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# **Diffusion Tensor Imaging tutorial**



Sonia Pujol, PhD

Surgical Planning Laboratory  
Harvard University

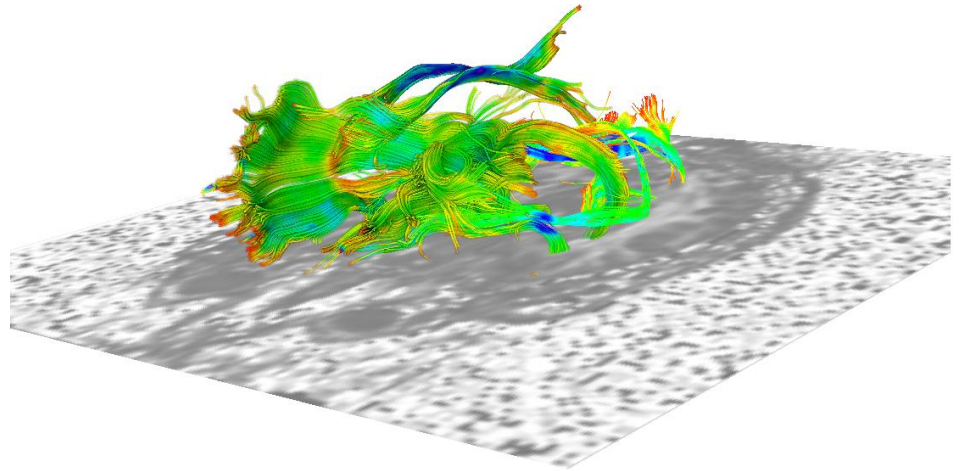
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# DTI tutorial

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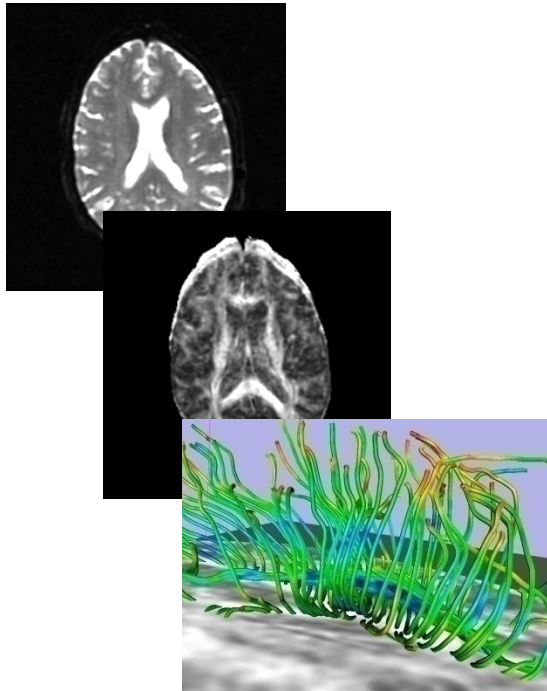
This tutorial is an introduction to the advanced **Diffusion MR** capabilities of the **Slicer3** software for medical image analysis.





# Outline

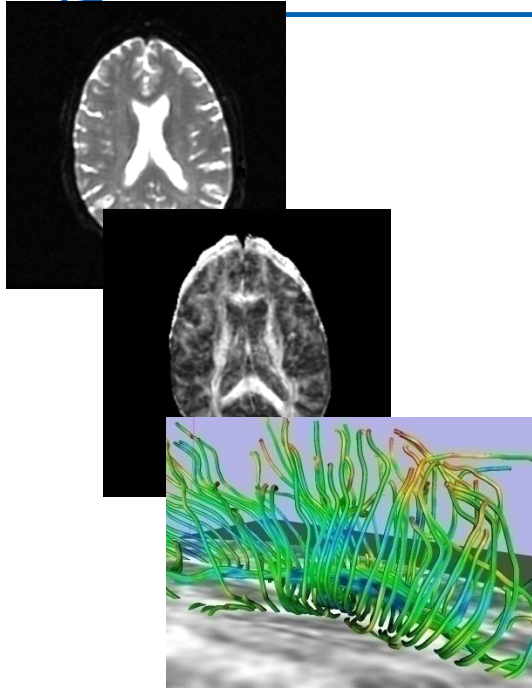
---



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



# Outline



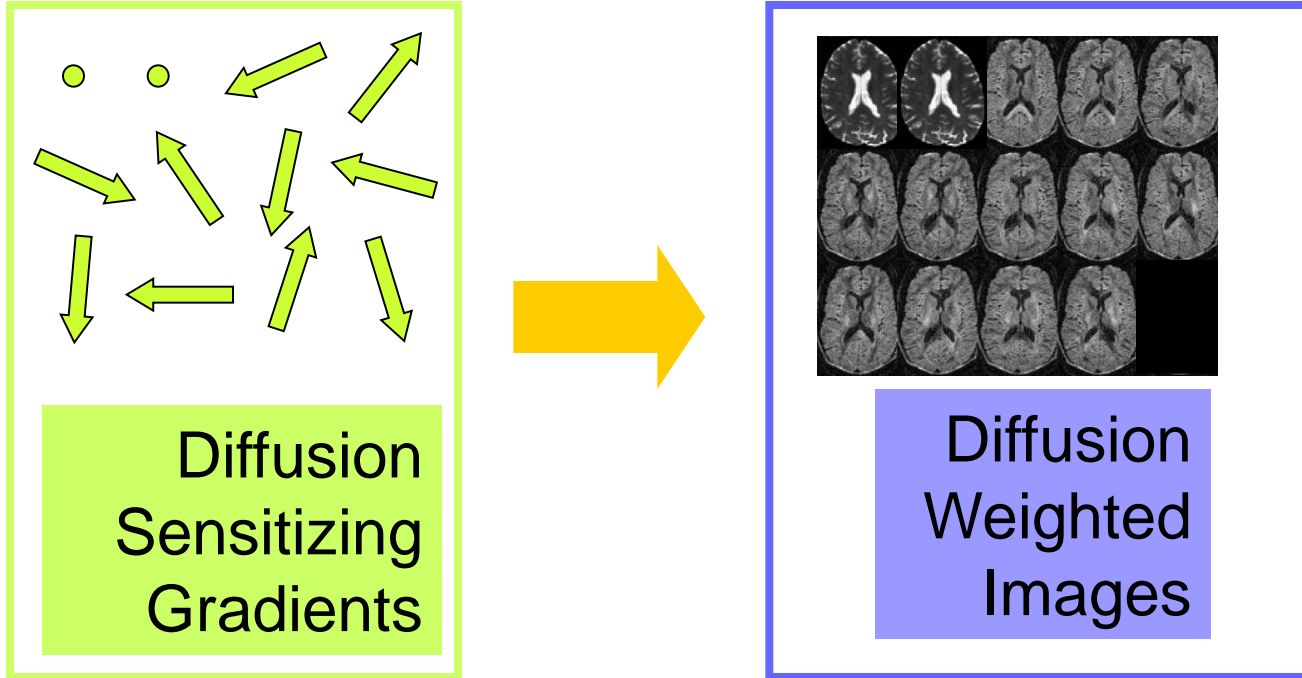
The processing pipeline uses **9 image analysis modules** of Slicer3.6

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



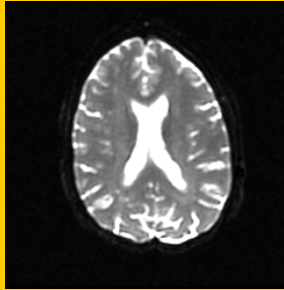
# Tutorial Dataset

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

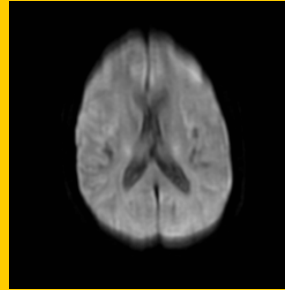




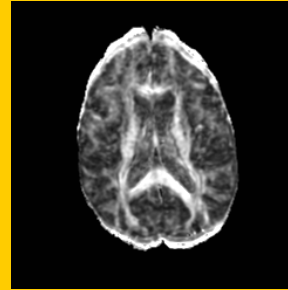
# DTI Processing Pipeline



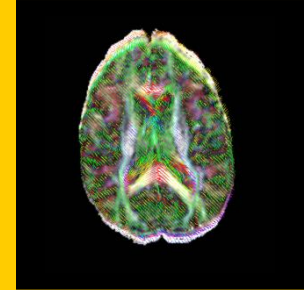
DWI  
Acquisition



Tensor  
Calculation



Scalar  
Maps



3D  
Visualization



# Start Slicer3

**Linux/Mac users**

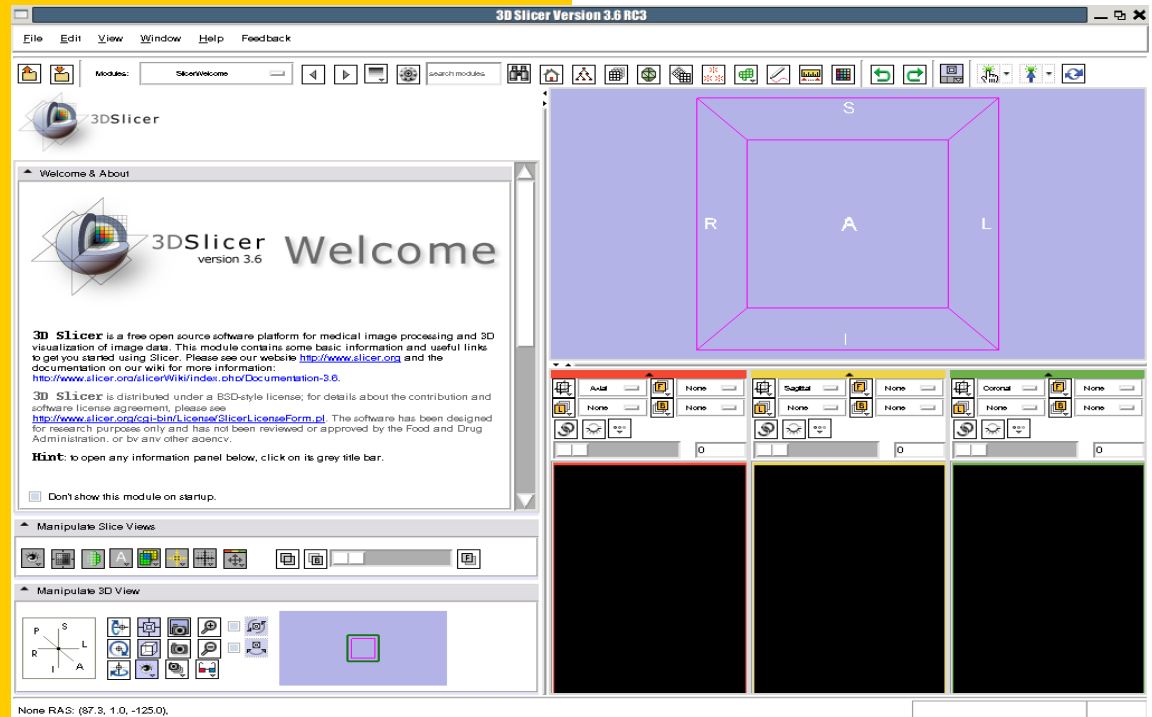
Launch the Slicer3 executable located in the Slicer3.6 directory

**Windows users**

Select

Start → All Programs

→ Slicer3-3.6-2011-03-04 → Slicer3





# Slicer Welcome

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

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

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.

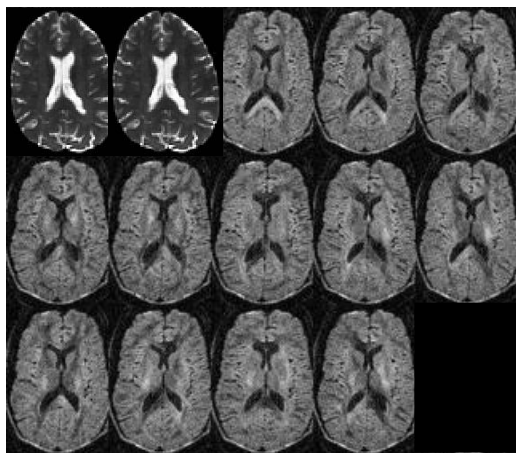
Don't show this module on startup.

Manipulate Slice Views

Manipulate 3D View

None RAS: (87.3, 1.0, -125.0)



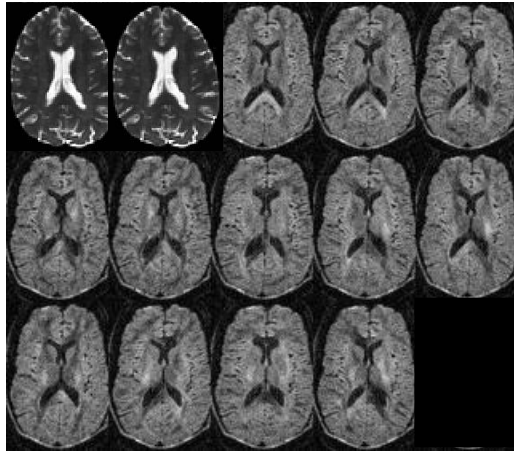


# Part 1:

# Diffusion data loading and tensor estimation

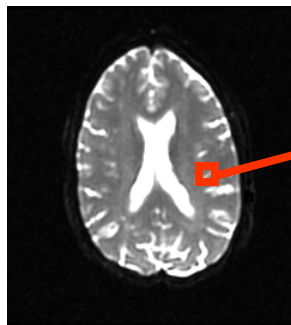


# Diffusion Tensor Imaging



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

(Stejskal and Tanner 1965, Basser 1994 )

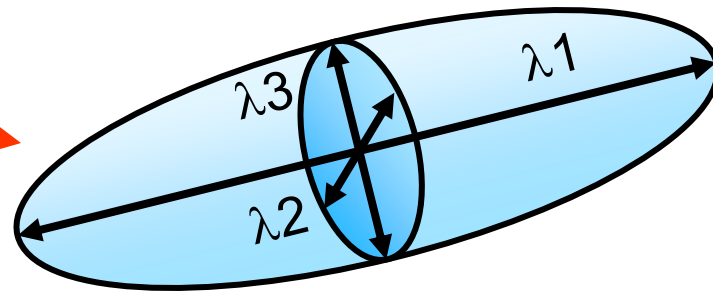
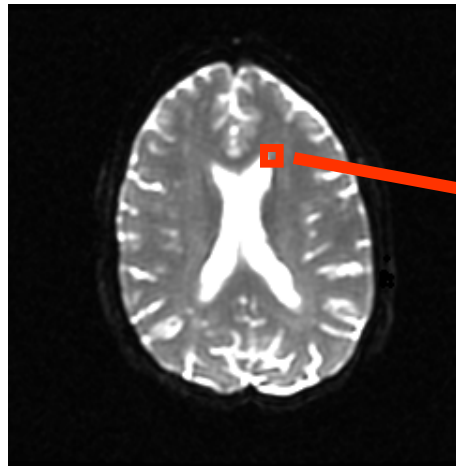


$$\underline{\mathbf{D}} = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{bmatrix}$$



# Physical Interpretation

The diffusion tensor  $\underline{D}$  in the voxel  $(I,J,K)$  can be visualized as an ellipsoidal isoprobability surface in which the principal axes correspond to the eigenvectors.





