

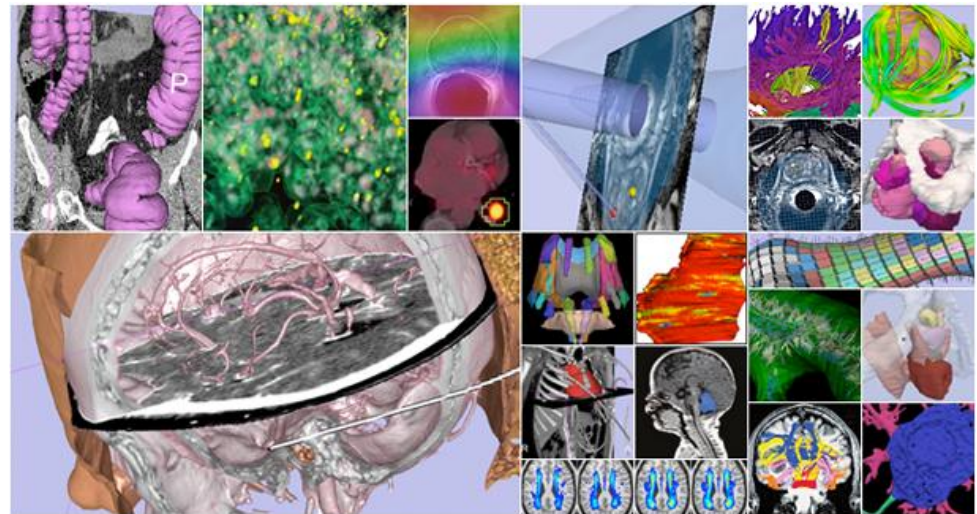
# Exploring Peritumoral White Matter Fibers for Neurosurgical Planning

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# 3D Slicer

- 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



# Download Slicer3.6



- Download and install the Slicer3.6.3 release version software from the Slicer web site

<http://www.slicer.org/pages/Special:SlicerDownloads>

## Disclaimer

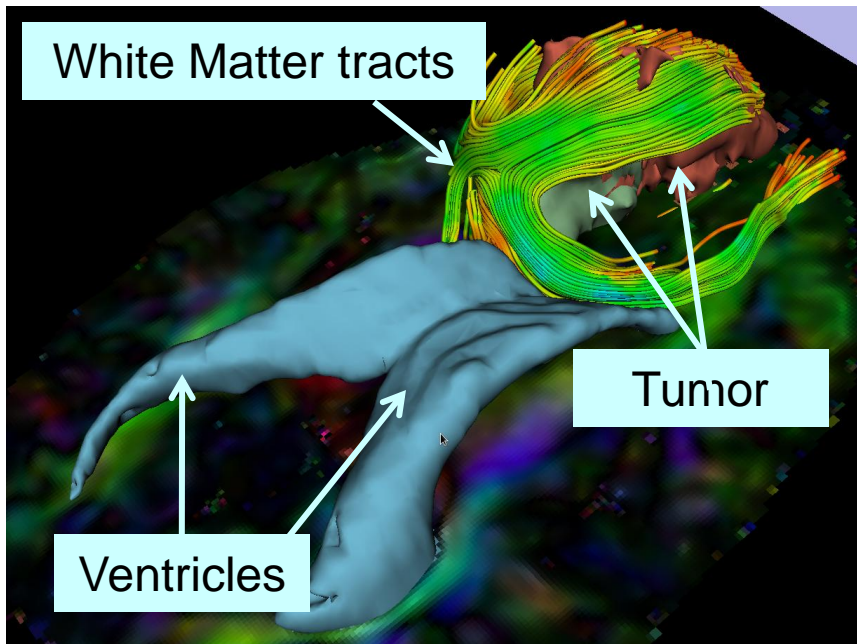
It is the responsibility of the user of 3DSlicer to comply with both the terms of the license and with the applicable laws, regulations and rules.

# Pre-Requirement

- This course supposes that you have taken the “*Slicer3 Data Loading and Visualization*” tutorial

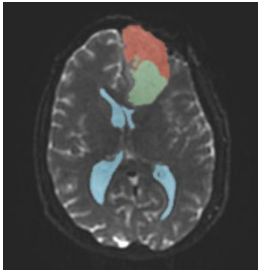
[http://www.slicer.org/slicerWiki/index.php/Slicer3.6:Training#Software\\_tutorials](http://www.slicer.org/slicerWiki/index.php/Slicer3.6:Training#Software_tutorials)

# Clinical Goal

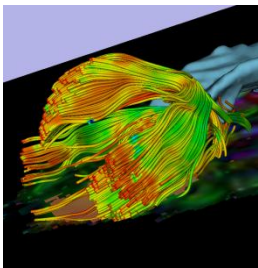


The goal of this tutorial is to explore white matter fibers surrounding a tumor using Diffusion Tensor Imaging (DTI) Tractography

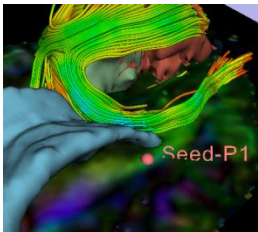
# Overview of the analysis pipeline



Part1: Segmentation of the ventricles, and solid and cystic parts of the tumor



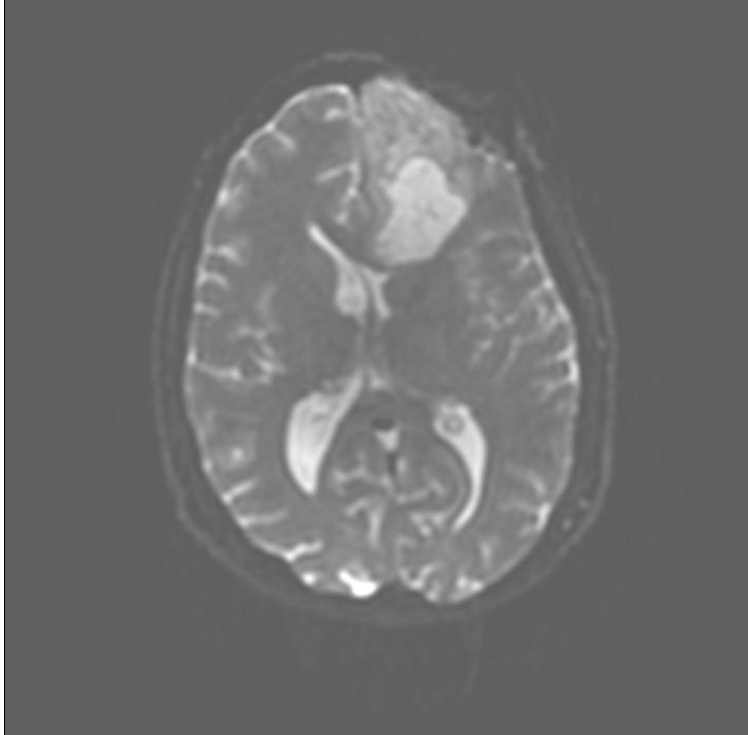
Part 2: Tractography reconstruction of the white matter fibers in the peritumoral volume



Part 3: Tractography exploration of the ipsilateral and contralateral fibers tracts

# Part 1: Diffusion Data Loading and Visualization

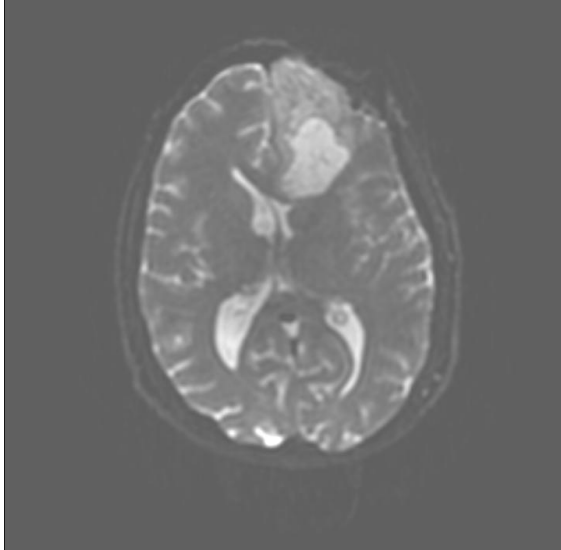
# Clinical Case



- 35 year-old male diagnosed with Glioblastoma multiforme (GBM)
- Diffusion Weighted Imaging (DWI) acquisition for neurosurgical planning



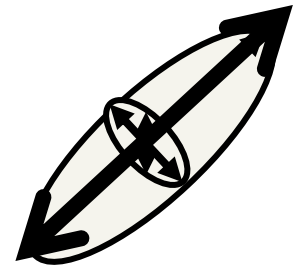
# Diffusion Tensor Imaging



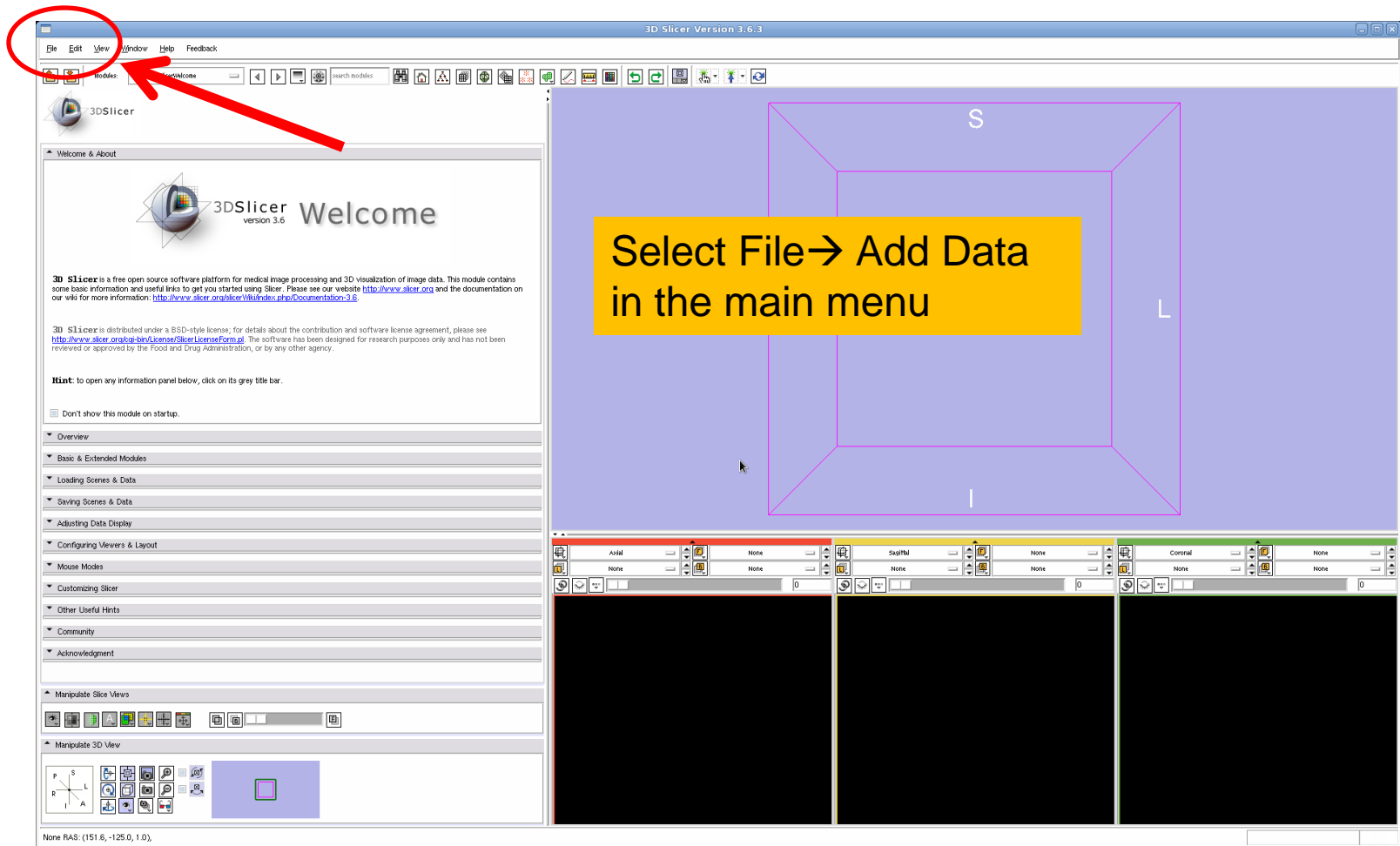
$$S_i = S_0 e^{-b \hat{u}^T \underline{D} \hat{u}}$$

(Stejskal and Tanner 1965, Basser 1994 )

