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

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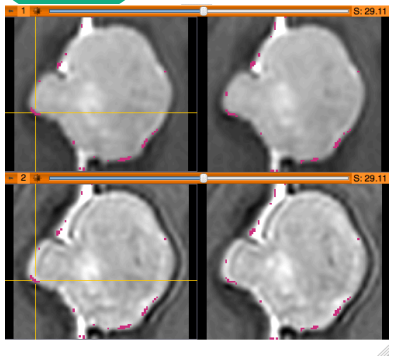
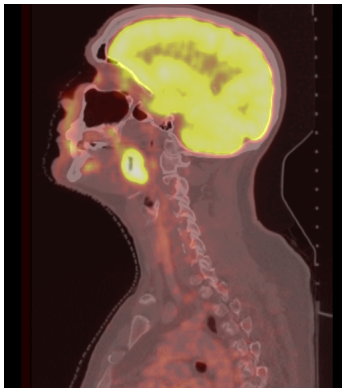
Brigham and Women's Hospital, Harvard Medical School,
Johns Hopkins University
Boston University Medical Center

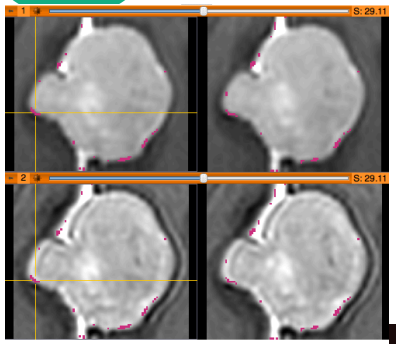
Quantitative Imaging Tutorial

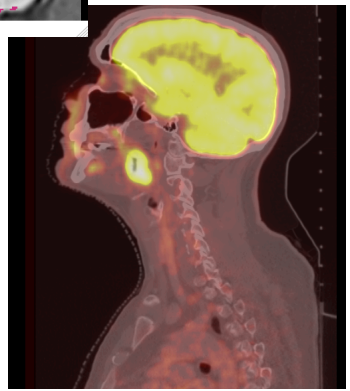




- Quantitative Imaging techniques can be used to give radiologists complementary information for interpreting images
- The hands-on aspect of the course is intended to give clinical researchers a **practical experience on the latest methods developed in medical research**

Quantitative Imaging Tutorial

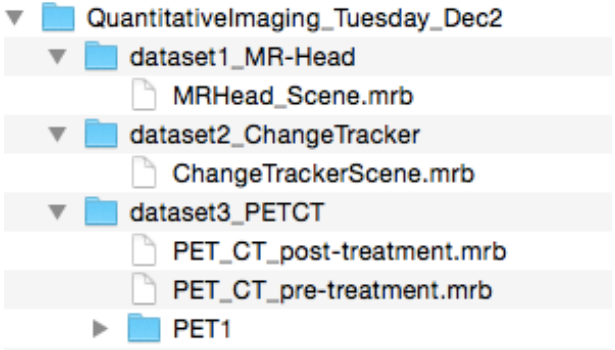




This tutorial is built upon a series of examples of quantitative imaging analysis:

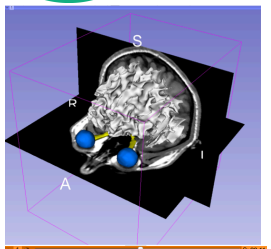
- **Morphology**: volumetric changes in brain and breast tumors
- **Function**: metabolic activity in squamous cell carcinoma

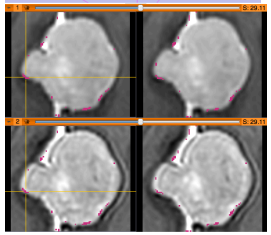
Tutorial Materials

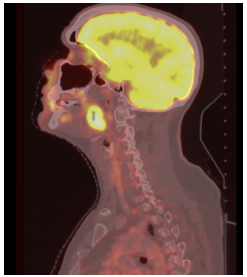


- **Software:** 3D Slicer
- **Datasets:** QuantitativeImaging_Tuesday_Dec2

Tutorial Overview







Part 1: Introduction to 3D Slicer

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

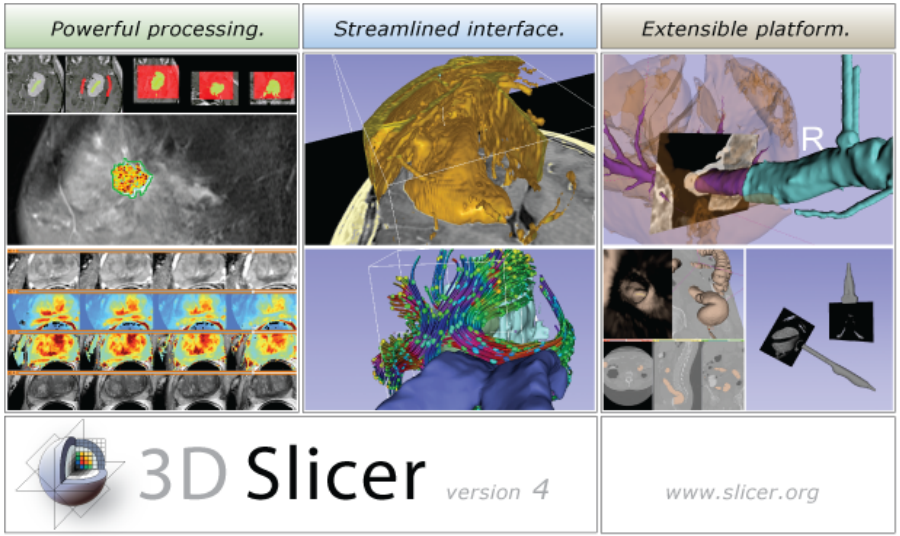
Part 3: Measurement of volumetric changes

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

Part 4: Measurement of metabolic activity

- squamous cell carcinoma case

3D Slicer



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

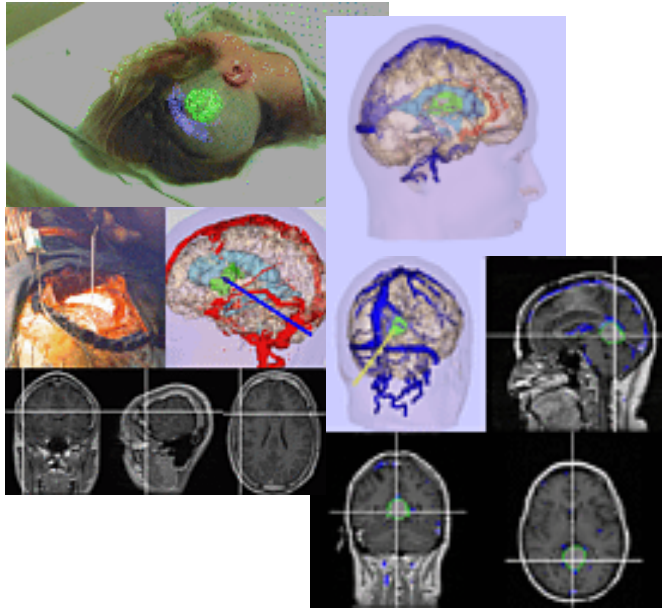
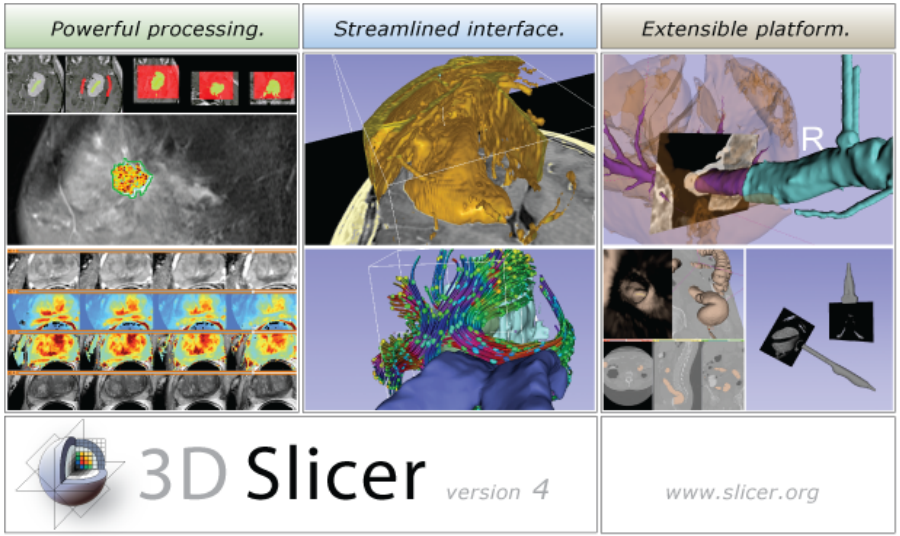


Image Courtesy of the CSAIL, MIT

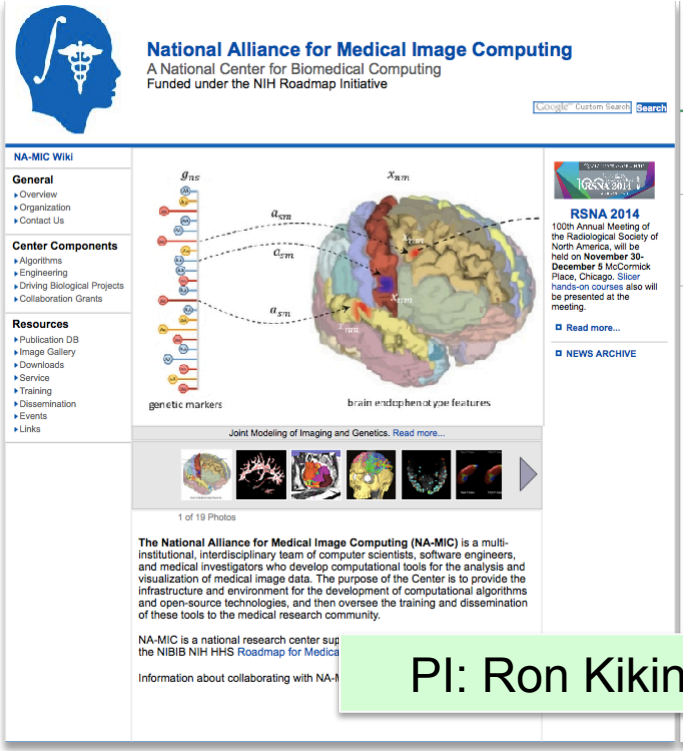
- 1997: Slicer started as a research project between the Surgical Planning Lab (Harvard) and the CSAIL (MIT)

3DSlicer History

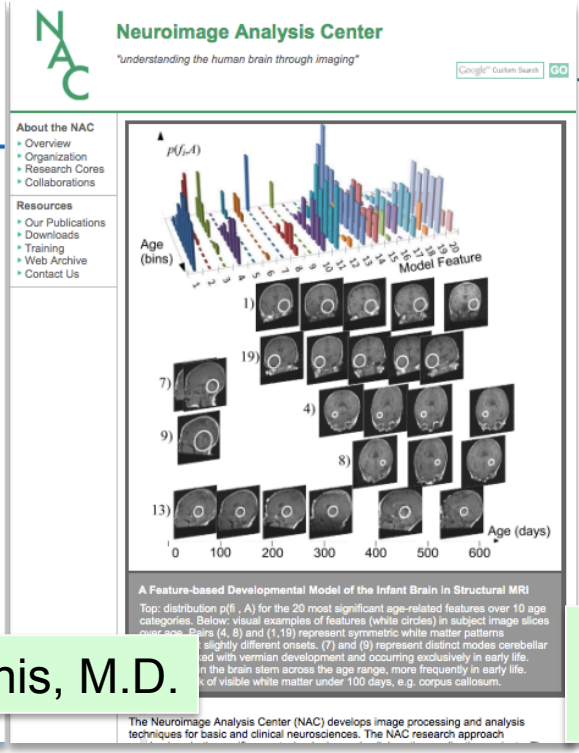


- 1997: Slicer started as a research project between the Surgical Planning Lab (Harvard) and the CSAIL (MIT)
- 2014: Multi-institution effort to share the latest advances in image analysis with clinicians and scientists

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

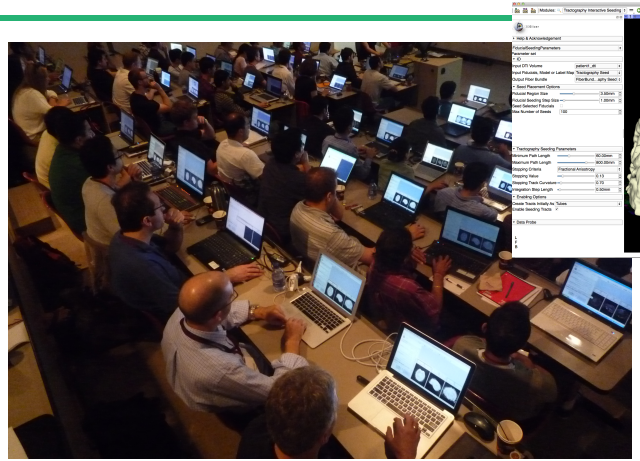


PI: Ron Kikinis, M.D.

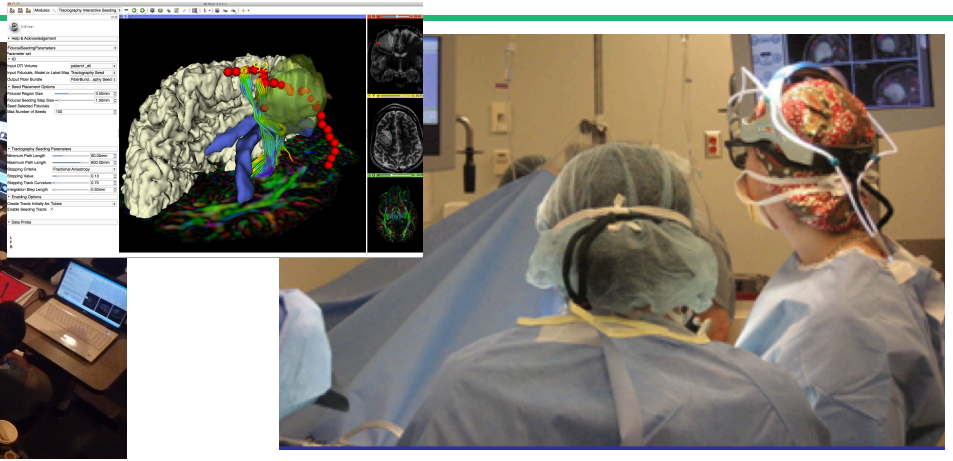


PIs: Ferenc Jolesz, M.D., Clare Tempany, M.D.

An interdisciplinary platform



An open-source environment for software developers



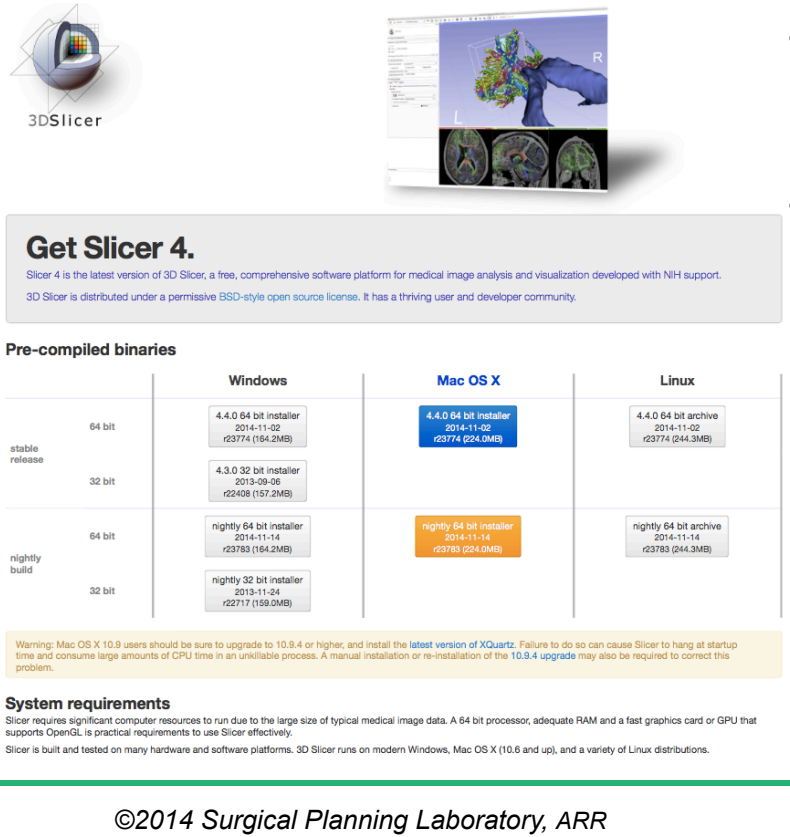
An end-user application for clinical investigators and scientists

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

An extensible platform

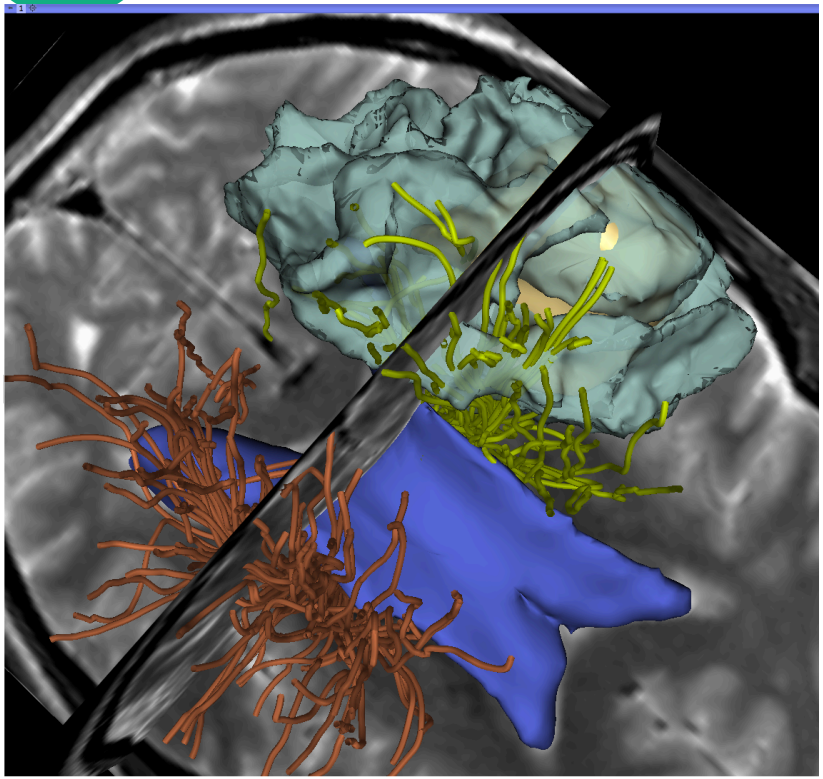
- 3D Slicer supports plug-ins called Slicer extensions available from the Extension Manager
- Allows end-users to select extensions useful to them, without having to download the entire extension archive.
- Built Nightly with Slicer

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

3D Slicer in practice



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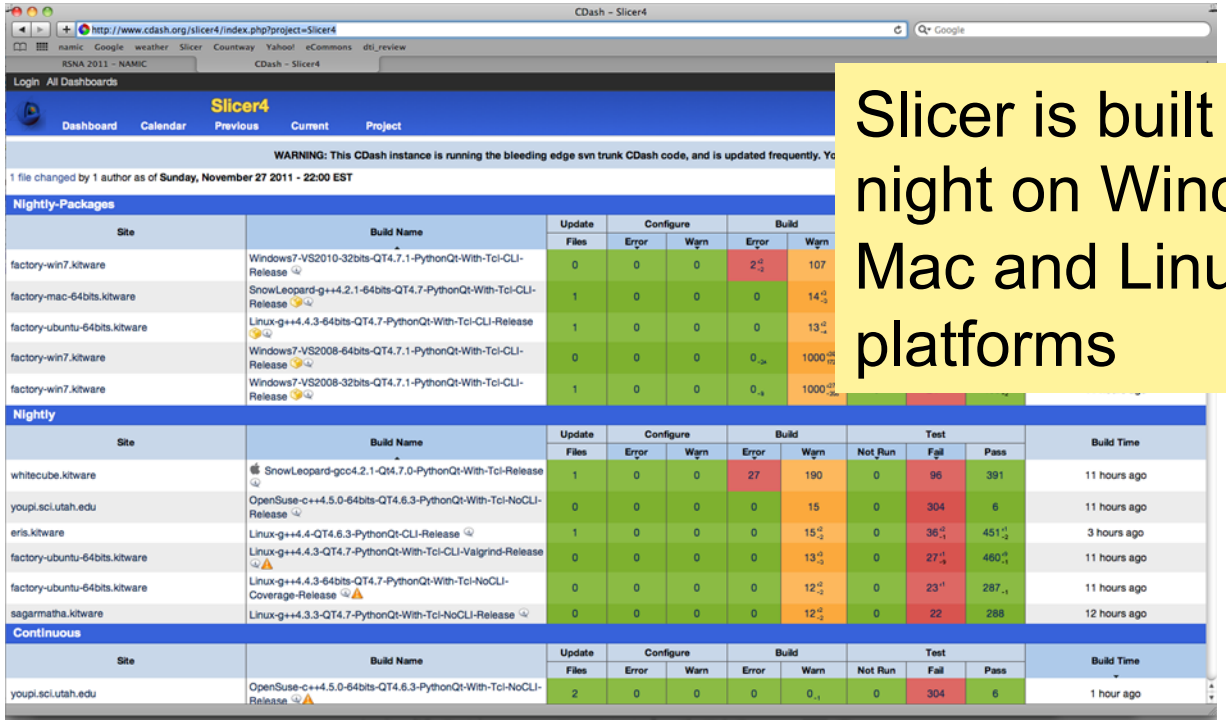
- Slicer is distributed under a BSD-style license agreement with no restriction on use
- 3D Slicer is for clinical research use only, and is not FDA approved or CE-marked.

Slicer: Behind the scenes



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

An extensible platform

- 3D Slicer supports plug-ins called Slicer extensions available from the Extension Manager
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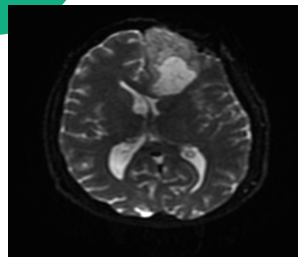
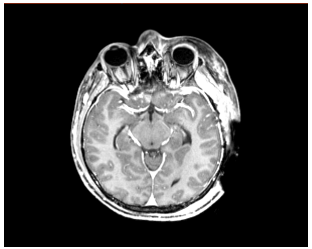
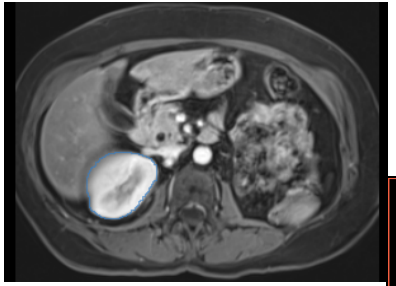
Training Portfolio

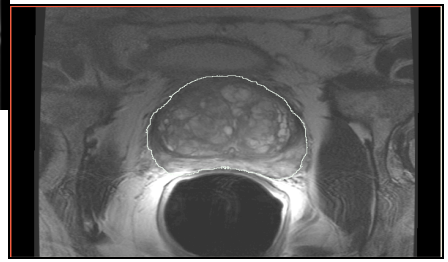
- Modular multi-level training for expert and non-expert community
- Tutorials and anonymized datasets for end-users and developers
- Cross platform testing for quality control

Slicer clinical applications



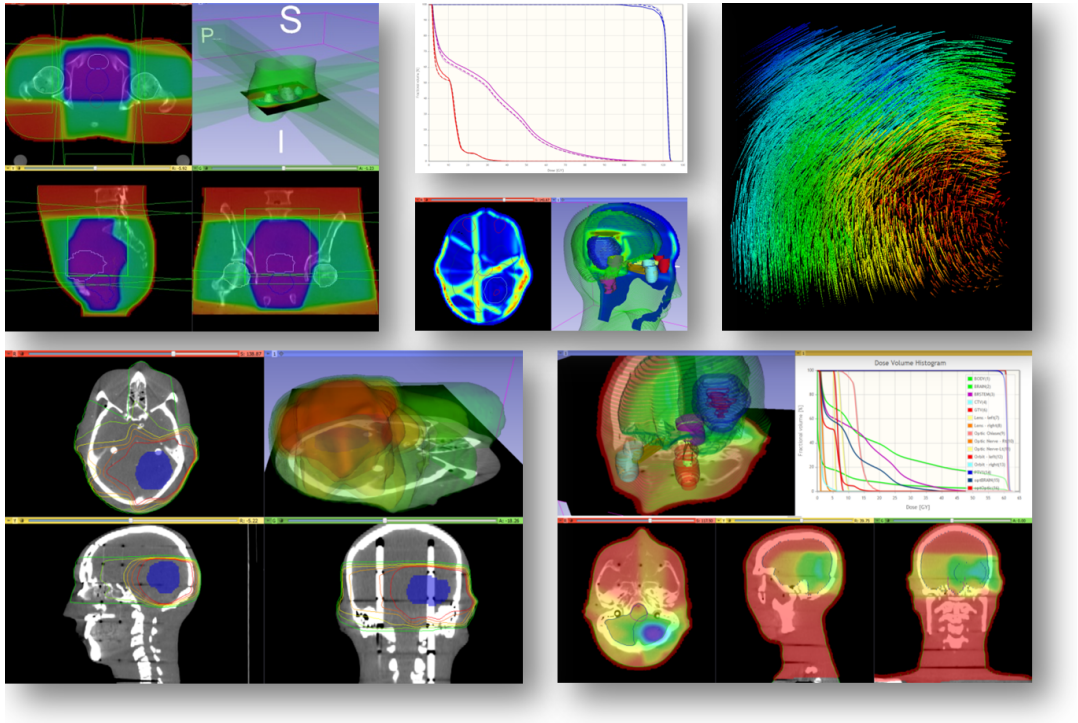






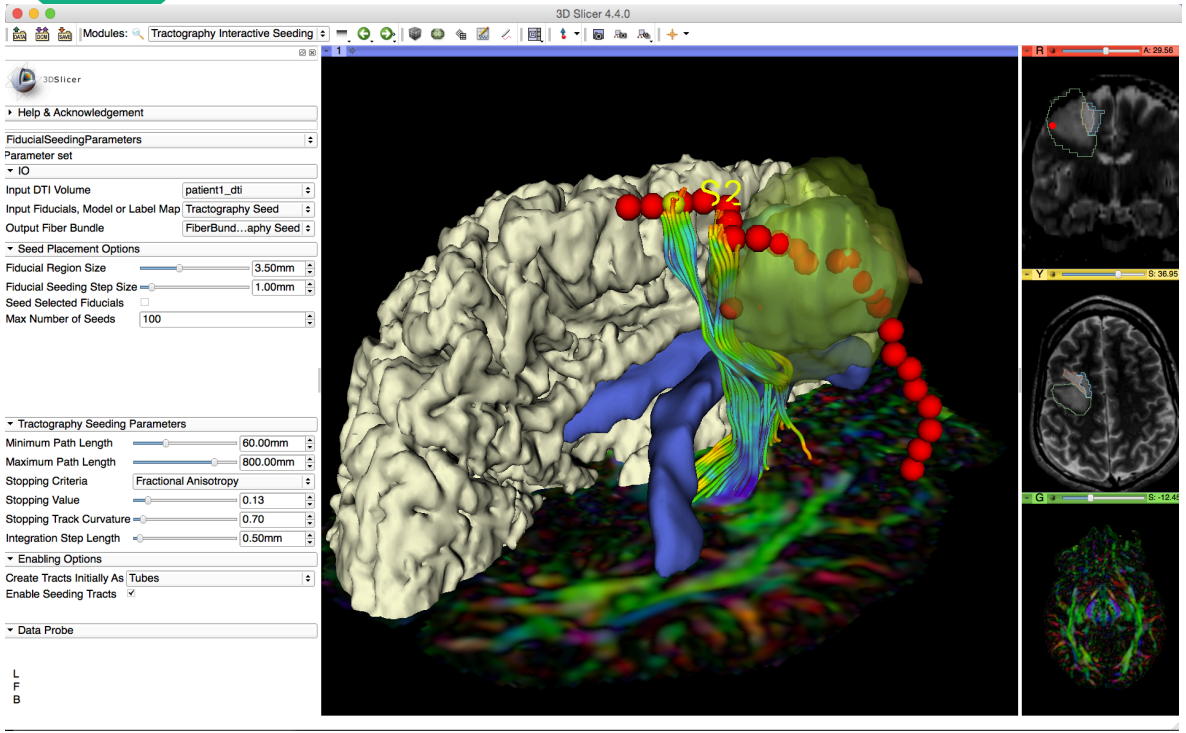
- Applied science oriented toward patient-specific analysis in the presence of pathology
- Driving Biological Projects leading to the development of new tools

Examples of clinical applications



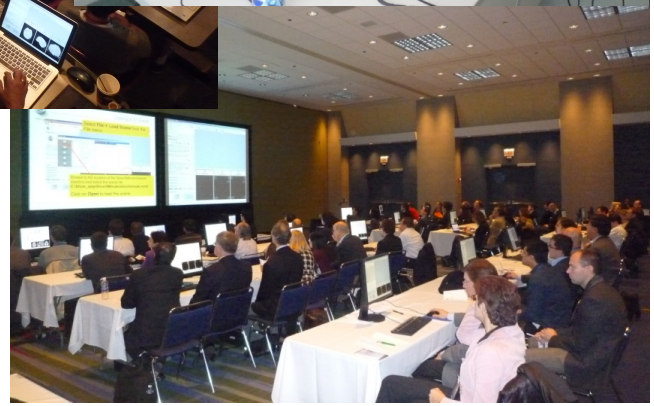
- Radiotherapy: RT-specific analysis dose accumulation and dose comparison (G.Fichtinger et al. Queen's University, Canada)

Examples of clinical applications



- Diffusion Tensor Imaging tractography for neurosurgical planning

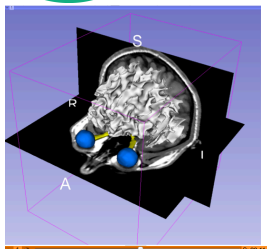
Slicer Training events

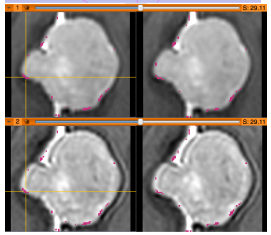


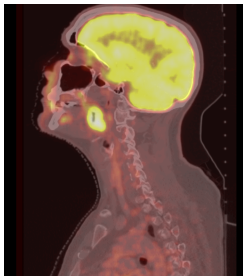
Major international conferences

- **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

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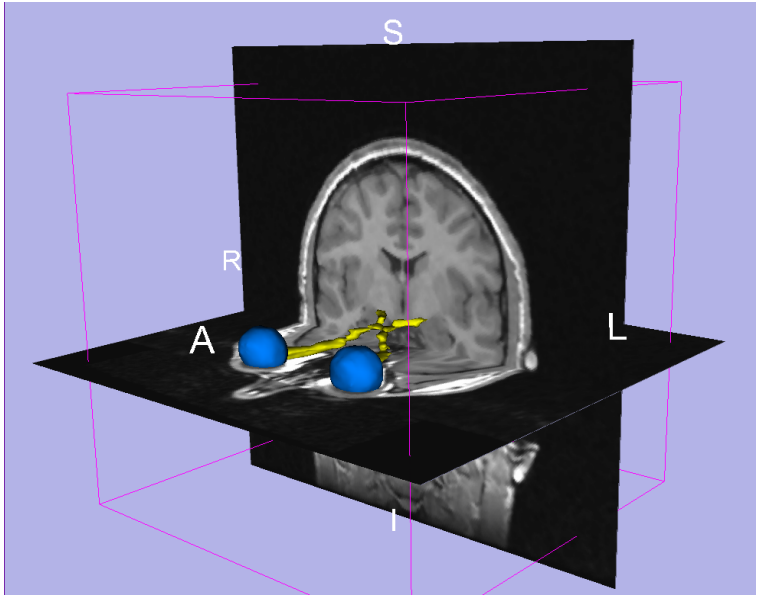
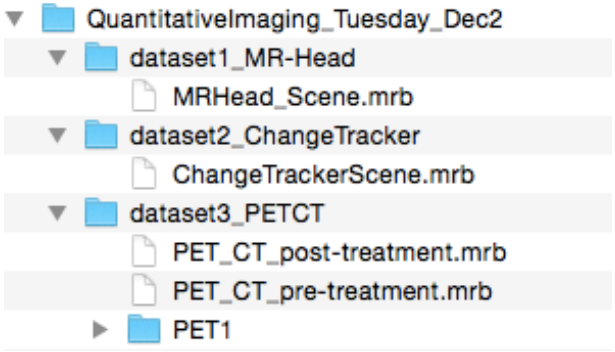


Part II: Basics of Data Loading and 3D Visualization

Course Datasets

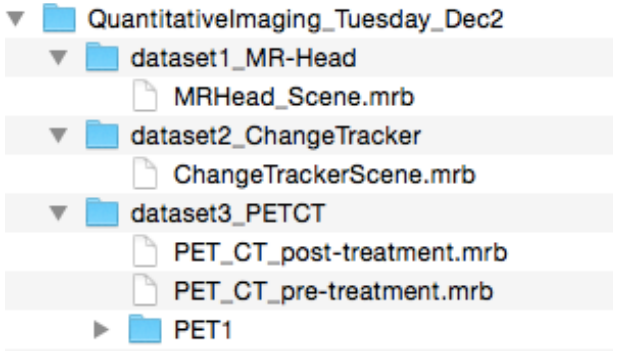


The **QuantitativeImaging_Tuesday_Dec2** directory contains three datasets located in the sub-directories:

- dataset1_MR_Head
- dataset2_ChangeTracker
- dataset3_PETCT

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

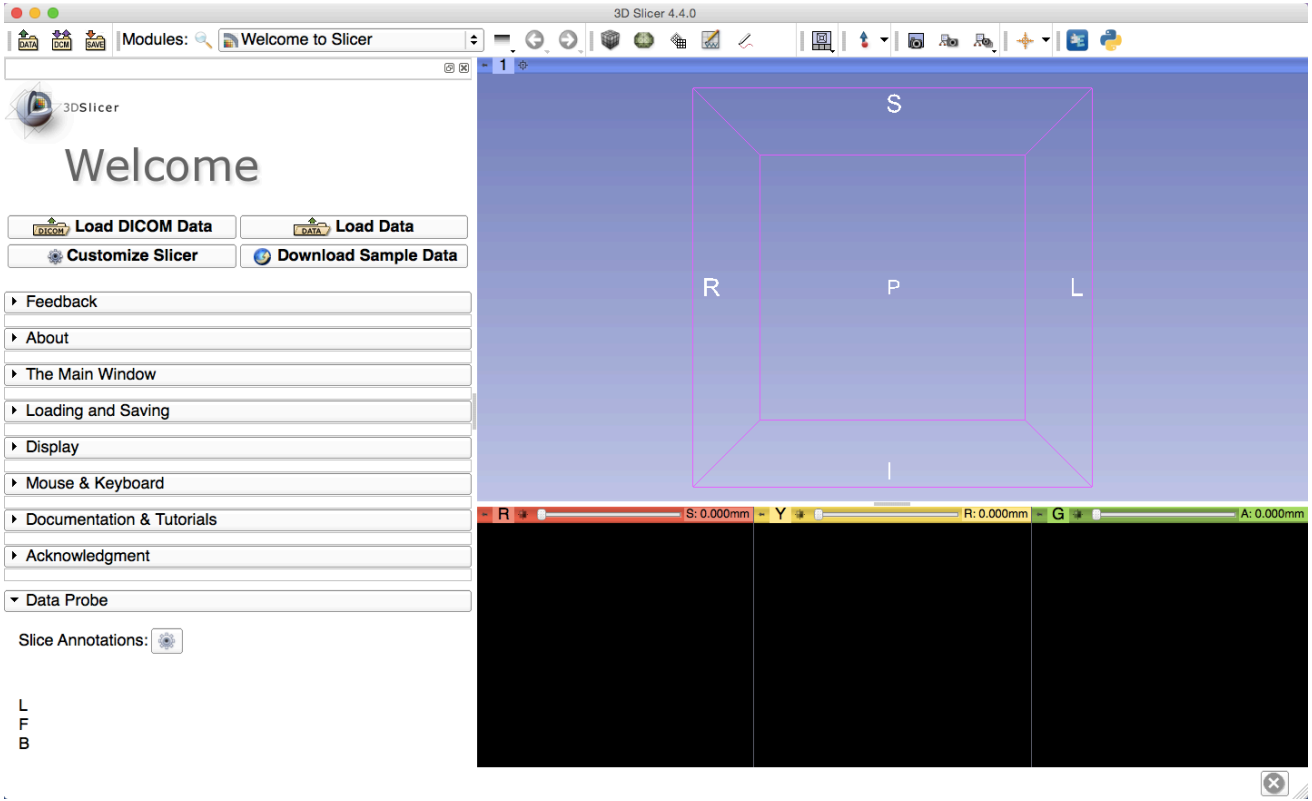
Slicer mrb file format



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.

