



Diffusion MRI Analysis

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Brain Anatomy



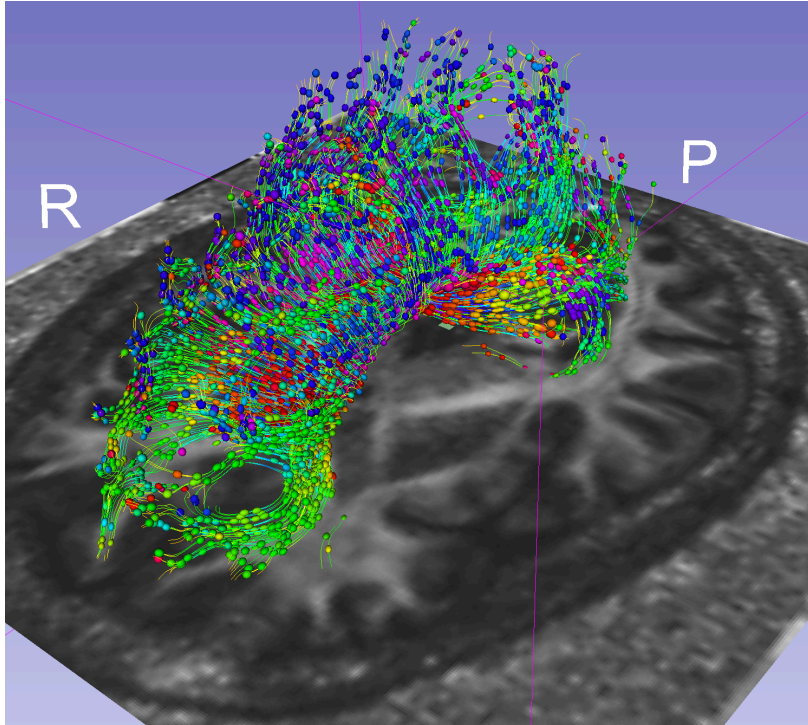
- White matter ~45% of the brain
- Myelinated nerve fibers (~ 10 μm axon diameter)

White Matter Exploration



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

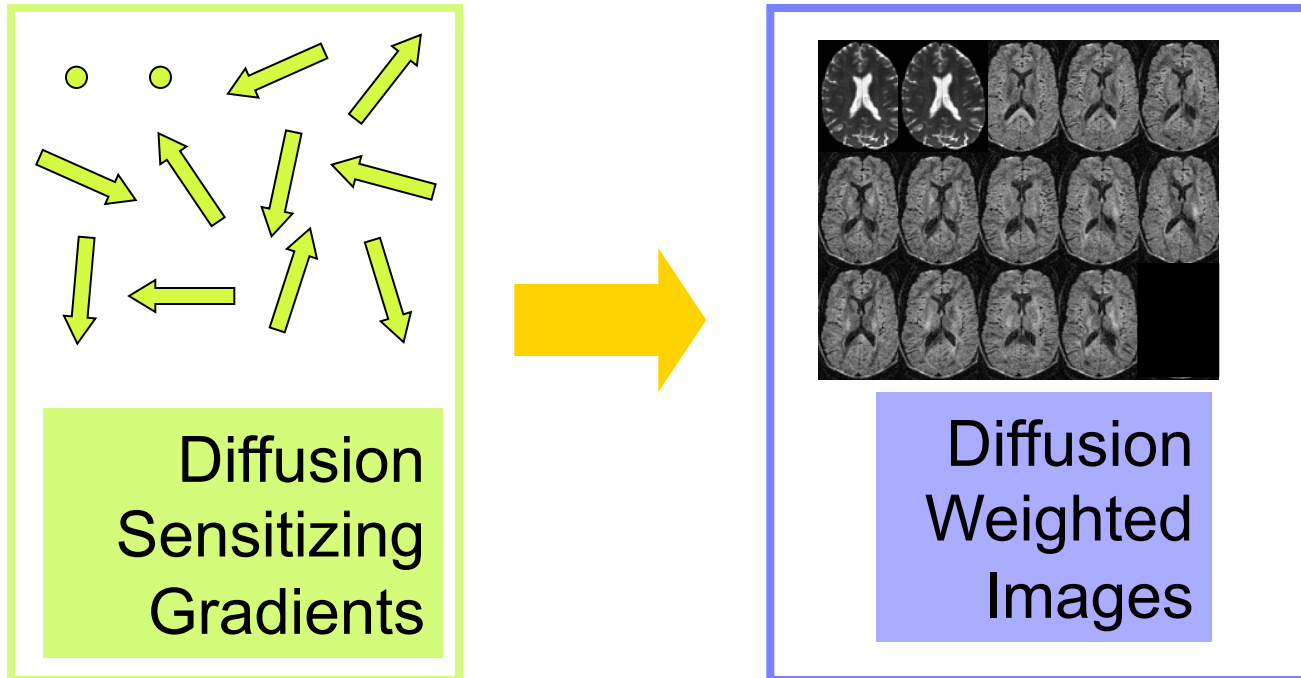
Tutorial Outline



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



The dataset is available on the Slicer Training Compendium (www.slicer.org)

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 description: "A multi-platform, free and open source software package for visualization and medical image computing". A search bar is located to the right of the description. Below the description 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." (showing MRI slices with a green region), "Streamlined interface." (showing a 3D model of a brain), and "Extensible platform." (showing a 3D model of a hand). Below these images is a large banner for "3D Slicer version 4.0" with the website URL "www.slicer.org".

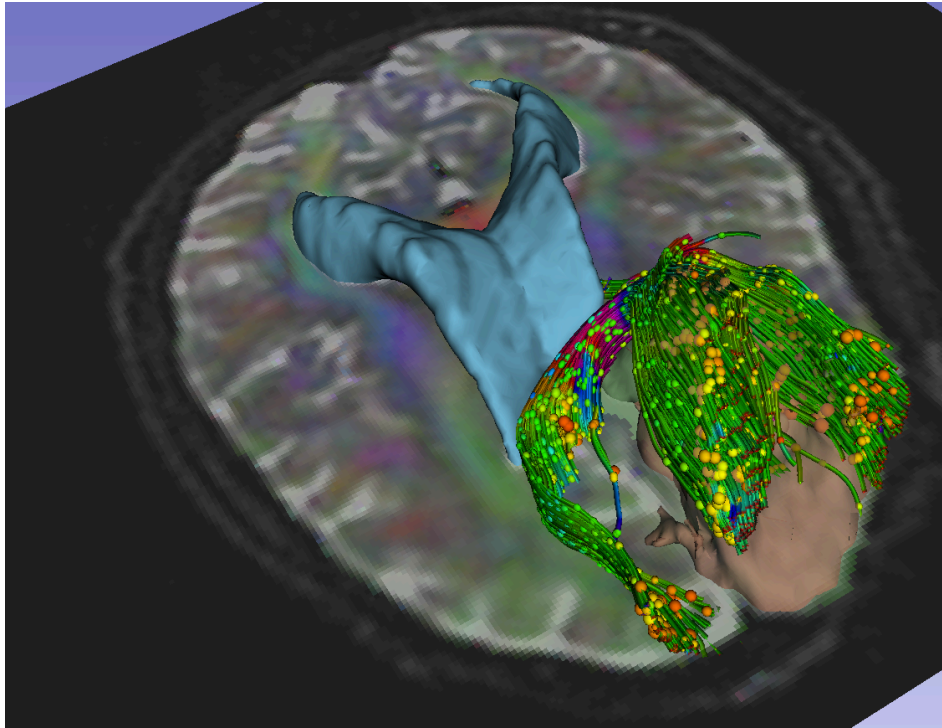
At the bottom of the page, there is a footer with copyright information: "Content of this site is Copyright 2012 BWH and 3D Slicer contributors, unless otherwise noted. Contact webmaster@bwh.harvard.edu for questions about the use of this site's content. See here for more information about the web infrastructure."

The tutorial uses the 3DSlicer version 4.1 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.

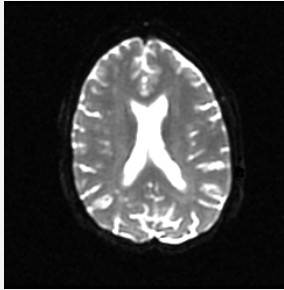
- An **end-user application** for image analysis
- An **open-source environment** for software development
- A software platform that is both **easy to use** for clinical researchers and **easy to extend** for programmers

Learning Objectives

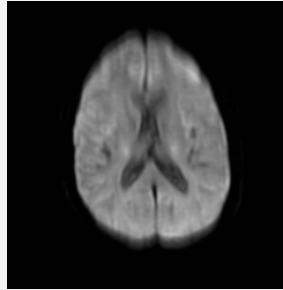
Following this tutorial, you'll be able to

- 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

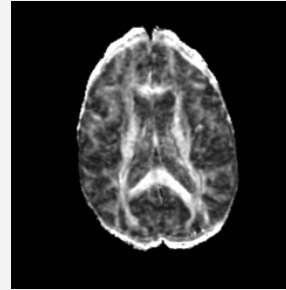
MR Diffusion Analysis Pipeline



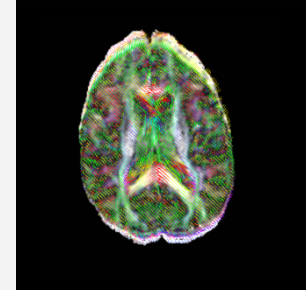
DWI
Acquisition



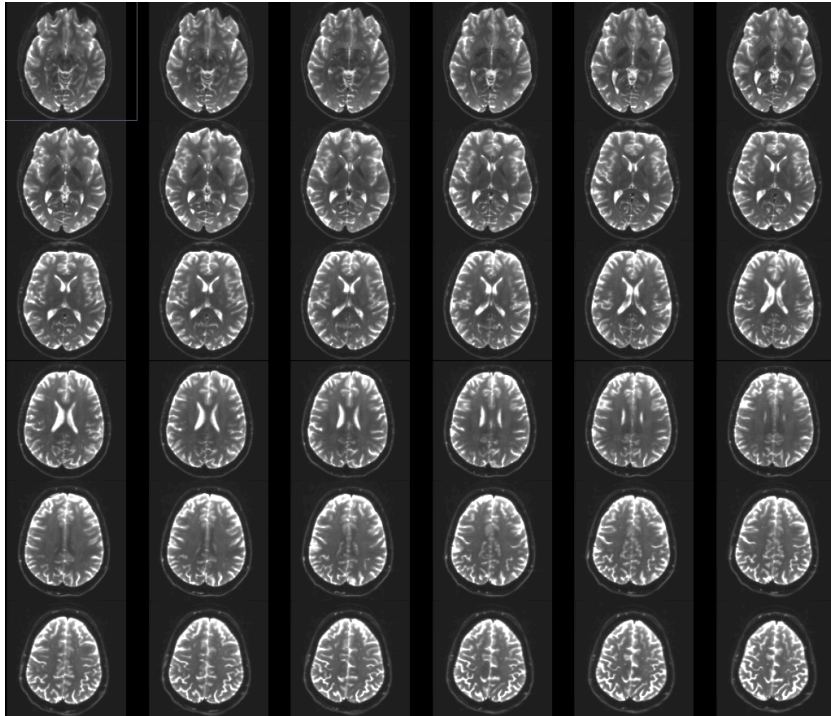
Tensor
Calculation



Scalar
Maps

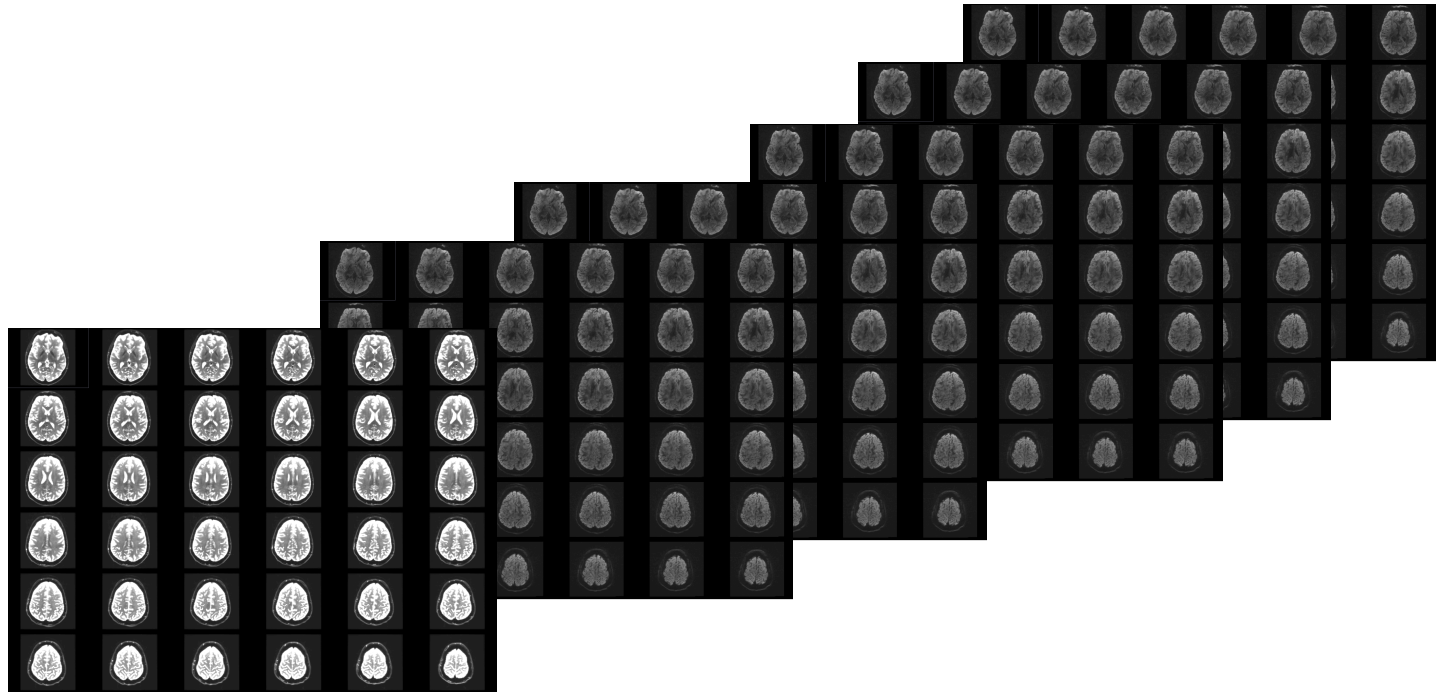


3D
Visualization



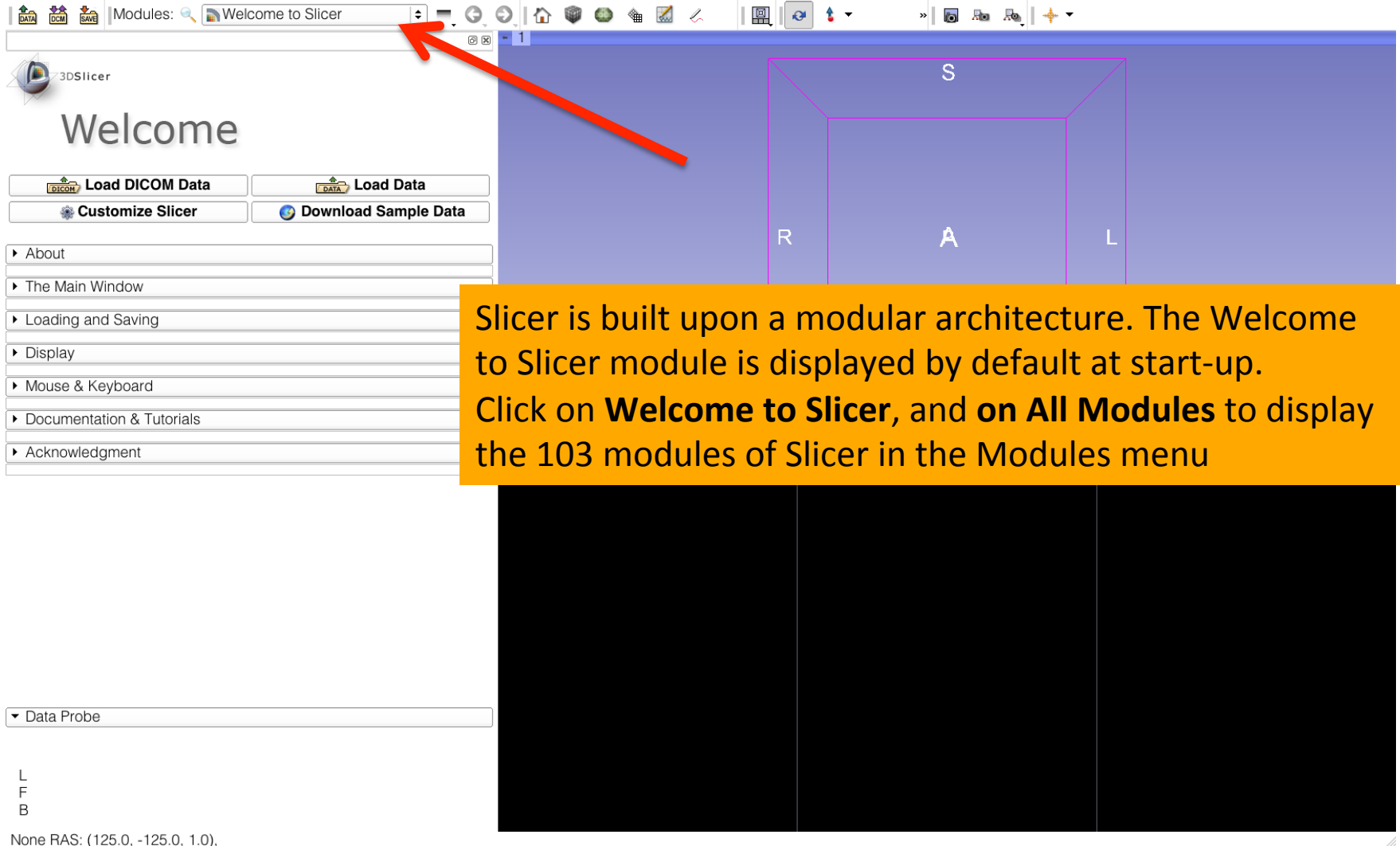
Part 1: From DWI images to Tensors

Understanding the DWI dataset



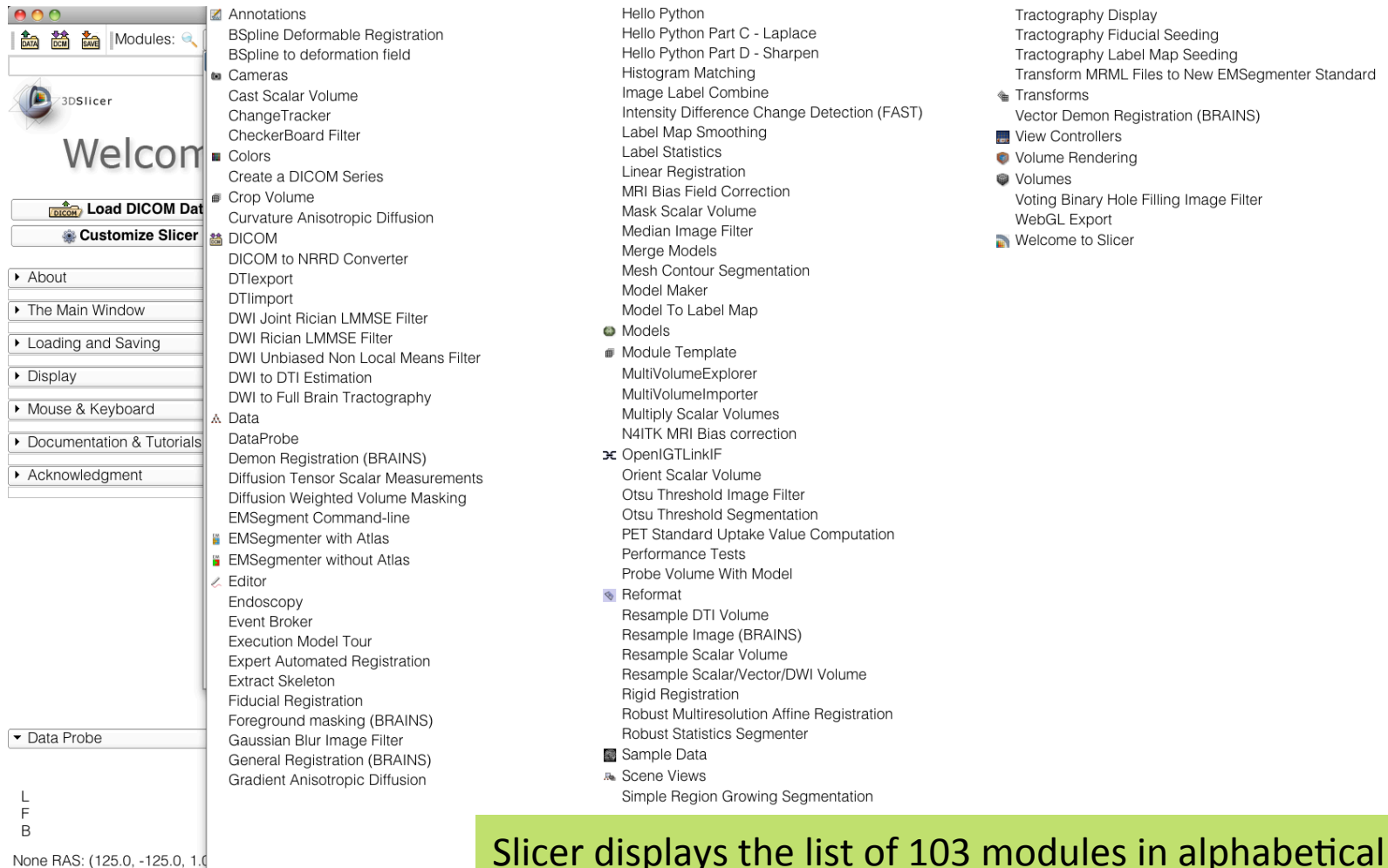
The DWI dataset is composed of 1 volume acquired without diffusion-sensitizing gradient, and 41 volumes acquired with 41 different diffusion-sensitizing gradients.

