



Diffusion MRI Analysis

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Brain Anatomy



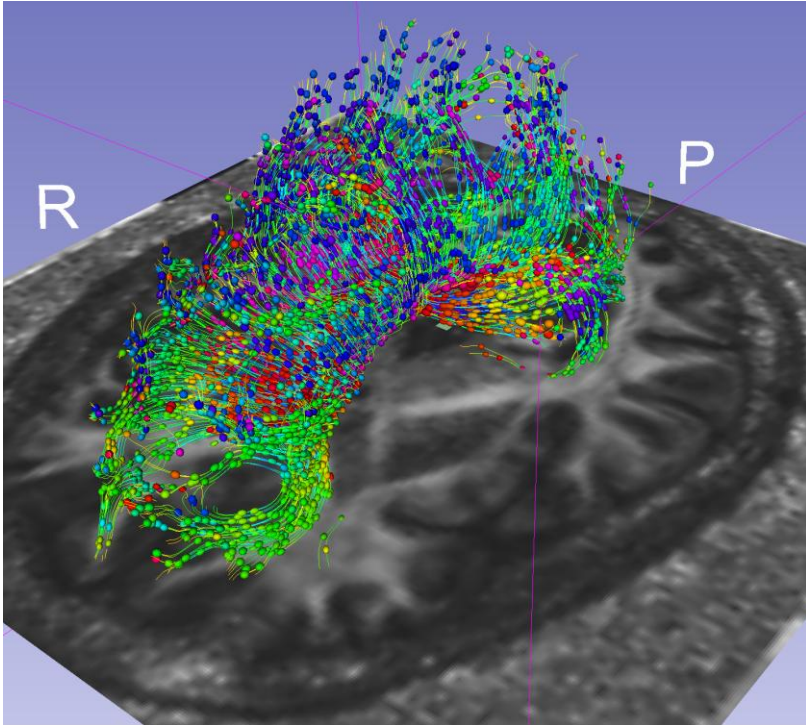
- White matter ~45% of the brain
- Myelinated nerve fibers (~ 10 μm axon diameter)

White Matter Exploration



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

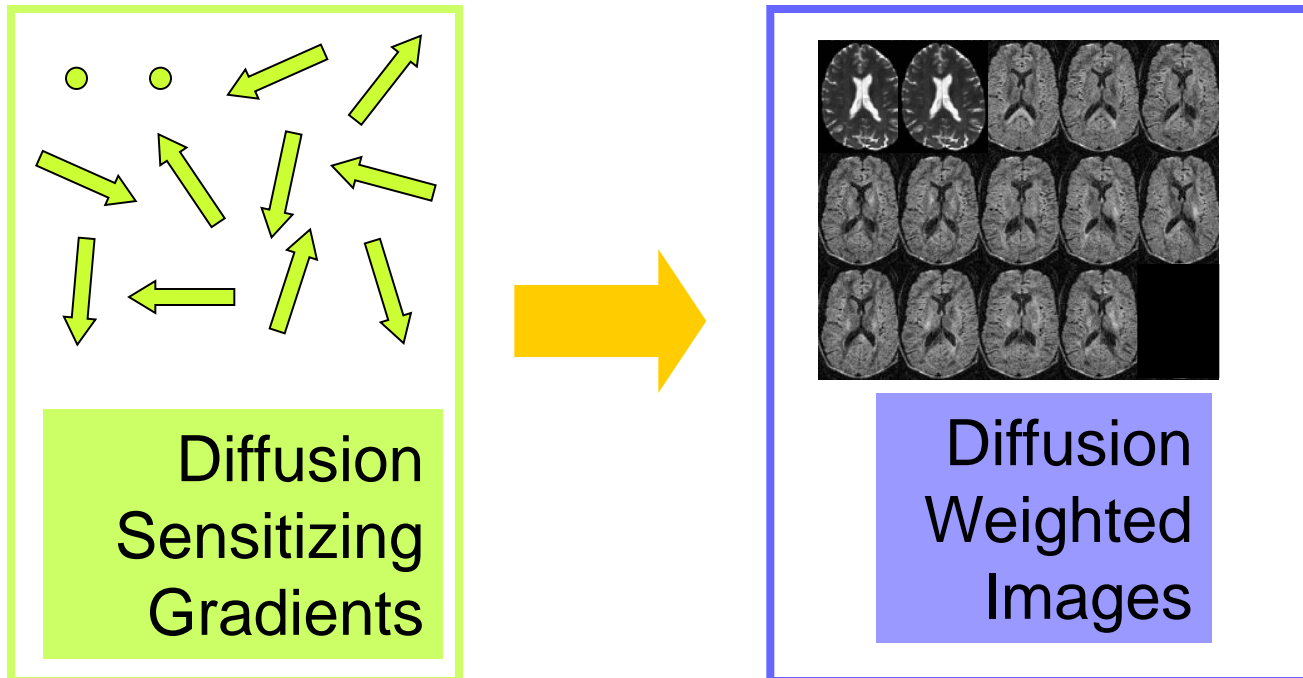
Tutorial Outline



This tutorial is an introduction to the fundamentals of 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.



Tutorial software



The screenshot shows the 3DSlicer website homepage. At the top left is the 3DSlicer logo, a stylized sphere with a grid. To its right is the text "3DSlicer" and a tagline: "A multi-platform, free and open source software package for visualization and medical image computing". A search bar is located in the top right corner. Below the tagline are four buttons: "Download", "Tutorials", "Reference", and "Feedback".

On the left side, there is a "Slicer Wiki" section with a "Download" button and a list of links: "About Slicer" (Introduction, Acknowledgments, Contact Us), "Resources" (For Users, For Developers, Commercial Use, NCIA, Publication DB, Image Gallery, Slicer Community, Source Code, Licensing, Mailing Lists, Web Archive).

The main content area features three columns of images illustrating the software's capabilities:

- Powerful processing.** Shows a series of brain slices with a green and yellow heatmap overlay.
- Streamlined interface.** Shows a 3D model of a brain with a yellow mesh overlay.
- Extensible platform.** Shows a 3D model of a brain with a purple and green mesh overlay.

At the bottom of the main content area, there is a large 3DSlicer logo and the text "3D Slicer version 4.0" and "www.slicer.org".

Below the main content area, there is a small text block: "The community of Slicer developers is proud to announce the release of Slicer 4.0. Find out more...".

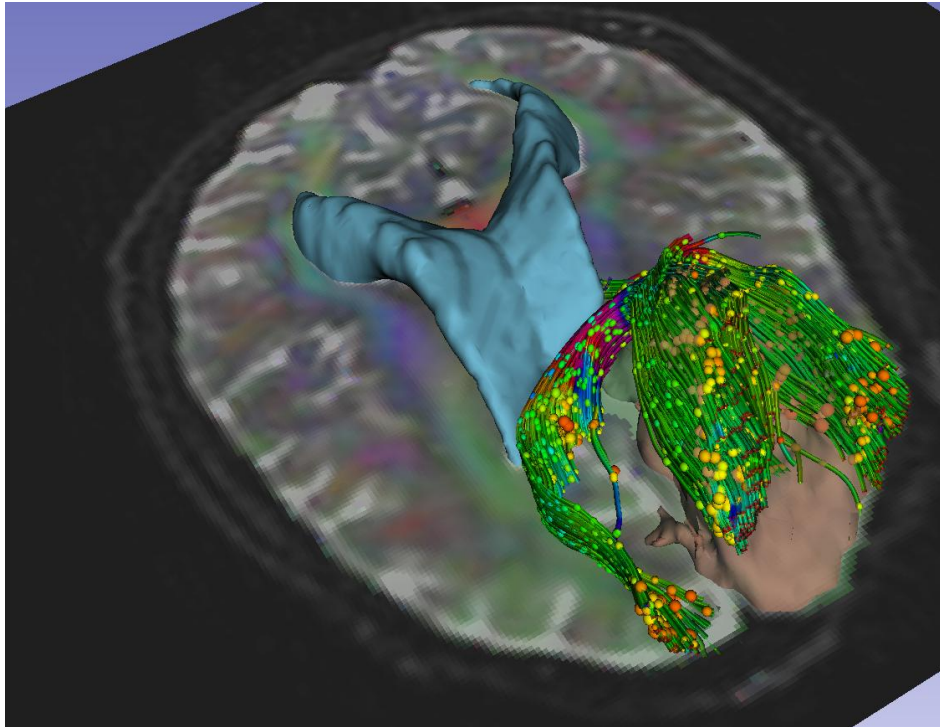
At the very bottom, there is a footer with copyright information: "Content of this site is Copyright 2012 BWH and 3D Slicer contributors, unless otherwise noted. Contact webmaster@bwh.harvard.edu for questions about the use of this site's content. See here for more information about the web infrastructure."

The tutorial uses the 3DSlicer version 4.0.1 (Slicer-4.0.1) software available at www.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.

3DSlicer



3D Slicer is a multi-institution effort supported by the National Institutes of Health.

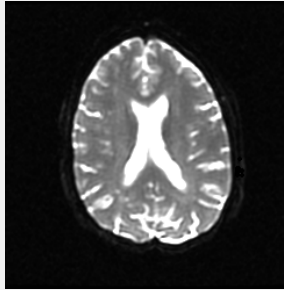
- An **end-user application** for image analysis
- An **open-source environment** for software development
- A software platform that is both **easy to use** for clinical researchers and **easy to extend** for programmers

Learning Objectives

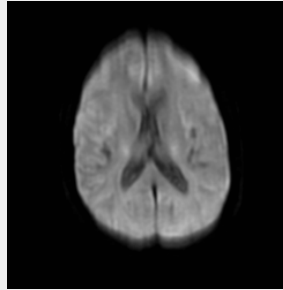
Following this tutorial, you'll be able to

- 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

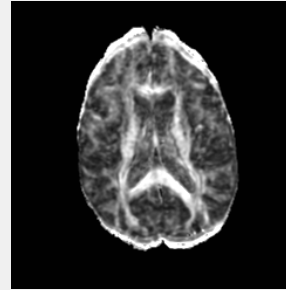
MR Diffusion Analysis Pipeline



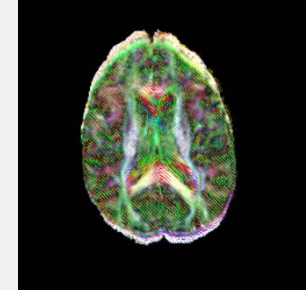
DWI
Acquisition



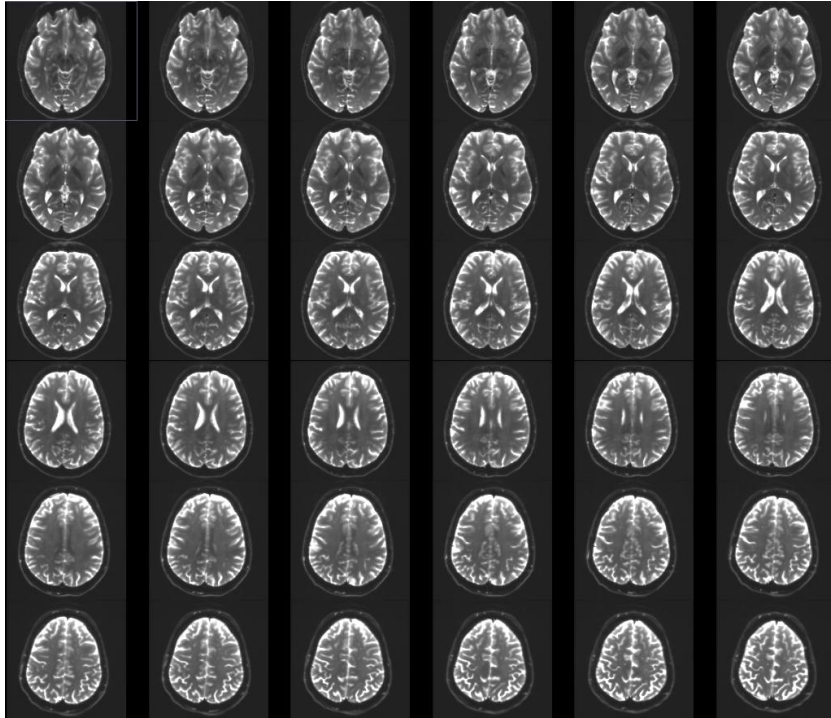
Tensor
Calculation



Scalar
Maps

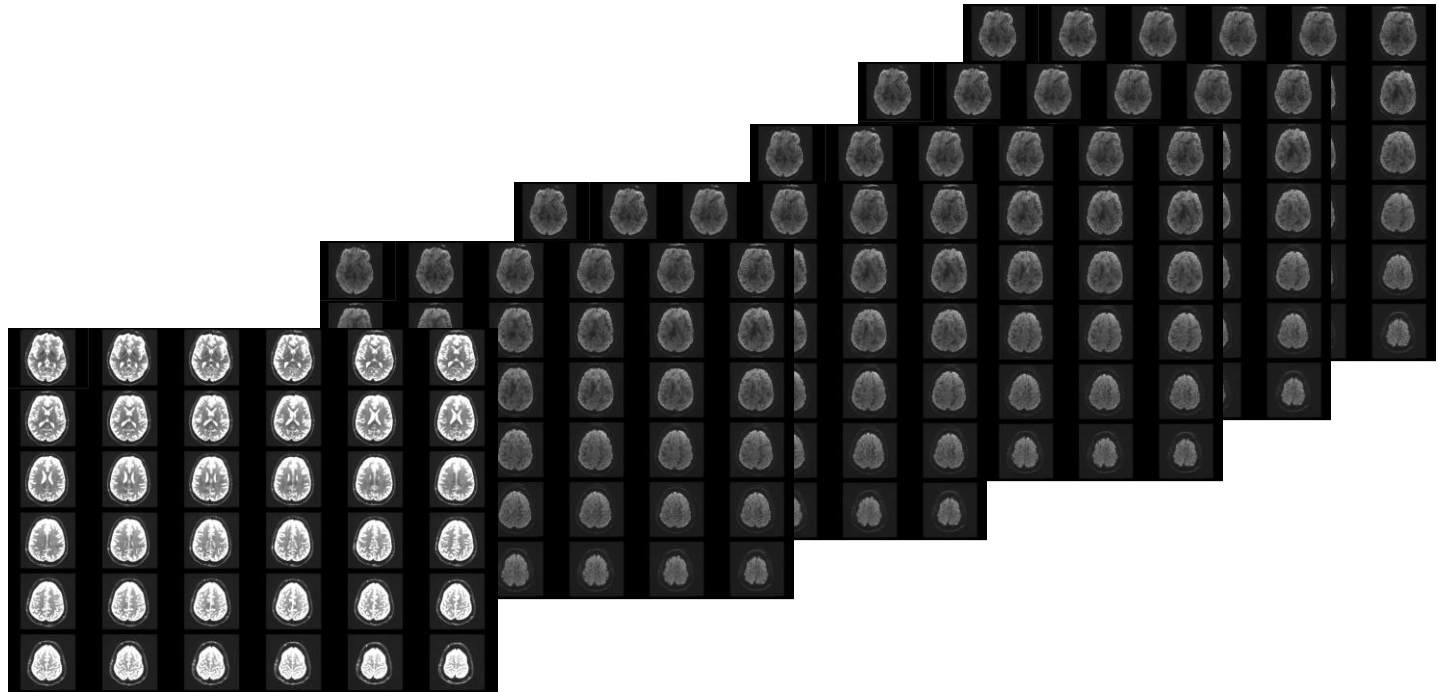


3D
Visualization



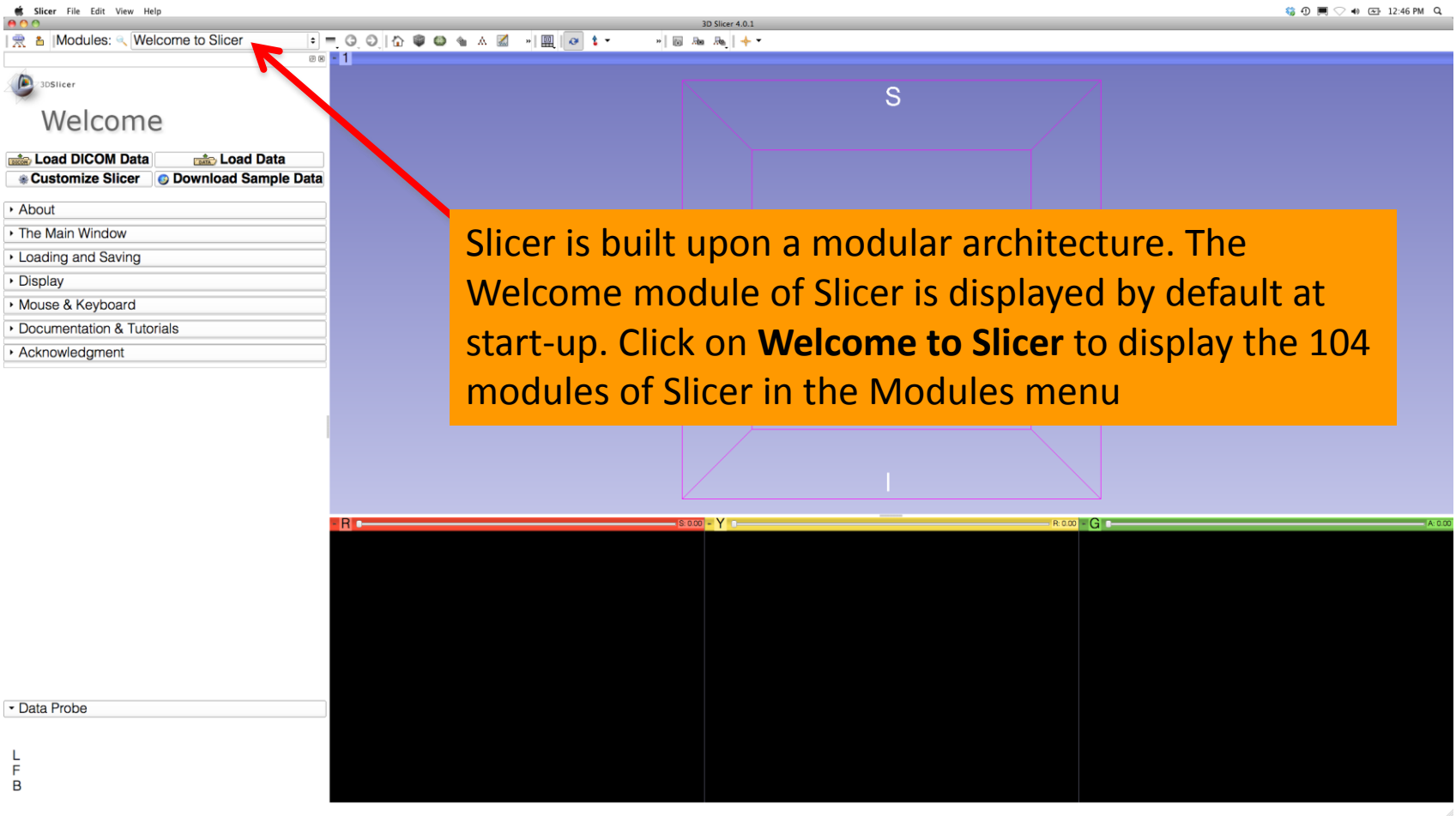
Part 1: From DWI images to Tensors

Understanding the DWI dataset



The DWI dataset is composed of 1 volume acquired without diffusion-sensitizing gradient, and 41 volumes acquired with 41 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 4.0.0

Modules: Welcome to Slicer

1

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

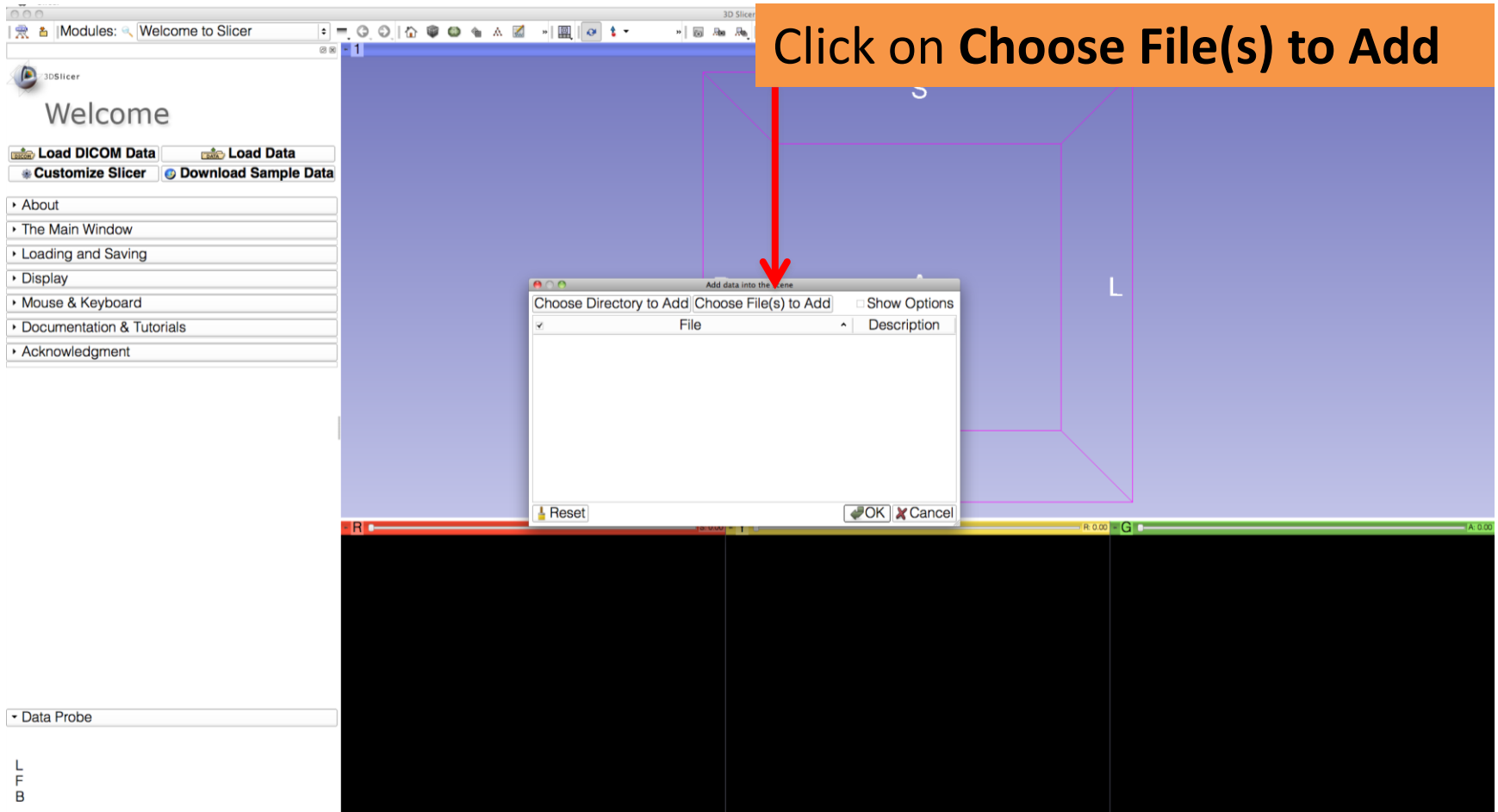
Red RAS: (-104.6, 63.4, -0.8) Axial Sp: 1.5

