



# Exploring Peritumoral White Matter Fibers for Neurosurgical Planning

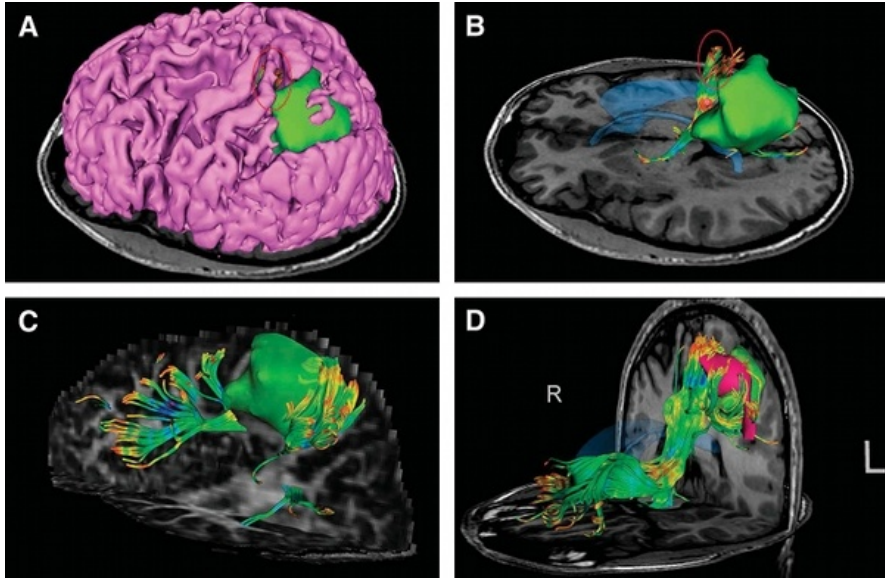
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Surgical Planning Laboratory

Harvard University

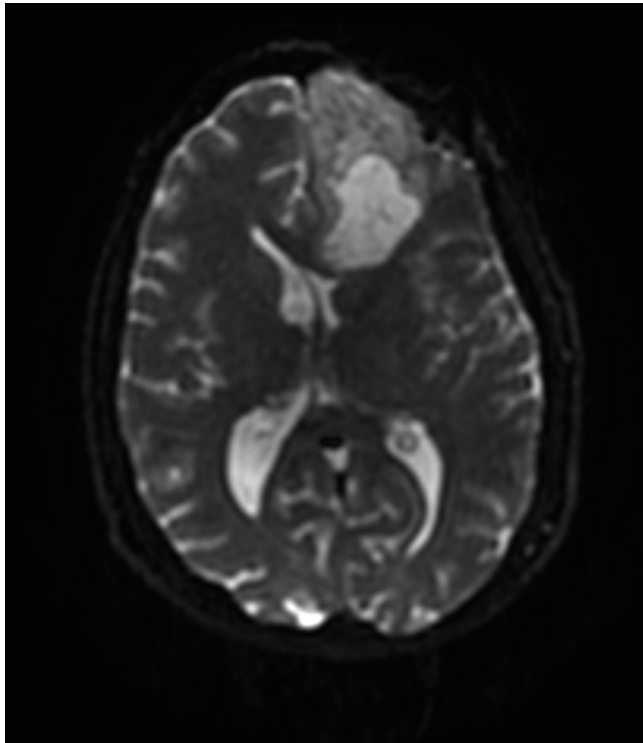
# Clinical Goal



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.

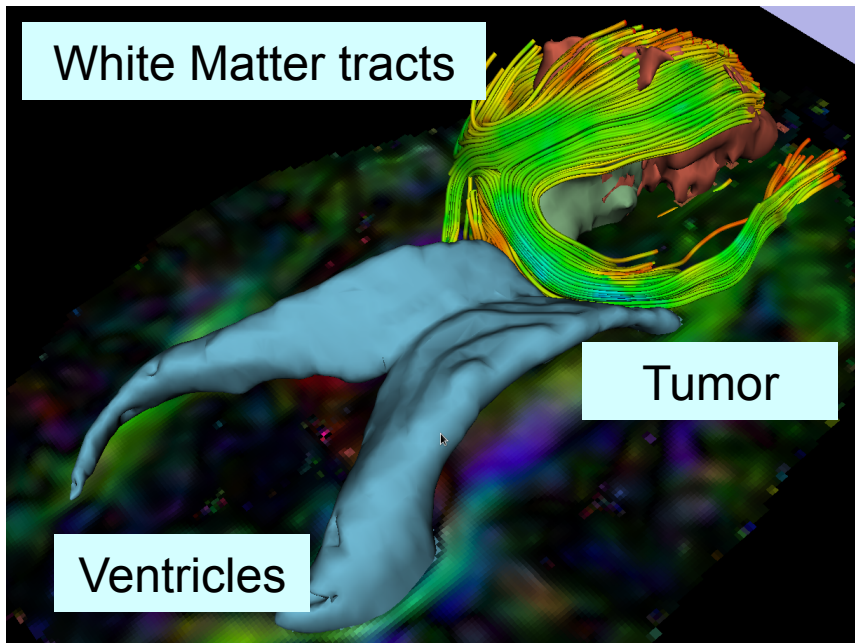
Image Courtesy of Dr. Alexandra Golby, Brigham and Women's Hospital, Boston, MA..

# Clinical Case



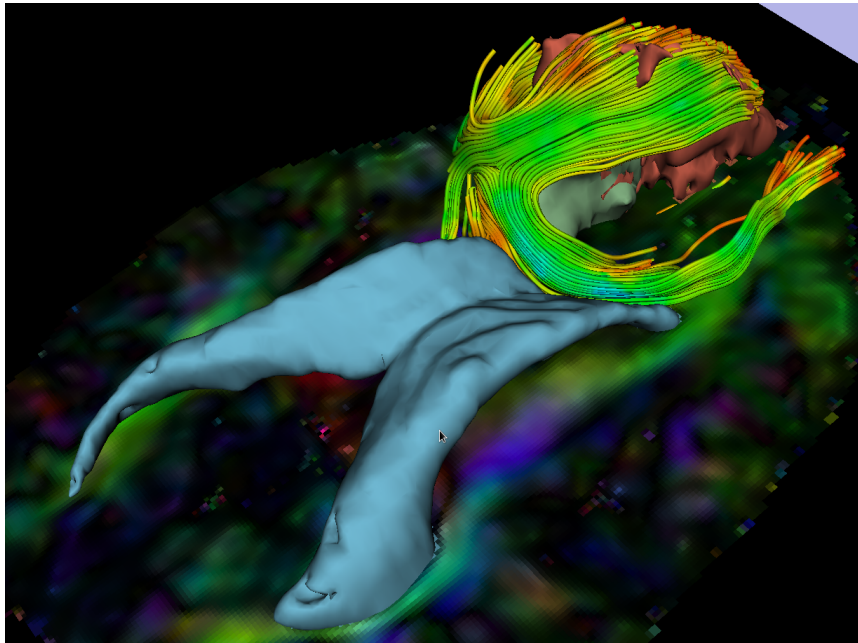
- 35 year-old male diagnosed with Glioblastoma multiforme (GBM)
- Diffusion Weighted Imaging (DWI) acquisition for neurosurgical planning

# Clinical Goal



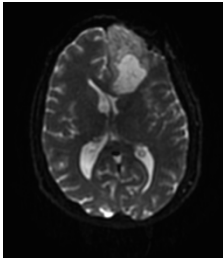
The goal of this tutorial is to explore white matter fibers surrounding a tumor using Diffusion Tensor Imaging (DTI) Tractography.

# Image Analysis Pipeline

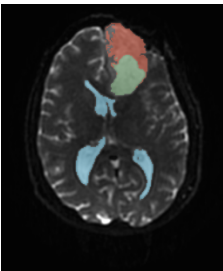


The image analysis pipeline described in this tutorial uses three different algorithms: the “Grow Cut” algorithm for segmentation of the tumor parts, the Marching Cube algorithm for surface modeling, and the single tensor streamline tractography algorithm for tract generation.

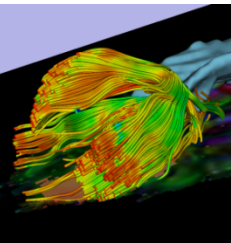
# Overview of the analysis pipeline



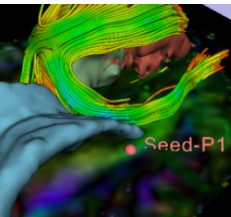
Part 1: Loading & Visualization of Diffusion Data



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

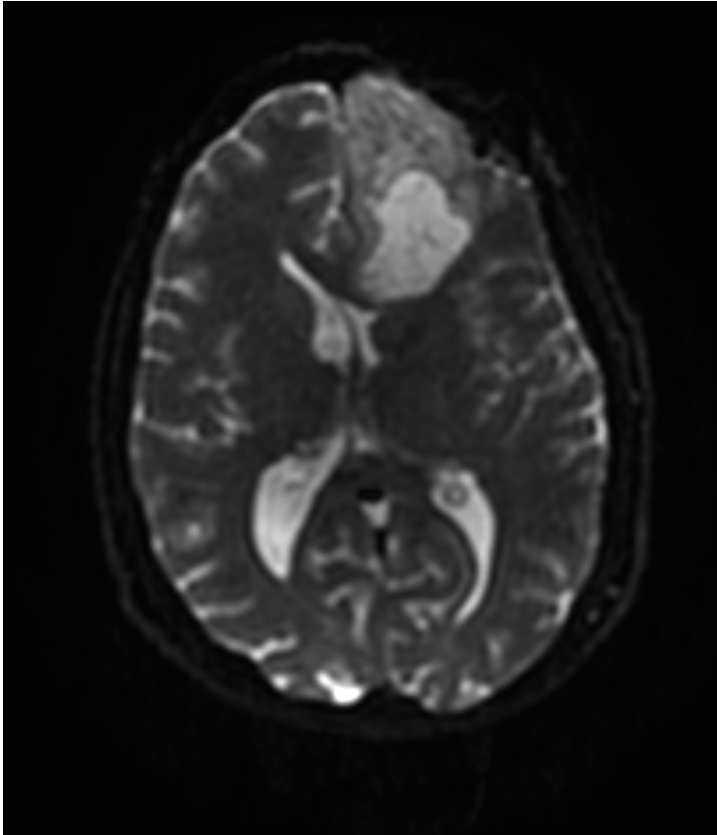


Part 3: Tractography reconstruction of the white matter fibers in the peri-tumoral volume



Part 4: Tractography exploration of the ipsilateral and contralateral side

# Part 1: Loading and Visualization of Diffusion Data

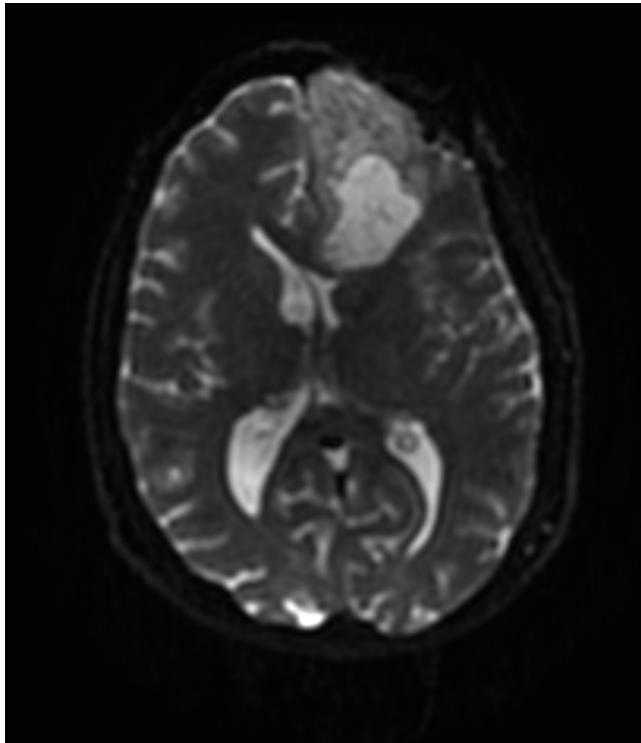
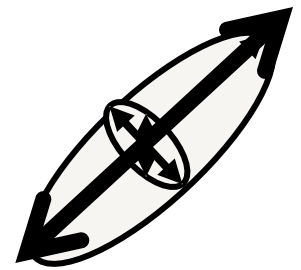


