



Diffusion MRI Analysis

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Harvard Medical School

Brain Anatomy



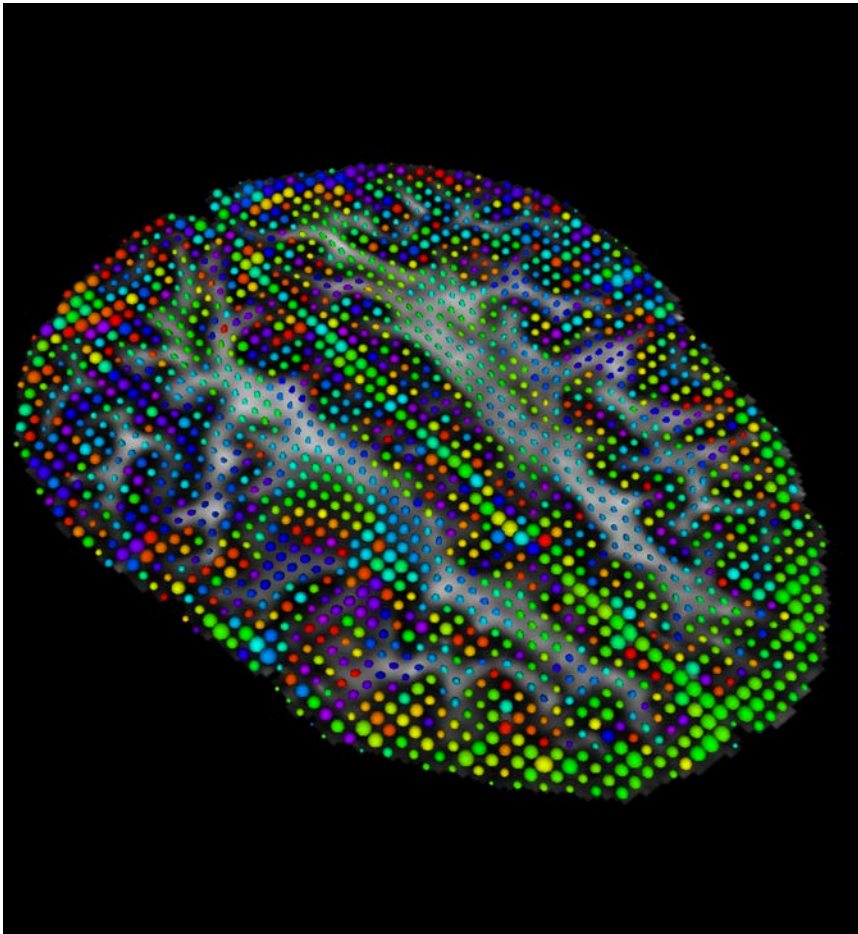
- White matter ~45% of the brain
- Myelinated nerve fibers (~ 10 μm axon diameter)

White Matter Exploration



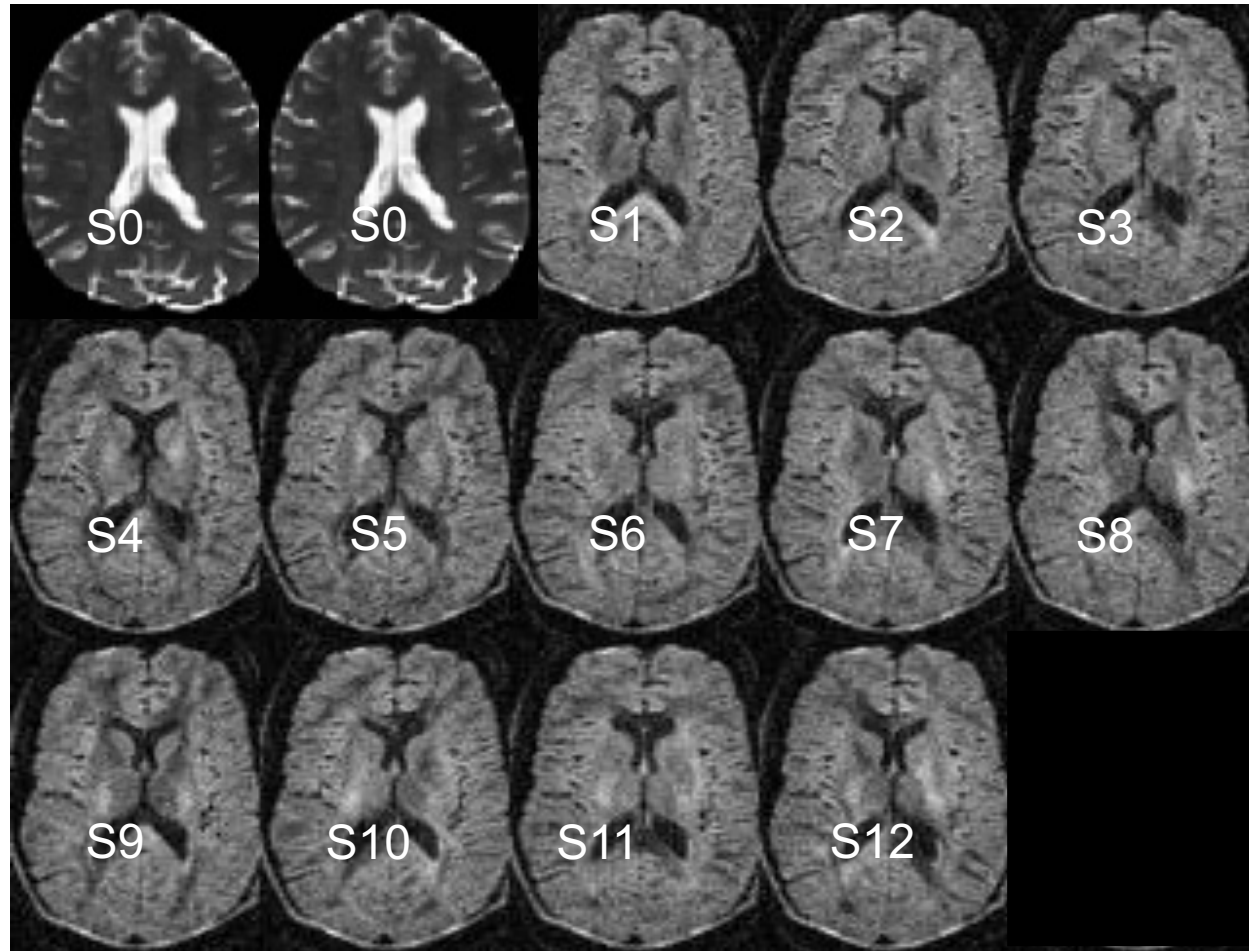
Jules Joseph Dejerine
(*Anatomie des centres
nerveux* (Paris, 1890-1901):
Atlas of Neuroanatomy based
on myelin stained preparation

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

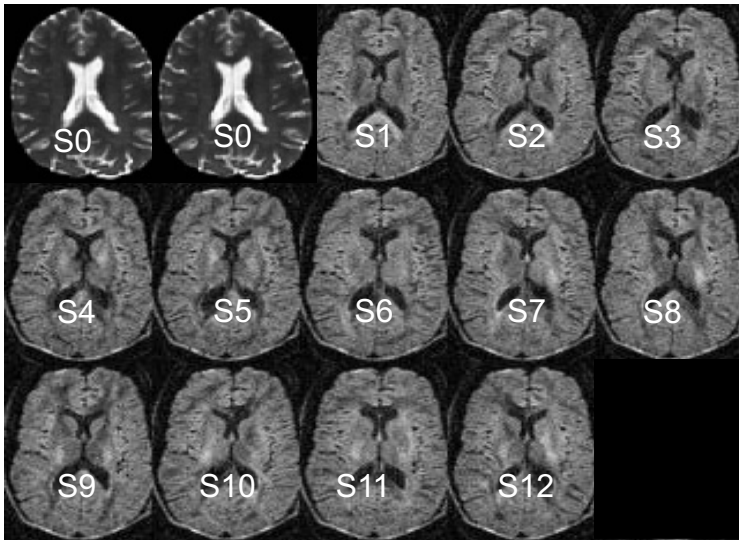
Diffusion Weighted Imaging (DWI)



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

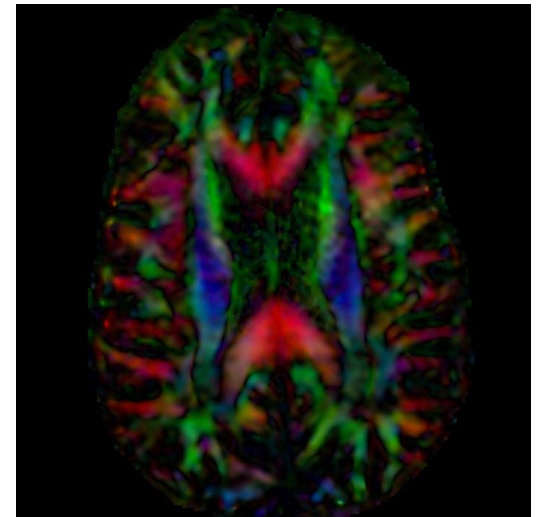
From DWI to DTI

DWI



DWI dataset acquired with 12 gradient and 2 baseline

DTI



DTI dataset

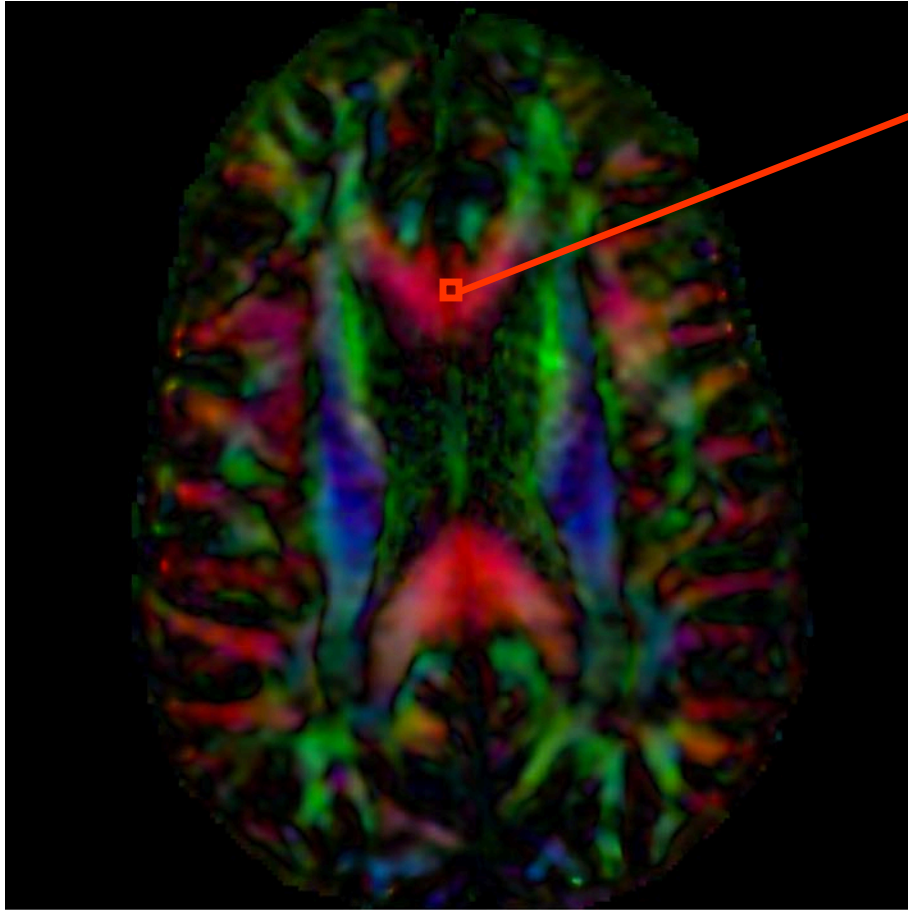
$$S_i = S_0 e^{-b \hat{g}_i^T \underline{D} \hat{g}_i}$$

Stejskal-Tanner (1965)

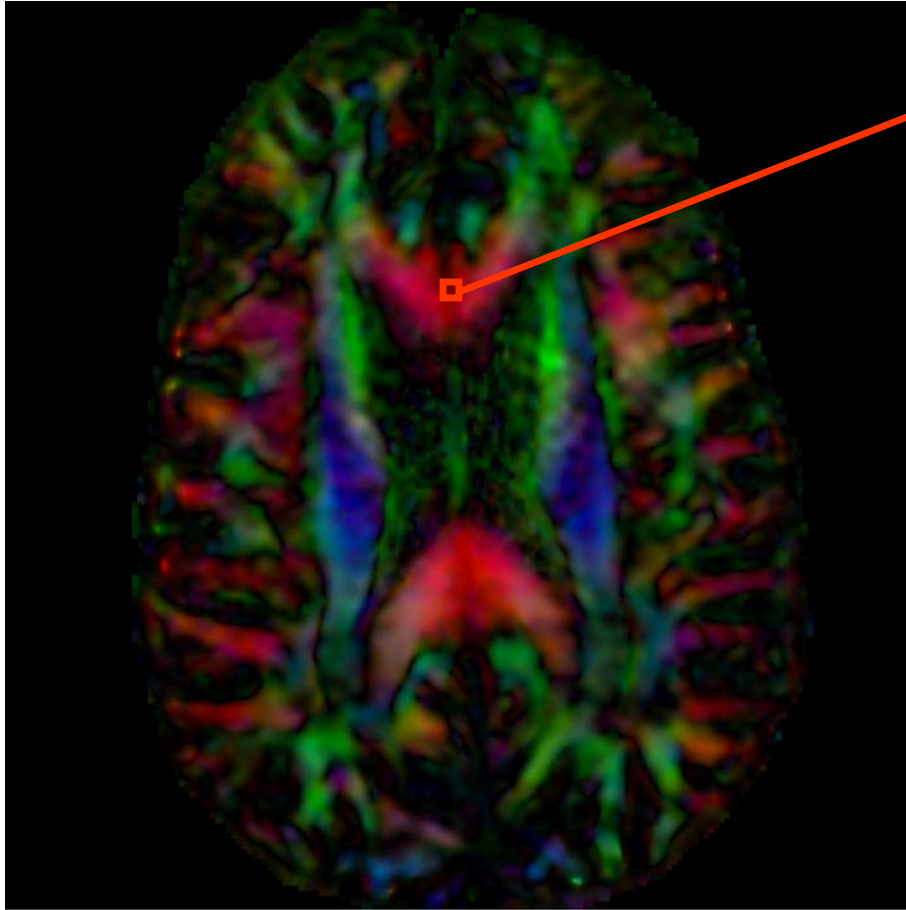
S_i : DWI volume acquired with
 i th gradient
 S_0 : Baseline volume

Diffusion Tensor Imaging

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



Diffusion Tensor Imaging

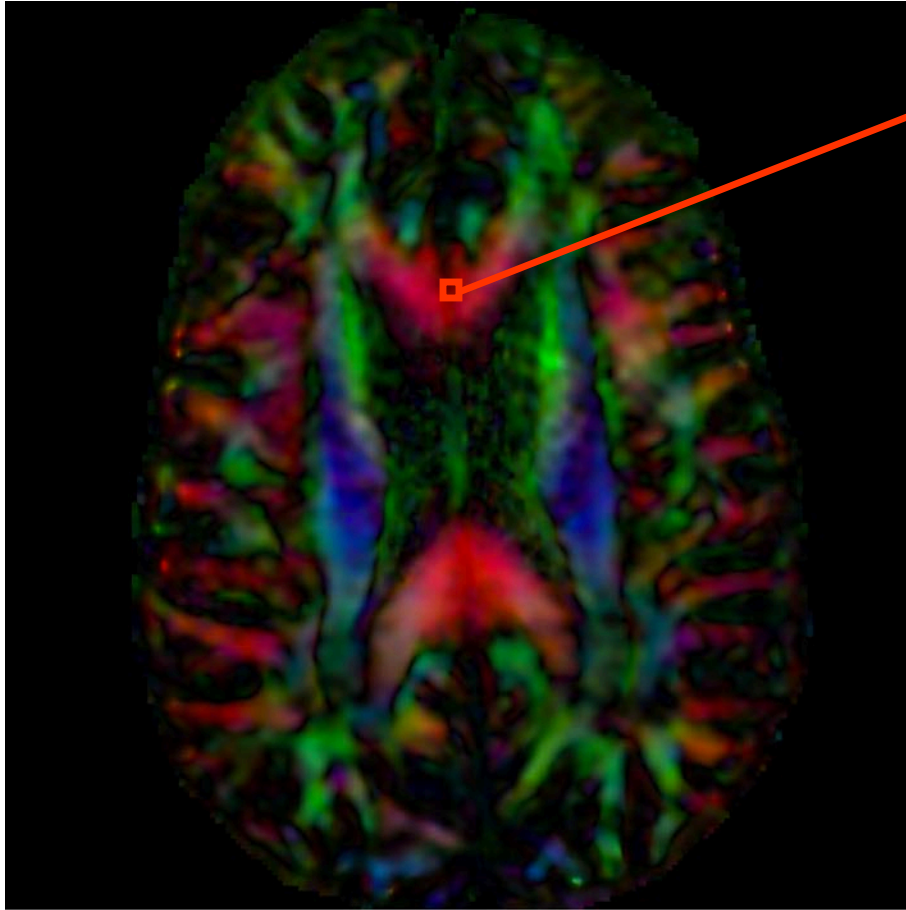


$$S_i = S_0 e^{-b \hat{g}_i^T \underline{D} \hat{g}_i}$$



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

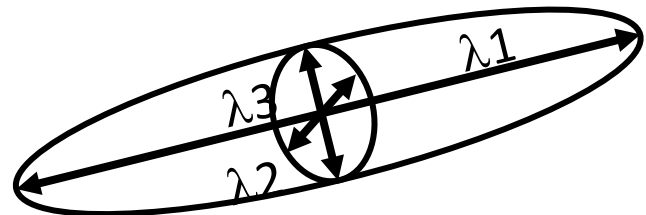
Diffusion Tensor Imaging



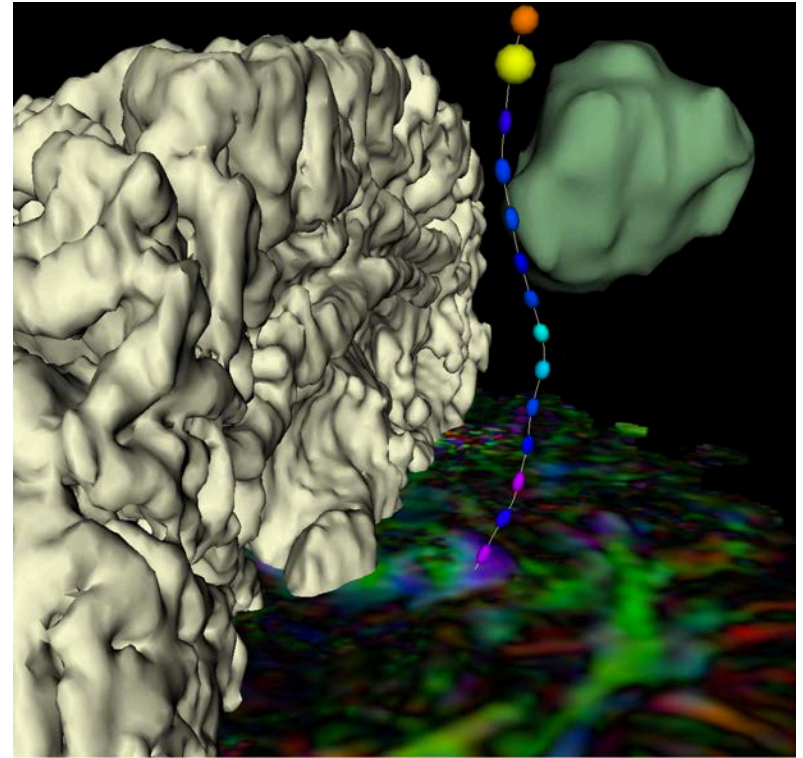
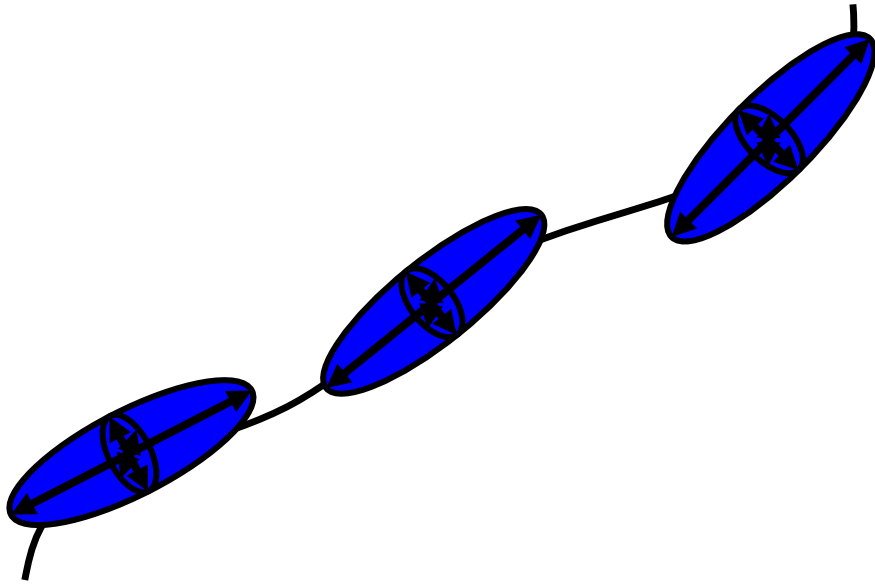
$$S_i = S_0 e^{-b\hat{g}_i^T \underline{D} \hat{g}_i}$$



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



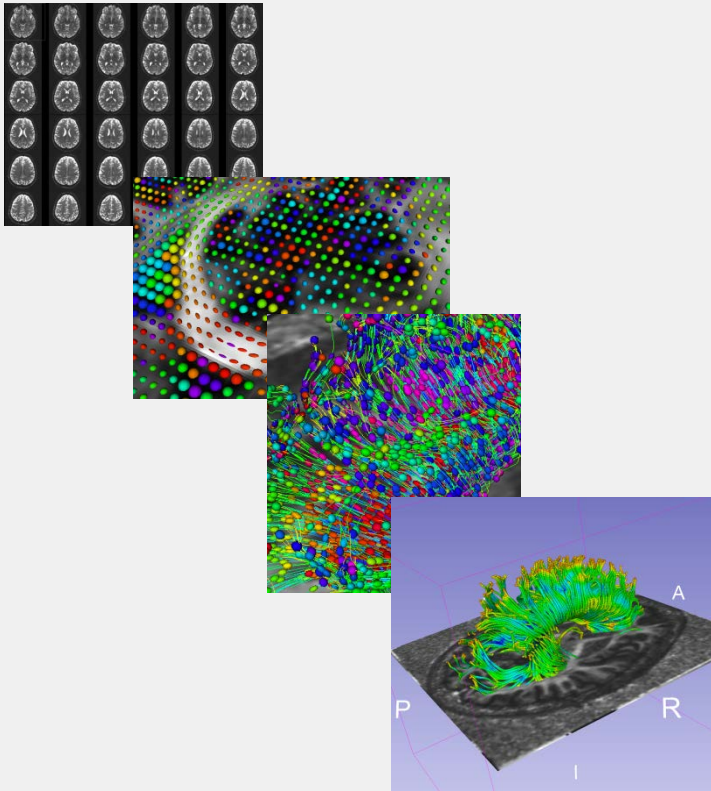
Tractography



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

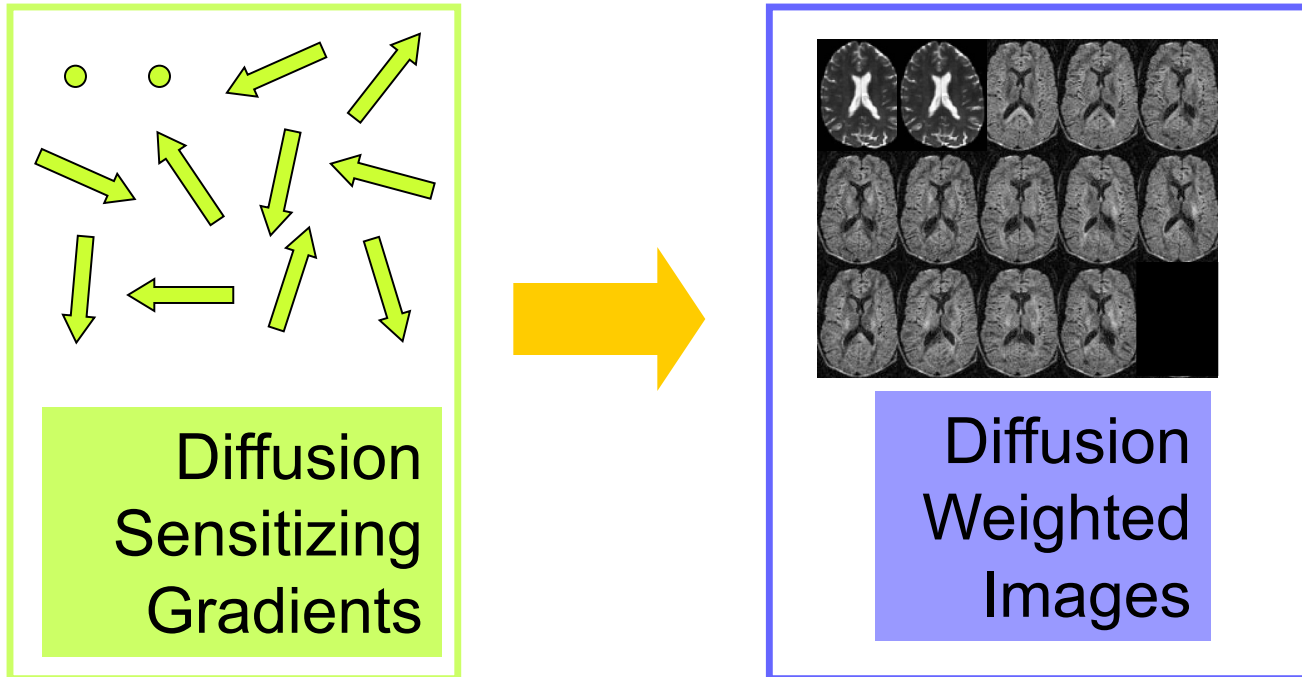
Tutorial Outline

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

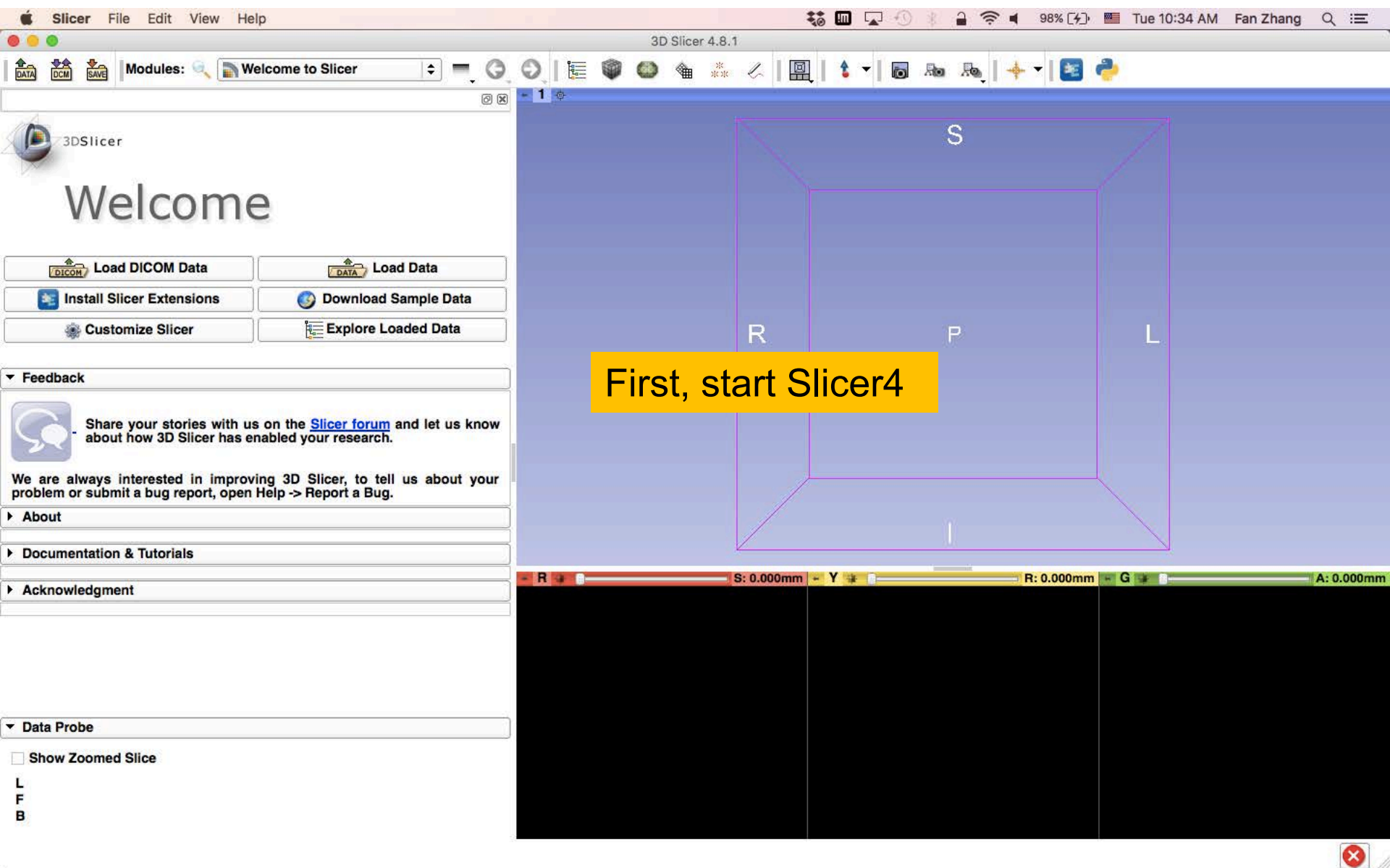
An open-source project to improve and extend diffusion magnetic resonance imaging software in 3D Slicer:

<http://dmri.slicer.org>

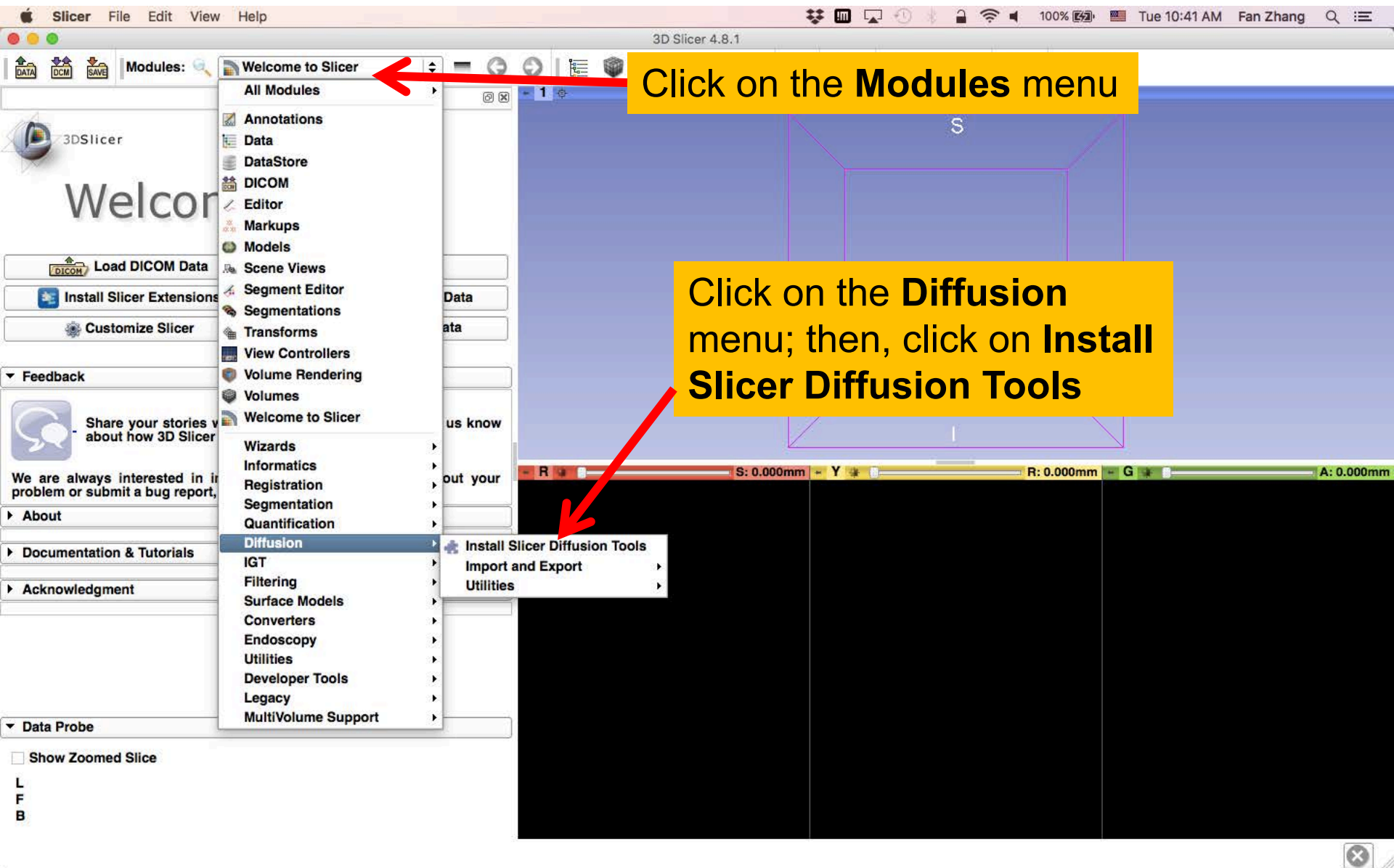
Disclaimer

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.

