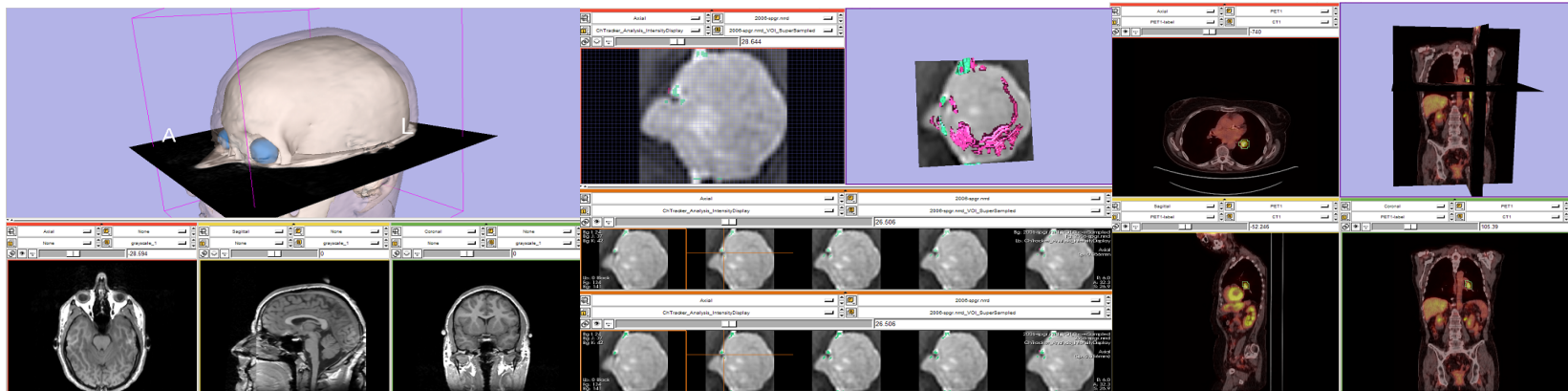


Quantitative Analysis and Visualization with 3D Slicer

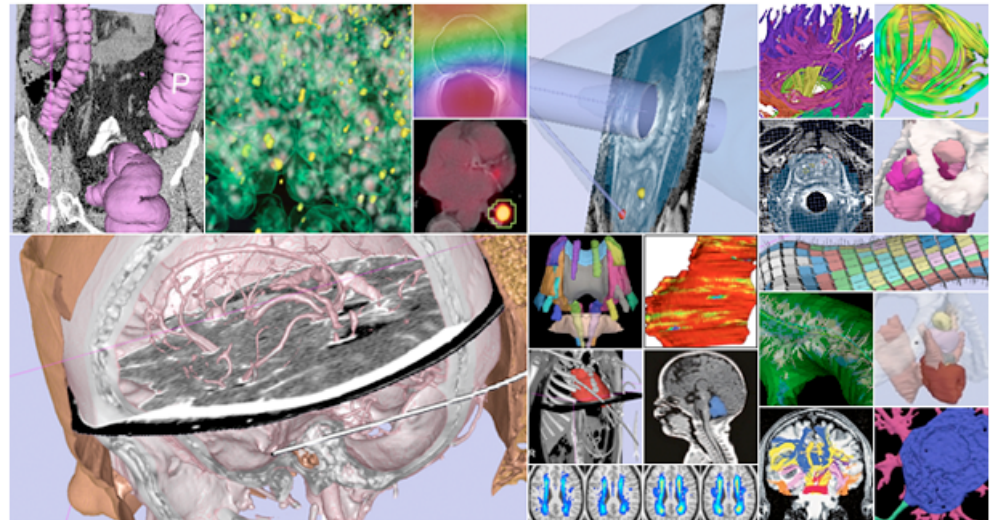


Jeffrey Yap, Ph.D.
Ron Kikinis, M.D.
Randy Gollub, M.D., Ph.D
Wendy Plesniak, Ph.D.
Kathryn Hayes, M.S.

Sonia Pujol, Ph.D.
Valerie Humblet, Ph.D.
Kilian Pohl, Ph.D.
Ender Konukoglu, Ph.D.
Andriy Fedorov, Ph.D.



- An **end-user application** for image analysis and visualization
- An **open-source environment** for software development
- A software platform that is both **easy to use** for clinical researchers and **easy to extend** for programmers

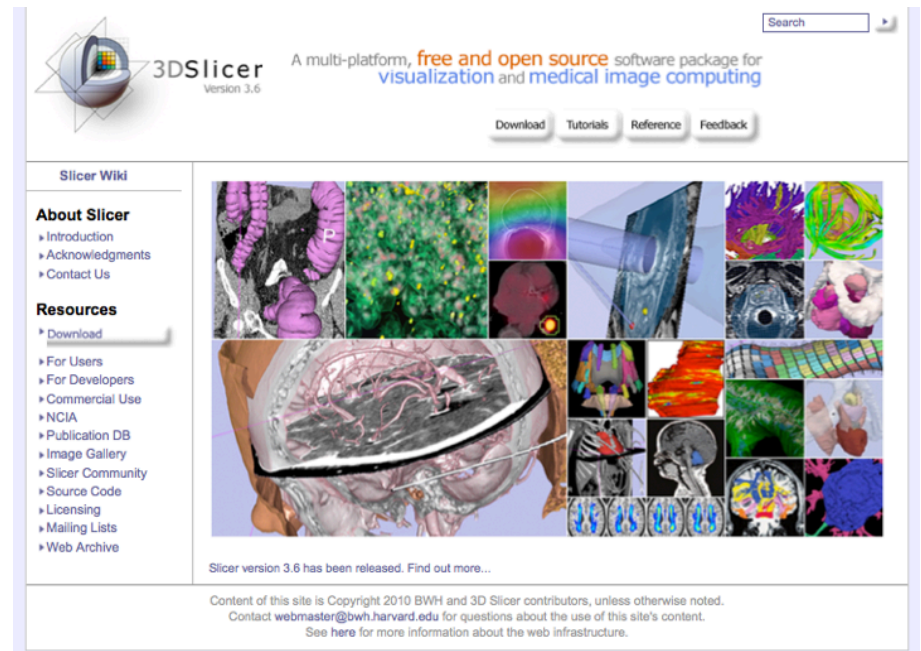




3D Slicer version 3 is a multi-platform software running on **Windows, Linux, and Mac OSX.**

Disclaimer

It is the responsibility of the user of 3DSlicer to comply with both the terms of the license and with the applicable laws, regulations and rules. **Slicer is a tool for research, and is not FDA approved.**





www.slicer.org

- This workshop uses the newest release of 3D Slicer (version 3.6.2).
- Visit the **Slicer download page** for Slicer 3.6 stable release, or for Slicer nightly builds.

A screenshot of the 3DSlicer website homepage. The page features the 3DSlicer logo and version number (3.6) at the top left. To the right, it states "A multi-platform, free and open source software package for visualization and medical image computing". Below this, there are navigation buttons for "Download", "Tutorials", "Reference", and "Feedback". The "Download" button is circled in orange. On the left side, there is a "Slicer Wiki" section with links for "About Slicer" (Introduction, Acknowledgments, Contact Us) and "Resources" (Download, For Users, For Developers, Commercial Use, NCI, Publication DB, Image Gallery, Slicer Community, Source Code, Licensing, Mailing Lists, Web Archive). The main content area displays a grid of various 3D medical image visualizations, including brain scans, organ models, and anatomical structures. At the bottom, there is a notice: "Slicer version 3.6 has been released. Find out more..." and a footer with copyright information and contact details for the webmaster at bwh.harvard.edu.



Tutorial Overview

- Getting Started: **Slicer3 Minute Tutorial**
- Quantitative Measurement of Volumetric Change:
ChangeTracker Tutorial
- Quantitative Measurements for Functional Imaging:
PETCTFusion Tutorial

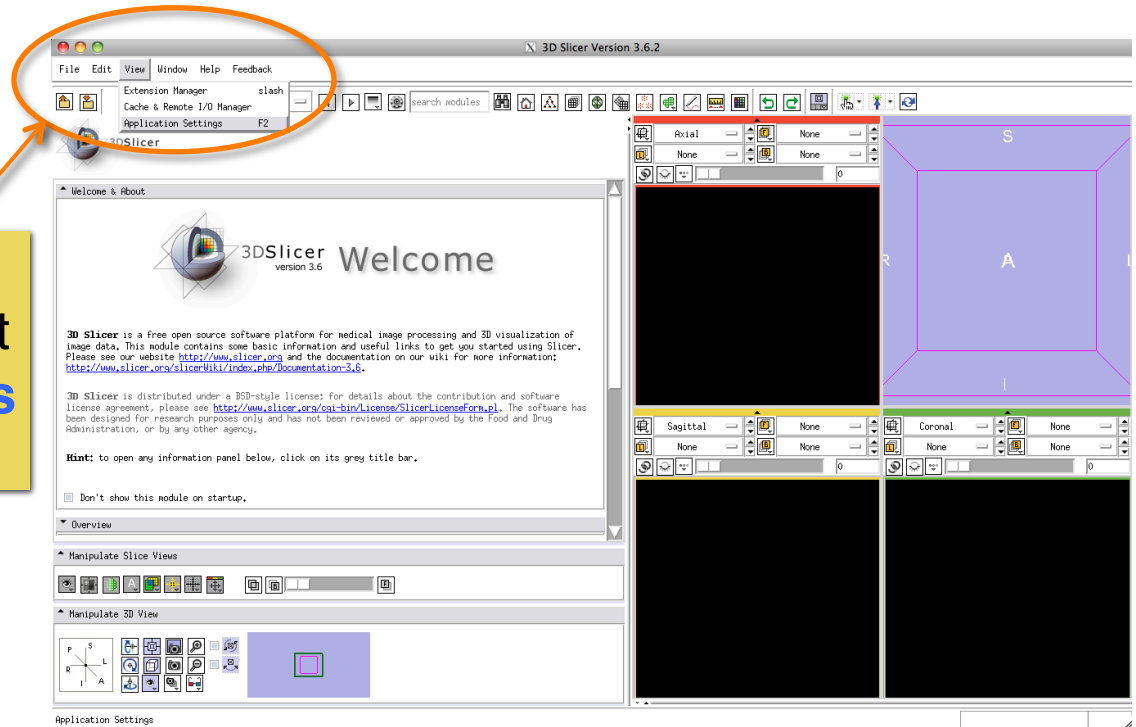
All Tutorial Datasets are located in `C:\slicer_data`



Tuning up...

Setting Font Size

In Slicer's main menu, select **View->Application Settings**



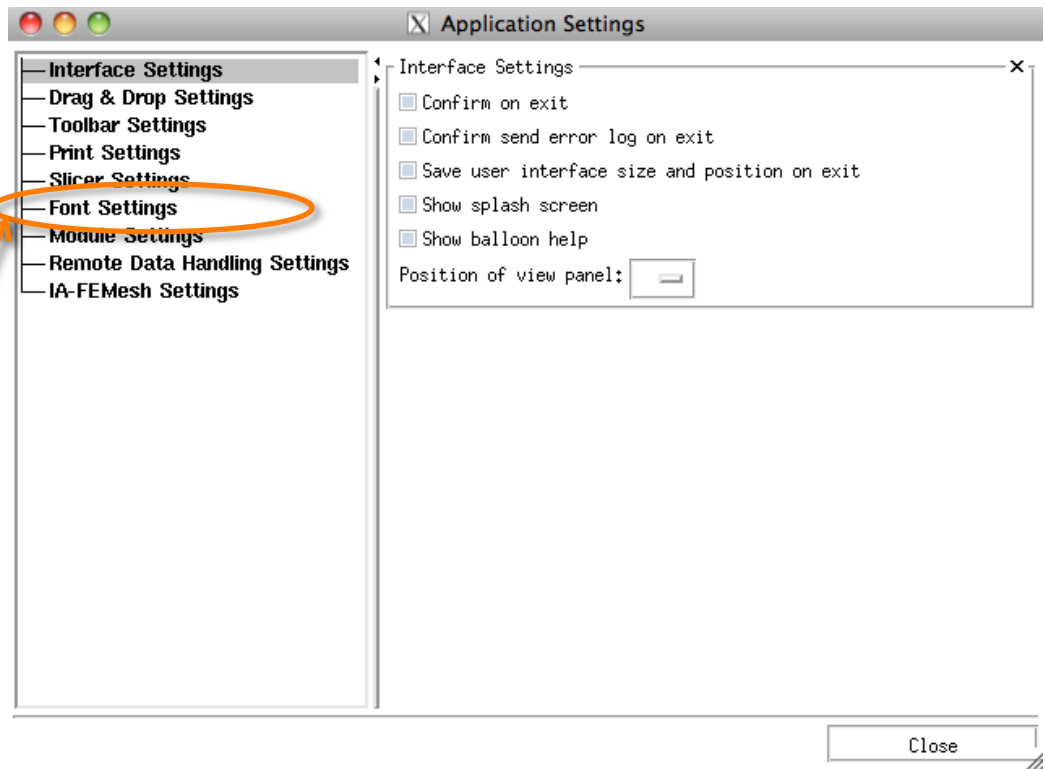


Tuning up...

Setting Font Size

This raises Slicer's
Application Settings
Interface

In the left panel, select
Font Settings



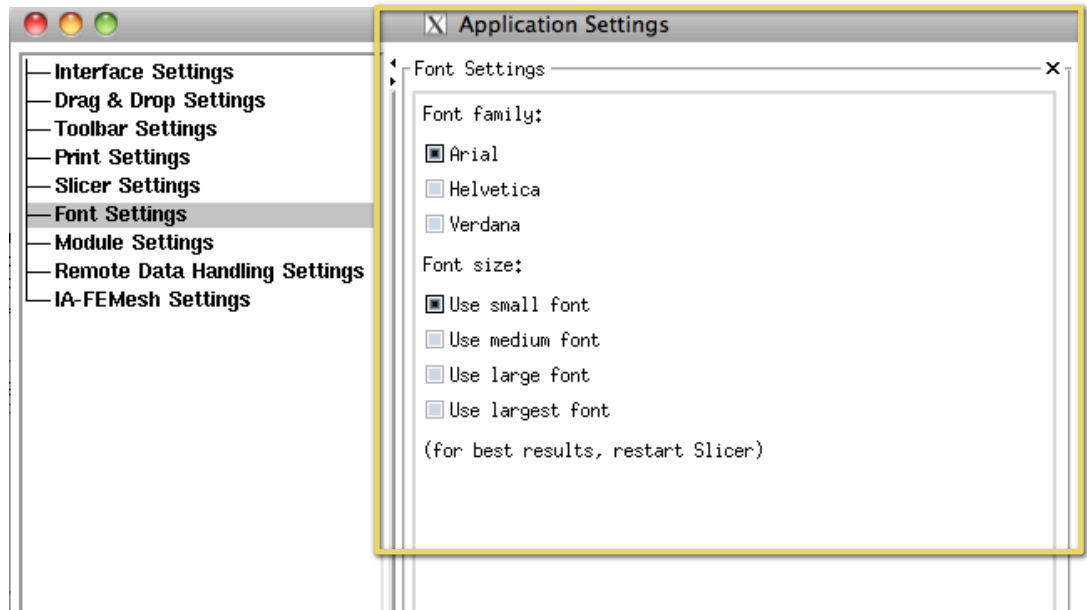


Tuning up...

Setting Font Size

This displays Slicer's **Font Family and Font Size options**

Choose among options until you find a font-size that works well for you.



Slicer will remember these settings next time you start the application.



3DSlicer

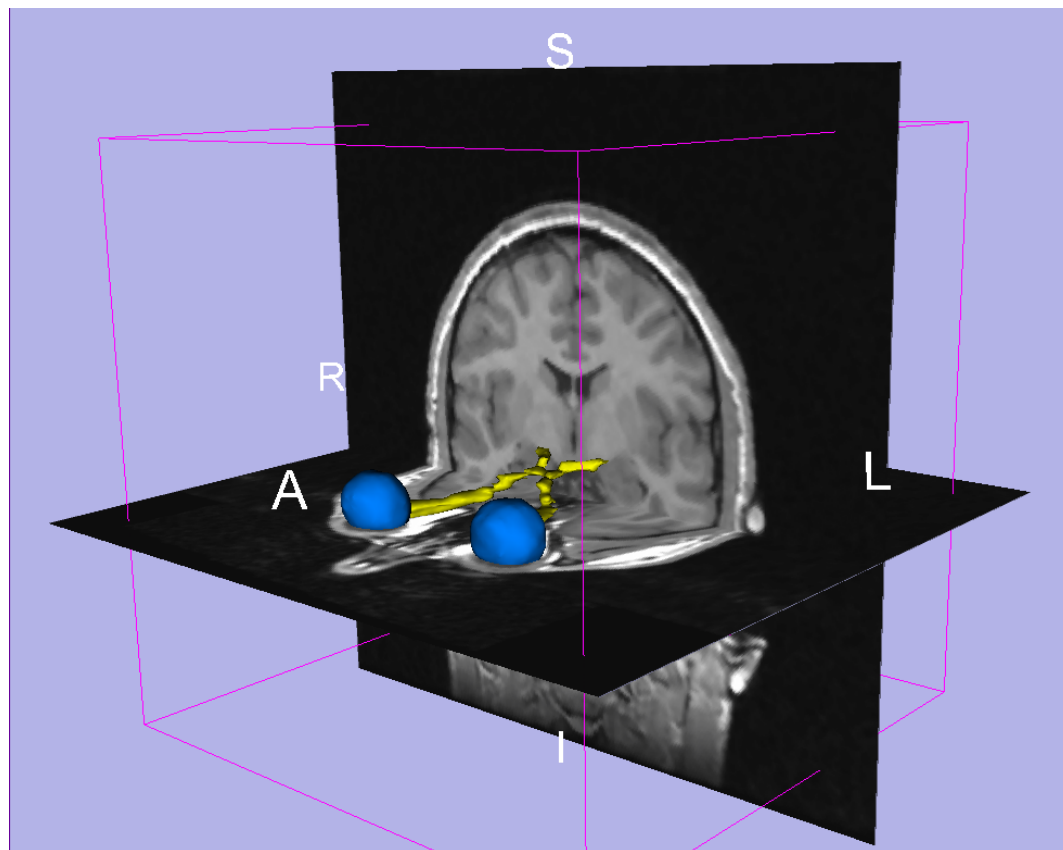
Slicer3 Minute Tutorial

Part I: Slicer3 Minute Tutorial

Sonia Pujol, PhD
Wendy Plesniak, PhD

This tutorial is a short introduction to the advanced **3D visualization capabilities** of the Slicer3 software for medical image analysis.