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

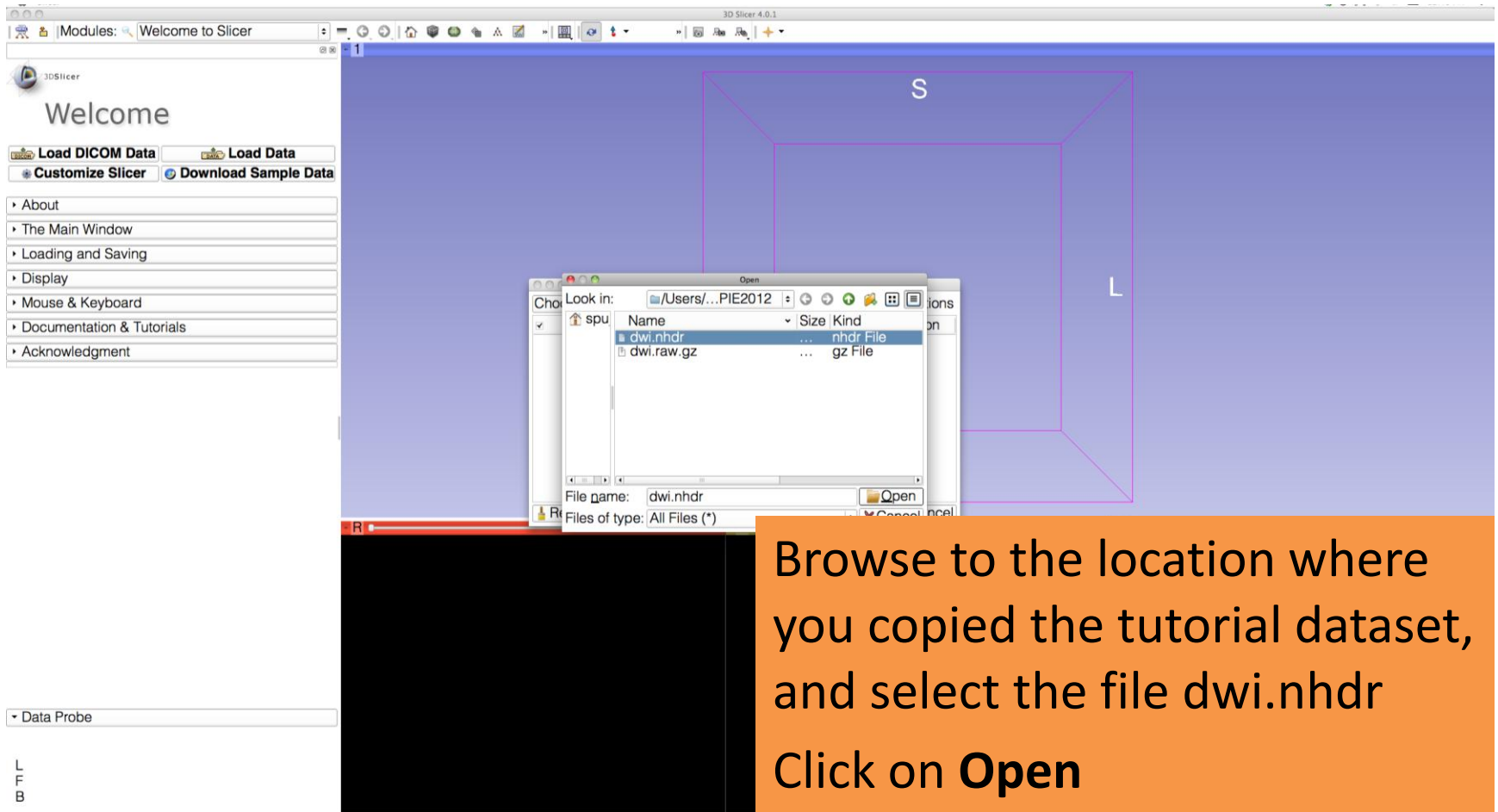
R A L

R S 0.00 -Y R 0.00 G A 0.00

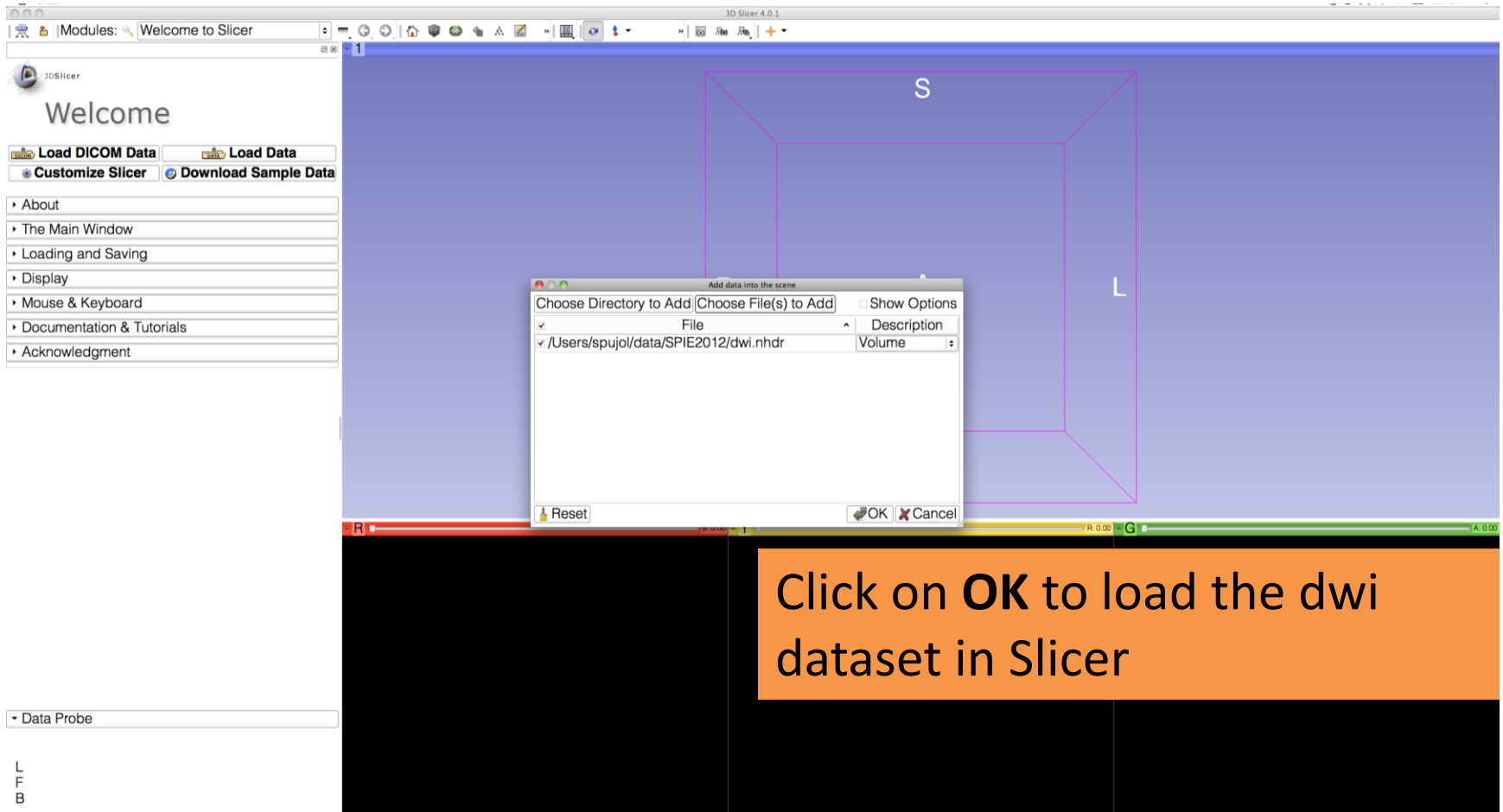
Loading the DWI dataset



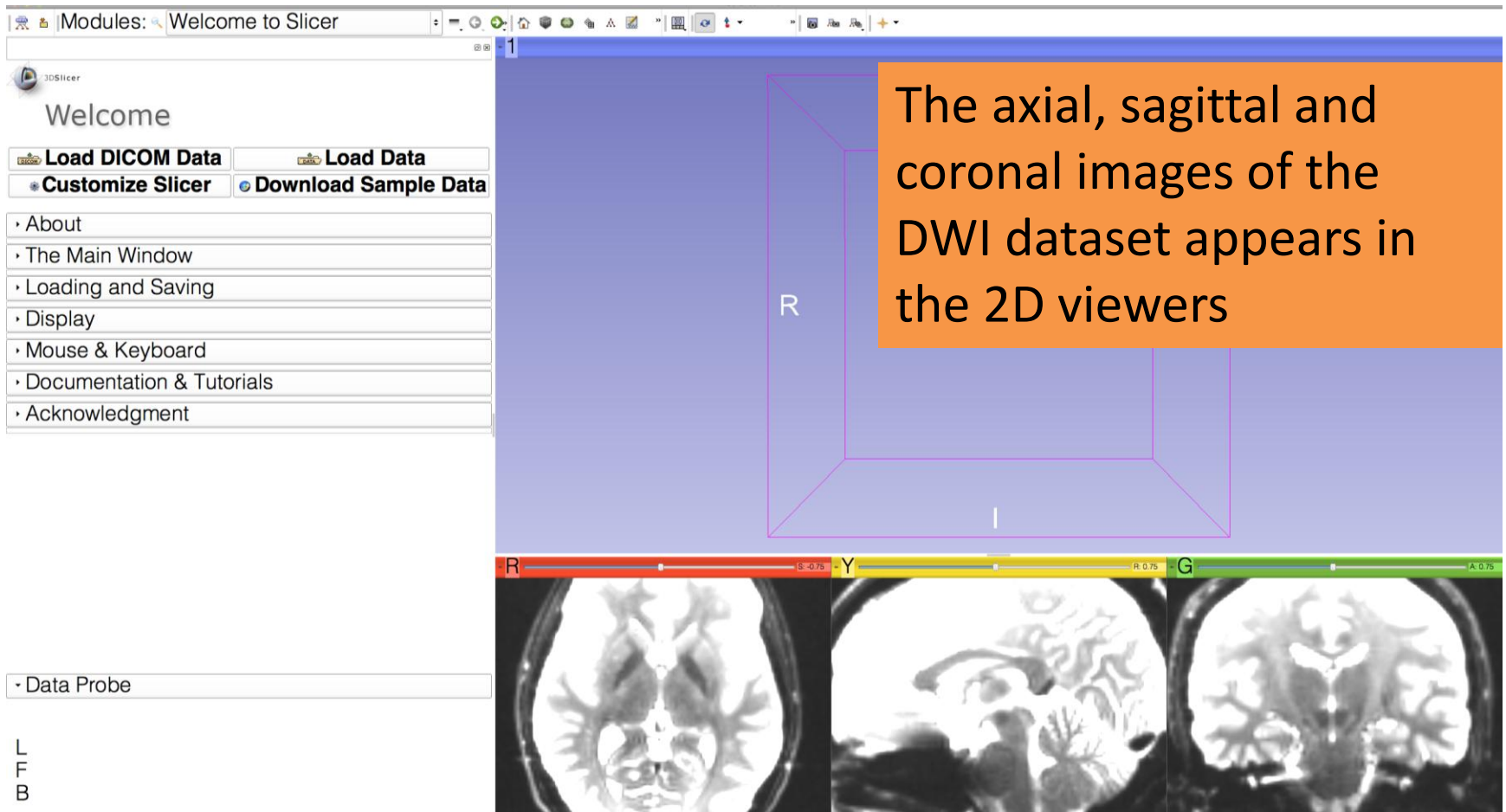
Loading the DWI dataset



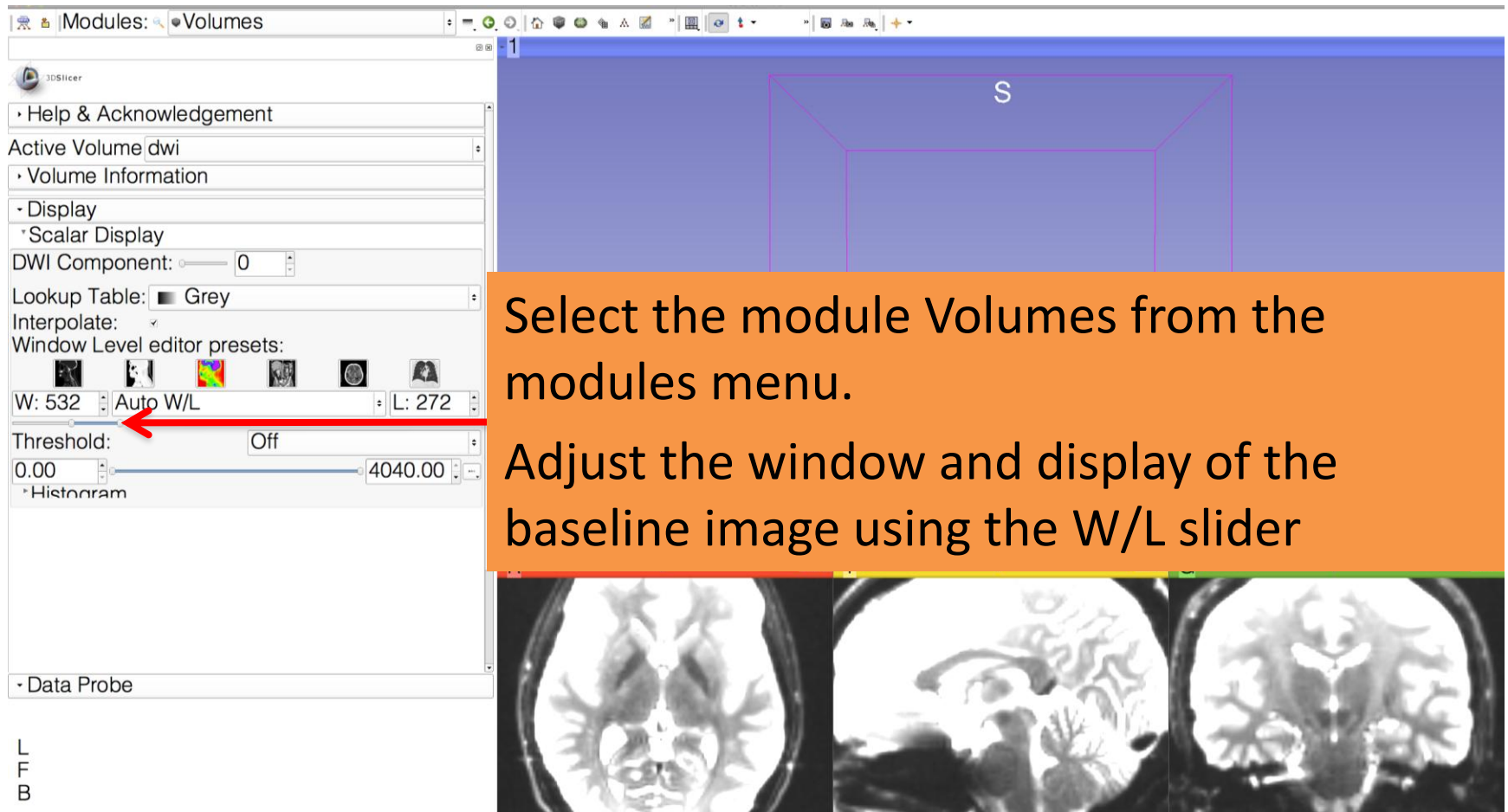
Loading the DWI dataset



Loading the DWI dataset



Adjusting Window and Level

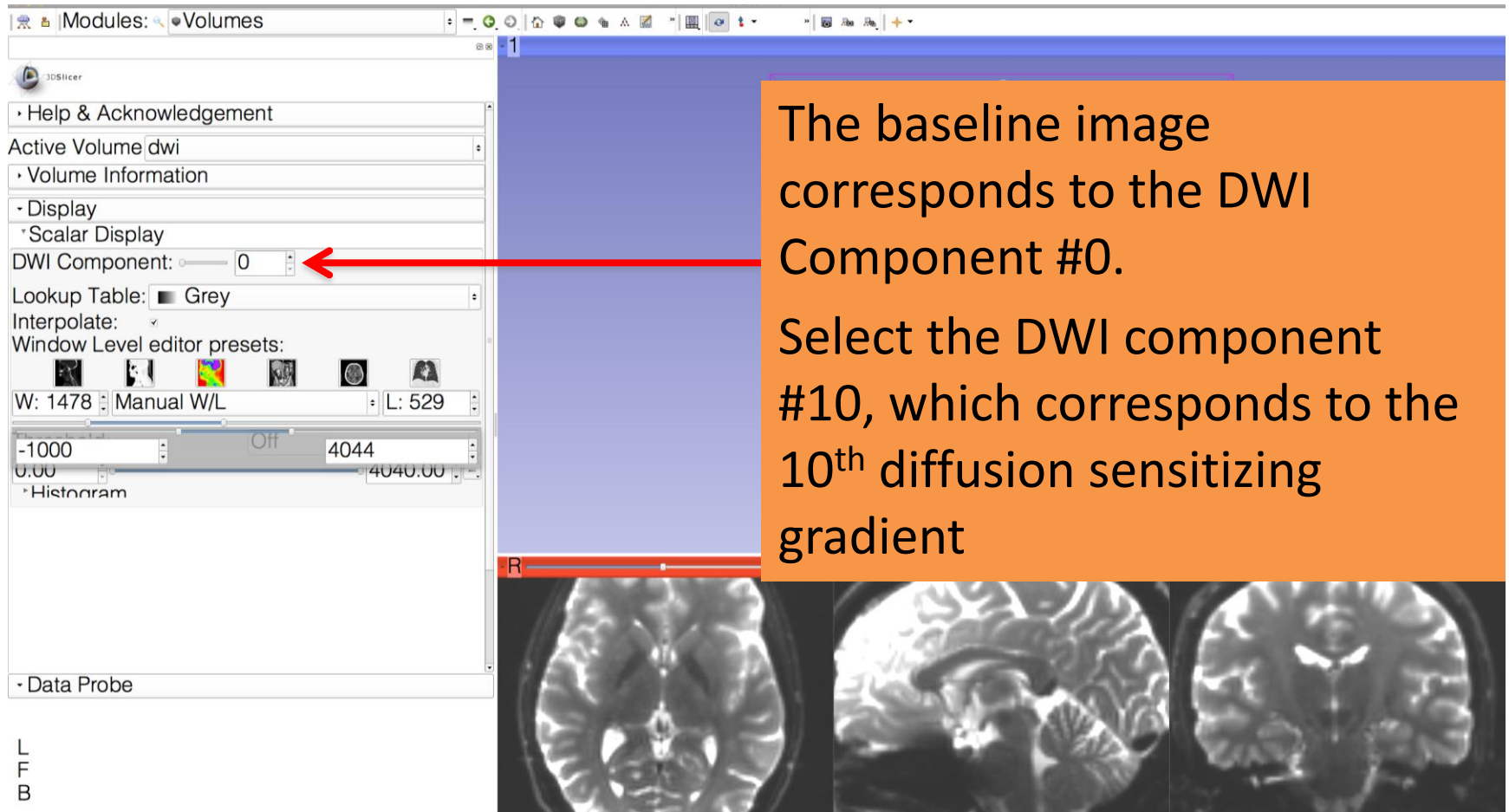


Select the module Volumes from the modules menu.

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

L
F
B

Exploring the DWI dataset

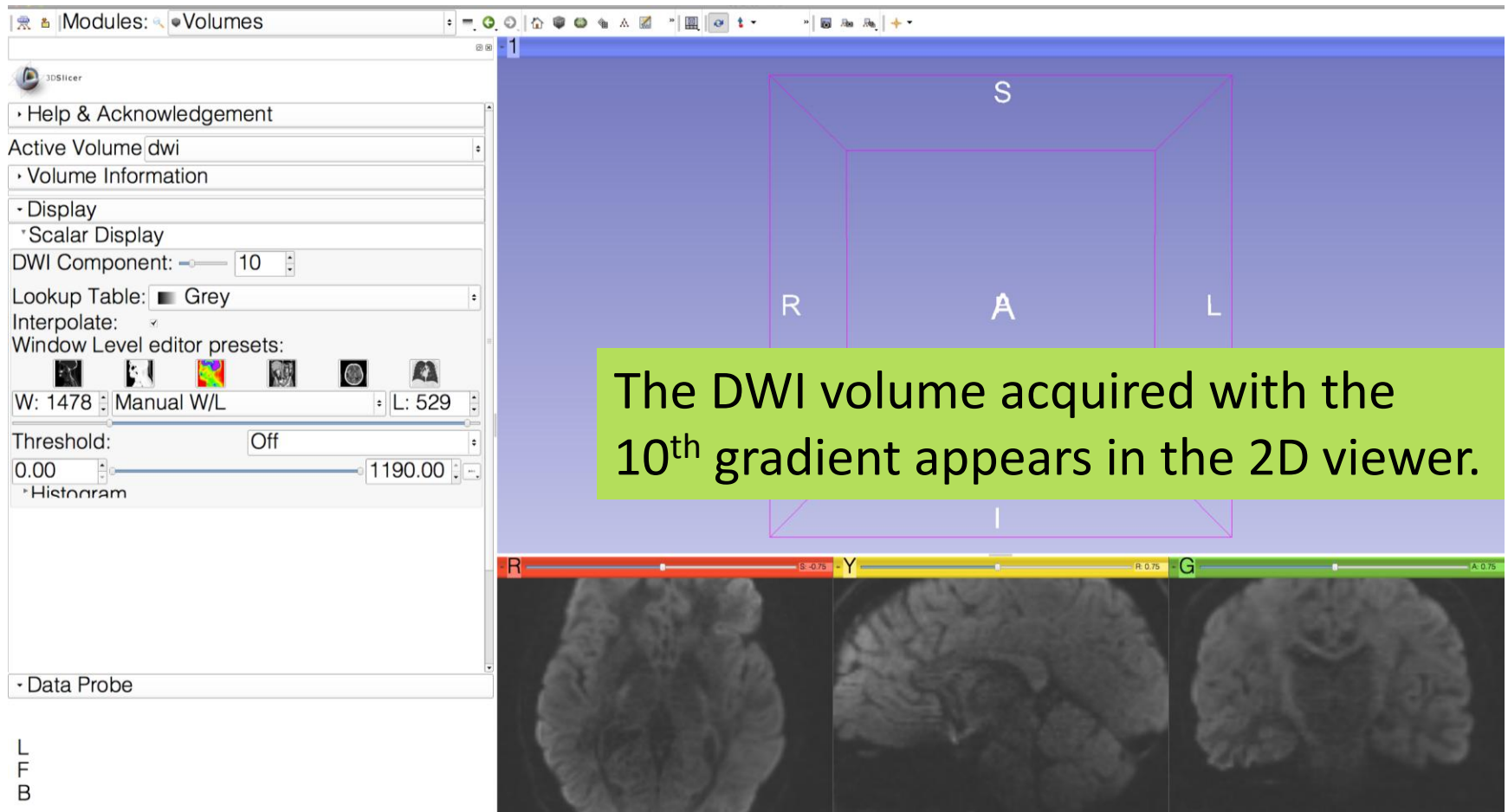


The screenshot shows the 3D Slicer software interface. On the left, the 'Volumes' panel is active, displaying the 'Active Volume dwi' section. The 'DWI Component' dropdown menu is set to '0', with a red arrow pointing to it. Below this, the 'Lookup Table' is set to 'Grey'. The 'Window Level editor' shows a range from -1000 to 4044. At the bottom, three axial brain MRI slices are displayed, with the middle slice showing a red 'R' marker.

The baseline image corresponds to the DWI Component #0.

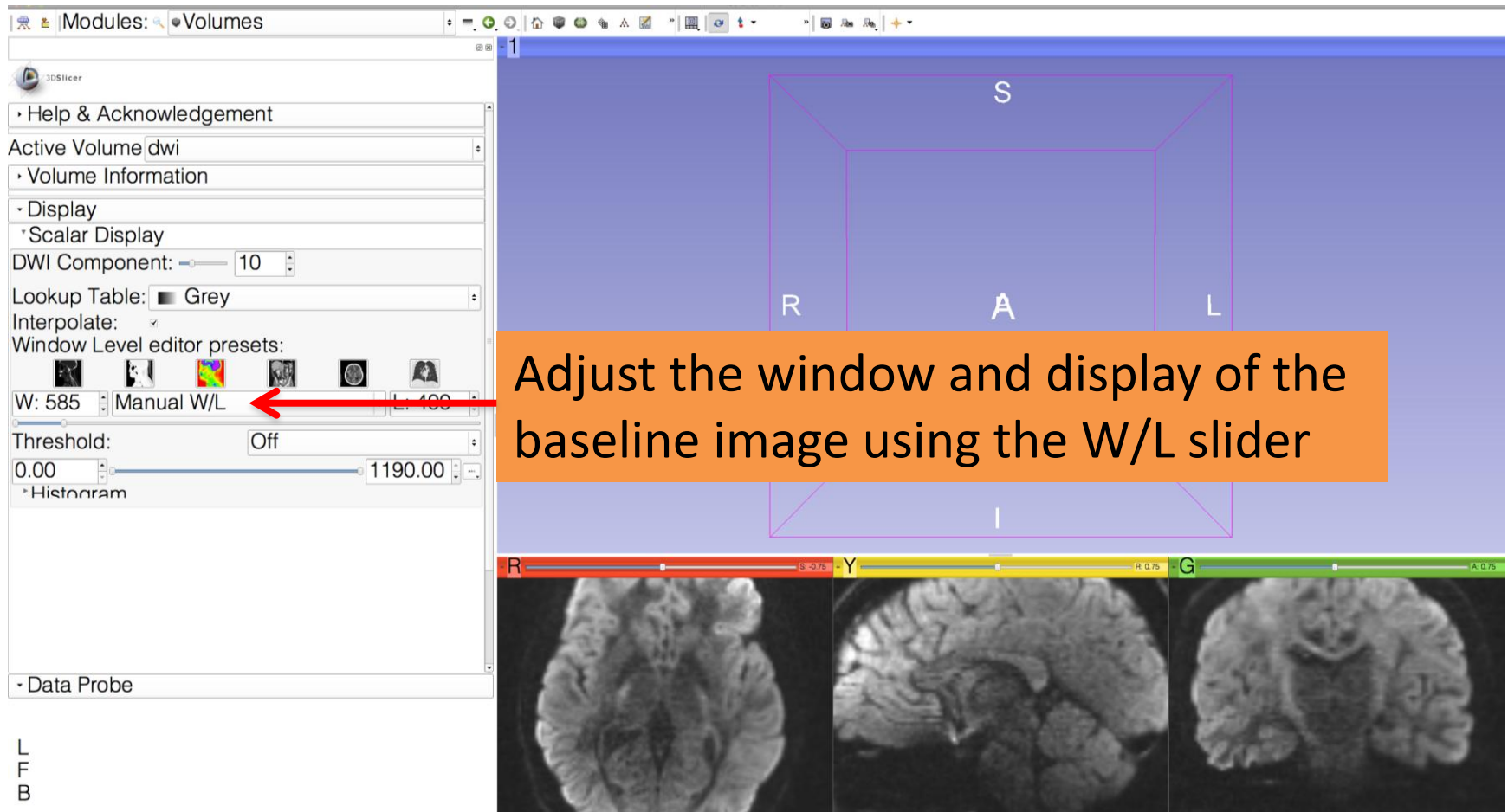
Select the DWI component #10, which corresponds to the 10th diffusion sensitizing gradient

Exploring the DWI dataset

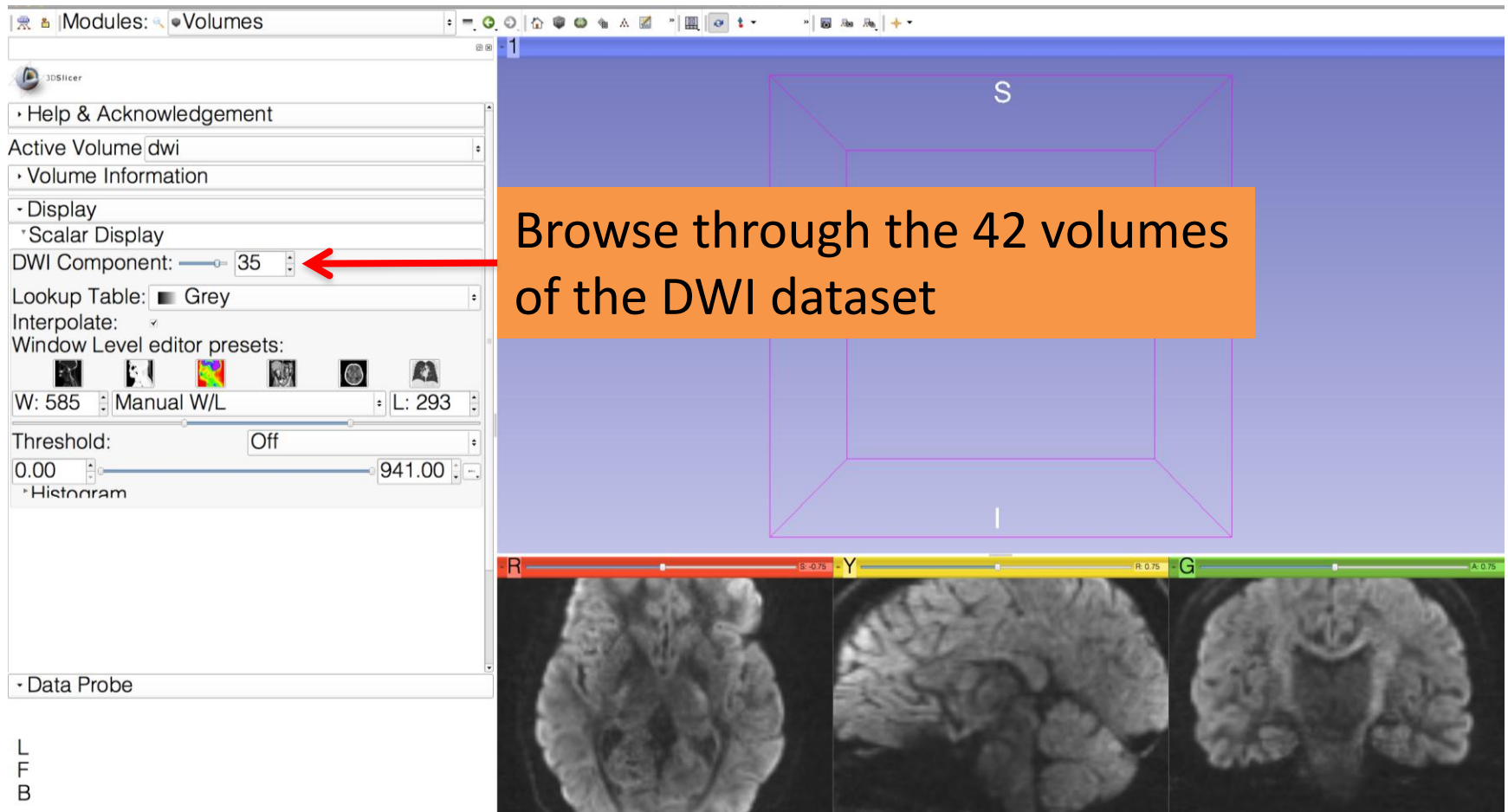


L
F
B


Exploring the DWI dataset





Exploring the DWI dataset



Exploring the DWI dataset

Left click on the push-pin icon  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 

