

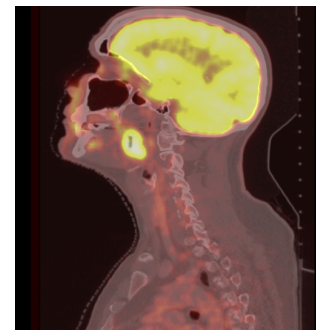
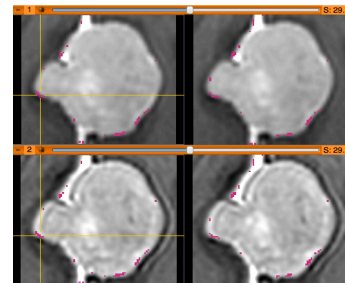


Surgical Planning Laboratory
Brigham and Women's Hospital
Boston, Massachusetts USA

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



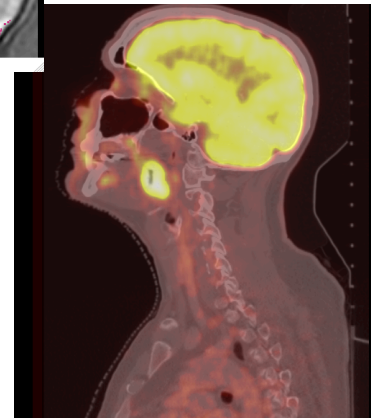
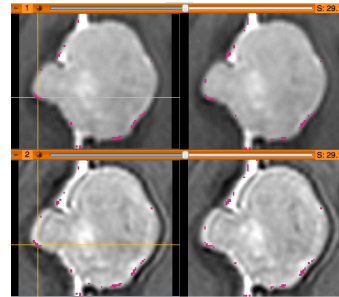


Quantitative Imaging Tutorial

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

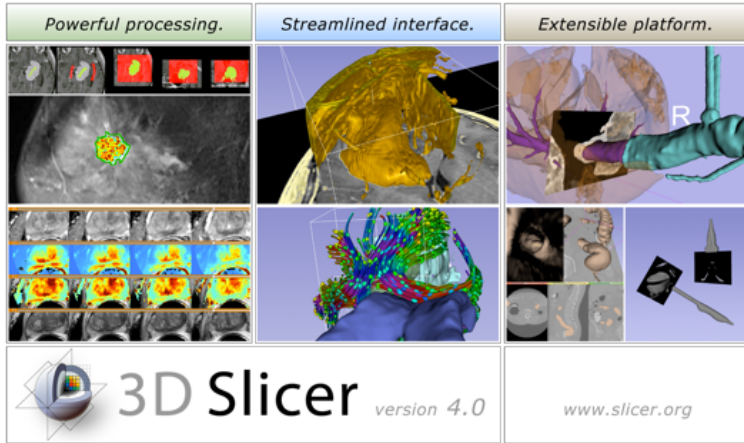
This tutorial is built upon two examples of quantitative imaging:

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





Quantitative Imaging: Software



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**.



Tutorial Overview

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

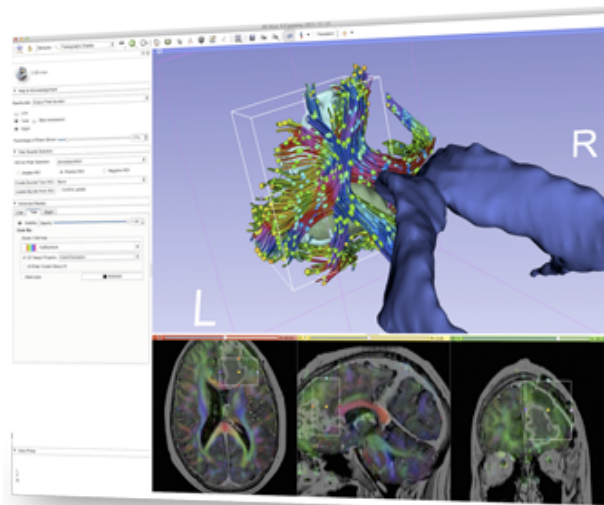
Part 2: Measurement of small Volumetric Changes in meningioma using the Change Tracker module

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



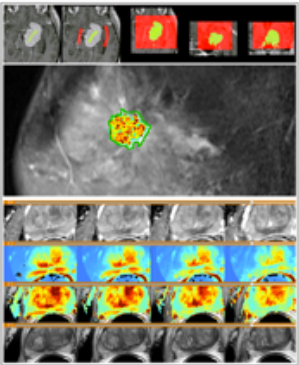
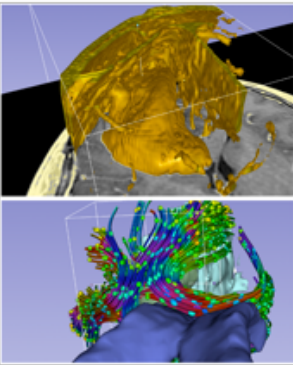
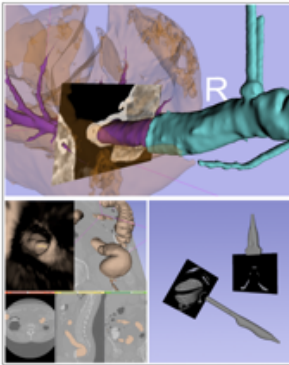

Introduction to the 3DSlicer software

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





3DSlicer

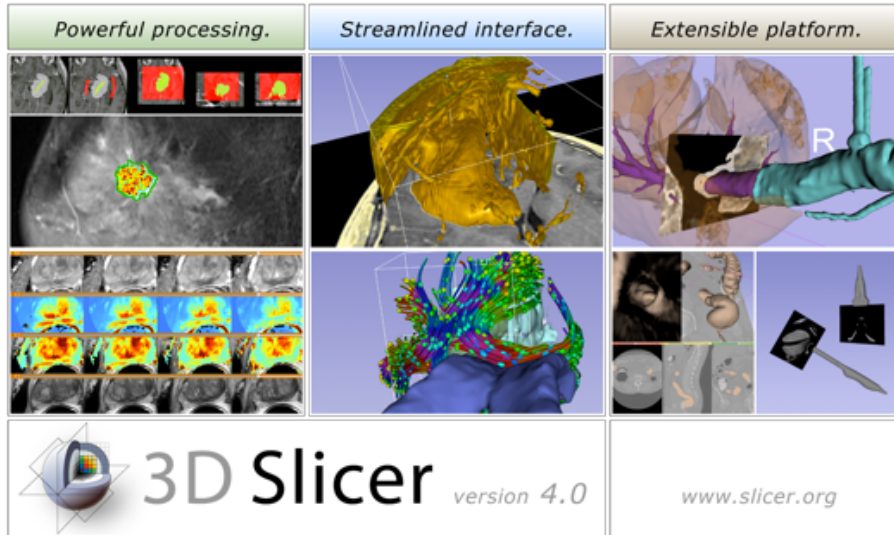
Powerful processing.	Streamlined interface.	Extensible platform.
		
 3D Slicer <i>version 4.0</i>		www.slicer.org

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

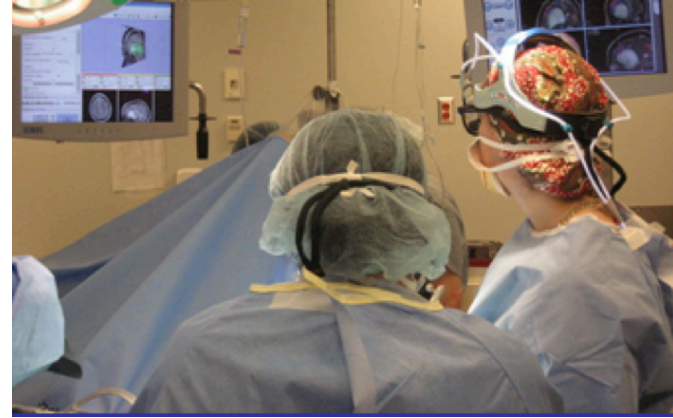
It is the responsibility of the user of 3DSlicer to comply with both the terms of the license and with the applicable laws, regulations and rules.



An interdisciplinary platform



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

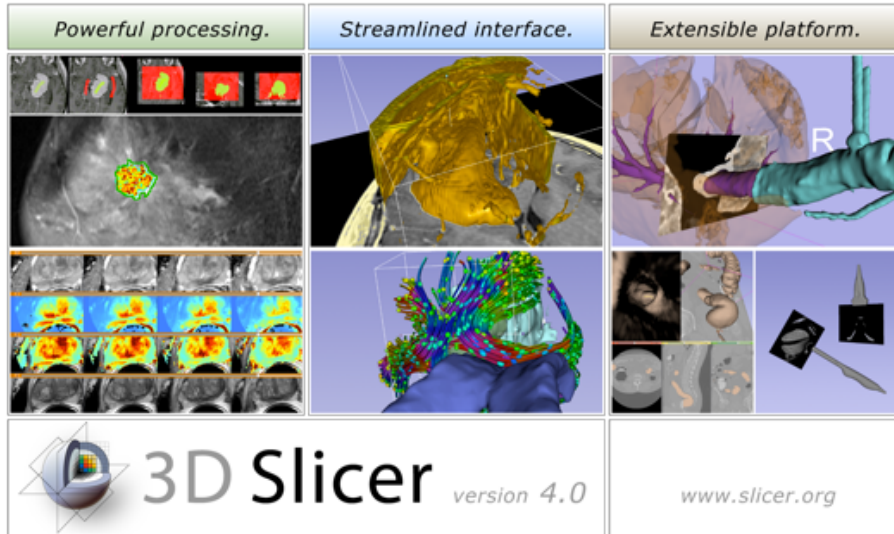


An **end-user application** for clinical investigators and scientists

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



3DSlicer History



- 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

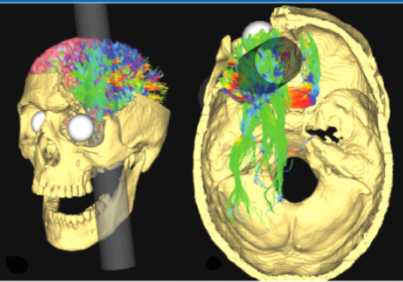
- Overview
- Organization
- Contact Us

Center Components

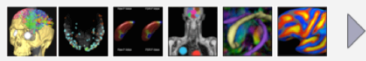
- Algorithms
- Engineering
- Driving Biological Projects
- Collaboration Grants

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
Information about collaborating with NA-MIC

PI: Ron Kikinis, M.D.

NAC **Neuroimage Analysis Center**
"understanding the human brain through imaging"

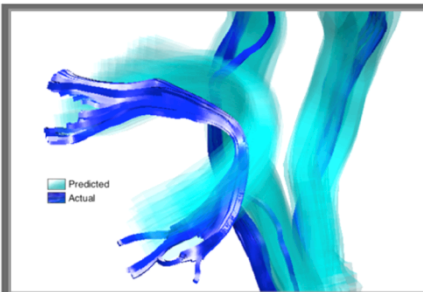
Google Custom Search **GO**

About the NAC

- Overview
- Organization
- Research Cores
- Collaborations

Resources

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




FMRI-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 individual peaks and gradient landmark AL plus the leave-one-out LDA from the other subjects, were used to predict the location of the 'A', left CST, and right CST. The true anatomies 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.

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 center supported by the National Center for Research Resources (2011) and the Institute of Biomedical Imaging and Bioengineering (NIBIB), National Institutes of Health.



National Center for Image-Guided Therapy

NCIGT Wiki

About Us

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

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- Publication DB
- Image Gallery
- Downloads
- AMIGO
- News and Events
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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 NCRRL and NIBIB Institutes

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



Slicer: Behind the scenes

CDash - Slicer4

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	Error	Warn		
factory-win7.kitware	Windows7-VS2010-32bits-QT4.7.1-PythonQt-With-Tcl-CLI-Release	0	0	0	2	0	107	0	0	
factory-mac-64bits.kitware	SnowLeopard-g++4.2.1-64bits-QT4.7-PythonQt-With-Tcl-CLI-Release	1	0	0	0	0	14	0	0	
factory-ubuntu-64bits.kitware	Linux-g++4.4.3-64bits-QT4.7-PythonQt-With-Tcl-CLI-Release	1	0	0	0	0	13	0	0	
factory-win7.kitware	Windows7-VS2008-64bits-QT4.7.1-PythonQt-With-Tcl-CLI-Release	0	0	0	0	0	1000	0	0	
factory-win7.kitware	Windows7-VS2008-32bits-QT4.7.1-PythonQt-With-Tcl-CLI-Release	1	0	0	0	0	1000	0	0	

Nightly

Site	Build Name	Update			Configure			Build			Test			Build Time
		Files	Error	Warn	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	0	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	0	15	0	304	6			11 hours ago	
eris.kitware	Linux-g++4.4-QT4.6.3-PythonQt-CLI-Release	1	0	0	0	0	15	0	36	451			3 hours ago	
factory-ubuntu-64bits.kitware	Linux-g++4.4.3-QT4.7-PythonQt-With-Tcl-CLI-Valgrind-Release	0	0	0	0	0	13	0	27	460			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	0	12	0	23	287			11 hours ago	
sagarmatha.kitware	Linux-g++4.3.3-QT4.7-PythonQt-With-Tcl-NoCLI-Release	0	0	0	0	0	12	0	22	288			12 hours ago	

Continuous

Site	Build Name	Update			Configure			Build			Test			Build Time
		Files	Error	Warn	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	0	0	0	304	6			1 hour ago

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



Slicer Training



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

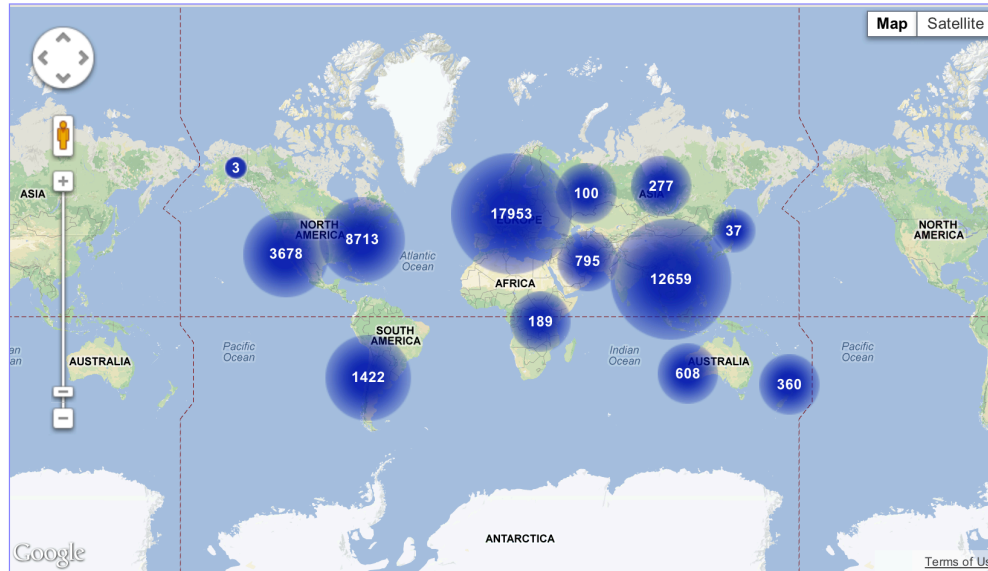
Update

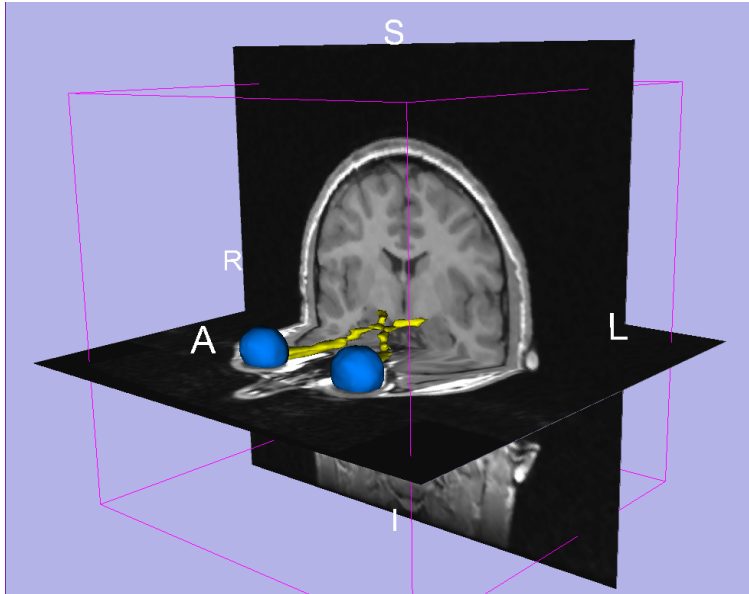
Download location

By Country

By Filename

By Month





Part I: 3D Data Loading and Visualization

Sonia Pujol, PhD
Wendy Plesniak, PhD



3D Data Loading and Visualization

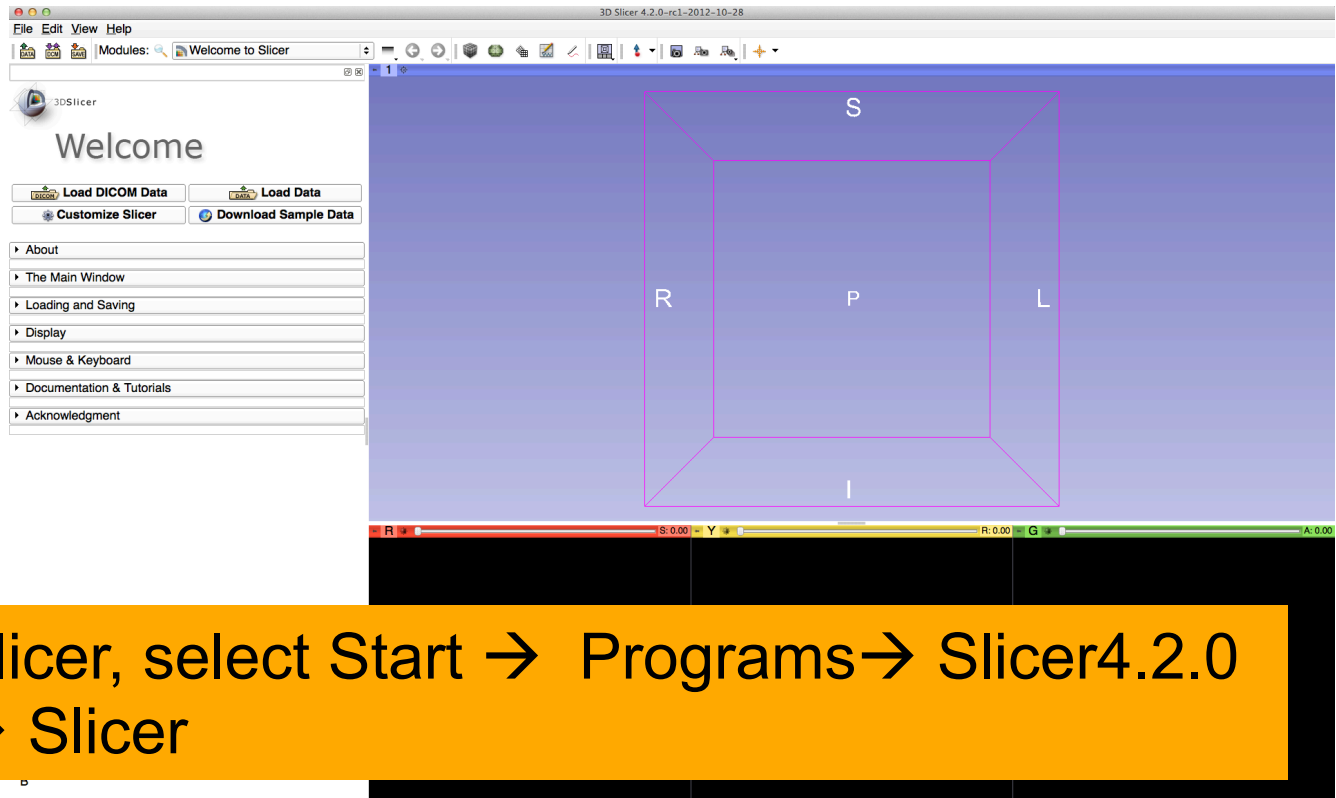


- This tutorial is a short introduction to the advanced **3D visualization capabilities Slicer**
- The Slicer4 Minute dataset is composed of an MR scan of the brain and 3D surface reconstructions of anatomical structures.
- The data are part of the SPL-PNL Brain Atlas developed by Talos, Jakab, Kikinis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

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



Welcome to Slicer4



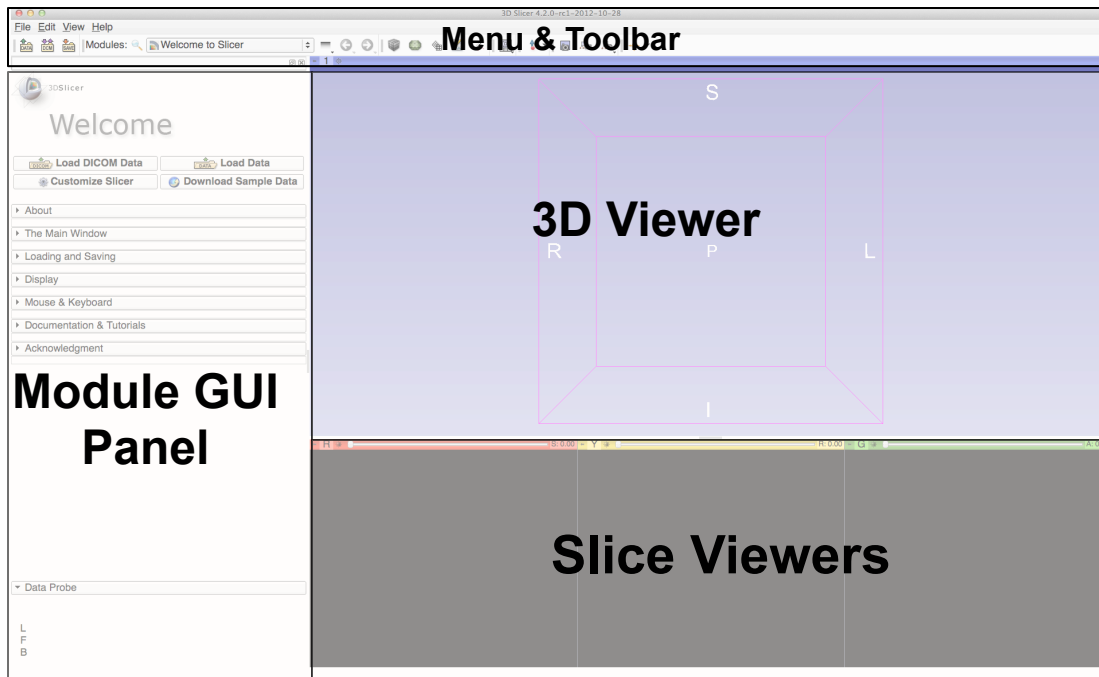
To start Slicer, select Start → Programs → Slicer4.2.0 (Win64) → Slicer



Slicer4 Minute Tutorial: Navigating the Application GUI

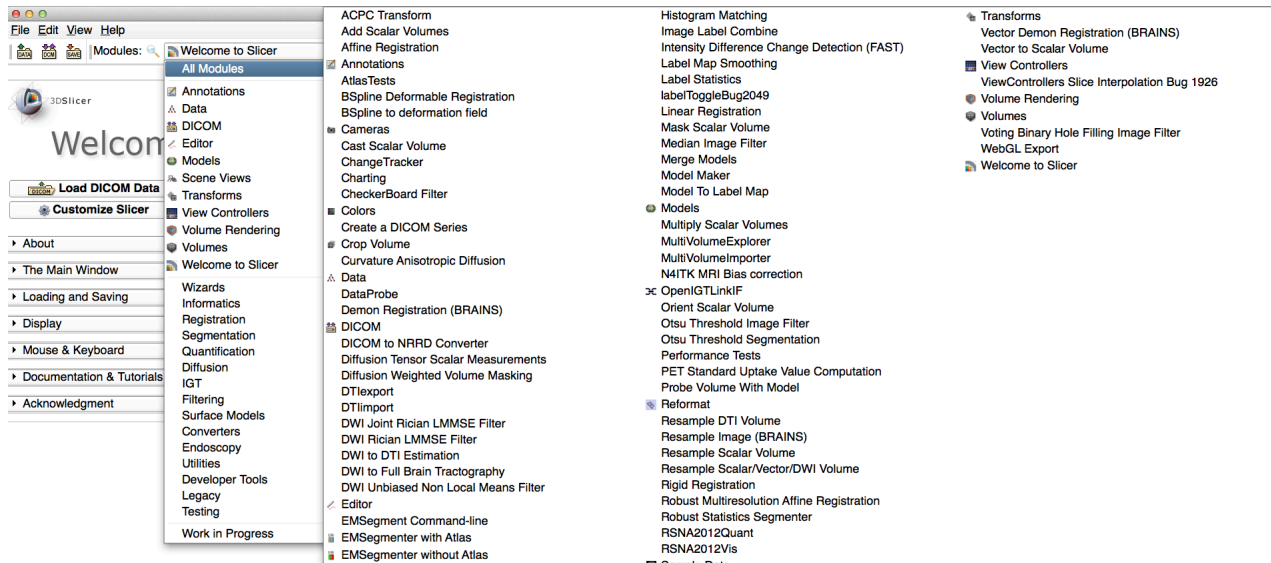
The Graphic User Interface (GUI) of Slicer4 integrates **four components**:

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





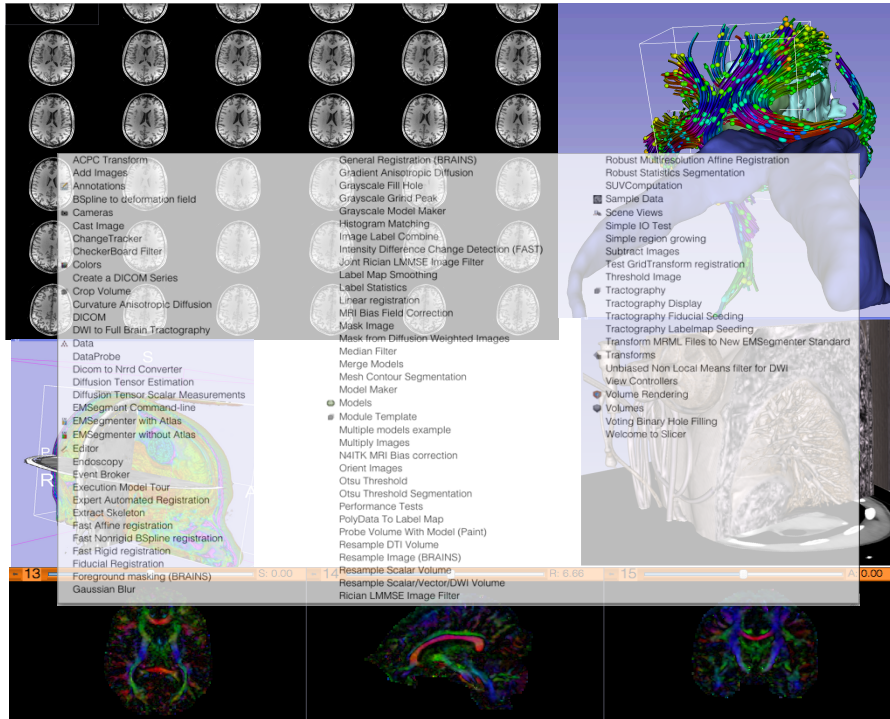
Welcome to Slicer4.2



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



Welcome to Slicer4



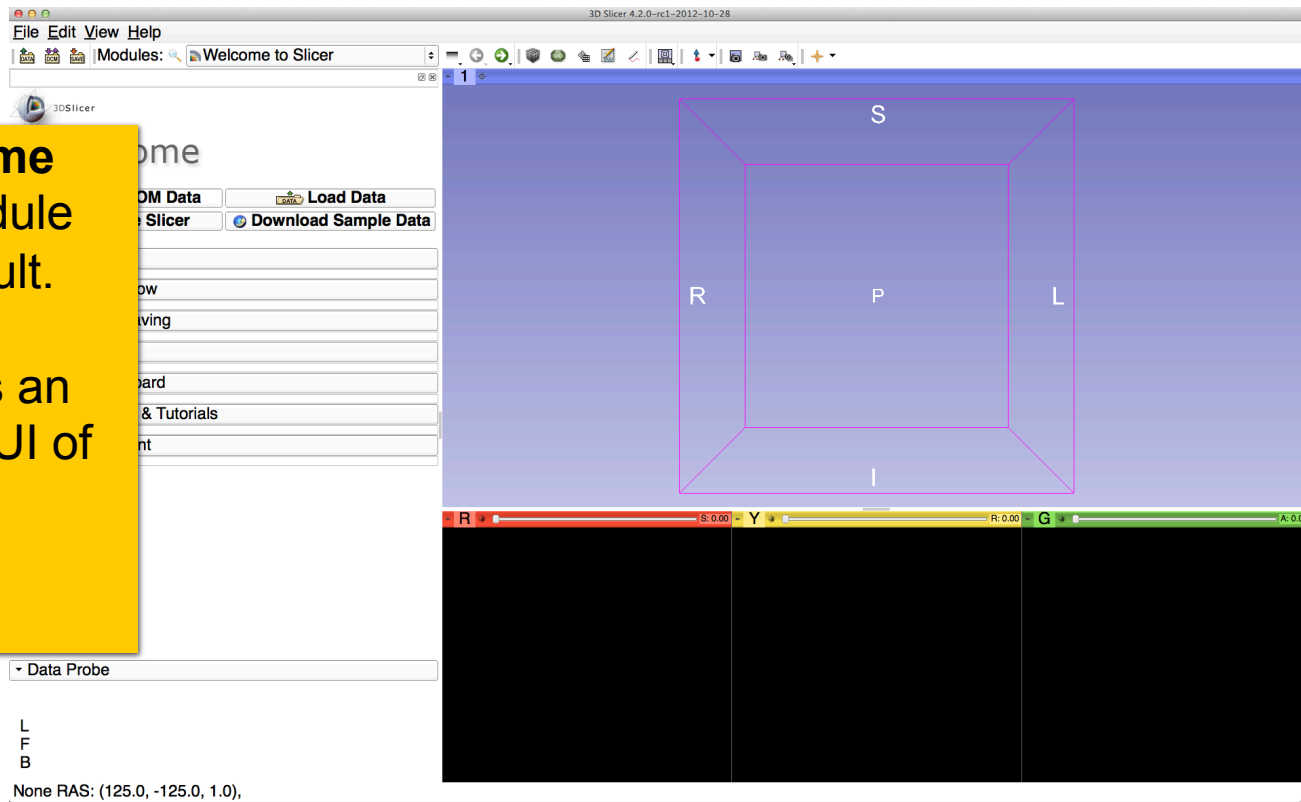
Slicer4.2 contains more than 100 modules for image segmentation, registration and 3D visualization of medical imaging data



Slicer4 Minute Tutorial: Welcome Module

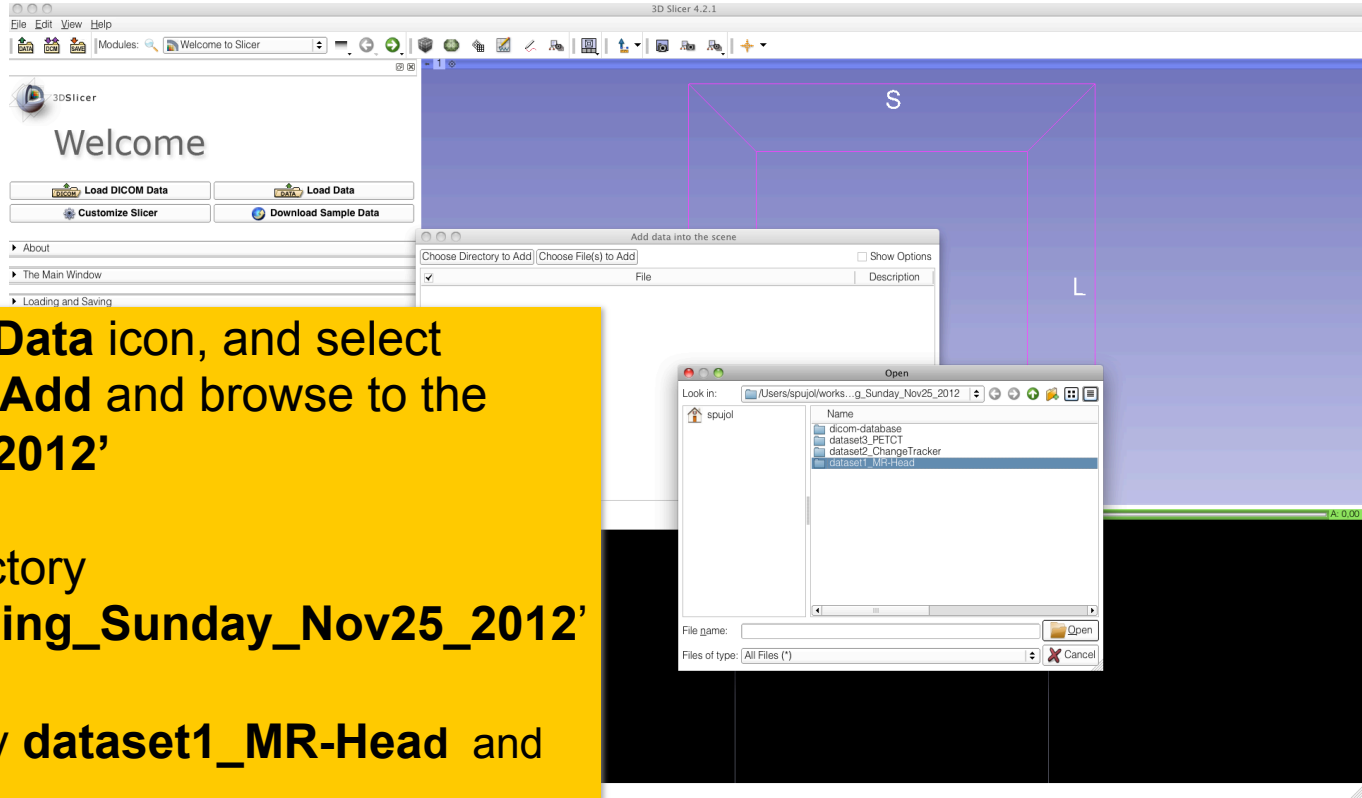
The **SlicerWelcome** module is the module displayed by default.

This module gives an overview of the GUI of Slicer4, and **data loading & saving functionalities**.