# Diffusion Tensor Imaging

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

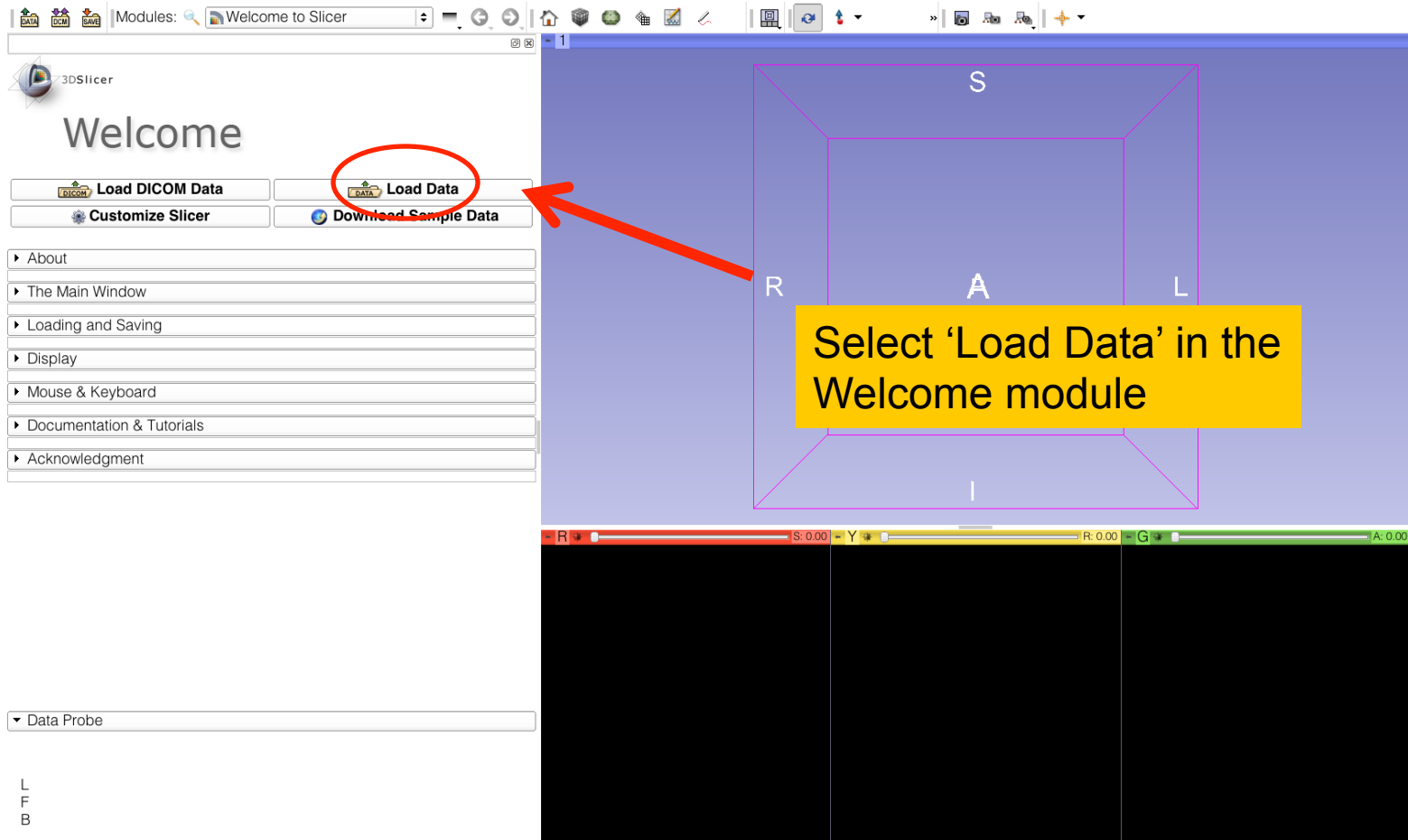
(Stejskal and Tanner 1965, Basser 1994 )

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

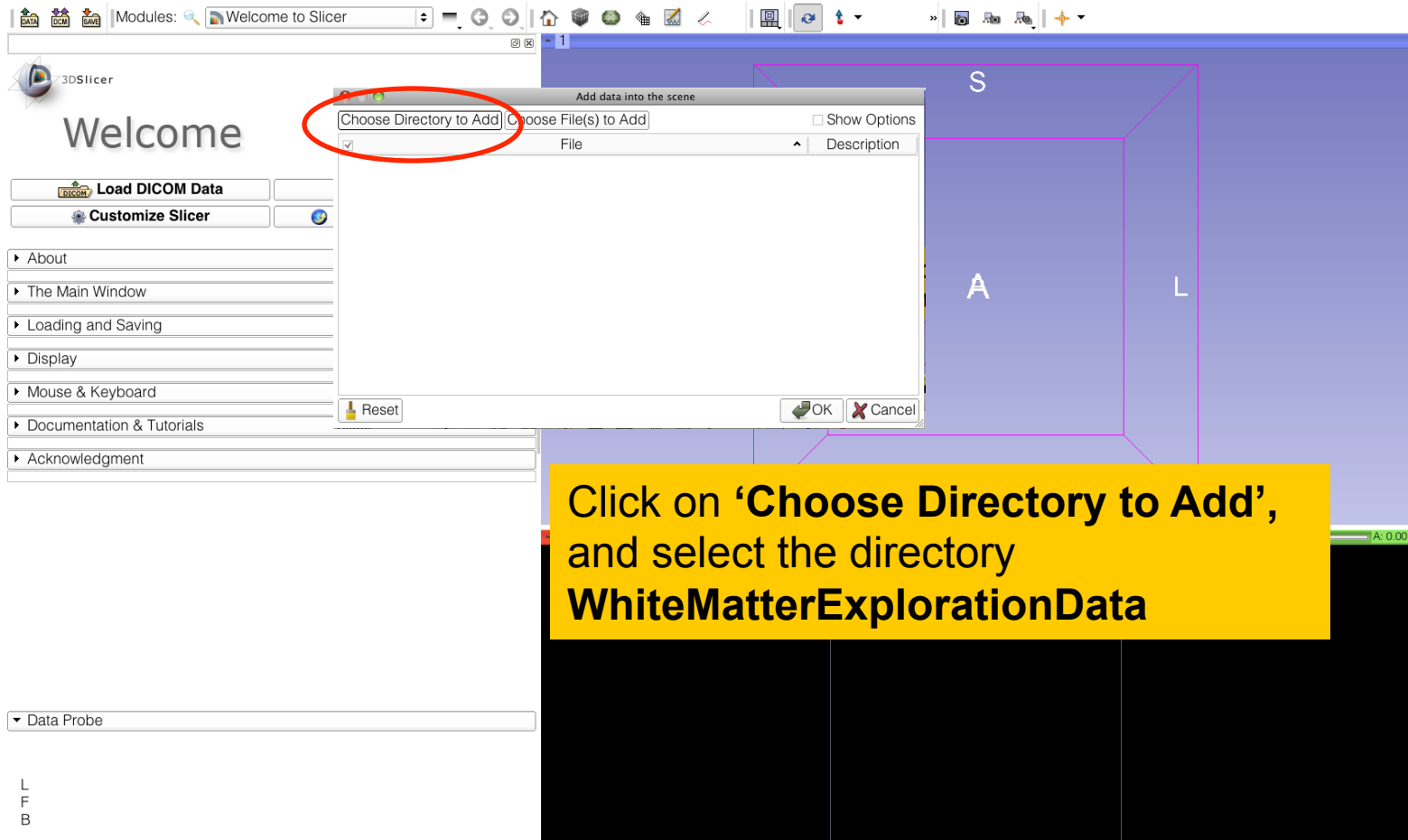




# Loading DTI and Baseline Data



# Loading DTI and Baseline Data



# Loading DTI and Baseline Data

The screenshot shows the Slicer software interface with a file selection dialog open. The dialog has two tabs: "Choose Directory to Add" and "Choose File(s) to Add". The "Choose File(s) to Add" tab is active, showing a list of files with checkboxes. The files listed are:

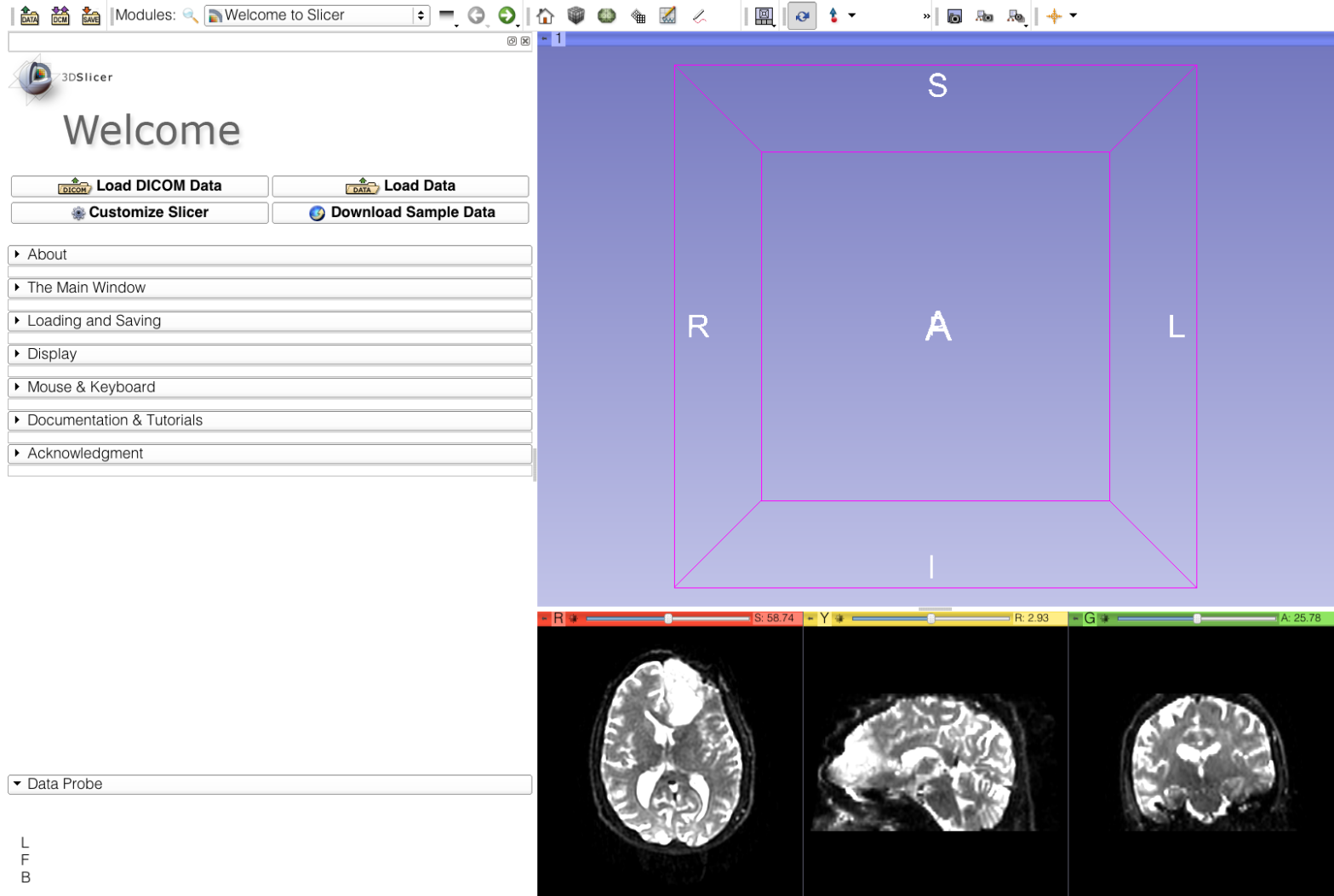
File	Description
<input type="checkbox"/> /Users/spujol/data/WhiteMatterExplorationData/DTIVolume.raw.gz	Volume
<input checked="" type="checkbox"/> /Users/spujol/data/WhiteMatterExplorationData/DTIVolume.nhdr	Volume
<input checked="" type="checkbox"/> /Users/spujol/data/WhiteMatterExplorationData/BaselineVolume.nrrd	Volume

The "Choose File(s) to Add" tab is highlighted with a red circle. The background shows a 3D brain model with axes labeled S (Superior), I (Inferior), A (Anterior), and L (Lateral). A yellow callout box contains the following instructions:

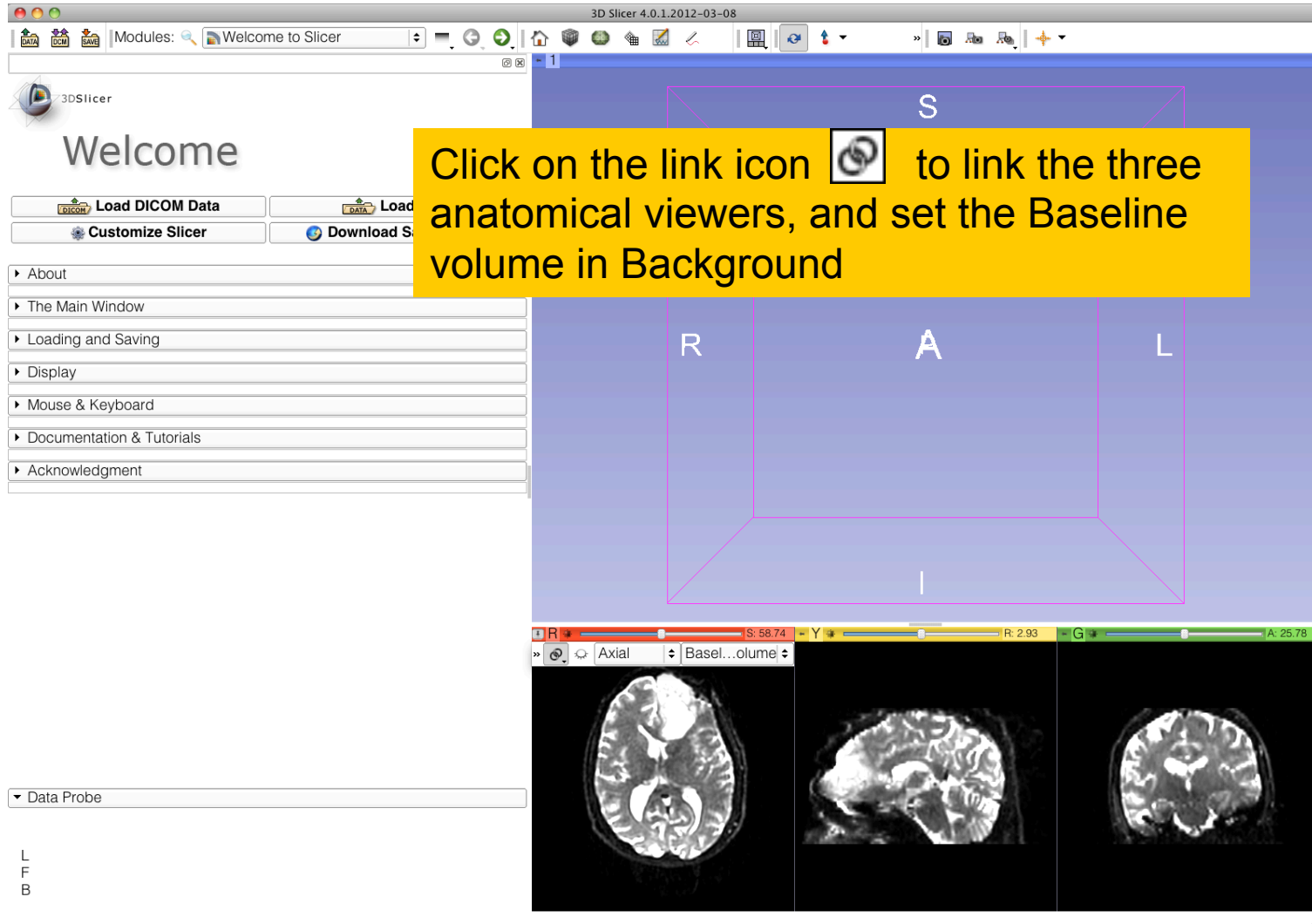
Select the directory  
**WhiteMatterExplorationData**