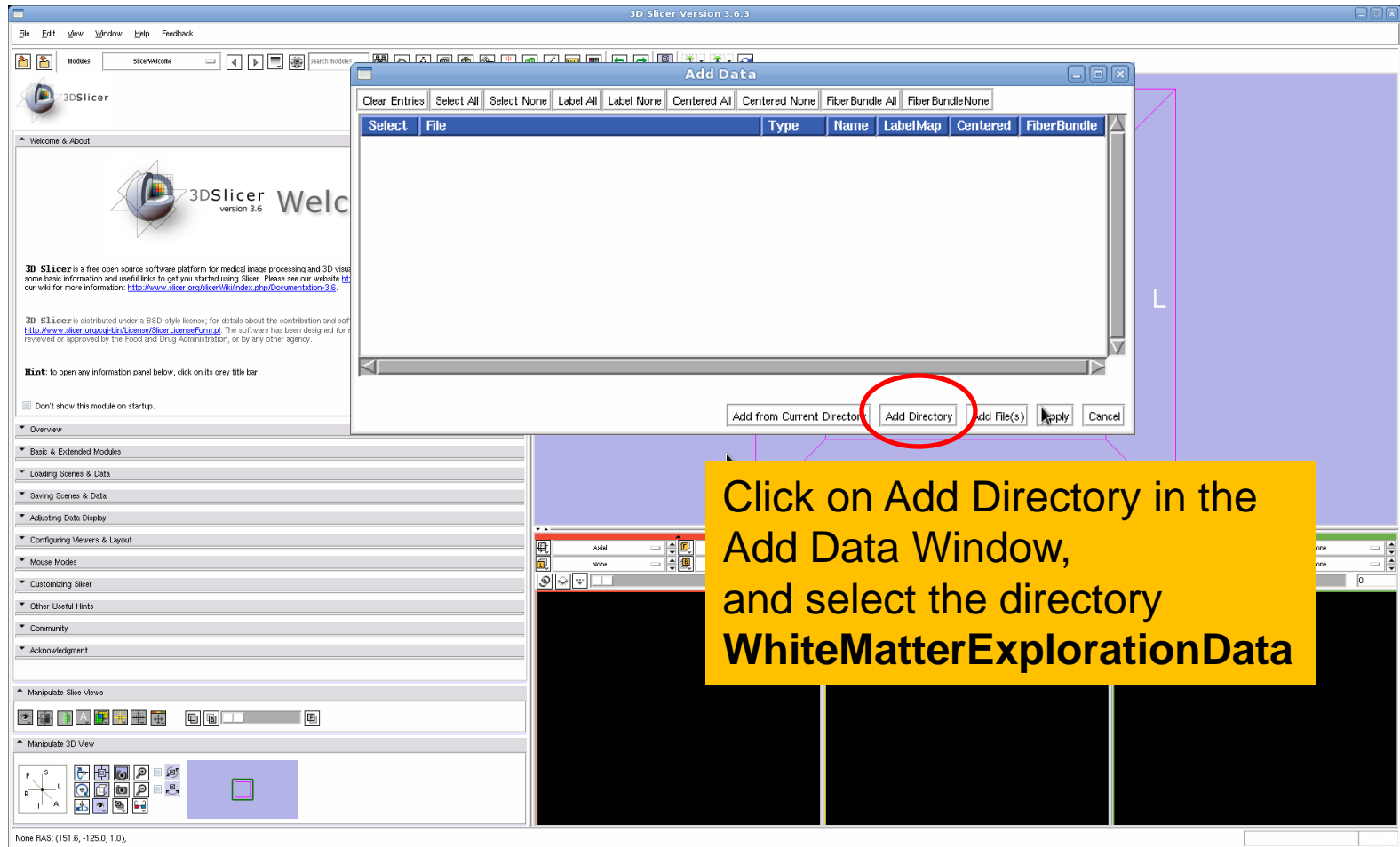
$$\underline{D} = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{bmatrix}$$



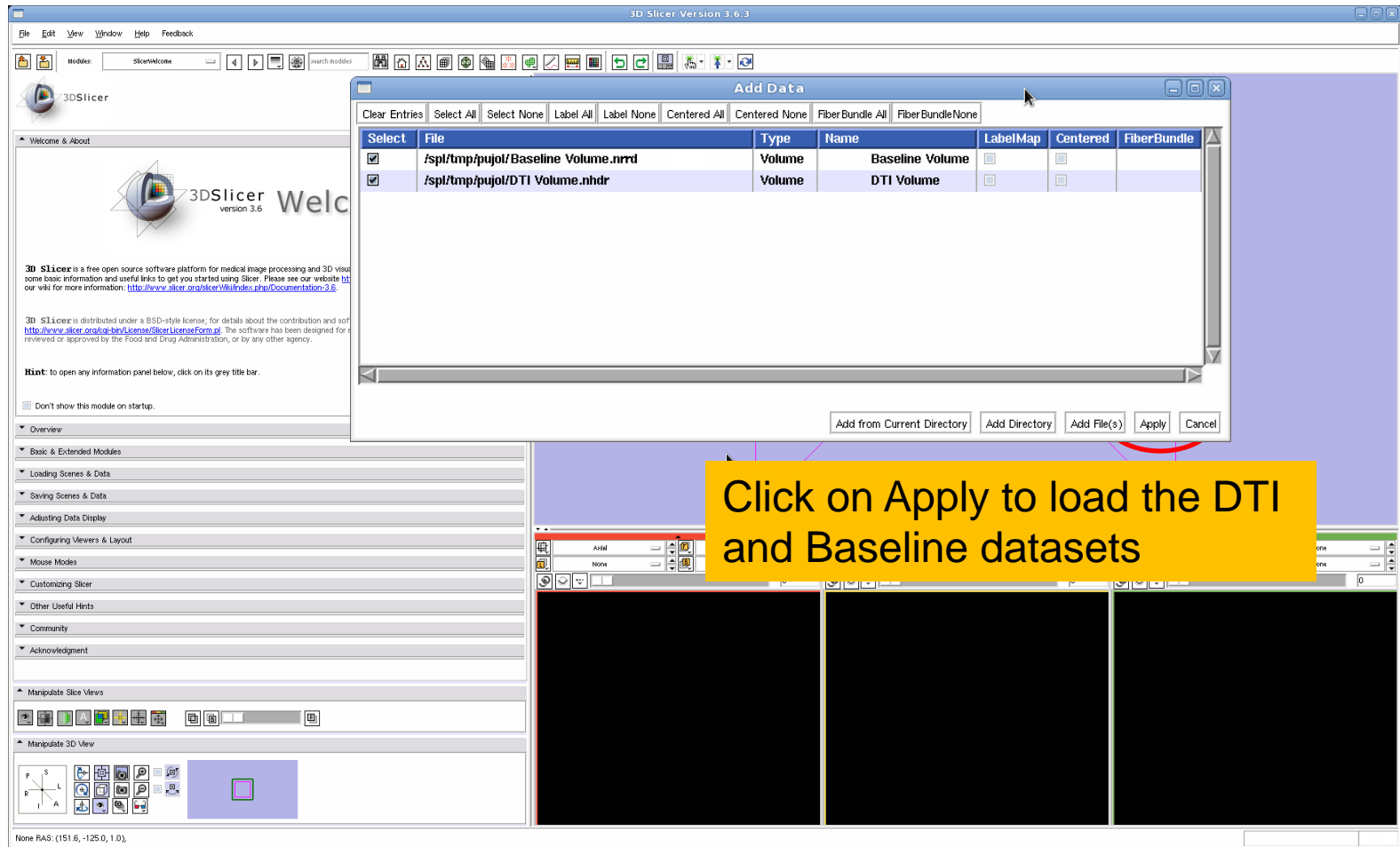
# Loading DTI and Baseline Data




# Loading DTI and Baseline Data



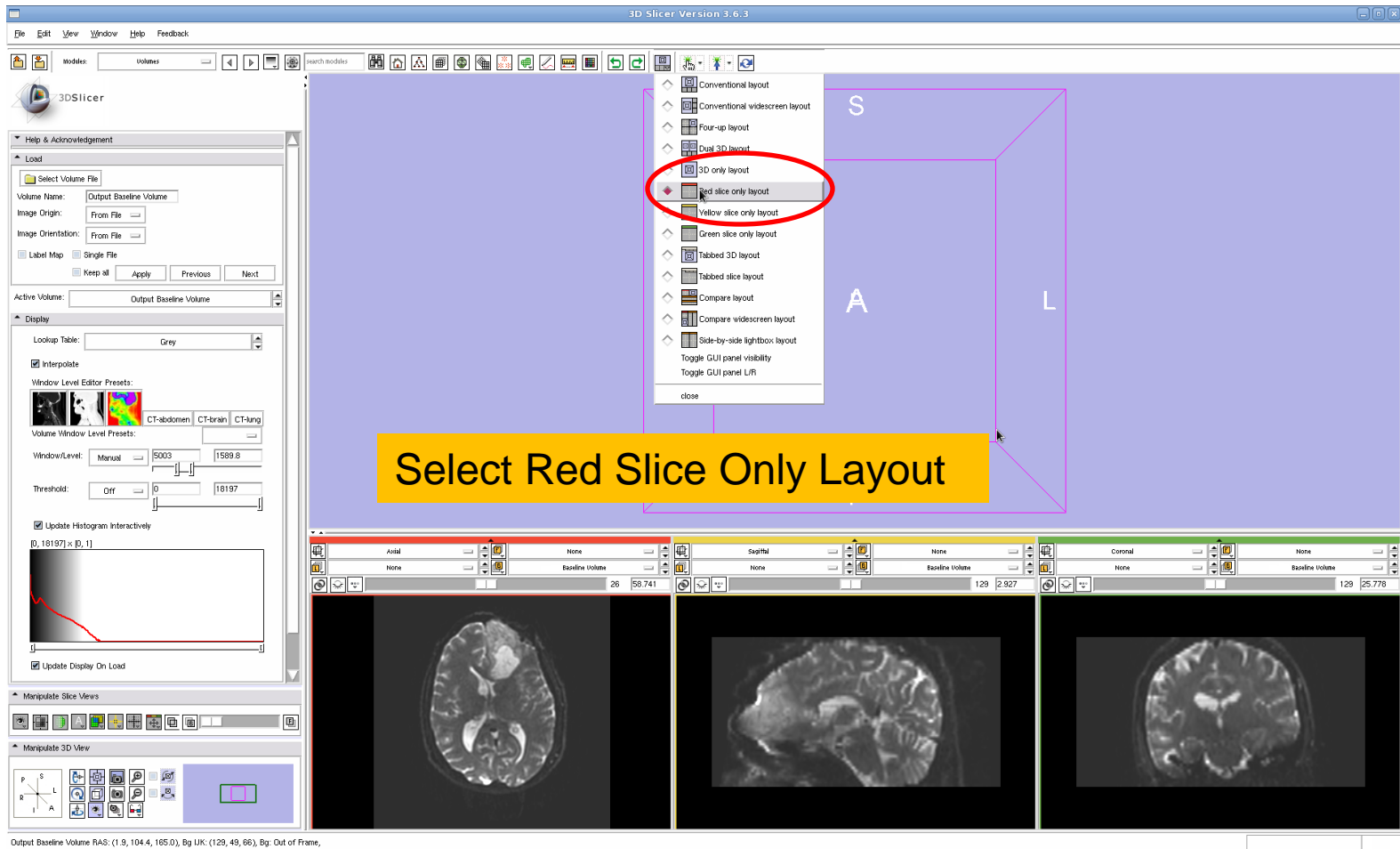
# Loading DTI and Baseline Data



# Loading DTI and Baseline Data

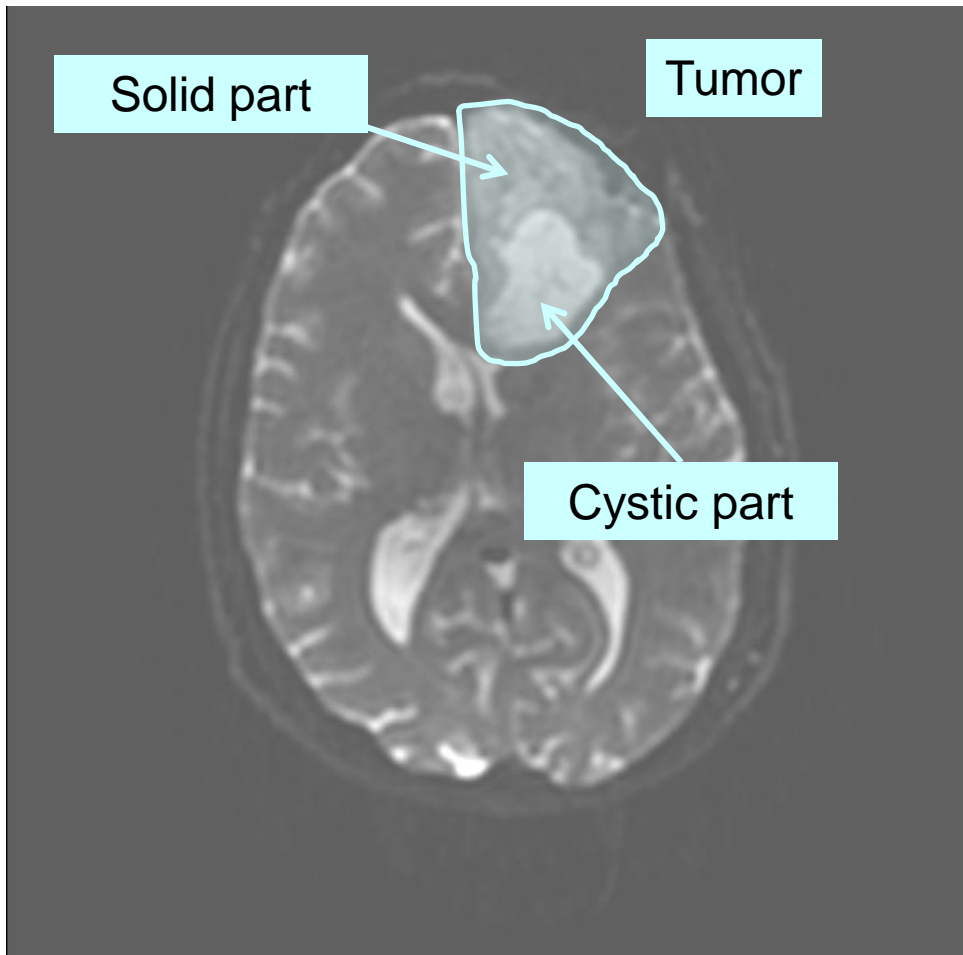
The screenshot displays the 3D Slicer software interface. The 'Volumes' module is selected in the top toolbar and circled in red. The 'Load' panel on the left shows 'Output Baseline Volume' as the active volume. The 'Display' panel shows the 'Window/Level' set to 'Manual' with a value of 5003, which is highlighted by a red arrow. The 'Manipulate Slice Views' panel at the bottom shows three anatomical views: Axial, Sagittal, and Coronal. A red circle highlights the link icon in the bottom toolbar. A yellow text box in the center reads: 'Select the module **Volumes** and adjust the Window and Level values of the Baseline Volume.' Another yellow text box at the bottom right reads: 'Click on the link icon  to link the three anatomical viewers'. The status bar at the bottom shows the RAS coordinates for the Baseline Volume: (129, 49, 66).