Slicer4 Minute Tutorial: Load a Scene



Click on the **Load Data** icon, and select **Choose File(s) to Add** and browse to the directory **'C:\Pujol2012'**

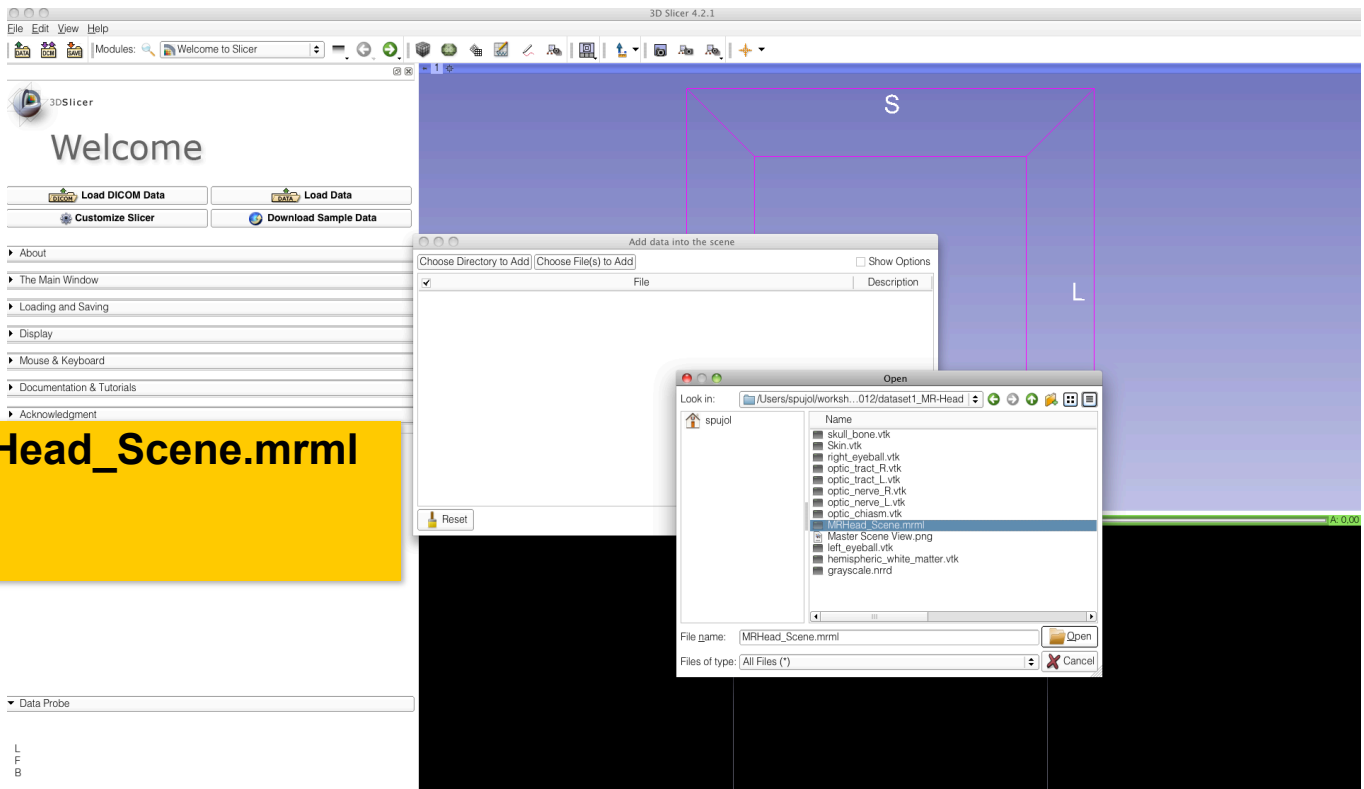
Select the subdirectory **'QuantitativeImaging_Sunday_Nov25_2012'**

Select the directory **dataset1_MR-Head** and click on **Open**



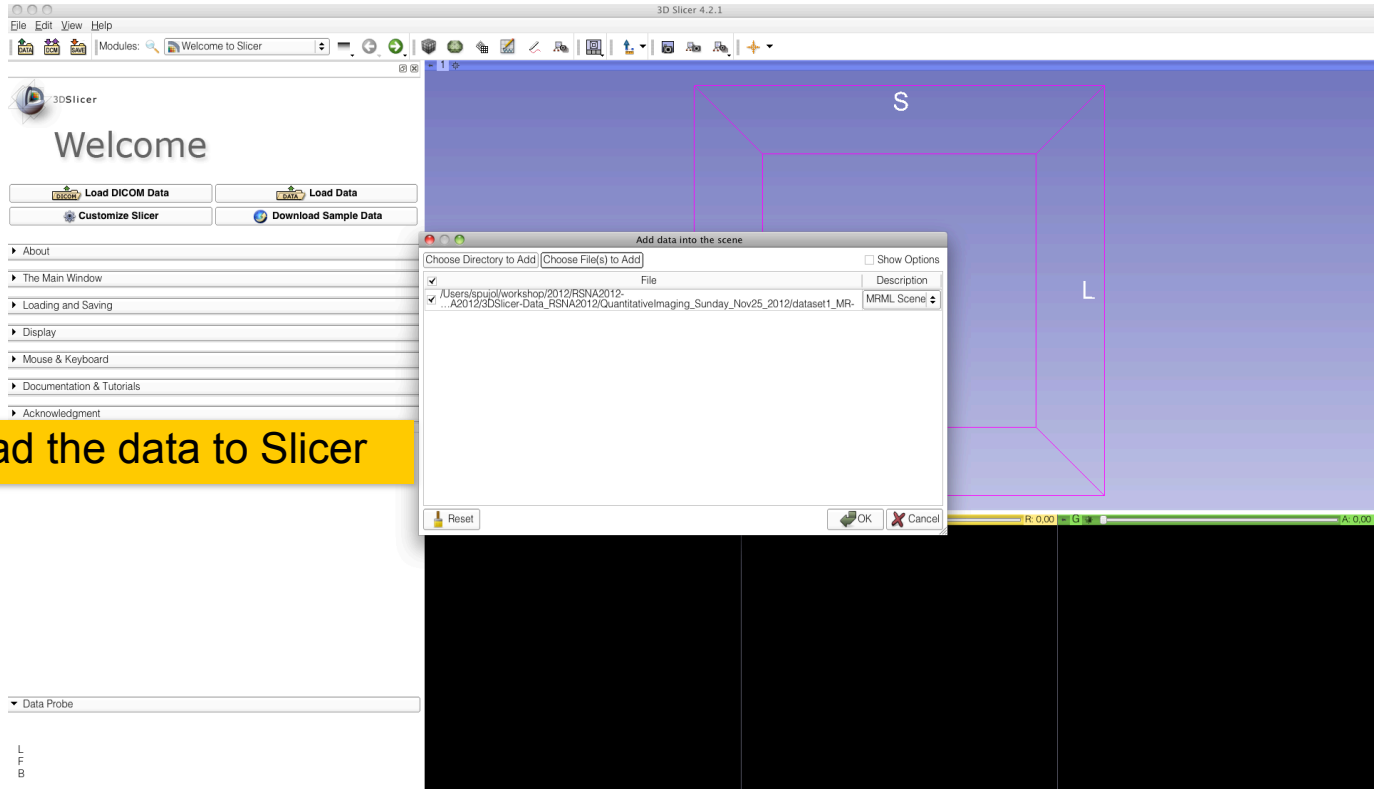
Slicer4 Minute Tutorial: Load a Scene

Select the file **MRHead_Scene.mrml** and click on **Open**





Slicer4 Minute Tutorial: Load a Scene

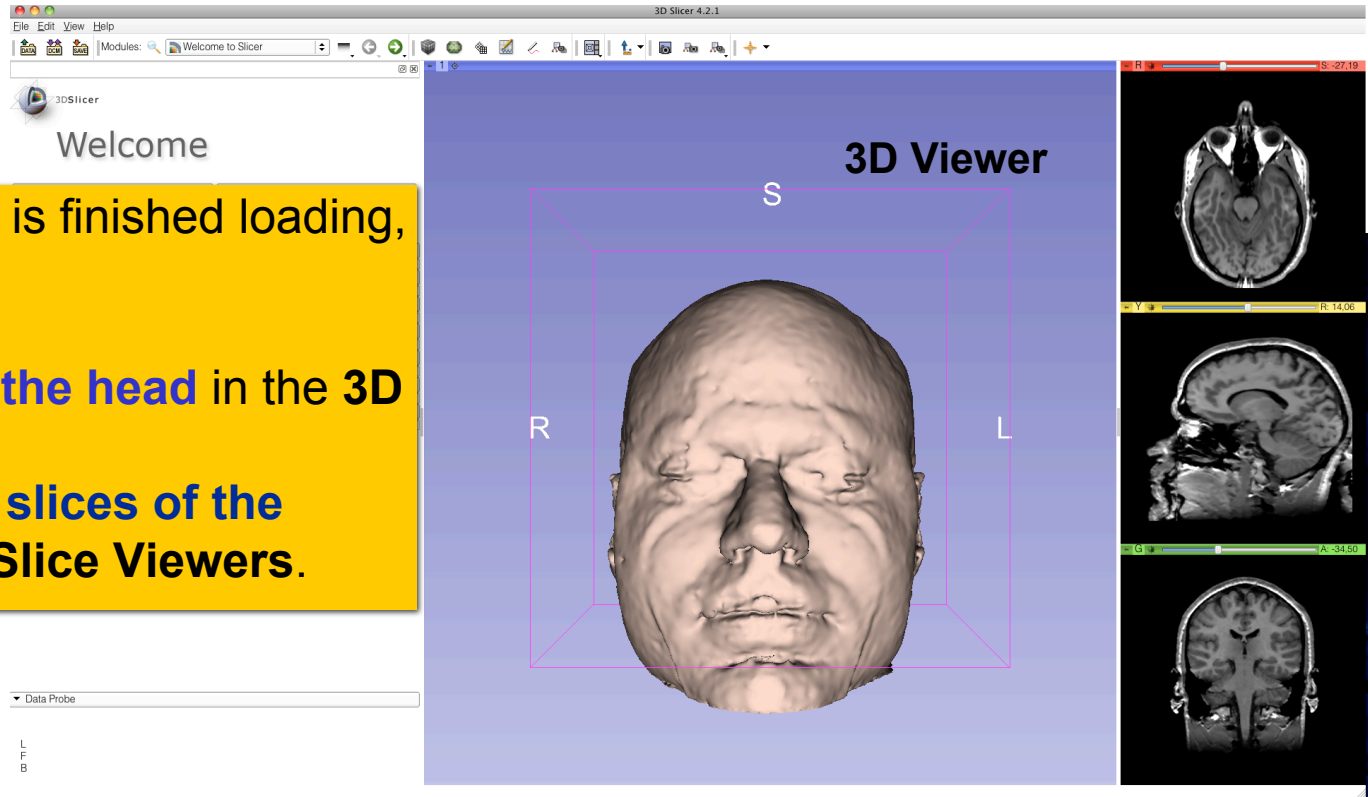




Slicer4 Minute Tutorial: Viewing the Scene

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**.

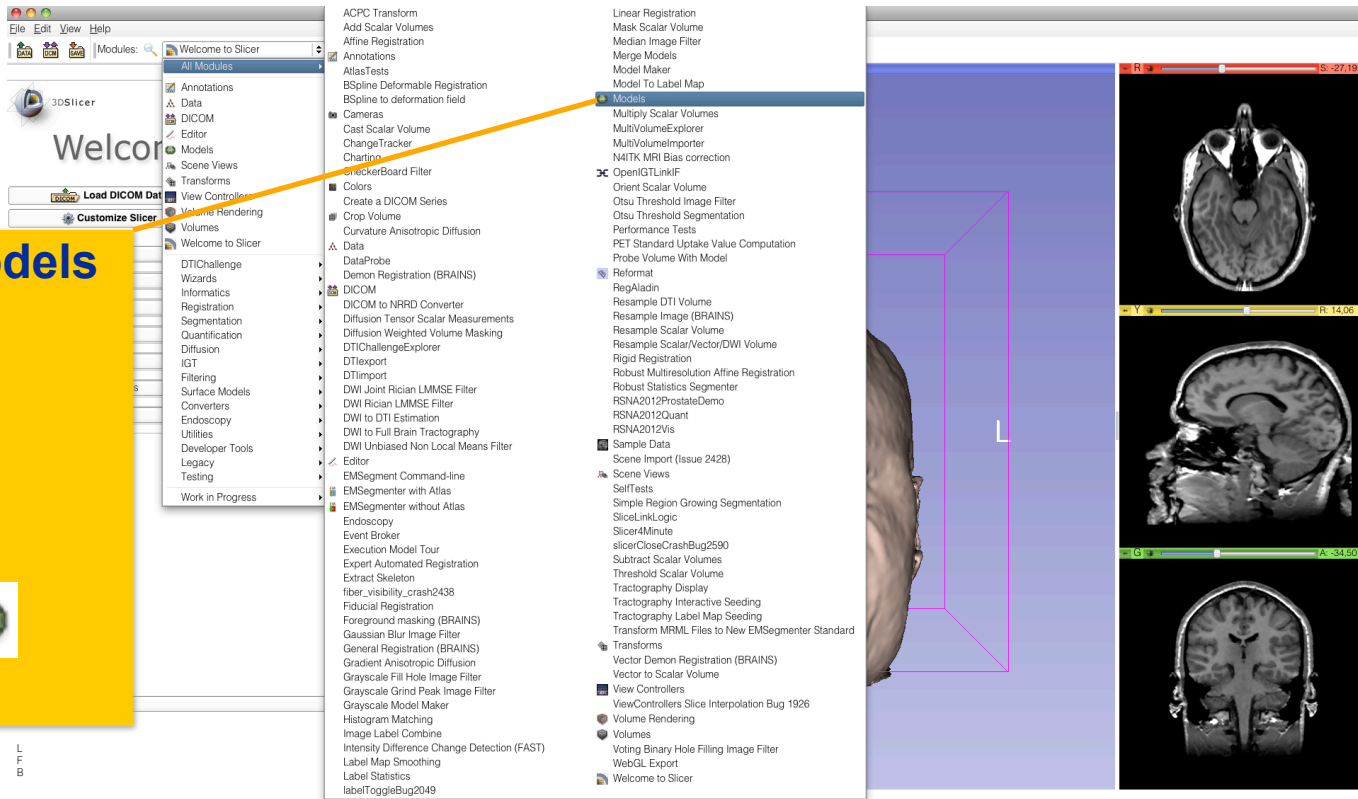




Slicer4 Minute Tutorial: Exploring Slicer's functionality

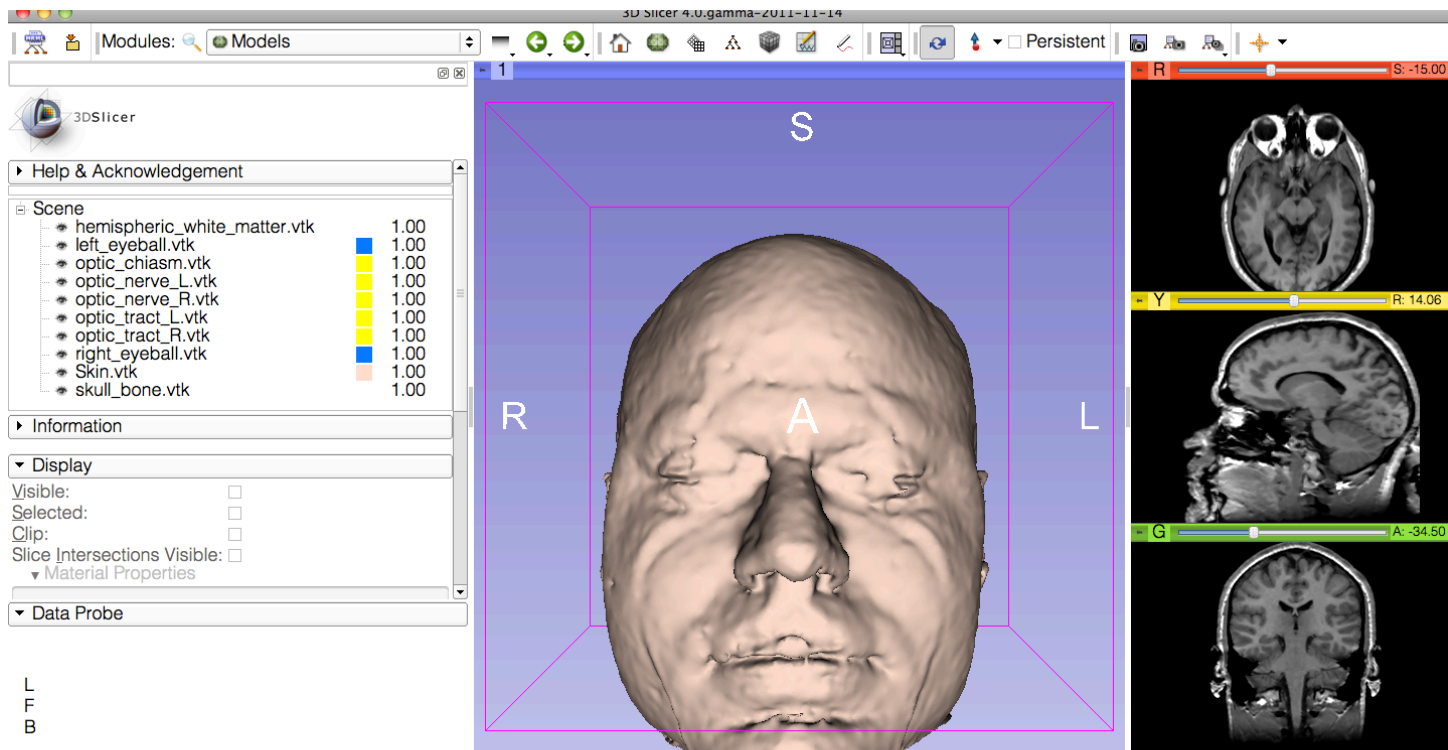
To access the **Models** module, browse through the list of modules...

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





Slicer4 Minute Tutorial: Switching to the Models Module

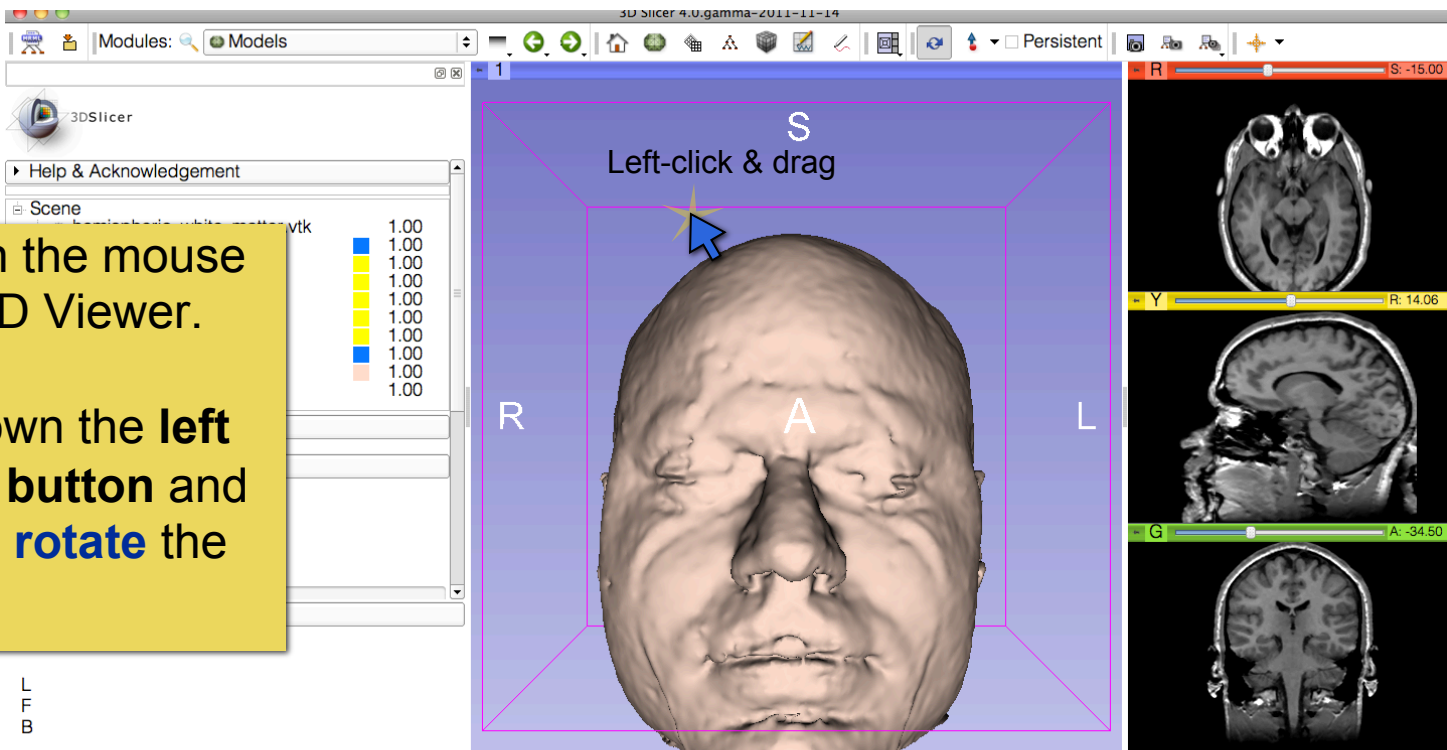




Slicer4 Minute Tutorial: Basic 3D Interaction

Position the mouse in the 3D Viewer.

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

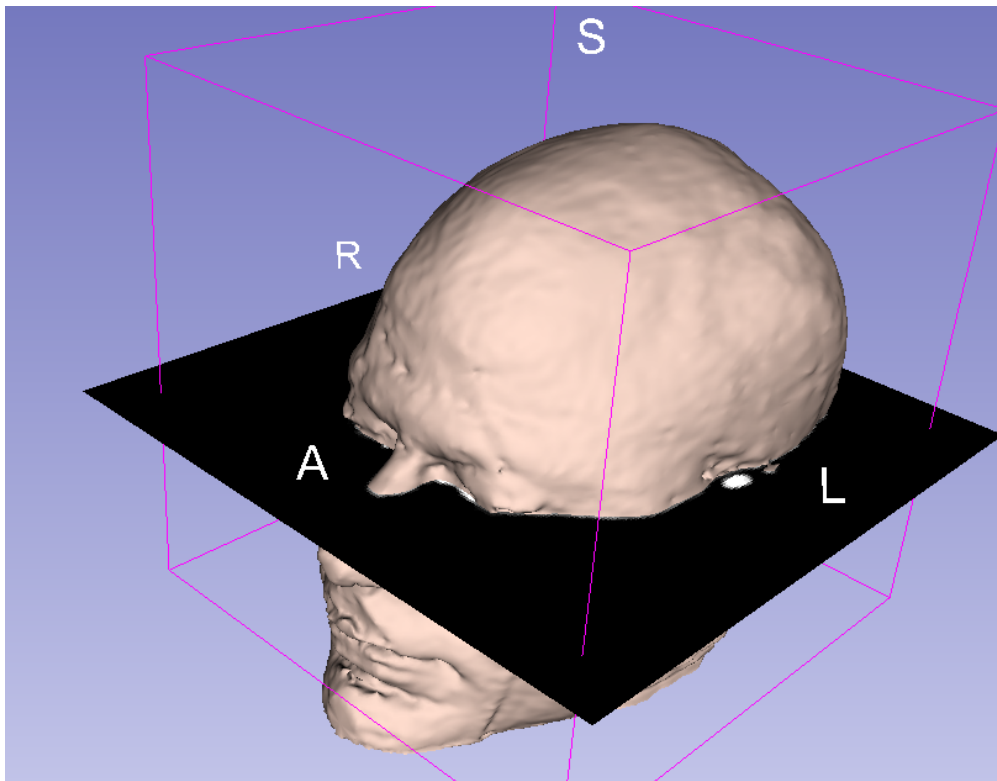


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Slicer4 Minute Tutorial: 3D Visualization

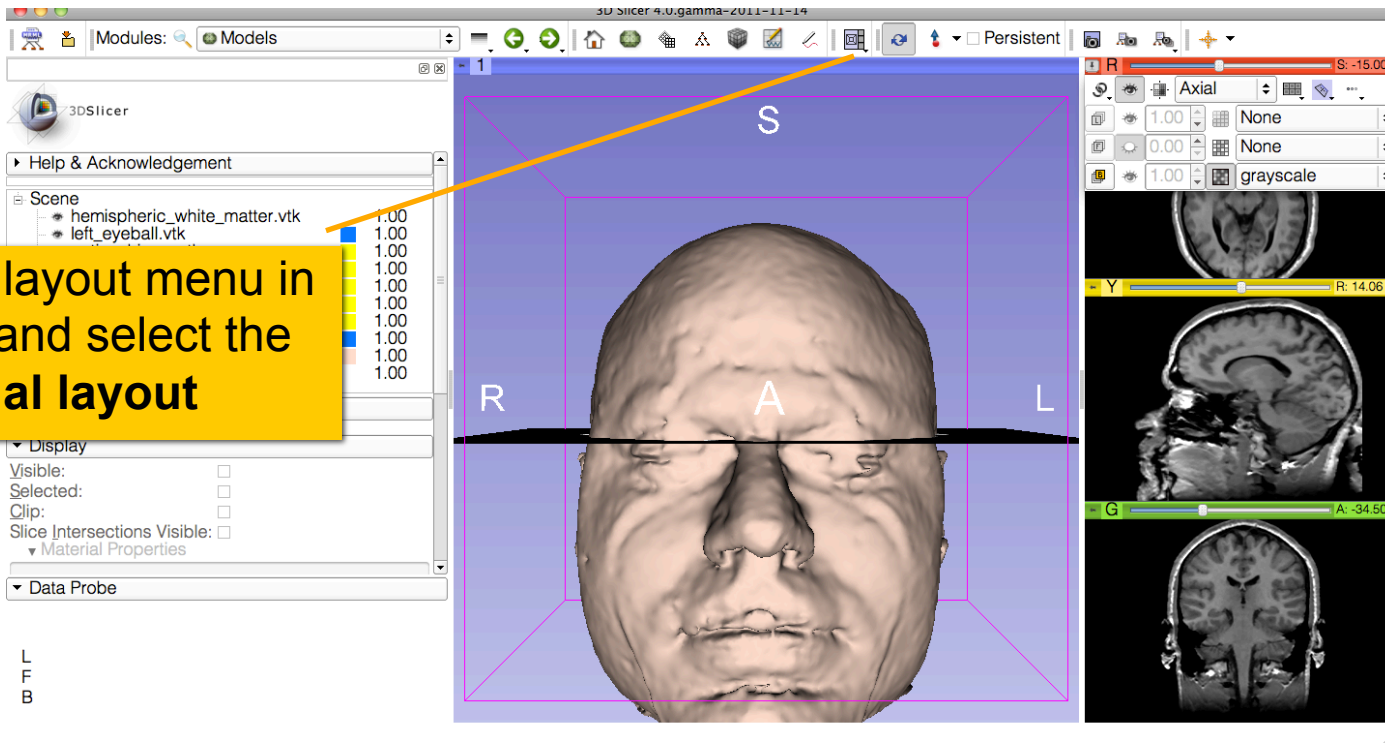
Slicer adds a view of the **Axial slice** in the 3D View.





Slicer4 Minute Tutorial: Viewing Slices in the 3D Viewer

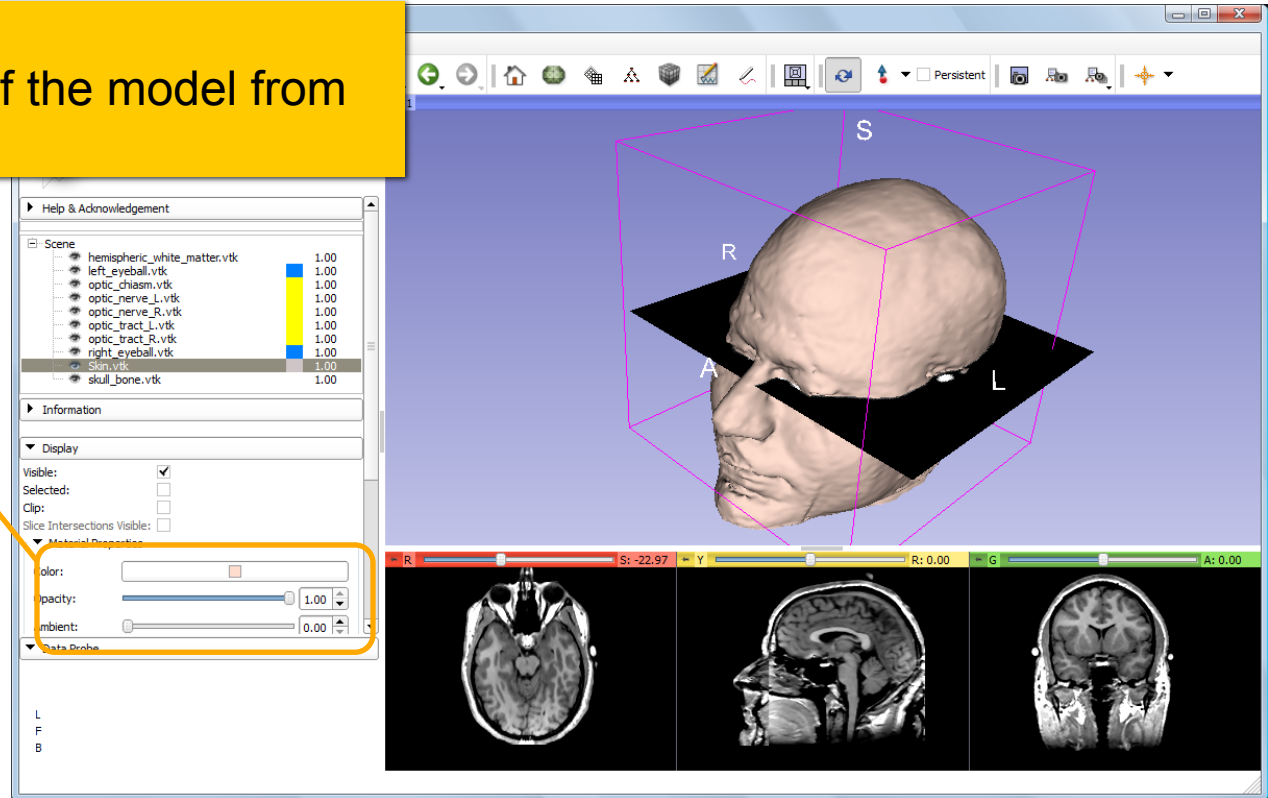
Click on the layout menu in the toolbar, and select the **Conventional layout**





Slicer4 Minute Tutorial: 3D Visualization

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

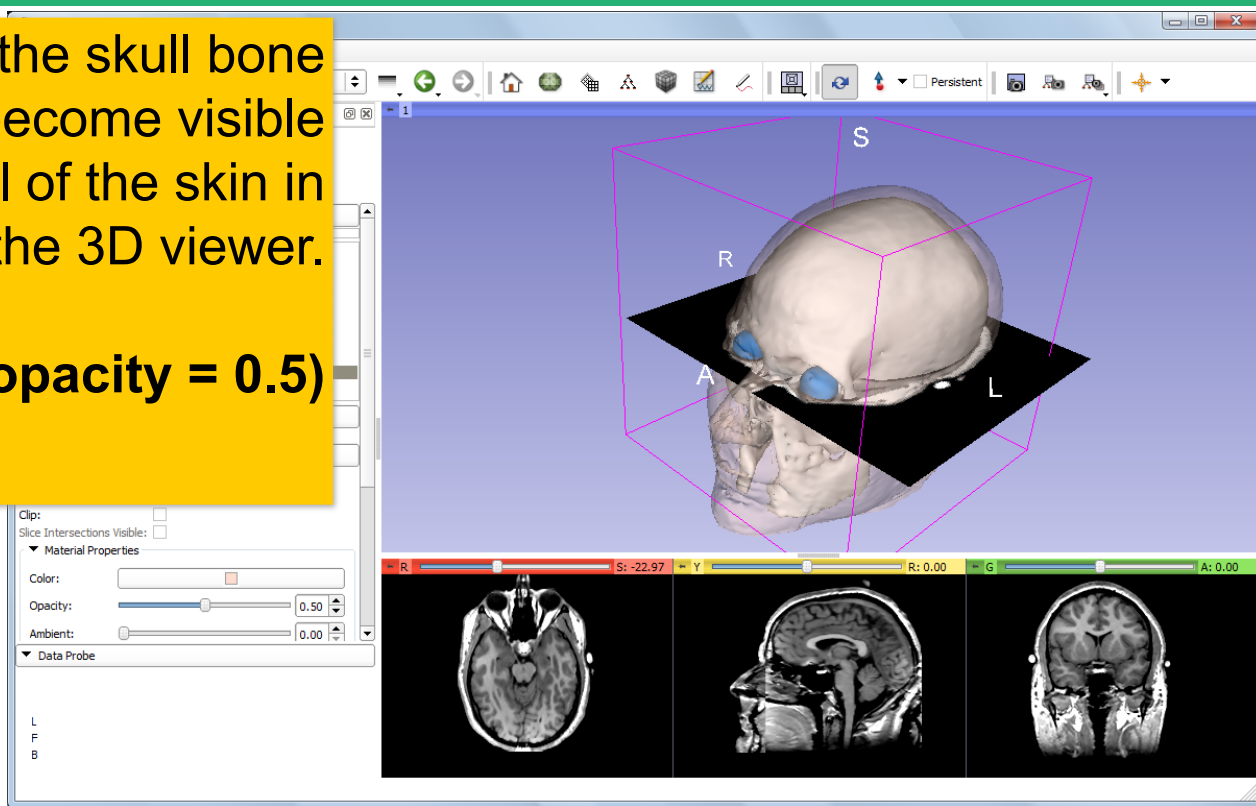




Slicer4 Minute Tutorial: 3D Visualization

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)

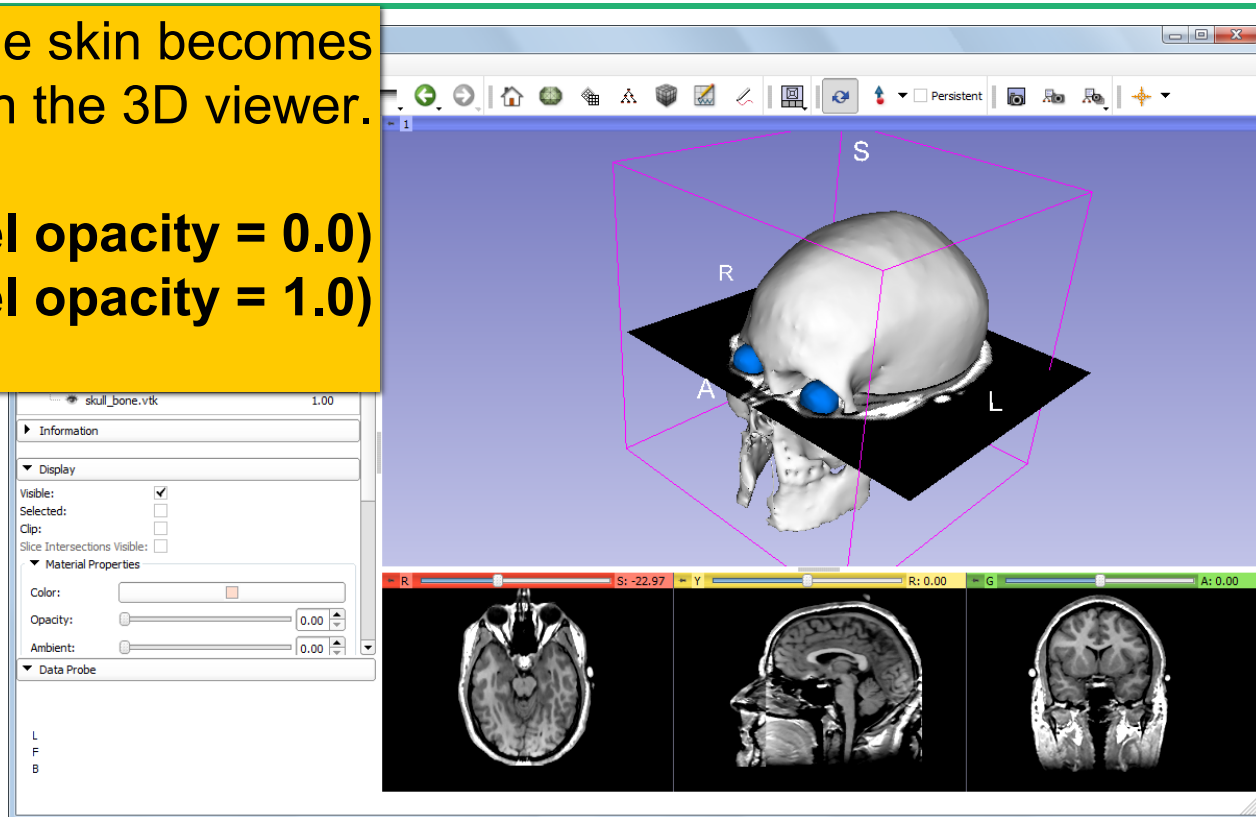




Slicer4 Minute Tutorial: 3D Visualization

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.



