

Exploring Peritumoral White Matter Fibers for Neurosurgical Planning

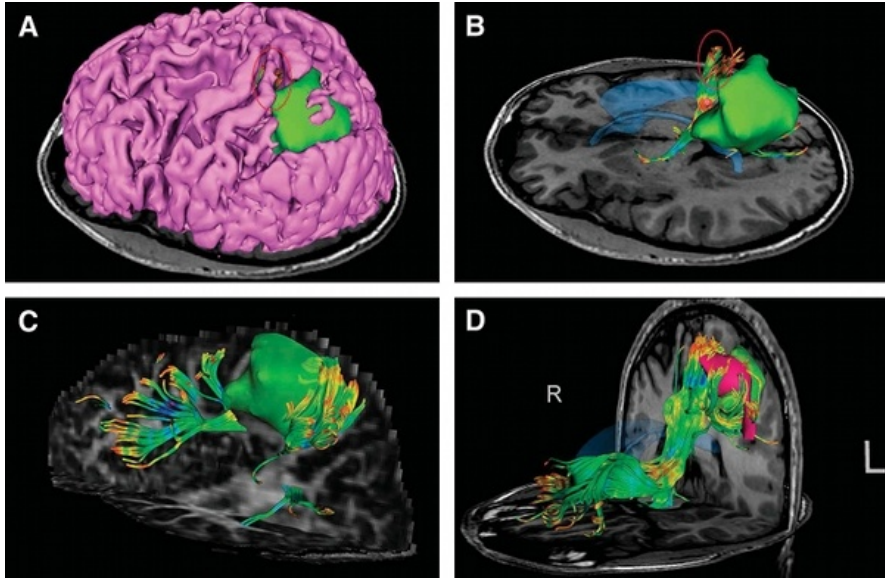
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Surgical Planning Laboratory

Harvard University

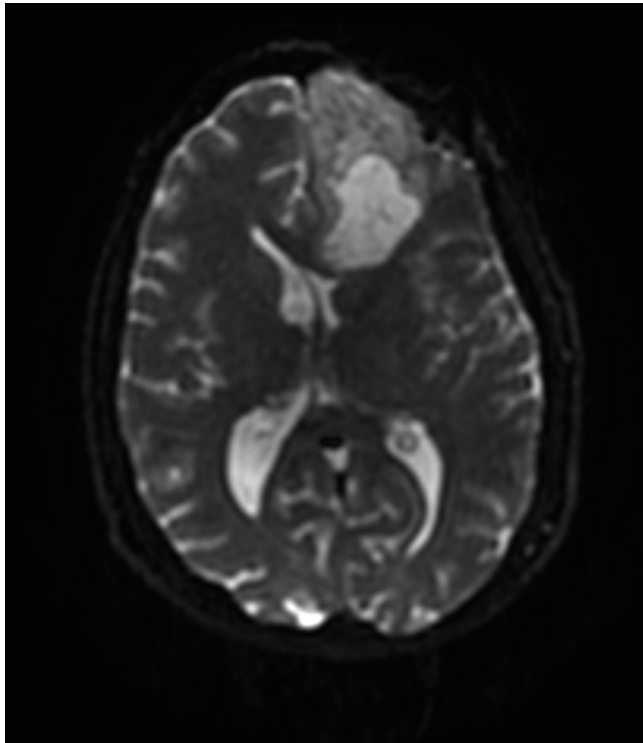
Clinical Goal



Diffusion Tensor Imaging (DTI) Tractography has the potential to bring valuable spatial information on tumor infiltration and tract displacement for neurosurgical planning of tumor resection.

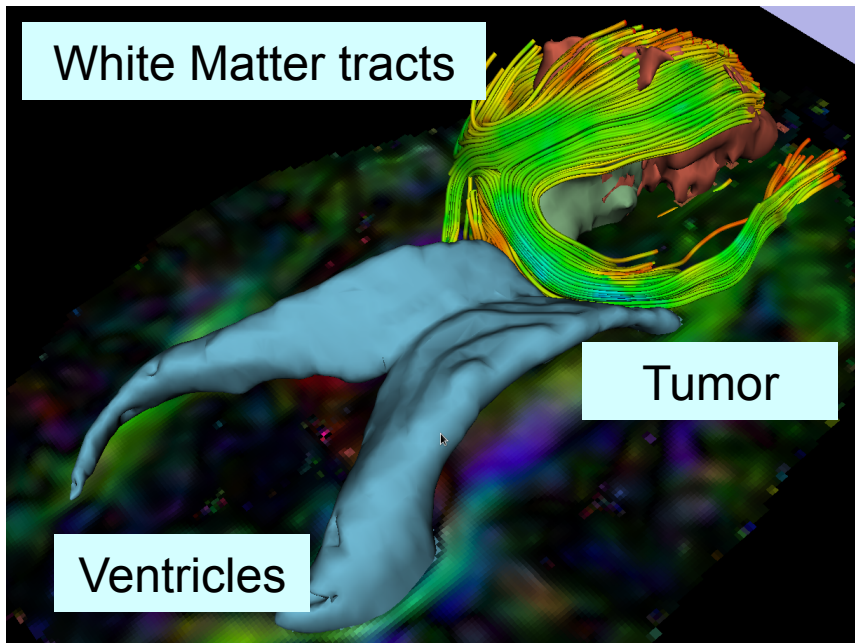
Image Courtesy of Dr. Alexandra Golby, Brigham and Women's Hospital, Boston, MA..

Clinical Case



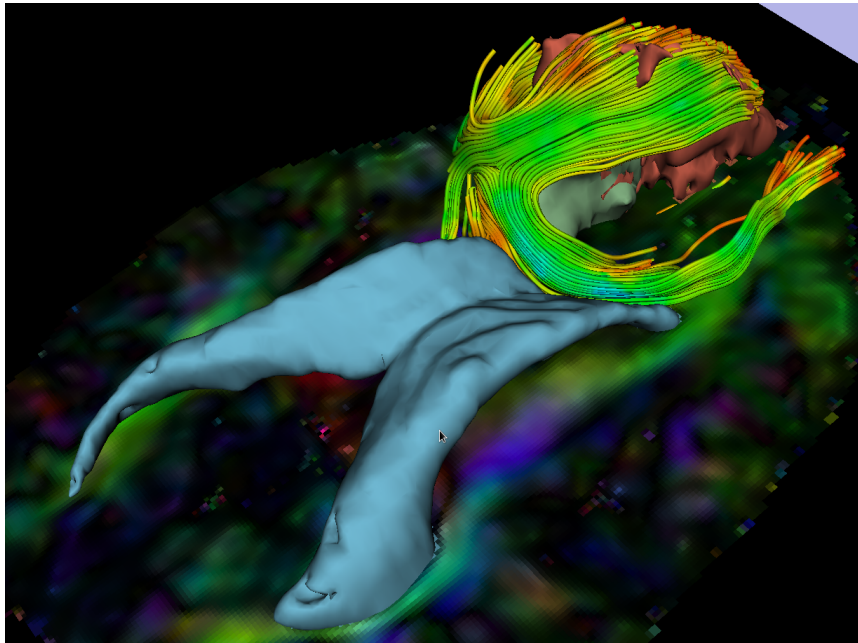
- 35 year-old male diagnosed with Glioblastoma multiforme (GBM)
- Diffusion Weighted Imaging (DWI) acquisition for neurosurgical planning

Clinical Goal



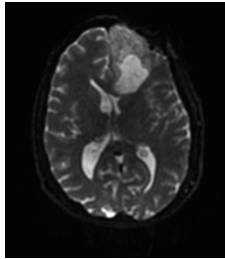
The goal of this tutorial is to explore white matter fibers surrounding a tumor using Diffusion Tensor Imaging (DTI) Tractography.

Image Analysis Pipeline

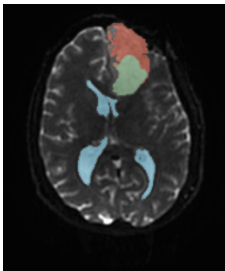


The image analysis pipeline described in this tutorial uses three different algorithms: the “Grow Cut” algorithm for segmentation of the tumor parts, the Marching Cube algorithm for surface modeling, and the single tensor streamline tractography algorithm for tract generation.

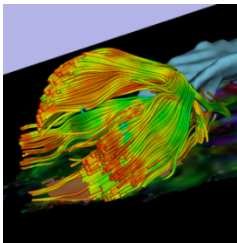
Overview of the analysis pipeline



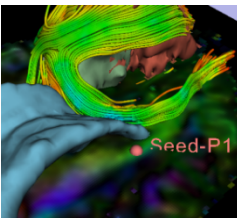
Part 1: Loading & Visualization of Diffusion Data



Part 2: Segmentation of the ventricles, and solid and cystic parts of the tumor

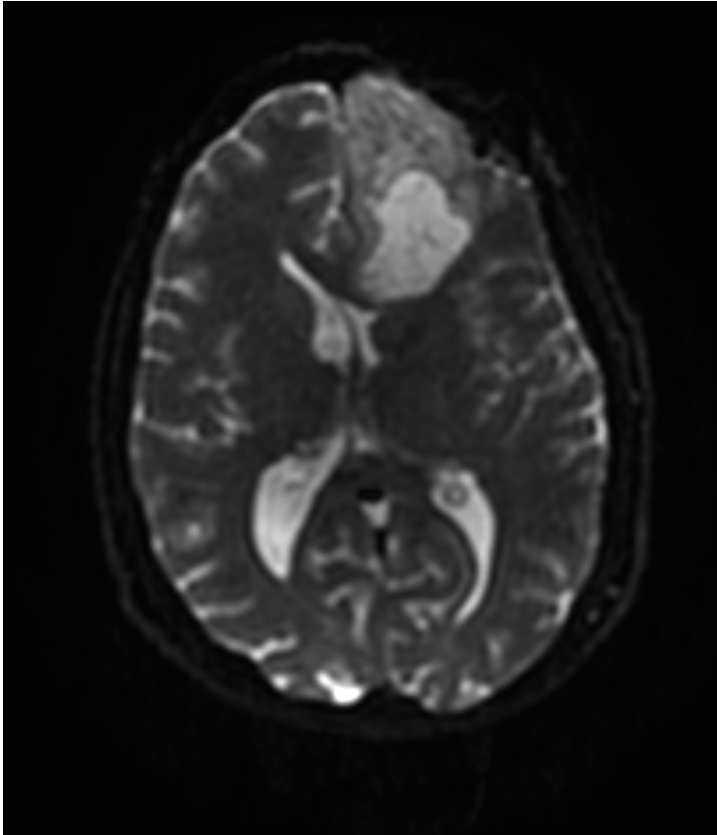


Part 3: Tractography reconstruction of the white matter fibers in the peri-tumoral volume



Part 4: Tractography exploration of the ipsilateral and contralateral side

Part 1: Loading and Visualization of Diffusion Data

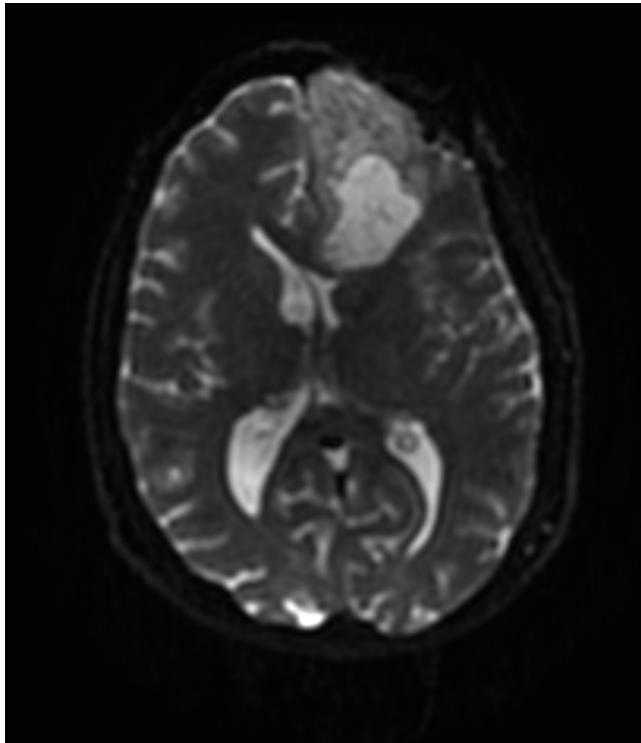
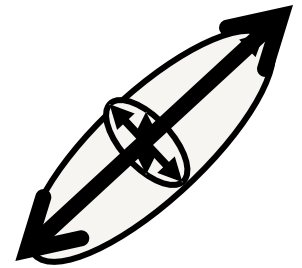


Diffusion Tensor Imaging

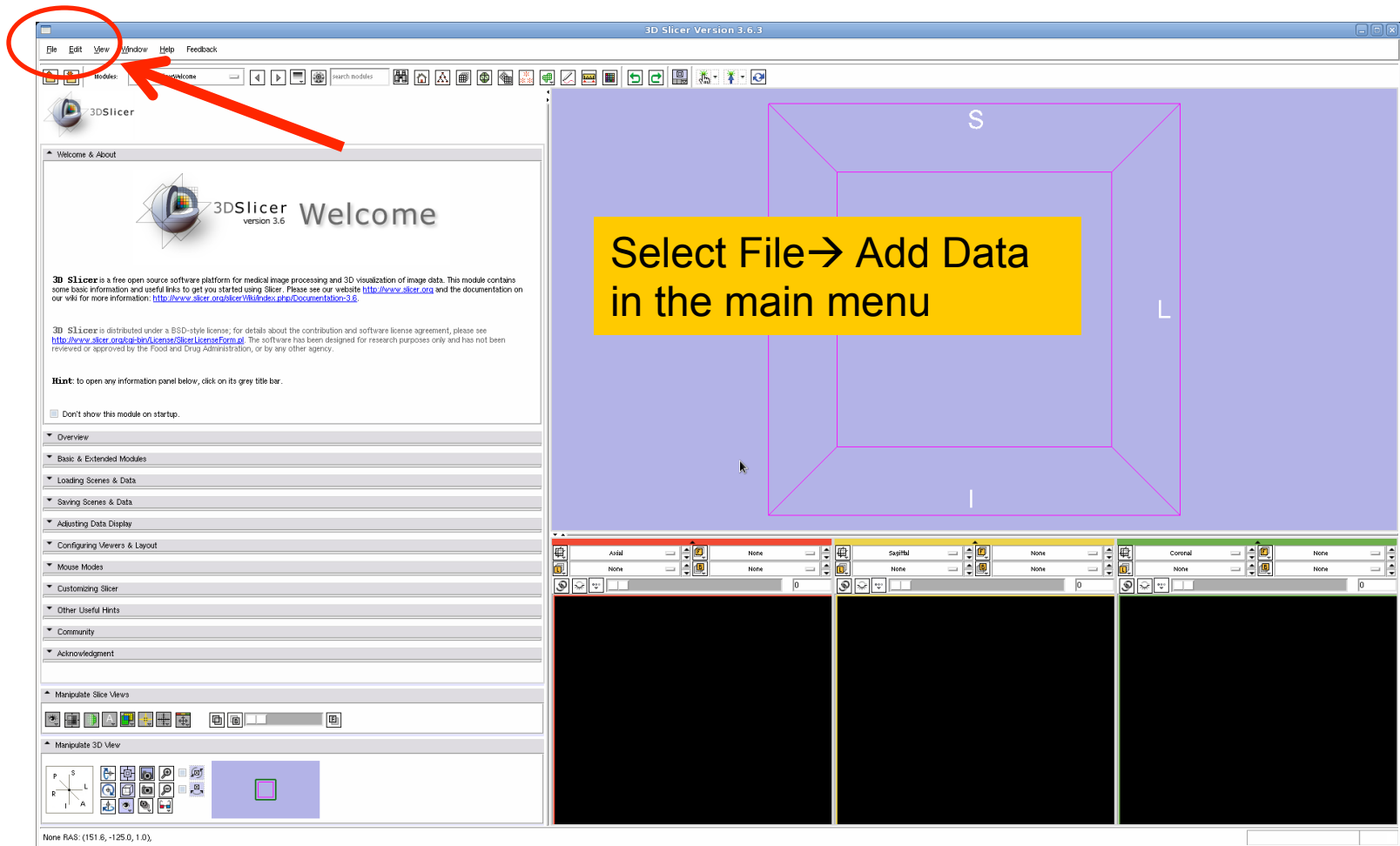
$$S_i = S_0 e^{-b \hat{g}_i^T \underline{D} \hat{g}_i}$$

(Stejskal and Tanner 1965, Basser 1994)