# Loading the DWI volume

**3D Slicer Version 3.6 RC3**

File Edit View Window Help Feedback

3DSlicer

Welcome & About

**3DSlicer**  
version 3.6

**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

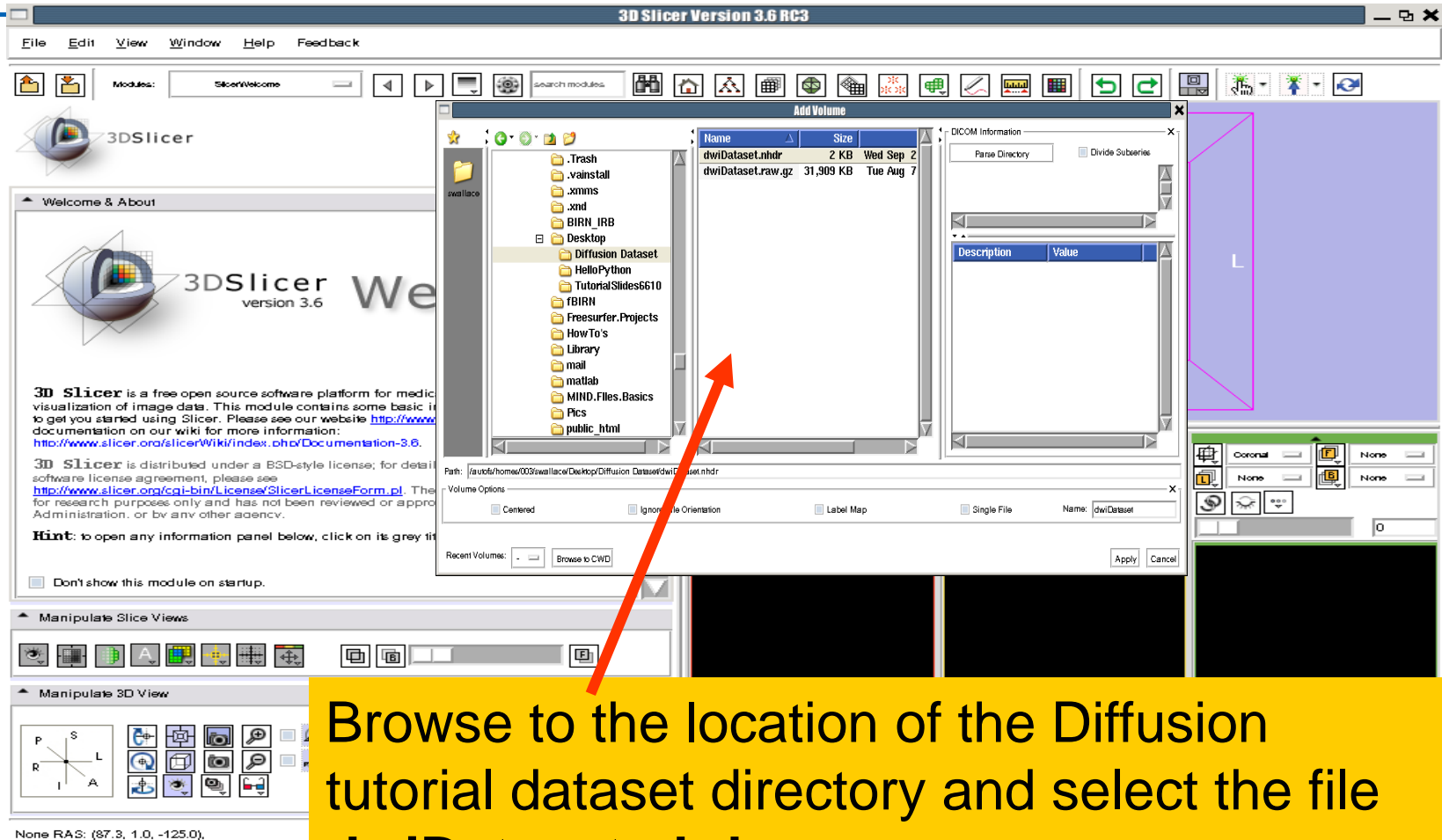
Manipulate 3D View

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

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



# Loading the DWI volume



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

Click on **Apply** to load the volume

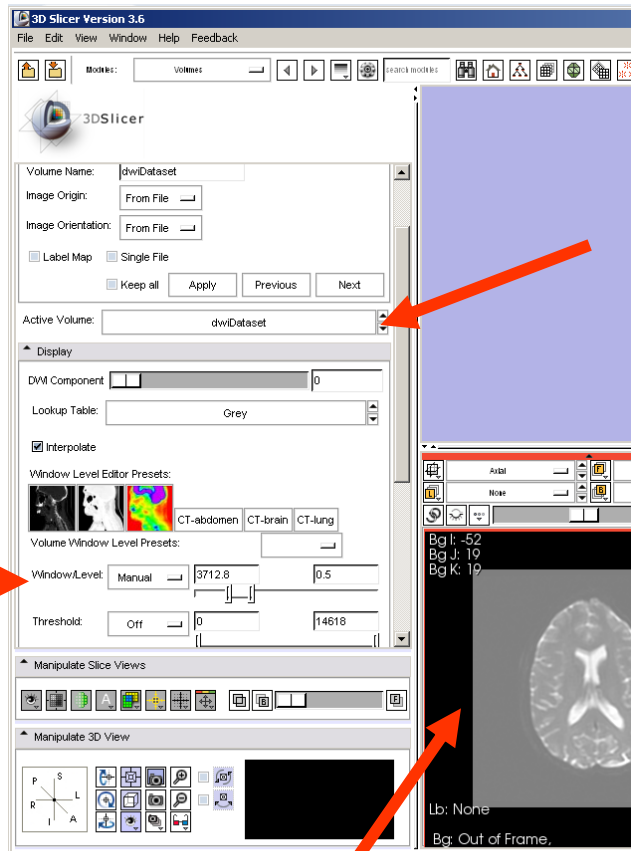


# Loading the DWI volume

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

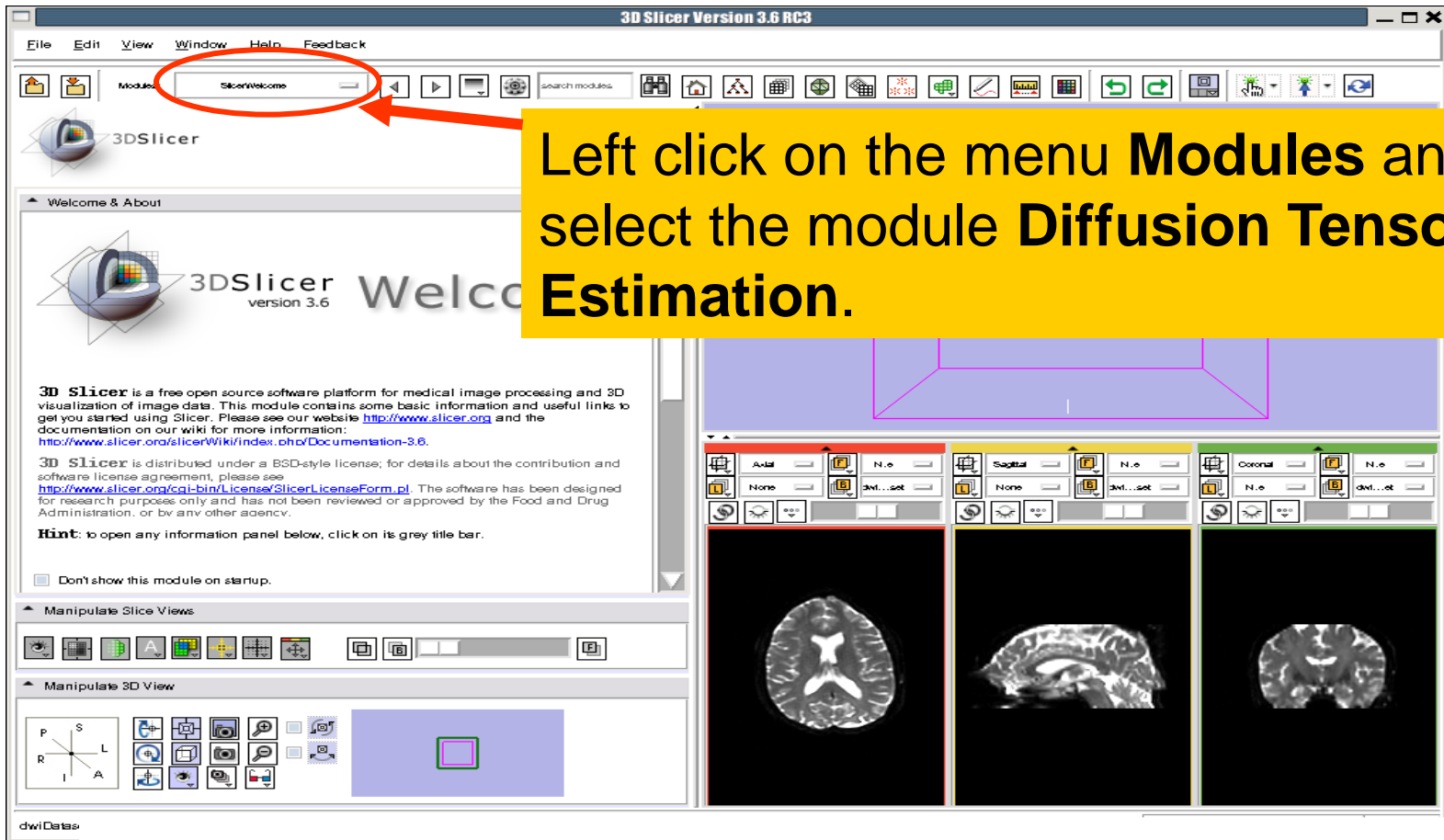


Select the Active Volume **dwiDataset** and adjust the Window/Level Parameters

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



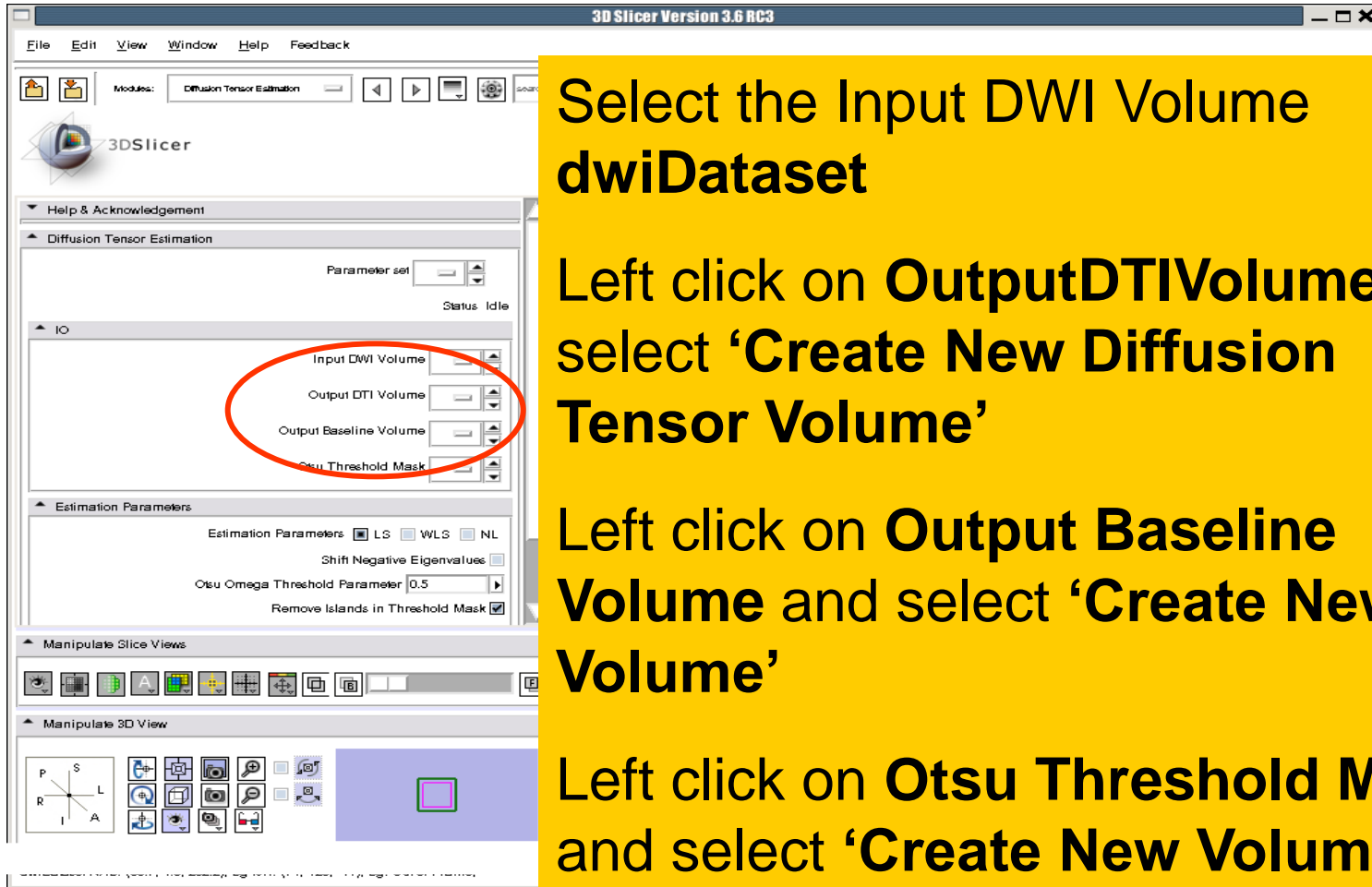
# Tensor Estimation







# 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

**Left click on Output Baseline Volume to display the list of volumes that have been computed by Slicer**

The screenshot shows the 3D Slicer interface with the Diffusion Tensor Estimation panel open. The panel includes sections for IO (Input DWM Volume, Output DTI Volume, Output Baseline Volume, Otsu Threshold Mask), Estimation Parameters (LS, WLS, NL, Otsu Omega Threshold Parameter, etc.), and Manipulate Slice Views. The main 3D view shows a brain slice with a purple bounding box. The bottom panel displays three slice views: Axial, Sagittal, and Coronal, each showing the Output Baseline Volume as a blue region.