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

# Loading DTI and Baseline Data



# Loading DTI and Baseline Data



# Loading DTI and Baseline Data

The screenshot displays the 3D Slicer software interface. The top toolbar includes icons for DATA, DICOM, SAVE, and other functions. The 'Modules' dropdown menu is set to 'Volumes'. The left sidebar shows the '3D Slicer' logo and a list of panels: 'Help & Acknowledgement', 'Active Volume: BaselineVolume', 'Volume Information', 'Display', 'Lookup Table: Grey', 'Interpolate: checked', 'Window Level editor presets' (with a red circle around the 'Manual W/L' button), 'W: 3200', 'Threshold: Off', and 'Histogram'. The main 3D view shows a brain scan with a purple wireframe bounding box labeled 'S' (Superior), 'I' (Inferior), 'R' (Right), and 'L' (Left). A yellow callout box with black text reads: 'Select the module **Volumes** and adjust the Window and Level values of the Baseline Volume.' Below the 3D view are three 2D viewports: 'R' (Right), 'S' (Superior), and 'A' (Anterior), each with a corresponding color-coded slider (red for R, yellow for S, green for A) and numerical values (R: 2.93, S: 58.74, A: 25.78). The bottom left corner shows 'L', 'F', 'B' labels.

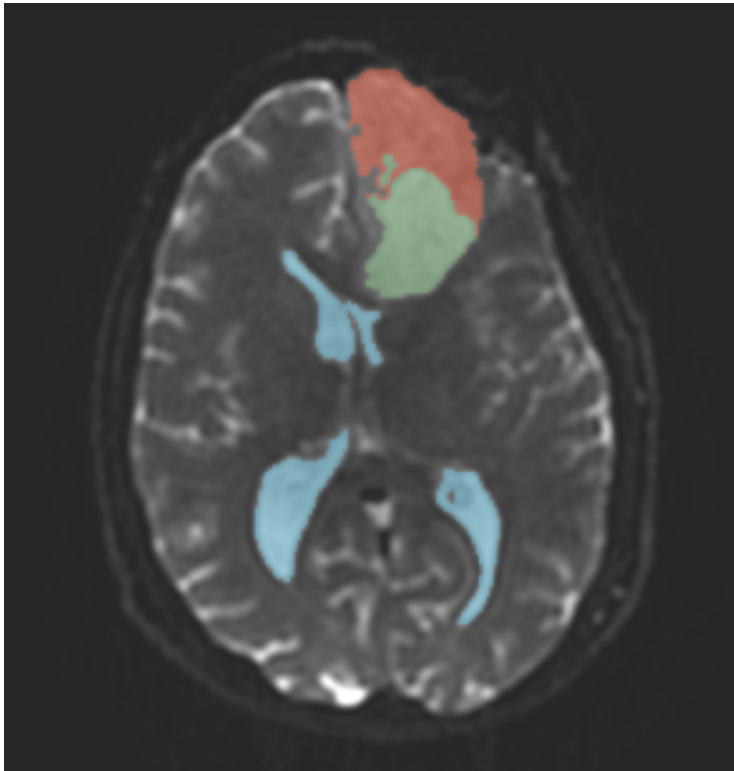
# Loading DTI and Baseline Data

The screenshot shows the 3D Slicer software interface. On the left, the 'Display' panel is visible, showing the 'Active Volume' as 'BaselineVolume' and various display settings like 'Lookup Table: Grey', 'Interpolate: checked', and 'Window Level editor presets'. The main window displays an axial MRI slice of a brain. A context menu is open over the slice, listing various layout options. The 'Red slice only' option is circled in red. A yellow callout box at the bottom of the image contains the text 'Select Red Slice Only Layout'. The status bar at the bottom left shows 'L', 'F', and 'B'.

- Conventional
- Conventional Widescreen
- Conventional Quantitative
- Four-Up
- Four-Up Quantitative
- Dual 3D
- Triple 3D
- 3D only
- Red slice only**
- Yellow slice only
- Green slice only
- Tabbed 3D
- Tabbed slice
- Compare
- Compare Widescreen
- Compare Grid
- Three over three
- Four over four
- Two over Two

Select Red Slice Only Layout

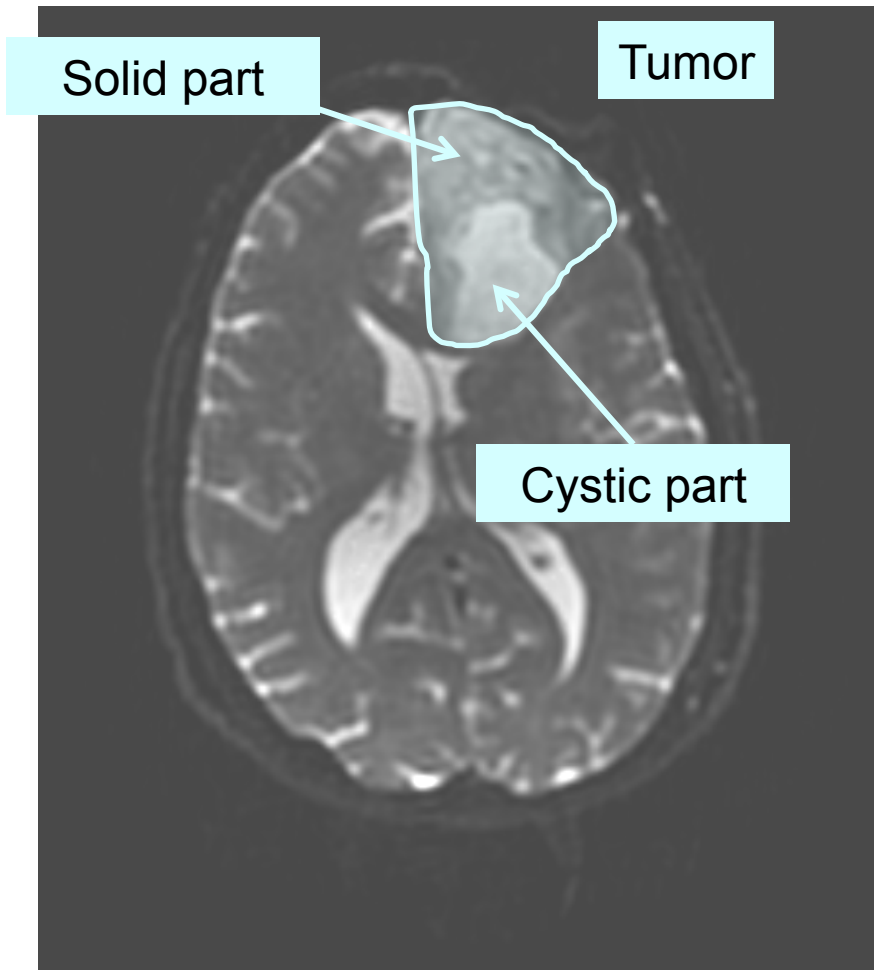
L  
F  
B



# Part 1: Segmenting the tumor and ventricles



# Tumor Segmentation



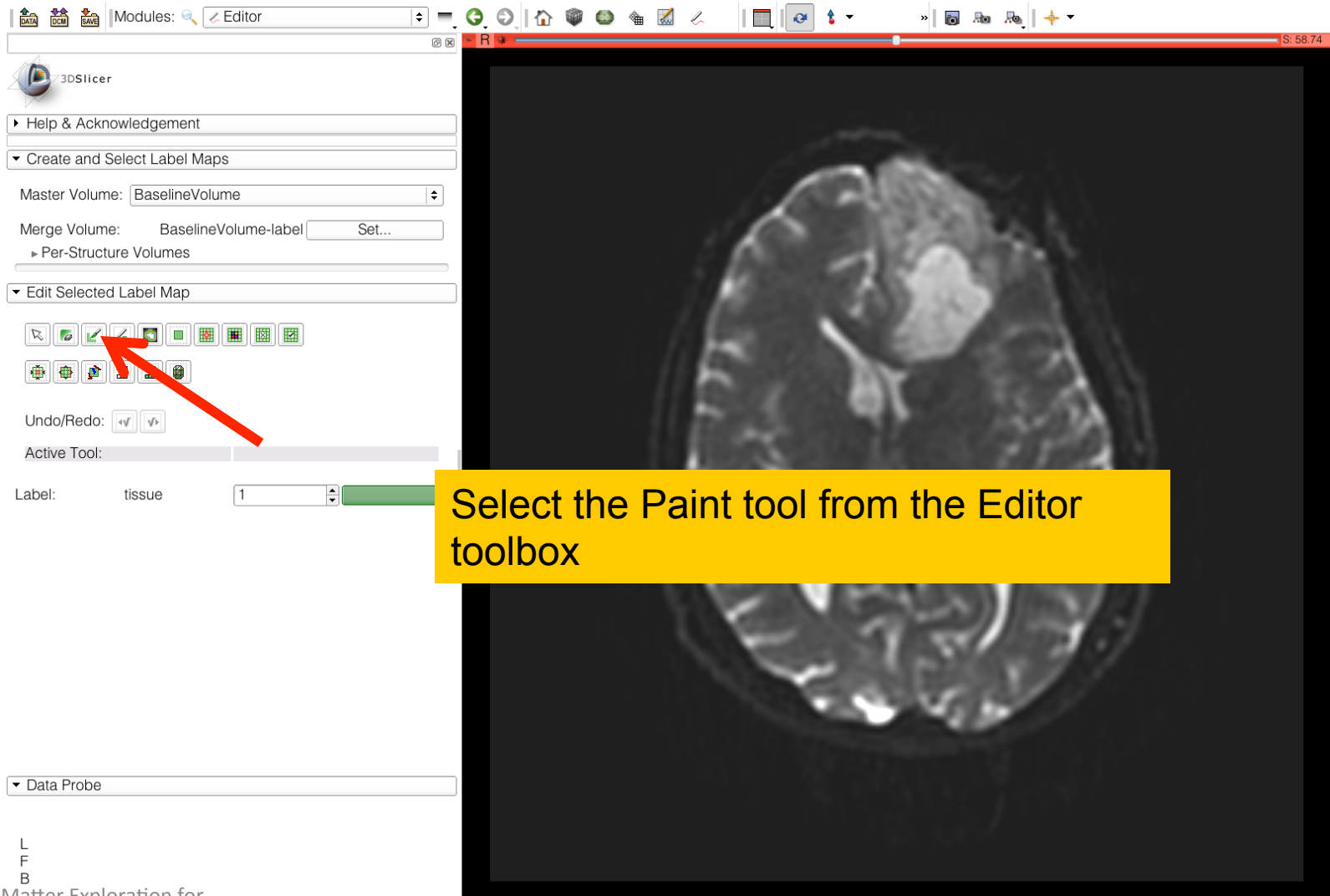
The tumor in this clinical case is composed of two parts: a solid part, and a cystic part.

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

# Tumor Segmentation

The screenshot shows the 3D Slicer software interface. The 'Modules' dropdown menu at the top left is open, and 'Editor' is selected and circled in red. A yellow callout box points to this selection with the text: 'Select the module **Editor** from the main menu'. Below the menu, the 'Create and Select Label Maps' panel is visible, showing 'Master Volume: BaselineVolume' and 'Merge Volume: None'. A dialog box is open in the center, containing the text: 'Create a merge label map for selected master volume BaselineVolume. New volume will be BaselineVolume-label. Select the color table node will be used for segmentation labels.' Below this text, a dropdown menu shows 'GenericAnatomyColors' selected. Two buttons, 'Apply' and 'Cancel', are at the bottom of the dialog. A red arrow points to the 'Apply' button. A yellow callout box at the bottom of the dialog area contains the text: 'Select the color table 'Generic Anatomy Colors' and click on Apply'. The background shows a 3D rendering of a brain MRI slice.

