



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

a teaching affiliate of
Harvard Medical School

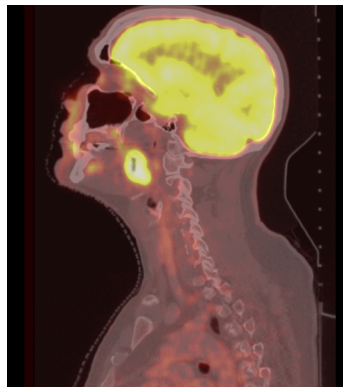
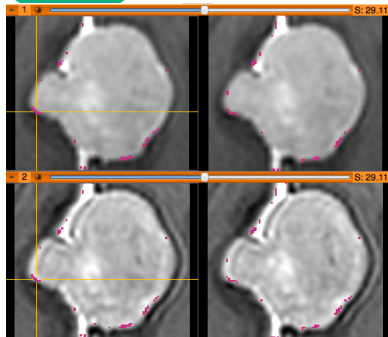
Quantitative Medical Imaging for Clinical Research and Practice

Sonia Pujol, PhD, Katarzyna Macura MD, PhD,
Kitt Shaffer, MD, PhD, Ron Kikinis, MD

Brigham and Women's Hospital, Harvard Medical School,
Johns Hopkins University
Boston University Medical Center



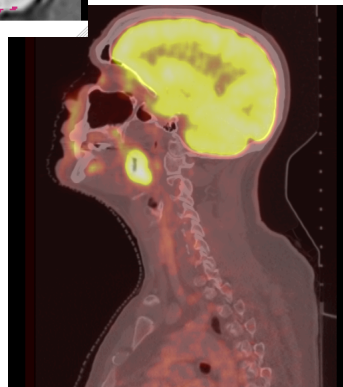
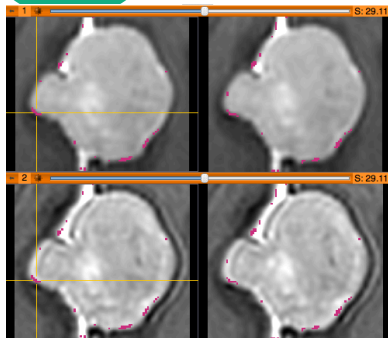
Quantitative Imaging Tutorial



- Quantitative Imaging techniques can be used to give radiologists complementary information for interpreting images
- The hands-on aspect of the course is intended to give clinical researchers a **practical experience on the latest methods developed in medical research**



Quantitative Imaging Tutorial

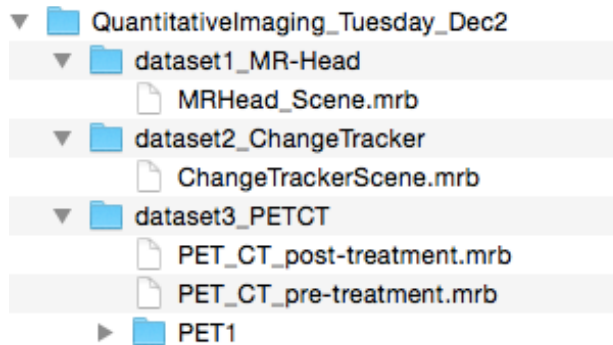


This tutorial is built upon a series of examples of quantitative imaging analysis:

- **Morphology:** volumetric changes in brain and breast tumors
- **Function:** metabolic activity in squamous cell carcinoma



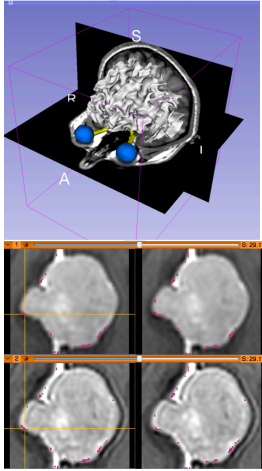
Tutorial Materials



- **Software:** 3D Slicer
- **Datasets:**
QuantitativeImaging_Tuesday_Dec2



Tutorial Overview



Part 1: Introduction to 3D Slicer

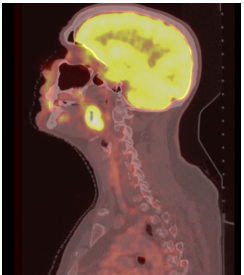
Part 2: Basics of data loading and 3D interactive visualization

Part 3: Measurement of volumetric changes

- large volumetric change: breast tumor case
- small volumetric change: meningioma case

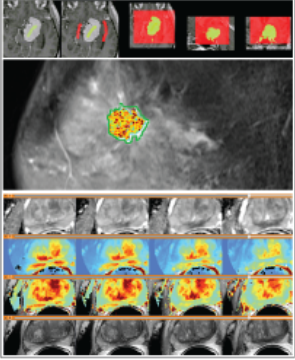
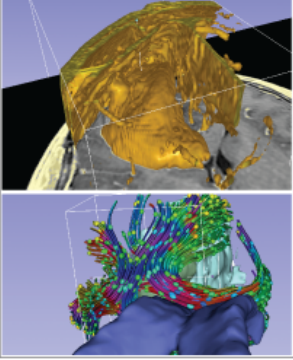
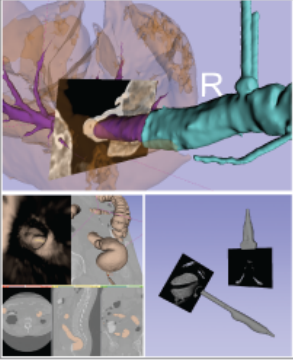

Part 4: Measurement of metabolic activity

- squamous cell carcinoma case





3D Slicer

Powerful processing.	Streamlined interface.	Extensible platform.
		
 3D Slicer <i>version 4</i>	www.slicer.org	

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

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



3DSlicer History

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

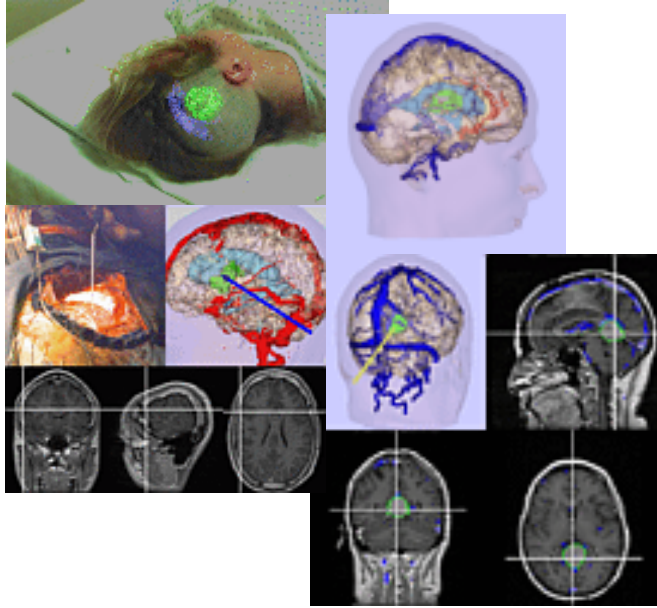
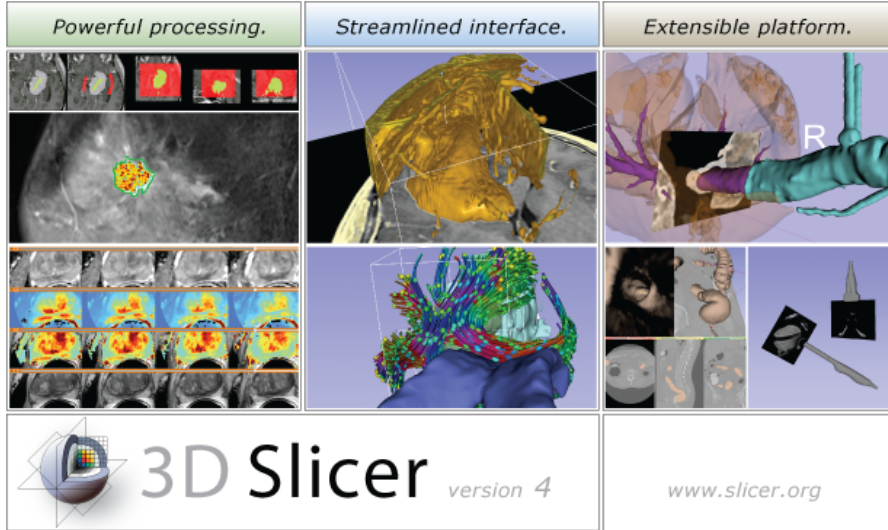


Image Courtesy of the CSAIL, MIT



3DSlicer History



- 1997: Slicer started as a research project between the Surgical Planning Lab (Harvard) and the CSAIL (MIT)
- 2014: 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

NA-MIC Wiki

General

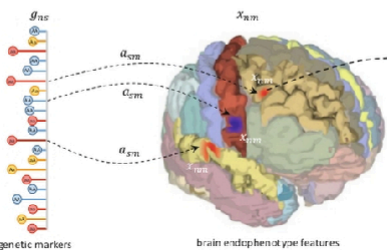
- Overview
- Organization
- Contact Us

Center Components

- Algorithms
- Engineering
- Driving Biological Projects
- Collaboration Grants

Resources

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



1 of 19 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 tools to the medical research community.

NA-MIC is a national research center supported by the NIBIB NIH HHS Roadmap for Medical Research. Information about collaborating with NA-MIC is available at [http://www.na-mic.org](#).

PI: Ron Kikinis, M.D.



Neuroimage Analysis Center

"understanding the human brain through imaging"

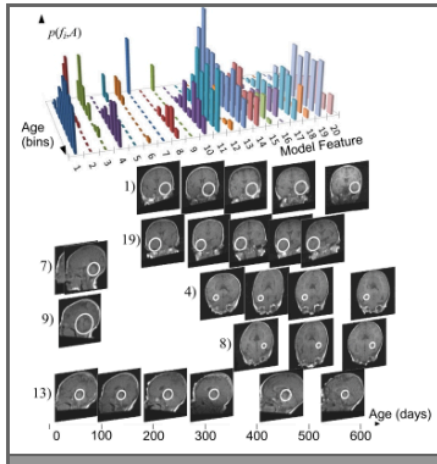
Google Custom Search

About the NAC

- Overview
- Organization
- Research Cores
- Collaborations

Resources

- Our Publications
- Downloads
- Training
- Web Archive
- Contact Us



A Feature-based Developmental Model of the Infant Brain in Structural MRI

Top: distribution $p(A)$ for the 20 most significant age-related features over 10 age categories. Below: visual examples of features (white circles) in subject image slices over age. Pairs (4, 8) and (1, 19) represent symmetric white matter patterns with slightly different onsets. (7) and (9) represent distinct modes cerebellar development and occurring exclusively in early life in the brain stem across the age range, more frequently in early life. (6) of visible white matter under 100 days, e.g. corpus callosum.

The Neuroimage Analysis Center (NAC) develops image processing and analysis techniques for basic and clinical neurosciences. The NAC research approach



National Center for Image Guided Therapy

Google Custom Search

NCIGT Wiki

About Us

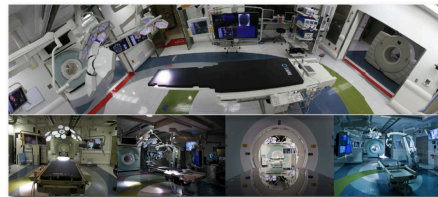
- Research Labs
- Collaborations
- People

Resources

- AMIGO
- Our Publications
- Downloads
- Training & Dissemination
- IGT Workshop Series
- News and Events
- Contact Us

Advanced Multimodality Image Guided Operating (AMIGO) Suite

The Advanced Multimodality Image-Guided Operating (AMIGO) suite is a clinical translational test-bed for research of the National Center for Image-Guided Therapy (NCIGT) at Brigham and Women's Hospital (BWH) and Harvard Medical School. NCIGT and AMIGO are funded under the Biomedical Technology Resource Centers program of the National Institute of Biomedical Imaging and Bioengineering. A unique resource for Image-Guided therapy, AMIGO represents and encourages multidisciplinary cooperation and collaboration among teams of surgeons, interventional radiologists, imaging physicists, computer scientists, biomedical engineers, nurses, and technologists to achieve the common goal of delivering the safest and the most effective state-of-the-art therapy to patients in a technologically advanced and patient-friendly environment. If you are a patient and would like to learn about the offerings of AMIGO, please visit the BWH AMIGO page [here](#).



Launched in 2011, AMIGO is one of the first operating suites in the world with a full array of imaging modalities for use during procedures, enabling less invasive, more effective therapy. Encompassing 5,700 square feet, divided into three separate, yet integrated sterile procedure rooms in which multidisciplinary teams treat patients using multiple imaging modalities. Each room has a separate entrance to the control corridor and support spaces.

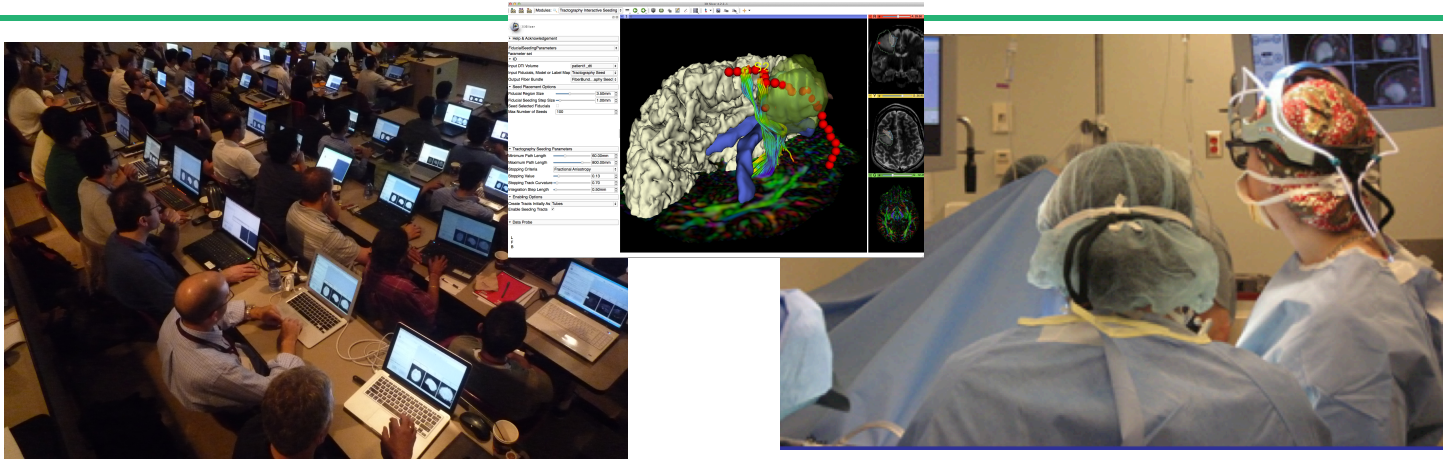
MRI Room

The Magnetic Resonance Imaging (MRI) room of AMIGO induces a high-performance high-field (3 Tesla) wide-room

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



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

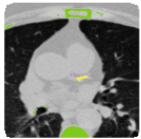


An extensible platform



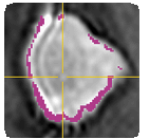
CleverExtension
Jonathan Bronson (SCL ...
★★★★★ (0)

INSTALL



CardiacAgastonMeas...
Jessica Forbes (Ulowa)...
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ChangeTracker
Andrey Fedorov (SPL), ...
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Pietro Nardelli (Univers...
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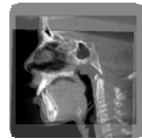
CornerAnnotation
Atsushi Yamada (Shiga...
★★★★★ (0)

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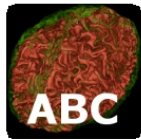
CurveMaker
Junichi Tokuda (BWH)
★★★★★ (0)

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CMFreg
Vinicius Boen (Univ of M...
★★★★★ (0)

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Marcel Prastawa (Unive...
★★★★★ (0)

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CarreraSlice
Ivan Kolesov, Liangjia ...
★★★★★ (0)

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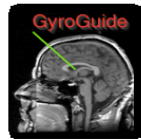
ErodeDilateLabel
Junichi Tokuda (Brigha...
★★★★★ (0)

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DiceComputation
Laurent Chauvin (BWH)
★★★★★ (0)

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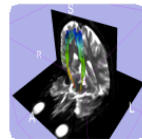
GyroGuide
Ruifeng Chen, Luping F...
★★★★★ (0)

UNINSTALL



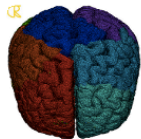
FastGrowCutEffect
Liangjia Zhu, Ivan Kole...
★★★★★ (0)

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Fotis Drakopoulos (CR...
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Csaba Pinter (PerkLab...
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Pengdong Xiao (Depar...
★★★★★ (0)

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LAScarSegmenter
Liangjia Zhu (SBU), Yi G...
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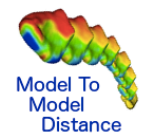
ImageMaker
Julien Finet (Kitware)
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IASem
Bradley Lowekamp
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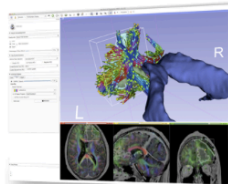
ModelToModelDistan...
Francois Budin (UNC), ...
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INSTALL

- 3D Slicer supports plug-ins called Slicer extensions available from the Extension Manager
- Allows end-users to select extensions useful to them, without having to download the entire extension archive.
- Built Nightly with Slicer



3D Slicer in practice



- Slicer works on Windows, Linux, and Mac
- Slicer is distributed under a BSD-style license agreement with no restriction on use

Get Slicer 4.

Slicer 4 is the latest version of 3D Slicer, a free, comprehensive software platform for medical image analysis and visualization developed with NIH support. 3D Slicer is distributed under a permissive BSD-style open source license. It has a thriving user and developer community.

Pre-compiled binaries

		Windows	Mac OS X	Linux
stable release	64 bit	4.4.0 64 bit installer 2014-11-02 r23774 (164.2MB)	4.4.0 64 bit installer 2014-11-02 r23774 (244.0MB)	4.4.0 64 bit archive 2014-11-02 r23774 (244.3MB)
	32 bit	4.3.0 32 bit installer 2013-09-06 r22408 (157.2MB)		
nightly build	64 bit	nightly 64 bit installer 2014-11-14 r23783 (164.2MB)	nightly 64 bit installer 2014-11-14 r23783 (244.0MB)	nightly 64 bit archive 2014-11-14 r23783 (244.3MB)
	32 bit	nightly 32 bit installer 2013-11-24 r22717 (159.0MB)		

Warning: Mac OS X 10.9 users should be sure to upgrade to 10.9.4 or higher, and install the latest version of XQuartz. Failure to do so can cause Slicer to hang at startup time and consume large amounts of CPU time in an unkillable process. A manual installation or re-installation of the 10.9.4 upgrade may also be required to correct this problem.

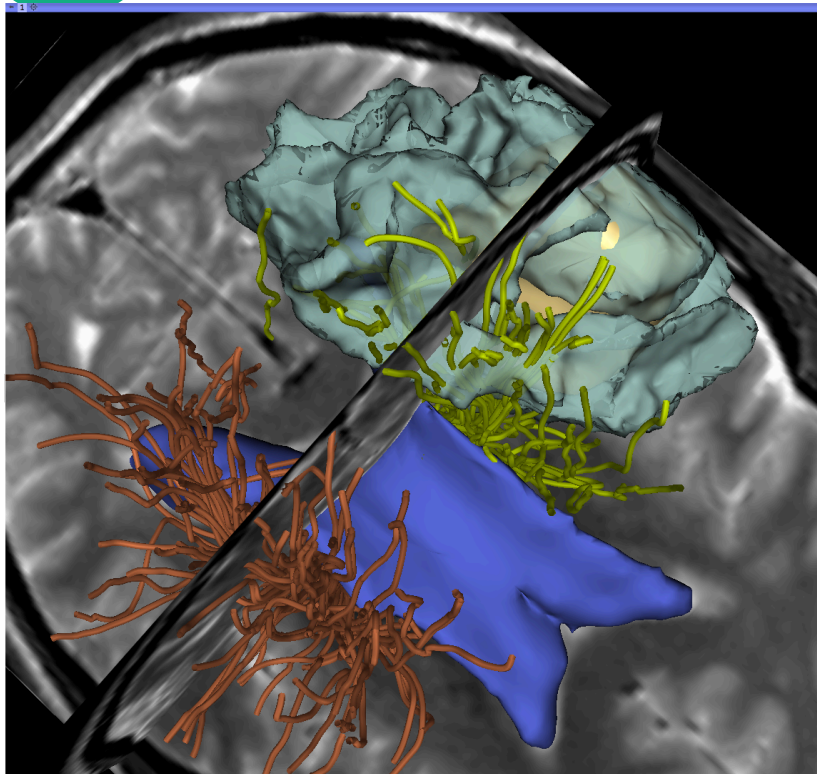
System requirements

Slicer requires significant computer resources to run due to the large size of typical medical image data. A 64 bit processor, adequate RAM and a fast graphics card or GPU that supports OpenGL is practical requirements to use Slicer effectively.

Slicer is built and tested on many hardware and software platforms. 3D Slicer runs on modern Windows, Mac OS X (10.6 and up), and a variety of Linux distributions.



3D Slicer in practice



- Slicer works on Windows, Linux, and Mac
- Slicer is distributed under a BSD-style license agreement with no restriction on use
- 3D Slicer is for clinical research use only, and is not FDA approved or CE-marked.



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	
factory-mac-64bits.kitware	SnowLeopard-g++4.2.1-64bits-QT4.7-PythonQt-With-Tcl-CLI-Release	1	0	0	0	0	14	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	
factory-win7.kitware	Windows7-VS2008-64bits-QT4.7.1-PythonQt-With-Tcl-CLI-Release	0	0	0	0	0	1000	0	
factory-win7.kitware	Windows7-VS2008-32bits-QT4.7.1-PythonQt-With-Tcl-CLI-Release	1	0	0	0	0	1000	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

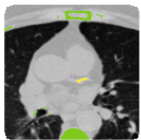


An extensible platform



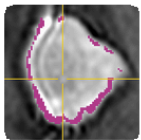
CleverExtension
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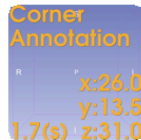
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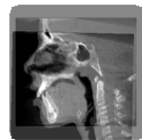
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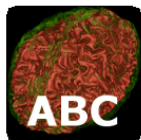
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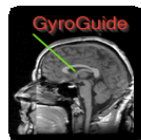
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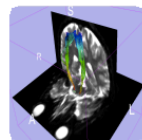
GyroGuide
Ruifeng Chen, Luping F...
★★★★★ (0)

UNINSTALL



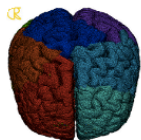
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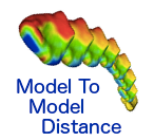
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- Built Nightly with Slicer



Training Portfolio

- Modular multi-level training for expert and non-expert community
- Tutorials and anonymized datasets for end-users and developers
- Cross platform testing for quality control

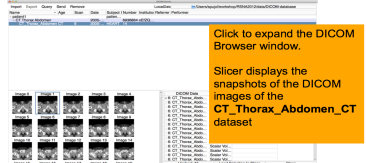
SPL Loading a DICOM volume

SLICER WELCOME TUTORIAL

- The SlicerWelcome tutorial is an introduction to Slicer based on the Web
- Author: Sonia Pujol, Ph.D.
- Audience: First time users who want a general introduction to the software
- Based on: 3D Slicer version 4.0

SLICER4MINUTE TUTORIAL

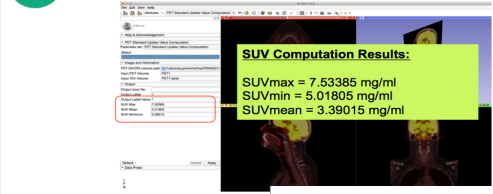
- The Slicer4Minute tutorial is a brief introduction to the advanced 3D view
- Author: Sonia Pujol, Ph.D.
- Audience: First time users who want to discover Slicer in 4 minutes.



Click to expand the DICOM Browser window.

Slicer displays the snapshots of the DICOM images of the CT_Thorax_Abdomen_CT dataset

SPL PET SUV Computation



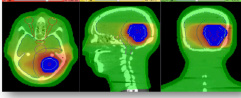

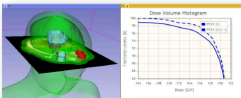
SUV Computation Results:

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

©2011 Surgical Planning Laboratory, ARR

Learning Objective

This tutorial demonstrates how to perform a radiation therapy research workflow using the SlicerRT extension:



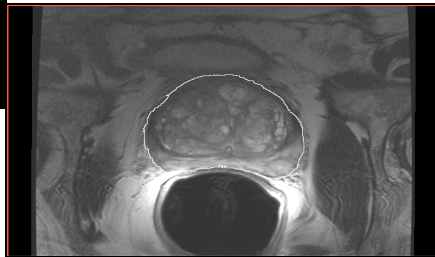
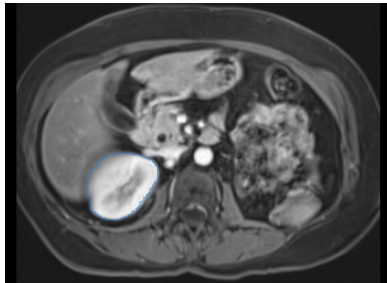
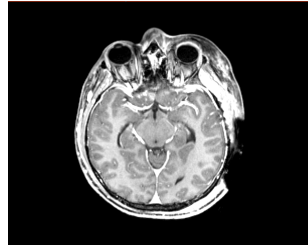
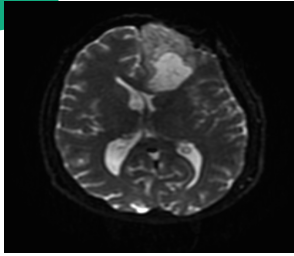
Evaluation of the isocenter shifting adaptation method

National Alliance for Medical Image Computing
<http://www.na-mic.org>

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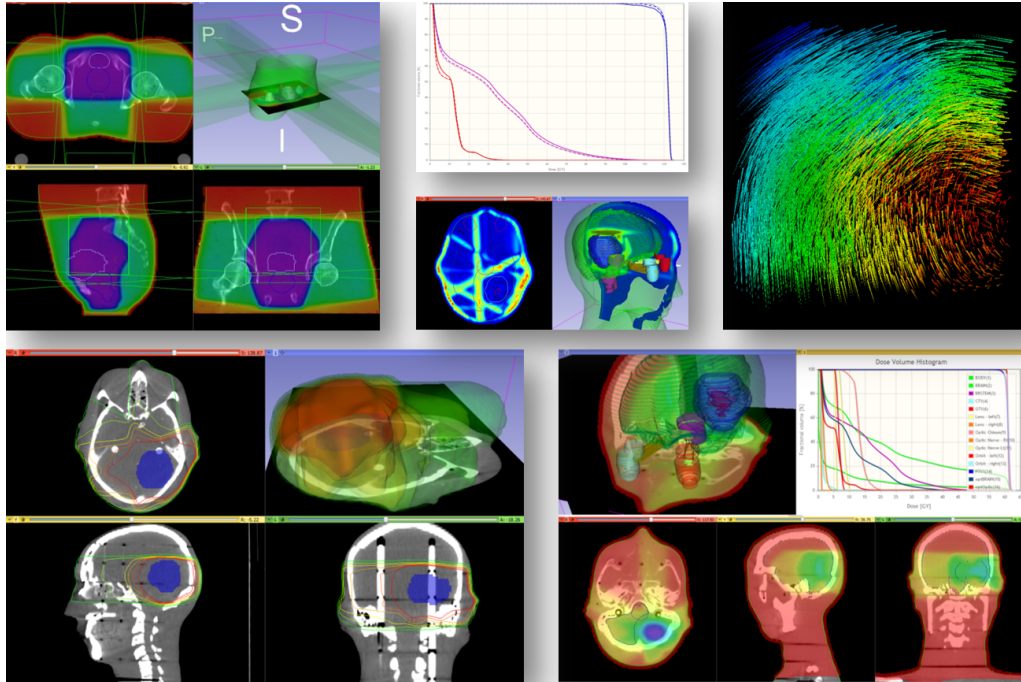
Slicer clinical applications



- Applied science oriented toward **patient-specific analysis** in the presence of pathology
- Driving Biological Projects leading to the development of new tools



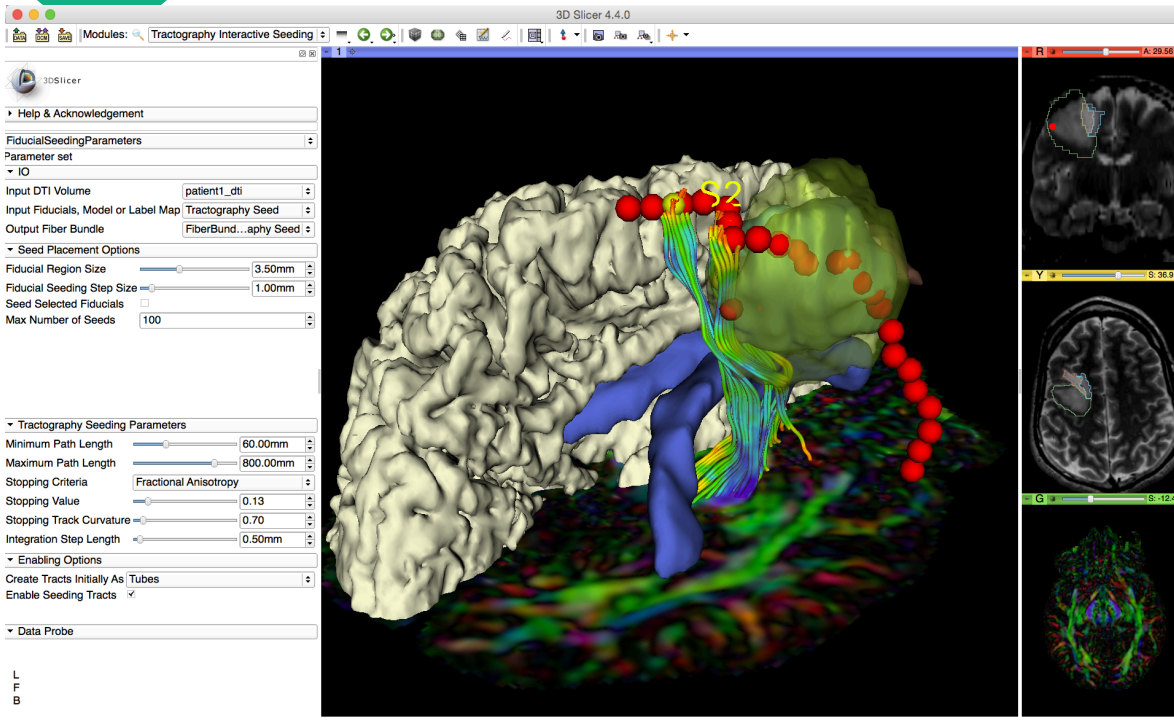
Examples of clinical applications



- Radiotherapy: RT-specific analysis dose accumulation and dose comparison (G.Fichtinger et al. Queen's University, Canada)



Examples of clinical applications



- Diffusion Tensor Imaging tractography for neurosurgical planning



Slicer Training events

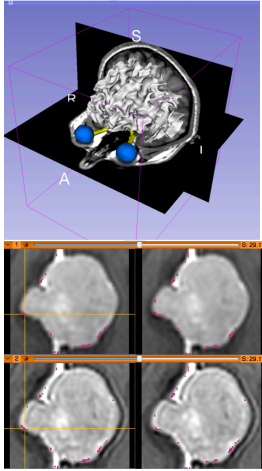
Major international conferences

- **RSNA** 2008, 2009, 2010, 2011, 2012, 2013, 2014
- **MICCAI** 2008, 2009, 2011, 2012, 2013, 2014
- **SfN** 2009, 2011
- **SPIE** 2012, 2013
- **CAOS** 2010
- **CARS** 2010, 2012, 2013





Tutorial Overview



Part 1: Introduction to 3D Slicer

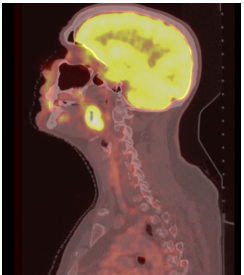
Part 2: Basics of data loading and 3D interactive visualization

