



Diffusion MRI Analysis

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Brain Anatomy



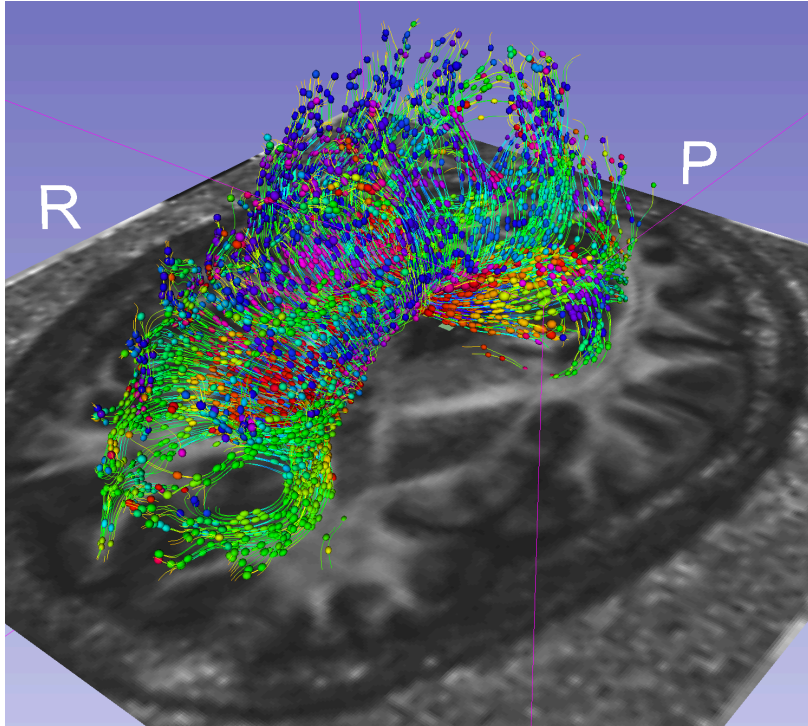
- White matter ~45% of the brain
- Myelinated nerve fibers (~ 10 μm axon diameter)

White Matter Exploration



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

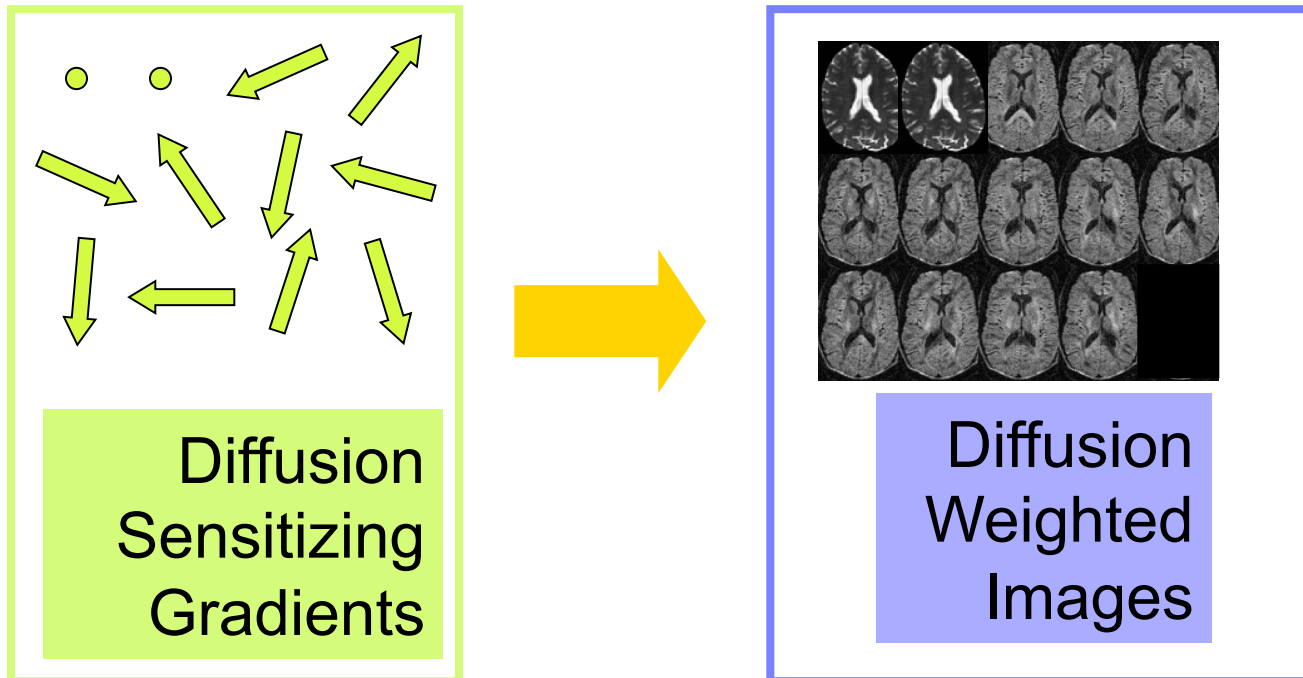
Tutorial Outline



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

Tutorial dataset

The tutorial dataset is a Diffusion Weighted MR scan of the brain acquired with 42 gradient directions and one baseline.

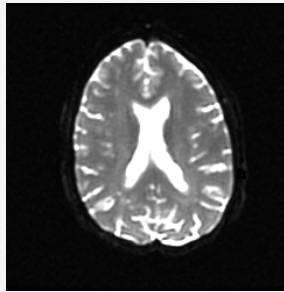


Learning Objectives

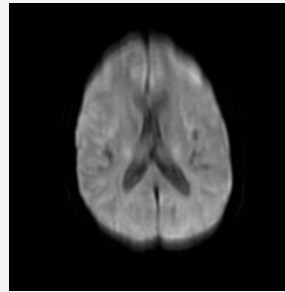
Following this tutorial, you'll be able to

- 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

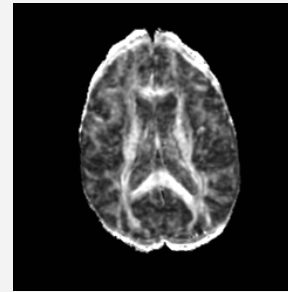
MR Diffusion Analysis Pipeline



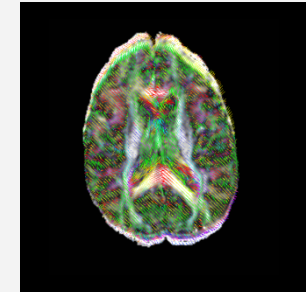
DWI
Acquisition



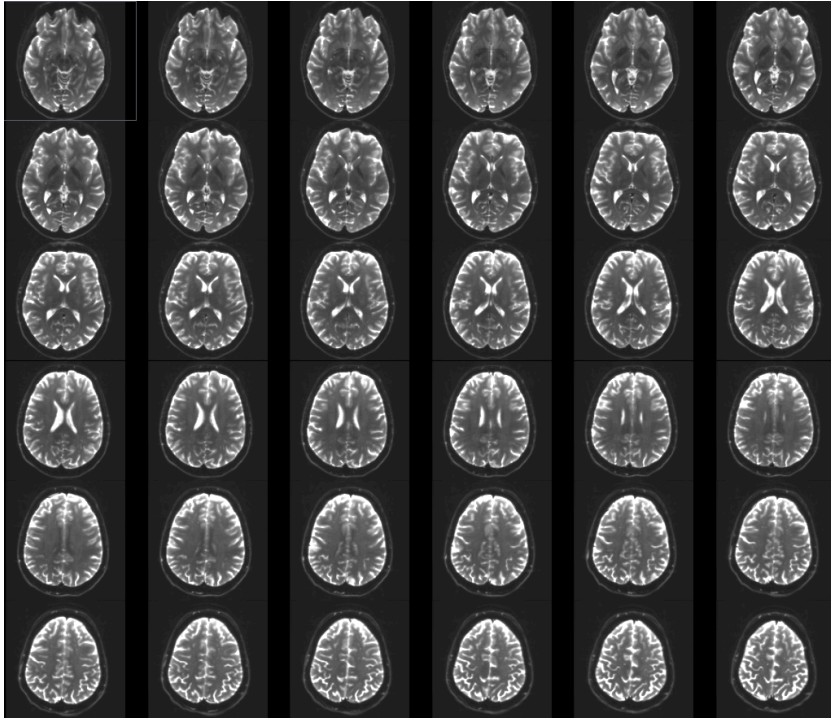
Tensor
Calculation



Scalar
Maps

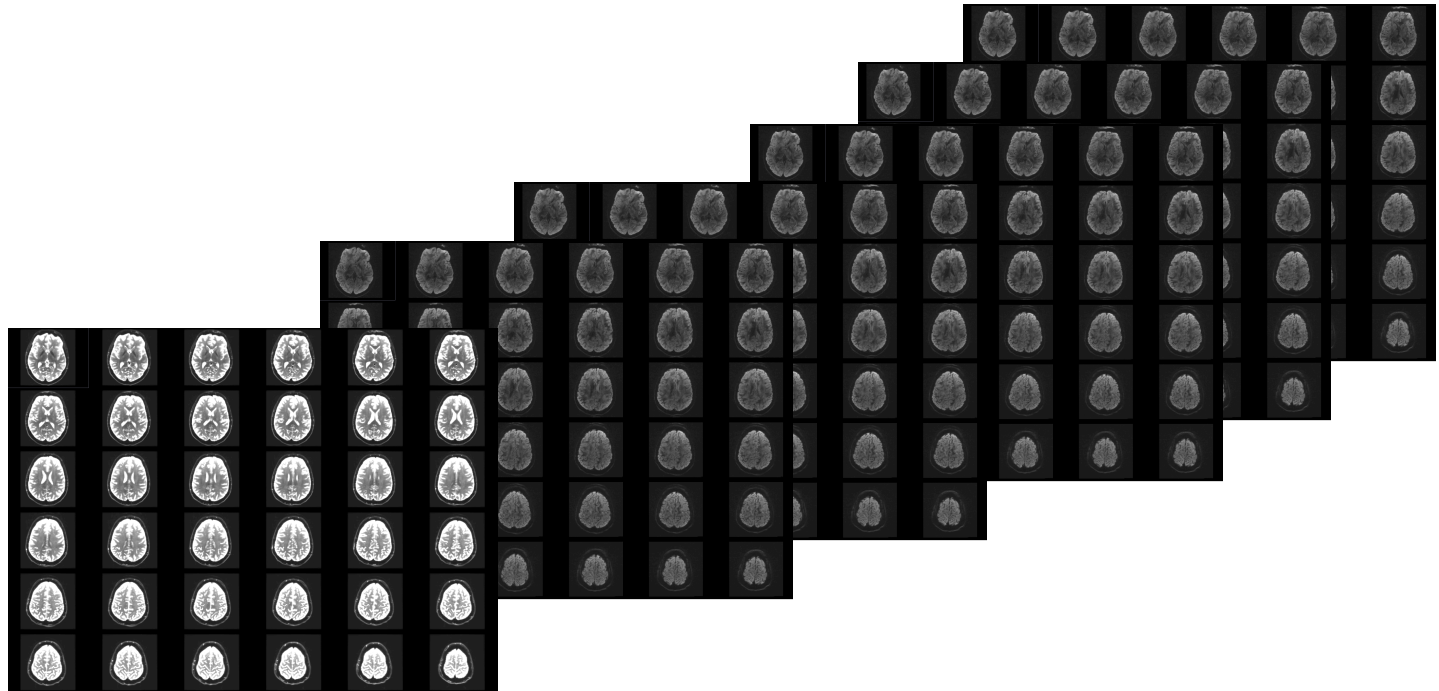


3D
Visualization



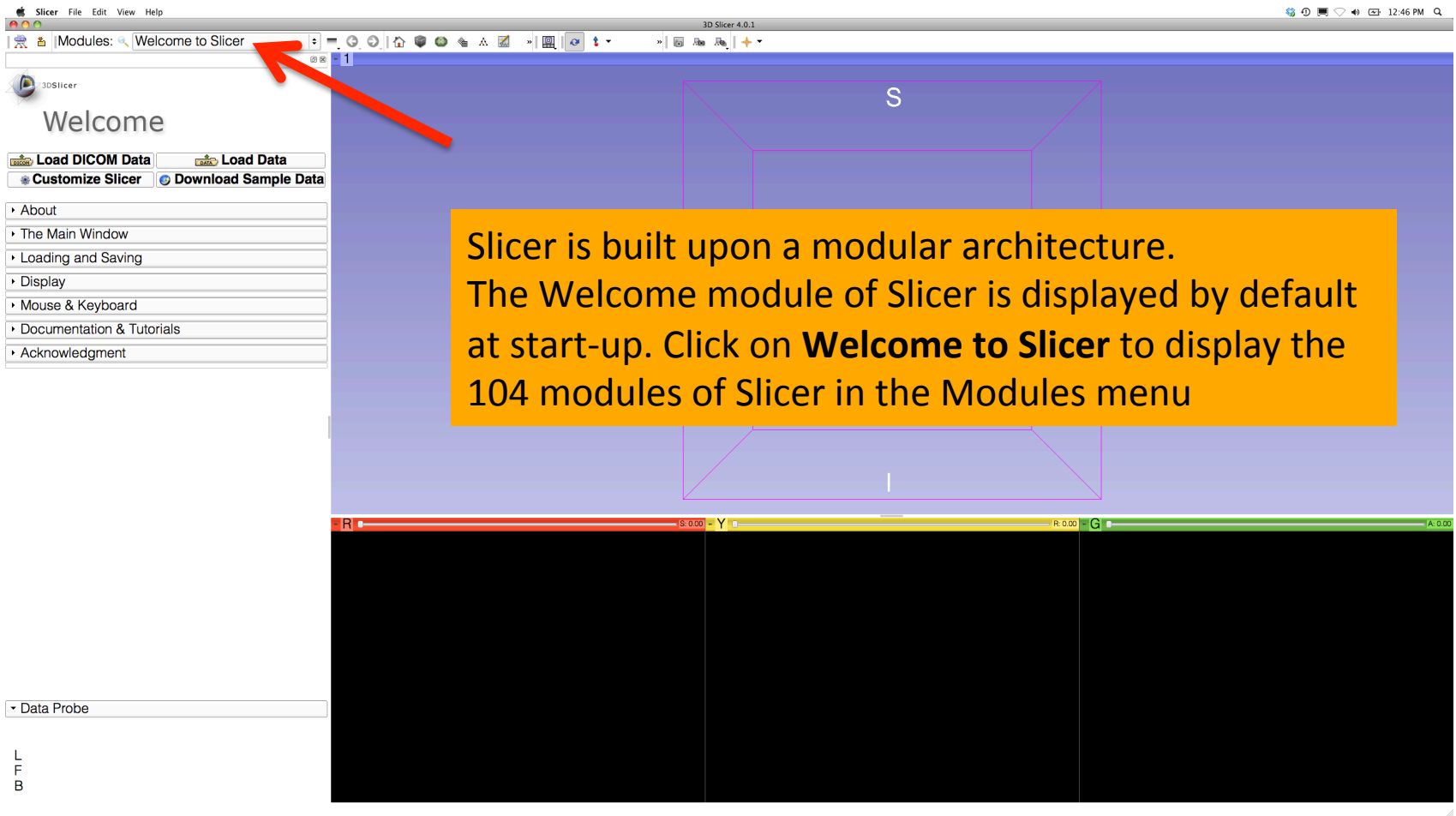
Part 1: From DWI images to Tensors

Understanding the DWI dataset

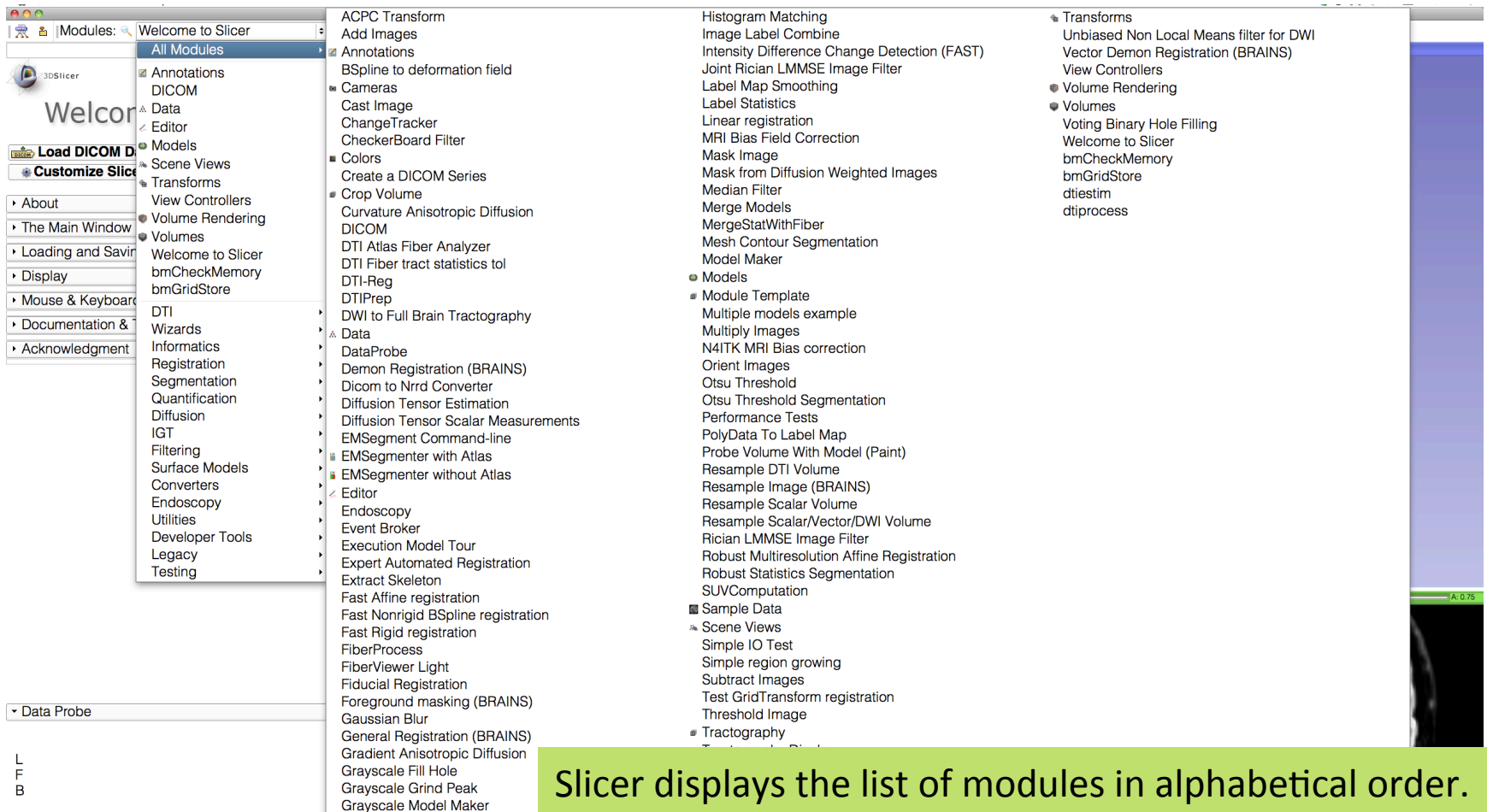


The DWI dataset is composed of one volume acquired without diffusion-sensitizing gradient, and 42 volumes acquired with 42 different diffusion-sensitizing gradients.

Loading the DWI dataset



Start the Slicer software



Loading the DWI dataset

Click on **Load Data** in the GUI panel of the Welcome menu.

3D Slicer 4.0.1

Modules: Welcome to Slicer

3DSlicer

Welcome

Load DICOM Data Load Data

Customize Slicer Download Sample Data

- About
- The Main Window
- Loading and Saving
- Display
- Mouse & Keyboard
- Documentation & Tutorials
- Acknowledgment

- Data Probe

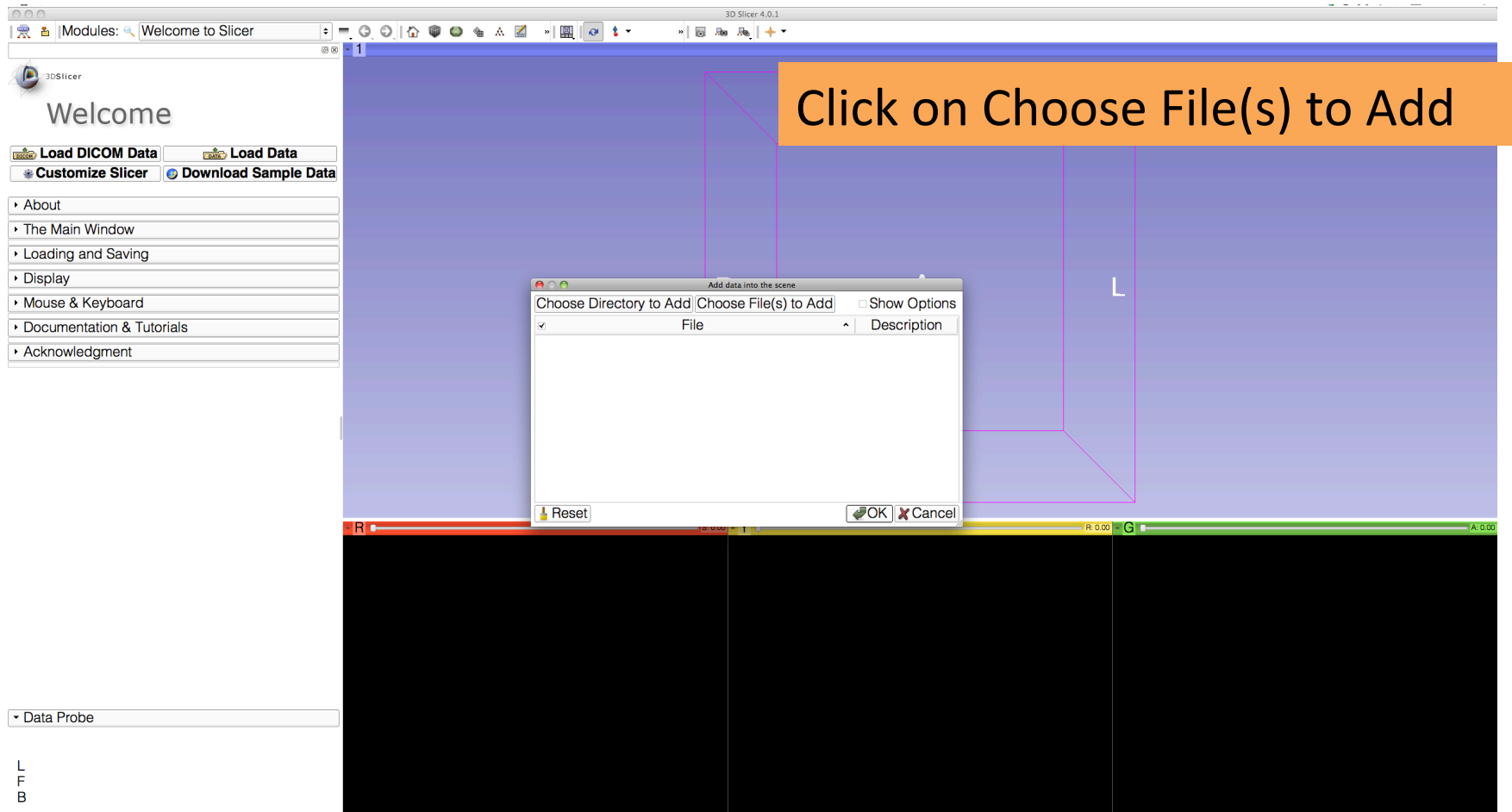
Red RAS: (-104.6, 63.4, -0.8) Axial Sp: 1.5

L None()
F None()
B None()

