Exploring Peritumoral White Matter Fibers for Neurosurgical Planning

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Harvard University

Clinical Goal

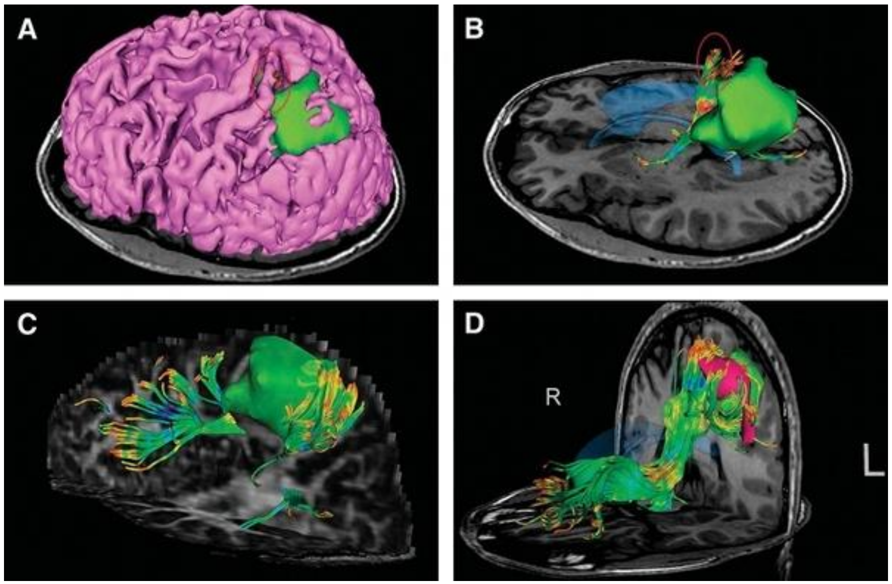

Image Courtesy of Dr. Alexandra Golby, Brigham and Women's Hospital, Boston, MA..

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.

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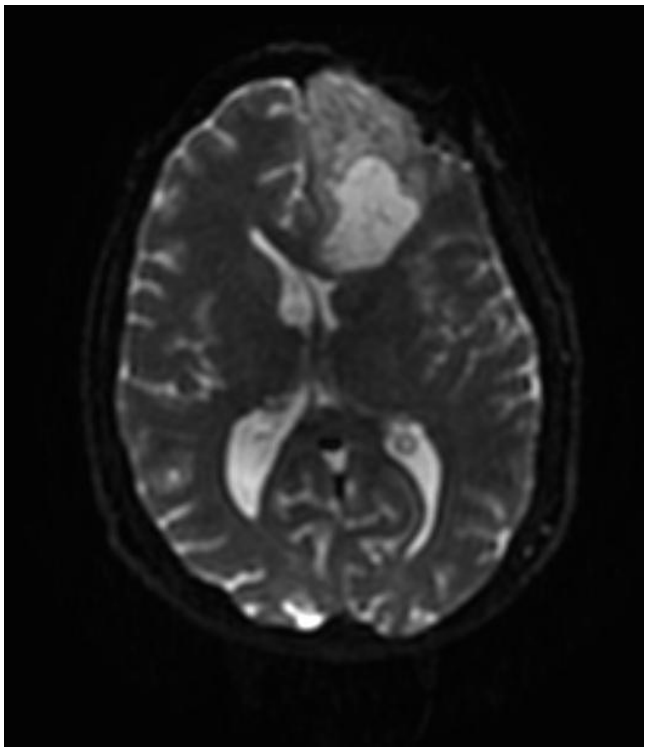
Clinical Case



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

(White Matter Exploration Dataset)

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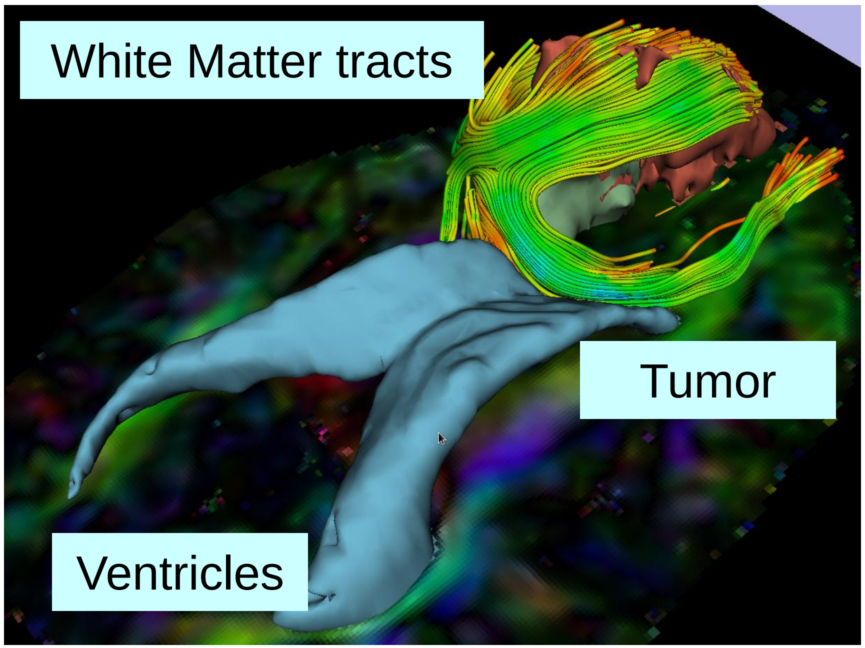
Clinical Goal



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

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Material

- This tutorial uses the Slicer3.6.3 release version available at www.slicer.org

- Windows XP: Slicer3-3.6.3-2011-03-04-win32.exe
- Mac OS: Slicer3-3.6.3-2011-03-04-darwin-x86
- Linux_x86: Slicer3-3.6.3-2011-03-04-linux-x86
- Linux_x86_64: Slicer3-3.6.3-2011-03-04-linux-x86_64

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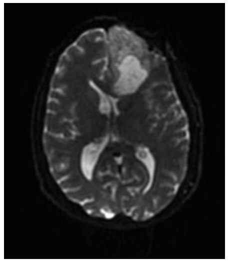
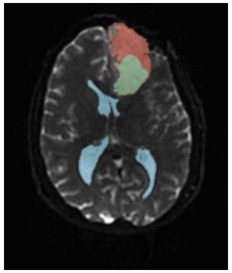
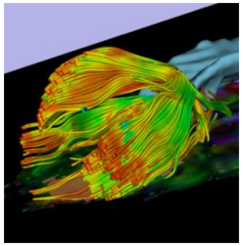
Overview of the analysis pipeline



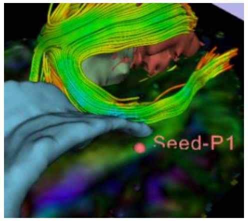
Part 1: Loading &Visualization of Diffusion Data



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

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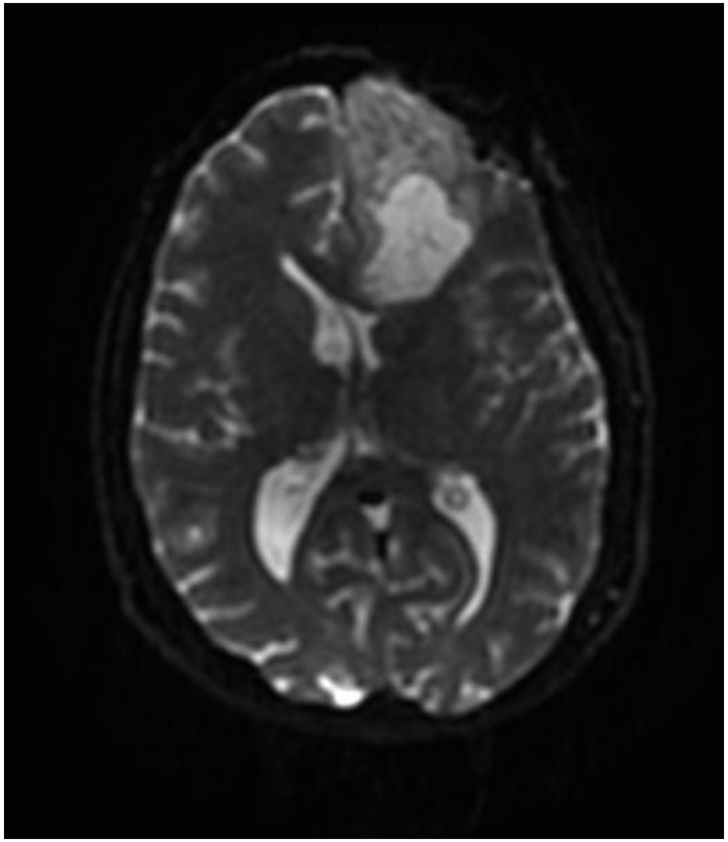

Part 1: Loading and Visualization of Diffusion Data

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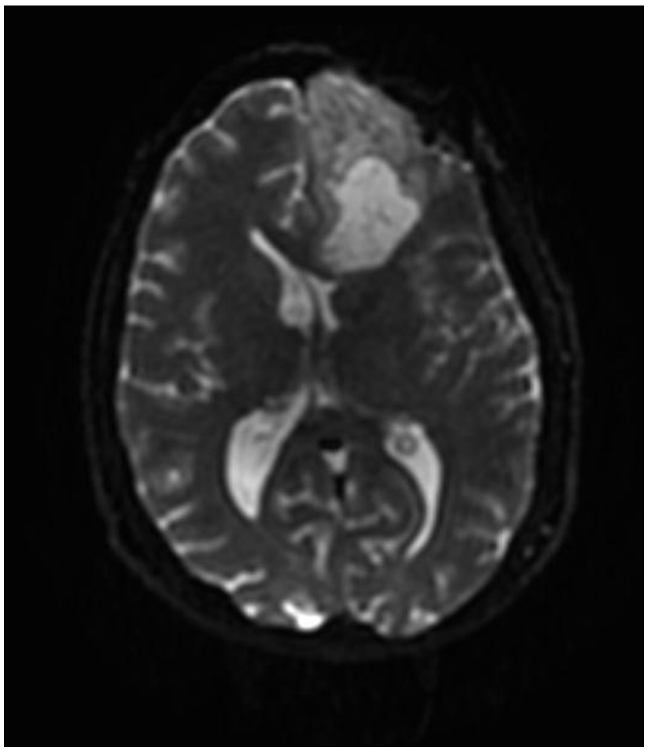
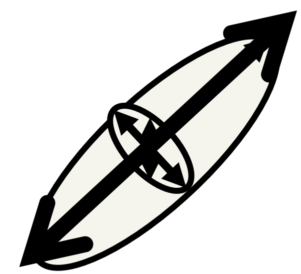
Diffusion Tensor Imaging



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

(Stejskal and Tanner 1965, Basser 1994)

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



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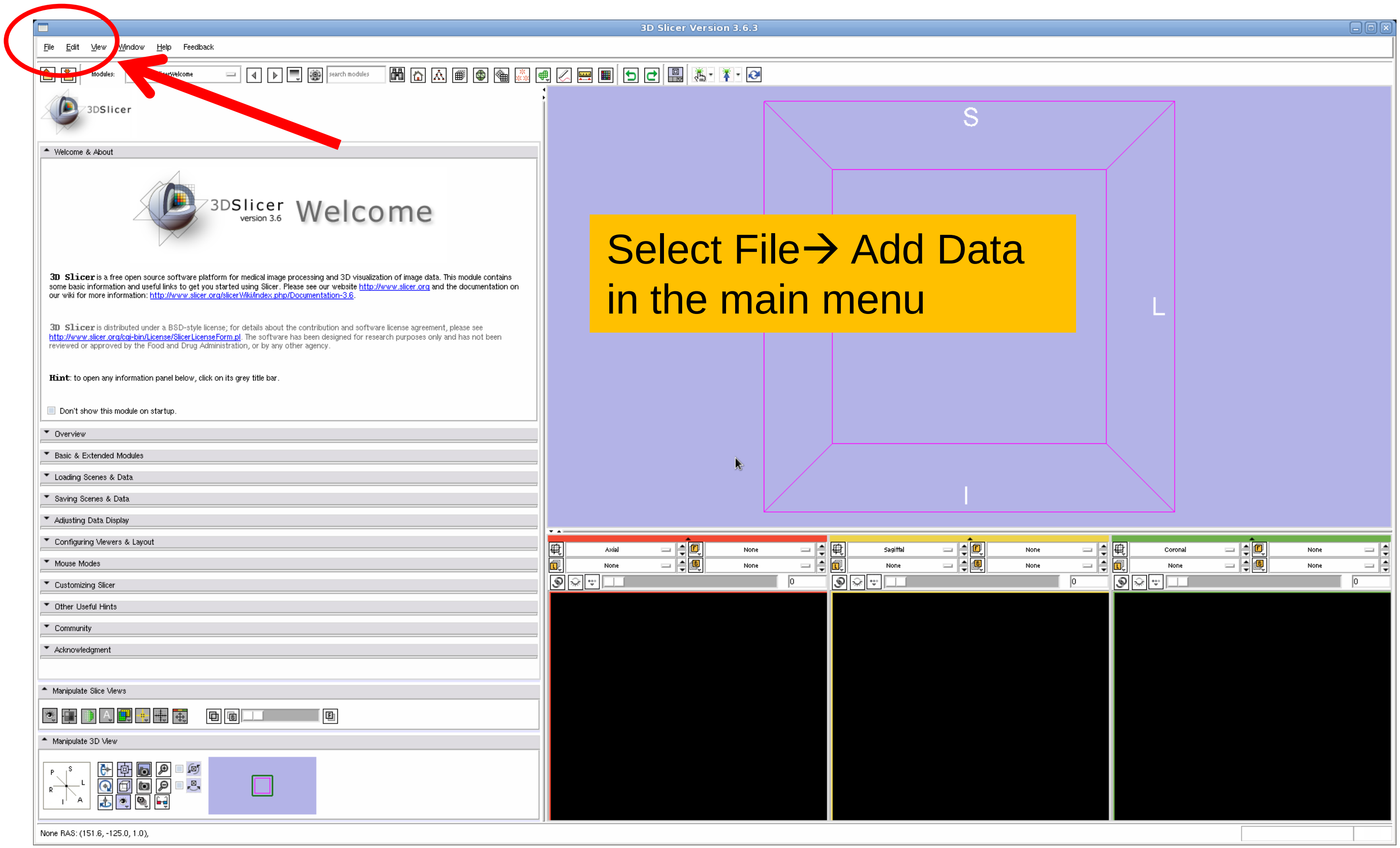
Loading DTI and Baseline Data



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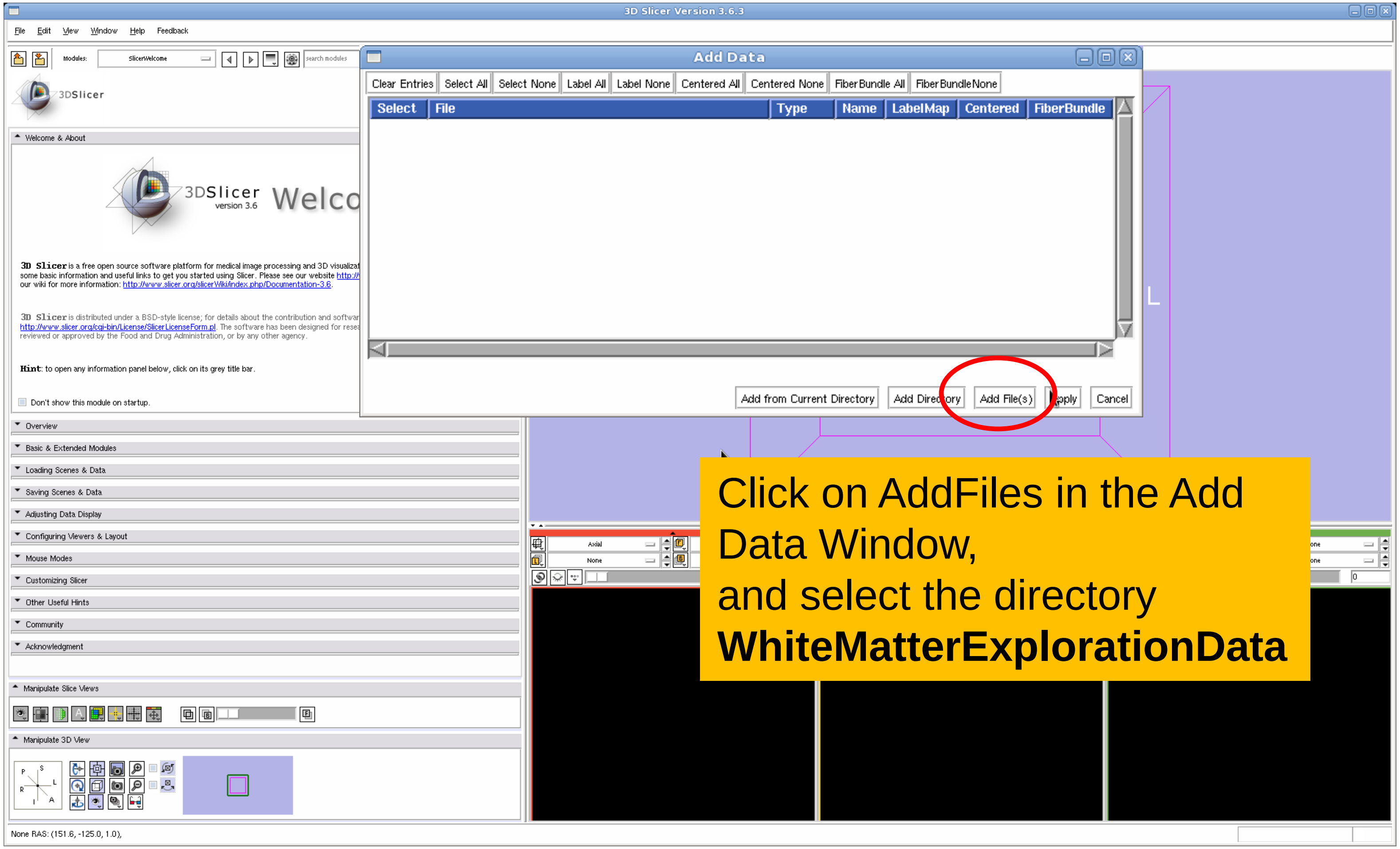
Loading DTI and Baseline Data



Click on AddFiles in the Add Data Window,
and select the directory
WhiteMatterExplorationData