It is designed to **quickly build a basic level of comfort** with the Slicer software.



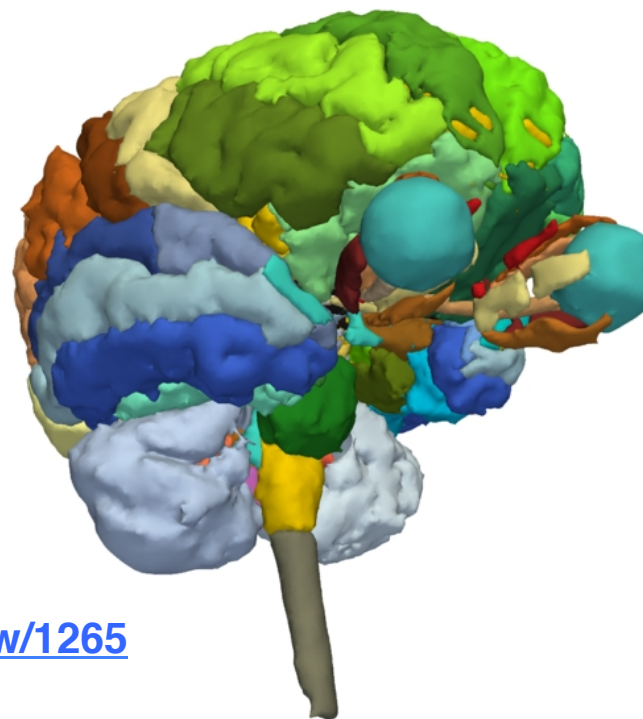


Slicer3 Minute Tutorial

The Slicer3Minute dataset is composed of
An MR scan of the brain and 3D surface
Reconstructions of anatomical structures.

The data are part of the SPL-PNL Brain Atlas
Developed by Talos *et al.* The atlas is available at:

<http://www.spl.harvard.edu/publications/item/view/1265>





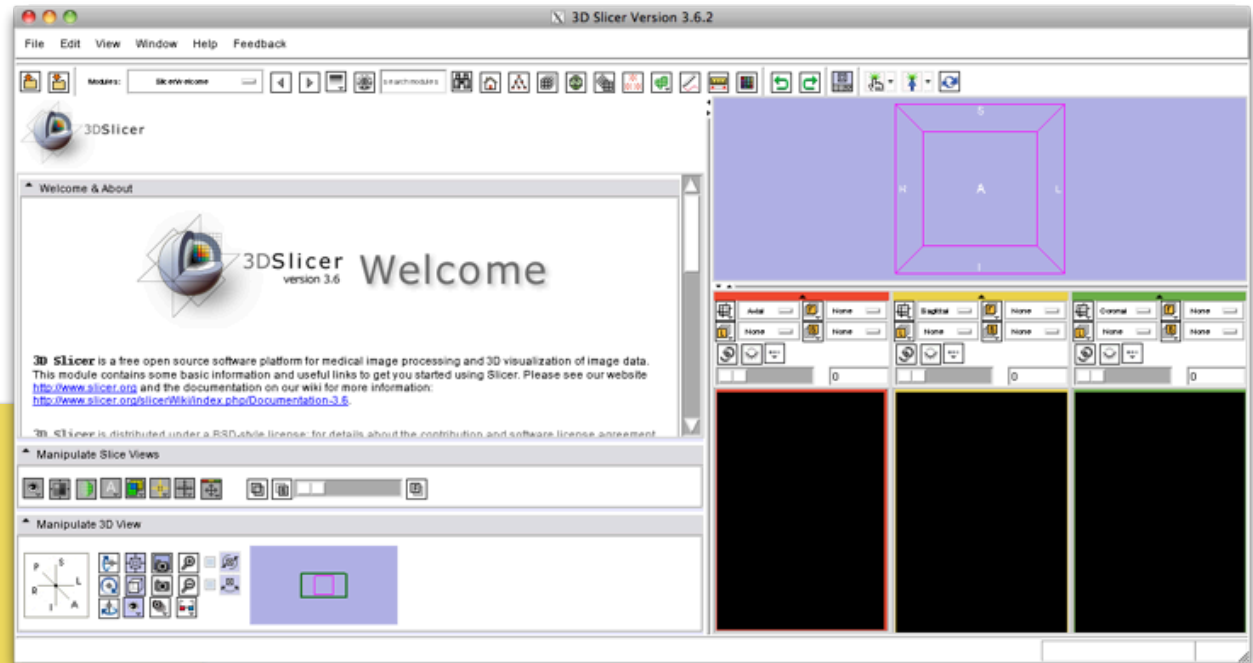
Slicer3 Minute Tutorial: Launch the Application

Windows users:

Double-Click the Shortcut to **Slicer3.exe** on the Desktop

or Select

Start ->All Programs ->Slicer3 3.6.2010-10-22->Slicer

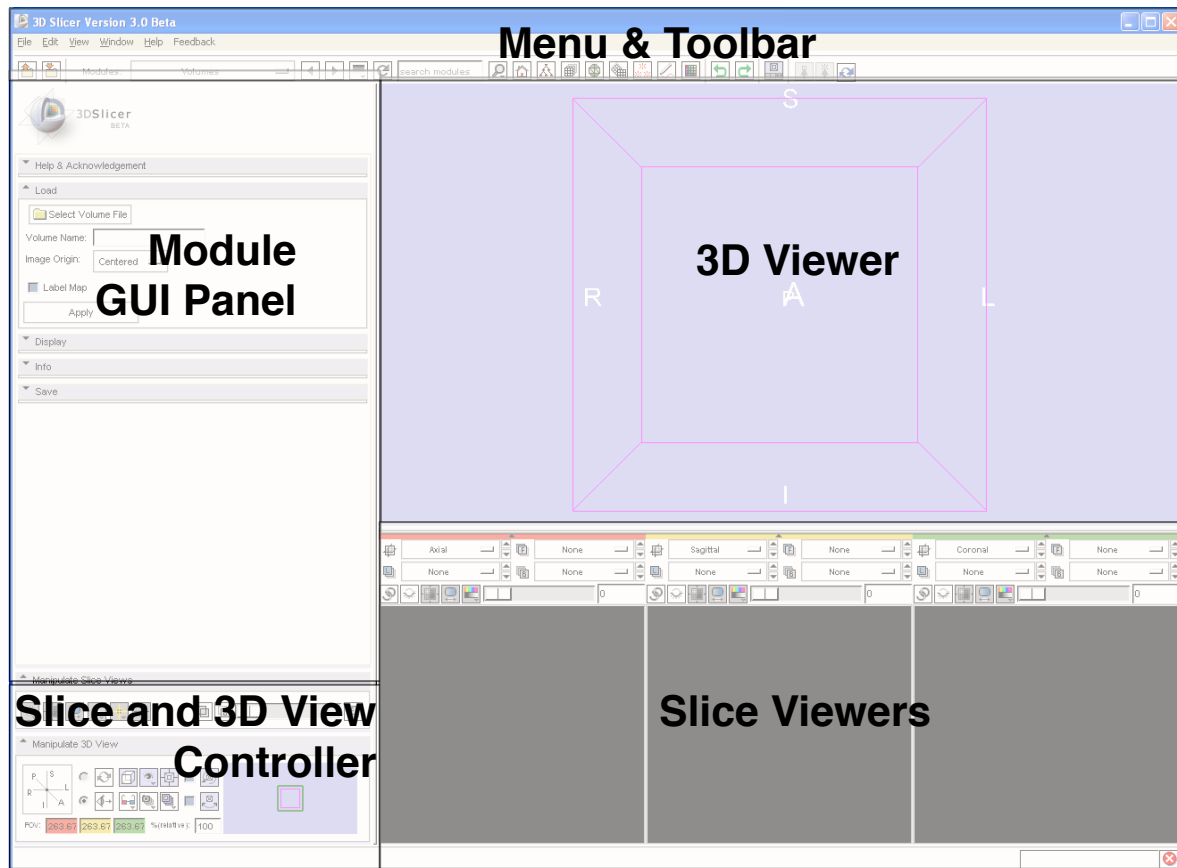




Slicer3 Minute Tutorial: Navigating the Application GUI

The Graphical User Interface (GUI) of Slicer3 integrates **five** components:

- the Menu Toolbar
- the Module GUI Panel
- the 3D Viewer
- the Slice Viewer
- the Slice and 3D View Controller

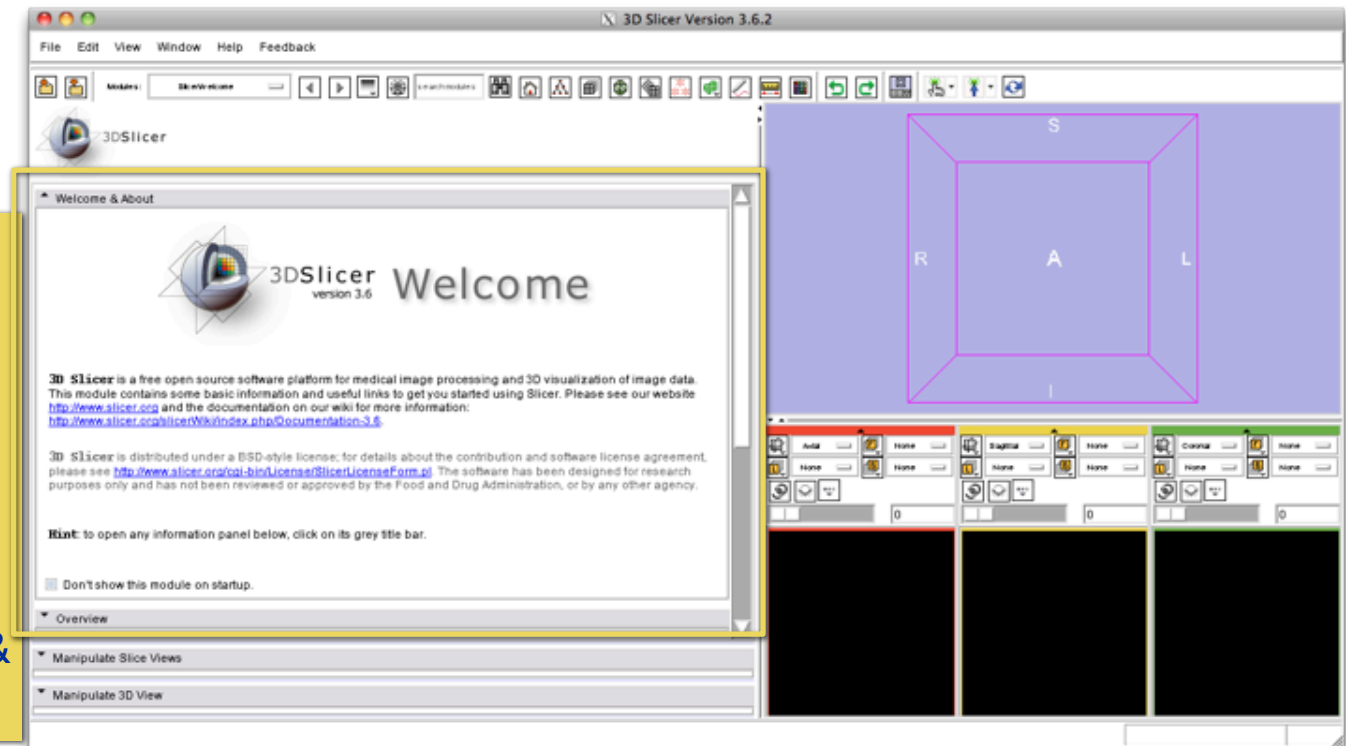




Slicer3 Minute Tutorial: Welcome Module

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

This module gives an overview of the GUI of Slicer3, and **data loading & saving functionalities**.

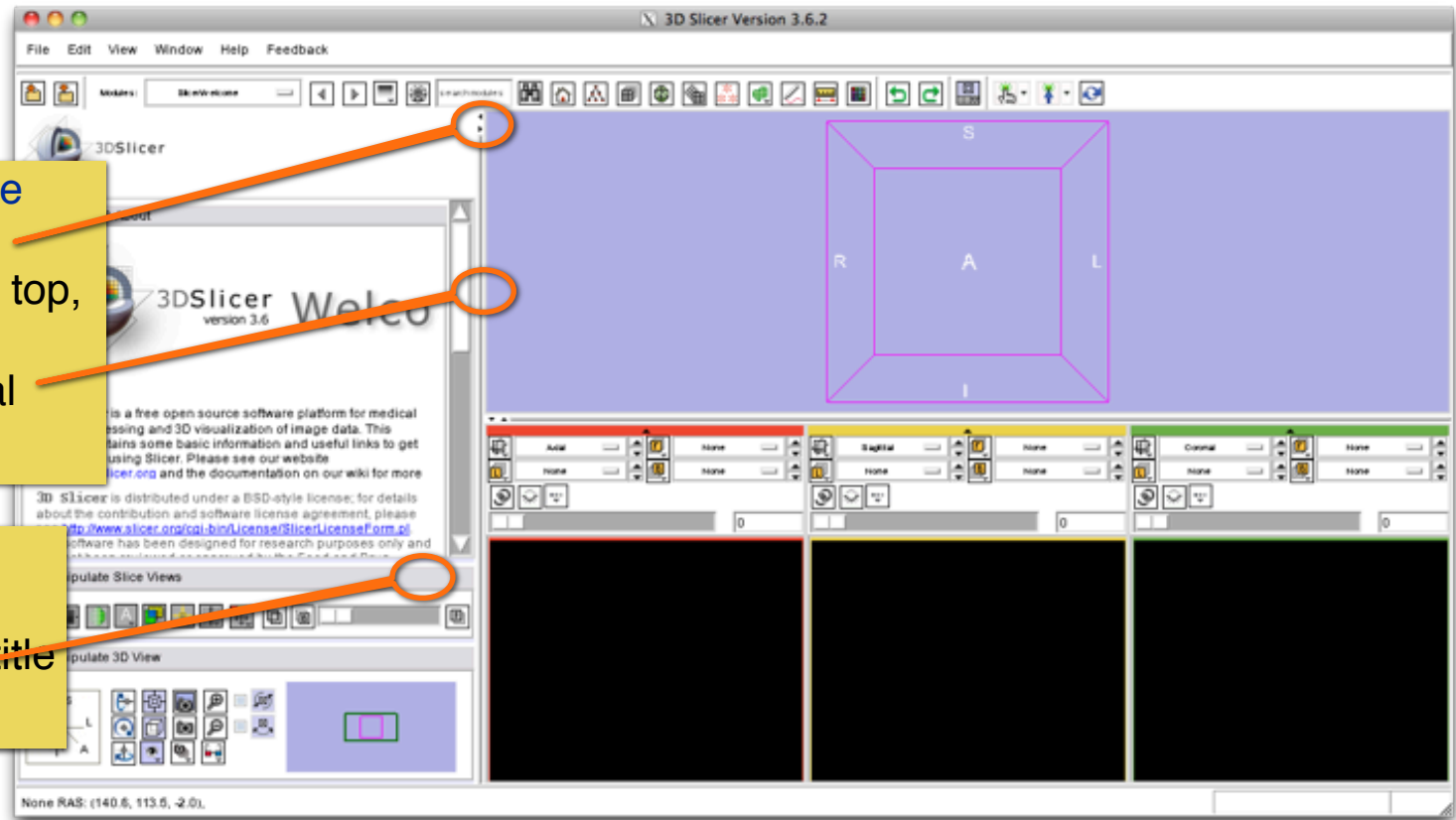




Slicer3 Minute Tutorial: GUI Basics

Expand or shrink the GUI panel with the arrows at the frame top, or by clicking and dragging the vertical separator

Expand or collapse any sub-panel by clicking on its grey title bar.






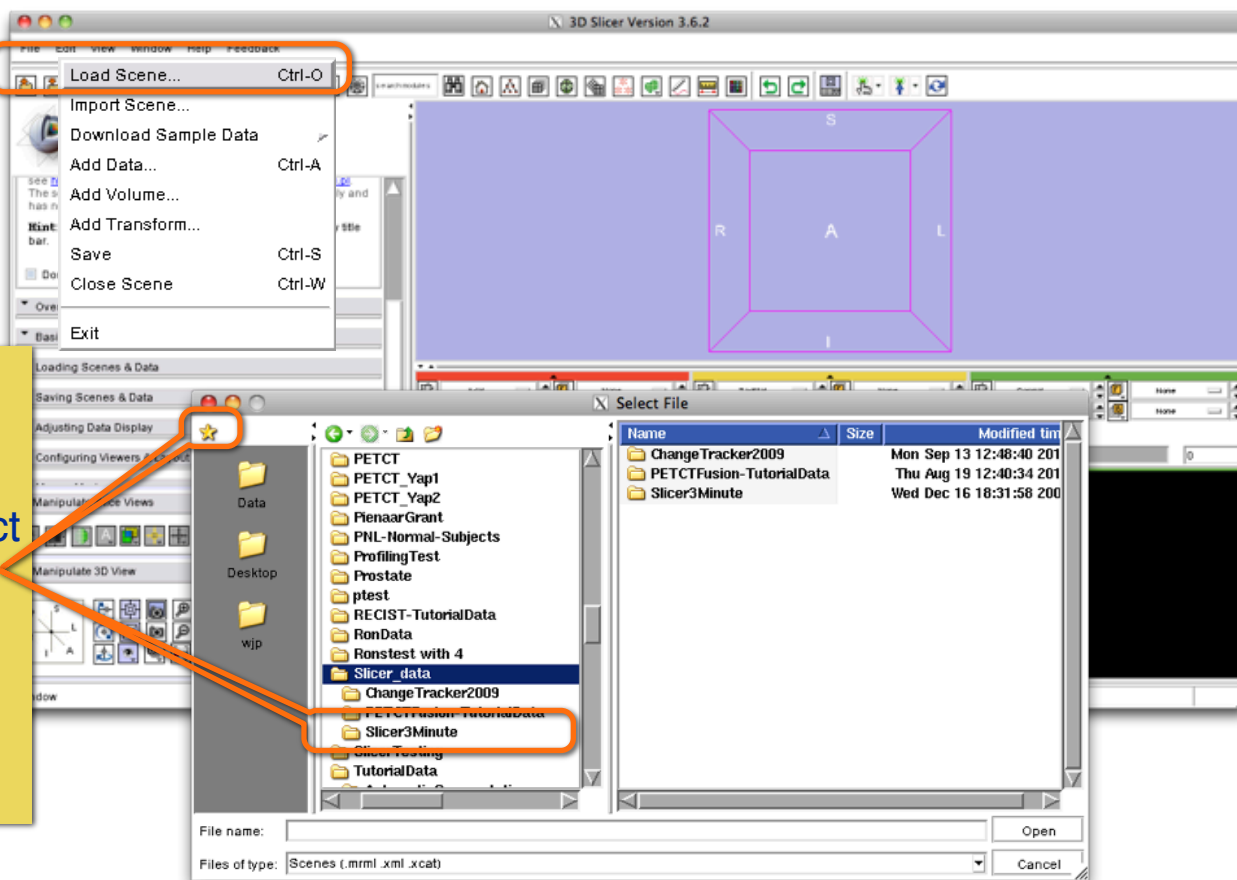
Slicer3 Minute Tutorial: Load A Scene

Select **File-> Load Scene** from the File menu

Browse to the location of the **Slicer_data** directory.