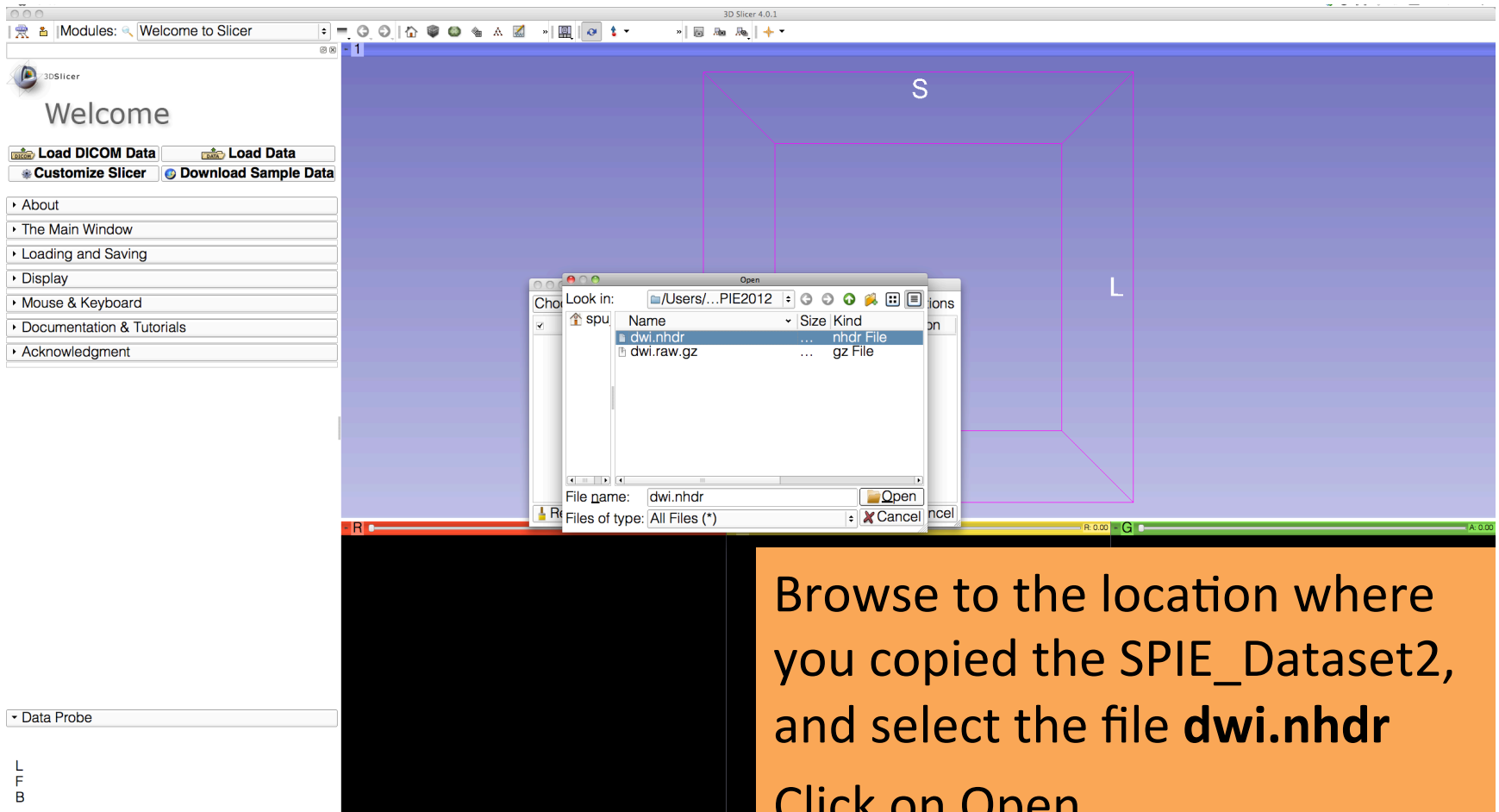
R A L

R S 0.00 -Y R 0.00 G -A 0.00

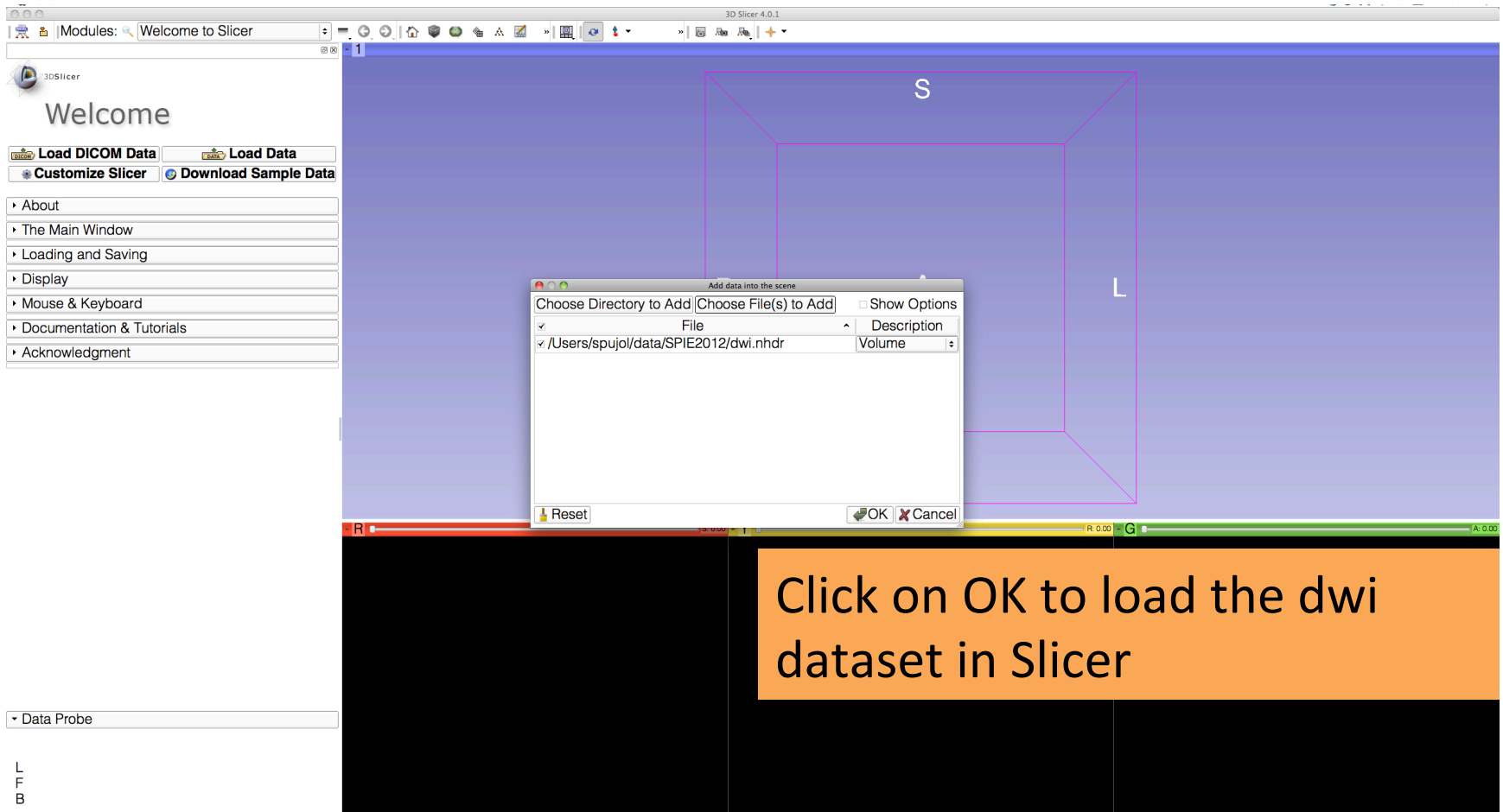
Loading the DWI dataset



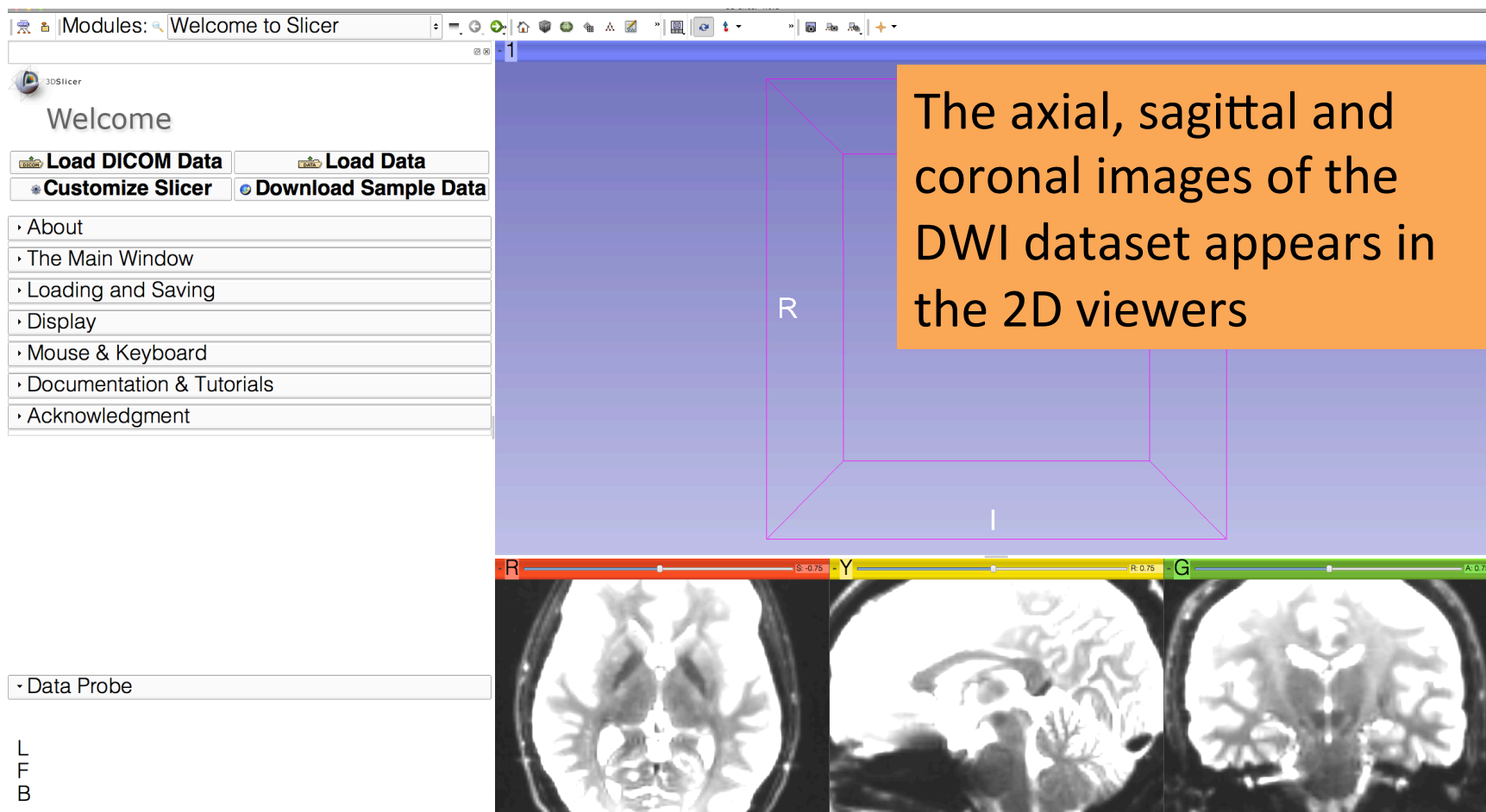
Loading the DWI dataset



Loading the DWI dataset



Loading the DWI dataset



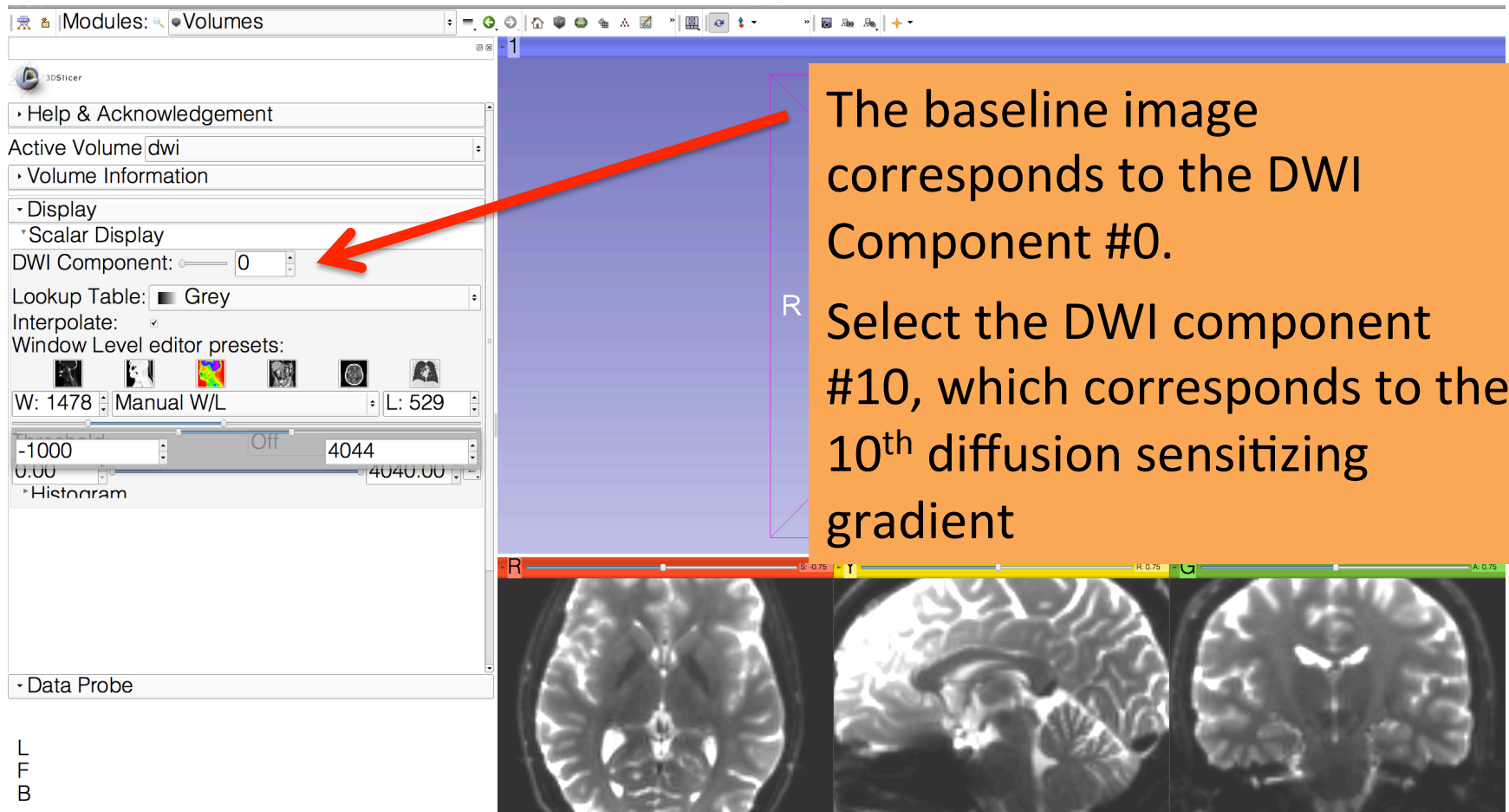
Adjusting Window and Level

The screenshot shows the 3D Slicer software interface. The 'Volumes' module is selected in the top menu. The left sidebar contains various settings for the active volume 'dwi'. A red arrow points to the 'Threshold' slider, which is currently set to 'Off' with a range from 0.00 to 4040.00. The 'W/L' (Window/Level) settings are set to 'Auto W/L' with a window width of 532 and a level of 272. The main 3D view shows a brain slice with a purple wireframe box and a white 'R' label. Below the 3D view are three 2D image thumbnails labeled 'R', 'Y', and 'G'. The 'R' thumbnail shows a coronal slice, the 'Y' thumbnail shows a sagittal slice, and the 'G' thumbnail shows an axial slice. The 'R' thumbnail has a red bar above it with 'S: -0.75', the 'Y' thumbnail has a yellow bar with 'R: 0.75', and the 'G' thumbnail has a green bar with 'A: 0.75'. The bottom left corner of the interface shows the letters 'L', 'F', and 'B' stacked vertically.

Select the module Volumes from the modules menu.

Adjust the window and display of the baseline image using the W/L slider

Exploring the DWI dataset



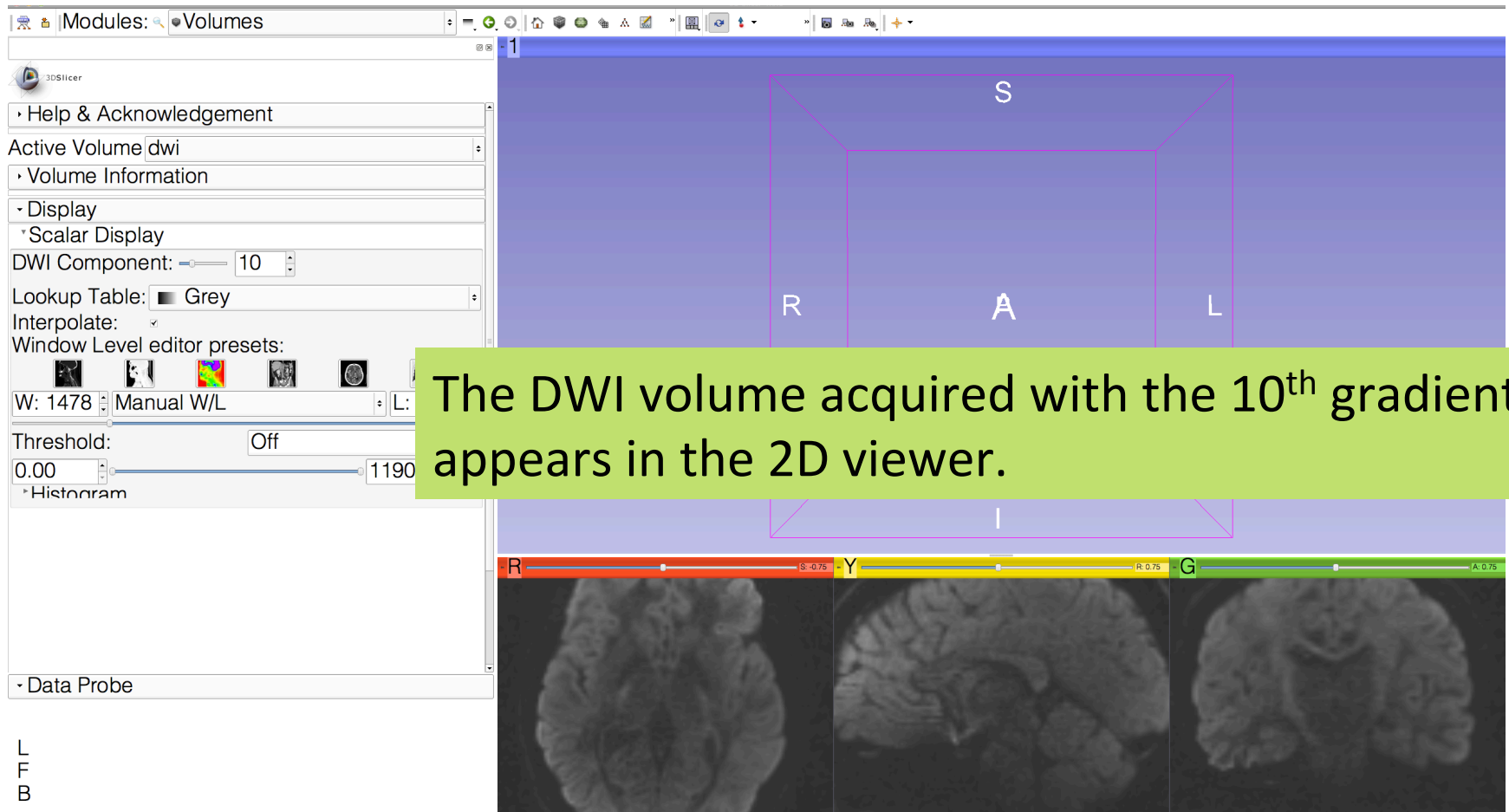
The screenshot shows the 3D Slicer software interface. The top toolbar includes icons for file operations, view manipulation, and volume management. The left sidebar contains the 'Volumes' panel with sections for 'Help & Acknowledgement', 'Active Volume | dwi', 'Volume Information', and 'Display'. Under 'Display', the 'Scalar Display' section is active, showing 'DWI Component' set to 0, 'Lookup Table' set to 'Grey', and 'Interpolate' checked. Below this are 'Window Level editor presets' and 'W/L' settings (W: 1478, L: 529). A red arrow points from the 'DWI Component' dropdown to the text box on the right. The main 3D view shows a blue volume with a red 'R' label. Below the 3D view are three 2D slices: axial (labeled 'R'), sagittal (labeled 'S: -0.75'), and coronal (labeled 'R: 0.75').

The baseline image corresponds to the DWI Component #0.

Select the DWI component #10, which corresponds to the 10th diffusion sensitizing gradient

L
F
B

Exploring the DWI dataset



Exploring the DWI dataset

Adjust the window and display of the baseline image using the W/L slider

W: 585 Manual W/L L: 400

Threshold: Off

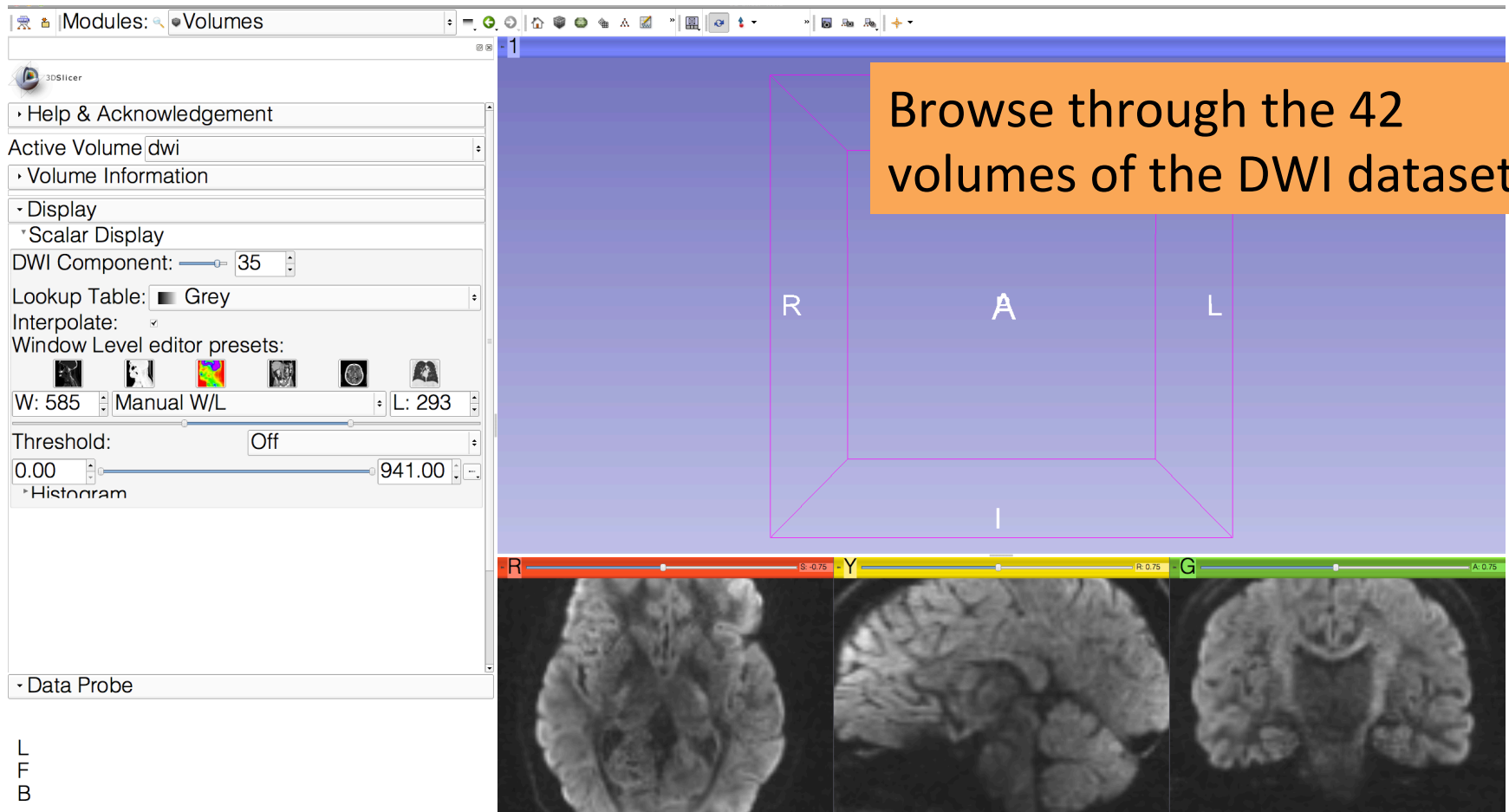
0.00 1190.00

R A L I

R Y G

L
F
B

Exploring the DWI dataset



Exploring the DWI dataset

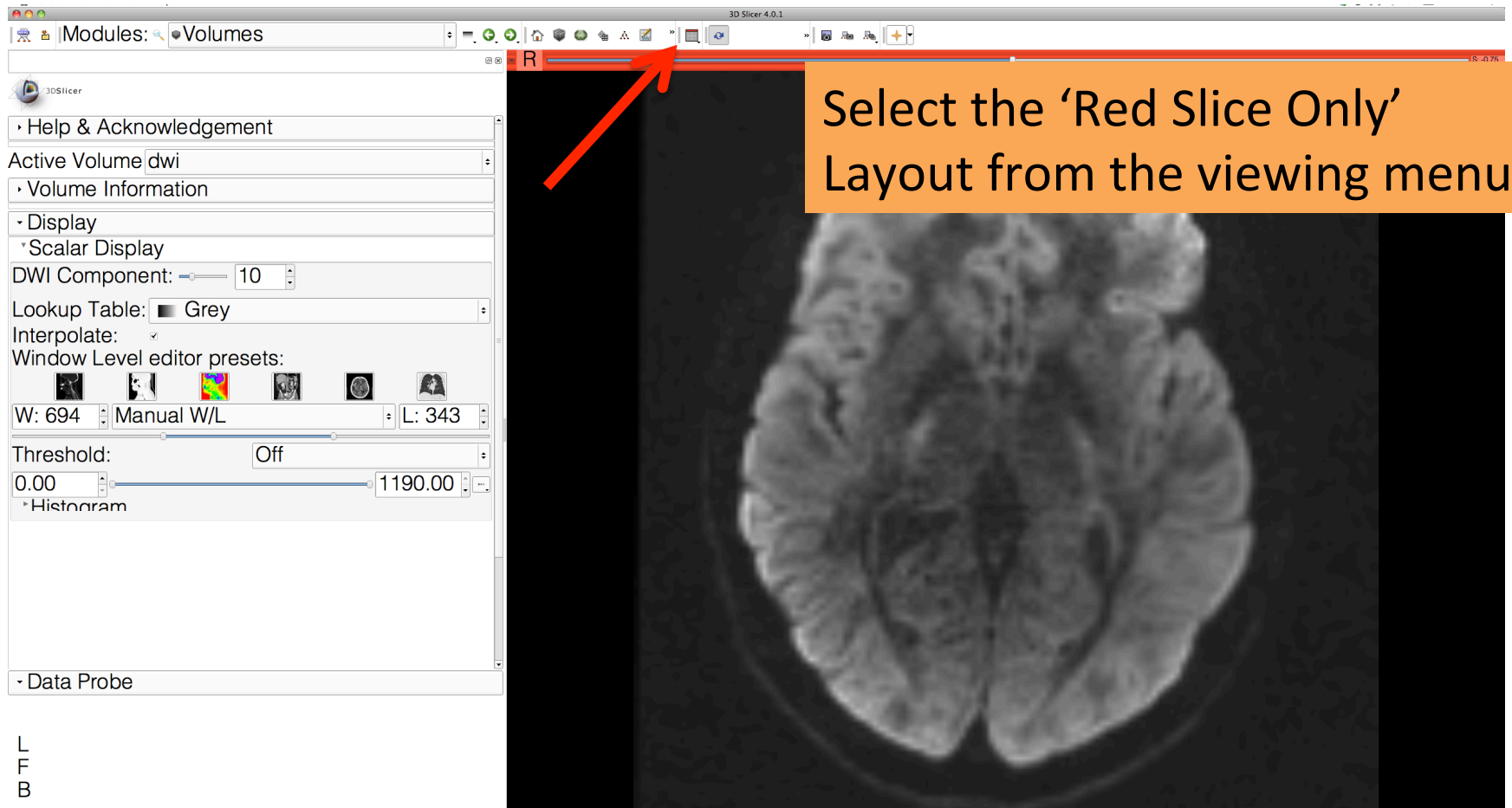
The screenshot shows the 3D Slicer software interface. On the left is the 'Volumes' panel with various settings for the active volume 'dwi', including 'Scalar Display', 'DWI Component' (set to 35), 'Lookup Table' (Grey), 'Interpolate' (checked), and 'Threshold' (Off). The main 3D view shows a purple volume with a red slice plane. A red arrow points to the 'R' label on the slice plane. Below the 3D view is a 'Slice Menu' with three rows: 'Axial' (1.00, None), 'Sagittal' (0.00, None), and 'Coronal' (1.00, dwi). The 'R' label is also present in the slice menu. An orange callout box on the right contains instructions: 'Left click on the pin button in the top left corner of the red viewer to display the slice menu.' and 'Click on the 'links' icon to link all three viewers, and click on the 'fit image to window icon'.

Left click on the pin button in the top left corner of the red viewer to display the slice menu.

Click on the 'links' icon to link all three viewers, and click on the 'fit image to window icon'.