W: 585 Manual W/L L: 293

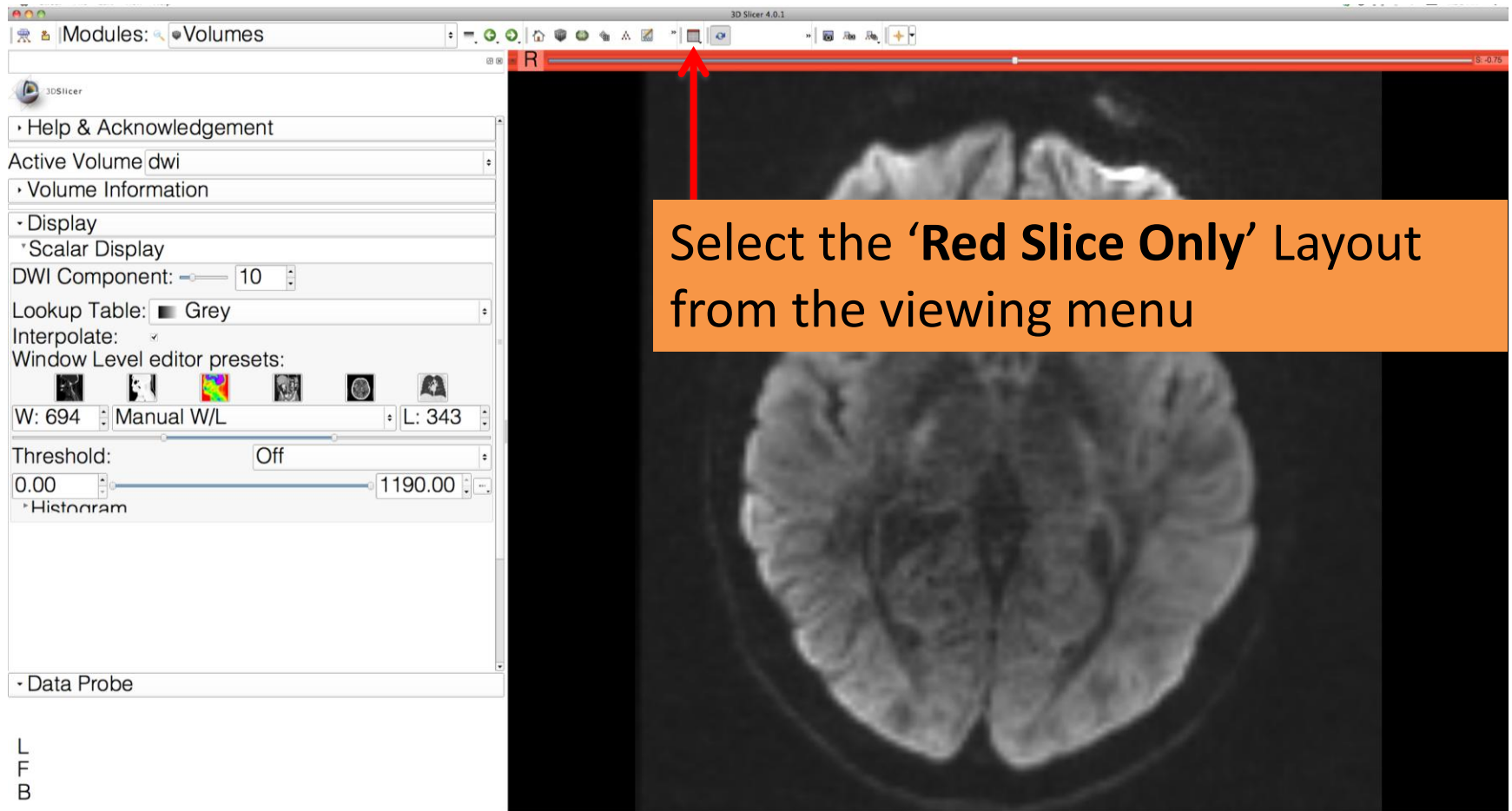
Threshold: Off 0.00 941.00

Axial

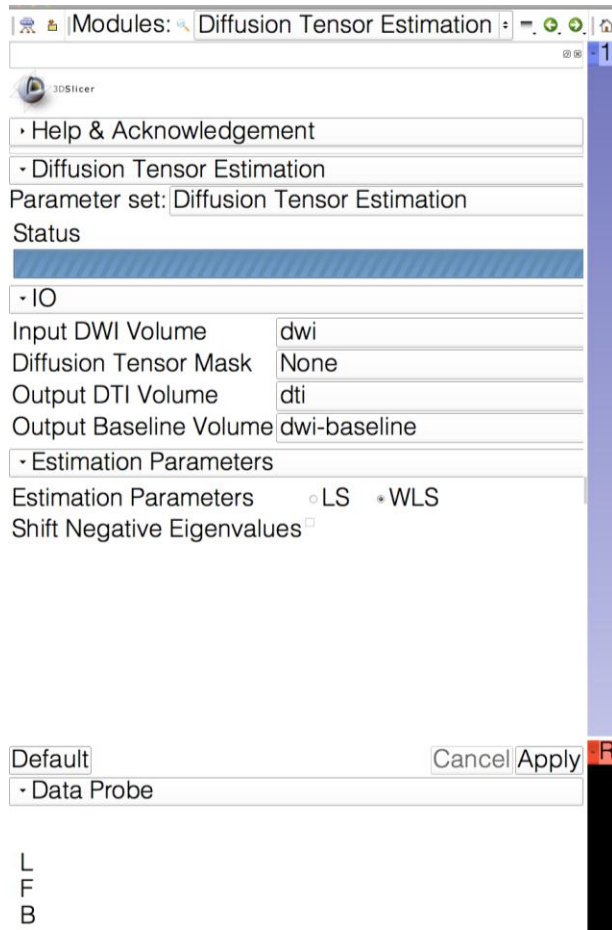
1.00	None
0.00	None
1.00	dwi

L
F
B

Exploring the DWI dataset



Diffusion Tensor Estimation



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

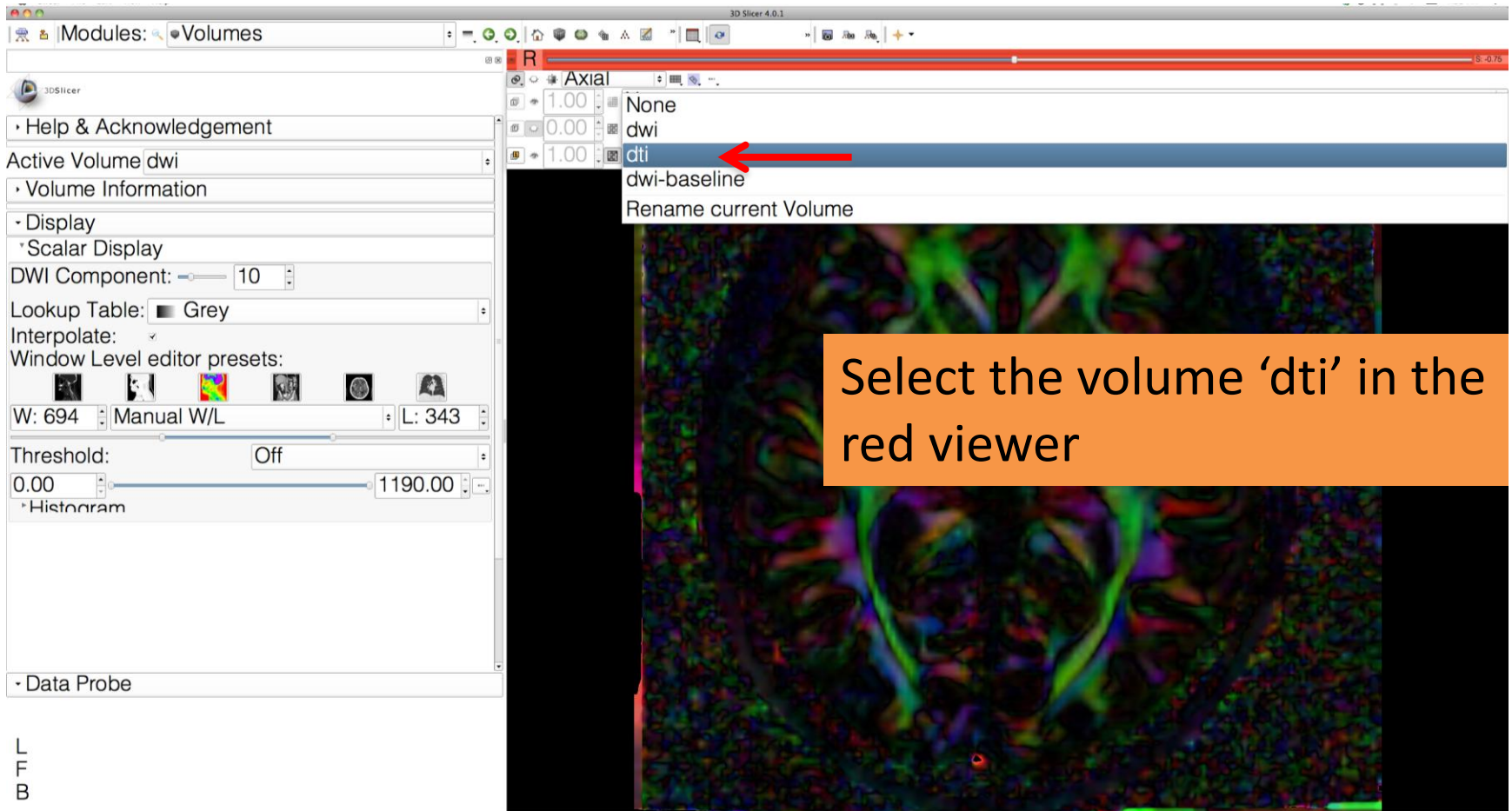
-set the **Input DWI volume** to 'dwi'

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

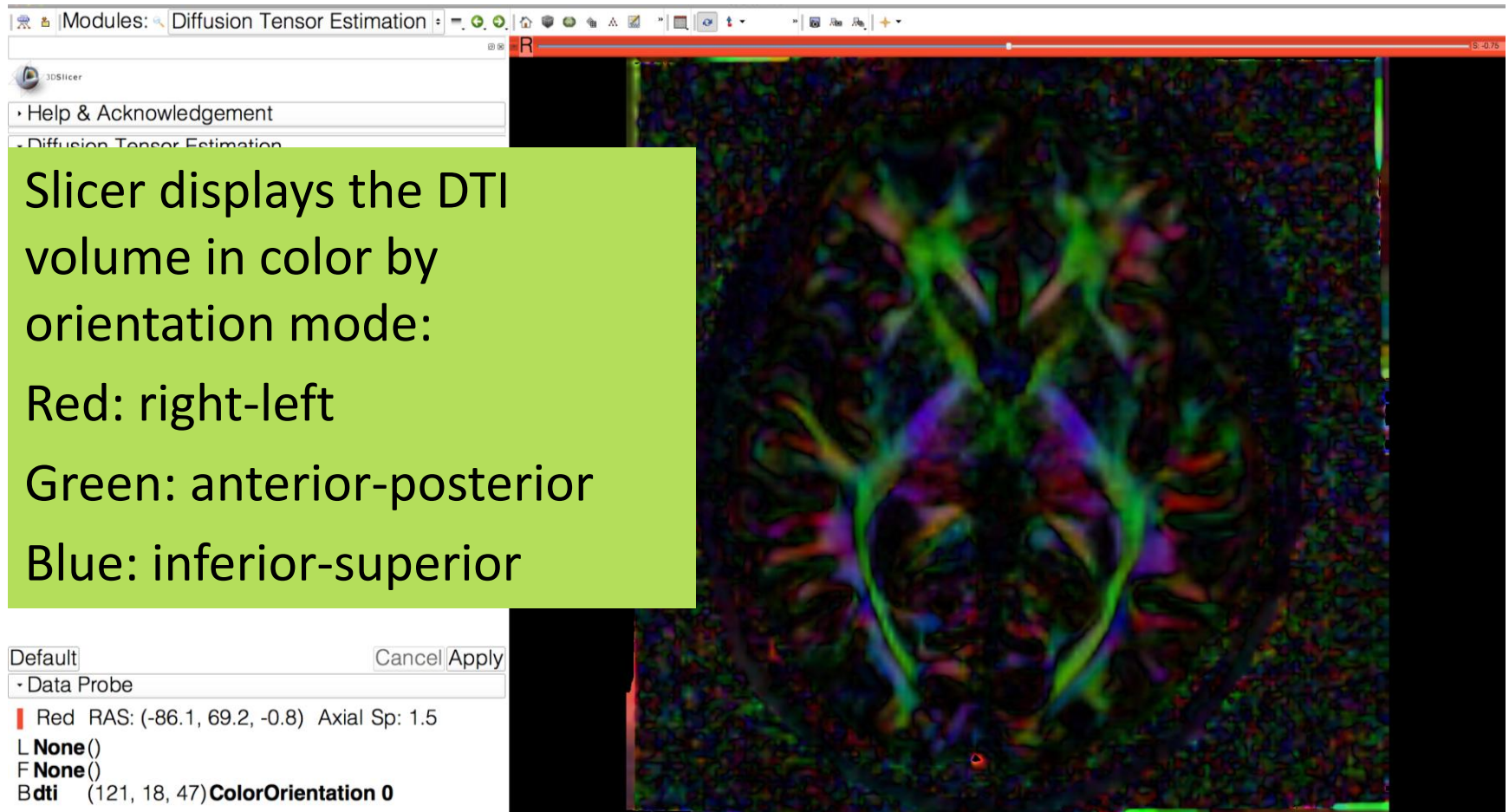
-select **Output Baseline Volume** 'Create new Volume', and rename it 'dwi-baseline'

-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

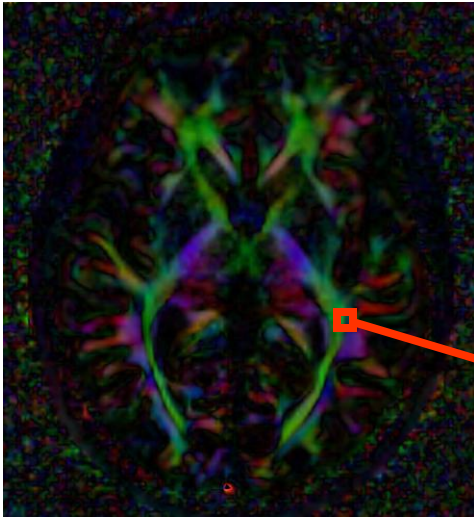
Red RAS: (-86.1, 69.2, -0.8) Axial Sp: 1.5

L **None**()

F **None**()

Bdti (121, 18, 47) **ColorOrientation 0**

Diffusion Tensor Data



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

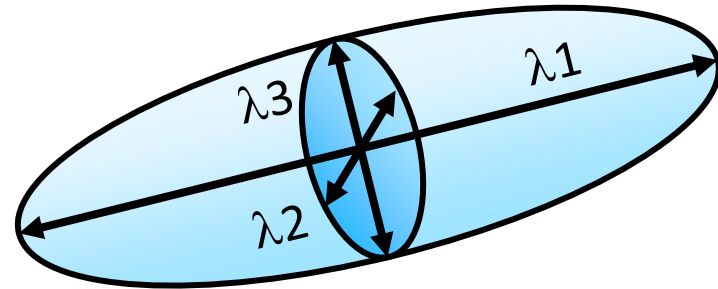
Stejskal-Tanner equation (1965)

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

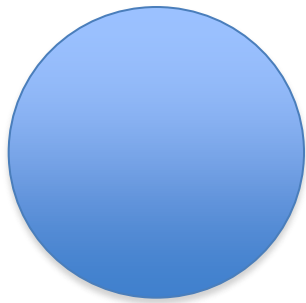
The diffusion tensor \underline{D} in the voxel (I,J,K) is a 3x3 symmetric matrix.

Diffusion Tensor

- The diffusion tensor \underline{D} in 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.

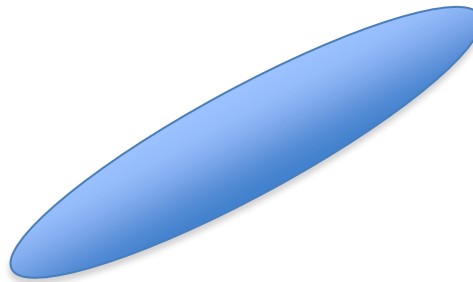


Diffusion Tensor Shape



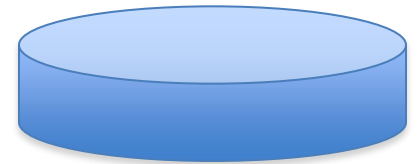
$$\lambda_1 = \lambda_2 = \lambda_3$$

Isotropic media
(CSF, gray matter)



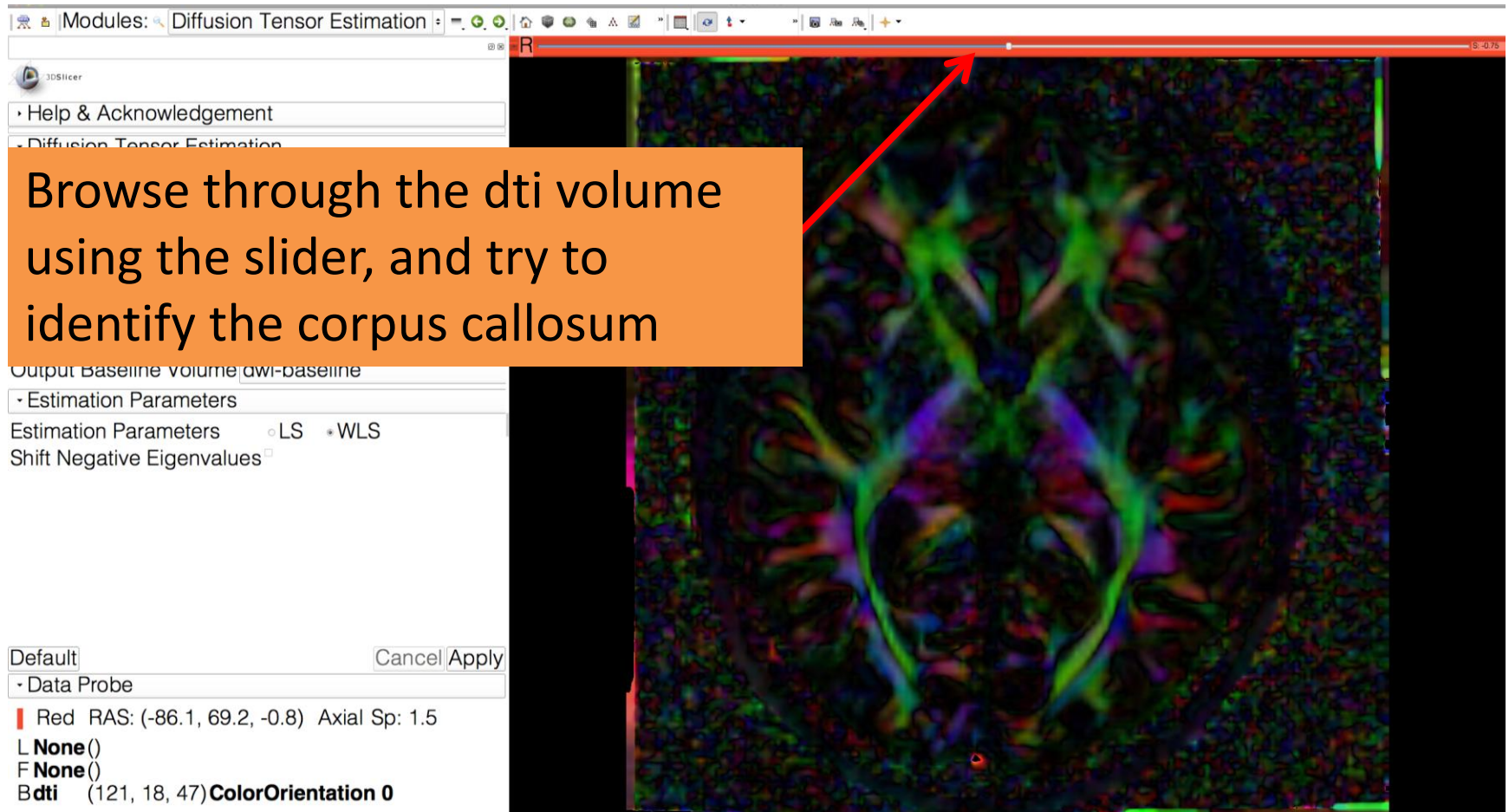
$$\lambda_1 \gg \lambda_2, \lambda_3$$

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 to identify the corpus callosum

Output Baseline volume | dwi-baseline

• Estimation Parameters

Estimation Parameters LS WLS

Shift Negative Eigenvalues

Default

• Data Probe

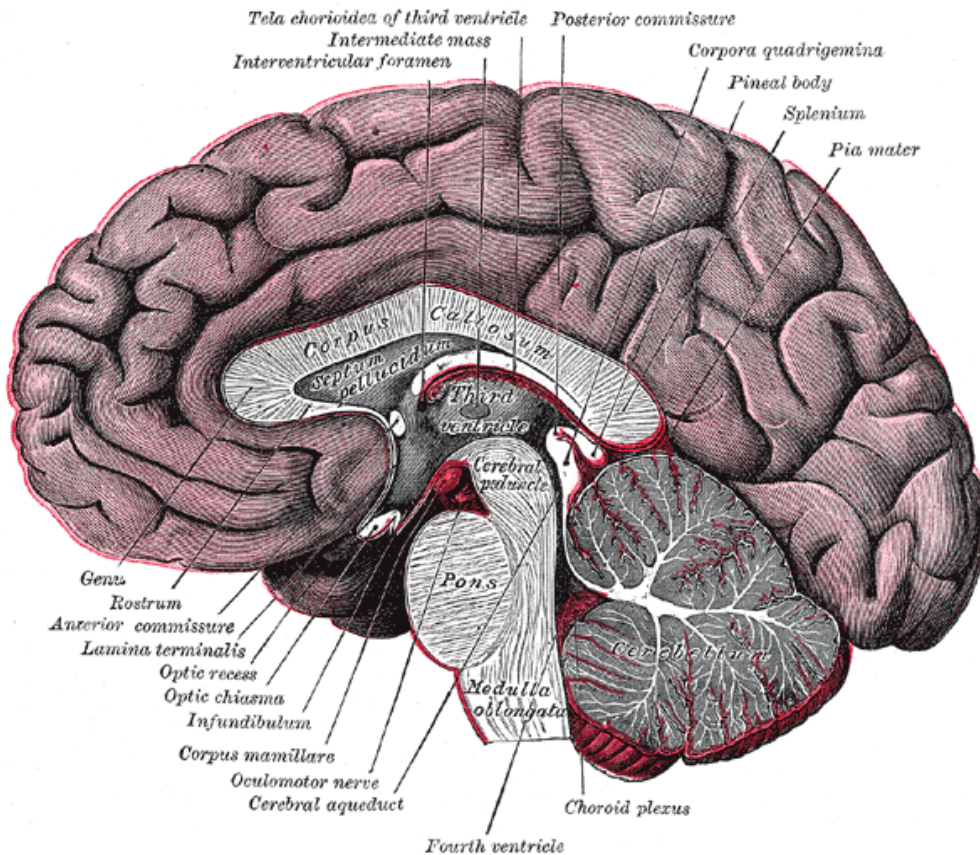
R Red RAS: (-86.1, 69.2, -0.8) Axial Sp: 1.5

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

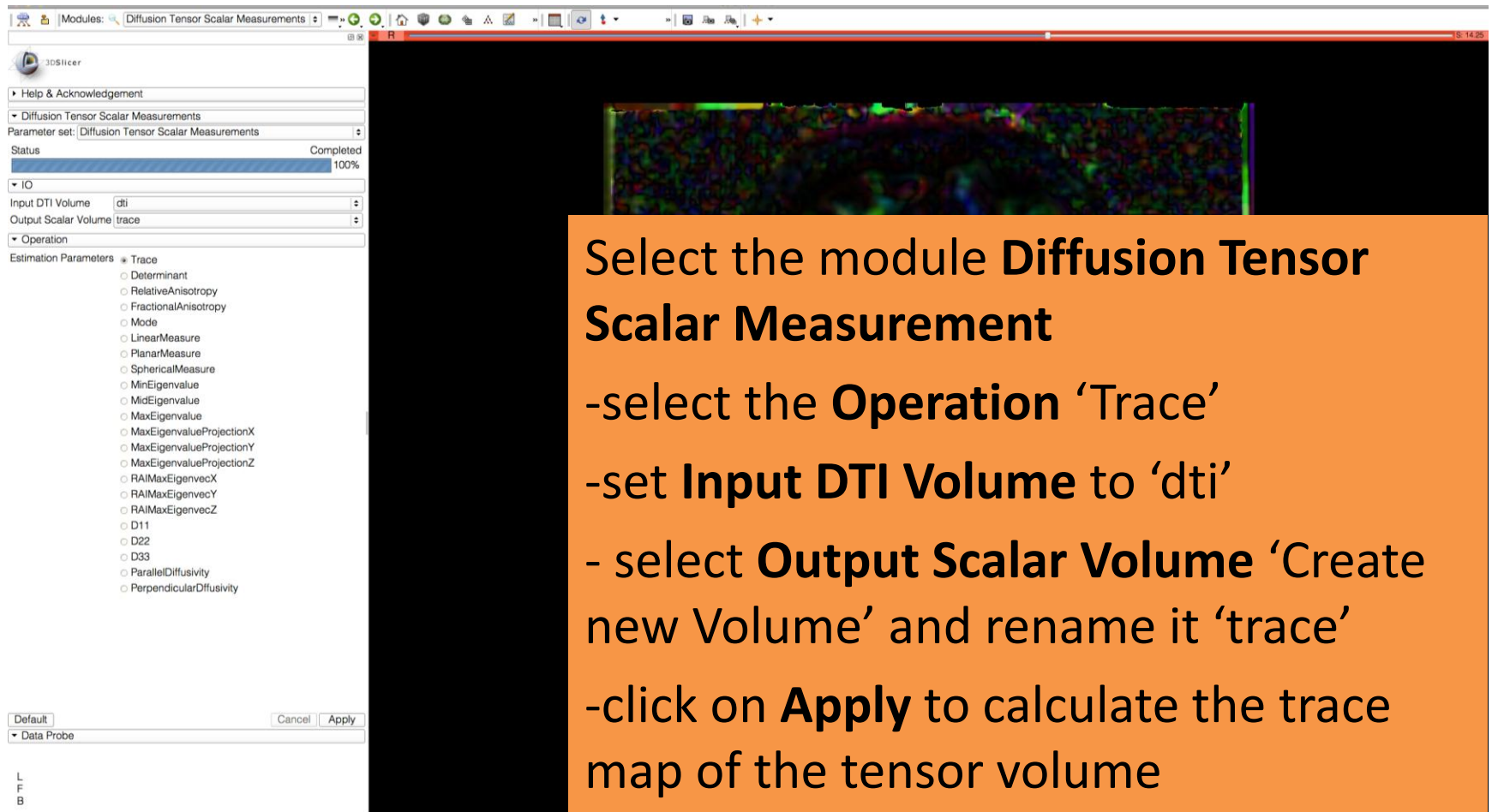
The main window shows an axial DTI brain scan with a color-coded fiber orientation map. A white arrow points from a green callout box labeled "Corpus Callosum" to the central white matter structure.

Characterizing the Shape of the tensor: Trace

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

- Trace(D) is intrinsic to the tissue and is independent of fiber orientation, and diffusion sensitizing gradient directions
- Trace(D) is a clinically relevant parameter for monitoring stroke and neurological condition
- Trace(D) is useful to characterize the size of the diffusion ellipsoid

Characterizing the Shape 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

The screenshot shows the 3D Slicer 4.0.1 interface. The 'Diffusion Tensor Scalar Measurements' module is active, with the 'IO' section showing 'Input DTI Volume' as 'dti' and 'Output Scalar Volume' as 'trace'. The 'Operation' section is set to 'Trace', with 'Determinant' selected. The '3D View' shows an axial slice of brain data with a red arrow pointing to the 'dti' volume in the foreground viewer and the 'trace' volume in the background viewer. The opacity of the 'dti' volume is set to 0.40.