# Loading DTI and Baseline Data



# Part 1: Segmenting the tumor

# Tumor Segmentation

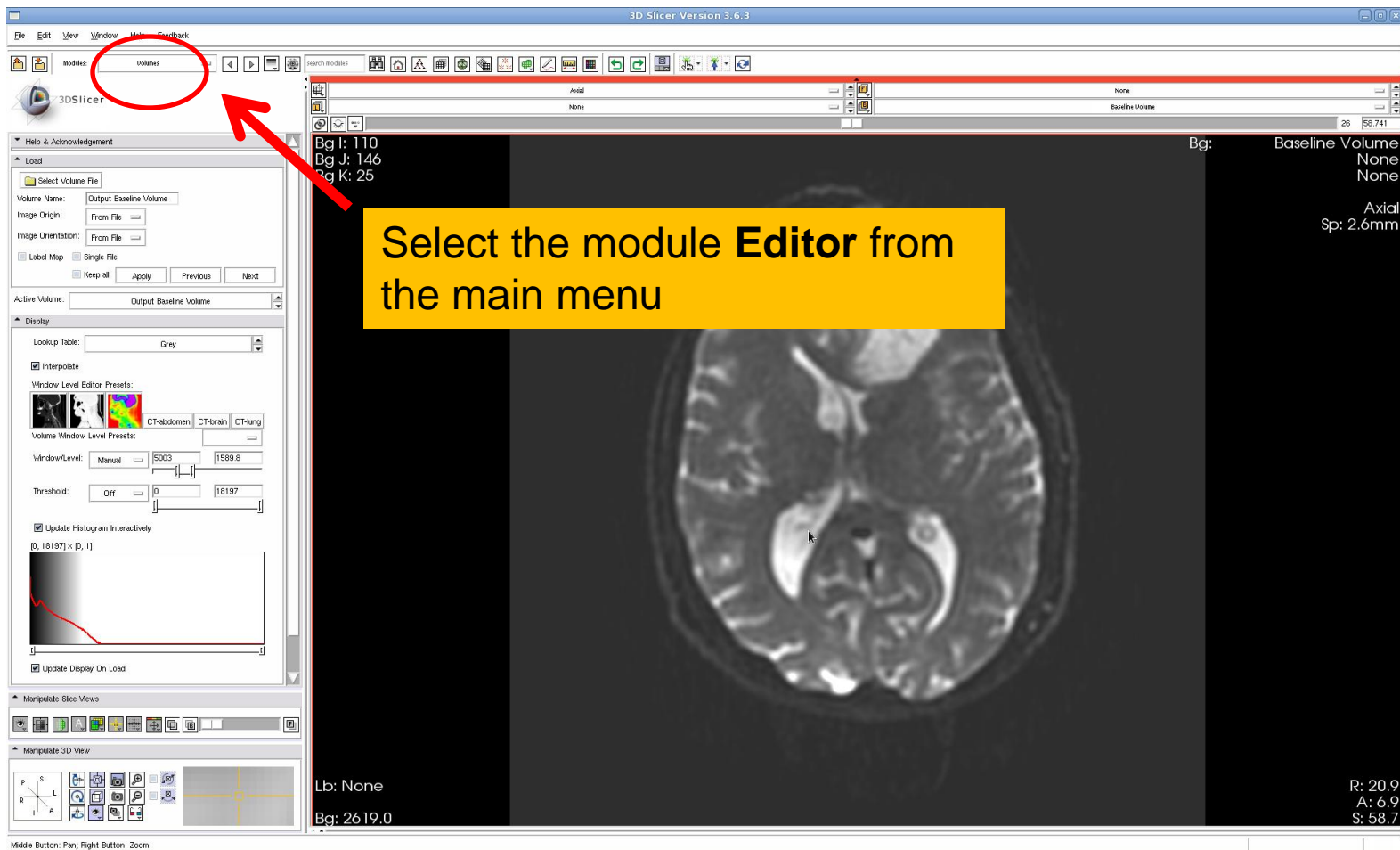


The tumor in this clinical case is composed of two parts: a solid part and a cystic part.

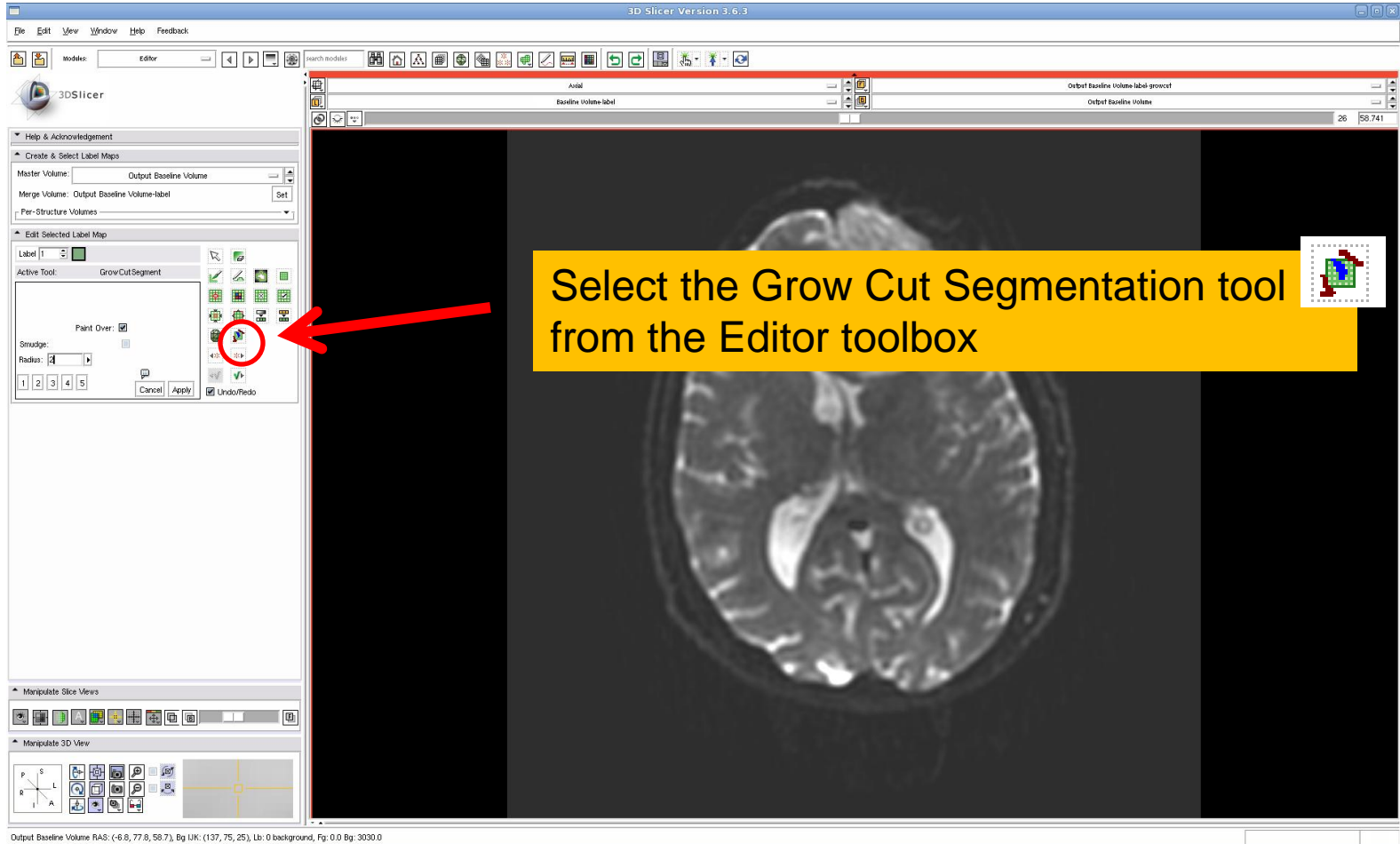
In this section, we'll segment the different parts of the tumor using a Grow Cut Segmentation algorithm.



# Editor Module



# Tumor Segmentation



# Grow Cut Segmentation

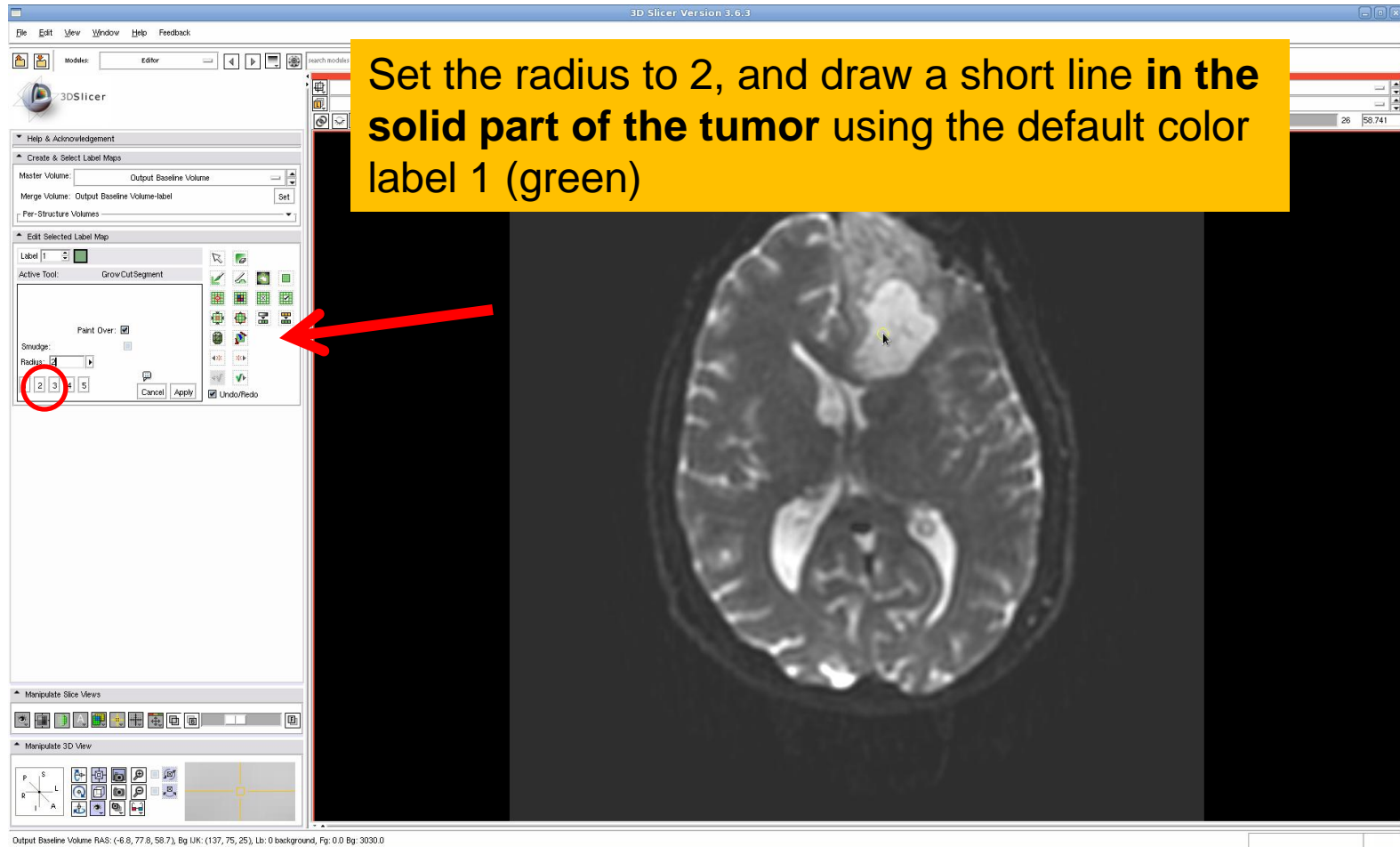
The **Grow Cut Segmentation module** is a competitive region growing algorithm using cellular automata.

The algorithm works by using a set of user input scribbles for foreground and background.