L
F
B

Exploring the DWI dataset



Exploring the DWI dataset

3D Slicer 4.0.1

Modules: Volumes

3D Slicer

Help & Acknowledgement

Active Volume: dwi

Volume Information

Display

Scalar Display

DWI Component: 10

Look up Table: Grey

Interpolate:

Window Level editor presets:

W: 694 Manual W/L L: 343

Threshold: Off

0.00 1190.00

Histogram

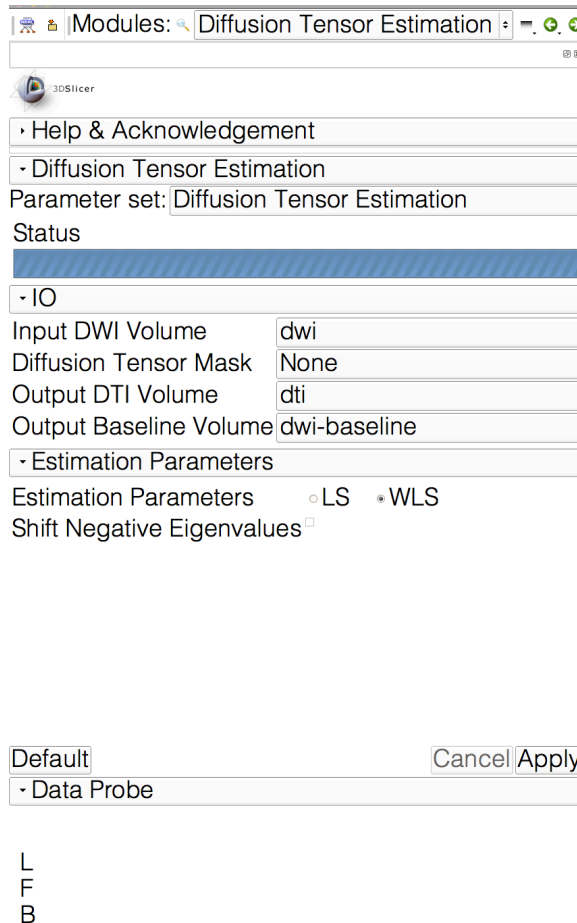
Data Probe

R

Select the 'Red Slice Only' Layout from the viewing menu

L
F
B

Diffusion Tensor Estimation



Select the module **Diffusion Tensor Estimation** in the modules menu:

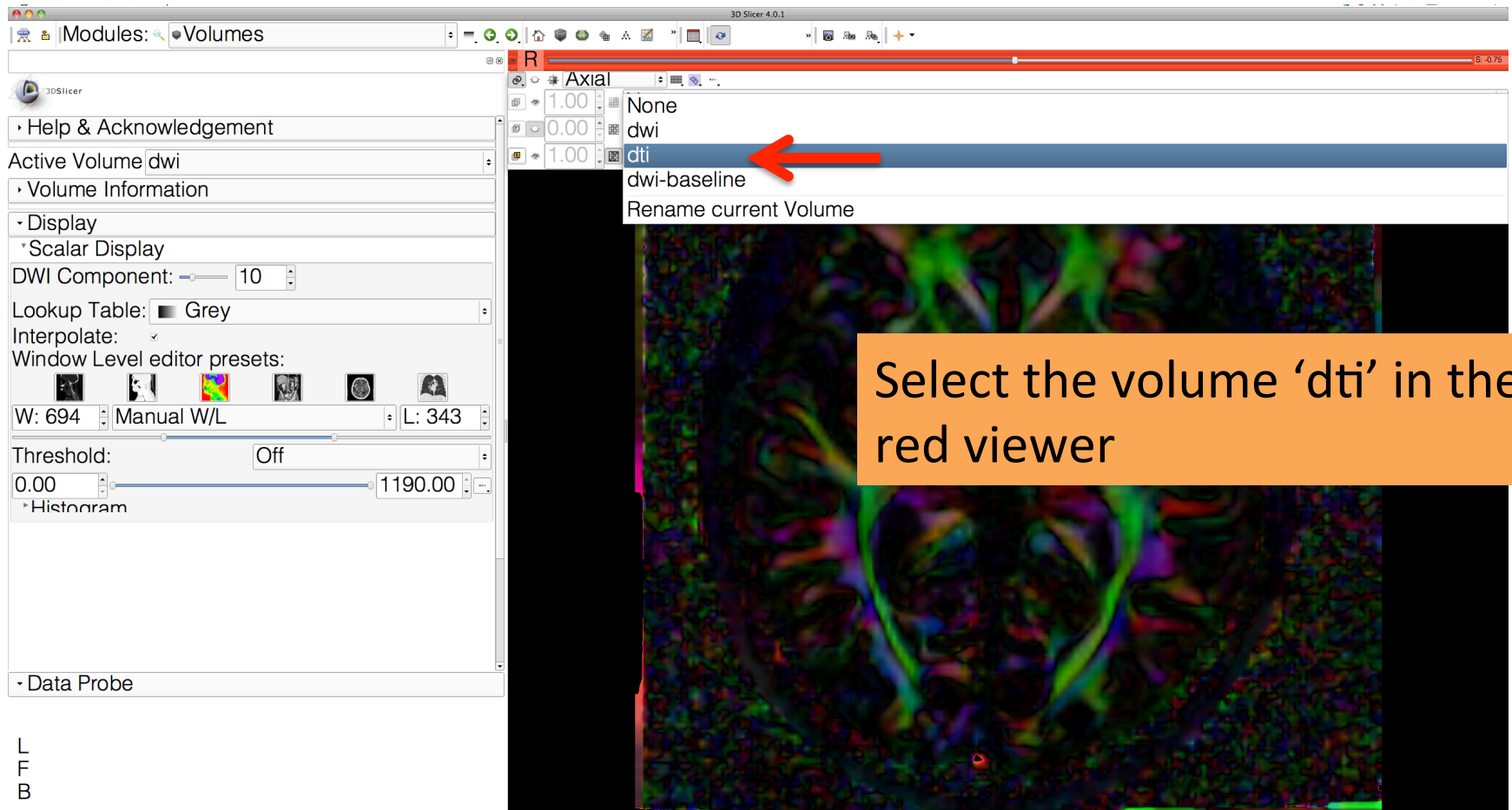
-select the Input DWI volume 'dwi'

-select Output DTI Volume 'Create New Diffusion Tensor Volume', and rename it 'dti'

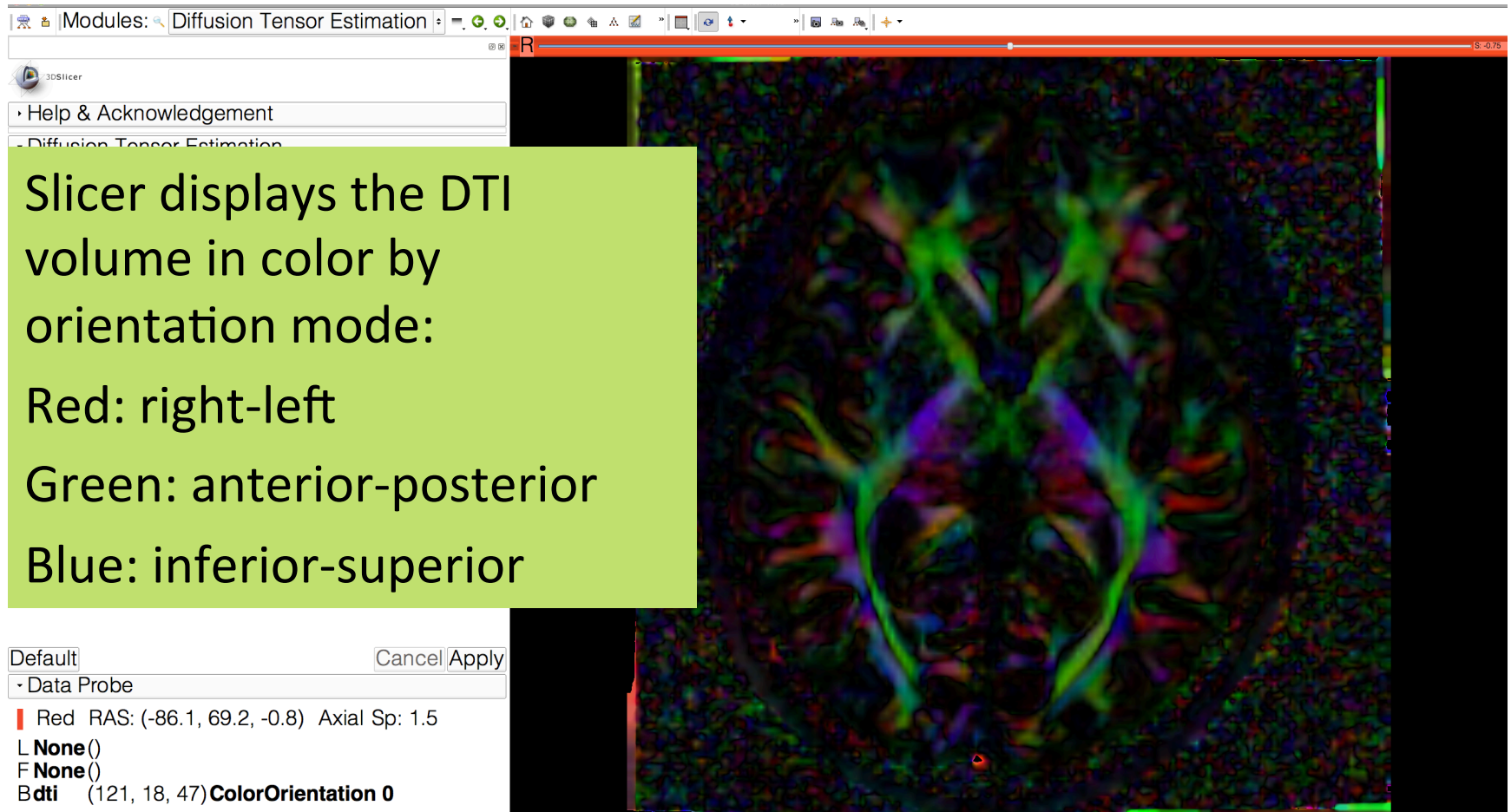
-select Output Baseline Volume 'Create new Volume', and rename it 'dwi-baseline'

-select the Estimation Method 'WLS' (Weighted Least Squares) and click on Apply.

Diffusion Tensor Estimation



Diffusion Tensor Estimation



Slicer displays the DTI volume in color by orientation mode:

- Red: right-left
- Green: anterior-posterior
- Blue: inferior-superior

Default

- Data Probe

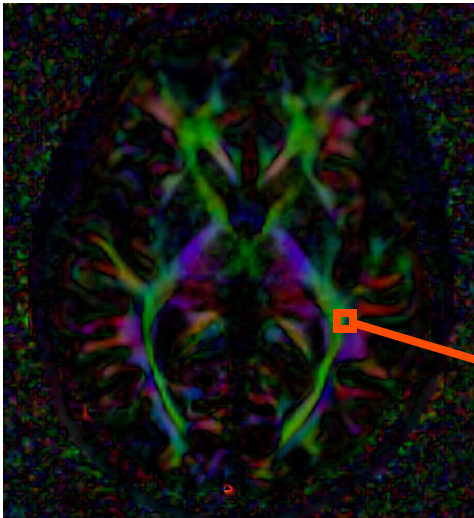
Red RAS: (-86.1, 69.2, -0.8) Axial Sp: 1.5

L None()

F None()

Bdti (121, 18, 47) ColorOrientation 0

Diffusion Tensor Data



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

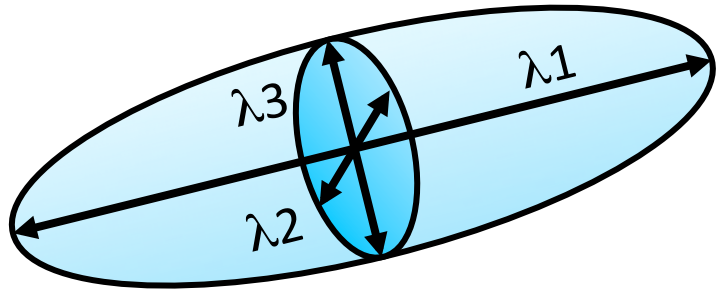
Stejskal-Tanner equation (1965)

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

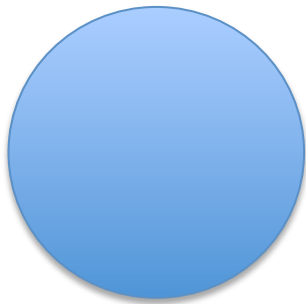
The diffusion tensor $\underline{\mathbf{D}}$ in the voxel (I,J,K) is a 3x3 symmetric matrix.

Diffusion Tensor

- The diffusion tensor \underline{D} in the voxel (I,J,K) can be visualized as an ellipsoid, with the eigenvectors indicating the directions of the principal axes, and the square root of the eigenvalues defining the ellipsoidal radii.
- 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.

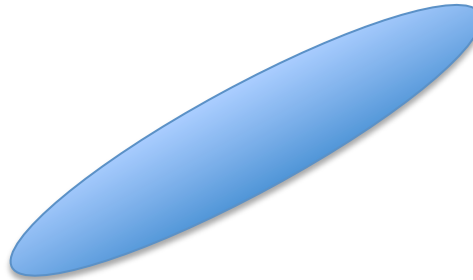


Diffusion Tensor Shape



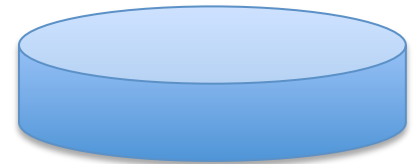
$$\lambda_1 = \lambda_2 = \lambda_3$$

Isotropic media
(CSF, gray matter)



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

Anisotropic media
(white matter)



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

Exploring the Diffusion Tensor Data

Browse through the dti volume using the slider, and try identify the corpus callosum

Default

- Data Probe

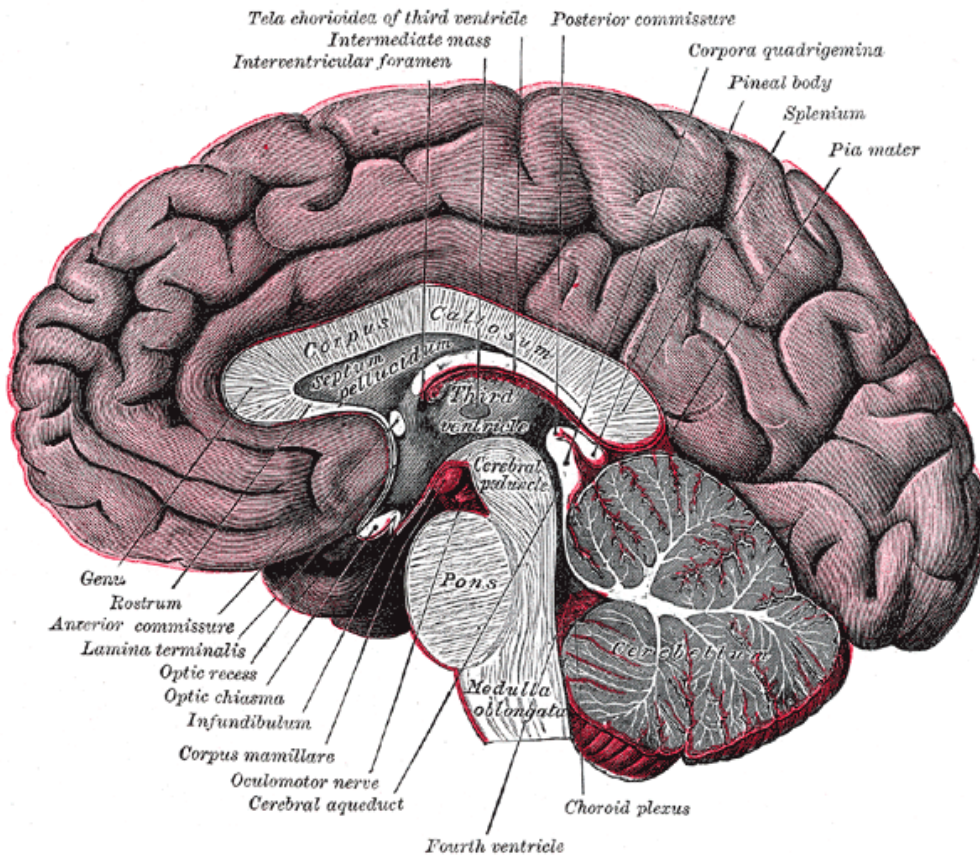
Red RAS: (-86.1, 69.2, -0.8) Axial Sp: 1.5

L None()

F None()

Bdti (121, 18, 47) ColorOrientation 0

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

Exploring the Diffusion Tensor Data

The screenshot displays the 3D Slicer interface for Diffusion Tensor Estimation. The left sidebar contains a parameter panel with the following sections:

- Help & Acknowledgement
- Diffusion Tensor Estimation
 - Parameter set: Diffus
 - Status
- IO
 - Input DWI Volume: dwi
 - Diffusion Tensor Mask: None
 - Output DTI Volume: dti
 - Output Baseline Volume: dwi-baseline
- Estimation Parameters
 - Estimation Parameters: LS WLS
 - Shift Negative Eigenvalues:
- Data Probe
 - Default:
 - Red RAS: (-2.9, 95.4, 18.8) Axial Sp: 1.5
 - L: None()
 - F: None()
 - Bdti: (66, 0, 60) ColorOrientation 0

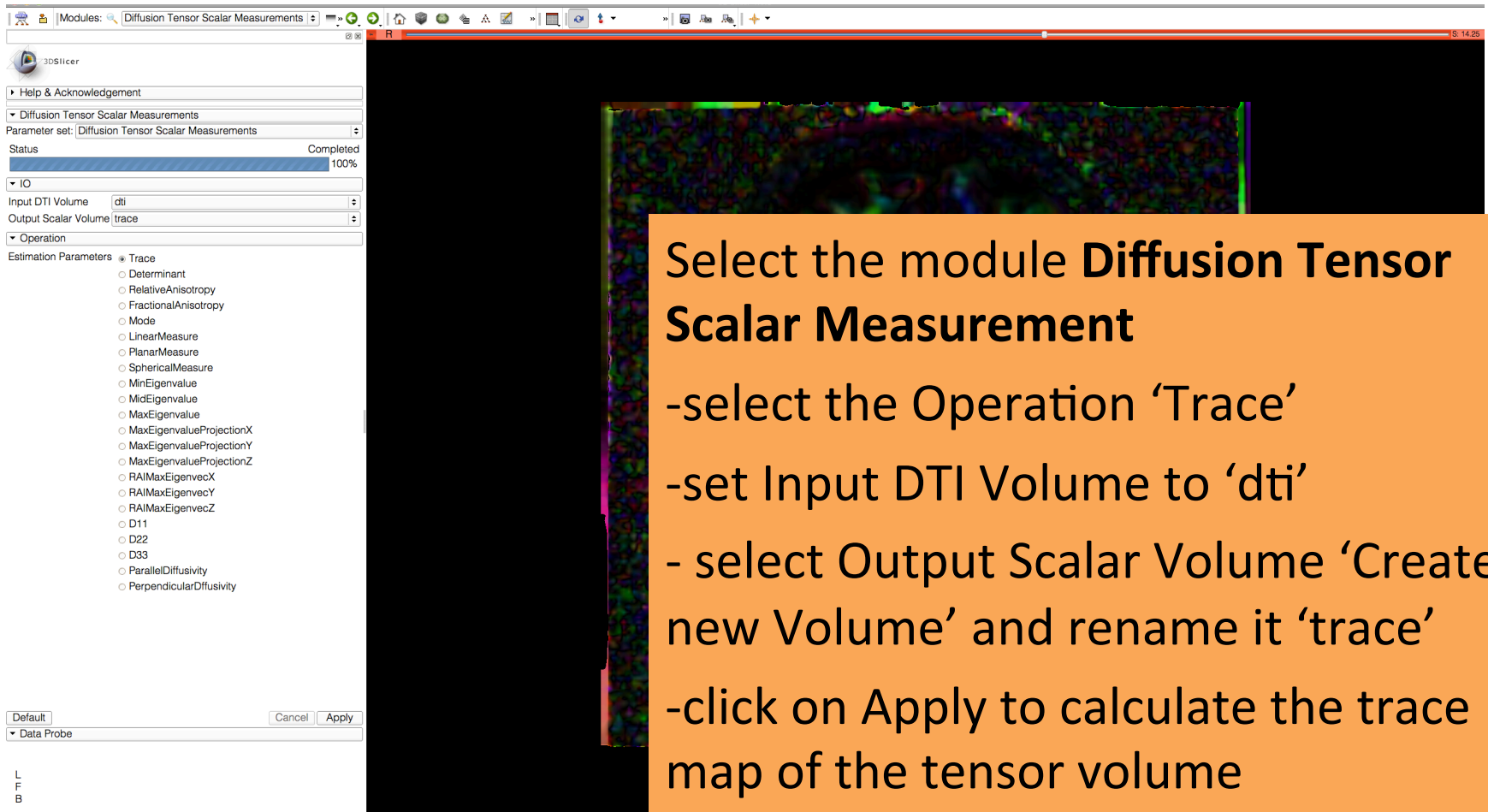
The main window shows an axial brain slice with a color-coded Diffusion Tensor Imaging (DTI) map. A red arrow points to the corpus callosum, which is highlighted in a light green box with the text "Corpus Callosum".

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
- $\text{Trace}(D)$ is useful to characterize the size of the diffusion ellipsoid

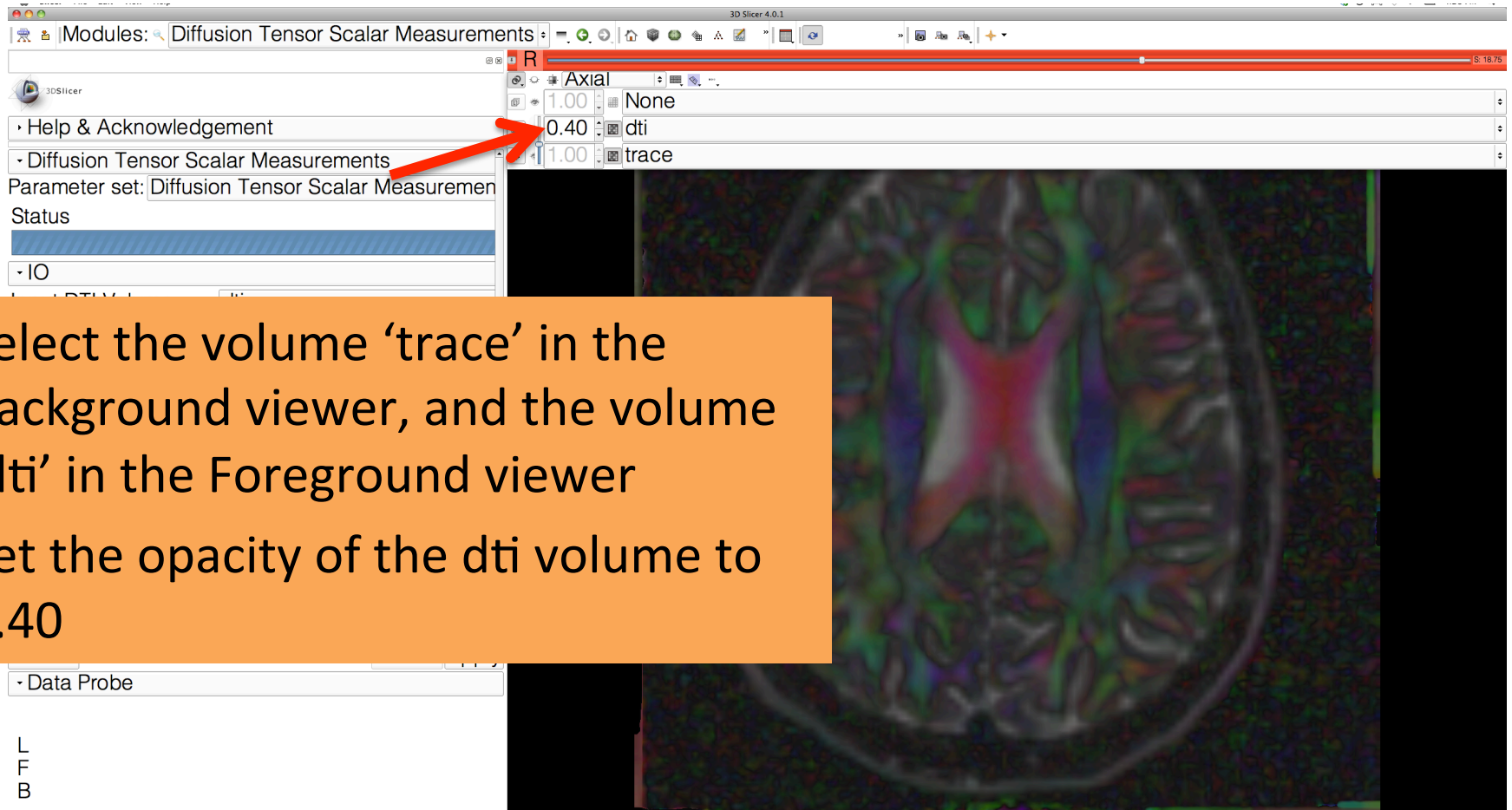
Characterizing the Size of the tensor: Trace



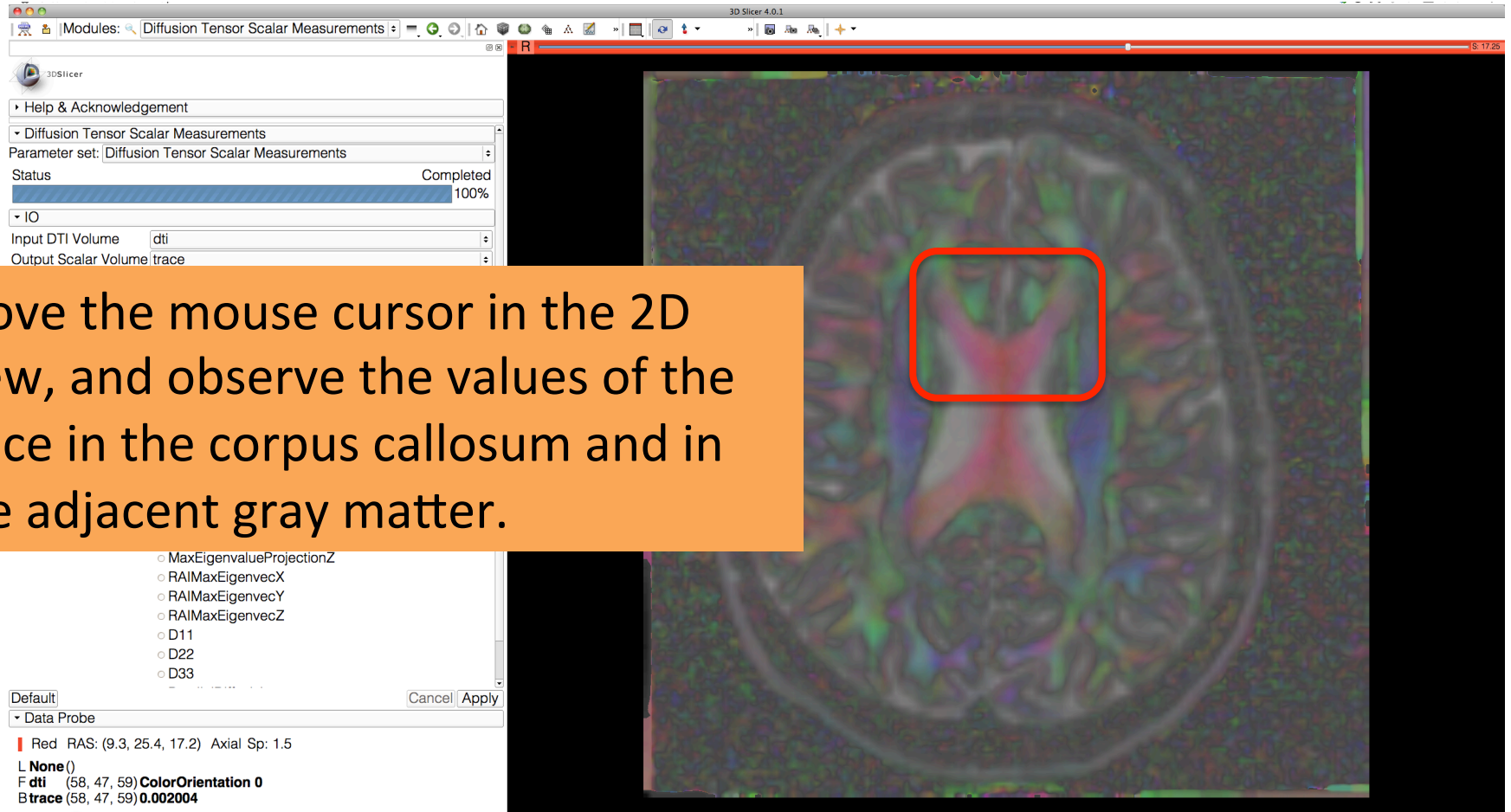
Select the module **Diffusion Tensor Scalar Measurement**