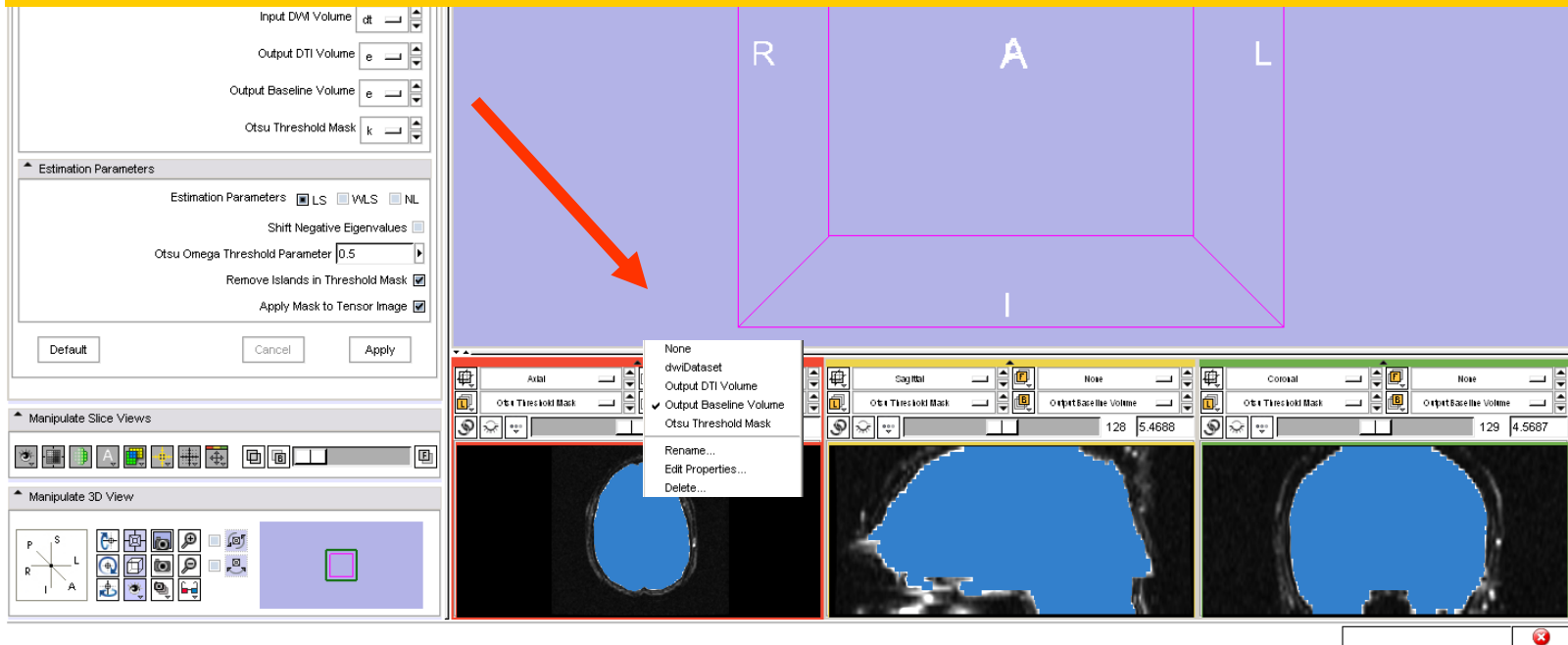


# Tensor Estimation

**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

Module: 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**

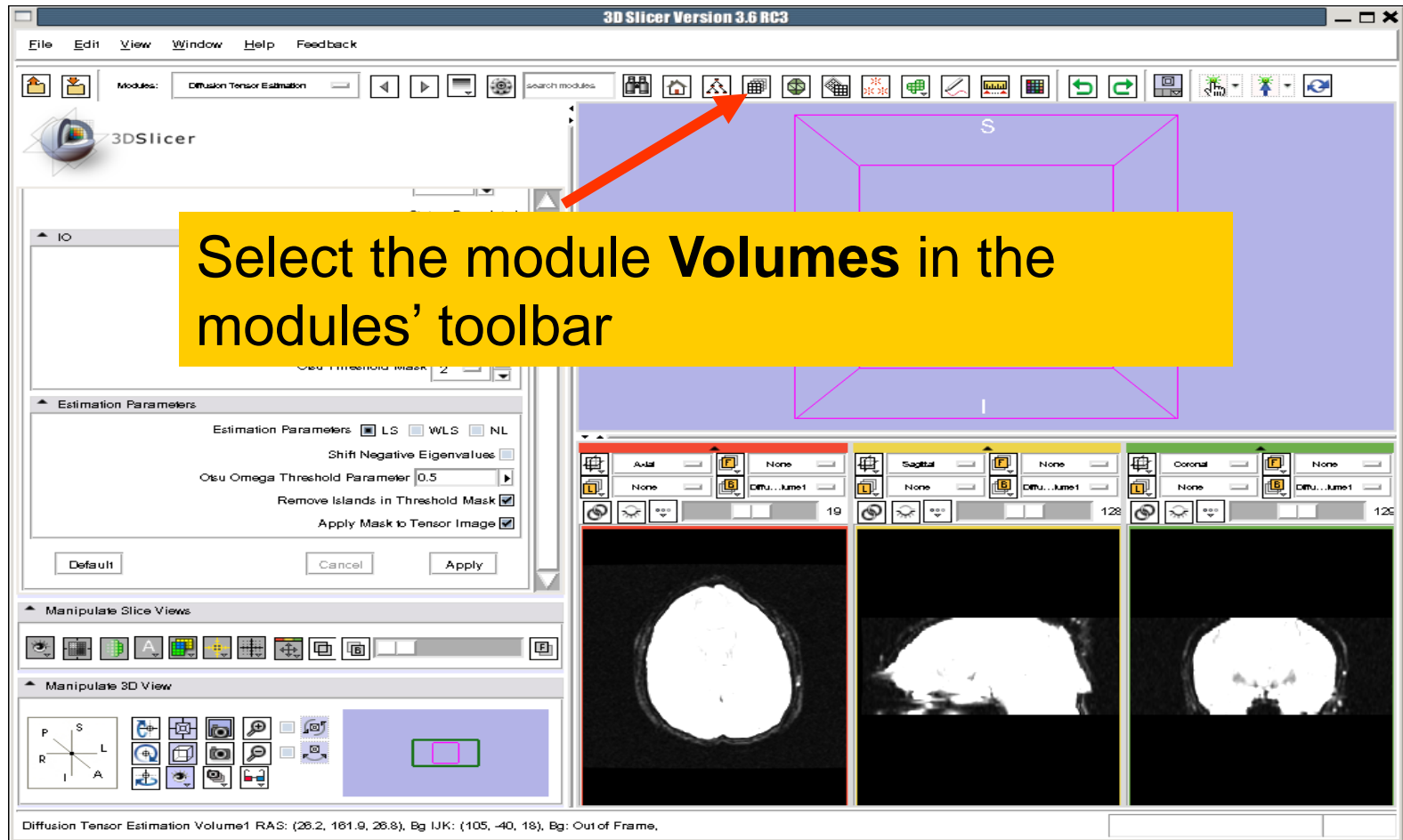
19 26.8

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

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

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-women 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

R A L

I

Axial None Output Baseline Volume 19 26.8

Sagittal None Output Baseline Volume 128 5.4688

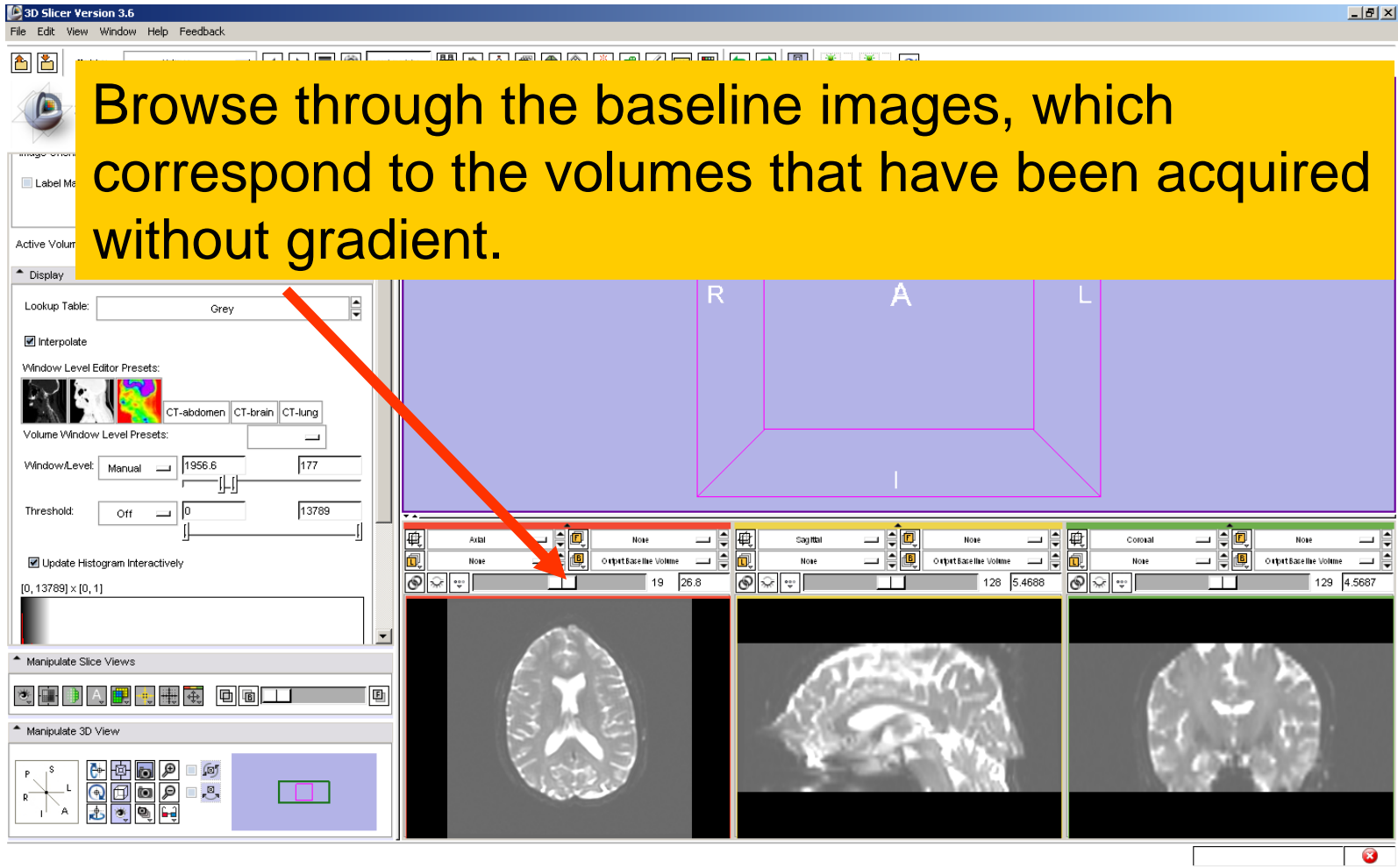
Coronal None Output Baseline Volume 129 4.5687

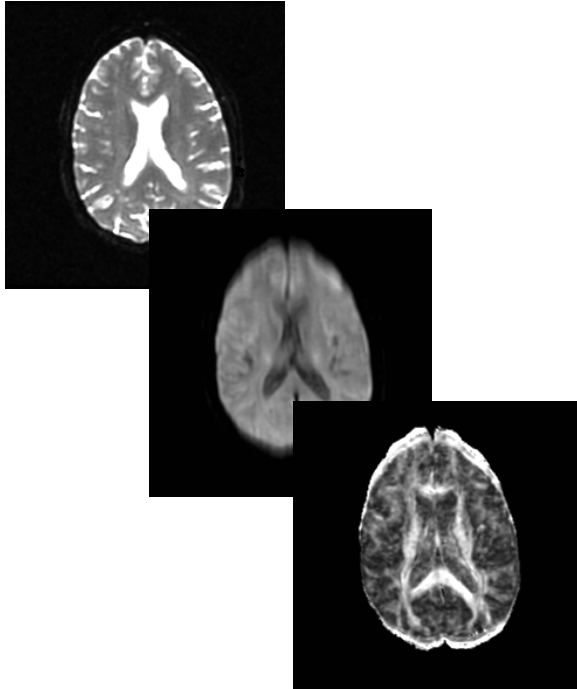




# Tensor Estimation

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





# Part2:

# Scalar Measurements



# Scalar Measurements

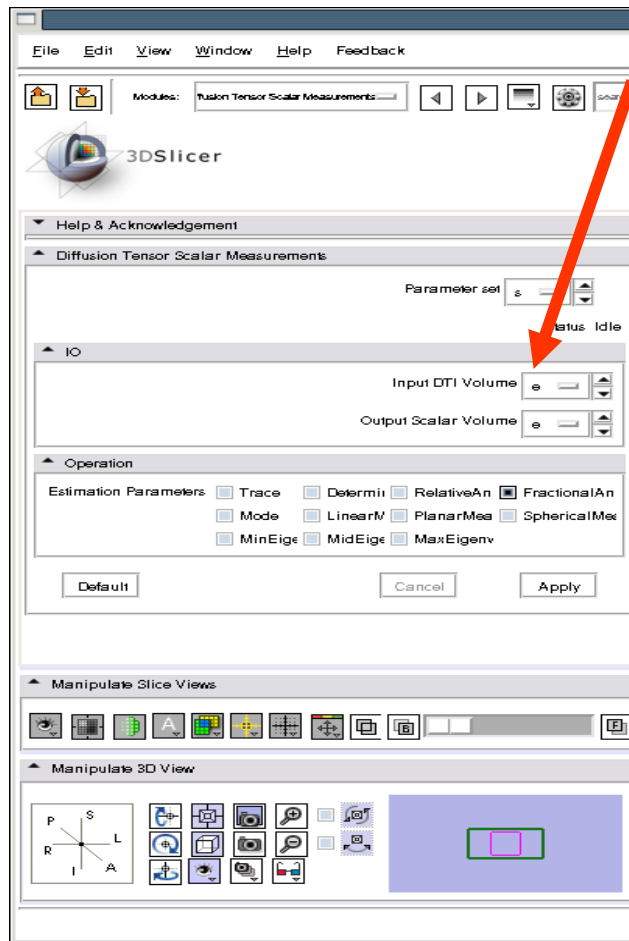
Select the category **Diffusion--> Utilities** from the list of modules, and left click on the **Diffusion Tensor Scalar Measurements** module.