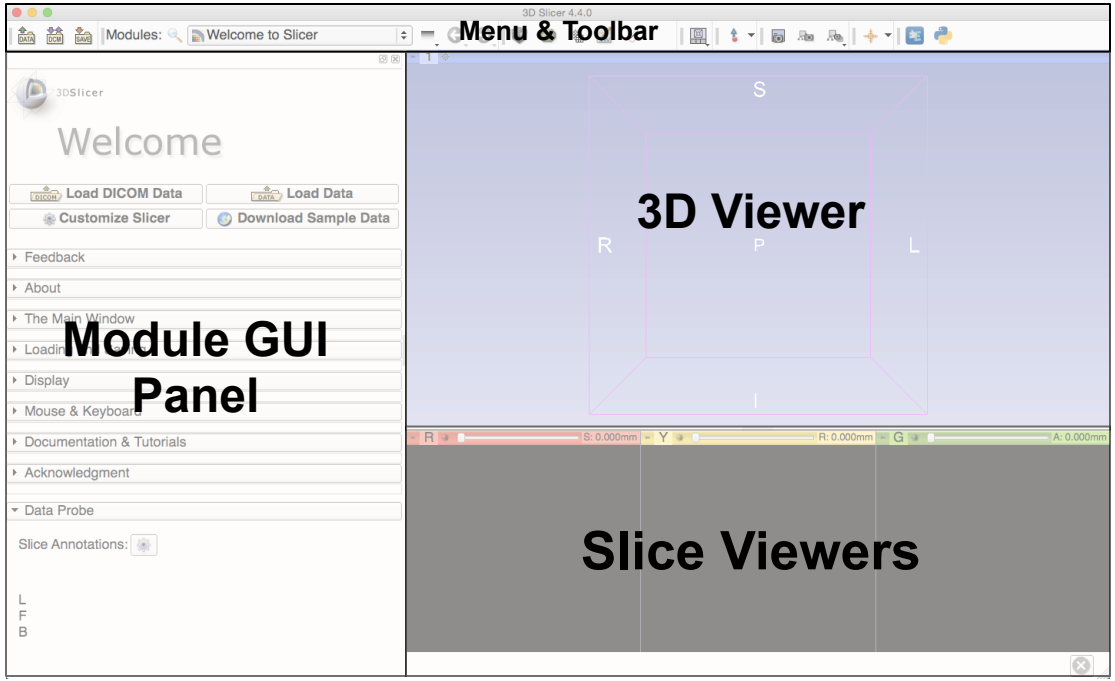
Welcome to Slicer4.4



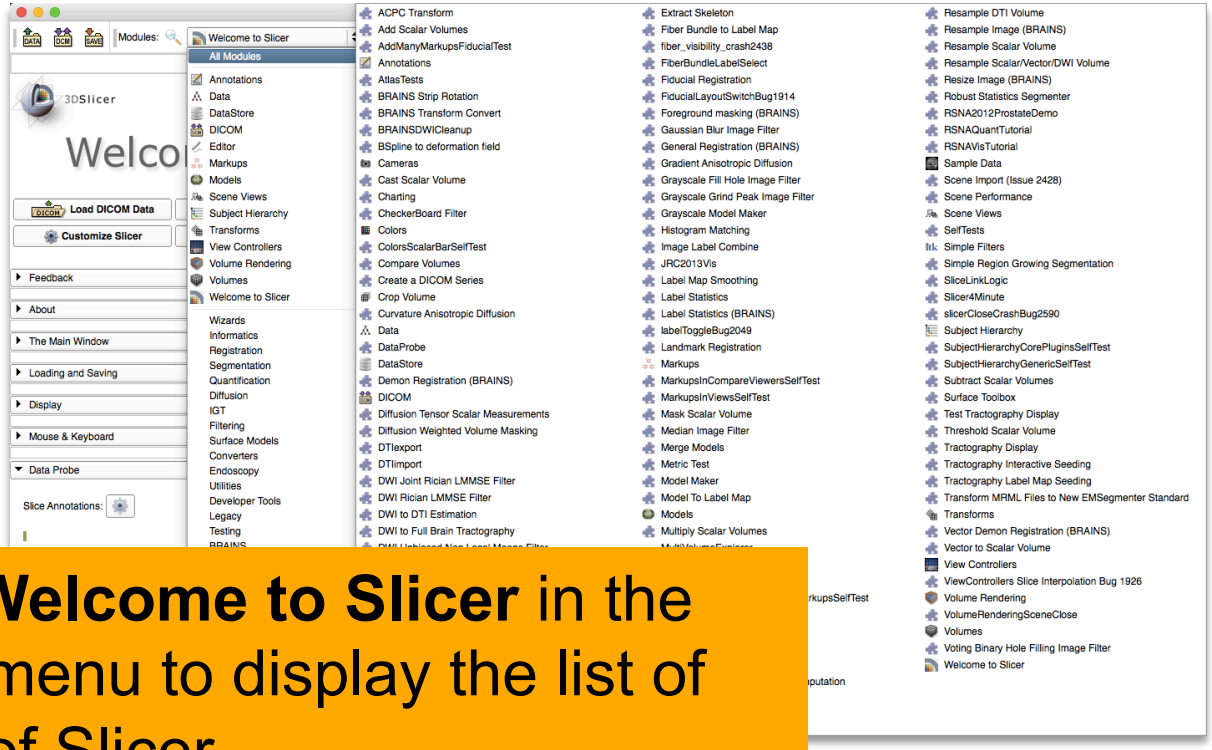
Slicer4 Minute Tutorial: Navigating the Application GUI

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

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

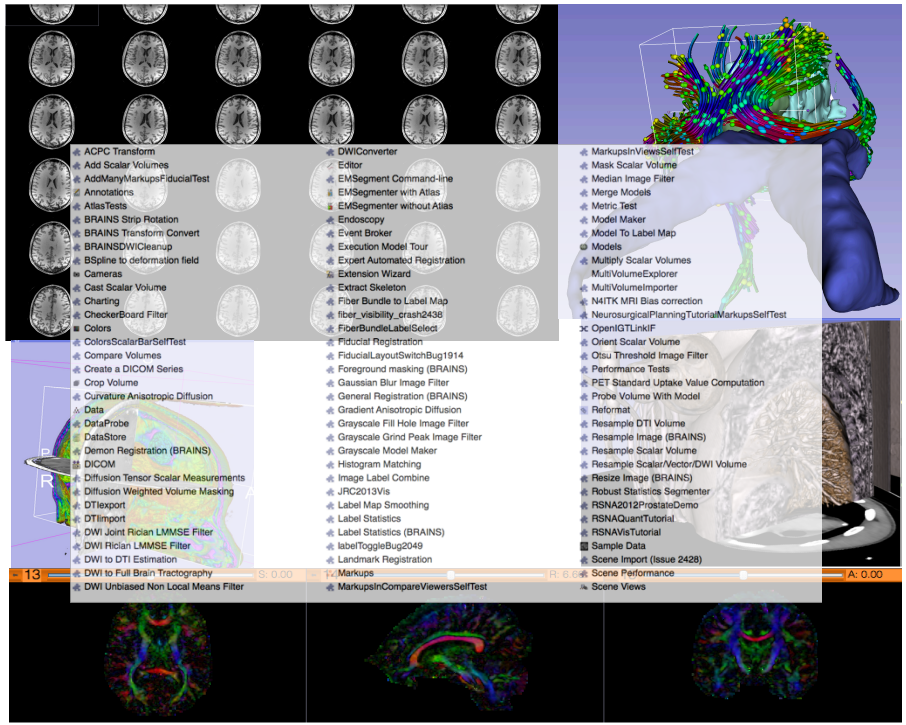


Welcome to Slicer4.4



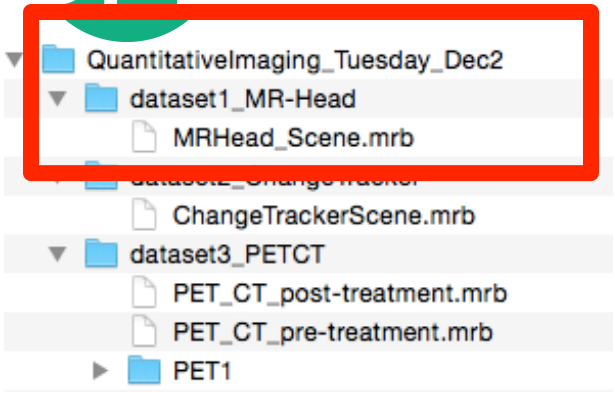
Click on **Welcome to Slicer** in the Modules menu to display the list of modules of Slicer

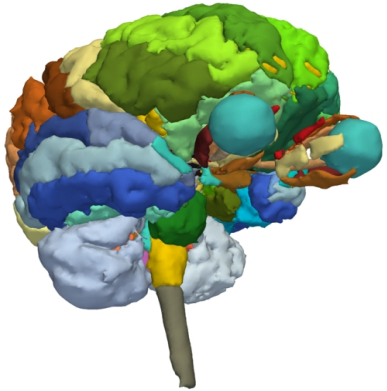
Welcome to Slicer4.4



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**

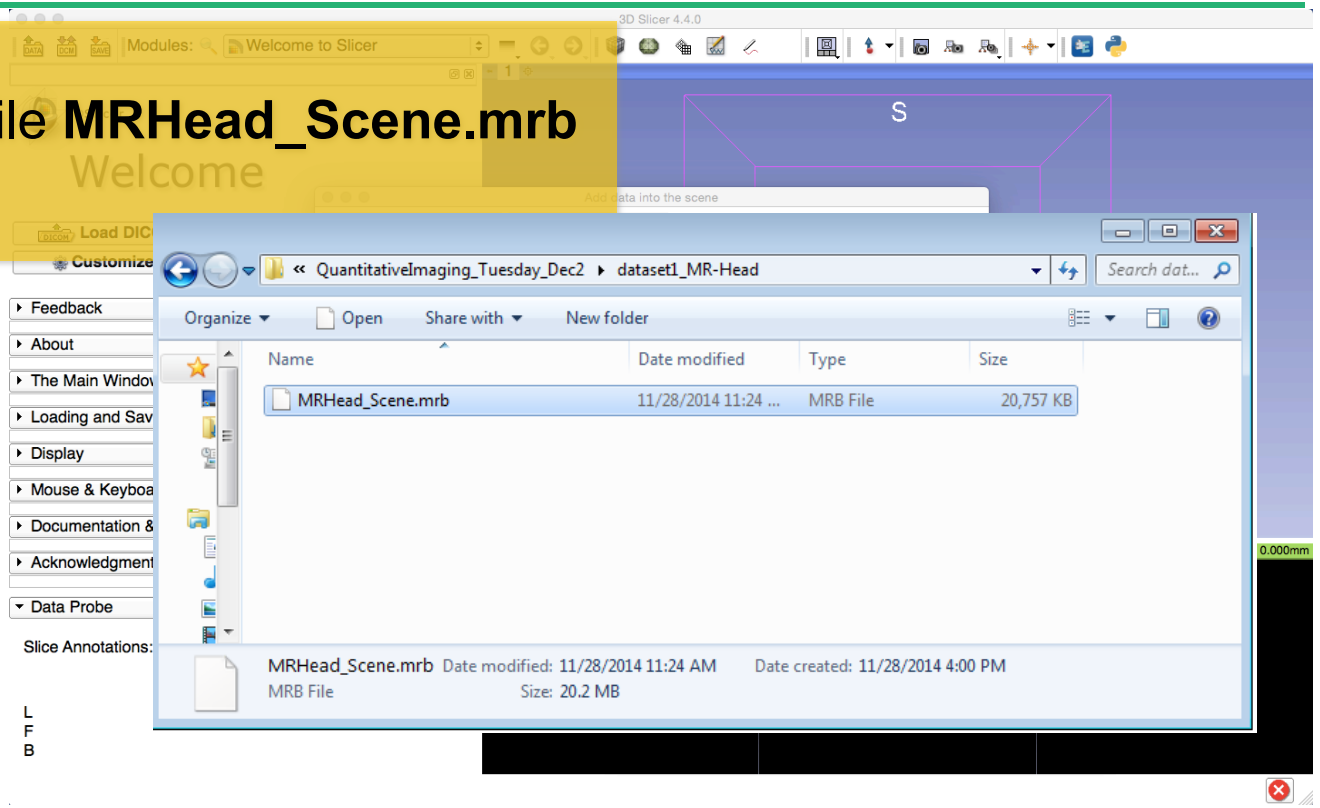
This file is composed of an MR scan of the brain and 3D surface reconstructions of anatomical structures, from

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

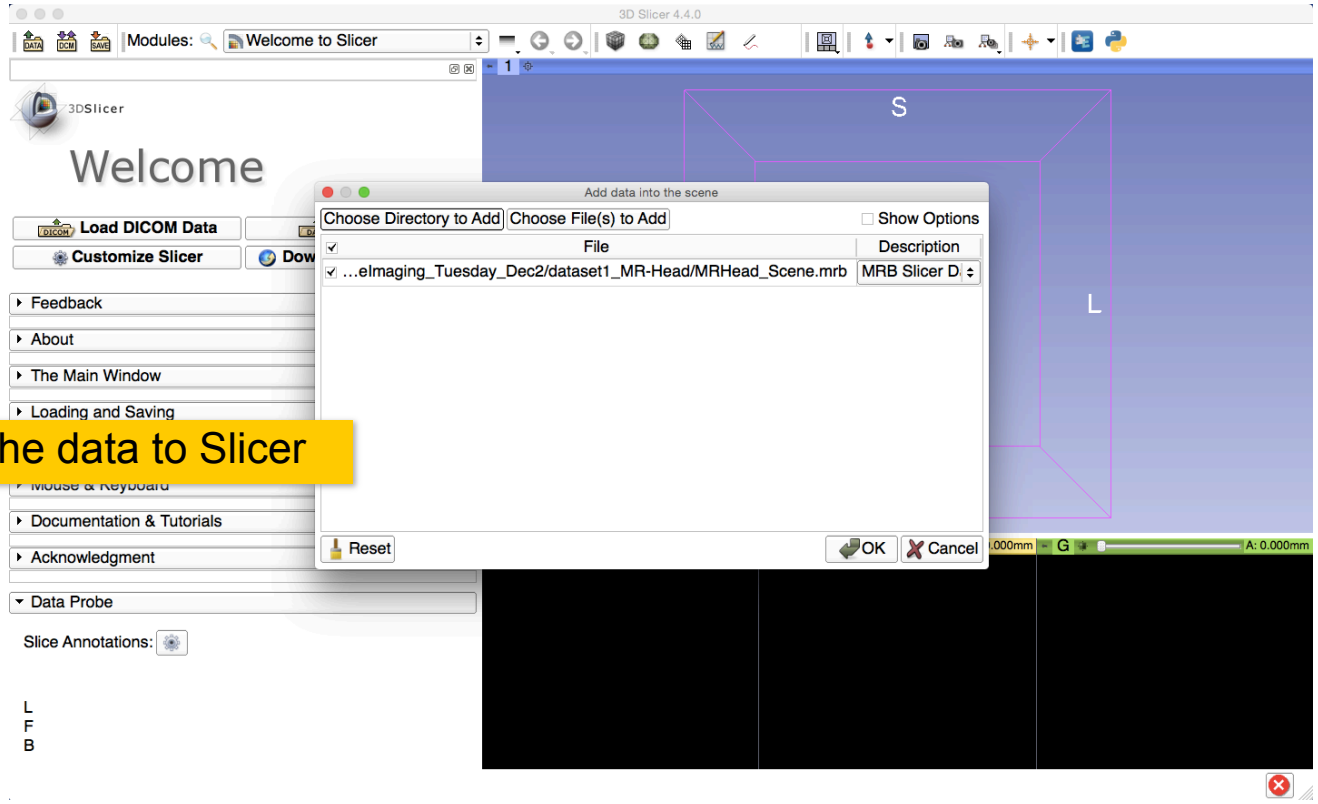
http://www.spl.harvard.edu/publications/item/view/2037

Slicer4 Minute Tutorial: Load a Scene

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



Slicer4 Minute Tutorial: Load a Scene

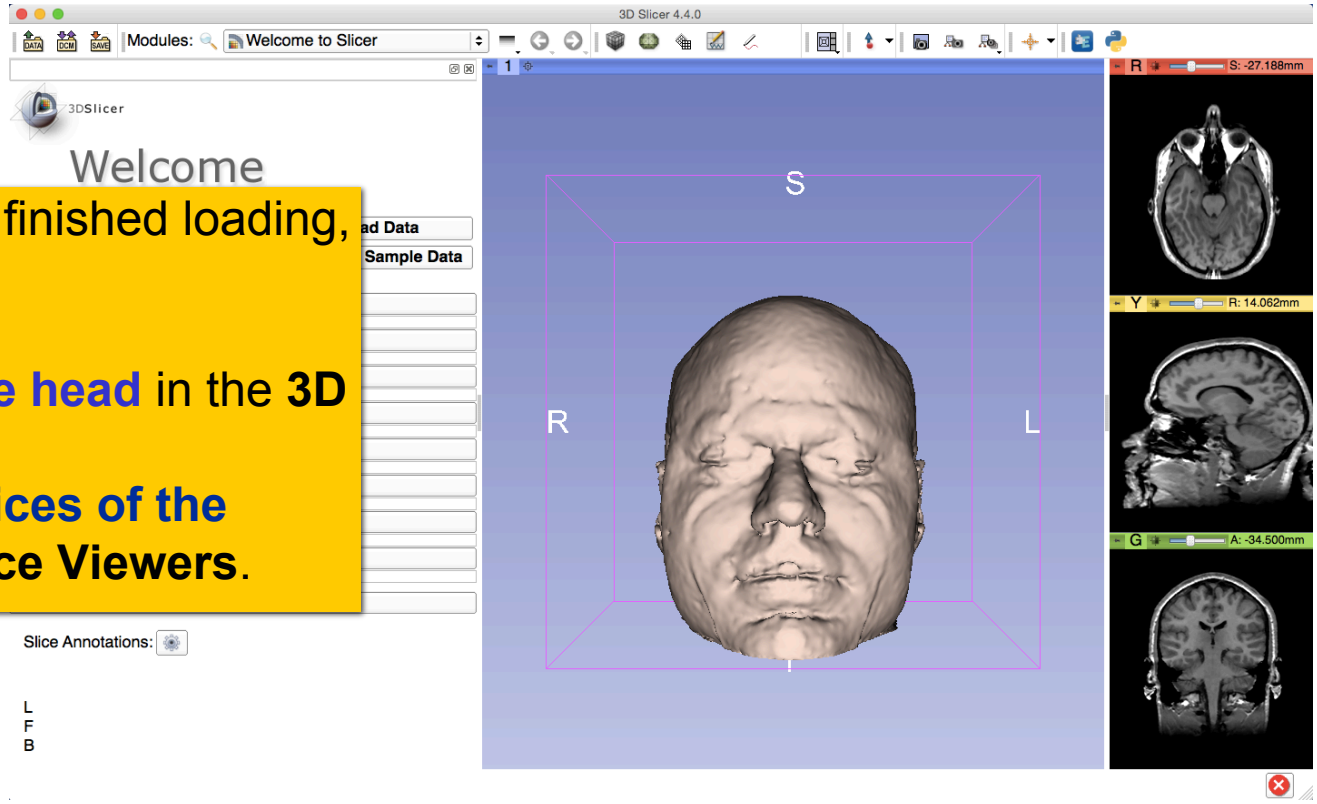


Click on **OK** to load the data to Slicer

Slicer4 Minute Tutorial: Viewing the Scene

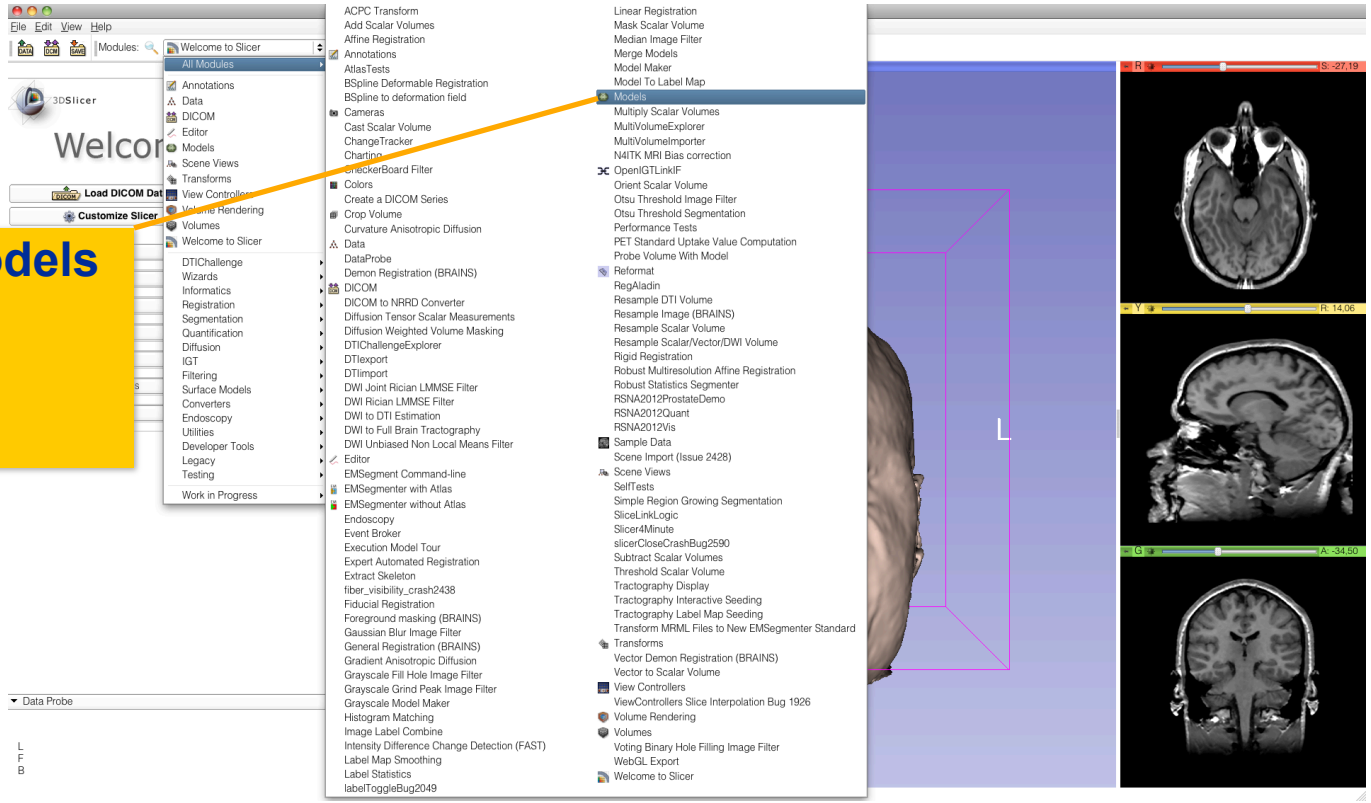
When the scene is finished loading, Slicer displays:

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

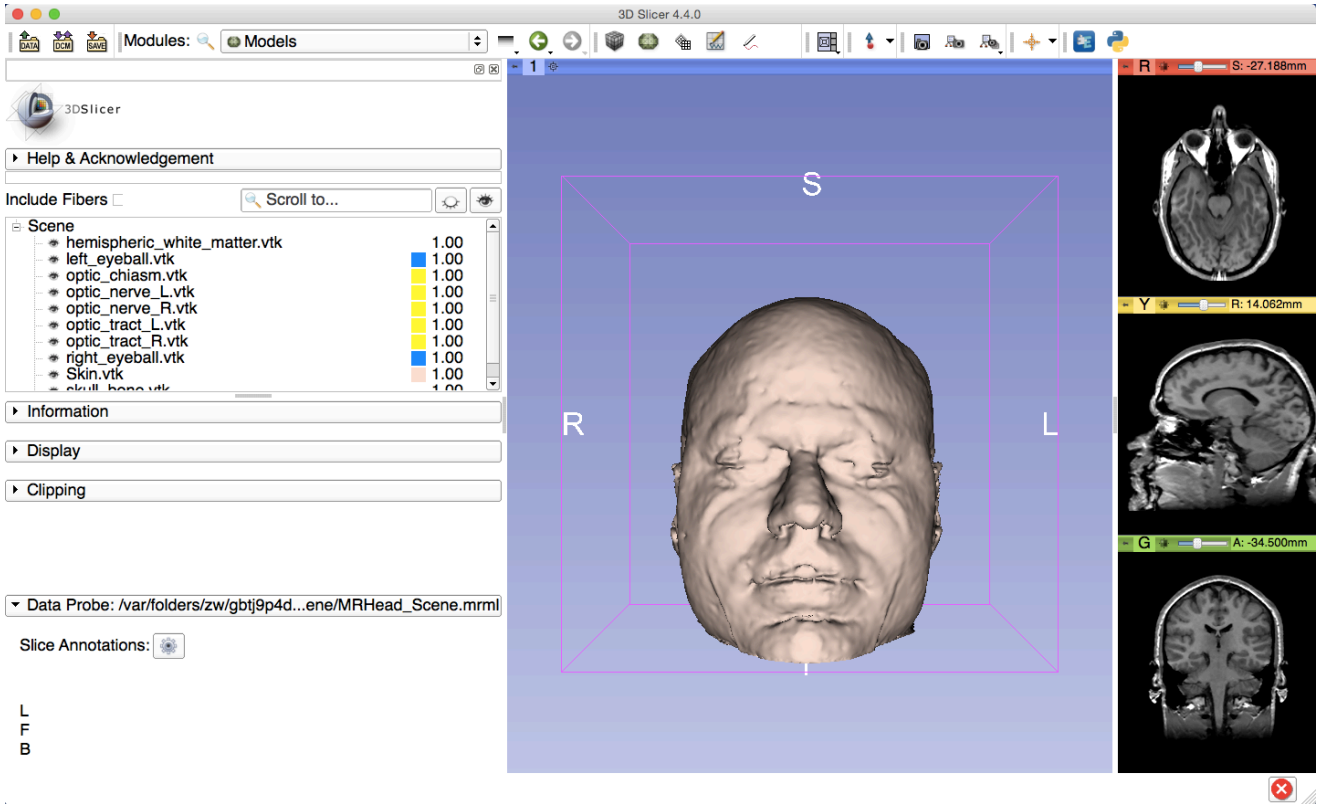


Slicer4 Minute Tutorial: Exploring Slicer's functionality

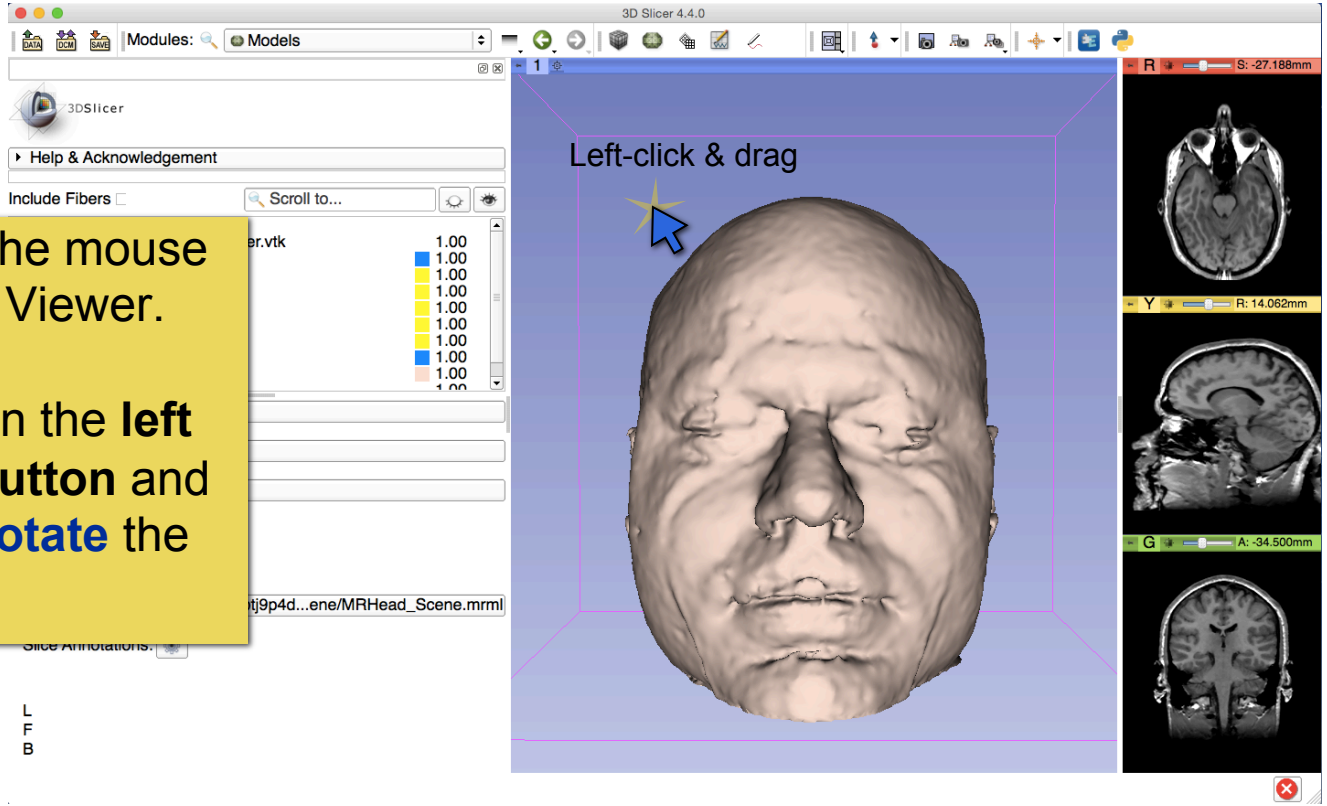
To access the **Models module**, browse through the list of modules…



Slicer4 Minute Tutorial: Switching to the Models Module



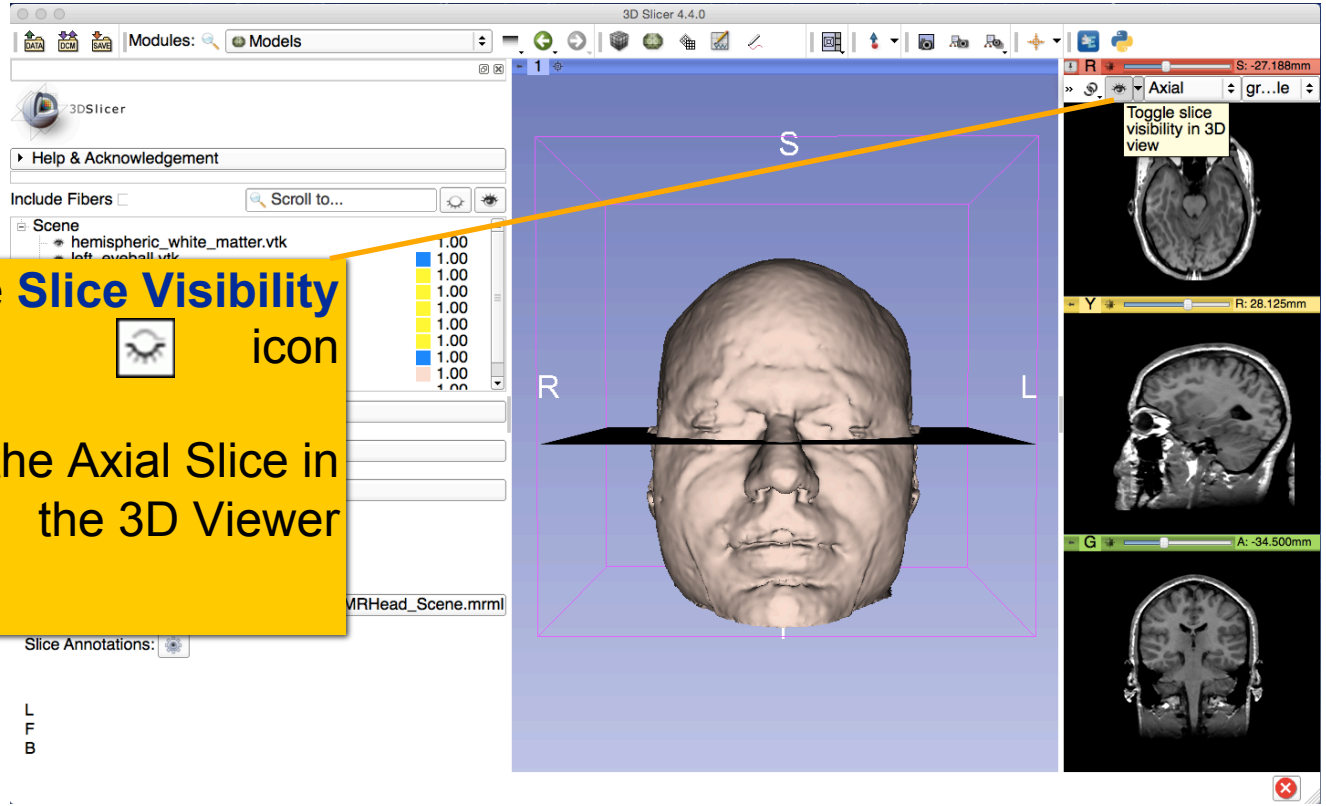
Slicer4 Minute Tutorial: Basic 3D Interaction



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

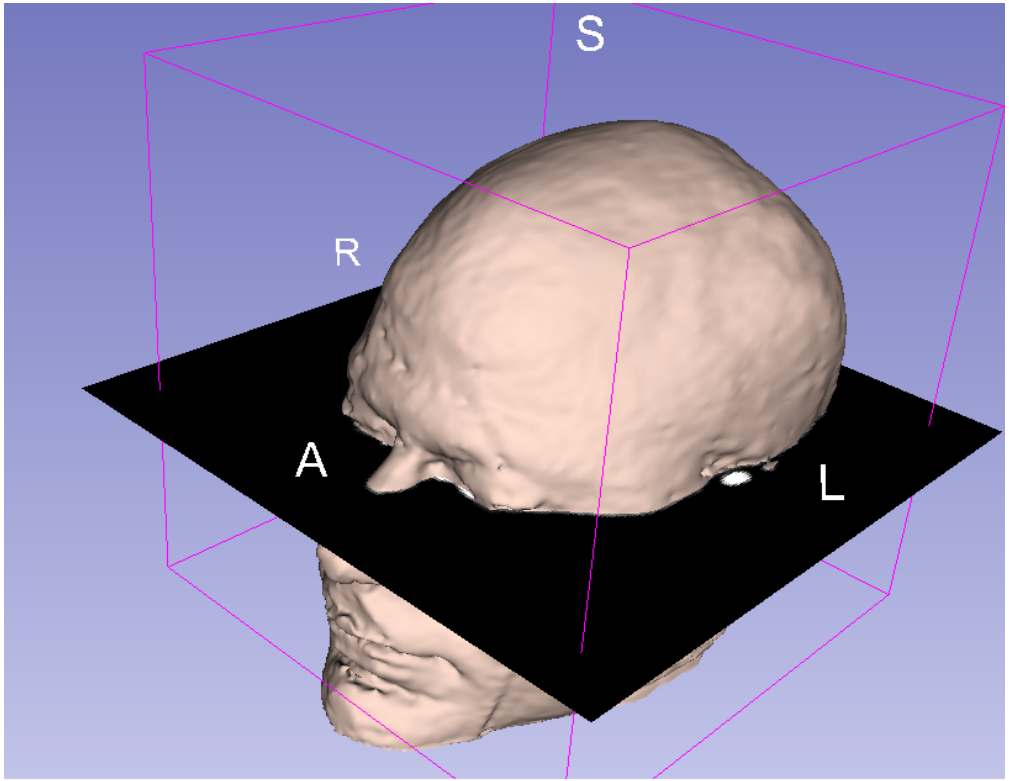


Click on the **Slice Visibility** icon

to display the Axial Slice in the 3D Viewer

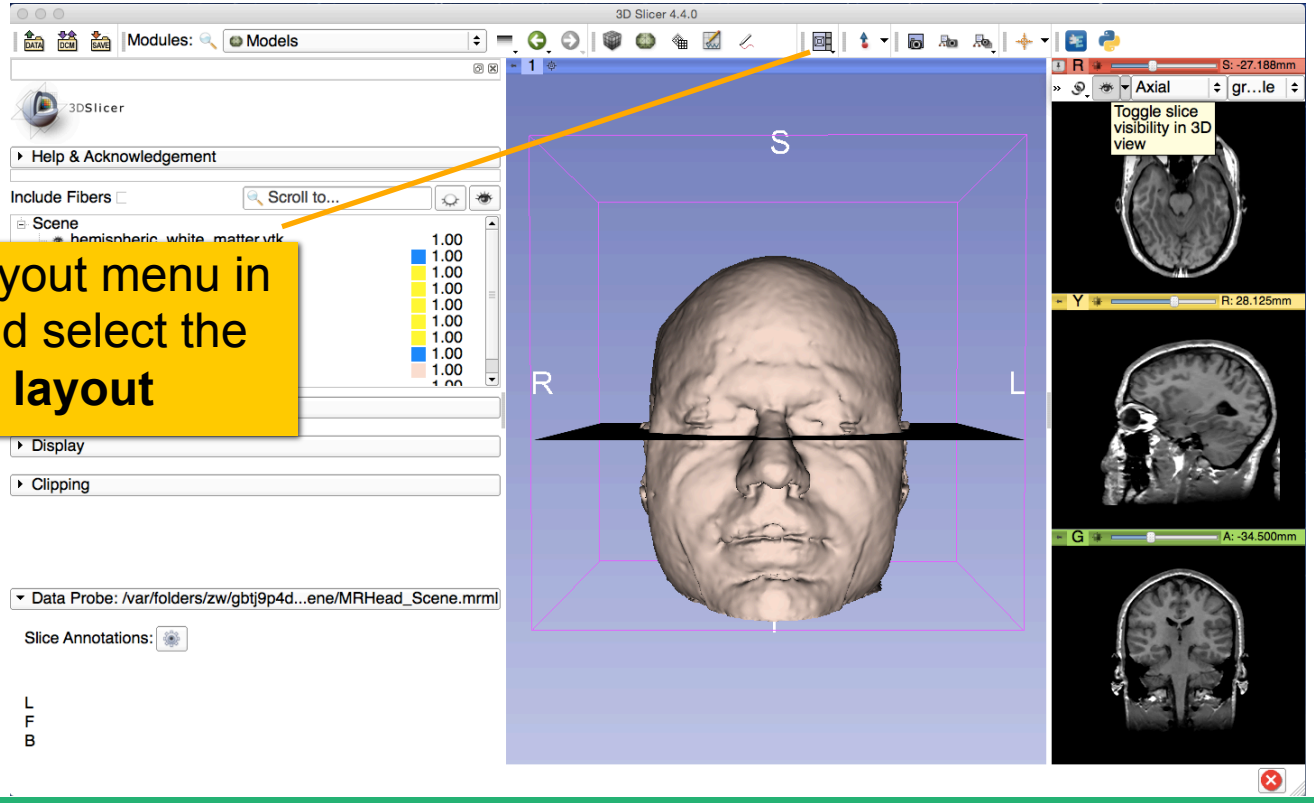
Slicer4 Minute Tutorial: 3D Visualization

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

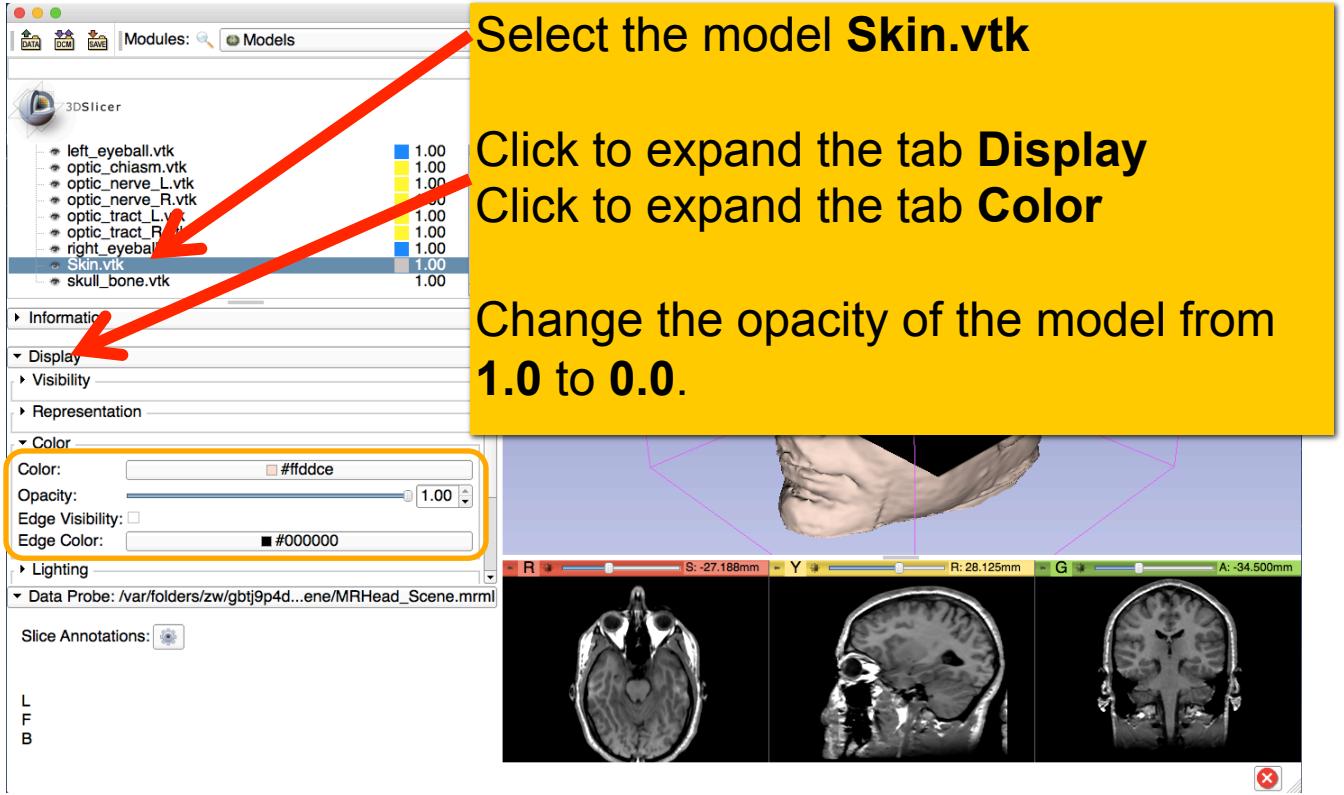


Slicer4 Minute Tutorial: Viewing Slices in the 3D Viewer

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



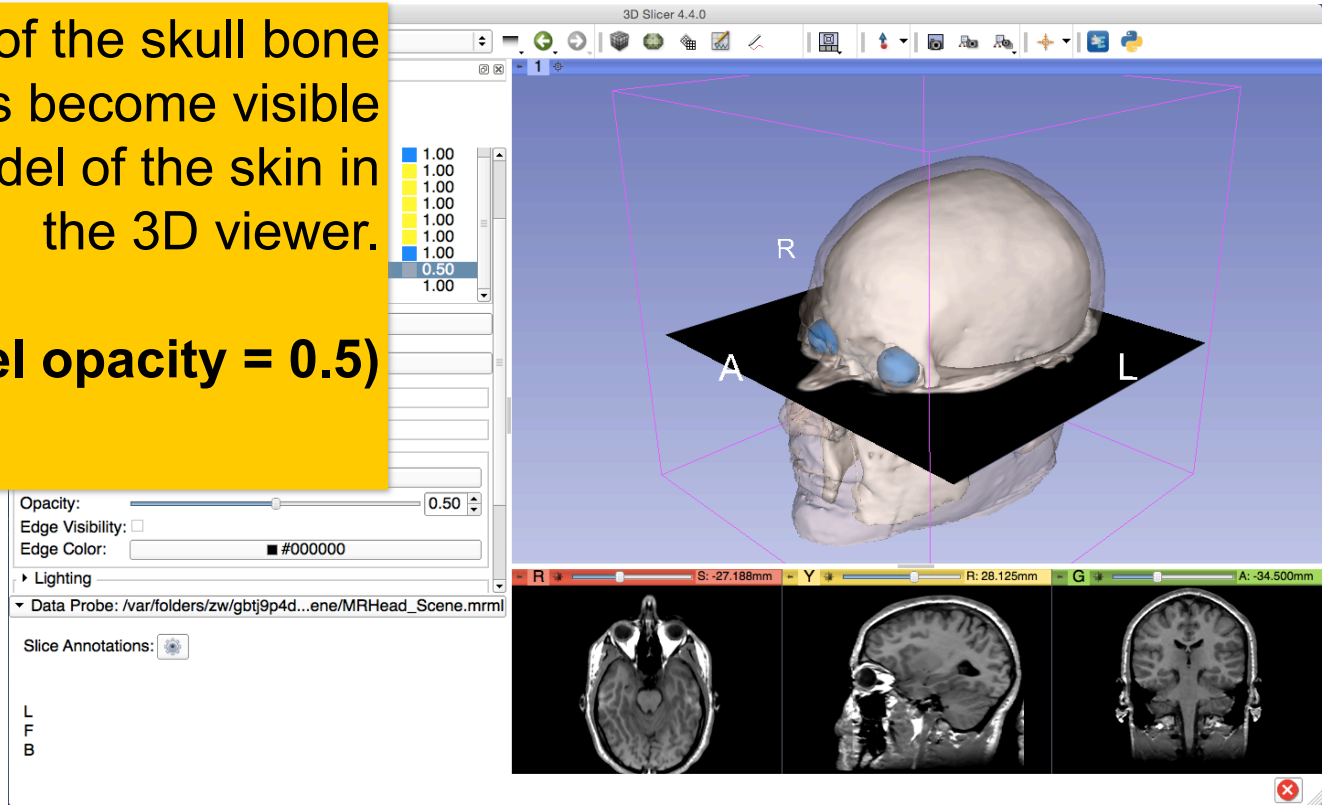
Slicer4 Minute Tutorial: 3D Visualization