Information

Display

Visible:

Selected:

Clip:

Slice Intersections Visible:

Material Properties

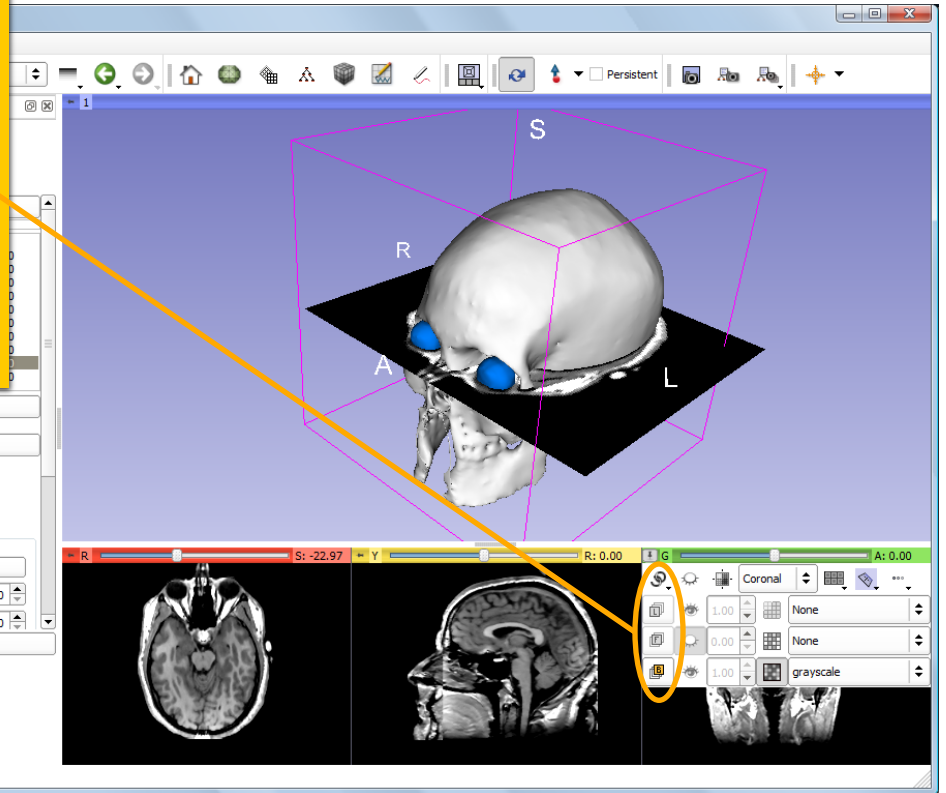
Color:

Opacity: 0.00

Ambient: 0.00

Data Probe

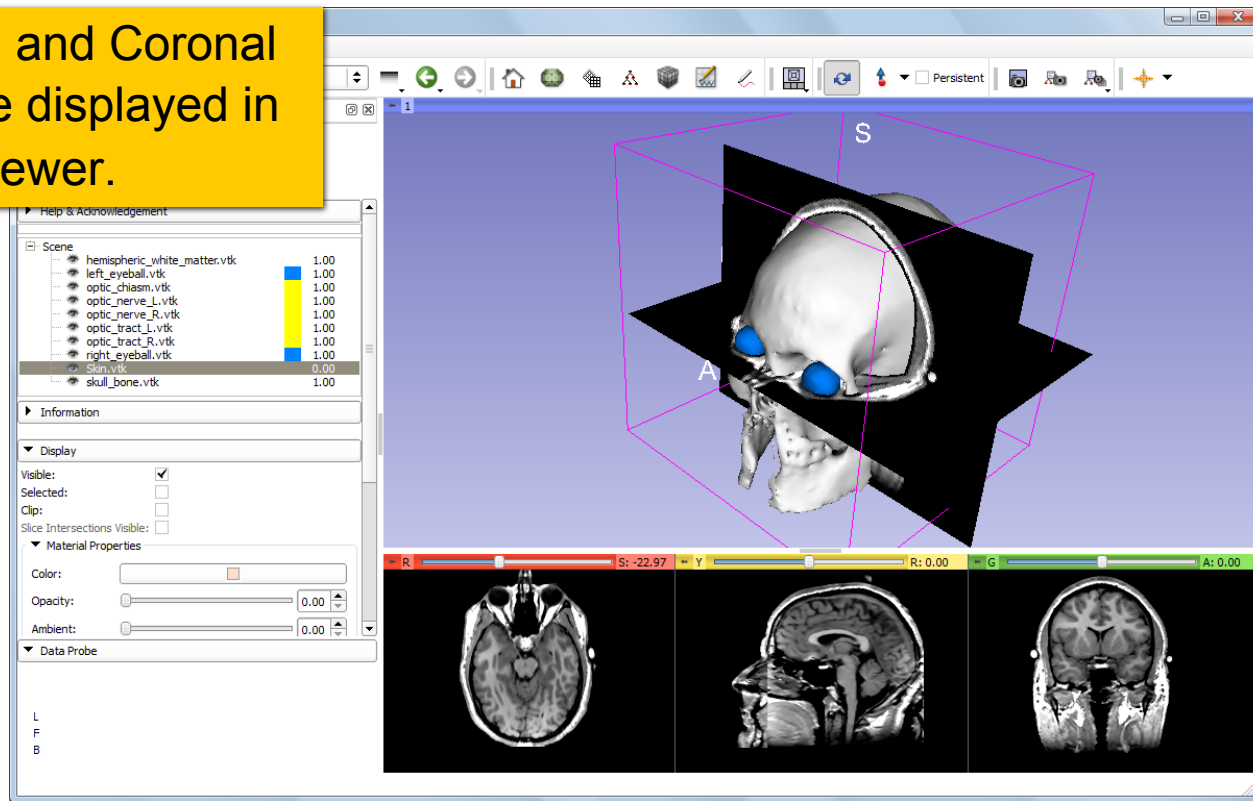
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F
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Slicer4 Minute Tutorial: 3D Visualization

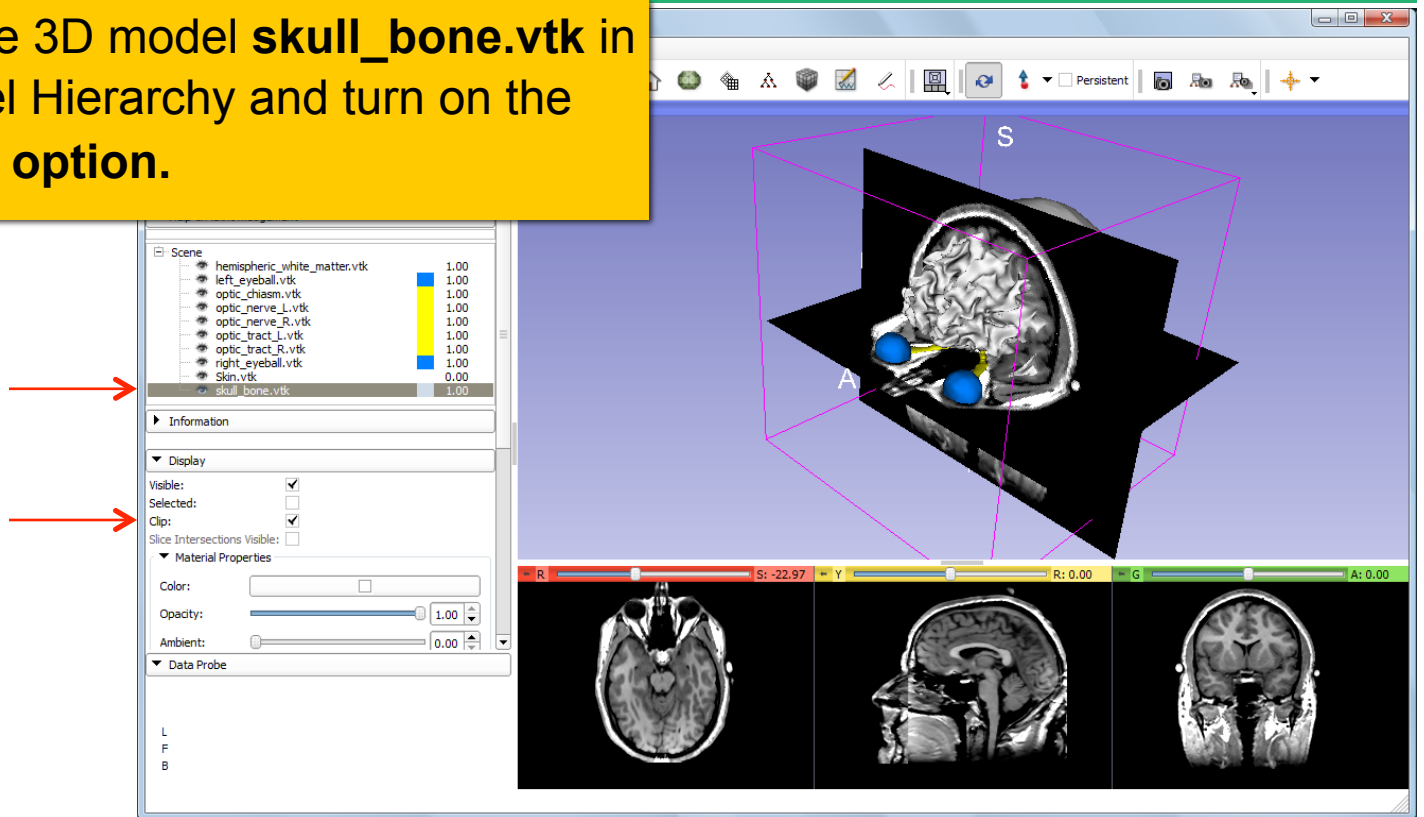
The Axial and Coronal Slices are displayed in the 3D Viewer.





Slicer4 Minute Tutorial: 3D Visualization

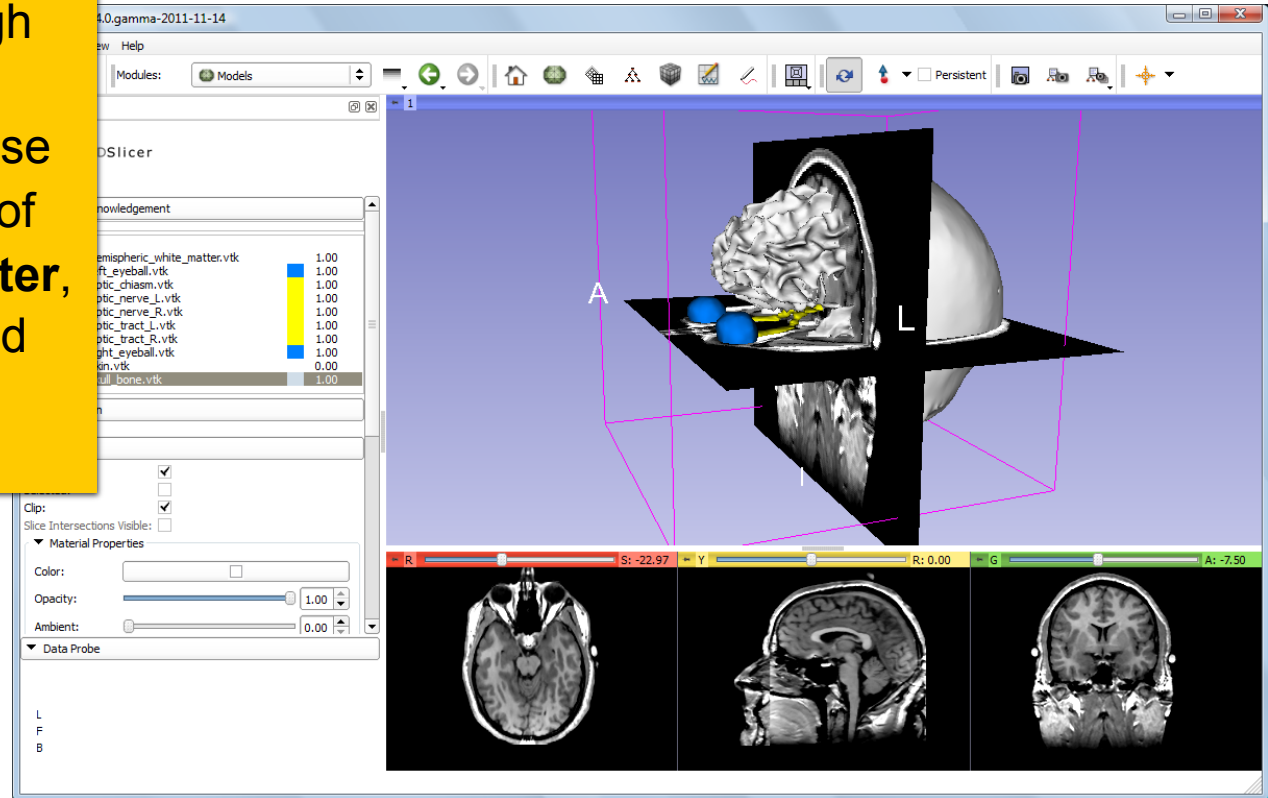
Select the 3D model **skull_bone.vtk** in the Model Hierarchy and turn on the **Clipping** option.





Slicer4 Minute Tutorial: 3D Visualization

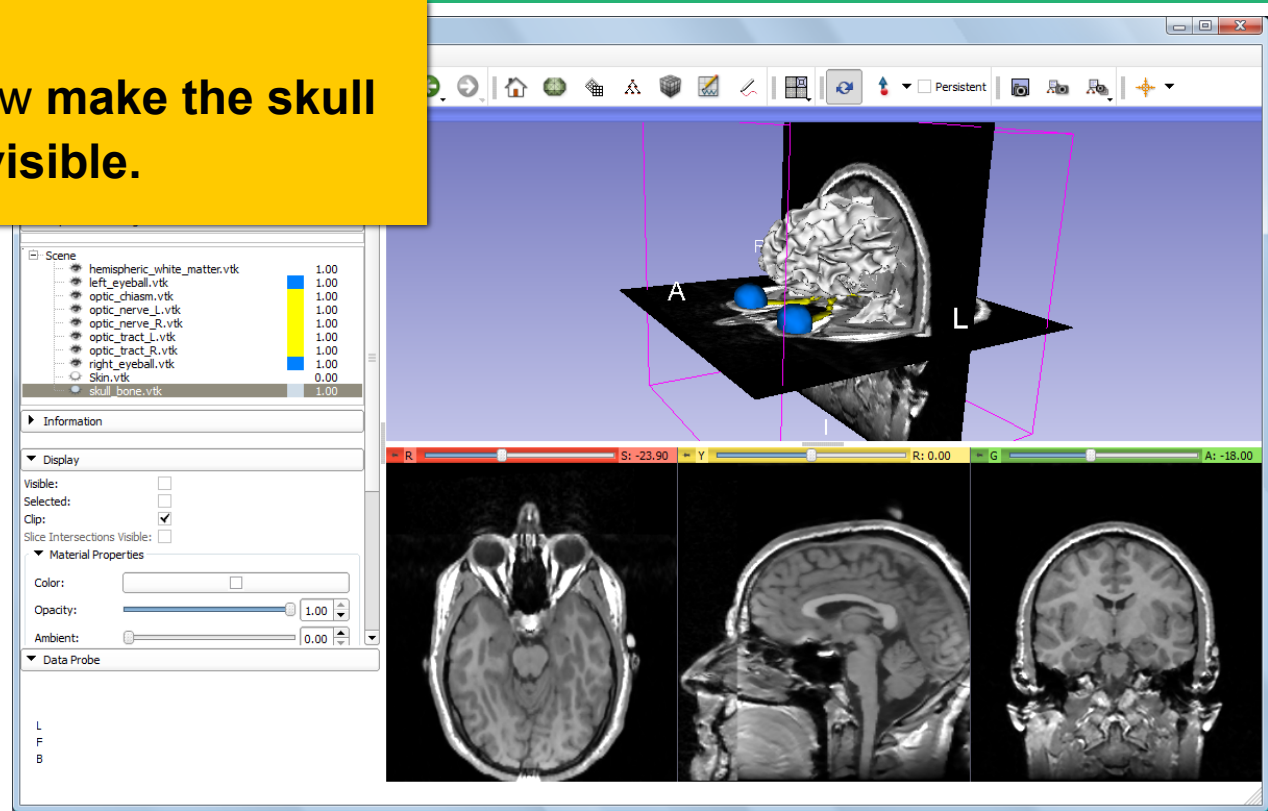
Browse through the **coronal slices** to expose the 3D model of the **white matter**, and the left and right **optic nerves**.





Slicer4 Minute Tutorial: 3D Visualization

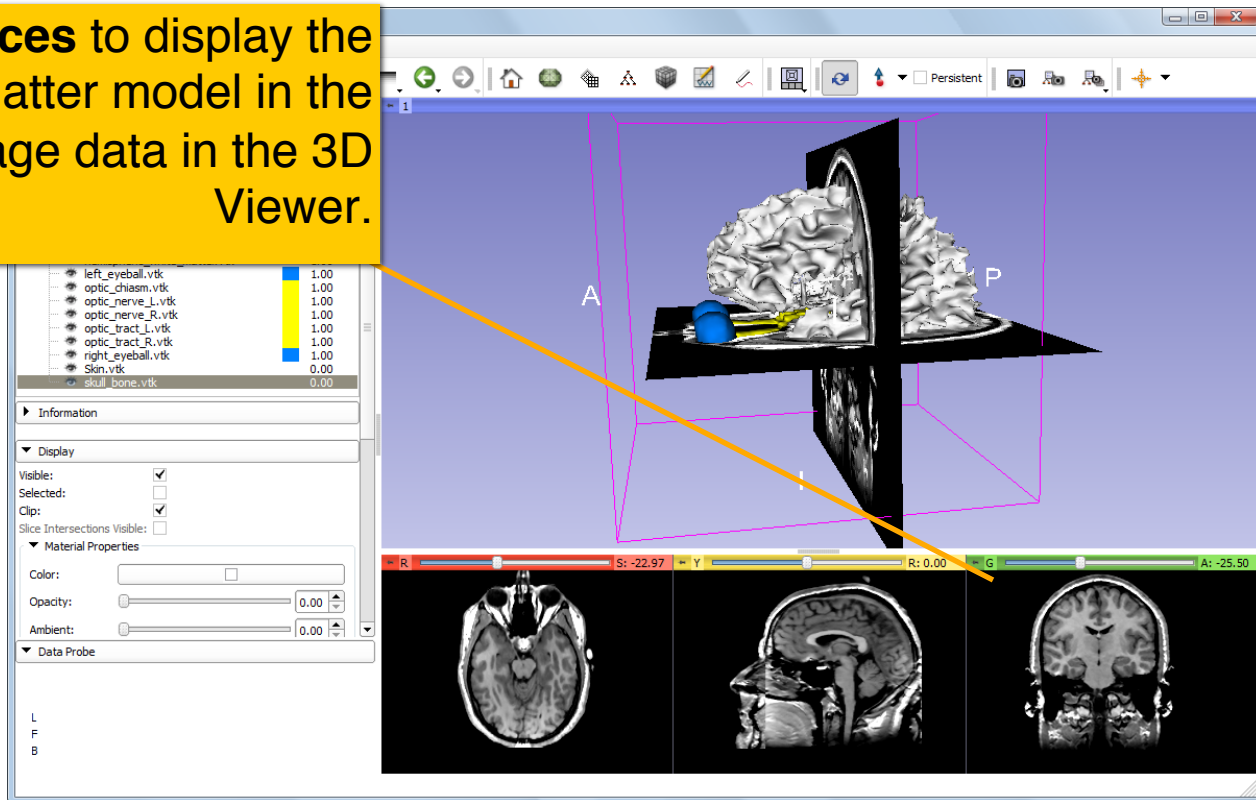
Now make the skull invisible.





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**.



Scene

- hemispheric_white_matter.vtk 1.00
- left_eyeball.vtk 1.00
- optic_chiasm.vtk 1.00
- optic_nerve_L.vtk 1.00
- optic_nerve_R.vtk 1.00
- optic_tract_L.vtk 1.00
- optic_tract_R.vtk 1.00
- right_eyeball.vtk 1.00
- Skln.vtk 0.00
- skull_bone.vtk 0.00

Information

Display

Visible:

Selected:

Clip:

Slice Intersections Visible:

Material Properties

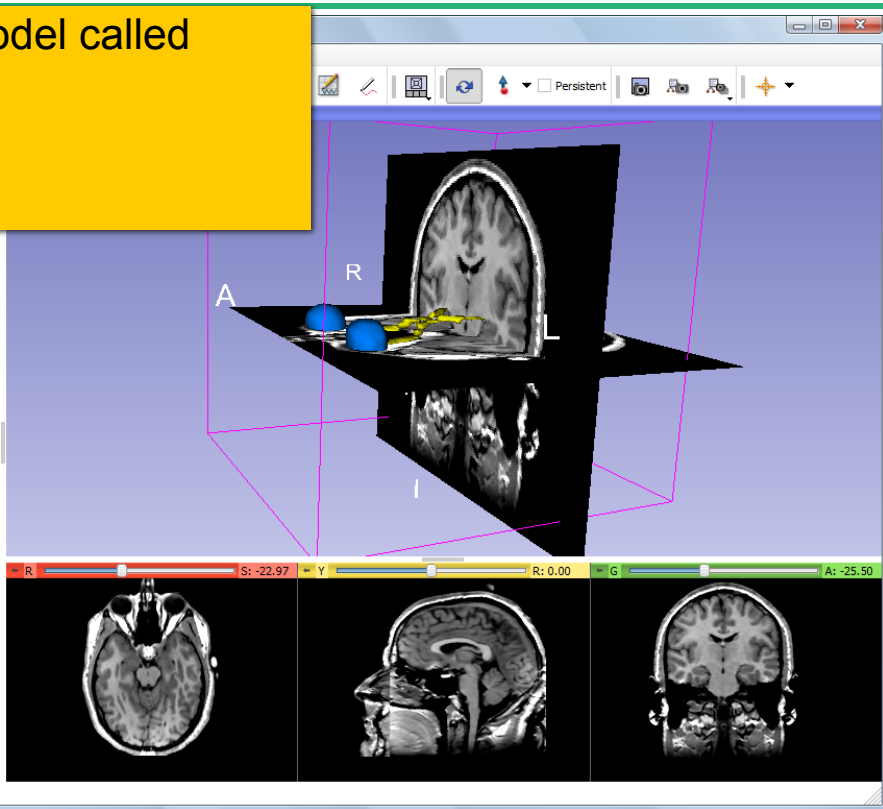
Color:

Opacity:

Ambient:

Data Probe

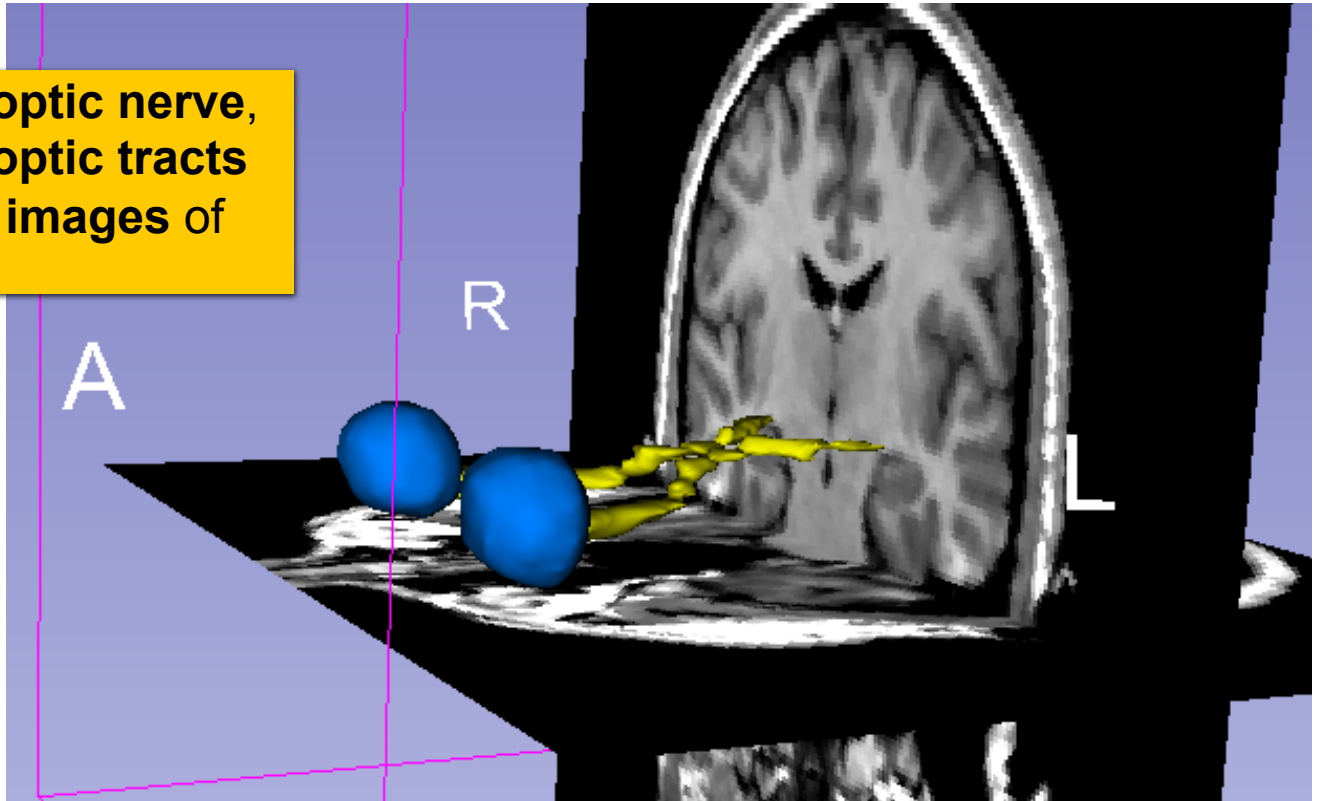
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Slicer4 Minute Tutorial: 3D Visualization

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

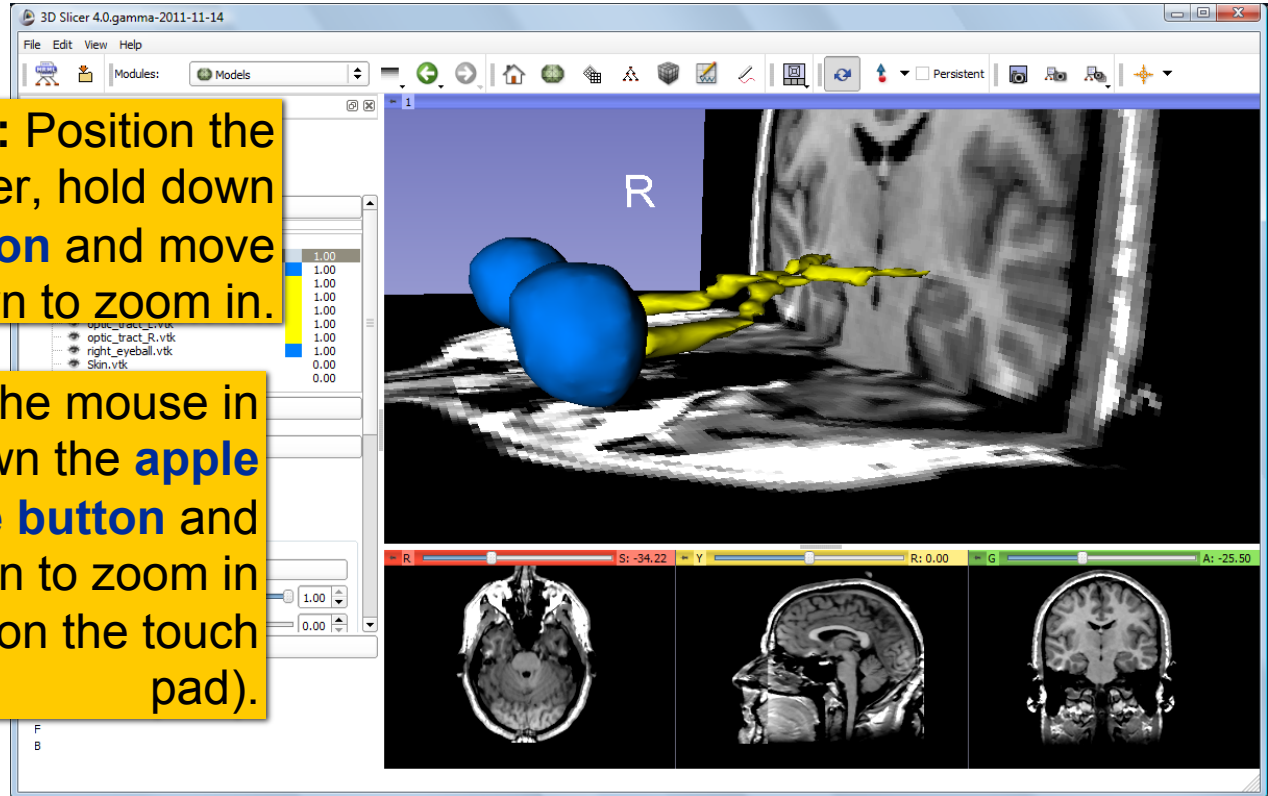




Slicer4 Minute Tutorial: 3D Visualization: Zoom the view

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

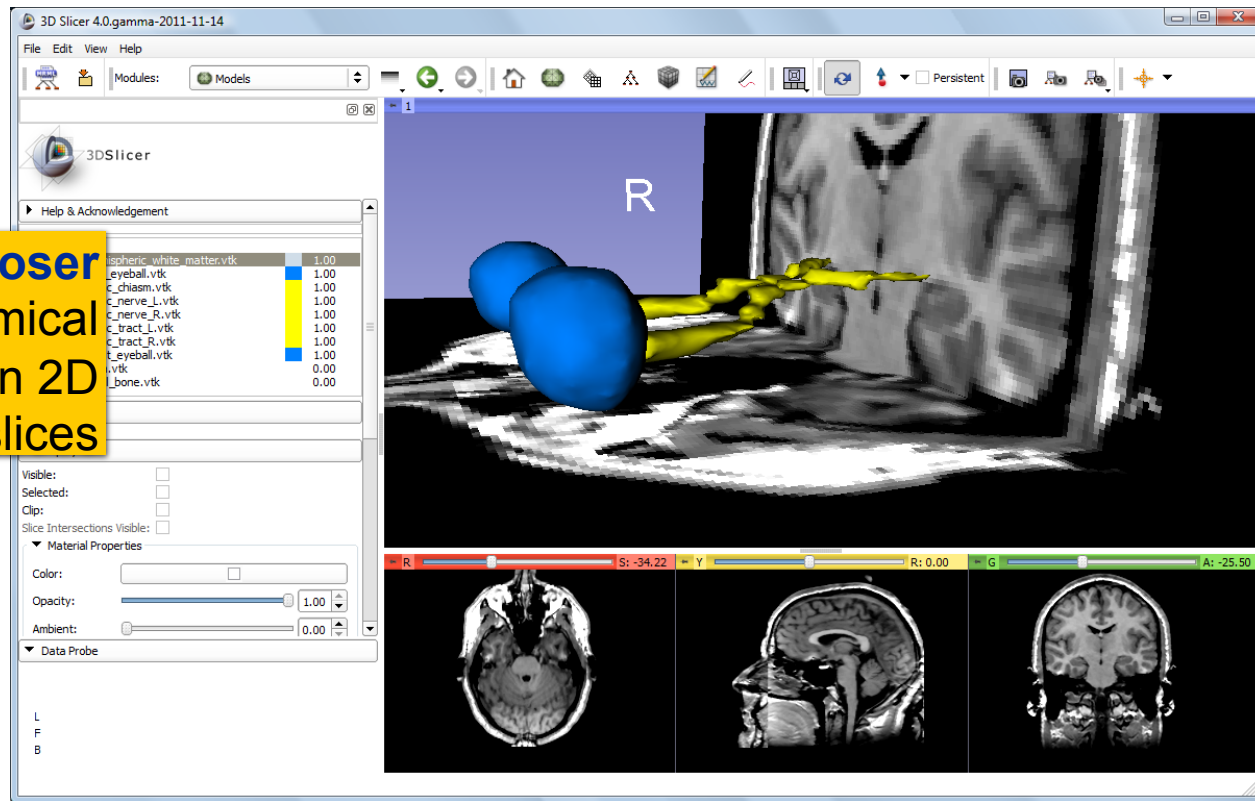
Mac users: Position the mouse in the 3D Viewer, hold down the **apple button and the mouse button** and move the mouse down to zoom in (or use two fingers on the touch pad).





