



Exploring Peritumoral White Matter Fibers for Neurosurgical Planning

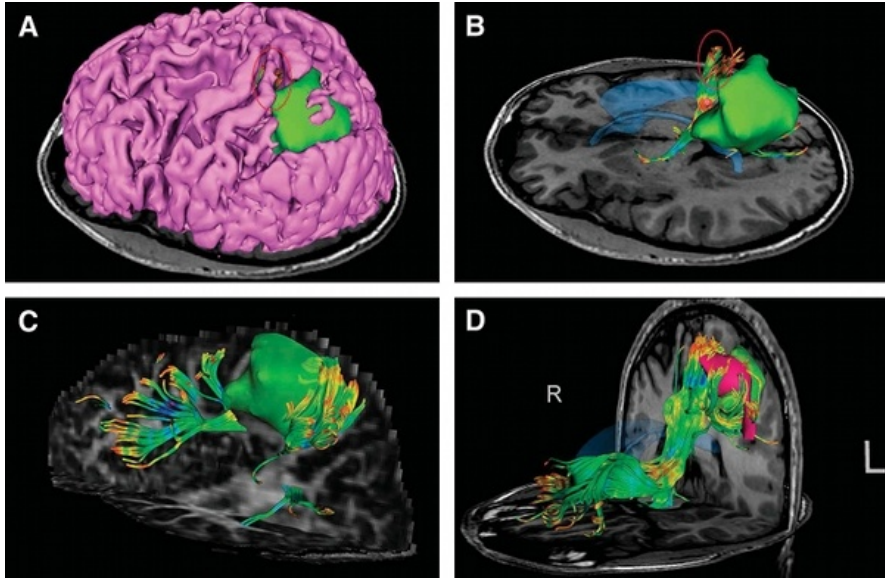
Sonia Pujol, Ph.D.

Ron Kikinis, M.D.

Surgical Planning Laboratory

Harvard University

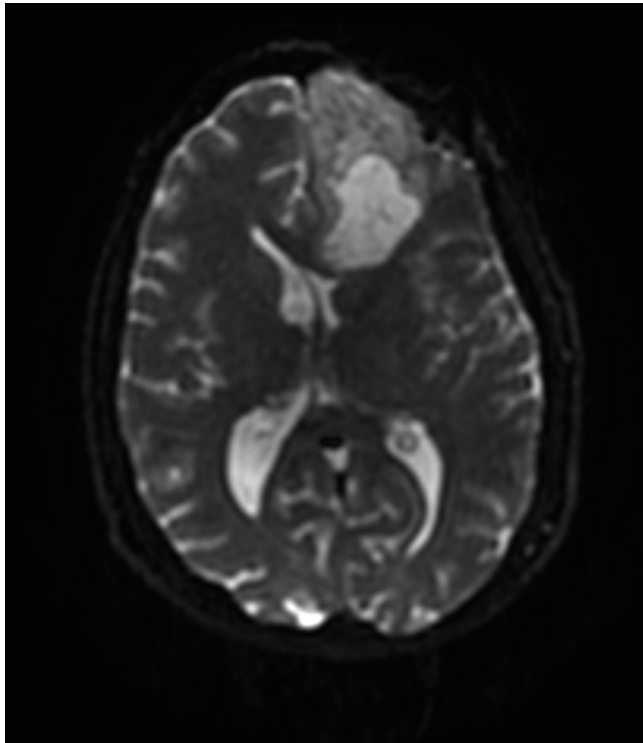
Clinical Goal



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.

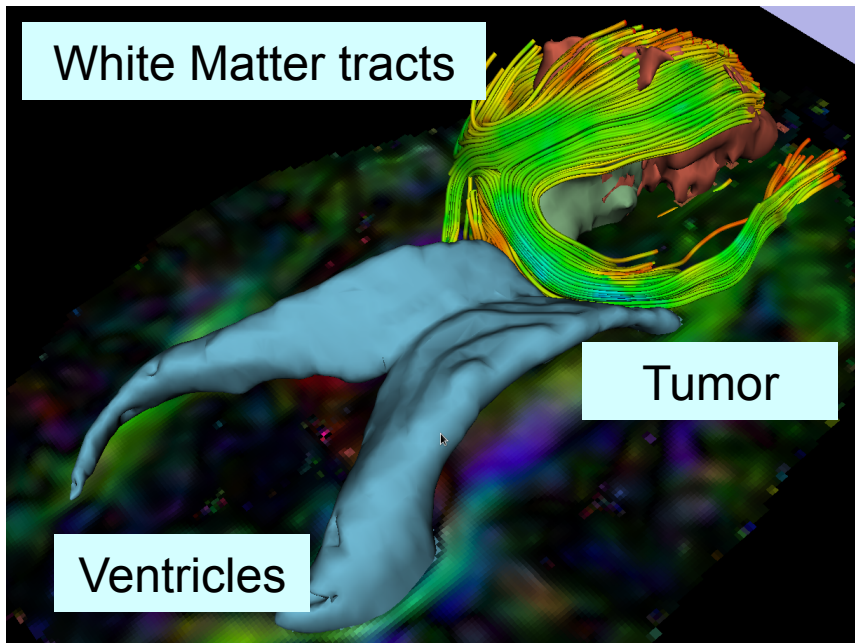
Image Courtesy of Dr. Alexandra Golby, Brigham and Women's Hospital, Boston, MA..

Clinical Case



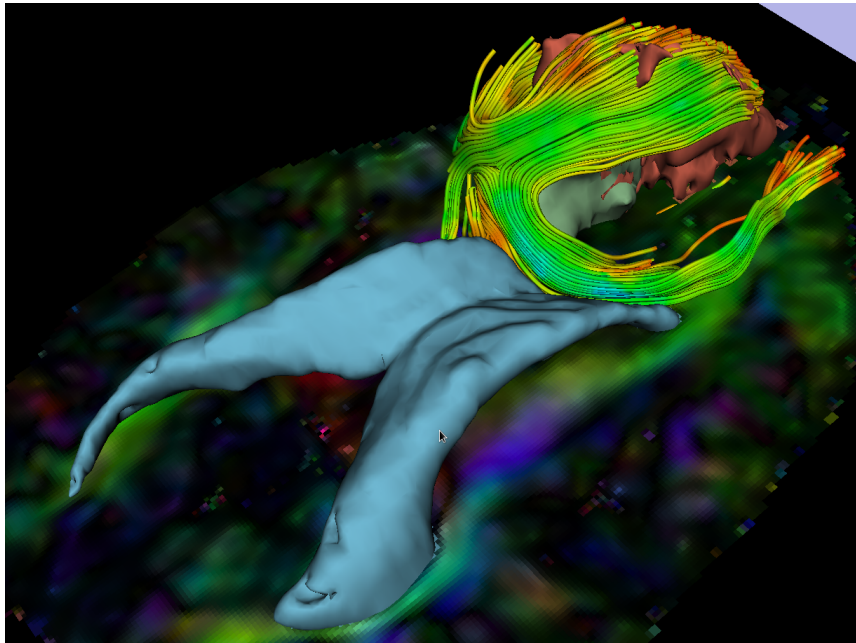
- 35 year-old male diagnosed with Glioblastoma multiforme
- Diffusion Weighted Imaging (DWI) acquisition for neurosurgical planning

Clinical Goal



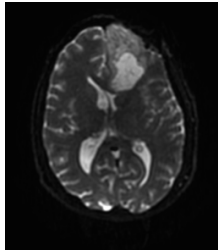
The goal of this tutorial is to explore white matter fibers surrounding a tumor using Diffusion Tensor Imaging (DTI) Tractography.

Image Analysis Pipeline

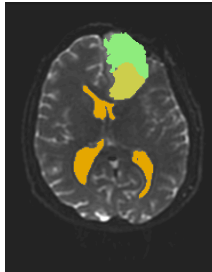


The image analysis pipeline described in this tutorial uses three different algorithms: the “Grow Cut” algorithm for segmentation of the tumor parts, the Marching Cube algorithm for surface modeling, and the single tensor streamline tractography algorithm for tract generation.

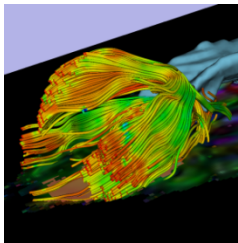
Overview of the analysis pipeline



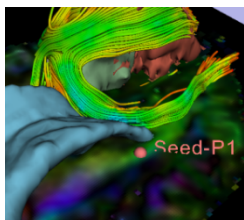
Part 1: Loading & Visualization of Diffusion Data



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

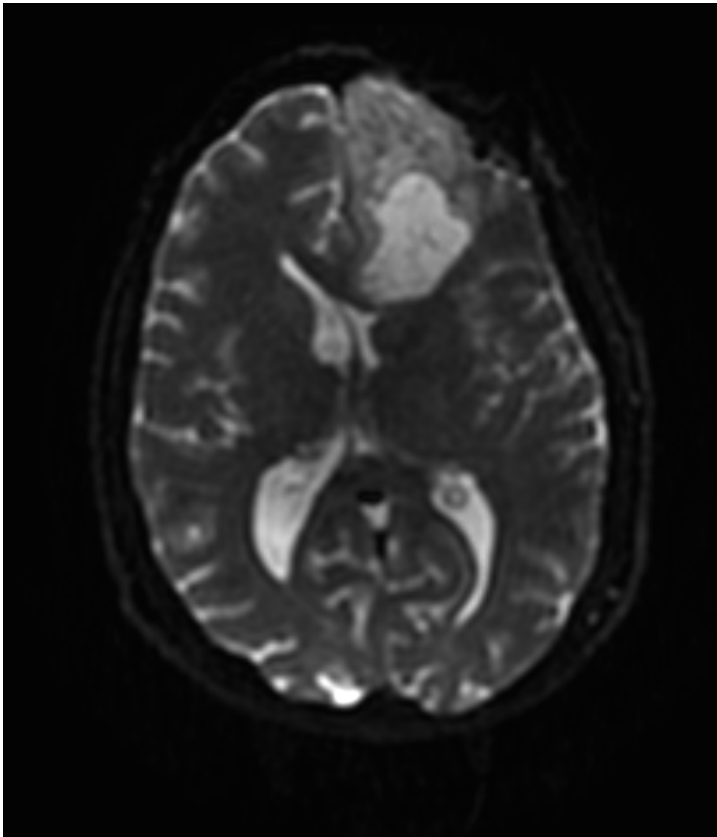


Part 3: Tractography reconstruction of the white matter fibers in the peri-tumoral volume



Part 4: Tractography exploration of the ipsilateral and contralateral side

Part 1: Loading and Visualization of Diffusion Data

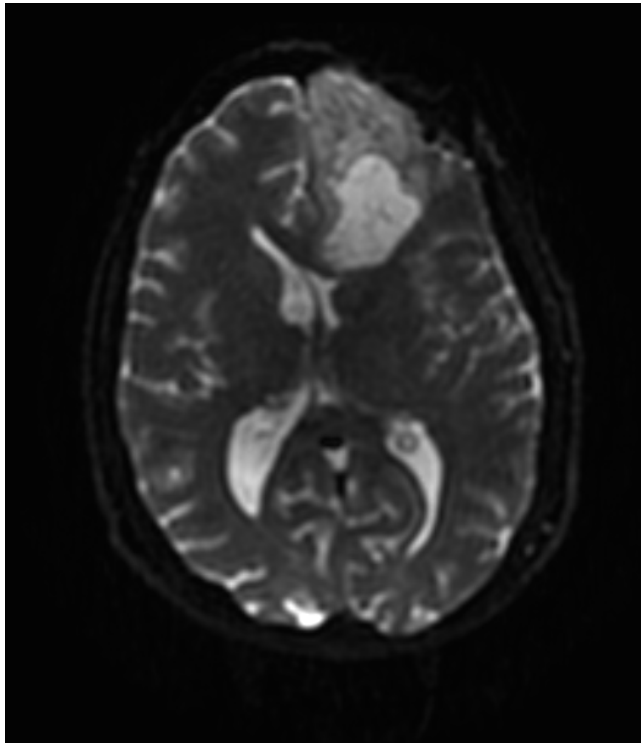
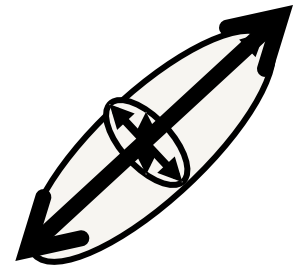