Modules: Diffusion Tensor Scalar Measurements

3D Slicer

• Help & Acknowledgement

• Diffusion Tensor Scalar Measurements

Parameter set: Diffusion Tensor Scalar Measurements

Status

• IO

Input DTI Volume dti

Output Scalar Volume trace

• Operation

Estimation Parameters • Trace

- Determinant
- RelativeAnisotropy
- FractionalAnisotropy
- Mode
- LinearMeasure
- PlanarMeasure
- SphericalMeasure
- MinEigenvalue
- MidEigenvalue

Default Cancel Apply

• Data Probe

L
F
B

Axial

1.00 None

0.40 dti

.00 trace

Select the volume 'dti' in the Foreground viewer and the volume 'trace' in the Background viewer
Set the opacity of the dti volume to 0.40

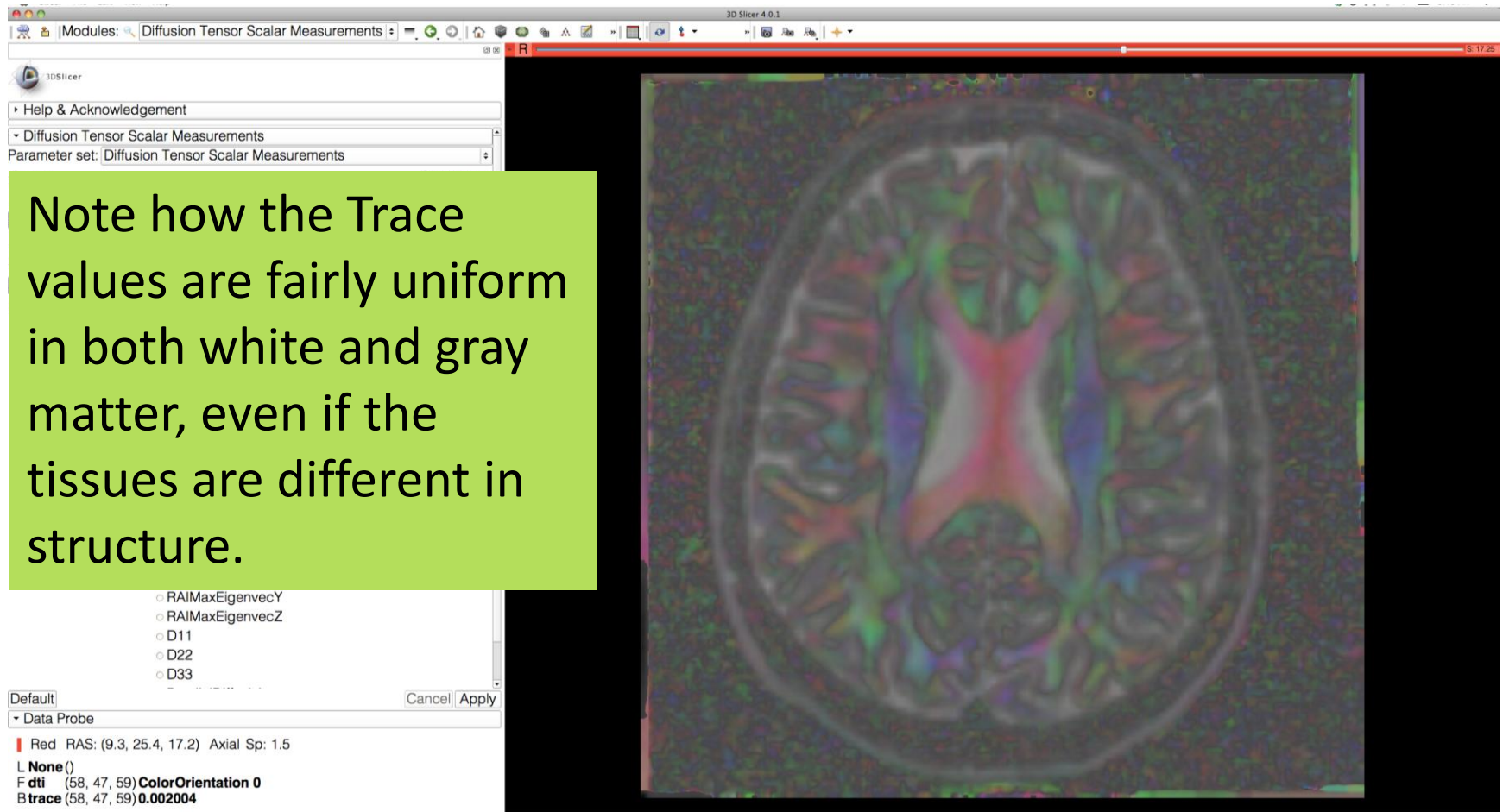
Exploring the Diffusion Tensor Data

Move the mouse cursor in the 2D view, and observe the values of the trace in the corpus callosum and in the adjacent gray matter.

MaxEigenvalueProjectionZ
RAI MaxEigvecX
RAI MaxEigvecY
RAI MaxEigvecZ
D11
D22
D33

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

Characterizing the Shape 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.

RAIMaxEigenvecY
RAIMaxEigenvecZ
D11
D22
D33

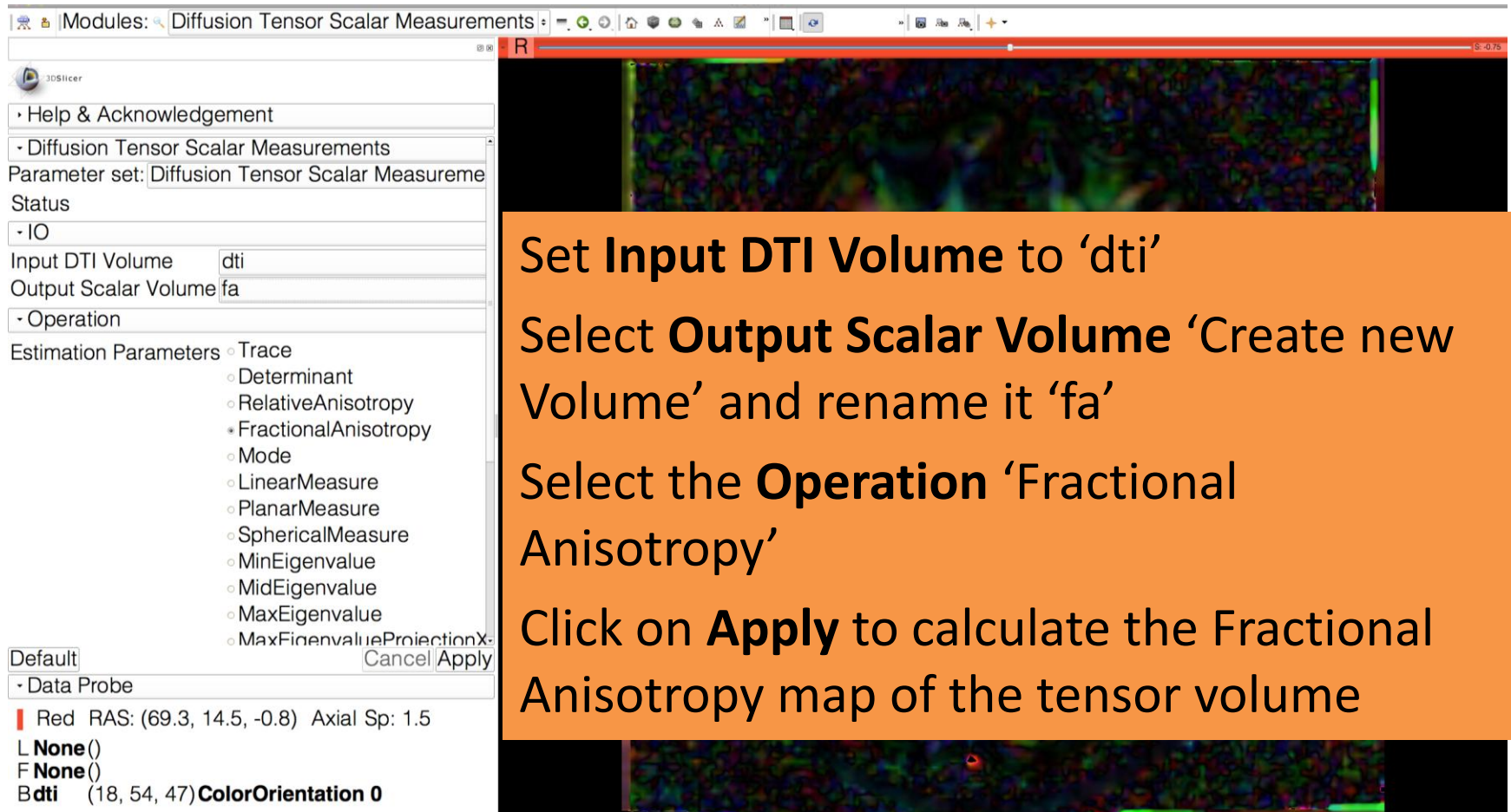
Default
Data Probe
Red RAS: (9.3, 25.4, 17.2) Axial Sp: 1.5
L None()
F dti (58, 47, 59) ColorOrientation 0
B trace (58, 47, 59) 0.002004

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



Set **Input DTI Volume** to 'dti'

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

Select the **Operation** 'Fractional Anisotropy'

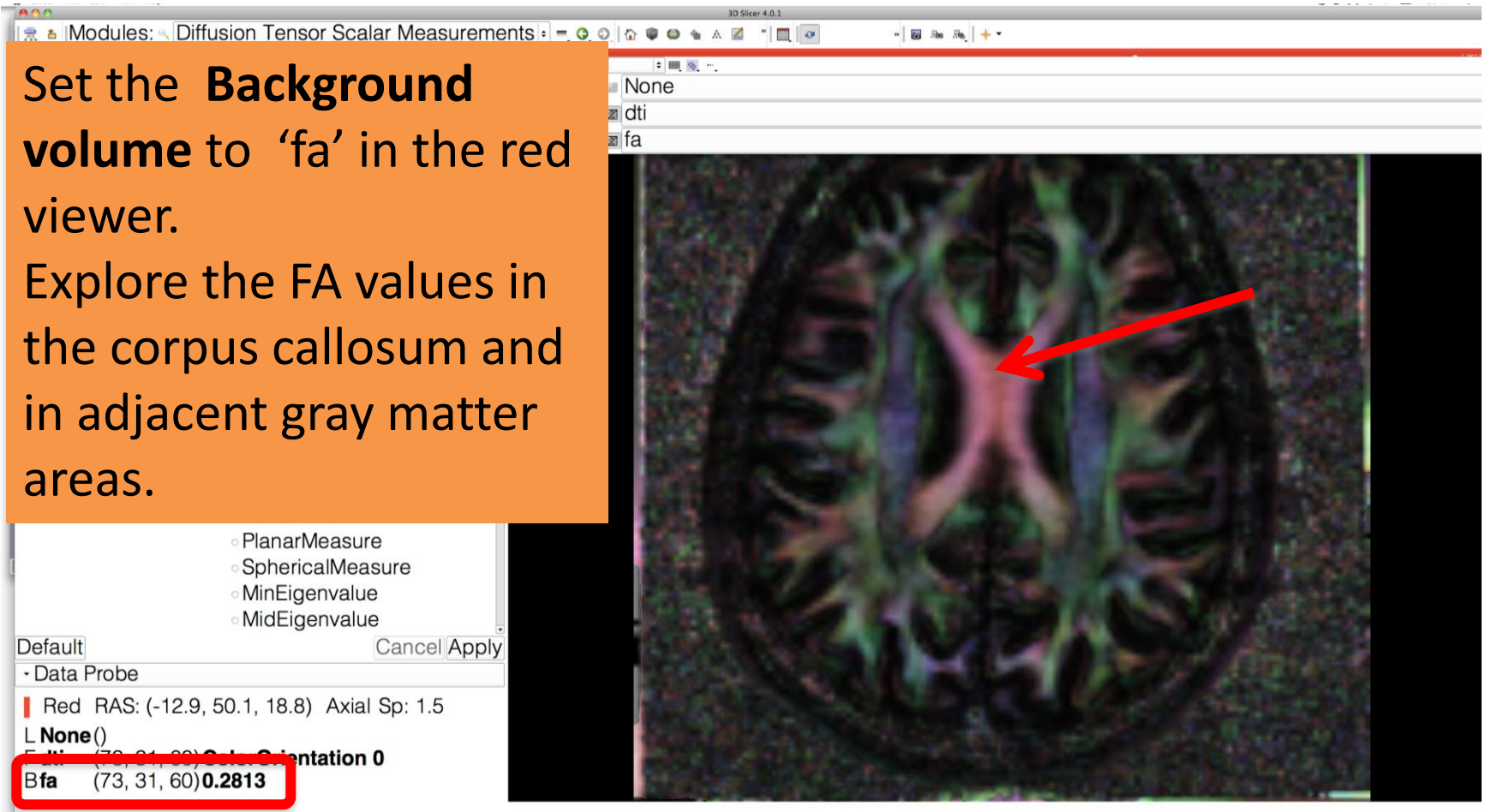
Click on **Apply** to calculate the Fractional Anisotropy map of the tensor volume

3D Slicer
Modules: Diffusion Tensor Scalar Measurements
Parameter set: Diffusion Tensor Scalar Measurements
Status
- IO
Input DTI Volume dti
Output Scalar Volume fa
- 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()
Bdti (18, 54, 47) ColorOrientation 0

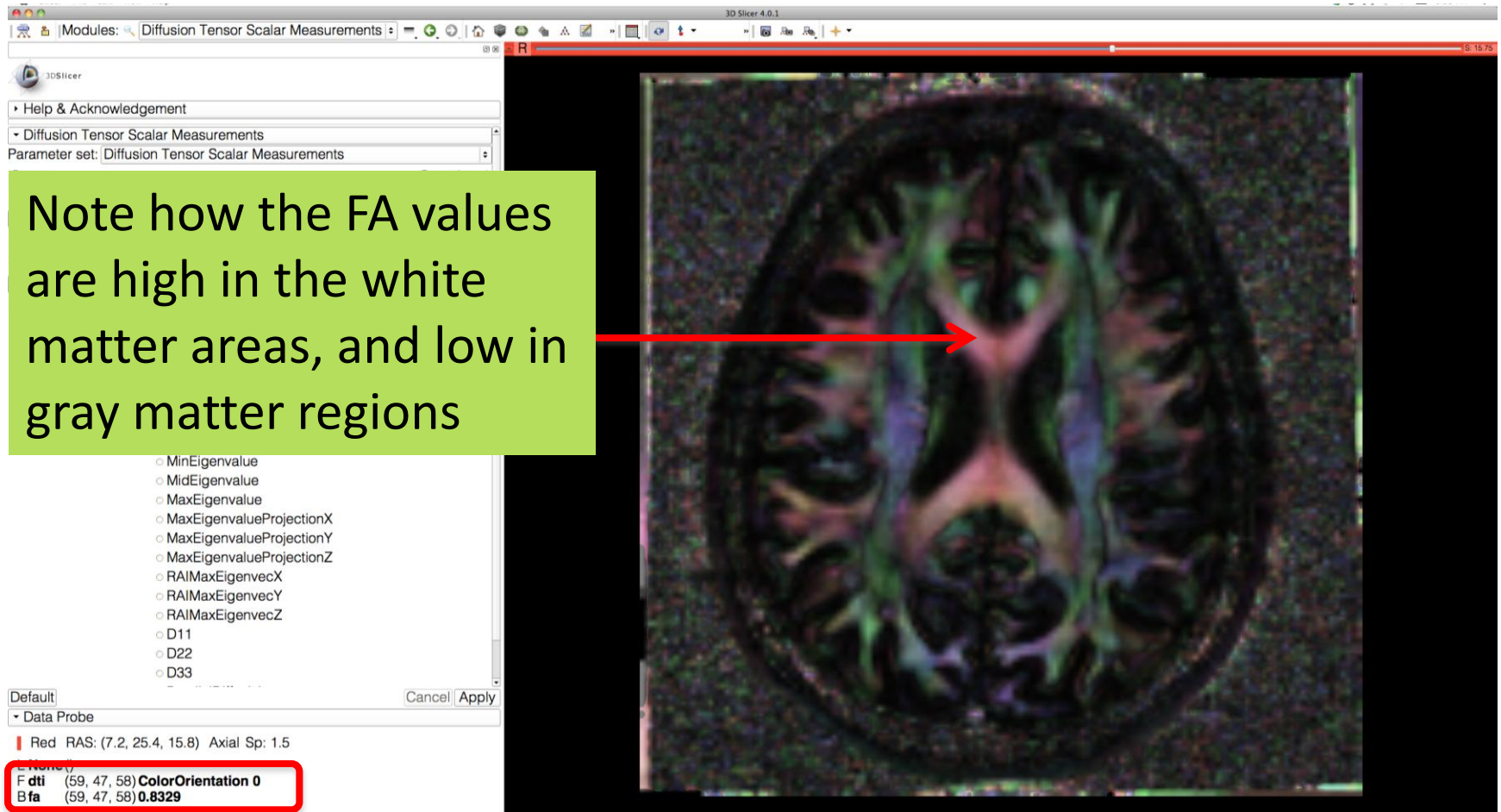
Fractional Anisotropy

Set the **Background volume** to 'fa' in the red viewer.

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

- 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

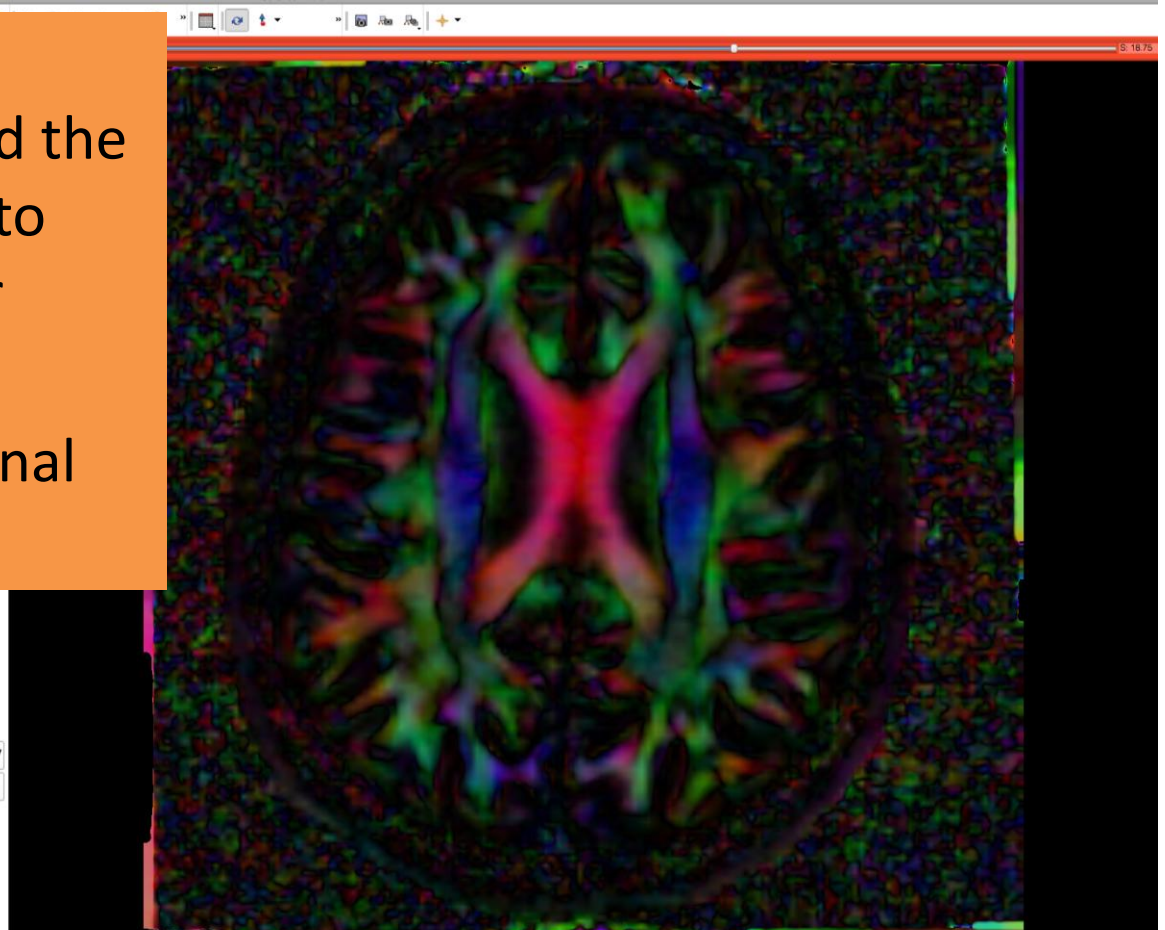
F dti	(59, 47, 58)	ColorOrientation 0
B fa	(59, 47, 58)	0.8329

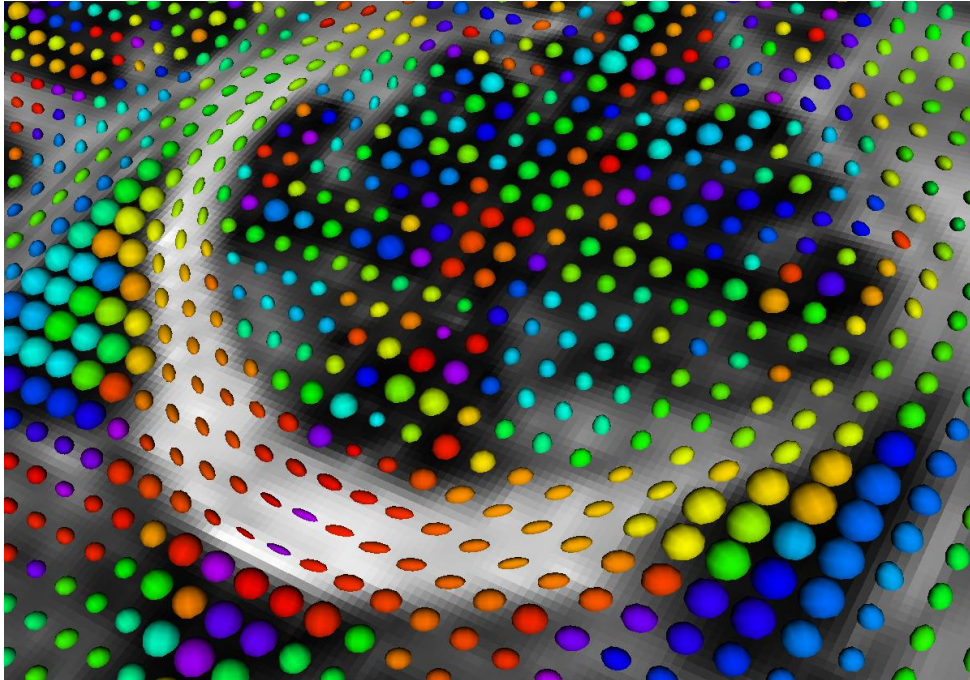
Fractional Anisotropy

Set the **Foreground volume** to 'None', and 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**()
B **dti** (66, 0, 60) **ColorOrientation 0**





Part 2: Visualizing the tensor data

3D Visualization: Glyphs

The screenshot shows the 3D Slicer software interface. The 'Volumes' module is active, and the 'Active Volume' is set to 'dti'. The 'Scalar Display' panel is visible, showing 'Scalar Mode' set to 'ColorOrientation'. The 'Lookup Table' is set to 'Grey'. The 'Interpolate' checkbox is checked. The 'Window Level editor presets' are shown. The 'Threshold' is set to 'Off'. The 'Histogram' is visible. The 'Glyphs on Slices Display' panel is visible, showing 'Slice Visibility' for Red, Yellow, and Green. The 'Opacity' is set to 1.00. The 'Scalar ColorMap' is set to 'Rainbow'. The 'Color by Scalar' is set to 'FractionalAnisotropy'. The 'Scalar Range' is set to 0.00 to 1.00. The 'Glyph Type' is set to 'Ellipsoids'. The 'Scale Factor' is set to 50.00. The 'Spacing' is set to 5.00. The 'Data Probe' panel is visible. The 3D view shows a cross-section of a brain with DTI glyphs (ellipsoids) colored by fractional anisotropy. The glyphs are colored in a rainbow spectrum, with red indicating high fractional anisotropy and blue indicating low fractional anisotropy. The glyphs are oriented along the principal diffusion directions. The 3D view is overlaid on a grid with axes labeled R (Red), Y (Yellow), and G (Green).

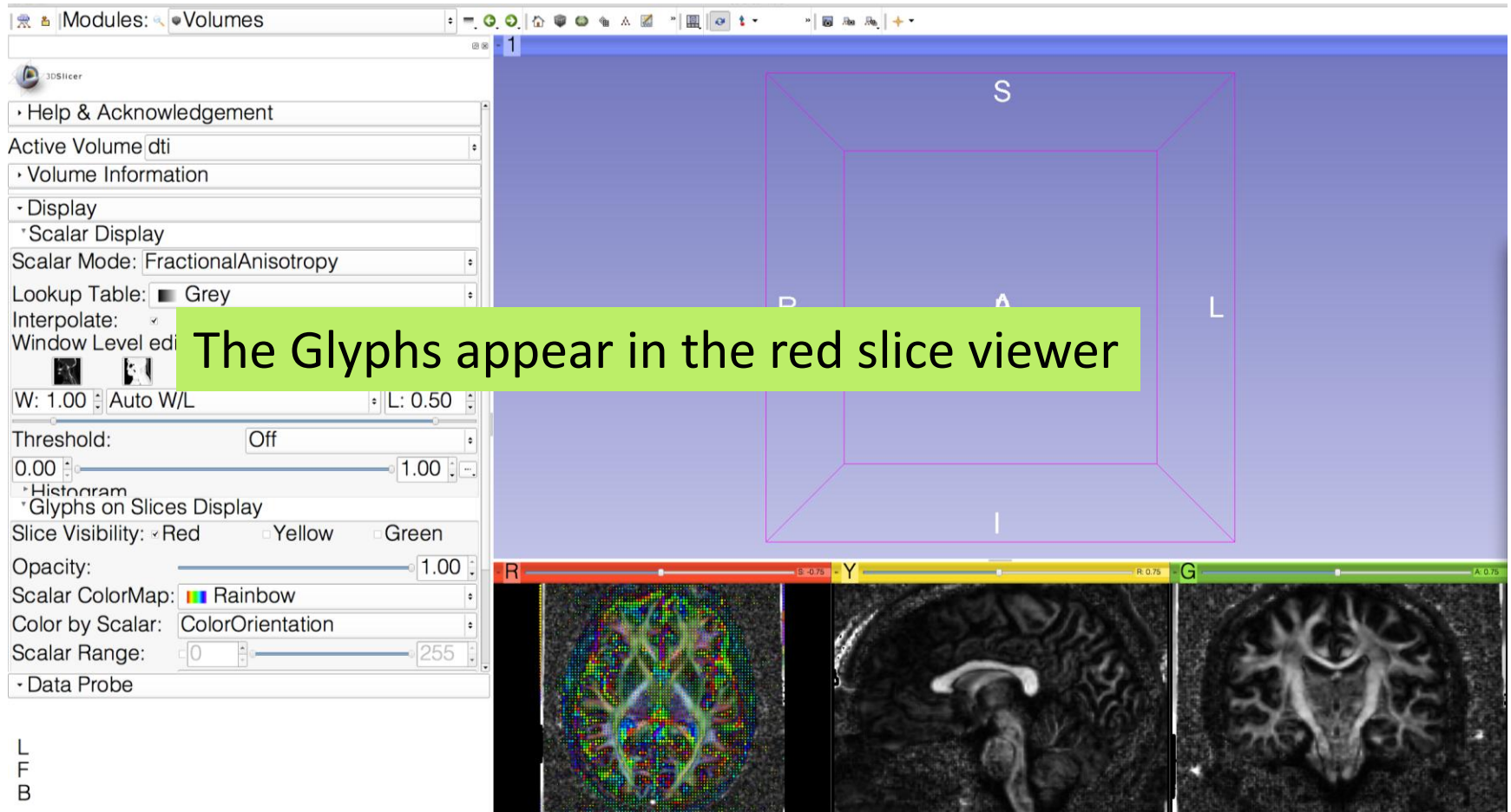
Select the module **Volumes**, and set the **Active Volume** to 'dti'

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


3D Visualization: Glyphs


The screenshot shows the 3D Slicer software interface. The 'Volumes' panel on the left contains the 'Glyphs on Slices Display' section, which is highlighted with a red box. This section includes settings for 'Slice Visibility' (with 'Red' selected), 'Opacity' (set to 1.00), 'Scalar ColorMap' (set to 'Rainbow'), 'Color by Scalar' (set to 'FractionalAnisotrop'), and 'Scalar Range' (set from 0.00 to 1.00). The main 3D view area shows a brain slice with 'R', 'A', and 'L' labels. An orange callout box points to the 'Auto W/L' button in the 'Window Level editor presets' section, with the text: 'Click on Auto W/L to adjust the Window and Level values of the display'. Another orange callout box at the bottom right contains the text: 'In the Glyphs on Slices Display panel, set the Color by Scalar parameter to 'ColorOrientation', and check 'Slice Visibility' 'Red''.

