



Diffusion MRI Analysis

Sonia Pujol, Ph.D.

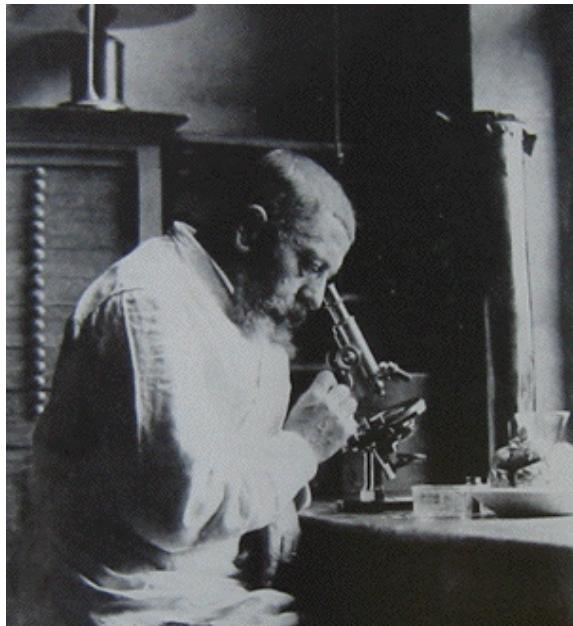
Surgical Planning Laboratory
Harvard University

Brain Anatomy



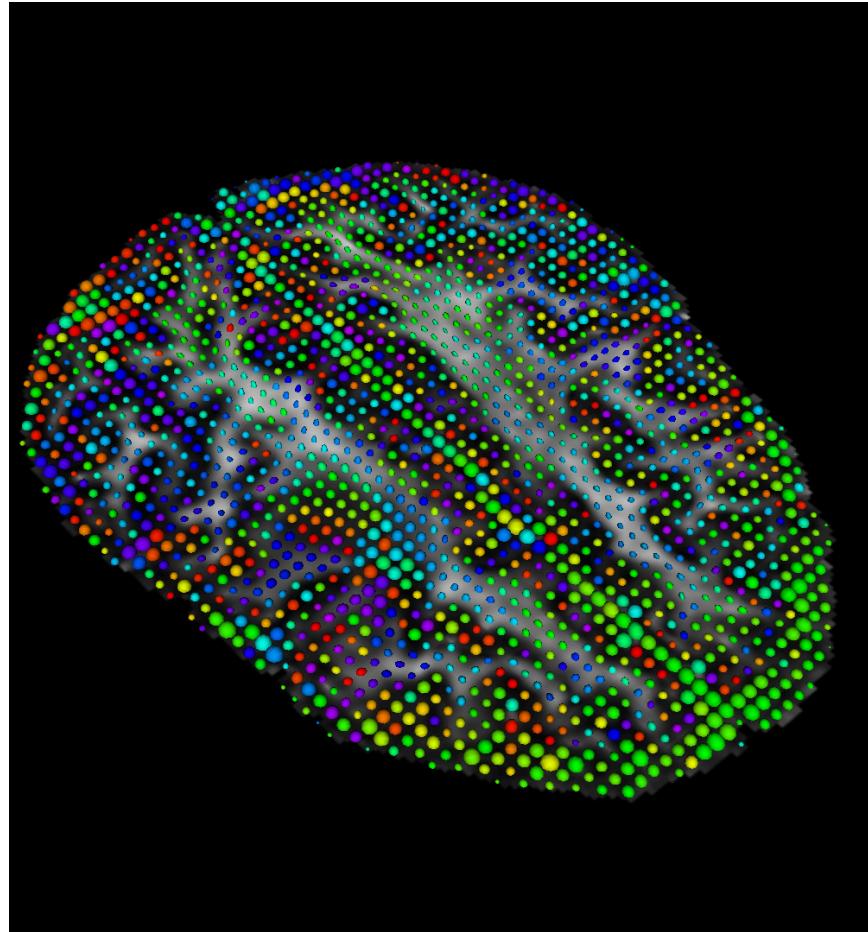
- White matter ~45% of the brain
- Myelinated nerve fibers (~ 10 μm axon diameter)

White Matter Exploration



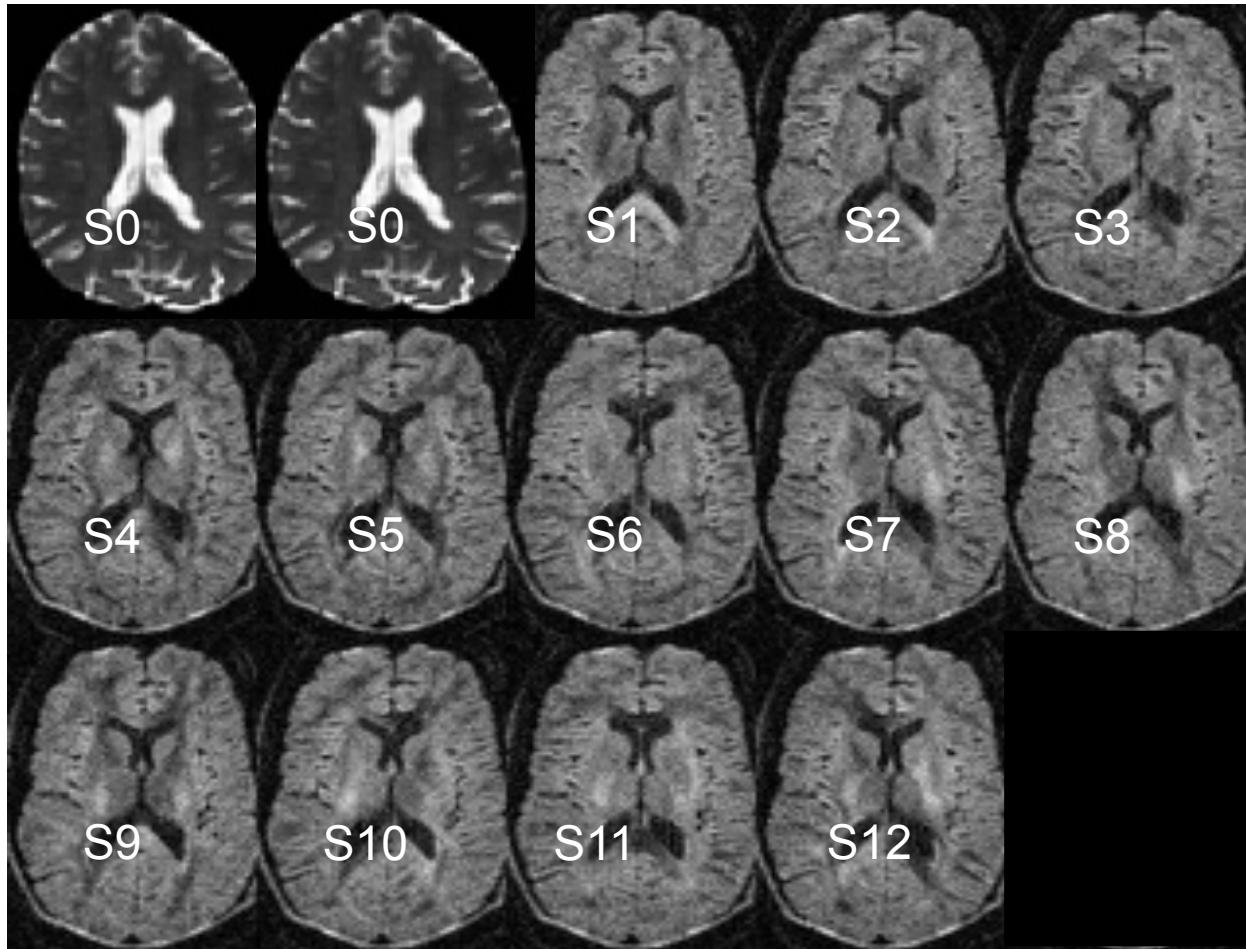
Jules Joseph Dejerine
*(Anatomie des centres
nerveux* (Paris, 1890-1901):
Atlas of Neuroanatomy based
on myelin stained preparation

Diffusion Tensor Imaging (DTI)



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

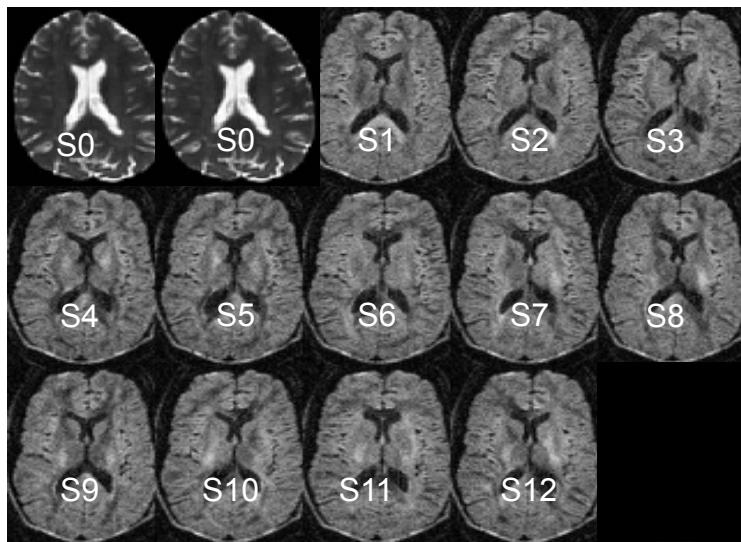
Diffusion Weighted Imaging (DWI)



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

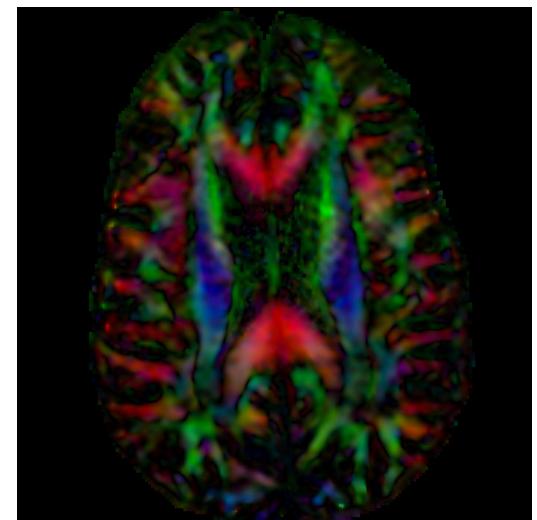
From DWI to DTI

DWI



DWI dataset acquired with
12 gradient and 2 baseline

DTI

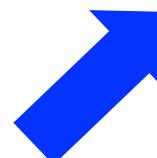


DTI dataset



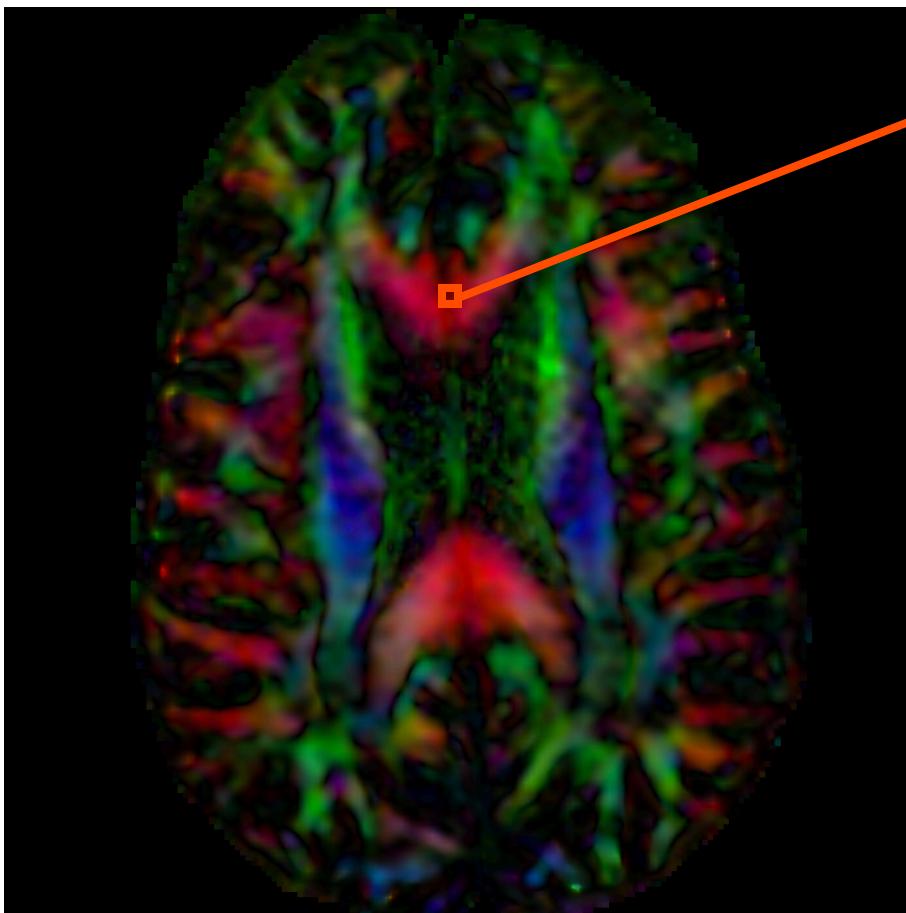
$$S_i = S_0 e^{-b \hat{g}^T D \hat{g}_i}$$

Stejskal-Tanner (1965)



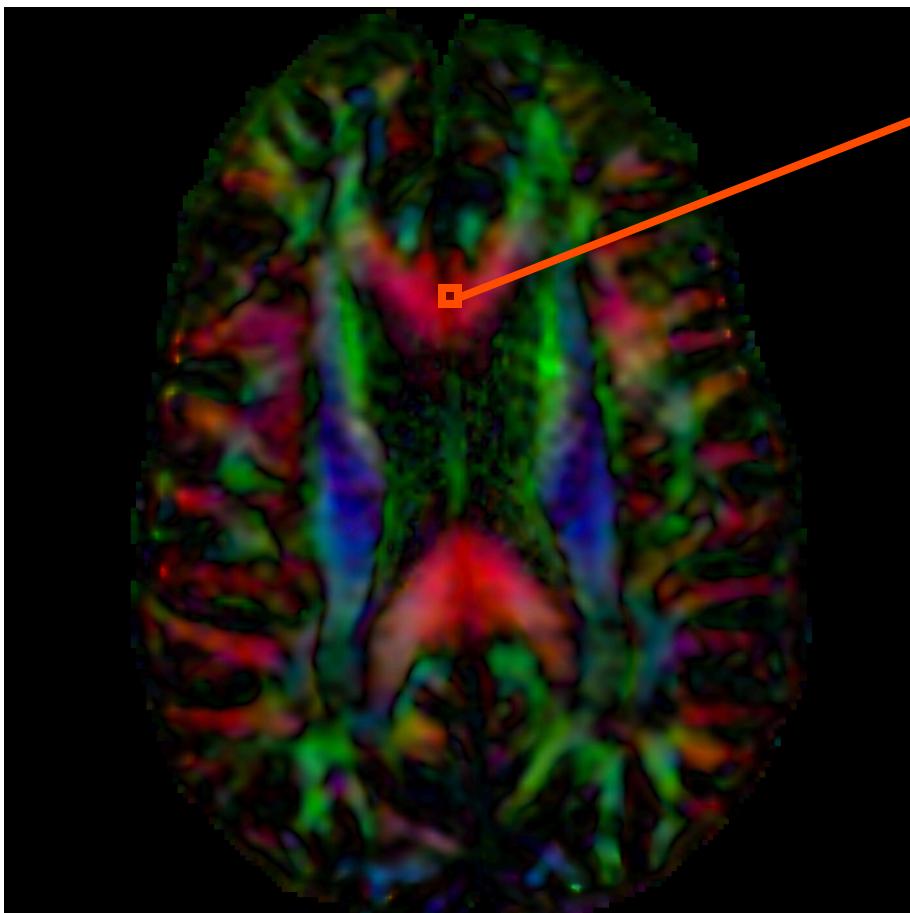
*S_i: DWI volume acquired with
ith gradient
S₀: Baseline volume*

Diffusion Tensor Imaging



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

Diffusion Tensor Imaging

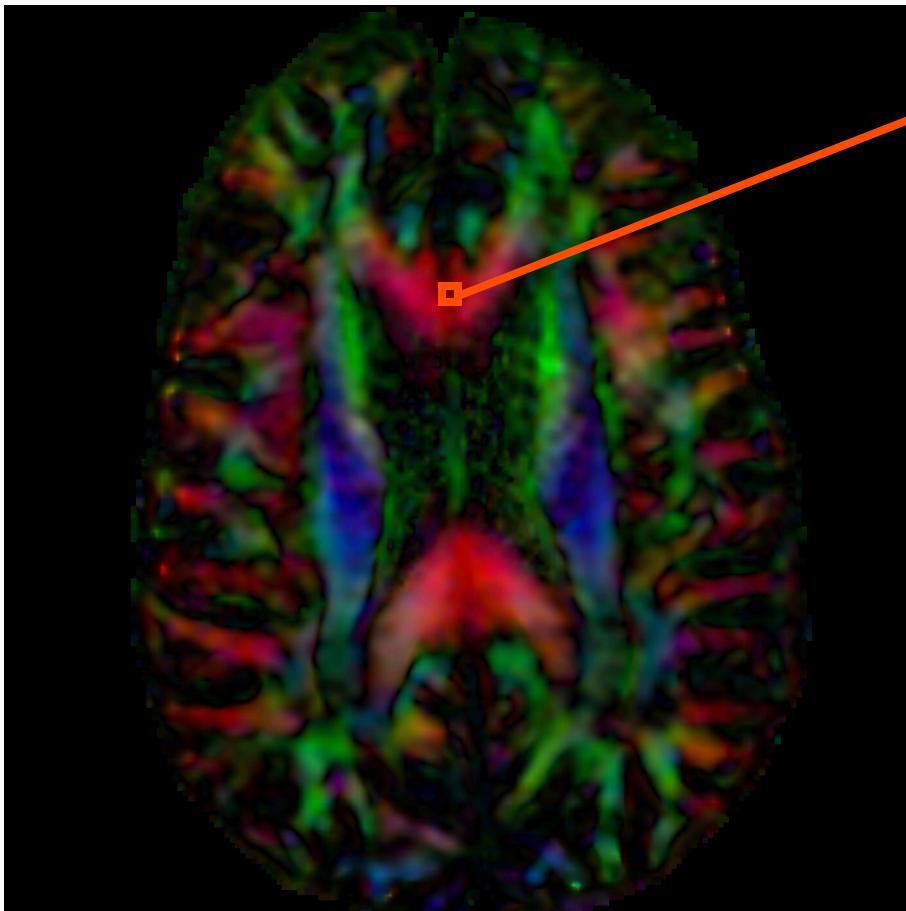


$$S_i = S_0 e^{-b \hat{g}_i^T \underline{D} \hat{g}_i}$$

↓

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

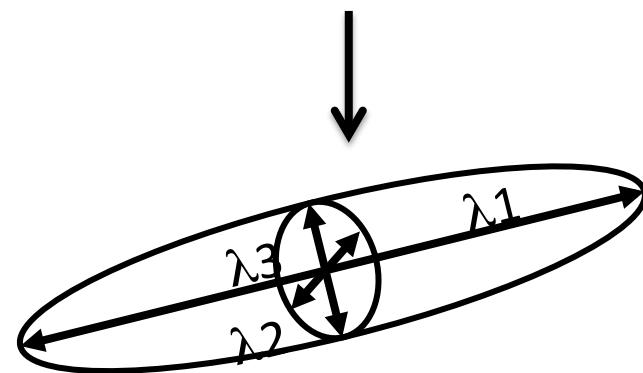
Diffusion Tensor Imaging



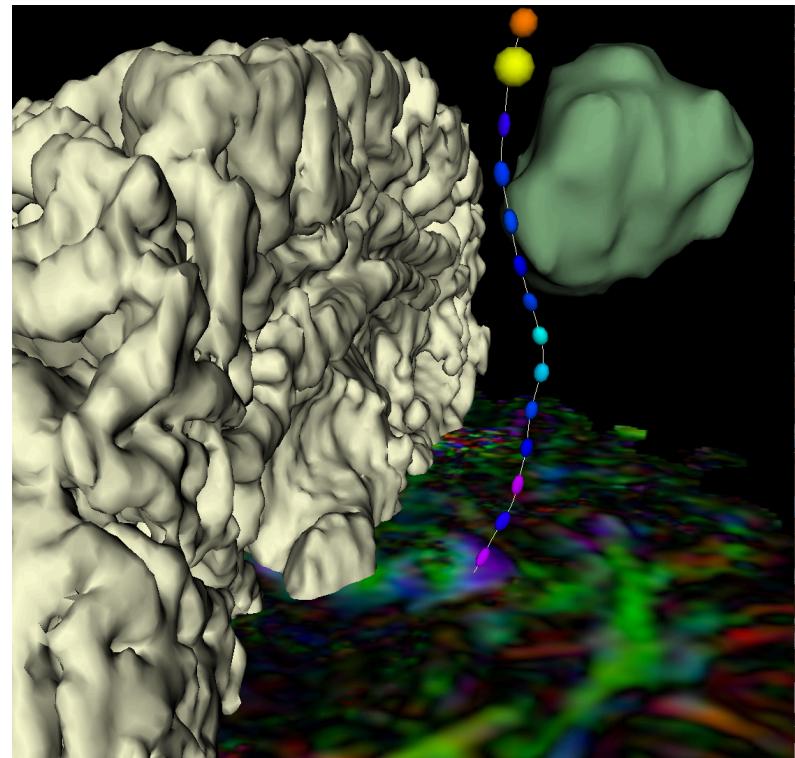
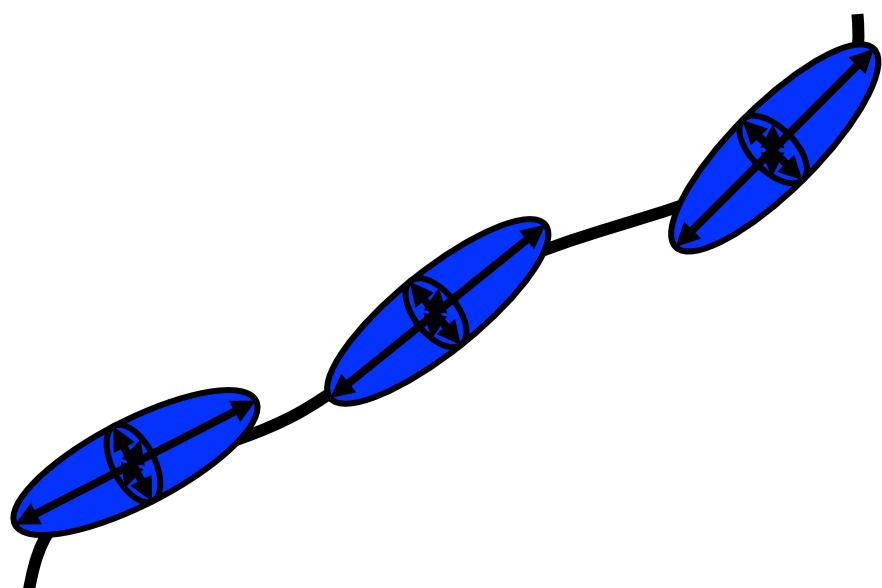
$$S_i = S_0 e^{-b \hat{g}^T \underline{D} \hat{g}_i}$$

↓

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

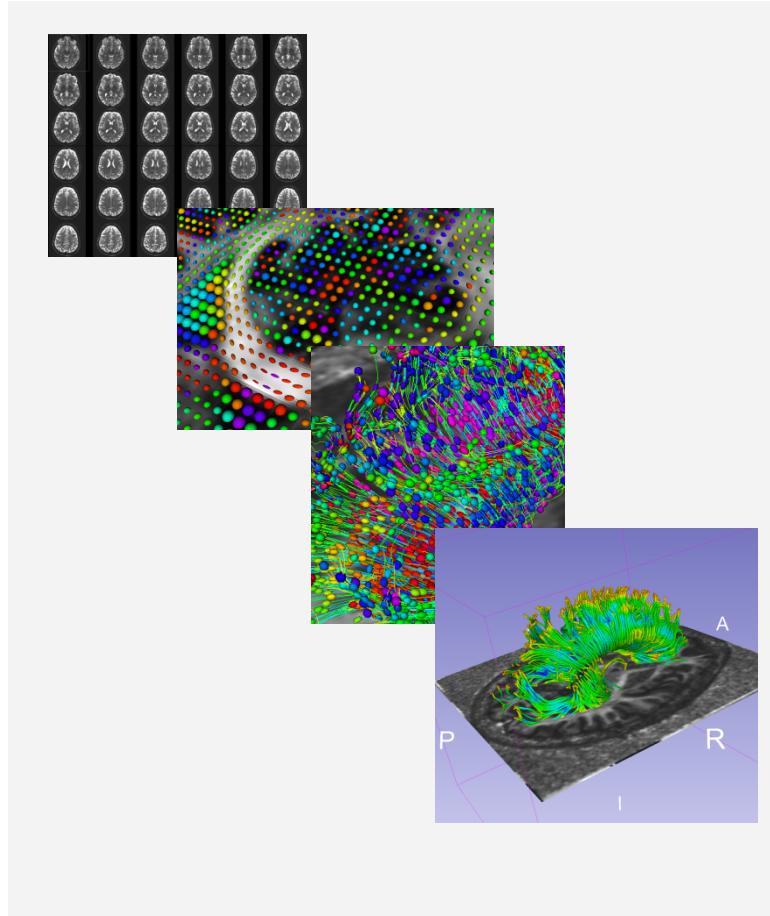


Tractography



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

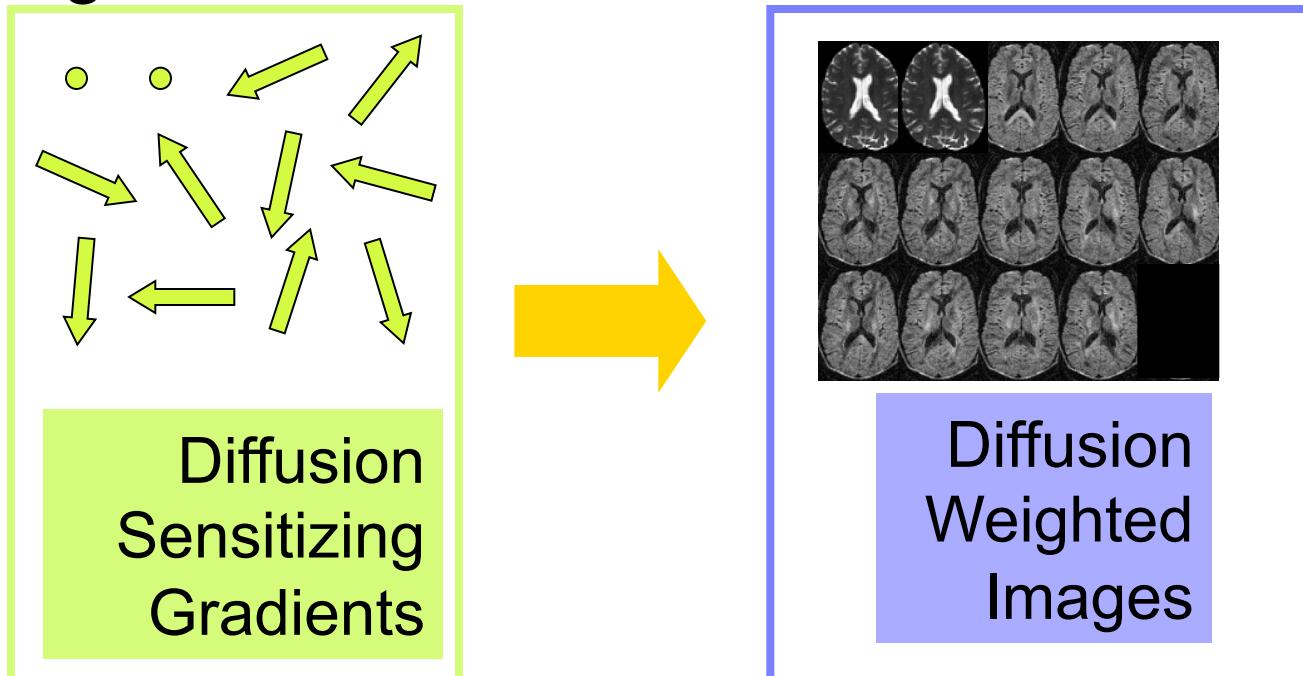
Tutorial Outline



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

Tutorial Dataset

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



3D Slicer

The tutorial uses the 3DSlicer (Version 4.6.2 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

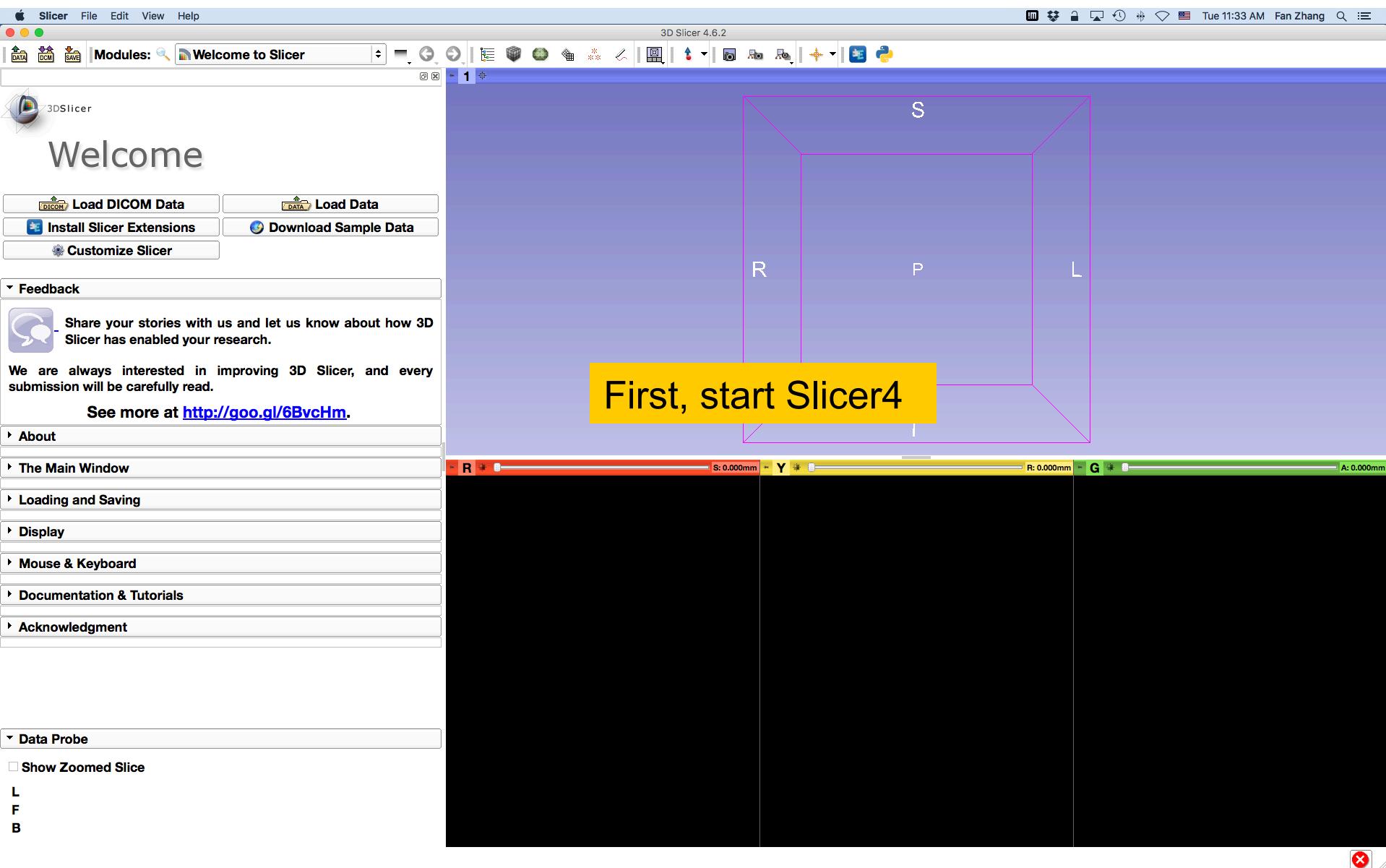
An open-source project to improve and extend diffusion magnetic resonance imaging software in 3D Slicer:

<http://slicerdmri.github.io>

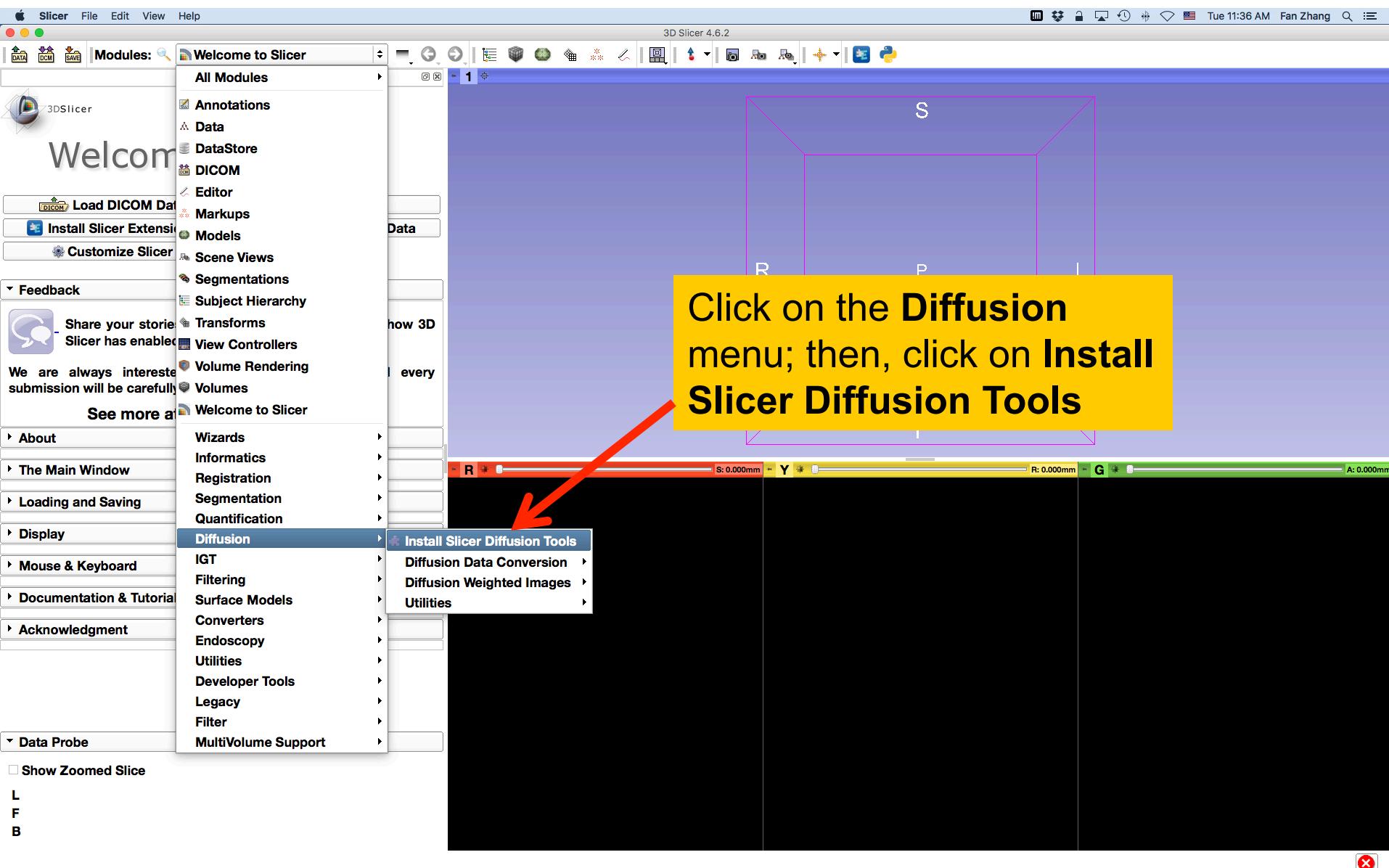
Disclaimer

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.