Diffusion Tensor Imaging

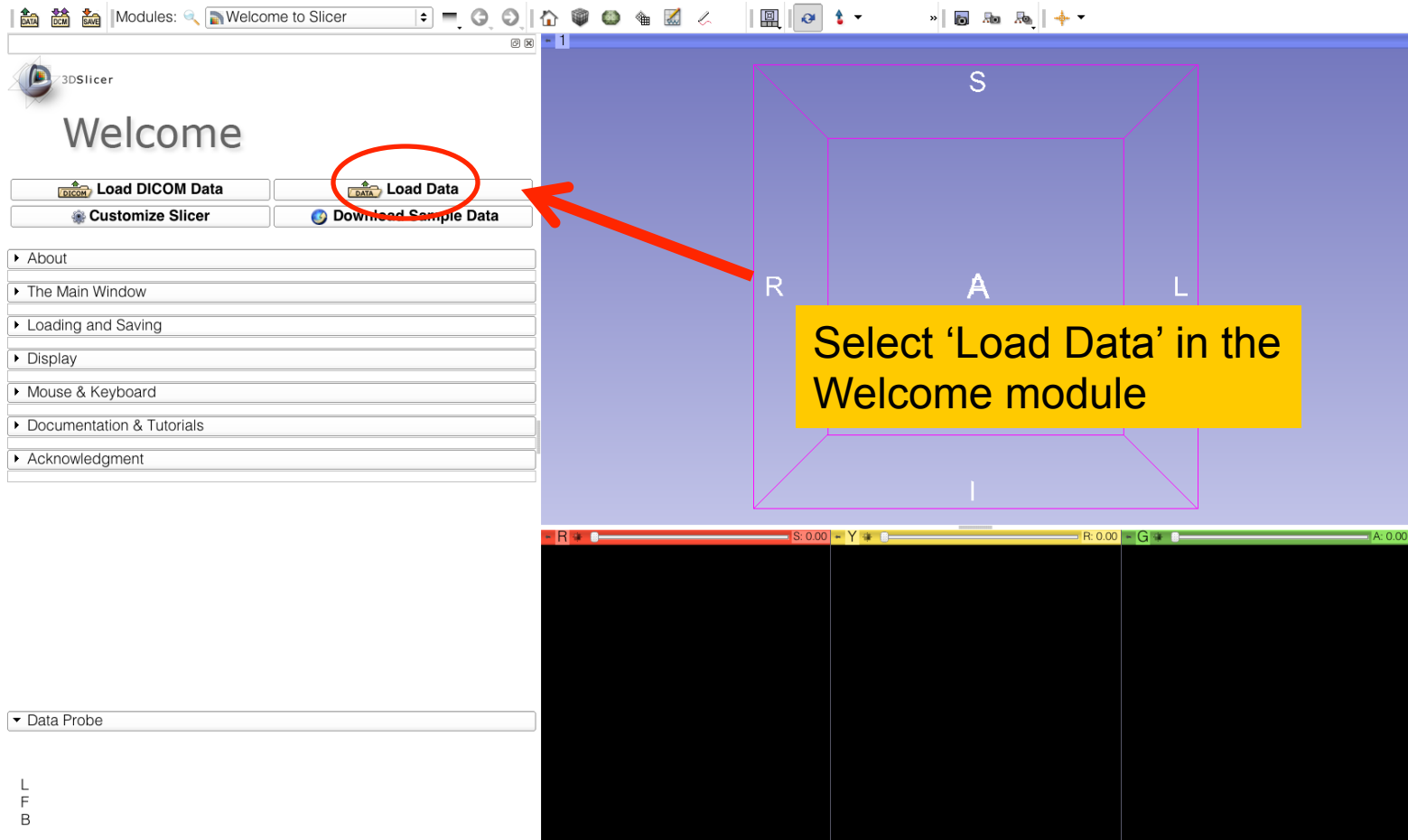
$$S_i = S_0 e^{-b \hat{g}_i^T \underline{D} \hat{g}_i}$$

(Stejskal and Tanner 1965, Basser 1994)

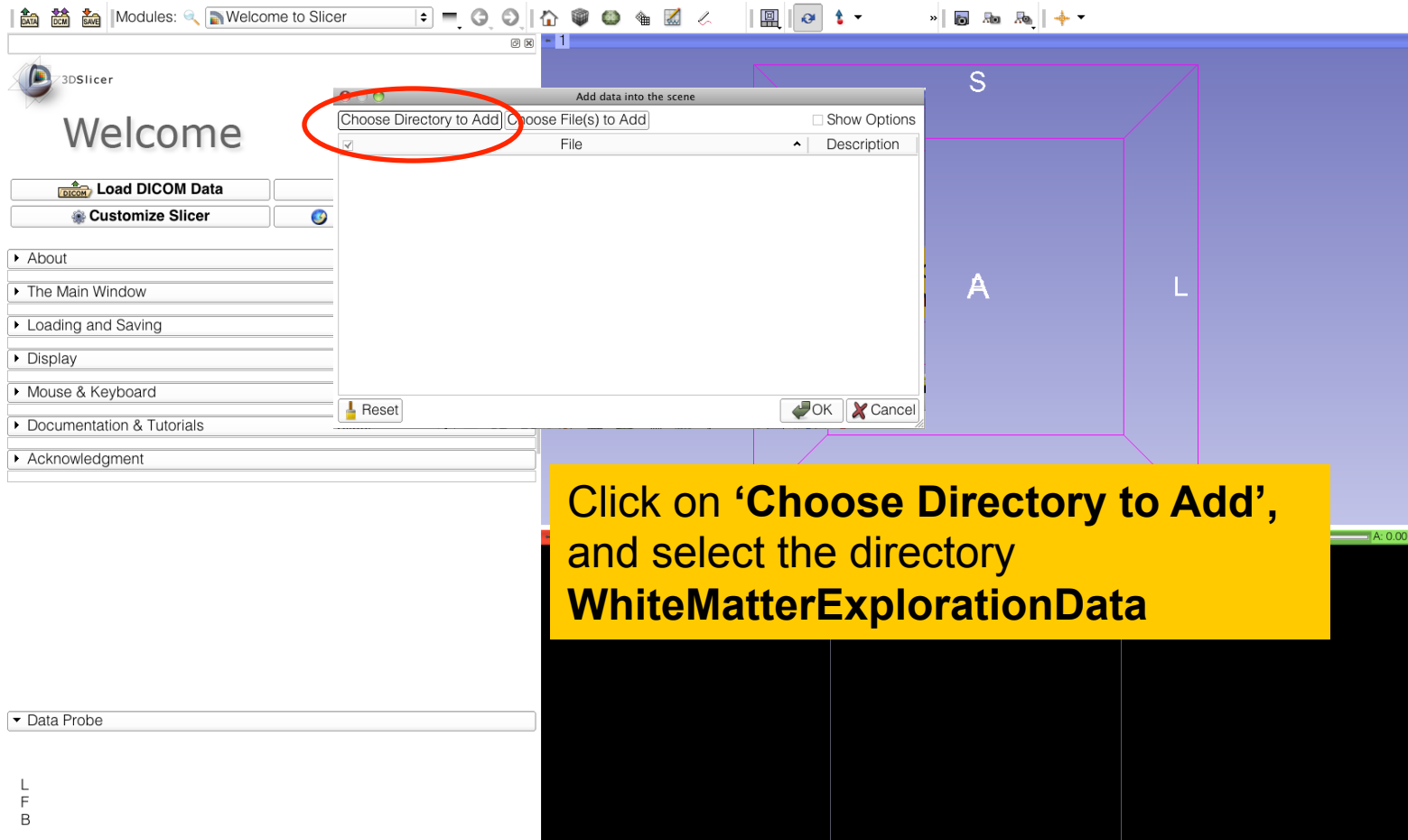
$$\underline{D} = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{bmatrix}$$



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:

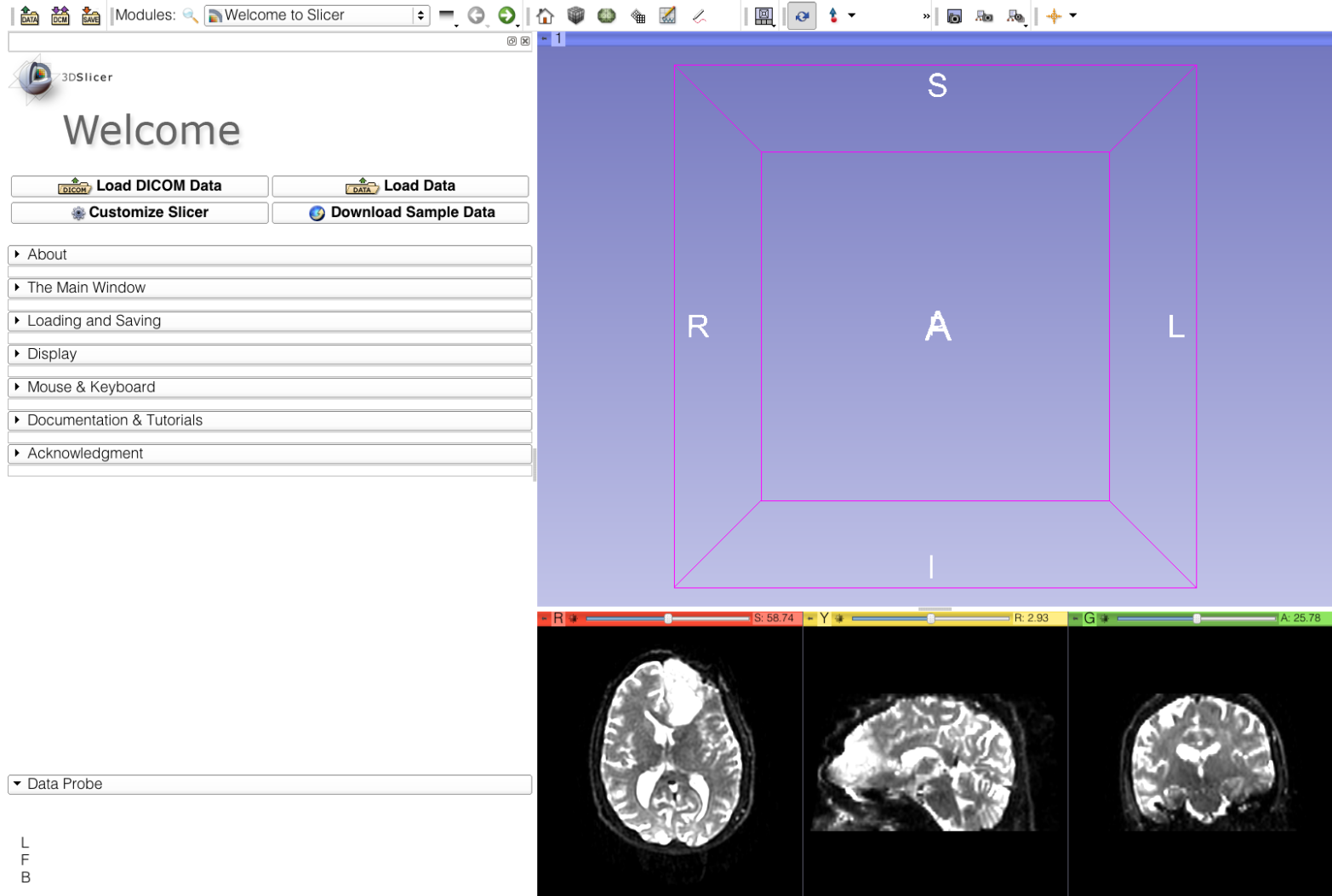
File	Description
<input type="checkbox"/> /Users/spujol/data/WhiteMatterExplorationData/DTIVolume.raw.gz	Volume
<input checked="" type="checkbox"/> /Users/spujol/data/WhiteMatterExplorationData/DTIVolume.nhdr	Volume
<input checked="" type="checkbox"/> /Users/spujol/data/WhiteMatterExplorationData/BaselineVolume.nrrd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

The file selection dialog is overlaid on a 3D brain scan visualization. The brain scan shows a cross-section with labels 'S' (Superior), 'I' (Inferior), 'A' (Anterior), and 'L' (Lateral). A yellow callout box with black text provides instructions:

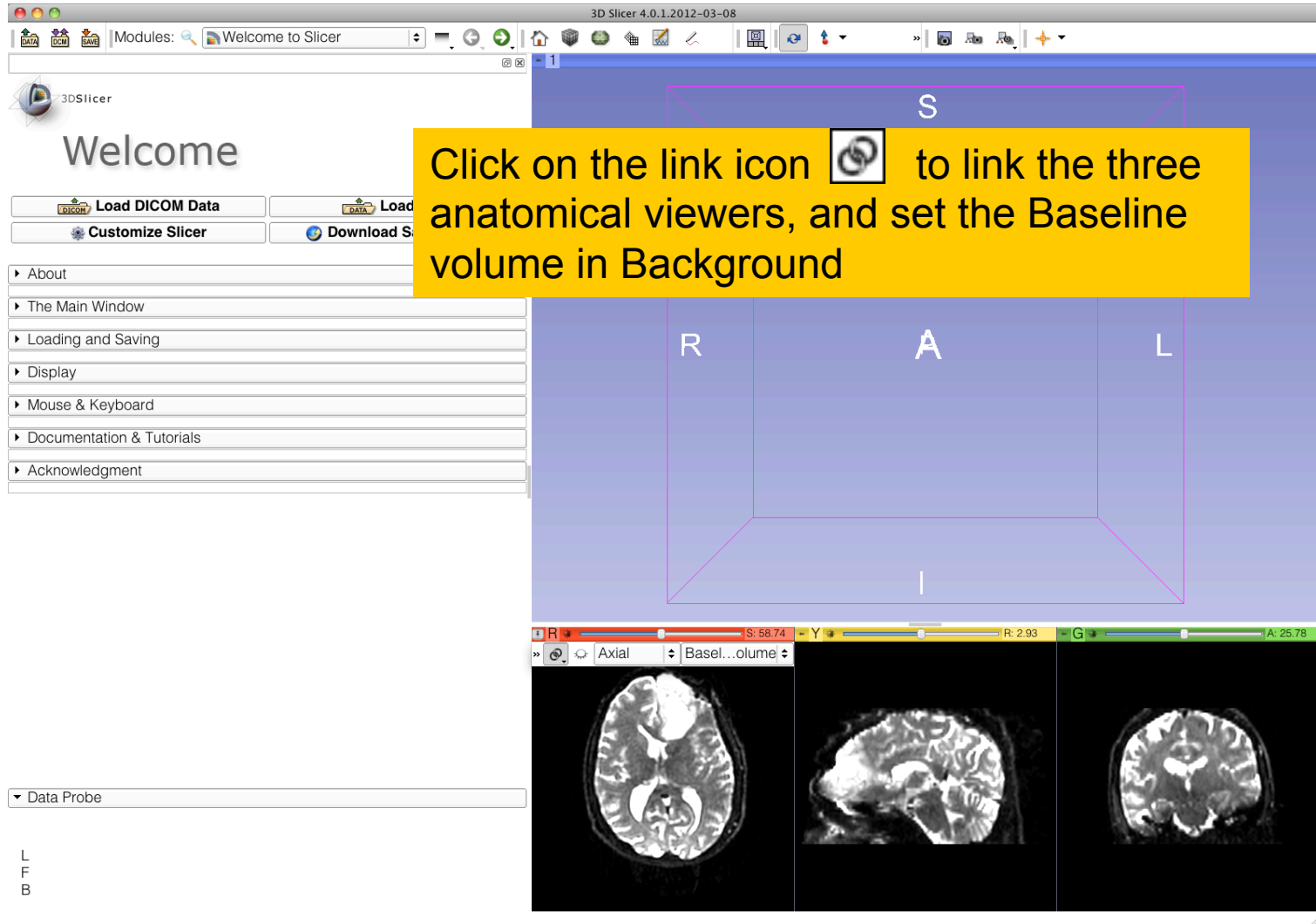
Select the directory
WhiteMatterExplorationData

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 blue brain model with a purple wireframe box. The box is labeled with '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 slice windows: an axial slice (labeled 'R'), a sagittal slice (labeled 'S'), and a coronal slice (labeled 'A'). Each slice window has a corresponding color-coded slider for windowing: red for R, yellow for S, and green for A. The bottom left corner of the interface shows the letters 'L', 'F', and 'B' stacked vertically.