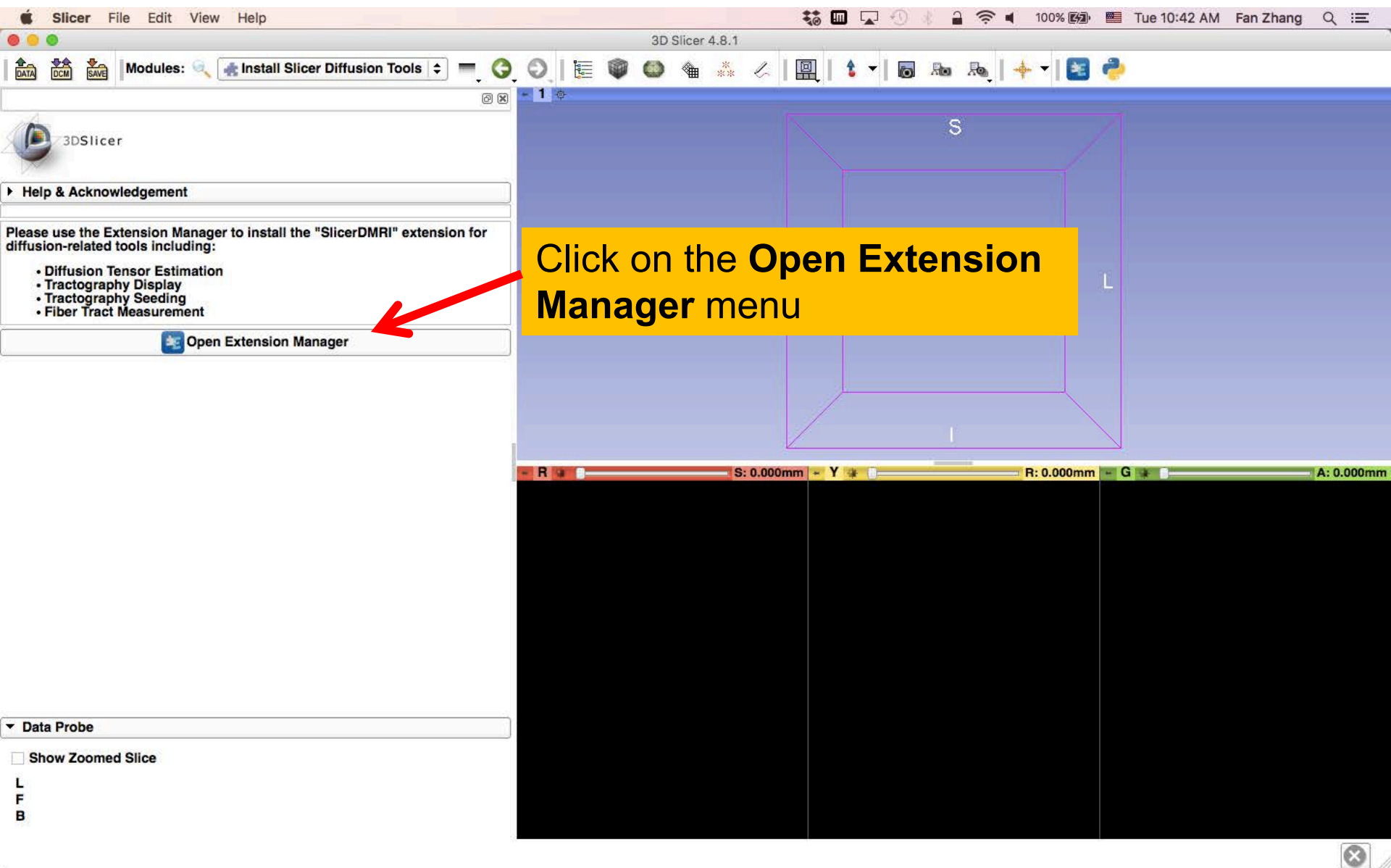
Install SlicerDMRI



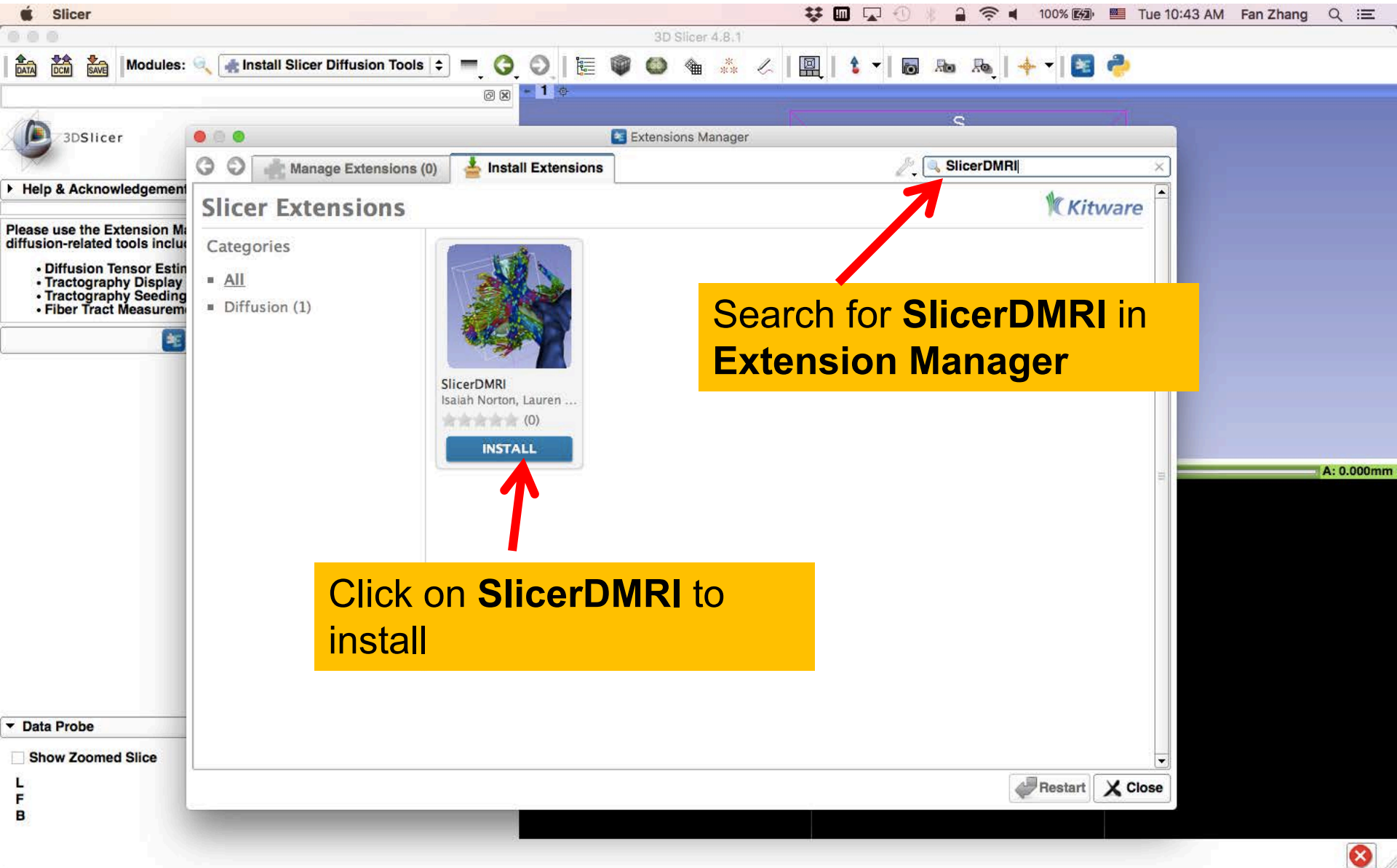
Install SlicerDMRI



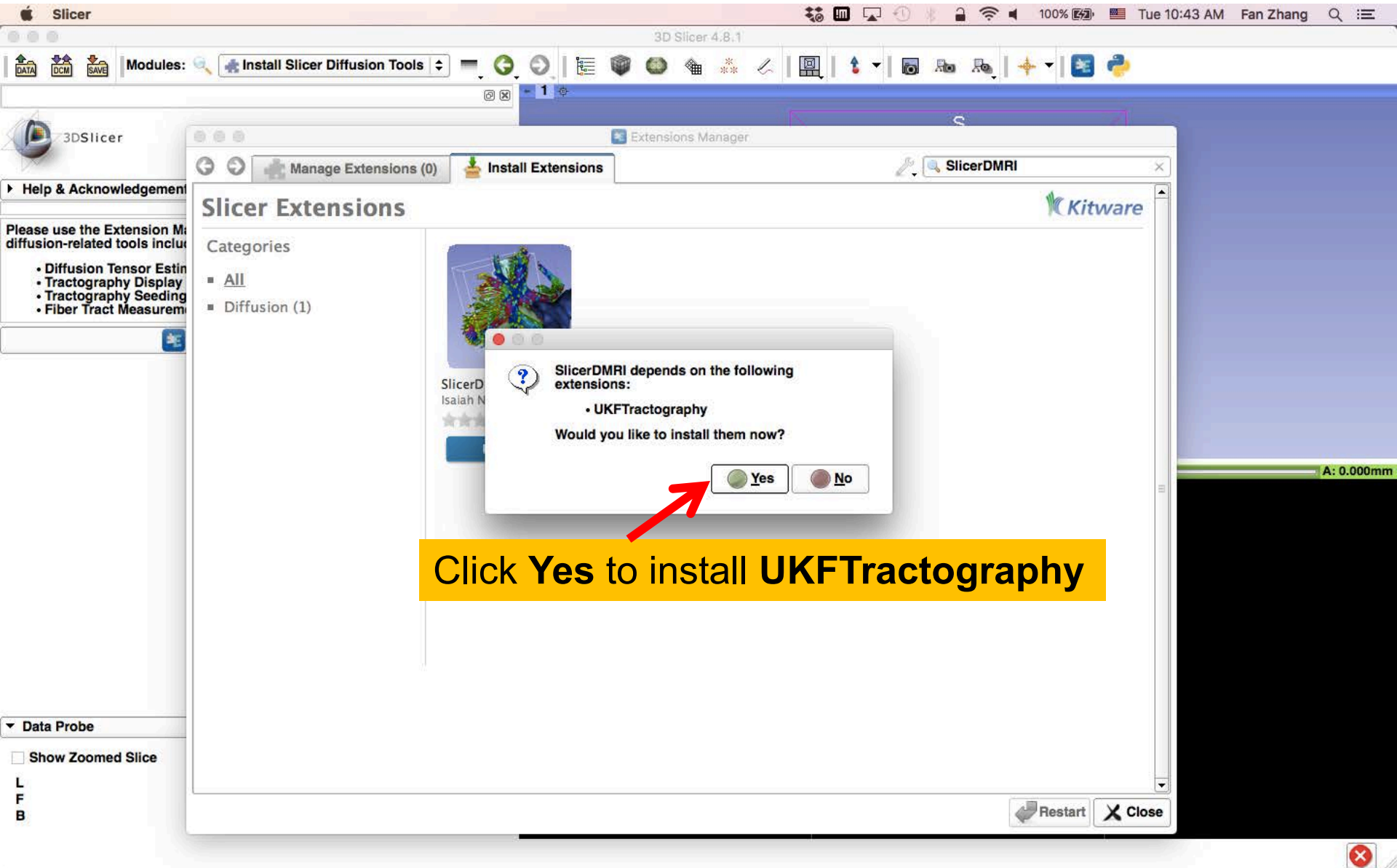
Install SlicerDMRI



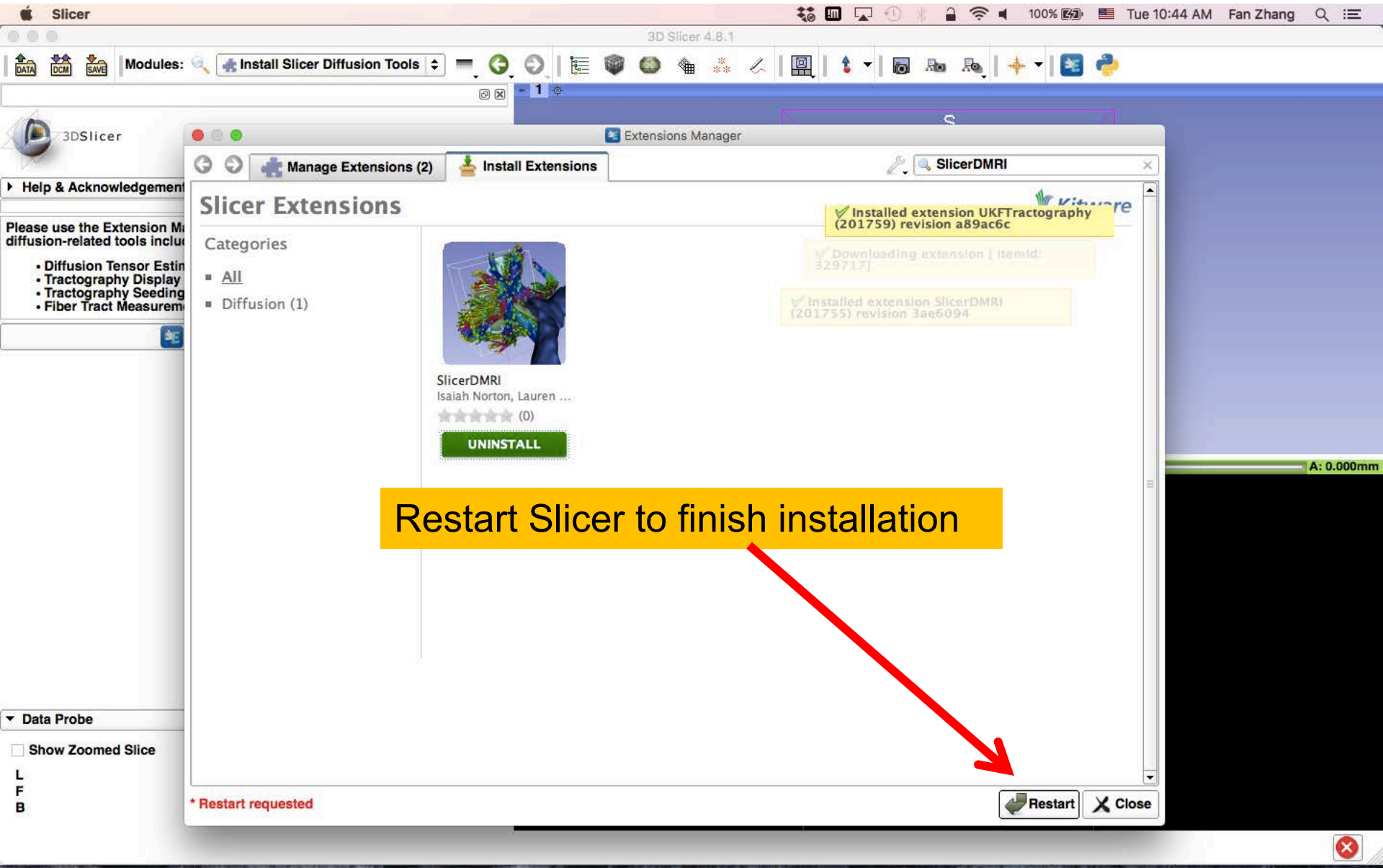
Install SlicerDMRI



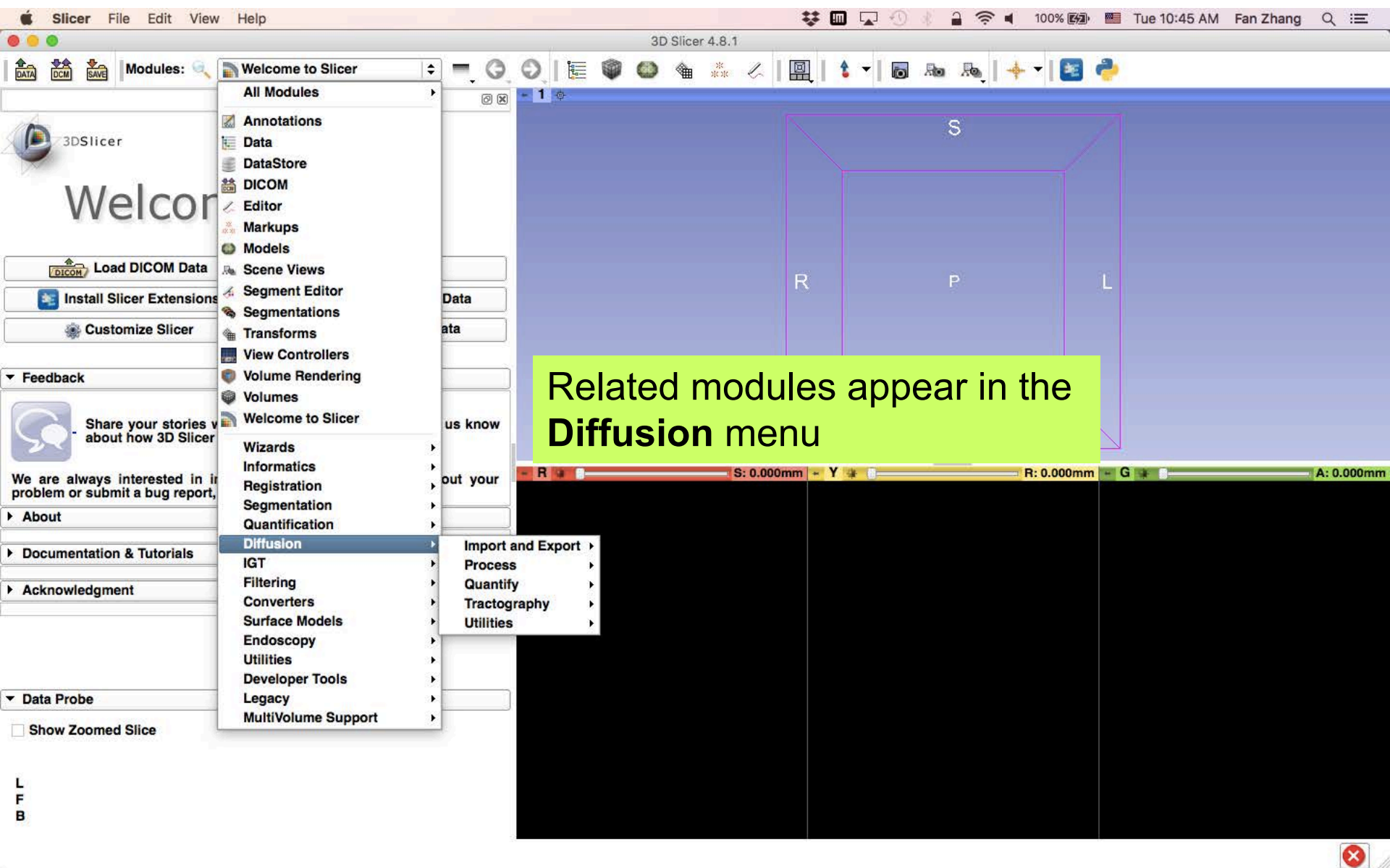
Install SlicerDMRI



Install SlicerDMRI



Install SlicerDMRI

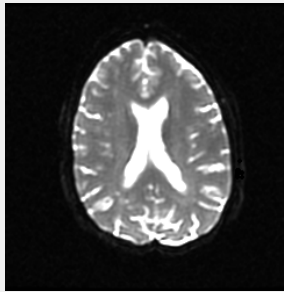


Learning Objectives

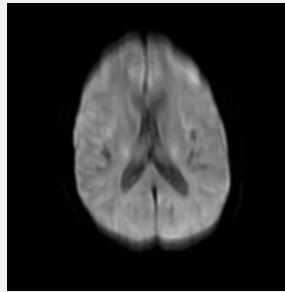
Following this tutorial, you'll be able to

- 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

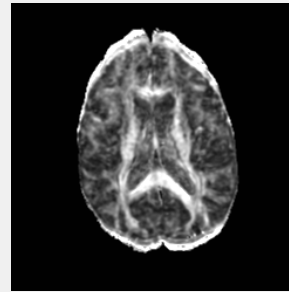
MR Diffusion Analysis Pipeline



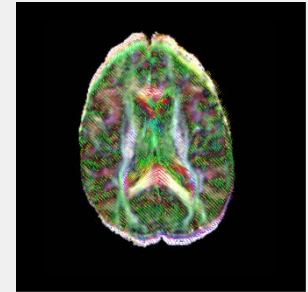
DWI
Acquisition



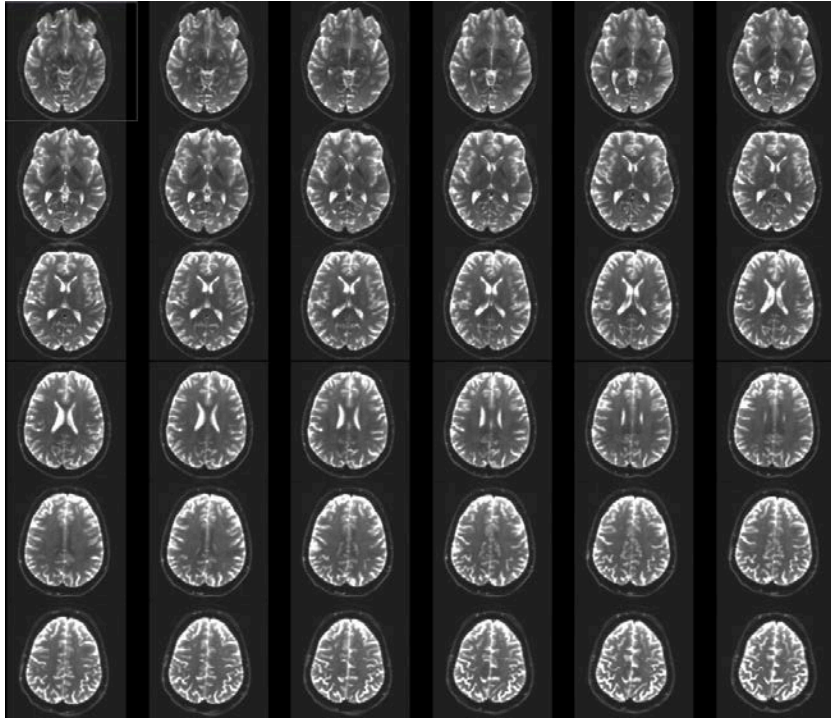
Tensor
Calculation



Scalar
Maps

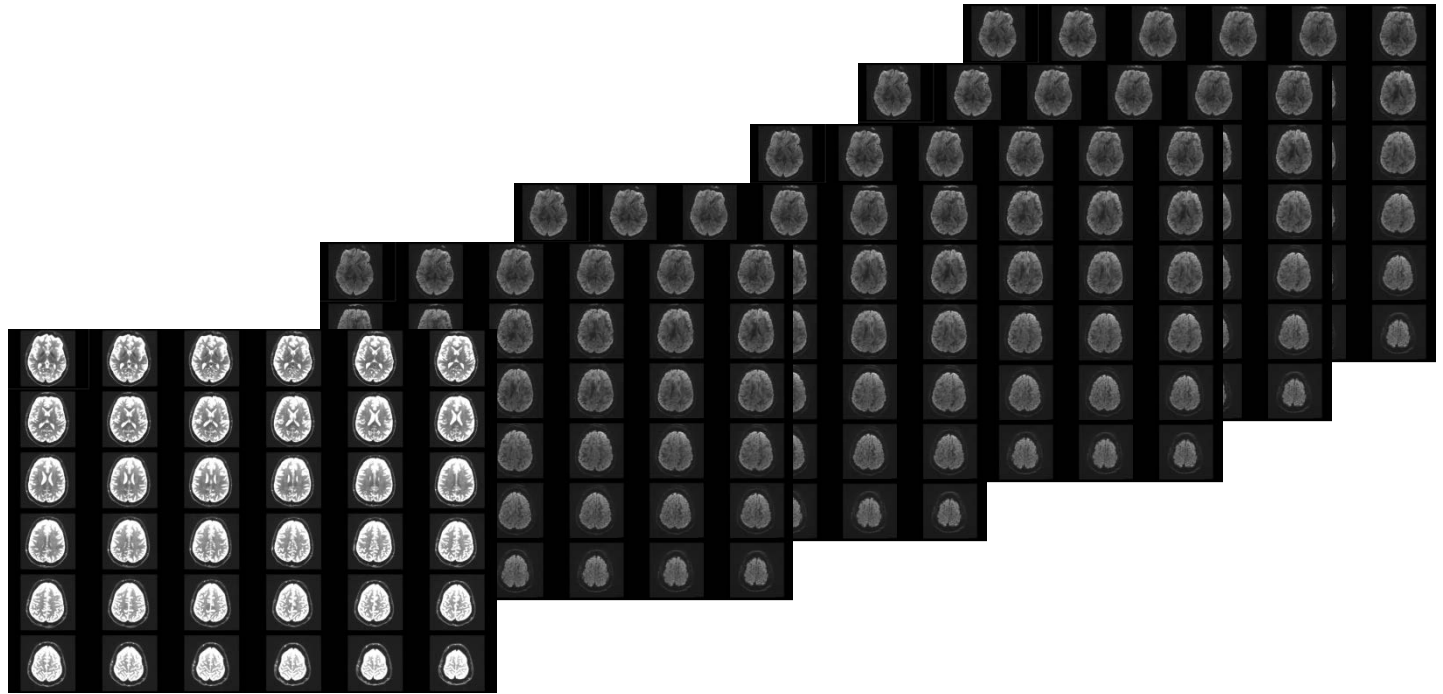


3D
Visualization



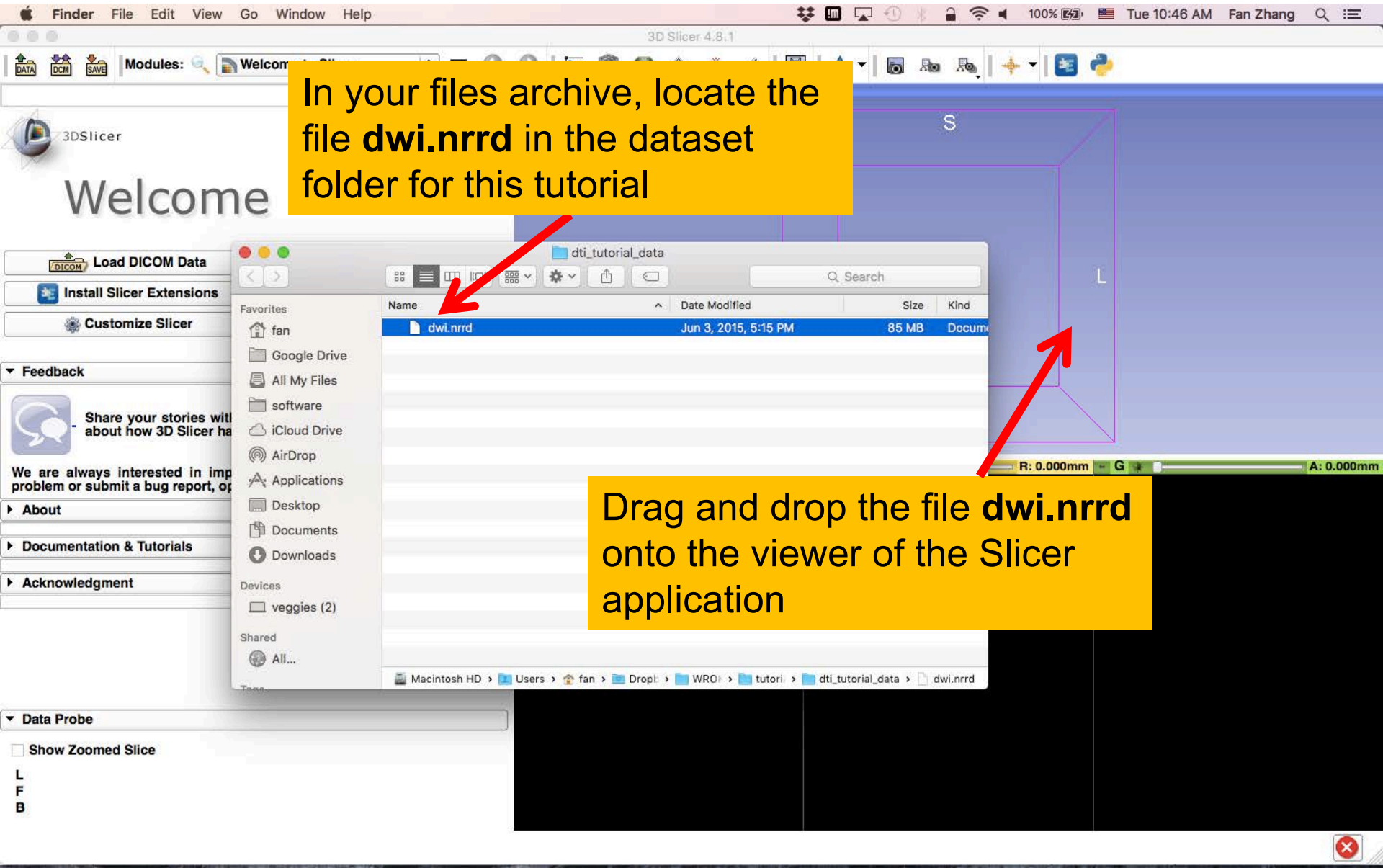
Part 1: From DWI images to Tensors

Understanding the DWI Dataset

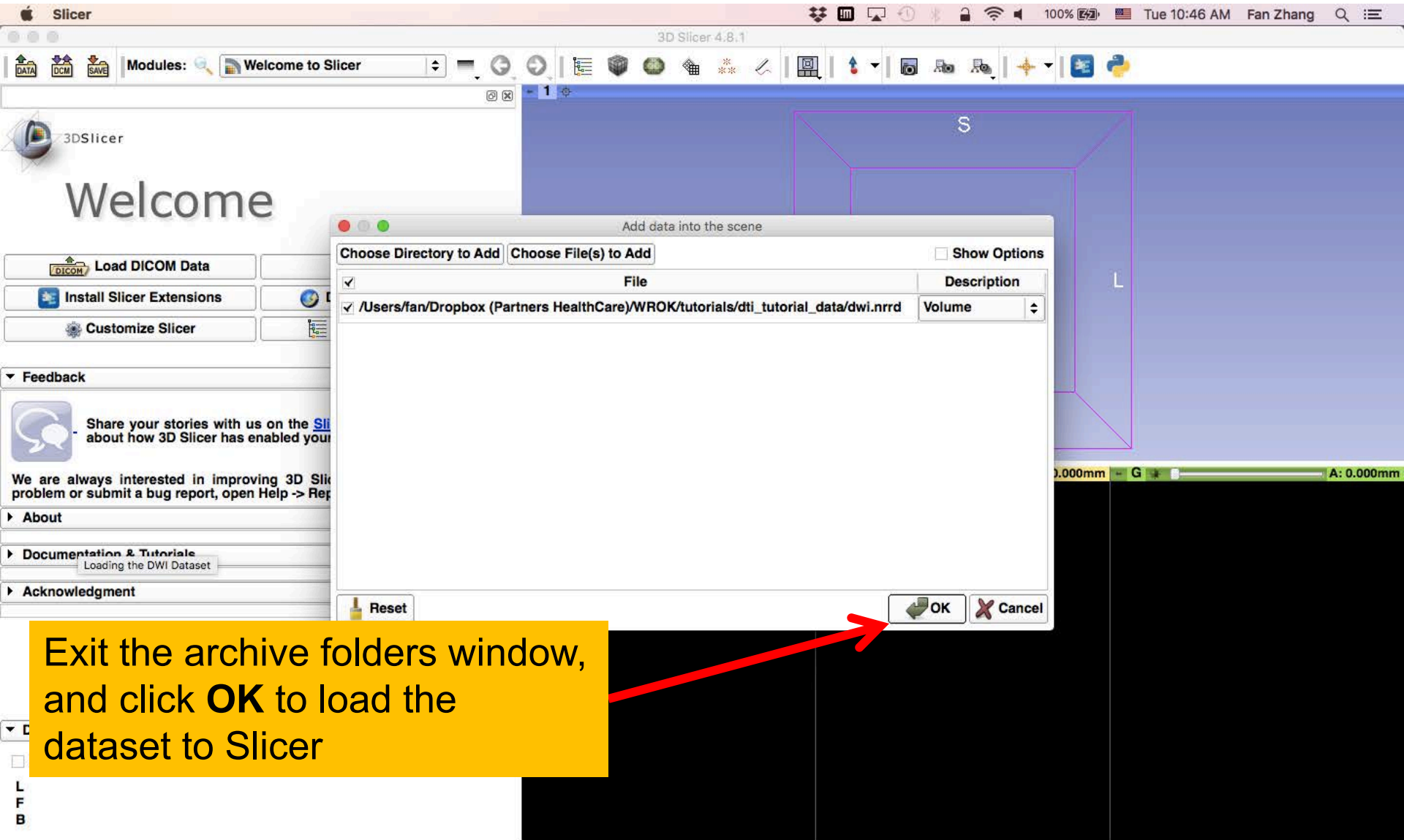


The Diffusion Weighted Imaging (DWI) dataset is composed of 41 volumes acquired with 41 different diffusion-sensitizing gradient directions, and one baseline image acquired without diffusion weighting.