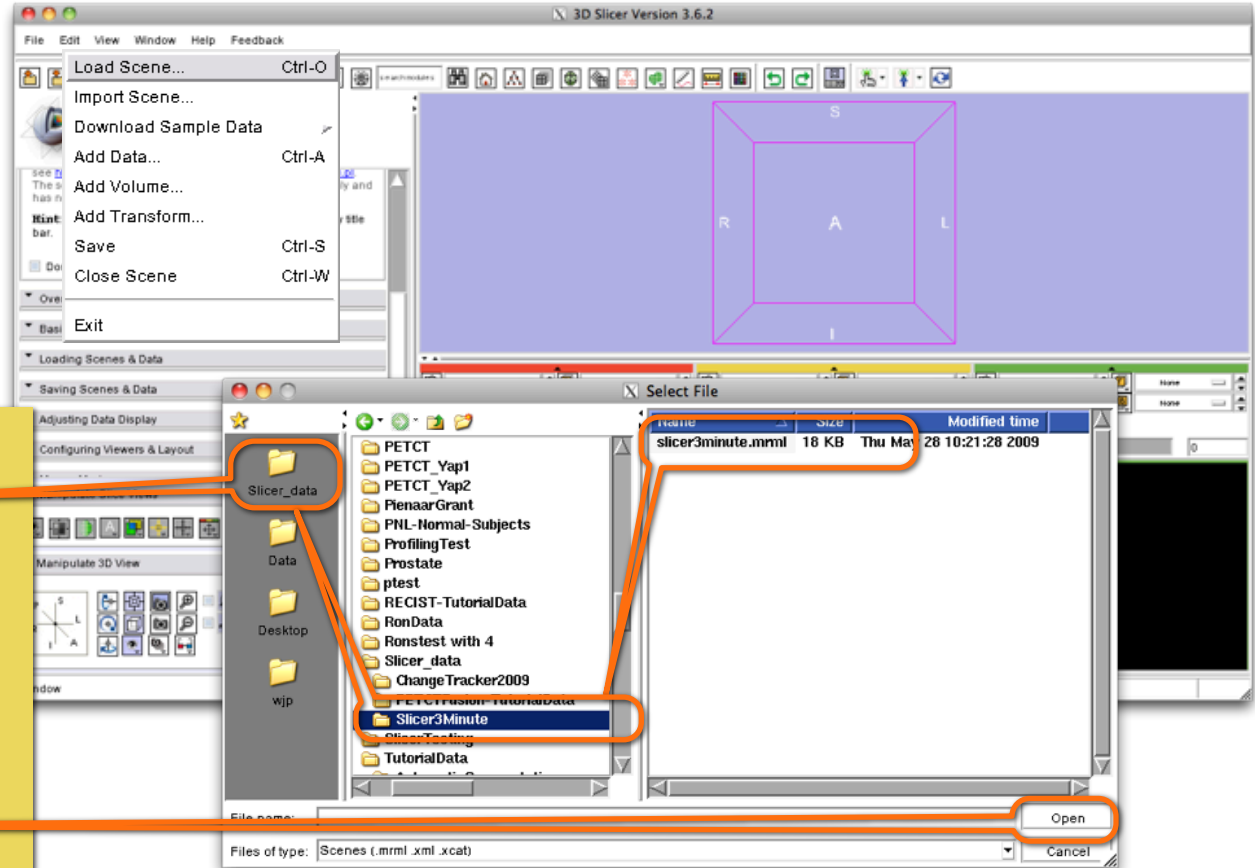
Select that directory and select the **Add To Favorites** icon 

This will make the directory easier to find later...





Slicer3 Minute Tutorial: Load A Scene



Browse to the location of the **Slicer3MinuteDataset** directory.

Select the scene file **slicer3minute.mrml**

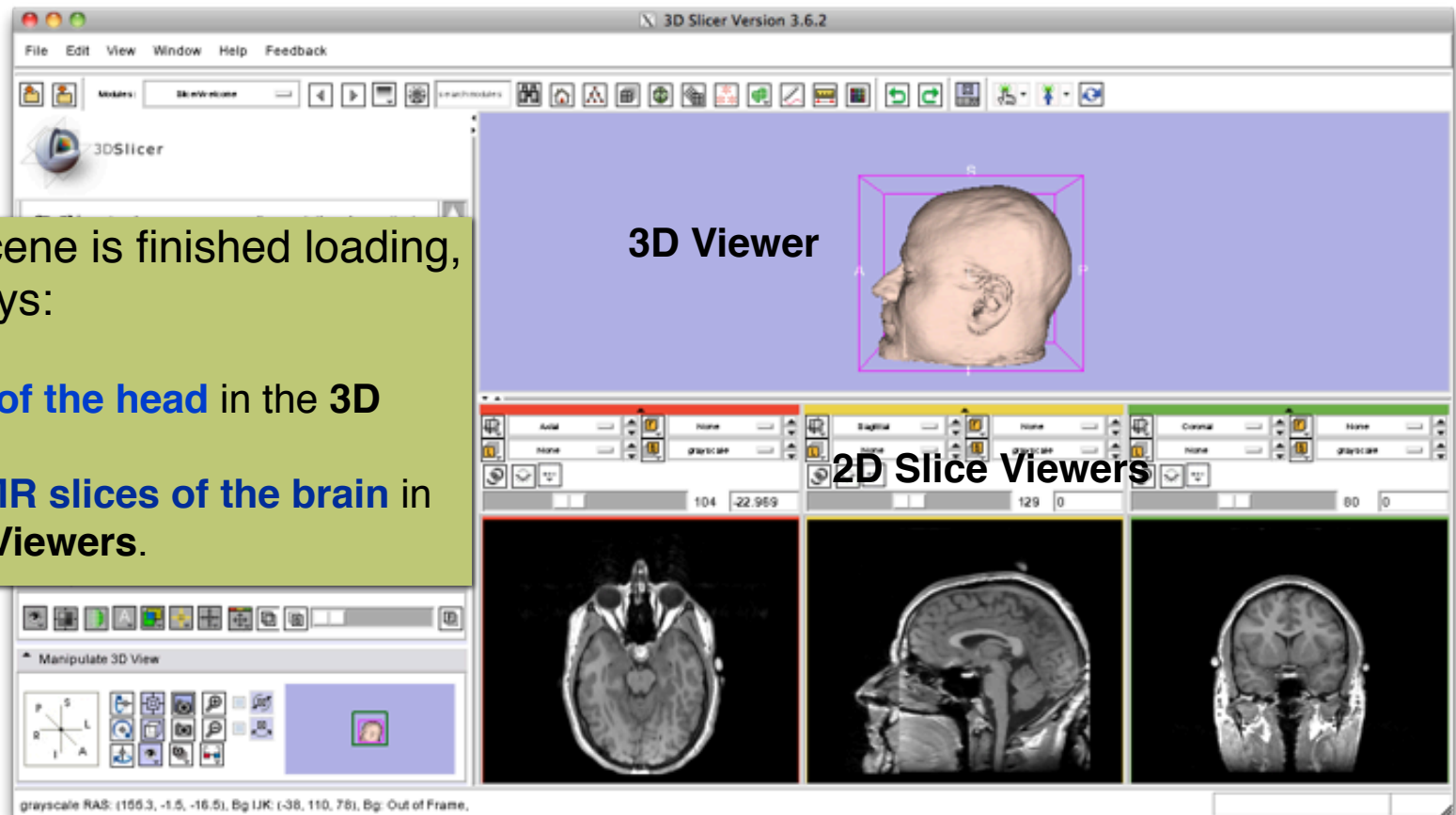
Click on **Open** to load the scene



Slicer3 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**.



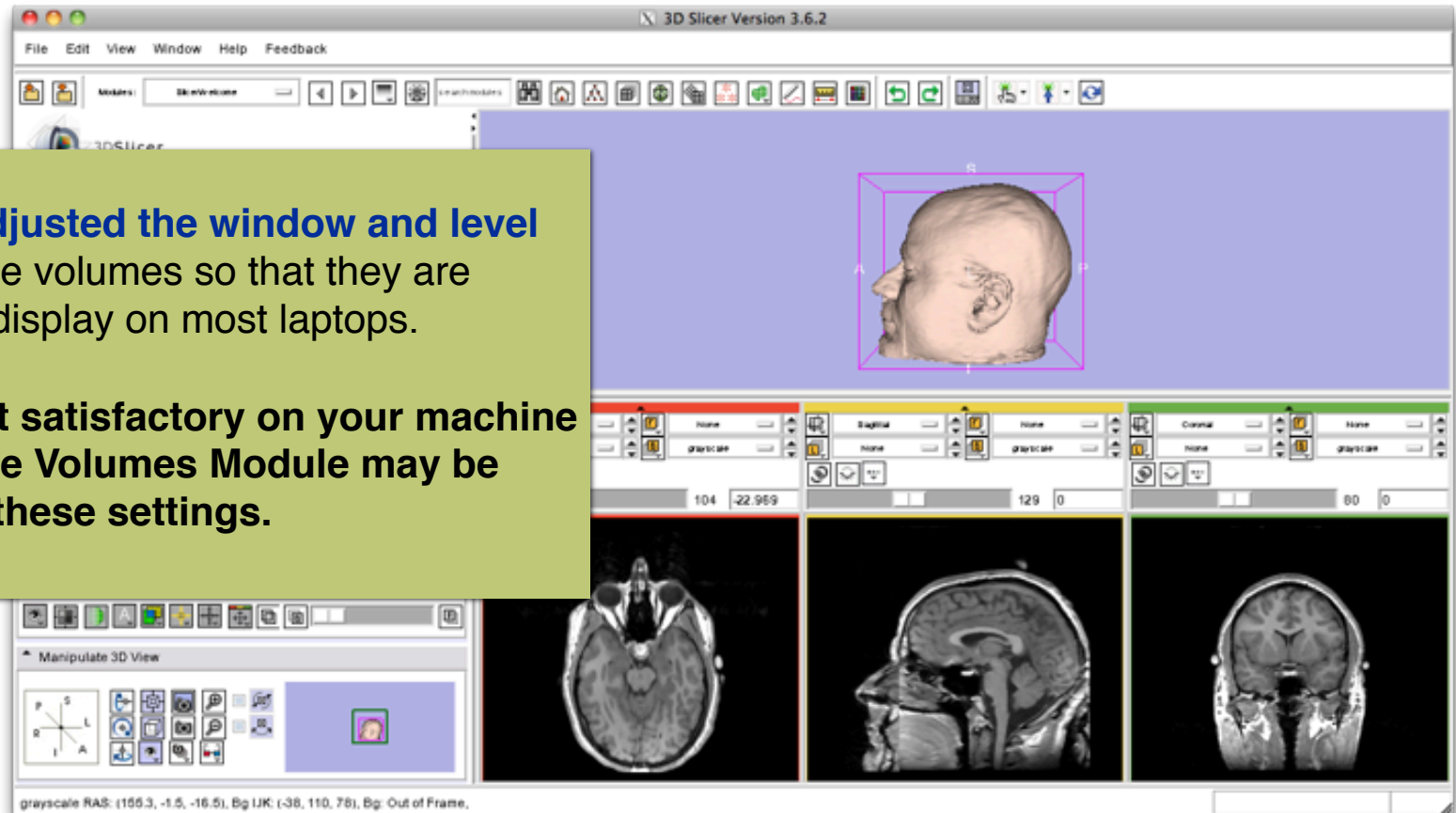


Slicer3 Minute Tutorial: Viewing the Scene

Note:

We have **pre-adjusted the window and level** settings for these volumes so that they are appropriate for display on most laptops.

If display is not satisfactory on your machine or projector, the Volumes Module may be used to refine these settings.

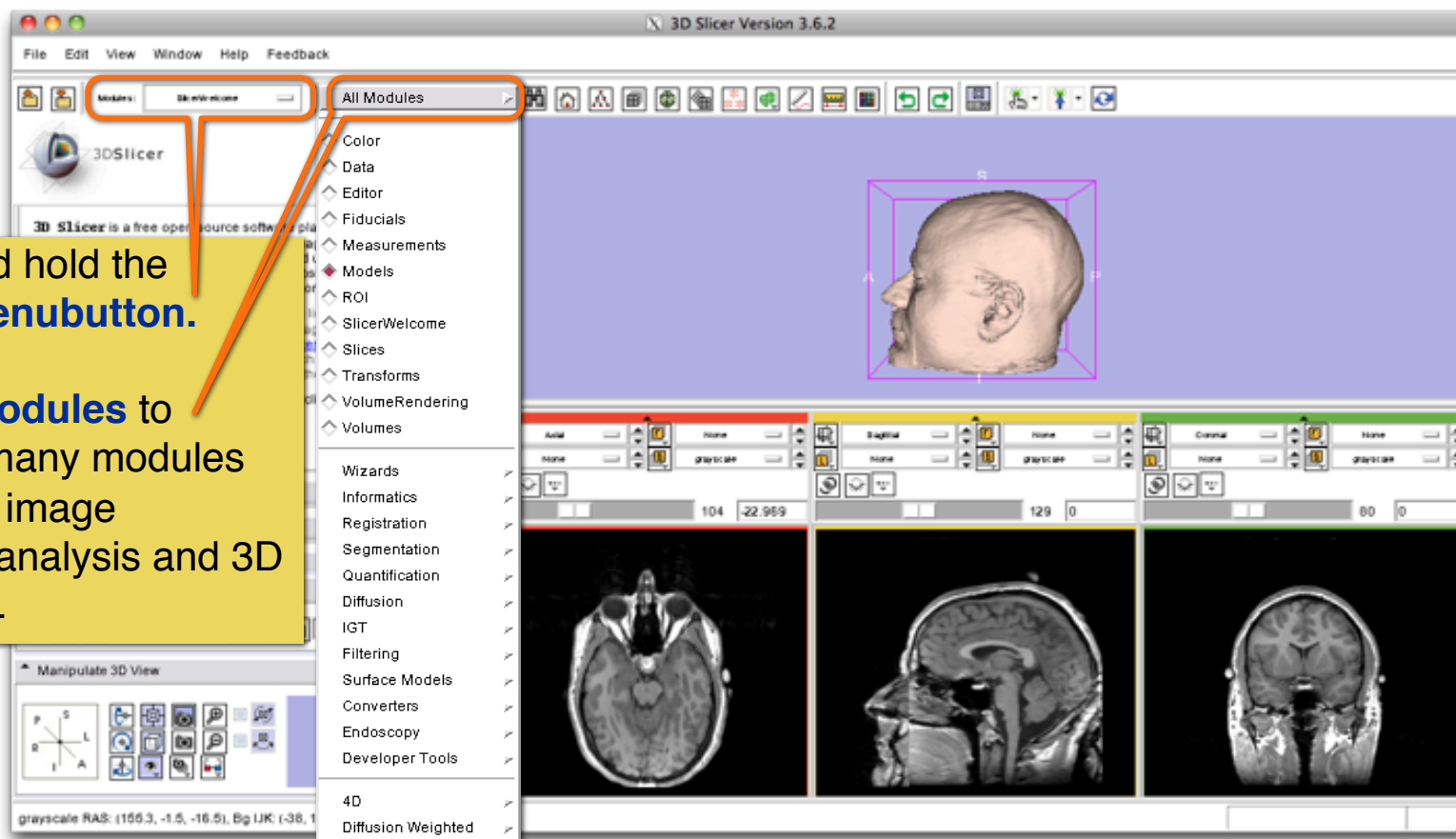




Slicer3 Minute Tutorial: Exploring Slicer's functionality

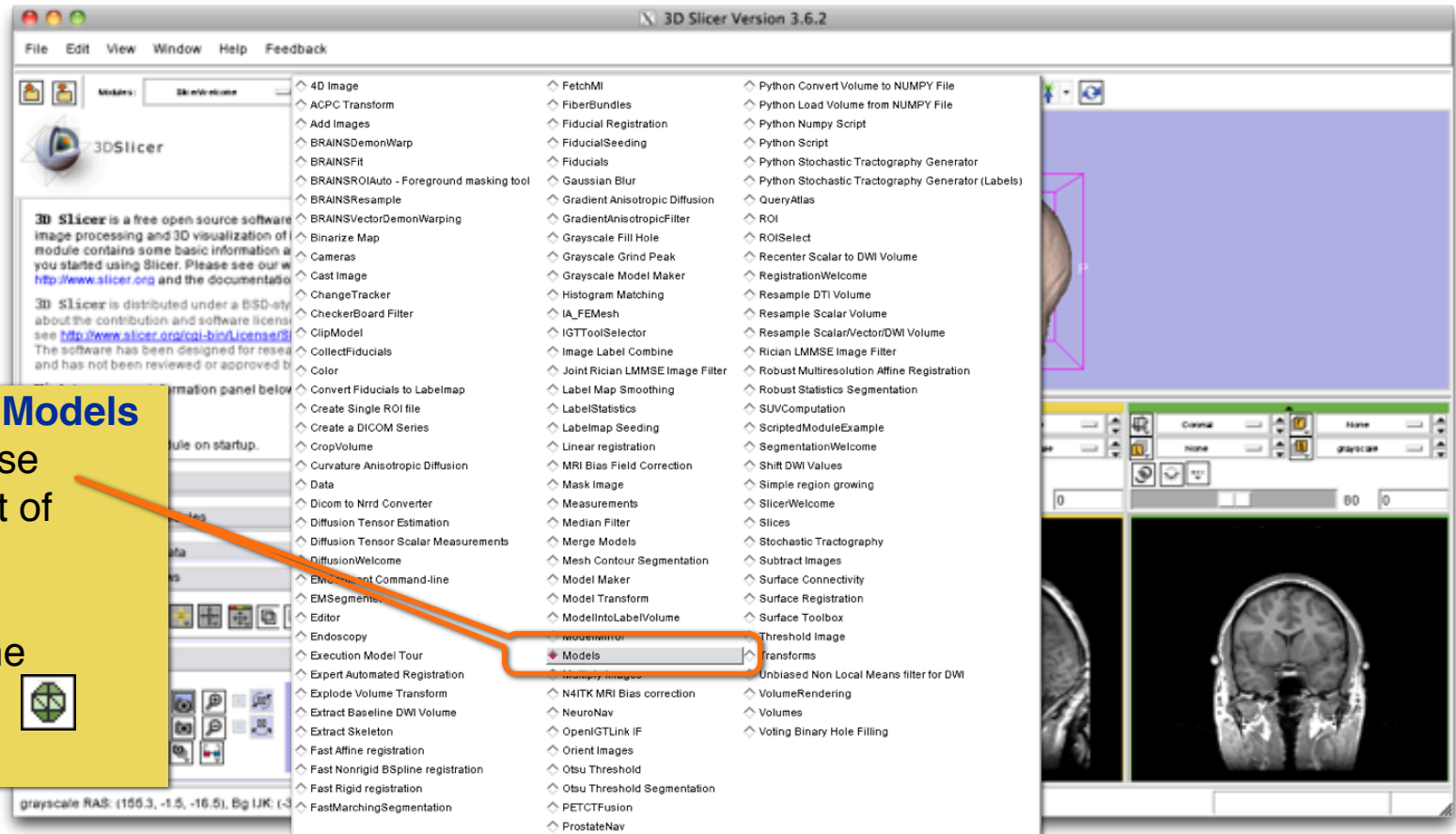
Left click and hold the **Modules** menubutton.