The screenshot shows the 3D Slicer software interface. The 'Utilities' menu is circled in red. The main window displays a 3D view of a brain slice with a purple bounding box. Below the 3D view are three 2D views: Axial, Sagittal, and Coronal. The bottom of the interface shows a table of scalar measurements for each view.

View	Measurement 1	Measurement 2	Measurement 3
Axial	19	26.8	
Sagittal	128	5.4688	
Coronal	129	4.5687	



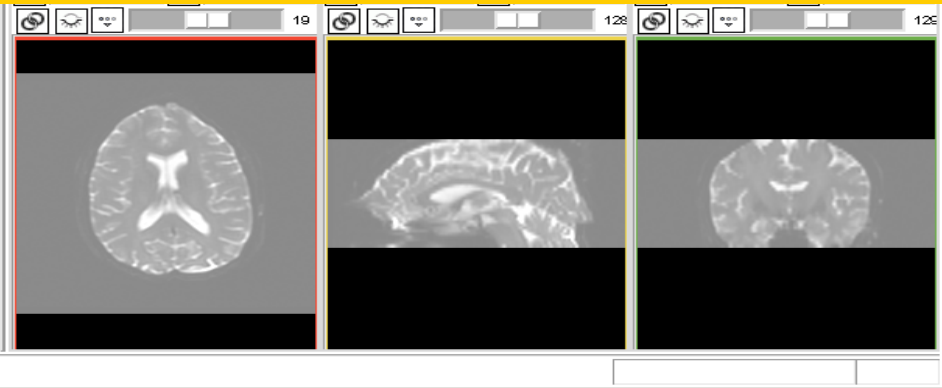
# Scalar Measurements



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

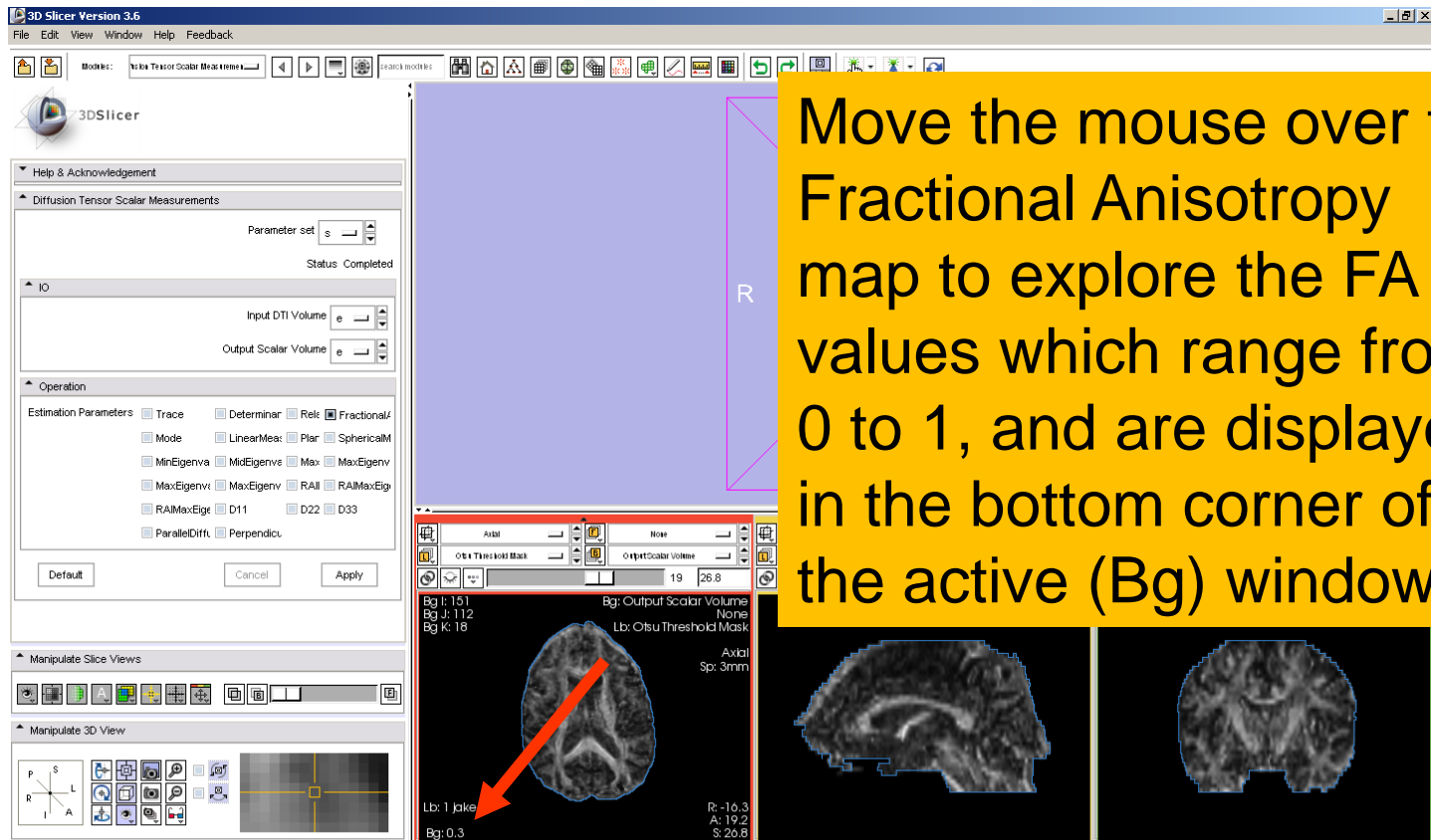
Select the Output Scalar Volume **'Create New Volume'**

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





# Fractional Anisotropy Volume



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

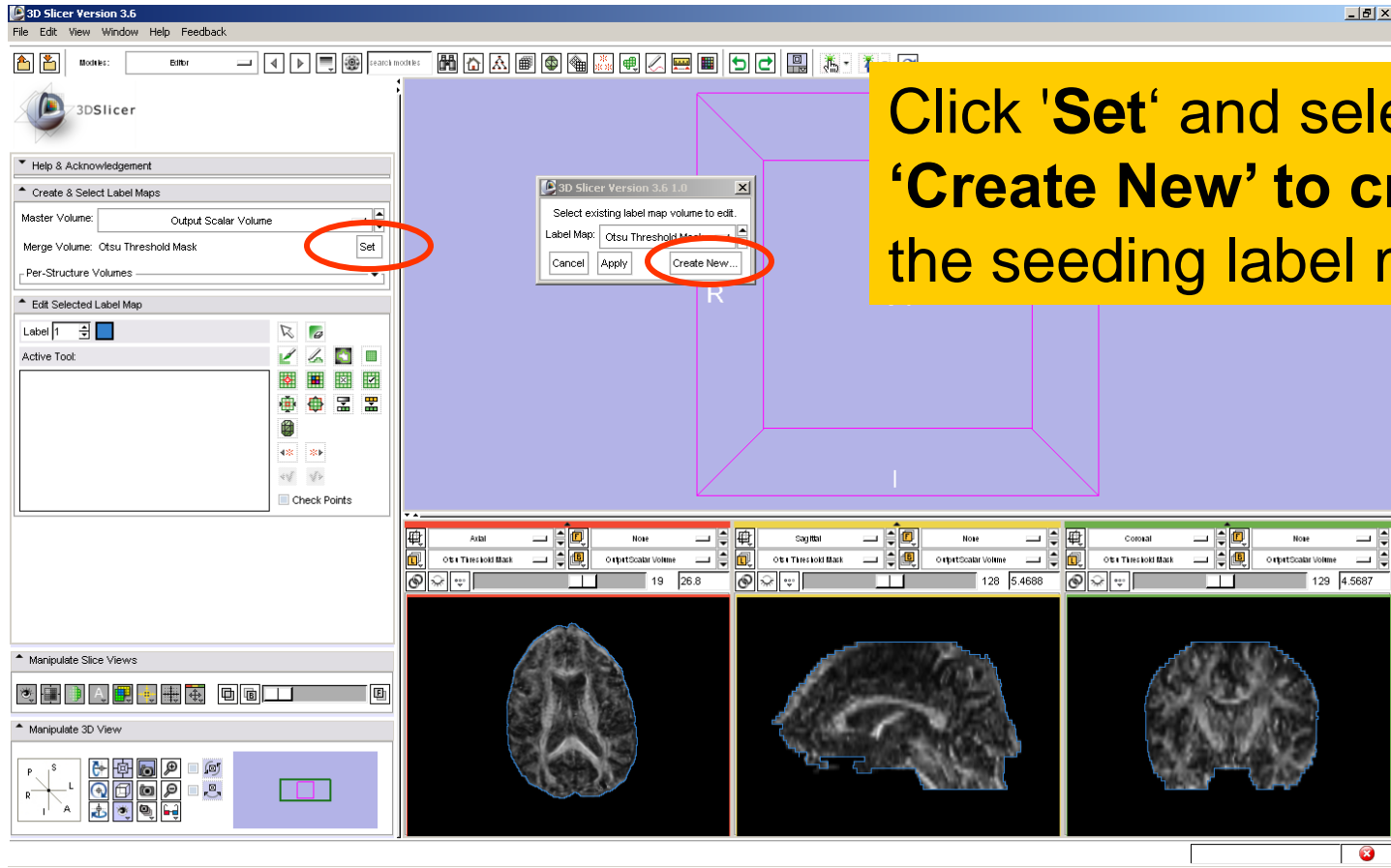
Select the module **Editor** in the modules menu.

Select the Master Volume as '**Output Scalar Volume**'

Output Scalar Volume RAS: (89.6, 148.7, 23.8), Bg LK: (38, -26, 19), Lb: Out of Frame, Bg: Out of Frame,



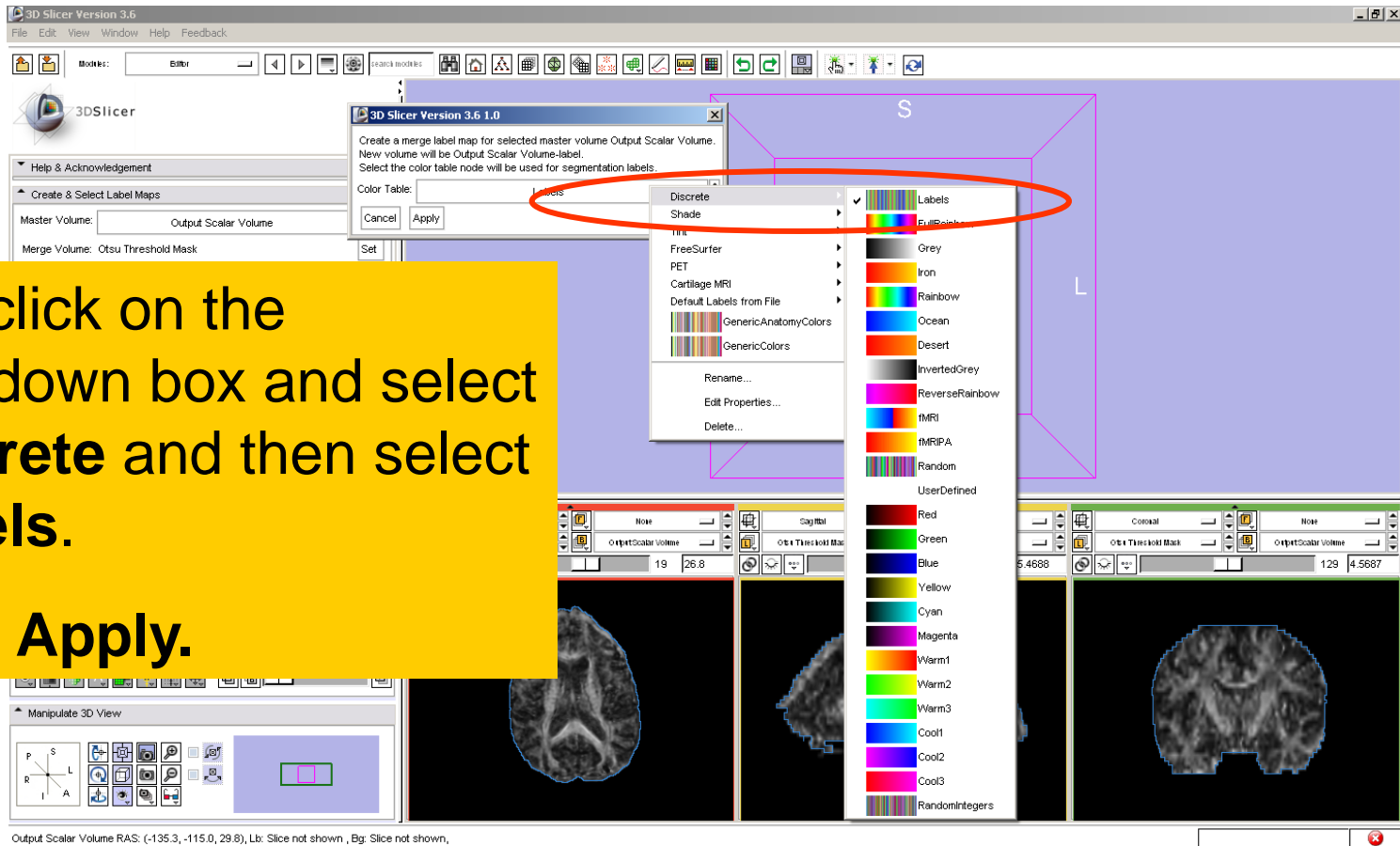
# Label Map Generation







# 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**

3D Slicer Version 3.6  
File Edit View Window Help Feedback

Help & About

Create & Select Label maps

Master Volume: Output Scalar Volume  
Merge Volume: Output Scalar Volume-label  
Per-Structure Volumes

Edit Selected Label Map

Label 2  
Active Tool: Paint  
Paint Over:   
Threshold Painting:   
Threshold: 0 1  
Radius: 23  
Smudge:   
Check Points