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

Exploring the Diffusion Tensor Data

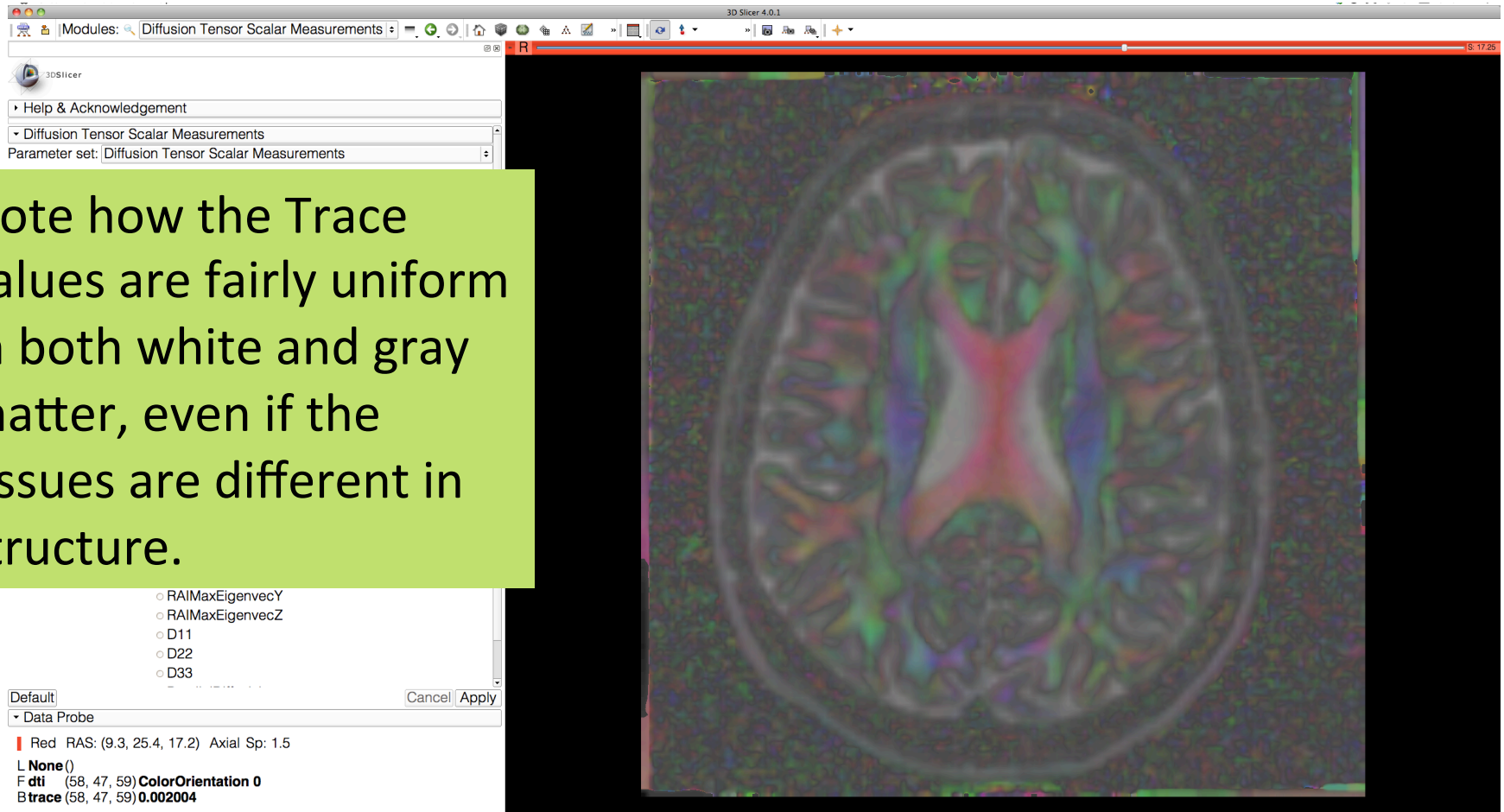


Exploring the Diffusion Tensor Data



Characterizing the Size of the tensor: Trace

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






The screenshot shows the 3D Slicer 4.0.1 interface. The main window displays an axial brain MRI slice with a color-coded tensor map overlaid. The tensor map shows a central region with a prominent red color, indicating high trace values, surrounded by a more uniform distribution of colors (green, blue, purple). The interface includes a menu bar with 'Modules: Diffusion Tensor Scalar Measurements' and a sidebar with 'Help & Acknowledgement' and 'Diffusion Tensor Scalar Measurements' sections. A 'Data Probe' window is open at the bottom left, showing the following information:

- RAIMaxEigenvecY
- RAIMaxEigenvecZ
- D11
- D22
- D33

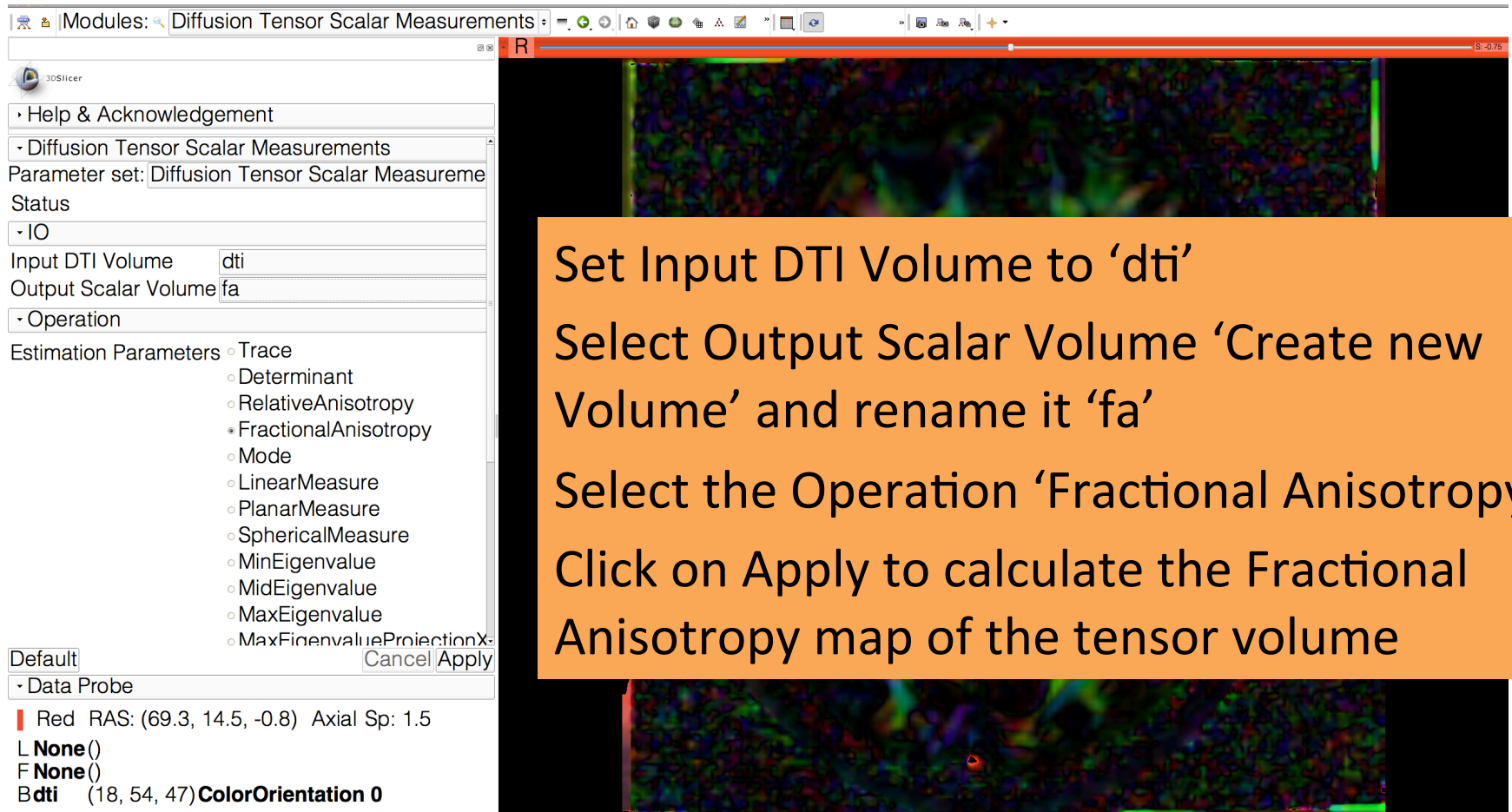
Default
Data Probe
Red RAS: (9.3, 25.4, 17.2) Axial Sp: 1.5
L None ()
F dti (58, 47, 59) ColorOrientation 0
B trace (58, 47, 59) 0.002004

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: 

Characterizing the Shape of the tensor: Fractional Anisotropy



3D Slicer

Modules: Diffusion Tensor Scalar Measurements

- Help & Acknowledgement
- Diffusion Tensor Scalar Measurements

Parameter set: Diffusion Tensor Scalar Measureme

Status

• IO

Input DTI Volume

Output Scalar Volume

• Operation

Estimation Parameters

- Trace
- Determinant
- RelativeAnisotropy
- FractionalAnisotropy
- Mode
- LinearMeasure
- PlanarMeasure
- SphericalMeasure
- MinEigenvalue
- MidEigenvalue
- MaxEigenvalue
- MaxEigenvalueProjectionX

Default

• Data Probe

Red RAS: (69.3, 14.5, -0.8) Axial Sp: 1.5

L None()

F None()

B dti (18, 54, 47) ColorOrientation 0

Set Input DTI Volume to 'dti'

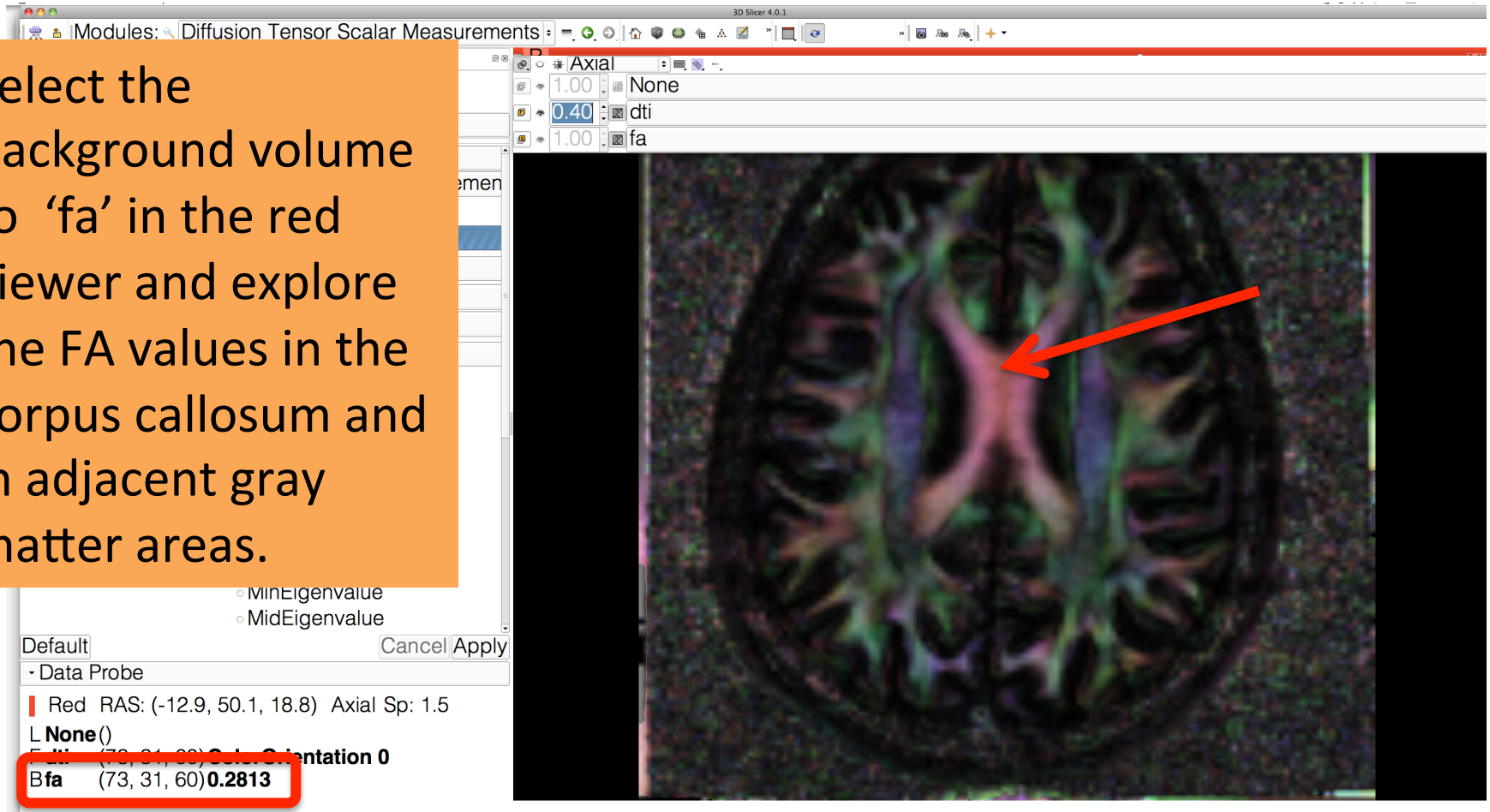
Select Output Scalar Volume 'Create new Volume' and rename it 'fa'

Select the Operation 'Fractional Anisotropy'

Click on Apply to calculate the Fractional Anisotropy map of the tensor volume

Fractional Anisotropy

Select the Background volume to 'fa' in the red viewer and explore the FA values in the corpus callosum and in adjacent gray matter areas.



Fractional Anisotropy

Note how the FA values are high in the white matter areas, and low in gray matter regions

The screenshot shows the 3D Slicer 4.0.1 interface. The 'Diffusion Tensor Scalar Measurements' window is open, displaying a list of parameters with radio buttons. The 'fa' parameter is selected and highlighted with a red box, showing a value of 0.8329. The main window displays an axial brain MRI slice with a color-coded Fractional Anisotropy (FA) map. A red arrow points to a white matter tract in the central region of the brain.

- MinEigenvalue
- MidEigenvalue
- MaxEigenvalue
- MaxEigenvalueProjectionX
- MaxEigenvalueProjectionY
- MaxEigenvalueProjectionZ
- RAI_MaxEigenvecX
- RAI_MaxEigenvecY
- RAI_MaxEigenvecZ
- D11
- D22
- D33

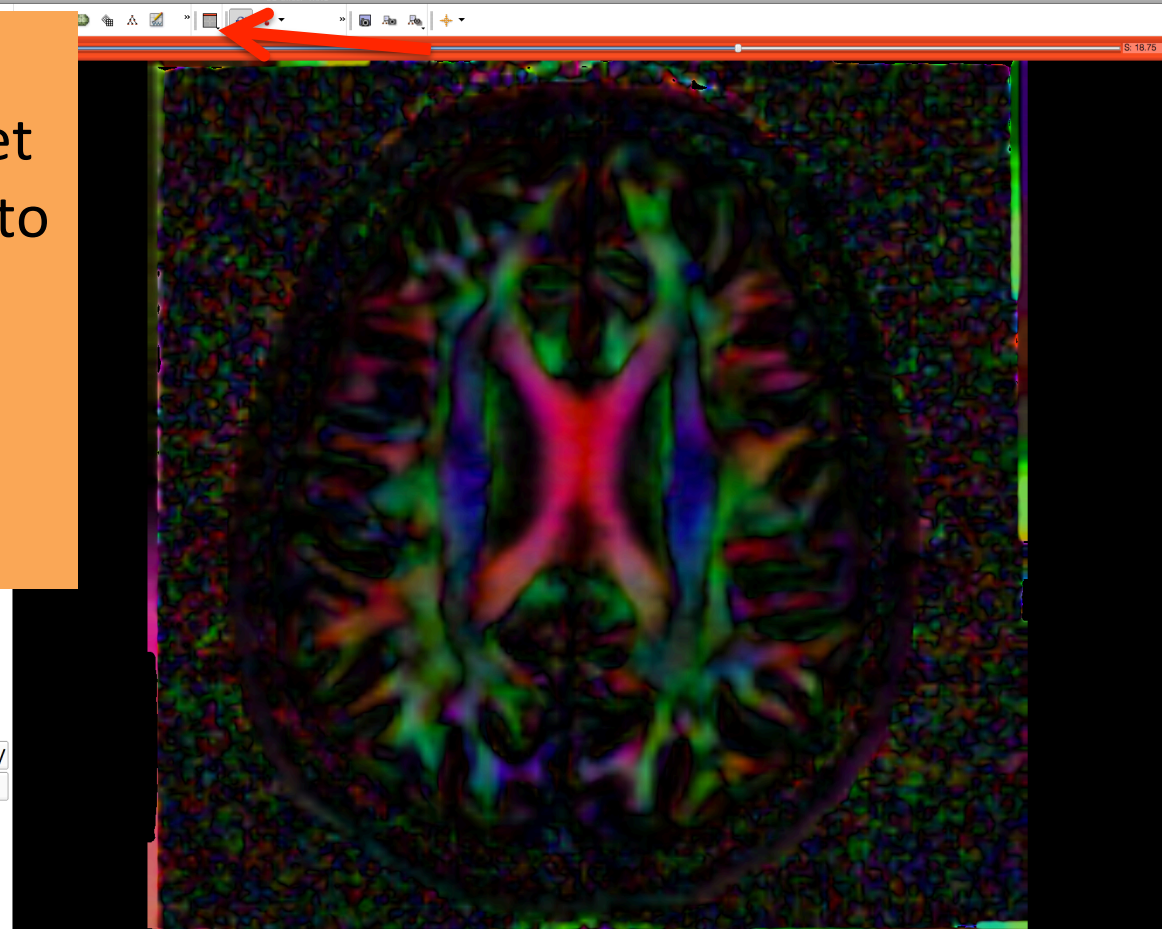
Default
Data Probe
Red RAS: (7.2, 25.4, 15.8) Axial Sp: 1.5

dti (59, 47, 58) ColorOrientation 0
fa (59, 47, 58) 0.8329

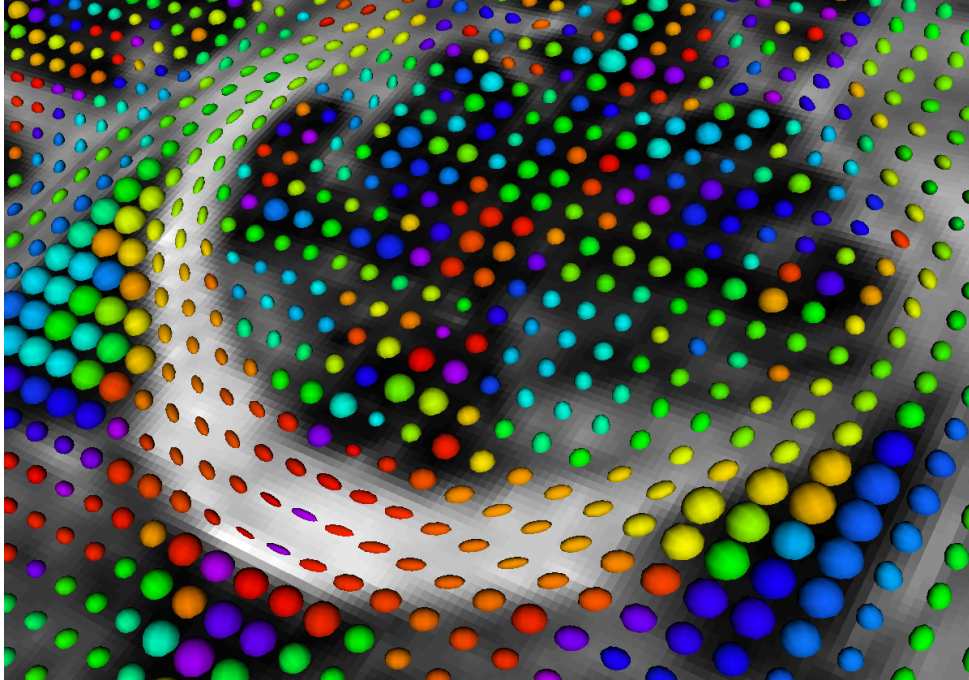
Fractional Anisotropy

Set the Foreground volume to 'None', and set the Background volume to 'dti' in the red viewer menu.

Go back to conventional layout

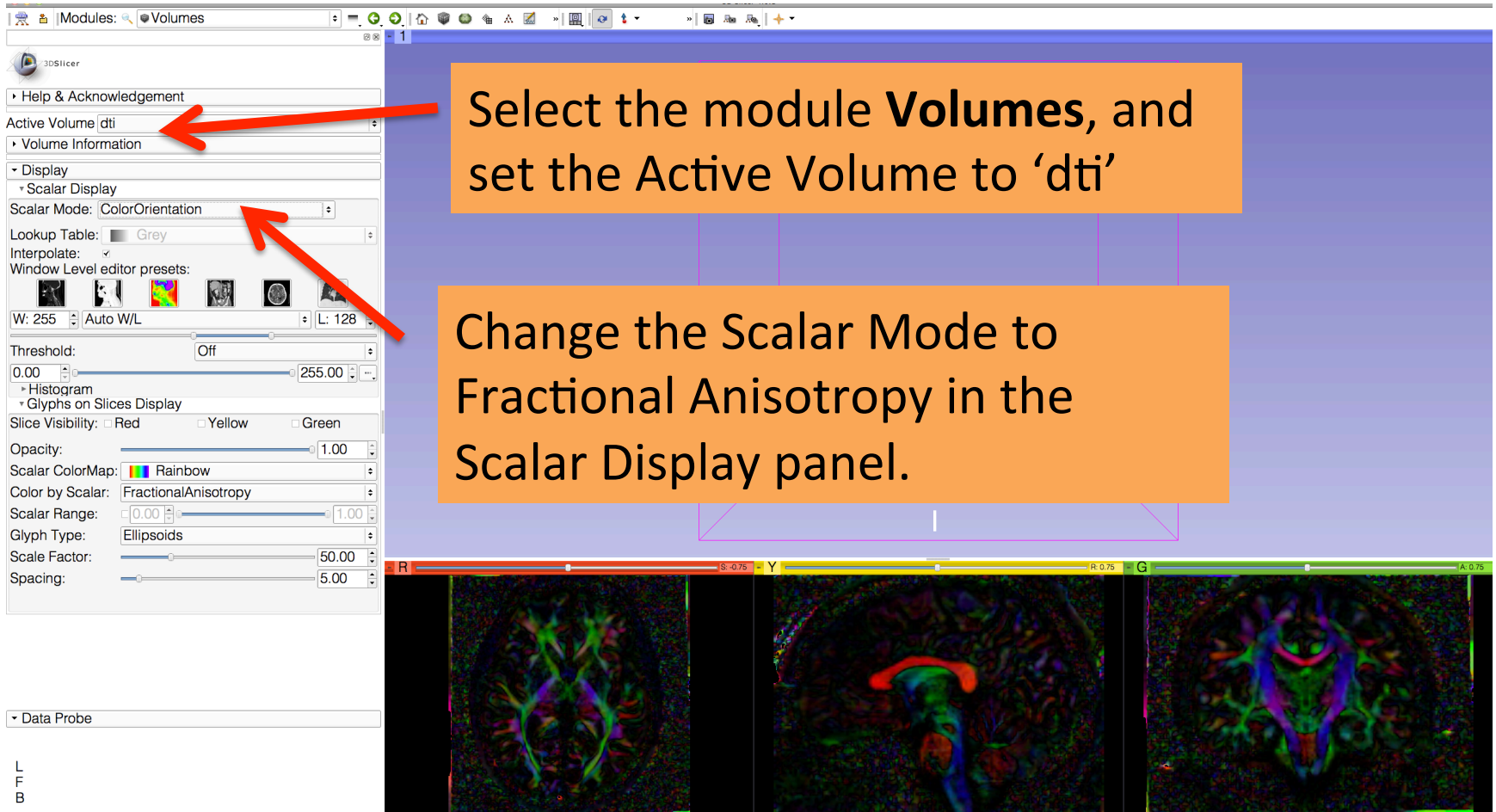


Default Cancel Apply
- Data Probe
Red RAS: (-2.9, 95.4, 18.8) Axial Sp: 1.5
L None()
F None()
Bdti (66, 0, 60) ColorOrientation 0



Part 2: Visualizing the tensor data

3D Visualization: Glyphs



Select the module **Volumes**, and set the Active Volume to 'dti'

Change the Scalar Mode to Fractional Anisotropy in the Scalar Display panel.