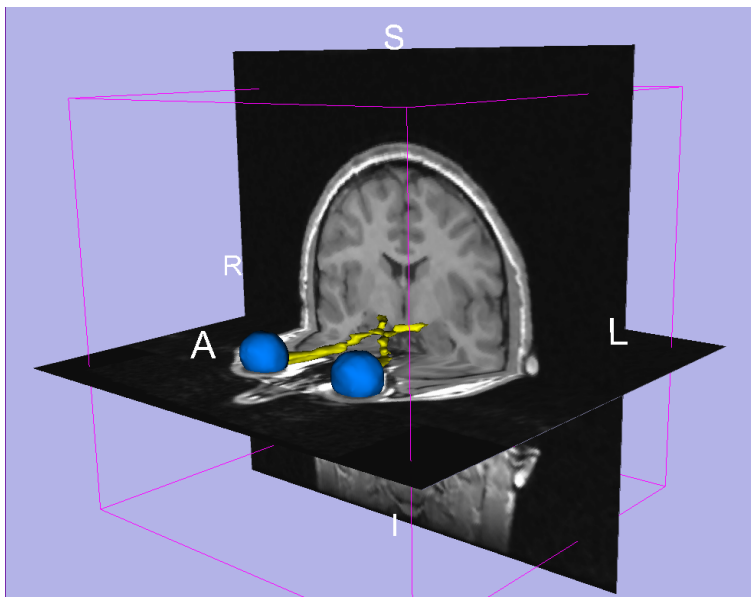
Part 3: Measurement of volumetric changes

- large volumetric change: breast tumor case
- small volumetric change: meningioma case

Part 4: Measurement of metabolic activity

- squamous cell carcinoma case

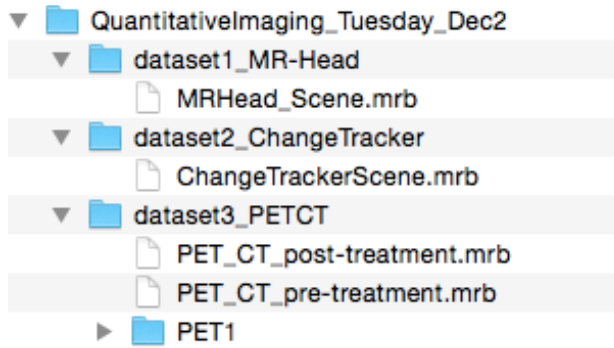




Part II: Basics of Data Loading and 3D Visualization



Course Datasets



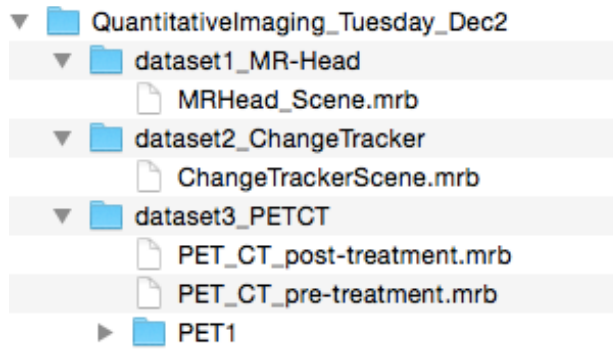
The **QuantitativeImaging_Tuesday_Dec2** directory contains three datasets located in the sub-directories:

- dataset1_MR_Head
- dataset2_ChangeTracker
- dataset3_PETCT

Each dataset is in **.mrb file format.**



Slicer mrb file format

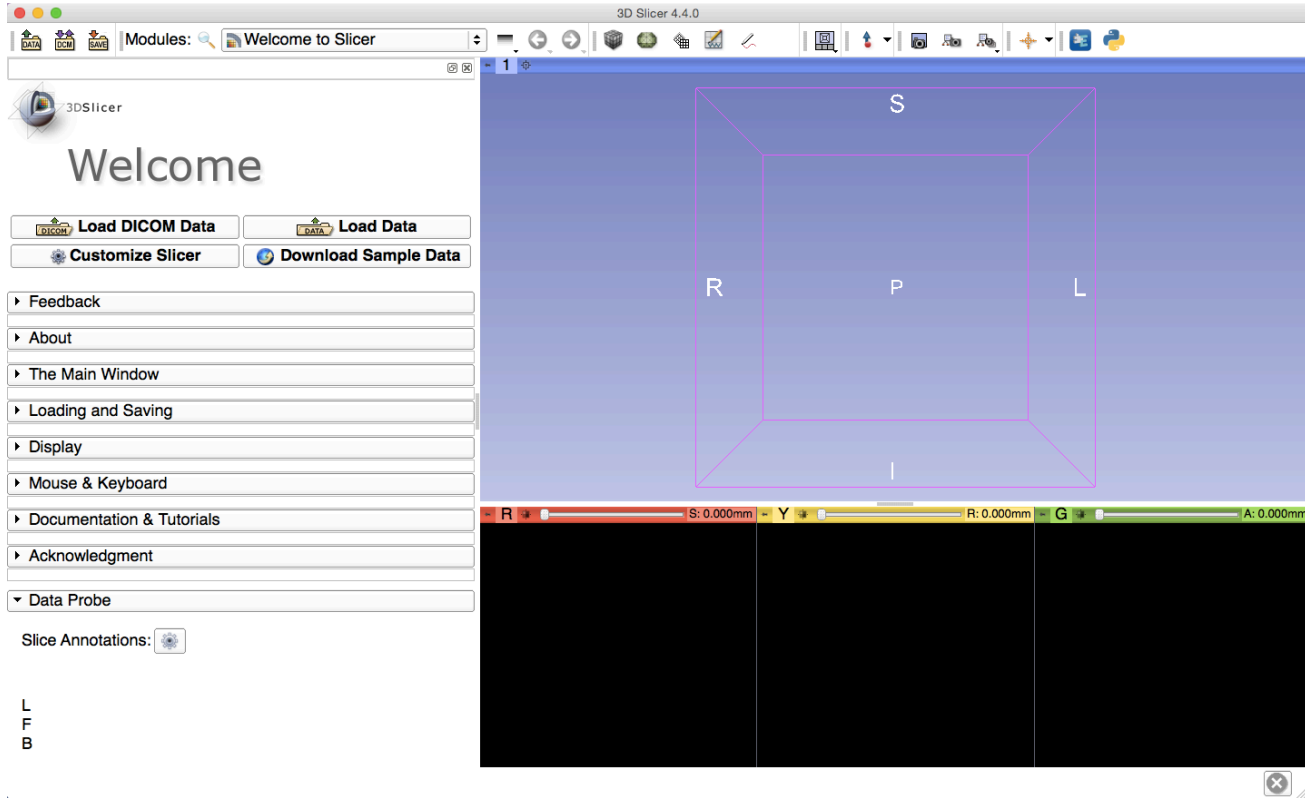


A Slicer mrb file is an archive file that contains all data for loading into Slicer4.

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



Welcome to Slicer4.4

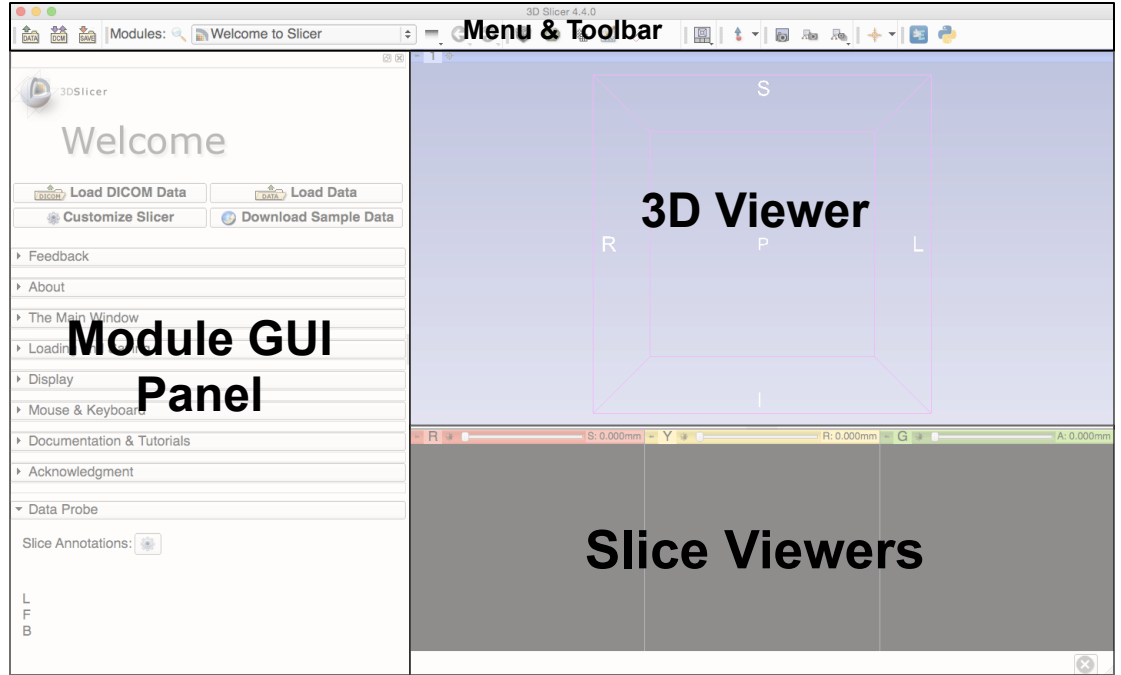




Slicer4 Minute Tutorial: Navigating the Application GUI

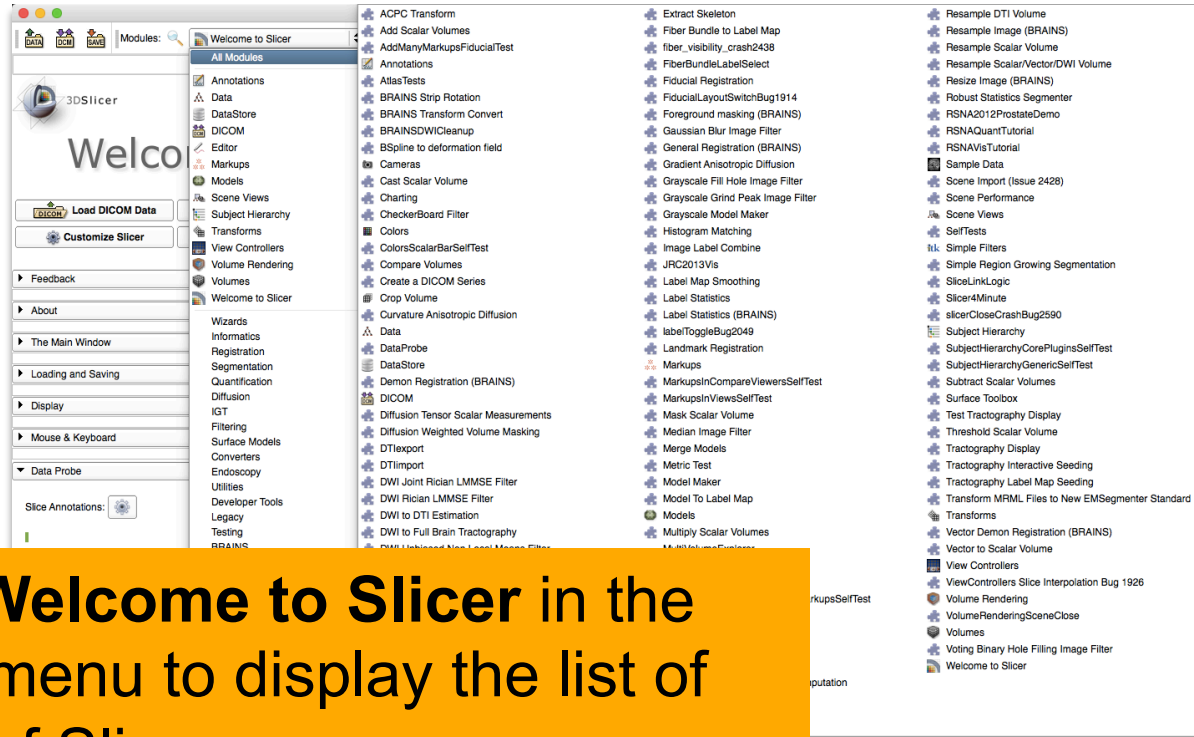
The Graphic User Interface (GUI) of Slicer4 integrates **four components**:

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





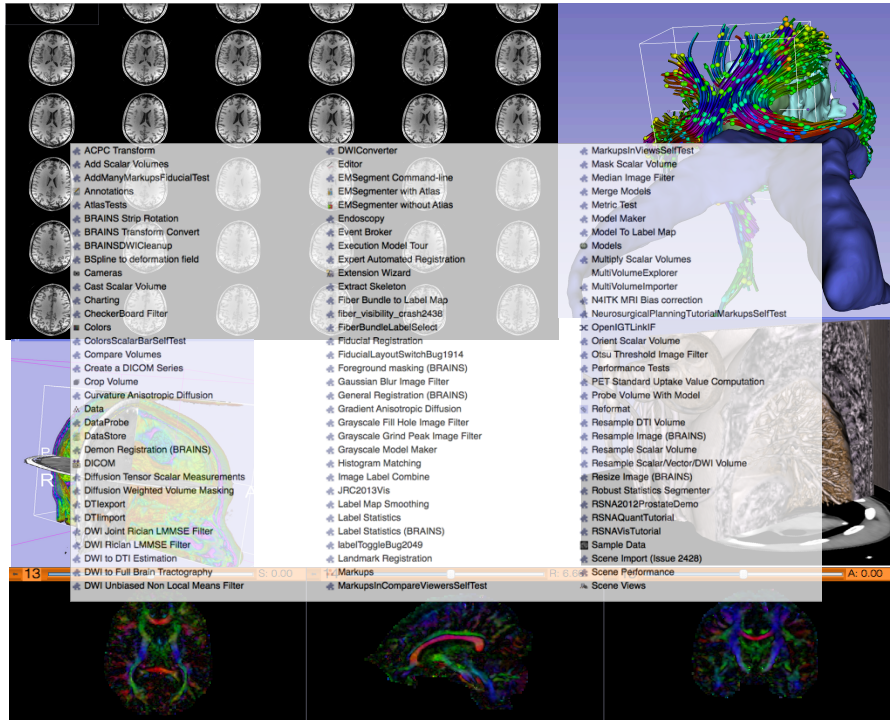
Welcome to Slicer4.4



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



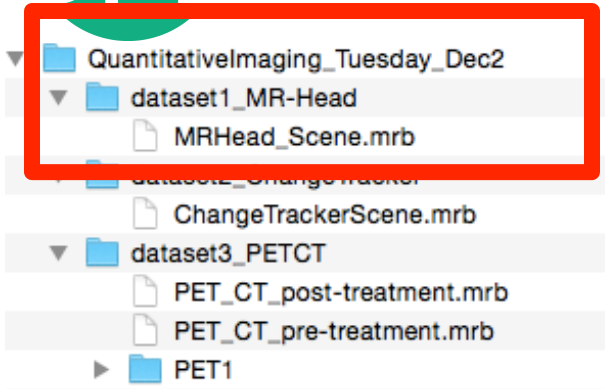
Welcome to Slicer4.4



Slicer4.4.0 contains more than 100 modules for image segmentation, registration and 3D visualization of medical imaging data



3D Data Loading and Visualization

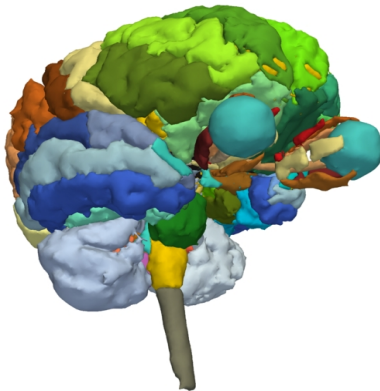


- Open the directory **QuantitativeImaging_Tuesday_Dec2** on the Desktop
- Select the directory **dataset1_MR-Head**
- Select the file **MRHead_Scene.mrb**

This file is composed of an MR scan of the brain and 3D surface reconstructions of anatomical structures, from

The data are part of the SPL-PNL Brain Atlas developed by Talos, Jakob, Kikinis et al. The atlas is freely available for download at:

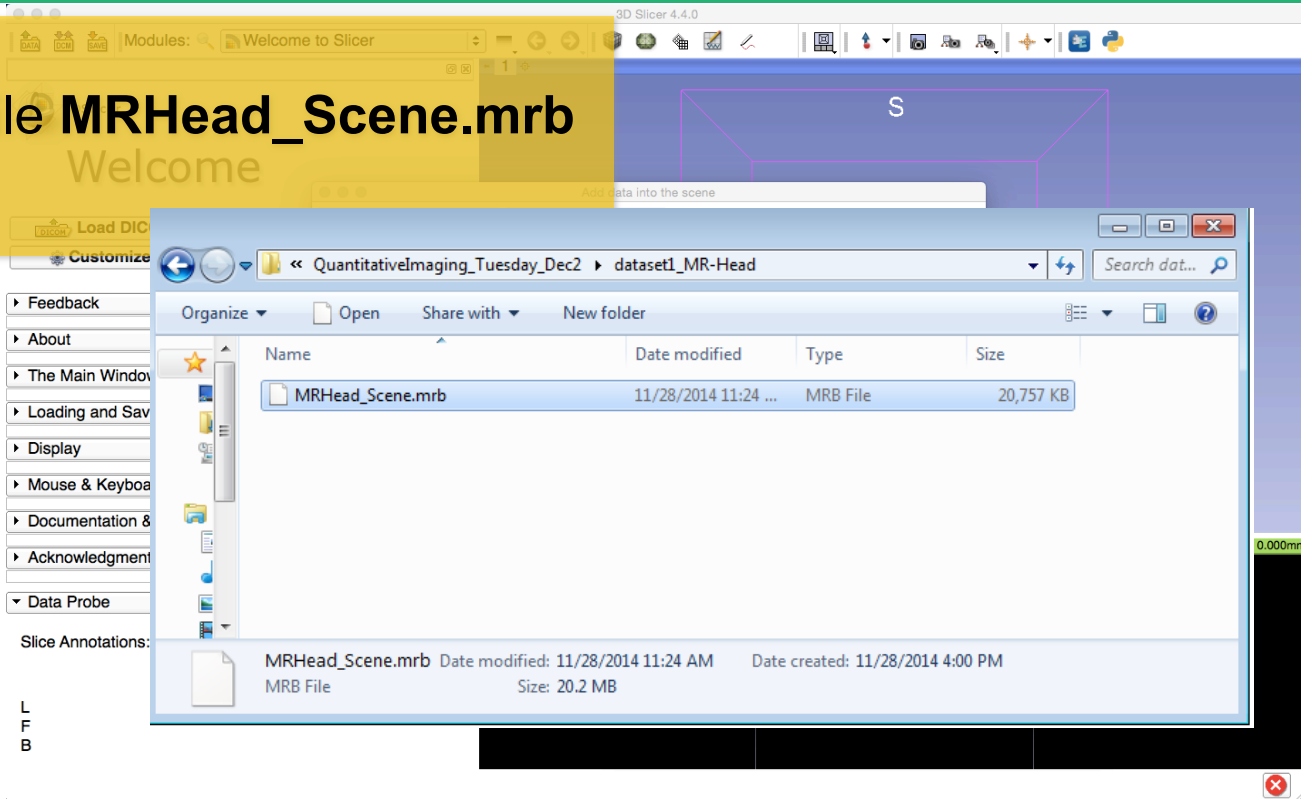
<http://www.spl.harvard.edu/publications/item/view/2037>





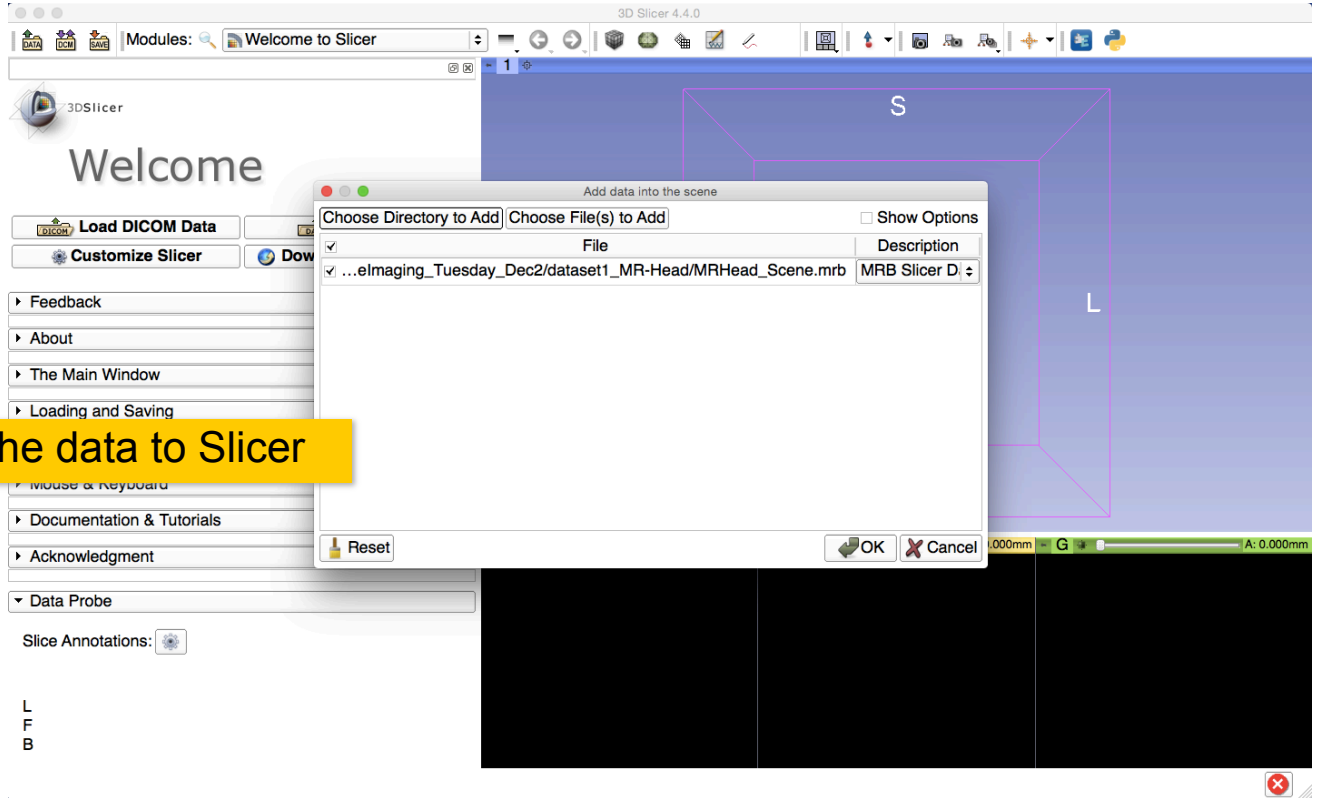
Slicer4 Minute Tutorial: Load a Scene

Drag and drop the file **MRHead_Scene.mrb**





Slicer4 Minute Tutorial: Load a Scene

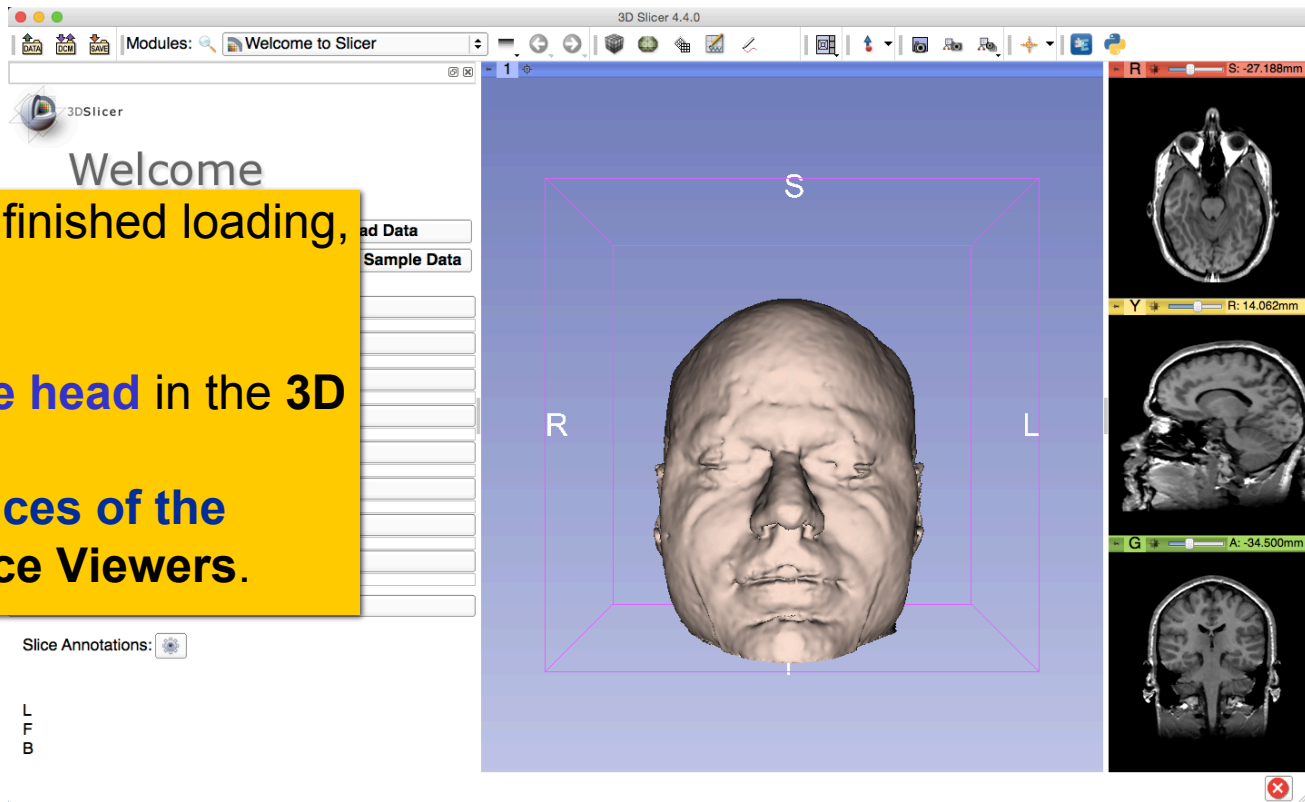




Slicer4 Minute Tutorial: Viewing the Scene

When the scene is finished loading, Slicer displays:

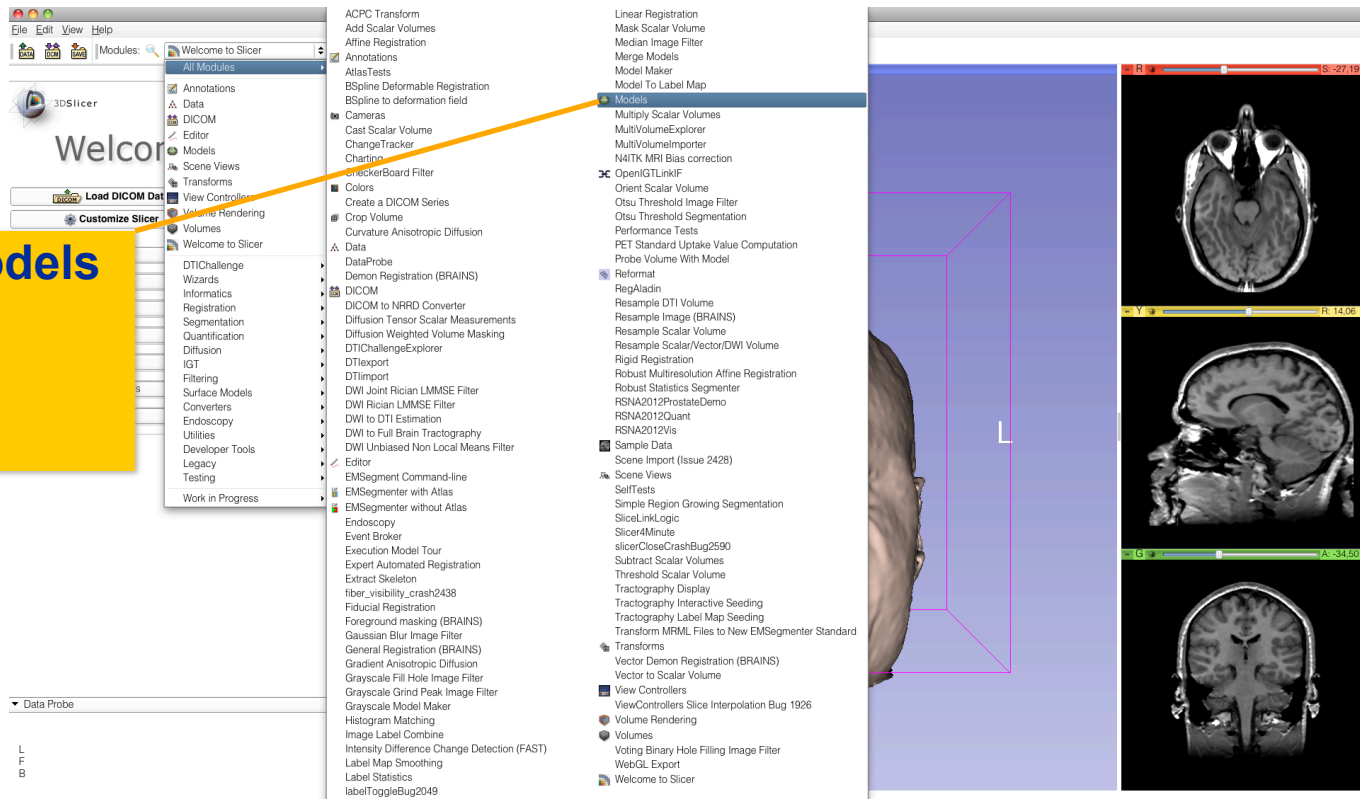
- a **3D model of the head** in the **3D Viewer**, and
- anatomical **MR slices of the brain** in the **2D Slice Viewers**.





