

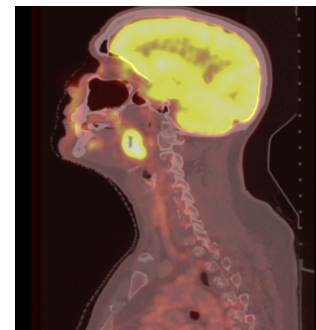
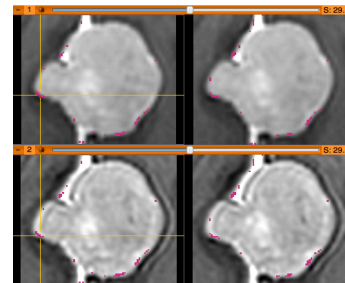


Surgical Planning Laboratory  
Brigham and Women's Hospital  
Boston, Massachusetts USA

a teaching affiliate of  
Harvard Medical School

# Quantitative Medical Imaging for Clinical Research and Practice

Sonia Pujol, PhD, Katarzyna Macura MD, PhD,  
Kitt Shaffer, MD, PhD, Hatsuho Mamata, MD,  
PhD, Andriy Fedorov, PhD, Wendy Plesniak,  
PhD, Ron Kikinis, MD



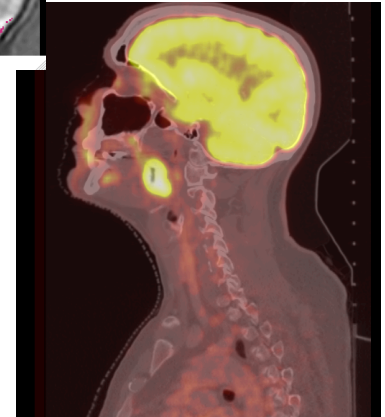
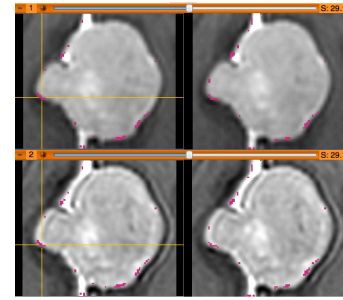


# Quantitative Imaging Tutorial

Quantitative imaging is the extraction of quantitative measurements from medical imaging.

This tutorial is built upon two examples of quantitative imaging:

- **Morphology:** small volumetric changes in slow growing tumors
- **Function:** metabolic activity in squamous cell carcinoma

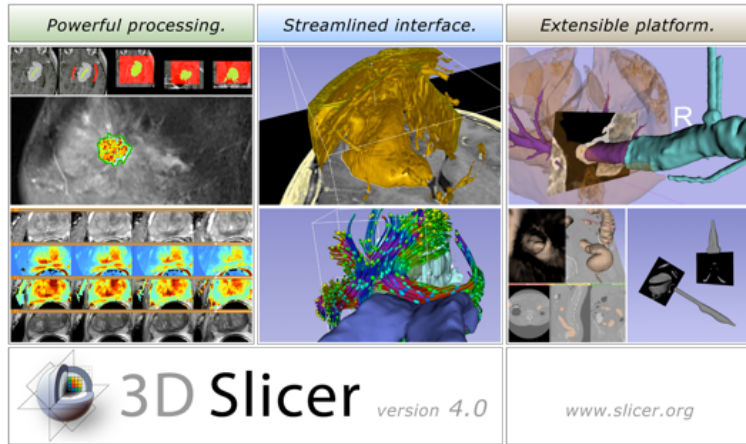






# Quantitative Imaging: Software

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[www.slicer.org](http://www.slicer.org)

- This hands-on tutorial will guide you step-by-step through the use of quantitative imaging modules of the [3DSlicer software](#).
- 3DSlicer is a freely available open-source platform for medical imaging research [supported by the National Institutes of Health](#).



# Course Overview

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**Part 1:** Basics of 3D Data Loading and interactive visualization in 3DSlicer

**Part 2:** Measurement of small Volumetric Changes in meningioma using the Change Tracker module

**Part 3:** Measurement Metabolic Activity in squamous cell carcinoma using the PET Standard Uptake Value Computation module



# Course Datasets

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The course data is located in the directory:

C:/3DSlicerData/QuantitativeImaging\_Tues\_Dec3

- dataset1\_MR\_Head
- dataset2\_ChangeTracker
- dataset3\_PETCT

Each dataset is in Slicer **.mrp** file format.



# Slicer mrb file format

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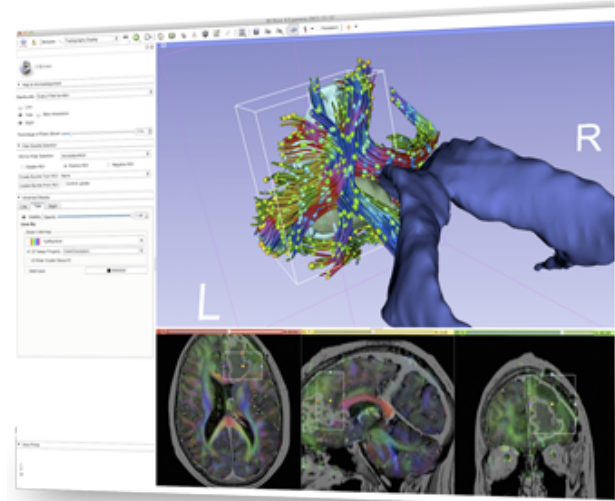
A Slicer mrb file is an archive file that contains all data for loading into Slicer4.

The .mrb file is a .zip file but with a different file extension.



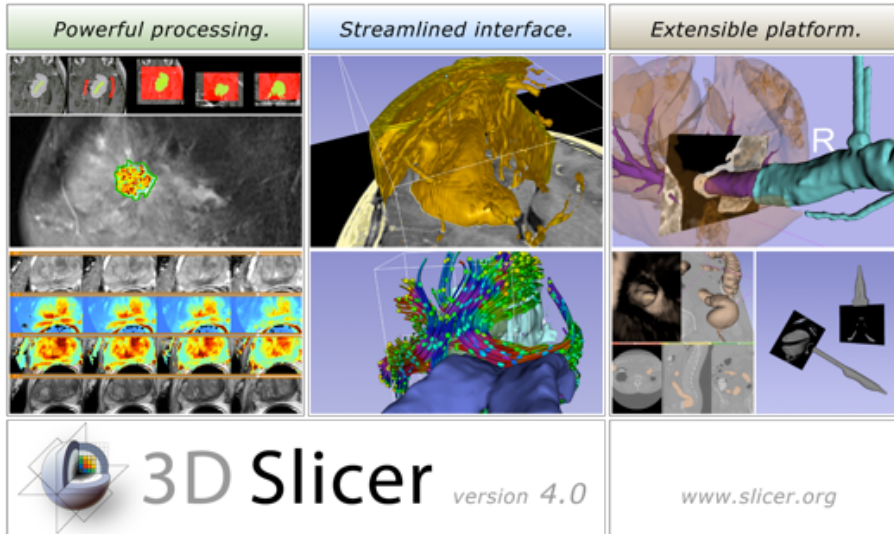
# ***Introduction to the 3DSlicer software***

Sonia Pujol, PhD  
Director of Training,  
National Alliance for Medical Image Computing  
Brigham and Women's Hospital, Boston, MA





# 3DSlicer

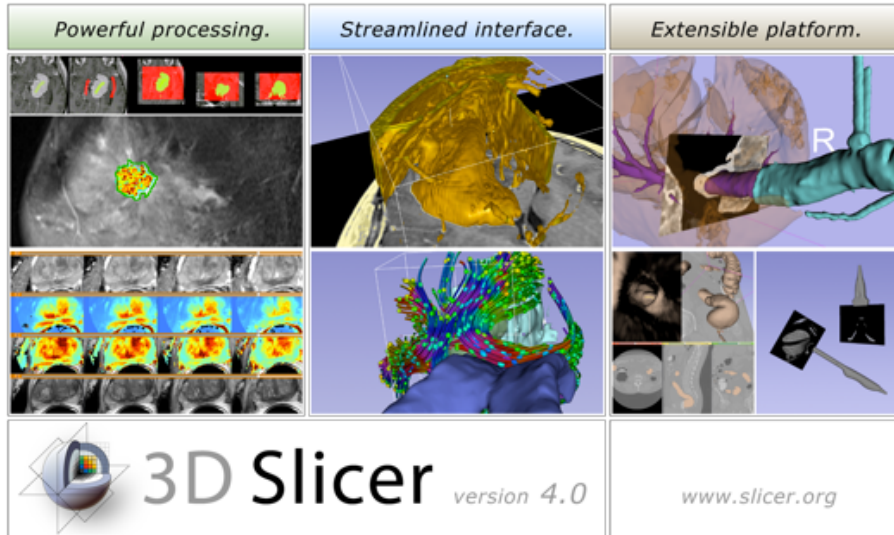


3DSlicer is a freely available **open-source** platform for segmentation, registration and 3D visualization of medical imaging data.

3DSlicer is a **multi-institutional effort** supported by the **National Institute of Health**.



# 3DSlicer



- 3DSlicer version 4.2 is a **multi-platform software** running on Windows, Linux, and Mac OSX
- Slicer is distributed under a **BSD license** with no restriction on use
- Slicer is a tool for research, and is **not FDA** approved

## Disclaimer

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

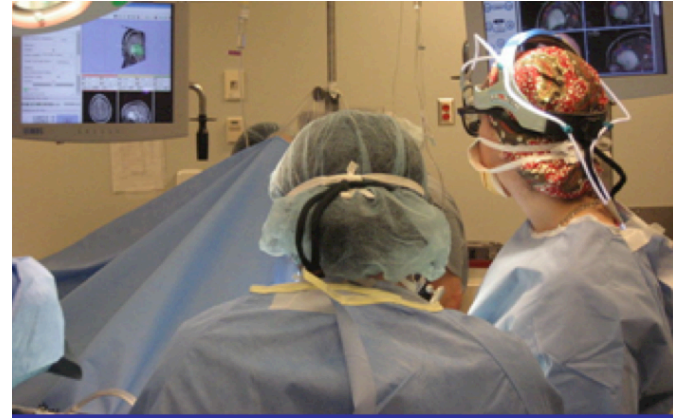


# An interdisciplinary platform

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An **open-source environment** for software developers



An **end-user application** for clinical investigators and scientists

A software platform that is both **easy to use** for clinical researchers and **easy to extend** for programmers





# 3DSlicer History

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- 1997: Slicer started as a research project between the Surgical Planning Lab (Harvard) and the CSAIL (MIT)

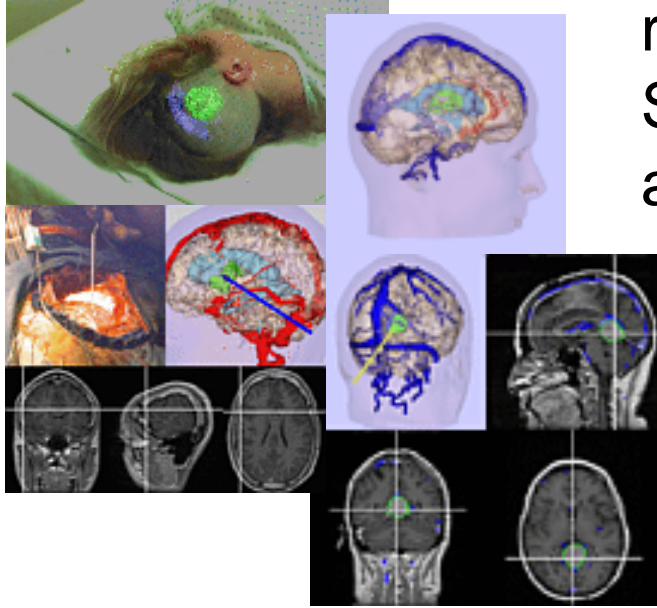
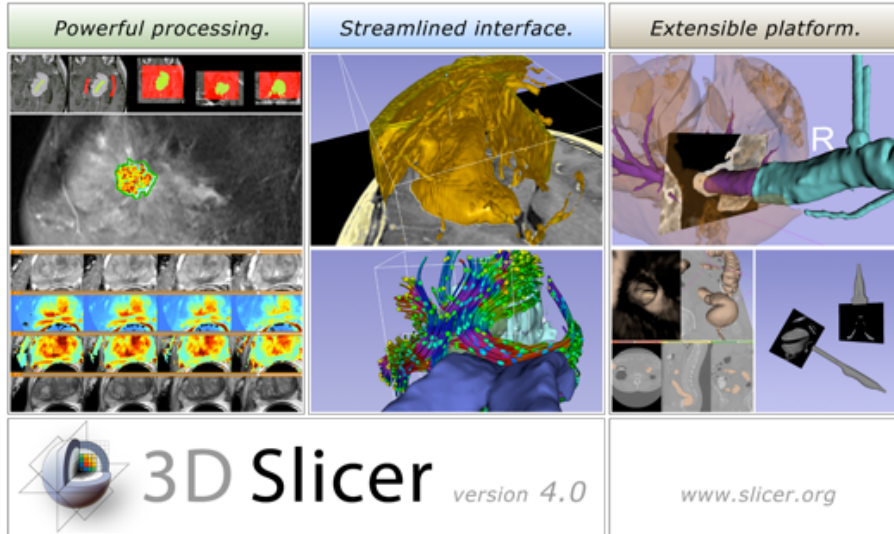


Image Courtesy of the CSAIL, MIT




# 3DSlicer History



- 1997: Slicer started as a research project between the Surgical Planning Lab (Harvard) and the CSAIL (MIT)
- 2012: Multi-institution effort to share the latest advances in image analysis with clinicians and scientists



# A multi-institution: NA-MIC, NAC, NCIGT



## National Alliance for Medical Image Computing

A National Center for Biomedical Computing  
Funded under the NIH Roadmap Initiative

Google Custom Search Search

### NA-MIC Wiki

**General**

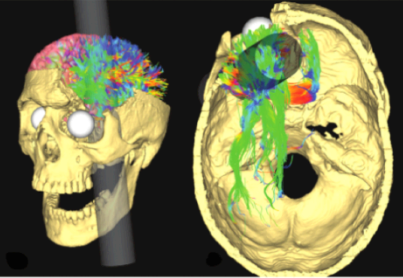
- Overview
- Organization
- Contact Us

**Center Components**

- Algorithms
- Engineering
- Driving Biological Projects
- Collaboration Grants

**Resources**

- Publication DB
- Image Gallery
- Downloads
- Service
- Training
- Dissemination
- Events
- Links



Modeling the path of the tamping iron through the Gage skull and its effects on white matter structure [Read more...](#)

1 of 24 Photos

**The National Alliance for Medical Image Computing (NA-MIC)** is a multi-institutional, interdisciplinary team of computer scientists, software engineers, and medical investigators who develop computational tools for the analysis and visualization of medical image data. The purpose of the Center is to provide the infrastructure and environment for the development of computational algorithms and open-source technologies, and then oversee the training and dissemination of these technologies to the research community.

Supported by the National Institutes of Health (NIH) and the National Science Foundation (NSF).

Information about collaborating with NA-MIC



## Neuroimage Analysis Center

"understanding the human brain through imaging"

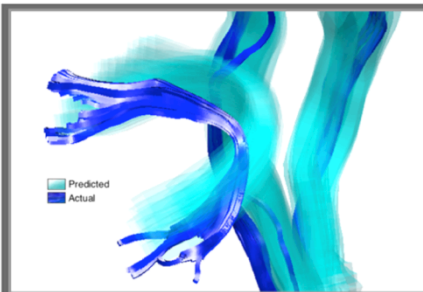
Google Custom Search GO

### About the NAC

- Overview
- Organization
- Research Cores
- Collaborations

### Resources

- Contact Us
- Publication DB
- Image Gallery
- Downloads
- Training
- Web Archive



**IMRI-DTI Modeling via Landmark Distance Atlases for Prediction and Detection of Fiber Tracts**


Leave-one-out prediction of tract location according to the landmark distance atlas (LDA). Each subject's MRI selection peaks and anatomical landmarks, plus the leave-one-out LDA from the other subjects, were used to predict the location of the AF, left CST, and right CST. The true dissections for each subject are shown in dark blue, and the 80% confidence interval for the predicted trajectory is shown in transparent cyan. These results provide an alternative visualization of the data in the learned landmark distance model and they demonstrate reasonable model generalization to novel subjects.

**More...**

**Featured Image Archive**

The Neuroimage Analysis Center (NAC) develops image processing and analysis techniques for basic and clinical neurosciences. The NAC research approach emphasizes both specific core technologies and collaborative application projects. The activities of the NAC are centered at the Harvard Medical School and the Surgical Planning Laboratory at the Brigham and Women's Hospital, with collaborators throughout the United States and the rest of the world.

Research supported by the National Center for Research Resources (NCRR) (P30 RR021311) and the Institute of Biomedical Imaging and Bioengineering (NIIB) at the National Institutes of Health.



## National Center for Image-Guided Therapy

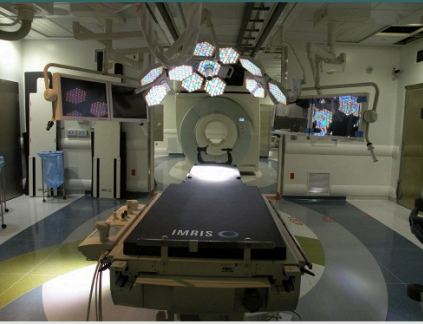
### NCIGT Wiki

**About Us**

- Overview
- Research Labs
- Research Cores
- Research Projects
- DBPs
- People

**Resources**

- Publication DB
- Image Gallery
- Downloads
- AMIGO
- News and Events
- Contact Us



**Advanced Multimodality Image Guided Operating (AMIGO) Suite**

The Advanced Multimodality Image Guided Operating (AMIGO) Suite is an innovative surgical and interventional environment that is the clinical translational test bed of the National Center for Image-Guided Therapy (NCIGT) at the Brigham and Women's Hospital (BWH) and Harvard Medical School. The AMIGO is an integrated, 5,700 square foot area divided into three sterile procedure rooms in which a multidisciplinary team will treat patients with the benefit of intra-operative imaging using multiple modalities. [More...](#)

[Featured Image Archive](#)

The National Center for Image Guided Therapy (NCIGT) is a Biomedical Technology Resource Center supported by the NCRR and NIBB Institutes

**PIs: Ferenc Jolesz, M.D., Clare Tempany, M.D.**

PI: Ron Kikinis, M.D.



# Slicer: Behind the scenes

CDash - Slicer4

http://www.cdash.org/slicer4/index.php?project=Slicer4

Dashboard Calendar Previous Current Project

WARNING: This CDash instance is running the bleeding edge svn trunk CDash code, and is updated frequently. You have 1 file changed by 1 author as of Sunday, November 27 2011 - 22:00 EST

### Nightly-Packages

Site	Build Name	Update	Configure			Build	
		Files	Error	Warn		Error	Warn
factory-win7.kitware	Windows7-VS2010-32bits-QT4.7.1-PythonQt-With-Tcl-CLI-Release	0	0	0		2 <sup>0</sup> <sub>0</sub>	107
factory-mac-64bits.kitware	SnowLeopard-g++4.2.1-64bits-QT4.7-PythonQt-With-Tcl-CLI-Release	1	0	0		0	14 <sup>0</sup> <sub>0</sub>
factory-ubuntu-64bits.kitware	Linux-g++4.4.3-64bits-QT4.7-PythonQt-With-Tcl-CLI-Release	1	0	0		0	13 <sup>0</sup> <sub>0</sub>
factory-win7.kitware	Windows7-VS2008-64bits-QT4.7.1-PythonQt-With-Tcl-CLI-Release	0	0	0		0 <sup>0</sup> <sub>0</sub>	1000 <sup>0</sup> <sub>0</sub>
factory-win7.kitware	Windows7-VS2008-32bits-QT4.7.1-PythonQt-With-Tcl-CLI-Release	1	0	0		0 <sup>0</sup> <sub>0</sub>	1000 <sup>0</sup> <sub>0</sub>

### Nightly

Site	Build Name	Update	Configure			Build			Test			Build Time
		Files	Error	Warn		Error	Warn		Not Run	Fail	Pass	
whitecube.kitware	SnowLeopard-gcc4.2.1-QT4.7.0-PythonQt-With-Tcl-Release	1	0	0		27	190		0	96	391	11 hours ago
youpi.sci.utah.edu	OpenSuse-c++4.5.0-64bits-QT4.6.3-PythonQt-With-Tcl-NoCLI-Release	0	0	0		0	15		0	304	6	11 hours ago
eris.kitware	Linux-g++4.4-QT4.6.3-PythonQt-CLI-Release	1	0	0		0	15 <sup>0</sup> <sub>0</sub>		0	36 <sup>0</sup> <sub>0</sub>	451 <sup>0</sup> <sub>0</sub>	3 hours ago
factory-ubuntu-64bits.kitware	Linux-g++4.4.3-QT4.7-PythonQt-With-Tcl-CLI-Vaigrind-Release	0	0	0		0	13 <sup>0</sup> <sub>0</sub>		0	27 <sup>0</sup> <sub>0</sub>	460 <sup>0</sup> <sub>0</sub>	11 hours ago
factory-ubuntu-64bits.kitware	Linux-g++4.4.3-64bits-QT4.7-PythonQt-With-Tcl-NoCLI-Coverage-Release	0	0	0		0	12 <sup>0</sup> <sub>0</sub>		0	23 <sup>0</sup> <sub>0</sub>	287 <sup>0</sup> <sub>0</sub>	11 hours ago
sagarmatha.kitware	Linux-g++4.3.3-QT4.7-PythonQt-With-Tcl-NoCLI-Release	0	0	0		0	12 <sup>0</sup> <sub>0</sub>		0	22	288	12 hours ago

### Continuous

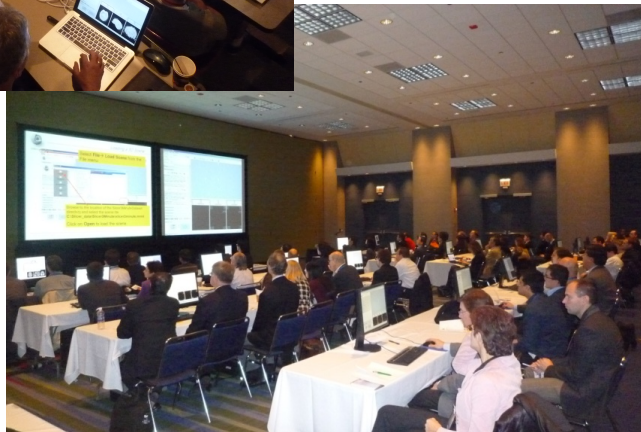
Site	Build Name	Update	Configure			Build			Test			Build Time
		Files	Error	Warn		Error	Warn		Not Run	Fail	Pass	
youpi.sci.utah.edu	OpenSuse-c++4.5.0-64bits-QT4.6.3-PythonQt-With-Tcl-NoCLI-Release	2	0	0		0	0 <sup>0</sup> <sub>0</sub>		0	304	6	1 hour ago

Slicer is built every night on Windows, Mac and Linux platforms



# Slicer Training

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RSNA 2011

- Hands-on training workshops at national and international venues
- More than 2,000 clinicians, clinical researchers and scientists trained since 2005



# Slicer Downloads



## Slicer 4 download statistics

Total matching  
downloads:  
**46794**

Date range:

past year

Release type:

any

Browser type:

desktop

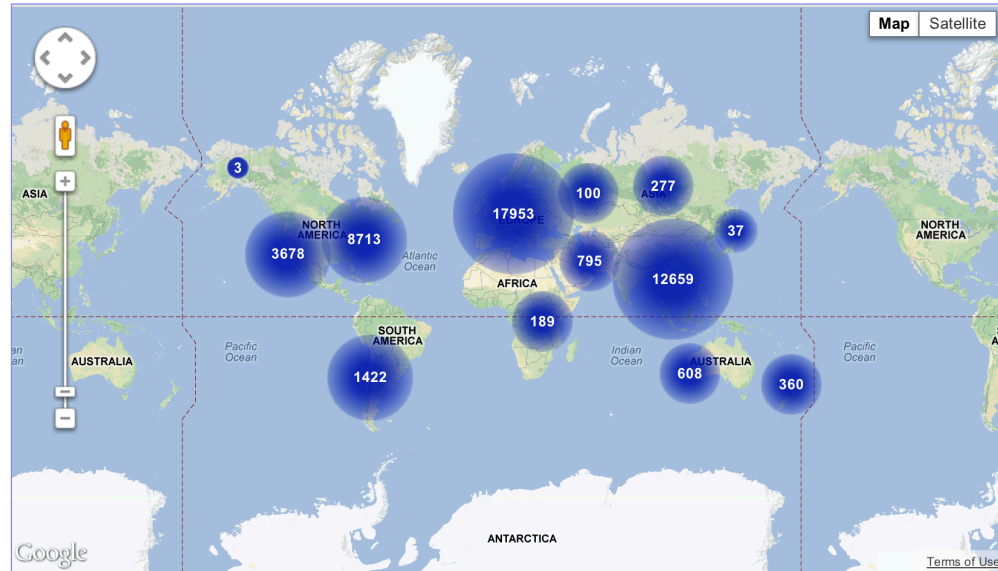
Update

Download location

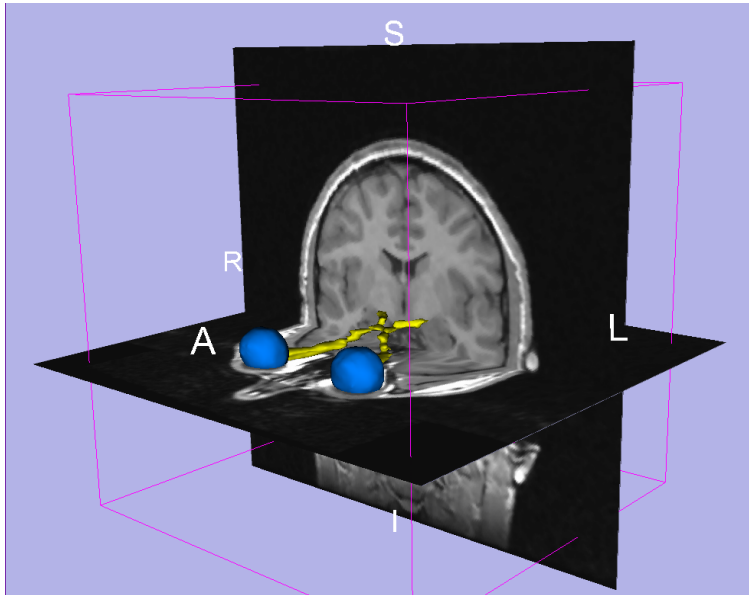
By Country

By Filename

By Month







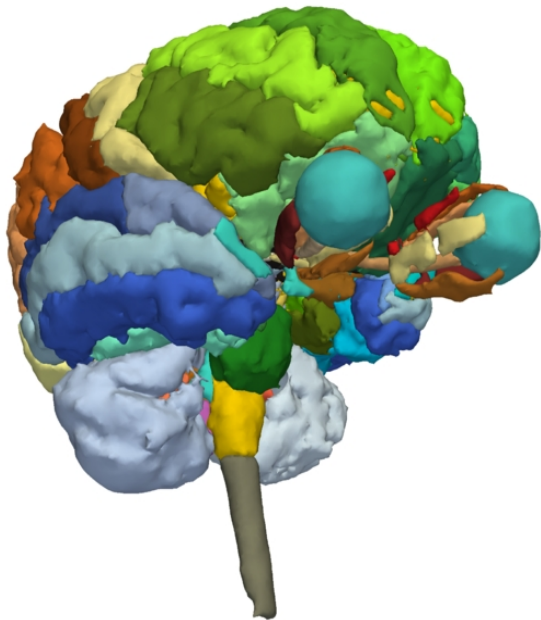
## Part I: 3D Data Loading and Visualization

Sonia Pujol, PhD  
Wendy Plesniak, PhD



# 3D Data Loading and Visualization

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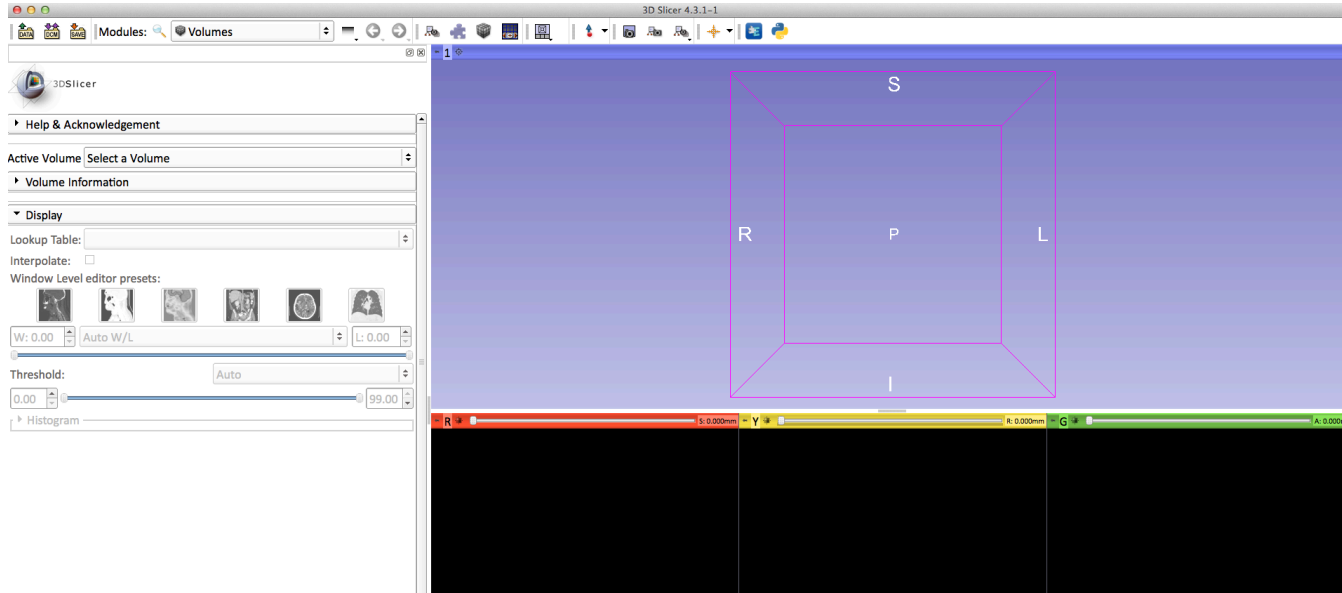
- This tutorial is a short introduction to the advanced **3D visualization capabilities Slicer**
- The Slicer4 Minute dataset is composed of an MR scan of the brain and 3D surface reconstructions of anatomical structures.
- The data are part of the SPL-PNL Brain Atlas developed by Talos, Jakab, Kikinis *et al.* The atlas is available at:

<http://www.spl.harvard.edu/publications/item/view/2037>





# Welcome to Slicer4



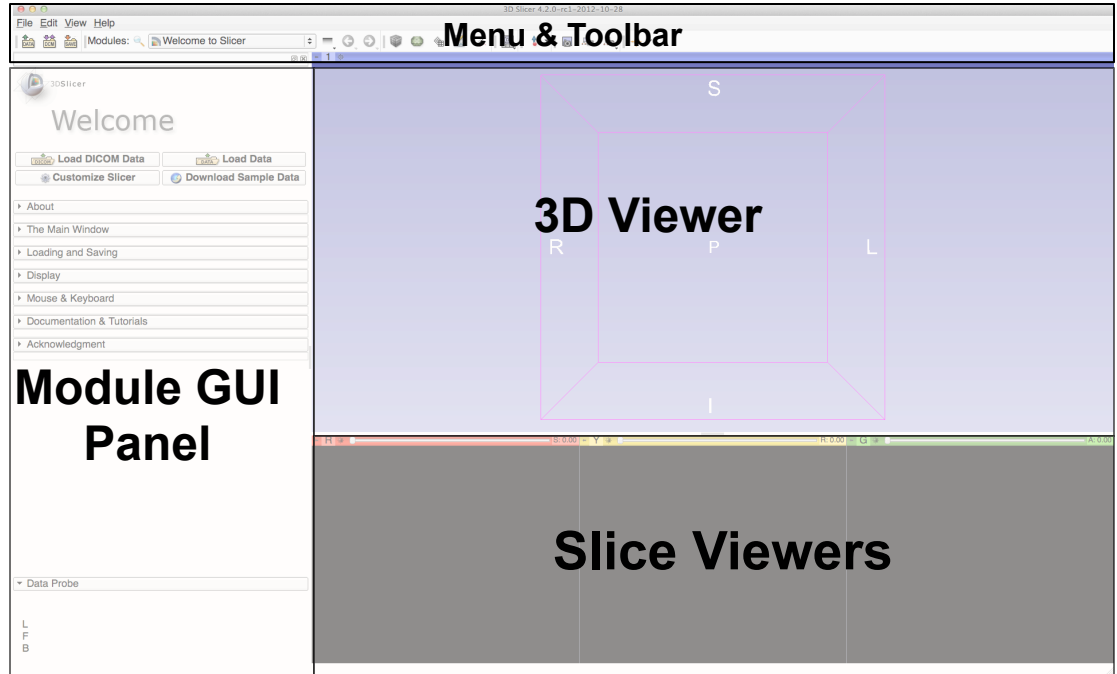
To start Slicer, select Start → Programs → Slicer4.3.1-1 (Win64) → Slicer