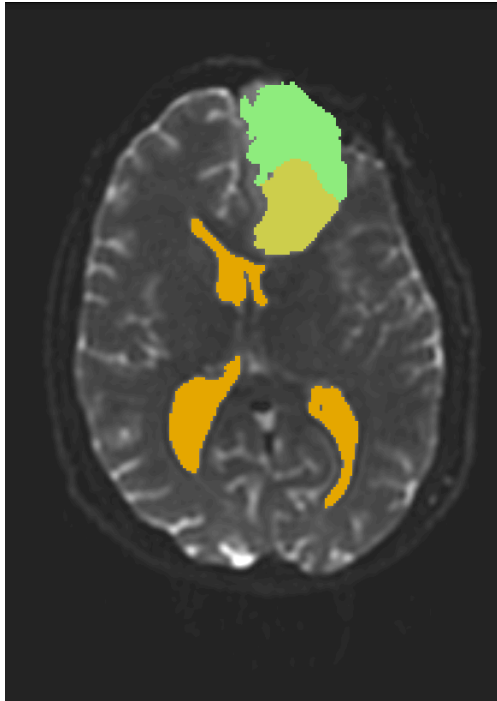
Loading DTI and Baseline Data

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

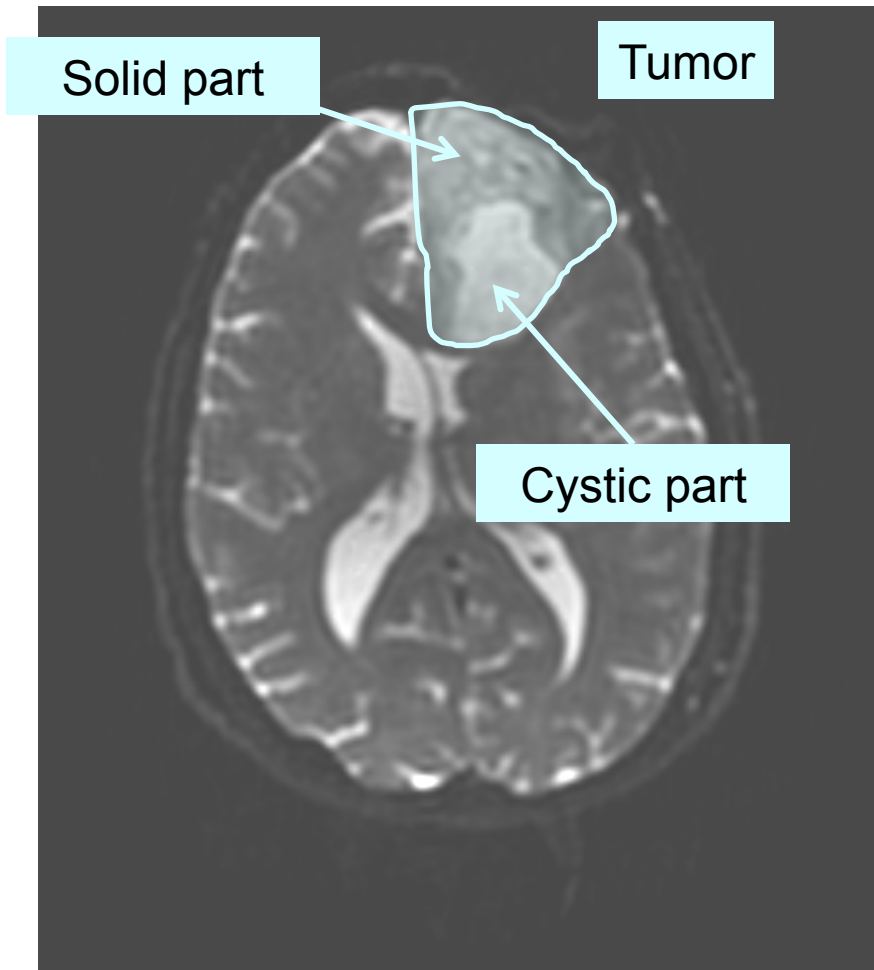
Select Red Slice Only Layout

L
F
B



Part 1: Segmenting the tumor and ventricles

Tumor Segmentation



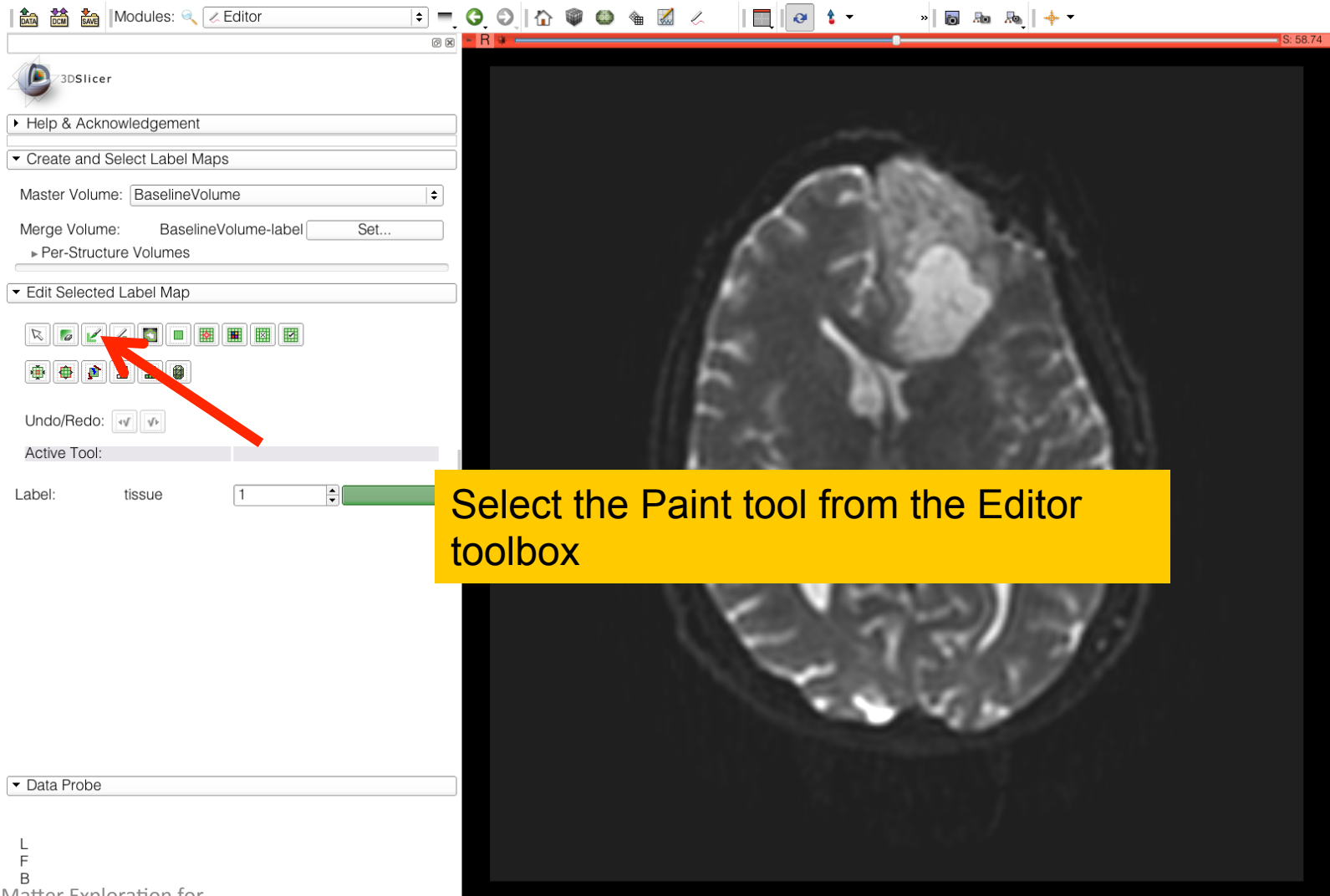
The tumor in this clinical case is composed of two parts: a solid part, and a cystic part.

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 the 'Editor' option is circled in red. A yellow callout box points to this menu 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'. In the bottom left corner, the letters 'L', 'F', and 'B' are stacked vertically. The top right corner of the window shows 'S: 58.74'.

Tumor Segmentation



Select the Paint tool from the Editor toolbox

Tumor Segmentation

3DSlicer

Modules: Editor

Set the label #309 'cyst' and draw a short line in the **cystic part of the tumor**

Help & Acknowledgement

Create and Select Label Maps

Master Volume: BaselineVolume

Merge Volume: BaselineVolume-label Set...

Per-Structure Volumes

Edit Selected Label Map

Undo/Redo: [Undo] [Redo]

Active Tool: [Tool]

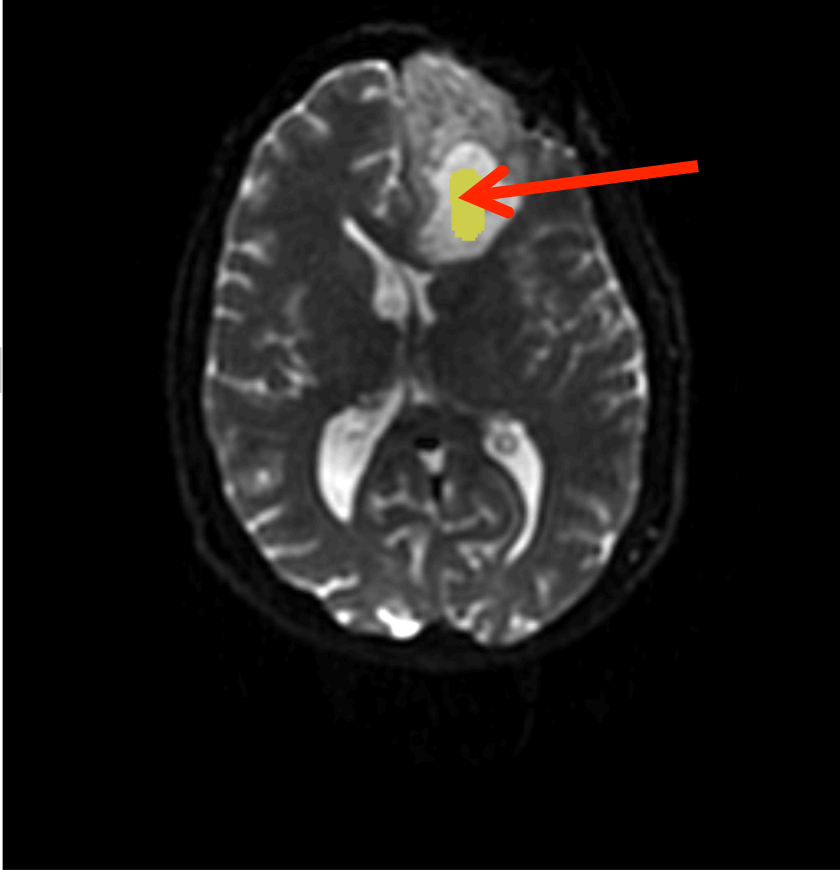
Label: cyst 309 [Color]

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 screenshot displays the 3DSlicer software interface. The top toolbar shows various icons for file operations and navigation. The left sidebar contains the '3DSlicer' logo and several panels: 'Help & Acknowledgement', 'Create and Select Label Maps', and 'Edit Selected Label Map'. The 'Edit Selected Label Map' panel is active, showing a grid of segmentation tools and a 'Label' dropdown menu set to 'cyst' with the value '309'. A yellow box at the bottom of the interface contains the instruction: "Select the label #7 (mass) and draw a short line in the solid part of the tumor". The main view shows an axial MRI slice of a brain with a tumor. A red arrow points to a green segmented region on the tumor, and a yellow segmented region is visible below it.

Tumor Segmentation

The screenshot shows the 3D Slicer interface. On the left, the 'Edit Selected Label Map' panel is active, showing various segmentation tools. The main window displays an axial MRI slice of a brain with a tumor region highlighted in yellow. A red arrow points to the yellow outline. A yellow text box overlaid on the image contains the instruction: 'Select the label # 295 region_3 and draw a line around the tumor'. The interface also shows a 'Redo' button and a 'Label: cyst' field.