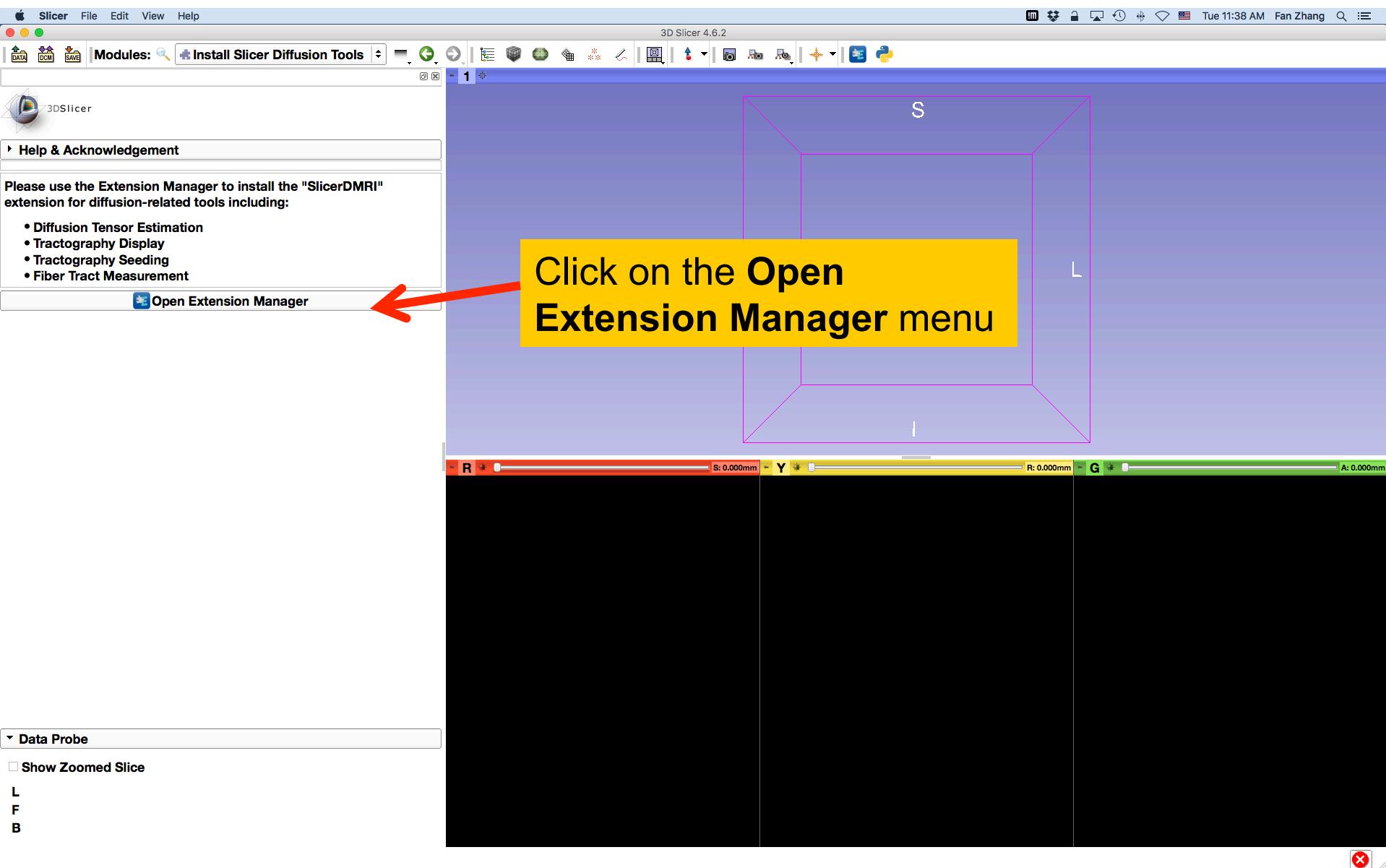
Install SlicerDMRI



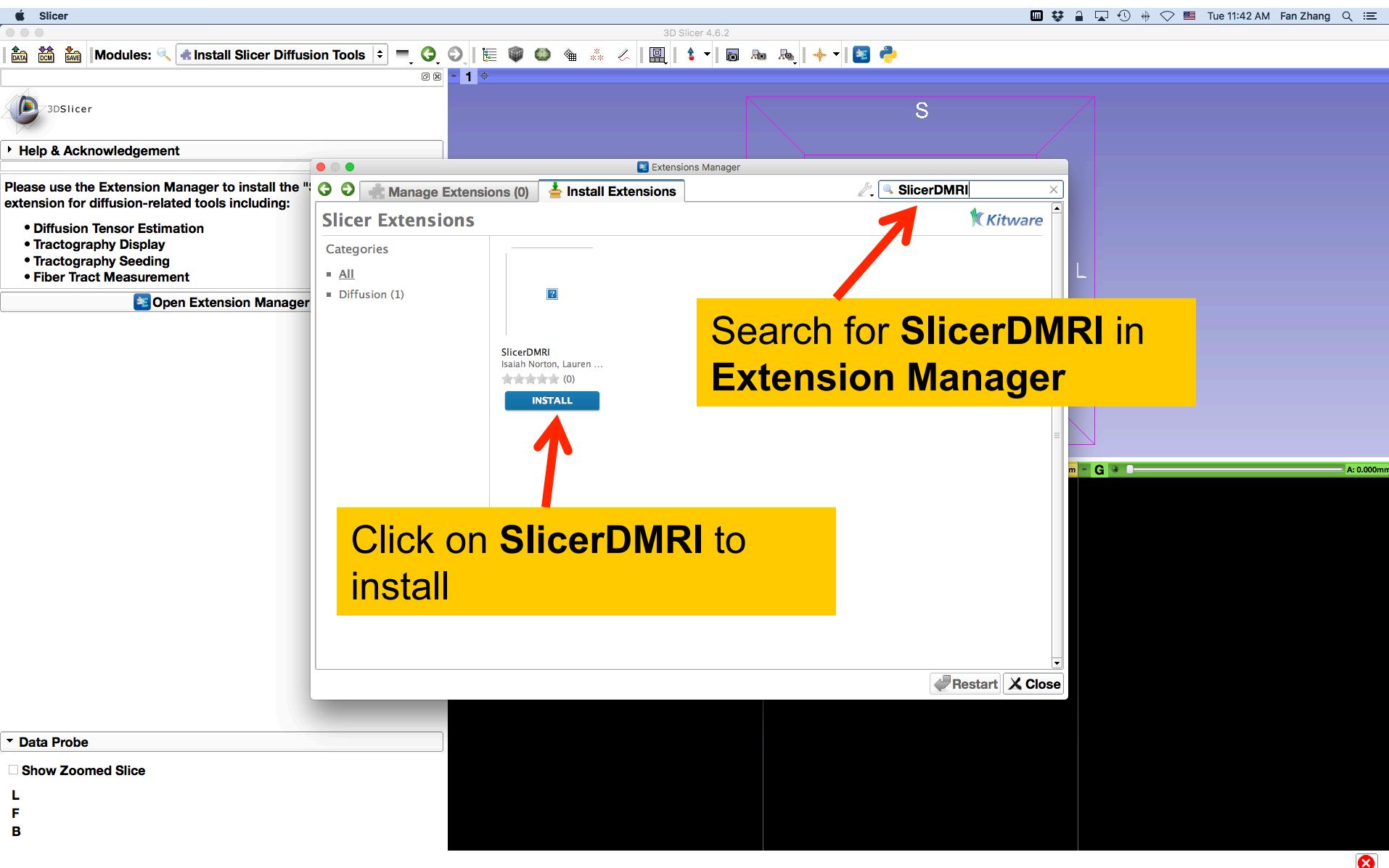
Install SlicerDMRI



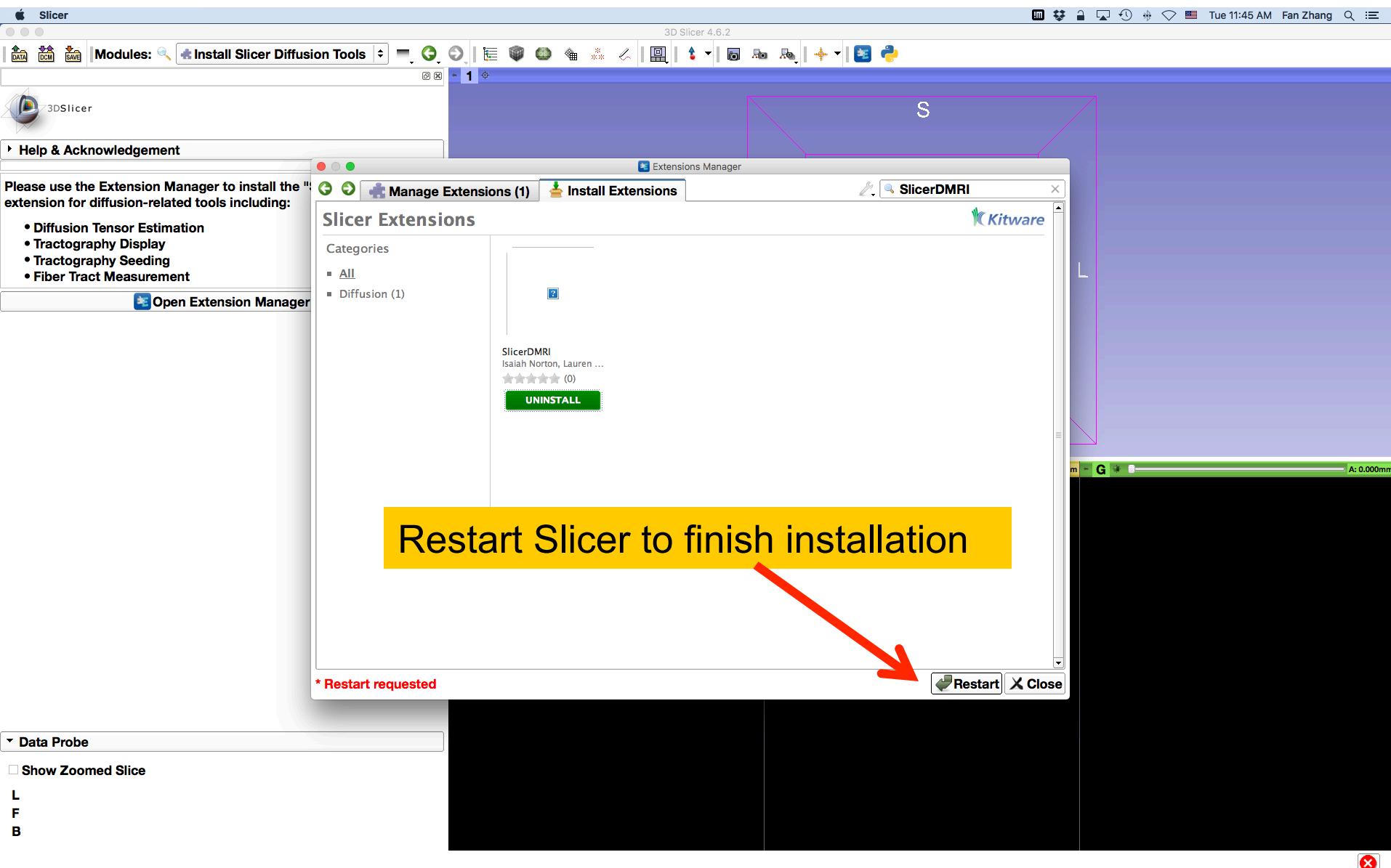
Install SlicerDMRI



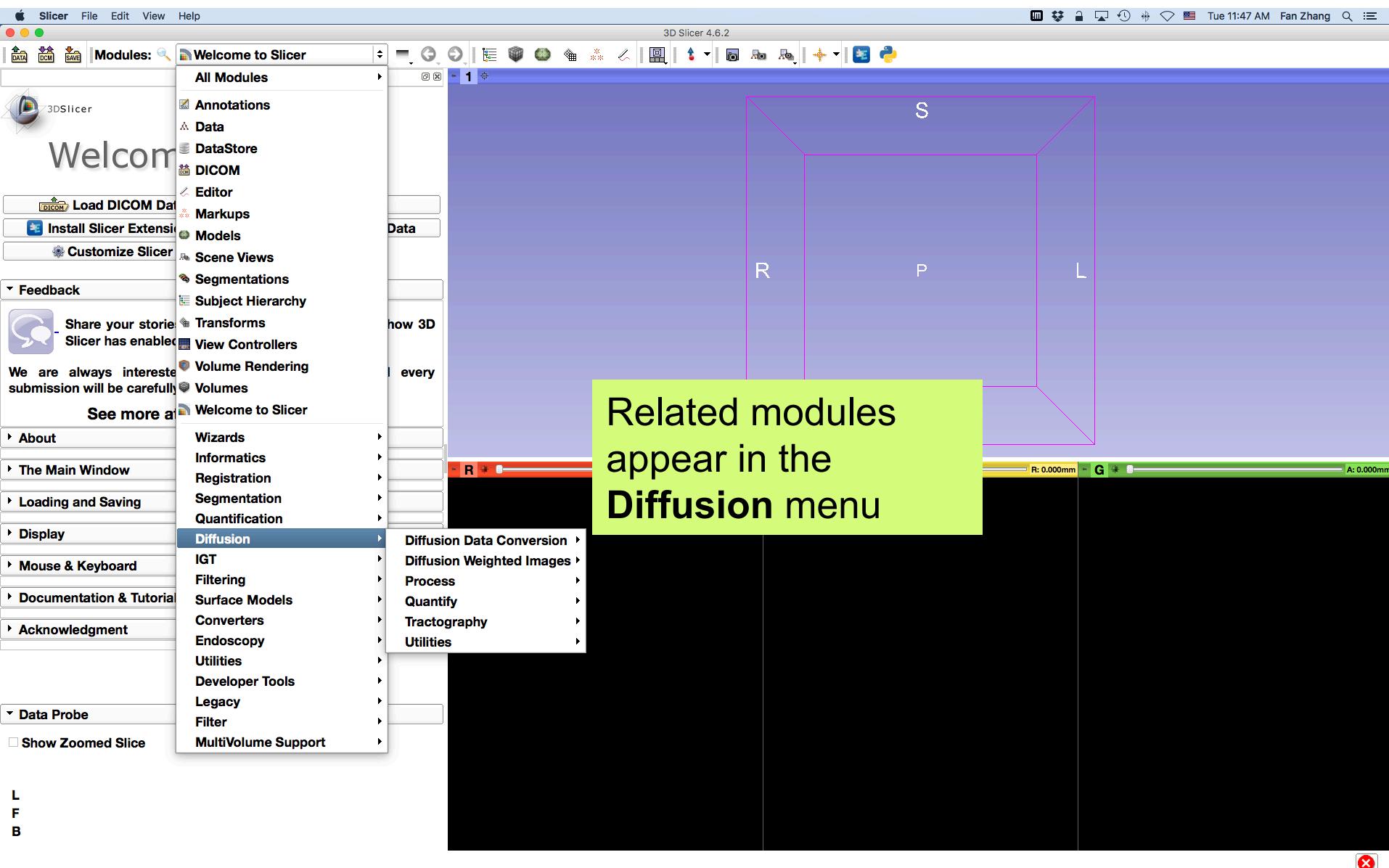
Install SlicerDMRI



Install SlicerDMRI



Install SlicerDMRI

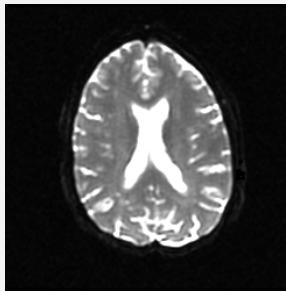


Learning Objectives

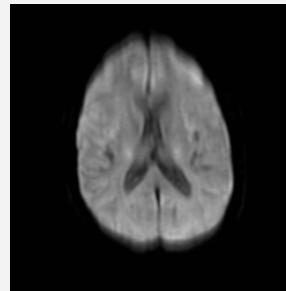
Following this tutorial, you'll be able to

- 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

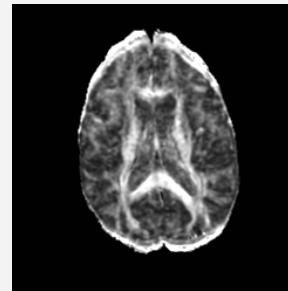
MR Diffusion Analysis Pipeline



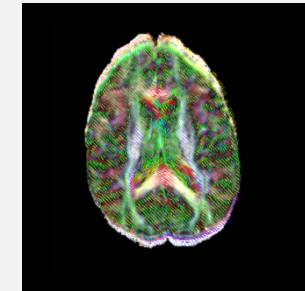
DWI
Acquisition



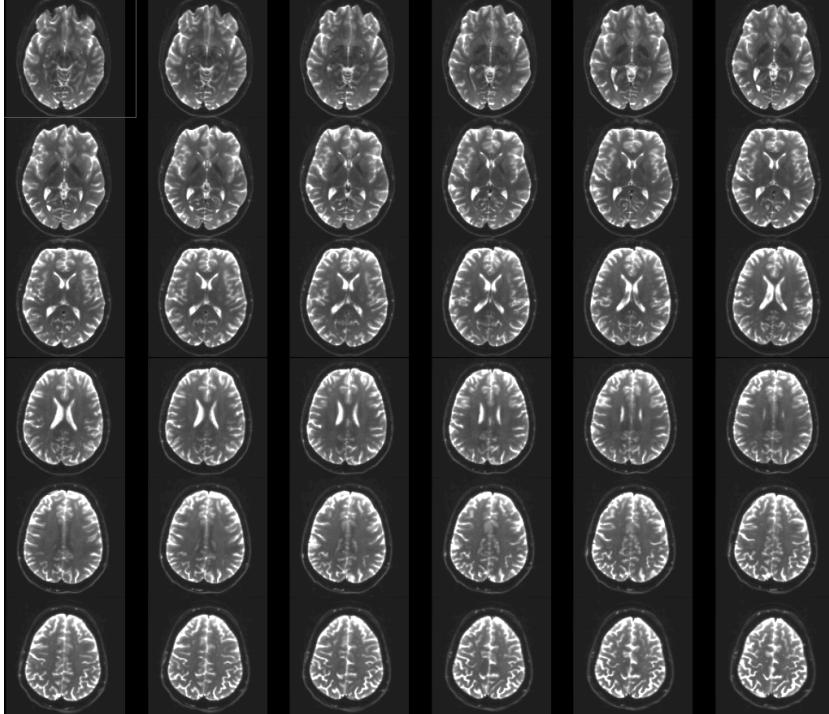
Tensor
Calculation



Scalar
Maps



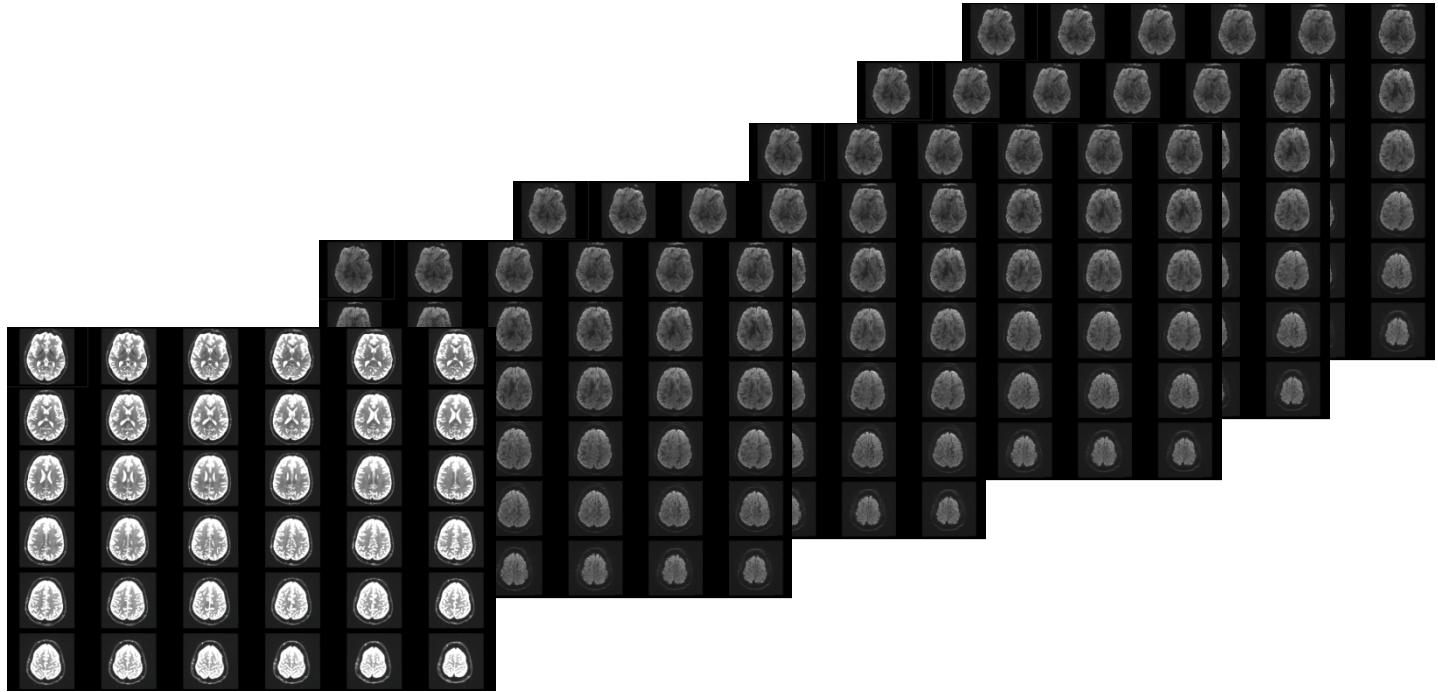
3D
Visualization



Part 1:

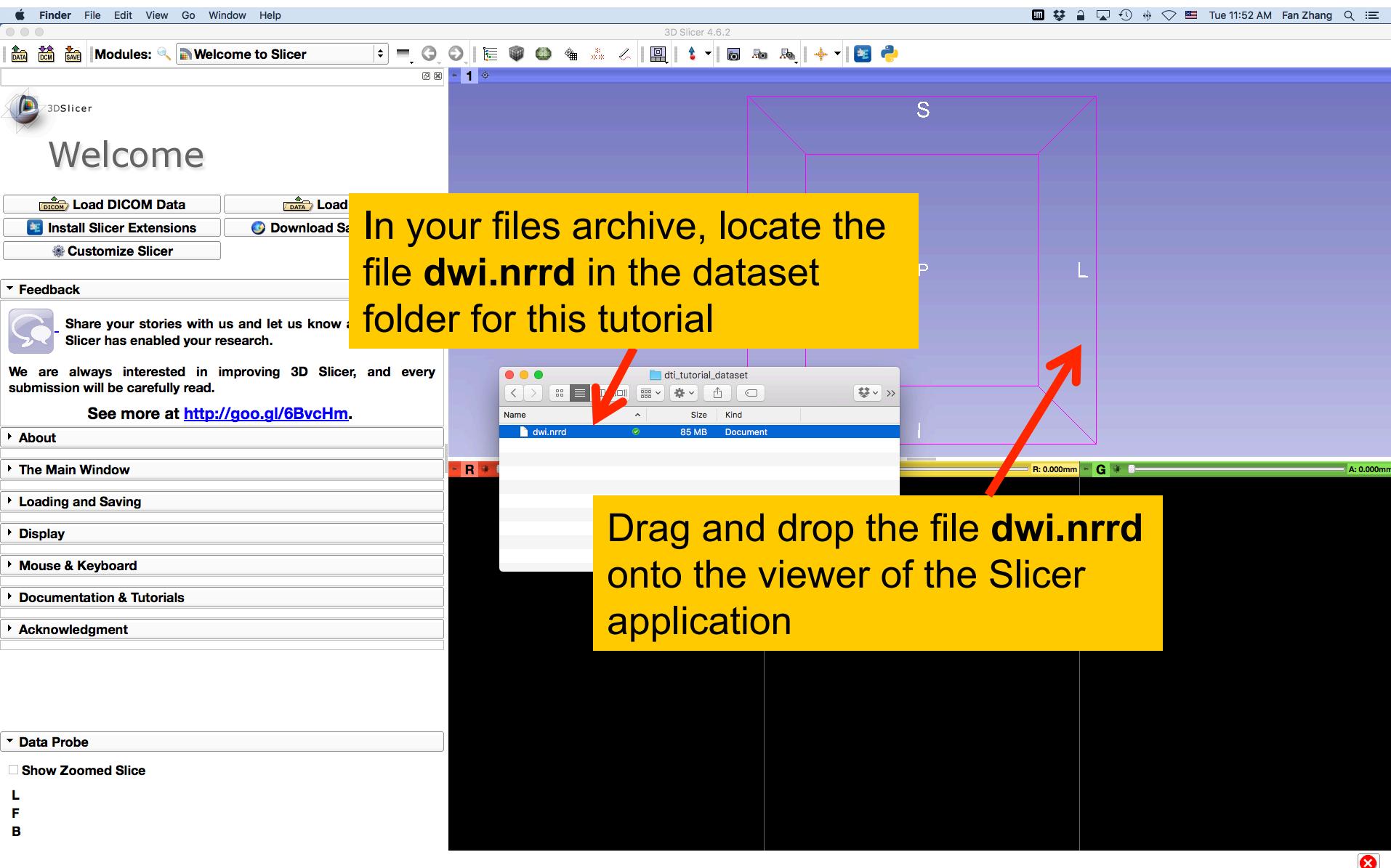
From DWI images to Tensors

Understanding the DWI Dataset

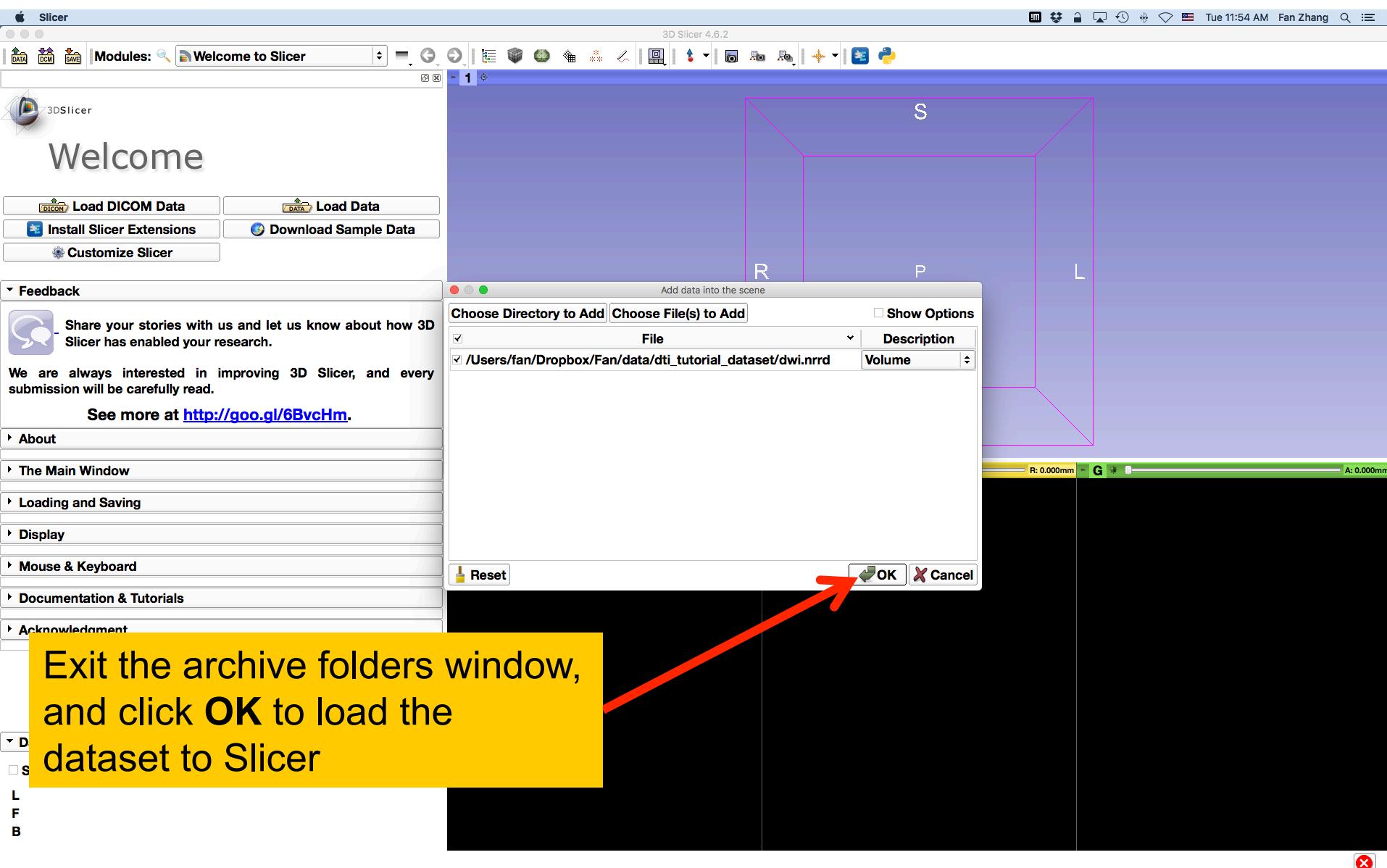


The Diffusion Weighted Imaging (DWI) dataset is composed of 41 volumes acquired with 41 different diffusion-sensitizing gradient directions, and one baseline image acquired without diffusion weighting.