Start the Slicer Software



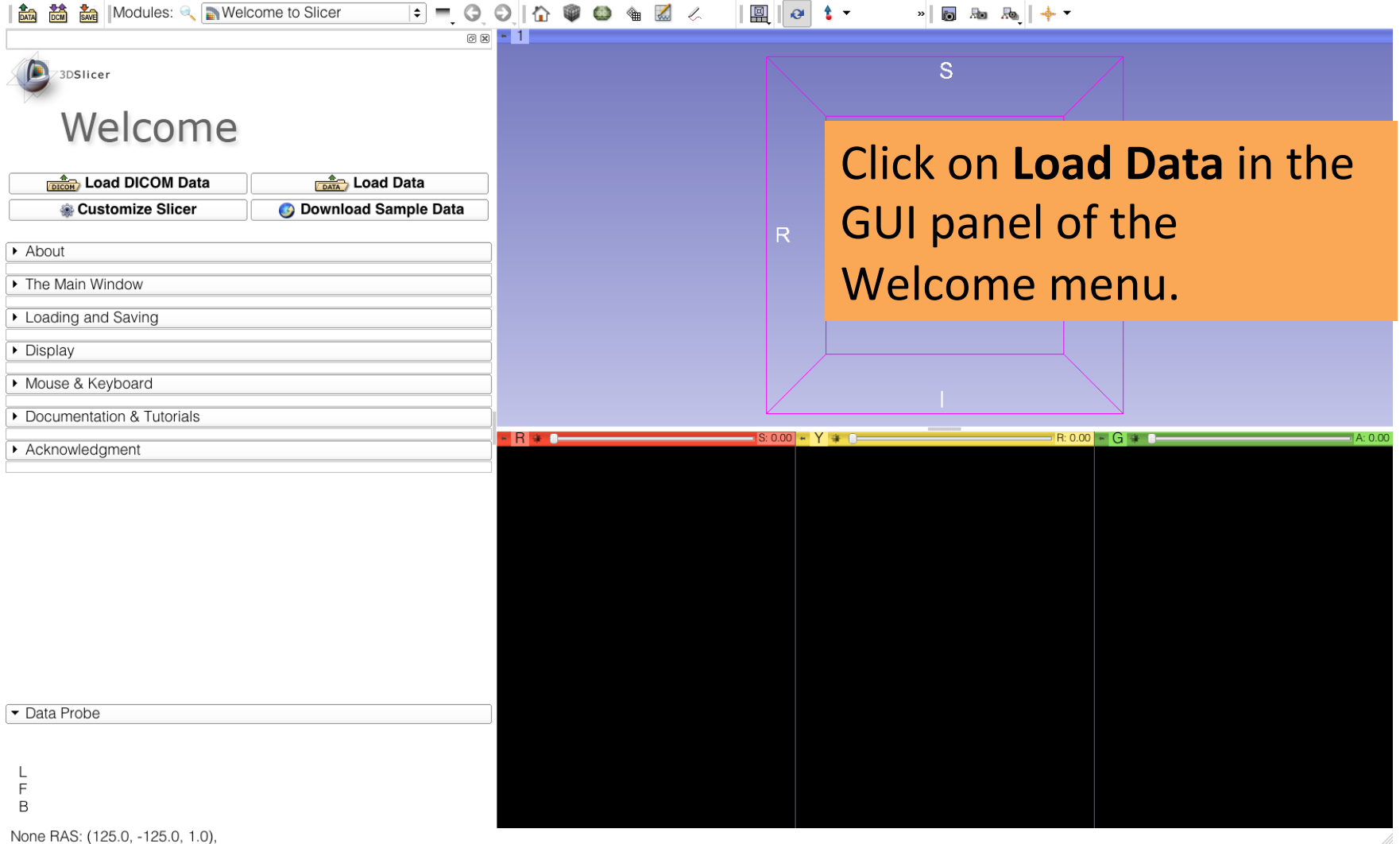
Slicer is built upon a modular architecture. The Welcome to Slicer module is displayed by default at start-up. Click on **Welcome to Slicer**, and on **All Modules** to display the 103 modules of Slicer in the Modules menu

Start the Slicer software

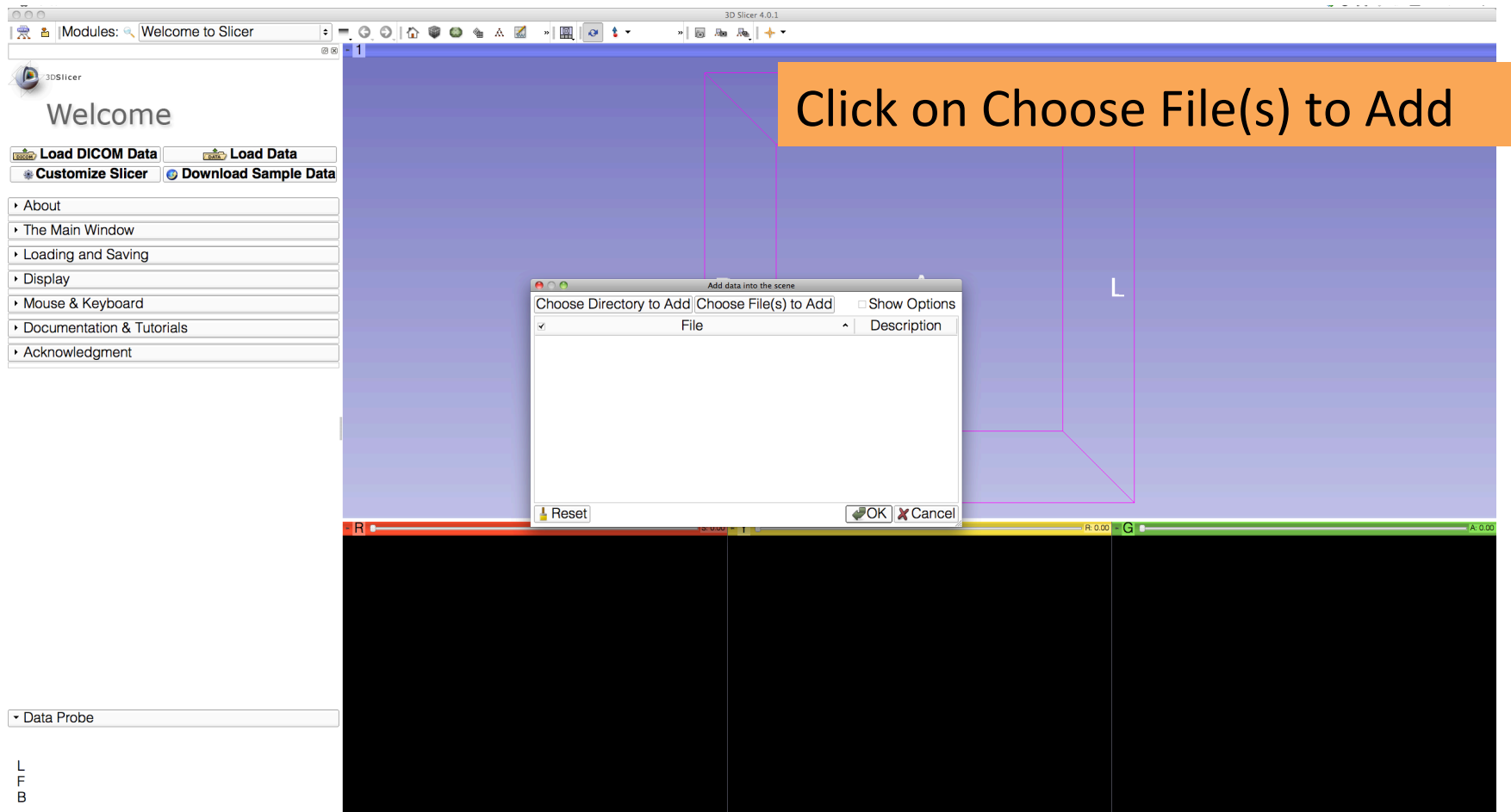


Slicer displays the list of 103 modules in alphabetical order.

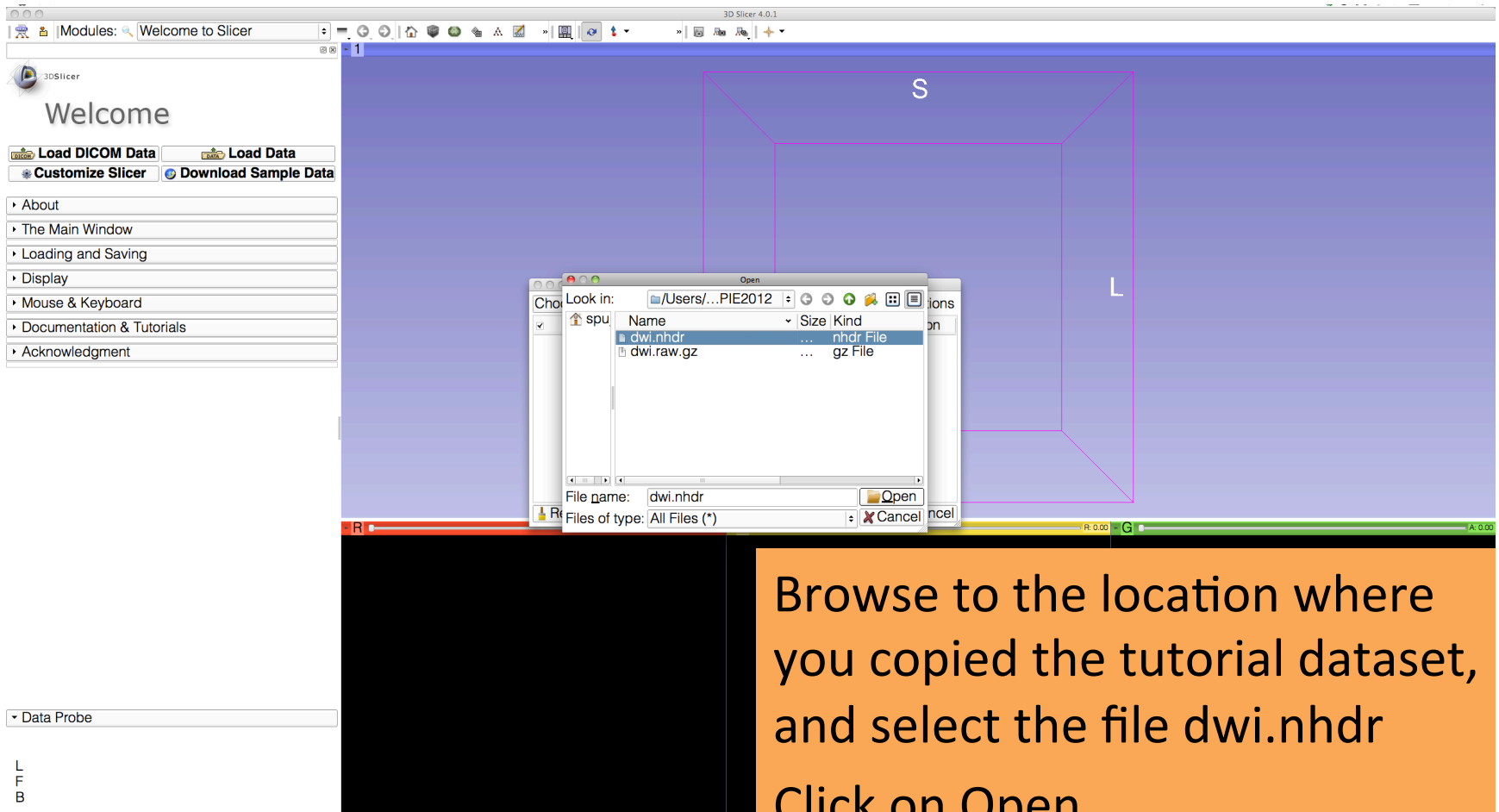
Loading the DWI dataset



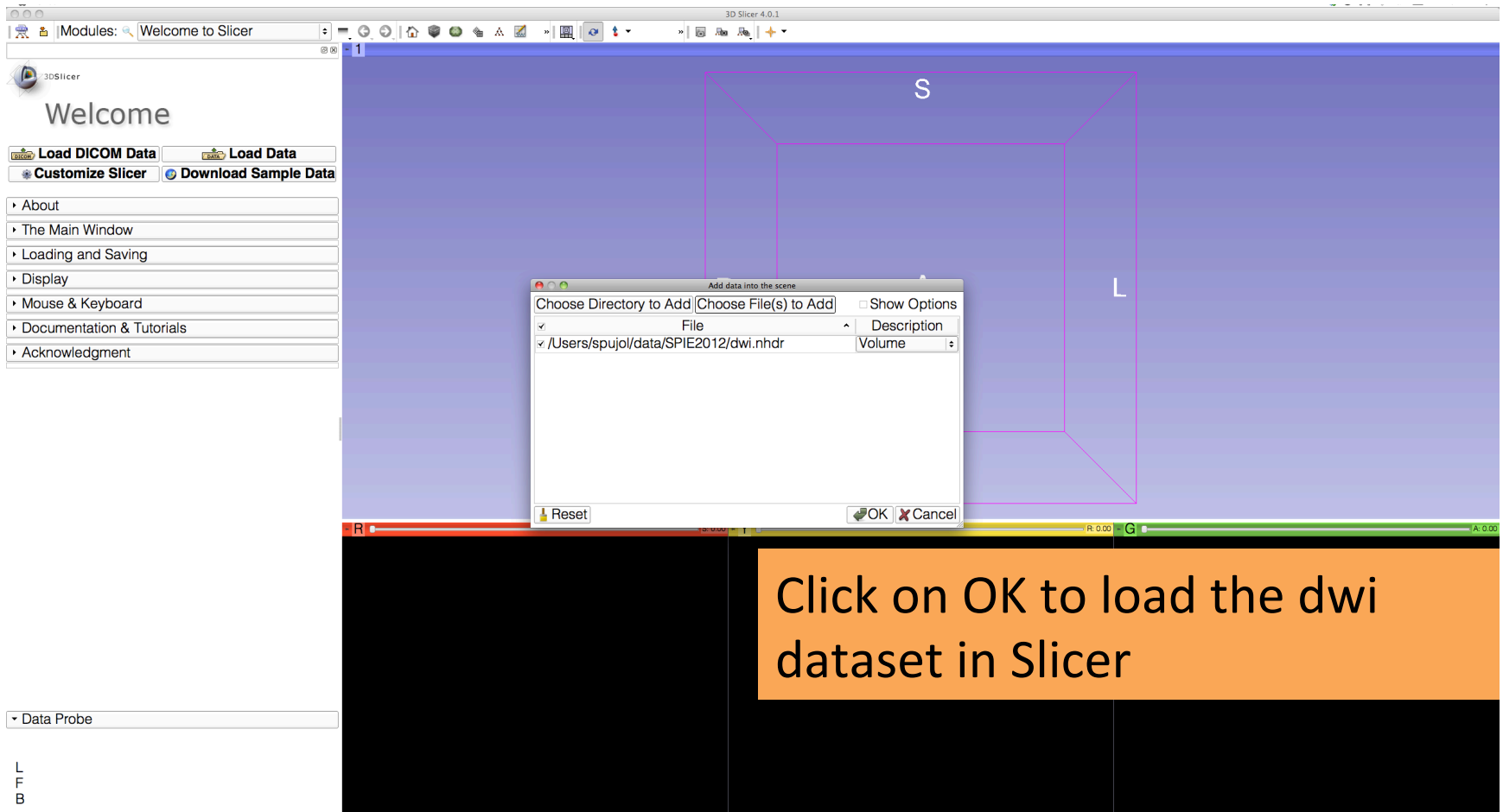
Loading the DWI dataset



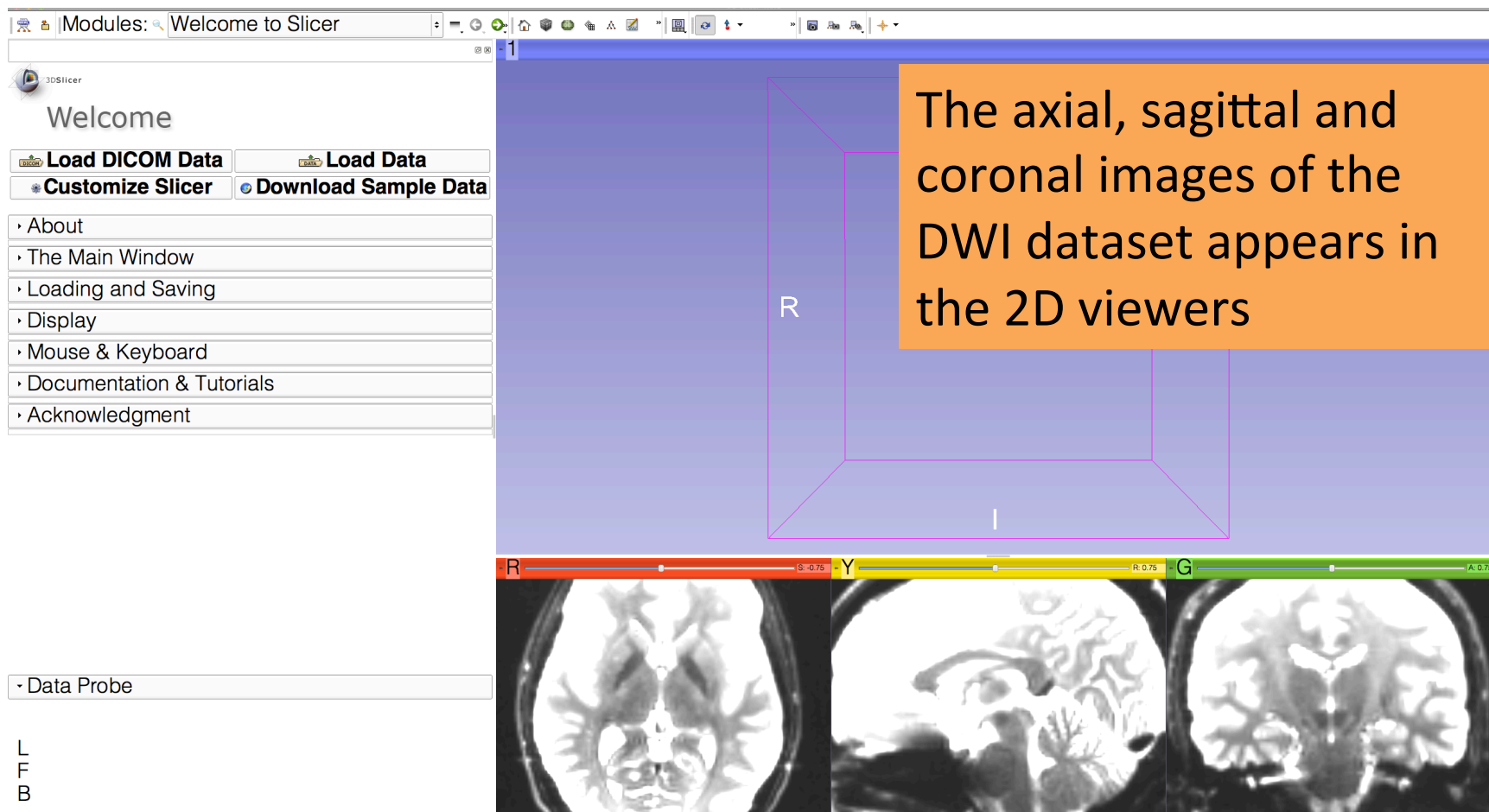
Loading the DWI dataset



Loading the DWI dataset



Loading the DWI dataset



Adjusting Window and Level

The screenshot shows the 3D Slicer software interface. The top menu bar includes 'Modules' and 'Volumes'. The left sidebar contains a 'Volumes' panel with various settings. 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 windows labeled 'R', 'Y', and 'G'. The 'R' window shows a coronal slice, the 'Y' window shows a sagittal slice, and the 'G' window shows an axial slice. The 'R' window has a red bar above it with 'R' and 'S: -0.75'. The 'Y' window has a yellow bar above it with 'Y' and 'R: 0.75'. The 'G' window has a green bar above it with 'G' and 'A: 0.75'. The bottom left corner has 'L', 'F', and 'B' labels.

Select the module Volumes from the modules menu.

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

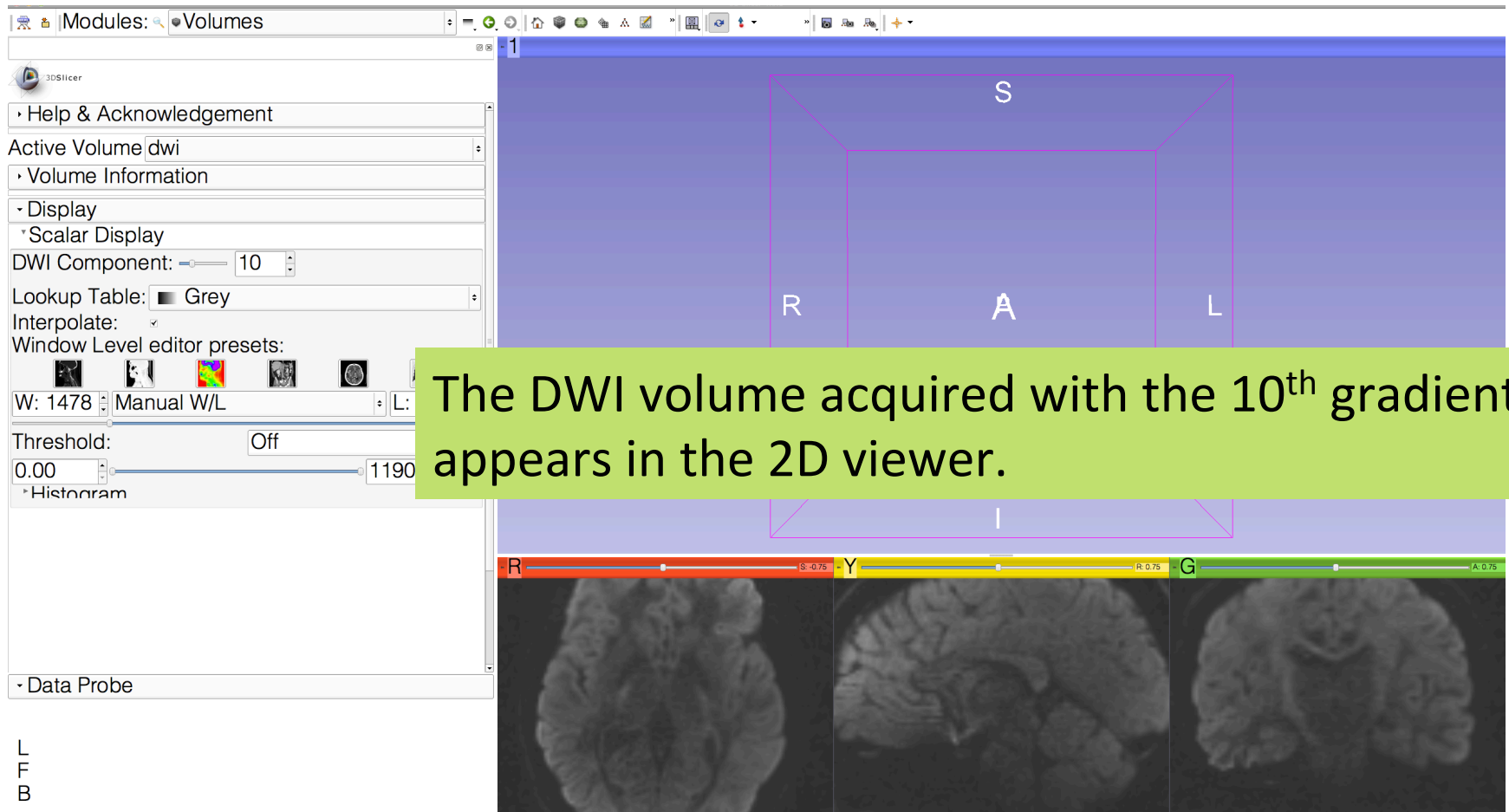
Exploring the DWI dataset

The screenshot shows the 3D Slicer software interface. The 'Volumes' module is active. In the 'Display' section, 'Scalar Display' is selected, and the 'DWI Component' is set to 0. A red arrow points to this dropdown menu. Below it, the 'Lookup Table' is set to 'Grey'. The 'Window Level editor' shows 'W: 1478' and 'L: 529'. The 'Histogram' section is visible at the bottom. The main view area shows a 3D volume with a red 'R' label and a purple '1' label. Below the 3D view are three 2D brain slices: axial (left), sagittal (middle), and coronal (right). The axial slice is labeled 'R' and 'S: -0.75'. The sagittal slice is labeled 'Y' and 'R: 0.75'. The coronal slice is labeled 'G' and 'A: 0.75'. The letters 'L', 'F', and 'B' are visible on the left side of the interface.

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

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

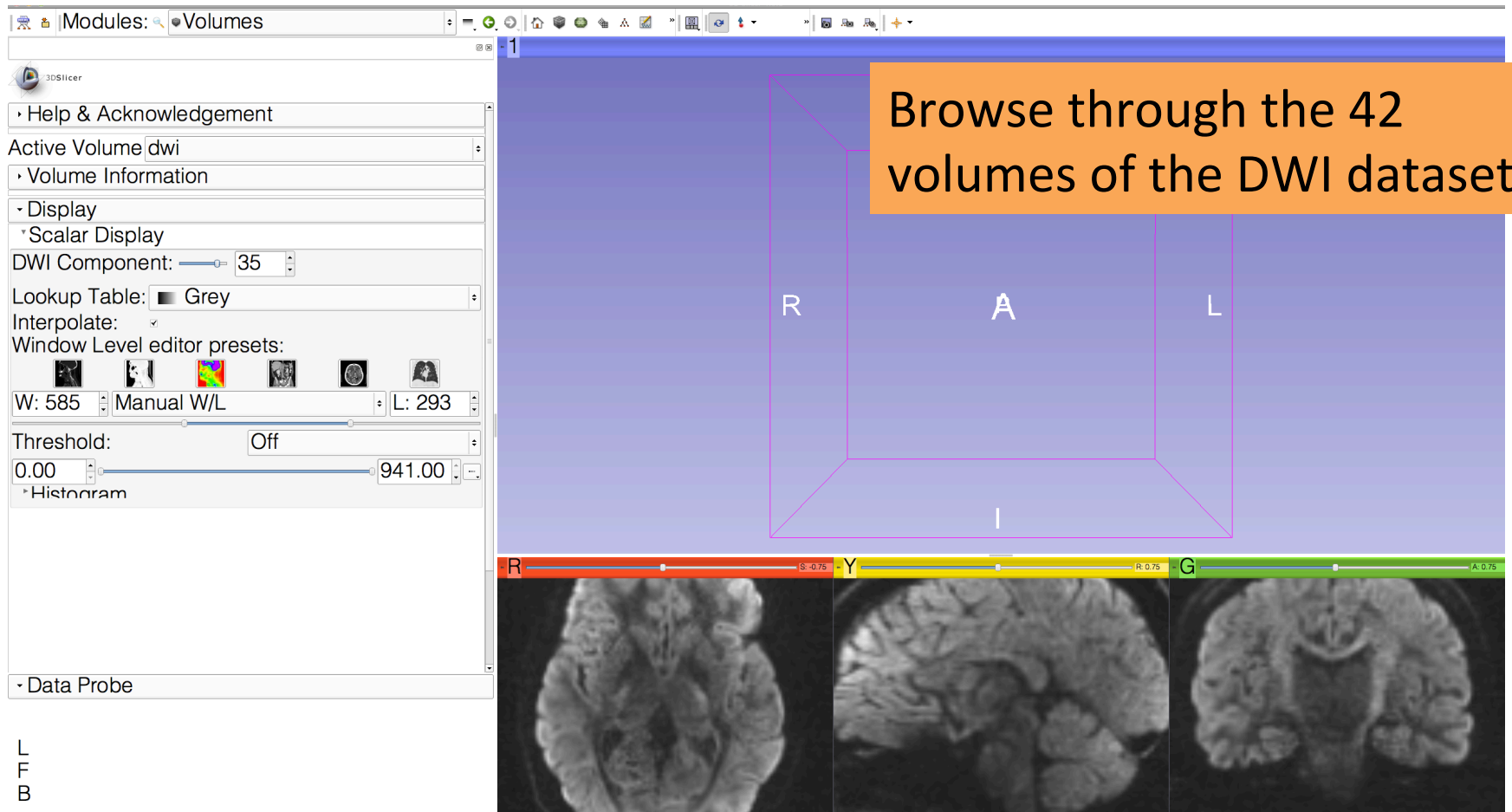
W: 585 Manual W/L L: 400

Threshold: Off

0.00 1190.00

L
F
B

Exploring the DWI dataset



Exploring the DWI dataset

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

The screenshot shows the 3D Slicer 4.0.1 interface. The top toolbar contains a viewing menu with icons for different layouts. A red arrow points to the 'R' icon, which represents the 'Red Slice Only' layout. An orange callout box with white text says: "Select the 'Red Slice Only' Layout from the viewing menu". The main window displays a grayscale axial brain slice. On the left, the 'Volumes' panel is open, showing settings for the active volume 'dwi', including 'DWI Component: 10', 'Lookup Table: Grey', and 'Threshold: Off'. The 'Data Probe' panel is also visible at the bottom left.