Tumor Segmentation

Select the Grow Cut segmentation algorithm




Master Volume:

Merge Volume:

► Per-Structure Volumes

▼ Edit Selected Label Map



Undo/Redo:

Active Tool: Redo

Label:

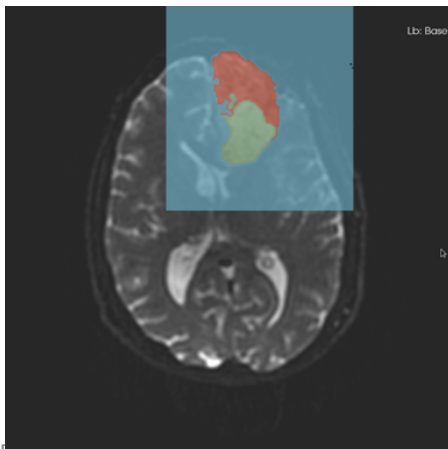
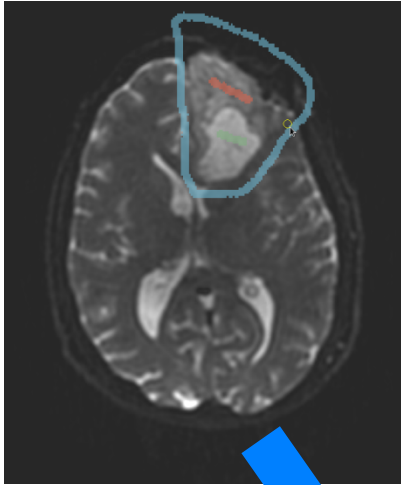
Run the GrowCut segmentation on the current label map.
This will use your current segmentation as an example
to fill in the rest of the volume.

▼ 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

The screenshot shows a software interface for tumor segmentation. The top toolbar includes icons for DATA, DCM, SAVE, and various navigation and editing tools. The central panel contains the following elements:

- Master Volume: BaselineVolume
- Merge Volume: BaselineVolume-label (with a Set... button)
- Per-Structure Volumes (dropdown menu)
- Edit Selected Label Map (dropdown menu)
- Tools: A grid of icons for various operations like selection, drawing, and editing.
- Undo/Redo: Two icons for undo and redo.
- Active Tool: GrowCutEffect
- Label: cyst (with a dropdown menu showing 309 and a color swatch)
- Instructions: 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: A button to execute the segmentation, highlighted with a red arrow.
- Data Probe: A dropdown menu.
- Orientation: L, F, B (Left, Front, Back).

The right side of the interface displays a brain MRI scan. A yellow outline highlights a region of interest in the upper part of the brain. Within this region, there are two distinct areas: a green one and a yellow one, representing segmented tumor components.

Tumor Segmentation

Slicer displays the results of the segmentation

Solid part

Cystic part

3DSlicer

Modules: Editor

Help & Acknowledgement

Create and Select Label Maps

Master Volume: BaselineVolume

Undo/Redo: [undo] [redo]

Active Tool: GrowCutEffect

Label: region_3 295

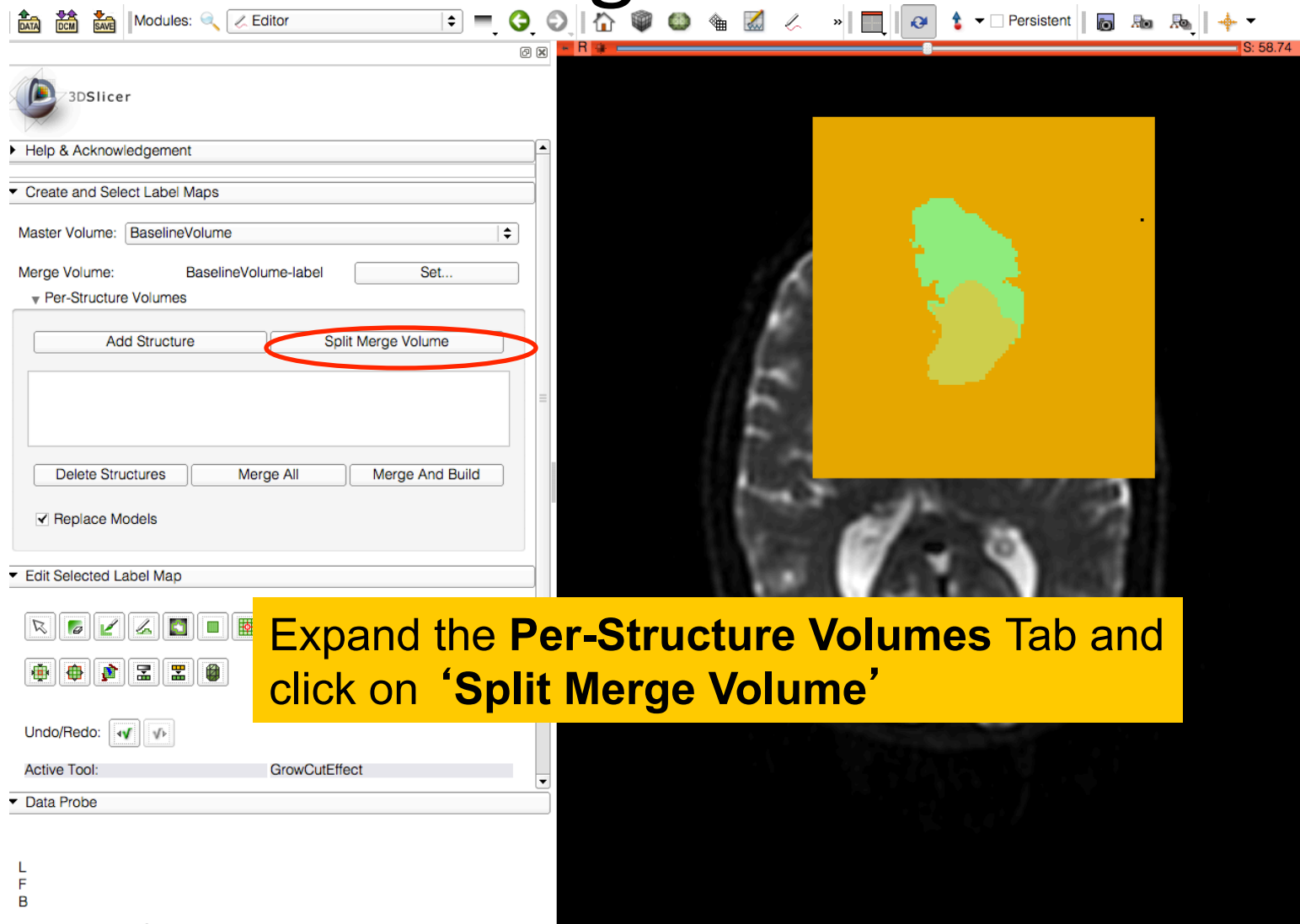
Run the GrowCut segmentation on the current label map. This will use your current segmentation as an example to fill in the rest of the volume.

Apply

Data Probe

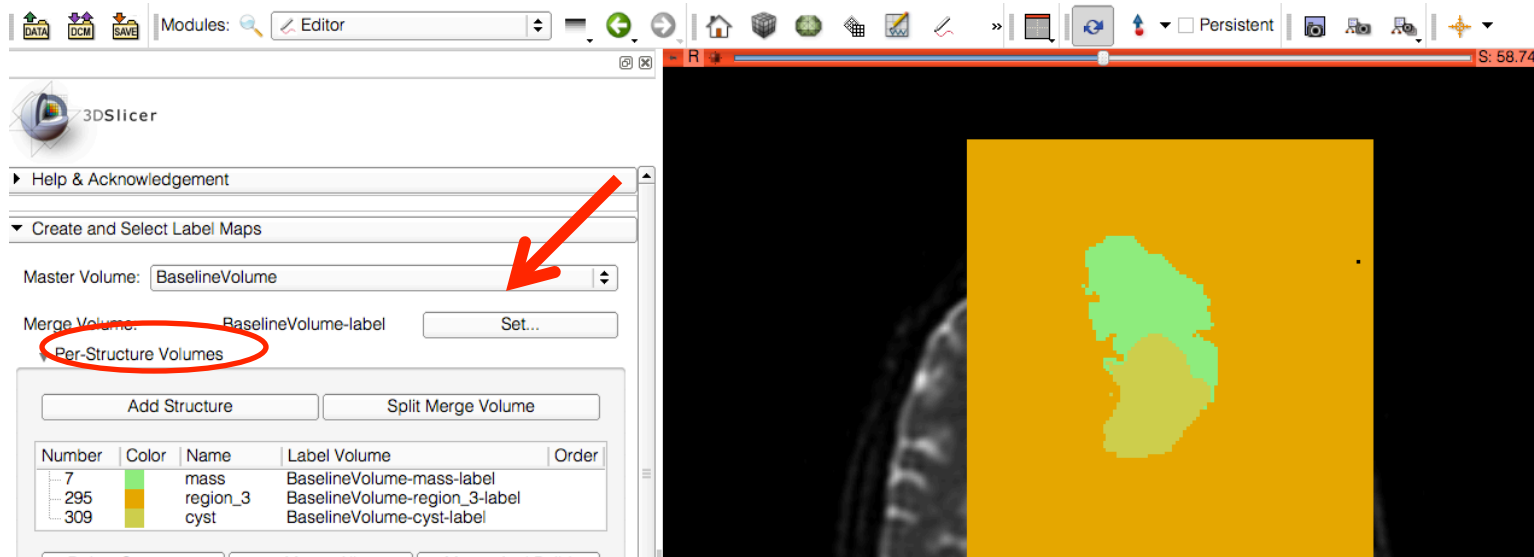
L
F
B

Tumor Segmentation



Expand the Per-Structure Volumes Tab and click on 'Split Merge Volume'

Tumor Segmentation



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

- BaselineVolume-mass-label**: solid part of the tumor
- BaselineVolume-cyst-label**: cystic part of the tumor
- BaselineVolume-region_3-label**: surrounding structures

Tumor Segmentation

The screenshot shows the 3DSlicer interface. At the top, the 'Modules' dropdown is set to 'Data'. The 'Nodes' list on the left includes: Scene, View, Default Scene Camera, BaselineVolume, BaselineVolume-label, BaselineVolume-mass-label, BaselineVolume-region_3-label, and BaselineVolume-cyst-label. The 'scene Model' is set to 'Transform'. The main 3D view displays an axial MRI slice with a segmented tumor region highlighted in green and yellow. A yellow text box at the bottom of the image reads: "Select the module Data and note the different label maps that have been generated".

Ventricles Segmentation






Go back to the Editor module

▼ Create and Select Label Maps

Master Volume:

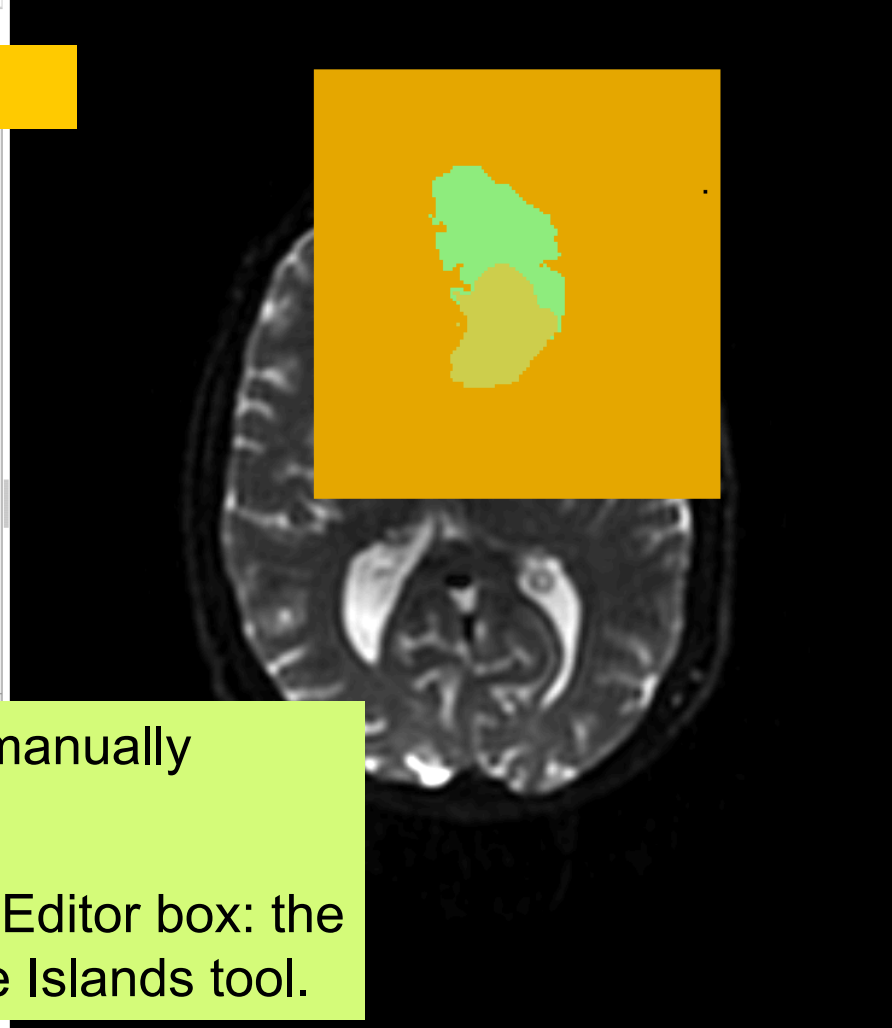

Merge Volume:

▼ Per-Structure Volumes

Number	Color	Name	Label Volume	Order
7		mass	BaselineVolume-mass-label	
295		region_3	BaselineVolume-region_3-label	
309		cyst	BaselineVolume-cyst-label	

Replace Models

▼ Edit Selected Label Map



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.

Ventricles Segmentation

Select the volume
'BaselineVolume-region_3-label'

Number	Color	Name	Label Volume	Order
7		mass	BaselineVol...	
295		region...	BaselineVol...	
309		cyst	BaselineVol...	

