



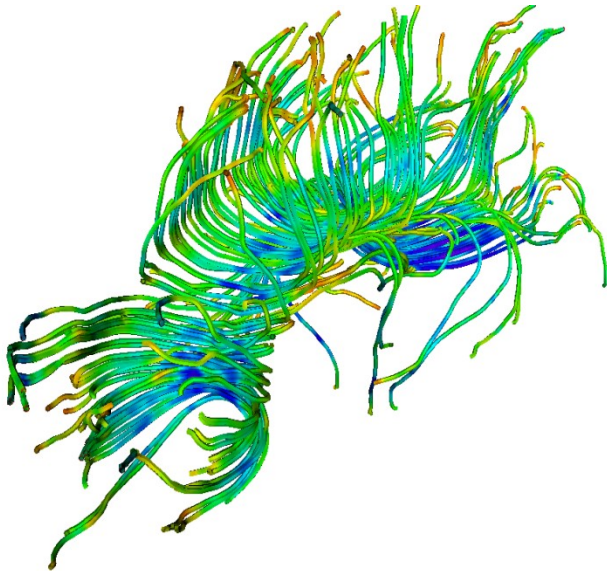
NA-MIC

*National Alliance for Medical Image Computing*

*<http://na-mic.org>*

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# **Diffusion Tensor Imaging tutorial**



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Harvard University

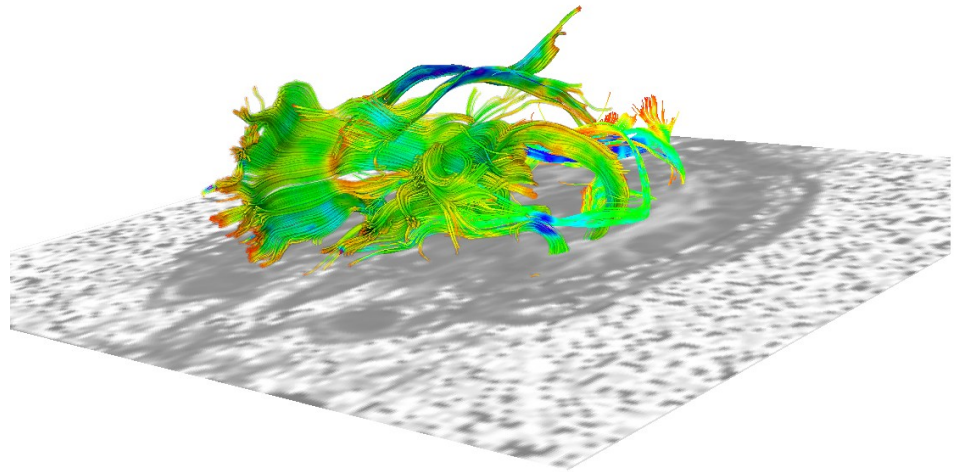
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# DTI tutorial

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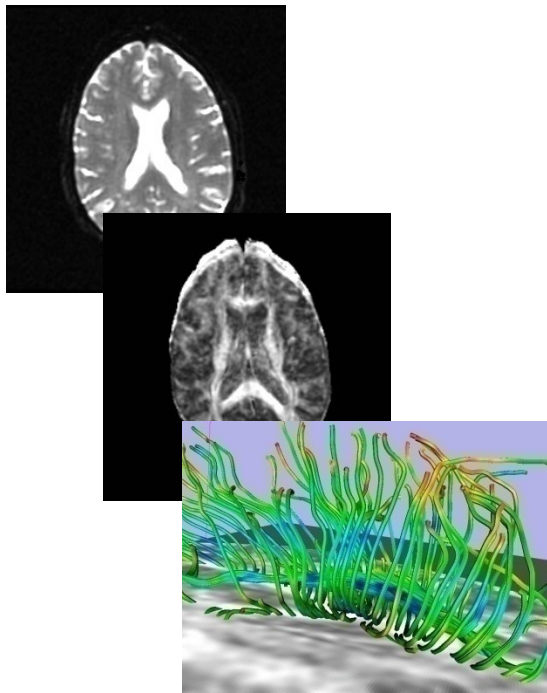
This tutorial is an introduction to the advanced **Diffusion MR** capabilities of the **Slicer3** software for medical image analysis.





# Outline

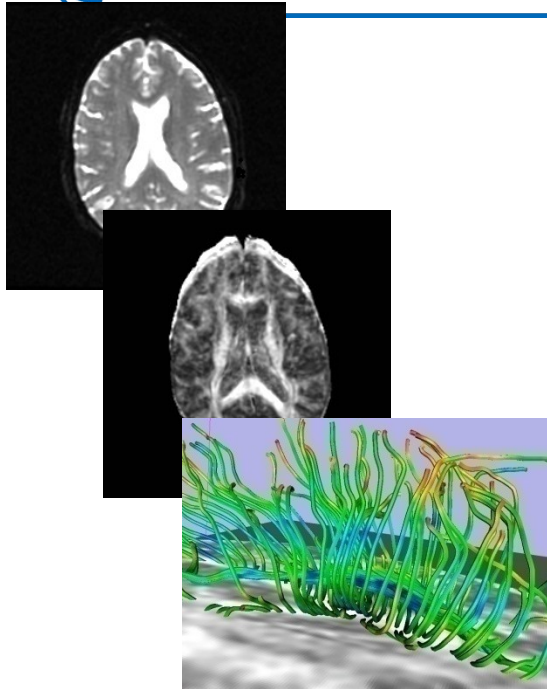
---



This tutorial guides you through the process of **loading diffusion MR data**, **estimating diffusion tensors**, and **performing tractography** of white matter bundles.



# Outline



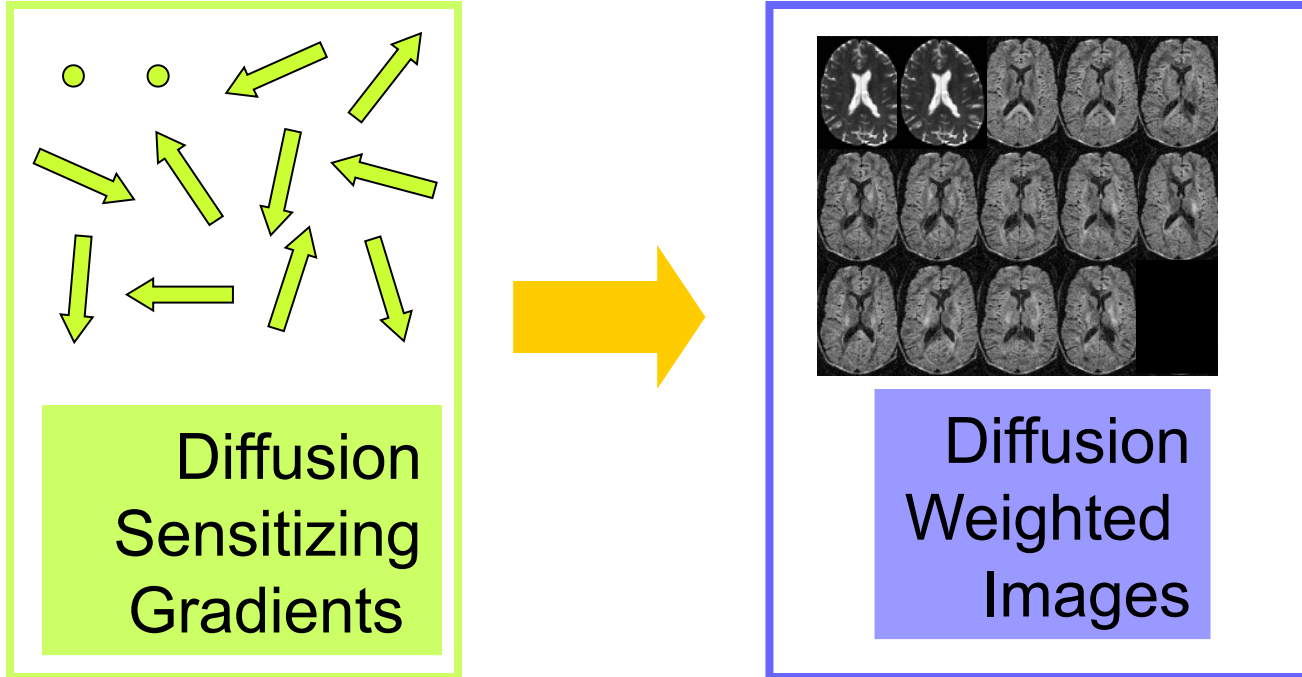
The processing pipeline uses **9 image analysis modules** of Slicer3.6

1. Data
2. Volumes
3. Diffusion Tensor Estimation
4. Diffusion Tensor Scalar Measurements
5. Editor
6. LabelMap Seeding
7. Fiber Bundles
8. Fiducials
9. Fiducial Seeding



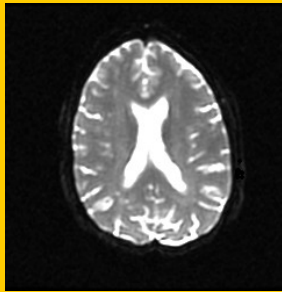
# Tutorial Dataset

The Diffusion MR tutorial dataset is composed of a **Diffusion Weighted MR scan** of the brain acquired with 12 gradient directions and 2 baseline.

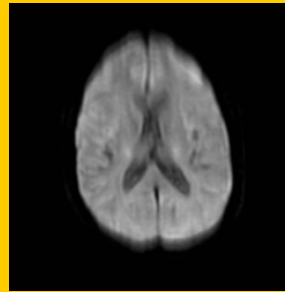




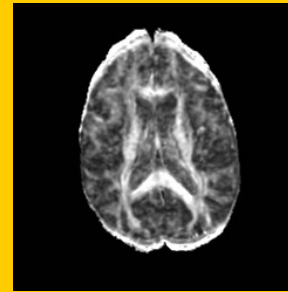
# DTI Processing Pipeline



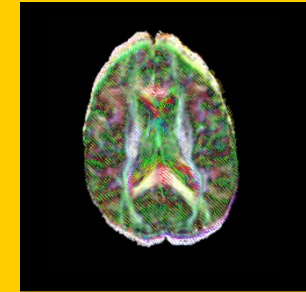
DWI  
Acquisition



Tensor  
Calculation



Scalar  
Maps



3D  
Visualization



# Start Slicer3

**Linux/Mac users**

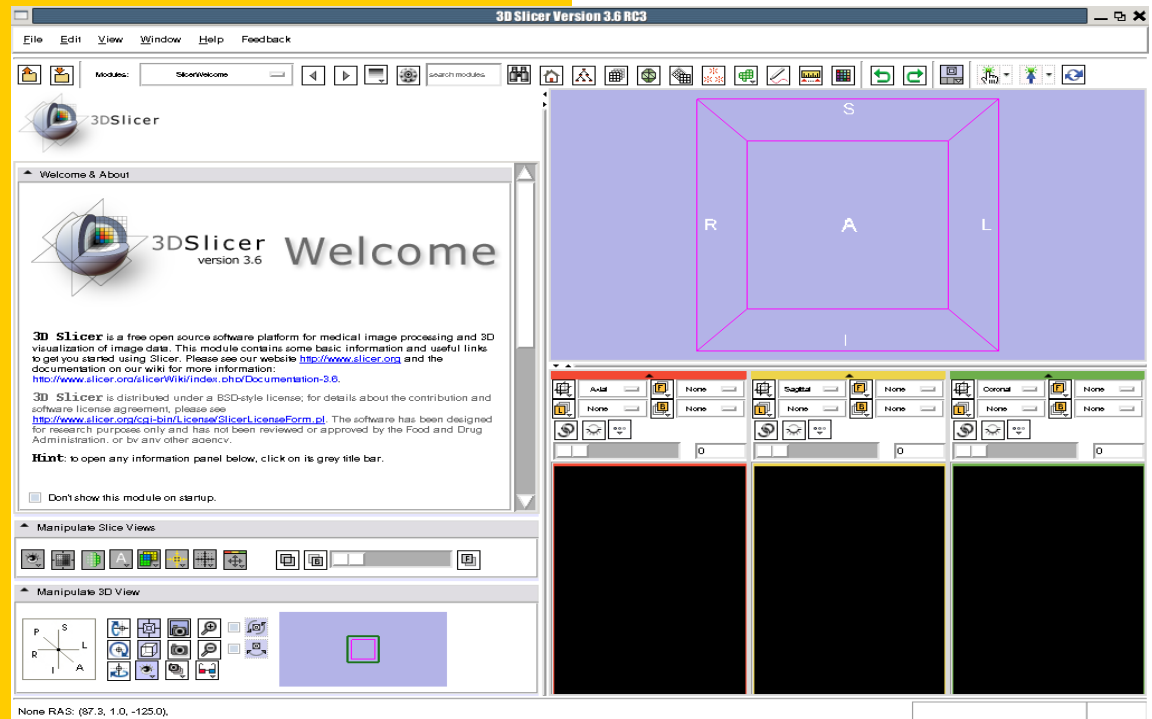
Launch the Slicer3 executable located in the Slicer3.6 directory

**Windows users**

Select

Start → All Programs

→ Slicer3-3.6-RC3-2010-06-04 → Slicer3





# Slicer Welcome

**3D Slicer Version 3.6 RC3**

File Edit View Window Help Feedback

Modules: SlicerWelcome

3DSlicer

Welcome & About

3DSlicer version 3.6

**3D Slicer** is a free open source software platform for visualization of image data. This module contains some information to get you started using Slicer. Please see our website for documentation on our wiki for more information: <http://www.slicer.org/slicerWiki/index.php/Documentation>

3D Slicer is distributed under a BSD-style license; see the software license agreement, please see <http://www.slicer.org/cgi-bin/License/SlicerLicenseForm.pl>. The software has been designed for research purpose only and has not been reviewed or approved by the Food and Drug Administration, or by any other agency.

**Hint:** to open any information panel below, click on its grey title bar.

Don't show this module on startup.

Manipulate Slice Views

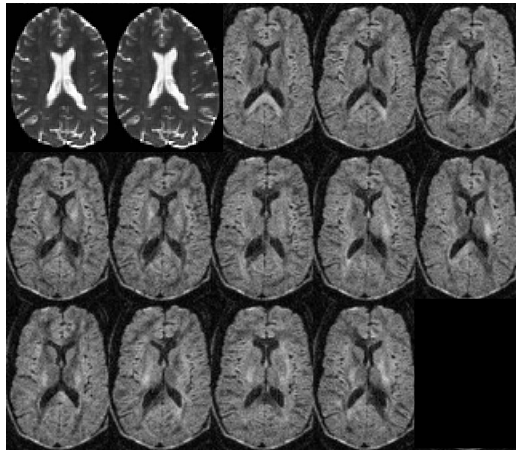
Manipulate 3D View

None RAS: (87.3, 1.0, -125.0)

The **SlicerWelcome** module is the module displayed by default.

This module gives an overview of the GUI of Slicer3, and data loading & saving functionalities.





## Part 1:

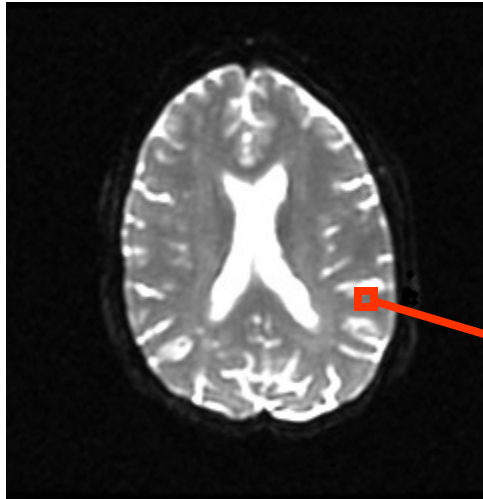
# Diffusion data loading and tensor estimation



# Diffusion Tensor

Stejskal-Tanner

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



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



# Loading the DWI volume

**File** Edit View Window Help Feedback

3DSlicer

3DSlicer version 3.6

**Select File → Add Volume from the File menu**

3D Slicer is a free open source software platform for medical image processing and 3D visualization of image data. This module contains some basic information and useful links to get you started using Slicer. Please see our website <http://www.slicer.org> and the documentation on our wiki for more information: <http://www.slicer.org/slicerWiki/index.php/Documentation-3.6>.

3D Slicer is distributed under a BSD-style license; for details about the contribution and software license agreement, please see <http://www.slicer.org/cgi-bin/License/SlicerLicenseForm.pl>. The software has been designed for research purpose only and has not been reviewed or approved by the Food and Drug Administration, or by any other agency.

**Hint:** to open any information panel below, click on its grey title bar.

Don't show this module on startup.

None RAS: (87.3, 1.0, -125.0).



# Loading the DWI volume

3D Slicer Version 3.6 RC3

File Edit View Window Help Feedback

Modules: SlicerWelcome

3DSlicer

Welcome & About

3DSlicer version 3.6

3D Slicer is a free open source software platform for medical visualization of image data. This module contains some basic information to get you started using Slicer. Please see our website <http://www.slicer.org> for more information: <http://www.slicer.org/slicerWiki/index.php/Documentation-3.6>.