Slicer4 Minute Tutorial: 3D Visualization: Zoom the view

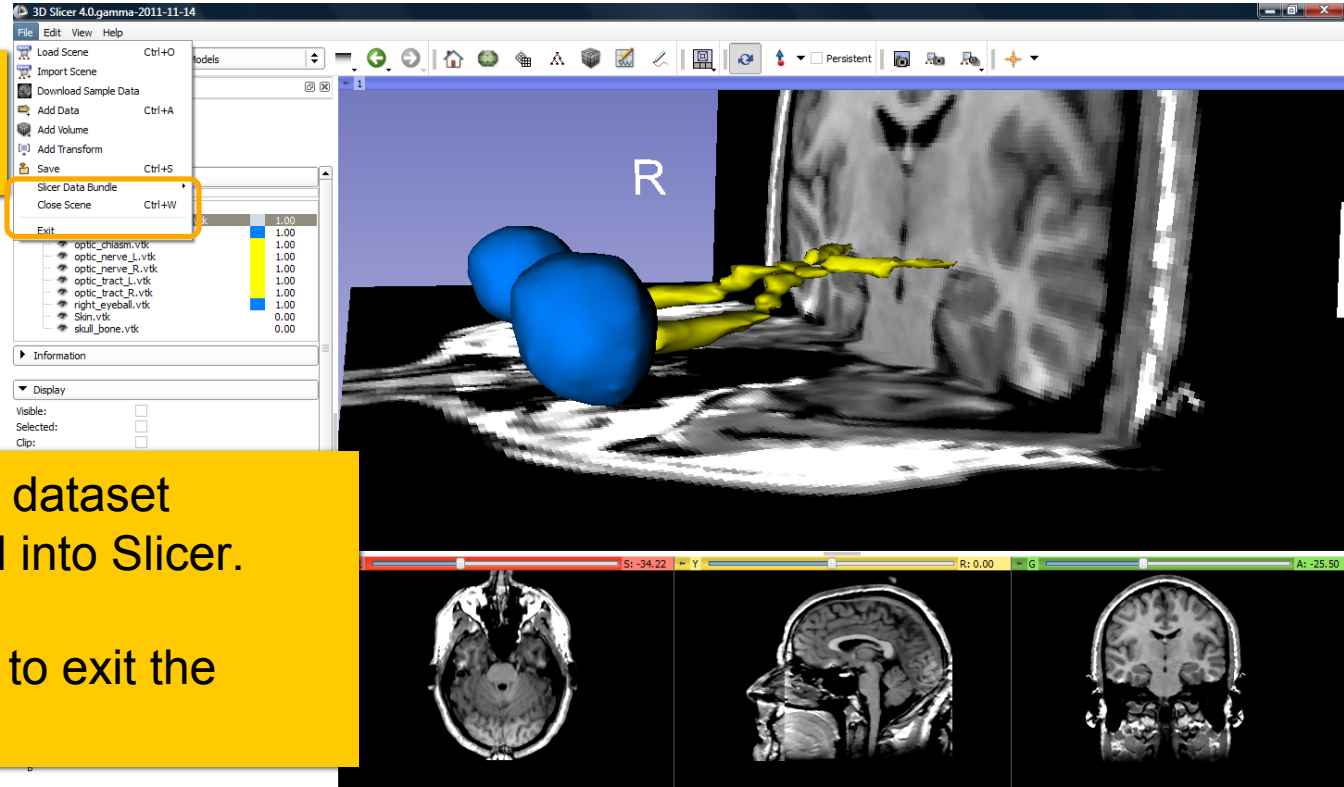
Slicer displays a **closer view** of 3D anatomical structures overlaid on 2D MR slices





Close the existing scene and all its data

Select **File->Close Scene**



This removes any dataset previously loaded into Slicer.

Select **File-> Exit** to exit the software

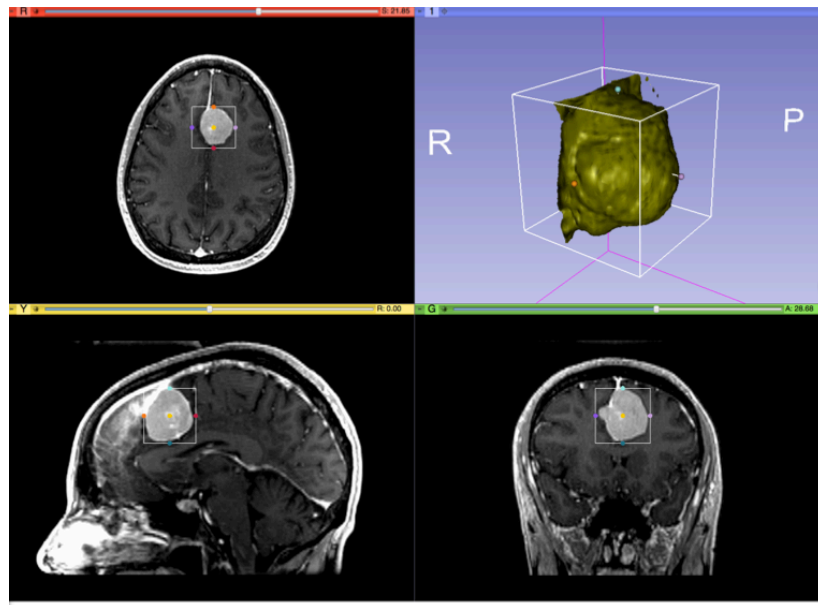


Part I: Summary

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.

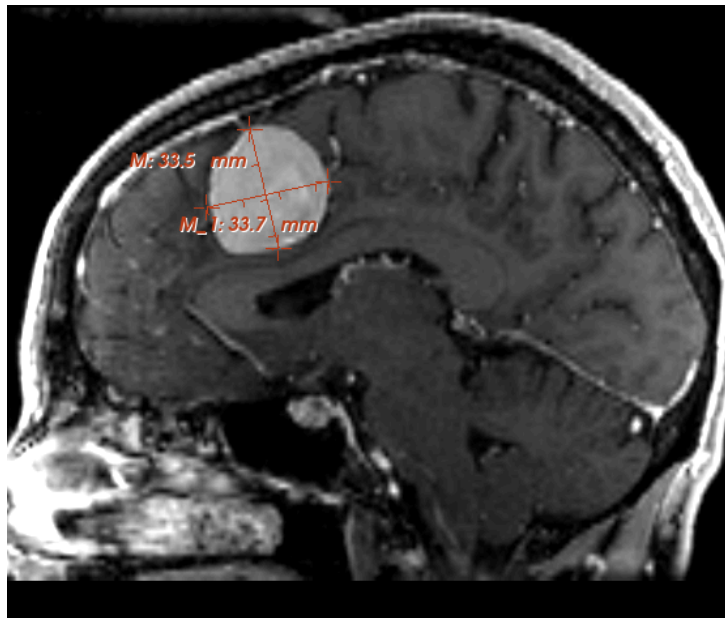


Part II: Analyzing Small Volumetric Changes

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



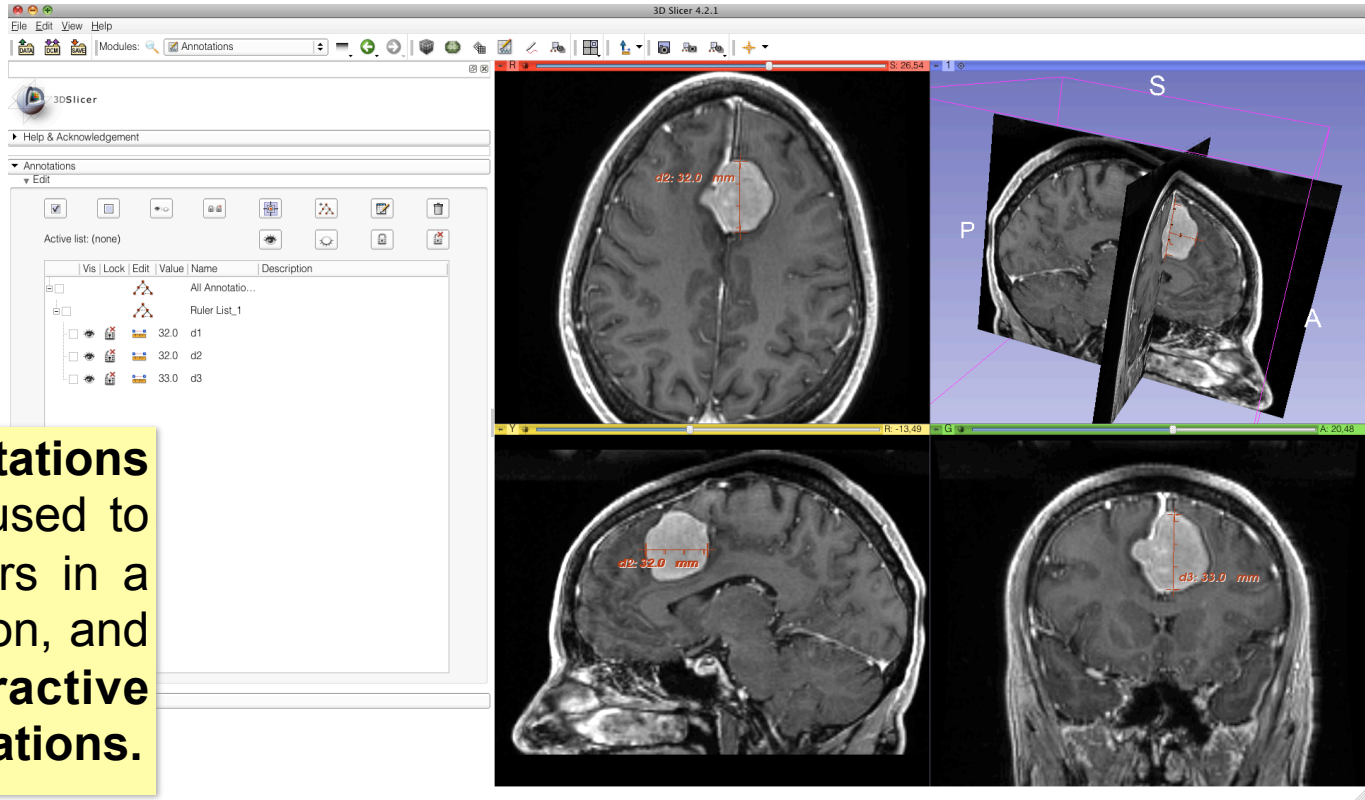
Conventional measures of tumor response



- 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



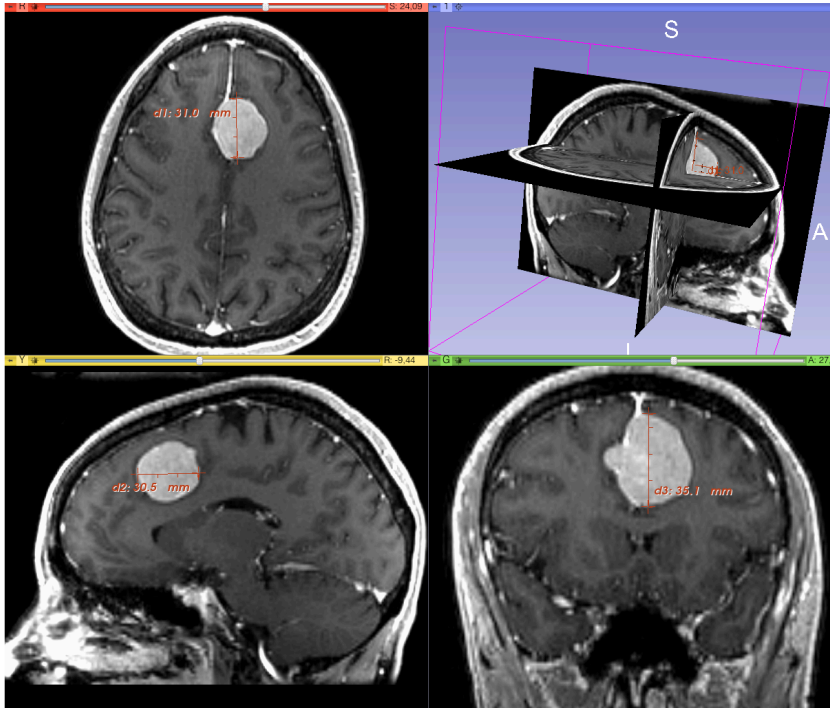
Conventional measures of tumor response



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



Clinical case: baseline scan

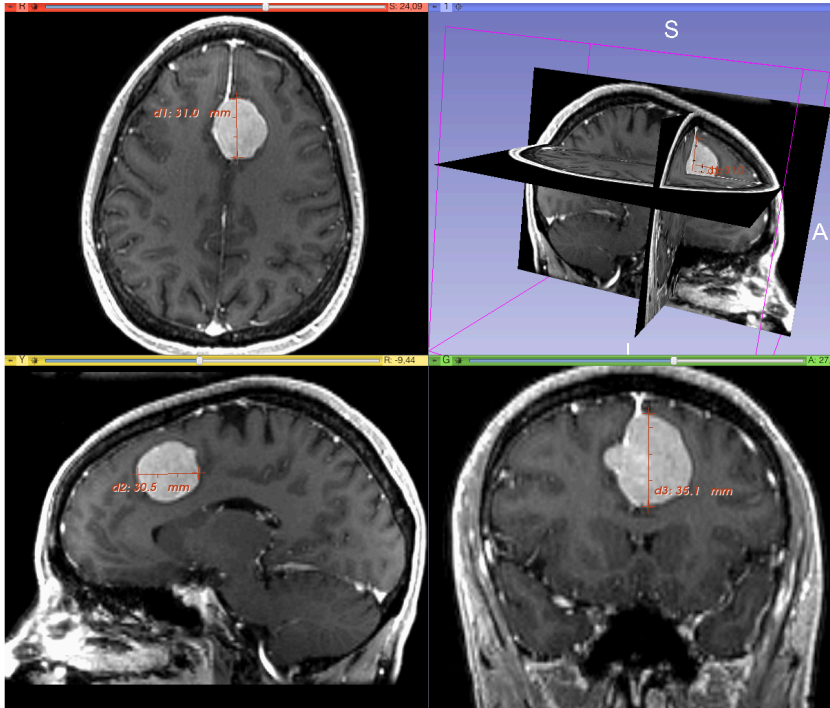


Baseline radiologist's clinical impression:

- 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

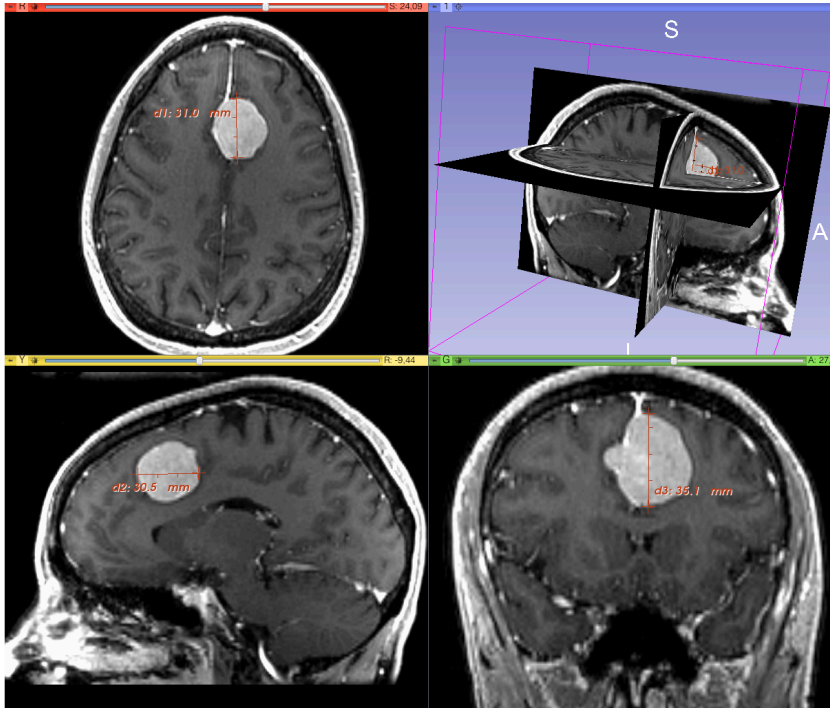


Follow-up radiologist's clinical impression:

- 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

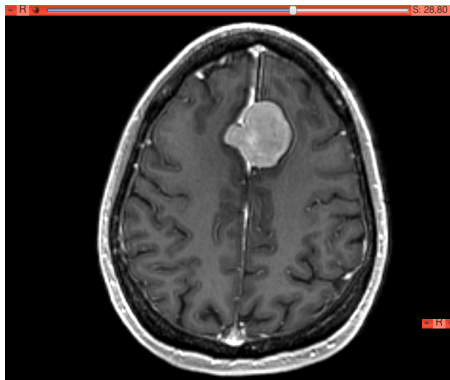
More accurate and precise methods for understanding volume changes may be useful when:

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

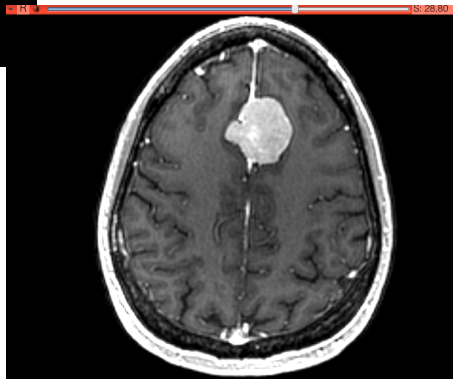


Goal of the tutorial

MR Scan1 June 2006



MR Scan2 June 2007



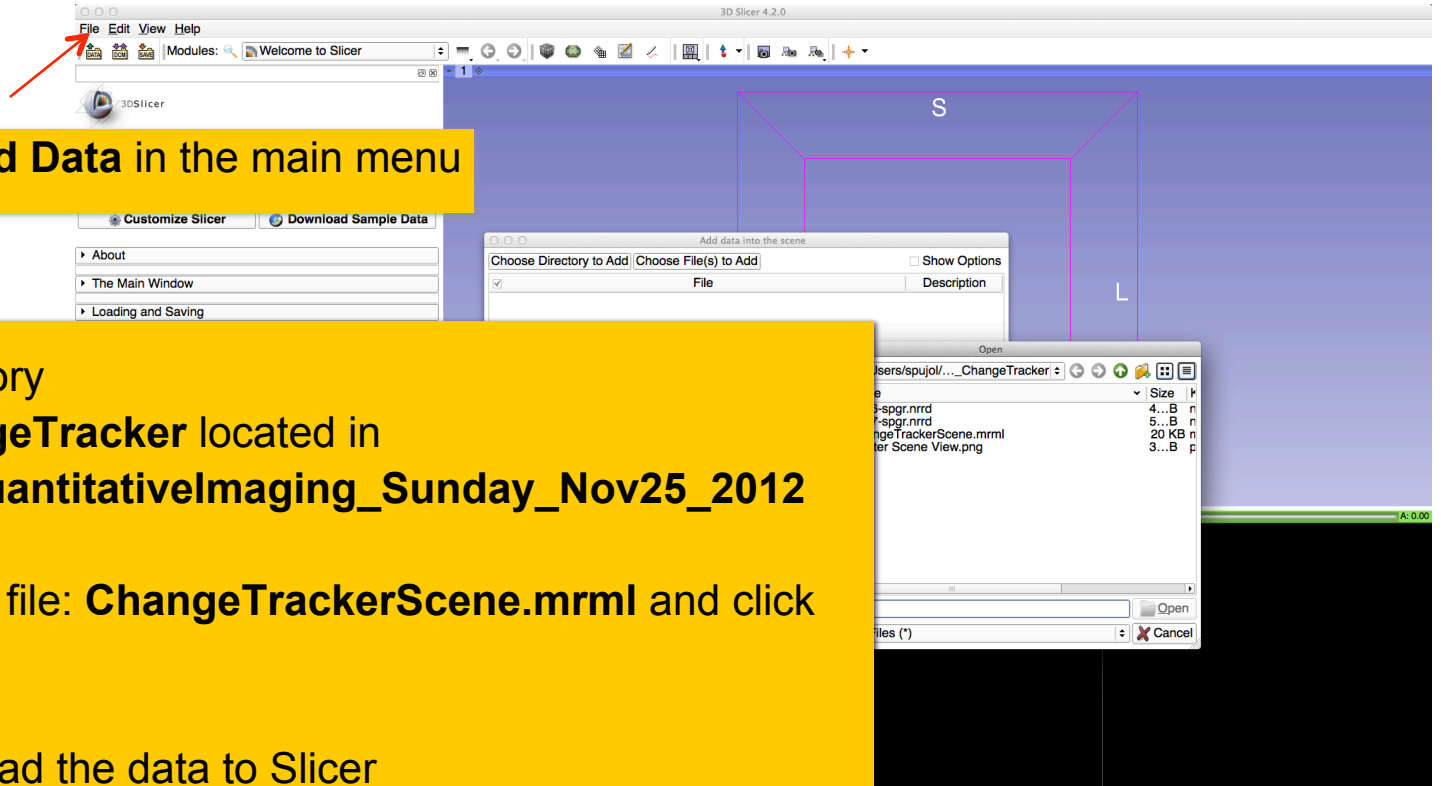
The following section will guide you step-by-step through the computation of small volumetric changes in a slow growing tumor.

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.

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



ChangeTracker: Load the dataset



Select **File** → **Add Data** in the main menu

Select the directory
dataset2_ChangeTracker located in
C:\Pujol2012\QuantitativeImaging_Sunday_Nov25_2012

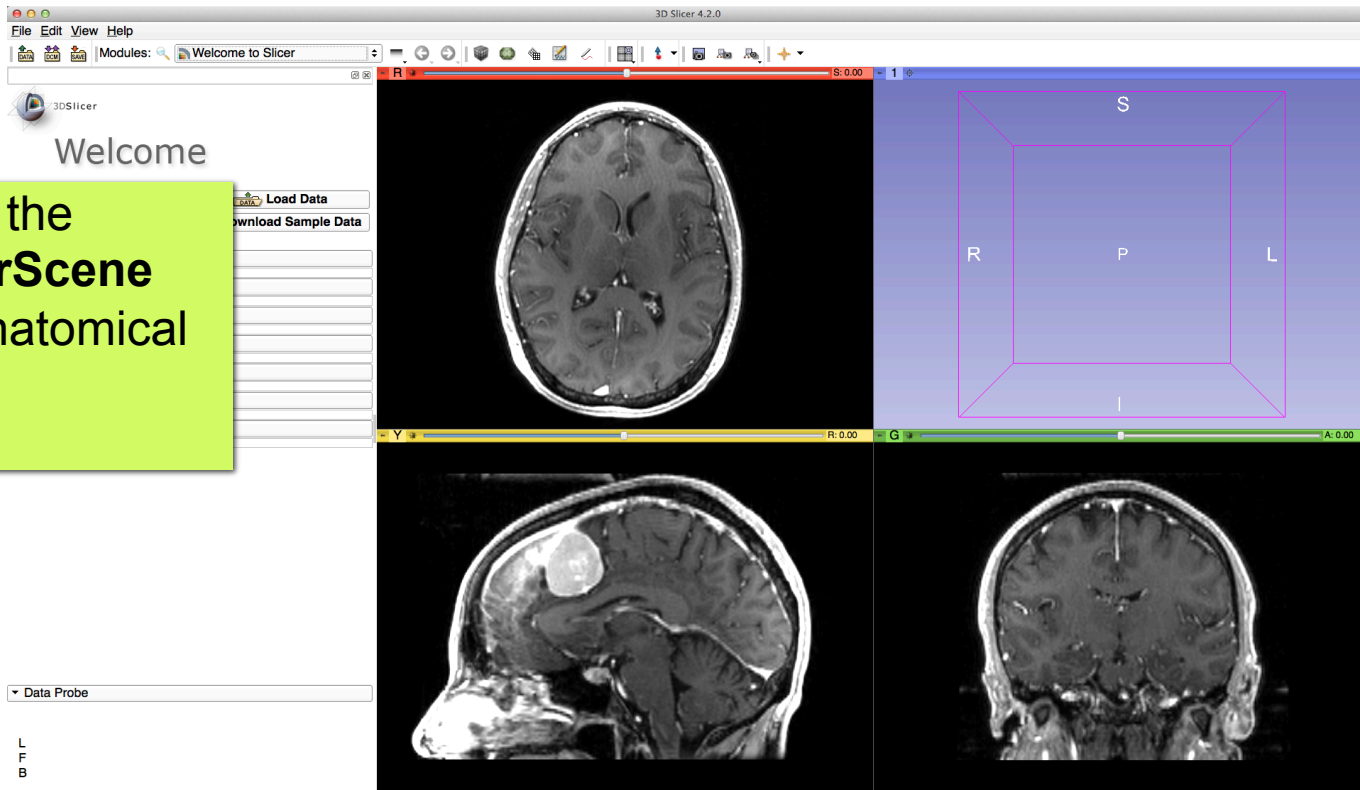
Select the scene file: **ChangeTrackerScene.mrml** and click
on **Open**

Click on **OK** to load the data to Slicer



Loading the data

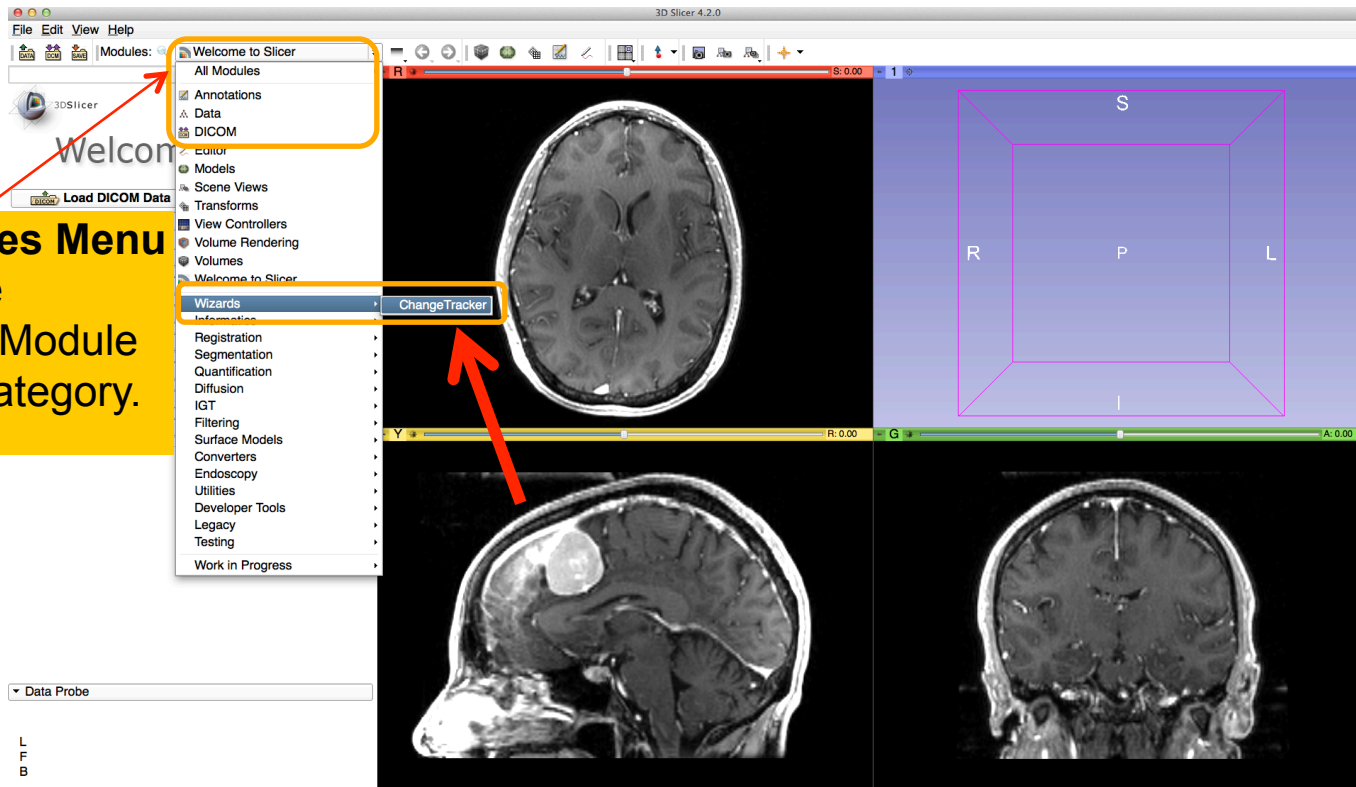
The datasets of the **ChangeTrackerScene** appear in the anatomical viewers.





ChangeTracker: exploring small volumetric changes

Using the **Modules Menu** button, select the **ChangeTracker** Module in the **Wizards** category.





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'

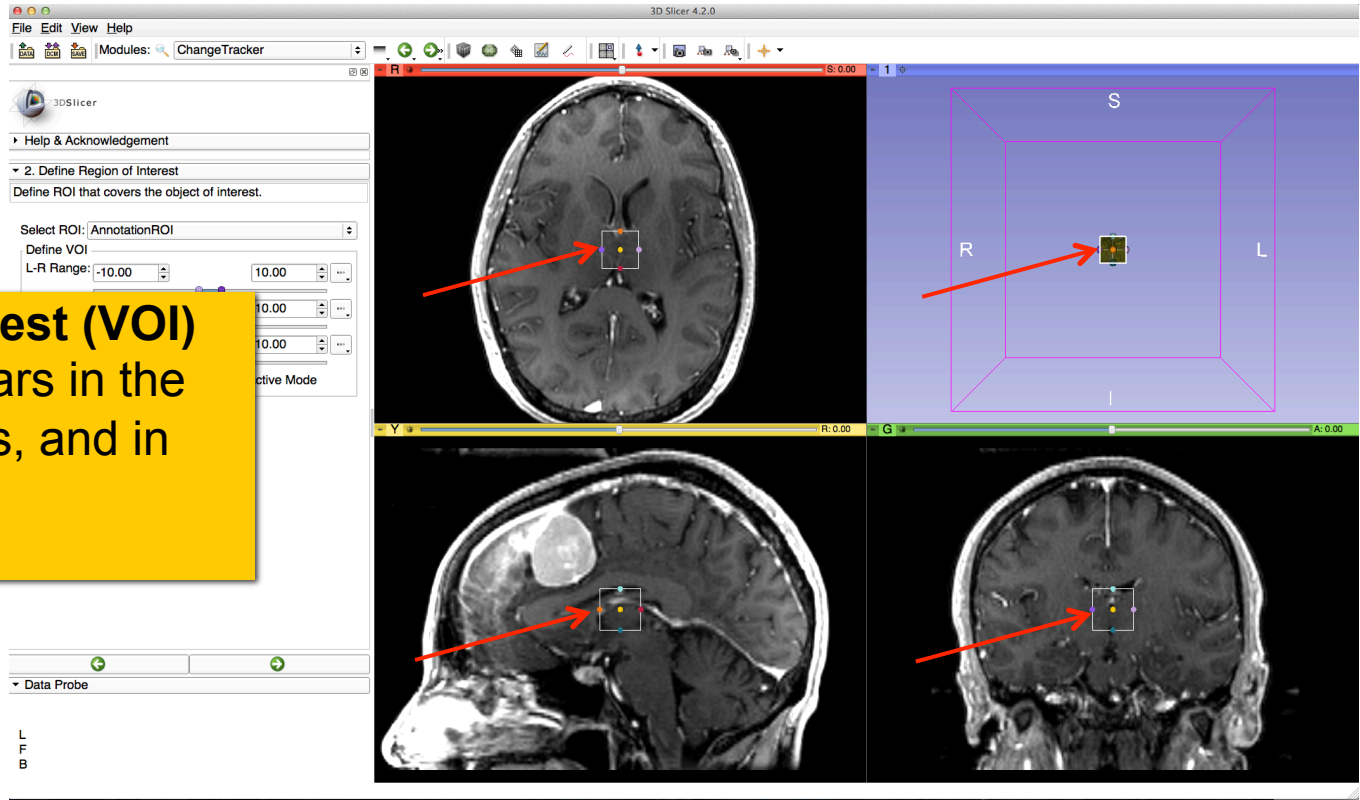
- Set the **Baseline scan** to **2006-spgr1**
- Set the **Follow up scan** to **2007-spgr1**

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.



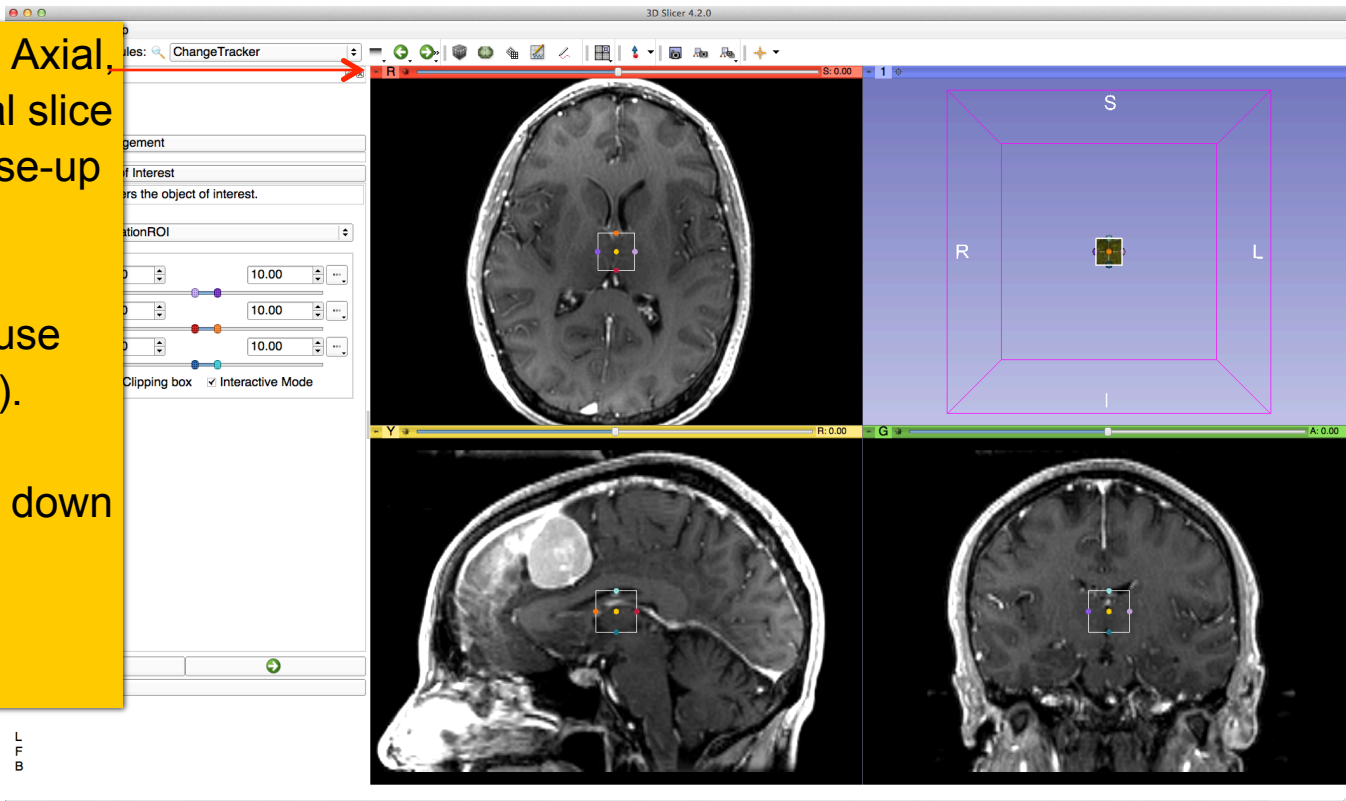


Step2: Define Region of interest

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

Center the VOI first:

Position the square in the center of the tumor in the slice viewer.