Buttons: 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

App


Data Probe

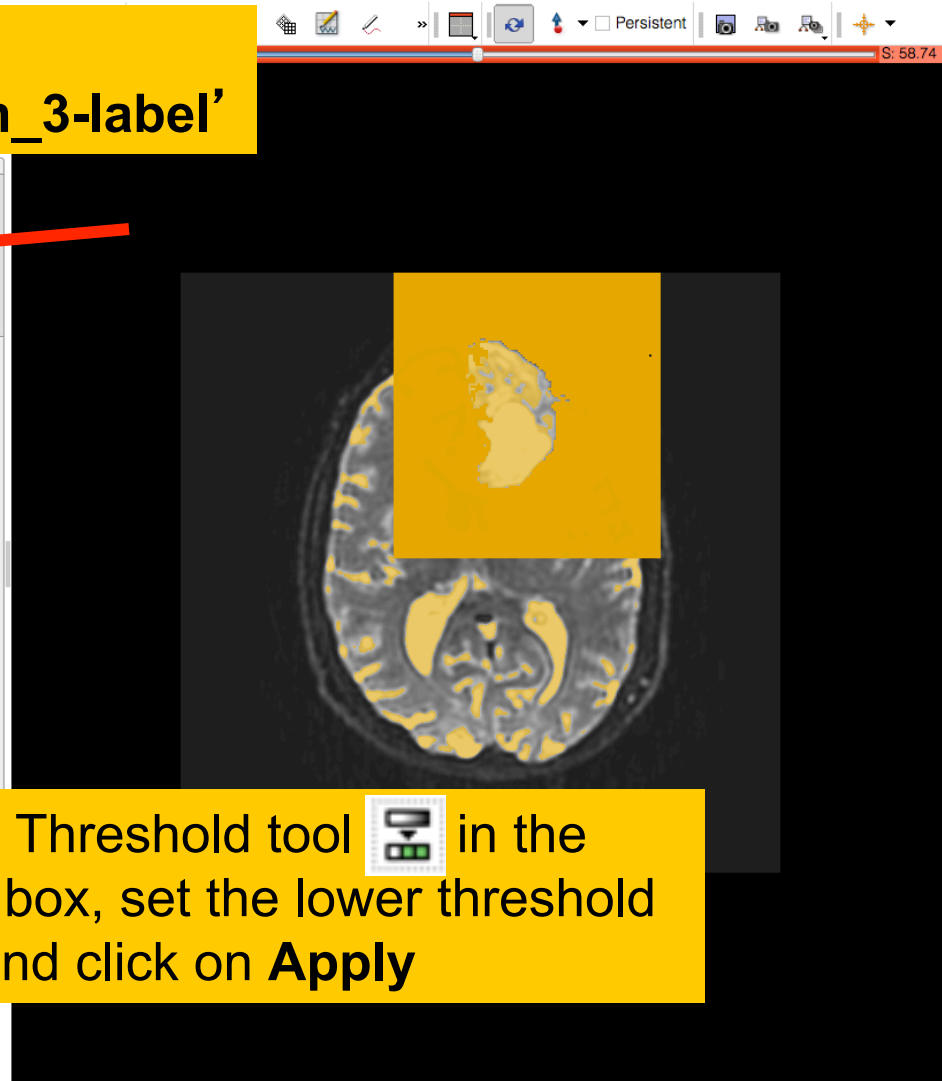
Red RAS: (148.9, -119.7, 58.7)

L BaselineVolume-region_3-label (-19, 273, 25) Out of Frame

F None (0)

B BaselineVolume (-19, 273, 25) Out of Frame

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

▼ Create and Select Label Maps

Master Volume:

Merge Volume:

▼ Per-Structure Volumes

Number	Color	Name	Label Volume	Order
7		mass	BaselineVol...	
295		region...	BaselineVol...	
309		cyst	BaselineVol...	

Replace Models

▼ Edit Selected Label Map

Undo/Redo:

Active Tool:

Label:

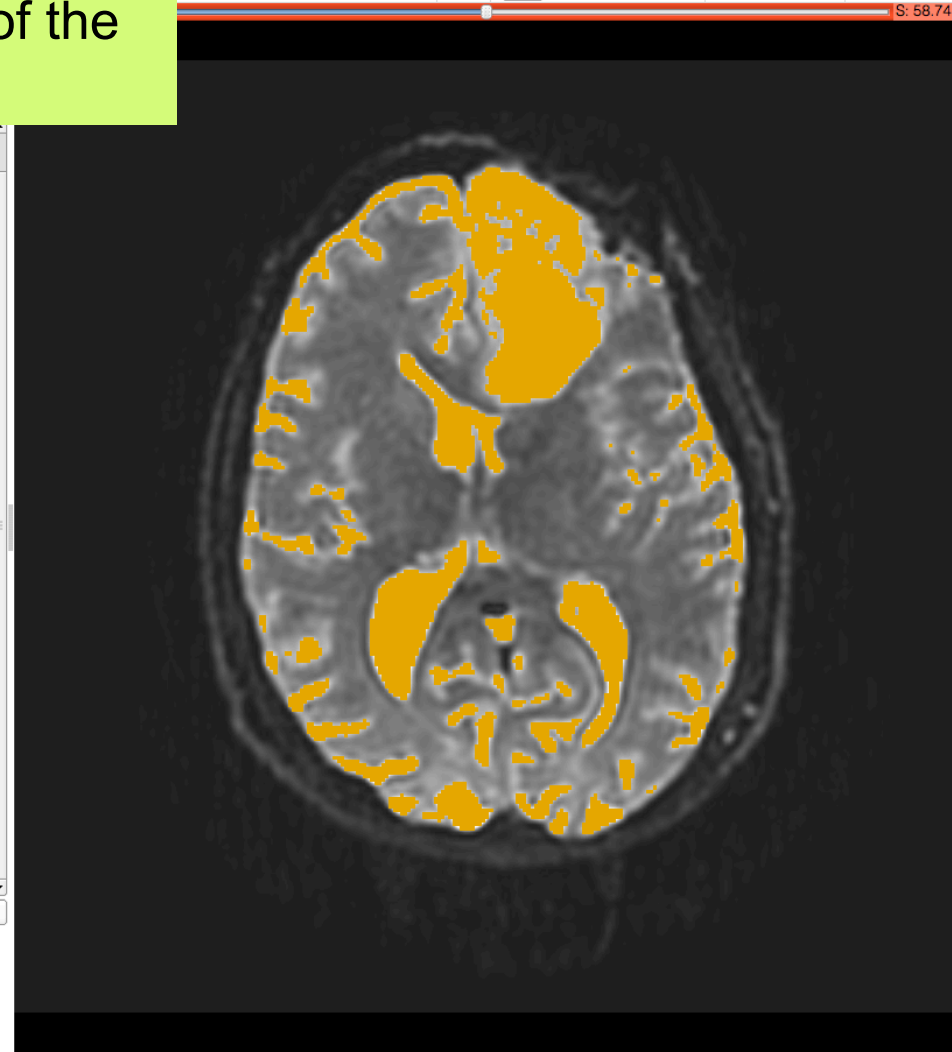
▼ Data Probe

Red RAS: (124.5, -15.6, 58.7) Axial Sp: 2.6

L **BaselineVolume-region_3-label** (6, 169, 25) **background** (0)

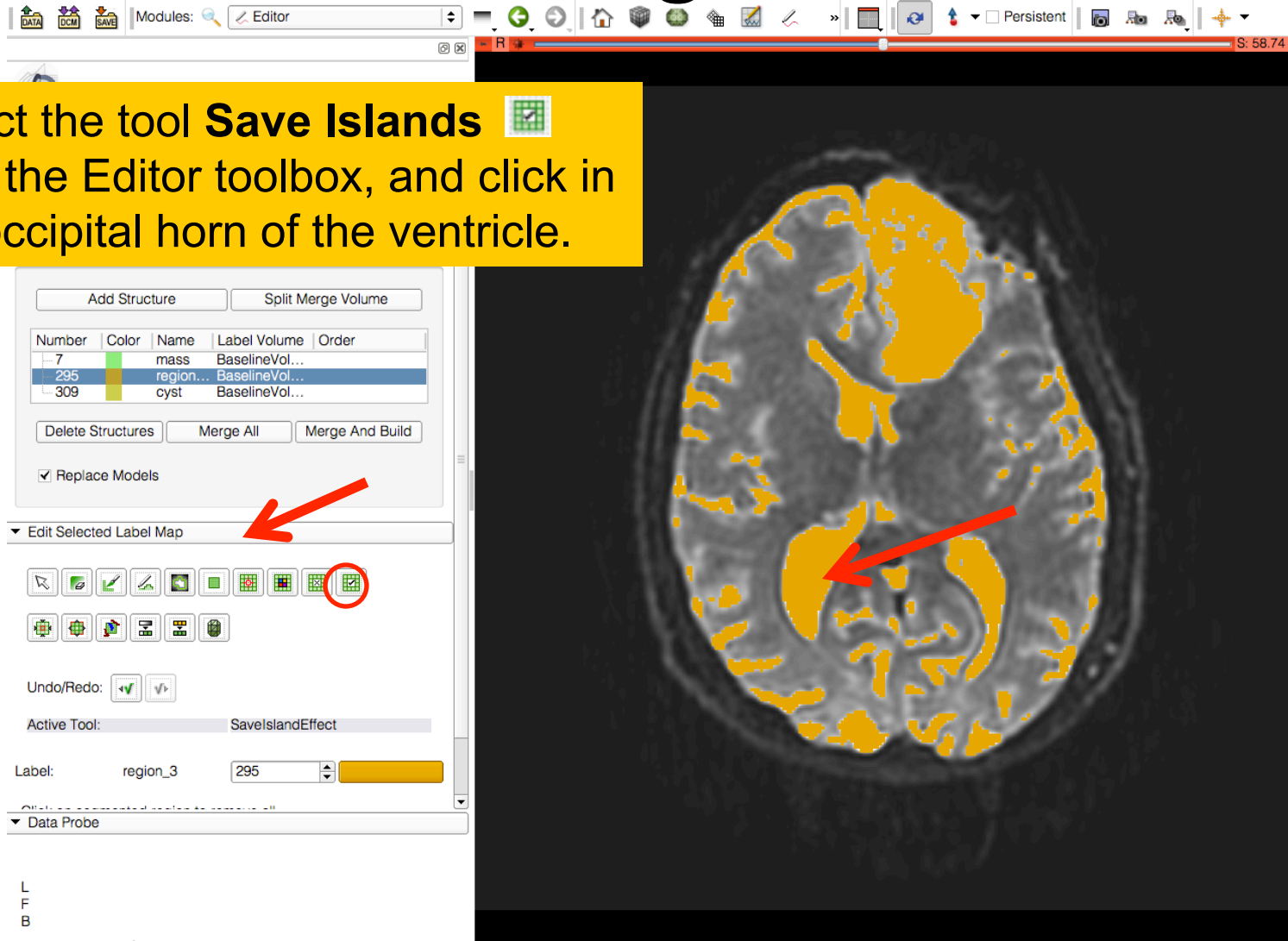
F **None** (0)

B **BaselineVolume** (6, 169, 25) **1**



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

The screenshot shows the 3D Slicer software interface. The main window displays an axial MRI slice of a brain with segmented ventricles highlighted in yellow. The left sidebar contains several panels:

- Create and Select Label Maps:** Master Volume: BaselineVolume; Merge Volume: BaselineVolume-label; Per-Structure Volumes section with a table:

Number	Color	Name	Label Volume	Order
7	Green	mass	BaselineVol...	
295	Yellow	region...	BaselineVol...	
309	Yellow	cyst	BaselineVol...	
- Edit Selected Label Map:** Contains various editing tools and a 'SavelandEffect' active tool.
- Data Probe:** Shows coordinates and volume information for the selected label map:

Red RAS: (21.1, -48.8, 58.7) Axial Sp: 2.6
L BaselineVolume-region_3-label (109, 202, 25) background (0)
F None (0)
B BaselineVolume (109, 202, 25) 1606

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 'Create and Select Label Maps' panel is active, displaying a table of structures and buttons for 'Merge All' and 'Merge And Build'. A red arrow points to the 'Merge And Build' button. Below the table, the 'Edit Selected Label Map' panel shows the 'region_3' label selected with value 295. At the bottom, the 'Data Probe' panel shows the current slice coordinates and volume information.

Number	Color	Name	Label Volume	Order
7		mass	BaselineVol...	
295		region...	BaselineVol...	
309		cyst	BaselineVol...	