L
F
B

Diffusion Tensor Estimation

Select the module **DWI to DTI 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 'baseline'
- select the Estimation Method 'WLS' (Weighted Least Squares) and click on Apply.

Diffusion Tensor Estimation

3D Slicer 4.1.0-rc1-2012-03-15

Modules: DWI to DTI Estimation

3DSlicer

Help & Acknowledgement

DWI to DTI Estimation

Parameter set: DWI to DTI Estimation

Status Completed 100%

IO

Input DWI Volume dwi

Diffusion Tensor Mask None

Output DTI Volume dti

Output Baseline Volume baseline

Estimation Parameters

Estimation Parameters LS WLS

Shift Negative Eigenvalues

Default

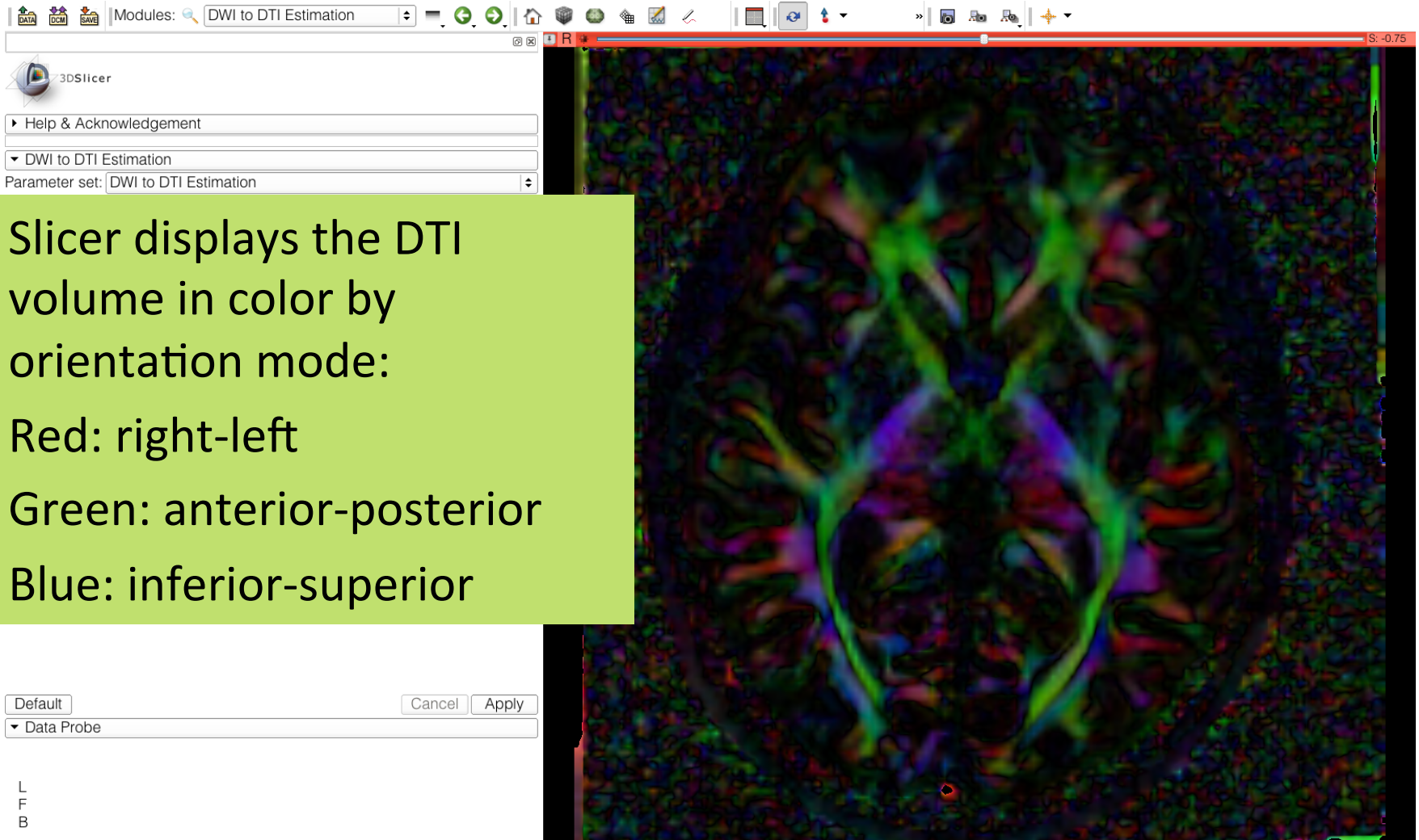
Cancel Apply

Data Probe

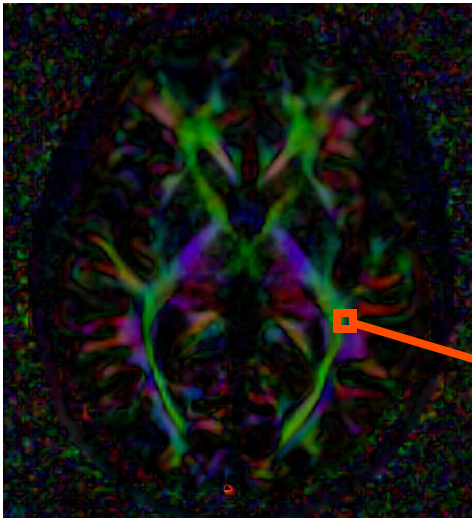
L
F
B

Select the volume 'dti' in the red viewer

Diffusion Tensor Estimation



Diffusion Tensor Data



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

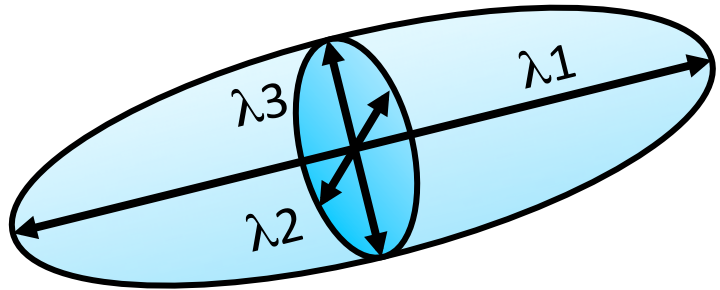
Stejskal-Tanner equation (1965)

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

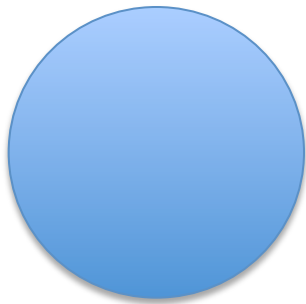
The diffusion tensor $\underline{\mathbf{D}}$ in the voxel (I,J,K) is a 3x3 symmetric matrix.

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.

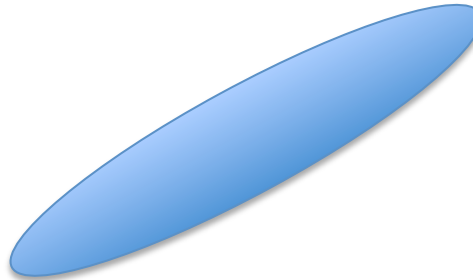


Diffusion Tensor Shape



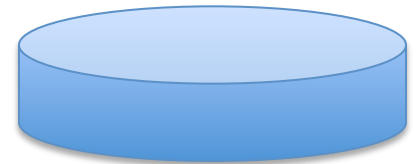
$$\lambda_1 = \lambda_2 = \lambda_3$$

Isotropic media
(CSF, gray matter)



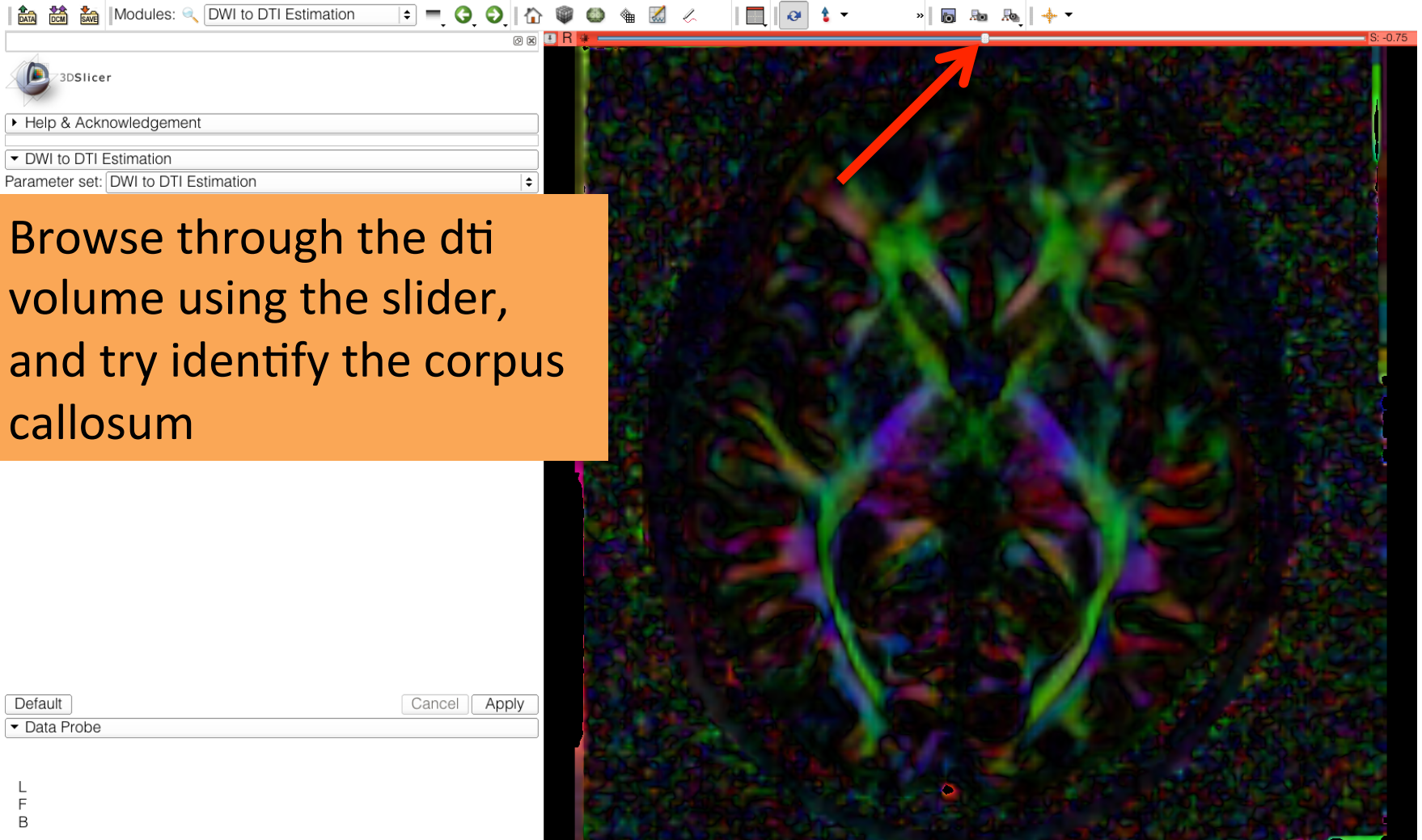
$$\lambda_1 \gg \lambda_2, \lambda_3$$

Anisotropic media
(white matter)



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

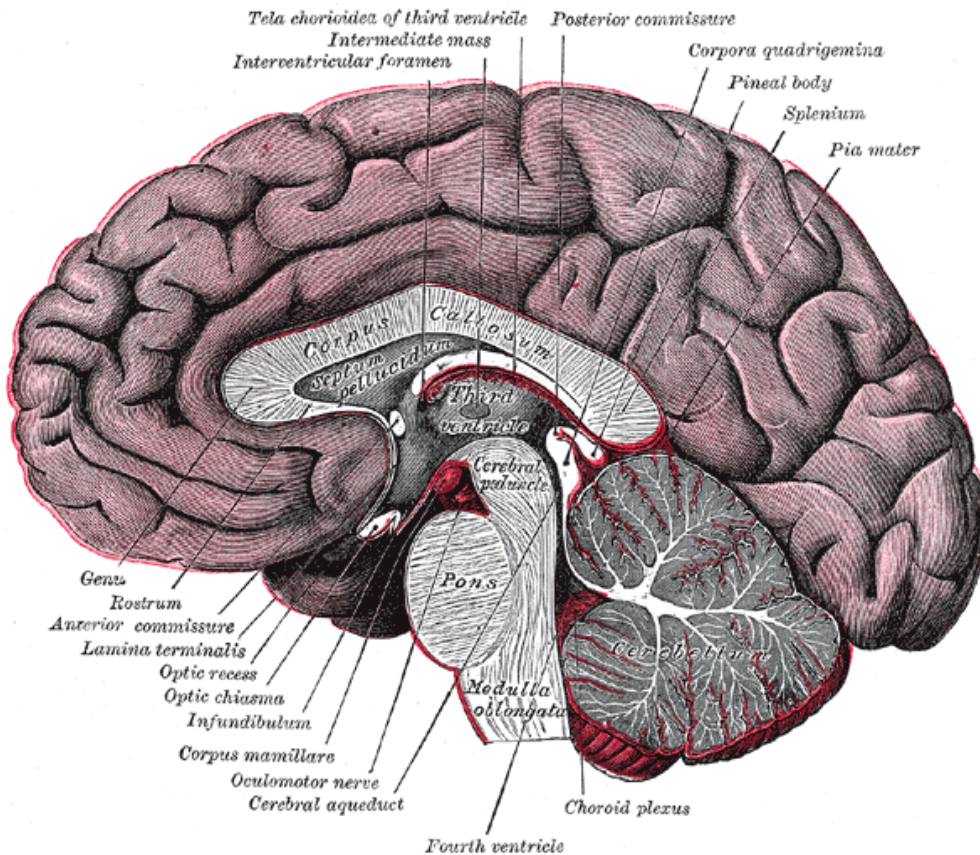
Exploring the Diffusion Tensor Data



The screenshot shows the 3DSlicer interface with the 'DWI to DTI Estimation' module active. The main view displays a colorful DTI volume. A red arrow points to a slider on the top toolbar, which is used to browse through the DTI volume. The interface includes a menu bar, a toolbar, and a sidebar with various options like 'Help & Acknowledgement' and 'DWI to DTI Estimation'. At the bottom, there are buttons for 'Default', 'Cancel', and 'Apply', and a 'Data Probe' dropdown menu.

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

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

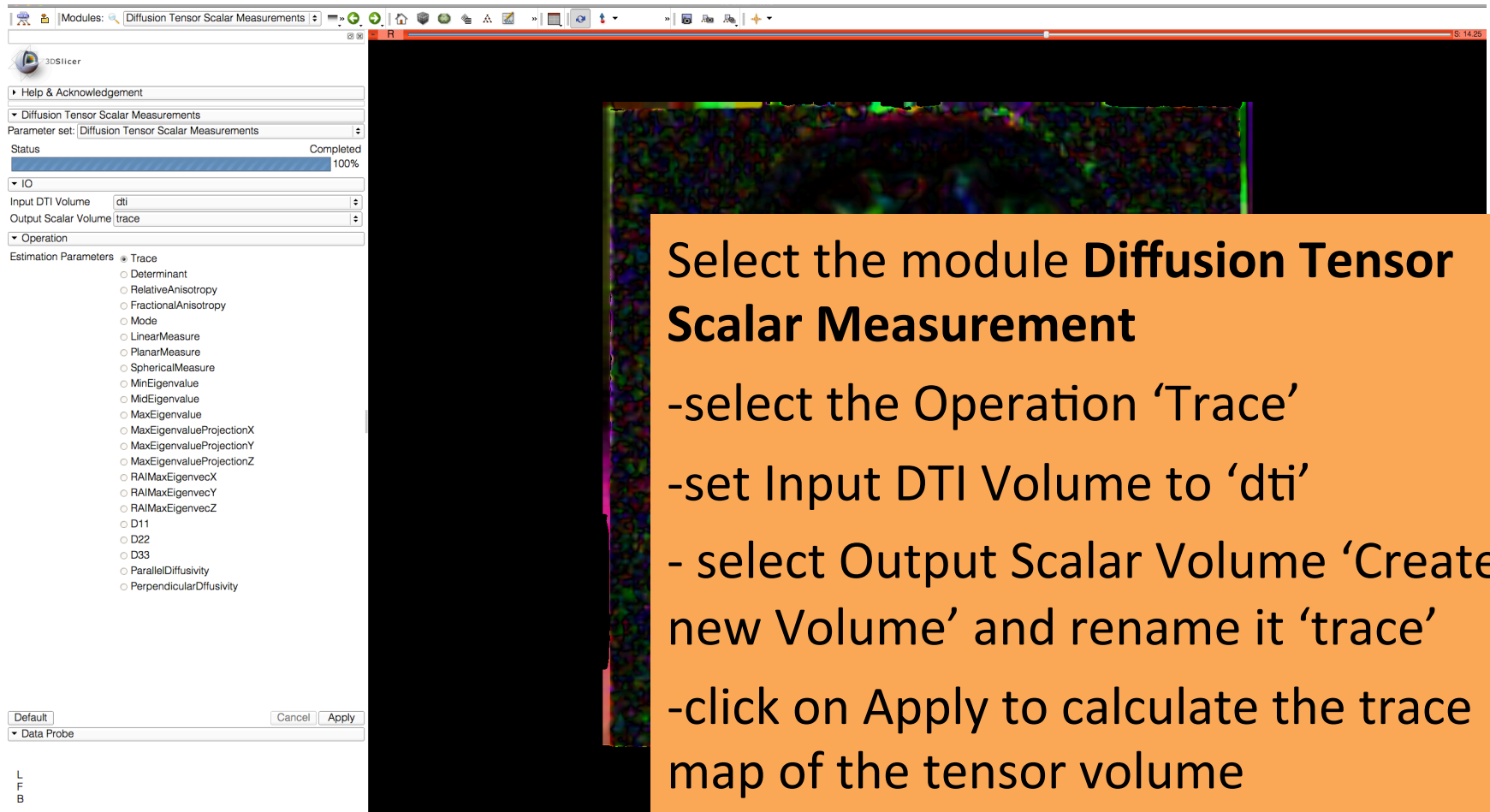
The image shows the 3DSlicer software interface. On the left, the 'DWI to DTI Estimation' module is active. The parameter set is 'DWI to DTI Estimation'. The status bar shows a progress indicator. The 'IO' section includes: Input DWI Volume (dwi), Diffusion Tensor Mask (None), Output DTI Volume (dti), and Output Baseline Volume (baseline). The 'Estimation Parameters' section has 'Estimation Parameters' set to 'WLS' (selected) and 'Shift Negative Eigenvalues' unchecked. At the bottom left, there are 'Default', 'Cancel', and 'Apply' buttons, and a 'Data Probe' dropdown. On the right, a brain DTI map is displayed in an axial view. A red arrow points to the corpus callosum, which is highlighted in red. A green box with the text 'Corpus Callosum' is overlaid on the image. The top status bar shows 'R' and 'S: 18.75'.

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

Trace

3DSlicer

Diffusion Tensor Scalar Measurements

Parameter set: Diffusion Tensor Scalar Measurements

Status Completed
100%

IO

Input DTI Volume dti

Output Scalar Volume trace

Operation

- LinearMeasure
- PlanarMeasure
- SphericalMeasure
- MinEigenvalue
- MidEigenvalue
- MaxEigenvalue
- MaxEigenvalueProjectionX
- MaxEigenvalueProjectionY
- MaxEigenvalueProjectionZ
- RAIMaxEigenvX

Default

Data Probe

Red RAS: (16.9, 30.4, -0.8) Axial Sp: 1.5

L None ()

F None ()

B trace (53, 44, 47) 0.001736

The trace image appears in the red viewer

Trace

3D Slicer 4.1.0-rc1-2012-03-15

Modules: Diffusion Tensor Scalar Measurements

3DSlicer

Help & Acknowledgement

Diffusion Tensor Scalar Measurements

Parameter set: Diffusion Tensor Scalar Measurements

Status Completed 100%

IO

Input DTI Volume dti

Output Scalar Volume trace

Operation

Estimation Parameters

- Trace
- Determinant
- RelativeAnisotropy
- FractionalAnisotropy
- Mode
- LinearMeasure
- PlanarMeasure
- SphericalMeasure

Default

Data Prob

L
F
B

Axial

1.00 None

0.40 dti

1.00 trace

Select the volume 'trace' in the Background viewer, and the volume 'dti' in the Foreground viewer

Set the opacity of the dti volume to 0.40

Trace

3D Slicer 4.1.0-rc1-2012-03-15

Modules: Diffusion Tensor Scalar Measurements

Diffusion Tensor Scalar Measurements
Parameter set: Diffusion Tensor Scalar Measurements
Status: Completed 100%

Input DTI Volume: dti
Output Scalar Volume: trace

1.00 None
0.40 dti
1.00 trace

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.