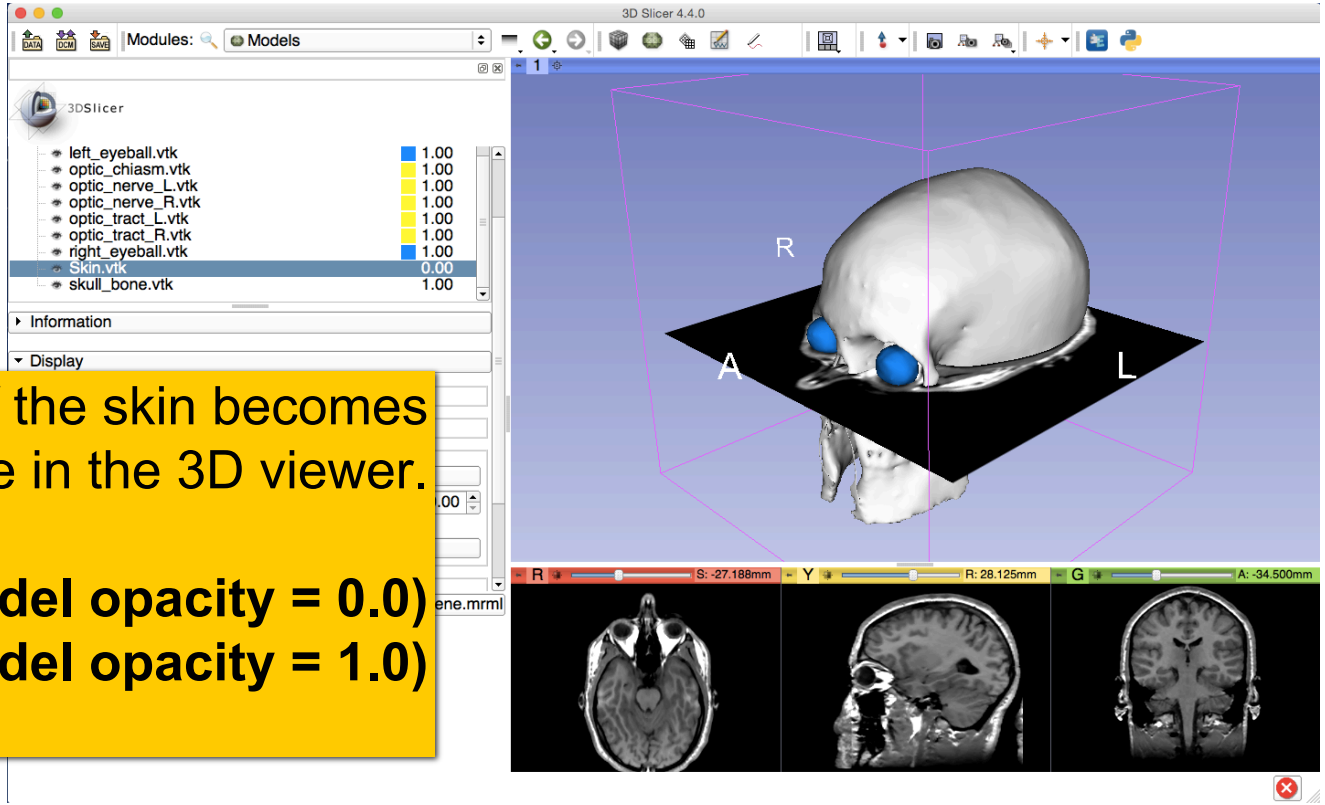
Slicer4 Minute Tutorial: 3D Visualization

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

(skin model opacity = 0.5)



Slicer4 Minute Tutorial: 3D Visualization

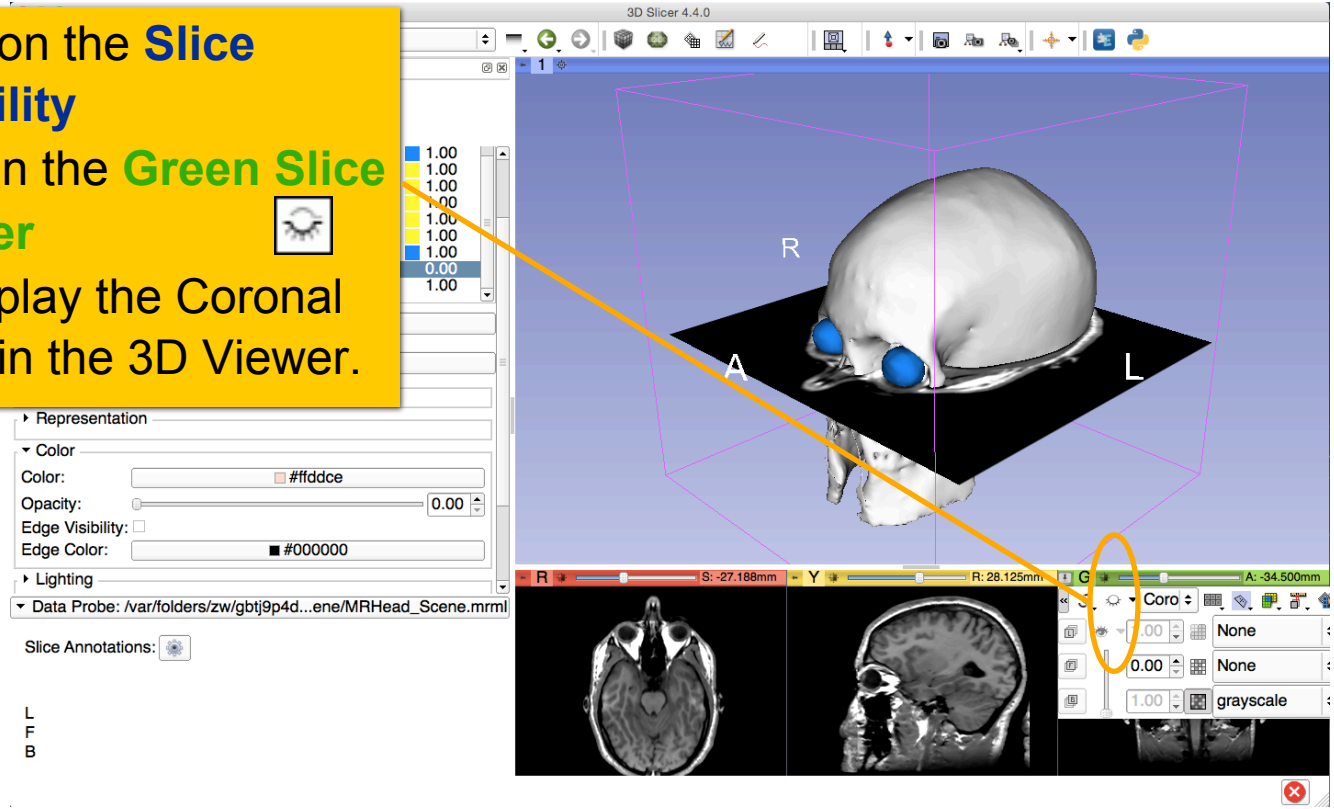


The model of the skin becomes invisible in the 3D viewer.

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

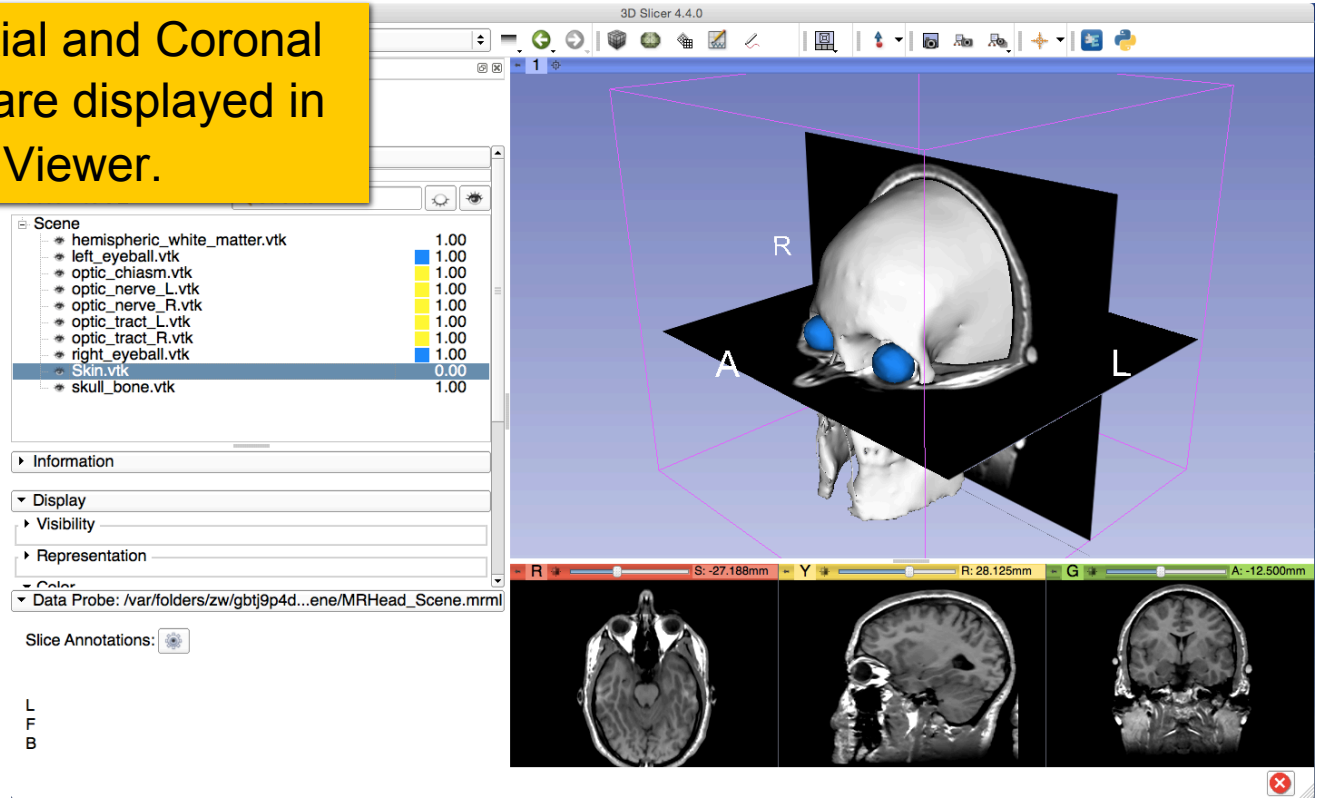
Slicer4 Minute Tutorial: 3D Visualization

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

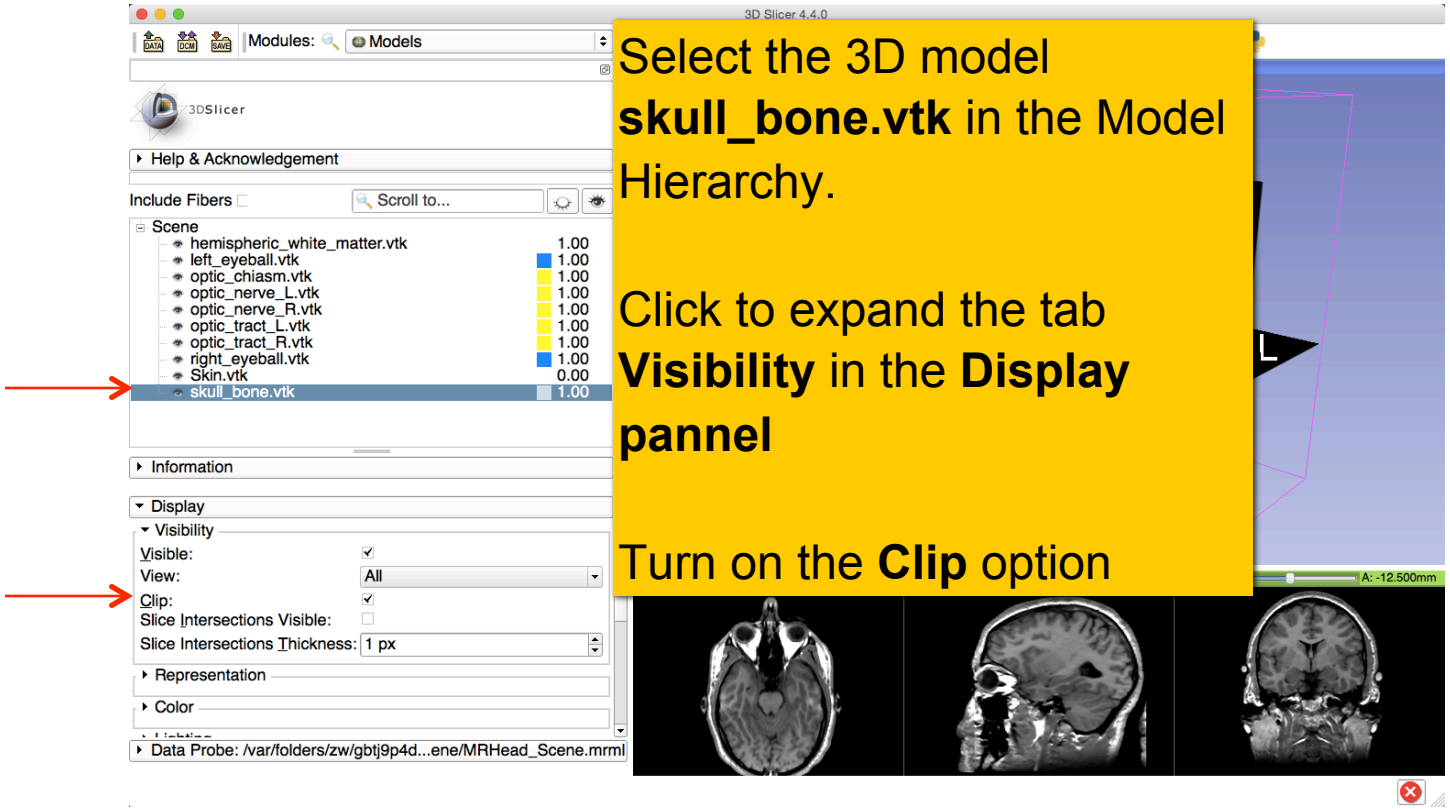


Slicer4 Minute Tutorial: 3D Visualization

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



Slicer4 Minute Tutorial: 3D Visualization



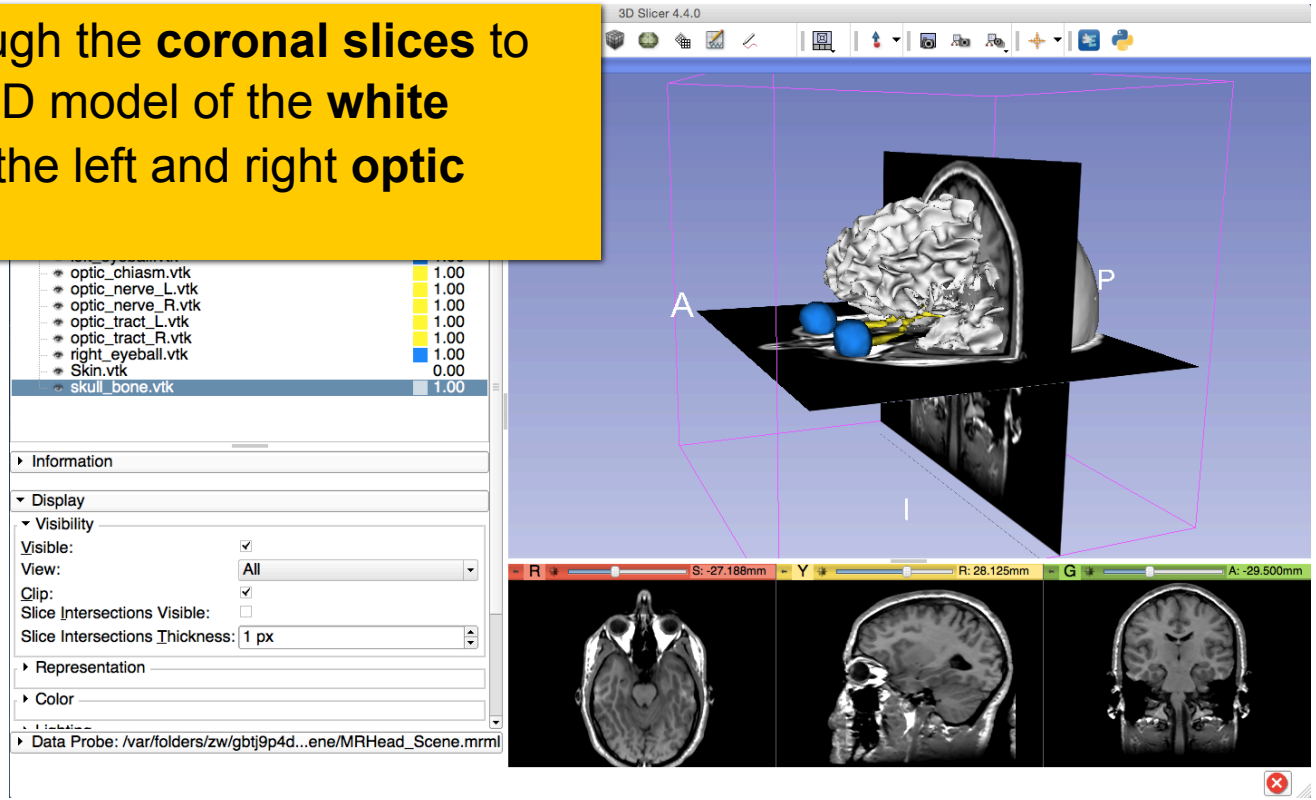
Select the 3D model **skull_bone.vtk** in the Model Hierarchy.

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

Turn on the **Clip** option

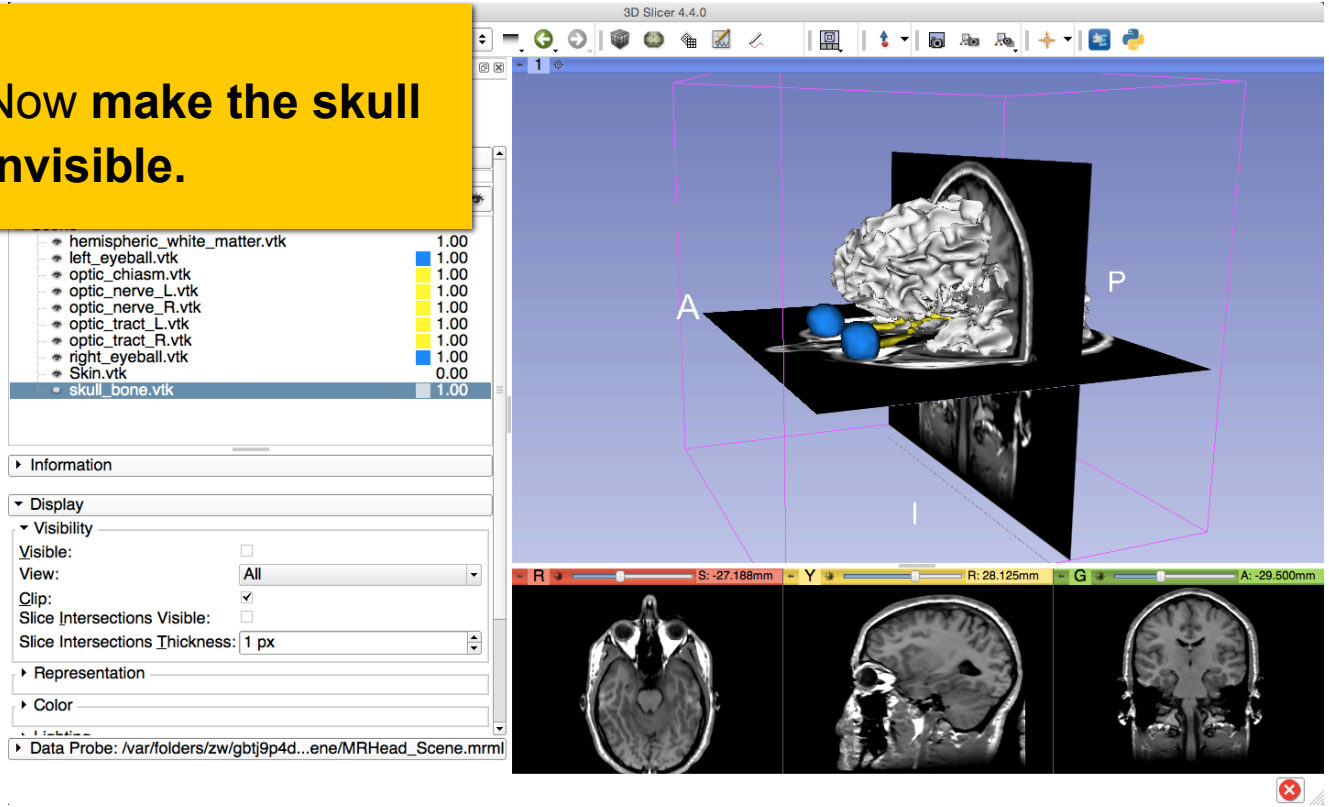
Slicer4 Minute Tutorial: 3D Visualization

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



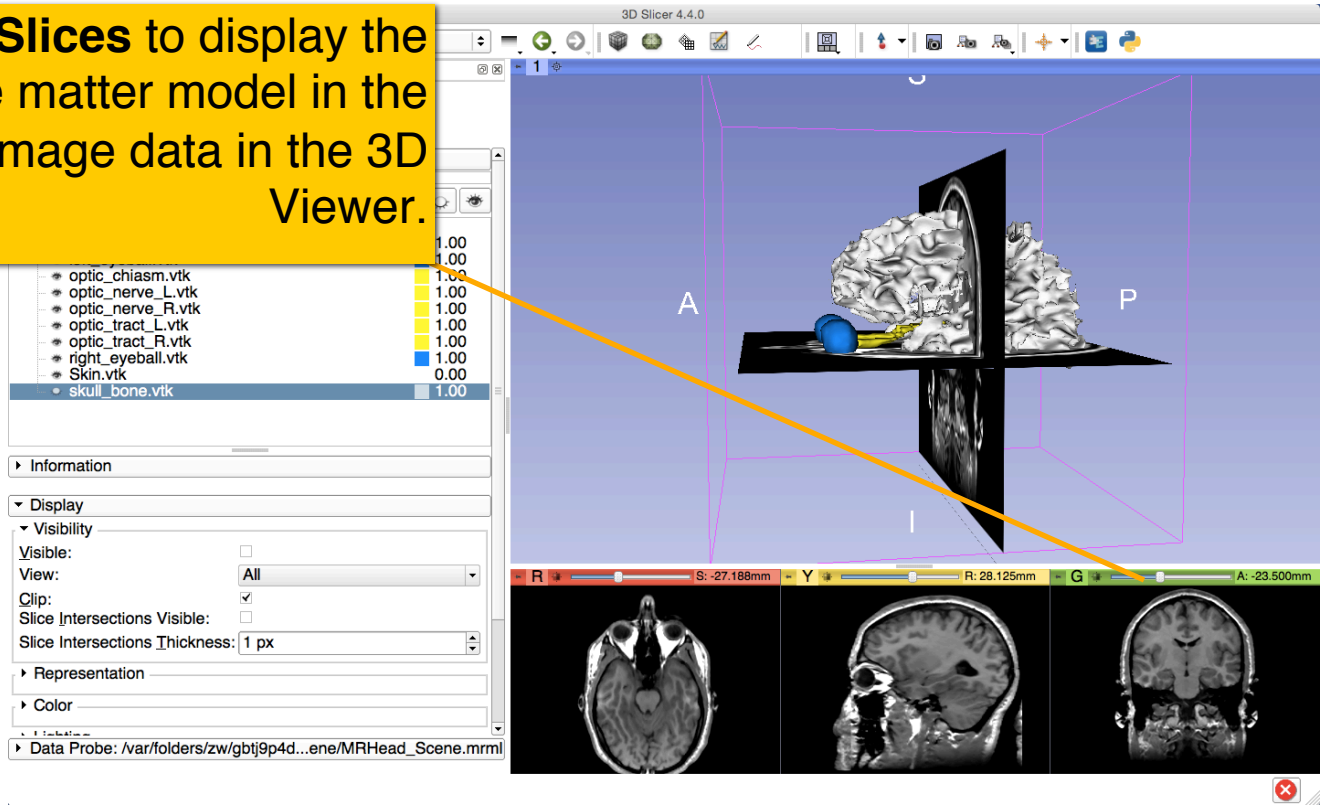
Slicer4 Minute Tutorial: 3D Visualization

Now **make the skull invisible.**



Slicer4 Minute Tutorial: 3D Visualization

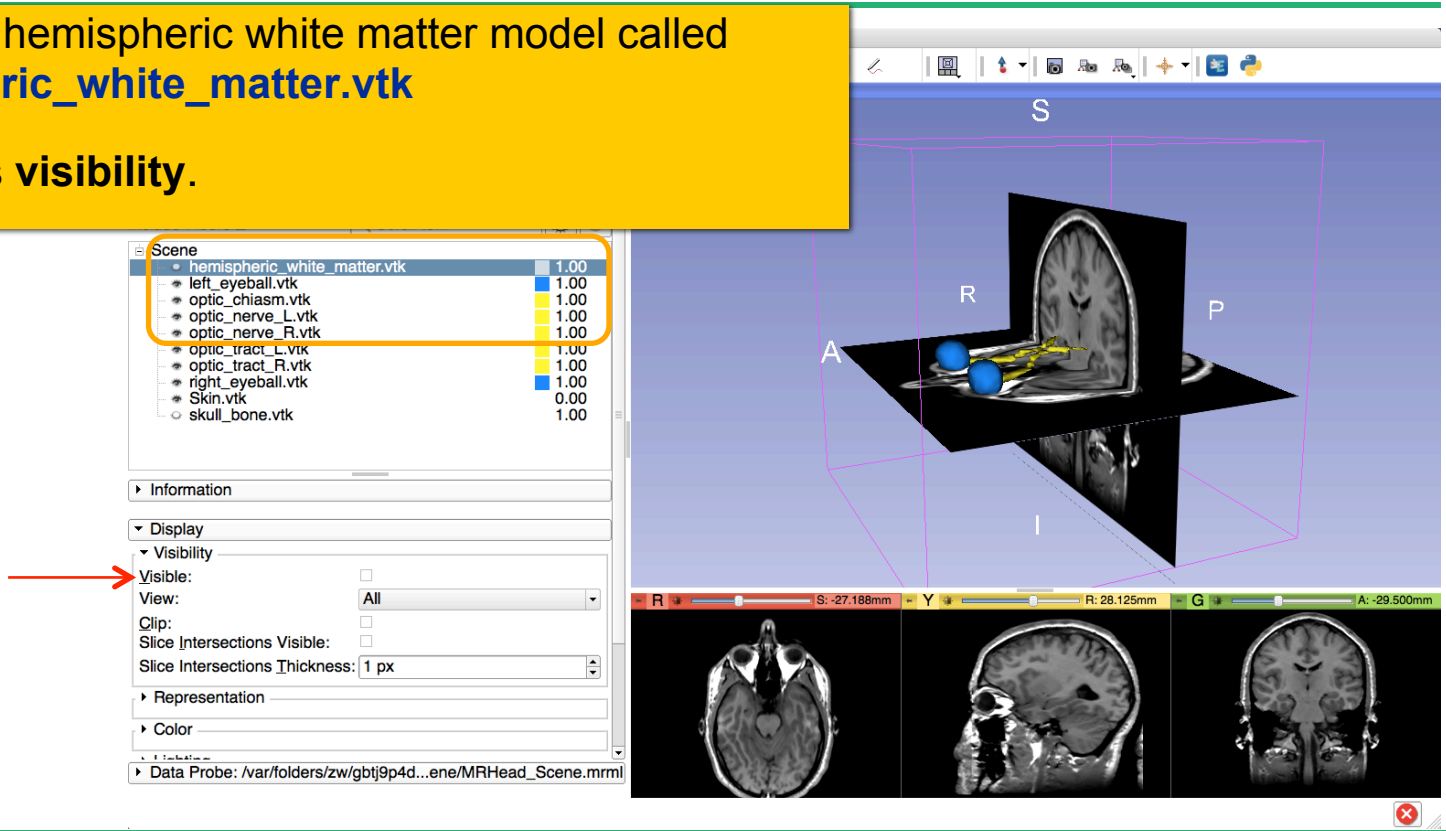
Scroll the **Coronal Slices** to display the hemispheric white matter model in the context of the image data in the 3D Viewer.



Slicer4 Minute Tutorial: 3D Visualization

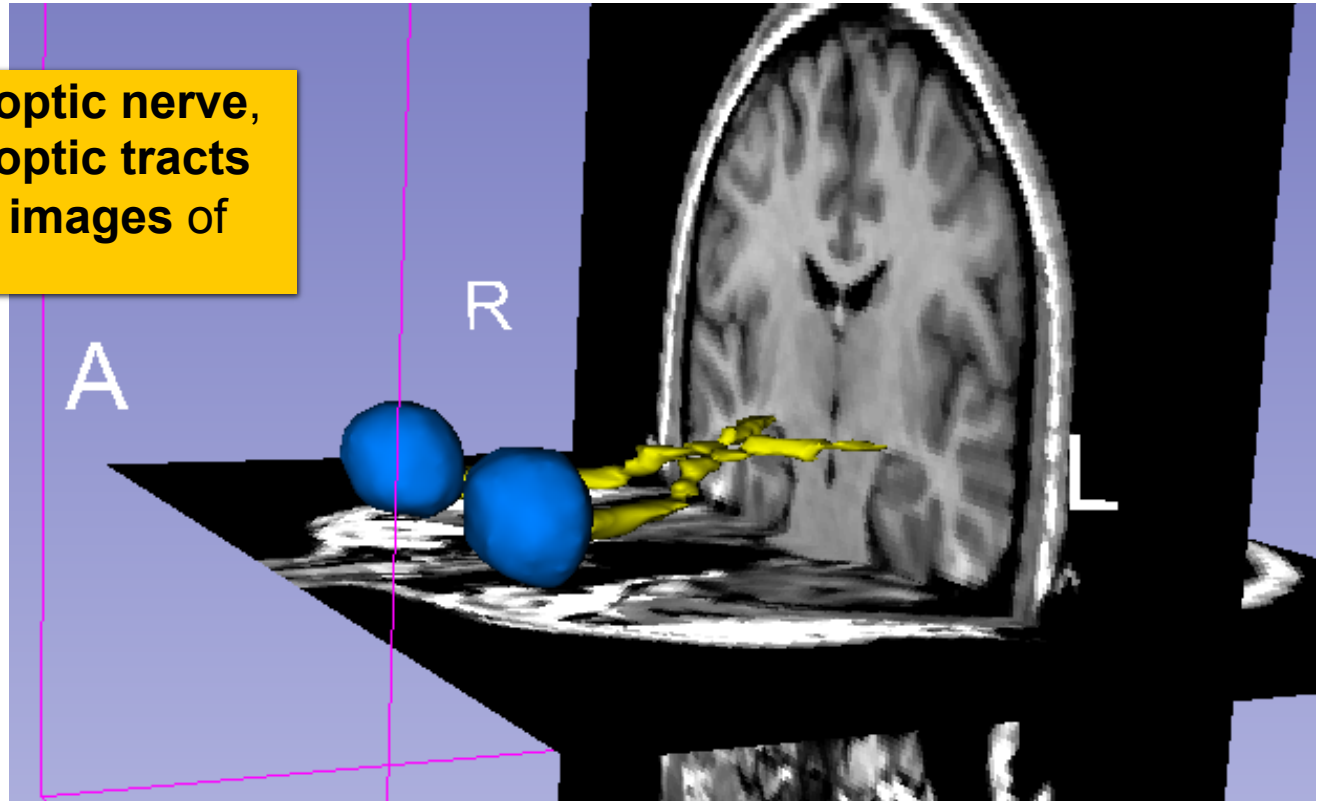
Select the hemispheric white matter model called **hemispheric_white_matter.vtk**

Turn off its **visibility**.

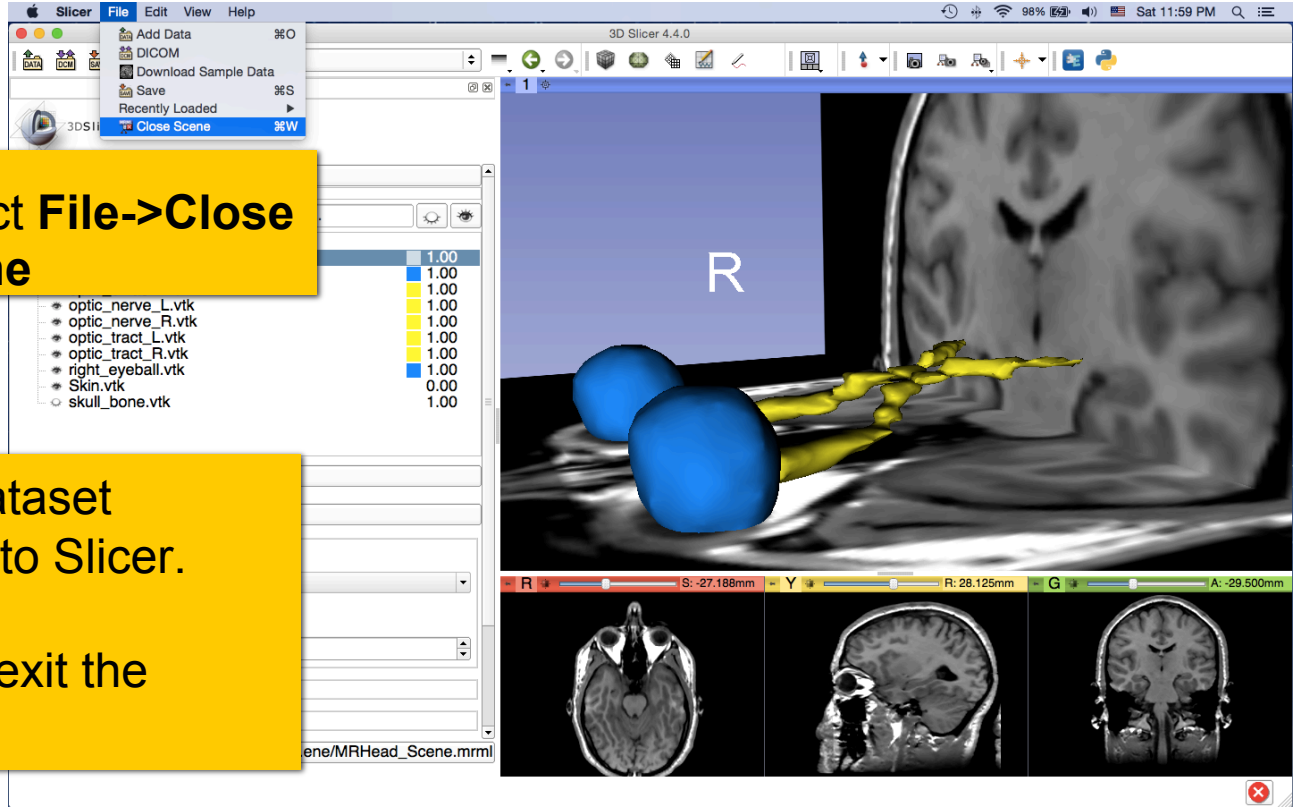


Slicer4 Minute Tutorial: 3D Visualization

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



Close the existing scene and all its data



Select **File->Close Scene**

This removes any dataset previously loaded into Slicer.