Select **All Modules** to display the many modules available for image processing, analysis and 3D visualization.



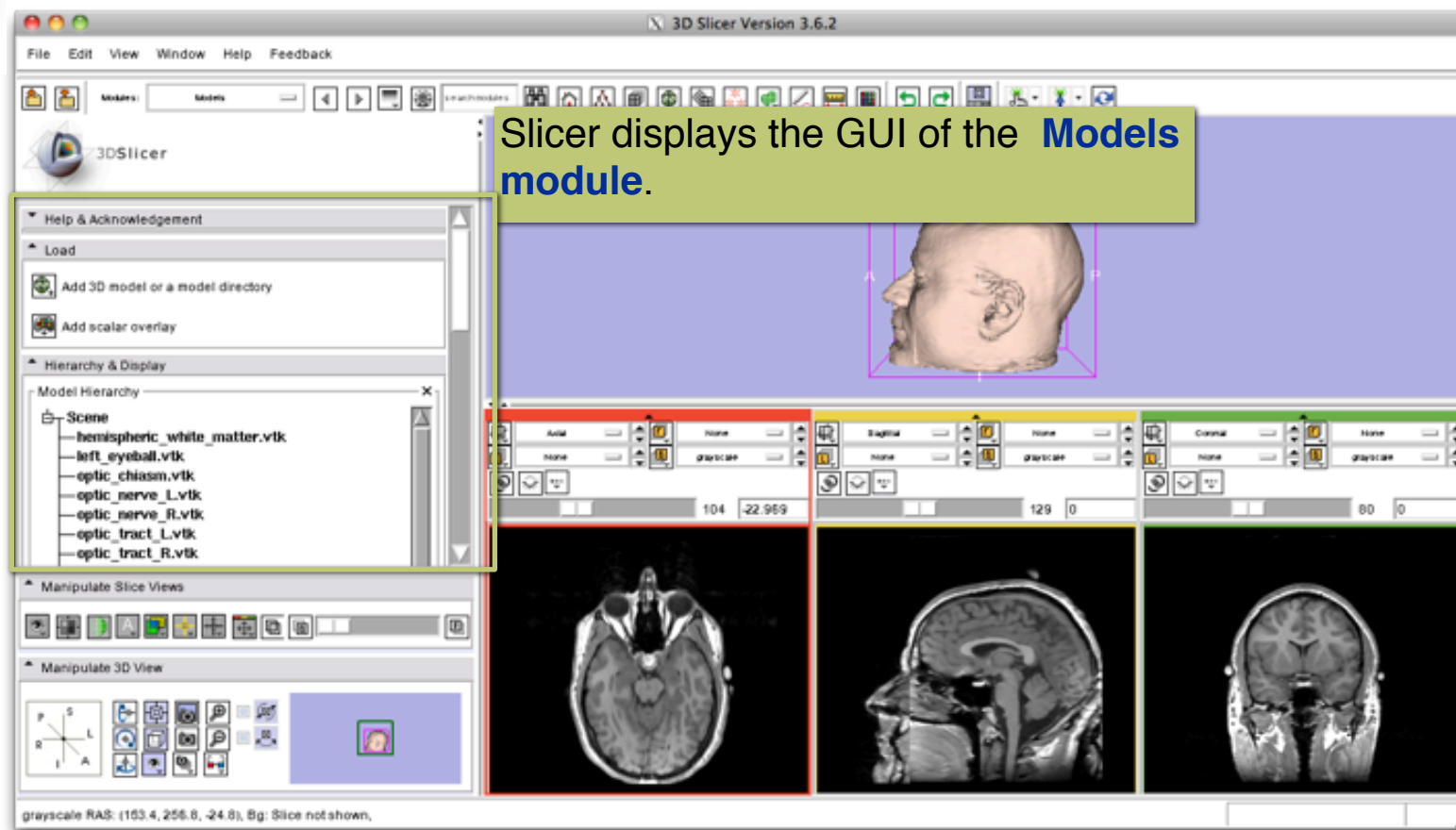


Slicer3 Minute Tutorial: Exploring Slicer's functionality





Slicer3 Minute Tutorial: Switching to the Models Module

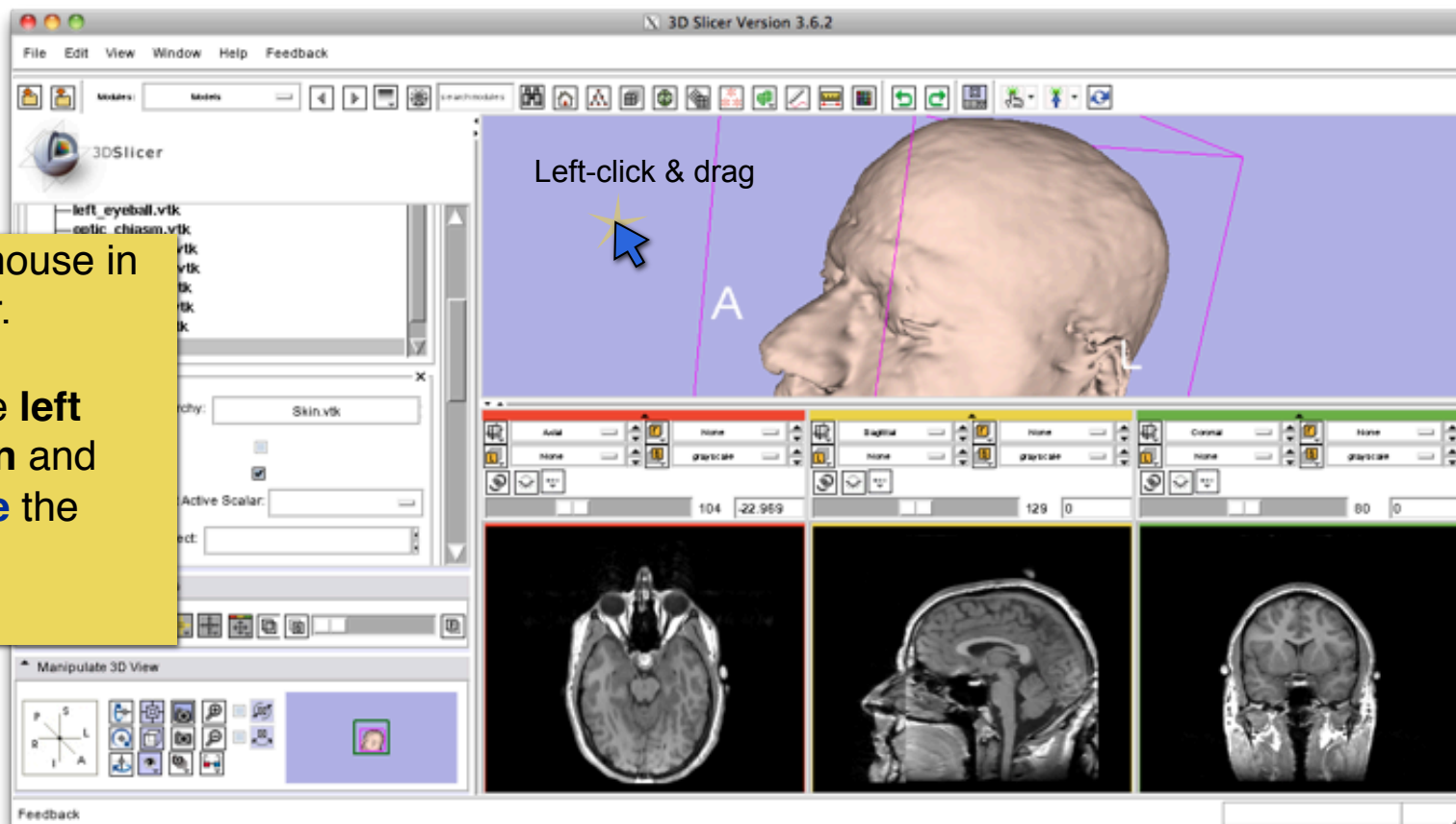




Slicer3 Minute Tutorial: Basic 3D Interaction

Position the mouse in the 3D Viewer.

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





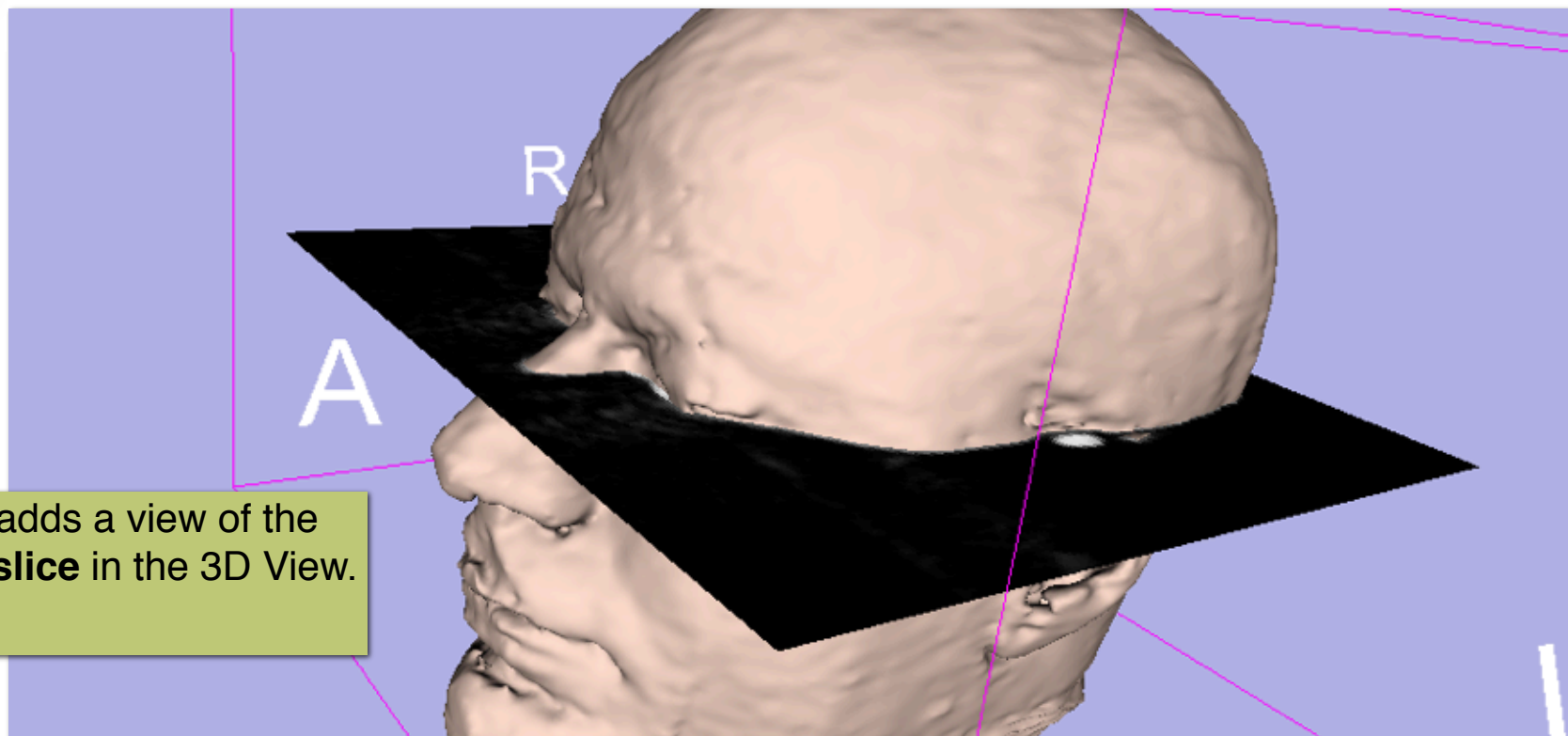
Slicer3 Minute Tutorial: Viewing Slices in the 3D Viewer

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

The screenshot shows the 3D Slicer 3.6.2 interface. The main 3D view displays a 3D model of a human head in profile, with a purple plane labeled 'A' indicating an axial slice. Below the 3D view are three slice view panels: Axial (red header), Sagittal (yellow header), and Coronal (green header). Each panel has a 'Slice Visibility' icon (a sun with rays) and a 'Map Select' dropdown. The Axial panel's 'Slice Visibility' icon is circled in orange, and a yellow callout box points to it with the text: 'Click on the **Slice Visibility** icon to display the Axial Slice in the 3D Viewer'. The 'Manipulate 3D View' panel at the bottom left shows a 3D coordinate system with 'A' (Anterior) and 'P' (Posterior) labels. The 'Feedback' panel is at the bottom.



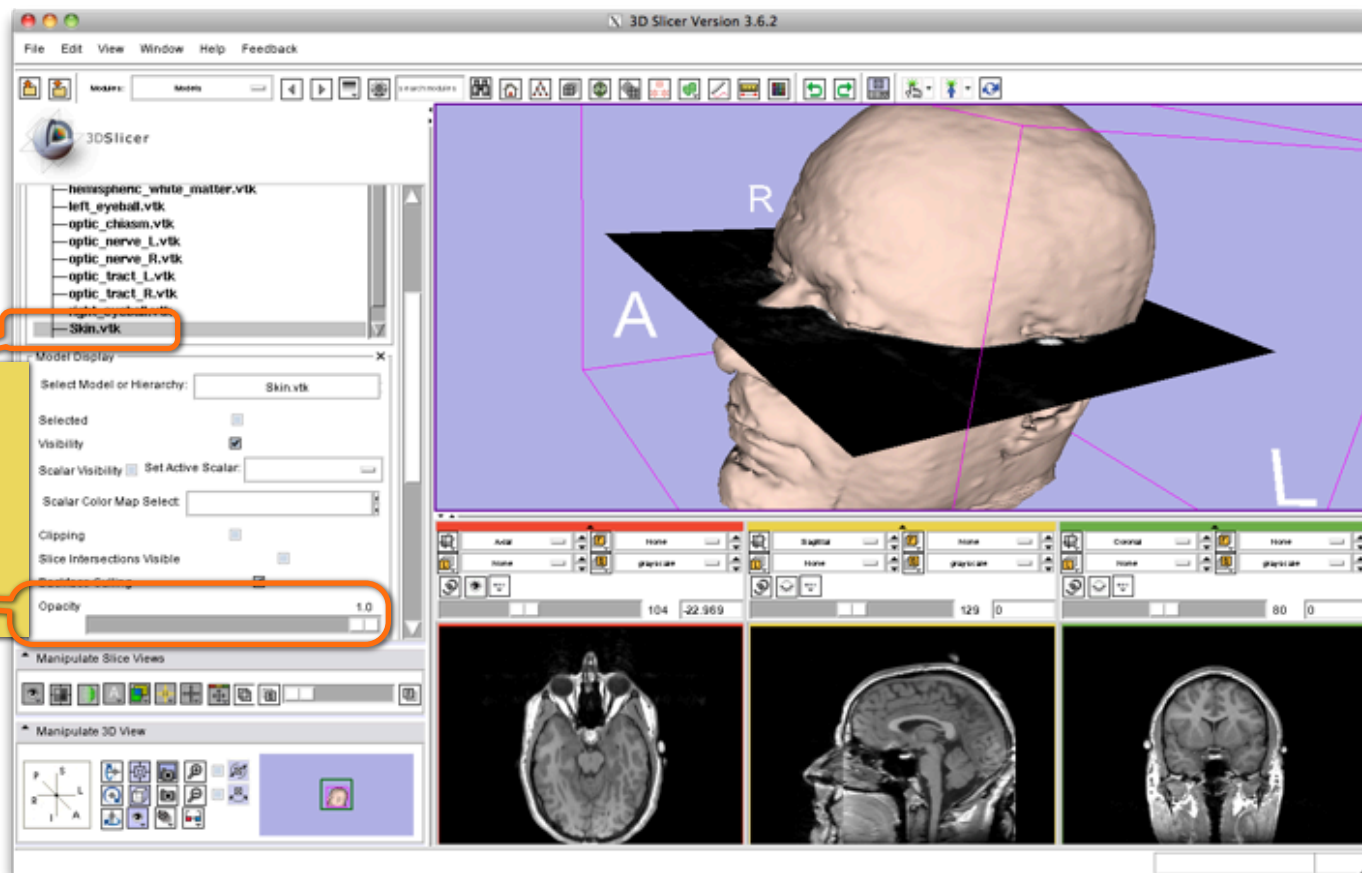
Slicer3 Minute Tutorial: 3D Visualization