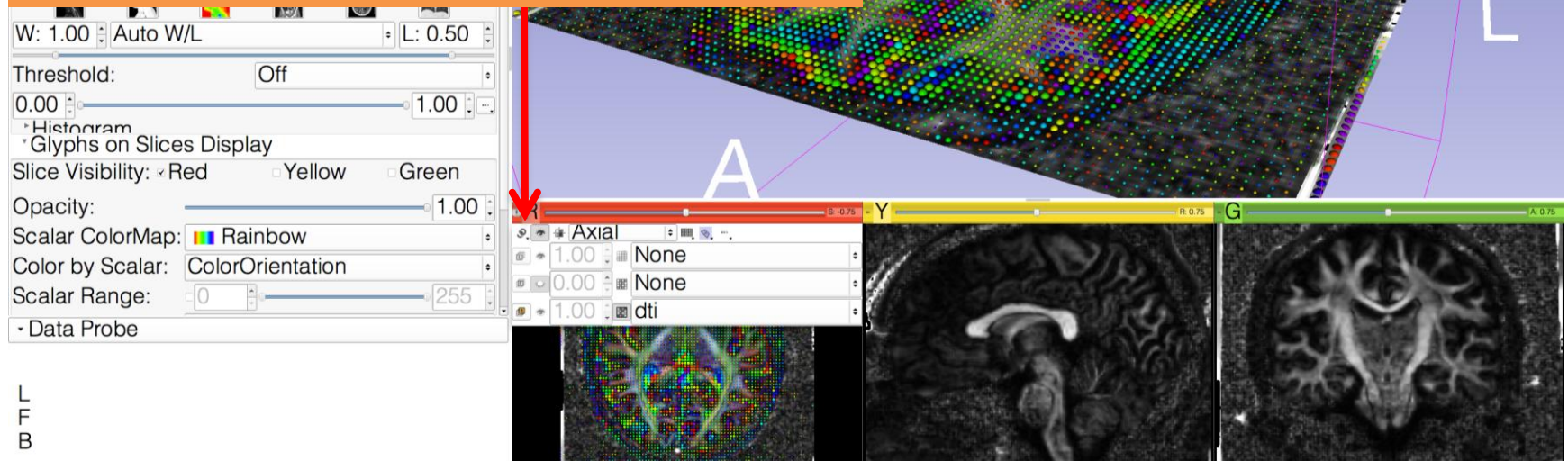
3D Visualization: Glyphs



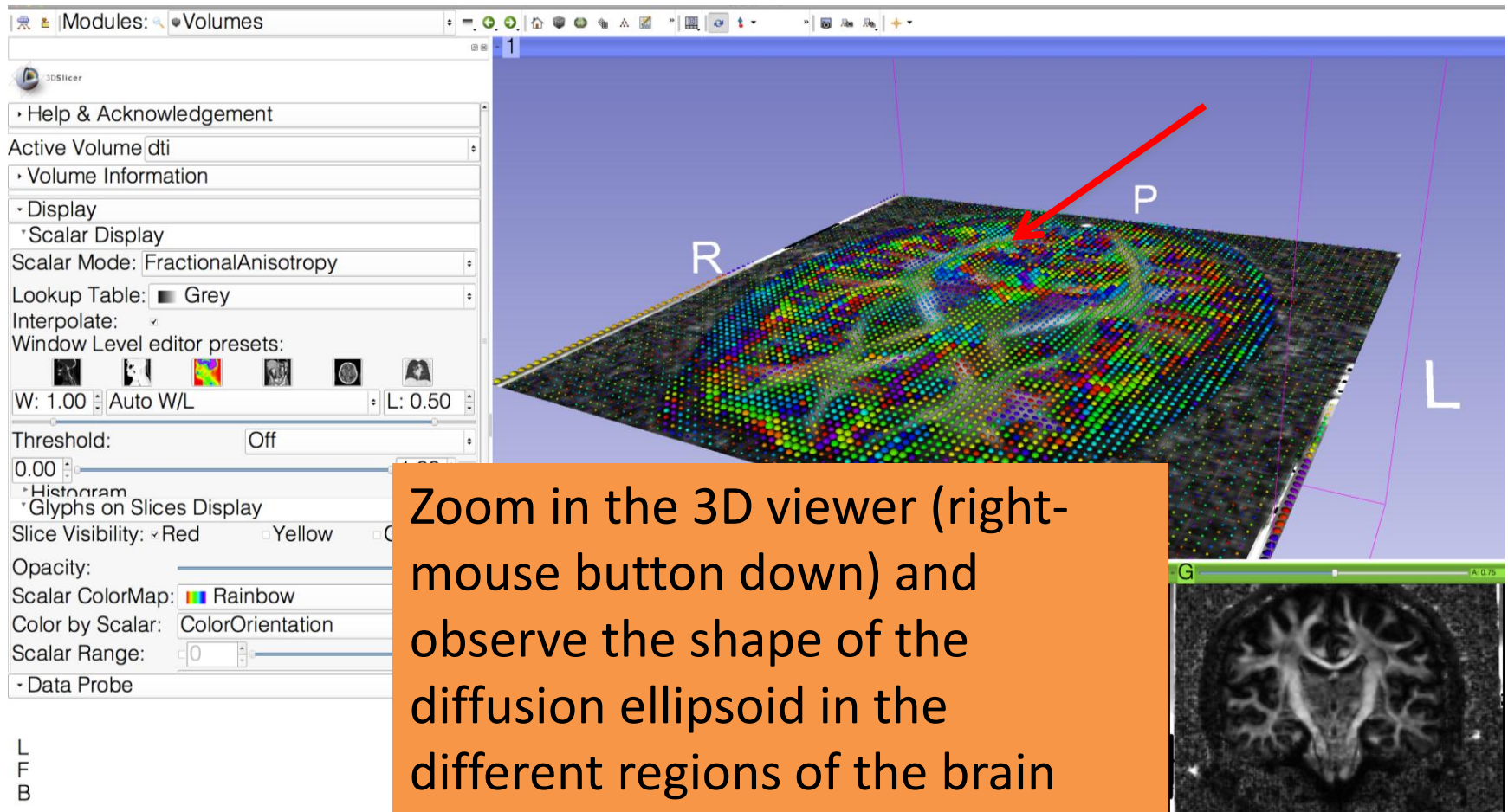
3D Visualization: Glyphs

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

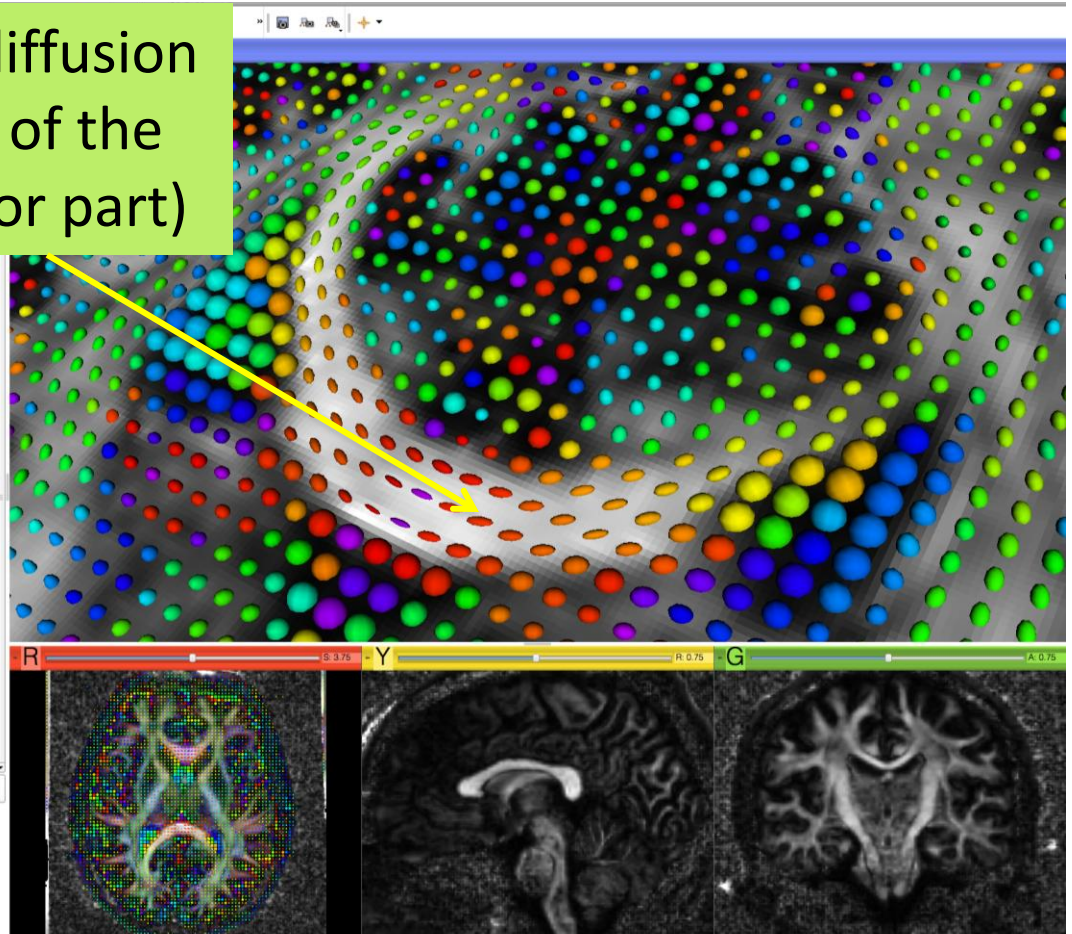
Scalar Range: 0 | 255

Glyph Type: Ellipsoids

Scale Factor: 45.00

Spacing: 5.00

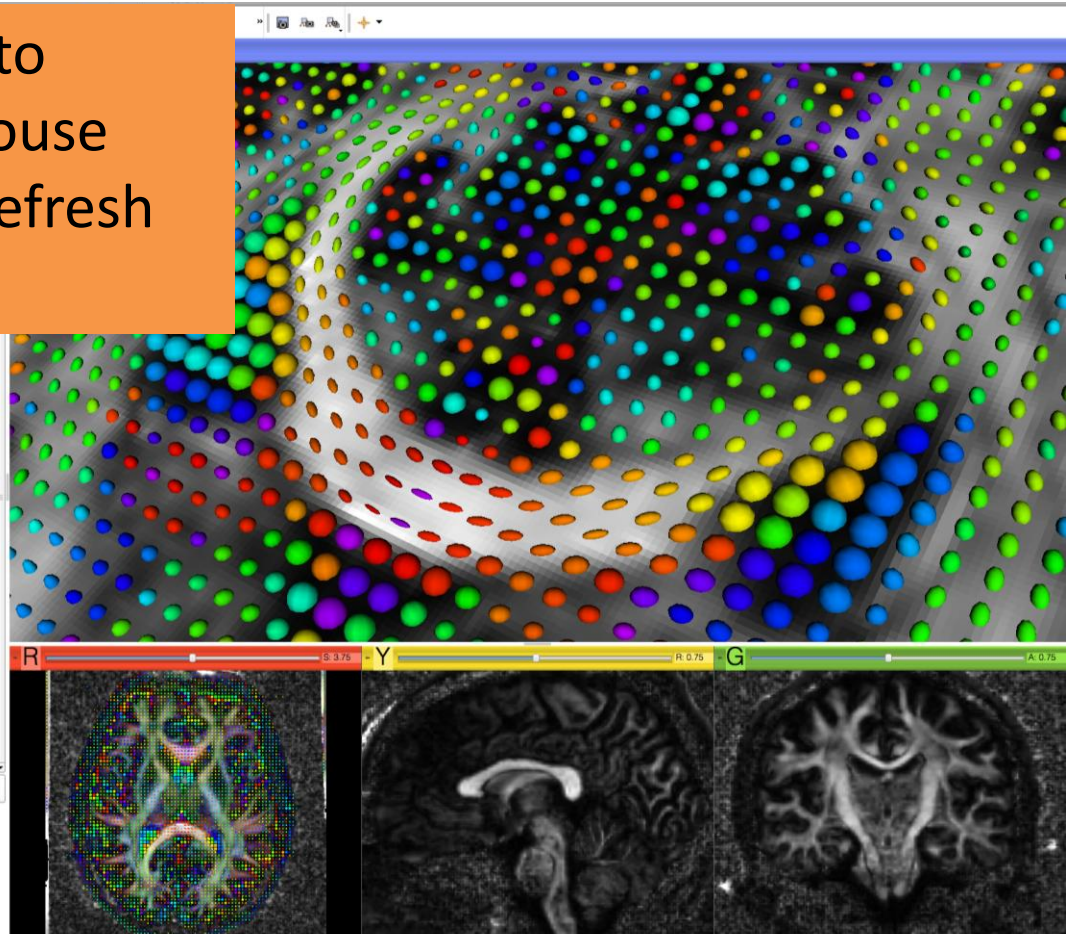
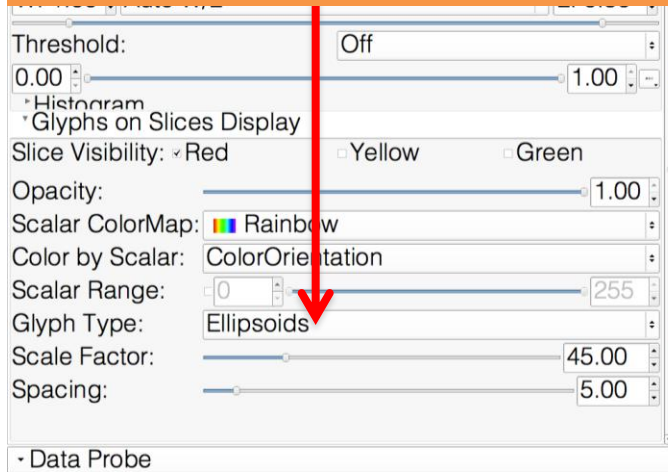
• Data Probe



L
F
B

3D Visualization: Glyphs

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



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

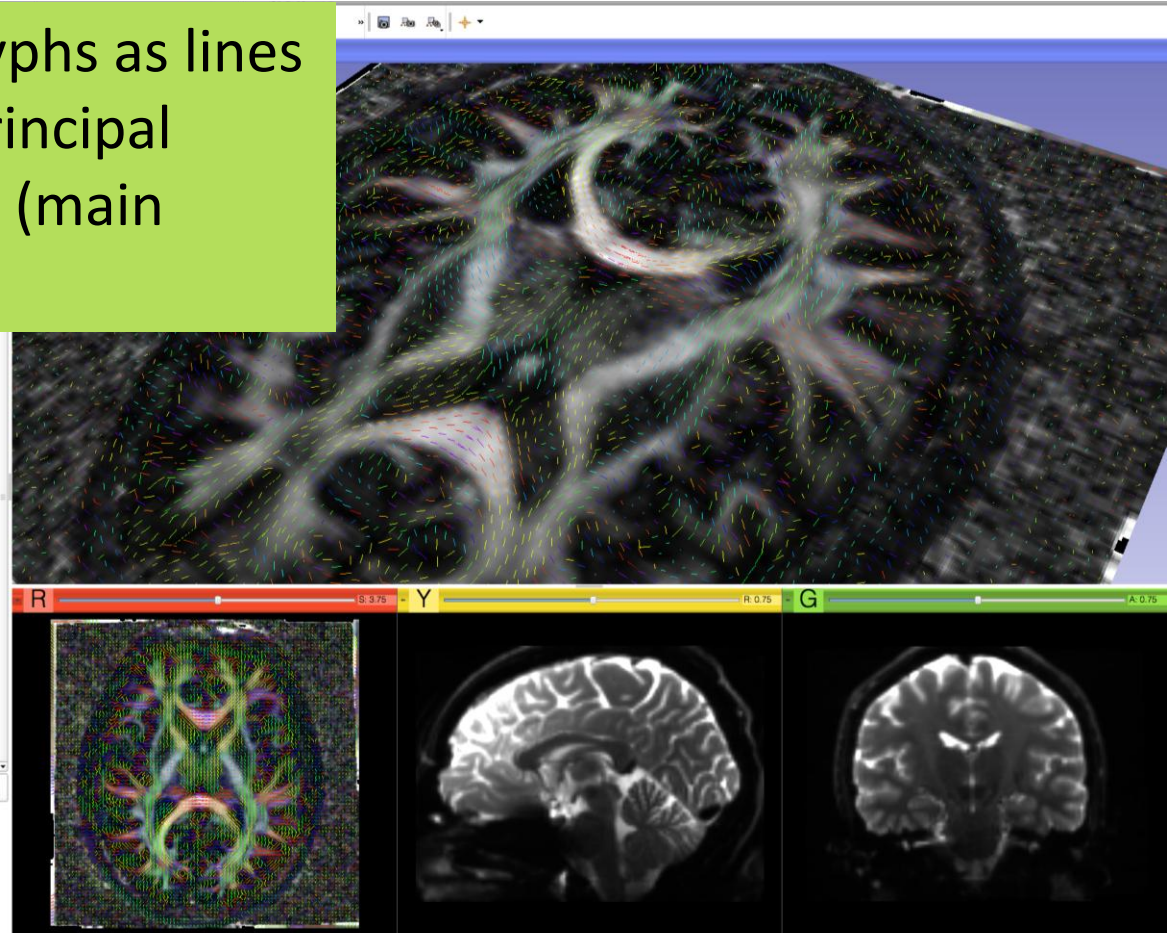
Glyph Type: Lines

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

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.

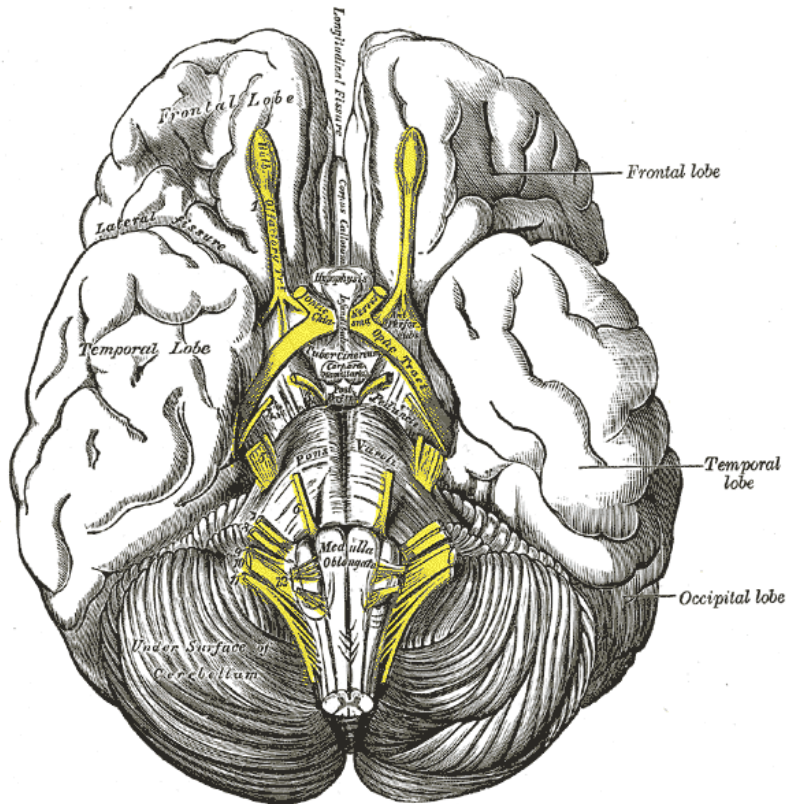
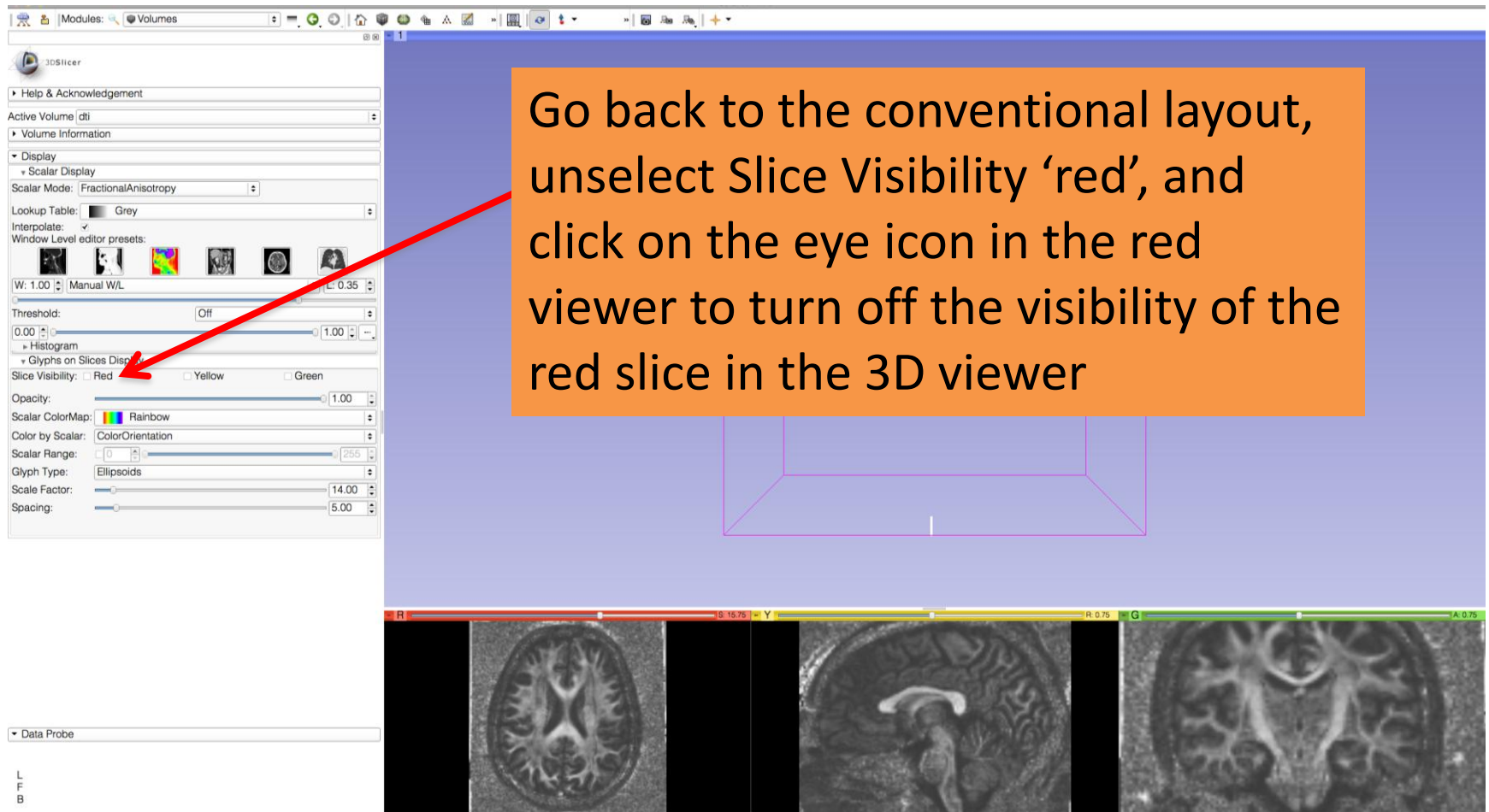
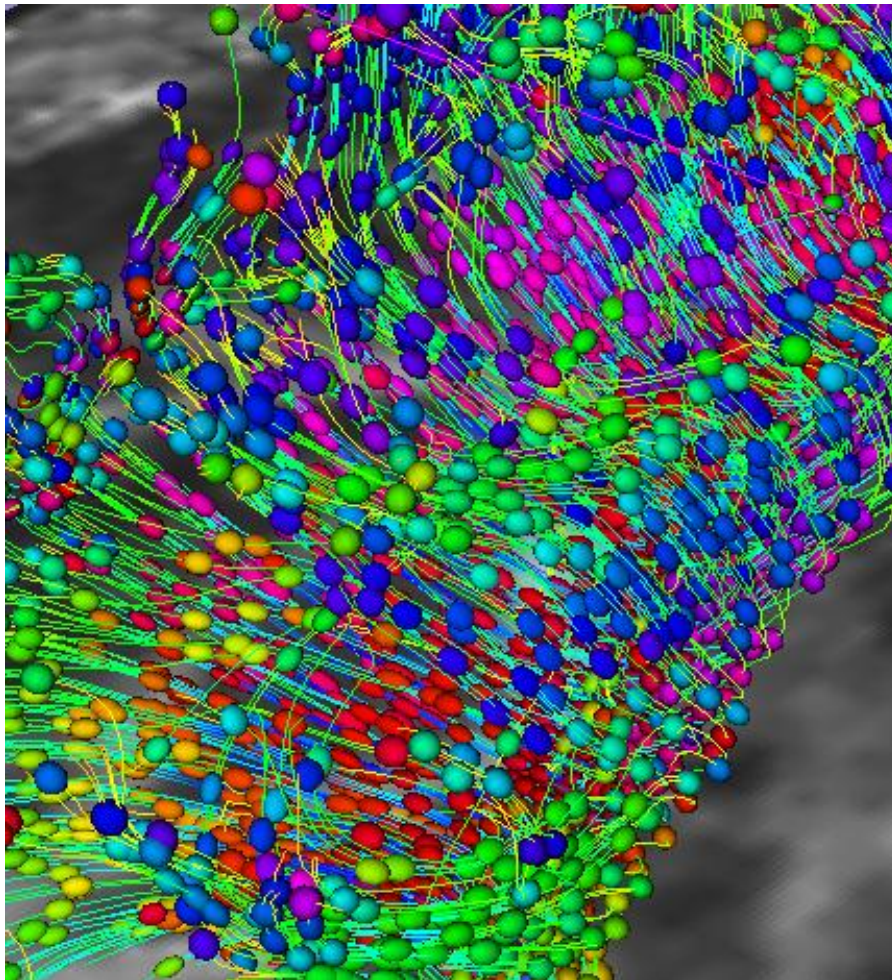