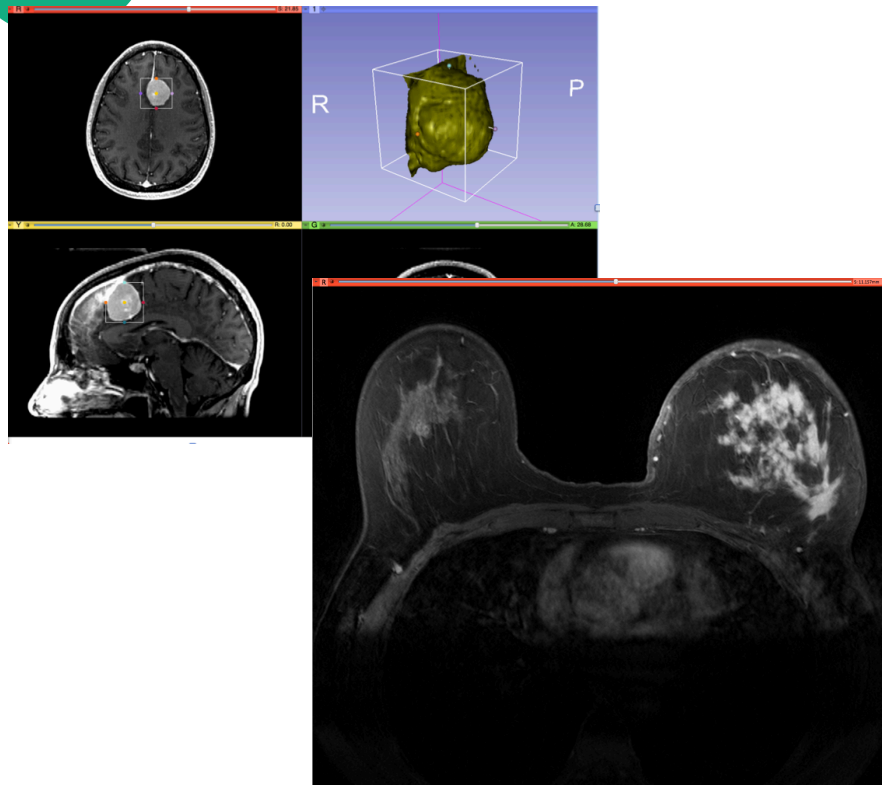
Select **File→Exit** to exit the software

Summary

This first part of the tutorial has demonstrated:

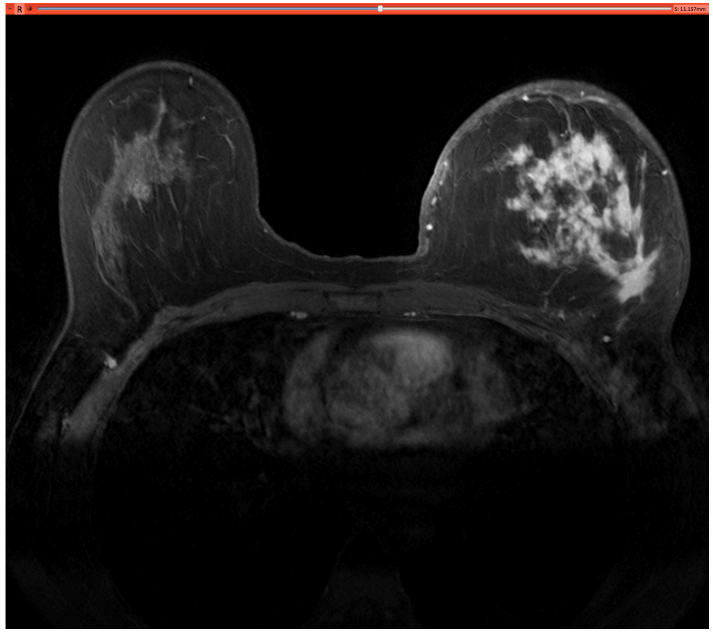
- Basic description of the Slicer4 Application Interface
- How to load a .mrb file containing volumes and models
- How to visualize these different datasets together

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



Part II: Analyzing Volumetric Changes

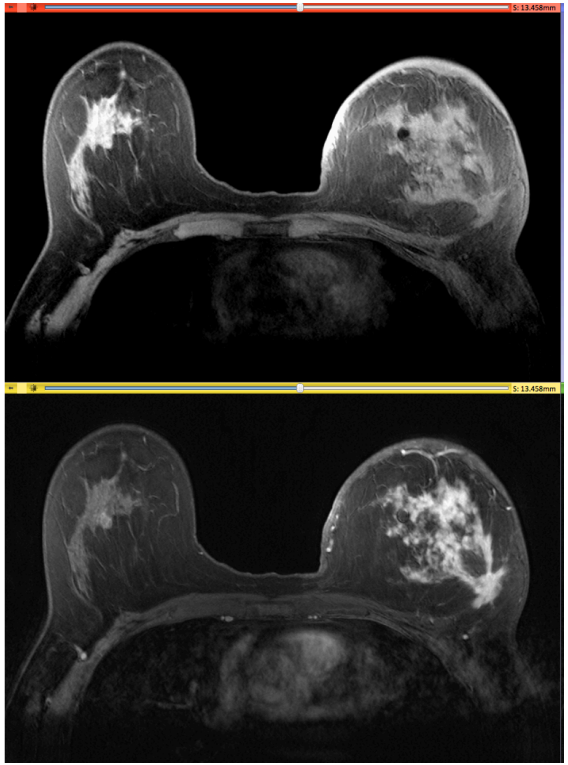
Example1: Large volumetric change



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

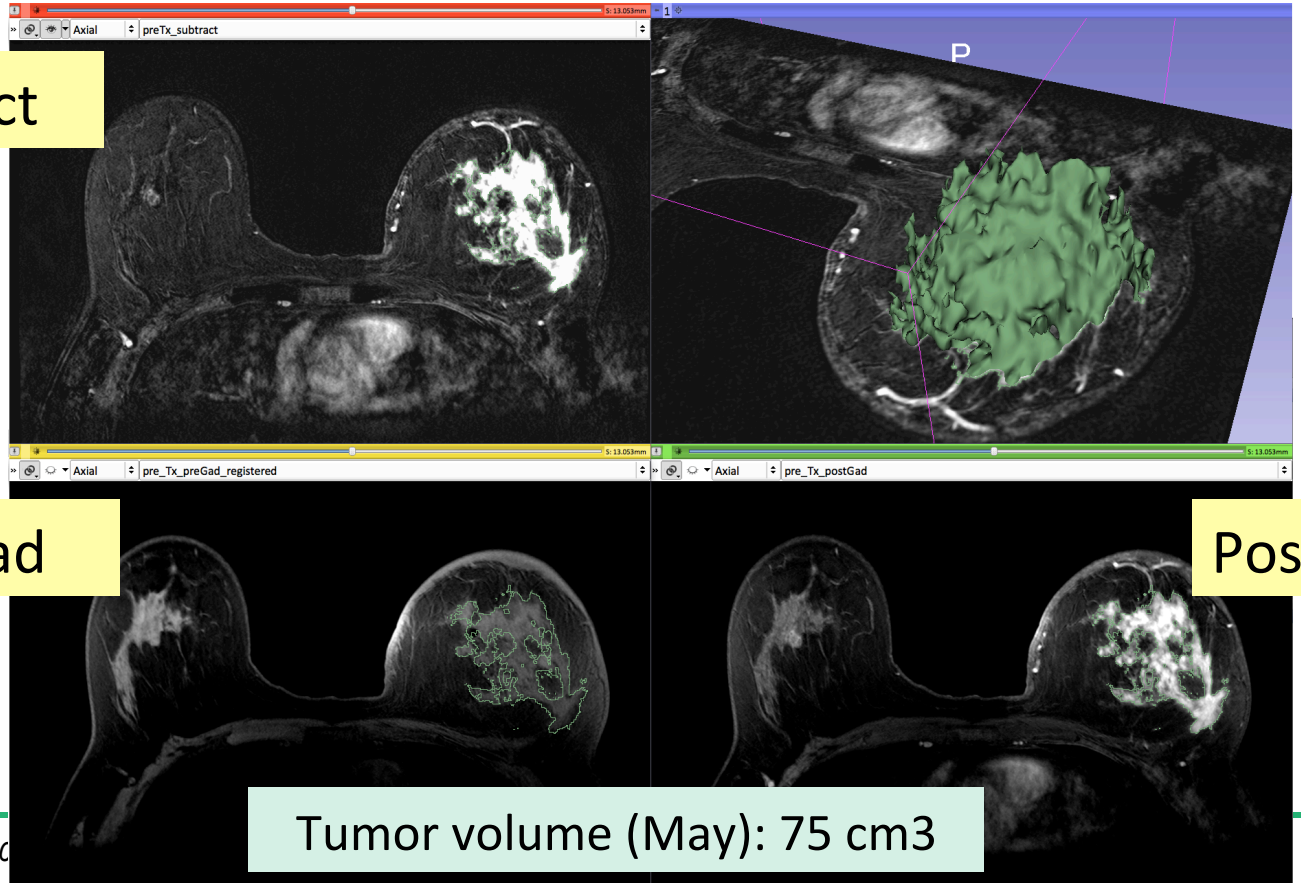
Step #4: **3D model creation**

Step #5: **Tumor volume computation**

Processing time ~5-7 min

Pre-therapy analysis (May 2013)

Subtract

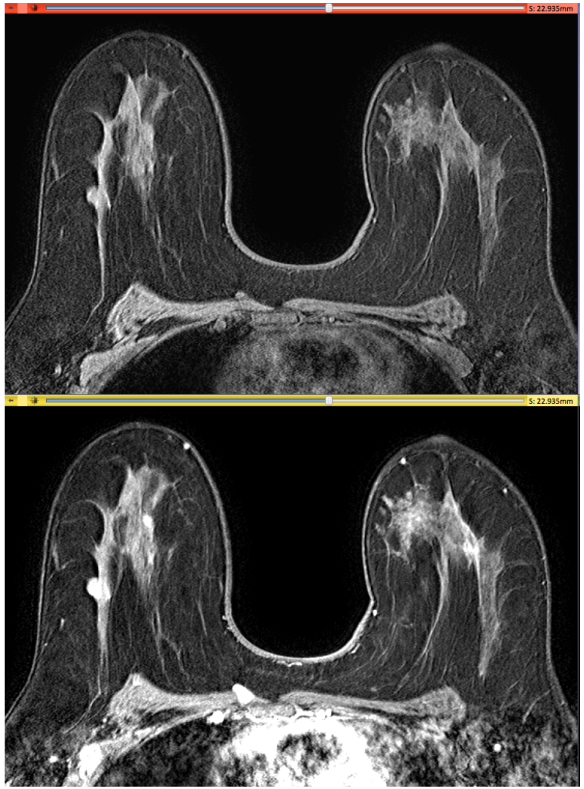


Pre-Gad

Post-Gad

Tumor volume (May): 75 cm3

PostTherapy acquisition

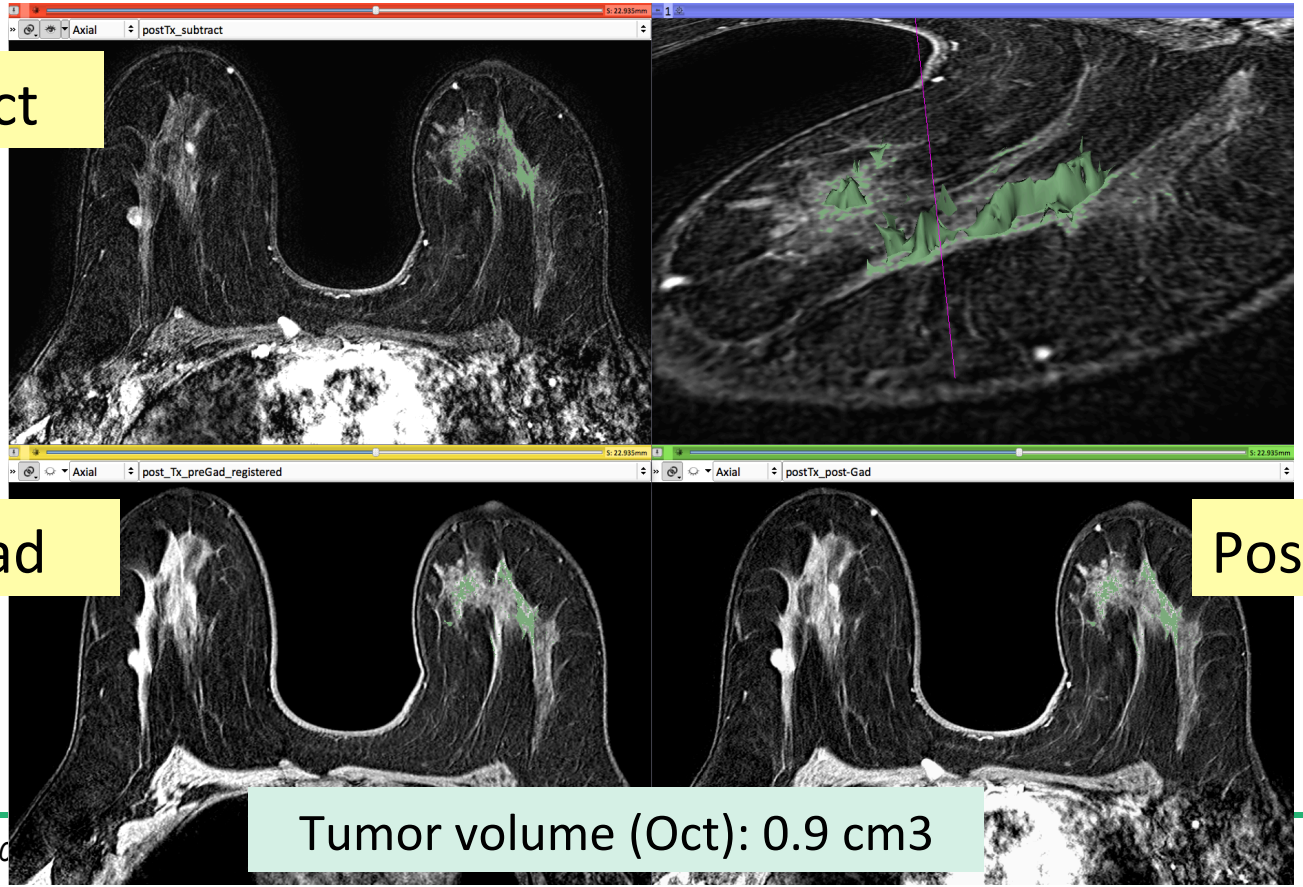


Pre-Gad High resolution scan

Post-Gad High resolution scan

Post-therapy analysis (Oct. 2013)

Subtract

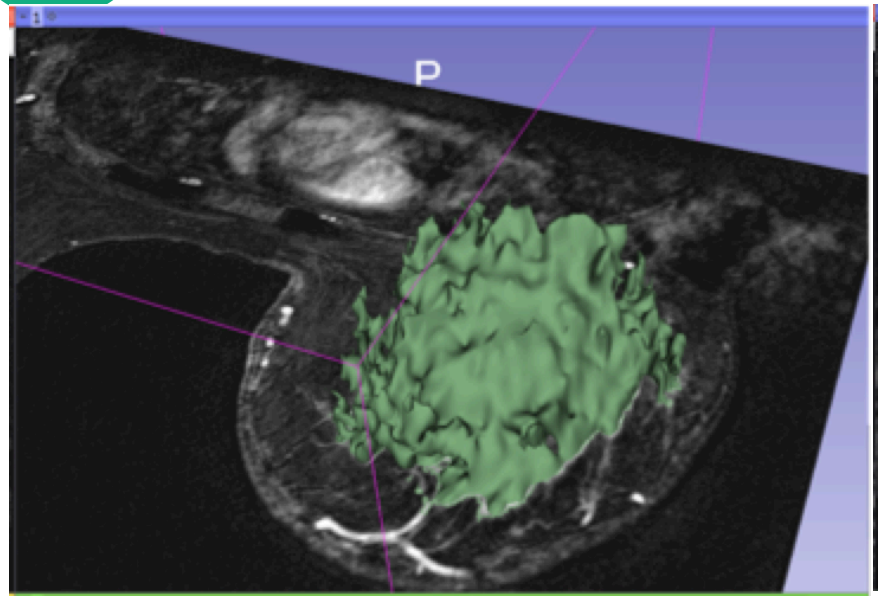


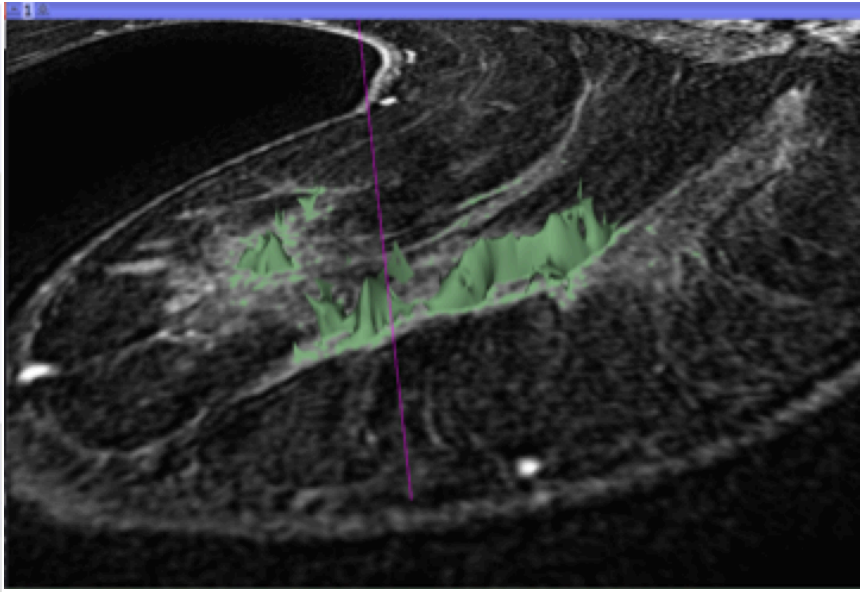
Pre-Gad

Post-Gad

Tumor volume (Oct): 0.9 cm3

Example1: Large Volumetric Change



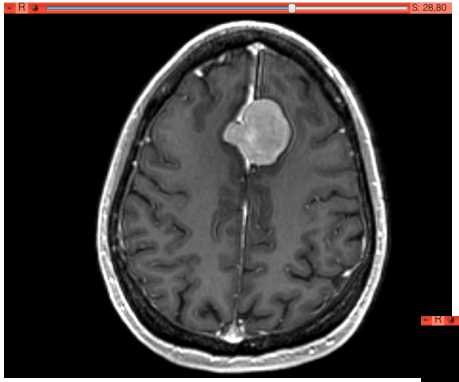


Tumor volume (May): 75 cm3

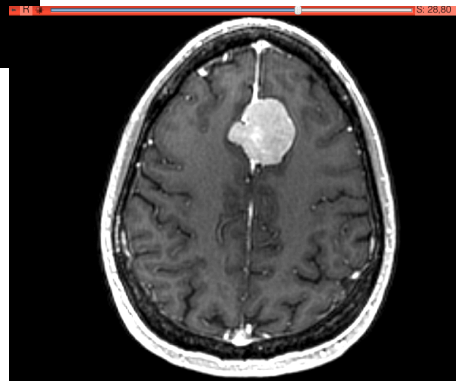
Tumor volume (Oct): 0.9 cm3

Example 2: Small volumetric change

MR Scan1 2006



MR Scan2 2007

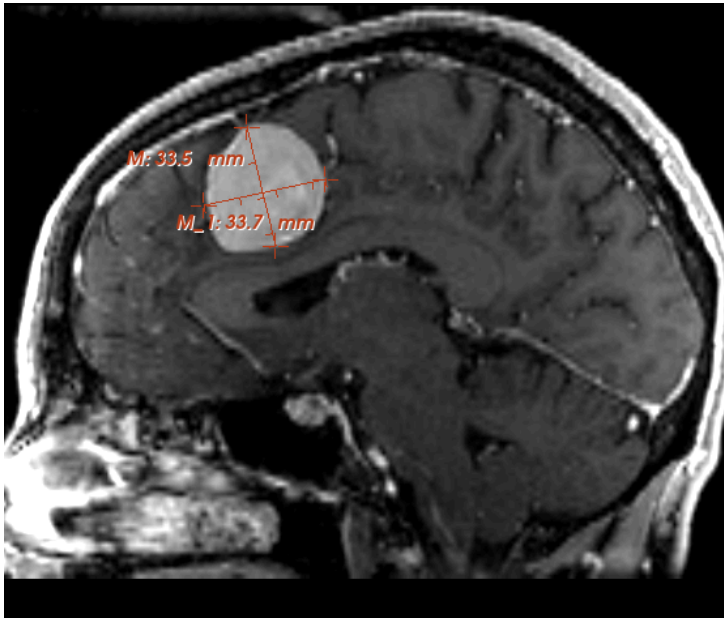


(Voxel dimension: 0.94mm x 0.94mm x 1.20mm, FOV: 240mm, Matrix: 256 x 256)

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.

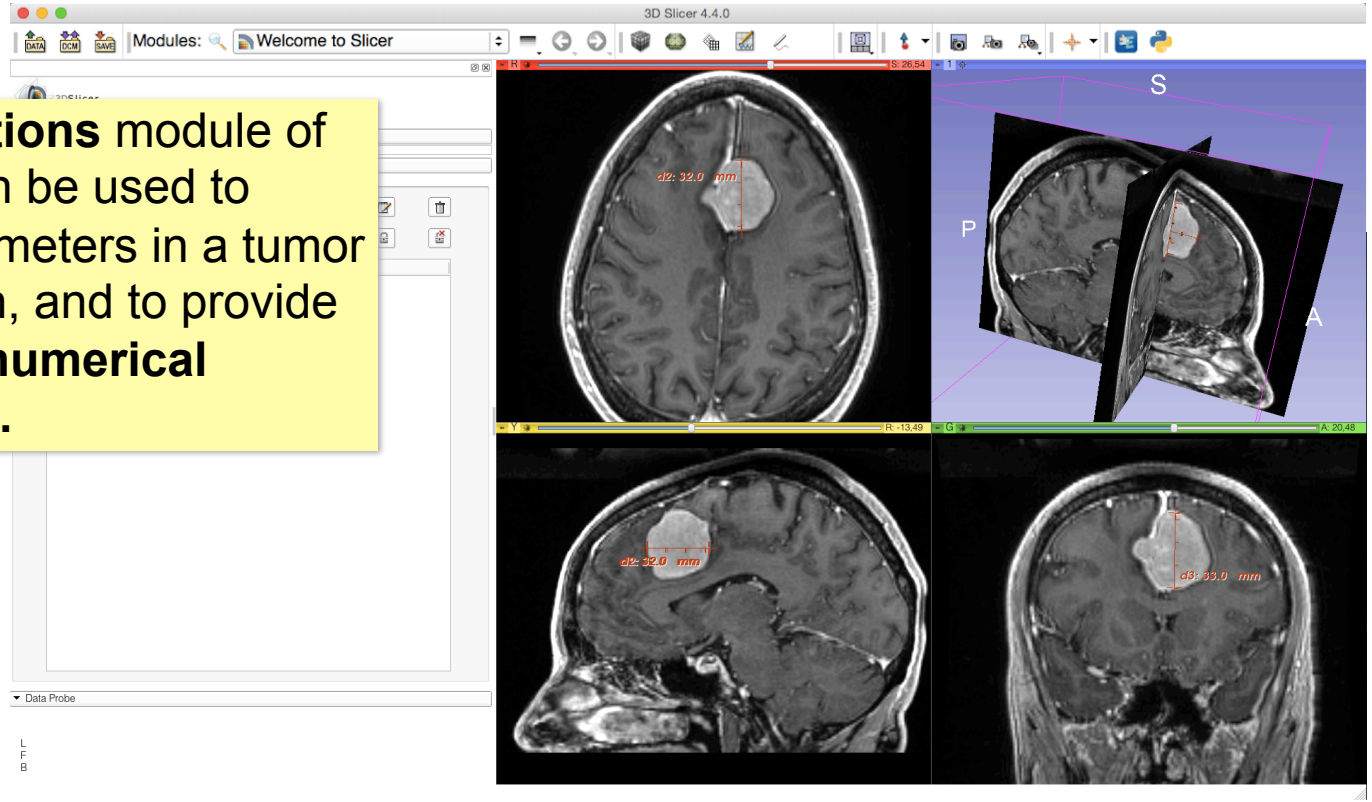
Conventional measures of tumor response



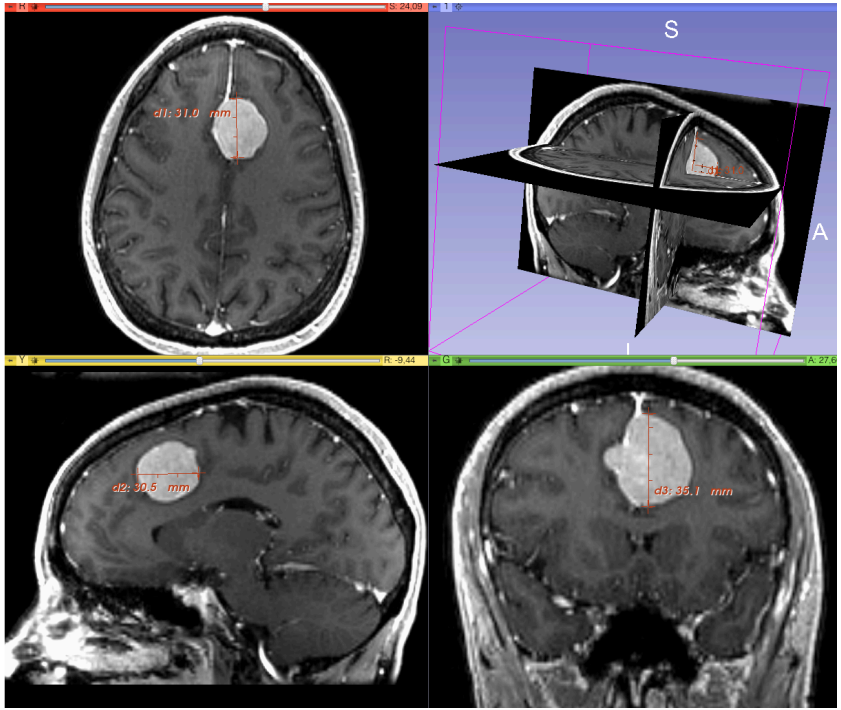
- Conventional anatomic imaging using CT or MRI are often used to evaluate tumor size and shape
- Most clinical trials that evaluate new chemotherapeutic drugs use changes in uni-dimensional or bi-dimensional measurements to assess response (*e.g.* RECIST)
- Slicer has several tools for applying RECIST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



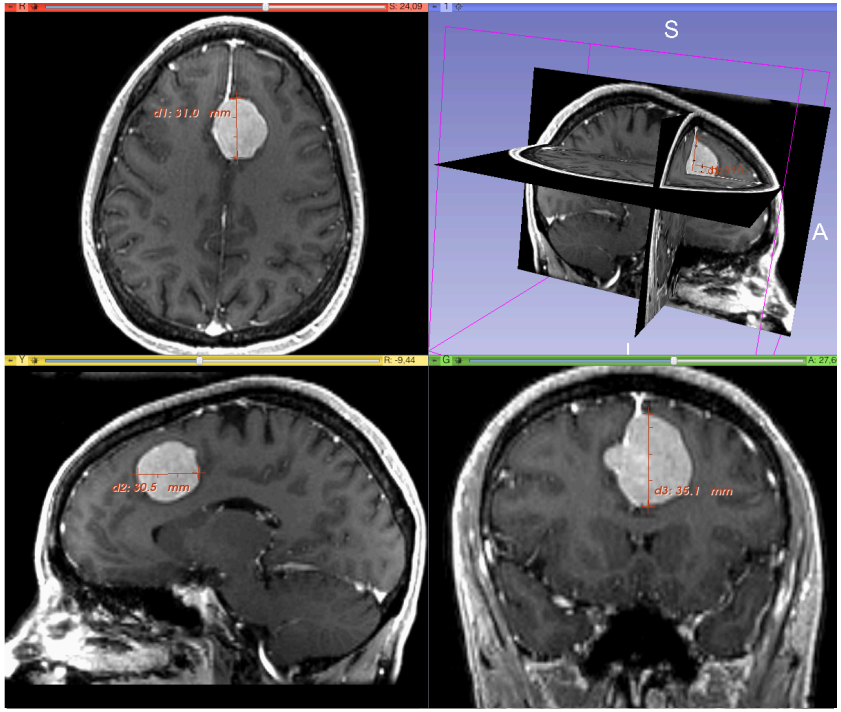
Clinical Case: baseline scan (2006)



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.

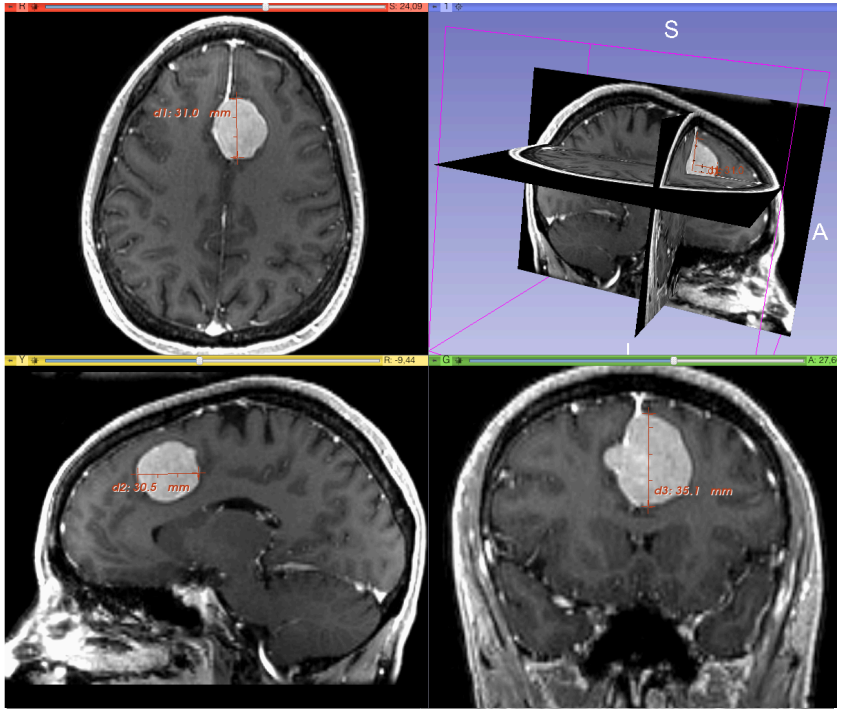
Clinical Case: follow-up scan (2007)



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.

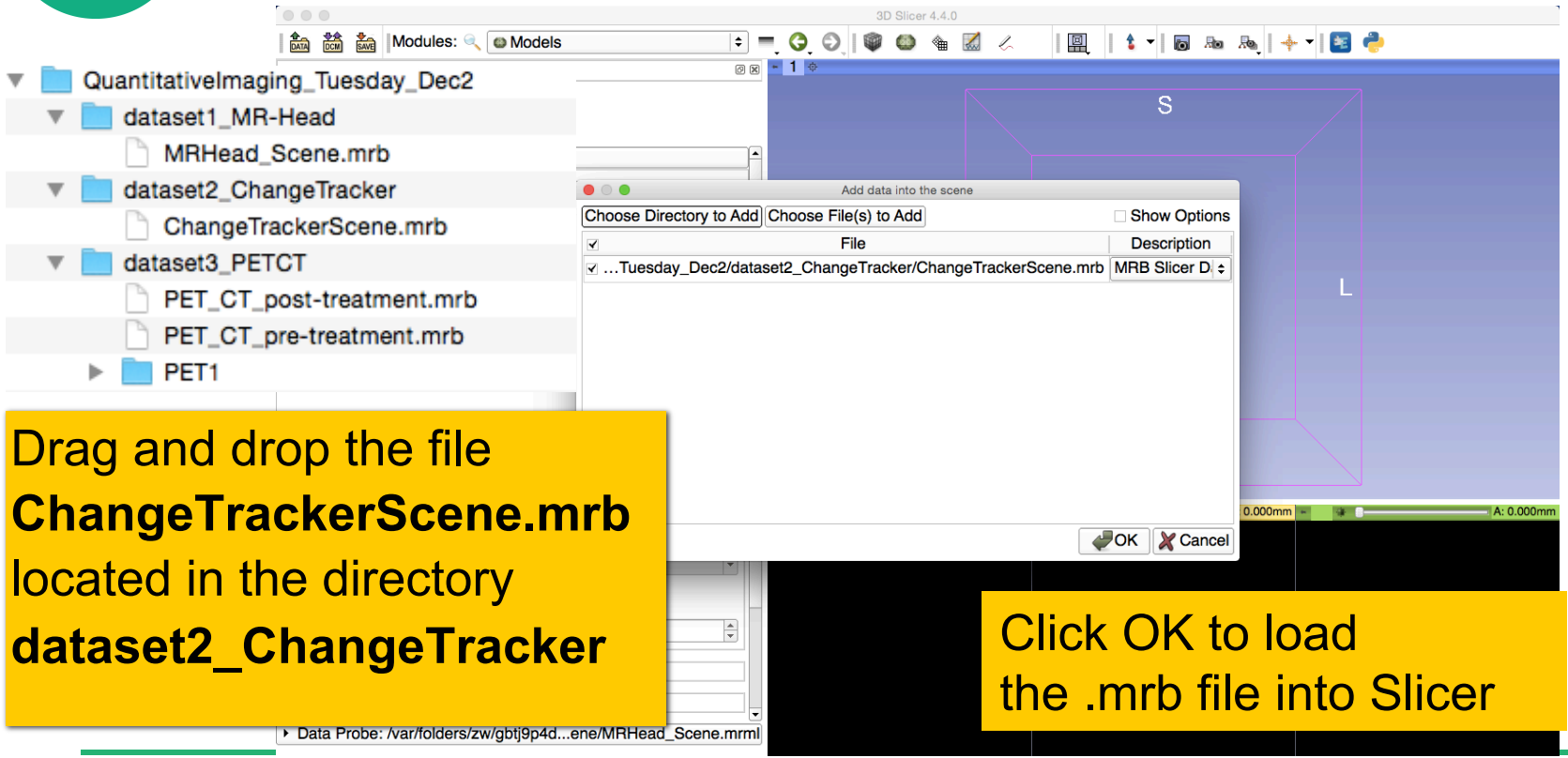
→ How has the tumor changed?

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



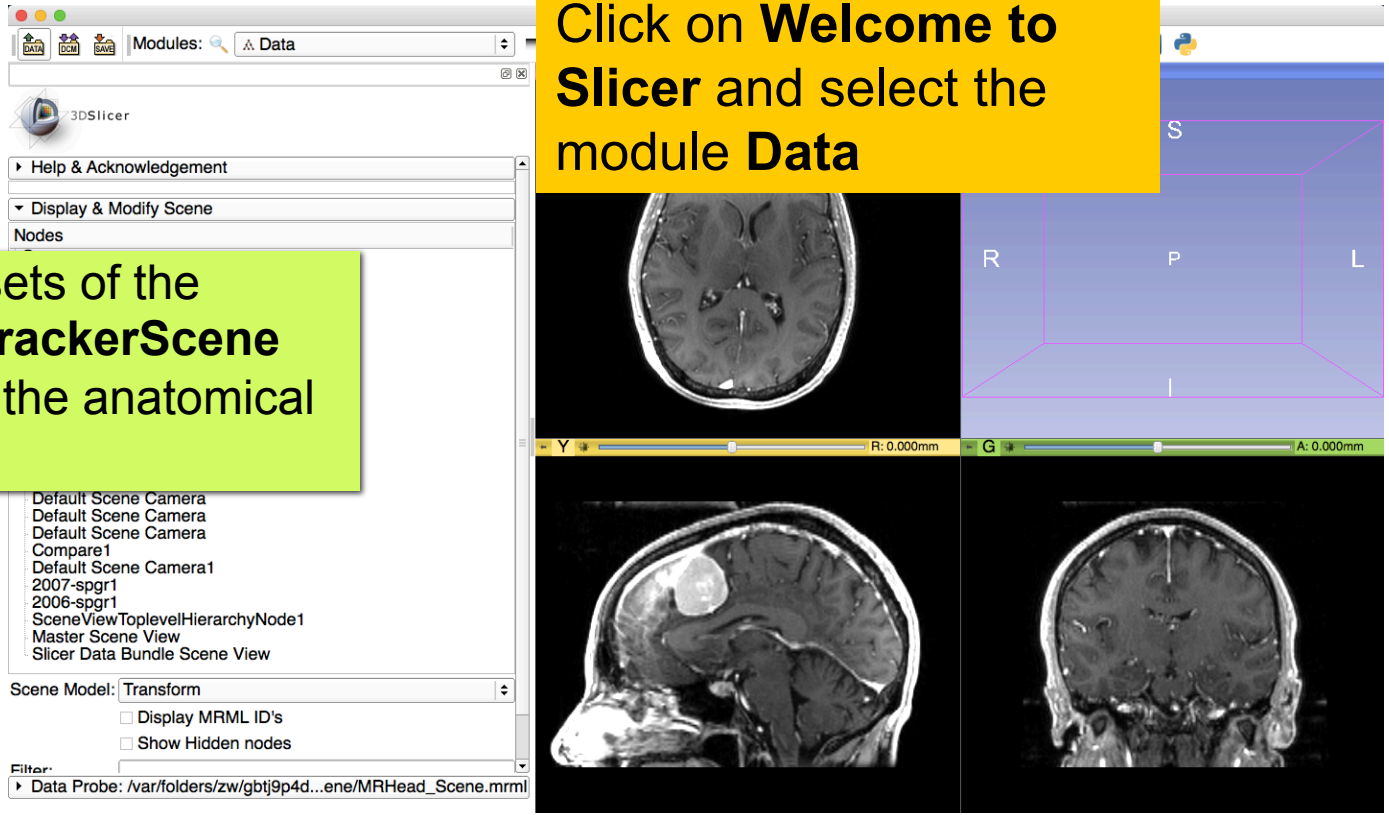
Drag and drop the file **ChangeTrackerScene.mrb** located in the directory **dataset2_ChangeTracker**

Click OK to load the .mrb file into Slicer

Loading the data

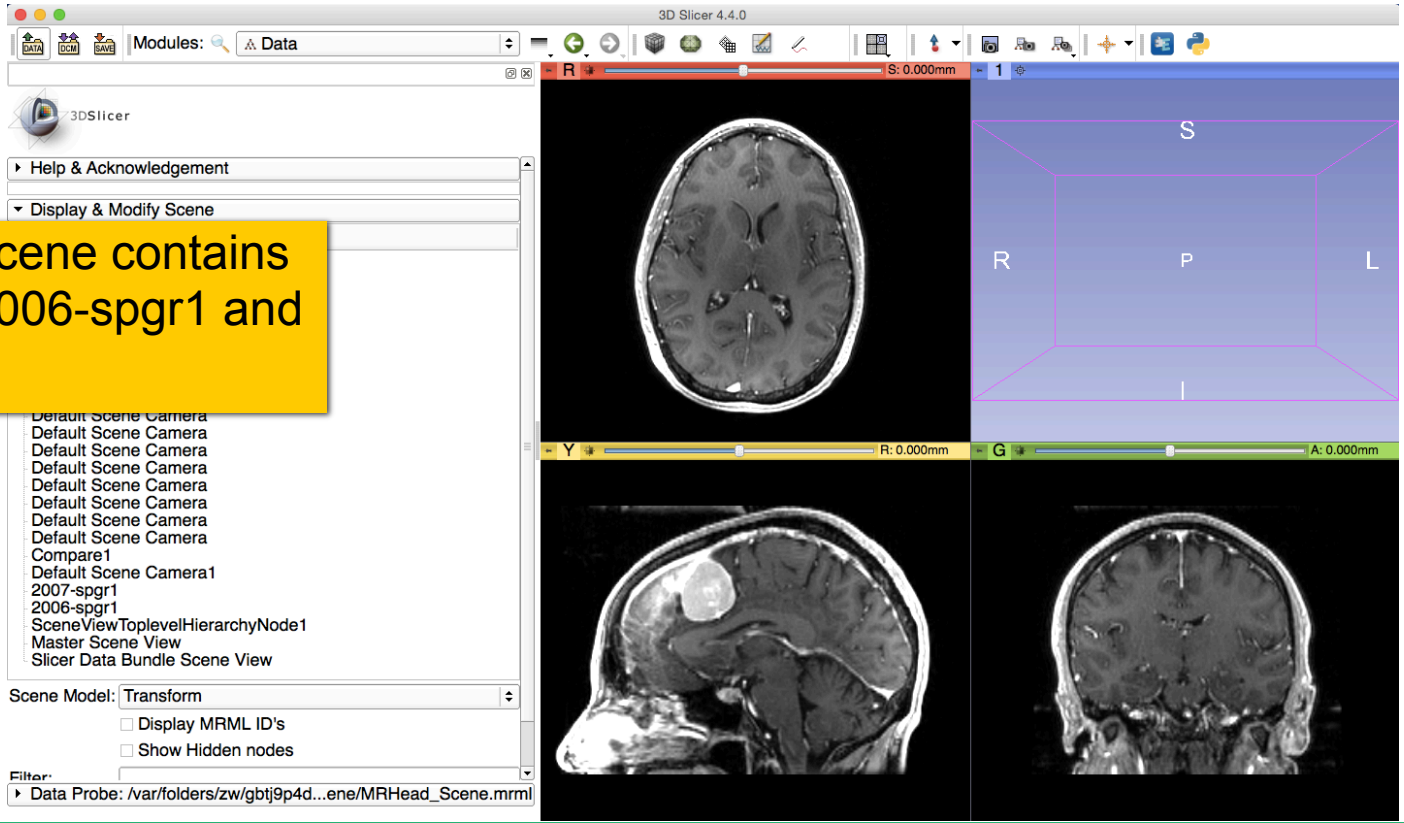
Click on **Welcome to Slicer** and select the module **Data**

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

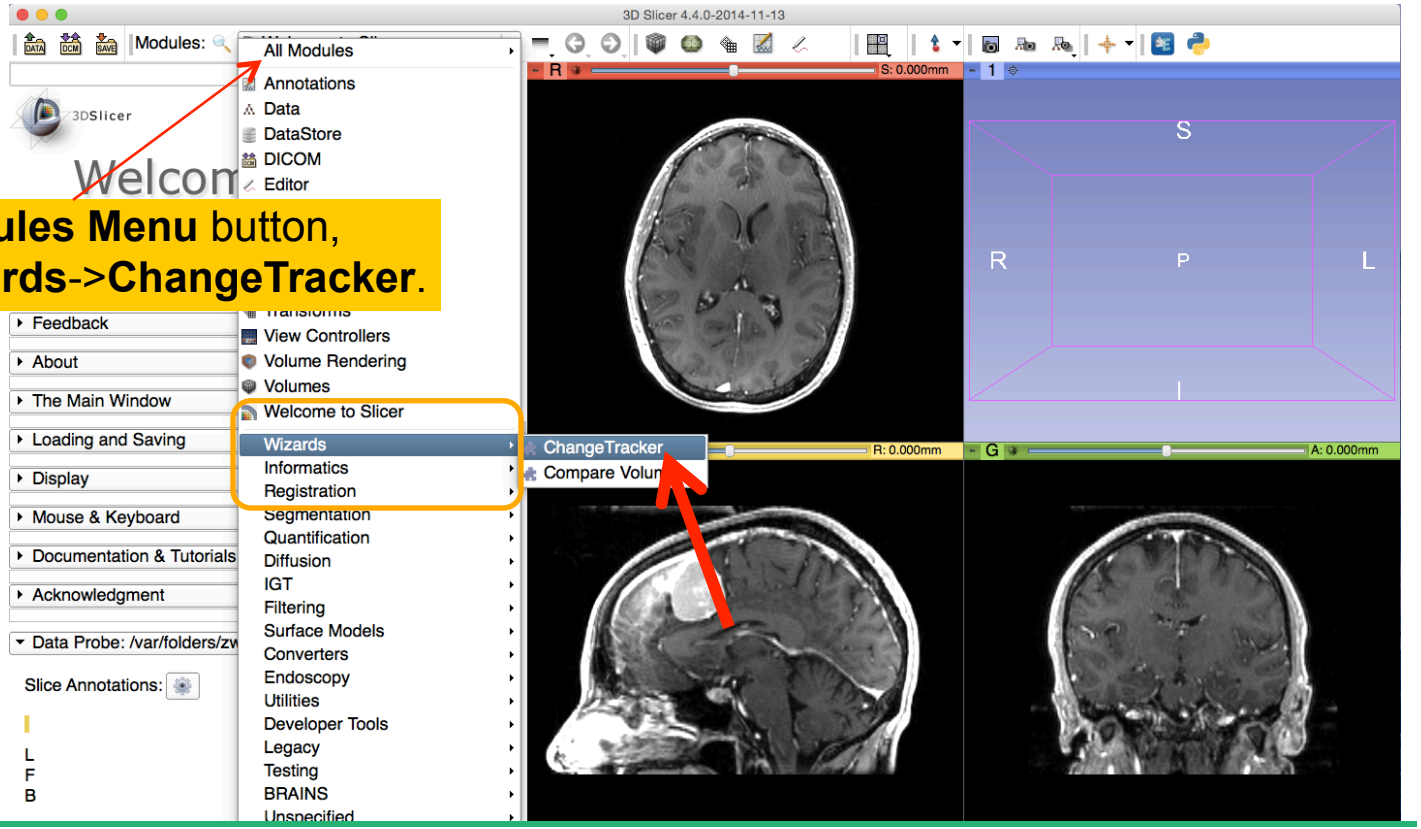


Loading the data

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



ChangeTracker: exploring small volumetric changes

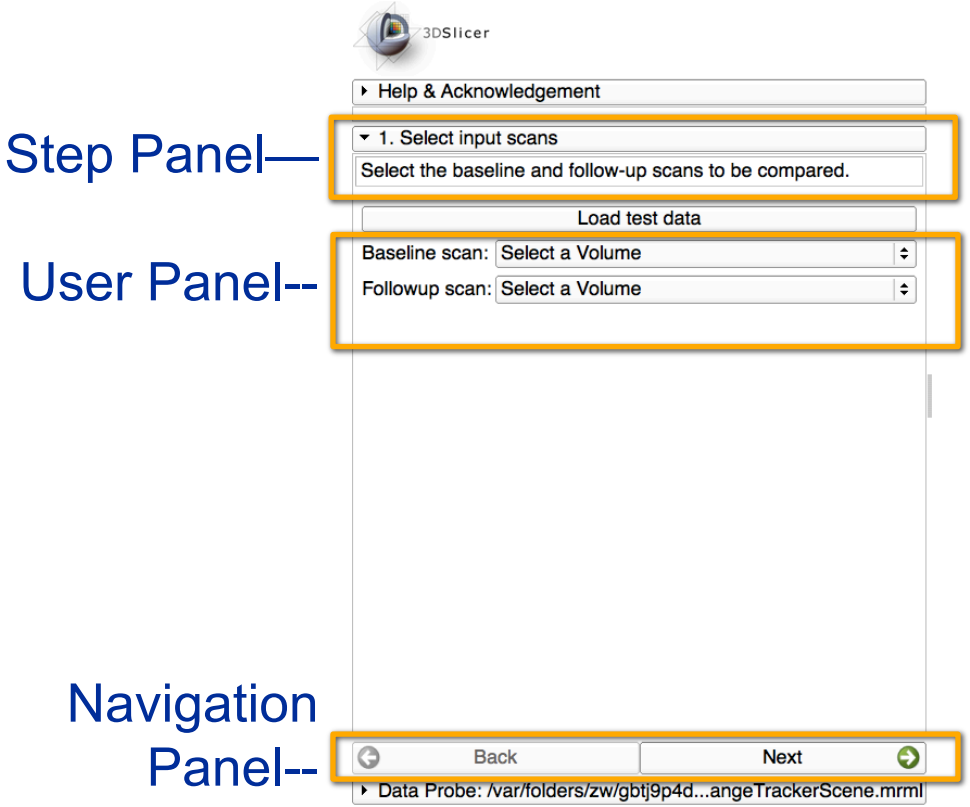


Using the **Modules Menu** button, select the **Wizards->ChangeTracker**.