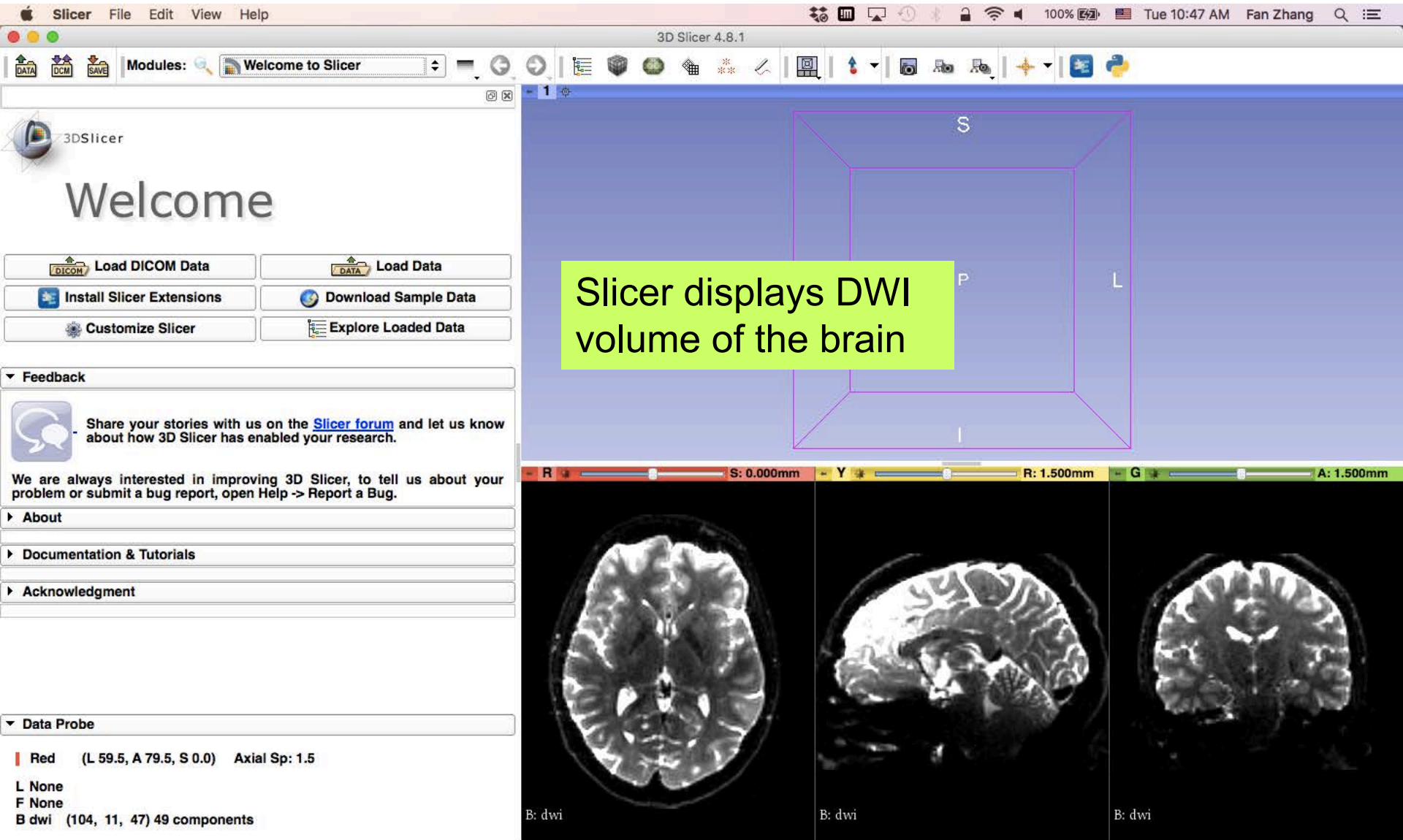
Loading the DWI Dataset



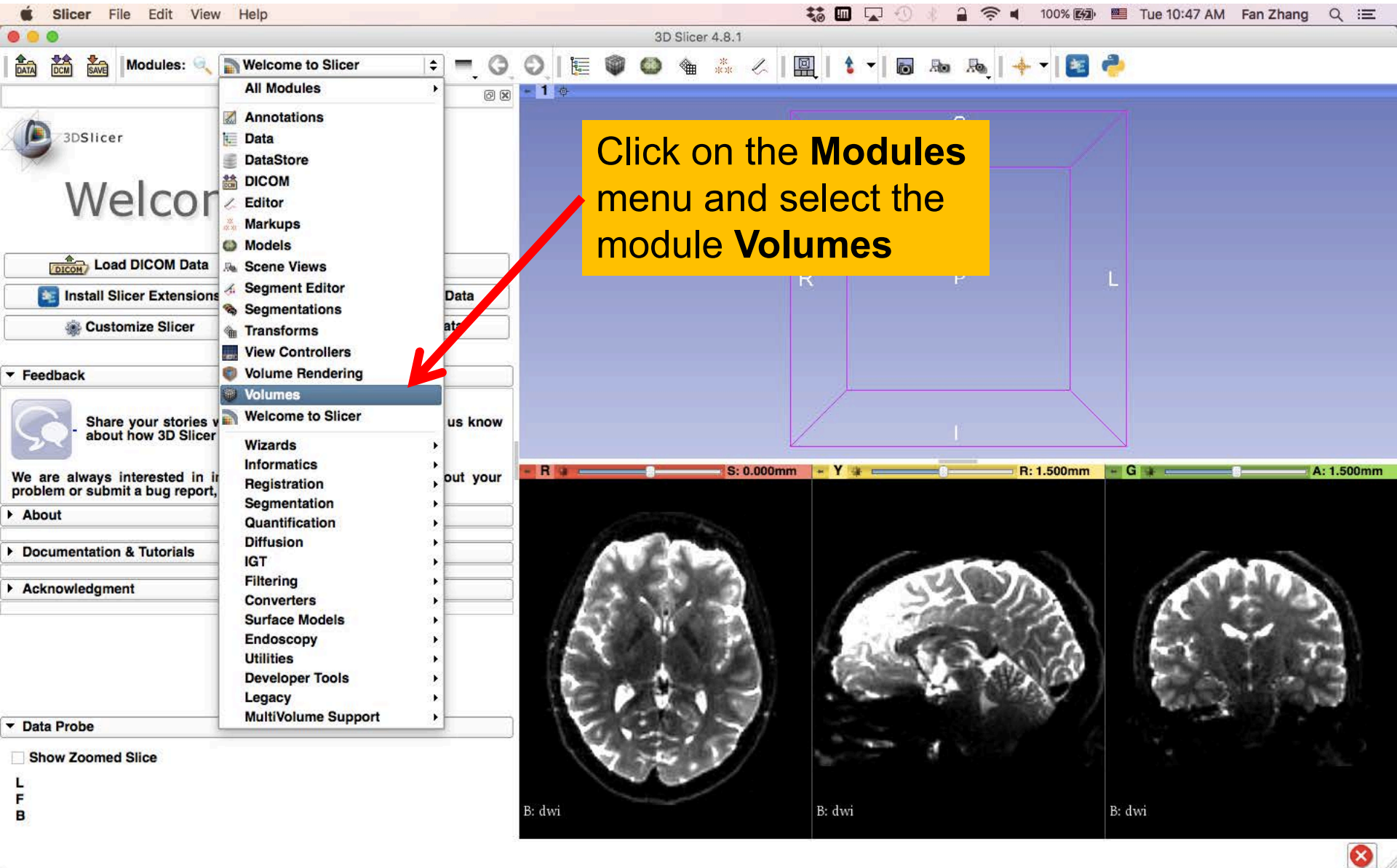
Loading the DWI Dataset



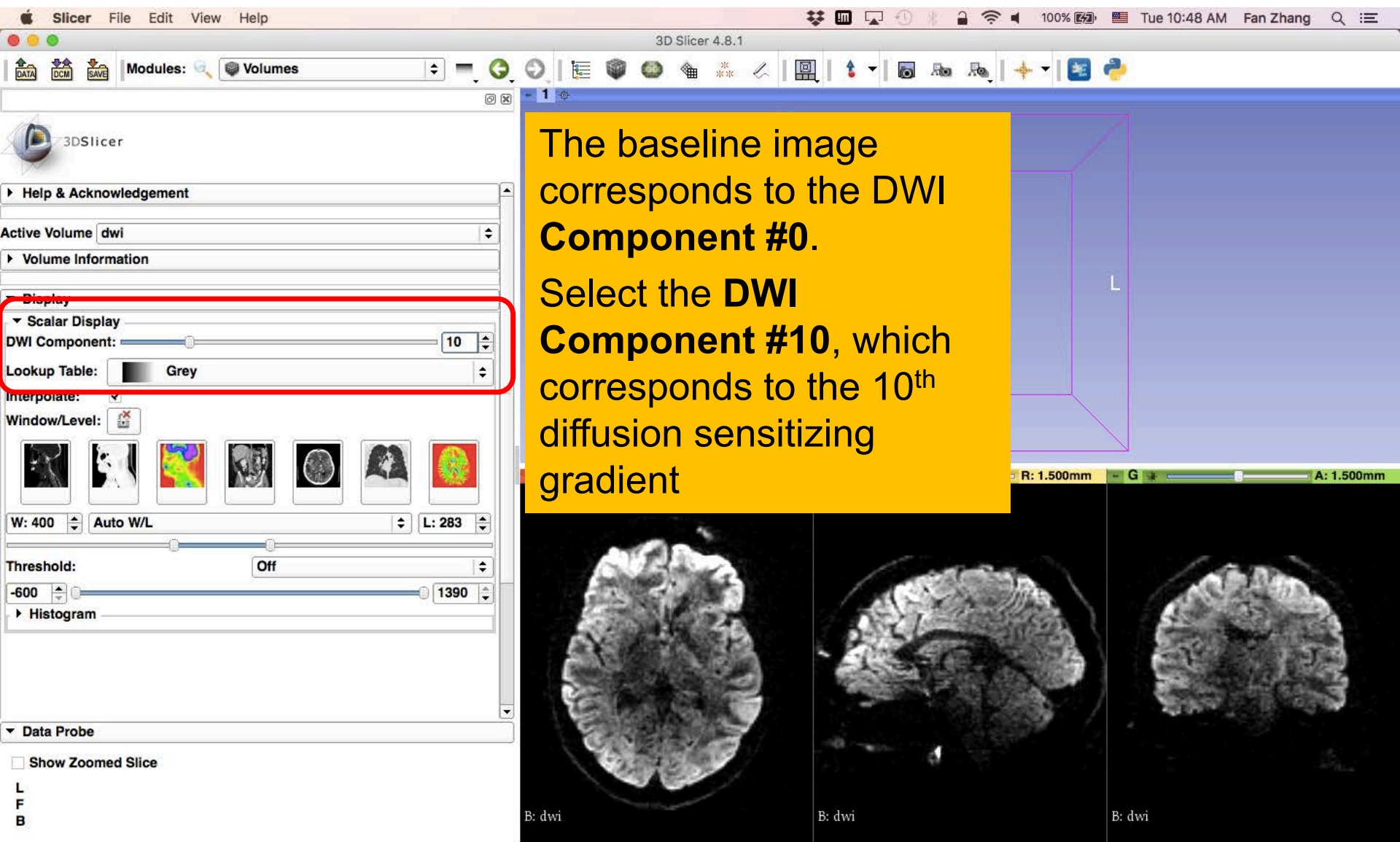
Loading the DWI Dataset



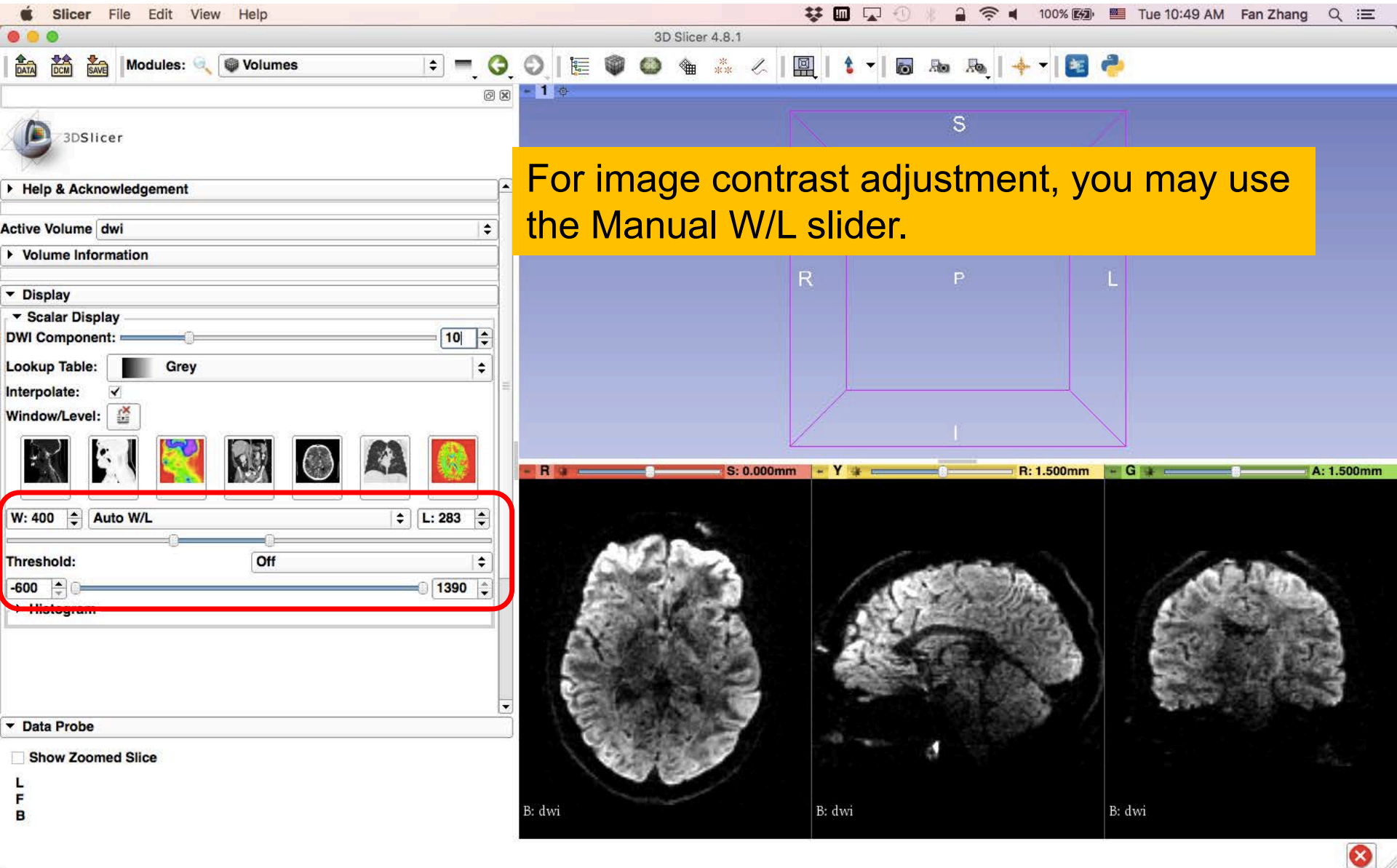
Loading the DWI Dataset



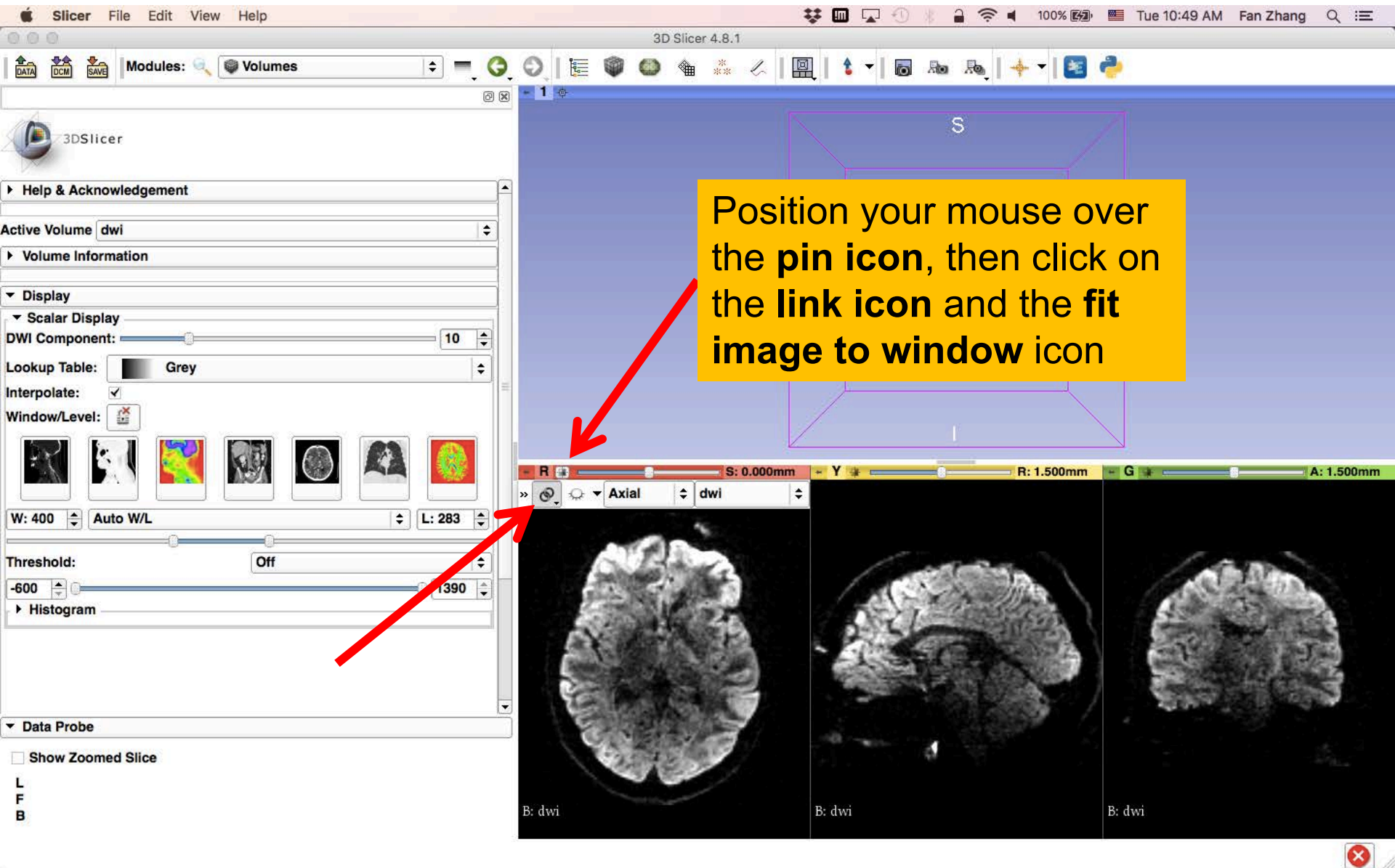
Loading the DWI Dataset



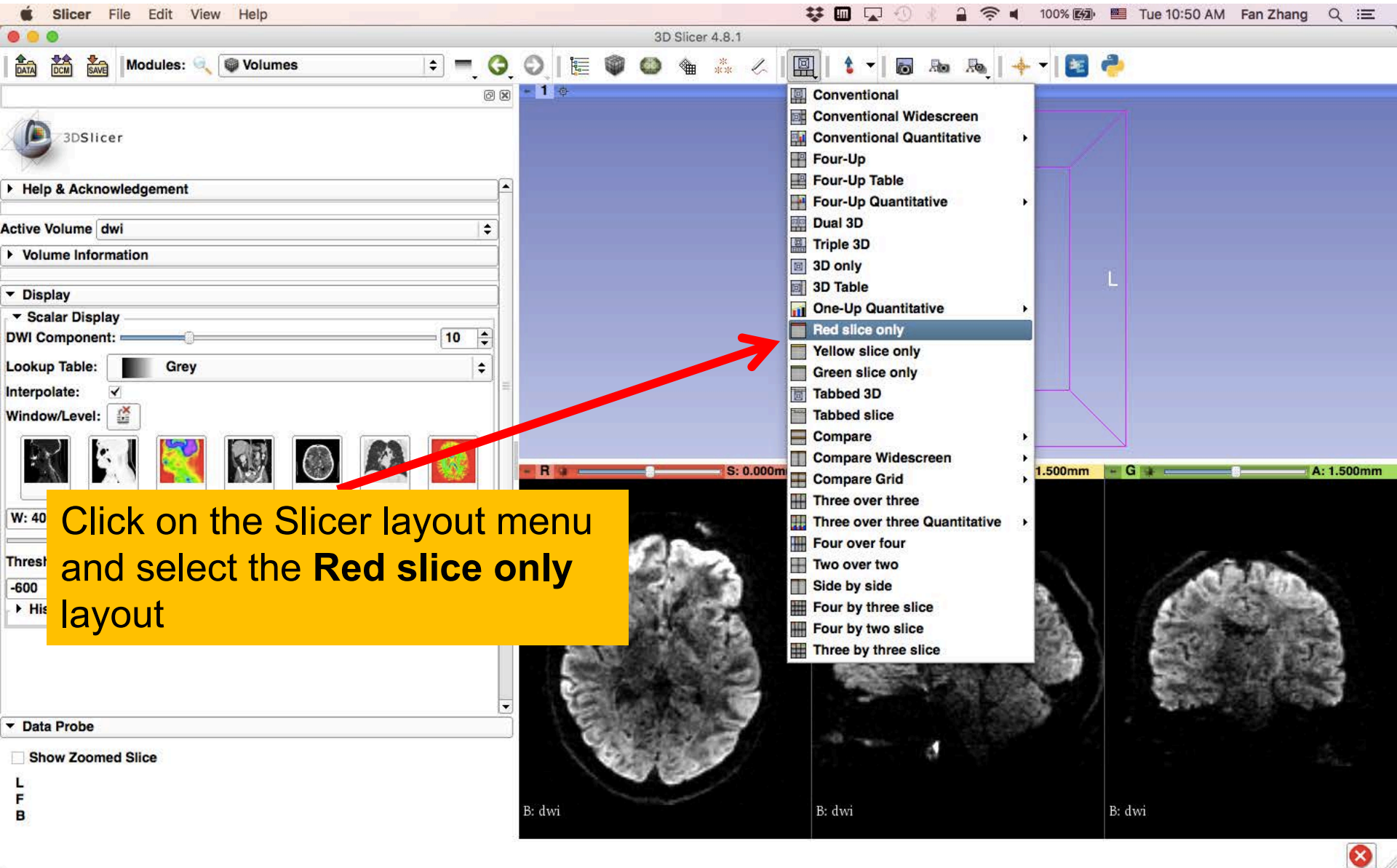
Loading the DWI Dataset



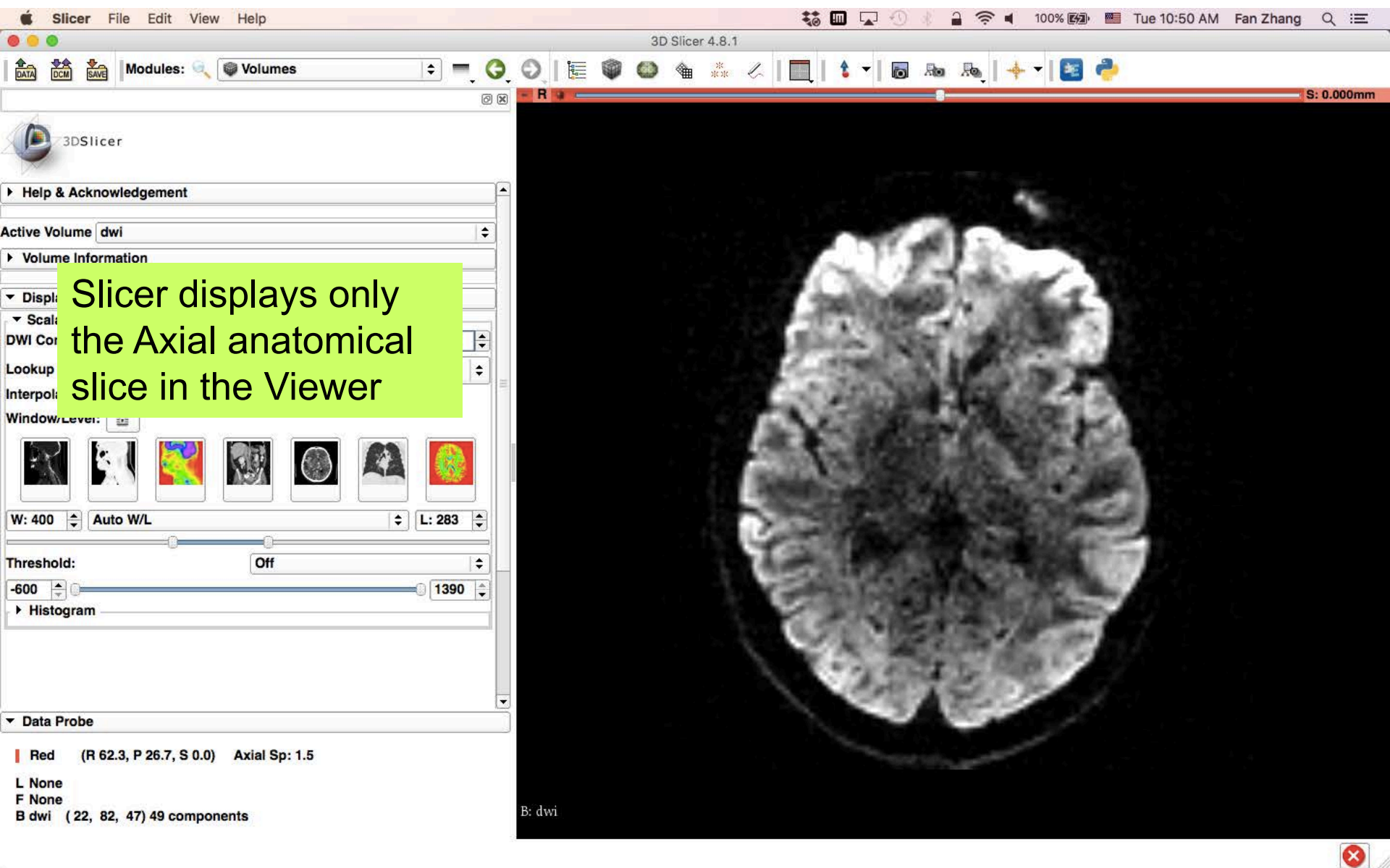
Loading the DWI Dataset



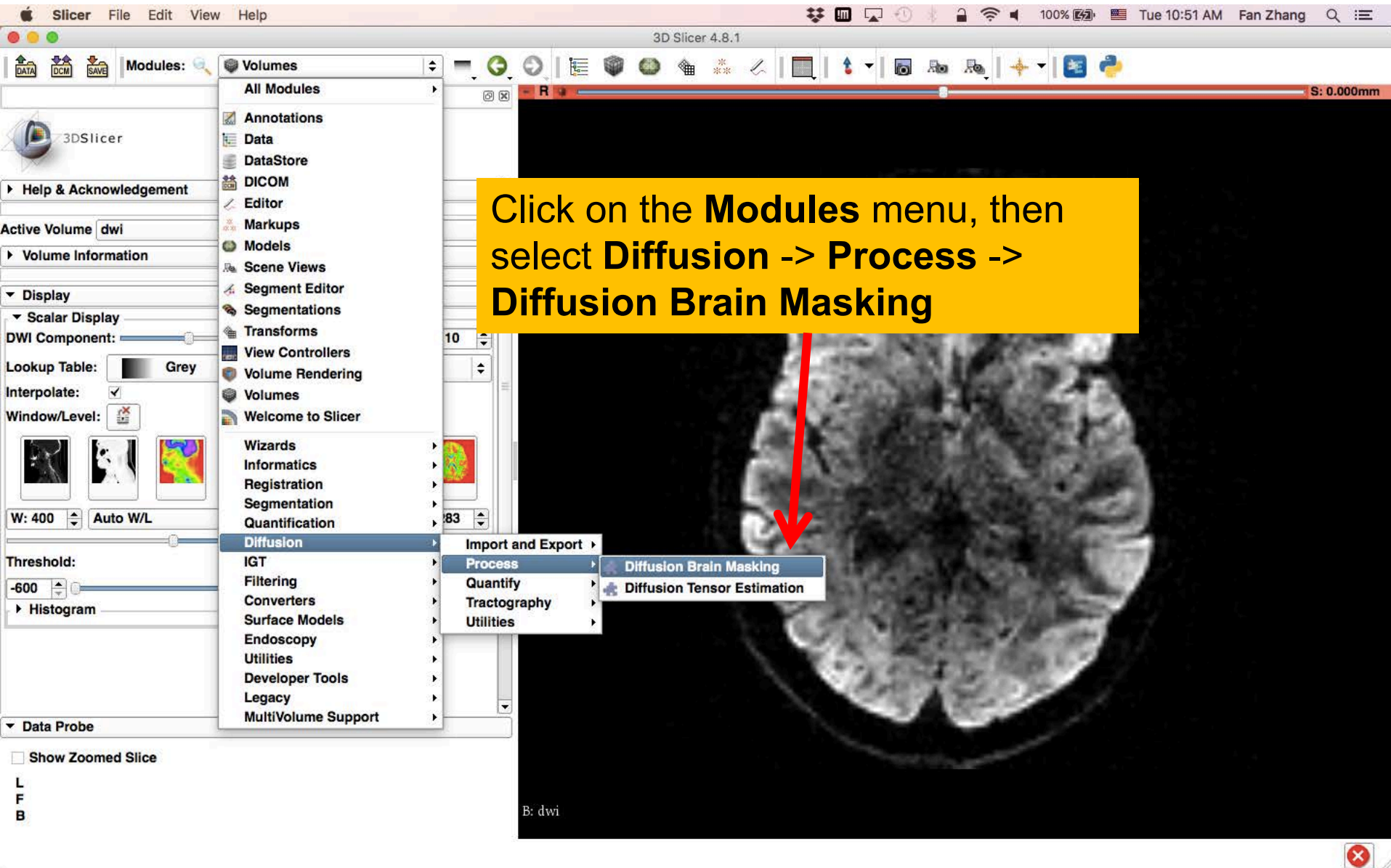
Loading the DWI Dataset



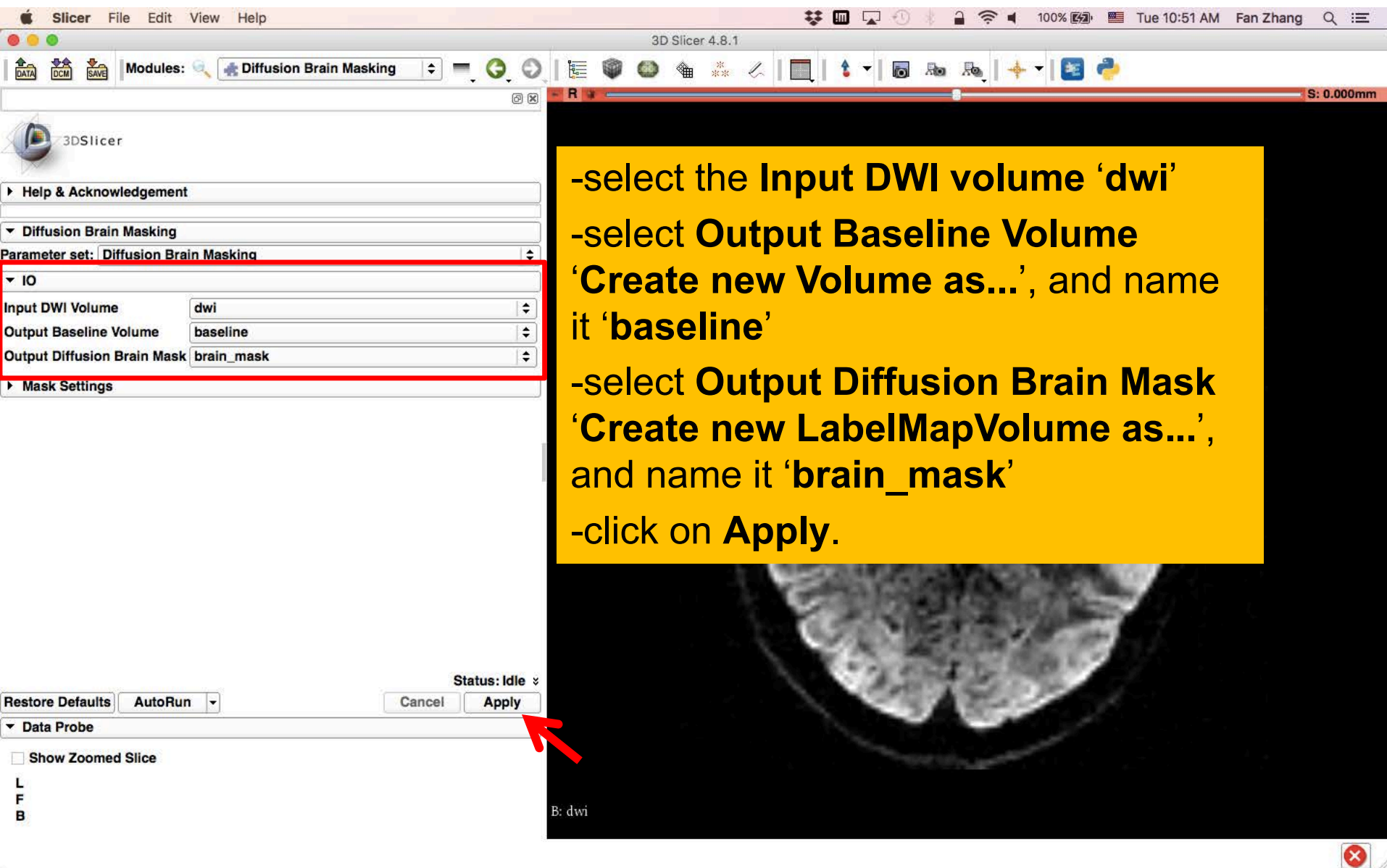
Loading the DWI Dataset



Creating a brain mask



Creating a brain mask



The screenshot shows the 3D Slicer 4.8.1 interface. The 'Diffusion Brain Masking' module is selected in the 'Modules' panel. The 'Parameter set' is 'Diffusion Brain Masking'. The 'IO' section is expanded, showing the following settings:

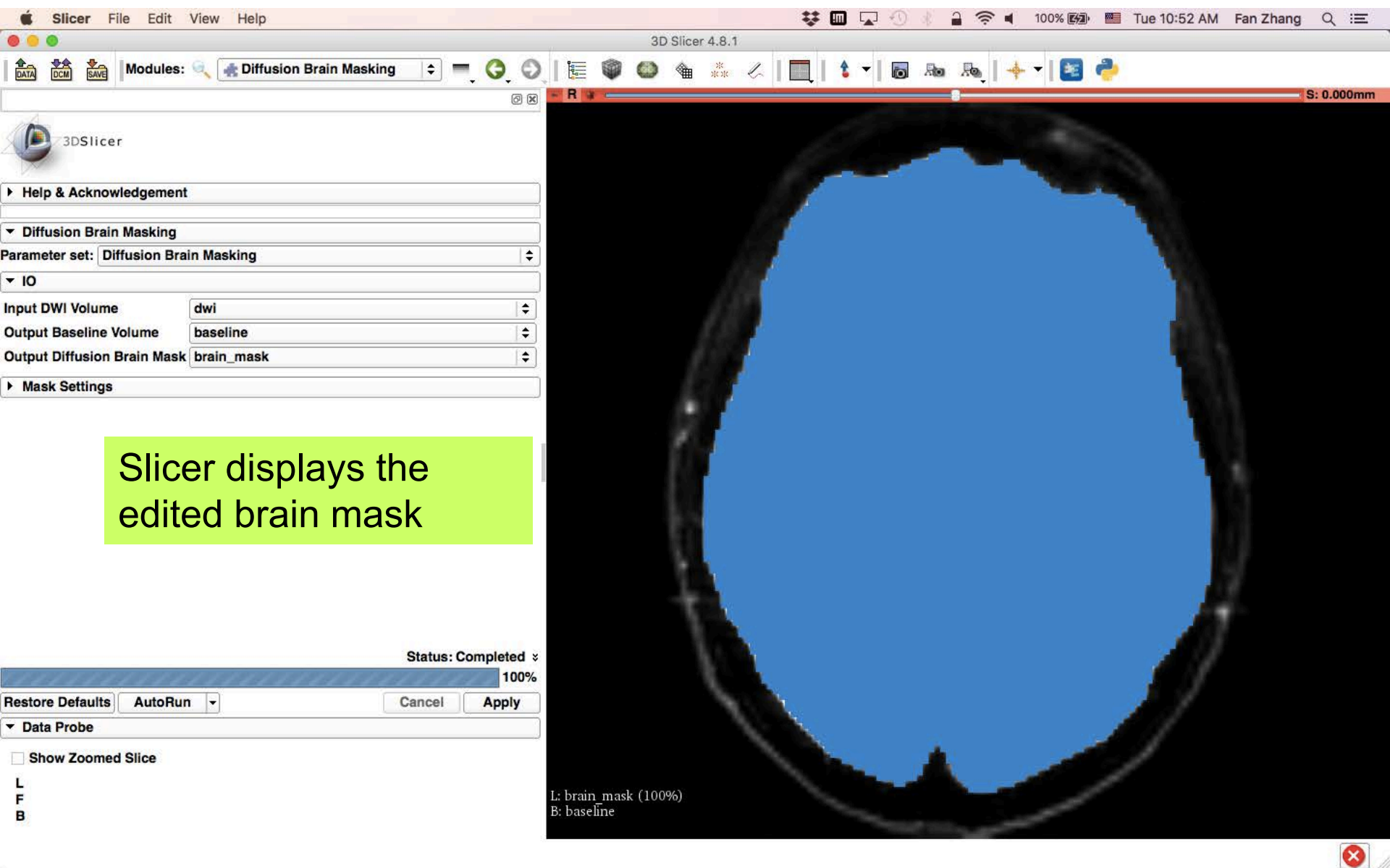
- Input DWI Volume: dwi
- Output Baseline Volume: baseline
- Output Diffusion Brain Mask: brain_mask

The 'Mask Settings' section is also visible. At the bottom, the 'Status' is 'Idle'. The 'Apply' button is highlighted with a red arrow.

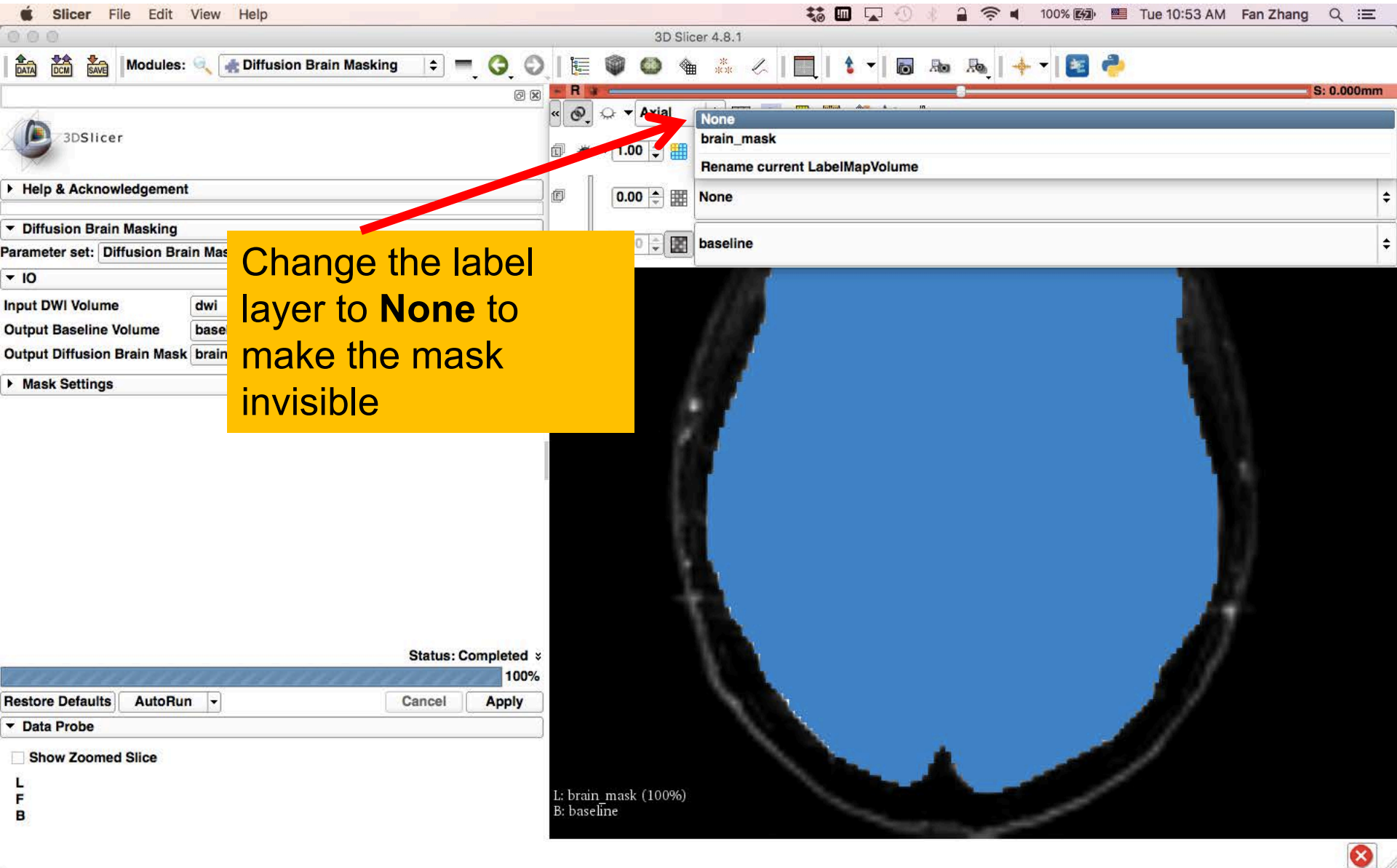
Instructions for creating a brain mask:

- 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**.

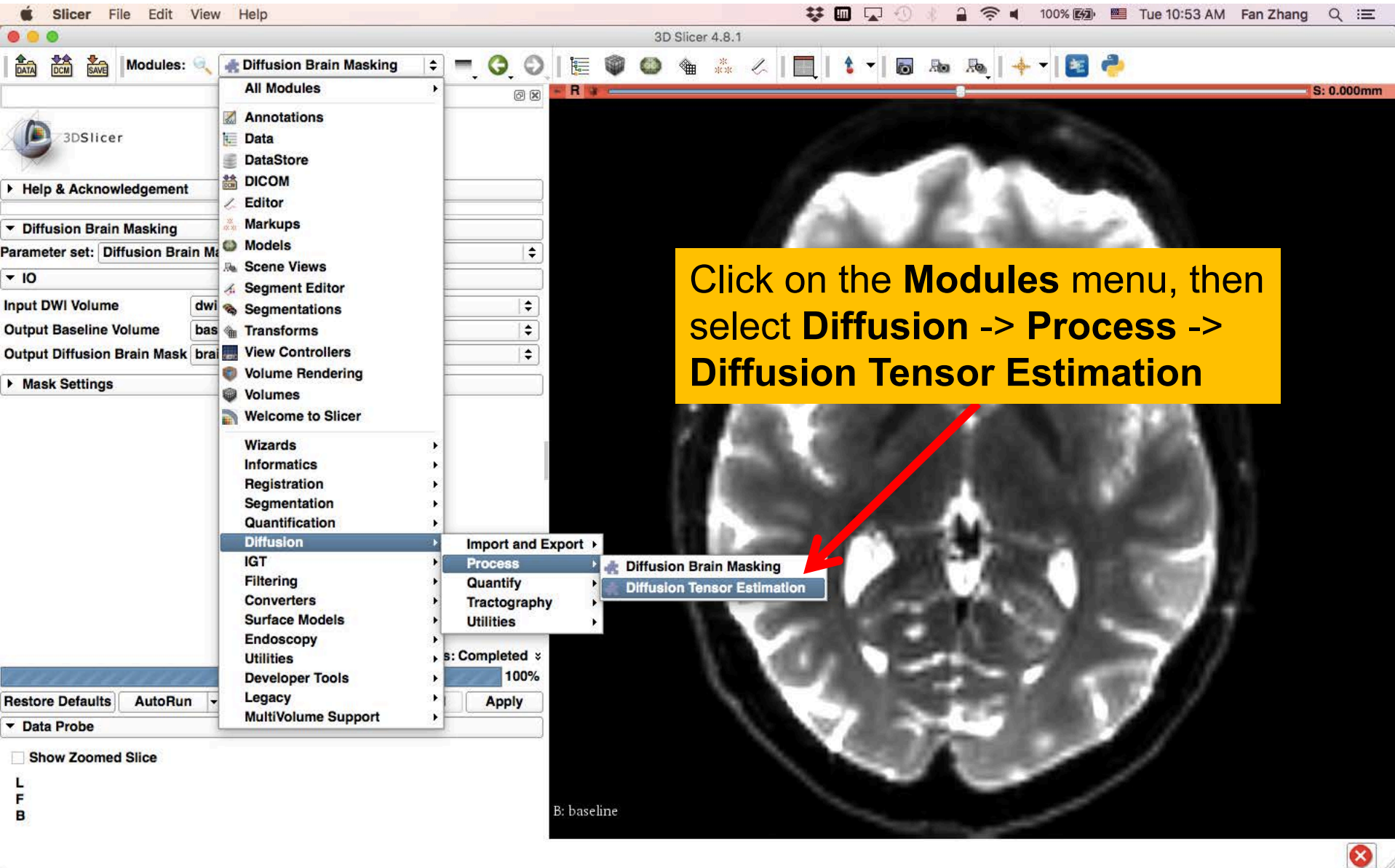
Creating a brain mask



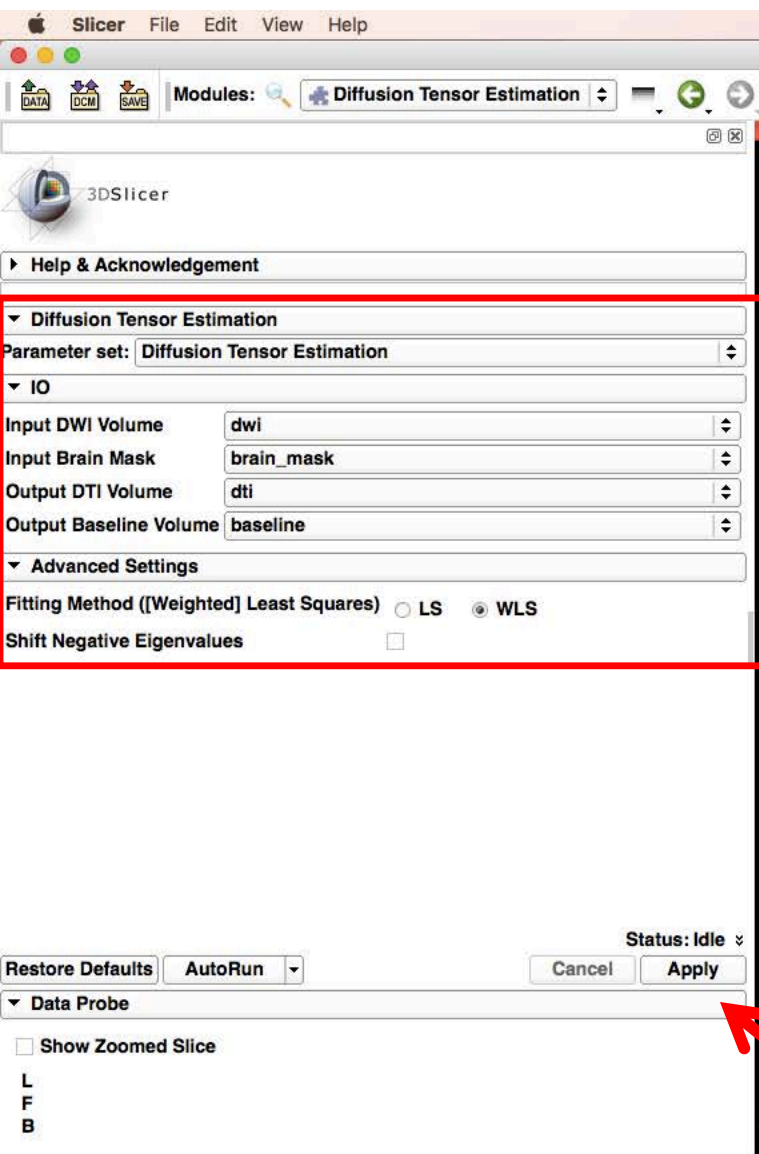
Creating a brain mask



Estimating the tensor



Estimating the tensor



The screenshot shows the 3D Slicer 4.8.1 application window. The 'Diffusion Tensor Estimation' module is selected in the 'Modules' panel. The 'Parameter set' is 'Diffusion Tensor Estimation'. The 'IO' section is expanded, showing the following settings:

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

The 'Advanced Settings' section is also expanded, showing:

- 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' is 'Idle'. The 'Data Probe' section is also visible at the bottom.