# Slicer4 Minute Tutorial: Navigating the Application GUI

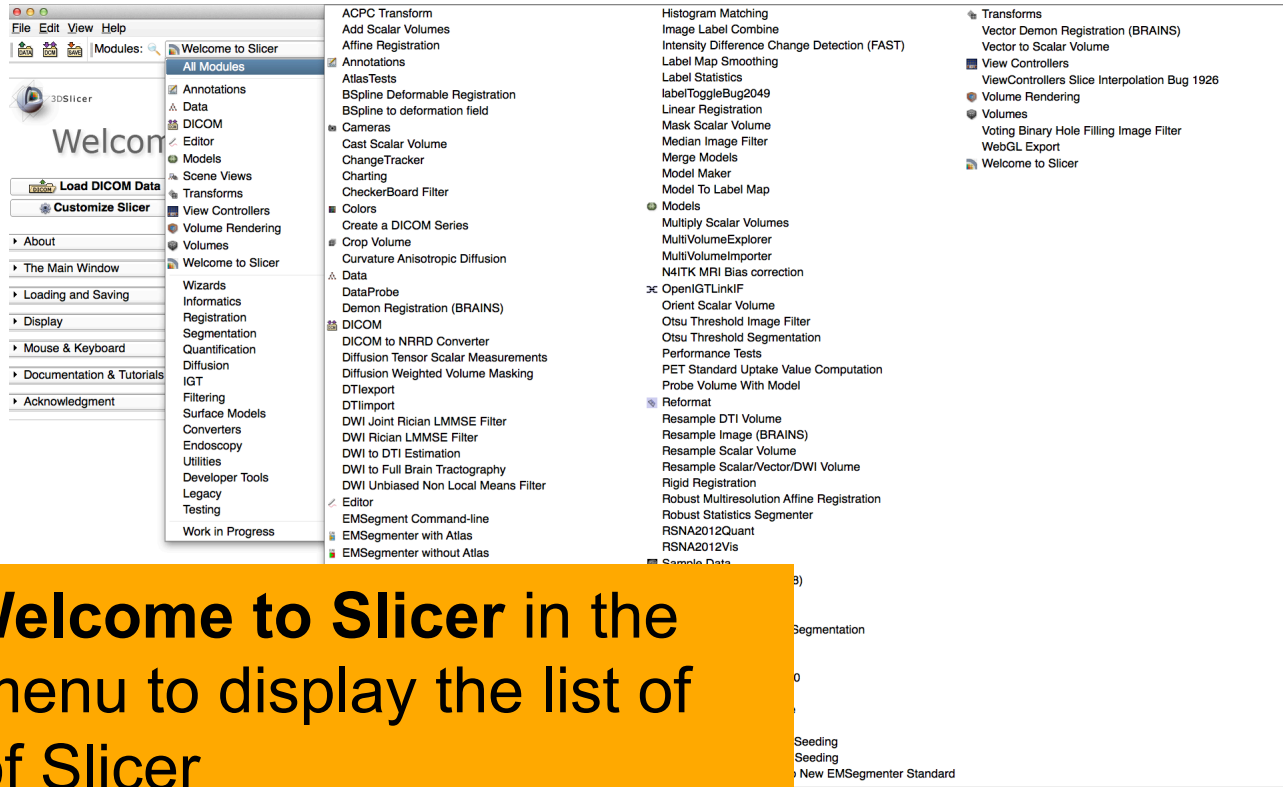
The Graphic User Interface (GUI) of Slicer4 integrates **four components**:

- the Menu Toolbar
- the Module GUI Panel
- the 3D Viewer
- the Slice Viewer





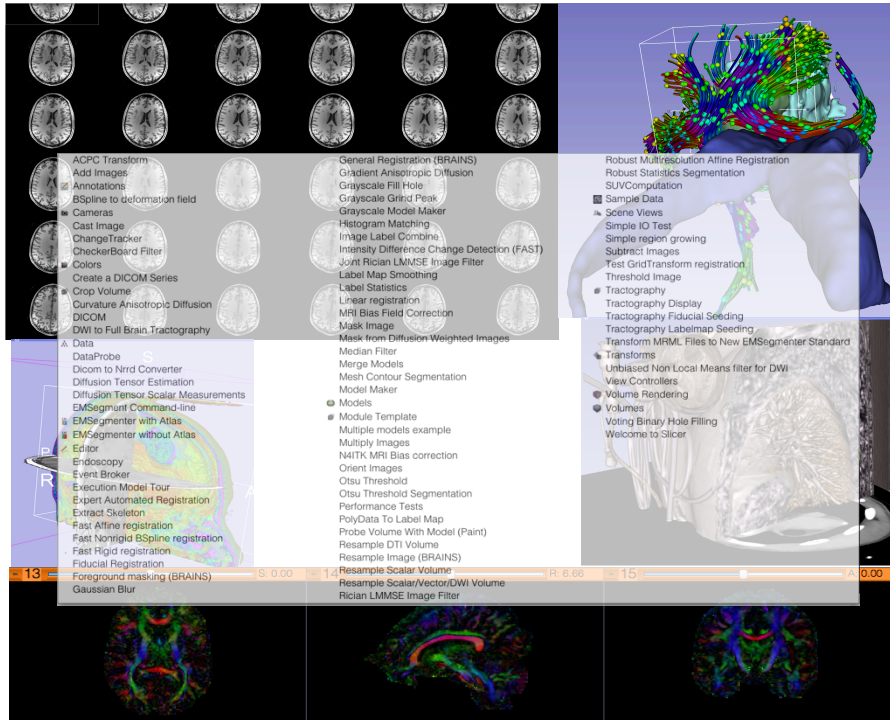
# Welcome to Slicer4.3



Click on **Welcome to Slicer** in the Modules menu to display the list of modules of Slicer



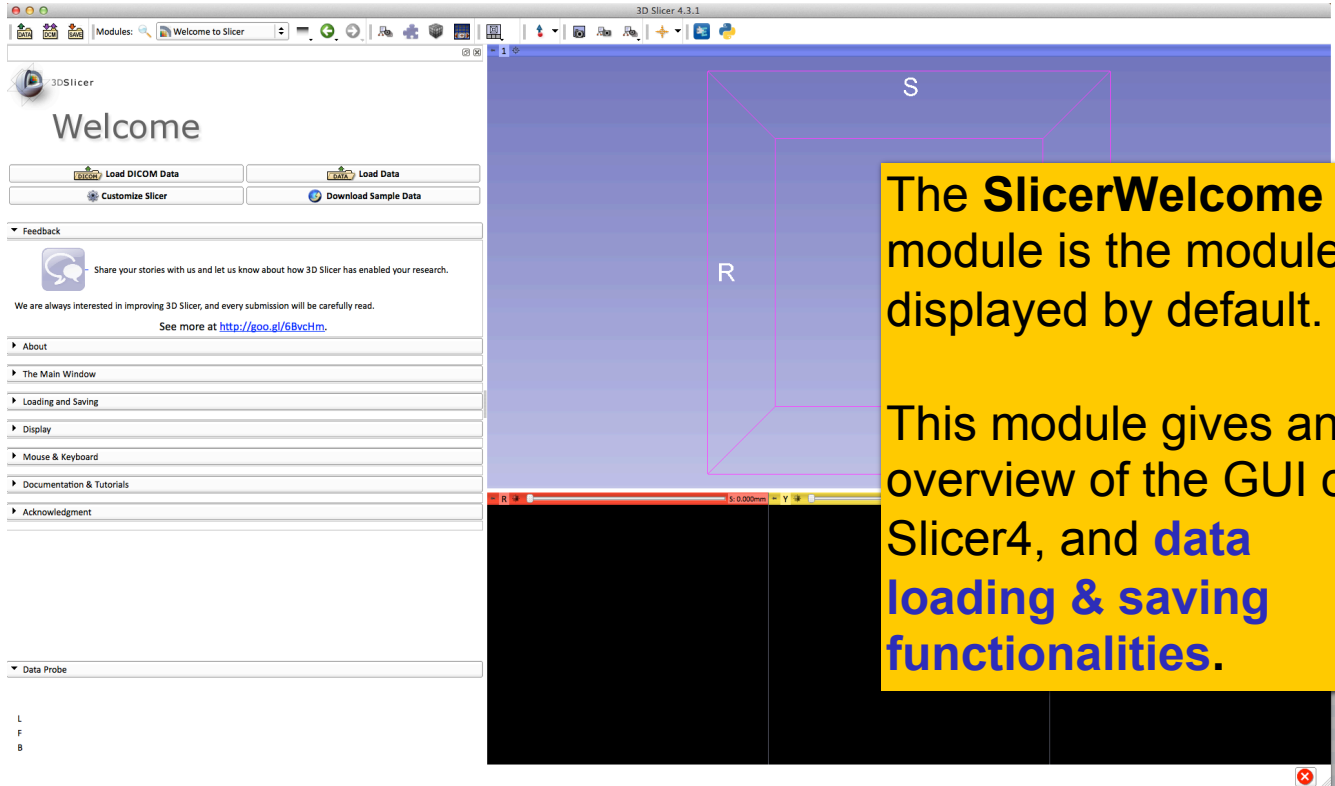
# Welcome to Slicer4



Slicer4.3 contains more than 100 modules for image segmentation, registration and 3D visualization of medical imaging data



# Slicer4 Minute Tutorial: Welcome Module



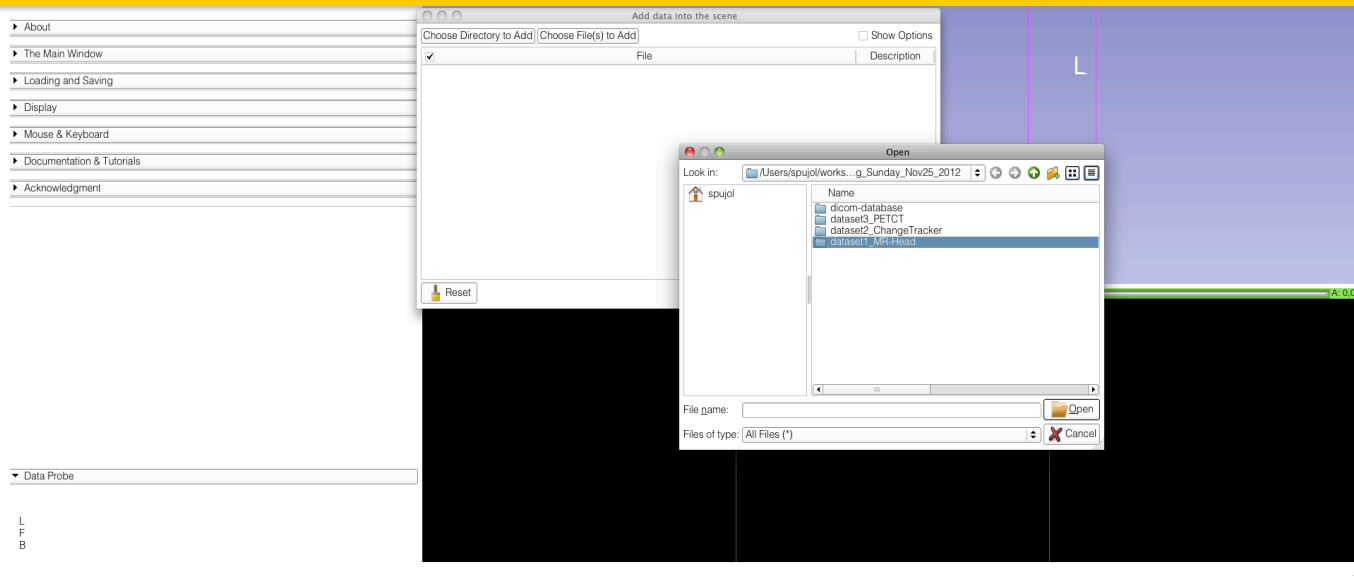


# Slicer4 Minute Tutorial: Load a Scene

Browse to the directory

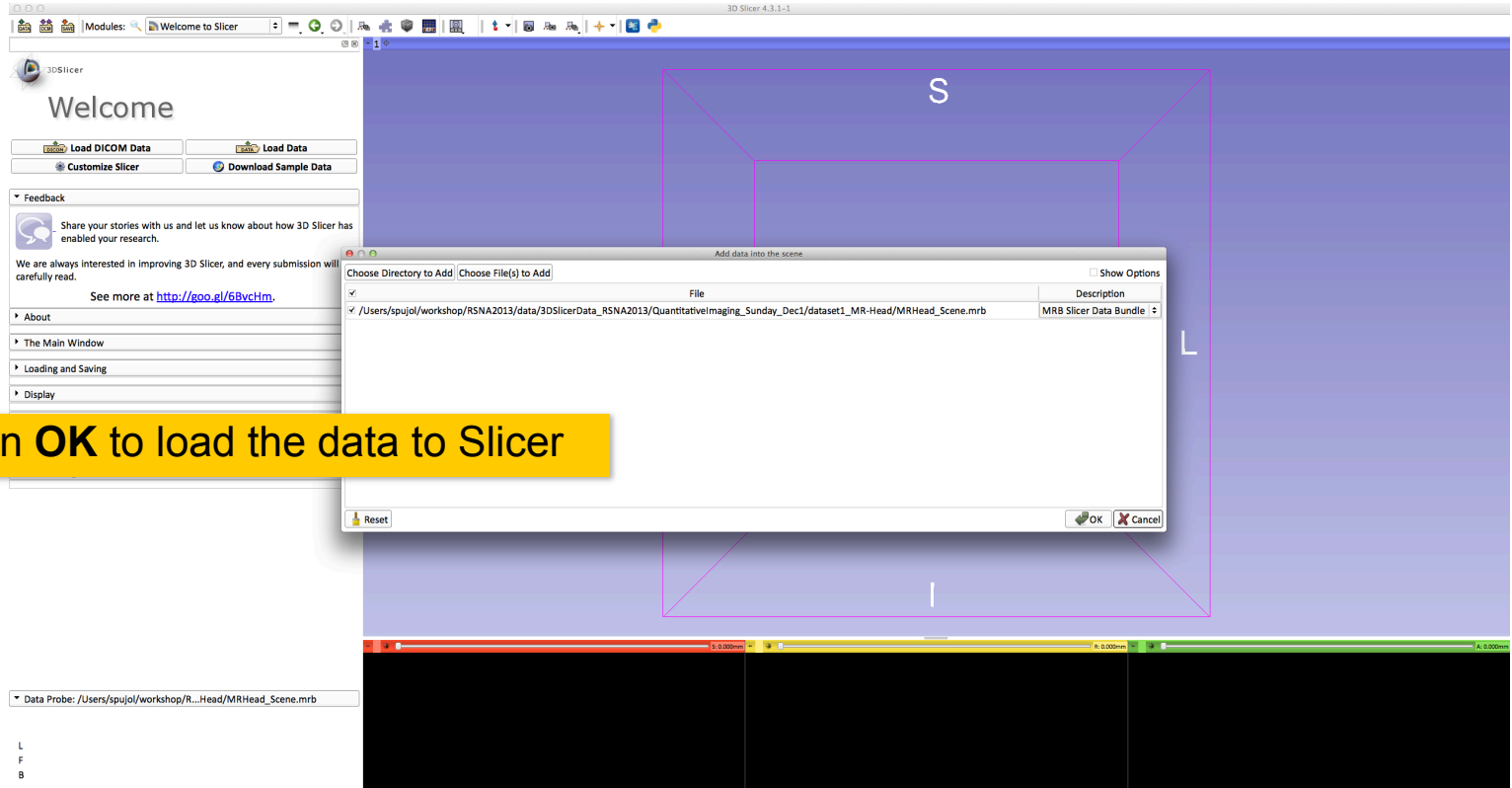
**'C:\3DSlicerData\QuantitativeImaging\_Sunday\_Dec1\dataset1\_MR-Head'**

Drag and drop the file **MRHead\_Scene.mrb**





# Slicer4 Minute Tutorial: Load a Scene

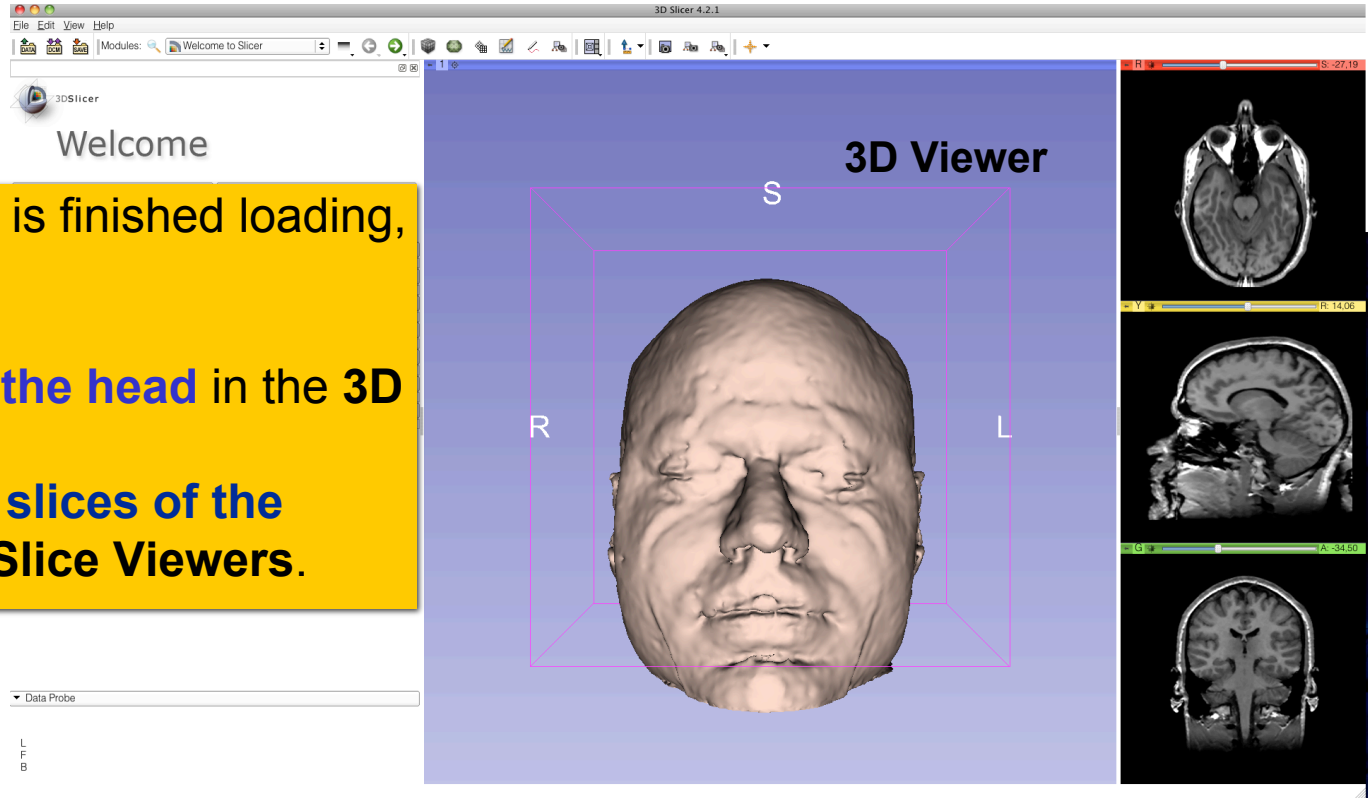




# Slicer4 Minute Tutorial: Viewing the Scene

When the scene is finished loading, Slicer displays:

- a **3D model of the head** in the **3D Viewer**, and
- anatomical **MR slices of the brain** in the **2D Slice Viewers**.



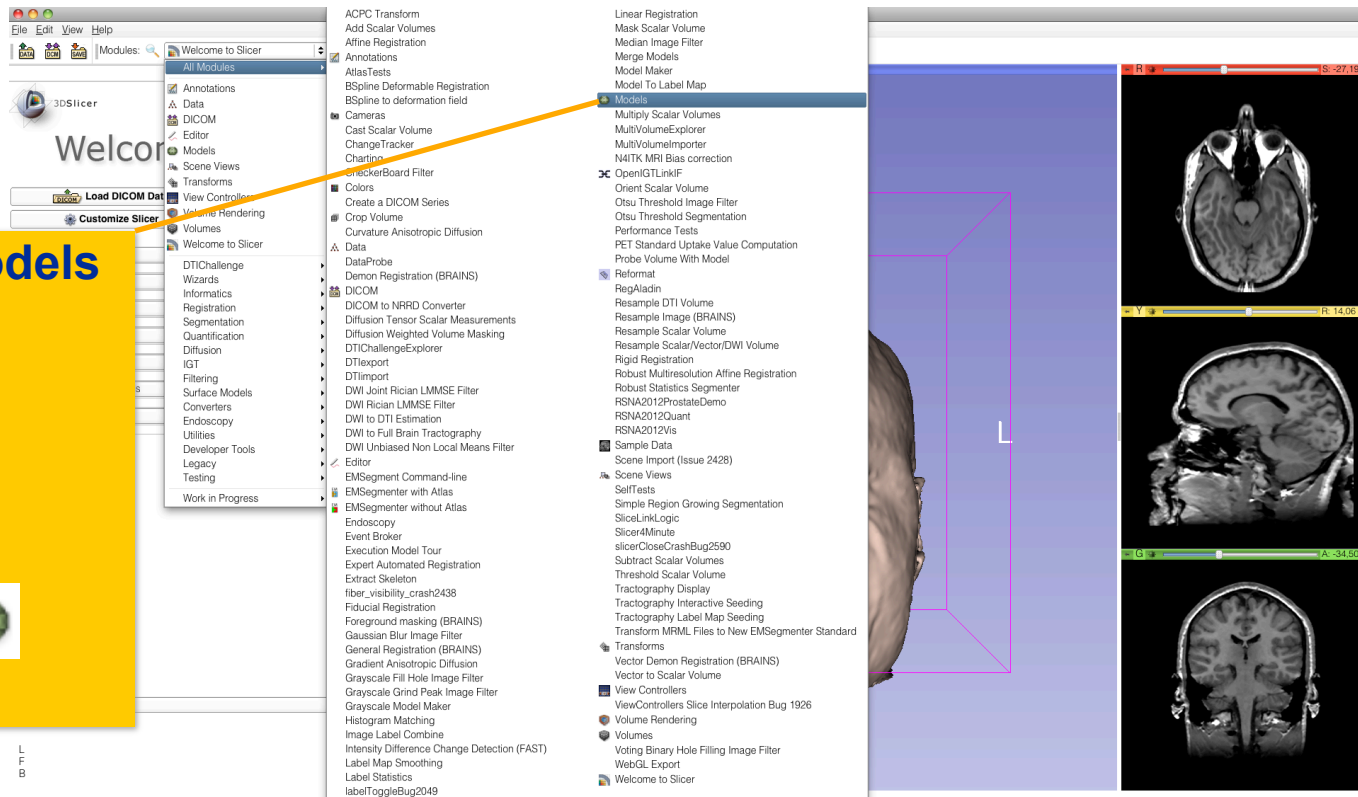




# Slicer4 Minute Tutorial: Exploring Slicer's functionality

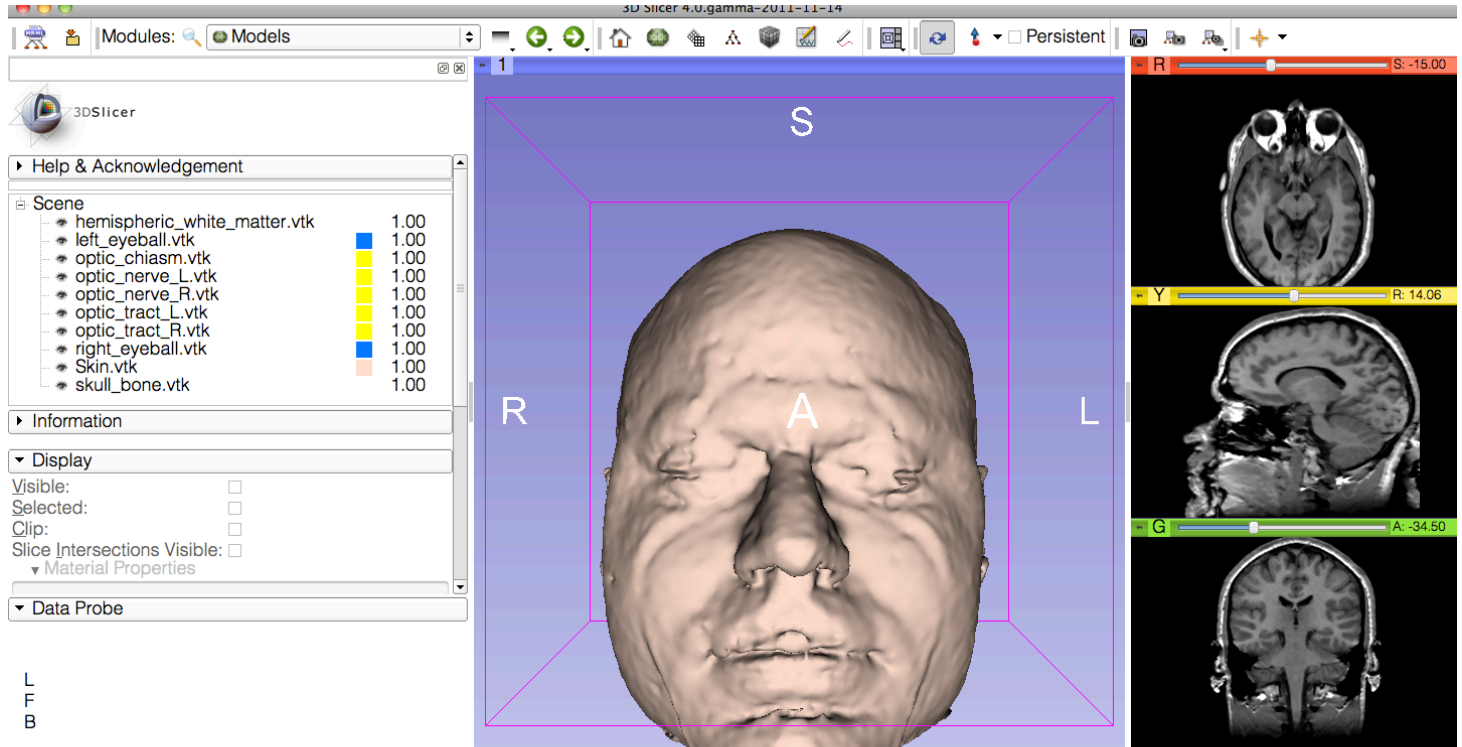
To access the **Models** module, browse through the list of modules...

...or click on the **models icon** in the toolbar





# Slicer4 Minute Tutorial: Switching to the Models Module

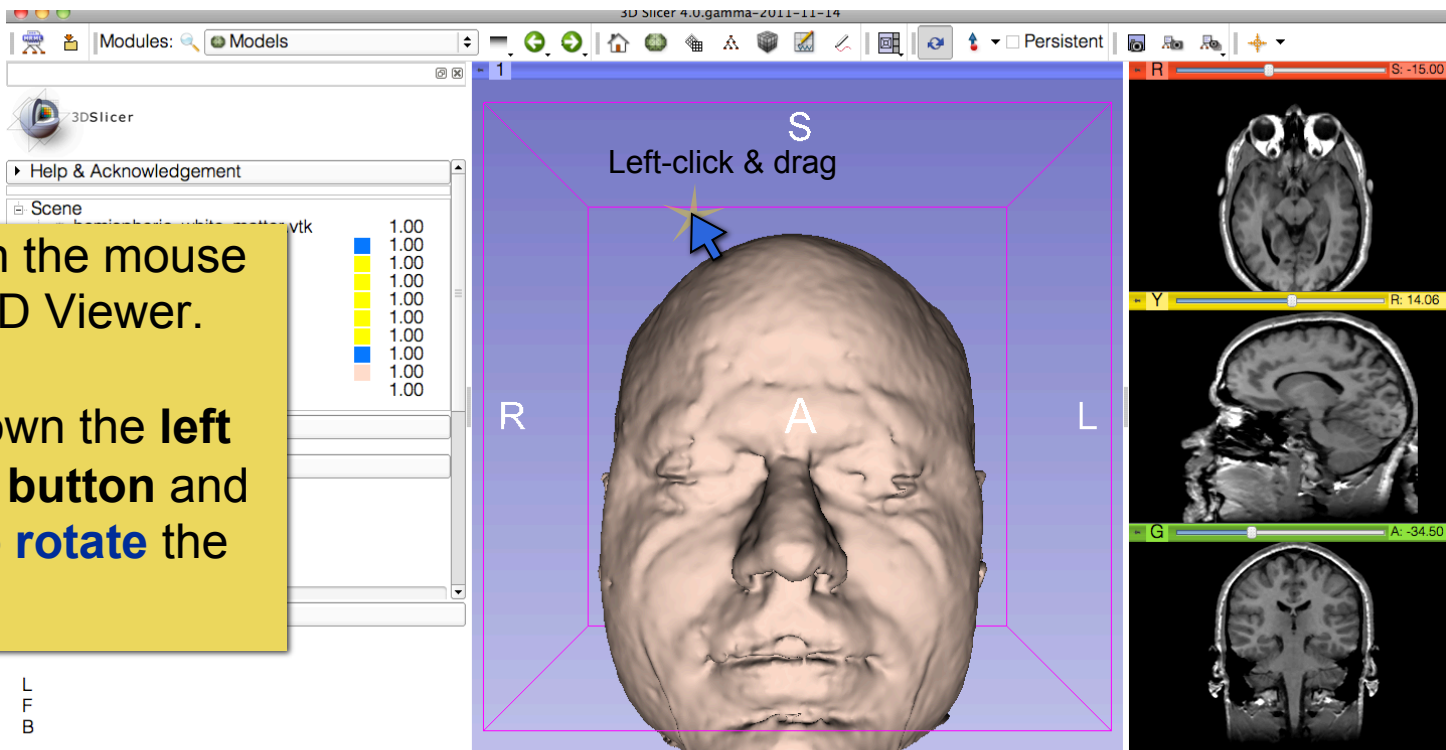




# Slicer4 Minute Tutorial: Basic 3D Interaction

Position the mouse  
in the 3D Viewer.

Hold down the **left  
mouse button** and  
**drag to rotate** the  
model.





# Slicer4 Minute Tutorial: Viewing Slices in the 3D Viewer

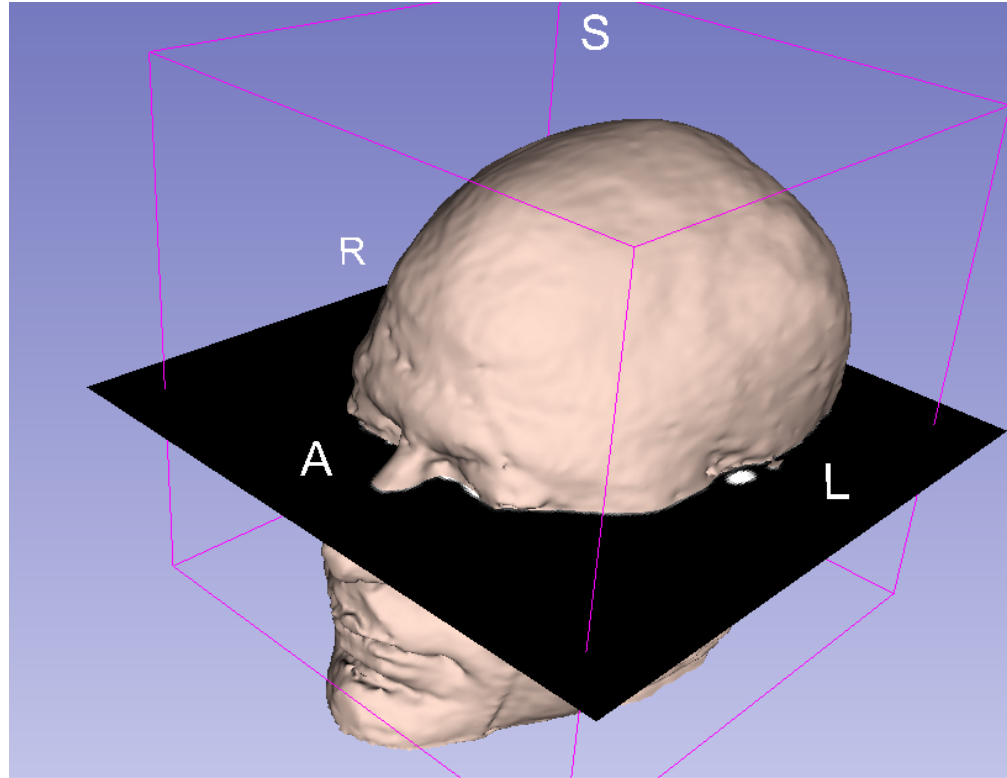
Click on the **Slice Visibility** icon to display the Axial Slice in the 3D Viewer

The screenshot shows the Slicer4 interface. The 'Scene' panel on the left lists 'hemispheric\_white\_matter.vtk' and 'left\_eyeball.vtk'. The '3D Slicer' window displays a 3D model of a head with a purple bounding box. The bounding box is labeled with 'S' (Superior), 'R' (Right), 'L' (Left), and 'A' (Anterior). A yellow callout box points to the 'Slice Visibility' icon in the 'Scene' panel. The '3D Slicer' window shows the 'Axial' slice view with a grayscale color map. The 'Y' and 'G' axes are visible on the right side of the 3D viewer.