Buttons: Add Structure, Split Merge Volume, Delete Structures, Merge All, Merge And Build

Replace Models:

Active Tool: SavelslandEffect

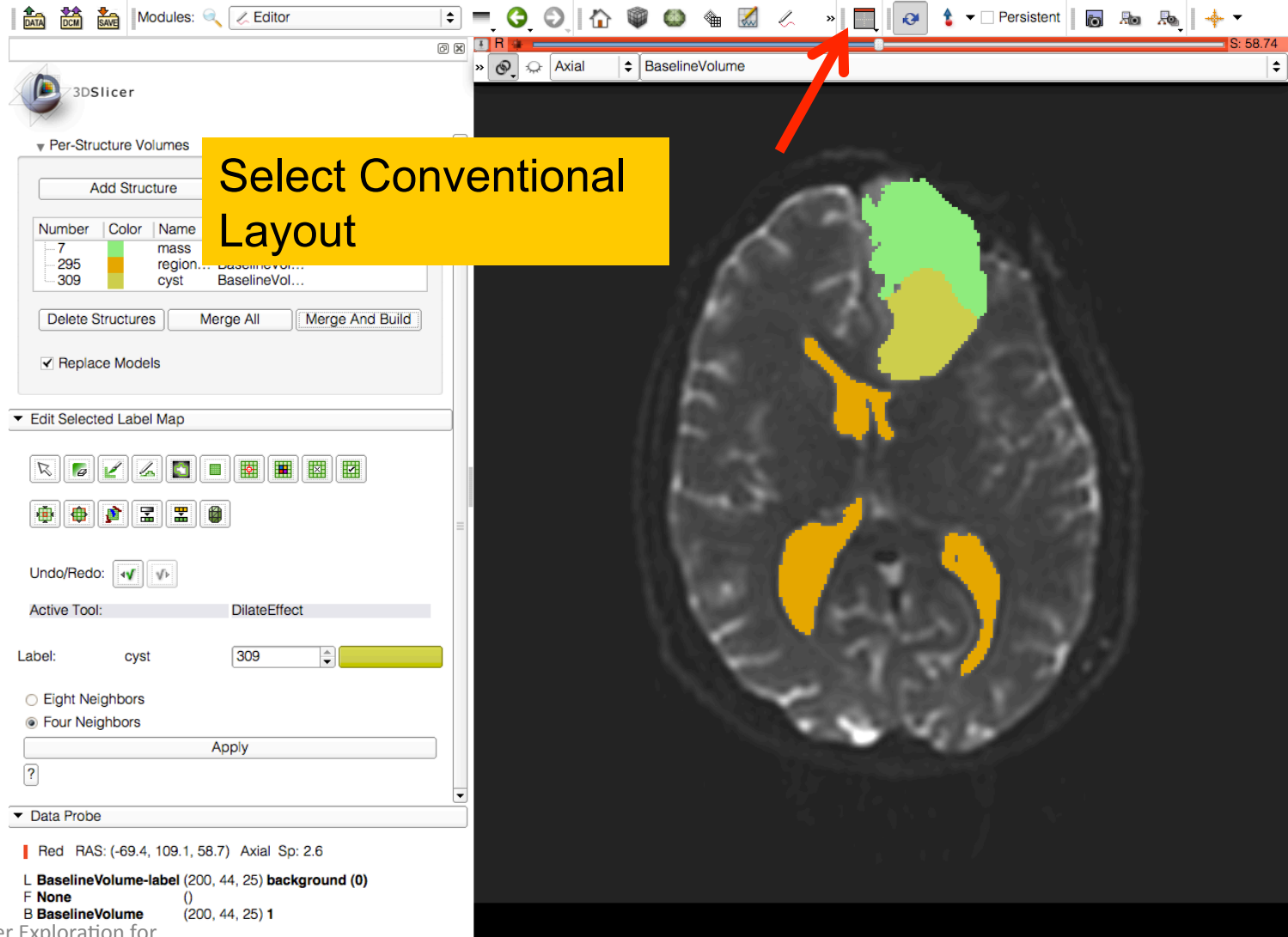
Label: region_3, 295

Data Probe:
Red RAS: (21.1, -48.8, 58.7) Axial Sp: 2.6
L BaselineVolume-region_3-label (109, 202, 25) background (0)
F None (0)
B BaselineVolume (109, 202, 25) 1606

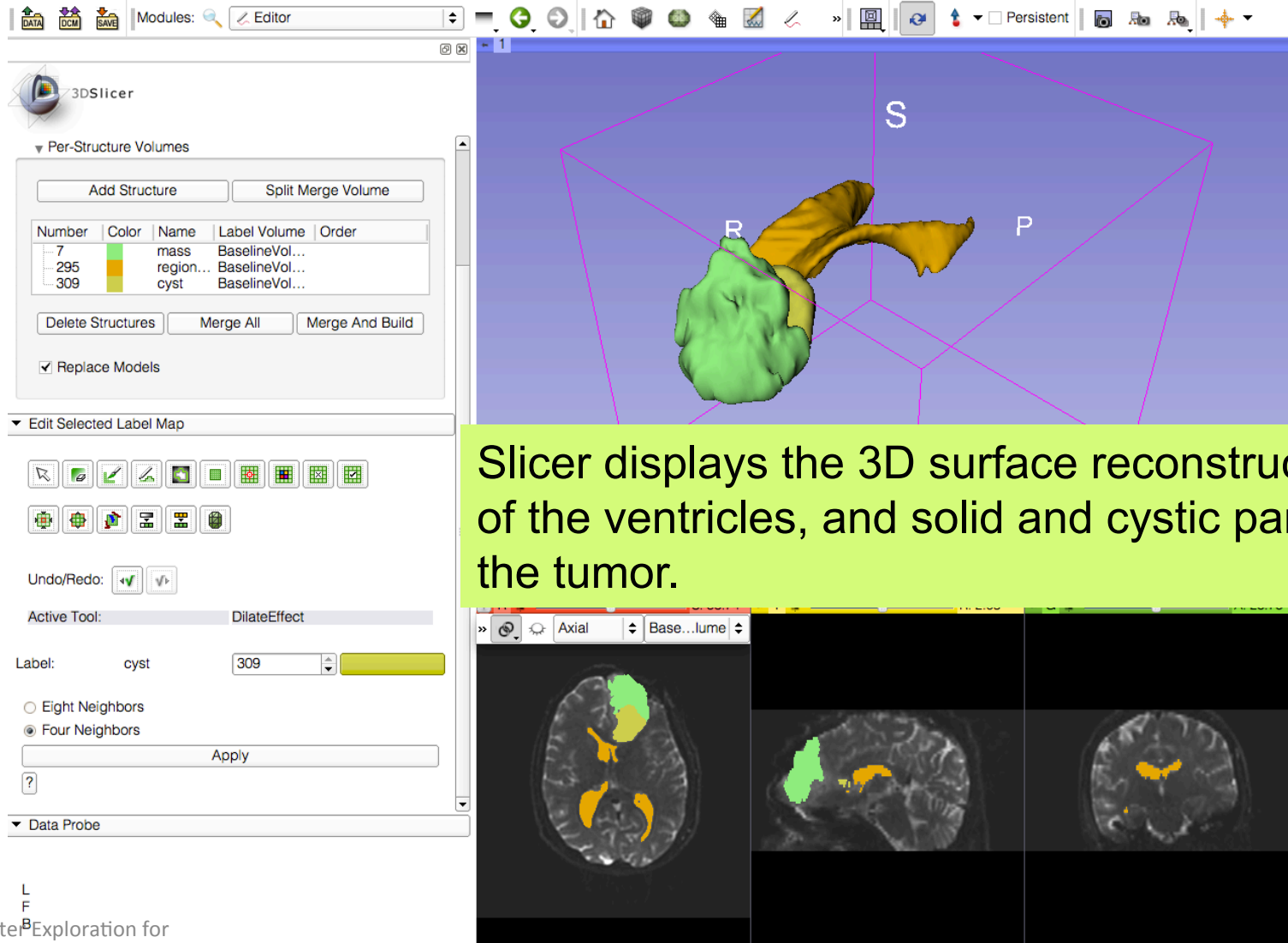
Click on **Merge and Build** to merge the different label maps, and generate the 3D models of the tumor and ventricles using a Marching Cubes algorithm

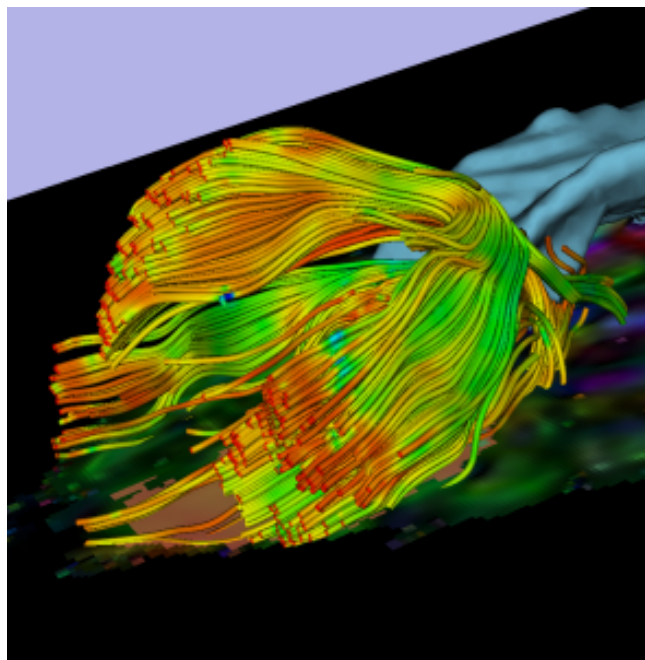
The 3D model shows a cross-section of a brain with segmented regions highlighted in yellow and orange, representing the tumor and ventricles.

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-cyst-label', and select the tool 'Dilate' in the Editor toolbox

The screenshot shows the 3D Slicer interface. On the left, the 'Structure Volumes' panel lists three volumes: 'mass', 'region...', and 'cyst'. The 'cyst' volume is selected. Below it, the 'Edit Selected Label Map' panel shows the 'Dilate' tool (a grid icon) circled in red. The 'Active Tool' is 'DilateEffect'. The 'Label' is 'cyst' with ID '309'. The 'Neighbors' are set to 'Four Neighbors'. The 'Data Probe' panel is visible at the bottom left. The main 3D view shows a brain model with a green cyst and a yellow peri-tumoral volume. The axes are labeled R (Right), P (Posterior), A (Anterior), and L (Left). The bottom status bar shows coordinates: R: 58.74, Y: -11.66, G: 78.00.

Definition of the peri-tumoral volume

The screenshot shows the 3DSlicer software interface. On the left, the 'Per-Structure Volumes' panel lists three structures: 'mass' (ID 7), 'region...' (ID 295), and 'cyst' (ID 309). The 'cyst' structure is selected. Below this, the 'Edit Selected Label Map' panel is active, showing various tools and an 'Apply' button circled in red. The main 3D view shows a brain scan with a green and yellow tumor model. A yellow text box is overlaid on the 3D view, and a red arrow points to the 'Apply' button.

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

Number	Color	Name	Label Volume
7		mass	BaselineVolume-mass-label
295		region...	BaselineVolume-region_3-l...
309		cyst	BaselineVolume-cyst-label

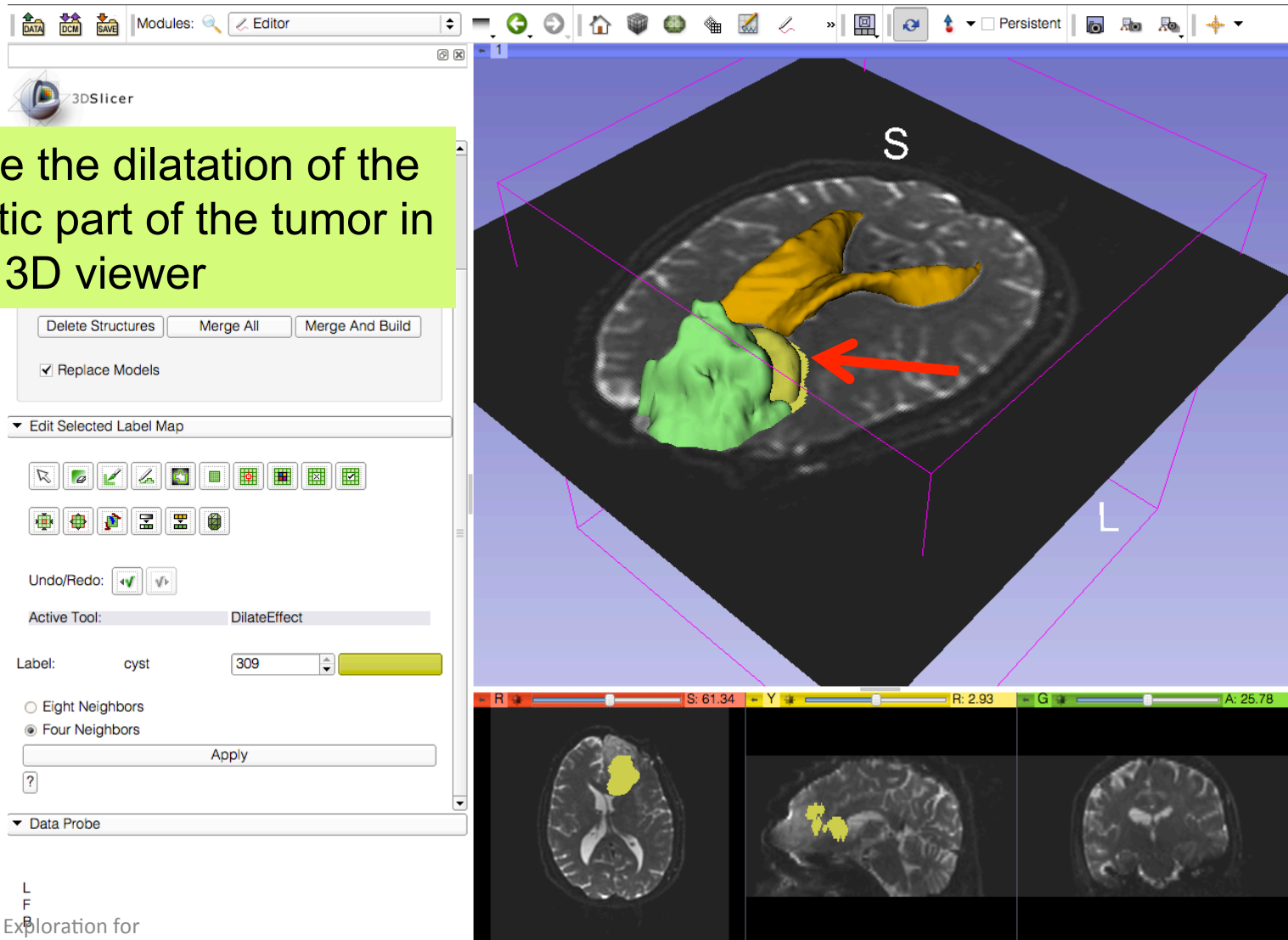
Active Tool: DilateEffect

Label: cyst 309

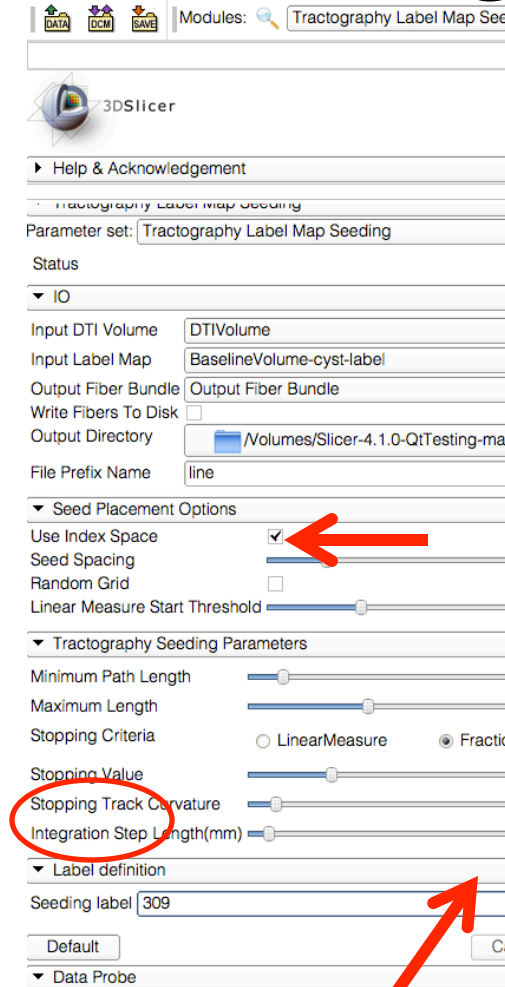
Apply

Visualization of the DTI Volume

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



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-cyst-label

Output Fiber Bundle: Create NewFiberBundle

- **Seed Placement Options**:

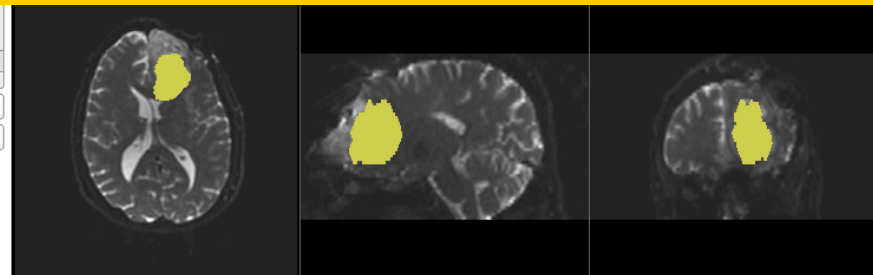
Check **Use Index Space**

- **Stopping Value**

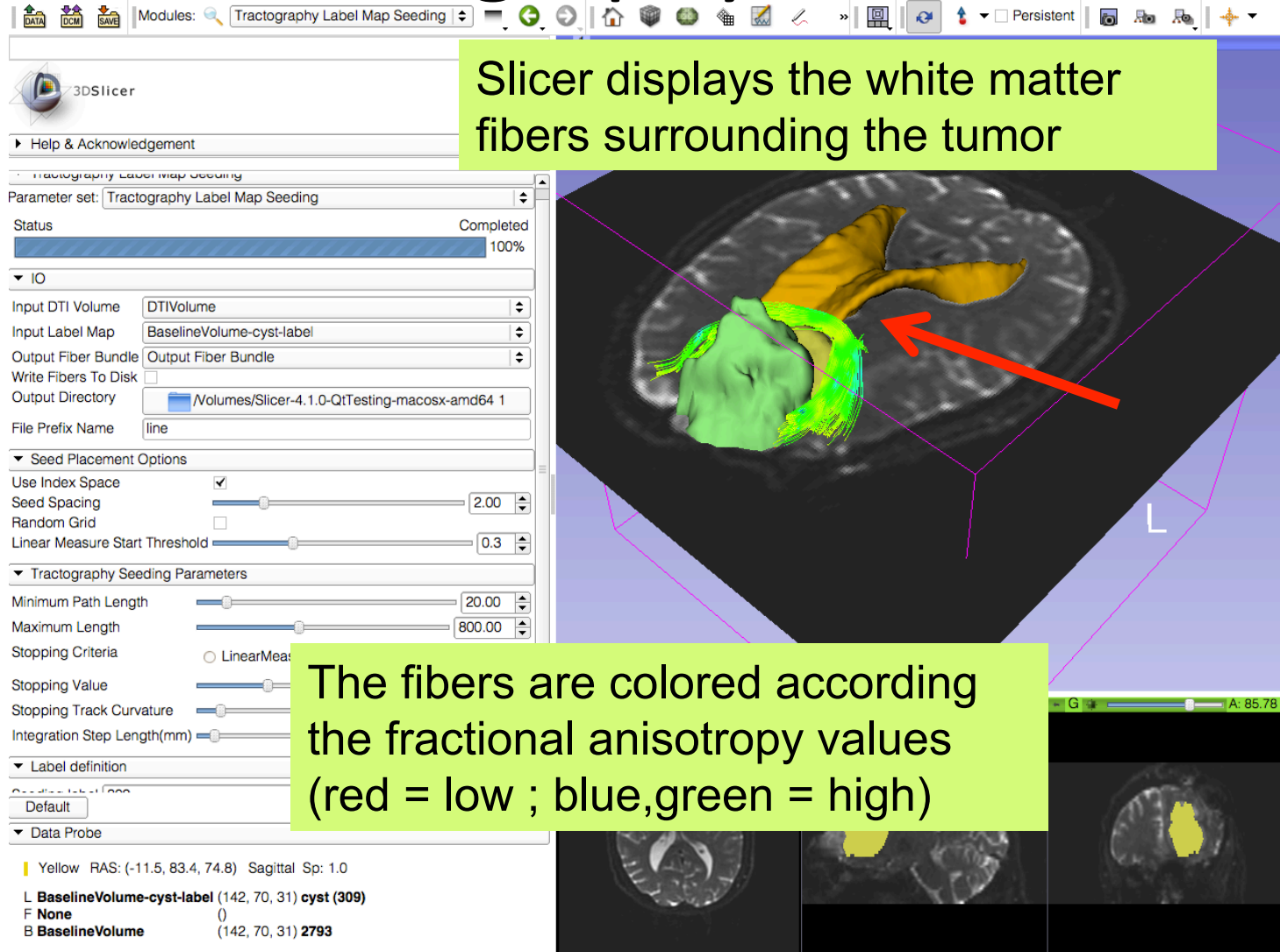
Set the FA threshold to 0.15

- **Label Definition**:

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



Tractography Results



Slicer displays the white matter fibers surrounding the tumor

The fibers are colored according to the fractional anisotropy values (red = low ; blue, green = high)

Parameter set: Tractography Label Map Seeding

Status: Completed 100%

IO

Input DTI Volume: DTIVolume

Input Label Map: BaselineVolume-cyst-label

Output Fiber Bundle: Output Fiber Bundle

Write Fibers To Disk:

Output Directory: /Volumes/Slicer-4.1.0-QtTesting-macosx-amd64 1

File Prefix Name: line

Seed Placement Options

Use Index Space:

Seed Spacing: 2.00

Random Grid:

Linear Measure Start Threshold: 0.3

Tractography Seeding Parameters

Minimum Path Length: 20.00

Maximum Length: 800.00

Stopping Criteria: LinearMea

Stopping Value: [Slider]

Stopping Track Curvature: [Slider]

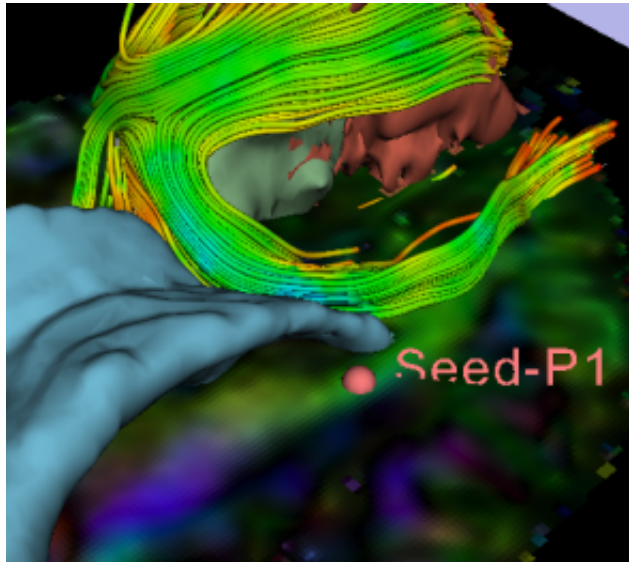
Integration Step Length(mm): [Slider]

Label definition

Default

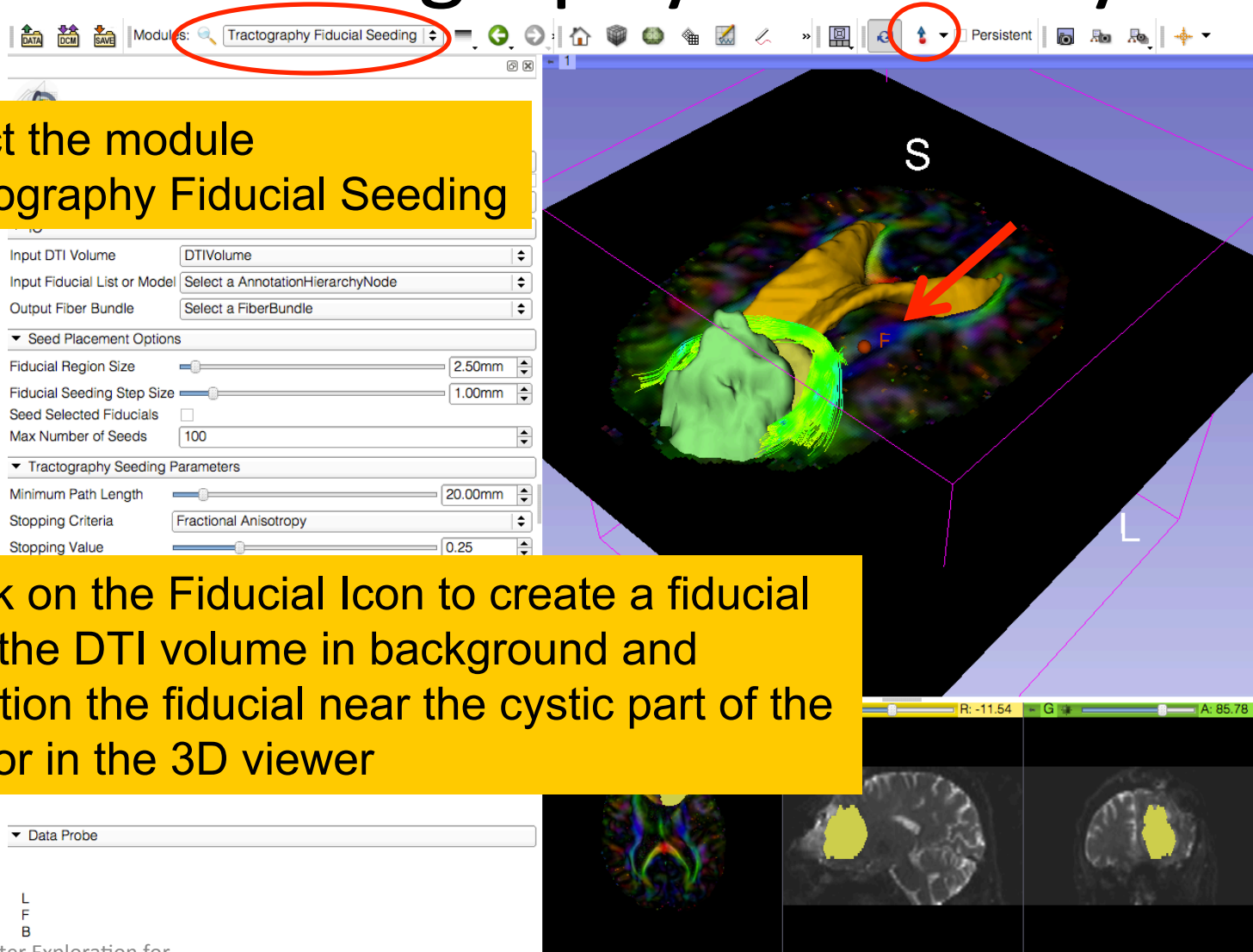
Data Probe

- Yellow RAS: (-11.5, 83.4, 74.8) Sagittal Sp: 1.0
- L BaselineVolume-cyst-label (142, 70, 31) cyst (309)
- F None (0)
- B BaselineVolume (142, 70, 31) 2793



Part 4: Tractography exploration of the ipsilateral and contralateral side

Tractography on-the-fly



Select the module
Tractography Fiducial Seeding

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

Tractography on-the-fly

3DSlicer

Modules: Tractography Fiducial Seeding

Parameter set: FiducialSeedingParameters

IO

Input DTI Volume: DTIVolume

Input Fiducial List or Model: Fiducials List

Output Fiber Bundle: FiberBundle_Fiducials List

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

R: 58.74, Y: -14.22, G: 47.35

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 ipsilateral side of the tumor

Modules: Tractography Fiducial Seeding

Parameter set: FiducialSeedingParameters

IO

Input DTI Volume: DTIVolume

Input Fiducial List or Model: Fiducials List

Output Fiber Bundle: FiberBundle_Fiducials List

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

R: 58.74 Y: -14.22 G: 47.35

Fiducial Seeding



Move the fiducial to the cingulum region 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_Fiducials List