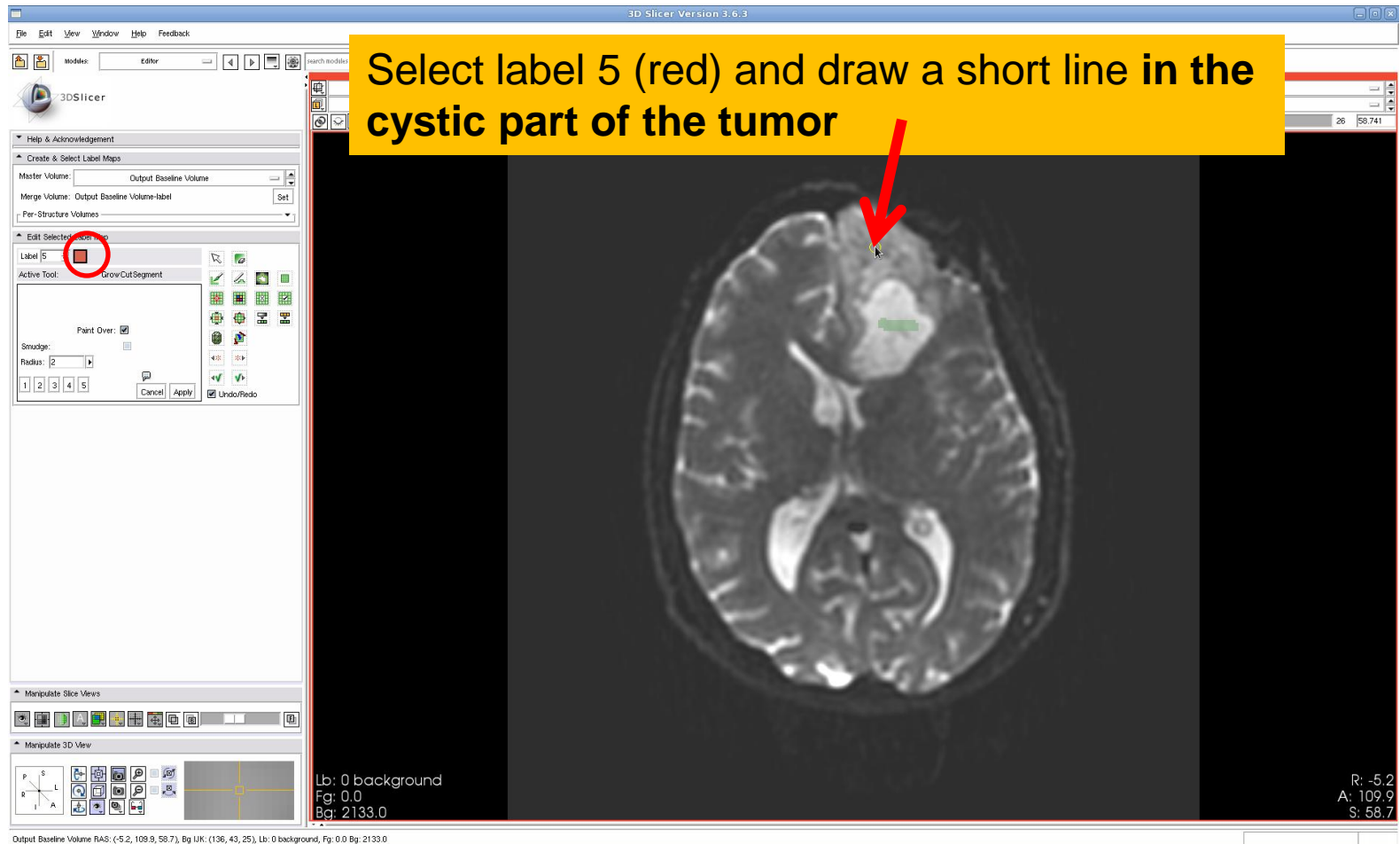
For N-class segmentation, the algorithm requires a set of scribbles corresponding the N classes, and a scribble for the other classes.



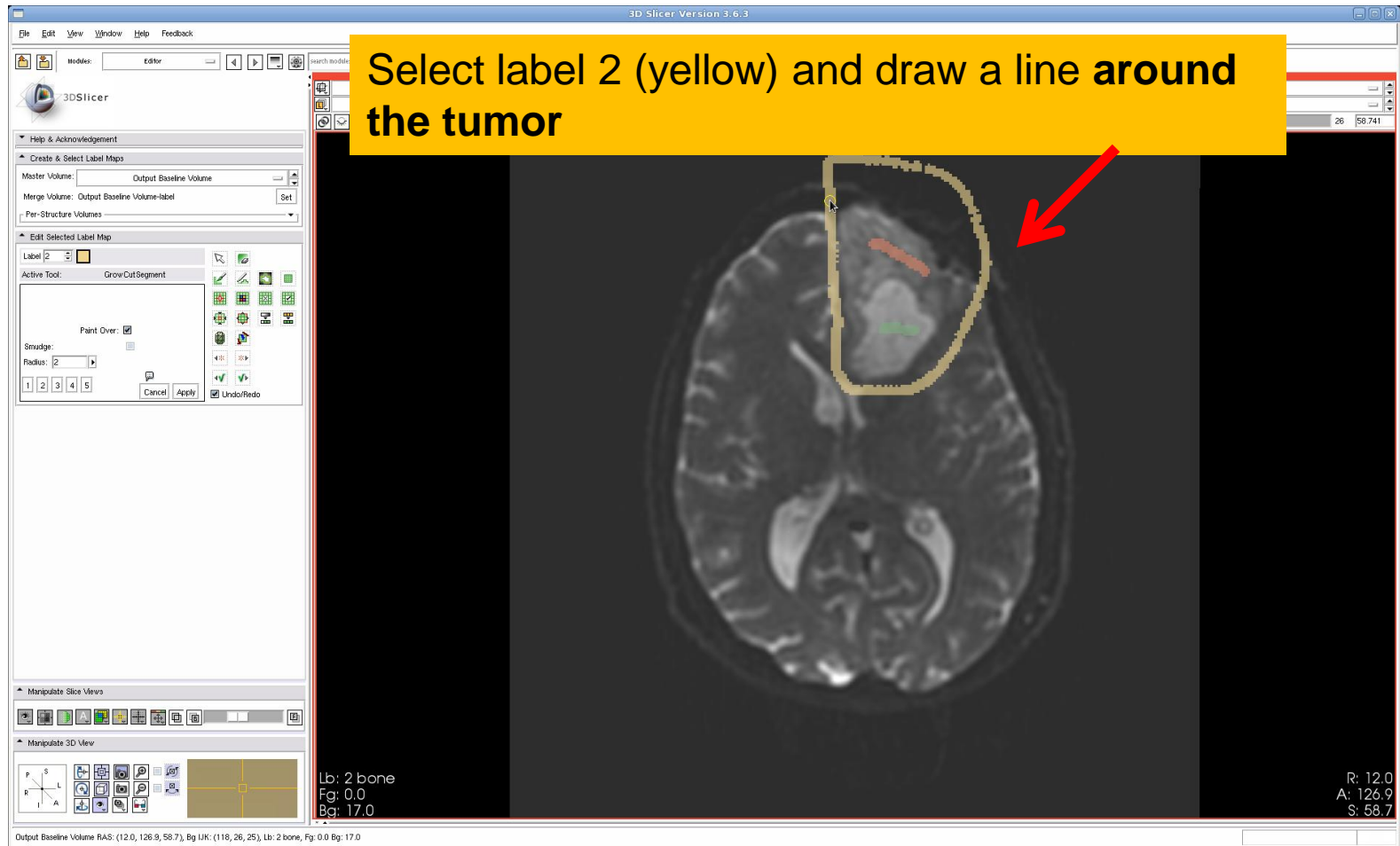
# Tumor Segmentation



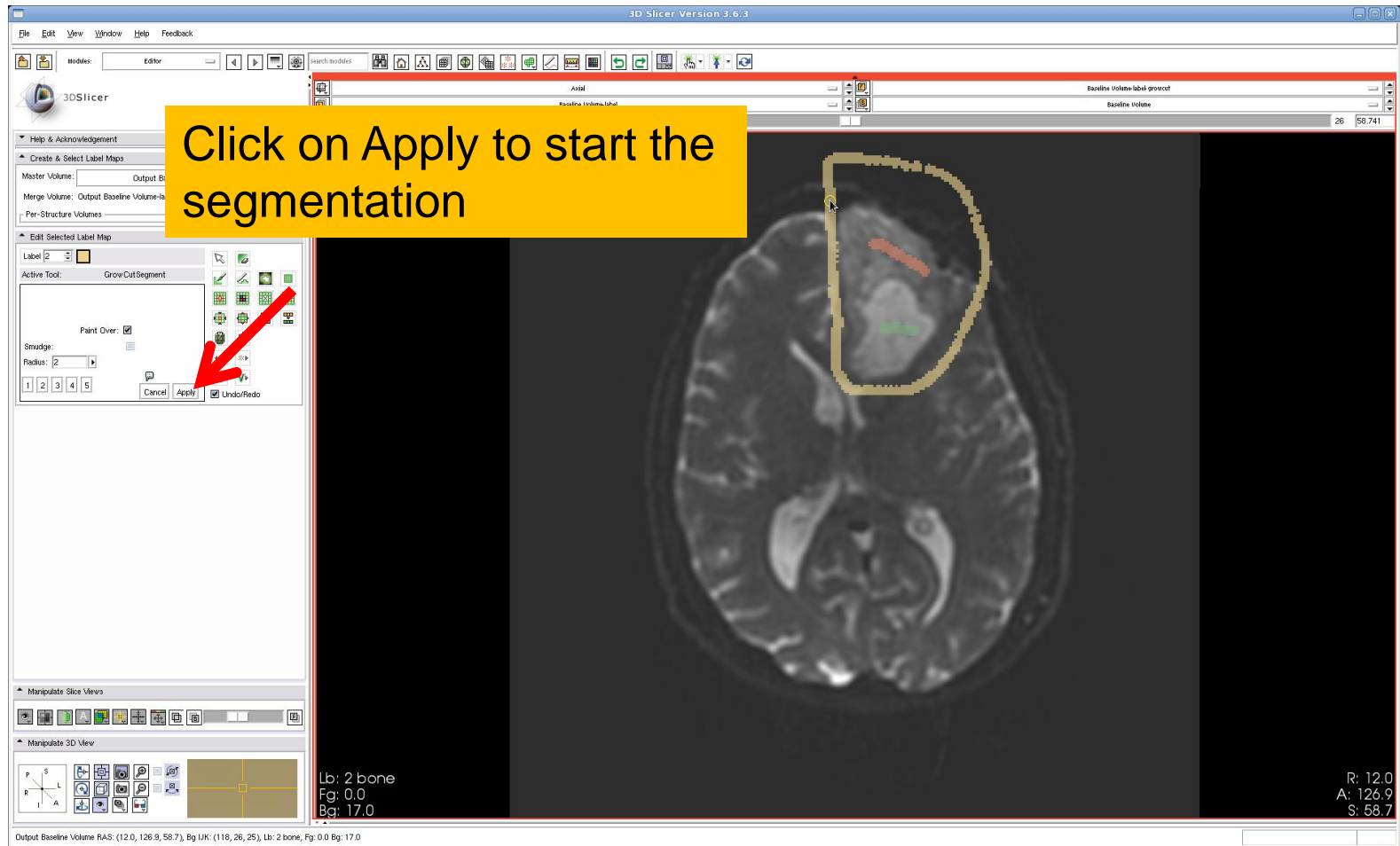
# Tumor Segmentation



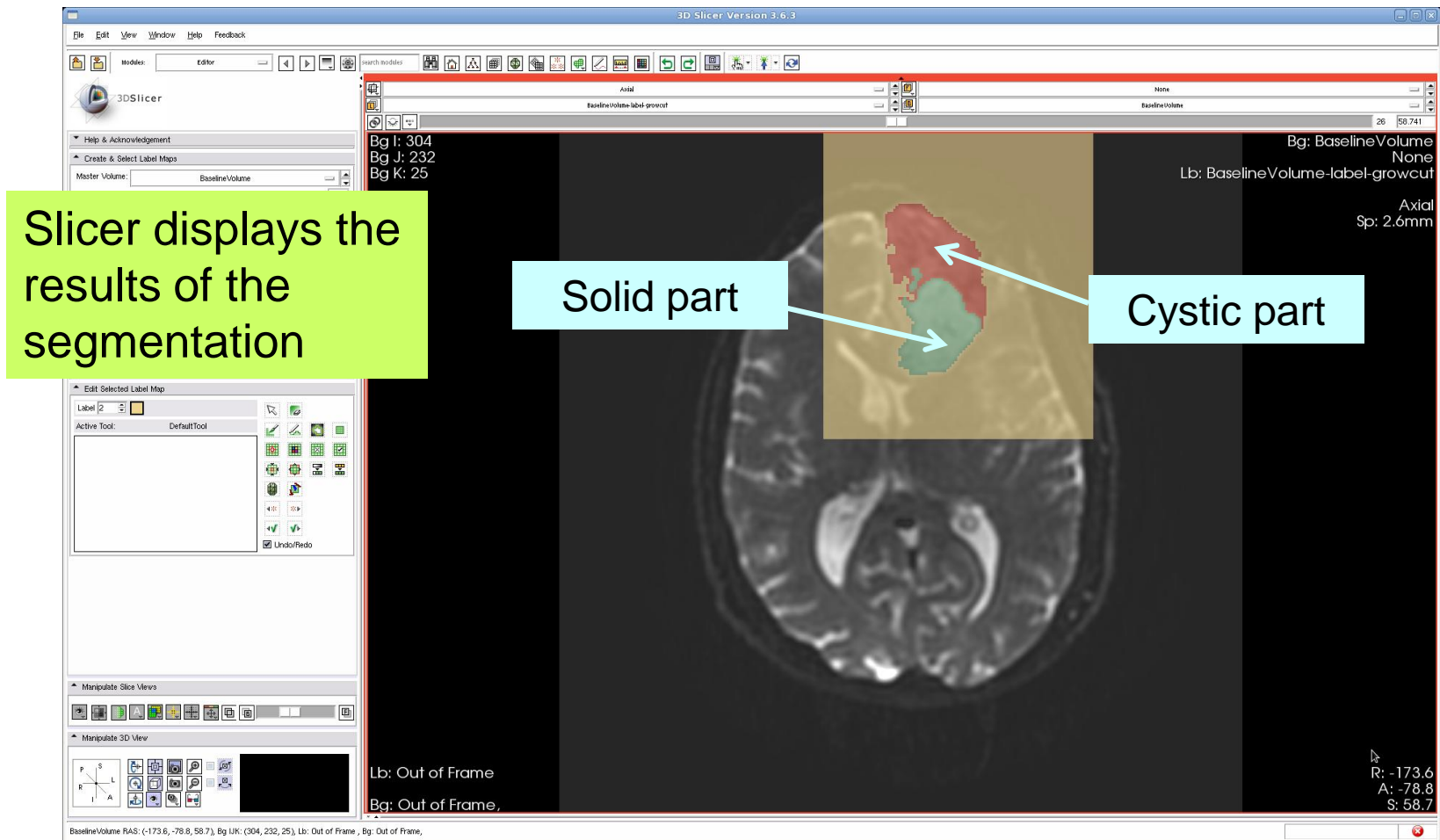
# Tumor Segmentation



# Tumor Segmentation



# Tumor Segmentation





# Tumor Segmentation

Click on Set, select Merge Volume 'BaselineVolume-label-growcut' and click on 'Split Merge Volume'

The screenshot shows the 3D Slicer interface. The 'Merge Volume' dropdown menu is open, showing 'BaselineVolume-label-growcut' selected. The 'Split Merge Volume' option is circled in red. A red arrow points to the 'Set' button. The main window displays an axial MRI slice with a segmented tumor region in red and green. The status bar at the bottom shows: BaselineVolume RAS: (-173.6, -78.8, 58.7), Bg UK: (304, 232, 25), Lb: Out of Frame, Bg: Out of Frame.