## Slicer4 Minute Tutorial: 3D Visualization

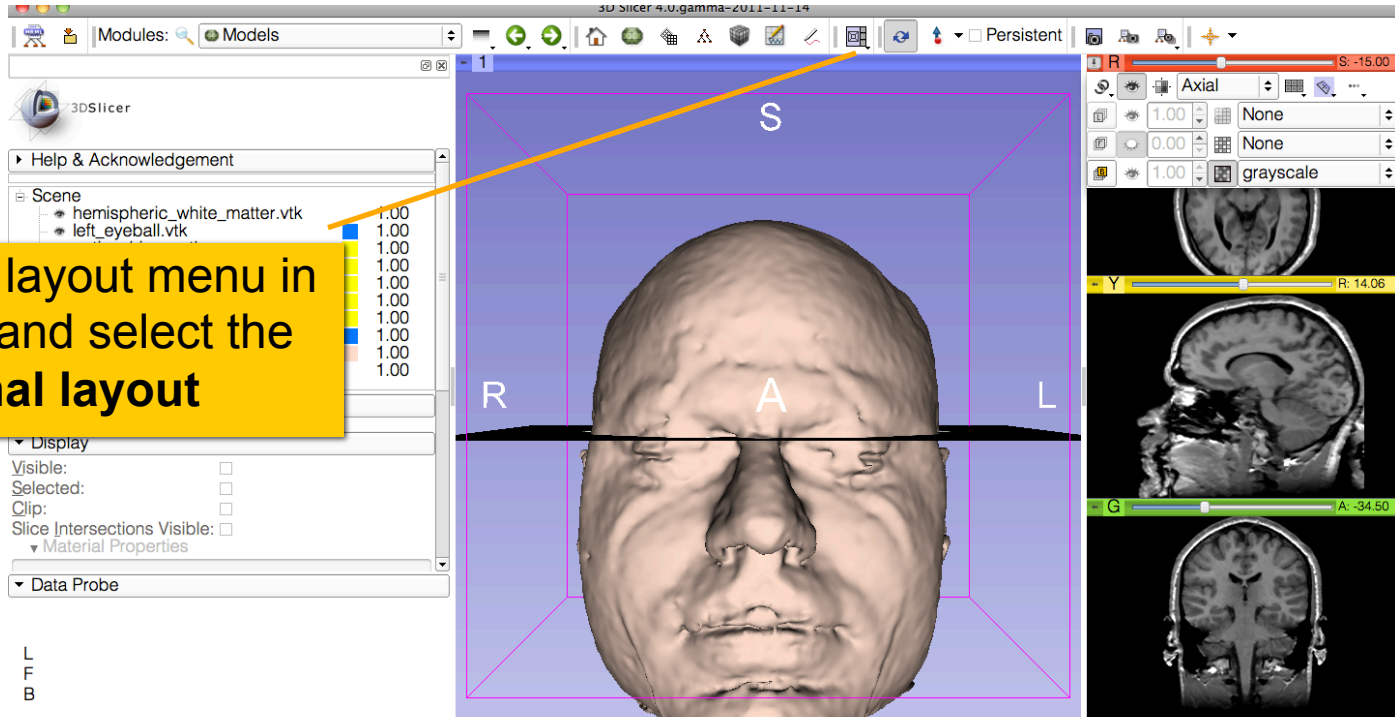
Slicer adds a view of the **Axial slice** in the 3D View.





# Slicer4 Minute Tutorial: Viewing Slices in the 3D Viewer

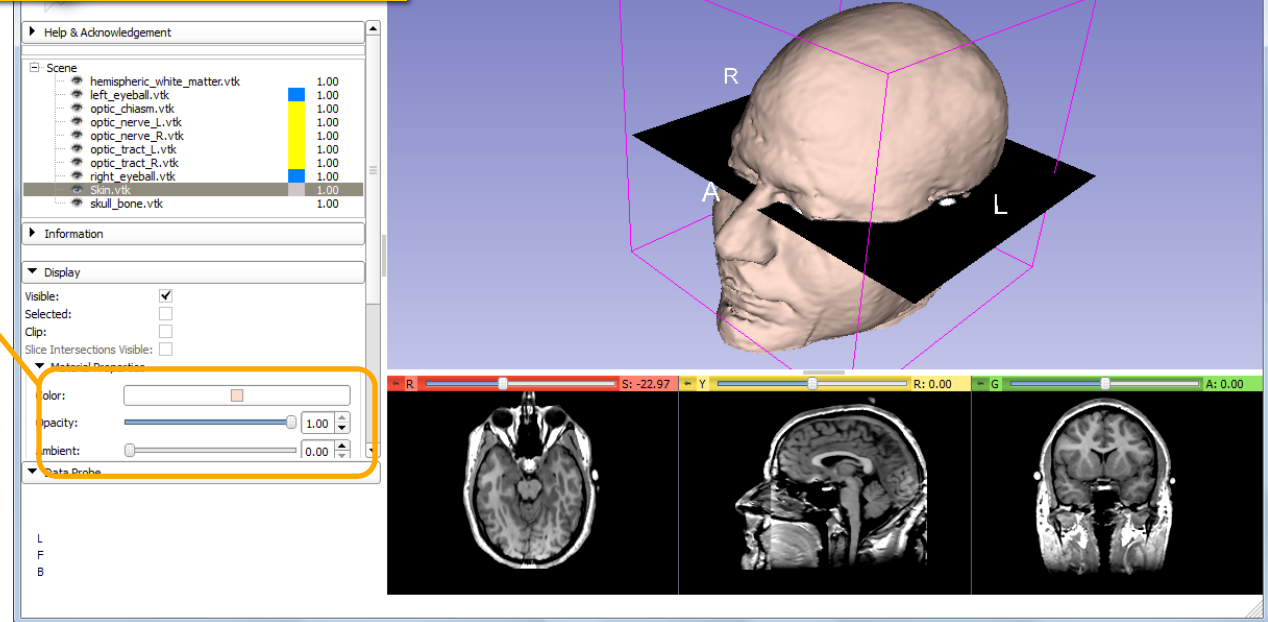
Click on the layout menu in the toolbar, and select the **Conventional layout**





## Slicer4 Minute Tutorial: 3D Visualization

Select the **Skin.vtk**  
Change the opacity of the model from  
**1.0 to 0.0**.

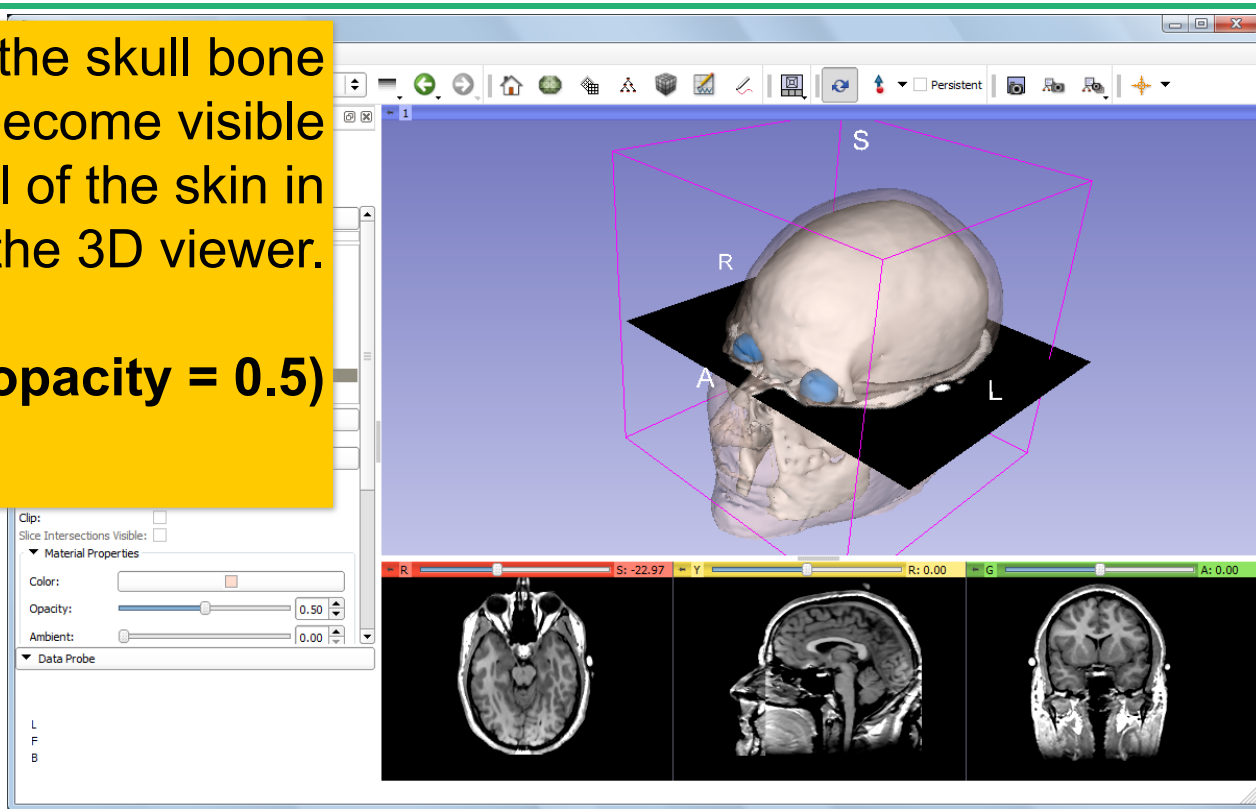




## Slicer4 Minute Tutorial: 3D Visualization

The model of the skull bone and eyeballs become visible through the model of the skin in the 3D viewer.

**(skin model opacity = 0.5)**



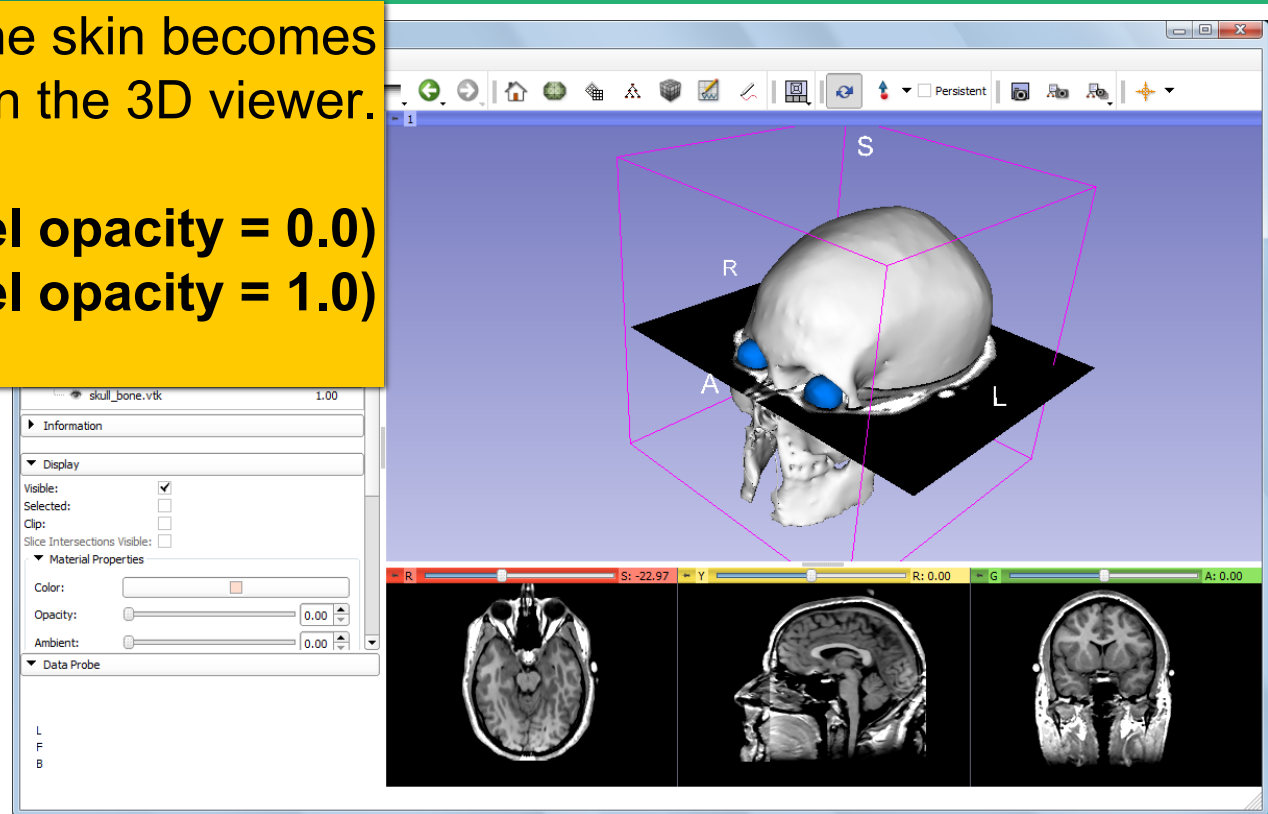




## Slicer4 Minute Tutorial: 3D Visualization

The model of the skin becomes invisible in the 3D viewer.

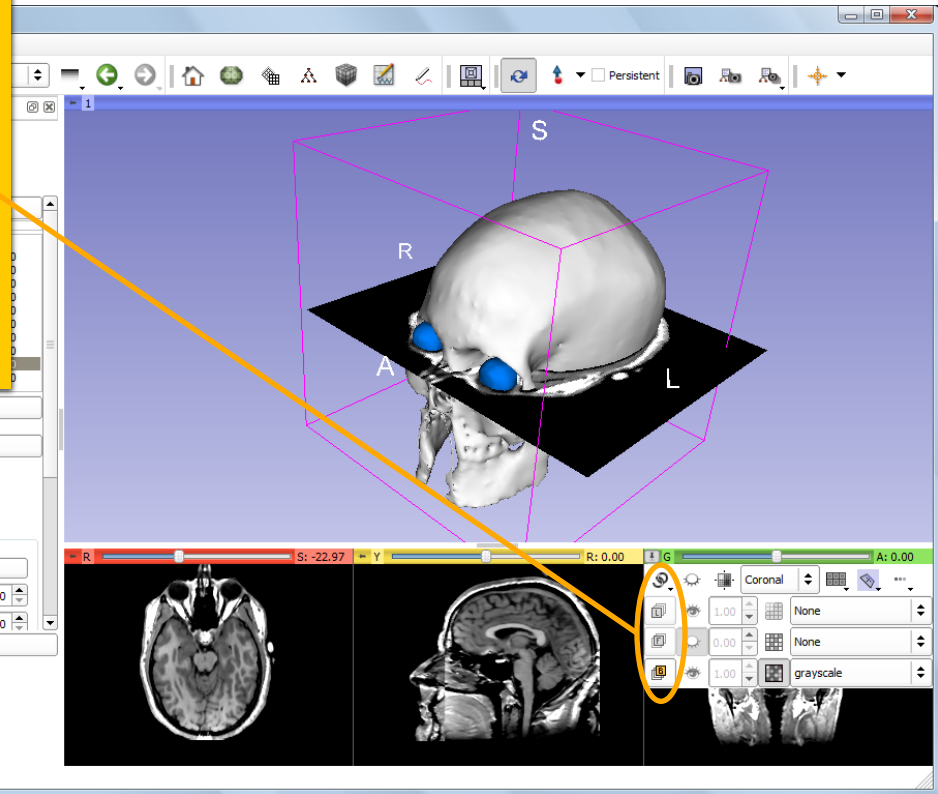
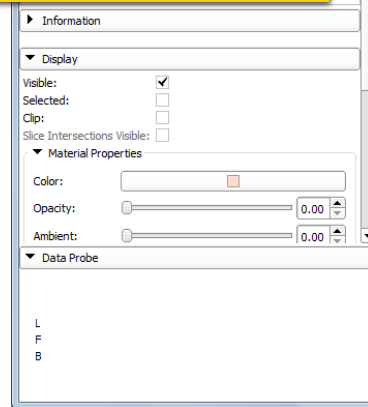
**(skin model opacity = 0.0)**  
**(skull model opacity = 1.0)**





## Slicer4 Minute Tutorial: 3D Visualization

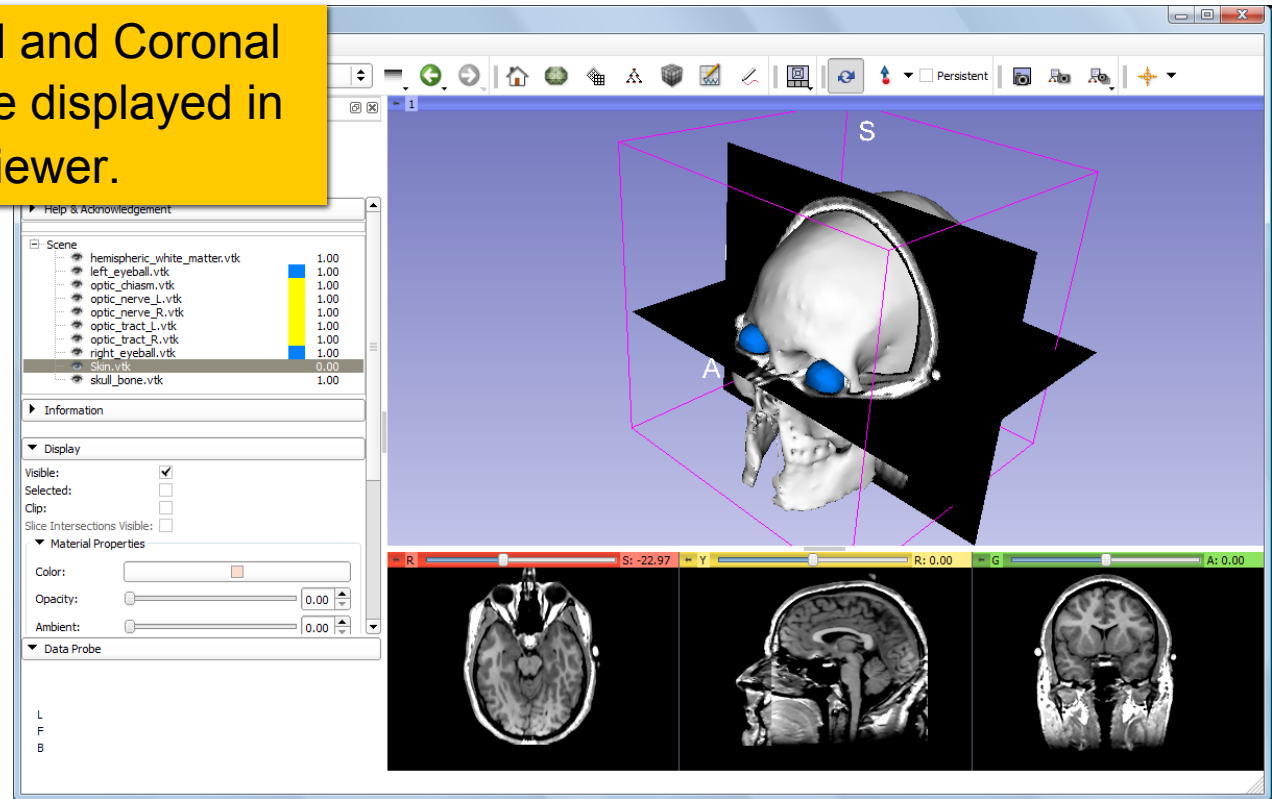
Click on the **Slice Visibility** icon in the **Green Slice Viewer** to display the Coronal Slice in the 3D Viewer.





## Slicer4 Minute Tutorial: 3D Visualization

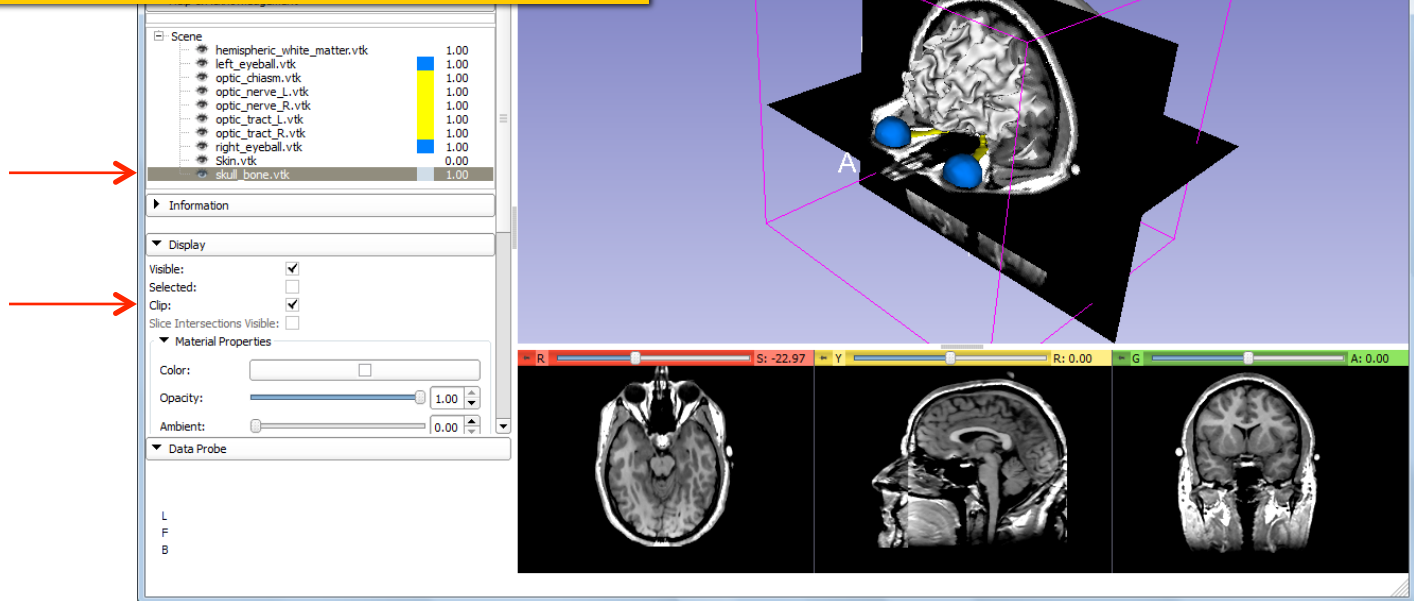
The Axial and Coronal Slices are displayed in the 3D Viewer.





## Slicer4 Minute Tutorial: 3D Visualization

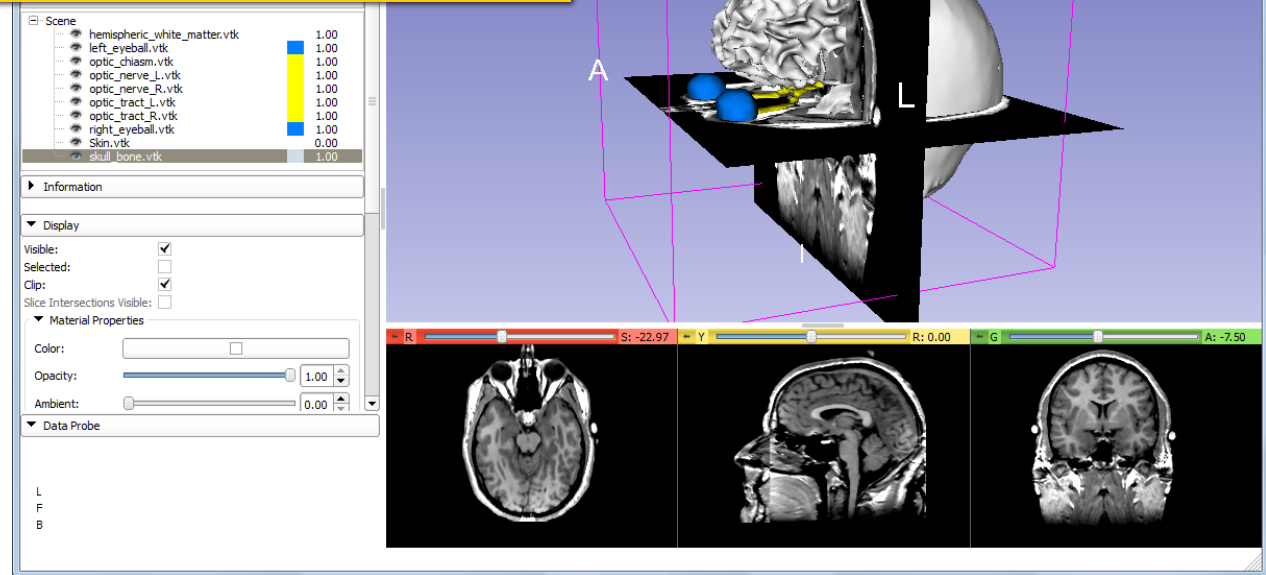
Select the 3D model **skull\_bone.vtk** in the Model Hierarchy and turn on the **Clipping** option.





## Slicer4 Minute Tutorial: 3D Visualization

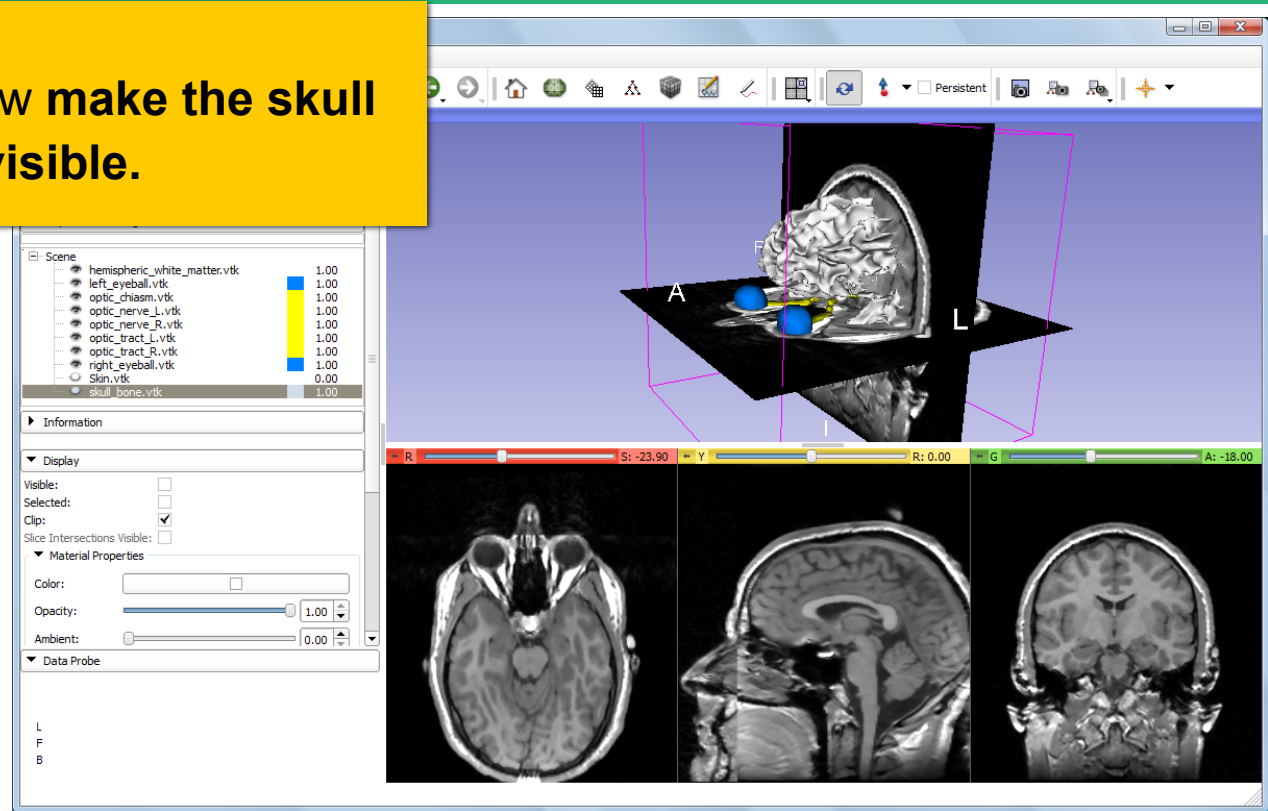
Browse through the **coronal slices** to expose the 3D model of the **white matter**, and the left and right **optic nerves**.





## Slicer4 Minute Tutorial: 3D Visualization

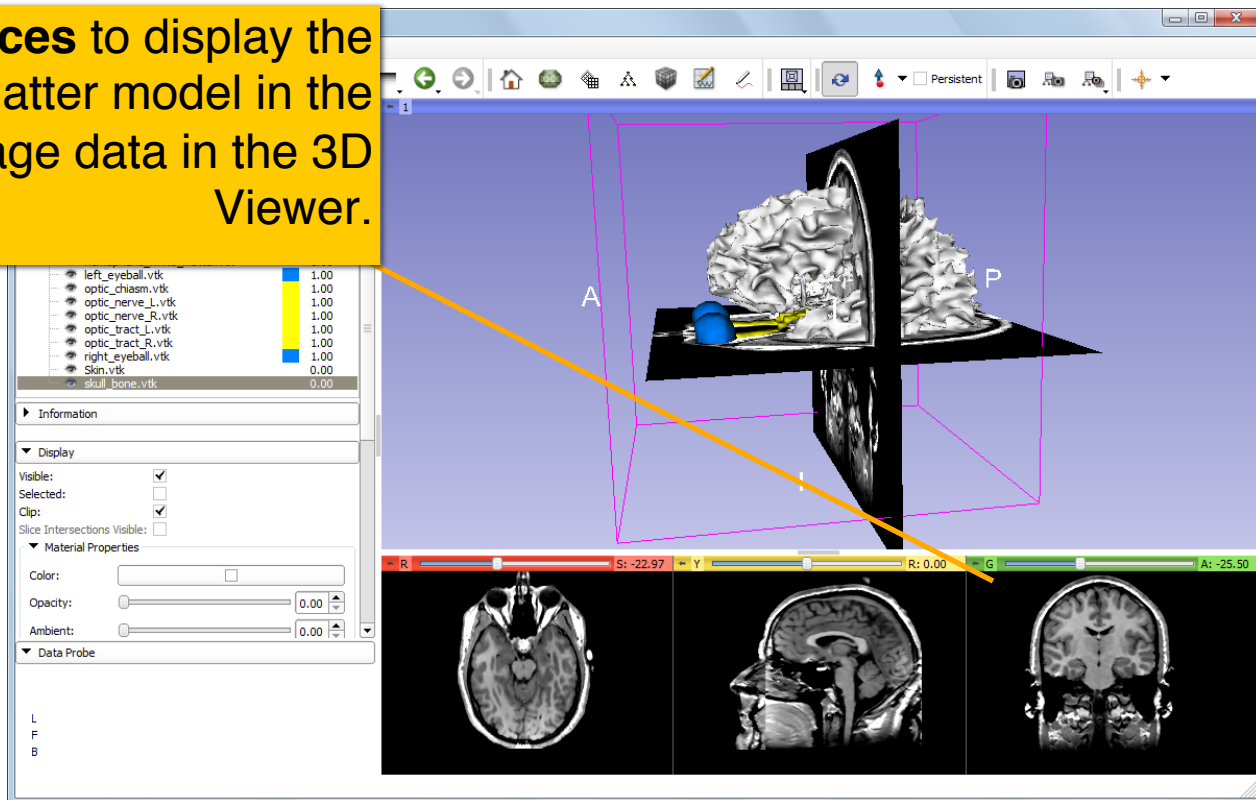
**Now make the skull invisible.**





## Slicer4 Minute Tutorial: 3D Visualization

Scroll the **Coronal Slices** to display the hemispheric white matter model in the context of the image data in the 3D Viewer.

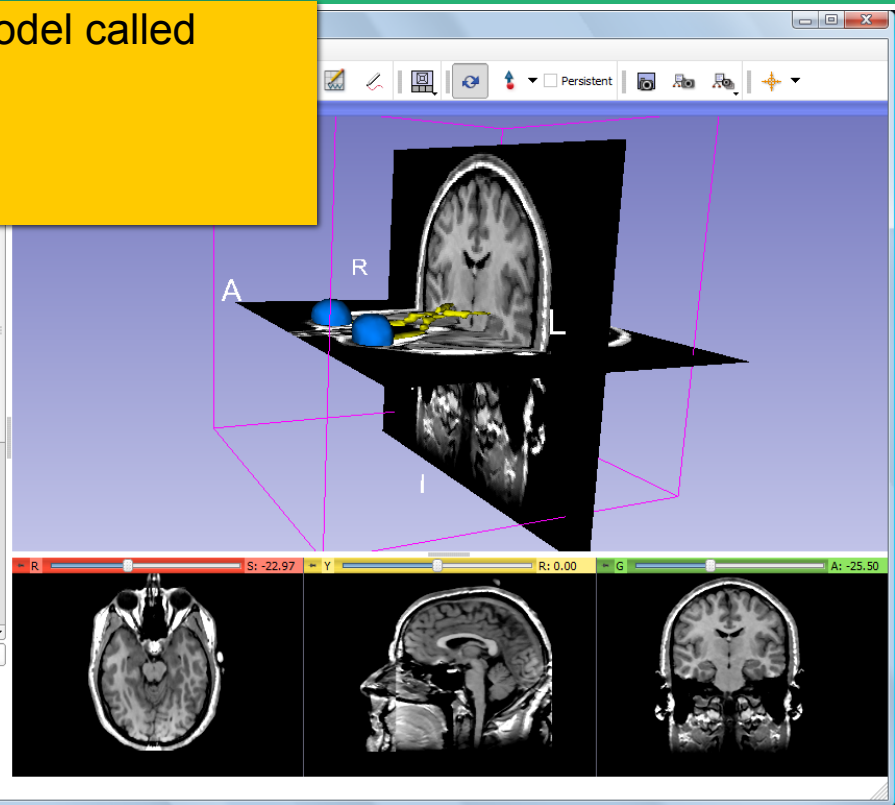
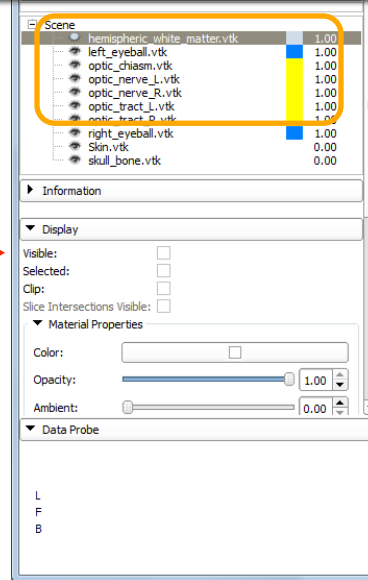




## Slicer4 Minute Tutorial: 3D Visualization

Select the hemispheric white matter model called **hemispheric\_white\_matter.vtk**

Turn off its **visibility**.

