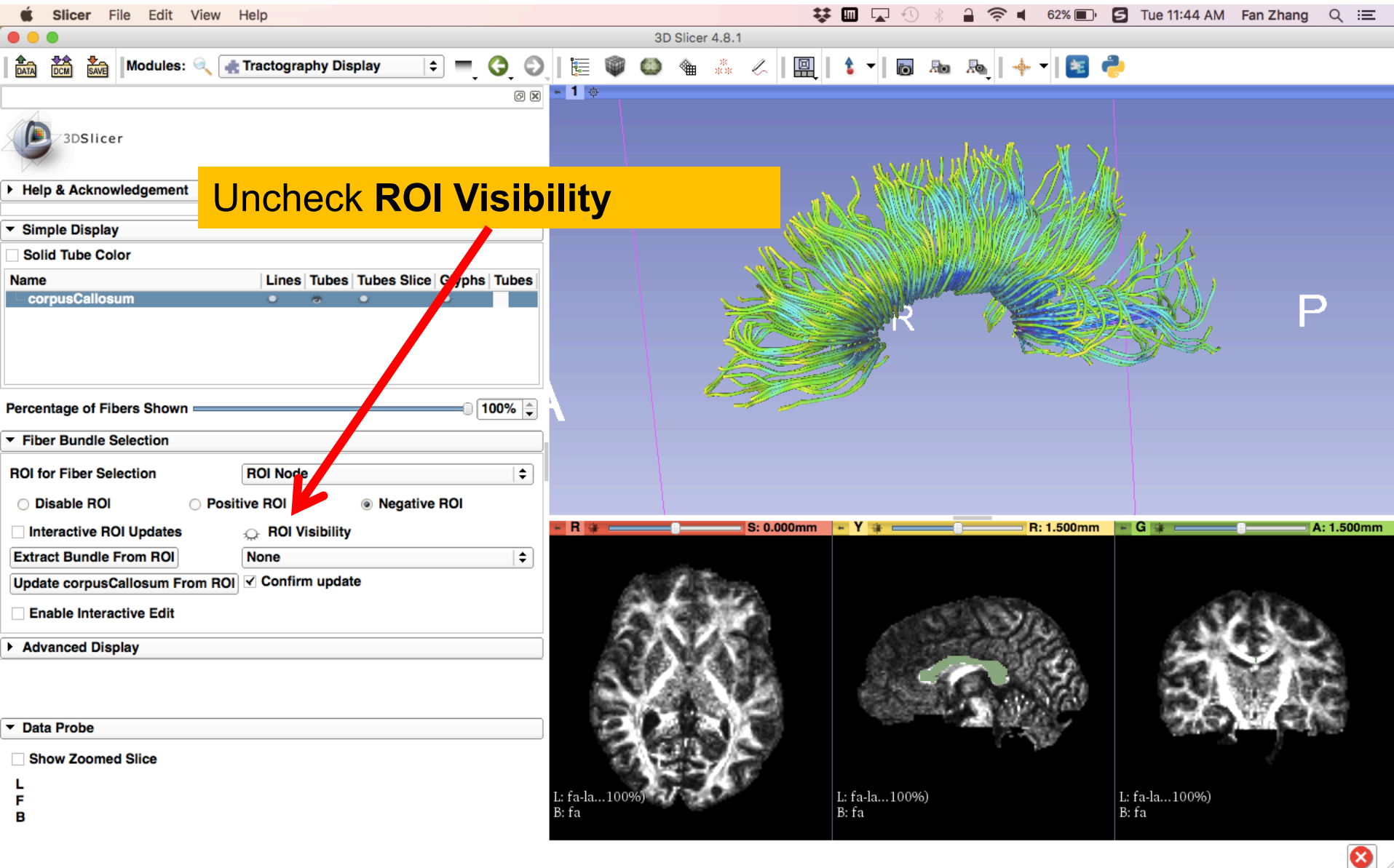
☐ Show Zoomed Slice

L: fa-la...100%) B: fa

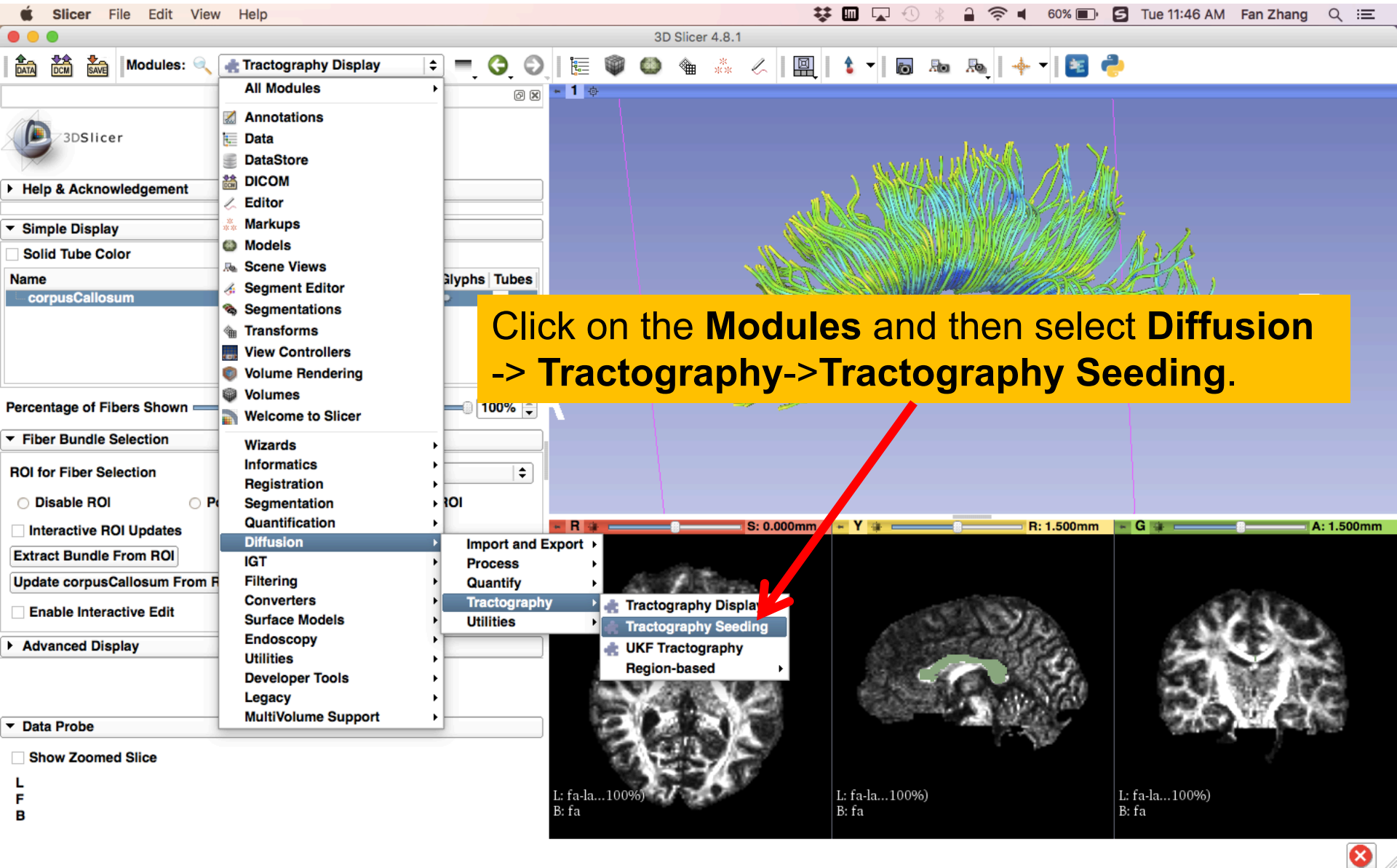
L: fa-la...100%) B: fa

L: fa-la...100%) B: fa

Step 4: Undesirable track removal

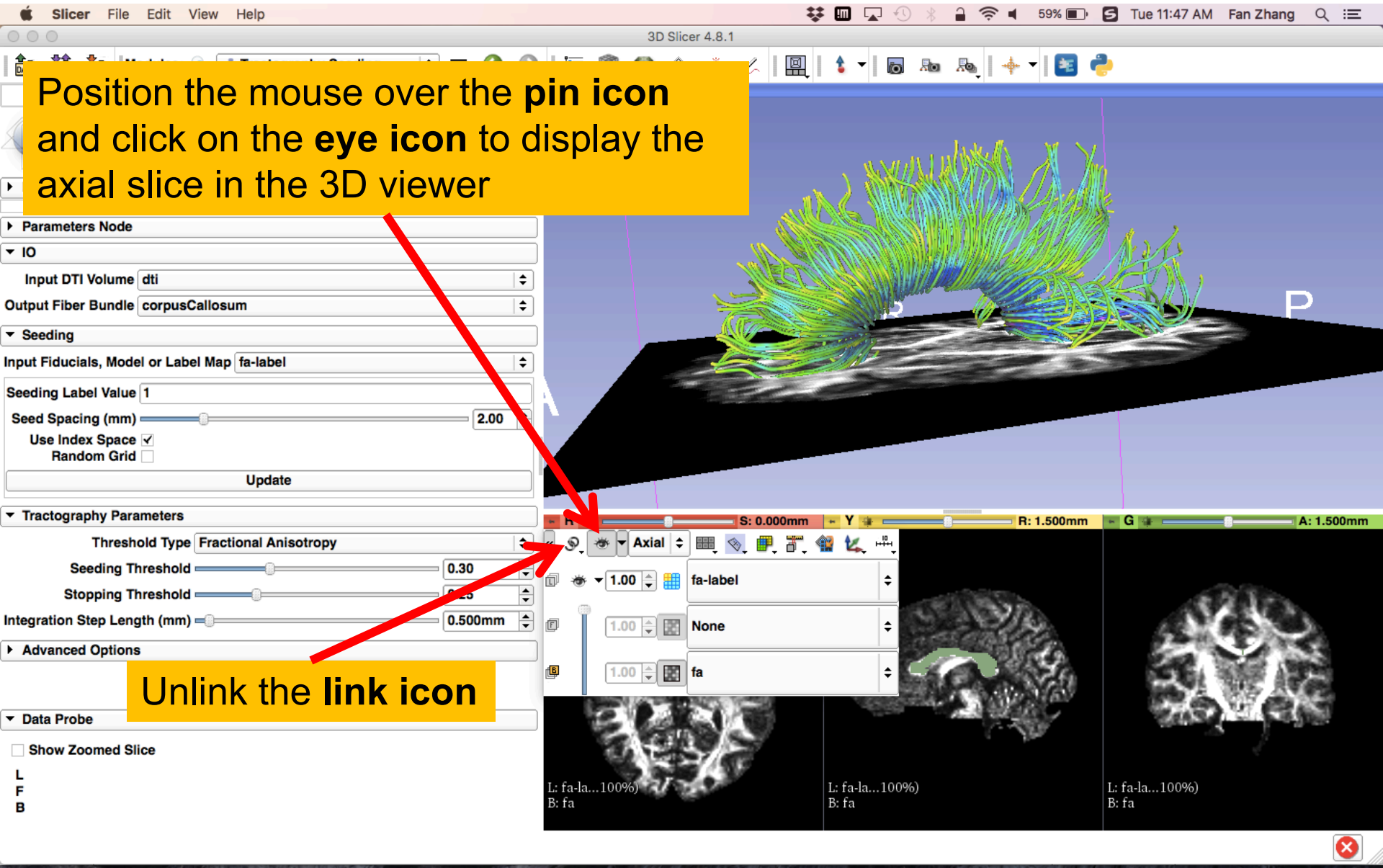


Fiducial Seeding



Fiducial Seeding

Position the mouse over the **pin icon** and click on the **eye icon** to display the axial slice in the 3D viewer



Unlink the **link icon**

Fiducial Seeding

Slicer File Edit View Help 58% Tue 11:48 AM Fan Zhang

Modules: Tractography Seeding

3DSlicer

Help & Acknowledgement

Parameters Node

IO

Input DTI Volume dti

Output Fiber Bundle corpusCallo

Seeding

Input Fiducials, Model or Label M

Seeding Label Value 1

Seed Spacing (mm) 2.00

Use Index Space ☒

Random Grid ☐

Fiducial Seeding

Tractography Parameters

Threshold Type Fra

Seeding Threshold

Stopping Threshold

Integration Step Length (mm)