BaselineVolume RAS: (-173.6, -78.8, 58.7), Bg UK: (304, 232, 25), Lb: Out of Frame, Bg: Out of Frame.

# Ventricles Segmentation

Number	Color	Name	LabelName
1		tissue	BaselineVolume-t
2		bone	BaselineVolume-l
5		blood	BaselineVolume-l

Select the volume **'BaselineVolume-label-bone'** (label 2)

Select the **threshold tool** from the Editor toolbox, **select the label 4 (blue)**, threshold the ventricles, and click on Apply

# Ventricles Segmentation

Select the tool **'Save Islands'** from the Editor toolbox, and click on the occipital horn of the ventricle

Number	Color	Name	LabelText
1	tissue	BaselineVolume-t	BaselineVolume-t
2	bone	BaselineVolume-l	BaselineVolume-l
5	blood	BaselineVolume-l	BaselineVolume-l

BaselineVolume RAS: (26.1, 5.1, 58.7), Bg UK: (104, 148, 25), Lb: 4 connective\_tissue, Bg: 3179.0

# Final Result of the Segmentation

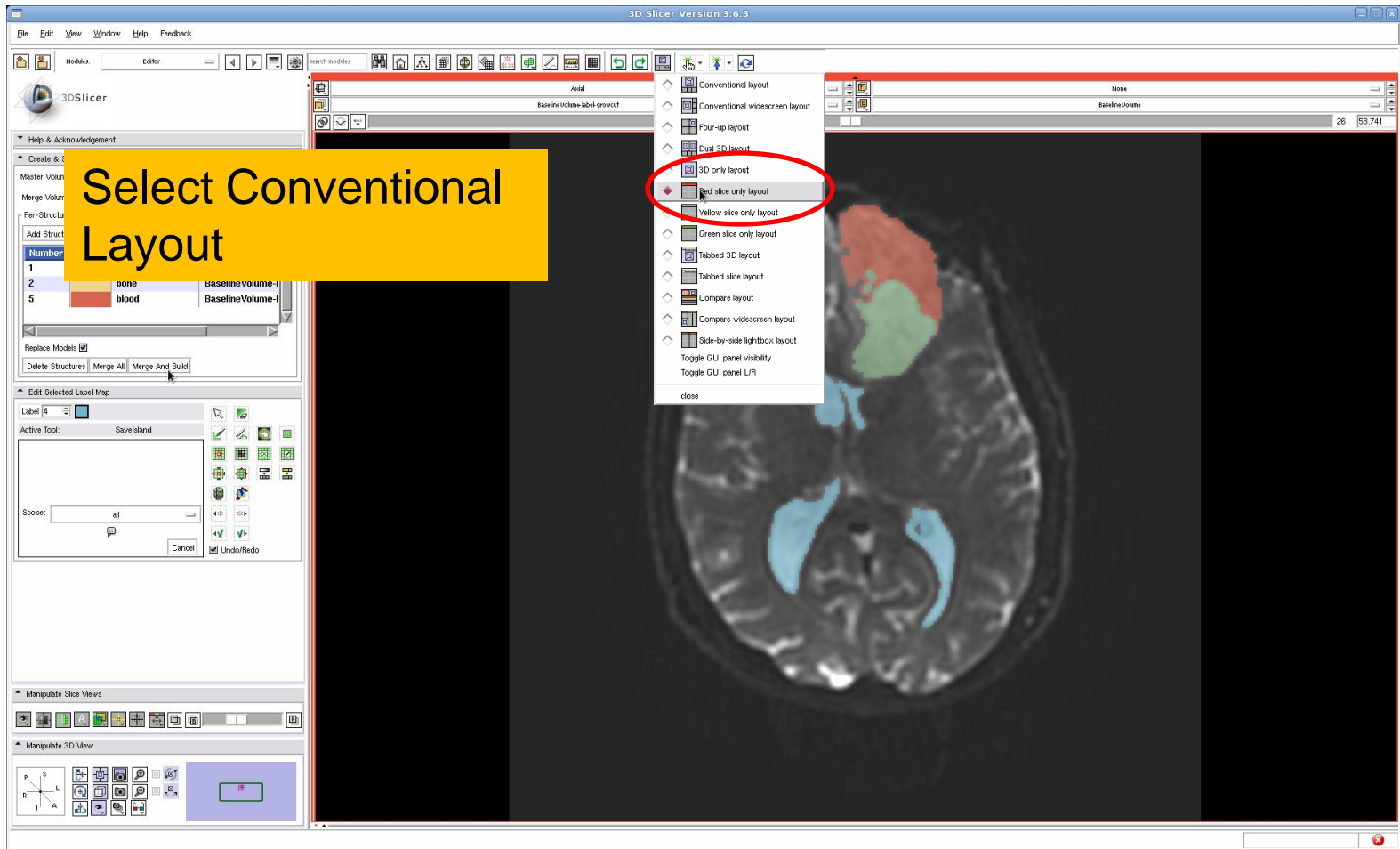
Click on **Merge** and **Build** to merge the different labelmaps and generate the 3D models of the tumor and ventricles

The screenshot shows the 3DSlicer interface. The 'Create & Select Label Maps' panel contains the following table:

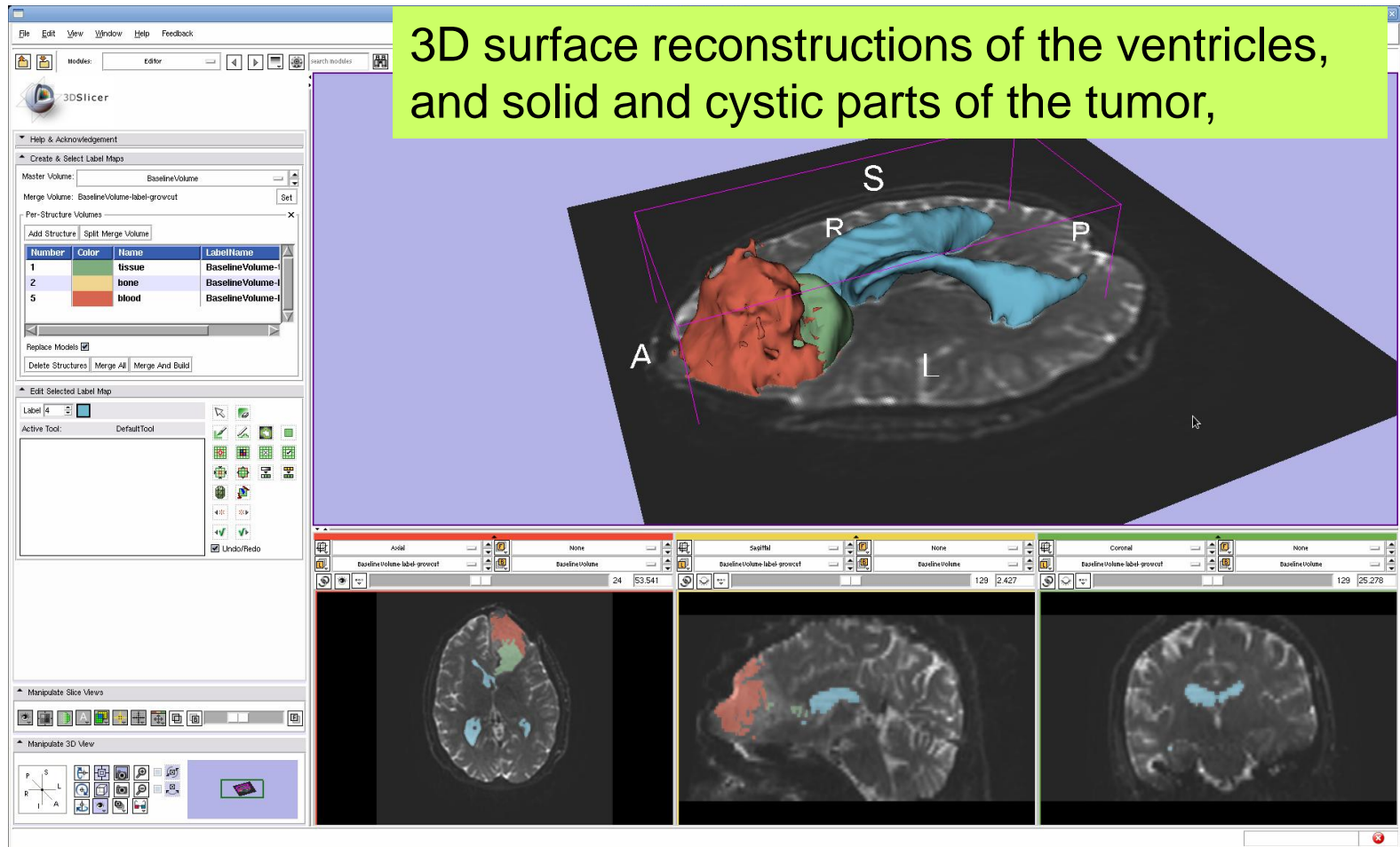
Number	Color	Name	LabelName
1	Green	tissue	BaselineVolume-t
2	Yellow	bone	BaselineVolume-t
5	Red	blood	BaselineVolume-t

The 'Edit Selected Label Map' panel shows 'Label 4' selected. The '3D View' shows an axial slice with segmented regions. The status bar at the bottom indicates: 'BaselineVolume RAS: (25.6, 7.0, 58.7), Bg UK: (105, 146, 25), Lb: 4 connective\_tissue, Bg: 2443.0'. The right side of the image shows 'Axial Sp: 2.6mm', 'R: 25.6', 'A: 7.0', and 'S: 58.7'.

# Final Result of the Segmentation



# Final Result of the Segmentation



# Part 2: Tractography exploration of peri-tumoral white matter fibers

# Definition of the peri-tumoral volume

Select the label map 'BaselineVolume-tissue' (label 1), and select the tool 'Dilate' in the Editor toolbox

Number	Color	Name	LabelName
1		tissue	BaselineVolume-t
2		bone	BaselineVolume-t
5		blood	BaselineVolume-t

Baselineslice RAS: (196.9, 24.5, 50.9), Bg UK: (-66, 129, 22), Lb: Out of Frame, Bg: Out of Frame.



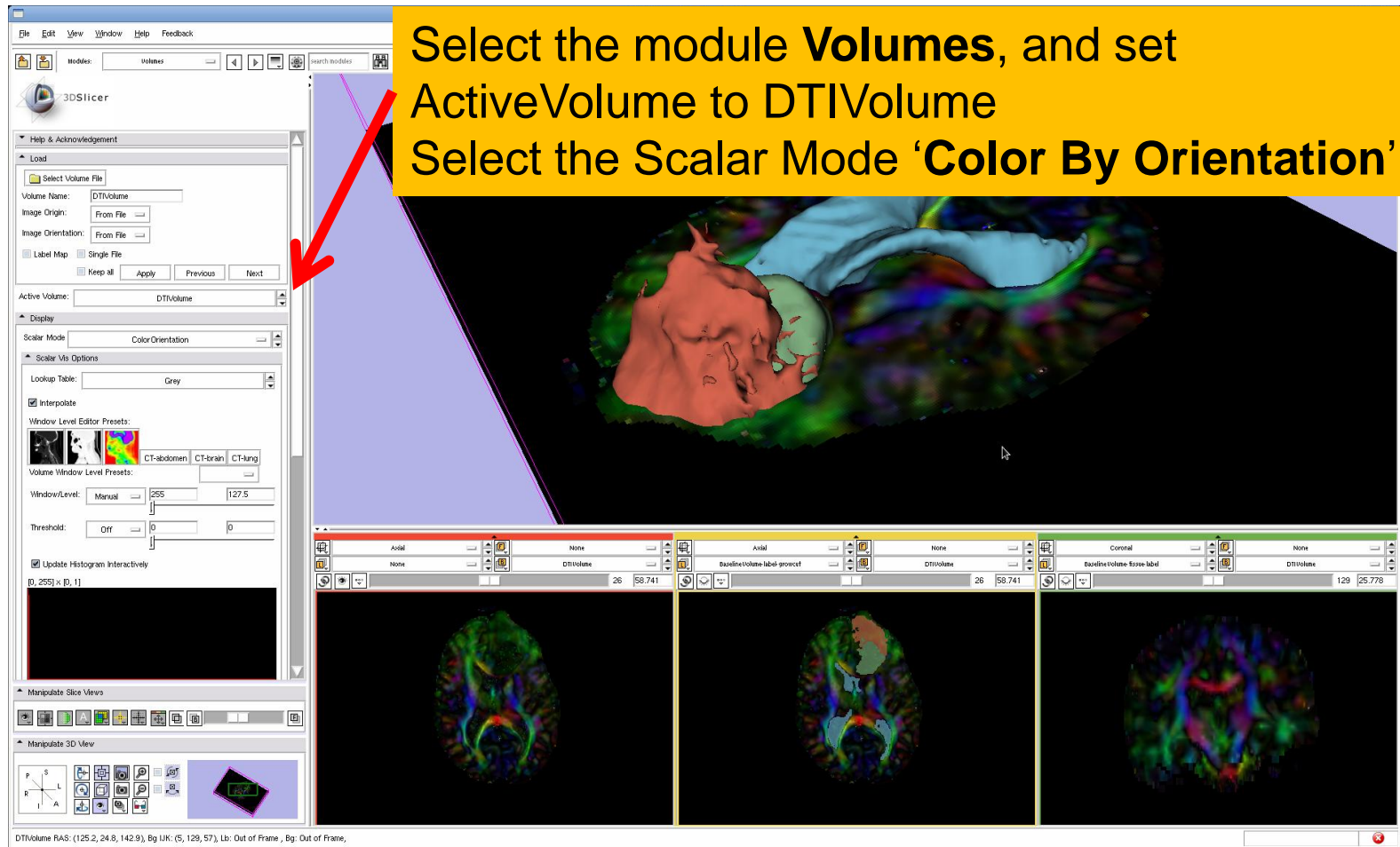
# Definition of the peri-tumoral volume

Click three times in the solid part of the tumor in the axial slice to generate the peritumoral volume