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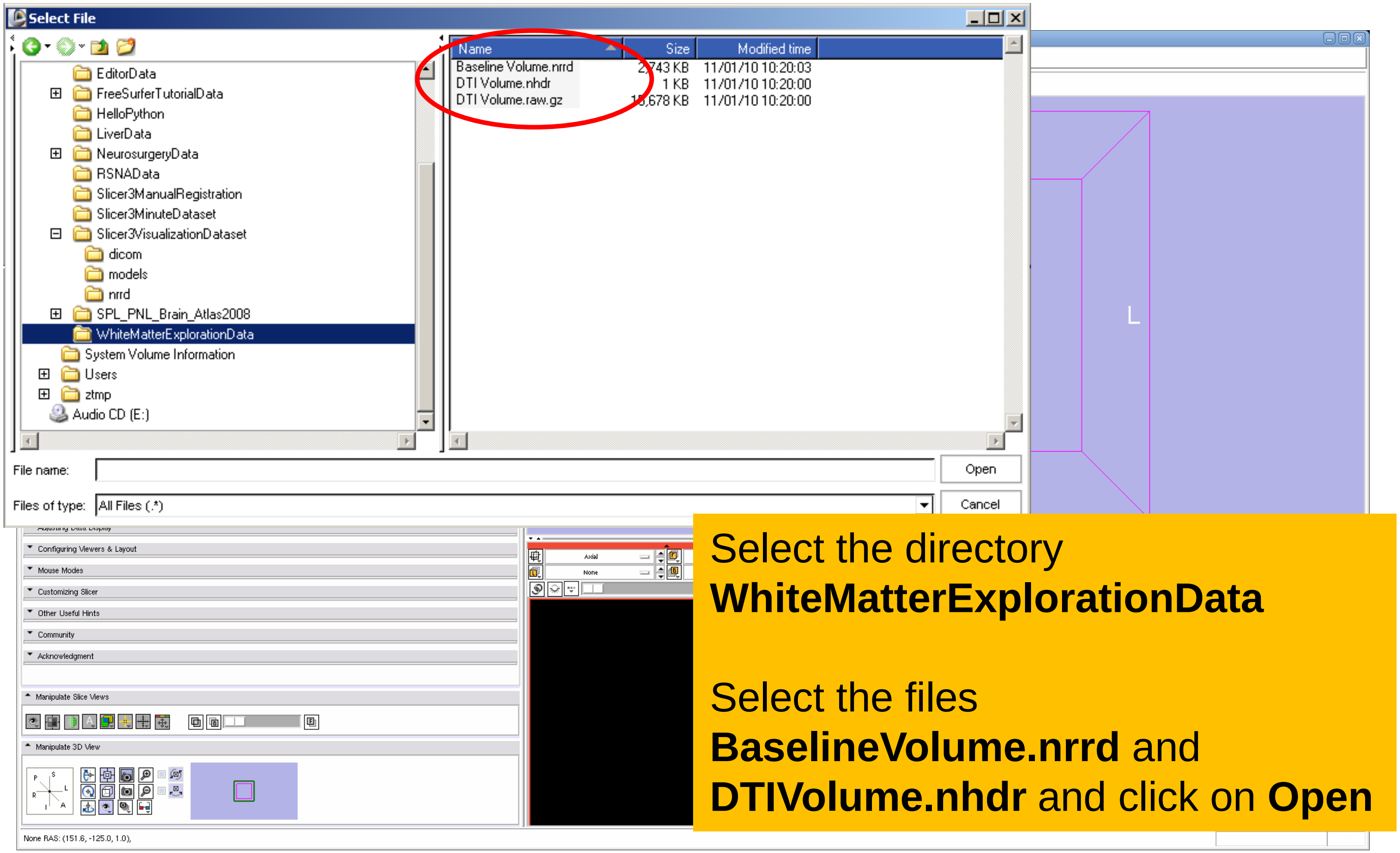
Loading DTI and Baseline Data



Select the directory **WhiteMatterExplorationData**

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

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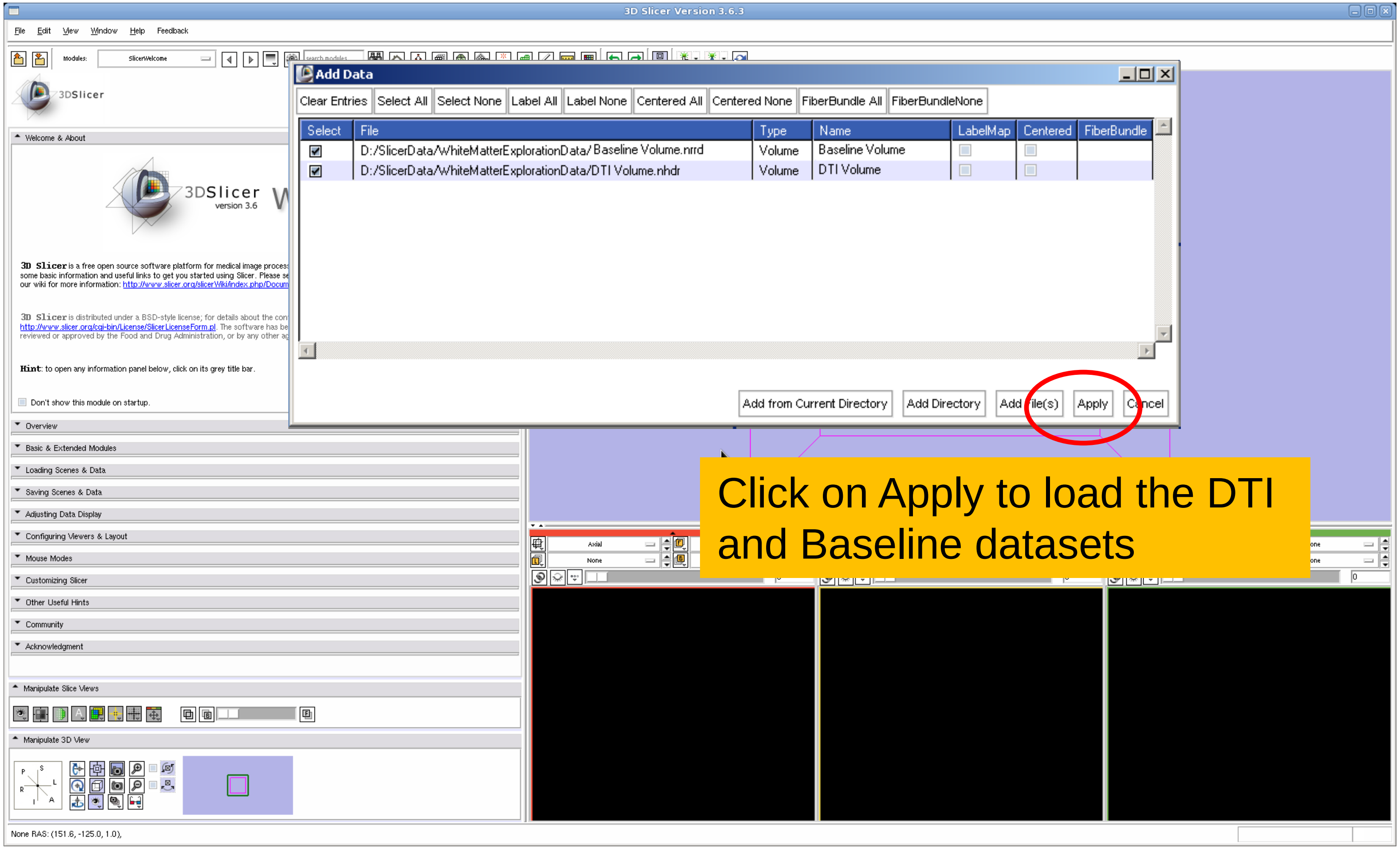
Loading DTI and Baseline Data



Click on Apply to load the DTI and Baseline datasets

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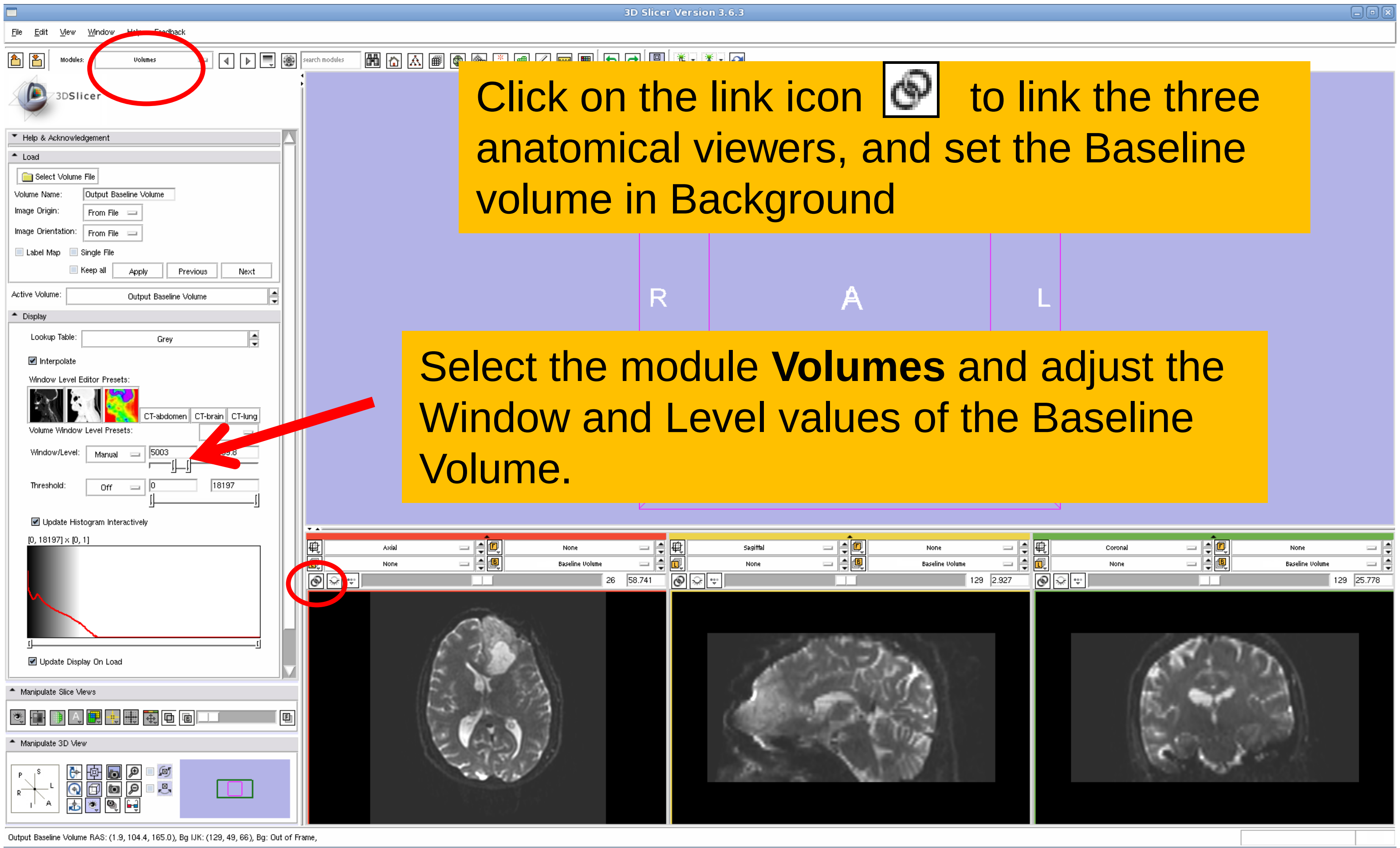
Loading DTI and Baseline Data



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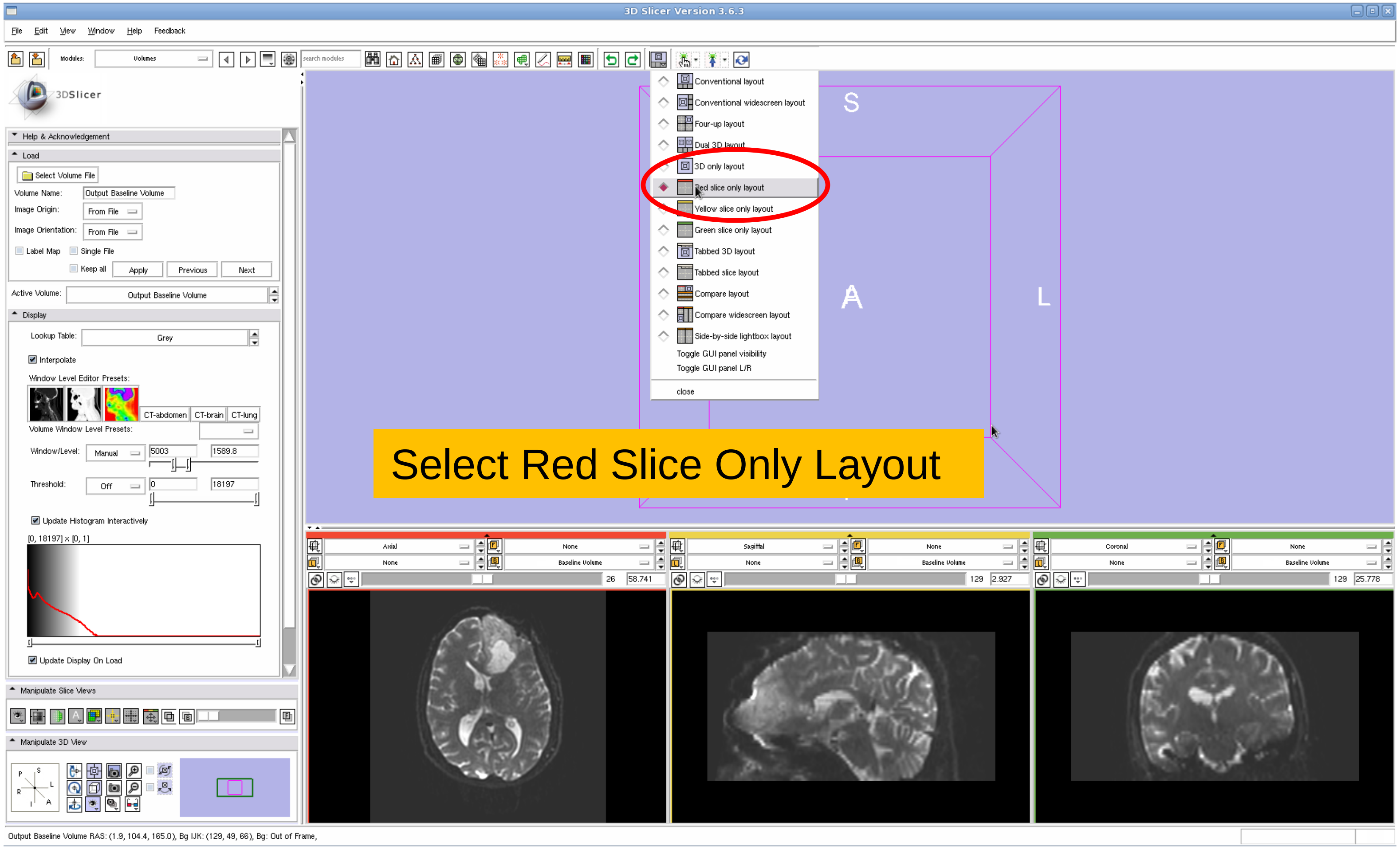
Loading DTI and Baseline Data



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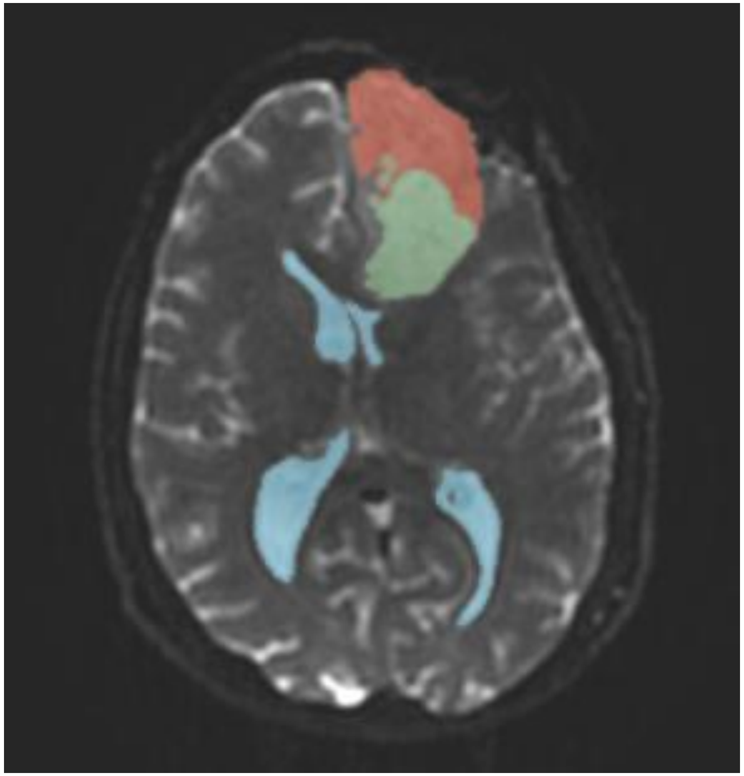

Part 1: Segmenting the tumor and ventricles

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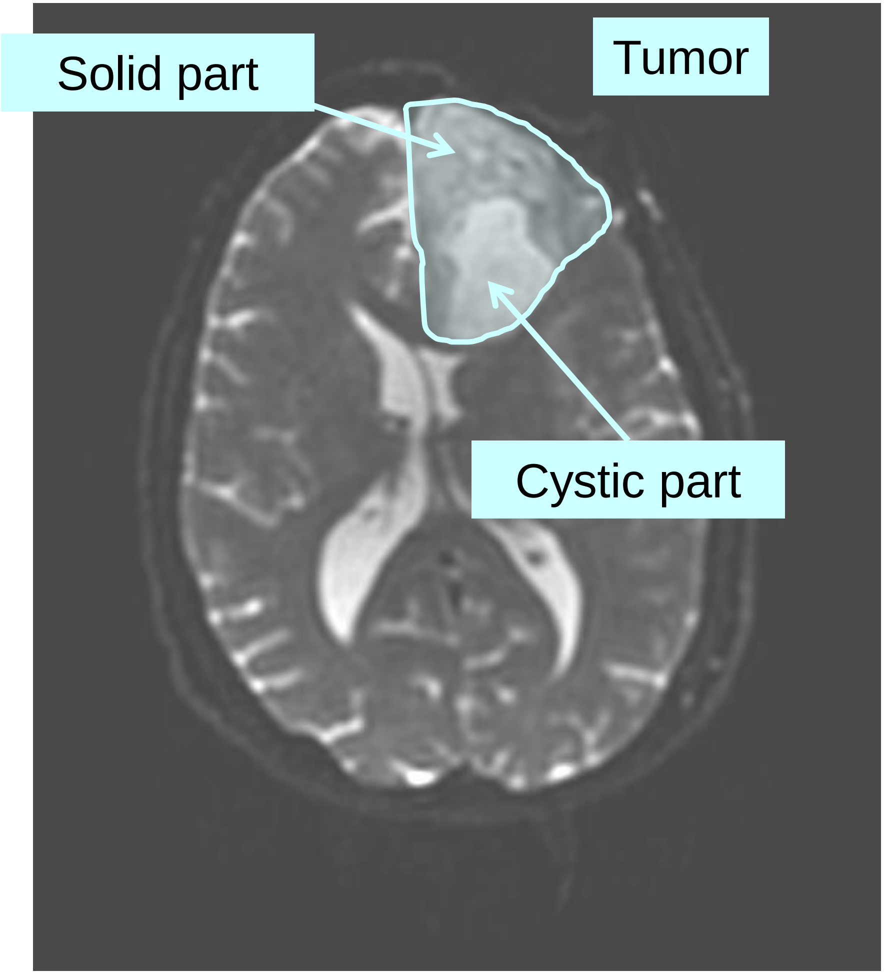
Tumor Segmentation



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.