W: 255 Auto W/L L: 128

Threshold: Off 0.00 255.00

Scalar ColorMap: Rainbow

Color by Scalar: FractionalAnisotropy

Scalar Range: 0.00 1.00

Glyph Type: Ellipsoids

Scale Factor: 50.00

Spacing: 5.00

R 0.75 Y 0.75 A 0.75 G 0.75

L
F
B

3D Visualization: Glyphs

The screenshot shows the 3D Slicer software interface. The 'Volumes' module is active. The 'Glyphs on Slices Display' panel is highlighted with a red box. The 'Color by Scalar' parameter is set to 'FractionalAnisotrop', and 'Slice Visibility' is checked for 'Red'. The 'Auto W/L' button is highlighted with a red arrow. The main display area shows three orthogonal slices (R, A, L) with a color scale from 0.00 to 1.00. The 'Glyphs on Slices Display' panel includes the following settings:

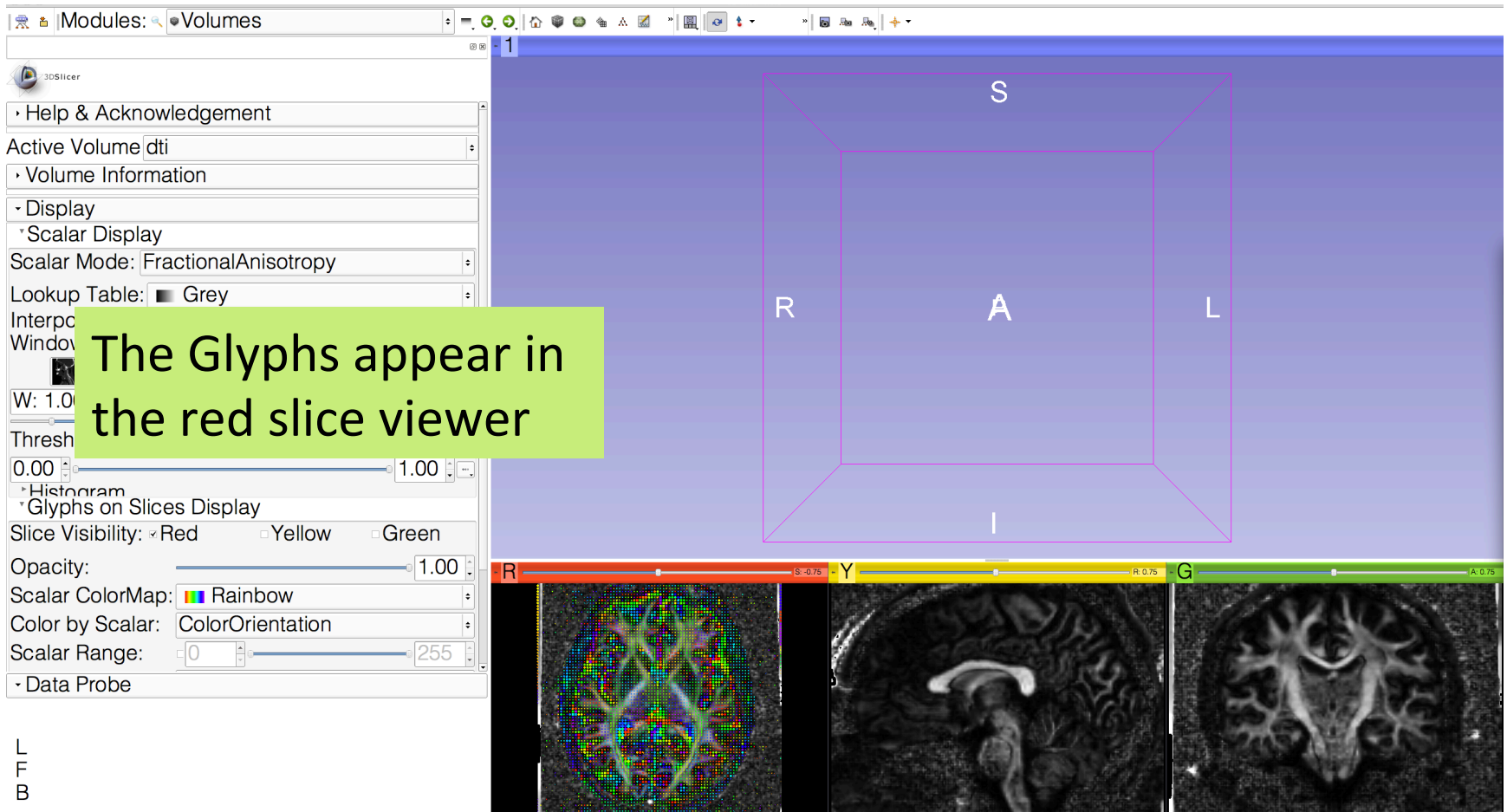
- Glyphs on Slices Display
- Slice Visibility: Red Yellow Green
- Opacity: 1.00
- Scalar ColorMap: Rainbow
- Color by Scalar: FractionalAnisotrop
- Scalar Range: 0.00 - 1.00
- Data Probe

Click on Auto W/L to adjust the Window and Level values of the display

In the **Glyphs on Slices Display** panel, set the Color by Scalar parameter to 'ColorOrientation', and check Slice Visibility 'Red' '

L
F
B

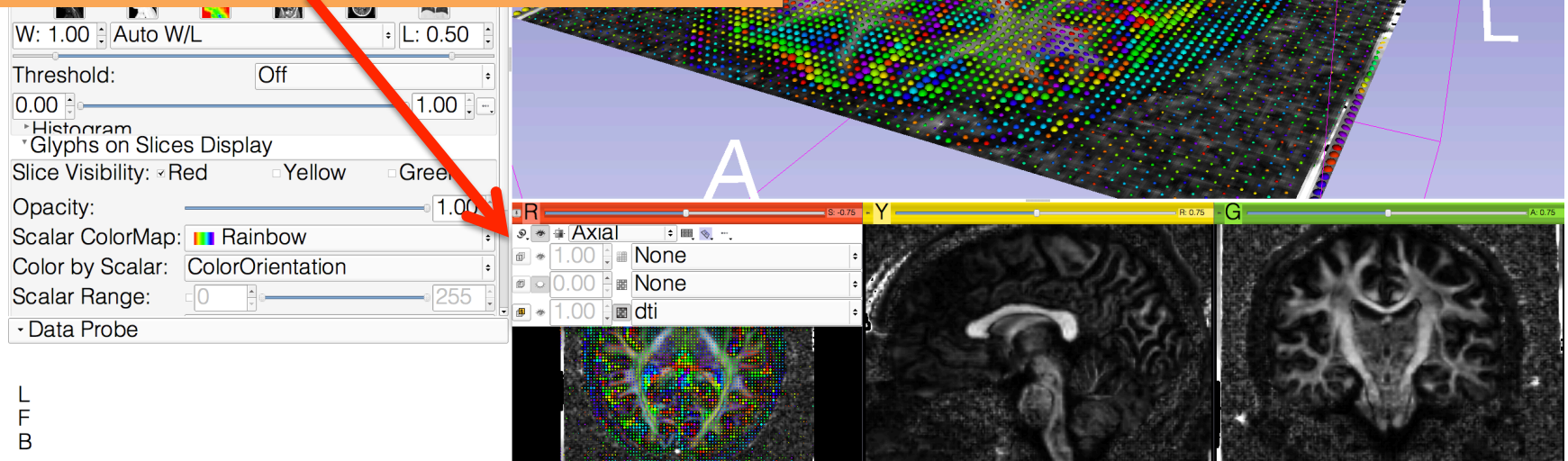
3D Visualization: Glyphs



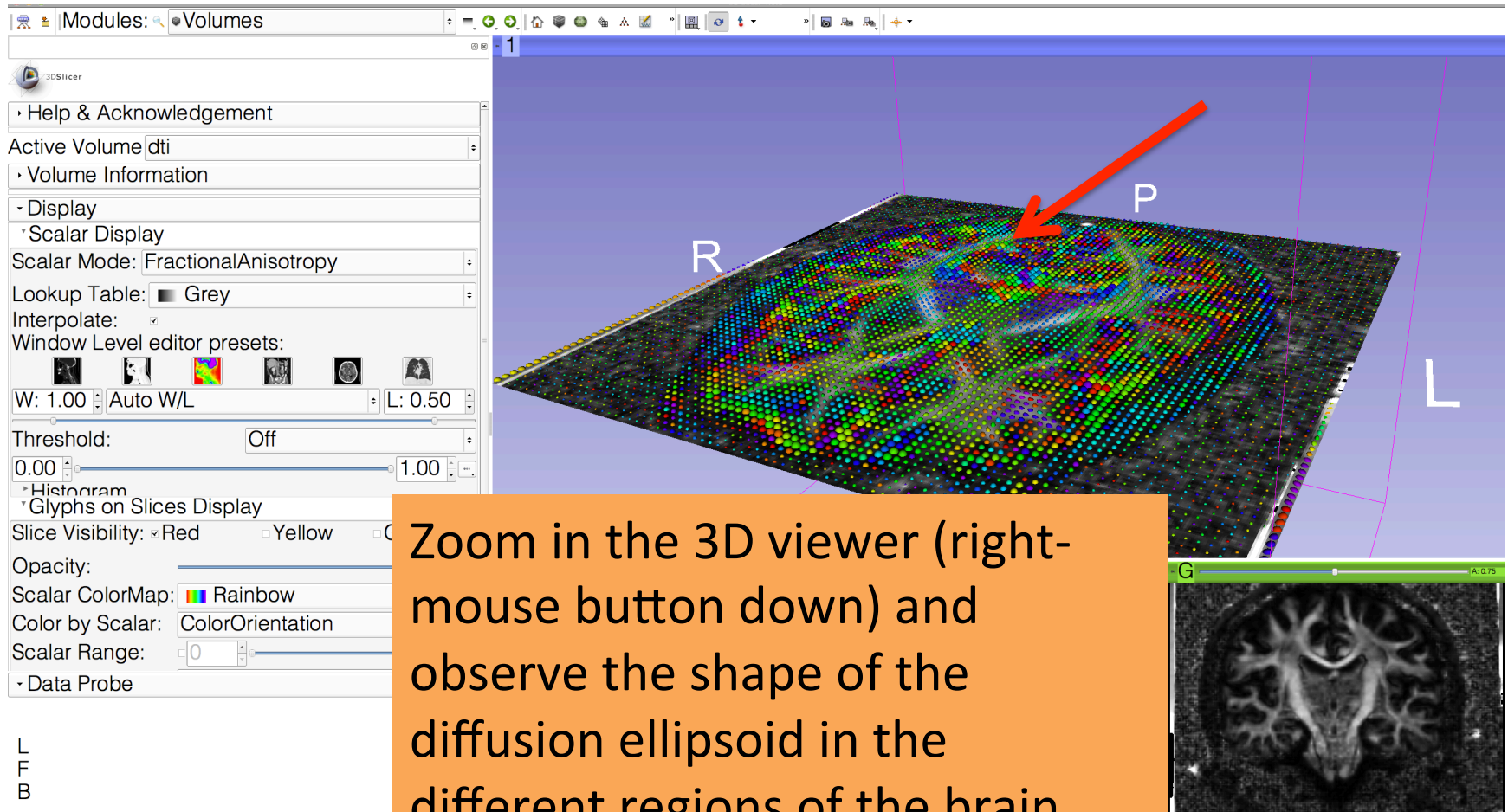
3D Visualization: Glyphs

Click on the link icon in the red slice viewer to unlink the three viewers.

Click on the eye icon to display the glyphs in the 3D Viewer



3D Visualization: Glyphs



3D Visualization: Glyphs

Note the orientation of diffusion ellipsoid of the splenium of the corpus callosum (posterior part)

Window Level editor presets.

W: 1.00 | Auto W/L | L: 0.50

Threshold: Off

0.00 | 1.00

Histogram

Glyphs on Slices Display

Slice Visibility: Red Yellow Green

Opacity: 1.00

Scalar ColorMap: Rainbow

Color by Scalar: ColorOrientation

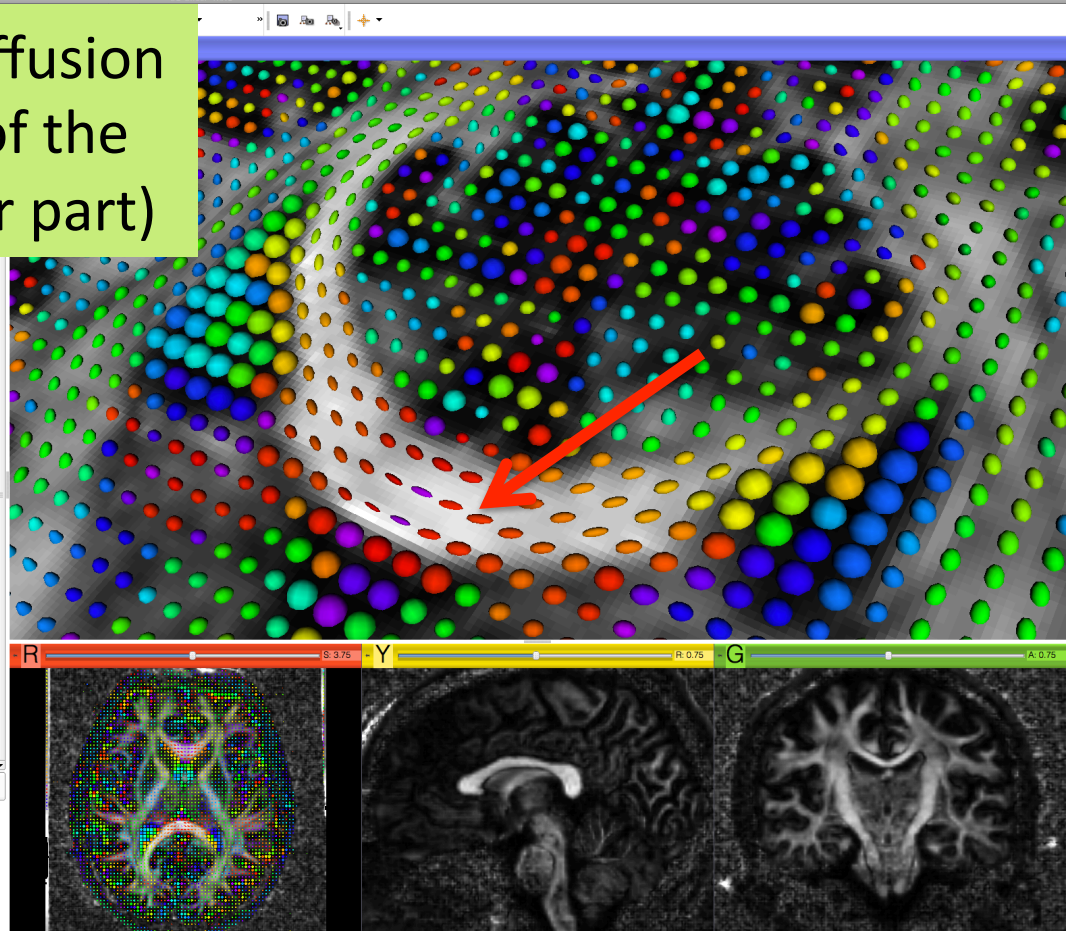
Scalar Range: 0 | 255

Glyph Type: Ellipsoids

Scale Factor: 45.00

Spacing: 5.00

- Data Probe



L
F
B

3D Visualization: Glyphs

Change the Glyph Type to 'Lines', and move the mouse inside the 3D viewer to refresh the display.

Threshold: Off

0.00 1.00

Histogram

Glyphs on Slices Display

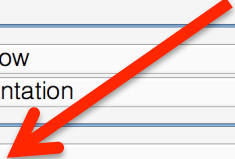
Slice Visibility: Red Yellow Green

Opacity: 1.00

Scalar ColorMap: Rainbow

Color by Scalar: ColorOrientation

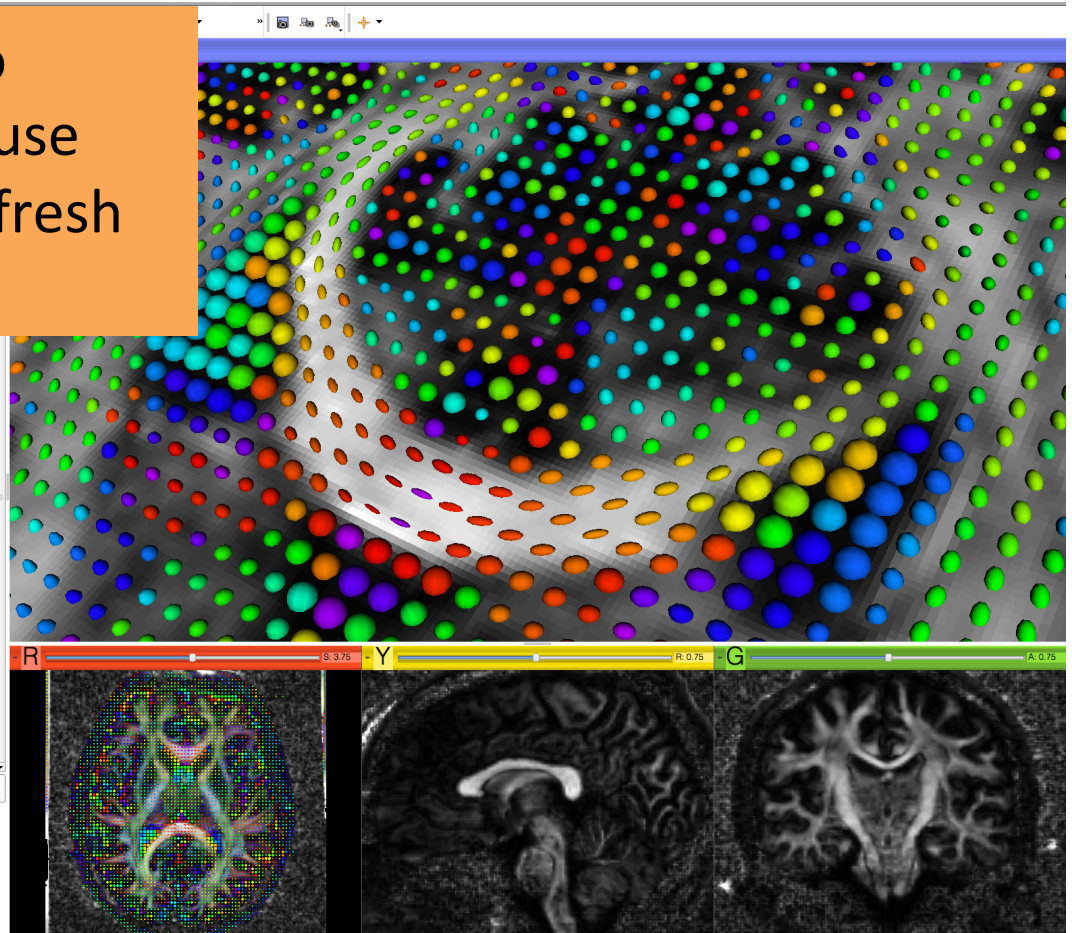
Scalar Range: 0 255

Glyph Type: Ellipsoids 

Scale Factor: 45.00

Spacing: 5.00

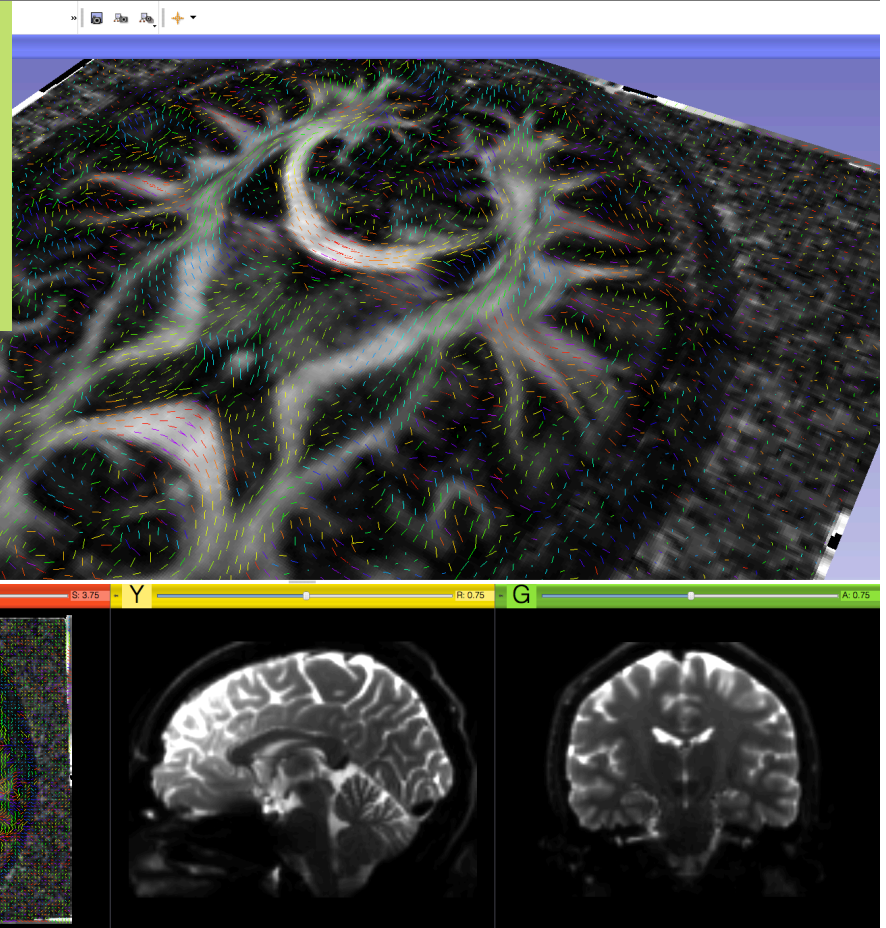
Data Probe



L
F
B

3D Visualization: Glyphs

Slicer displays the glyphs as lines that represent the principal direction of diffusion (main eigenvector)



Threshold: Off

0.00 0.00

Histogram

Glyphs on Slices Display

Slice Visibility: Red Yellow Green

Opacity: 1.00

Scalar ColorMap: Rainbow

Color by Scalar: ColorOrientation

Scalar Range: 0 255

Glyph Type: Lines

Scale Factor: 45.00

Spacing: 5.00

Glyph EigenVector: Major

Data Probe

L
F
B

3D Visualization: Glyphs

Select Red Slice Only layout in the layout menu

Window Level editor presets:

W: 1.00 | Auto W/L | L: 0.50

Threshold: Off
0.00 | 0.00

Histogram
Glyphs on Slices Display

Slice Visibility: Red Yellow Green

Opacity: 1.00

Scalar ColorMap: Rainbow

Color by Scalar: ColorOrientation

Scalar Range: 0 | 255

Glyph Type: Lines

Scale Factor: 18.00

Spacing: 15.00

Glyph EigenVector: Major

Data Probe

Red RAS: (-36.4, 27.1, -18.8) Axial Sp: 1.5

L None()

F dti (88, 46, 35) FractionalAnisotropy 0.07395

B dti (88, 46, 35) FractionalAnisotropy 0.07395

Change the Scale Factor to 18.00 and the Spacing to 15.00, and explore the glyphs in the optic chiasm area (slice S: -18.75)

Optic Chiasm

The optic chiasm corresponds to the part of the brain where the optic nerves cross.

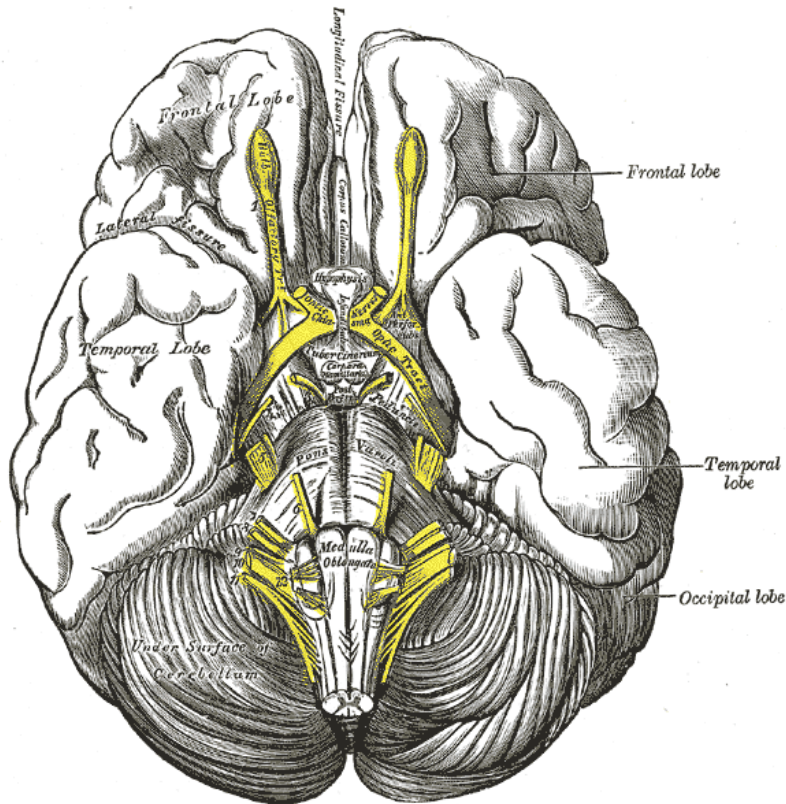


Image from Gray's Anatomy

3D Visualization: Glyphs

Go back to the conventional layout, unselect Slice Visibility 'red', and click on the eye icon in the red viewer to turn off the visibility of the red slice in the 3D viewer

3D Slicer

Help & Acknowledgement

Active Volume | dti

Volume Information

Display

Scalar Display

Scalar Mode: FractionalAnisotropy

Lookup Table: Grey

Interpolate:

Window Level editor presets:

W: 1.00 Manual W/L 0.35

Threshold: Off

0.00 1.00

Histogram

Glyphs on Slices Display

Slice Visibility: Red Yellow Green

Opacity: 1.00

Scalar ColorMap: Rainbow

Color by Scalar: ColorOrientation

Scalar Range: 0 255

Glyph Type: Ellipsoids

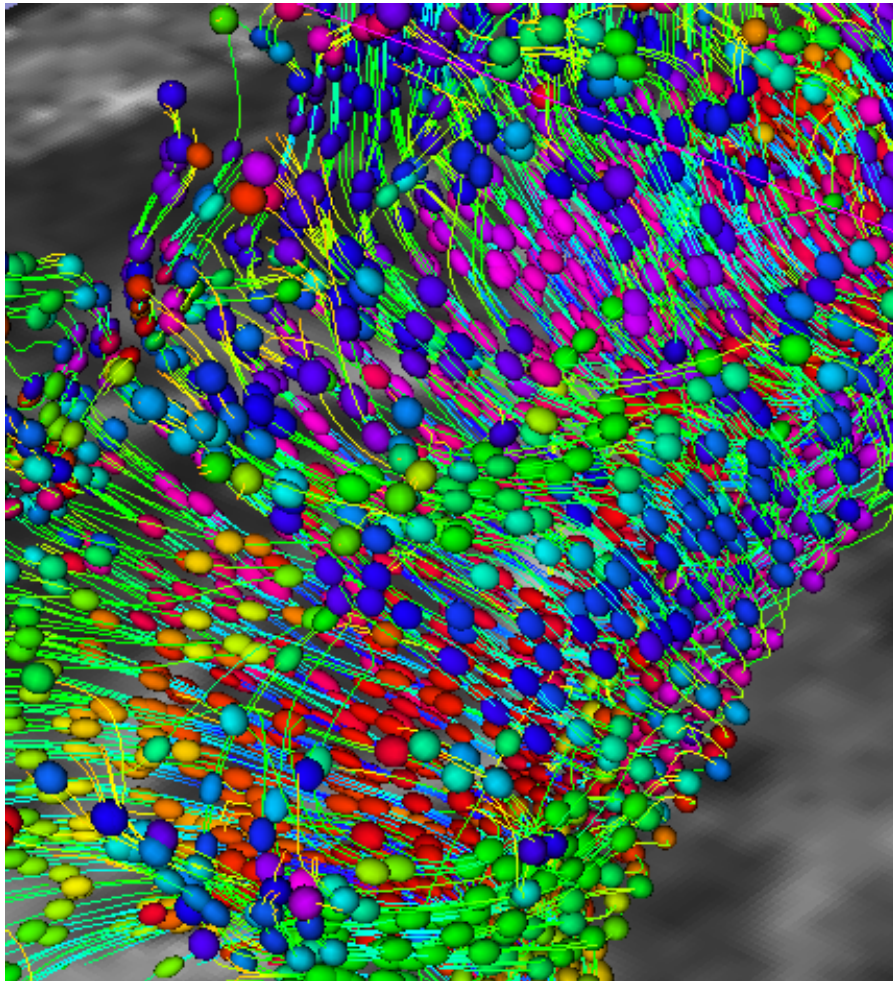
Scale Factor: 14.00

Spacing: 5.00

Data Probe

L
F
B

R S Y R G A

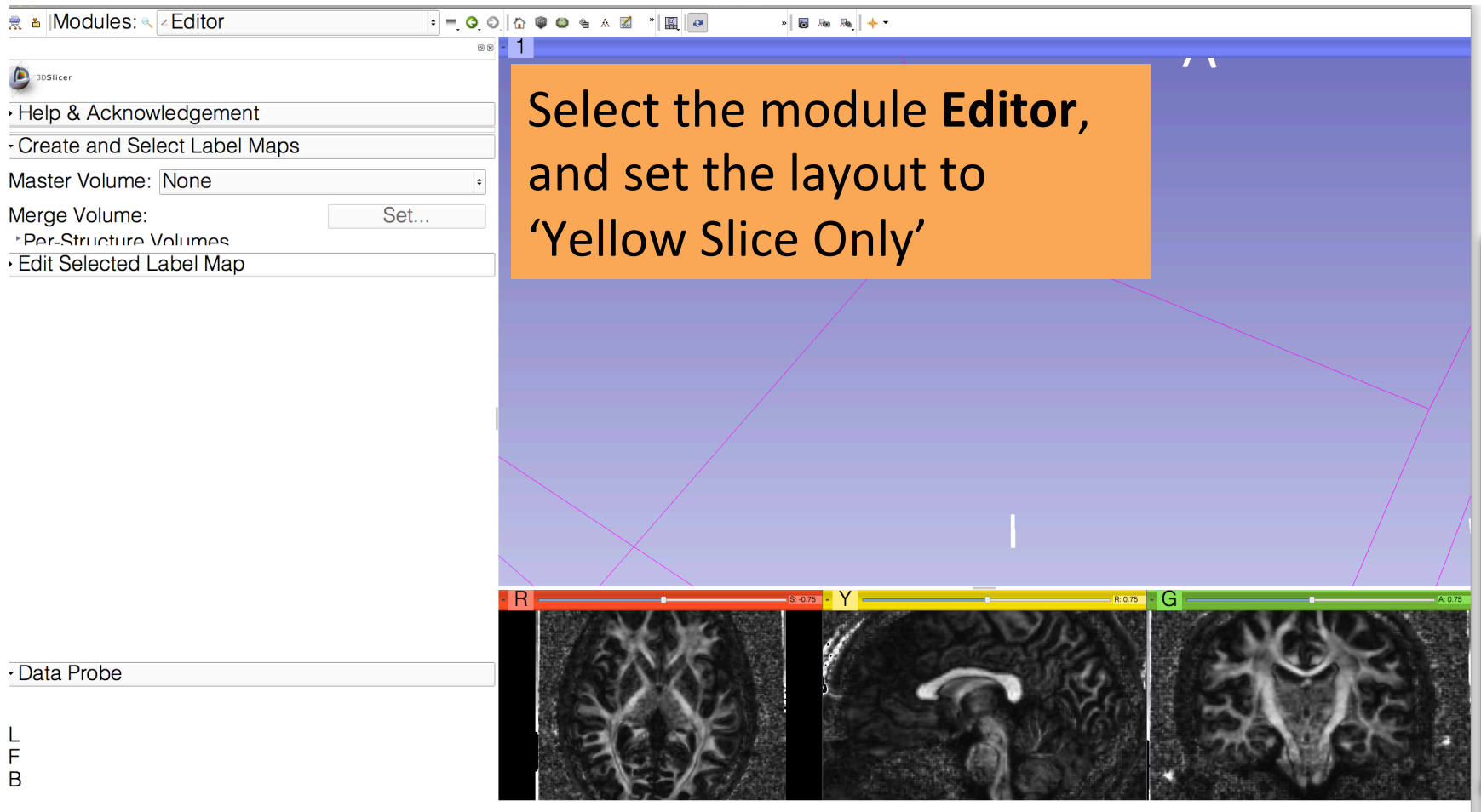


Part 3: From tensors to tracts

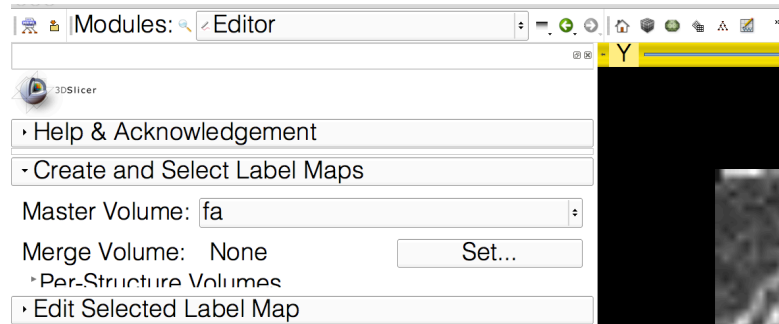
Diffusion MRI tractography

- Tractography can be defined as the virtual reconstruction of the trajectory of water molecules along white matter bundles.
 - DTI tracts provide a mathematical representation of the underlying white matter anatomy.
 - Each voxel contains hundreds of thousands of axon fibers: size of a voxel $\sim 1-5$ mm; diameter of an axon $\sim 0.1-10$ μm
- A DTI tract is not equivalent to a real fiber.

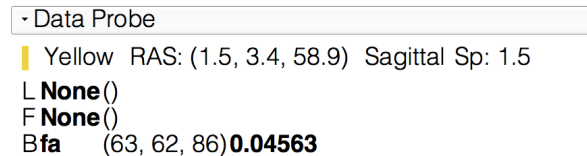
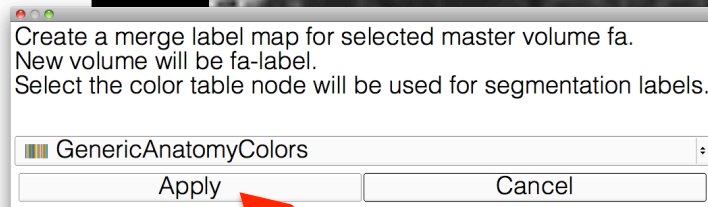
Tractography Seeding: ROI definition



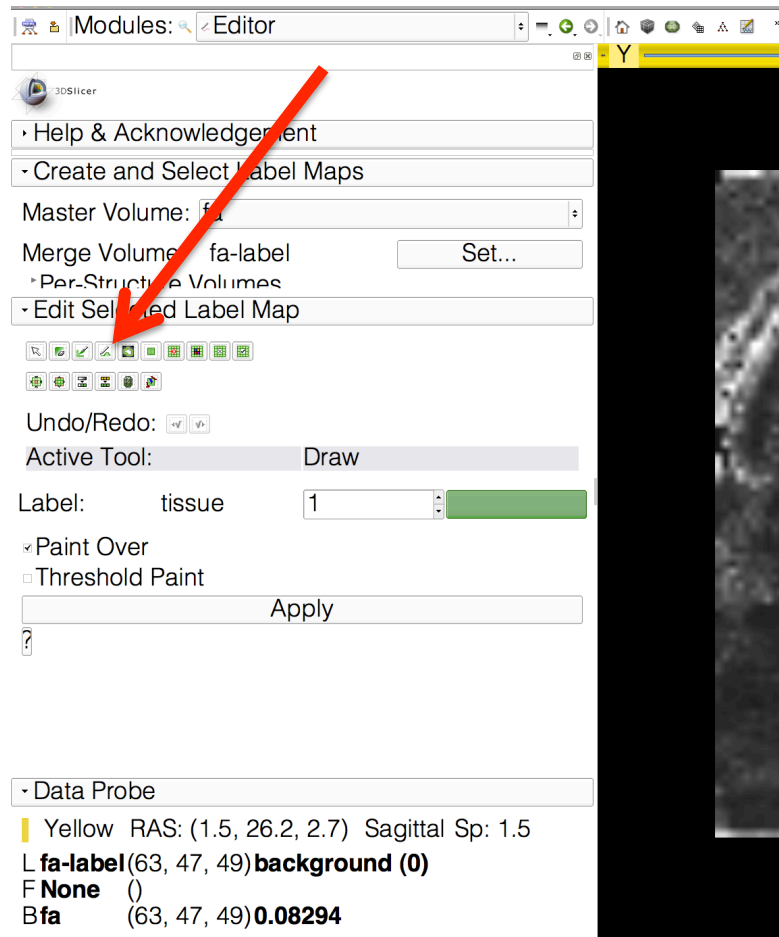
ROI Definition



Set the Master Volume to 'fa'
Click on Apply in the pop-up window to create an empty labelmap 'fa-label'



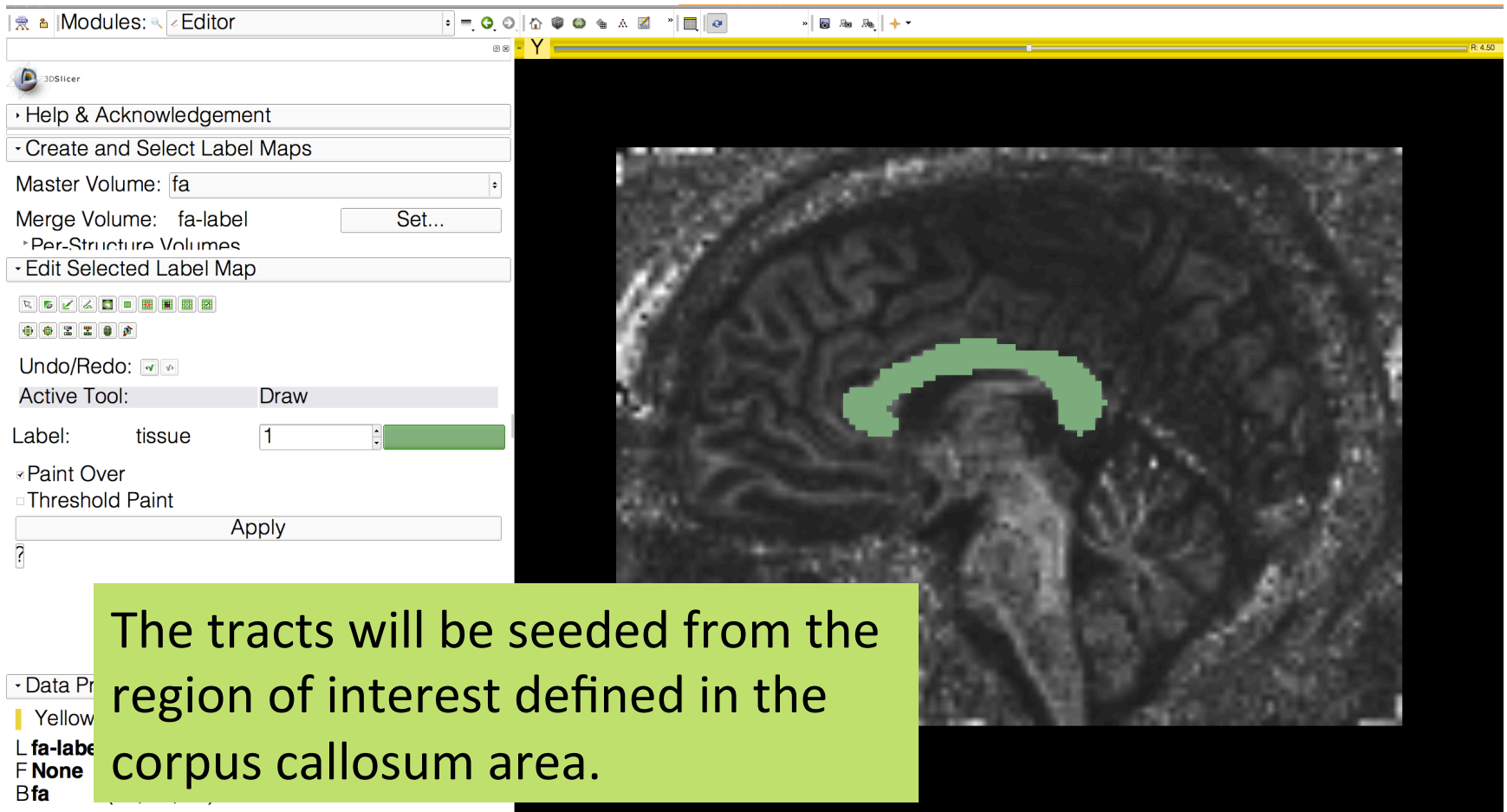
ROI Drawing



Use the draw tool to outline the contour of the corpus callosum in the sagittal slice, and press Enter. Repeat the same operation on 3 adjacent sagittal slices.



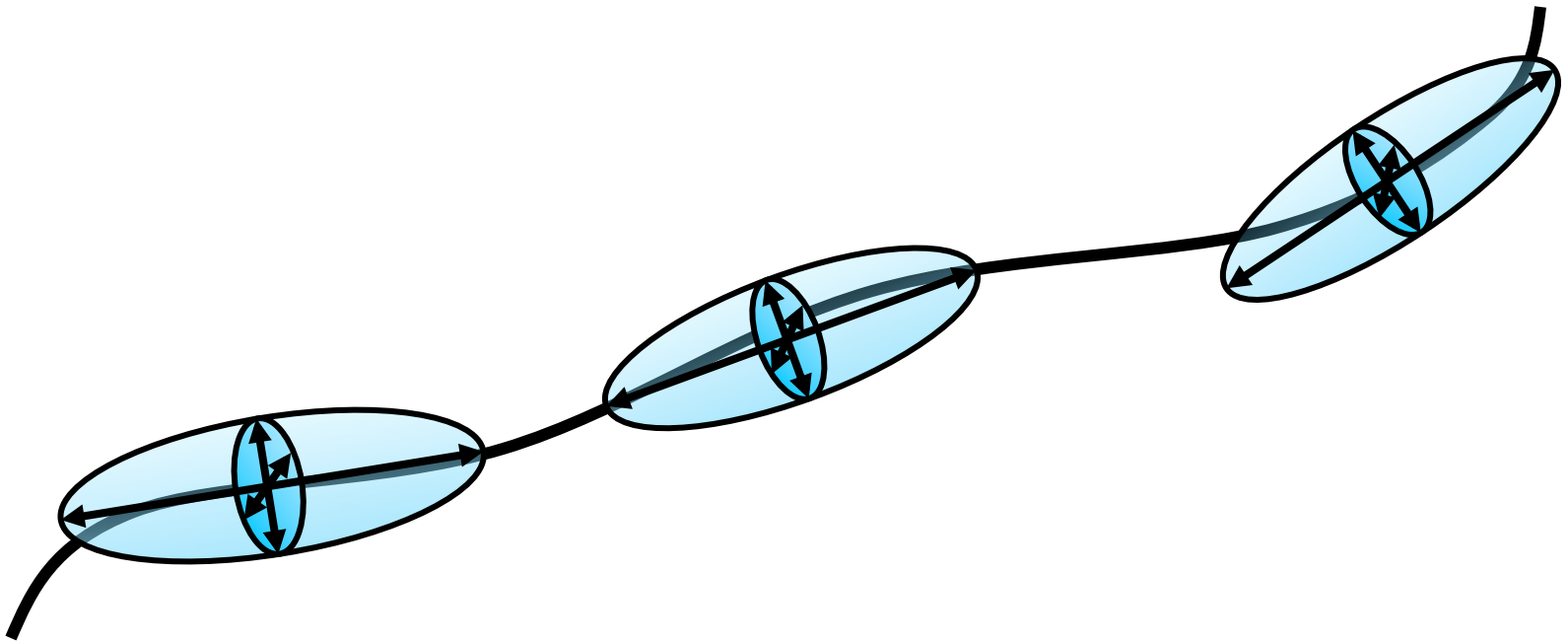
ROI Drawing



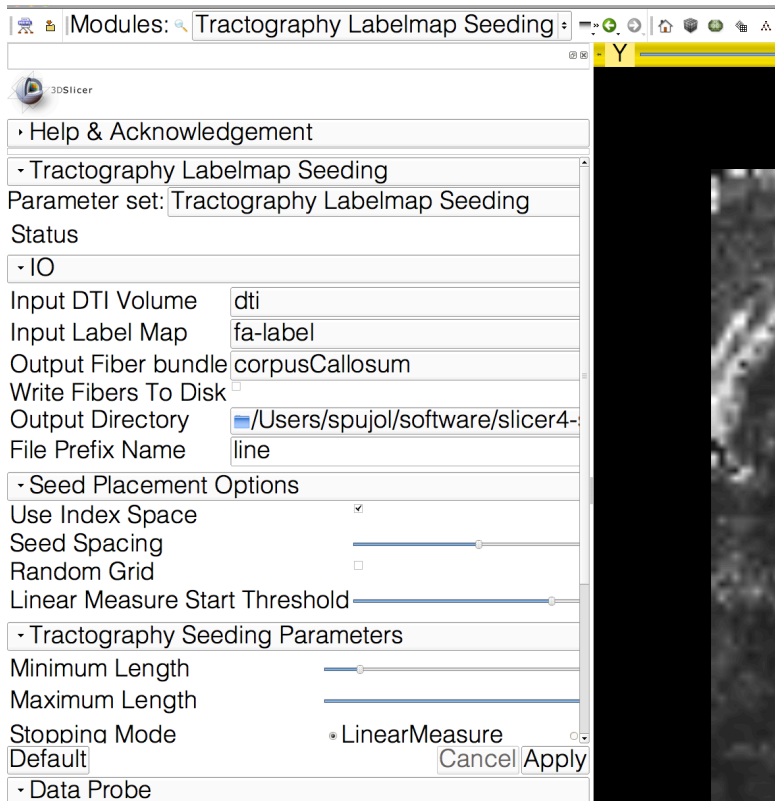
The screenshot shows the 3D Slicer software interface. The top menu bar includes 'Modules: Editor'. The left sidebar contains a '3D Slicer' logo and several menu items: 'Help & Acknowledgement', 'Create and Select Label Maps', 'Master Volume: fa', 'Merge Volume: fa-label' (with a 'Set...' button), 'Per-Structure Volumes', and 'Edit Selected Label Map'. Below these are various tool icons, an 'Undo/Redo' section, and an 'Active Tool: Draw' dropdown. The 'Label:' section is set to 'tissue' with a value of '1' and a green color swatch. There are checkboxes for 'Paint Over' (checked) and 'Threshold Paint' (unchecked), and an 'Apply' button. The main view area shows a grayscale axial MRI slice of a brain with a green, semi-circular region of interest (ROI) drawn over the corpus callosum. A green text box is overlaid on the bottom left of the image, containing the text: 'The tracts will be seeded from the region of interest defined in the corpus callosum area.'

Streamline tractography

Underlying Assumption: the orientation of the fibers is collinear with the direction of the principal eigenvector



Labelmap Seeding: I/O



Select the module **Tractography Labelmap Seeding**

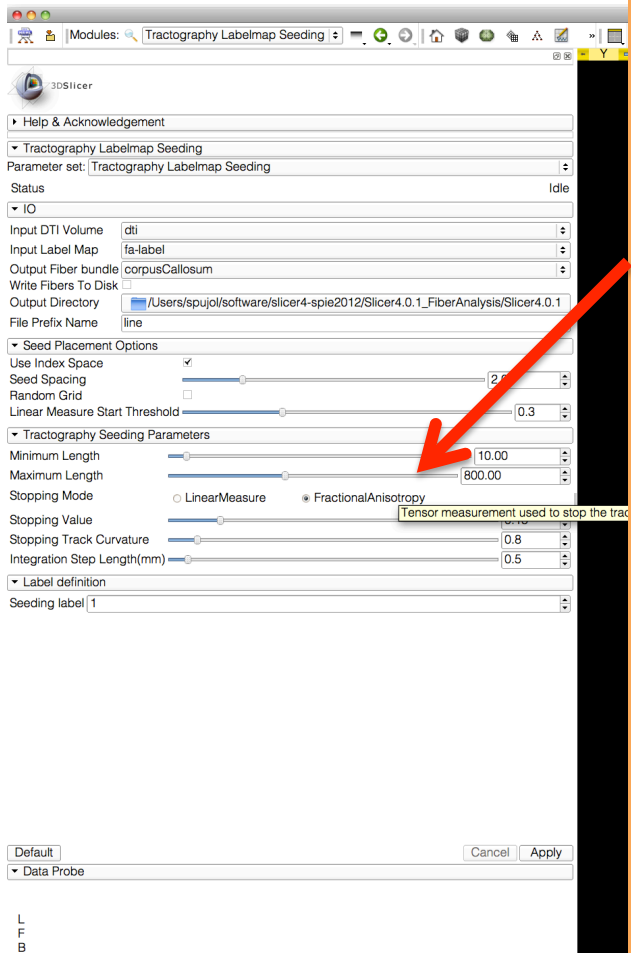
Set the Input DTI Volume to 'dti'

Set the Input Label Map to 'fa-label'

Set Output Fiber Bundle to 'Create New Fiber Bundle' and rename it 'corpusCallosum'

L
F
B

Labelmap Seeding: parameters



Select the Seed Placement Options to 'Use Index Space'.

Select Stopping Mode 'Fractional Anisotropy'

Select the default tractography Seeding parameters:

-Minimum length: 10 mm

-Maximum length: 800 mm

-Stopping value: 0.15

-Stopping track curvature: 0.8

-Integration step length: 0.5 mm

Click on **Apply**

Labelmap Seeding: Tracts

Select the layout 'Conventional Widescreen'

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

3D Slicer 4.0.1

Modules: Tractography Labelmap Seeding

3DSlicer

Help & Acknowledgement

Tractography Labelmap Seeding

Parameter set: Tractography Labelmap Seeding

Status Completed 100%

IO

Input DTI Volume dti

Input Label Map fa-label

Output Fiber bundle corpusCallosum

Write Fibers To Disk

Output Directory /Users/spujol/software/slicer4-spie2012/Slicer4.0.1_FiberAnalysis/Slicer4.0.1