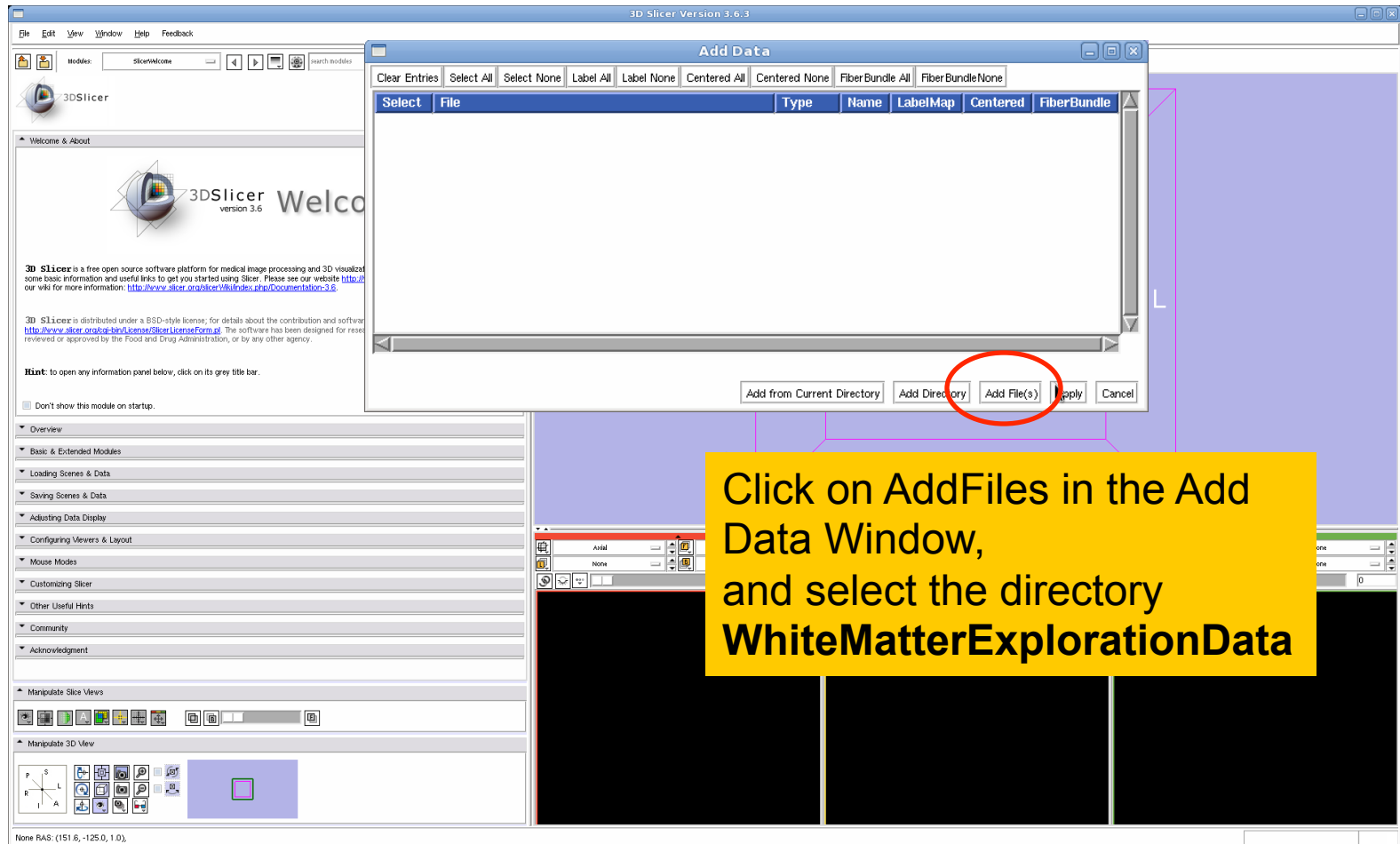
$$\underline{D} = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{bmatrix}$$



Loading DTI and Baseline Data



Loading DTI and Baseline Data



Loading DTI and Baseline Data

Name	Size	Modified time
Baseline Volume.nrrd	2,743 KB	11/01/10 10:20:03
DTI Volume.nhdr	1 KB	11/01/10 10:20:00
DTI Volume.raw.gz	18,678 KB	11/01/10 10:20:00

File name:

Files of type: All Files (*.*)

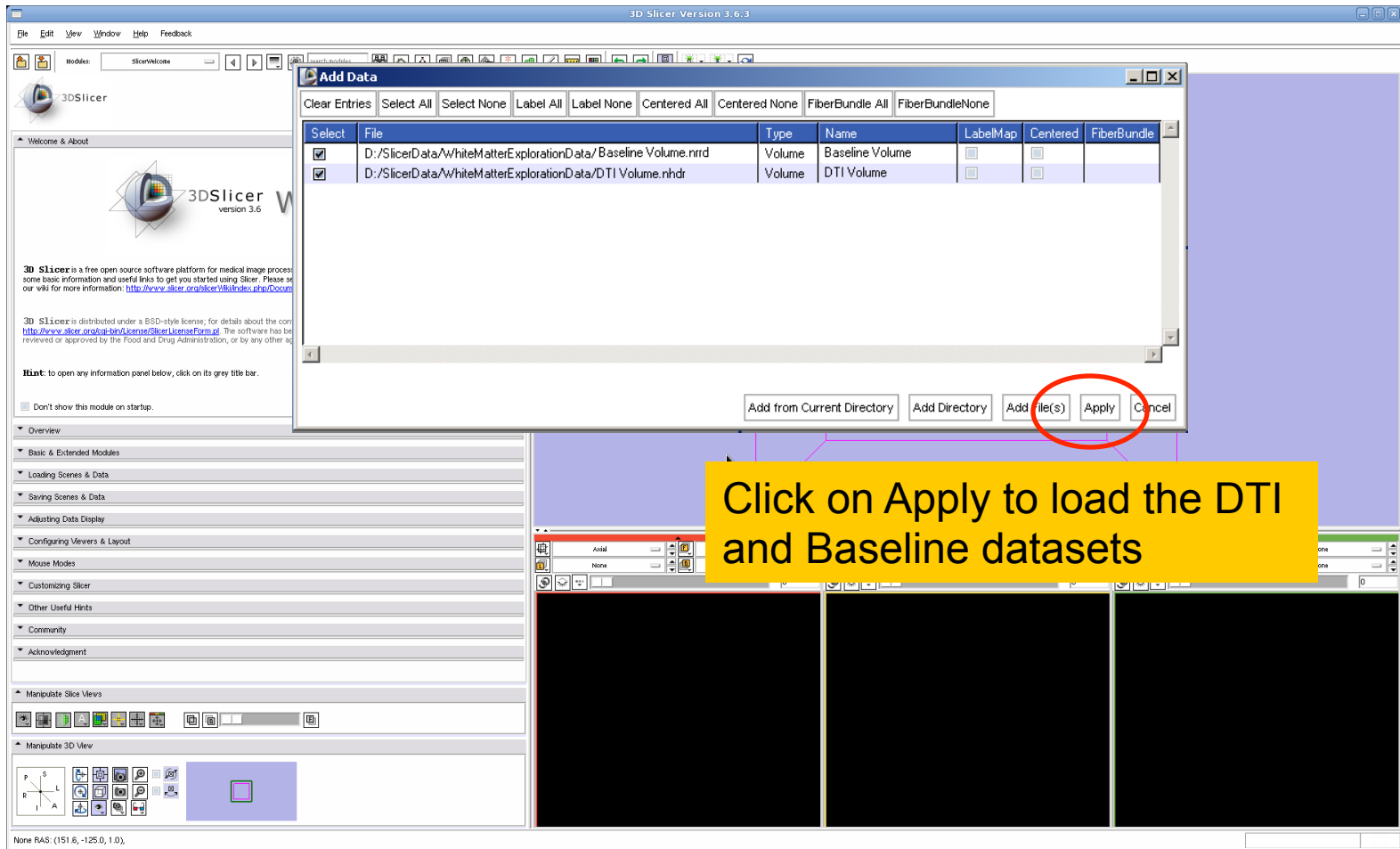
Open Cancel

None RAS: (151 8, -125 0, 1 0).

Select the directory **WhiteMatterExplorationData**

Select the files **BaselineVolume.nrrd** and **DTIVolume.nhdr** and click on **Open**

Loading DTI and Baseline Data




Loading DTI and Baseline Data

3D Slicer Version 3.6.3

File Edit View Window Help Feedback

modules Volumes

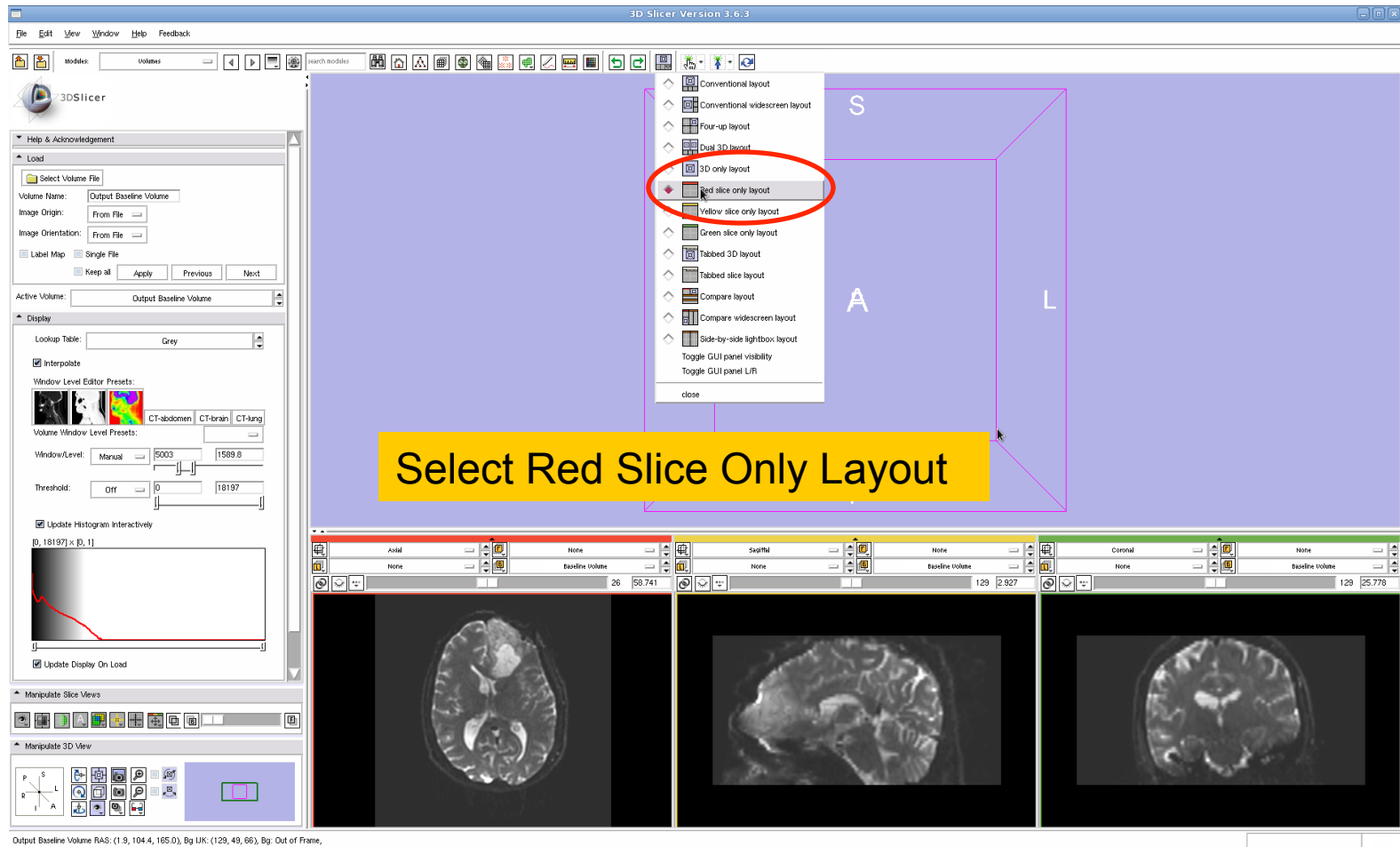
Click on the link icon  to link the three anatomical viewers, and set the Baseline volume in Background

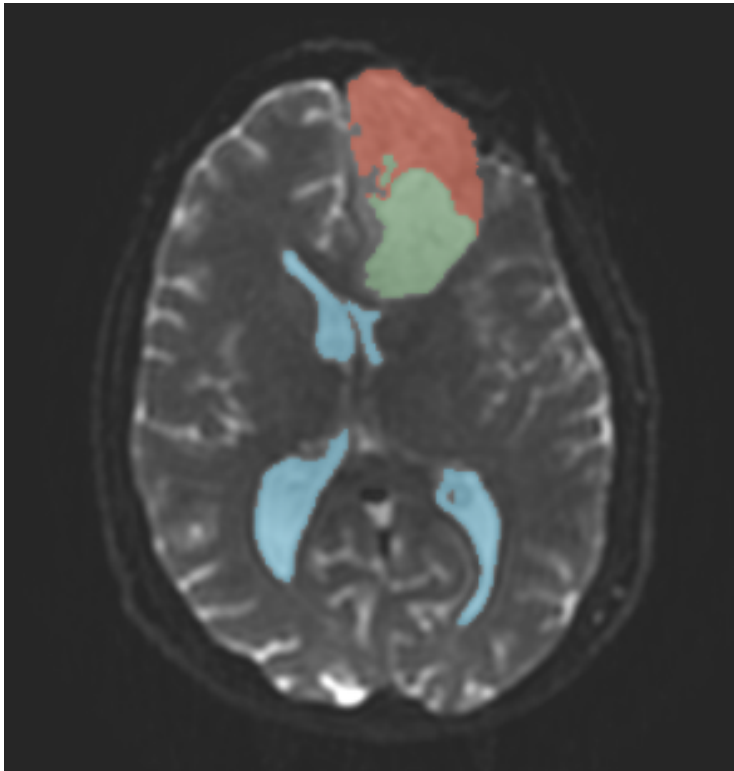
R A L

Select the module **Volumes** and adjust the Window and Level values of the Baseline Volume.

Output Baseline Volume RAS: (1.9, 104.4, 165.0), Bg IJK: (129, 49, 66), Bg: Out of Frame.