Manipulate Slice Views

Manipulate 3D View

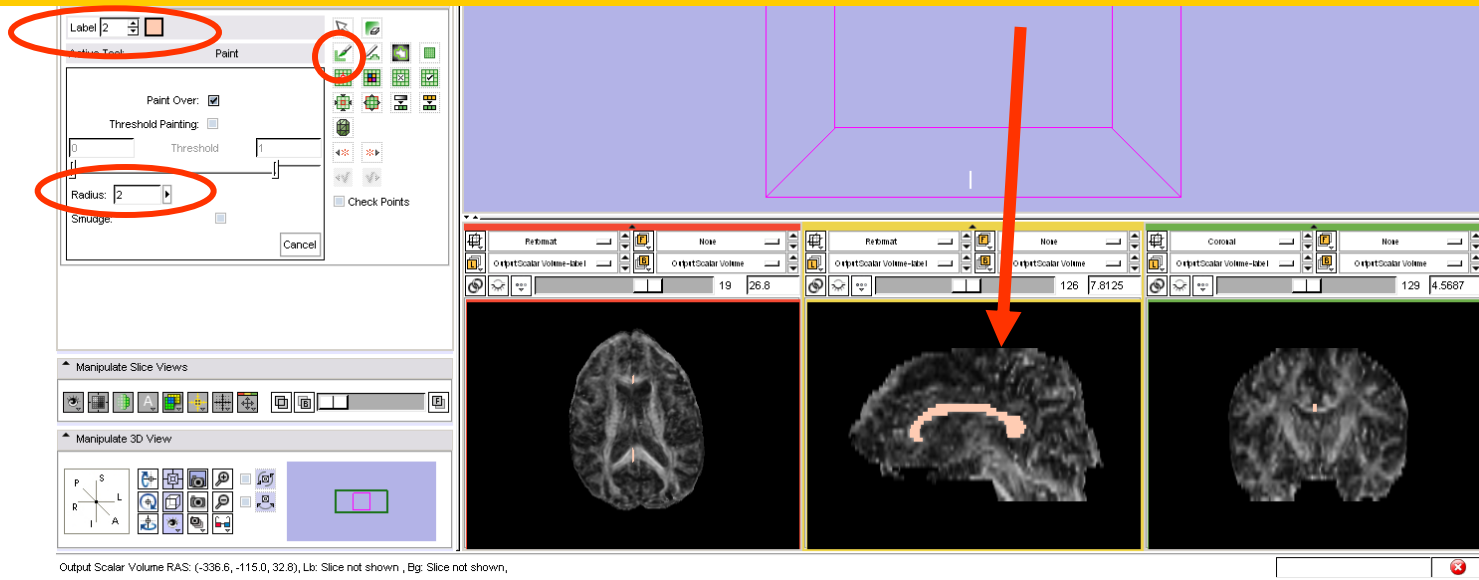
Don't show label volume outlines

Fit to window  
Rotate to Volume Plane  
Adjust label map opacity  
Don't show label volume outlines  
Show reformat widget  
Compositing  
Slice spacing mode  
Lightbox view  
Adjust display  
tear off control panel  
close



# 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

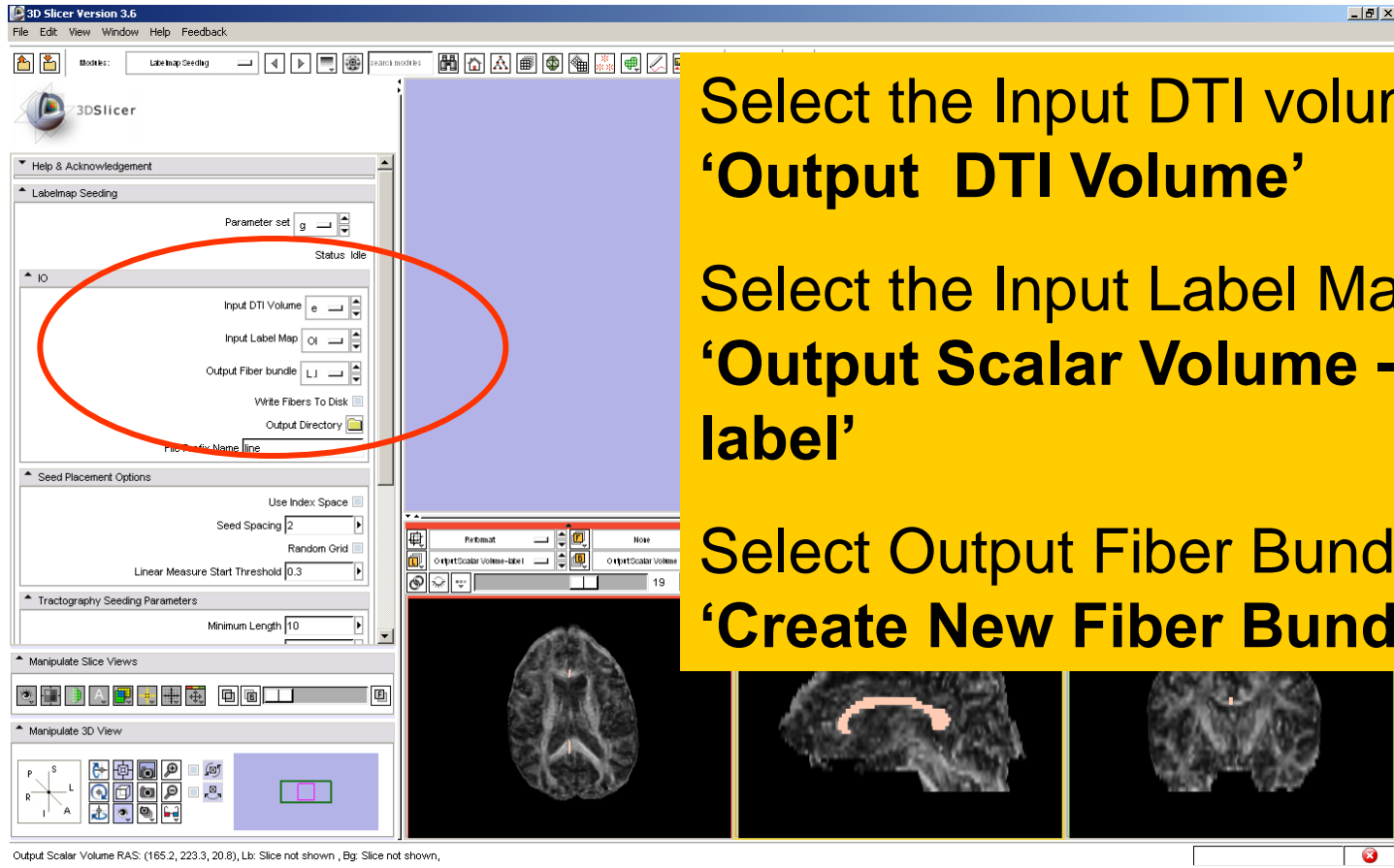
Manipulate 3D View

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

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



# LabelMap Seeding



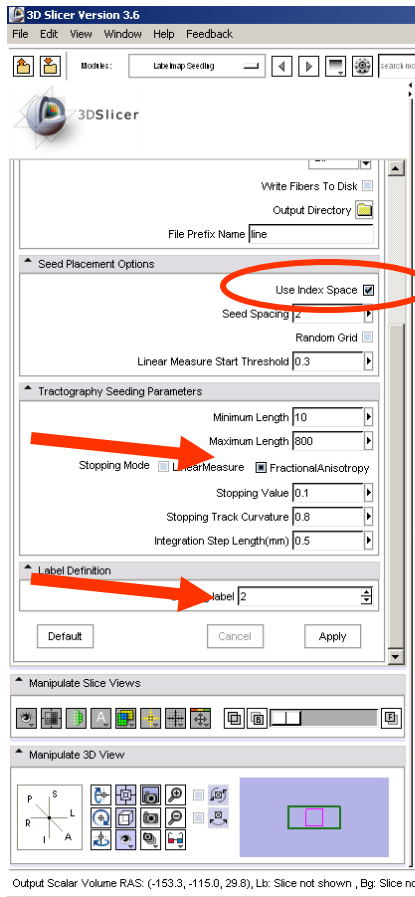
Select the Input DTI volume  
**'Output DTI Volume'**

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

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



# 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.

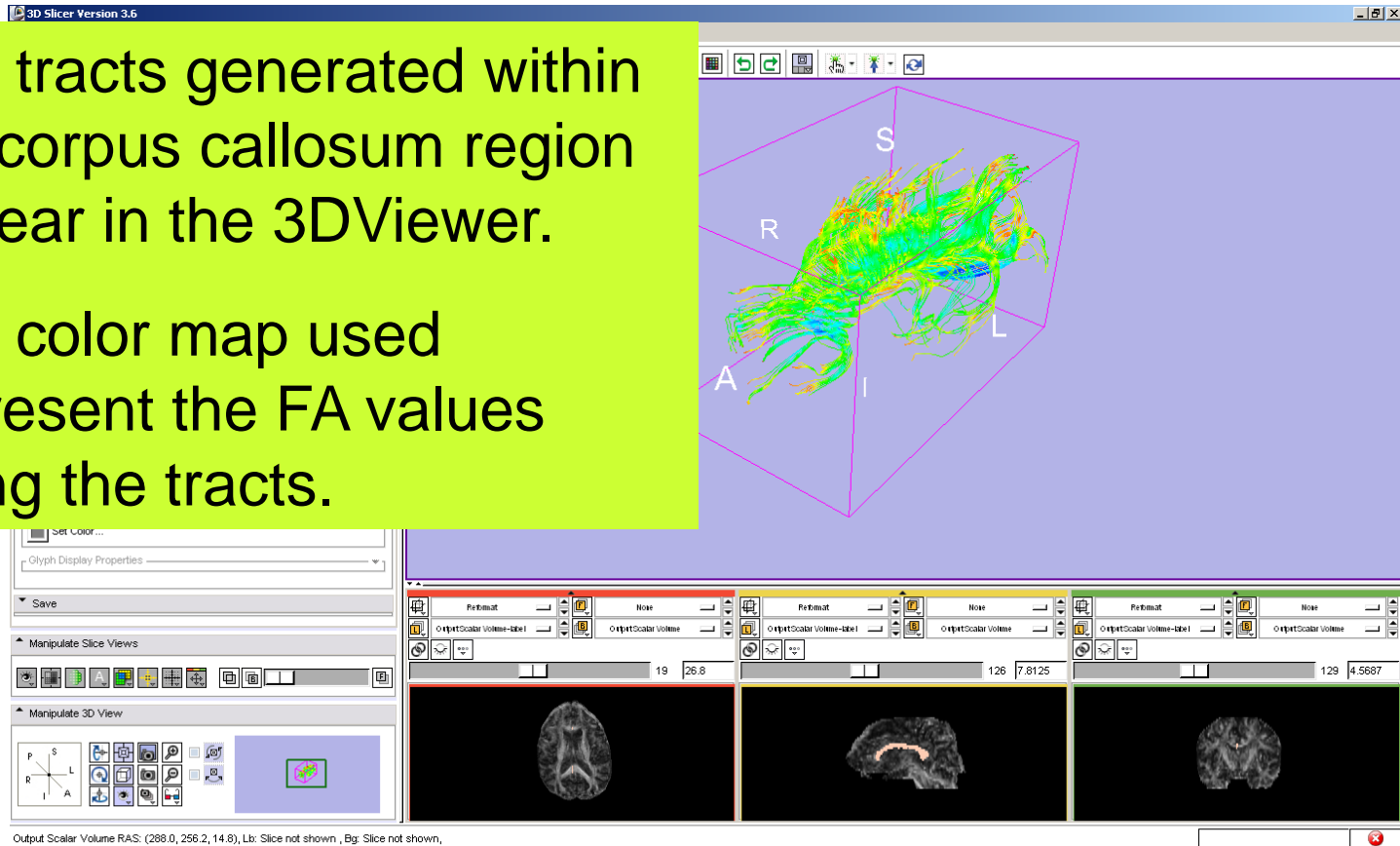
In the Label Definition tab, set 'Seeding label' to label 2, and click on **Apply**



