

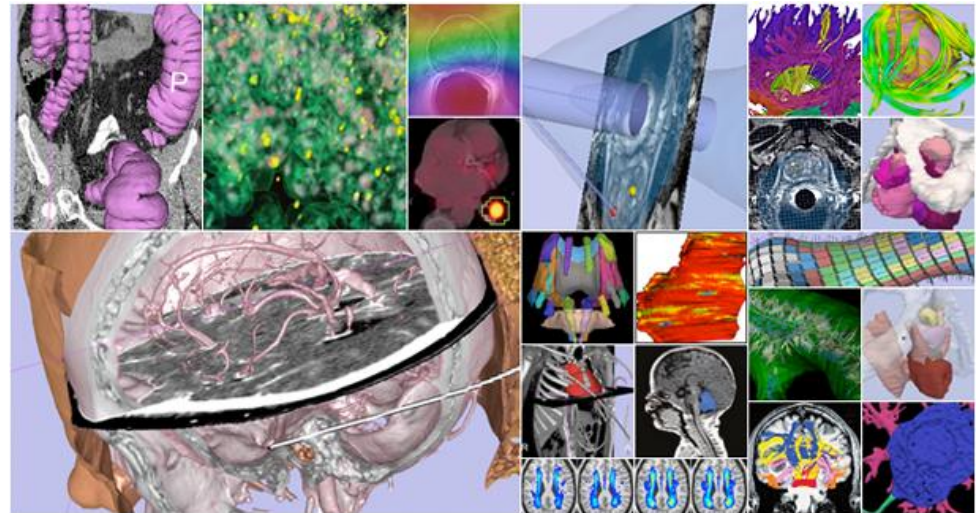
Exploring Peritumoral White Matter Fibers for Neurosurgical Planning

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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

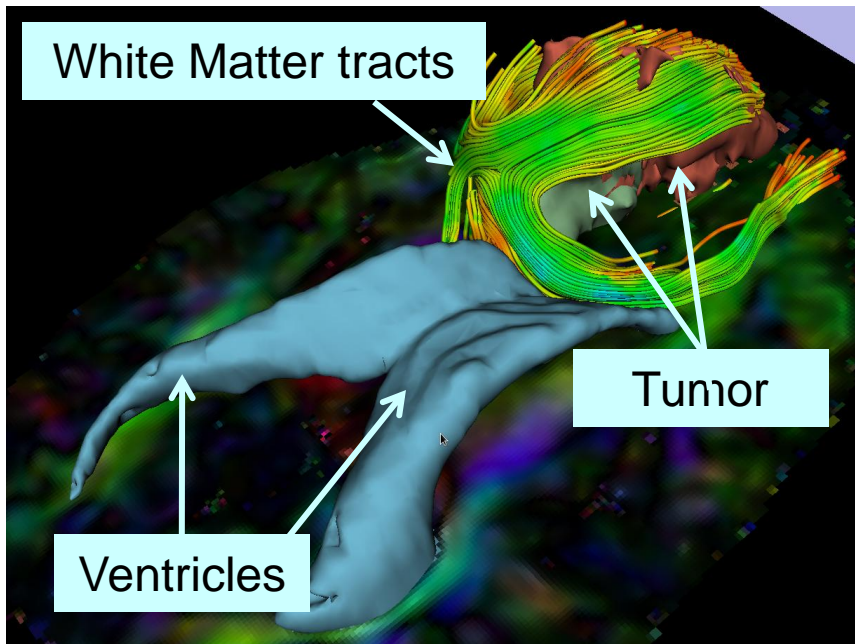
It is the responsibility of the user of 3DSlicer to comply with both the terms of the license and with the applicable laws, regulations and rules.

Pre-Requisite

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

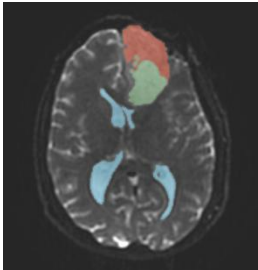
http://www.slicer.org/slicerWiki/index.php/Slicer3.6:Training#Software_tutorials

Clinical Goal

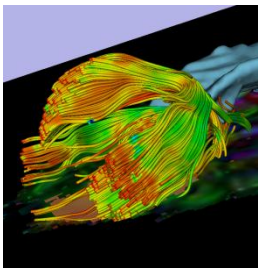


The goal of this tutorial is to explore white matter fibers surrounding a tumor using Diffusion Tensor Imaging (DTI) Tractography

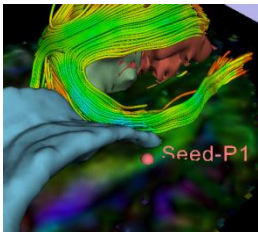
Overview of the analysis pipeline



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



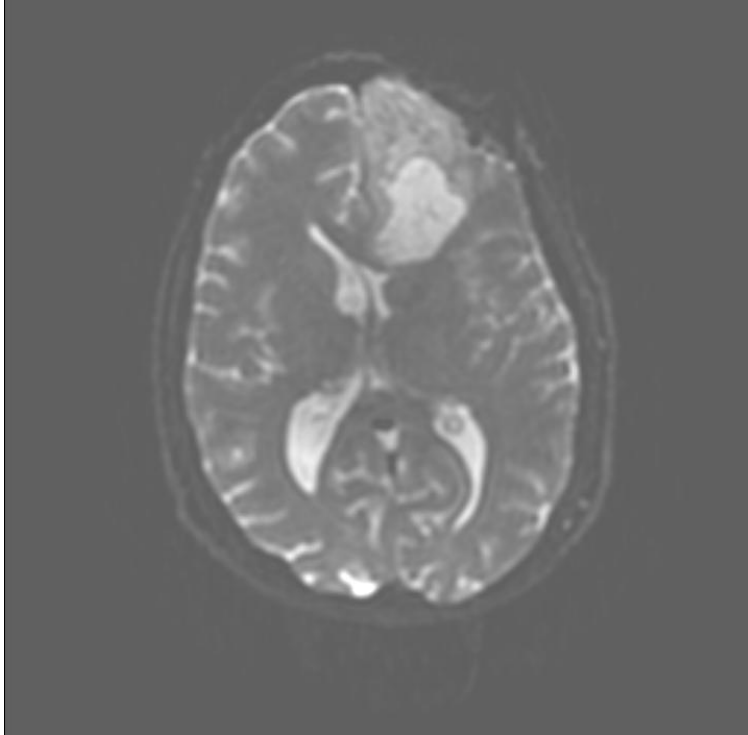
Part 2: Tractography reconstruction of the white matter fibers in the peritumoral volume



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

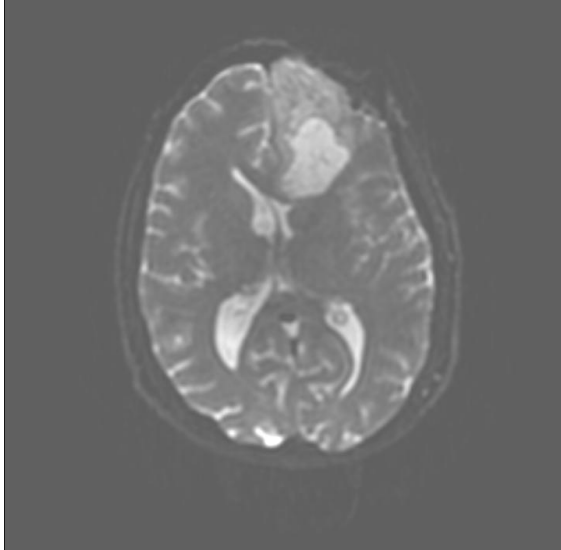
Part 1: Diffusion Data Loading and Visualization

Clinical Case



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

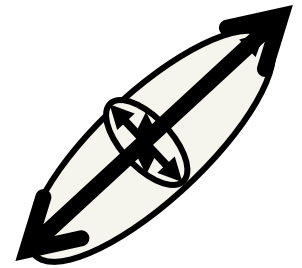
Diffusion Tensor Imaging



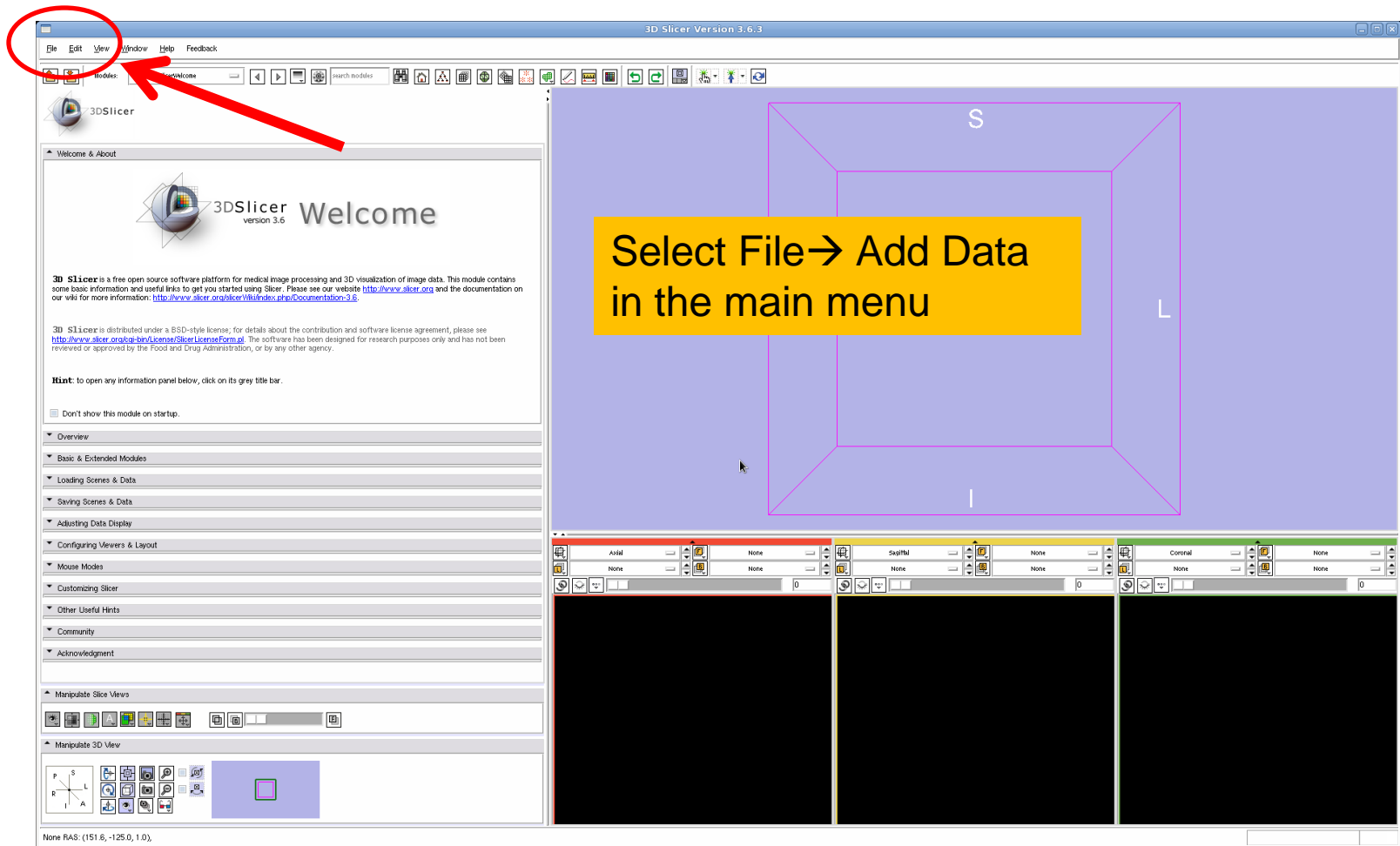
$$S_i = S_0 e^{-b \hat{u}^T \underline{D} \hat{u}}$$

(Stejskal and Tanner 1965, Basser 1994)