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



Slicer3 Minute Tutorial: 3D Visualization



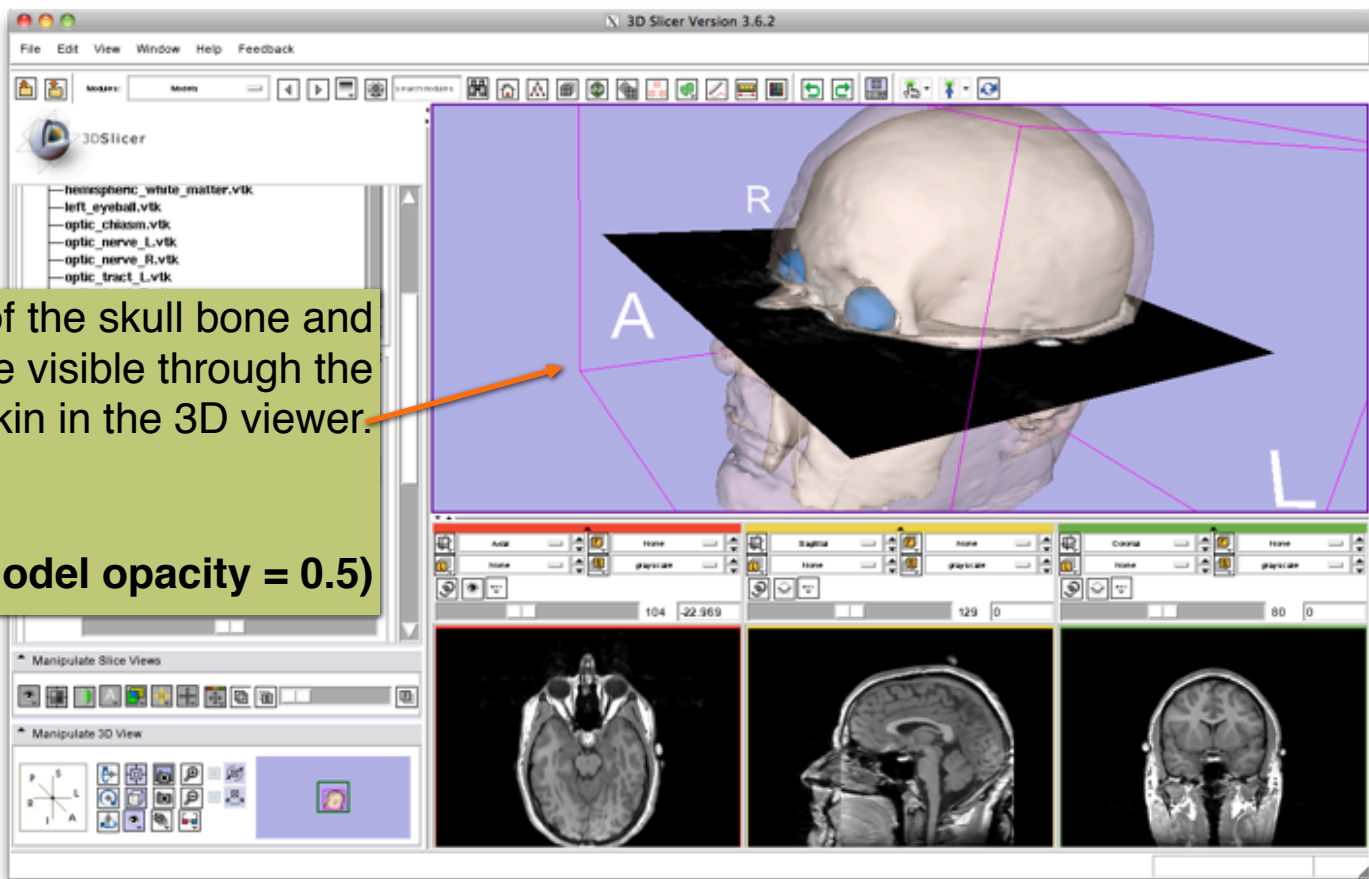
Select the **Skin model**.

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



Slicer3 Minute Tutorial: 3D Visualization

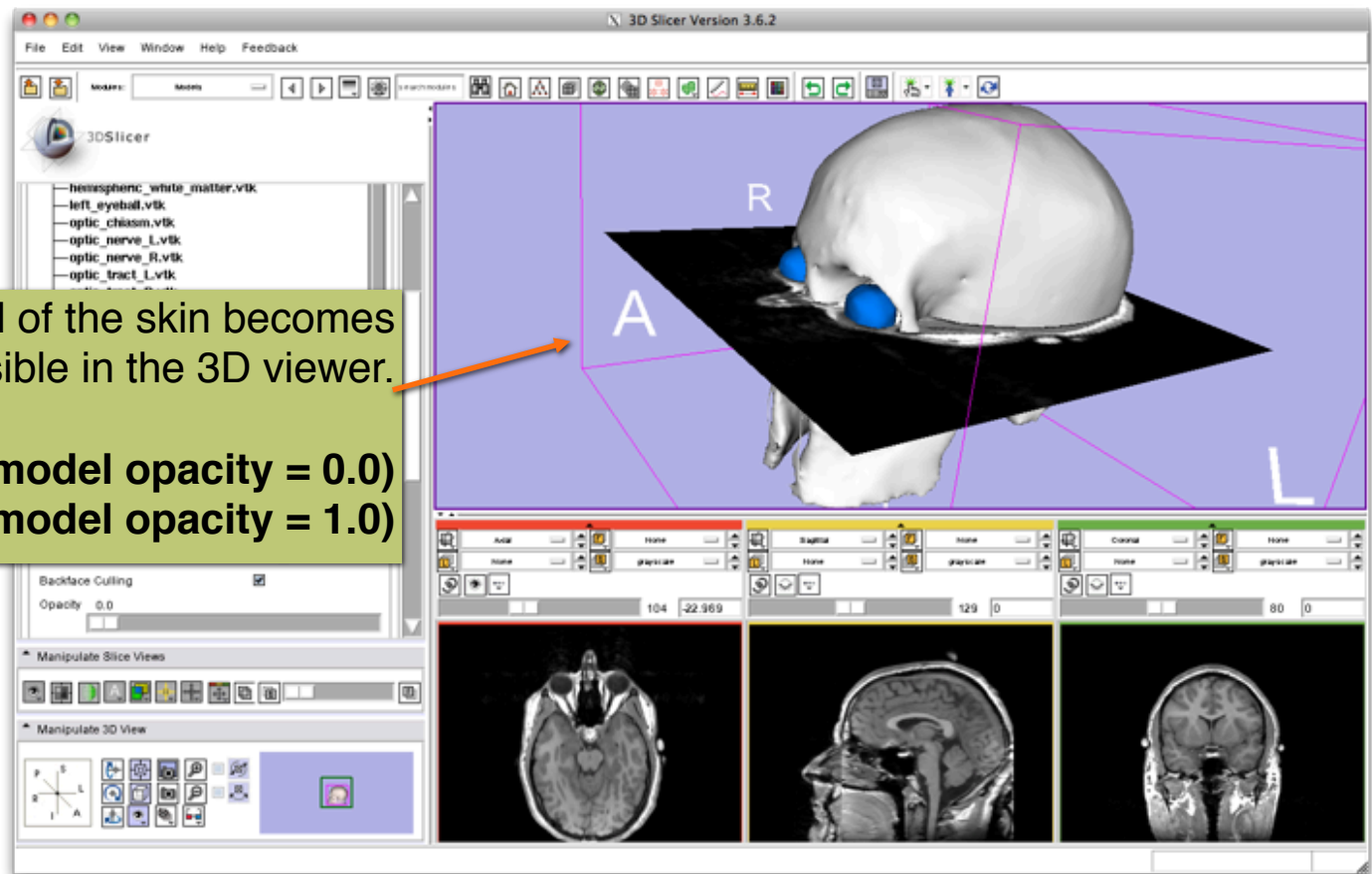
The model of the skull bone and eyeballs become visible through the model of the skin in the 3D viewer.
(skin model opacity = 0.5)





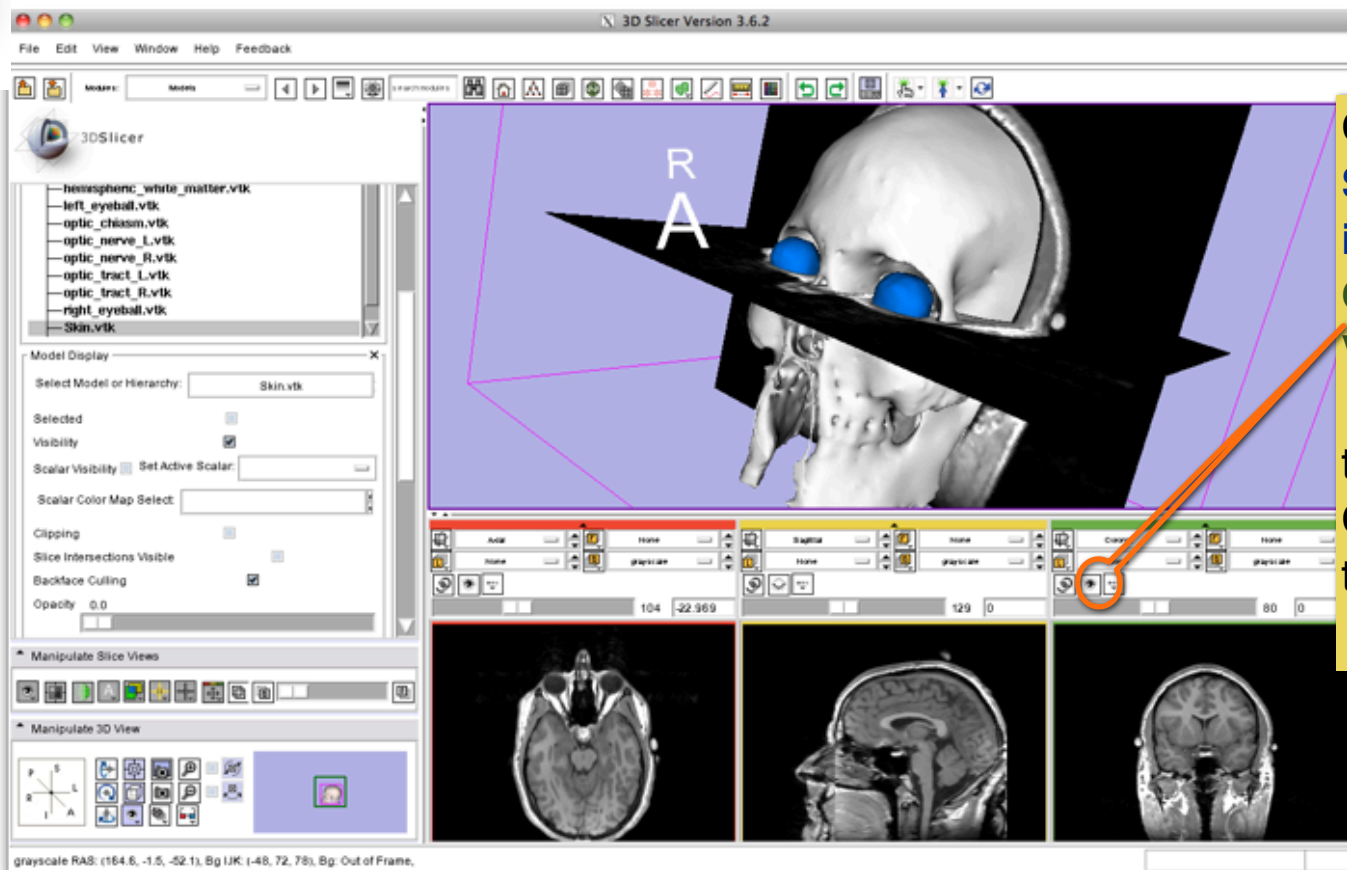
Slicer3 Minute Tutorial: 3D Visualization

The model of the skin becomes invisible in the 3D viewer.
(skin model opacity = 0.0)
(skull model opacity = 1.0)





Slicer3 Minute Tutorial: 3D Visualization

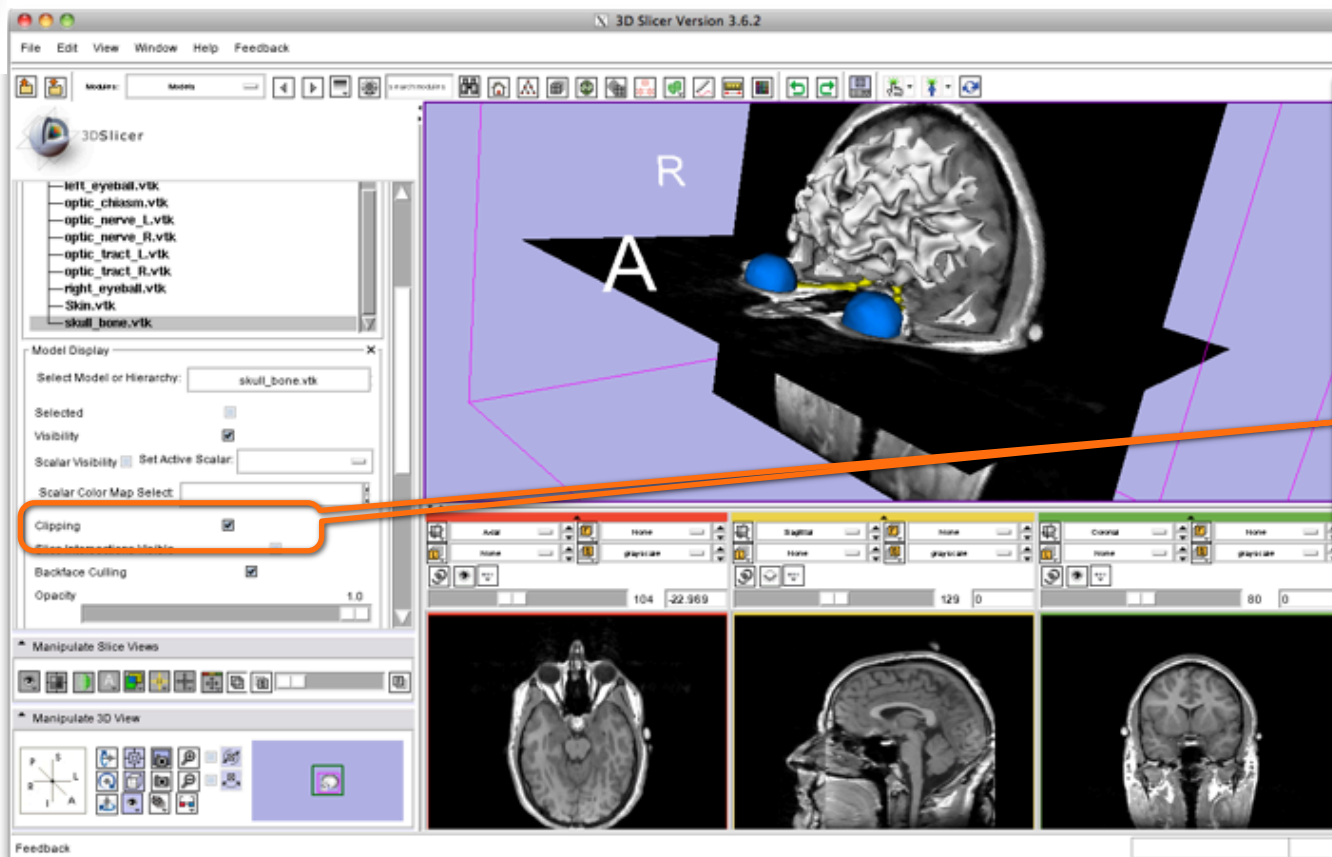


Click on the **Slice Visibility icon** in the **Green Slice Viewer**

to display the **Coronal Slice** in the 3D Viewer.



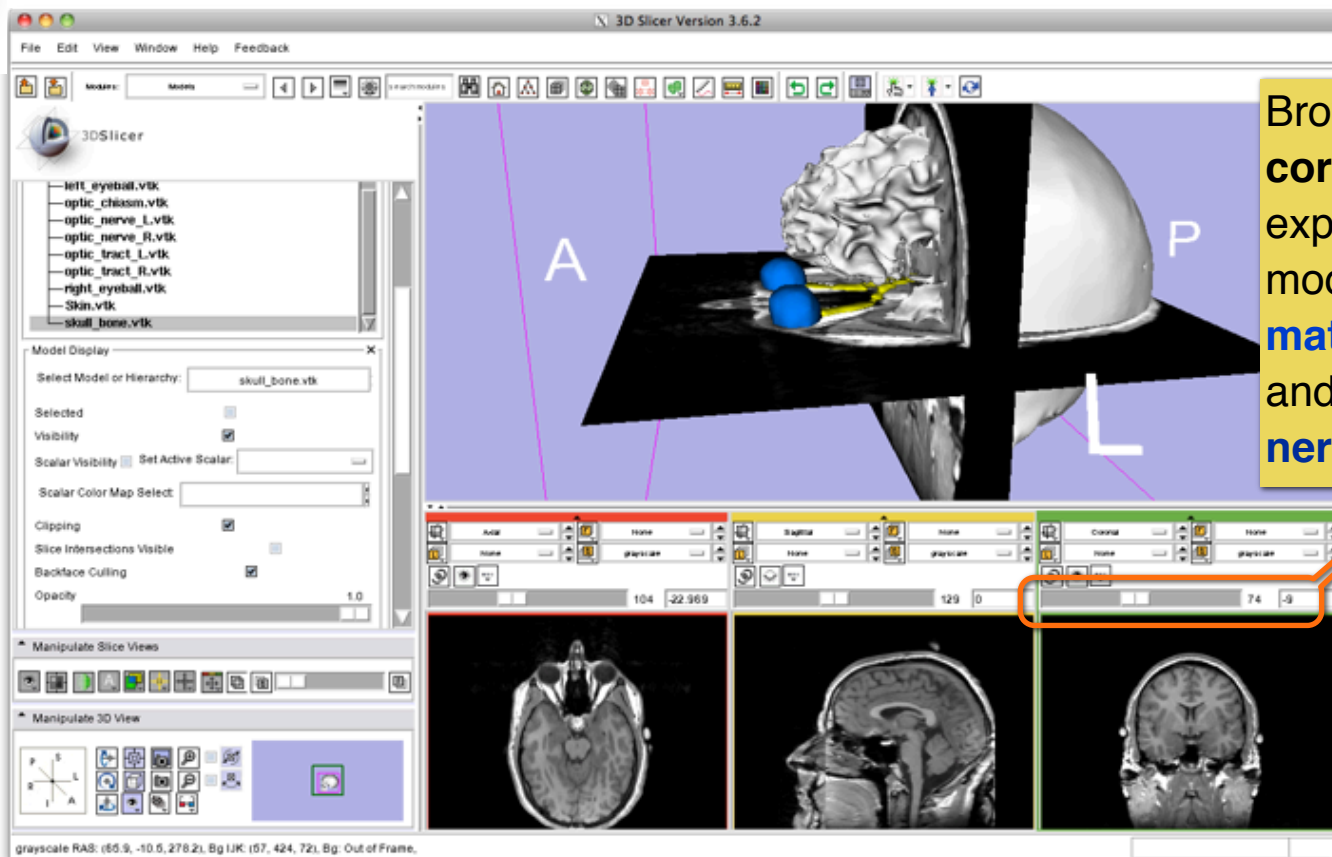
Slicer3 Minute Tutorial: 3D Visualization