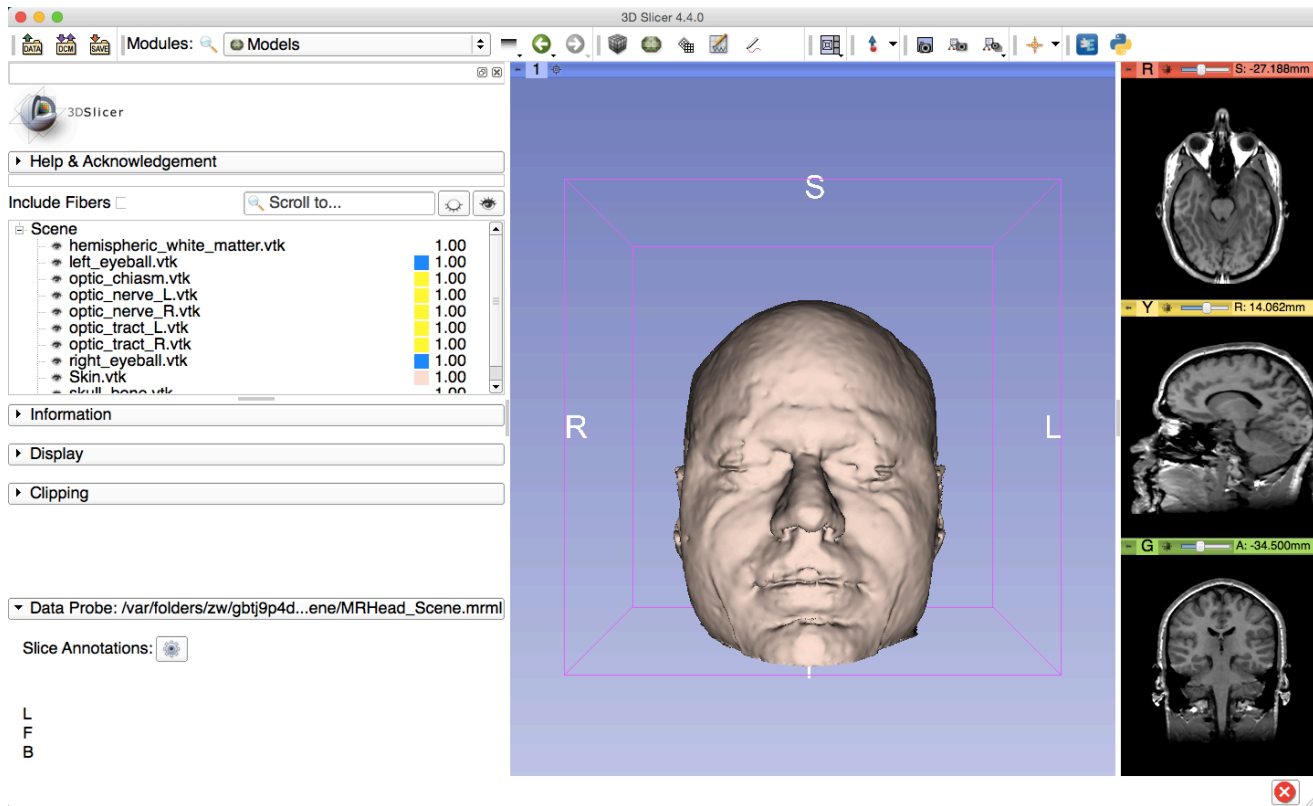
Slicer4 Minute Tutorial: Exploring Slicer's functionality

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





Slicer4 Minute Tutorial: Switching to the Models Module

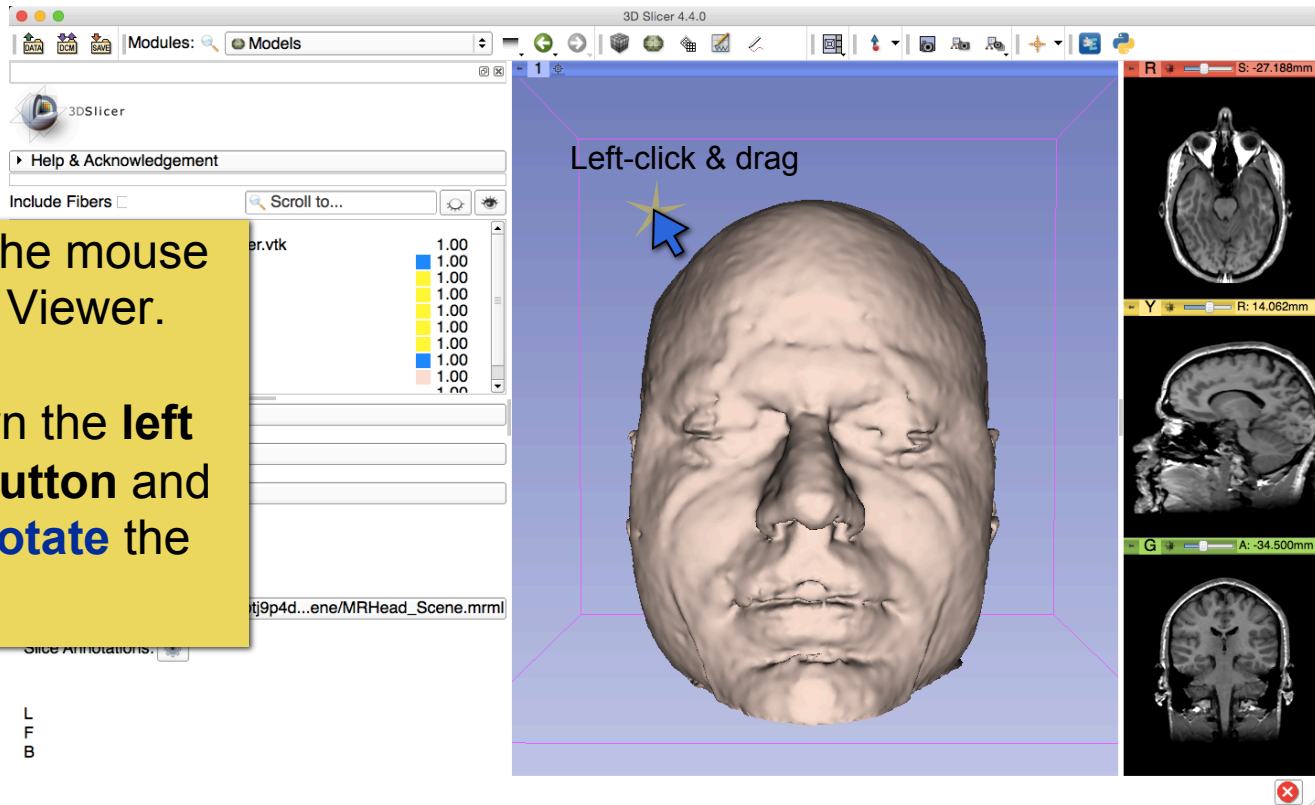




Slicer4 Minute Tutorial: Basic 3D Interaction


Position the mouse in the 3D Viewer.

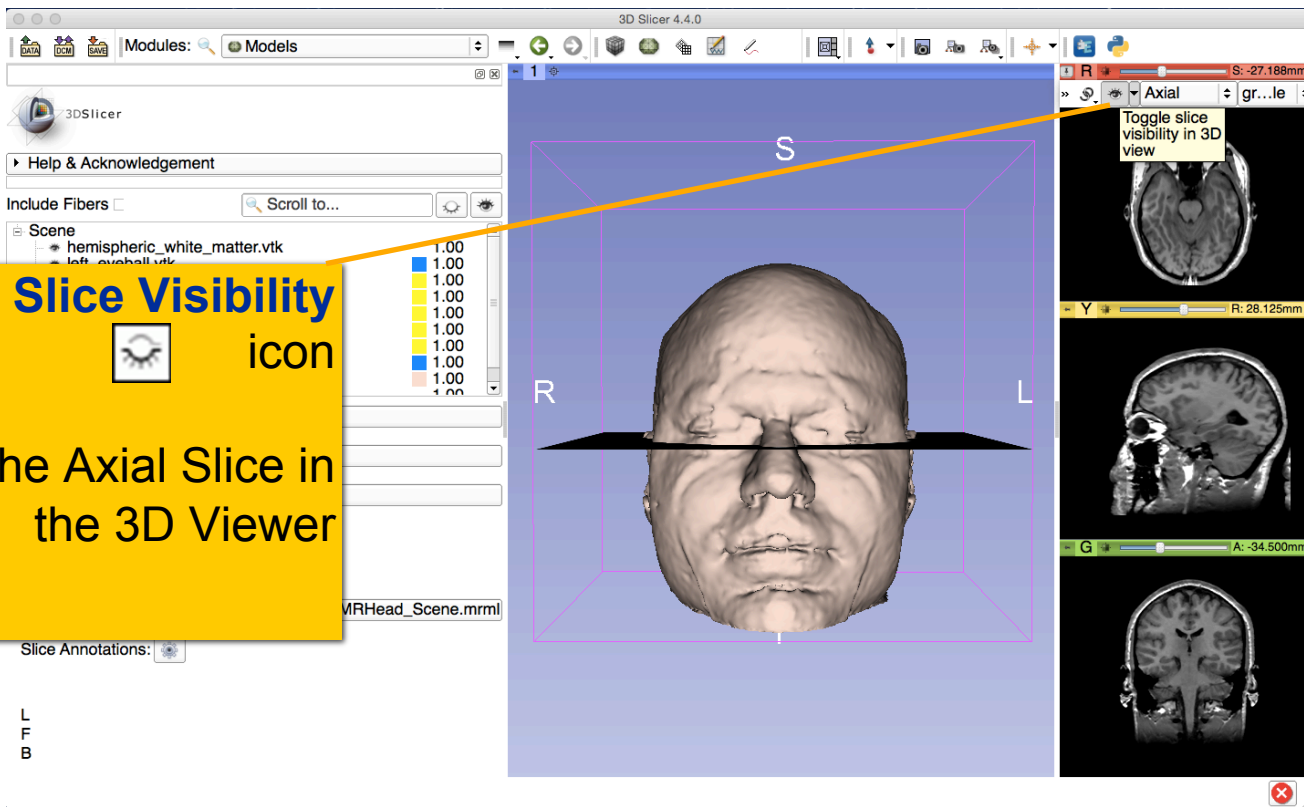
Hold down the **left mouse button** and **drag to rotate** the model.





Slicer4 Minute Tutorial: Viewing Slices in the 3D Viewer

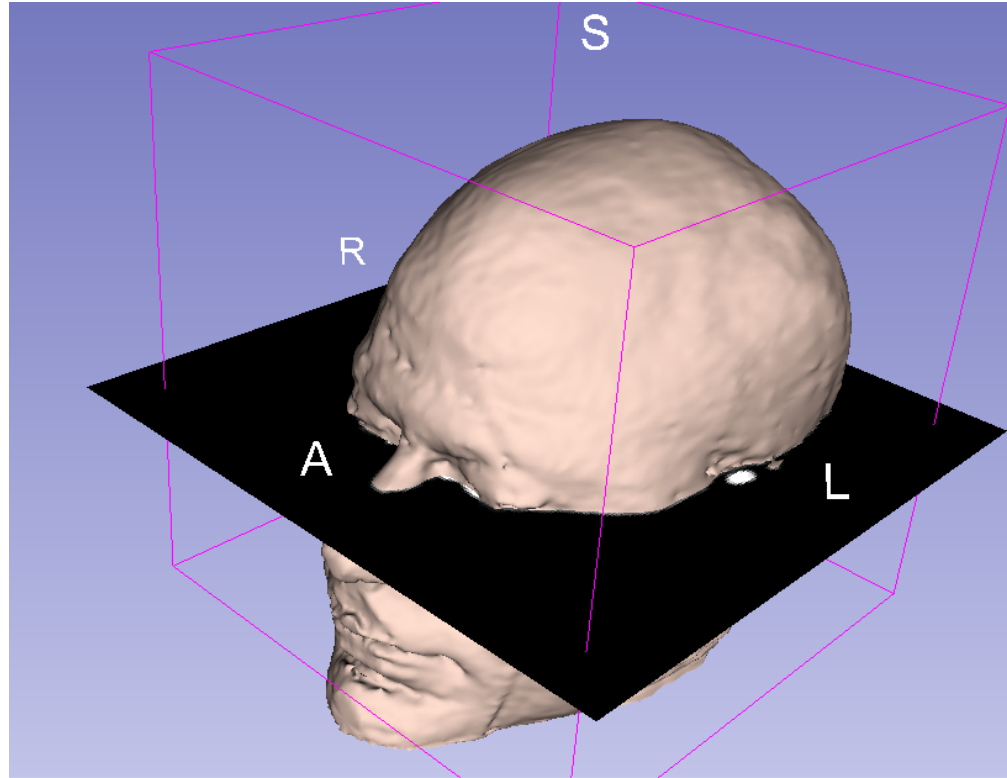
Click on the **Slice Visibility** icon
 icon
to display the Axial Slice in the 3D Viewer





Slicer4 Minute Tutorial: 3D Visualization

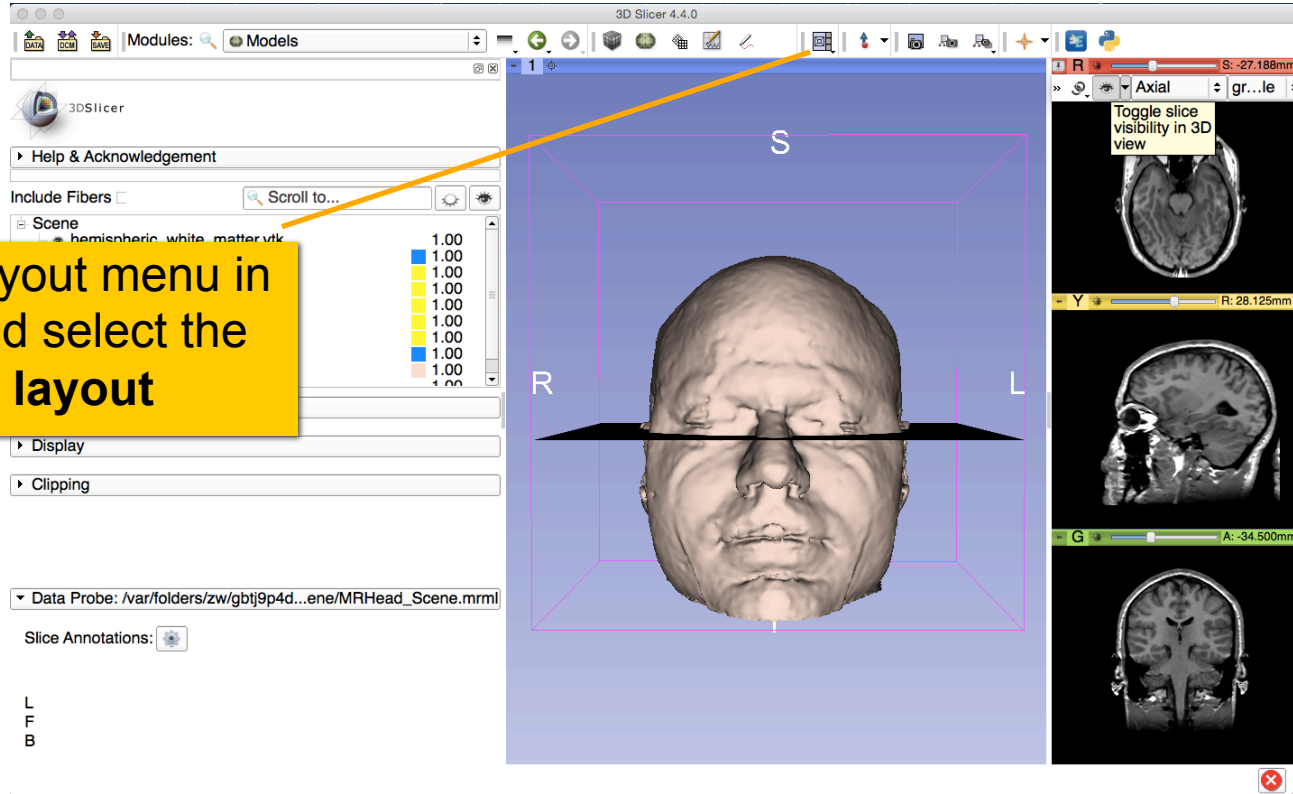
Slicer adds a view of the **Axial slice** in the 3D View.





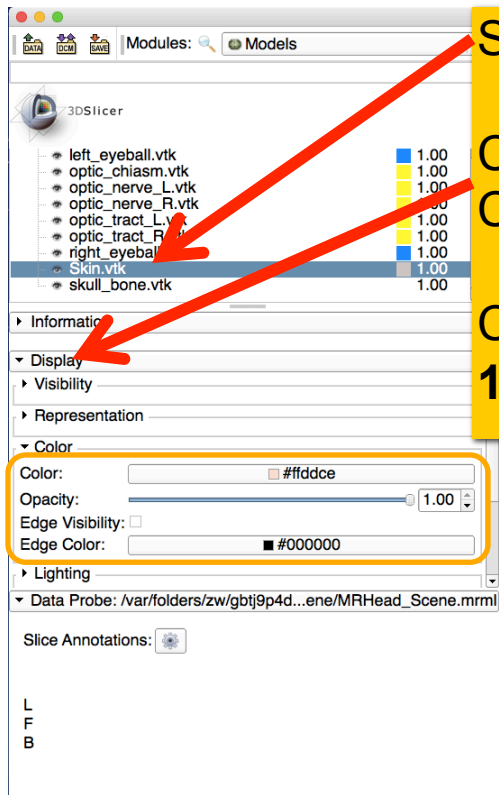
Slicer4 Minute Tutorial: Viewing Slices in the 3D Viewer

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





Slicer4 Minute Tutorial: 3D Visualization

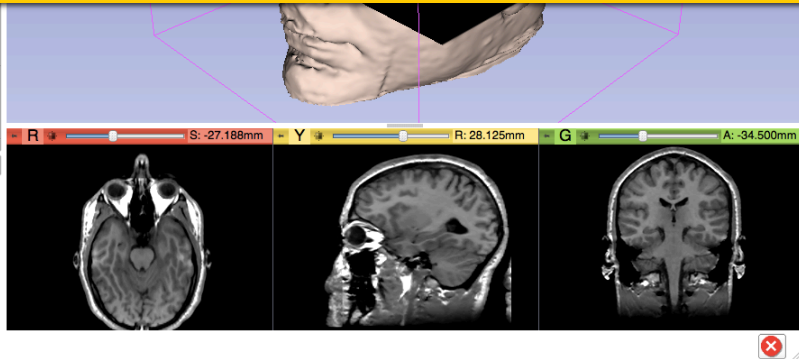


Select the model **Skin.vtk**

Click to expand the tab **Display**

Click to expand the tab **Color**

Change the opacity of the model from **1.0** to **0.0**.

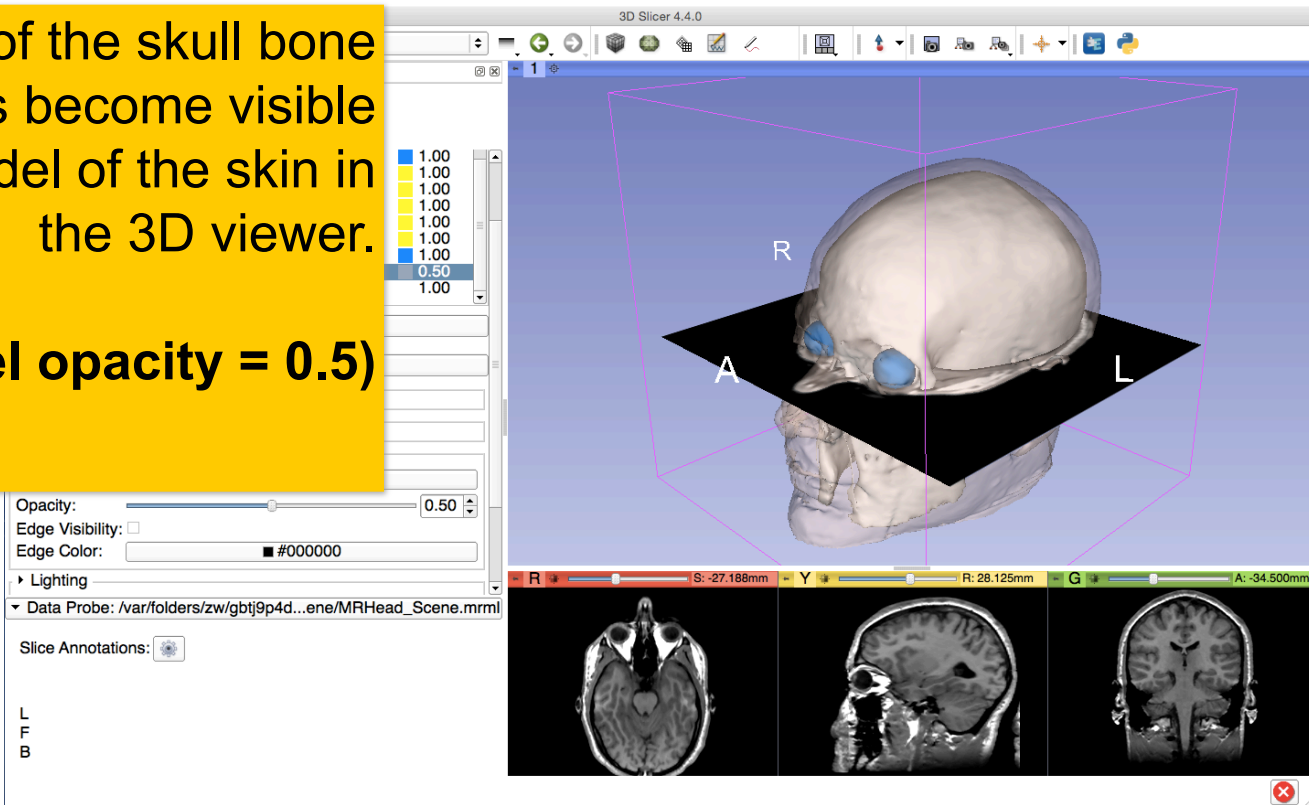




Slicer4 Minute Tutorial: 3D Visualization

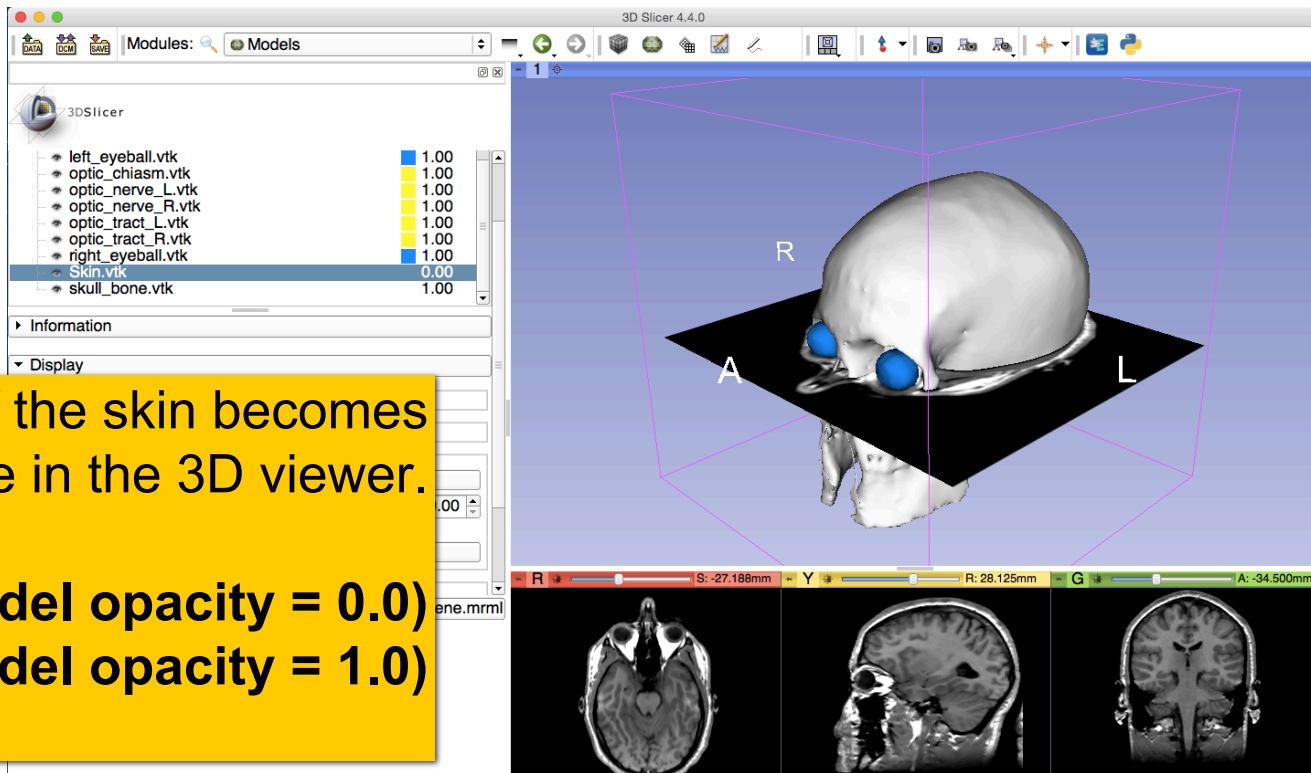
The model of the skull bone and eyeballs become visible through the model of the skin in the 3D viewer.

(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.



Representation

Color

Color: #ffddce

Opacity: 0.00

Edge Visibility:

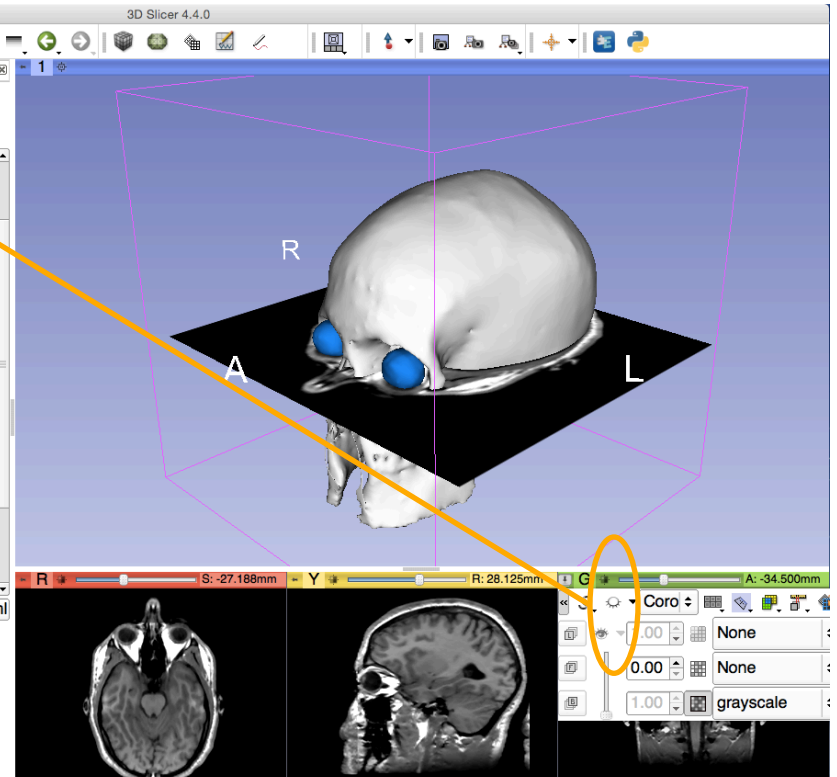
Edge Color: #000000

Lighting

Data Probe: /var/folders/zw/gbtj9p4d...ene/MRHead_Scene.mrml

Slice Annotations:

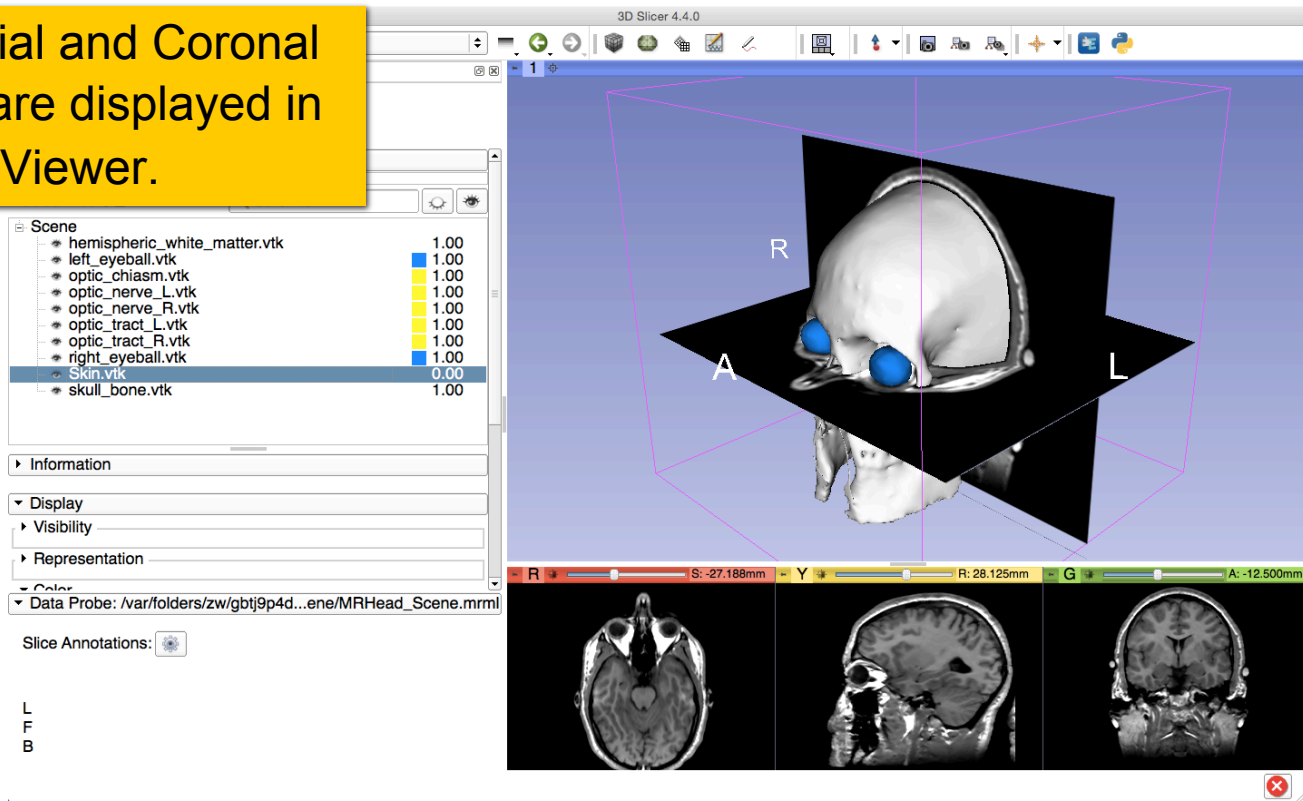
L
F
B





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.

Click to expand the tab **Visibility** in the Display panel

Turn on the **Clip** option

The screenshot shows the 3D Slicer 4.4.0 interface. The Model Hierarchy panel on the left lists several models, with **skull_bone.vtk** selected and highlighted by a red arrow. The Display panel below it shows the Visibility section expanded, with the **Clip** checkbox checked, also indicated by a red arrow. The main 3D view on the right shows a 3D reconstruction of a skull. At the bottom, three axial MRI slices are displayed.



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**.

The screenshot shows the 3D Slicer 4.4.0 interface. On the left, the 'Data Probe' panel lists the following data sets with their visibility and opacity settings:

Data Set	Visibility	Opacity
optic_chiasm.vtk	Visible	1.00
optic_nerve_L.vtk	Visible	1.00
optic_nerve_R.vtk	Visible	1.00
optic_tract_L.vtk	Visible	1.00
optic_tract_R.vtk	Visible	1.00
right_eyeball.vtk	Visible	1.00
Skin.vtk	Visible	0.00
skull_bone.vtk	Visible	1.00

Below the list, the 'Display' section is expanded to show 'Visibility' settings:

- Visible:
- View: All
- Clip:
- Slice Intersections Visible:
- Slice Intersections Thickness: 1 px

The main 3D view shows a brain model with a coronal slice. The slice is labeled with 'A' (Anterior), 'P' (Posterior), and 'I' (Inferior). The slice is currently set to 'Coronal' (G). The slice position is indicated by the 'S' slider at -27.188mm. The 'R' (Right) and 'L' (Left) sliders are at 28.125mm and -29.500mm, respectively. The 'Data Probe' at the bottom shows the current scene: /var/folders/zw/gbtj9p4d...ene/MRHead_Scene.mrml.



Slicer4 Minute Tutorial: 3D Visualization

Now make the skull invisible.