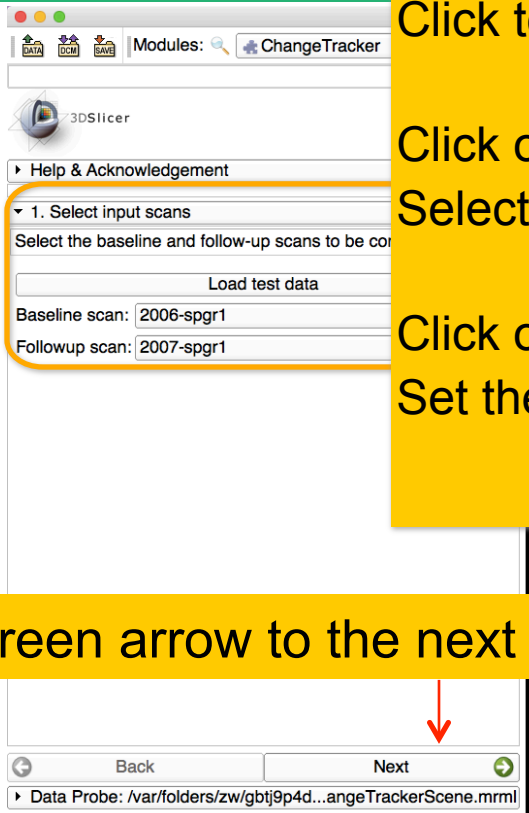
ChangeTracker: a note about the Workflow wizard

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



Step1: Select input scans

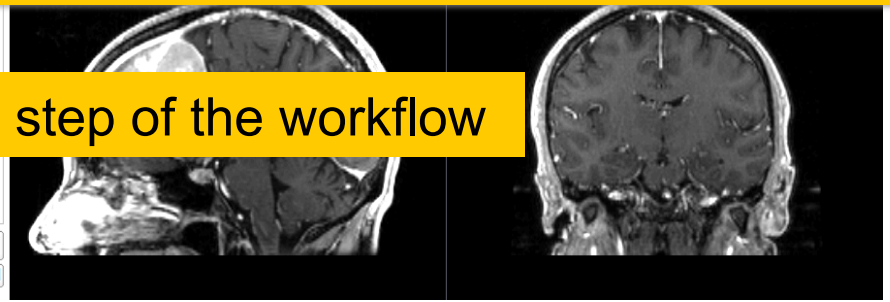


Click to expand the tab **'1.Select input scans'**

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

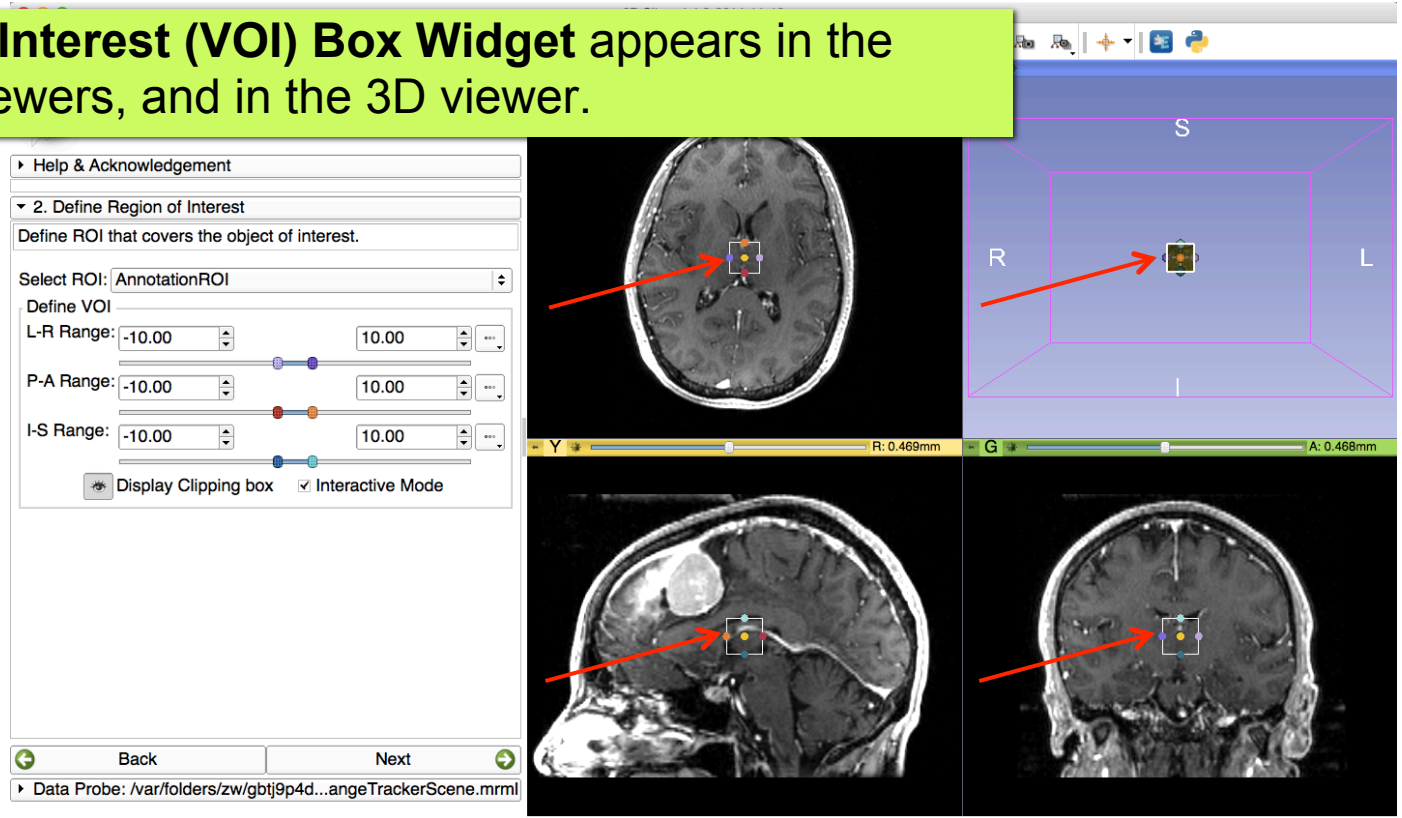
Click on **Select a Volume** next to **Follow up Scan**
Set the volume **2007-spgr1**

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.

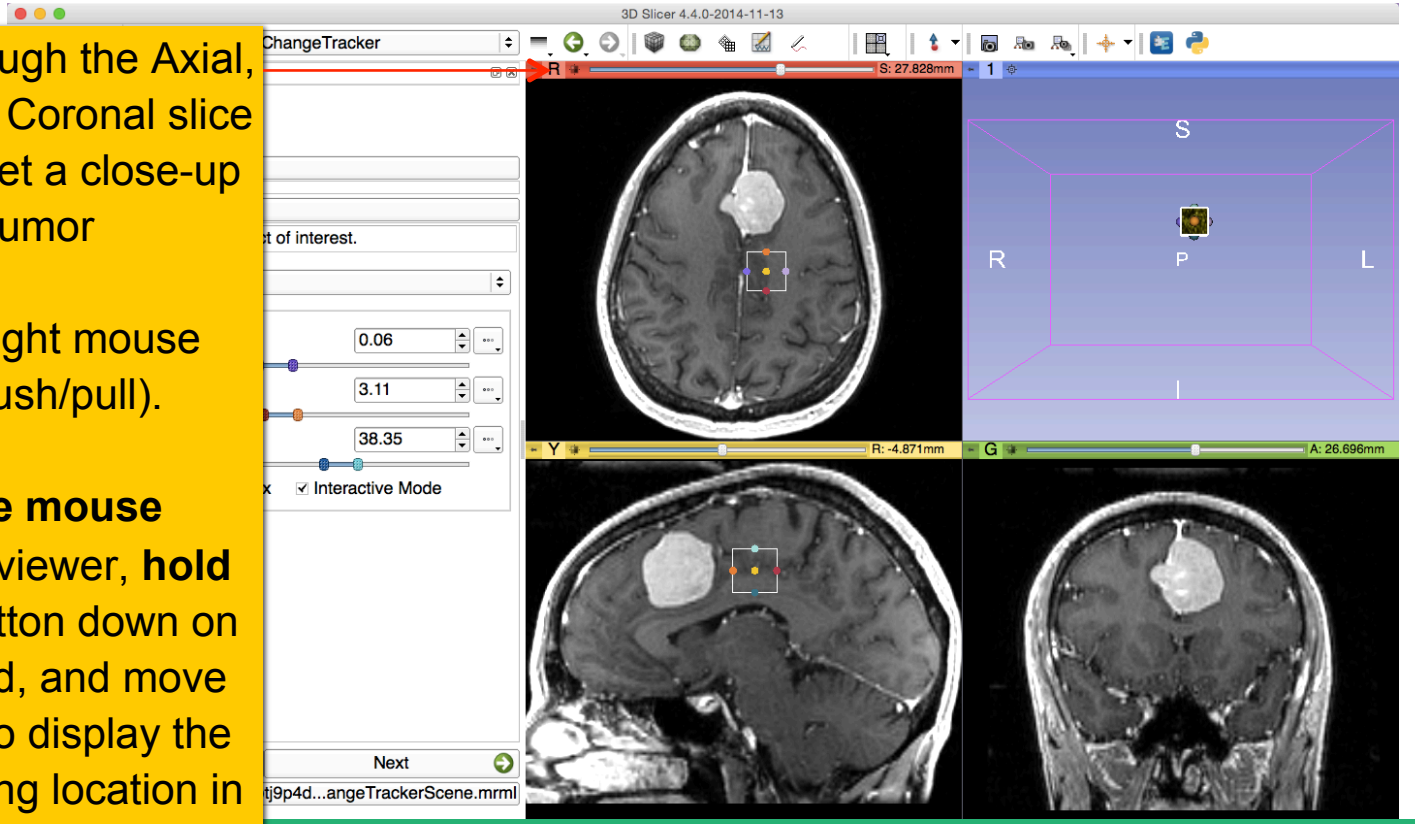


Step2: Define Region of interest

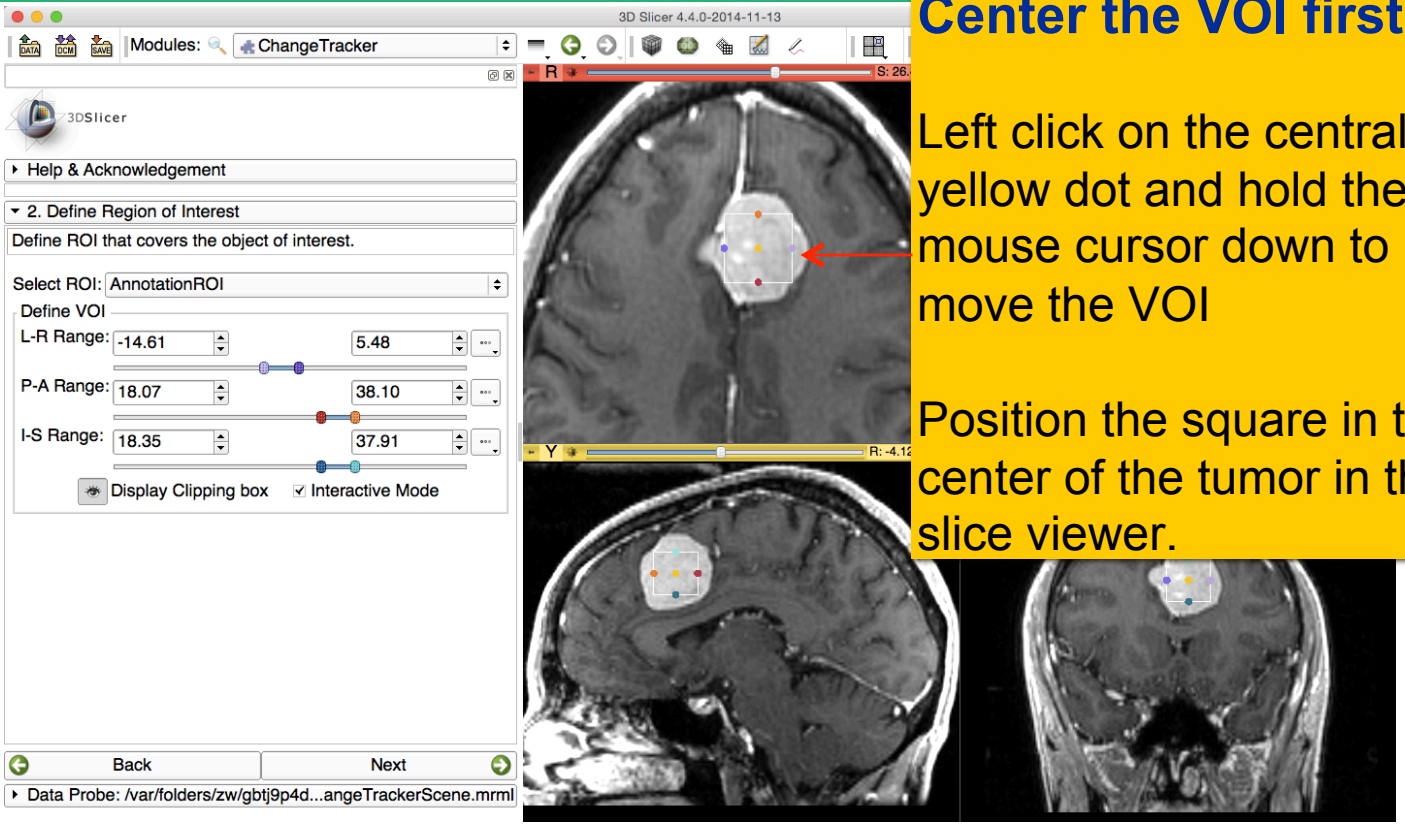
Browse through the Axial, Sagittal and Coronal slice viewers to get a close-up view of the tumor

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

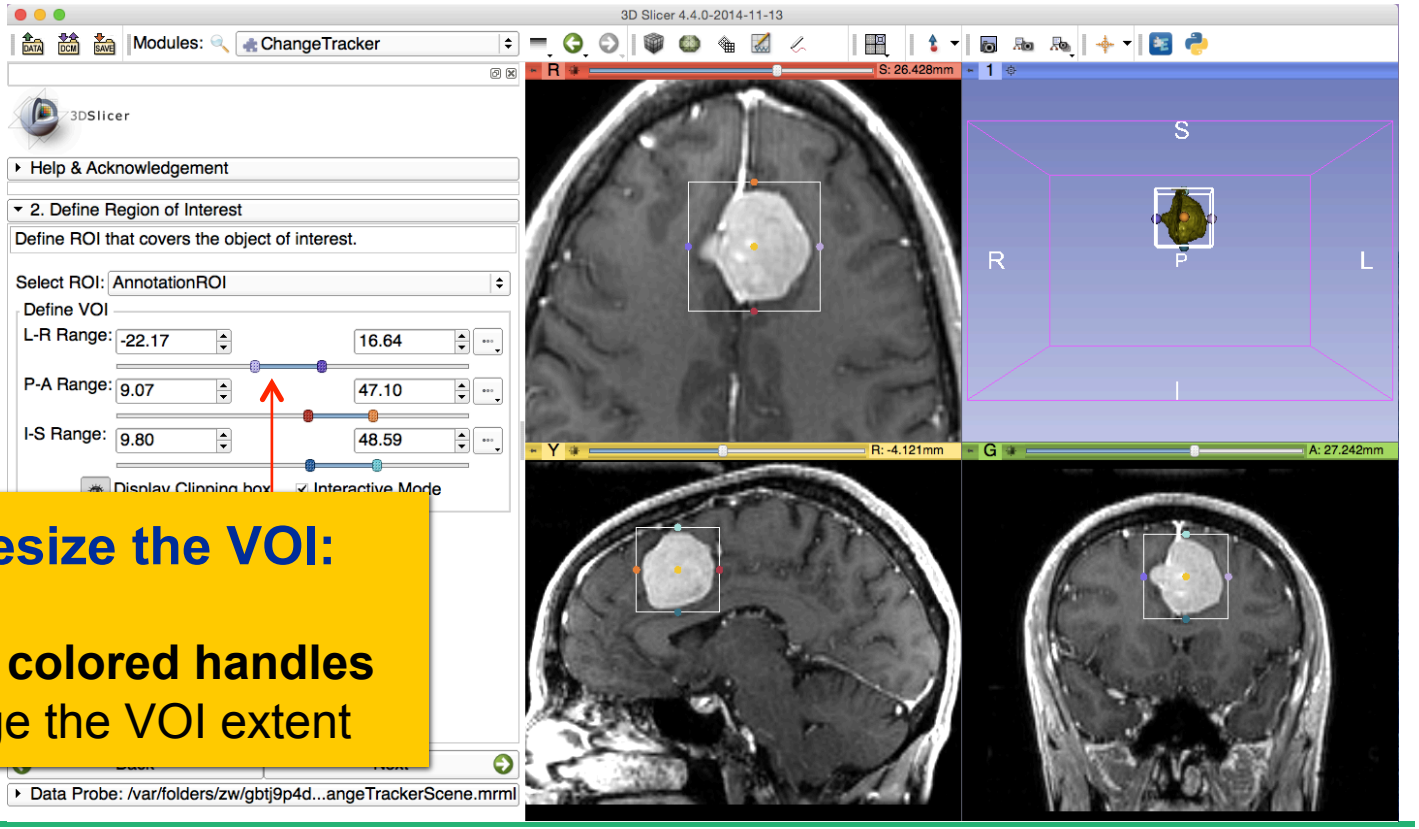


Center the VOI first:

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.

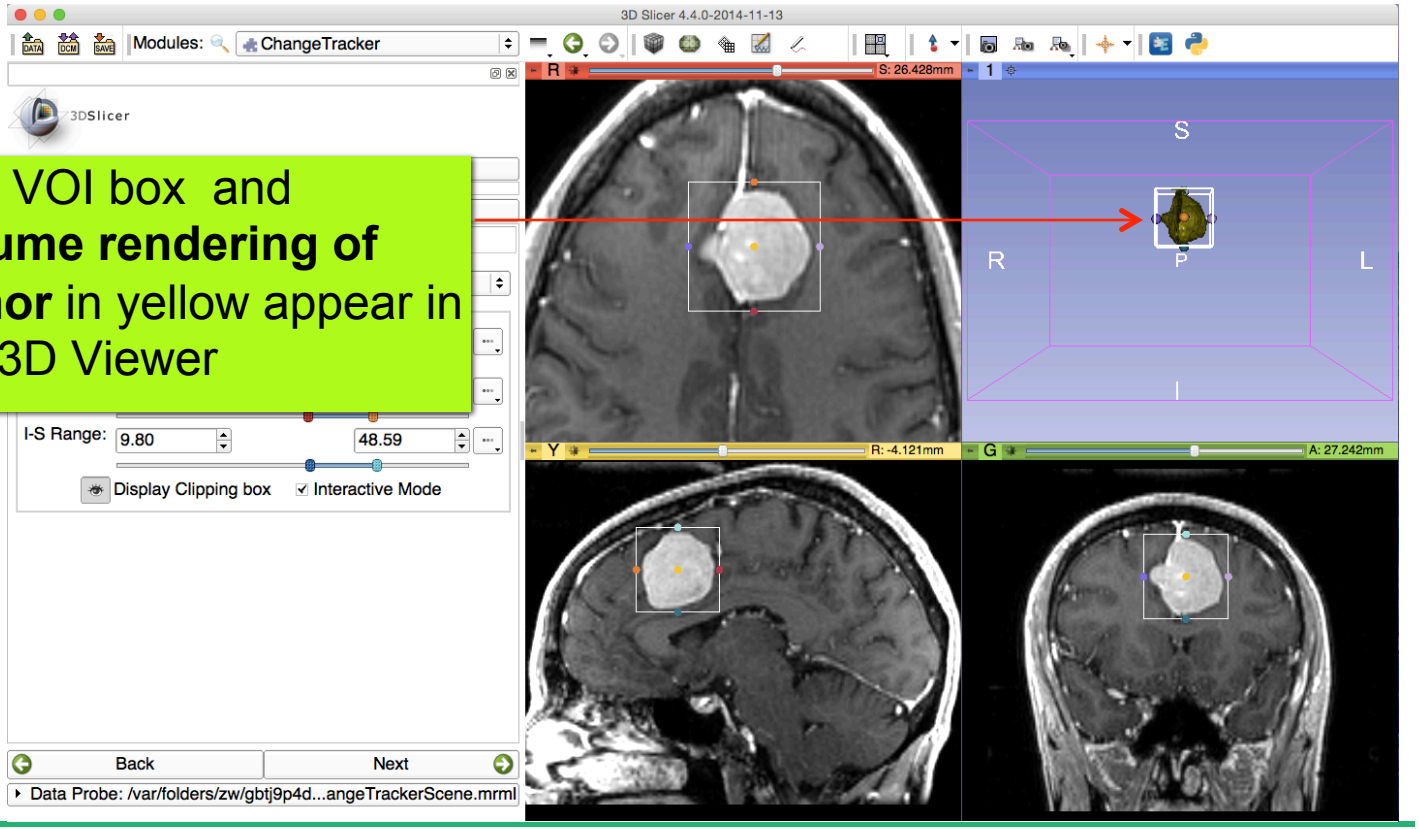
Step2: Define Region of interest



Next, resize the VOI:

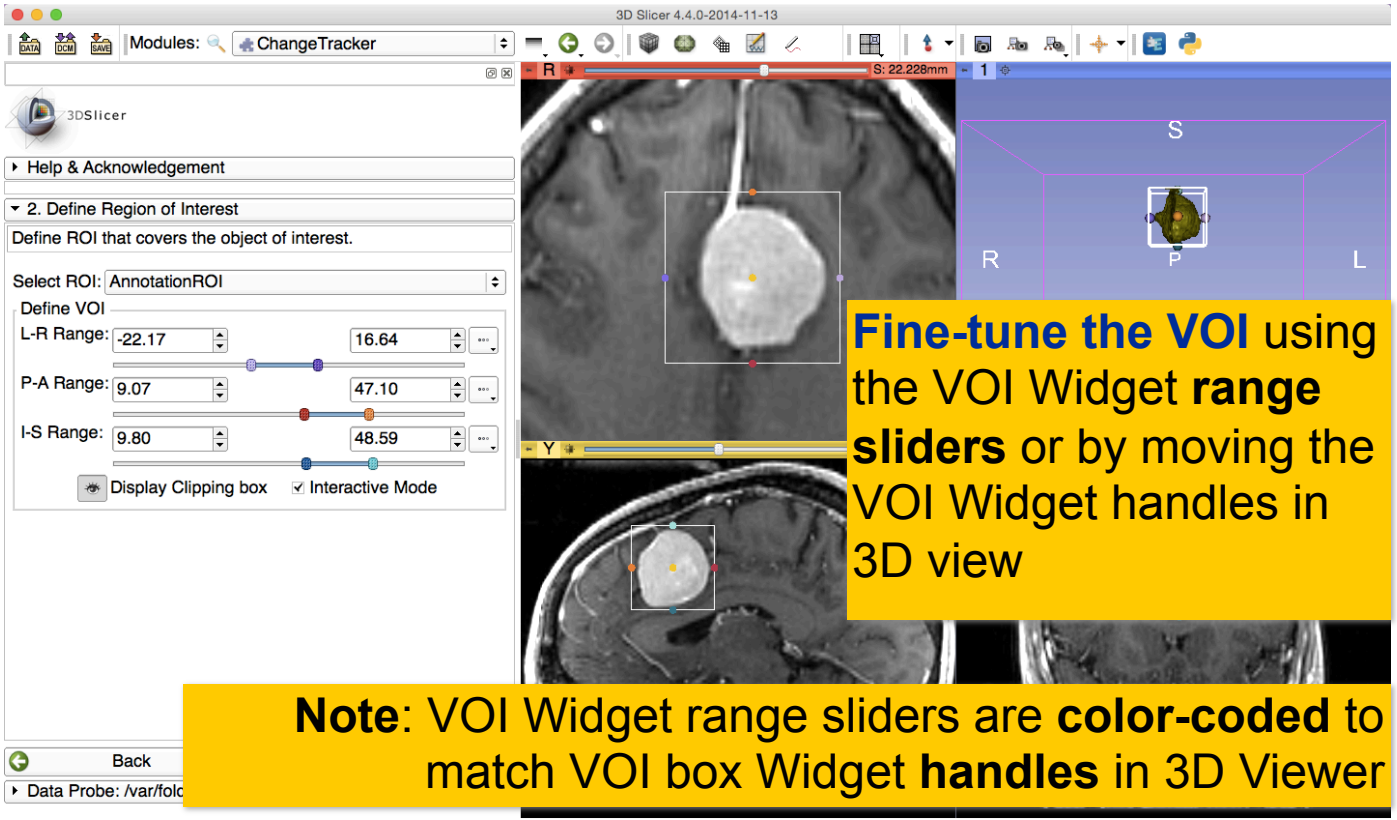
Use the colored handles
to change the VOI extent

Step2: Define Region of interest



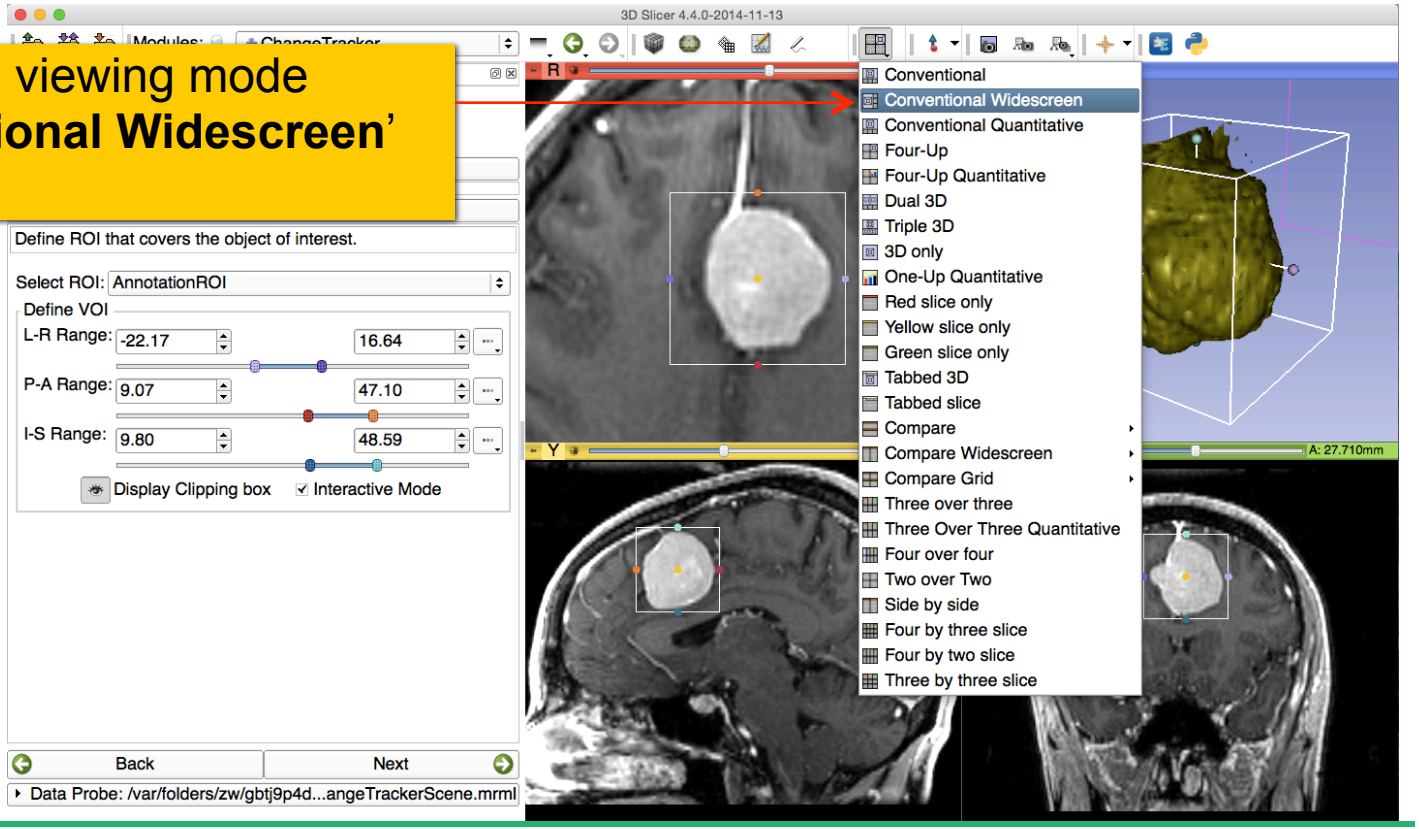
The VOI box and **volume rendering of tumor** in yellow appear in the 3D Viewer

Step2: Define Region of interest

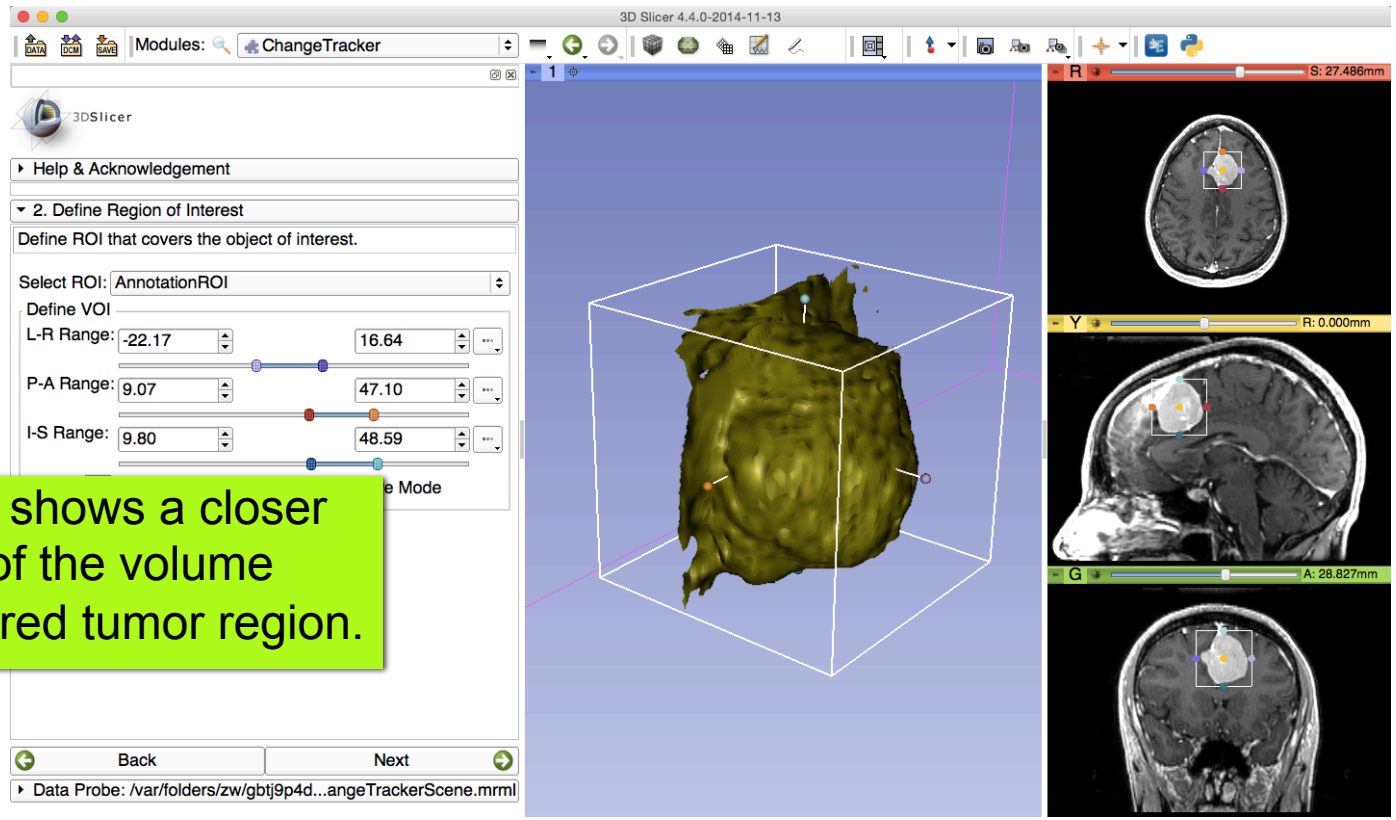


Step2: Define Region of interest

Select the viewing mode ‘**Conventional Widescreen**’

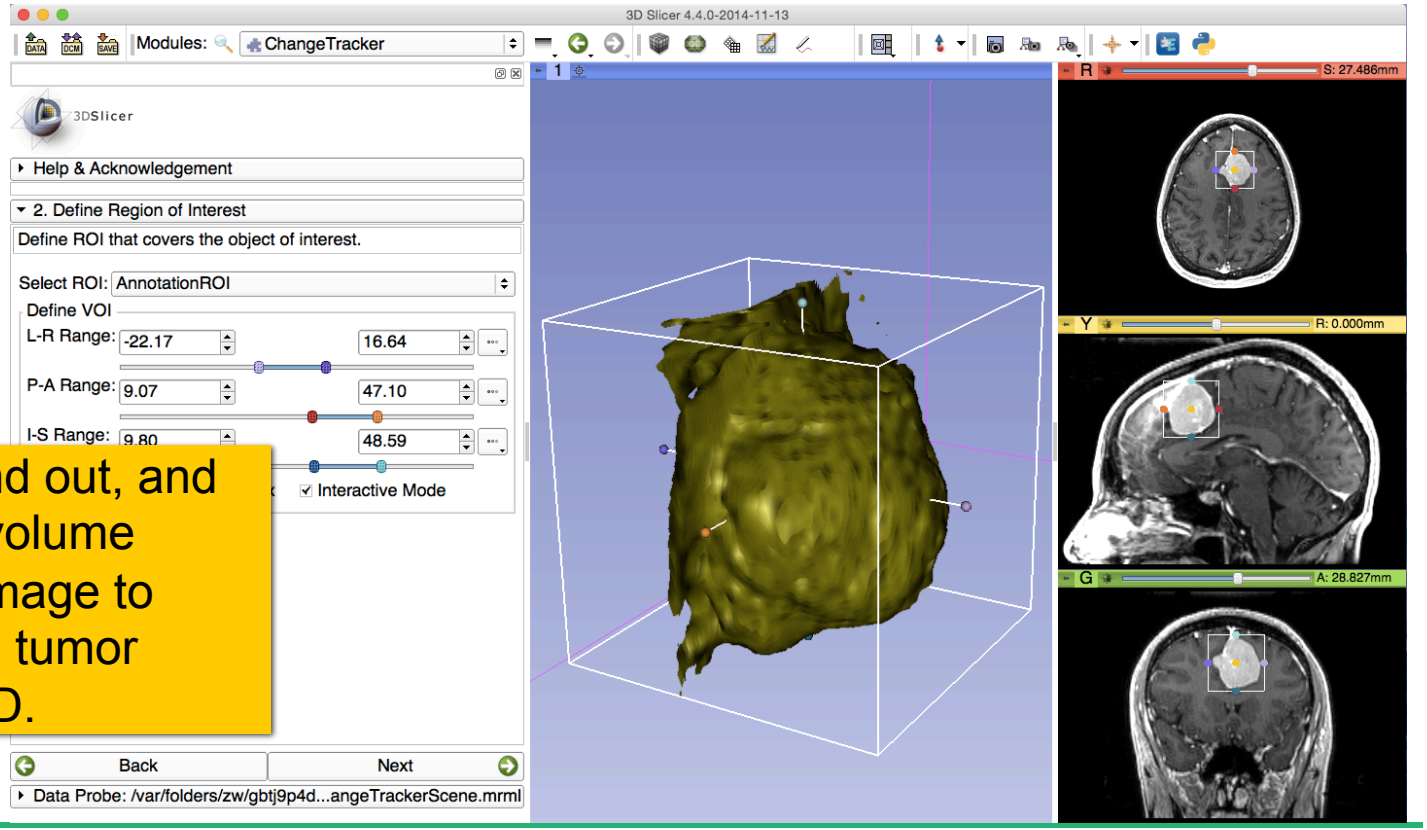


Step2: Define Region of interest



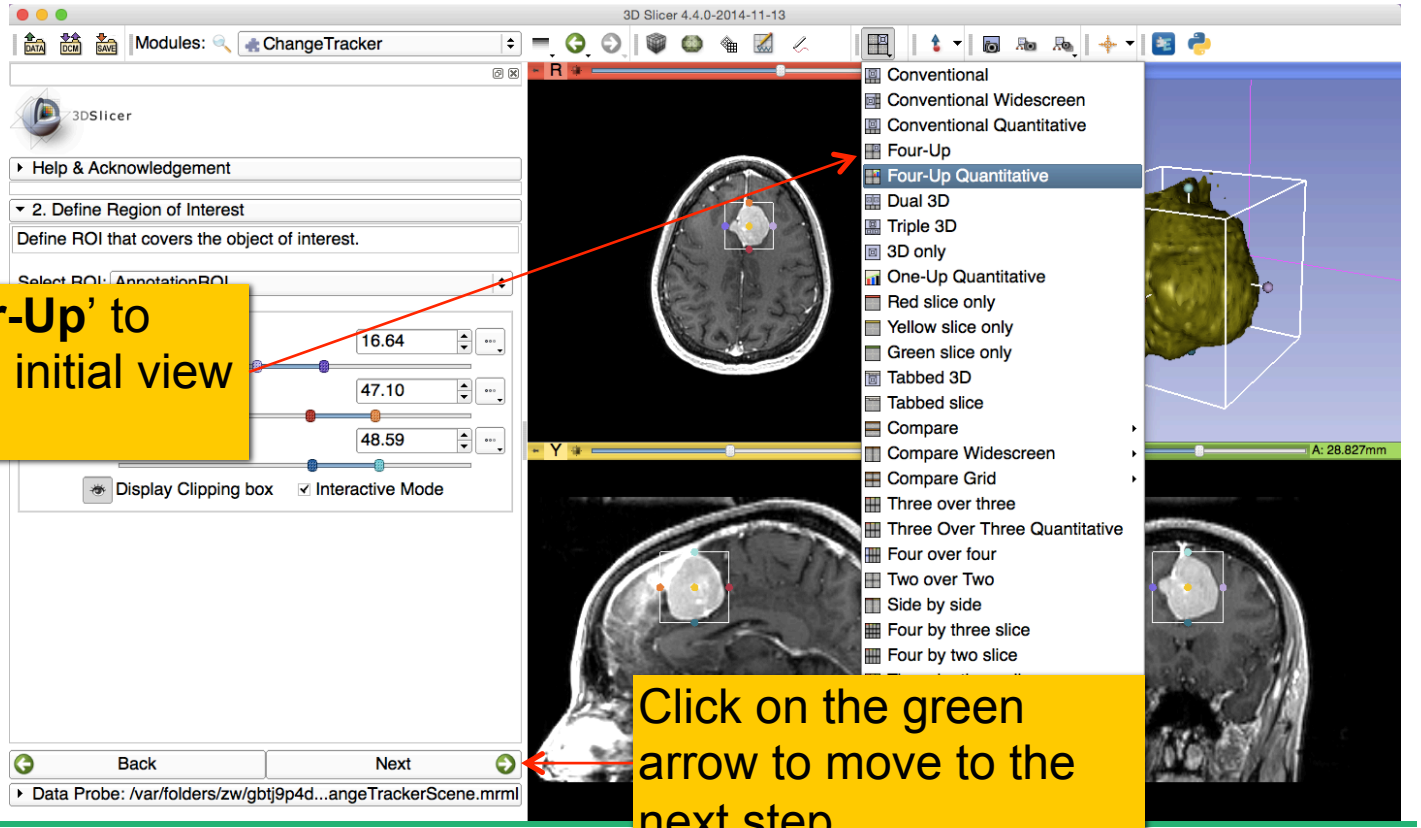
Slicer shows a closer view of the volume rendered tumor region.