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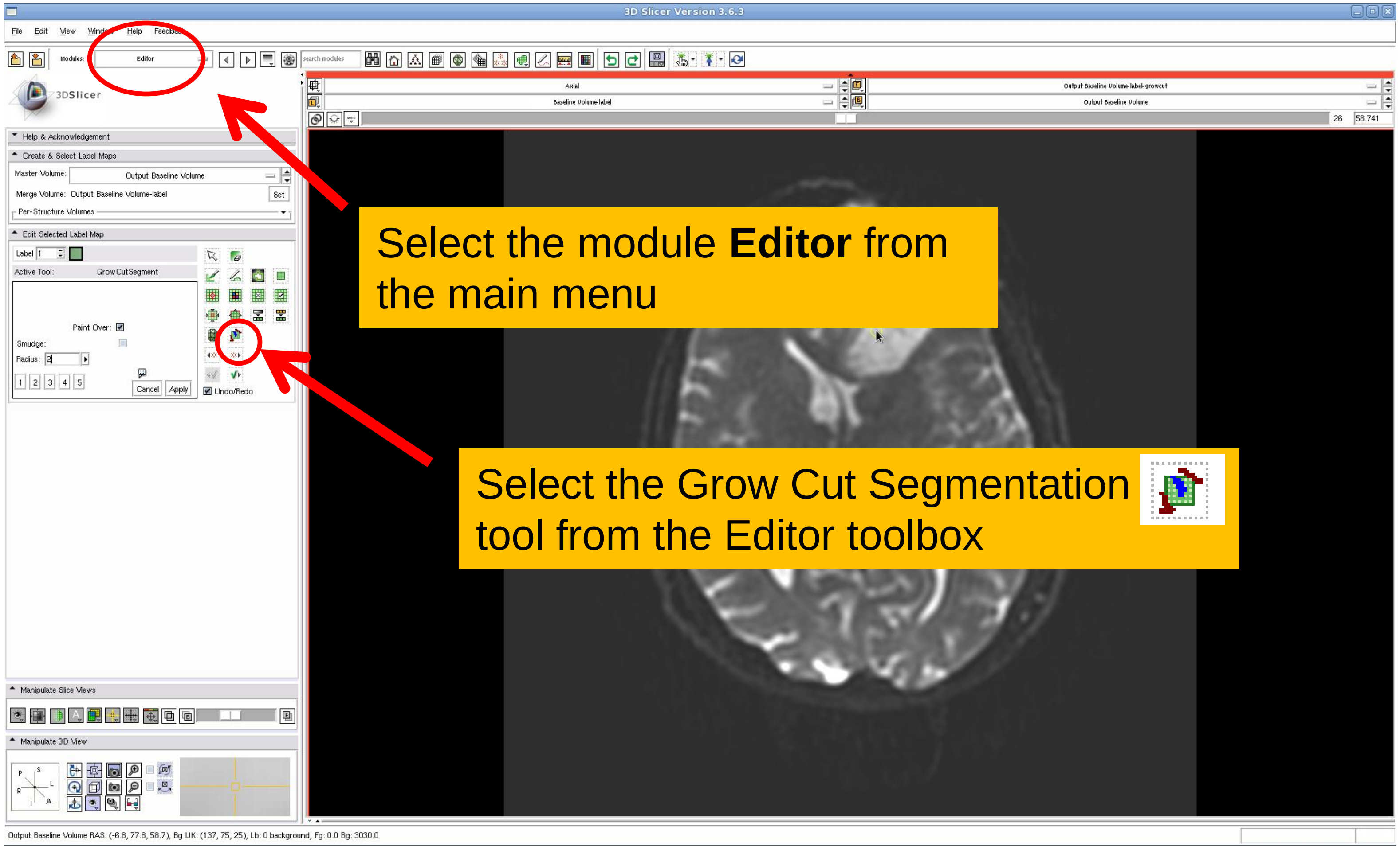
Tumor Segmentation



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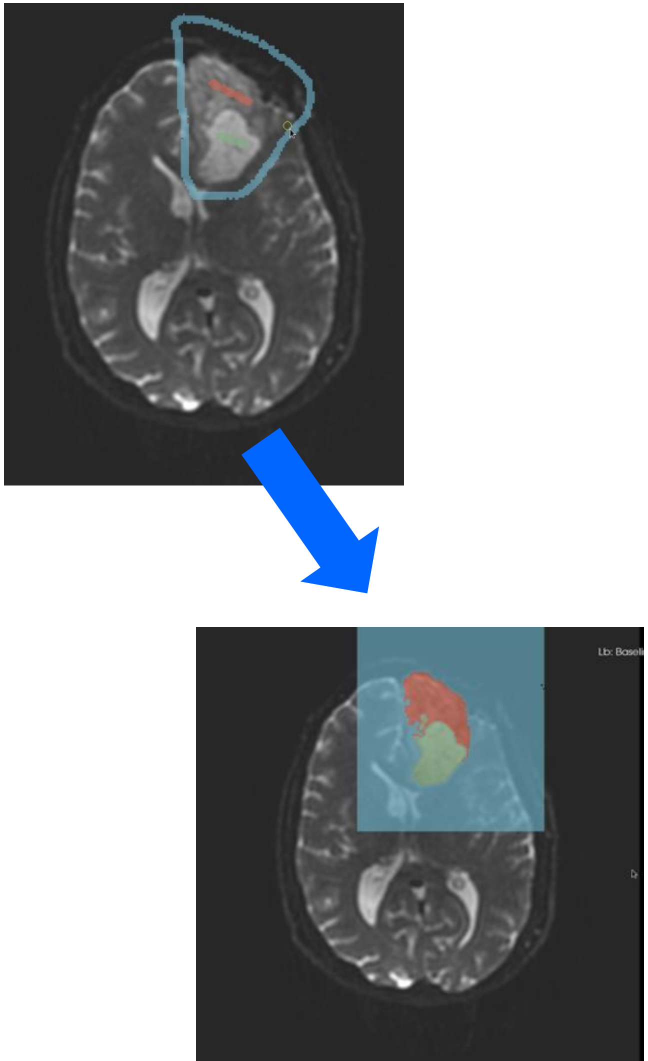
Grow Cut Segmentation



- 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.

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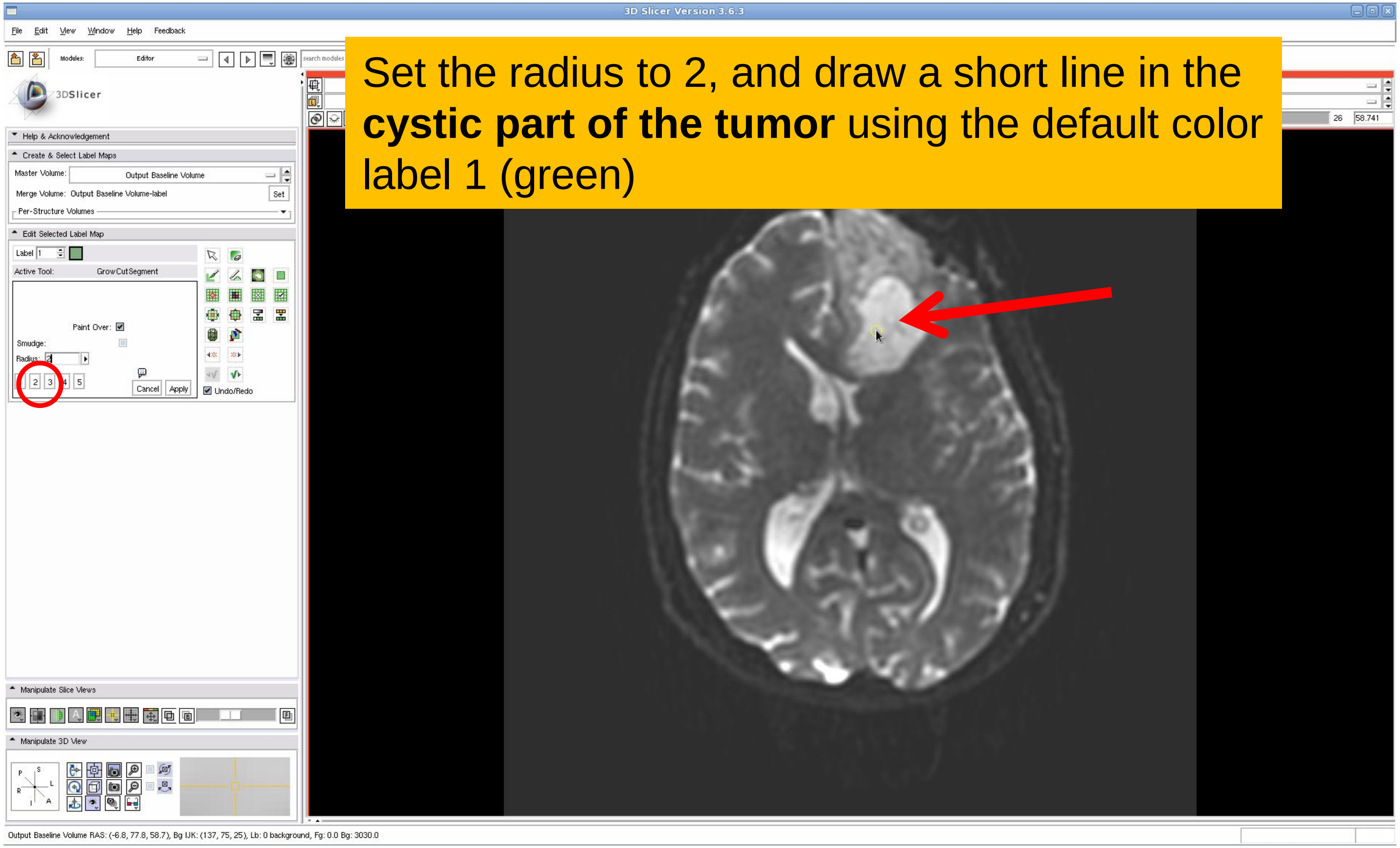
Tumor Segmentation

Set the radius to 2, and draw a short line in the **cystic part of the tumor** using the default color label 1 (green)



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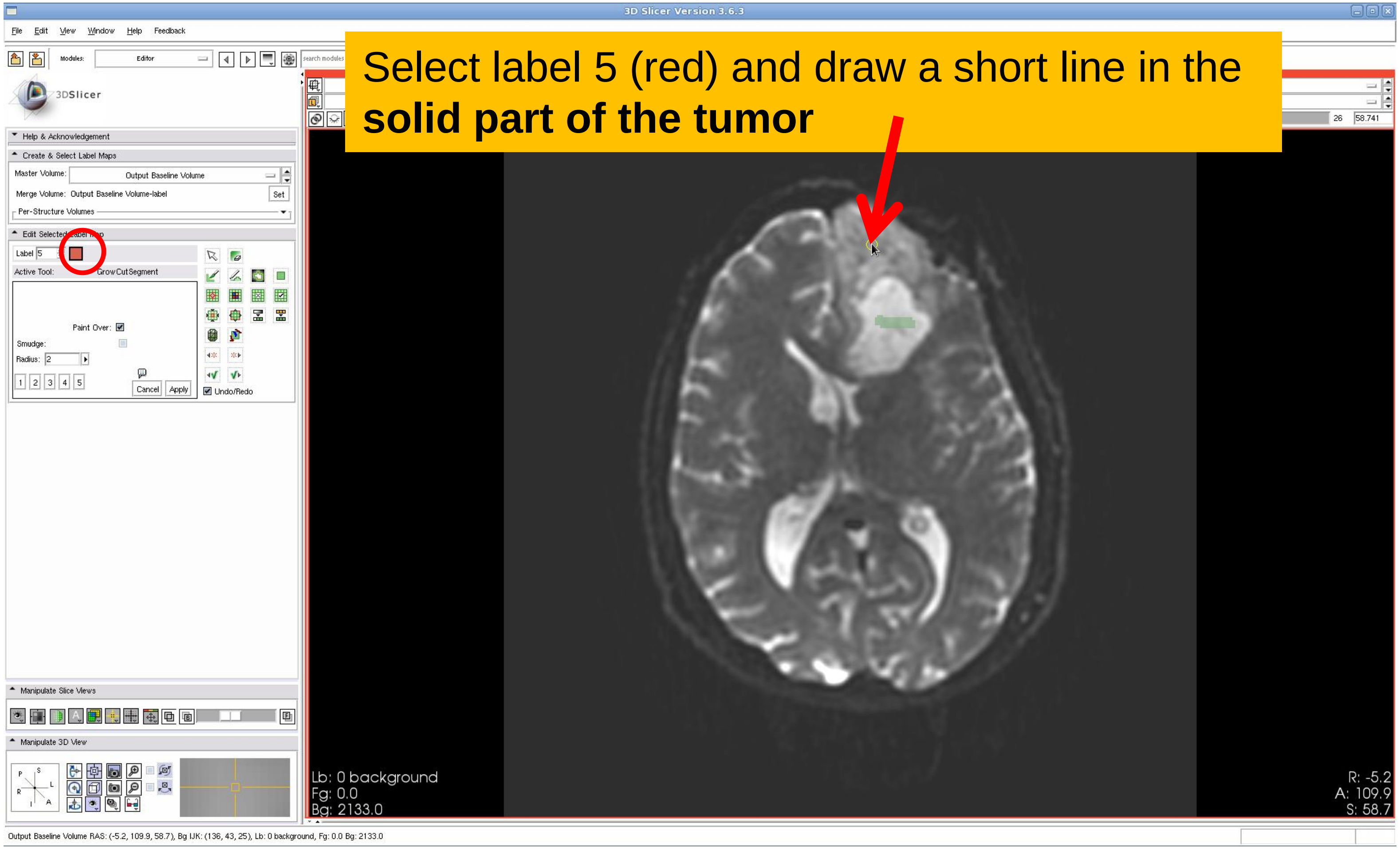
Tumor Segmentation



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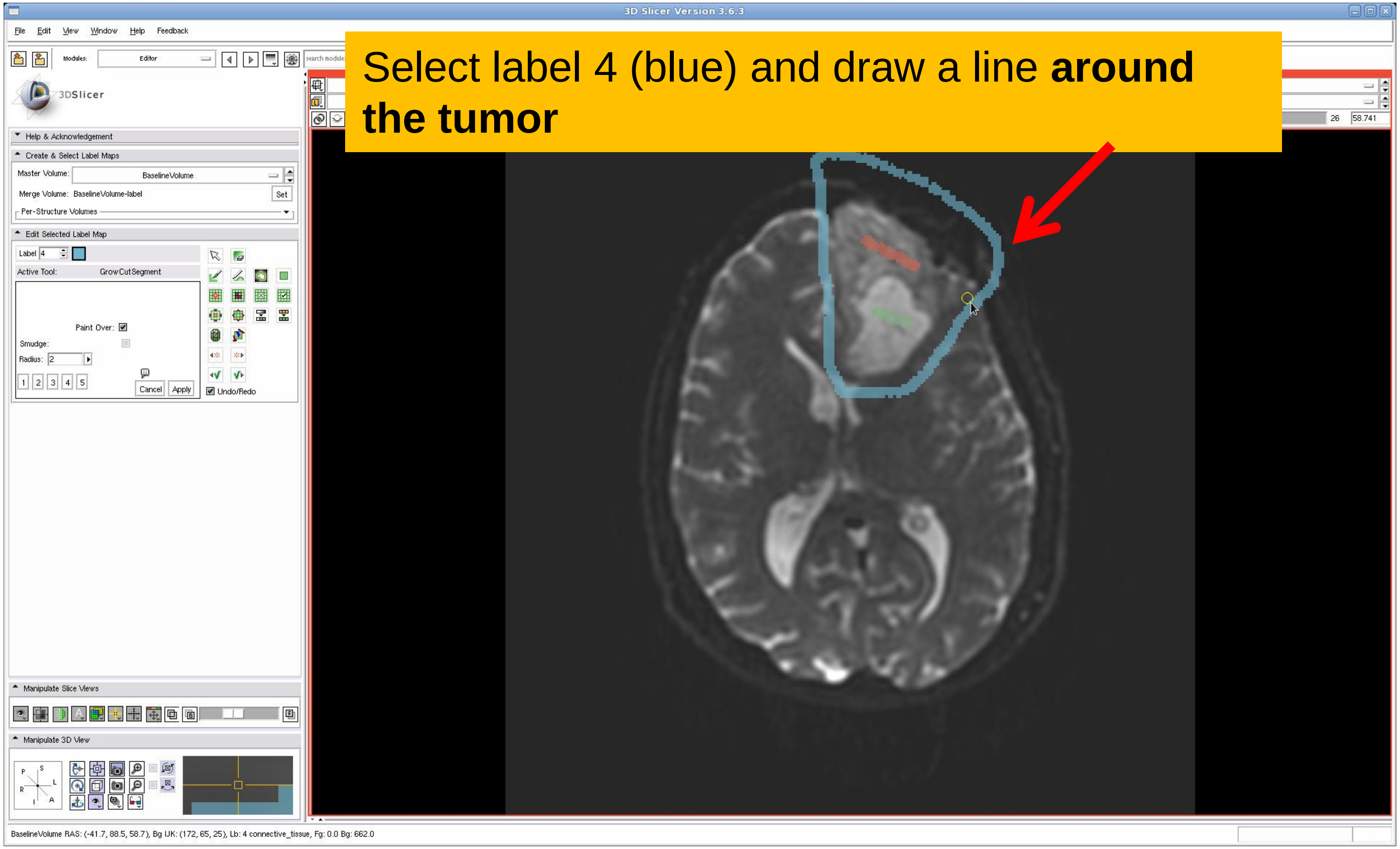
Tumor Segmentation