3D Slicer is distributed under a BSD-style license; for detailed software license agreement, please see <http://www.slicer.org/cgi-bin/License/SlicerLicenseForm.pl>. This software is for research purposes only and has not been reviewed or approved by any other agency.

**Hint:** to open any information panel below, click on its grey title bar.

Don't show this module on startup.

Manipulate Slice Views

Manipulate 3D View

None RAS: (87.3, 1.0, -125.0).

**Add Volume**

Name	Size	Modified
dwiDataset.nhdr	2 KB	Wed Sep 2
dwiDataset.raw.gz	31,309 KB	Tue Aug 7

Path: /a/ufdz/home/003swallace/Desktop/Diffusion Dataset/dwiDataset.nhdr

Volume Options

Centered  Ignore Orientation  Label Map  Single File Name: dwiDataset

Recent Volumes:

DICOM Information

Parse Directory  Divide Subseries

Description	Value
-------------	-------

Coronal None

None None

0

Browse to the location of the Diffusion tutorial dataset directory and select the file **dwiDataset.nhdr**

Click on **Apply** to load the volume



# Loading the DWI volume

Left click on the menu **Modules** and select **All Modules** to display the list of **95 modules** available for image analysis and 3D visualization.

Select the module **Volumes**



# Loading the DWI volume

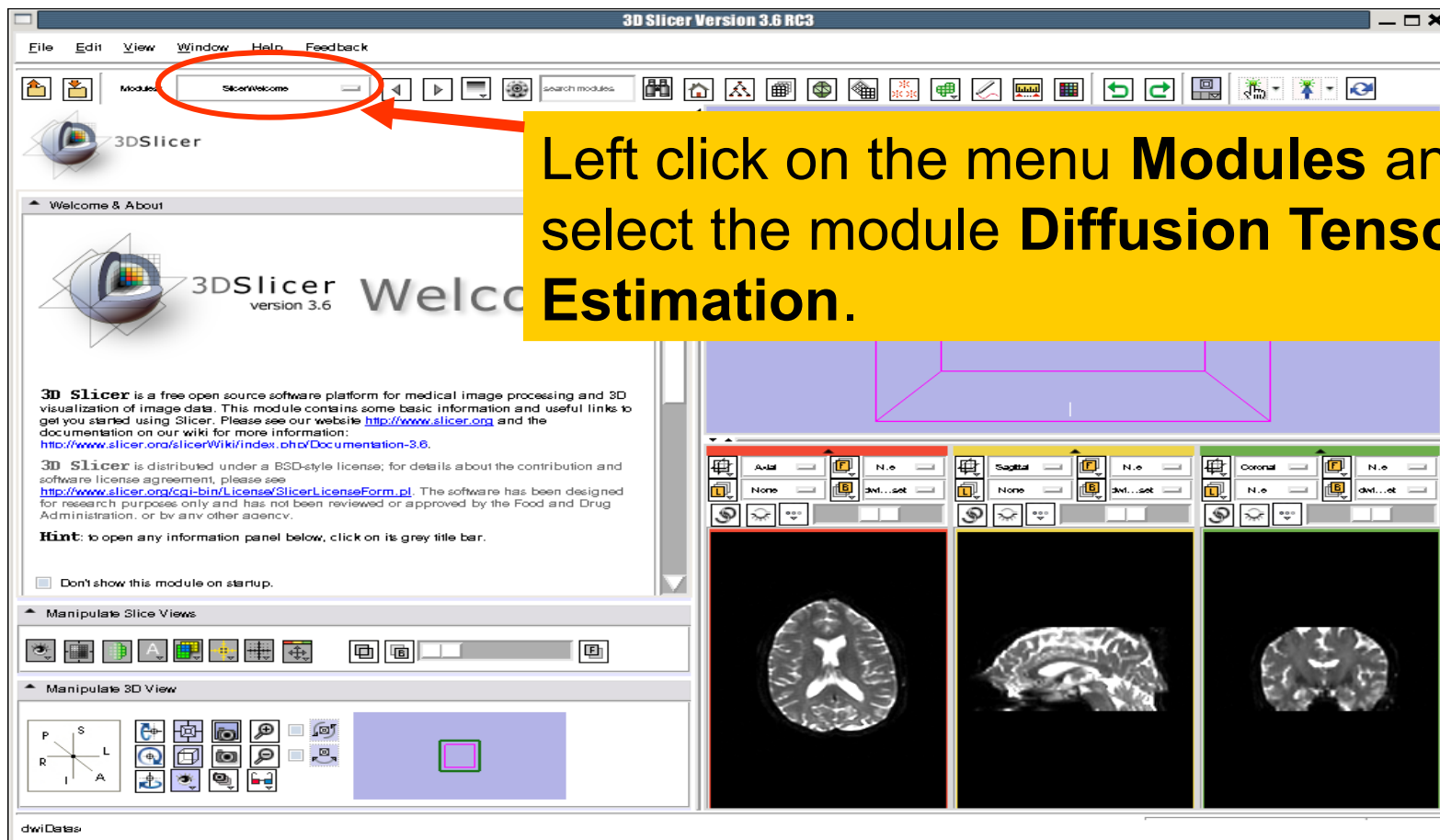
Select the Active Volume **dwiDataset** and adjust the Window/Level Parameters

The screenshot shows the 3D Slicer 3.6 interface. The Volume Browser on the left lists 'dwiDataset' as the Active Volume. The Display panel shows 'DWM Component' set to 0 and 'LookUp Table' set to 'Grey'. The 'Window/Level' section is set to 'Manual' with a level of 3712.8 and a threshold of 0. The 2D Slice Viewer displays three anatomical views: Axial, Sagittal, and Coronal. The Axial view shows a brain slice with a level of -52 and a spacing of 3mm. The Sagittal view shows a brain slice with a level of 128 and a spacing of 5.4698. The Coronal view shows a brain slice with a level of -24 and a spacing of 0.938mm. The background is set to 'dwiDataset'.

Slicer displays the anatomical views of the baseline volume of the diffusion dataset in the 2D Slice Viewer.

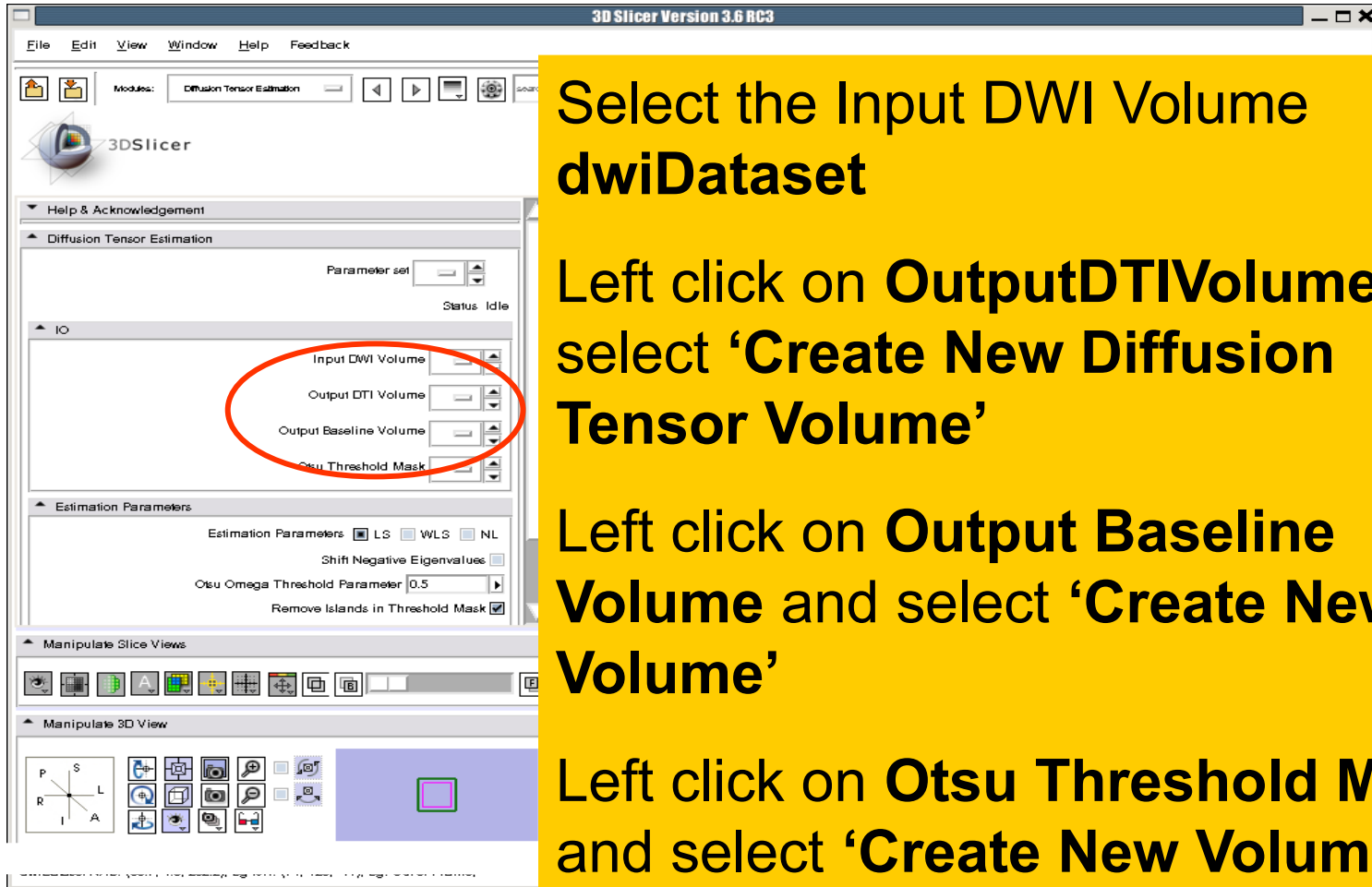


# Tensor Estimation





# Tensor Estimation



**Select the Input DWI Volume  
dwiDataset**

**Left click on **OutputDTIVolume** and  
select '**Create New Diffusion  
Tensor Volume**'**

**Left click on **Output Baseline  
Volume** and select '**Create New  
Volume**'**

**Left click on **Otsu Threshold Mask**  
and select '**Create New Volume**'**





# Tensor Estimation

Select the Tensor Estimation Algorithm **LS** ( Least Squares), and click on **Apply** to estimate the tensors.



# Tensor Estimation

The screenshot shows the 3D Slicer Version 3.6 interface. The main window displays a 3D view of a brain slice with a yellow callout box overlaid. The callout box contains the text: "Left click on **Output Baseline Volume** to display the list of volumes that have been computed by Slicer".

The left sidebar contains the following panels:

- Help & Acknowledgement**
- Diffusion Tensor Estimation**
  - Parameter set: n
  - Status: Complete
  - IO
    - Input DWM Volume: dt
    - Output DTI Volume: e
    - Output Baseline Volume: e
    - Otsu Threshold Mask: k
  - Estimation Parameters
    - Estimation Parameters:  LS  WLS  NL
    - Shift Negative Eigenvalues:
    - Otsu Omega Threshold Parameter: 0.5
    - Remove Islands in Threshold Mask:
    - Apply Mask to Tensor Image:
  - Buttons: Default, Cancel, Apply
- Manipulate Slice Views**
- Manipulate 3D View**

The bottom of the interface shows three slice views (Axial, Sagittal, Coronal) with their respective volume names and values:

View	Volume	Value 1	Value 2
Axial	Otsu Threshold Mask	19	26.8
Sagittal	Otsu Threshold Mask	128	5.4688
Coronal	Otsu Threshold Mask	129	4.5687



# Tensor Estimation

**Output DTI Volume** is the volume of estimated tensors

**Output Baseline Volume** is the Baseline volume

**Output Threshold Mask** is the tensor mask (blue)



# Tensor Estimation

3D Slicer Version 3.6

File Edit View Window Help Feedback

Modals: Diffuska Tensor Estimation

3DSlicer

Help & Acknowledgement

Diffusion Tensor Estimation

IO

Input DWM Volume dt

Output DTI Volume e

Output Baseline Volume e

Otsu Threshold Mask k

Estimation Parameters

Estimation Parameters  LS  VMLS  NL

Shift Negative Eigenvalues

Otsu Omega Threshold Parameter 0.5

Remove Islands in Threshold Mask

Apply Mask to Tensor Image

Default Cancel Apply

Manipulate Slice Views

Manipulate 3D View

Output Threshold Mask

Click on the link icon, left click on **Output Threshold Mask** and select **None**

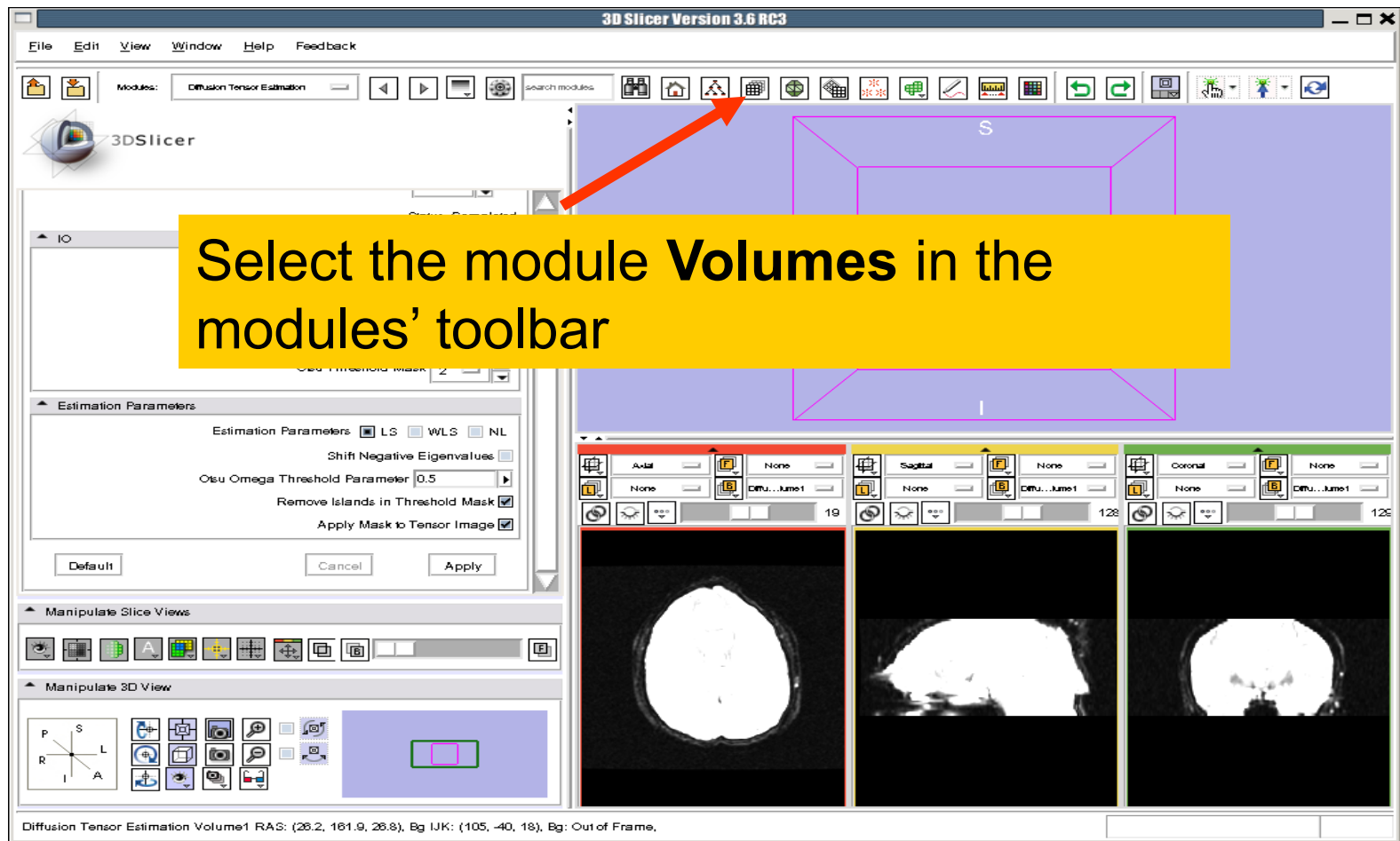
19 26.8

128 5.4688

129 4.5687



# Tensor Estimation





# Tensor Estimation

Select the **Active Volume** 'Output Baseline Volume' and click on the tab **Display**