# 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.

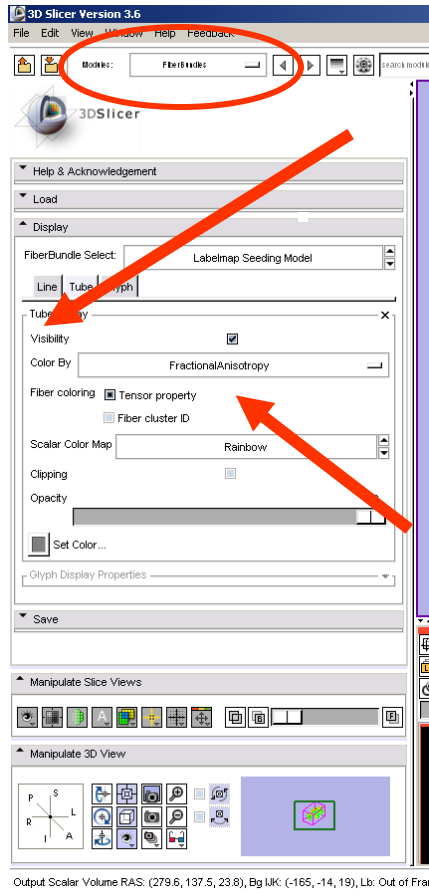




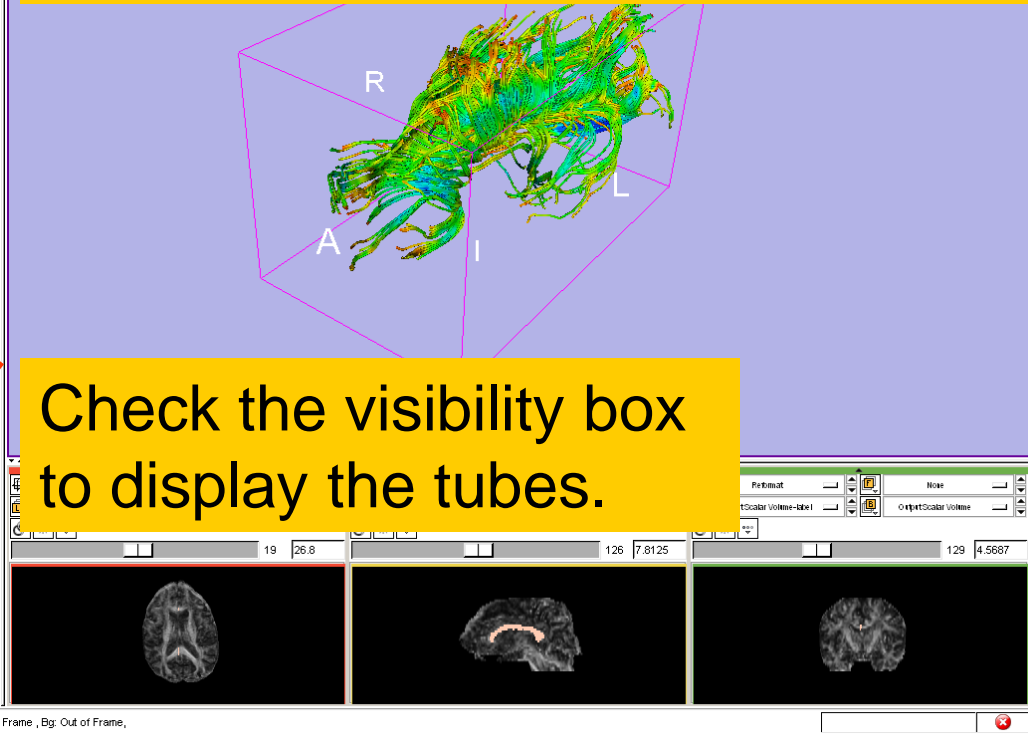


# LabelMap Seeding

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



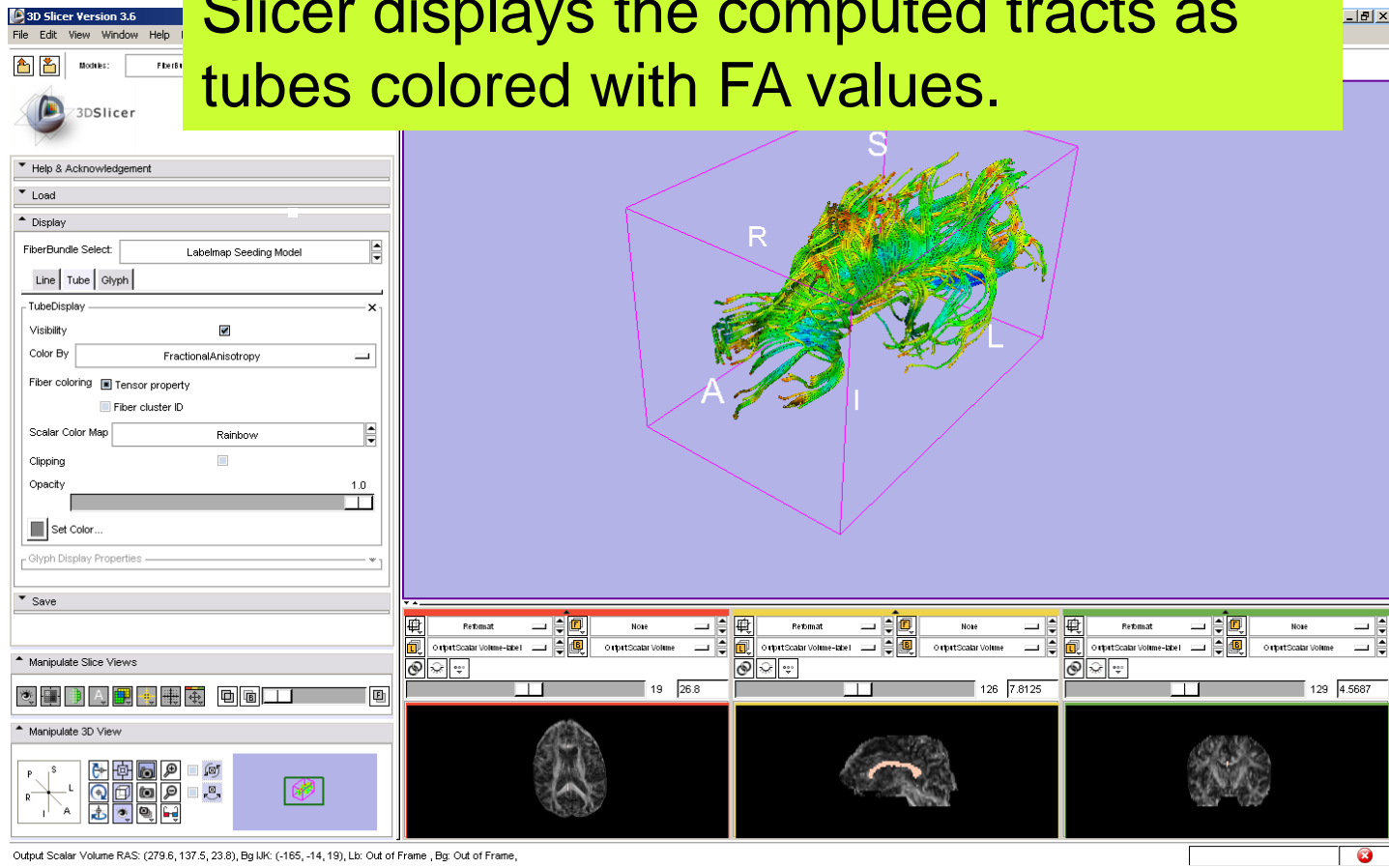
Check the visibility box to display the tubes.

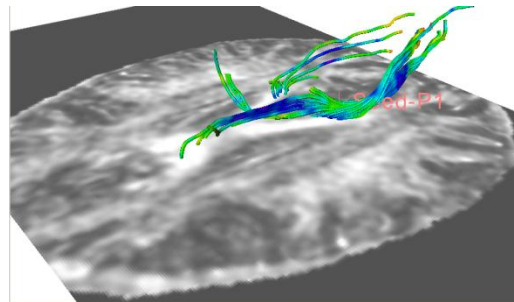
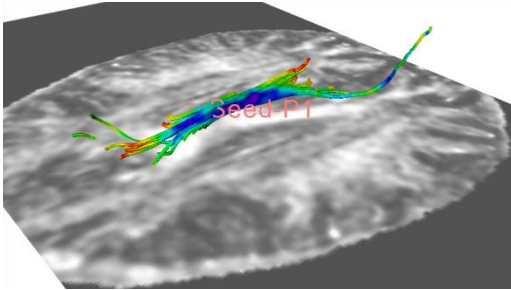
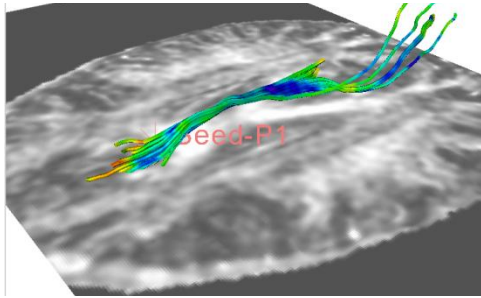




# LabelMap Seeding

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





## Part 4:

# Tractography on-the-fly



# Fiducial Seeding

3D Slicer Version 3.6

Select the module **Fiducials**

Help & Acknowledgement

Modify All Fiducial Lists & Their Fiducial Points

Modify A Selected Fiducial List & Its Fiducials

Fiducial List: FiducialList

Modify List: [Add] [Remove] [Refresh]

Other List Display Properties

Add & Modify Individual Fiducials

Name	X	Y	Z
------	---	---	---

Distance: List Distance:

Renumber Fiducials: Rename Fiducials

Numbering Scheme: UseID

Manipulate Slice Views

Manipulate 3D View

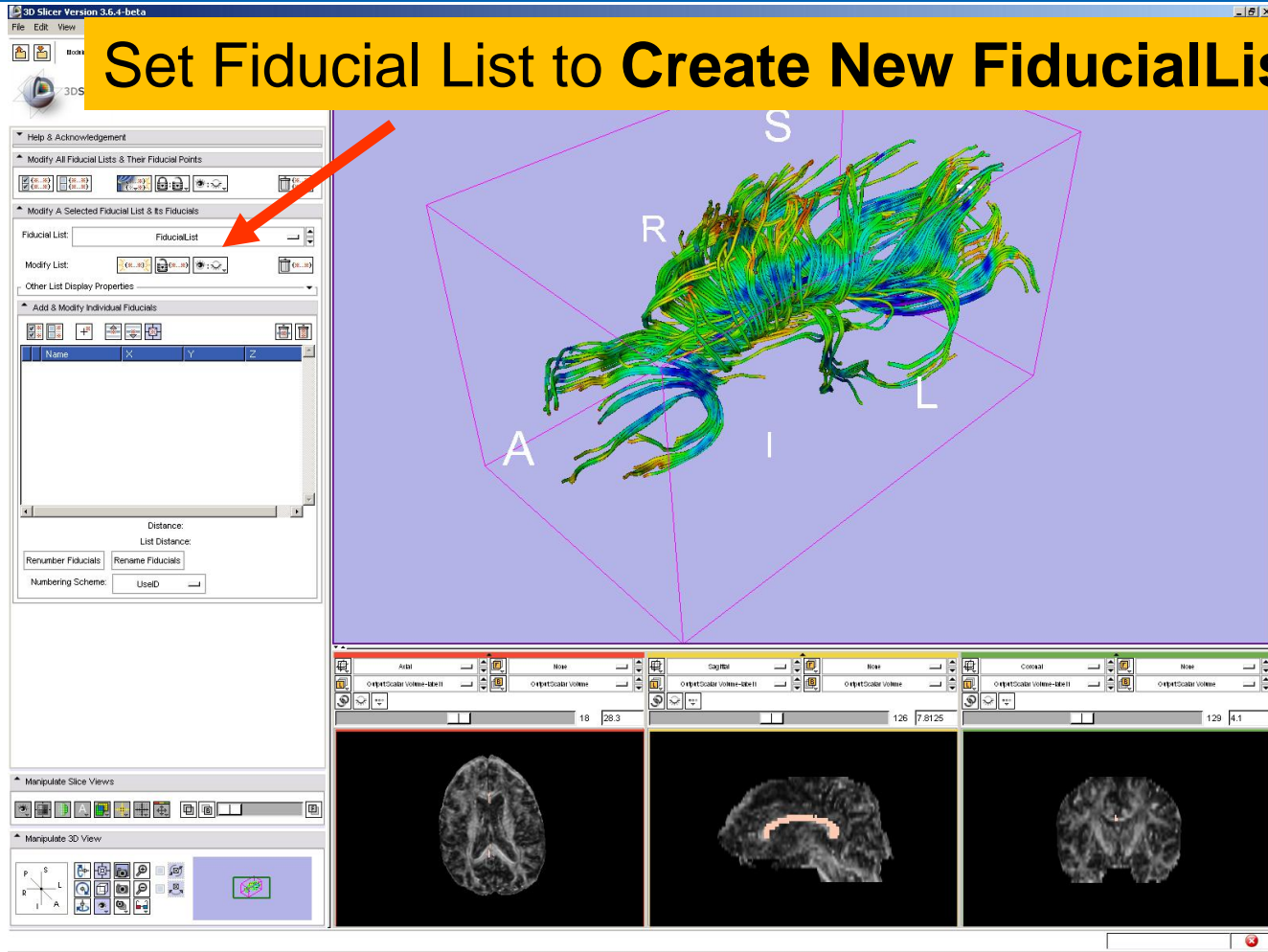
Axial: None | Sagittal: None | Coronal: None