Select label 4 (blue) and draw a line **around the tumor**

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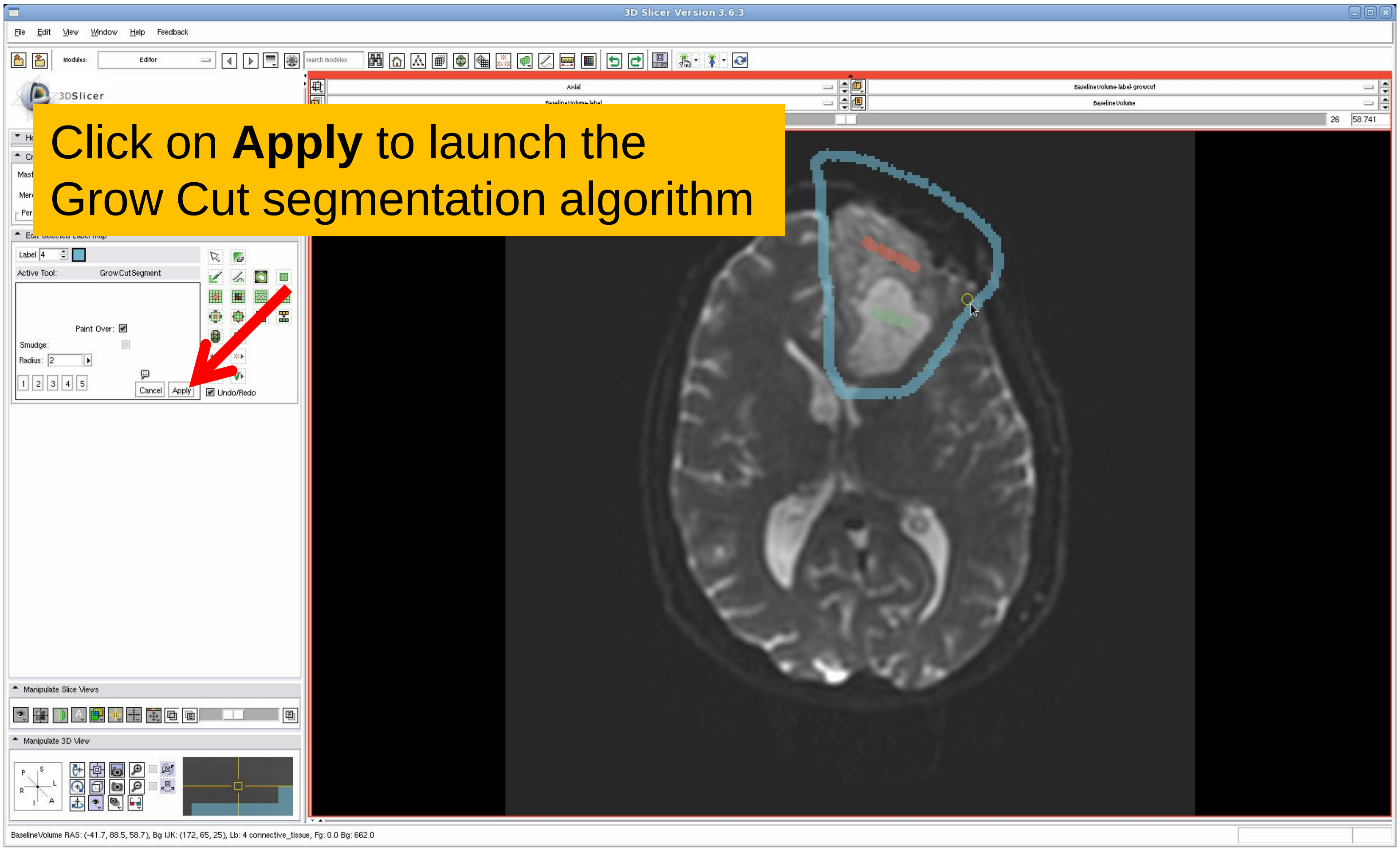
Tumor Segmentation



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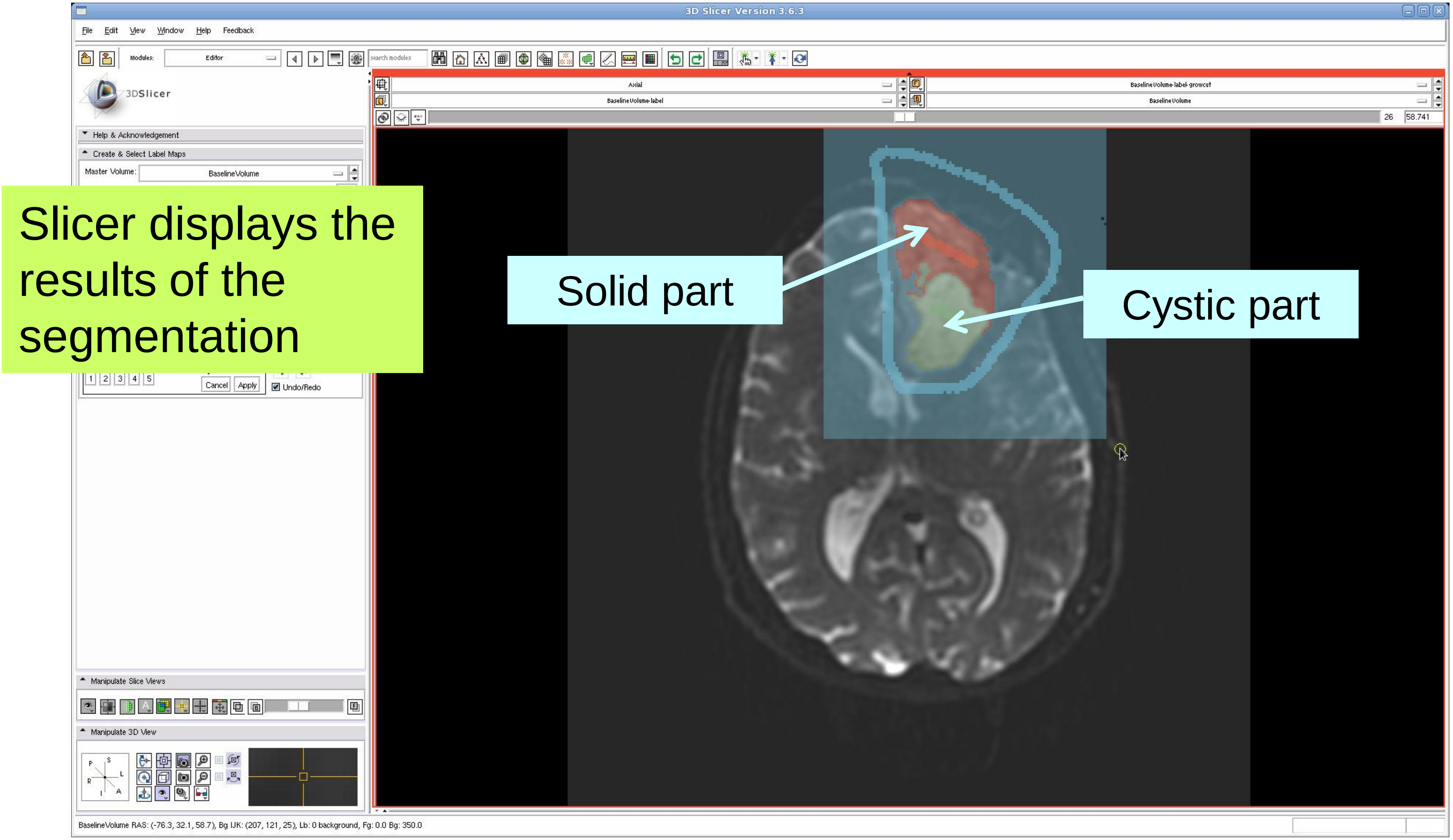
Tumor Segmentation



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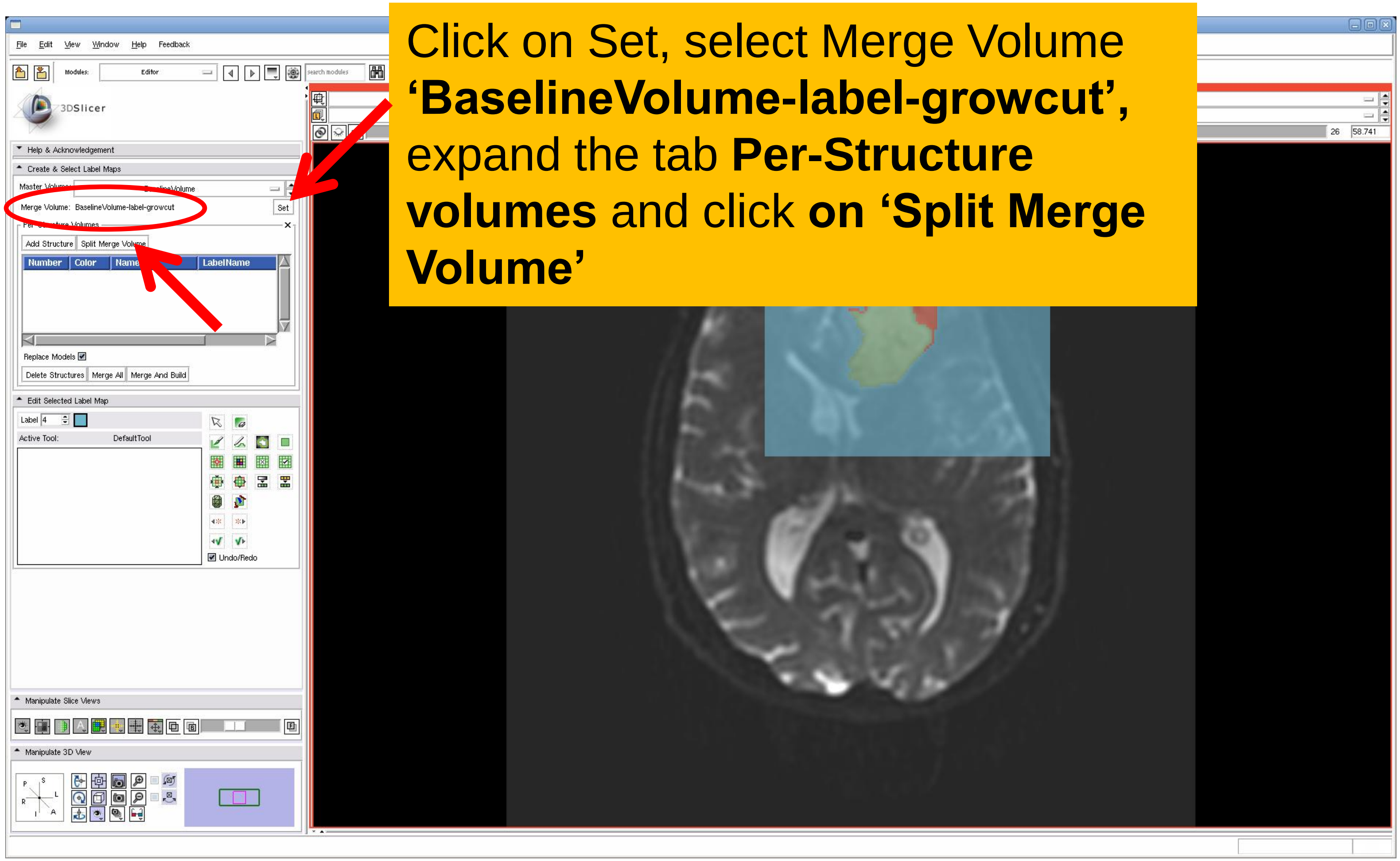
Tumor Segmentation

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



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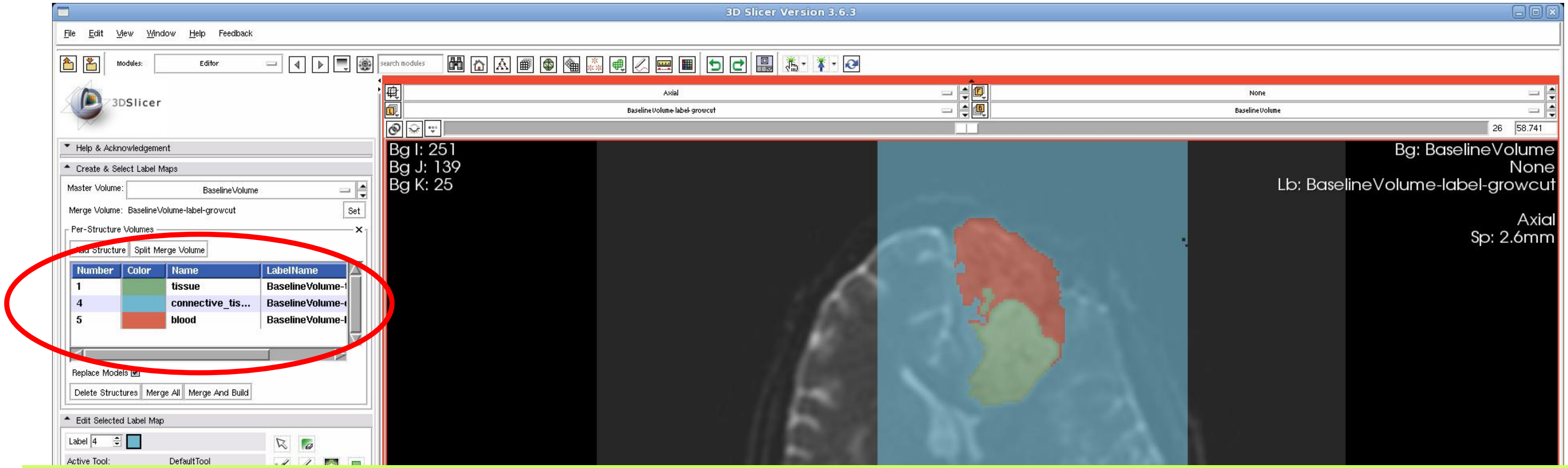
Tumor Segmentation



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

-**BaselineVolume-tissue-label** (label1): cystic part of the tumor
-**BaselineVolume-connective_tissue-label** (label 4): ventricles
-**BaselineVolume-blood-label** (label 5): solid part of the tumor

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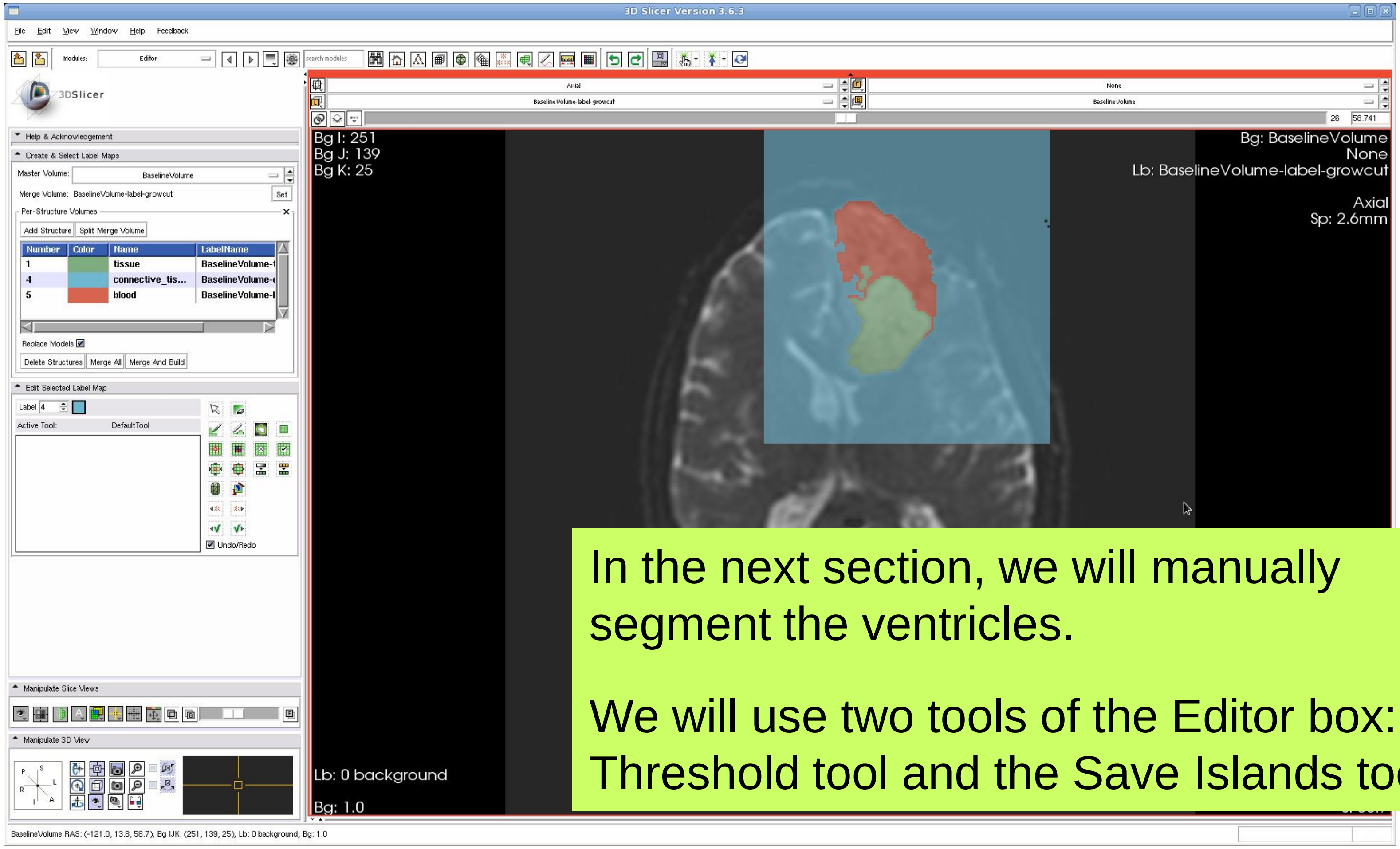
Ventricles Segmentation



In the next section, we will manually segment the ventricles.

We will use two tools of the Editor box: the Threshold tool and the Save Islands tool.