# Tumor Segmentation



Select the Paint tool from the Editor toolbox

# Tumor Segmentation

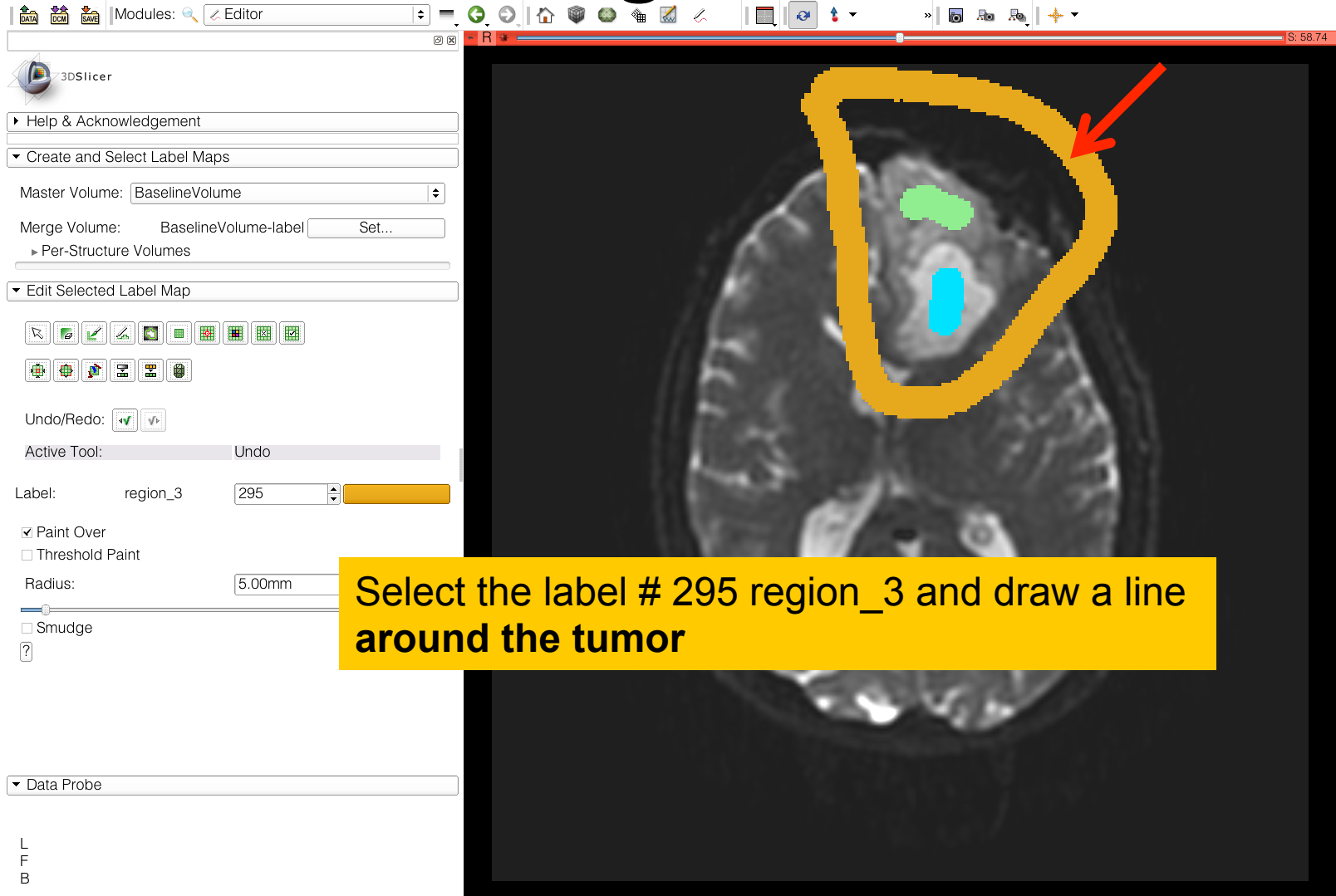
The screenshot displays the 3D Slicer software interface. The top toolbar includes icons for DATA, DCM, SAVE, and various editing tools. The main window shows an axial MRI slice of a brain with a cyan-colored region highlighted in the center, representing a tumor. A red arrow points to this region. The left sidebar contains several panels: 'Help & Acknowledgement', 'Create and Select Label Maps', 'Edit Selected Label Map', and 'Data Probe'. The 'Edit Selected Label Map' panel is active, showing a 'Label' dropdown set to 'region\_1' with a value of '293' and a cyan color swatch. Below this, there are checkboxes for 'Paint Over' (checked), 'Threshold Paint', and 'Smudge'. A 'Radius' slider is set to '5.00mm'. The 'Data Probe' panel is also visible at the bottom of the sidebar.

# Tumor Segmentation

The screenshot displays the 3D Slicer software interface. On the left, the 'Edit Selected Label Map' panel is active, showing the 'Label' set to 'mass' with a value of '7' and a green color swatch. The 'Radius' is set to '5.00mm'. The main view shows an axial MRI brain slice with a green segmented region (labeled #7) and a blue segmented region. A red arrow points to the green region. A yellow text box at the bottom of the image contains the following text:

Select the label #7 (mass) and draw a short line in the **solid part of the tumor**

# Tumor Segmentation



The screenshot shows the 3DSlicer software interface. The main view displays an axial MRI slice of a brain with a tumor region highlighted in yellow. A red arrow points to the yellow boundary. The left sidebar contains various tool panels, including 'Create and Select Label Maps' and 'Edit Selected Label Map'. The 'Edit Selected Label Map' panel shows the 'Active Tool' set to 'Undo' and the 'Label' set to 'region\_3' with a value of '295'. A yellow text box is overlaid on the image with the instruction: 'Select the label # 295 region\_3 and draw a line around the tumor'.

# Tumor Segmentation

Select the Grow Cut segmentation algorithm

Merge Volume: BaselineVolume-label Set...

Per-Structure Volumes

Edit Selected Label Map

Undo/Redo: [undo] [redo]

Active Tool: GrowCutEffect

Label: region\_3 295

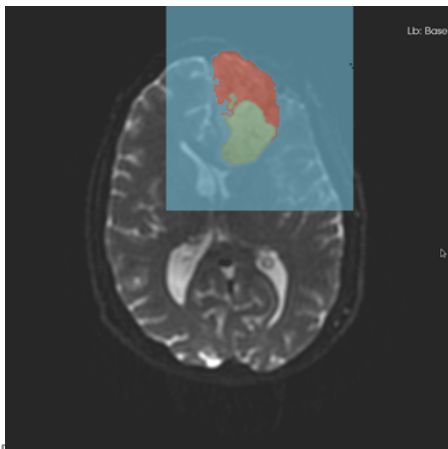
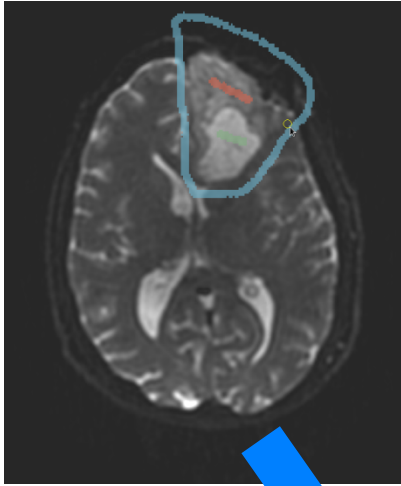
Run the GrowCut segmentation on the current label map. This will use your current segmentation as an example to fill in the rest of the volume.

Apply

Data Probe

L  
F  
B

# 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

Click on Apply to start the Grow Cut segmentation algorithm

Merge Volume: BaselineVolume-label Set...  
► Per-Structure Volumes

▼ Edit Selected Label Map

Undo/Redo: [undo] [redo]

Active Tool: GrowCutEffect

Label: region\_3 295

Run the GrowCut segmentation on the current label map. This will use your current segmentation as an example to fill in the rest of the volume.

Apply

▼ Data Probe

L  
F  
B

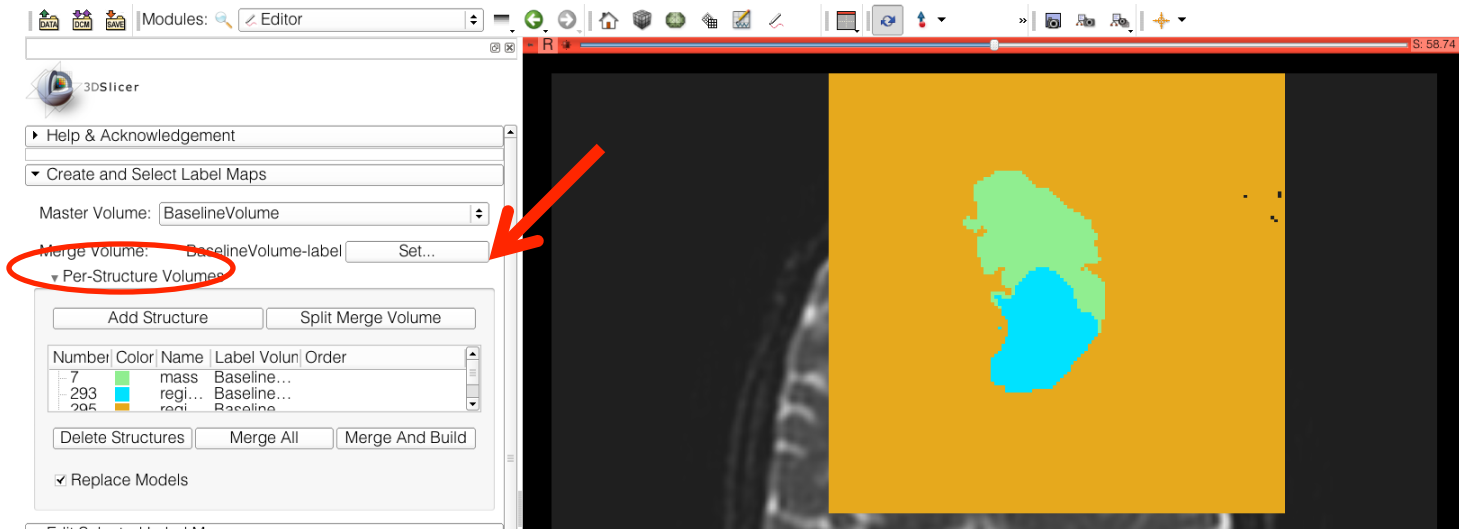
# Tumor Segmentation

The image shows the 3DSlicer software interface. On the left, the 'Create and Select Label Maps' panel is visible, showing 'Master Volume: BaselineVolume' and 'Merge Volume: BaselineVolume-label'. A yellow box highlights the segmentation results, and a green box contains the text 'Slicer displays the results of the segmentation'. The main window displays an axial MRI slice of a brain with a tumor. The tumor is segmented into two parts: a solid part (green) and a cystic part (blue). A yellow box highlights the segmentation results, and a green box contains the text 'Slicer displays the results of the segmentation'. A light blue box labeled 'Solid part' points to the green region, and another light blue box labeled 'Cystic part' points to the blue region. The software interface includes a top toolbar with various icons and a bottom status bar showing 'L', 'F', and 'B'.

# Tumor Segmentation

The screenshot shows the 3D Slicer software interface. On the left, the 'Per-Structure Volumes' tab is selected and circled in red. A red arrow points to the 'Split Merge Volume' button. The central 3D view displays a brain slice with segmented regions in green, blue, and orange. A yellow box at the bottom contains the instruction: 'Expand the Per-Structure Volumes Tab and click on 'Split Merge Volume''. The interface also shows a 'Merge Volume' dropdown set to 'BaselineVolume-label' and a 'Set...' button. The 'Edit Selected Label Map' section contains various icons for editing the segmentation. The 'Data Probe' section is visible at the bottom left.

# Tumor Segmentation

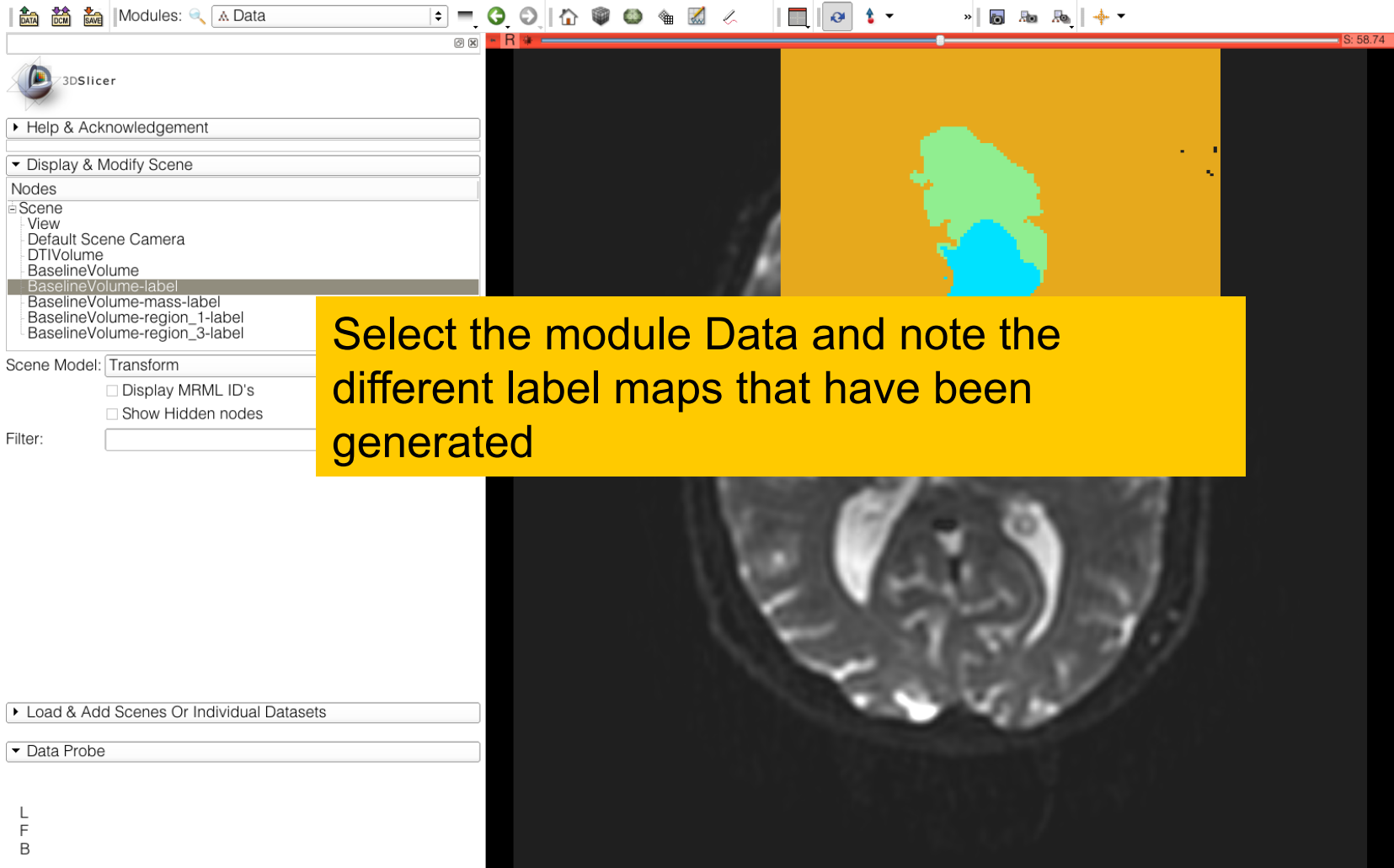


The label map **BaselineVolume-label** has been split into three volumes:

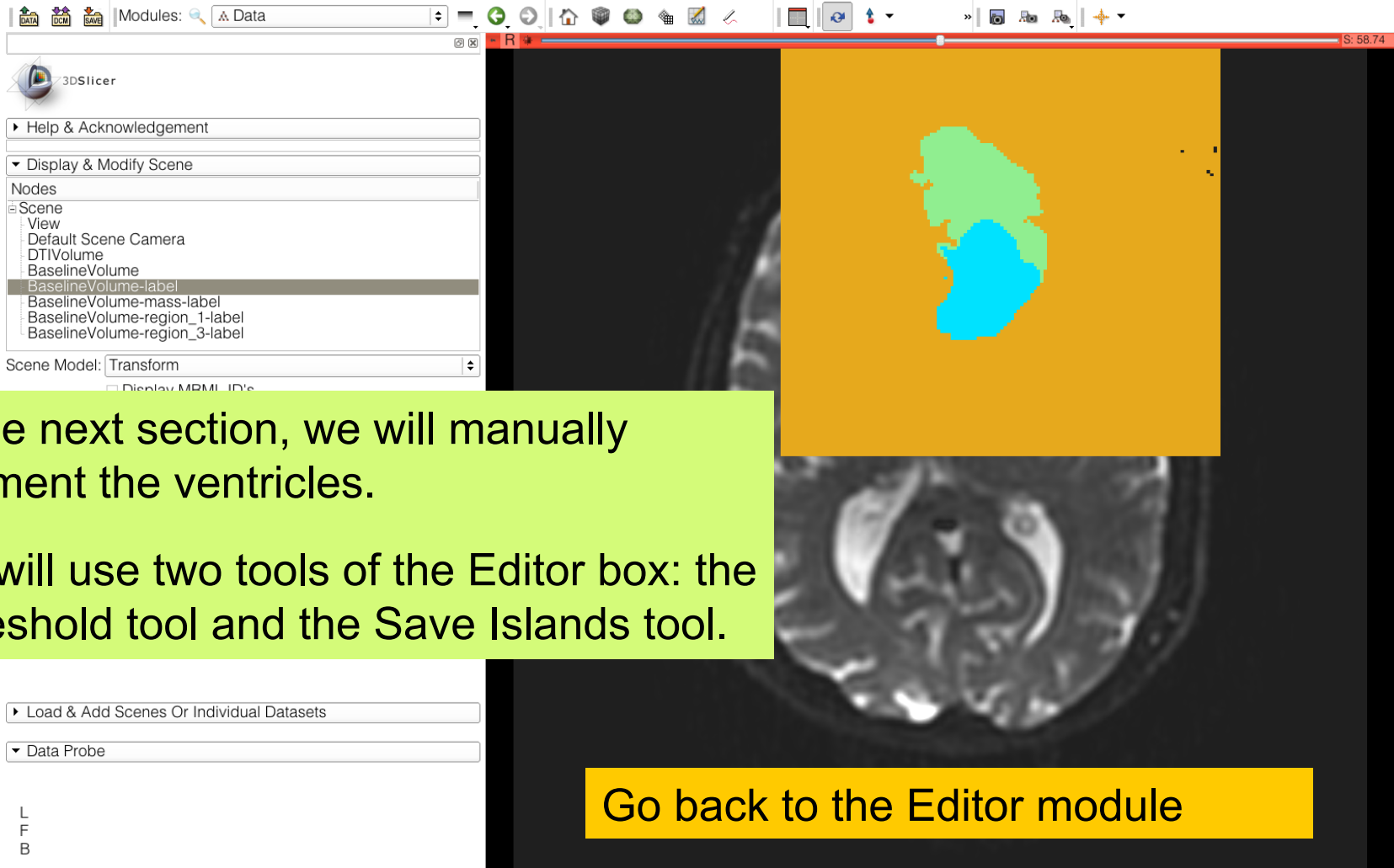
- BaselineVolume-mass-label**: solid part of the tumor
- BaselineVolume-region\_1-label**: cystic part of the tumor
- BaselineVolume-region\_3-label**: surrounding structures

L  
F  
B

# Tumor Segmentation



# 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.

Go back to the Editor module

# Ventricles Segmentation

Select the volume  
'BaselineVolume-region\_3-label'

Add Structure   Split Merge Volume

Number	Color	Name	Label Volume	Order
293	■	regi...	BaselineVolume-region_1-...	
295	■	regi...	BaselineVolume-region_3-...	

Delete Structures   Merge All   Merge And Build

Replace Models

▼ Edit Selected Label Map

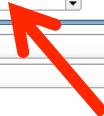


Undo/Redo:  

Active Tool: ThresholdEffect

Label: region\_3   295

Threshold Range: 1700.00   18197.00

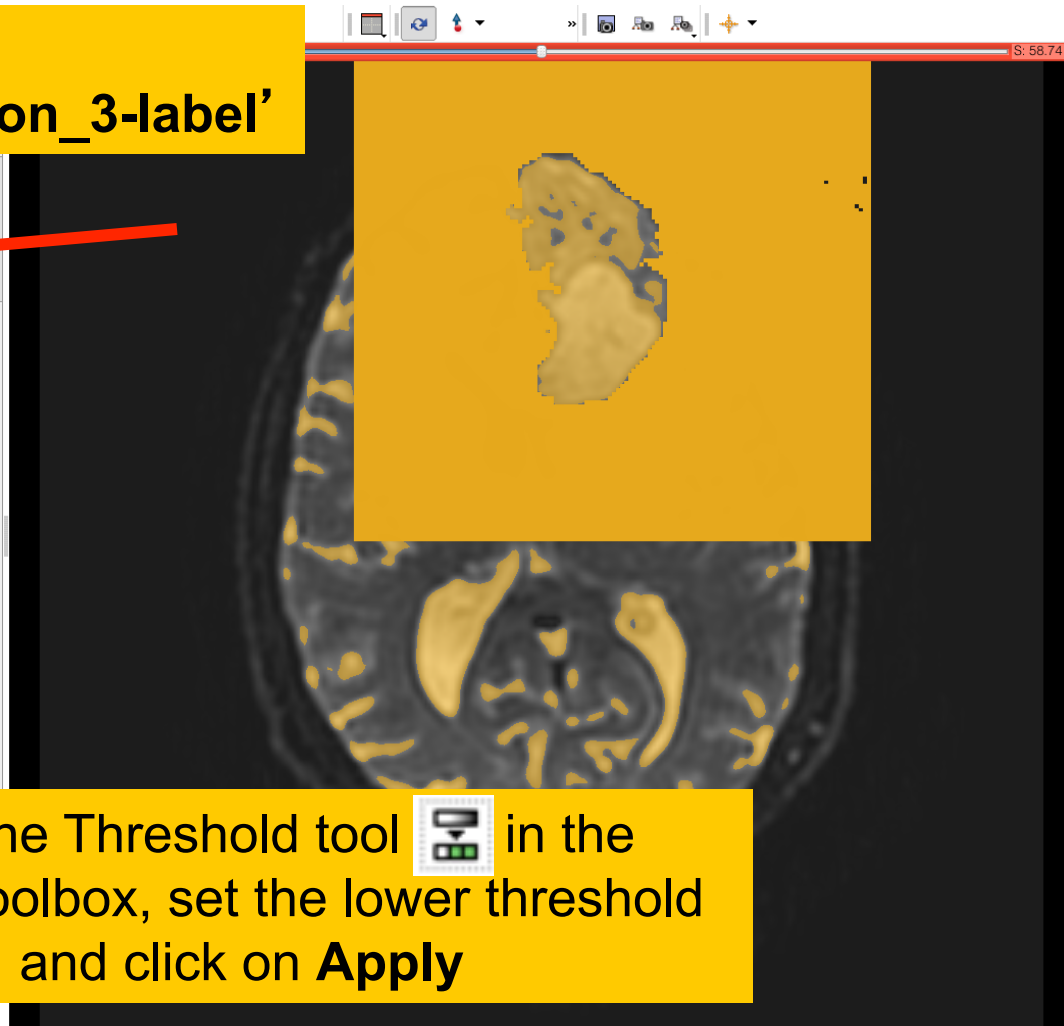



Use For Paint

Apply

▼ Data Probe

L  
F  
B



Select the Threshold tool  in the Editor toolbox, set the lower threshold to 1700, and click on **Apply**

# Ventricles Segmentation

Slicer displays the result of the threshold

Master Volume: BaselineVolume

Merge Volume: BaselineVolume-label Set...

Per-Structure Volumes

Number	Color	Name	Label Volume	Order
7	Green	mass	BaselineVolume-mass-label	
293	Blue	regi...	BaselineVolume-region_1-...	
295	Yellow	regi...	BaselineVolume-region_3	

Delete Structures Merge All Merge And Build

Replace Models

Edit Selected Label Map

Undo/Redo: [Undo] [Redo]