File Prefix Name line

Seed Placement Options

Use Index Space

Seed Spacing 2.00

Random Grid

Linear Measure Start Threshold 0.3

Tractography Seeding Parameters

Minimum Length 10.00

Maximum Length 800.00

Stopping Mode LinearMeasure FractionalAnisotropy

Stopping Value 0.15

Stopping Track Curvature 0.8

Integration Step Length(mm) 0.5

Label definition

Seeding label 1

Default

Data Pr

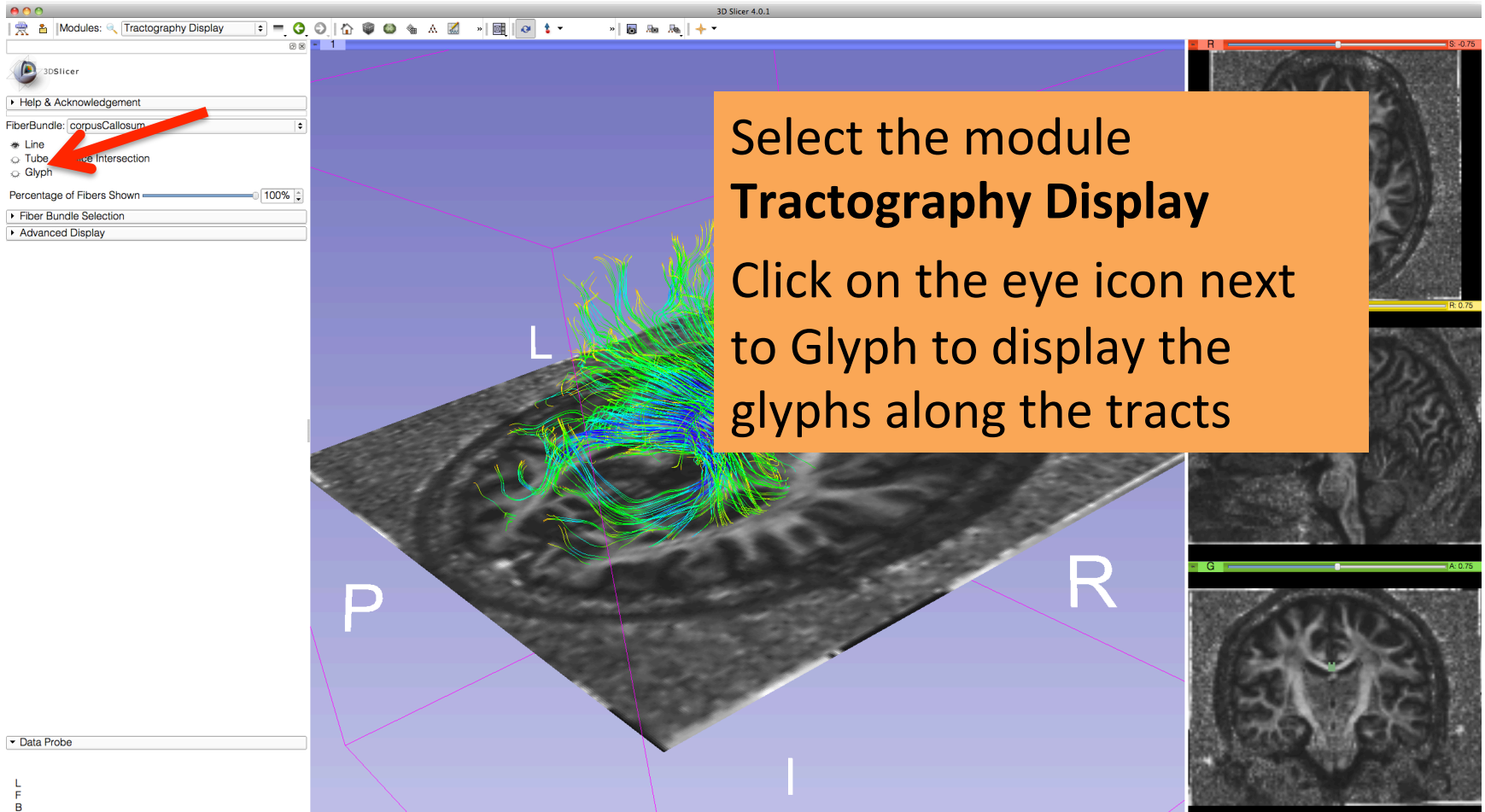
L
F
B

R
S: 0.00

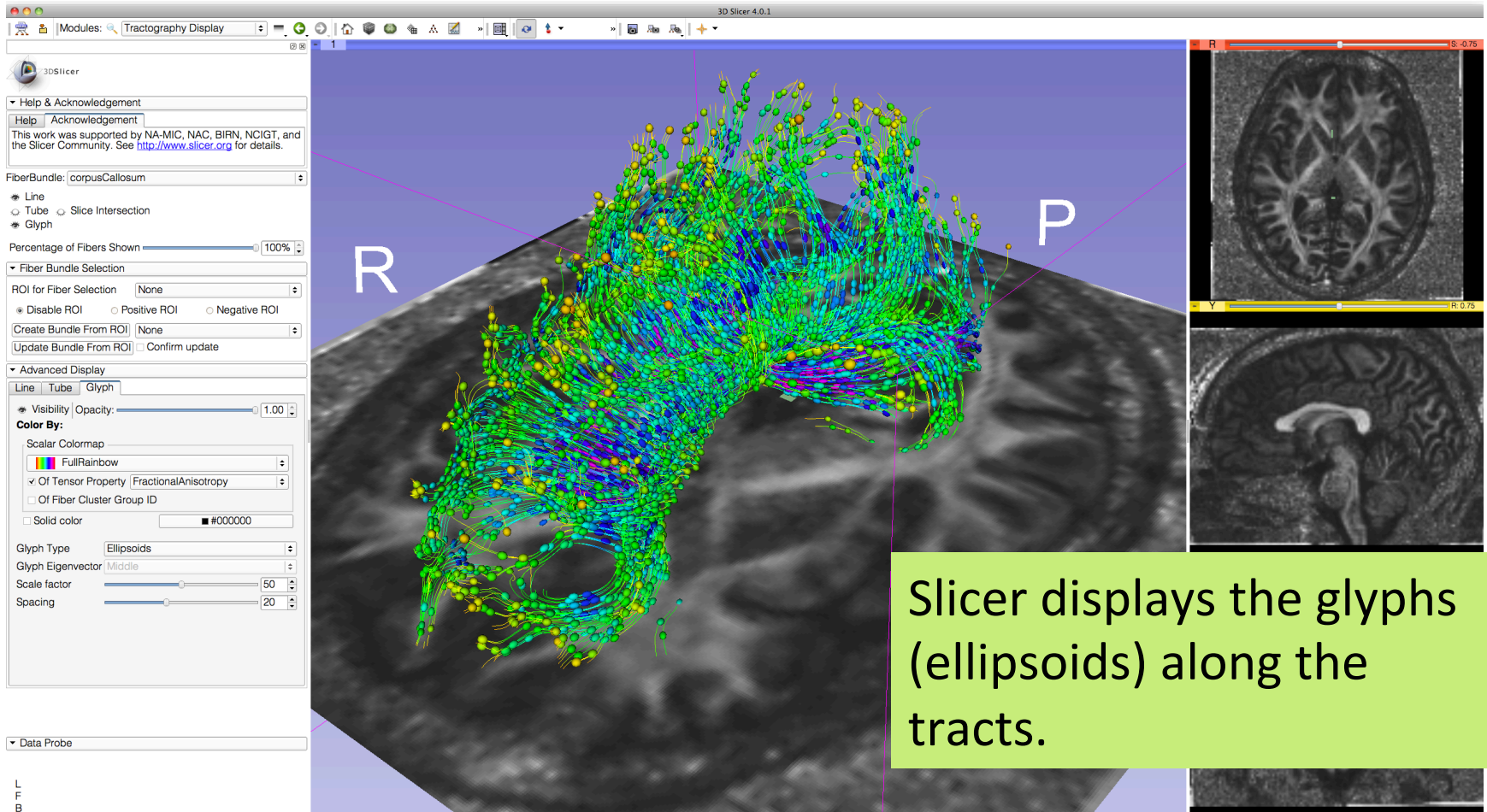
Y
R: 4.50

G
A: 1.50

Labelmap Seeding: Tracts

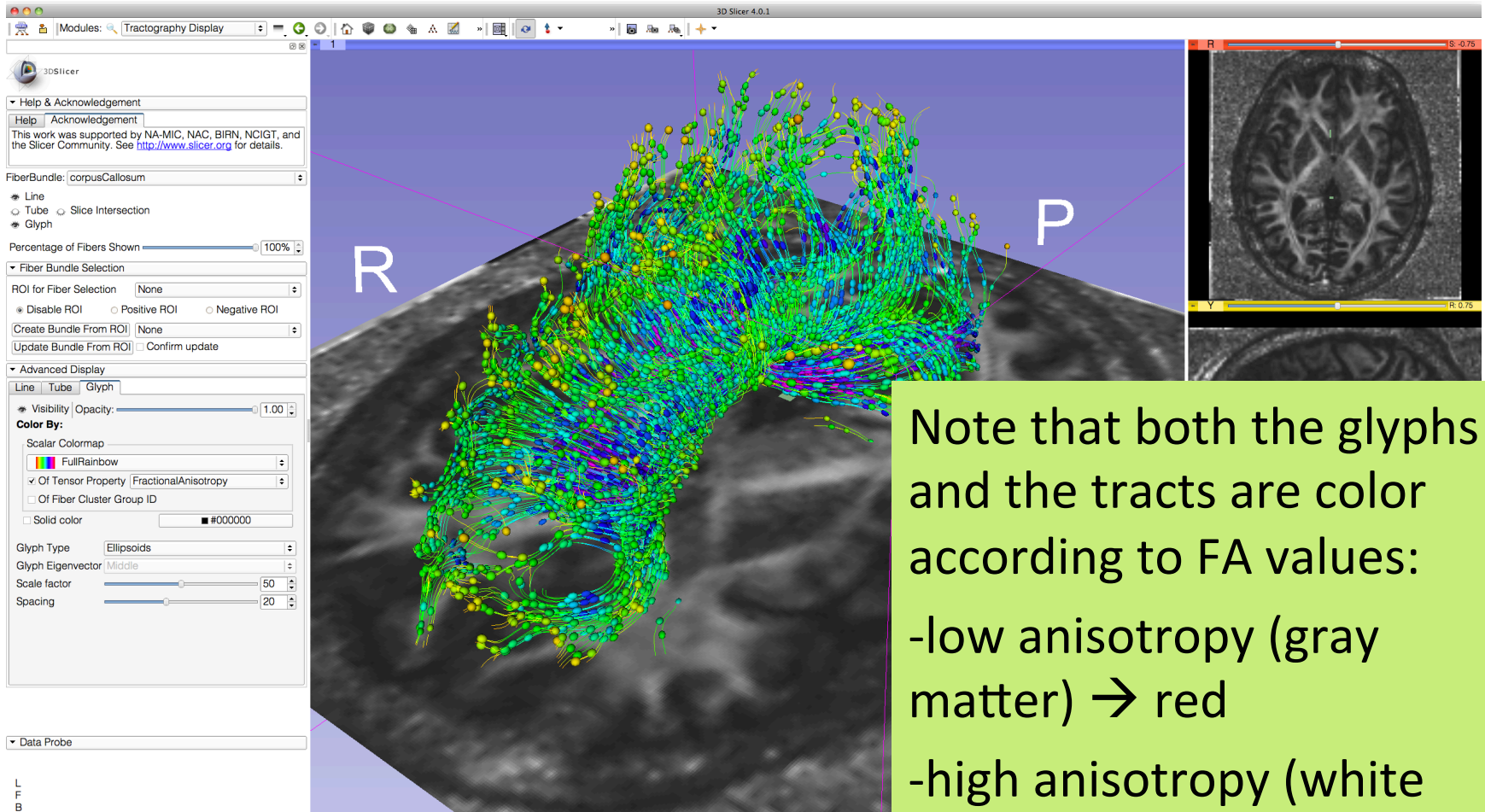


Tractography Results



Slicer displays the glyphs (ellipsoids) along the tracts.

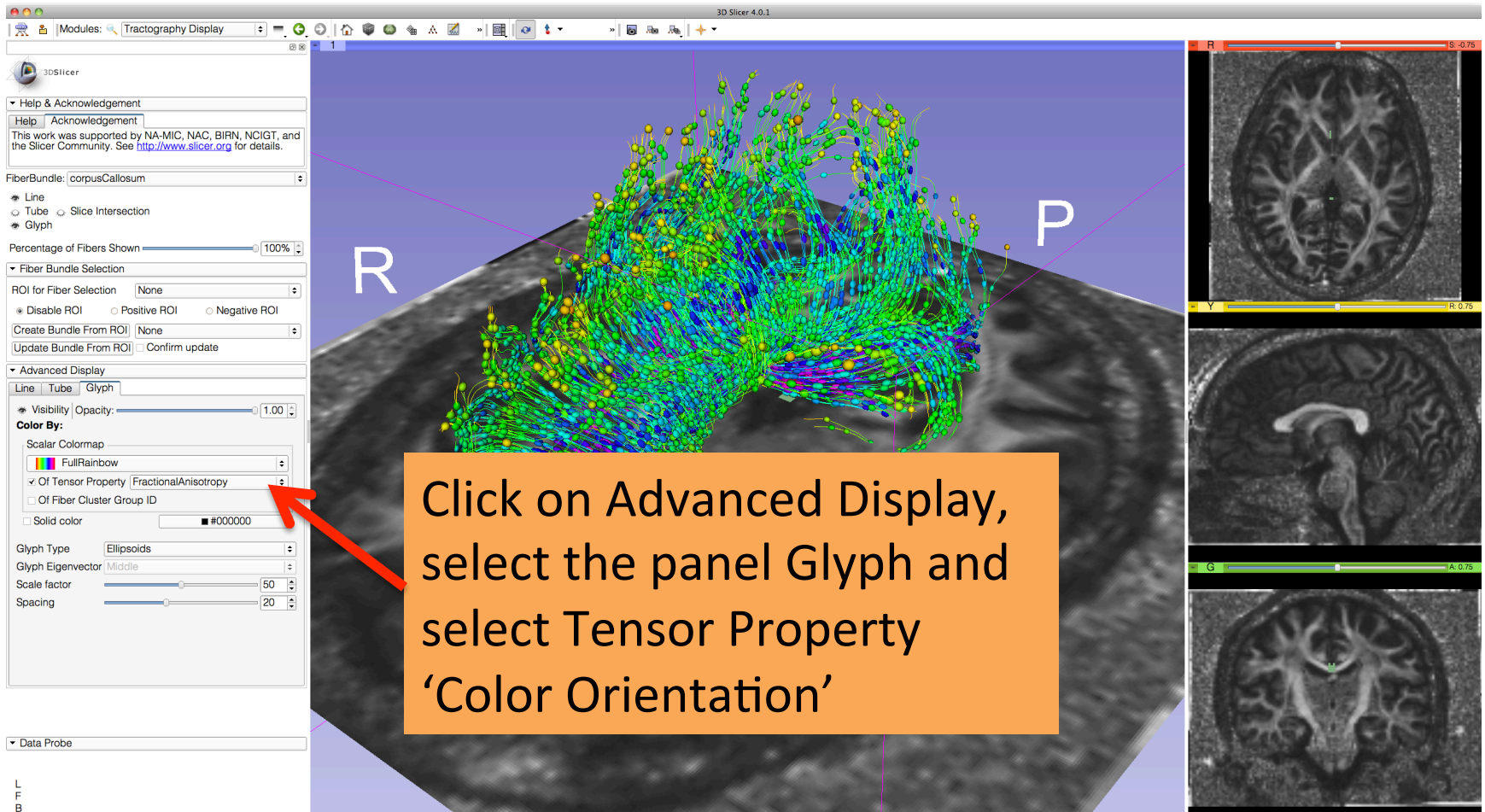
Tractography Results



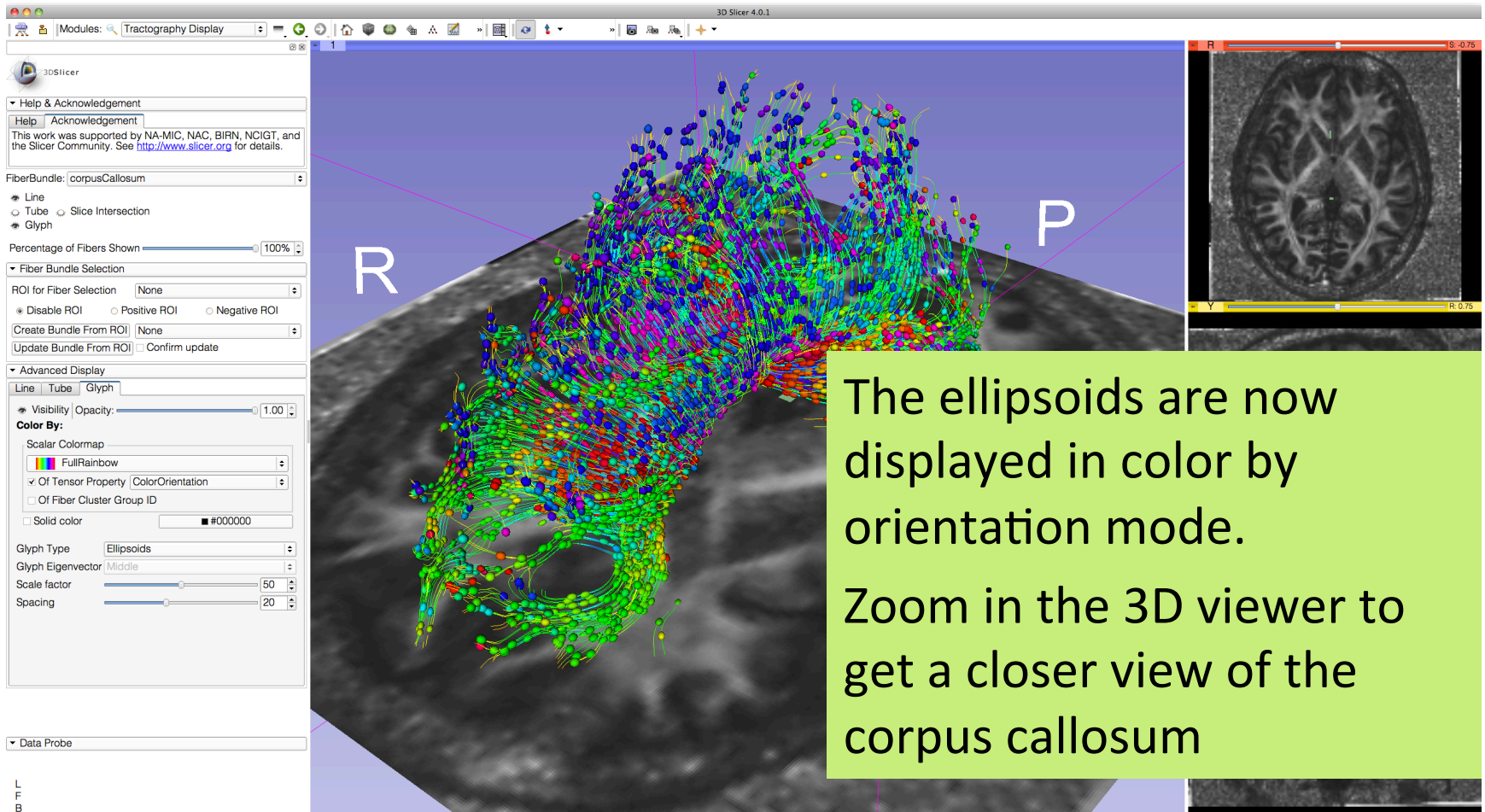
Note that both the glyphs and the tracts are color according to FA values:

- low anisotropy (gray matter) → red
- high anisotropy (white matter) → blue

Tractography Results



Tractography Results

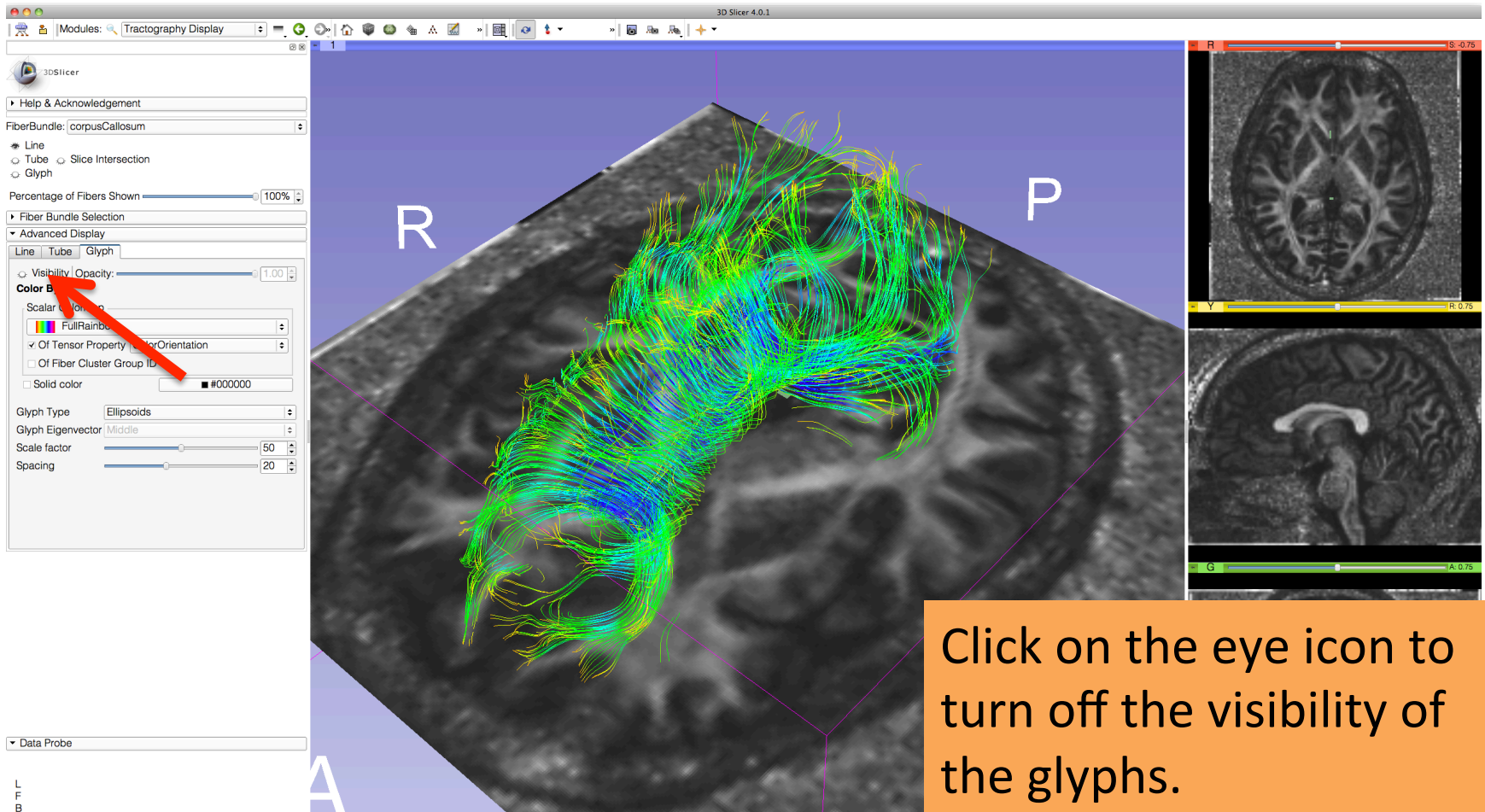


Tractography Results



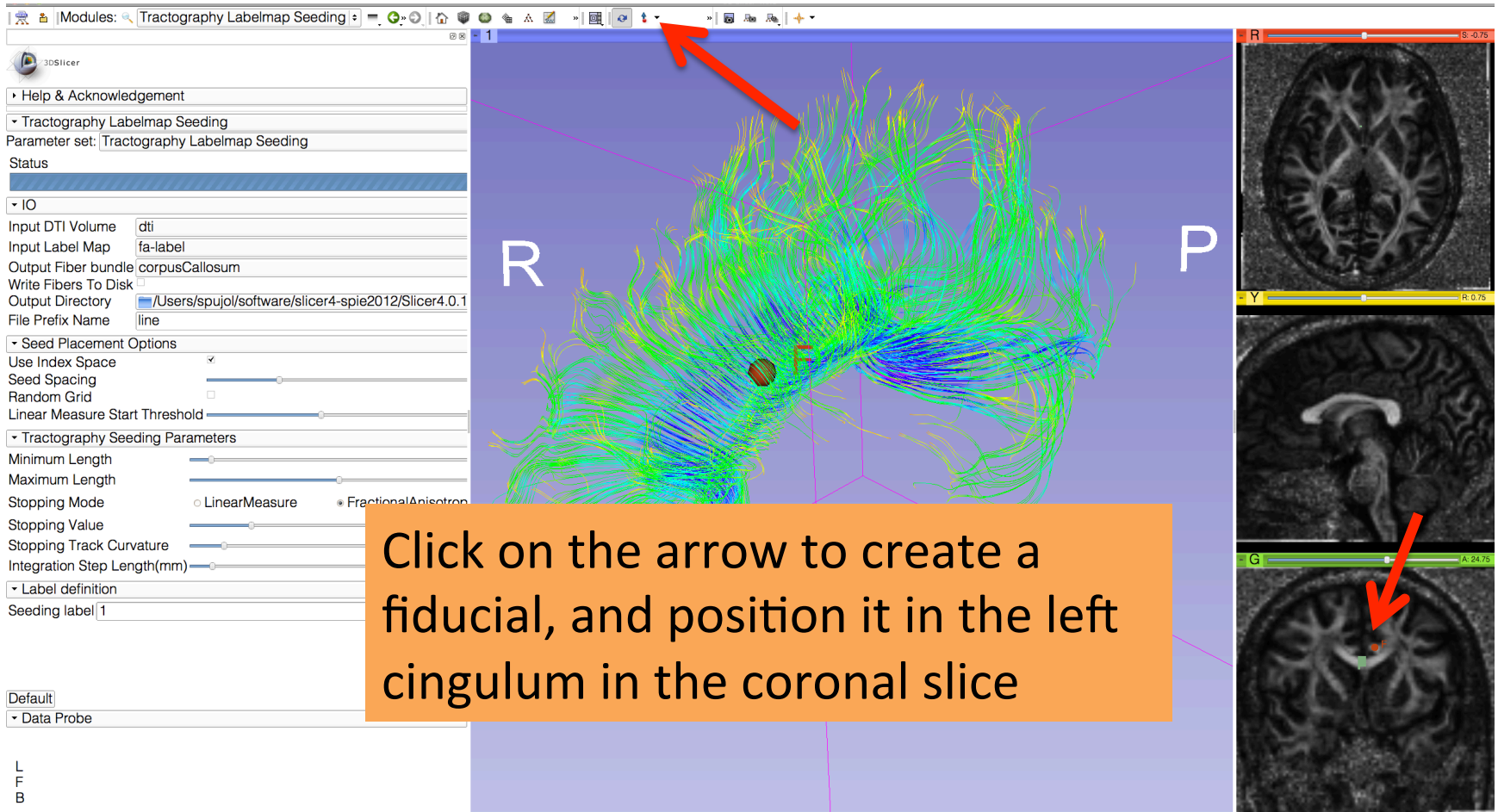
Explore the shape and orientation of the glyphs in the body of the corpus callosum.

Tractography Results



Click on the eye icon to turn off the visibility of the glyphs.

Fiducial Seeding



Fiducial Seeding

Select the Annotations module in the modules menu

Select the Fiducial F, and rename it 'Left Cingulum'

Vis	Lock	Edit	Value	Name	Description
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		All Annotations	
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		Fiducials List	
<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	-3.5, 18.8, 26.1	Left Cingulum	

L
F
B

Fiducial Seeding

Select the module **Tractography Fiducial Seeding**

Select the DTI volume 'dti'

Select the Fiducial List 'Fiducials List'

Select the Output Fiber Bundle 'Create New Fiber Bundle' and rename it 'Cingulum'

Parameters: FiducialSeedingParameters

DTI Volume: dti

Fiducial List or Model: All Annotations

Output Fiber Bundle: Select a FiberBundle

Stopping Criteria: Linear Measure

Stopping Value: 0.15

Stopping Track Curvature: 0.80

Integration Step Length (mm): 0.50

Minimum Path Length (mm): 10.00

Fiducial Region Size (mm): 2.50

Fiducial Seeding Step Size: 1.00

Seed Selected Fiducials

Maximum Number Of Seeds: 100

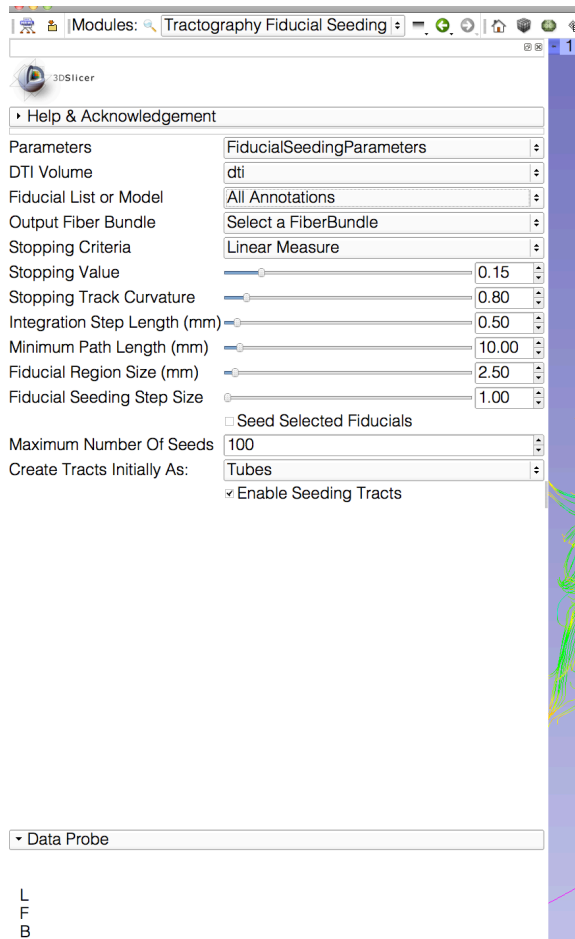
Create Tracts Initially As: Tubes

Enable Seeding Tracts

Data Probe

L
F
B

Fiducial Seeding



Set the tractography parameters as follows:

-Stopping Criteria: Fractional Anisotropy

-Stopping Value: 0.15

-Stopping Track Curvature: 0.8

-Integration step length: 0.5 mm

-Minimum length: 10 mm

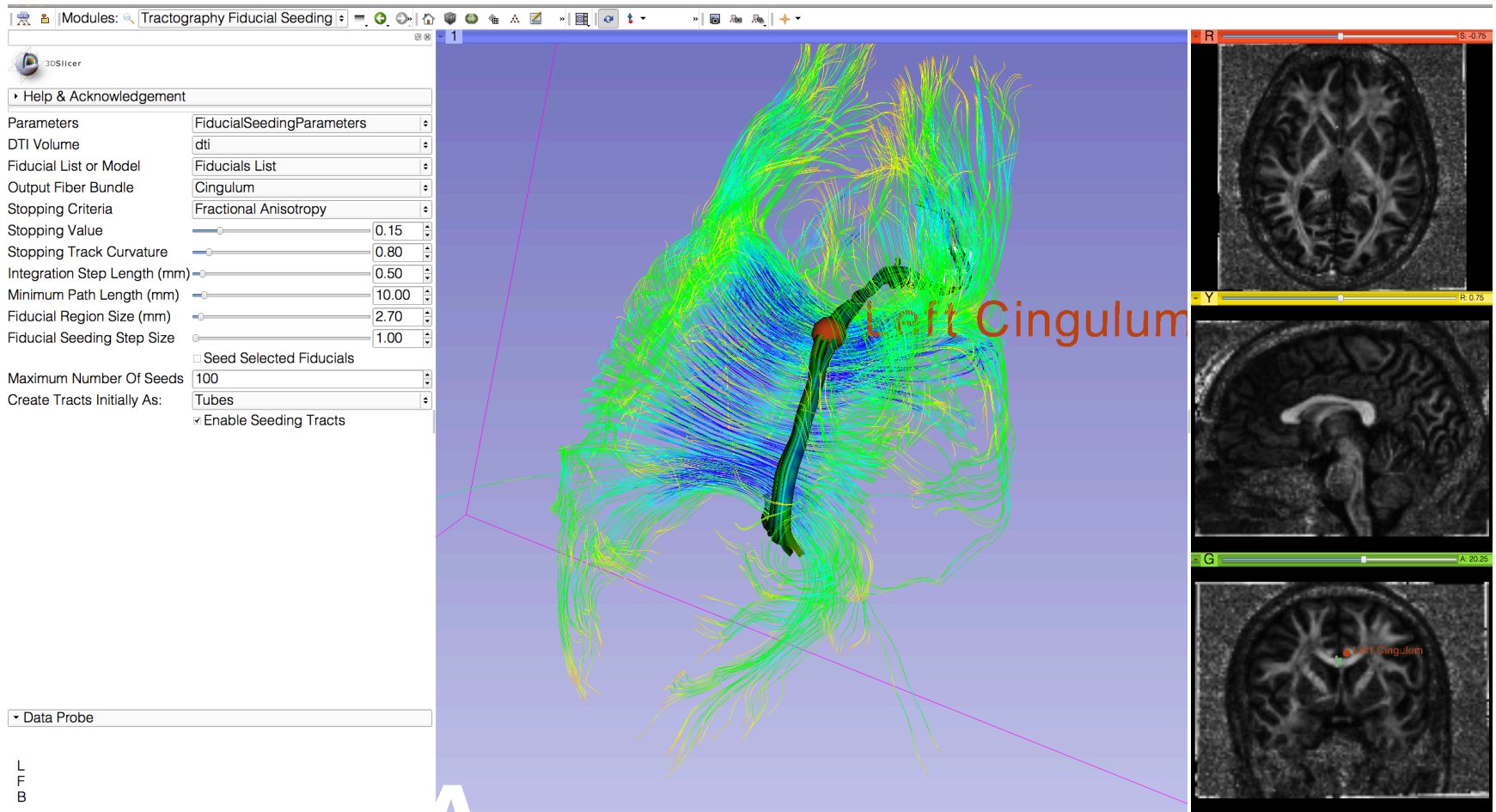
-Fiducial regions size: 2.5 mm

-Fiducial step size: 1.0

-Maximum number of seeds: 100

-Create Tracts Initially as Tubes

Fiducial Seeding



Fiducial Seeding

Click on the arrow icon to create a new fiducial, and position it in the right cingulum area.