MaxEigenvalue
MaxEigenvalueProjectionX
MaxEigenvalueProjectionY
MaxEigenvalueProjectionZ
RAIMaxEigenvecX

Default Cancel Apply

Data Probe

Red RAS: (10.3, 23.7, 18.8) Axial Sp: 1.5
L None ()
F dti (57, 48, 60) ColorOrientation 0
B trace (57, 48, 60) 0.002243

Trace

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

3D Slicer 4.1.0-rc1-2012-03-15

Modules: Diffusion Tensor Scalar Measurements

Diffusion Tensor Scalar Measurements

Parameter set: Diffusion Tensor Scalar Measurements

Status: Completed 100%

MaxEigenvalueProjectionX
MaxEigenvalueProjectionY
MaxEigenvalueProjectionZ
RAIMaxEigenvecX

Default Cancel Apply

Data Probe

Red RAS: (10.3, 23.7, 18.8) Axial Sp: 1.5




L None ()

F dti (57, 48, 60) ColorOrientation 0

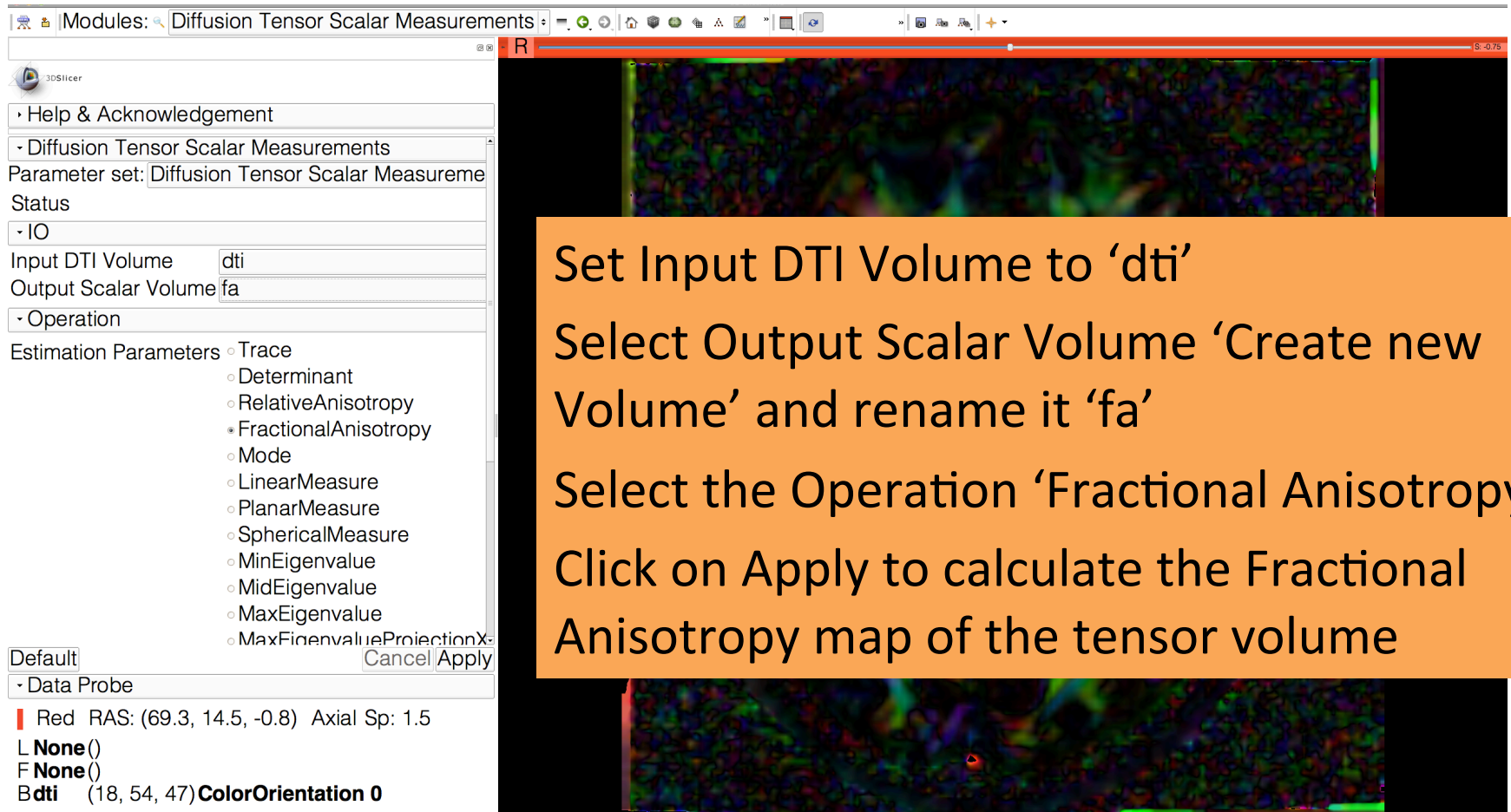
B trace (57, 48, 60) 0.002243

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 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()

B dti (18, 54, 47) ColorOrientation 0

Set Input DTI Volume to 'dti'

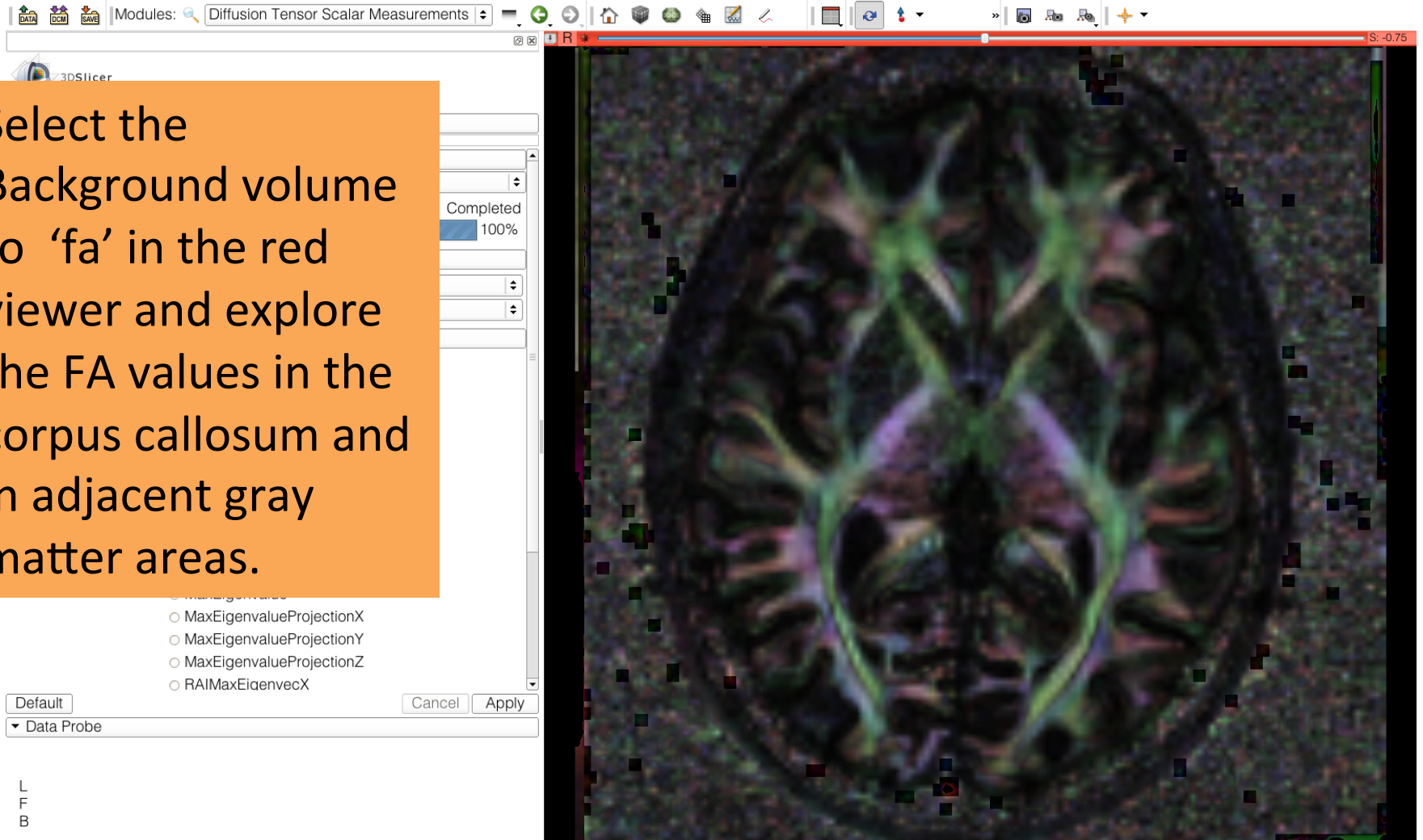
Select Output Scalar Volume 'Create new Volume' and rename it 'fa'

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 for the 'Data Probe' at RAS coordinates (7.2, 25.4, 15.8) with an axial slice spacing of 1.5. The 'fa' parameter is highlighted with a red box, showing a value of 0.8329. The main window displays an axial brain MRI slice with a color-coded FA map. A red arrow points to a white matter region, indicating high FA values.

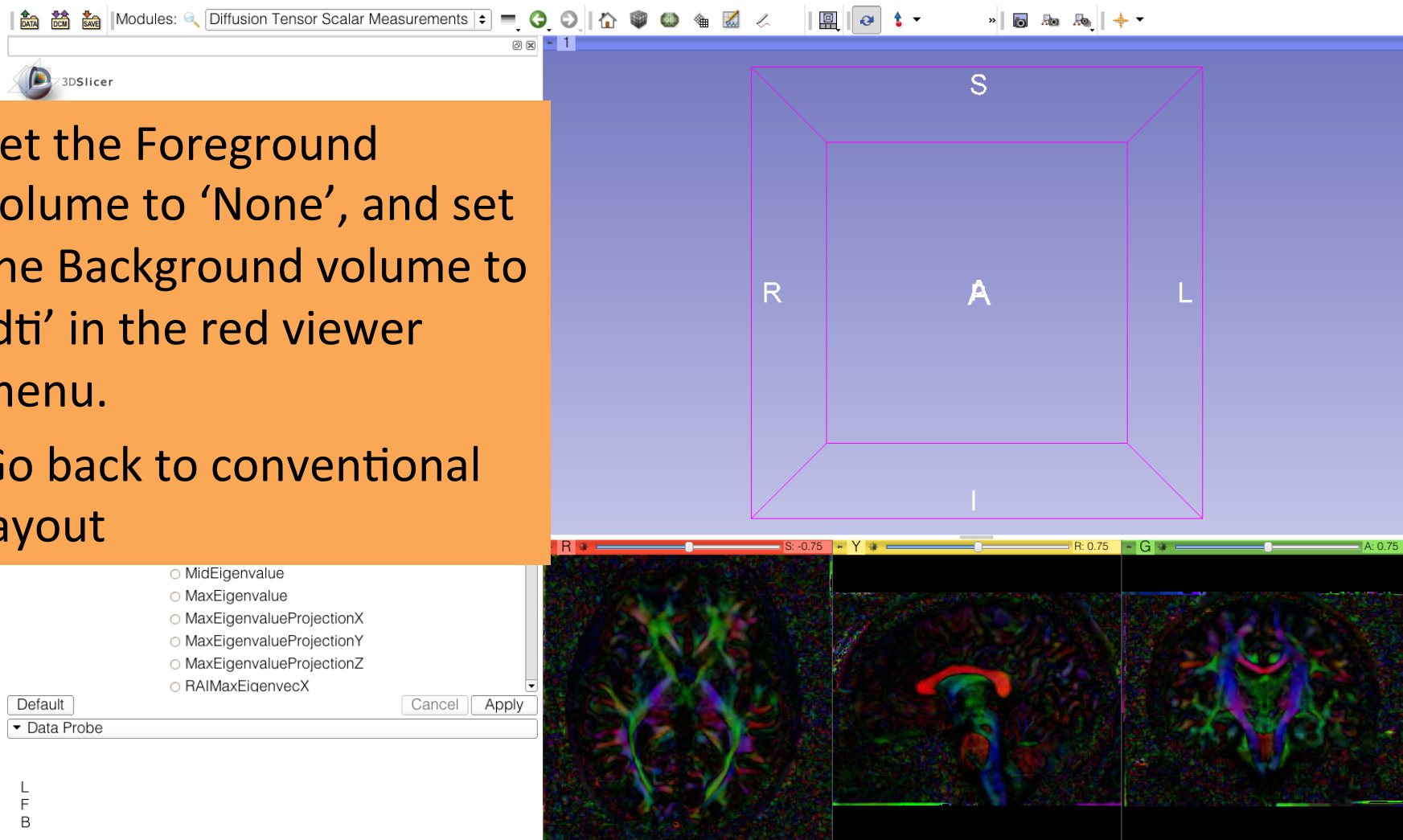
- MinEigenvalue
- MidEigenvalue
- MaxEigenvalue
- MaxEigenvalueProjectionX
- MaxEigenvalueProjectionY
- MaxEigenvalueProjectionZ
- RAI_MaxEigenvecX
- RAI_MaxEigenvecY
- RAI_MaxEigenvecZ
- D11
- D22
- D33

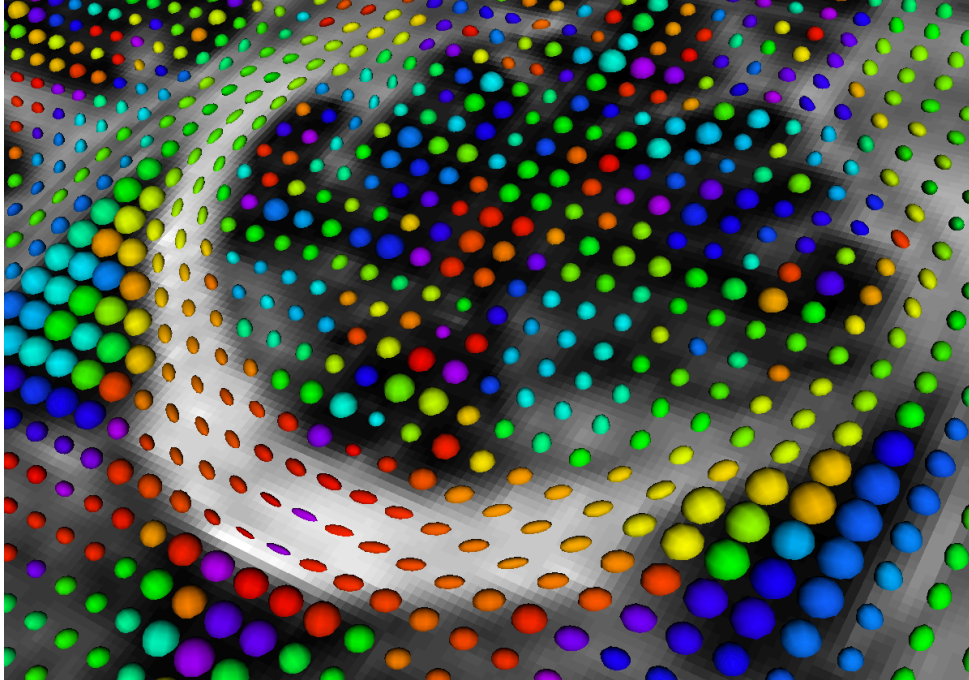
Default
Data Probe
Red RAS: (7.2, 25.4, 15.8) Axial Sp: 1.5
dti (59, 47, 58) ColorOrientation 0
fa (59, 47, 58) 0.8329

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





Part 2: Visualizing the tensor data

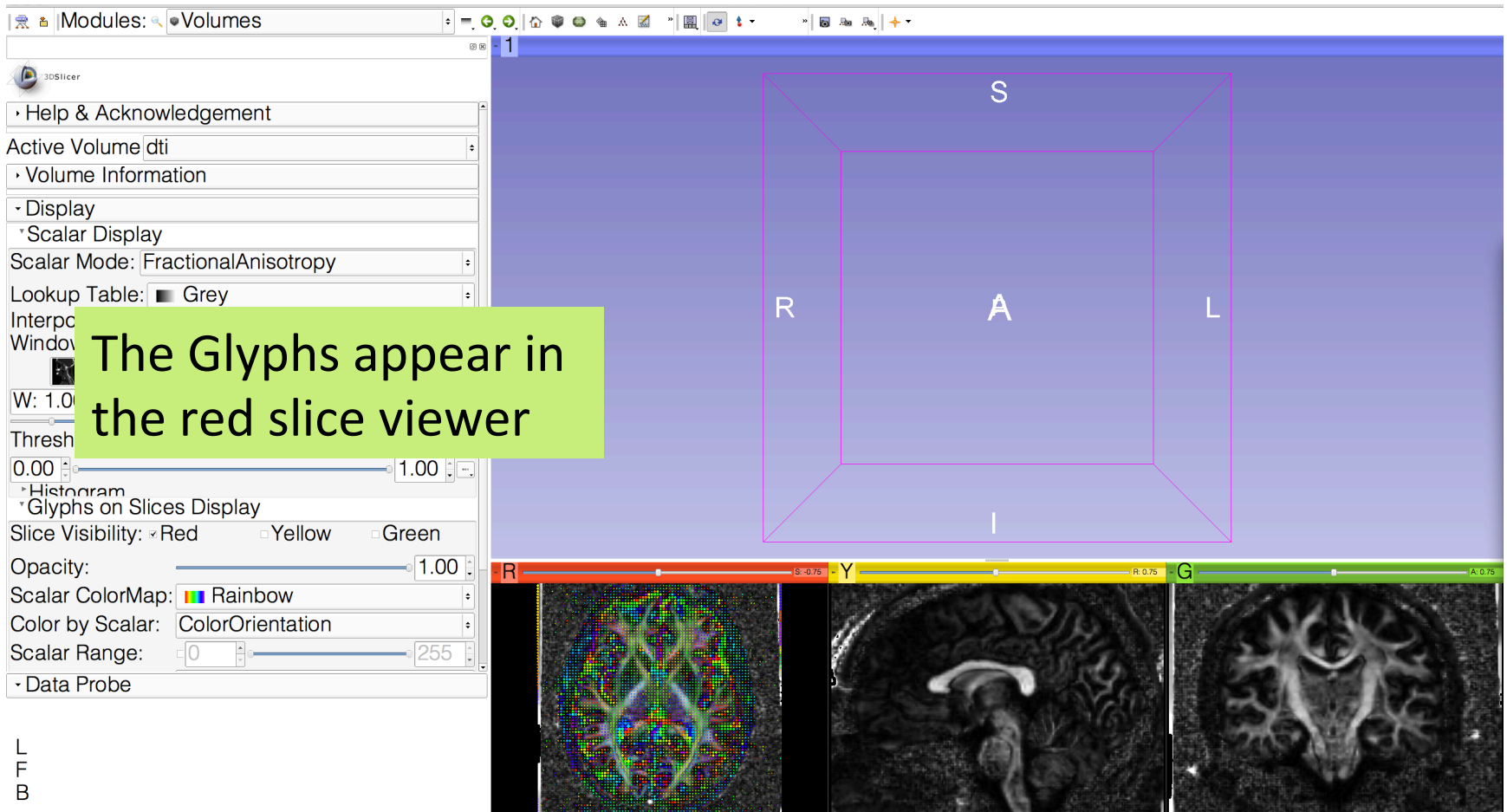
3D Visualization: Glyphs

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

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

L
F
B

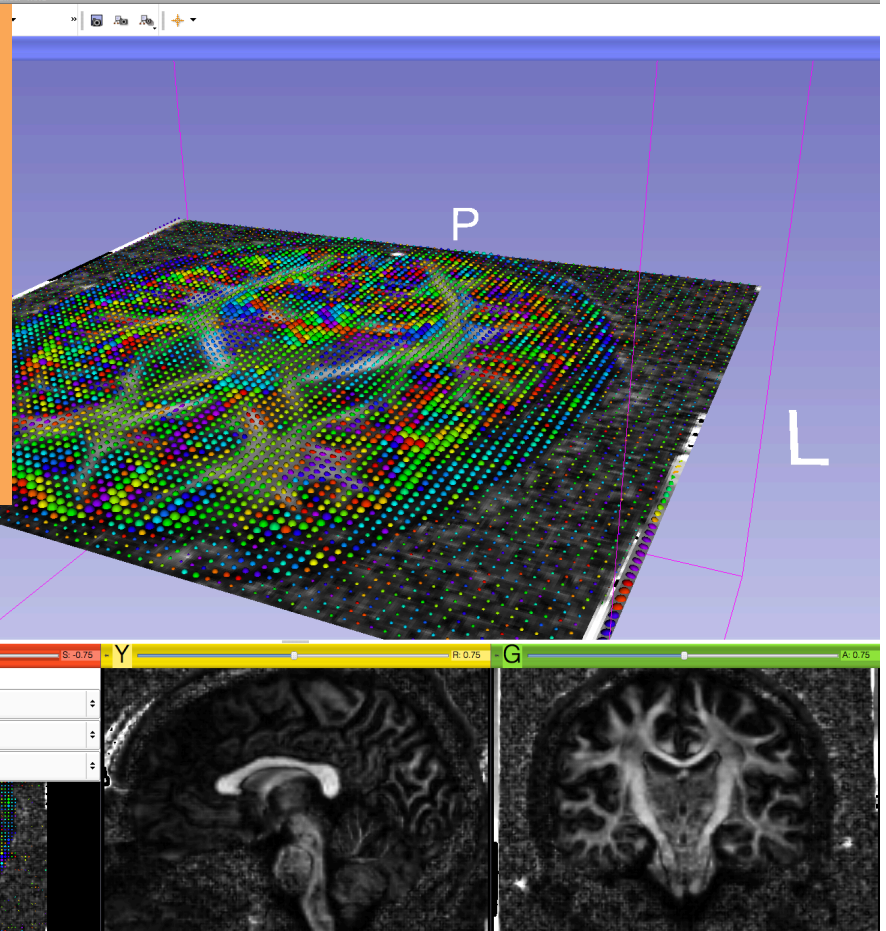
3D Visualization: Glyphs



3D Visualization: Glyphs

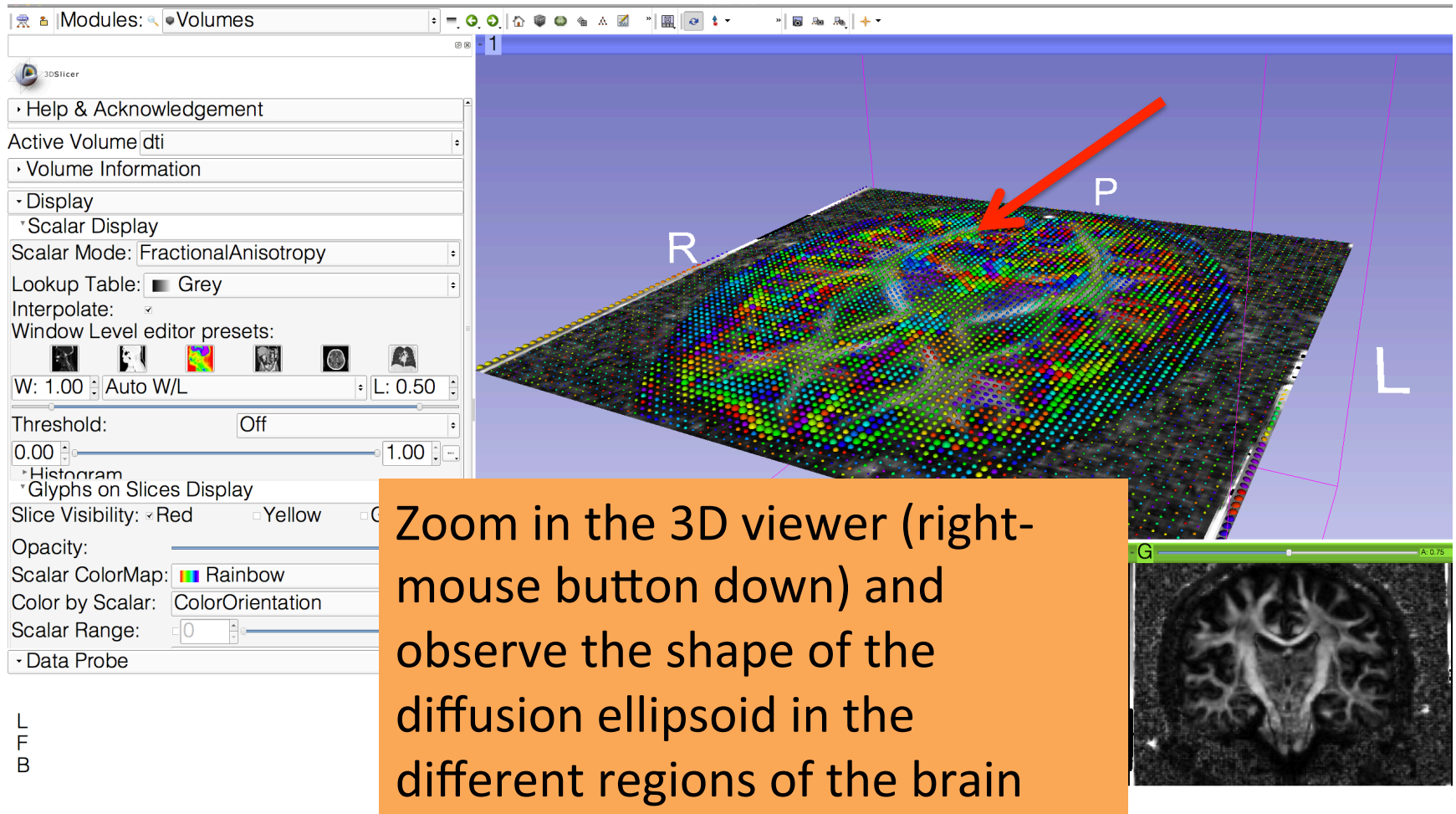
Click on the link icon in the red slice viewer to unlink the three viewers.