Active Tool: DefaultTool

Label: region\_3 295

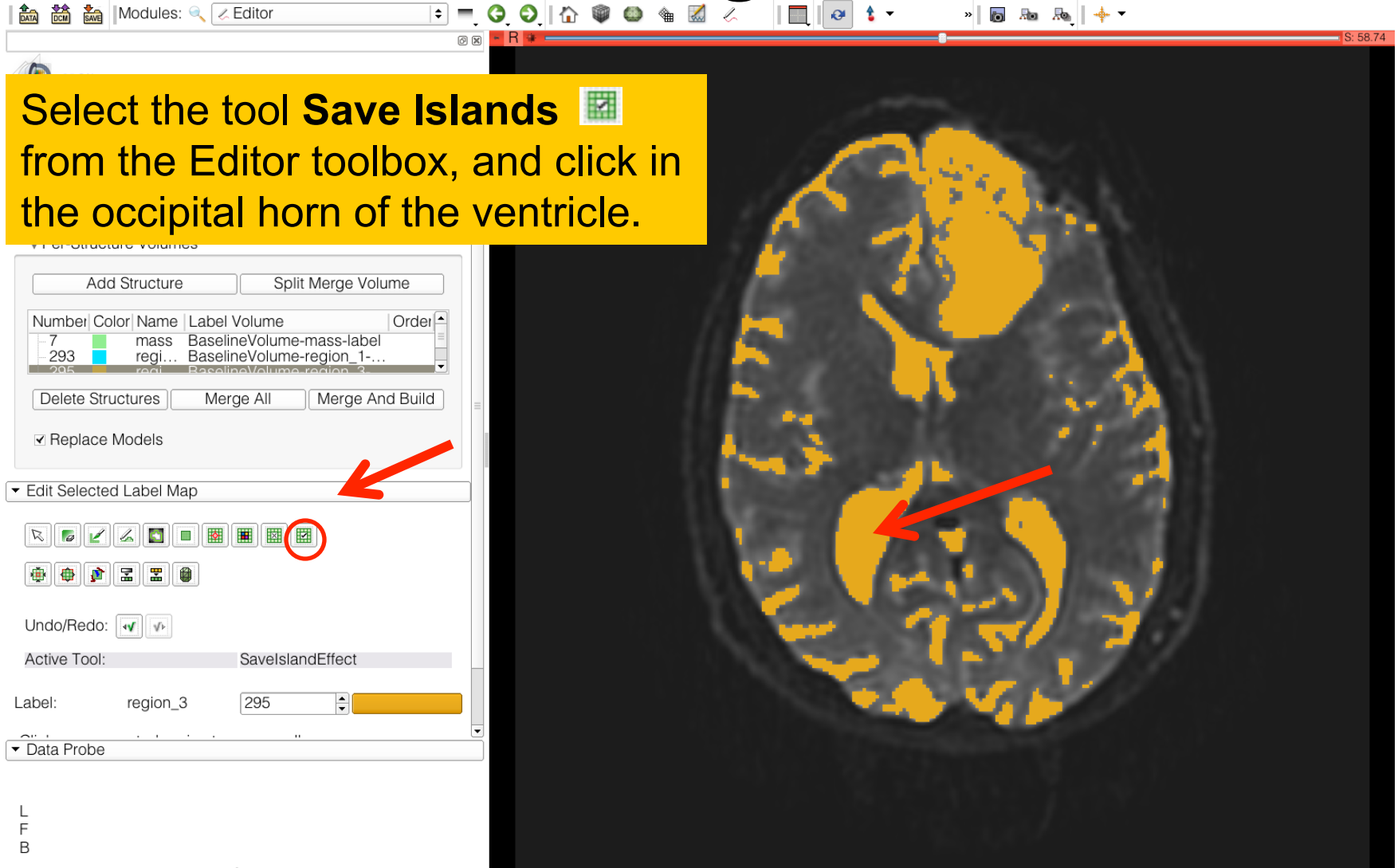
Data Probe

L  
F  
B

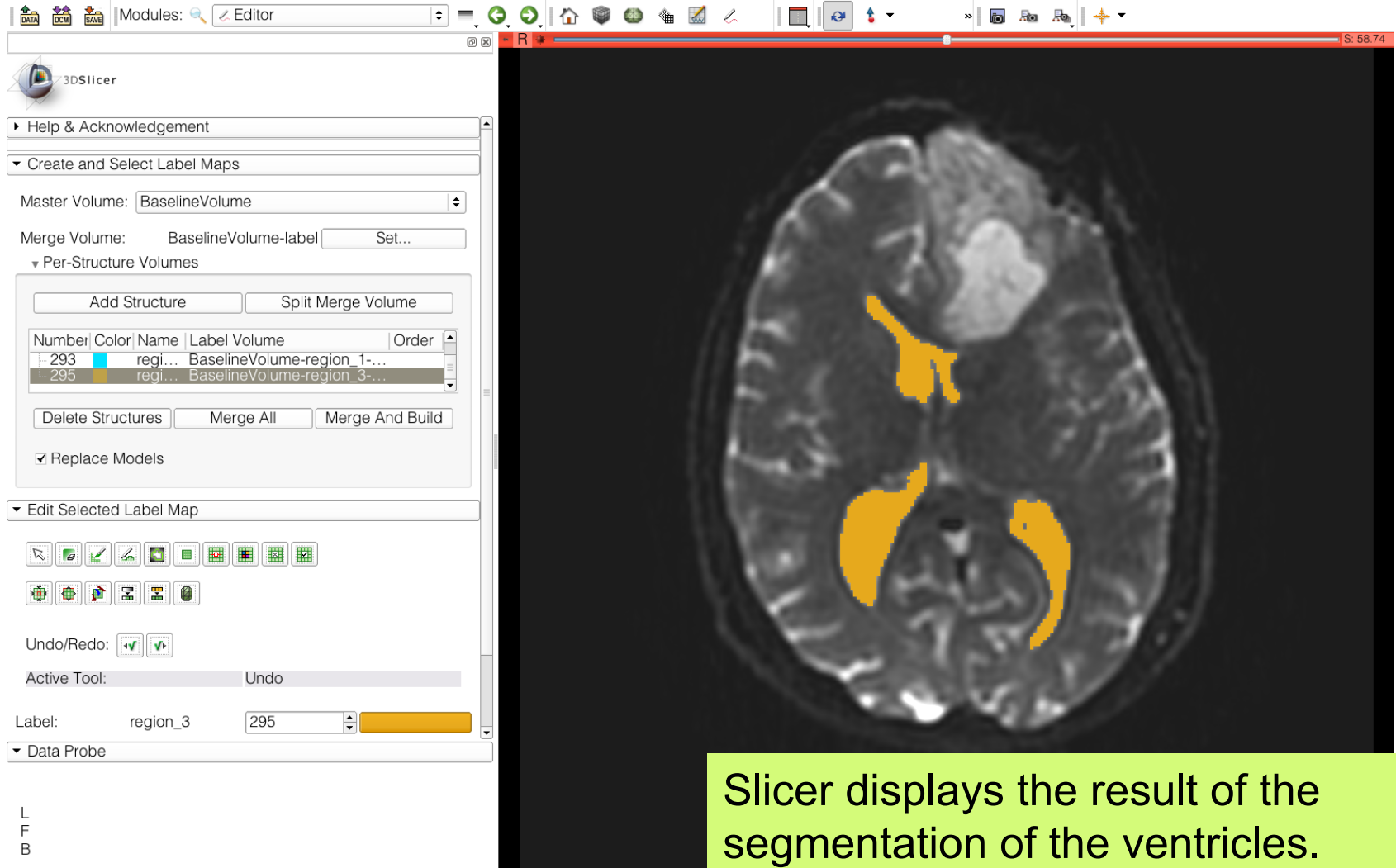


# Ventricles Segmentation

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



# Final Result of the Segmentation



Slicer displays the result of the segmentation of the ventricles.

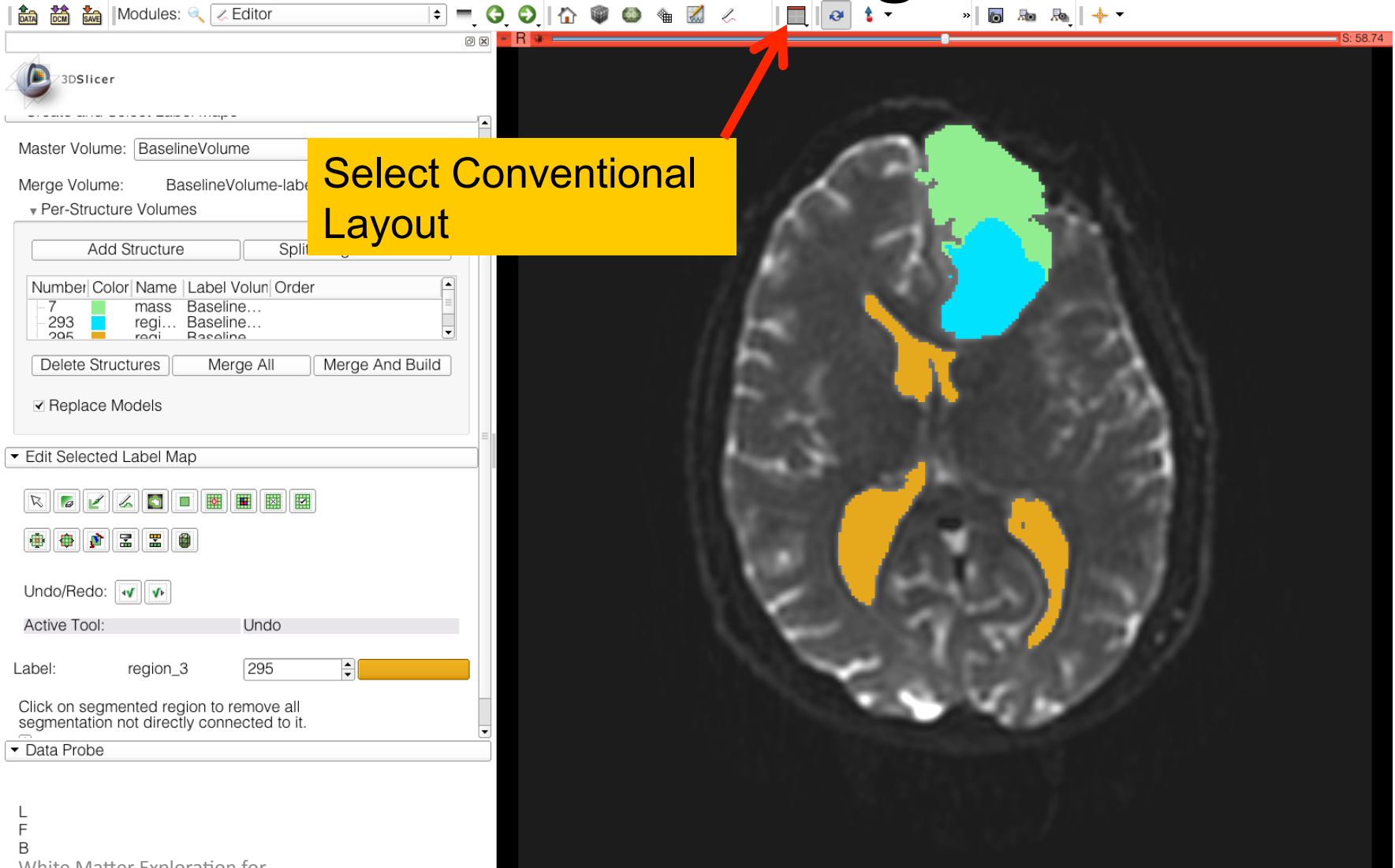
# Final Result of the Segmentation

The screenshot shows the 3D Slicer software interface. On the left, the 'Per-Structure Volumes' panel is visible, containing a table of segmented volumes and a 'Merge And Build' button highlighted with a red arrow. The main window displays a brain scan with two yellow highlighted regions.

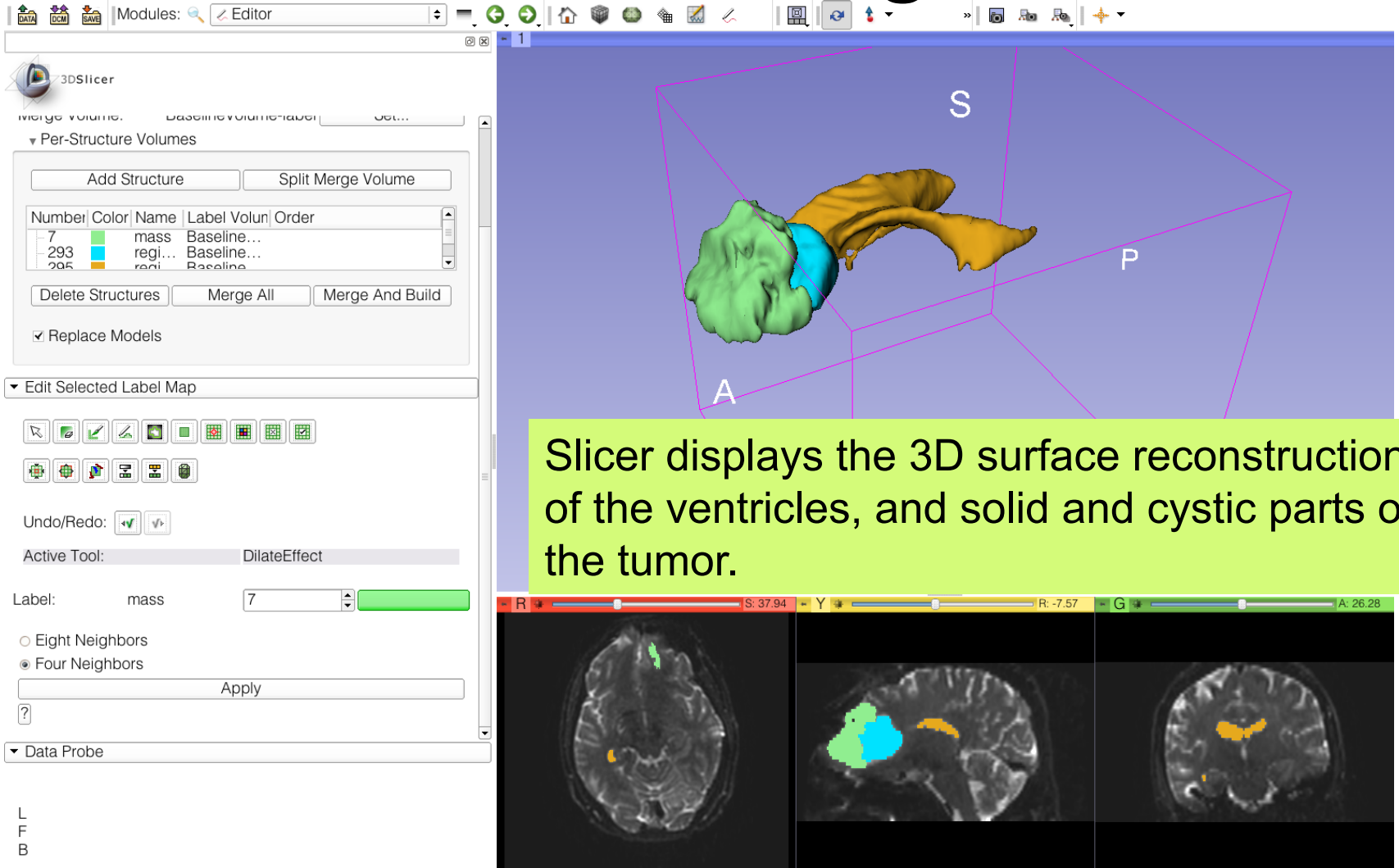
Number	Color	Name	Label Volu	Order
7	Green	mass	Baseline...	
293	Blue	regi...	Baseline...	
295	Yellow	radi...	Baseline...	

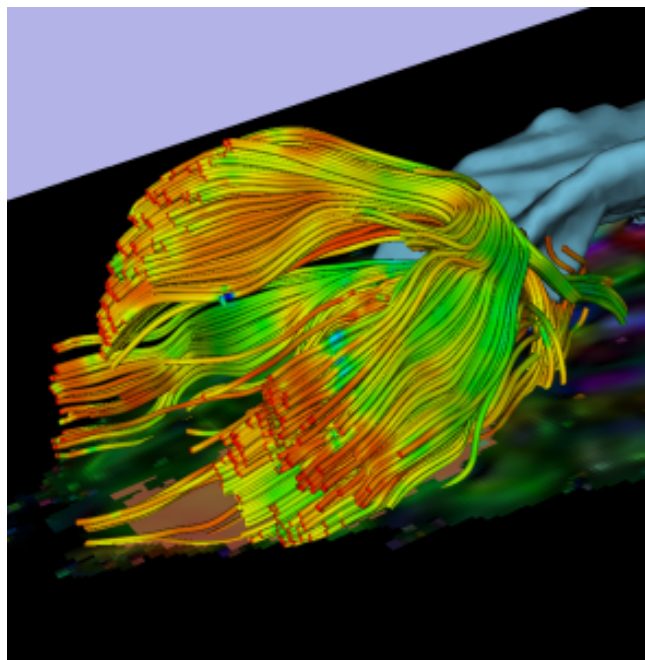
Click on **Merge and Build** to merge the different label maps, and generate the 3D models of the tumor and ventricles using a Marching Cubes algorithm