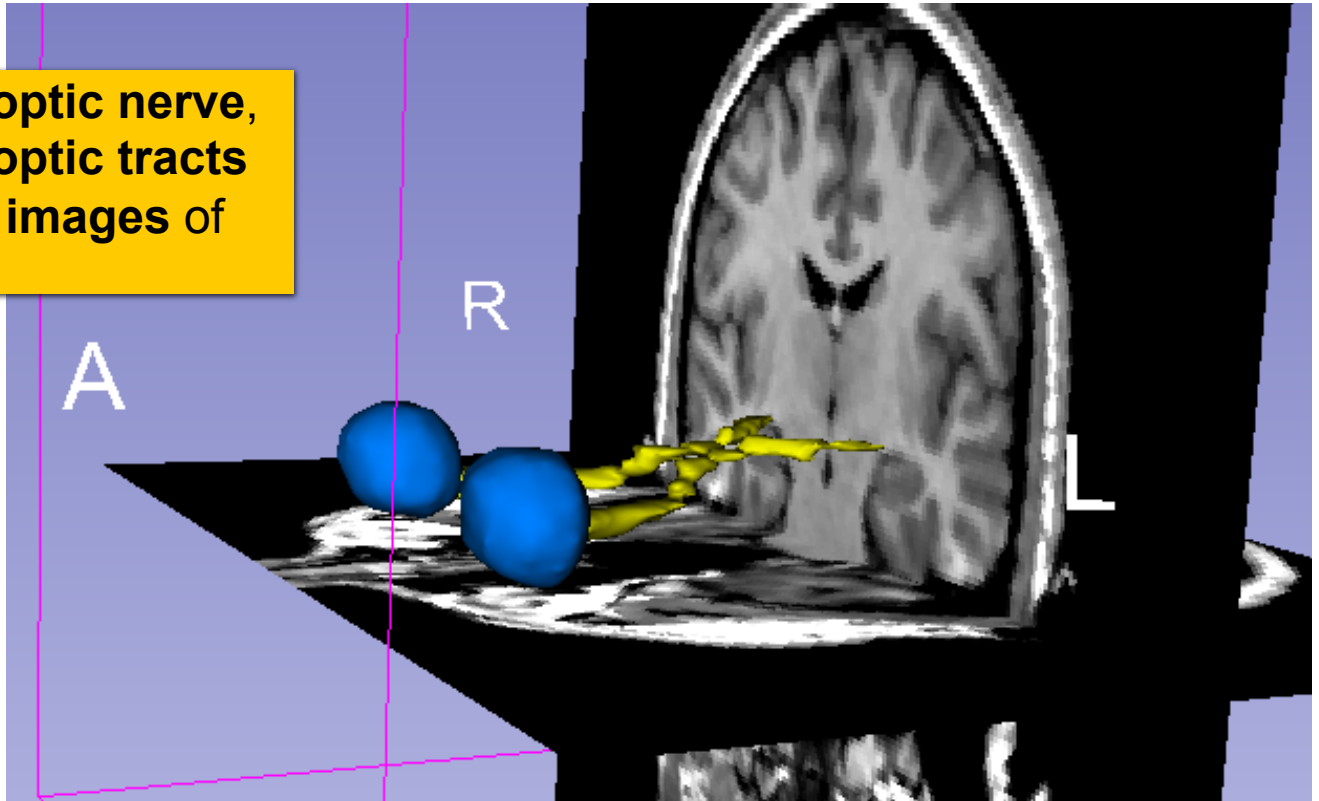






## Slicer4 Minute Tutorial: 3D Visualization

Slicer displays the **optic nerve**, **optic chiasm** and **optic tracts** overlaid on the **MR images** of the brain.

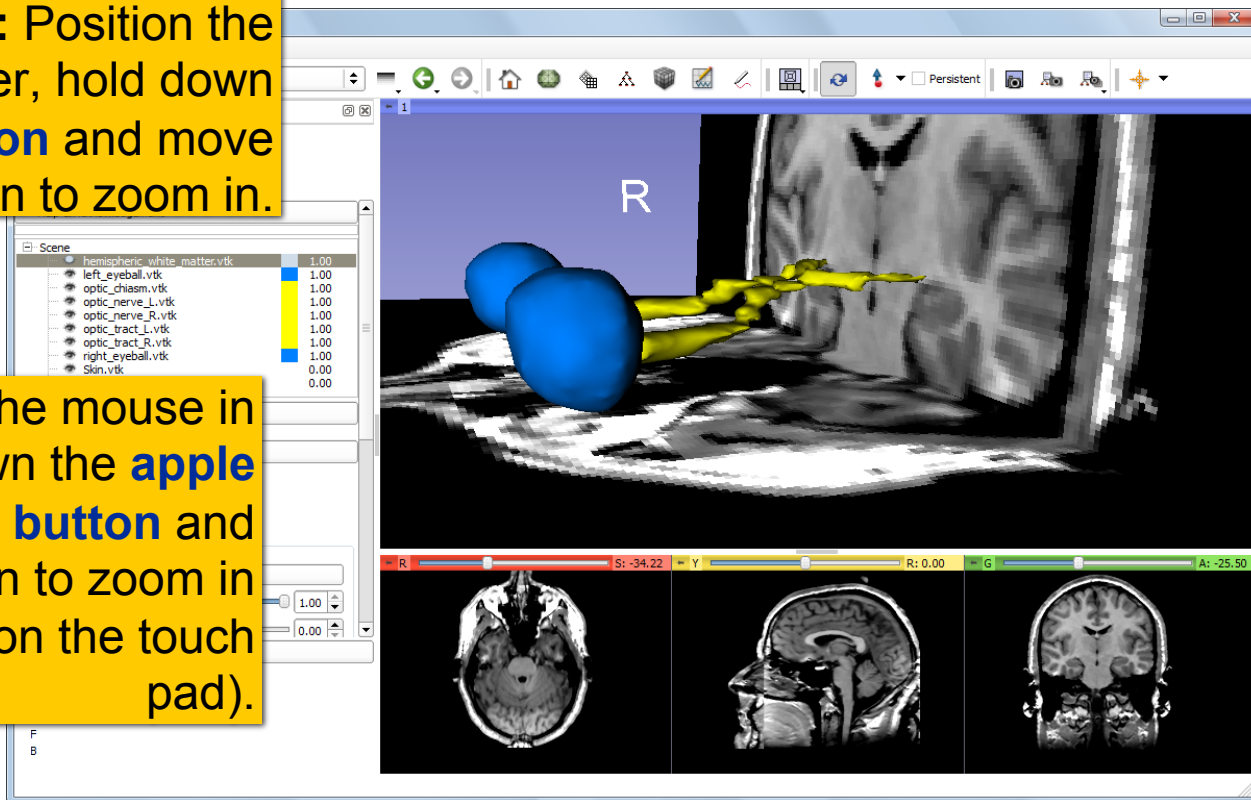




## Slicer4 Minute Tutorial: 3D Visualization: Zoom the view

**Windows/Linux users:** Position the mouse in the 3D Viewer, hold down the **right mouse button** and move the mouse down to zoom in.

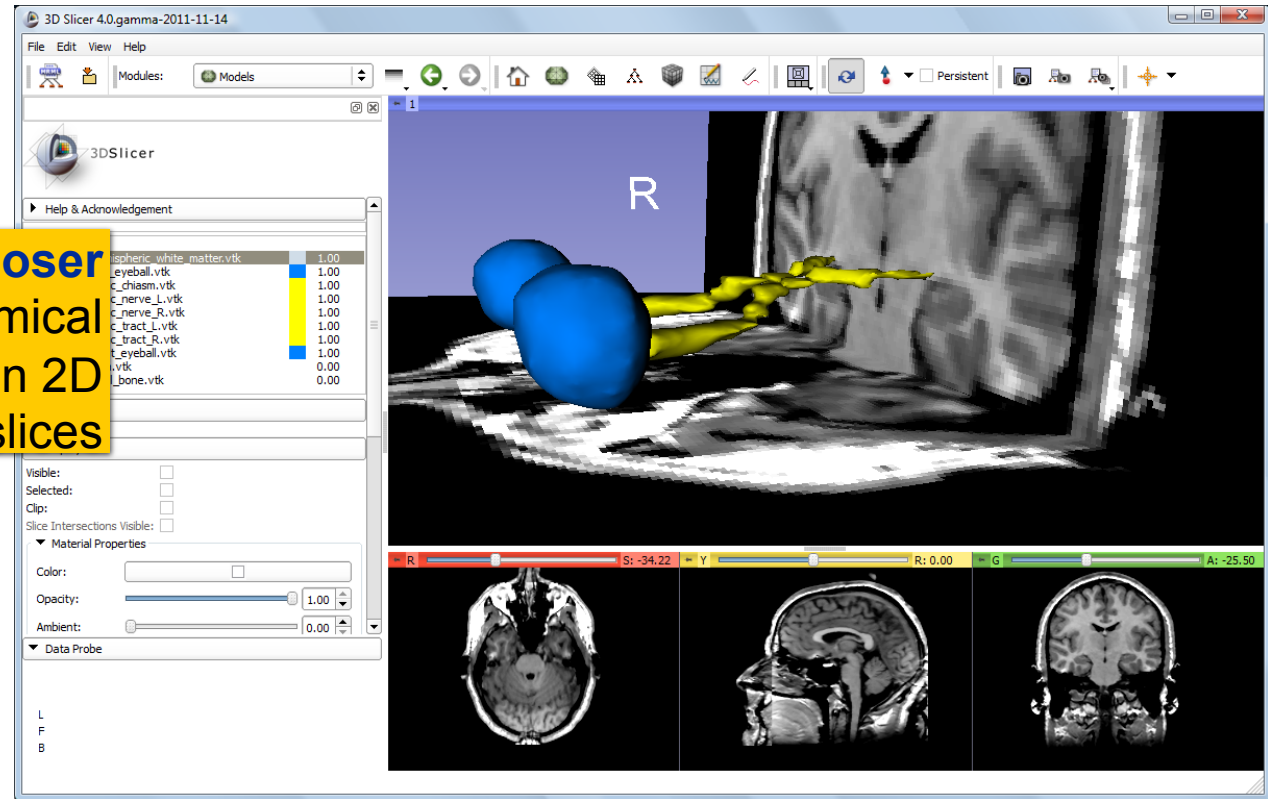
**Mac users:** Position the mouse in the 3D Viewer, hold down the **apple button and the mouse button** and move the mouse down to zoom in (or use two fingers on the touch pad).





# Slicer4 Minute Tutorial: 3D Visualization: Zoom the view

Slicer displays a **closer view** of 3D anatomical structures overlaid on 2D MR slices



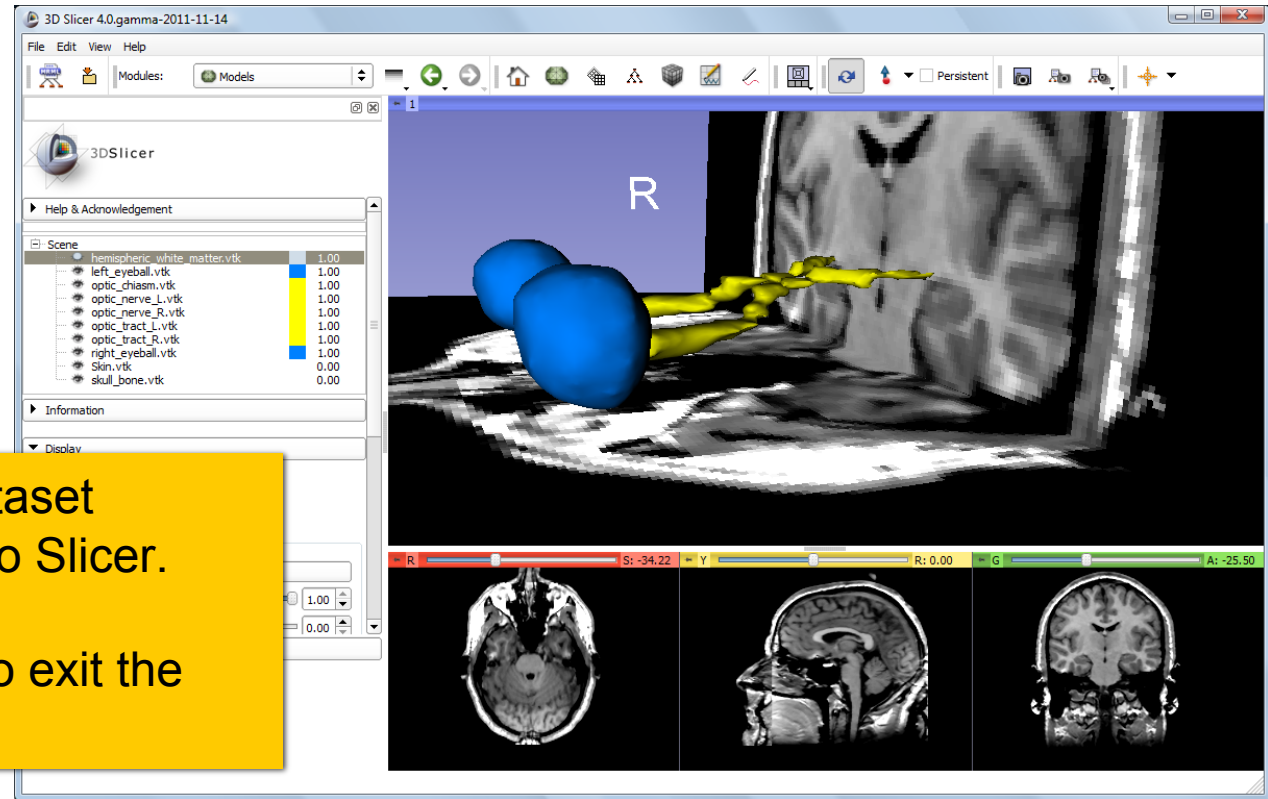


# Close the existing scene and all its data

Select **File->Close Scene**

This removes any dataset previously loaded into Slicer.

Select **Slicer->Quit** to exit the software





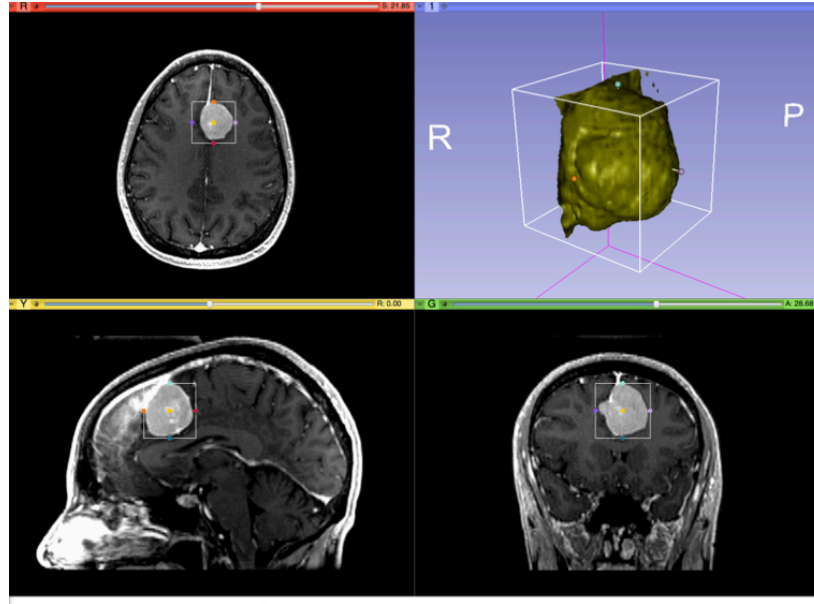
## Part I: Summary

---

This first part of the tutorial has demonstrated:

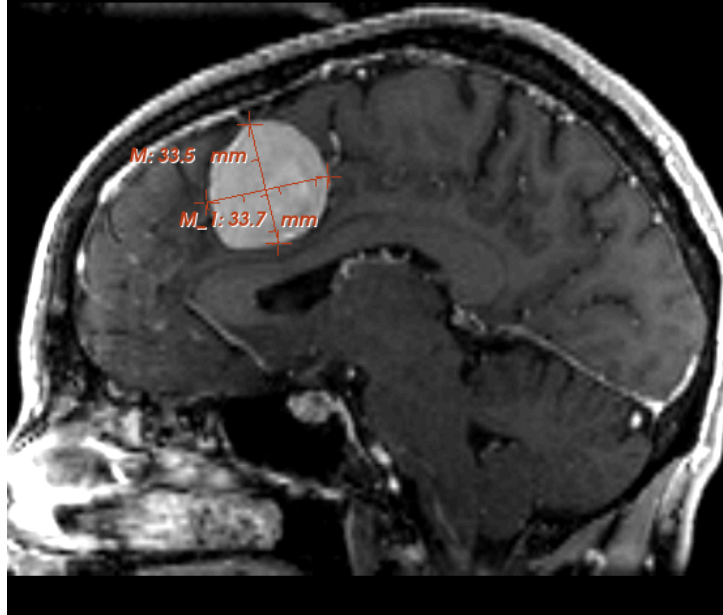
- Basic description of the Slicer4 Application Interface
- How to load a scene containing volumes and models
- How to visualize these different datasets together

Next, we will use these building blocks to perform image analysis and visualize quantitative results.



## Part II: Analyzing Small Volumetric Changes

Sonia Pujol, PhD  
 Kilian M Pohl, PhD  
 Andriy Fedorov, PhD  
 Ender Konukoglu, PhD  
 Ron Kikinis, MD

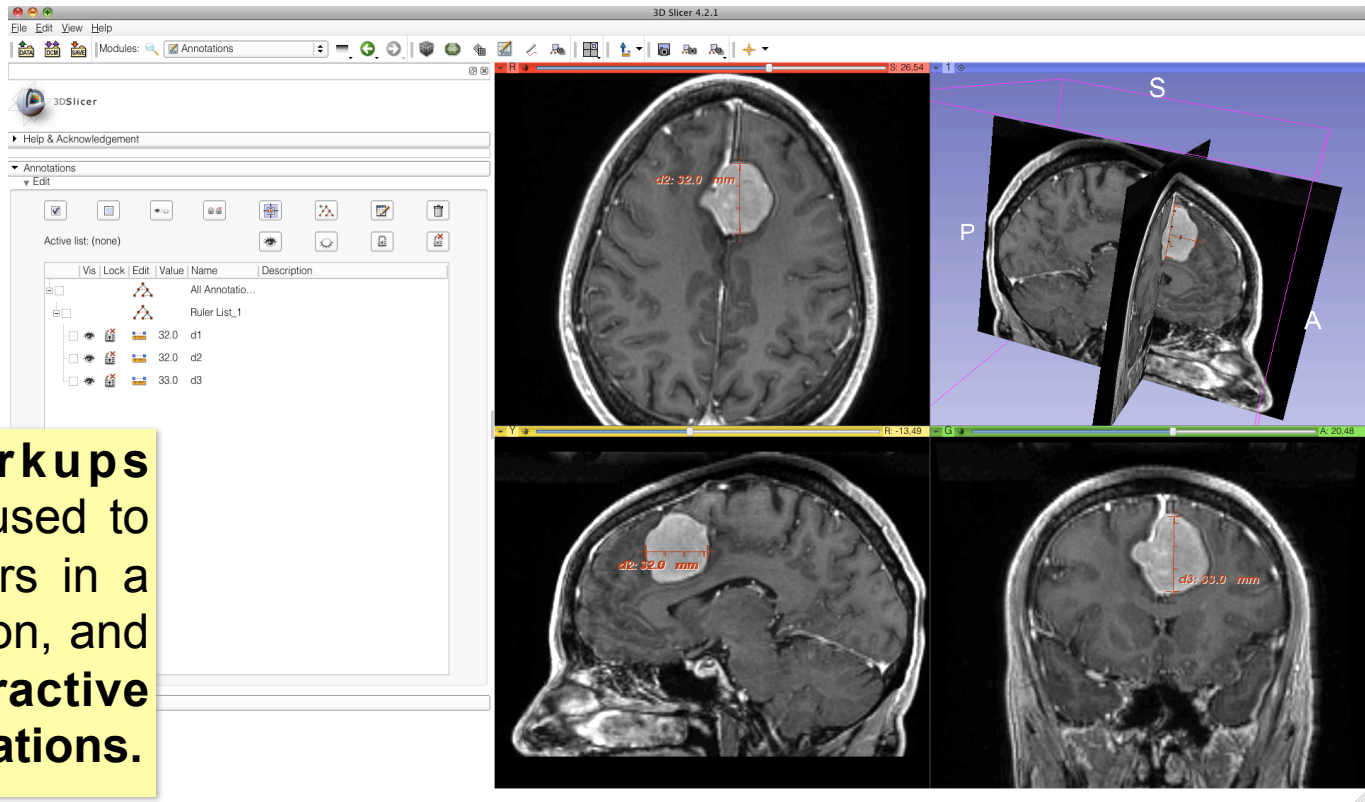


- Conventional anatomic imaging using CT or MRI are often used to evaluate tumor size and shape
- Most clinical trials that evaluate new chemotherapeutic drugs use changes in uni-dimensional or bi-dimensional measurements to assess response (e.g. RECIST)
- Slicer has several tools for applying RECIST methodologies



# Conventional measures of tumor response

3D Slicer **Markups** module can be used to measure diameters in a tumor cross section, and to provide **interactive numerical annotations**.

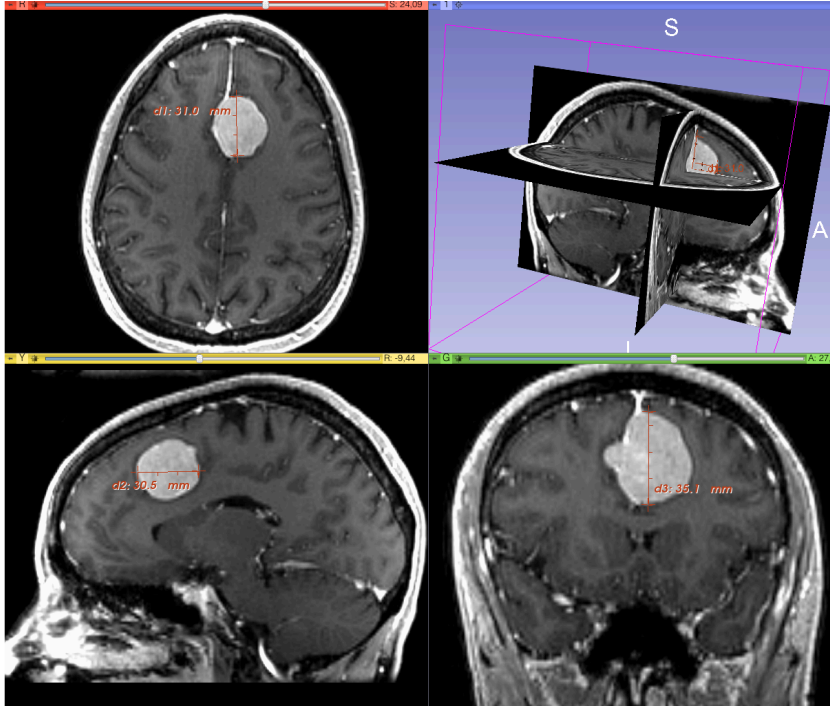




## Clinical case: baseline scan

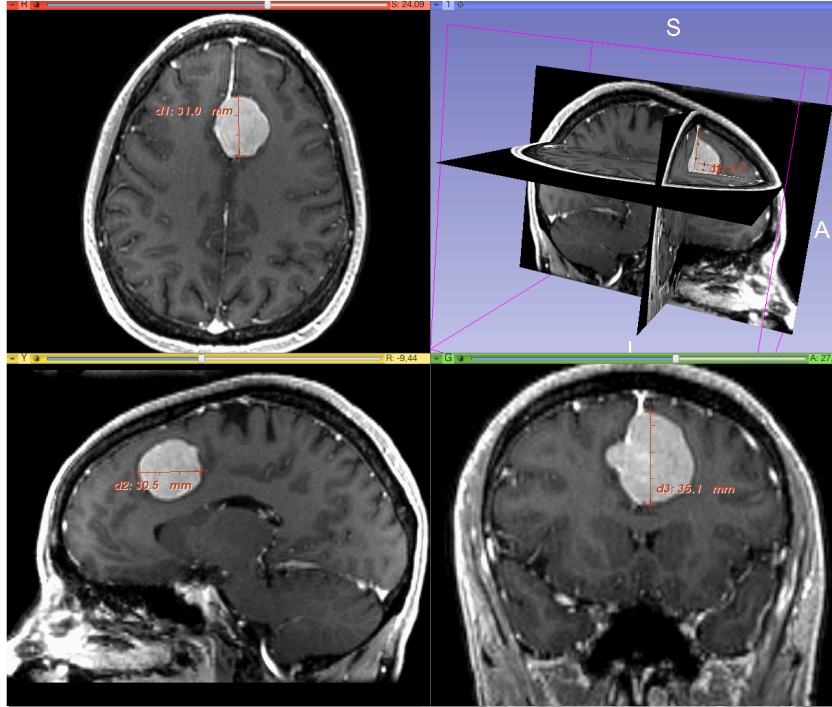
### Baseline radiologist's clinical impression:

- large falcine lesion is identified.
- measures 3.10 cm anteroposteriorly and 3.51 cm in height.
- enhances moderately on post gadolinium imaging.





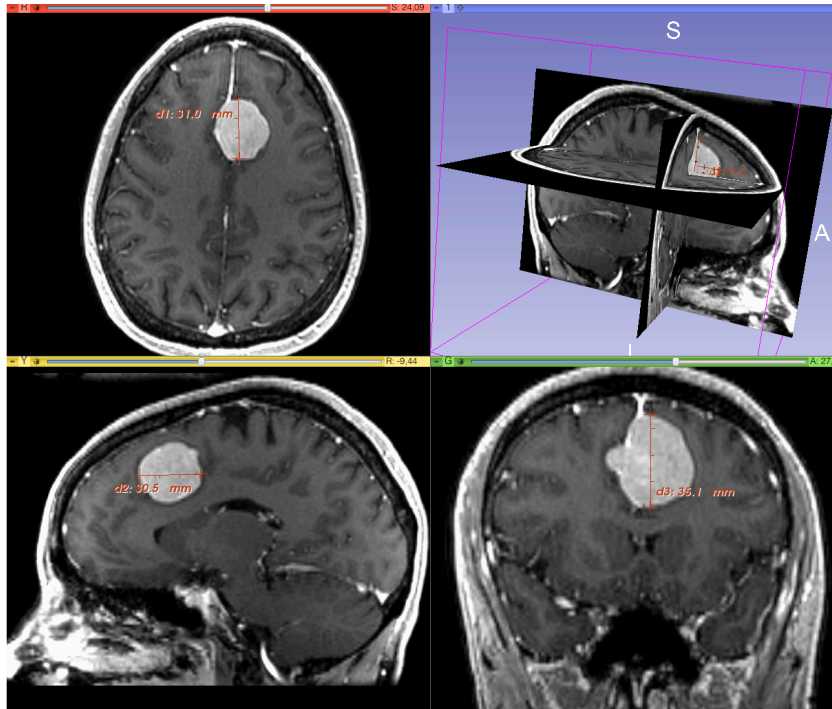
## Clinical Case: follow-up scan



### Follow-up radiologist's clinical impression:

- left frontal lobe mass appears unchanged on all series.
- measures 3.3 x 3.2 cm in maximum dimension.
- enhances moderately on post gadolinium imaging.

## Clinical Case: follow-up scan



### Follow-up radiologist's clinical impression:

- left frontal lobe mass appears unchanged on all series.
- measures 3.3 x 3.2 cm in maximum dimension.
- enhances moderately on post gadolinium imaging.

→ How has the tumor changed?



# ChangeTracker: rationale for new approaches

---

More accurate and precise methods for understanding volume changes may be useful when:

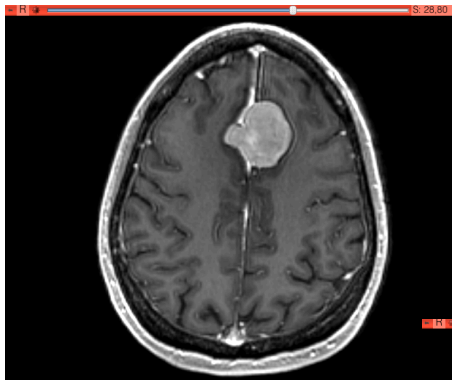
- **benign tumor change** is being monitored, or
- where **small changes may be clinically significant** but difficult to assess with RECIST



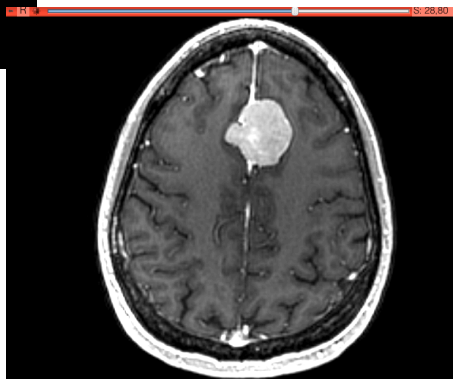
# Goal of the tutorial

---

MR Scan1 June 2006



MR Scan2 June 2007



(Voxel dimension: 0.94mm x 0.94mm x 1.20mm, FOV: 240mm, Matrix: 256 x 256)

The following section will guide you step-by-step through the computation of small volumetric changes in a slow growing tumor.

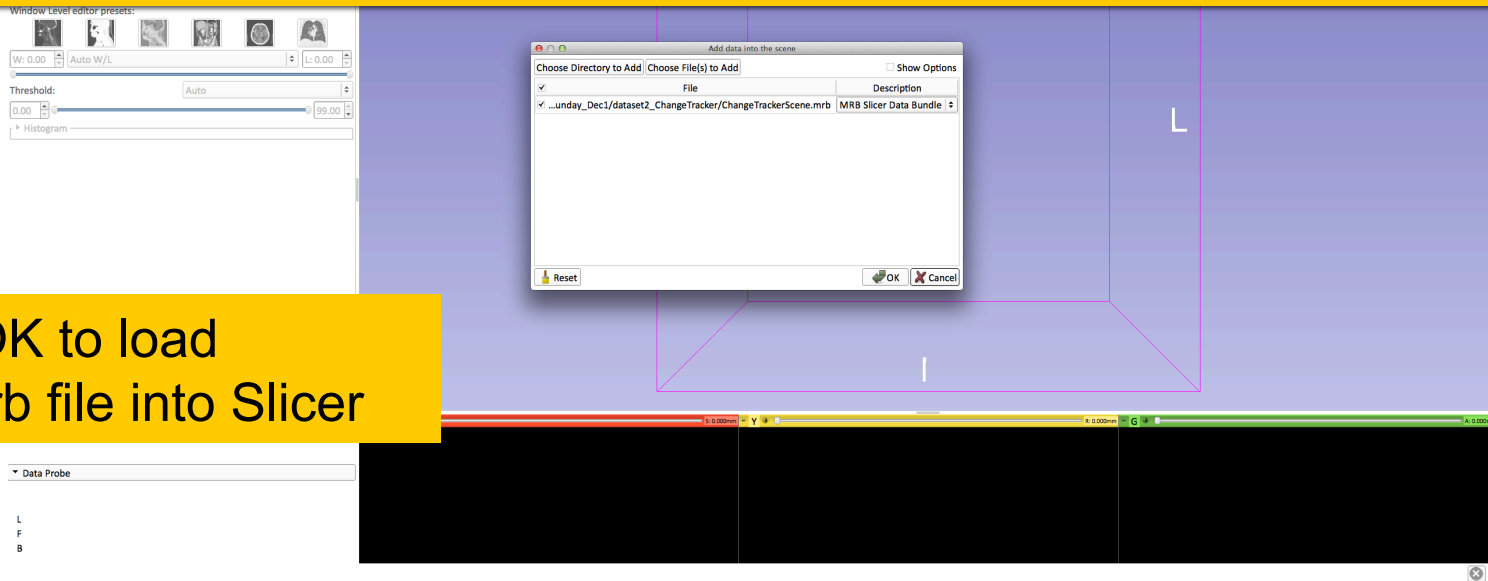
This tutorial is built upon two scans (Axial 3D SPGR T1 post Gadolinium) of a patient with meningioma, and uses the Change Tracker module of Slicer.