Number	Color	Name	LabelText
1	tissue	BaselineVolume-t	BaselineVolume-t
2	bone	BaselineVolume-l	BaselineVolume-l
5	blood	BaselineVolume-l	BaselineVolume-l

BaselineVolume RAS: (-102.8, 46.8, 53.5), Bg IJK: (233, 106, 23), Lb: 0 background, Bg: 1.0

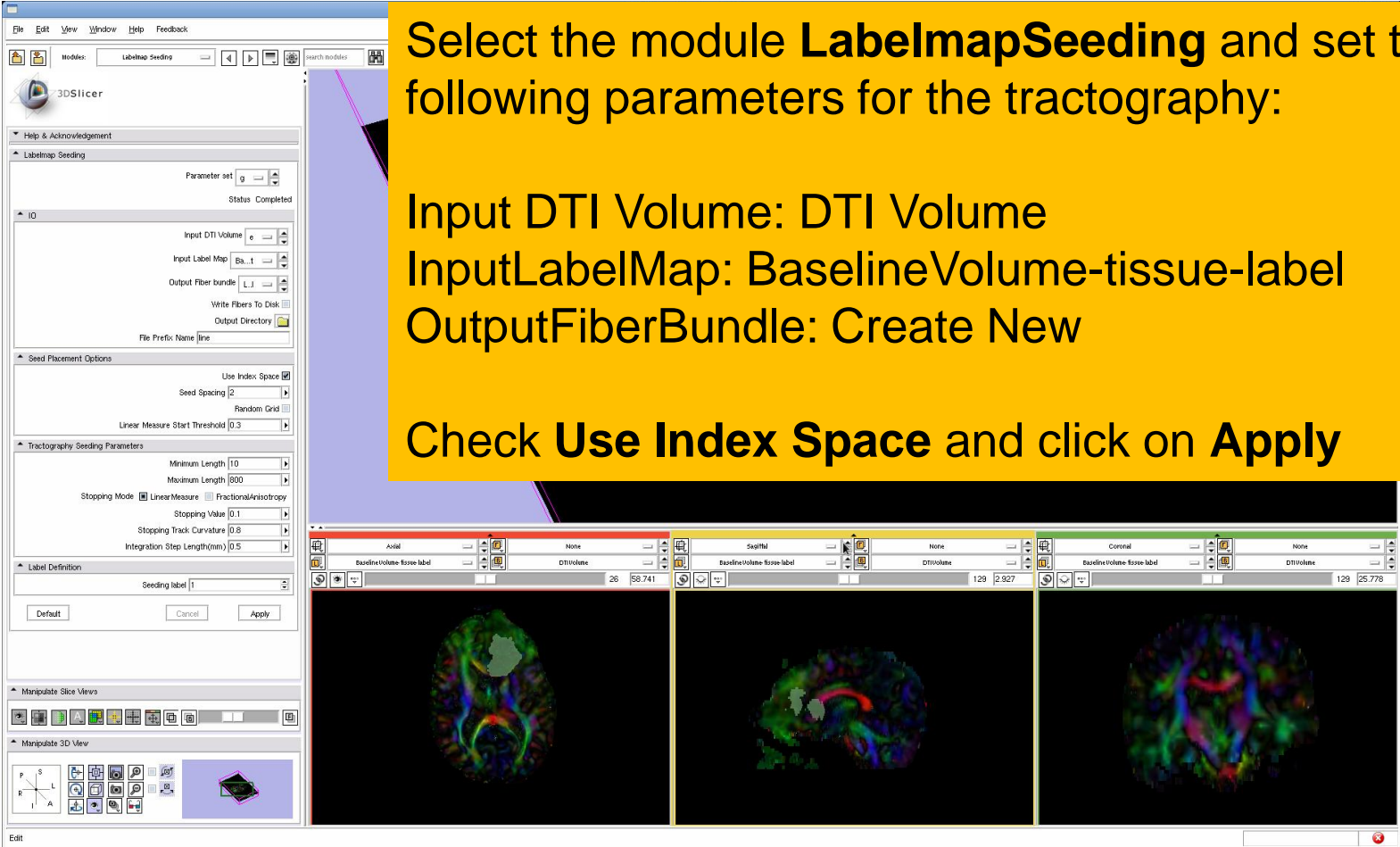
# Visualization of the DTI Volume



Select the module **Volumes**, and set ActiveVolume to DTIVolume  
Select the Scalar Mode '**Color By Orientation**'

The screenshot displays the 3DSlicer interface. The 'Volumes' module is selected in the top toolbar. The 'Active Volume' dropdown is set to 'DTIVolume'. In the 'Display' section, the 'Scalar Mode' is set to 'Color Orientation'. The main 3D view shows a brain slice with a red and blue structure overlaid on a colorful DTI volume. Below the main view are three smaller windows showing different orientations: Axial, Coronal, and Sagittal. A red arrow points from the 'Volumes' module in the toolbar to the 'DTIVolume' dropdown in the 'Active Volume' section.

# Tractography Parameters

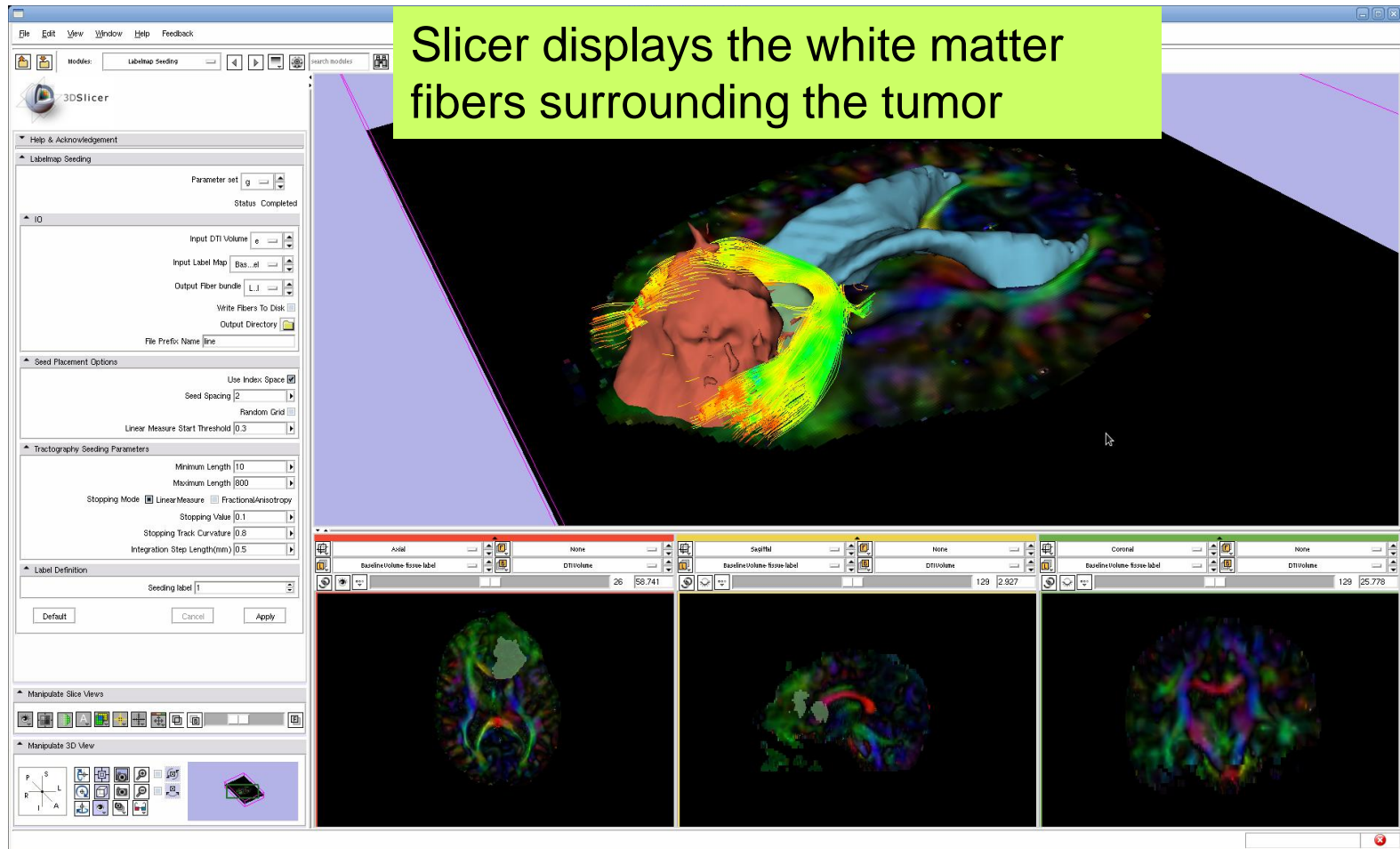


Select the module **LabelmapSeeding** and set the following parameters for the tractography:

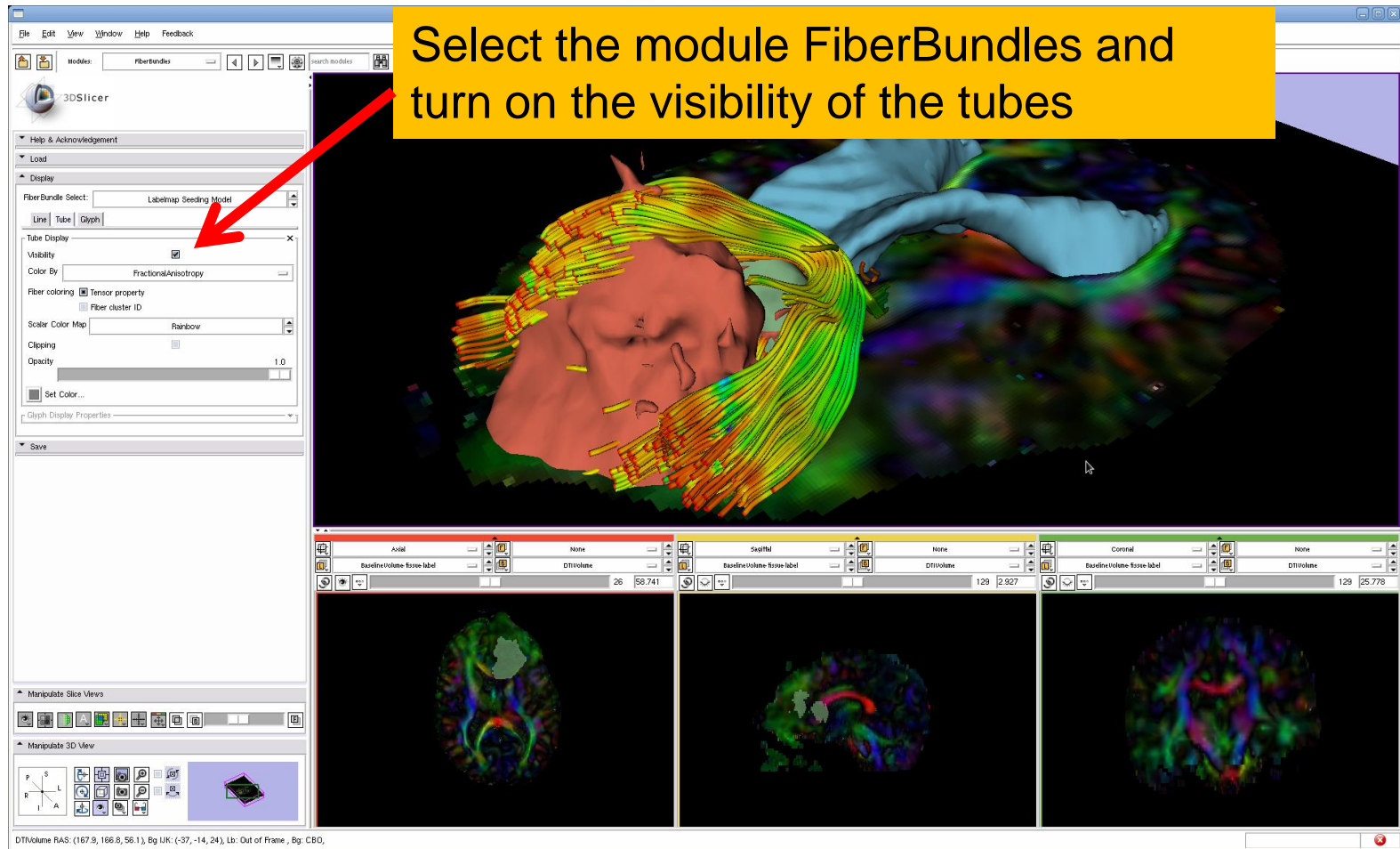
- Input DTI Volume: DTI Volume
- InputLabelMap: BaselineVolume-tissue-label
- OutputFiberBundle: Create New