- 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
- Skin.vtk 0.00
- skull_bone.vtk 1.00

Information

Display

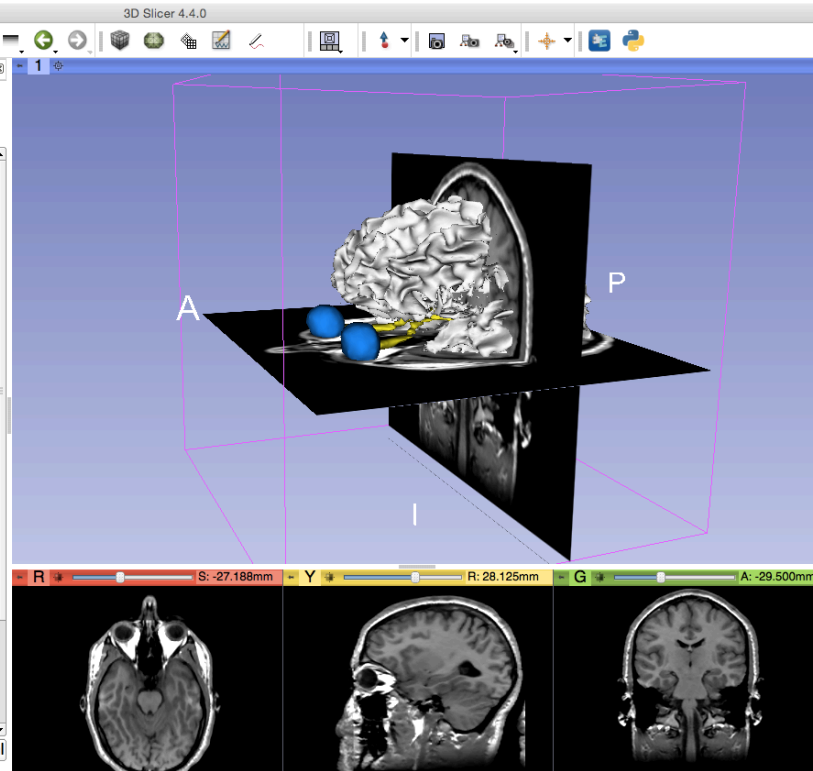
Visibility

- Visible:
- View: All
- Clip:
- Slice Intersections Visible:
- Slice Intersections Thickness: 1 px

Representation

Color

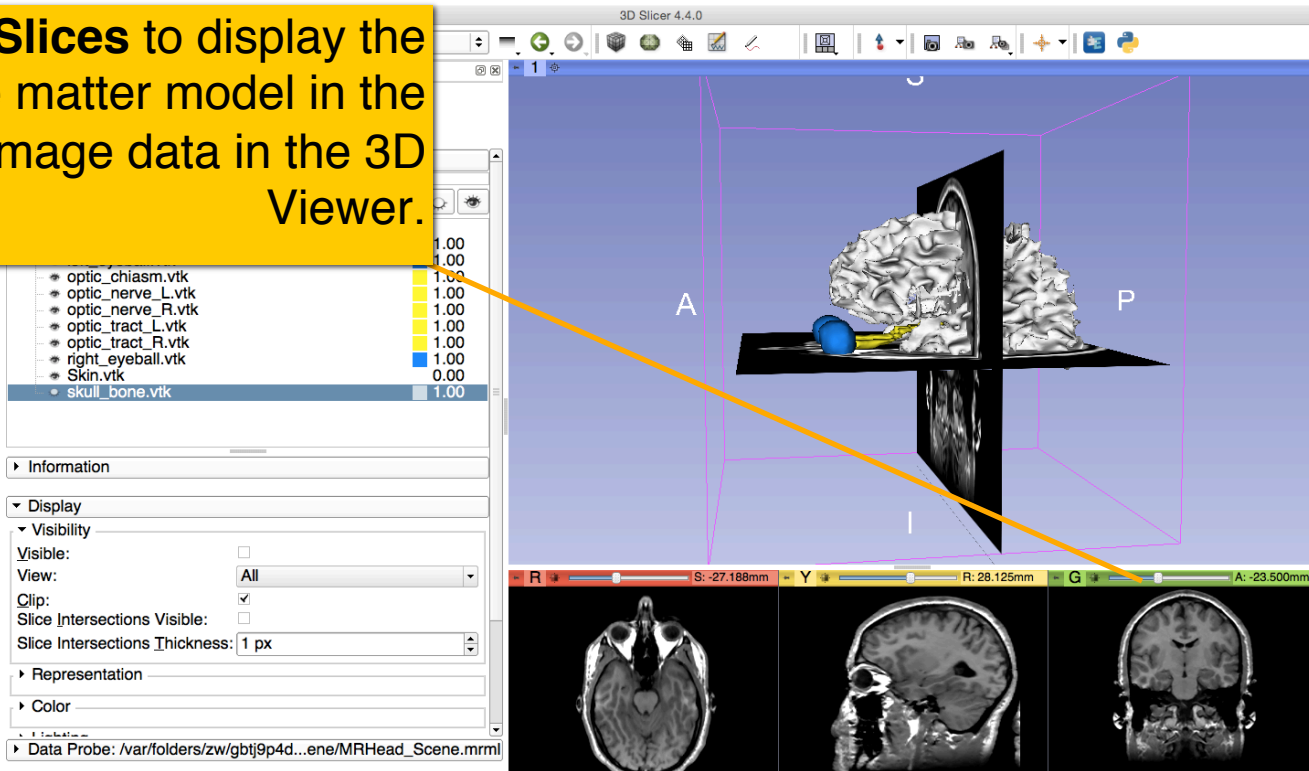
Data Probe: /var/folders/zw/gbtj9p4d...ene/MRHead_Scene.mrml





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
- Skin.vtk 0.00
- skull_bone.vtk 1.00

Information

Display

Visibility

Visible:

View: All

Clip:

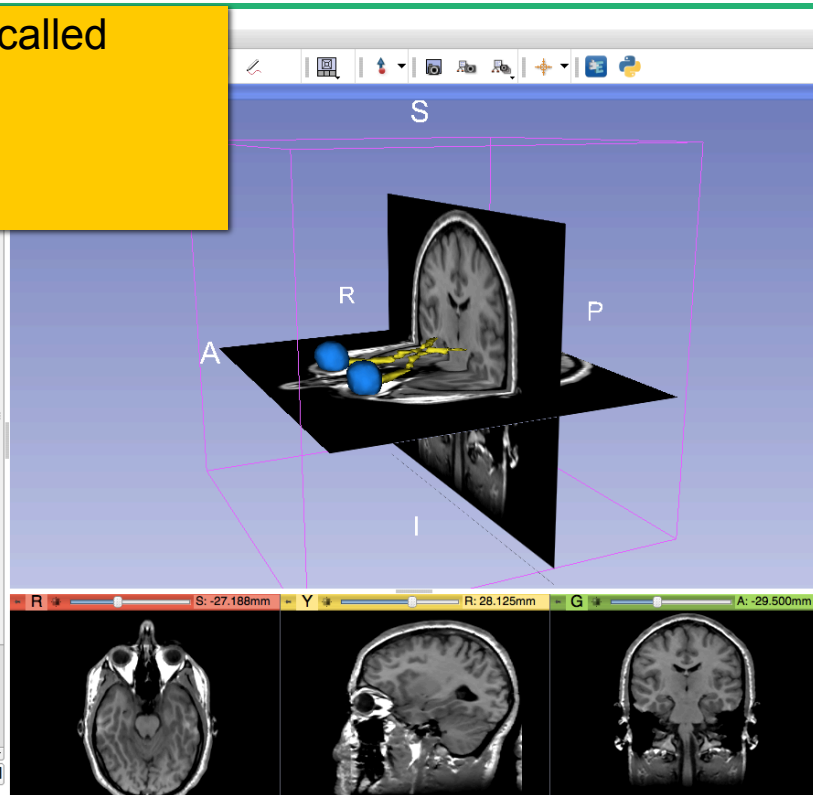
Slice Intersections Visible:

Slice Intersections Thickness: 1 px

Representation

Color

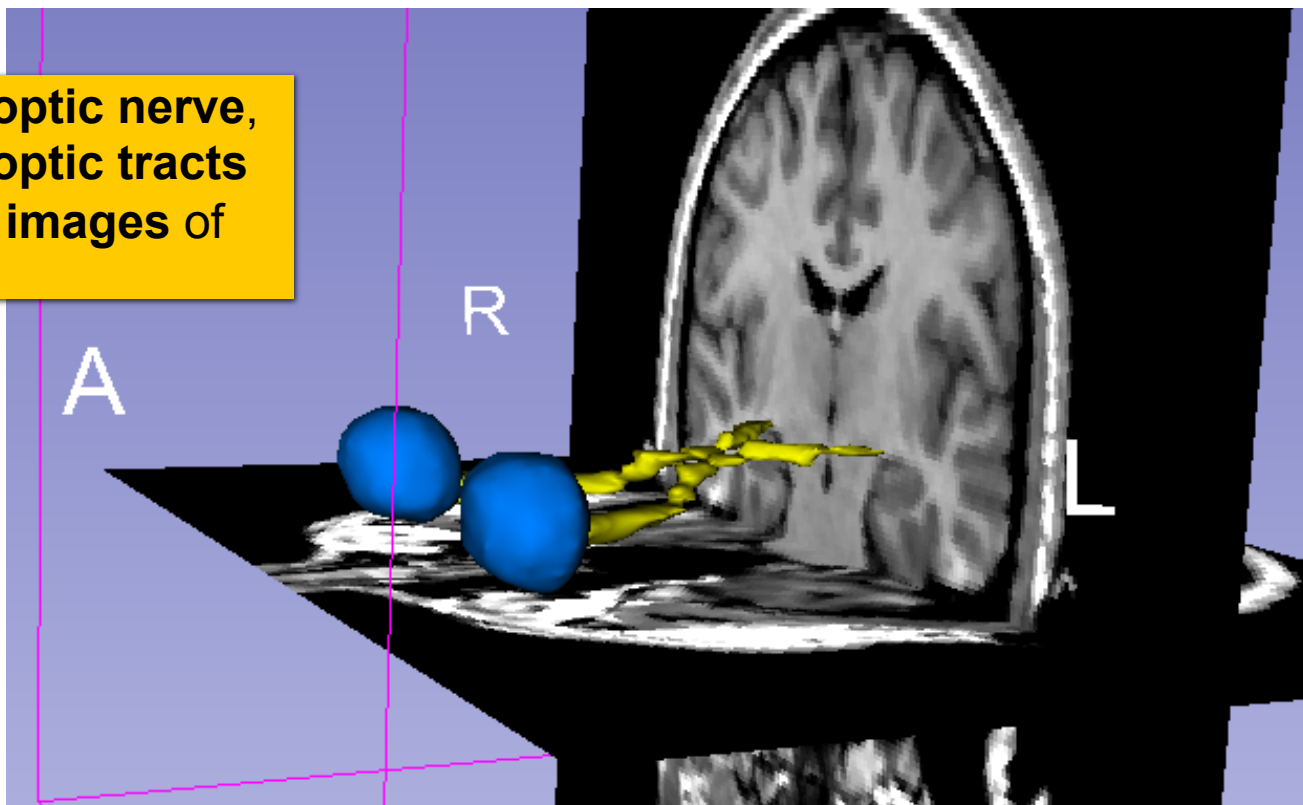
Data Probe: /var/folders/zw/gbtj9p4d...ene/MRHead_Scene.mrml





Slicer4 Minute Tutorial: 3D Visualization

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



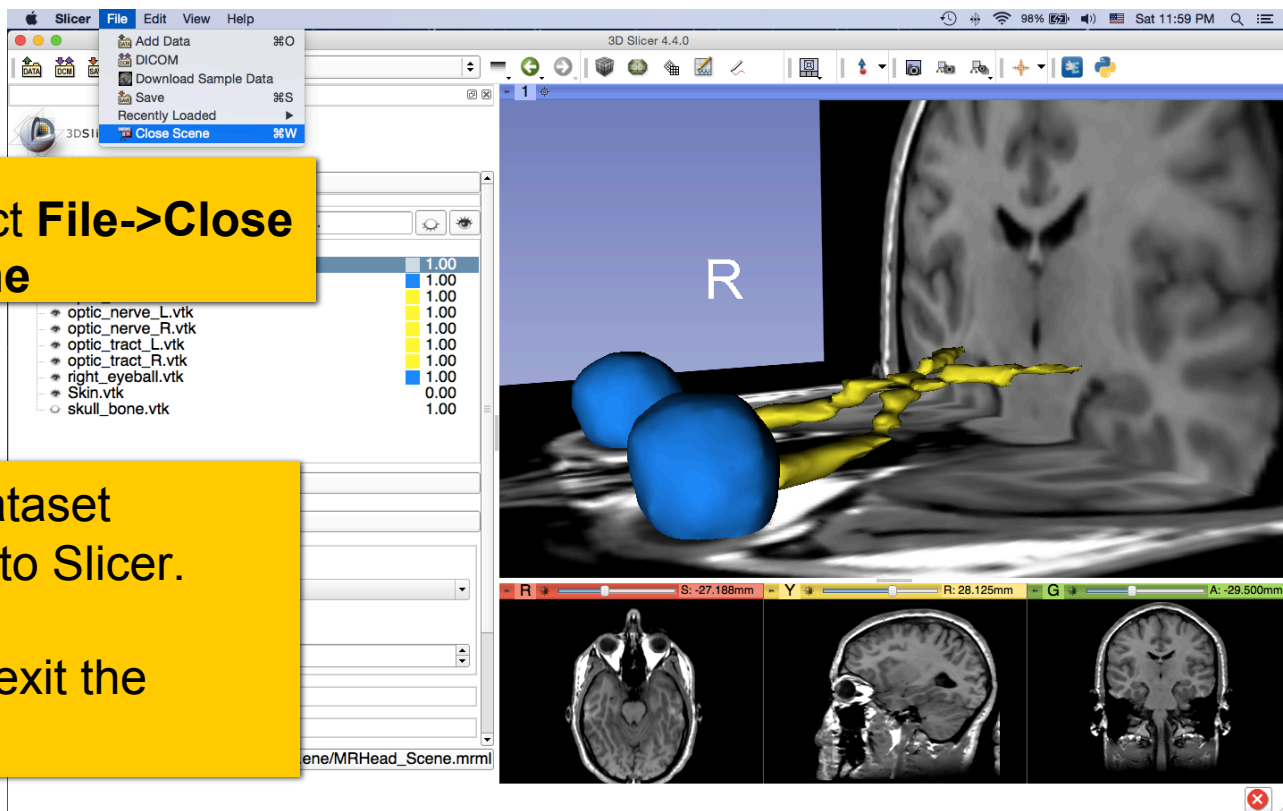


Close the existing scene and all its data

Select **File->Close Scene**

This removes any dataset previously loaded into Slicer.

Select **File→Exit** to exit the software



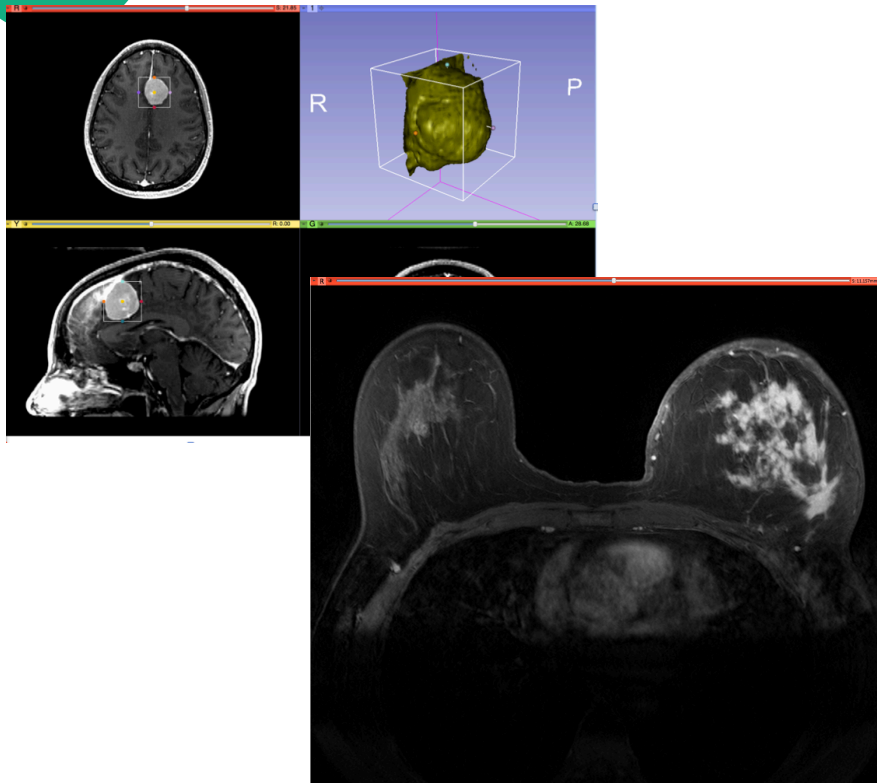


Summary

This first part of the tutorial has demonstrated:

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

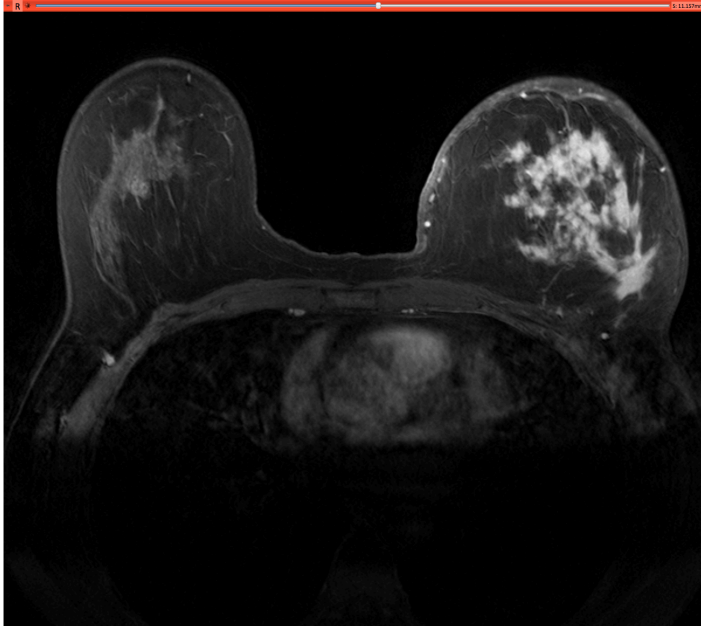
Next, we will use these building blocks to perform image analysis and visualize quantitative results.



Part II: Analyzing Volumetric Changes



Example 1: Large volumetric change

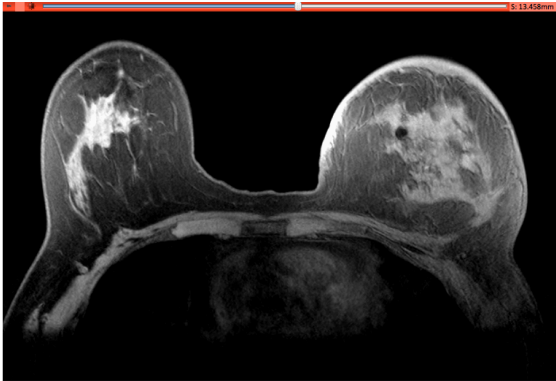


Case Courtesy of Dr. Macura, JHU

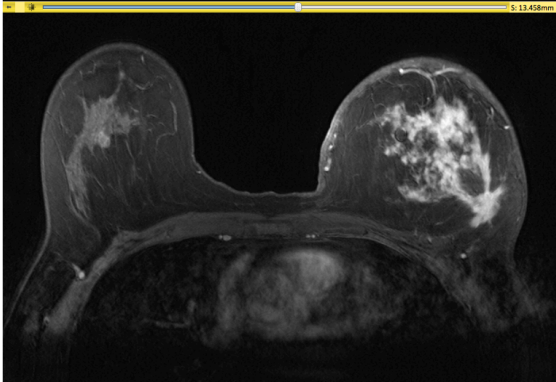
- Clinical case: 45 y-o woman presenting with an infiltrating ductal carcinoma in left breast
- Pre- and post-treatment imaging shows large volumetric difference in tumor size



PreTherapy acquisition



Pre-Gad High resolution MR scan



Post-Gad High resolution MR scan



Quantitative Imaging Processing Pipeline

Step #1: **Non-rigid Registration** of pre-Gad image to post-Gad image

Step #2: **Subtraction** of registered pre-Gad image to the post-Gad image

Step #3: **Semi-automated segmentation** of the subtracted image

Step #4: **3D model creation**

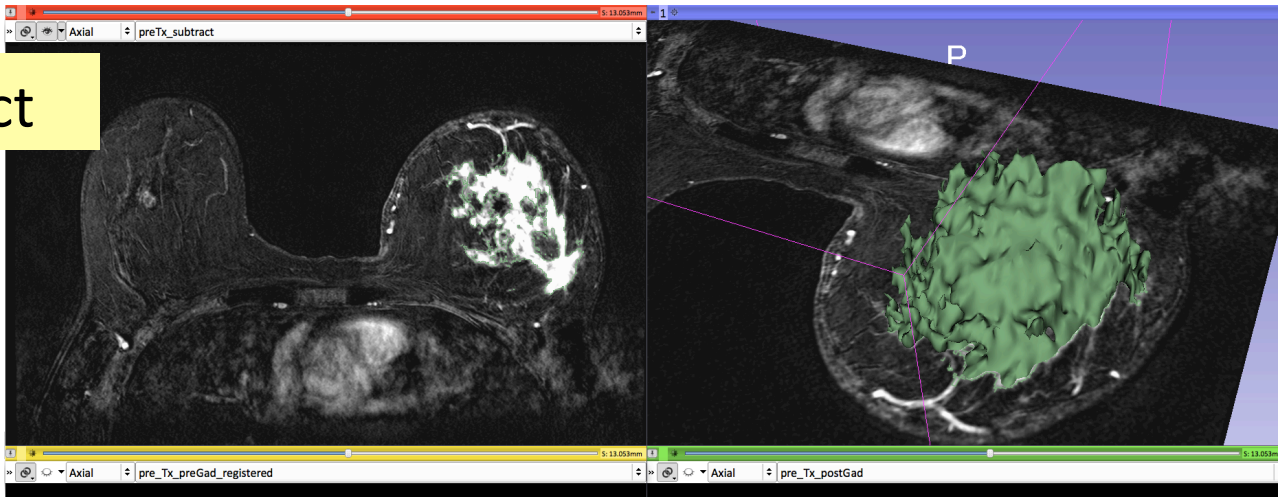
Step #5: **Tumor volume computation**

Processing time ~5-7 min

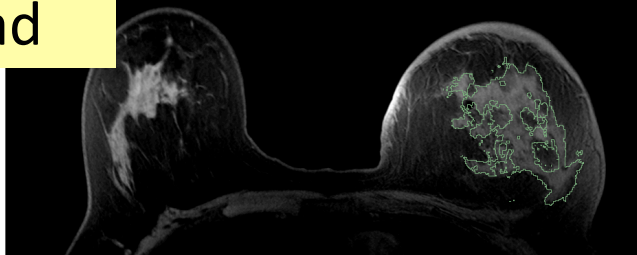


Pre-therapy analysis (May 2013)

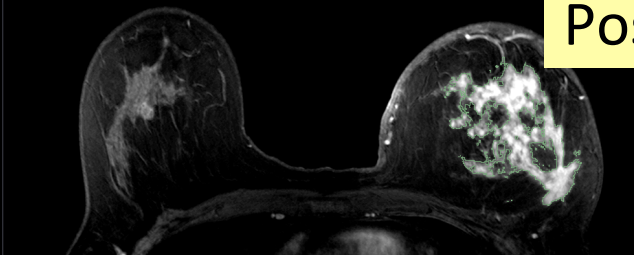
Subtract



Pre-Gad



Post-Gad



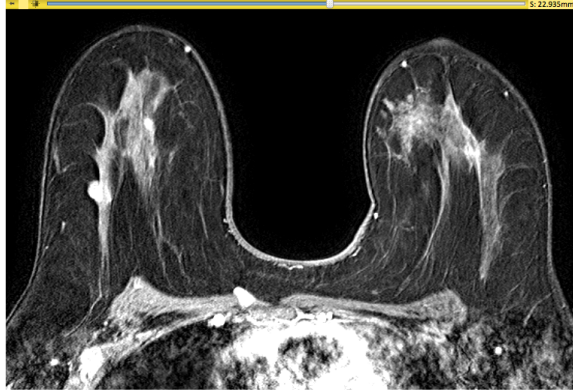
Tumor volume (May): 75 cm³



PostTherapy acquisition



Pre-Gad High resolution scan

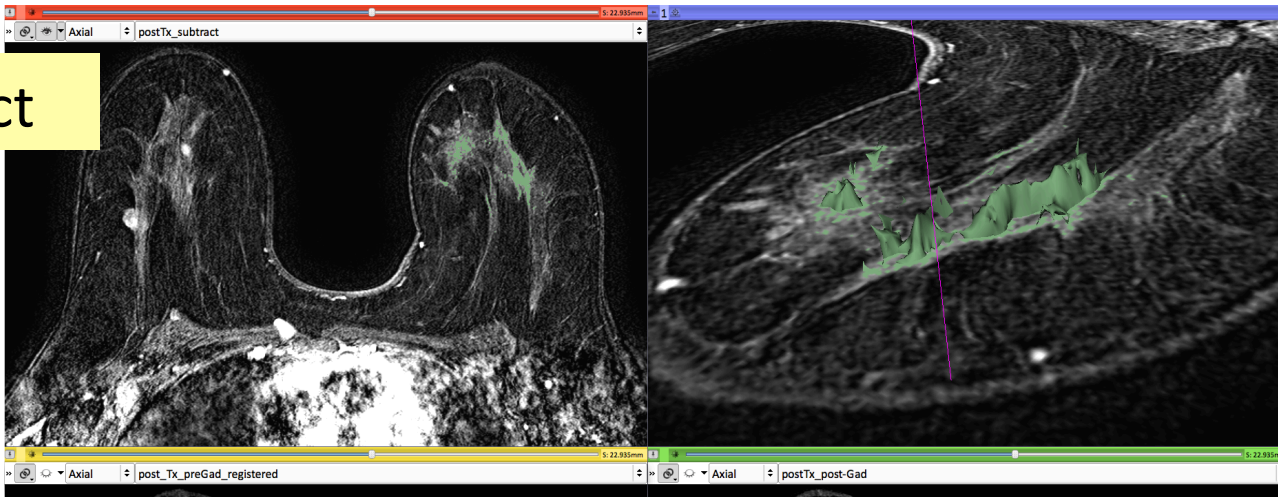


Post-Gad High resolution scan

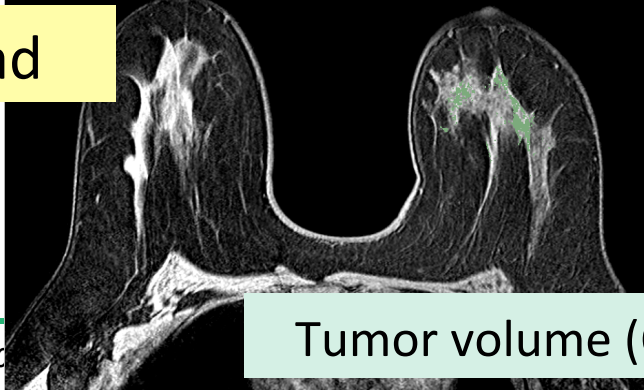


Post-therapy analysis (Oct. 2013)

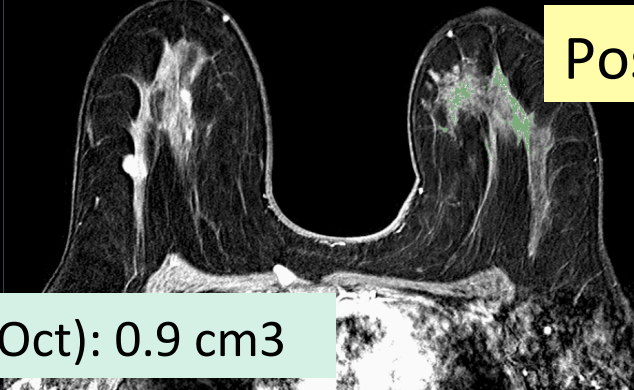
Subtract



Pre-Gad



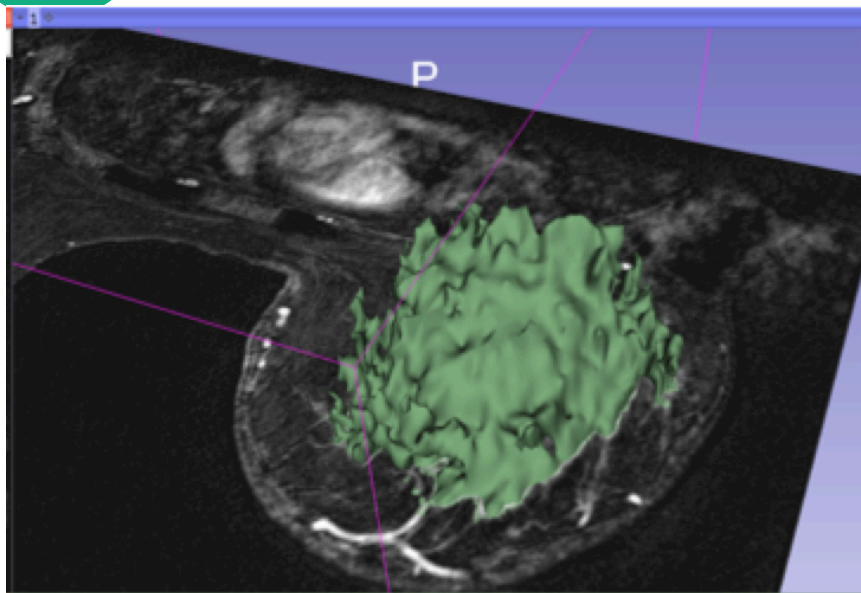
Post-Gad



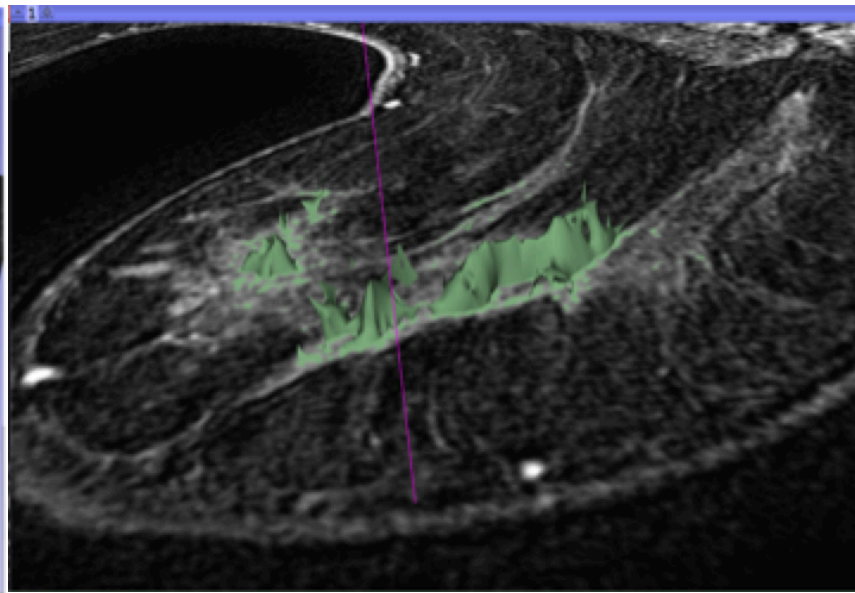
Tumor volume (Oct): 0.9 cm³



Example 1: Large Volumetric Change



Tumor volume (May): 75 cm³

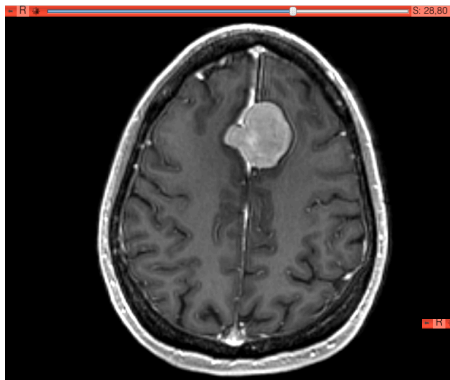


Tumor volume (Oct): 0.9 cm³



Example 2: Small volumetric change

MR Scan1 2006



MR Scan2 2007



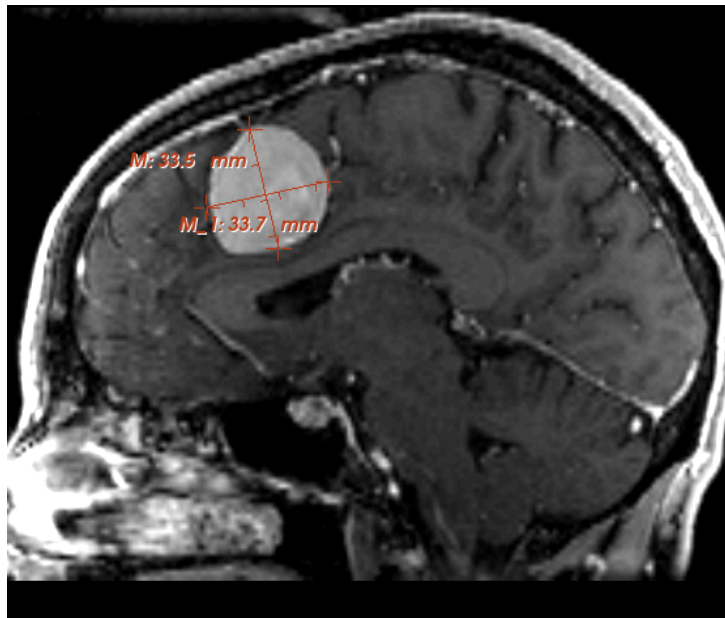
The second example is built upon MR datasets of a meningioma case.

The following section will guide you step-by-step through the computation of small volumetric changes between the baseline (2006) and follow-up (2007) using the Change Tracker module.