# ChangeTracker: Load the dataset

Drag and drop the file **ChangeTrackerScene.mrb** located in

**C:\3DSlicerData\_RSNA2013\QuantitativeImaging\_Sunday\_Dec1\dataset2\_ChangeTracker**

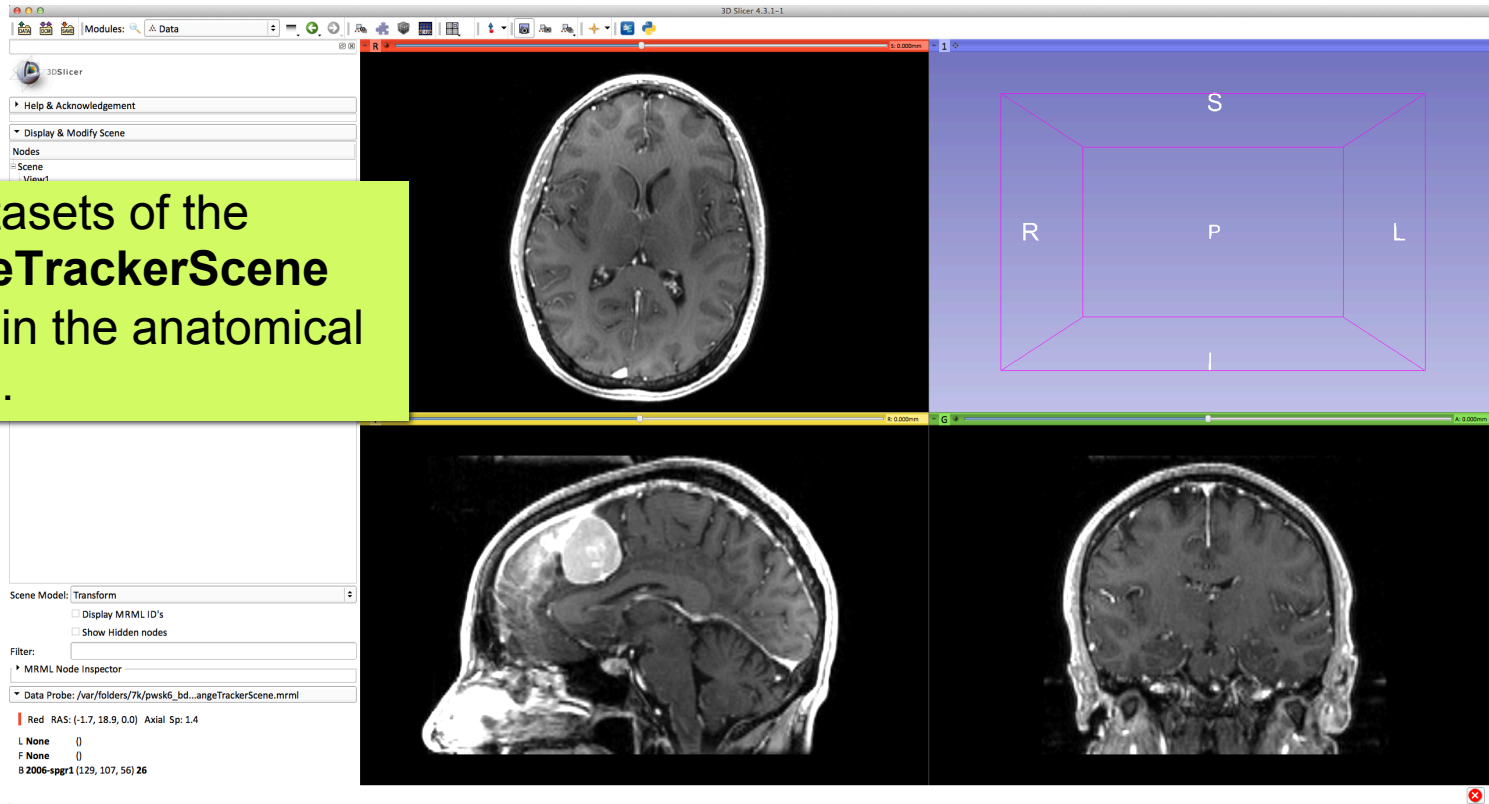


Click OK to load  
the .mrb file into Slicer



# Loading the data

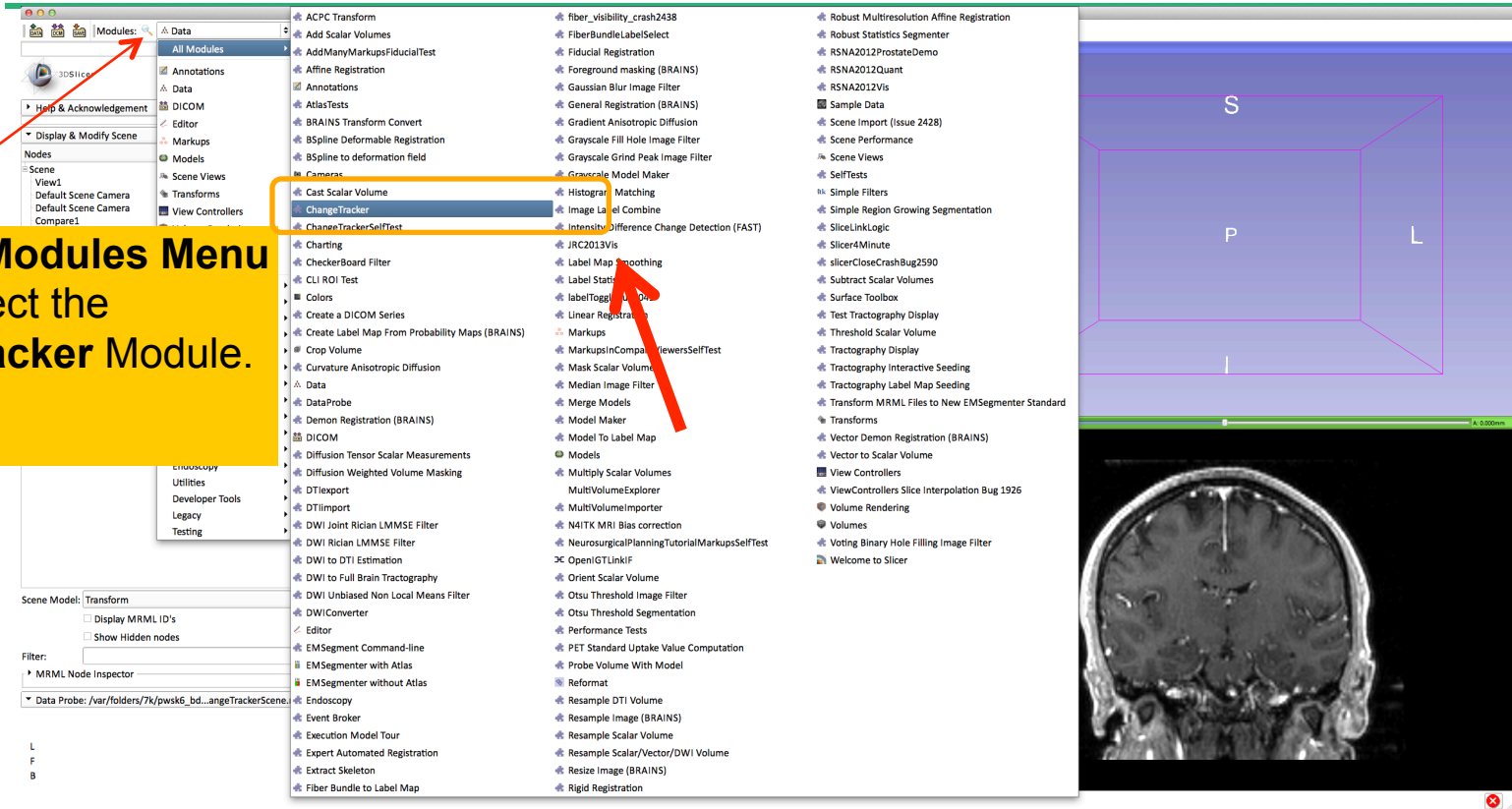
The datasets of the **ChangeTrackerScene** appear in the anatomical viewers.





# ChangeTracker: exploring small volumetric changes

Using the **Modules Menu** button, select the **ChangeTracker** Module.







## ChangeTracker: a note about the Workflow wizard

The **Workflow Wizard** guides the user through a sequence of steps and has the following components:

- the Step Panel
- the User Panel
- the Navigation Panel

Step Panel--

User Panel--

Navigation Panel--

3DSlicer

► Help & Acknowledgement

▼ 1. Select input scans

Select the baseline and follow-up scans to be compared.

Load test data

Baseline scan: Select a Volume

Followup scan: Select a Volume

◀ ▶

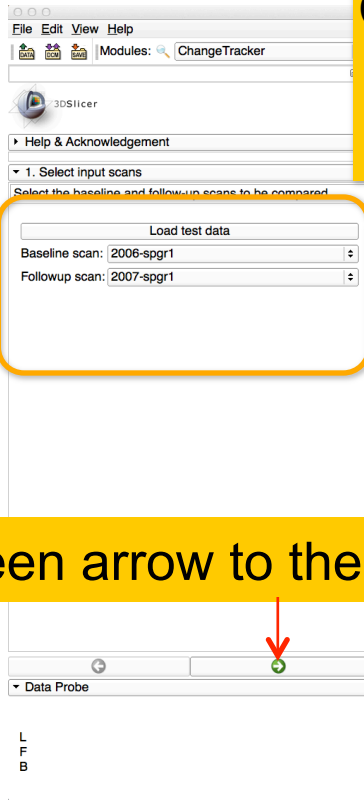
▼ Data Probe



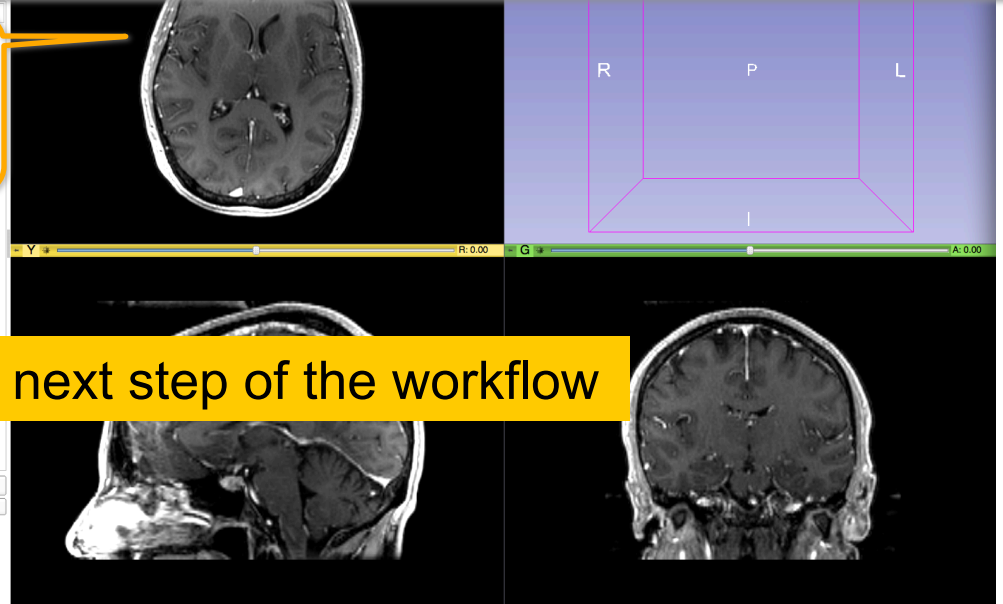
# Step1: Select input scans

Click to expand the tab '1.Select input scans'

- Set the **Baseline scan** to 2006-spgr1
- Set the **Follow up scan** to 2007-spgr1



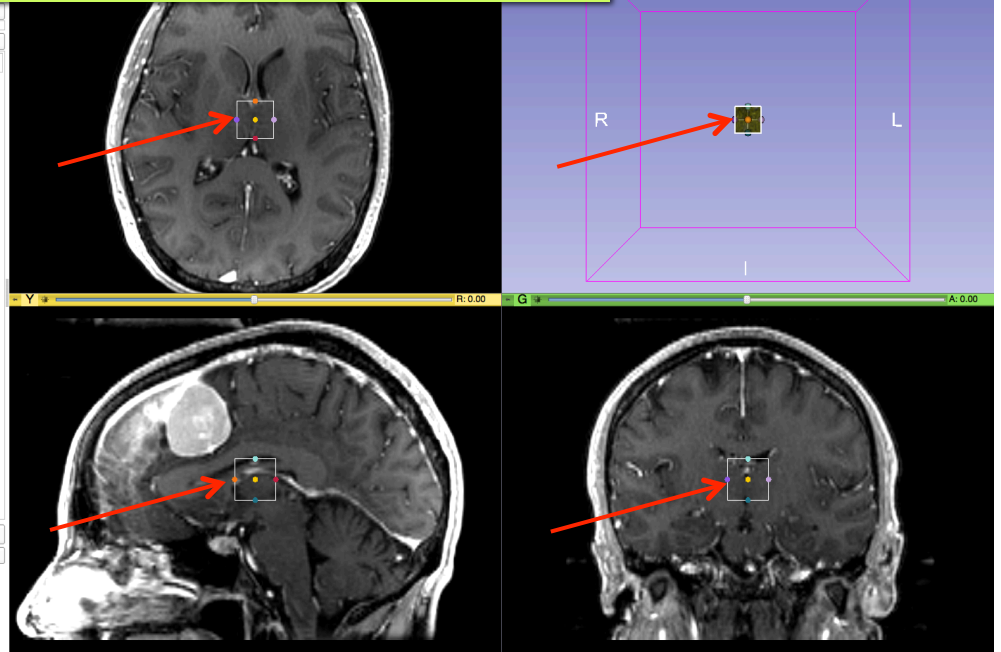
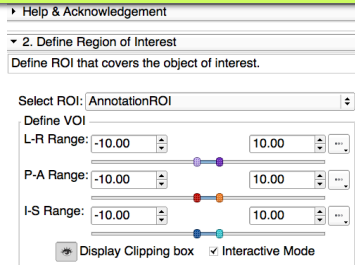
Click on the green arrow to the next step of the workflow





## Step2: Define Region of interest

A **Volume of Interest (VOI) Box Widget** appears in the anatomical viewers, and in the 3D viewer.



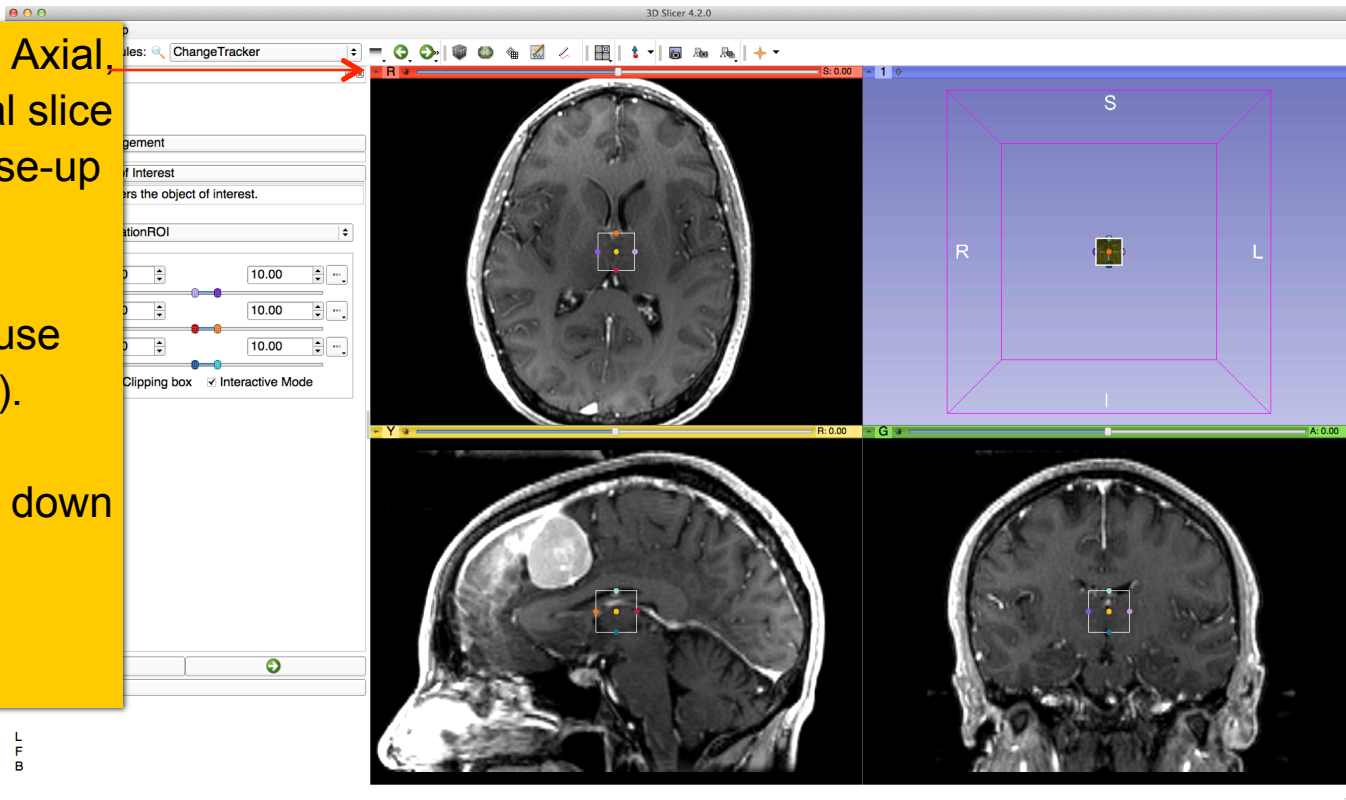


## Step2: Define Region of interest

Browse through the Axial, Sagittal and Coronal slice viewers to get a close-up view of the tumor

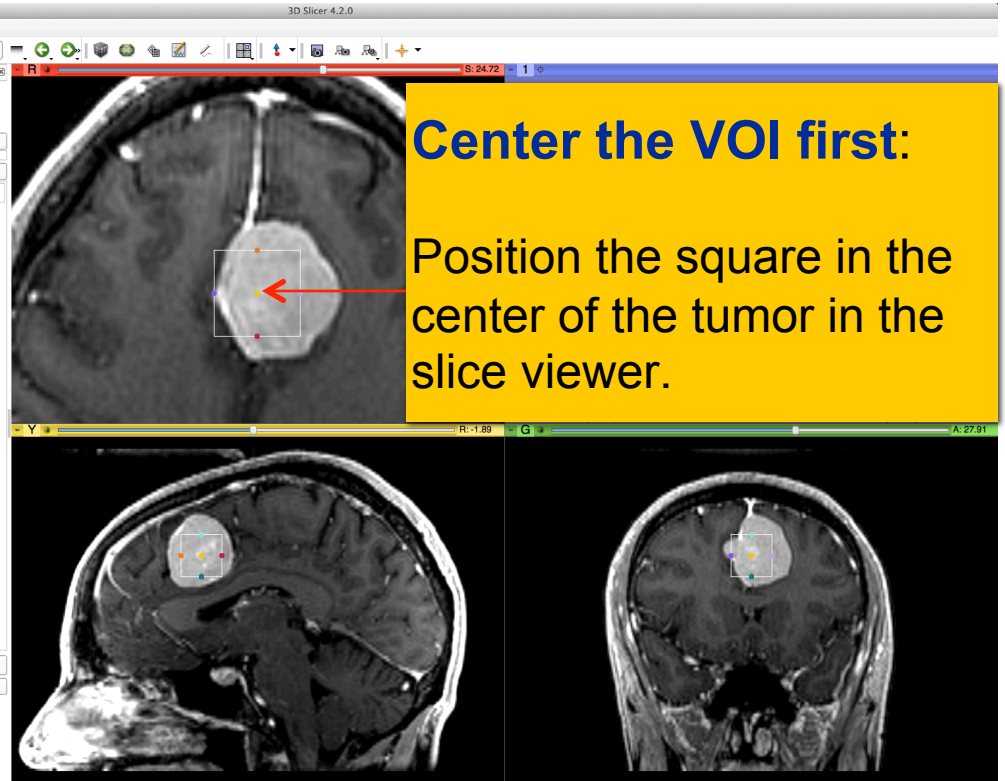
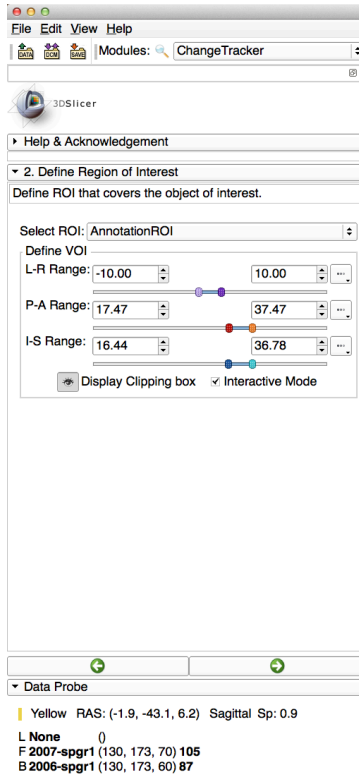
**Zoom in** (Right mouse down and push/pull).

**Pan** (Middle mouse down and move)



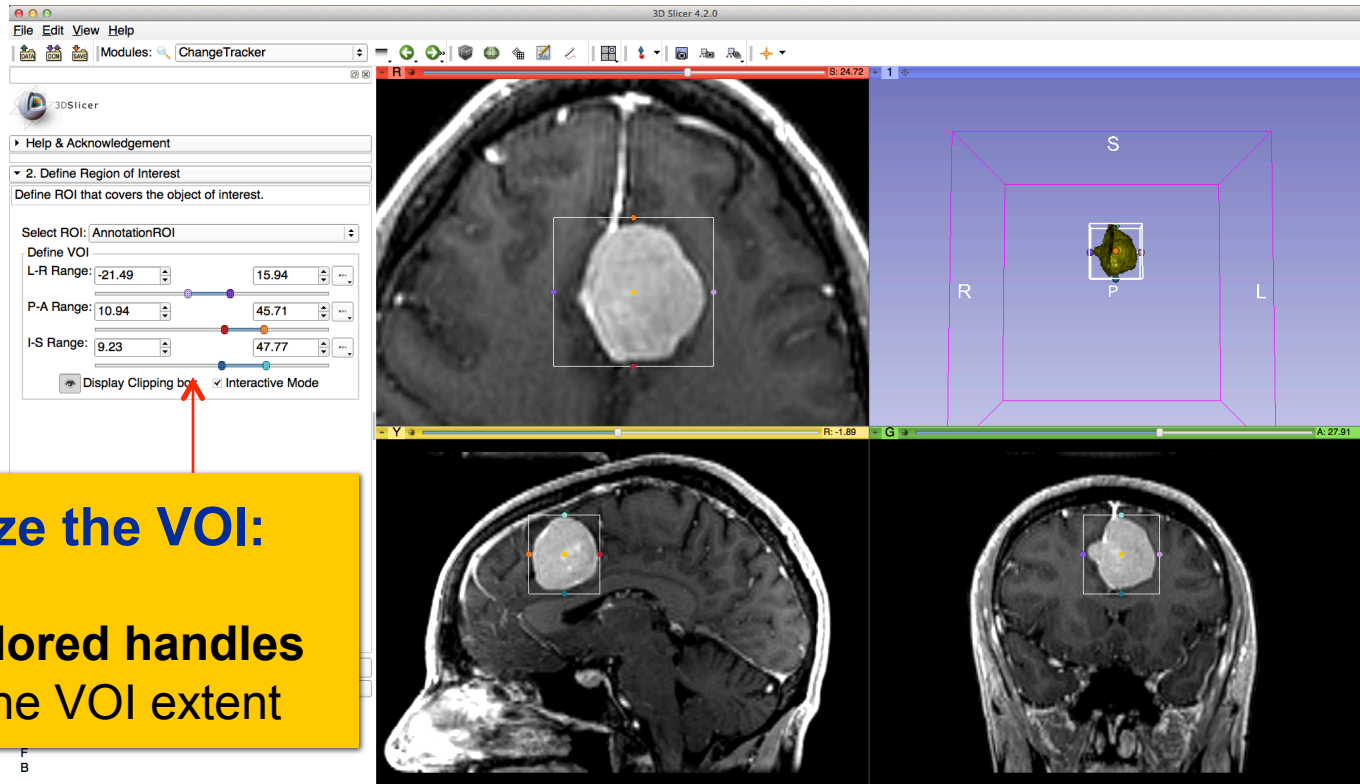


## Step2: Define Region of interest





## Step2: Define Region of interest



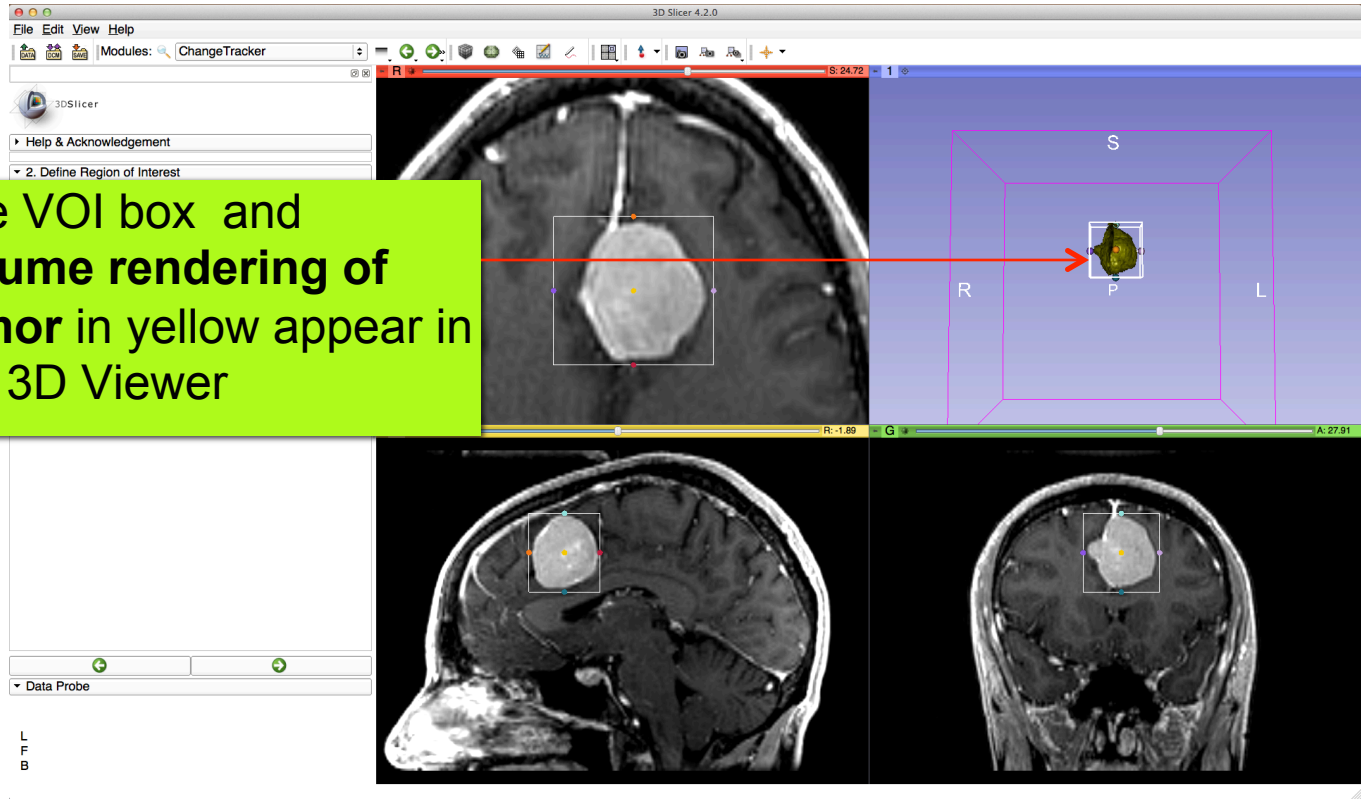
**Next, resize the VOI:**

**Use the colored handles  
to change the VOI extent**



## Step2: Define Region of interest

The VOI box and volume rendering of tumor in yellow appear in the 3D Viewer





## Step2: Define Region of interest

3D Slicer 4.2.0

File Edit View Help

Modules: ChangeTracker

3DSlicer

Help & Acknowledgement

2. Define Region of Interest

Define ROI that covers the object of interest.

Select ROI: AnnotationROI

Define VOI

L-R Range: -20.67 14.46

P-A Range: 10.94 45.05

I-S Range: 9.23 47.77

☐ Display Clipping box ☒ Interactive Mode

VOI Widget range sliders are color-coded to match VOI box Widget handles in 3D Viewer

Fine-tune the VOI using the VOI Widget range sliders or by moving the VOI Widget handles in 3D view

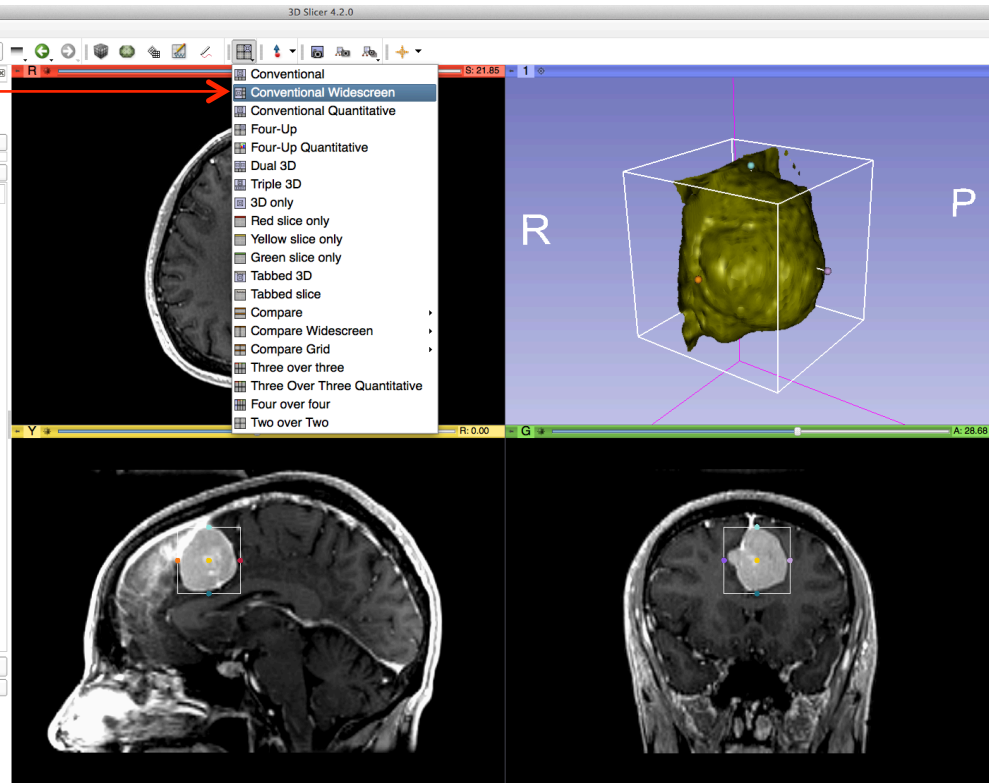
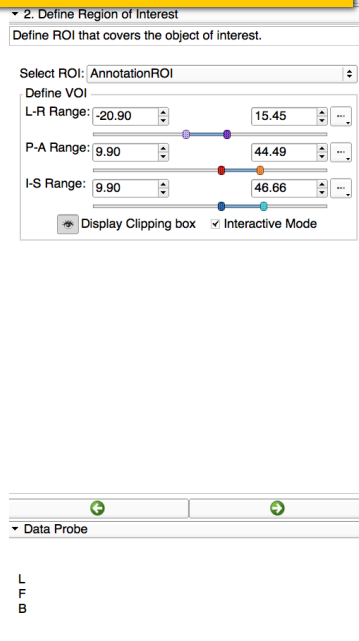
Note: VOI Widget range sliders are color-coded to match VOI box Widget handles in 3D Viewer





## Step2: Define Region of interest

Select the viewing mode  
**'Conventional Widescreen'**





## Step2: Define Region of interest

3D Slicer 4.2.0

File Edit View Help

Modules: ChangeTracker

3DSlicer

Help & Acknowledgement

2. Define Region of Interest

Define ROI that covers the object of interest.

Select ROI: AnnotationROI

Define VOI

L-R Range: -20.90 15.45

P-A Range: 9.90 44.49

I-S Range: 9.90 46.66

☐ Display Clipping box ☒ Interactive Mode

Slicer shows a closer view of the volume rendered tumor region.