Check **Use Index Space** and click on **Apply**

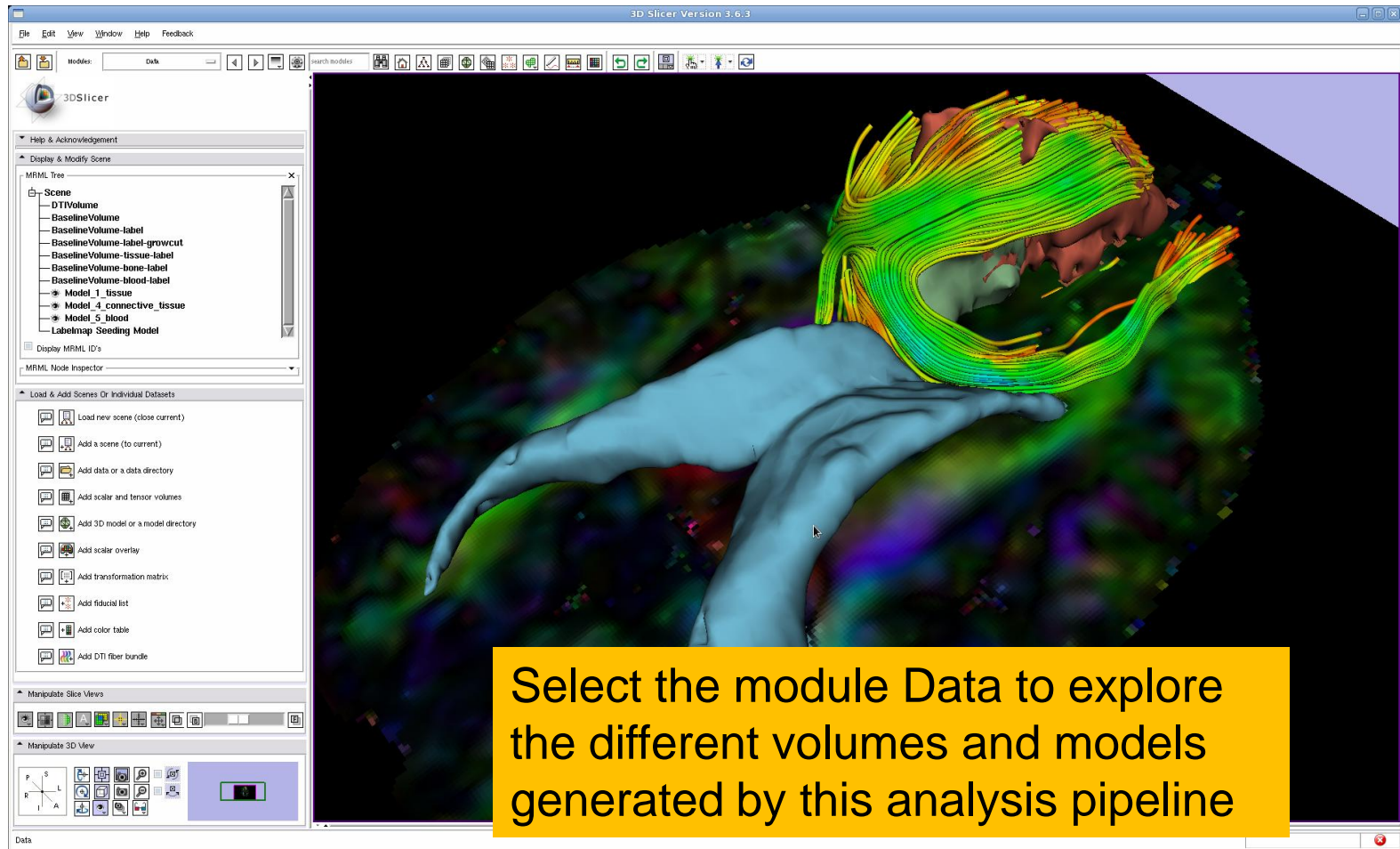
# Tractography Results



# Tractography Results

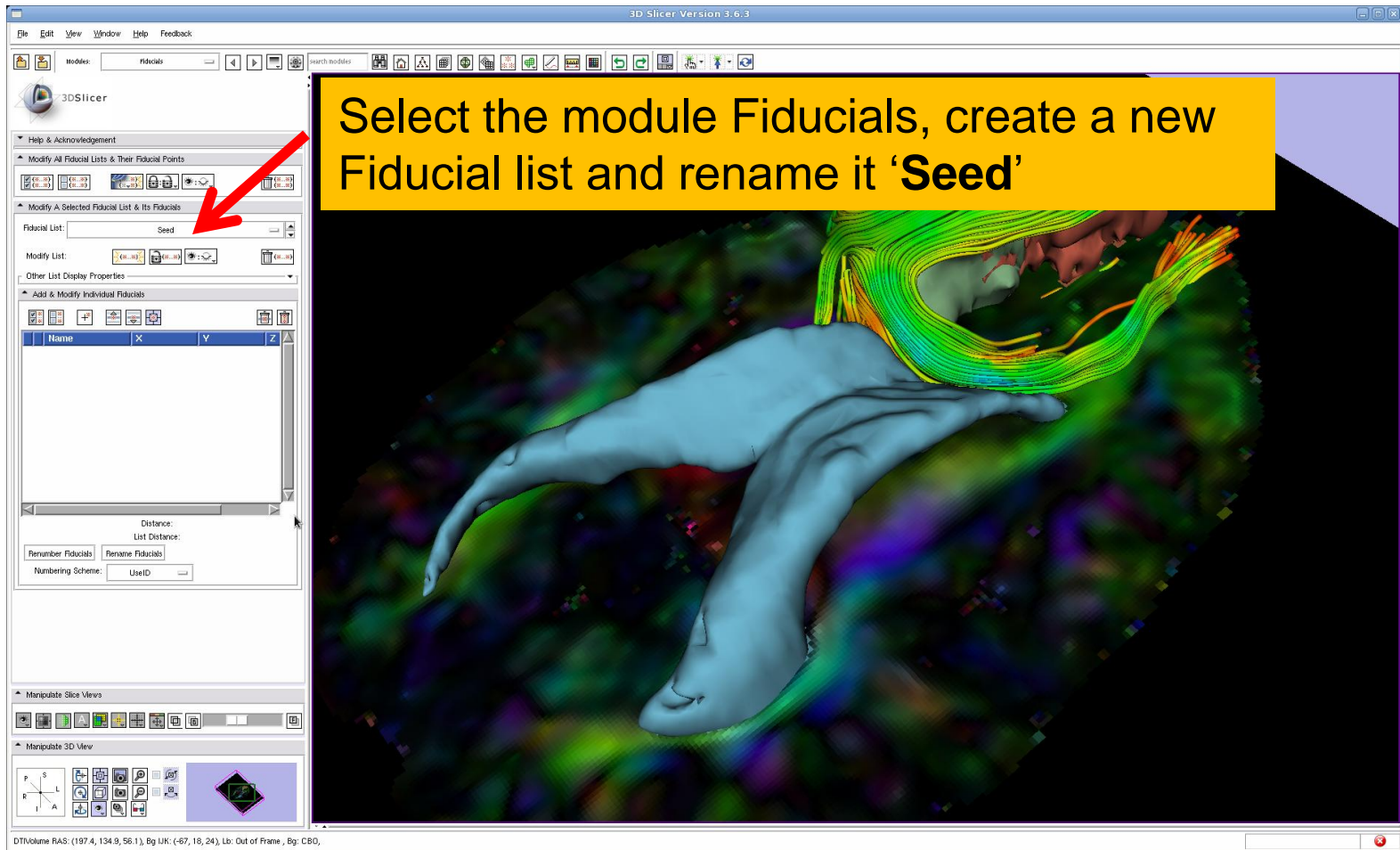


# Tractography Results



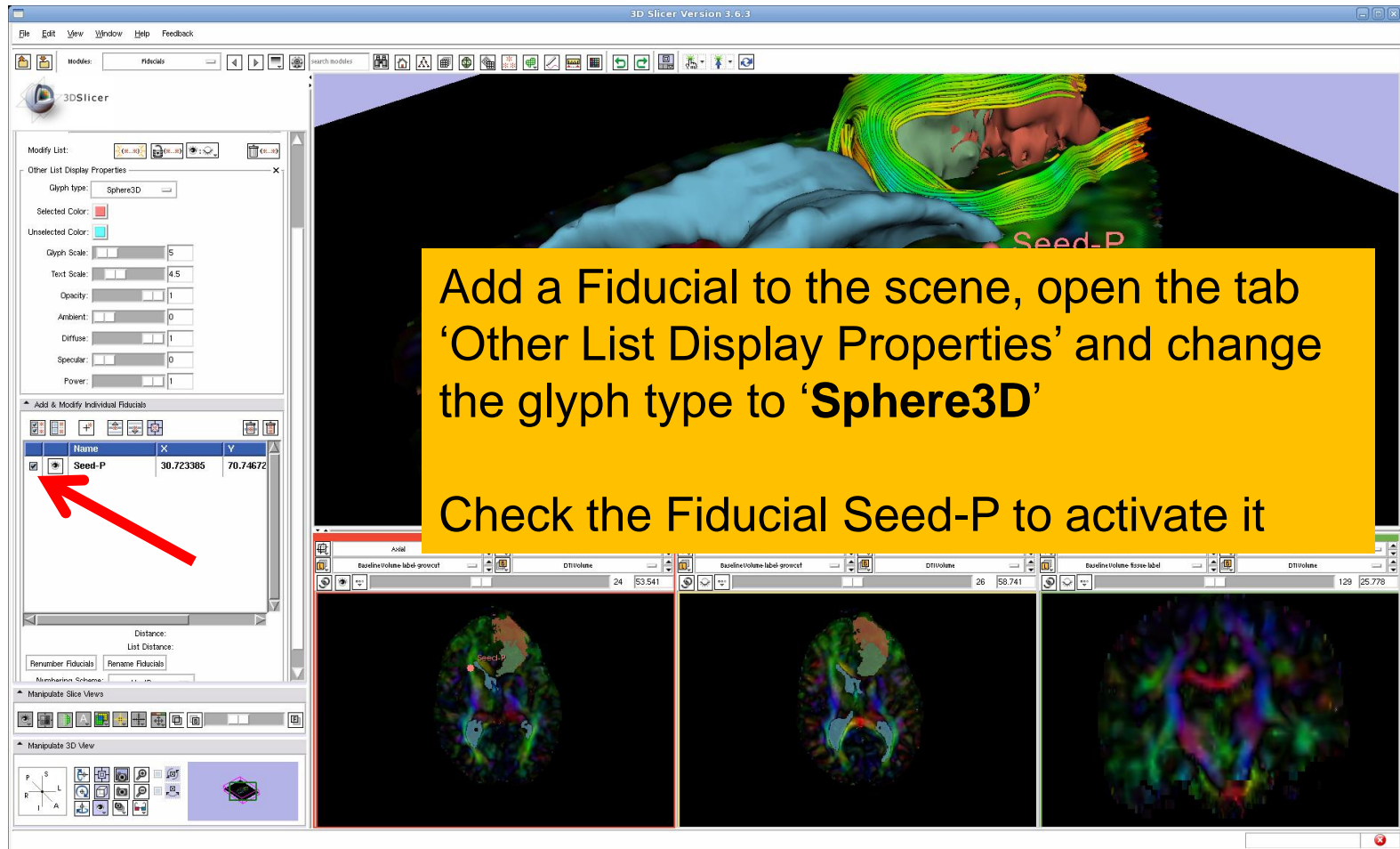
# Part 3: Tractography exploration of the contralateral side

# Tractography on-the-fly





# Fiducial Seeding



The screenshot shows the 3D Slicer interface with a brain scan. A yellow text box is overlaid on the main 3D view, providing instructions on how to activate a fiducial. The 'Add & Modify Individual Fiducials' panel is visible on the left, with a red arrow pointing to the 'Seed-P' entry in the table. The table has columns for Name, X, and Y. Below the table are buttons for 'Renumber Fiducials' and 'Rename Fiducials'. The bottom of the interface shows three orthogonal views of the brain scan.