Advanced Options

Data Probe

Show Zoomed Slice

L
F
B

All Modules

Annotations

Data

DataStore

DICOM

Editor

Markups

Models

Scene Views

Segment Editor

Segmentations

Transforms

View Controllers

Volume Rendering

Volumes

Welcome to Slicer

Wizards

Informatics

Registration

Segmentation

Quantification

Diffusion

IGT

Filtering

Converters

Surface Models

Endoscopy

Utilities

Developer Tools

Legacy

MultiVolume Support

Select the module **Markups**

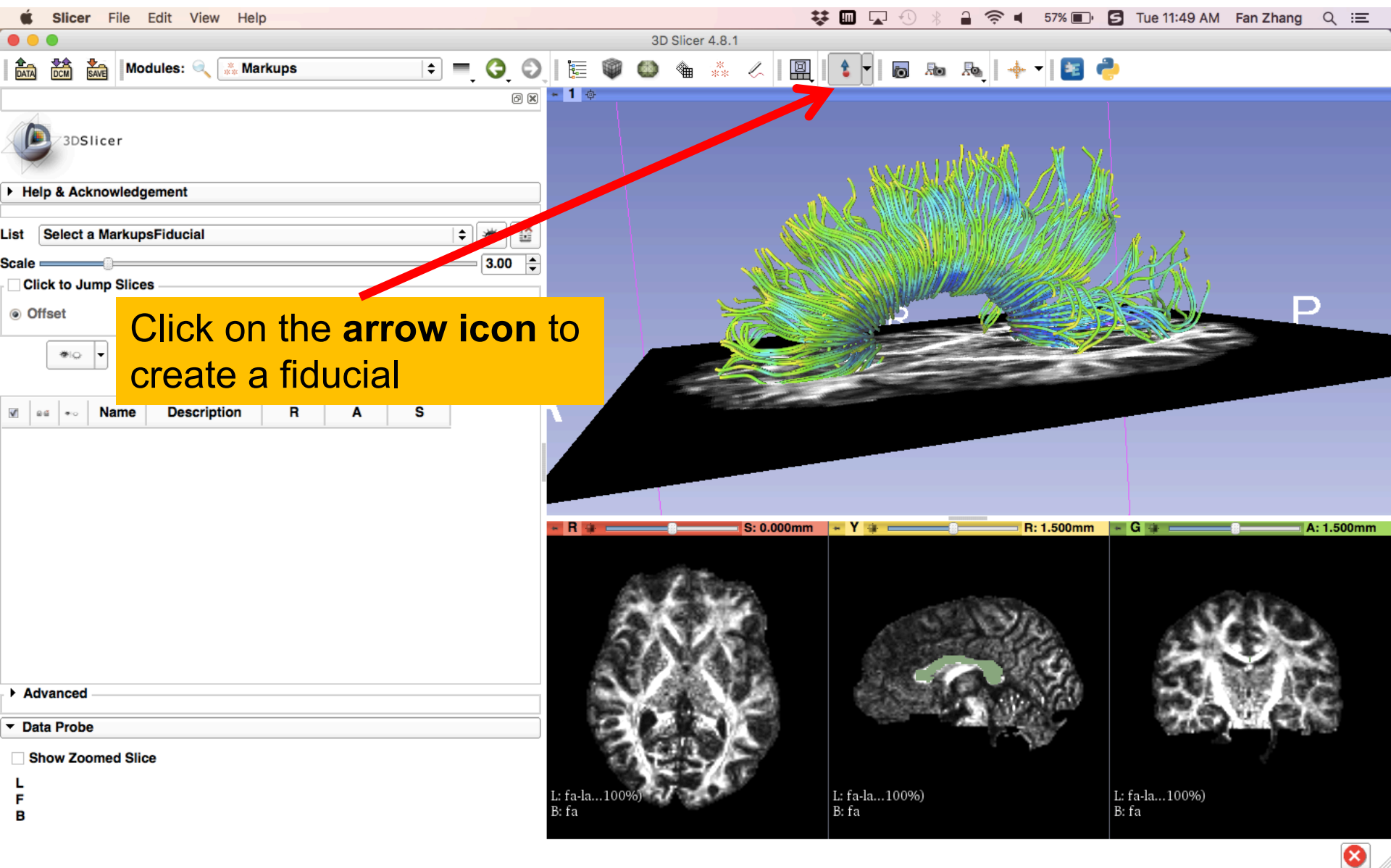
3D View: Fiber bundle visualization (green/yellow lines) on a brain slice (black/white).

2D Views: Axial, Sagittal, and Coronal slices showing the fiber bundle (green/yellow lines) overlaid on the brain slice (black/white).

Navigation: R (Right), S (Superior), Y (Inferior), R (Right), G (Growth), A (Anterior).

Labels: L: fa-la...100%, B: fa

Fiducial Seeding



Fiducial Seeding

3D Slicer 4.8.1

Modules: Markups

Position the fiducial in the left cingulum of the coronal slice

Transformed Hide RAS

	Name	Description	R	A	S
1	F-1		10.317	1.500	25.642

Advanced

Data Probe

Red (R 6.4, A 67.4, S 0.0) Axial Sp: 1.5

L fa-label (60, 19, 47) background (0)

F None

B fa (60, 19, 47) 0.109656

R: 15.000mm Y: 1.500mm G: 1.500mm

L: fa-la...100%) B: fa

L: fa-la...100%) B: fa

L: fa-la...100%) B: fa

Fiducial Seeding

3D Slicer 4.8.1

Modules: Markups

Scale: 3.00

Click to Jump Slices

Offset Centered Show Slice Intersections

Transformed Hide RAS

	Name	Description	R	A	S
1	LeftCingulum		10.317	1.500	25.642

Advanced

Data Probe

Show Zoomed Slice

L F B

P

LeftCingulum

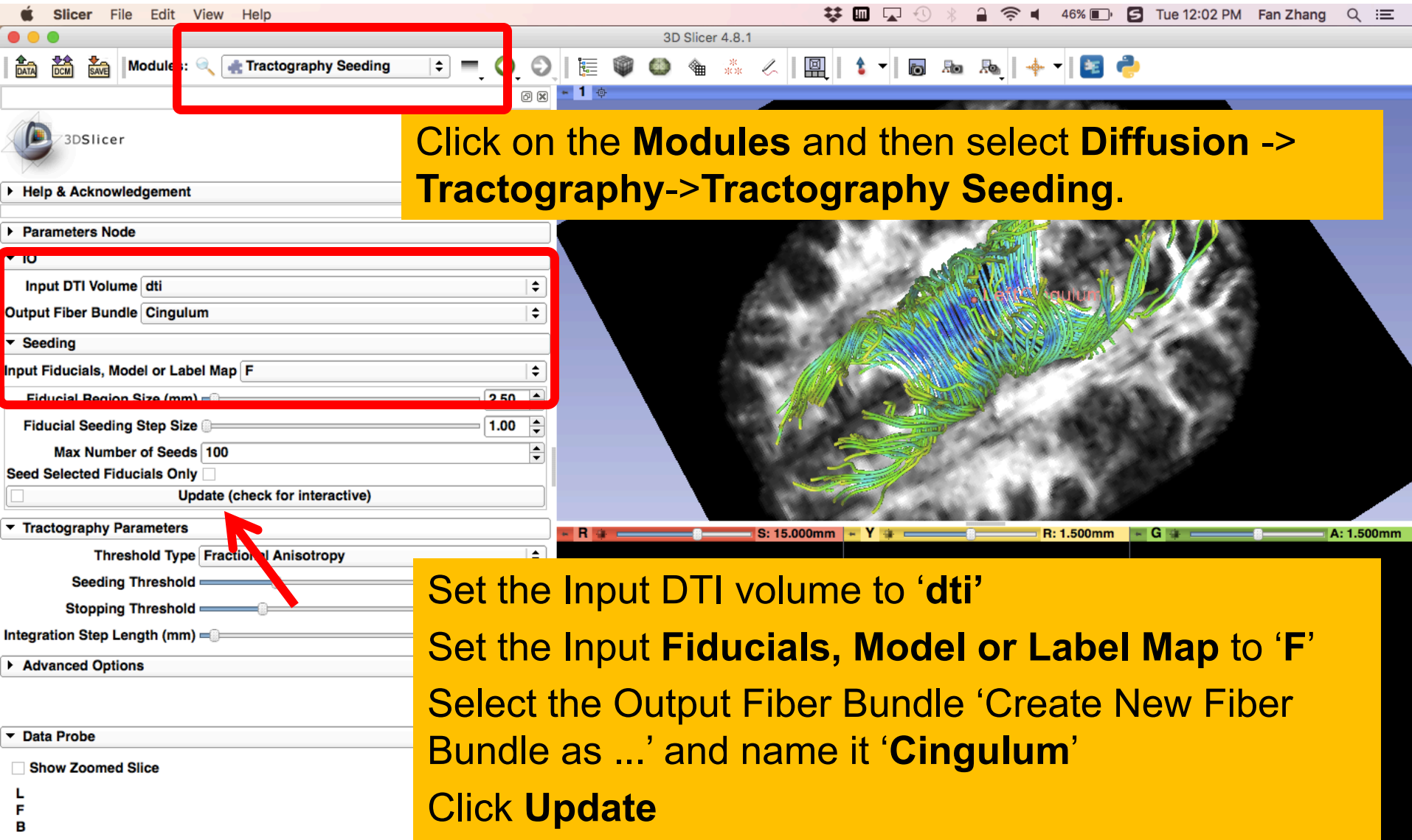
R: 15.000mm Y: 15.000mm R: 15.000mm G: 15.000mm A: 1.500mm