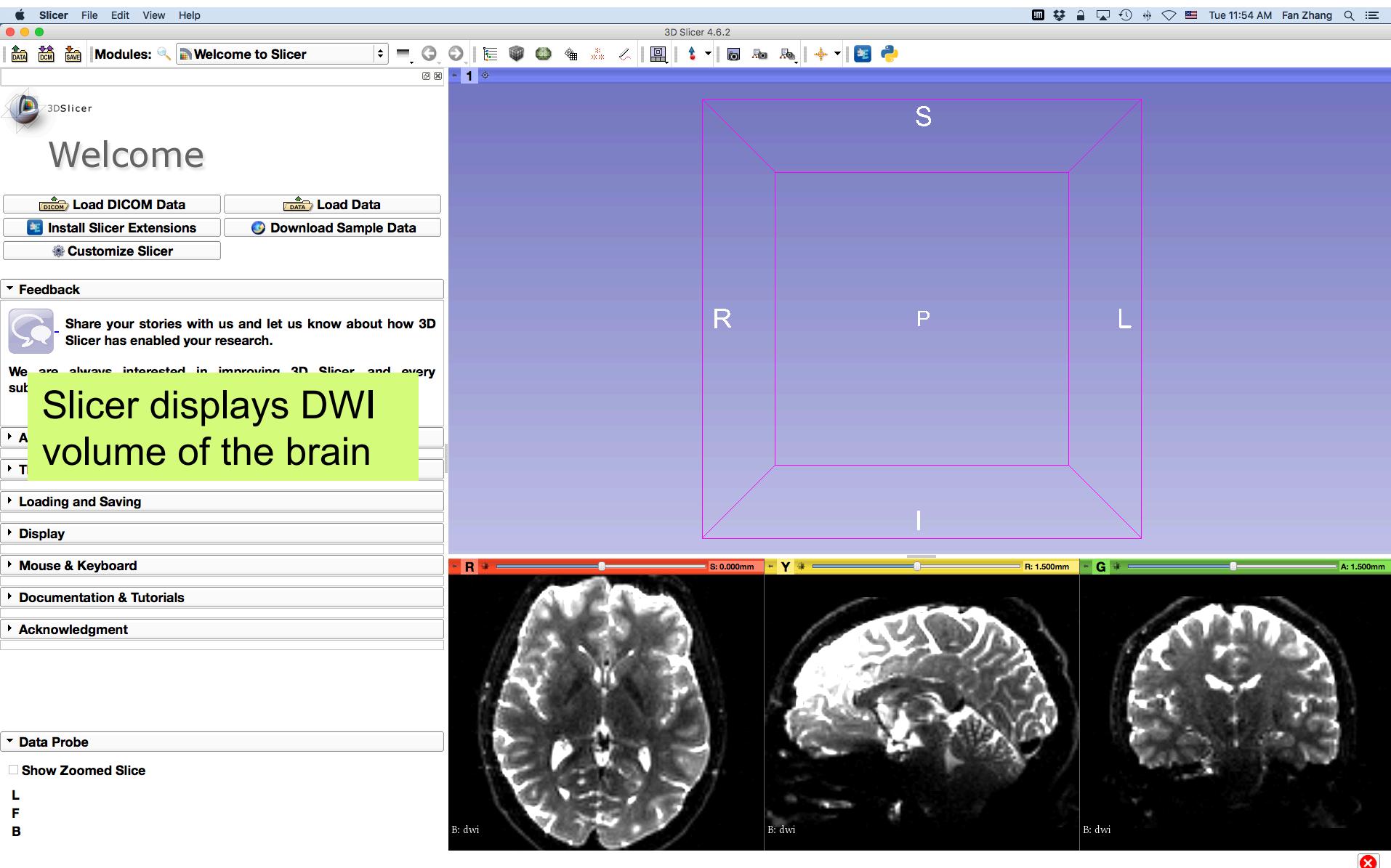
Loading the DWI Dataset



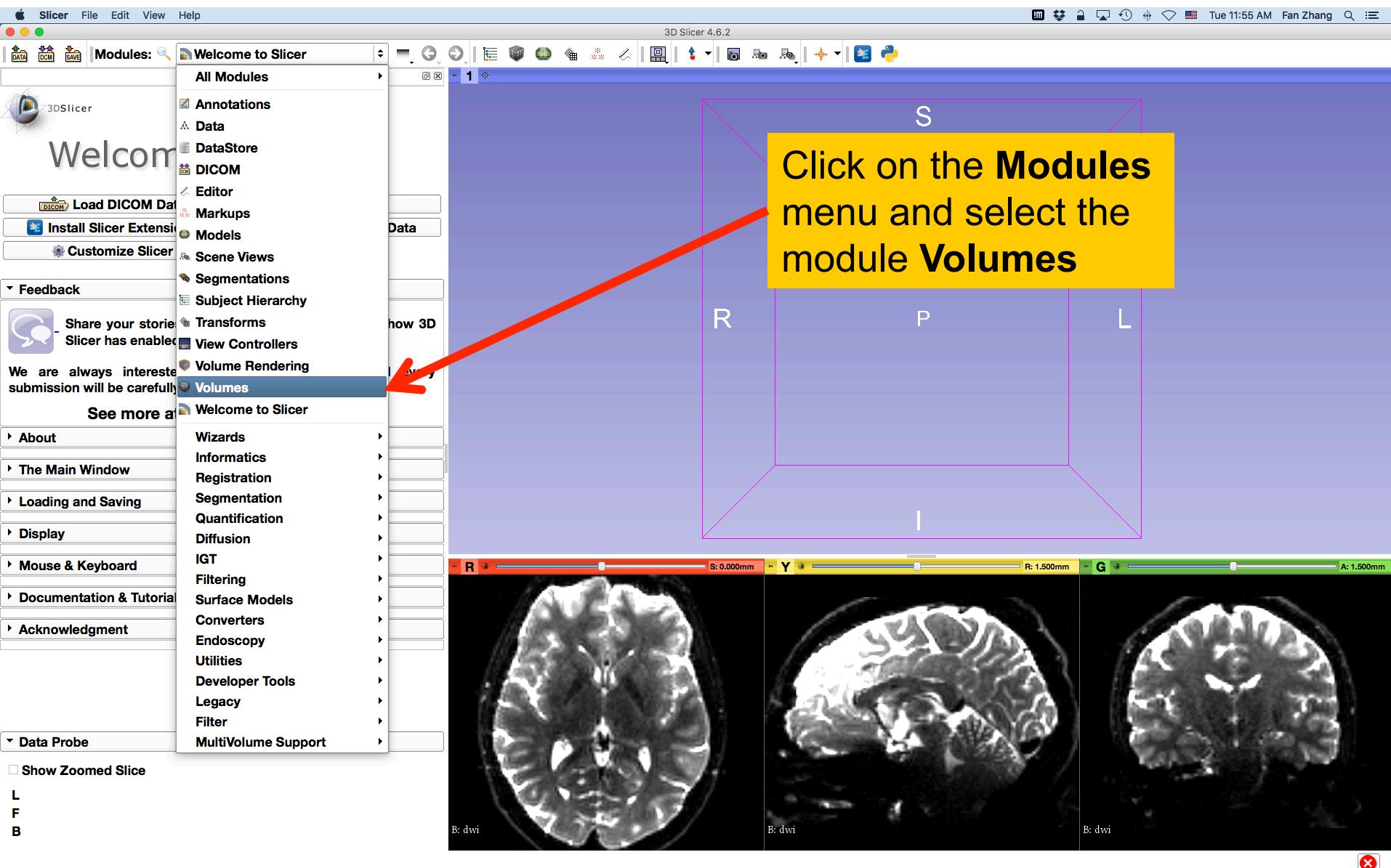
Loading the DWI Dataset



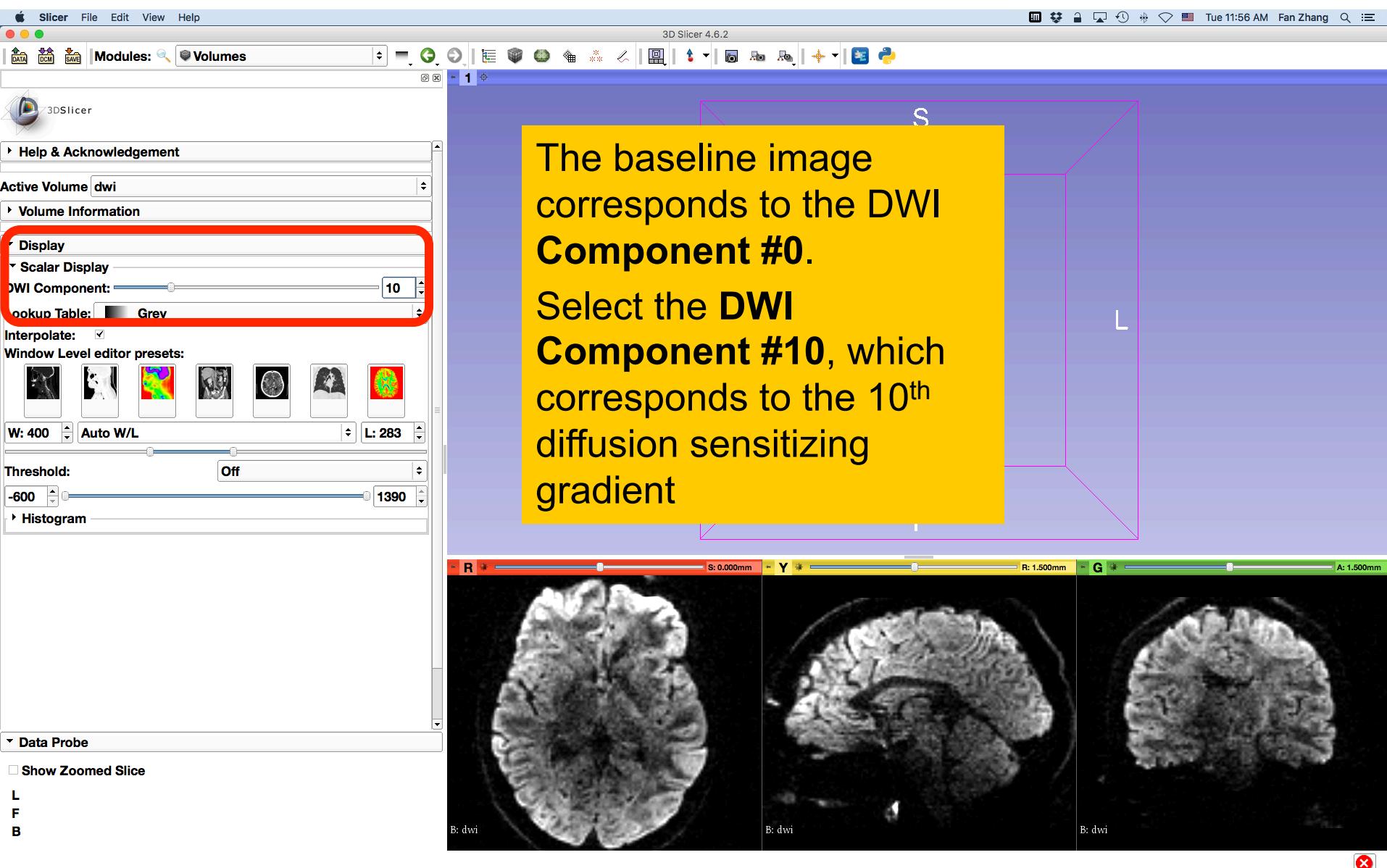
Loading the DWI Dataset



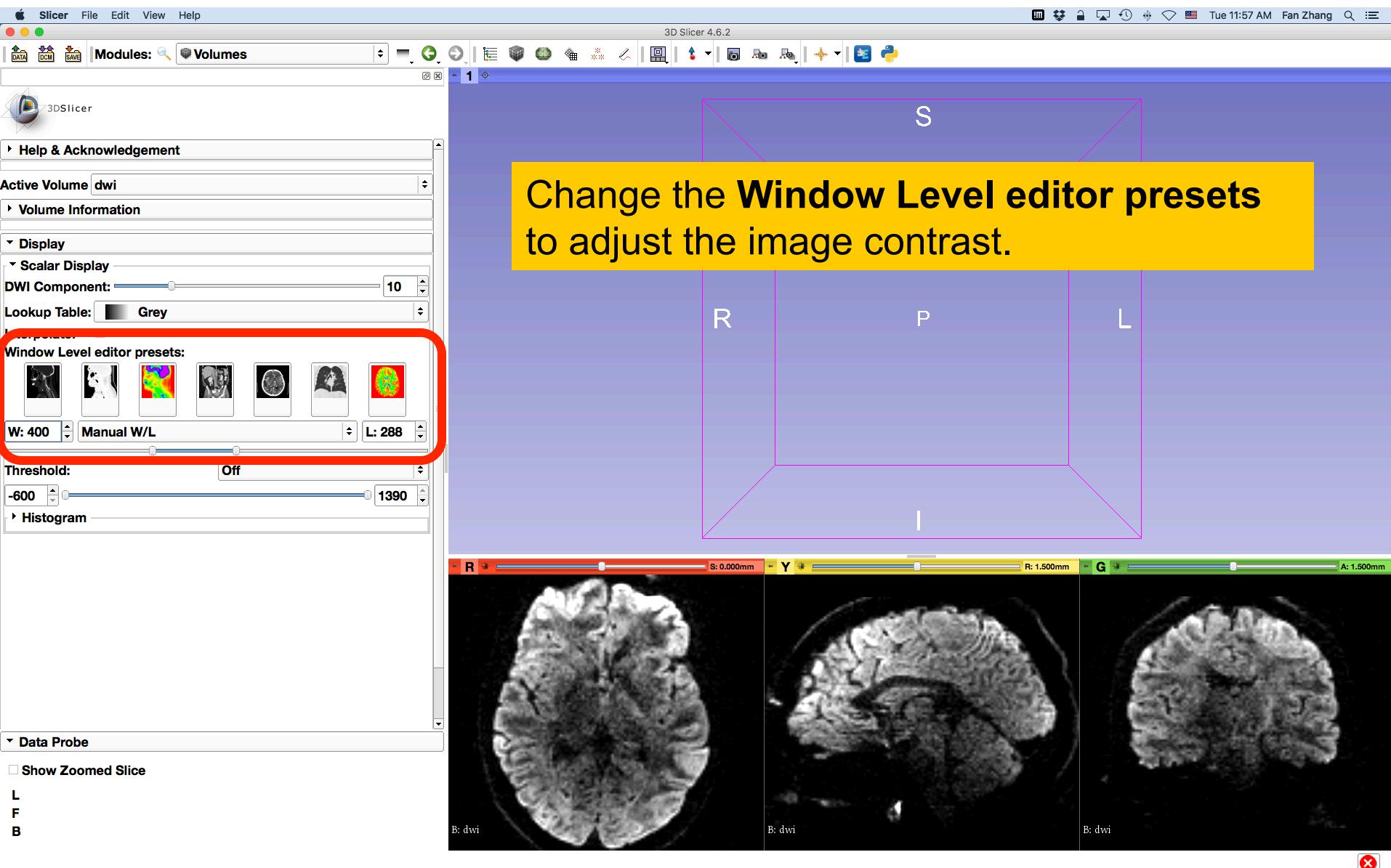
Loading the DWI Dataset



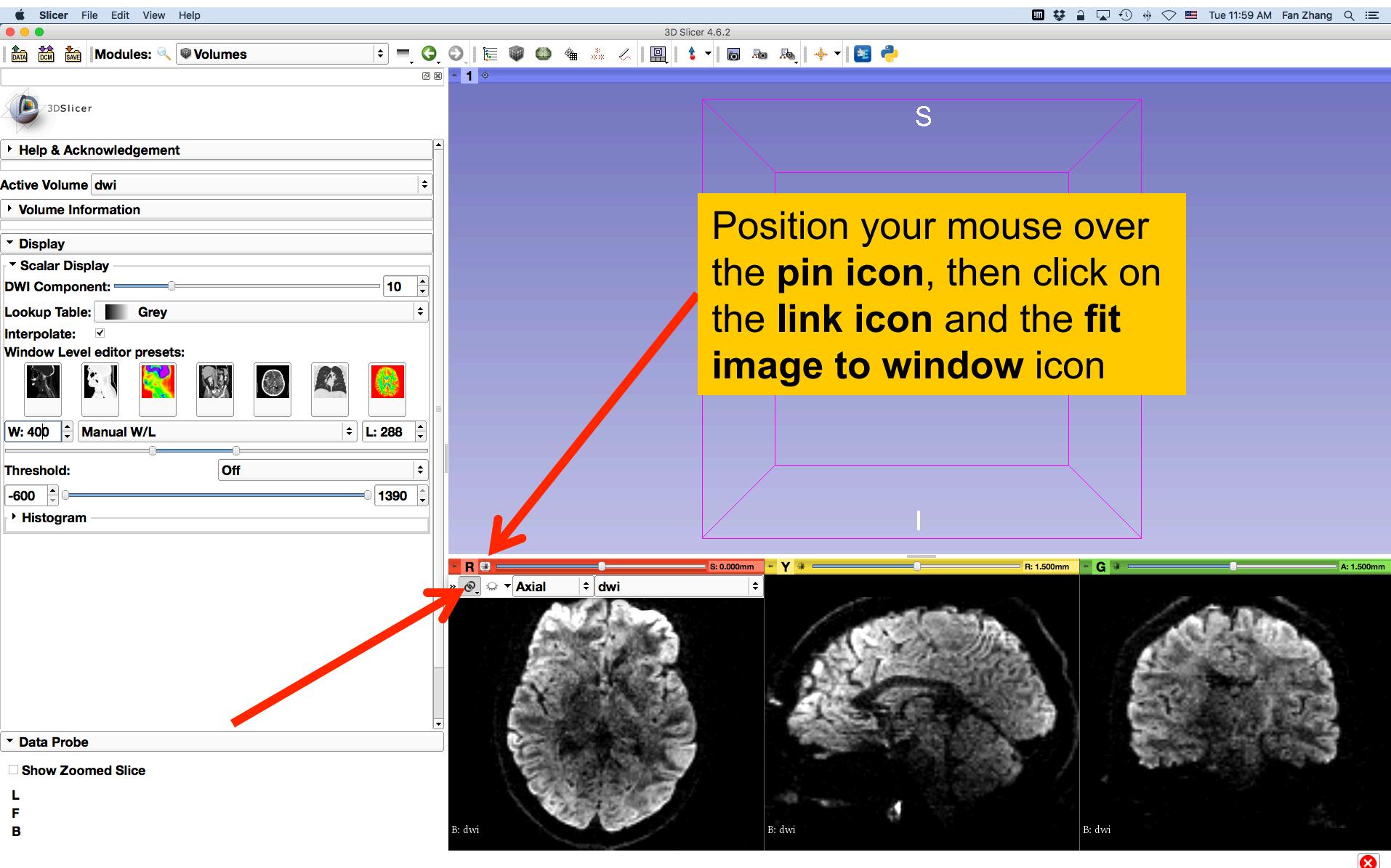
Loading the DWI Dataset



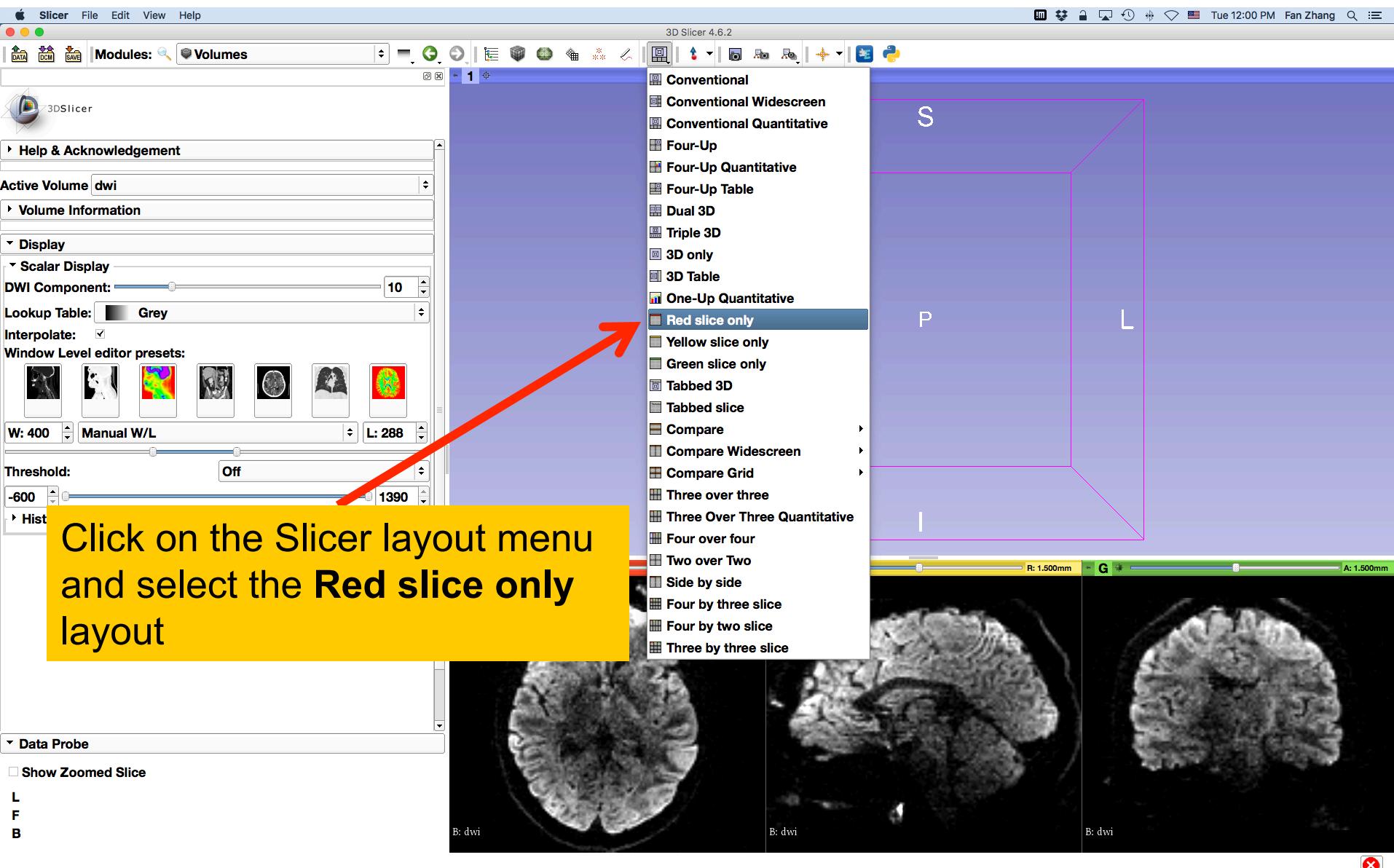
Loading the DWI Dataset



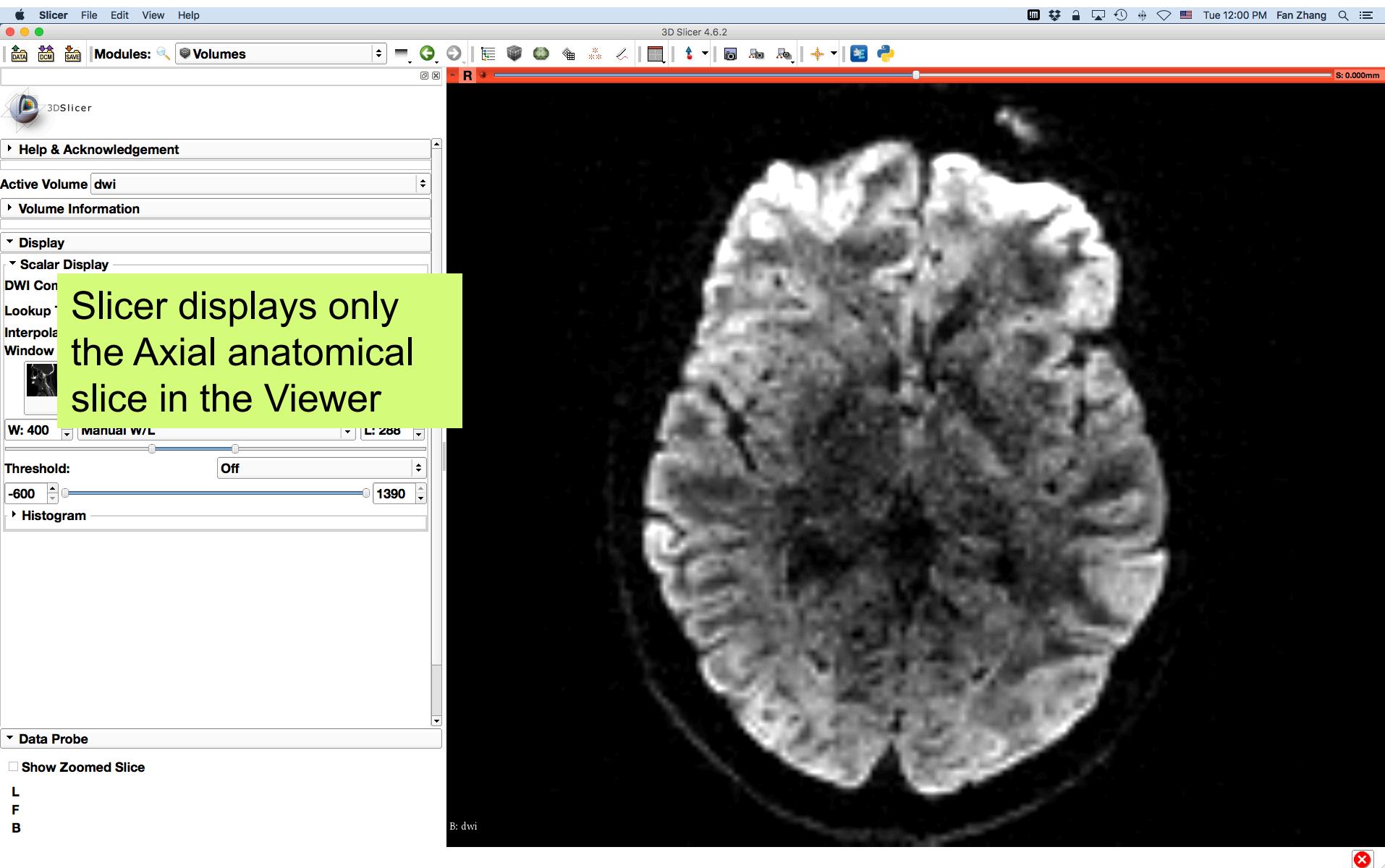
Loading the DWI Dataset



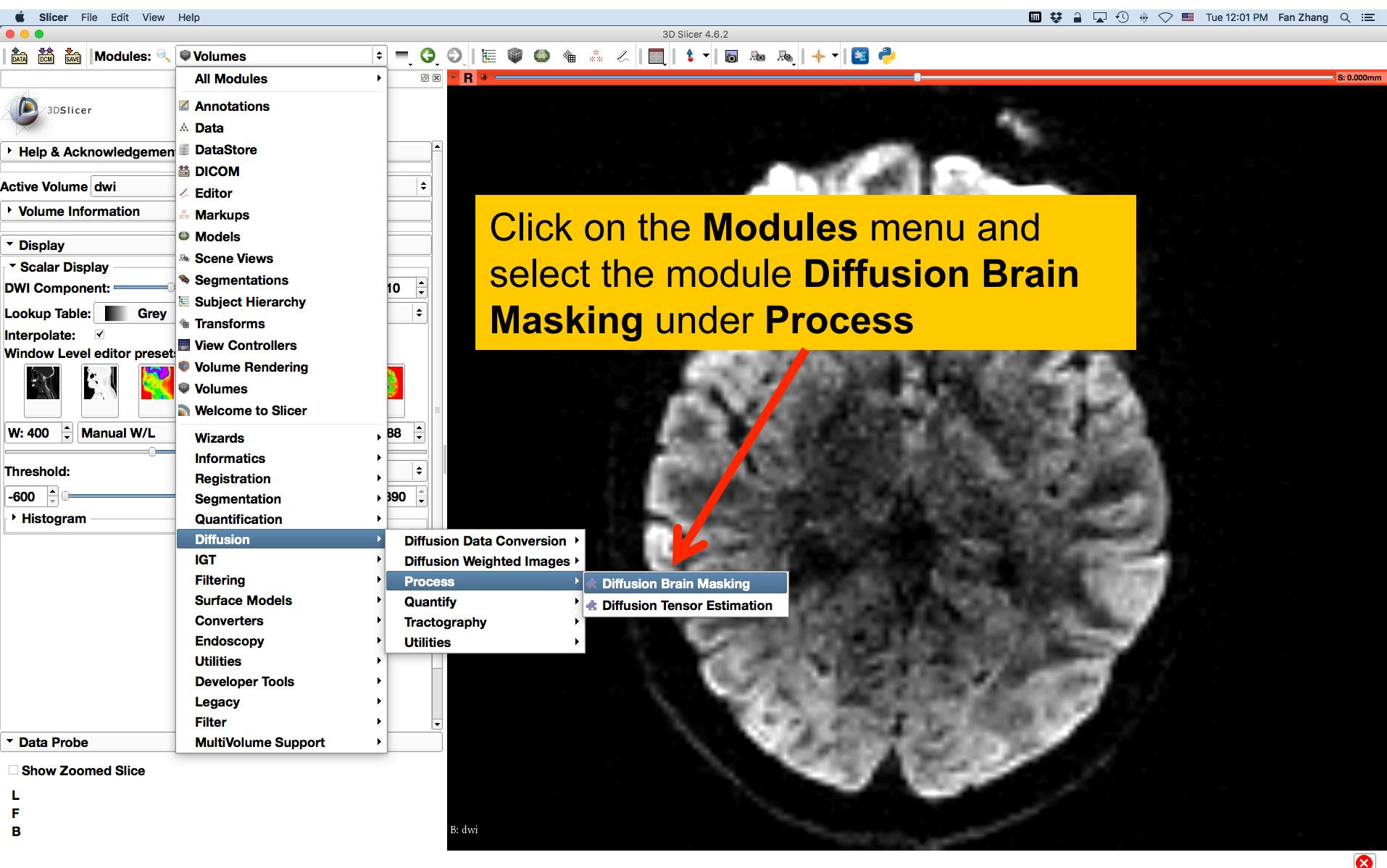
Loading the DWI Dataset



Loading the DWI Dataset



Creating a brain mask



Creating a brain mask

The screenshot shows the 3D Slicer interface with the 'Diffusion Brain Masking' module selected. The parameter settings are as follows:

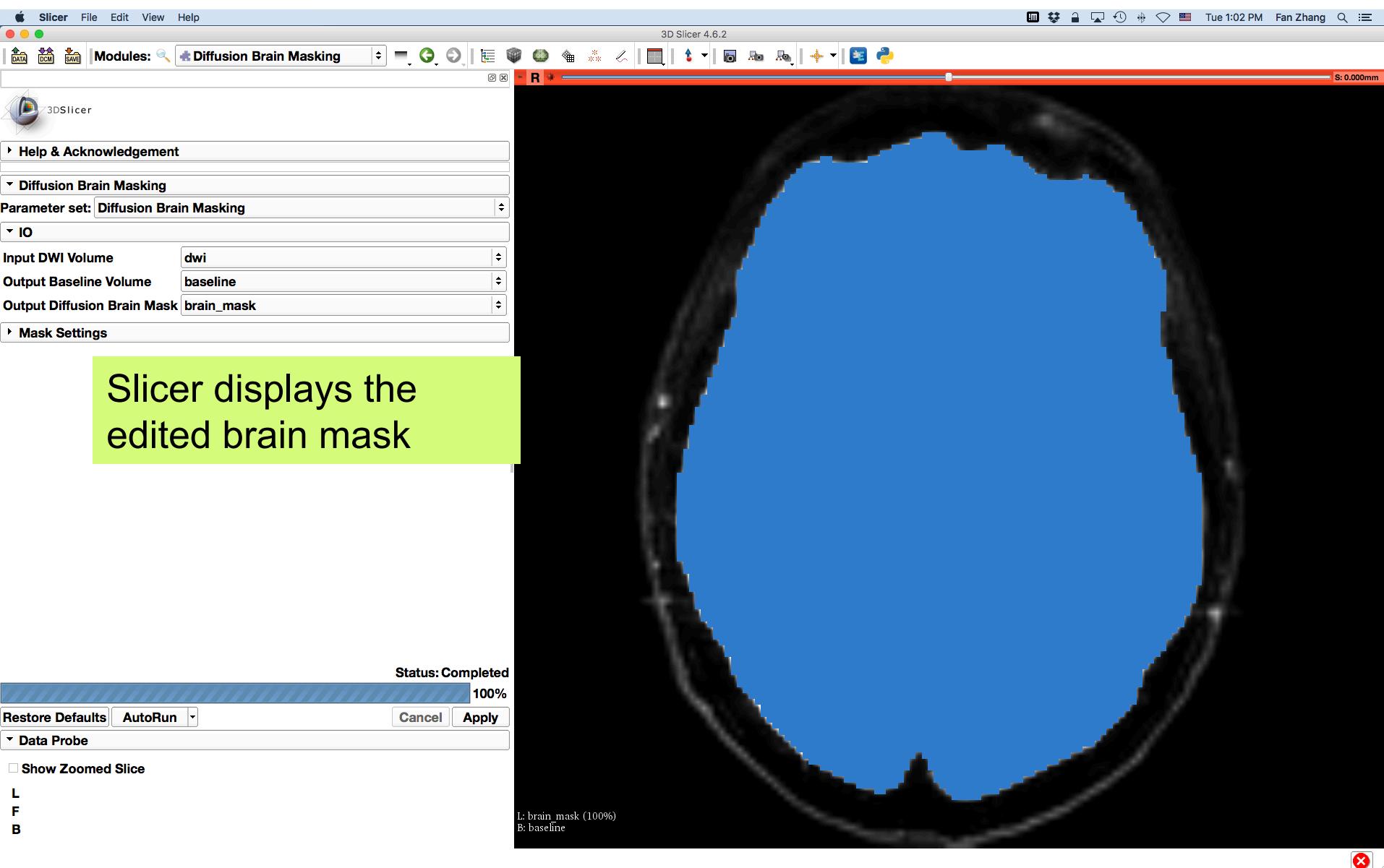
- Input DWI Volume: dwi
- Output Baseline Volume: baseline
- Output Diffusion Brain Mask: brain_mask

A yellow callout box contains the following instructions:

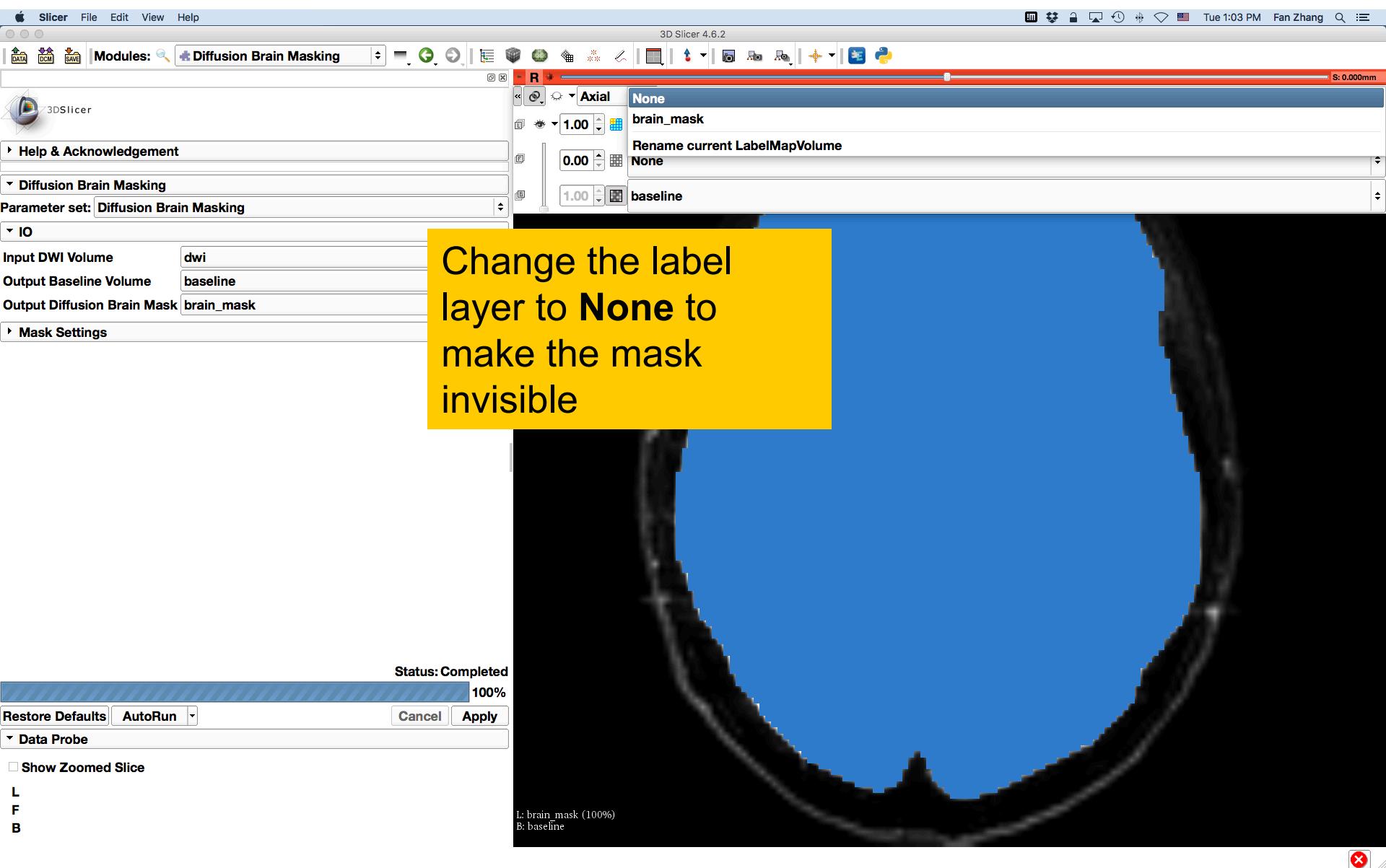
- select the **Input DWI volume 'dwi'**
- select **Output Baseline Volume**
'Create new Volume as...', and name it '**baseline**'
- select **Output Diffusion Brain Mask**
'Create new LabelMapVolume as...', and name it '**dwi_mask**'
- click on **Apply**.

The main window displays a grayscale axial slice of a brain, labeled 'B: dwi' at the bottom left.

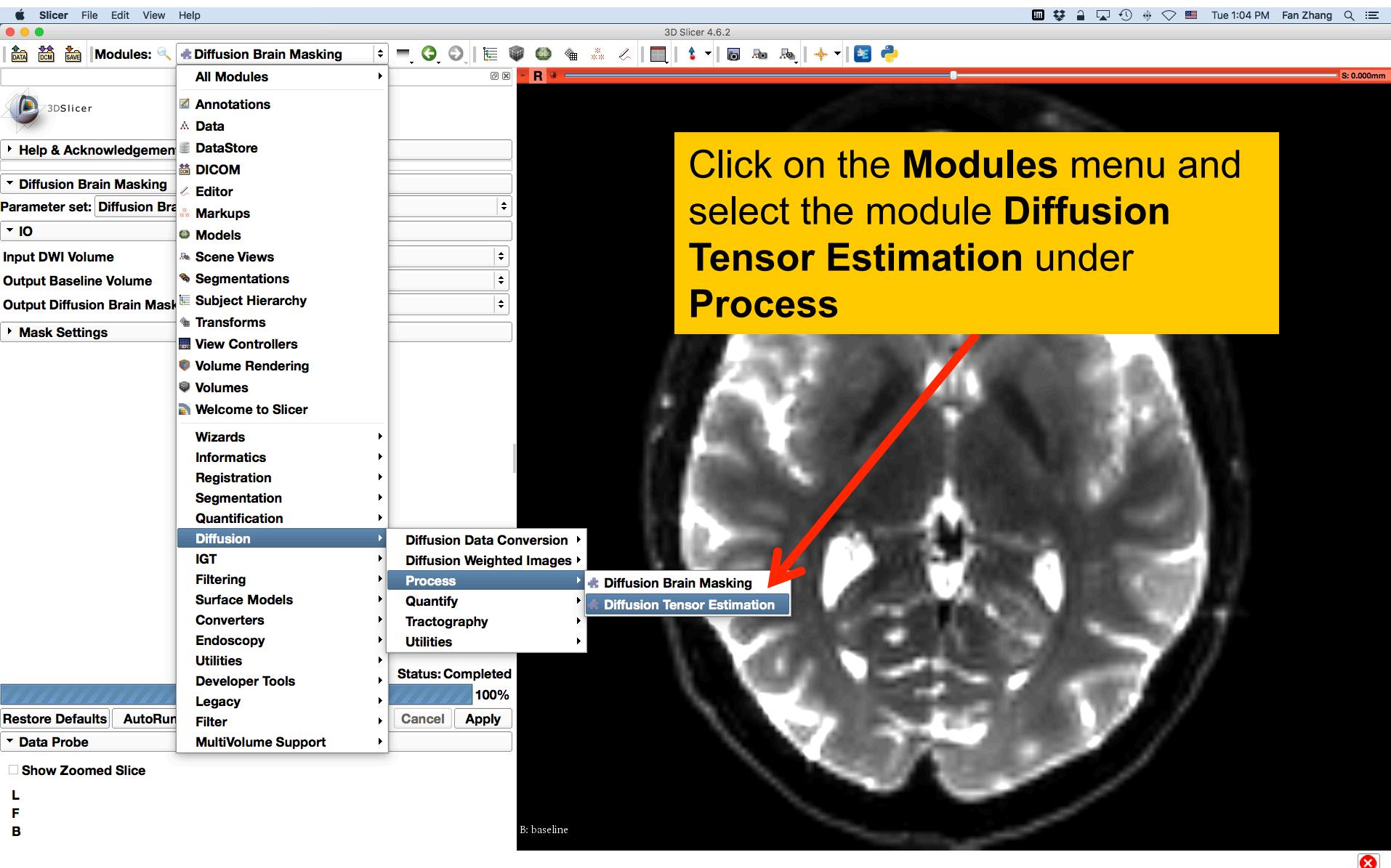
Creating a brain mask



Creating a brain mask



Estimating the tensor



Estimating the tensor

The screenshot shows the 3D Slicer interface with the 'Diffusion Tensor Estimation' module selected. A red box highlights the parameter settings for this module:

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

Below these settings, under 'Advanced Settings', the 'Fitting Method' is set to 'WLS' (Weighted Least Squares), indicated by a checked radio button. A red arrow points to the 'Apply' button at the bottom of the module panel.