Instructions for Estimating the tensor:

- 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

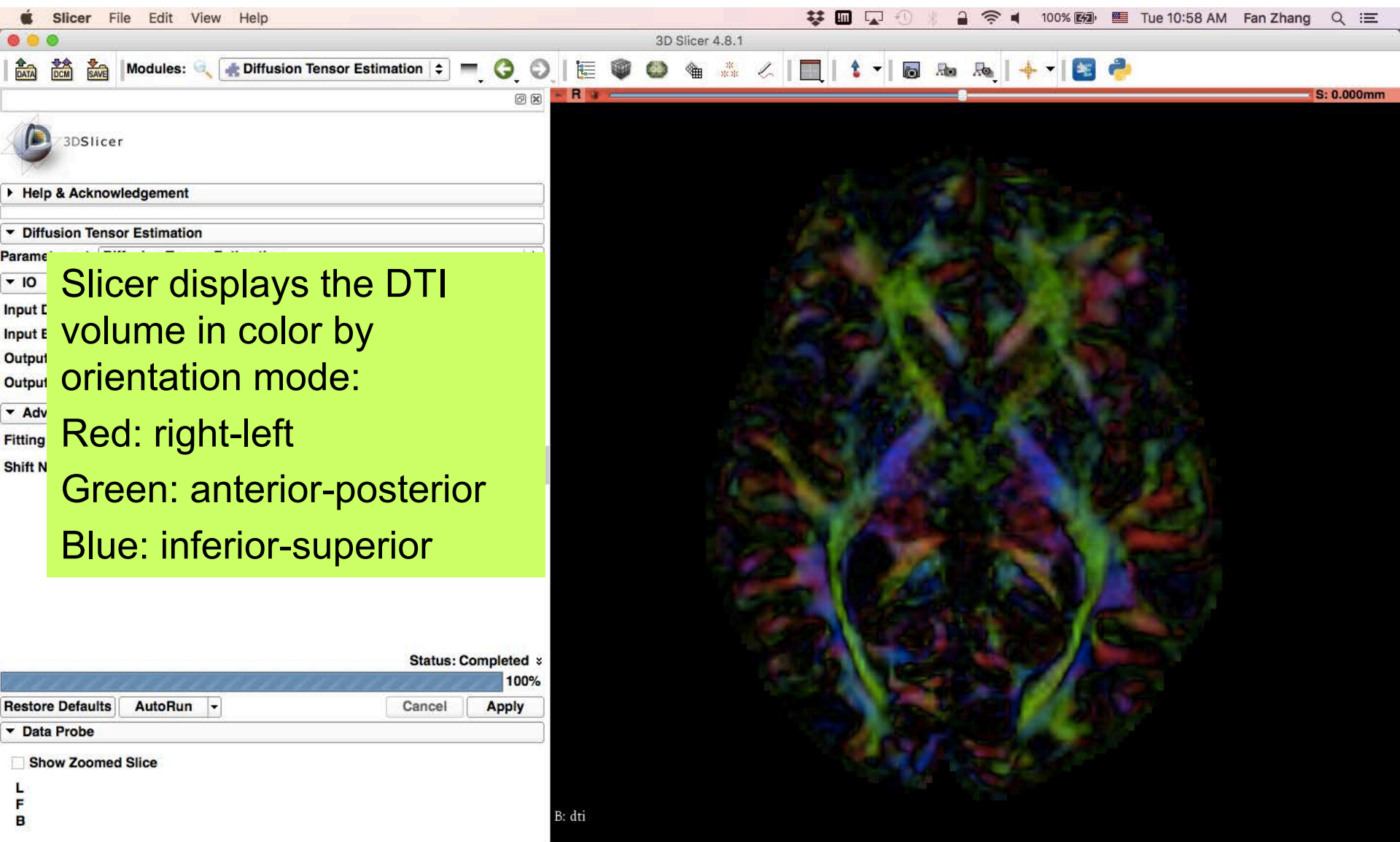
Data Probe

Show Zoomed Slice

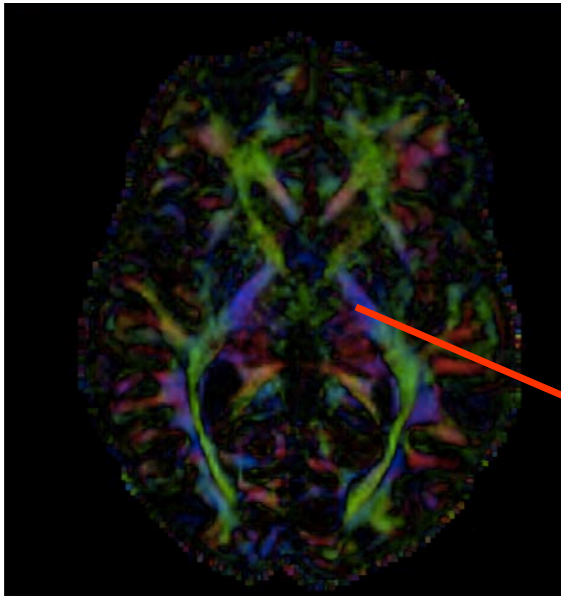
L: brain_mask (100%)
B: dti

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



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

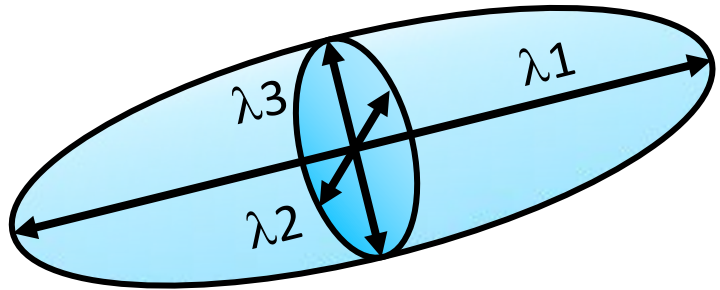
Stejskal-Tanner equation (1965)

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

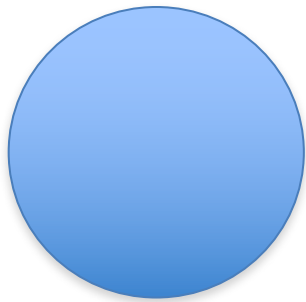
The diffusion tensor $\underline{\mathbf{D}}$ in the voxel (I,J,K) is a 3x3 symmetric matrix.

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.

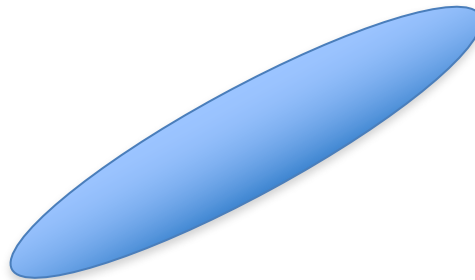


Diffusion Tensor Shape



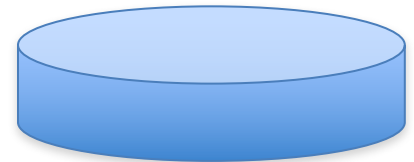
$$\lambda_1 = \lambda_2 = \lambda_3$$

Isotropic media
(Cerebrospinal
Fluid, gray matter)



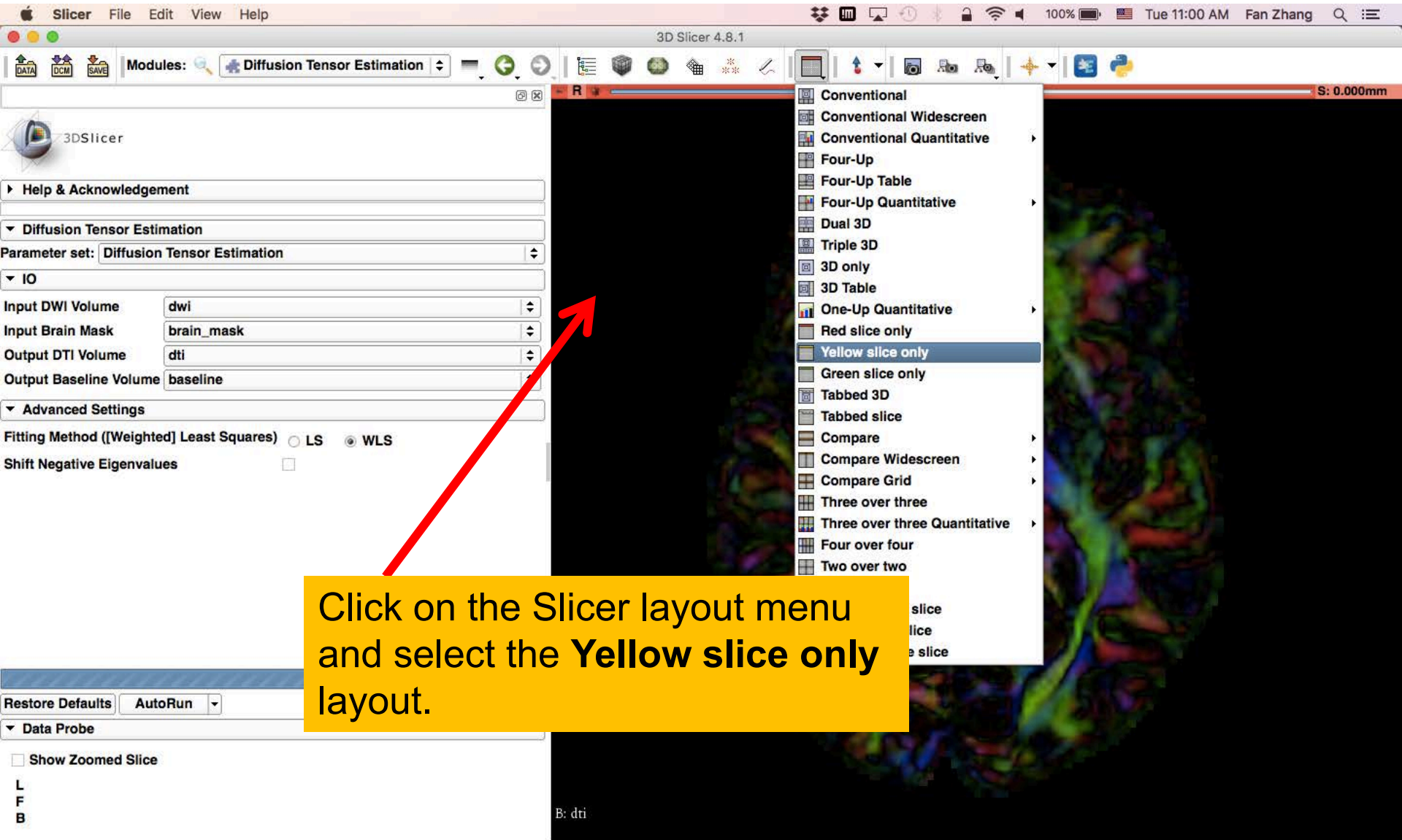
$$\lambda_1 \gg \lambda_2, \lambda_3$$

Anisotropic media
(white matter)

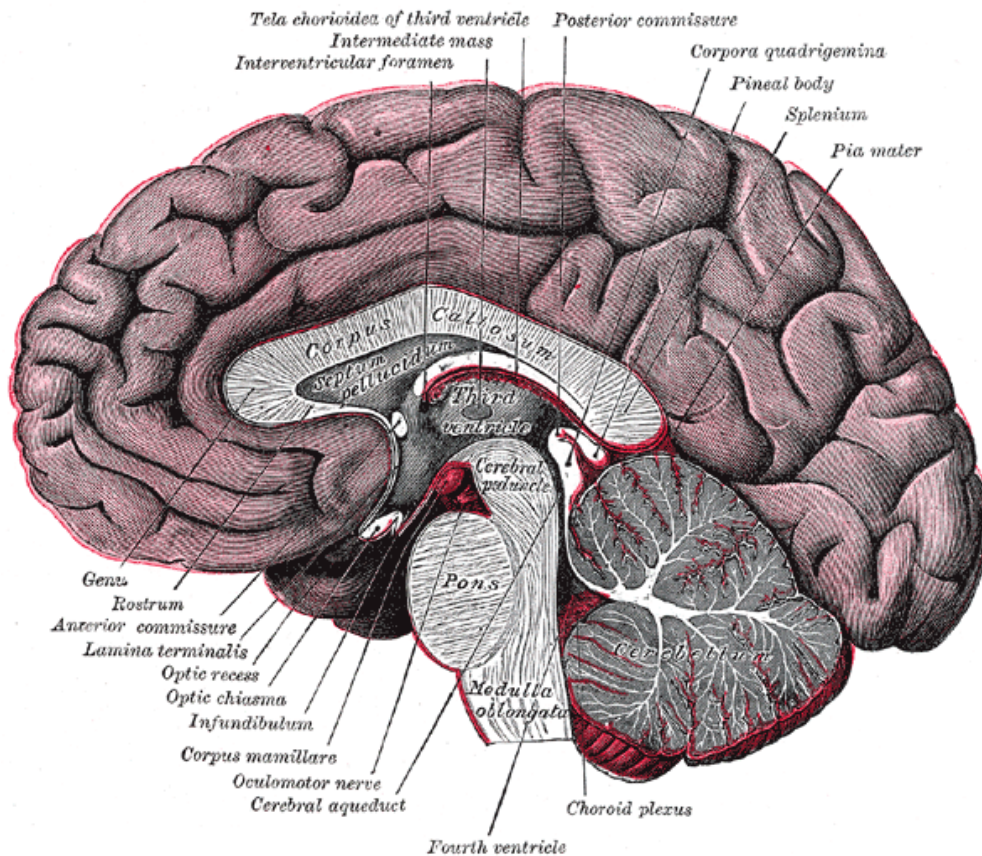


$$\lambda_1 \sim \lambda_2 \gg \lambda_3$$

Exploring the DWI Dataset



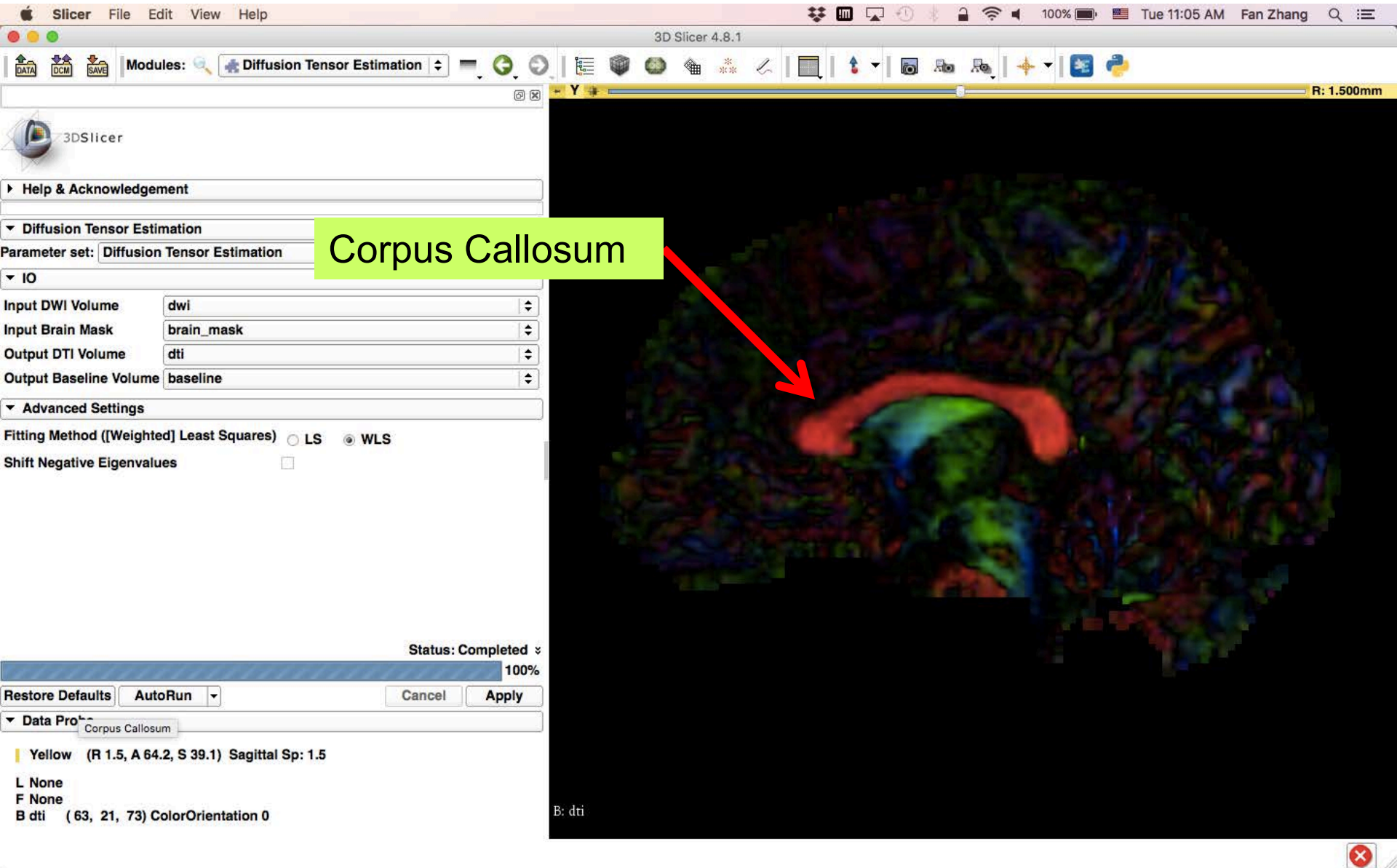
Corpus Callosum



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

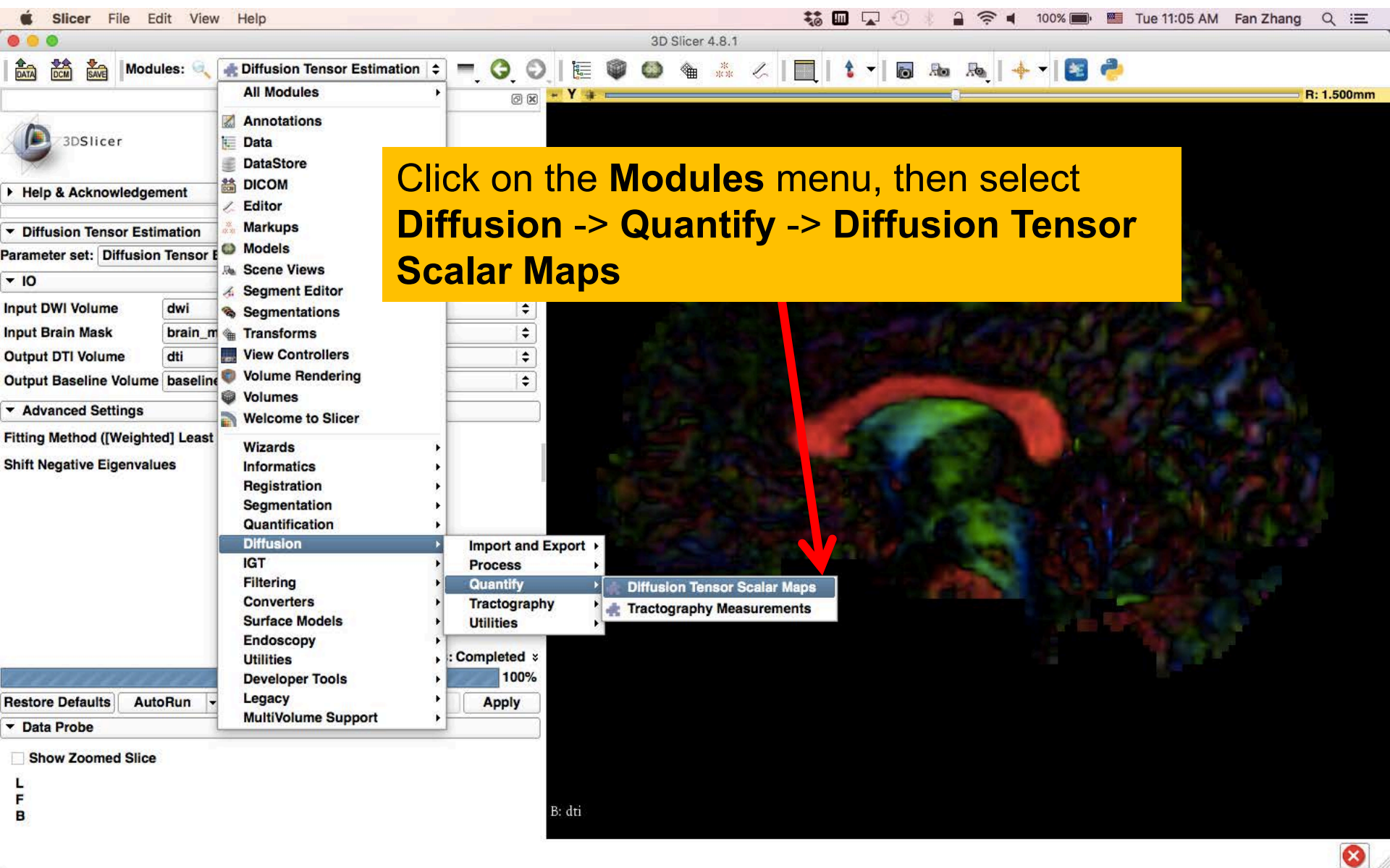


Characterizing the Size of the tensor: Trace

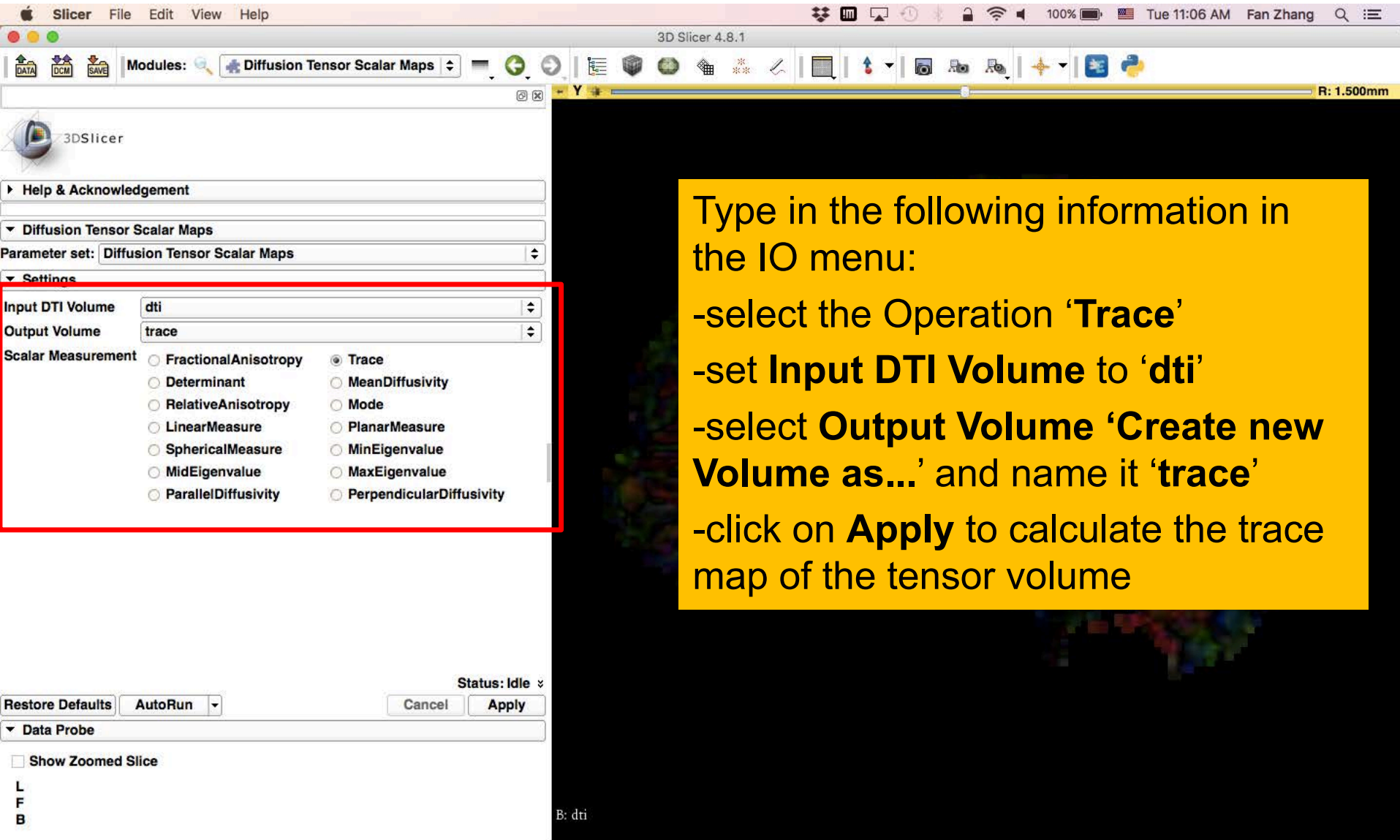
$$\text{Trace}(D) = \lambda_1 + \lambda_2 + \lambda_3$$

- $\text{Trace}(D)$ 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



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

The screenshot shows the 3D Slicer 4.8.1 interface. The 'Diffusion Tensor Scalar Maps' module is active. The 'Settings' panel on the left shows 'Input DTI Volume' set to 'dti', 'Output Volume' set to 'trace', and 'Scalar Measurement' set to 'Trace'. A red arrow points from a yellow box labeled 'Set L as none.' to the 'None' dropdown in the 'Sagittal' view. The 'trace' image is visible in the yellow viewer. A green box at the bottom left states 'The trace image appears in the yellow viewer'. The status bar at the bottom indicates 'Status: Completed' and '100%'. The 'Data Probe' section shows 'Show Zoomed Slice' is unchecked. The 'L', 'F', and 'B' buttons are visible at the bottom left.

Set L as none.

The trace image appears in the yellow viewer

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

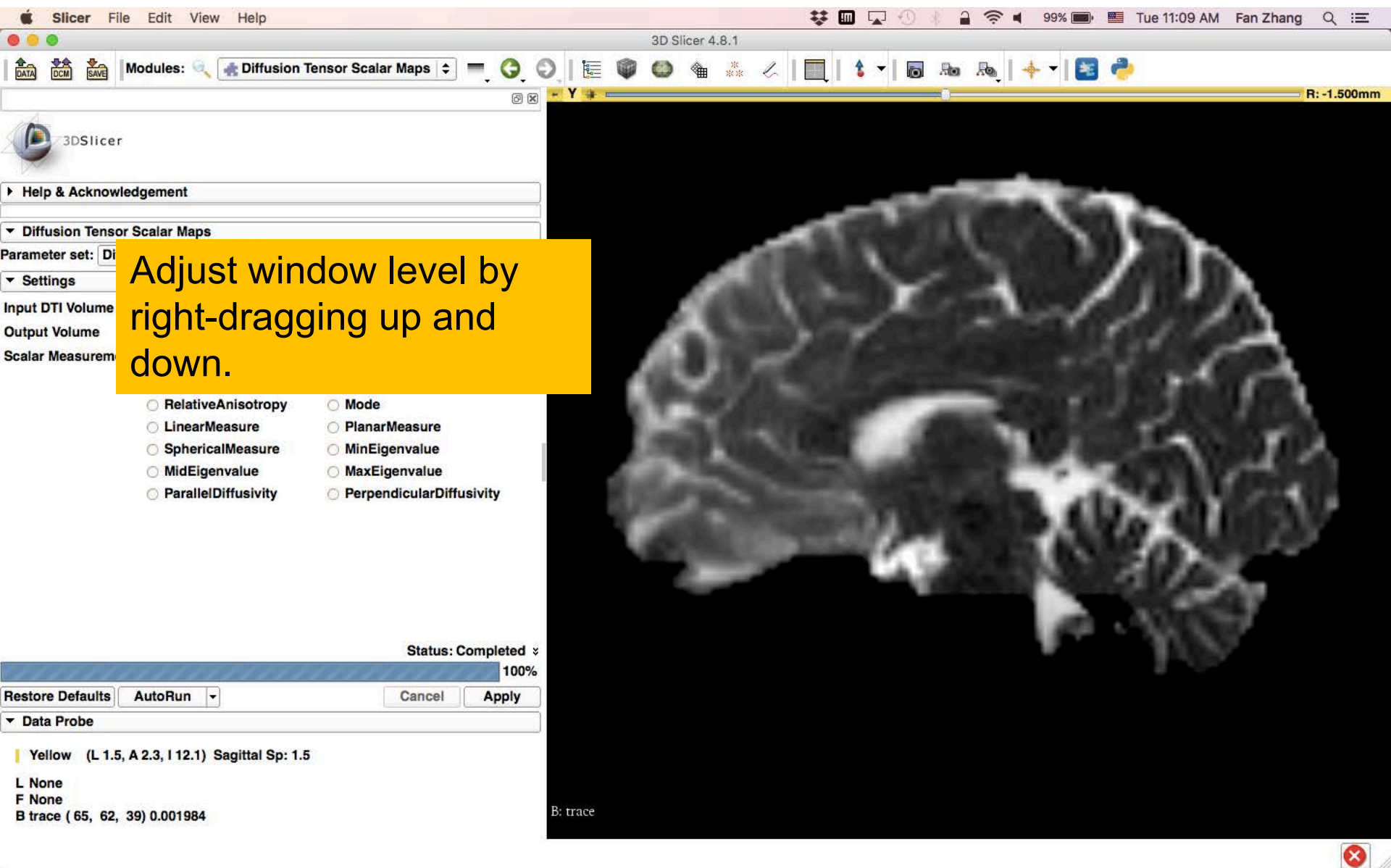
Data Probe

Show Zoomed Slice

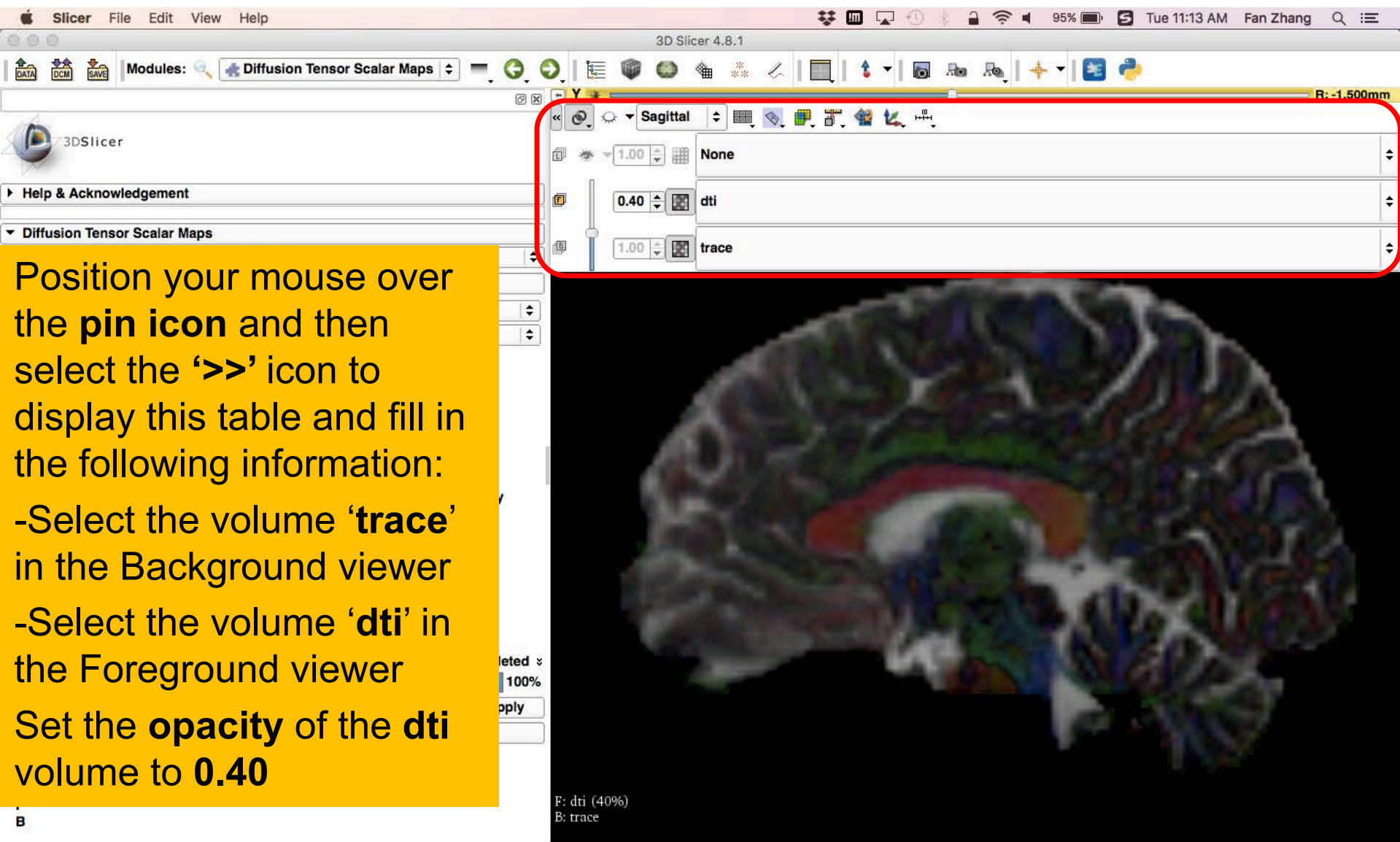
L
F
B

B: trace

Trace



Trace



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

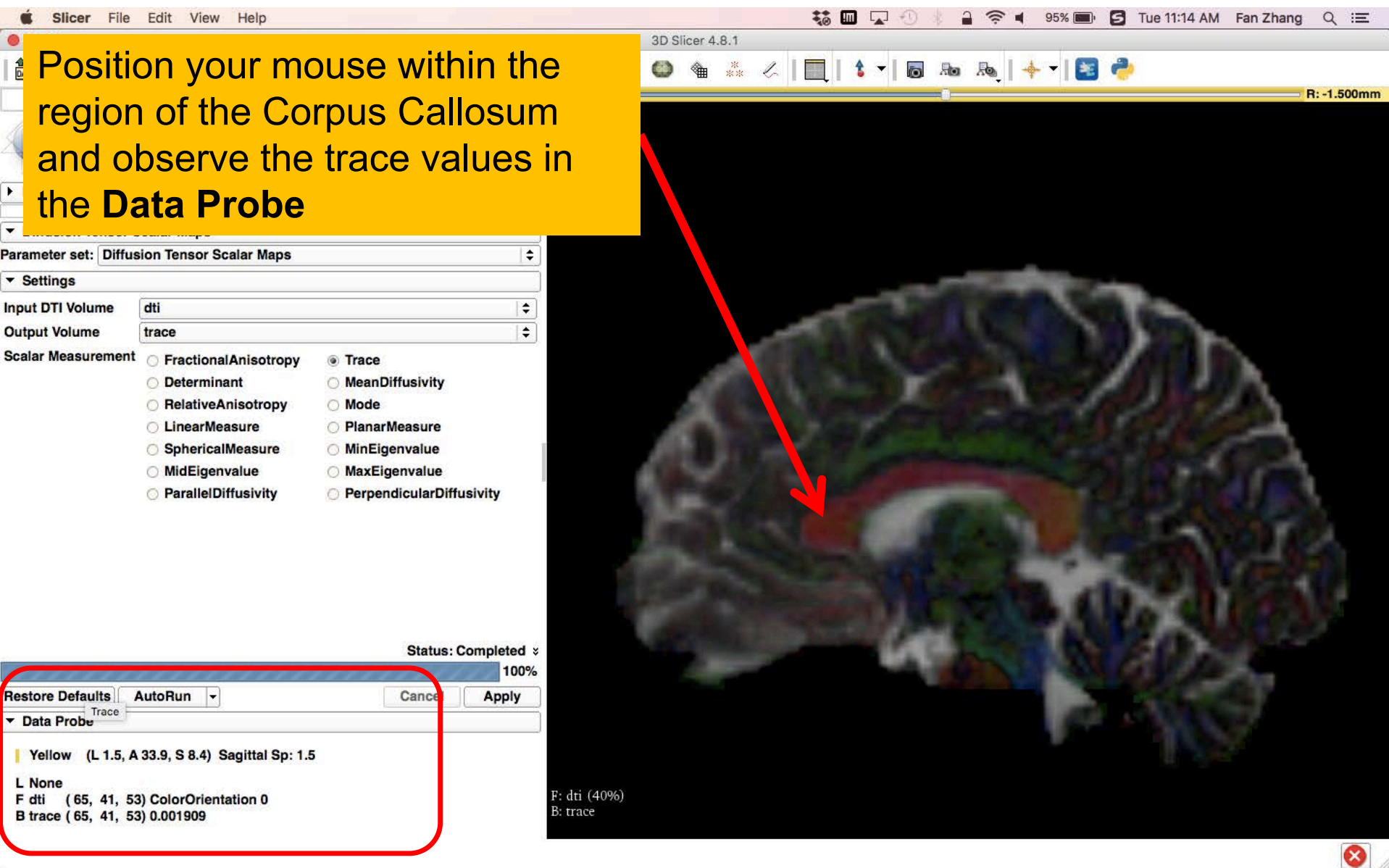
- Select the volume '**trace**' in the Background viewer
- Select the volume '**dti**' in the Foreground viewer

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

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.

3D Slicer 4.8.1

Modules: Diffusion Tensor Scalar Maps

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%)

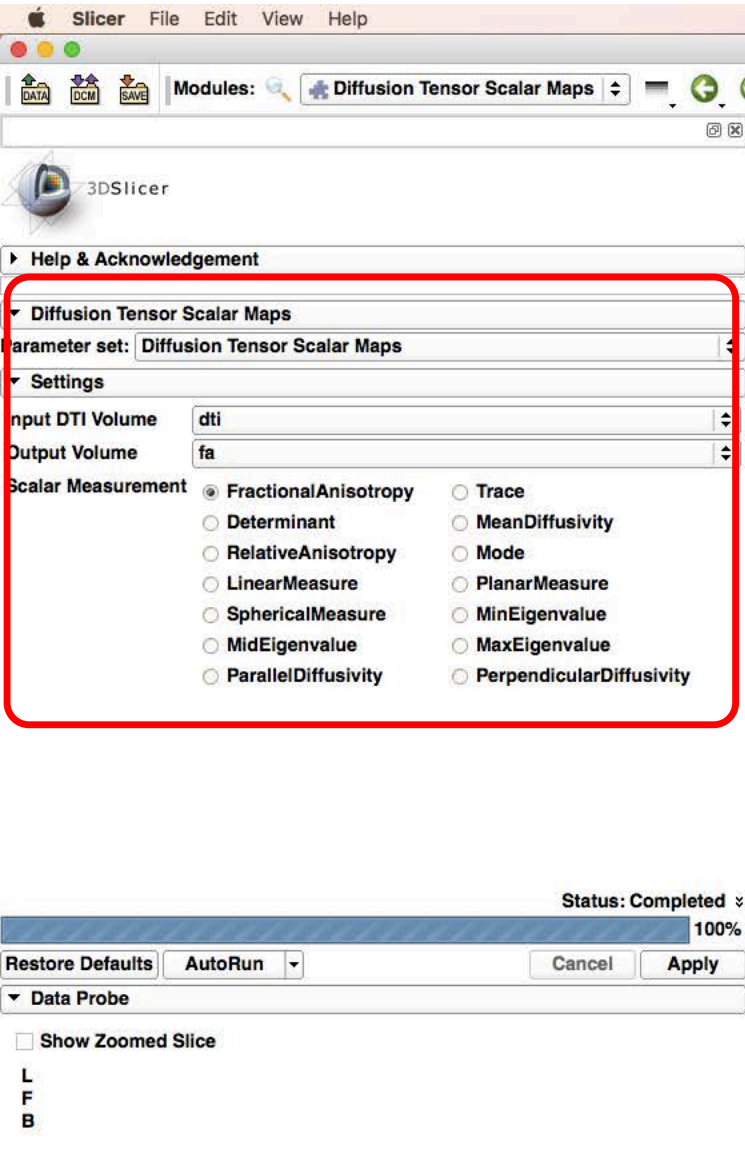
B: trace

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



The screenshot shows the 3D Slicer 4.8.1 interface. The 'Diffusion Tensor Scalar Maps' module is selected in the 'Modules' panel. The 'Settings' section is expanded, showing the following configuration:

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

The 'Status: Completed' bar is at 100%. The 'Data Probe' section is visible at the bottom left, showing 'L', 'F', and 'B' views. The 'Apply' button is highlighted.