Data Probe

Red RAS: (-110.7, 28.3, 21.9) Axial Sp: 1.4

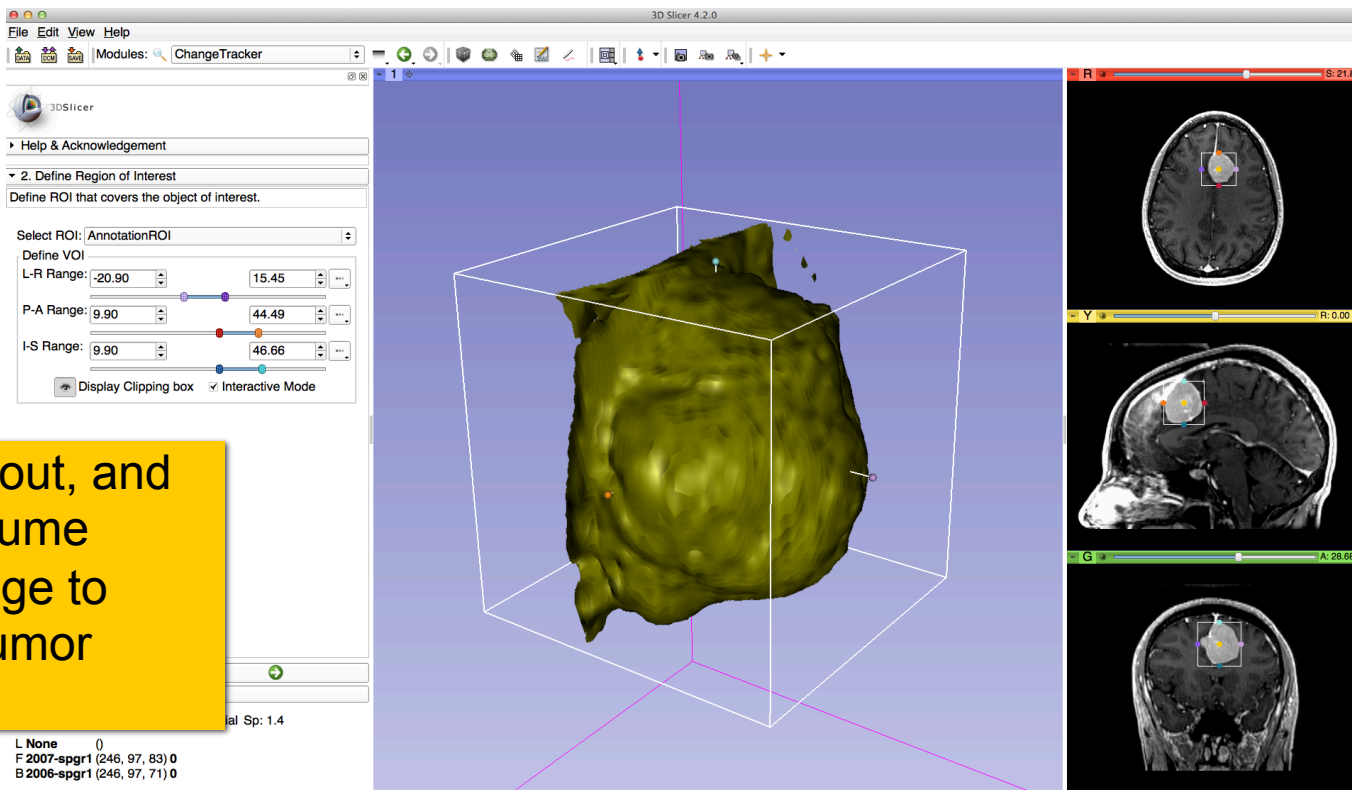
L None 0

F 2007-spgr1 (246, 97, 83) 0

B 2006-spgr1 (246, 97, 71) 0



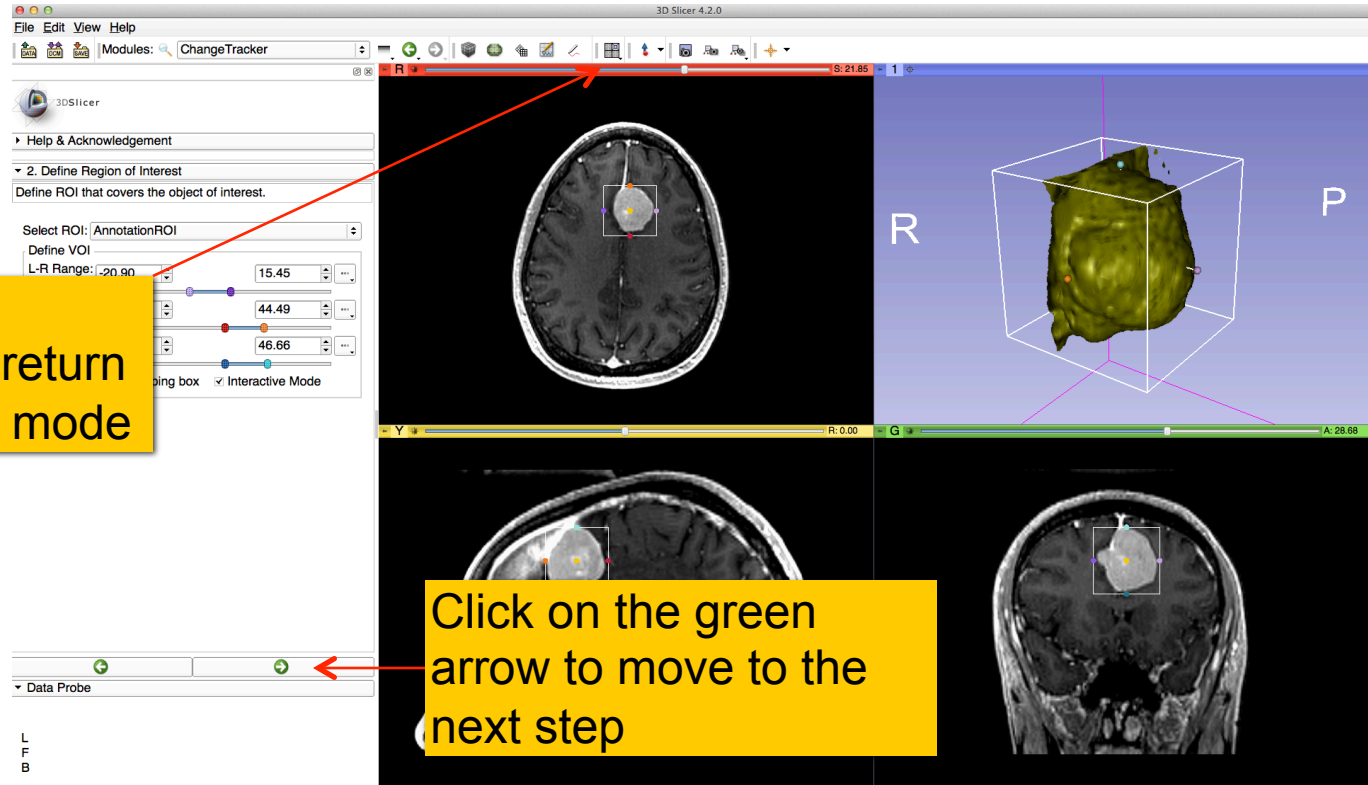
## Step2: Define Region of interest





## Step2: Define Region of interest

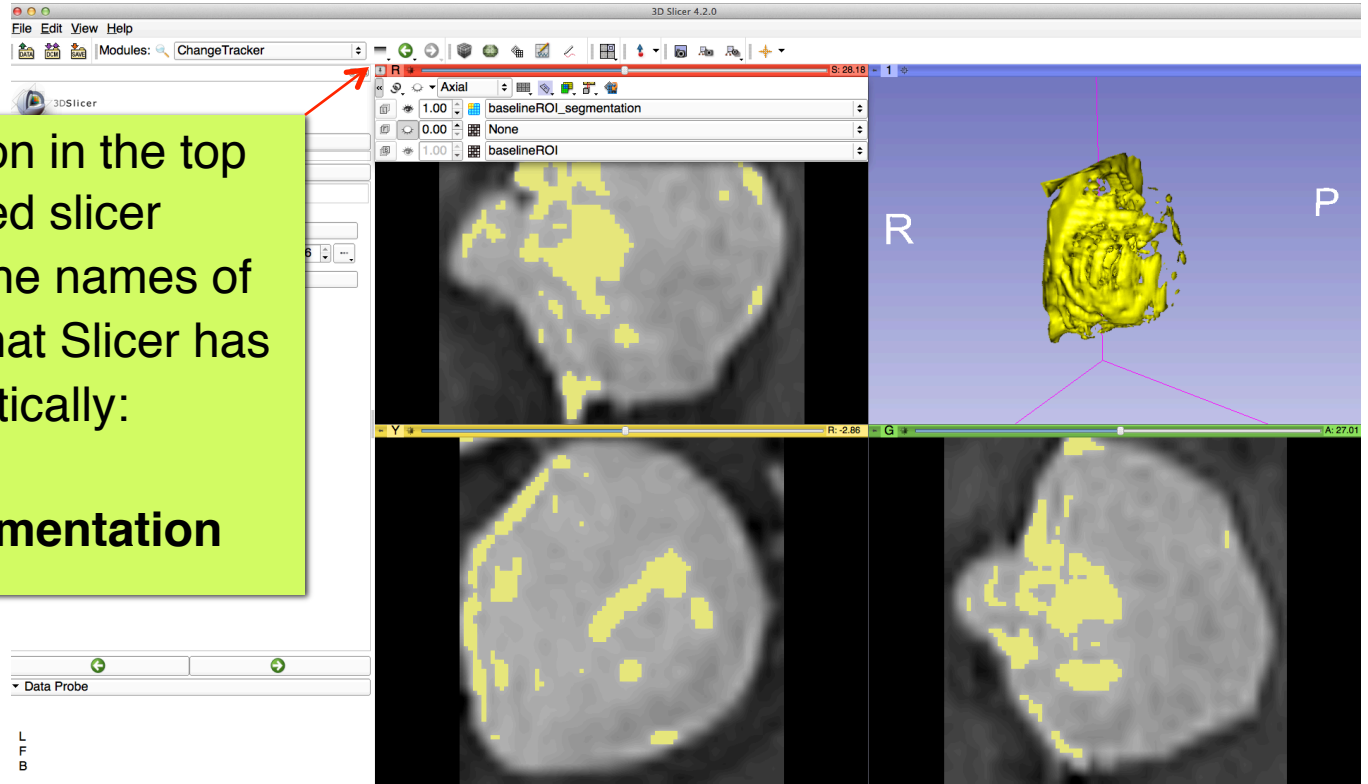
Select '**Four-Up Quantitative**' to return to the initial view mode





## Step3: Segment the tumor

Click on the pin icon in the top left corner of the red slicer viewer to display the names of the two volumes that Slicer has generated automatically:  
**baselineROI** and  
**baselineROI\_segmentation**



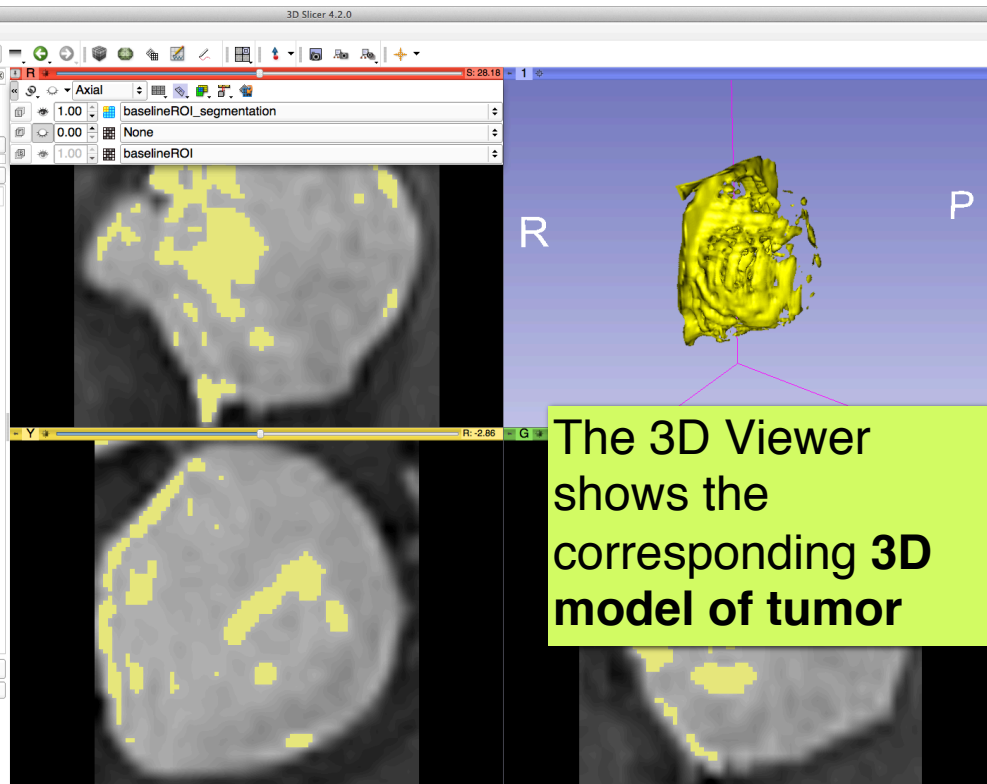


## Step3: Segment the tumor

**'baselineROI'** (background viewer) is the subvolume that corresponds to the previous VOI

**'baselineROI\_segmentation'** (labelmap viewer) is the current segmentation of the tumor.

In the current settings, Slicer displays the segmentation overlaid on the spgr volume





## Step3: Segment the tumor

Select the **layout FourUp** in the layout menu to display the volume rendered segmentation

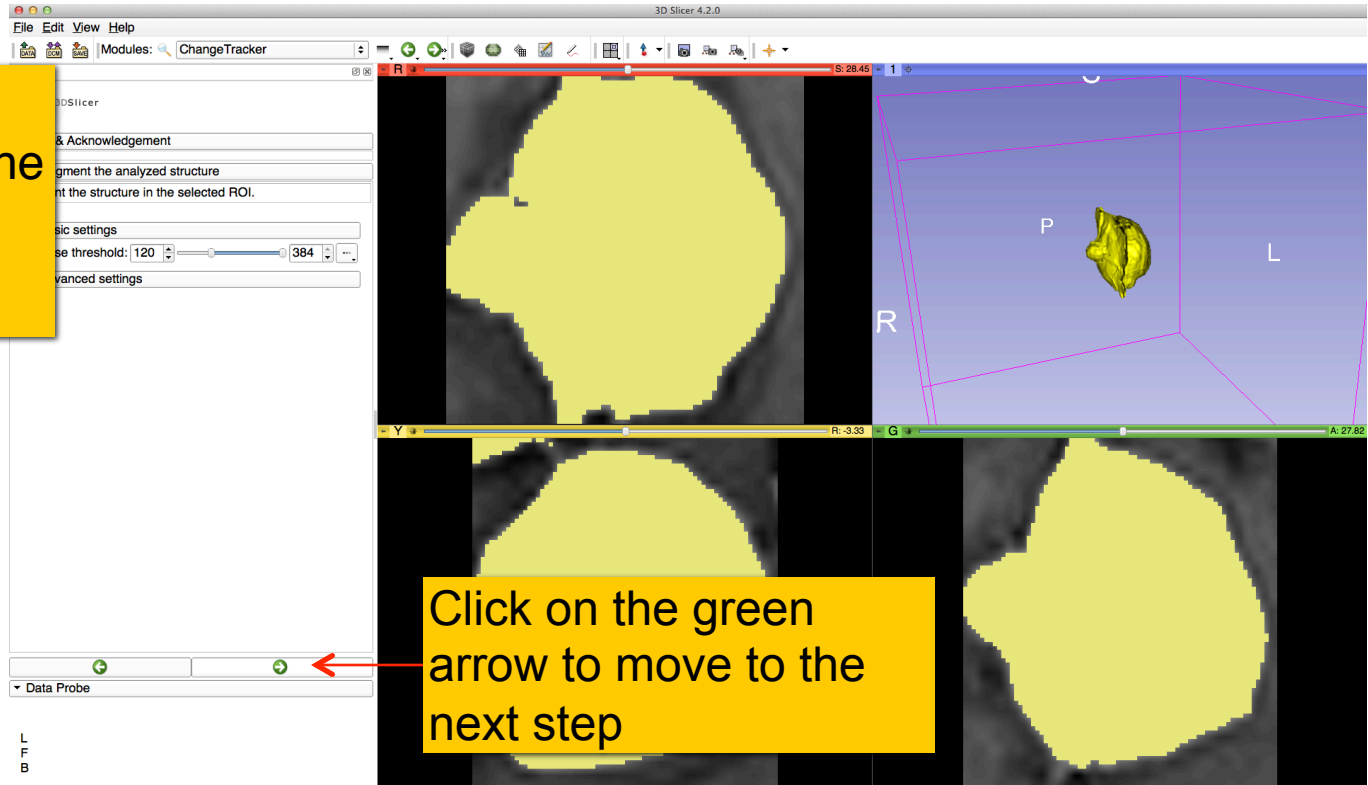
Modify the segmentation of the tumor by moving the **threshold range slider**

The screenshot shows the 3D Slicer software interface. On the left, the '3D Slicer' sidebar is visible with a section titled '3. Segment the analyzed structure' and a sub-section 'Segment the structure in the selected ROI'. Below this, the 'Basic settings' section contains a 'Choose threshold' slider ranging from 188 to 366. A red arrow points to this slider. On the right, the 'Layout' menu is open, showing various layout options. A red arrow points to the 'FourUp' layout option. The main window displays a 3D volume rendering of a tumor (yellow) and several 2D axial, sagittal, and coronal slices of the same volume. The tumor is segmented based on a threshold range.



## Step3: Segment the tumor

Scroll through the slices until the segmentation appears optimal.

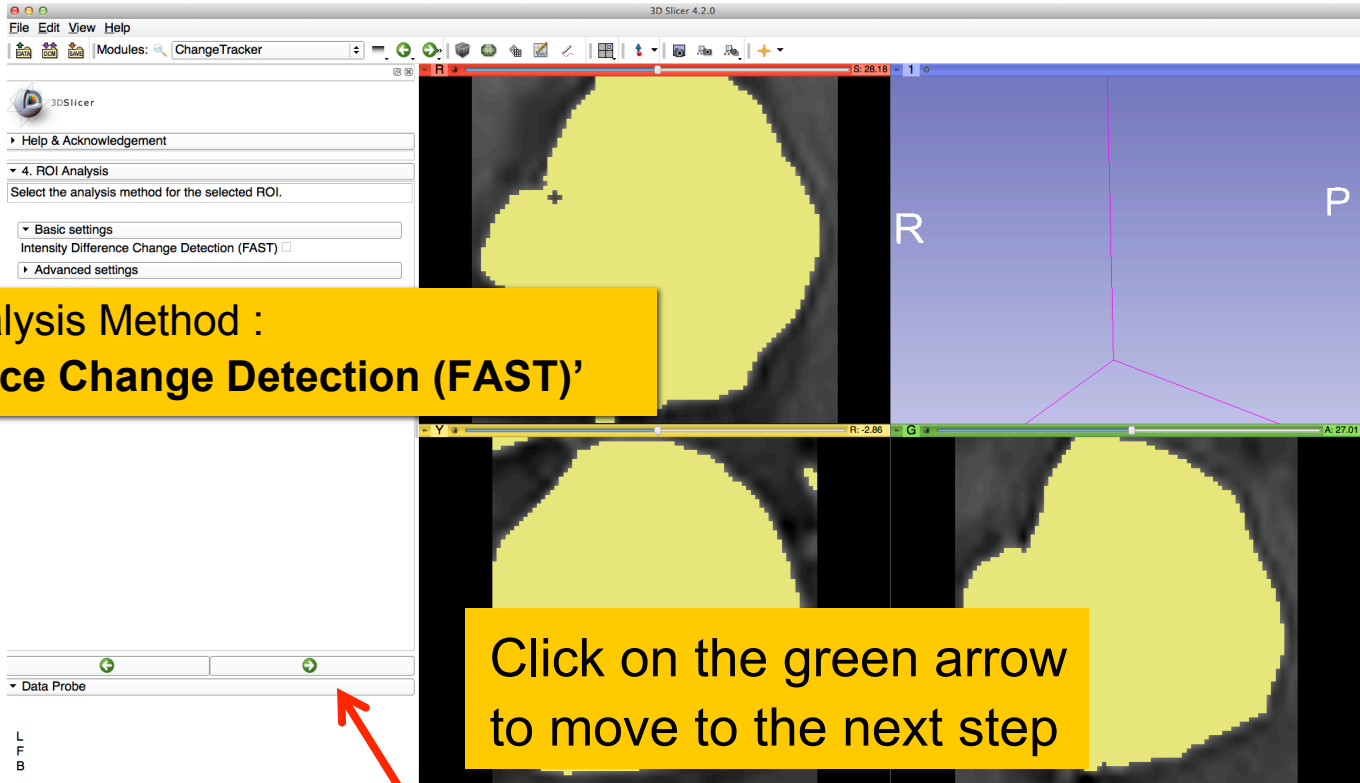


Click on the green arrow to move to the next step





## Step4: Select the Analysis Method

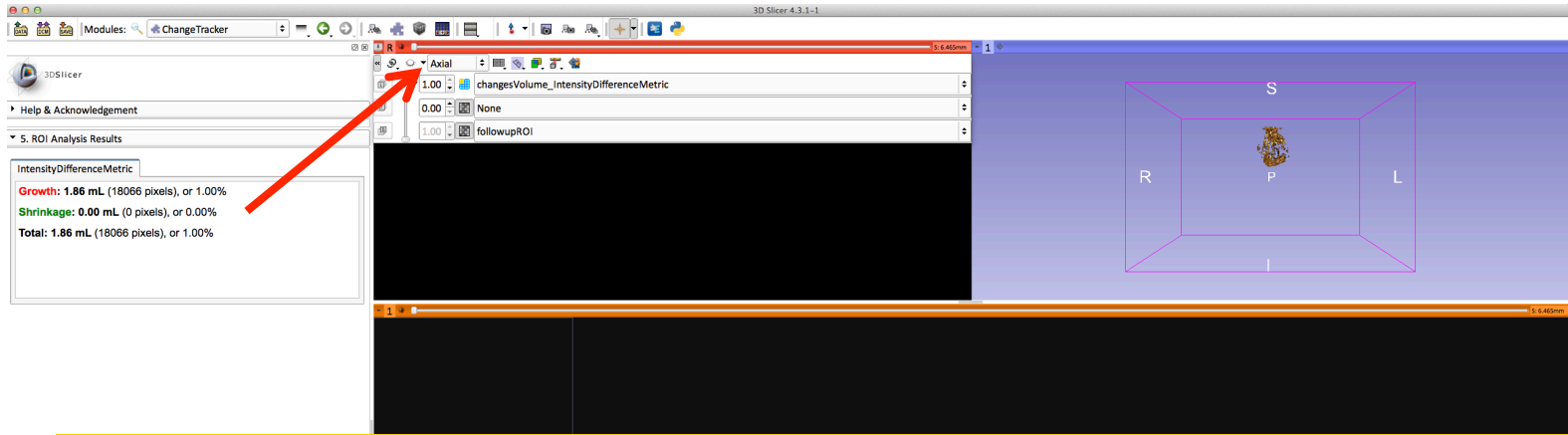


Select the ROI Analysis Method :  
**'Intensity Difference Change Detection (FAST)'**

Click on the green arrow  
to move to the next step



## Step4: Select the Analysis Method

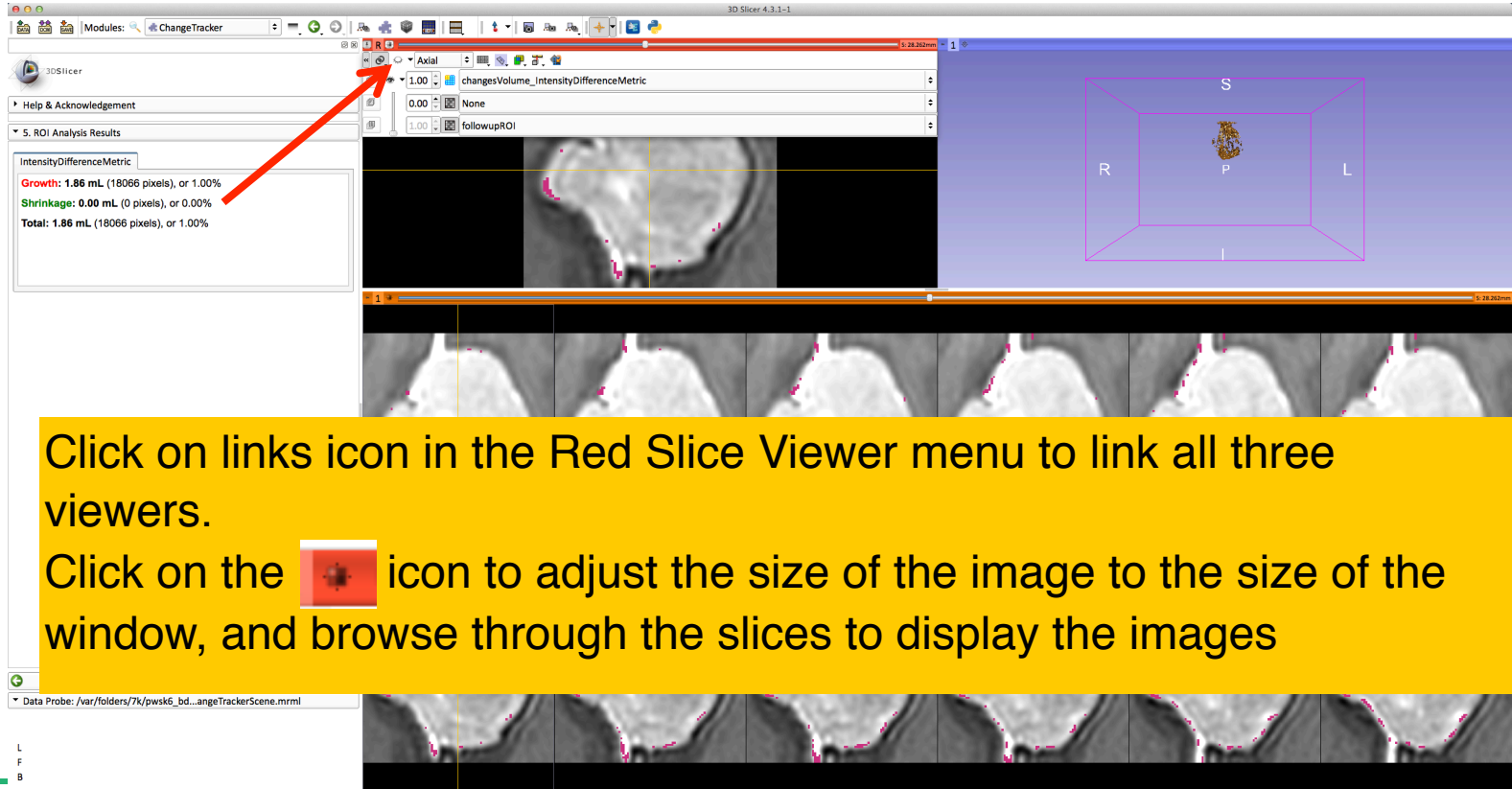


Left click on the slice menu to display the volumes that have been generated:


- **followupROI** correspond to the subvolume that has been extracted around the tumor in the 2007-spgr\_1 dataset
- **changesVolume\_IntensityDifferenceMetric** corresponds to the change between the 2006 and 2007 scans



## Step4: Select the Analysis Method



Click on links icon in the Red Slice Viewer menu to link all three viewers.

Click on the  icon to adjust the size of the image to the size of the window, and browse through the slices to display the images

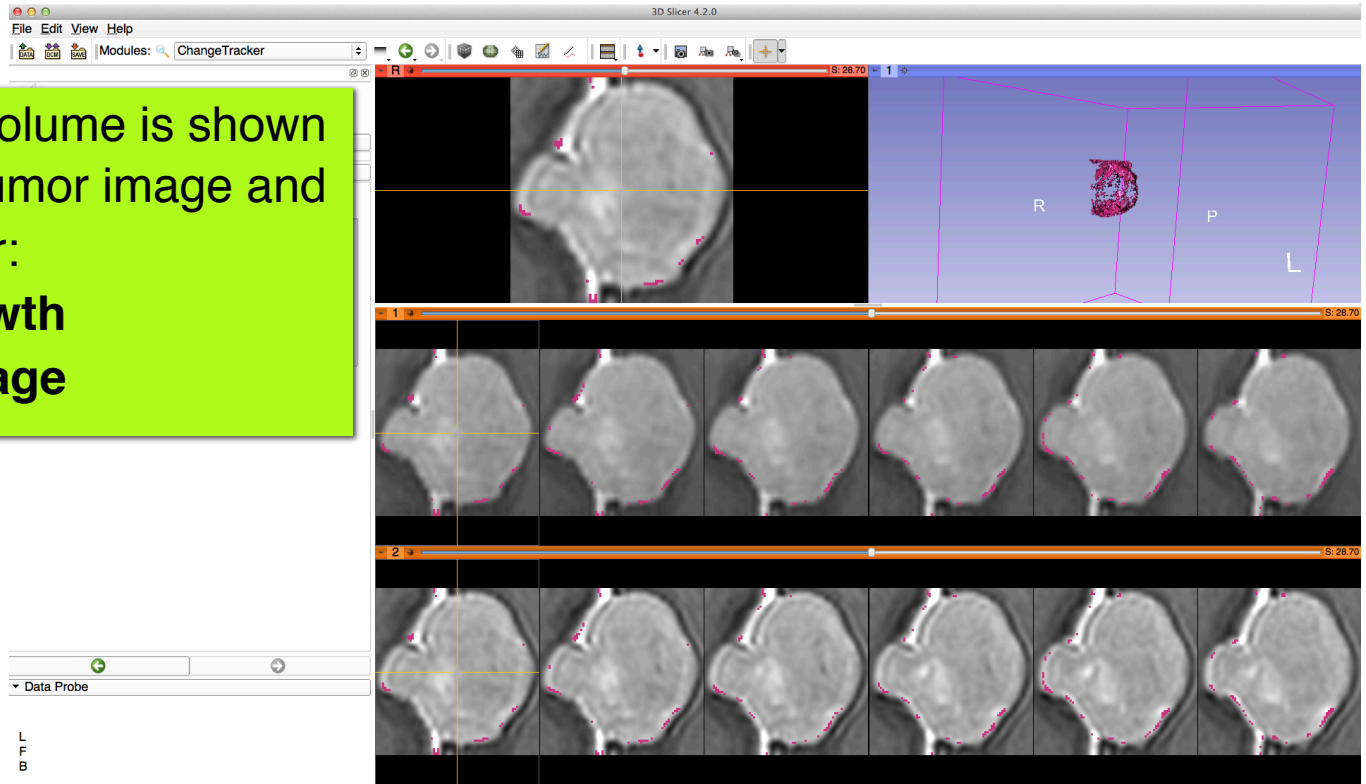


# Final Step: Change Tracker Results

The change in volume is shown  
overlaying the tumor image and  
in the 3D Viewer:

**magenta** = growth

**green** = shrinkage

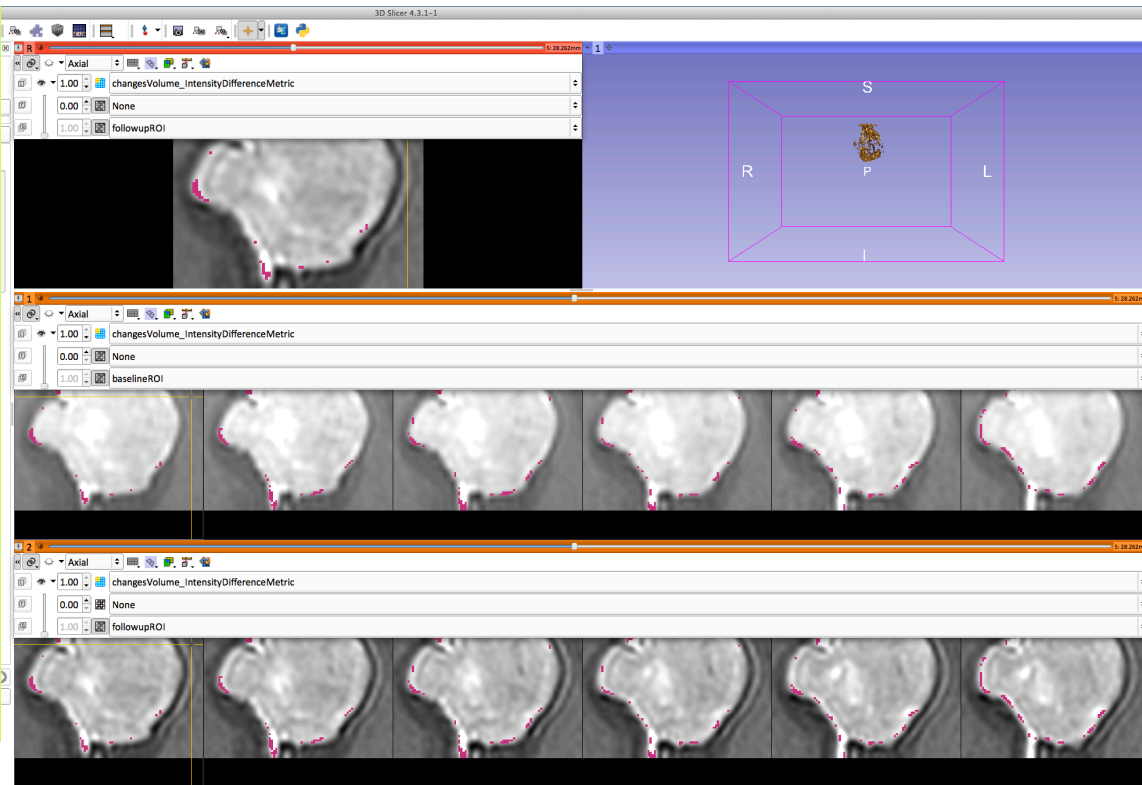




# Visualization of the change in pathology

The results of the analysis are displayed in the “**Compare View**” layout

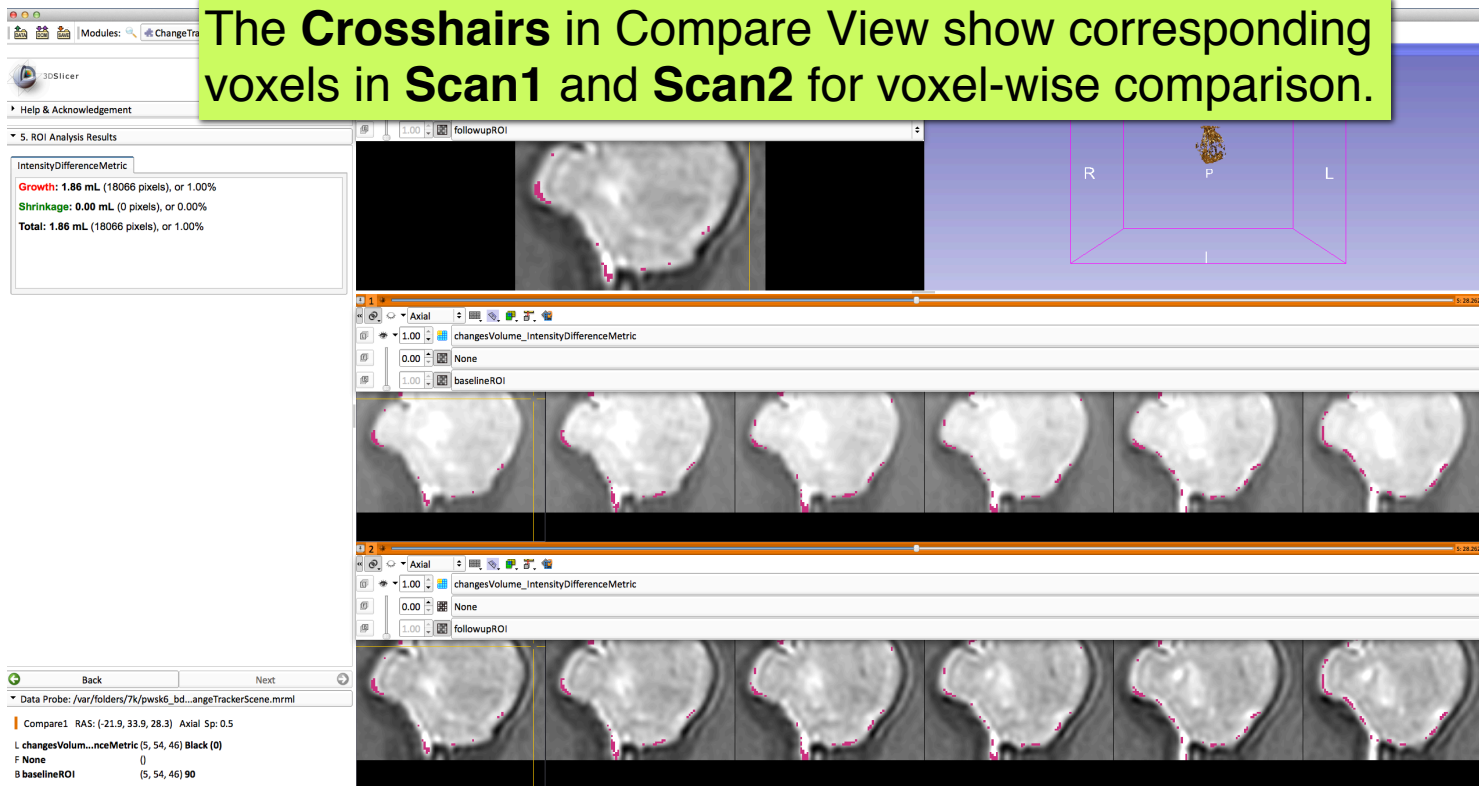
- Six consecutive slices for the VOI in Scan1 (**top row**), and
- Six corresponding consecutive slices for the VOI in Scan2 (**bottom row**).
- A zoomed view of the axial slice in the red slicer viewer