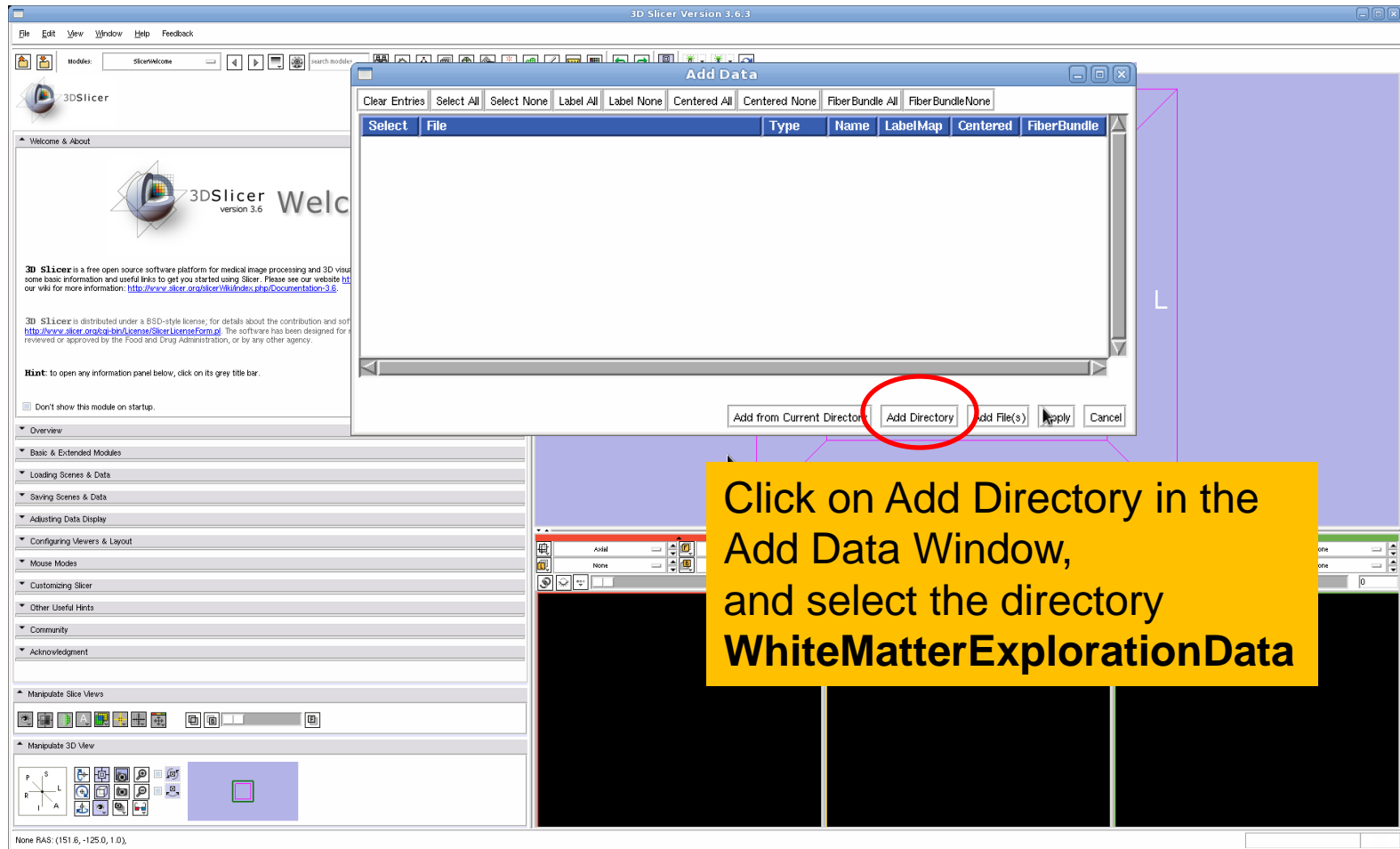
$$\underline{D} = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{bmatrix}$$



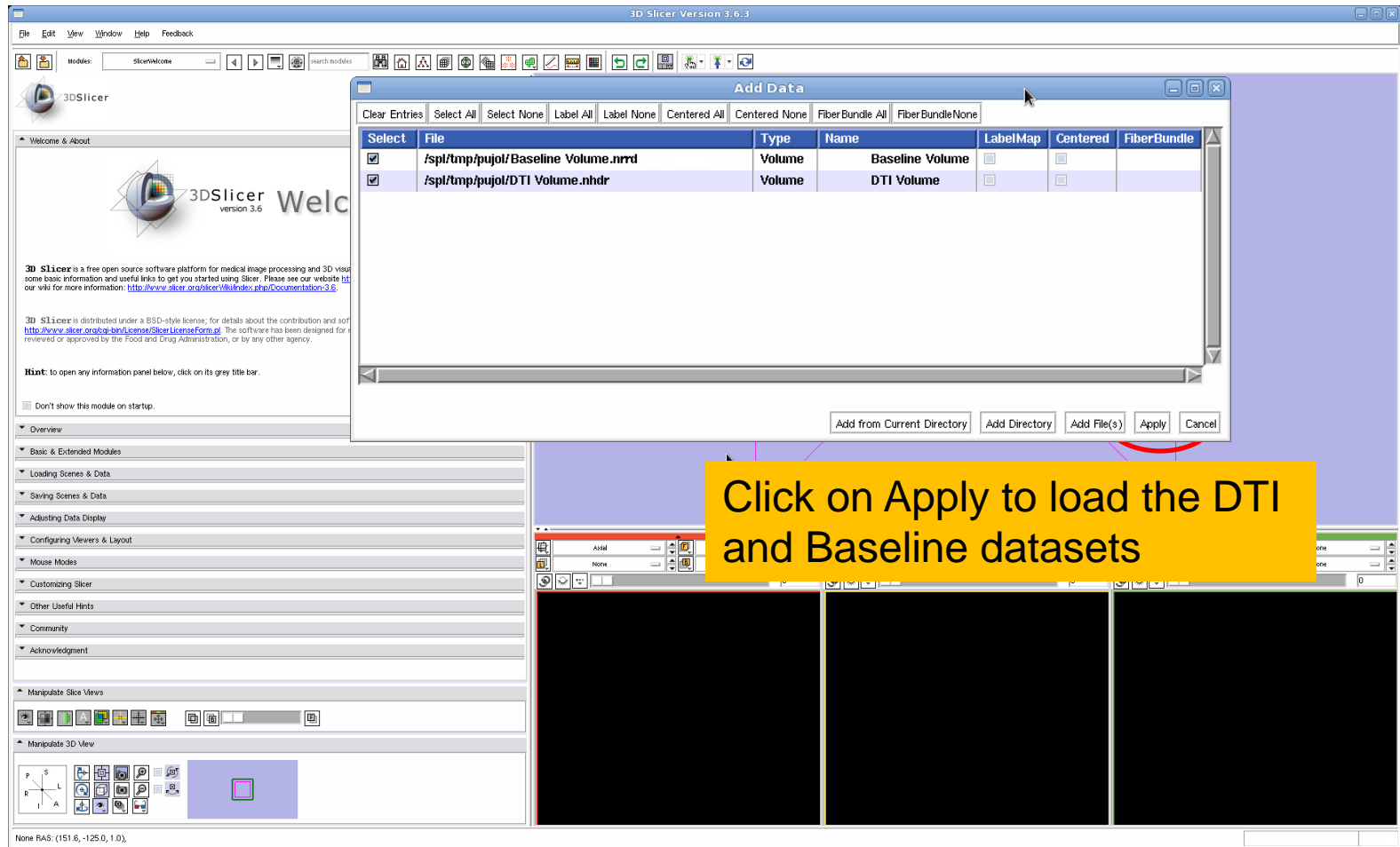
Loading DTI and Baseline Data




Loading DTI and Baseline Data



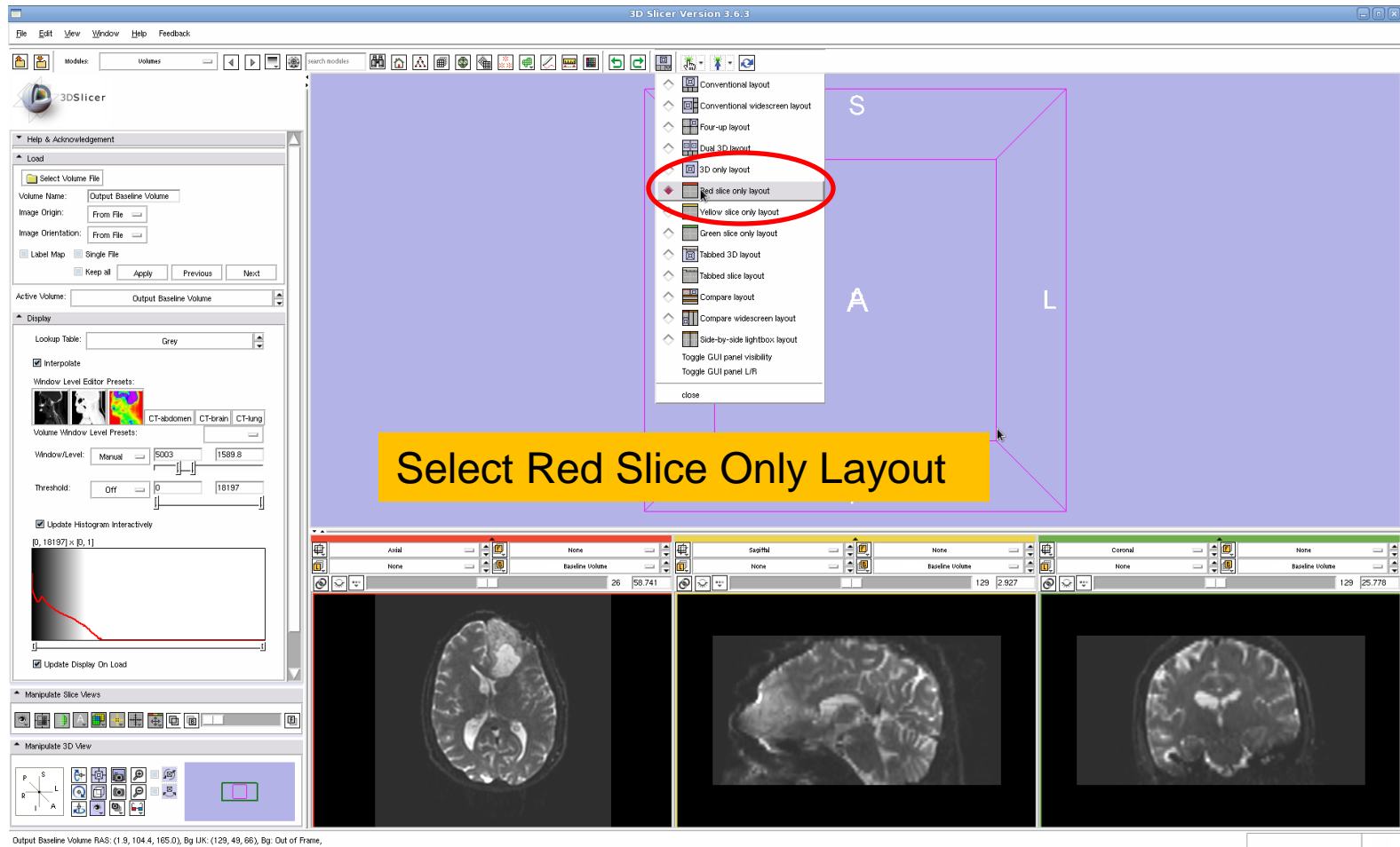
Loading DTI and Baseline Data



Loading DTI and Baseline Data

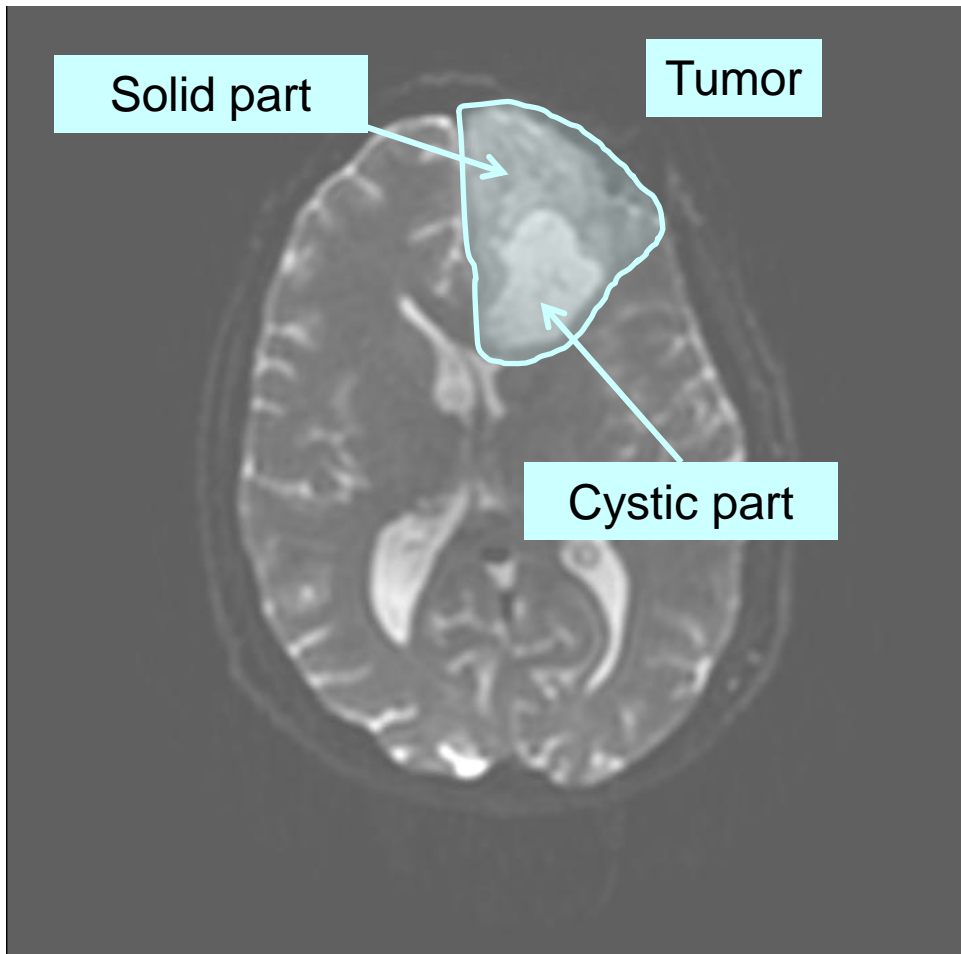
The screenshot displays the 3D Slicer Version 3.6.3 interface. The 'Volumes' module is selected in the top toolbar and circled in red. The 'Load' panel on the left shows 'Output Baseline Volume' as the active volume. The 'Display' panel shows the 'Window/Level' set to 'Manual' with a value of 5003, and a red arrow points to this value. The 'Manipulate Slice Views' panel at the bottom shows three anatomical views (Axial, Sagittal, Coronal) with a link icon circled in red. 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