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

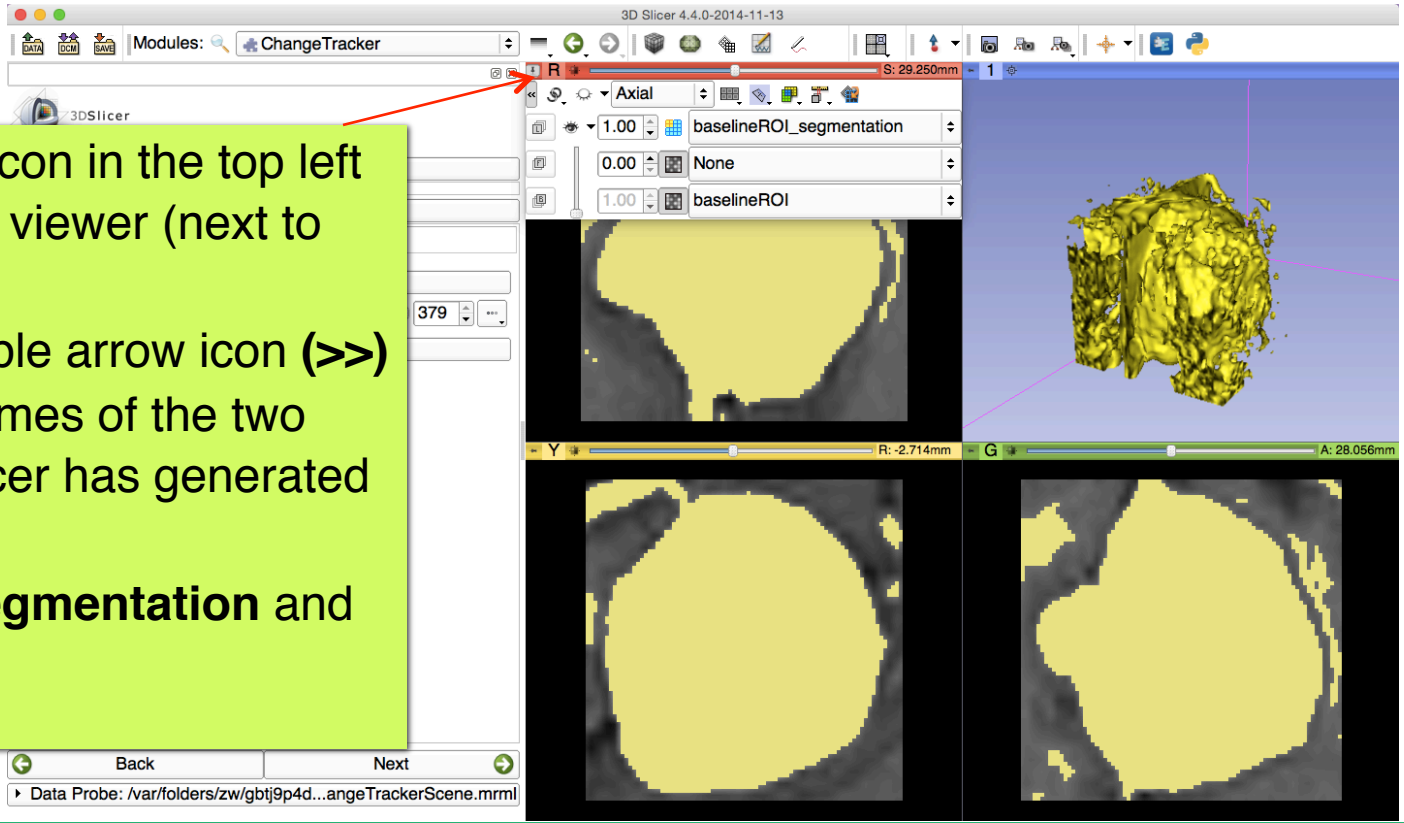


Select '**Four-Up**' to return to the initial view mode

Click on the green arrow to move to the next step

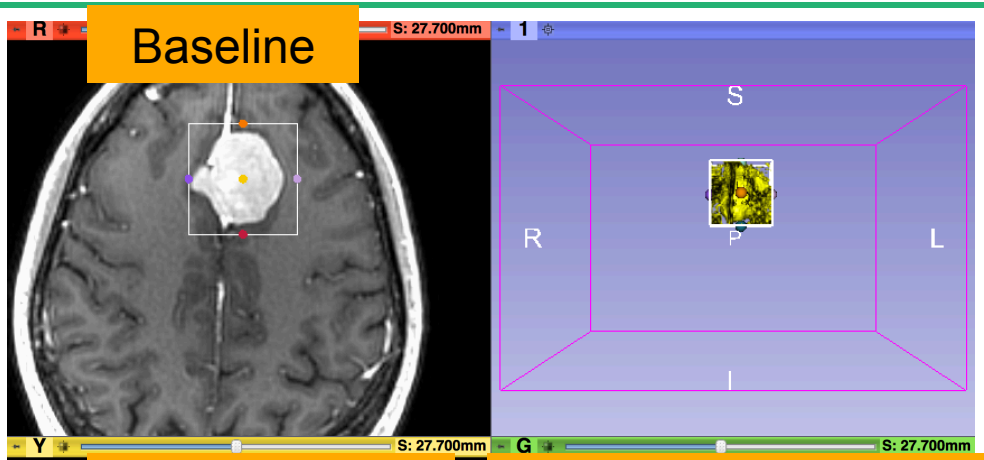
Step3: Segment the tumor

Click on the pin icon in the top left corner of the red 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**

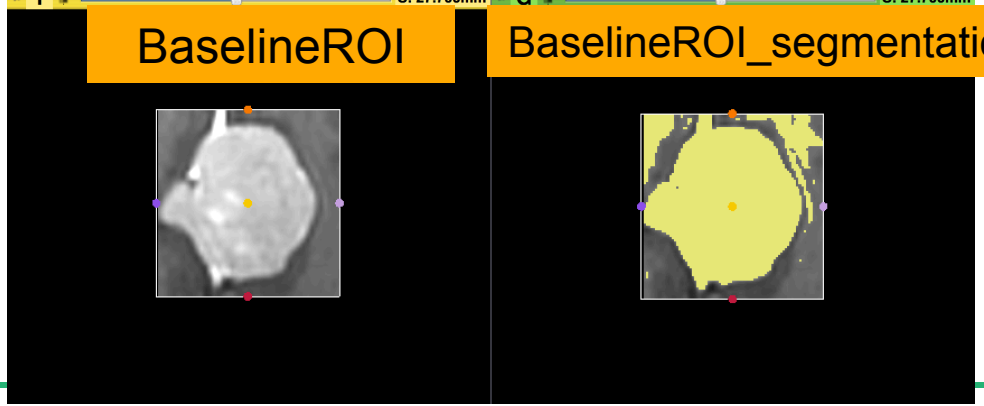


Segment the tumor

Step 1:
VOI
definition

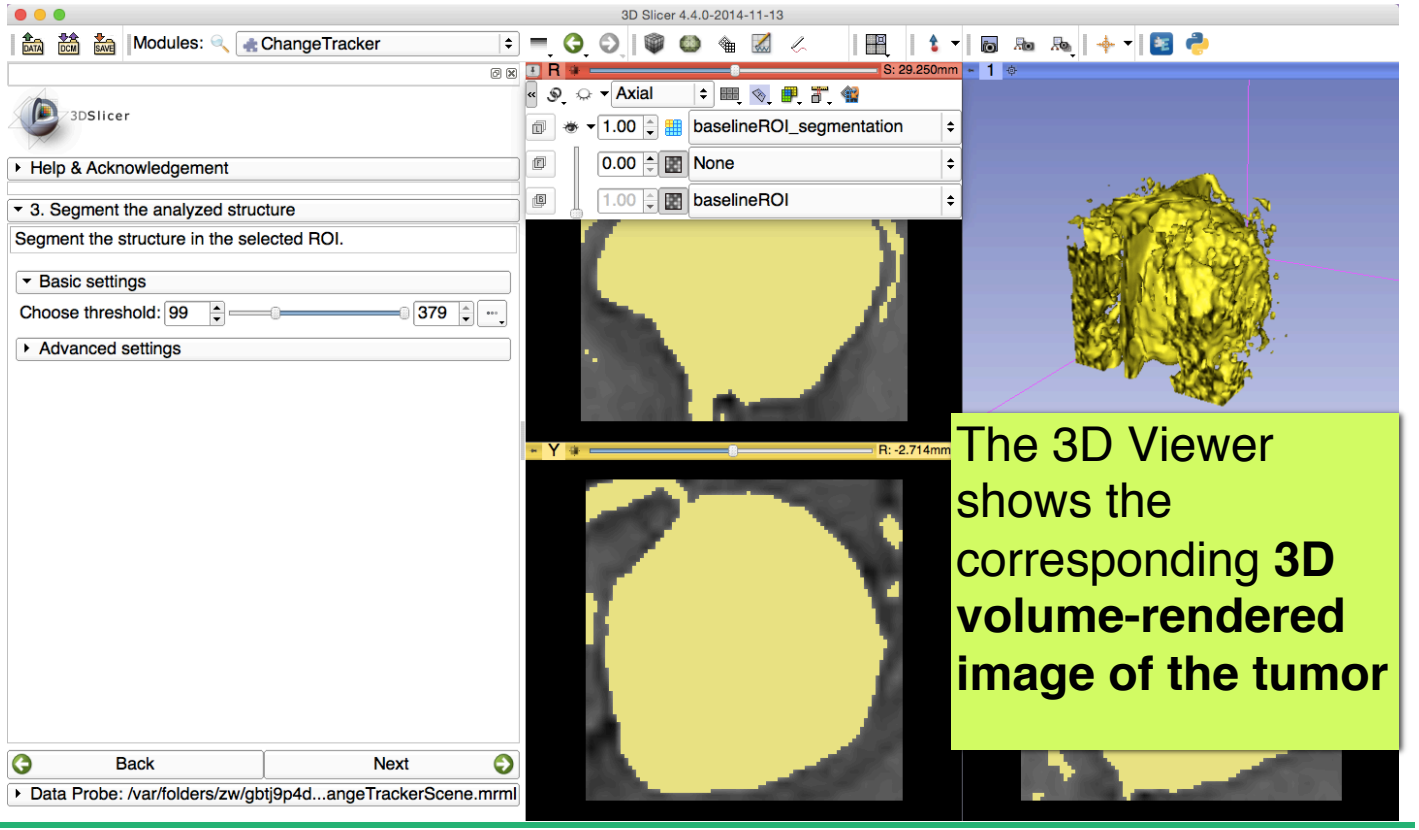


Step 2:
VOI
extraction

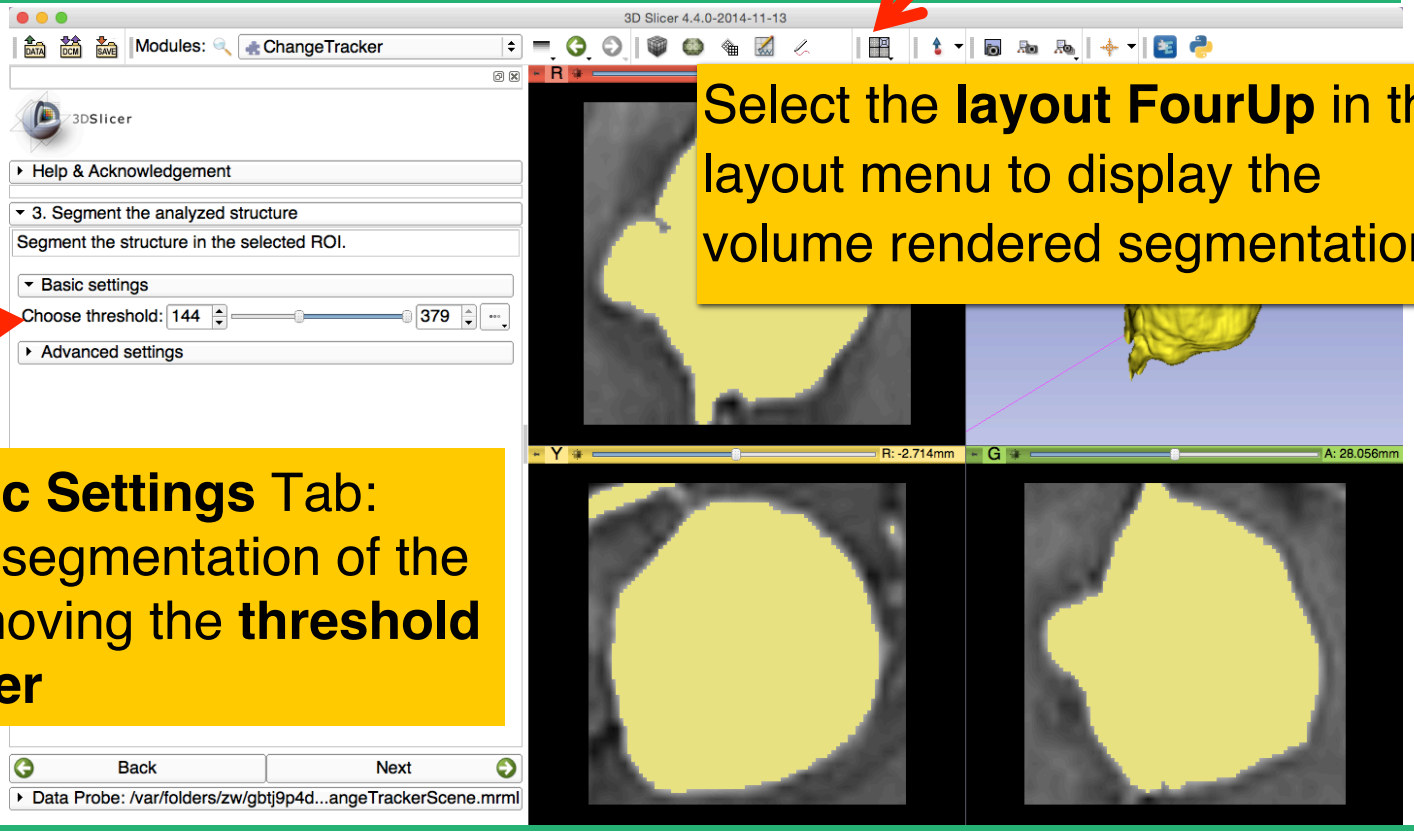


Step 3:
Segmentation

Step3: Segment the tumor



Step3: Segment the tumor

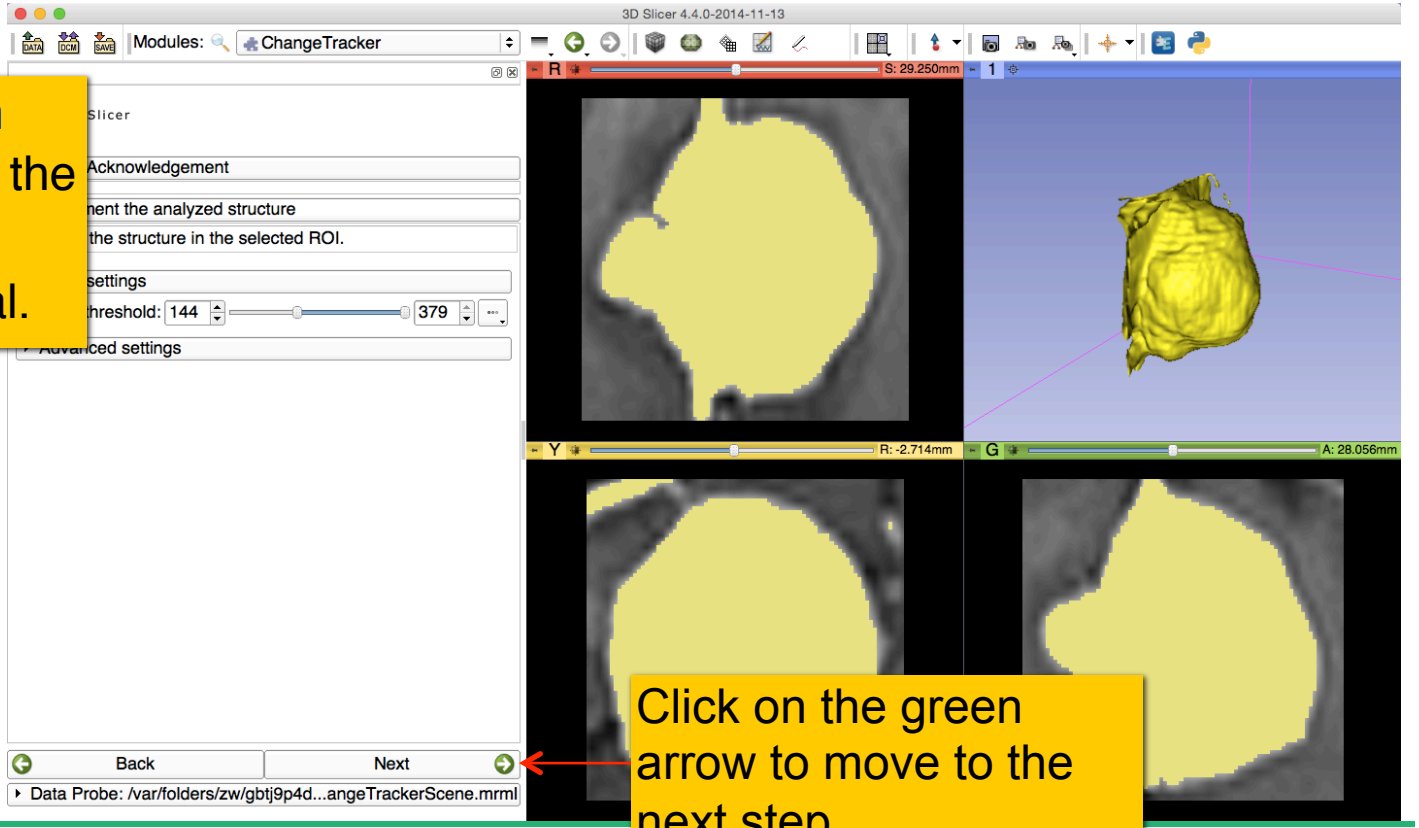


Select the **layout FourUp** in the layout menu to display the volume rendered segmentation

In the **Basic Settings** Tab: Modify the segmentation of the tumor by moving the **threshold range slider**

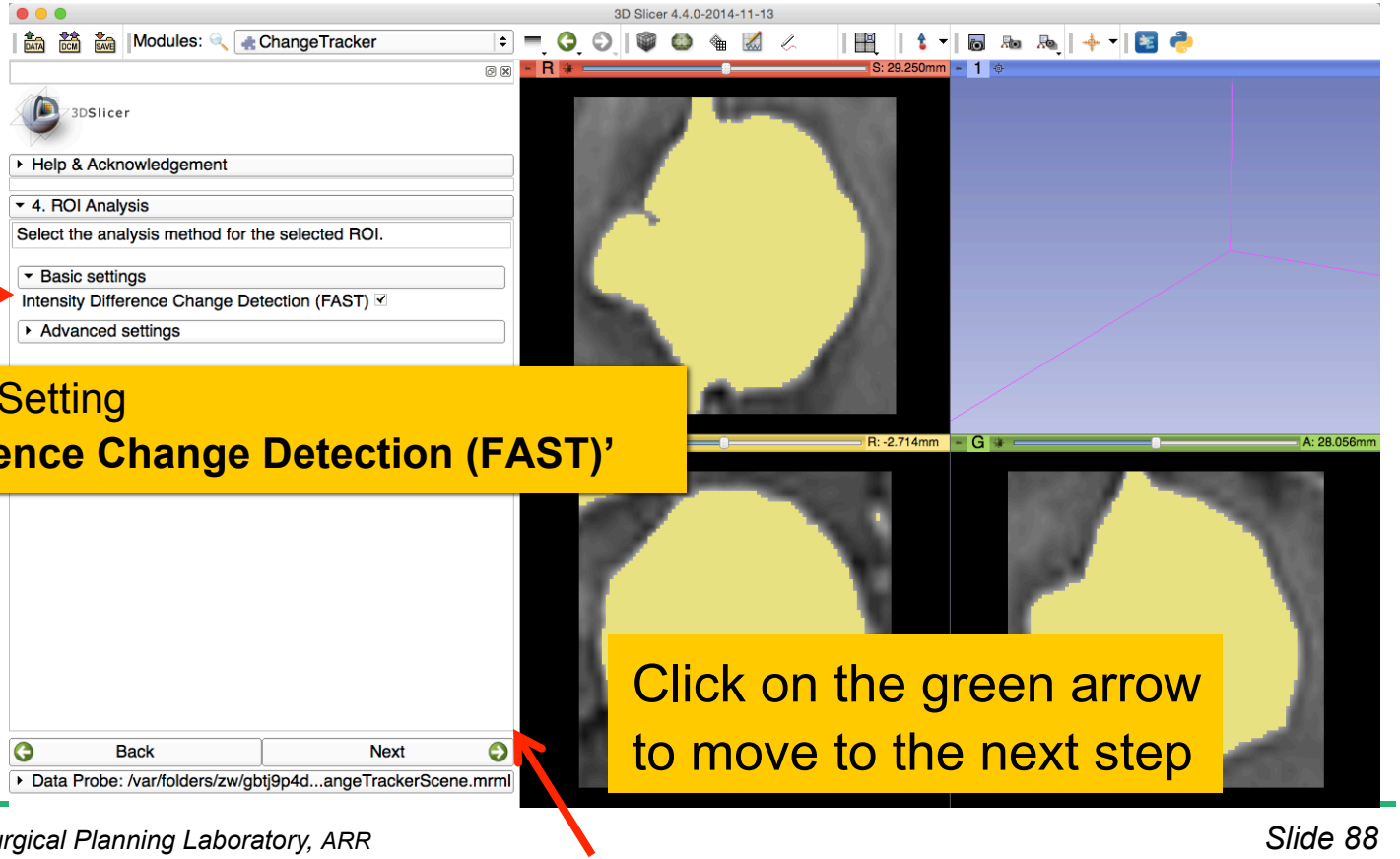
Step3: Segment the tumor

Scroll through the slices until the segmentation appears optimal.



Click on the green arrow to move to the next step

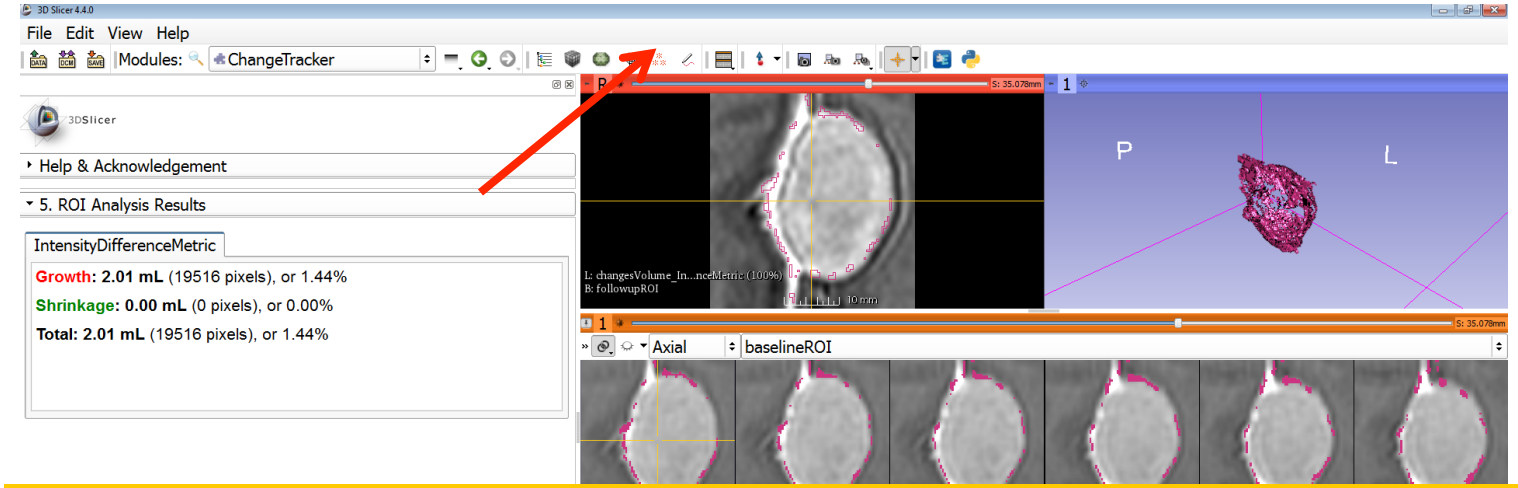
Step4: Select the Analysis Method



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

Click on the green arrow to move to the next step

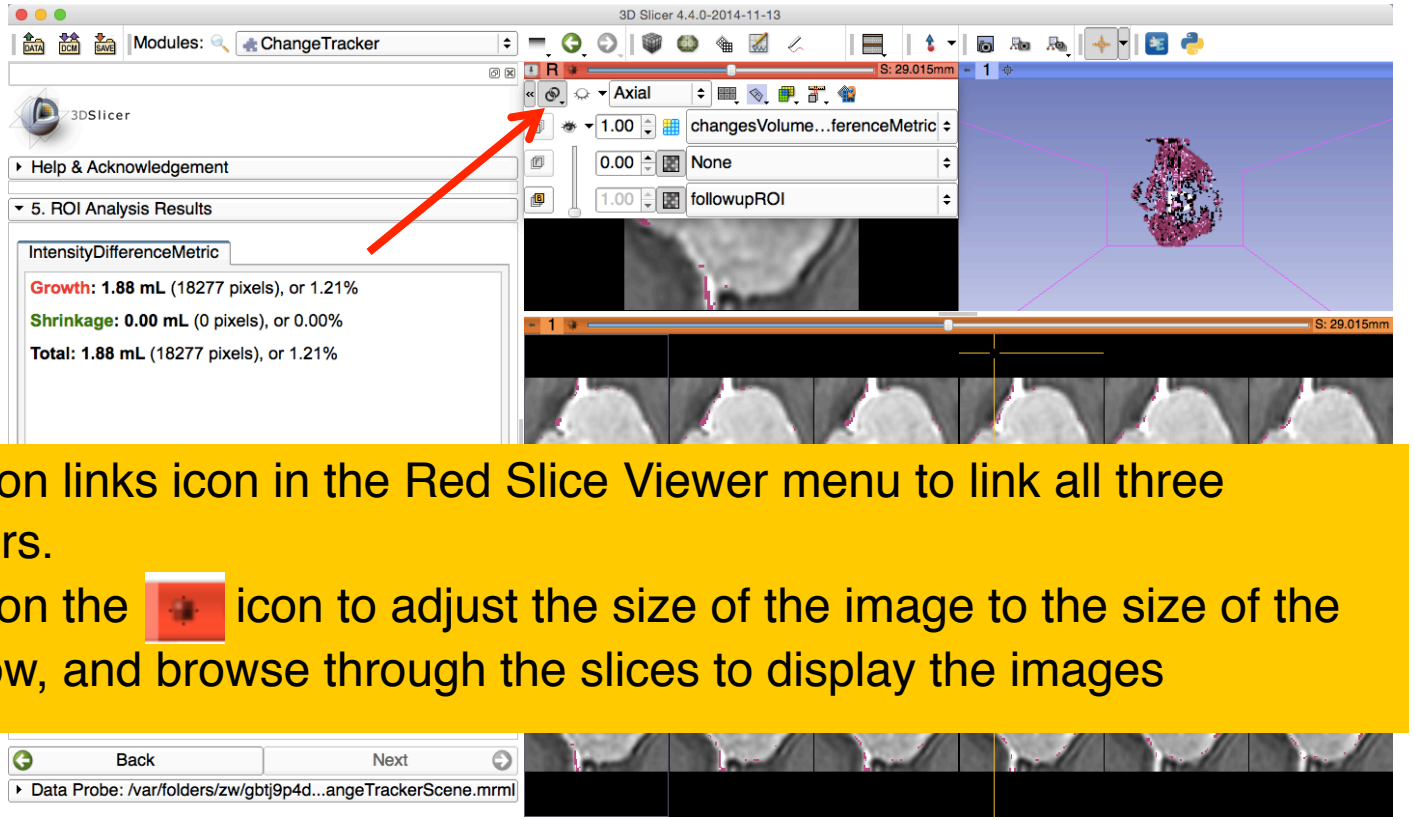
Step4: Select the Analysis Method



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.

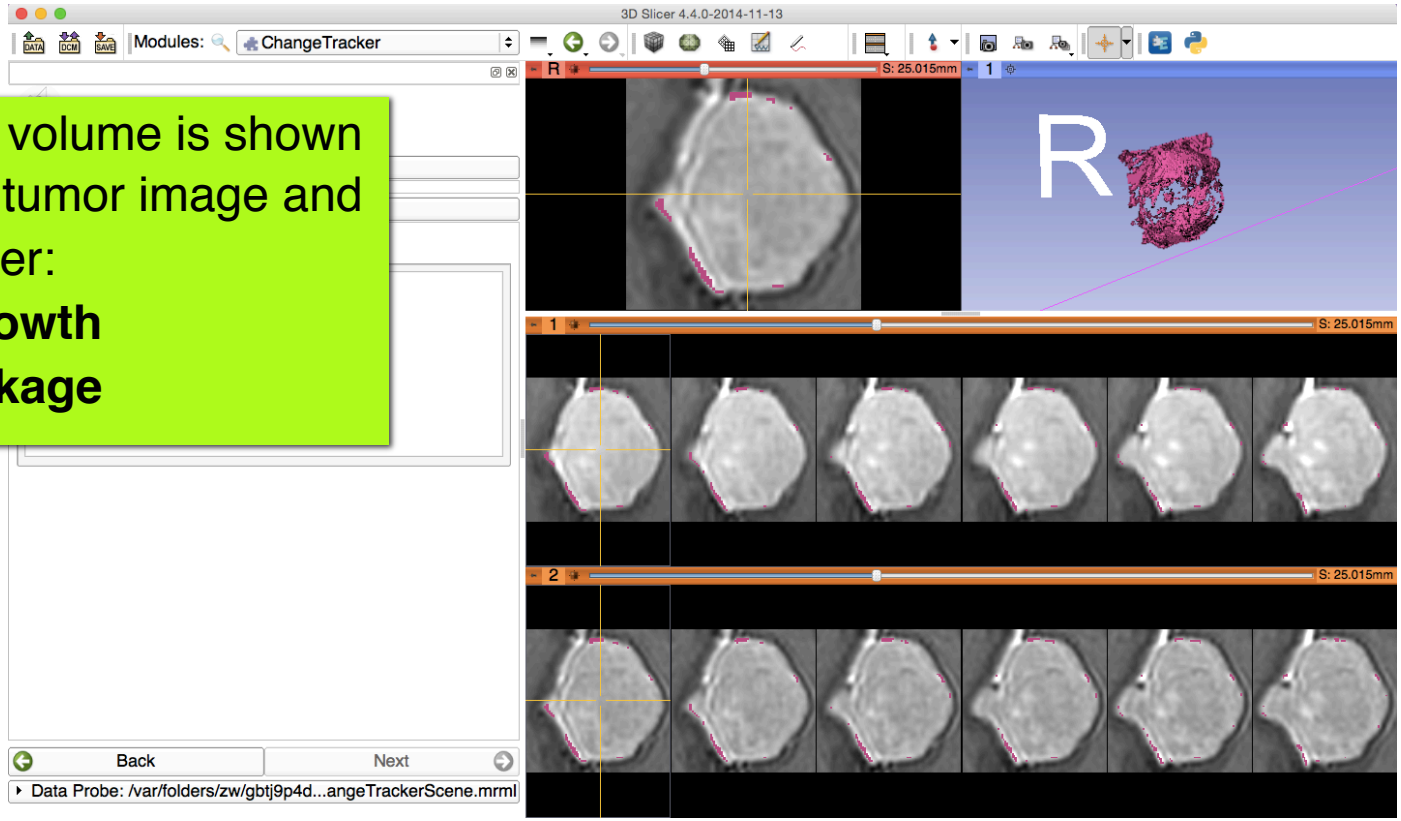
Click on the icon to adjust the size of the image to the size of the window, and browse through the slices to display the images

Final Step: Change Tracker Results

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

magenta = growth

green = shrinkage



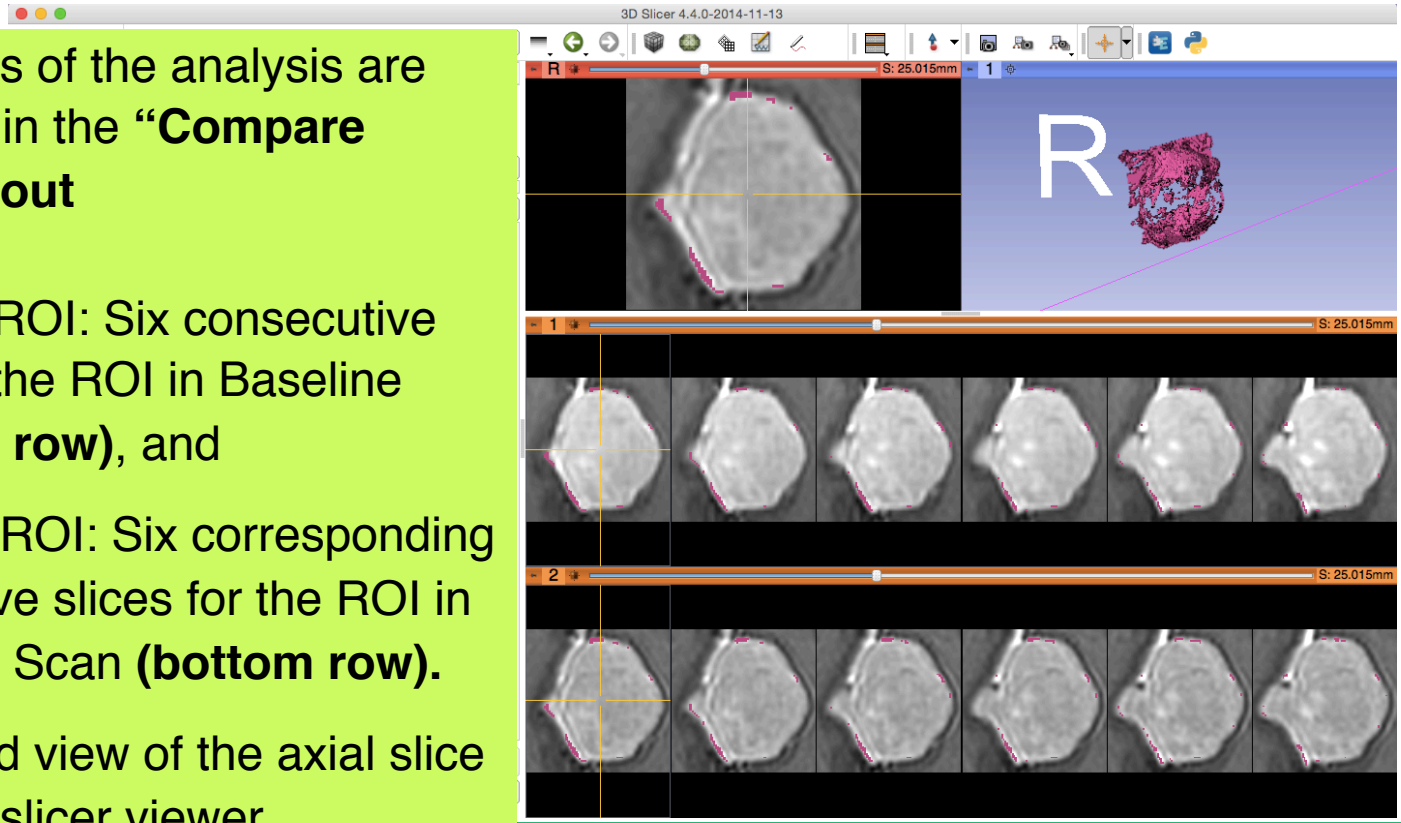
Visualization of the change in pathology

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

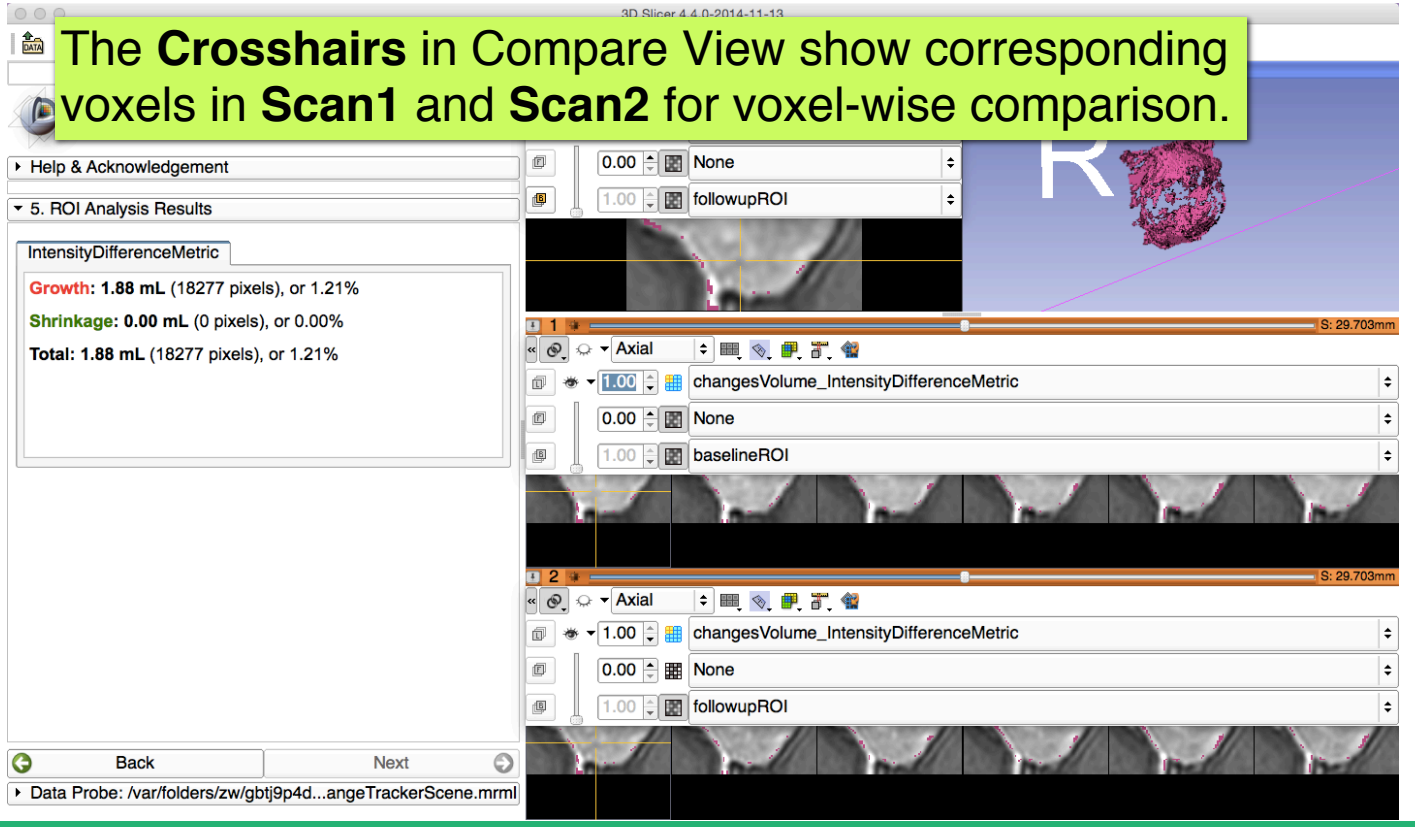
•BaselineROI: Six consecutive slices for the ROI in Baseline Scan **(top row)**, and

•FollowupROI: Six corresponding consecutive slices for the ROI in Follow Up Scan **(bottom row).**