Change the name of the new fiducial to 'Right Cingulum' in the Annotations module

Vis	Lock	Edit	Value	Name	Descriptio
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		All Annotations	
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		Fiducials List	
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	-2.3, 20.2, 23.1	Left Cingulum	
<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	7.9, 20.2, 26.1	Right Cingulum	

L
F
B

Fiducial Seeding

Go back to the **Tractography Fiducial Seeding** module

Uncheck and check again the 'Enable Seeding Tracts' to update the 3D viewer

Parameters: FiducialSeedingParameters

DTI Volume: dti

Fiducial List or Model: Fiducials List

Output Fiber Bundle: Cingulum

Stopping Criteria: Fractional Anisotropy

Stopping Value: 0.15

Stopping Track Curvature: 0.80

Integration Step Length (mm): 0.50

Minimum Path Length (mm): 10.00

Fiducial Region Size (mm): 2.70

Fiducial Seeding Step Size: 1.00

Seed Selected Fiducials

Maximum Number Of Seeds: 100

Create Tracts Initially As: Tubes

Enable Seeding Tracts

Data Probe

L
F
B

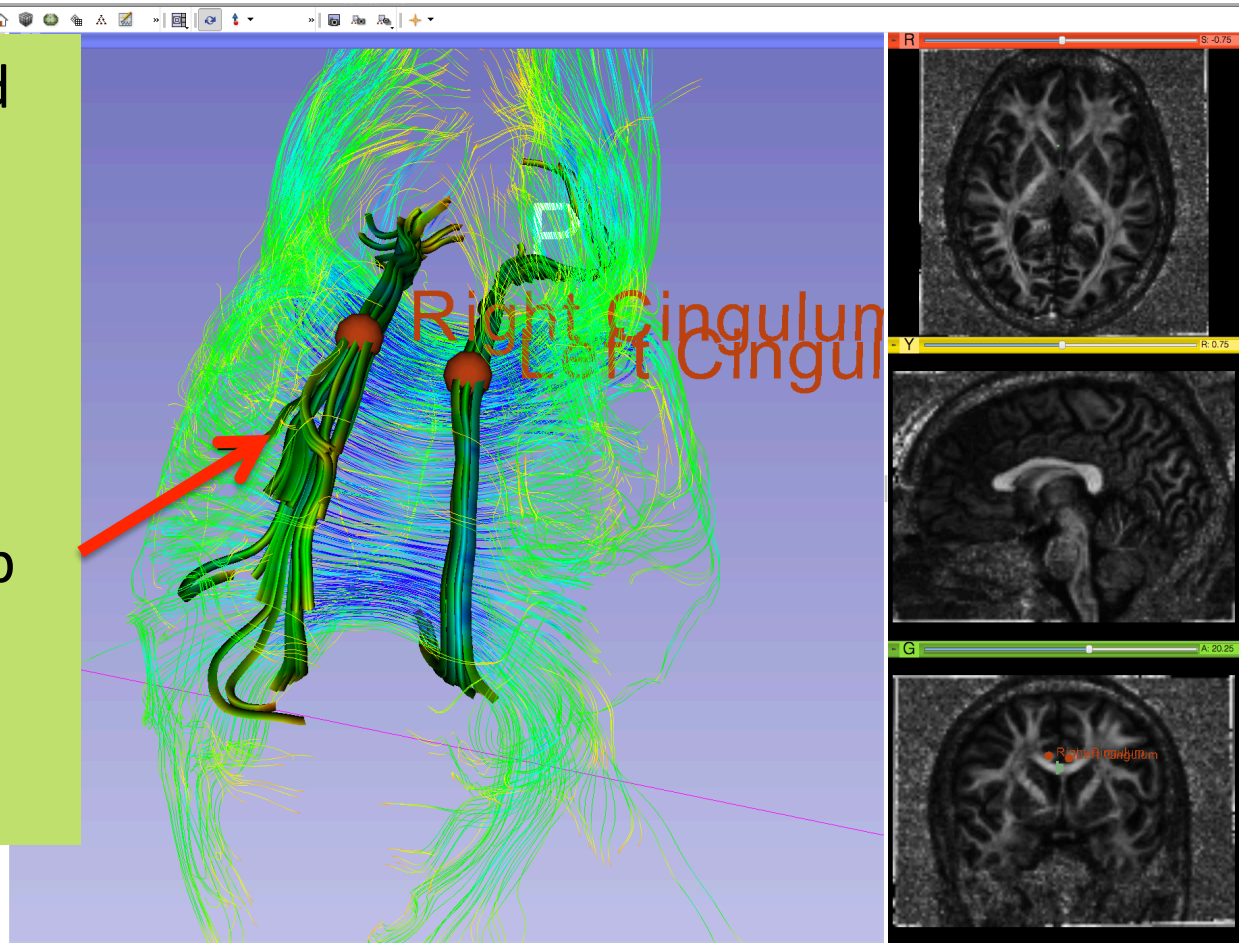
R
Y
G
A: 20.25

Right Cingulum

Fiducial Seeding

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

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



L
F
B

Fiducial Seeding

3D Slicer

Modules: Tractography Fiducial Seeding

Help & Acknowledgement

Parameters: FiducialSeedingParameters

DTI Volume: dti

Fiducial List or Model: Fiducials List

Output Fiber Bundle: Cingulum_Fiducials List

Stopping Criteria: Fractional Anisotropy

Stopping Value: 0.15

Stopping Track Curvature: 0.80

Integration Step Length (mm): 0.50

Minimum Path Length (mm): 10.00

Fiducial Region Size (mm): 2.70

Fiducial Seeding Step Size: 1.00

Seed Selected Fiducials

Maximum Number Of Seeds: 100

Create Tracts Initially As: Tubes

Enable Seeding Tracts

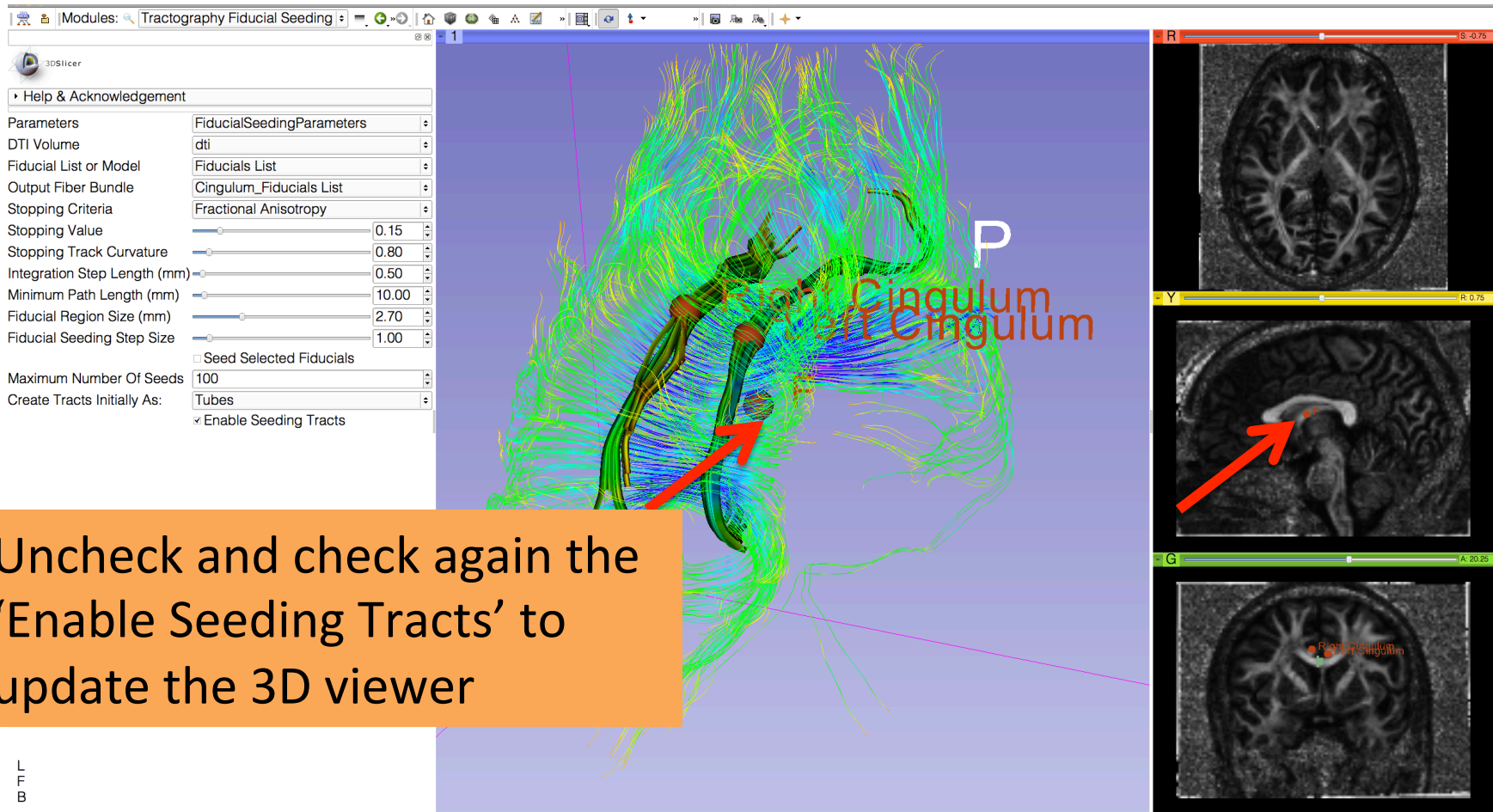
Data Probe

L
F
B

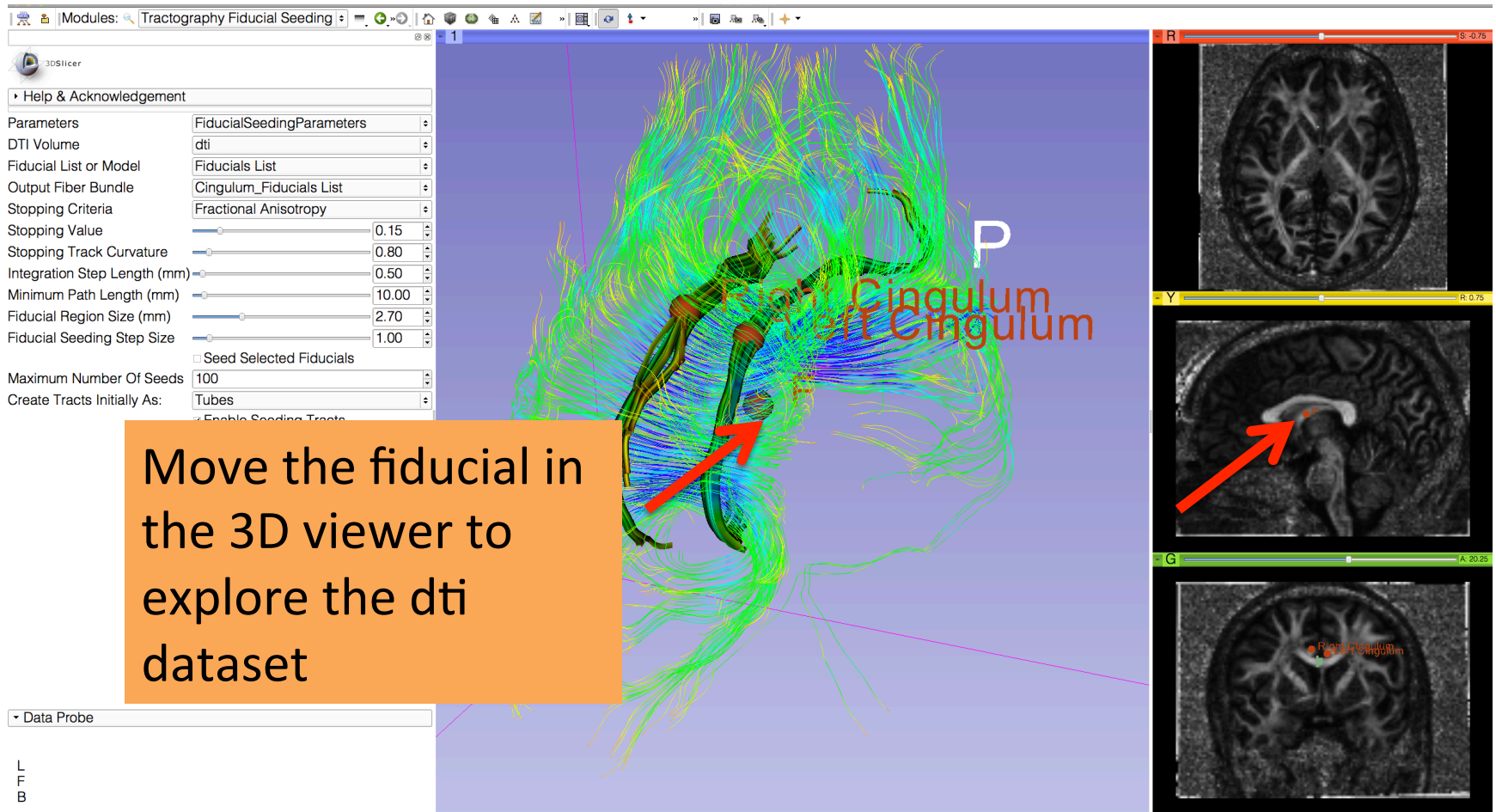
Click on the arrow icon to create a new fiducial

Right Cingulum

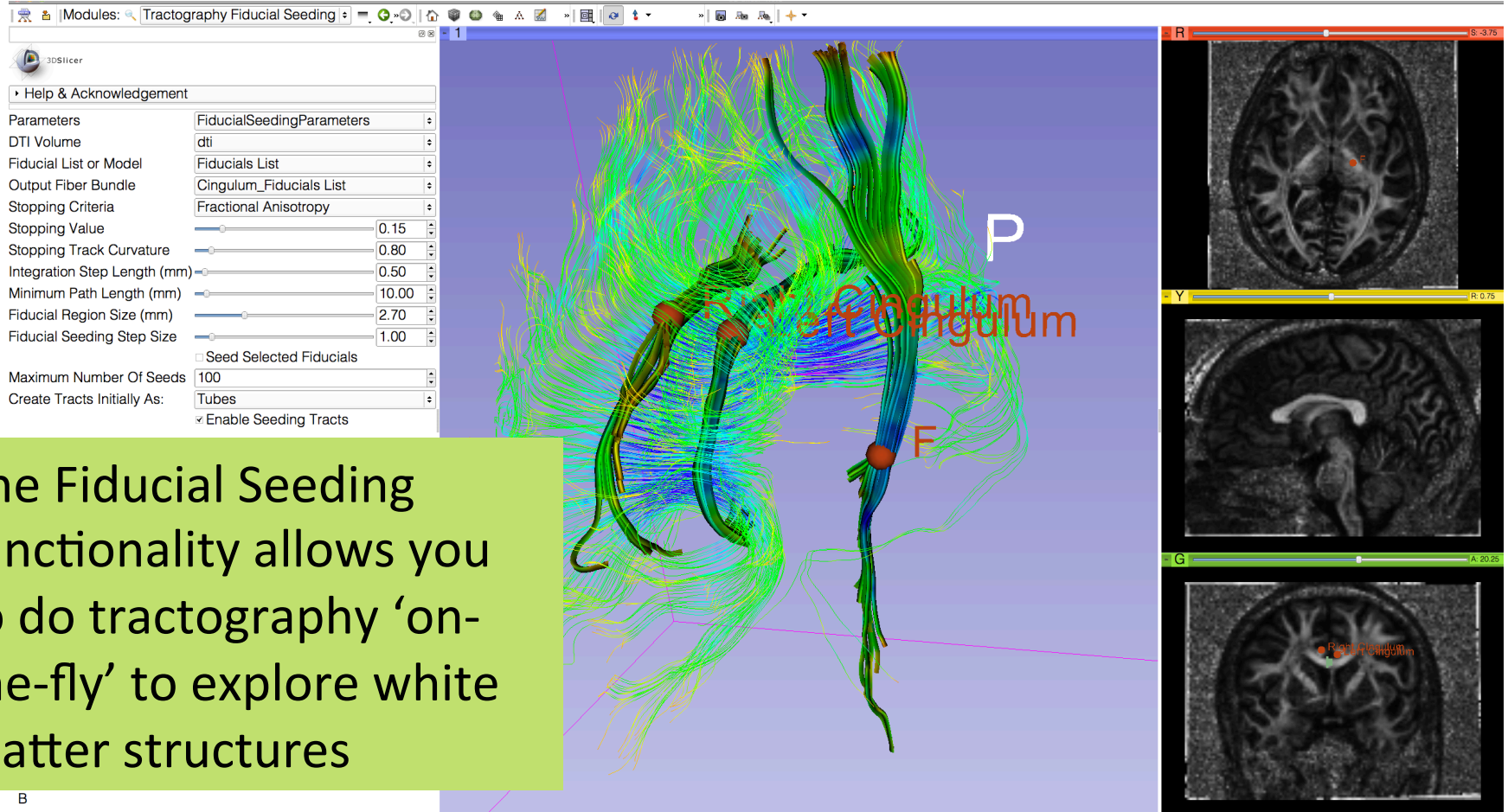
Fiducial Seeding



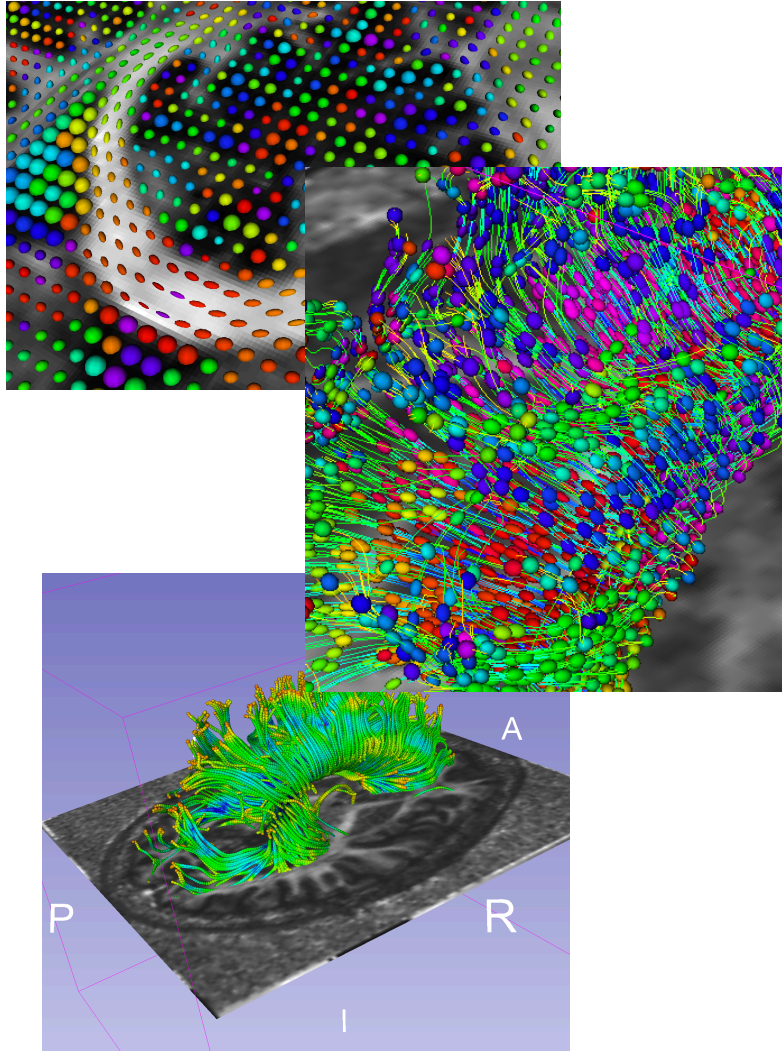
Fiducial Seeding



Tractography 'on-the-fly'



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 brain white matter pathways.

Acknowledgments



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NIH P41RR013218

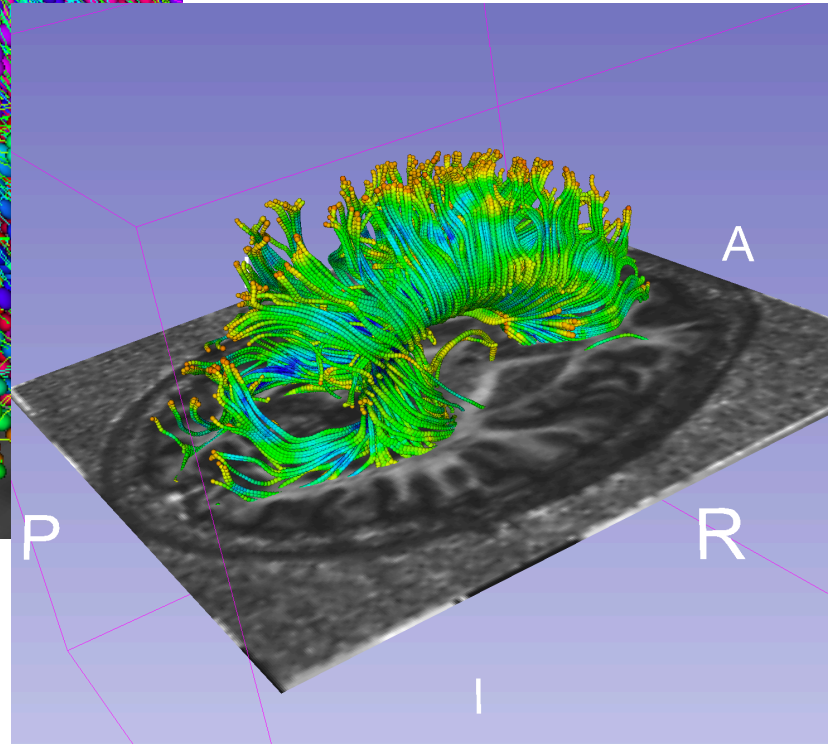
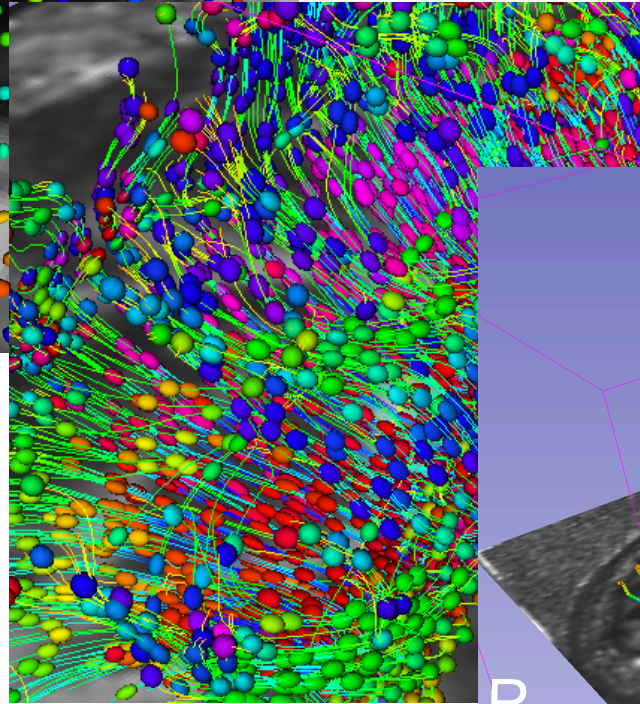
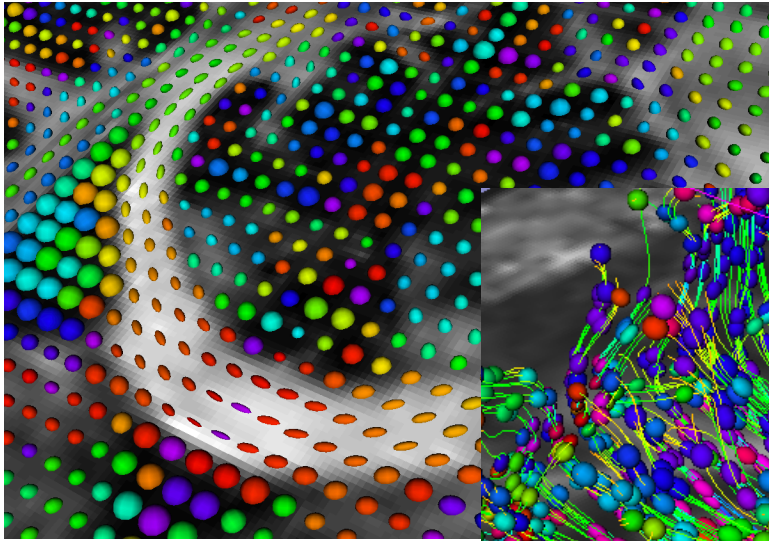
Slicer Community

- www.slicer.org

- Mailing lists:

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spujol@bwh.harvard.edu