Image from Gray's Anatomy

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

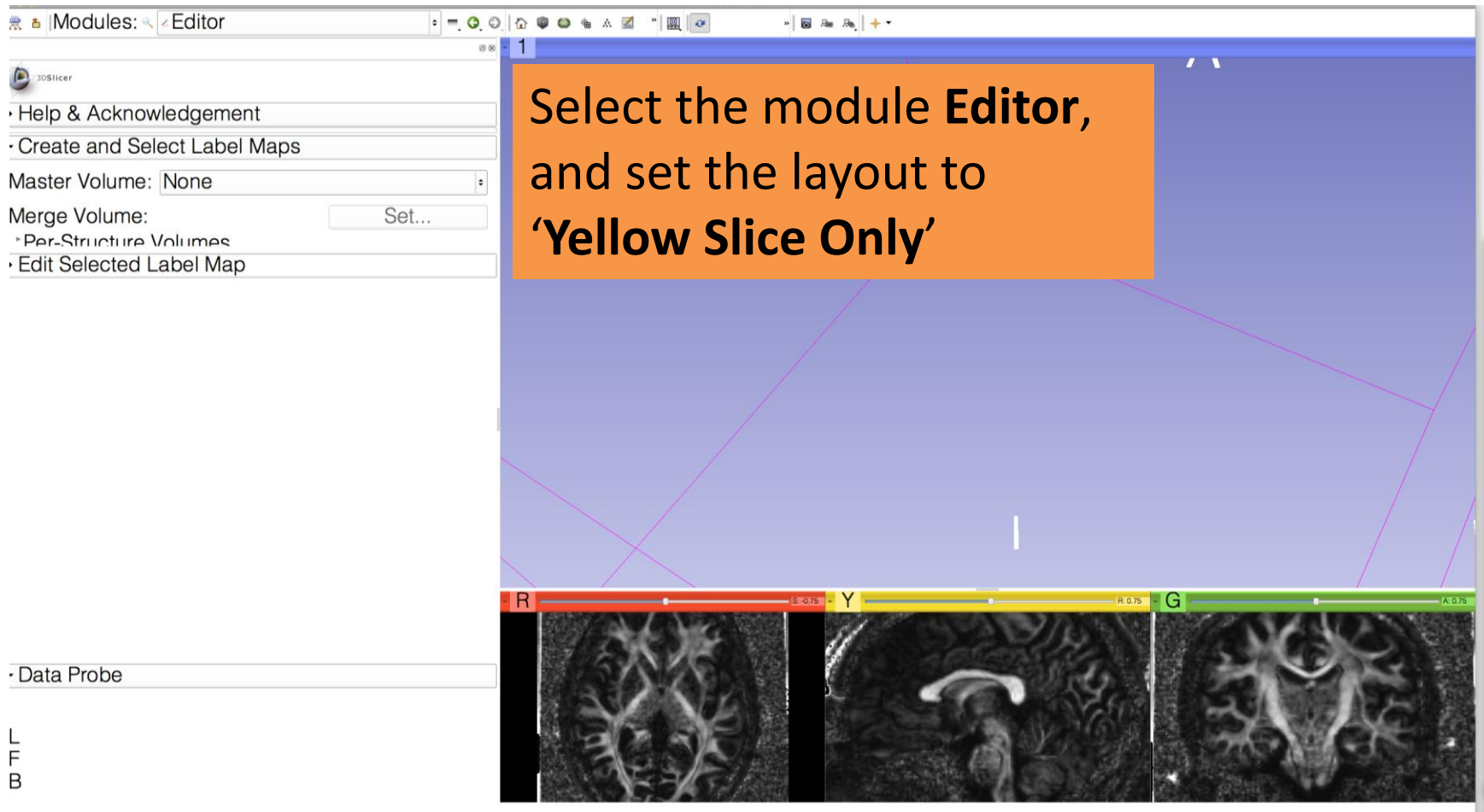


Part 3: From tensors to tracts

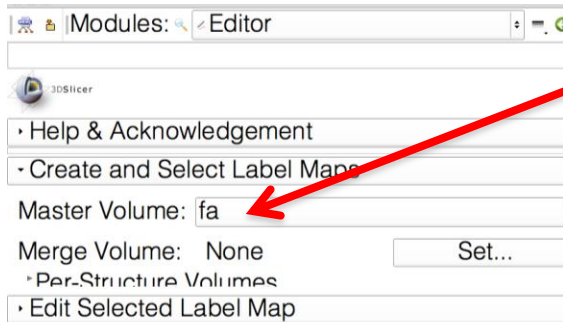
Diffusion MRI tractography

- 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

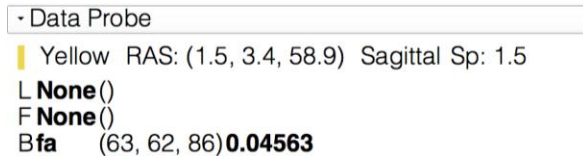
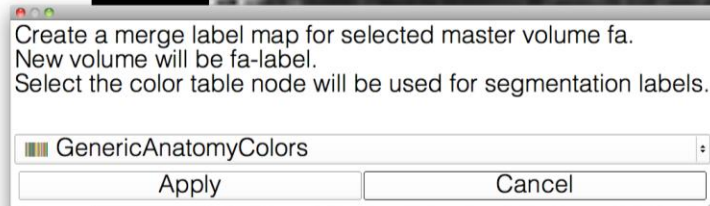


ROI Definition

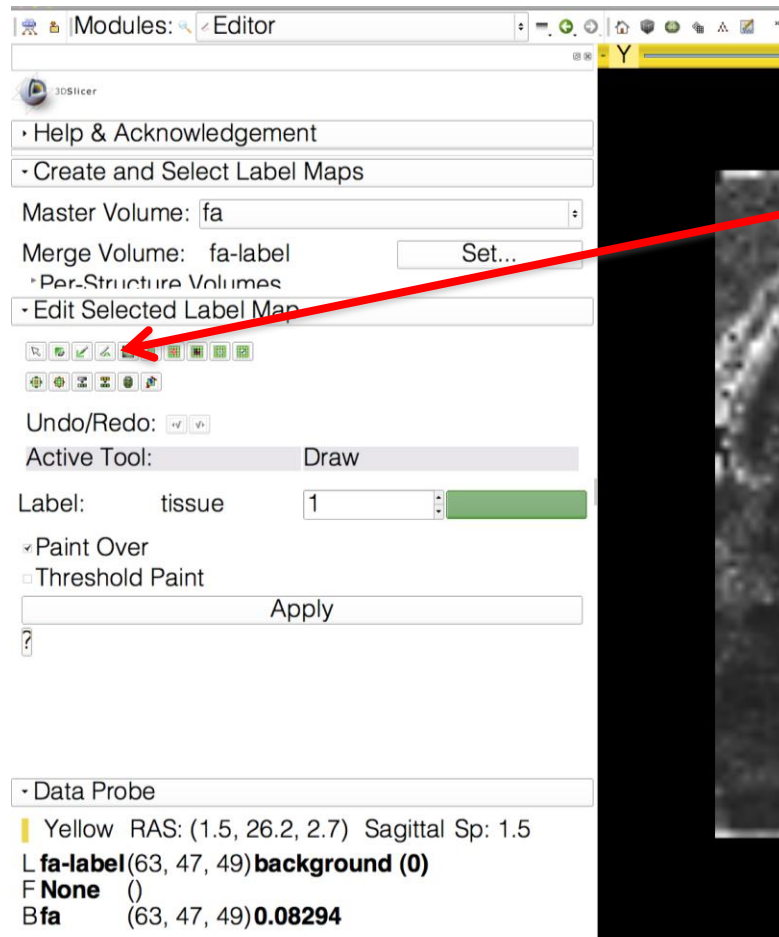



Set the **Master Volume** to 'fa'

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

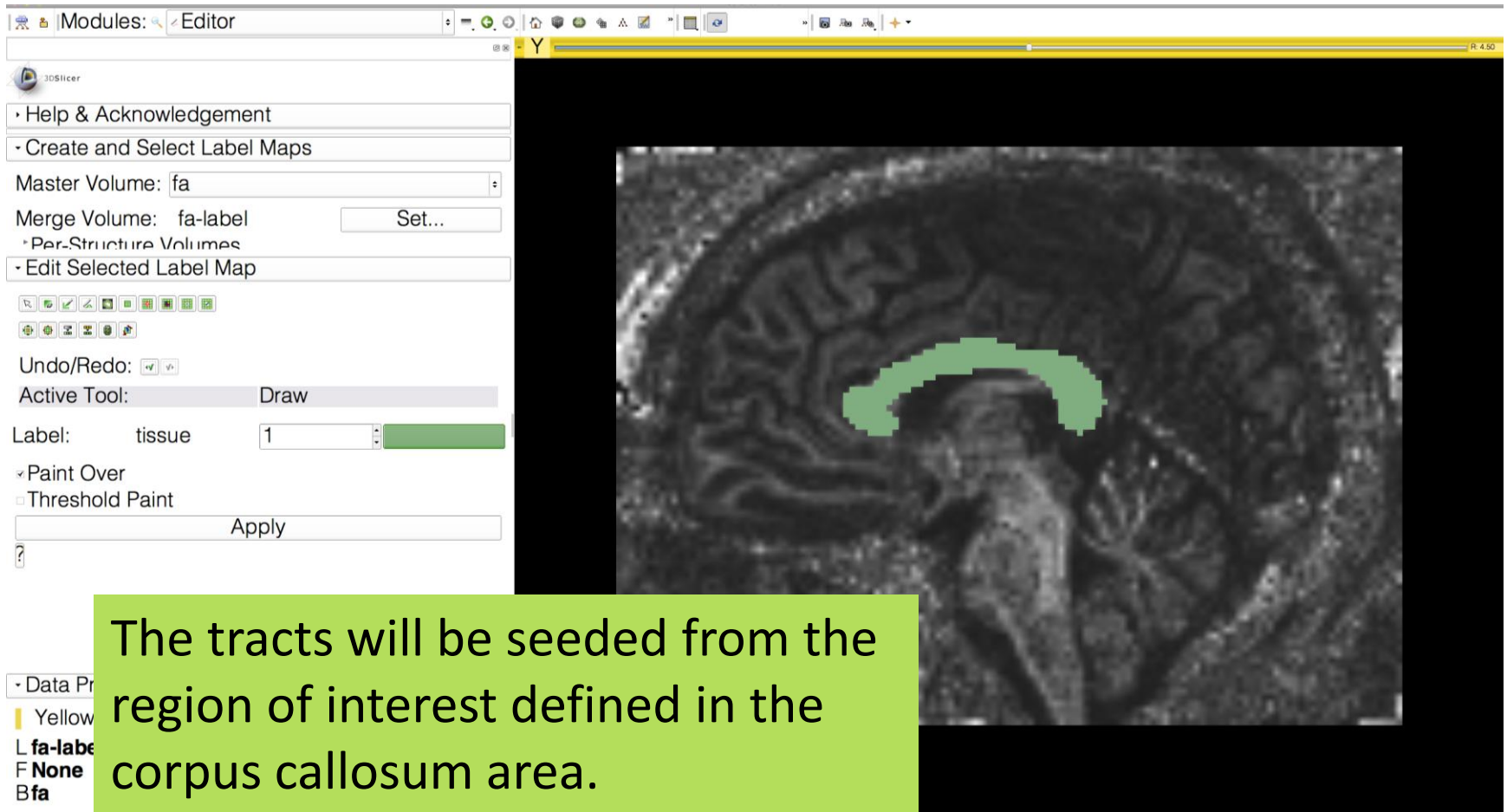


ROI Drawing



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

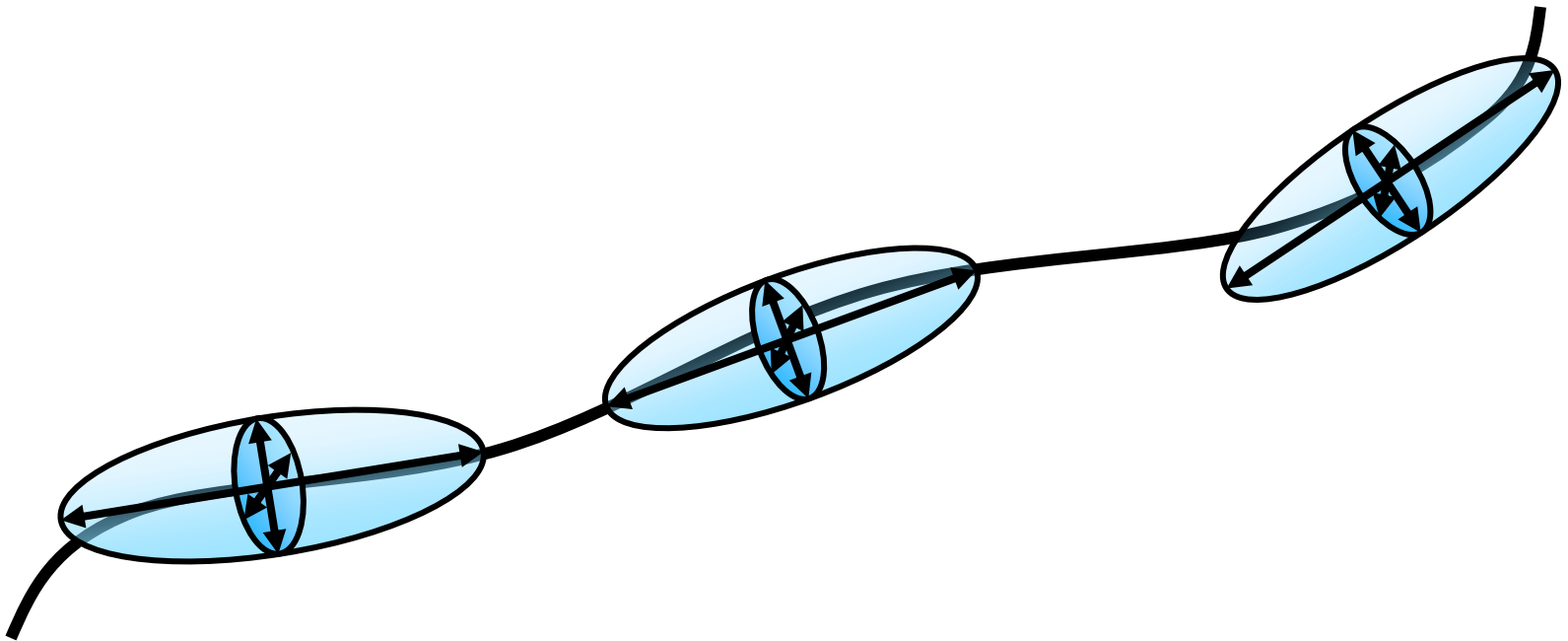


The screenshot shows the 3D Slicer software interface. The main window displays a coronal MRI slice of a brain with a green, semi-circular region of interest (ROI) drawn over the corpus callosum. The left sidebar contains the 'Editor' module, which is currently active. The 'Editor' module has several sections: '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' dropdown set to 'Draw'. The 'Label' section shows 'tissue' selected with a value of '1' and a green color swatch. There are also checkboxes for 'Paint Over' and 'Threshold Paint', and an 'Apply' button. At the bottom left, a 'Data Panel' is partially visible, showing a list of volumes: 'Yellow', 'L fa-label', 'F None', and 'B fa'.

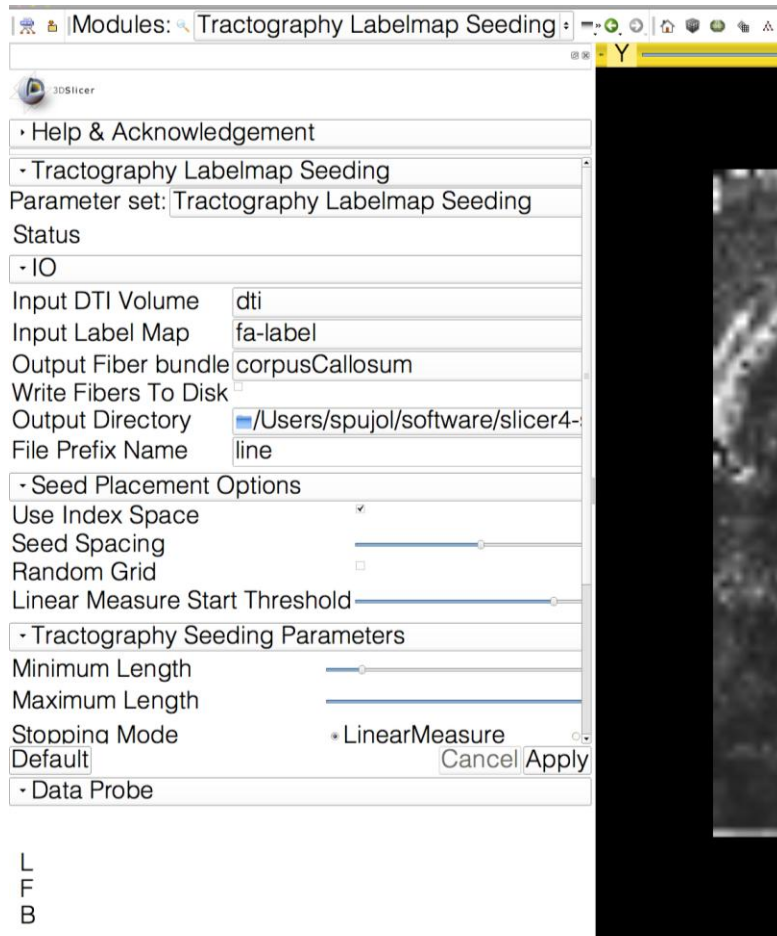
The tracts will be seeded from the region of interest defined in the corpus callosum area.

Streamline tractography

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



Labelmap Seeding: I/O



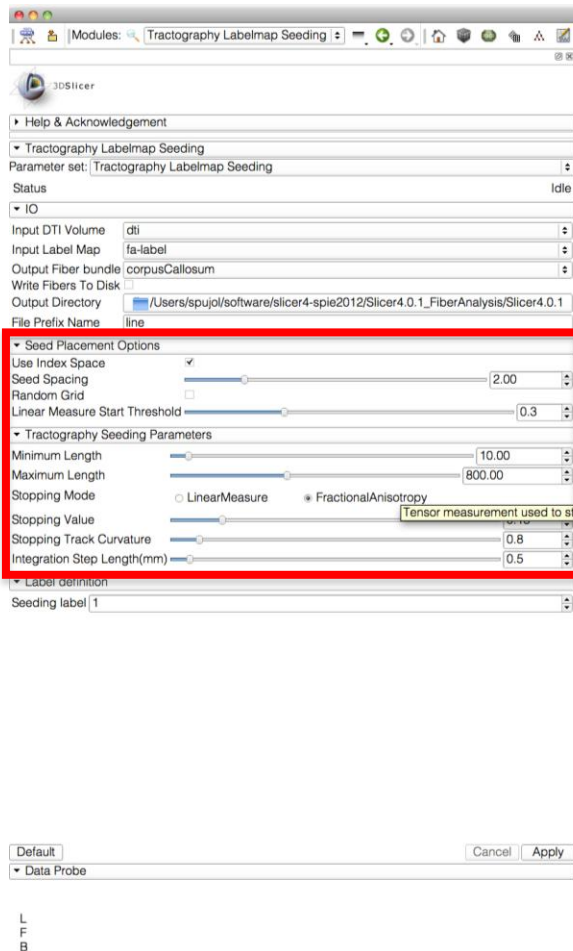
Select the module **Tractography Labelmap Seeding**

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'

Labelmap Seeding: parameters



Set 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**

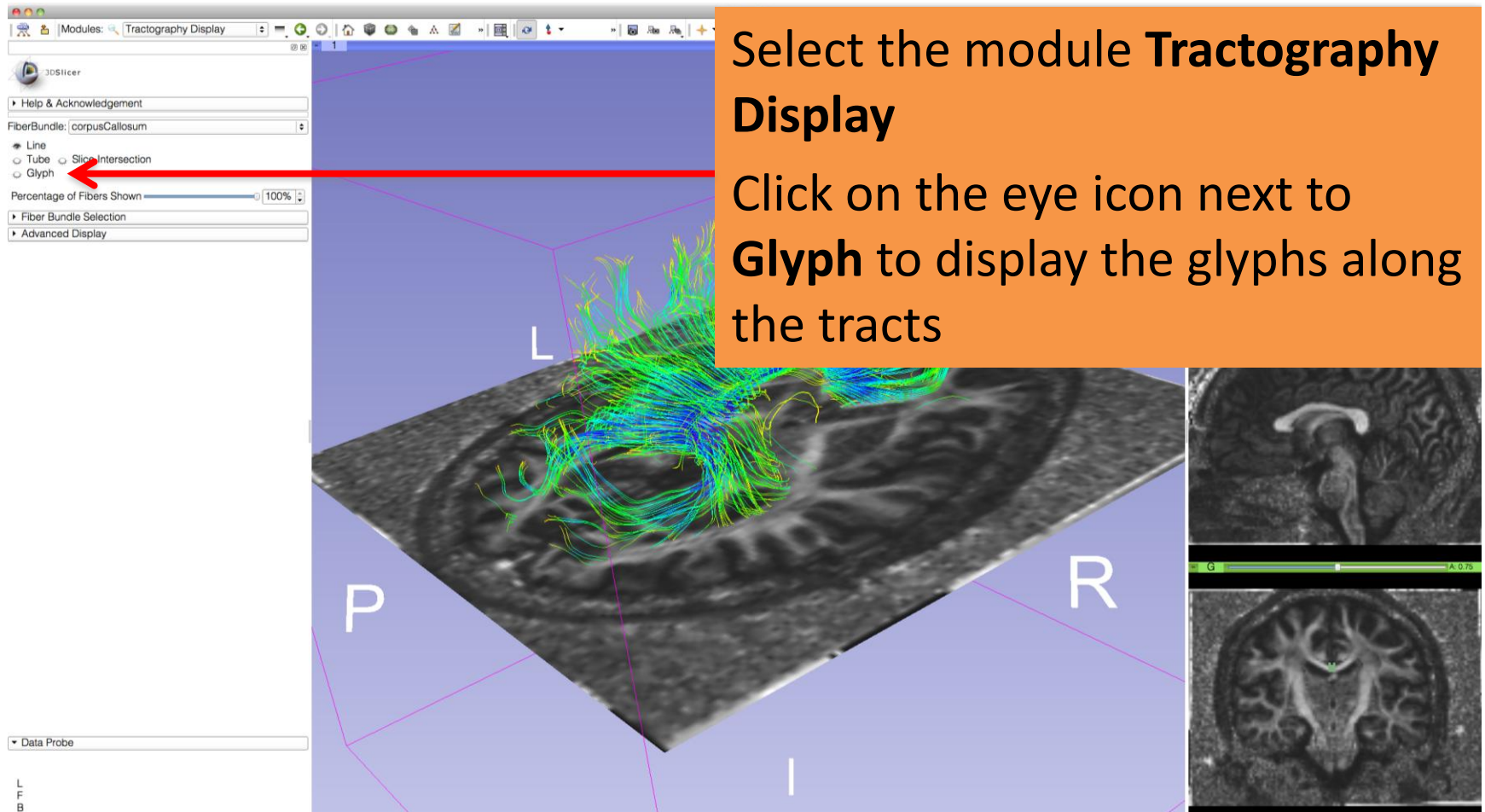
Labelmap Seeding: Tracts

The screenshot displays the 3D Slicer software interface. On the left, the 'Tractography Labelmap Seeding' module is active, showing various parameters such as 'Input DTI Volume' (dti), 'Input Label Map' (fa-label), and 'Output Fiber bundle' (corpusCallosum). The 'Seed Placement Options' and 'Tractography Seeding Parameters' sections are visible, with sliders for 'Seed Spacing' (2.00), 'Linear Measure Start Threshold' (0.3), 'Minimum Length' (10.00), and 'Maximum Length' (800.00). The 'Stopping Mode' is set to 'Fractional Anisotropy'. The 'Label definition' section shows 'Seeding label' set to 1. The main 3D viewer shows a brain slice with a dense bundle of fiber tracts in the corpus callosum area, colored with a gradient from blue to green. The axes are labeled L (Left), A (Anterior), and I (Inferior). An orange callout box with a red arrow points to the 'Conventional Widescreen' layout button in the top toolbar. A green callout box at the bottom left explains the tracts. On the right, three axial brain slices show the corpus callosum area with a green highlight indicating the seeding region.

Select the layout 'Conventional Widescreen'

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

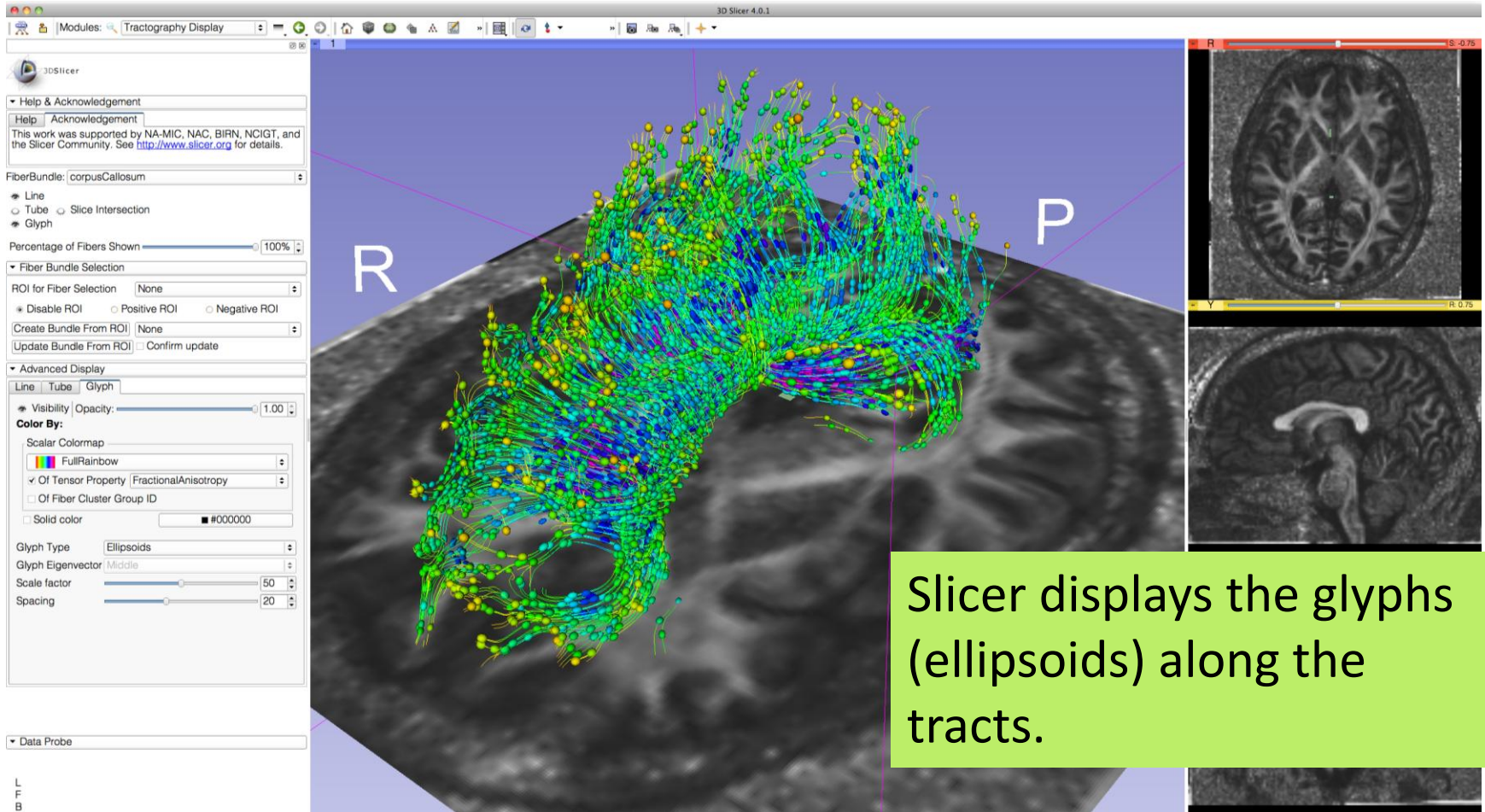
Labelmap Seeding: Tracts



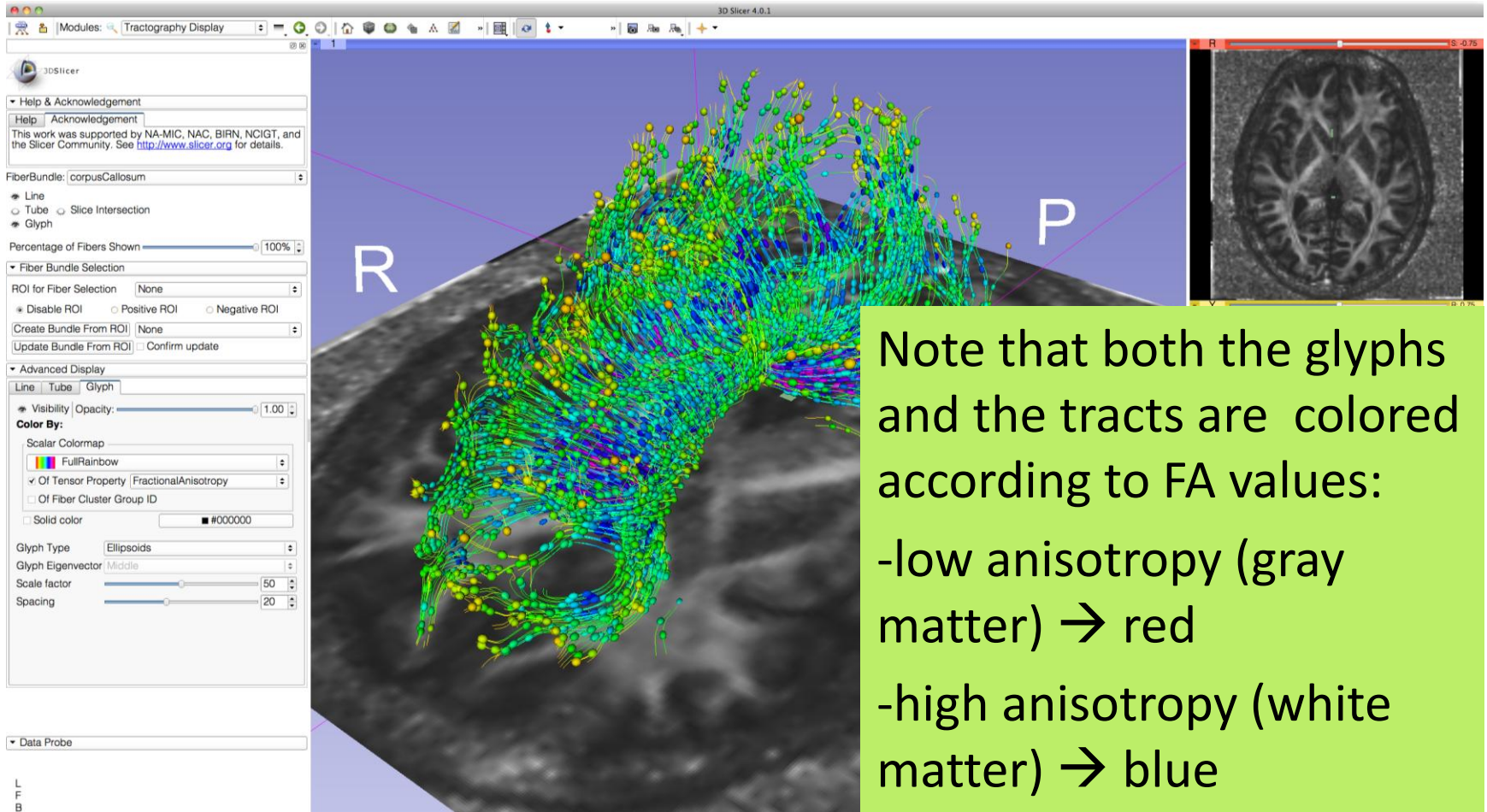
Select the module **Tractography Display**