3D Slicer Version 3.6.3

File Edit View Window Help Feedback

Models: Fiducials

3DSlicer

Modify List: [List of fiducials]

Other List Display Properties

Glyph type: Sphere3D

Selected Color: [Red]

Unselected Color: [Cyan]

Glyph Scale: 5

Text Scale: 45

Opacity: 1

Ambient: 0

Diffuse: 1

Specular: 0

Power: 1

Add & Modify Individual Fiducials

	Name	X	Y
<input checked="" type="checkbox"/>	Seed-P	30.723385	70.74672

Distance: [Field]

List Distance: [Field]

Renumber Fiducials

Rename Fiducials

Manipulate Slice Views

Manipulate 3D View

BaselineVolume label-growcut DTIVolume 24 [53.541]

BaselineVolume label-growcut DTIVolume 26 [50.741]

BaselineVolume fssse label DTIVolume 129 [25.778]

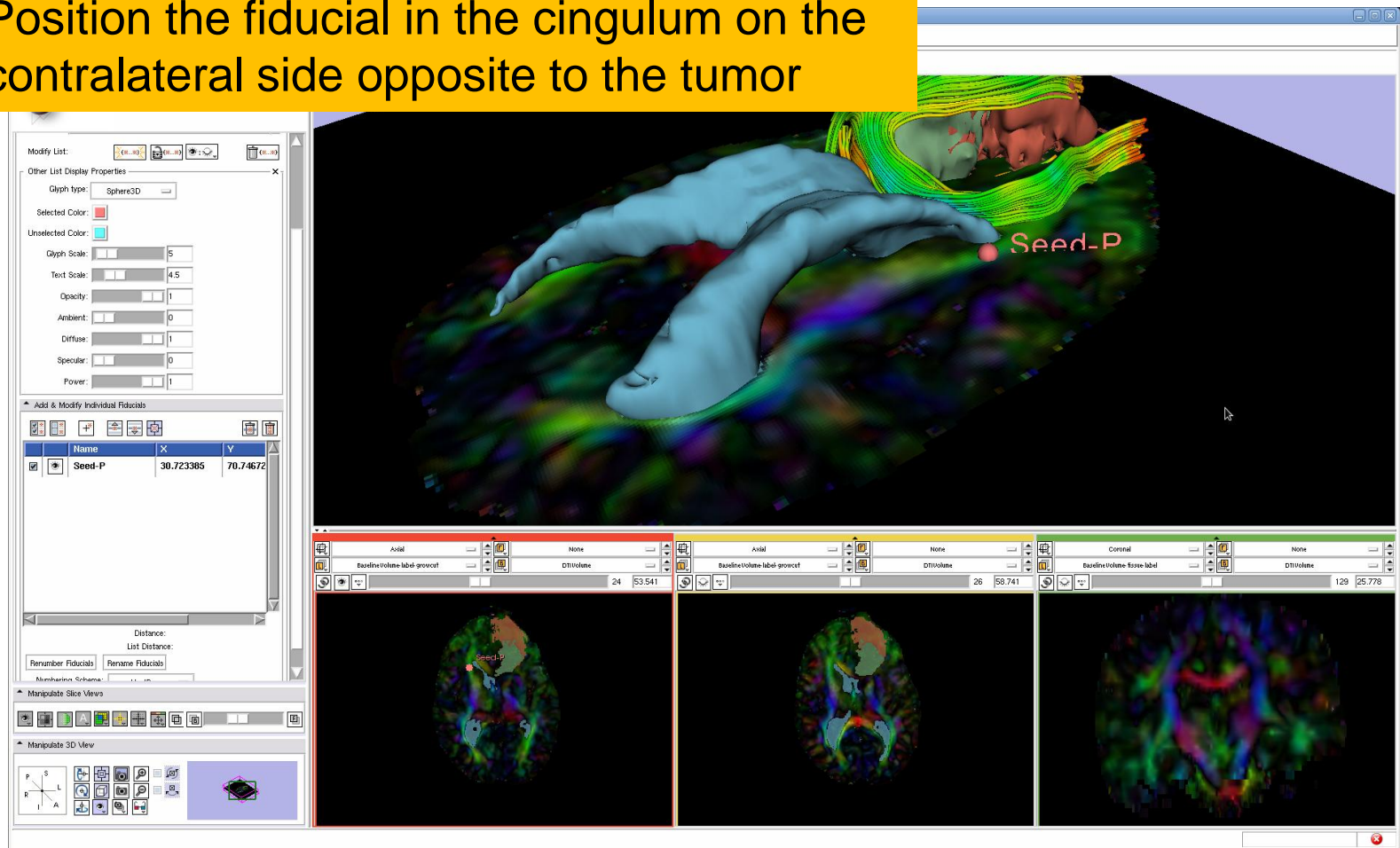
Seed-P

Add a Fiducial to the scene, open the tab 'Other List Display Properties' and change the glyph type to 'Sphere3D'

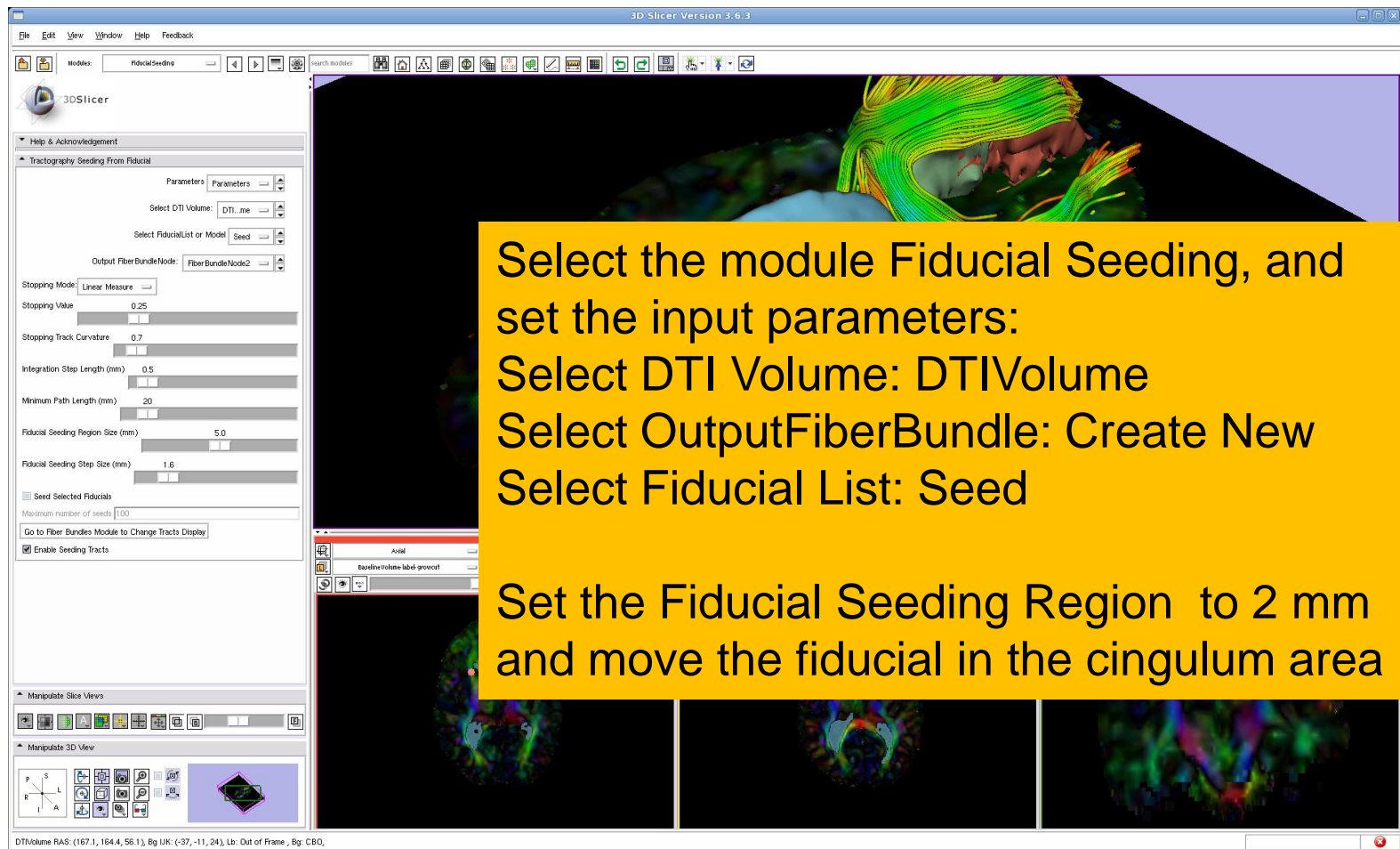
Check the Fiducial Seed-P to activate it

# Fiducial Seeding

Position the fiducial in the cingulum on the contralateral side opposite to the tumor



# Tractography on-the-fly



The screenshot displays the 3D Slicer Version 3.6.3 interface. The main window shows a 3D brain model with green and yellow fiber tracts. The left sidebar contains the 'Fiducial Seeding' module parameters. A yellow text box is overlaid on the right side of the interface, providing instructions for setting up the module.

**Select the module Fiducial Seeding, and set the input parameters:**  
Select DTI Volume: DTIVolume  
Select OutputFiberBundle: Create New  
Select Fiducial List: Seed

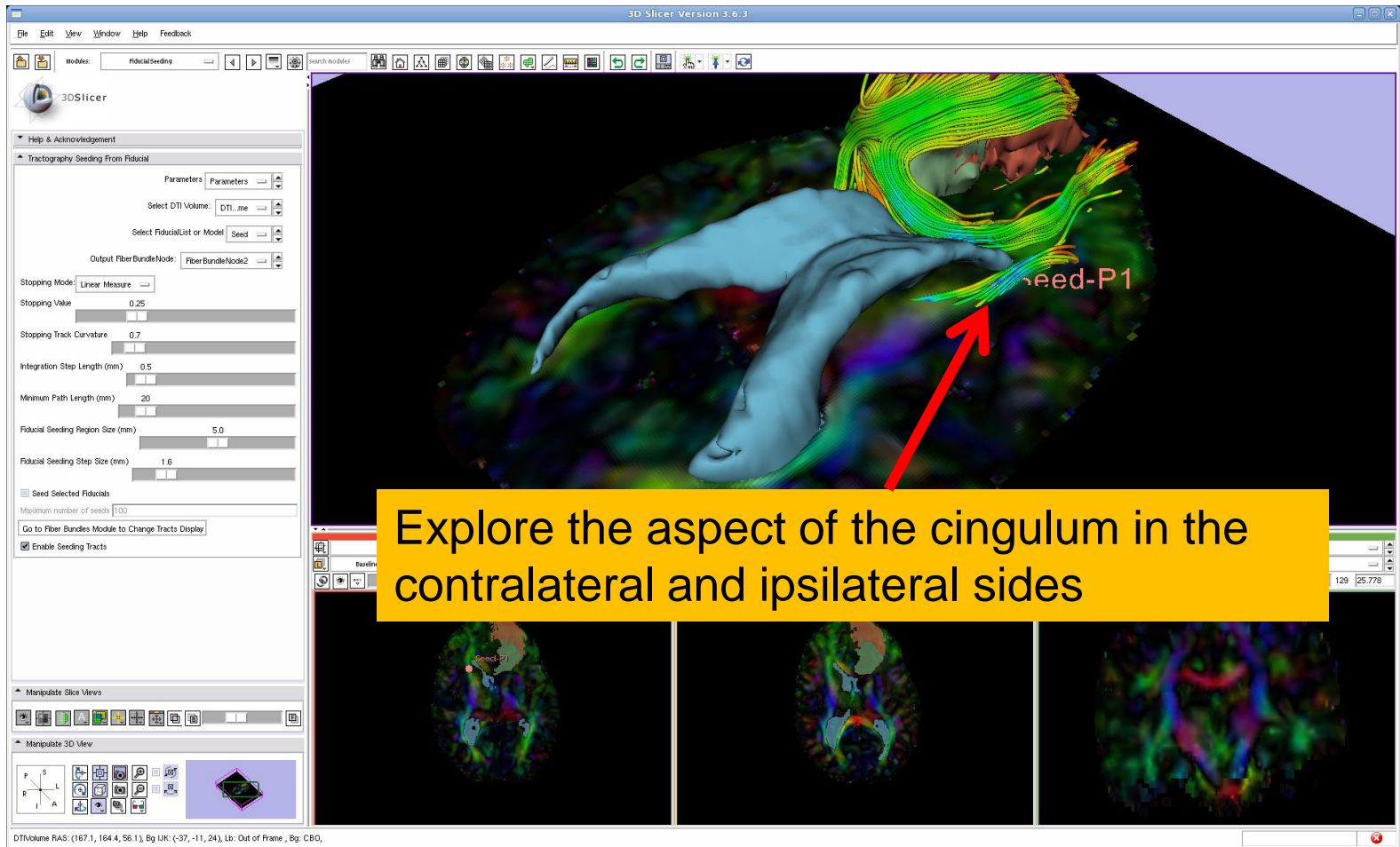
**Set the Fiducial Seeding Region to 2 mm and move the fiducial in the cingulum area**

The 'Fiducial Seeding' module parameters are as follows:

- Parameters: Parameters
- Select DTI Volume: DTI...me
- Select FiducialList or Model: Seed
- Output FiberBundleNode: FiberBundleNode2
- Stopping Mode: Linear Measure
- Stopping Value: 0.25
- Stopping Track Curvature: 0.7
- Integration Step Length (mm): 0.5
- Minimum Path Length (mm): 20
- Fiducial Seeding Region Size (mm): 5.0
- Fiducial Seeding Step Size (mm): 1.6
- Seed Selected Fiducials
- Maximum number of seeds: 100
- 
- Enable Seeding Tracts

The bottom of the interface shows three viewports: a 3D view, a sagittal slice view, and an axial slice view. The status bar at the bottom indicates: DTIVolume RAS: (167.1, 164.4, 56.1), By IJK: (-37, -11, 24), Lb: Out of Frame , Bg: C80.

# Tractography on-the-fly



# Conclusion

- Fully integrated pipeline for semi-automated tumor segmentation and white matter tract reconstruction
- 3D interactive exploration of the white matter tracts surrounding a tumor (peri-tumoral tracts) for neurosurgical planning

# Acknowledgments



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