-Set the Input DWI volume to 'dwi'

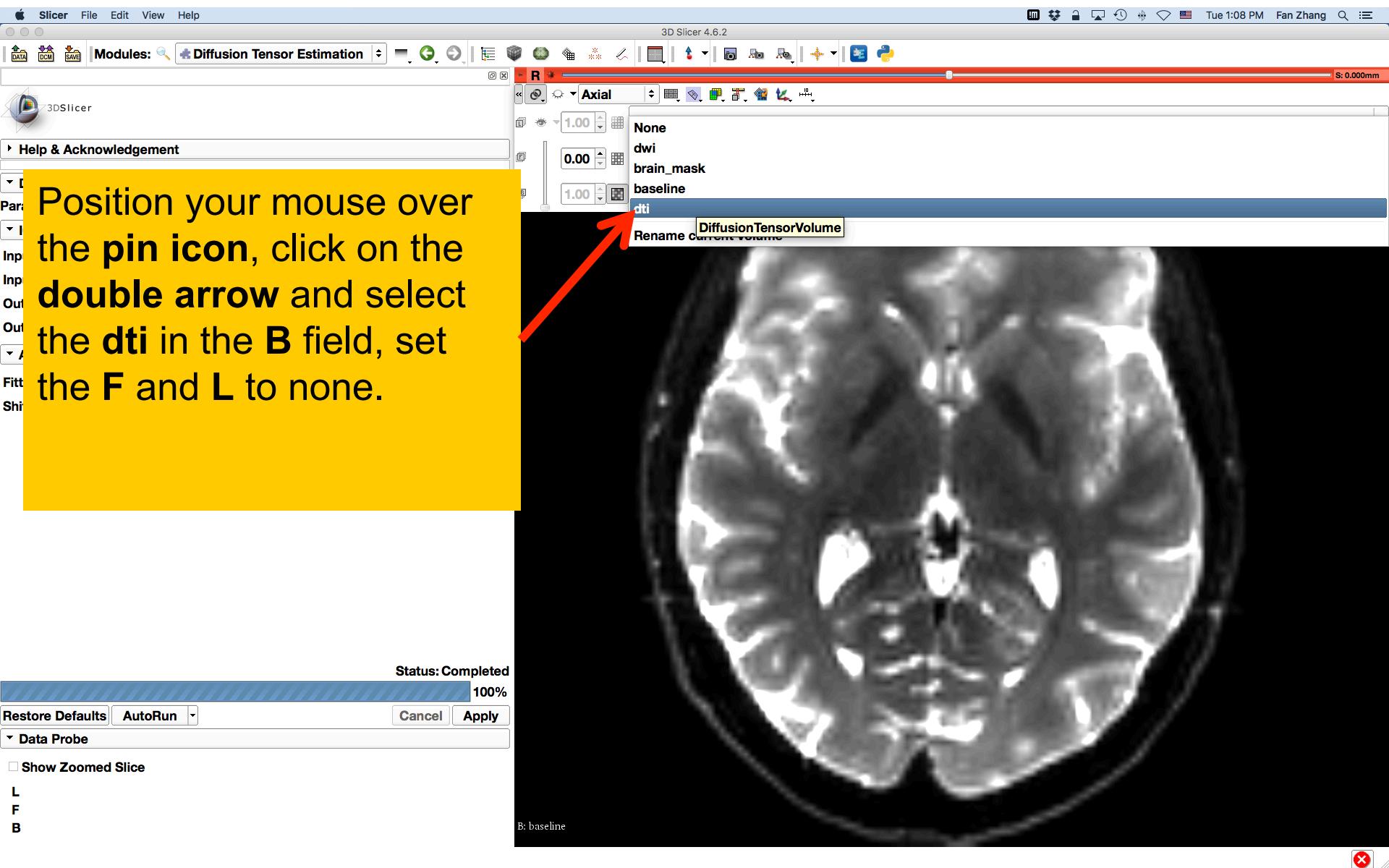
-Set the Input Brain Mask to 'dwi_mask'

- Select Output DTI Volume 'Create DiffusionTensorVolume as ...', and name it 'dti'

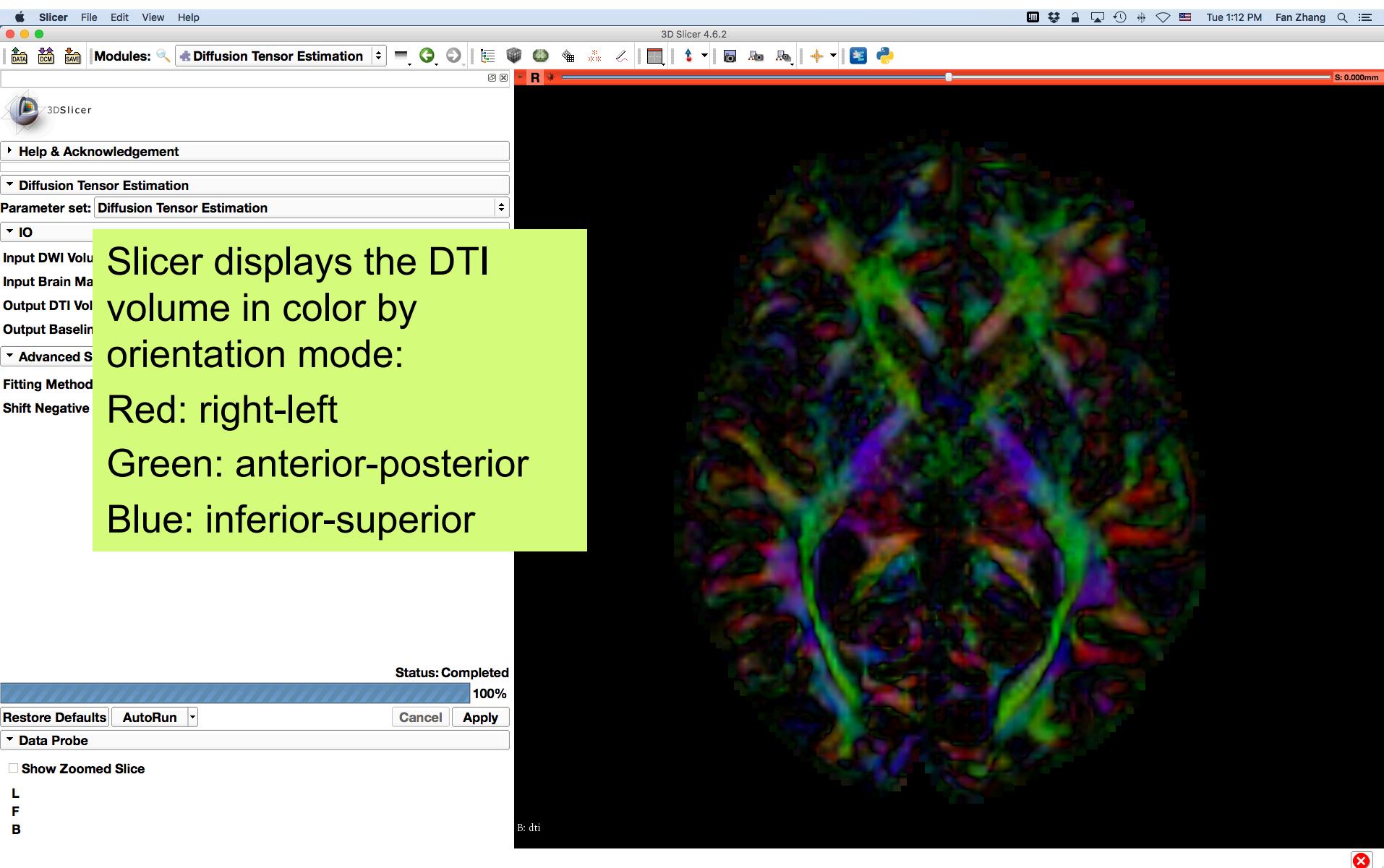
-Set Output Baseline Volume to 'baseline'

-Select the Estimation Parameters 'WLS' (Weighted Least Squares) and click on Apply.

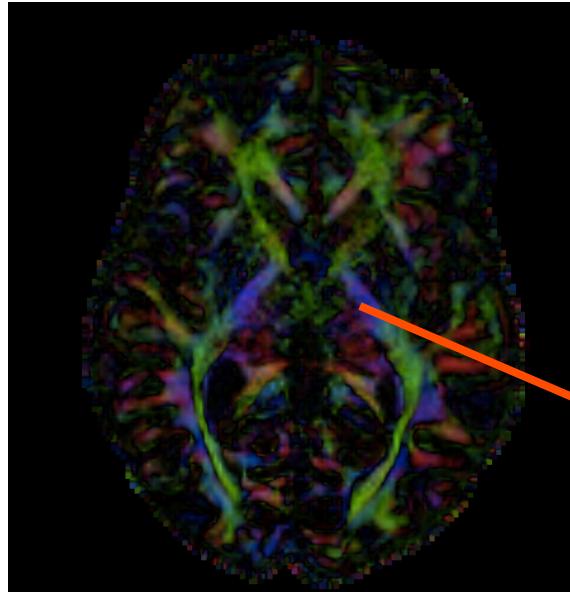
Estimating the tensor



Exploring the DWI Dataset



Diffusion Tensor Data



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

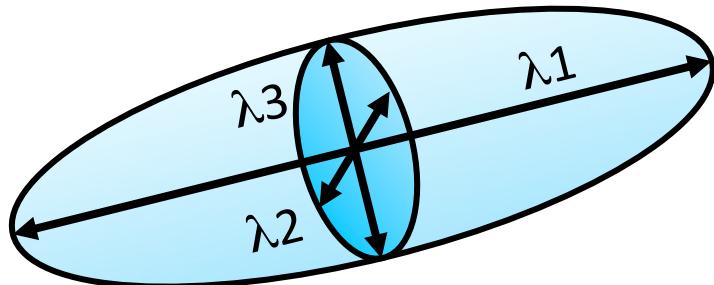
Stejskal-Tanner equation (1965)

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

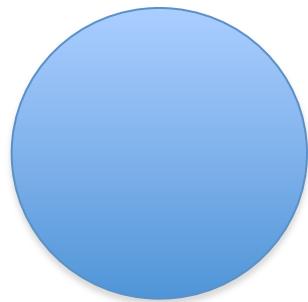
The diffusion tensor \underline{D} in the voxel (I,J,K) is a 3x3 symmetric matrix.

Diffusion Tensor

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

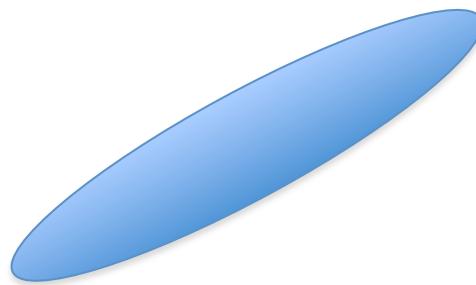


Diffusion Tensor Shape



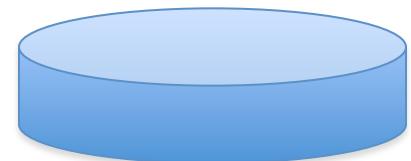
$$\lambda_1 = \lambda_2 = \lambda_3$$

Isotropic media
(Cerebrospinal
Fluid, gray matter)



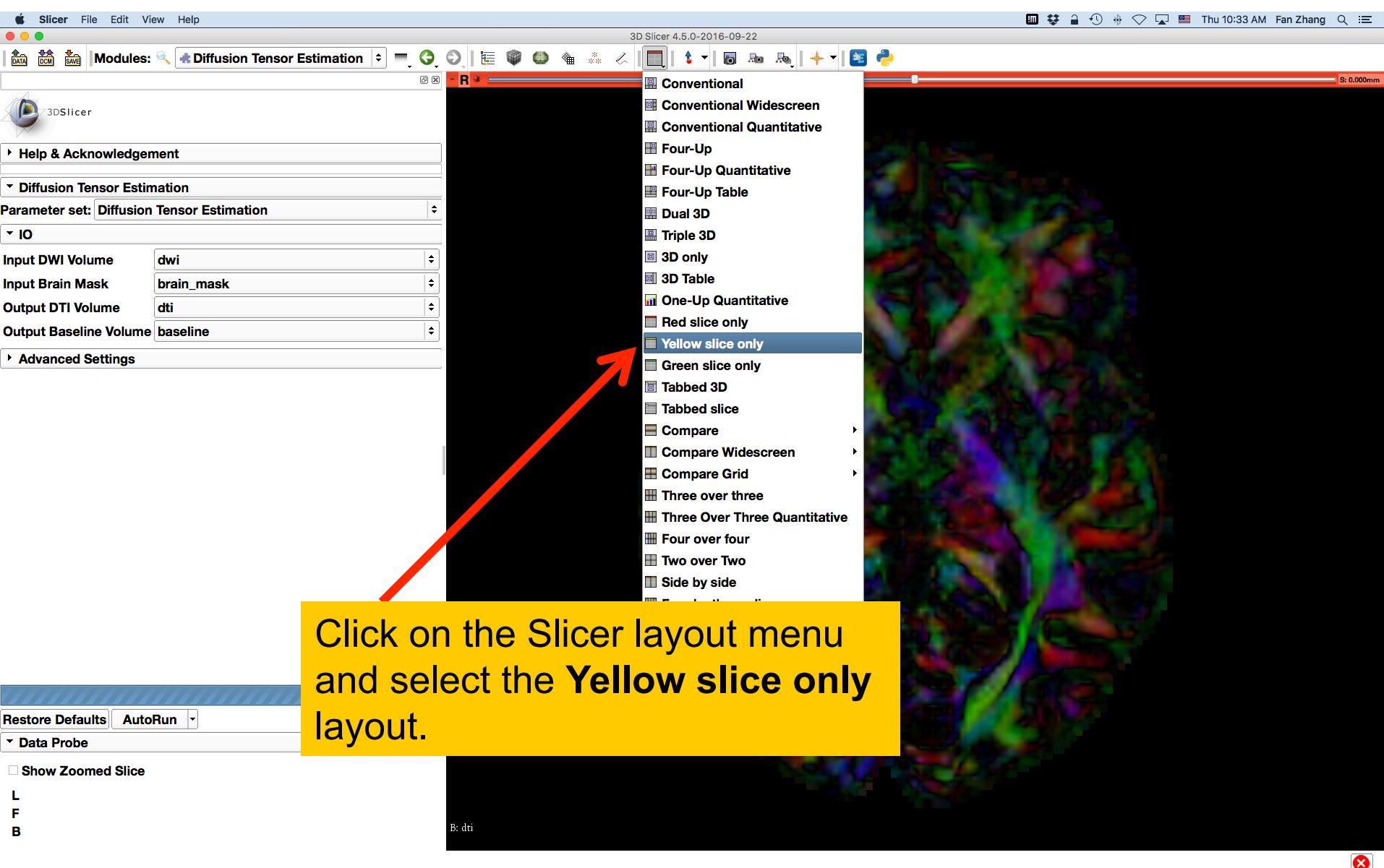
$$\lambda_1 >> \lambda_2, \lambda_3$$

Anisotropic media
(white matter)



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

Exploring the DWI Dataset



Corpus Callosum

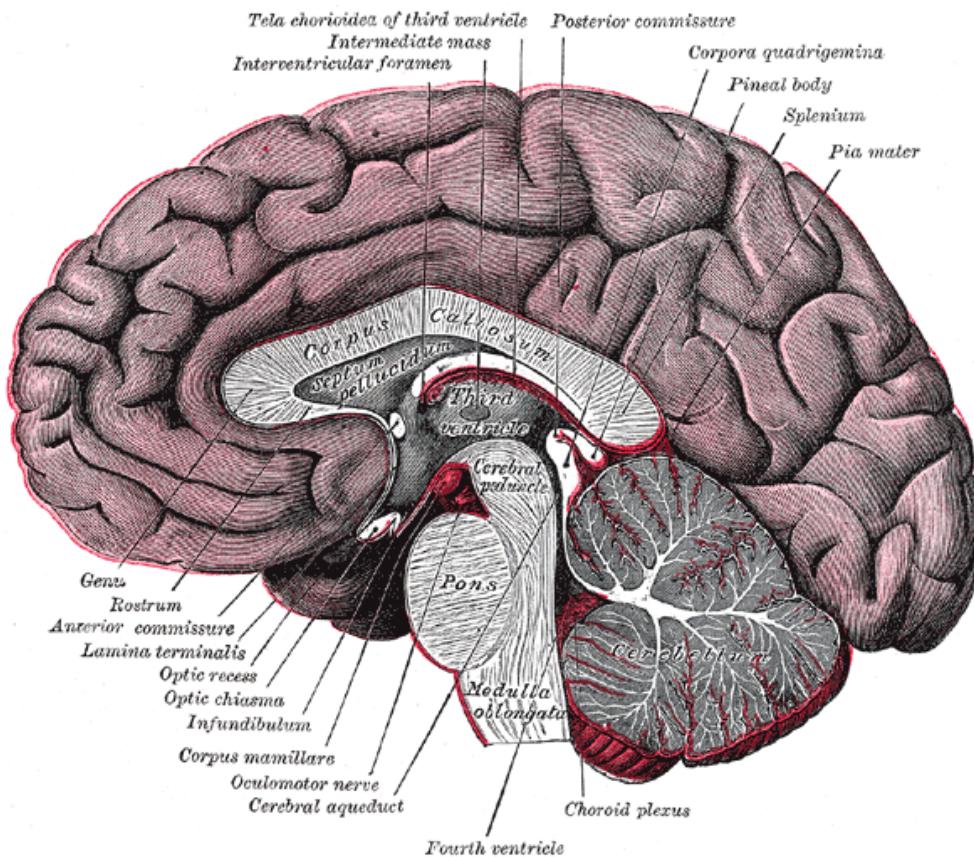
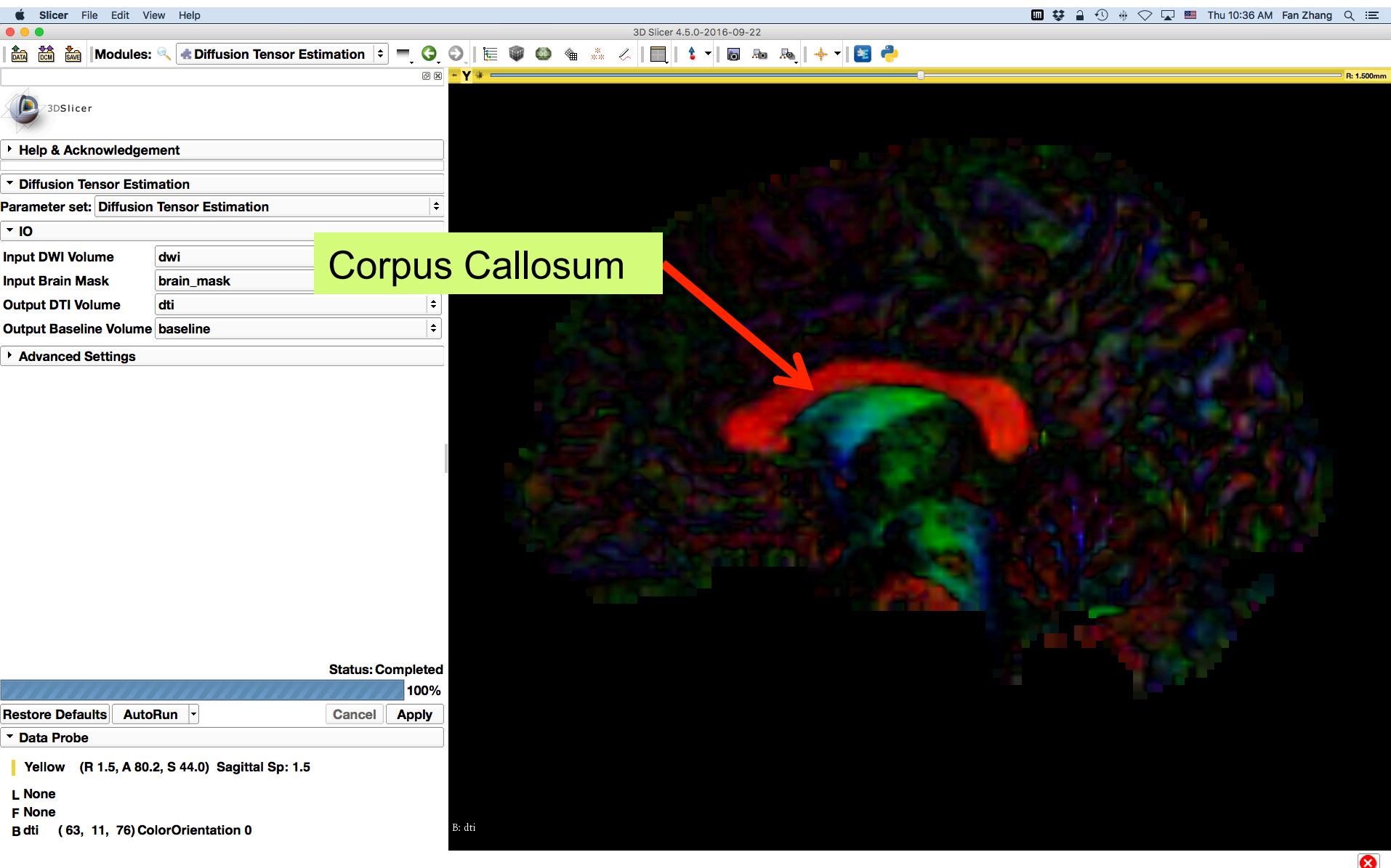


Image from Gray's Anatomy

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

Corpus Callosum

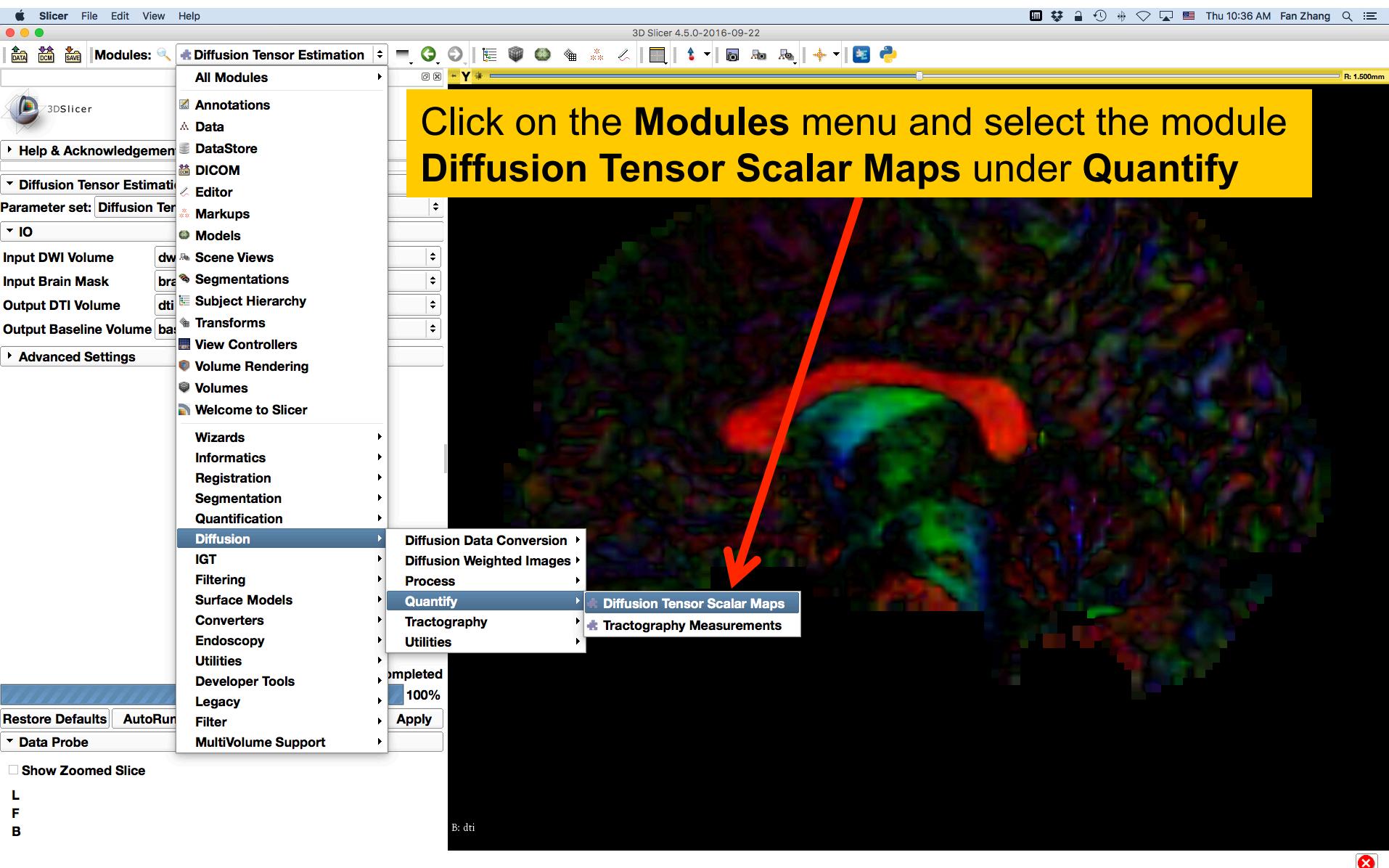


Characterizing the Size of the tensor: Trace

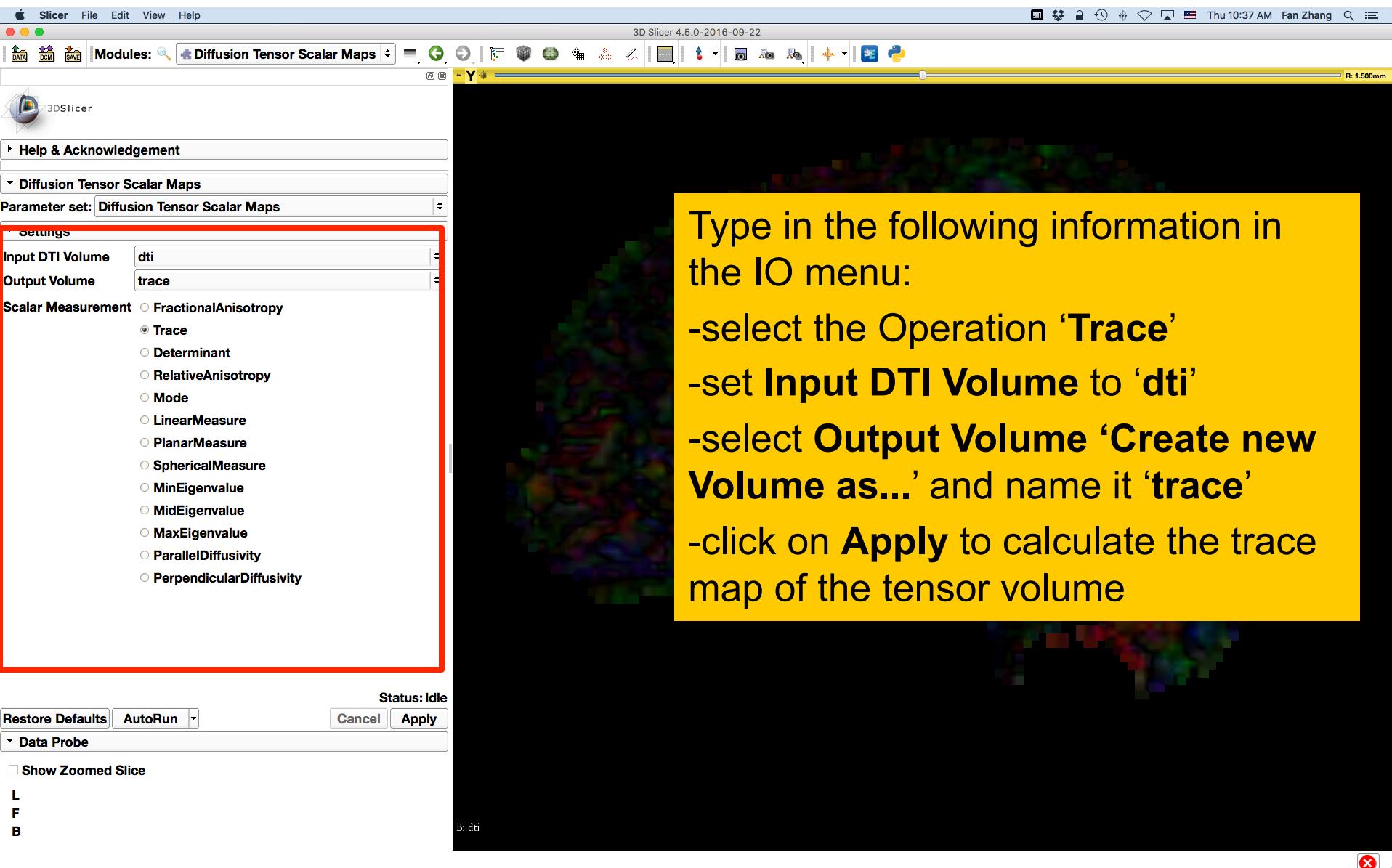
$$\text{Trace}(D) = \lambda_1 + \lambda_2 + \lambda_3$$

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

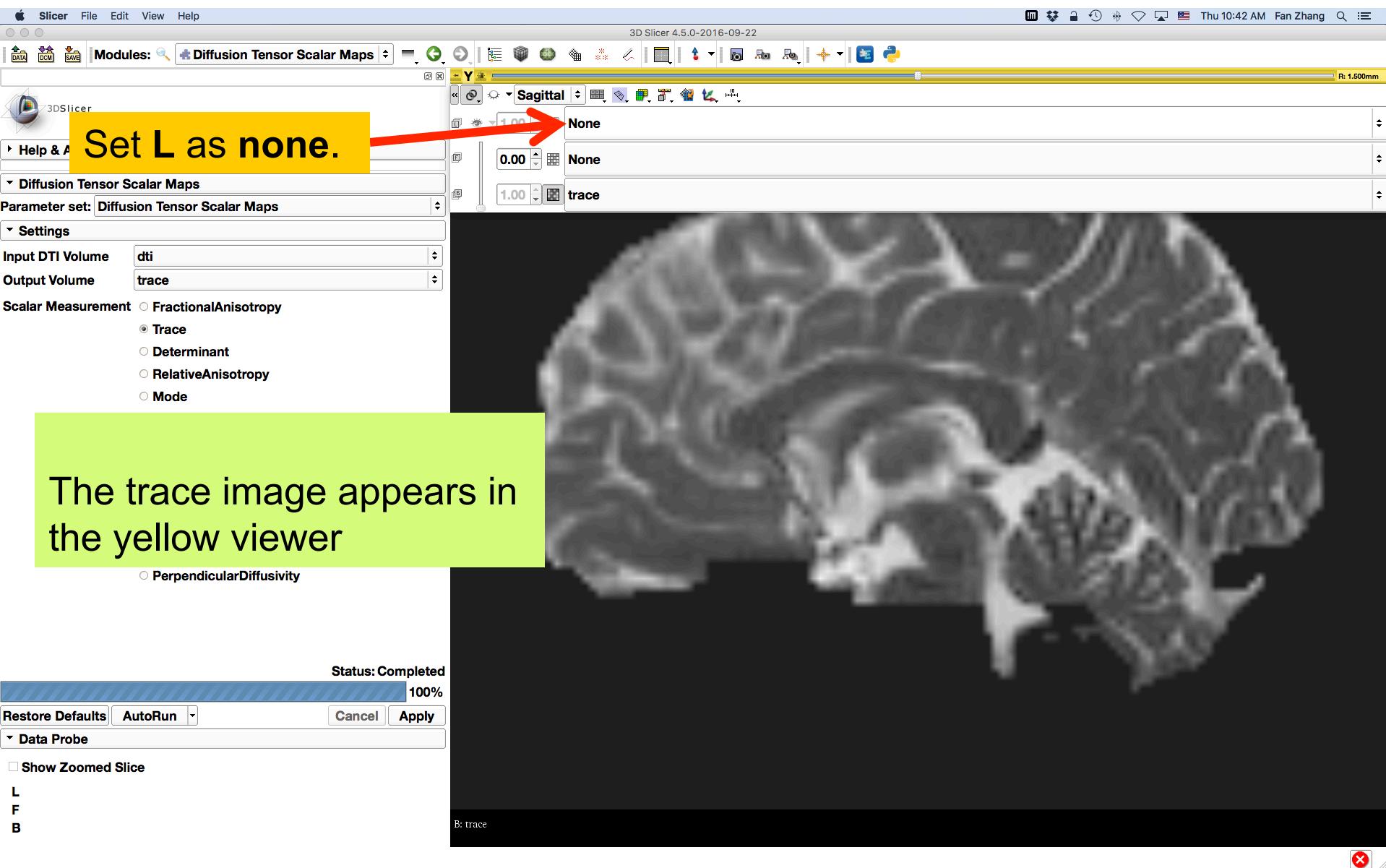
Trace



Trace



Trace



Trace

Slicer File Edit View Help

3D Slicer 4.5.0-2016-09-22

Modules: Diffusion Tensor Scalar Maps

3DSlicer

Help & Acknowledgement

Diffusion Tensor Scalar Maps

Parameter set: Diffusion Tensor Scalar Maps

Settings

Input Output Scale

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**

The screenshot shows a 3D brain model in a sagittal view. A red box highlights the 'Sagittal' module panel. Inside the panel, there are three dropdown menus: 'None' (set to 1.00), 'dti' (set to 0.40), and 'trace' (set to 1.00). The background viewer displays a multi-colored brain surface, and the foreground viewer shows a semi-transparent red and green trace overlay.

Trace

Slicer File Edit View Help

3D Slicer 4.5.0-2016-09-22

R: 1.500mm

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

Input DTI Volume: dti

Output Volume: trace

Scalar Measurement: Trace

FractionalAnisotropy

Determinant

RelativeAnisotropy

Mode

LinearMeasure

PlanarMeasure

SphericalMeasure

MinEigenvalue

MidEigenvalue

MaxEigenvalue

ParallelDiffusivity

PerpendicularDiffusivity

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

Data Probe

Yellow (R 1.5, A 27.6, S 11.5) Sagittal Sp: 1.5

L None

F dti (63, 46, 55) ColorOrientation 0

B trace (63, 46, 55) 0.002213

A red arrow points from the yellow callout box to the red-colored region of the corpus callosum in the brain image.

Trace

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

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

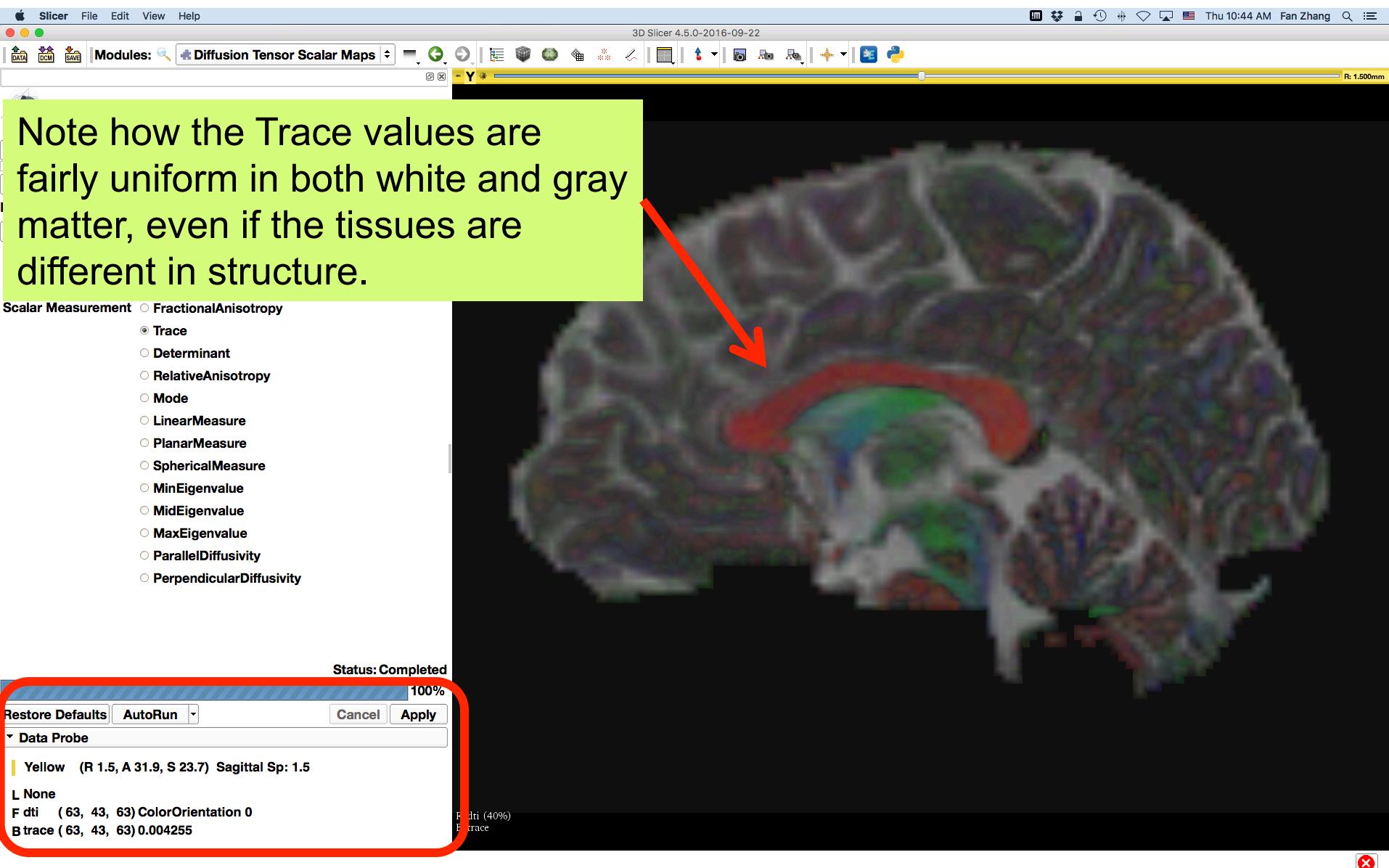
Status: Completed 100%

Restore Defaults AutoRun ▾ Cancel Apply

▼ Data Probe

Yellow (R 1.5, A 31.9, S 23.7) Sagittal Sp: 1.5

L None
F dti (63, 43, 63) ColorOrientation 0
B trace (63, 43, 63) 0.004255



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 interface with the 'Diffusion Tensor Scalar Maps' module selected. A red box highlights the 'Settings' section of the module panel, which includes fields for 'Input DTI Volume' (set to 'dti') and 'Output Volume' (set to 'fa'). Below these are various scalar measurement options, with 'FractionalAnisotropy' selected. The main window displays a 3D brain volume with color-coded regions representing different diffusion properties. A yellow callout box on the right provides instructions for calculating the Fractional Anisotropy map.

Fill in the following information:

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

Status: Completed
100%

Yellow (R 1.5, A 65.1, I 45.8) Sagittal Sp: 1.5

L None
F dti (63, 21, 16) ColorOrientation 0
B trace (63, 21, 16) 0

F: dti (40%)
B: trace

Fractional Anisotropy

Slicer File Edit View Help

3D Slicer 4.5.0-2016-09-22

DATA DCM SAVE Modules: Diffusion Tensor Scalar Maps

3DSlicer

Help & A

Diffusion Tensor Scalar Maps

Parameter set: Diffusion Tensor Scalar Maps

Setting

Input DT

Output V

Scalar M

Set L as **none**.