Click on the eye icon next to **Glyph** to display the glyphs along the tracts

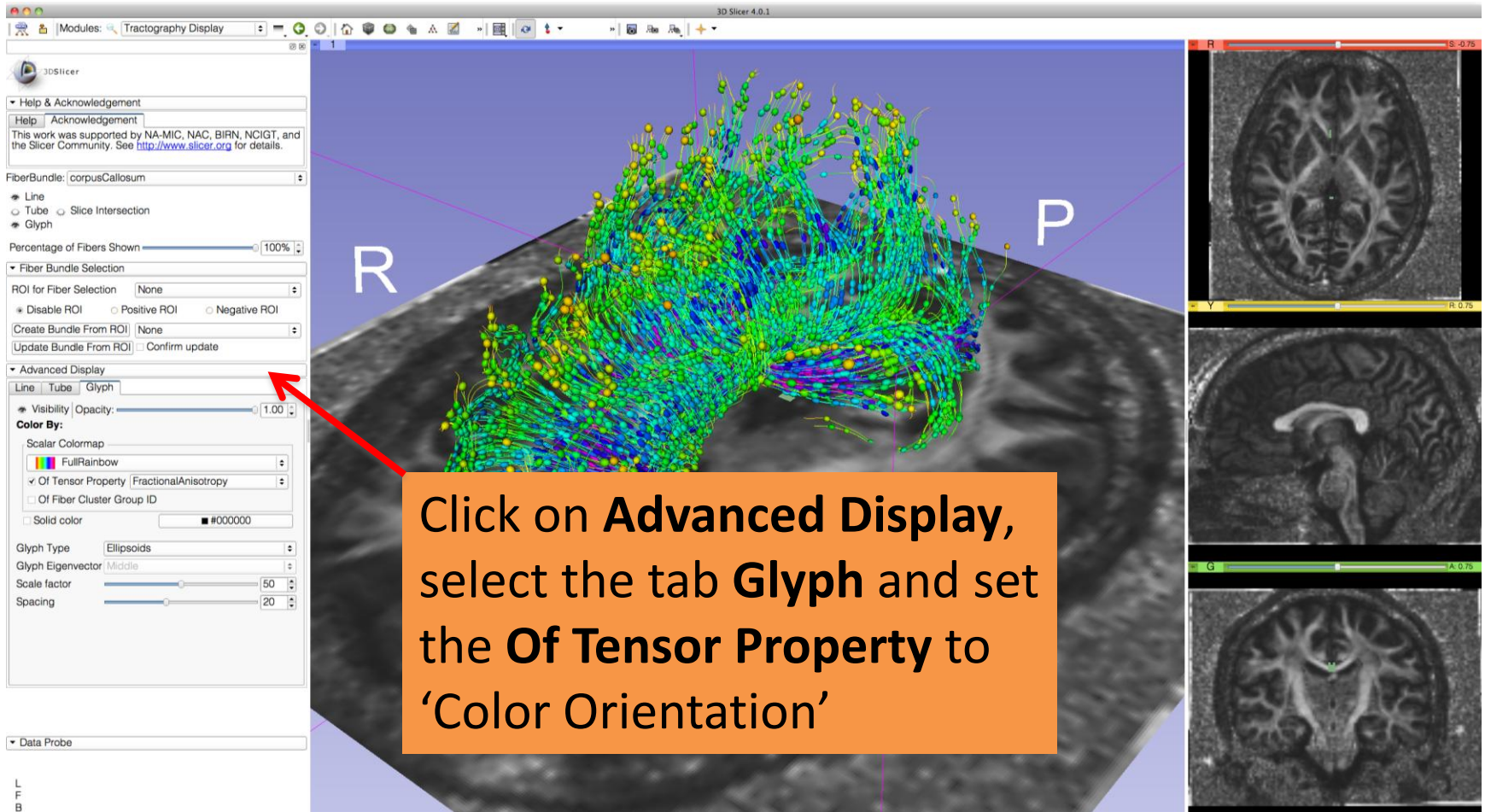
Tractography Results



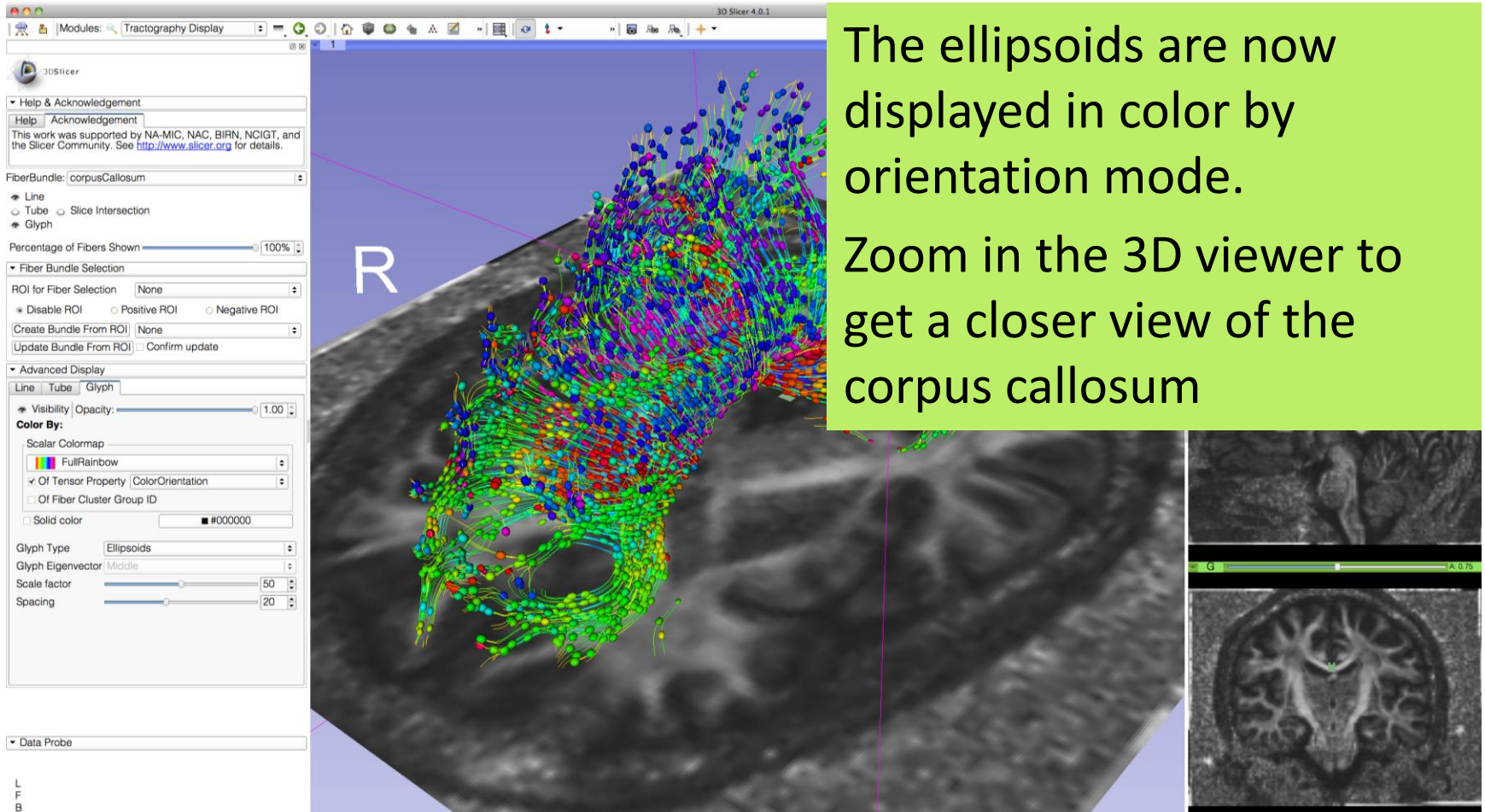
Tractography Results



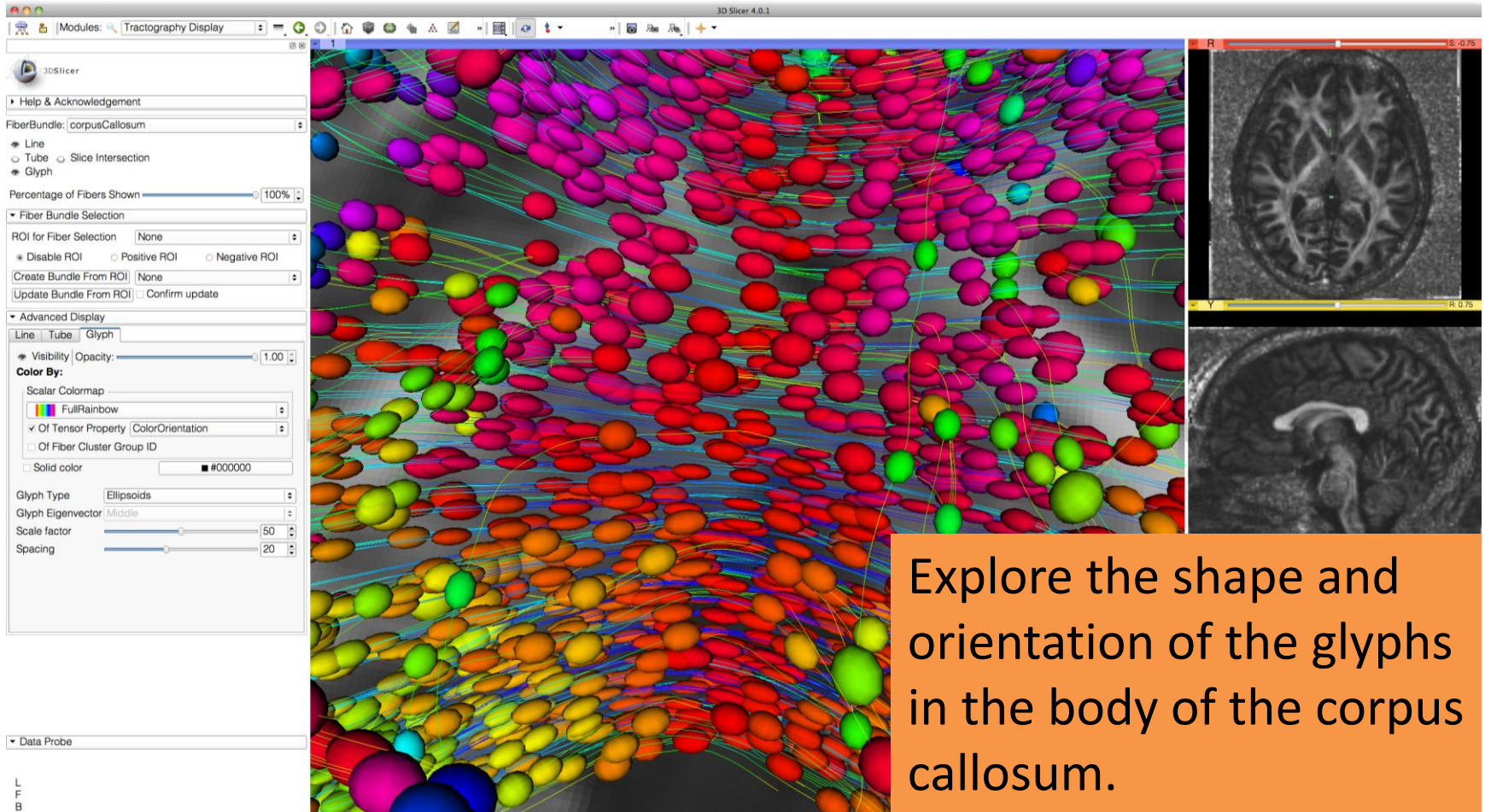
Tractography Results



Tractography Results

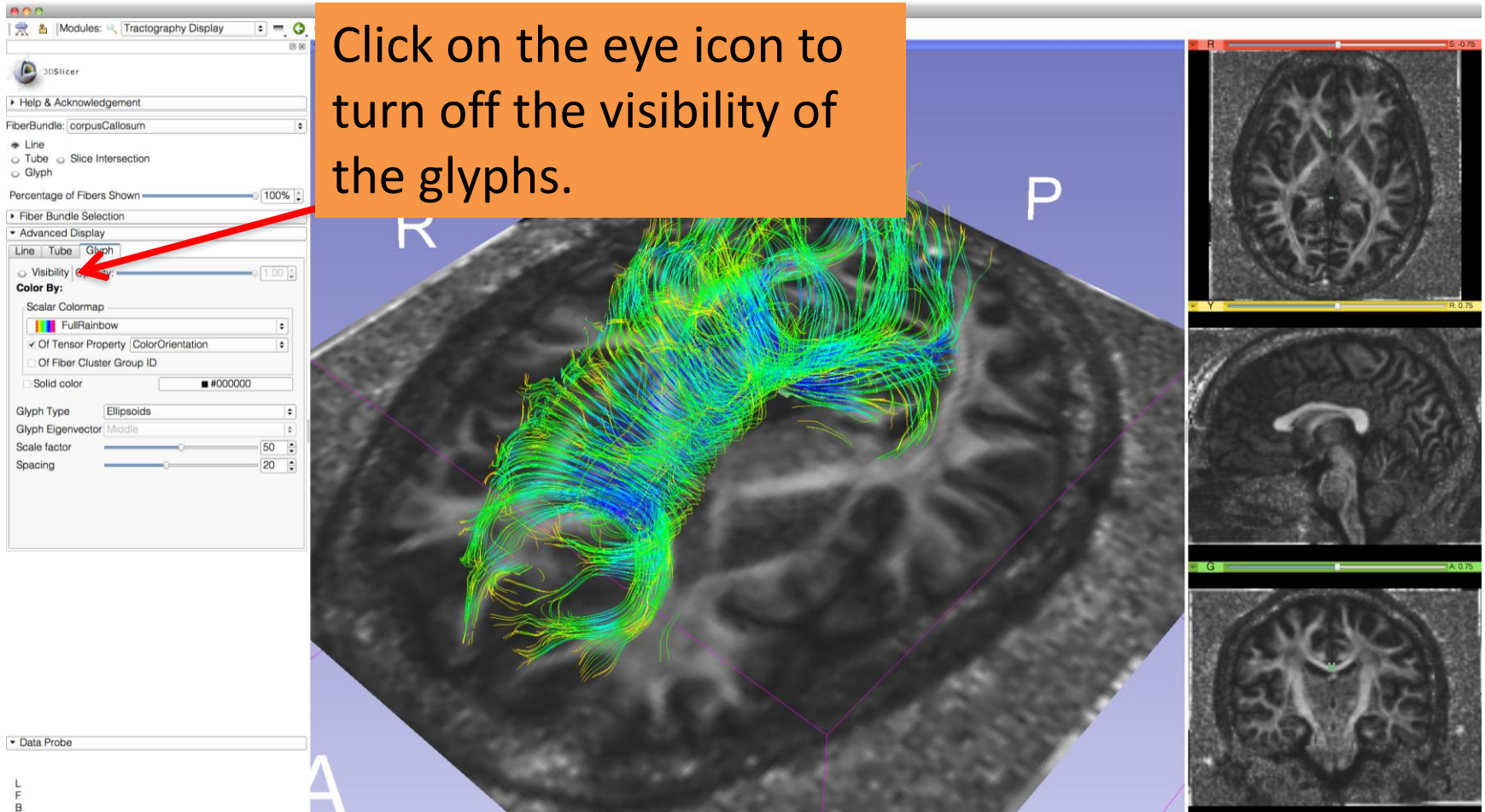


Tractography Results

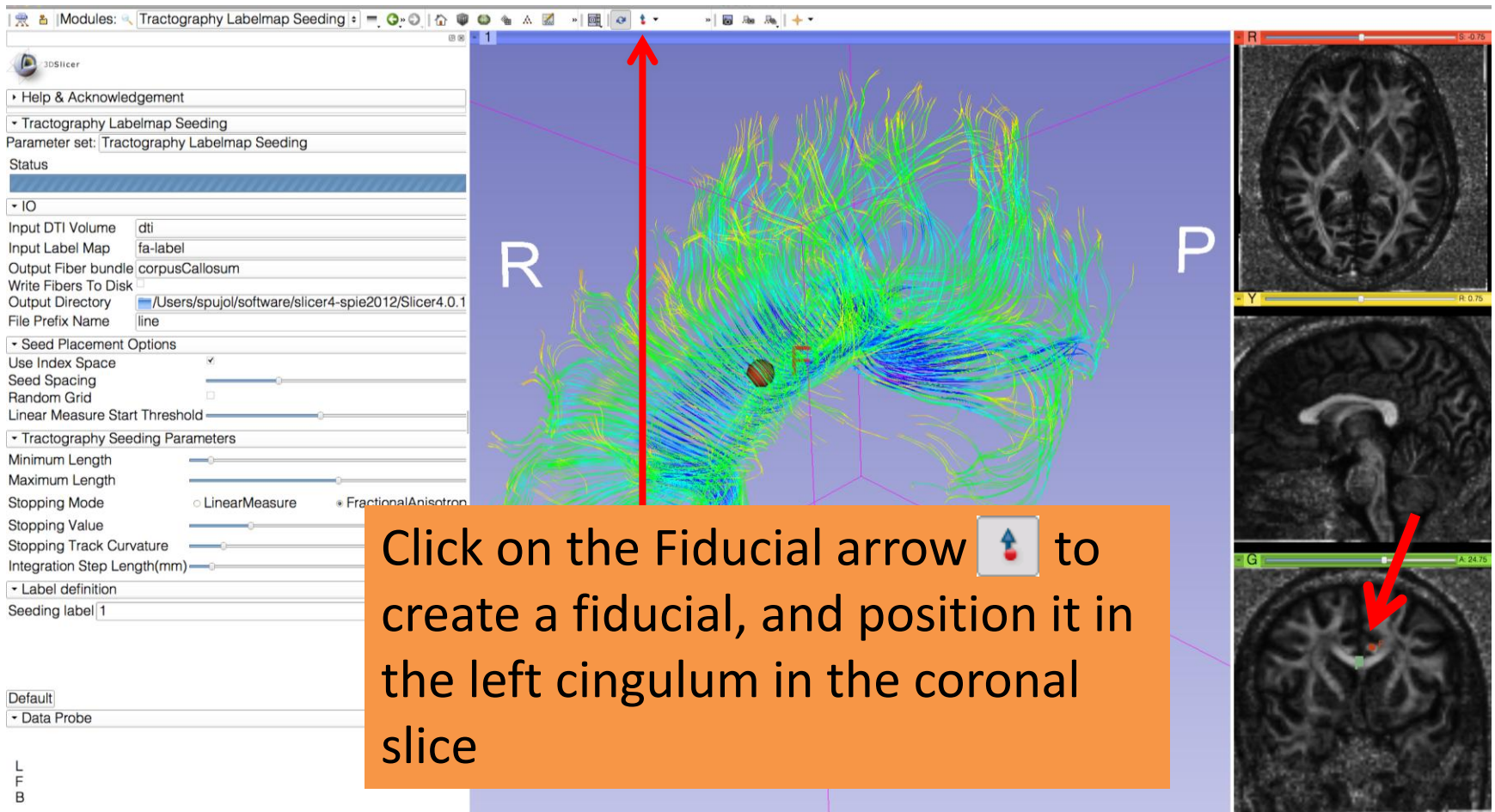


Explore the shape and orientation of the glyphs in the body of the corpus callosum.

Tractography Results



Fiducial Seeding



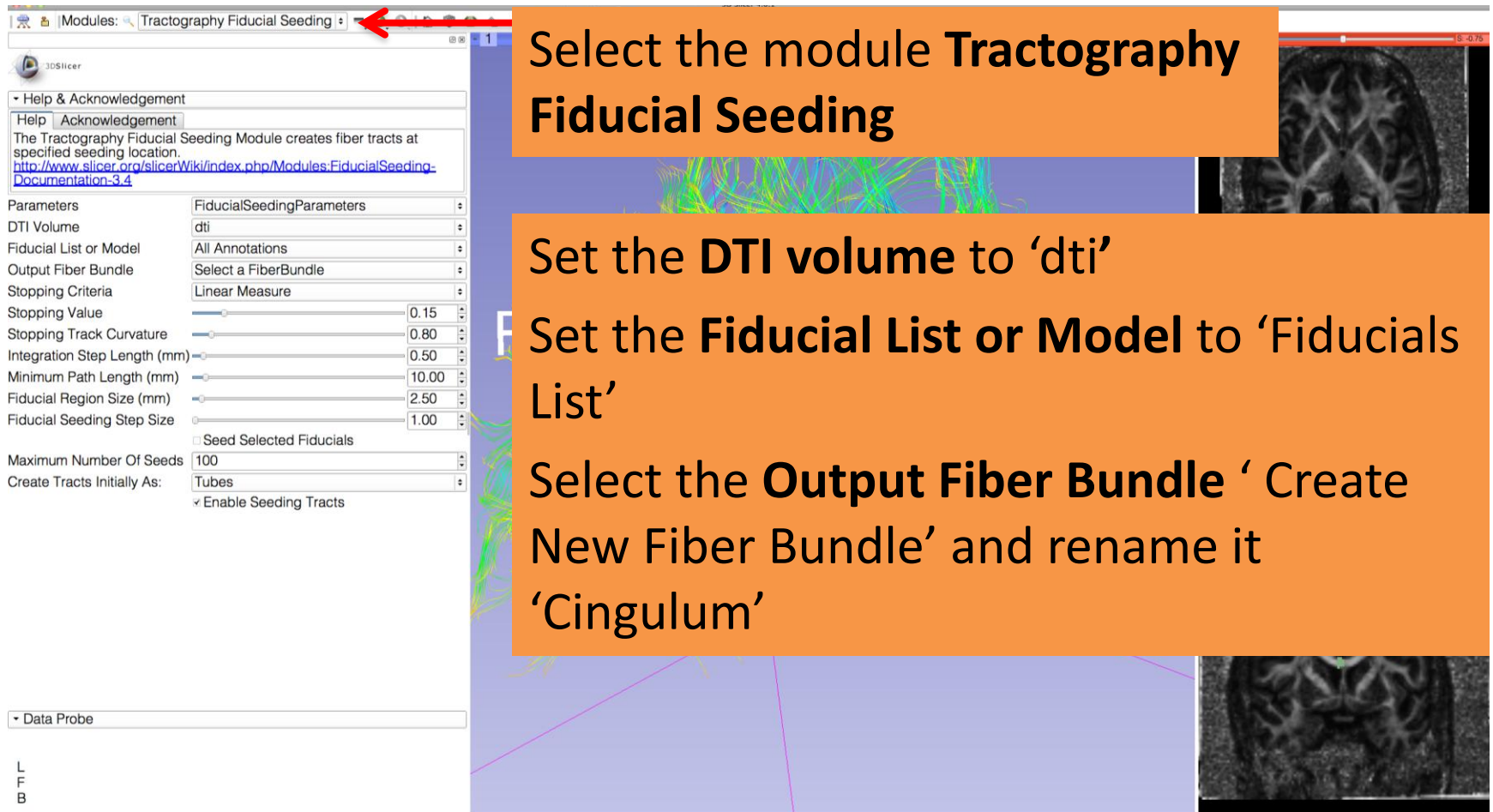
Fiducial Seeding

The image shows a 3D Slicer interface with the Annotations module active. The main window displays a brain MRI with a green and blue streamline visualization. A red arrow points to the 'Annotations' module in the top menu bar. Another red arrow points to a fiducial point labeled 'F' in the 'Fiducials List' table, which is highlighted and renamed 'Left Cingulum'. The table shows the following data:

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	

On the right, three orthogonal MRI slices (axial, sagittal, and coronal) are shown. The axial slice at the bottom has a red dot labeled 'Left Cingulum' on the brain's surface. The main window has 'R' (Right), 'P' (Posterior), and 'L' (Left) orientation markers. The bottom left corner has 'L', 'F', and 'B' markers.