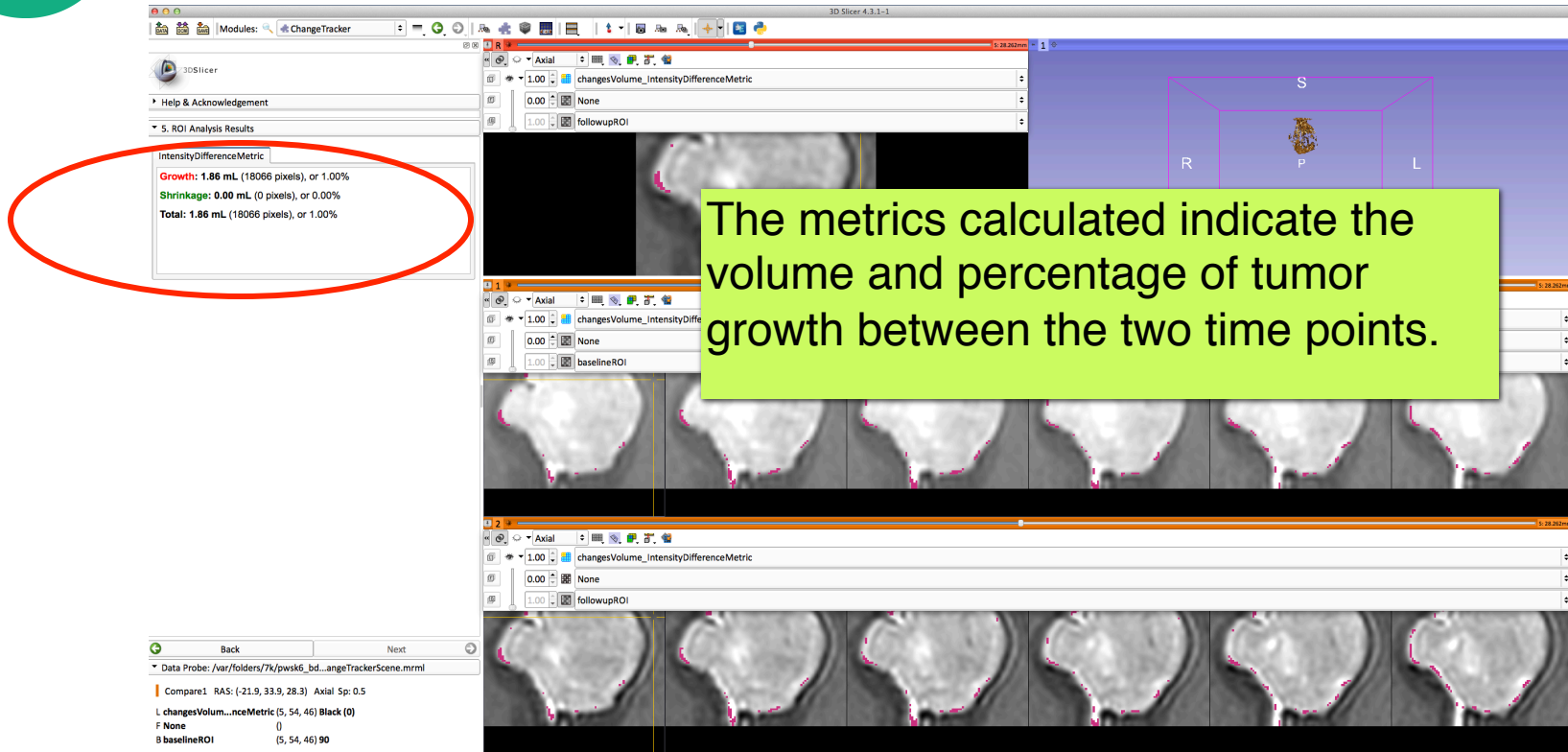
# Visualization of the change in pathology

The **Crosshairs** in Compare View show corresponding voxels in **Scan1** and **Scan2** for voxel-wise comparison.





# Change Tracker Results





## Change Tracker module

---

- This tutorial demonstrated the use of the change tracker module in Slicer on axial 3D SPGR T1 post Gadolinium scans
  - **Tumor boundary should be clear**
  - **Only for contrast enhanced images**
  - **Need homogenous enhancement across timepoints.**
- The Change Tracker module has not been tested for tumors with changing necrosis.





## ChangeTracker: Exploring small volumetric changes

---

This tutorial demonstrated:

- a method to quantify small volumetric changes in pathology.
- visualization of these changes in the anatomical context
- use of Slicer's “**Compare Viewer**” to simultaneously explore baseline and followup studies.

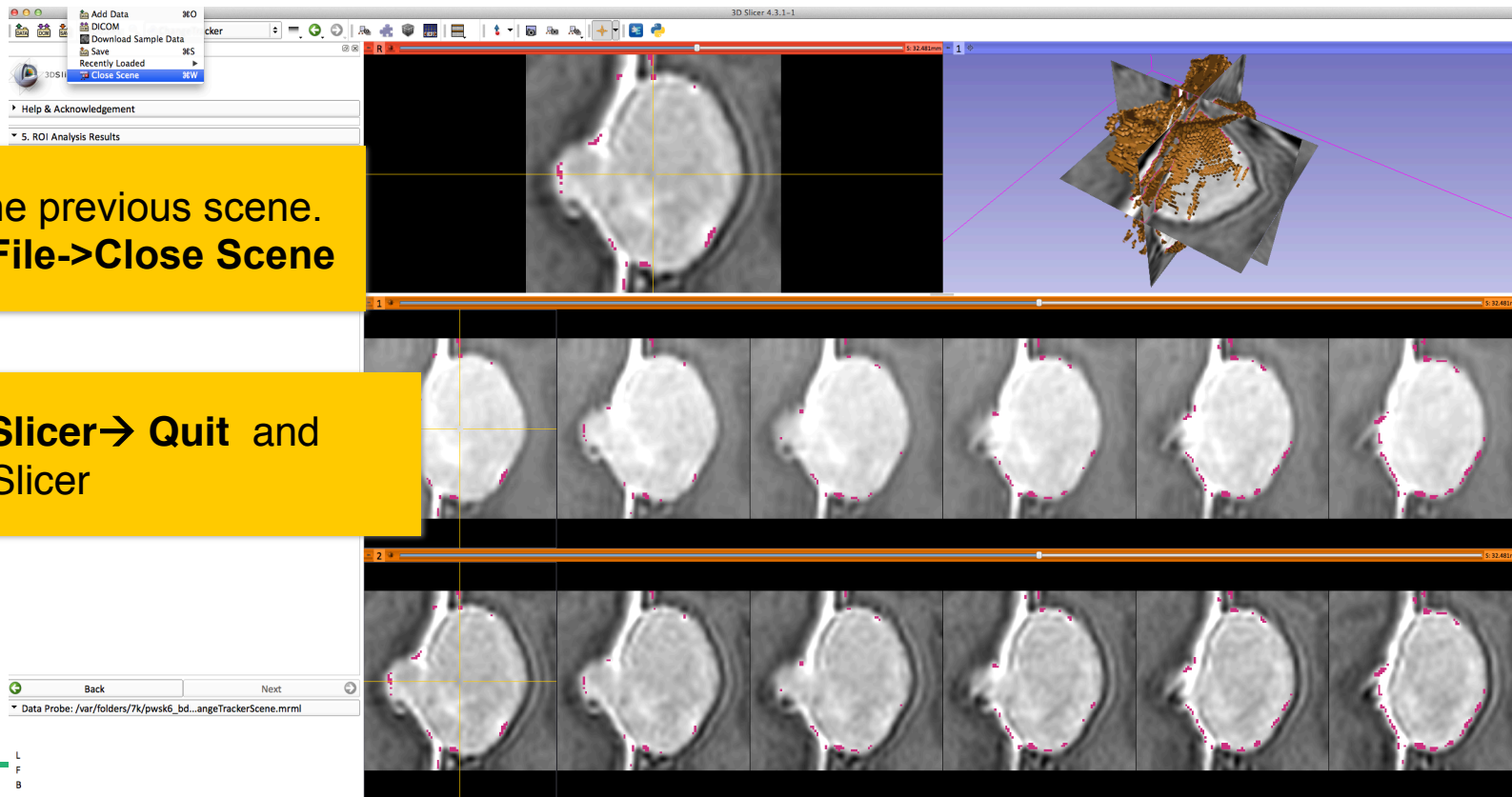
Next, we will demonstrate combined visualization of PET/CT studies and SUV computation.



# Clear the scene and its data

Clear the previous scene.  
Select **File**→**Close Scene**

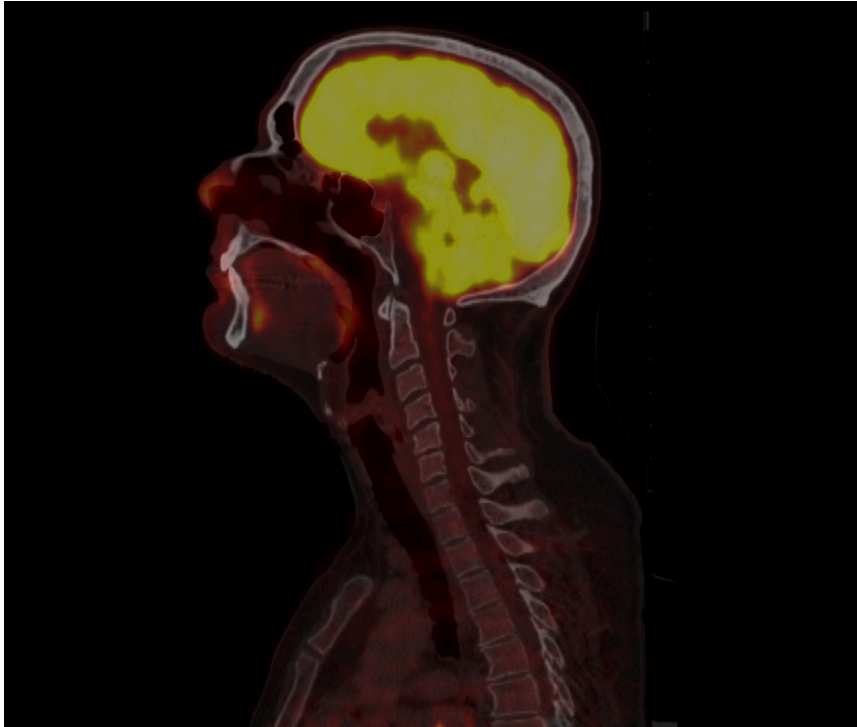
Select **Slicer**→**Quit** and  
restart Slicer





# PET/CT Visualization and Analysis

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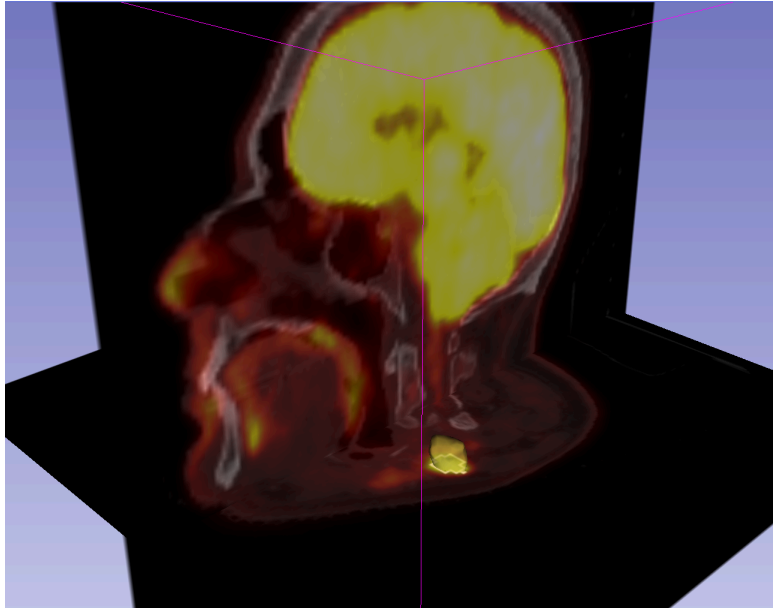
## Part III: PET/CT Analysis

Sonia Pujol, PhD  
Kitt Shaffer, MD, PhD  
Hatsuho Mamata, MD, PhD  
Ron Kikinis, MD



# Goal of the tutorial

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The goal of this tutorial is to guide you step-by-step through the SUV computation of PETCT data of a squamous cell carcinoma case pre- and post- treatment



# FDG-PET SUV

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- Standardized Uptake Value (SUV) is a semi-quantitative measure derived from the determination of tissue activity obtained from a clinical PET study

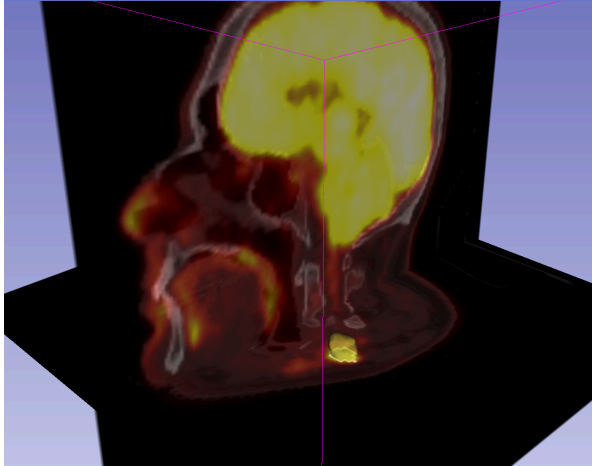
$$\text{SUV} = \frac{\text{Tissue Concentration of Radioactive Tracer} \times \text{Patient Weight}}{\text{Injected Dose}}$$

- Under certain circumstances, 18-F Fluorodeoxyglucose (FDG) SUV correlates with metabolic rate of glucose and/or the number of viable tumor cells



# Tutorial Case

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- Pathology: poorly differentiated squamous cell carcinoma
- Treatment: radiotherapy and chemotherapy (weekly cis-platin)
- Two 18F-FDG PET and CT scans acquired within a 5-month interval.



# PETCT tutorial: Clinical Case and Data

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The datasets are located in

**C:\3DSlicerData\_RSNA2013\QuantitativeImagingSunday\_Dec1\dataset3\_PETCT**

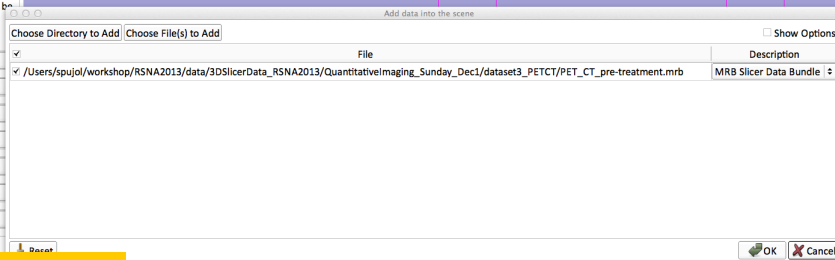
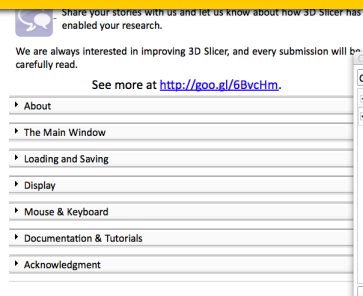
- **PETCT1 dataset** is located in the **pre-treatment directory** corresponds to the baseline
- **PETCT2 dataset** is located in the **post-treatment directory** corresponds to the follow-up scan.



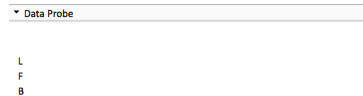
# Loading the PETCT scene

Drag and drop the file **PETCT\_pre-treatment.mrb** located in

**C:\3DSlicerData\_RSNA2013\QuantitativeImaging\_Sunday\_Dec1\dataset3\_PETCT**



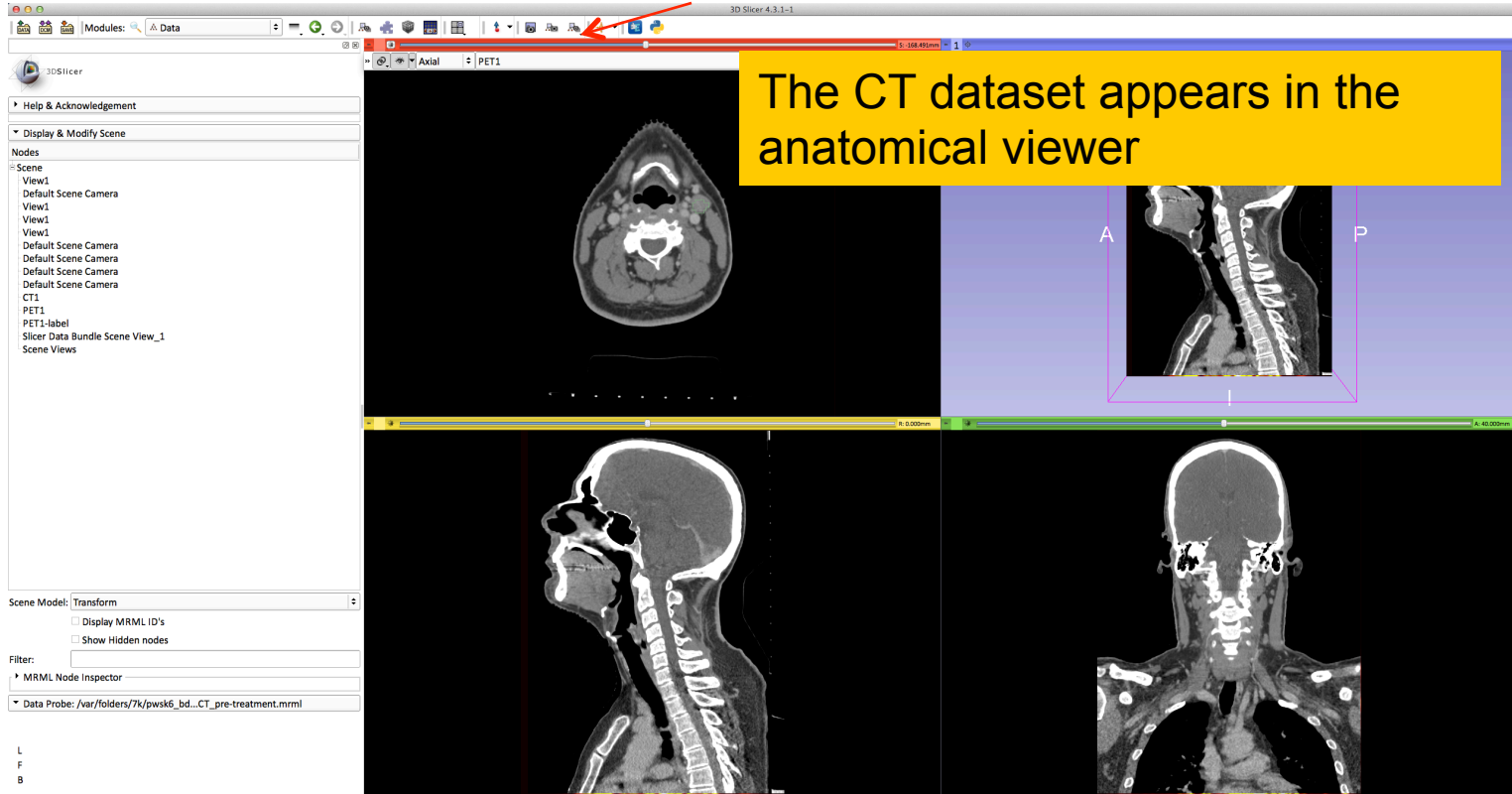
Click OK to load  
the .mrb file into Slicer





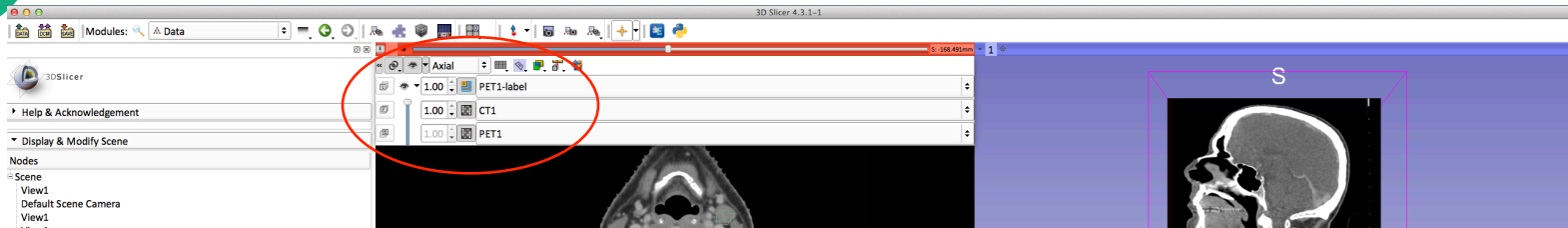


# Loading the PETCT scene





# Loading a PETCT dataset



Left click on the pin icon in the top left corner to display the red slice viewer menu.

The **CT1** volume is displayed in the Foreground viewer

The **PET1** volume is displayed in the Background viewer

The **PET1-Label** is displayed in the Labelmap viewer

Use the slider to fade between the Bg viewer and the Fg viewer to display the PET volume overlaid on the CT volume



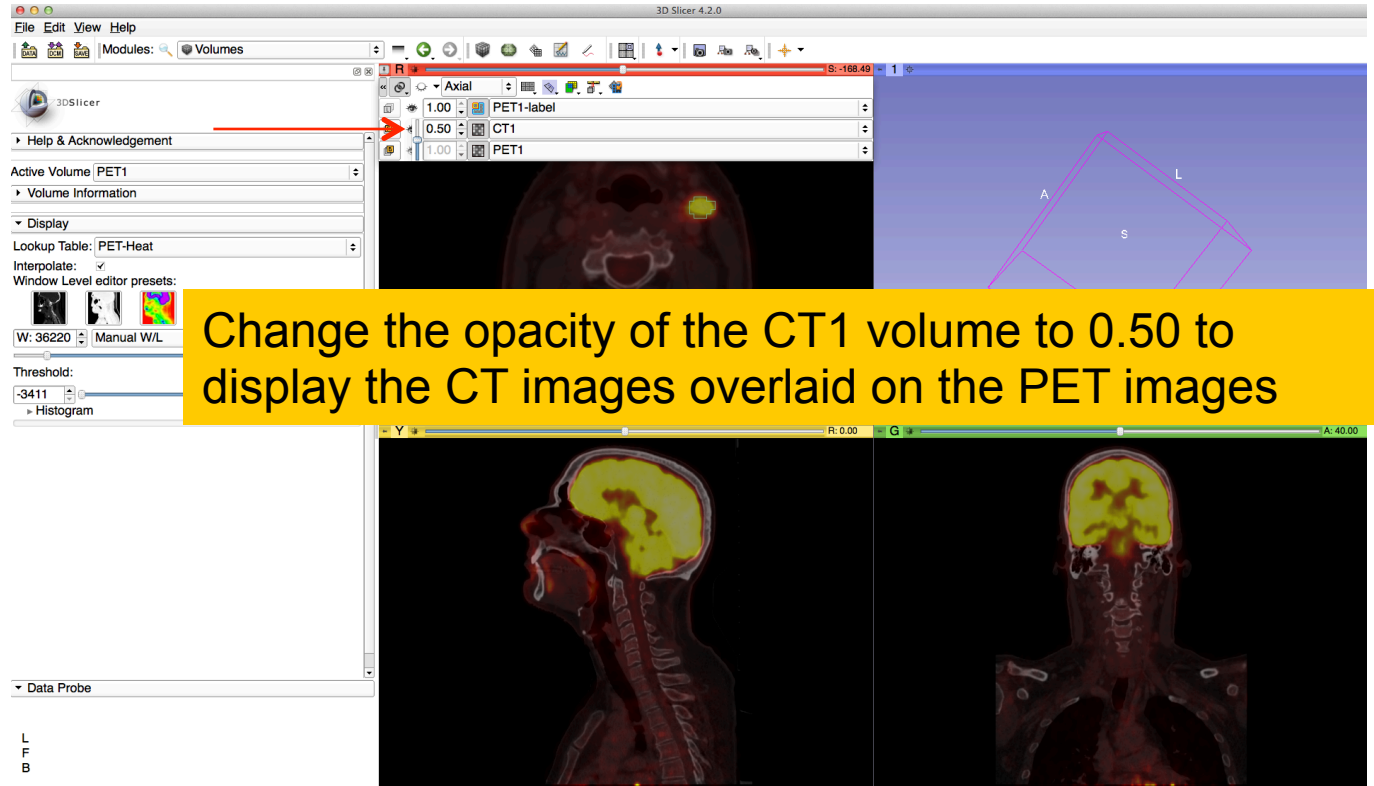
mode for segmentation viewer

The outline of a lesion appears in the anatomical viewers

The outline of a lesion appears in the anatomical viewers




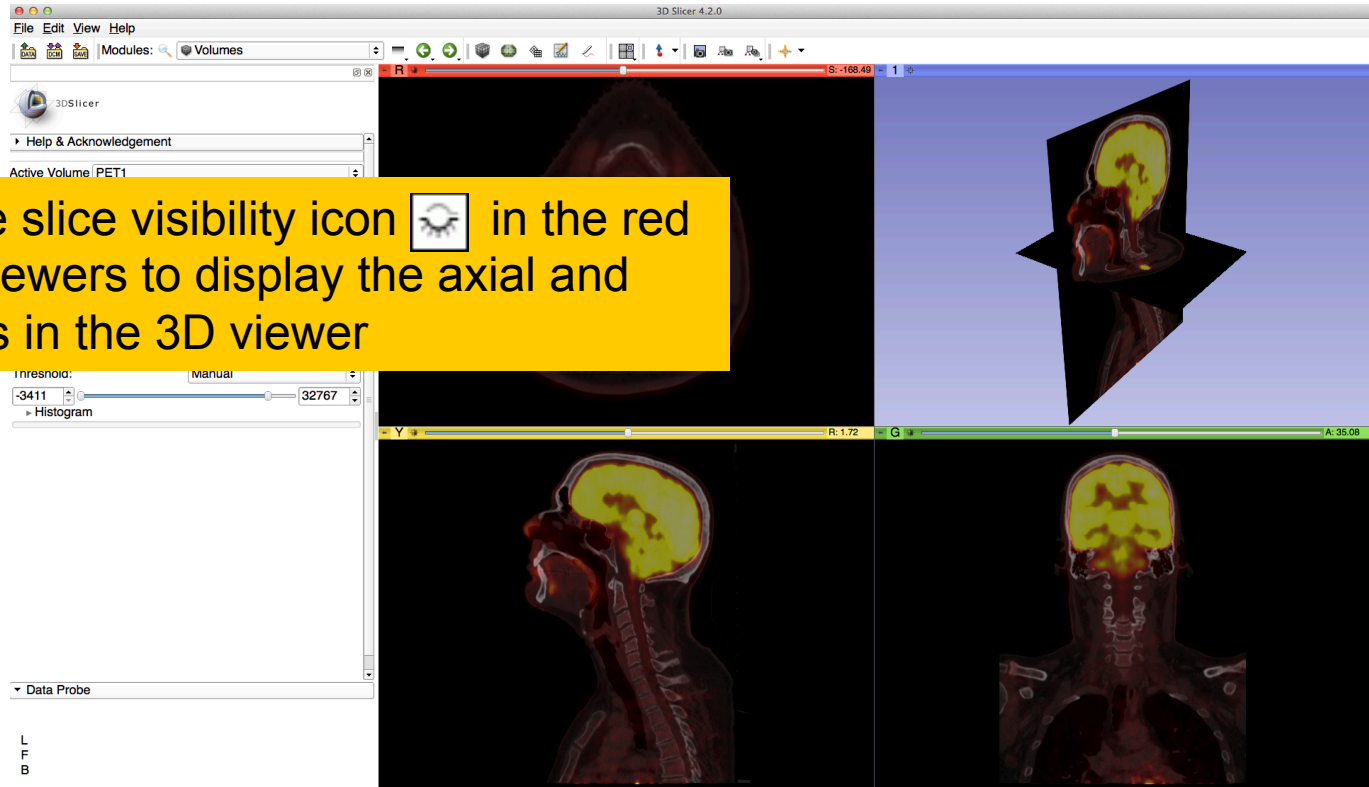
# Visualization of PETCT data





# Visualization of PETCT data

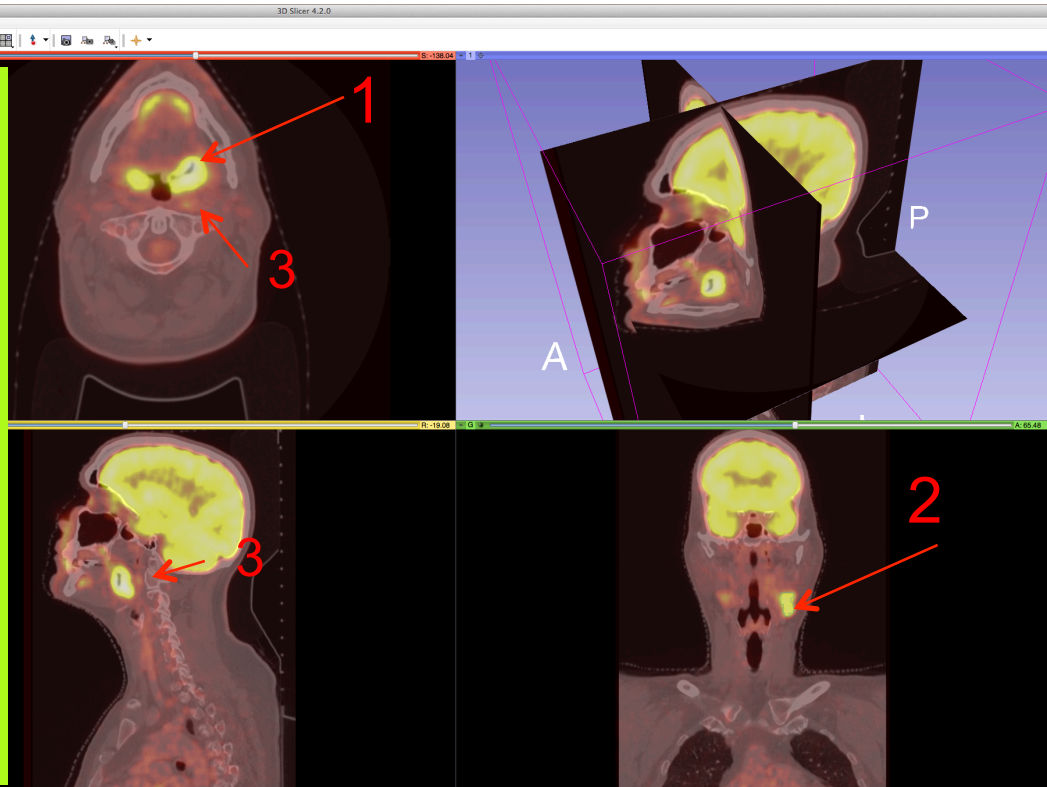
Check on the slice visibility icon  in the red and yellow viewers to display the axial and sagittal slices in the 3D viewer





# PET uptake findings

Note an intense uptake in  
1) left oropharyngeal mass  
involving the base of tongue  
and left glossotonsillar  
fossa and,  
2) in left level IIA/III lymph  
nodes as well as a small  
adjacent left level III node.  
3) a possible small  
metastasis in the left  
retropharyngeal region at  
level of C1

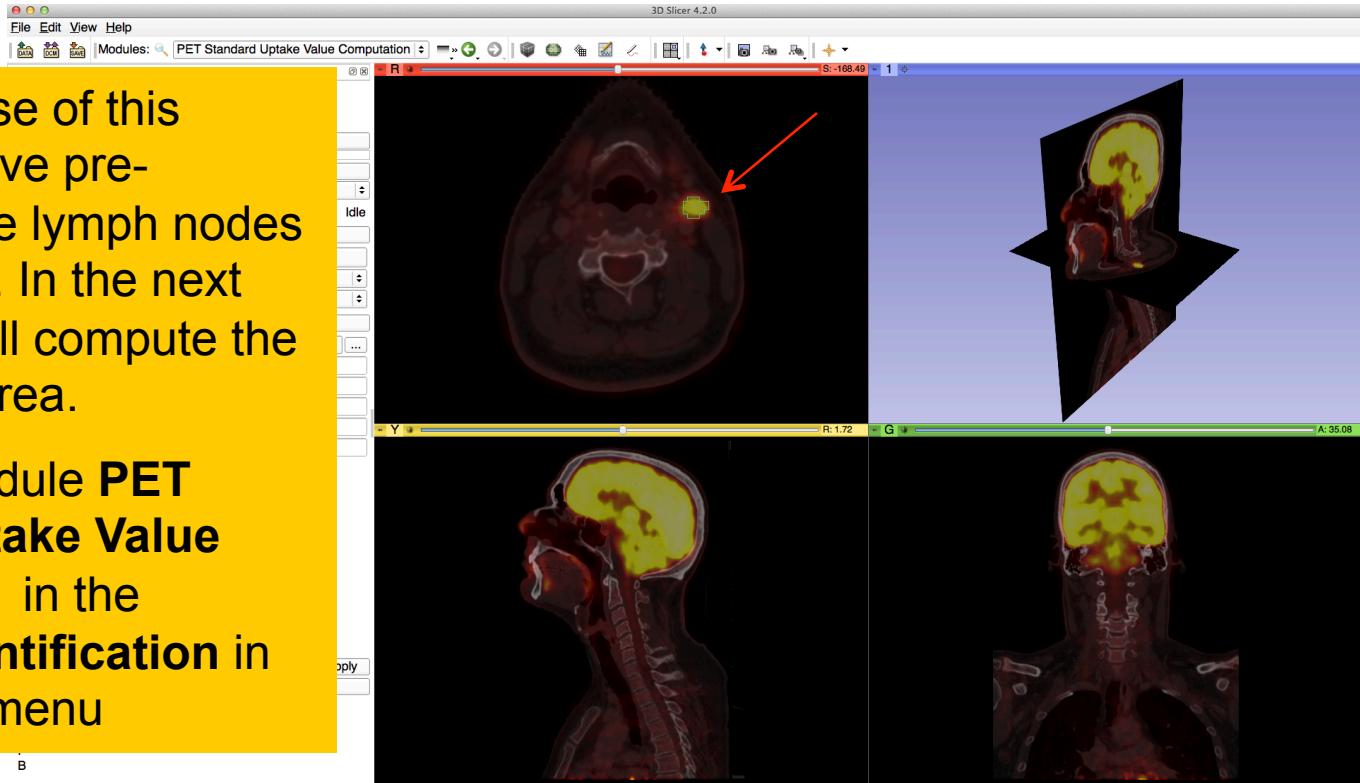




# PET SUV Computation

For the purpose of this tutorial, we have pre-segmented the lymph nodes uptake region. In the next section, we will compute the SUV for this area.