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



L
F
B

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

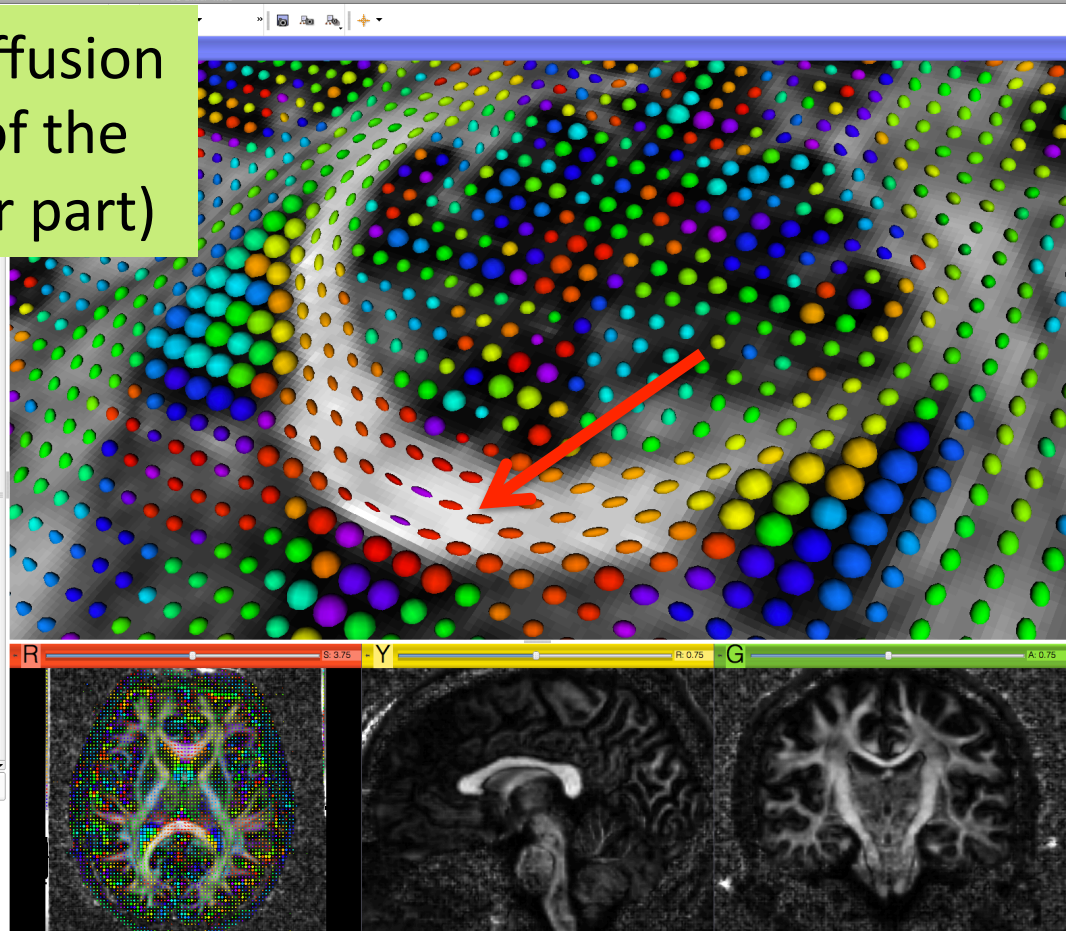
Scalar Range: 0 | 255

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

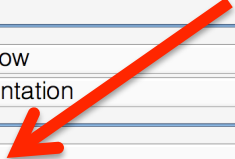
Slice Visibility: Red Yellow Green

Opacity: 1.00

Scalar ColorMap: Rainbow

Color by Scalar: ColorOrientation

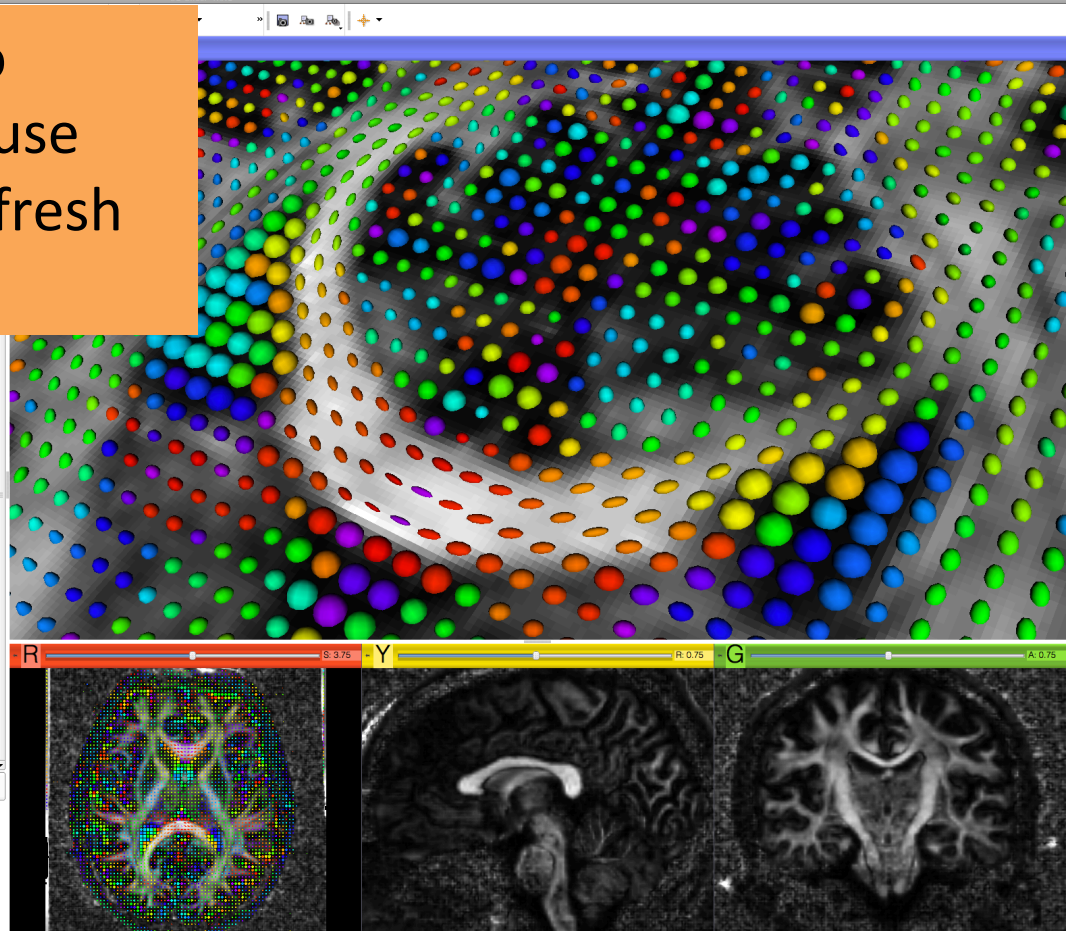
Scalar Range: 0 255

Glyph Type: Ellipsoids 

Scale Factor: 45.00

Spacing: 5.00

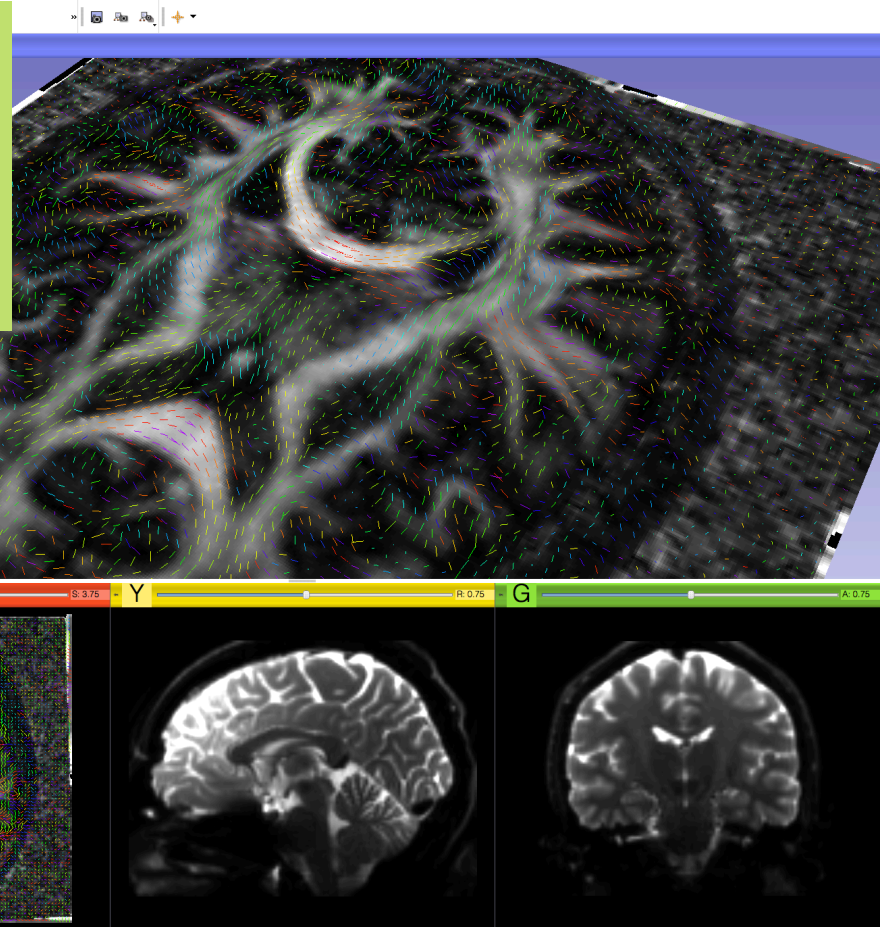
Data Probe



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

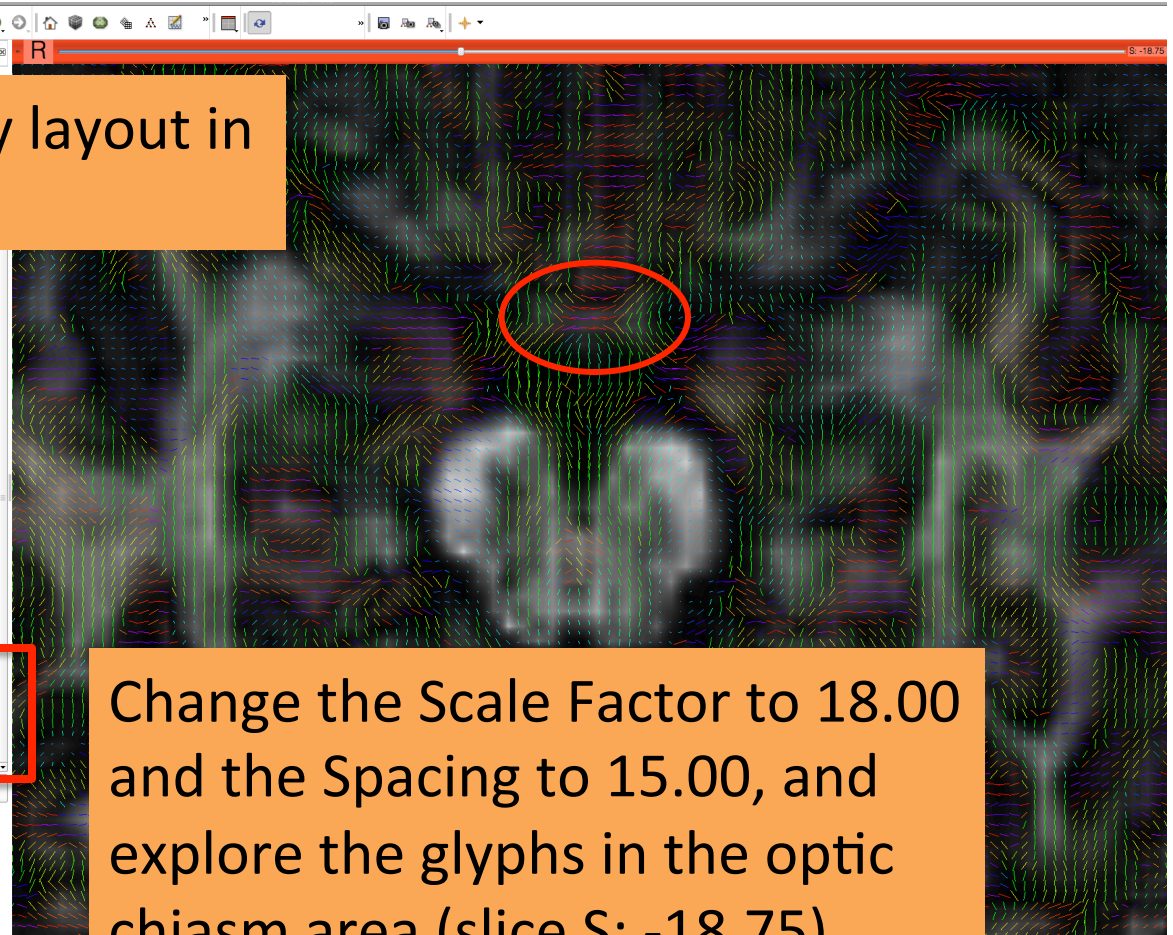
Data Probe

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.

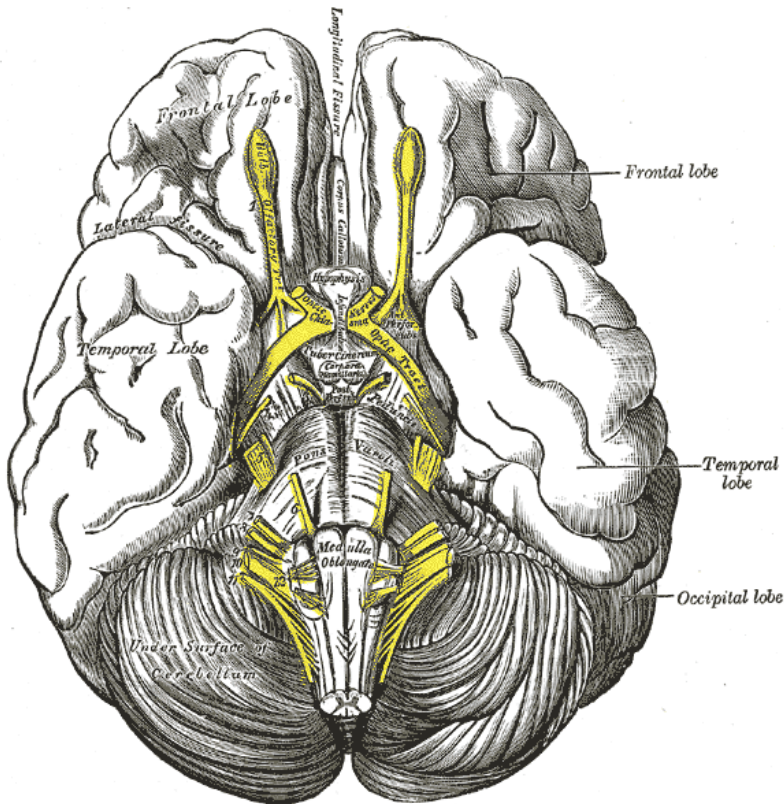
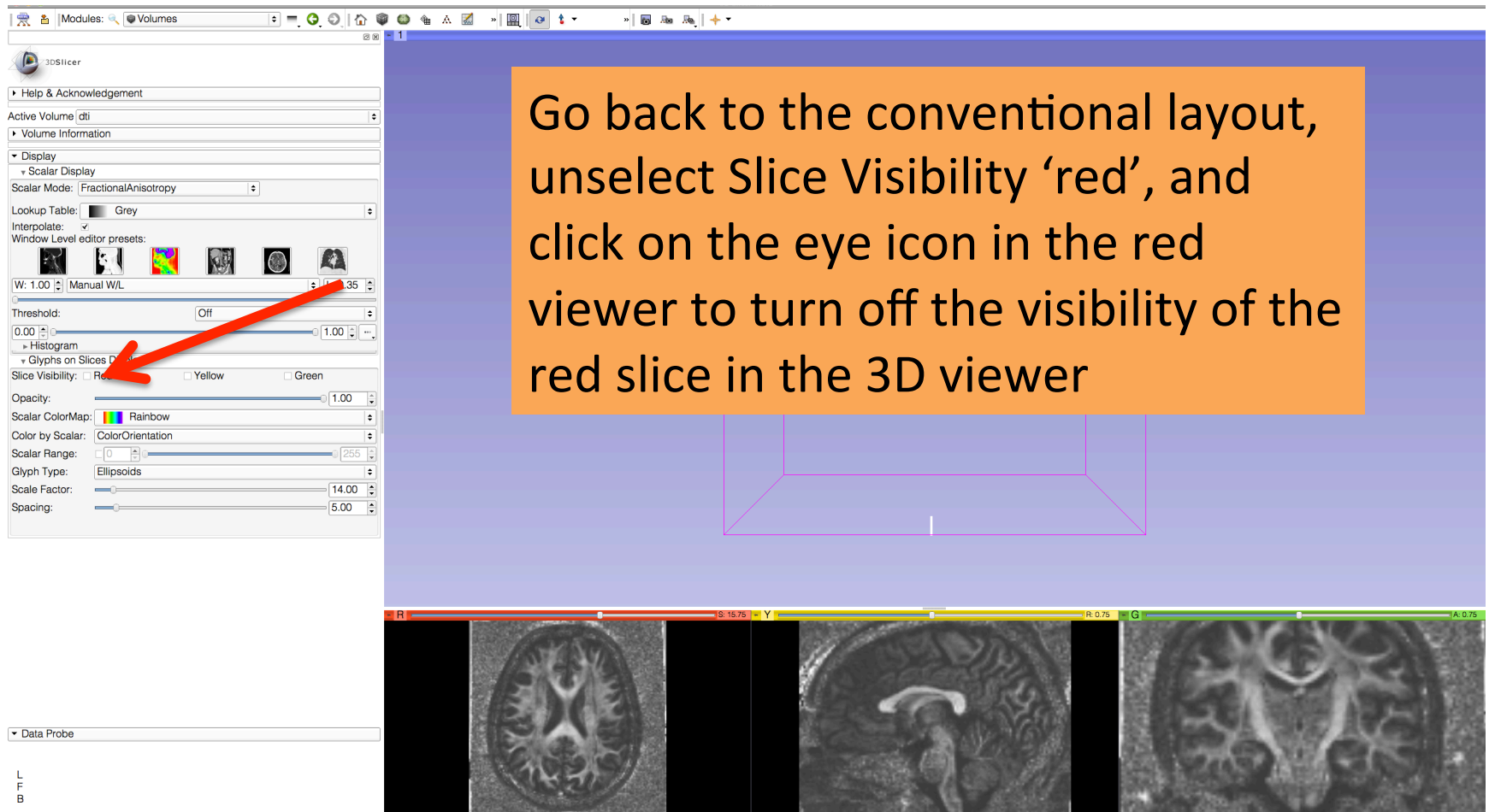


Image from Gray's Anatomy

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

Modules: Volumes

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

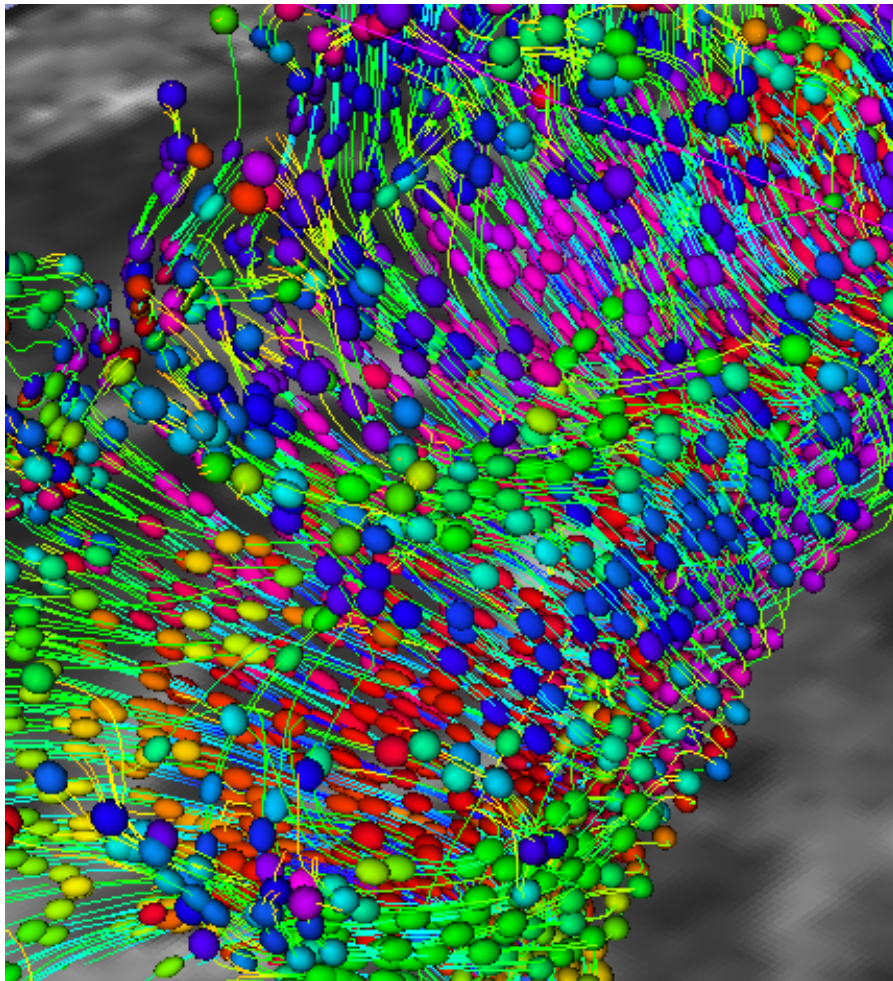
Scale Factor: 14.00

Spacing: 5.00

Data Probe

L
F
B

R S Y R G A

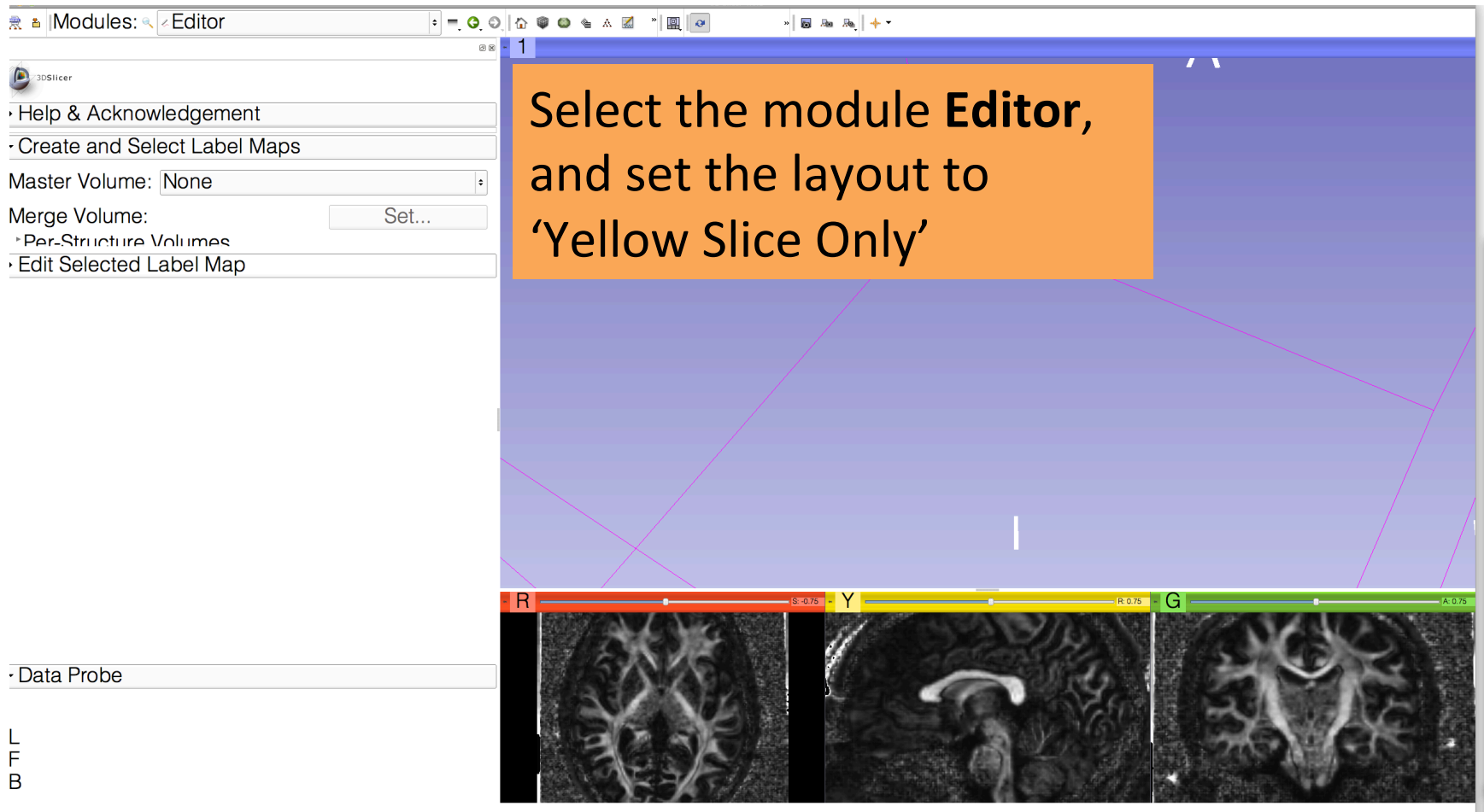


Part 3: From tensors to tracts

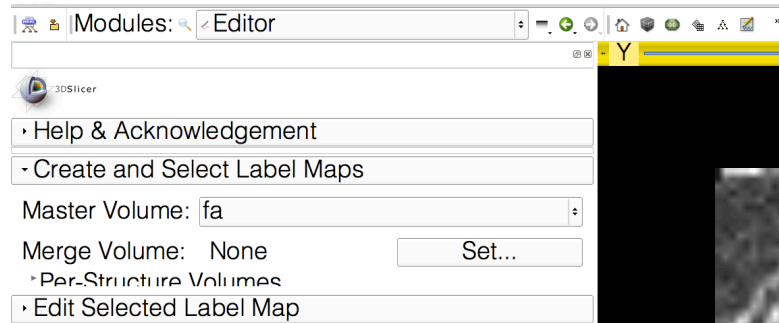
Diffusion MRI tractography

- 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 $\sim 1\text{-}5\text{ mm}$; diameter of an axon $\sim 0.1\text{-}10\text{ }\mu\text{m}$
- A DTI tract is not equivalent to a real fiber.