3D Slicer Version 3.6

File Edit View Window Help Feedback

Load

Select Volume File

Volume Name: Output Baseline Volume

Image Origin: From File

Image Orientation: From File

Label Map  Single File

Keep all Apply Previous Next

Active Volume: Output Baseline Volume

Display

Diffusion Editor

Info

Manipulate Slice Views

Manipulate 3D View

Axial None Output Baseline Volume 19 26.8

Sagittal None Output Baseline Volume 128 5.4688

Coronal None Output Baseline Volume 129 4.5687

Output Baseline Volume RAS: (-156.1, -115.0, 32.8), Bg: Slice not shown



# Tensor Estimation

3D Slicer Version 3.6

File Edit View Window Help Feedback

Adjust the Window/Level parameters of the baseline volume using the slider

Active Volume: Output Baseline Volume

Display

Lookup Table: Grey

Interpolate

Window Level Editor Presets: CT-brain CT-lung

Volume Window Level Presets: CT-brain

Window/Level: Manual 1956.6 177

Threshold: Off 0 13789

Update Histogram Interactively

[0, 13789] x [0, 1]

Manipulate Slice Views

Manipulate 3D View

R A L

I

Axial None Output Baseline Volume 19 26.8

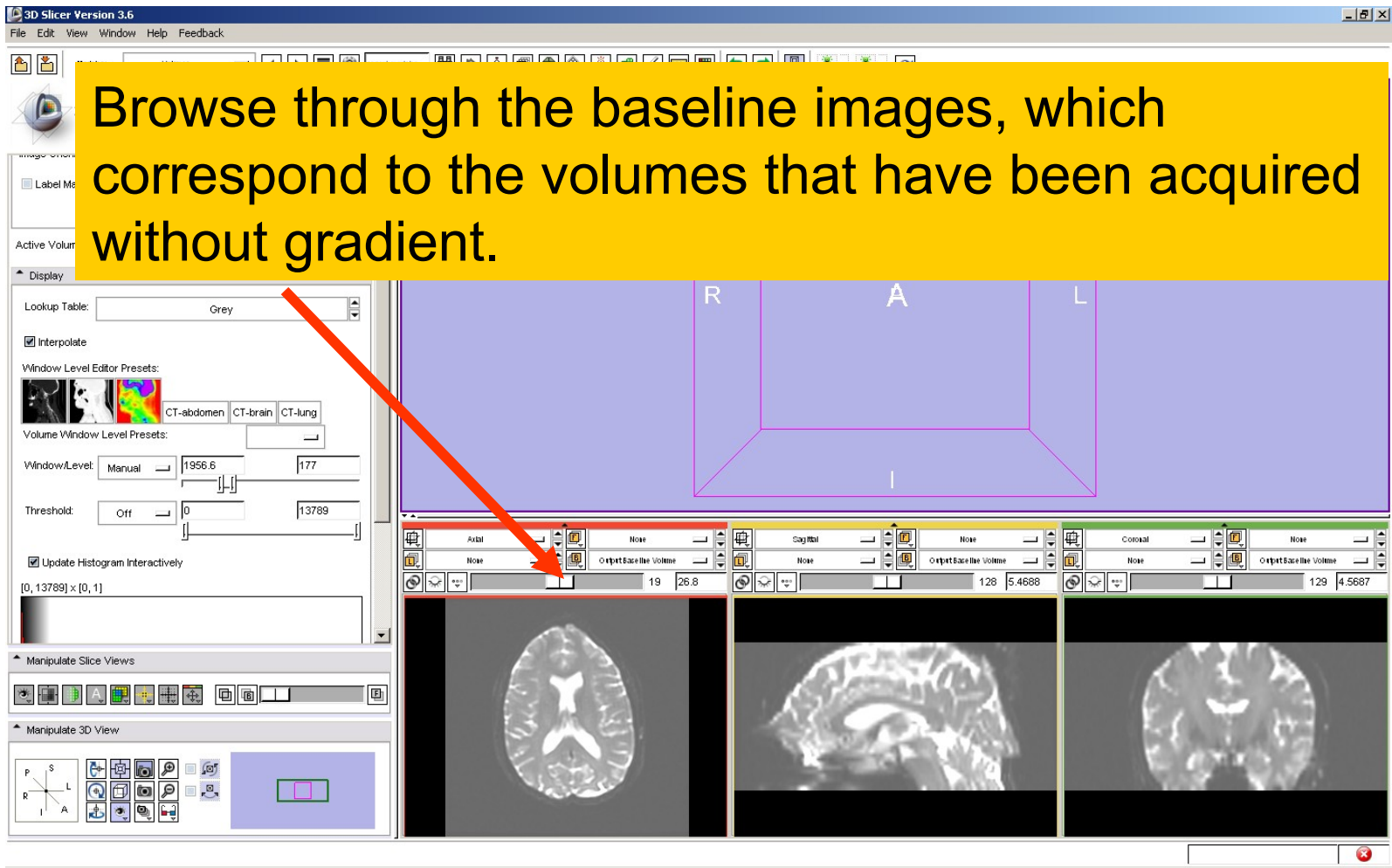
Sagittal None Output Baseline Volume 128 5.4688

Coronal None Output Baseline Volume 129 4.5687

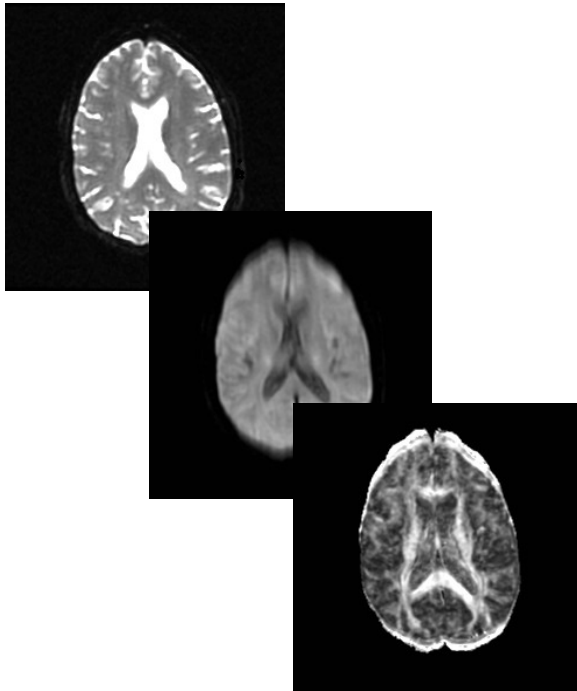


# Tensor Estimation

Browse through the baseline images, which correspond to the volumes that have been acquired without gradient.







# Part2:

# Scalar Measurements



# Scalar Measurements

3D Slicer Version 3.6

File Edit View Window Help Feedback

Model Volume

3DSlicer

Image Orientation: From File

Label Map Single File

Keep all Apply Previous Next

Active Volume: Output Baseline Volume

Display

Lookup Table: Grey

Interpolate

Window Level Editor Presets:

CT-abdomen CT-brain CT-lung

Volume Window Level Presets:

Window Level: Manual 1956.6 177

Threshold: Off 0 13789

Update Histogram Interactively

[0, 13789] x [0, 1]

Manipulate Slice Views

Manipulate 3D View

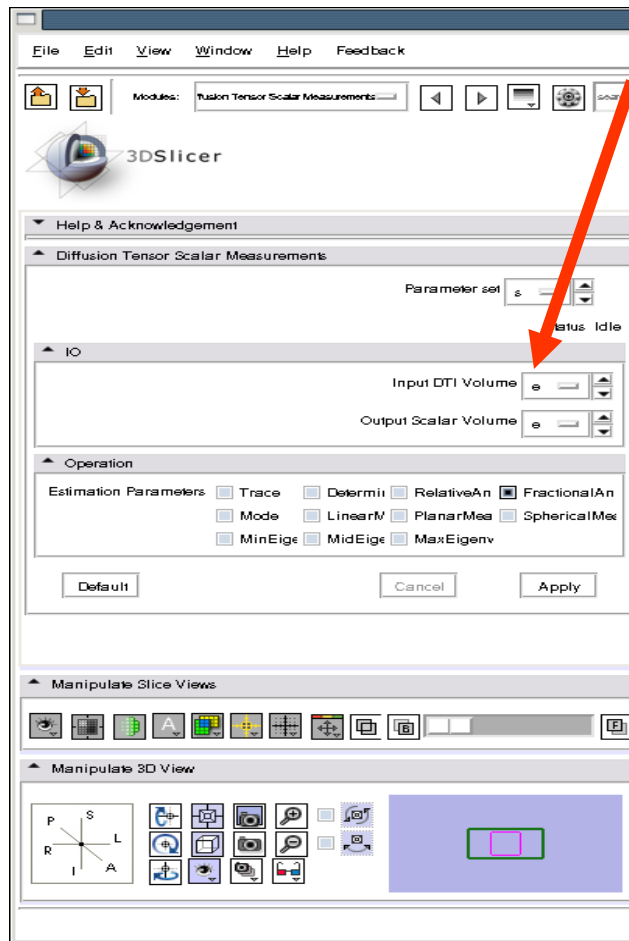
Diffusion Tensor Scalar Measurements

Select the category **Diffusion**--> **Utilities** from the list of modules, and left click on the **Diffusion Tensor Scalar Measurements** module.

3D Slicer interface showing the Diffusion Tensor Scalar Measurements module selected in the Utilities category. The interface displays various window level and threshold settings, and a 3D view of a brain slice with a purple bounding box around a region of interest.



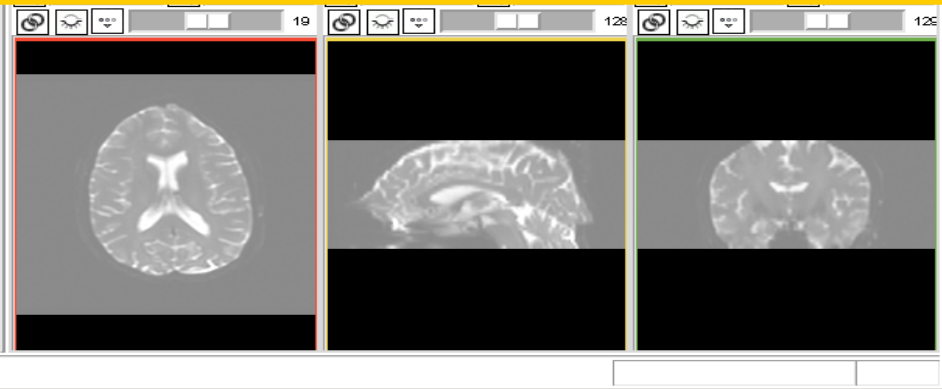
# Scalar Measurements



Select the Input DTI Volume **Output DTI Volume**

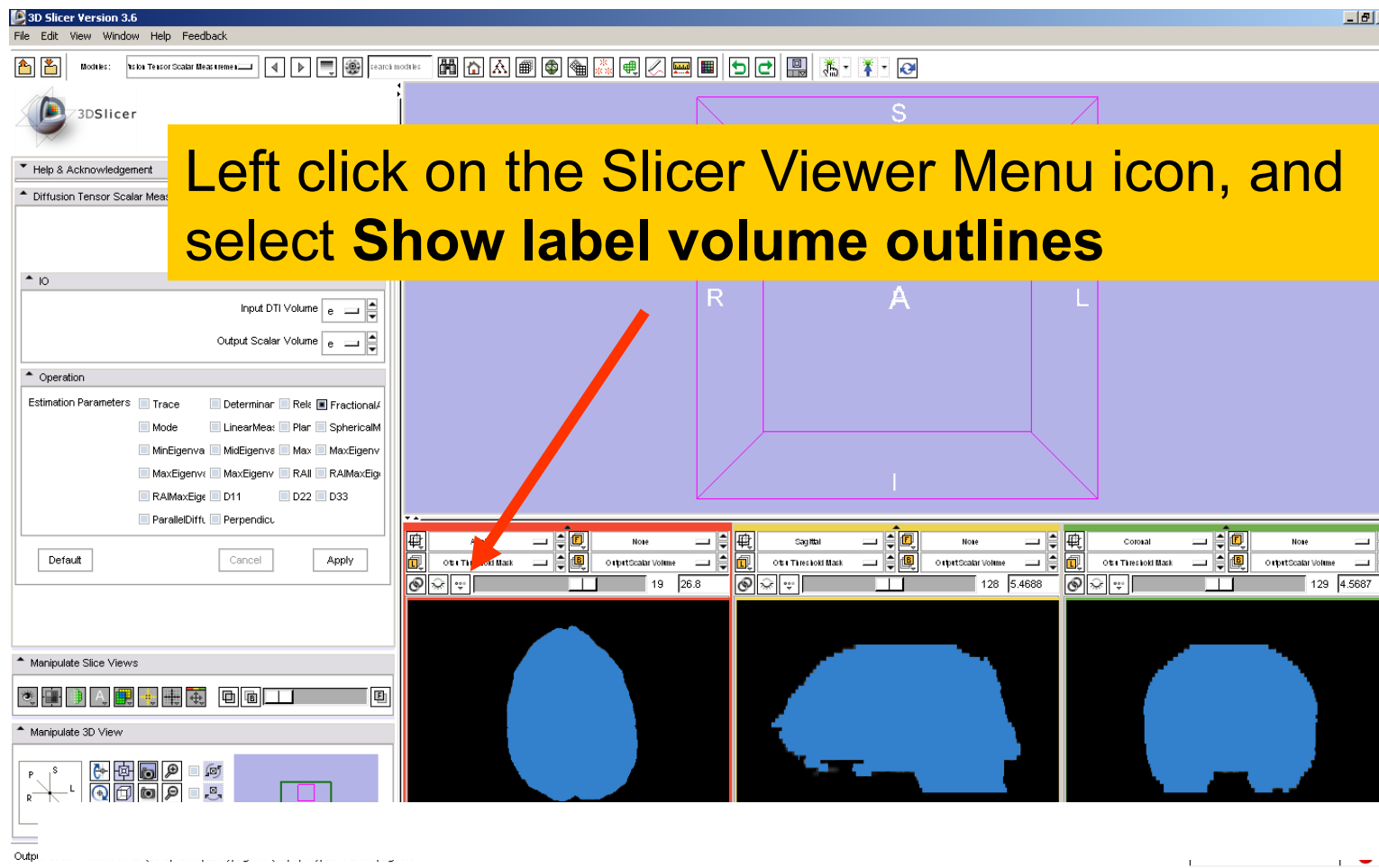
Select the Output Scalar Volume **'Create New Volume'**

Select the Operation **Fractional Anisotropy**, and click on **Apply**





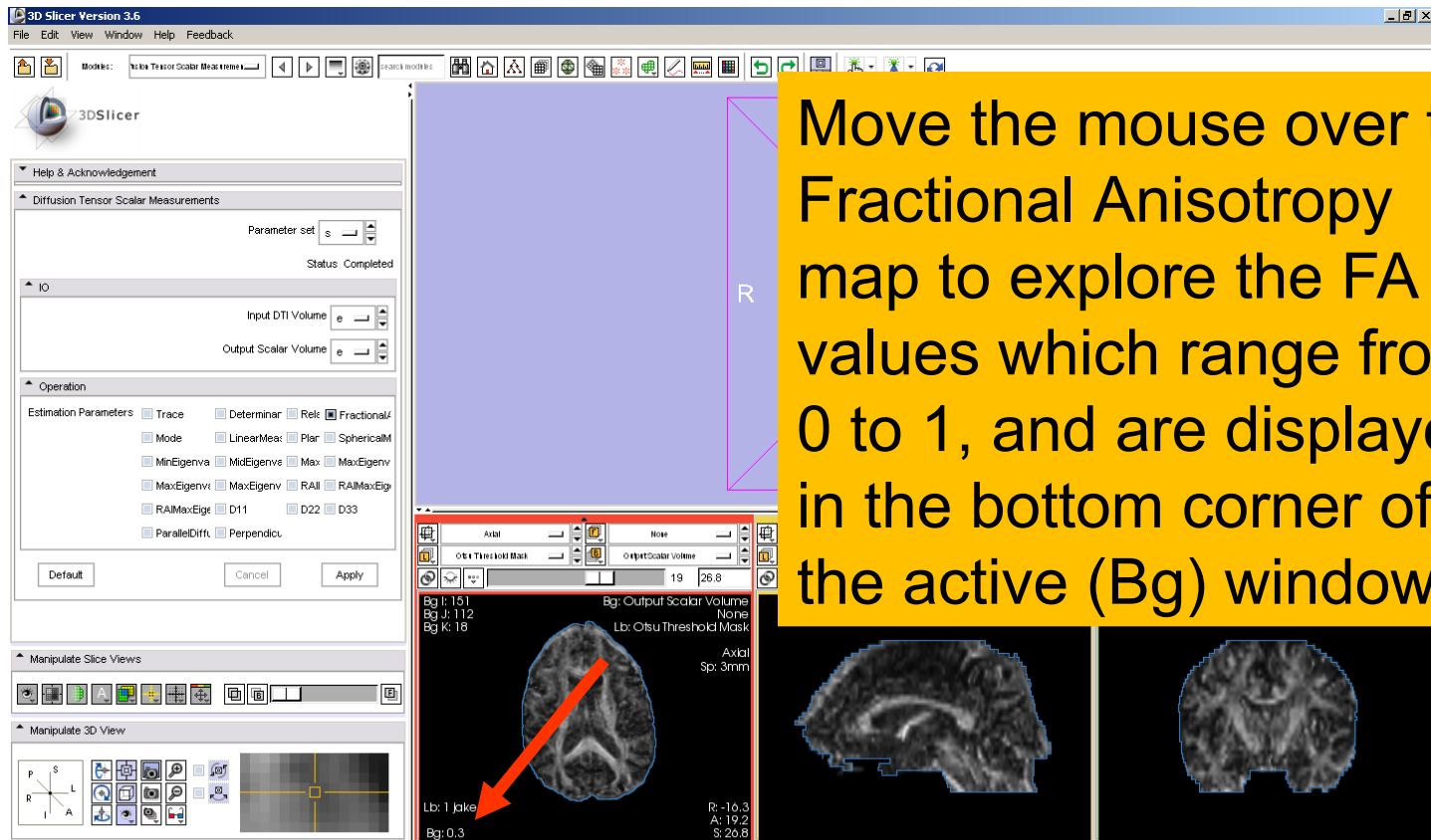
# Fractional Anisotropy Volume







# Fractional Anisotropy Volume



Move the mouse over the Fractional Anisotropy map to explore the FA values which range from 0 to 1, and are displayed in the bottom corner of the active (Bg) window.