# Final Result of the Segmentation



# Final Result of the Segmentation

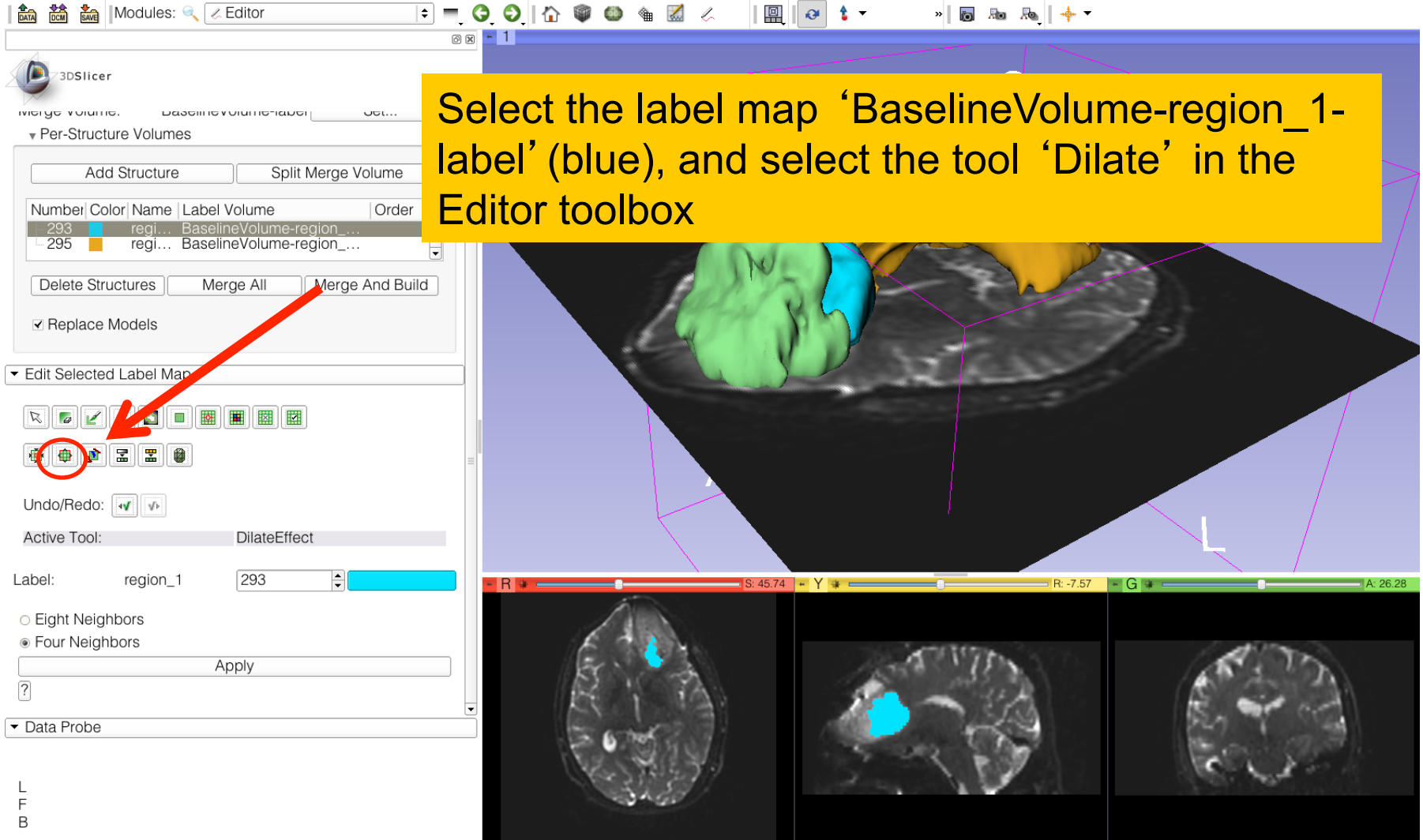




## Part 2: Tractography exploration of peri- tumoral white matter fibers

# Definition of the peri-tumoral volume

Select the label map 'BaselineVolume-region\_1-label' (blue), and select the tool 'Dilate' in the Editor toolbox



# 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

3D Slicer

Per-Structure Volumes

Number	Color	Name	Label Volume
293	Blue	regi... BaselineVolume-region_1-label	
295	Orange	regi... BaselineVolume-region_3-label	

Edit Selected Label Map

Label: region\_1 293

Four Neighbors

Apply

L  
F  
B



# Visualization of the DTI Volume

Note the dilatation of the cystic part of the tumor in the 3D viewer

3D Slicer

Modules: Editor

Delete Structures Merge All Merge And Build

Replace Models

Edit Selected Label Map

Undo/Redo:

Active Tool: DilateEffect

Label: region\_1 293

Eight Neighbors  
 Four Neighbors

Apply

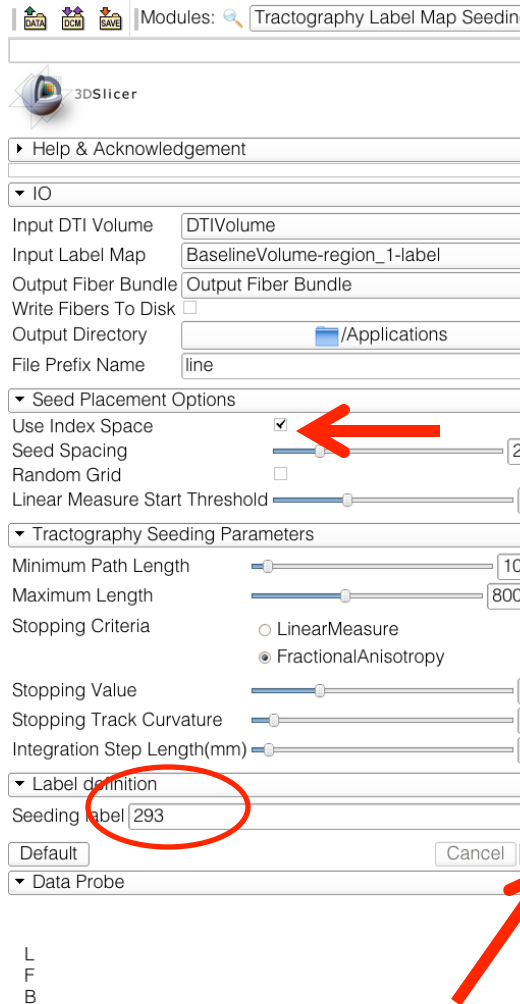
Data Probe

L  
F  
B

S  
A  
L

R S: 58.74 Y R: -7.57 G A: 26.28

# Tractography Parameters



Select the module **Tractography Label Map Seeding**

- **I/O**: Set the following input and output volume:

**Input DTI Volume**: DTIVolume

**Input Label Map**: BaselineVolume-region\_1-label

**Output Fiber Bundle**: Create NewFiberBundle

- **Seed Placement Options**:

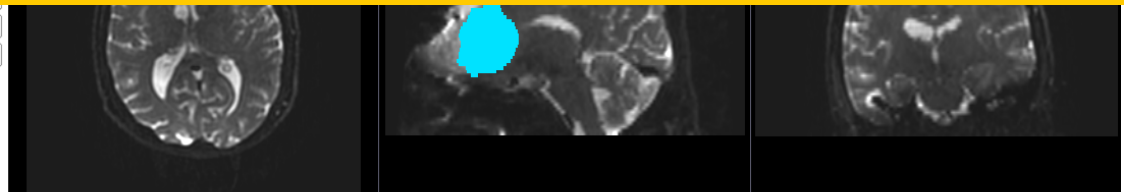
Check **Use Index Space**

- **Stopping Value**

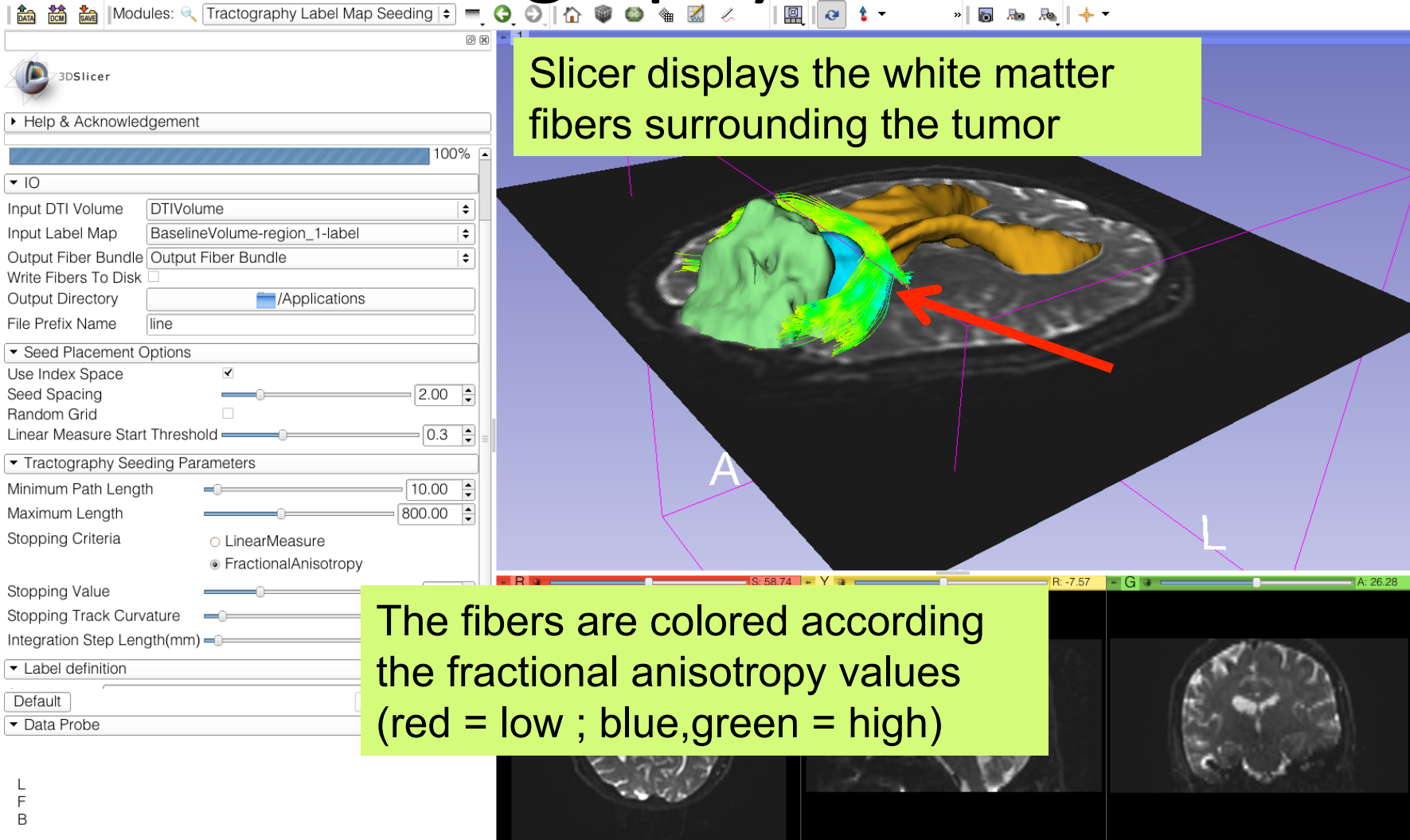
Set the FA threshold to 0.15

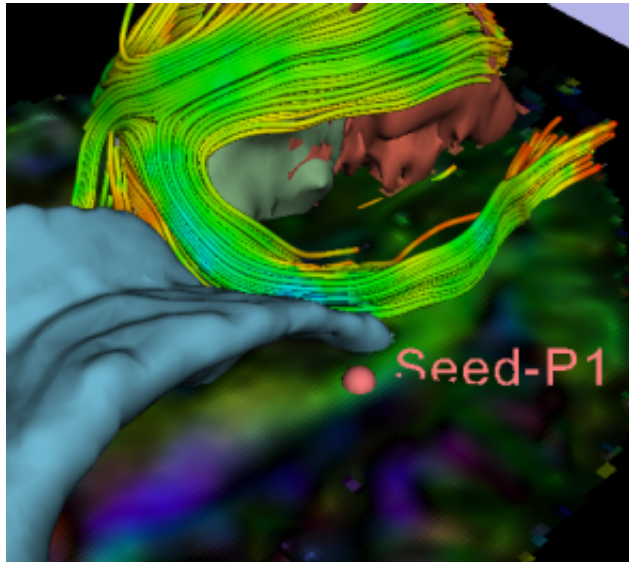
- **Label Definition**:

Enter Seeding Label **293**, and Click on **Apply**



# Tractography Results





## Part 4: Tractography exploration of the ipsilateral and contralateral side

# Tractography on-the-fly



Select the module  
Tractography Fiducial Seeding

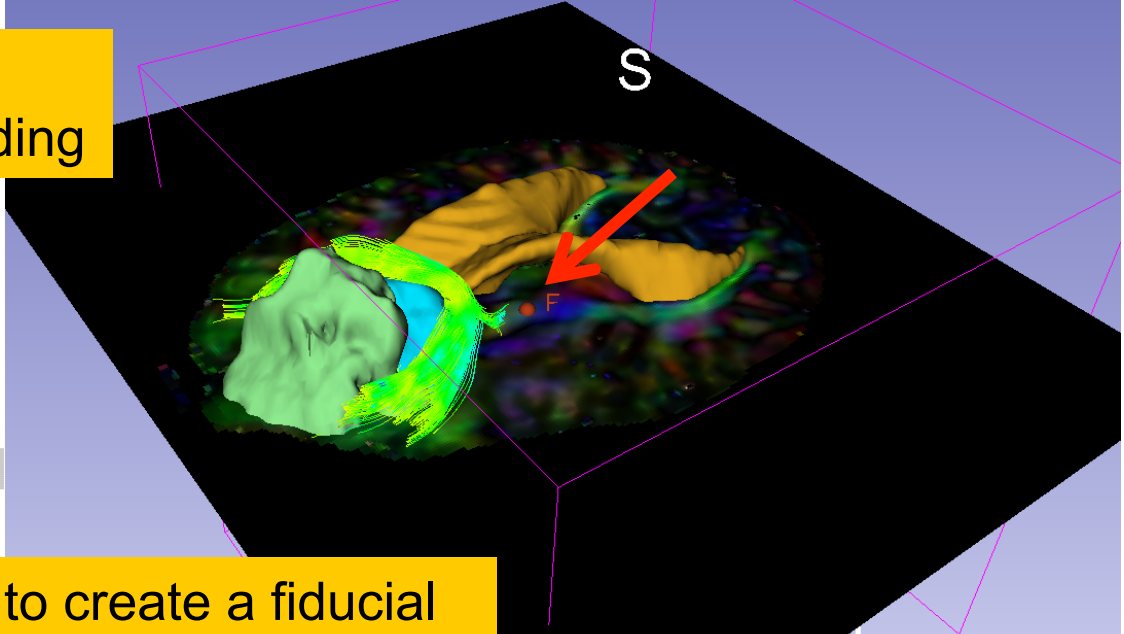
Input DTI Volume: DTIVolume  
Input Fiducial List or Model: Select a AnnotationHierarchyNode  
Output Fiber Bundle: Select a FiberBundle