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: [-10.00, 10.00]

P-A Range: [17.47, 37.47]

I-S Range: [16.44, 36.78]

Display Clipping box Interactive Mode

Data Probe

Yellow RAS: (-1.9, -43.1, 6.2) Sagittal Sp: 0.9

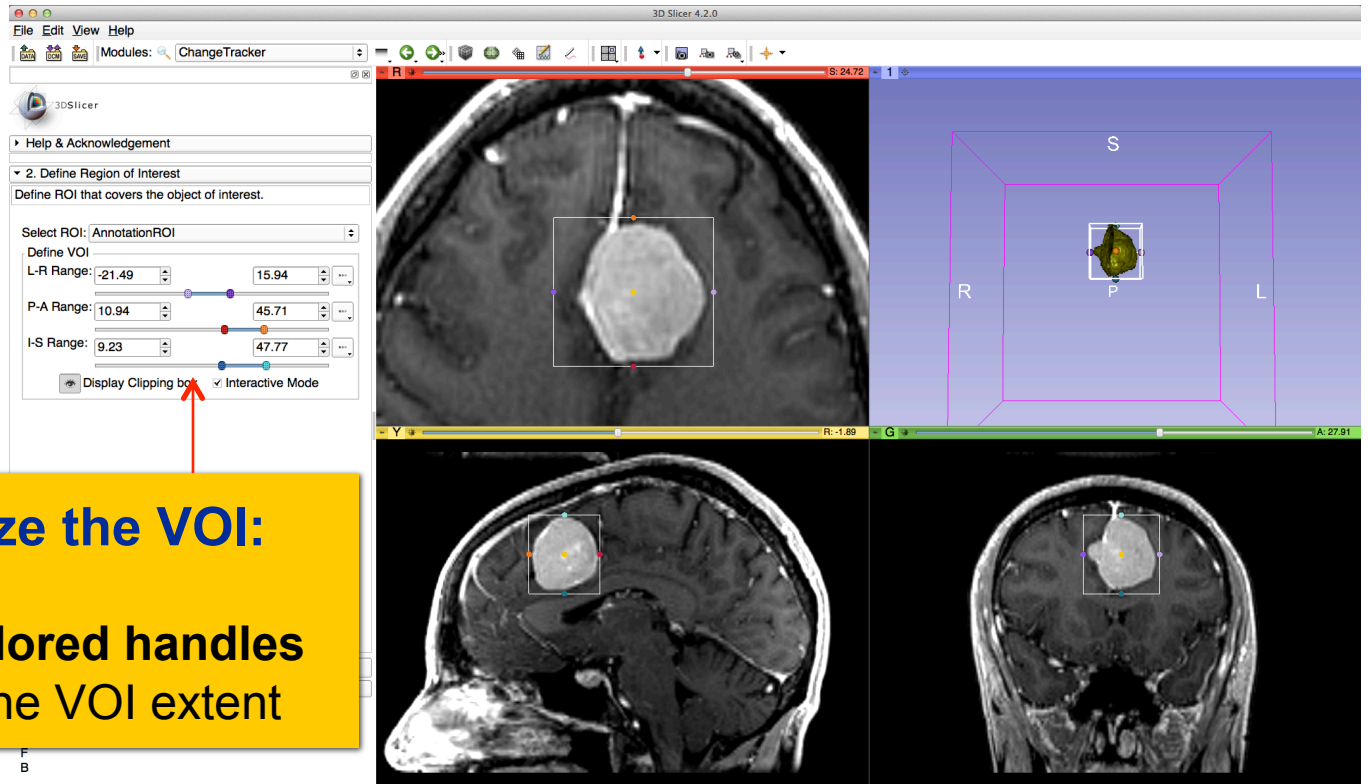
L None ()

F 2007-spg1 (130, 173, 70) 105

B 2006-spg1 (130, 173, 60) 87



Step2: Define Region of interest



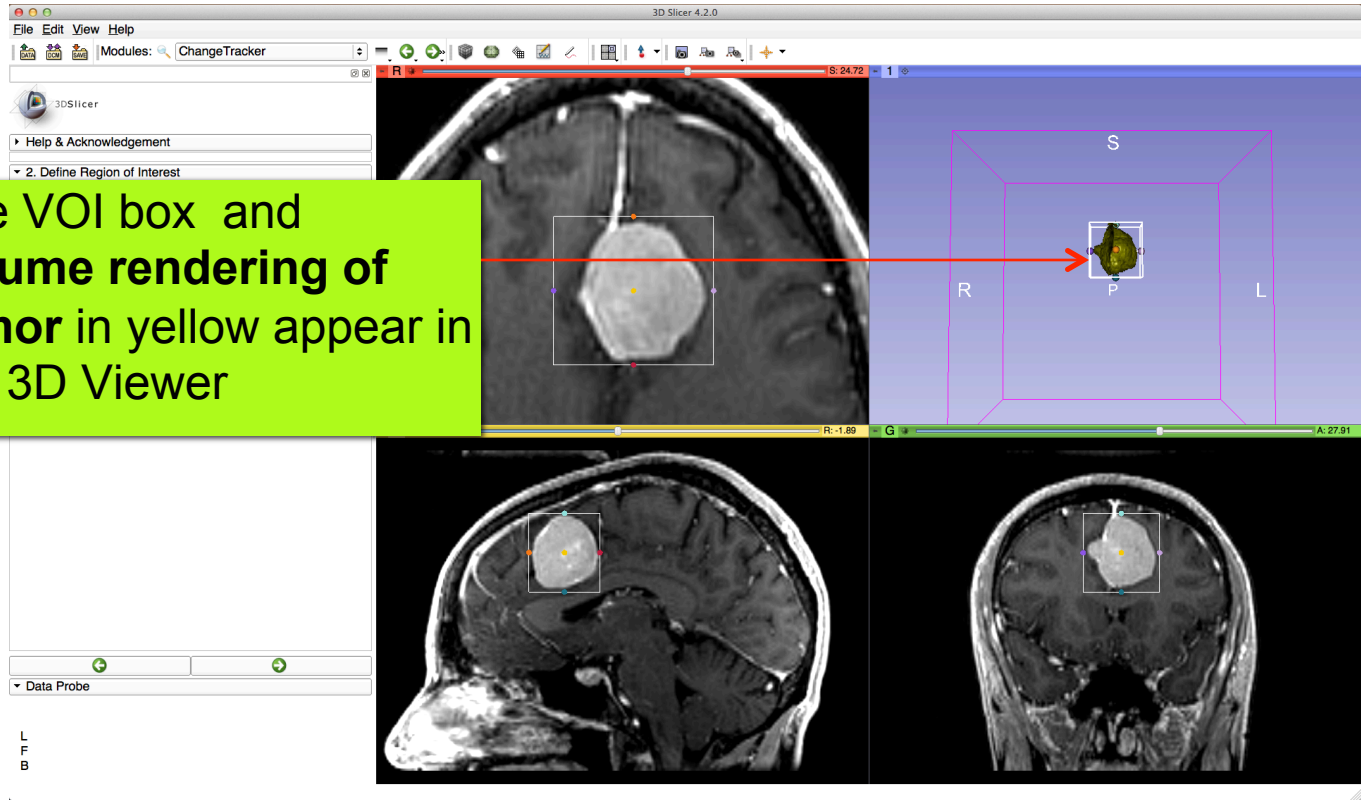
Next, resize the VOI:

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

L
F
B

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'

3D Slicer 4.2.0

File Edit View Help

Modules: ChangeTracker

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

View menu options:

- 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
- Three Over Three Quantitative
- Four over four
- Two over Two

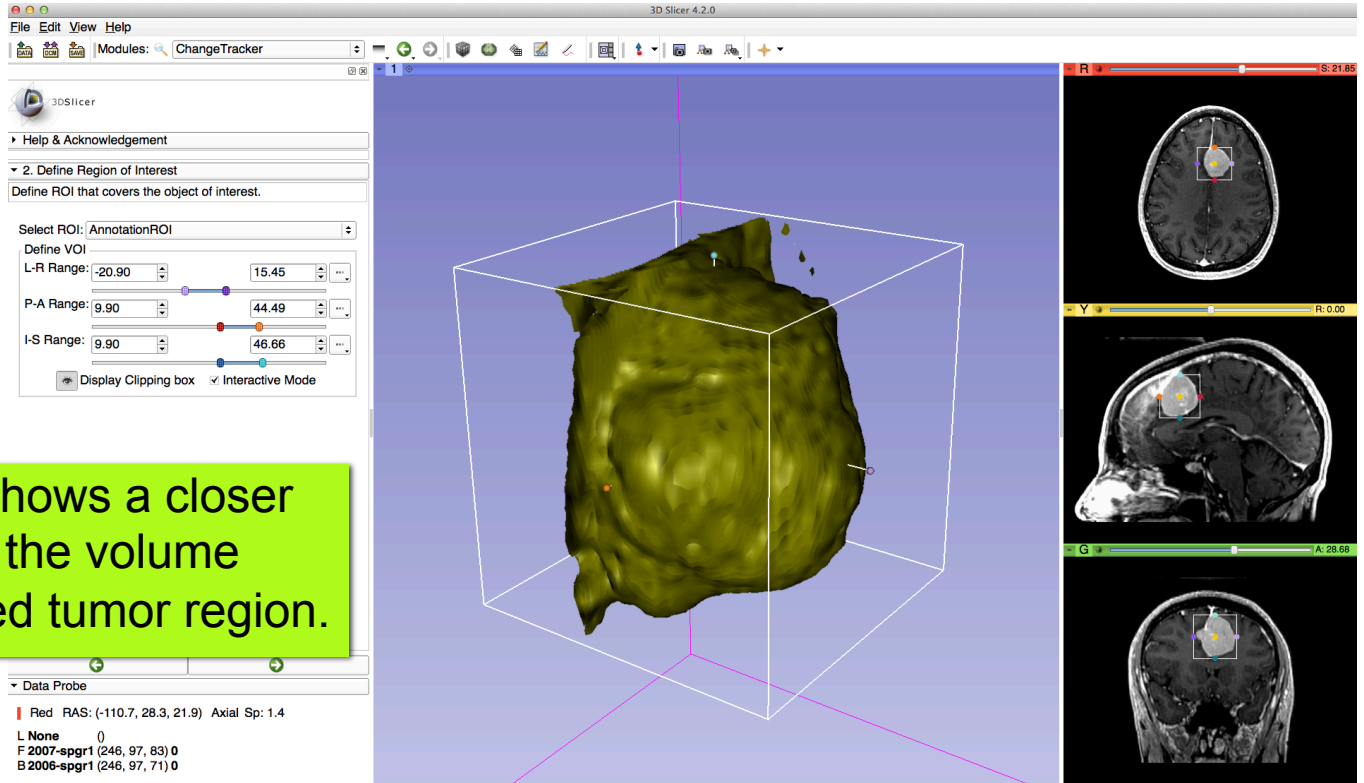
Viewing mode: R, G, A: 28.68

Data Probe

L
F
B



Step2: Define Region of interest



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



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

Zoom in and out, and rotate the volume rendered image to explore the tumor region in 3D.

L None 0
F 2007-spr1 (246, 97, 83) 0
B 2006-spr1 (246, 97, 71) 0

al Sp: 1.4

R S: 21.85

Y R: 0.00

G A: 26.68



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

44.49

46.66

Interactive Mode

Data Probe

L
F
B

R

P

R: 0.00

G

A: 28.68

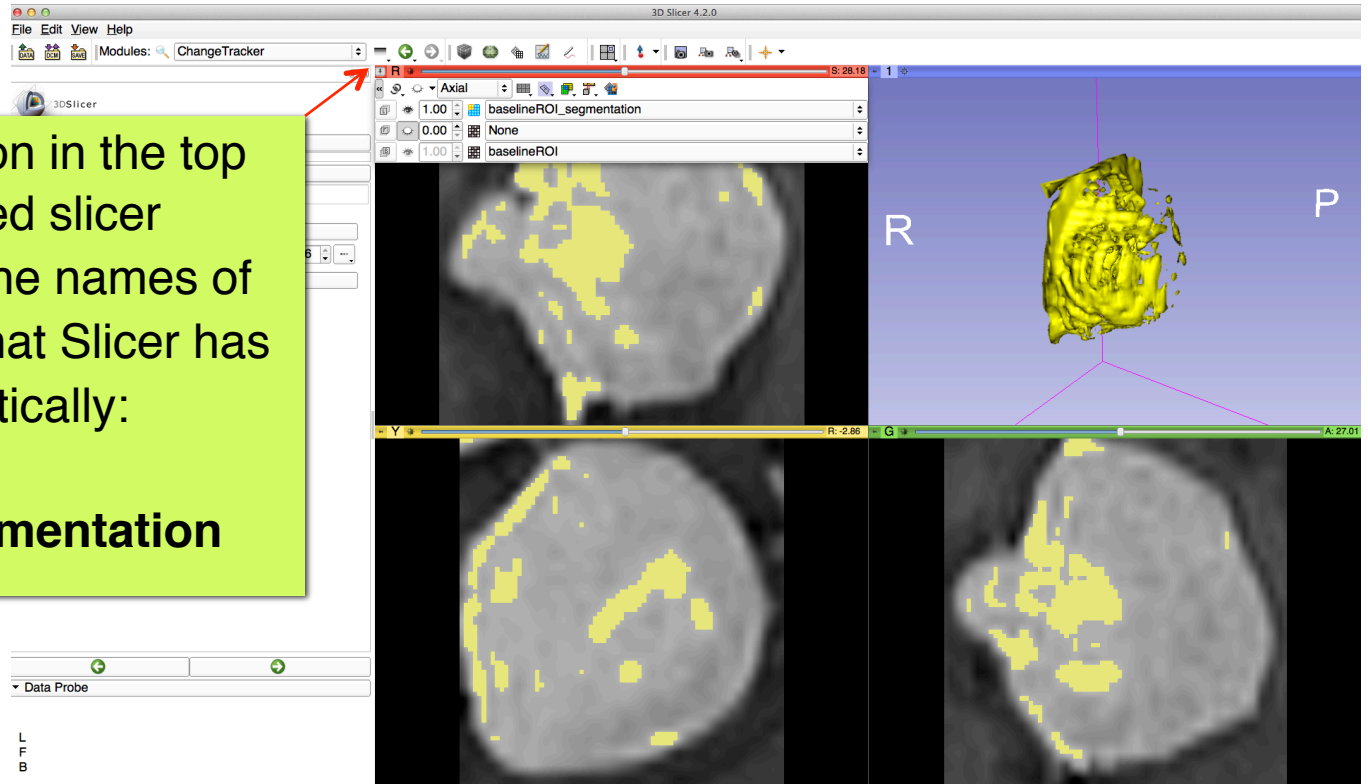
Select 'Four-Up Quantitative' to return to the initial view mode

Click on the green arrow to move to the next step



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



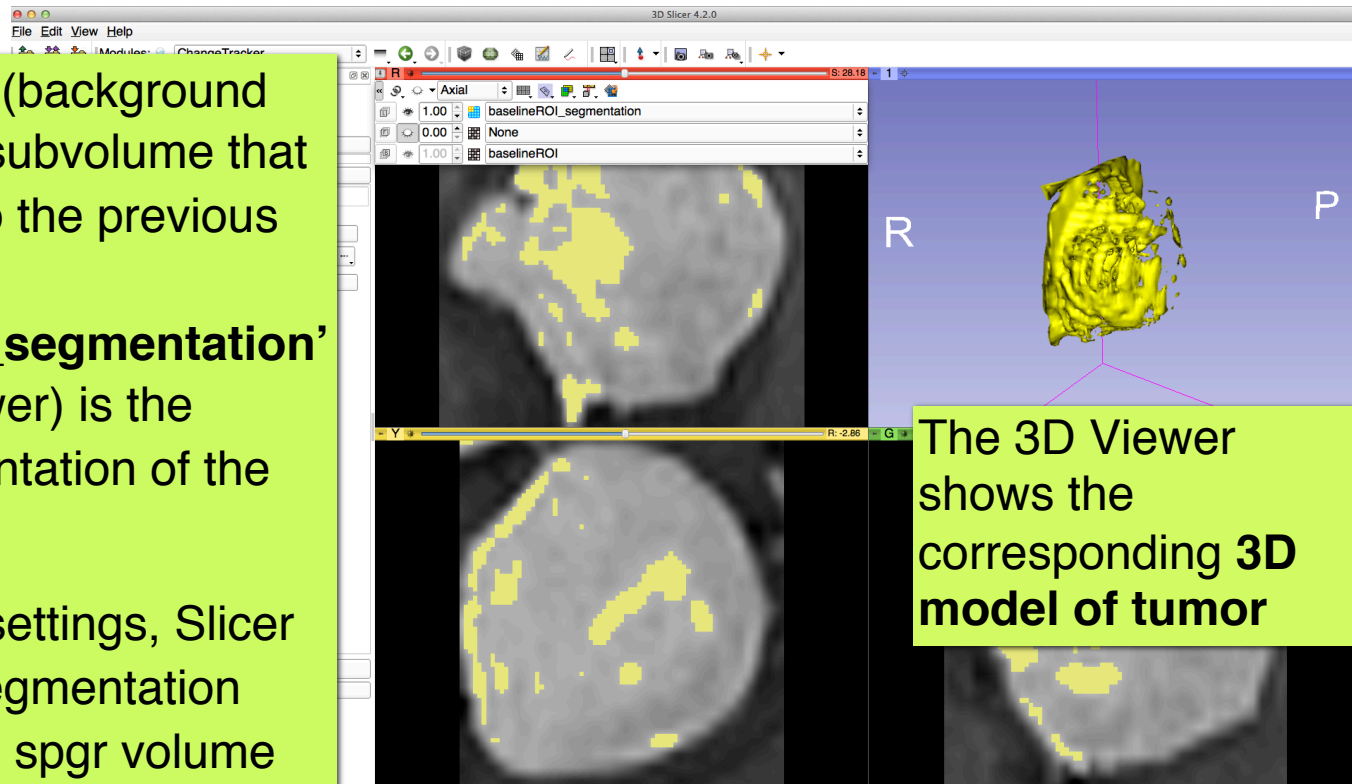


Step3: Segment the tumor

'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



The 3D Viewer shows the corresponding **3D model of tumor**



Step3: Segment the tumor

The screenshot shows the 3DSlicer software interface. On the left, the '3. Segment the analyzed structure' panel is active, with the 'Basic settings' section expanded. A red arrow points to the 'Choose threshold' slider, which is currently set to 188 and has a maximum value of 366. On the right, the 'Layout' menu is open, and a red arrow points to the 'FourUp' layout option. A yellow callout box contains the text: 'Select the layout FourUp in the layout menu to display the volume rendered segmentation'. The main view area displays a 3D volume rendering of a tumor in yellow, along with several 2D axial, sagittal, and coronal slices of the tumor. At the bottom, a 'Data Probe' panel is visible, and the orientation is set to L (Left), F (Front), and B (Back).

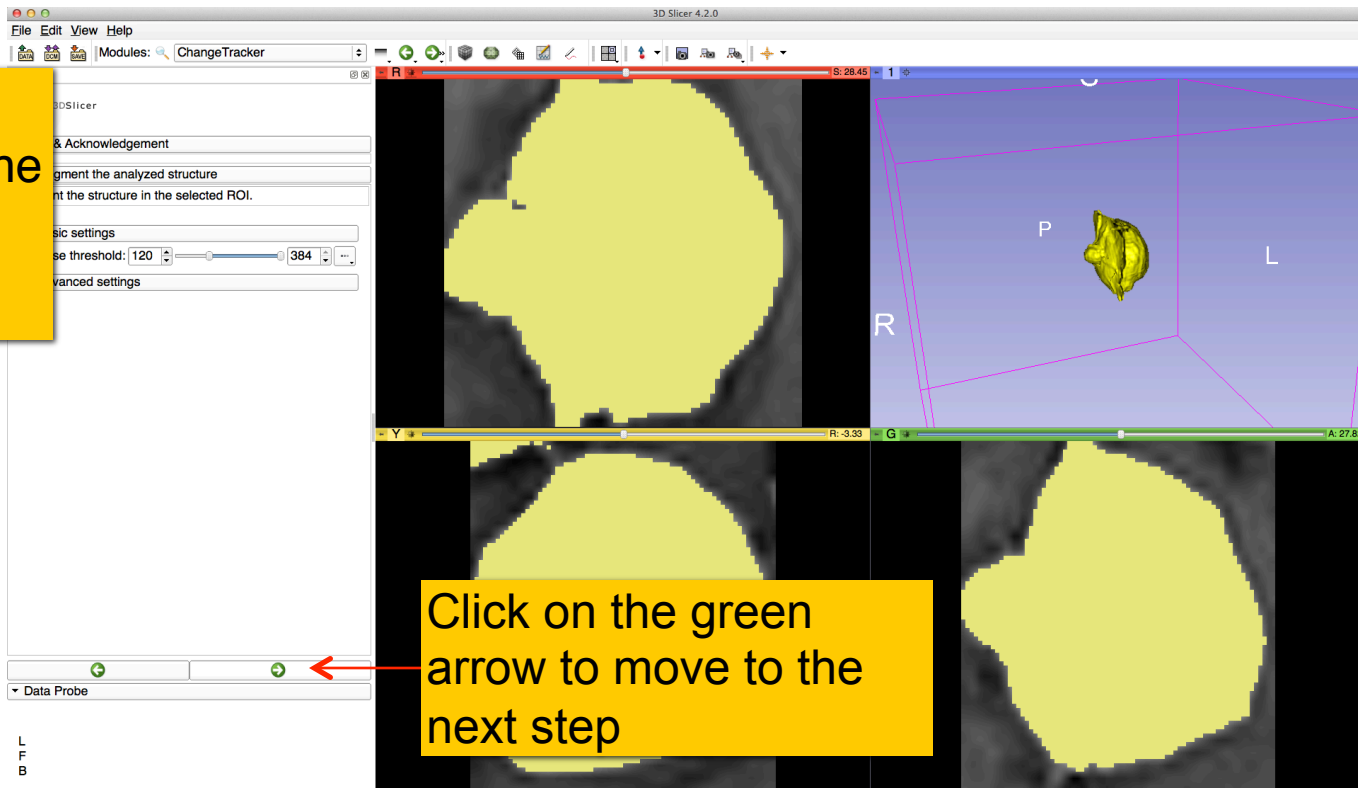
Select the **layout FourUp** in the layout menu to display the volume rendered segmentation

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



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

3D Slicer 4.2.0

File Edit View Help

Modules: ChangeTracker

3DSlicer

Help & Acknowledgement

4. ROI Analysis

Select the analysis method for the selected ROI.

Basic settings

Intensity Difference Change Detection (FAST)

Advanced settings

R P

Y R: 2.85 G A: 27.01

Data Probe

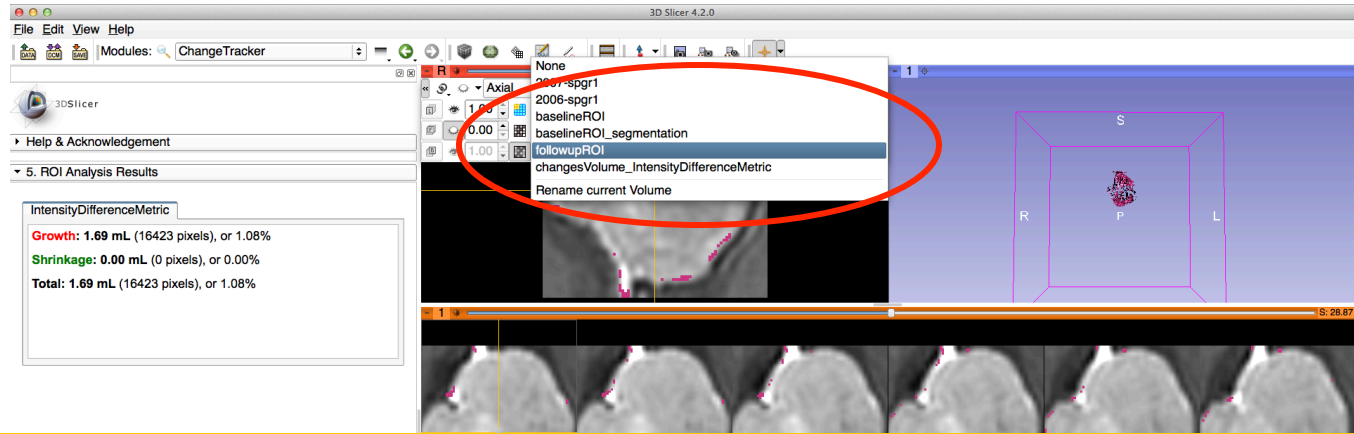
L F B

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

Click on the green arrow
to move to the next step



Final Step: Change Tracker Results



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

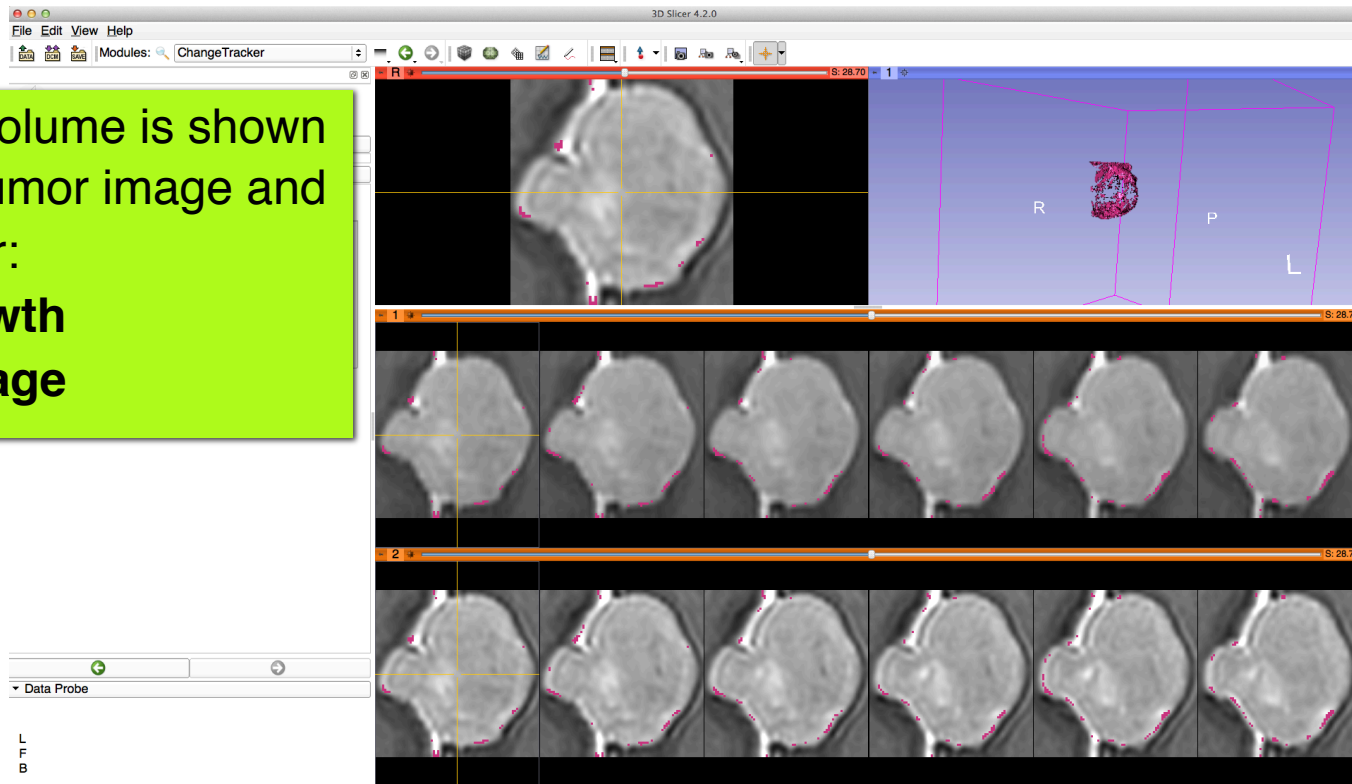


Final Step: Change Tracker Results

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

magenta = growth

green = shrinkage

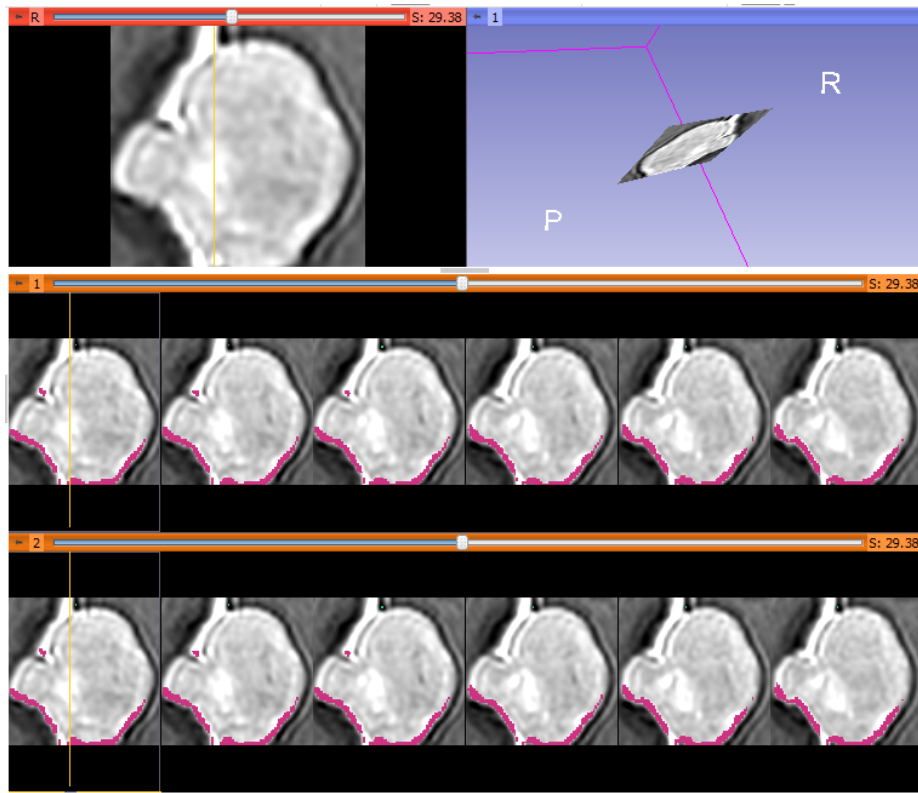




Visualization of the change in pathology

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

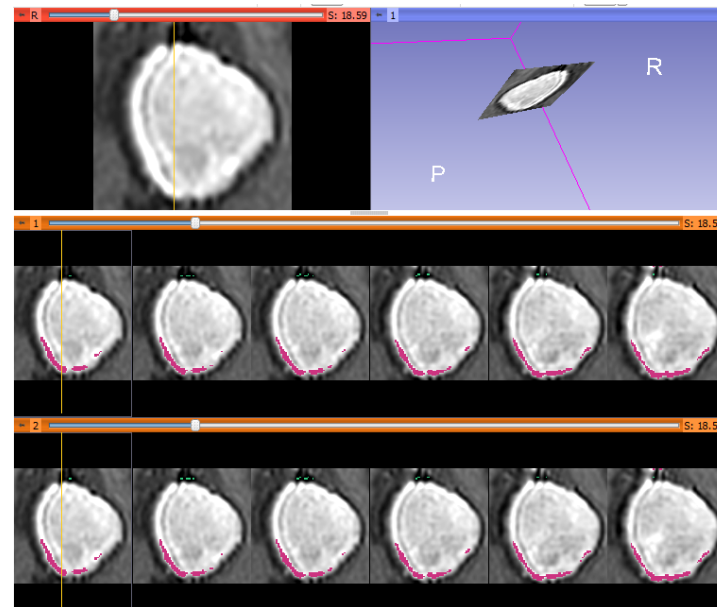
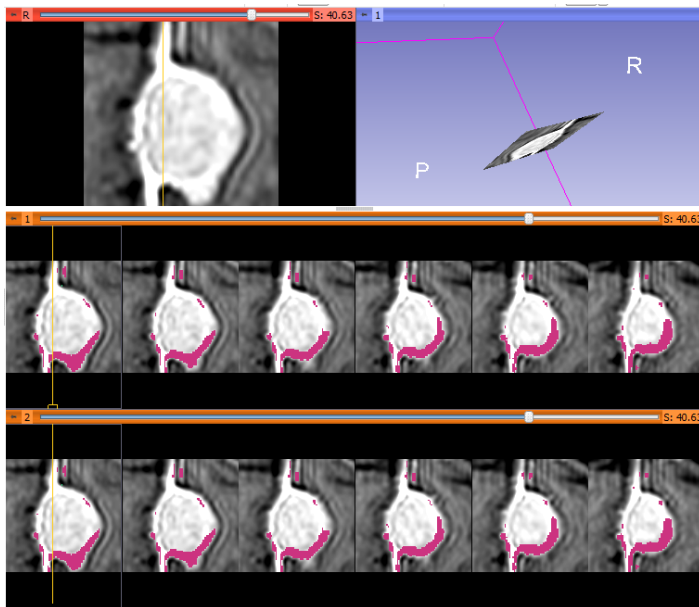
- Six consecutive slices for the VOI in Scan1 (**top row**), and
- Six corresponding consecutive slices for the VOI in Scan2 (**bottom row**).
- A zoomed view of the axial slice in the red slicer viewer