Fiducial Seeding



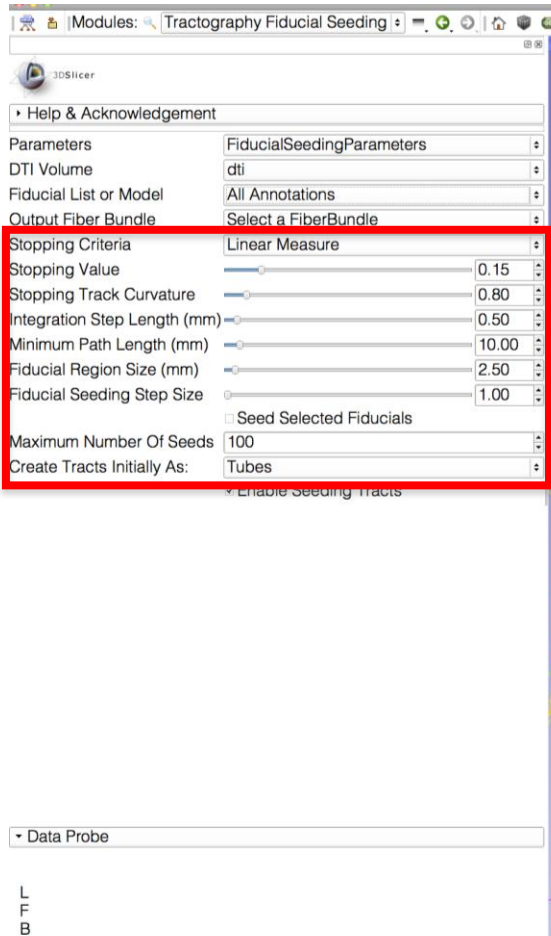
Select the module **Tractography Fiducial Seeding**

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

Set the **Fiducial List or Model** to 'Fiducials List'

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

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

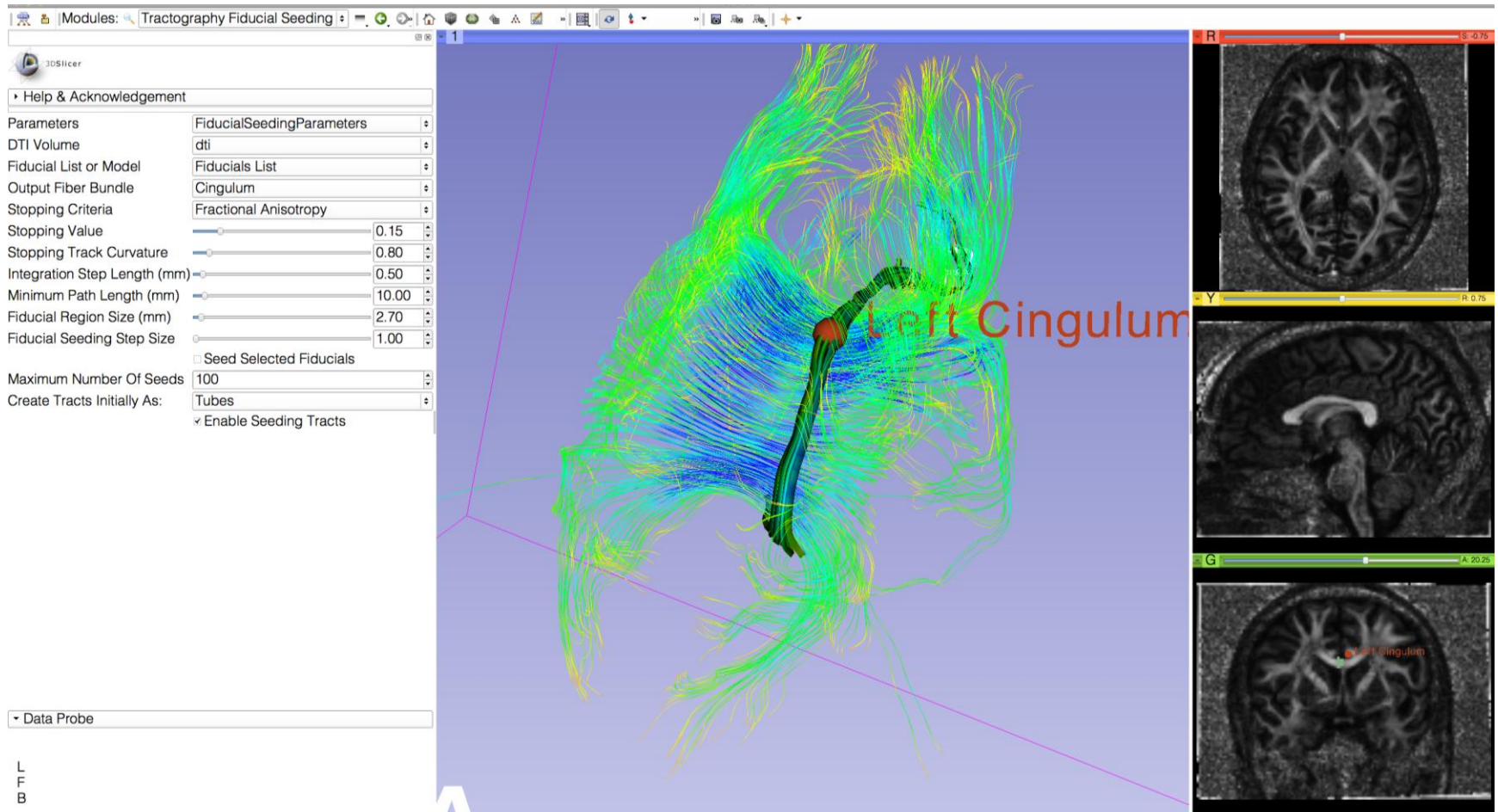
-Fiducial regions size: 2.5 mm

-Fiducial step size: 1.0

-Maximum number of seeds: 100


-Create Tracts Initially as Tubes

Fiducial Seeding



Fiducial Seeding

The screenshot shows the 3D Slicer software interface. The top menu bar includes 'Modules' and 'Annotations'. The left sidebar shows the 'Annotations' module selected. The main window displays a 3D brain model with green and blue streamlines. A red arrow points to the 'Annotations' module in the sidebar. Another red arrow points to the 'Fiducial' icon in the top toolbar. A third red arrow points to the 'Right Cingulum' entry in the 'Fiducials List' table. A fourth red arrow points to the 'Right Cingulum' label on the brain model. Two inset images on the right show axial MRI slices with a red dot and the label 'Right Cingulum' placed on the brain.

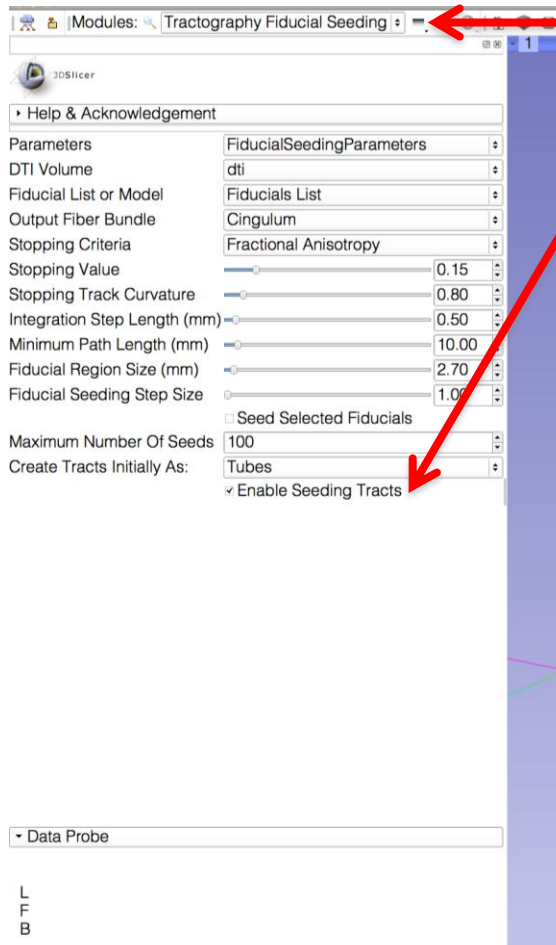
Click on the Fiducial arrow  icon to create a new fiducial, and position it in the right cingulum area.

Select the **Annotations** module in the modules menu
Change the name of the new fiducial to 'Right Cingulum'

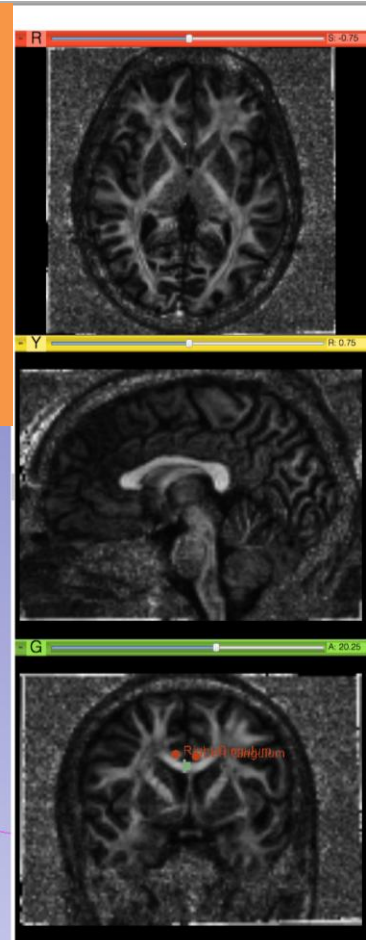
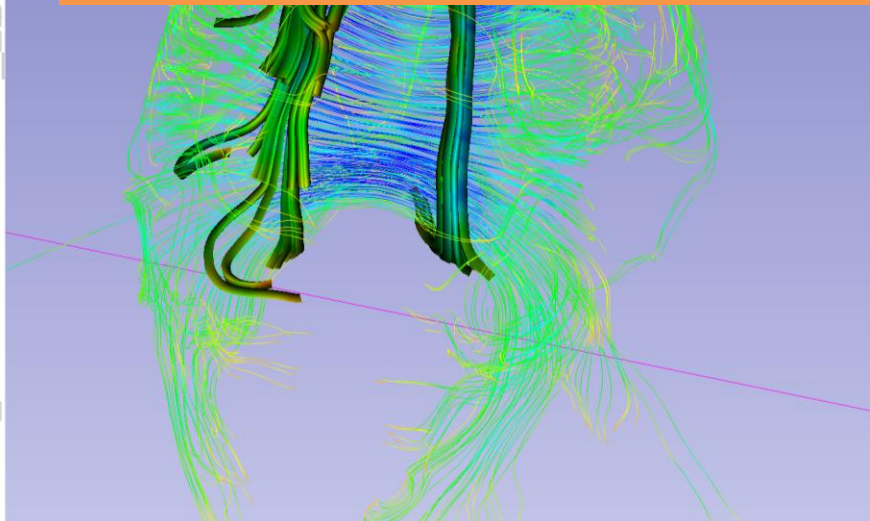
Vis	Lock	Edit	Value	Name	Description
				All Annotations	
				Fiducials List	
			-2.3, 20.2, 23.1	Left Cingulum	
			7.9, 20.2, 26.1	Right Cingulum	

L
F
B

Fiducial Seeding



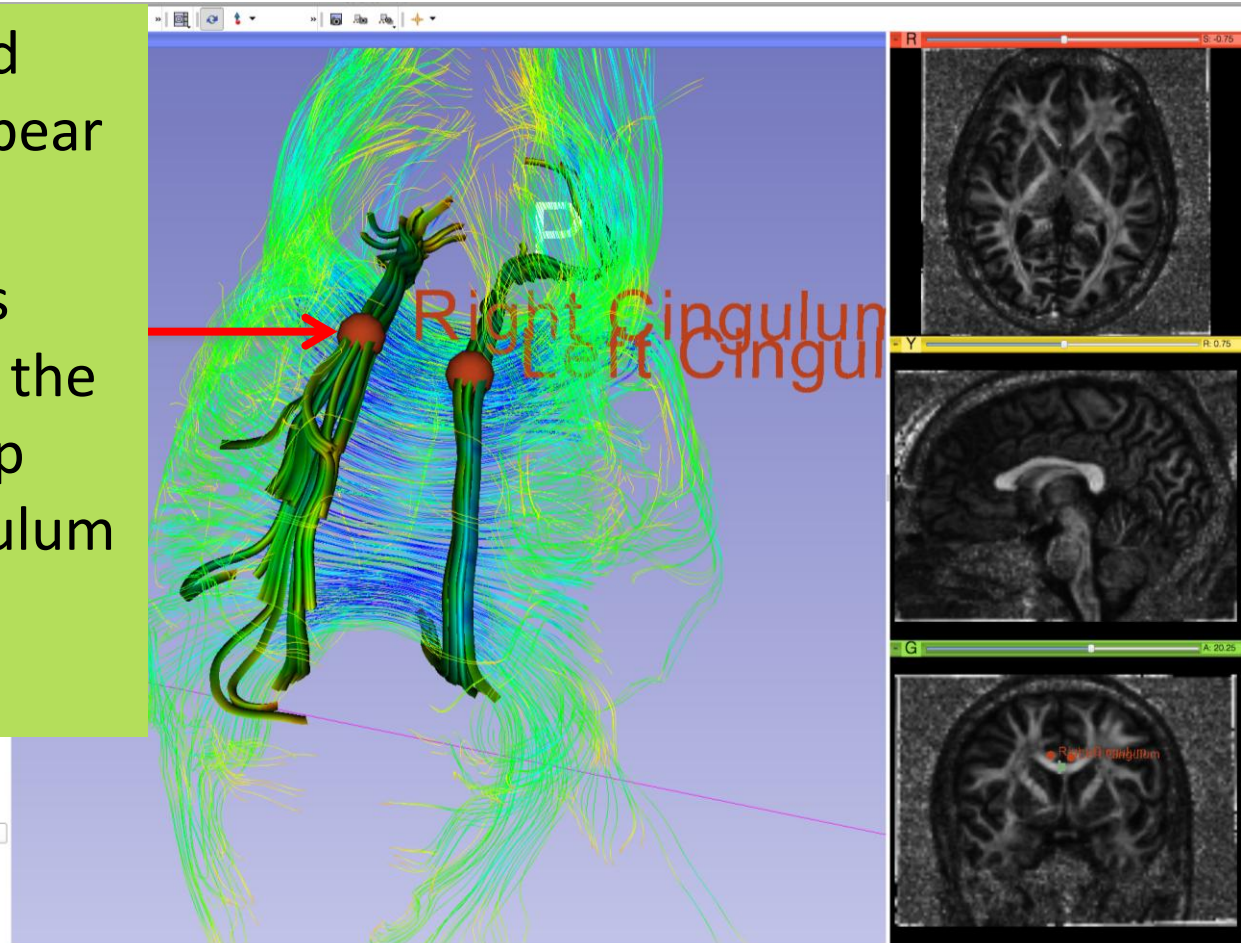
Go back to the **Tractography Fiducial Seeding** module
Uncheck and check again the 'Enable Seeding Tracts' to update the 3D viewer



Fiducial Seeding

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

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



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

Left Cingulum

Right Cingulum

Fiducial Seeding

Modules: Tractography Fiducial Seeding

3D Slicer

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

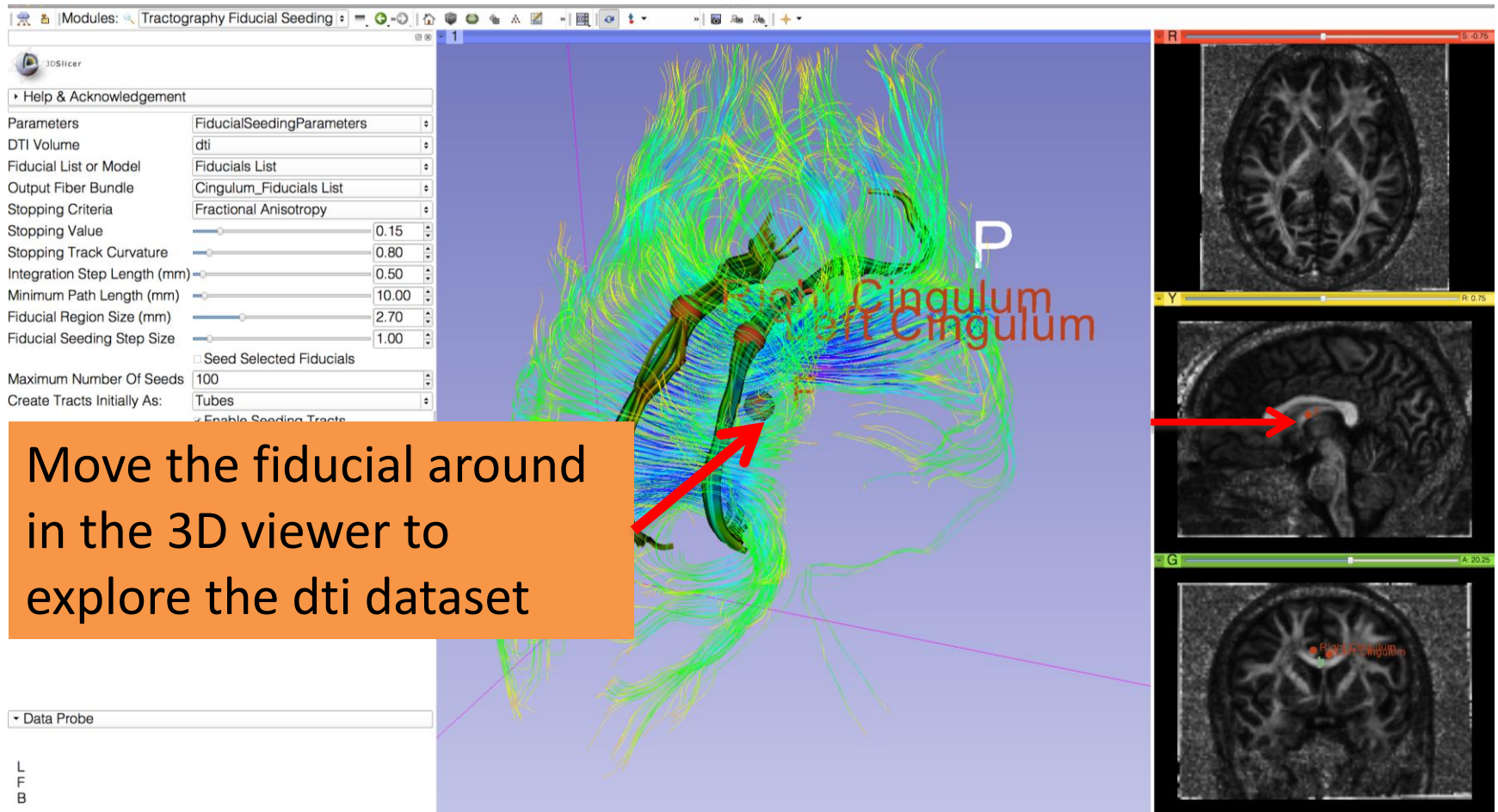
Uncheck and check again the 'Enable Seeding Tracts' to update the 3D viewer

Cingulum
Left Cingulum

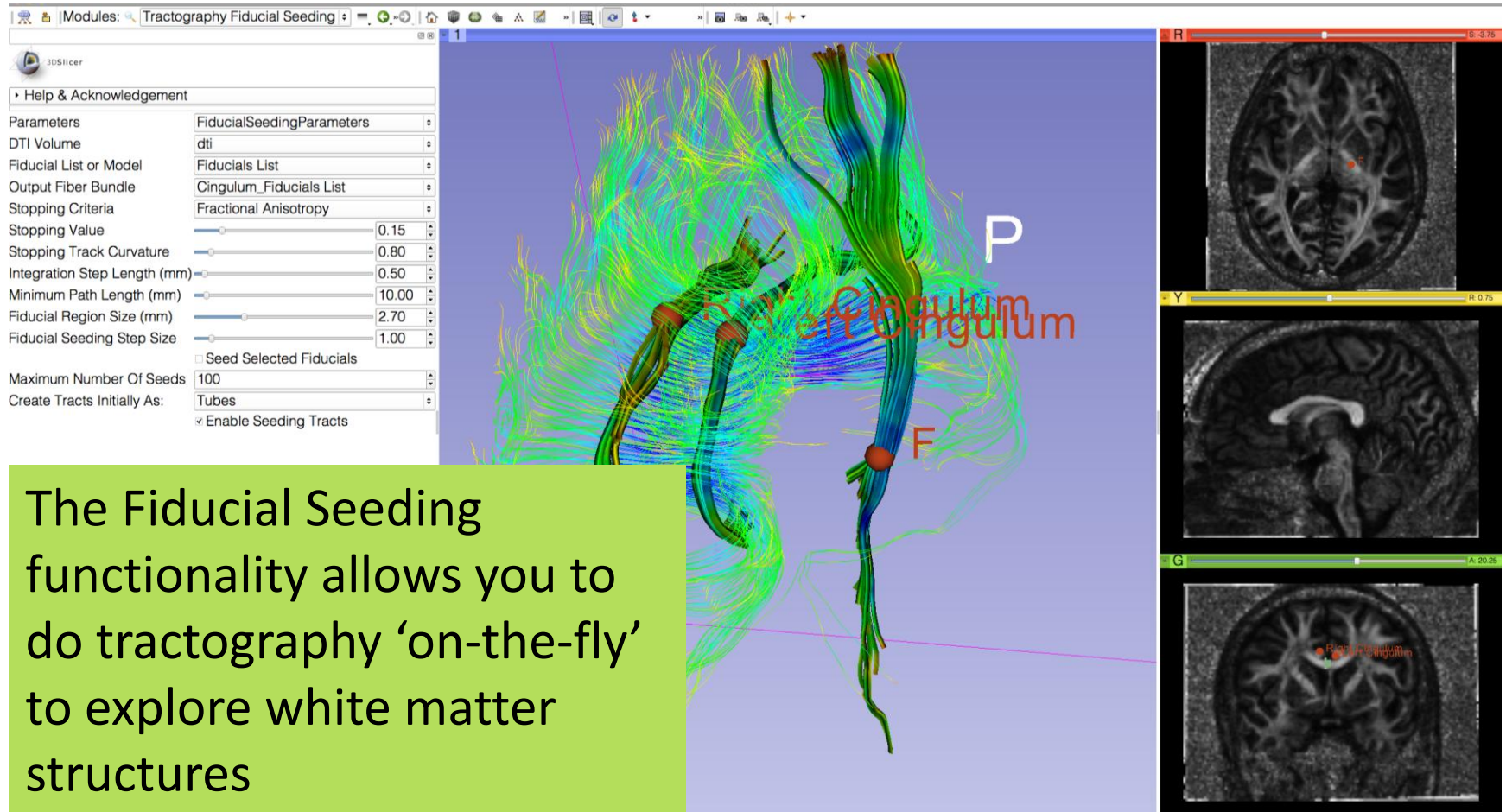
Right Cingulum
Left Cingulum

L
F
B

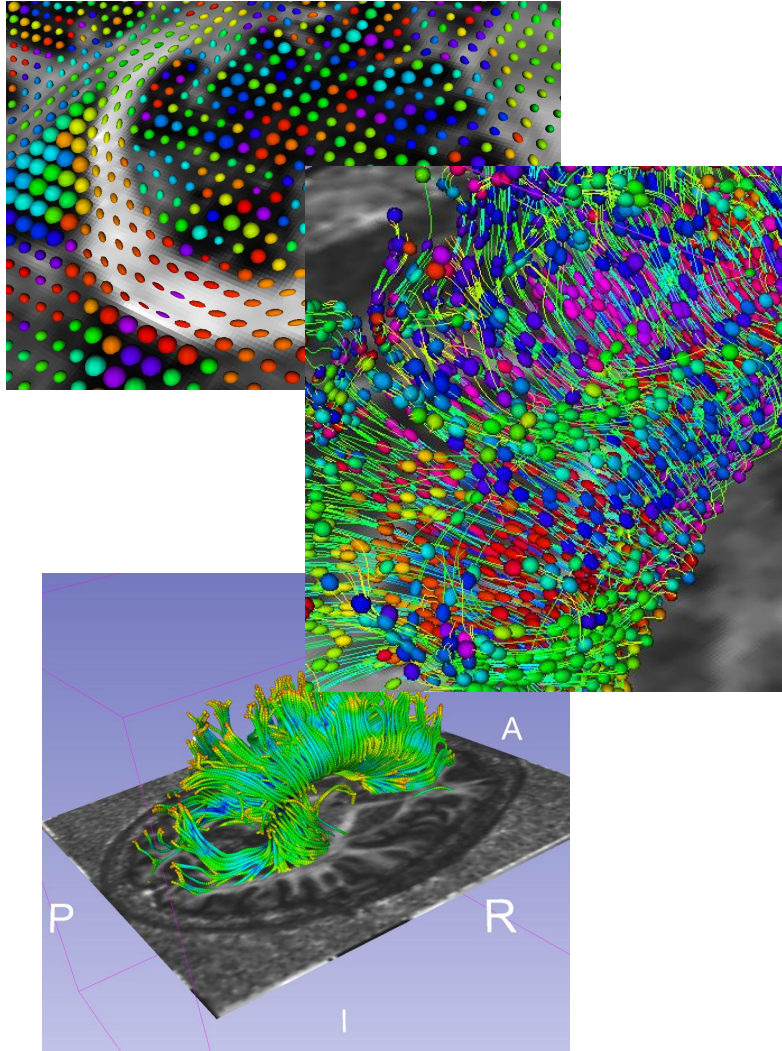
Fiducial Seeding



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



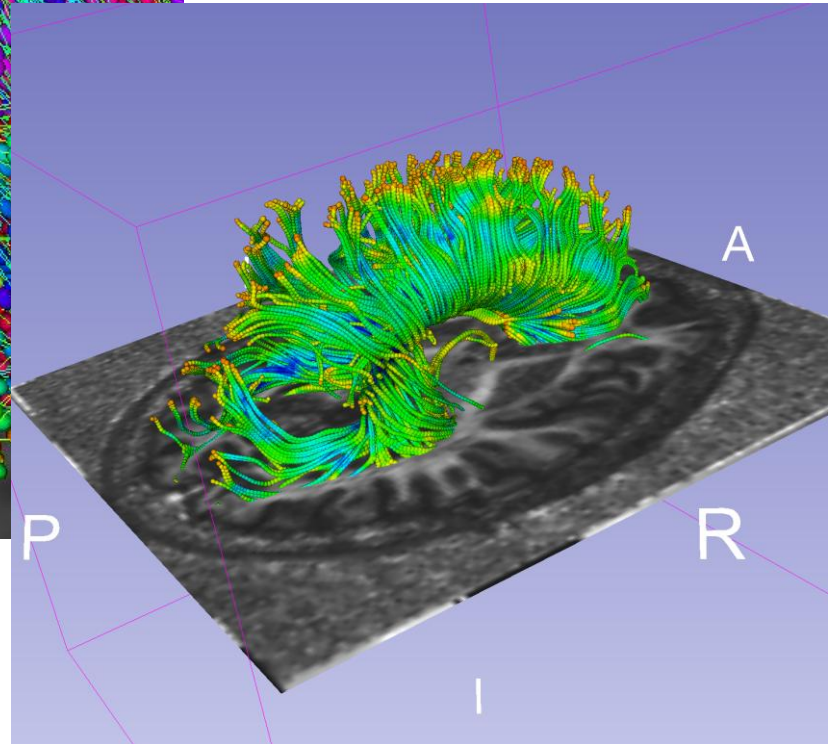
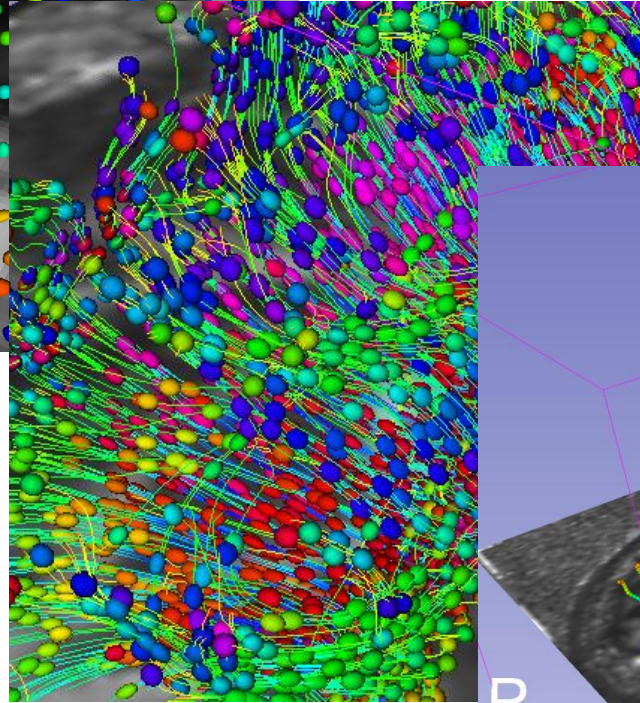
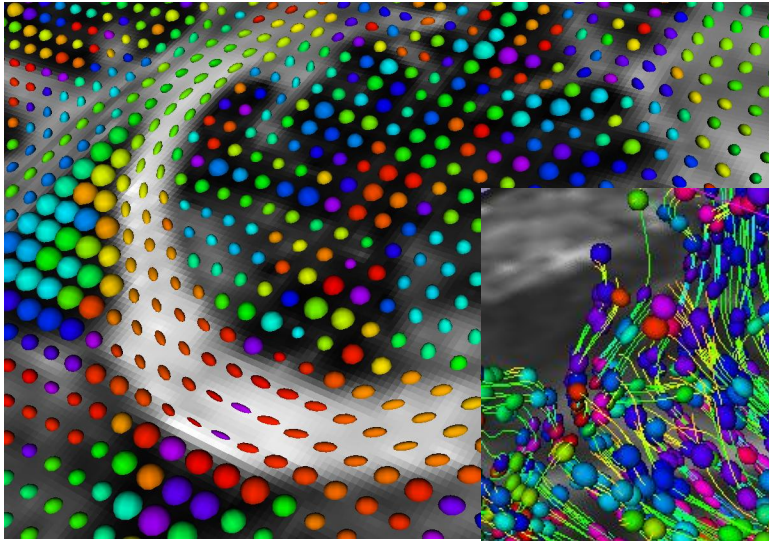
National Alliance for Medical Image Computing
NIH U54EB005149



Neuroimage Analysis Center
NIH P41RR013218

Slicer Community

- www.slicer.org
- Mailing lists:
slicer-users@bwh.harvard.edu
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Contact: spujol@bwh.harvard.edu