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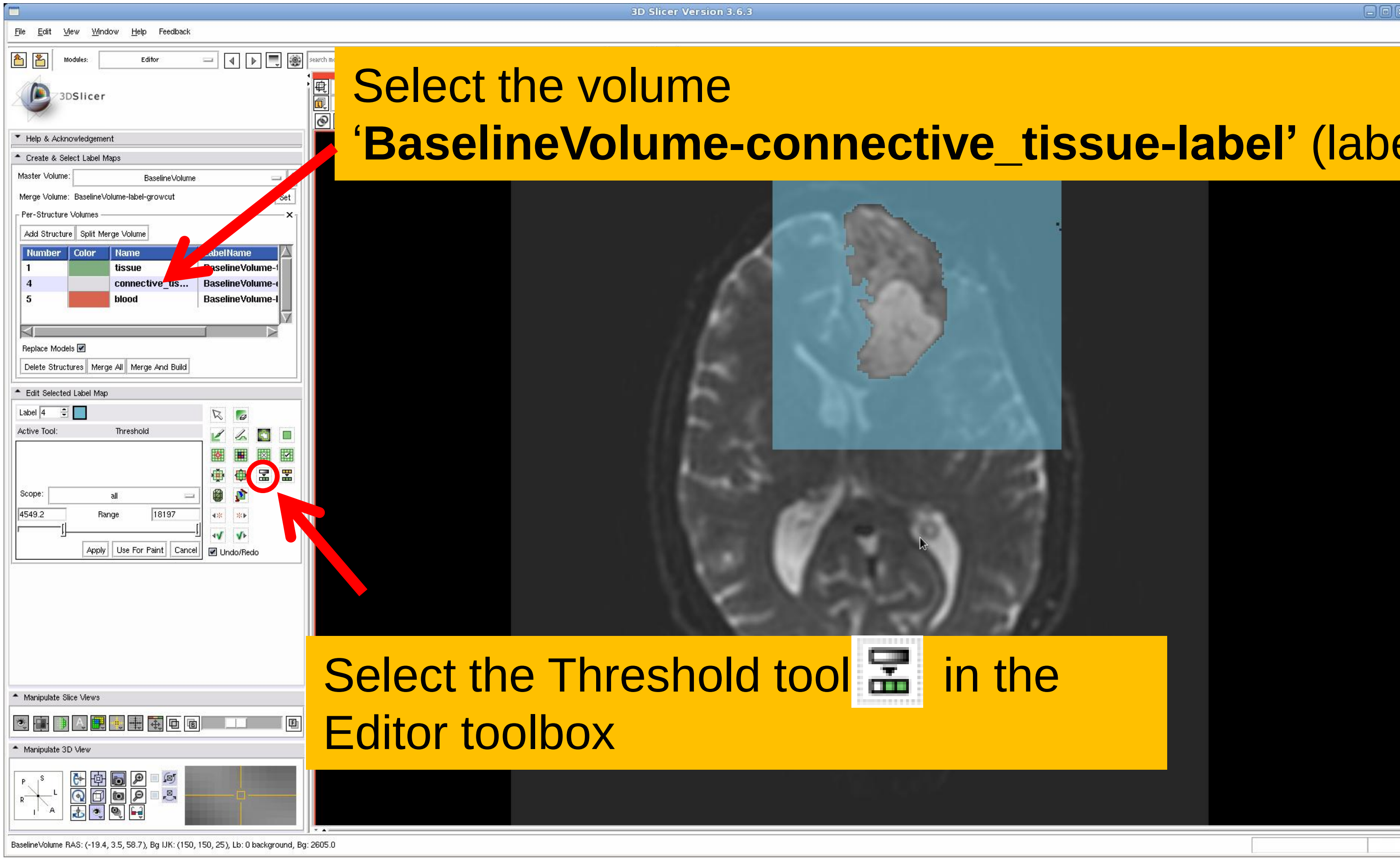
Ventricles Segmentation



Select the volume ‘**BaselineVolume-connective_tissue-label**’ (label 4)

Select the Threshold tool in the Editor toolbox

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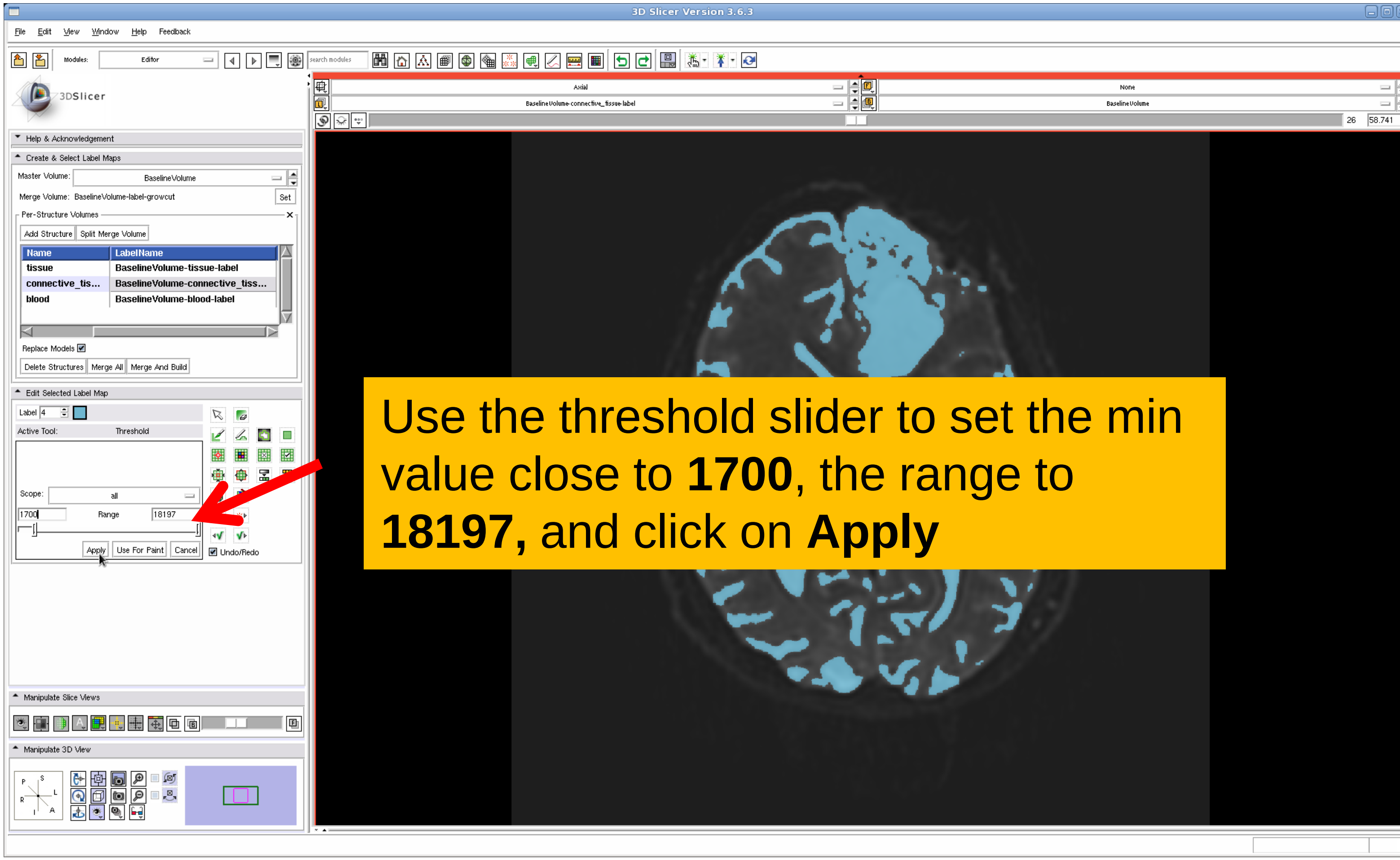
Ventricles Segmentation



Use the threshold slider to set the min value close to **1700**, the range to **18197,** and click on **Apply**

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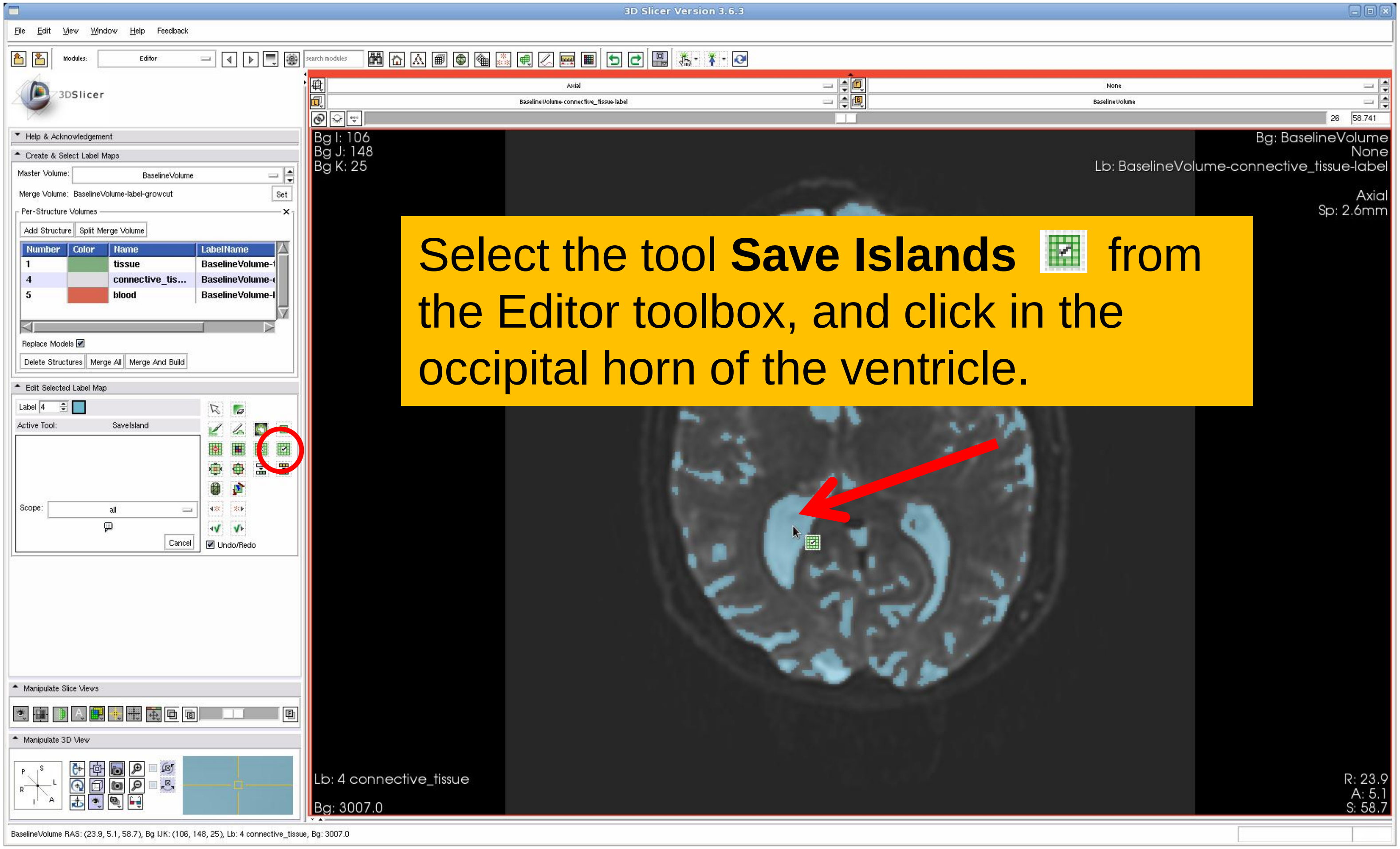
Ventricles Segmentation



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Final Result of the Segmentation

Slicer displays the result of the segmentation of the ventricles.

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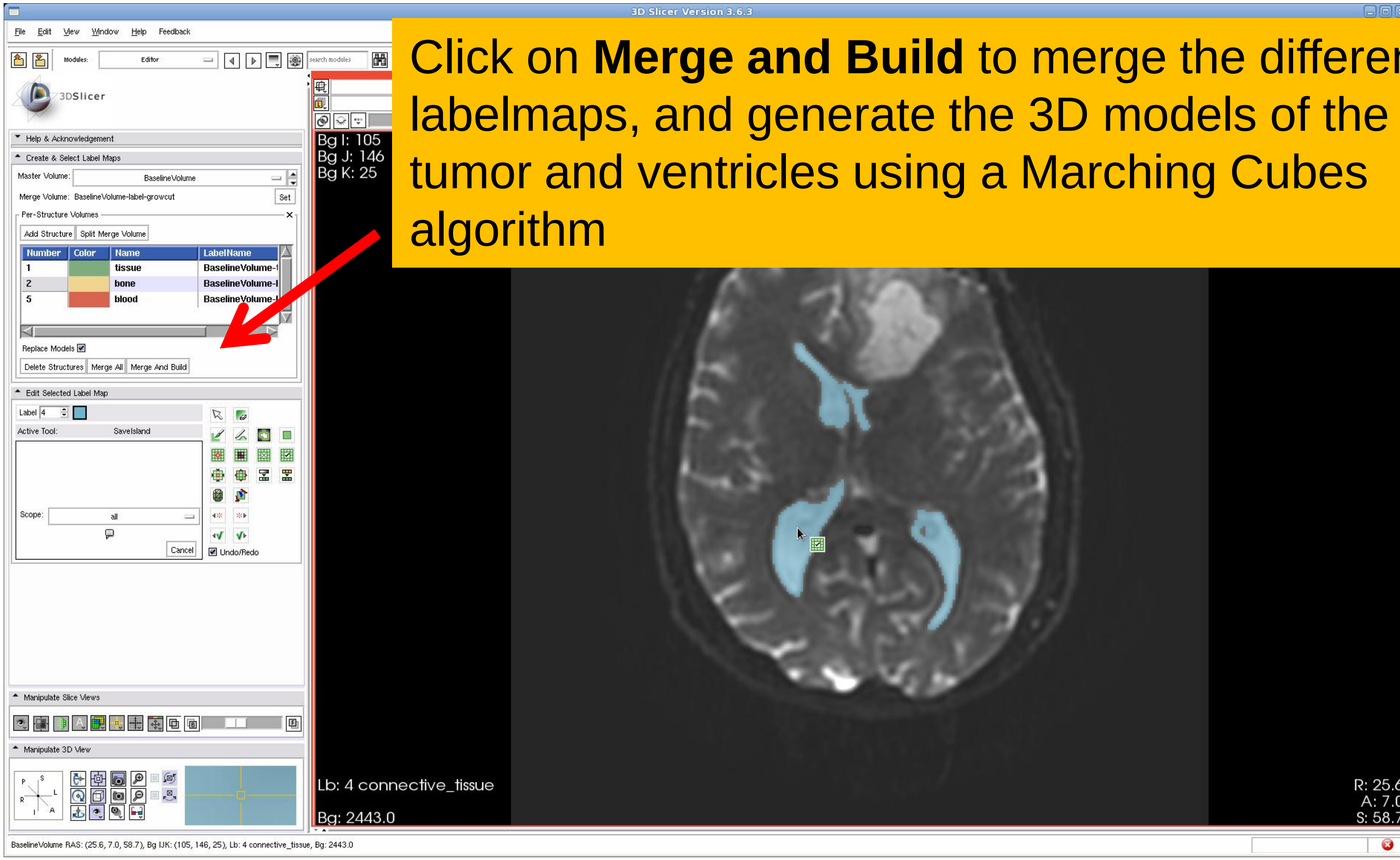
Final Result of the Segmentation



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

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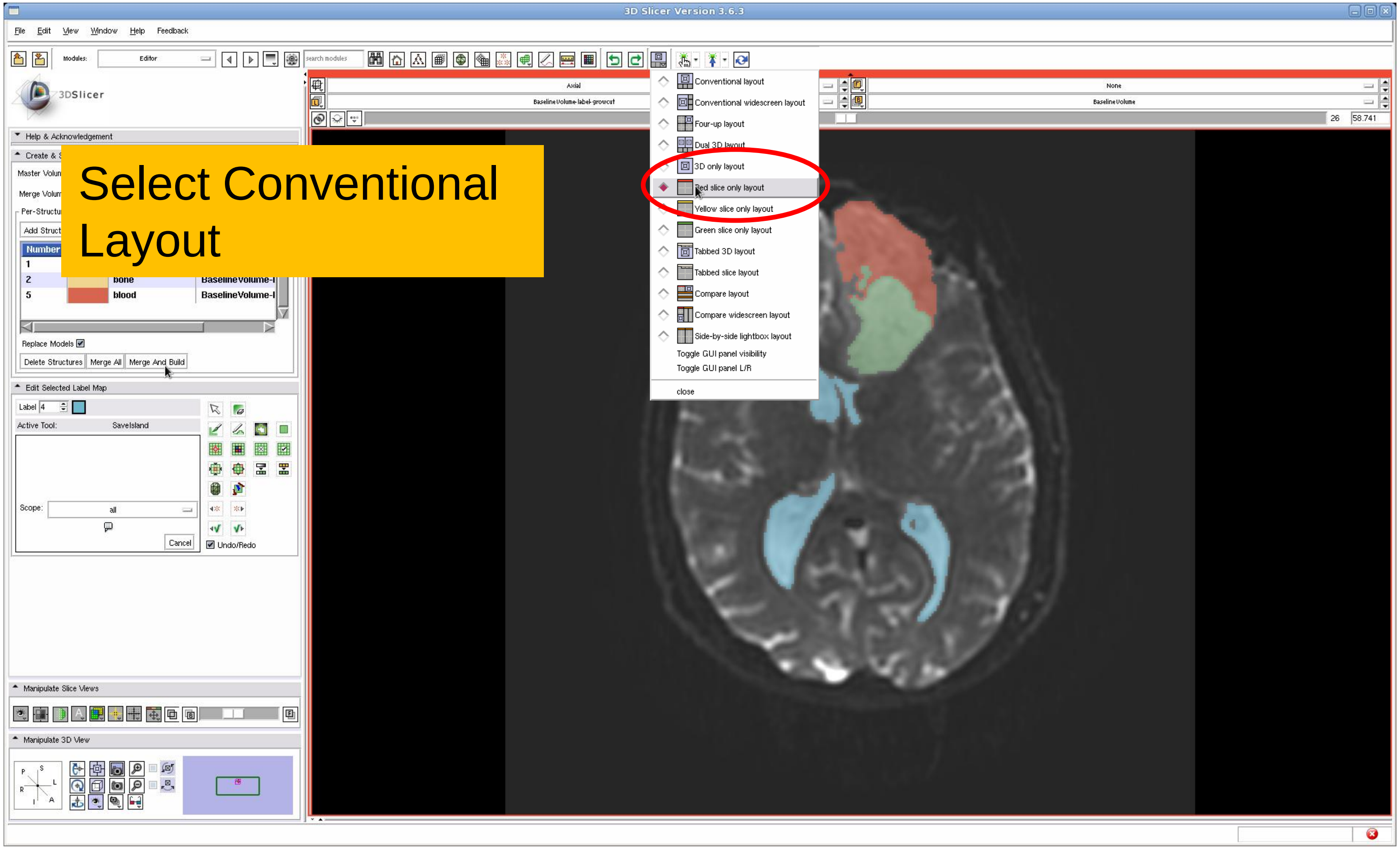
Final Result of the Segmentation