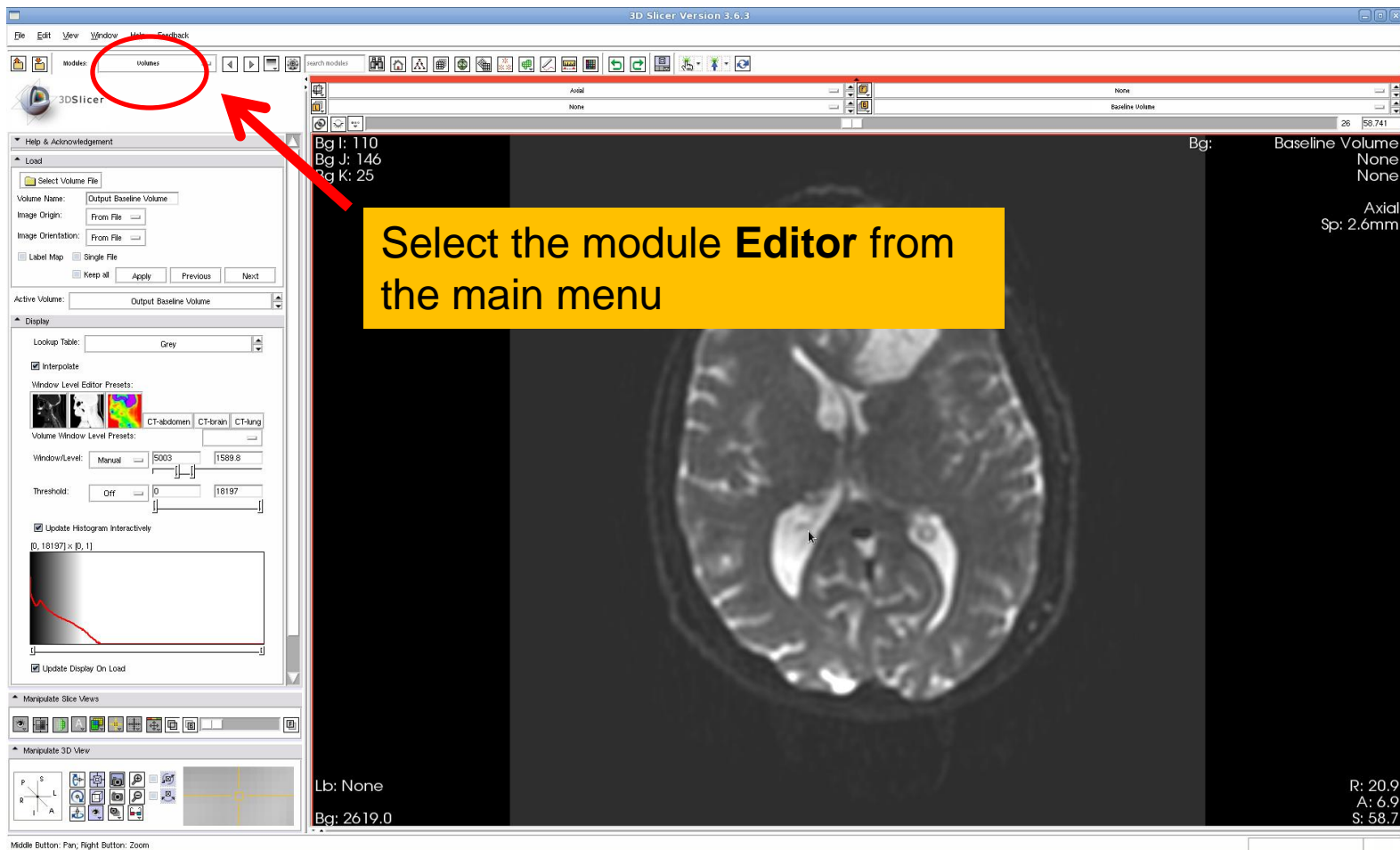
Tumor Segmentation



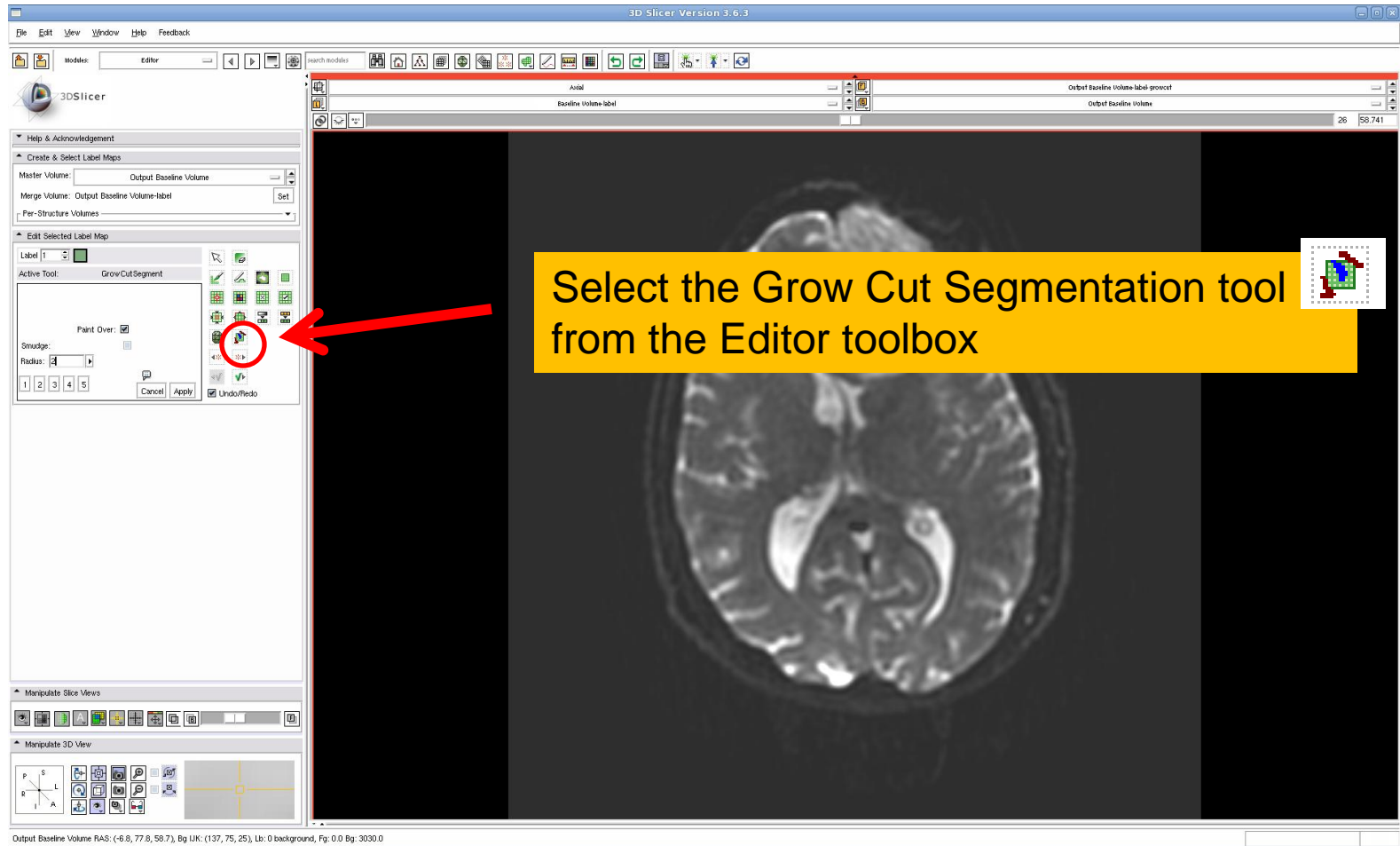
The tumor in this clinical case is composed of two parts: a solid part and a cystic part.

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

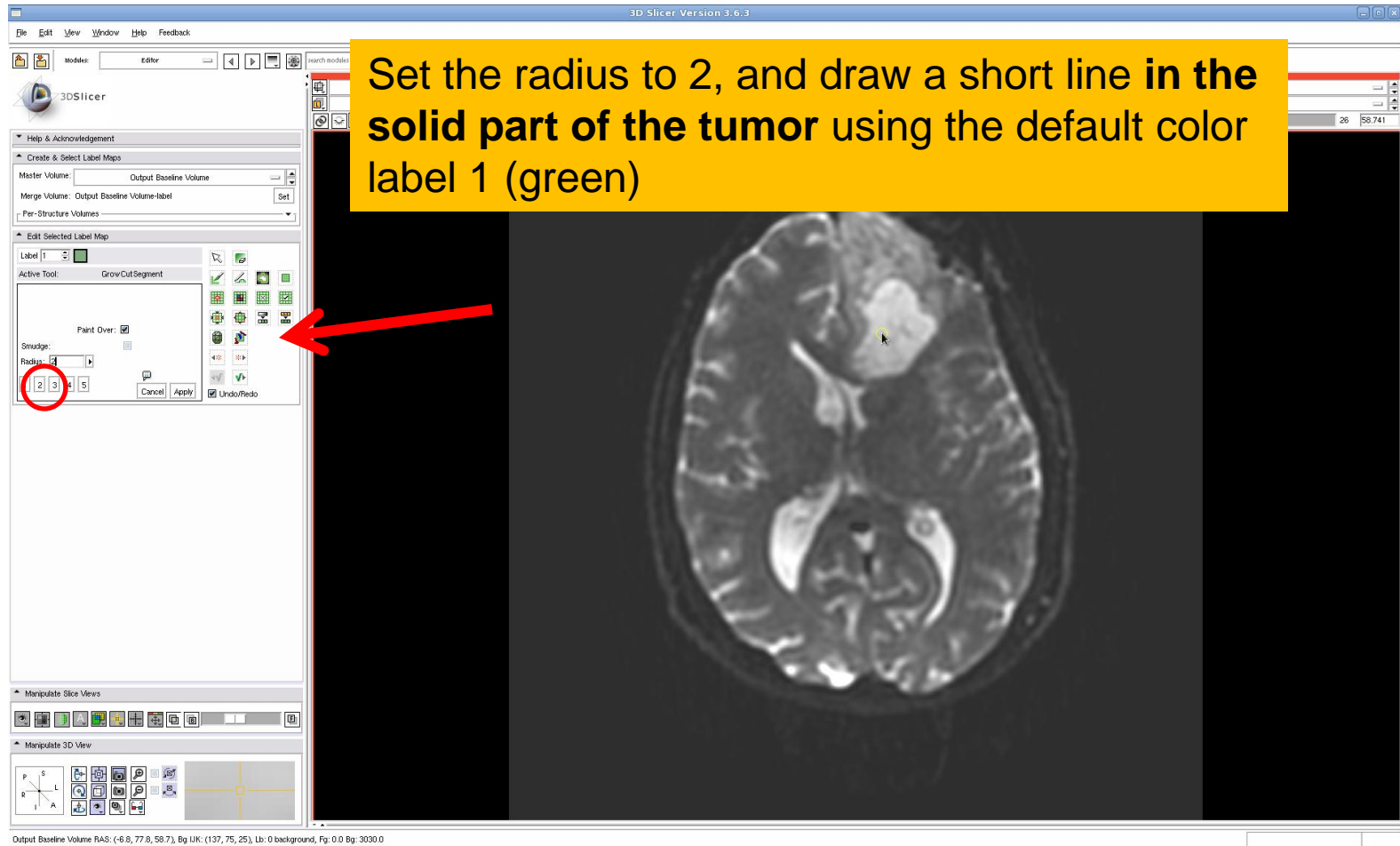
The **Grow Cut Segmentation module** is a competitive region growing algorithm using cellular automata.

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

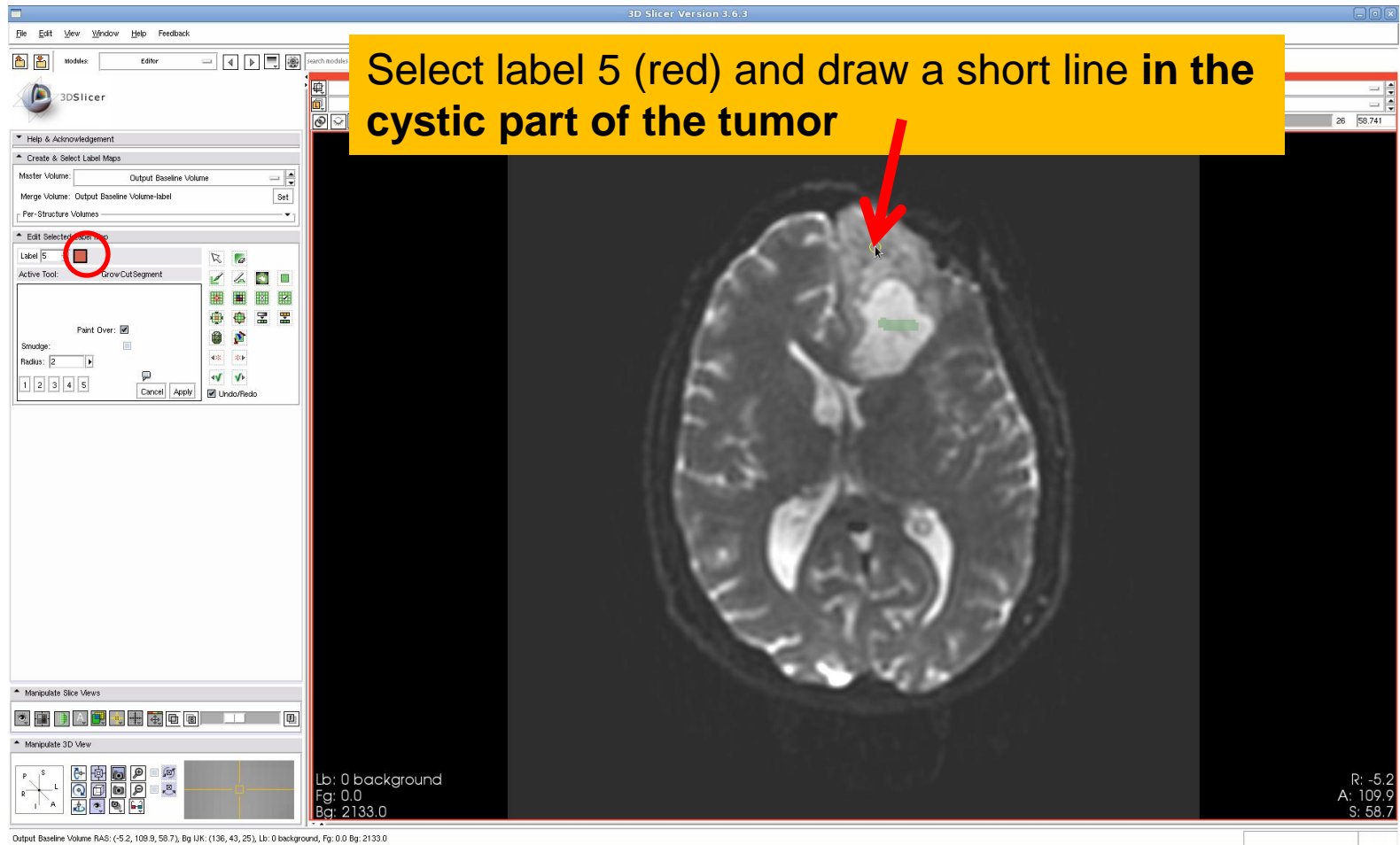
For N-class segmentation, the algorithm requires a set of scribbles corresponding the N classes, and a scribble for the other classes.