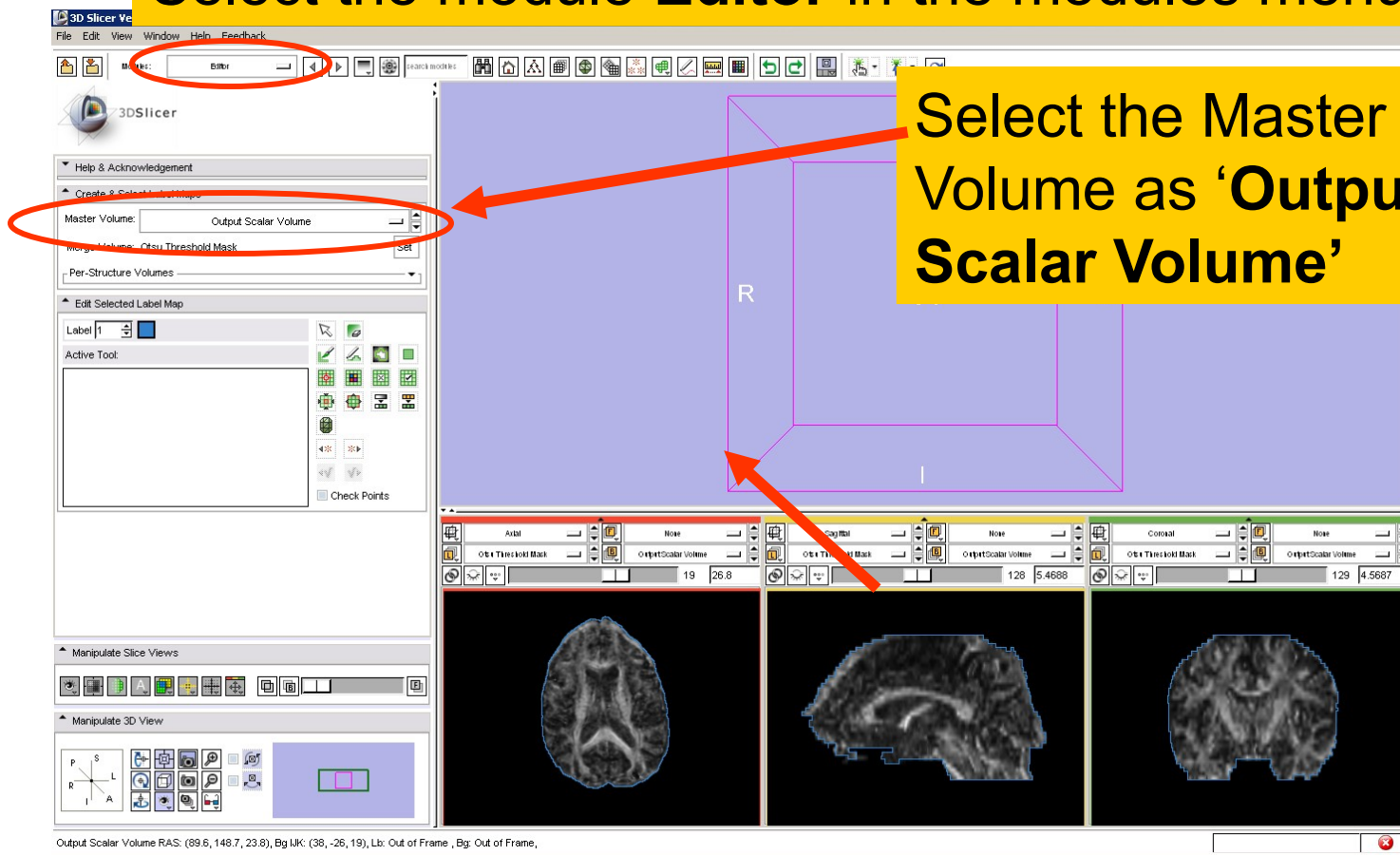
## Part 3:

# Region of Interest based Tractography



# LabelMap Generation

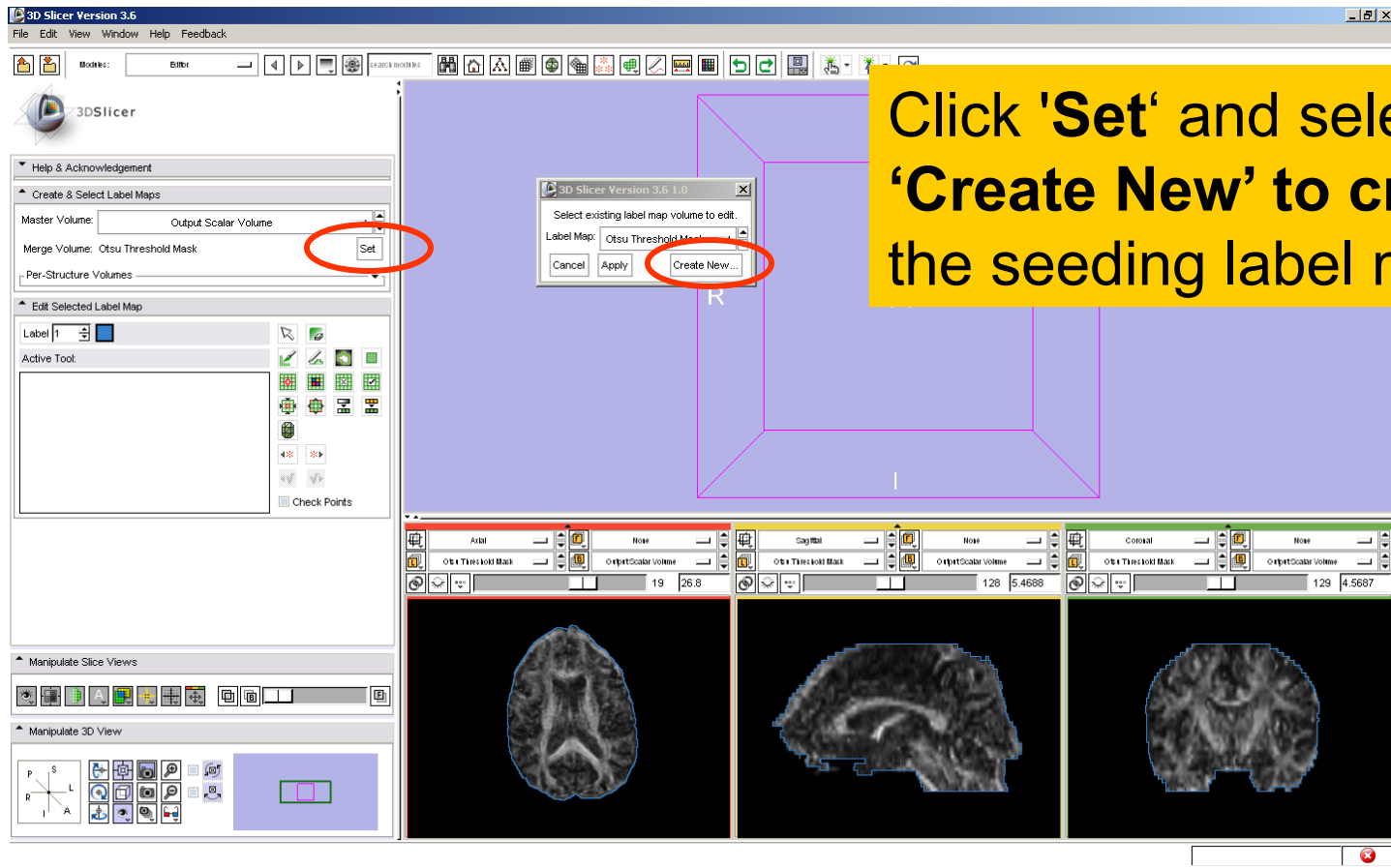
Select the module **Editor** in the modules menu.





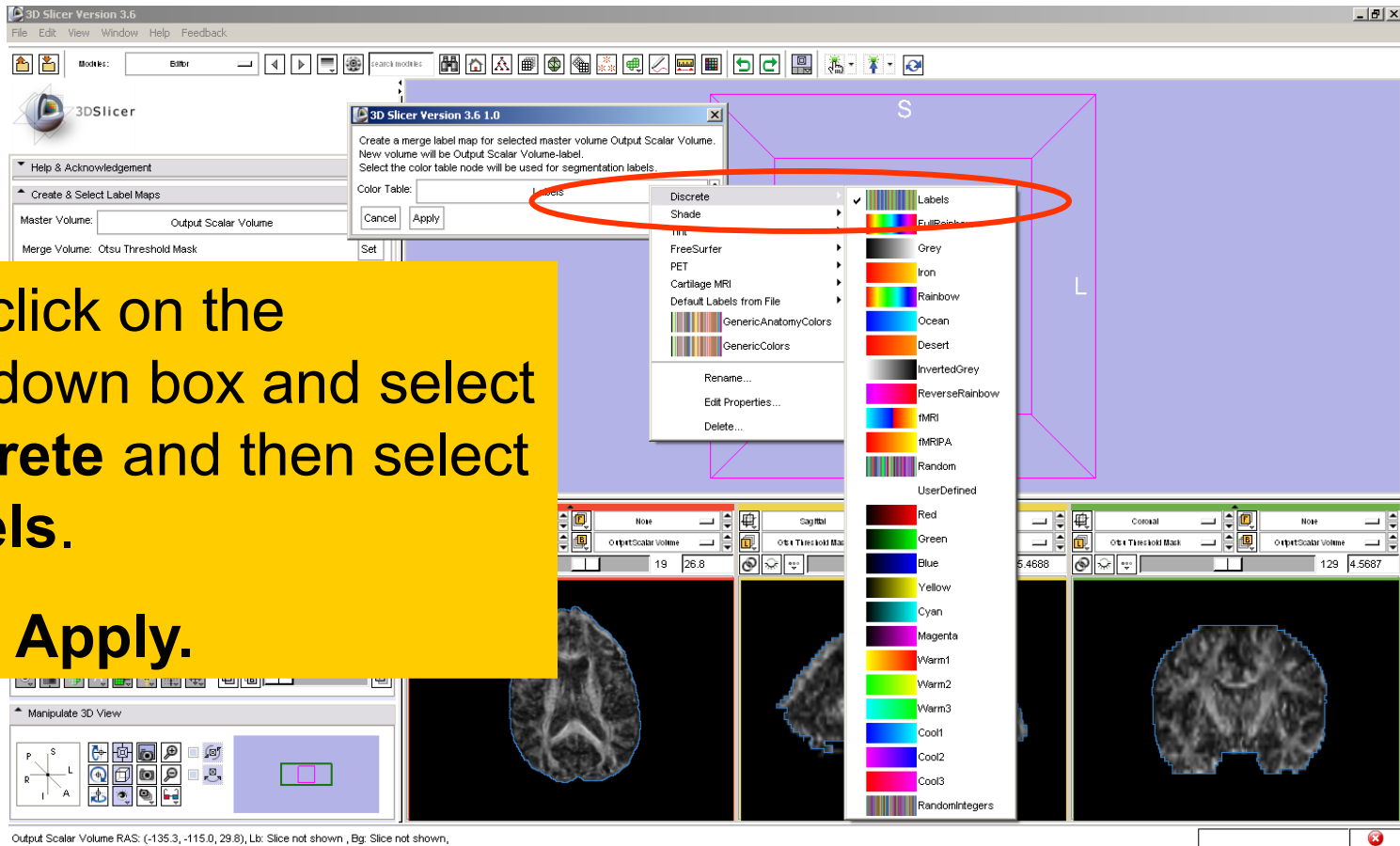


# Label Map Generation





# LabelMap Generation



Left click on the dropdown box and select **Discrete** and then select **Labels**.

Click **Apply**.



# LabelMap Generation

Left click on the Slicer Viewer Menu icon, and select the label map **Output Scalar Volume-label**

Output Scalar Volume RAS: (96.2, 126.0, 23.8), Bg LK: (31, -2, 19), Lb: Out of Frame, Bg: Out of Frame,



# LabelMap Generation

3D Slicer Version 3.6  
File Edit View Window Help Feedback

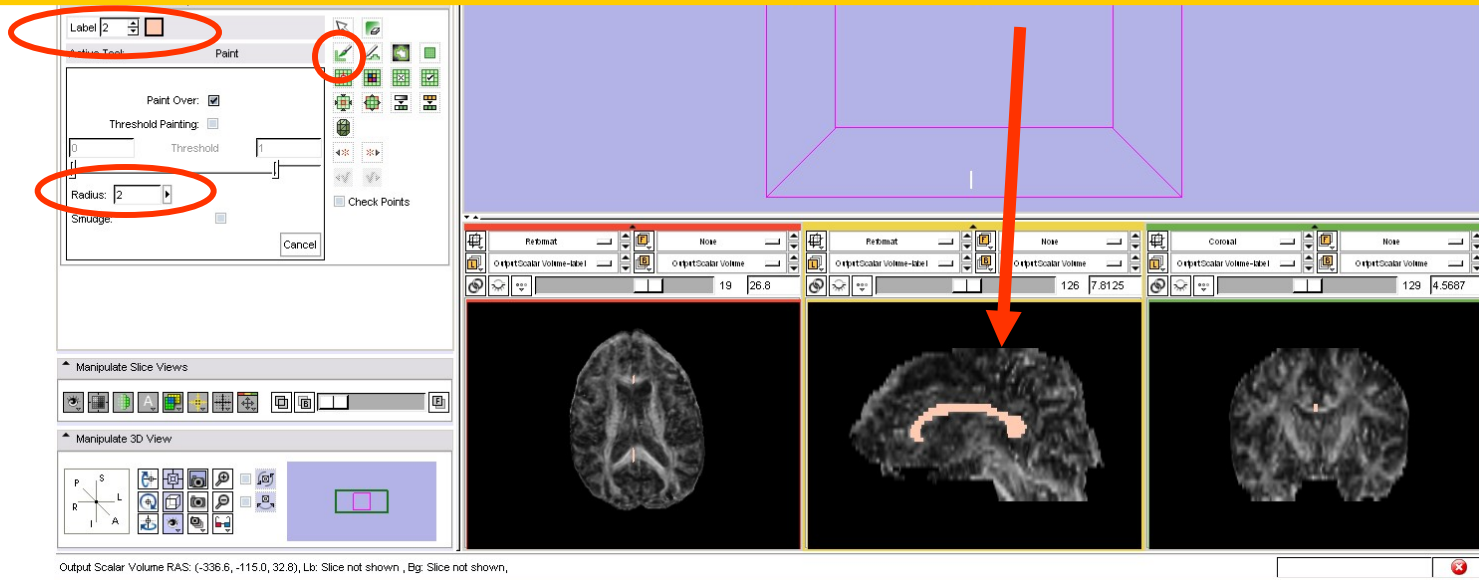
Left click on the Slicer Viewer Menu icon, and select **Don't Show label volume outlines**

The screenshot displays the 3D Slicer software interface. A yellow banner at the top contains the instruction: "Left click on the Slicer Viewer Menu icon, and select **Don't Show label volume outlines**". A red arrow points from this text to the Slicer Viewer menu icon in the bottom-left corner of the software window. The menu is open, showing the option "Don't show label volume outlines" selected. The interface includes a "Create & Select Label Maps" panel on the left, an "Edit Selected Label Map" panel below it, and three viewports (Sagittal, Coronal, and Axial) at the bottom right showing a brain slice with a label map overlay. The status bar at the bottom indicates "Don't show label volume outlines".