L: fa-la...100%) B: fa

L: fa-la...100%) B: fa

L: fa-la...100%) B: fa

Fiducial Seeding

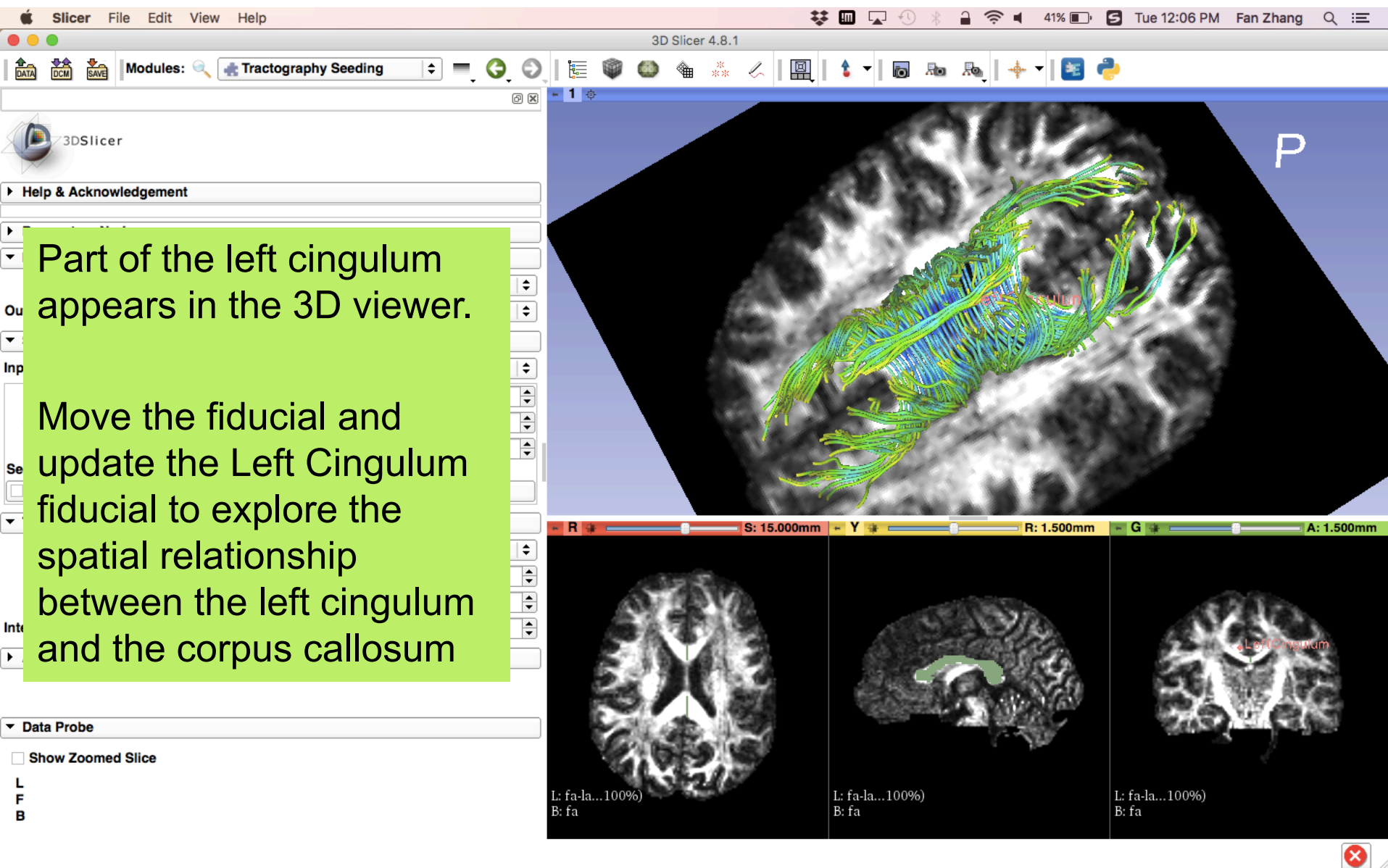


The screenshot shows the 3D Slicer 4.8.1 interface. The 'Modules' panel on the left has 'Tractography Seeding' selected and highlighted with a red box. The 'Parameters Node' on the left has the 'IO' section expanded and highlighted with a red box. Within this section, 'Input DTI Volume' is set to 'dti', 'Output Fiber Bundle' is set to 'Cingulum', and 'Input Fiducials, Model or Label Map' is set to 'F'. The 'Seeding' section is also expanded, showing 'Fiducial Region Size (mm)' set to 2.50, 'Fiducial Seeding Step Size' set to 1.00, 'Max Number of Seeds' set to 100, and 'Seed Selected Fiducials Only' unchecked. The 'Tractography Parameters' section is expanded, showing 'Threshold Type' set to 'Fractional Anisotropy', 'Seeding Threshold' set to 0.5, 'Stopping Threshold' set to 0.2, and 'Integration Step Length (mm)' set to 0.5. A red arrow points to the 'Update (check for interactive)' button. The main 3D view on the right shows a brain slice with green and blue fiber bundles. The bottom status bar shows 'R: 15.000mm', 'Y: 1.500mm', 'G: 1.500mm', and 'A: 1.500mm'.