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



Conventional measures of tumor response

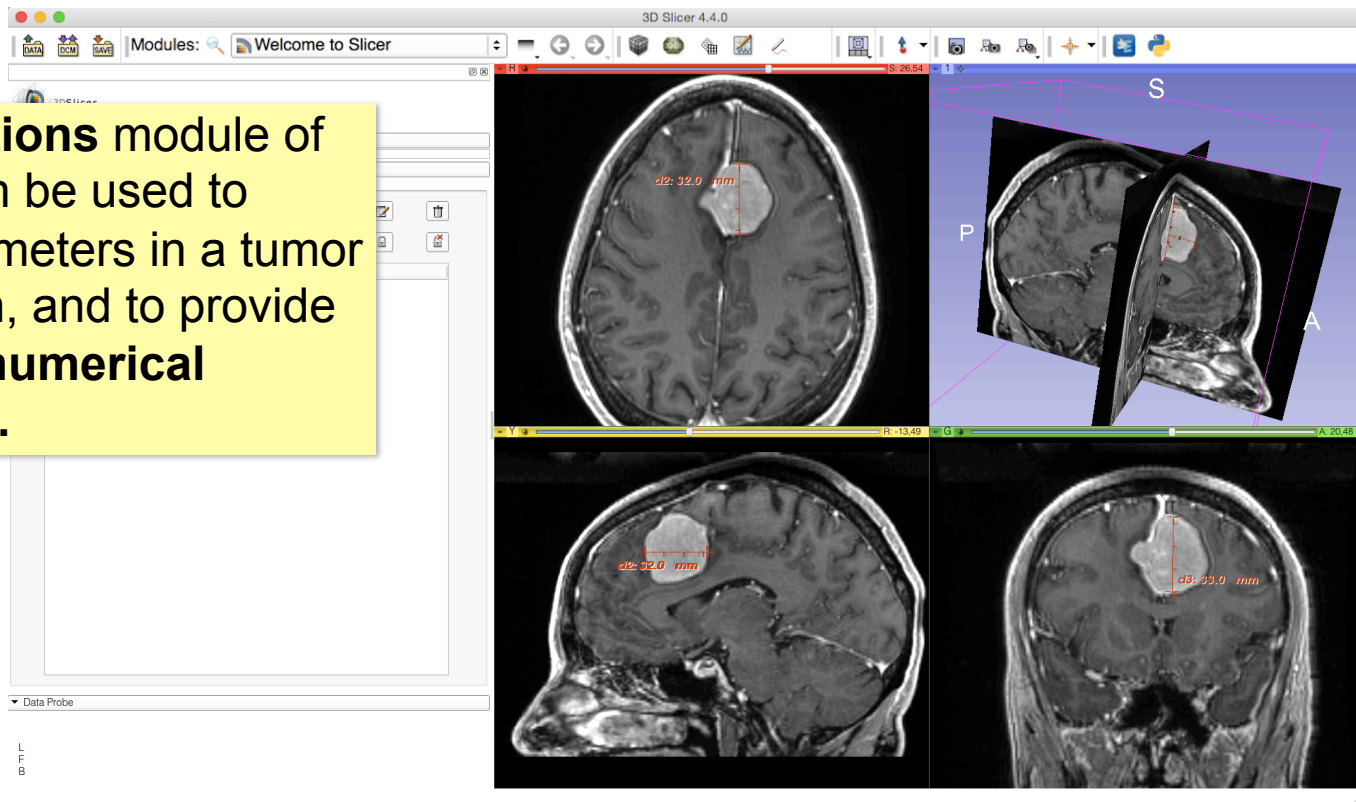


- Conventional anatomic imaging using CT or MRI are often used to evaluate tumor size and shape
- Most clinical trials that evaluate new chemotherapeutic drugs use changes in uni-dimensional or bi-dimensional measurements to assess response (*e.g.* RECIST)
- Slicer has several tools for applying RECIST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



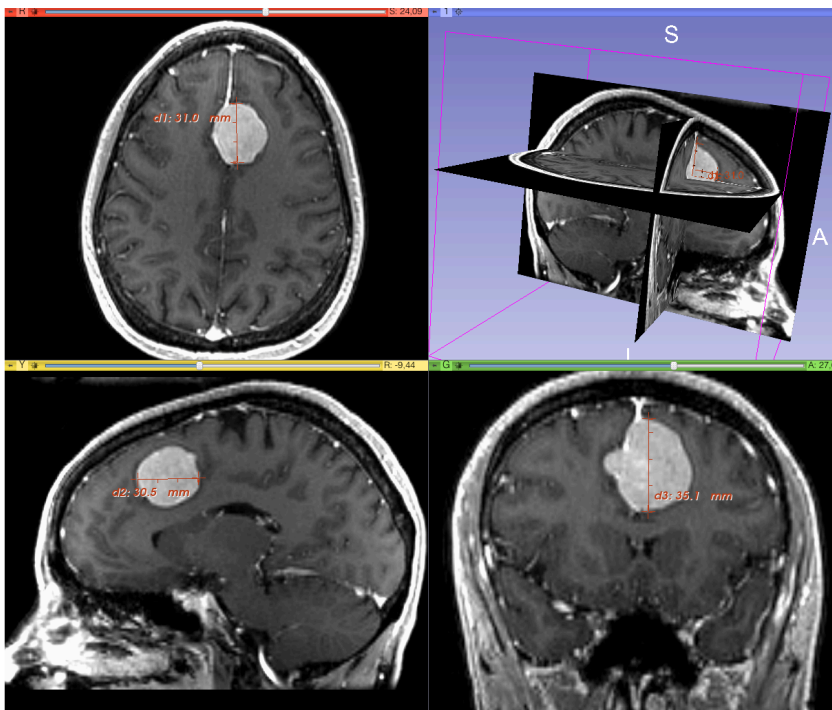
Conventional measures of tumor response

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





Clinical Case: baseline scan (2006)

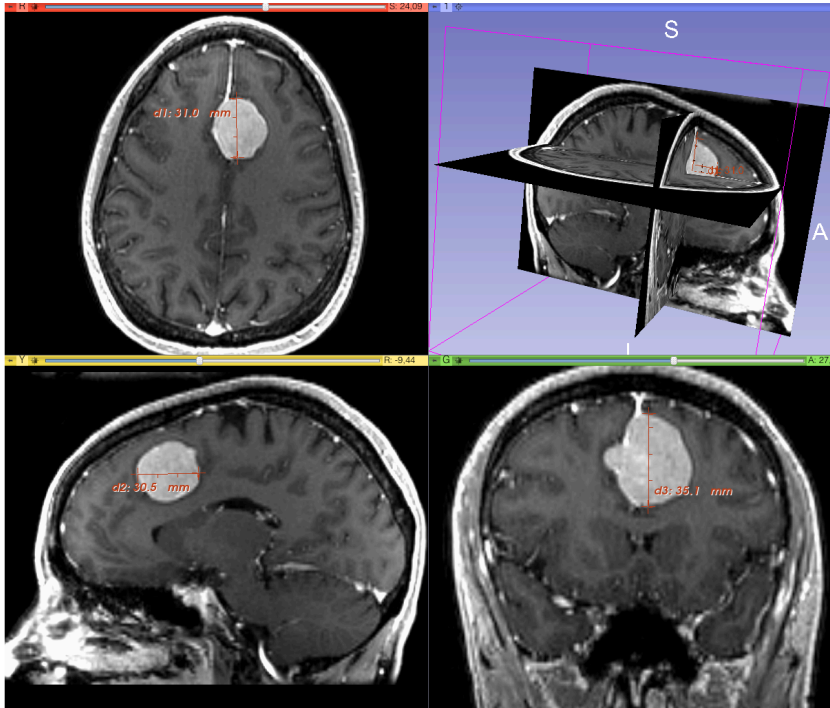


Baseline radiologist's clinical impression:

- 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 (2007)

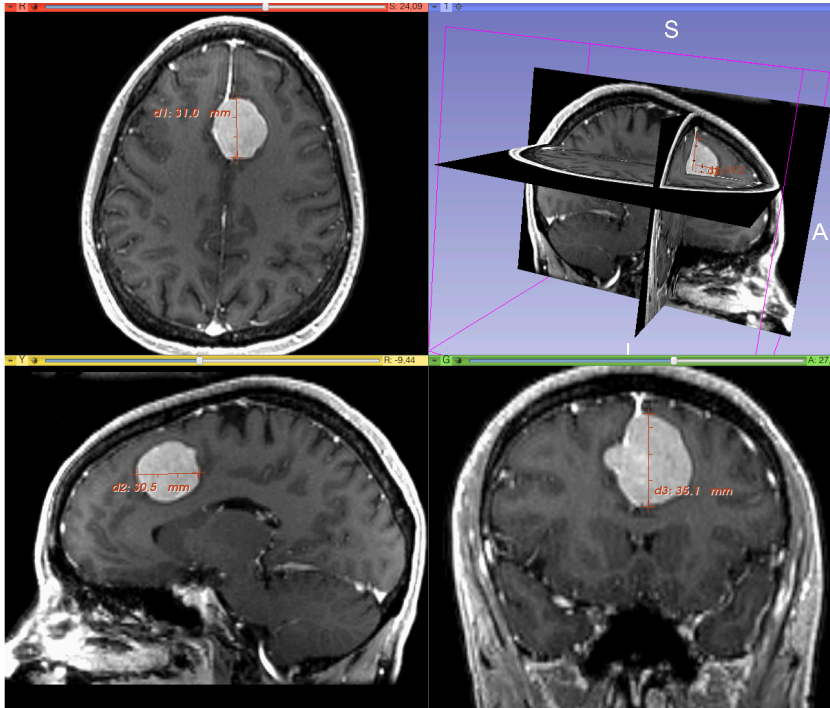


Follow-up radiologist's clinical impression:

- 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?



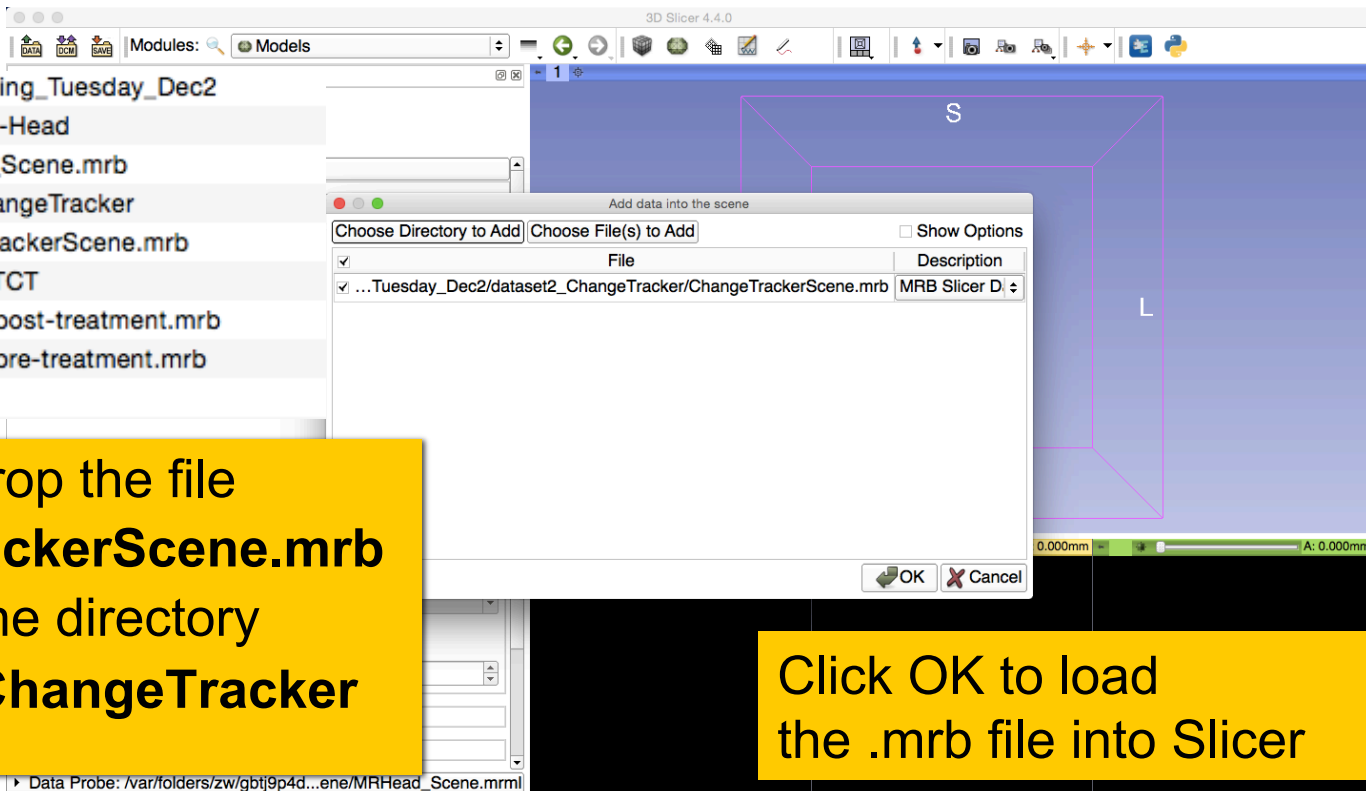
ChangeTracker: rationale for new approaches

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



ChangeTracker: Load the dataset



Drag and drop the file **ChangeTrackerScene.mrb** located in the directory **dataset2_ChangeTracker**

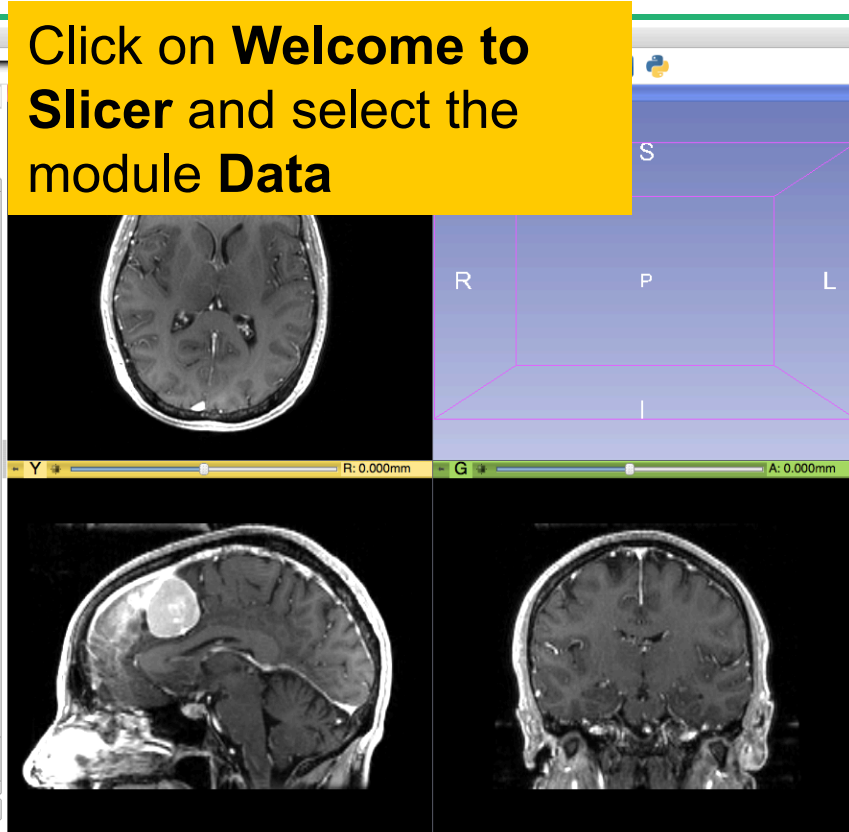
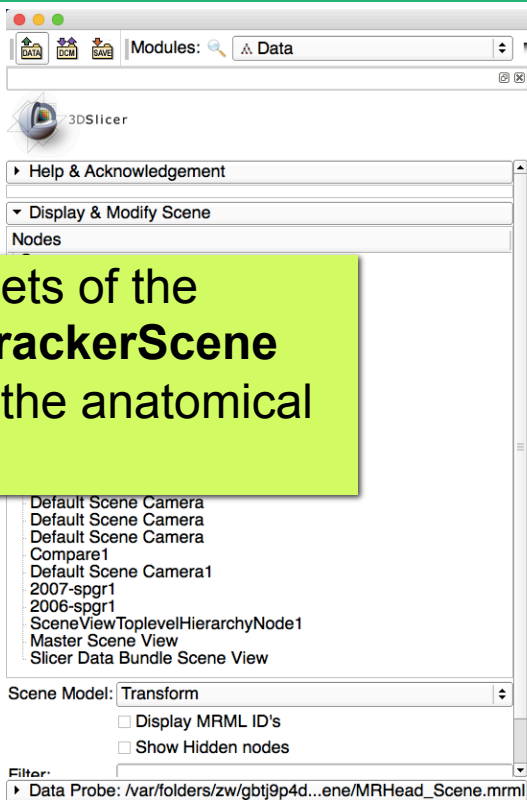
Click OK to load the .mrb file into Slicer



Loading the data

Click on **Welcome to Slicer** and select the module **Data**

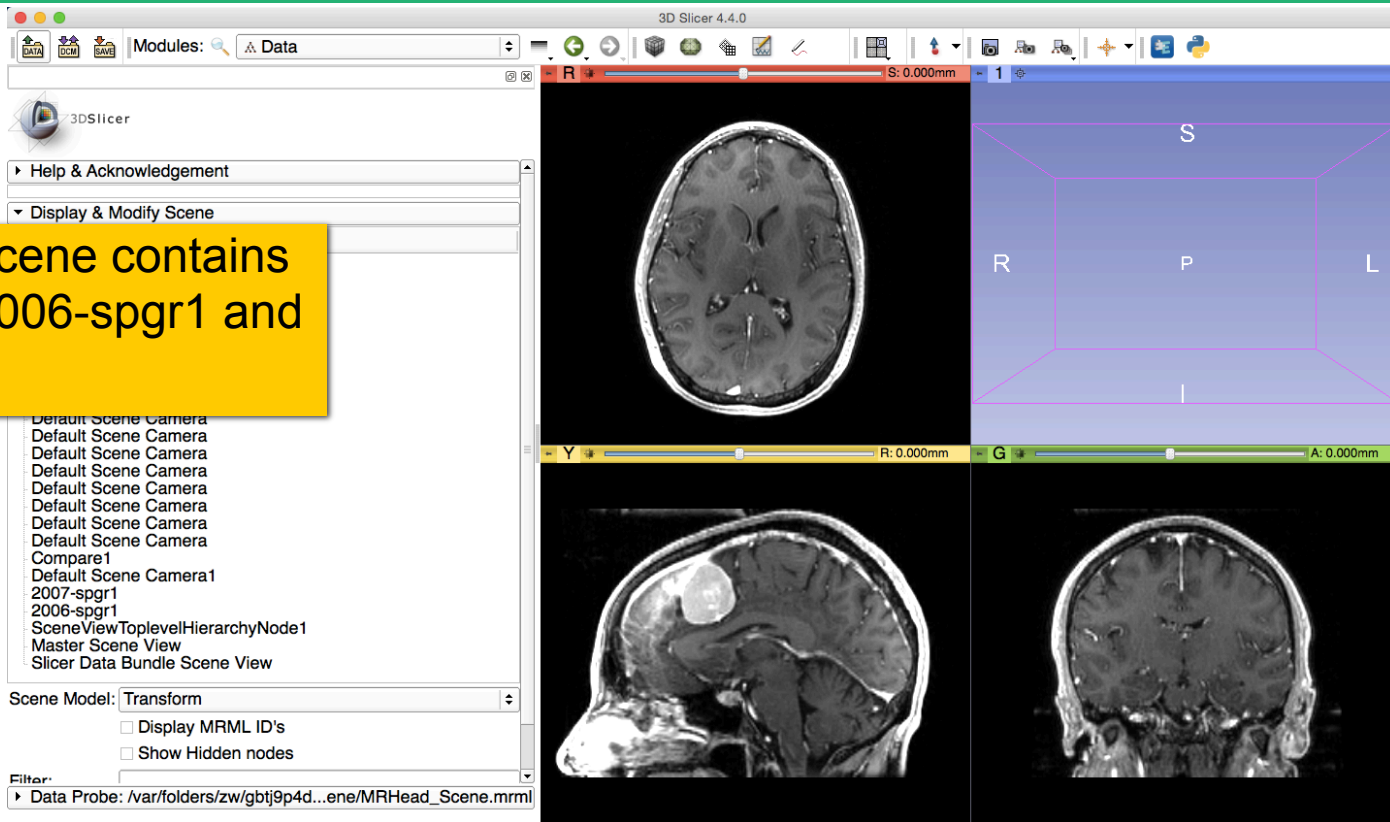
The datasets of the **ChangeTrackerScene** appear in the anatomical viewers.





Loading the data

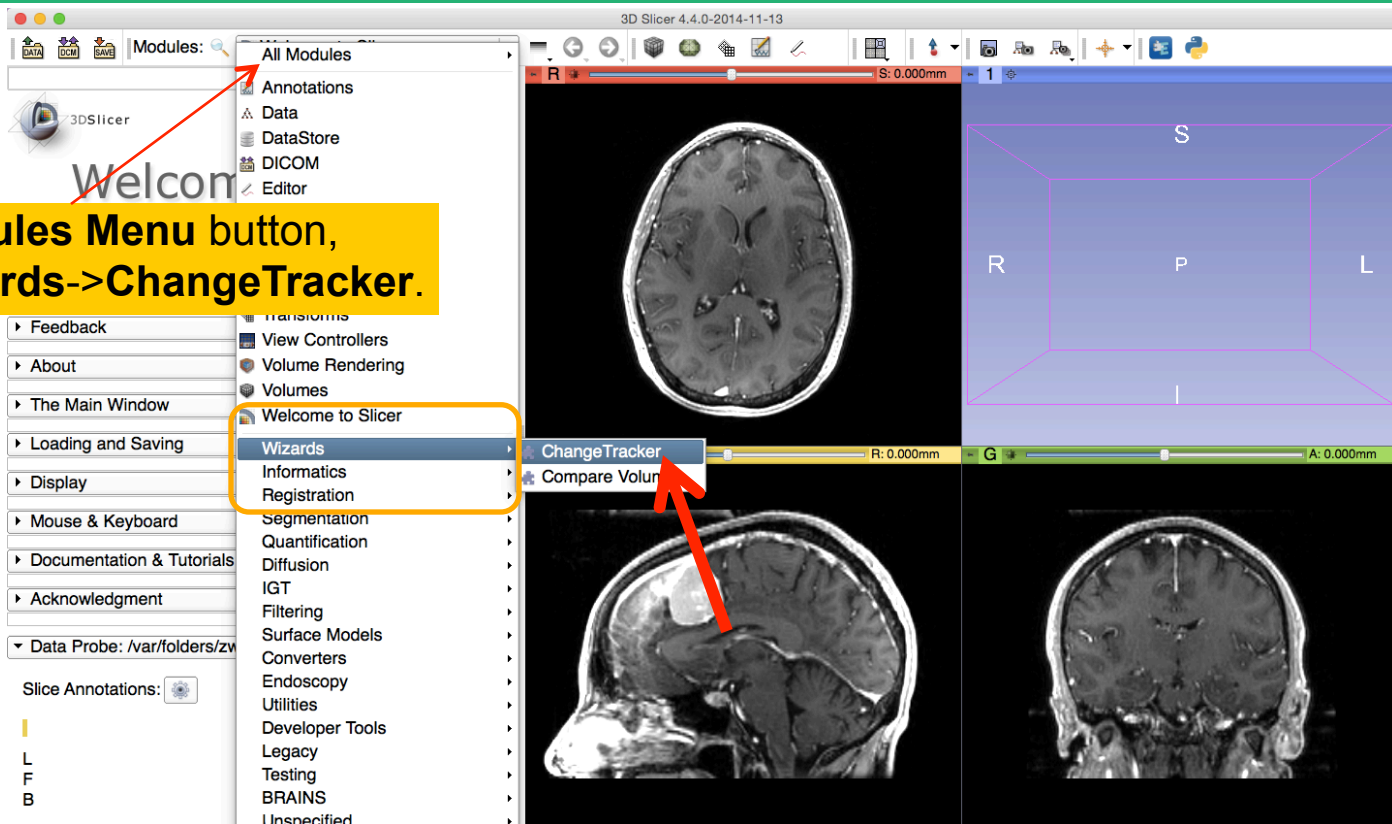
The Slicer scene contains two scans 2006-spgr1 and 2007-spgr1.





ChangeTracker: exploring small volumetric changes

Using the **Modules Menu** button, select the **Wizards->ChangeTracker**.





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

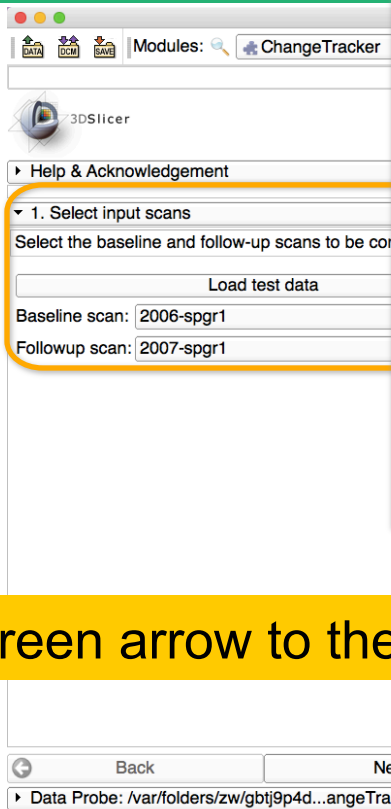
Followup scan: Select a Volume

Back Next

▸ Data Probe: /var/folders/zw/gbtj9p4d...angeTrackerScene.mrml



Step1: Select input scans

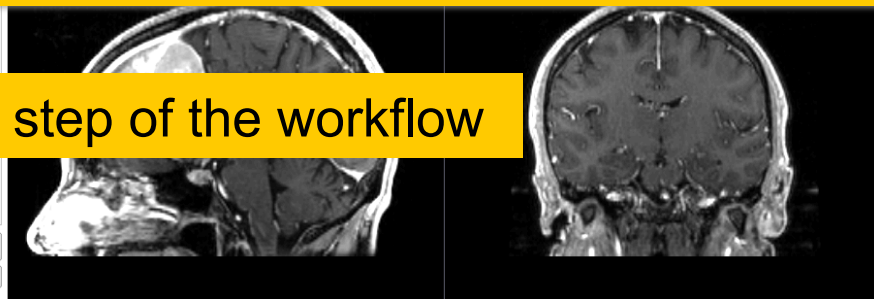


Click to expand the tab '1.Select input scans'

Click on **Select a Volume** next to **Baseline Scan**
Select the volume **2006-spgr1**

Click on **Select a Volume** next to **Follow up Scan**
Set the volume **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.

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

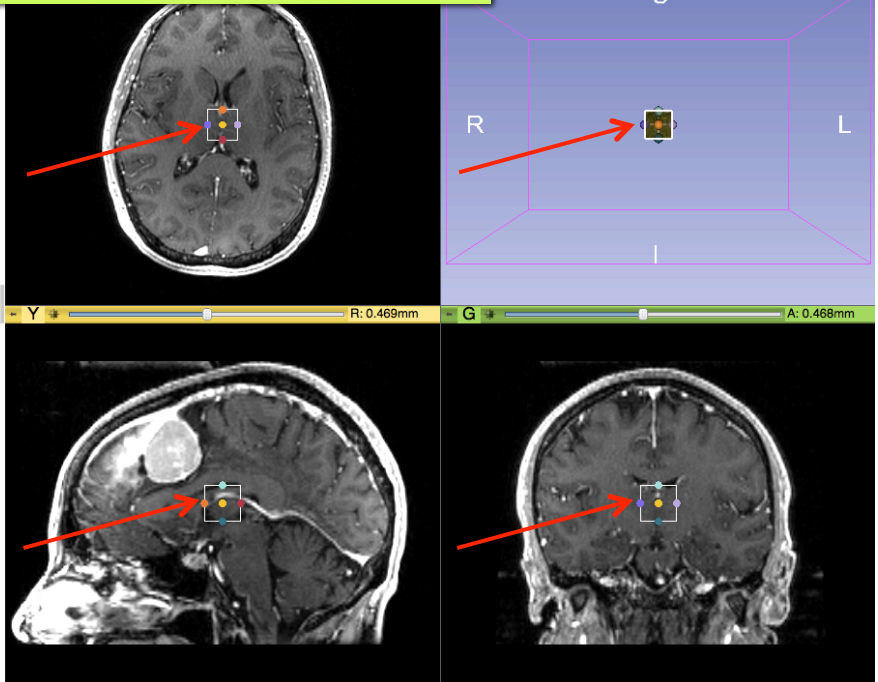
P-A Range: -10.00 10.00

I-S Range: -10.00 10.00

Display Clipping box Interactive Mode

Back Next

Data Probe: /var/folders/zw/gbtj9p4d...angeTrackerScene.mrml



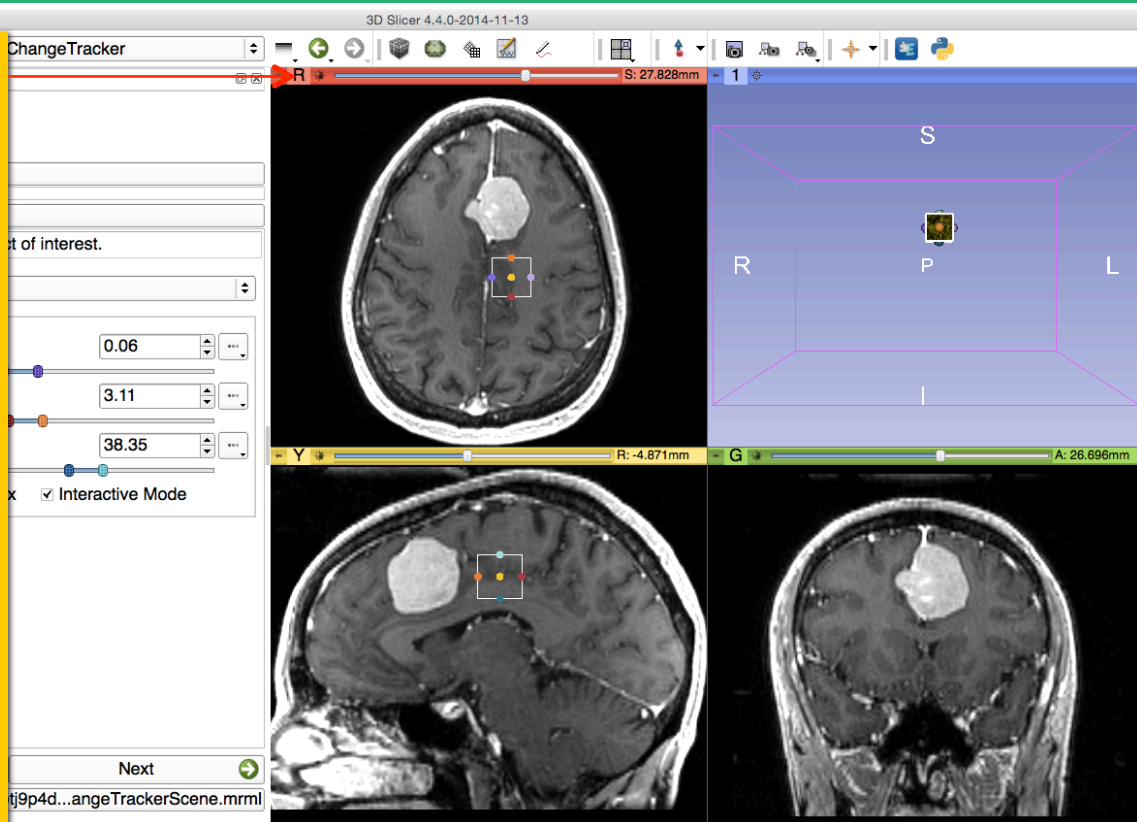


Step2: Define Region of interest

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

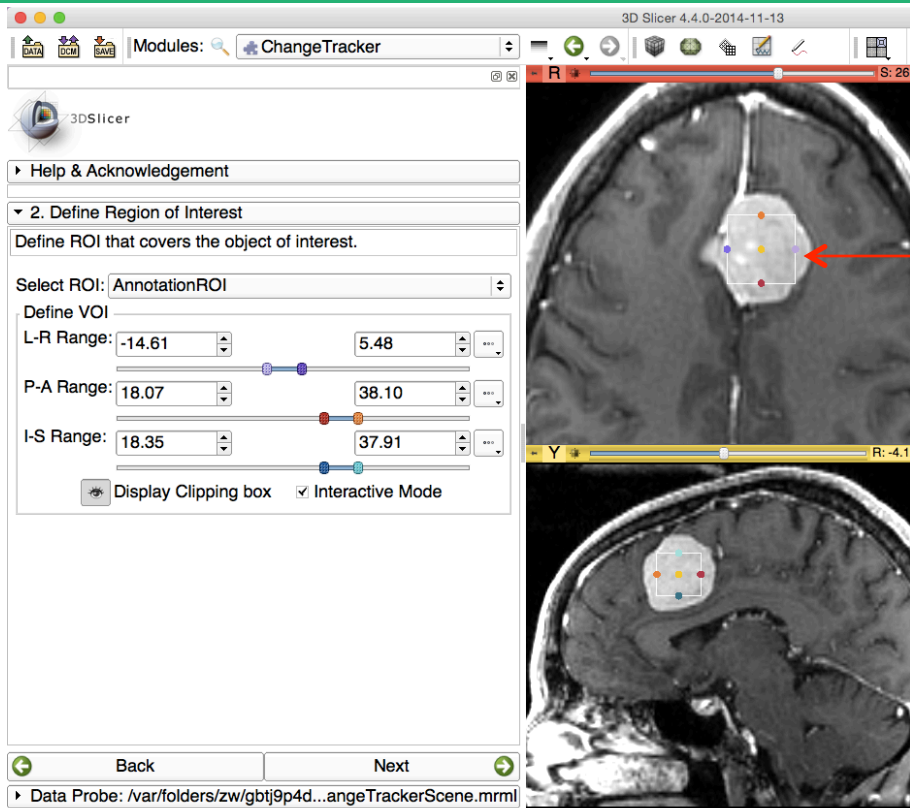
Zoom in (Right mouse down and push/pull).