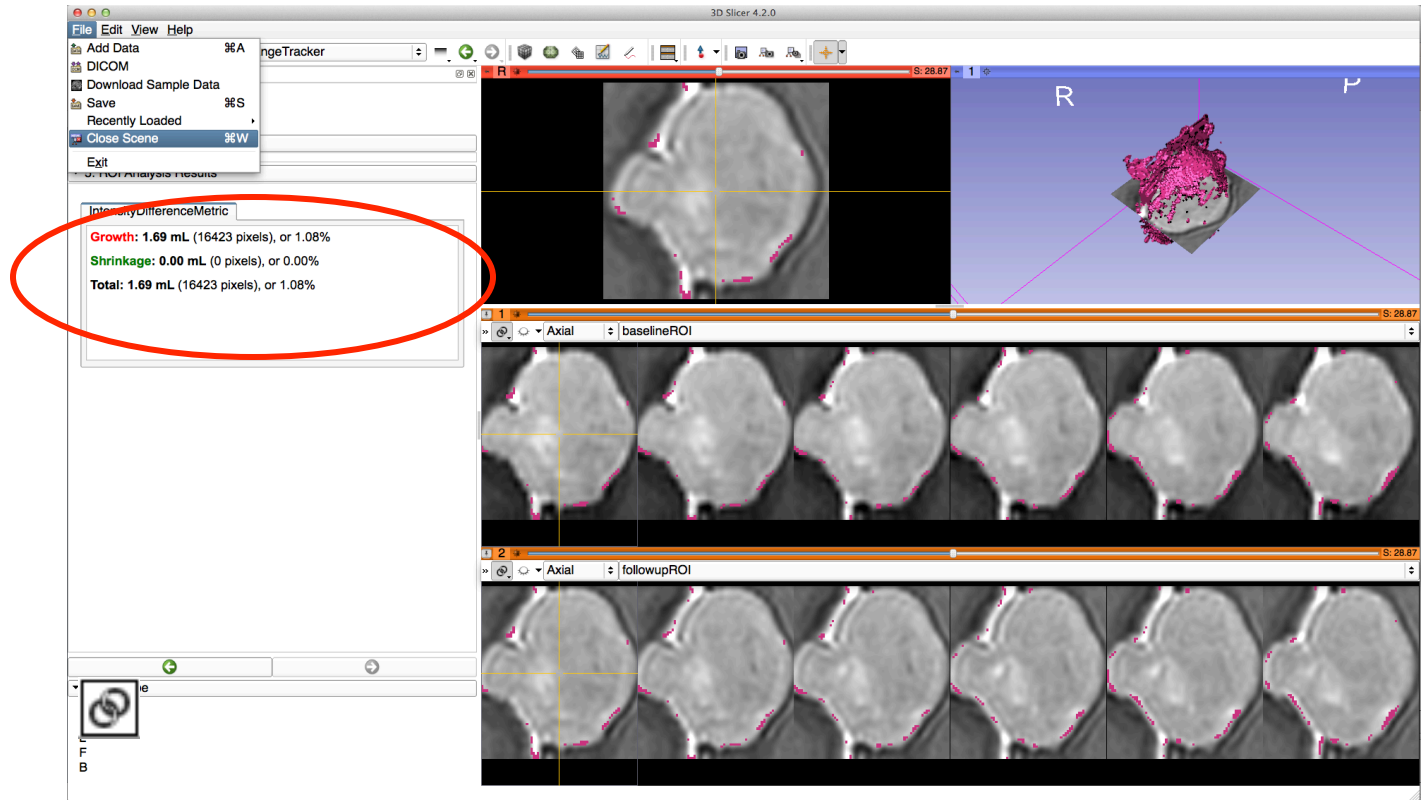
Visualization of the change in pathology

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

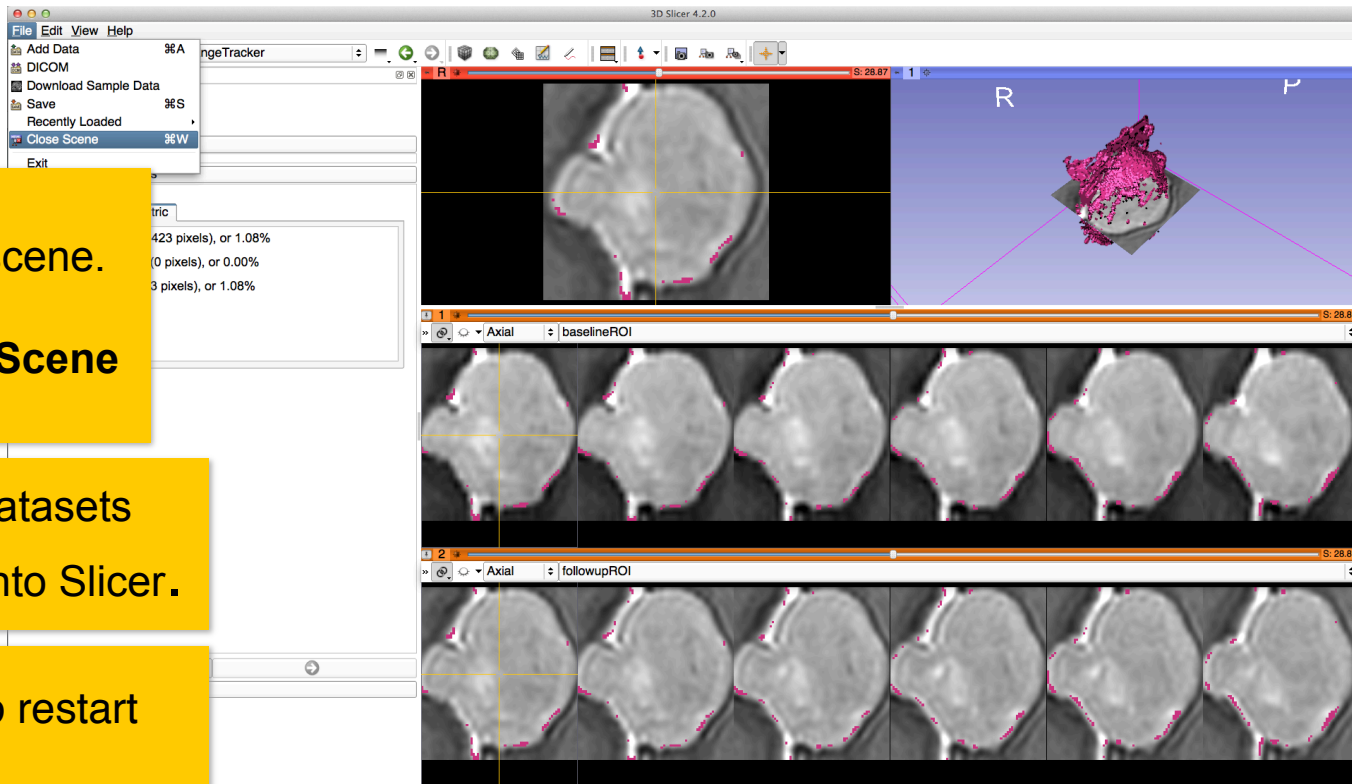
This tutorial demonstrated:

- 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.

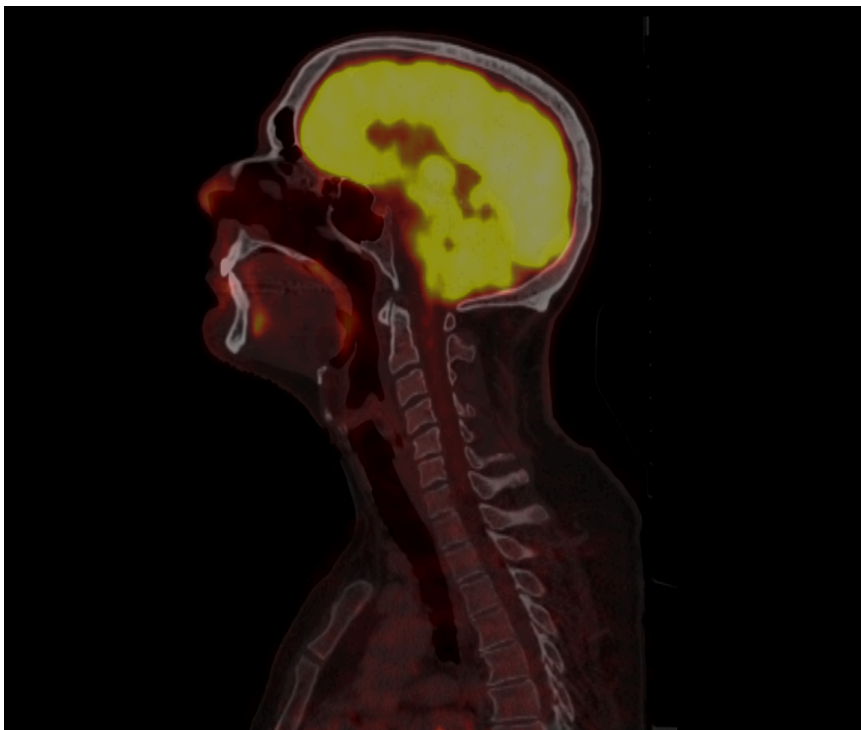
Select **File->Close Scene**

This removes any datasets previously loaded into Slicer.

Select **File** → **Exit** to restart Slicer



PET/CT Visualization and Analysis

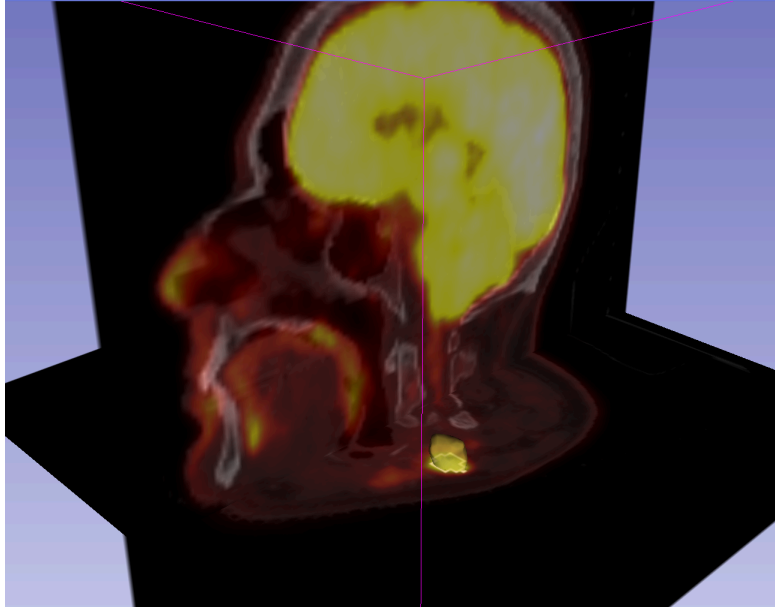


Part III: PET/CT Analysis

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



Goal of the tutorial



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

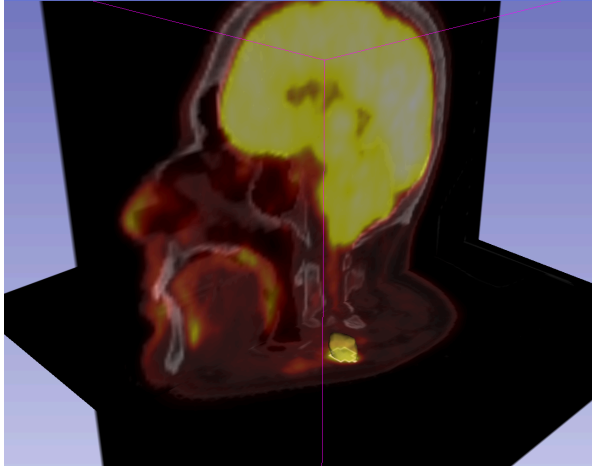
- Standardized Uptake Value (SUV) is a semi-quantitative measure derived from the determination of tissue activity obtained from a clinical PET study

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

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



Tutorial Case



- 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

The datasets are located in

**C:\Pujol2012\QuantitativeImagingSunday_Nov25_2012
\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.



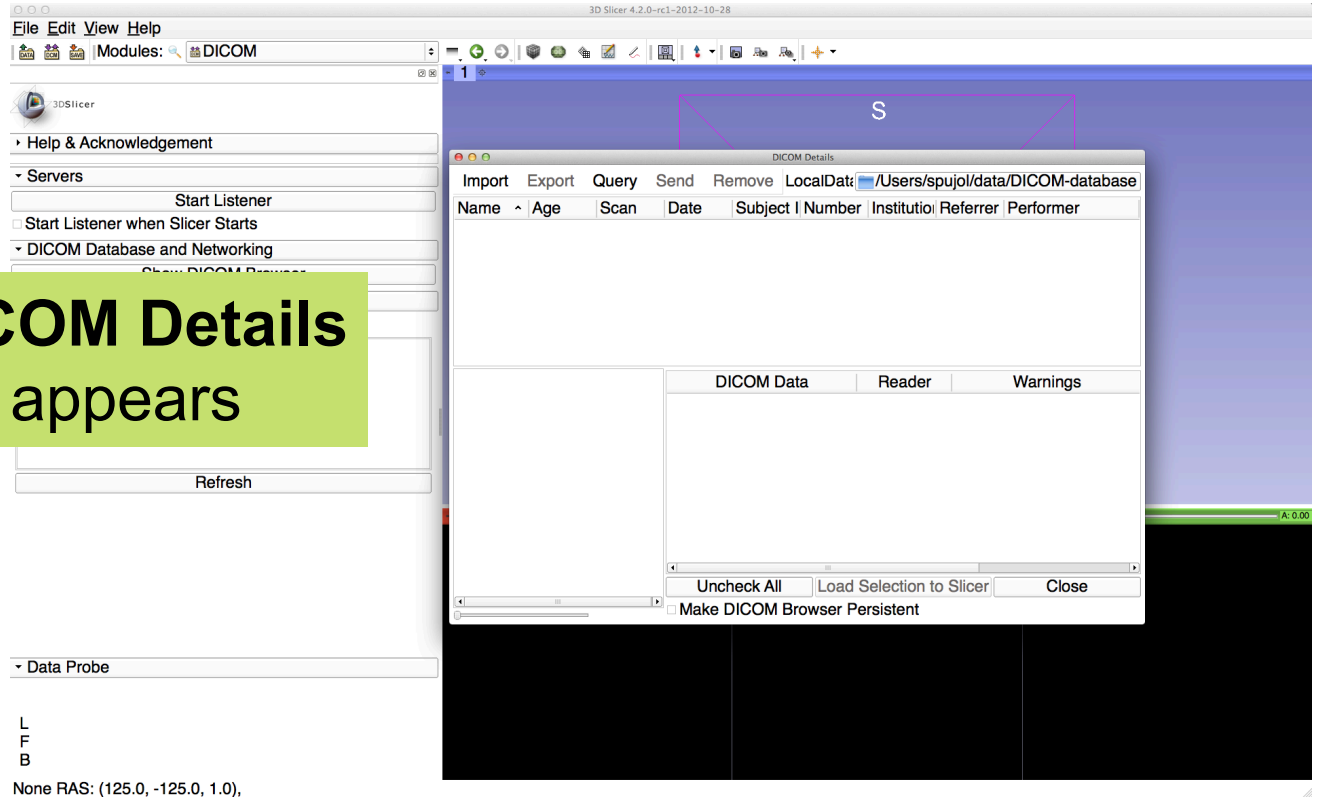
Select DICOM Database Directory

The screenshot shows the 3D Slicer 4.2.0-rc1-2012-10-28 interface. The 'Welcome' panel is visible on the left, with the 'Load DICOM Data' button circled in red. A large orange text box is overlaid on the right side of the interface, containing the instruction: 'Click on Load DICOM Data in the panel of the Welcome to Slicer module'. The main 3D view area is currently empty, showing a purple wireframe box. The bottom status bar displays 'R: 0.00', 'Y: 0.00', 'G: 0.00', and 'A: 0.00'. The bottom left corner shows 'None RAS: (125.0, -125.0, 1.0)'.



Select DICOM Database Directory

The **DICOM Details** window appears





Select DICOM Database Directory

The window **Select DICOM Database Directory** appears when you use the DICOM module for the first time

Browse to the directory:

C:\Pujol2012\QuantitativeImaging_Sunday_Nov25_2012

Select the sub-directory **dicom-database**

Click on **Choose**



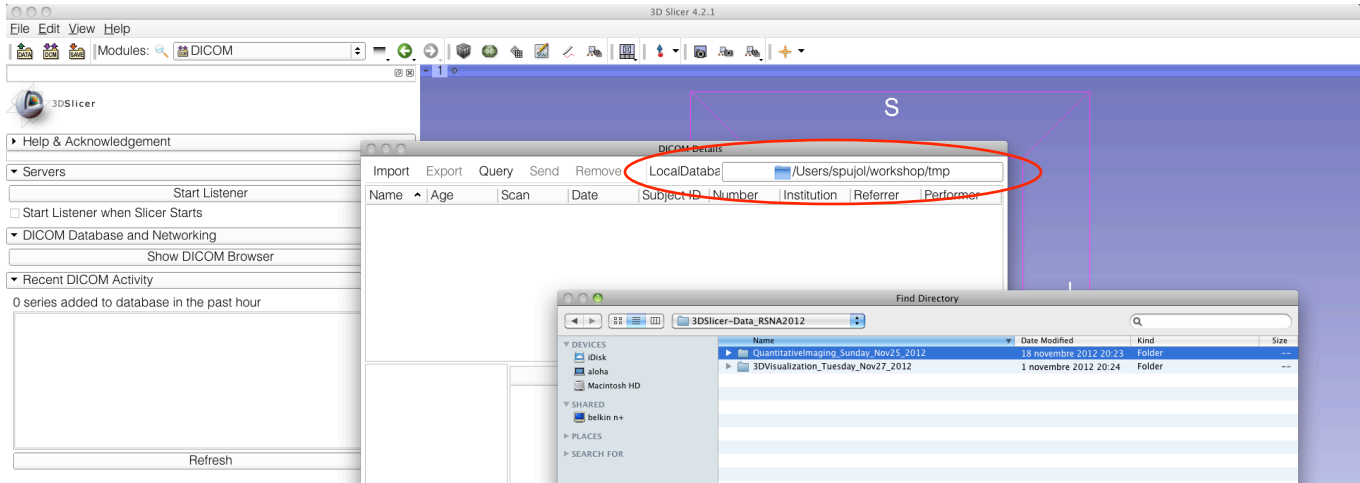
Select DICOM Database Directory

Slicer's local DICOM database is now set to:

**C:/Pujol2012/QuantitativeImaging_Sunday_Nov25_2012/
dicom-database**



Loading a DICOM Volume (Mac Users)



Mac Users: Click on the directory next to **Local Database**, and browse to the location of the **QuantitativeImaging_Sunday_Nov25_2012** directory, located in the **3DSlicer-Data_RSNA2012** directory



Loading a DICOM Volume (Mac Users)

The screenshot shows the 3D Slicer 4.2.1 interface. The main window displays a DICOM volume labeled 'S'. A 'DICOM Details' dialog is open, showing a table of DICOM series. A 'Find Directory' window is also open, showing a list of directories. The 'dicom-database' directory is selected, and the 'Choose' button is circled in red.

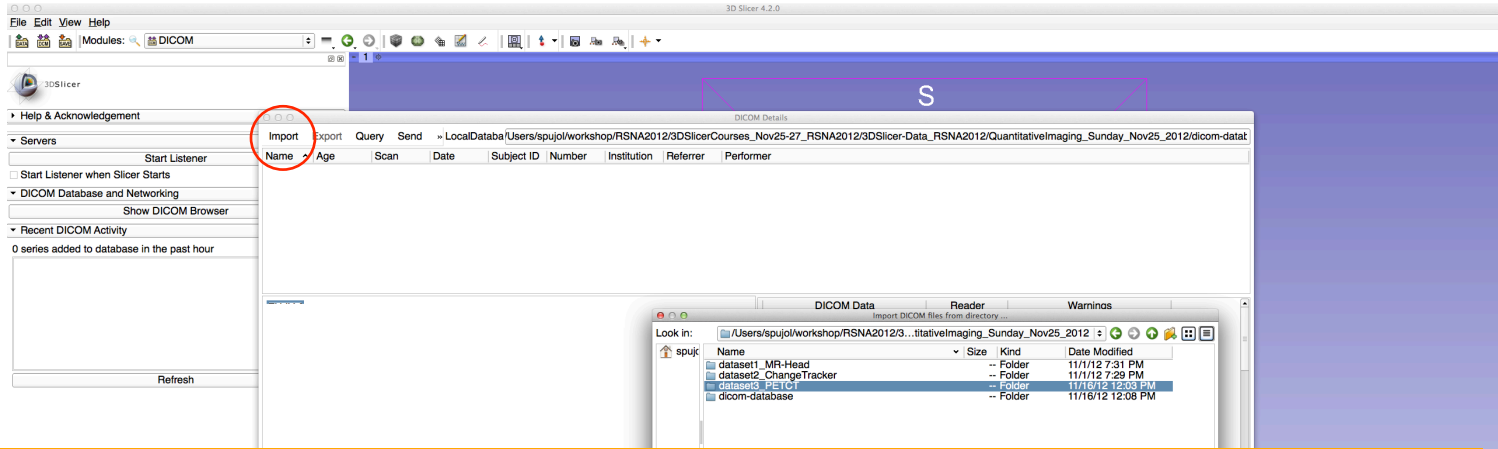
Name	Age	Scan	Date	Subject ID	Number	Institution	Referrer	Performer
dataset1_MR-Head			1 novembre 2012 19:31					
dataset2_ChangeTracker			1 novembre 2012 19:29					
dataset3_PETCT			17 novembre 2012 00:55					
dicom-database			18 novembre 2012 20:23					

Name	Date Modified	Kind	Size
dataset1_MR-Head	1 novembre 2012 19:31	Folder	--
dataset2_ChangeTracker	1 novembre 2012 19:29	Folder	--
dataset3_PETCT	17 novembre 2012 00:55	Folder	--
dicom-database	18 novembre 2012 20:23	Folder	--

Select the directory **dicom-database** and click on **Choose**



Loading a DICOM Volume

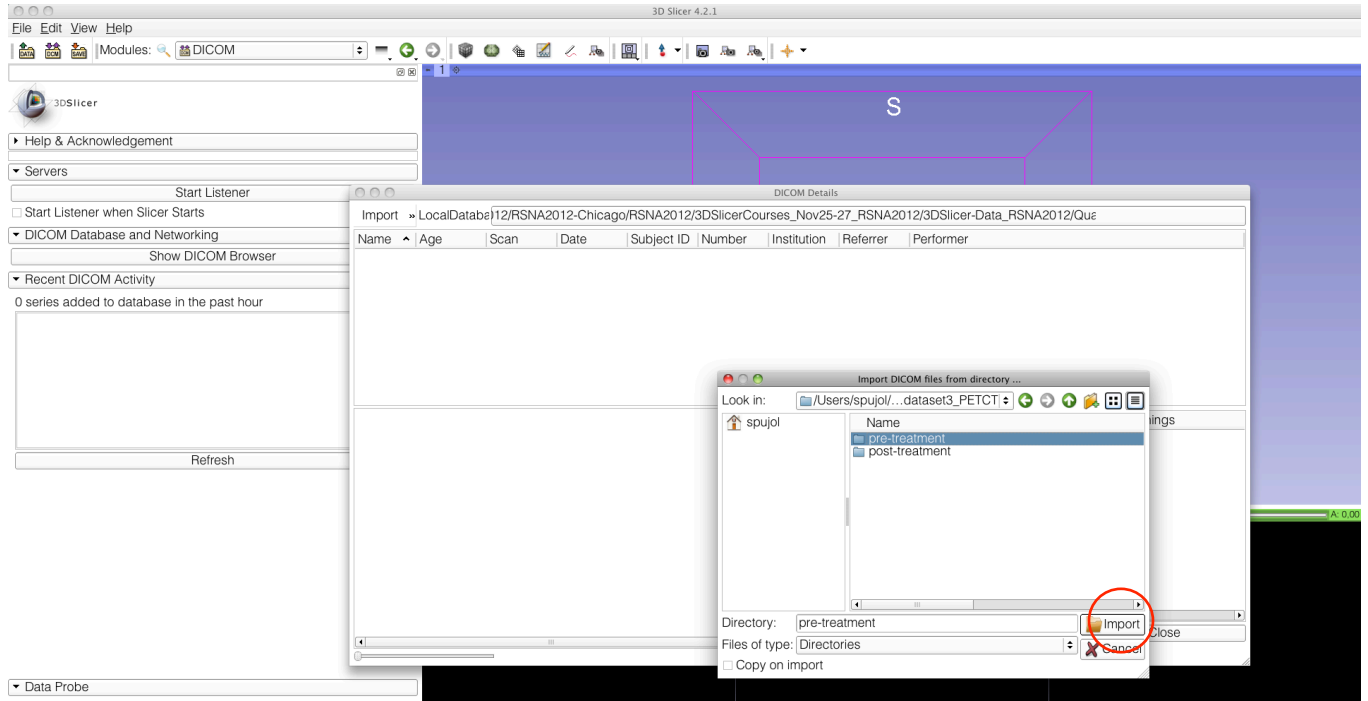


Click on **Import** and browse to the location of the directory
C:\Pujol2012\QuantitativeImaging_Sunday_Nov25_2012

Click on the dataset '**dataset3_PETCT**' located in this directory, and select the subdirectory **pre-treatment**



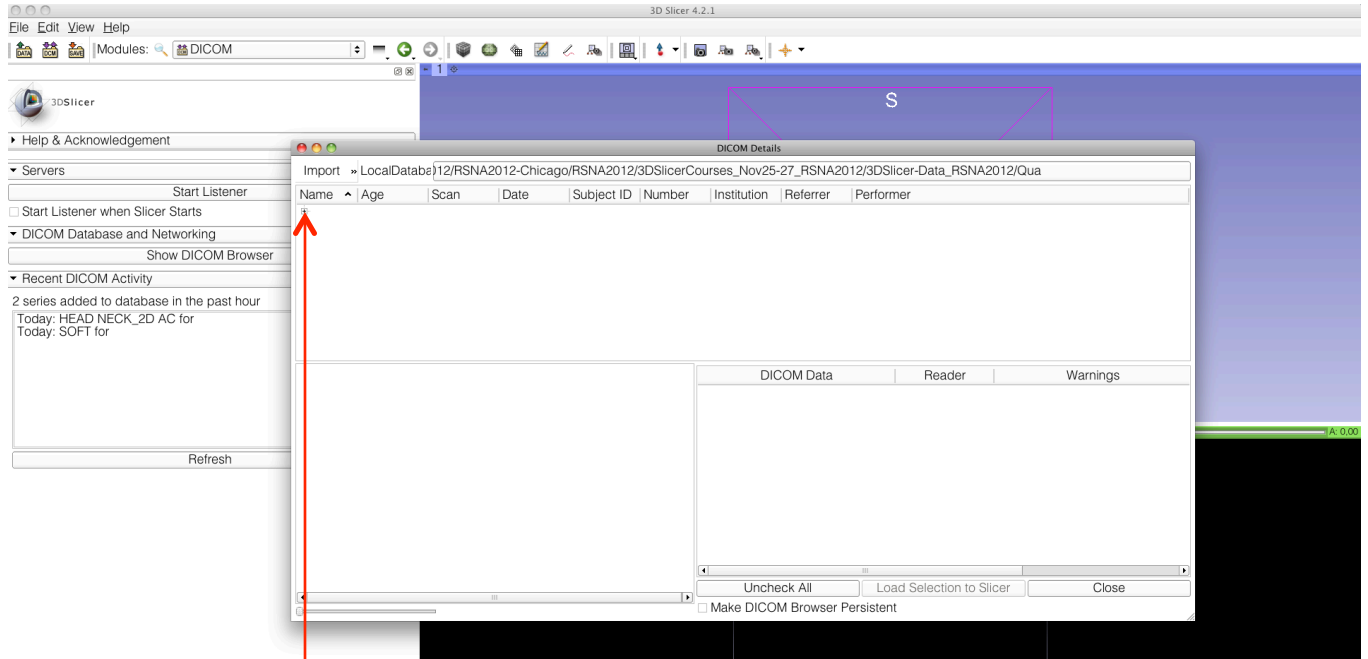
Loading a DICOM Volume



Select the **pre-treatment** directory and click on **Import**



Loading a DICOM Volume



Click to expand the list of DICOM volumes accessible via the DICOM browser



Loading a DICOM Volume

Select the series **PET Skull to MID Thigh Plus DCT Chest W Ini**

Name	Age	Scan	Date	Subject ID	Number	Institution	Referrer	Performer
PET Skull to Mid Thigh Plus DCT Chest W Ini			2012-06-07					
SOFT	CT	3	2012-06-07		1			
HEAD NECK_2D AC	PT	401	2012-06-07		0			

Slicer displays the list of DICOM volumes located in the pre-treatment directory:

- **'SOFT'** is the CT dataset
- **'HEAD NECK_2D AC'** is the PET dataset (note: this may take a few minutes)



Loading a DICOM Volume

Slicer displays a snapshot of the DICOM volumes:

- 'SOFT' is the CT dataset
- 'HEAD NECK_2D AC' is the PET dataset

The screenshot shows the 3D Slicer 4.2.1 interface. At the top, a menu bar includes 'File', 'Edit', 'View', and 'Help'. Below the menu, a window titled 'DICOM Details' displays a table of DICOM series. The table has columns for 'Object ID', 'Number', 'Institution', 'Referrer', and 'Performer'. The first row shows '1' and '0'. Below this, a 'DICOM Data' table is visible with columns for 'DICOM Data', 'Reader', and 'Warnings'. The 'DICOM Data' table contains several rows, with the first two rows checked: '3: SOFT' (Scalar Volume) and '401: HEAD NECK_2D AC' (Scalar Volume). Below the table are buttons for 'check All', 'Load Selection to Slicer', and 'Close'. A red arrow points to the 'Load Selection to Slicer' button. In the center of the interface, two thumbnail images are shown: 'SOFT' (a CT scan) and 'HEAD NECK_2D AC' (a PET scan). To the left of these thumbnails is a 'Refresh' button. At the bottom left, a 'Data Probe' window shows 'Green RAS: (7.3, 0.0, -6.5) Coronal Sp: 1.0' and 'L None ()', 'F None ()', 'B None ()'.

Object ID	Number	Institution	Referrer	Performer
1	0			

DICOM Data	Reader	Warnings
<input checked="" type="checkbox"/> 3: SOFT	Scalar Volume	
<input checked="" type="checkbox"/> 401: HEAD NECK_2D AC	Scalar Volume	
<input type="checkbox"/> 3: SOFT for contentType of 1...	Scalar Volume	Images are not equally spaced ...
<input type="checkbox"/> 3: SOFT for contentType of 1...	Scalar Volume	Images are not equally spaced ...
<input type="checkbox"/> 3: SOFT for contentType of 1...	Scalar Volume	Images are not equally spaced ...
<input type="checkbox"/> 3: SOFT for contentType of 1...	Scalar Volume	Images are not equally spaced ...
<input type="checkbox"/> 3: SOFT for contentType of 1...	Scalar Volume	Images are not equally spaced ...
<input type="checkbox"/> 3: SOFT for contentType of 1...	Scalar Volume	Images are not equally spaced ...
<input type="checkbox"/> 3: SOFT for contentType of 1...	Scalar Volume	Images are not equally spaced ...
<input type="checkbox"/> 3: SOFT for contentType of 1...	Scalar Volume	Images are not equally spaced ...

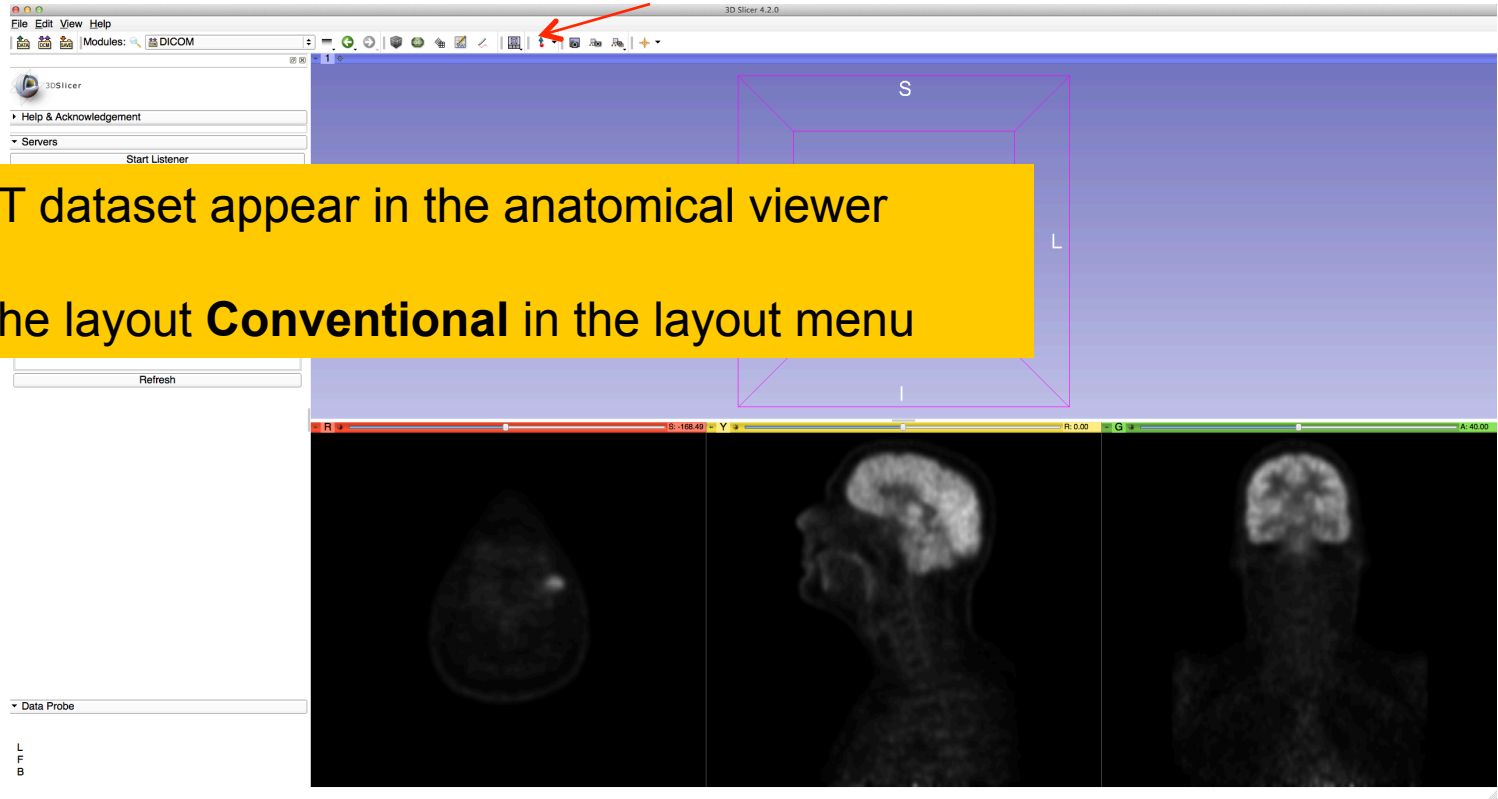
check All Load Selection to Slicer Close

OM Browser Persistent

Click on **Load Selection to Slicer**



Loading a DICOM Volume



The PET dataset appear in the anatomical viewer
Select the layout **Conventional** in the layout menu



Loading a DICOM Volume

The screenshot shows the 3D Slicer 4.2.0 interface. The 'Modules' menu is open, and 'Data' is highlighted. A context menu is also open over the volume '401: HEAD NECK_2D AC', with 'Rename' selected. The main 3D view shows three orthogonal slices of a head scan.