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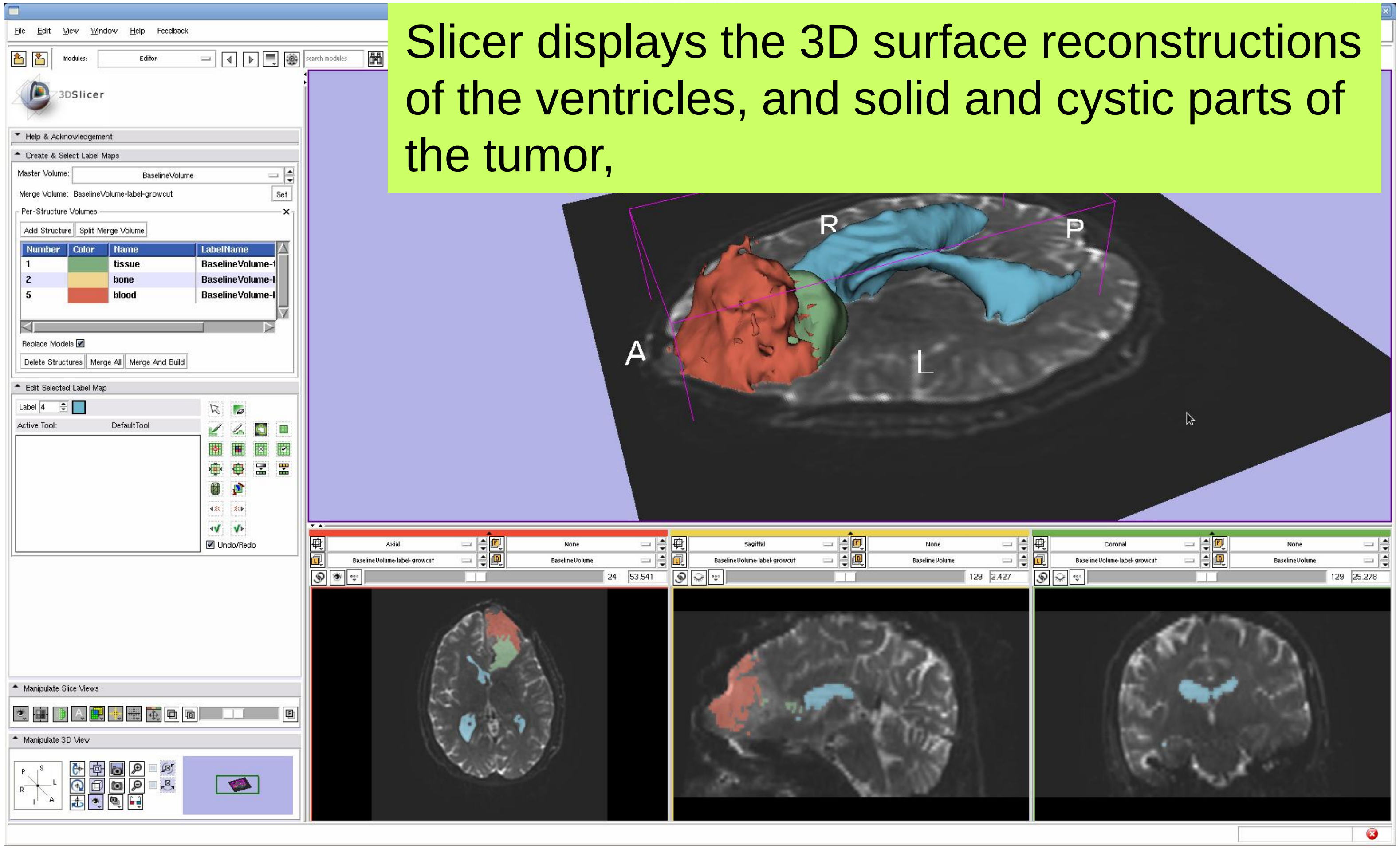
Final Result of the Segmentation

Slicer displays the 3D surface reconstructions of the ventricles, and solid and cystic parts of the tumor,



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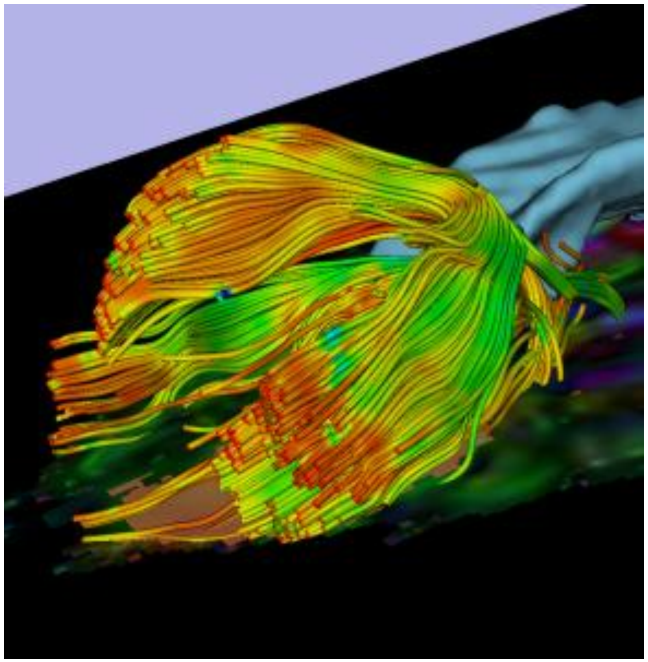

Part 2: Tractography exploration of peri-tumoral white matter fibers

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Definition of the peri-tumoral volume

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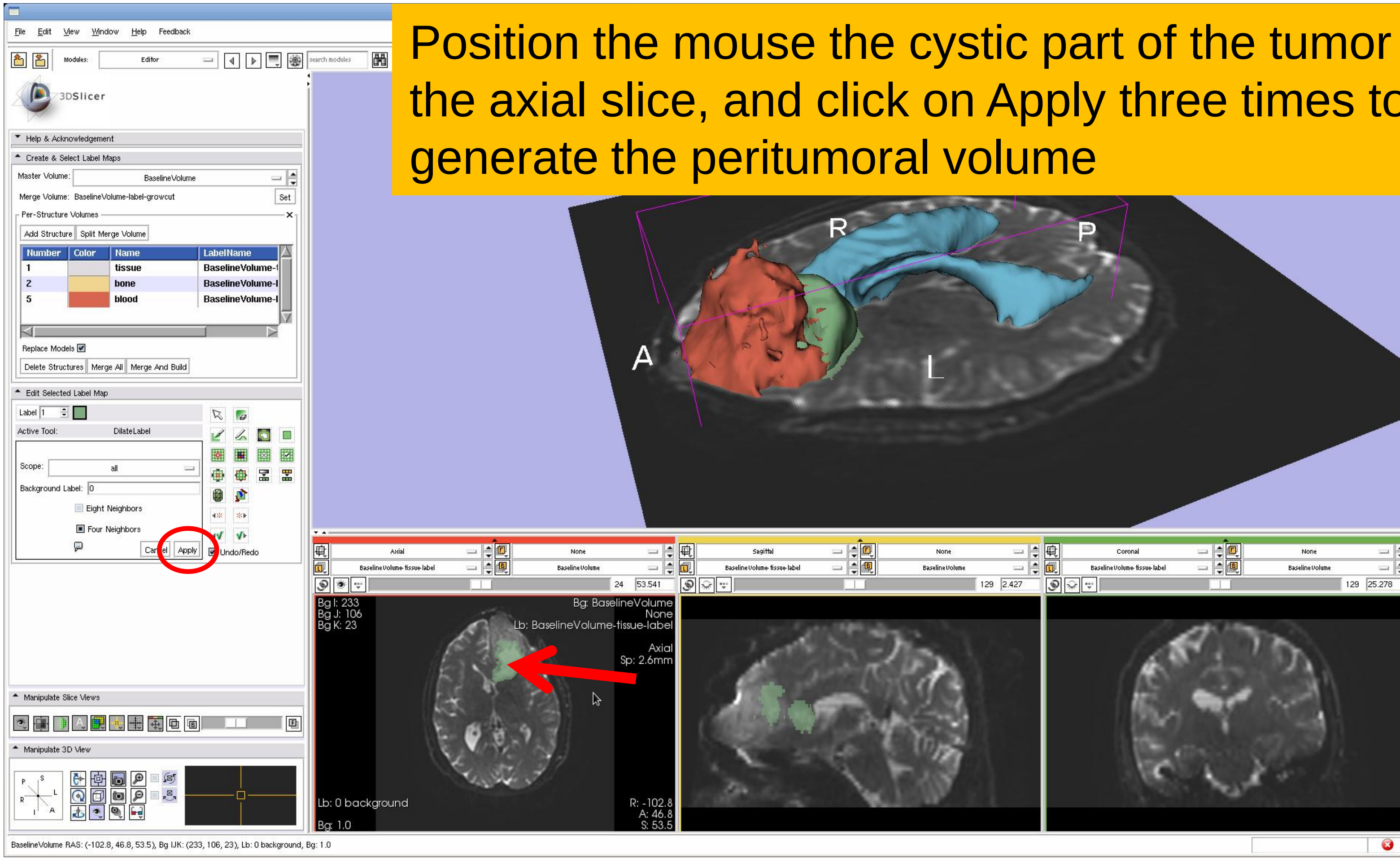
Definition of the peri-tumoral volume



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

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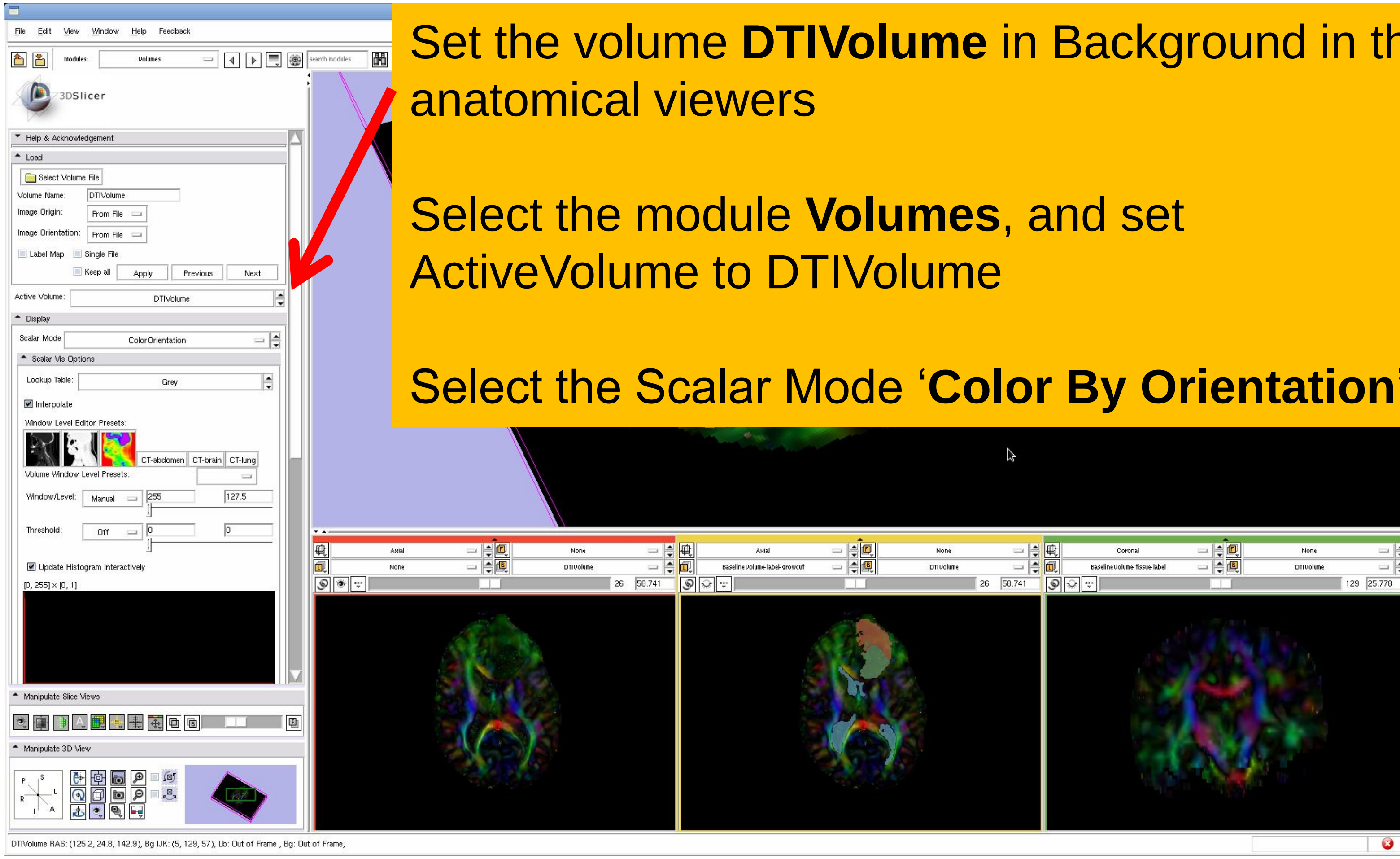
Visualization of the DTI Volume



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**’

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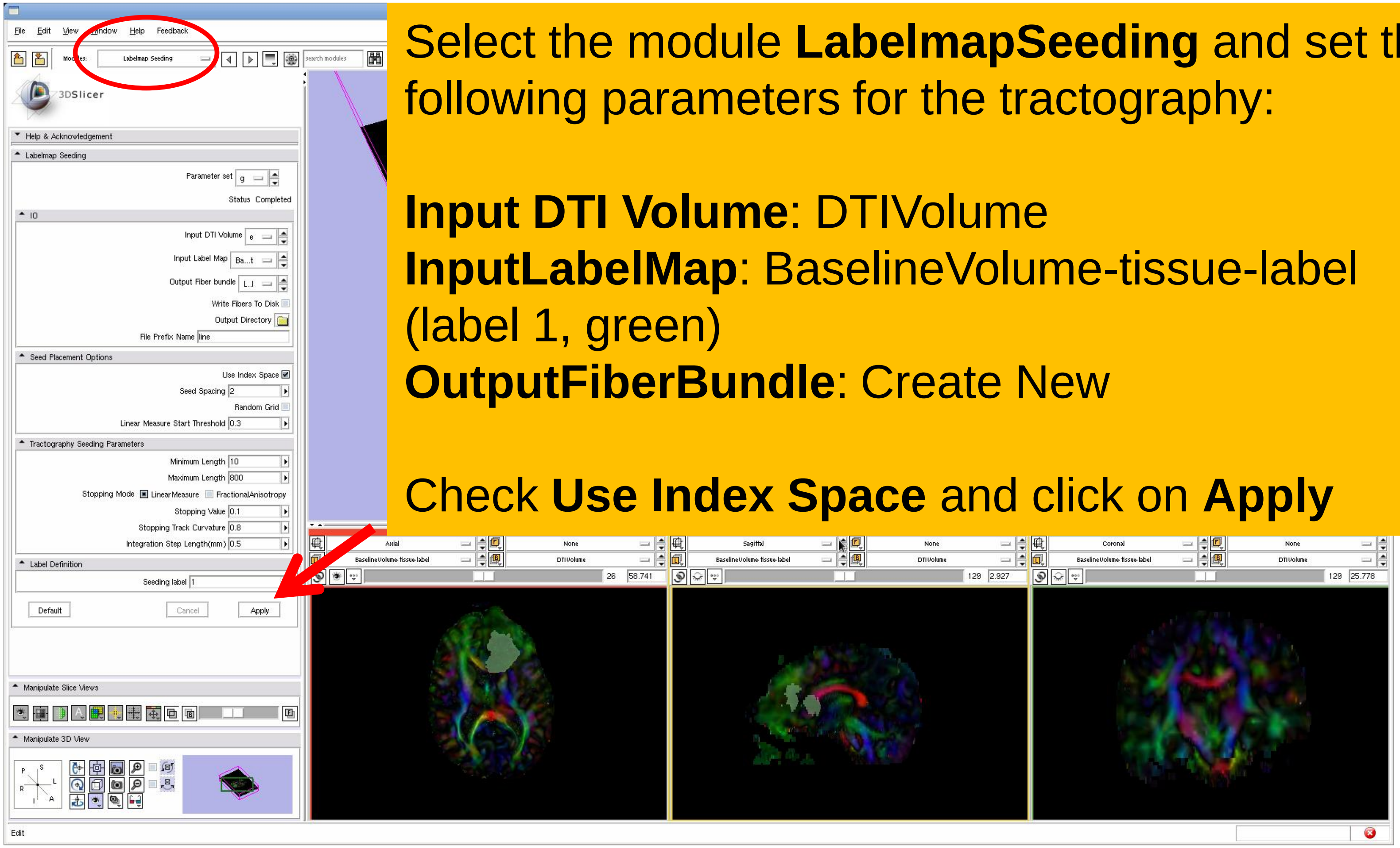
Tractography Parameters



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**

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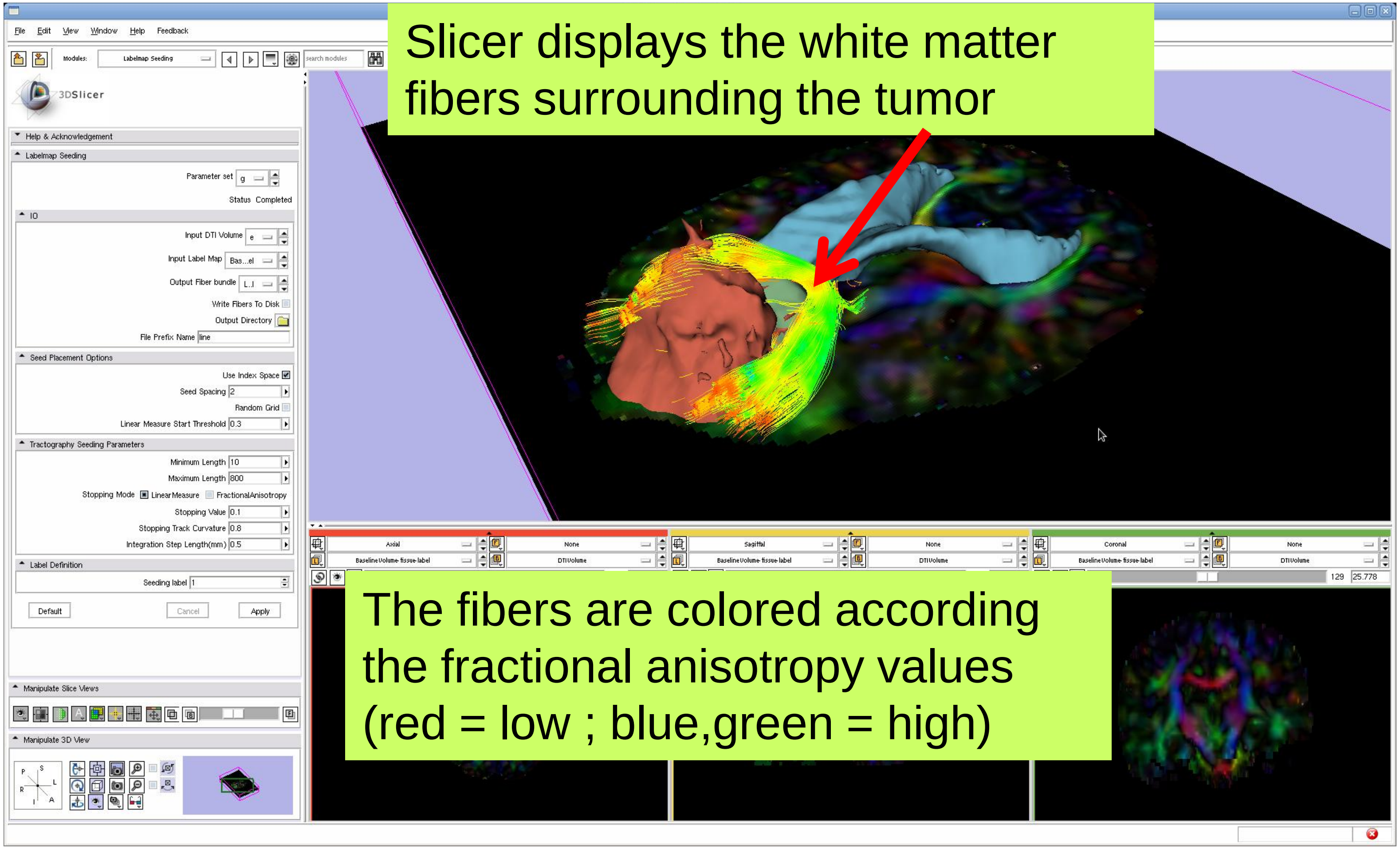
Tractography Results