18 28.3 | 126 7.8125 | 129 4.1



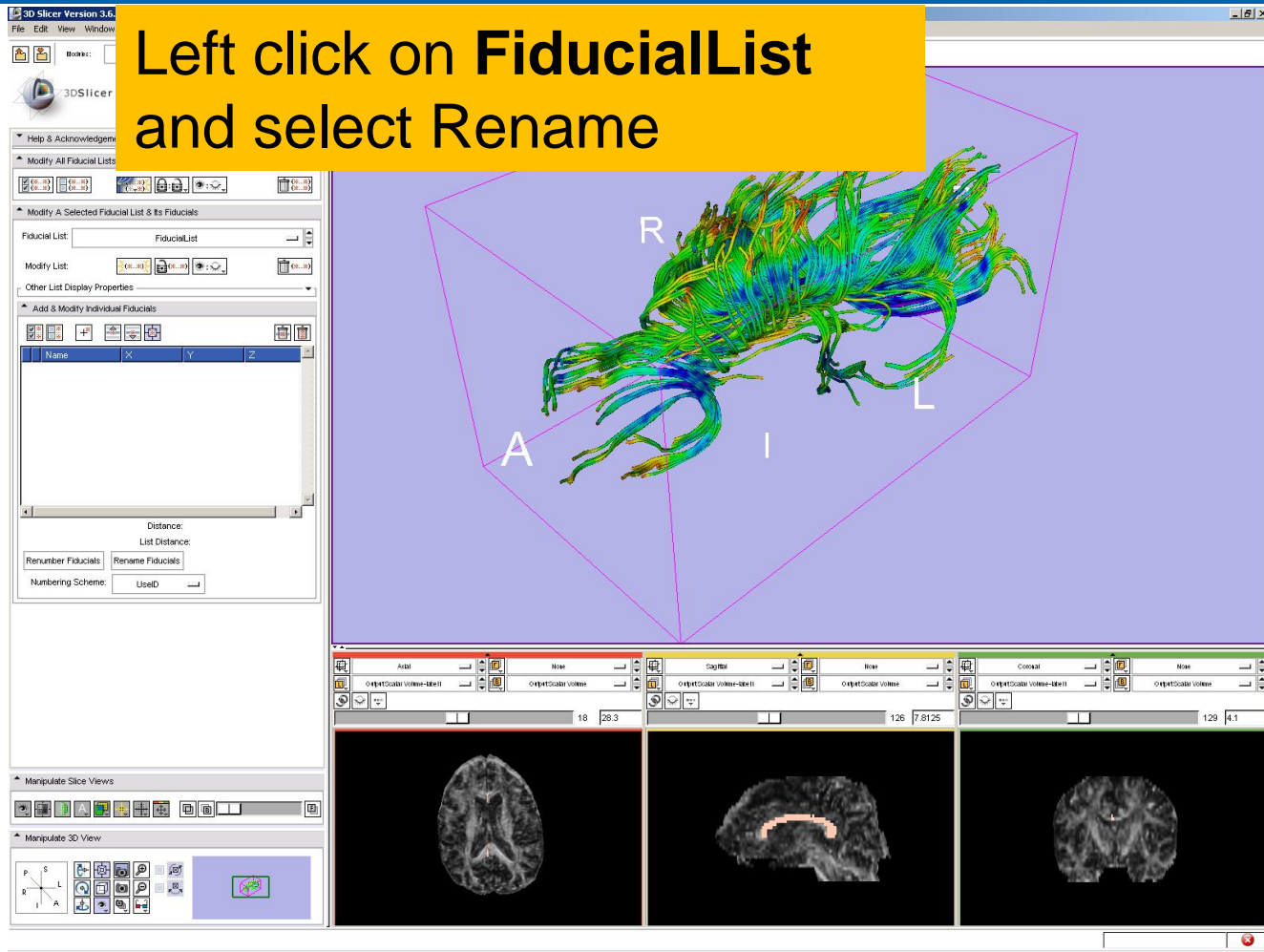
# Fiducial Seeding

Set Fiducial List to **Create New FiducialList**





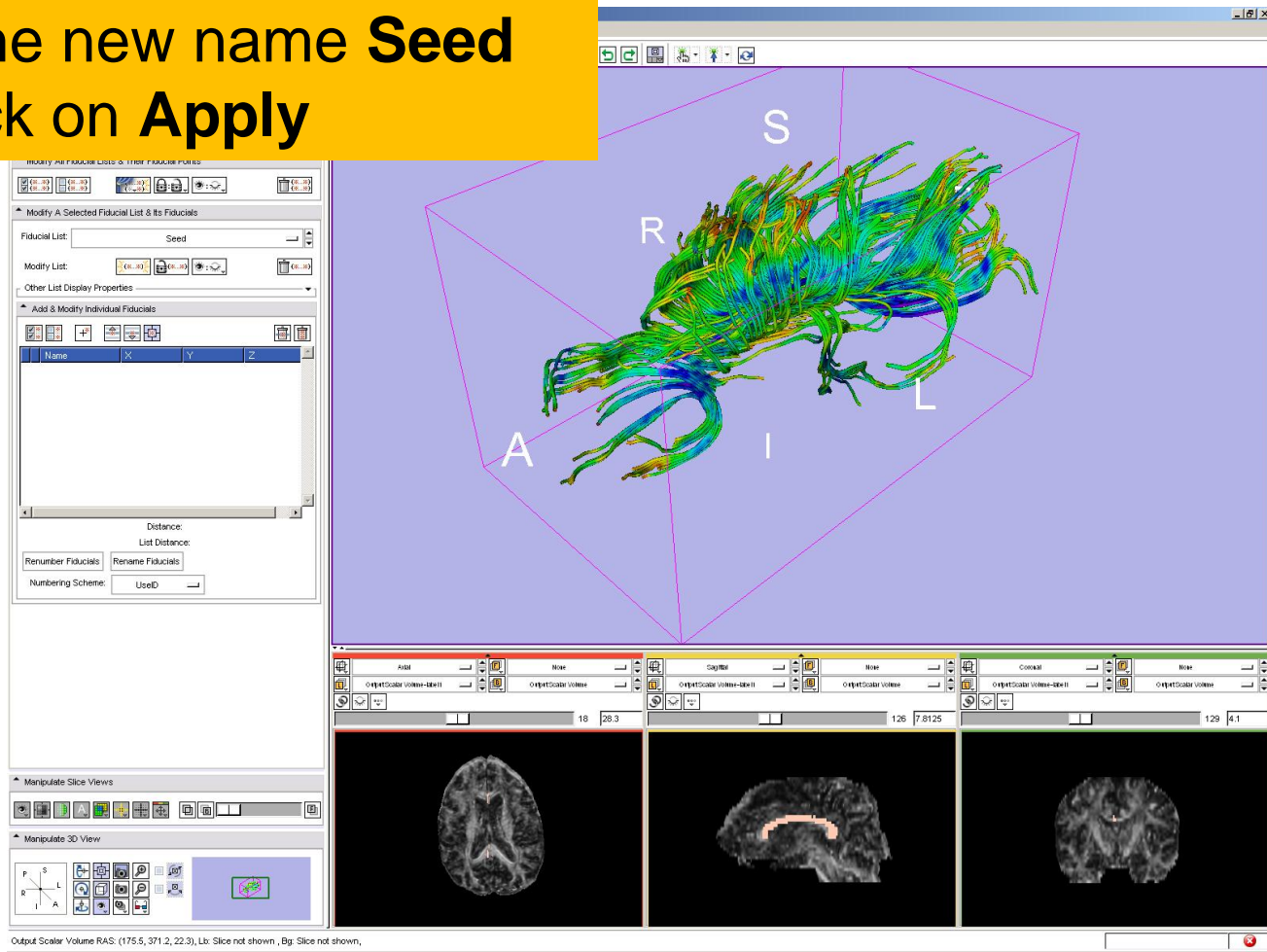
# Fiducial Seeding






# Fiducial Seeding

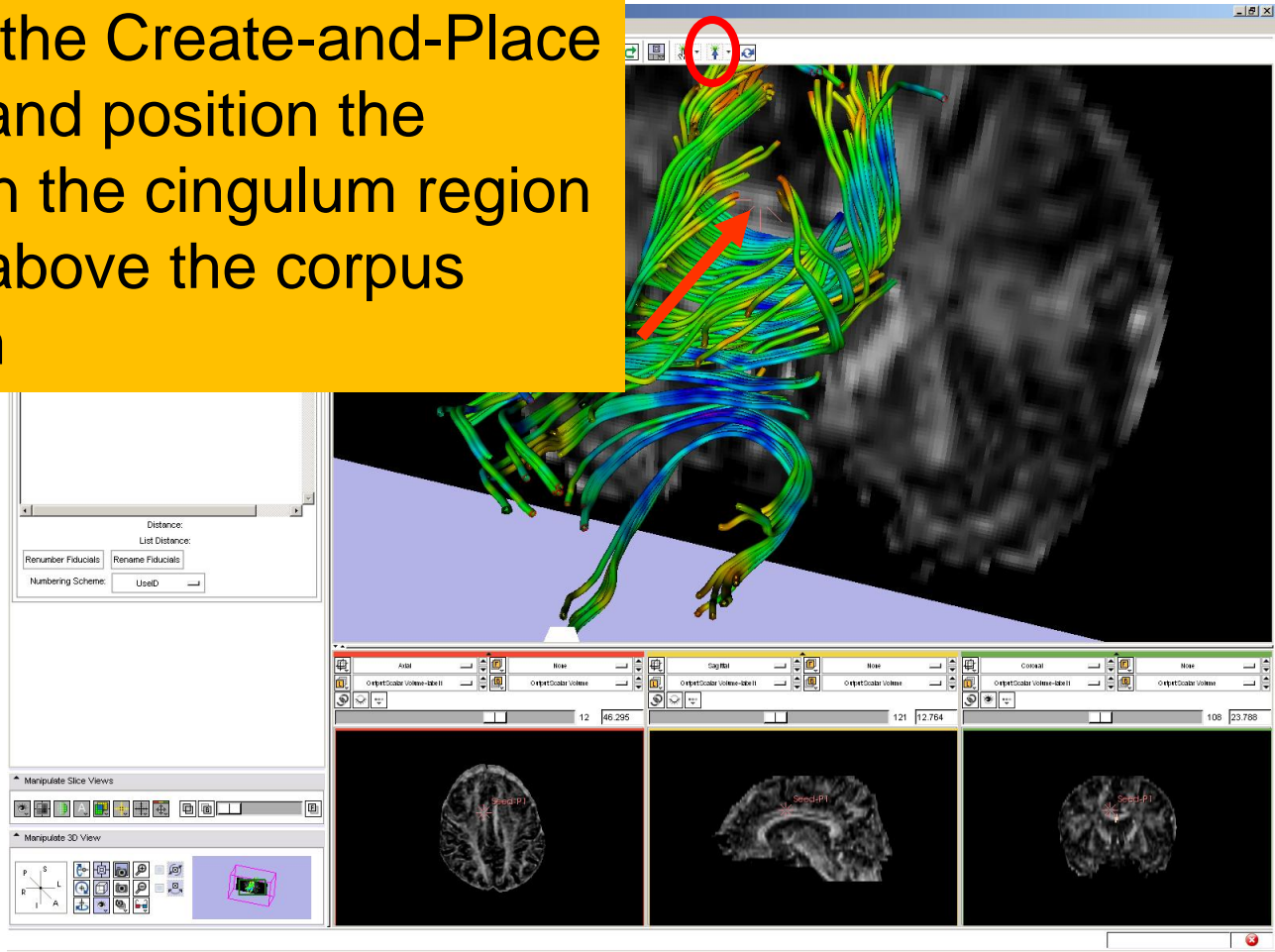
Enter the new name **Seed**  
and click on **Apply**





# Fiducial Seeding

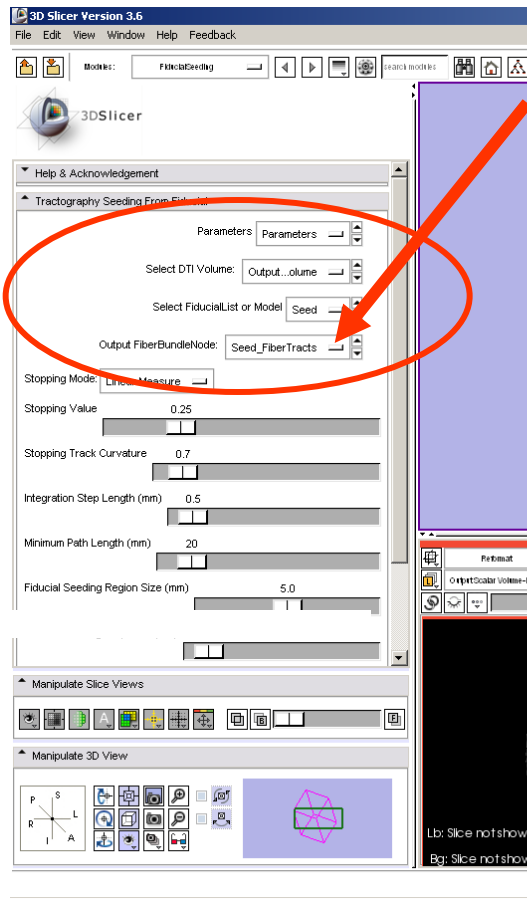
Click on the Create-and-Place icon  and position the fiducial in the cingulum region located above the corpus callosum







# Fiducial Seeding



Select the module **Fiducial Seeding**

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

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



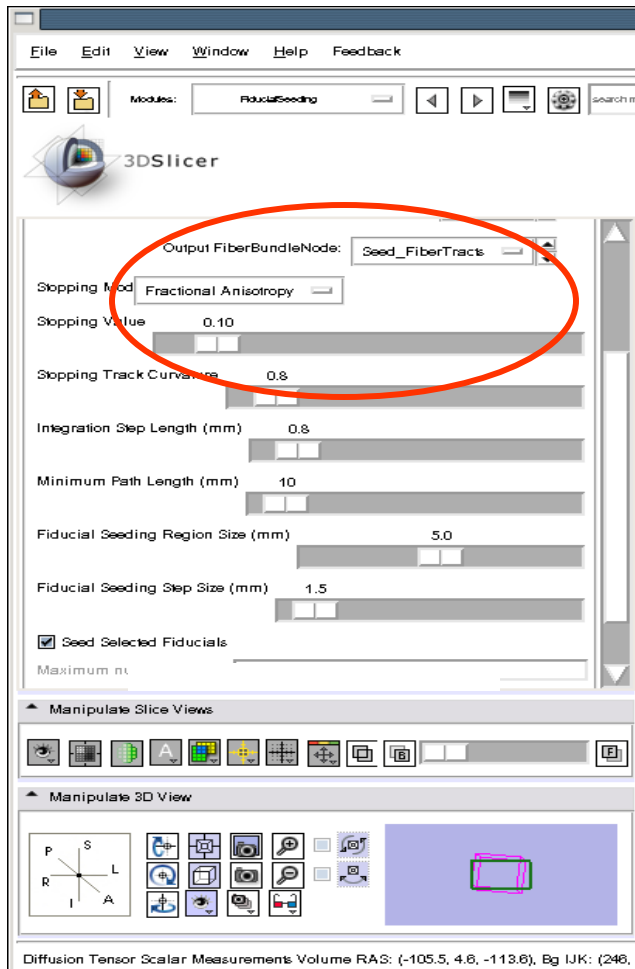
# Fiducial Seeding

**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**

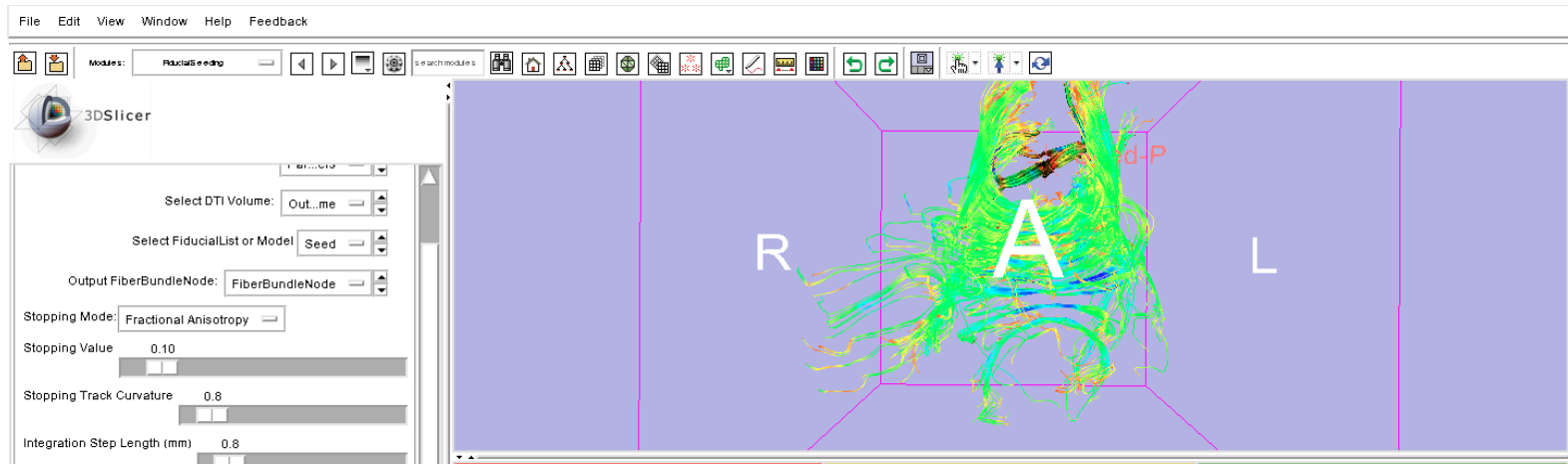
**Step Length: 0.8 mm**

**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

3D Slicer Version 3.6  
File Edit View Window Help Feedback

Books: FiducialSeeding

3DSlicer

Help & Acknowledgement

Tractography Seeding From Fiducial

Select DTI Volume

Select Fiducial

Output FiberBundleNodes

Stopping Mode: Fractional Anisotropy

Stopping Value: 0.10

Stopping Track Curvature: 0.8

Integration Step Length (mm): 0.8

Minimum Path Length (mm): 10

Fiducial Seeding Region Size (mm): 5.0

Fiducial Seeding Step Size (mm): 1.5

Manipulate Slice Views

Manipulate 3D View

FiducialSeeding

Move the fiducial **Seed-P** from the left cingulum to the corresponding region in the right cingulum in the coronal slice.