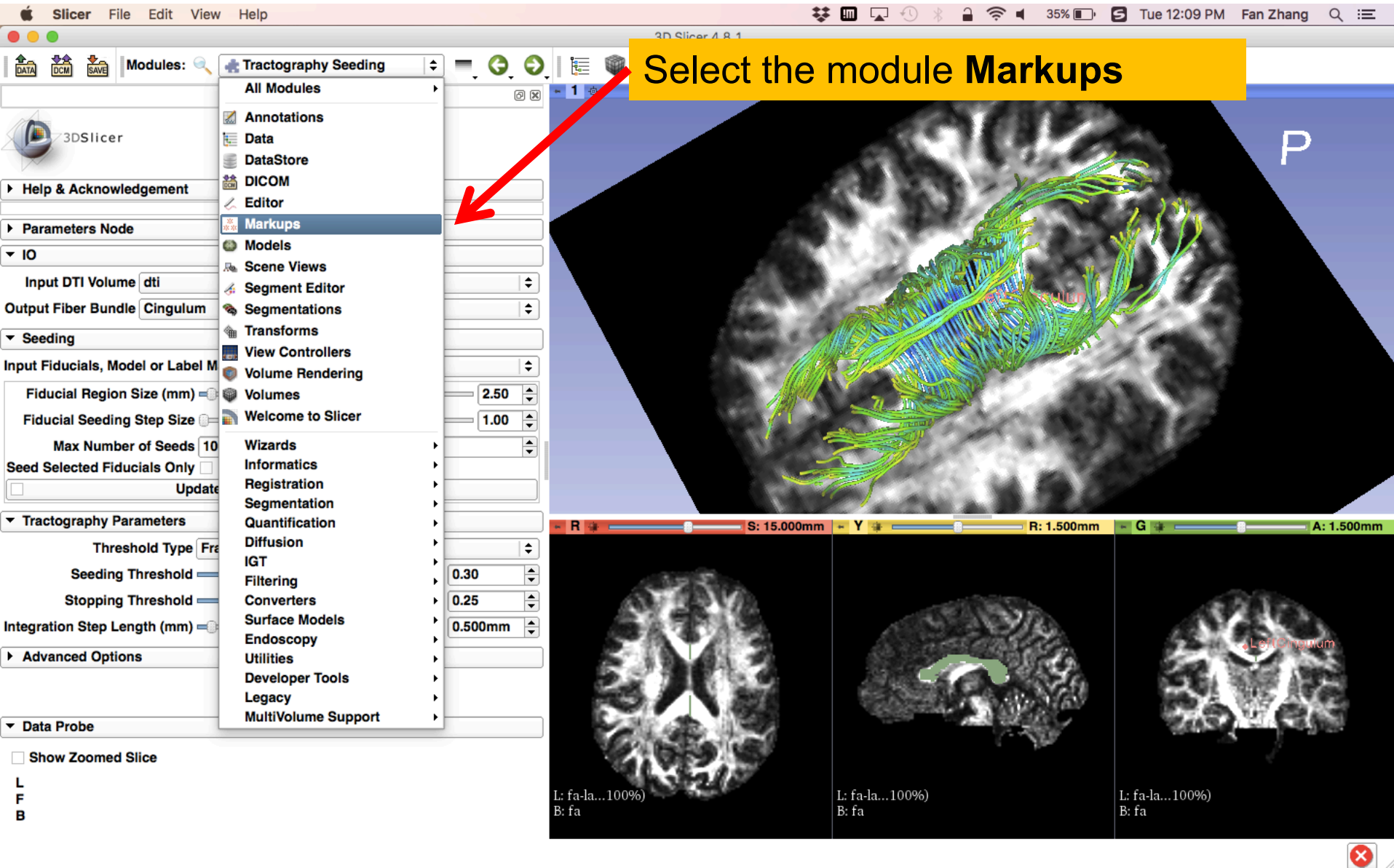
Click on the **Modules** and then select **Diffusion -> Tractography->Tractography Seeding**.

Set the Input DTI volume to 'dti'
Set the Input **Fiducials, Model or Label Map** to 'F'
Select the Output Fiber Bundle 'Create New Fiber Bundle as ...' and name it '**Cingulum**'
Click **Update**