The FA image appears in the yellow viewer

None

0.40 None

1.00 fa

None

irace Determinant RelativeAnisotropy Mode LinearMeasure PlanarMeasure SphericalMeasure MinEigenvalue MidEigenvalue MaxEigenvalue ParallelDiffusivity PerpendicularDiffusivity

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

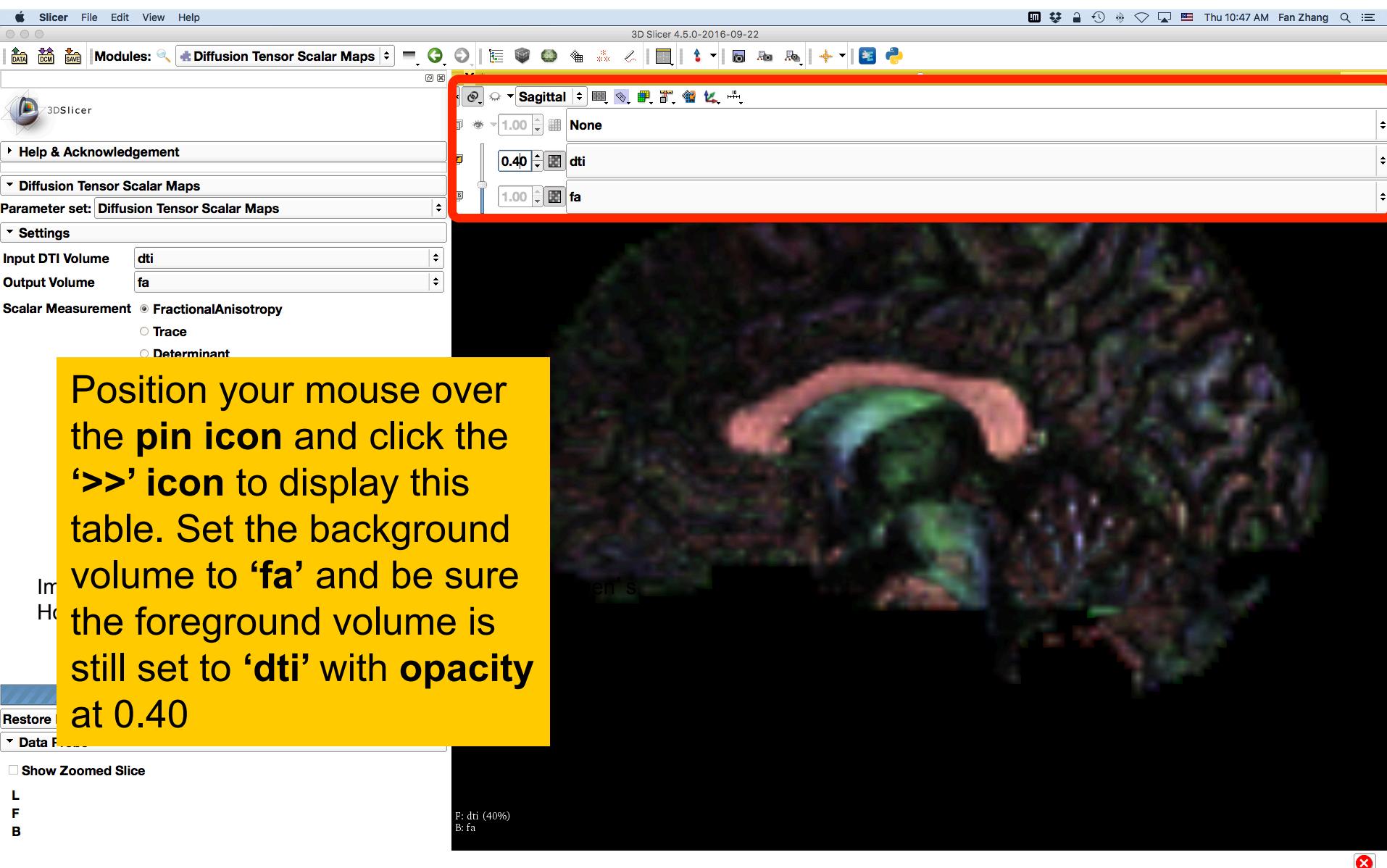
Data Probe

Show Zoomed Slice

L F B

B: fa

Fractional Anisotropy



Fractional Anisotropy

Slicer File Edit View Help

3D Slicer 4.5.0-2016-09-22

DATA DCM SAVE Modules: Diffusion Tensor Scalar Maps

R: 1.500mm

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

Determinant
RelativeAnisotropy
Mode
LinearMeasure
PlanarMeasure
SphericalMeasure
MinEigenvalue
MidEigenvalue
MaxEigenvalue
ParallelDiffusivity
PerpendicularDiffusivity

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

Data Probe

Yellow (R 1.5, A 33.5, S 7.2) Sagittal Sp: 1.5

L None
F dti (63, 42, 52) ColorOrientation 0
B fa (63, 42, 52) 0.757985

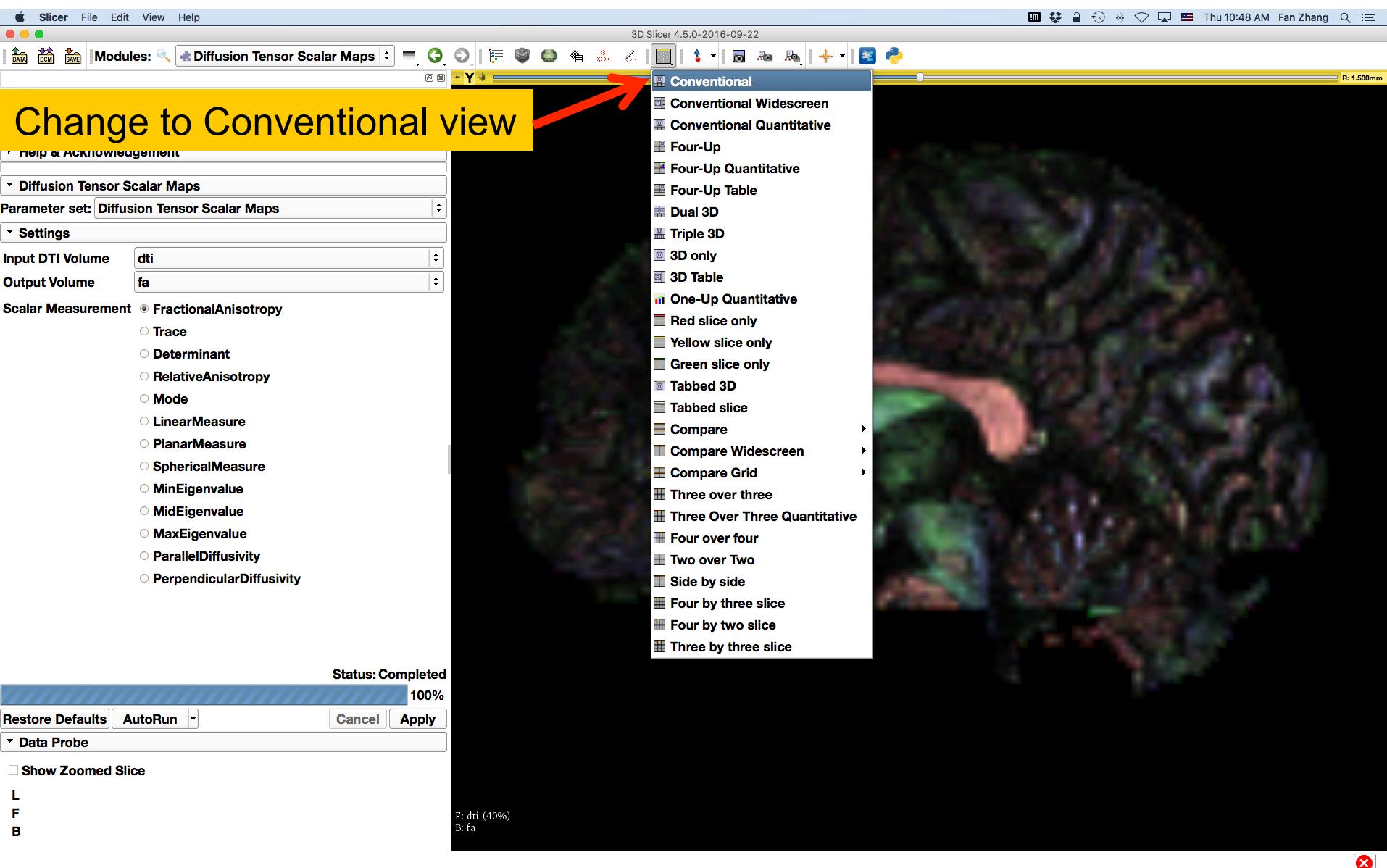
Yellow (R 1.5, A 33.5, S 7.2) Sagittal Sp: 1.5

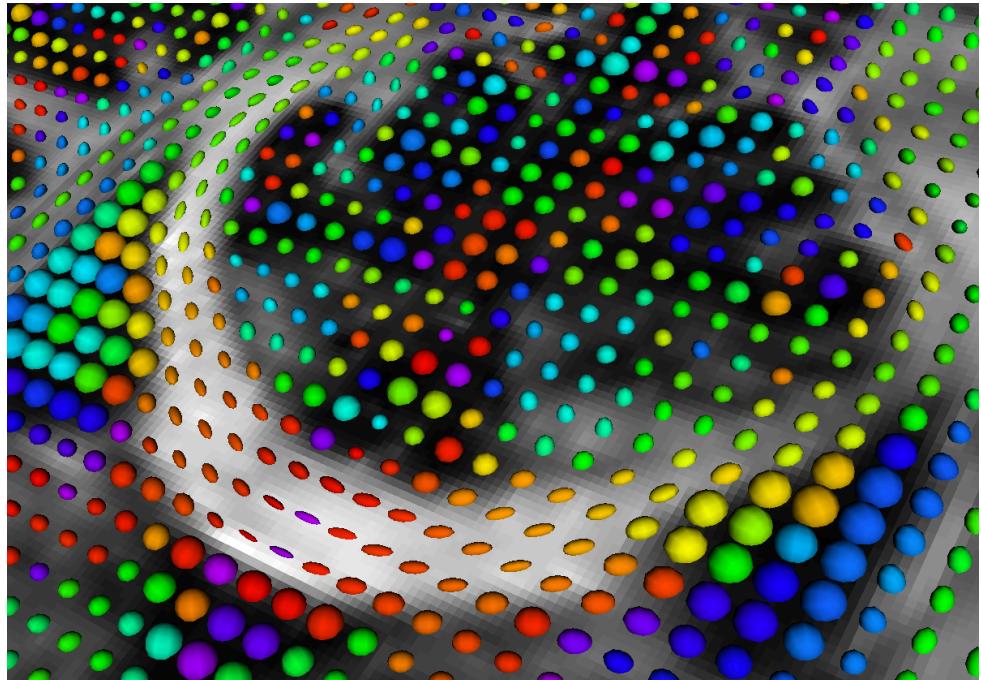
F dti (40%)

B fa (40%)

A red box highlights the 'Data Probe' section of the Slicer interface, which displays the coordinates (R 1.5, A 33.5, S 7.2), the slice type (Sagittal), the spatial step (Sp: 1.5), and the measured FA value (0.757985) at that specific location.

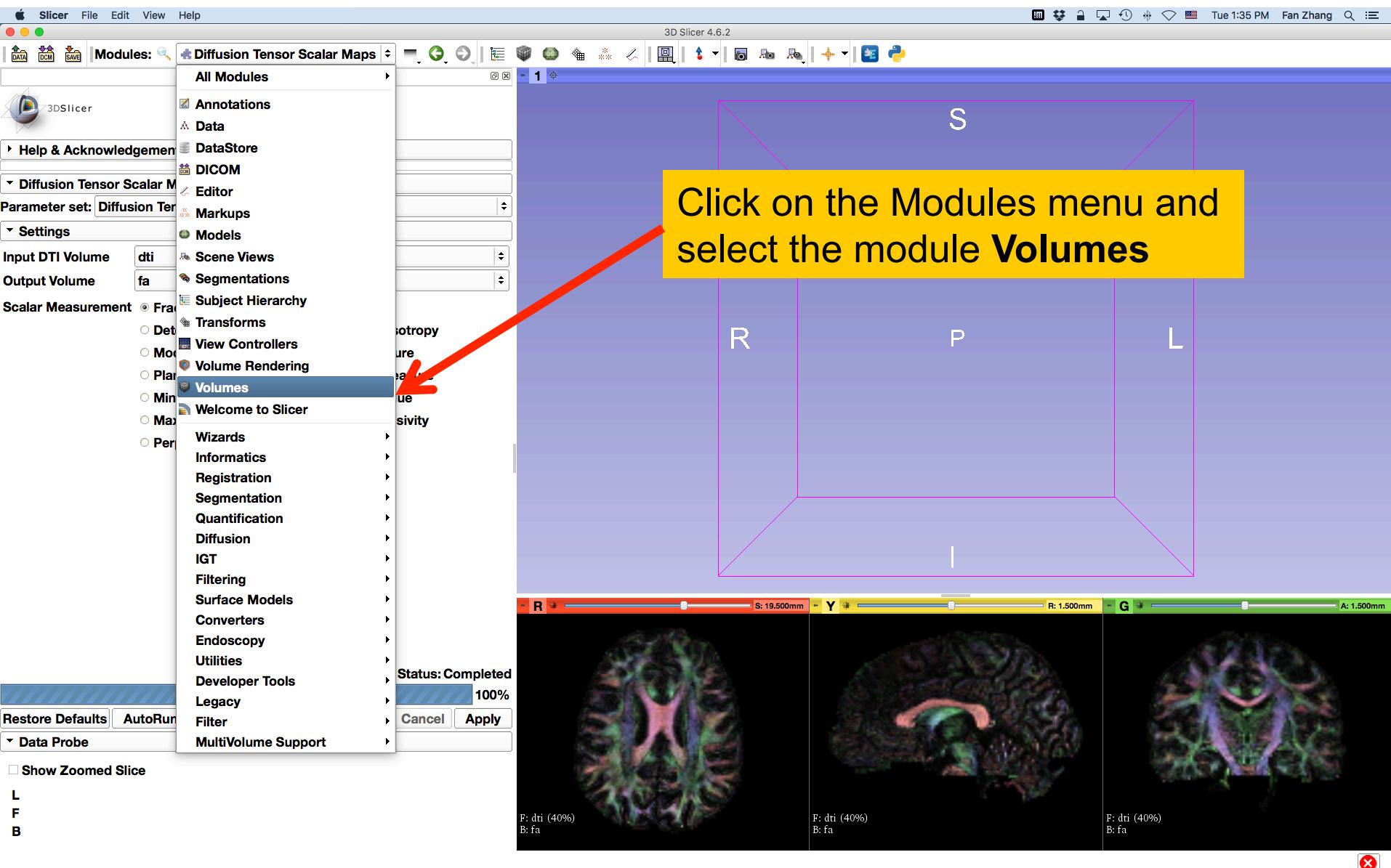
Fractional Anisotropy



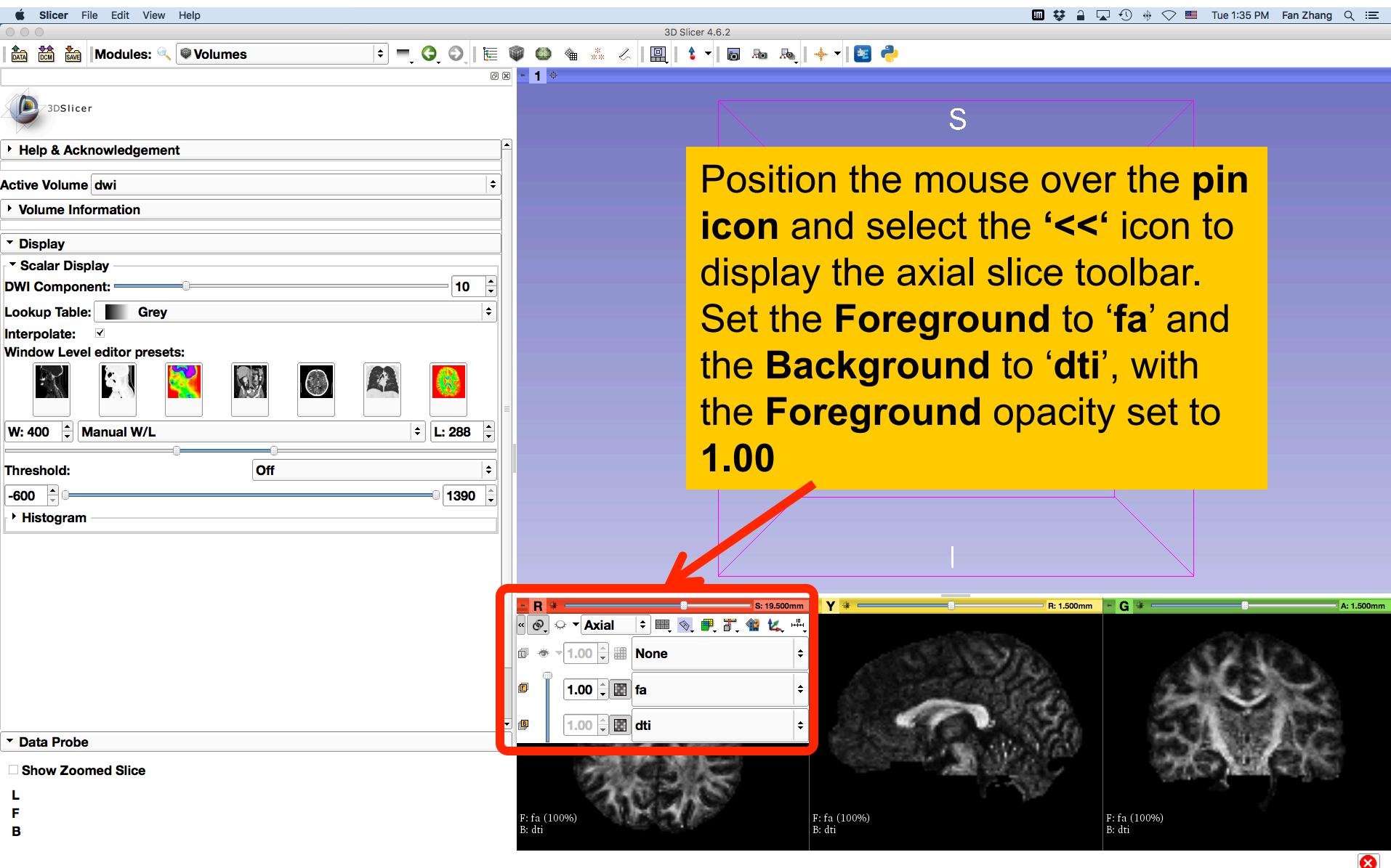


Part 2: Visualizing the tensor data

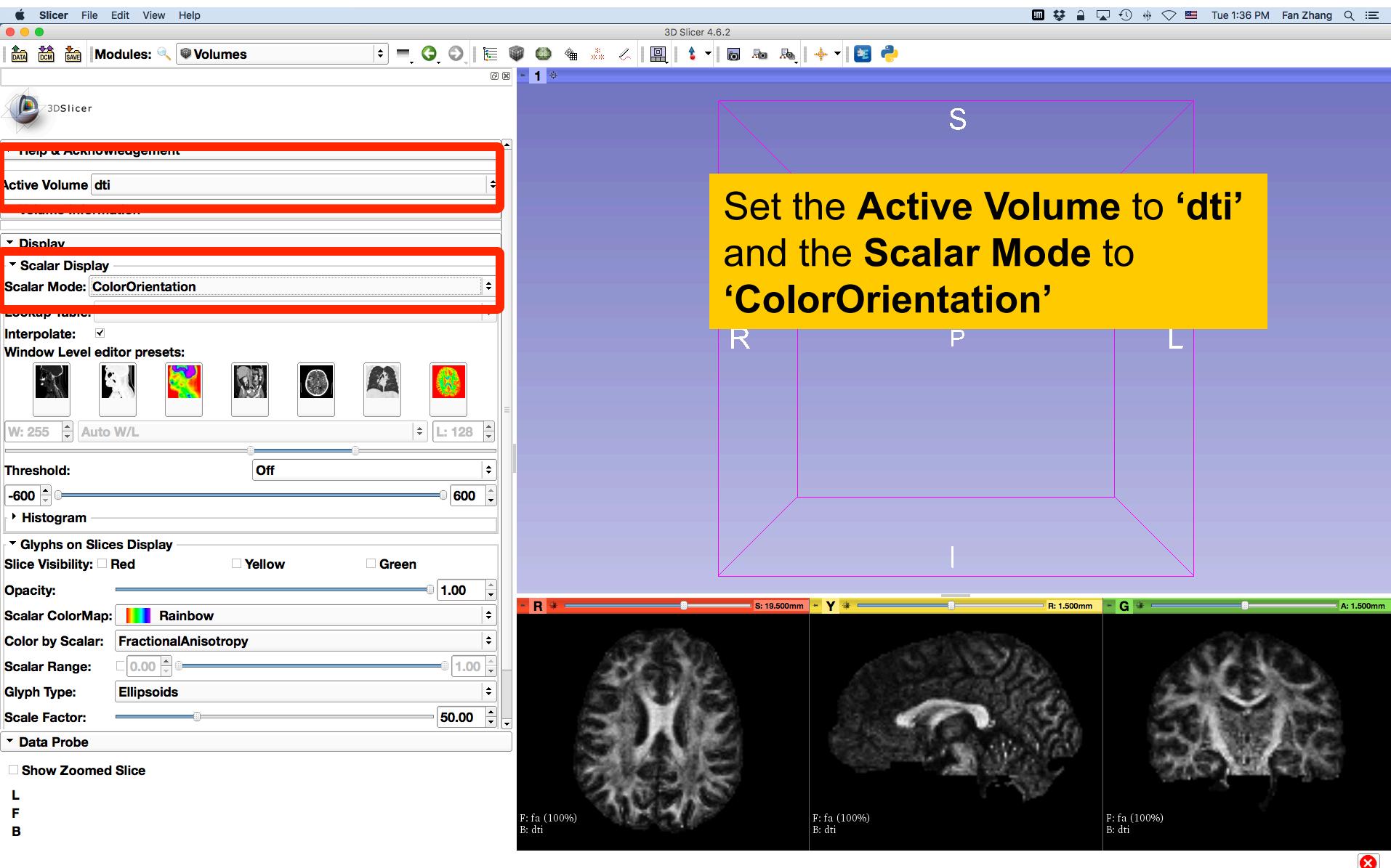
3D Visualization: Glyphs



3D Visualization: Glyphs



3D Visualization: Glyphs



3D Visualization: Glyphs

The screenshot shows the 3D Slicer 4.6.2 interface. On the left, the '3DSlicer' module panel is open, displaying various volume rendering parameters. A red box highlights the 'Glyphs on Slices Display' section, which includes 'Slice Visibility' (Red, Yellow, Green checked), 'Opacity' (1.00), 'Scalar ColorMap' (FullRainbow), 'Color by Scalar' (ColorOrientation), 'Glyph Type' (Ellipsoids selected), and 'Scale Factor' (50.00). Below this, the 'Data Probe' and 'Show Zoomed Slice' options are visible. The letters L, F, and B are listed at the bottom left.

3D Slicer 4.6.2

Help & Acknowledgement

Active Volume dti

Volume Information

Display

Scalar Display

Scalar Mode: ColorOrientation

Lookup Table:

Interpolate:

Window Level editor presets:

W: 255 Auto W/L

Threshold: Off

-600 600

Histogram

Glyphs on Slices Display

Slice Visibility: Red Yellow Green

Opacity: 1.00

Scalar ColorMap: FullRainbow

Color by Scalar: ColorOrientation

Glyph Type: Ellipsoids

Scale Factor: 50.00

Data Probe

Show Zoomed Slice

L

F

B

F: fa (100%)
B: dti

F: fa (100%)
B: dti

F: fa (100%)
B: dti

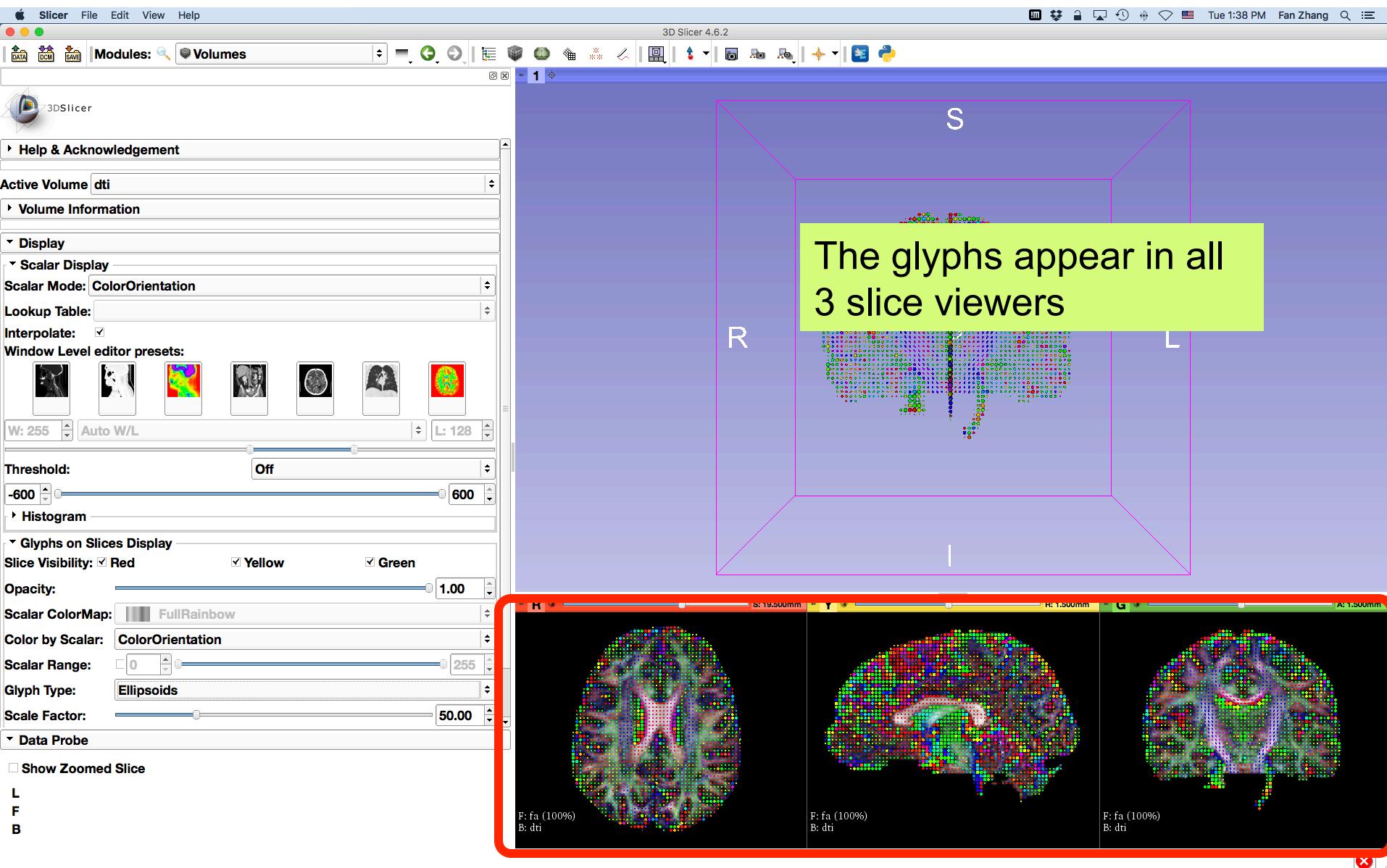
S

Scroll down the module panel and in the **Glyphs on Slices Display** section:
-Check off the option for **Red, Yellow, and Green Slice Visibility**

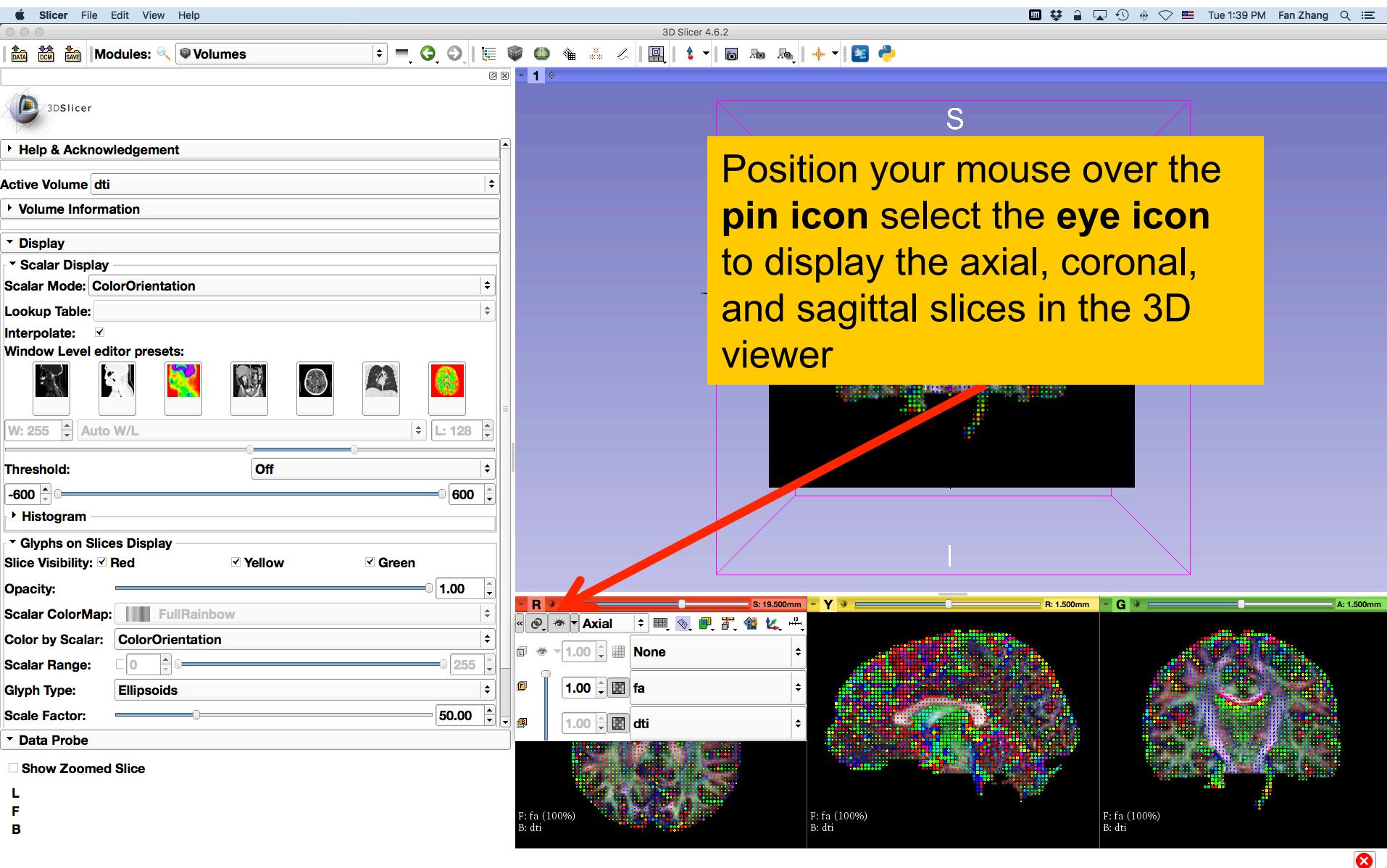
-Set the **Color by Scalar** parameter to '**ColorOrientation**'