Select the module **PET Standard Uptake Value Computation** in the category **Quantification** in the modules' menu





# PET SUV Computation

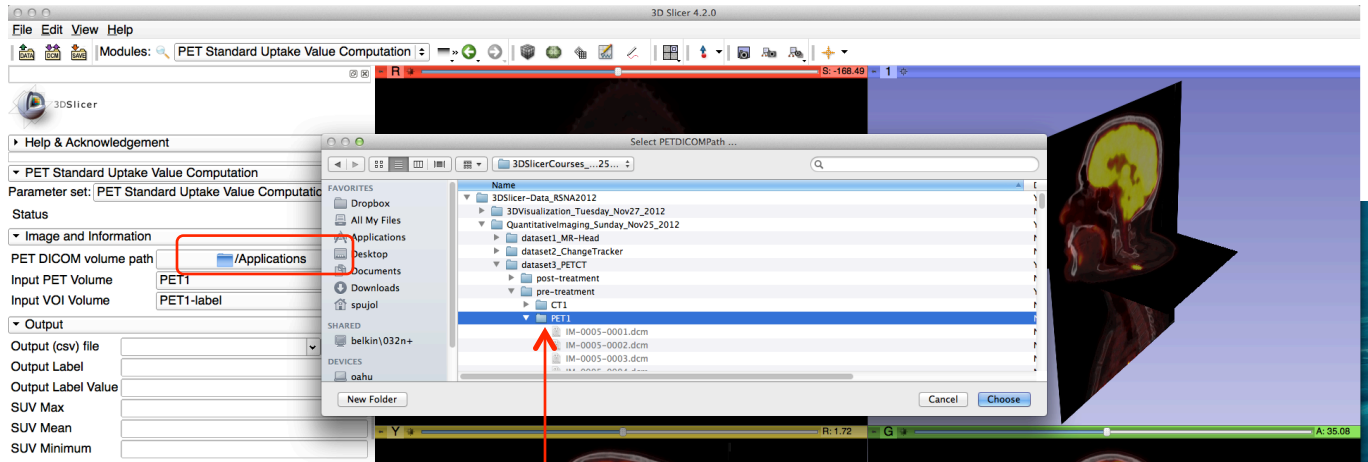
**Step1: Input volumes selection**  
Select Input PET Volume 'PET1'  
Select Input VOI Volume 'PET1-label'

	Red	RAS: (63.4, -9.2, -168.5)	Axial Sp: 3.3
L PET1-label	(36, 84, 63)	0 (0)	
F CT1	(148, 325, 164)	-995	
B PET1	(36, 84, 63)	661.377441	





# PET SUV Computation



## **Step2: Path to the DICOM PET header**

**Click on /Applications in the PET DICOM volume path, and select the PET1 subdirectory located under C:/3DSlicer\_RSNA2013/QuantitativImaging\_Sunday\_Dec1/PETCT/PET1**

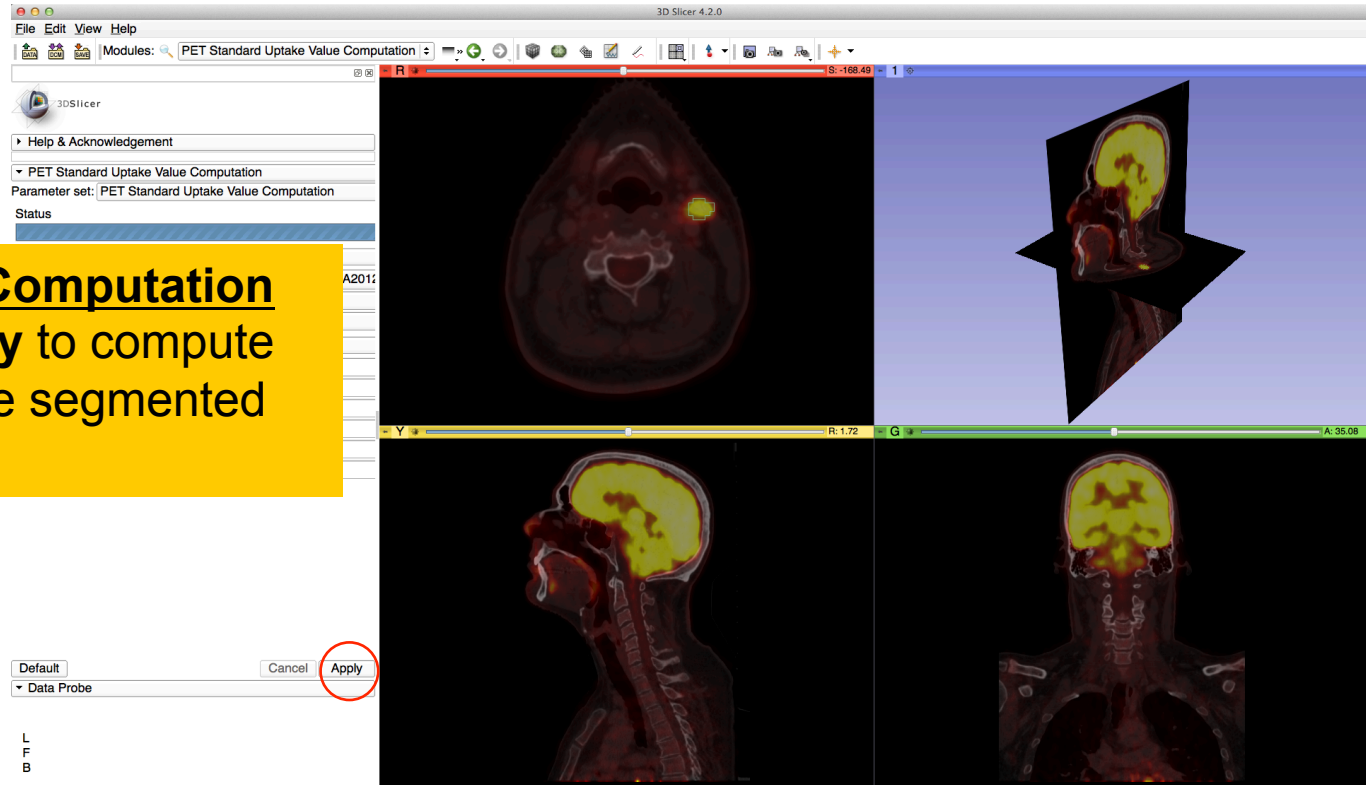
L  
F  
B



# PET SUV Computation

## Step3: SUV Computation

Click on **Apply** to compute the SUV in the segmented region





# PET SUV Computation

3D Slicer 4.2.0

File Edit View Help

Modules: PET Standard Uptake Value Computation

3DSlicer

Help & Acknowledgement

PET Standard Uptake Value Computation

Parameter set: PET Standard Uptake Value Computation

Status

Image and Information

PET DICOM volume path: /Users/spujol/workshop/RSNA2012

Input PET Volume: PET1

Input VOI Volume: PET1-label

Output

Output (csv) file:

Output Label: 1

Output Label Value: 1

SUV Max	7.53385
SUV Mean	5.01805
SUV Minimum	3.39015

Default Cancel Apply

Data Probe

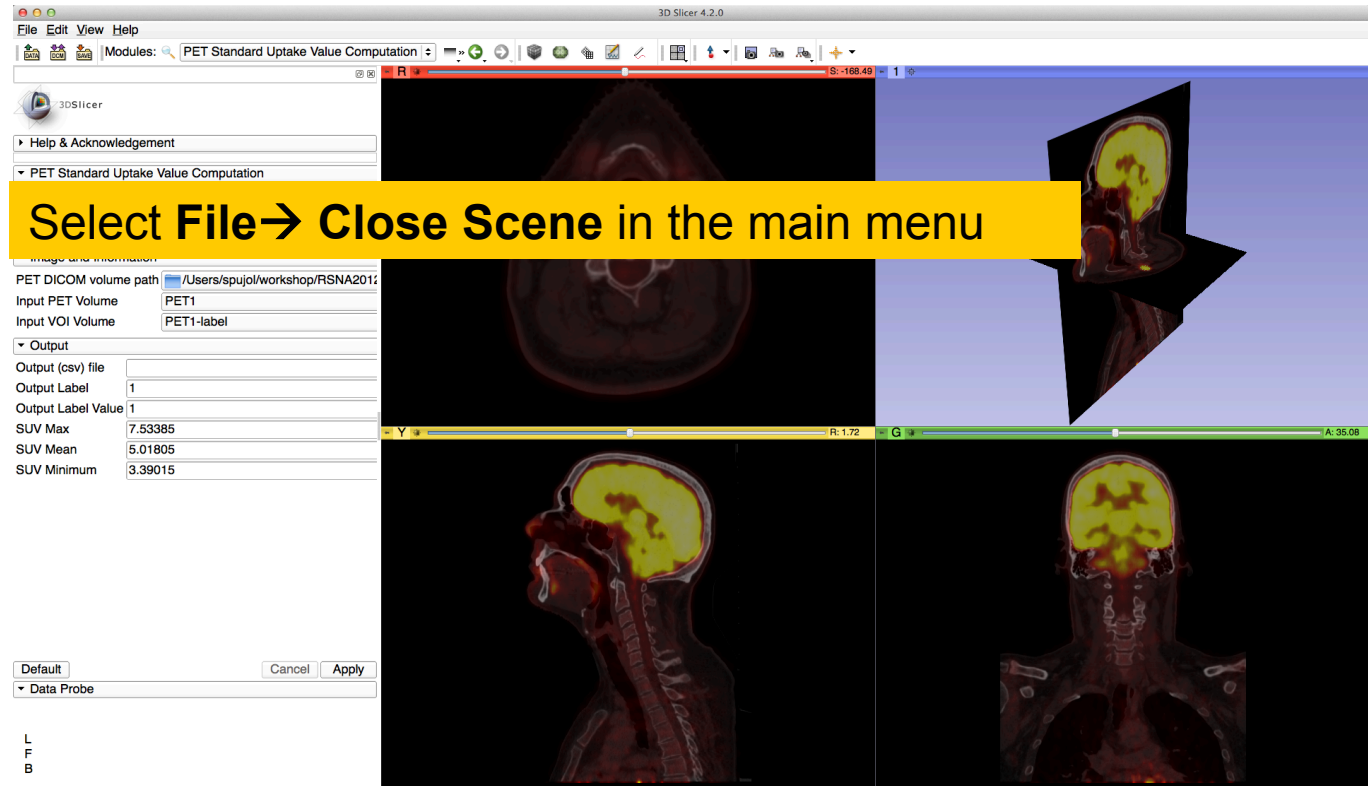
L  
F  
B

## SUV Computation Results:

SUVmax = 7.53385 mg/ml  
SUVmin = 5.01805 mg/ml  
SUVmean = 3.39015 mg/ml



# PET SUV Computation

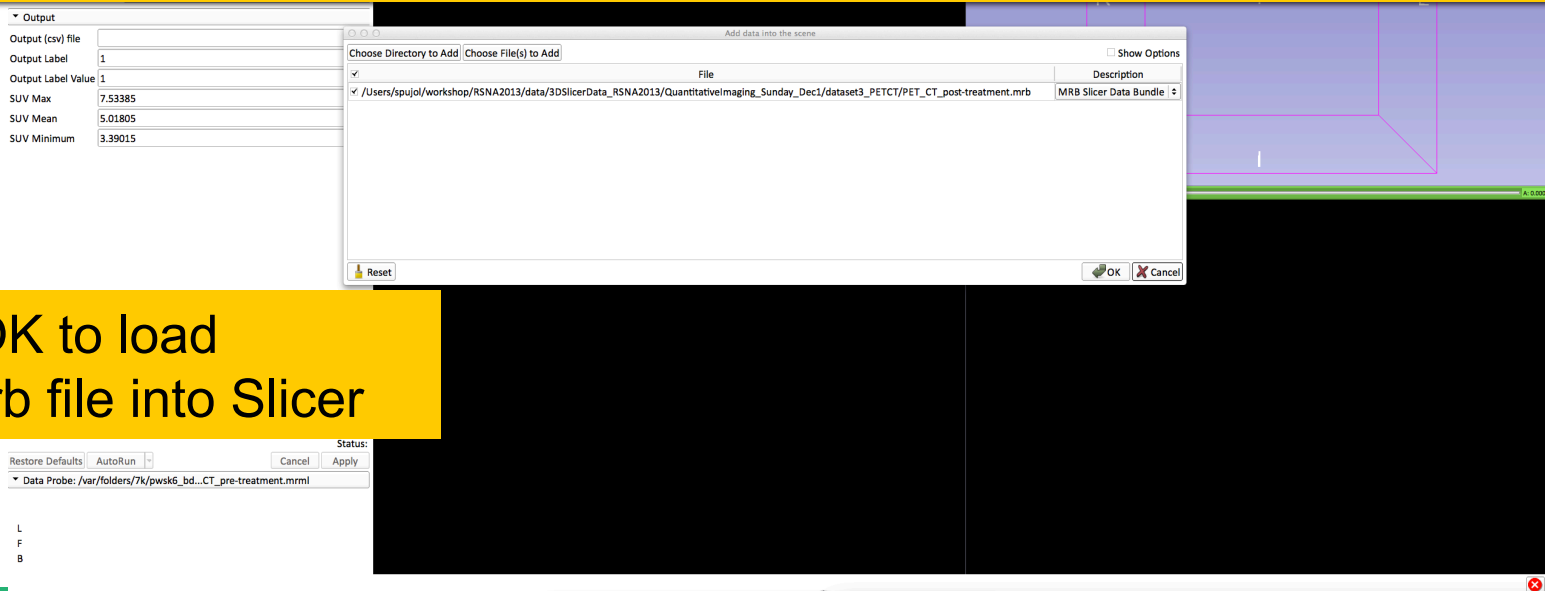




# Loading the PETCT scene

Drag and drop the file **PETCT\_post-treatment.mrb** located in

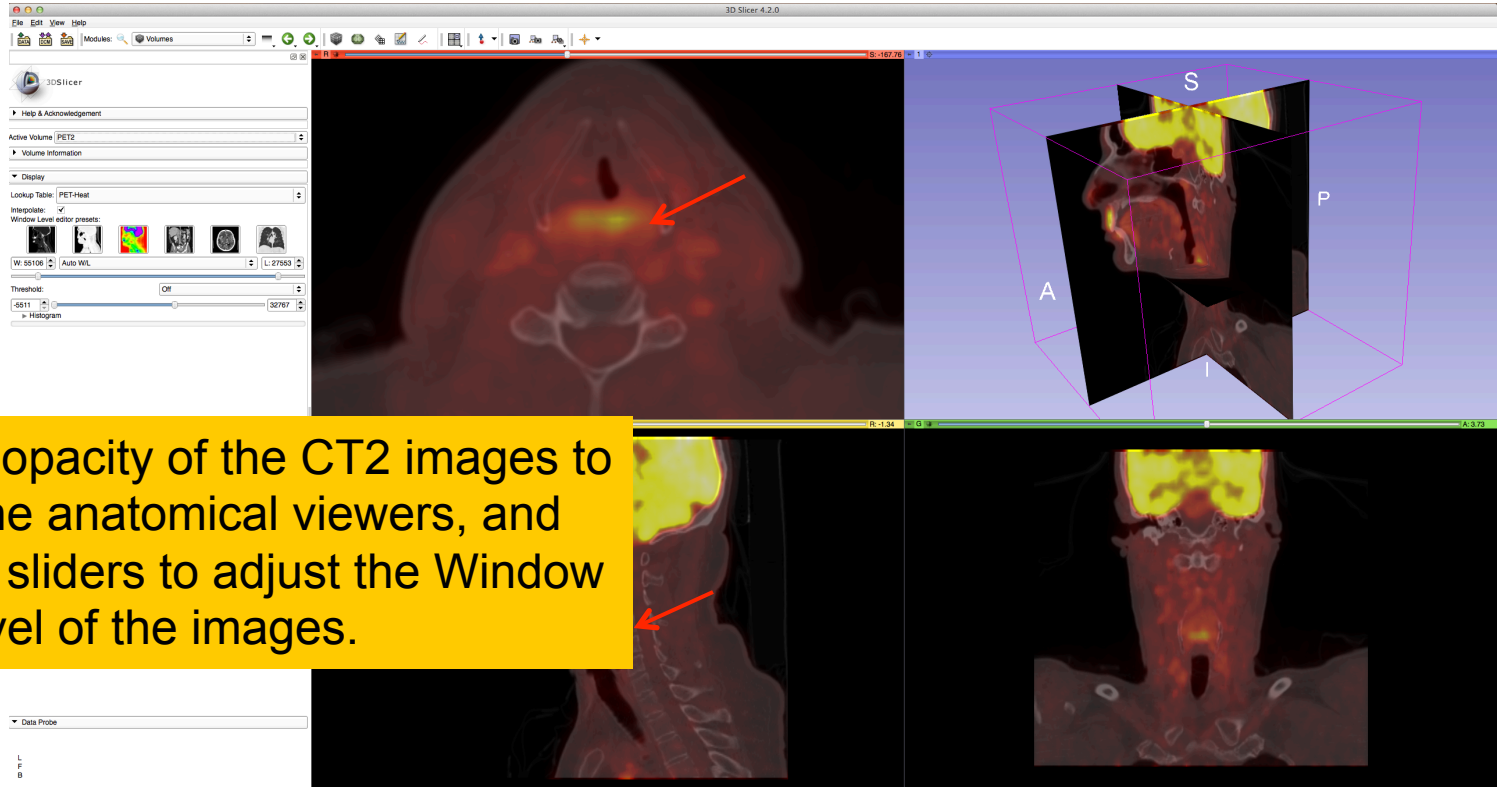
**C:\3DSlicerData\_RSNA2013\QuantitativeImaging\_Sunday\_Dec1\dataset3\_PETCT**



Click OK to load the .mrb file into Slicer



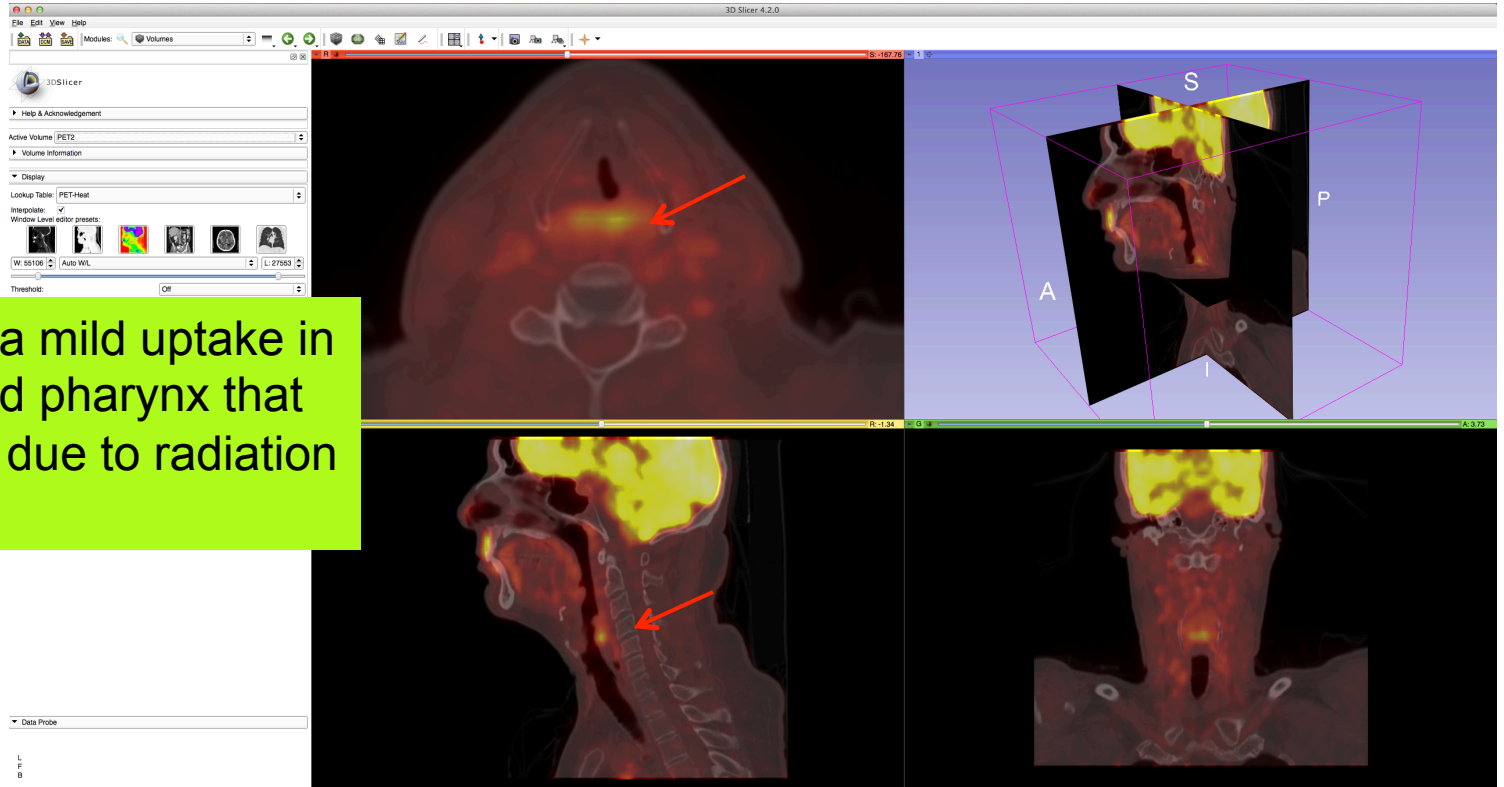
# PET uptake findings



Set the opacity of the CT2 images to 0.5 in the anatomical viewers, and use the sliders to adjust the Window and Level of the images.



# PET uptake findings

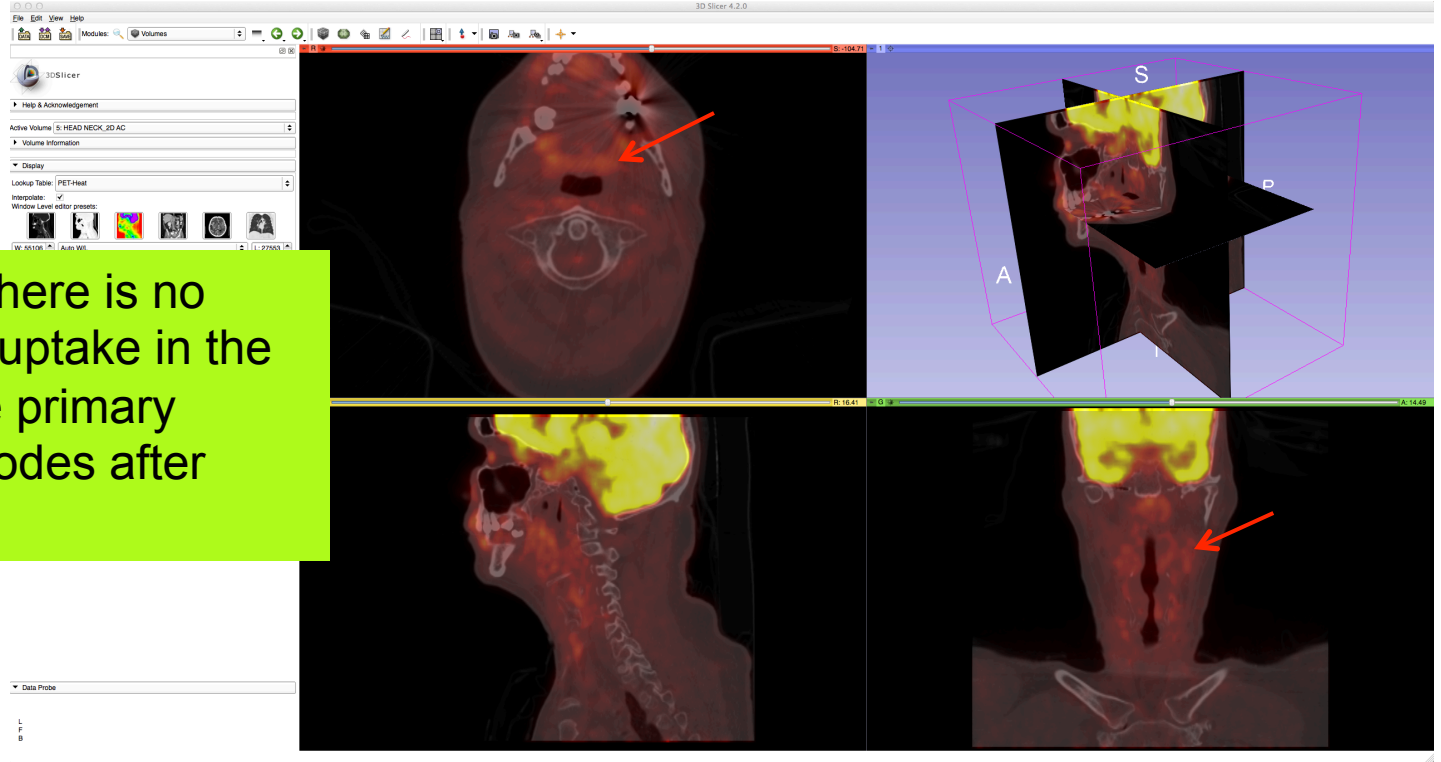


Observe a mild uptake in larynx and pharynx that are likely due to radiation effect.



# PET uptake findings

Note that there is no remaining uptake in the area of the primary tumor or nodes after treatment







# Conclusion

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- This tutorial has demonstrated how to do 3D data visualization, quantitative measurement of small changes in tumor size, and PET CT SUV computation in Slicer
- 3DSlicer is for research use only, and is not FDA approved
- 3DSlicer is a free open-source software for medical image computing and supported by the NIH



# Acknowledgments

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# 3DSlicer at RSNA 2013

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## Quantitative Imaging Reading Room Exhibit QIRR 1028

- Sun. Dec.1-Fri. Dec.6, 8:00-6:00
- 3DSlicer: An Open Source Platform for Segmentation, Registration, Quantitative Imaging, and 3D Visualization of Multi-Modal Image Data.
- Sonia Pujol, PhD, Steve Pieper, PhD, Andriy Fedorov, PhD, Ron Kikinis, MD,



# Additional Related Hands-on courses

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*All courses are in this Advanced Imaging Classroom: S401CD  
(except Monday when it is in S401AB)*

**Sunday 4:00 pm** – Structured Annotation and Image Markup (AIM) Template and Toolsets (ICIW12)

**Monday 4:30 pm** – Clinical Trials Software for Clinical Trials and Research (ICIW24)

**Wed 10:30 am** – Open Access Imaging Data Resources: NIH Cancer Imaging Archive (ICIA41)

**Wed 12:30 pm** – Correlating Imaging with Human Genomics (ICIA42)



# 3DSlicer at RSNA

Sunday, December 1	Monday, December 2	Tuesday, December 3	Wednesday, December 4	Thursday, December 5	Friday, December 6
<b>8:00am-11:00am: 3D Slicer</b> Exhibit: <a href="#">Quantitative Imaging Reading Room</a> . Lakeside Learning Center Hall E, Exhibit LL-QRR3007.	<b>8:00am-11:00am: 3D Slicer</b> Exhibit: <a href="#">Quantitative Imaging Reading Room</a> . Lakeside Learning Center Hall E, Exhibit LL-QRR3007.	<b>8:00am-11:00am: 3D Slicer</b> Exhibit: <a href="#">Quantitative Imaging Reading Room</a> . Lakeside Learning Center Hall E, Exhibit LL-QRR3007.		<b>8:00am-12:15pm: 3D Slicer</b> Exhibit: <a href="#">Quantitative Imaging Reading Room</a> . Lakeside Learning Center Hall E, Exhibit LL-QRR3007.	
<b>11:00am-12:30pm: RSNA</b> Refresher Course: "Quantitative Medical Imaging for Clinical Research and Practice: Hands-on Workshop." Sonia Pujol, Katarzyna Macura, Ron Kikinis Room S401CD.	<b>12:30pm-1:30pm: Meet-The-Experts Session</b> , 3D Slicer Exhibit: <a href="#">Quantitative Imaging Reading Room</a> . Lakeside Learning Center Hall E, Exhibit LL-QRR3007.	<b>12:30pm-2:00pm: RSNA</b> Refresher Course: "3D Interactive Visualization of DICOM Images for Radiology Applications: Hands-on Workshop." Sonia Pujol, Kitt Shaffer, Ron Kikinis Room S401CD.	<b>8:00am-12:15pm: 3D Slicer</b> Exhibit: <a href="#">Quantitative Imaging Reading Room</a> . Lakeside Learning Center Hall E, Exhibit LL-QRR3007.	<b>12:30pm-1:30pm: 3D Slicer</b> Exhibit: <a href="#">Quantitative Imaging Reading Room</a> . Lakeside Learning Center Hall E, Exhibit LL-QRR3007.	<b>8:00am-12:45pm: 3D Slicer</b> Exhibit: <a href="#">Quantitative Imaging Reading Room</a> . Lakeside Learning Center Hall E, Exhibit LL-QRR3007.
<b>12:30pm-1:30pm: Meet-The-Experts Session</b> , 3D Slicer Exhibit: <a href="#">Quantitative Imaging Reading Room</a> . Lakeside Learning Center Hall E, Exhibit LL-QRR3007.	<b>1:30pm-6:00pm: 3D Slicer Exhibit: Quantitative Imaging Reading Room</b> . Lakeside Learning Center Hall E, Exhibit LL-QRR3007.	<b>12:30pm-1:30pm: Meet-The-Experts Session</b> , 3D Slicer Exhibit: <a href="#">Quantitative Imaging Reading Room</a> . Lakeside Learning Center Hall E, Exhibit LL-QRR3007. ---	<b>1:30pm-6:00pm: 3D Slicer Exhibit: Quantitative Imaging Reading Room</b> . Lakeside Learning Center, Hall E, Exhibit LL-QRR3007.	<b>1:30pm-6:00pm: 3D Slicer Exhibit: Quantitative Imaging Reading Room</b> . Lakeside Learning Center Hall E, Exhibit LL-QRR3007.	
<b>1:30pm-6:00pm: 3D Slicer Exhibit: Quantitative Imaging Reading Room</b> . Lakeside Learning Center Hall E, Exhibit LL-QRR3007.		<b>1:30pm-6:00pm: 3D Slicer Exhibit: Quantitative Imaging Reading Room</b> . Lakeside Learning Center Hall E, Exhibit LL-QRR3007.			

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