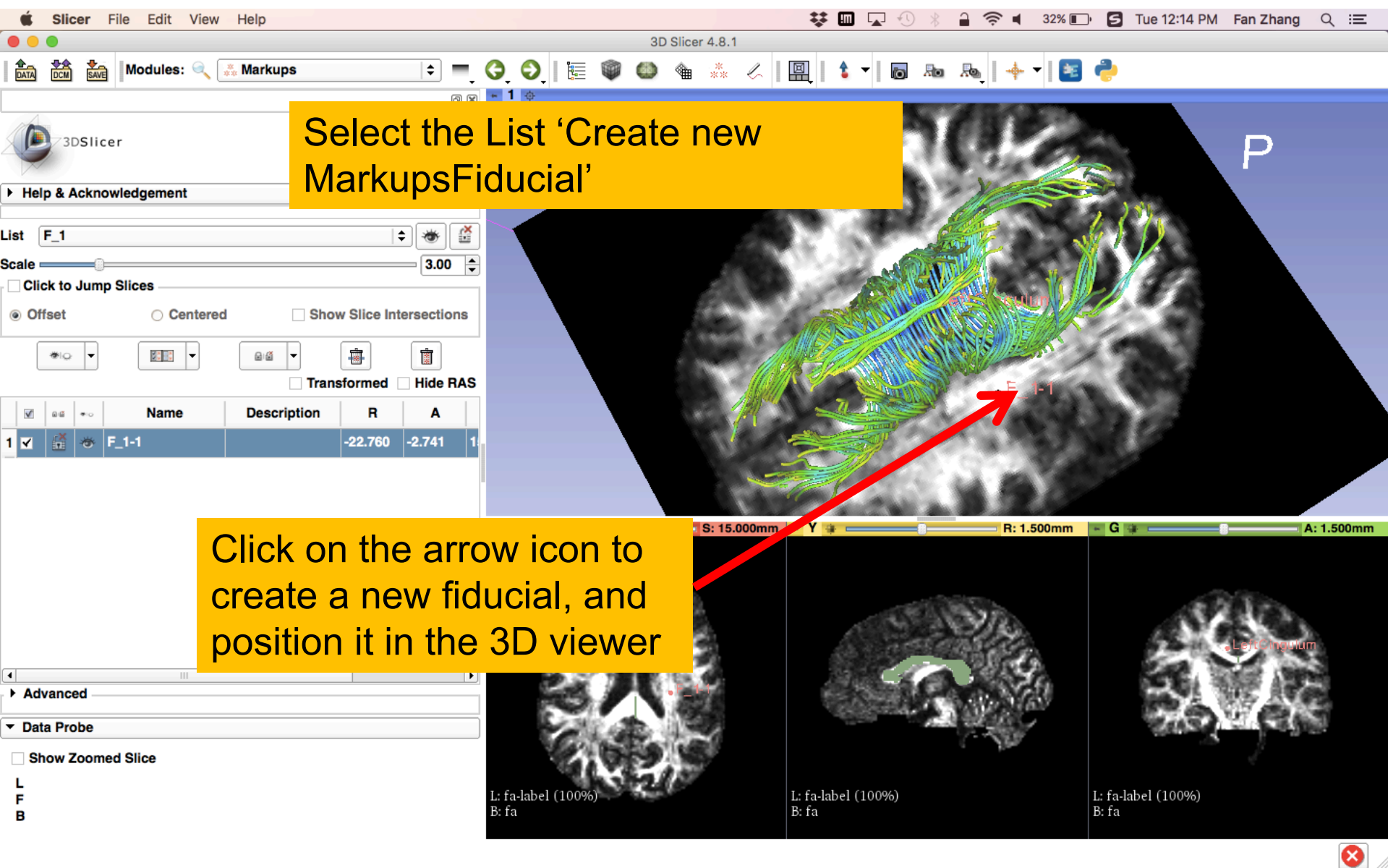
Fiducial Seeding



Tractography 'on-the-fly'



Tractography 'on-the-fly'



The screenshot displays the 3D Slicer 4.8.1 interface. The main 3D view shows a brain with green and blue fiber-like tractography results. A red arrow points from a text box to a red dot labeled 'F_1-1' in the 3D view. The left sidebar contains a 'Markups' panel with a list of markups. A yellow box highlights the text 'Select the List 'Create new MarkupsFiducial'' pointing to the 'F_1-1' entry. Another yellow box highlights the text 'Click on the arrow icon to create a new fiducial, and position it in the 3D viewer' pointing to the arrow icon in the 'F_1-1' row. The bottom of the interface shows three orthogonal views (axial, sagittal, and coronal) of the brain, each with a red dot labeled 'F_1-1'.

Select the List 'Create new MarkupsFiducial'

Click on the arrow icon to create a new fiducial, and position it in the 3D viewer

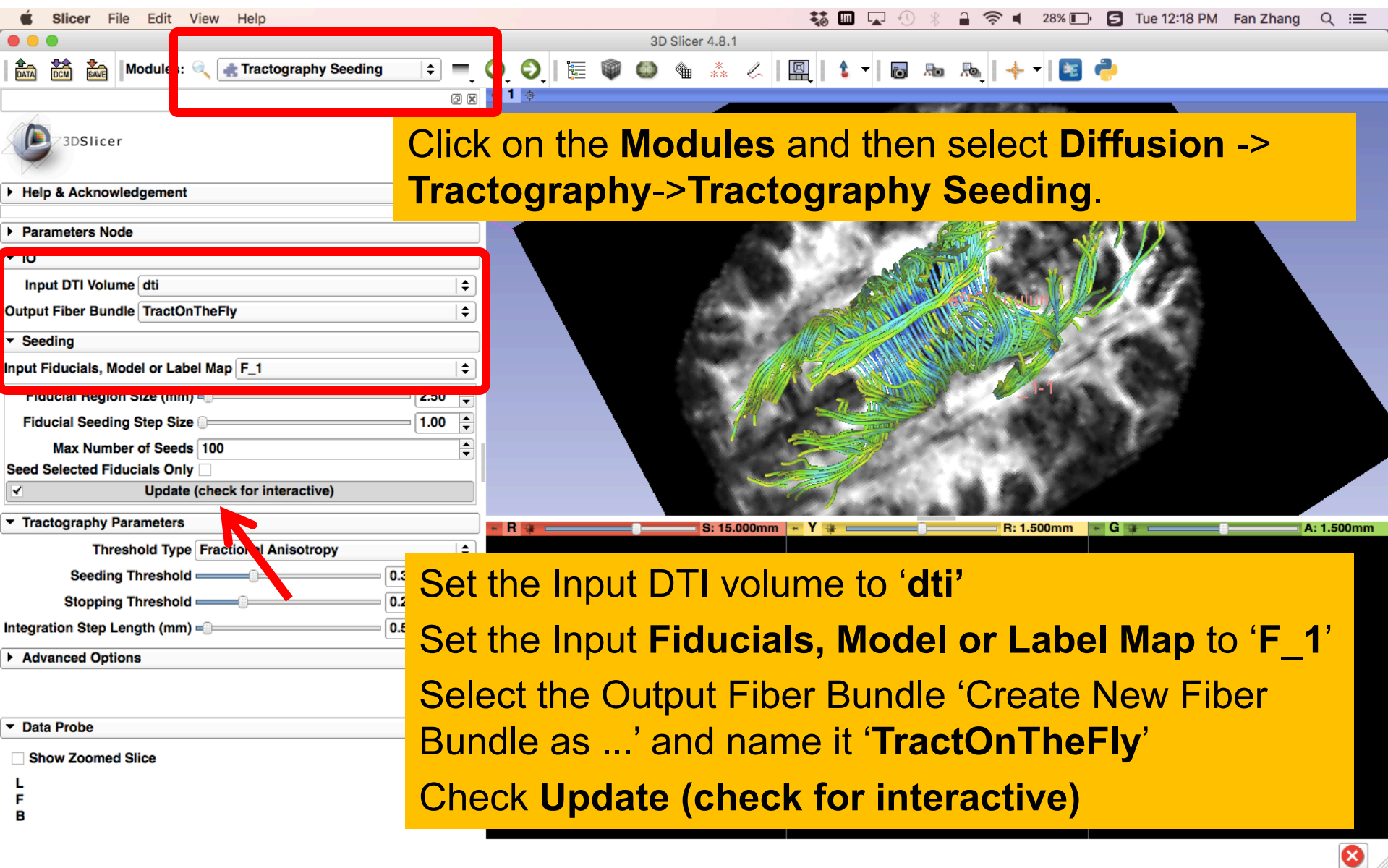
	Name	Description	R	A
1	F_1-1		-22.760	-2.741

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

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

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

Tractography 'on-the-fly'