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



Slicer3 Minute Tutorial: 3D Visualization

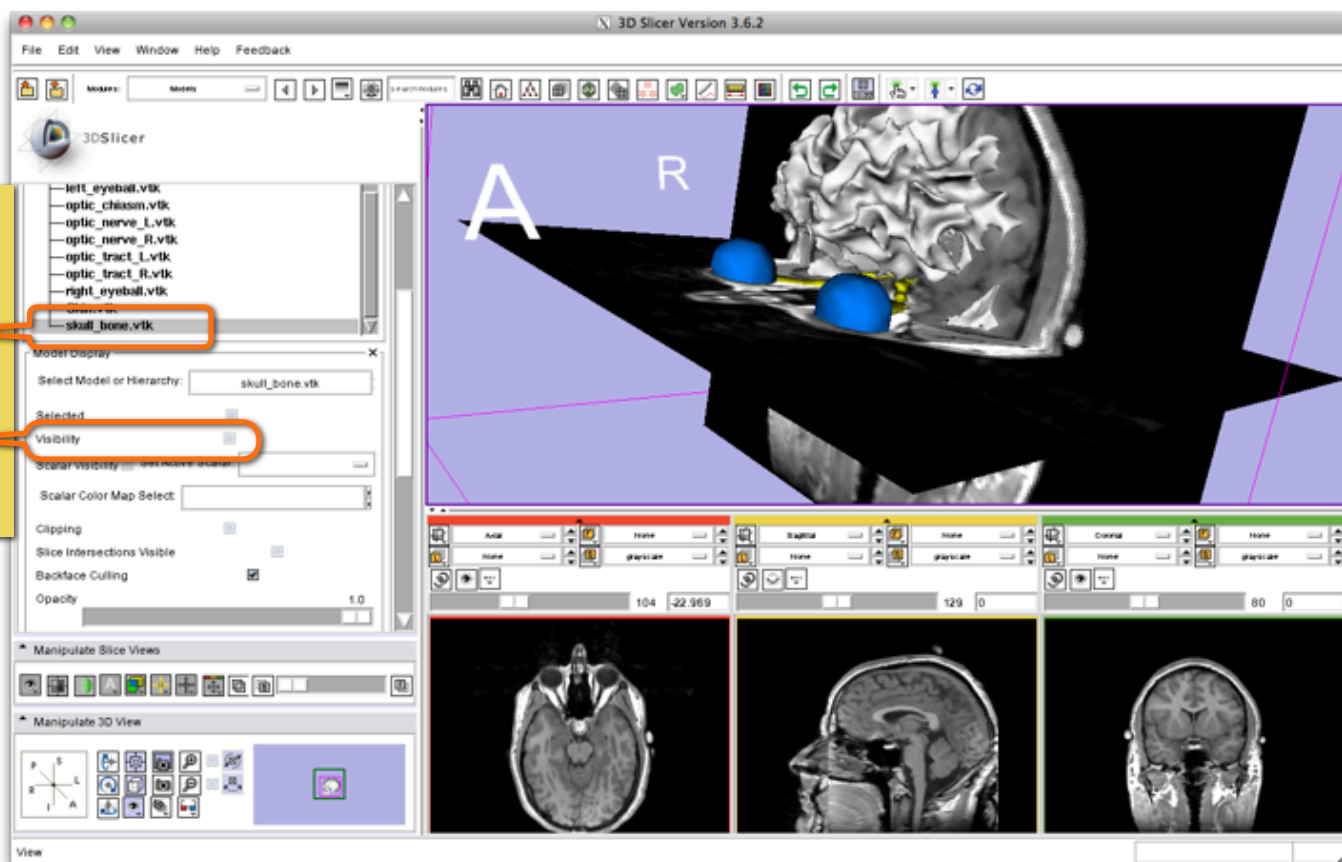


Browse through the **coronal slices** to expose the 3D model of the **white matter**, and the left and right **optic nerves**.



Slicer3 Minute Tutorial: 3D Visualization

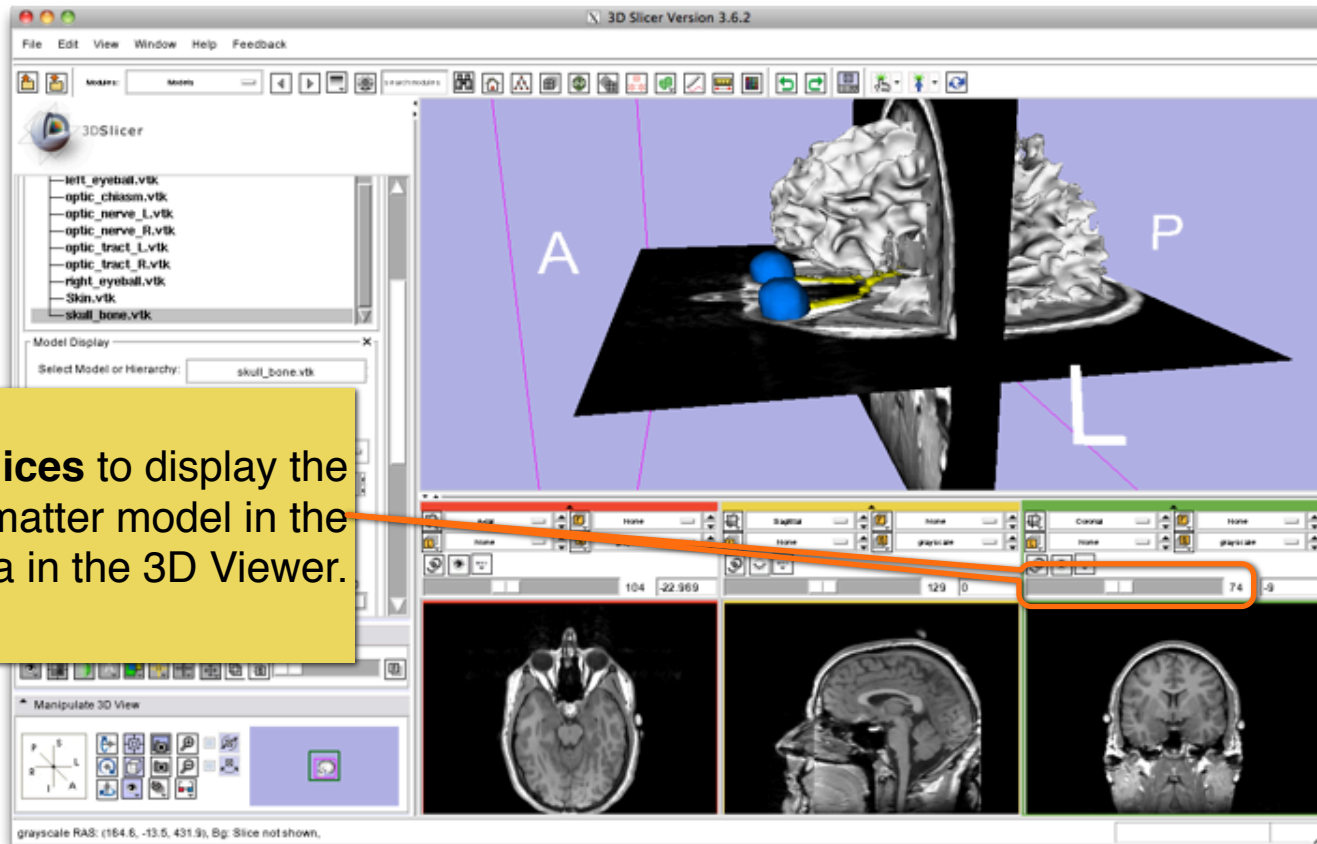
Select the 3D model
“skull_bone” in the
Model Hierarchy, and
turn off its Visibility





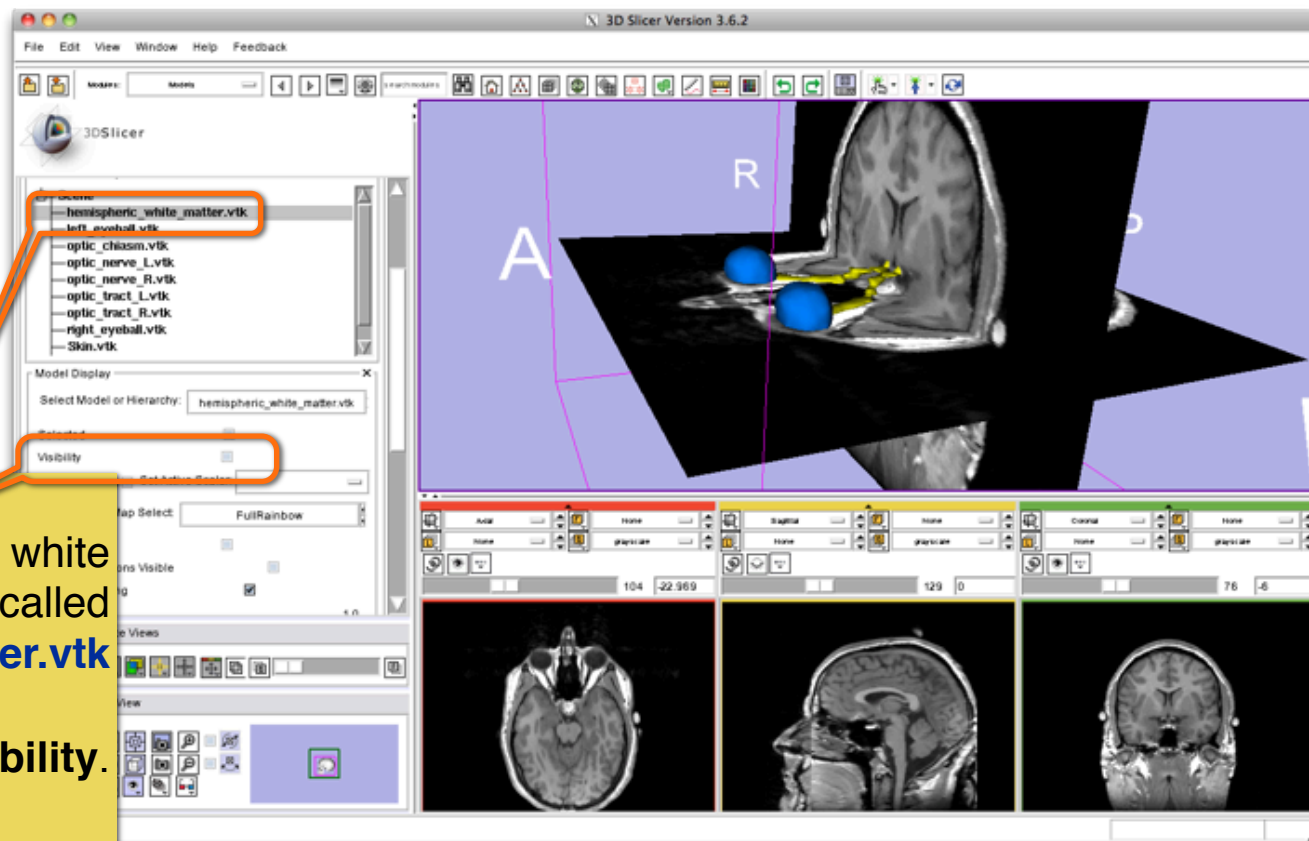
Slicer3 Minute Tutorial: 3D Visualization

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





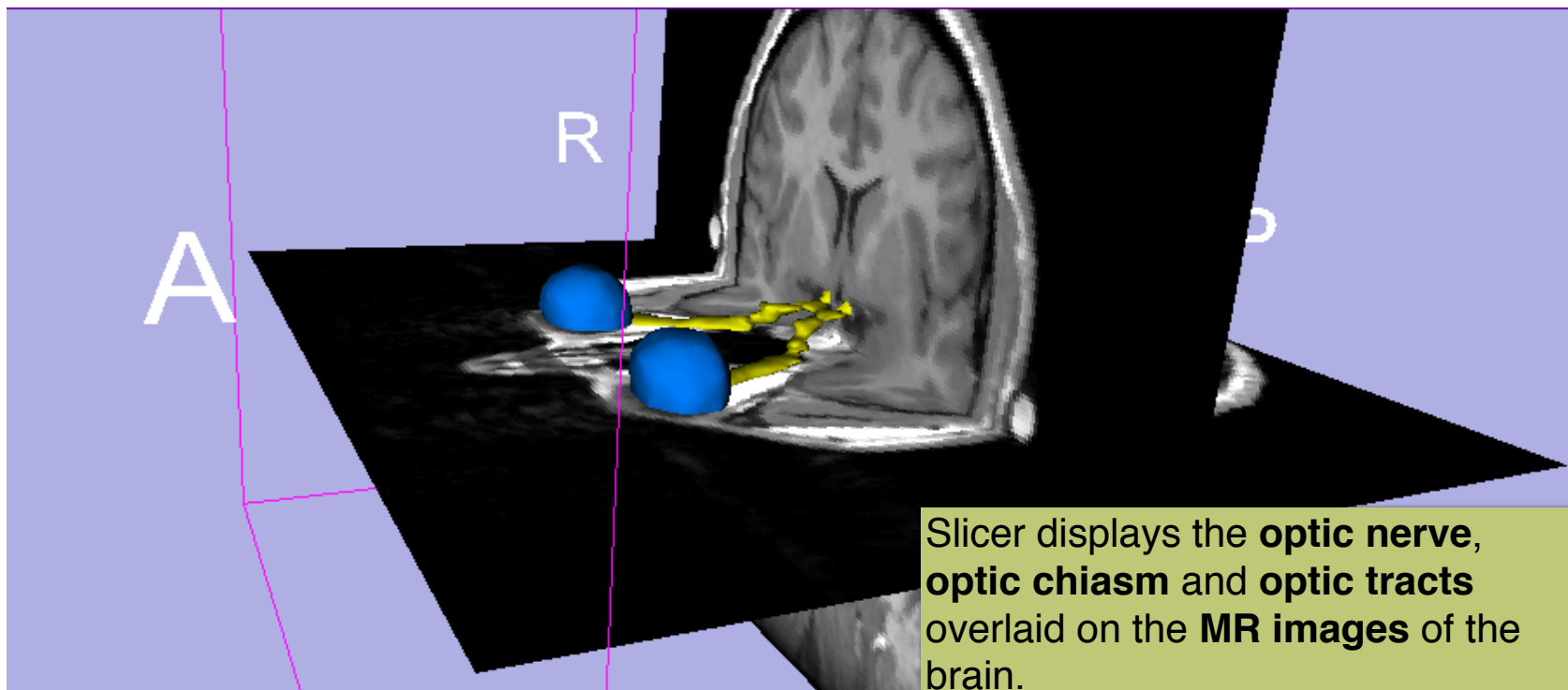
Slicer3 Minute Tutorial: 3D Visualization



Select the hemispheric white matter model called **hemispheric_white_matter.vtk**.
Turn off its **visibility**.



Slicer3 Minute Tutorial: 3D Visualization



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

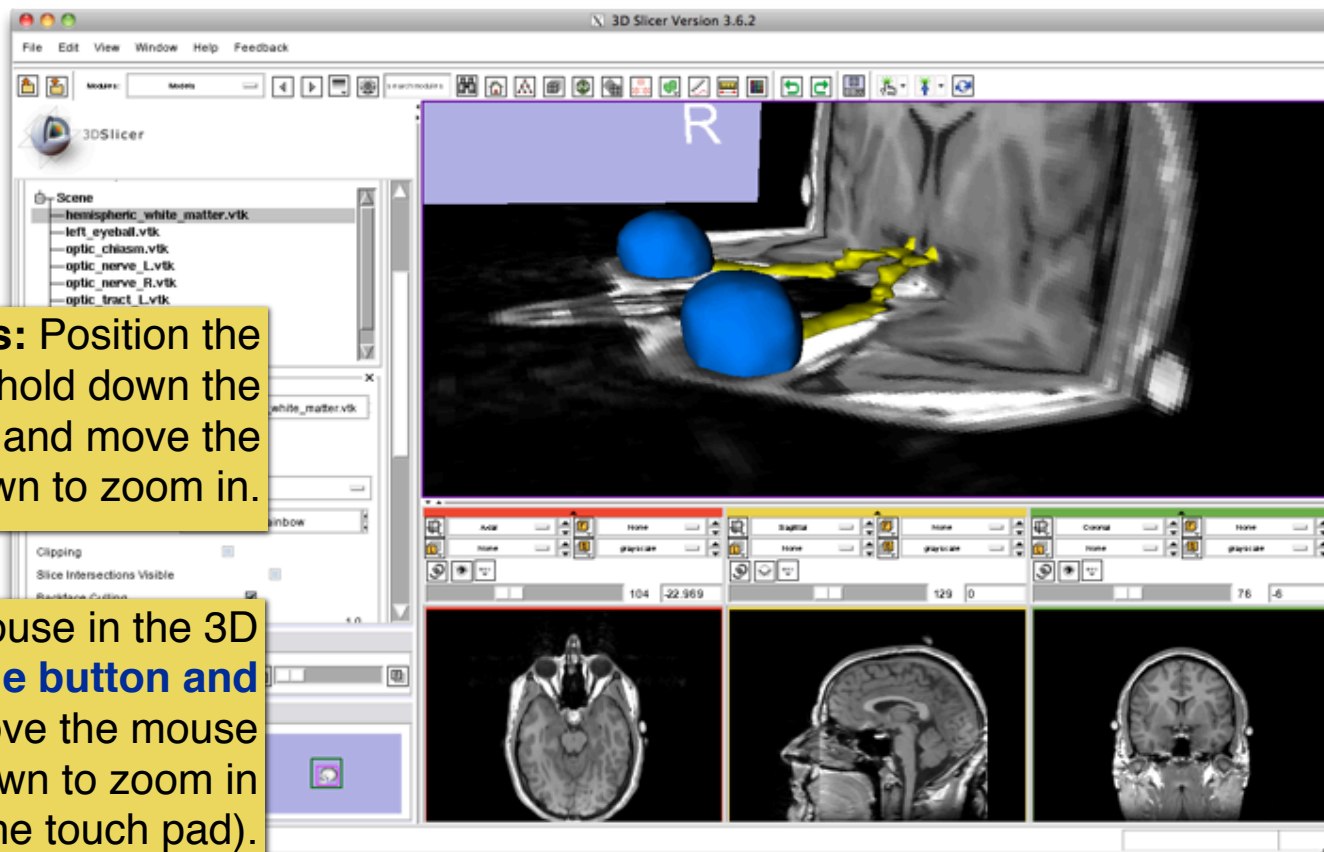


Slicer3 Minute Tutorial: 3D Visualization: Zoom the view

To Zoom:

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

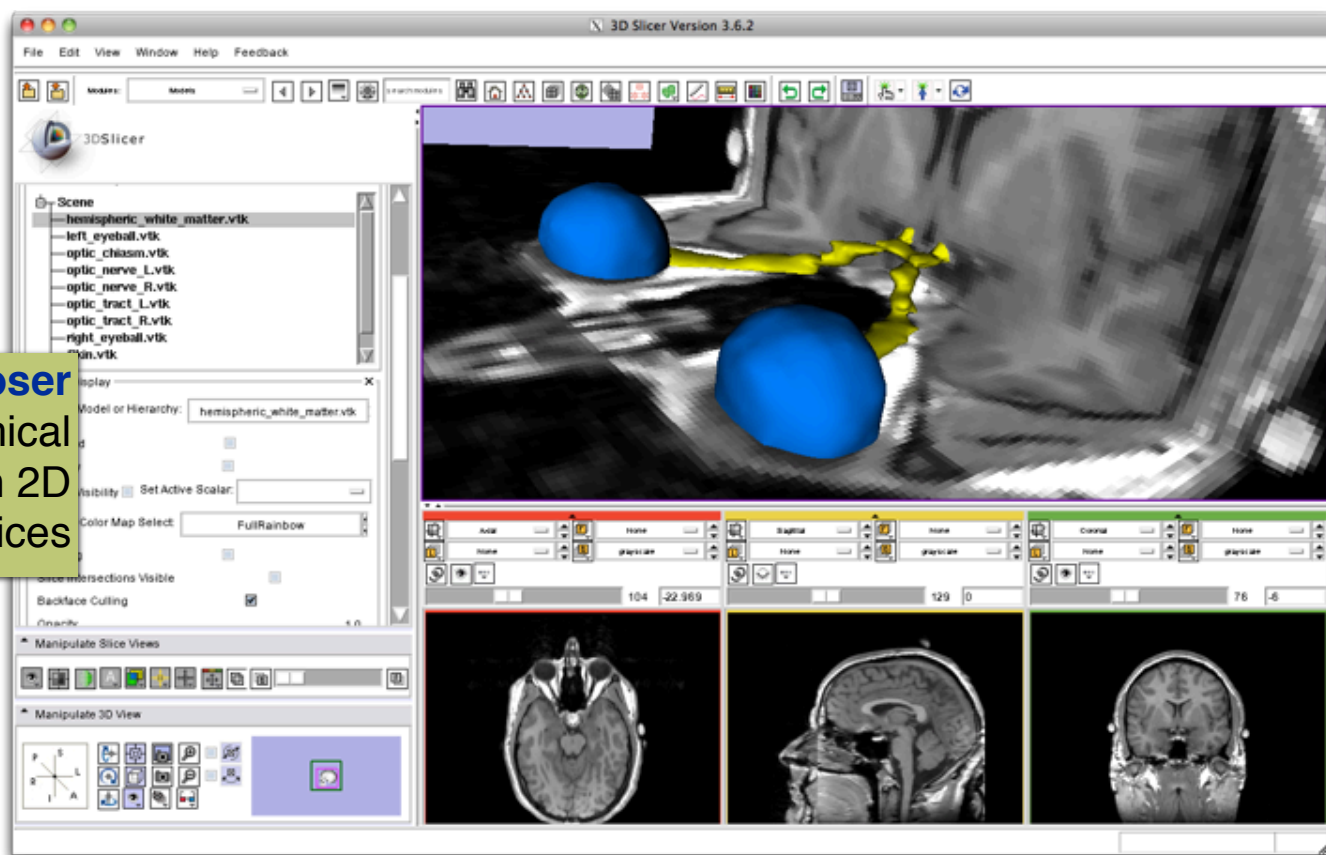
Mac users: Position the mouse in the 3D Viewer, hold down the **apple button and the mouse button** and move the mouse down to zoom in (or use two fingers on the touch pad).





Slicer3 Minute Tutorial: 3D Visualization

Slicer3 displays a **closer view** of 3D anatomical structures overlaid on 2D MR slices





Slicer3 Minute Tutorial: **Summary**

This tutorial has demonstrated:

- Basic description of the Slicer3 Application Interface
- How to load a scene containing volumes and models
- How to visualize these different datasets together

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

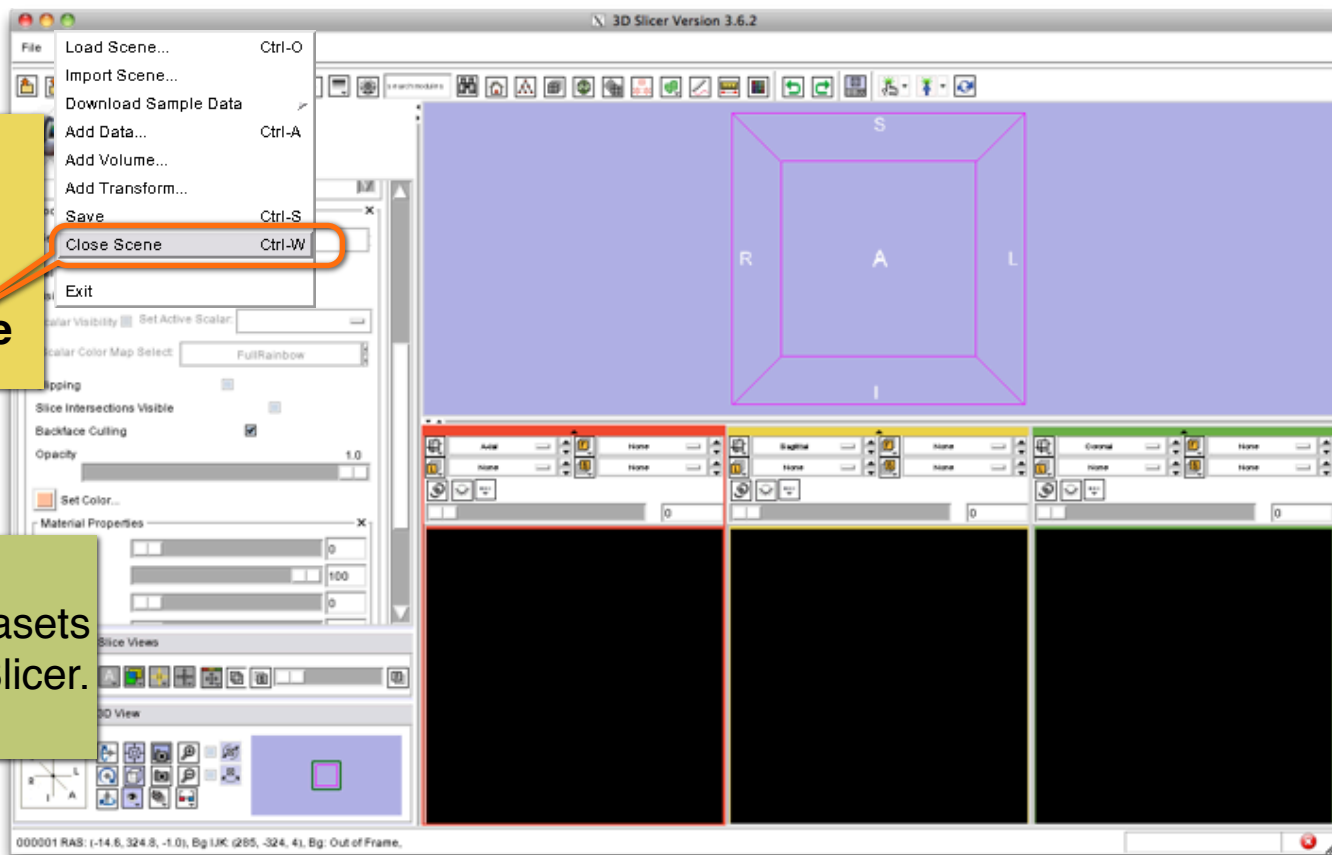


Close the existing scene and all its data

Clear the previous scene.

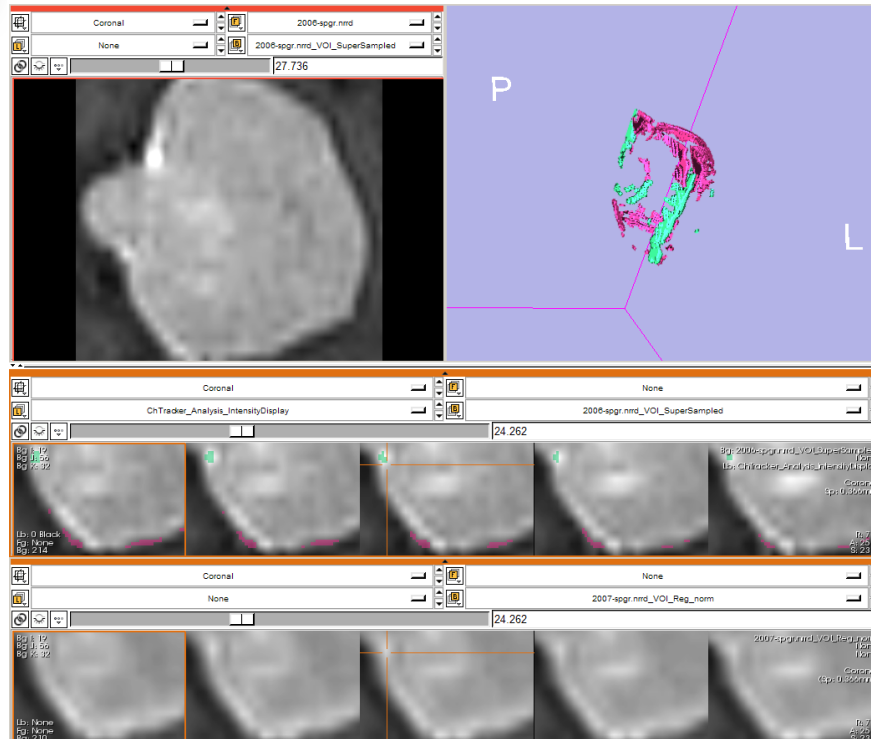
Select **File->Close Scene**

This removes any datasets previously loaded into Slicer.





ChangeTracker: exploring small volumetric changes



Part II: Analyzing Small Volumetric Changes using the ChangeTracker Module

Kilian M Pohl, PhD
Ender Konukoglu, PhD
Andriy Fedorov, PhD

The module described in this tutorial was tested on Axial 3D SPGR T1 post Gadolinium scans (Voxel dimension: 0.94mm x 0.94mm x 1.20mm, FOV: 240mm, Matrix: 256 x 256)



ChangeTracker: 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

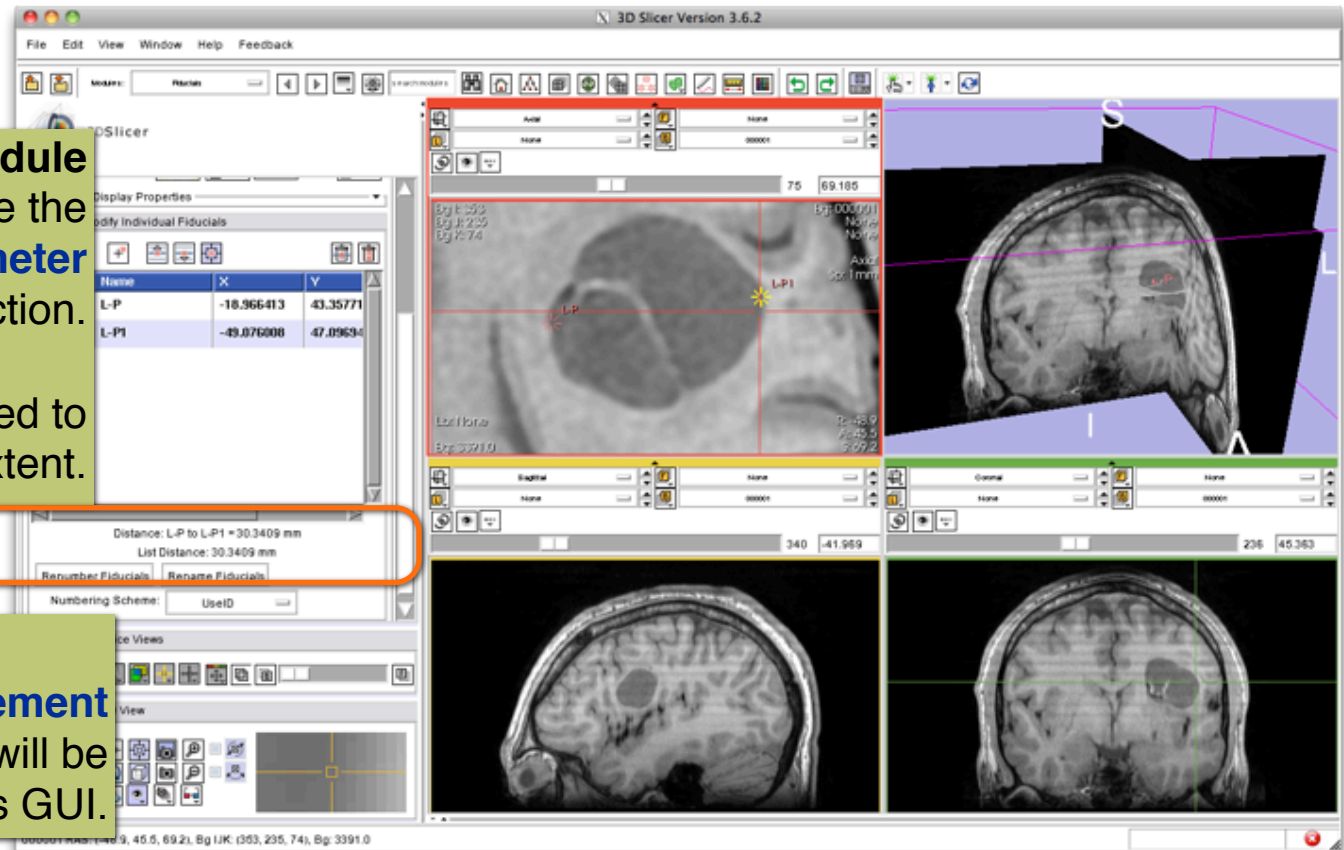


Quantifying tumor change: Conventional measures of tumor response

3D Slicer's **Fiducials Module** can be used to measure the **longest diameter** in a tumor cross section.

Two fiducials may be used to mark the tumor's extent.

The **distance measurement** (mm) between fiducials will be updated in the Fiducial's GUI.

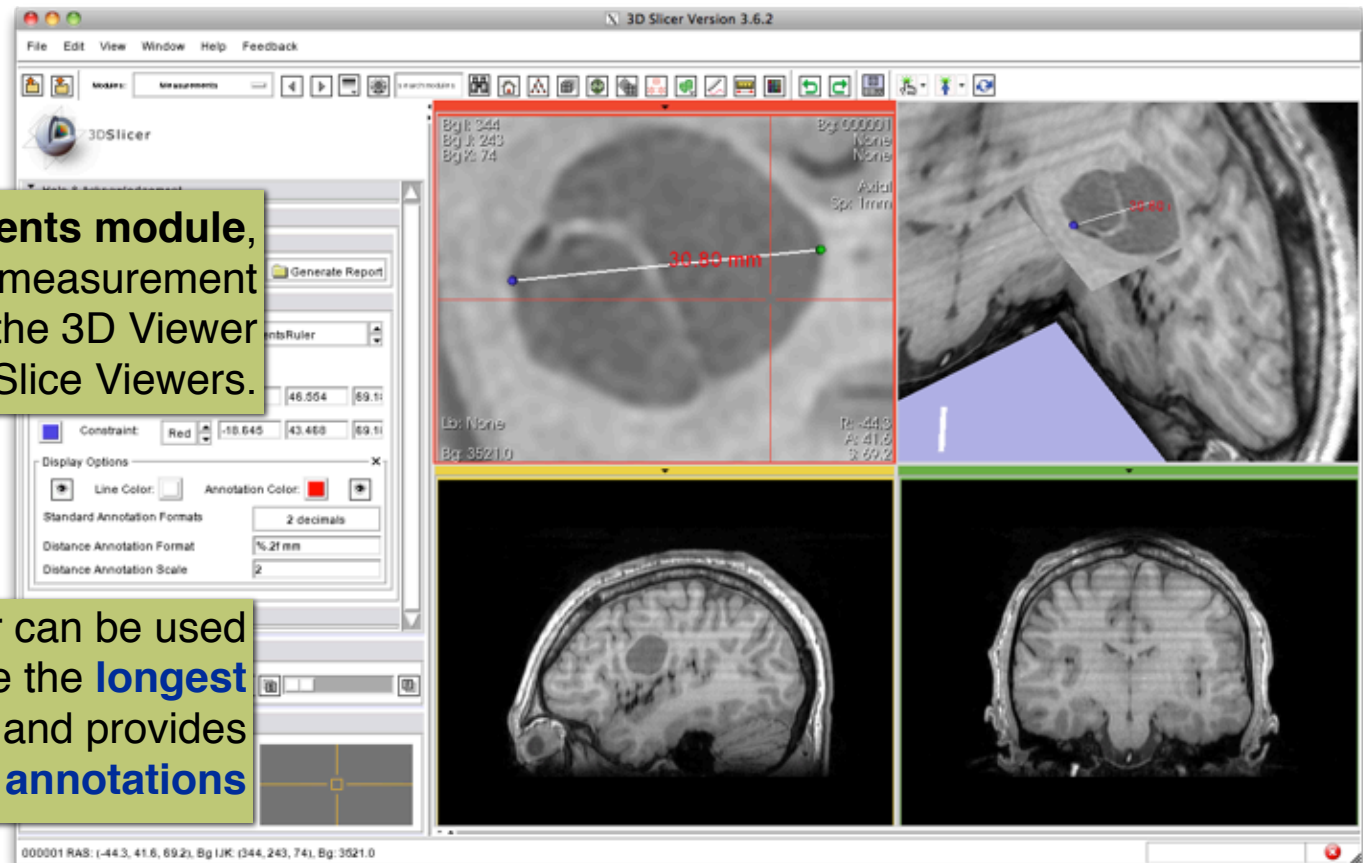




Quantifying tumor change: **Conventional measures of tumor response**

3D Slicer's **Measurements** module, provides interactive measurement tools that operate in the 3D Viewer and the Slice Viewers.