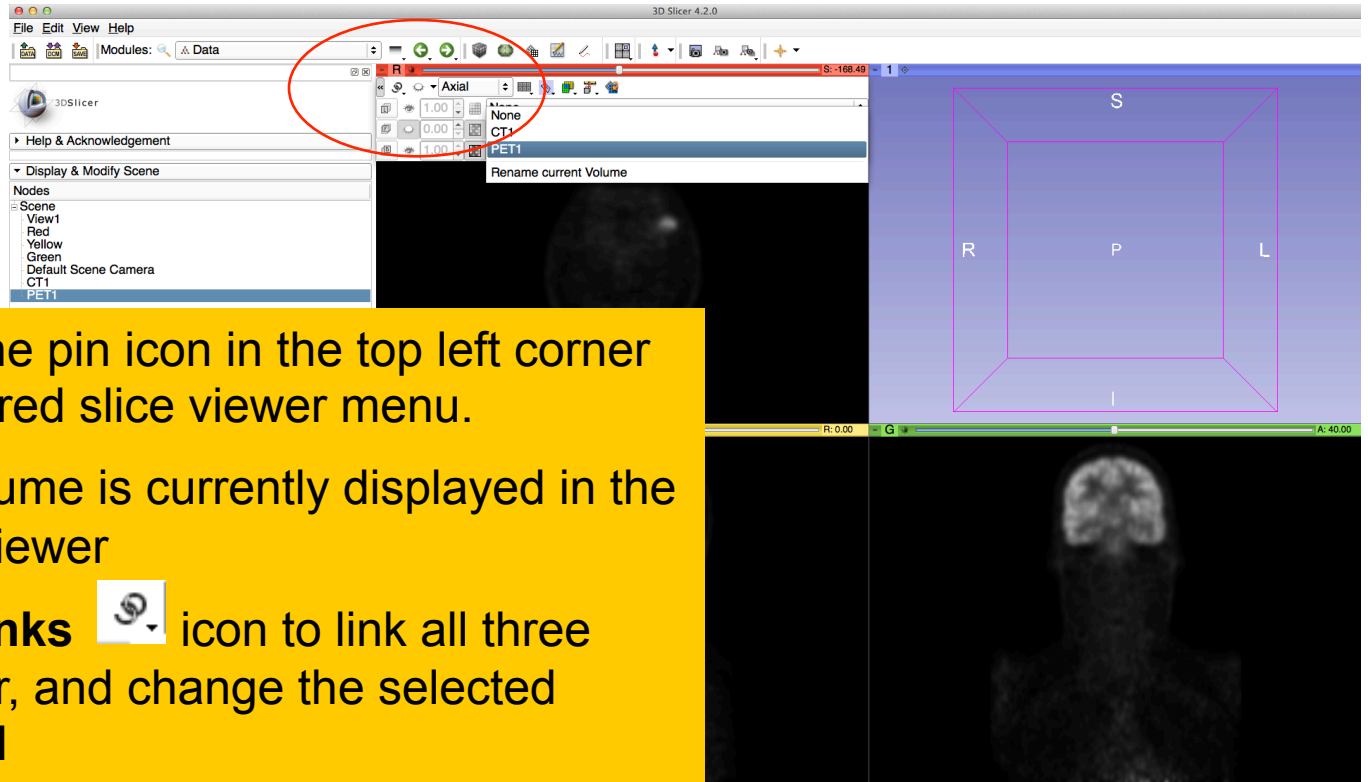
Select the module **Data** in the modules menu

Right click on the volume '**3: SOFT**' and rename it **CT1**

Right click on the volume '**401: HEAD NECK_2D AC**' and rename it **PET1**




Loading a PETCT dataset



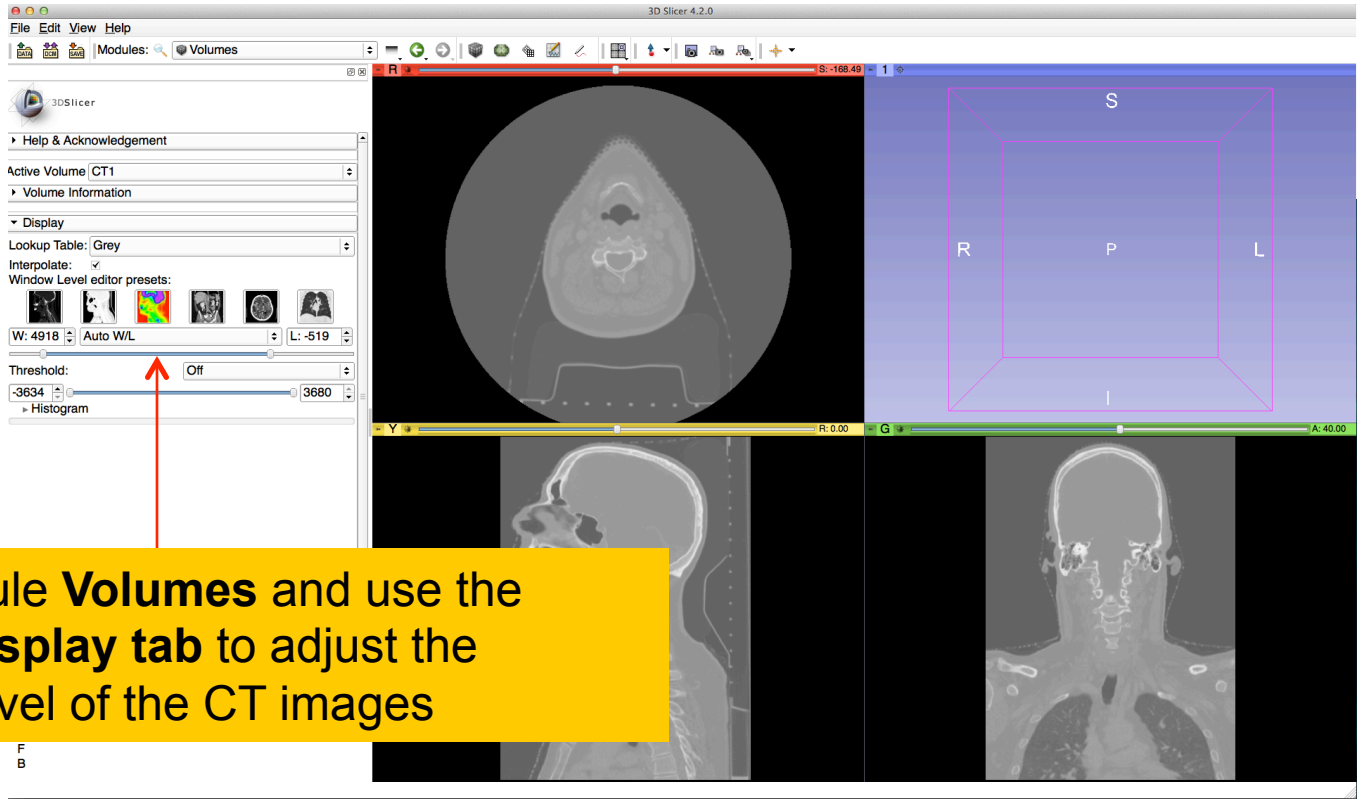
Left click on the pin icon in the top left corner to display the red slice viewer menu.

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

Click on the **links**  icon to link all three views together, and change the selected volume to **CT1**



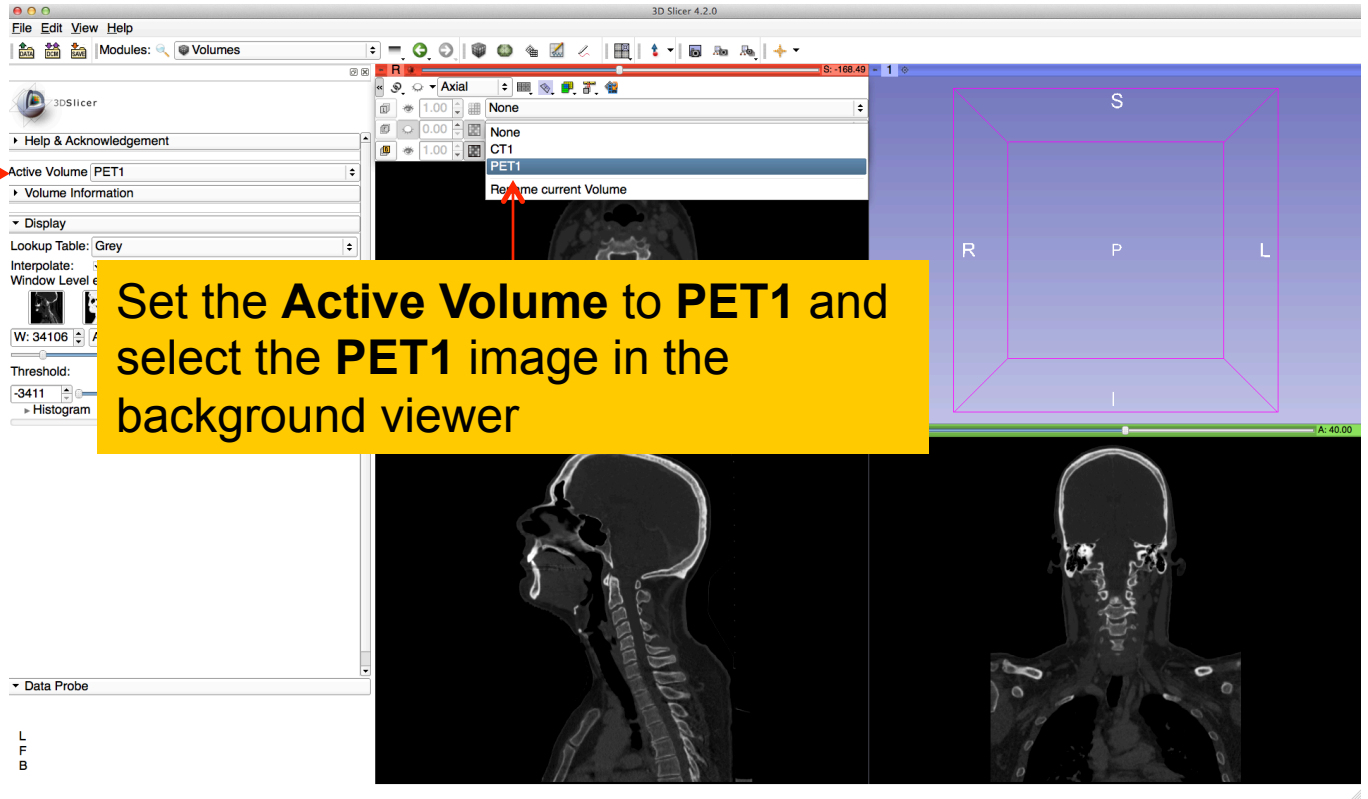
Loading a PETCT dataset



Select the module **Volumes** and use the sliders in the **Display tab** to adjust the Window and Level of the CT images



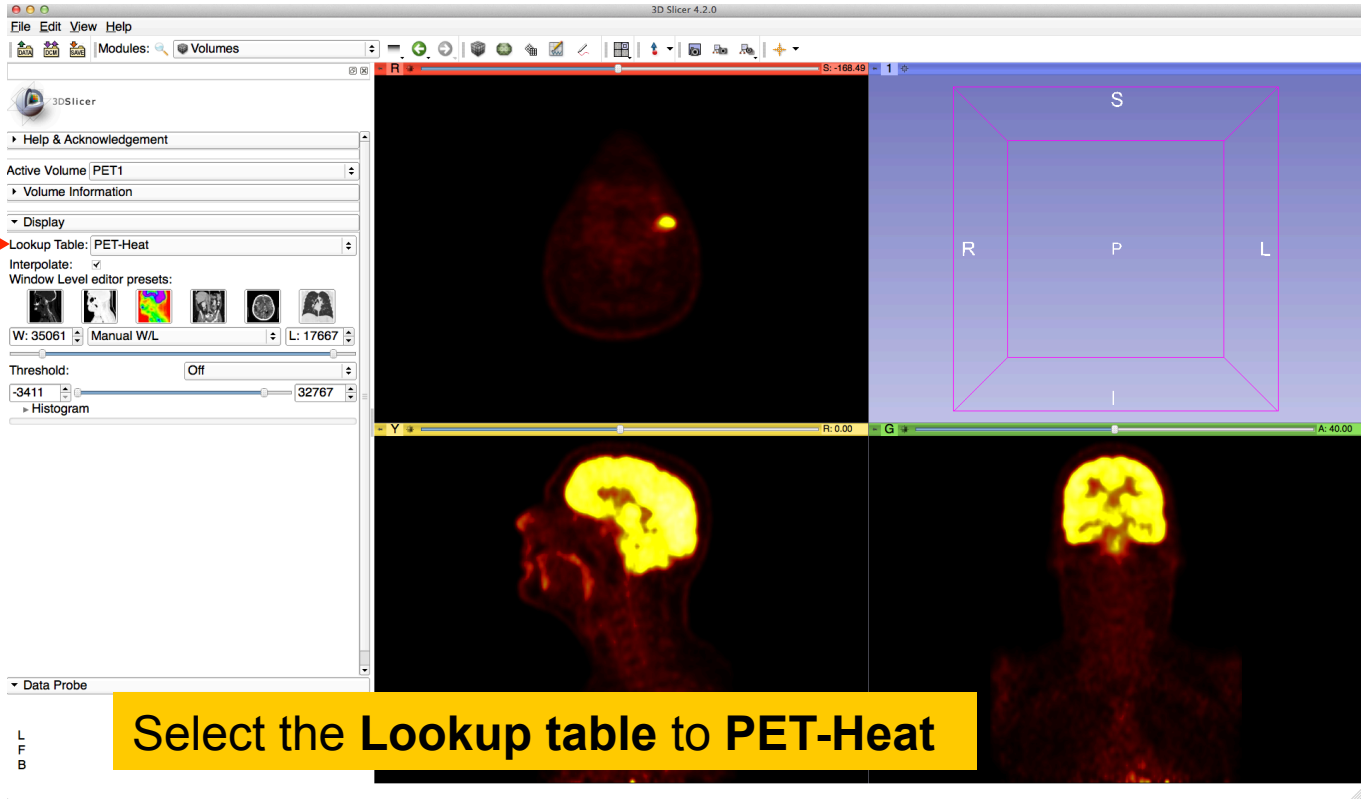
Visualization of PETCT data



Set the Active Volume to PET1 and select the PET1 image in the background viewer



Visualization of PETCT data

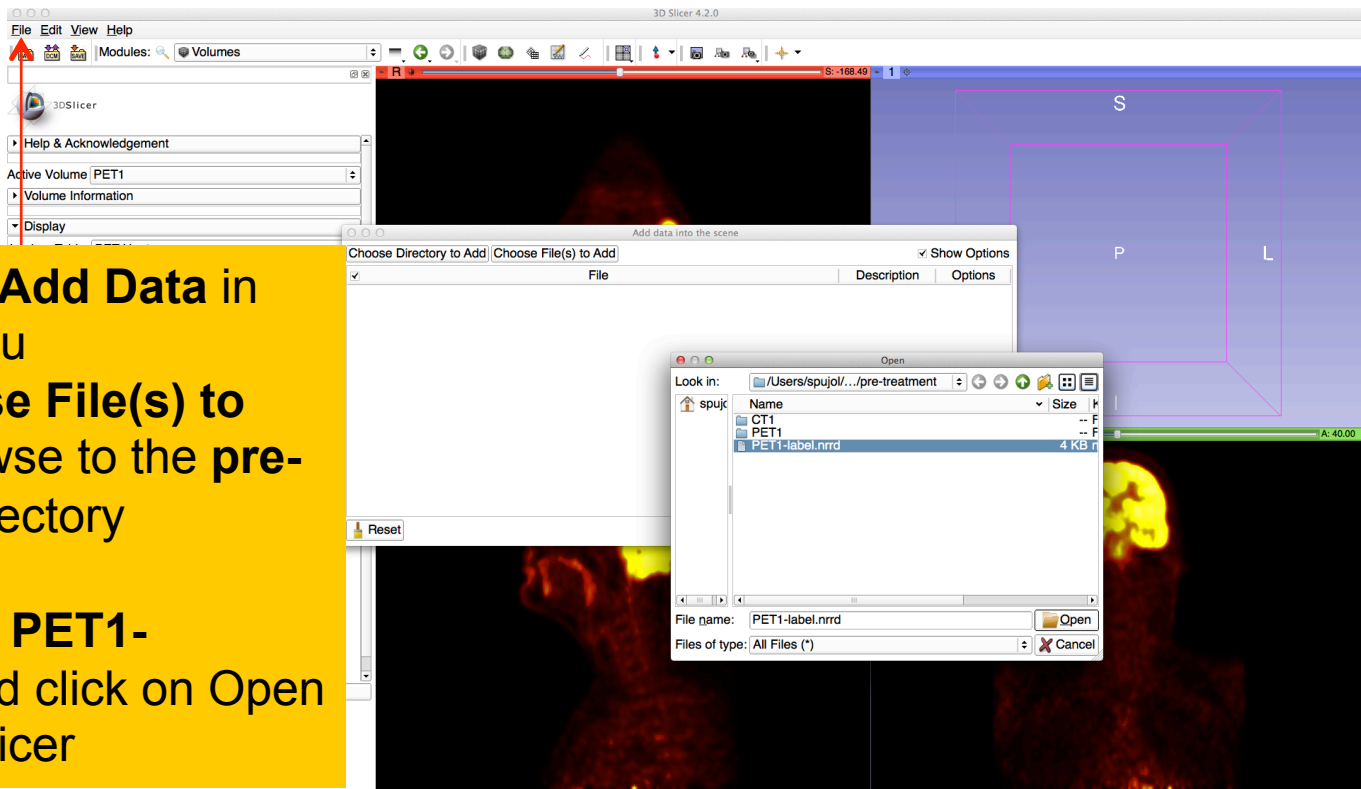




Visualization of PETCT data

Select **File** → **Add Data** in the main menu
Select **Choose File(s) to Add** and browse to the **pre-treatment** directory

Select the file **PET1-label.nrrd** and click on **Open** to load it in Slicer





Visualization of PETCT data

3D Slicer 4.2.0

File Edit View Help

Modules: Volumes

3DSlicer

Help & Acknowledgement

Active Volume: PET1

Volume Information

Display

Lookup Table: PET-Heat

Interpolate:

Window Level editor presets:

W: 35061 | Manual W/L | L: 17667

Threshold: Off | 32767

► Histogram

Data Probe

L
F
B

Add data into the scene

Choose Directory to Add | Choose File(s) to Add

Show Options

File	Description	Options
...ETCT/pre-	Volume	PET1-label

Centered Ignore Orientation Label Map Single File

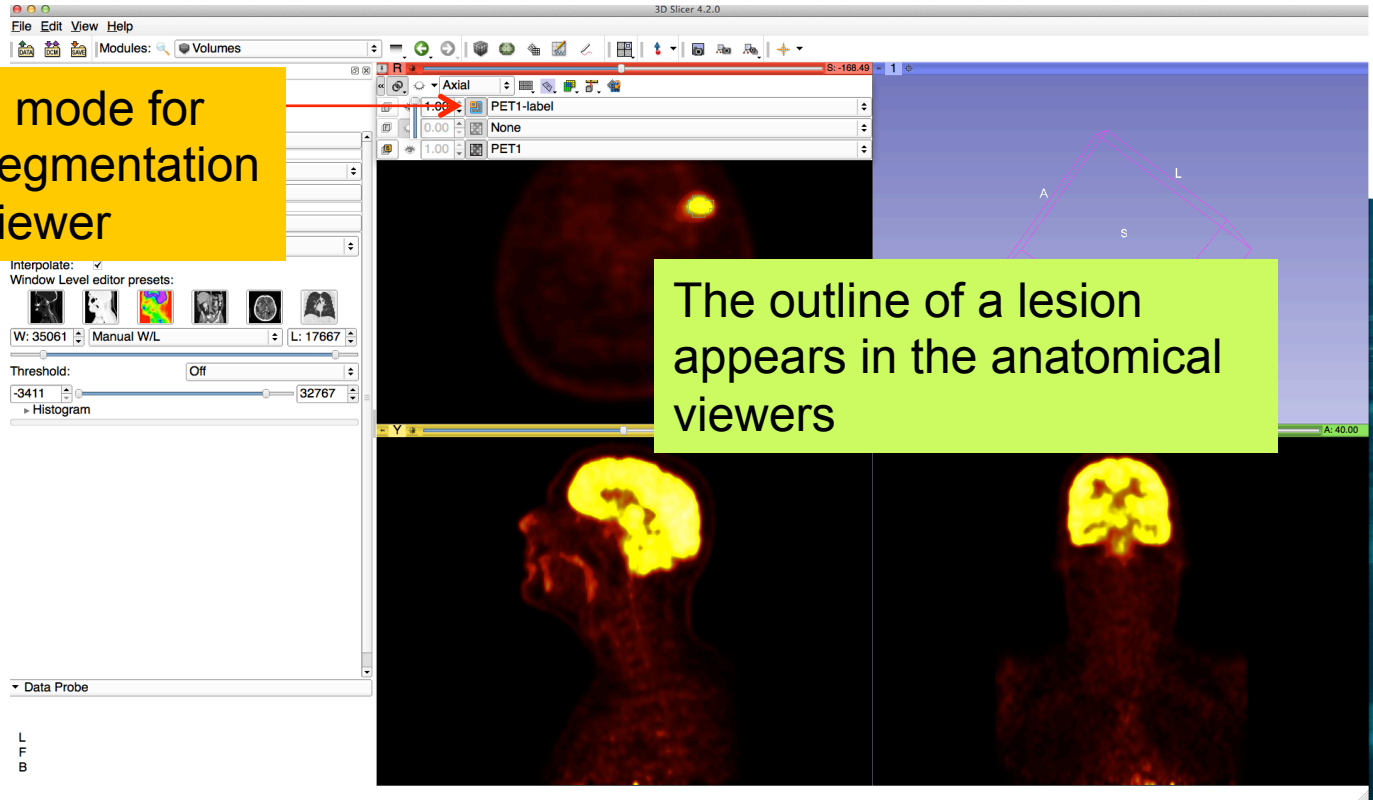
OK Cancel

Check the 'Show Options' box, and check that the option 'Label Map' is selected. Select the file **PET1-label.nrrd** and click on **OK** to load it in Slicer



Visualization of PETCT data

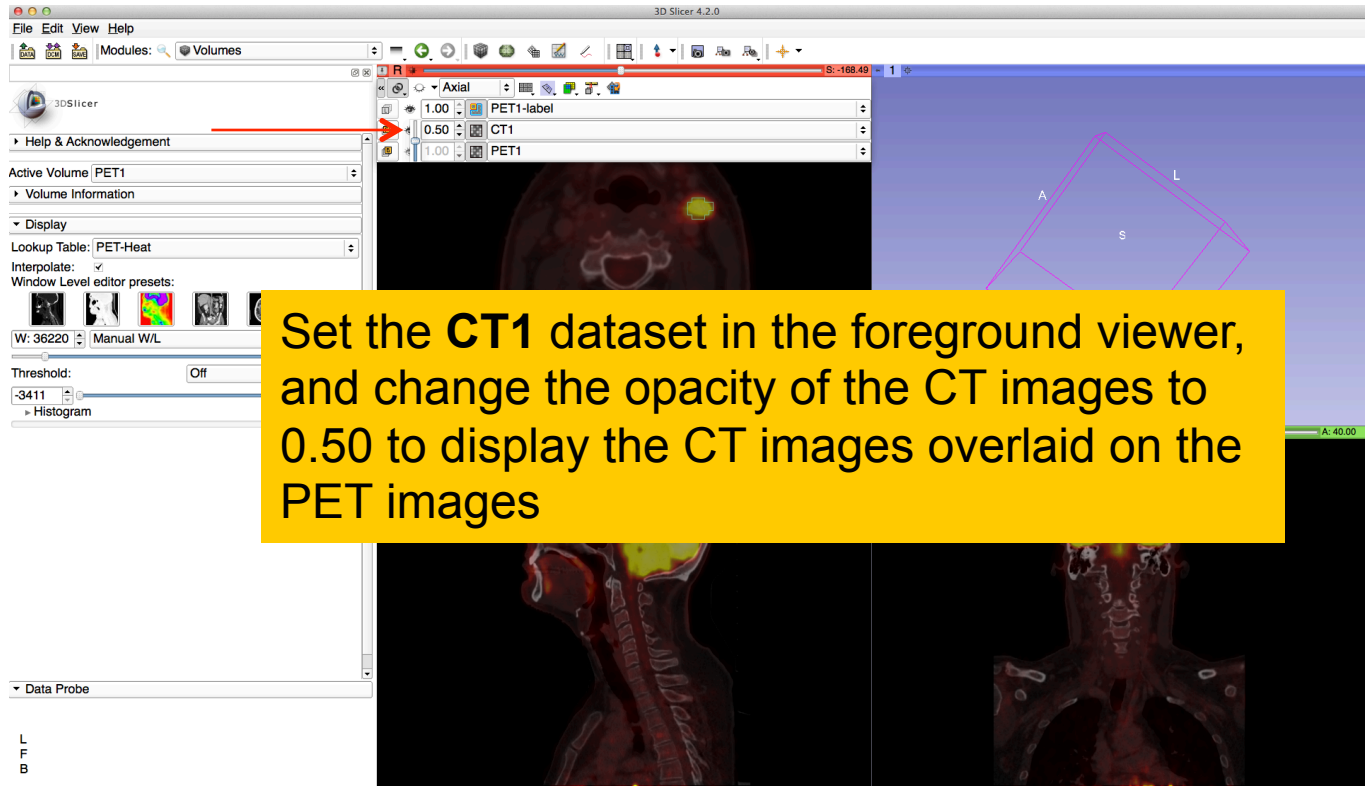
Select the outline mode for the **PET1-label** segmentation in the labelmap viewer



The outline of a lesion appears in the anatomical viewers




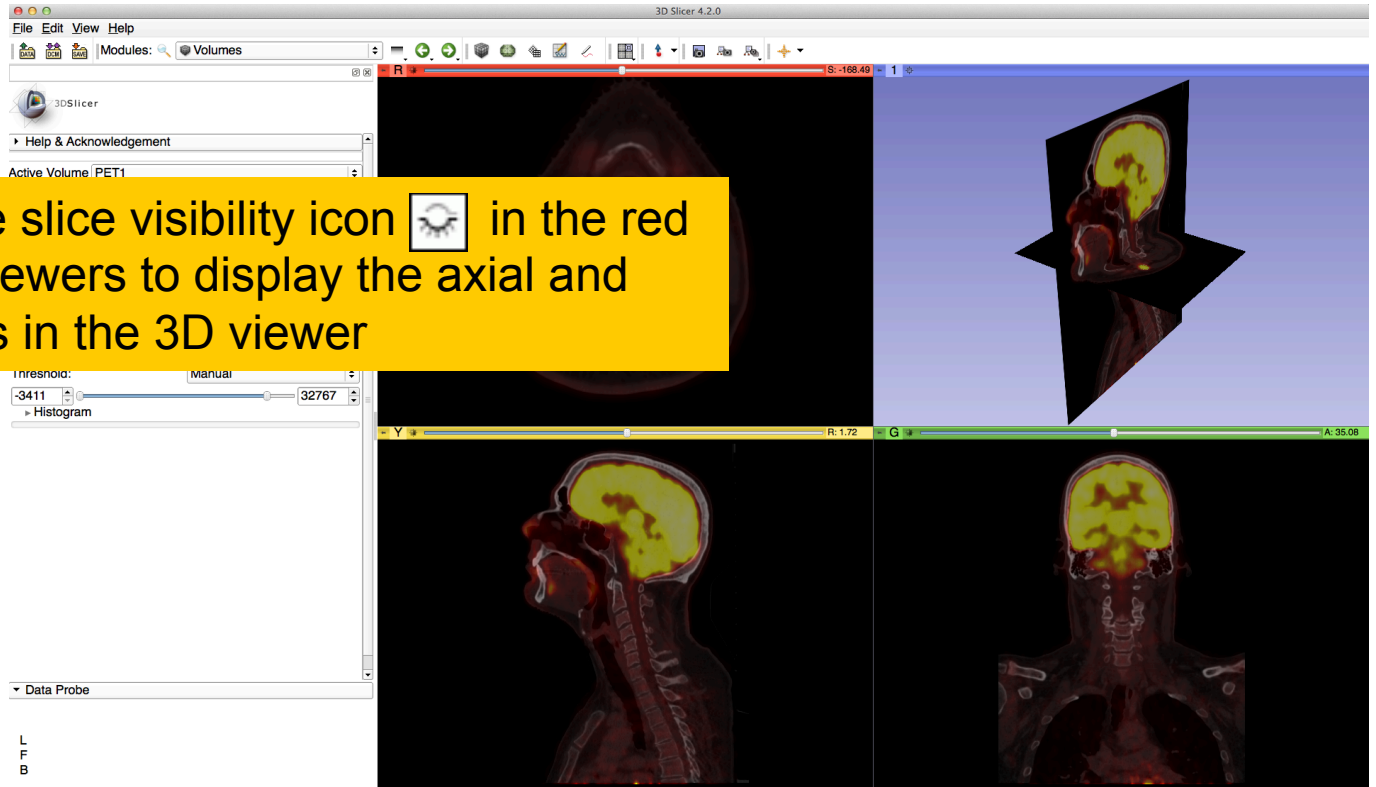
Visualization of PETCT data





Visualization of PETCT data

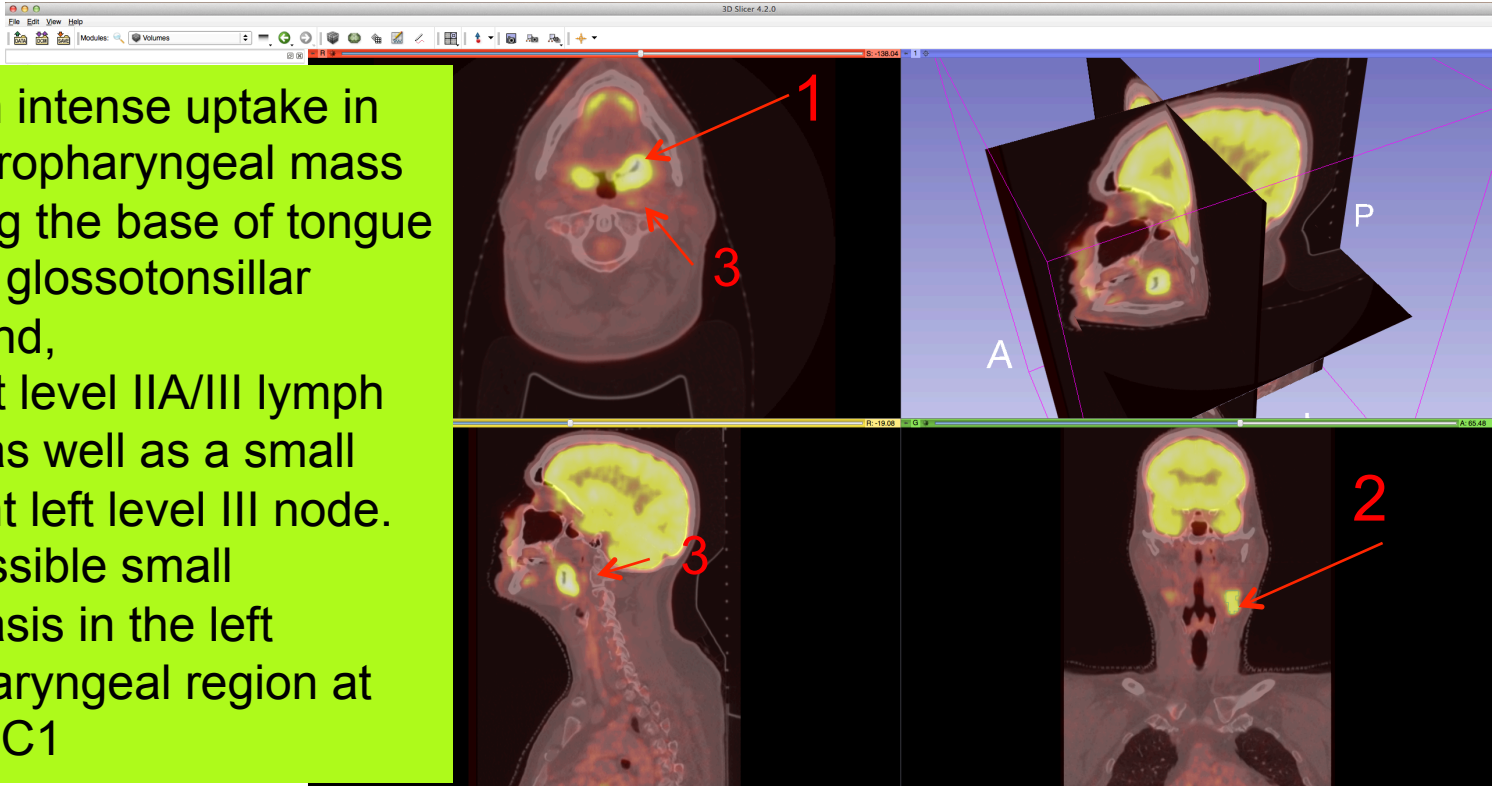
Check on the slice visibility icon  in the red and yellow viewers to display the axial and sagittal slices in the 3D viewer