Seed Placement Options

Fiducial Region Size: 2.50mm  
Fiducial Seeding Step Size: 1.00mm  
Seed Selected Fiducials:   
Max Number of Seeds: 100

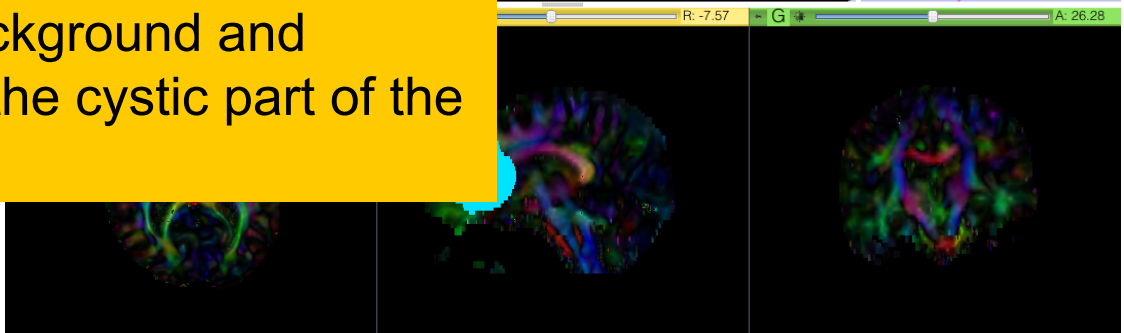
Tractography Seeding Parameters

Minimum Path Length: 20.00mm  
Stopping Criteria: Fractional Anisotropy  
Stopping Value: 0.25



Click on the Fiducial Icon to create a fiducial  
Set the DTI volume in background and  
position the fiducial near the cystic part of the  
tumor in the 3D viewer

L  
F  
B



# Tractography on-the-fly

Modules: Tractography Fiducial Seeding

3DSlicer

Parameter set: FiducialSeedingParameters

IO

Input DTI Volume: DTIVolume

Input Fiducial List or Model: Fiducials List

Output Fiber Bundle: FiberBundle

Seed Placement Options

Fiducial Region Size: 2.00mm

Fiducial Seeding Step Size: 1.00mm

Seed Selected Fiducials:

Max Number of Seeds: 100

Tractography Seeding Parameters

Minimum Path Length: 10.00mm

Stopping Criteria: Fractional Anisotropy

Stopping Value: 0.15

Stopping Track Curvature: 0.70

Integration Step Length: 0.50mm

Enabling Options

Create Tracts Initially As: Tubes

Enable Seeding Tracts:

Data Probe

L  
F  
B

S: 48.34 Y R: -7.57 G A: 26.28

Set Input DTI Volume to **DTIVolume**  
Set Fiducial List or Model to **FiducialsList**  
Set Output Fiber Bundle to **Create new Fiber Bundle**  
Set the Minimum Path Length to 10 mm  
Set the FA Stopping Criteria to 0.15

# Fiducial Seeding

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

Parameter set: FiducialSeedingParameters

IO

Input DTI Volume: DTIVolume

Input Fiducial List or Model: Fiducials List

Output Fiber Bundle: FiberBundle

Seed Placement Options

Fiducial Region Size: 2.00mm

Fiducial Seeding Step Size: 1.00mm

Seed Selected Fiducials:

Max Number of Seeds: 100

Tractography Seeding Parameters

Minimum Path Length: 10.00mm

Stopping Criteria: Fractional Anisotropy

Stopping Value: 0.15

Stopping Track Curvature: 0.70

Integration Step Length: 0.50mm

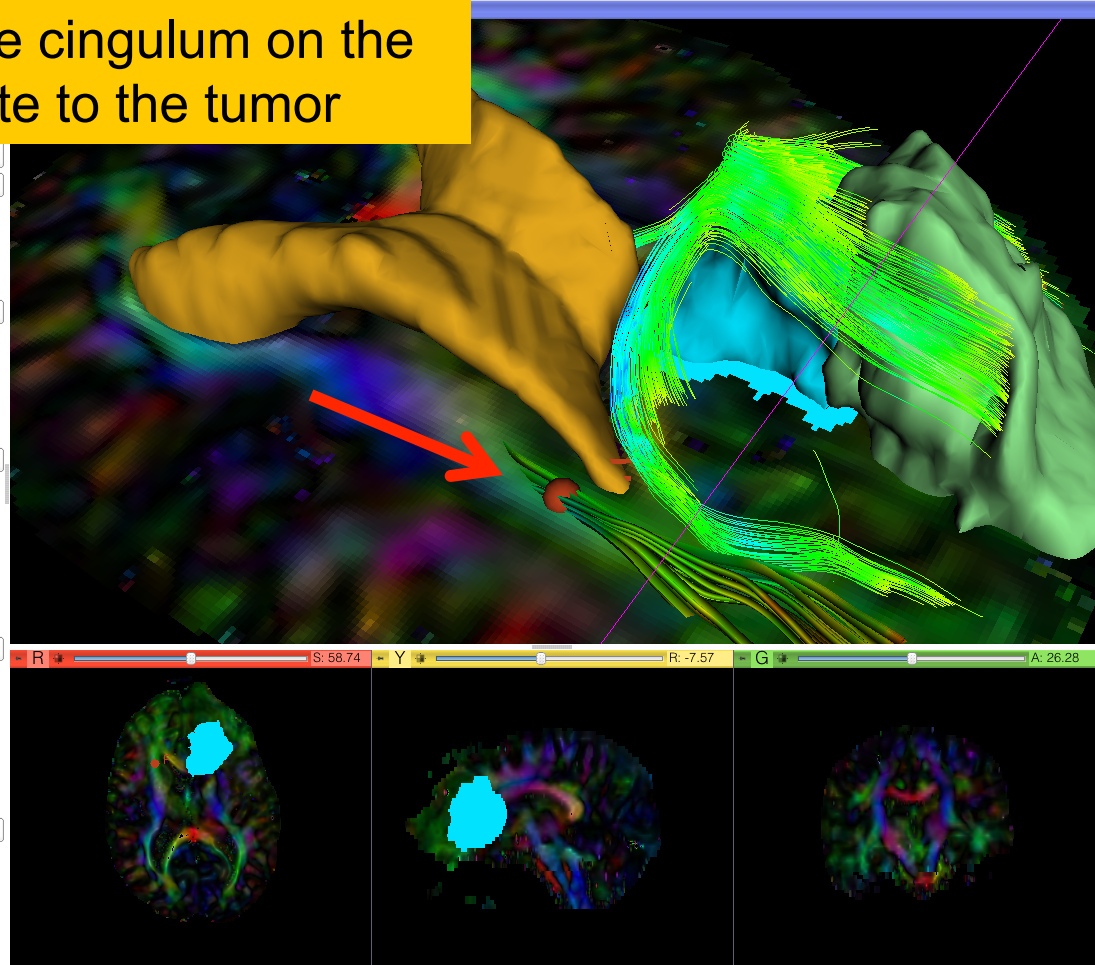
Enabling Options

Create Tracts Initially As: Tubes

Enable Seeding Tracts:

Data Probe

L  
F  
B



# Tractography on-the-fly

Explore the aspect of the cingulum in the contralateral and ipsilateral sides

3DSlicer

Modules: Tractography Fiducial Seeding

Help & Acknowledgement

Output Fiber Bundle: FiberBundle

Seed Placement Options

- Fiducial Region Size: 2.00mm
- Fiducial Seeding Step Size: 1.00mm
- Seed Selected Fiducials:
- Max Number of Seeds: 100

Tractography Seeding Parameters

- Minimum Path Length: 10.00mm
- Stopping Criteria: Fractional Anisotropy
- Stopping Value: 0.15
- Stopping Track Curvature: 0.70
- Integration Step Length: 0.50mm

Enabling Options

- Create Tracts Initially As: Tubes
- Enable Seeding Tracts:

Data Probe

L  
F  
B

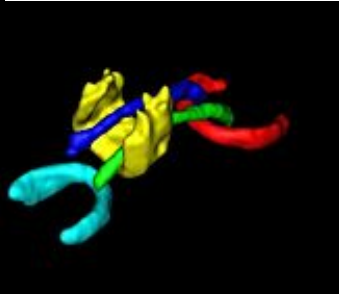
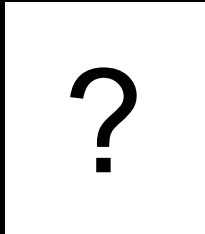
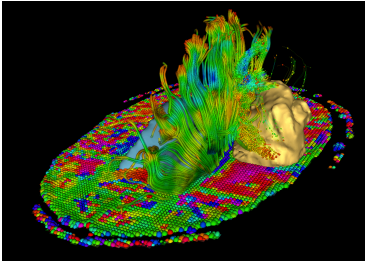
S: 58.74 Y: R: -7.57 G: A: 26.28



# 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

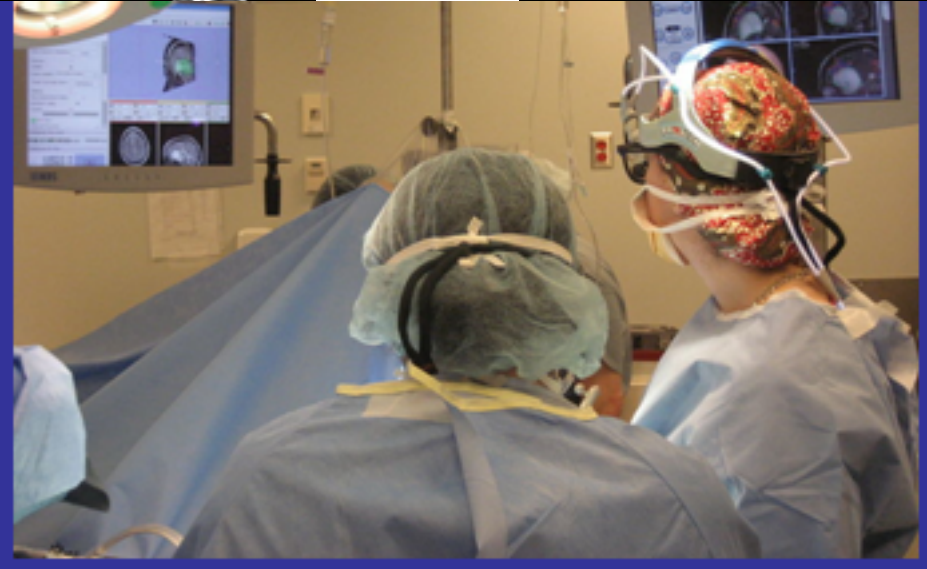
# Going Further: How to choose ?



Neurosurgeons face the challenge of selecting the appropriate tractography method and tract selection strategy

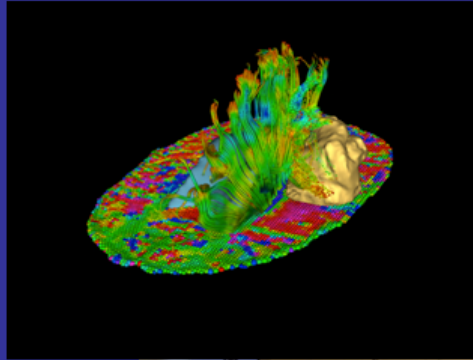


Need for validation to accelerate clinical use of DT-MRI findings



# MICCAI 2011 DTI Challenge

14<sup>th</sup> International Conference on Medical Image Computing and Computer Assisted Intervention



## DTI Tractography for Neurosurgical Planning: A Grand Challenge



**MICCAI 2011 Workshop**  
**Sunday September 18, 9am-6pm**  
**Westin Harbour Castle**  
**Toronto, Canada**

### Workshop Faculty

*Sonia Pujol, PhD, Surgical Planning Laboratory, Harvard Medical School*  
*Ron Kikinis, MD, Surgical Planning Laboratory, Harvard Medical School*  
*Alexandra Golby, MD, Brigham and Women's Hospital, Harvard Medical School*  
*Guido Gerig, PhD, The Scientific Computing and Imaging Institute, University of Utah*  
*Martin Styner, PhD, Neuroimage Research and Analysis Laboratory, University of North Carolina*  
*William Wells, PhD, Surgical Planning Laboratory, Harvard Medical School*  
*Carl-Fredrik Westin, PhD, Laboratory of Mathematics in Imaging, Harvard Medical School*  
*Sylvain Gouttard, MSc, The Scientific Computing and Imaging Institute, University of Utah*

National Alliance for Medical Image Computing

[http://www.na-mic.org/Wiki/index.php/Events\\_DTI\\_Tractography\\_Challenge\\_MICCAI\\_2011](http://www.na-mic.org/Wiki/index.php/Events_DTI_Tractography_Challenge_MICCAI_2011)

# Neurosurgical Planning Workshop, October 1<sup>st</sup>, 2012 – Nice, France

## MICCAI 2012 DTI Tractography Challenge Second Edition

INTRODUCTION THE CHALLENGE FACULTY KEYNOTE SPEAKER DATA LOGISTICS CONTACT

+ add new ⚙

Welcome to the 2nd edition of the MICCAI DTI Tractography Challenge. The workshop will be held on Monday October 1st, 2012 as part of the 15th International Conference on Medical Image Computing and Computer Assisted Intervention (MICCAI 2012).



## DTI Tractography for Neurosurgical Planning: A Grand Challenge

MICCAI 2012 Conference  
Acropolis Convention Center  
Nice, France

[www.miccai-org](http://www.miccai-org)

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