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

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

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

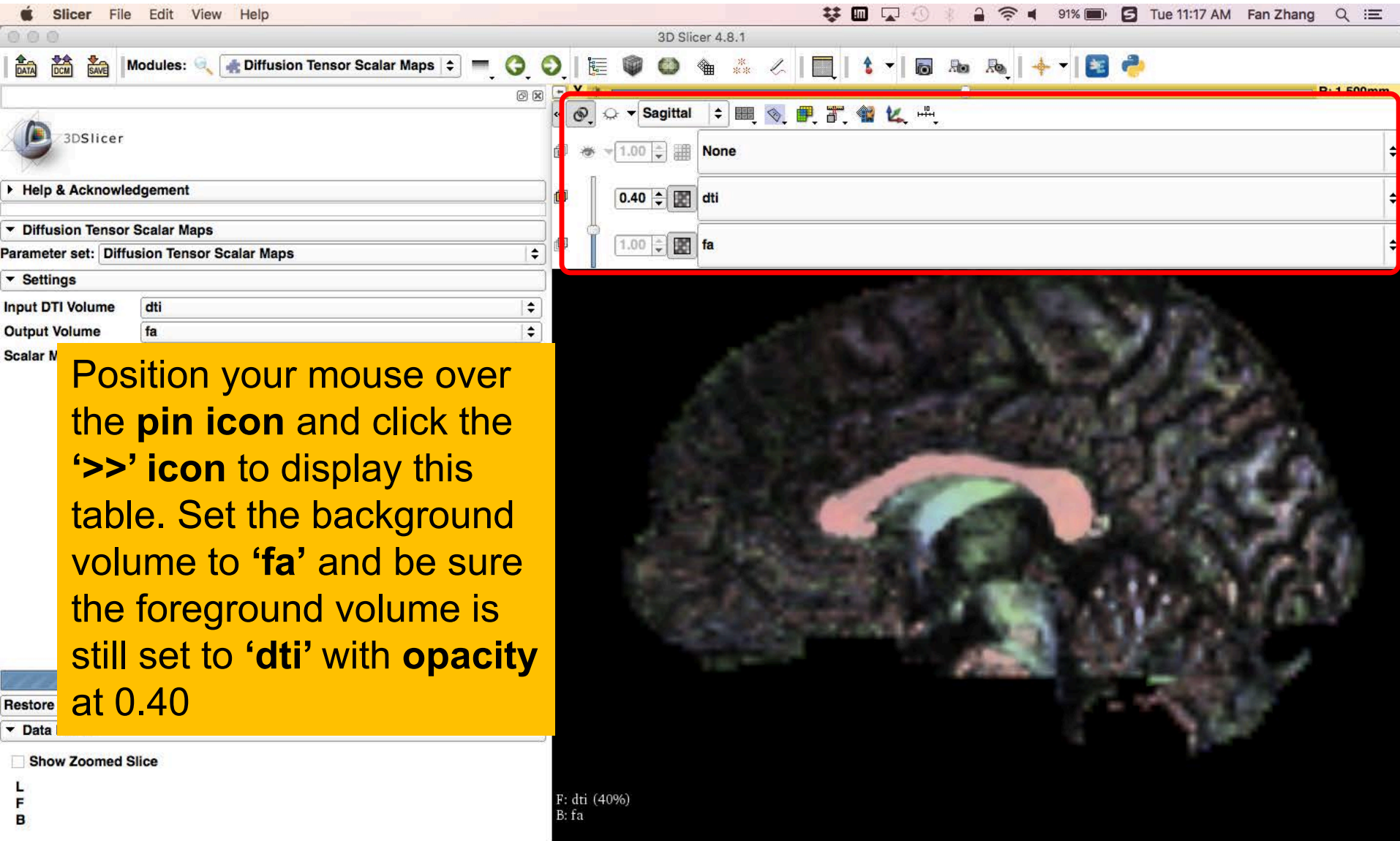
Sagittal

None
None
fa

R: 1.500mm

B: 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 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

3D Slicer 4.8.1

Modules: Diffusion Tensor Scalar Maps

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

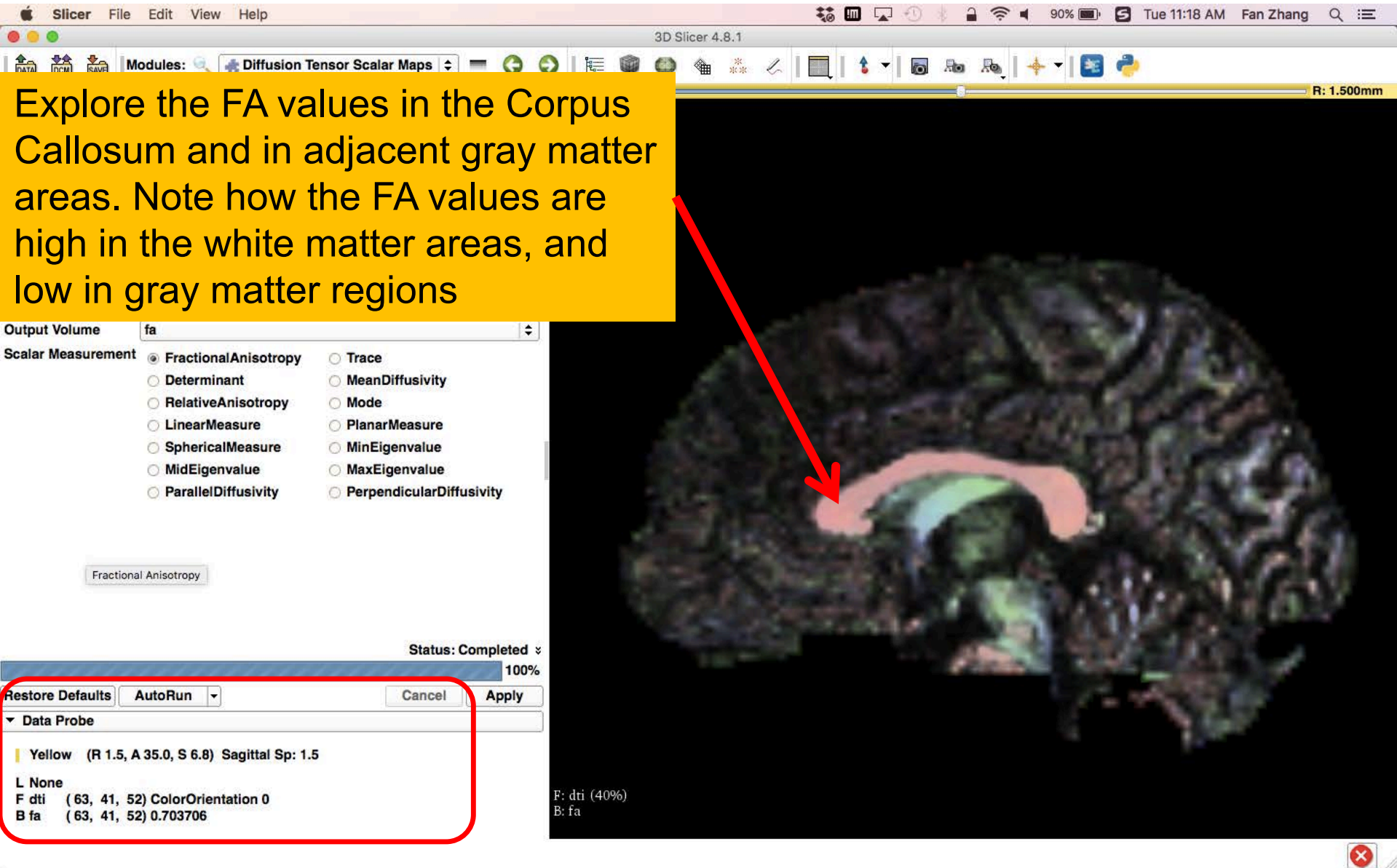
L None

F dti (63, 41, 52) ColorOrientation 0

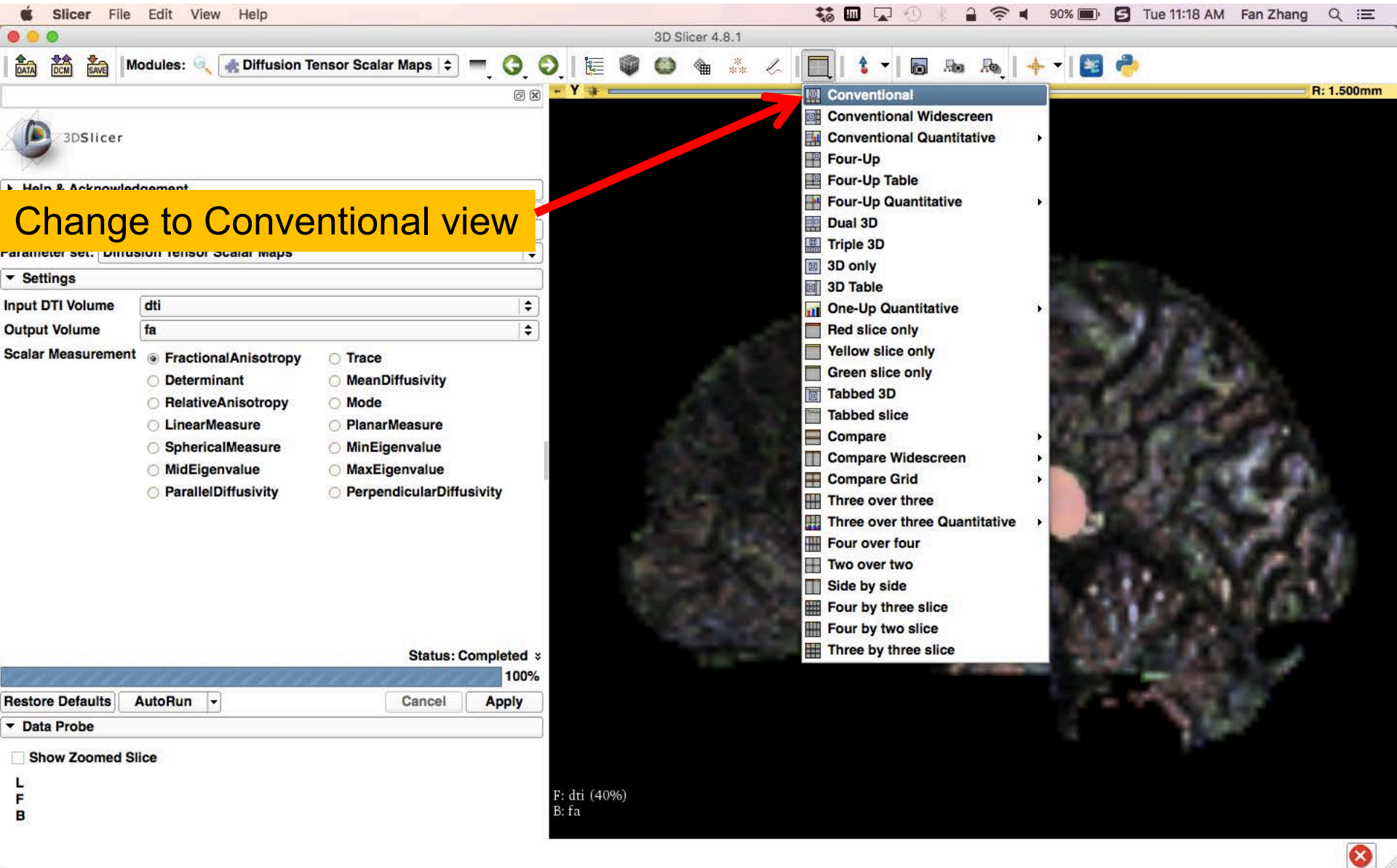
B fa (63, 41, 52) 0.703706

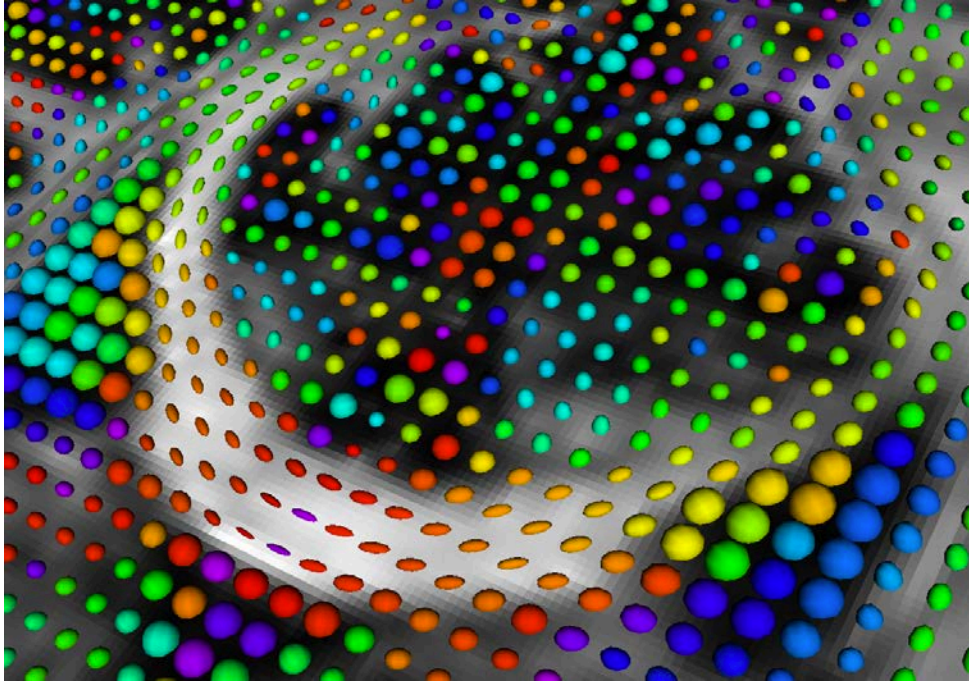
F: dti (40%)

B: fa



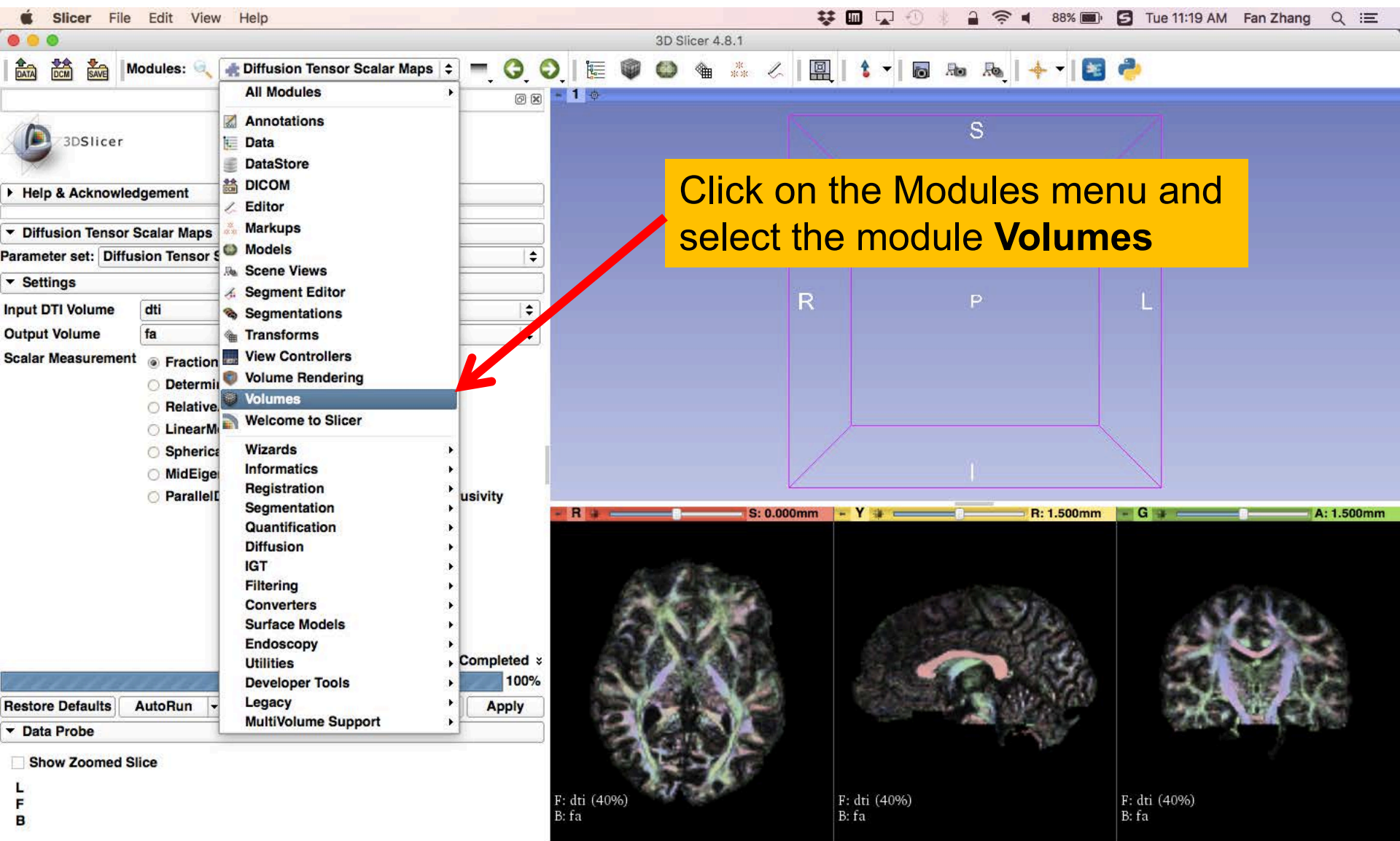
Fractional Anisotropy





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 File, Edit, View, and Help. The top toolbar contains various icons for file operations and viewing. The left sidebar shows the 'Modules' panel with 'Volumes' selected. Below it, the '3DSlicer' logo and 'Help & Acknowledgement' link are visible. The 'Active Volume' is set to 'trace'. The 'Volume Information' panel is empty. The 'Display' panel shows the 'Lookup Table' set to 'Grey', 'Interpolate' checked, and 'Window/Level' set to 'W: 0.0076' and 'L: 0.0050'. The 'Threshold' is set to 'Off' with a range from -0.0025 to 0.0108. The 'Data Probe' panel is at the bottom left, with 'Show Zoomed Slice' unchecked. The main 3D view shows a brain slice. A yellow text box is overlaid on the 3D view, containing the following text:

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

The bottom right of the interface shows a 3D visualization of brain data. The 'Axial' slice is selected. The 'Foreground' is set to 'fa' and the 'Background' is set to 'dti'. The 'Opacity' is set to 1.00. The 'F: fa (100%)' and 'B: dti' labels are visible in the bottom right corner of the 3D view.

3D Visualization: Glyphs

3D Slicer 4.8.1

Modules: Volumes

Active Volume: dti

Volume Information

Display

Scalar Display

Scalar Mode: ColorOrientation

Lookup Table:

Interpolate: ☒

Window/Level:

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

S

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

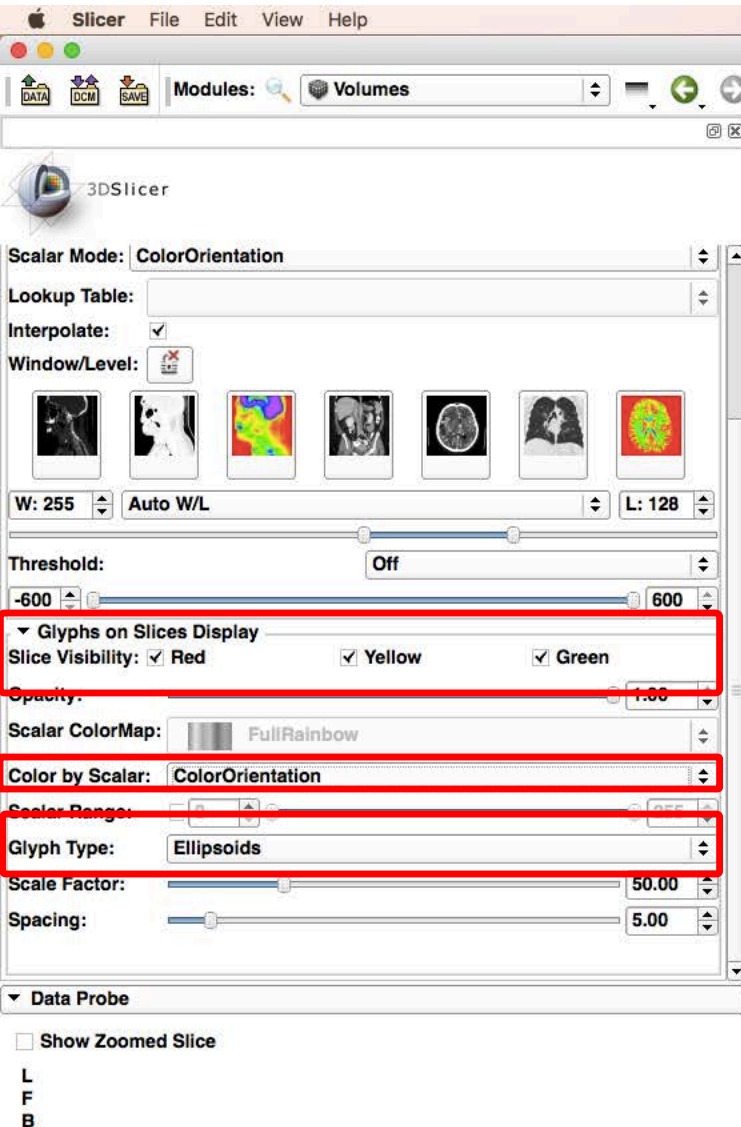
F: fa (100%)
B: dti

F: fa (100%)
B: dti

F: fa (100%)
B: dti

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

3D Visualization: Glyphs

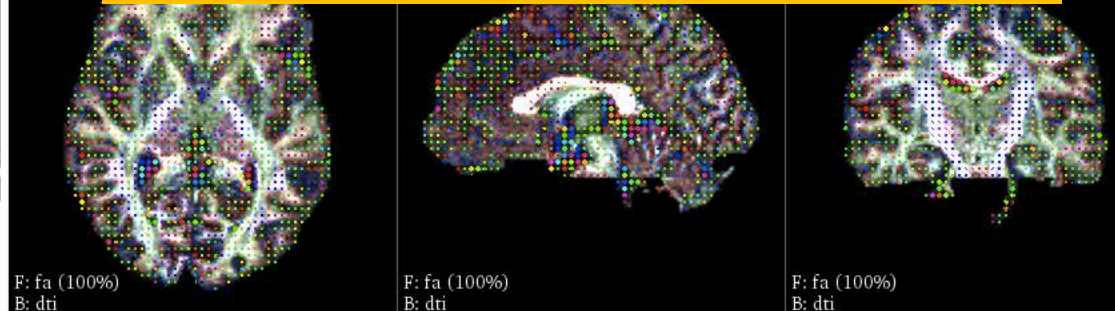


Scroll down the module panel and in the **Glyphs on Slices Display** section:

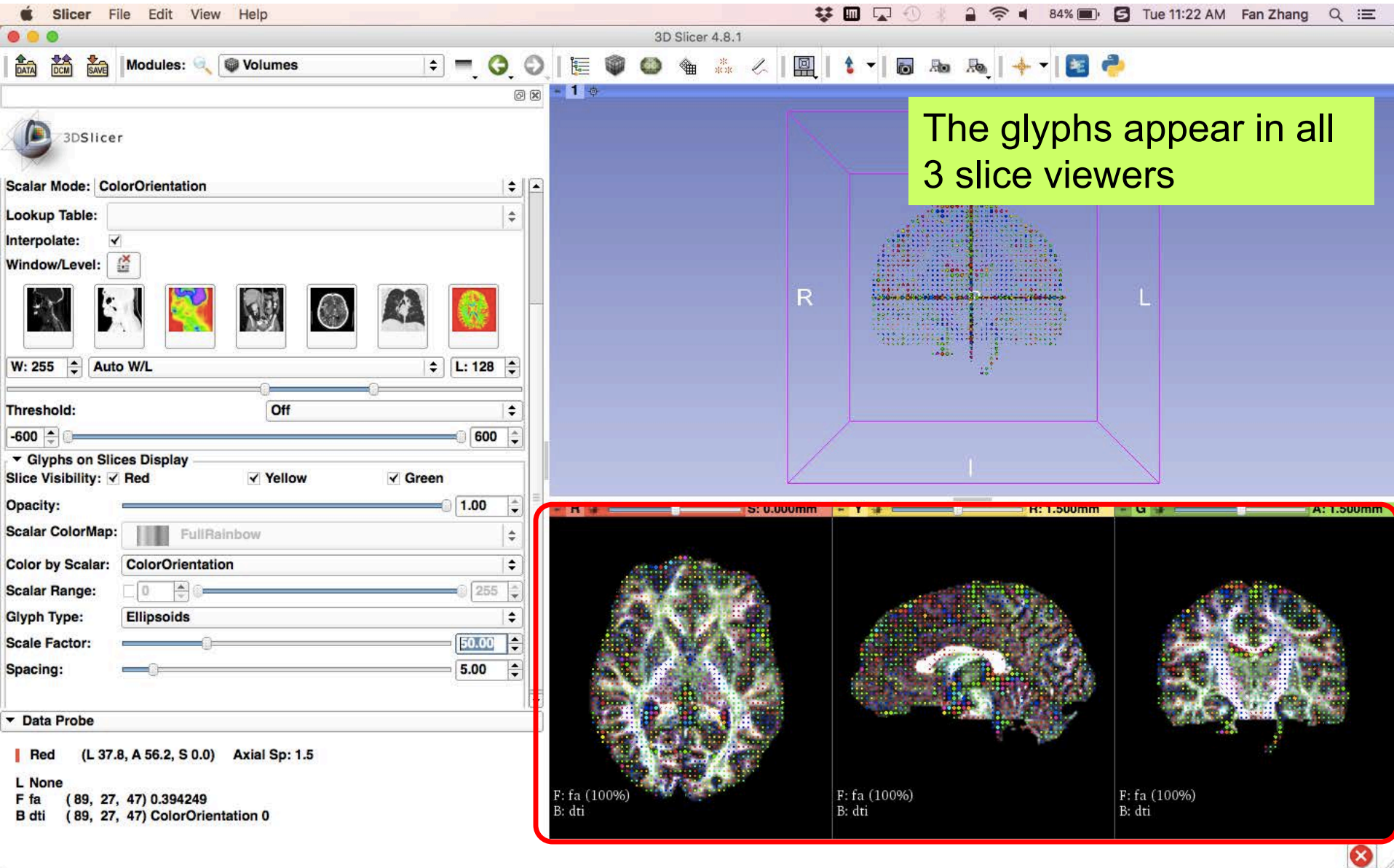
- Check off the option for **Red, Yellow, and Green Slice Visibility**

- Set the **Color by Scalar** parameter to '**ColorOrientation**'

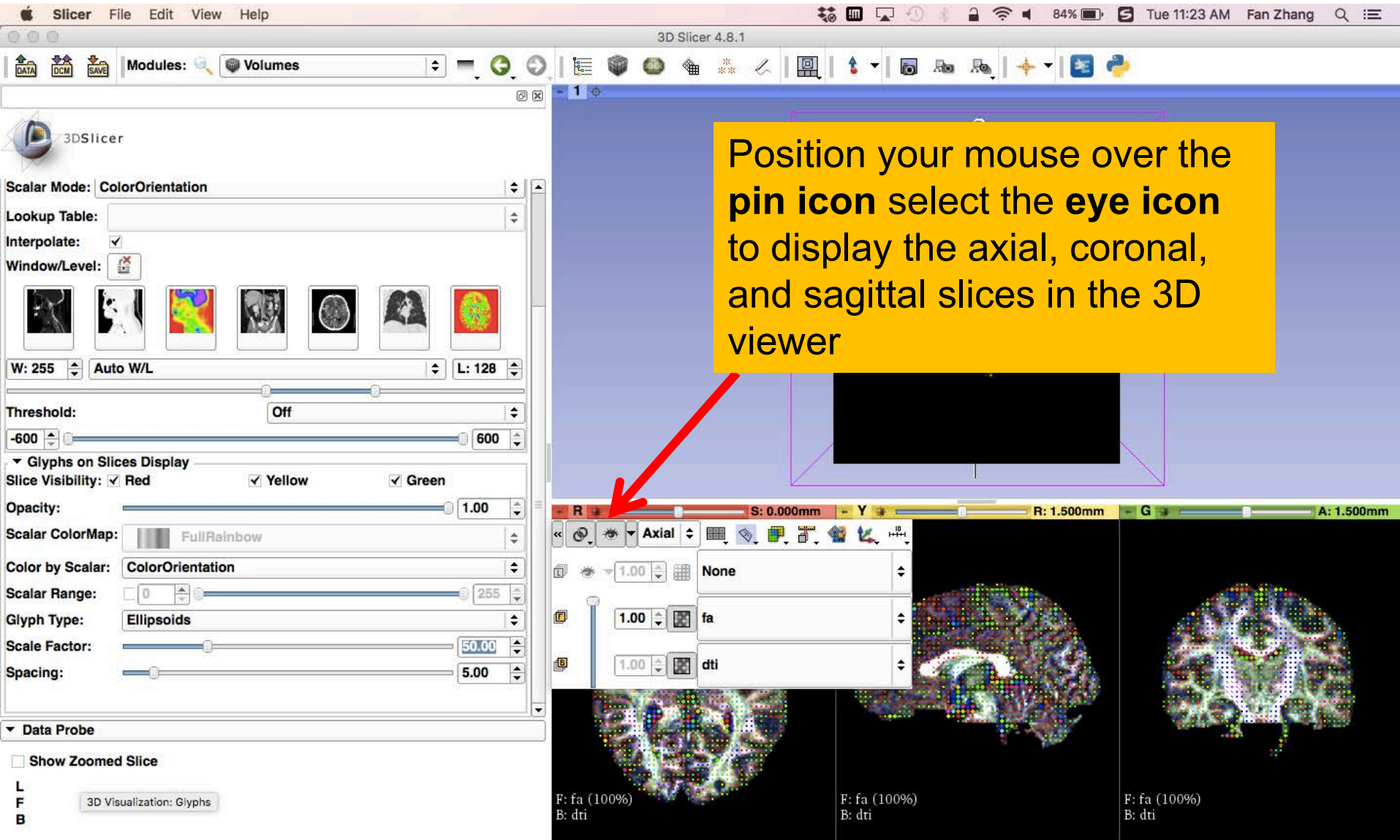
- Set the **Glyph Type** to '**Ellipsoids**'



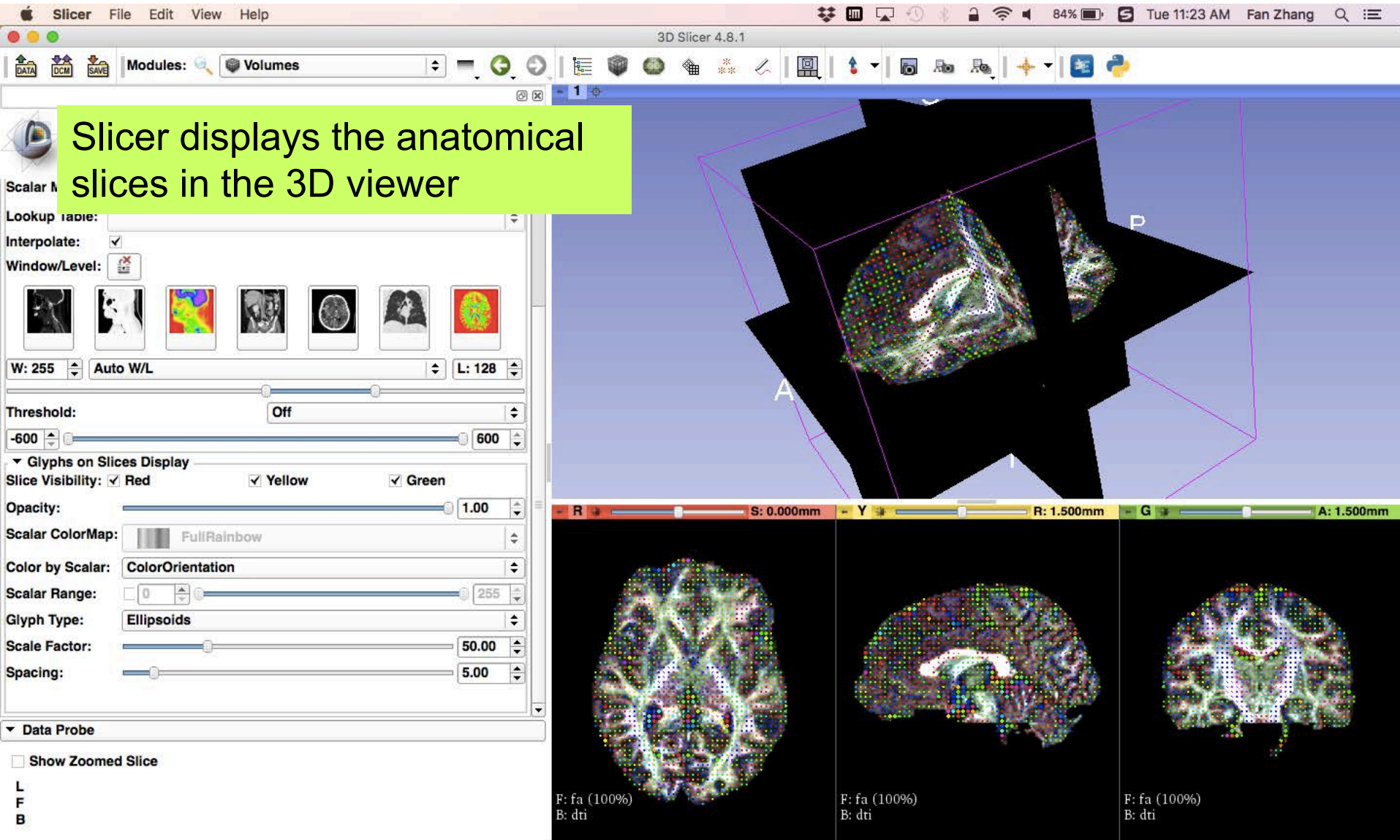
3D Visualization: Glyphs



3D Visualization: Glyphs



3D Visualization: Glyphs



3D Visualization: Glyphs

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

The screenshot displays the 3D Slicer 4.8.1 interface. The main 3D view shows a volume with a grid of colorful ellipsoids representing the principal direction of diffusion. 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 zoomed slices: Axial (A), Sagittal (S), and Coronal (C). The 'Data Probe' panel also shows the 'Glyphs on Slices Display' settings, including 'Slice Visibility' (Red, Yellow, Green), 'Opacity' (1.00), 'Scalar ColorMap' (FullRainbow), 'Color by Scalar' (ColorOrientation), 'Scalar Range' (0 to 255), 'Glyph Type' (Ellipsoids), 'Scale Factor' (50), and 'Spacing' (5.00).