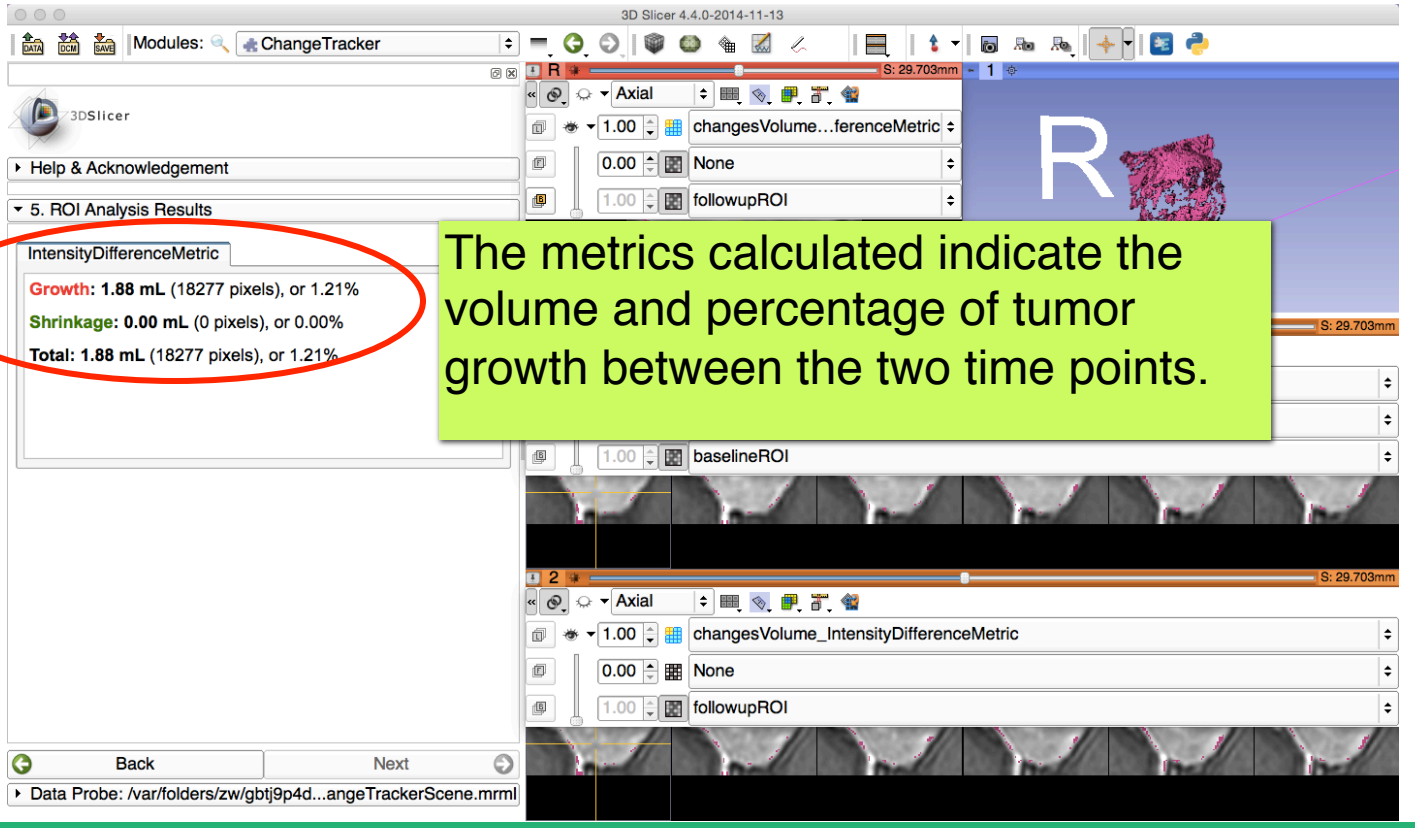
•A zoomed view of the axial slice in the red slicer viewer



Visualization of the change in pathology



Change Tracker Results



Change Tracker module

- The 3D Slicer ChangeTracker module is a research tool for evaluating volumetric changes and bring additional complementary information to RECIST measurements

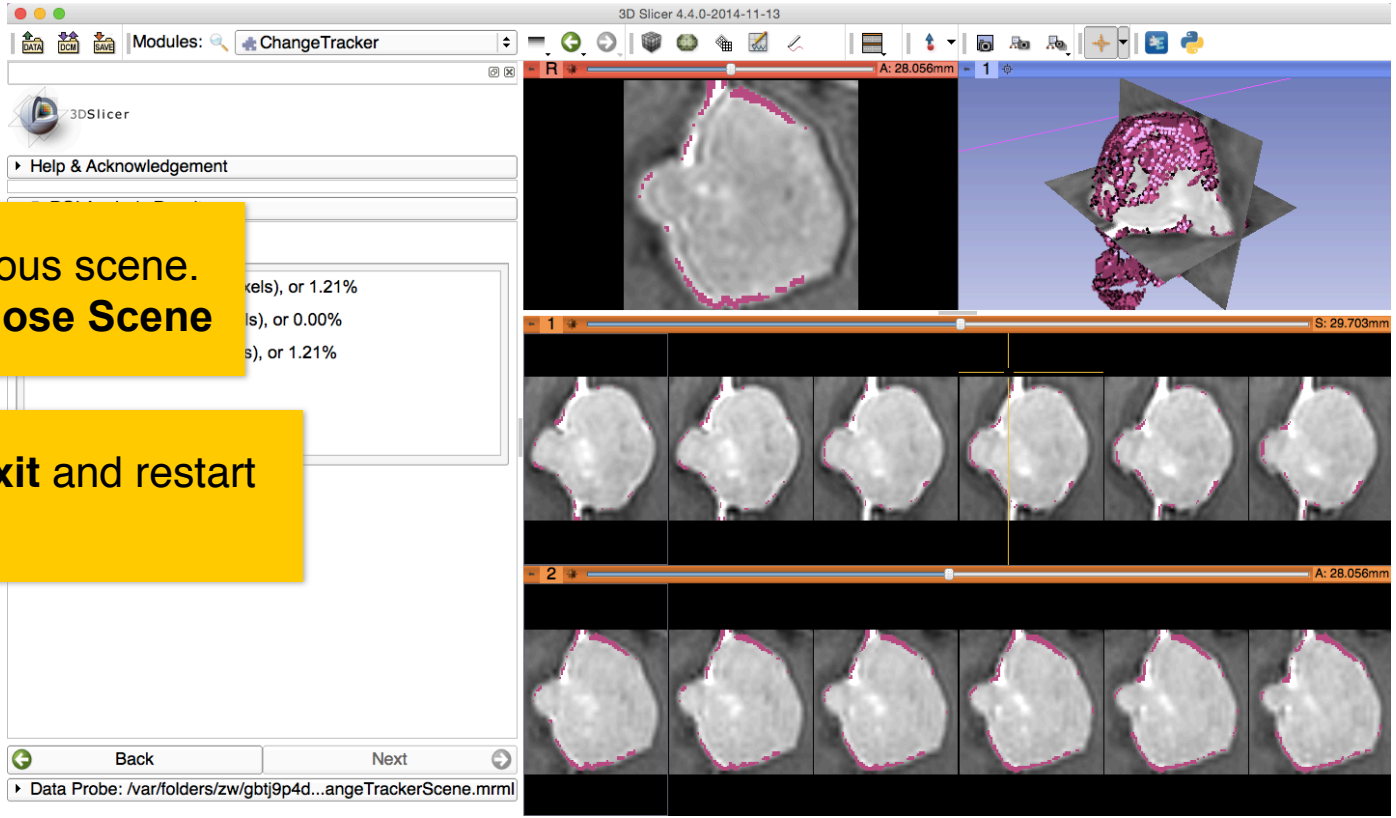
- However, three current requirements are needed for Change Tracker to produce adequate measurements:
  1) **Clear Tumor boundaries**
  2) **Contrast enhanced images only**
  3) **Homogenous enhancement across timepoints**

- 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



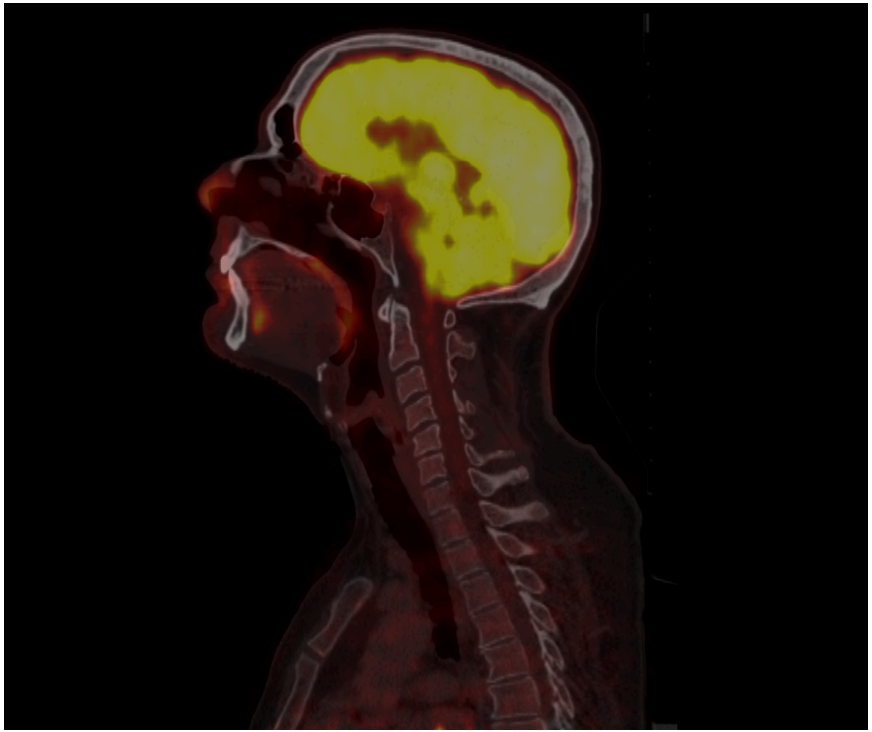
ChangeTracker: Exploring small volumetric changes

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.

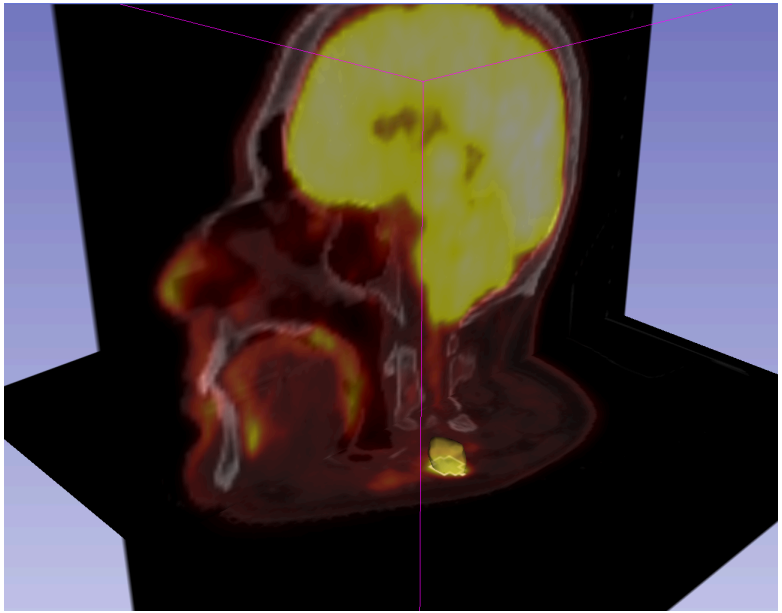
PET/CT Visualization and Analysis



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

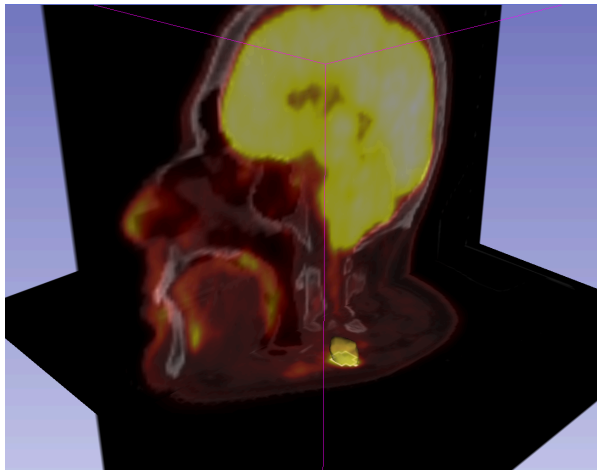
FDG-PET SUV

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

SUV = Tissue Concentration of Radioactive Tracer x
Patient Weight / Injected Dose

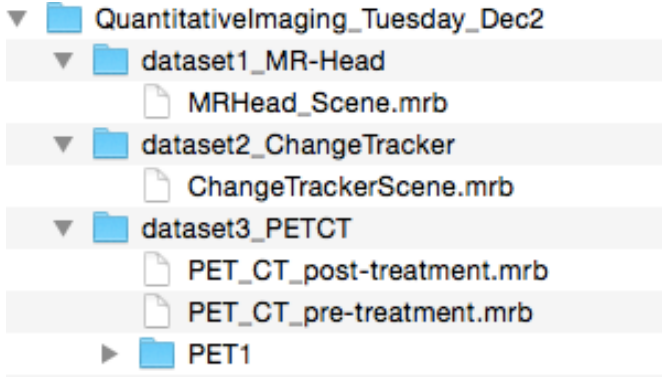
- Under certain circumstances, 18-F Fluorodeoxyglucose (FDG) SUV correlates with metabolic rate of glucose and/or the number of viable tumor cells

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

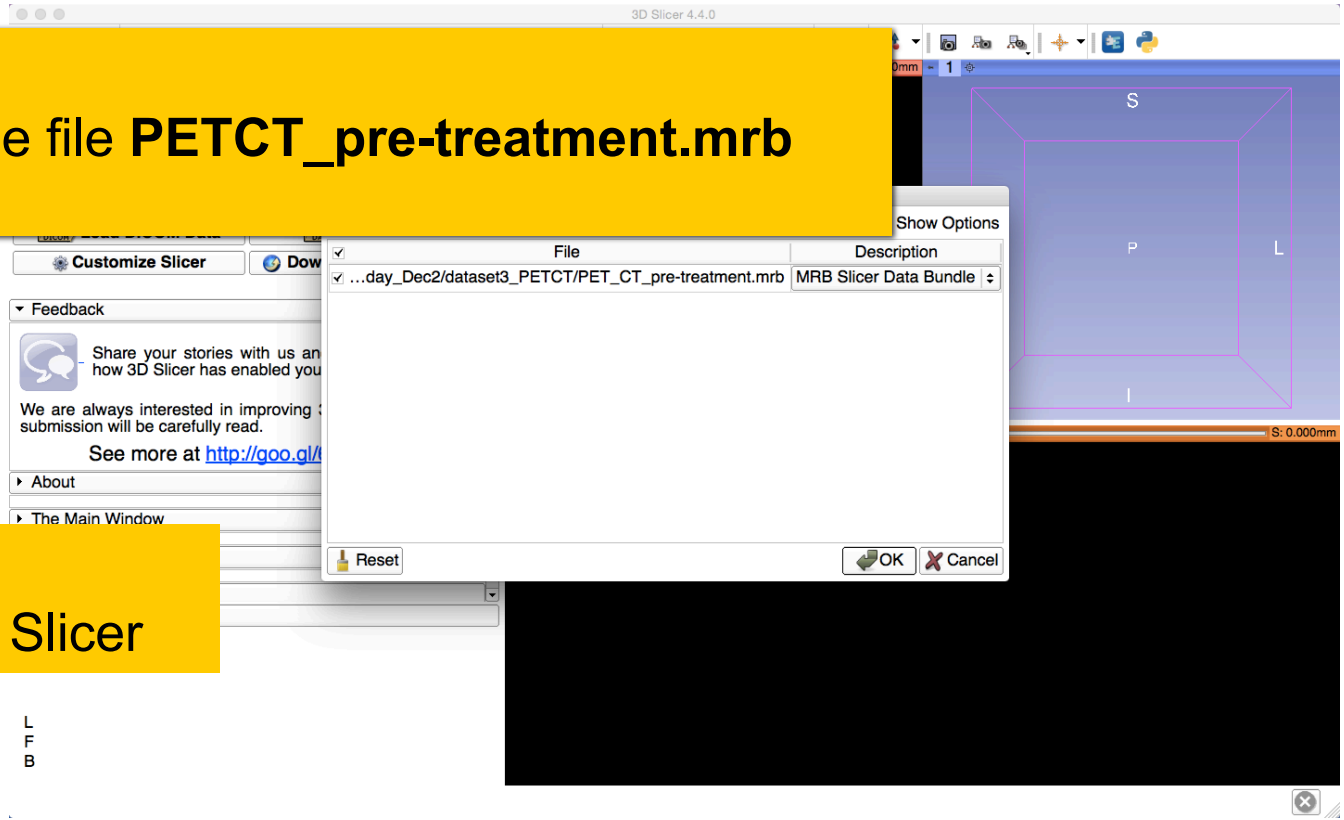


The datasets are located in
\dataset3_PETCT
The directory contains two .mrb files

- 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**

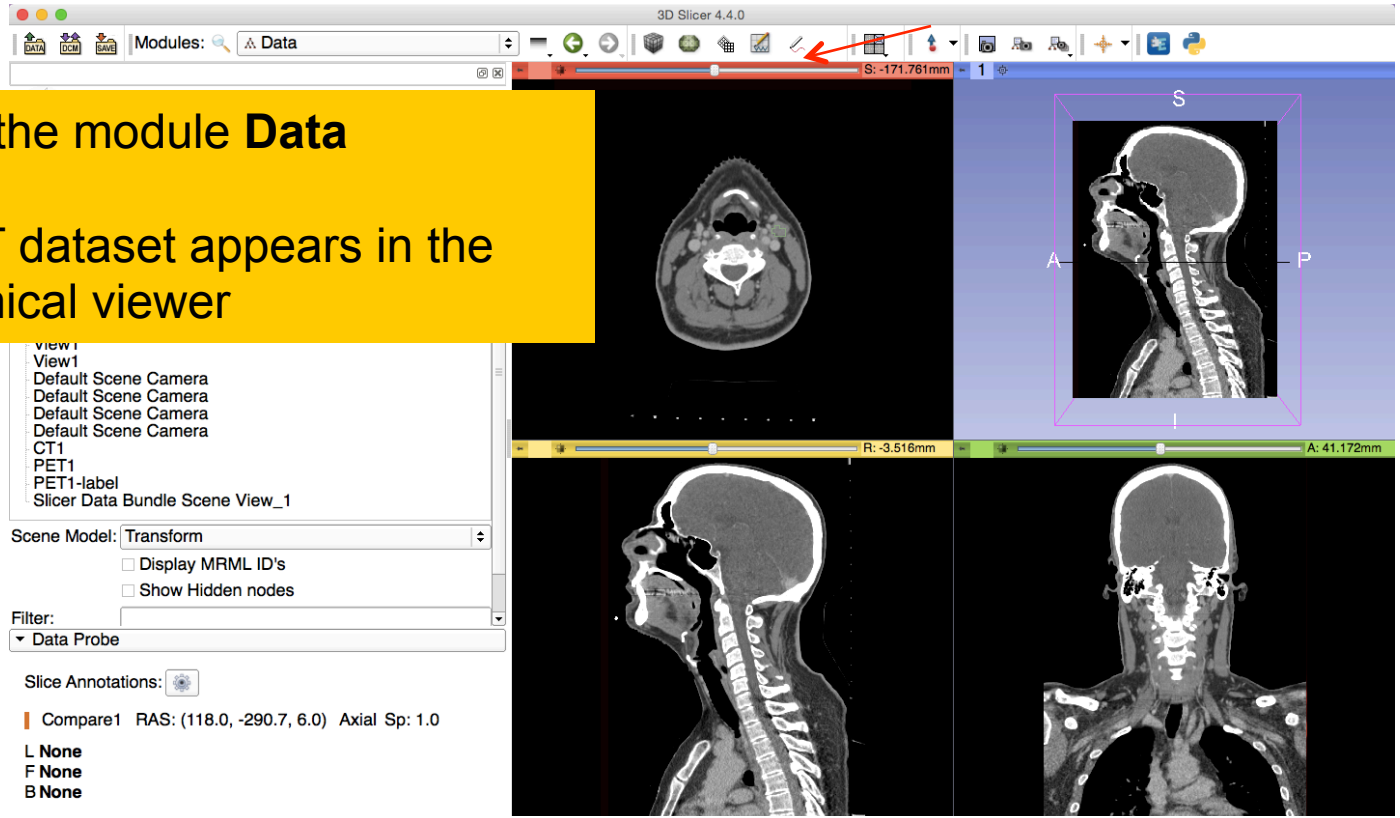


Click OK to load
the .mrb file into Slicer

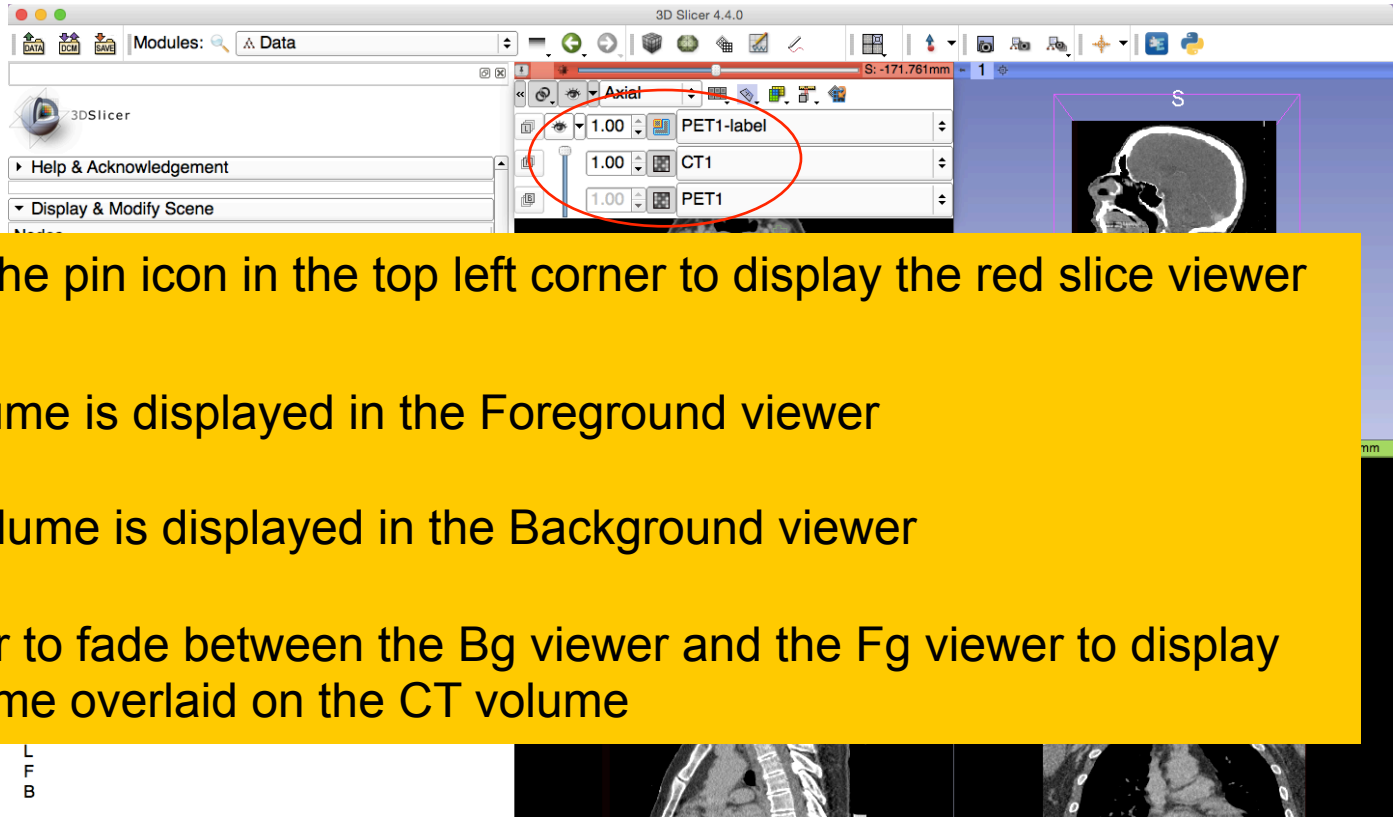
Loading the PETCT scene

Select the module **Data**

The CT dataset appears in the anatomical viewer



Loading a PETCT dataset



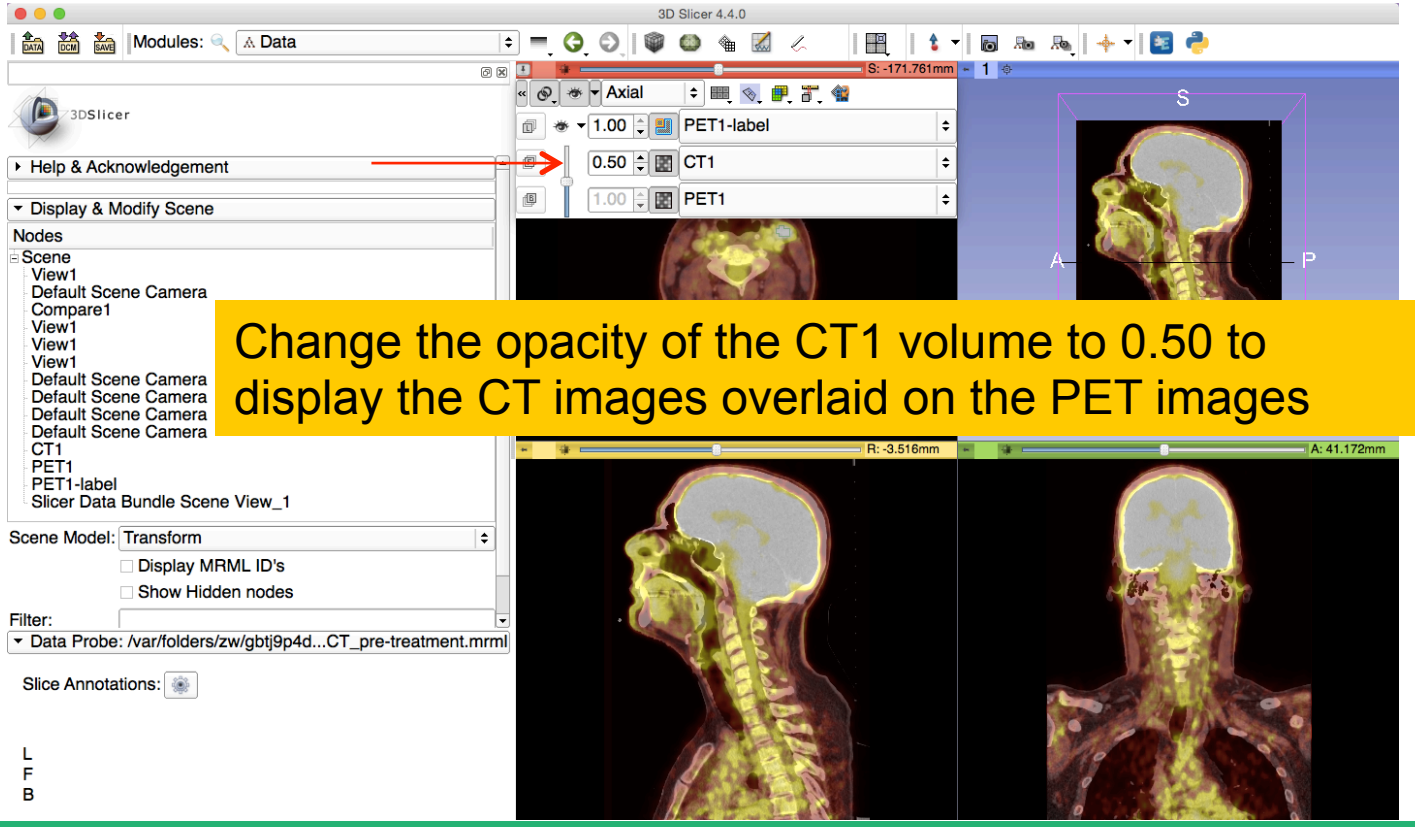
Left click on the pin icon in the top left corner to display the red slice viewer menu.

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

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

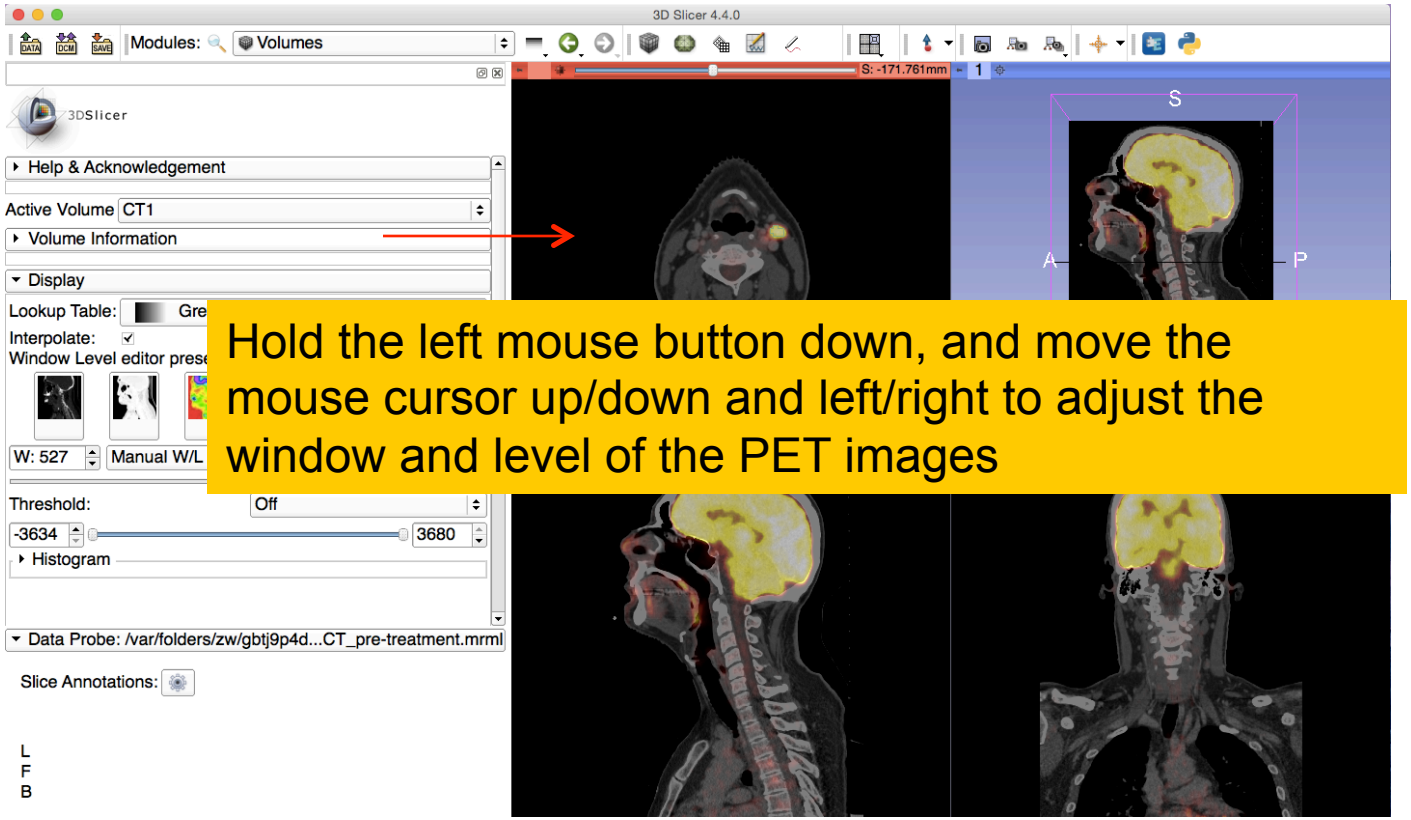
Use the slider to fade between the Bg viewer and the Fg viewer to display the PET volume overlaid on the CT volume

Visualization of PETCT data



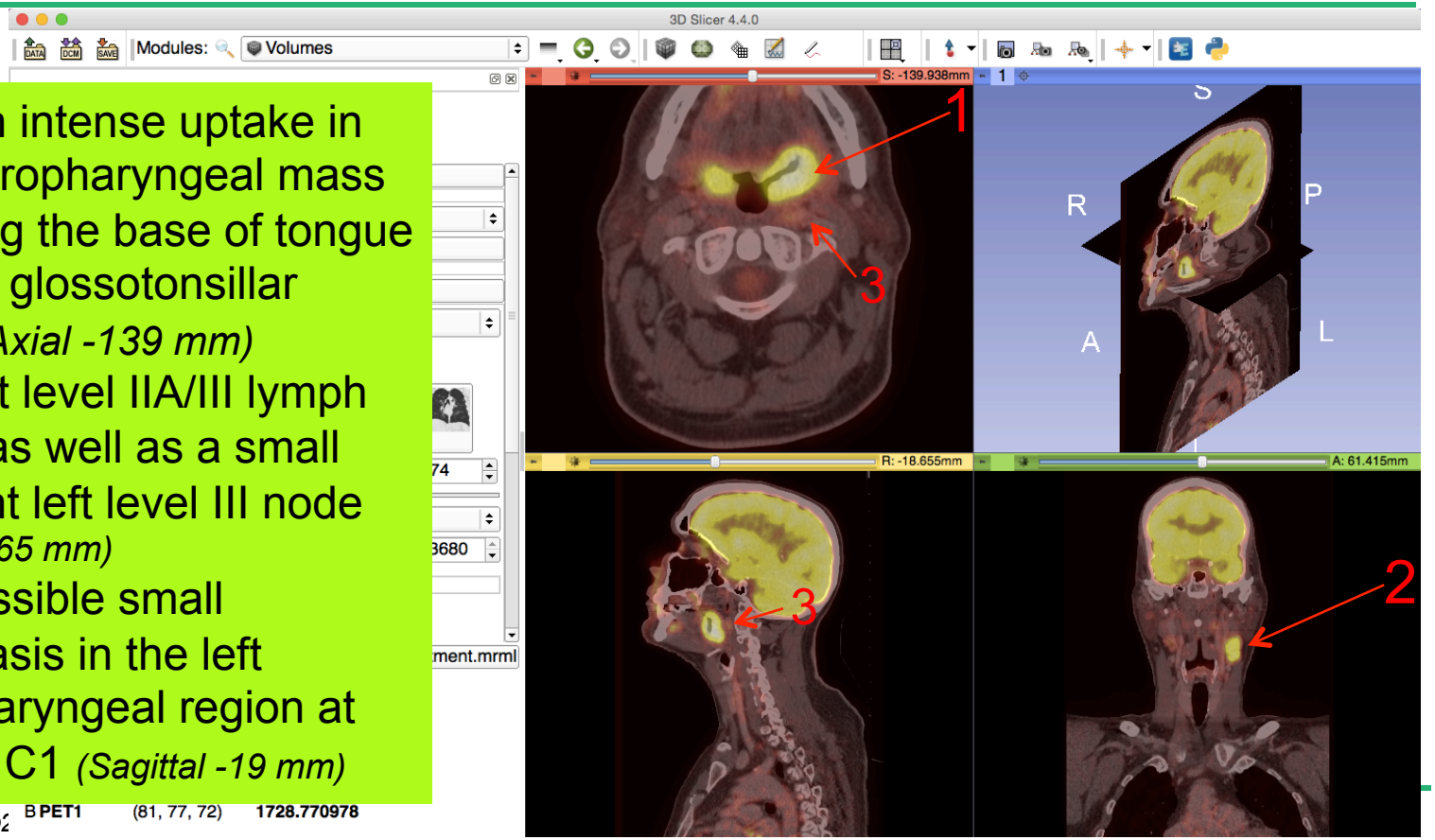
Change the opacity of the CT1 volume to 0.50 to display the CT images overlaid on the PET images

Visualization of PETCT data



PET uptake findings

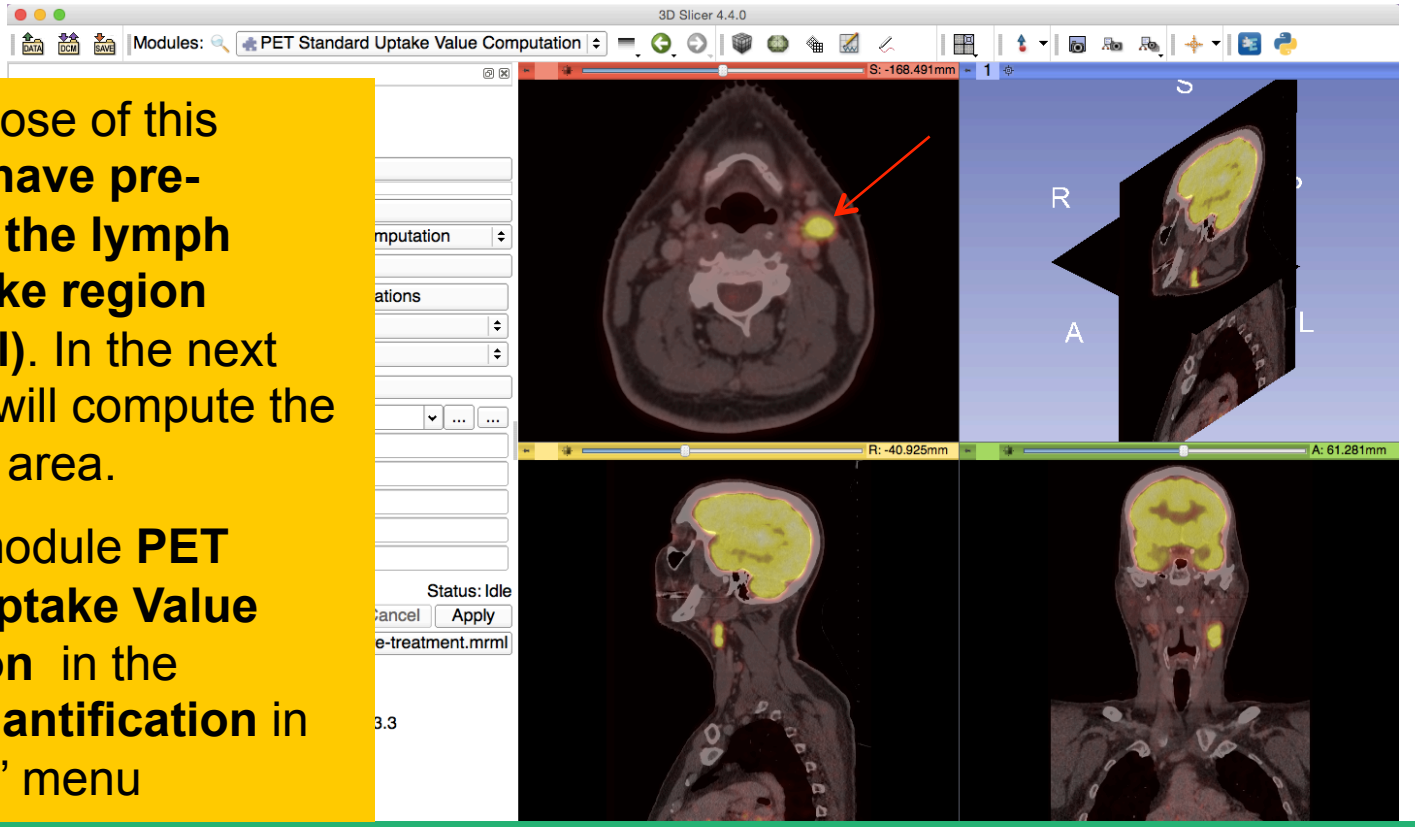
Note an intense uptake in
1) left oropharyngeal mass involving the base of tongue and left glossotonsillar fossa *(Axial -139 mm)*
2) in left level IIA/III lymph nodes as well as a small adjacent left level III node *(Coronal 65 mm)*
3) a possible small metastasis in the left retropharyngeal region at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



PET SUV Computation

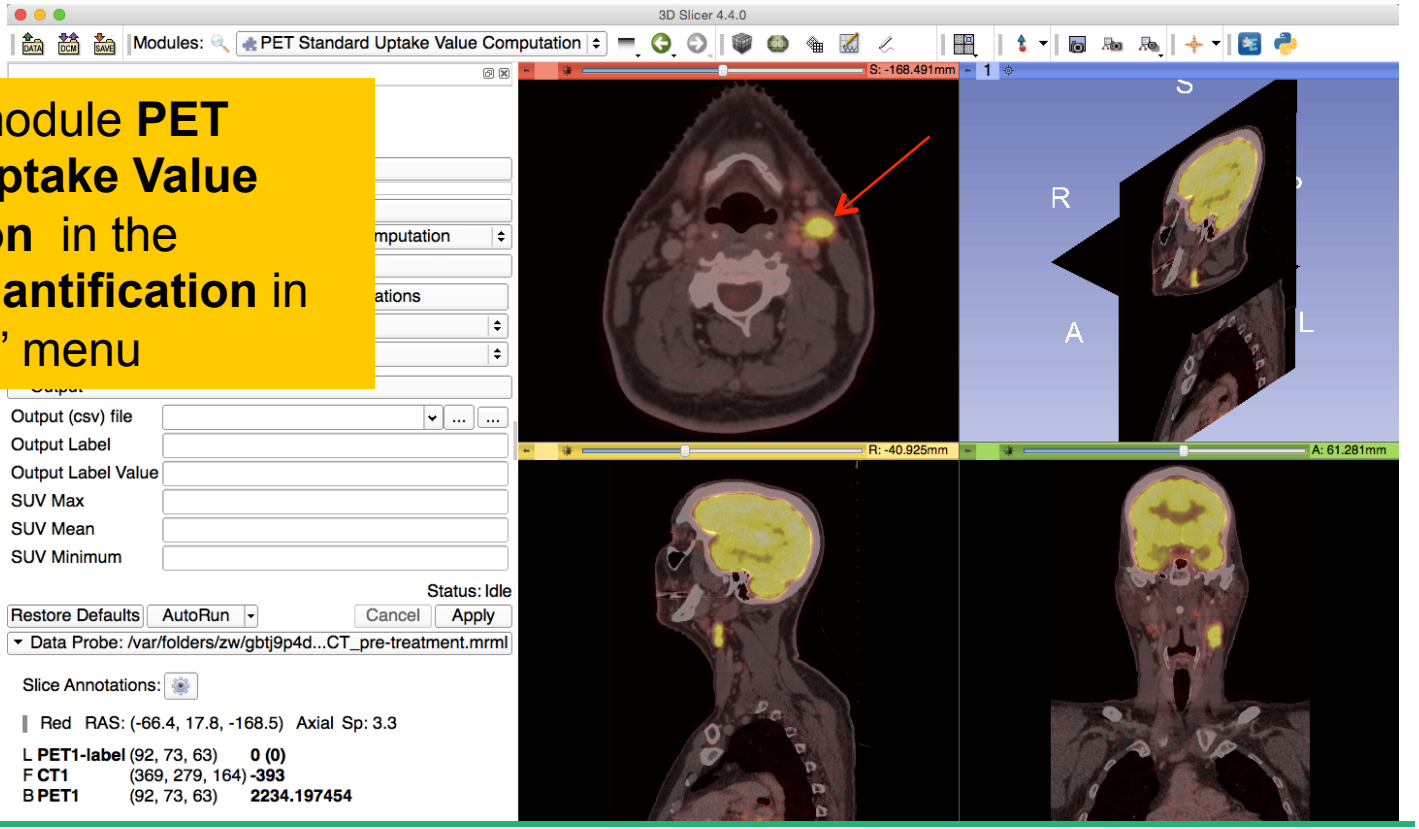
For the purpose of this tutorial, **we have pre-segmented the lymph nodes uptake region (PET1_label)**. In the next section, we will compute the SUV for this area.