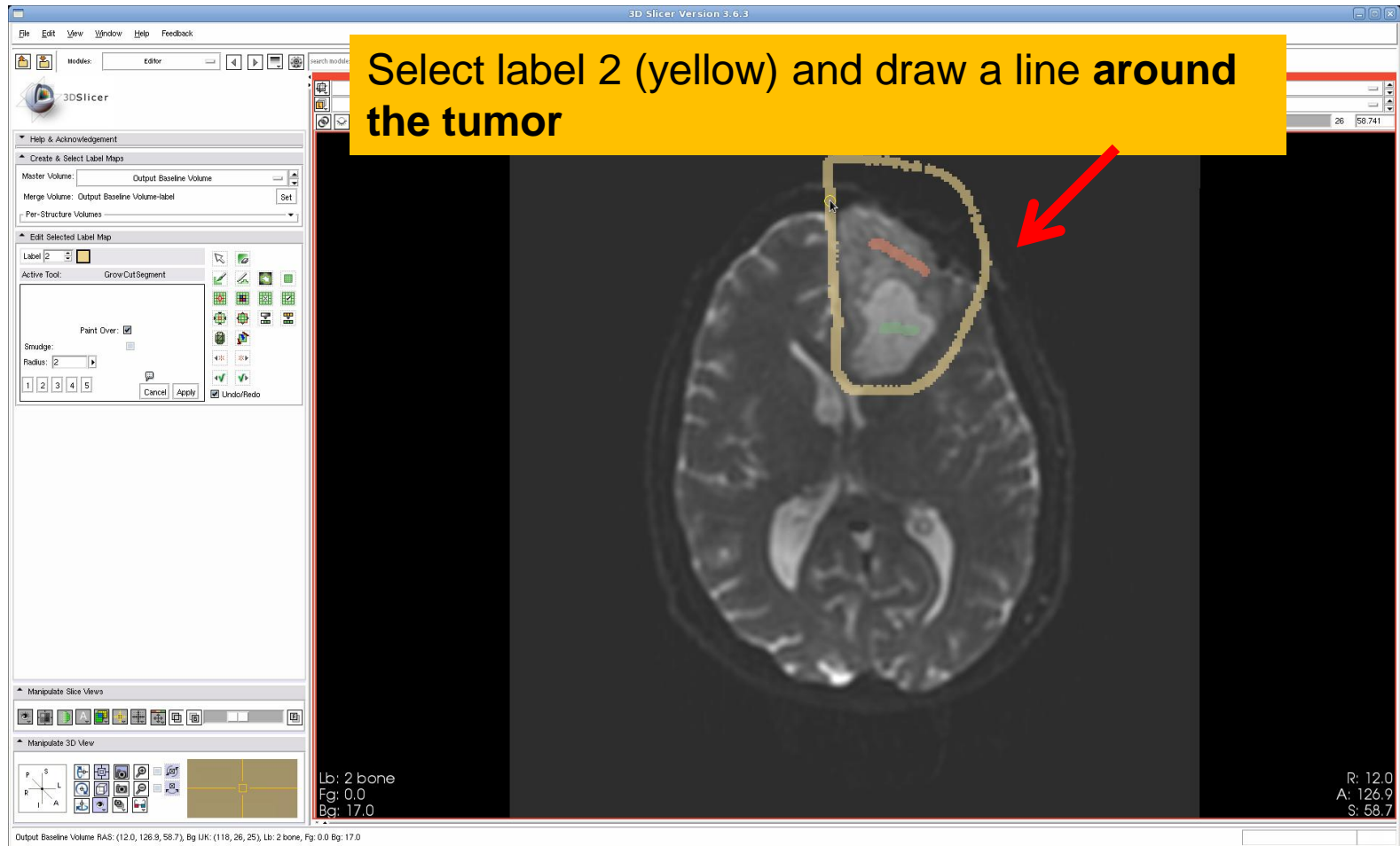
Tumor Segmentation



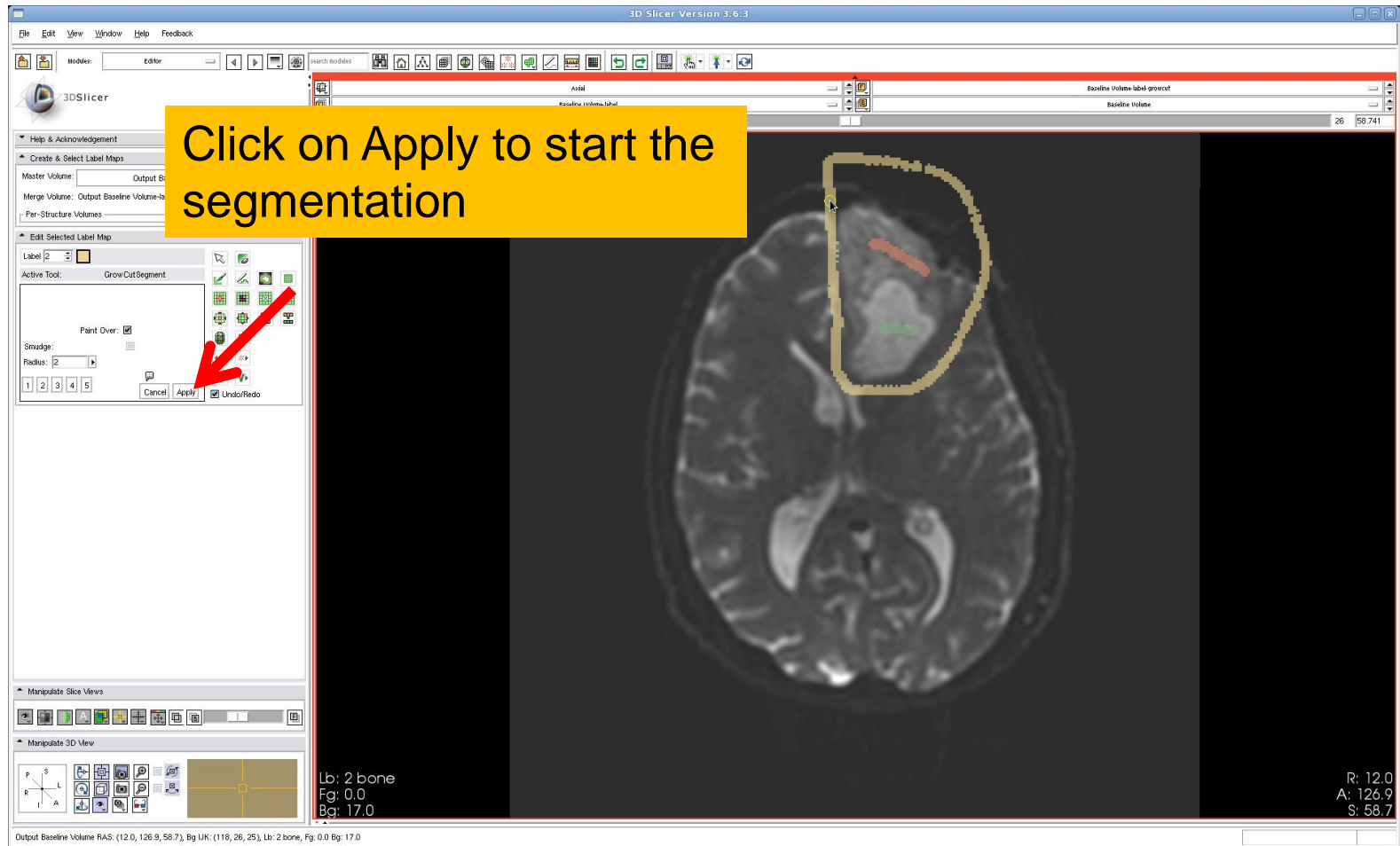
Tumor Segmentation



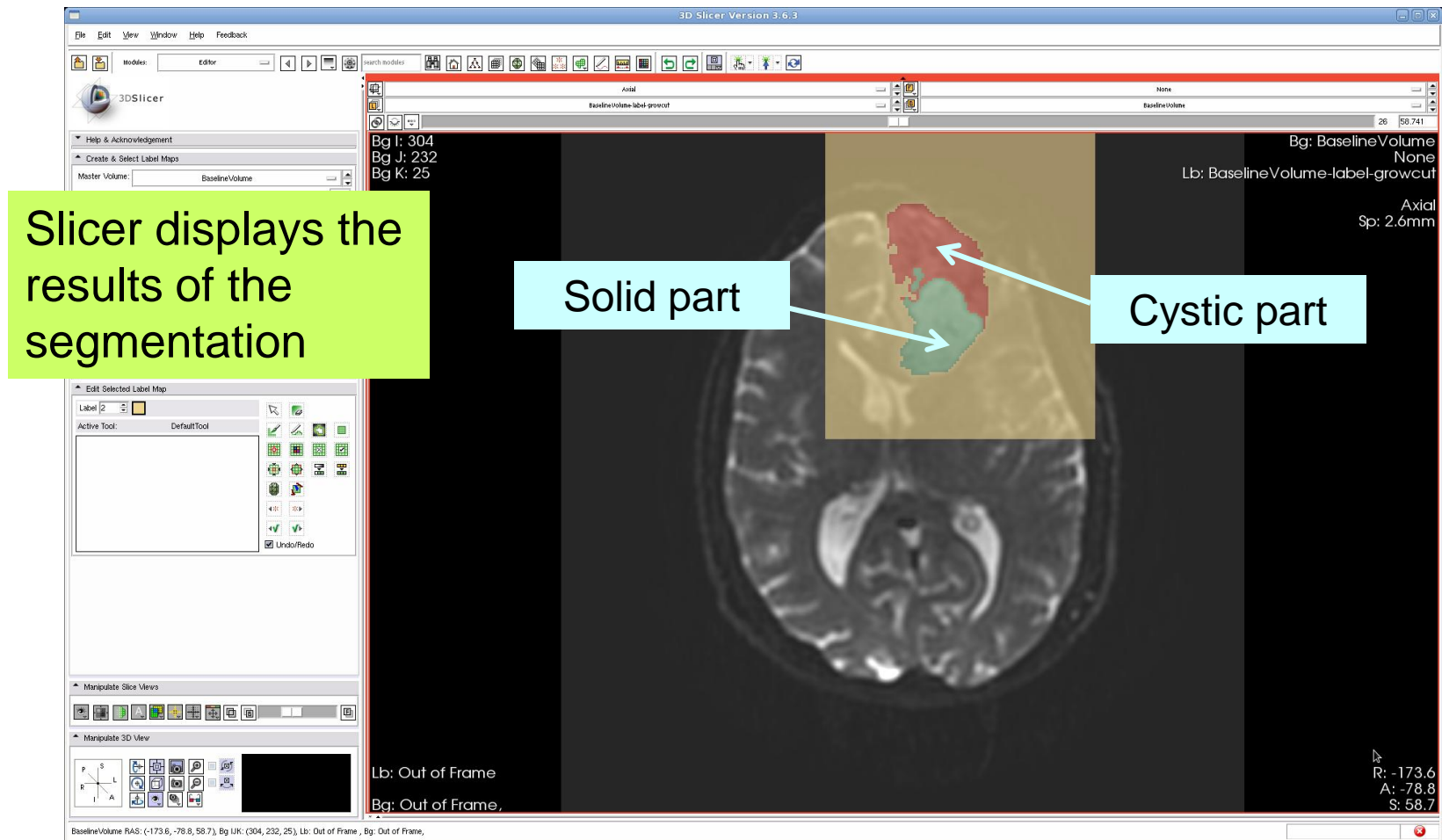
Tumor Segmentation



Tumor Segmentation



Tumor Segmentation

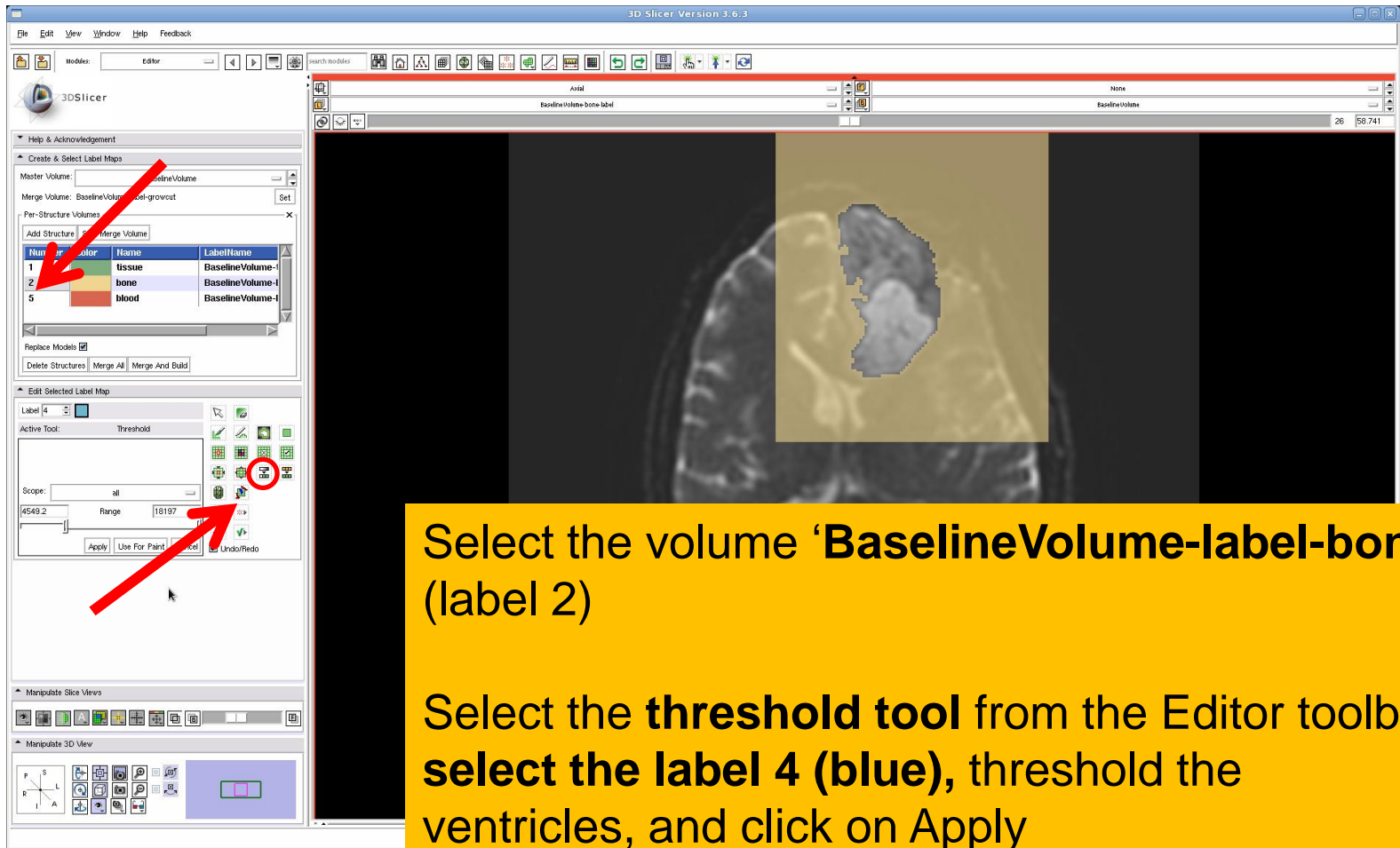


Tumor Segmentation

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

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

Ventricles Segmentation



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