W: 255 Auto W/L L: 128

Threshold: Off

-600 600

▼ Glyphs on Slices Display

Slide 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

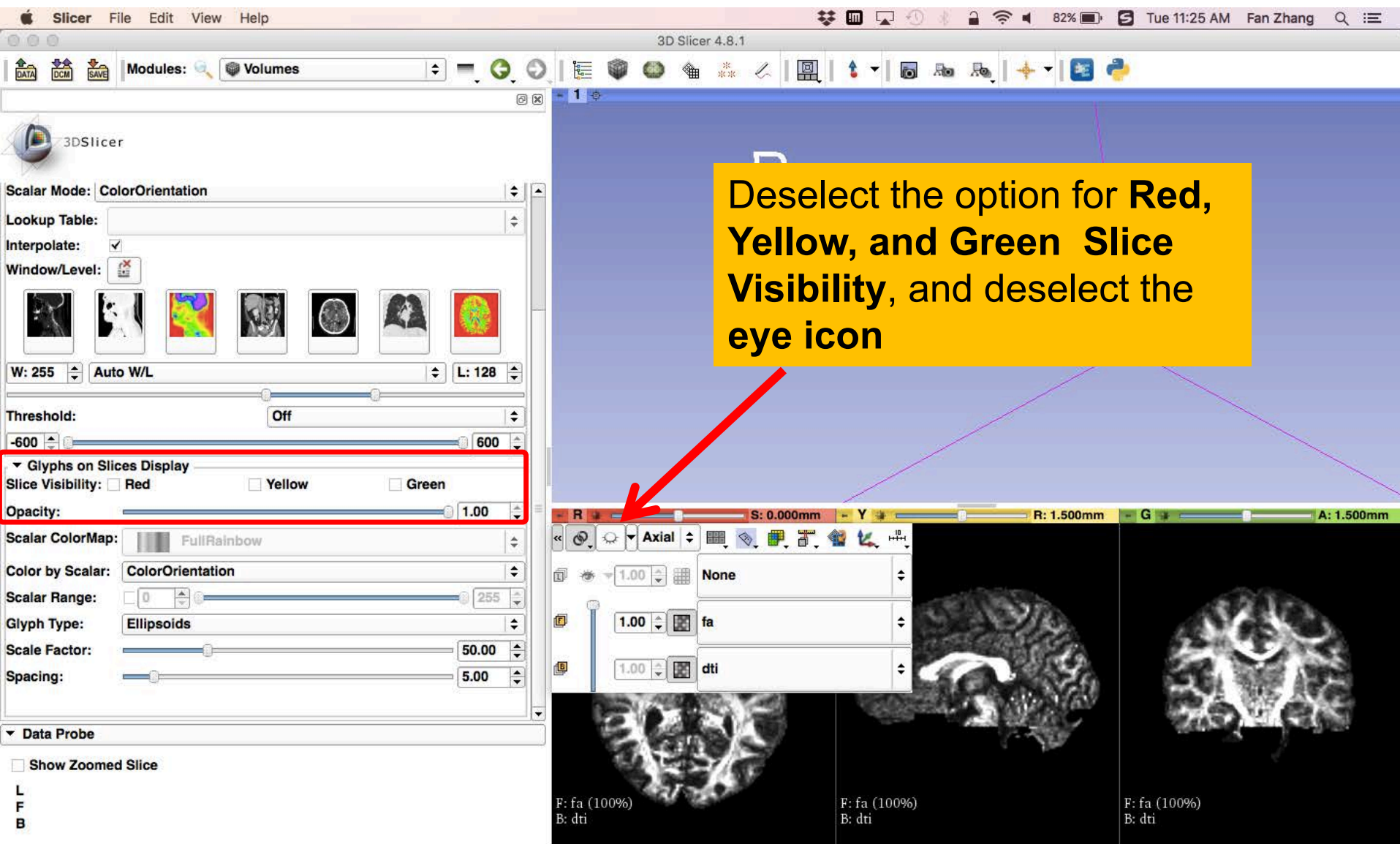
R S: 0.000mm Y R: 1.500mm G A: 1.500mm

F: fa (100%)
B: dti

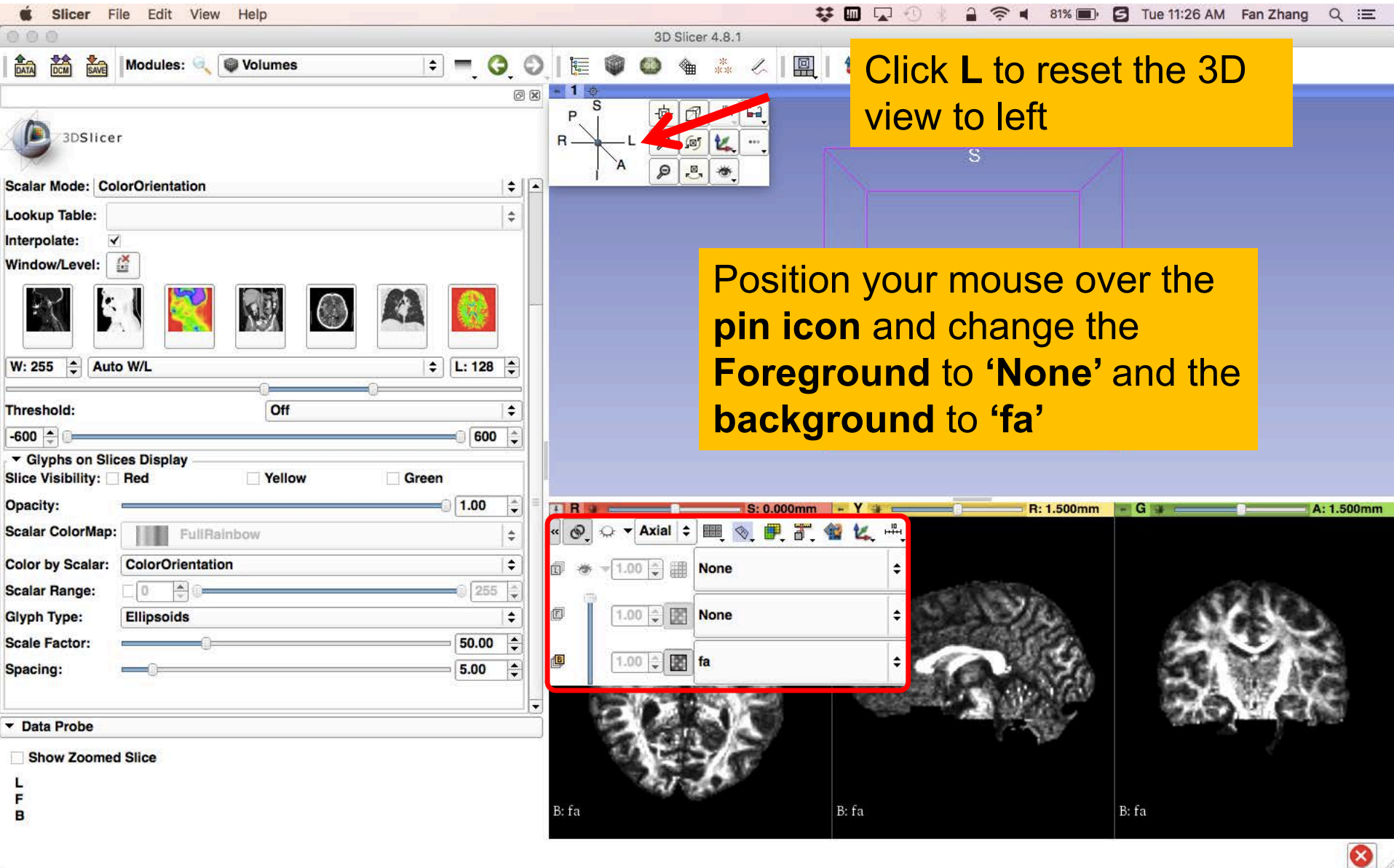
F: fa (100%)
B: dti

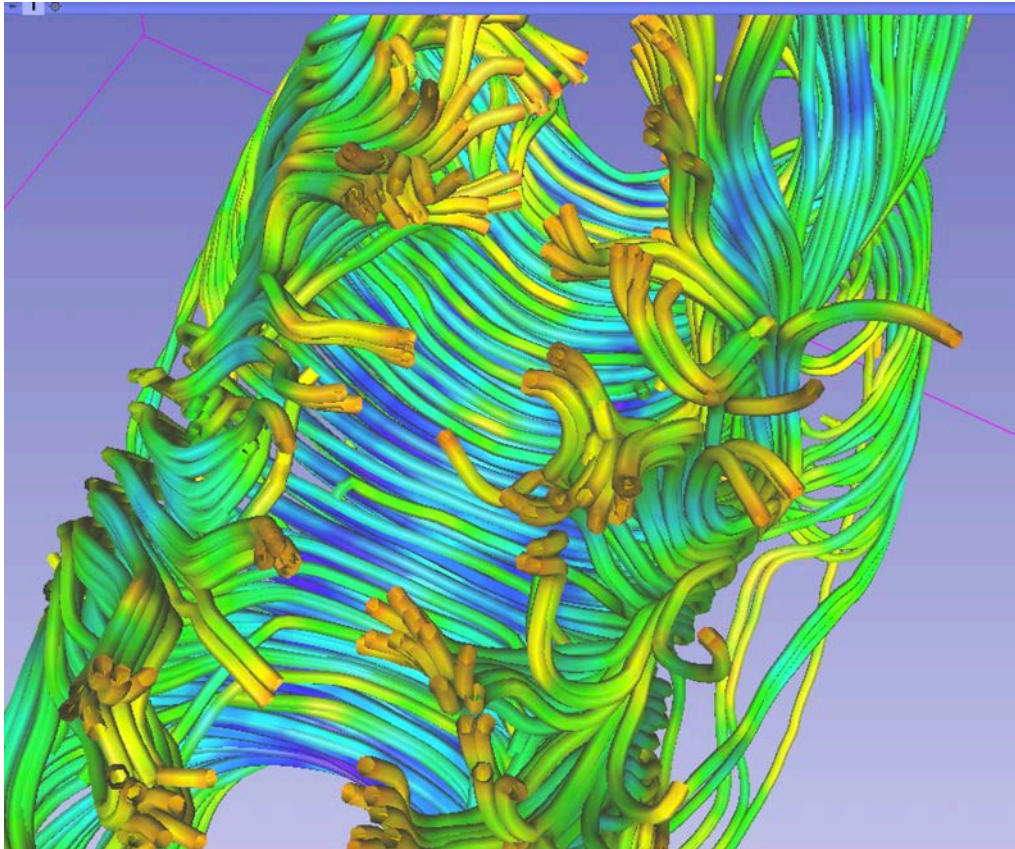
F: fa (100%)
B: dti

Diffusion MRI tractography



Diffusion MRI tractography



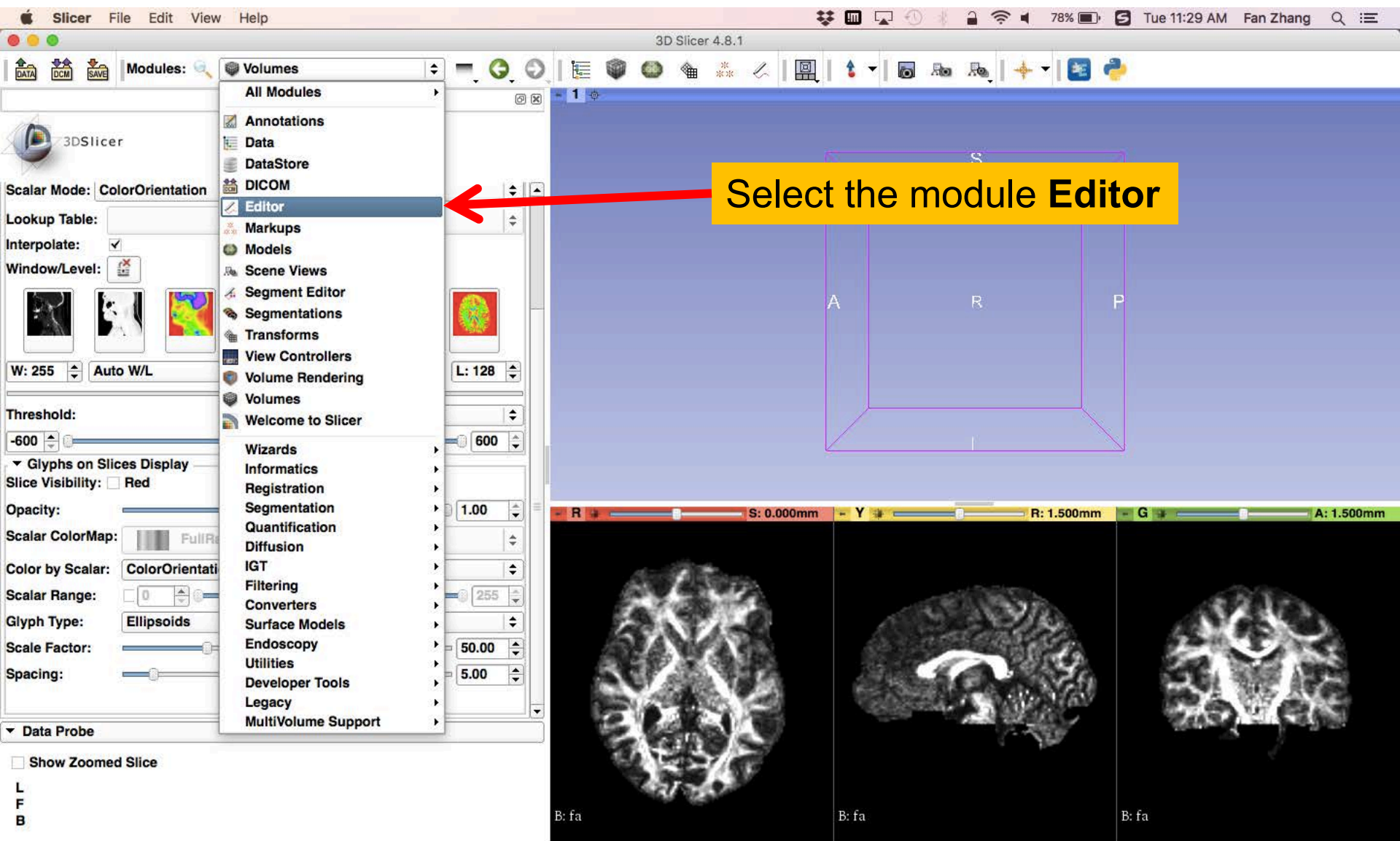


Part 3: From tensors to tracts

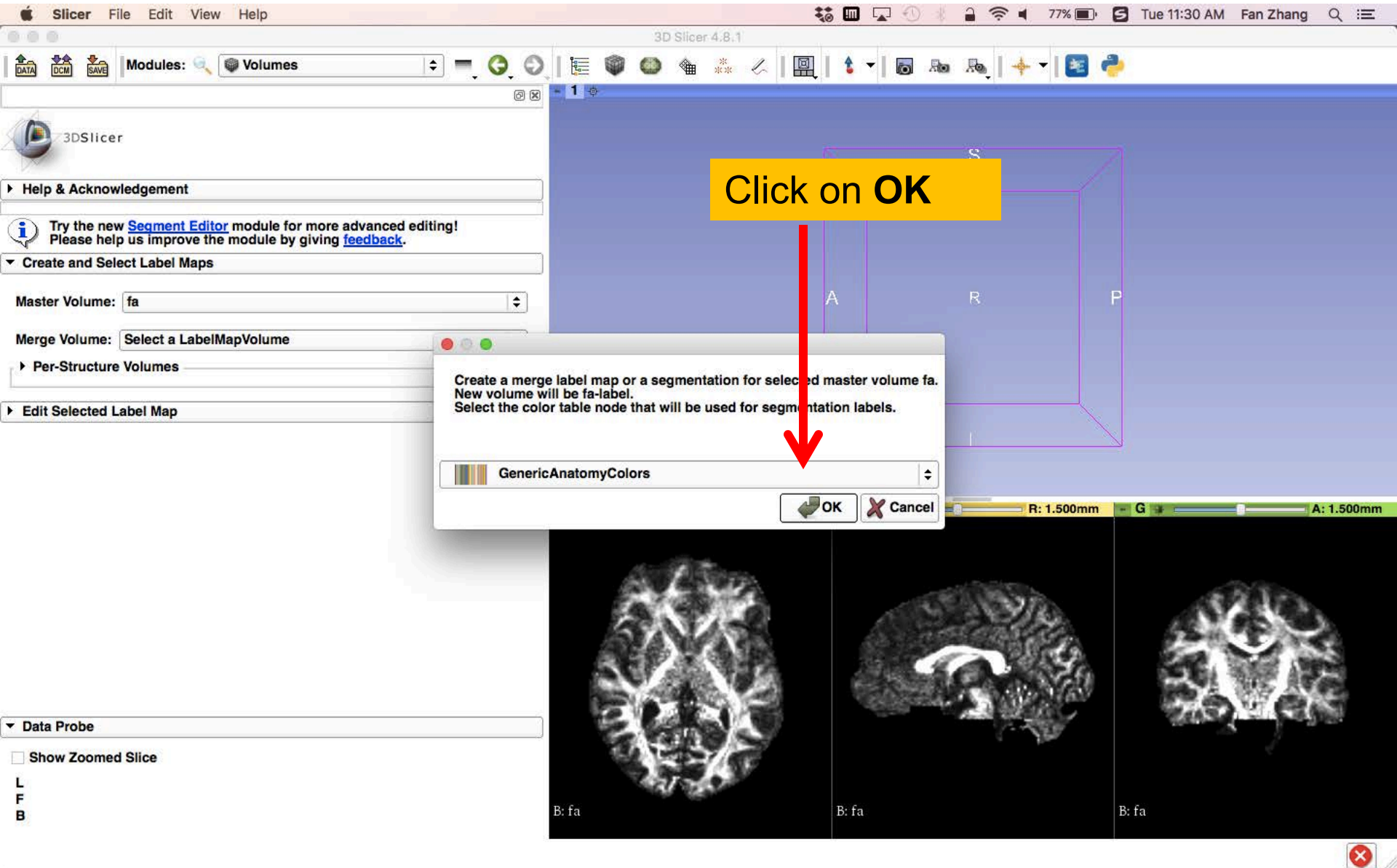
DTI tractography

- 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)

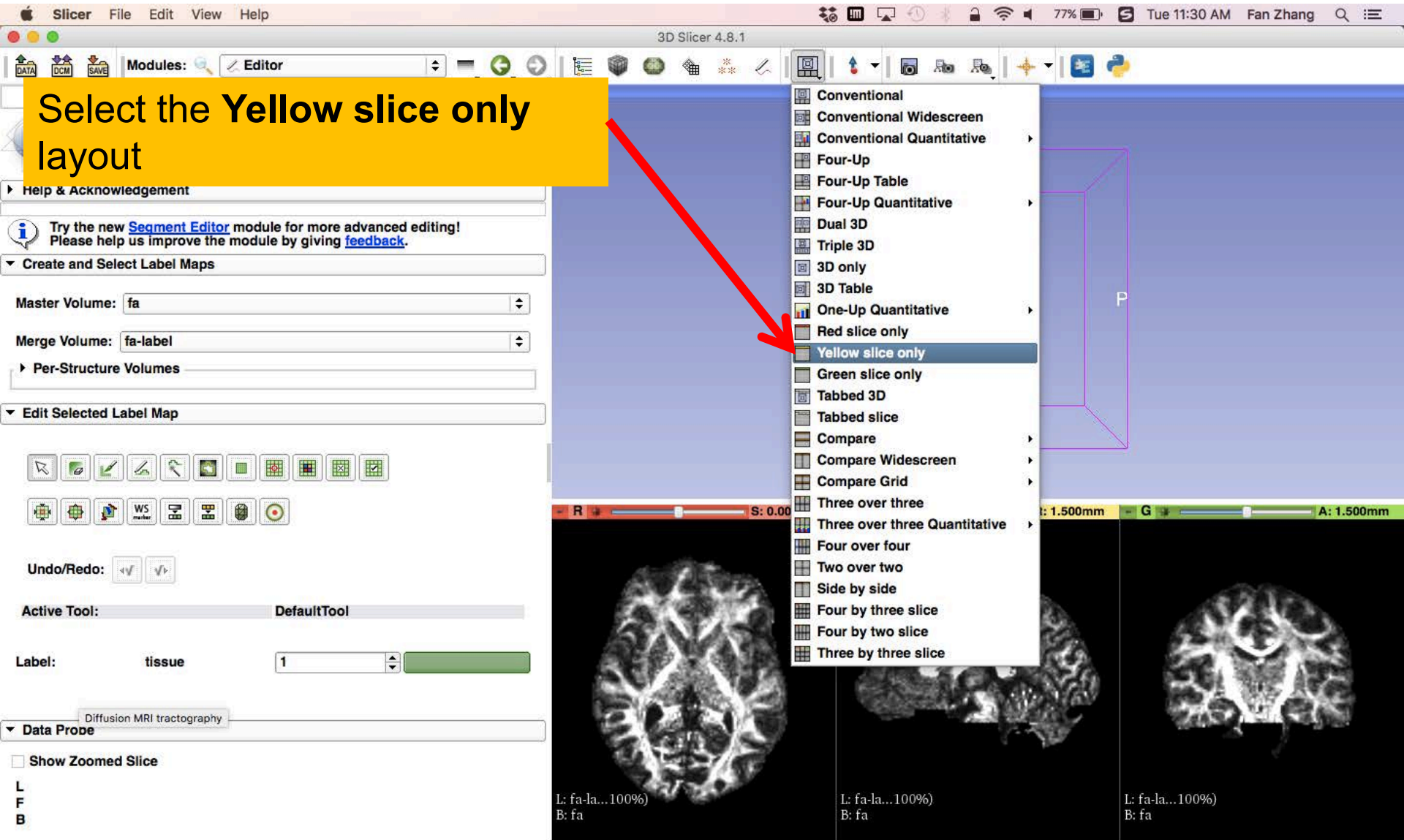
Diffusion MRI tractography



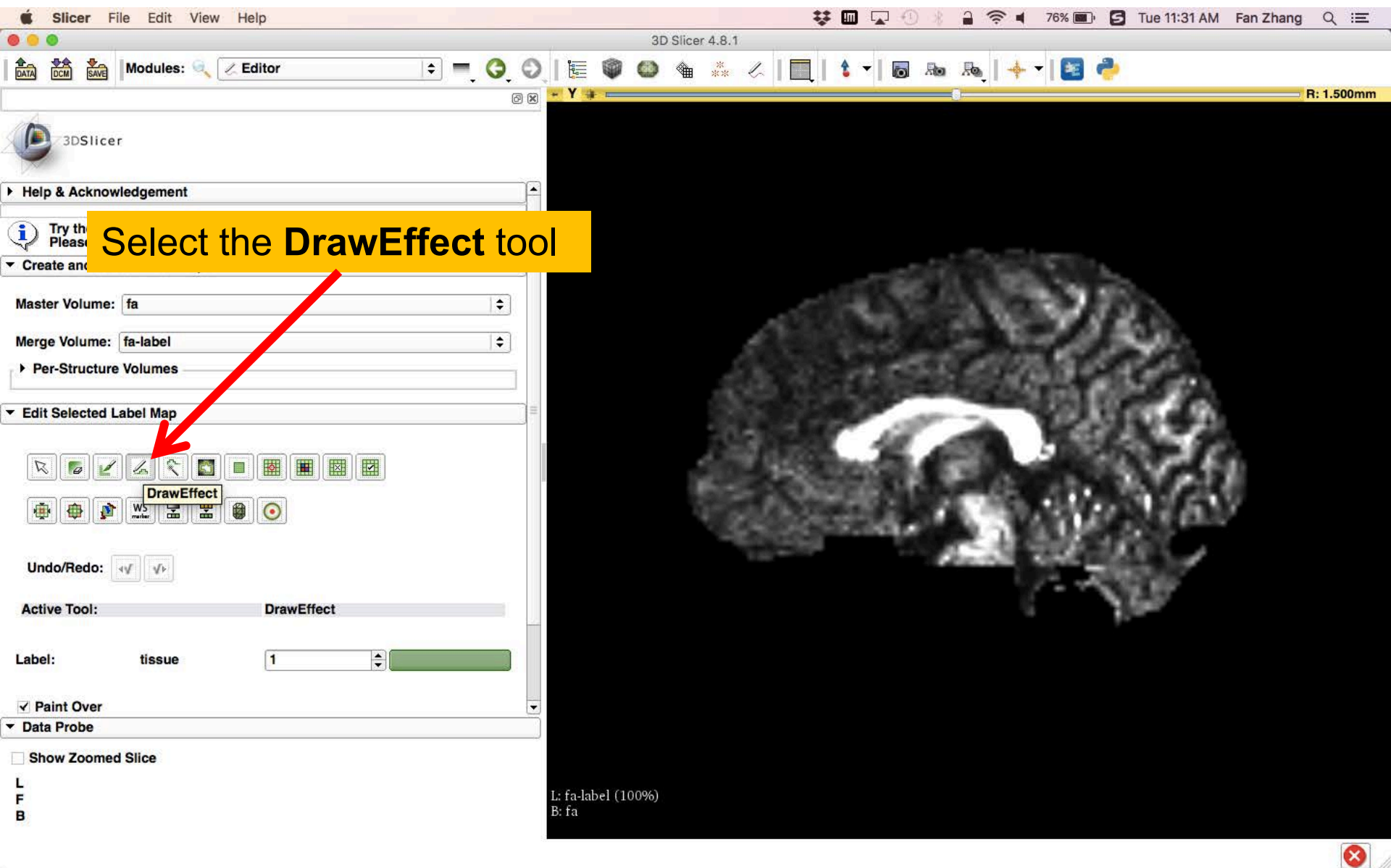
Diffusion MRI tractography



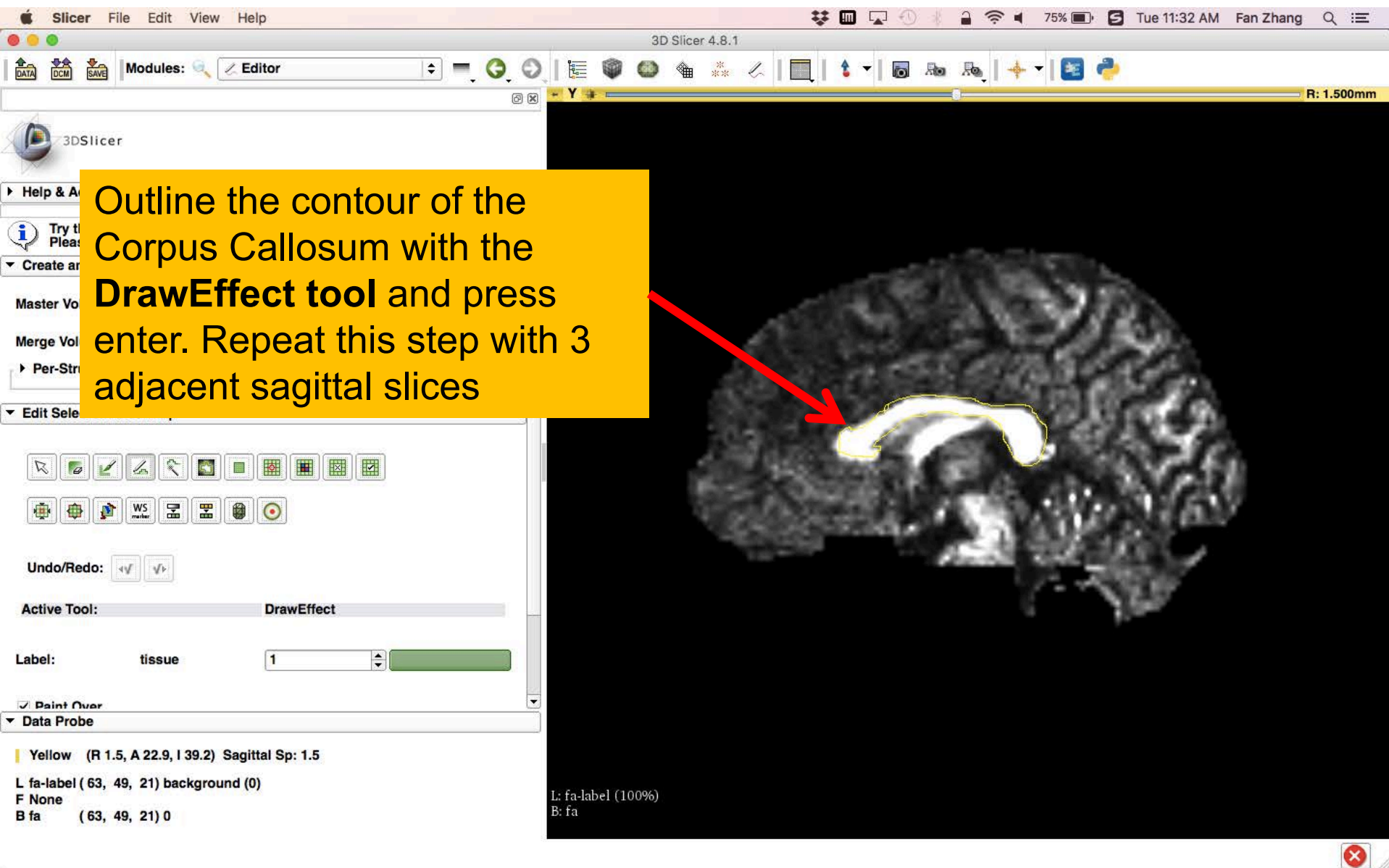
Diffusion MRI tractography



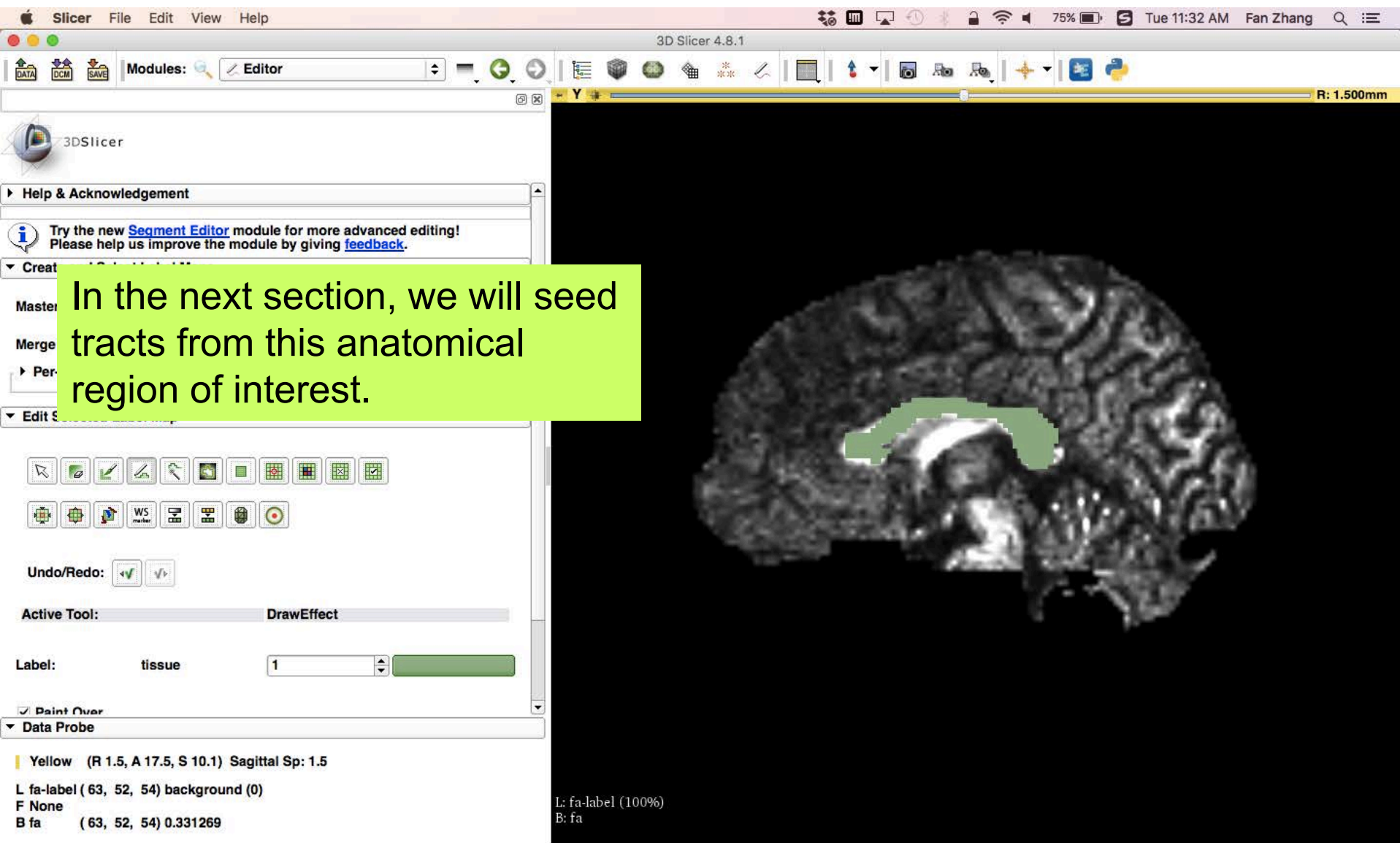
Diffusion MRI tractography



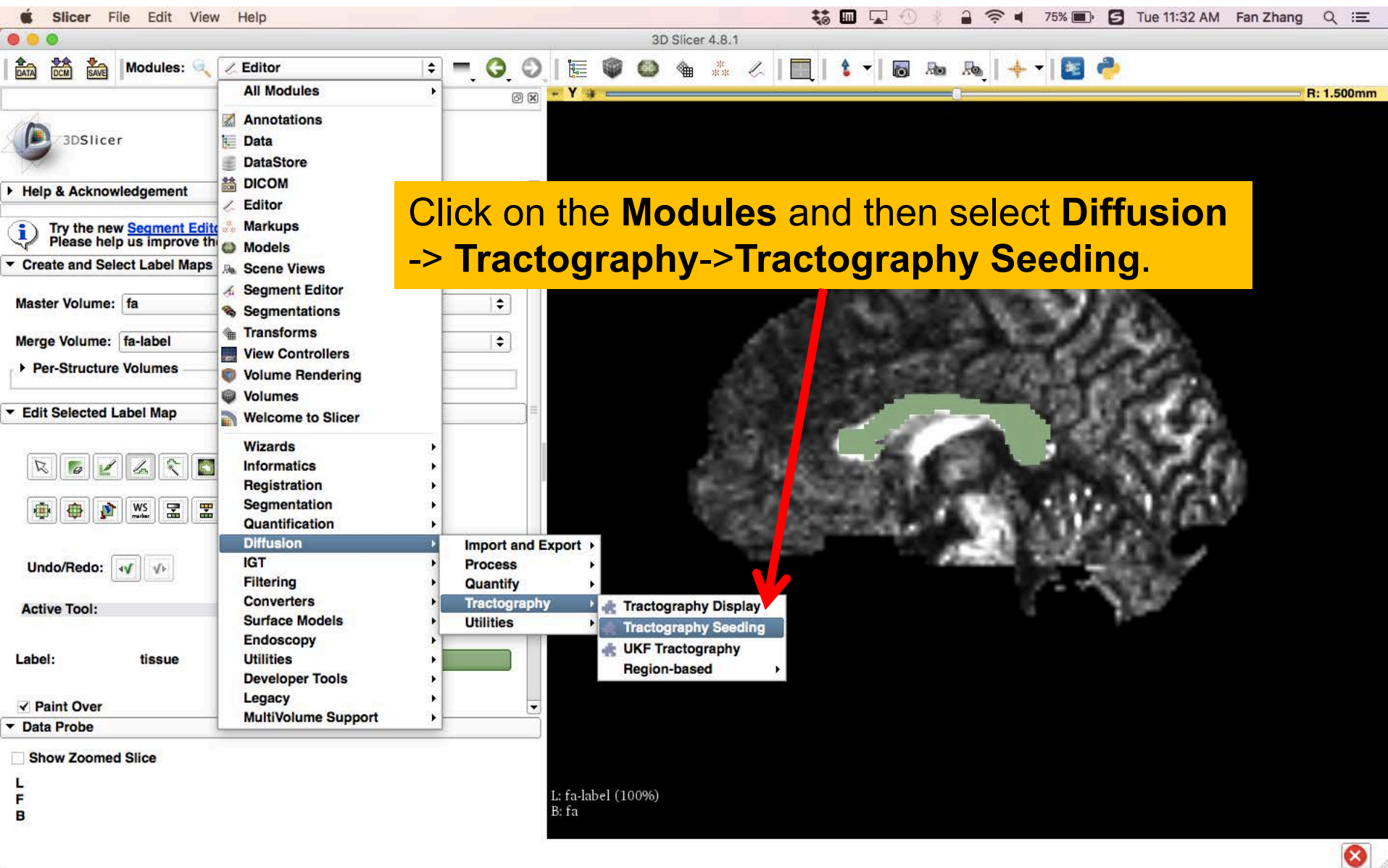
Diffusion MRI tractography



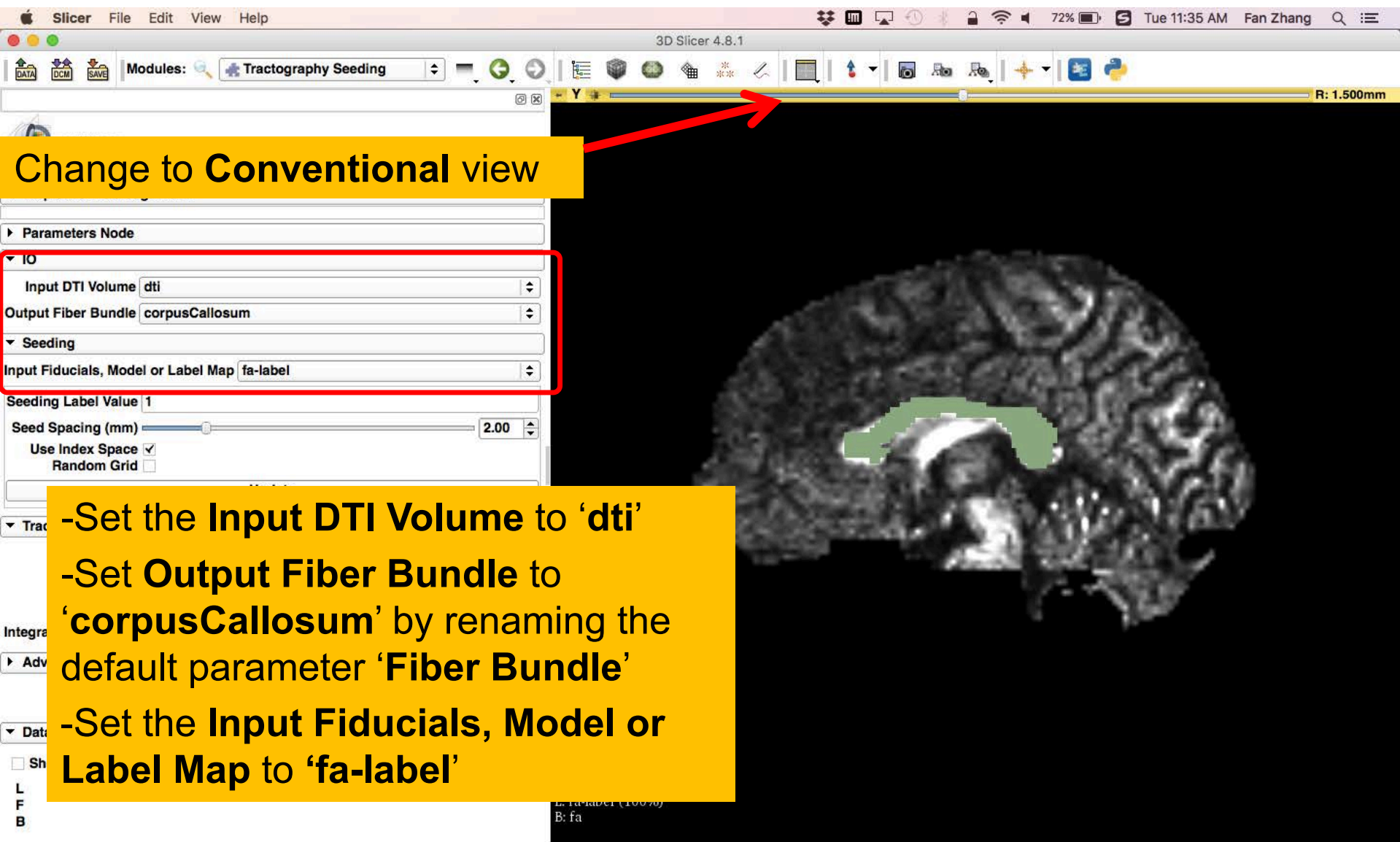
Diffusion MRI tractography



Diffusion MRI tractography



Step1: I/O



Change to **Conventional** view

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) 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

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): 1

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

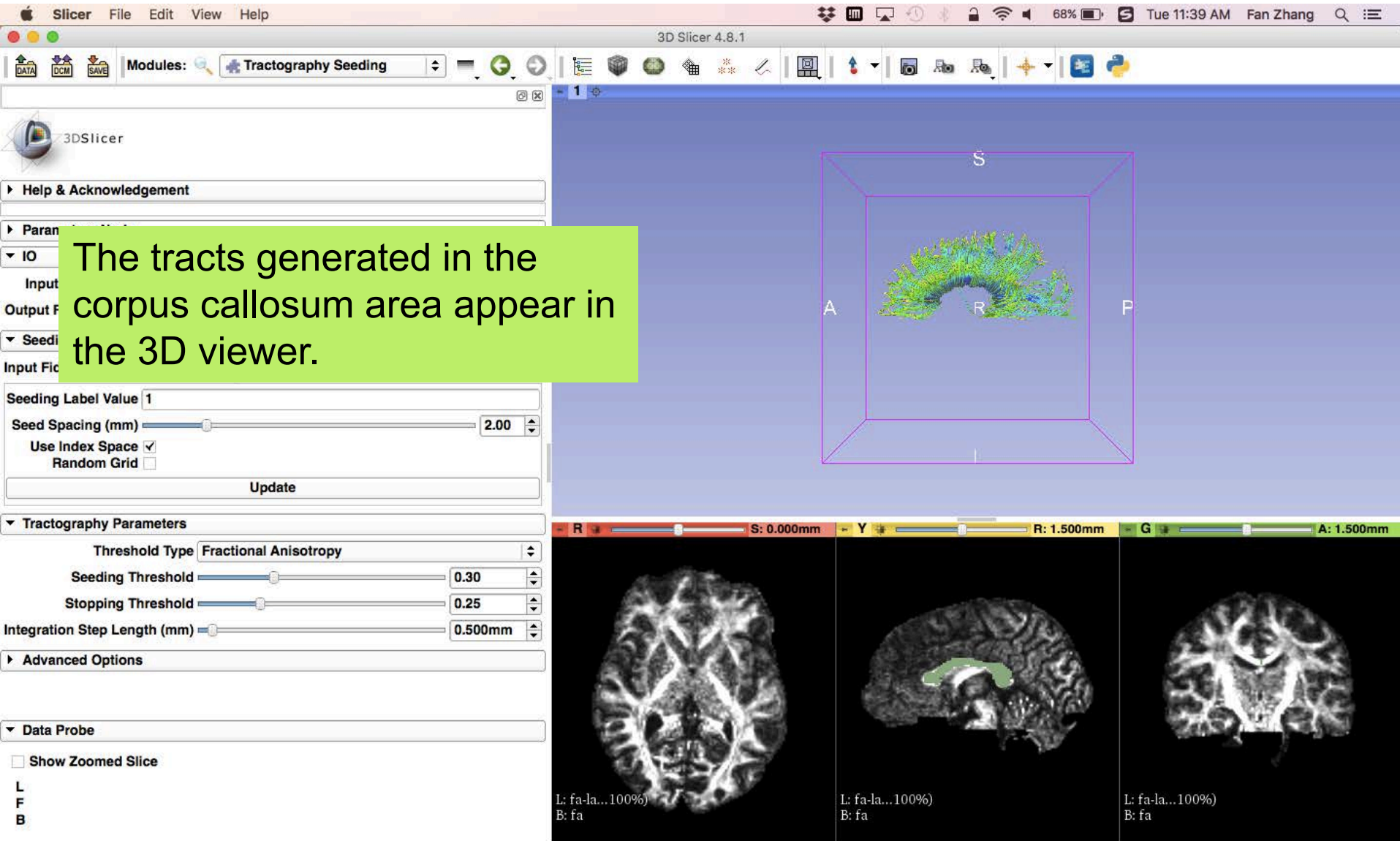
L: fa-label (100%)
B: fa

Select the default Tractography Seeding parameters:

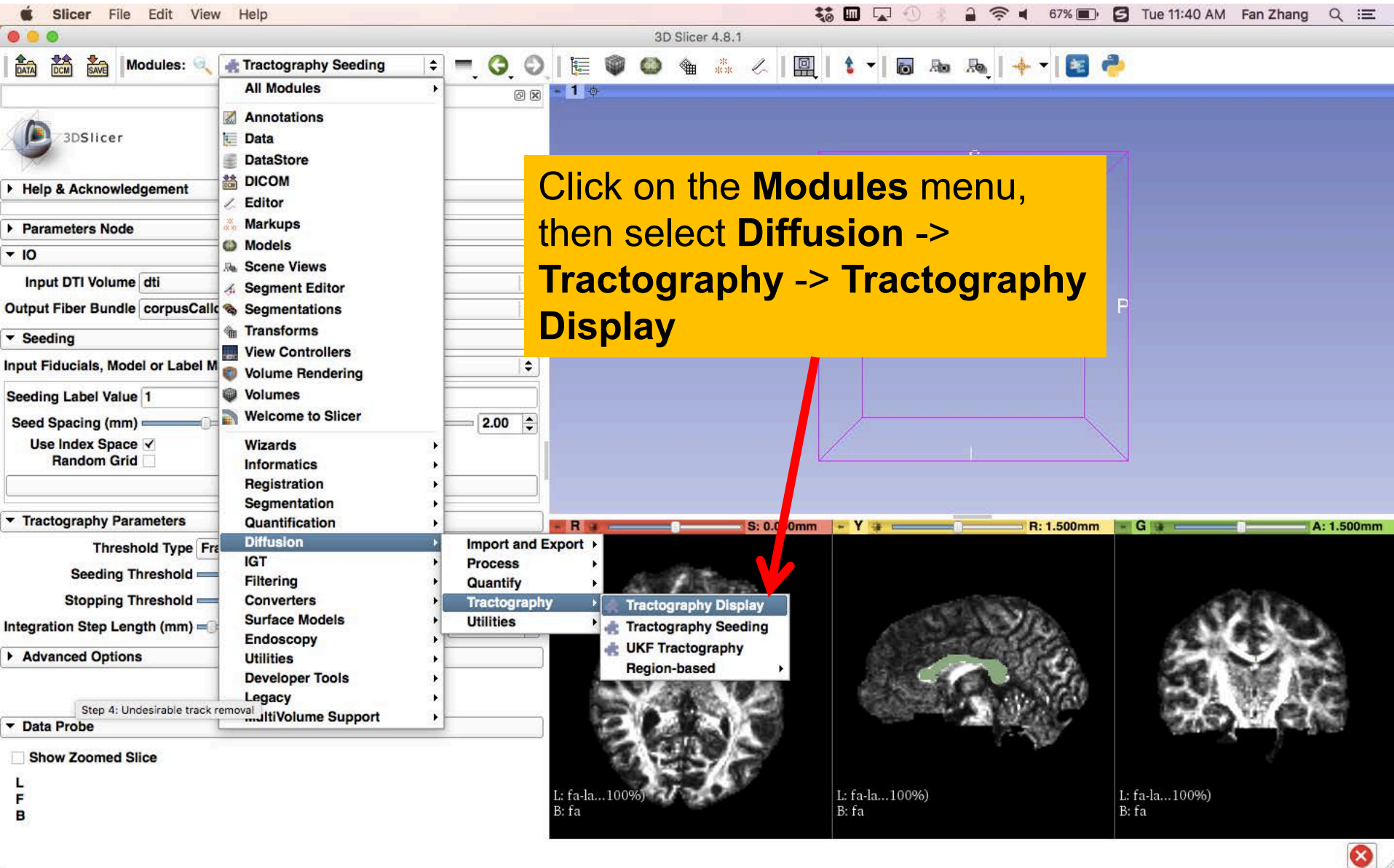
- Threshold Type: FractionalAnistropy
- Seeding Threshold:0.30
- Stopping Threshold: 0.25

Click **Update** to generate tractography

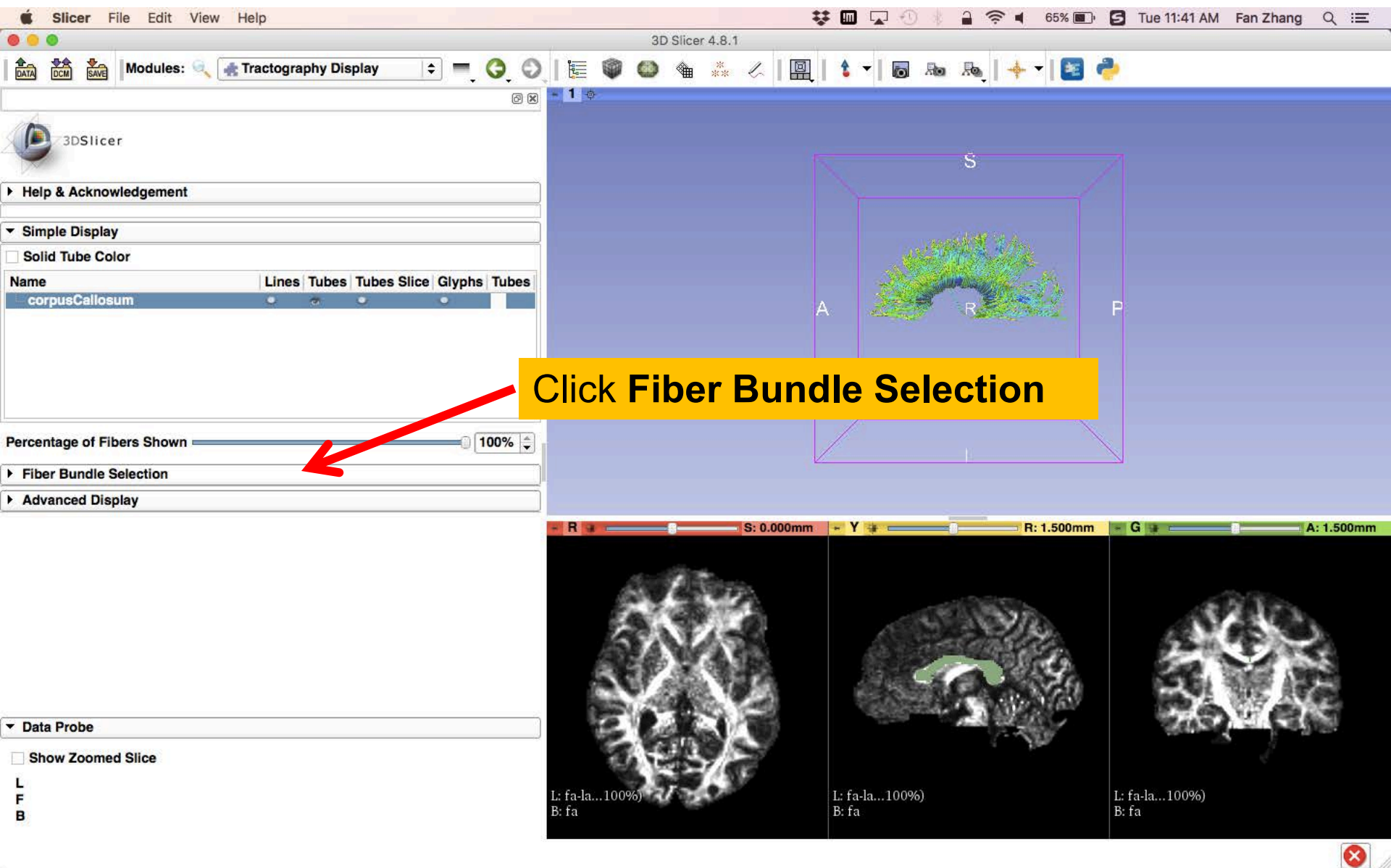
Step 3: Generate Tracts



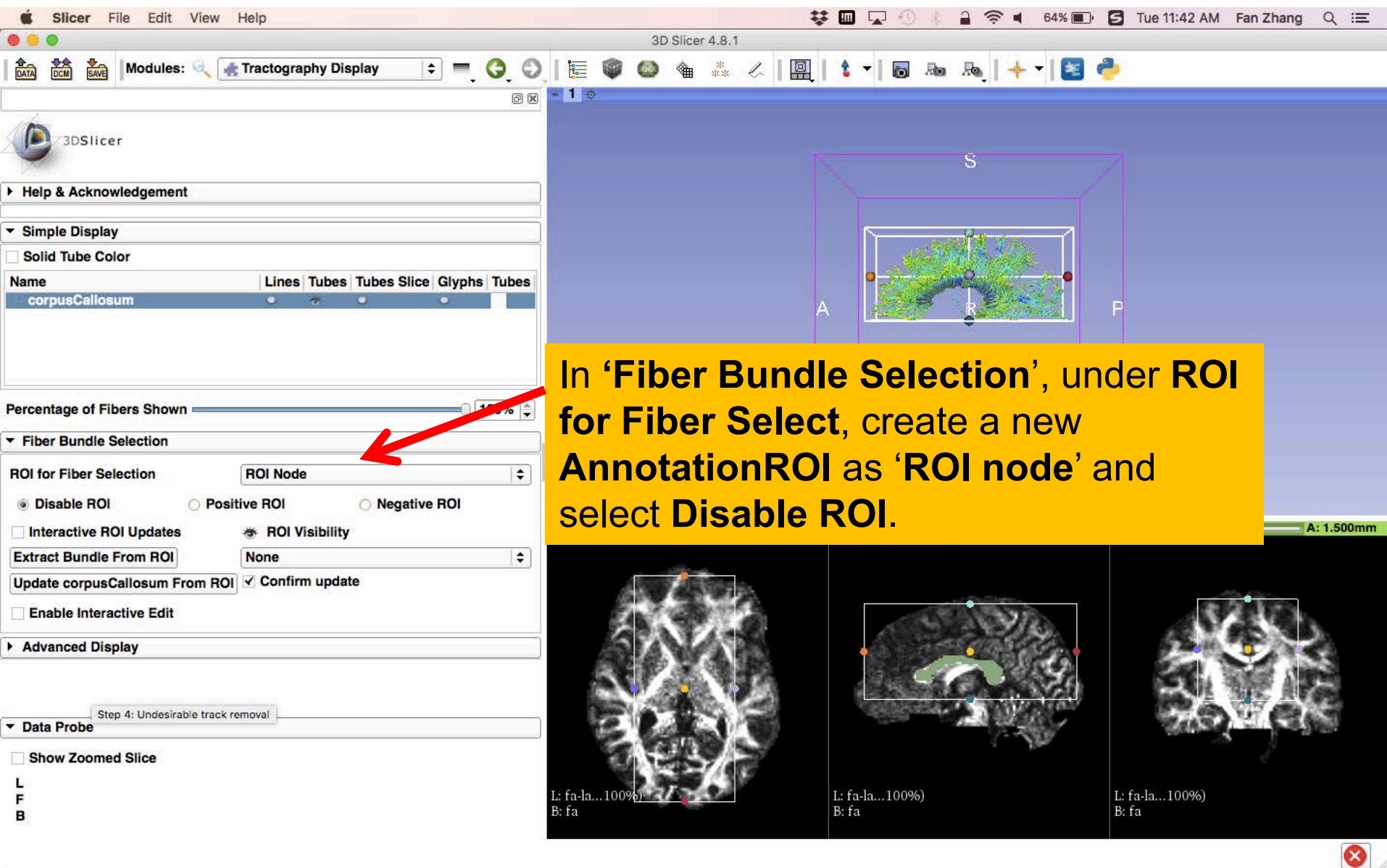
Step 4: Undesirable track removal



Step 4: Undesirable track removal



Step 4: Undesirable track removal



3D Slicer 4.8.1

Modules: **Tractography Display**

Simple Display

- ☐ Solid Tube Color

| Name | Lines | Tubes | Tubes Slice | Glyphs | Tubes |
|----------------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| corpusCallosum | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> |

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**.