# LabelMap Generation

Select the label 2 (pink), click on the icon **Paint** , set the radius to **2** and draw a region of interest within the corpus callosum in the sagittal view on a set of 2 or 3 slices





# LabelMap Seeding

3D Slicer Version 3.6

File Edit View Window Help Feedback

LabelMap Seeding

Parameter set

Status: idle

IO

Input DTI Volume

Input Label Map

Output Fiber bundle

Write Fibers To Disk

Output Directory

File Prefix Name: line

Seed Placement Options

Use Index Space

Seed Spacing: 2

Random Grid

Linear Measure Start Threshold: 0.3

Tractography Seeding Parameters

Minimum Length: 10

Manipulate Slice Views

Manipulate 3D View

Output Scalar Volume RAS: (-63.5, -114.0, 26.8), Bg UK: (201, 254, 18), Lb: 0 Black, Bg: 0.0

Select the module  
**Labelmap Seeding** from  
the Modules' menu



# LabelMap Seeding

**Select the Input DTI volume  
'Output DTI Volume'**

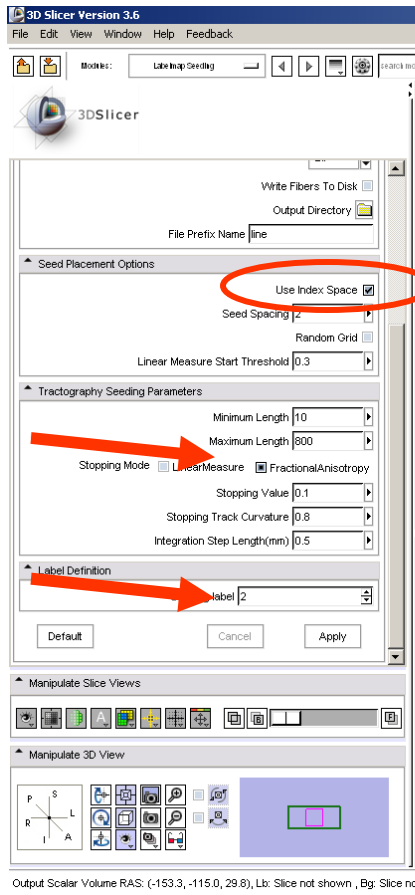
**Select the Input Label Map  
'Output Scalar Volume  
-label'**

**Select Output Fiber Bundle  
'Create New Fiber Bundle'**

3D Slicer Version 3.6  
File Edit View Window Help Feedback  
3DSlicer  
Help & Acknowledgement  
Labelmap Seeding  
Parameter set: g  
Status: Idle  
IO  
Input DTI Volume: e  
Input Label Map: O1  
Output Fiber bundle: L1  
Write Fibers To Disk  
Output Directory  
Seed Placement Options  
Use Index Space  
Seed Spacing: 2  
Random Grid  
Linear Measure Start Threshold: 0.3  
Tractography Seeding Parameters  
Minimum Length: 10  
Manipulate Slice Views  
Manipulate 3D View  
Output Scalar Volume RAS: (165.2, 223.3, 20.8), Lx: Slice not shown, Bx: Slice not shown



# LabelMap Seeding



In the Seed Placement Options tab, select **Use Index Space**.

In the Tractography Seeding Parameters tab, select the 'Stopping Mode' **Fractional Anisotropy**, and use the default parameters for the minimum and maximum tract length, stopping value, stopping track curvature and integration step length.

In the Label Definition tab, set 'Seeding label' to label 2, and click on **Apply**

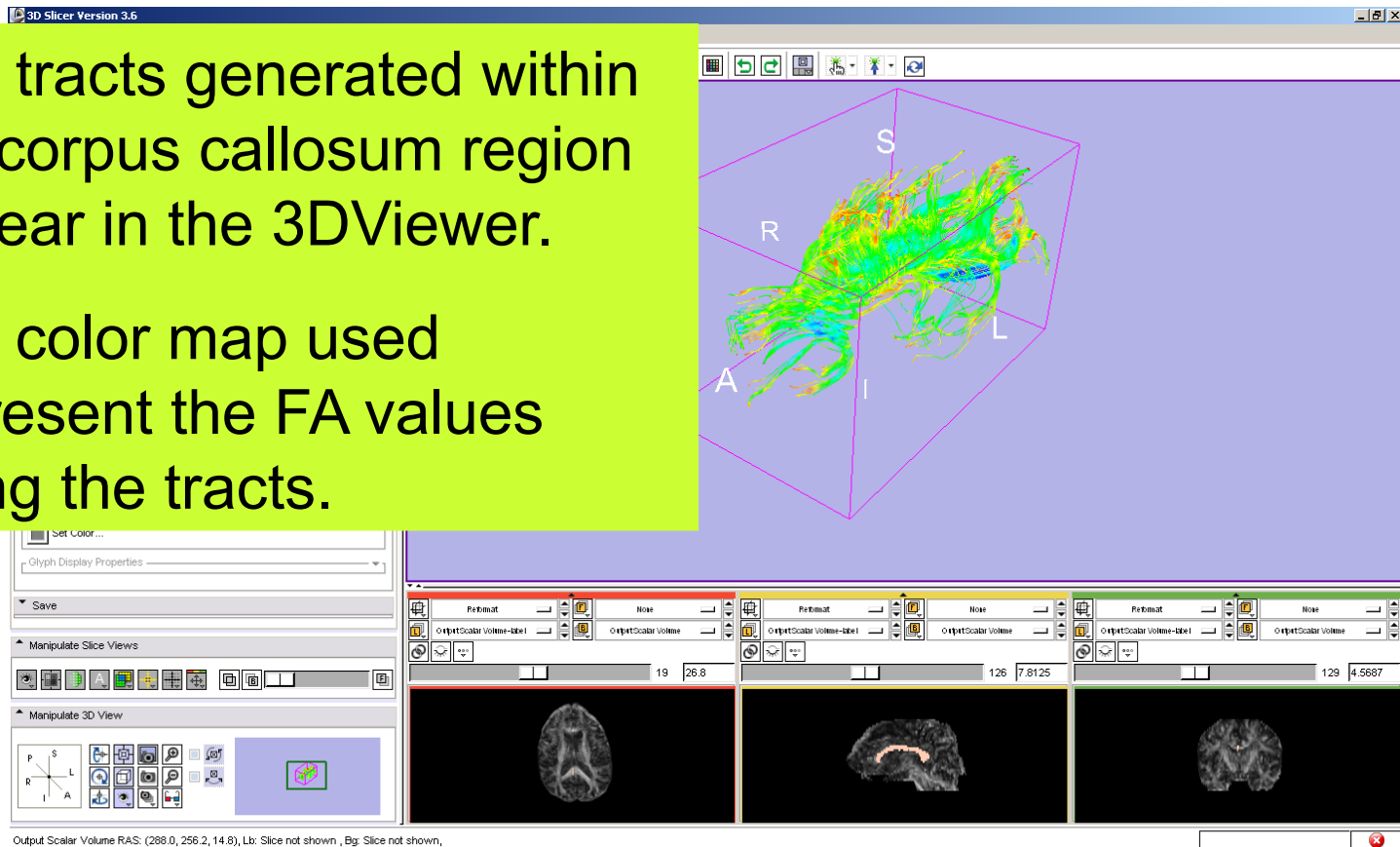




# LabelMap Seeding

The tracts generated within the corpus callosum region appear in the 3DViewer.

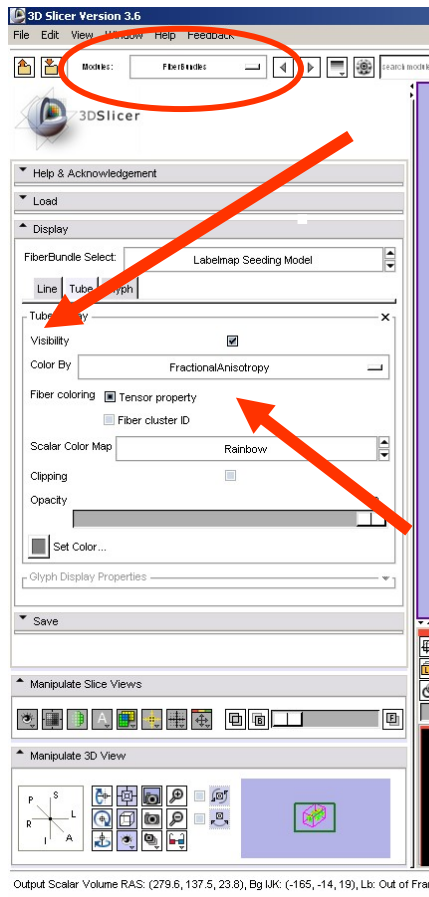
The color map used represent the FA values along the tracts.



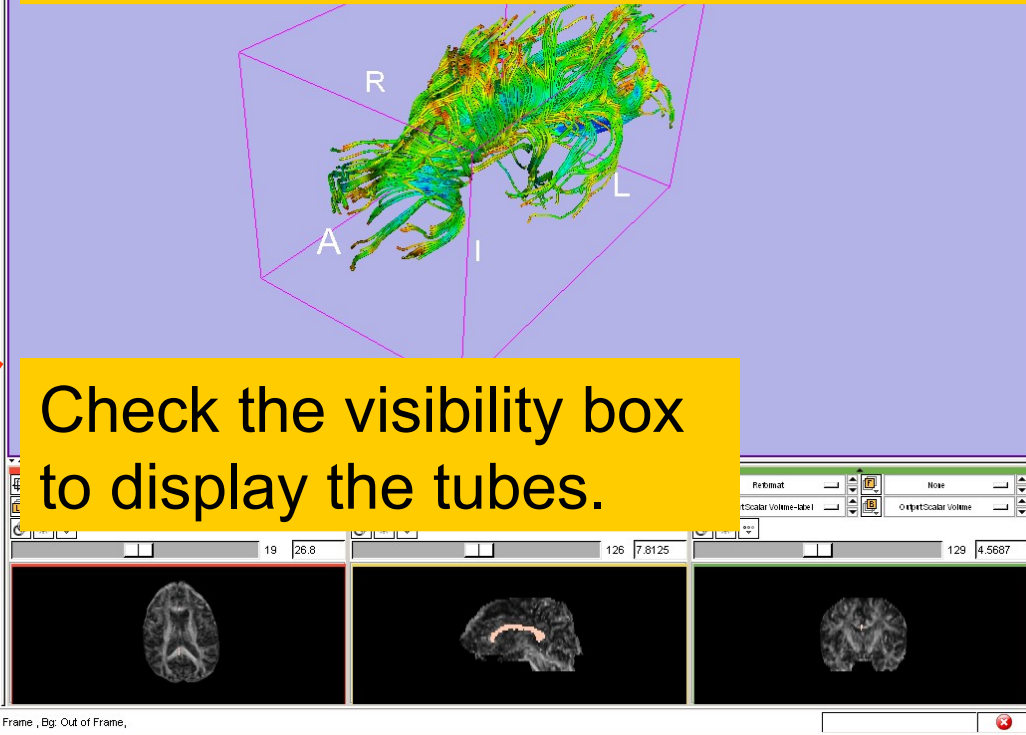


# LabelMap Seeding

Select the module **FiberBundles**, and click on the tab **Tube** in the Display panel



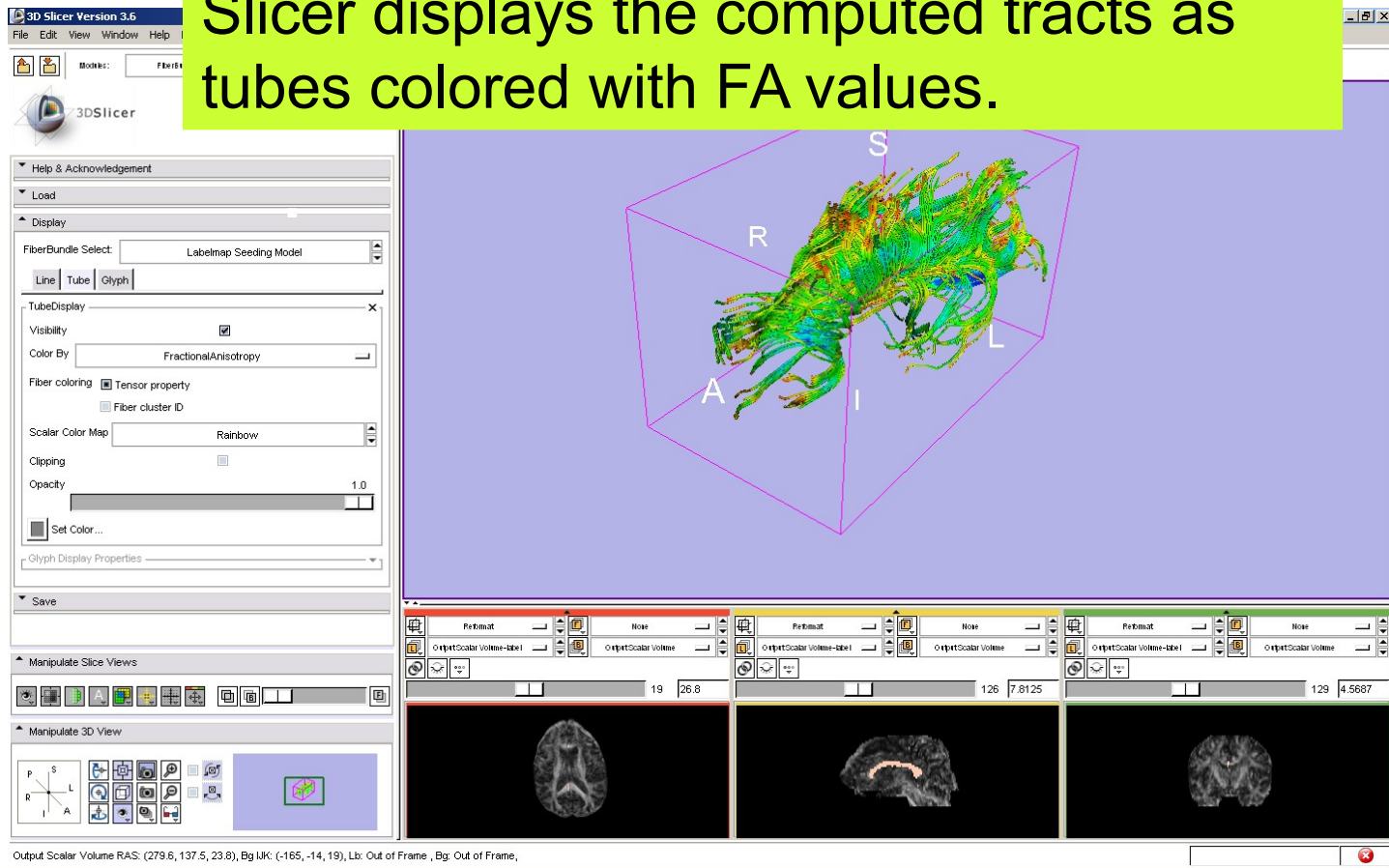
Check the visibility box to display the tubes.

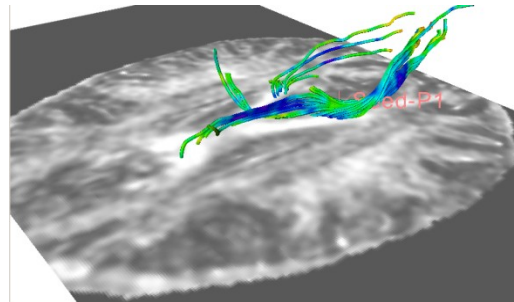
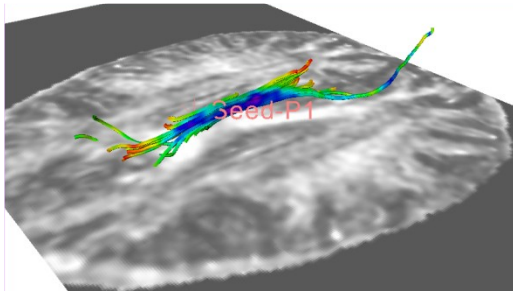
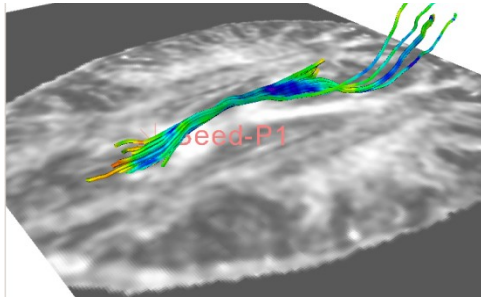




# LabelMap Seeding

Slicer displays the computed tracts as tubes colored with FA values.