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

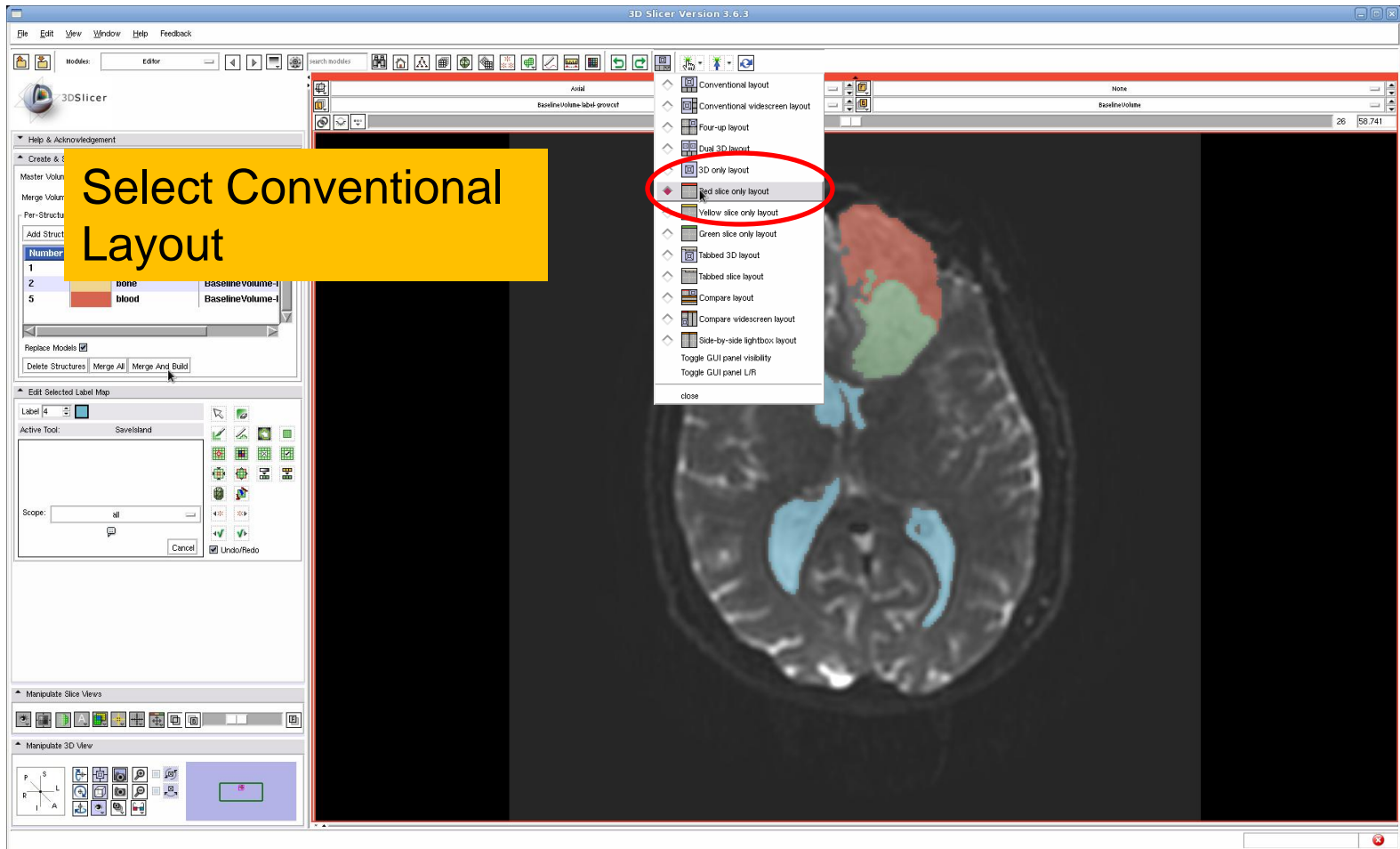
BaselineVolume RAS: (25.6, 7.0, 58.7), Bg UK: (105, 146, 25), Lb: 4 connective_tissue, Bg: 2443.0

Axis: Axial
Sp: 2.6mm

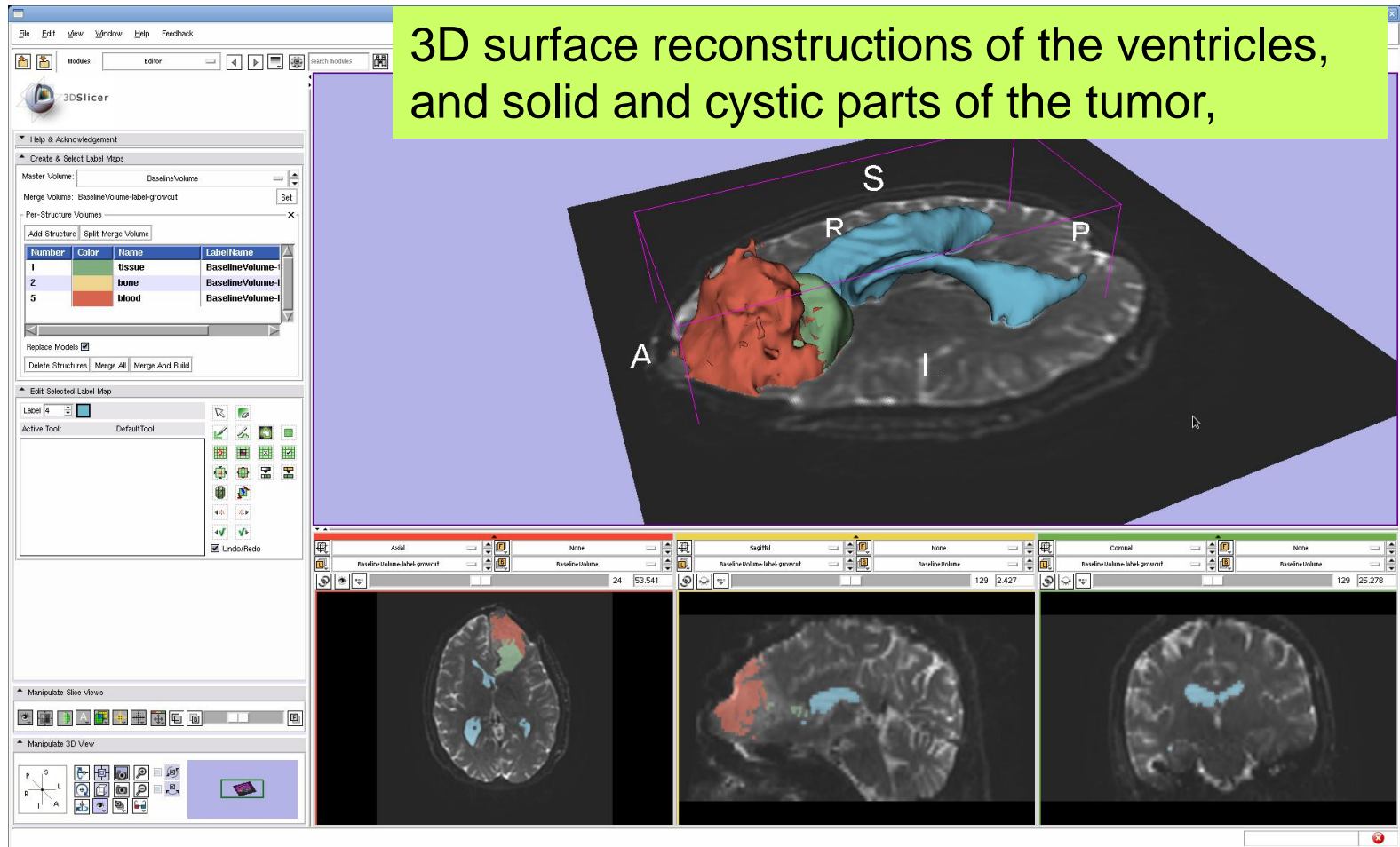
R: 25.6
A: 7.0
S: 58.7

Lb: 4 connective_tissue
Bg: 2443.0

Final Result of the Segmentation

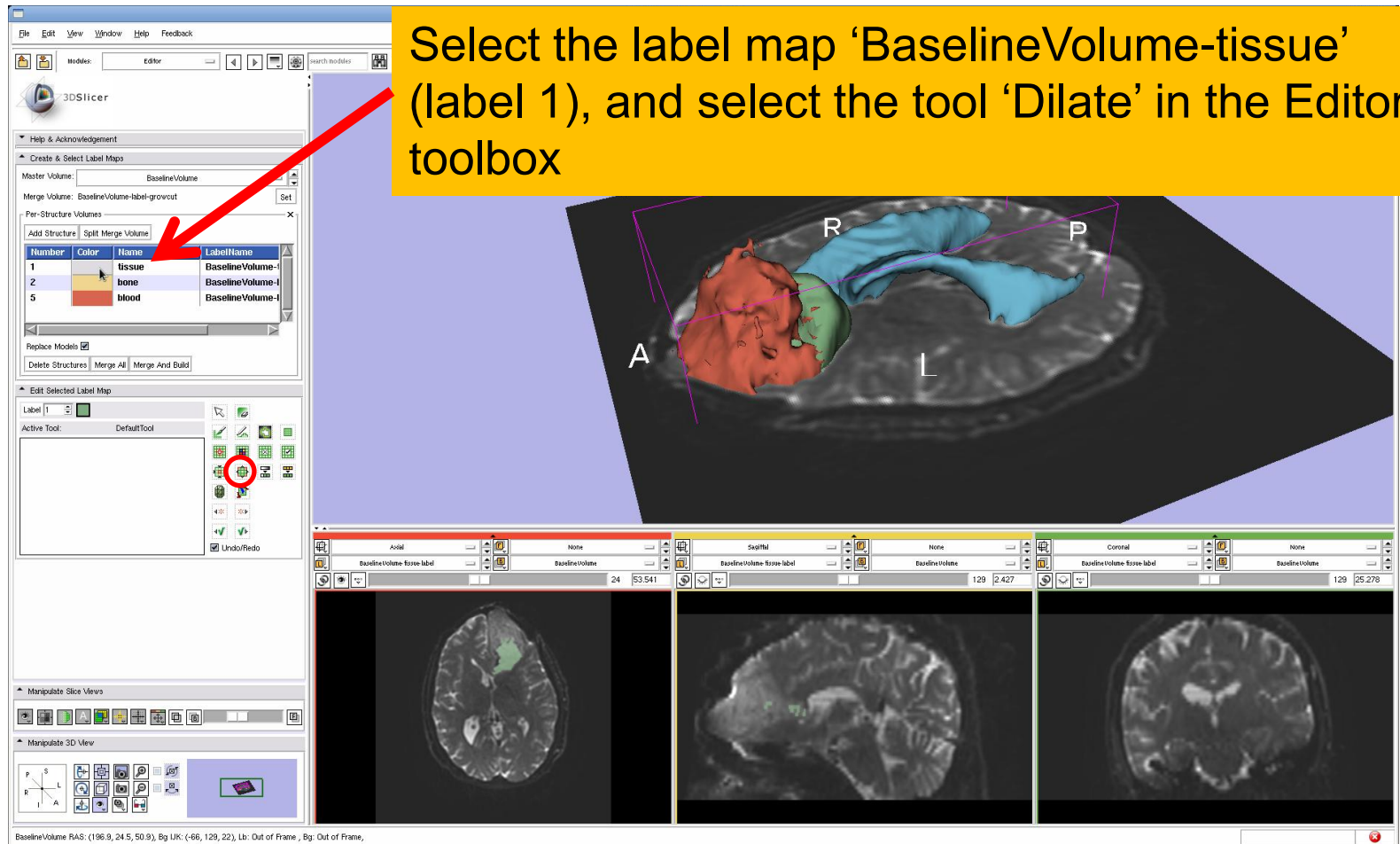


Final Result of the Segmentation



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.