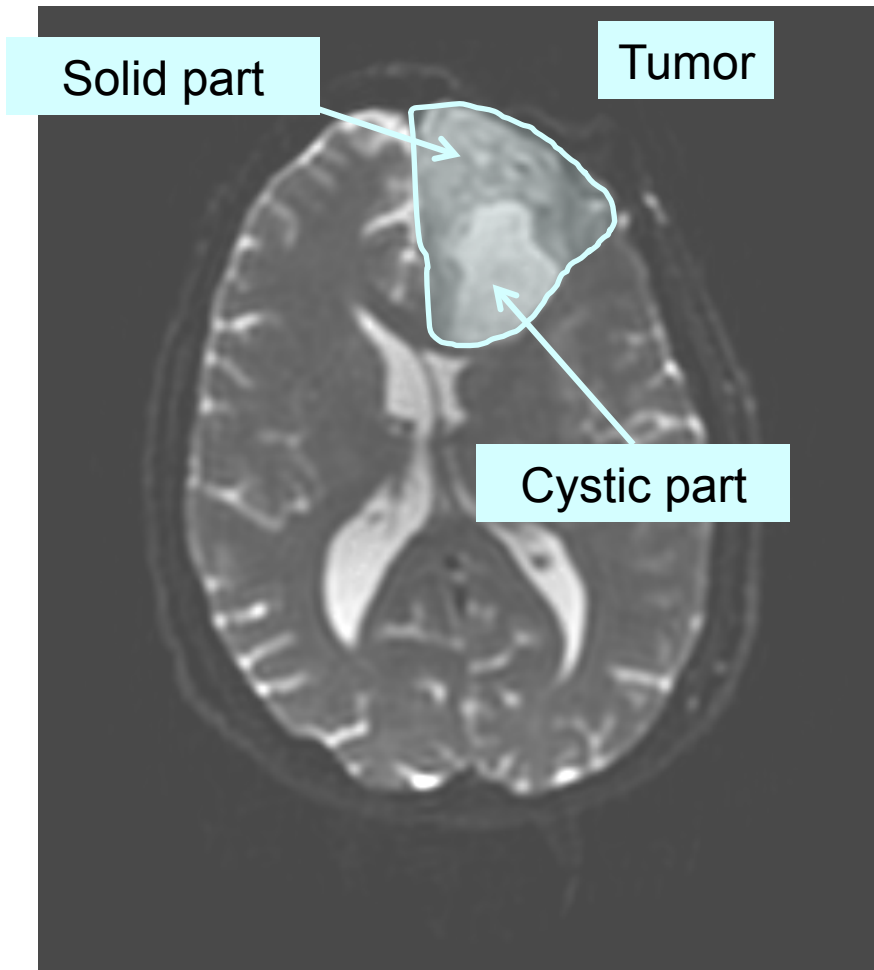
Loading DTI and Baseline Data





Part 1: Segmenting the tumor and ventricles

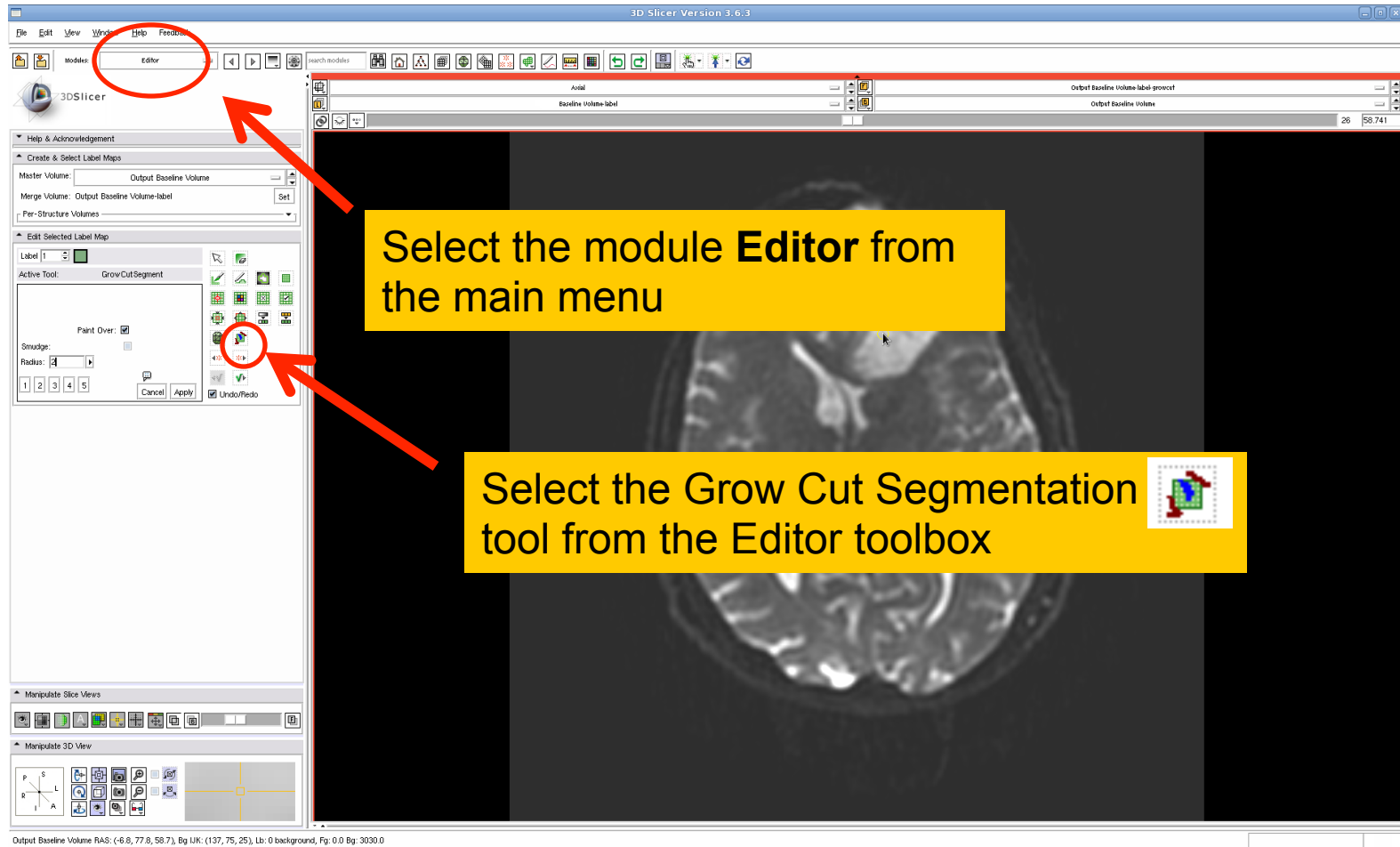
Tumor Segmentation



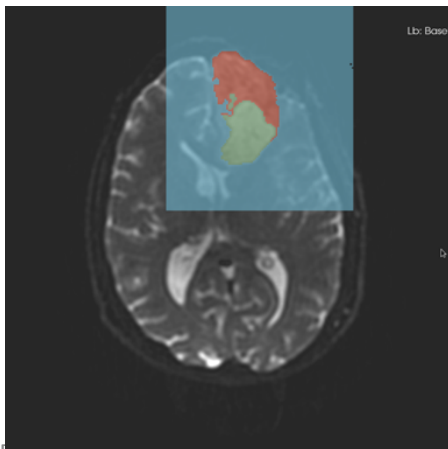
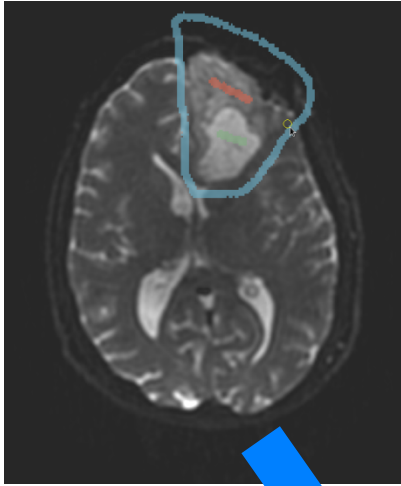
The tumor in this clinical case is composed of two parts: a solid part, and a cystic part.

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

Tumor Segmentation

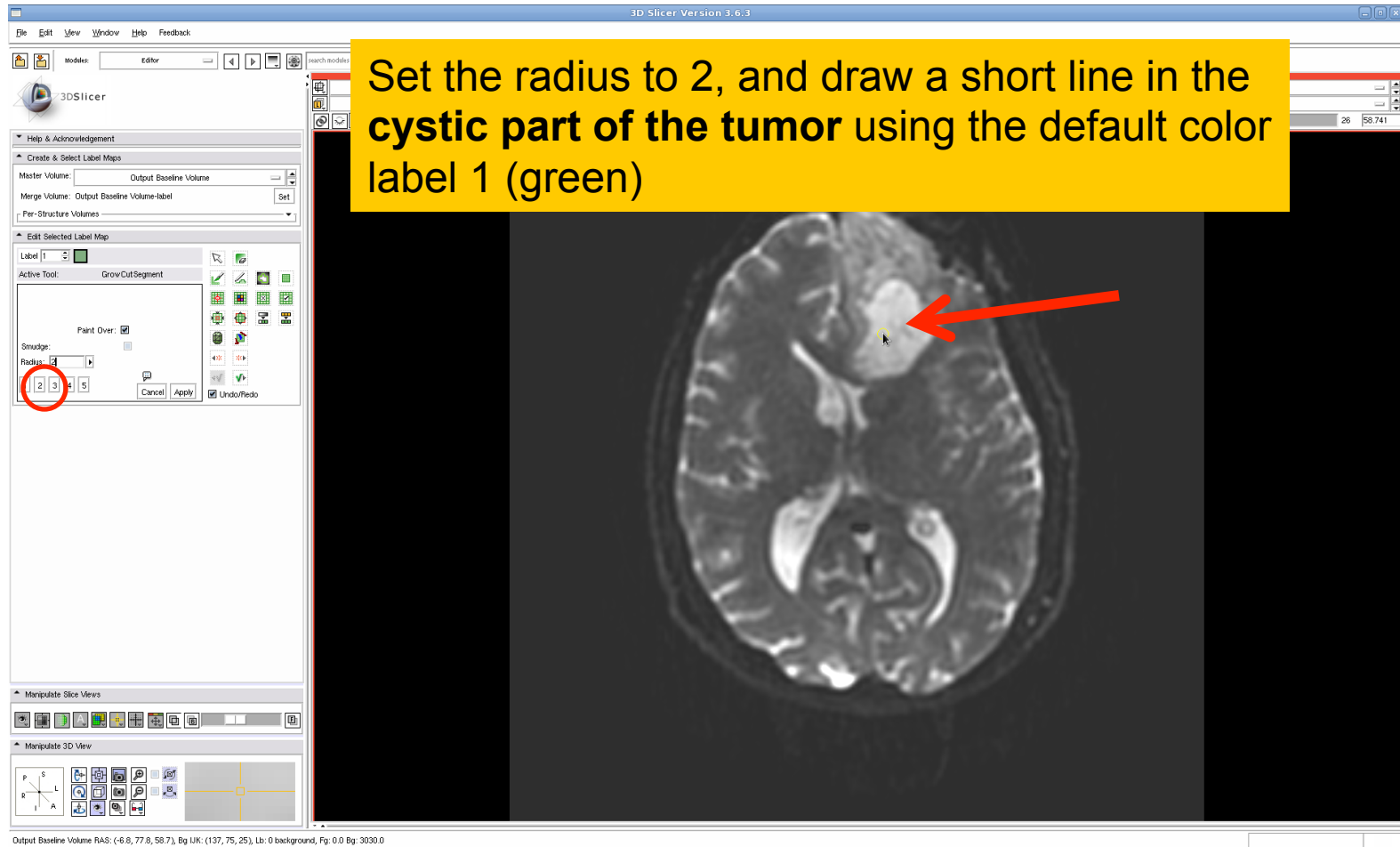


Grow Cut Segmentation

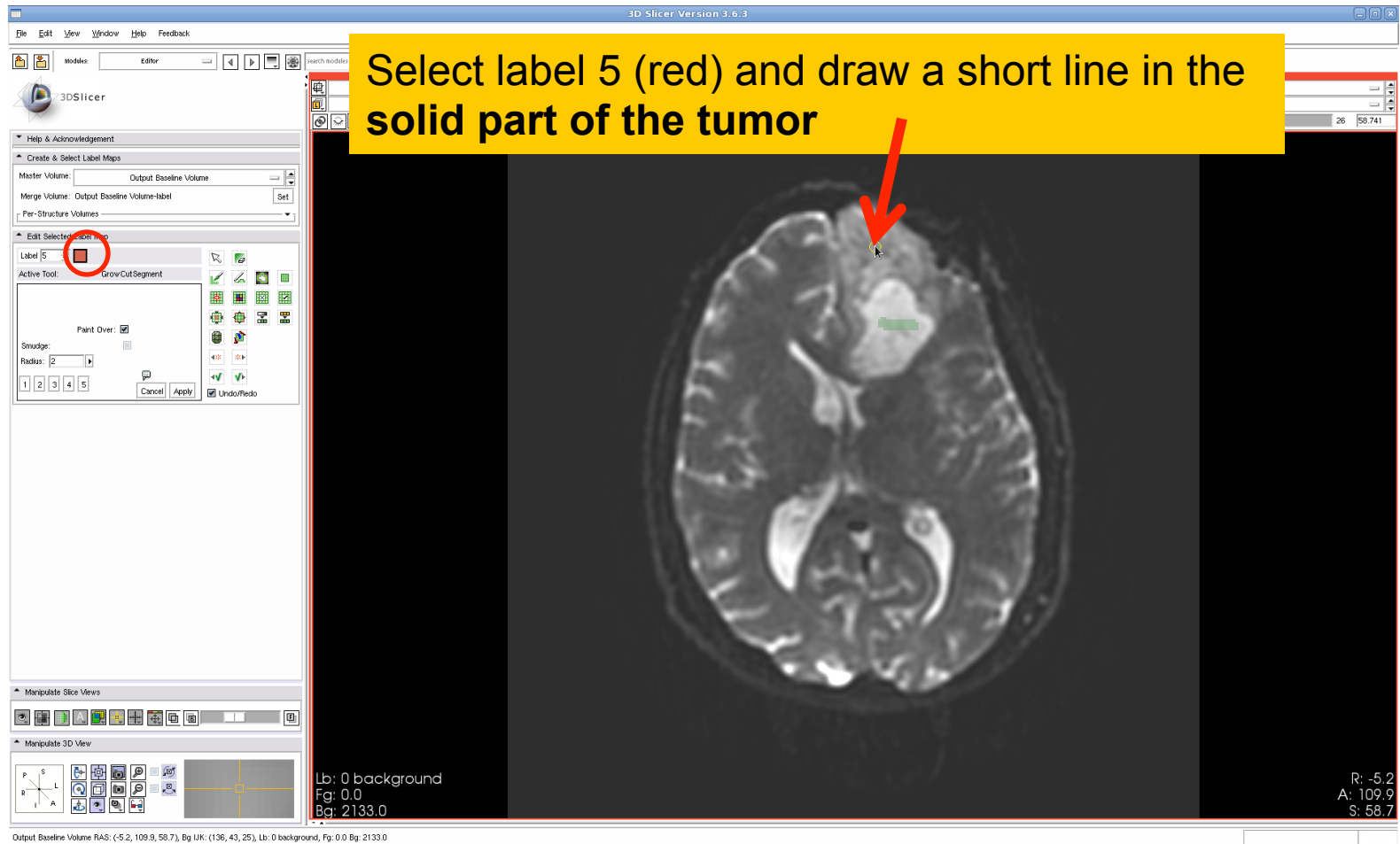


- The **Grow Cut Segmentation** method is a competitive region growing algorithm using Cellular Automata.
- The algorithm performs multi-label image segmentation using a set of user input scribbles.
- V. Vezhnevets, V. Konouchine. "Grow-Cut" - Interactive Multi-Label N-D Image Segmentation". *Proc. Graphicon*. 2005 . pp. 150–156.