Position the mouse cursor in a viewer, **hold the shift** button down on the keyboard, and move the mouse to display the corresponding location in the two other viewers





Step2: Define Region of interest



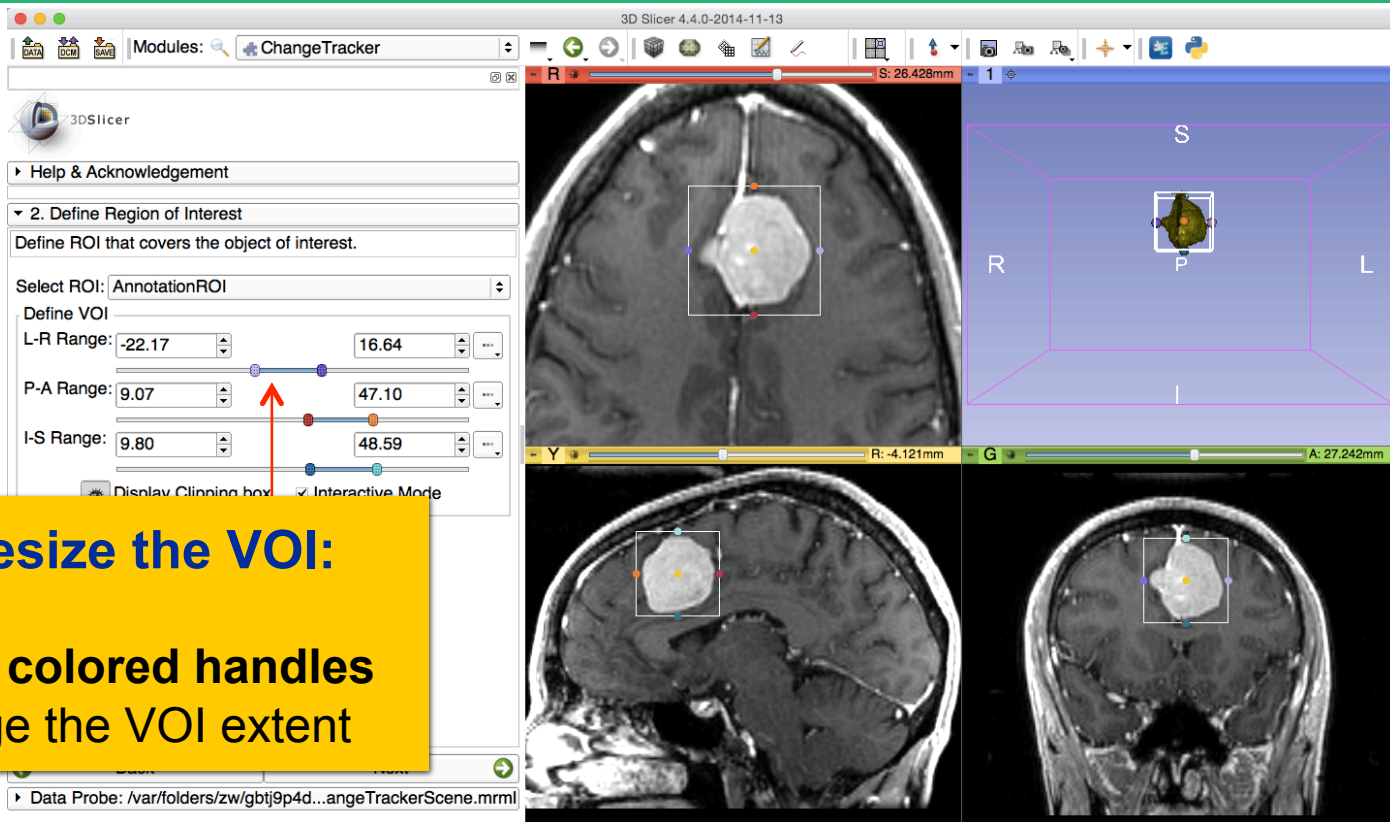
Center the VOI first:

Left click on the central yellow dot and hold the mouse cursor down to move the VOI

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



Step2: Define Region of interest



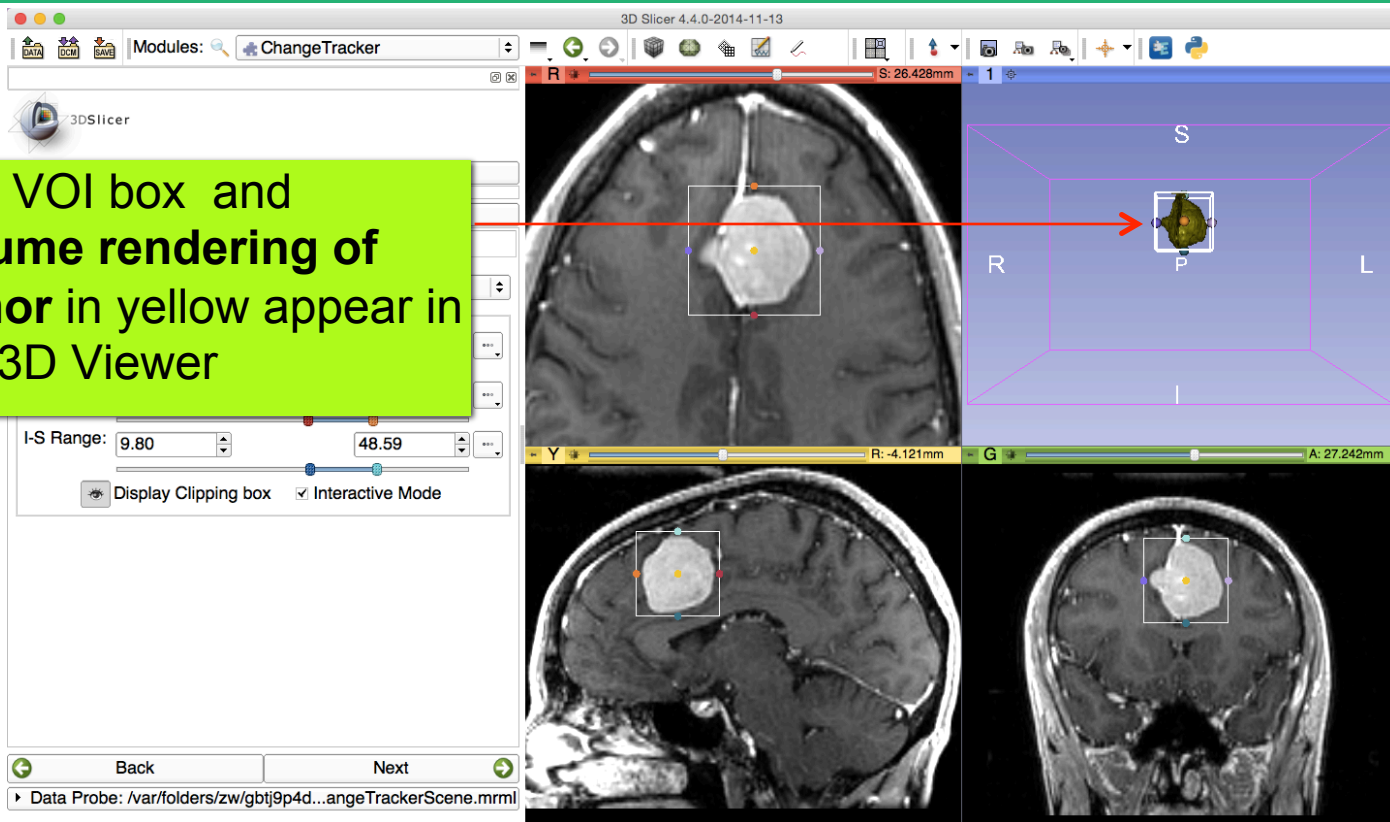
Next, resize the VOI:

**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

The screenshot displays the 3D Slicer 4.4.0-2014-11-13 interface. The left sidebar shows the '2. Define Region of Interest' panel with the following settings:

- Select ROI: AnnotationROI
- Define VOI
- L-R Range: -22.17 to 16.64
- P-A Range: 9.07 to 47.10
- I-S Range: 9.80 to 48.59
- Display Clipping box:
- Interactive Mode:

The main 3D view shows a brain slice with a green VOI box and a yellow dot. A yellow callout box on the right contains the text: **Fine-tune the VOI using the VOI Widget range sliders or by moving the VOI Widget handles in 3D view**

A yellow callout box at the bottom contains the text: **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 4.4.0-2014-11-13

Define ROI that covers the object of interest.

Select ROI: AnnotationROI

Define VOI

L-R Range: -22.17 to 16.64

P-A Range: 9.07 to 47.10

I-S Range: 9.80 to 48.59

Display Clipping box Interactive Mode

- Conventional
- Conventional Widescreen**
- Conventional Quantitative
- Four-Up
- Four-Up Quantitative
- Dual 3D
- Triple 3D
- 3D only
- One-Up Quantitative
- 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
- Side by side
- Four by three slice
- Four by two slice
- Three by three slice

Back Next

Data Probe: /var/folders/zw/gbtj9p4d...angeTrackerScene.mrml



Step2: Define Region of interest

3D Slicer 4.4.0-2014-11-13

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: -22.17 to 16.64

P-A Range: 9.07 to 47.10

I-S Range: 9.80 to 48.59

Back Next

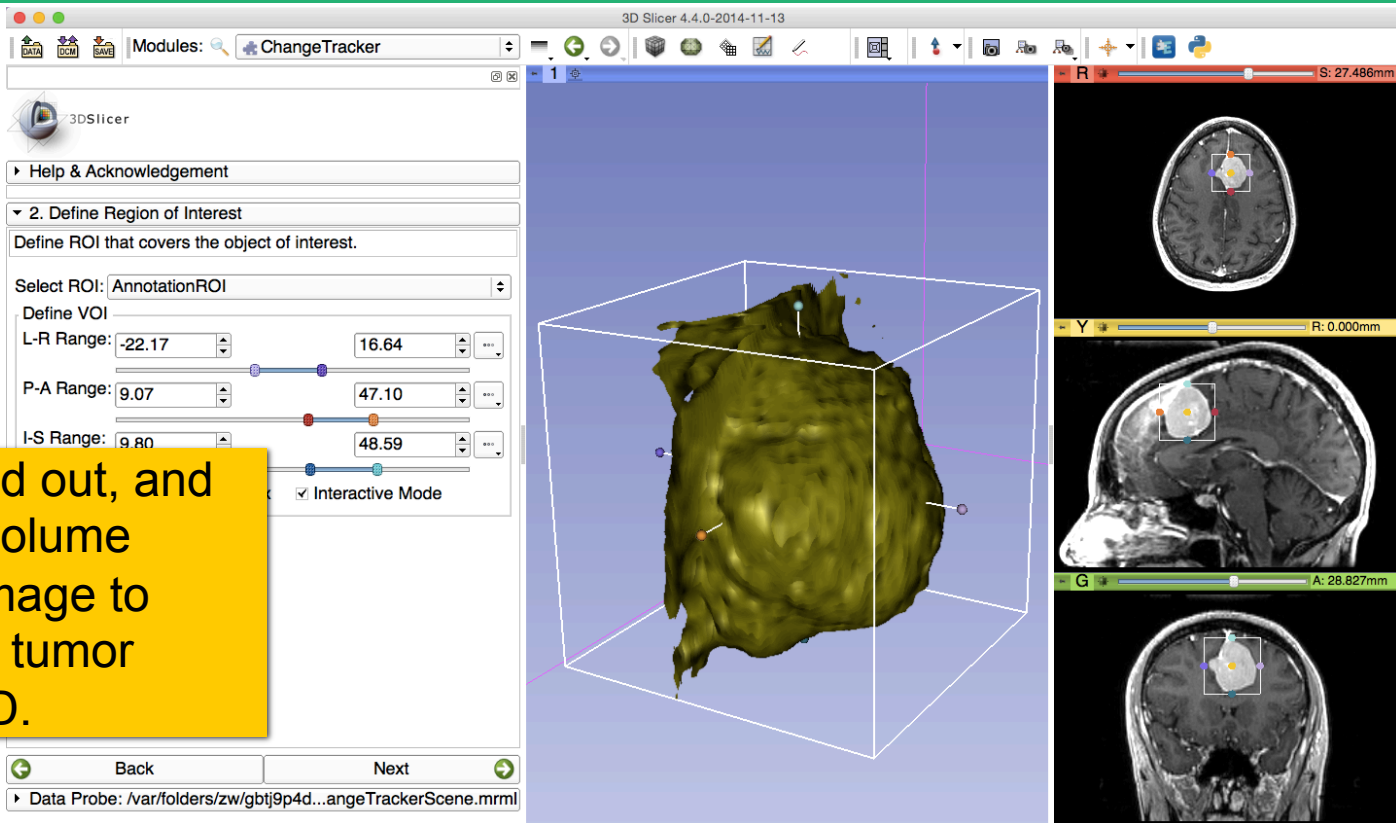
Data Probe: /var/folders/zw/gbtj9p4d...angeTrackerScene.mrml

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



Step2: Define Region of interest

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





Step2: Define Region of interest

3DSlicer

2. Define Region of Interest

Define ROI that covers the object of interest.

Select ROI: AnnotationROI

16.64

47.10

48.59

Display Clipping box Interactive Mode

Back Next

Data Probe: /var/folders/zw/gbtj9p4d...angeTrackerScene.mrml

- Conventional
- Conventional Widescreen
- Conventional Quantitative
- Four-Up
- Four-Up Quantitative**
- Dual 3D
- Triple 3D
- 3D only
- One-Up Quantitative
- 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
- Side by side
- Four by three slice
- Four by two slice

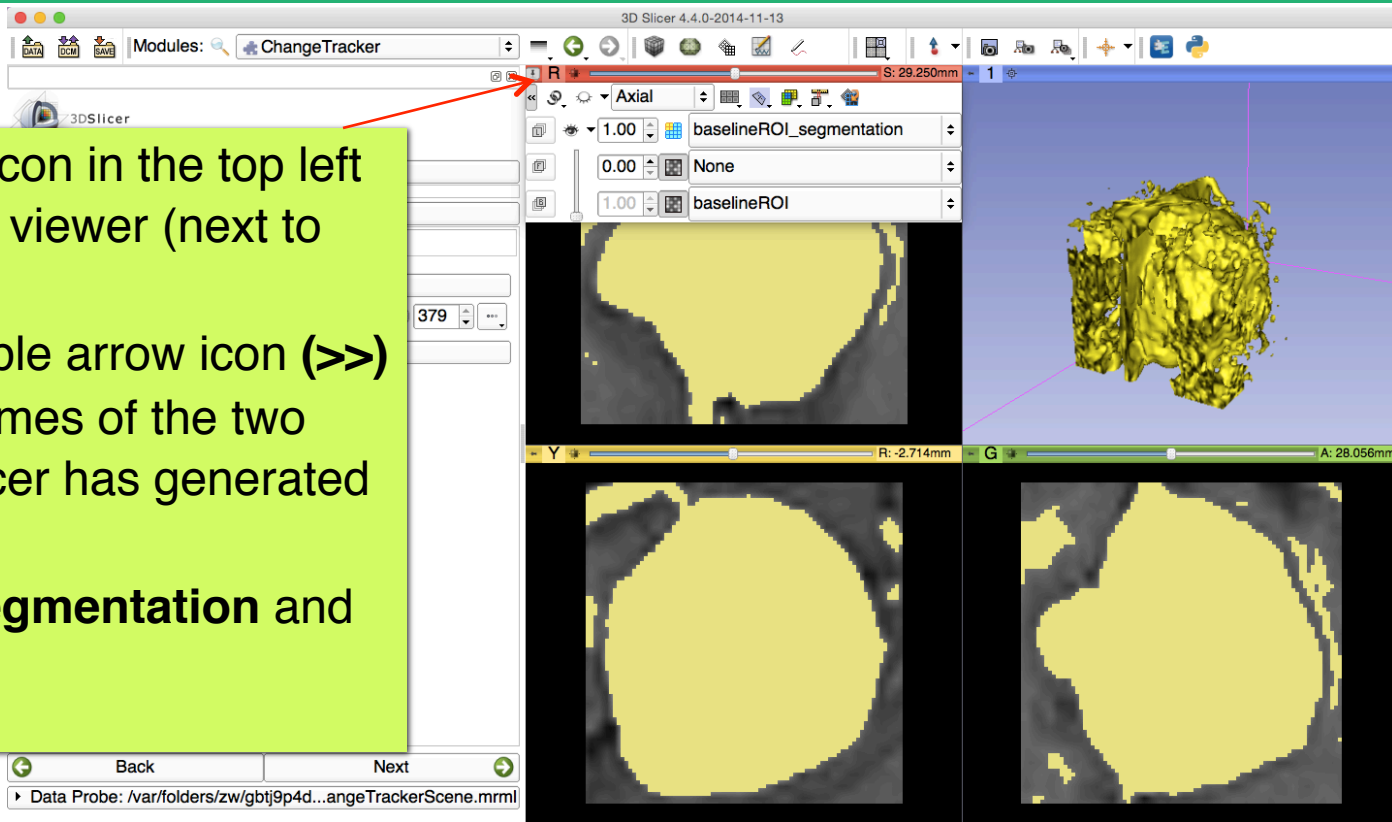
A: 28.827mm



Step3: Segment the tumor

Click on the pin icon in the top left corner of the red viewer (next to the letter **R**)

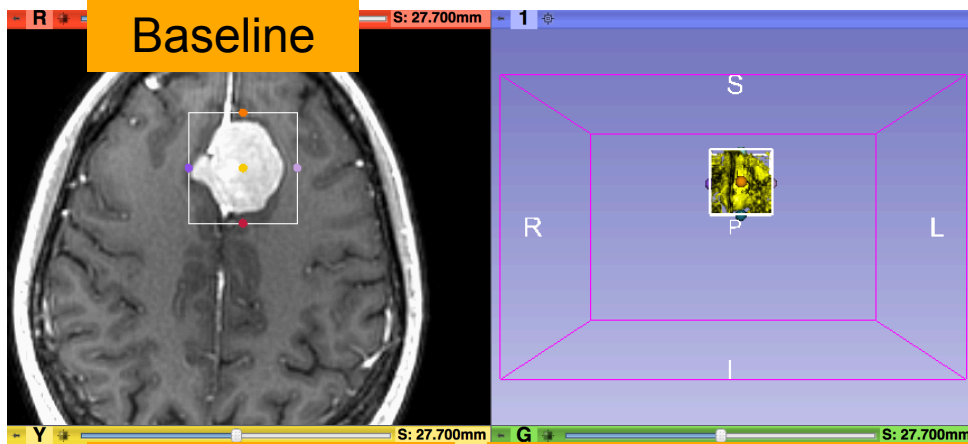
Click on the double arrow icon (**>>**) to display the names of the two volumes that Slicer has generated automatically:
baselineROI_segmentation and **baselineROI**



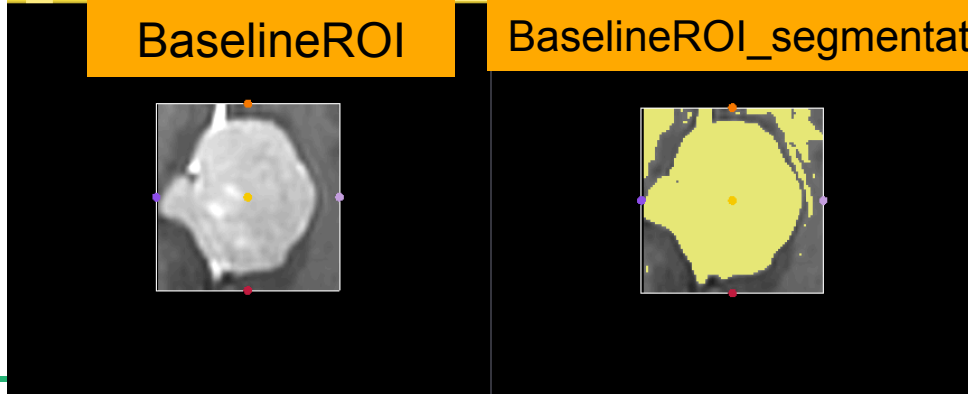


Segment the tumor

Step 1:
VOI
definition



Step 2:
VOI
extraction



Step 3:
Segmentation



Step3: Segment the tumor

A screenshot of the 3D Slicer software interface. The left sidebar shows the '3DSlicer' application with a menu for '3. Segment the analyzed structure'. The 'Basic settings' section is expanded, showing a 'Choose threshold' slider set to 379. The main window displays three views: a top-down axial view, a side view, and a 3D volume-rendered view of the segmented tumor in yellow. The 3D view is highlighted by a green callout box.

3D Slicer 4.4.0-2014-11-13

Modules: ChangeTracker

3DSlicer

Help & Acknowledgement

3. Segment the analyzed structure

Segment the structure in the selected ROI.

Basic settings

Choose threshold: 99 379

Advanced settings

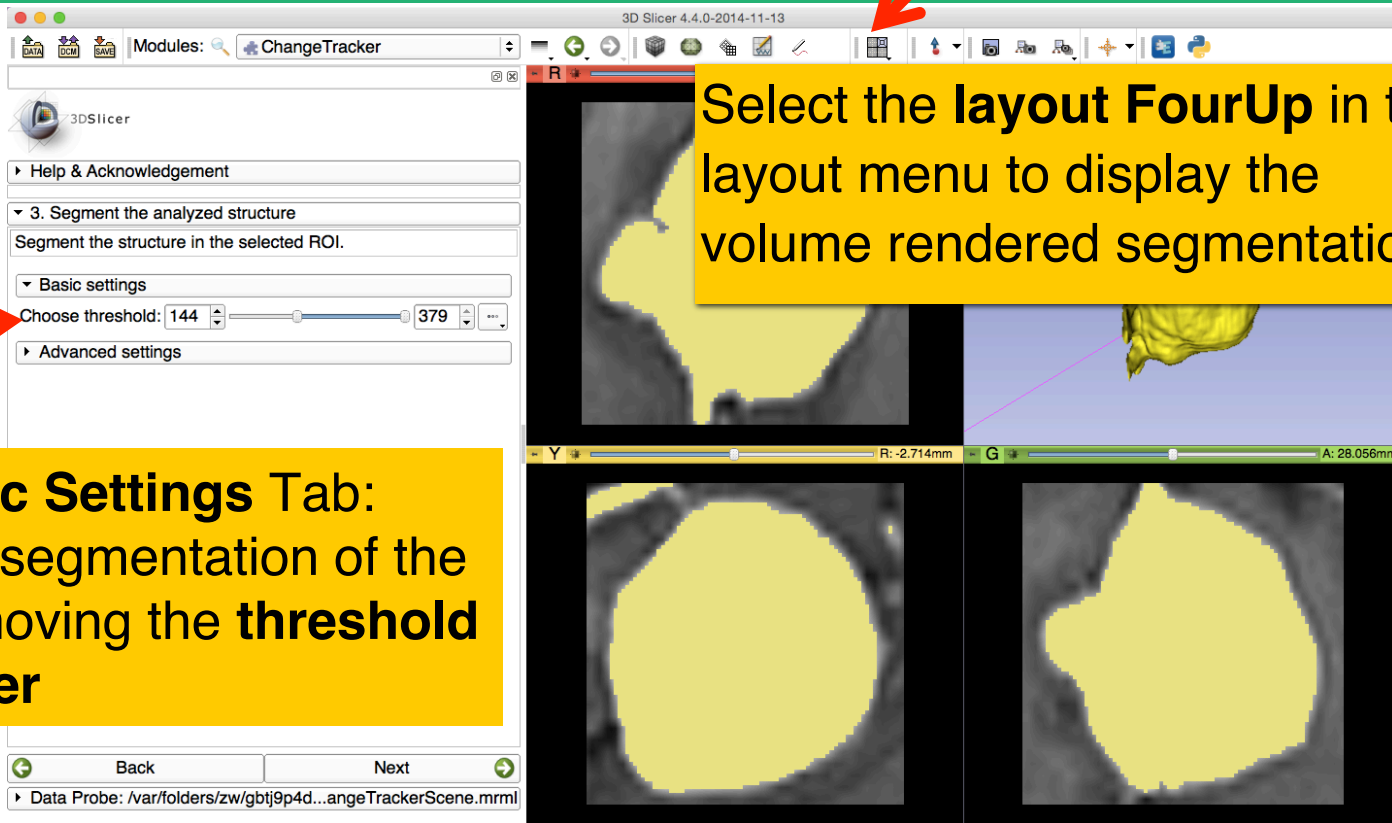
Back Next

Data Probe: /var/folders/zw/gbtj9p4d...angeTrackerScene.mrml

3D Viewer shows the corresponding 3D volume-rendered image of the tumor



Step3: Segment the tumor



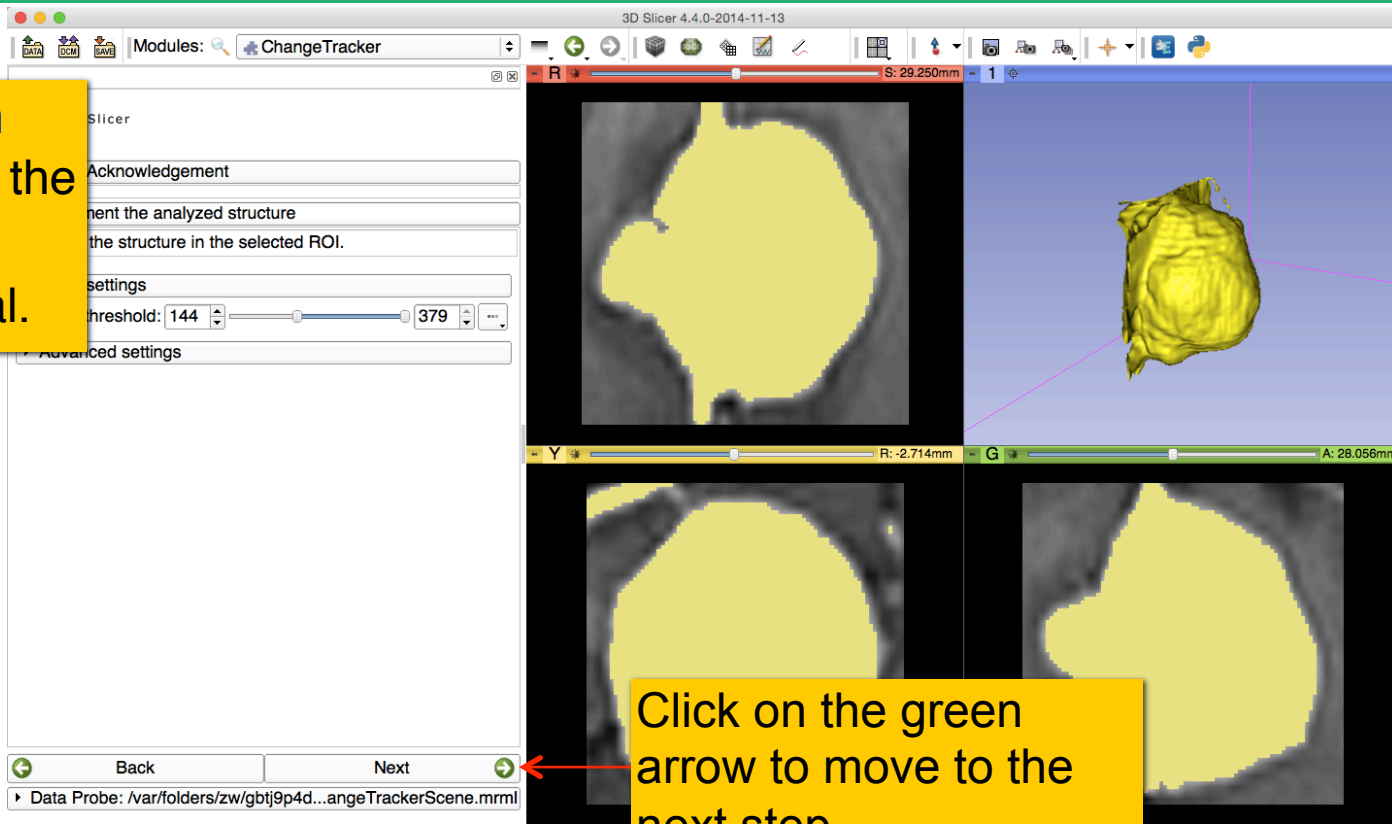
Select the **layout FourUp** in the layout menu to display the volume rendered segmentation

In the **Basic Settings** Tab: 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 4.4.0-2014-11-13

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

Back Next

Data Probe: /var/folders/zw/gbtj9p4d...angeTrackerScene.mrml

S: 29.250mm 1

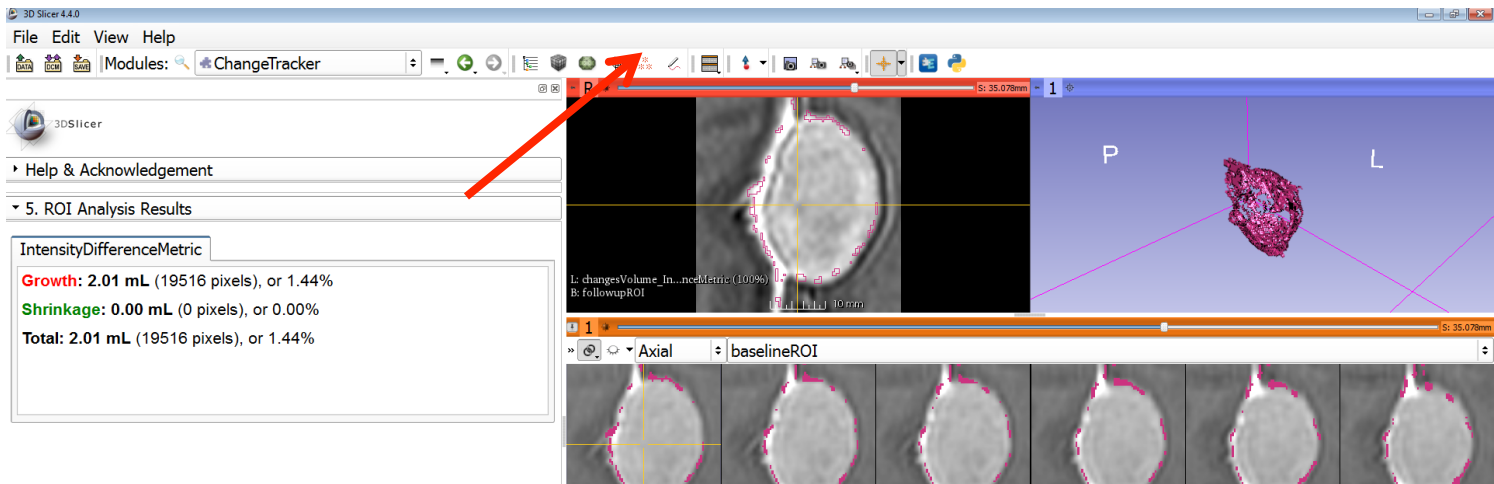
R: -2.714mm G: A: 28.056mm

Select the Basic Setting
'Intensity Difference Change Detection (FAST)'