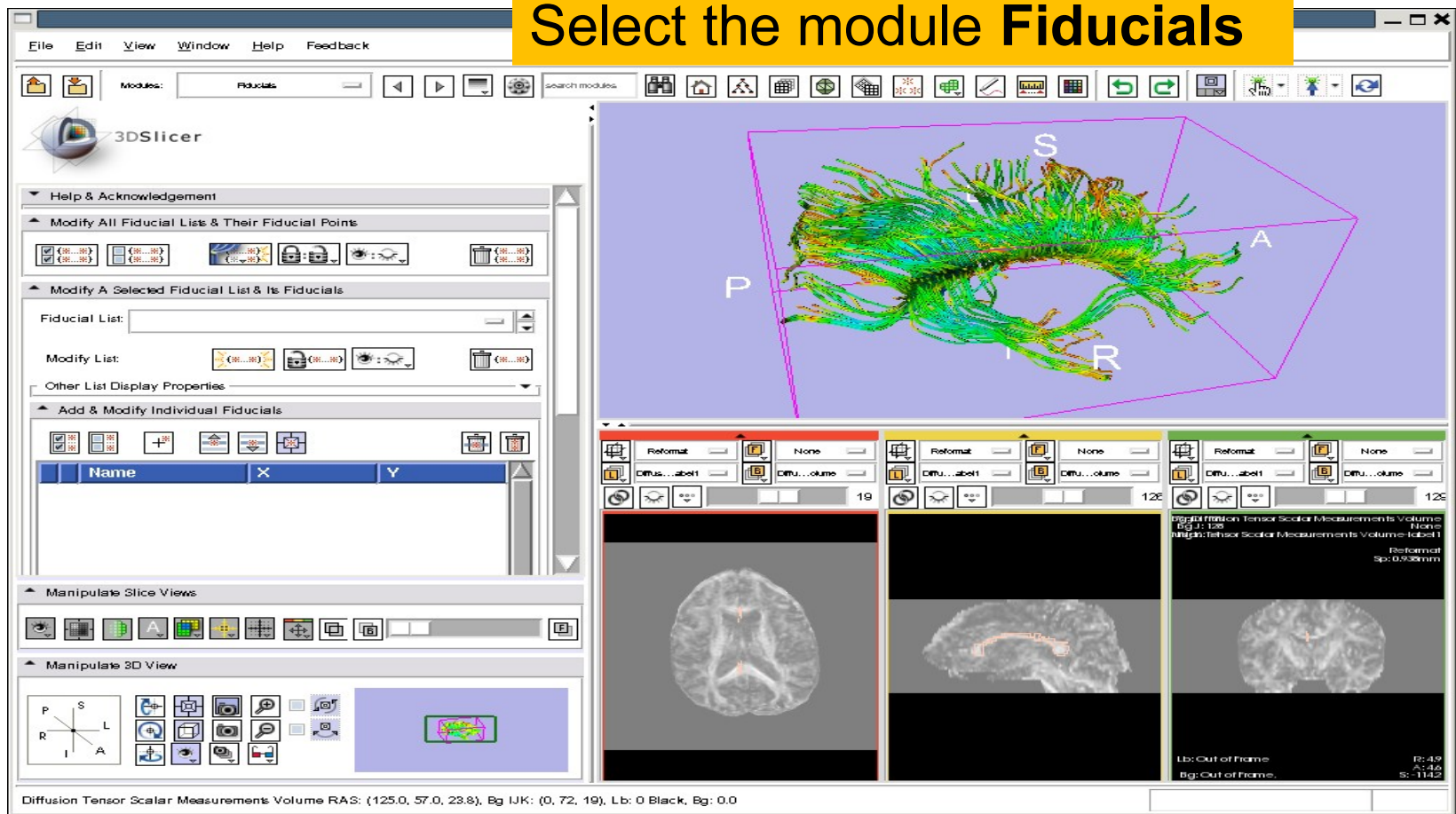
**Part 4:**

**Tractography  
on-the-fly**



# Fiducial Seeding

Select the module **Fiducials**





# Fiducial Seeding

Set Fiducial List to Create New FiducialList

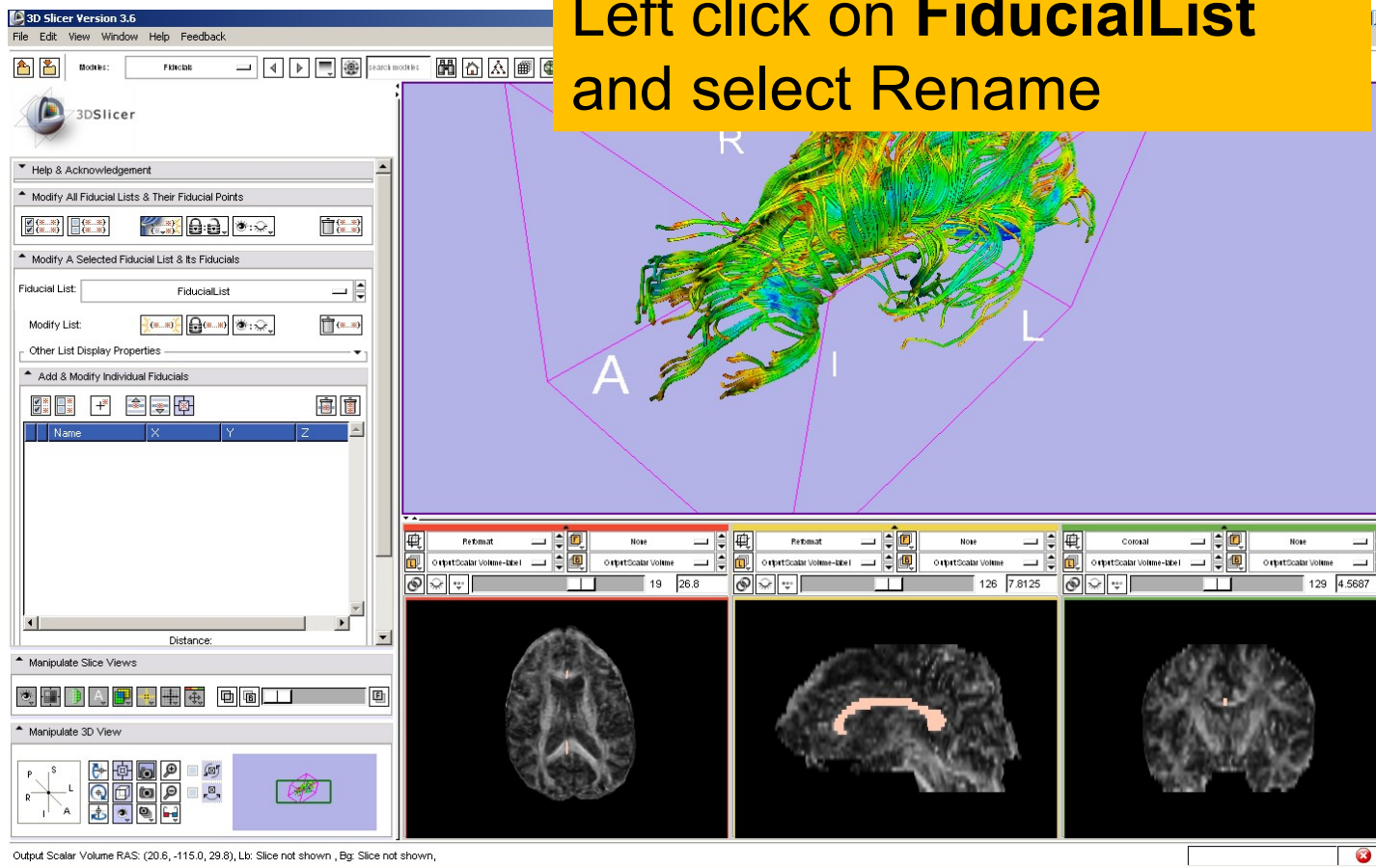
The screenshot displays the 3DSlicer software interface. On the left, the 'Fiducial List' panel is open, showing options to 'Modify All Fiducial Lists & Their Fiducial Points' and 'Modify A Selected Fiducial List & Its Fiducial'. A red arrow points from the 'Set Fiducial List to Create New FiducialList' text to the 'Fiducial List' input field. The main 3D view shows a brain model with a purple bounding box and axes labeled P, S, I, R, A. Below the 3D view are three slice views (axial, sagittal, and coronal) showing the brain model in different orientations. The status bar at the bottom indicates the current volume and its properties: 'Diffusion Tensor Scalar Measurements Volume RAS: (125.0, 57.0, 23.8), Bg IJK: (0, 72, 19), Lb: 0 Black, Bg: 0.0'.





# Fiducial Seeding

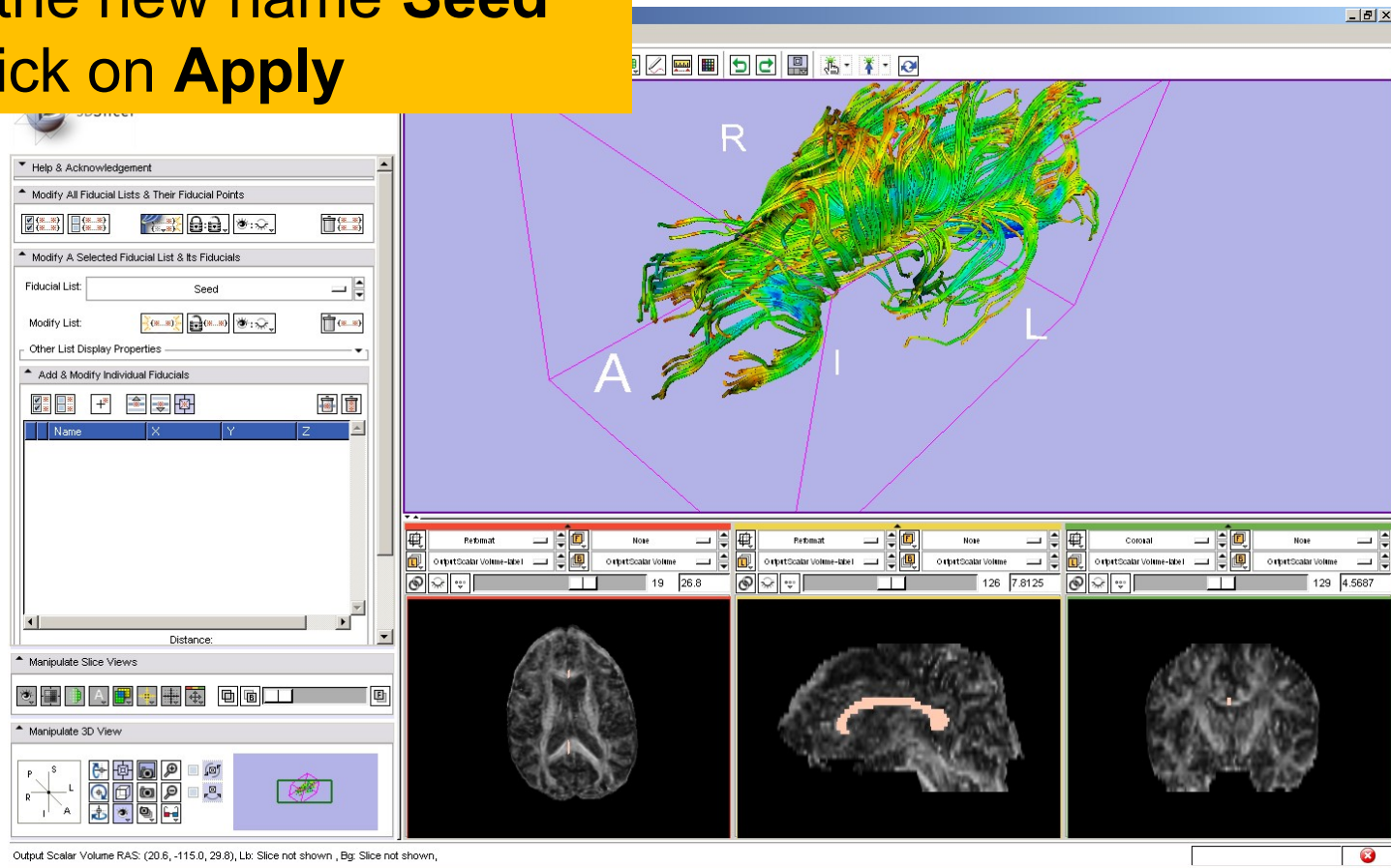
Left click on **FiducialList**  
and select **Rename**





# Fiducial Seeding

Enter the new name **Seed**  
and click on **Apply**

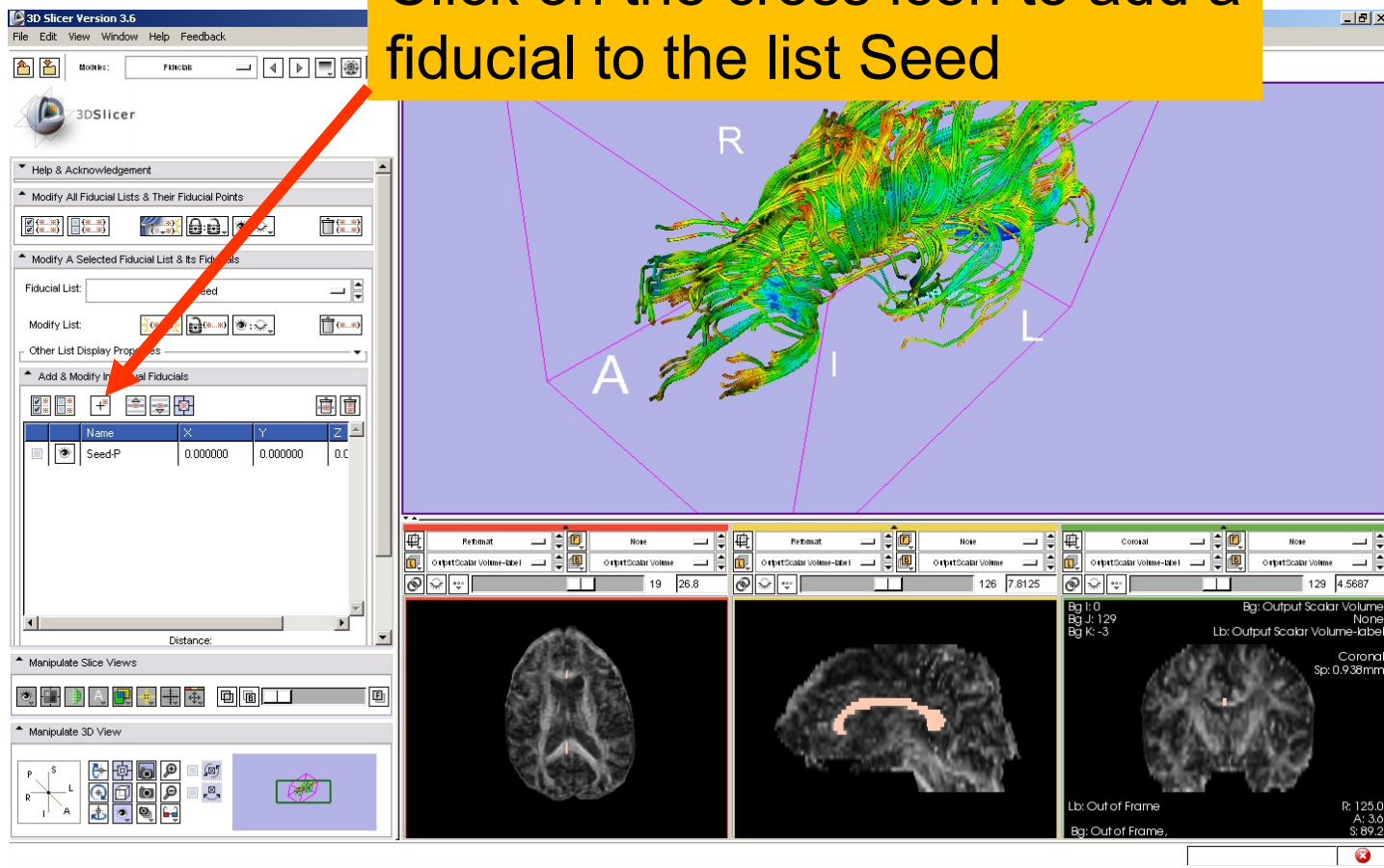






# Fiducial Seeding

Click on the cross icon to add a fiducial to the list Seed





# Fiducial Seeding

The fiducial **Seed-P** appears in the 3D Viewer

The screenshot displays the 3D Slicer software interface. On the left, the 'Fiducial List' panel shows a table with the following data:

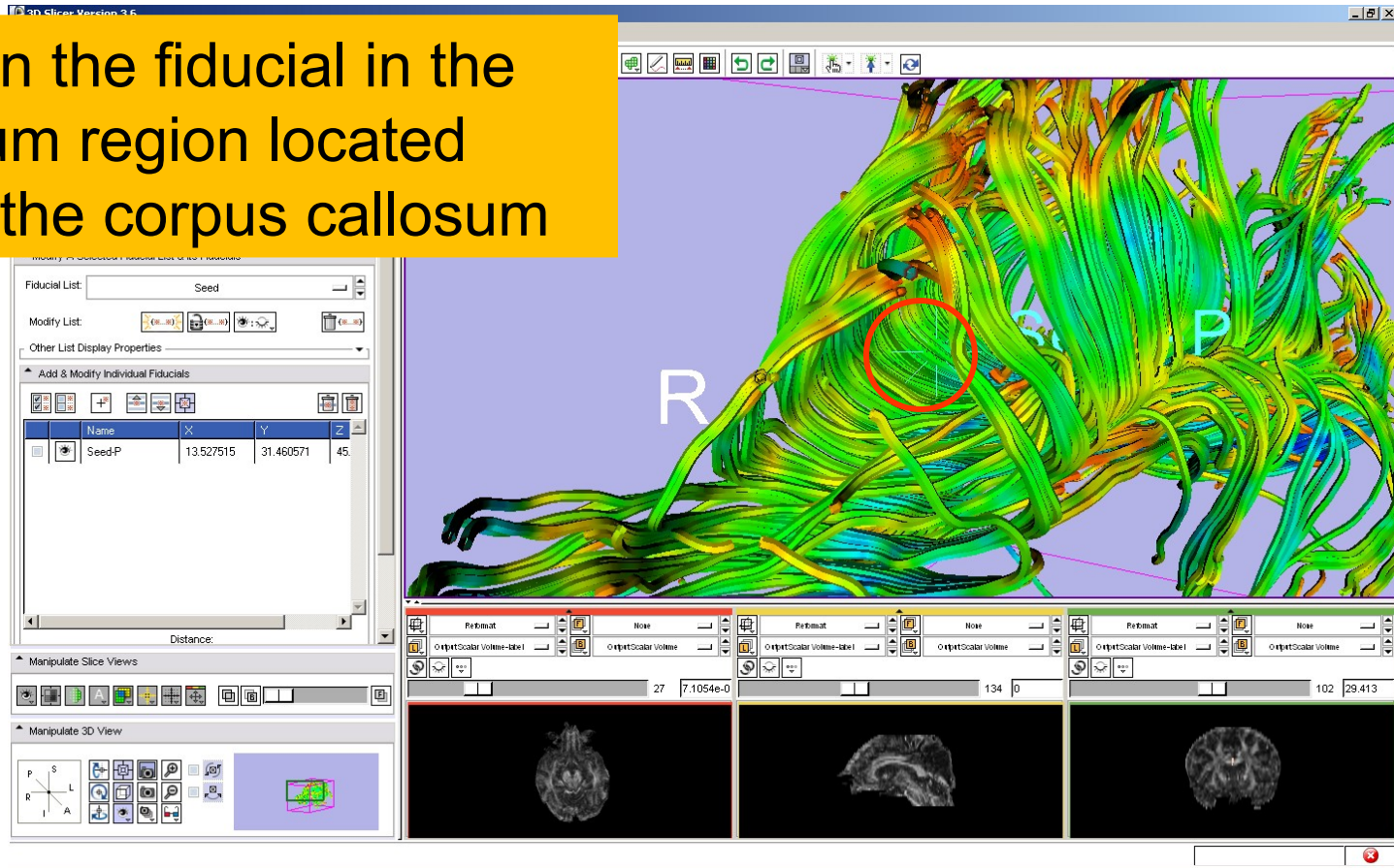
Name	X	Y	Z
Seed-P	0.000000	0.000000	0.0

The main 3D viewer shows a brain model with a red arrow pointing to a red circle labeled 'Seed-P'. The model is labeled with 'S' (Superior), 'I' (Inferior), 'R' (Right), 'L' (Left), 'A' (Anterior), and 'P' (Posterior). Below the 3D viewer are three slice views: Axial, Sagittal, and Coronal. The status bar at the bottom indicates: 'Output Scalar Volume RAS: (-84.3, 233.7, 23.8), Bg IJK: (223, -117, 19), Ltr: Out of Frame, Bg: Out of Frame.'



# Fiducial Seeding

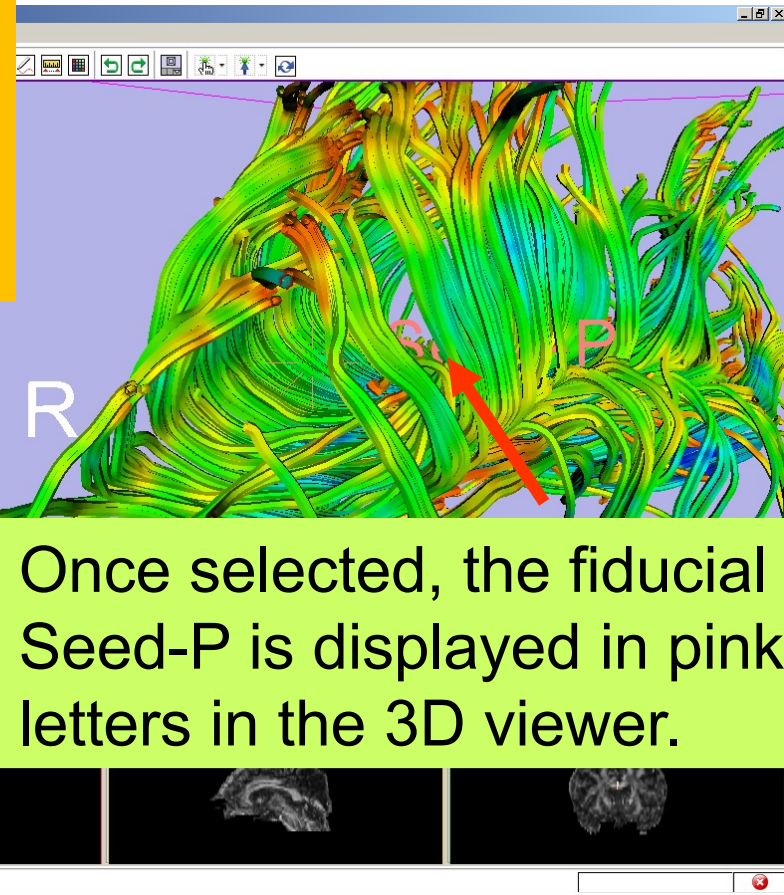
Position the fiducial in the cingulum region located above the corpus callosum



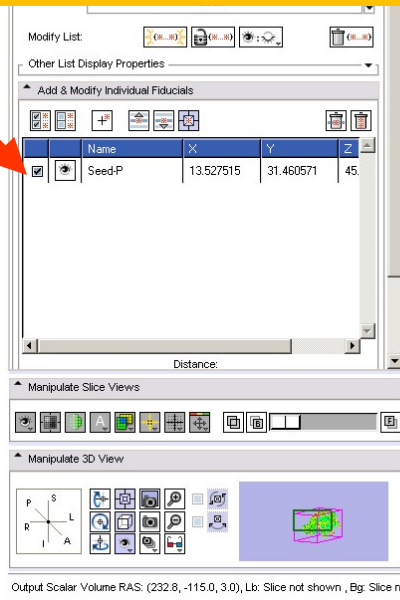


# Fiducial Seeding

**Check the box to select the 'Seed-P' fiducial:** we will use this fiducial to drive the tractography



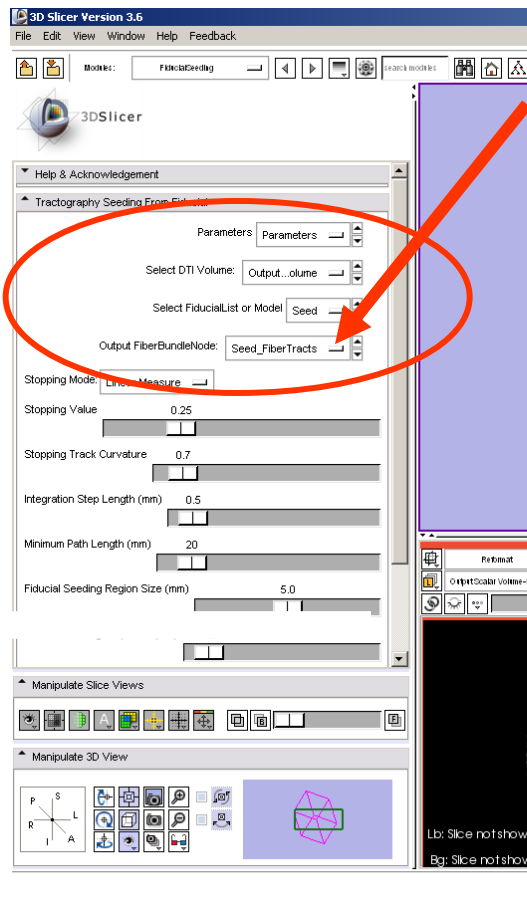
Once selected, the fiducial Seed-P is displayed in pink letters in the 3D viewer.







# Fiducial Seeding



Set the Output FiberBundleNode to **Create New FiberBundle**

**Important:** this step must be done first

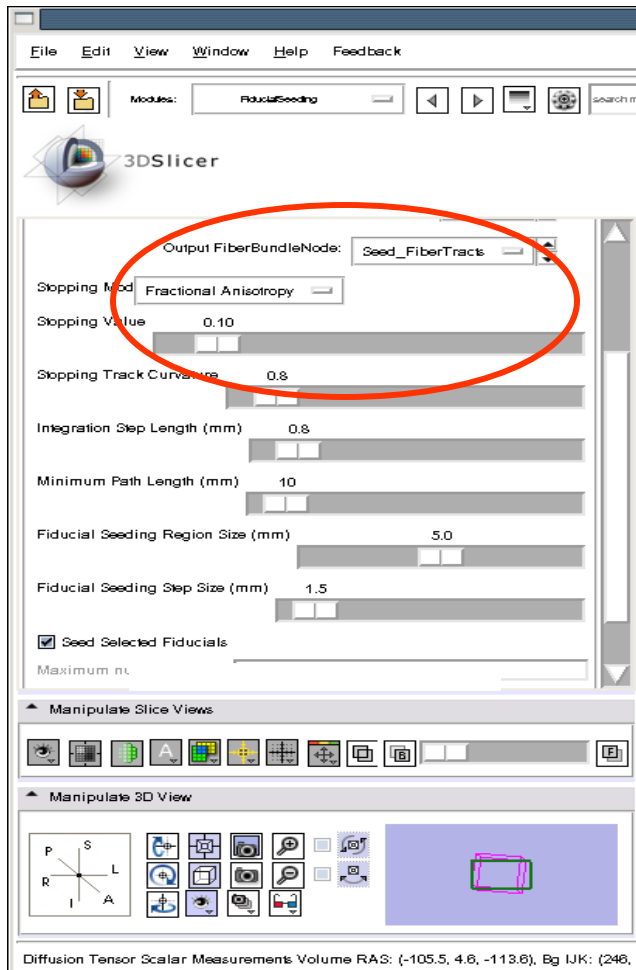
Select the module **Fiducial Seeding**

Set the DTI Volume to **Output DTI Volume**

Select the Fiducial List **Seed**



# Fiducial Seeding



Set the Stopping Mode to **Fractional Anisotropy** and set the tractography parameters to the values that we used for the corpus callosum:

**Stopping Value: 0.1**

**Stopping Track Curvature: 0.8**

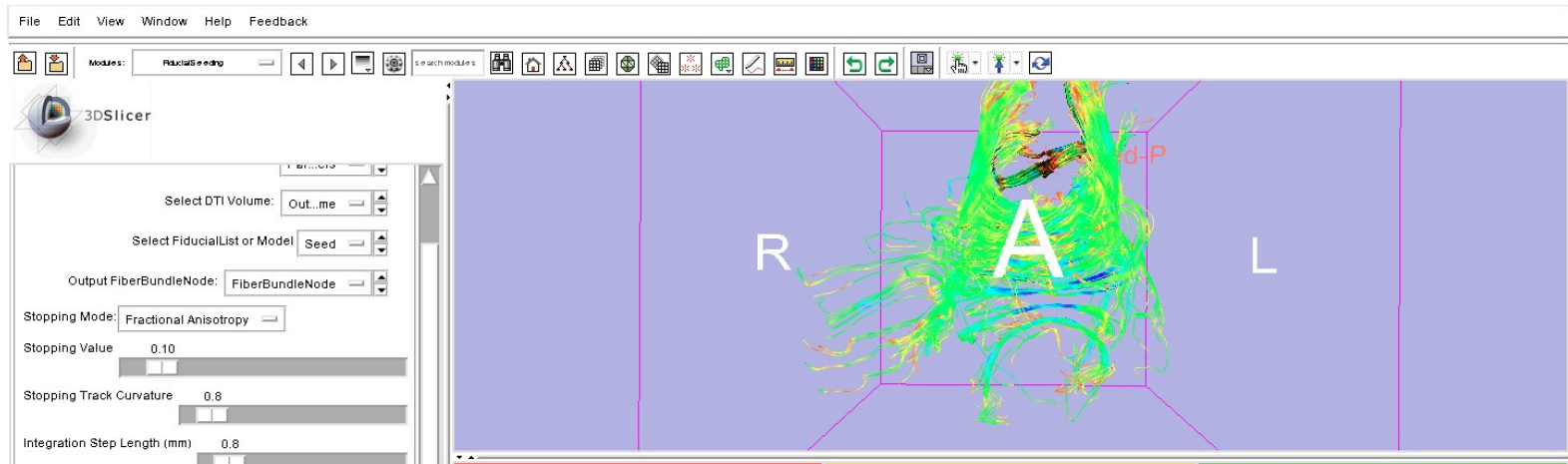
**Step Length: 0.8 mm**

**Minimum Path Length: 10 mm**

**Fiducial Stepping Size: 1.5 mm**



# Fiducial Seeding



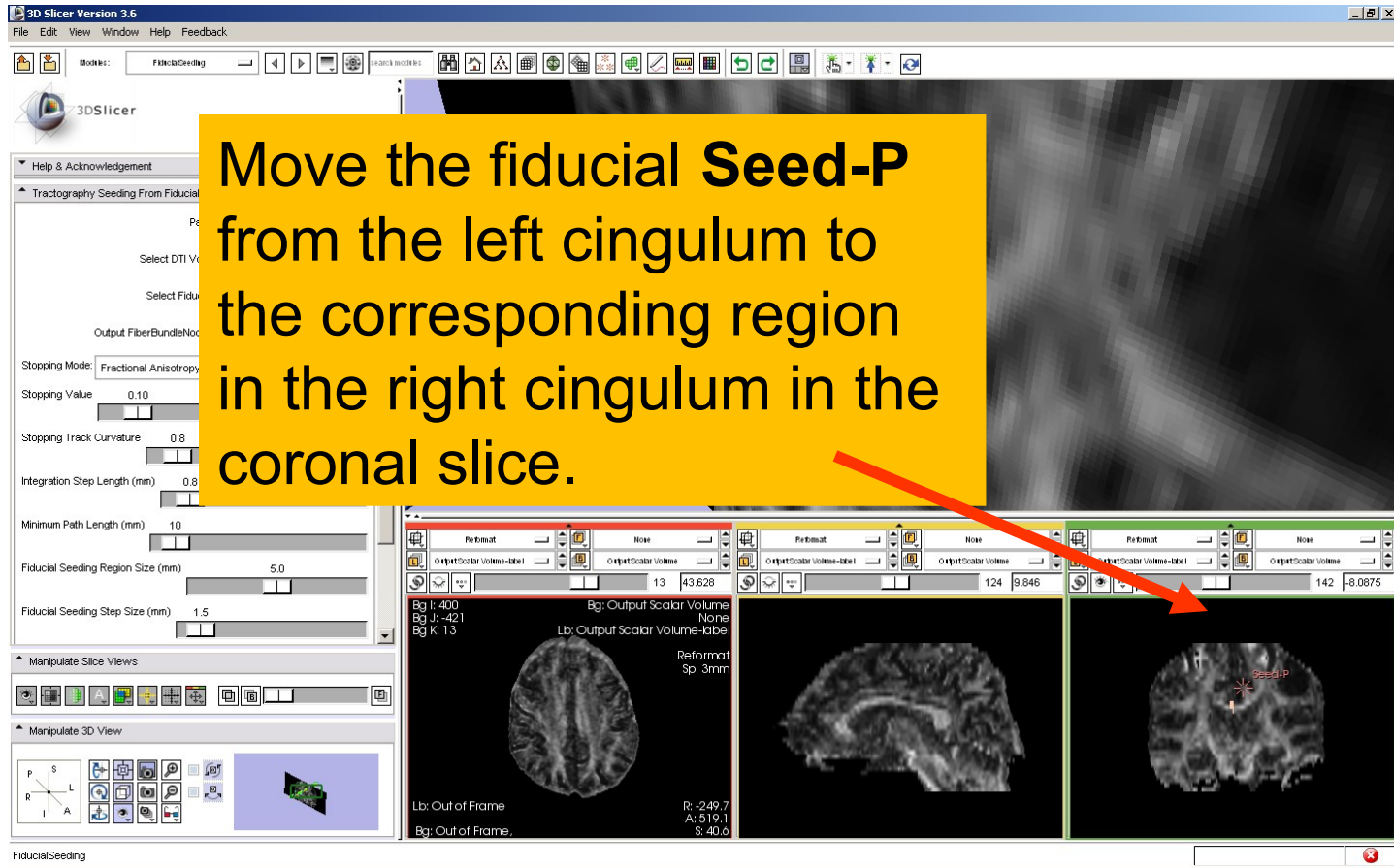
Slicer displays the tracts seeded from the Fiducial Seed-P.