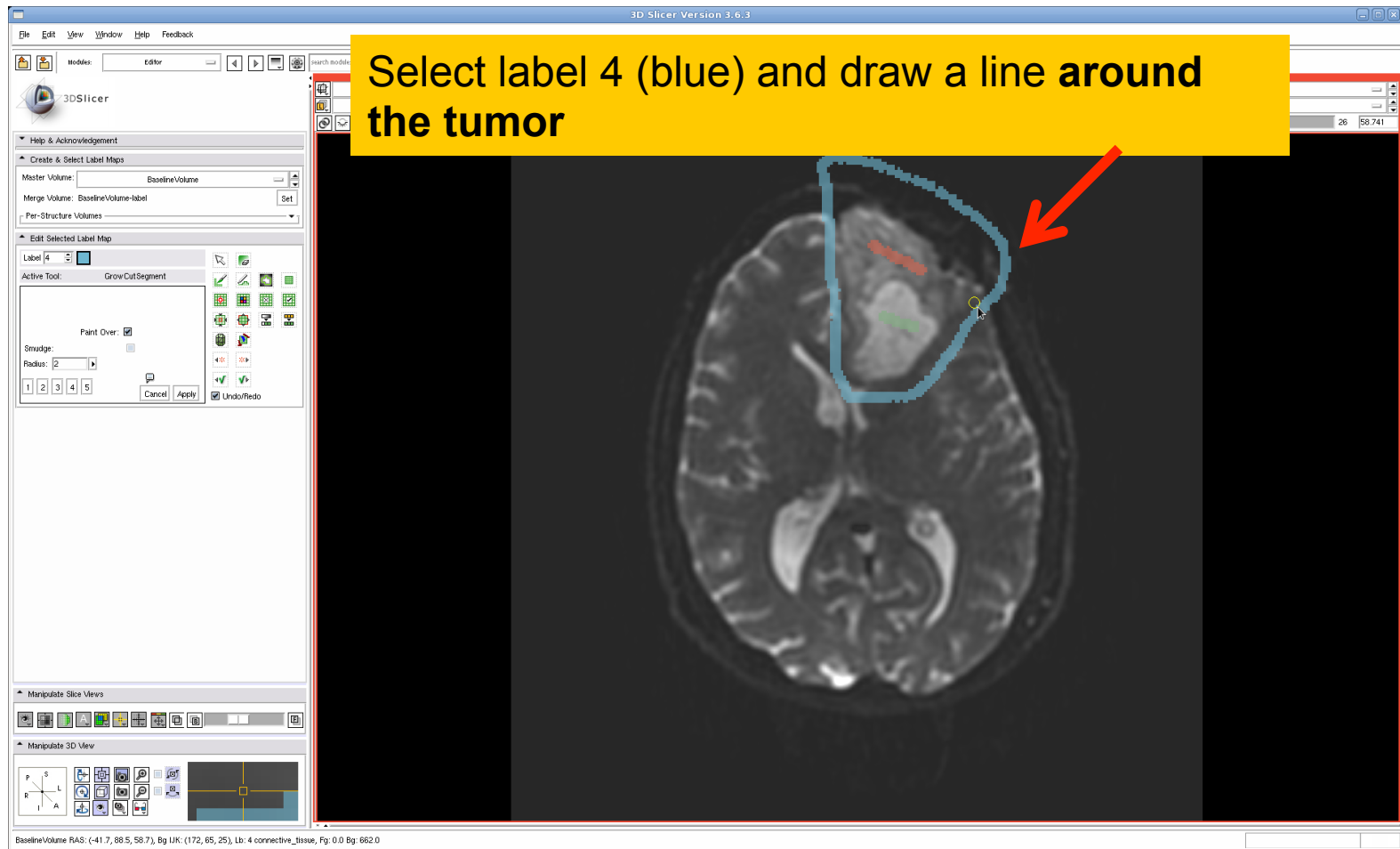
Tumor Segmentation



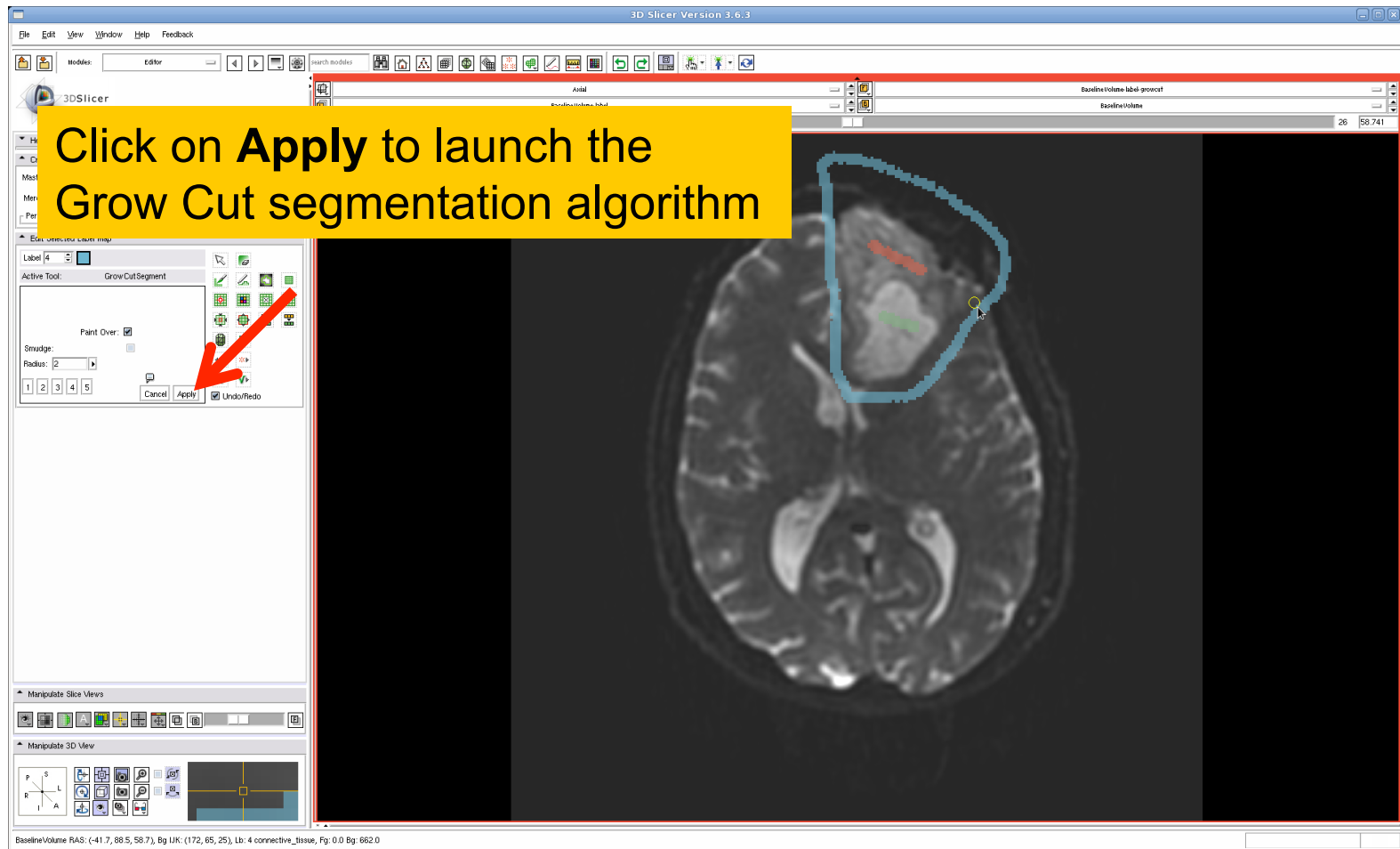
Tumor Segmentation



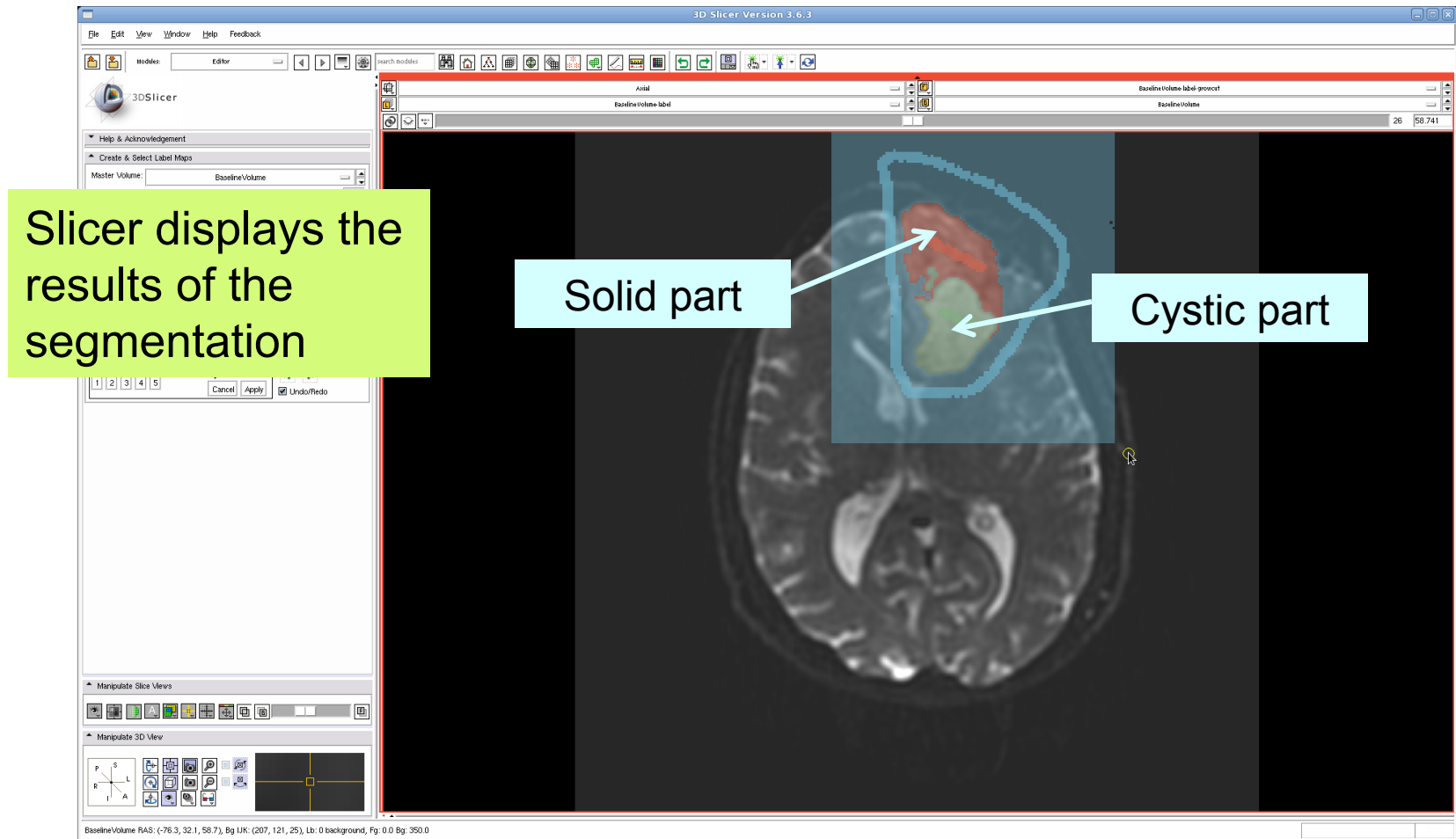
Tumor Segmentation



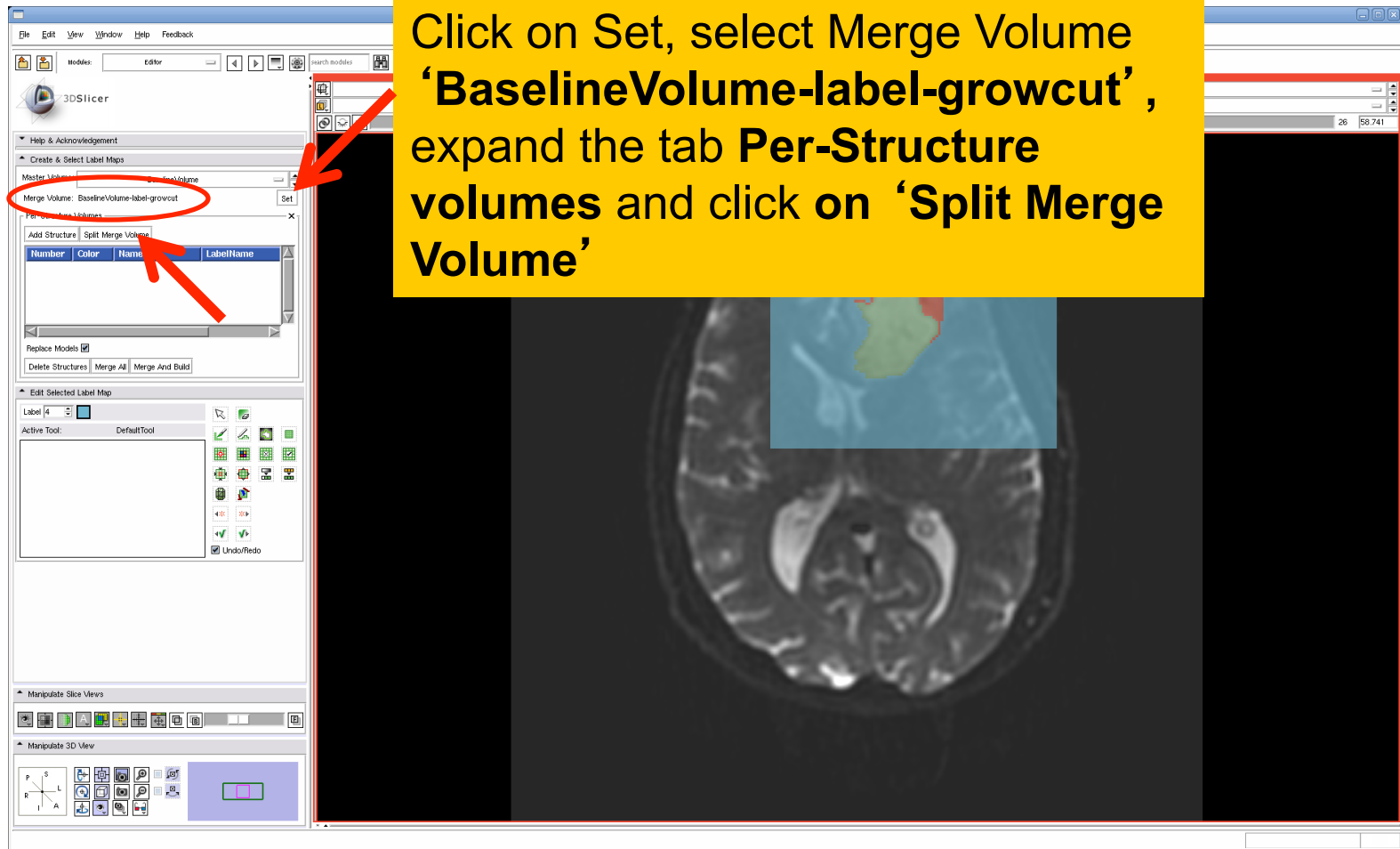
Tumor Segmentation



Tumor Segmentation



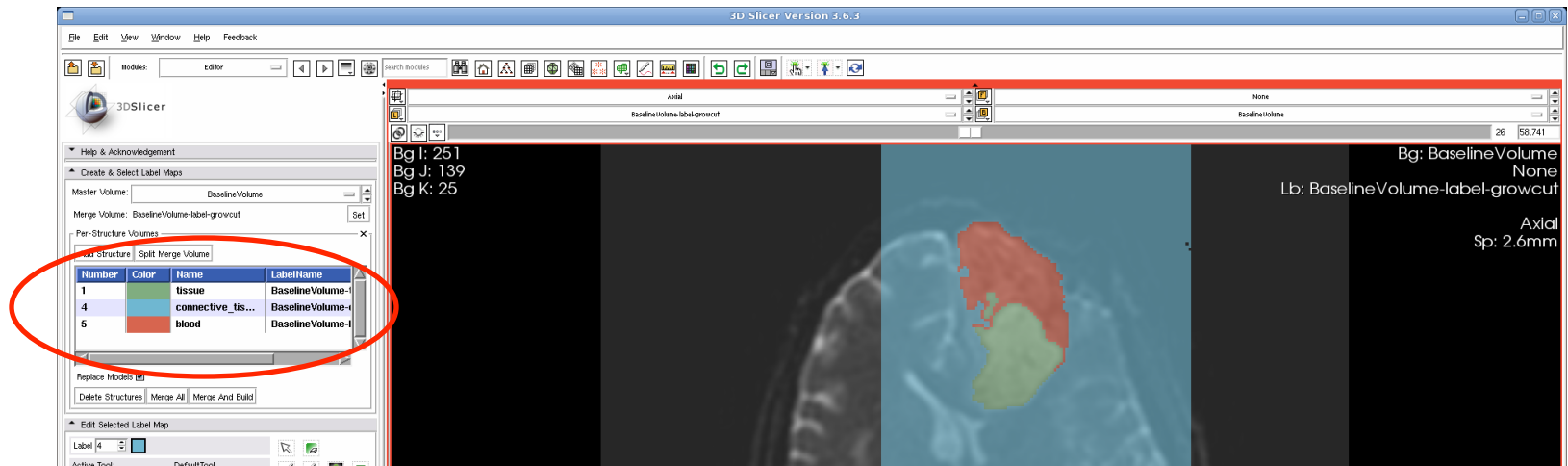
Tumor Segmentation



The screenshot displays the 3DSlicer software interface. On the left, the 'Create & Select Label Maps' panel is visible. The 'Merge Volume: BaselineVolume-label-growcut' entry is circled in red. Below it, the 'Split Merge Volume' button is also highlighted with a red arrow. The main 3D view shows a brain MRI slice with a segmented tumor region highlighted in blue and green. A yellow text box with black text is overlaid on the right side of the interface, providing instructions: 'Click on Set, select Merge Volume 'BaselineVolume-label-growcut', expand the tab Per-Structure volumes and click on 'Split Merge Volume''. The interface includes a menu bar at the top, a toolbar, and various panels for editing and visualization.

Click on Set, select Merge Volume 'BaselineVolume-label-growcut', expand the tab **Per-Structure volumes** and click on 'Split Merge Volume'

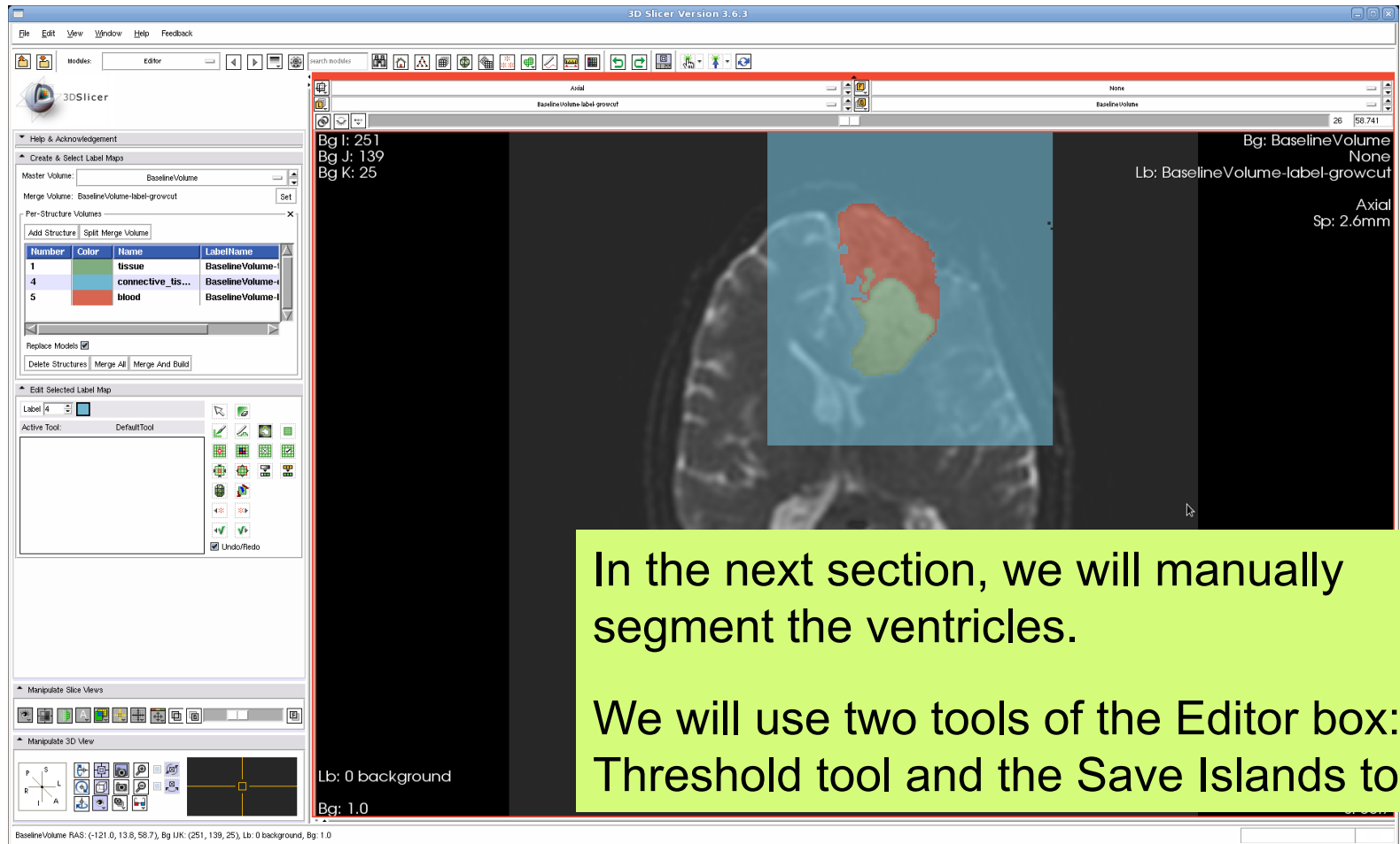
Tumor Segmentation



The label map **BaselineVolume-label-growcut** has been split into three volumes:

- BaselineVolume-tissue-label** (label 1): cystic part of the tumor
- BaselineVolume-connective_tissue-label** (label 4): ventricles
- BaselineVolume-blood-label** (label 5): solid part of the tumor


Ventricles Segmentation



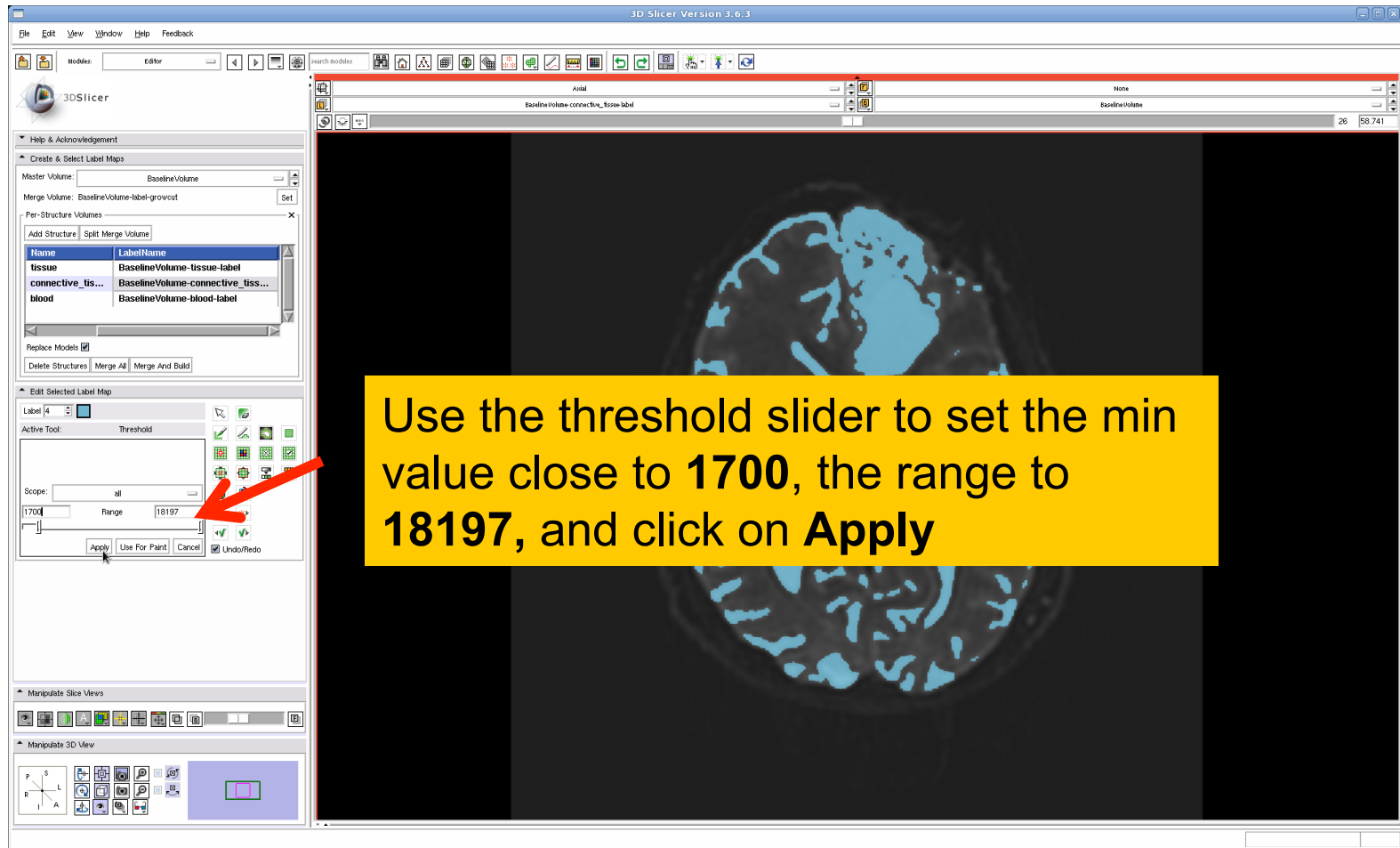
Ventricles Segmentation

Select the volume
'BaselineVolume-connective_tissue-label' (label 4)

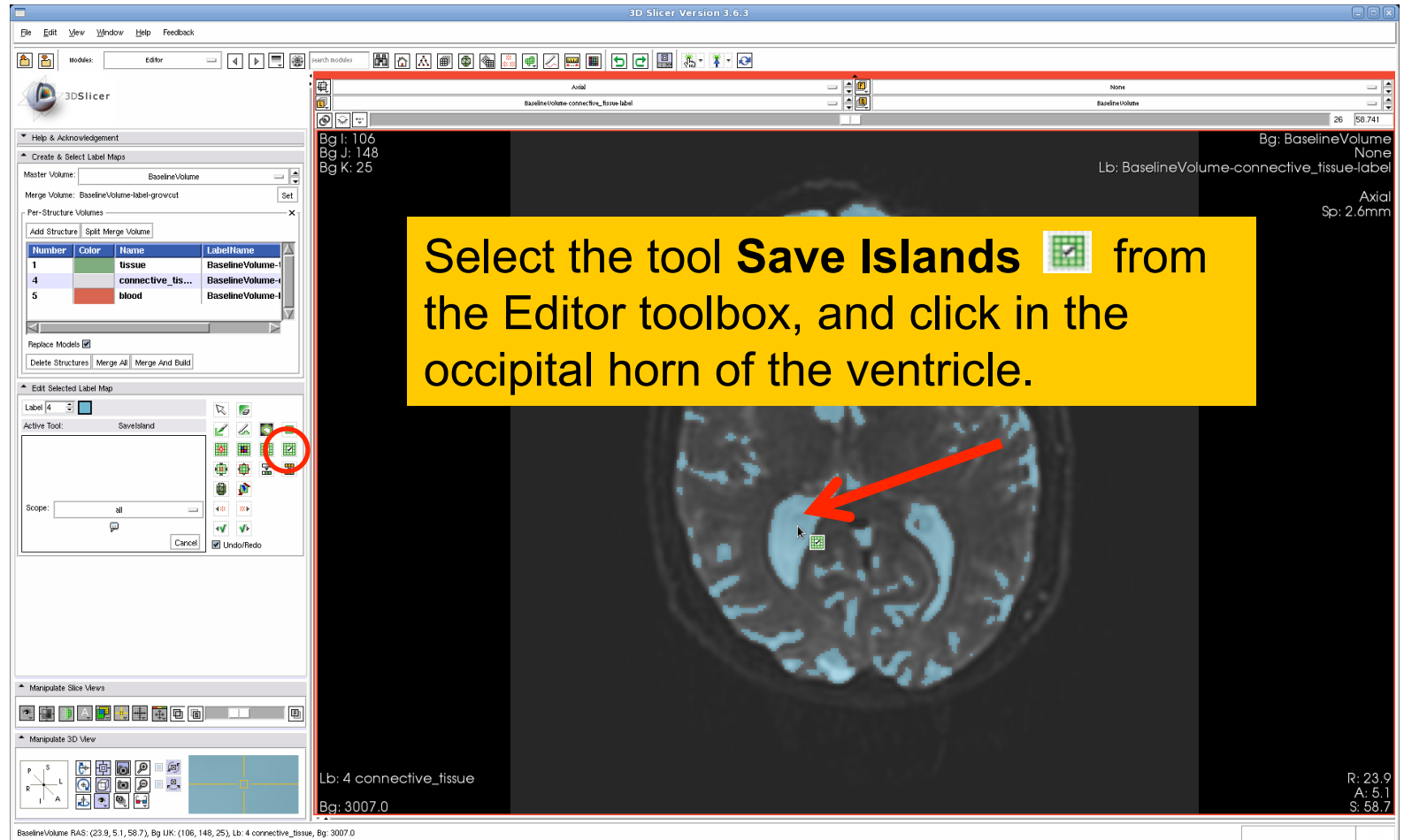
Number	Color	Name	LabelName
1	Green	tissue	BaselineVolume-t...
4	Grey	connective_tis...	BaselineVolume-t...
5	Red	blood	BaselineVolume-t...

Select the Threshold tool  in the Editor toolbox

Ventricles Segmentation



Ventricles Segmentation



Final Result of the Segmentation



Final Result of the Segmentation

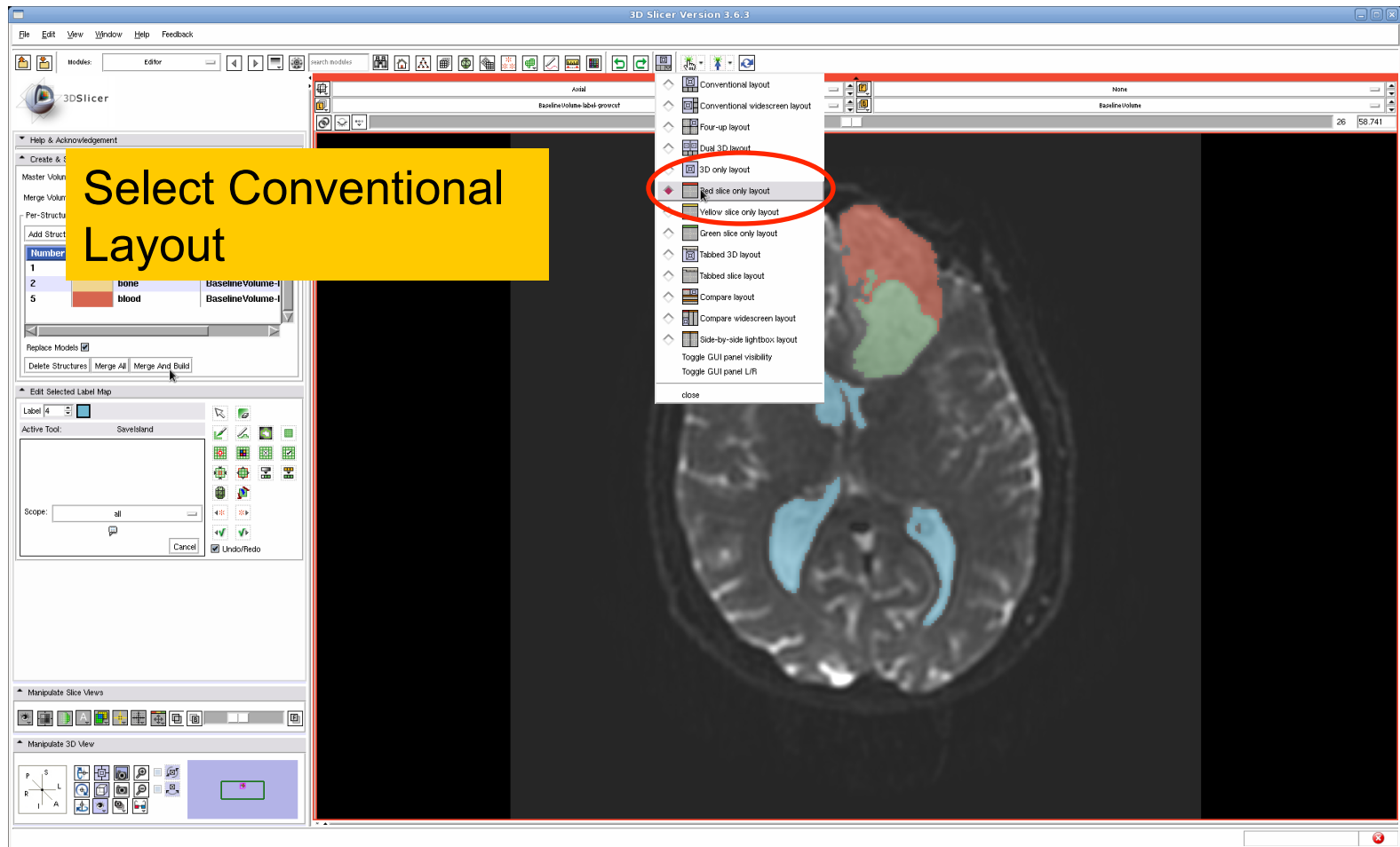
Click on **Merge and Build** to merge the different labelmaps, and generate the 3D models of the tumor and ventricles using a Marching Cubes algorithm

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

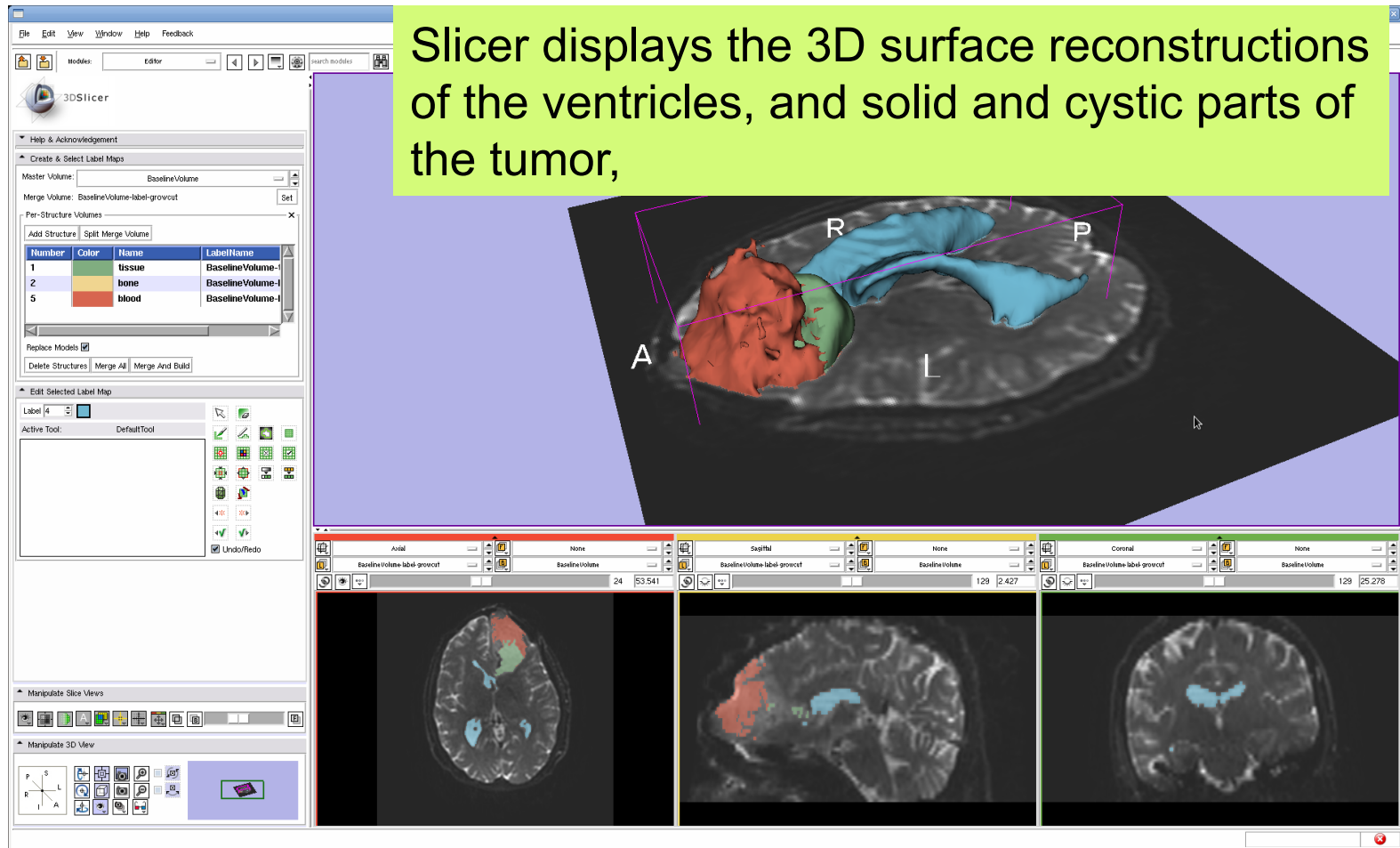
BaselineVolume RAS: (25.6, 7.0, 58.7), Bg UK: (105, 146, 25), Lb: 4 connective_tissue, Bg: 2443.0