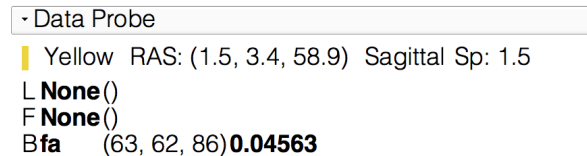
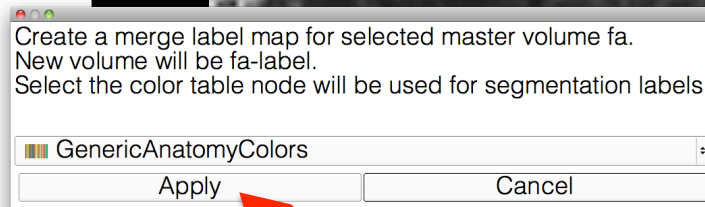
Tractography Seeding: ROI definition



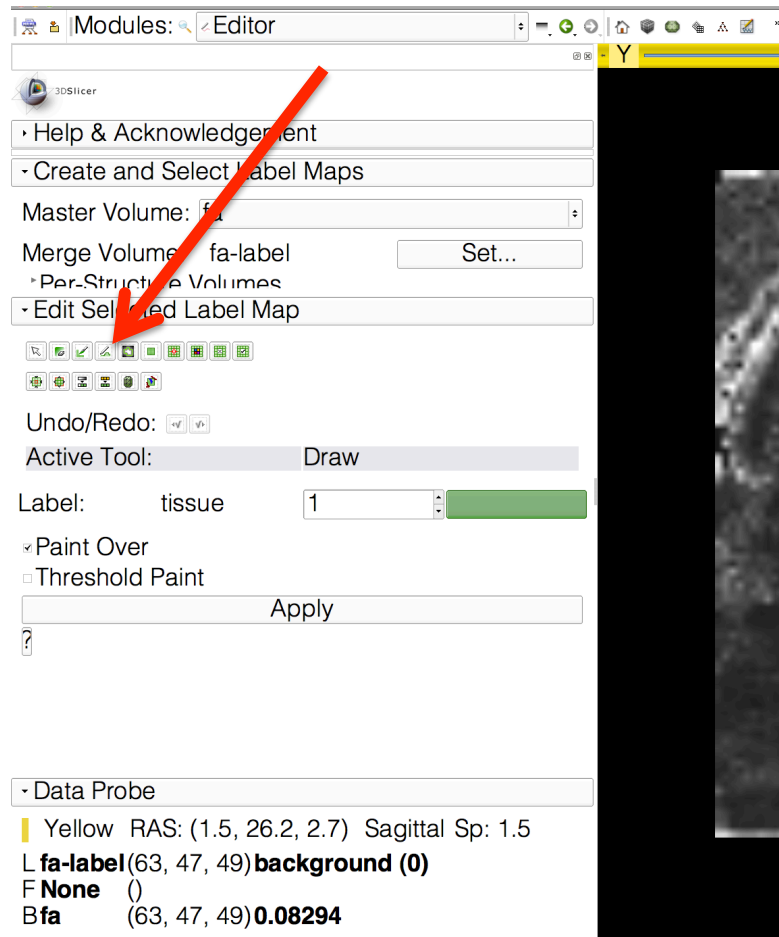
ROI Definition



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



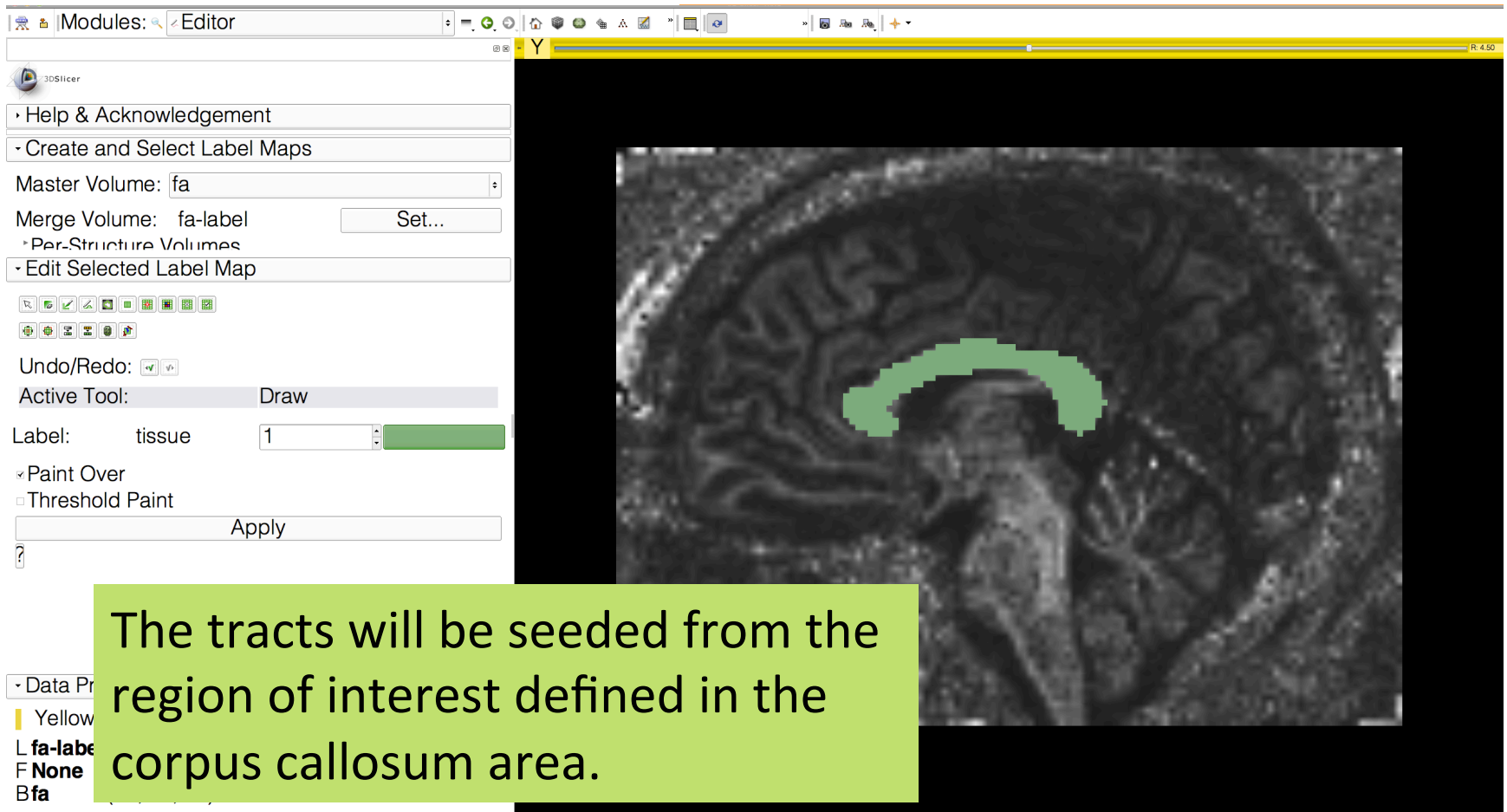
ROI Drawing



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.



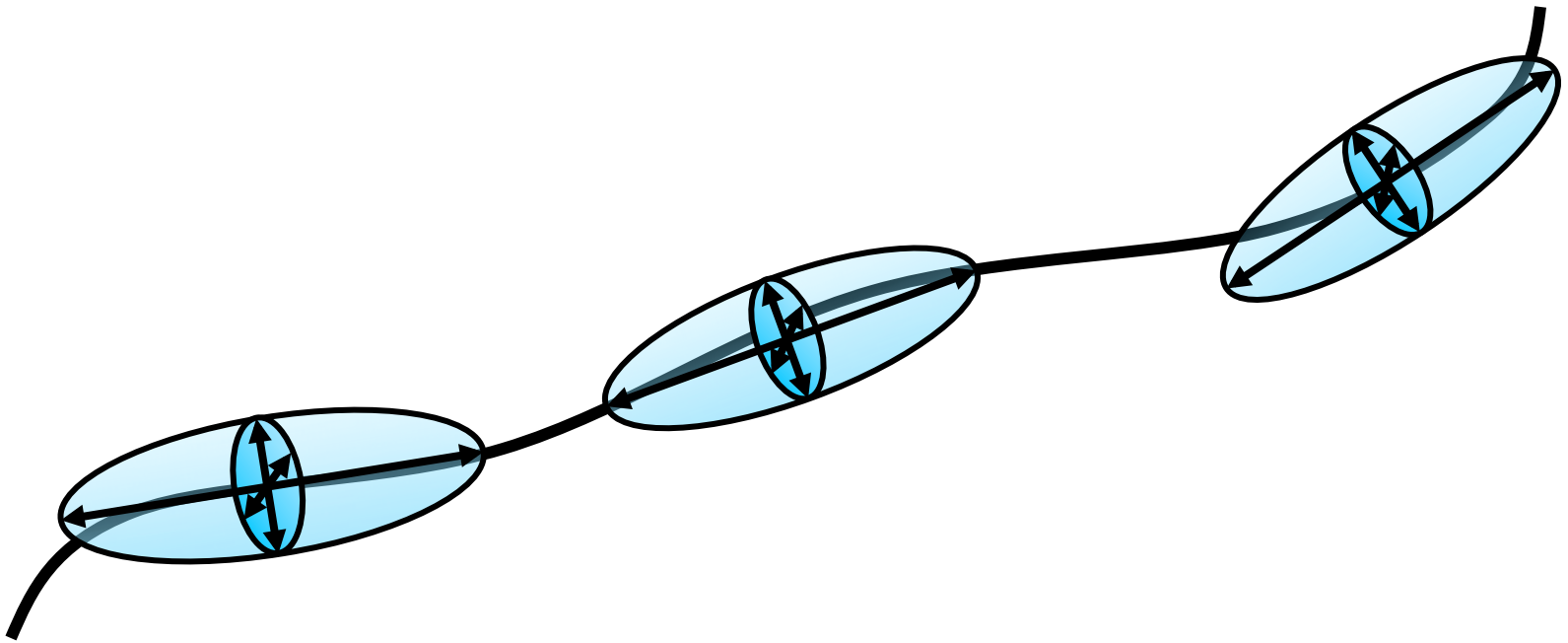
ROI Drawing



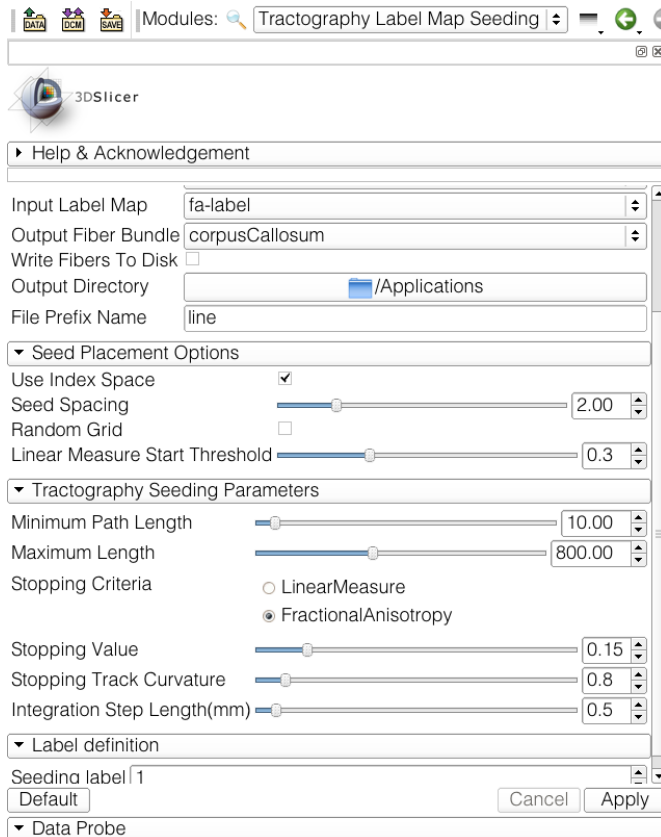
The screenshot shows the 3D Slicer software interface. The top menu bar includes 'Modules: Editor'. The left sidebar contains a '3D Slicer' logo and several menu items: 'Help & Acknowledgement', 'Create and Select Label Maps', 'Master Volume: fa', 'Merge Volume: fa-label', 'Per-Structure Volumes', and 'Edit Selected Label Map'. Below these are various tool icons, an 'Undo/Redo' section, and an 'Active Tool: Draw' dropdown. The 'Label:' field 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 light 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



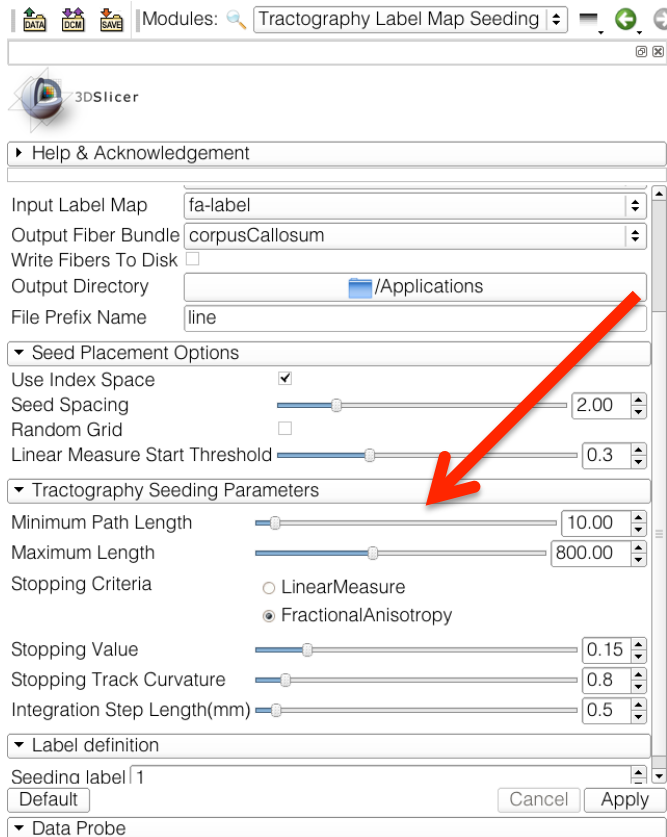
Select the module **Tractography Label Map Seeding**

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

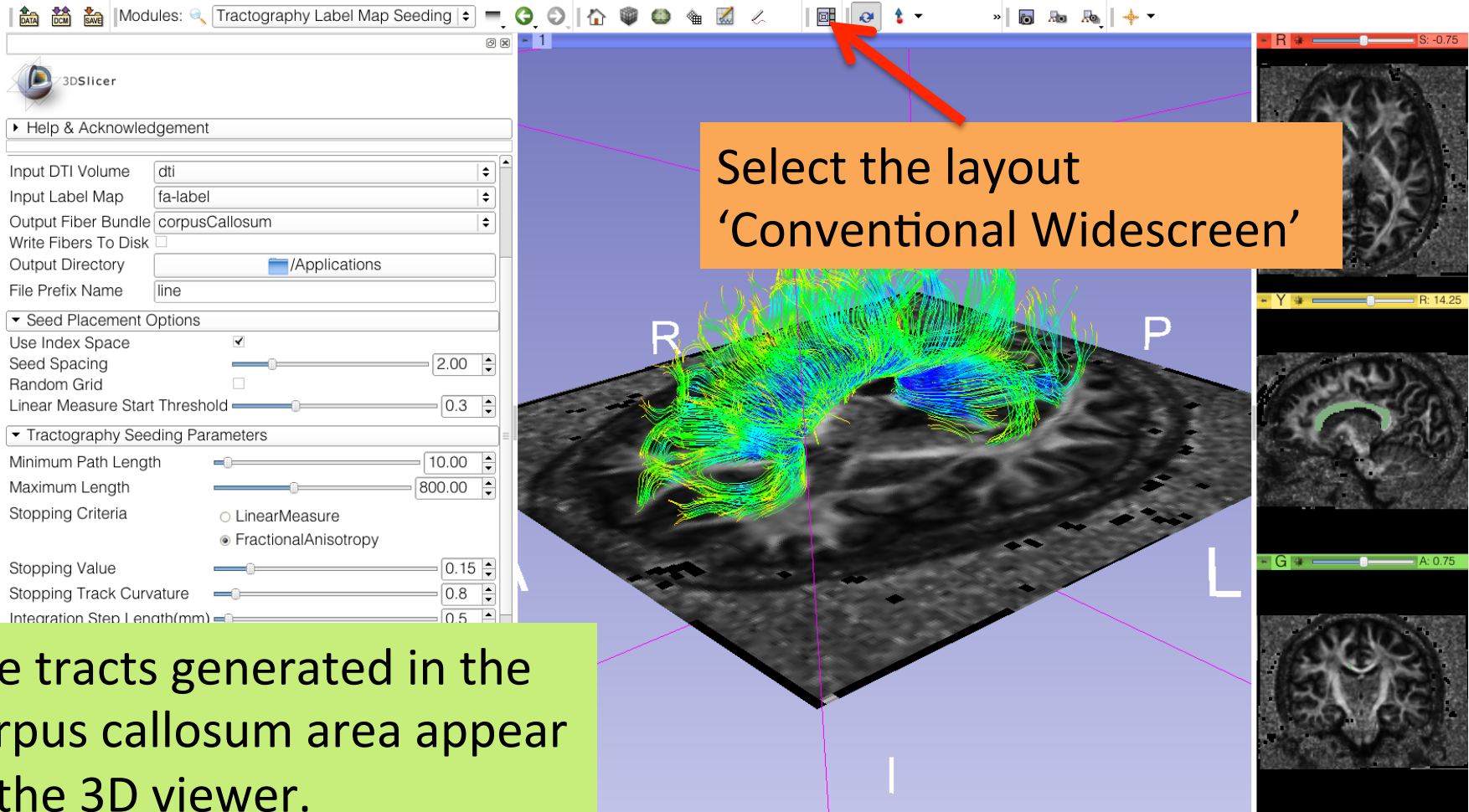
-Stopping value: 0.15

-Stopping track curvature: 0.8

-Integration step length: 0.5 mm

Click on **Apply**

Labelmap Seeding: Tracts



Labelmap Seeding: Tracts

The screenshot displays the 3DSlicer software interface. On the left, the 'Tractography Label Map Seeding' module is active, showing various configuration options:

- Input DTI Volume:** dti
- Input Label Map:** fa-label
- Output Fiber Bundle:** corpusCallosum
- Write Fibers To Disk:**
- Output Directory:** /Applications
- 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 Path Length:** 10.00
- Maximum Length:** 800.00
- Stopping Criteria:** LinearMeasure, FractionalAnisotropy
- Stopping Value:** 0.15
- Stopping Track Curvature:** 0.8
- Integration Step Length(mm):** 0.5

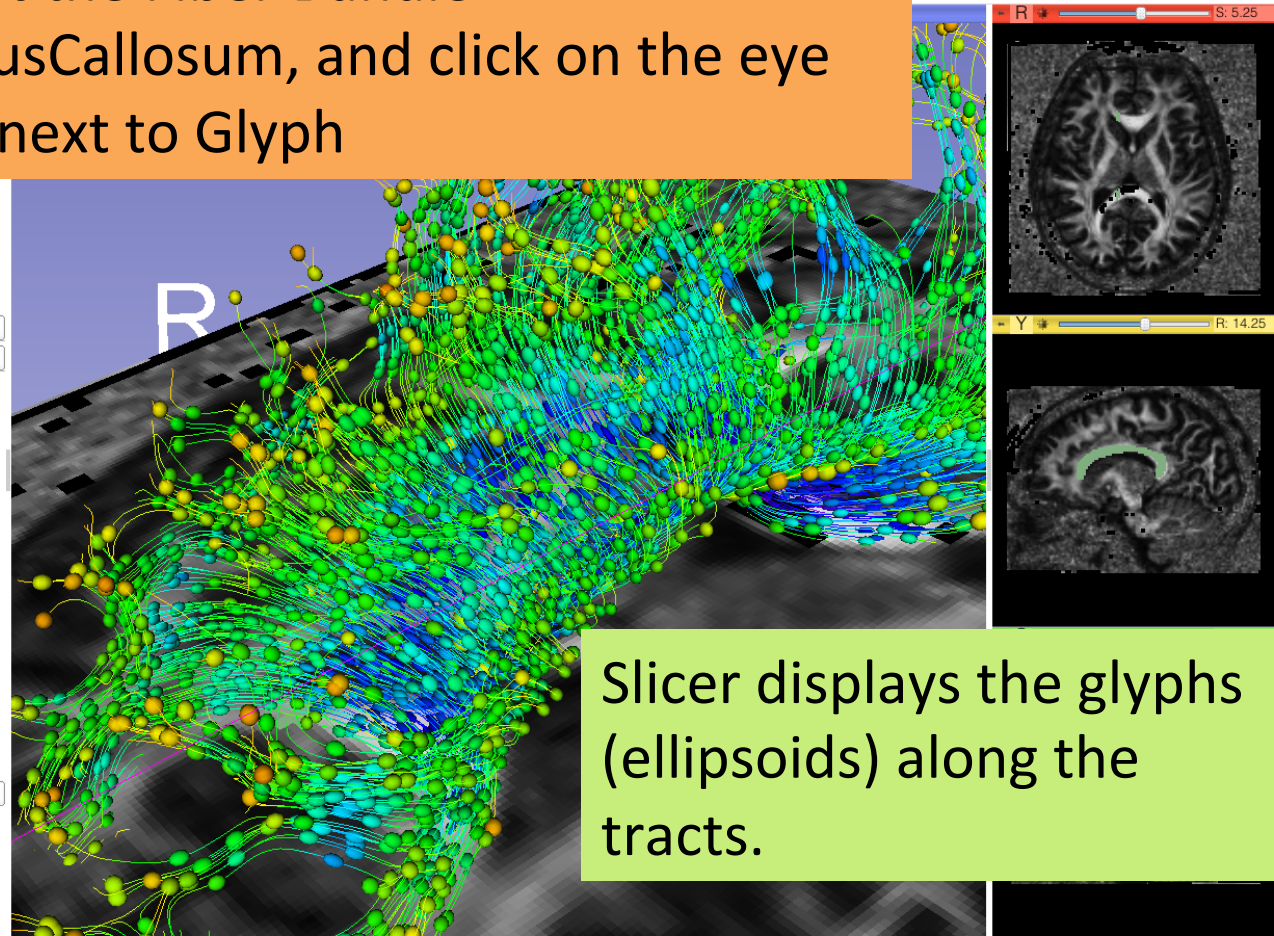
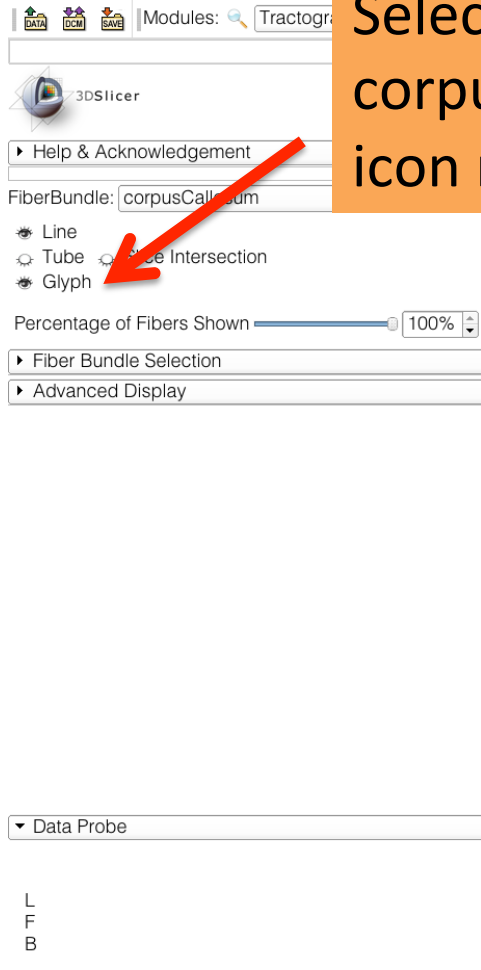
Label definition: Default

Data Probe: (Buttons: Cancel, Apply)

The main 3D view shows a brain slice with a bundle of tracts colored in a gradient from green to blue. The axes are labeled R (Right), P (Posterior), L (Left), and I (Inferior). An orange callout box with the text 'Select the module Tractography Display' points to the 3D view. On the right, a vertical stack of three axial brain slices is shown, with the top slice labeled 'R' and 'S: -0.75', the middle slice labeled 'Y' and 'R: 14.25', and the bottom slice labeled 'G' and 'A: 0.75'.

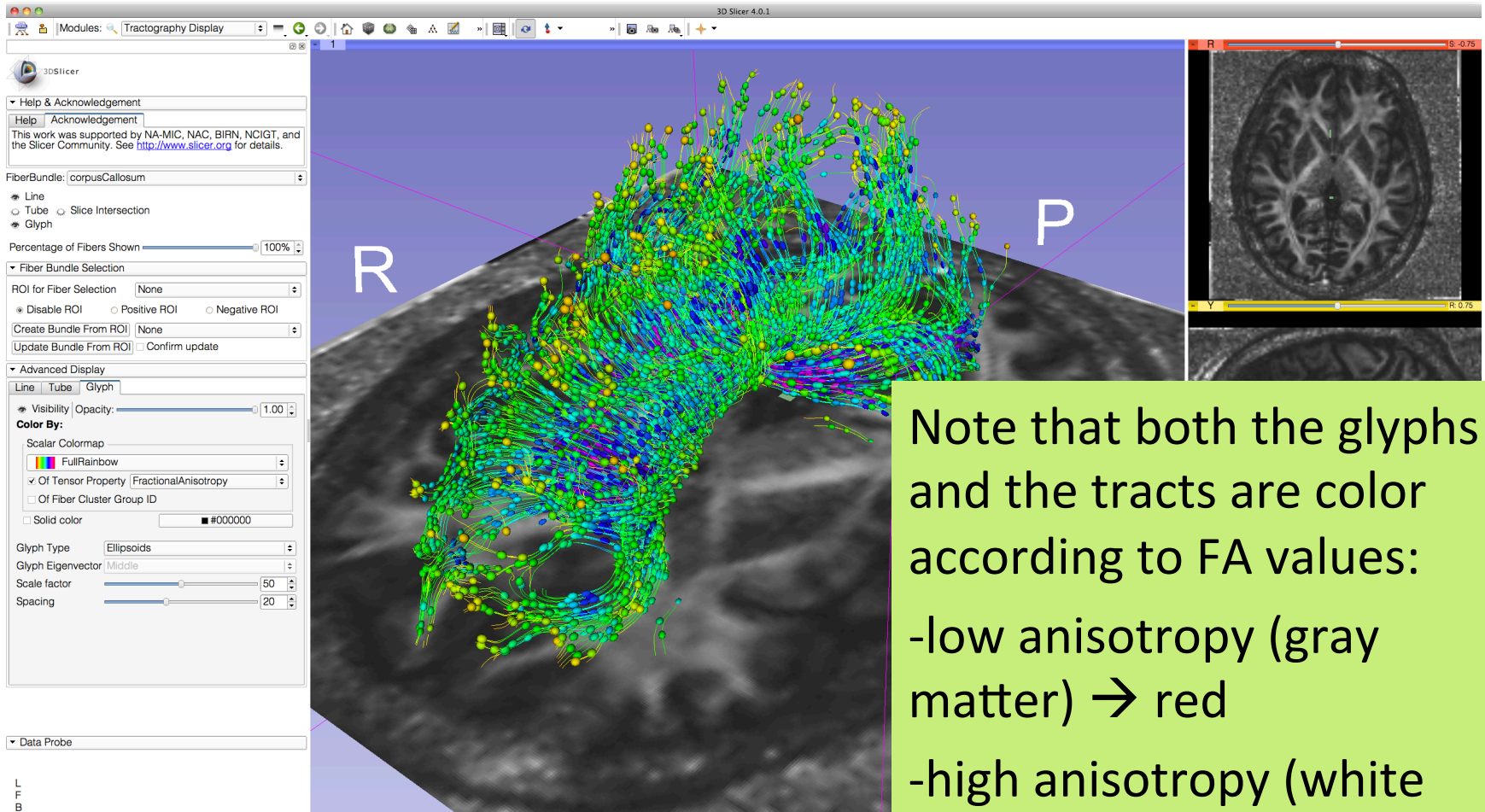
Tractography Results

Select the Fiber Bundle corpusCallosum, and click on the eye icon next to Glyph



Slicer displays the glyphs (ellipsoids) along the tracts.