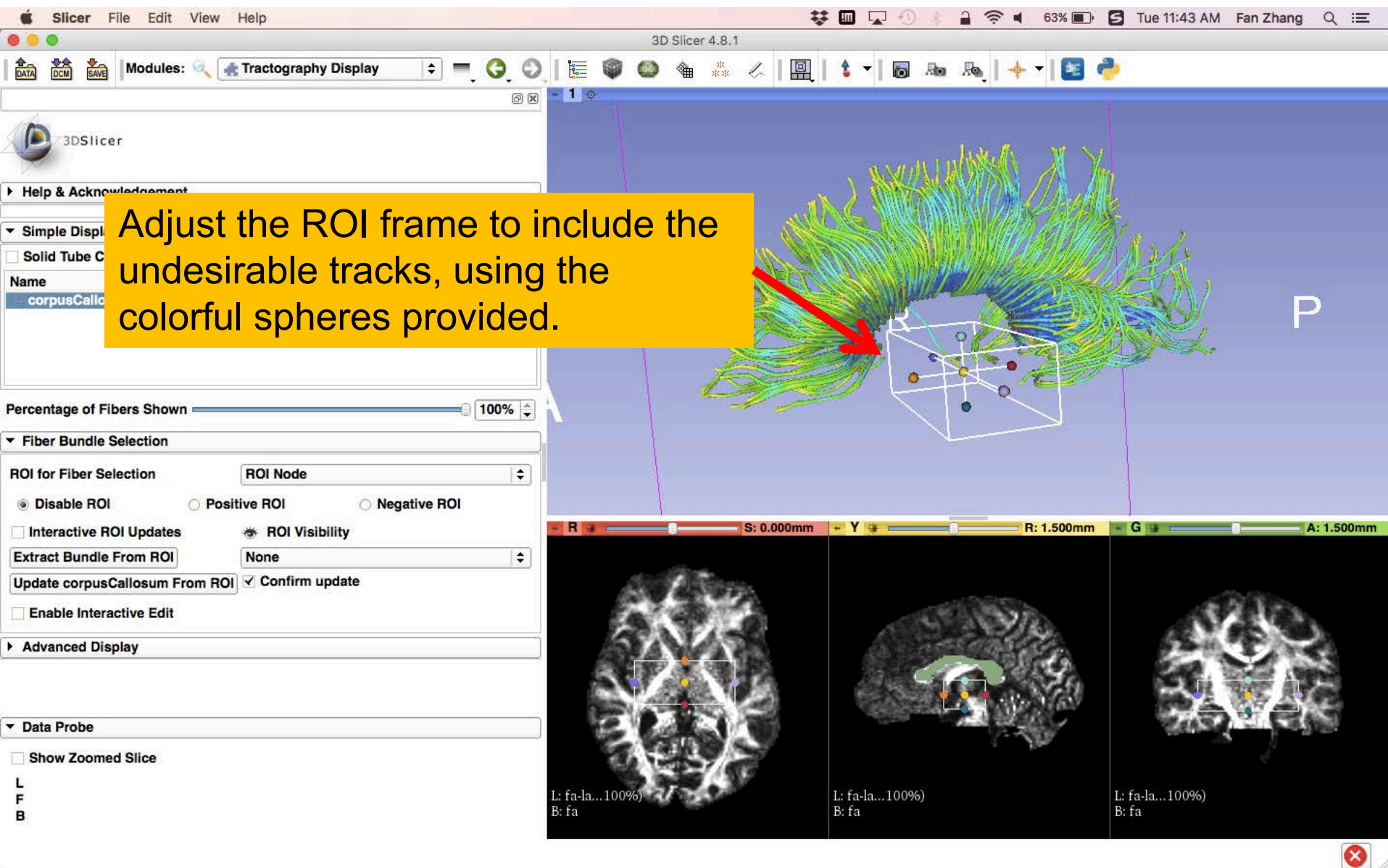
A: 1.500mm

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

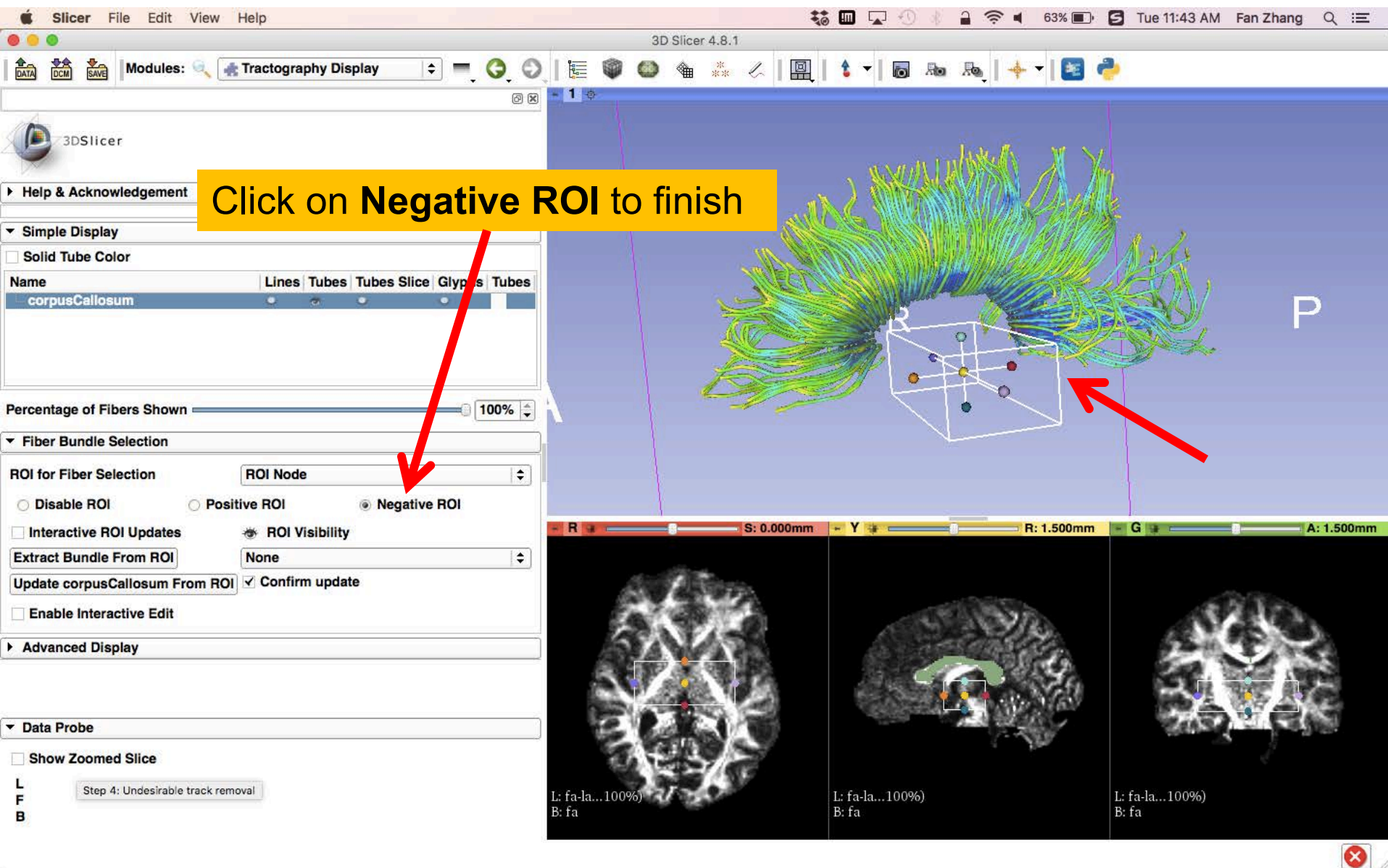
L: fa-la...100%)
B: fa

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

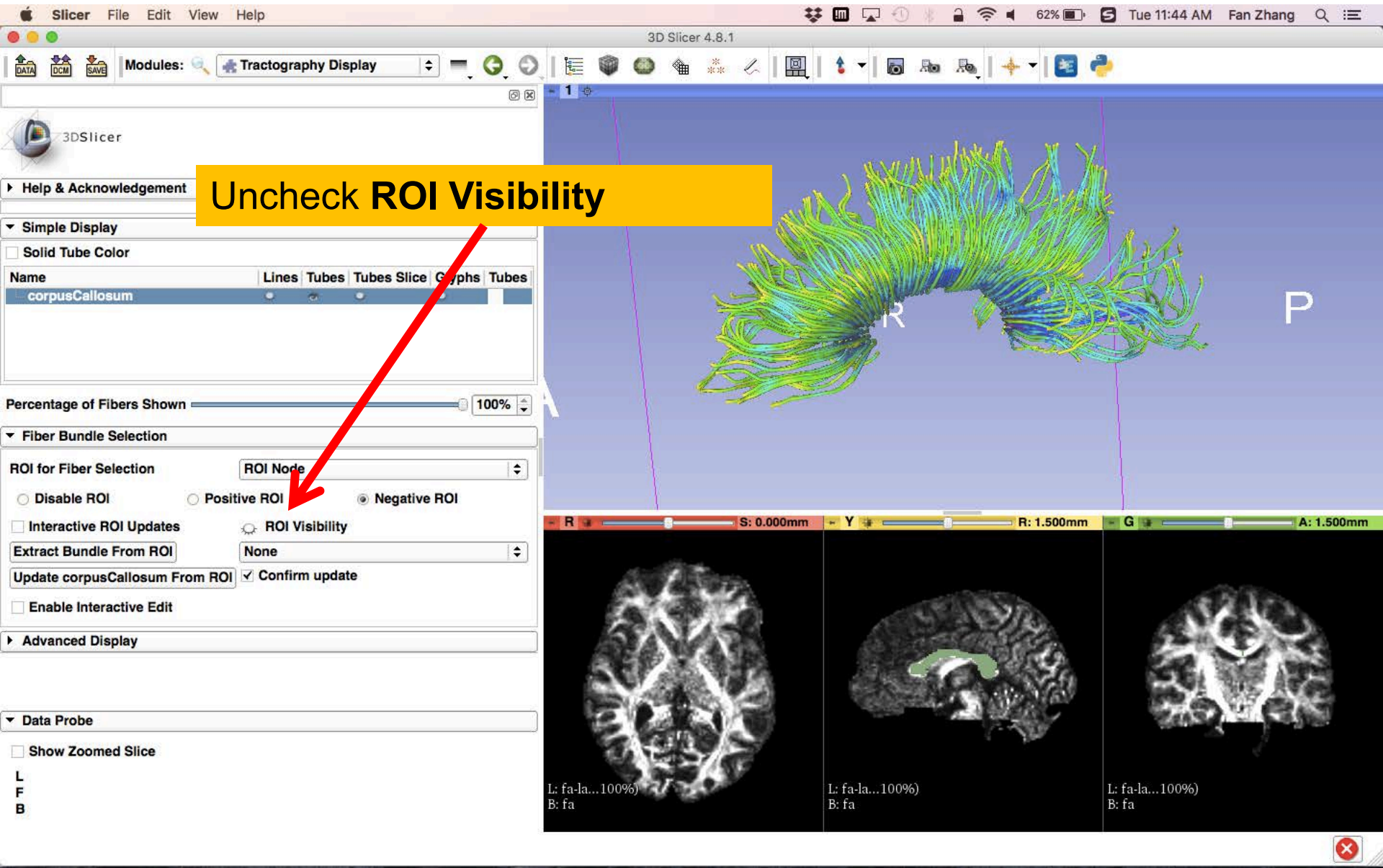
Step 4: Undesirable track removal



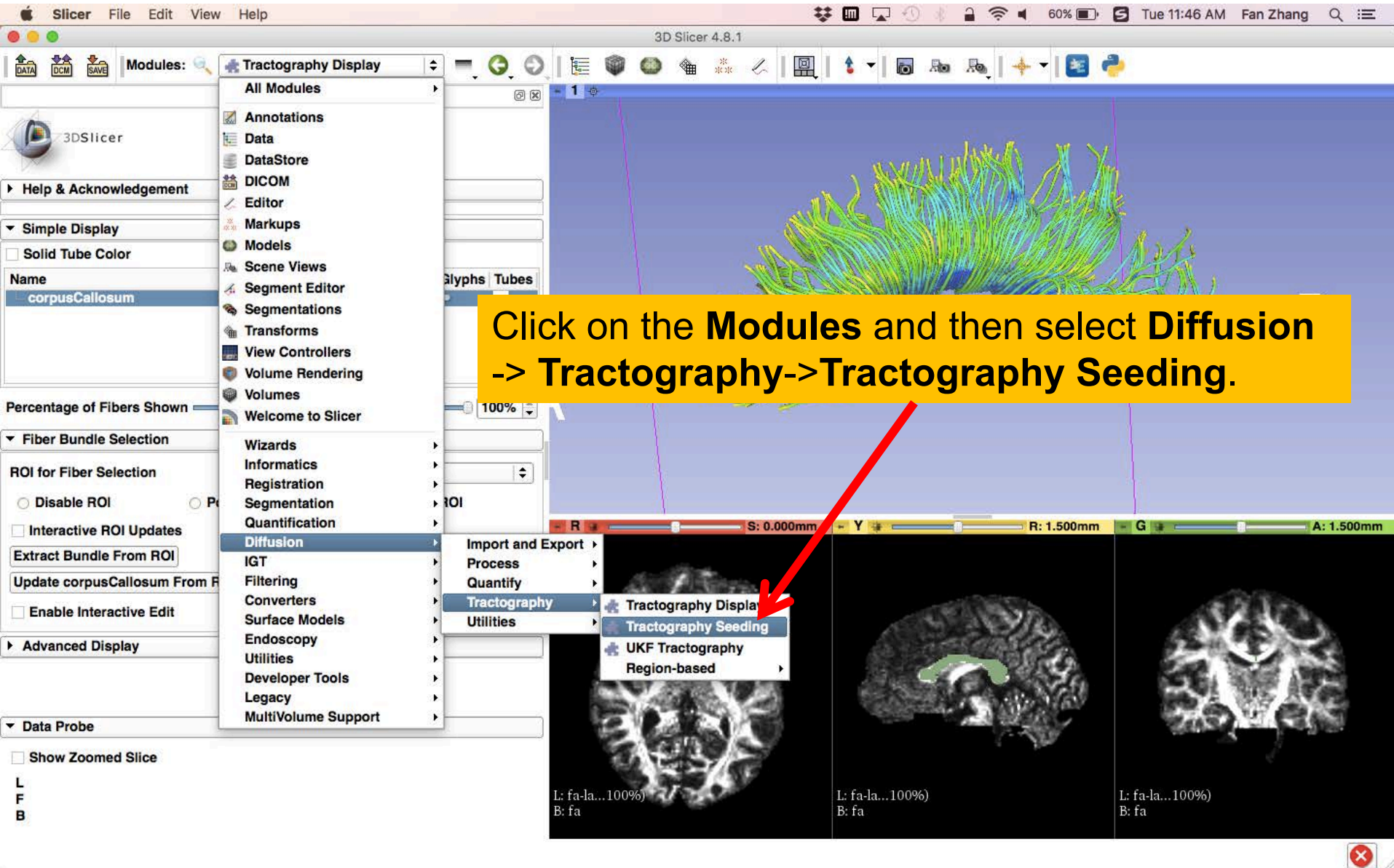
Step 4: Undesirable track removal



Step 4: Undesirable track removal

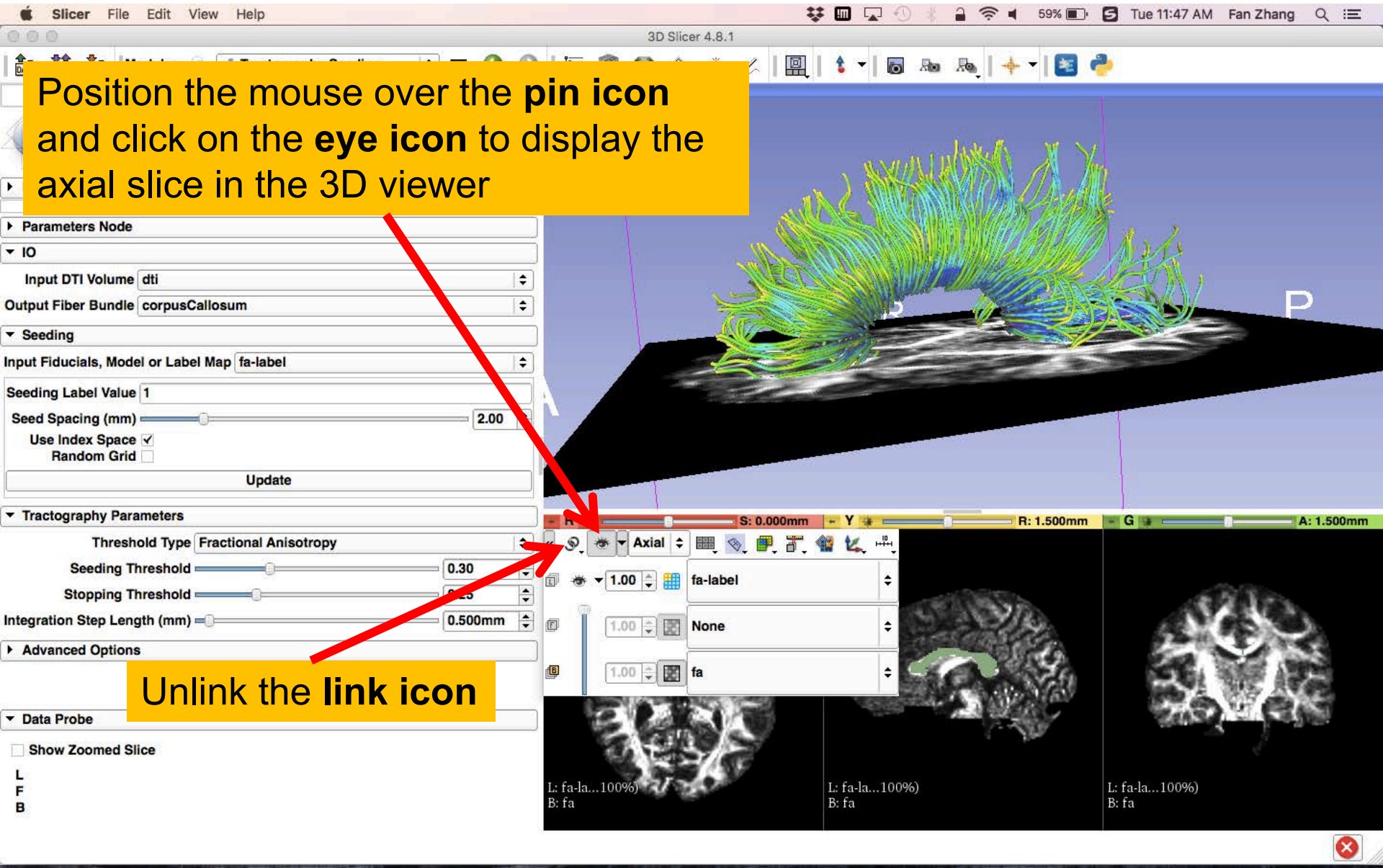


Fiducial Seeding



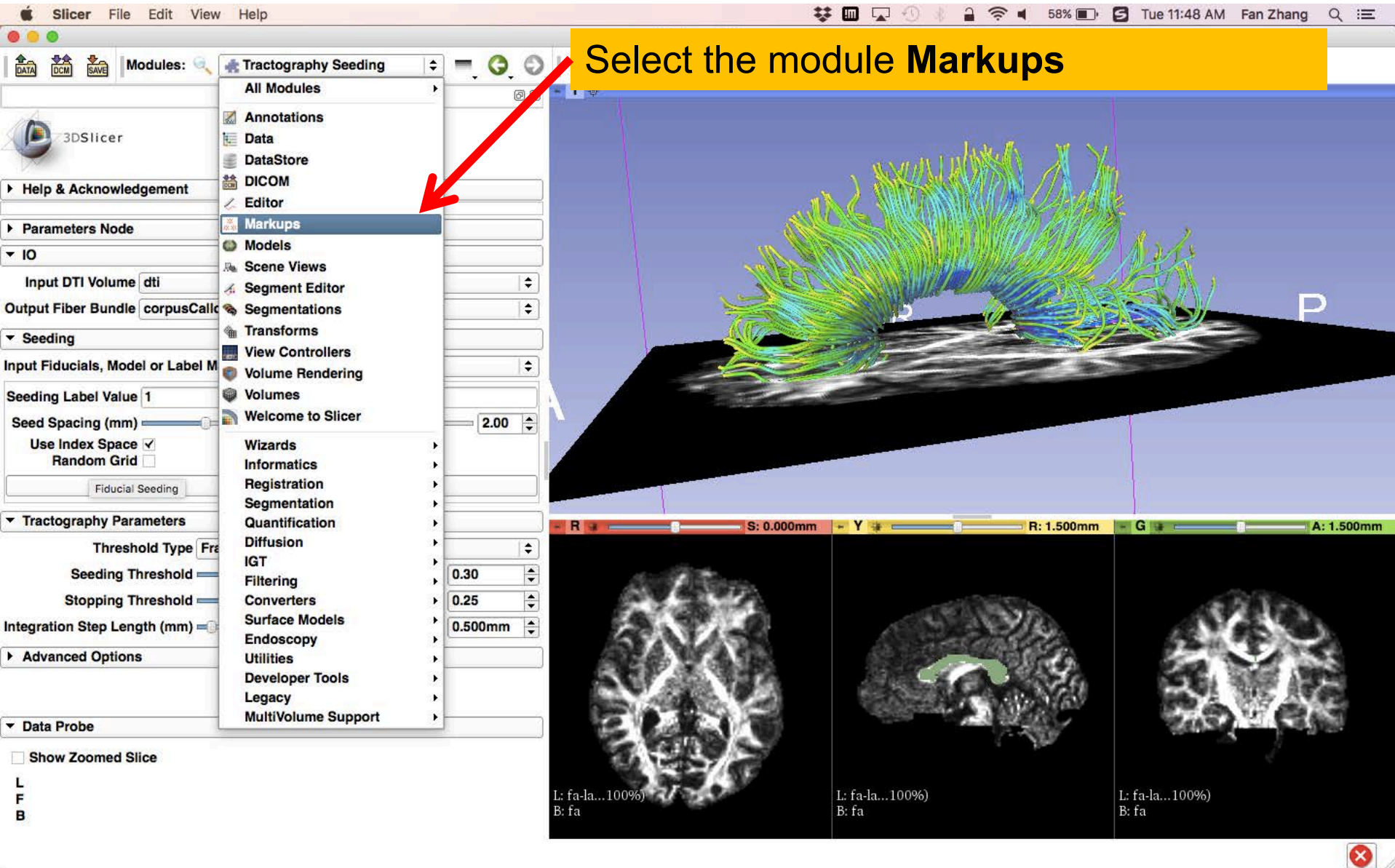
Fiducial Seeding

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

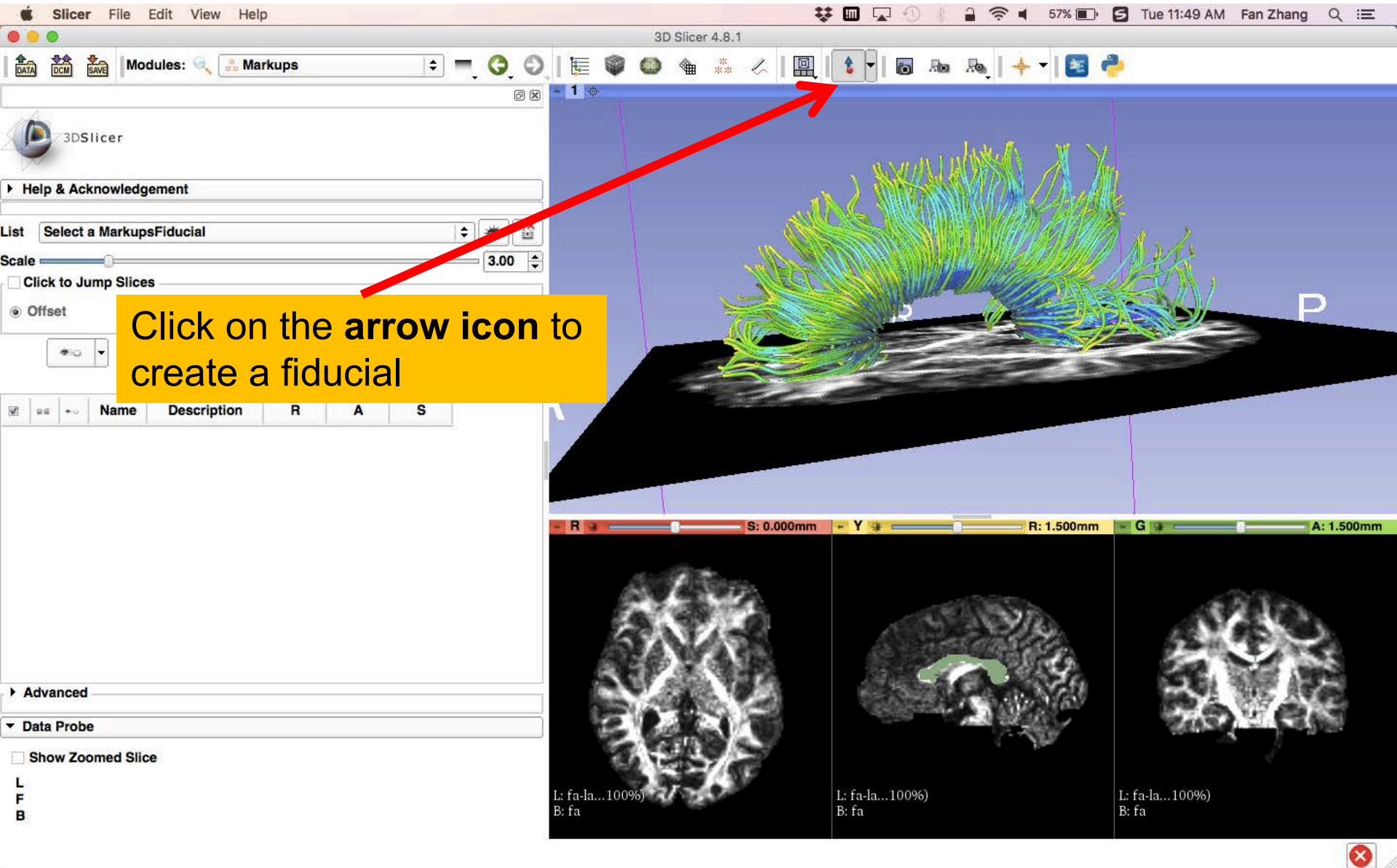


Unlink the **link icon**

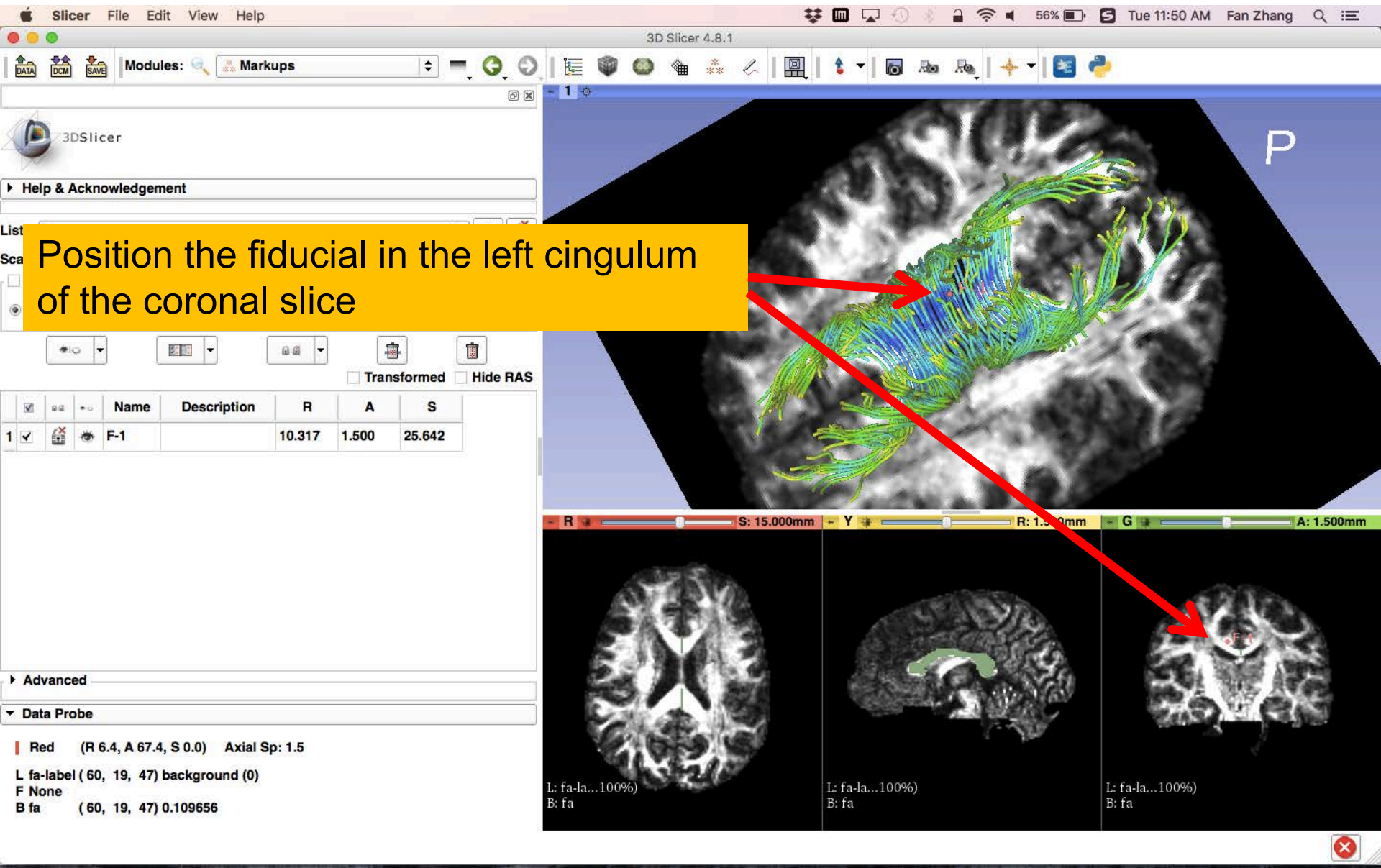
Fiducial Seeding



Fiducial Seeding



Fiducial Seeding



Fiducial Seeding

Double click on the fiducial and change the name to **LeftCingulum**

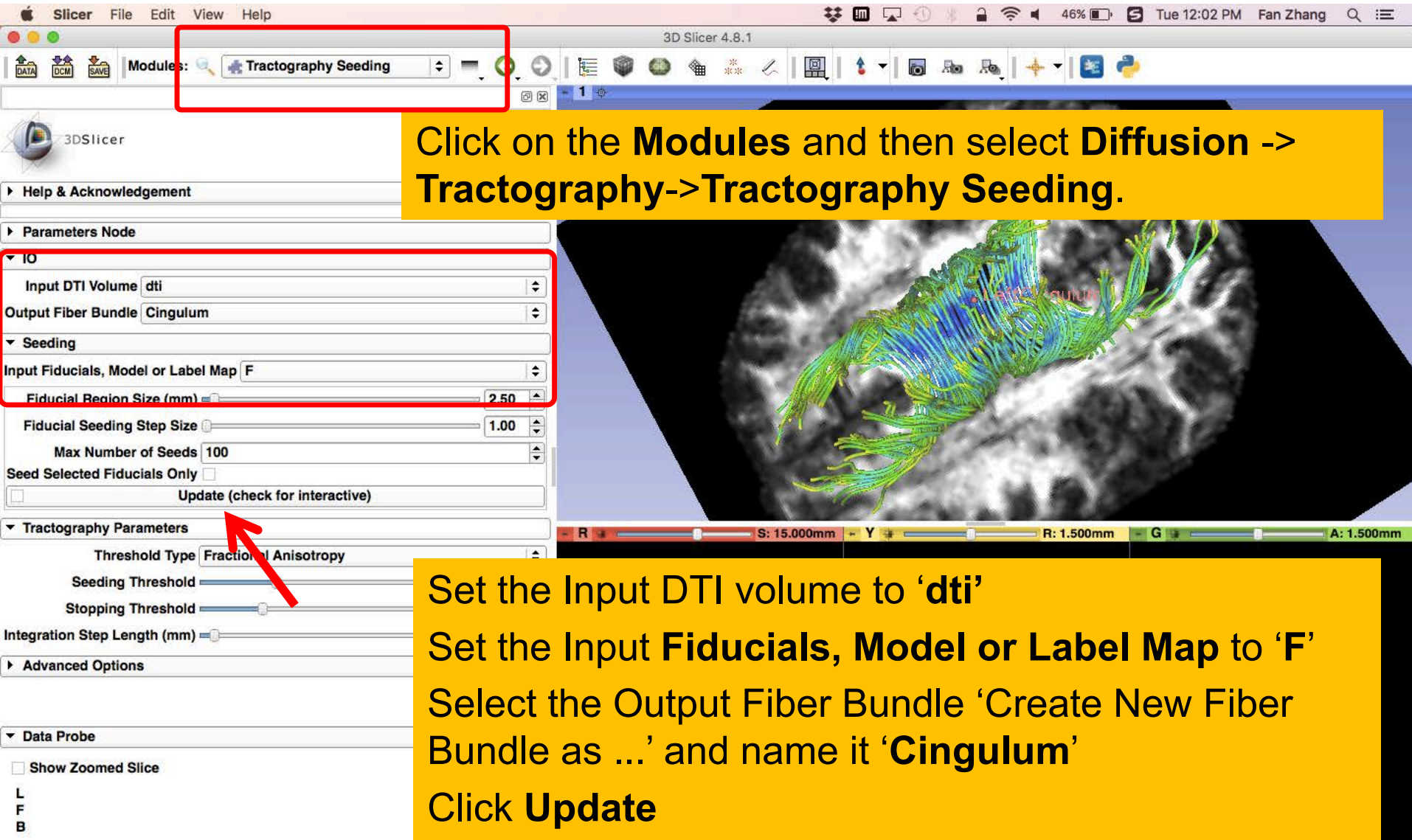
The screenshot shows the 3D Slicer 4.8.1 interface. The main 3D view displays a brain MRI slice with a green and blue fiber tract. A yellow box contains the instruction 'Double click on the fiducial and change the name to **LeftCingulum**'. Red arrows point from this box to a fiducial point on the tract in the main 3D view and to the 'LeftCingulum' entry in the 'Markups' table.

The 'Markups' table shows the following data:

| | Name | Description | R | A | S |
|---|--------------|-------------|--------|-------|--------|
| 1 | LeftCingulum | | 10.317 | 1.500 | 25.642 |

The bottom panel shows three orthogonal views (Axial, Sagittal, Coronal) of the brain MRI. The Coronal view shows the 'LeftCingulum' fiducial point.

Fiducial Seeding

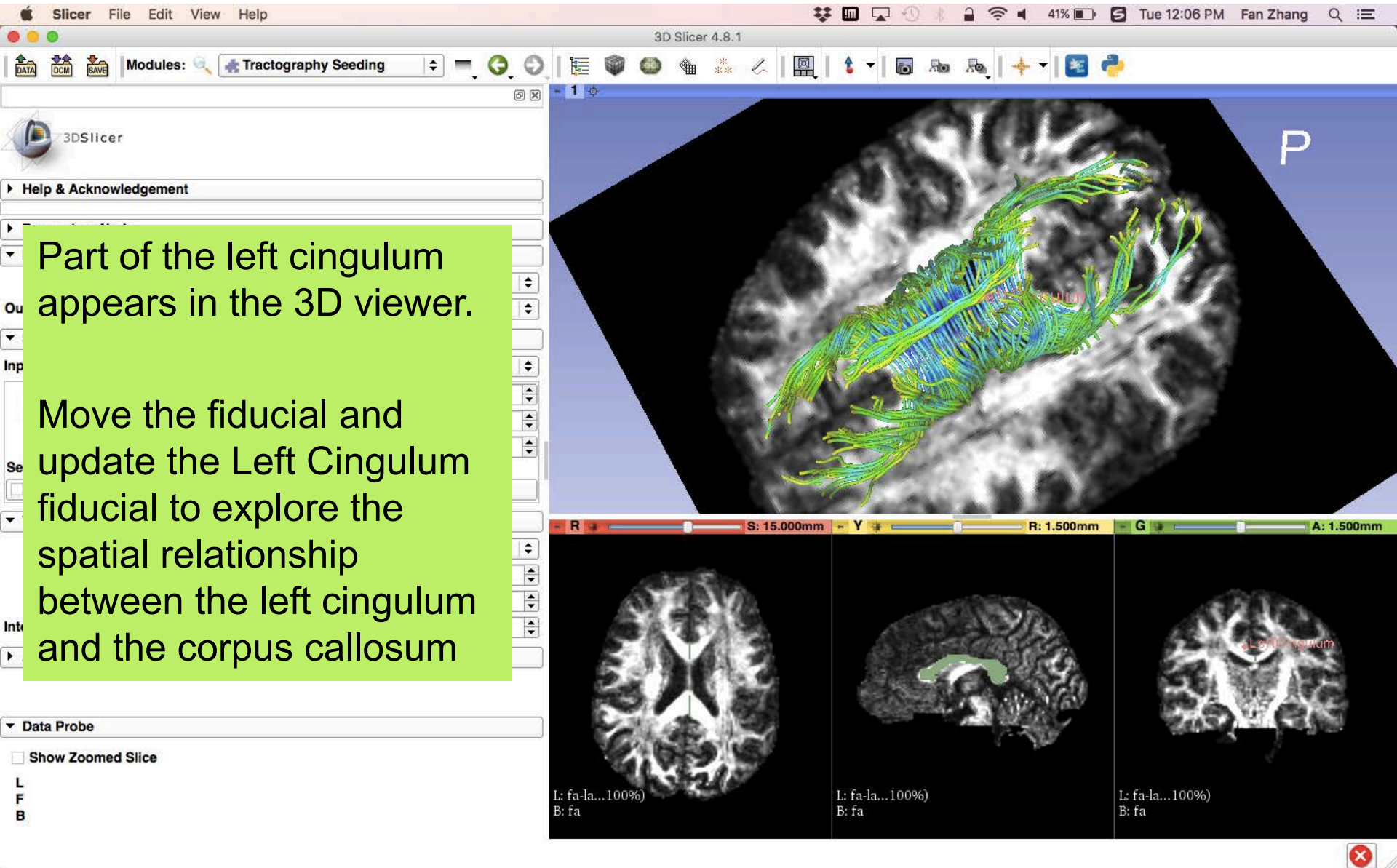


The screenshot shows the 3D Slicer 4.8.1 interface. The 'Modules' dropdown menu is highlighted with a red box, showing 'Tractography Seeding' selected. The 'Parameters Node' on the left is also highlighted with a red box, showing the 'IO' section with 'Input DTI Volume' set to 'dti' and 'Output Fiber Bundle' set to 'Cingulum'. The 'Seeding' section is also highlighted with a red box, showing 'Input Fiducials, Model or Label Map' set to 'F', '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' checked. The 'Tractography Parameters' section is highlighted with a red box, showing 'Threshold Type' set to 'Fractional Anisotropy', 'Seeding Threshold' set to 0.5, 'Stopping Threshold' set to 0.5, and 'Integration Step Length (mm)' set to 0.5. A red arrow points to the 'Update (check for interactive)' button. The main 3D view 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'.

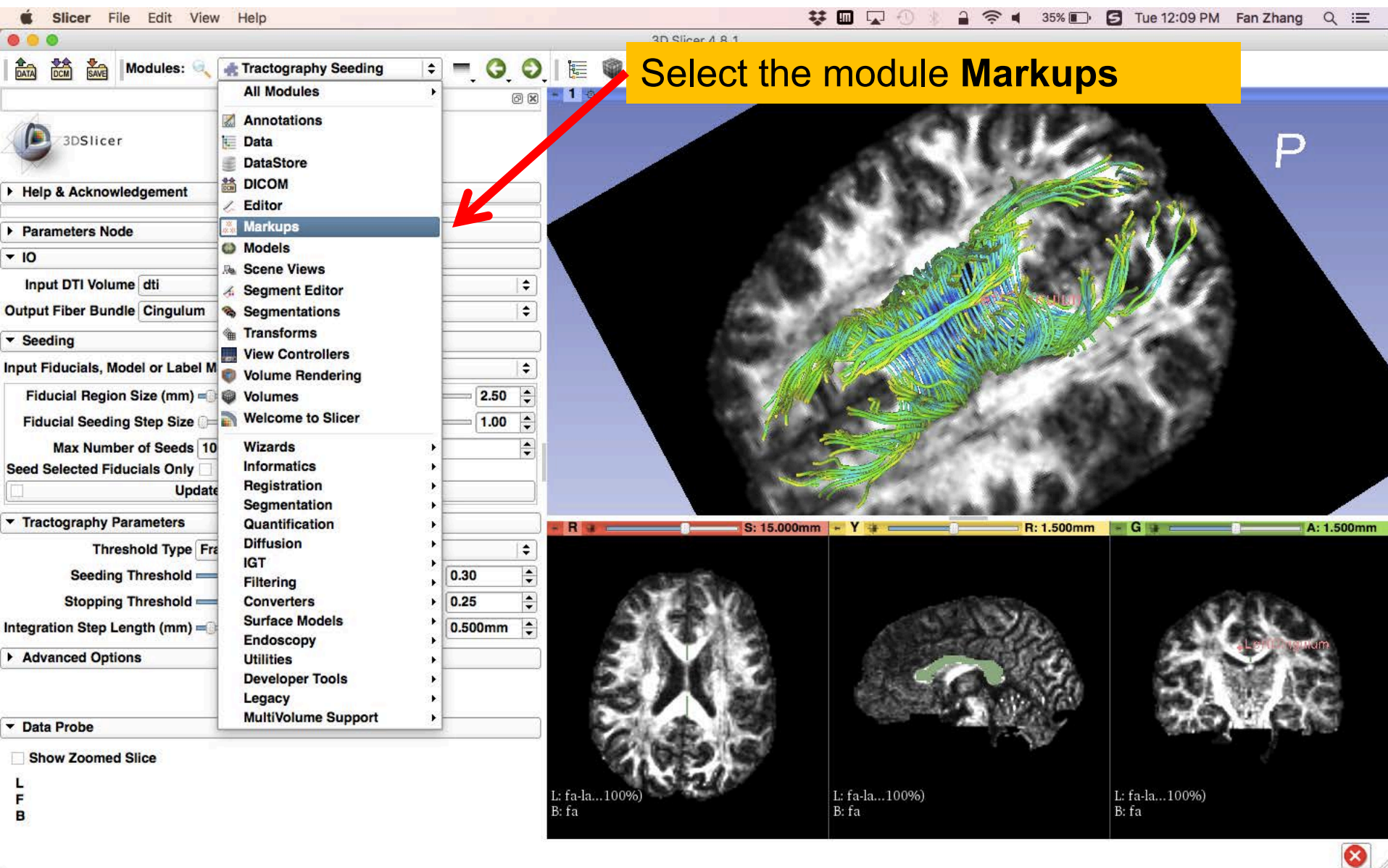
Click on the **Modules** and then select **Diffusion -> Tractography->Tractography Seeding**.

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**

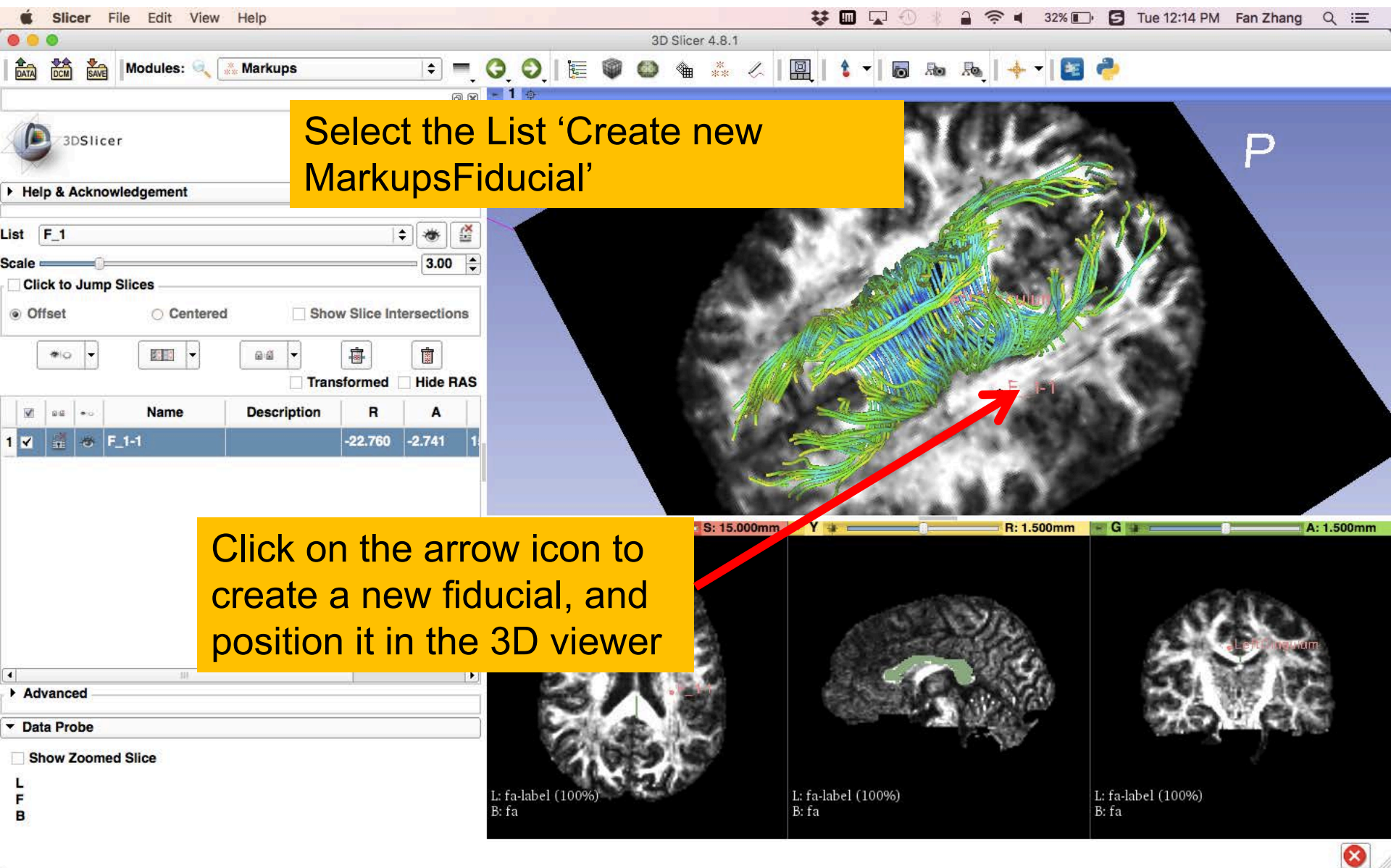
Fiducial Seeding



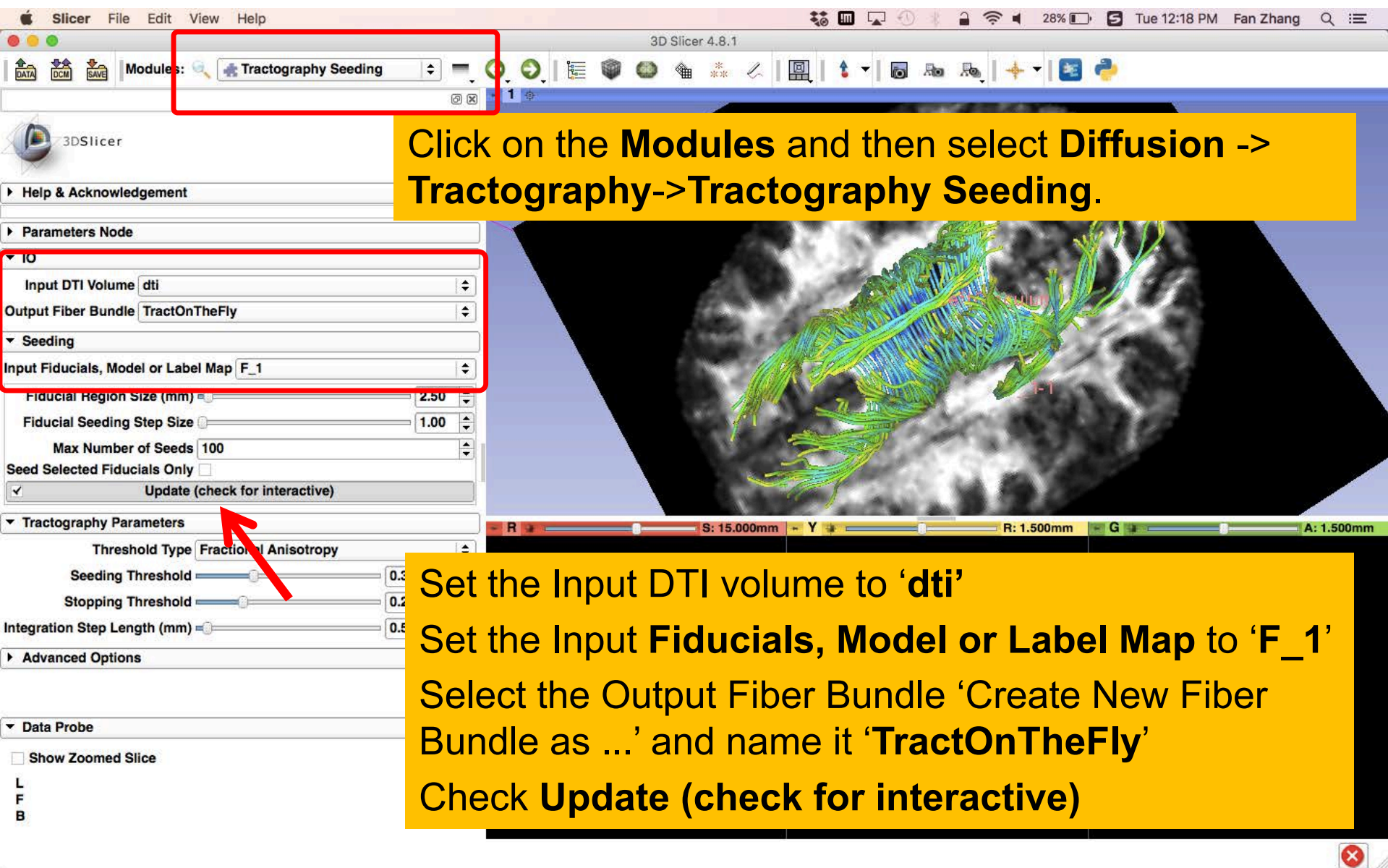
Tractography 'on-the-fly'



Tractography 'on-the-fly'



Tractography 'on-the-fly'

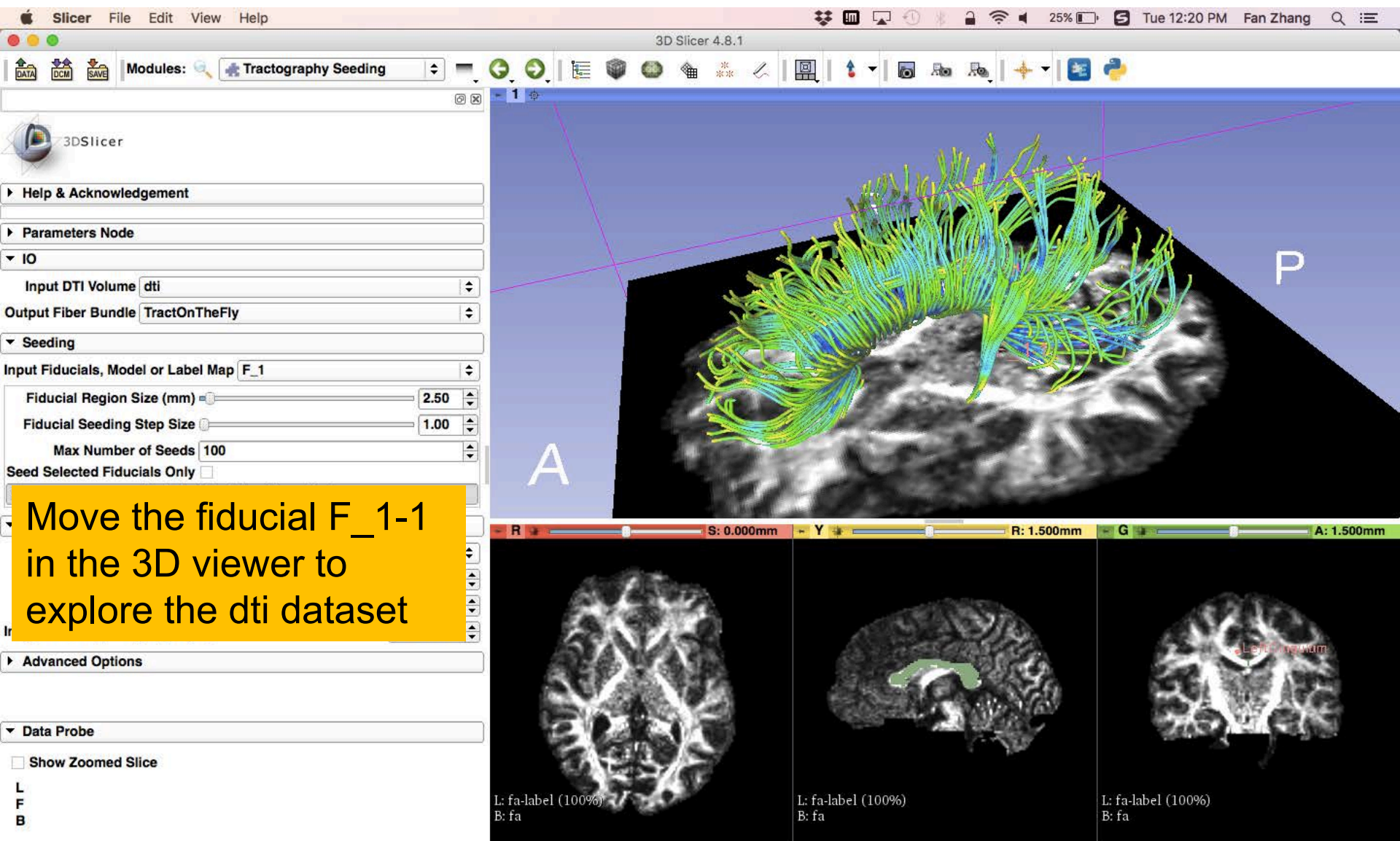


The screenshot shows the 3D Slicer 4.8.1 interface. The 'Modules' dropdown menu is highlighted with a red box, showing 'Tractography Seeding' selected. The 'Parameters Node' on the left is also highlighted with a red box, showing the 'IO' section with 'Input DTI Volume' set to 'dti', 'Output Fiber Bundle' set to 'TractOnTheFly', and 'Input Fiducials, Model or Label Map' set to 'F_1'. The 'Seeding' section is also highlighted with a red box, 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 highlighted with a red box, showing 'Threshold Type' set to 'Fractional Anisotropy', 'Seeding Threshold' set to 0.3, 'Stopping Threshold' set to 0.2, and 'Integration Step Length (mm)' set to 0.5. A red arrow points to the 'Seeding Threshold' slider. The 'Advanced Options' section is also visible. The 'Data Probe' section at the bottom shows 'Show Zoomed Slice' unchecked. The main 3D view on the right 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'.

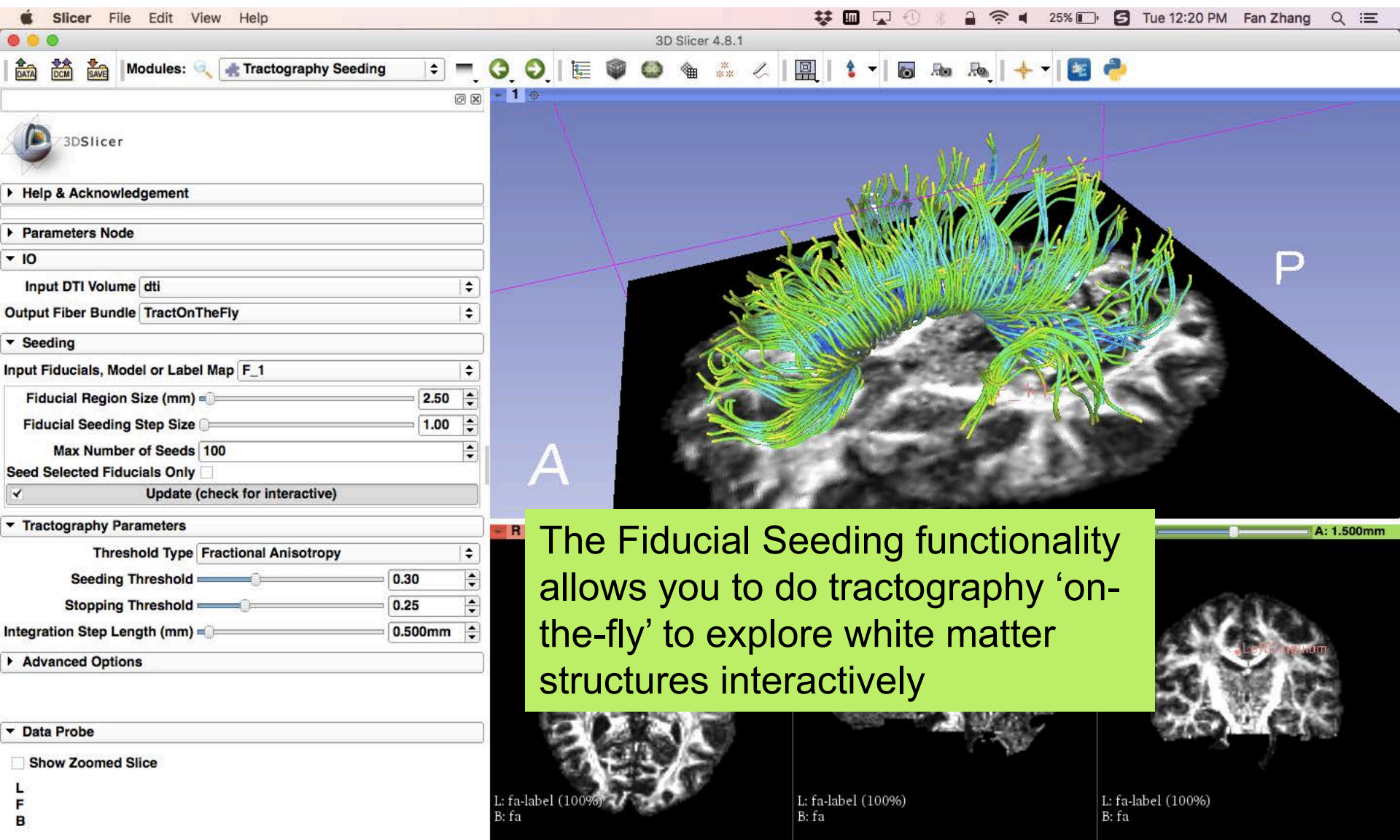
Click on the **Modules** and then select **Diffusion -> Tractography->Tractography Seeding**.

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)**

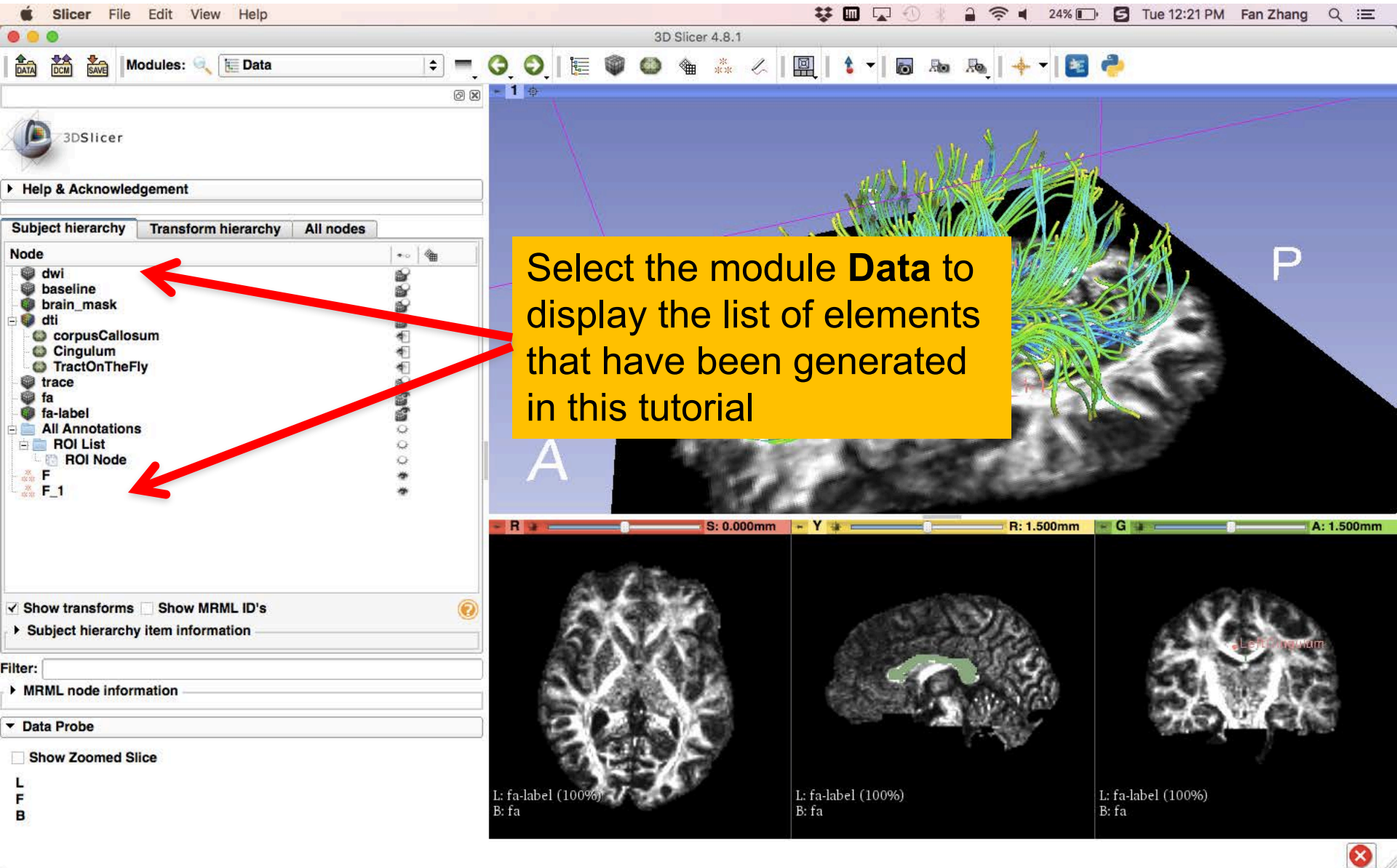
Tractography 'on-the-fly'



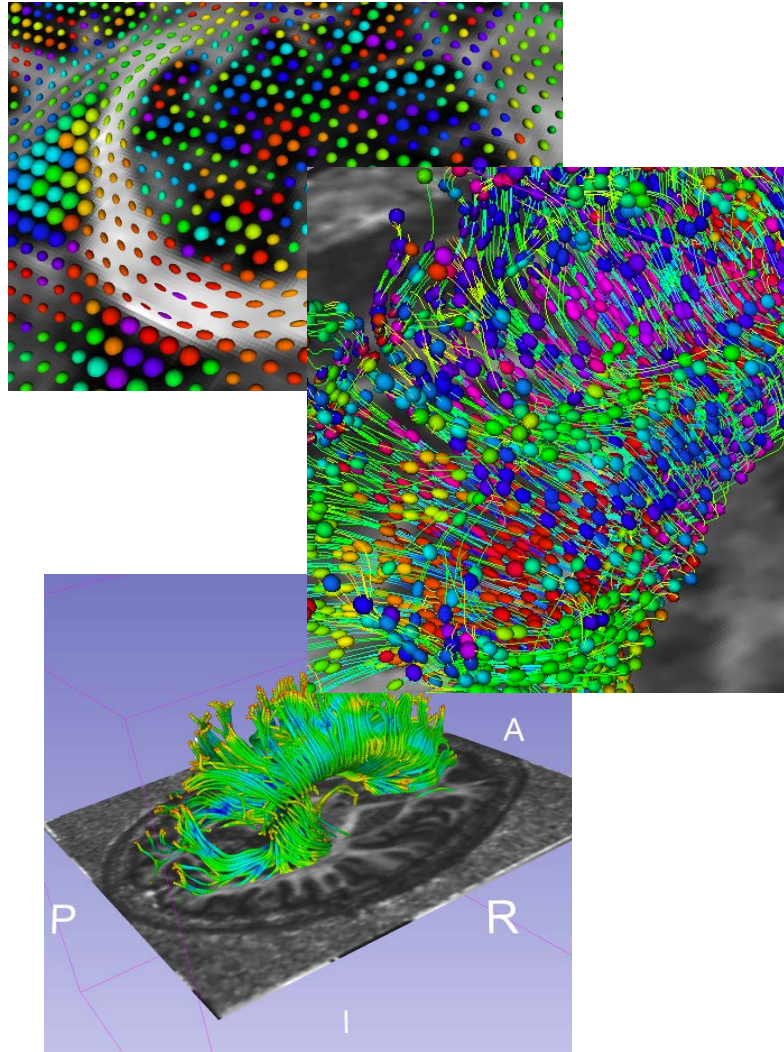
Tractography 'on-the-fly'



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.

Acknowledgments



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NIH P41EB015898



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NIH P41EB015902

- **Fan Zhang, Ph.D.**
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