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

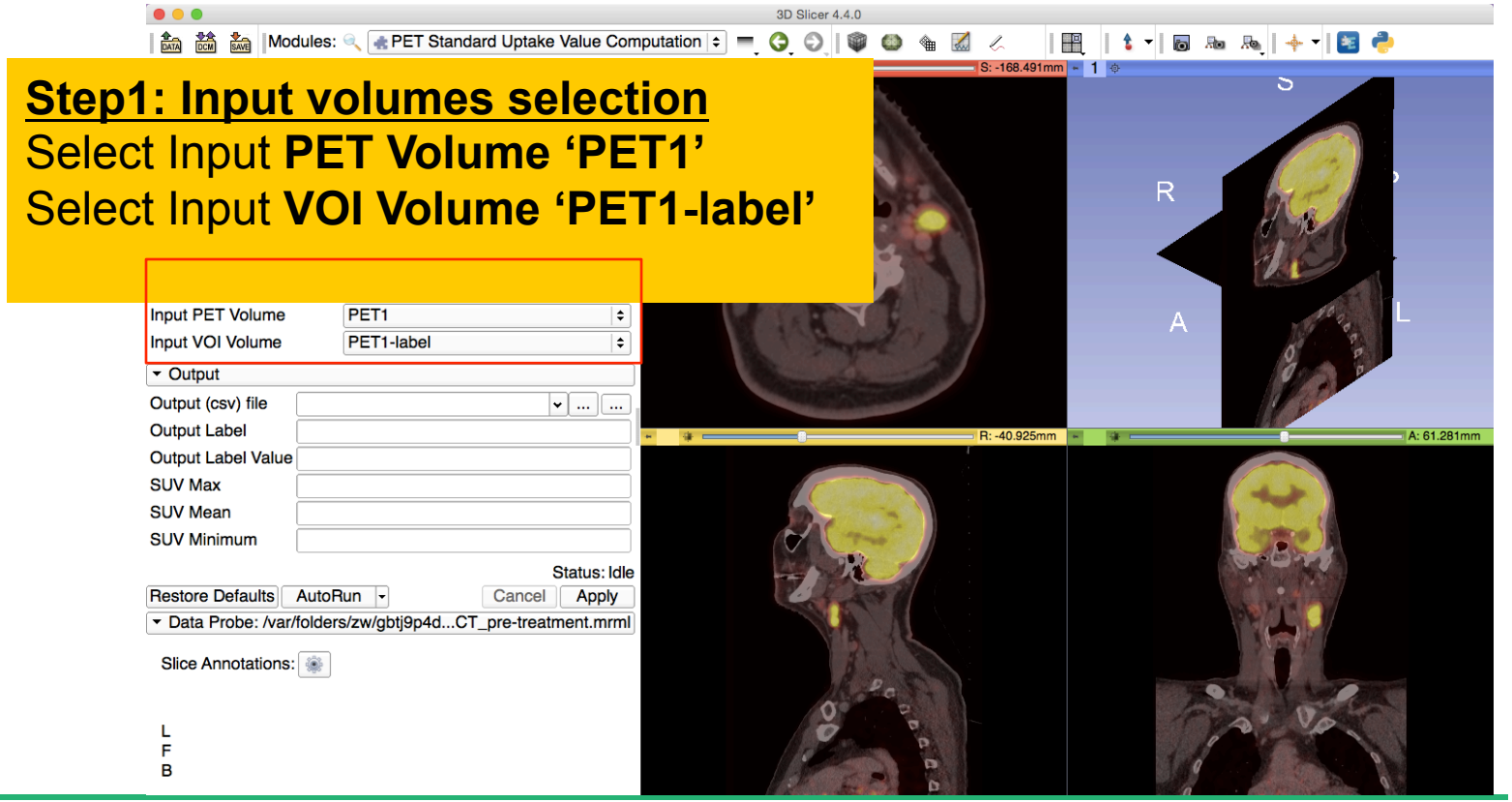


PET SUV Computation

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

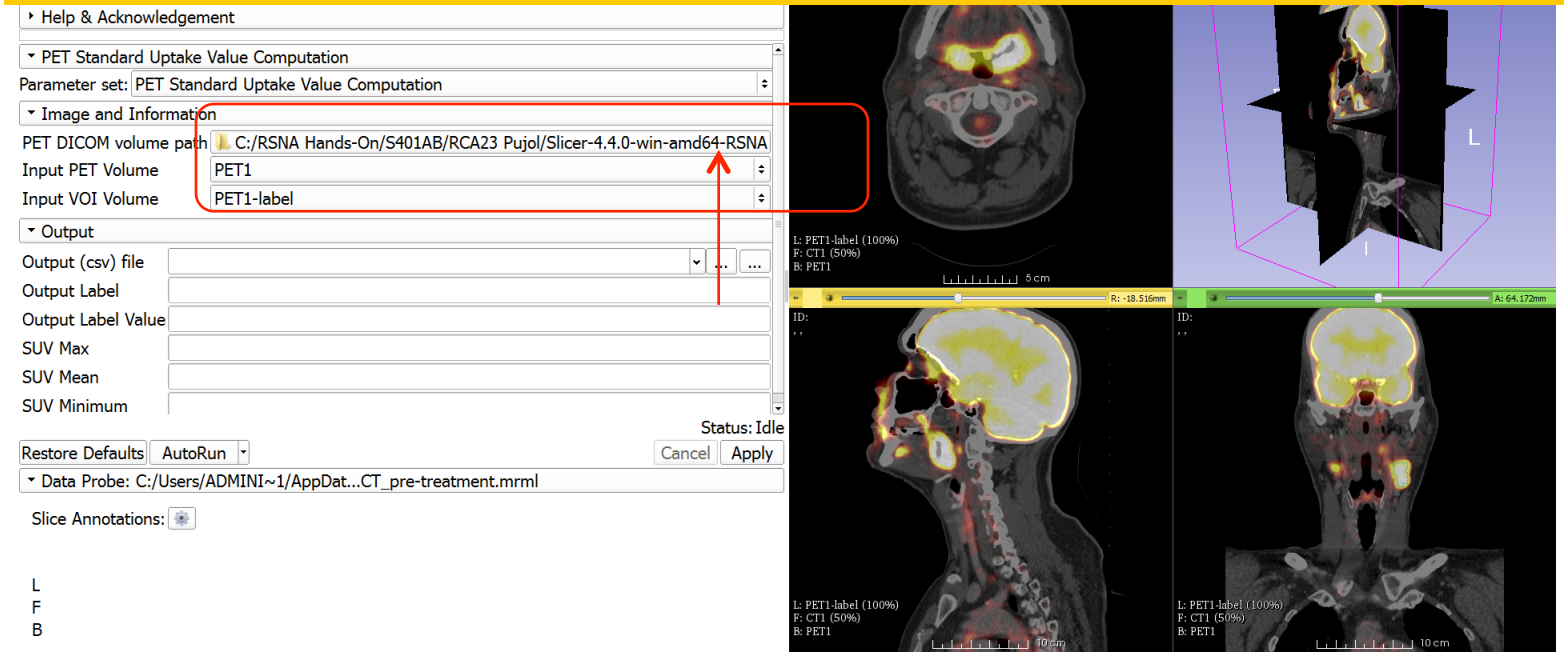


PET SUV Computation

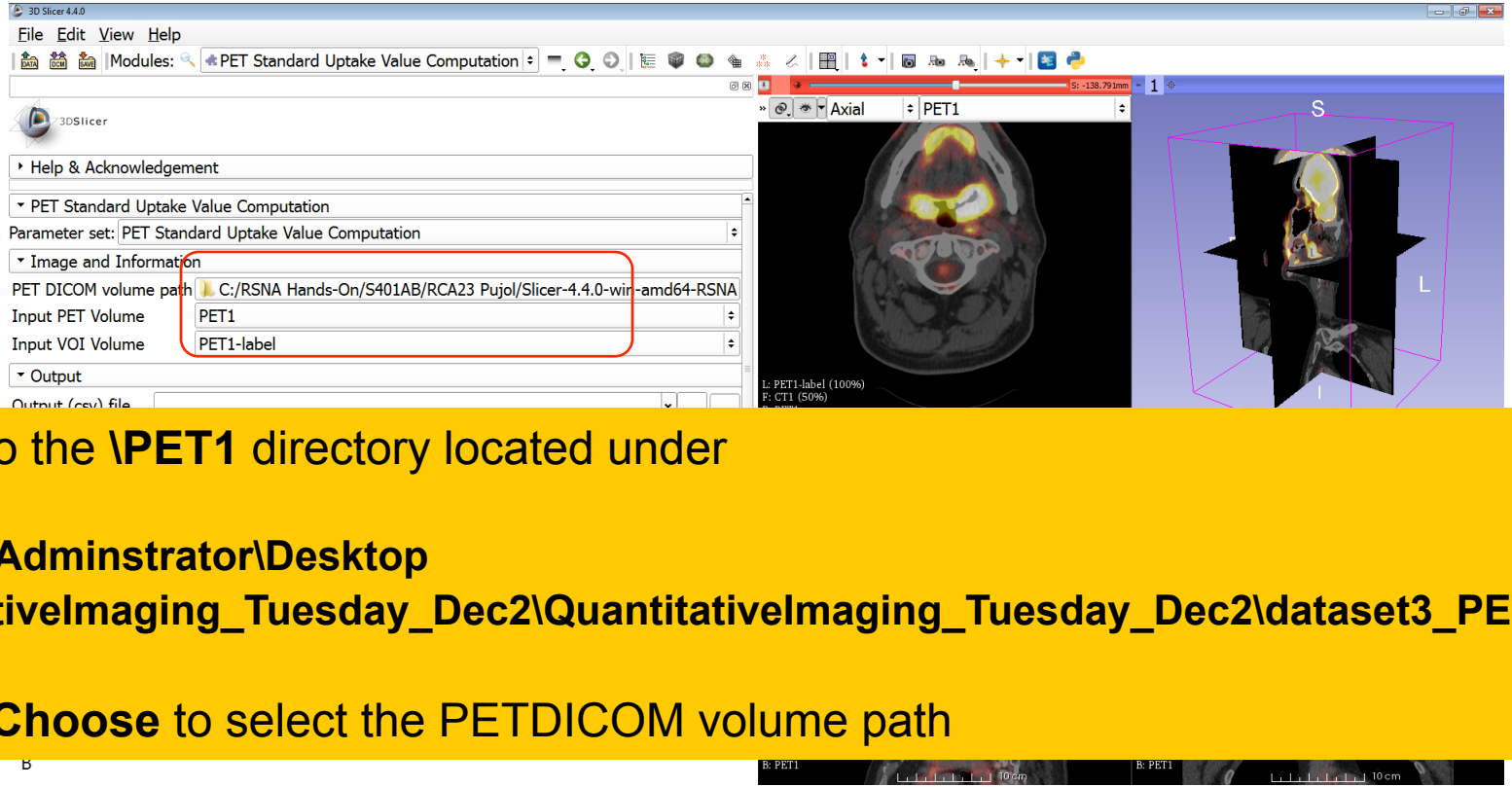


Step2: Path to the DICOM PET header

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



PET SUV Computation



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

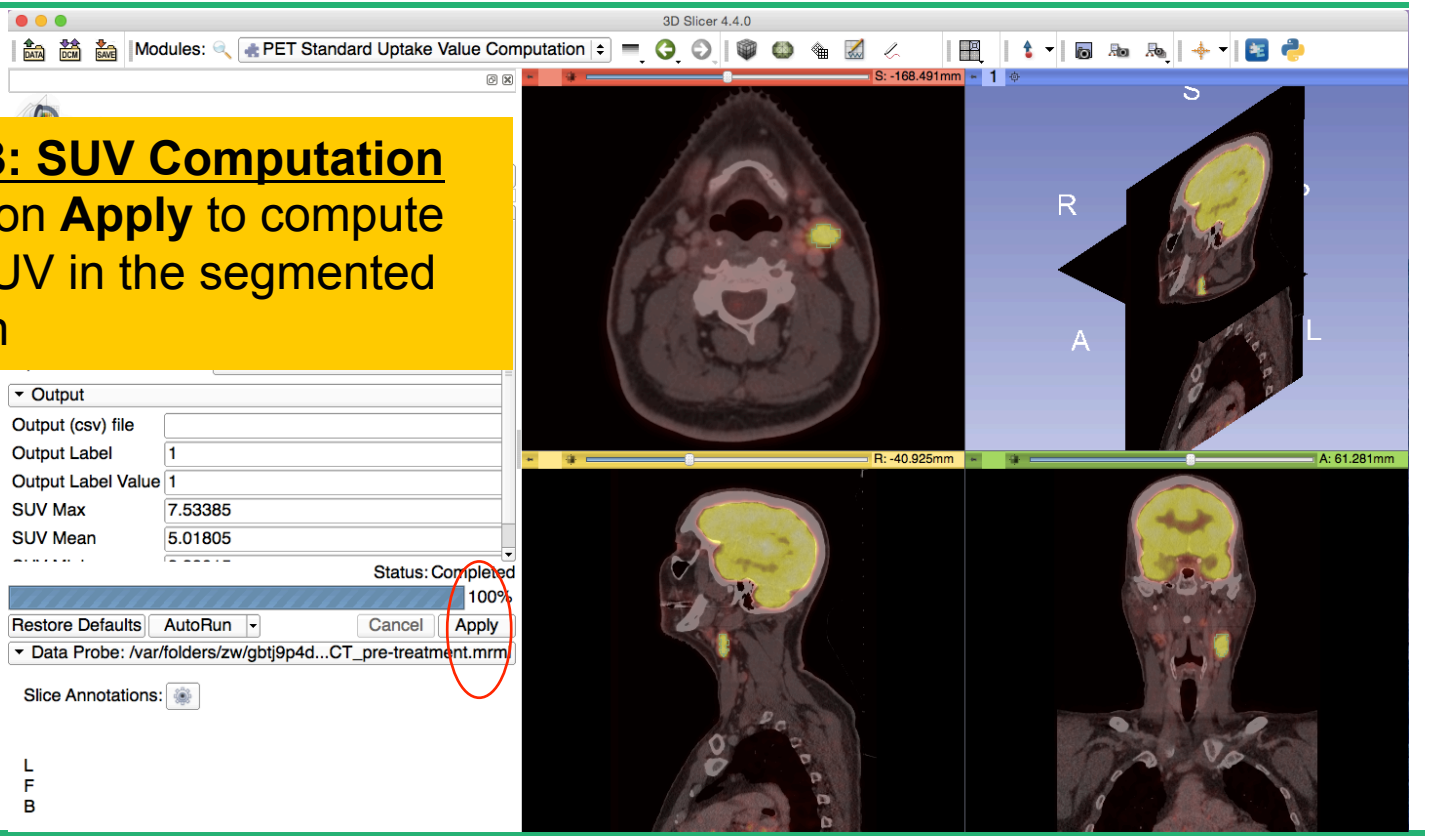
C:\Users\Adminstrator\Desktop
\QuantitativeImaging_Tuesday_Dec2\QuantitativeImaging_Tuesday_Dec2\dataset3_PETCT

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

PET SUV Computation

Step3: SUV Computation

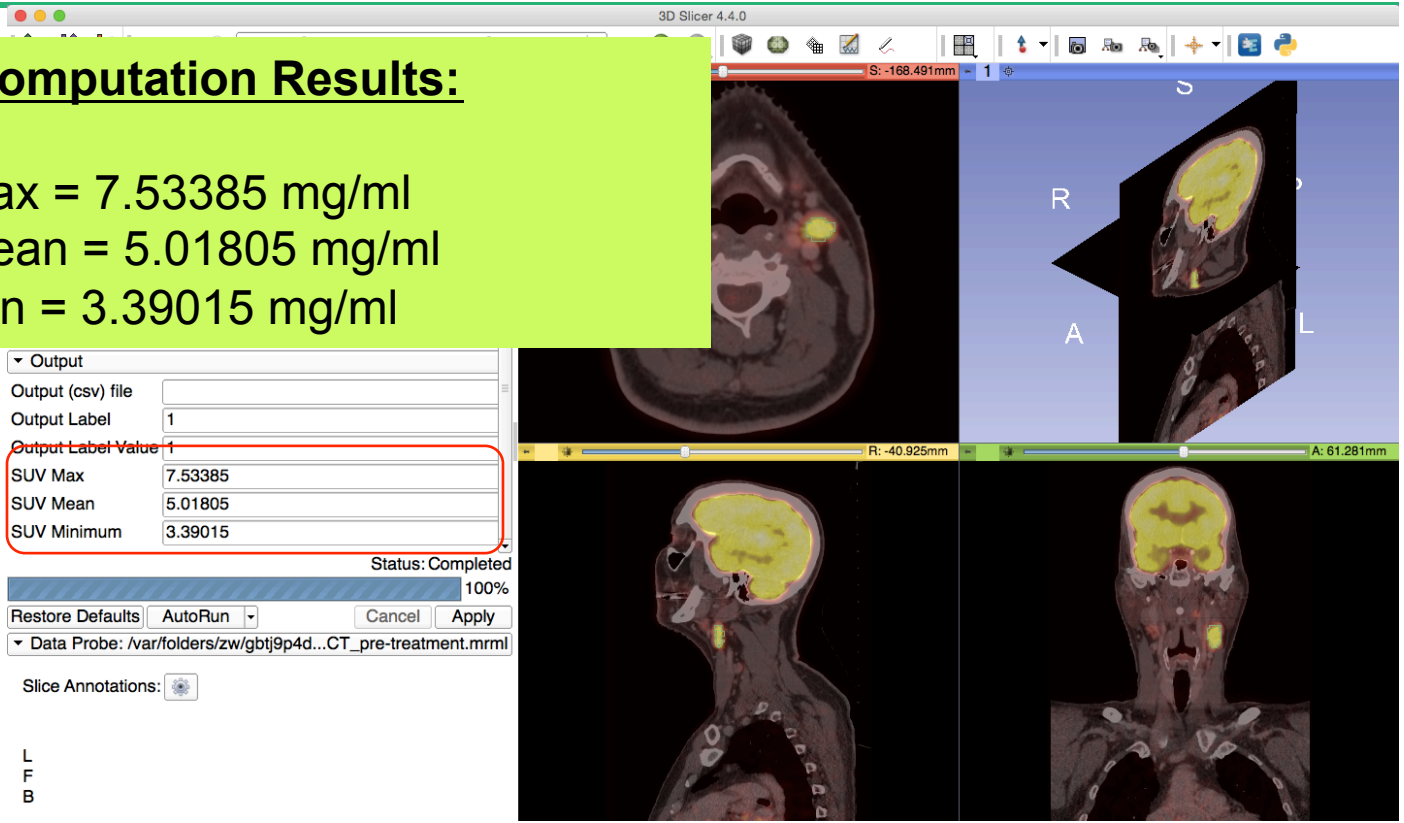
Click on **Apply** to compute the SUV in the segmented region



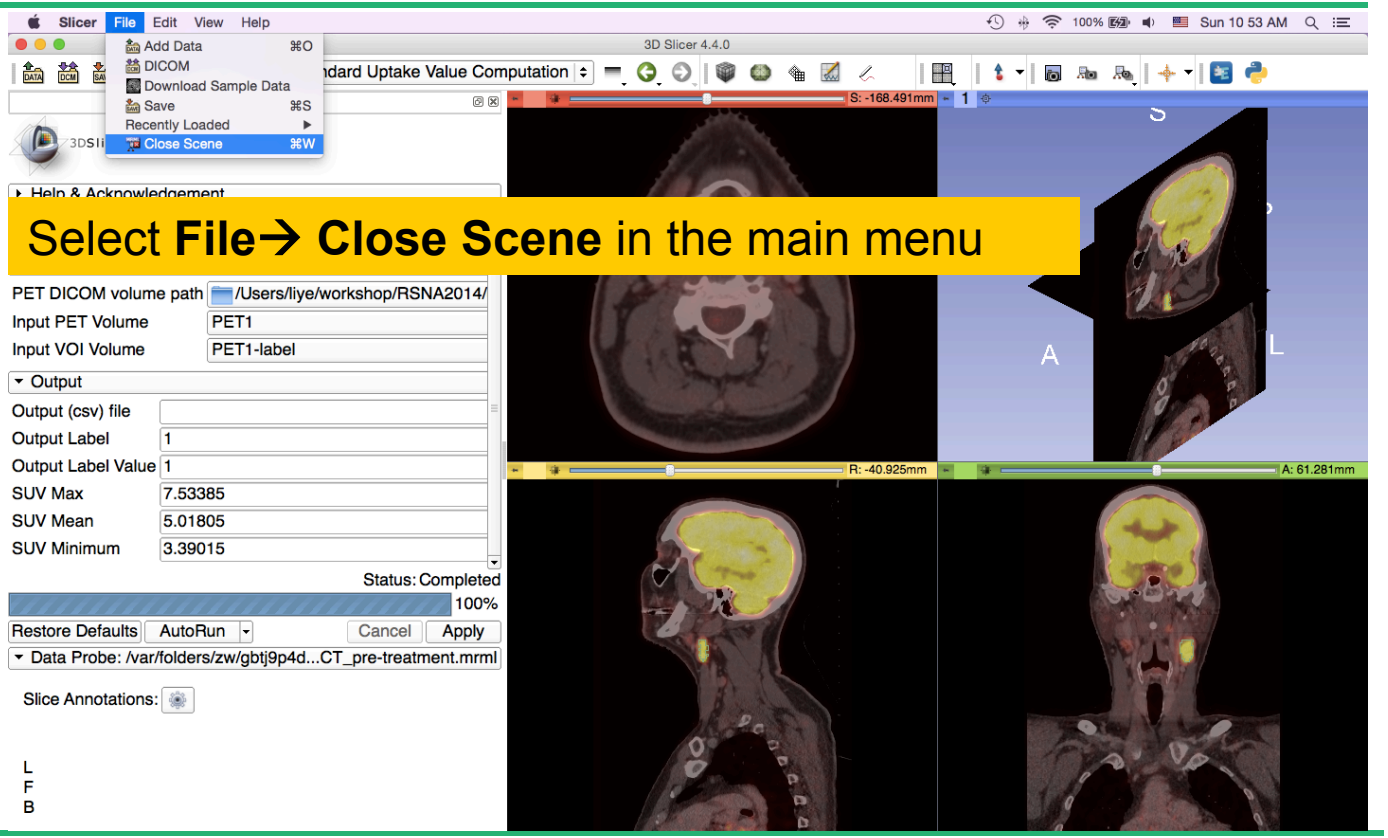
PET SUV Computation

SUV Computation Results:

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

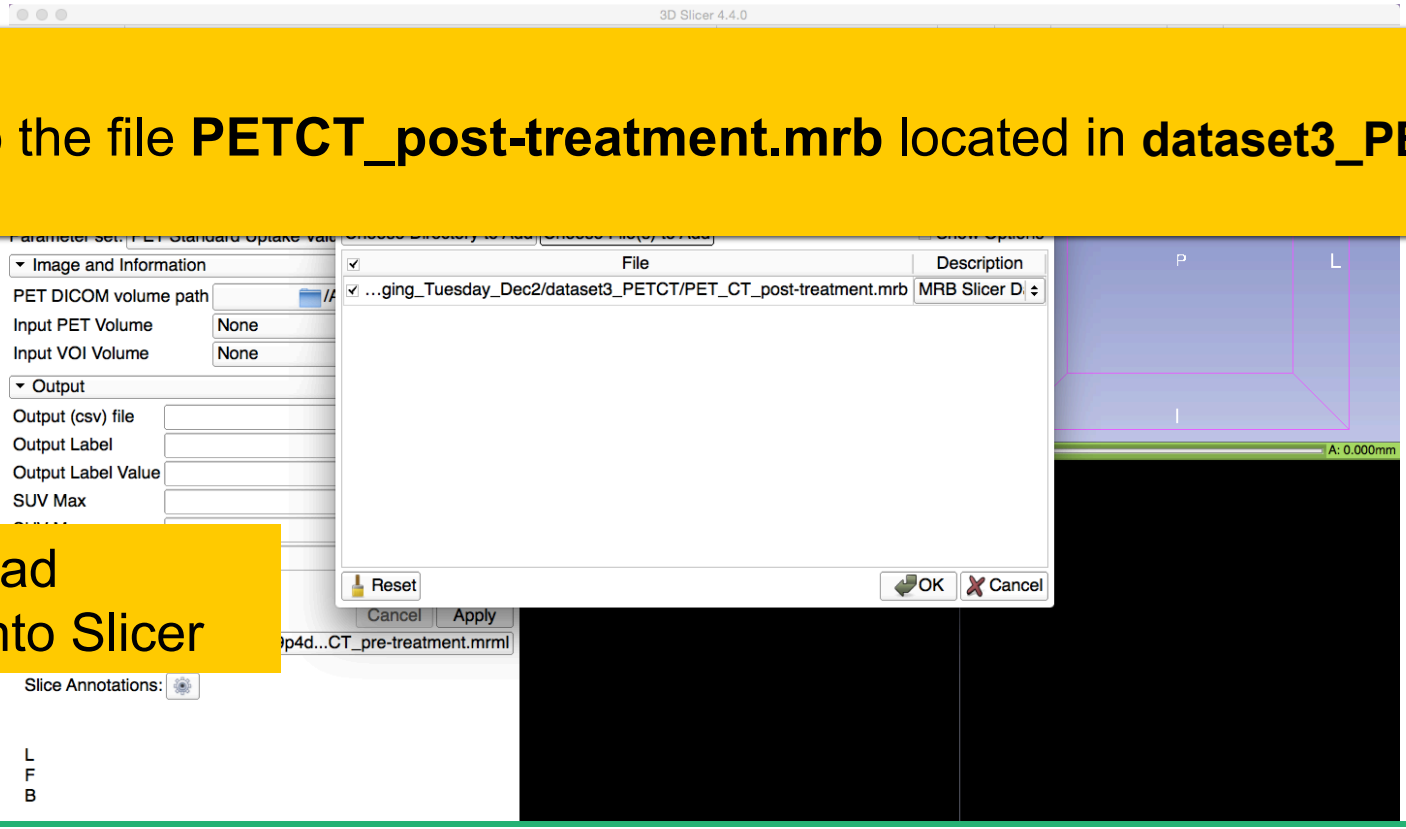


PET SUV Computation



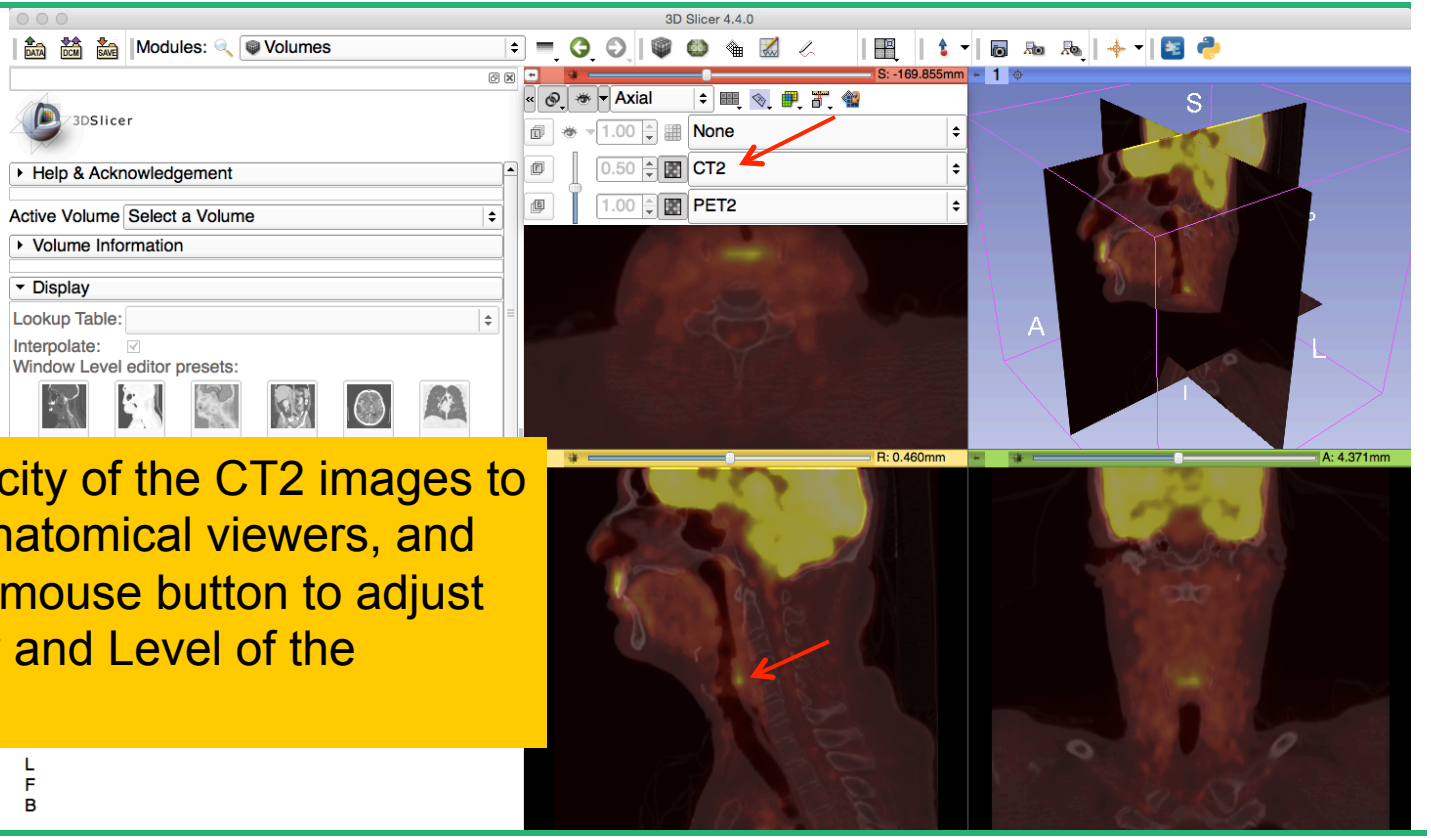
Loading the PETCT scene

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



Click OK to load the .mrb file into Slicer

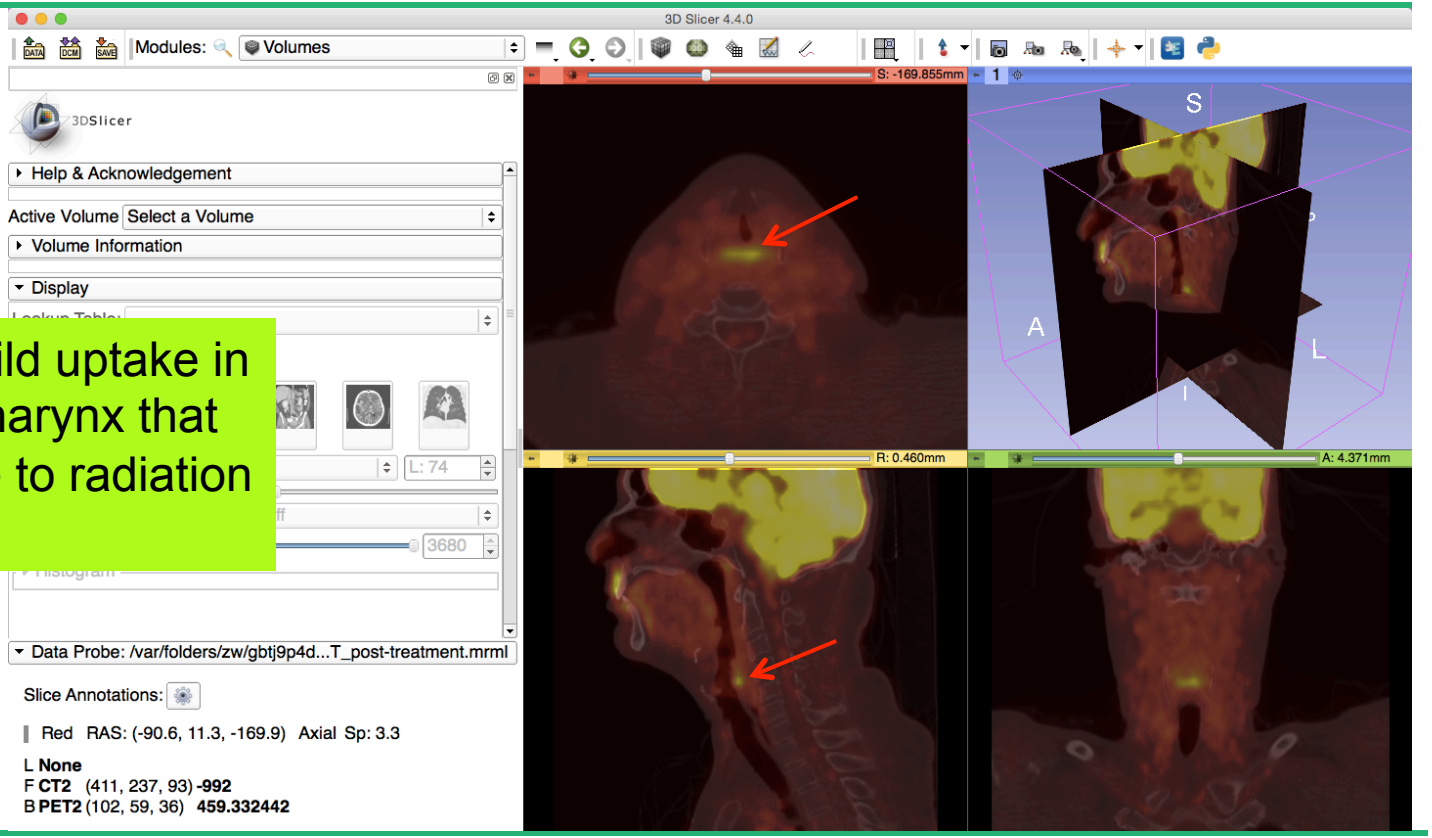
PET uptake findings



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

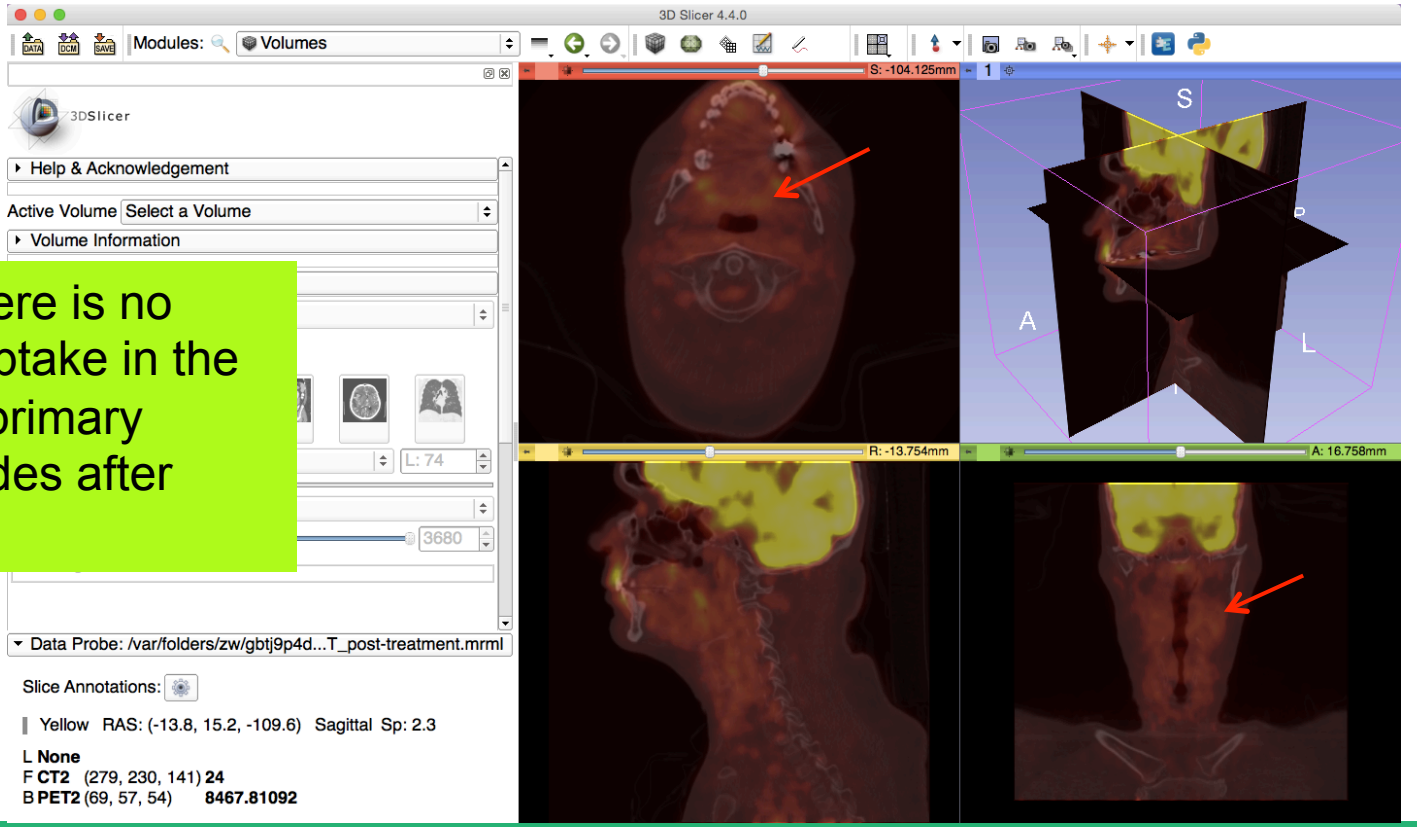
PET uptake findings

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 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

Acknowledgments

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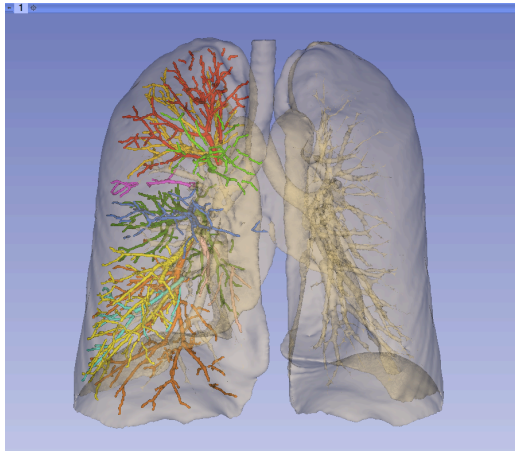
- Marianna Jakab, MS, Brigham & Women's Hospital
- Ye Li, MD, PLA General Hospital/ Brigham & Women's Hospital
- Franklin King, Queen's University

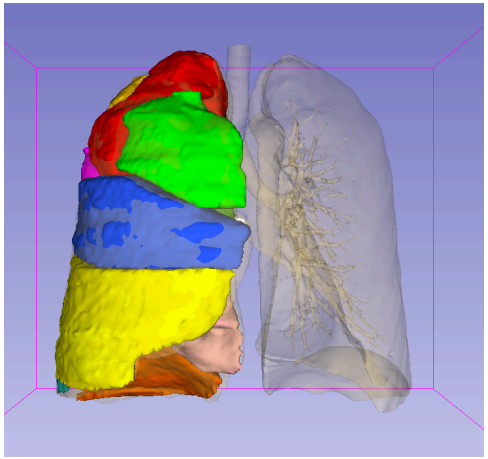
3DSlicer at RSNA 2014

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





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spujol@bwh.harvard.edu