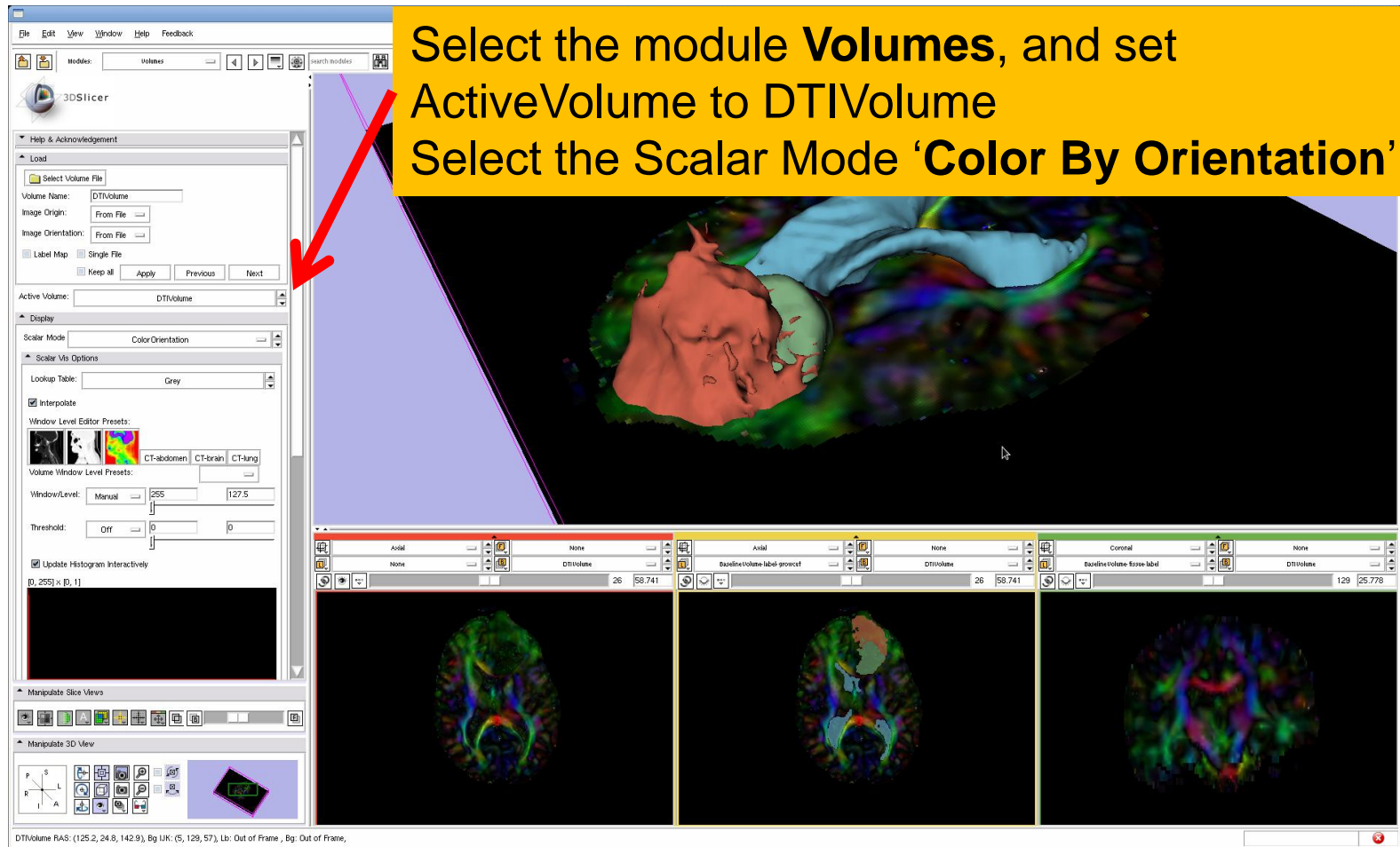
Definition of the peri-tumoral volume

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

The image shows the 3DSlicer interface. The main 3D view displays a brain model with a tumor (red) and surrounding tissue (blue). The tumor is labeled with 'S' (Superior), 'R' (Right), 'P' (Posterior), 'L' (Left), and 'A' (Anterior). The bottom panel shows three axial slices. The leftmost slice has a red arrow pointing to a green highlighted region, which is the peri-tumoral volume. The middle and right slices show the same region in different views. The interface includes a menu bar, a toolbar, and several panels for volume management and editing.

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

Visualization of the DTI Volume

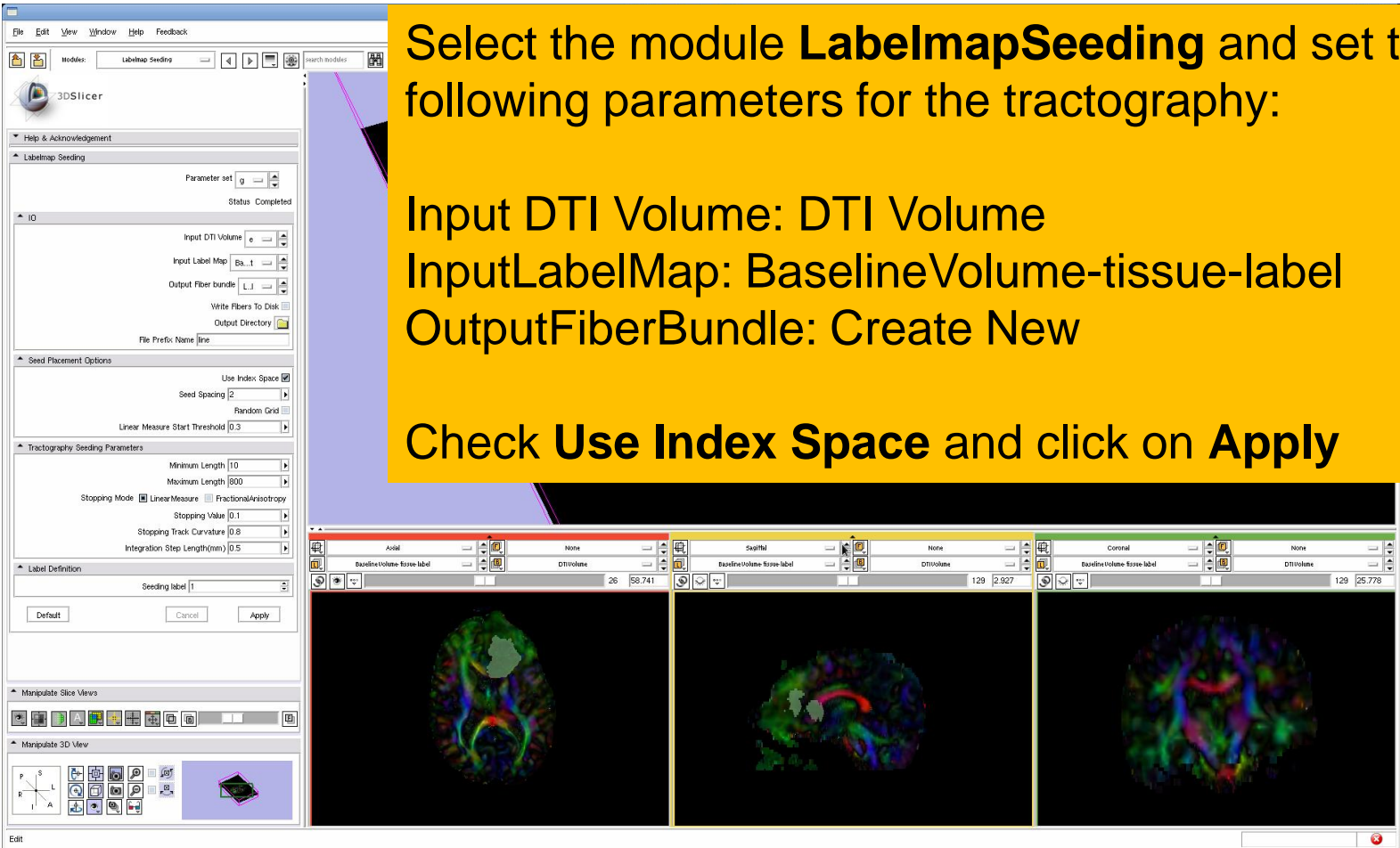


The screenshot displays the 3DSlicer interface. On the left, the 'Volumes' module is selected in the 'Modules' panel. The 'Active Volume' is set to 'DTIVolume'. In the 'Display' section, the 'Scalar Mode' is set to 'Color Orientation'. A yellow text box with a red arrow pointing to the 'Volumes' module contains the following instructions:

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

The main 3D view shows a brain slice with a red and white structure overlaid on a colorful DTI volume. Below the 3D view are three 2D slice views (Axial, Coronal, and Sagittal) showing the same data. The status bar at the bottom indicates 'DTIVolume RAS: (125.2, 24.8, 142.9), Bx LH: (S, 129, 57), Lb: Out of Frame, Bq: Out of Frame'.

Tractography Parameters

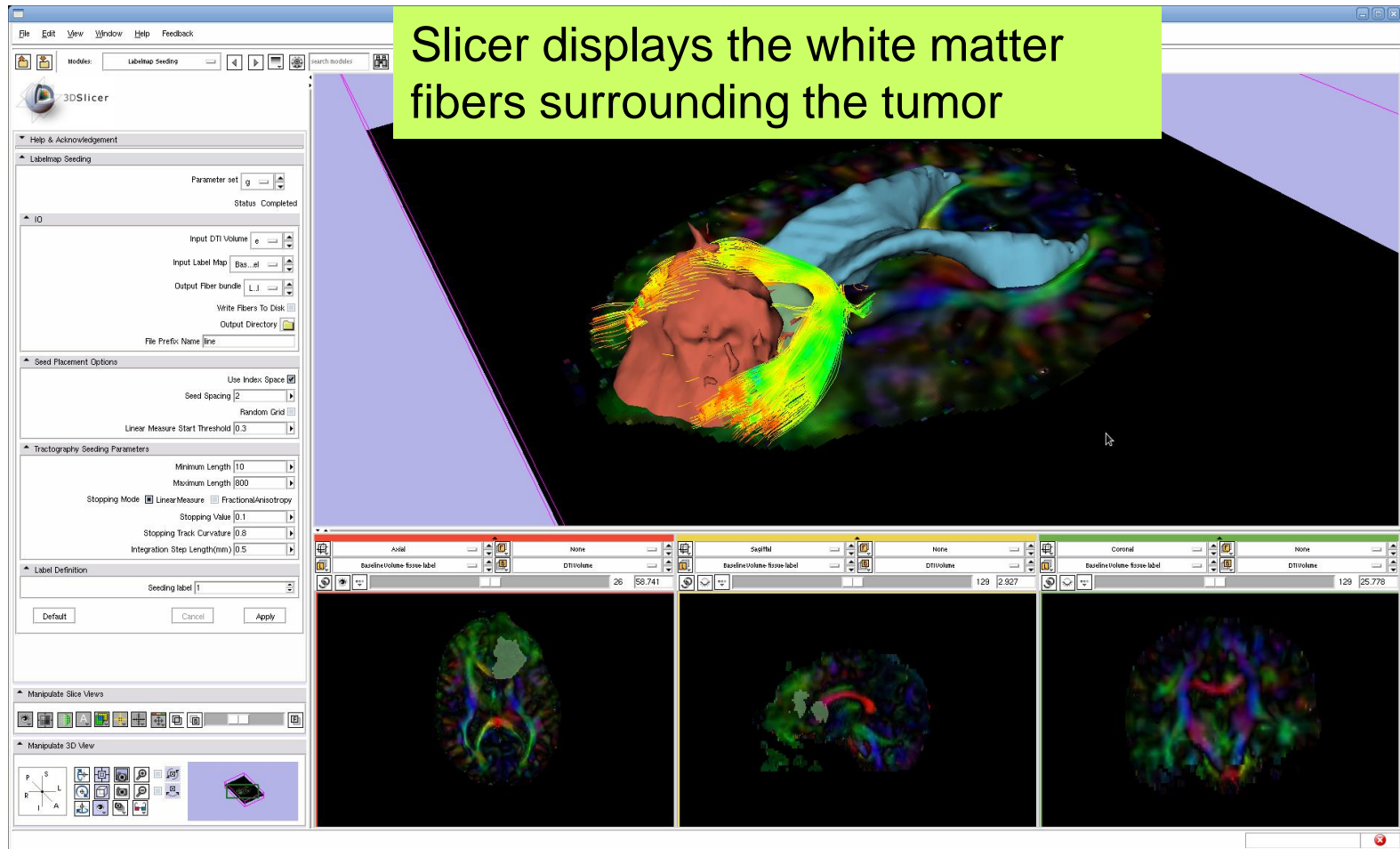


Select the module **LabelmapSeeding** and set the following parameters for the tractography:

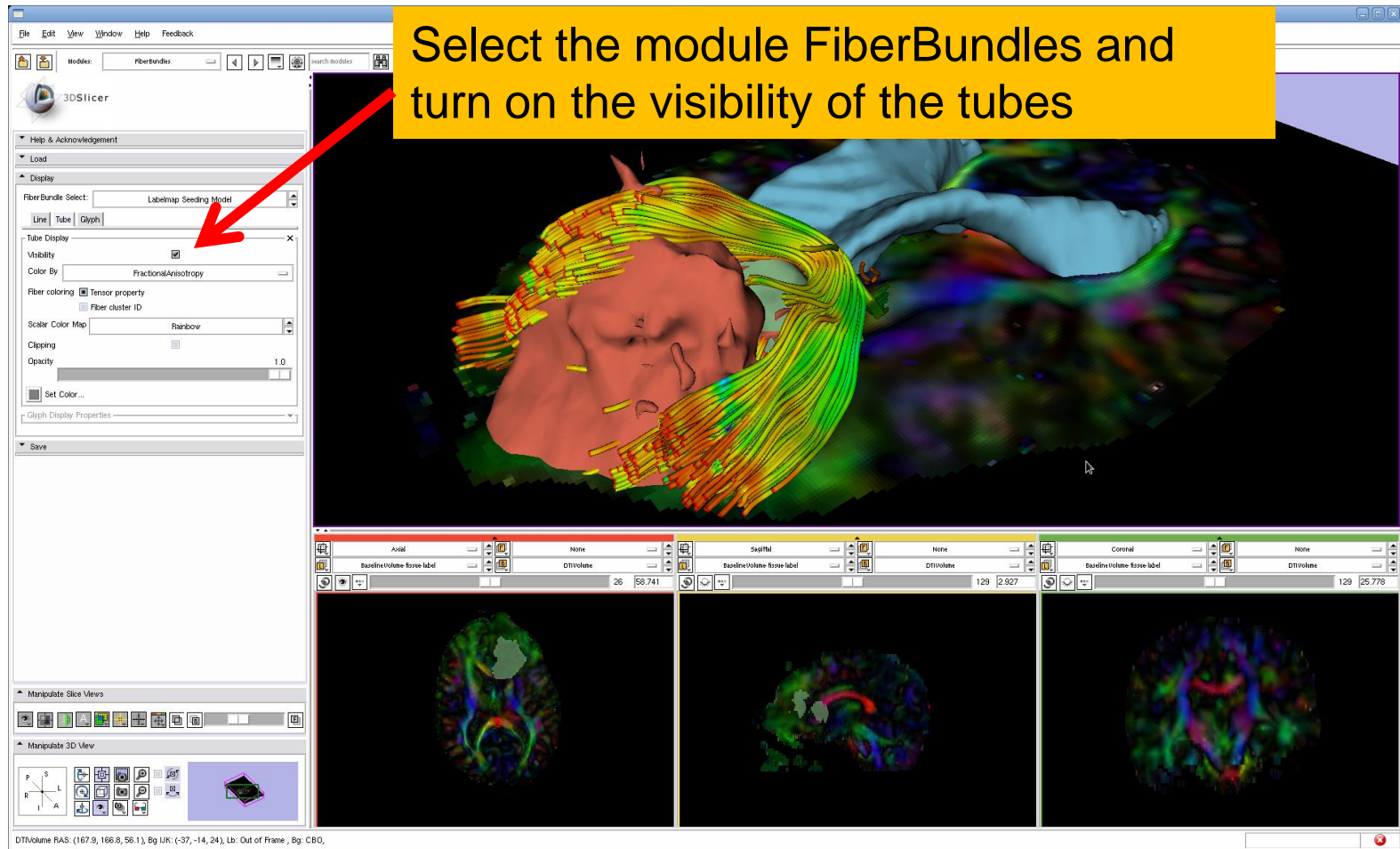
- Input DTI Volume: DTI Volume
- InputLabelMap: BaselineVolume-tissue-label
- OutputFiberBundle: Create New