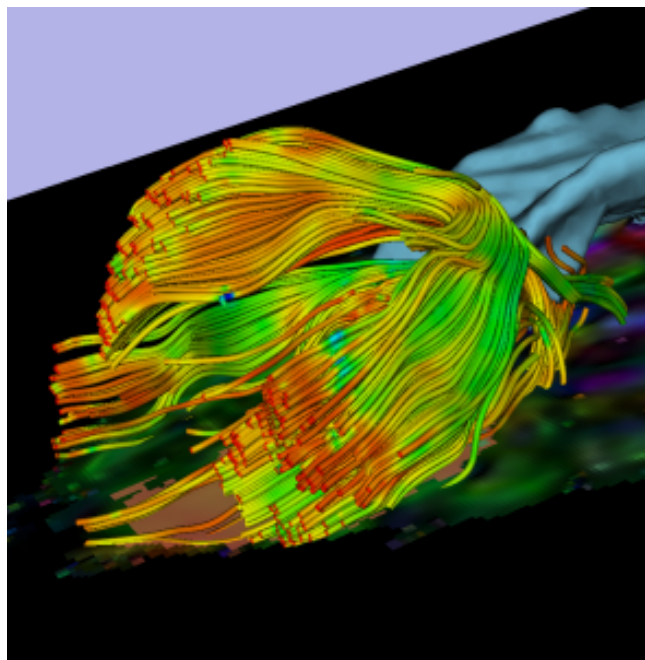
R: 25.6
A: 7.0
S: 58.7

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, green), and select the tool 'Dilate' in the Editor toolbox

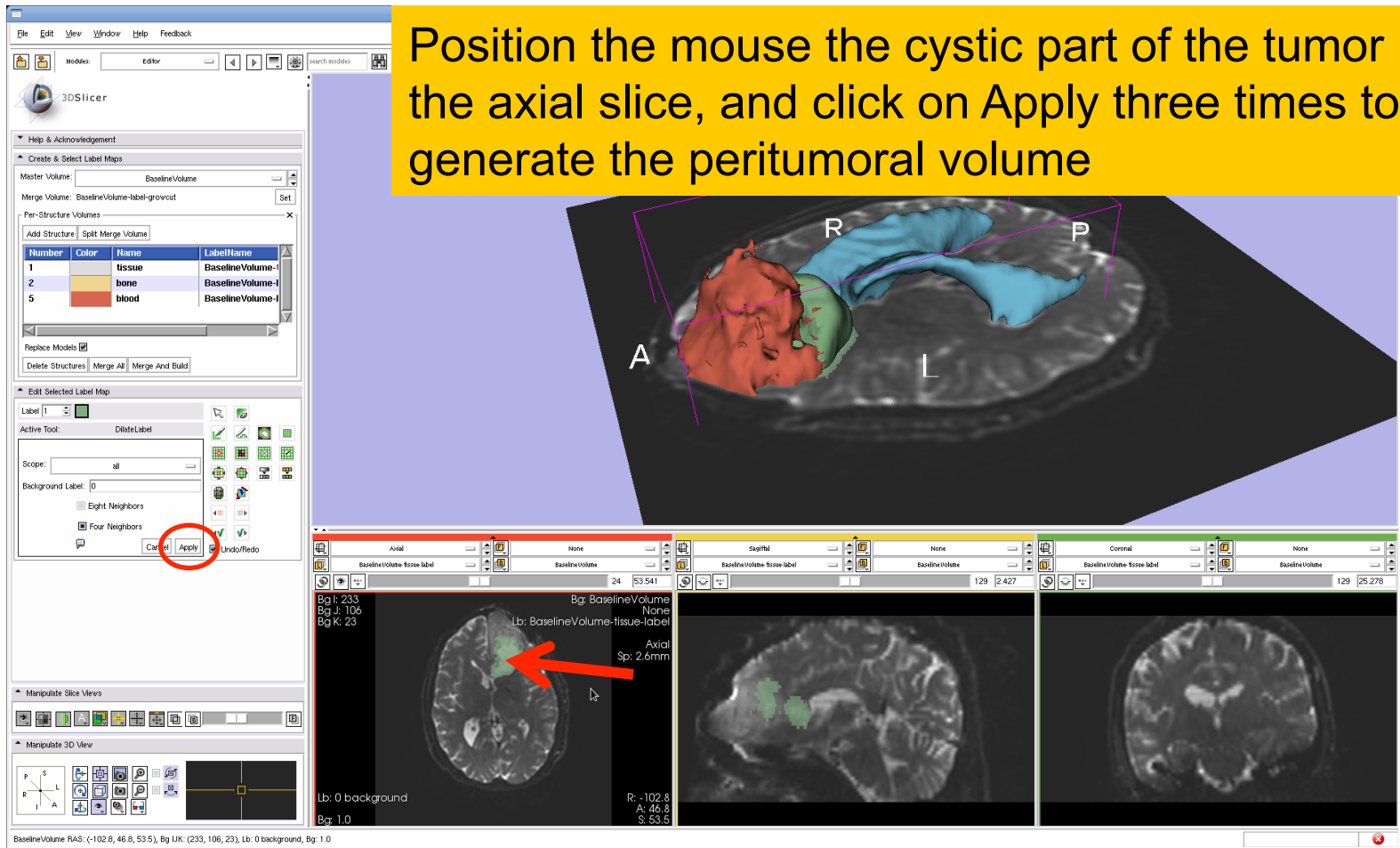
The screenshot displays the 3D Slicer software interface. On the left, the 'Create & Select Label Maps' panel shows a table of label maps:

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

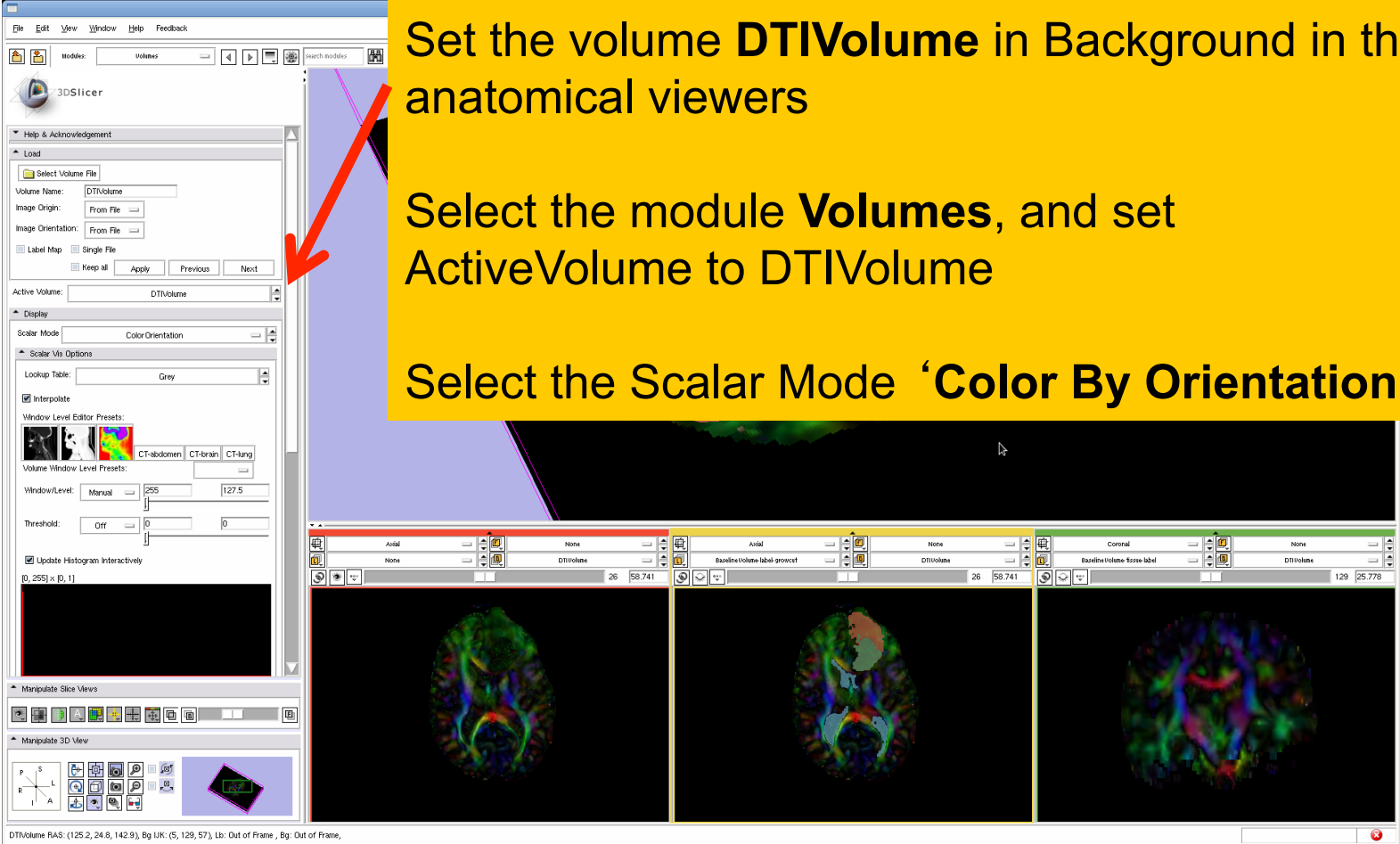
A red arrow points from the text box to the 'tissue' label map. Below this, the 'Edit Selected Label Map' panel shows the 'Active Tool' set to 'Dilate', which is circled in red. The main 3D view shows a brain slice with a green tumor volume and a red peri-tumoral volume. Anatomical markers A, R, L, and P are visible. The bottom of the interface shows three orthogonal views (Axial, Sagittal, Coronal) and a status bar at the bottom with coordinates: 'BaselineVolume 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

Position the mouse the cystic part of the tumor in the axial slice, and click on Apply three times to generate the peritumoral volume



Visualization of the DTI Volume



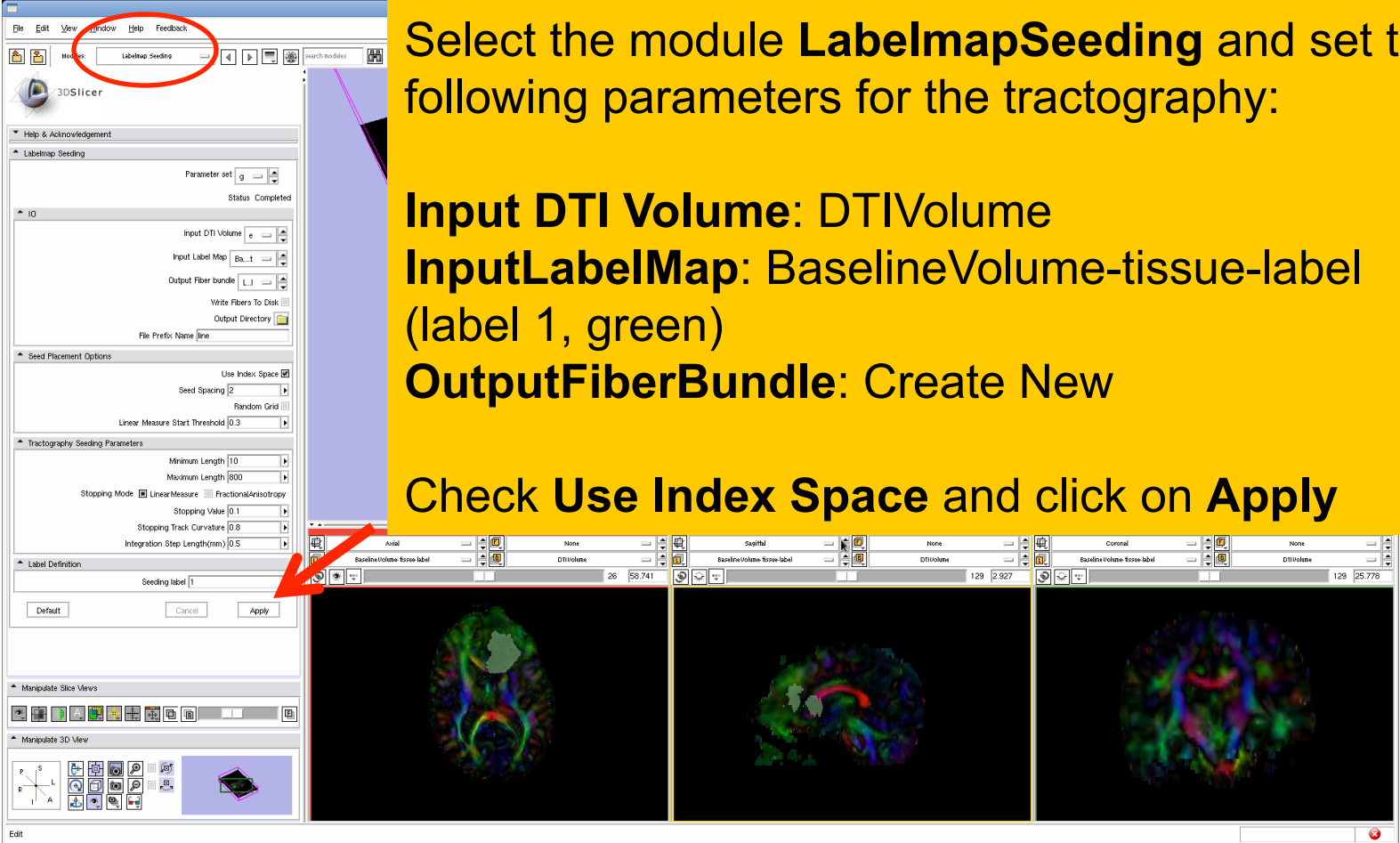
The screenshot shows the 3DSlicer interface with the 'Volumes' module selected. The 'Load' section shows 'DTIVolume' as the active volume. The 'Display' section shows 'Color Orientation' as the scalar mode. The 'Scalar Via Options' section shows 'Interpolate' checked and 'Color By Orientation' selected. The 'Window Level Editor' and 'Volume Window Level Presets' are also visible. The main 3D view shows a brain slice with DTI volume visualization in three orthogonal planes (Axial, Coronal, and Sagittal).

Set the volume **DTIVolume** in Background in the anatomical viewers

Select the module **Volumes**, and set ActiveVolume to DTIVolume

Select the Scalar Mode '**Color By Orientation**'

Tractography Parameters

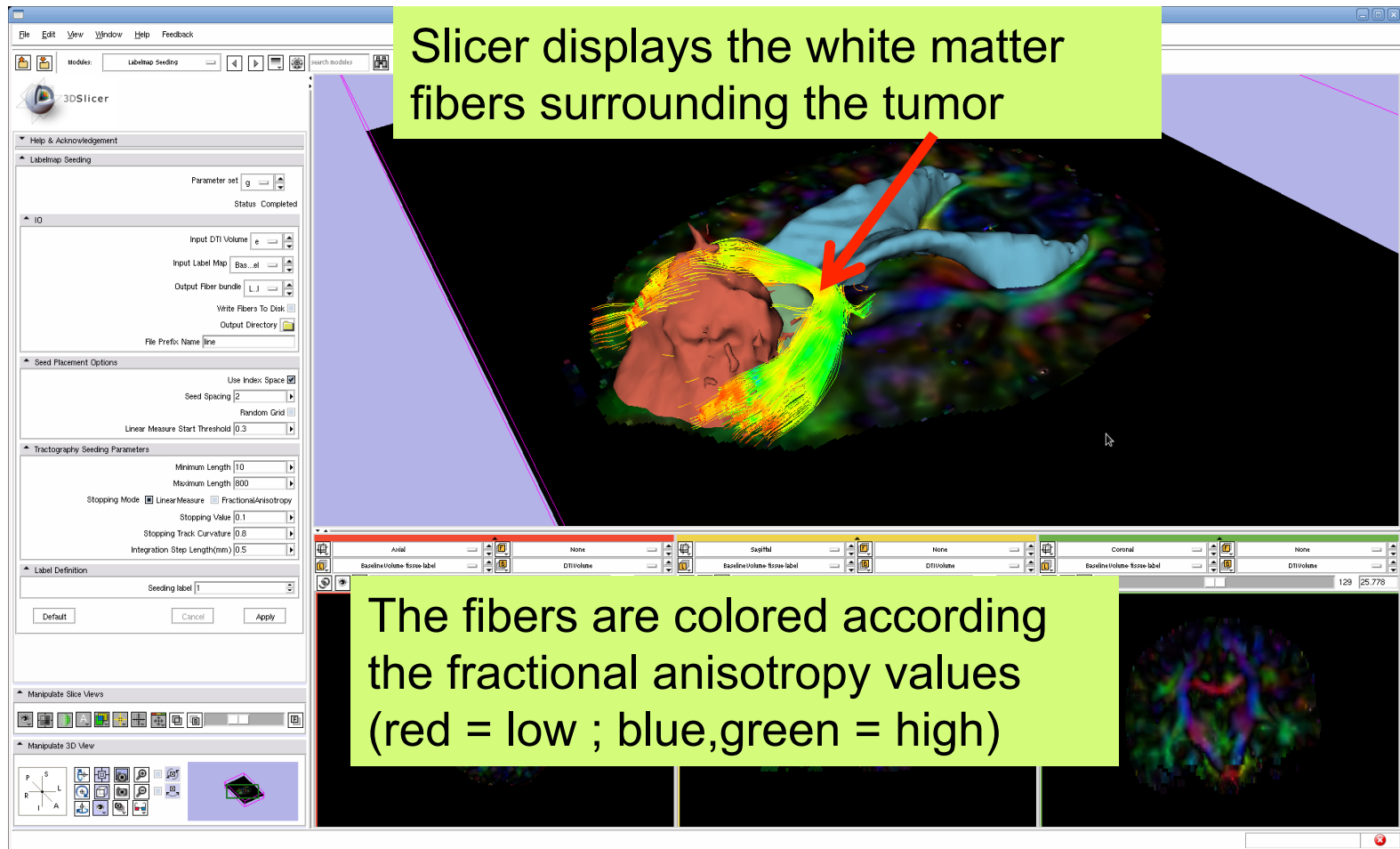


Select the module **LabelmapSeeding** and set the following parameters for the tractography:

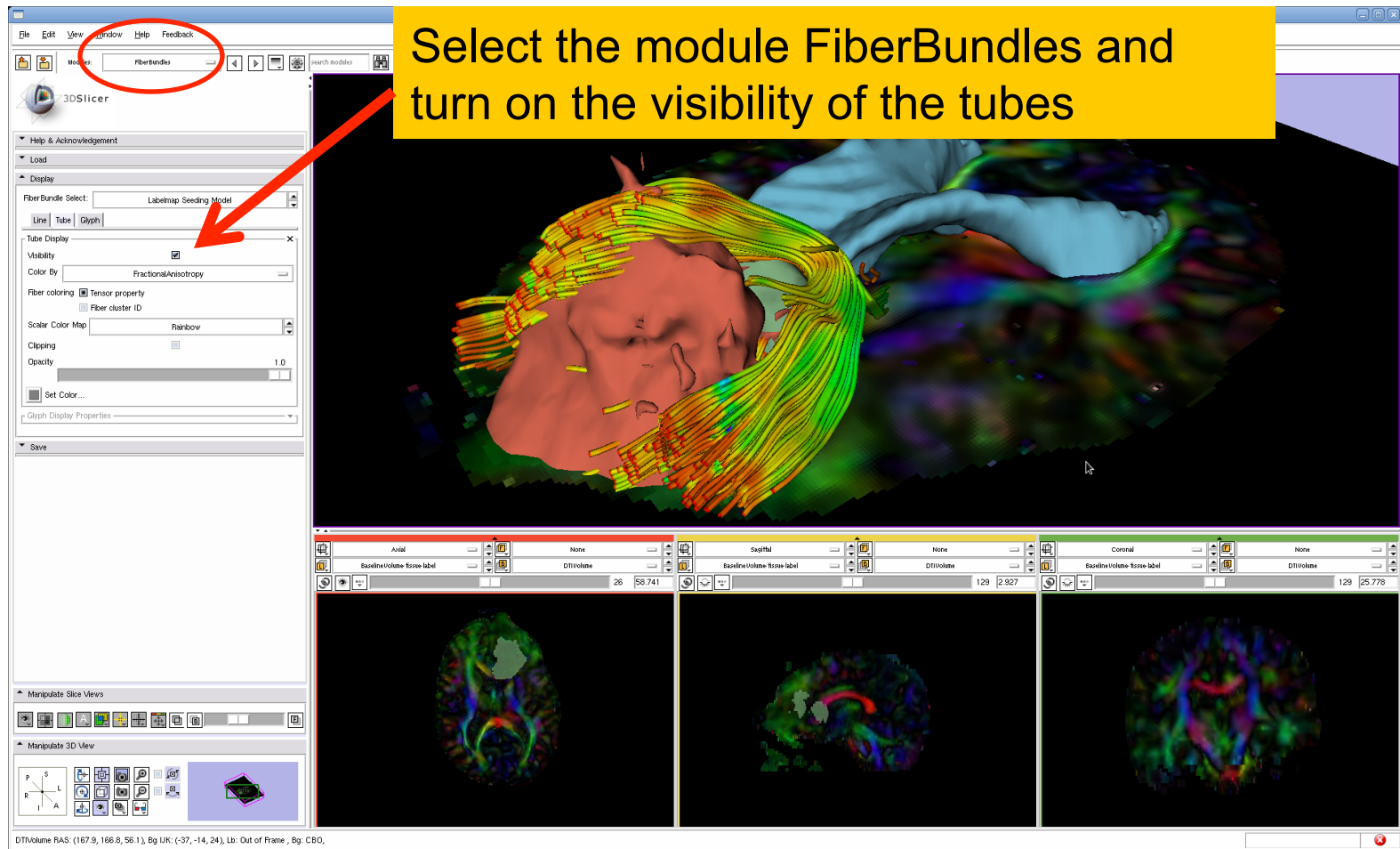
- Input DTI Volume:** DTIVolume
- InputLabelMap:** BaselineVolume-tissue-label (label 1, green)
- OutputFiberBundle:** Create New