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

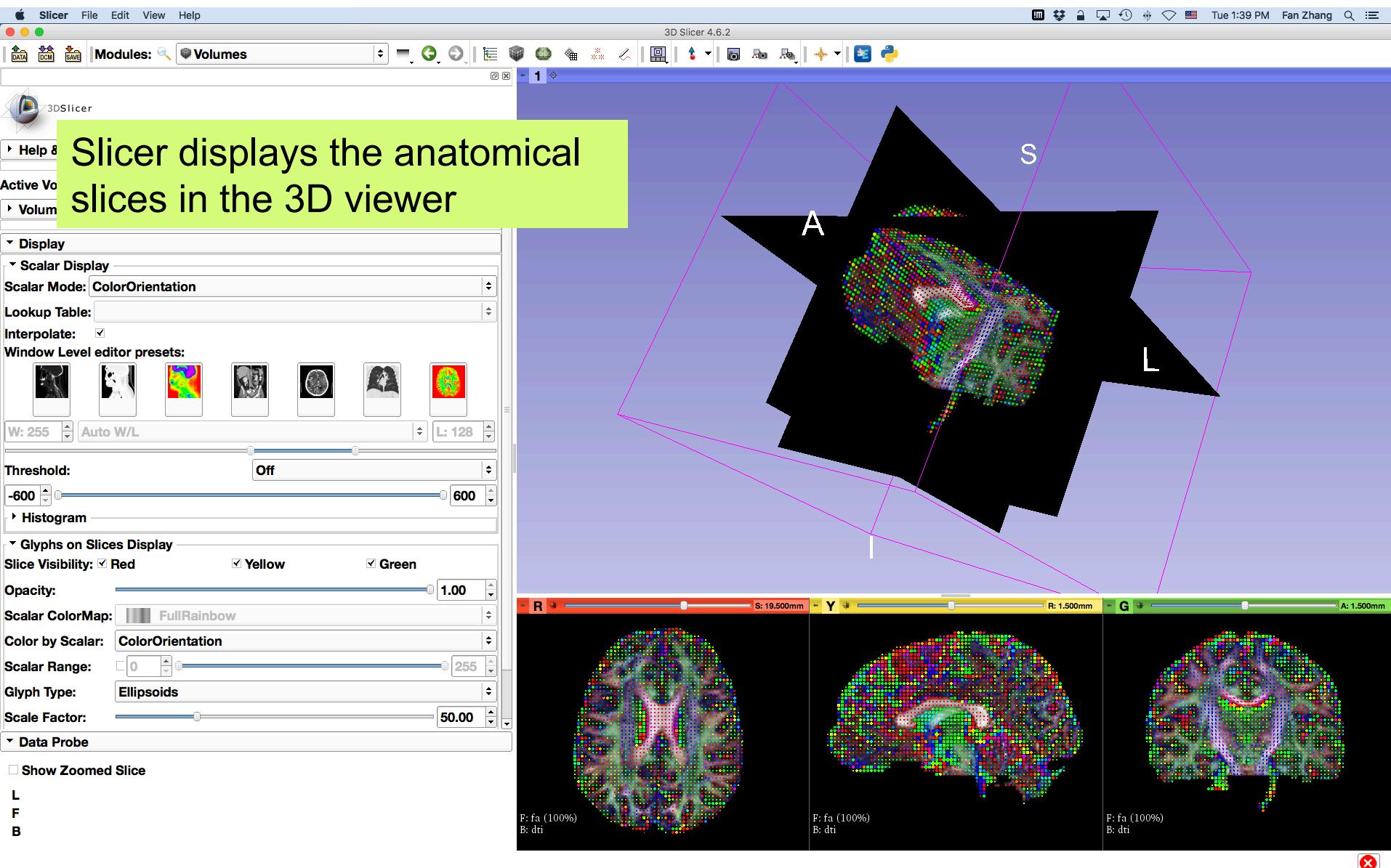
3D Visualization: Glyphs



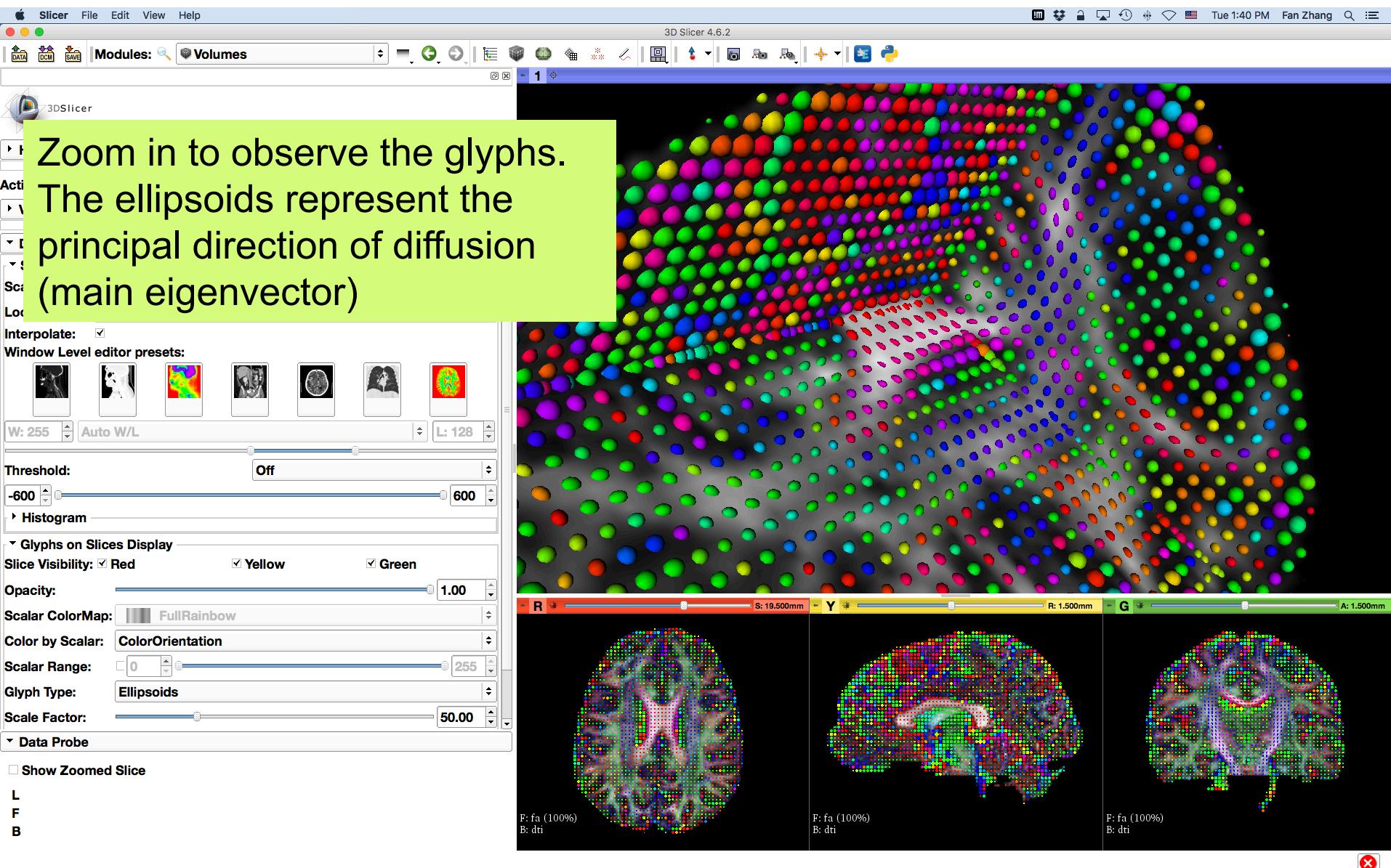
3D Visualization: Glyphs



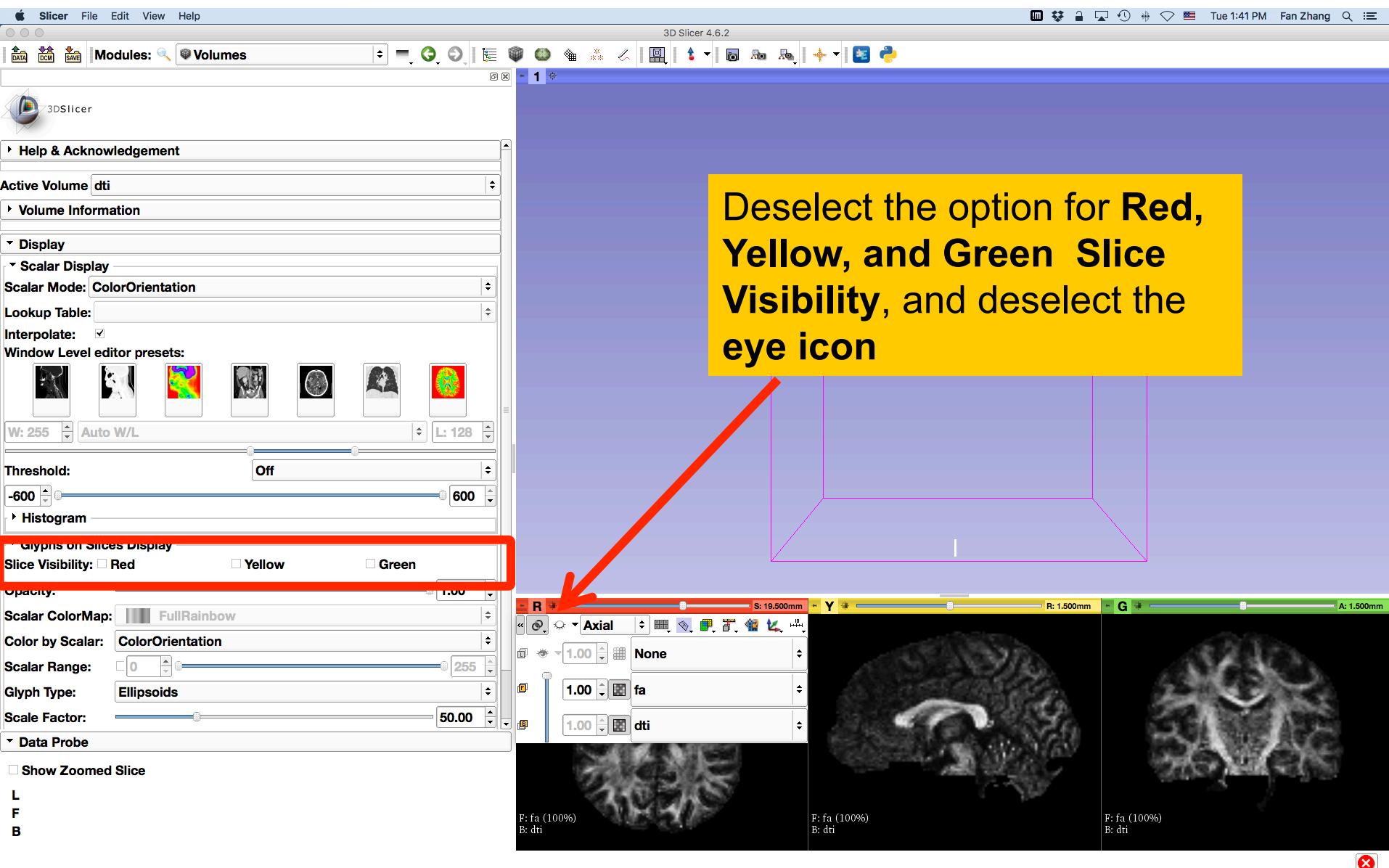
3D Visualization: Glyphs



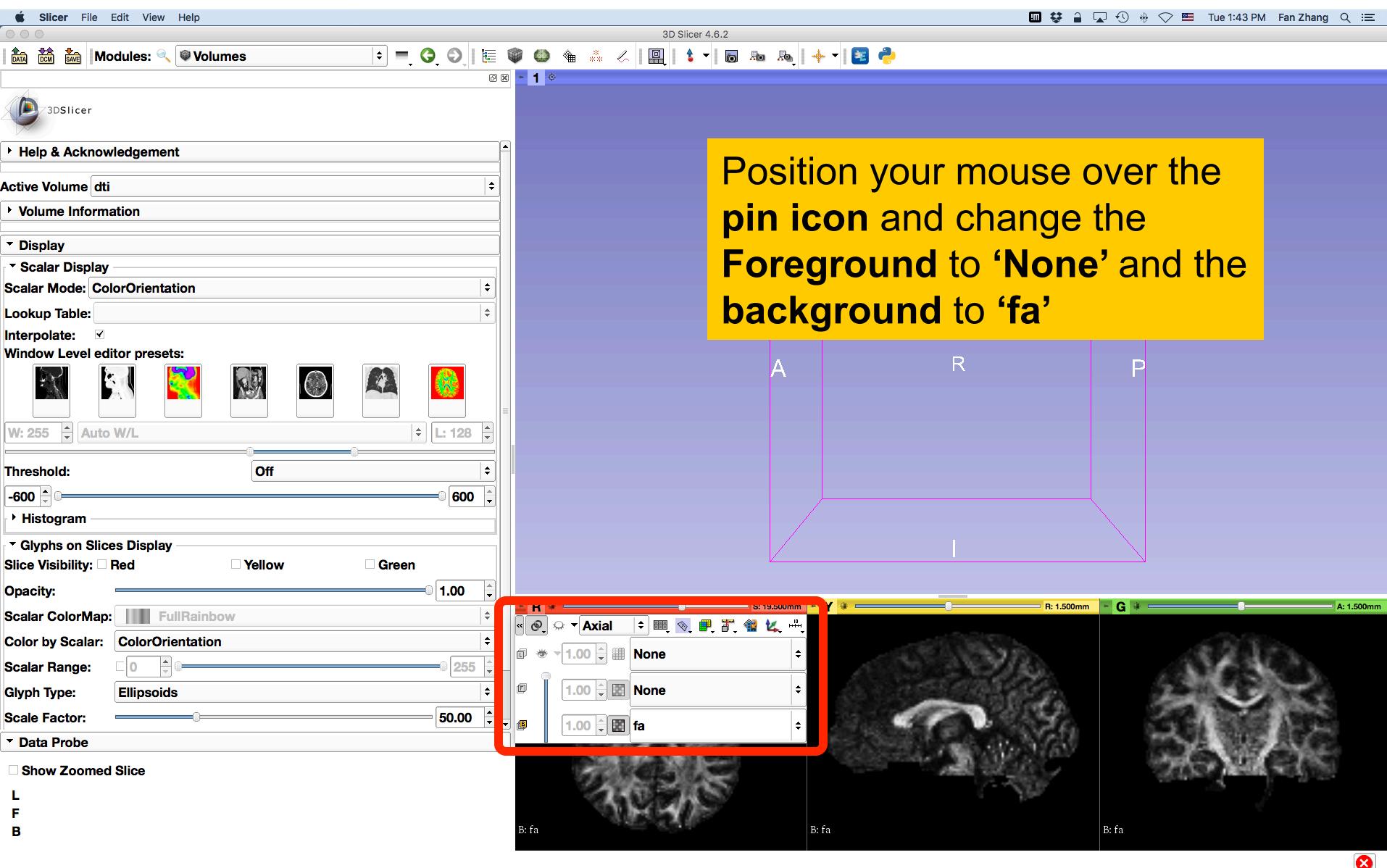
3D Visualization: Glyphs

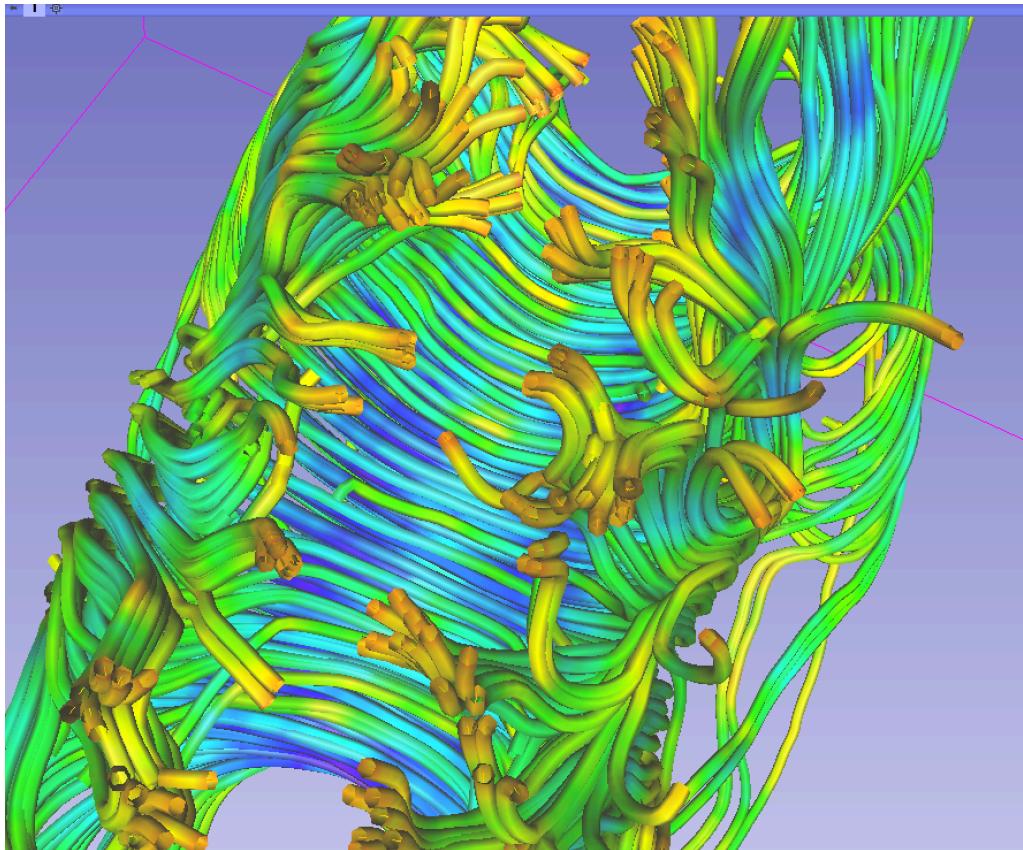


Diffusion MRI tractography



Diffusion MRI tractography



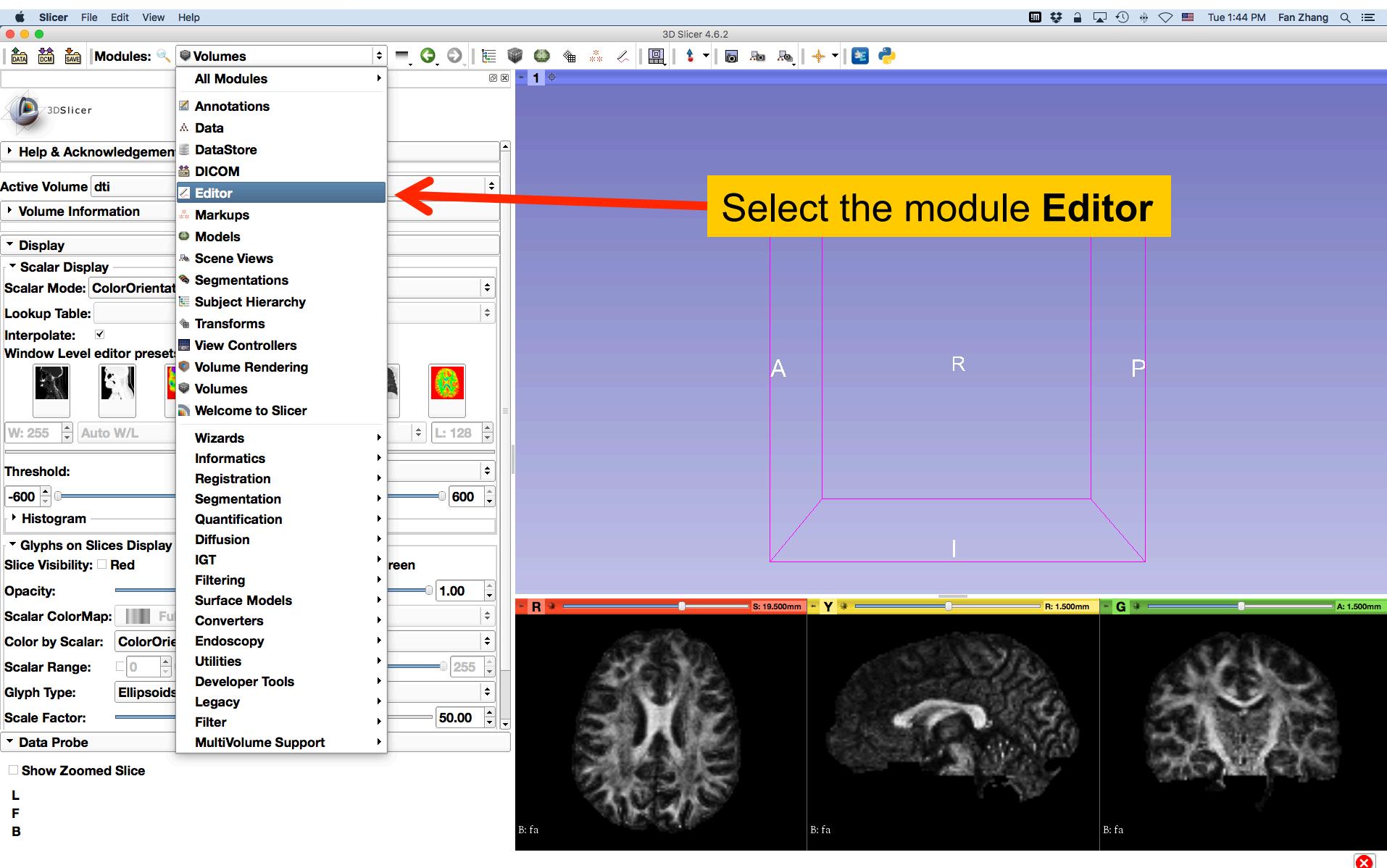


Part 3: From tensors to tracts

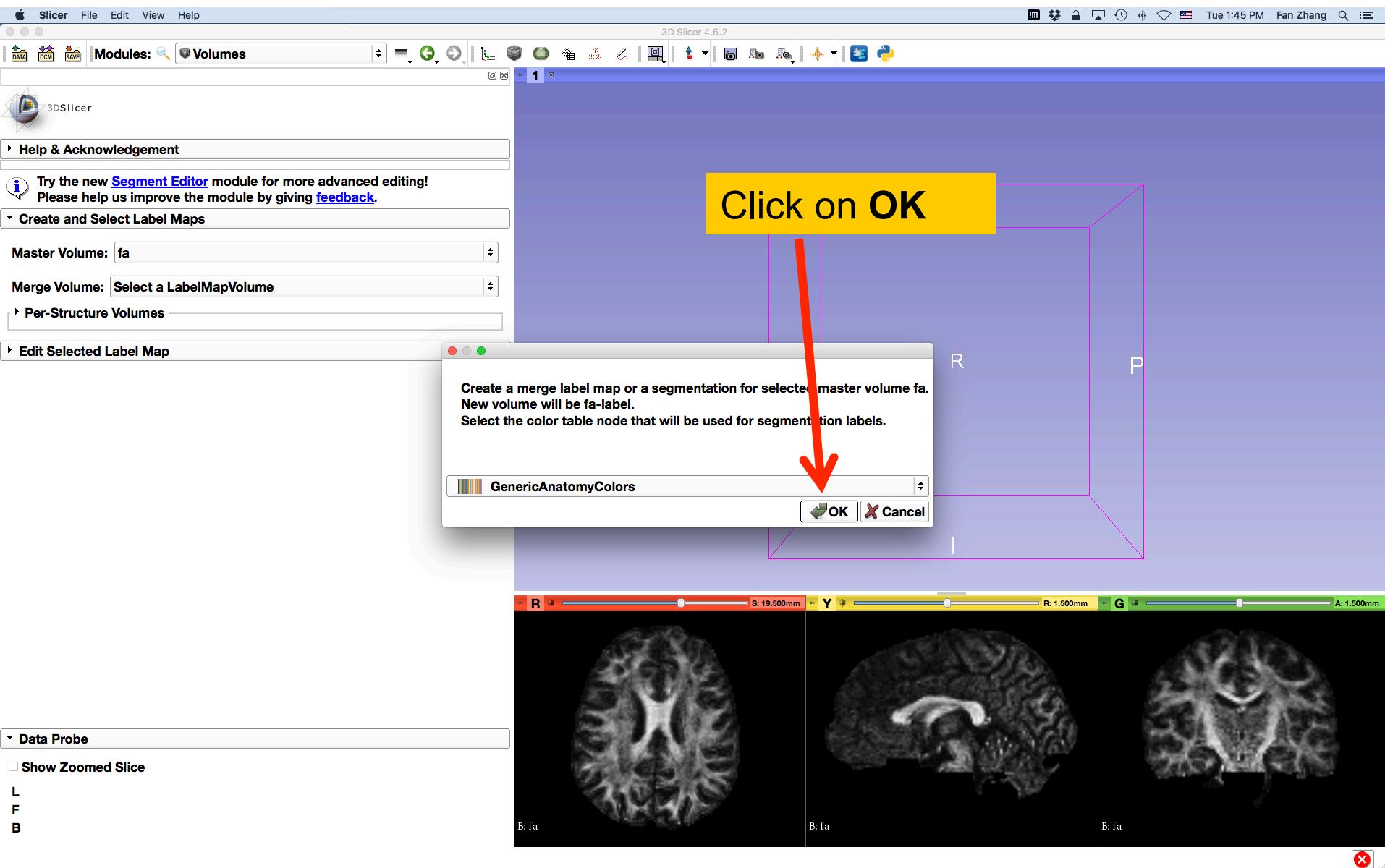
DTI tractography

- 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

Select the **Yellow slice only** layout

Please help us improve the module by giving [feedback](#).

Master Volume: fa

Merge Volume: fa-label

Per-Structure Volumes

Edit Selected Label Map

Active Tool: DefaultTool

Label: tissue 1

Terminology

Category: Tissue

Type: Tissue

Modifier:

Show Zoomed Slice

L
F
B

3D Slicer 4.6.2

S

R

P

I

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

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

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

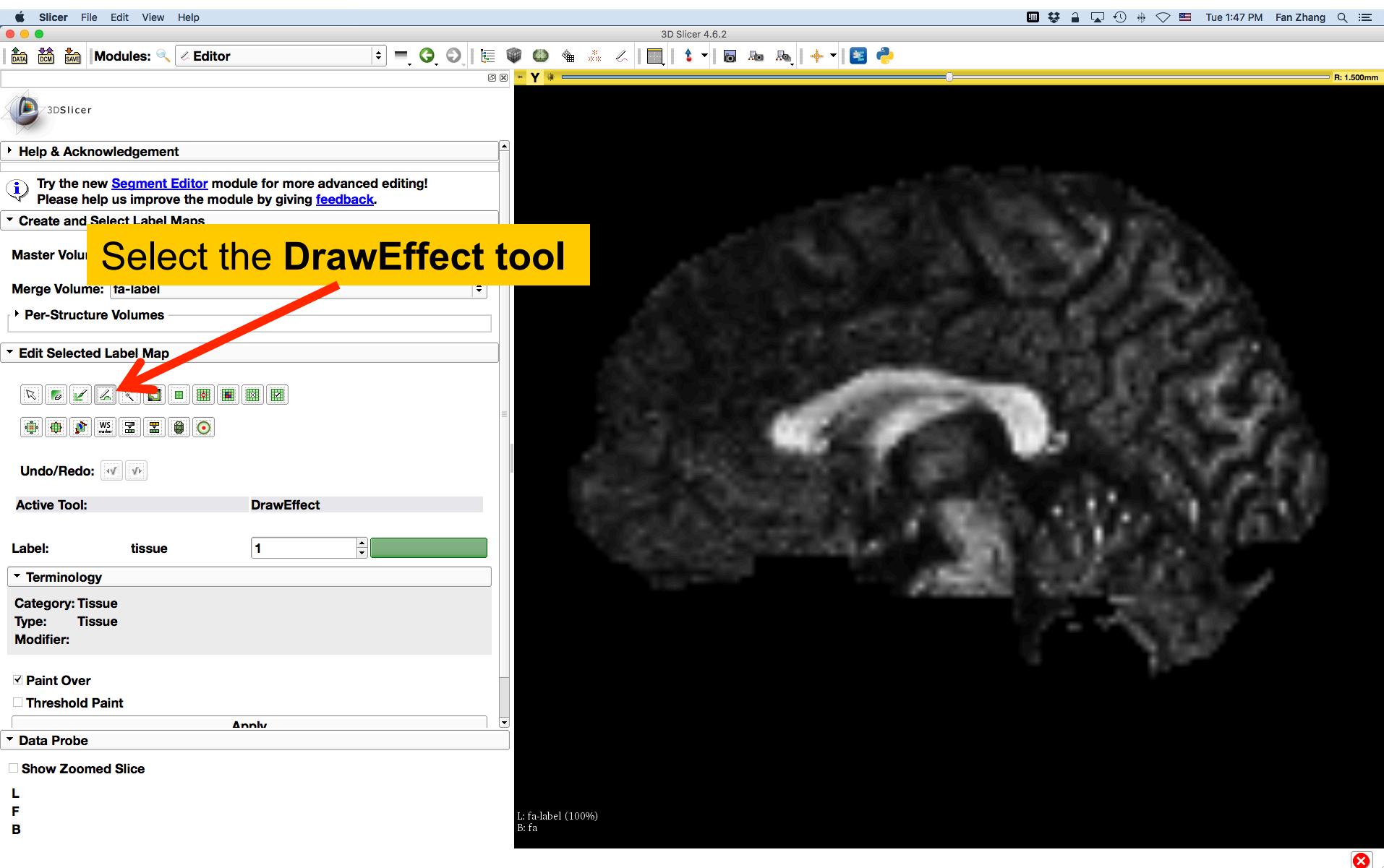
A: 1.500mm

G

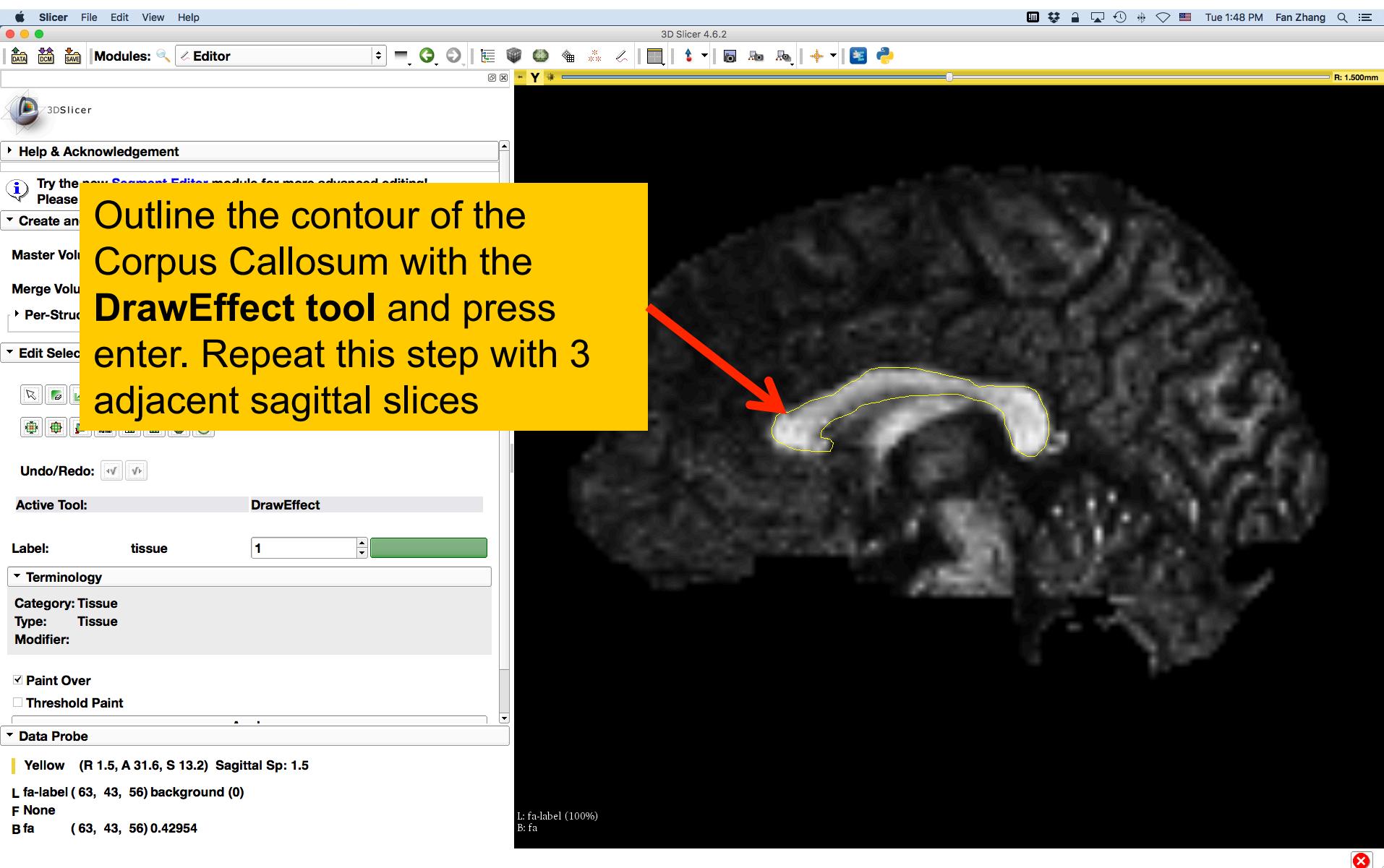
R: 1.500mm

The screenshot shows the Slicer 4.6.2 interface with a yellow overlay box highlighting the text "Select the Yellow slice only layout". A red arrow points from this text to the "Layout" dropdown menu in the top right corner. The "Layout" menu is open, showing various options like "Conventional", "Yellow slice only" (which is highlighted in blue), and "Red slice only". The main workspace displays a 3D brain volume with pink coordinate axes (Sagittal, Coronal, Axial) and three 2D brain slices at the bottom labeled L, R, and G. The L slice is labeled "L: fa-label (100%) B: fa". The R slice is labeled "R: 1.500mm". The G slice is labeled "G". The bottom status bar shows "A: 1.500mm".

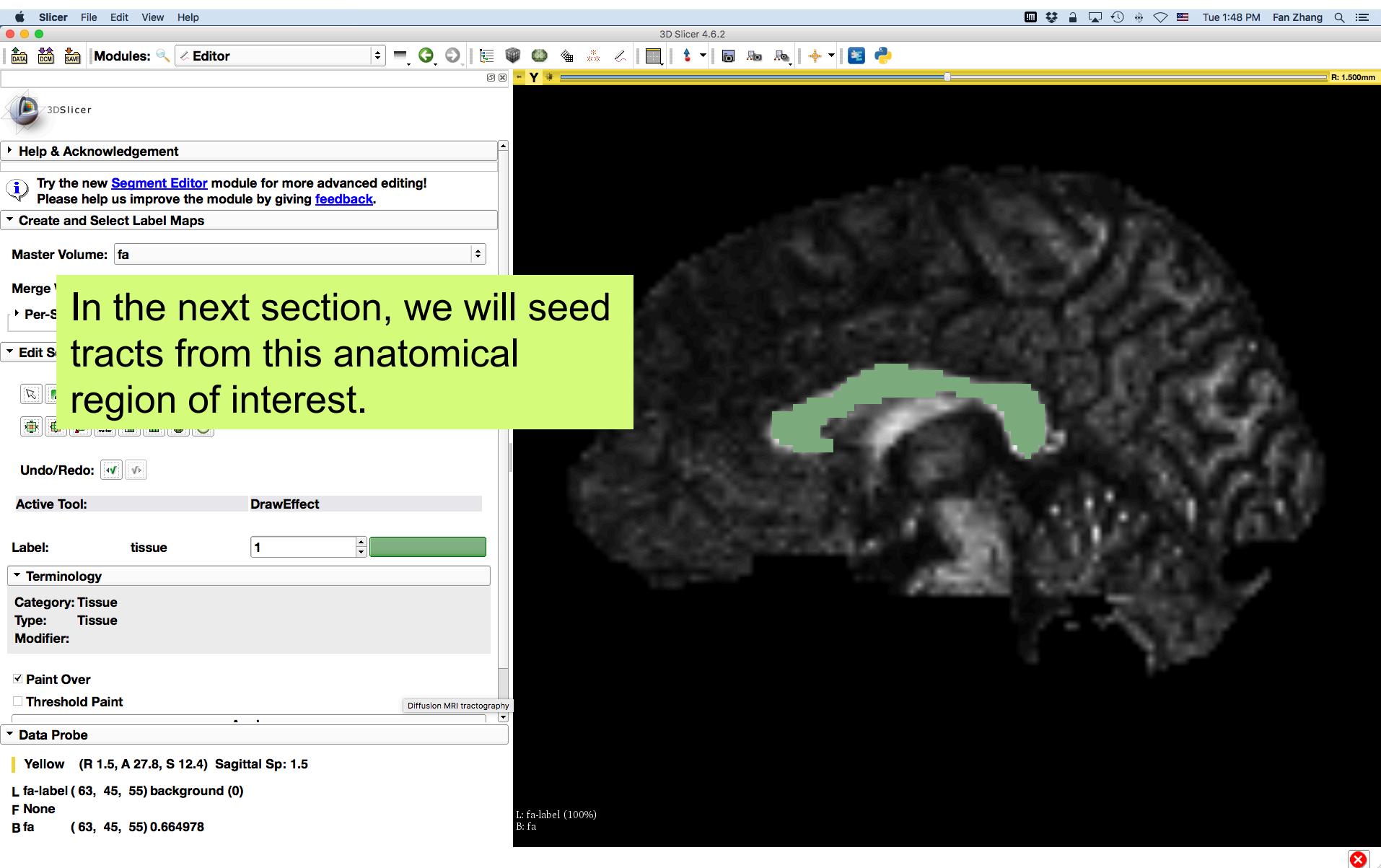
Diffusion MRI tractography



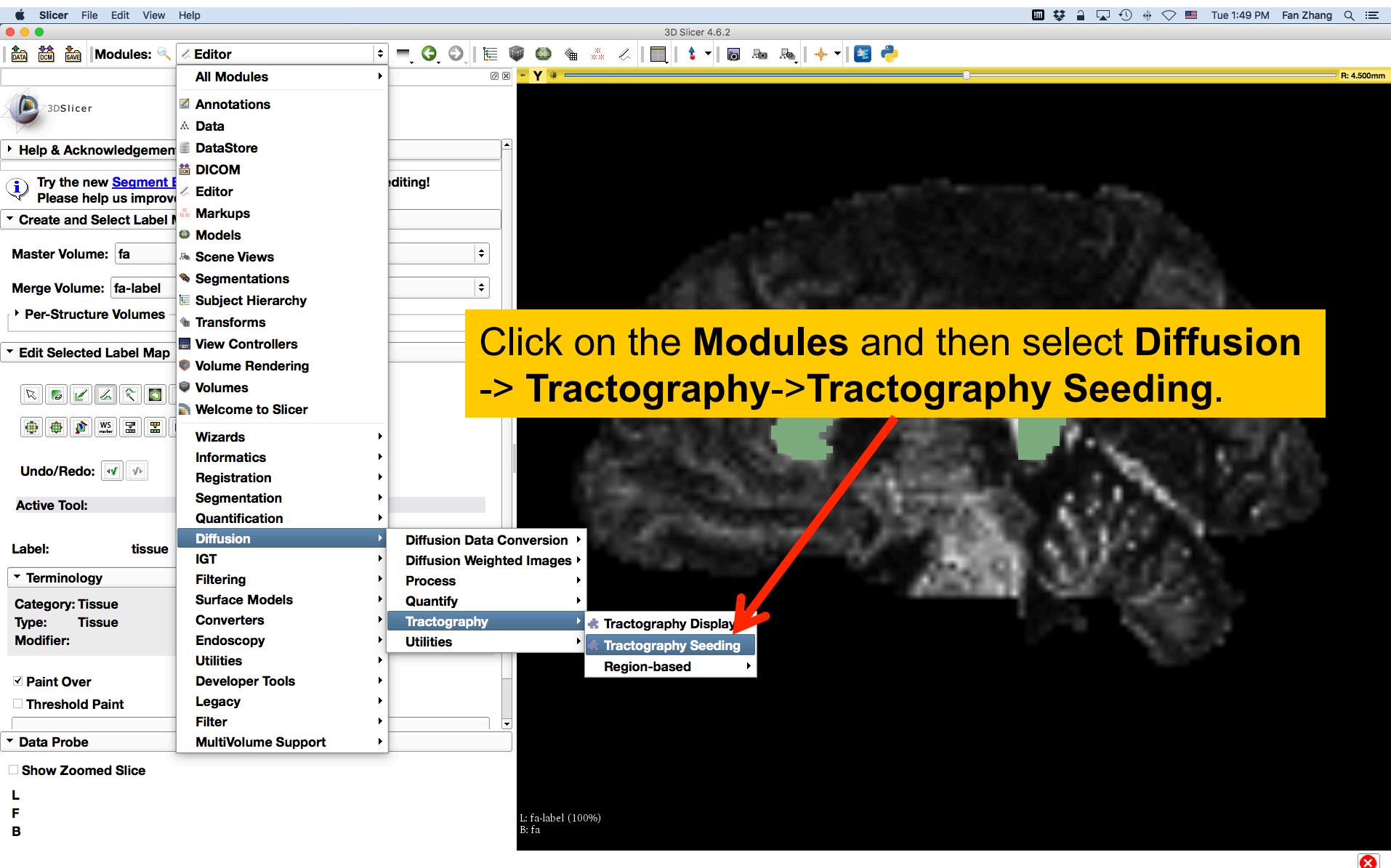
Diffusion MRI tractography



Diffusion MRI tractography



Diffusion MRI tractography



Step1: I/O

Change to Conventional view

3D Slicer 4.6.2

Conventional

- Conventional Widescreen
- Conventional Quantitative
- Four-Up
- Four-Up Quantitative
- Four-Up Table
- Dual 3D
- Triple 3D
- 3D only
- 3D Table
- One-Up Quantitative
- Red slice only
- Yellow slice only
- Green slice only
- Tabbed 3D
- Tabbed slice
- Compare
- Compare Widescreen
- Compare Grid
- Three over three
- Three Quantitative