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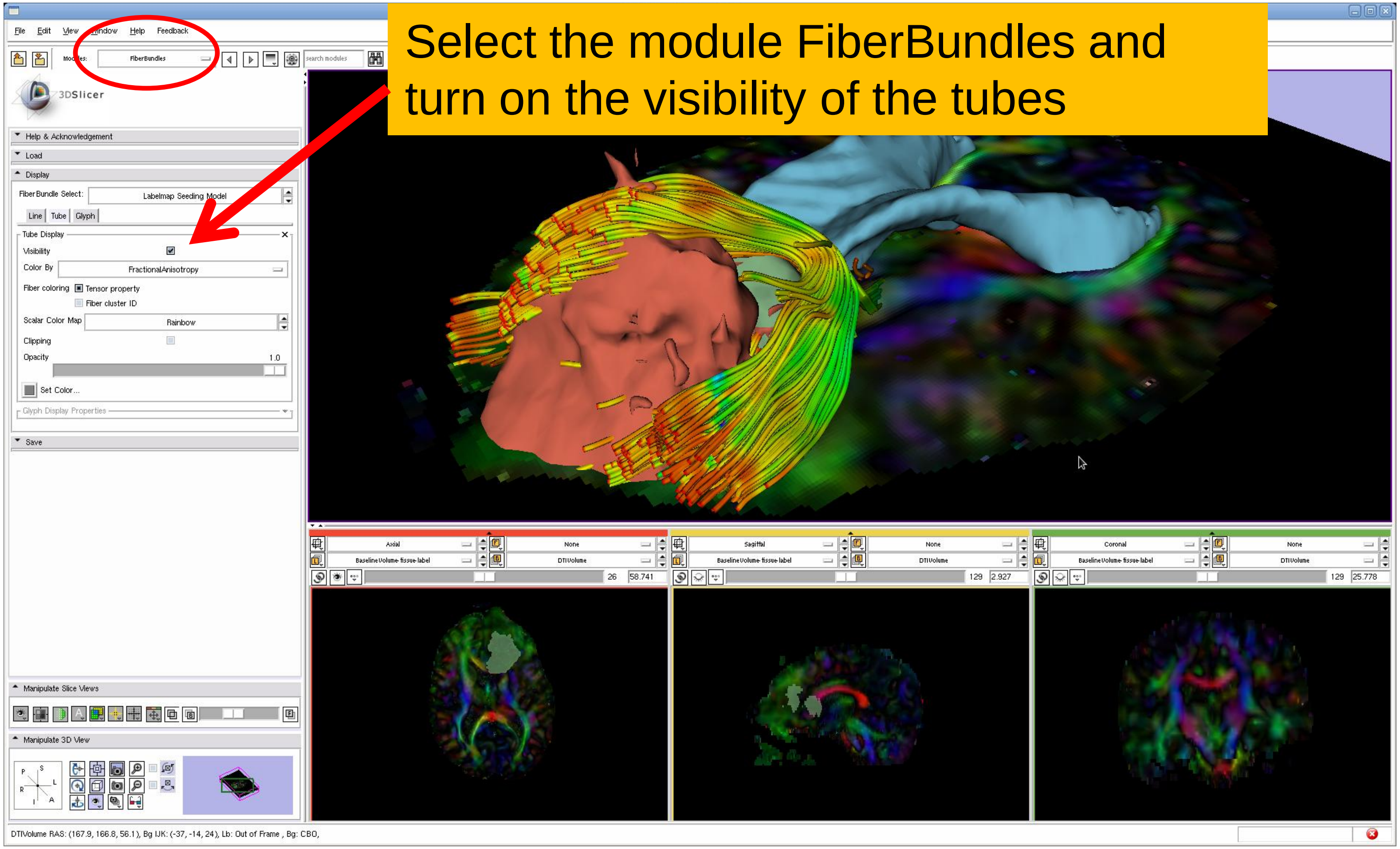
Tractography Results



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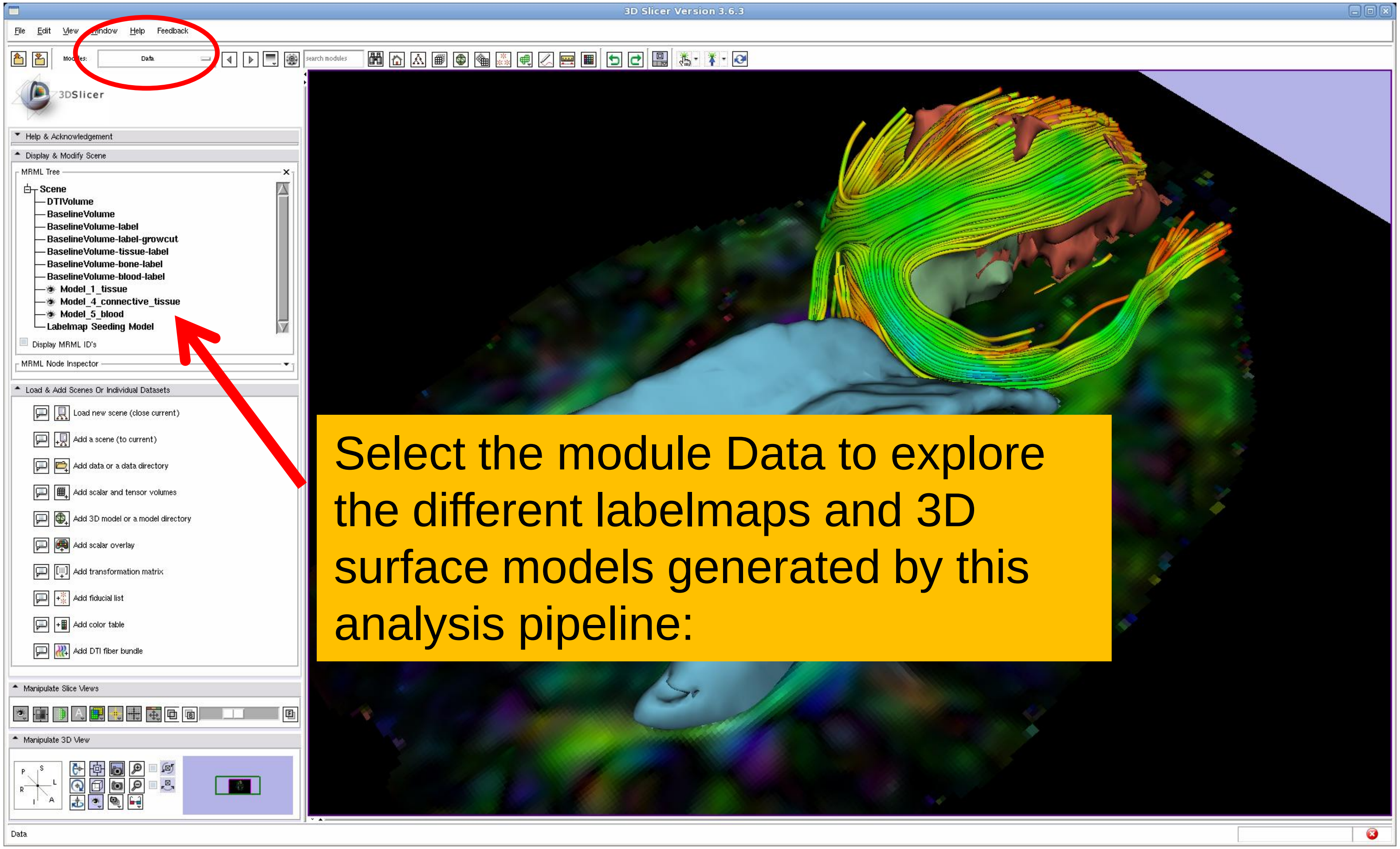
Tractography Results



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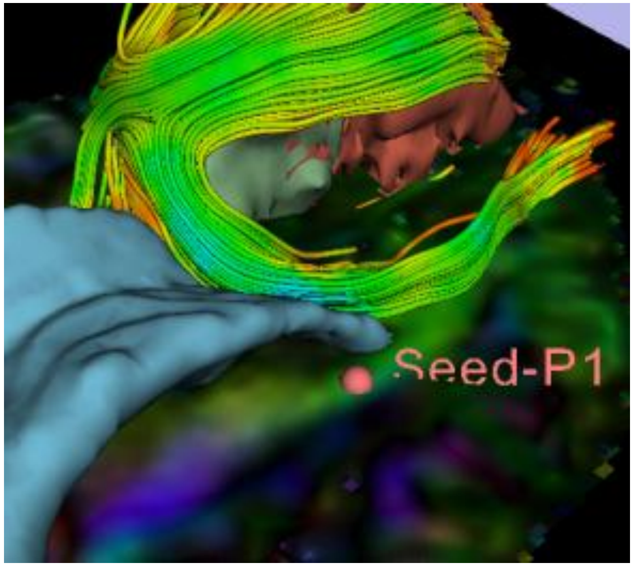

Part 4: Tractography exploration of the ipsilateral and contralateral side

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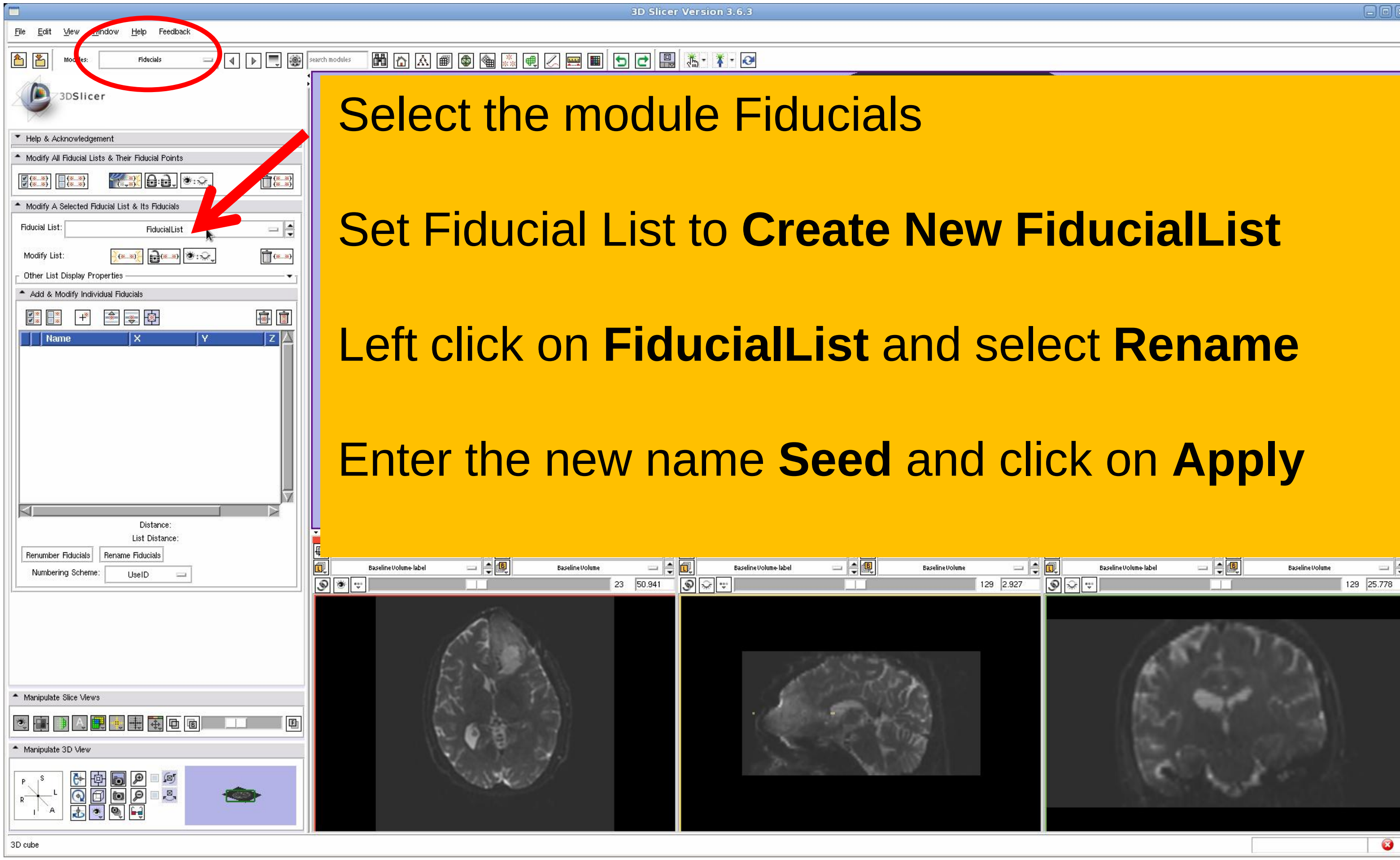
Tractography on-the-fly



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**

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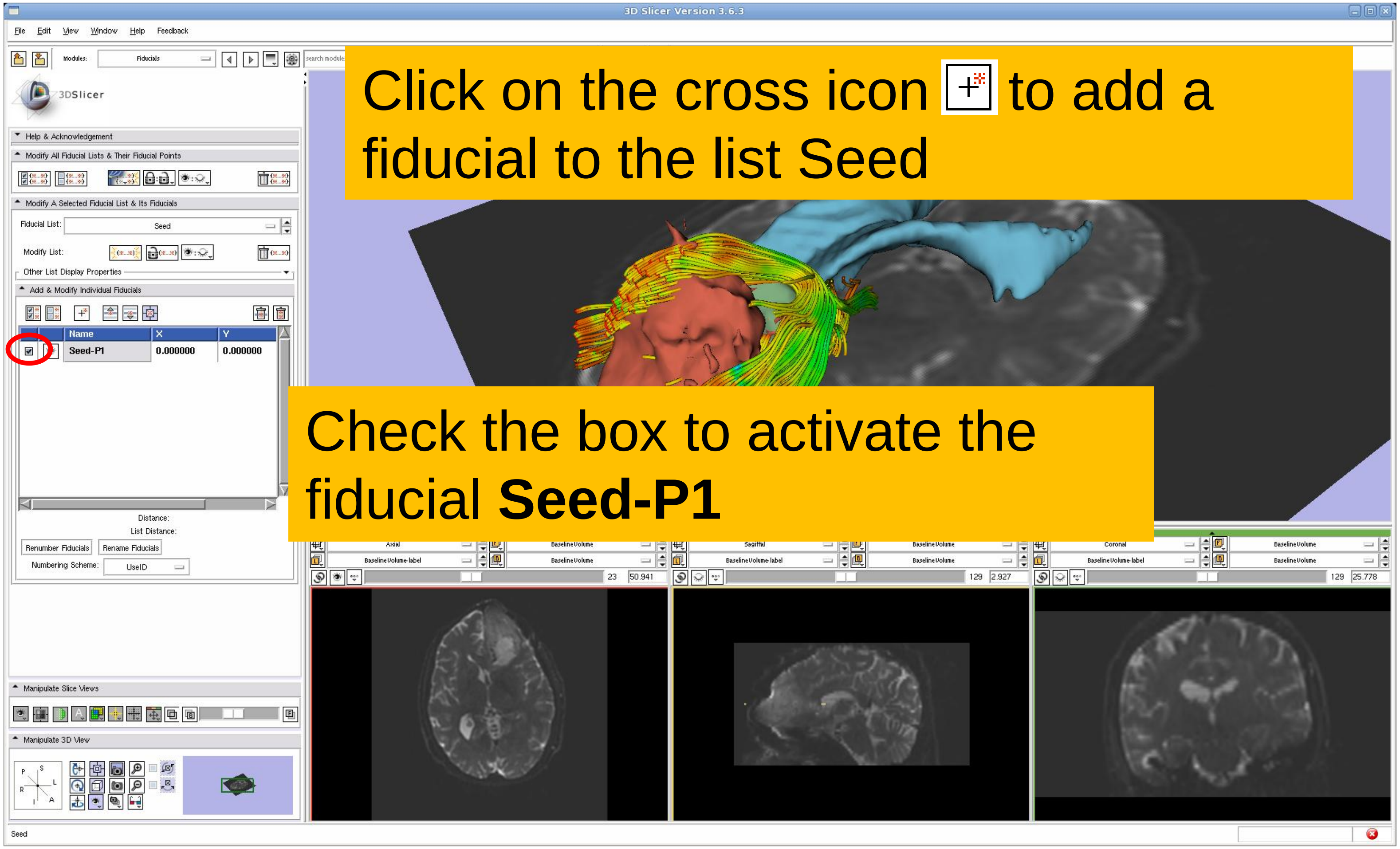
Tractography on-the-fly



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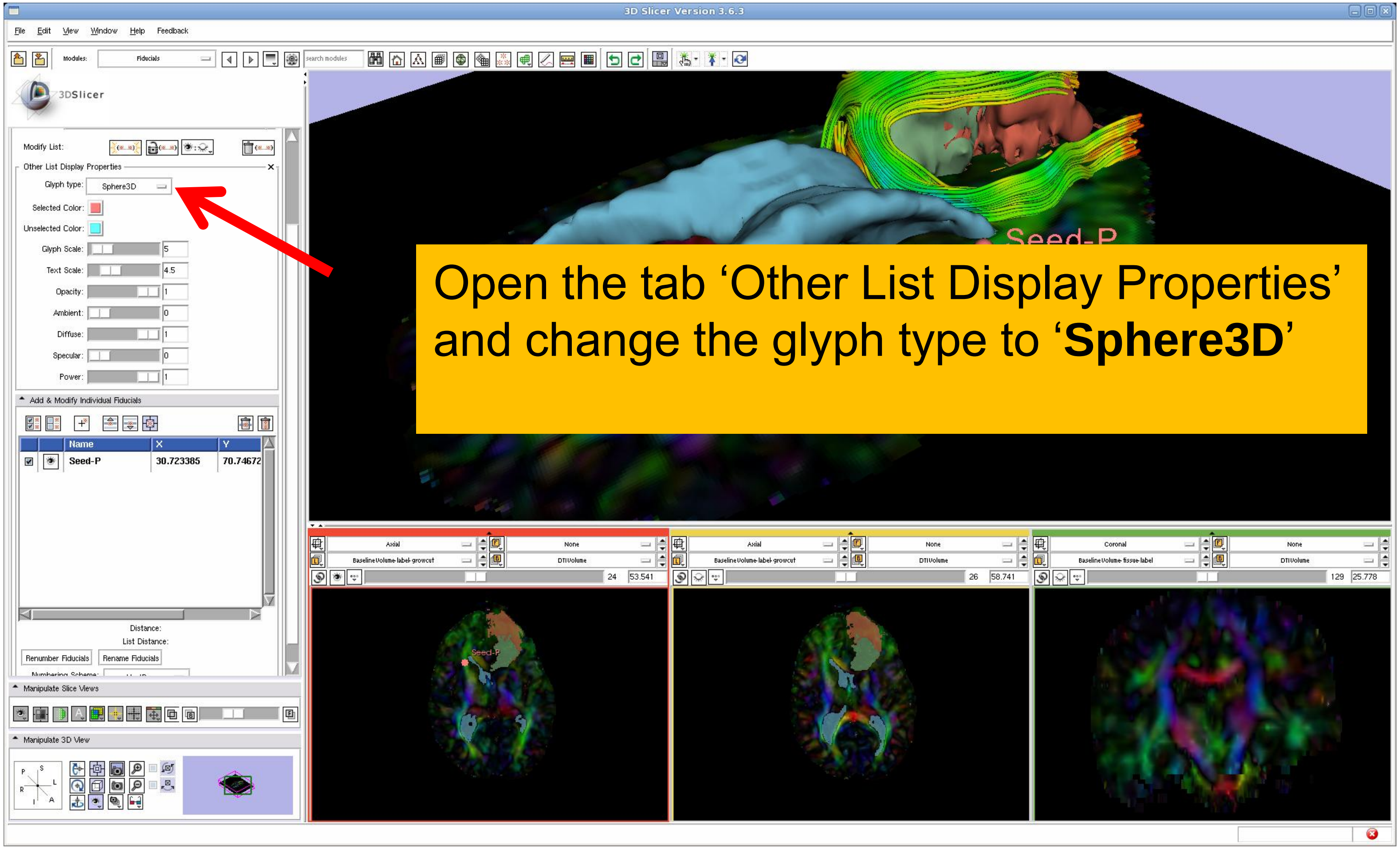
Fiducial Seeding