The tracts correspond to the region of the cingulum located above the corpus callosum.

For better visualization, uncheck the visibility box under **Tubes** in the **Fiber Bundles** module (Slide 42).



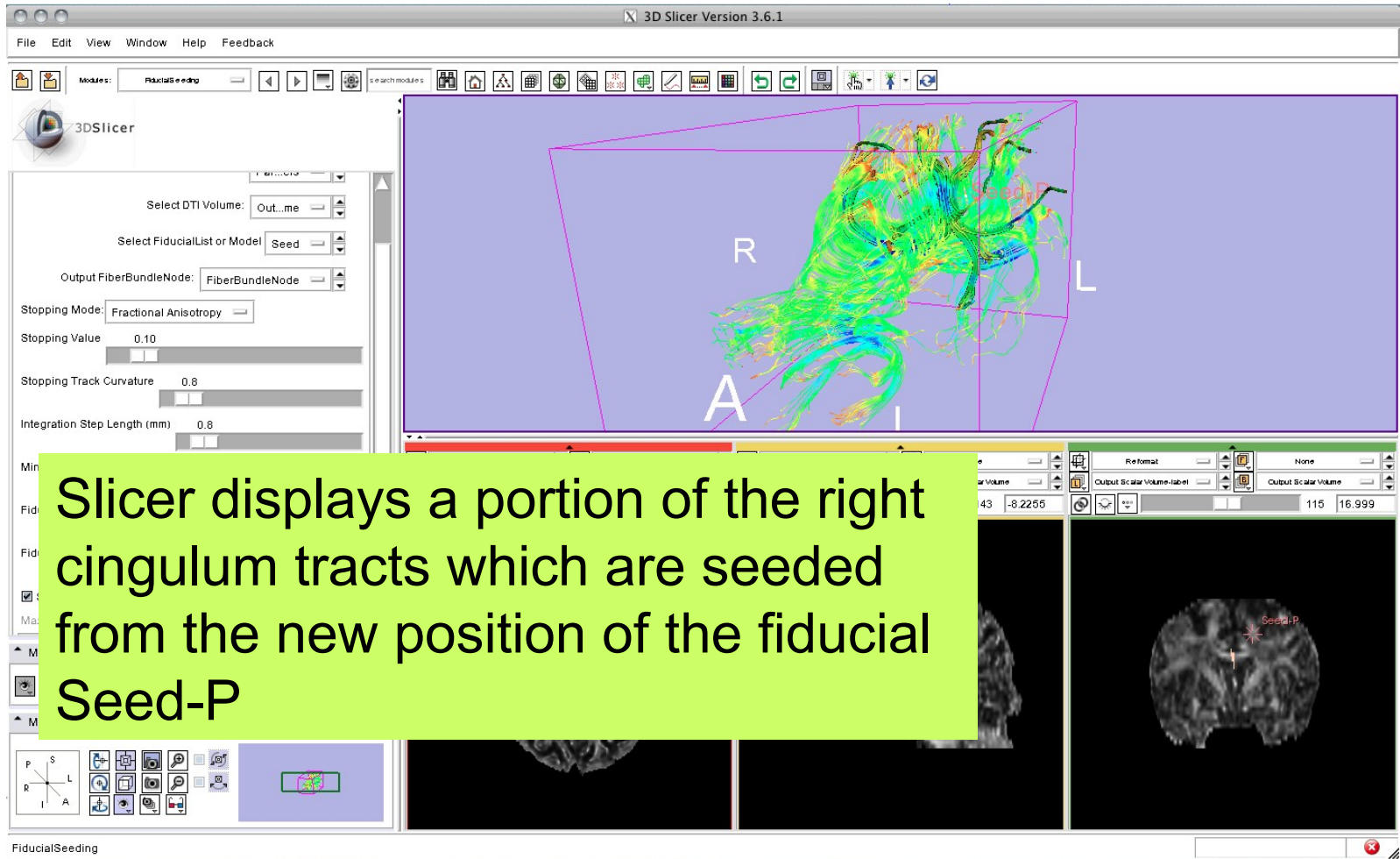
# Fiducial Seeding

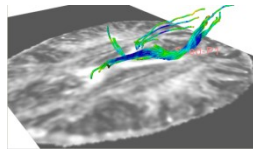
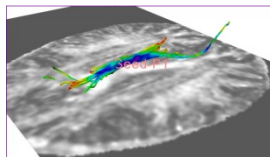
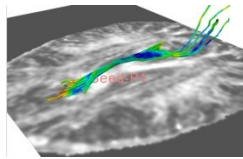
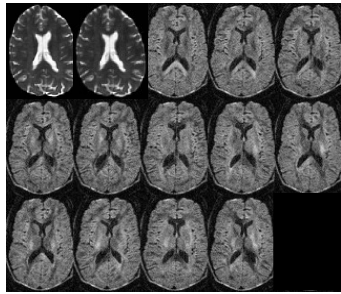






# Fiducial Seeding





## Part 5:

# Saving a DTI Scene



# DTI Scene

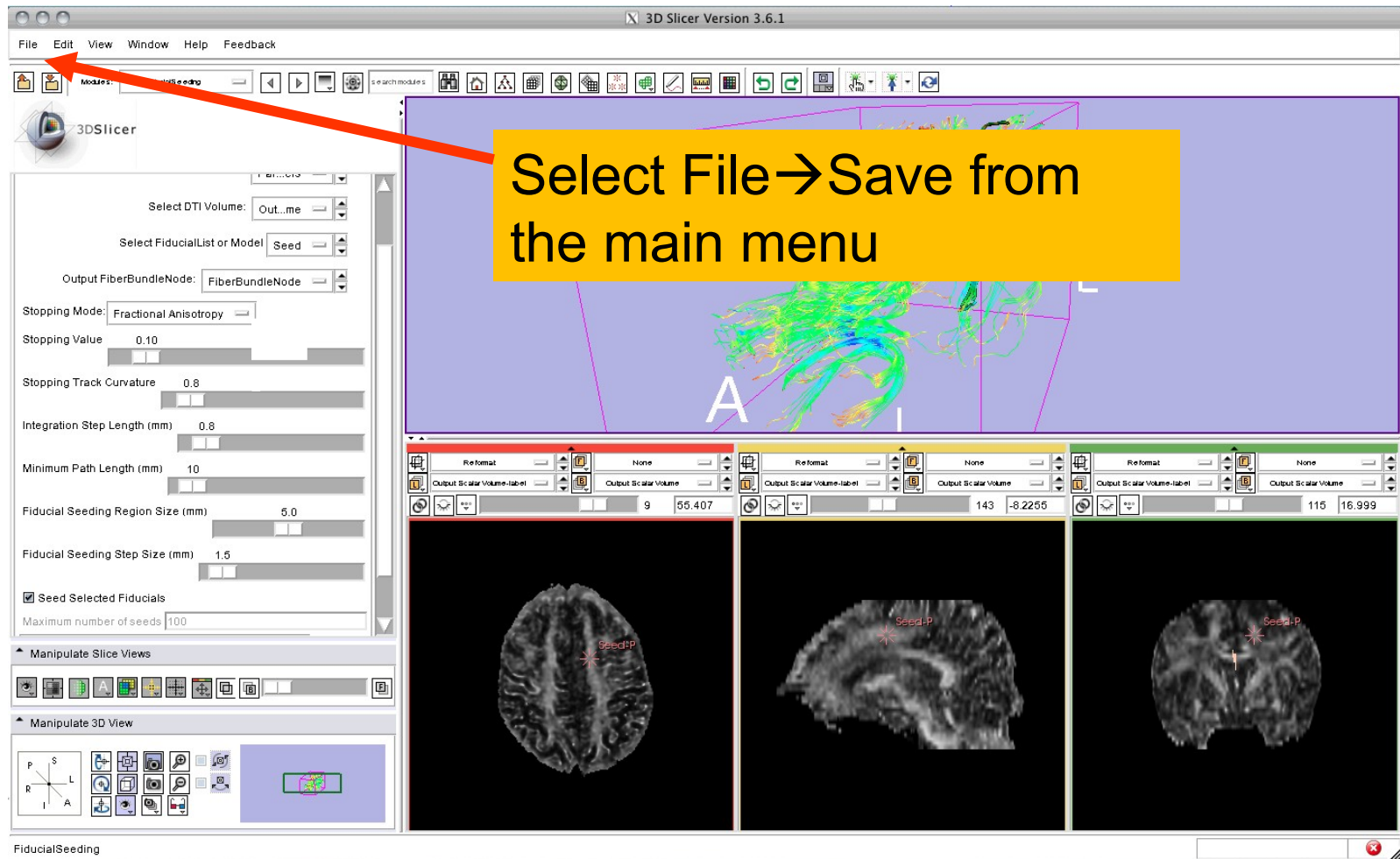
Select the module Data

Slicer displays the list of volumes and models generated in this tutorial

Volume Name	Size (MB)	Memory (MB)
Output Scalar Volume-label	19	26.8
Output Scalar Volume	128	5,4688
Output Scalar Volume-label	129	4,5687



# Saving a DTI Scene





# Saving a DTI Scene

Browse to a directory where you would like to save the data. Once you have selected a directory, select all the files that have been created during this tutorial and click on **Save Selected**

Save Scene & Data Options

Change Destination for All Selected: D:/SlicerData/DiffusionDataset/

Select	Node Name	Node Type	Node Status	File Format	File Name	Data Directory
<input checked="" type="checkbox"/>	[Scene Description]	[SCENE]	Modified	MRML (.mrm)	SlicerScene1	D:/SlicerData/DiffusionDataset/
<input type="checkbox"/>	dwiDataset	DiffusionWei...	Not Modified	NRRD (.nhdr)	dwiDataset.nhdr	D:/SlicerData/DiffusionDataset/
<input checked="" type="checkbox"/>	Output DTI Volume	DiffusionTen...	Not Modified	NRRD (.nhdr)	Output DTI Volume.nhdr	D:/SlicerData/DiffusionDataset/
<input checked="" type="checkbox"/>	Output Baseline Volume	Volume	Modified	NRRD (.nrrd)	Output Baseline Volum...	D:/SlicerData/DiffusionDataset/
<input checked="" type="checkbox"/>	Otsu Threshold Mask	Volume	Modified	NRRD (.nrrd)	Otsu Threshold Mask.n...	D:/SlicerData/DiffusionDataset/
<input checked="" type="checkbox"/>	Output Scalar Volume	Volume	Modified	NRRD (.nrrd)	Output Scalar Volume...	D:/SlicerData/DiffusionDataset/
<input checked="" type="checkbox"/>	Output Scalar Volume-label	Volume	Modified	NRRD (.nrrd)	Output Scalar Volume-l...	D:/SlicerData/DiffusionDataset/
<input checked="" type="checkbox"/>	Labelmap Seeding Model	FiberBundle	Modified	Poly Data (.vtk)	Labelmap Seeding Mo...	D:/SlicerData/DiffusionDataset/
<input checked="" type="checkbox"/>	Seed	FiducialList	Modified	Fiducial List CSV (.fcsv)	Seed.fcsv	D:/SlicerData/DiffusionDataset/
<input checked="" type="checkbox"/>	Seed_FiberTracts	FiberBundle	Modified	Poly Data (.vtk)	Seed_FiberTracts.vtk	D:/SlicerData/DiffusionDataset/

Save Selected Cancel



# Saving a DTI Scene

**Select File → Close Scene to close the current DTI Scene**

3D Slicer Version 3.6 RC3

File Edit View Window Help

Modules: SlicerWelcome

3DSlicer

Welcome & About

3DSlicer version 3.6 Welcome

3D Slicer is a free open source software platform for medical image processing and 3D visualization of image data. This module contains some basic information and useful links to get you started using Slicer. Please see our website <http://www.slicer.org> and the documentation on our wiki for more information: <http://www.slicer.org/slicerWiki/index.php/Documentation-3.6>.

3D Slicer is distributed under a BSD-style license; for details about the contribution and software license agreement, please see <http://www.slicer.org/cgi-bin/License/SlicerLicenseForm.pl>. The software has been designed for research purposes only and has not been reviewed or approved by the Food and Drug Administration, or by any other agency.

**Hint:** to open any information panel below, click on its grey title bar.

Don't show this module on startup.

Manipulate Slice Views

Manipulate 3D View

None RAS: (87.3, 1.0, -125.0)



# Loading a DTI Scene

**Select File** → **Load Scene** and browse to the location where you saved the scene **SlicerScene1.mrml**

3D Slicer Version 3.6 RC3

File Edit View Window Help

Modules: SlicerWelcome

3DSlicer

Welcome & About

3DSlicer version 3.6 Welcome

3D Slicer is a free open source software platform for medical image processing and 3D visualization of image data. This module contains some basic information and useful links to get you started using Slicer. Please see our website <http://www.slicer.org> and the documentation on our wiki for more information: <http://www.slicer.org/slicerWiki/index.php/Documentation-3.6>.

3D Slicer is distributed under a BSD-style license; for details about the contribution and software license agreement, please see <http://www.slicer.org/cgi-bin/License/SlicerLicenseForm.pl>. The software has been designed for research purposes only and has not been reviewed or approved by the Food and Drug Administration, or by any other agency.

**Hint:** to open any information panel below, click on its grey title bar.

Don't show this module on startup.

Manipulate Slice Views

Manipulate 3D View

None RAS: (87.3, 1.0, -125.0)





# Loading a DTI Scene

3D Slicer Version 3.6 RC3

Select the scene **SlicerScene1.mrml** and click on **Open**

The screenshot shows the 3D Slicer interface with a 'Select File' dialog box open. The dialog box displays a list of files and folders. The file 'SlicerScene1.mrml' is selected, and the 'Open' button is circled in red. The background shows the 3D Slicer interface with a 3D view of a brain slice and various toolbars.

Name	Size	Modified time
SlicerScene1.mrml	28 KB	07/31/10 16:13:36

File name: SlicerScene1.mrml  
Files of type: Scenes (.mrml;.xml;.xcat)

None RAS: (87.3, 1.0, -125.0)





# Loading a DTI Scene

3D Slicer Version 3.6.1

Select the module **Data**

The screenshot shows the 3D Slicer software interface. The top toolbar has a dropdown menu with 'Data' selected, which is circled in red. A yellow callout box points to this menu with the text 'Select the module Data'. The main 3D view displays a brain with colorful fiber bundles. The left sidebar contains the MRML Tree, which lists various nodes including 'Scene', 'View', 'Default Scene Camera', 'dwiDataset', 'Output DTI Volume', 'Output Baseline Volume', 'Otsu Threshold Mask', 'Output Scalar Volume', 'Output Scalar Volume-label', 'Labelmap Seeding Model', 'Seed', and 'FiberBundleNode'. The bottom of the interface shows three orthogonal slice views (Axial, Sagittal, Coronal) with a 'Seed.P' marker.



# Loading a DTI Scene

3D Slicer Version 3.6.1

File Edit View Window Help Feedback

Modules: Data

3DSlicer

Help & Acknowledgement

Display & Modify Scene

MRML Tree

- Scene
  - View
    - Default Scene Camera
    - dwiDataset
      - Output DTI Volume
      - Output Baseline Volume
      - Otsu Threshold Mask
      - Output Scalar Volume
      - Output Scalar Volume-label
      - Labelmap Seeding Model
      - Seed
      - FiberBundleNode

Display MRML ID's

MRML Node Inspector

Load & Add Scenes Or Individual Datasets

- Load new scene (close current)
- Add a scene (to current)
- Add data or a data directory

Manipulate Slice Views

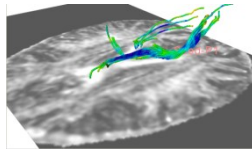
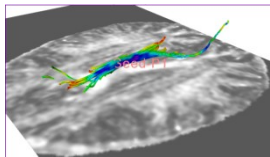
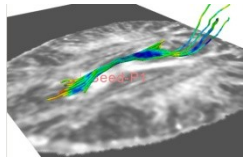
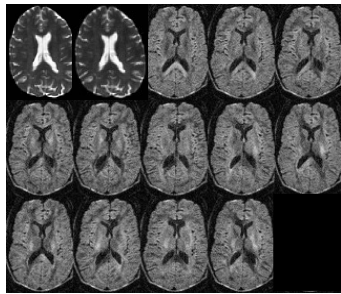
Manipulate 3D View

9 55.407 143 -8.2255 115 16.999

Slicer loads all the elements of the DTI Scene that were previously computed.



# Conclusion



This tutorial guided you through some of the **Diffusion MR** capabilities of the **Slicer3** software for studying the brain white matter pathways.

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# Acknowledgments

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