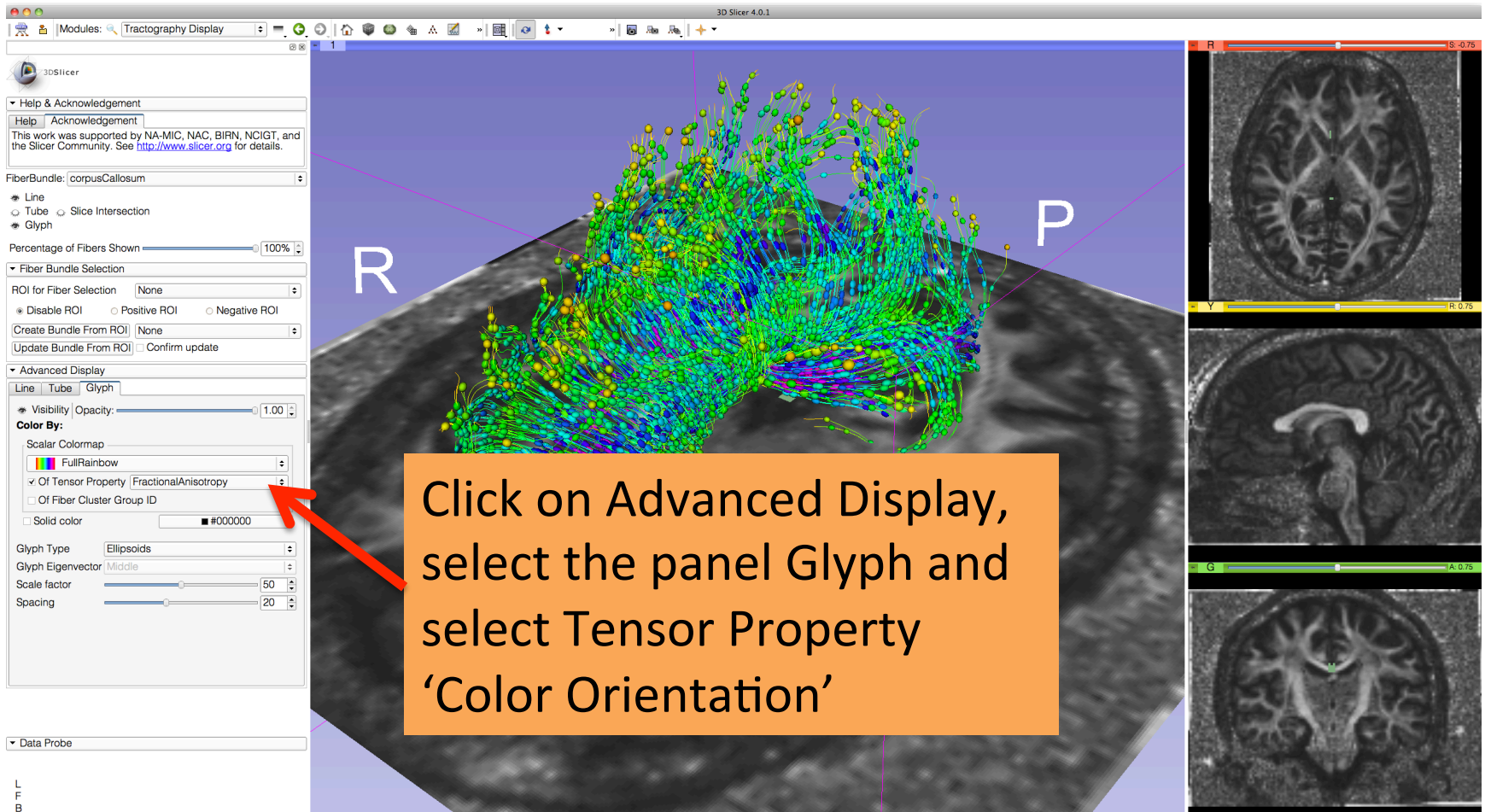
Tractography Results



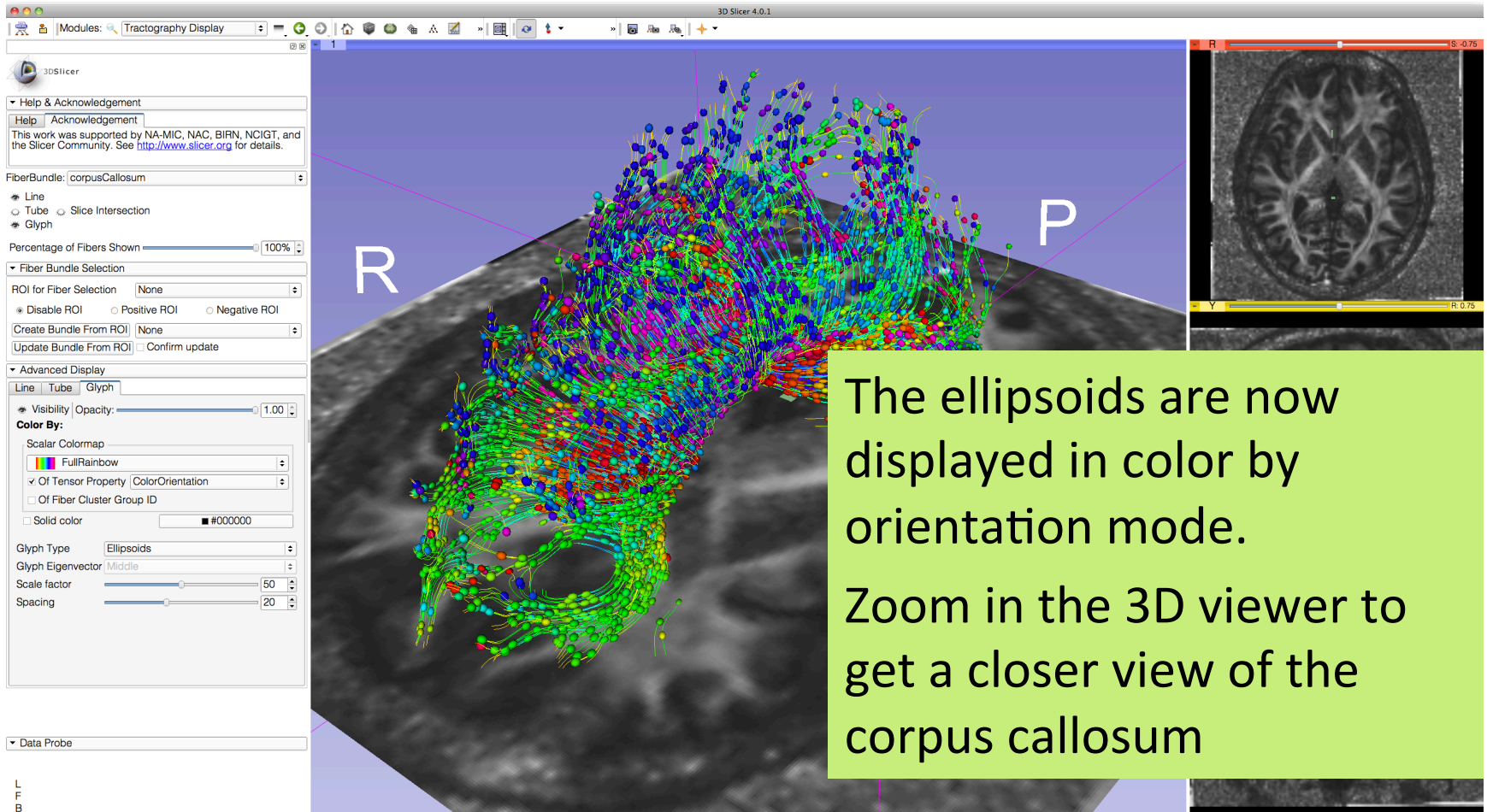
Note that both the glyphs and the tracts are color according to FA values:

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

Tractography Results



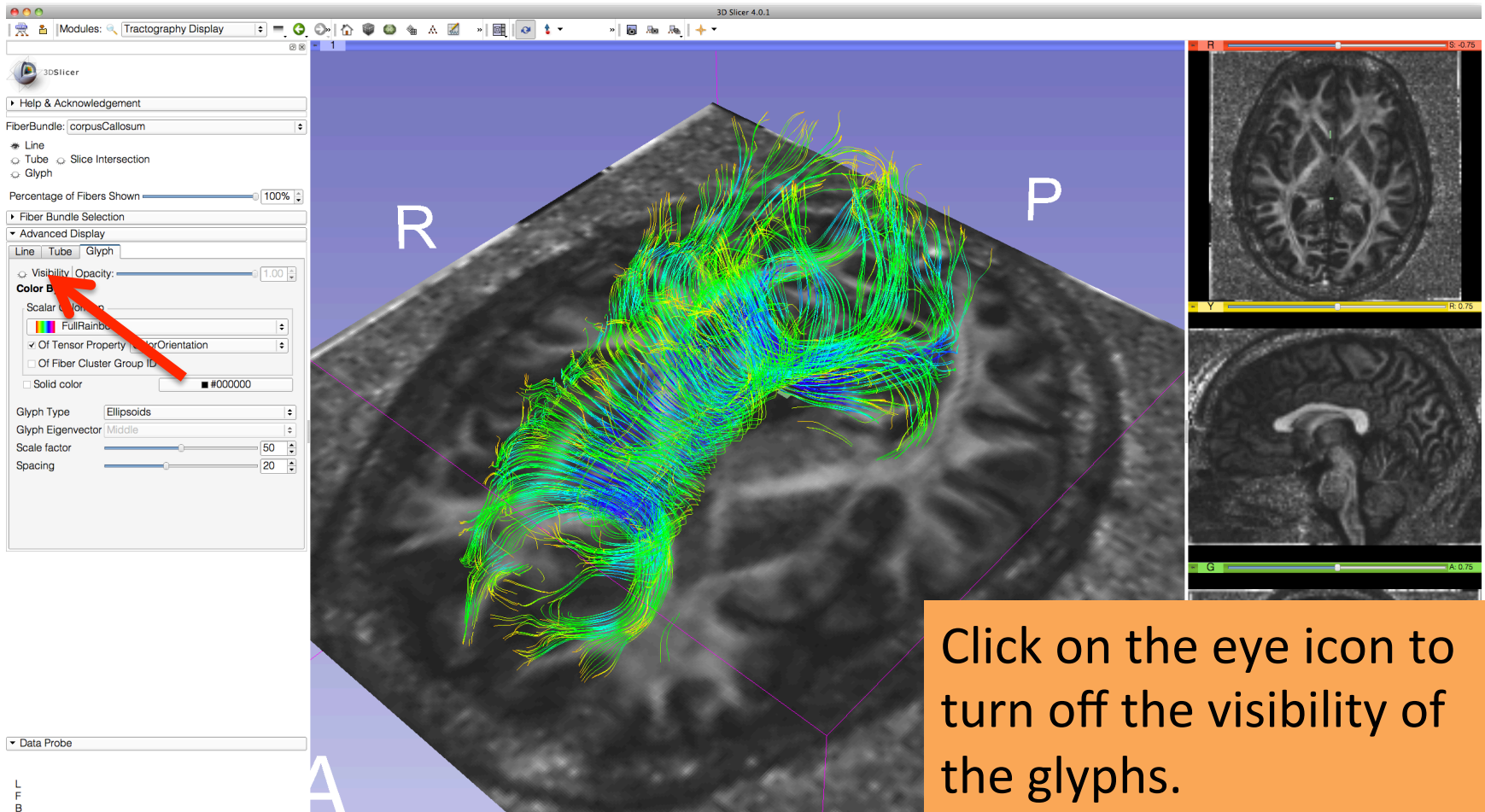
Tractography Results



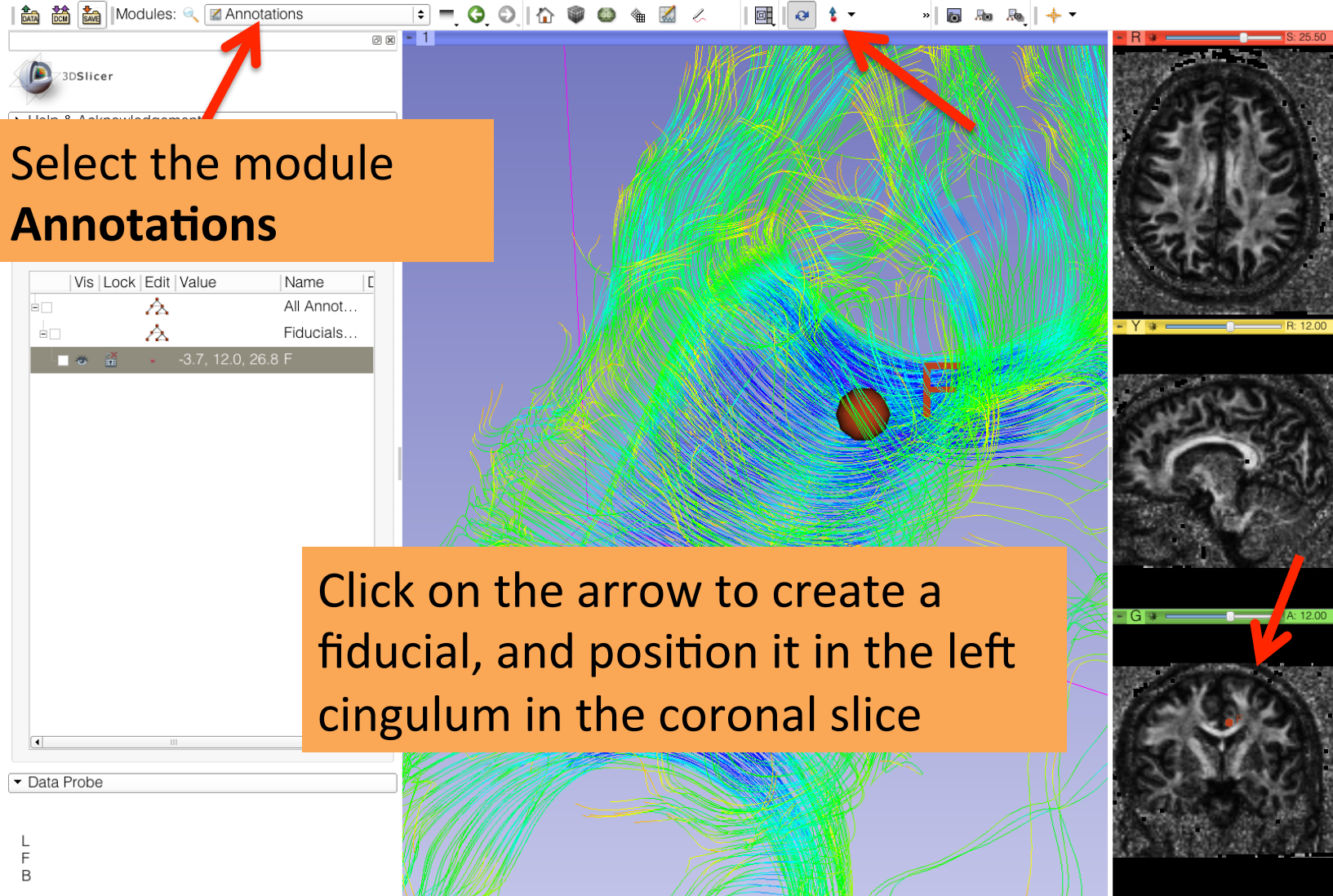
Tractography Results



Tractography Results



Fiducial Seeding

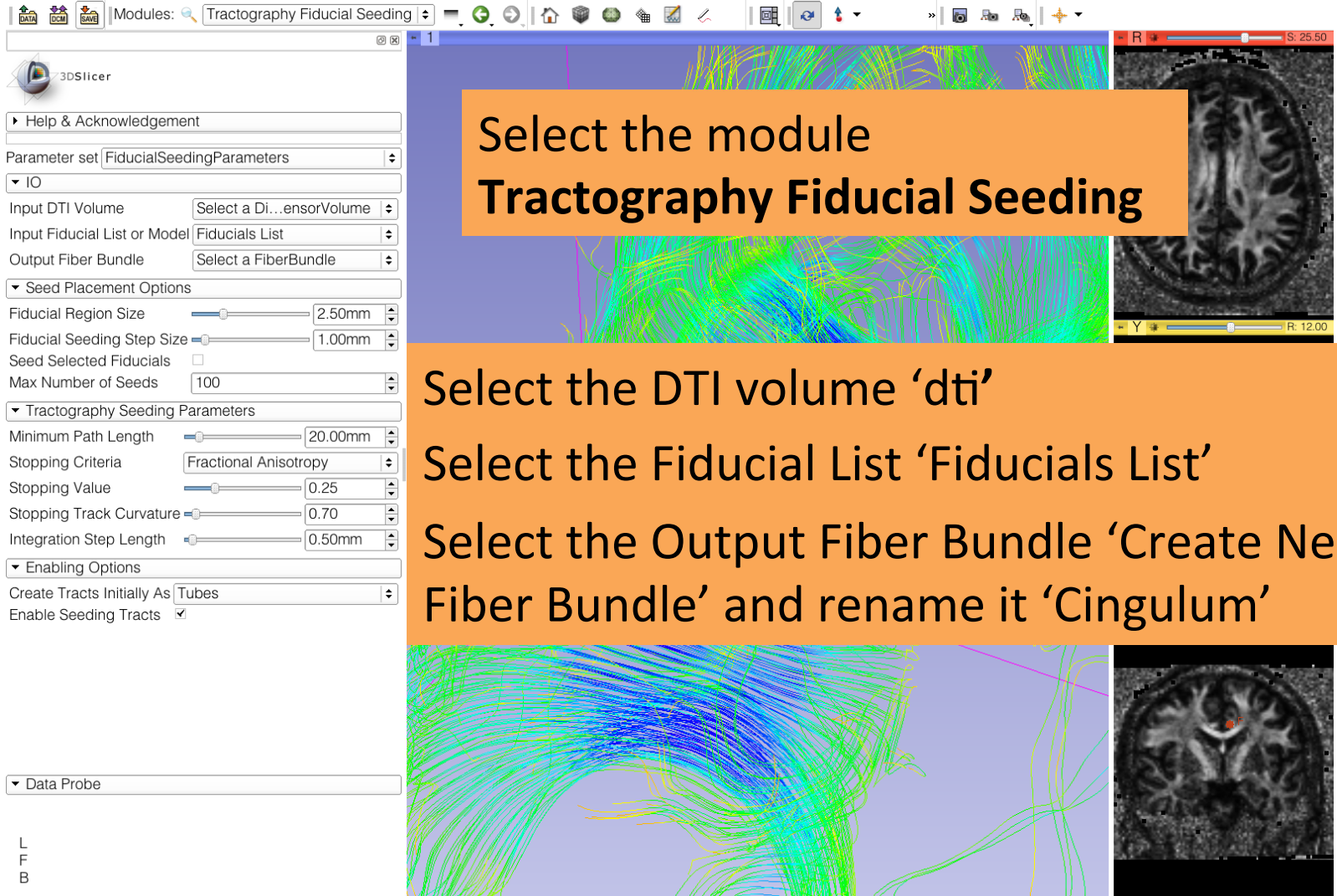


Fiducial Seeding

Change the name of the fiducial to 'LeftCingulum'

The screenshot displays the 3D Slicer interface. The top toolbar includes icons for Data, DICOM, SAVE, and various navigation tools. The 'Modules' dropdown is set to 'Annotations'. The main 3D view shows a brain with a complex network of fiber-like structures in various colors (green, blue, yellow). A red sphere, representing a fiducial, is placed on one of the fibers and is labeled 'LeftC' in red text. To the left of the 3D view, a panel titled 'Annotations' contains a table with columns for 'Vis', 'Lock', 'Edit', 'Value', and 'Name'. Under the 'Fiducials...' section, a single entry is visible: '-3.7, 12.0, 26.8 LeftCing...'. A red arrow points from the text box to this entry. To the right of the 3D view, three orthogonal MRI slices are displayed: an axial slice at the top, a sagittal slice in the middle, and a coronal slice at the bottom. The coronal slice has a red dot and the label 'LeftCingulum' next to it. The bottom left corner of the interface shows the letters 'L', 'F', and 'B' stacked vertically, representing the Left, Frontal, and Back views.

Fiducial Seeding

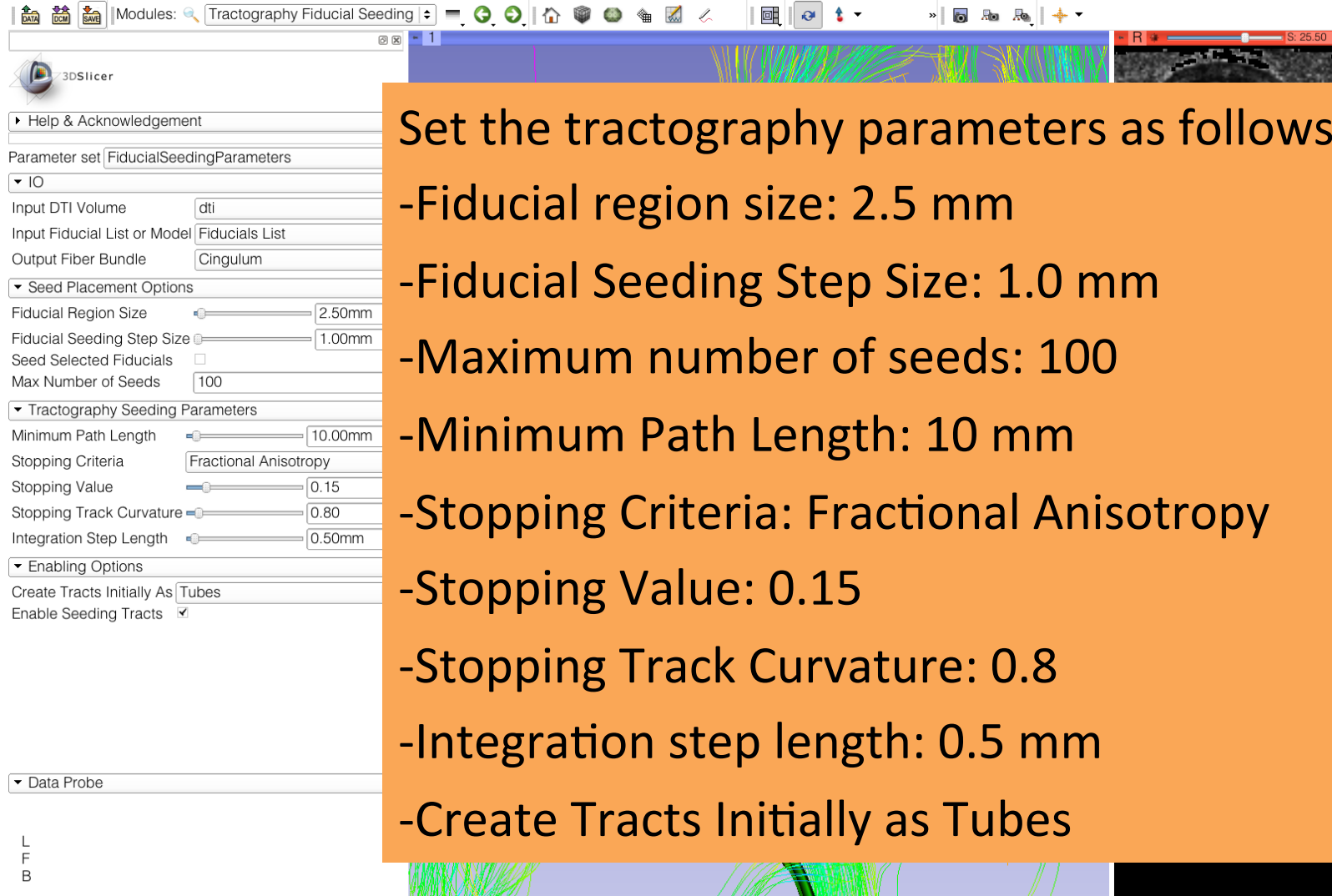


Select the module
Tractography Fiducial Seeding

Select the DTI volume 'dti'
Select the Fiducial List 'Fiducials List'
Select the Output Fiber Bundle 'Create New Fiber Bundle' and rename it 'Cingulum'