R: 4.500mm

- Set the Input DTI Volume to 'dti'
- Set the Input Label Map to 'fa-label'
- Set Output Fiber Bundle to 'Create New Fiber Bundle' and rename it 'corpusCallosum'
- Uncheck Enable Seeding Tracks

Step 2: Seeding parameters

The screenshot shows the 3D Slicer interface with the 'Tractography Seeding' module selected. The left panel contains the following configuration:

- Presets:** Slicer4 Interactive Seeding Defaults
- IO:**
 - Input DTI Volume: dti
 - Input Fiducials, Model or Label Map: fa-label
 - Output Fiber Bundle: corpusCallosum
 - Enable Seeding Tracts:
- Label Map Options:**
 - Use index Space:
 - Seed spacing (mm): 100
 - Random Grid:
 - Linear Measure Start Threshold: 0.30
- ROI Labels:** 1
- Write Fibers To Disk:**
- Output Directory:** /Applications
- File Prefix:**
- Tractography Seeding Parameters:**
 - Minimum Length (mm): 20.000mm
 - Maximum Length (mm): 800.000mm
 - Stopping Criteria: Fractional Anisotropy
 - Stopping Value: 0.15
 - Stopping Track Curvature: 0.70
 - Integration Step Length (mm): 0.500mm
- Enabling Options:**
 - Create Tracts Initially As: Tubes
- Data Probe:**
- Show Zoomed Slice:**

The right panel displays a 3D brain volume with a green fiber bundle tractography. A 2D grayscale zoomed slice is shown at the bottom. A yellow callout box on the right side provides instructions for selecting default tractography seeding parameters:

Select the default Tractography Seeding parameters:

- Check Use index Space
- Stopping Criteria: Fractional Anisotropy
- Stopping Value: 0.15

Step 3: Generate Tracts

Slicer File Edit View Help

3D Slicer 4.6.2

Modules: Tractography Seeding

Presets Slicer4 Interactive Seeding Defaults

IO

Input DTI Volume dti

Input Fiducials, Model or Label Map fa-label

Output Fiber Bundle corpusCallosum

Enable Seeding Tracts

Label Map Options

Use index Space

Seed Spacing (mm) 2.00

Random Grid

Linear Measure Start Threshold 0.30

ROI Labels 1

Check Enable Seeding Tracks

Tractography Seeding Parameters

Minimum Length (mm) 20.000mm

Maximum Length (mm) 800.000mm

Stopping Criteria Fractional Anisotropy

Stopping Value 0.15

Stopping Track Curvature 0.70

Integration Step Length (mm) 0.500mm

Enabling Options

Create Tracts Initially As Tubes

Data Probe

Show Zoomed Slice

L

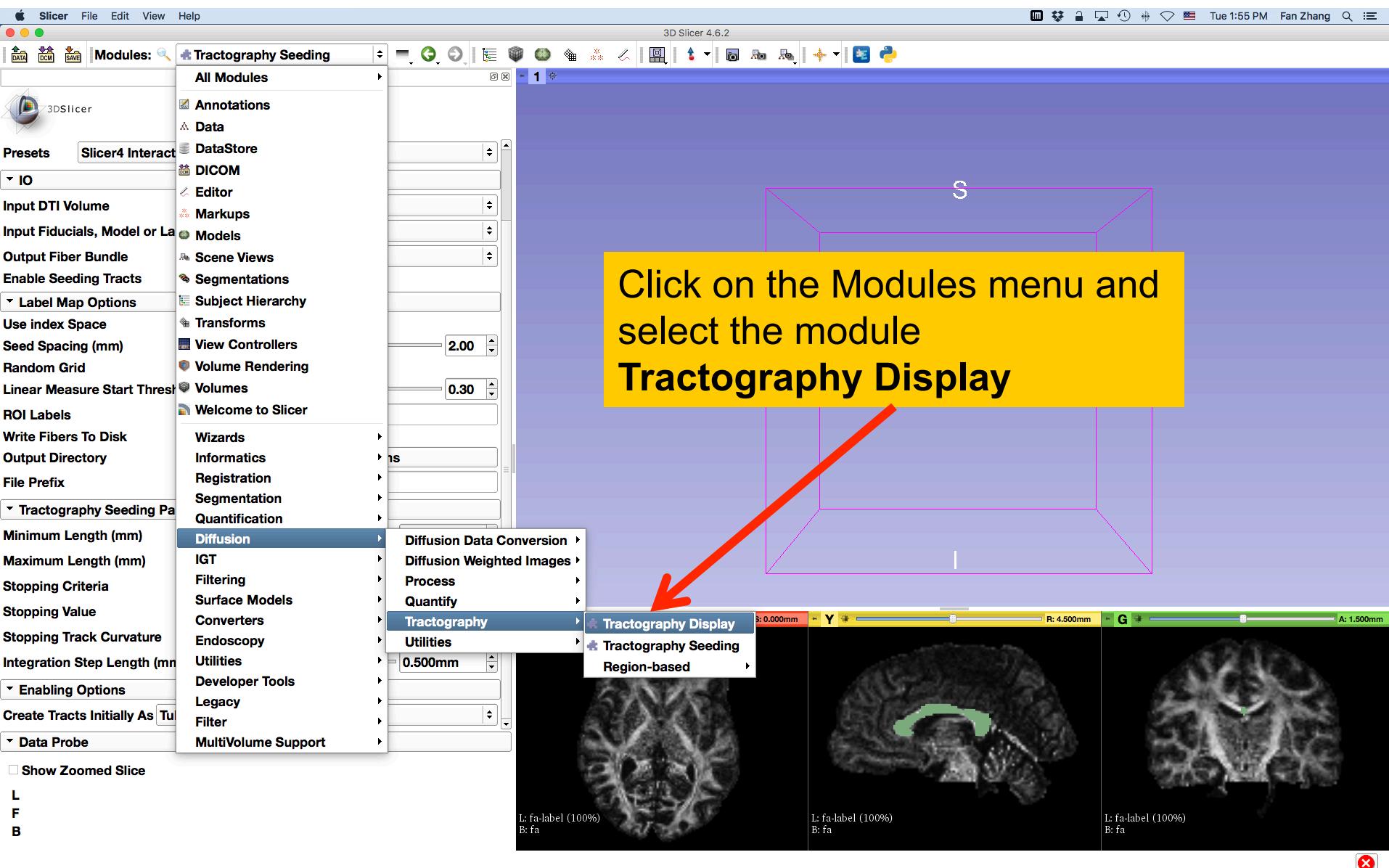
F

B

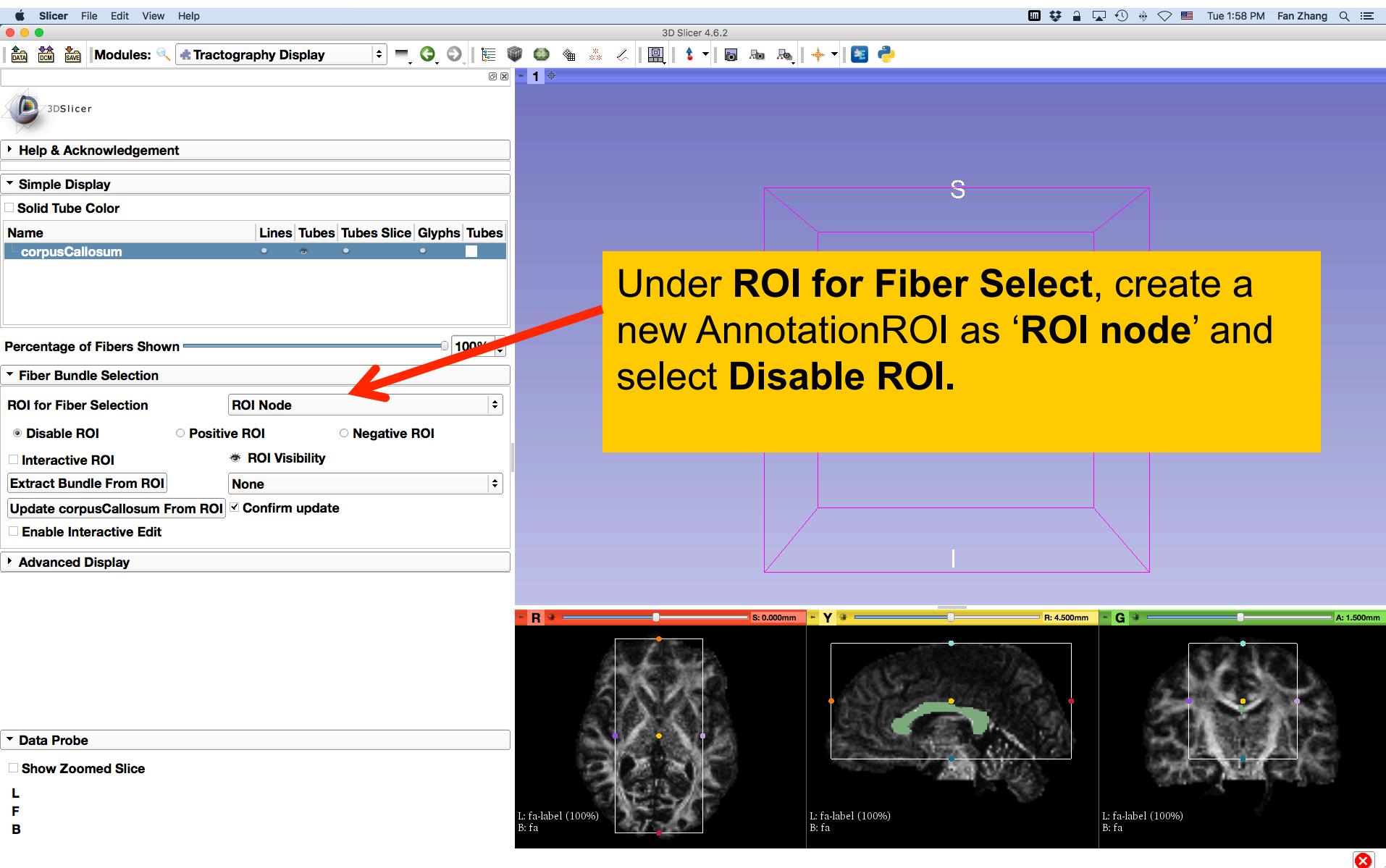
The tracts generated in the corpus callosum area appear in the 3D viewer.

The 3D Slicer interface displays a 3D volume rendering of a brain. A pink rectangular region highlights the corpus callosum area. Within this region, numerous colored fibers represent the generated tracts, primarily in shades of green, yellow, and blue. The 3D viewer has axes labeled A (Anterior), P (Posterior), and S (Superior). Below the 3D viewer, there are three smaller 2D grayscale brain slices: axial, coronal, and sagittal. The axial slice shows a green outline of the corpus callosum. The coronal and sagittal slices show internal brain structures. A red arrow points from the 'Enable Seeding Tracts' checkbox in the module panel to the text 'Check Enable Seeding Tracks' in a yellow box. A green box contains the text 'The tracts generated in the corpus callosum area appear in the 3D viewer.'