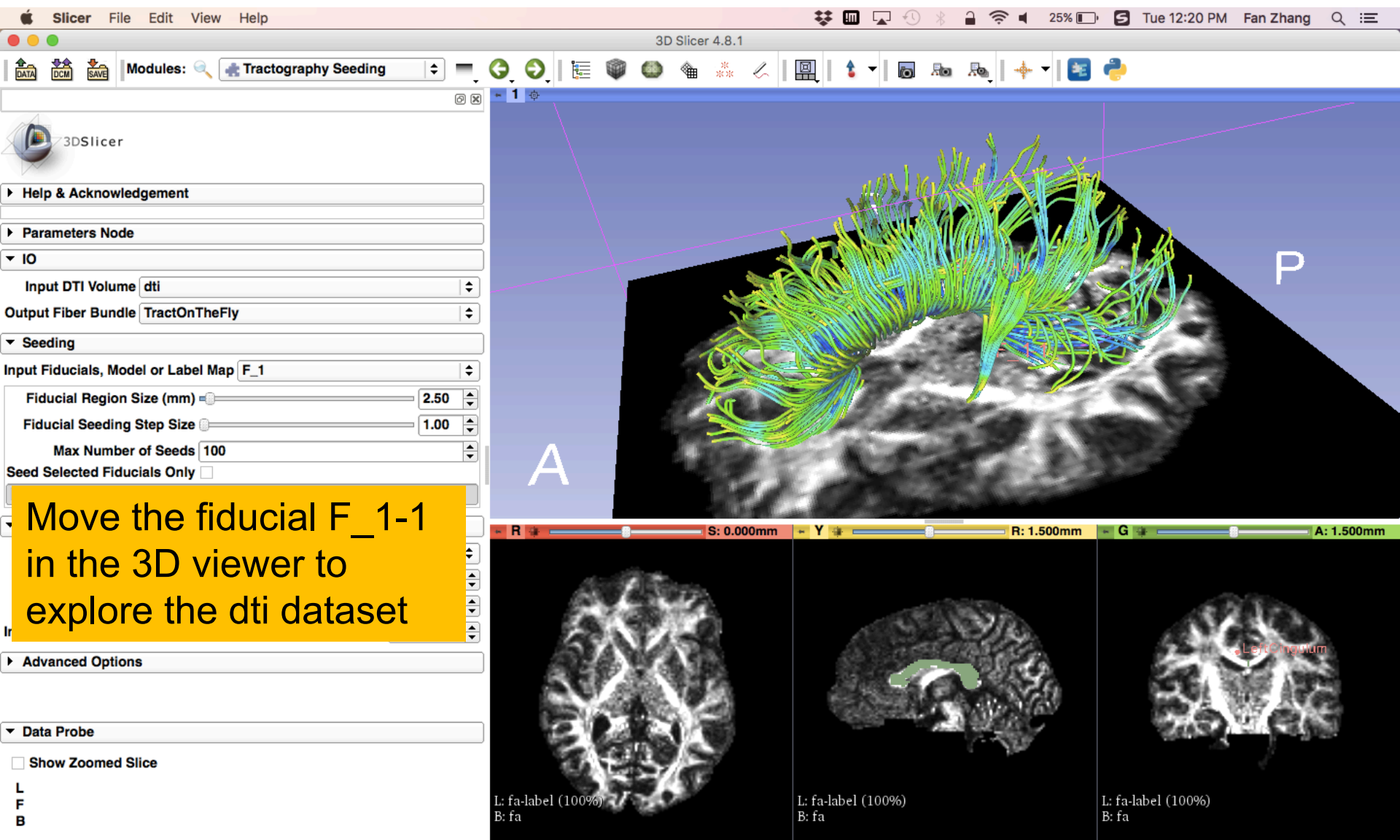


The screenshot shows the 3D Slicer 4.8.1 interface. The 'Modules' dropdown menu is highlighted with a red box, showing 'Tractography Seeding' selected. The 'Parameters Node' on the left is also highlighted with a red box, showing the 'Tractography Seeding' module's parameters. A red arrow points to the 'Fractional Anisotropy' threshold type. The main 3D view shows a brain slice with green and blue fiber bundles. The status bar at the bottom shows 'R: 15.000mm', 'Y: 1.500mm', 'G: 1.500mm', and 'A: 1.500mm'.

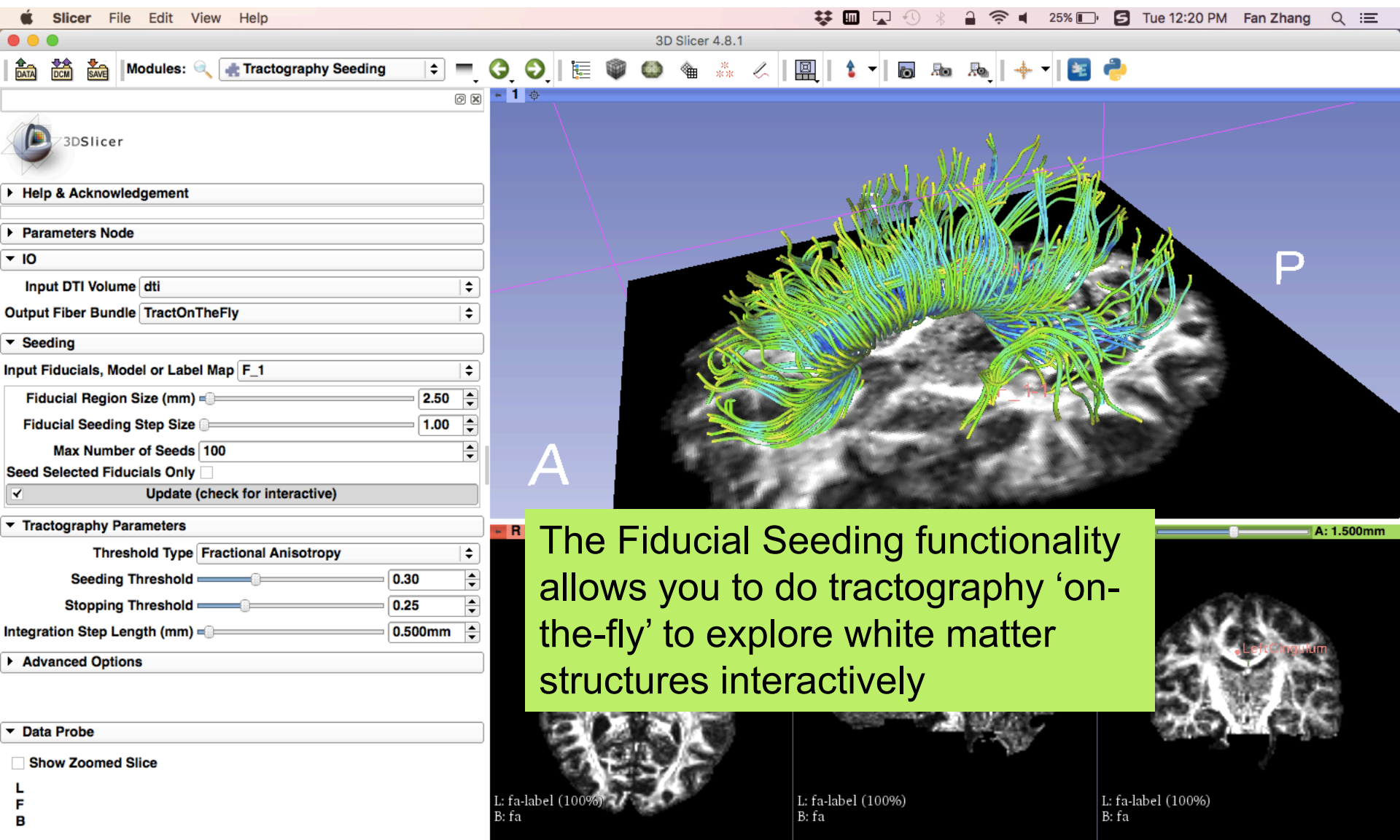
Click on the **Modules** and then select **Diffusion -> Tractography->Tractography Seeding**.