▼ 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

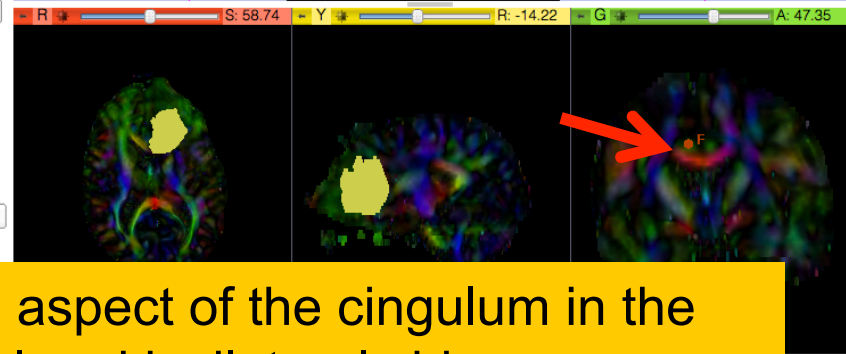
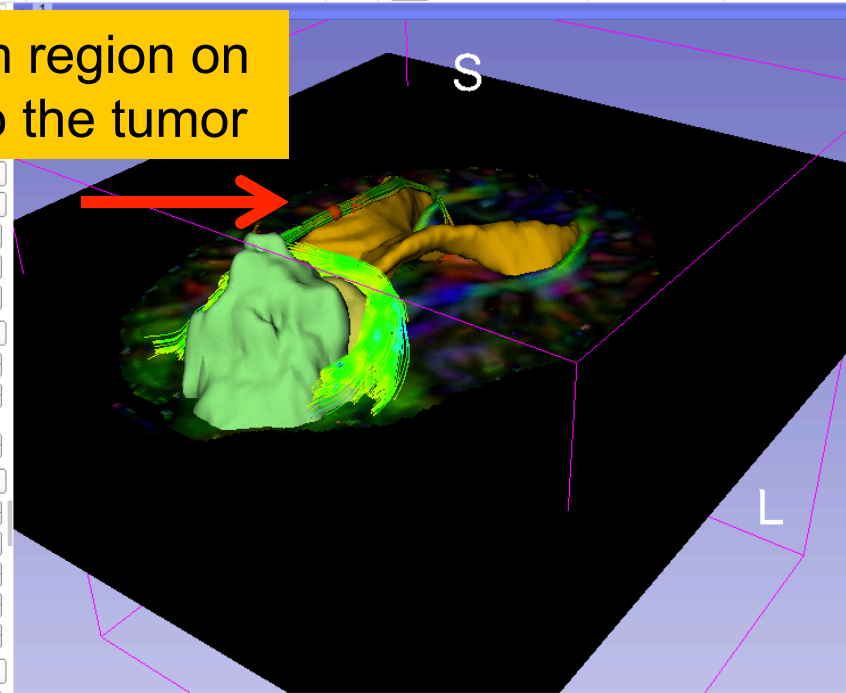
Integration Step Length: 0.50mm

▼ Enabling Options

Create Tracts Initially As: Tubes

Enable Seeding Tracts:

▼ Data Probe



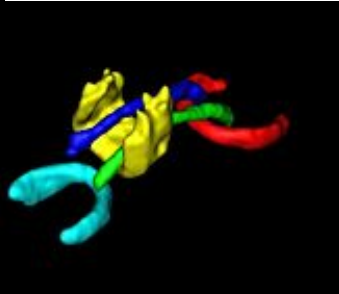
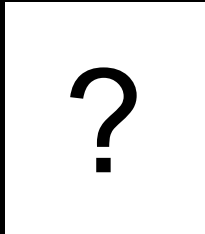
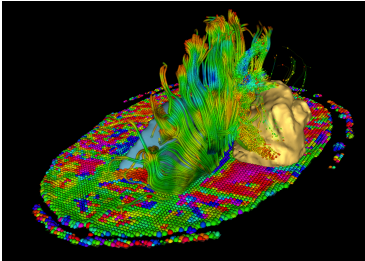
L
F
B

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

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

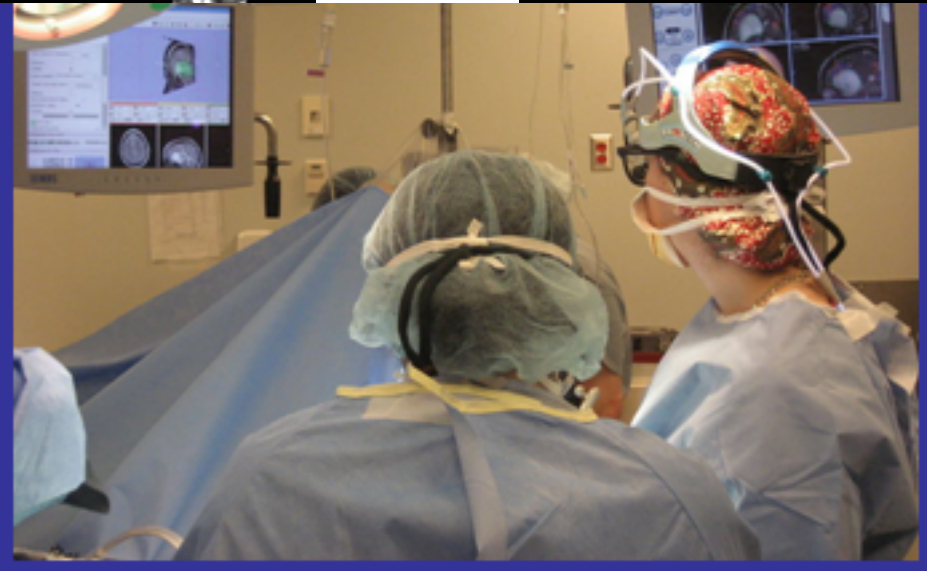
Going Further: How to choose ?



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

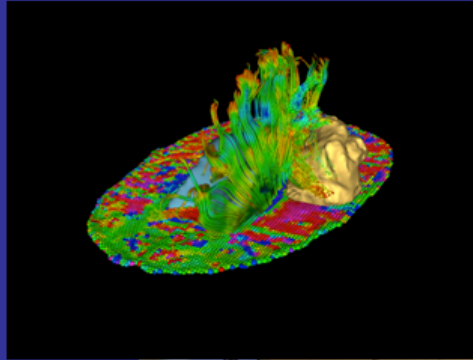


Need for validation to accelerate clinical use of DT-MRI findings



MICCAI 2011 DTI Challenge

14th 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

MICCAI 2011 Workshop

- 8 international teams
- 10-hour long workshop
- 25 participants
- 352 corticospinal tracts generated
- 6,600 visits on challenge webpage



DTI Tractography for Neurosurgical Planning: A Grand Challenge

Welcome to the DTI Tractography for Neurosurgical Planning: A Grand Challenge workshop. The goal of the initiative is to provide neurosurgeons with an overview of the state-of-the-art in the field of Diffusion Tensor Imaging (DTI) tractography and to provide neurosurgeons with an overview of the state-of-the-art in the field of Diffusion Tensor Imaging (DTI) tractography and to provide neurosurgeons with an overview of the state-of-the-art in the field of Diffusion Tensor Imaging (DTI) tractography.

Overview

Diffusion Tensor Imaging (DTI) tractography has a crucial potential for neurosurgical planning since it provides a virtual representation of white matter pathways. This workshop will provide neurosurgeons with an overview of the state-of-the-art in the field of Diffusion Tensor Imaging (DTI) tractography and to provide neurosurgeons with an overview of the state-of-the-art in the field of Diffusion Tensor Imaging (DTI) tractography.

Faculty

- Boris Poon, Ph.D., Surgical Planning Laboratory, Brigham and Women's Hospital, Harvard Medical School
- Ben Adams, M.D., Surgical Planning Laboratory, Brigham and Women's Hospital, Harvard Medical School
- Alexander Goh, M.D., Department of Neurosurgery, Brigham and Women's Hospital, Harvard Medical School
- Guohua Gao, Ph.D., The Scientific Computing and Imaging Institute, University of Utah
- Mark Spitzer, Ph.D., NeuroImage Research and Analysis Laboratory, University of North Carolina
- William Wells, Ph.D., Surgical Planning Laboratory, Brigham and Women's Hospital, Harvard Medical School
- Christophoros Pantazis, Ph.D., Laboratory of Radiology and Imaging Sciences, Brigham and Women's Hospital, Harvard Medical School
- Tyler Gauthier, M.Sc., The Scientific Computing and Imaging Institute, University of Utah
- Paul Mullen, M.D., Department of Neurosurgery, University Hospital Schleswig-Holstein, Kiel, Germany
- Mathias Marnett, M.D., Ph.D., Department of Radiology, Brigham and Women's Hospital, Harvard Medical School

Workshop Agenda

- 08:30-09:00: Start of the workshop
- 09:00-09:30: Welcome and registration
- 09:30-10:00: Morning keynote
- 10:00-10:30: DTI Tractography and Neurosurgical Planning
- 10:30-11:00: Presentation of the DTI Tractography Challenge
- 11:00-11:30: Lunch
- 11:30-12:00: DTI Tractography Basics
- 12:00-12:30: Diffusion Tensor Imaging
- 12:30-13:00: DTI Tractography Applications
- 13:00-13:30: DTI Tractography Applications
- 13:30-14:00: DTI Tractography Applications
- 14:00-14:30: DTI Tractography Applications
- 14:30-15:00: DTI Tractography Applications
- 15:00-15:30: DTI Tractography Applications
- 15:30-16:00: DTI Tractography Applications
- 16:00-16:30: DTI Tractography Applications
- 16:30-17:00: DTI Tractography Applications
- 17:00-17:30: DTI Tractography Applications
- 17:30-18:00: DTI Tractography Applications
- 18:00-18:30: DTI Tractography Applications
- 18:30-19:00: DTI Tractography Applications
- 19:00-19:30: DTI Tractography Applications
- 19:30-20:00: DTI Tractography Applications
- 20:00-20:30: DTI Tractography Applications
- 20:30-21:00: DTI Tractography Applications
- 21:00-21:30: DTI Tractography Applications
- 21:30-22:00: DTI Tractography Applications
- 22:00-22:30: DTI Tractography Applications
- 22:30-23:00: DTI Tractography Applications
- 23:00-23:30: DTI Tractography Applications
- 23:30-24:00: DTI Tractography Applications
- 24:00-24:30: DTI Tractography Applications
- 24:30-25:00: DTI Tractography Applications
- 25:00-25:30: DTI Tractography Applications
- 25:30-26:00: DTI Tractography Applications
- 26:00-26:30: DTI Tractography Applications
- 26:30-27:00: DTI Tractography Applications
- 27:00-27:30: DTI Tractography Applications
- 27:30-28:00: DTI Tractography Applications
- 28:00-28:30: DTI Tractography Applications
- 28:30-29:00: DTI Tractography Applications
- 29:00-29:30: DTI Tractography Applications
- 29:30-30:00: DTI Tractography Applications
- 30:00-30:30: DTI Tractography Applications
- 30:30-31:00: DTI Tractography Applications
- 31:00-31:30: DTI Tractography Applications
- 31:30-32:00: DTI Tractography Applications
- 32:00-32:30: DTI Tractography Applications
- 32:30-33:00: DTI Tractography Applications
- 33:00-33:30: DTI Tractography Applications
- 33:30-34:00: DTI Tractography Applications
- 34:00-34:30: DTI Tractography Applications
- 34:30-35:00: DTI Tractography Applications
- 35:00-35:30: DTI Tractography Applications
- 35:30-36:00: DTI Tractography Applications
- 36:00-36:30: DTI Tractography Applications
- 36:30-37:00: DTI Tractography Applications
- 37:00-37:30: DTI Tractography Applications
- 37:30-38:00: DTI Tractography Applications
- 38:00-38:30: DTI Tractography Applications
- 38:30-39:00: DTI Tractography Applications
- 39:00-39:30: DTI Tractography Applications
- 39:30-40:00: DTI Tractography Applications
- 40:00-40:30: DTI Tractography Applications
- 40:30-41:00: DTI Tractography Applications
- 41:00-41:30: DTI Tractography Applications
- 41:30-42:00: DTI Tractography Applications
- 42:00-42:30: DTI Tractography Applications
- 42:30-43:00: DTI Tractography Applications
- 43:00-43:30: DTI Tractography Applications
- 43:30-44:00: DTI Tractography Applications
- 44:00-44:30: DTI Tractography Applications
- 44:30-45:00: DTI Tractography Applications
- 45:00-45:30: DTI Tractography Applications
- 45:30-46:00: DTI Tractography Applications
- 46:00-46:30: DTI Tractography Applications
- 46:30-47:00: DTI Tractography Applications
- 47:00-47:30: DTI Tractography Applications
- 47:30-48:00: DTI Tractography Applications
- 48:00-48:30: DTI Tractography Applications
- 48:30-49:00: DTI Tractography Applications
- 49:00-49:30: DTI Tractography Applications
- 49:30-50:00: DTI Tractography Applications
- 50:00-50:30: DTI Tractography Applications
- 50:30-51:00: DTI Tractography Applications
- 51:00-51:30: DTI Tractography Applications
- 51:30-52:00: DTI Tractography Applications
- 52:00-52:30: DTI Tractography Applications
- 52:30-53:00: DTI Tractography Applications
- 53:00-53:30: DTI Tractography Applications
- 53:30-54:00: DTI Tractography Applications
- 54:00-54:30: DTI Tractography Applications
- 54:30-55:00: DTI Tractography Applications
- 55:00-55:30: DTI Tractography Applications
- 55:30-56:00: DTI Tractography Applications
- 56:00-56:30: DTI Tractography Applications
- 56:30-57:00: DTI Tractography Applications
- 57:00-57:30: DTI Tractography Applications
- 57:30-58:00: DTI Tractography Applications
- 58:00-58:30: DTI Tractography Applications
- 58:30-59:00: DTI Tractography Applications
- 59:00-59:30: DTI Tractography Applications
- 59:30-60:00: DTI Tractography Applications



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

Neurosurgical Planning Workshop, October 1st, 2012 – Nice, France

MICCAI 2012 DTI Tractography Challenge Second Edition

INTRODUCTION THE CHALLENGE FACULTY KEYNOTE SPEAKER DATA LOGISTICS CONTACT

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

Acknowledgments



National Alliance for Medical Image
Computing (NA-MIC)

NIH U54EB005149



Neuroimage Analysis Center (NAC)

NIH P41RR013218