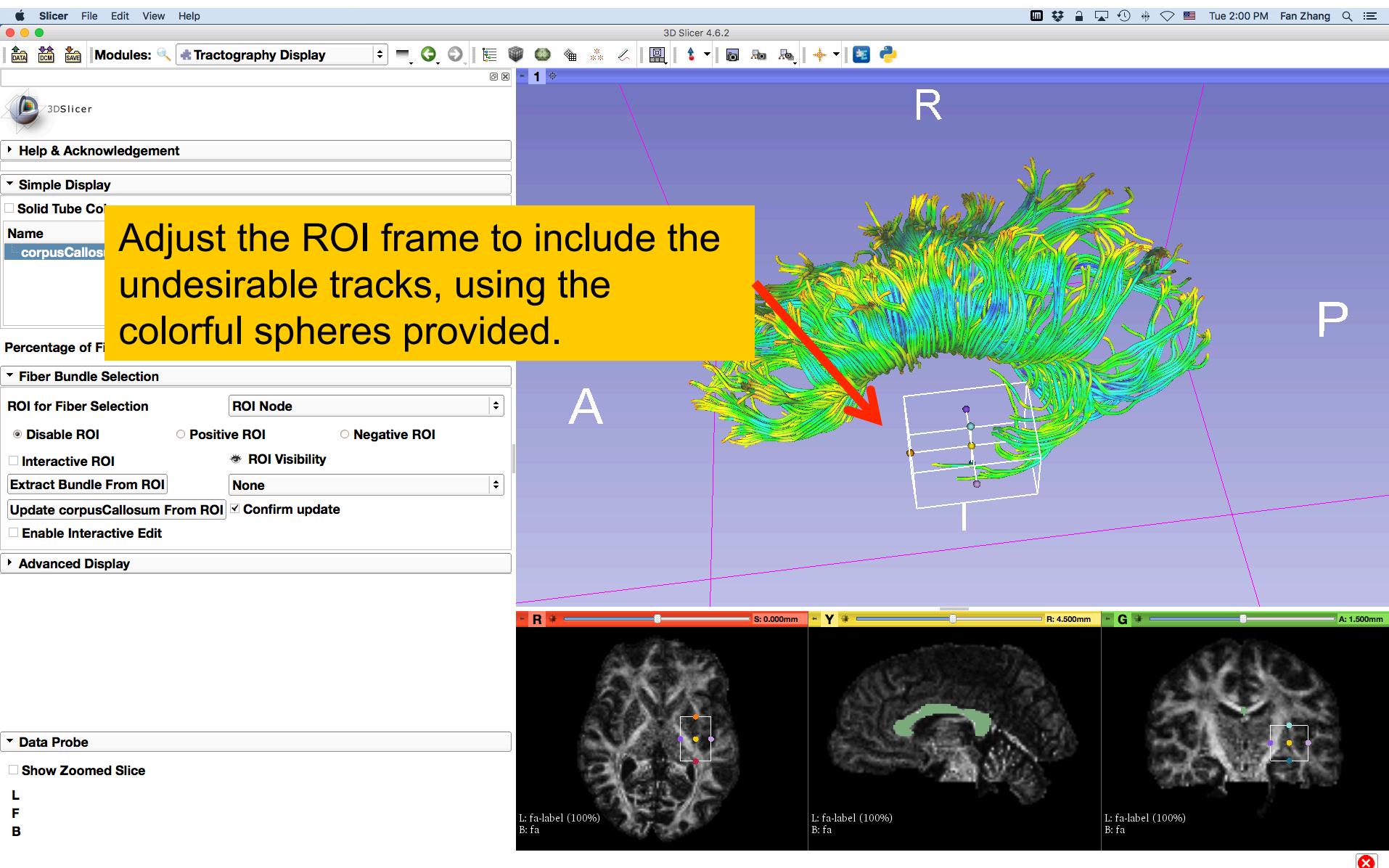
Step 4: Undesirable track removal



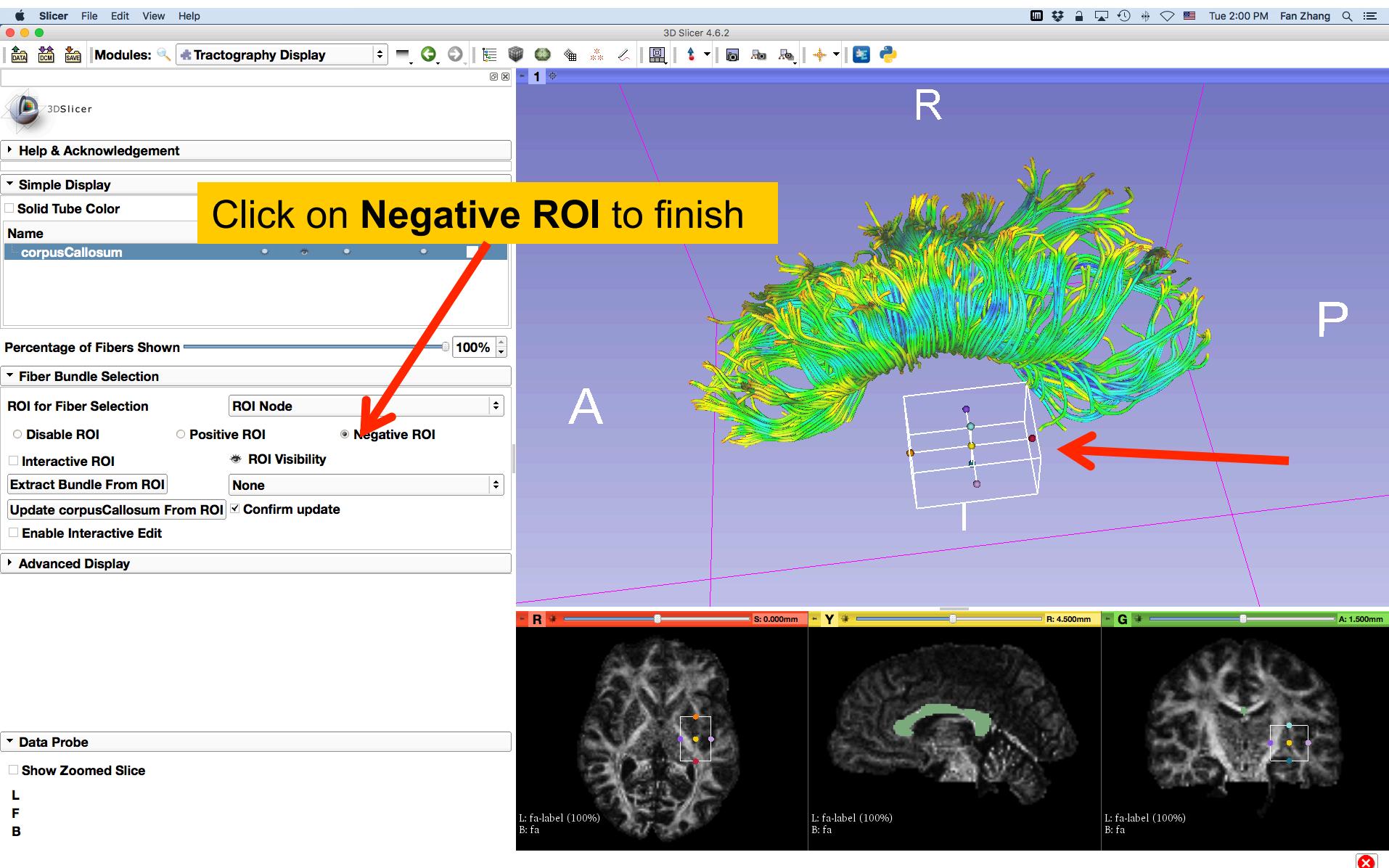
Step 4: Undesirable track removal



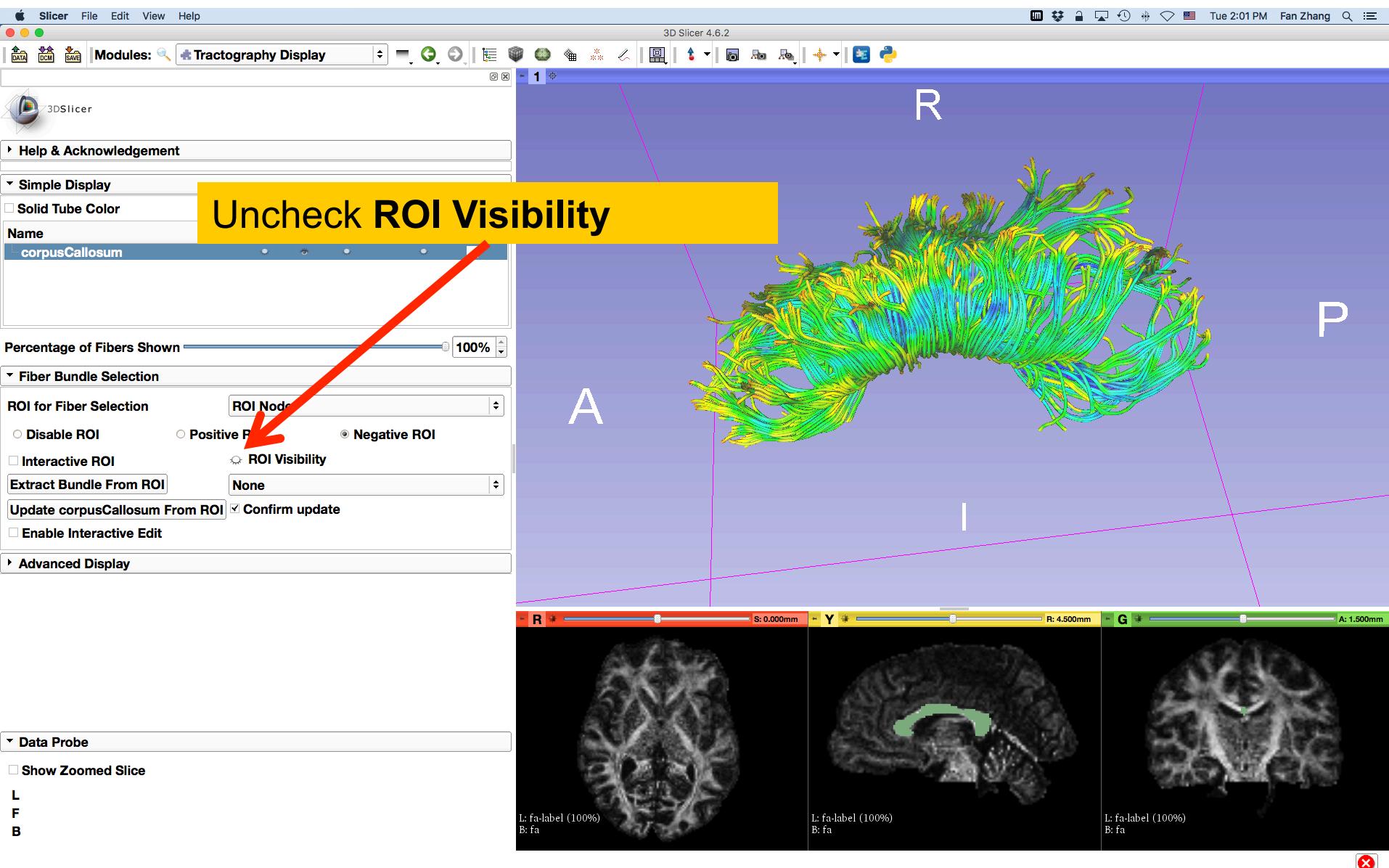
Step 4: Undesirable track removal



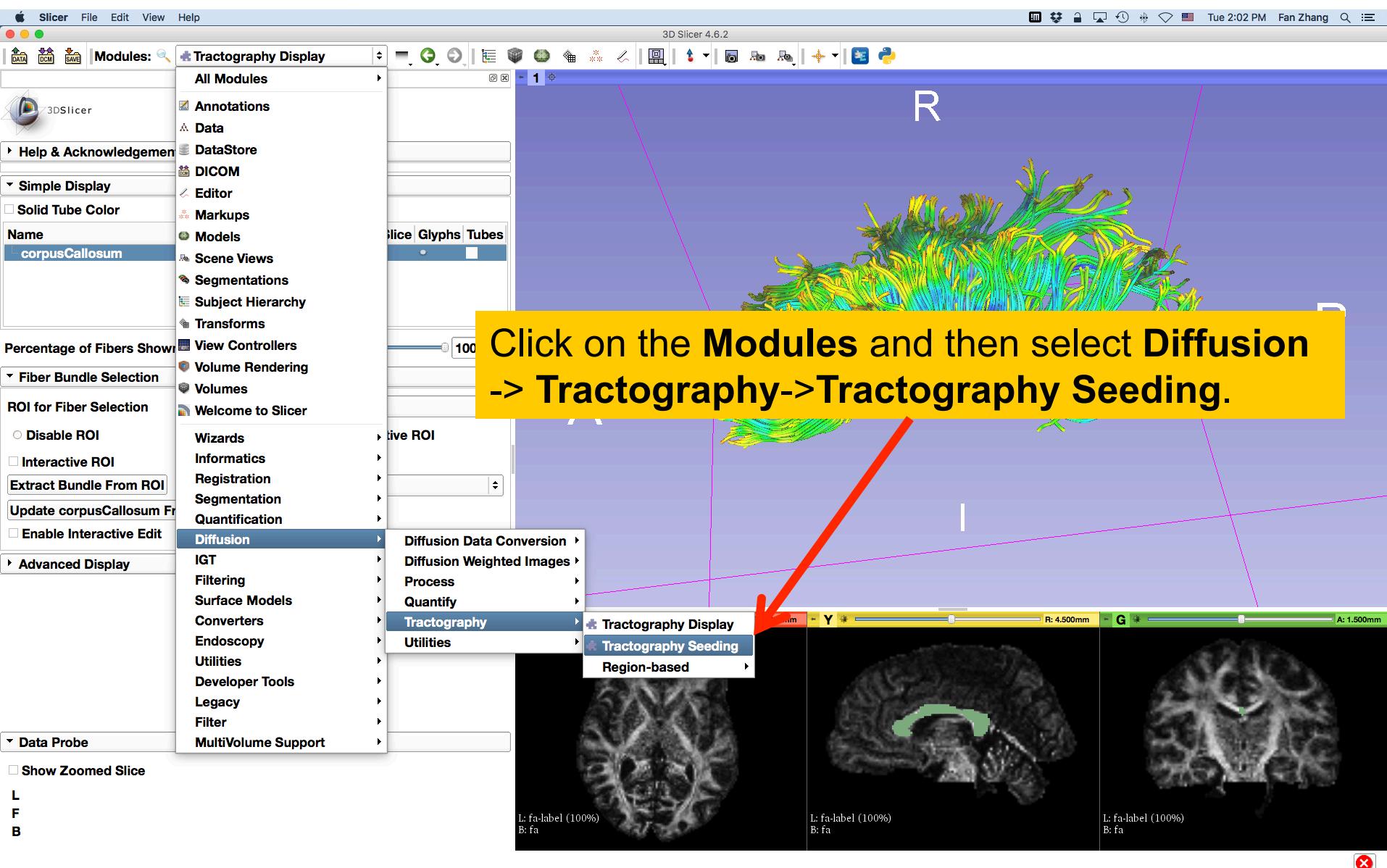
Step 4: Undesirable track removal



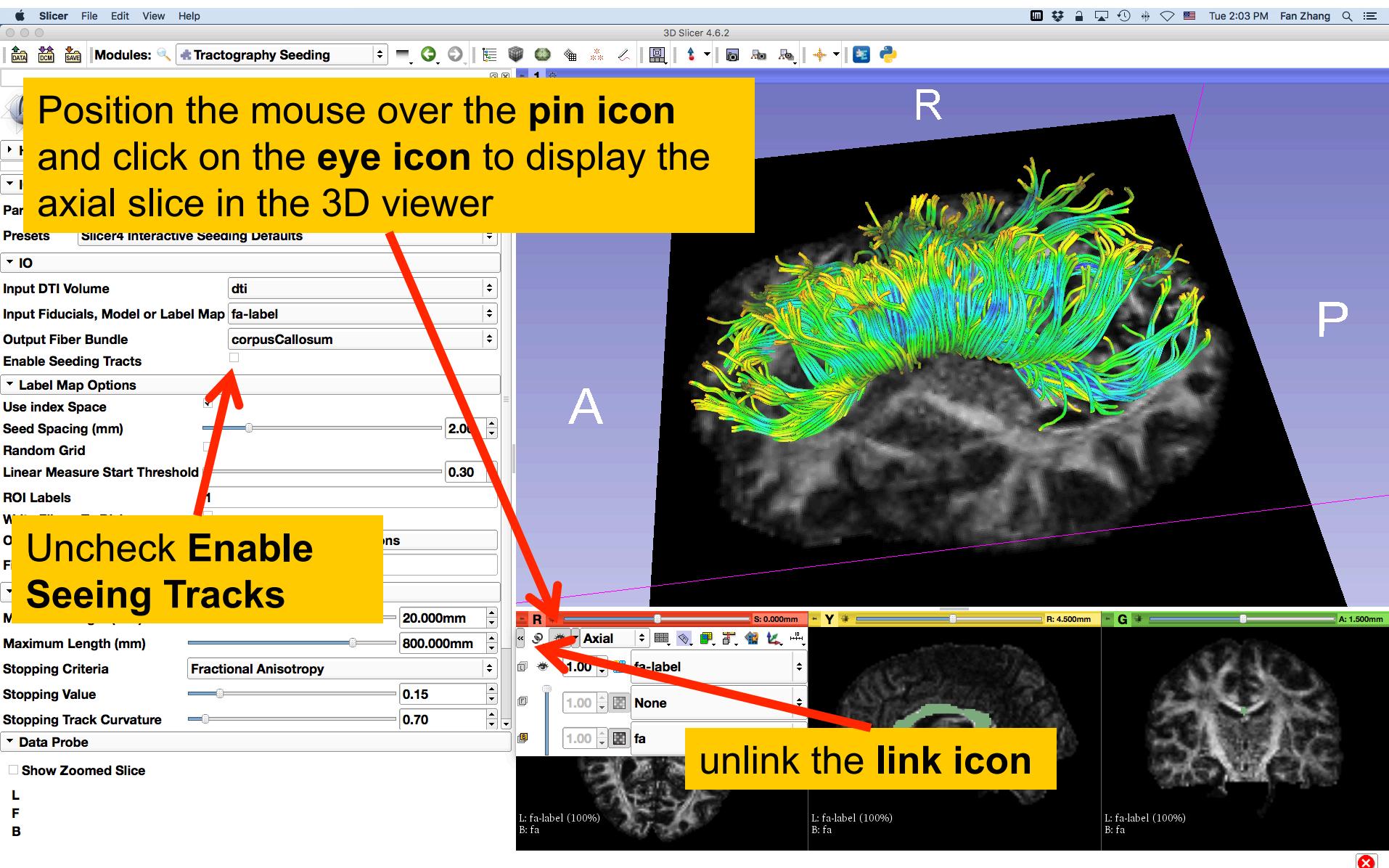
Step 4: Undesirable track removal



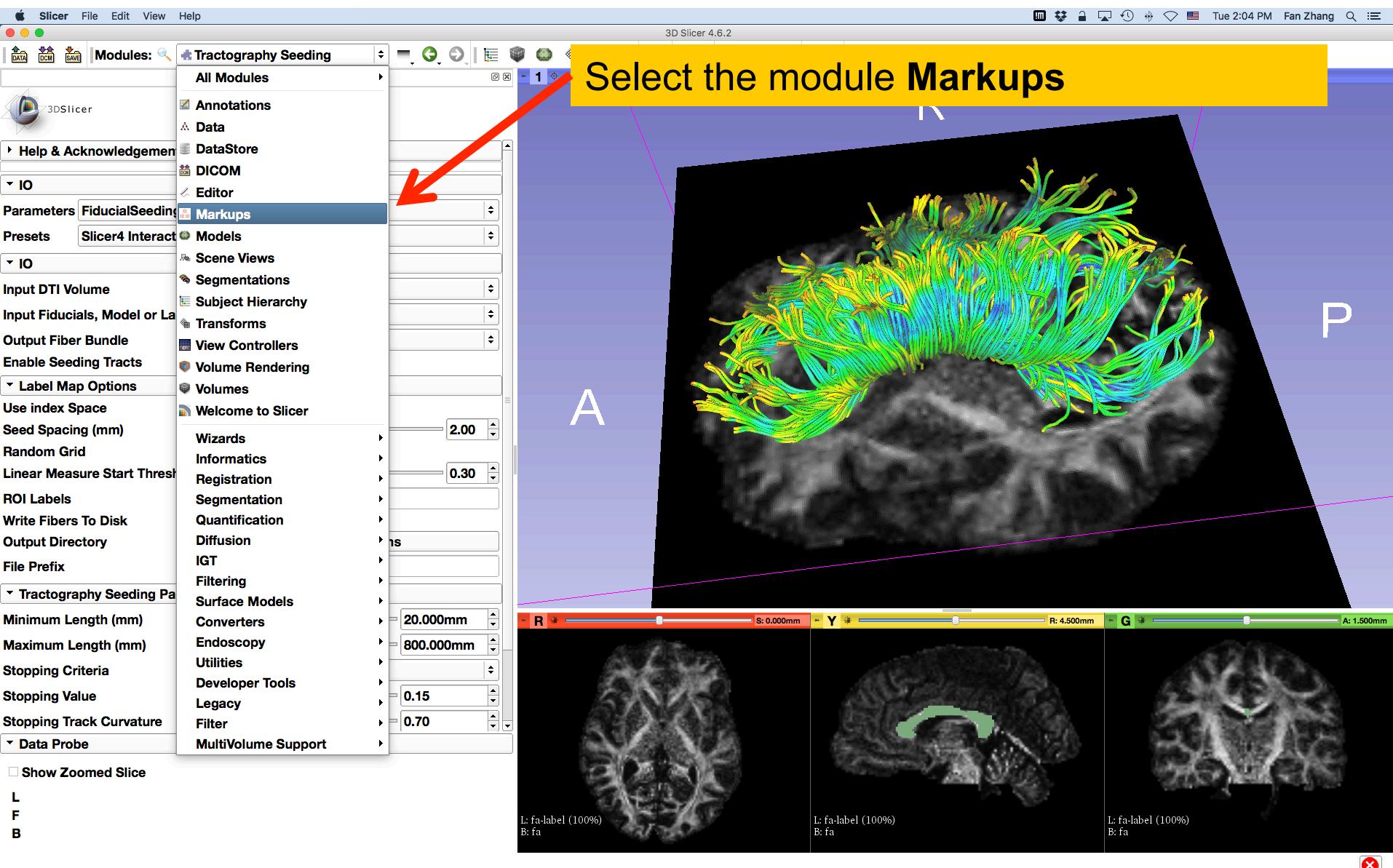
Labelmap Seeding: Tracts



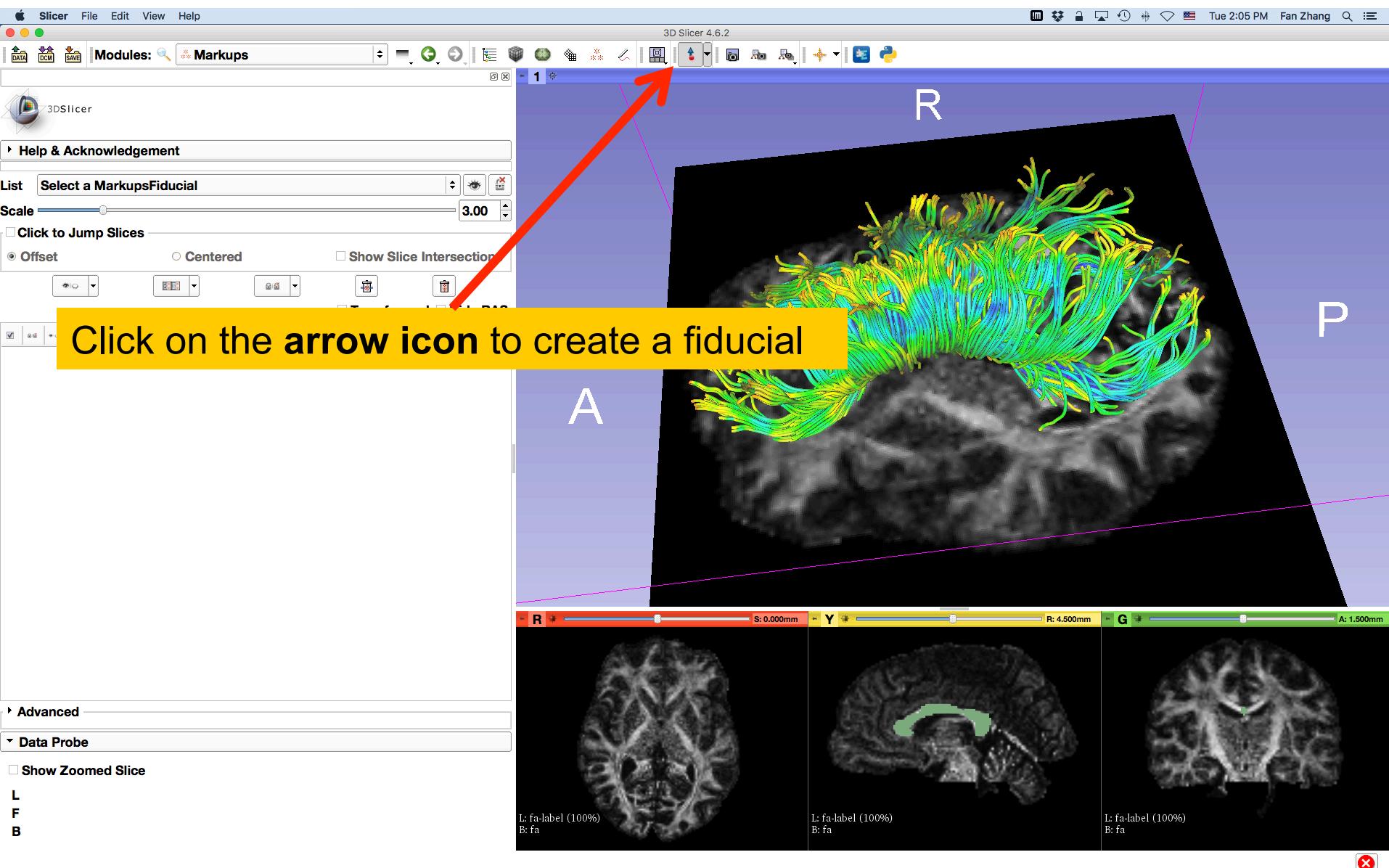
Tractography Results



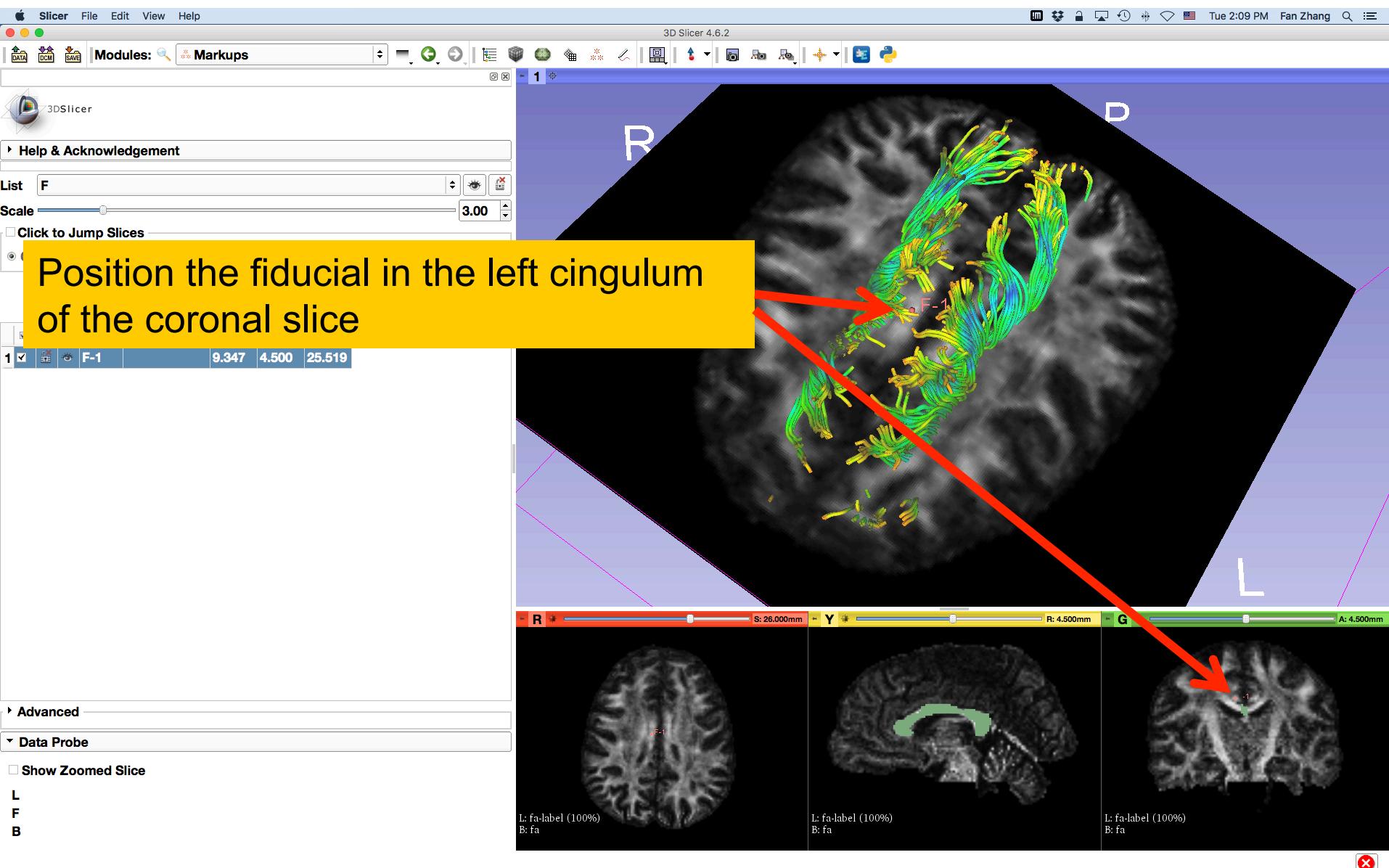
Fiducial Seeding



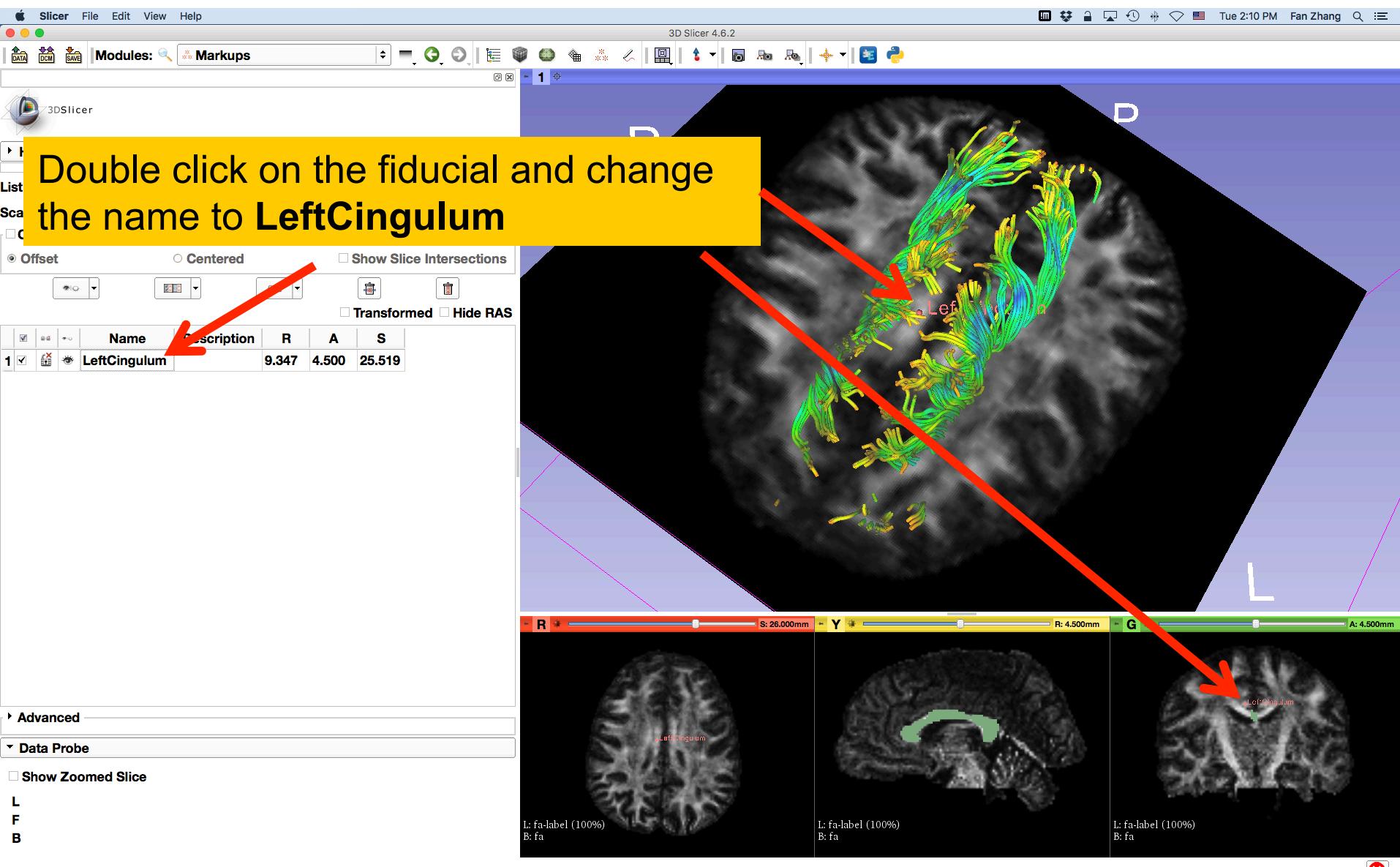
Fiducial Seeding



Fiducial Seeding



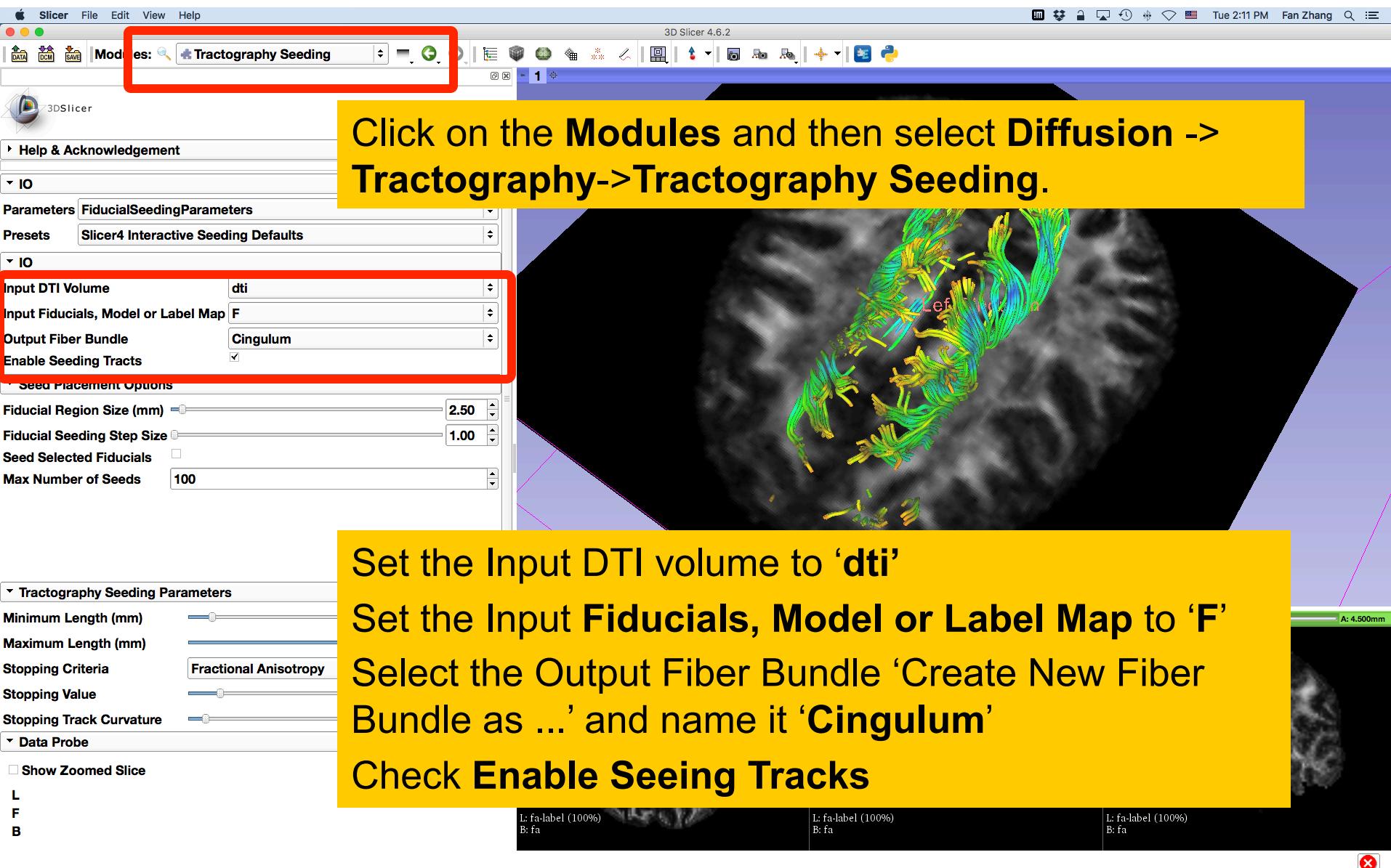
Fiducial Seeding



Fiducial Seeding

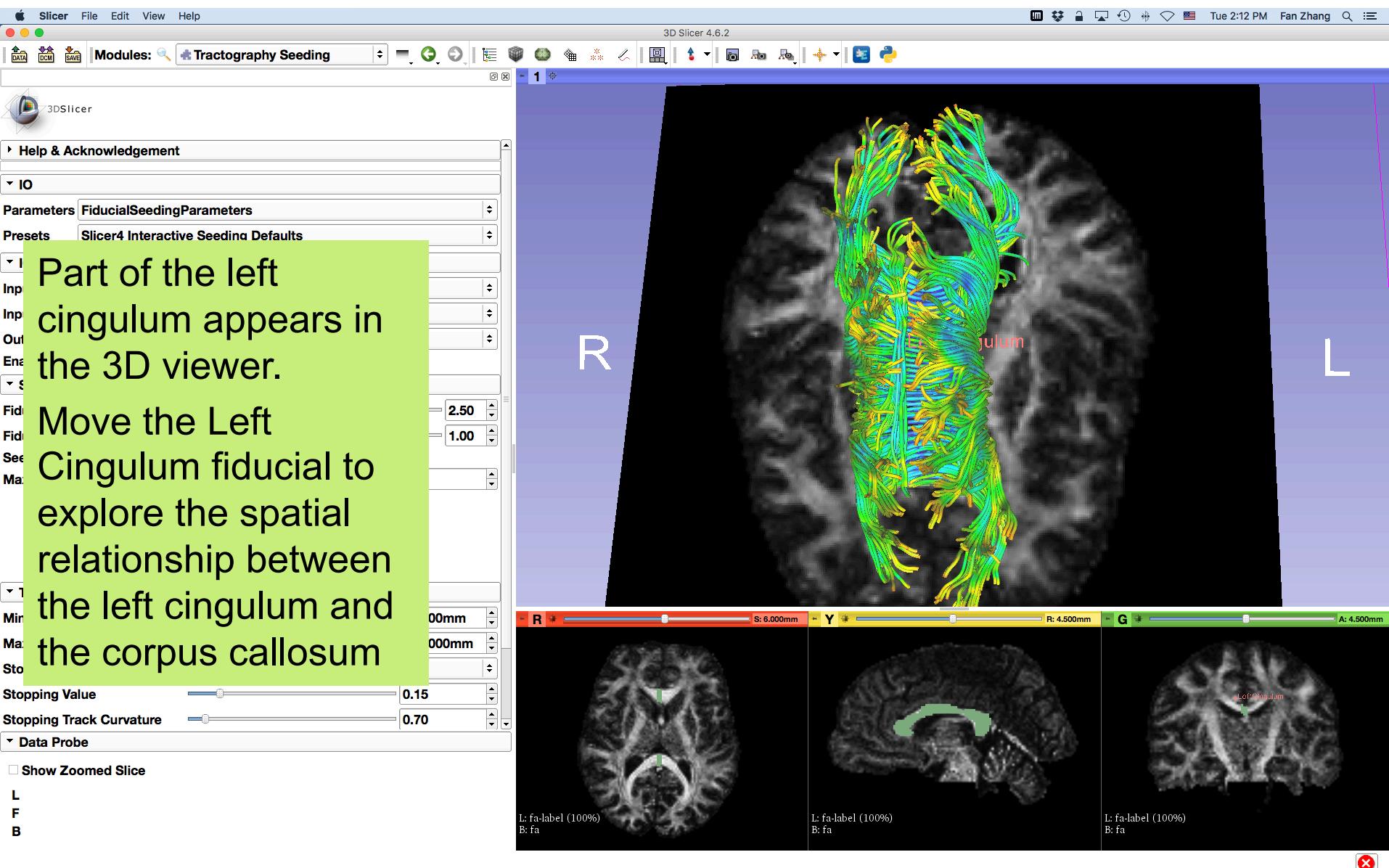
Click on the **Modules** and then select **Diffusion -> Tractography->Tractography Seeding**.

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**'
Check **Enable Seeing Tracks**



The screenshot shows the 3D Slicer interface version 4.6.2. The top bar includes the Slicer logo, menu options (File, Edit, View, Help), and a status bar indicating 'Tue 2:11 PM Fan Zhang'. A red box highlights the 'Modules' dropdown menu. Below the modules, a yellow box contains the instructions. Another red box highlights the 'Input DTI Volume' field set to 'dti'. To the right is a 3D brain model with green and yellow fiber tracts labeled 'Left Cingulum'. At the bottom, a yellow box lists the parameter settings: Minimum Length (mm), Maximum Length (mm), Stopping Criteria (Fractional Anisotropy), Stopping Value, and Stopping Track Curvature. It also shows the 'Data Probe' section and the 'Show Zoomed Slice' checkbox.

Fiducial Seeding



Fiducial Seeding

Slicer File Edit View Help

3D Slicer 4.6.2

Modules: **Markups**

Go to the **Markups** module

3DSlicer

Help & Acknowledgement

List F Scale 3.00

Click to Jump Slices Offset Centered Show Slice Intersections Transformed Hide RAS

	Name	Description	R	A	S
1	LeftCingulum		9.347	4.500	25.519
2	RightCingulum		-2.593	4.500	24.563

Place a fiducial for right cingulum, similar to the process for **LeftCingulum**.

Double click on the Name and change it to **RightCingulum**

L R P

LeftCingulum RightCingulum

R: 4.500mm A: 4.500mm

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

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

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

L F B

Advanced

Data Probe

Show Zoomed Slice

L F B

3D Slicer

Tue 2:14 PM Fan Zhang

Fiducial Seeding

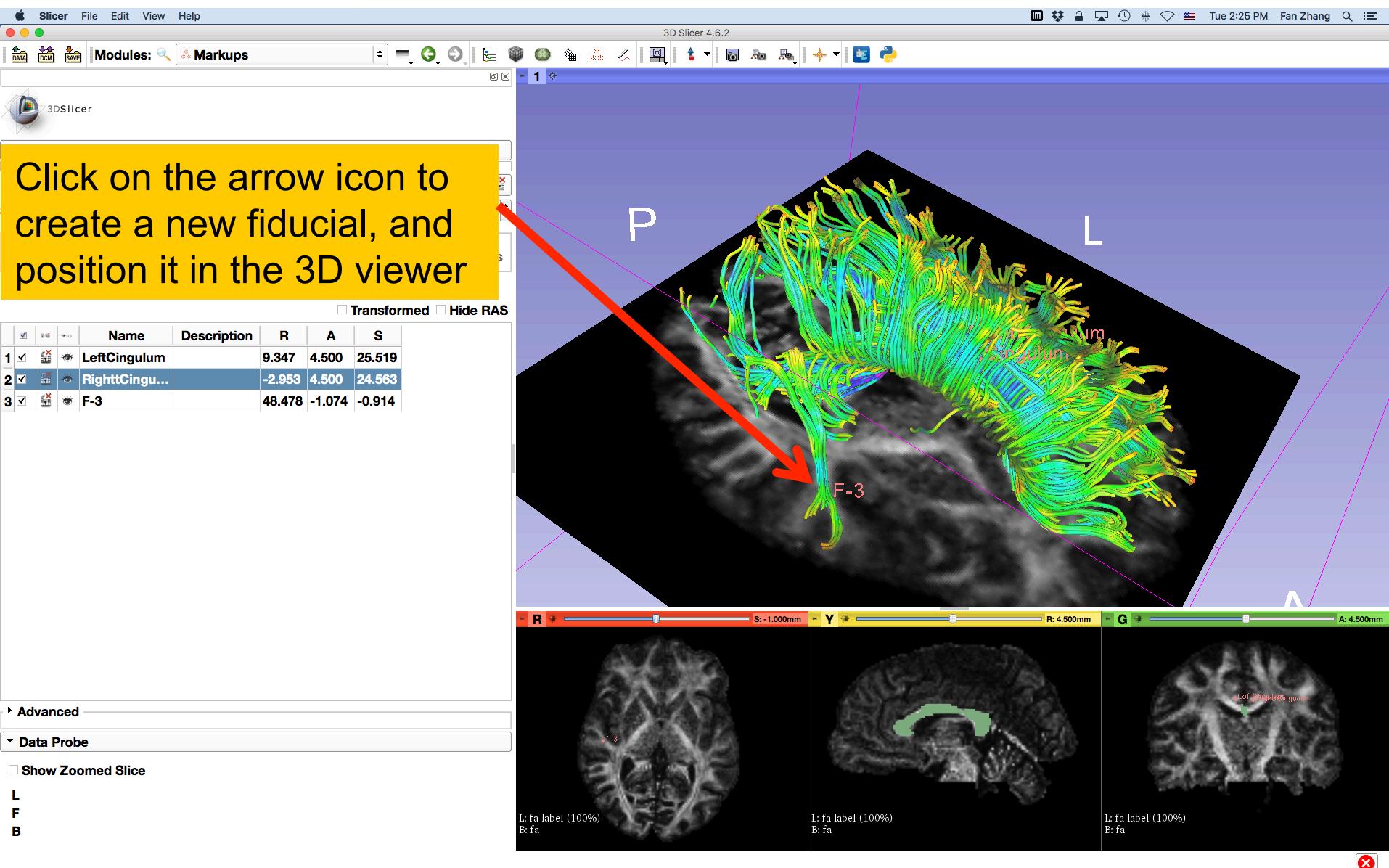
Part of the left and right cingulum appear in the 3D viewer.

Move the fiducials to explore the spatial relationship between the left and right cingulum, and the corpus callosum

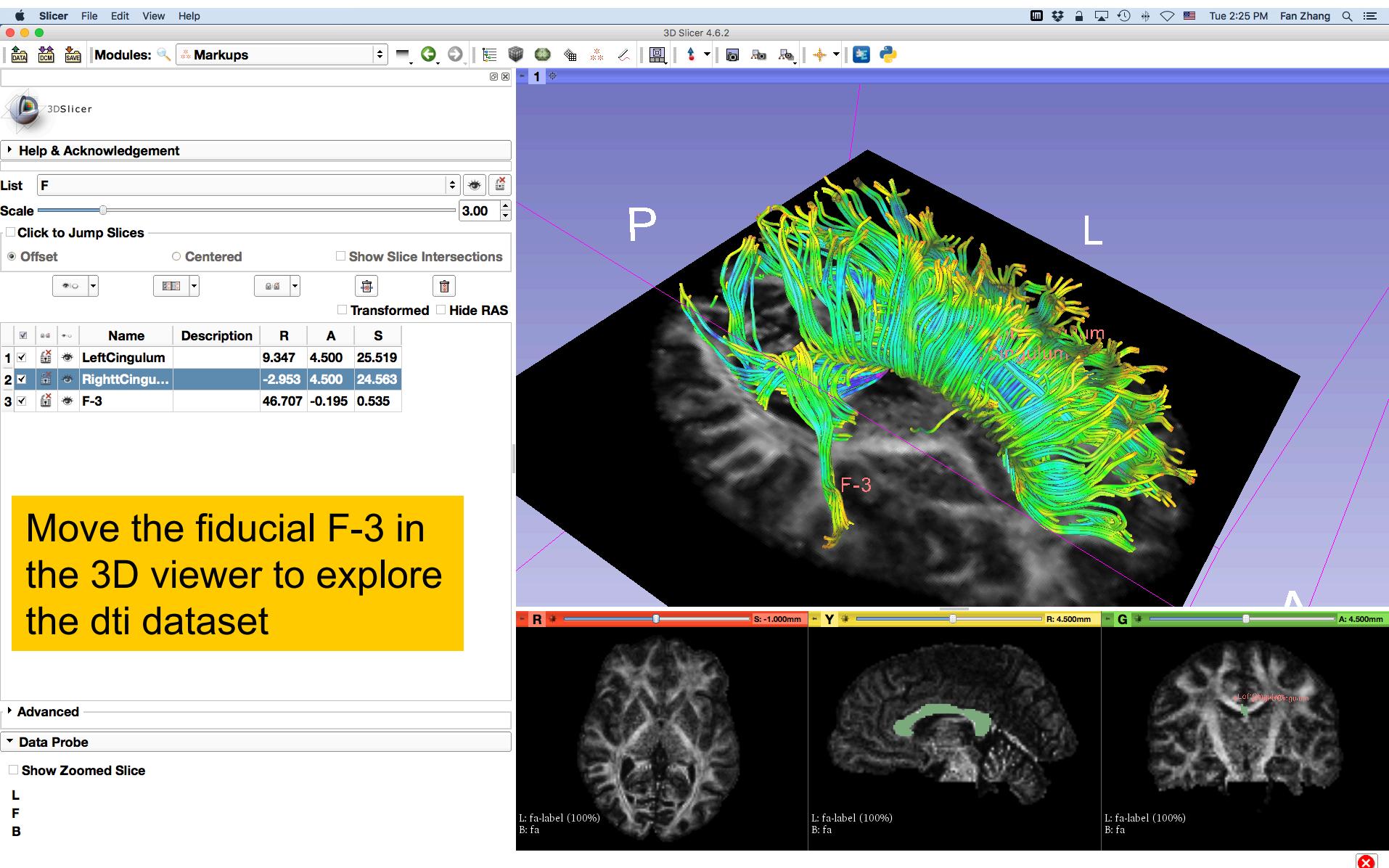
The image shows the 3D Slicer software interface. On the left, there's a control panel with buttons for 'DATA', 'DCM', 'SAVE', 'Modules' (with 'Markups' selected), and 'Help & Acknowledgement'. Below it are sliders for 'Scale' and 'Offset' (set to 'Offset'). A table lists two fiducials: 'LeftCingulum' at R: 9.347, A: 4.500 and 'RightCingulum' at R: -2.593, A: 4.500. At the bottom left, there are buttons for 'Advanced' and 'Data Probe', and a checkbox for 'Show Zoomed Slice'.

The main window displays a 3D brain volume with colored tracts (green, yellow) representing the cingulum and corpus callosum. Labels 'Left Cingulum' and 'Right Cingulum' are placed near their respective structures. A large purple slice on the right is labeled 'L' (left). Below the 3D view are three 2D axial slices. The left slice shows a green dot labeled 'fa-label (100%)' and 'B: fa'. The middle slice shows a green outline labeled 'fa-label (100%)' and 'B: fa'. The right slice shows a green dot labeled 'Left Cingulum' and 'fa-label (100%)' and 'B: fa'. Navigation sliders at the bottom indicate positions S: 6.000mm, R: 4.500mm, and G: 4.500mm.

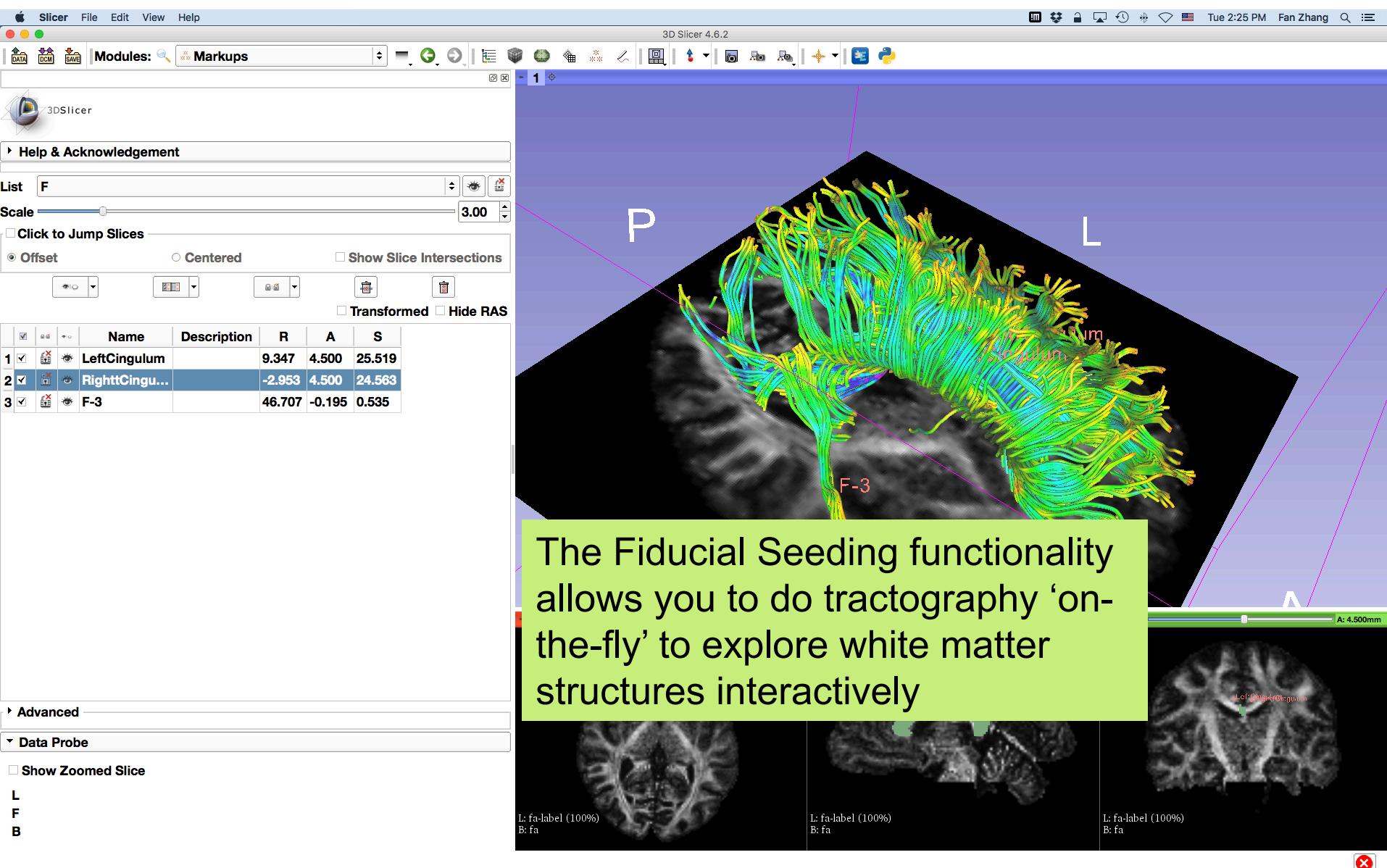
Fiducial Seeding



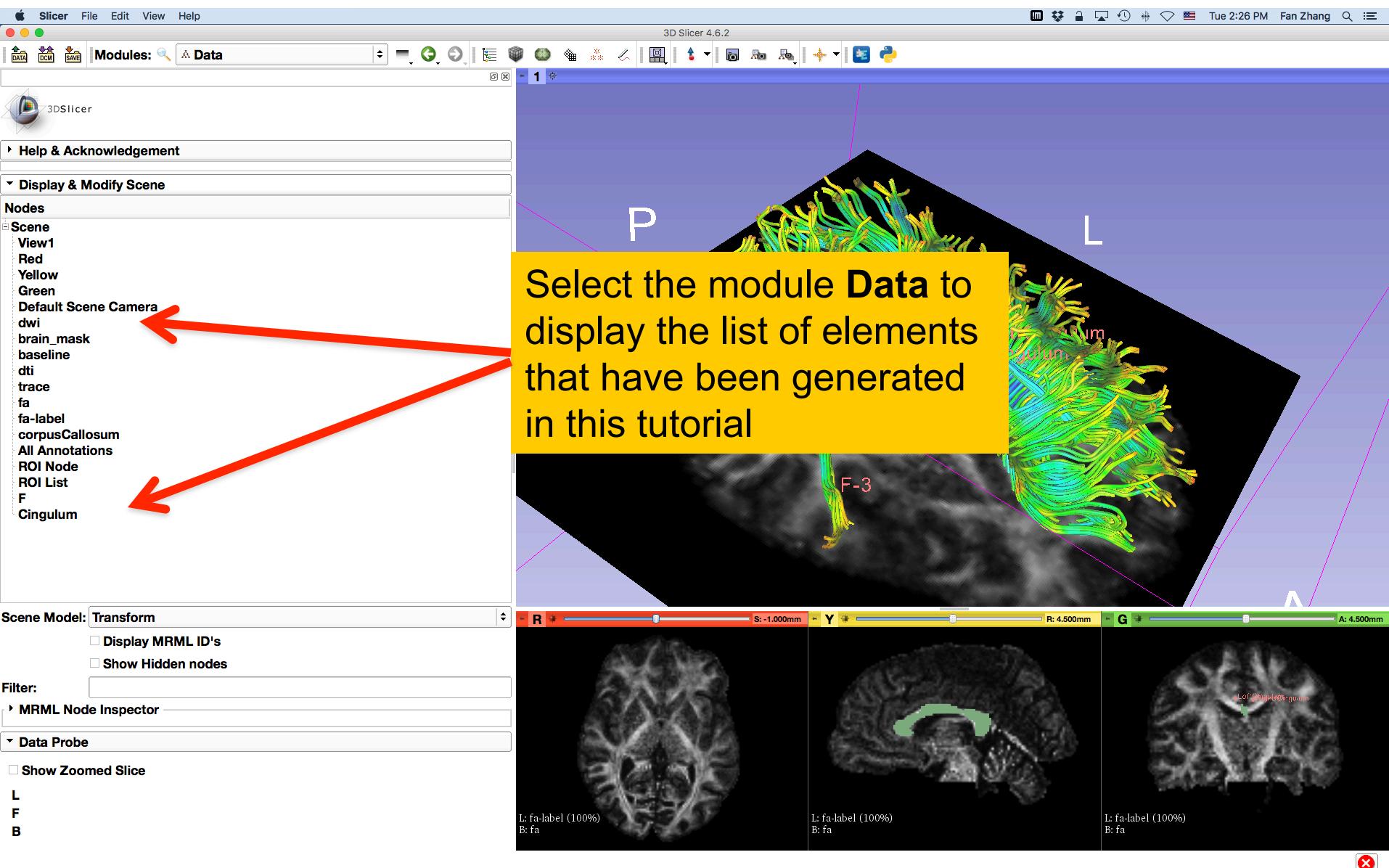
Fiducial Seeding



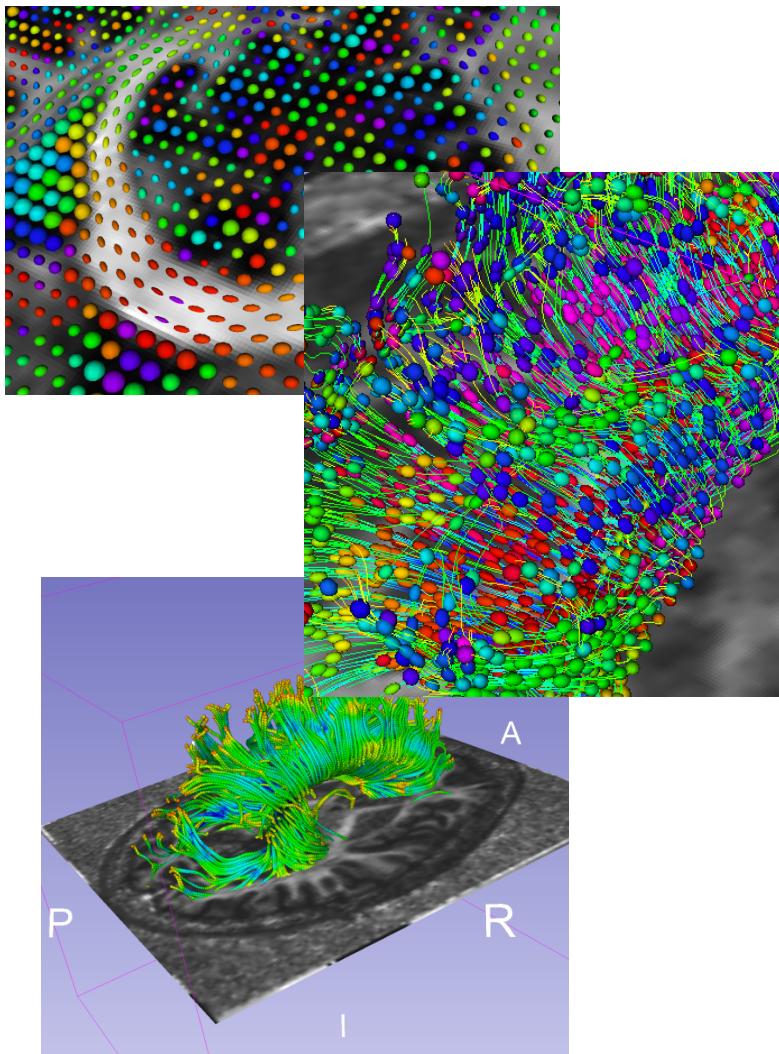
Tractography ‘on-the-fly’



DTI Analysis



Conclusion



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

Acknowledgments



- **Open Source Diffusion MRI Technology For Brain Cancer Research** NIH U01CA199459
- **National Center for Image Guided Therapy (NCIGT)**
NIH P41EB015898
- **Neuroimage Analysis Center (NAC)**
NIH P41EB015902
- Fan Zhang, Brigham and Women's Hospital, Harvard Medical School