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)**

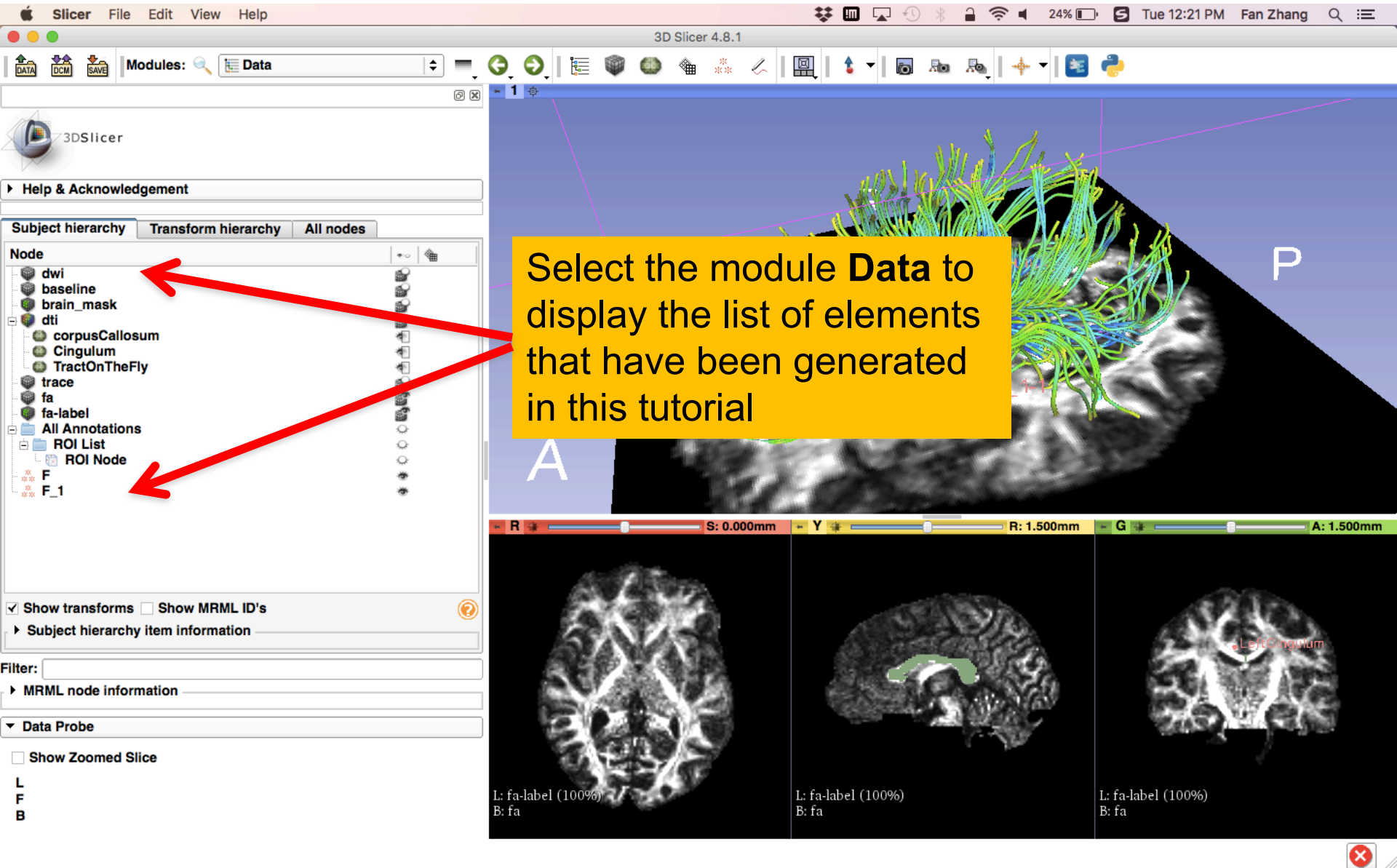
Tractography 'on-the-fly'



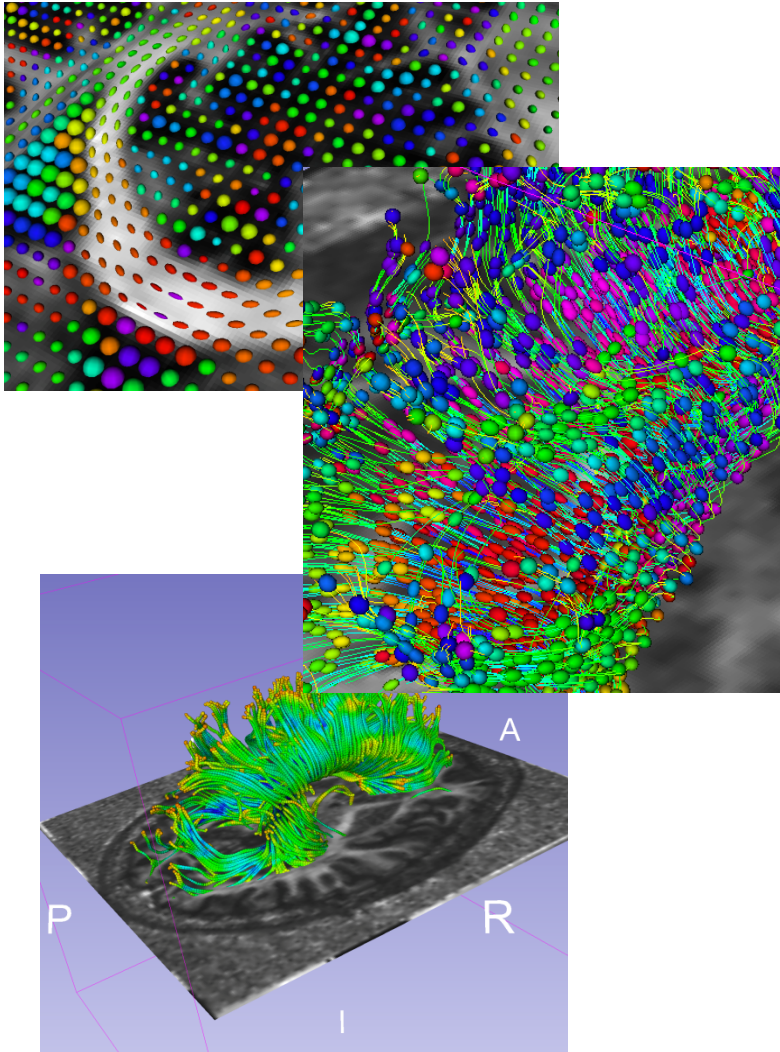
Tractography 'on-the-fly'



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.

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- **Fan Zhang, Ph.D.**
Brigham and Women's Hospital, Harvard Medical School