Output Scalar Volume-label: None  
Output Scalar Volume: 13 43.628

Output Scalar Volume-label: None  
Output Scalar Volume: 124 9.846

Output Scalar Volume-label: None  
Output Scalar Volume: 142 -8.0875

Bg I: 400  
Bg J: -421  
Bg K: 13

Bg: Output Scalar Volume  
None  
Lb: Output Scalar Volume-label

Reformat  
Sp: 3mm

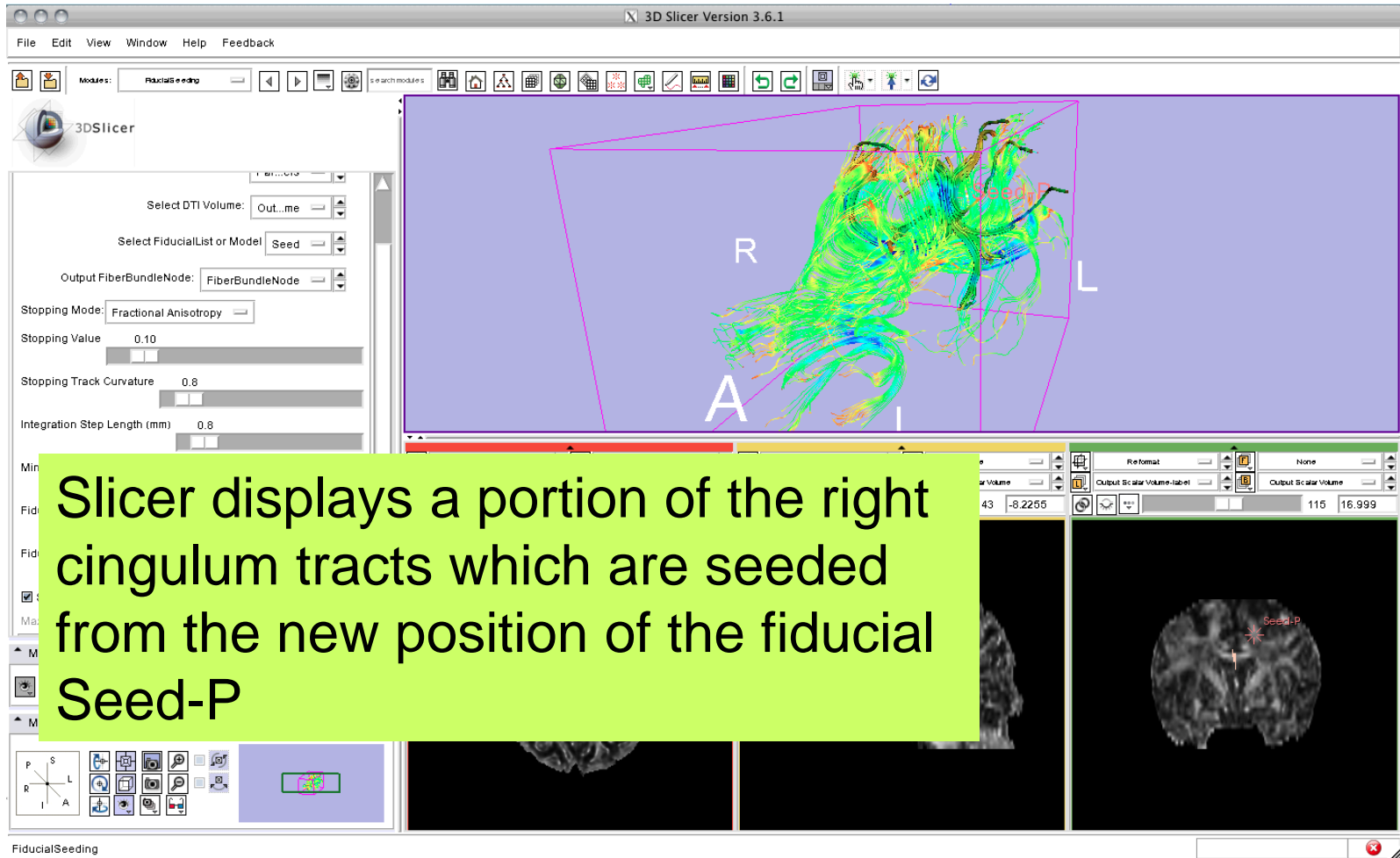
Lb: Out of Frame  
Bg: Out of Frame

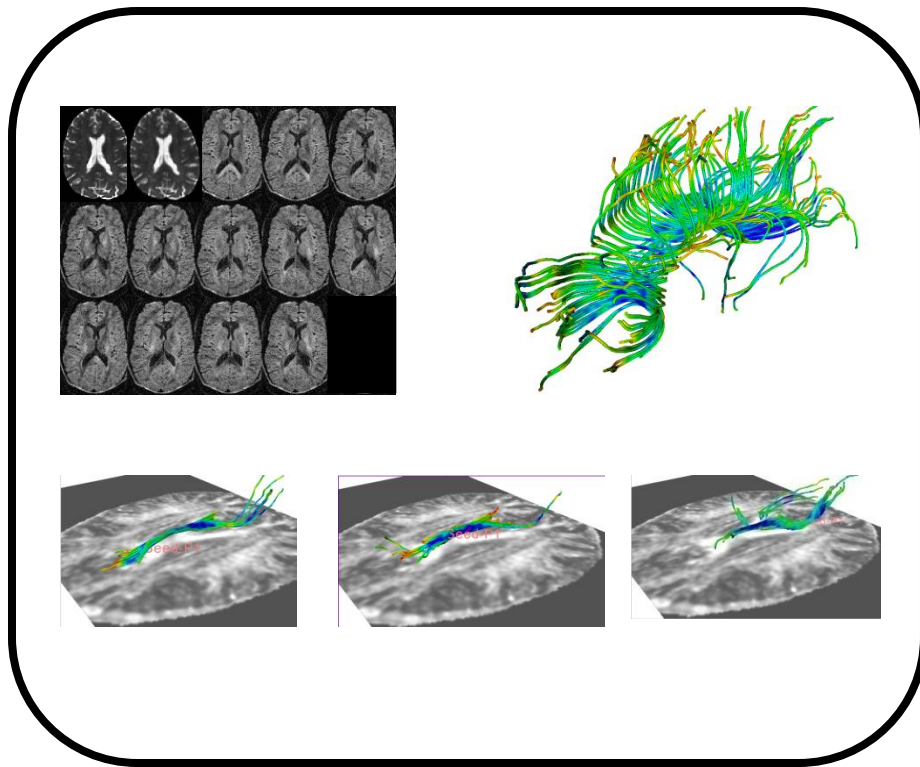
R: -249.7  
A: 519.1  
S: 40.6

Seed-P



# Fiducial Seeding





## Part 5:

# Saving a DTI Scene



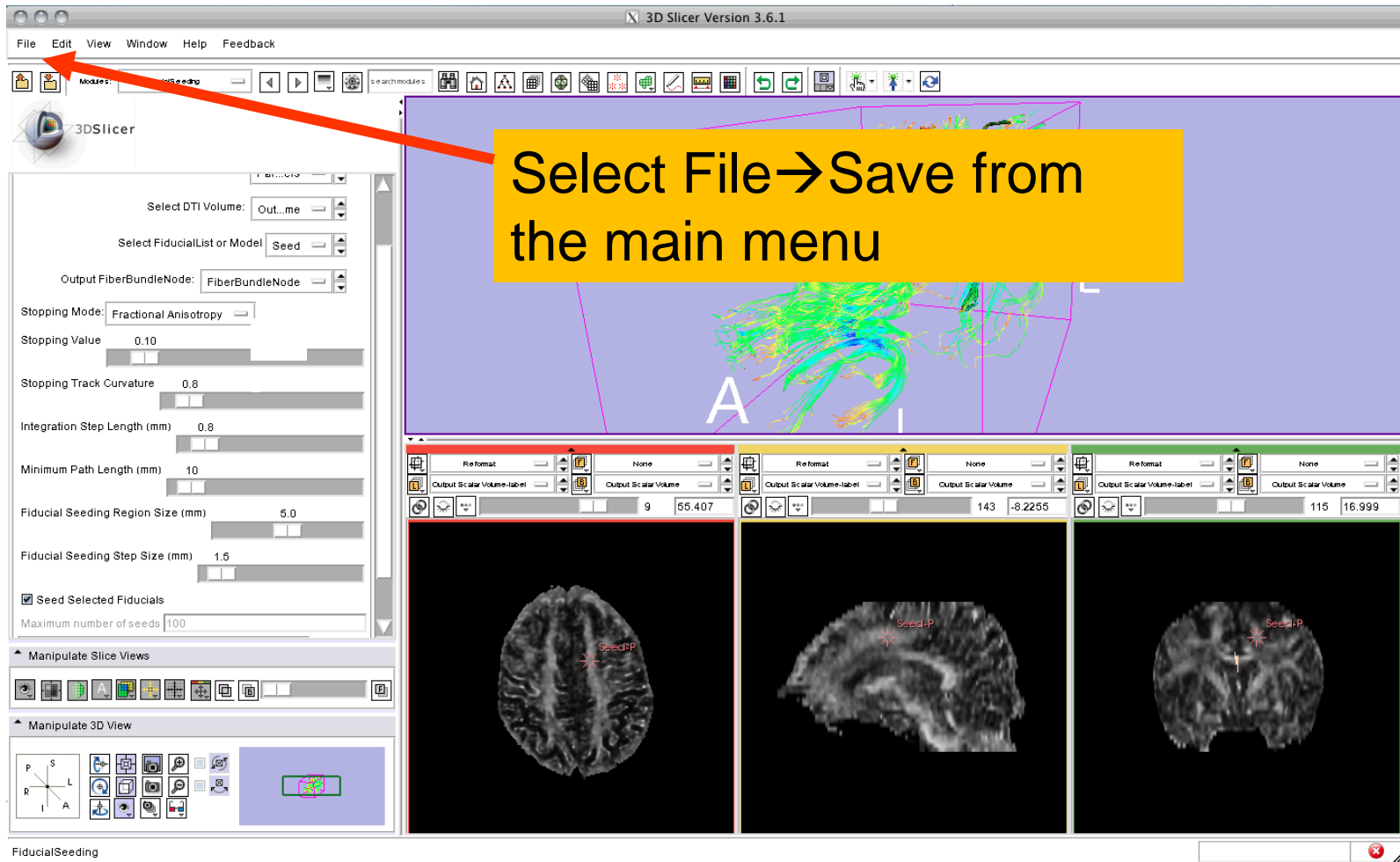
# DTI Scene

The screenshot shows the 3D Slicer software interface. The main window displays a 3D view of a brain with fiber bundles. The MRML Tree on the left lists the following nodes: 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 'Data' module is selected in the top toolbar. A yellow box highlights the text 'Select the module Data'. A green box highlights the text 'Slicer displays the list of volumes and models generated in this tutorial'. The bottom of the interface shows three slice views: a coronal slice, a sagittal slice, and an axial slice.





# 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

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

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)

Open  
Cancel

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 interface. The 'Data' module is selected in the top toolbar and circled in red. The main 3D view shows a fiber bundle reconstruction of a brain region with axes labeled R (Right), L (Left), A (Anterior), and I (Inferior). Below the 3D view are three orthogonal slice views: Axial, Sagittal, and Coronal. The Axial slice shows a red star labeled 'Seed.P'. The Sagittal and Coronal slices also show a red star labeled 'Seed.P'. The left sidebar contains the MRML Tree and other tool panels.



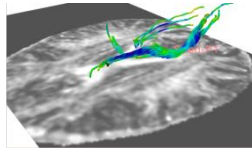
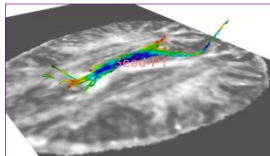
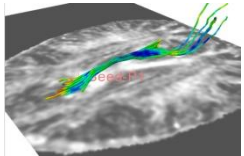
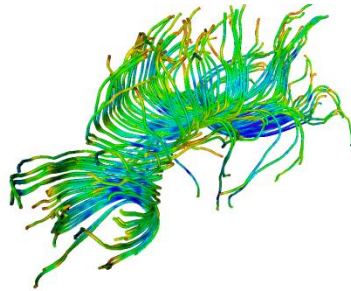
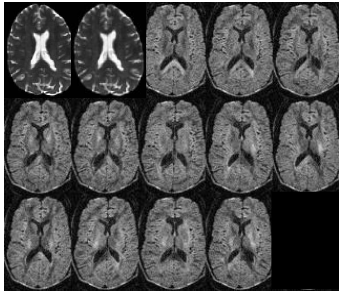
# Loading a DTI Scene

The screenshot displays the 3D Slicer Version 3.6.1 interface. The main window shows a 3D view of a brain with fiber bundles rendered in various colors (green, blue, red, yellow). The scene is oriented with 'R' (Right), 'L' (Left), 'A' (Anterior), and 'I' (Inferior) labels. The left sidebar contains the MRML Tree, MRML Node Inspector, and options for loading and manipulating scenes and slice views. The bottom of the interface shows three slice views: Axial, Sagittal, and Coronal, each with its own controls and numerical values.

**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.

spujol@bwh.harvard.edu





# Slicer Community

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[www.slicer.org](http://www.slicer.org)

Mailing lists:

[slicer-users@bwh.harvard.edu](mailto:slicer-users@bwh.harvard.edu)

[slicer-devel@bwh.harvard.edu](mailto:slicer-devel@bwh.harvard.edu)



# Acknowledgments

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## **National Alliance for Medical Image Computing**

NIH U54EB005149



## **Neuroimage Analysis Center**

NIH P41RR013218