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

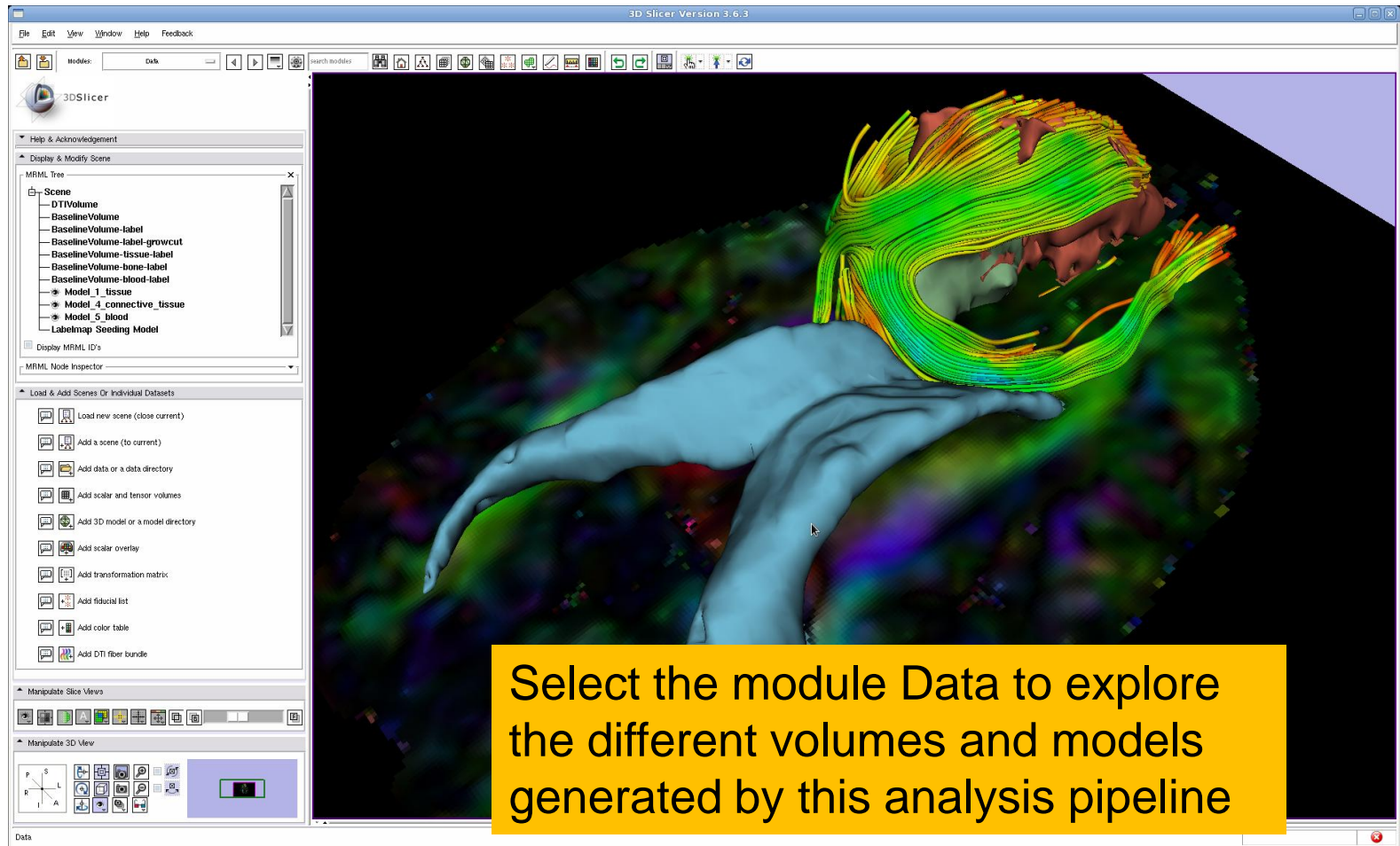
Tractography Results



Tractography Results

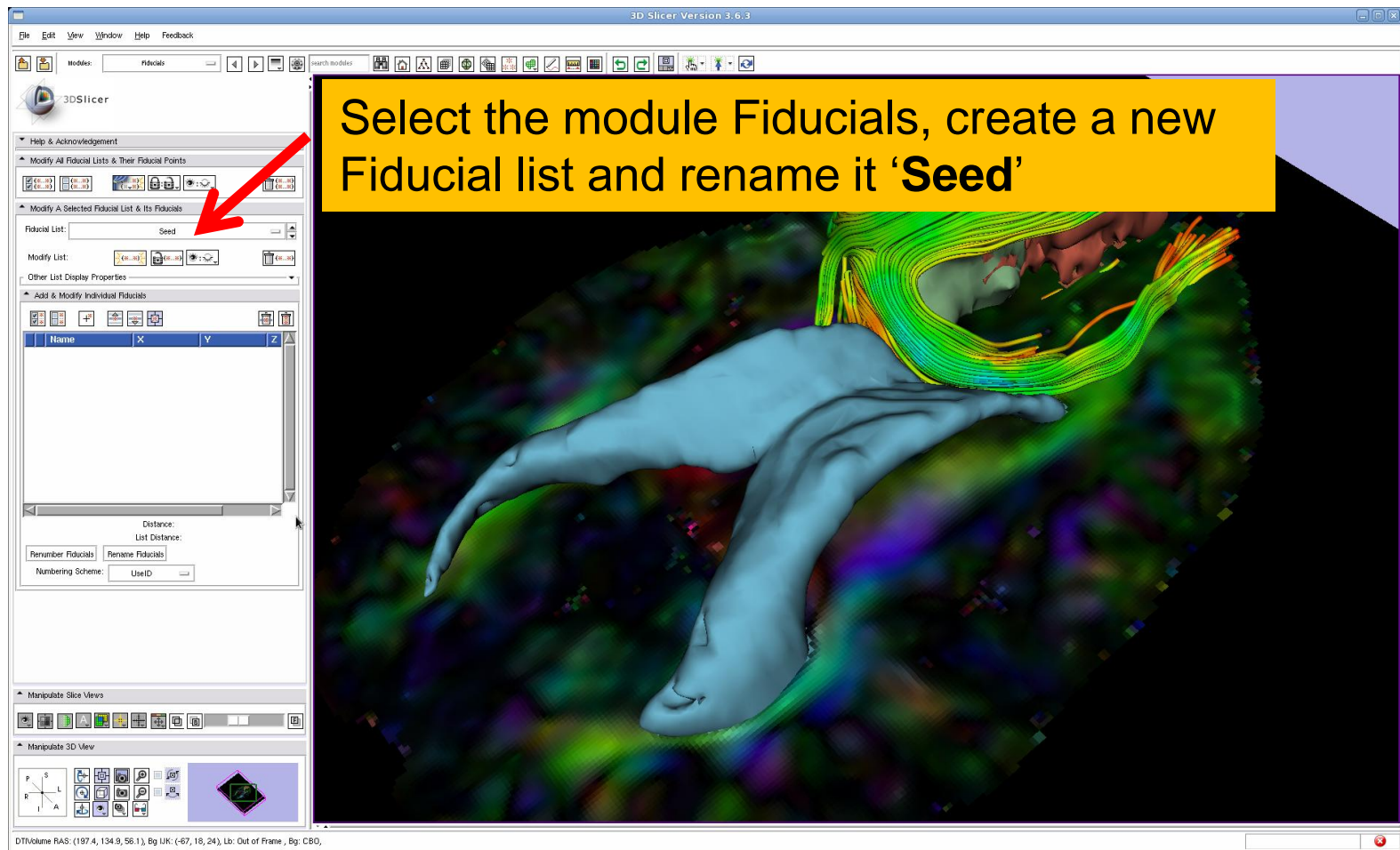


Tractography Results

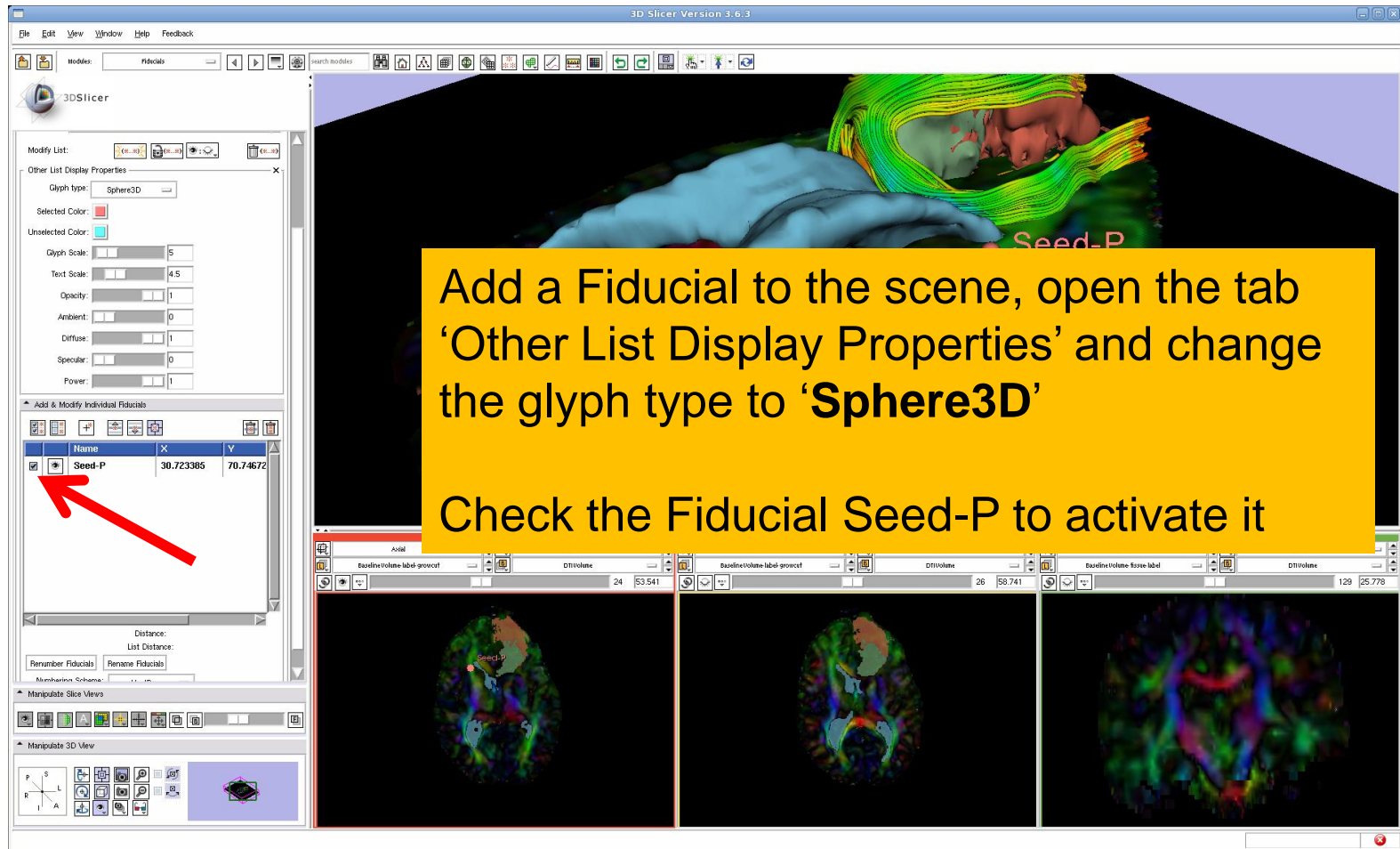


Part 3: Tractography exploration of the contralateral side

Tractography on-the-fly

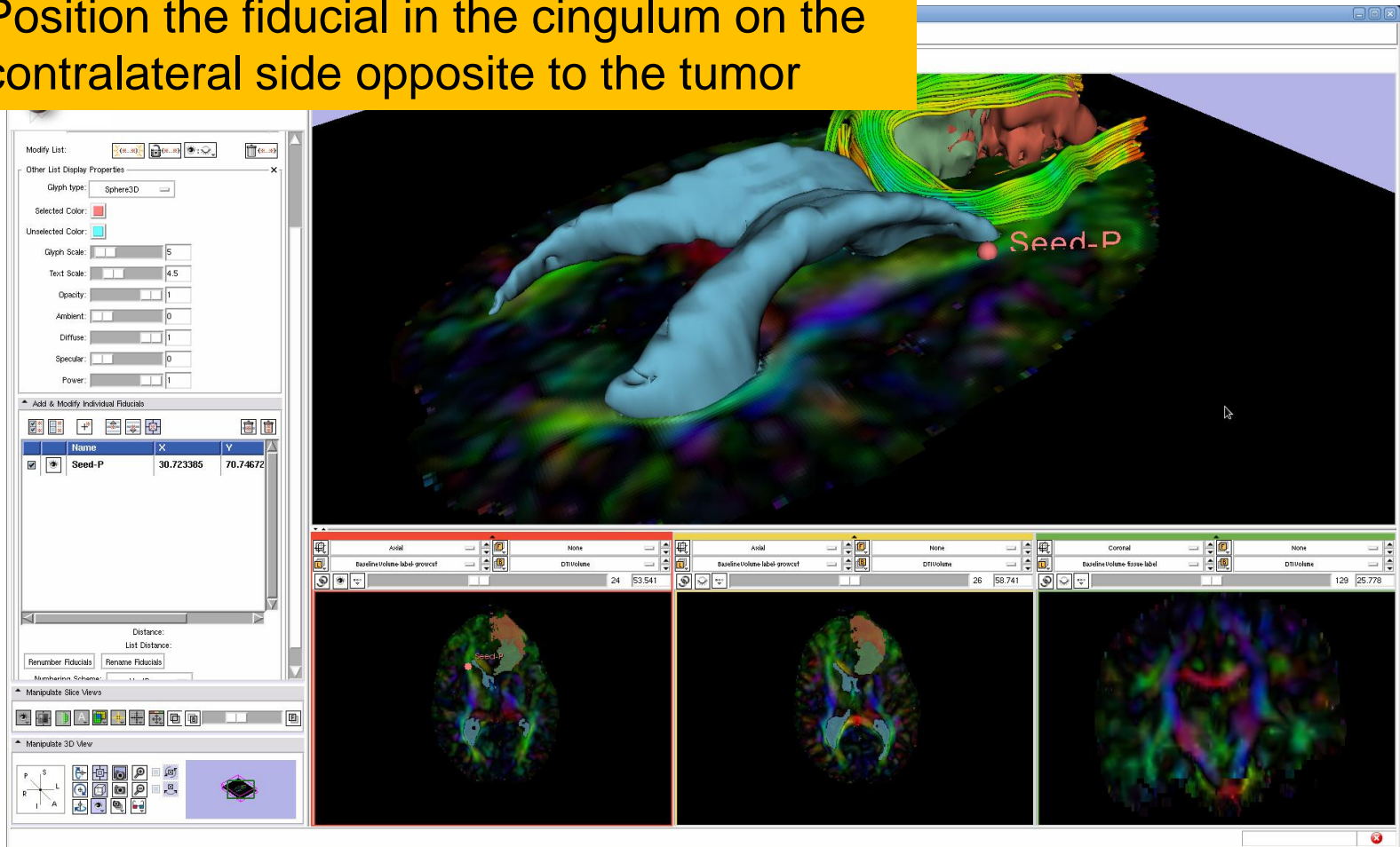


Fiducial Seeding

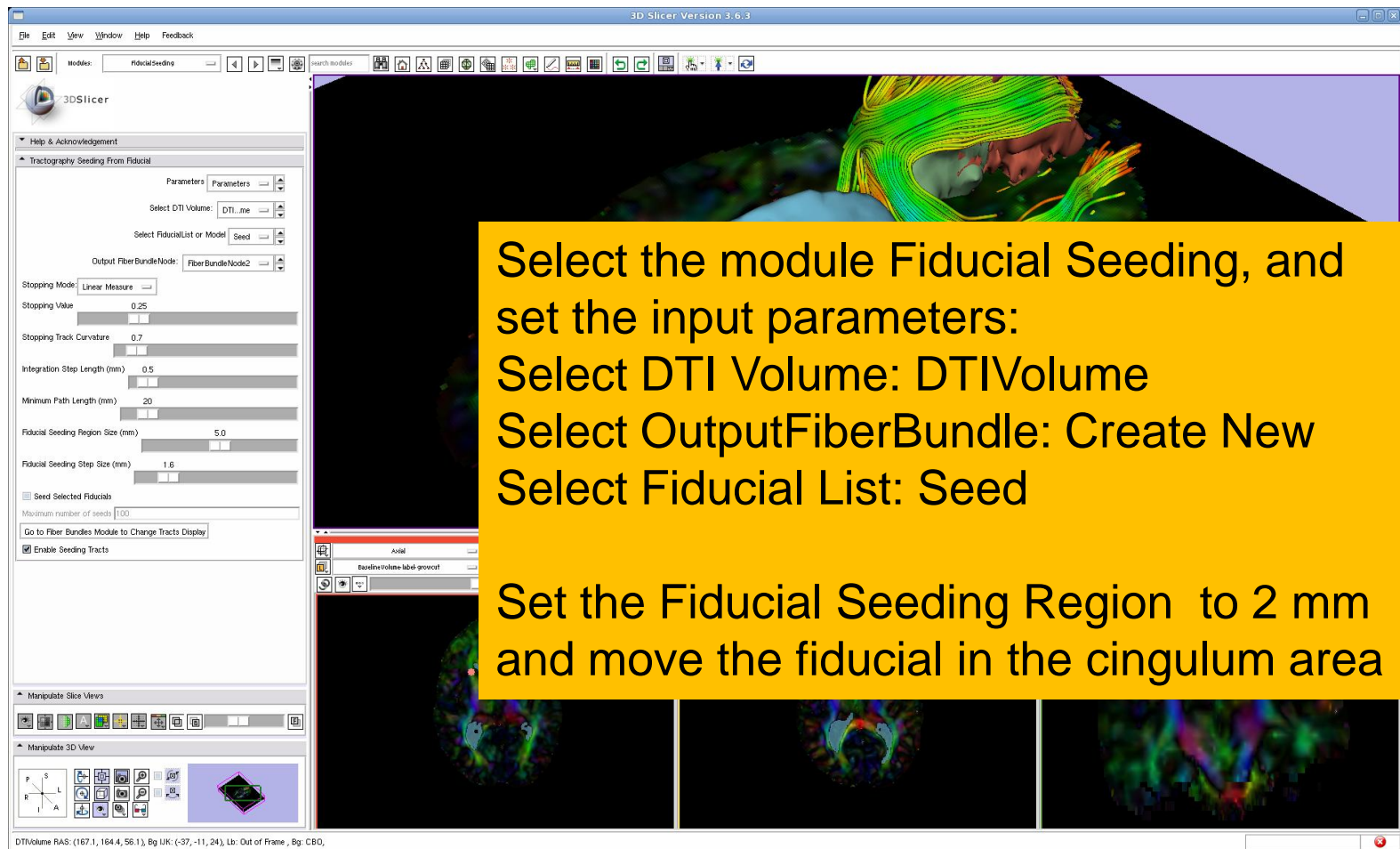


Fiducial Seeding

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



Tractography on-the-fly

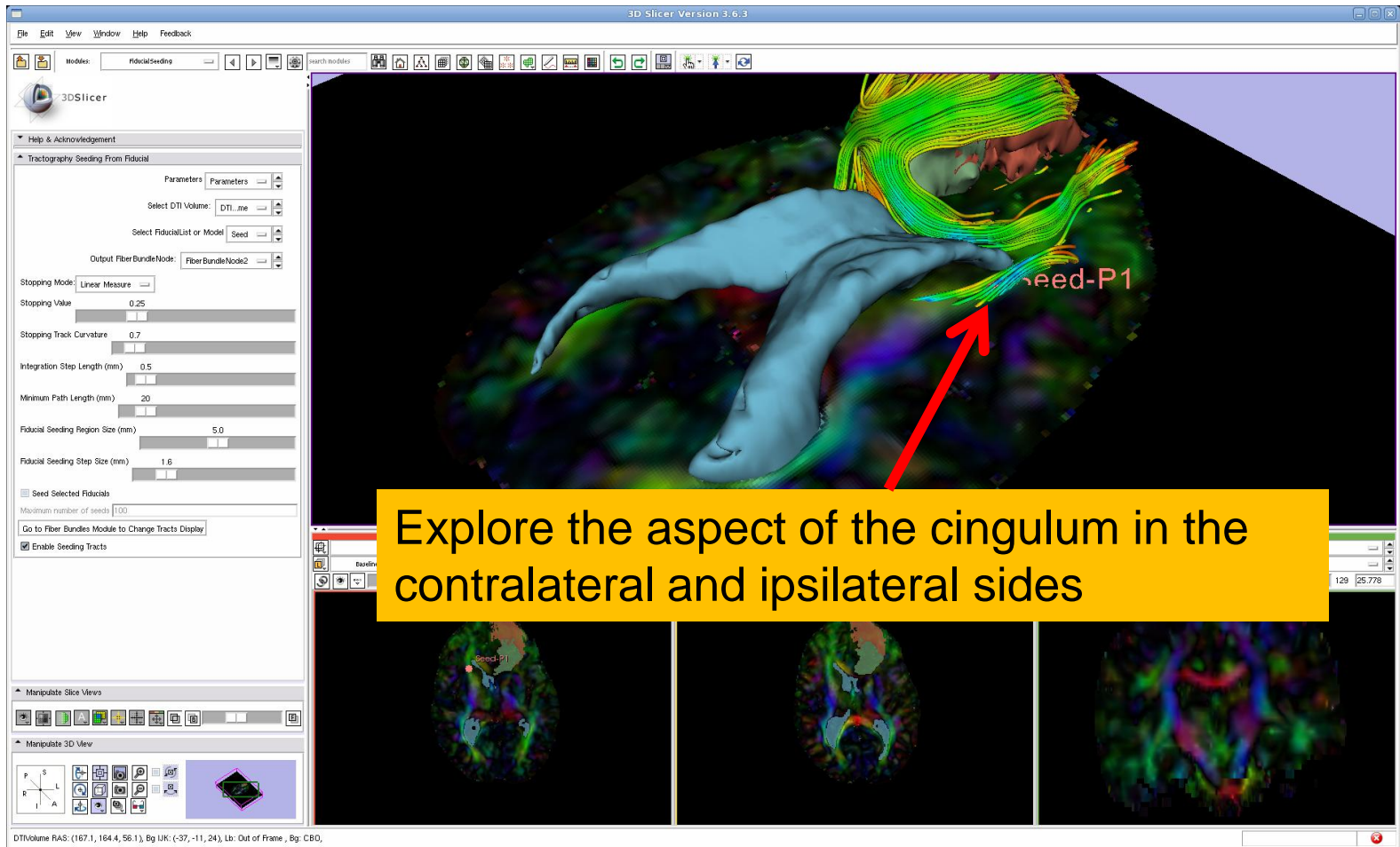


The screenshot displays the 3D Slicer Version 3.6.3 interface. The main window shows a 3D brain model with green and yellow fiber tracts. The left sidebar contains the 'Fiducial Seeding' module parameters. A yellow text box is overlaid on the right side of the interface, providing instructions on how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

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



National Alliance for Medical Image
Computing (NA-MIC)

NIH U54EB005149



Neuroimage Analysis Center (NAC)

NIH P41RR013218