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

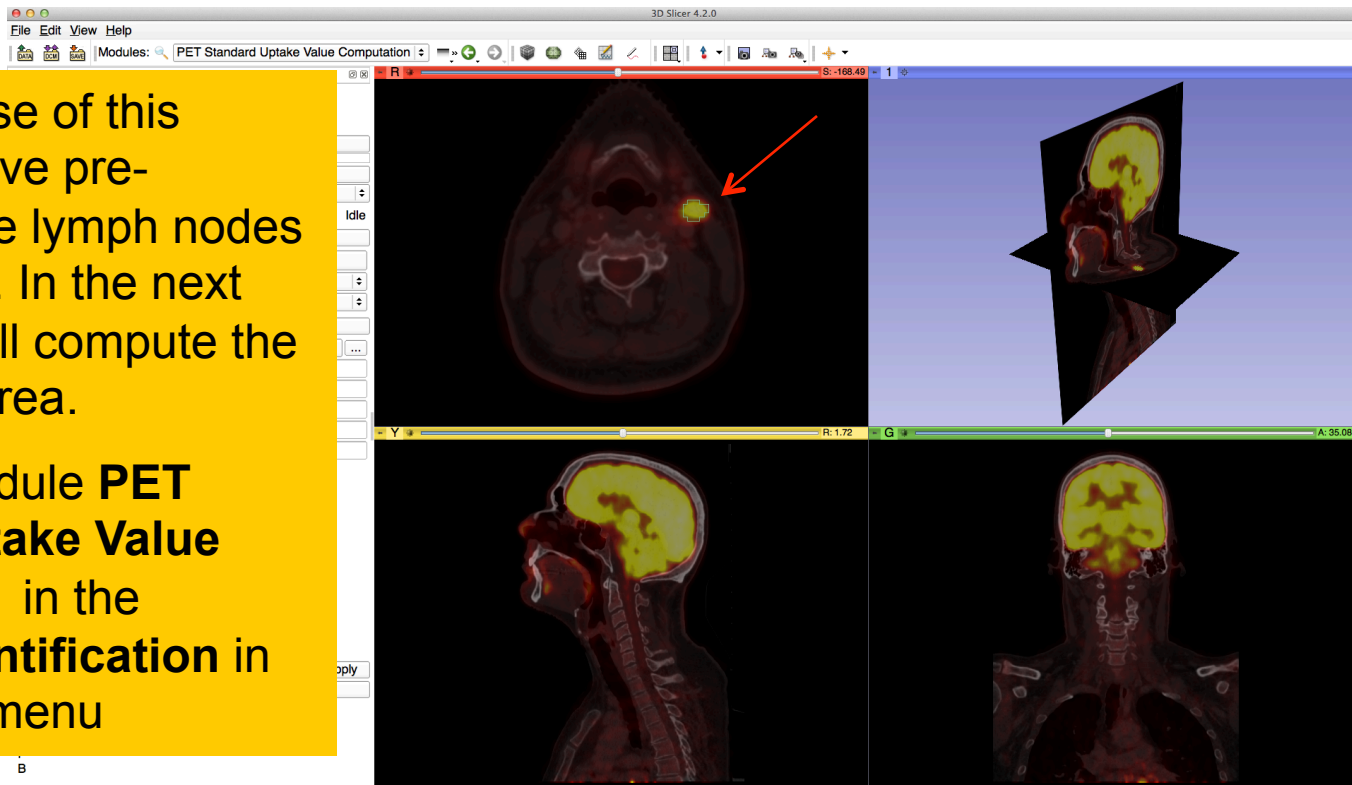




PET SUV Computation

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

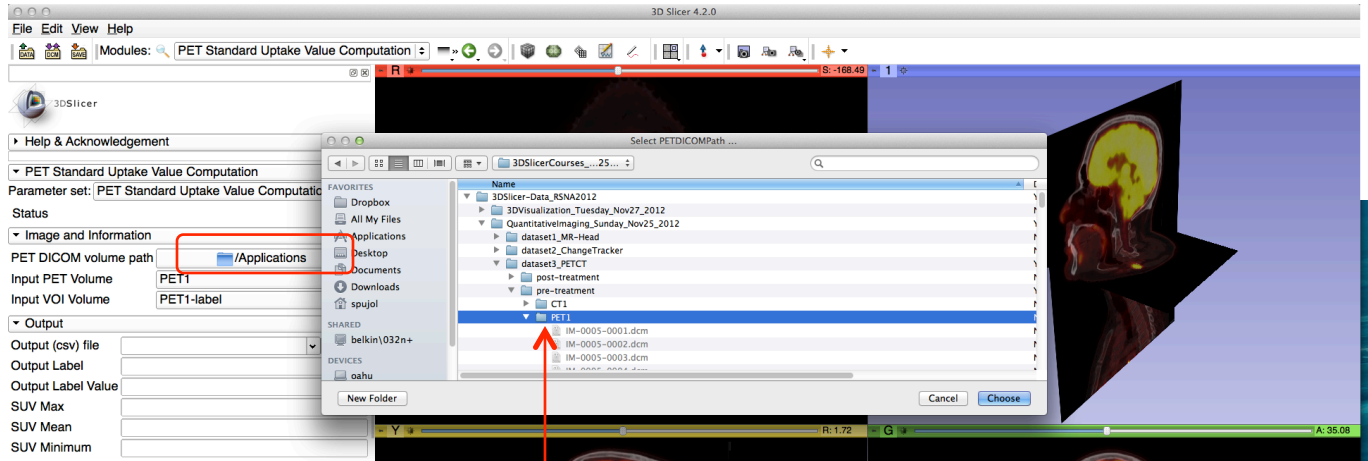
Step 1: Input volumes selection
Select Input PET Volume 'PET1'
Select Input VOI Volume 'PET1-label'

The screenshot shows the 3D Slicer 4.2.0 interface with the 'PET Standard Uptake Value Computation' module active. The 'Input PET Volume' is set to 'PET1' and the 'Input VOI Volume' is set to 'PET1-label'. The 'Output' section is empty. The 'Data Probe' section shows the following data:

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:/Pujol2012/**

QuantitativImaging_Sunday_Nov25_2012/dataset3_PETCT/pre-treatment/PET1

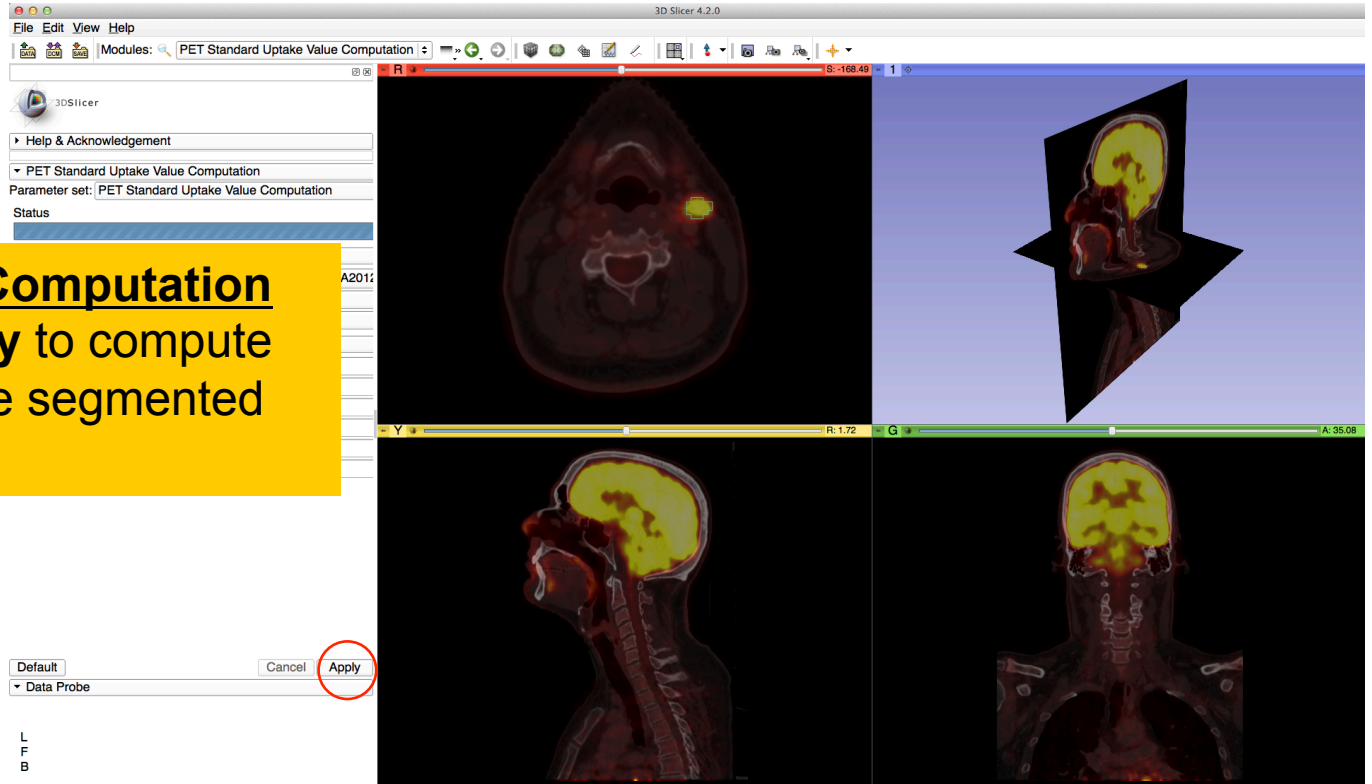
L
F
B



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: [empty]

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

Select File → Close Scene in the main menu

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

Input PET Volume: PET1

Input VOI Volume: PET1-label

Output

Output (csv) file: [empty]

Output Label: 1

Output Label Value: 1

SUV Max	7.53385
SUV Mean	5.01805
SUV Minimum	3.39015

Default [] Cancel [] Apply []

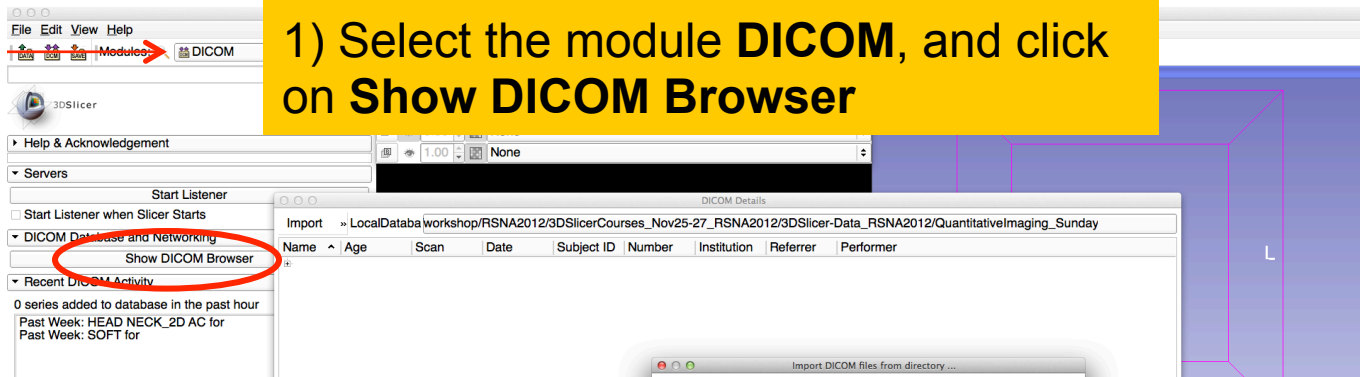
Data Probe []

L
F
B



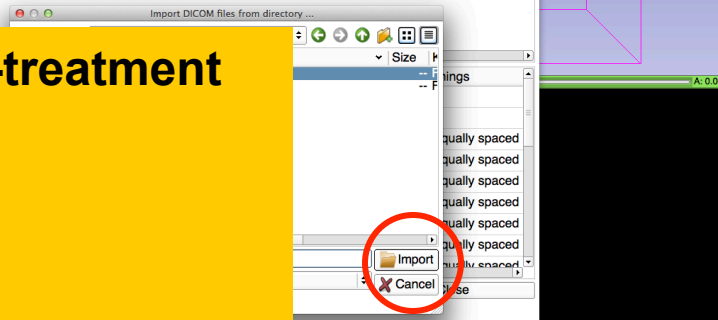
Loading the post-treatment dataset

1) Select the module **DICOM**, and click on **Show DICOM Browser**



2) Click on **Import** and select the dataset **post-treatment** located in the directory

**C:/Pujol2012/
QuantitativeImaging_Sunday_Nov25_2012/
dataset3_PETCT/post-treatment/**



F
B



Loading the post-treatment dataset

Click to expand the DICOM files tree

DICOM Details

Import » LocalDatabase\workshop\RSNA2012\3DSlicerCourses_Nov25-27_RSNA2012\3DSlicer-Data_RSNA2012\QuantitativeImaging_Sunday

Name	Age	Scan	Date	Subject ID	Number	Institution	Referrer	Performer
<input checked="" type="checkbox"/> SOFT	NECK							

DICOM Data	Reader	Warnings
<input checked="" type="checkbox"/> 3: SOFT	Scalar Volume	
<input checked="" type="checkbox"/> 5: HEAD NECK_2D AC	Scalar Volume	
<input type="checkbox"/> 3: SOFT for contentTime of 1...	Scalar Volume	Images are not equally spaced
<input type="checkbox"/> 3: SOFT for contentTime of 1...	Scalar Volume	Images are not equally spaced
<input type="checkbox"/> 3: SOFT for contentTime of 1...	Scalar Volume	Images are not equally spaced
<input type="checkbox"/> 3: SOFT for contentTime of 1...	Scalar Volume	Images are not equally spaced
<input type="checkbox"/> 3: SOFT for contentTime of 1...	Scalar Volume	Images are not equally spaced
<input type="checkbox"/> 3: SOFT for contentTime of 1...	Scalar Volume	Images are not equally spaced
<input type="checkbox"/> 3: SOFT for contentTime of 1...	Scalar Volume	Images are not equally spaced
<input type="checkbox"/> 3: SOFT for contentTime of 1...	Scalar Volume	Images are not equally spaced

Uncheck All Load Selection to Slicer Close

Make DICOM Browser Persistent

Most recent DICOM Database addition: Sat Nov 17 21:15:01 2012



Loading the post-treatment dataset

3D Slicer 4.2.0

File Edit View Help

Modules: DICOM

3DSlicer

Help & Acknowledgement

Servers

Start Listener

Start Listener when Slicer Starts

DICOM Database and Networking

Show DICOM Browser

Recent DICOM Activity

2 series added to database in the past hour
Today: HEAD NECK_2D AC for
Today: SOFT for
Past Week: HEAD NECK_2D AC for
Past Week: SOFT for

Refresh

DICOM Details

Import LocalData\workshop\RSNA2012\3DSlicerCourses_Nov25-27_RSNA2012\3DSlicer-Data_RSNA2012\QuantitativeImaging_Sunday

Name	Age	Scan	Date	Subject ID	Number	Institution	Referrer	Performer
PET Skull to Mid Thigh Plus DCT Chest W Ini			2012-06-07					
PET SKULL-MID THIGH PL			2012-11-06					
SOFT	CT	3	2012-11-06		1			
HEAD NECK_2D AC	PT	5	2012-11-06		0			

SOFT NECK_

DICOM Data	Reader	Warnings
<input checked="" type="checkbox"/> 3: SOFT	Scalar Volume	
<input checked="" type="checkbox"/> 5: HEAD NECK_2D AC	Scalar Volume	
<input type="checkbox"/> 3: SOFT for contentTime of 1...	Scalar Volume	Images are not equally spaced
<input type="checkbox"/> 3: SOFT for contentTime of 1...	Scalar Volume	Images are not equally spaced
<input type="checkbox"/> 3: SOFT for contentTime of 1...	Scalar Volume	Images are not equally spaced
<input type="checkbox"/> 3: SOFT for contentTime of 1...	Scalar Volume	Images are not equally spaced
<input type="checkbox"/> 3: SOFT for contentTime of 1...	Scalar Volume	Images are not equally spaced
<input type="checkbox"/> 3: SOFT for contentTime of 1...	Scalar Volume	Images are not equally spaced
<input type="checkbox"/> 3: SOFT for contentTime of 1...	Scalar Volume	Images are not equally spaced
<input type="checkbox"/> 3: SOFT for contentTime of 1...	Scalar Volume	Images are not equally spaced

Uncheck All Load Selection to Slicer Close

Make DICOM Browser Persistent

Select the 2nd series **PET SKULL-MID THIGH PL** and click in **Load Selection to Slicer** to load the follow-up PET and CT scans to Slicer



Loading the post-treatment dataset

Select the module **Data** and rename the CT scan '3:SOFT' to **CT2** and the PET scan '5: HEAD NECK_2D AC' to **PET2**

Scene Model: Transform
 Display MRML ID's
 Show Hidden nodes

Filter:
MRML Node Inspector

Load & Add Scenes Or Individual Datasets

Data Probe

L
F
B



Loading the post-treatment dataset

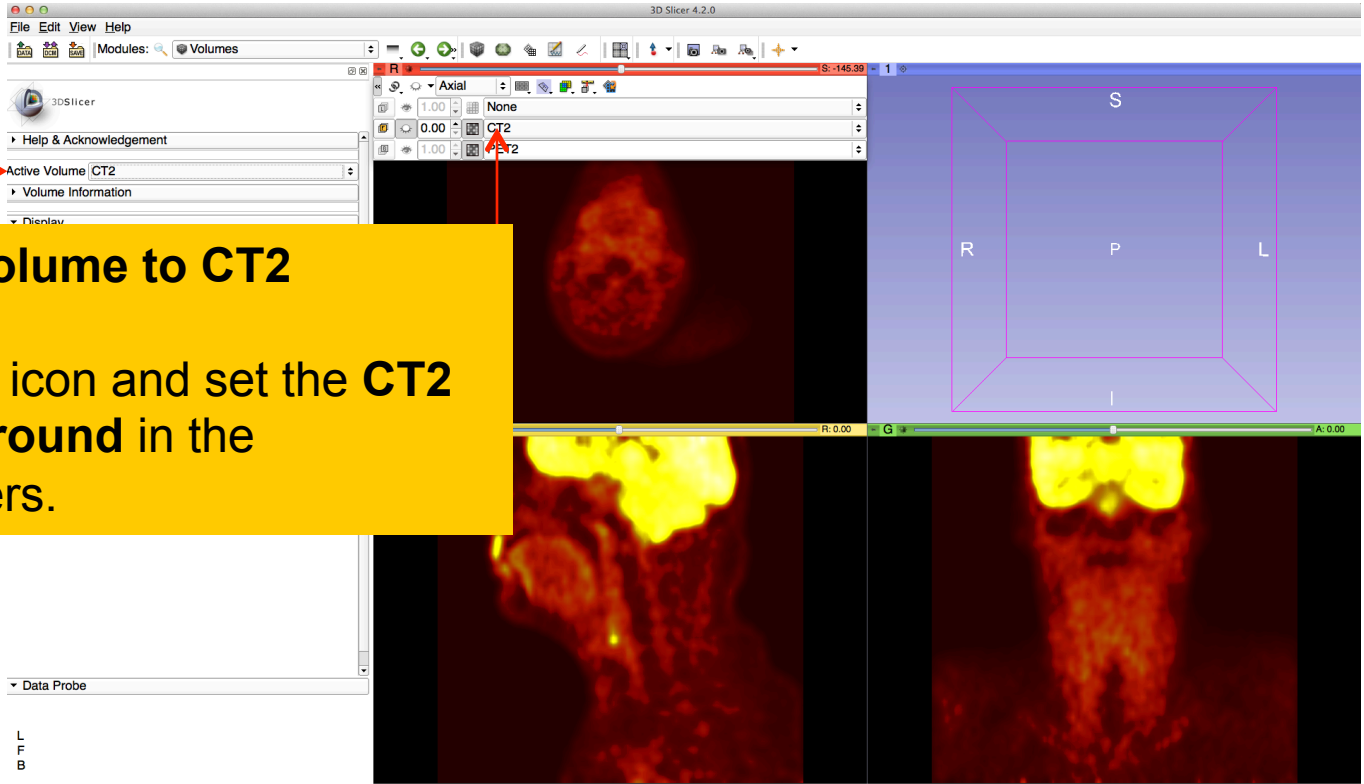
The screenshot shows the 3D Slicer 4.2.0 interface. The 'Volumes' module is active. The 'Volume Information' panel shows 'Active Volume: PET2'. The 'Lookup Table' dropdown is set to 'PET-Heat'. A red arrow points to the 'PET-Heat' option in the list. A yellow text box contains the following instructions:

- Select the module **Volumes**
- Select the **Active Volume PET2**
- Set the Lookup table to **PET-Heat**

The main view shows a 3D rendering of a brain slice with a purple bounding box. The bottom panel shows two grayscale PET scan slices. The interface includes a menu bar (File, Edit, View, Help), a toolbar, and a sidebar with various tool icons. The status bar at the bottom indicates 'L', 'F', and 'B' for orientation.



Loading the post-treatment dataset

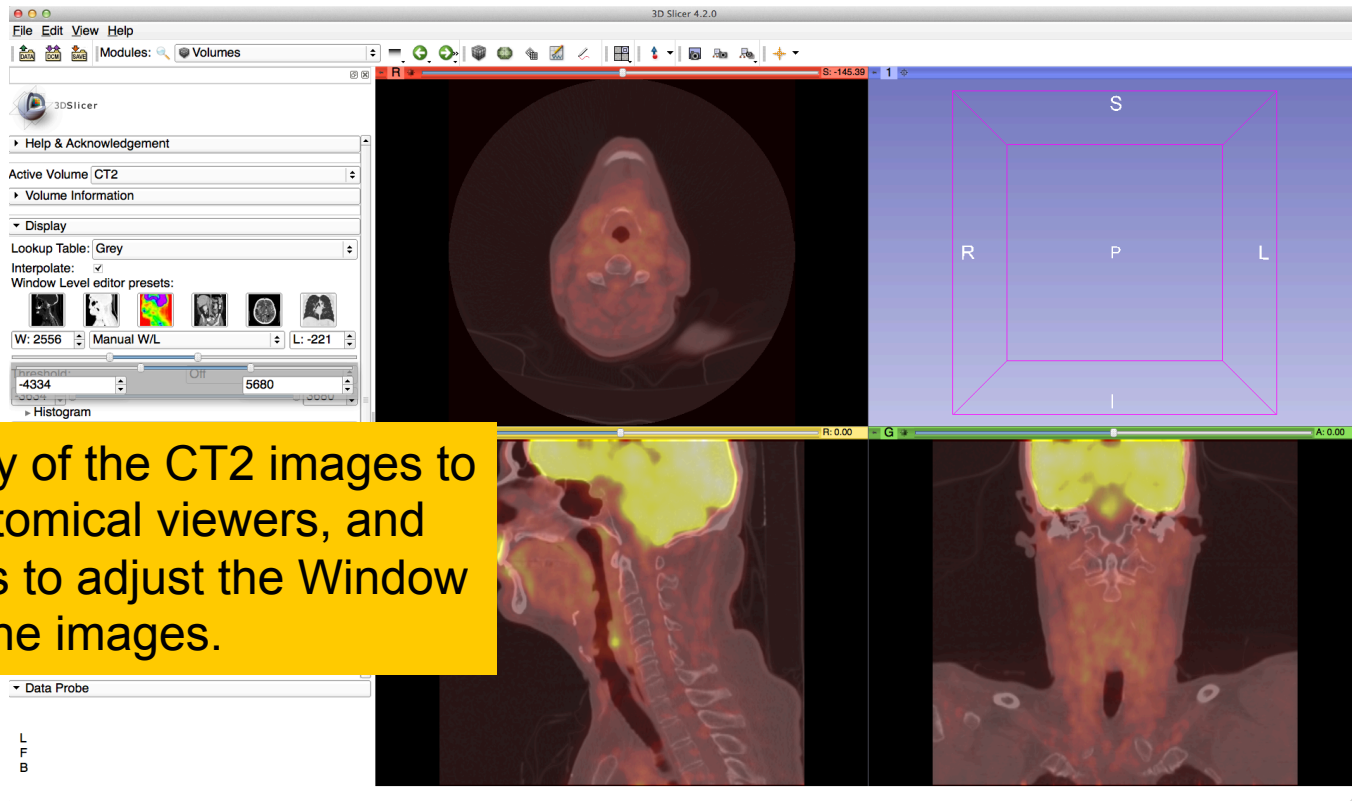


Set the **Active Volume** to **CT2**

Click on the links icon and set the **CT2** volume in **Foreground** in the anatomical viewers.



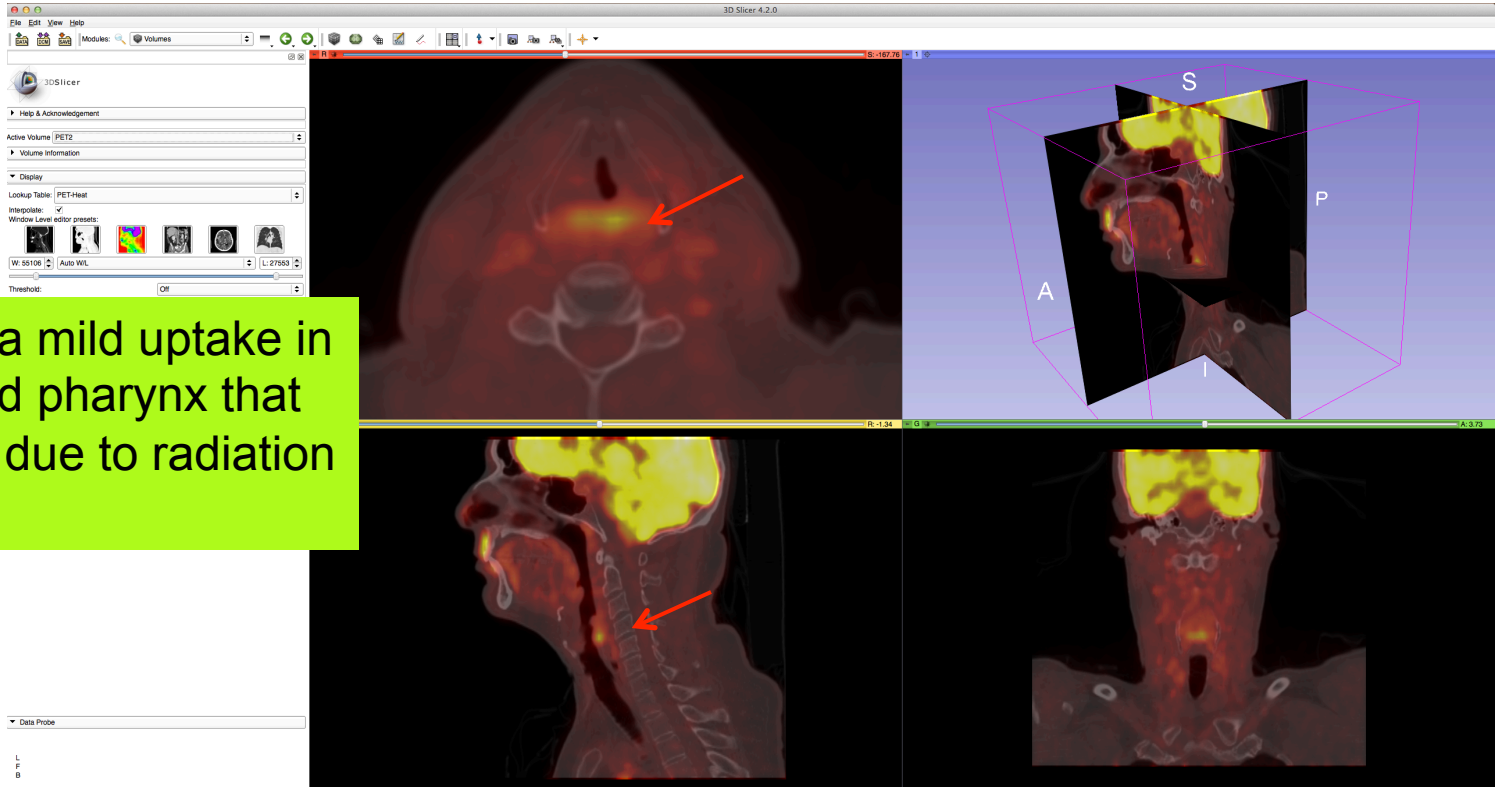
Loading the post-treatment dataset



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.



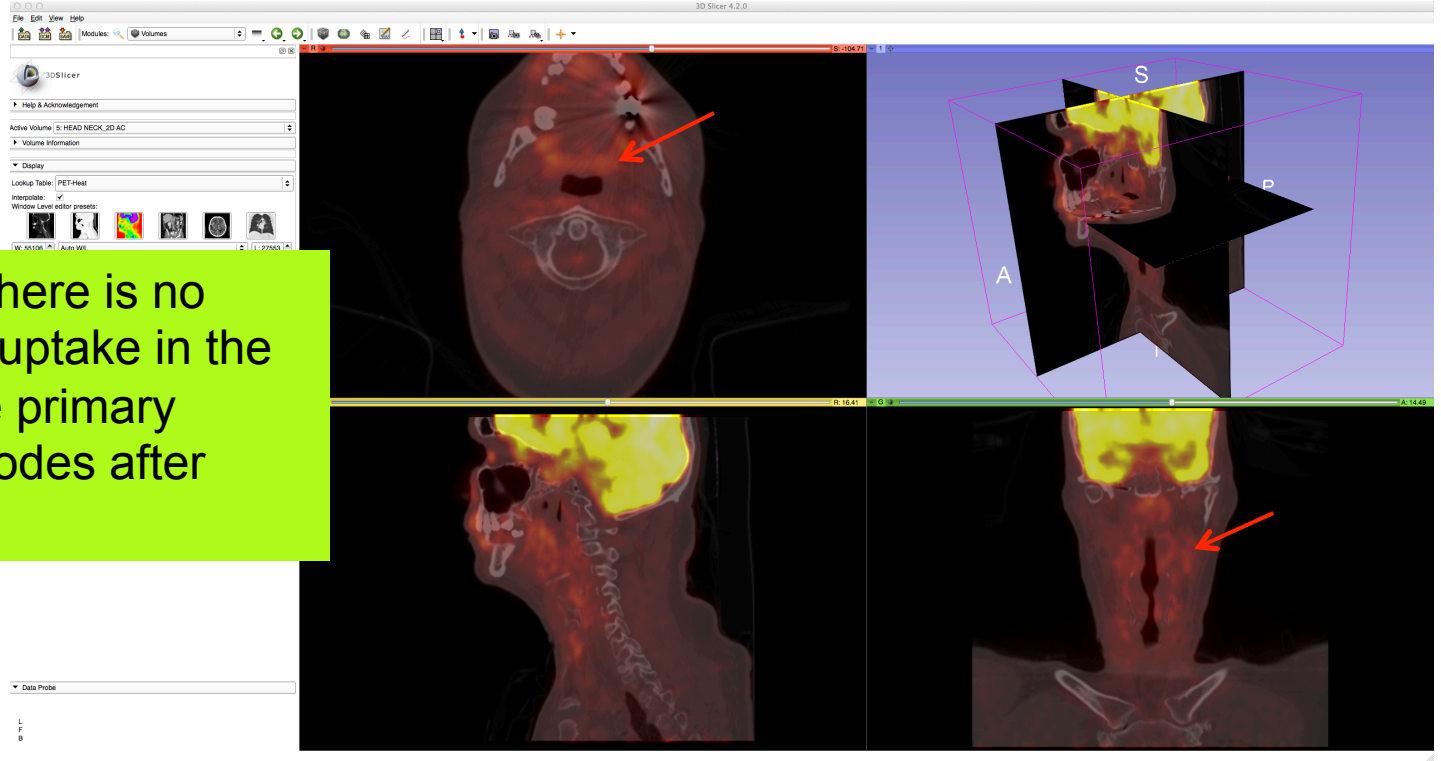
PET uptake findings



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

- 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



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- Marianna Jakab, MS, Brigham & Women's Hospital



3DSlicer at RSNA 2012

Hands-on courses:

- Tues. Nov.27, 12:30 pm -2 pm: 3DVisualization of DICOM images for Radiological Applications. Sonia Pujol, PhD, Kitt Shaffer, MD, PhD, Ron Kikinis, MD (SCD401)
- Wed. Nov. 28, 10:30 am – 12:00 pm: The NIH/NCI Cancer Imaging Archive (TCIA): A Comprehensive Source of DICOM Imaging Data for Research – Hands-on. C. Carl Jaffe MD, John B. Freymann BS, Justin Kirby, Fred William Prior, PhD, Lawrence R. Tarbox PhD



3DSlicer at RSNA 2012

Oral presentations:

- Mon. Nov. 26, 11:40-11:50: Computer-aided Diagnosis of Pure DCIS from DCE-MRI: Quantitative Results in 19 Patients. Jayender Jagadeesan, PhD
- Mon. Nov 26, 02:30-04:00: Open Source Applications for Medical Imaging Research (SCD401). Ricardo Avila, MS Wesley Turner PhD, Julien Finet MSc



3DSlicer at RSNA 2012

Quantitative Imaging Reading Room Exhibit QIRR 3007

- Sun. Nov 26-Fri. Nov 30, 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,



3DSlicer at RSNA

Sunday, November 25	Monday, November 26	Tuesday, November 27	Wednesday, November 28	Thursday, November 29	Friday, November 30
<p>8:00am-11:00am. 3D Slicer Exhibit ↗, Quantitative Imaging Reading Room, Lakeside Learning Center, Hall E, LL-QRR3007</p> <p>-</p> <p>11:00am-12:30pm. RSNA Refresher Course: "Quantitative Medical Imaging for Clinical Research and Practice" Katarzyna Macura, Sonia Pujol, Ron Kikinis ↗. Room S401CD</p> <p>-</p> <p>12:30pm-6:00 pm. 3D Slicer Exhibit ↗ Quantitative Imaging, Lakeside Learning Center, Hall E</p>	<p>8:00am-11:00am. 3D Slicer Exhibit ↗, Quantitative Imaging Reading Room, Lakeside Learning Center, Hall E</p> <p>-</p> <p>12:15pm-1:15pm. Meet-The-Experts Session ↗, Quantitative Imaging Reading Room, Lakeside Learning Center, Hall E</p> <p>-</p> <p>1:15pm-6:00 pm. 3D Slicer Exhibit ↗, Quantitative Imaging, Lakeside Learning Center, Hall E</p>	<p>8:00am-11:00am. 3D Slicer Exhibit ↗, Quantitative Imaging Reading Room, Lakeside Learning Center, Hall E</p> <p>-</p> <p>12:30pm-2:00pm. RSNA Refresher Course: "3D Visualization of DICOM images for Radiology Applications" Sonia Pujol, Kitt Shaffer, Ron Kikinis ↗. Room S401CD</p> <p>-</p> <p>12:30pm-6:00 pm. 3D Slicer Exhibit ↗, Quantitative Imaging, Lakeside Learning Center, Hall E</p>	<p>8:00am-12:15pm. 3D Slicer Exhibit ↗ Quantitative Imaging Reading Room, Lakeside Learning Center, Hall E</p> <p>-</p> <p>12:15pm-1:15pm. Meet-The-Experts Session ↗, Quantitative Imaging Reading Room, Lakeside Learning Center, Hall E</p> <p>-</p> <p>1:15pm-6:00 pm. 3D Slicer Exhibit ↗, Lakeside Learning Center, Hall E</p> <p>-</p>	<p>8:00am-12:15pm. 3D Slicer Exhibit ↗, Quantitative Imaging Reading Room, Lakeside Learning Center, Hall E</p> <p>-</p> <p>12:15pm-1:15pm. Meet-The-Experts Session ↗, Quantitative Imaging Reading Room, Lakeside Learning Center, Hall E</p> <p>-</p> <p>1:15pm-6:00pm. 3D Slicer Exhibit ↗, Quantitative Imaging Reading Room, Lakeside Learning Center, Hall E</p>	<p>8:00am-12:45pm. 3D Slicer Exhibit ↗, Quantitative Imaging Reading Room, Lakeside Learning Center, Hall E</p>

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