Click on the green arrow
to move to the next step



Step4: Select the Analysis Method

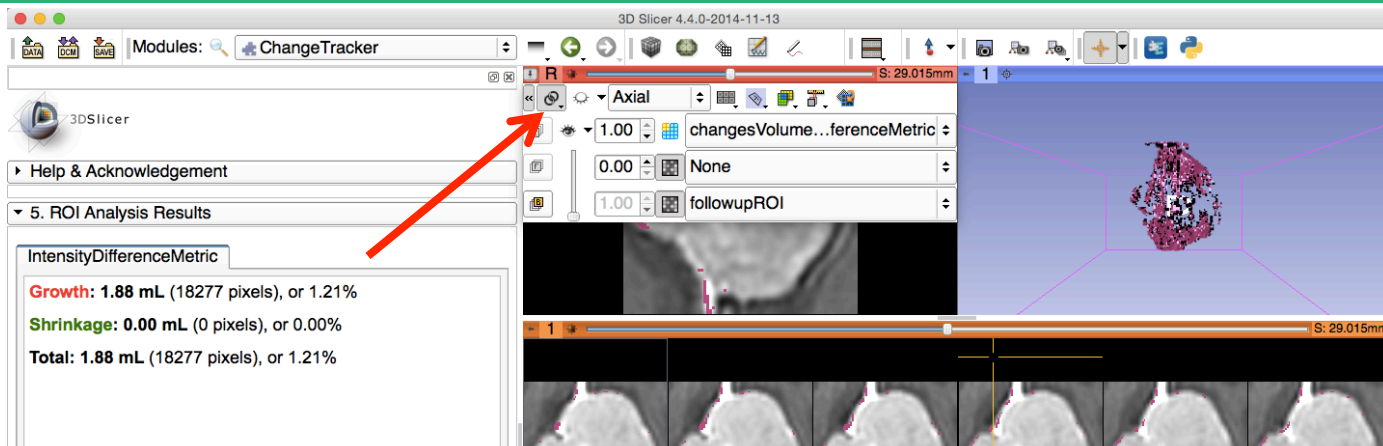


Left click on the slice menu to display the volumes that have been generated:


- **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

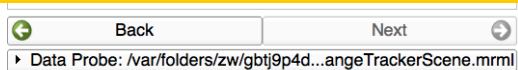


Step4: Select the Analysis Method



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

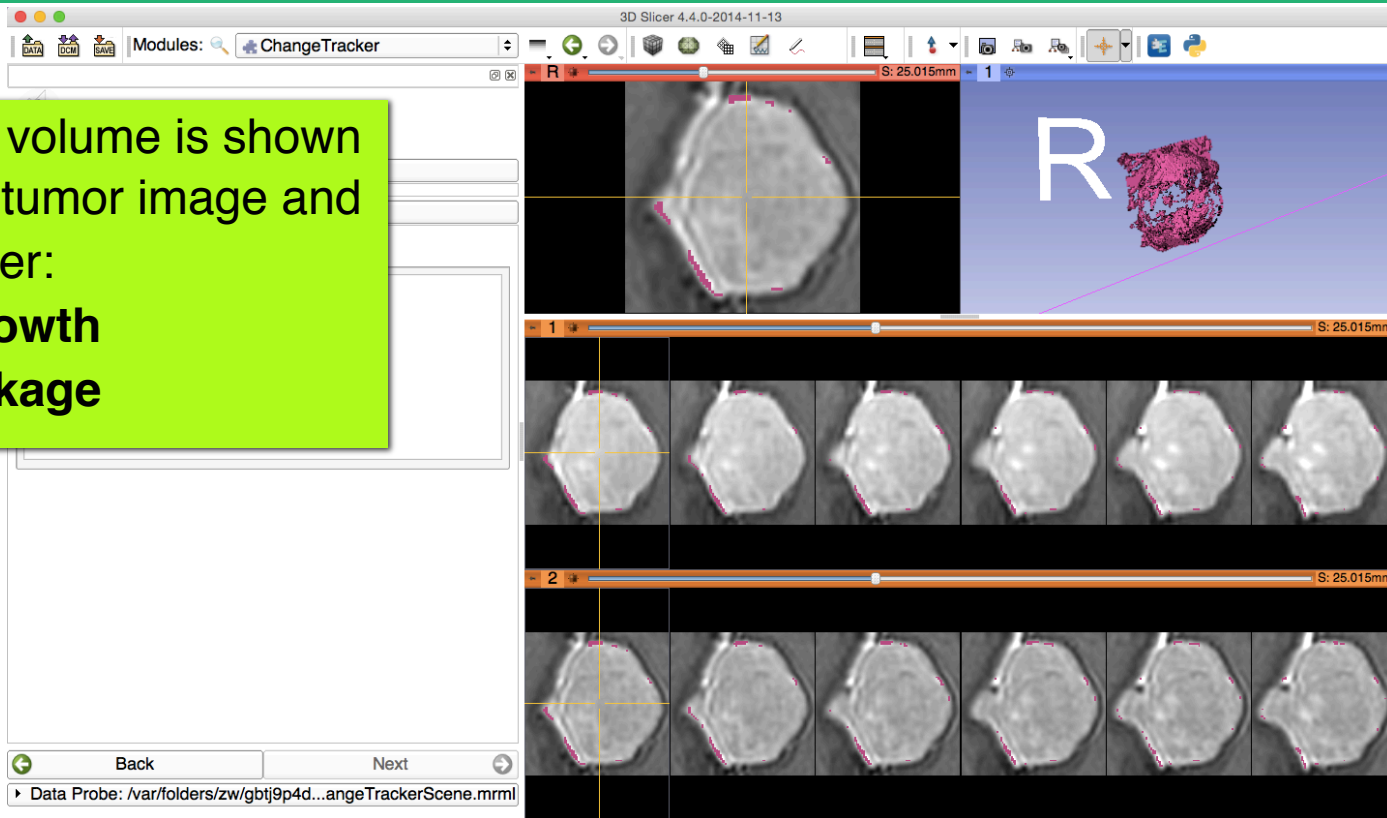




Final Step: Change Tracker Results

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

magenta = growth
green = shrinkage

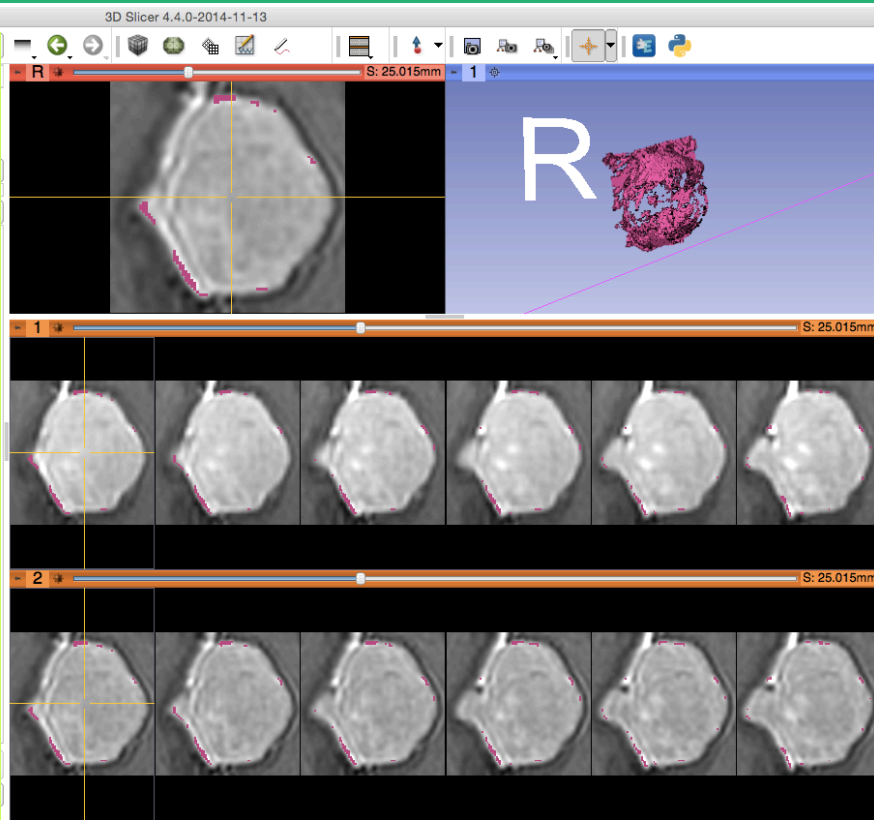




Visualization of the change in pathology

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

- BaselineROI: Six consecutive slices for the ROI in Baseline Scan (**top row**), and
- FollowupROI: Six corresponding consecutive slices for the ROI in Follow Up Scan (**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.

5. ROI Analysis Results

IntensityDifferenceMetric

Growth: 1.88 mL (18277 pixels), or 1.21%

Shrinkage: 0.00 mL (0 pixels), or 0.00%

Total: 1.88 mL (18277 pixels), or 1.21%

Back Next

Data Probe: /var/folders/zw/gbtj9p4d...angeTrackerScene.mrml



Change Tracker Results

3D Slicer 4.4.0-2014-11-13

Modules: ChangeTracker

3DSlicer

Help & Acknowledgement

5. ROI Analysis Results

IntensityDifferenceMetric

Growth: 1.88 mL (18277 pixels), or 1.21%

Shrinkage: 0.00 mL (0 pixels), or 0.00%

Total: 1.88 mL (18277 pixels), or 1.21%

The metrics calculated indicate the volume and percentage of tumor growth between the two time points.

changesVolume...ferenceMetric

1.00

0.00

1.00

None

followupROI

R

S: 29.703mm

1

baselineROI

changesVolume_IntensityDifferenceMetric

1.00

0.00

1.00

None

followupROI

2

S: 29.703mm

Back

Next

Data Probe: /var/folders/zw/gbtj9p4d...angeTrackerScene.mrml



Change Tracker module

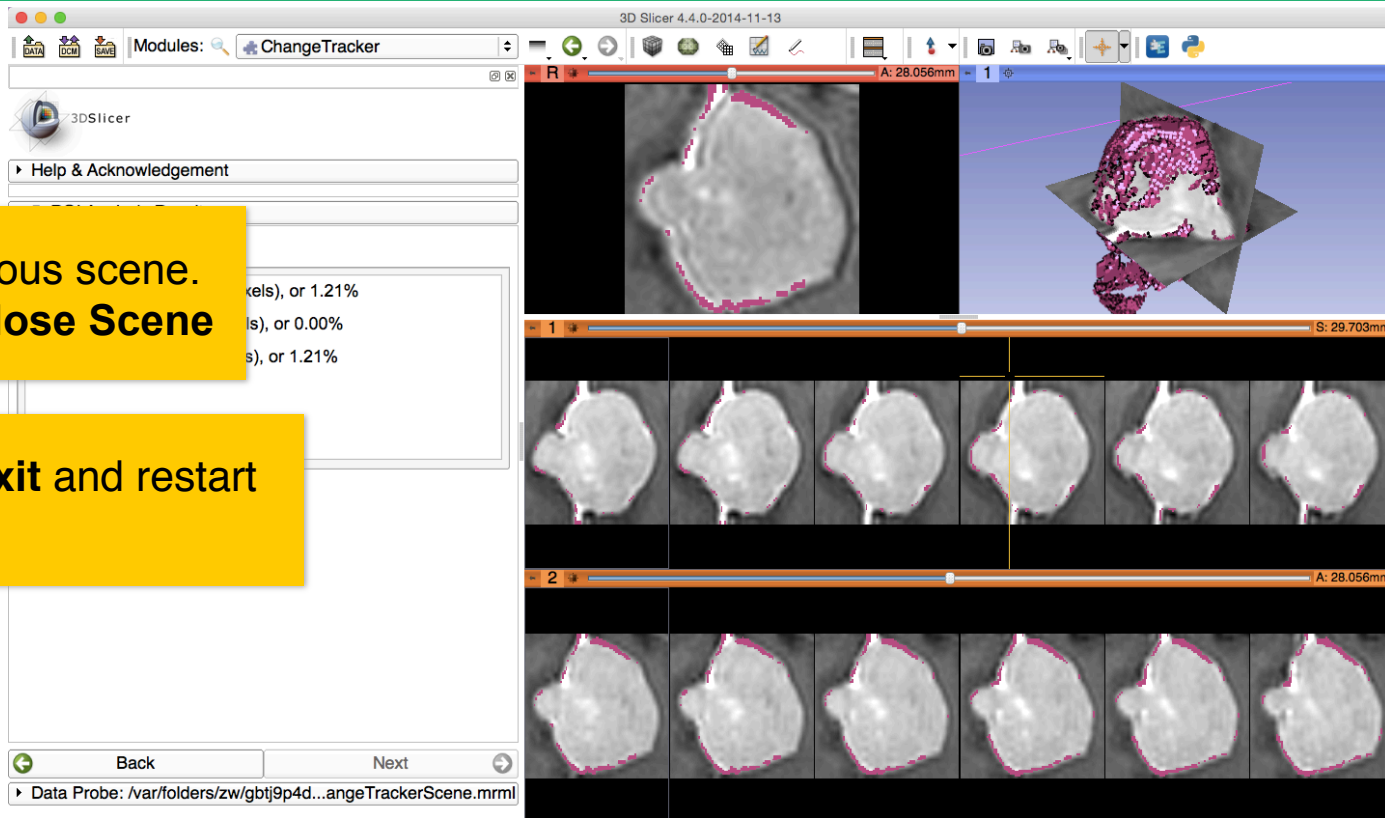
- The 3D Slicer ChangeTracker module is a research tool for evaluating volumetric changes and bring additional complementary information to RECIST measurements
- However, three current requirements are needed for Change Tracker to produce adequate measurements:
 - 1) **Clear Tumor boundaries**
 - 2) **Contrast enhanced images only**
 - 3) **Homogenous enhancement across timepoints**
- The Change Tracker module has not been tested for tumors with changing necrosis.



Clear the scene and its data

Clear the previous scene.
Select **File**->**Close Scene**

Select **File**->**Exit** and restart
Slicer





ChangeTracker: Exploring small volumetric changes

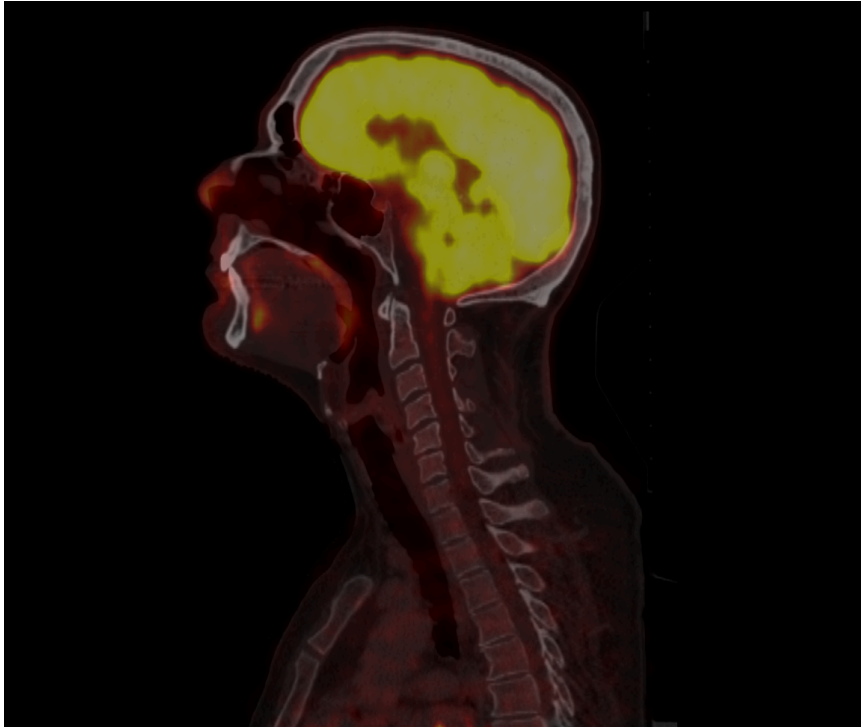
This tutorial demonstrated:

- 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.



PET/CT Visualization and Analysis

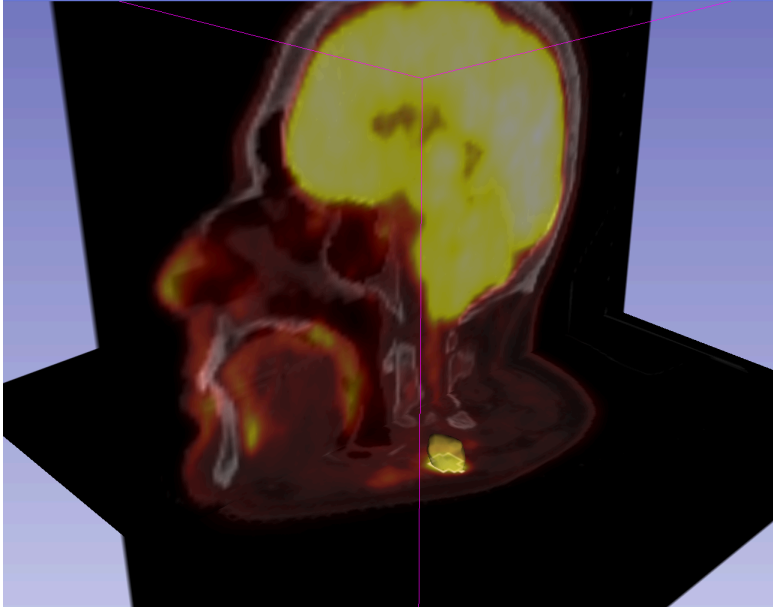


Part III: PET/CT Analysis

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 Standard Uptake Value (SUV) computation of PETCT data of a squamous cell carcinoma case, pre- and post- treatment



FDG-PET SUV

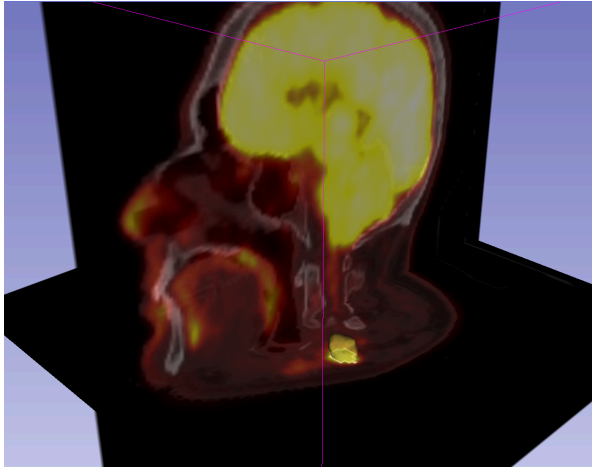
- Standardized Uptake Value (SUV) is a semi-quantitative measure derived from the determination of tissue activity obtained from a clinical PET study

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

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



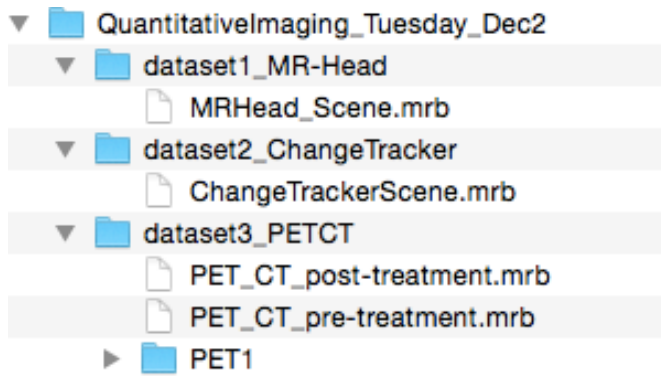
Tutorial Case



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



PETCT tutorial: Clinical Case and Data



The datasets are located in

\dataset3_PETCT

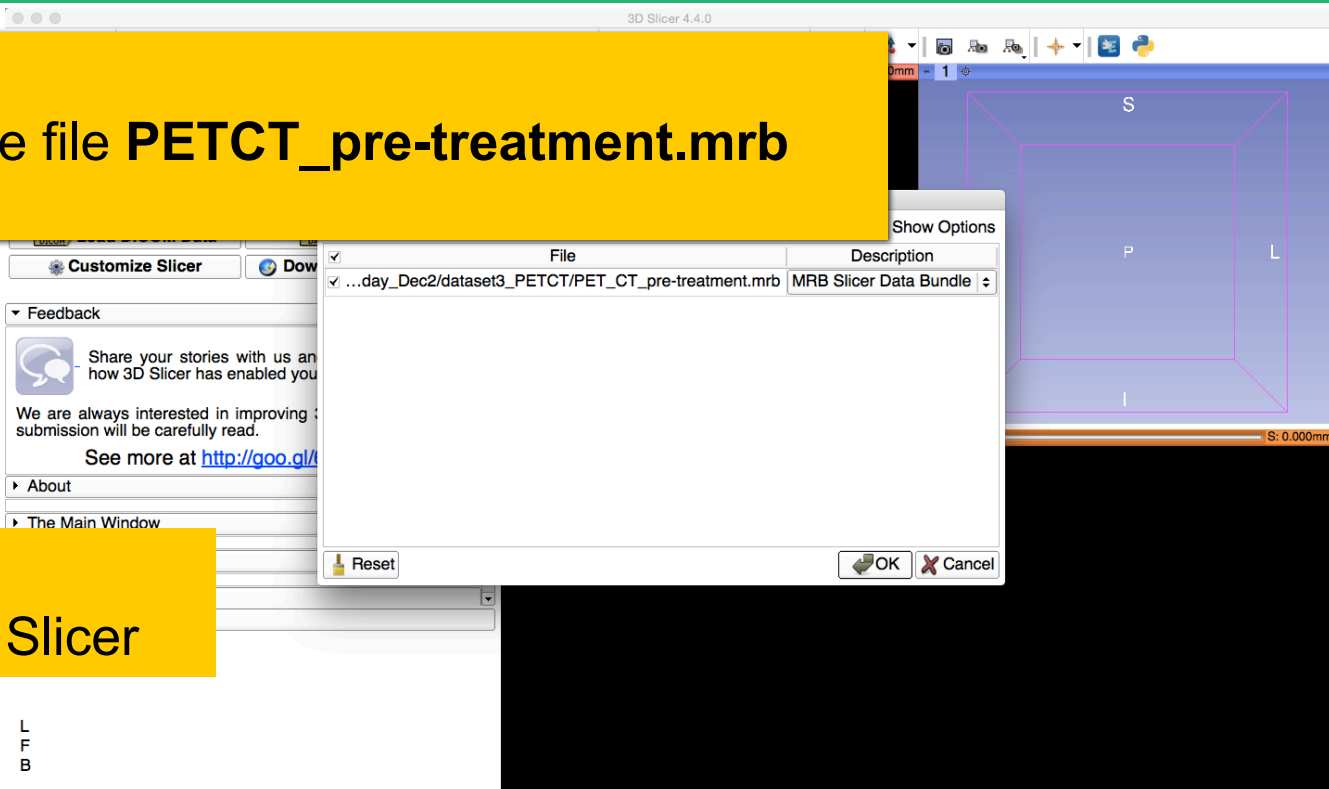
The directory contains two .mrb files

- **PET_CT_pre-treatment.mrb**
corresponds to the baseline
- **PET_CT_post-treatment.mrb**
corresponds to the follow-up scan.



Loading the PETCT scene

Drag and drop the file **PETCT_pre-treatment.mrb**



L
F
B

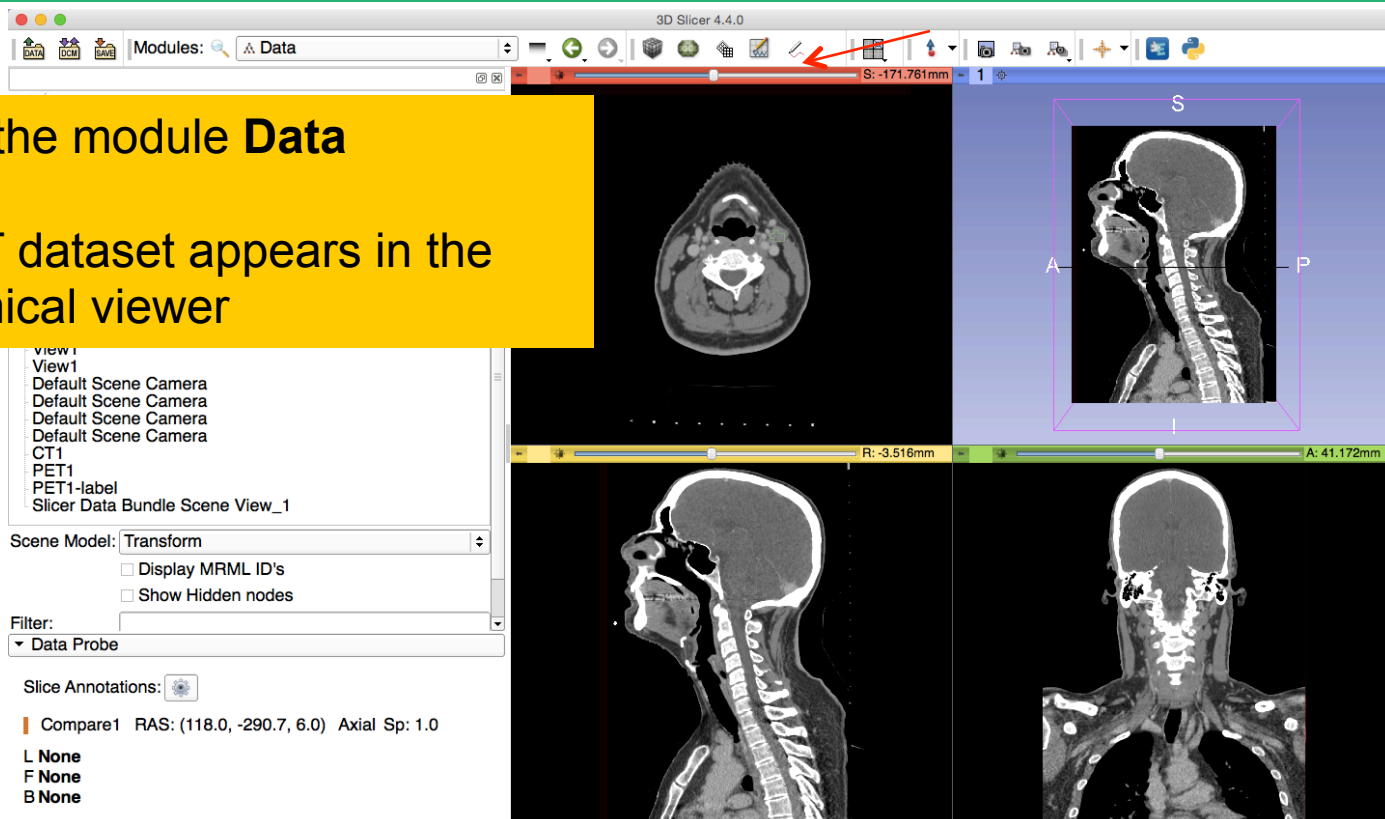
Click OK to load the .mrb file into Slicer



Loading the PETCT scene

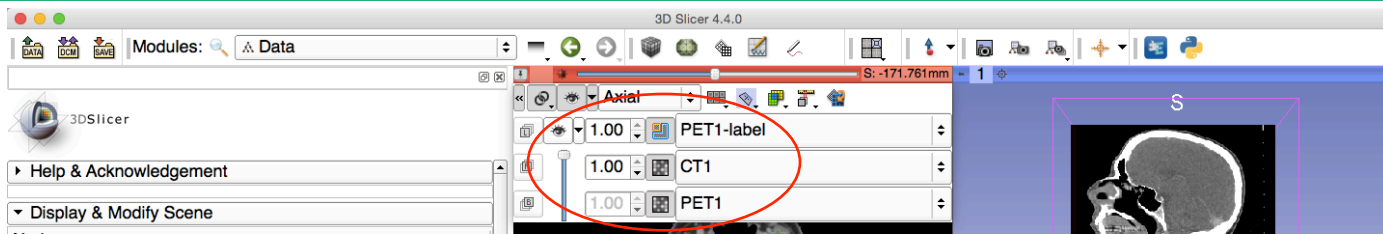
Select the module **Data**

The CT dataset appears in the anatomical viewer





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

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

L
F
B





Visualization of PETCT data

3D Slicer 4.4.0

Modules: Data

Axial S: -171.761mm

1

3DSlicer

Help & Acknowledgement

Display & Modify Scene

Nodes

- Scene
 - View1
 - Default Scene Camera
 - Compare1
 - View1
 - View1
 - View1
 - Default Scene Camera
 - Default Scene Camera
 - Default Scene Camera
 - Default Scene Camera
 - CT1
 - PET1
 - PET1-label
 - Slicer Data Bundle Scene View_1

Scene Model: Transform

- Display MRML ID's
- Show Hidden nodes

Filter:

Data Probe: /var/folders/zw/gbtj9p4d...CT_pre-treatment.mrml

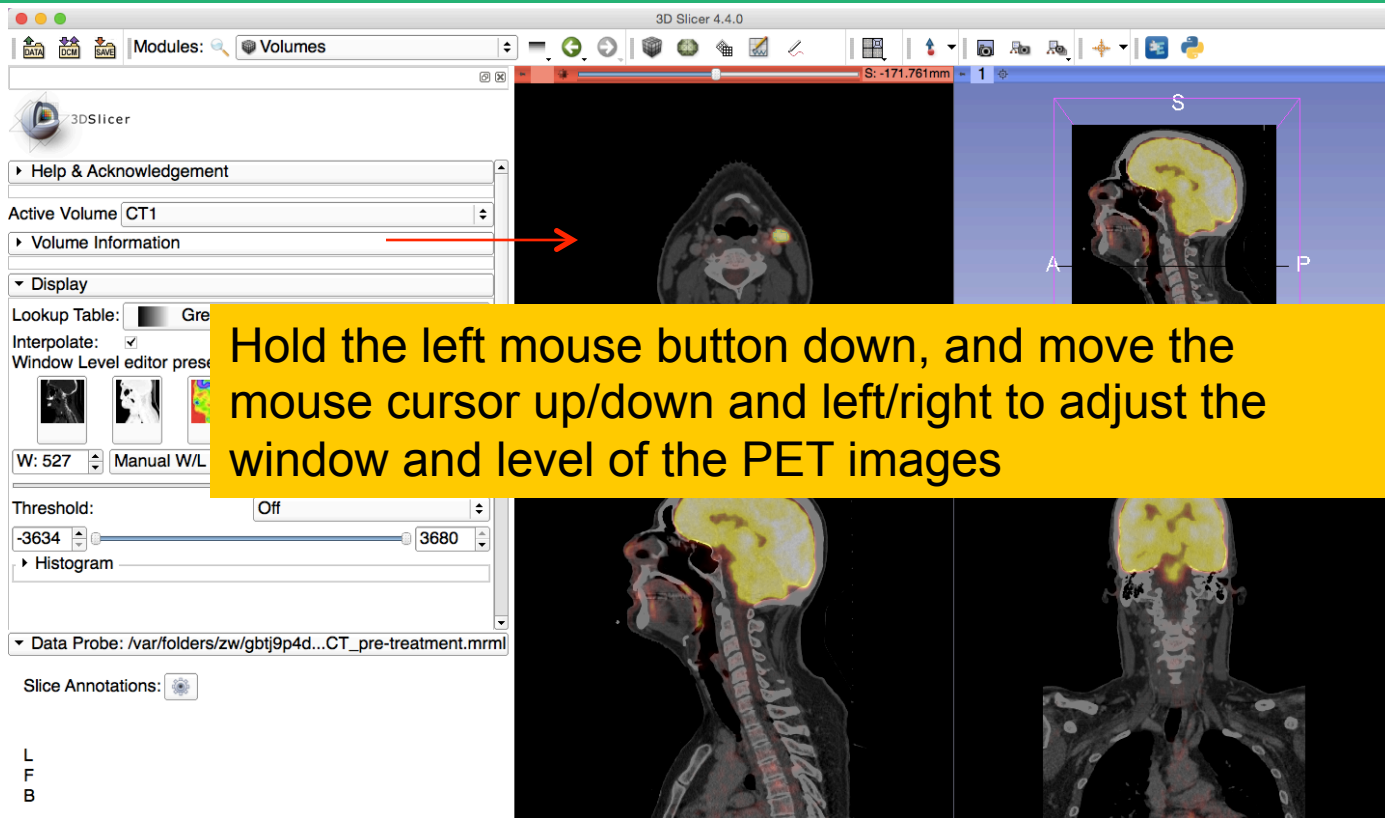
Slice Annotations:

L
F
B

Change the opacity of the CT1 volume to 0.50 to display the CT images overlaid on the PET images