3DSlicer
Modules: Tractography Fiducial Seeding
Parameter set: FiducialSeedingParameters
IO
Input DTI Volume: Select a Di...ensorVolume
Input Fiducial List or Model: Fiducials List
Output Fiber Bundle: Select a FiberBundle
Seed Placement Options
Fiducial Region Size: 2.50mm
Fiducial Seeding Step Size: 1.00mm
Seed Selected Fiducials:
Max Number of Seeds: 100
Tractography Seeding Parameters
Minimum Path Length: 20.00mm
Stopping Criteria: Fractional Anisotropy
Stopping Value: 0.25
Stopping Track Curvature: 0.70
Integration Step Length: 0.50mm
Enabling Options
Create Tracts Initially As: Tubes
Enable Seeding Tracts:
Data Probe
L
F
B

Fiducial Seeding

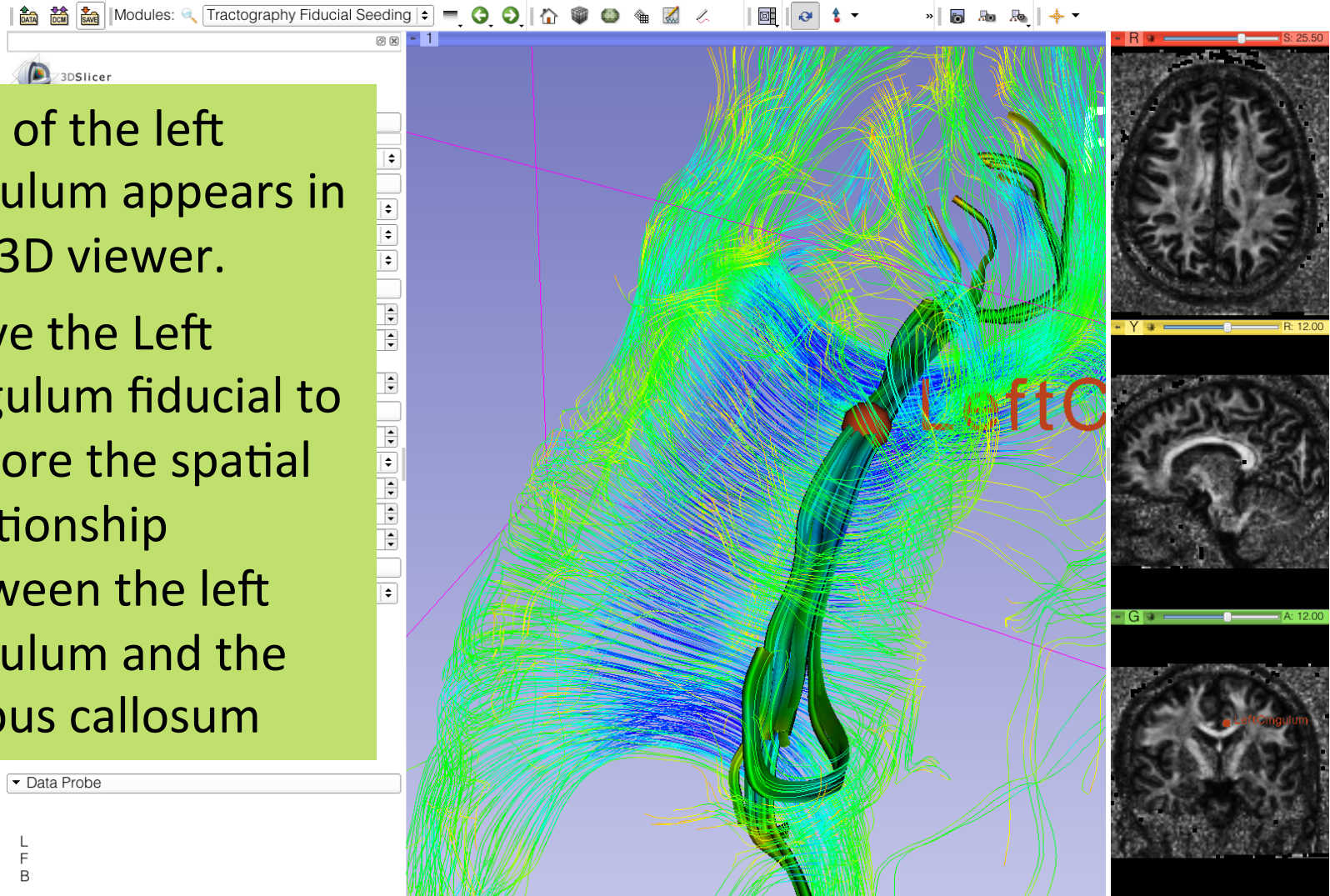


Set the tractography parameters as follows:

- Fiducial region size: 2.5 mm
- Fiducial Seeding Step Size: 1.0 mm
- Maximum number of seeds: 100
- Minimum Path Length: 10 mm
- Stopping Criteria: Fractional Anisotropy
- Stopping Value: 0.15
- Stopping Track Curvature: 0.8
- Integration step length: 0.5 mm
- Create Tracts Initially as Tubes

Fiducial Seeding

Part of the left cingulum appears in the 3D viewer.
Move the Left Cingulum fiducial to explore the spatial relationship between the left cingulum and the corpus callosum



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

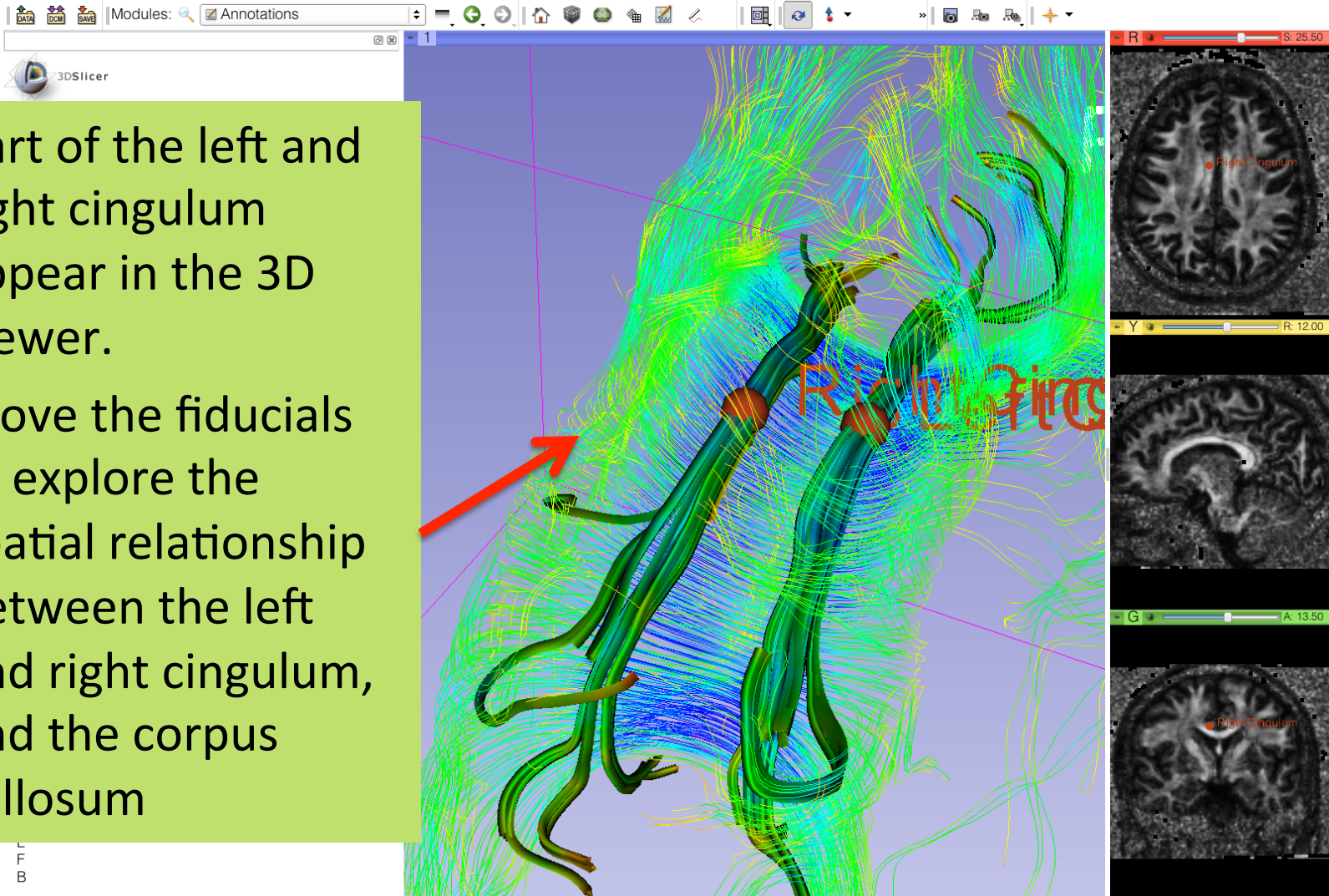
Vis	Lock	Edit	Value	Name	D
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		All Annot...	
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		Fiducials...	
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	-3.7, 12.0, 26.8	LeftCing...	
<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	8.5, 12.9, 24.9	RightCin...	

L
F
B

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



Fiducial Seeding

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

8.5, 12.9, 24.9 RightCin...
-14.7, 0.4, 7.8 F_2

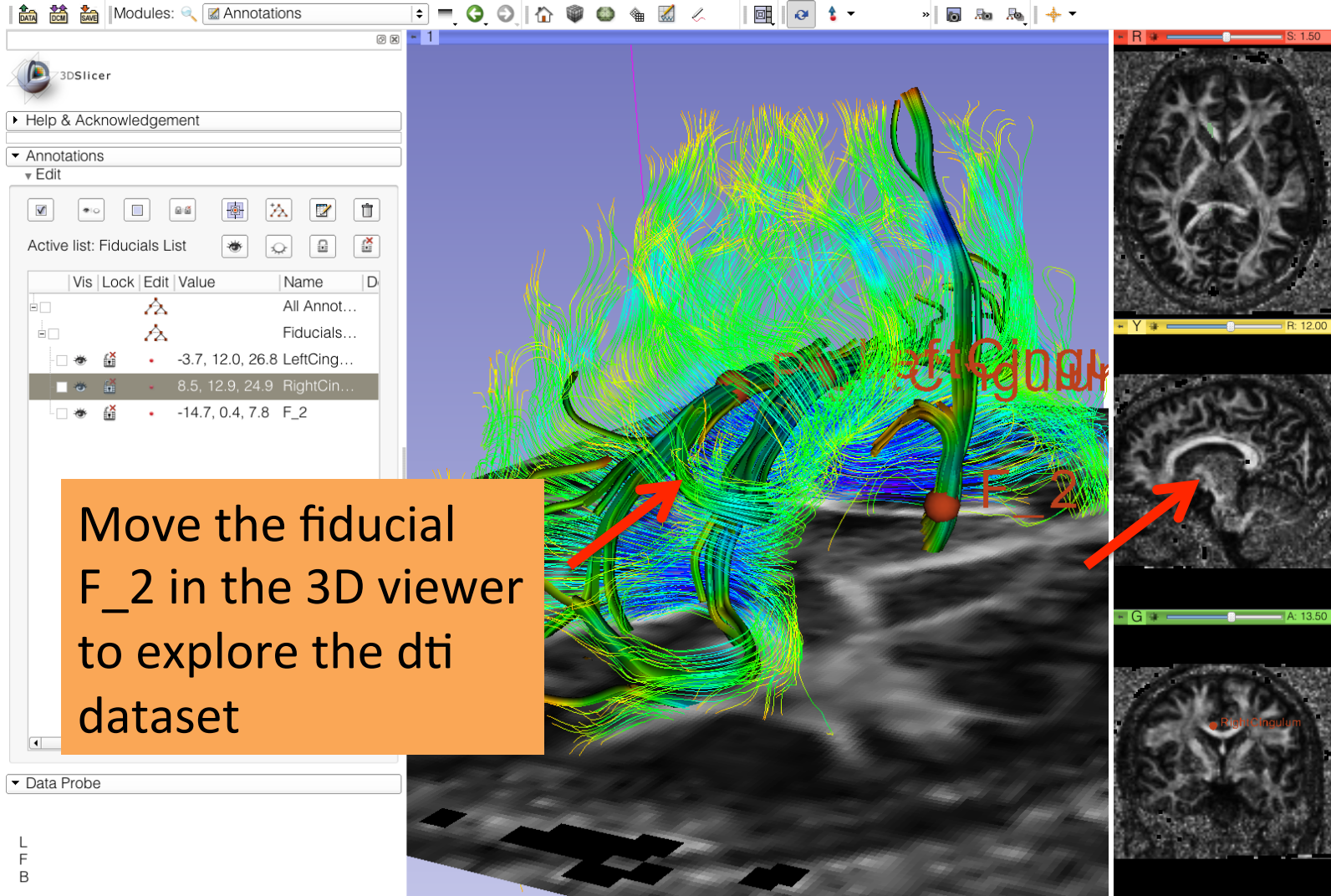
Data Probe

L
F
B

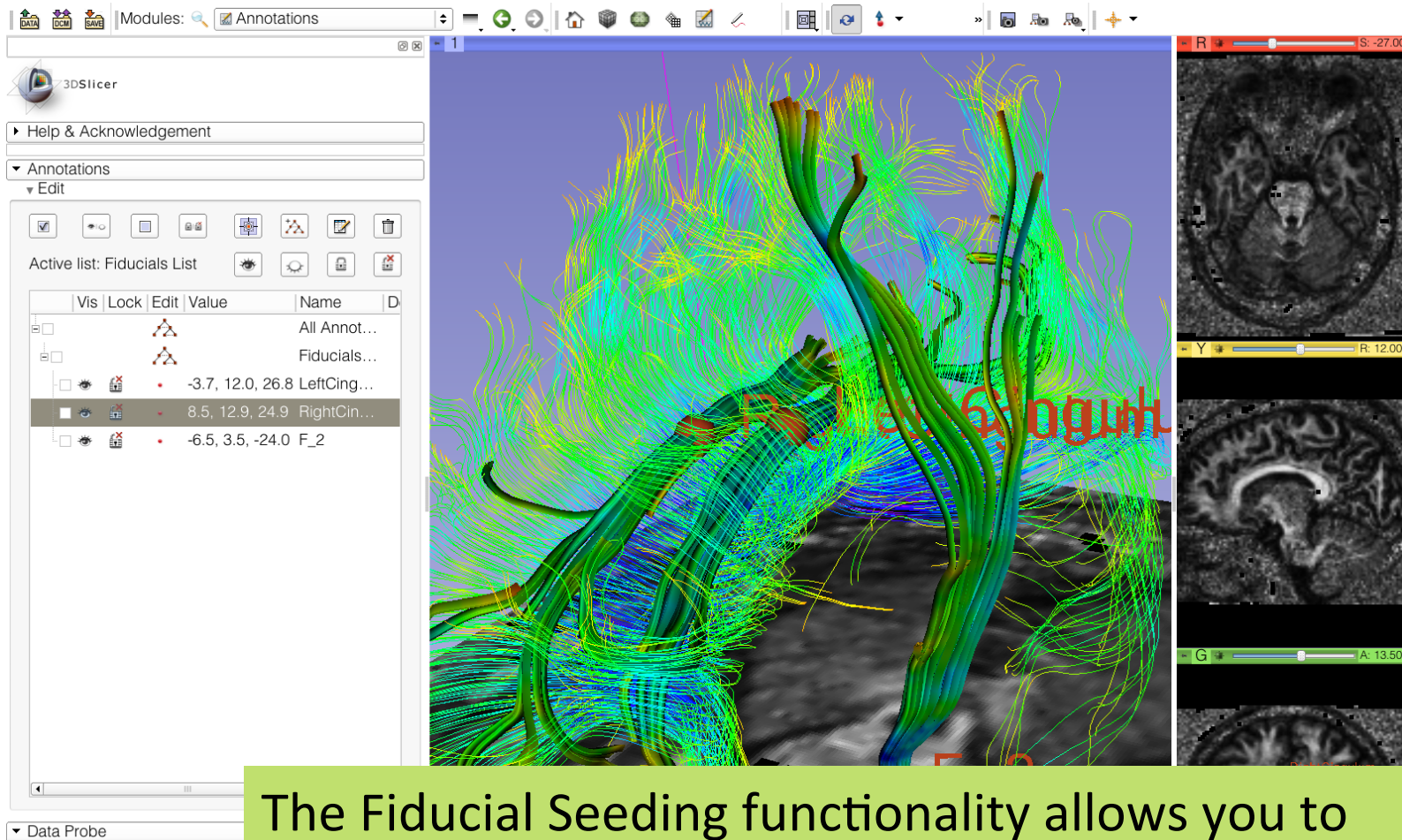
RightCinulum

S: 1.50
R: 12.00
A: 13.50

Fiducial Seeding



Tractography 'on-the-fly'



The Fiducial Seeding functionality allows you to do tractography 'on-the-fly' to explore white matter structures interactively

DTI Analysis

Select the module Data to display the list of elements that have been generated in this tutorial

3DSlicer

Modules: Data

Help & Acknowledgement

Display & Modify Scene

Nodes

- Scene
 - View
 - Default Scene Camera
 - dwi
 - dti
 - baseline
 - baseline-label
 - trace
 - fa
 - corpusCallosum
 - All Annotations
 - LeftCingulum
 - Fiducials List
 - Cingulum
 - RightCingulum
 - F_2
 - SceneViewToplevelHierarchyNode
 - Master Scene View

Scene Model: Transform

- Display MRML ID's
- Show Hidden nodes

Filter:

Load & Add Scenes Or Individual Datasets

Data Probe

L
F
B

R S: -27.00

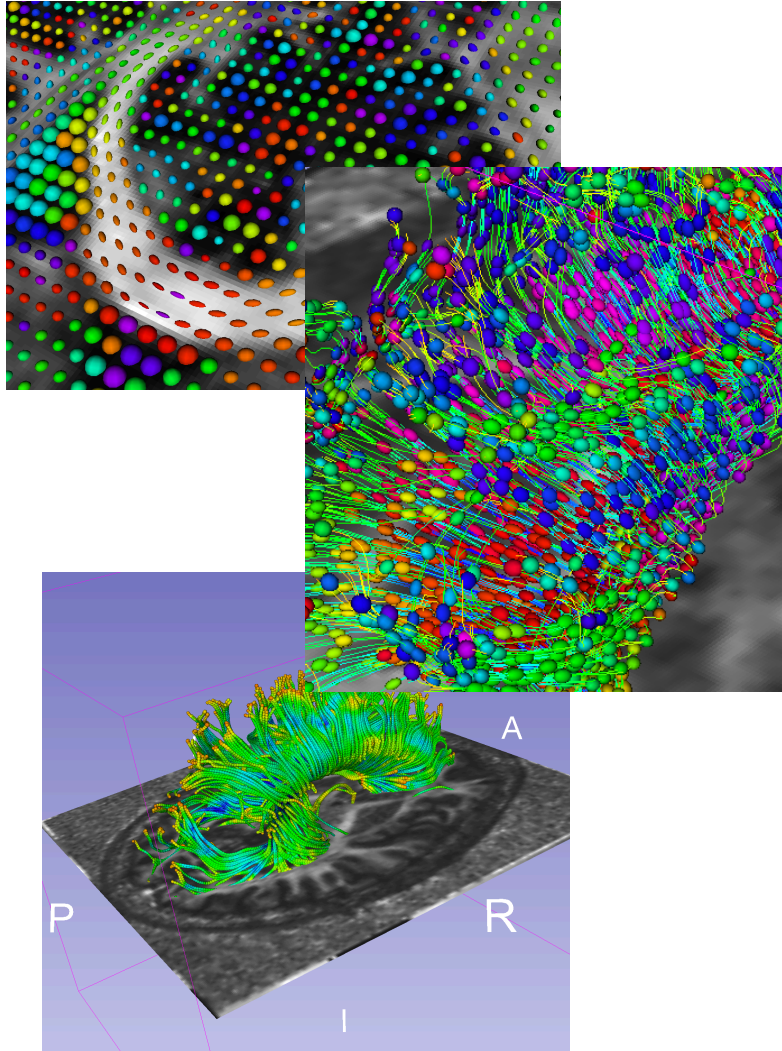
Y R: 12.00

G A: 13.50

Right Cingulum

F_2

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.

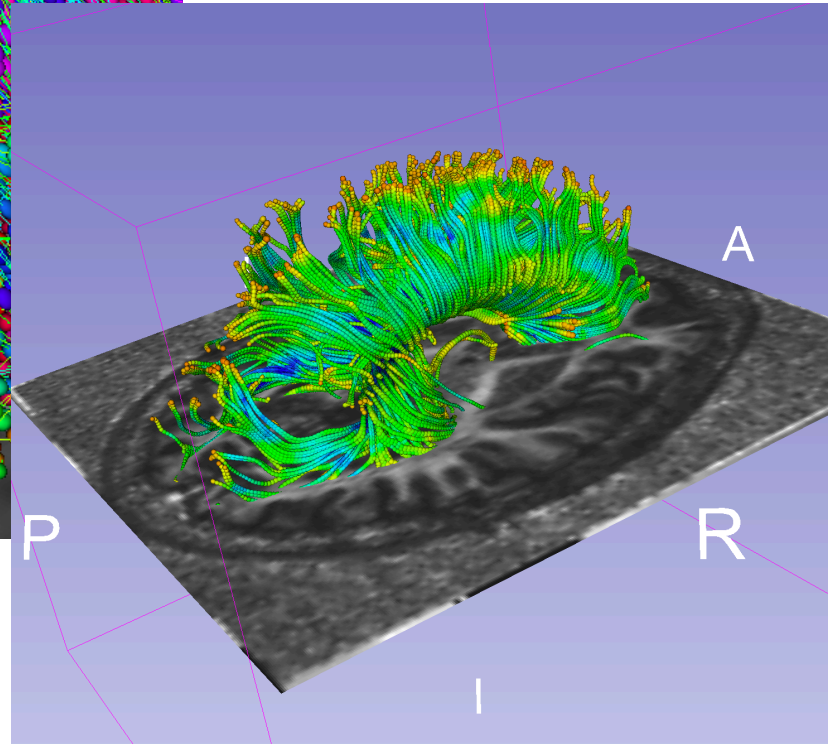
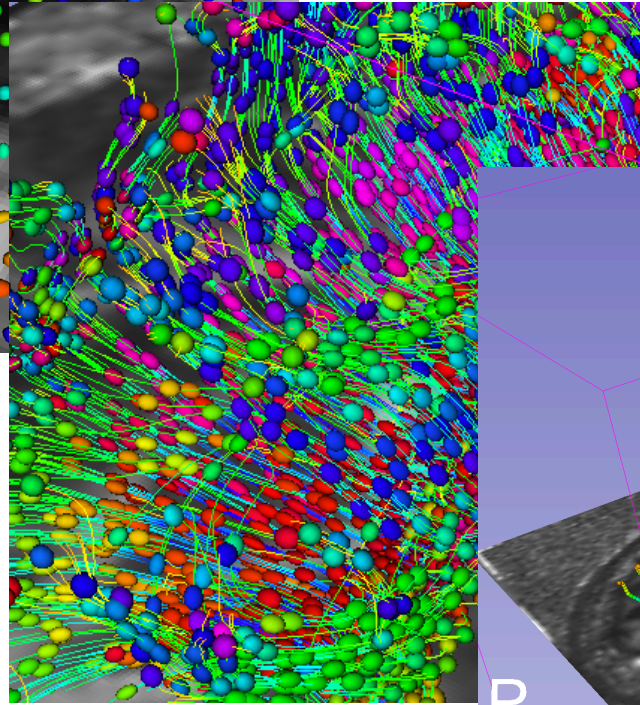
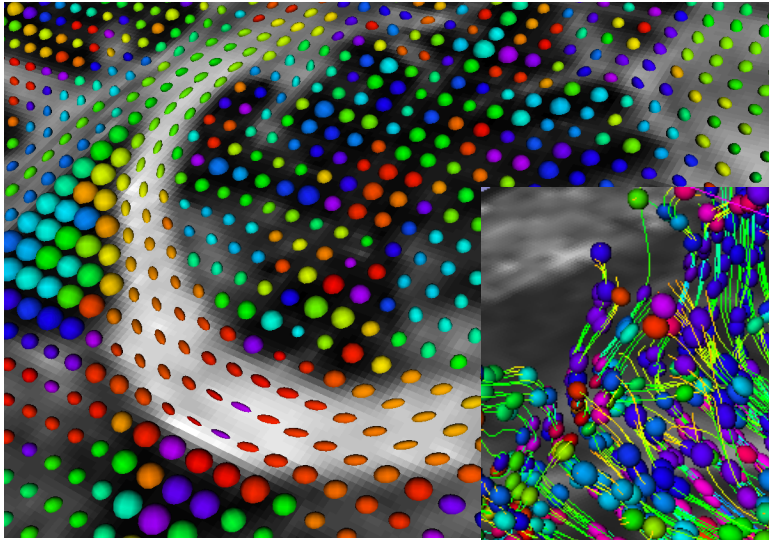
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NIH U54EB005149



Neuroimage Analysis Center
NIH P41RR013218



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