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

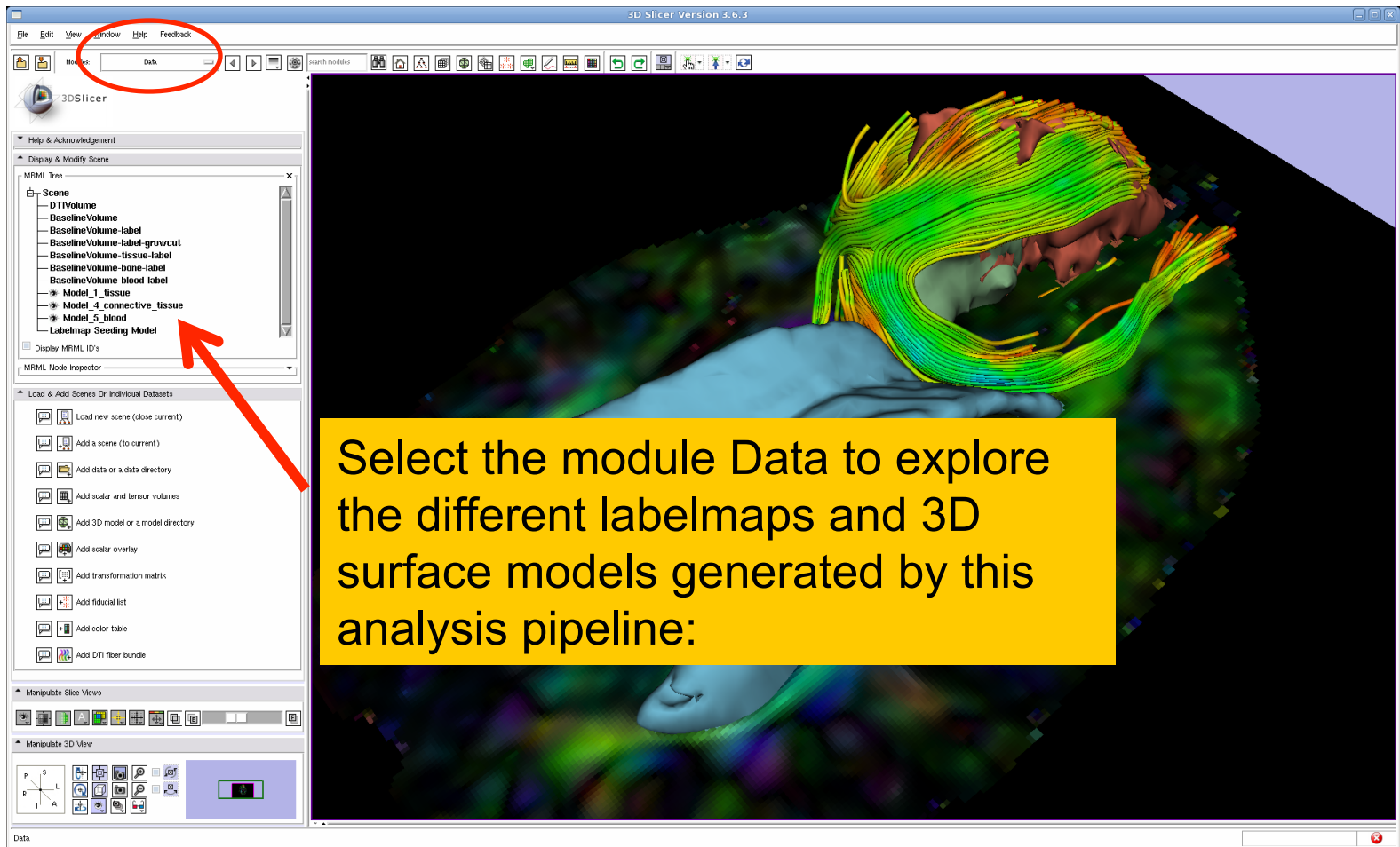
Tractography Results

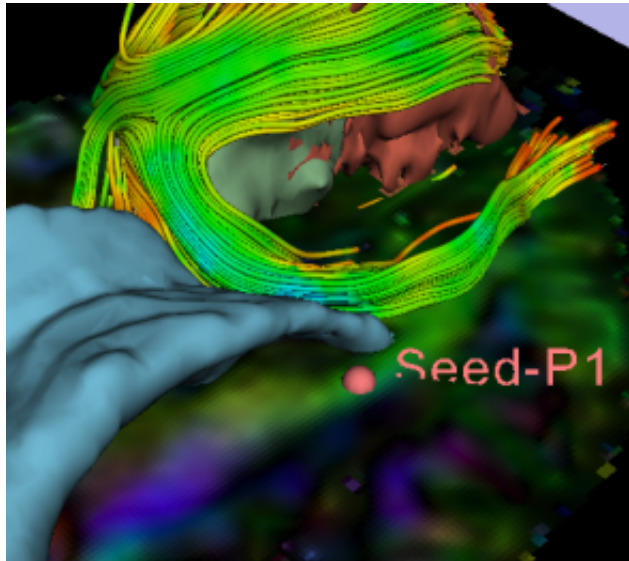


Tractography Results



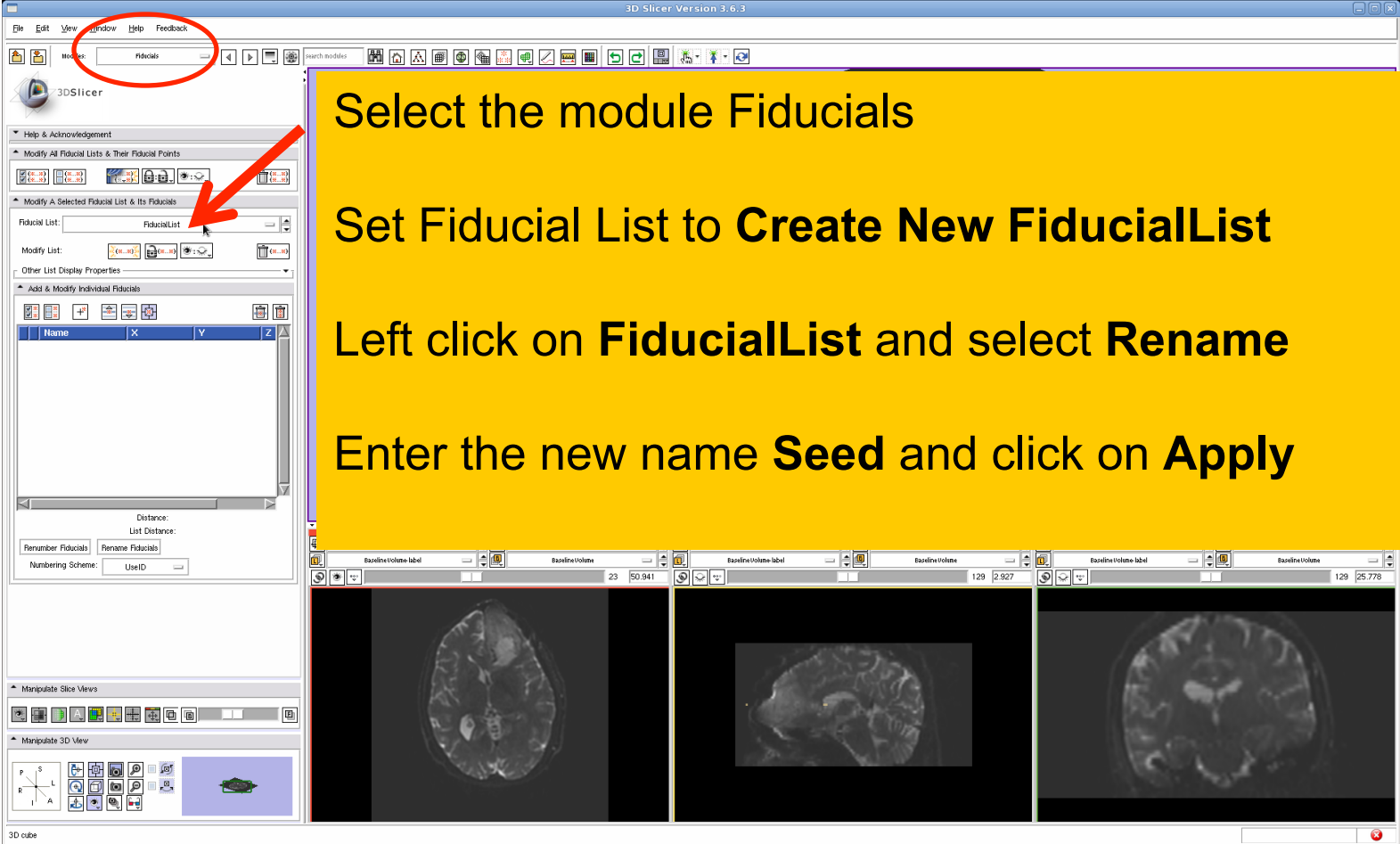
Tractography Results





Part 4: Tractography exploration of the ipsilateral and contralateral side

Tractography on-the-fly




Select the module **Fiducials**

Set Fiducial List to **Create New FiducialList**

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

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

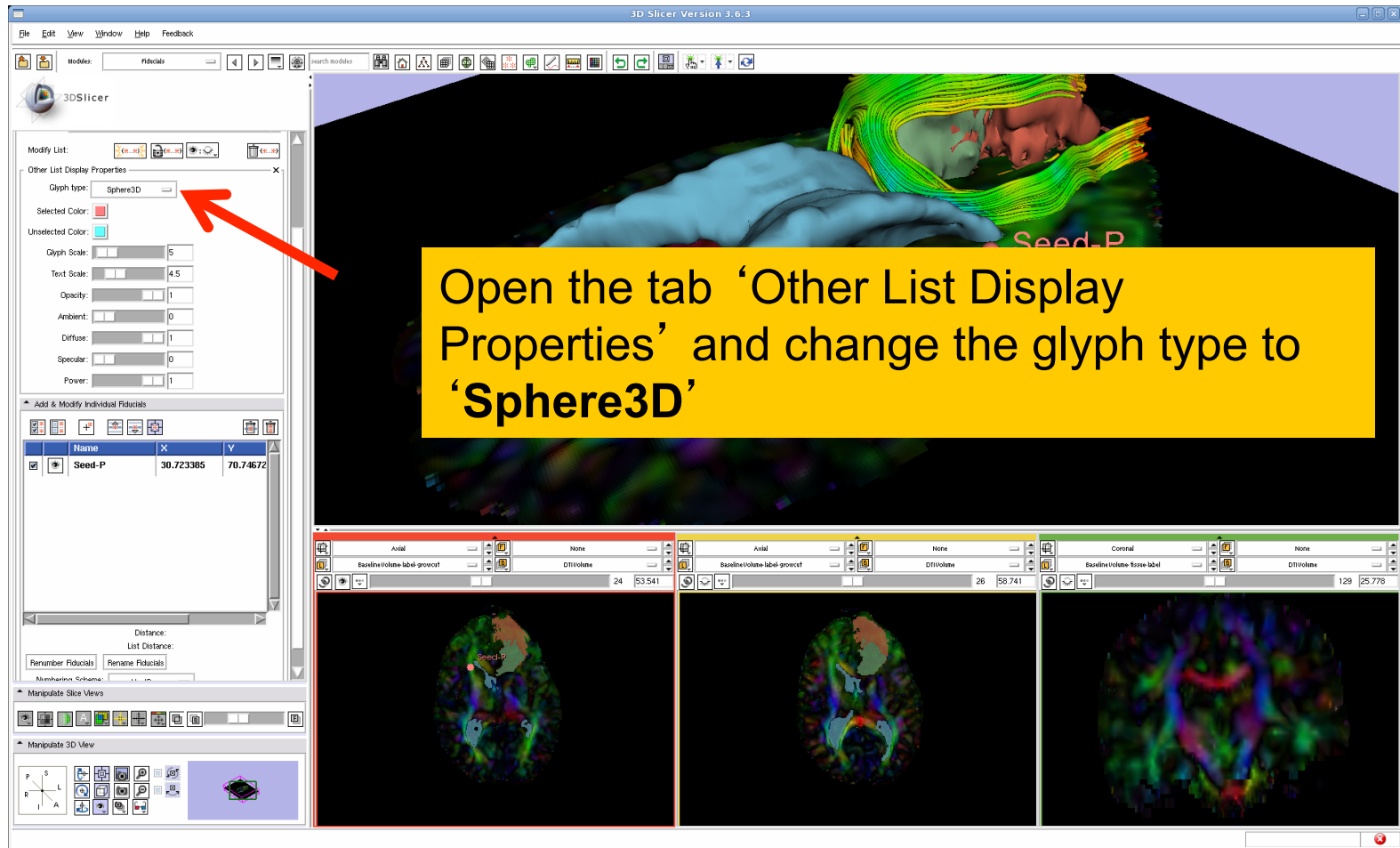
Tractography on-the-fly

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

Check the box to activate the fiducial **Seed-P1**

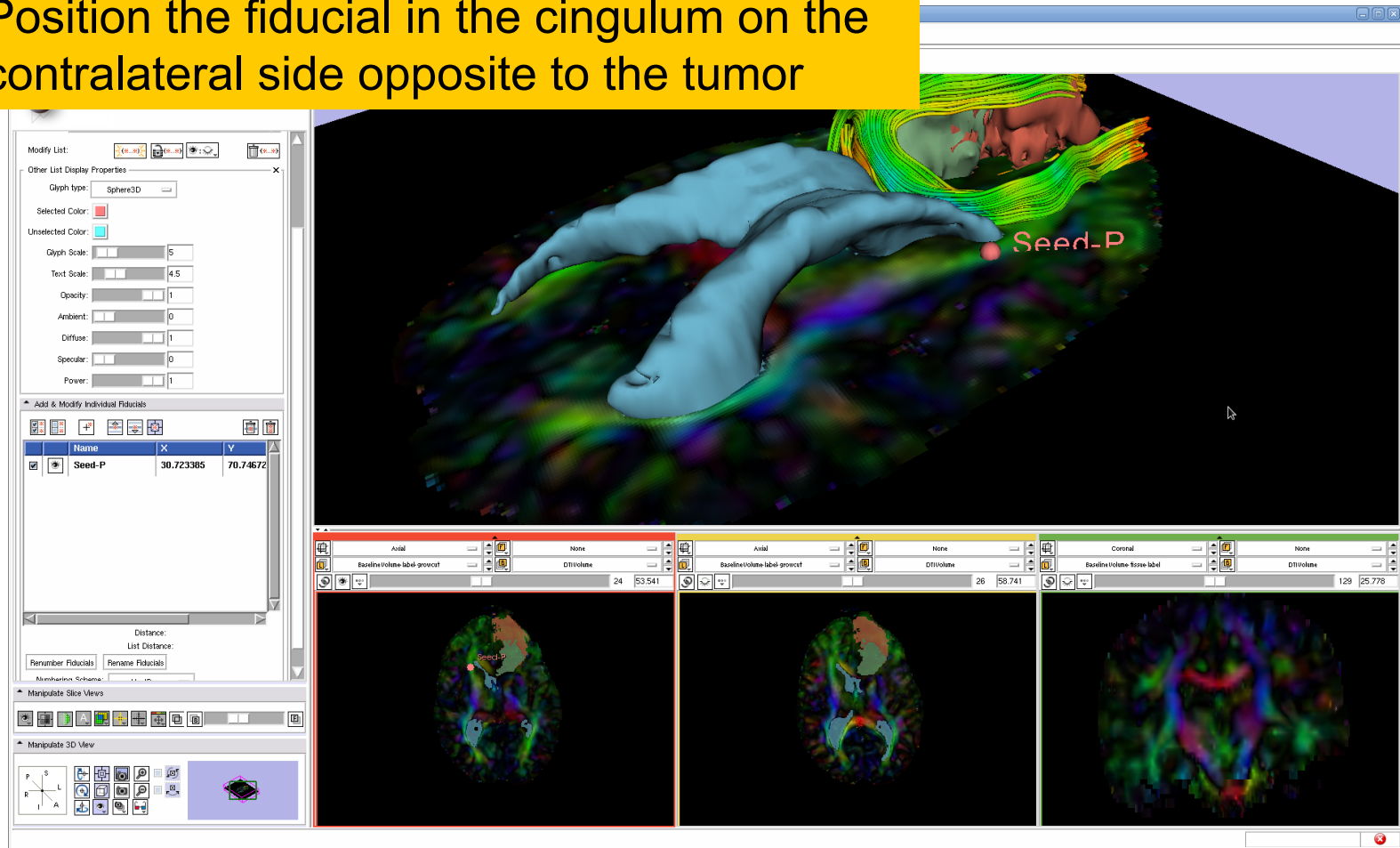
Name	X	Y
Seed-P1	0.000000	0.000000

Fiducial Seeding

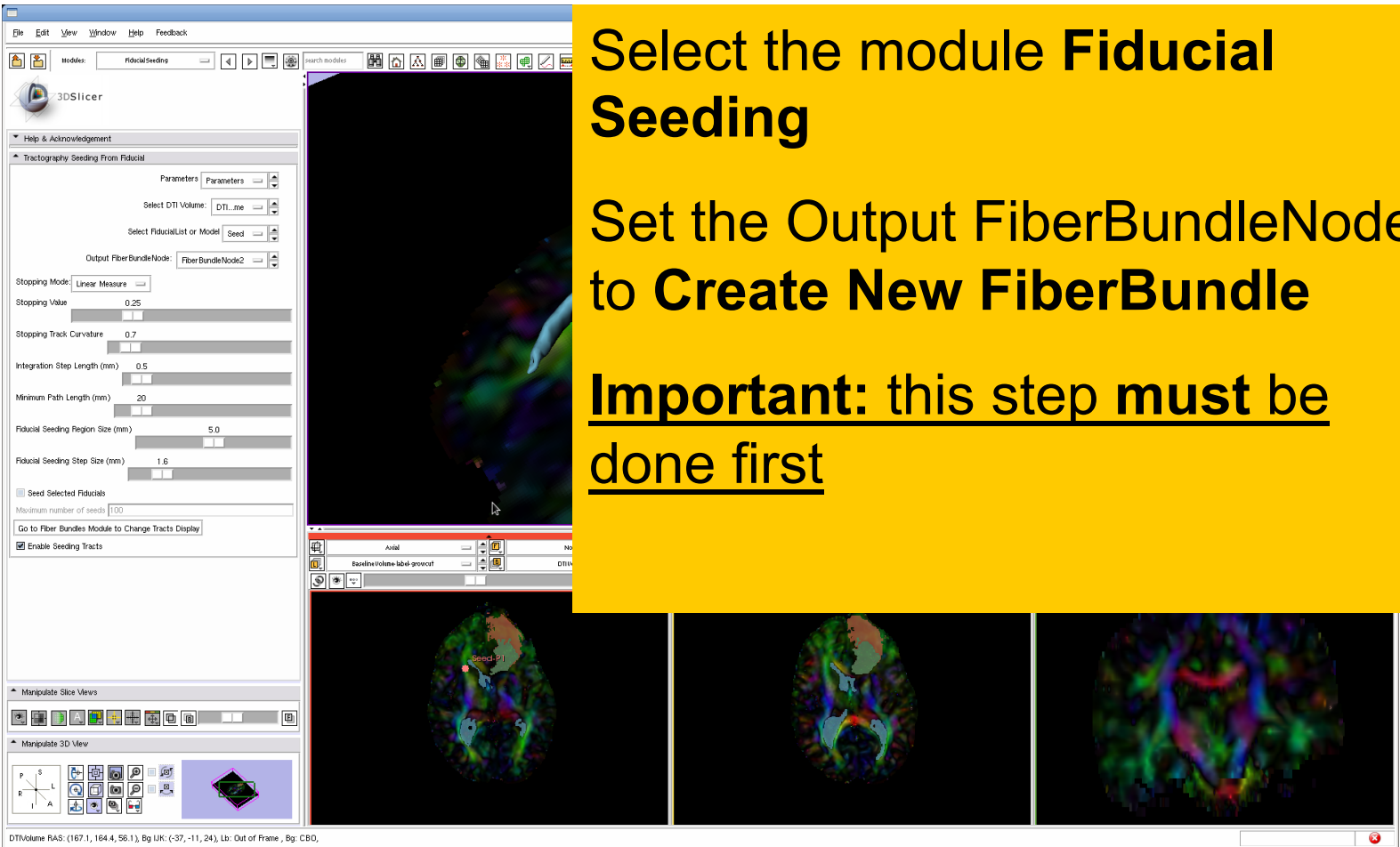


Fiducial Seeding

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



Tractography on-the-fly

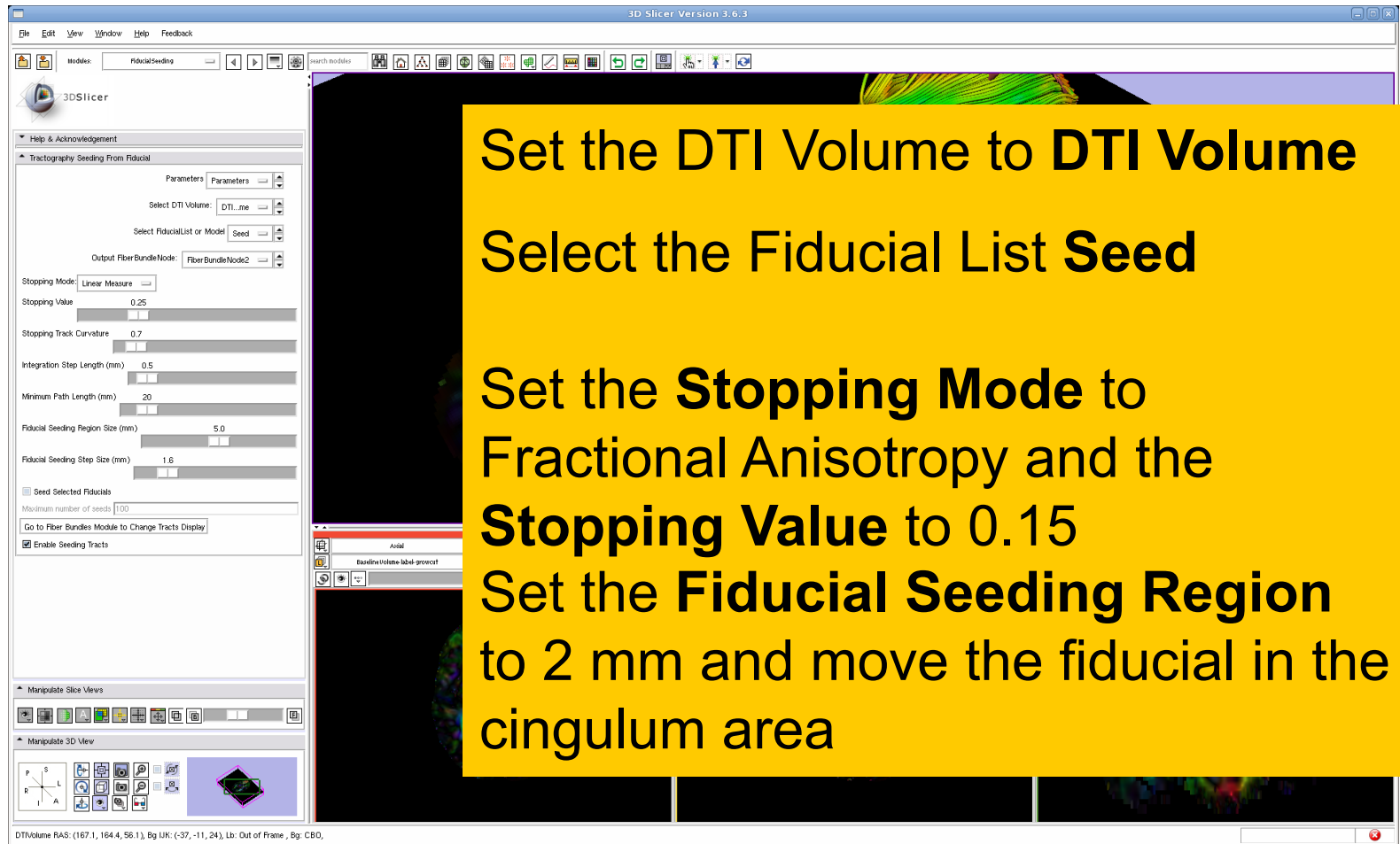


Select the module **Fiducial Seeding**

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

Important: this step must be done first

Tractography on-the-fly



3D Slicer Version 3.6.3

File Edit View Window Help Feedback

Models: FiducialSeeding

3DSlicer

Help & Acknowledgement

Tractography, Seeding From Fiducial

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

Manipulate Slice Views

Manipulate 3D View

DTIVolume RAS: (167.1, 164.4, 56.1), By LJK: (-37, -11, 24), Lb: Out of Frame , Bg: C80.

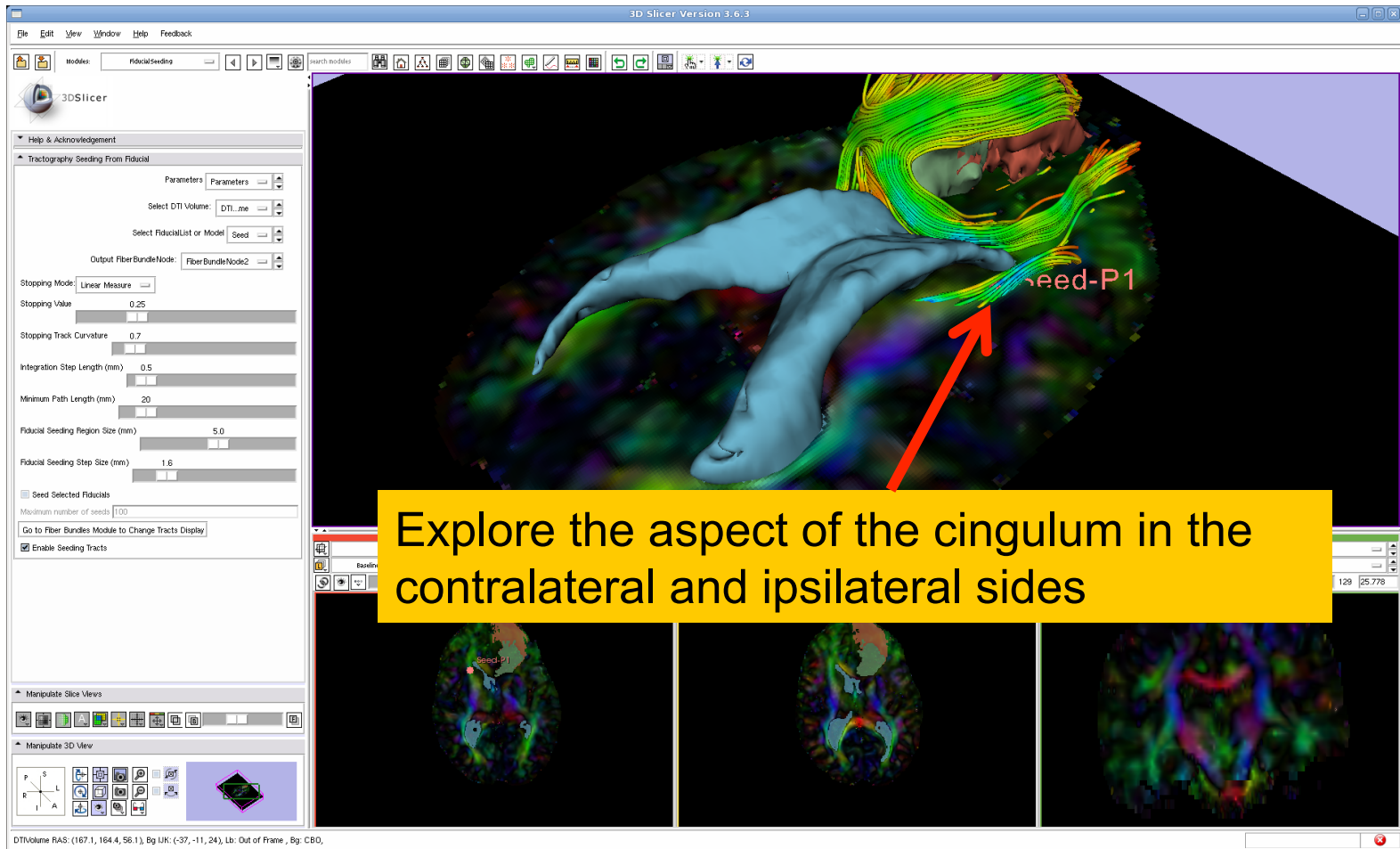
Set the DTI Volume to DTI Volume

Select the Fiducial List Seed

Set the Stopping Mode to Fractional Anisotropy and the Stopping Value to 0.15

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



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