Visualization of PETCT data

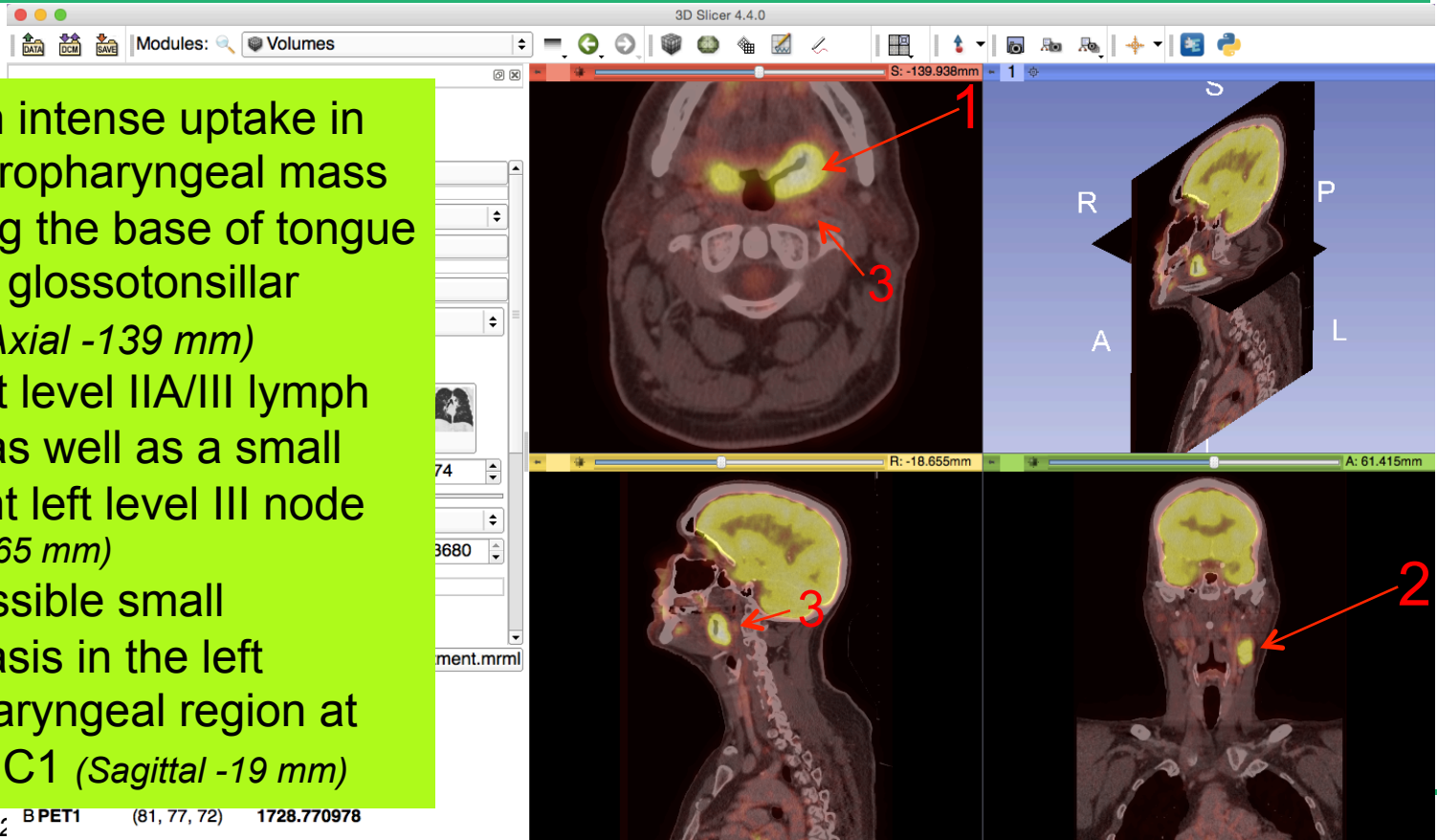




PET uptake findings

Note an intense uptake in

- 1) left oropharyngeal mass involving the base of tongue and left glossotonsillar fossa (*Axial -139 mm*)
- 2) in left level IIA/III lymph nodes as well as a small adjacent left level III node (*Coronal 65 mm*)
- 3) a possible small metastasis in the left retropharyngeal region at level of C1 (*Sagittal -19 mm*)

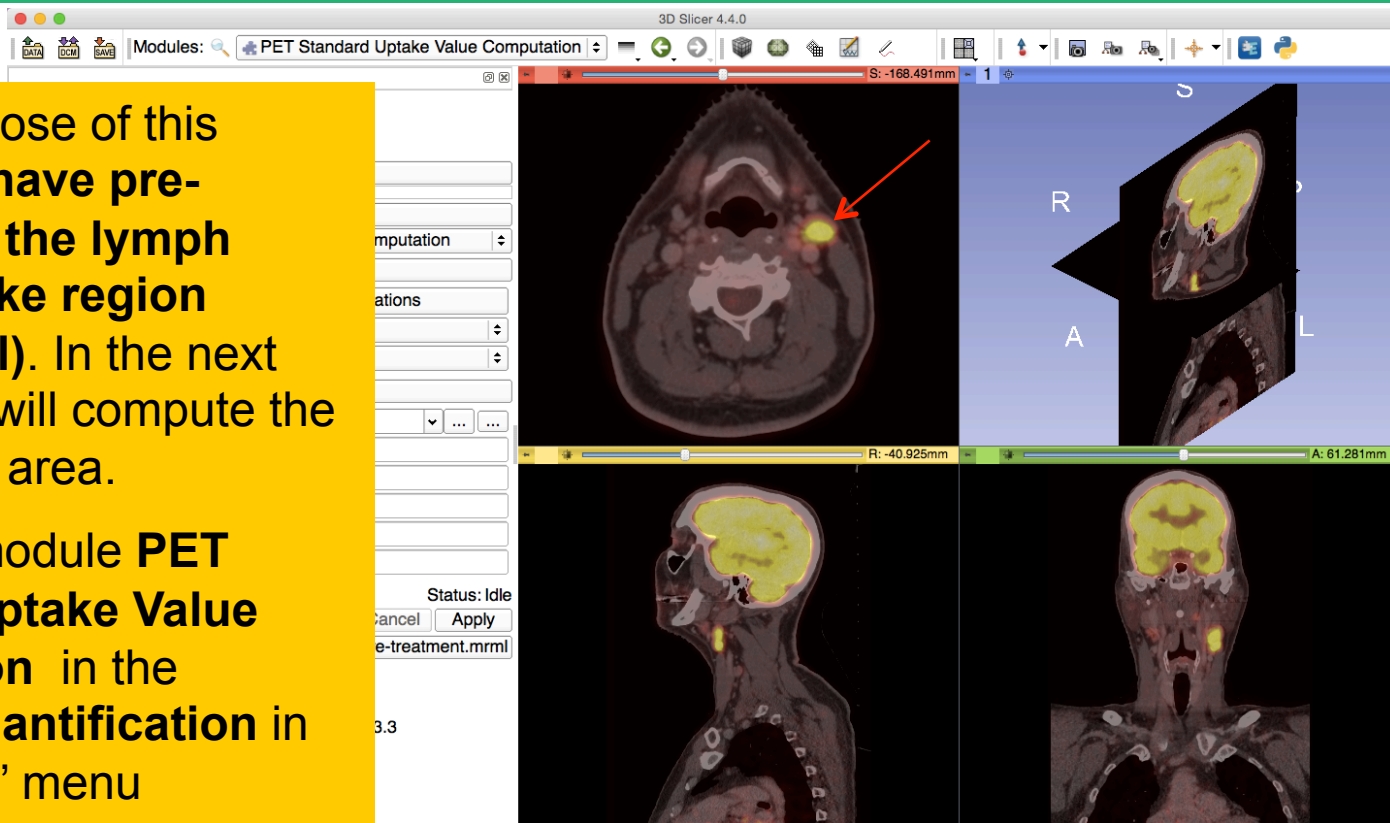




PET SUV Computation

For the purpose of this tutorial, we have **pre-segmented the lymph nodes uptake region (PET1_label)**. 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

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

3D Slicer 4.4.0

Modules: PET Standard Uptake Value Computation

Output:

Output (csv) file: []

Output Label: []

Output Label Value: []

SUV Max: []

SUV Mean: []

SUV Minimum: []

Status: Idle

Restore Defaults AutoRun Cancel Apply

Data Probe: /var/folders/zw/gbtj9p4d...CT_pre-treatment.mrml

Slice Annotations: []

Red RAS: (-66.4, 17.8, -168.5) Axial Sp: 3.3

L PET1-label (92, 73, 63) 0 (0)

F CT1 (369, 279, 164) -393

B PET1 (92, 73, 63) 2234.197454



PET SUV Computation

Step1: Input volumes selection

Select Input PET Volume 'PET1'

Select Input VOI Volume 'PET1-label'

Input PET Volume: PET1

Input VOI Volume: PET1-label

Output

Output (csv) file: []

Output Label: []

Output Label Value: []

SUV Max: []

SUV Mean: []

SUV Minimum: []

Status: Idle

Restore Defaults | AutoRun | Cancel | Apply

Data Probe: /var/folders/zw/gbtj9p4d...CT_pre-treatment.mrml

Slice Annotations: []

L
F
B



Step2: Path to the DICOM PET header

Click on **C:/RSNA Hands-on/S401AB/RCA23 Pujol/Slicer-4.4.0-win-
amd64-RSNA**

▸ Help & Acknowledgement

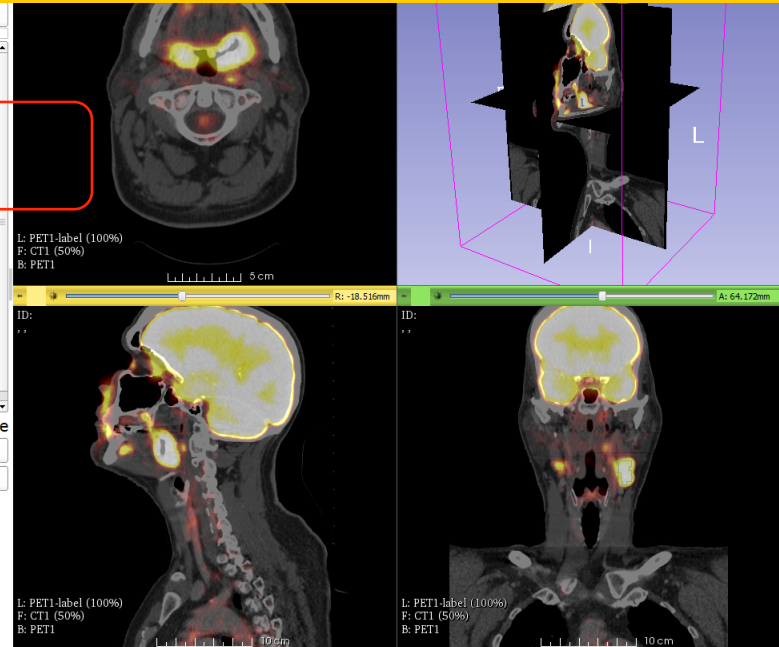
▾ PET Standard Uptake Value Computation
Parameter set: PET Standard Uptake Value Computation

▾ Image and Information
PET DICOM volume path **C:/RSNA Hands-On/S401AB/RCA23 Pujol/Slicer-4.4.0-win-amd64-RSNA**
Input PET Volume PET1
Input VOI Volume PET1-label

▾ Output
Output (csv) file
Output Label
Output Label Value
SUV Max
SUV Mean
SUV Minimum

Status: Idle
Restore Defaults AutoRun Cancel Apply

▾ Data Probe: C:/Users/ADMINI~1/AppDat...CT_pre-treatment.mrml

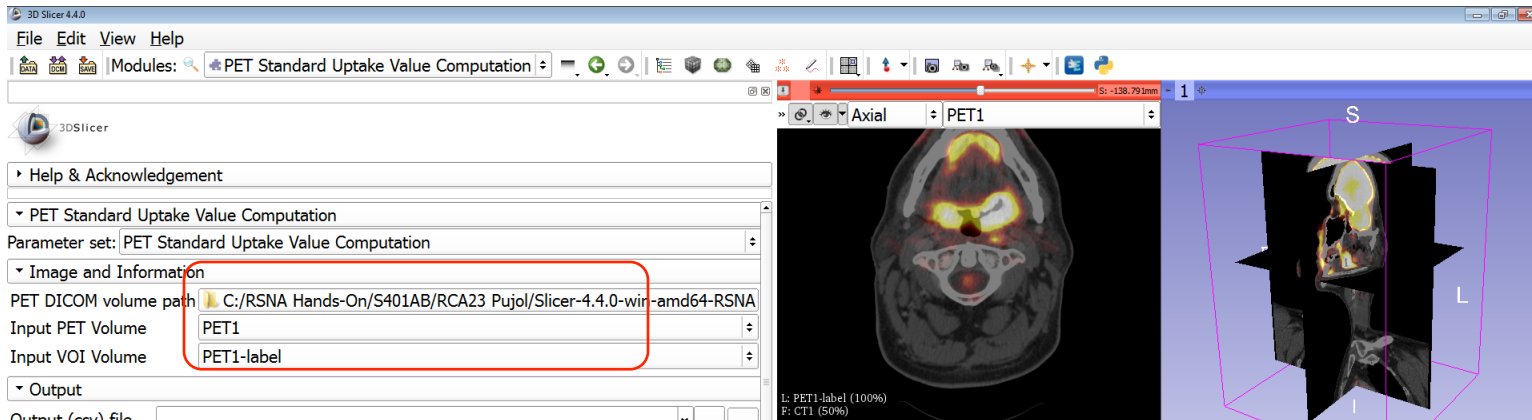


L
F
B





PET SUV Computation



Browse to the **\PET1** directory located under

C:\Users\Administrator\Desktop

\QuantitativeImaging_Tuesday_Dec2\QuantitativeImaging_Tuesday_Dec2\dataset3_PETCT

Click on **Choose** to select the PETDICOM volume path





PET SUV Computation

Step3: SUV Computation

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

3D Slicer 4.4.0

Modules: PET Standard Uptake Value Computation

S: -168.491mm

Output

Output (csv file)

Output Label 1

Output Label Value 1

SUV Max 7.53385

SUV Mean 5.01805

Status: Completed 100%

Restore Defaults AutoRun Cancel **Apply**

Data Probe: /var/folders/zw/gbtj9p4d...CT_pre-treatment.mrm

Slice Annotations: [icon]

L
F
B

R
A
L

R: -40.925mm A: 61.281mm



PET SUV Computation

SUV Computation Results:

SUVmax = 7.53385 mg/ml

SUVmean = 5.01805 mg/ml

SUVmin = 3.39015 mg/ml

▼ Output

Output (csv file)

Output Label

Output Label Value 1

SUV Max	7.53385
SUV Mean	5.01805
SUV Minimum	3.39015

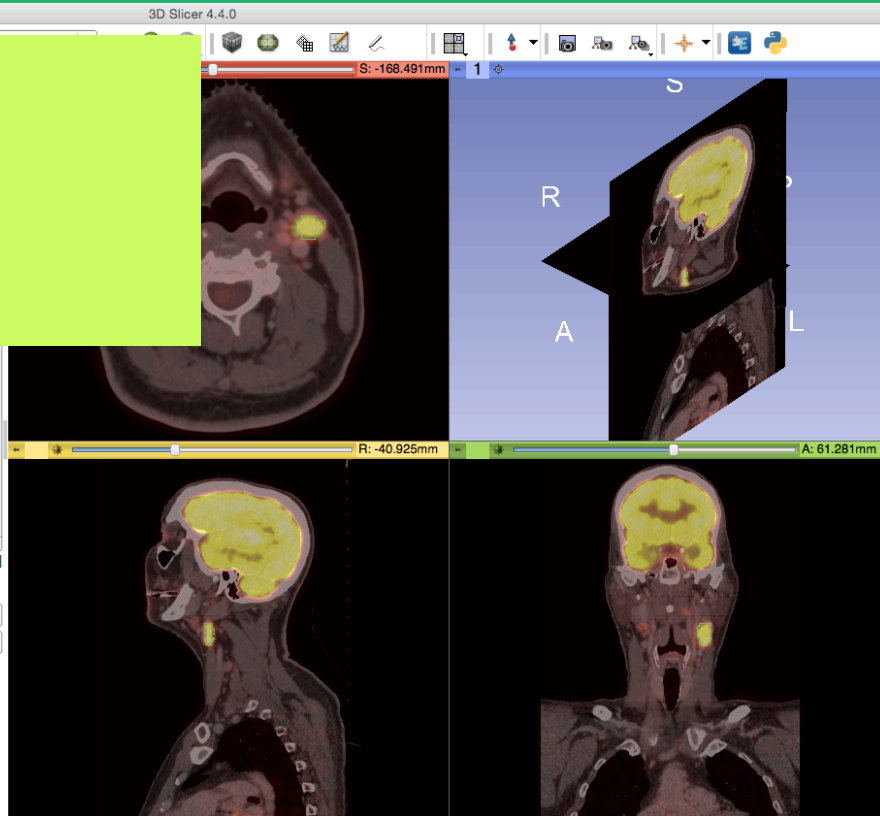
Status: Completed

100%

Restore Defaults AutoRun Cancel Apply

▼ Data Probe: /var/folders/zw/gbtj9p4d...CT_pre-treatment.mrml

L
F
B





PET SUV Computation

Select File → Close Scene in the main menu

PET DICOM volume path

Input PET Volume

Input VOI Volume

Output

Output (csv) file

Output Label

Output Label Value

SUV Max

SUV Mean

SUV Minimum

Status: Completed

Data Probe:

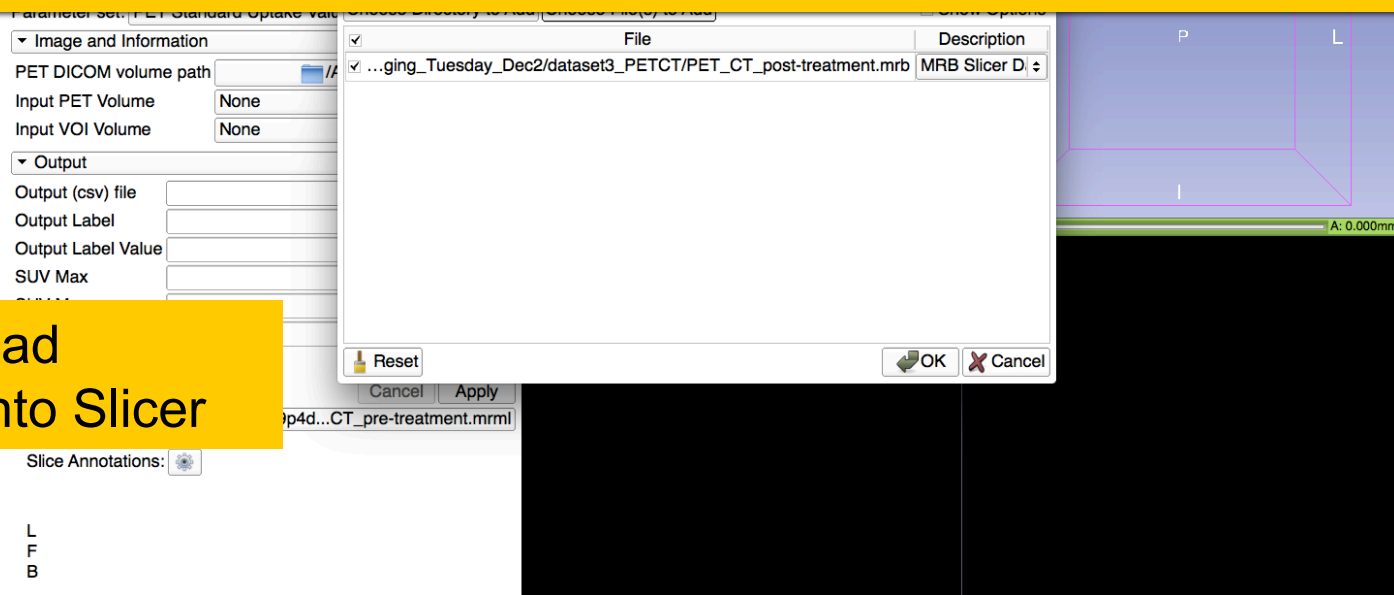
Slice Annotations:

L
F
B



Loading the PETCT scene

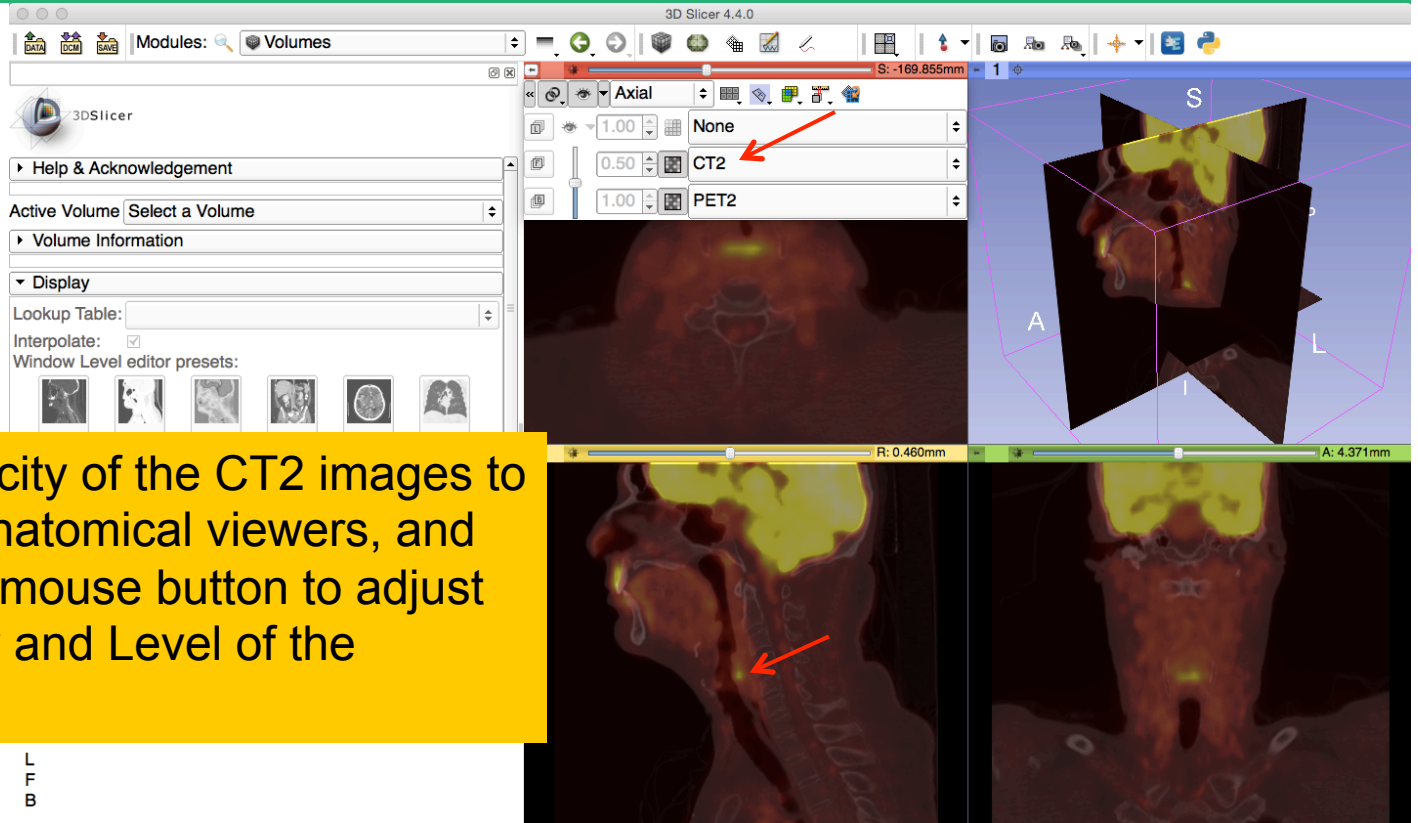
Drag and drop the file **PETCT_post-treatment.mrb** located in **dataset3_PETCT**



Click OK to load the .mrb file into Slicer



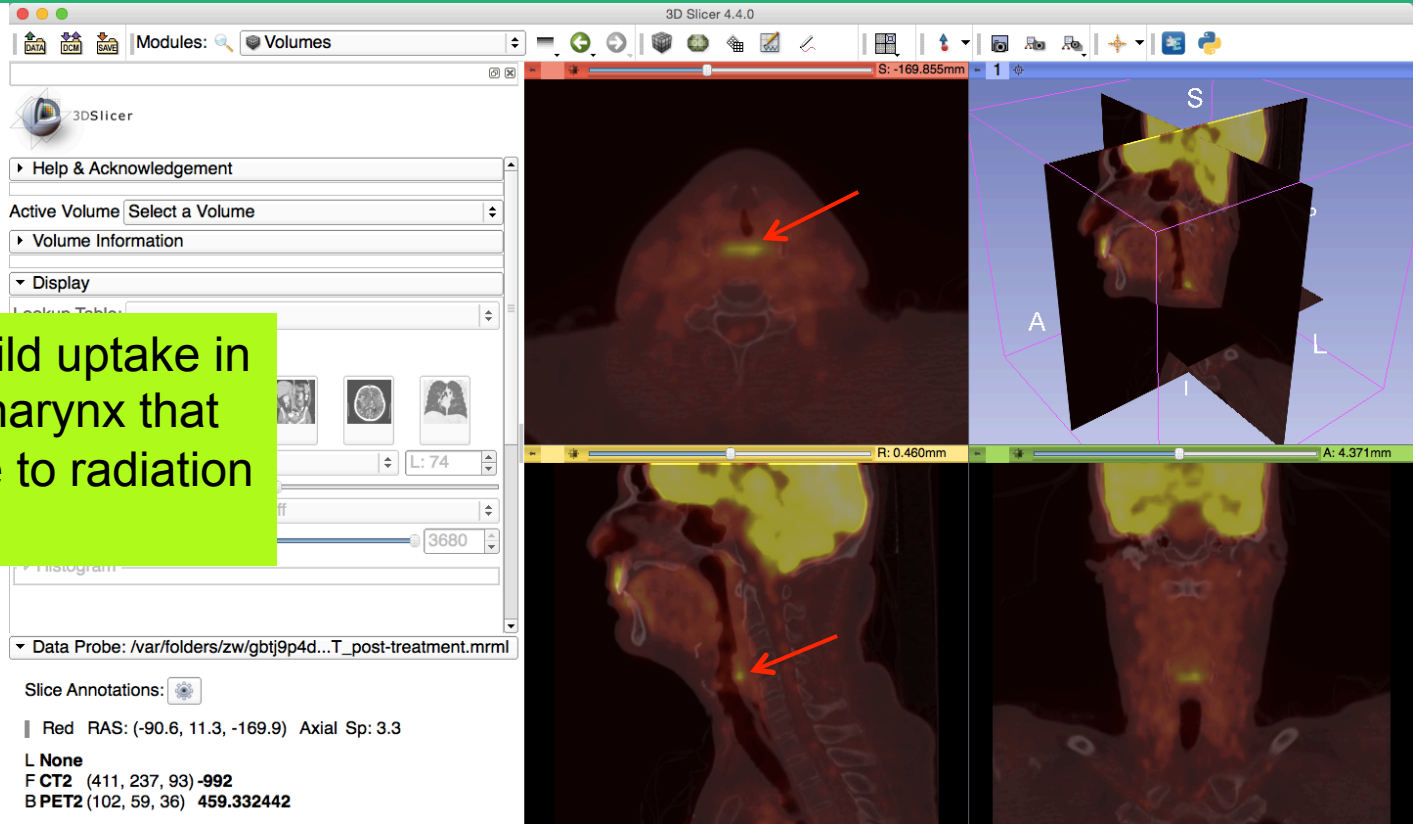
PET uptake findings





PET uptake findings

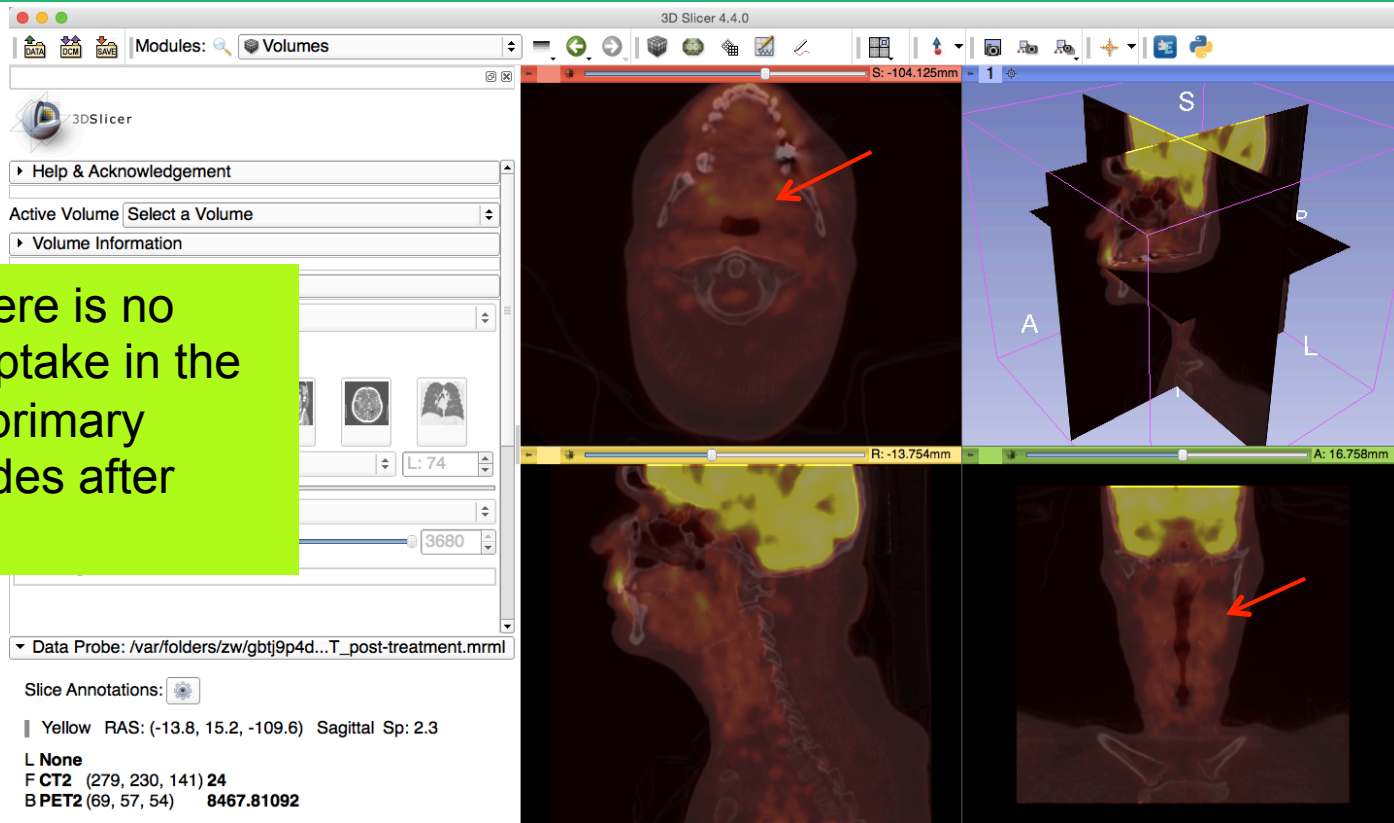
Observe a mild uptake in larynx and pharynx that are likely due to radiation effect.





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 the 3D Slicer modules for quantitative imaging
- Continuous advances are being made in imaging technology and post-processing software tools
- The intersection of quantitative and clinical sciences offers great promise to help improve outcome prediction and tumor response to therapy



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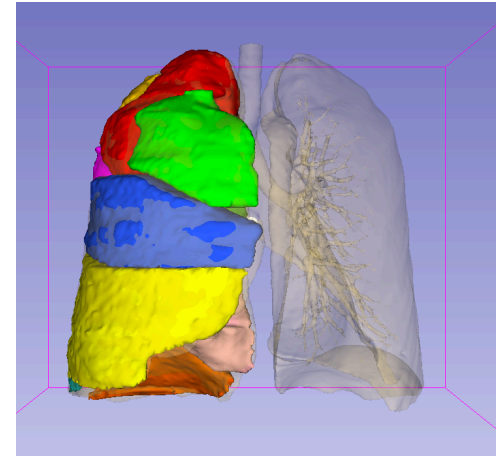
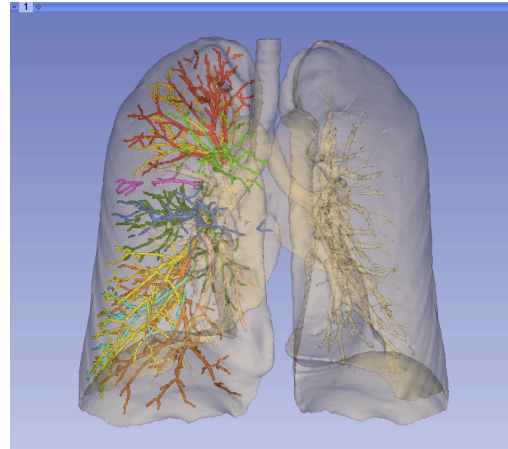


3DSlicer at RSNA 2014

Quantitative Imaging Reading Room, Exhibit LL-QRR3007

- Tue. Dec.2-Fri. Dec.5, 8:00-6:00
- 3D Slicer: 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,

www.slicer.org



Questions and comments:

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