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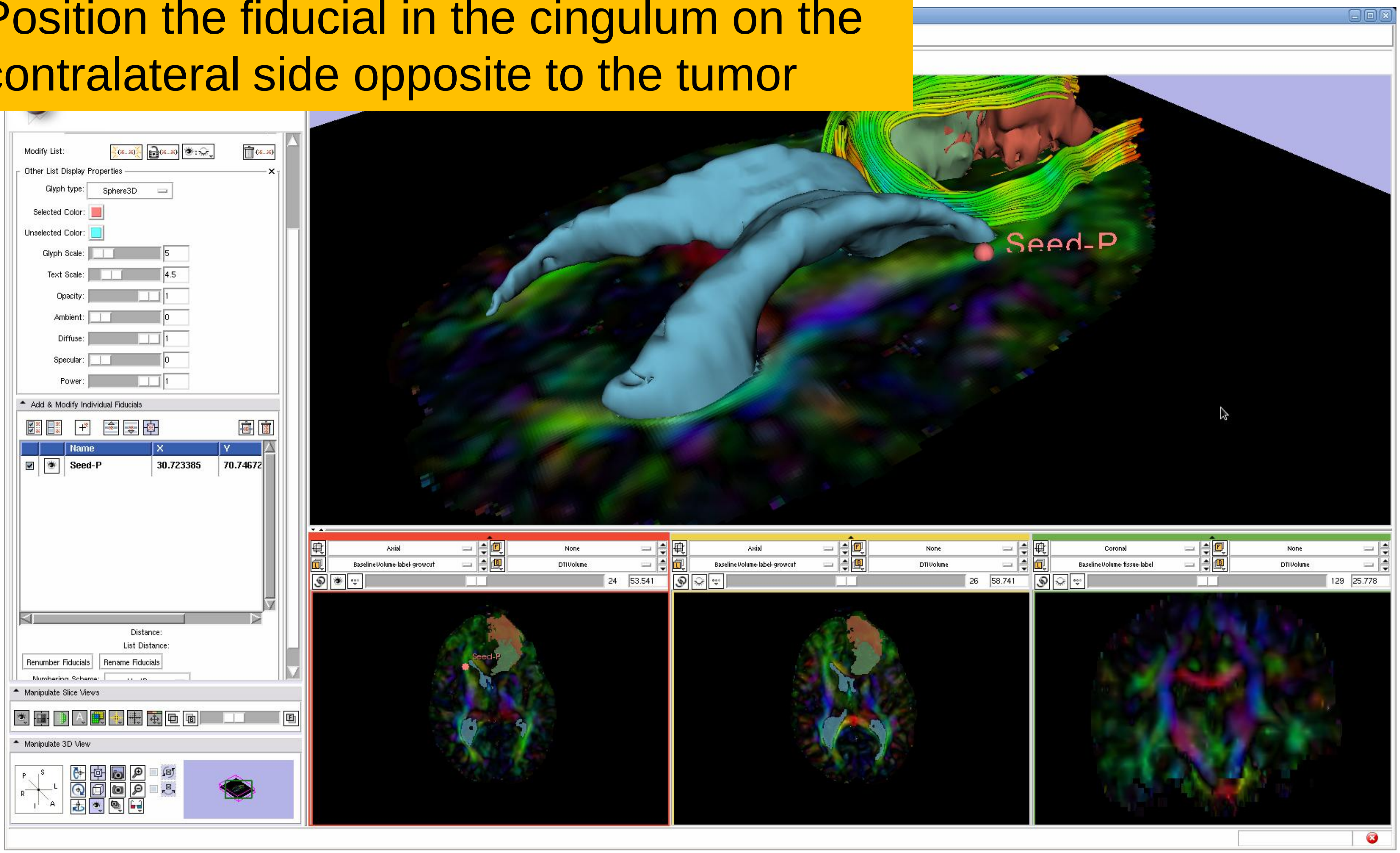
Fiducial Seeding

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



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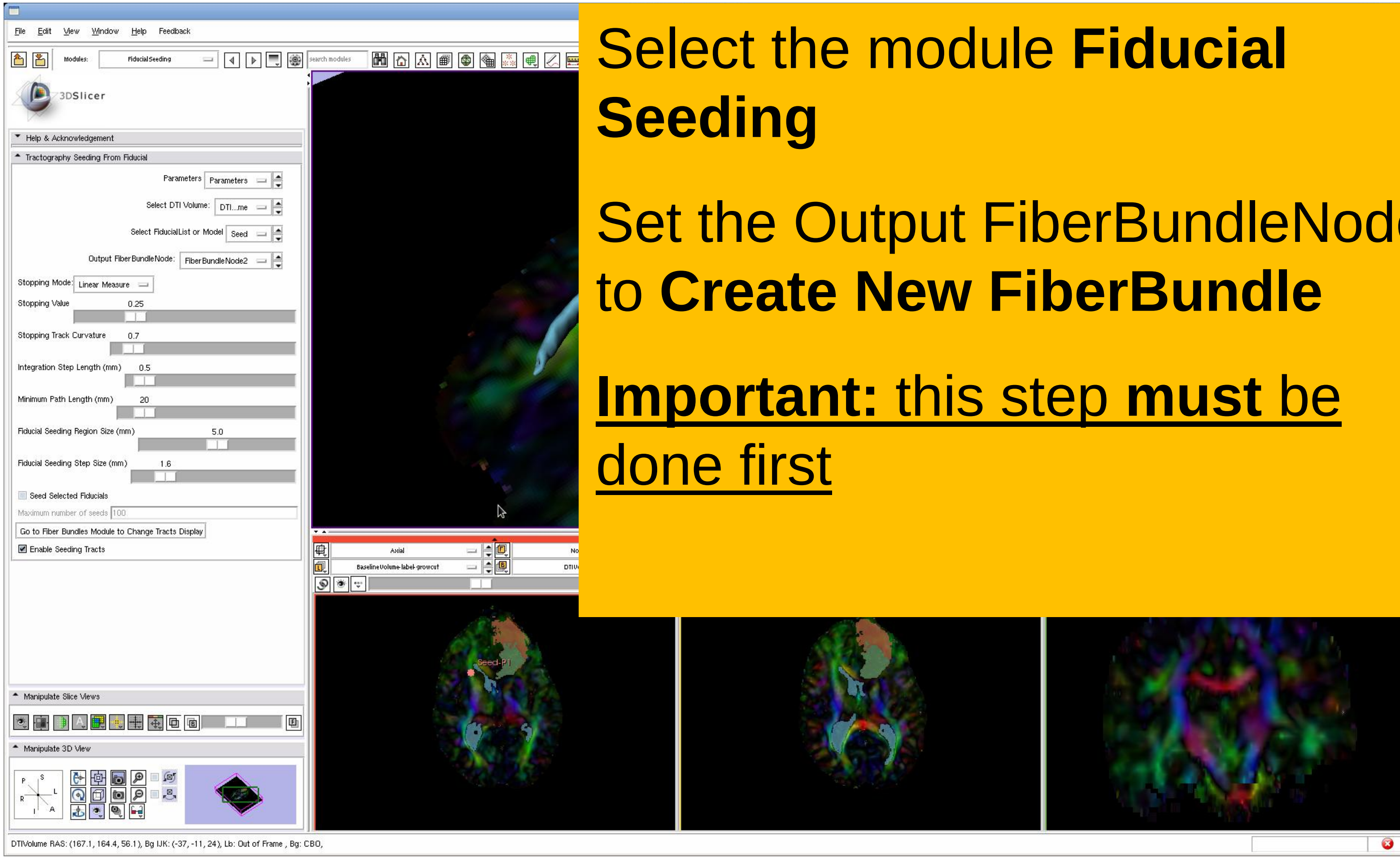
Tractography on-the-fly



Select the module **Fiducial Seeding**

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

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

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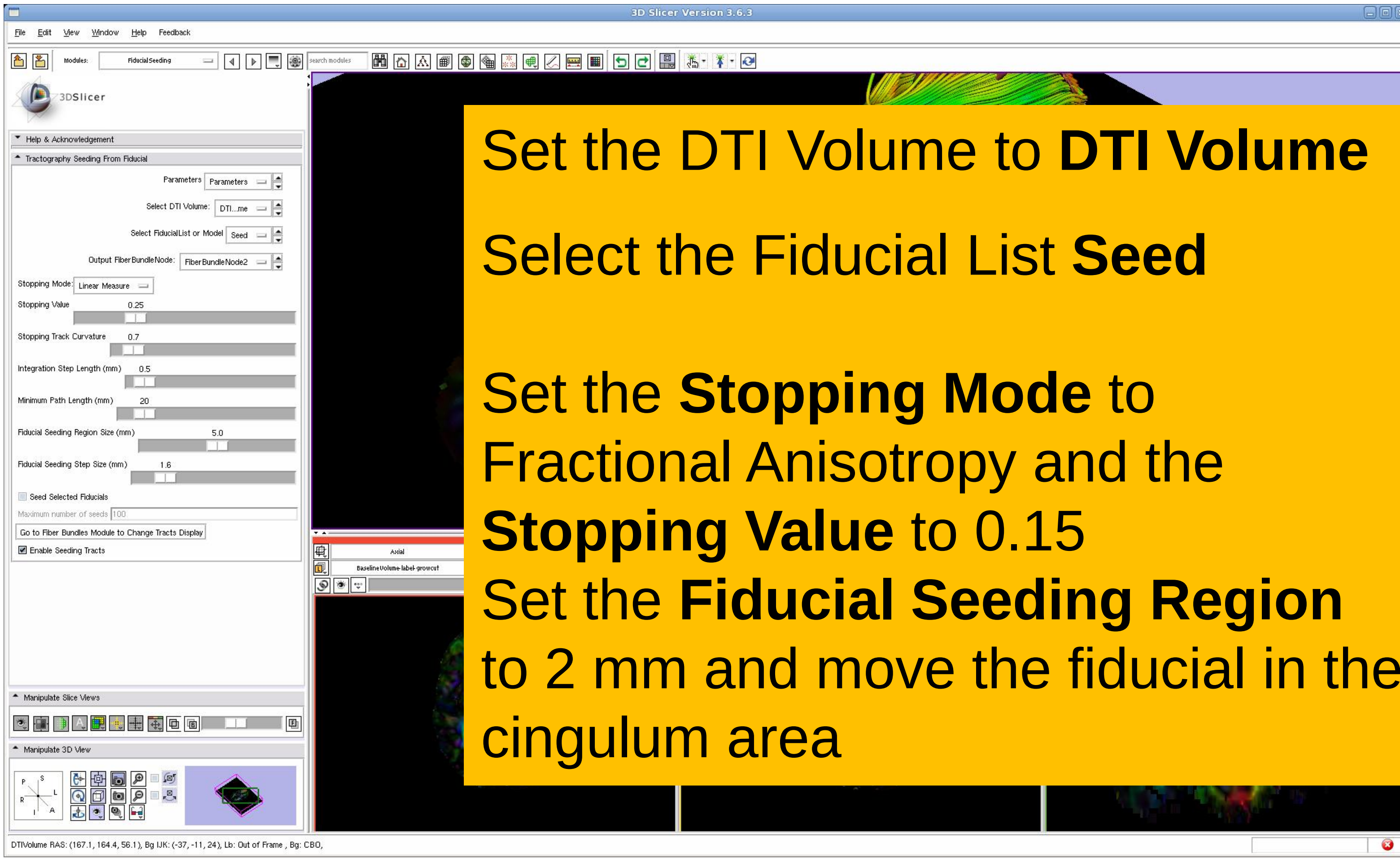
Tractography on-the-fly



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

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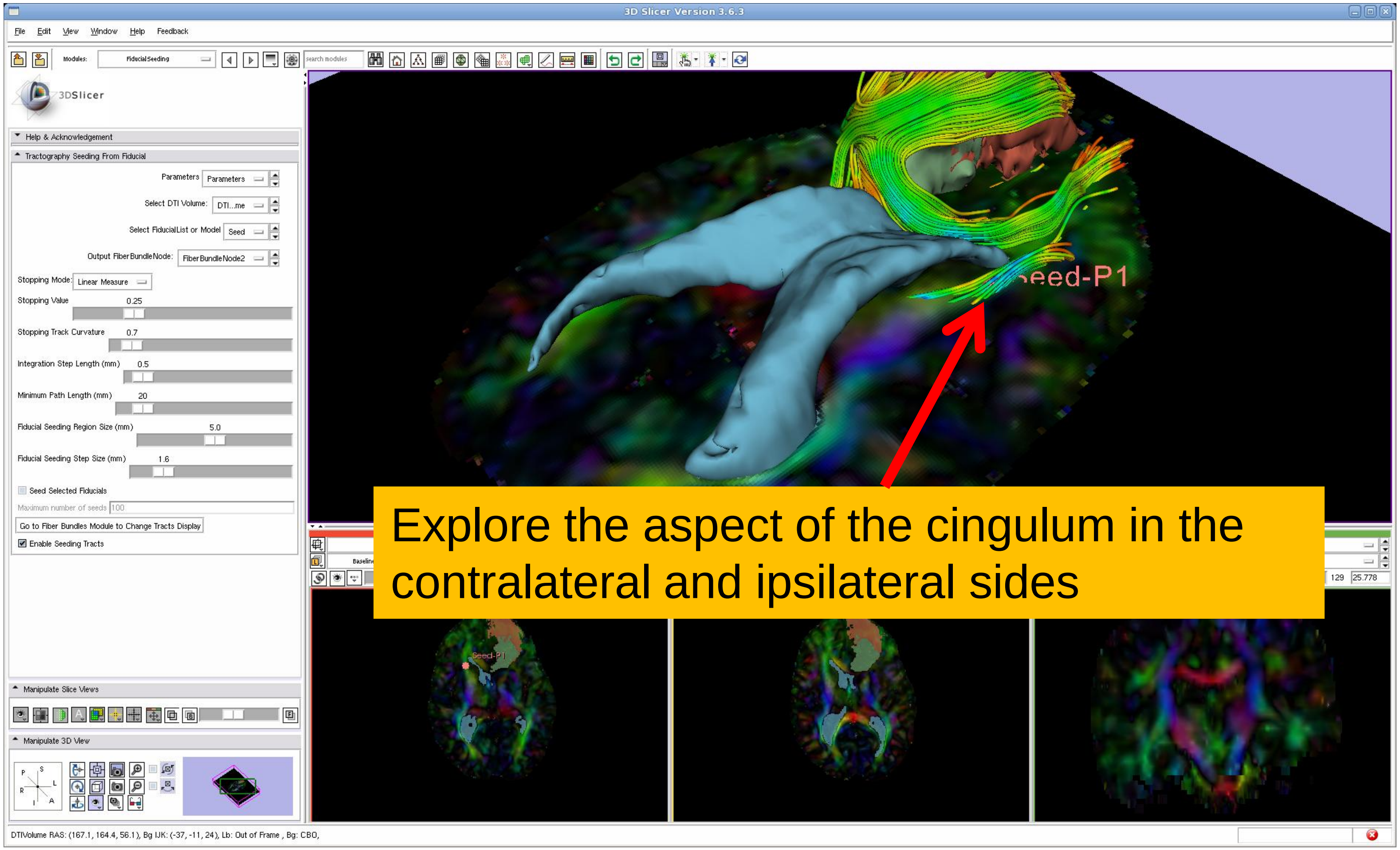
Tractography on-the-fly



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Neurosurgical Planning Workshop,

September 18, 2011 - Toronto


page discussion view source history

Events: DTI Tractography Challenge MICCAI 2011

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18-22 September MICCAI 2011 Toronto, CANADA

14th International Conference on Medical Image Computing and Computer Assisted Intervention

DTI Tractography for Neurosurgical Planning: A Grand Challenge

Welcome to the 'DTI Tractography for Neurosurgical Planning: A Grand Challenge' workshop. The goal of this initiative is to compare Diffusion Tensor Imaging Tractography algorithms for reconstructing white matter bundles for pre-surgical planning. The workshop is part of the 14th International Conference on Medical Image Computing and Computer Assisted Intervention MICCAI 2011, to be held from 18th to 22th September 2011 in Toronto, Canada.

Overview

Diffusion Tensor Imaging (DTI) tractography has a unique potential for neurosurgical planning since it provides a window on the complex organization of white matter pathways *in-vivo*. During the past decade, the MICCAI community has been a major contributor to the development and refinement of a wide variety of advanced tractography techniques. Still the transfer of these cutting-edge algorithms to clinical routine is hindered by the difficulties of validating tractography results. The DTI Tractography Challenge workshop will give participants the opportunity to evaluate the performances of their tractography algorithms in a neurosurgical context. Participants will gain insights on the currently available gold-standard for evaluating tractography results in the Operating Room, in the absence of ground truth.

Neurosurgical case with left frontoparietal tumor. Neurosurgery 2011 Feb; 68(2):496-505. Image courtesy of Dr. Alexandra Golby.

Faculty

- Sonia Pujol, Ph.D., Surgical Planning Laboratory, Brigham and Women's Hospital, Harvard Medical School
- Ron Kikinis, M.D., Surgical Planning Laboratory, Brigham and Women's Hospital, Harvard Medical School
- Alexandra Golby, M.D., Department of Neurosurgery, Brigham and Women's Hospital, Harvard Medical School
- Guido Gerig, Ph.D.,The Scientific Computing and Imaging Institute, University of Utah
- Martin Styner, Ph.D., Neuro Image Research and Analysis Laboratory, University of North Carolina
- William Wells, Ph.D., Surgical Planning Laboratory, Brigham and Women's Hospital, Harvard Medical School
- Carl-Fredrik Westin, Ph.D., Laboratory of Mathematics in Imaging, Brigham and Women's Hospital, Harvard Medical School
- Sylvain Gouttard, M.Sc.,The Scientific Computing and Imaging Institute, University of Utah

DTI Tractography for Neurosurgical Planning: A Grand Challenge

September 18, 2011
MICCAI 2011 Conference
The Westin Harbor Castle
Toronto, Canada

http://www.na-mic.org/Wiki/index.php/Events:_DTI_Tractography_Challenge_MICCAI_2011

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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

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