Interactive ruler can be used to measure the **longest diameter** and provides numerical **annotations**

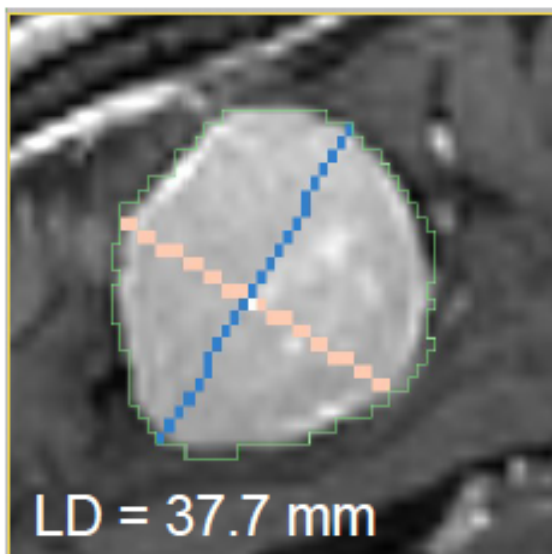




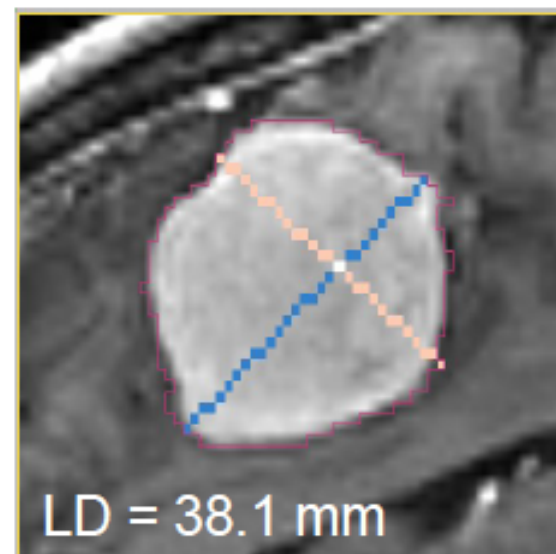
Quantifying tumor change: **Conventional measures of tumor response**

3D Slicer's **LabelDiameterEstimation (extension) module** will automatically compute the largest tumor diameter and **orthogonal** dimension.

This analysis requires an **initial segmentation (VOI)**.



Baseline: June 2006



Follow-up: June 2007



ChangeTracker: **rationale for new approaches**

- However, 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 Module** is a tool to measure **volumetric change at the voxel level.**



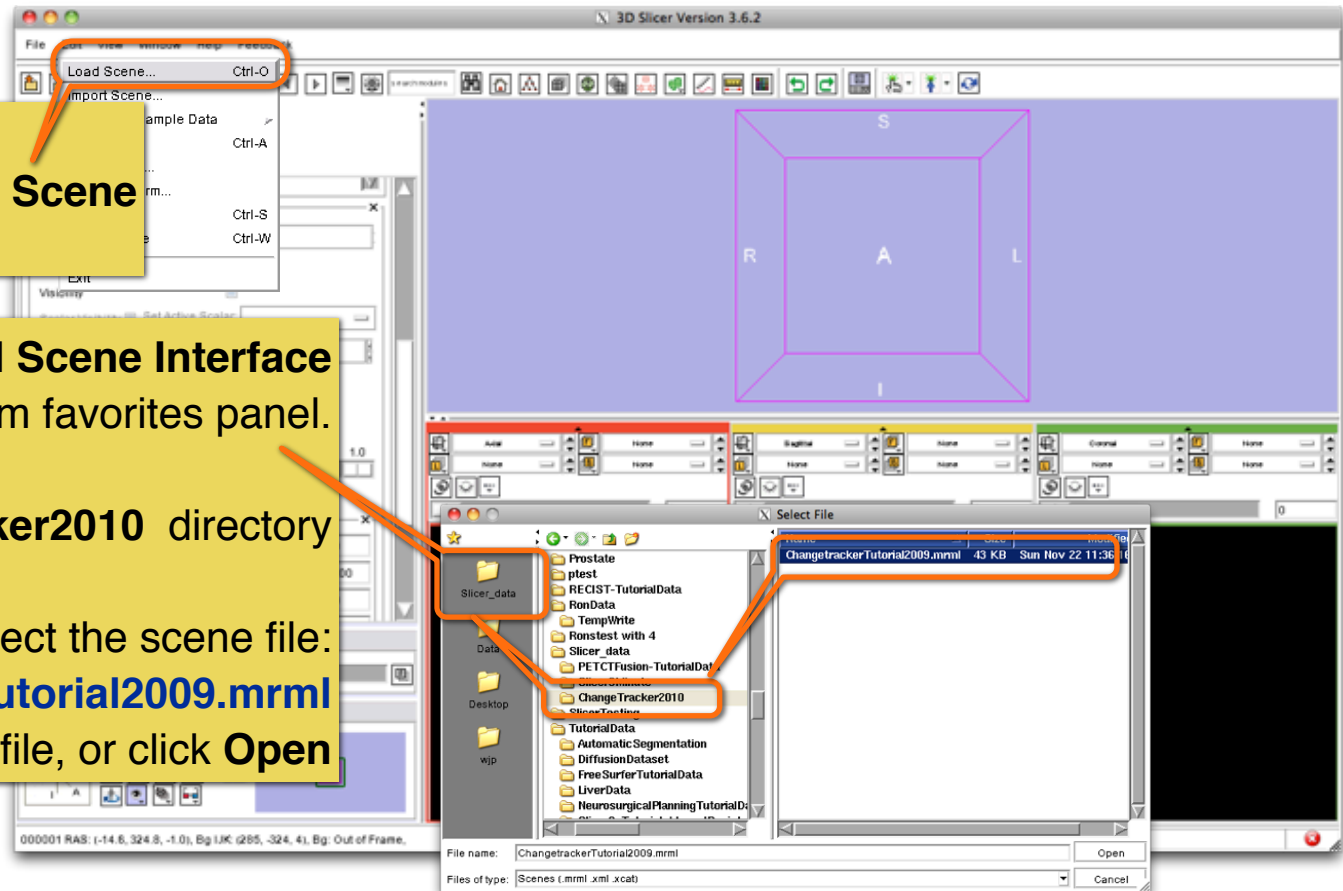
ChangeTracker: Load the training dataset

Select **File->Load Scene**

This raises the **Load Scene Interface**
Select **Slicer_data** from favorites panel.

Select the **ChangeTracker2010** directory

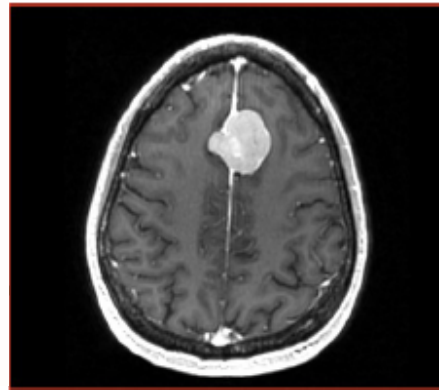
And select the scene file:
ChangetrackerTutorial2009.mrml
double click the file, or click **Open**



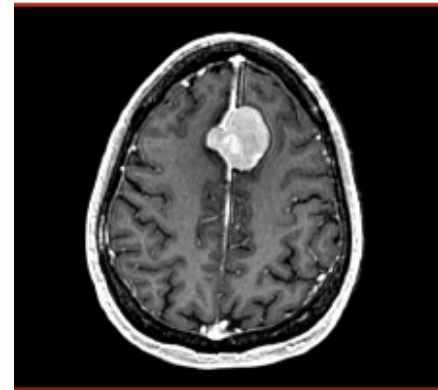


ChangeTracker: [about the data...](#)

This course is built upon two scans of a patient with meningioma:



MR Scan 1



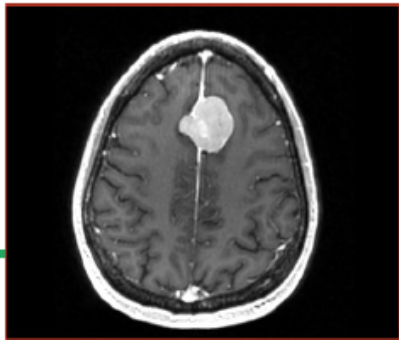
MR Scan 2

Please note: we have **pre-adjusted the window and level settings** for these volumes so that they are appropriate for display on most laptops. If display is not satisfactory on your machine or projector, the Volumes Module may be used to refine these settings.

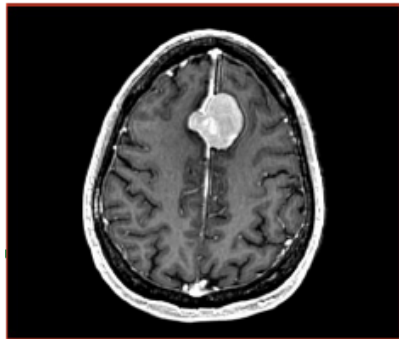


ChangeTracker: Clinical context

SCAN1
Baseline:
June 2006



SCAN2
Follow-up:
June 2007



Meningioma

- Usually benign slow-growing tumors

Baseline radiologist's clinical impression:

- large falcine lesion is identified.
- measures 3.1 cm anteroposteriorly, 3.05 cm from side-to-side, 3.5 cm in height.
- enhances moderately on post gadolinium imaging.

Follow-up radiologist's clinical impression:

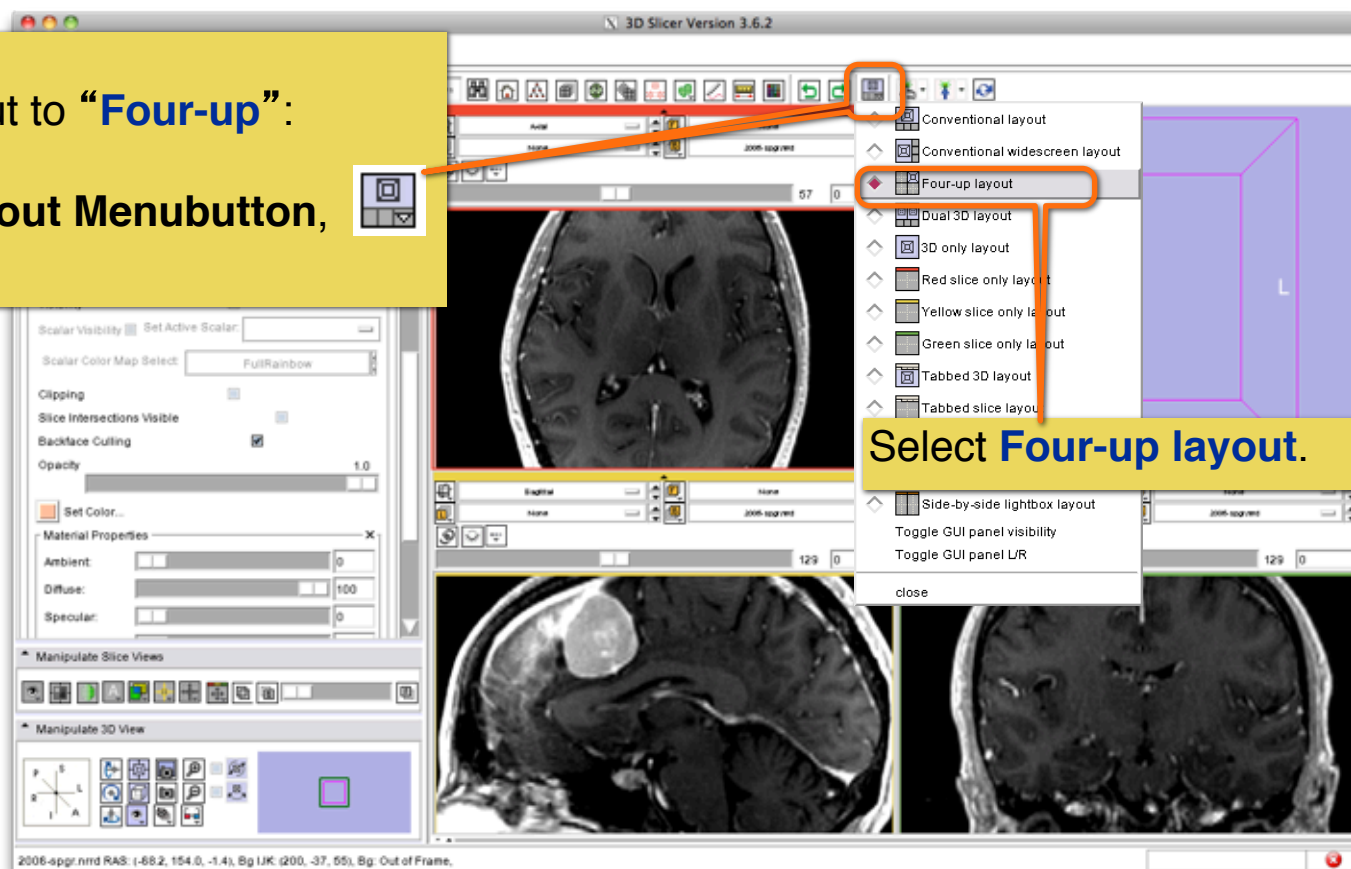
- left frontal lobe mass appears unchanged on all series.
- measures 3.3 x 3.2 cm in maximum dimension.
- enhances moderately on post gadolinium imaging.

How has the tumor changed?



ChangeTracker: exploring small volumetric changes

Change Layout to **“Four-up”**:
Using the **Layout Menubutton**,

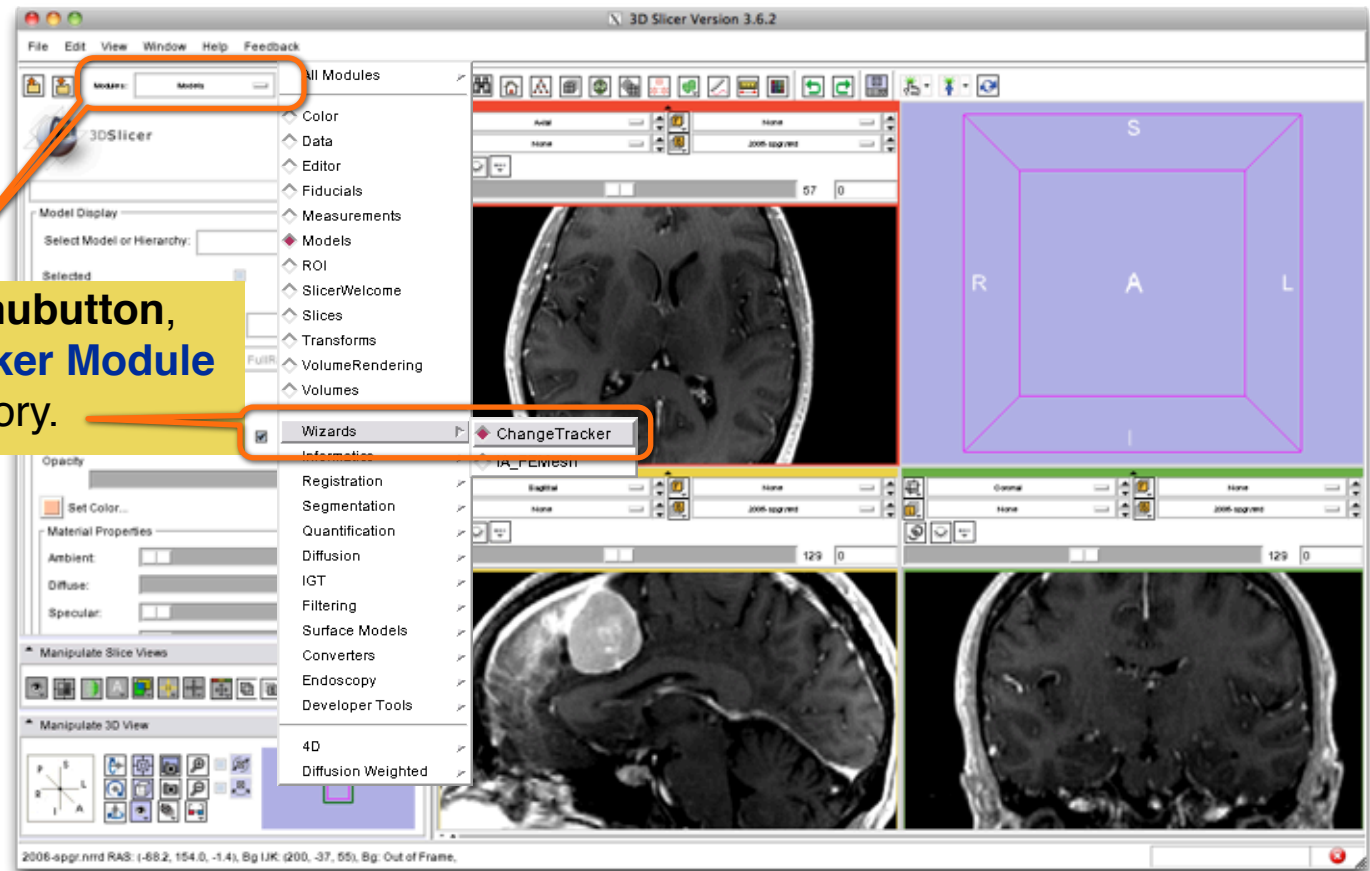


Select **Four-up layout.**



ChangeTracker: exploring small volumetric changes

Using the **Modules** Menubutton, Select the **ChangeTracker Module** from the **Wizards** category.





ChangeTracker: a note about the Workflow Wizard

A **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--

The screenshot shows a software interface with a sidebar on the left containing a tree view with 'Help & Acknowledgement' and 'Wizard'. The 'Wizard' section is expanded to show '1/4. Define Scans' with the instruction 'Select first and second scan of patient'. The main area is divided into three panels: the Step Panel (top, light blue), the User Panel (middle, white), and the Navigation Panel (bottom, white). The User Panel contains a 'Select Scan' section with two rows: '1. Scan' and '2. Scan', each with a dropdown menu currently set to 'None' and a small navigation icon. The Navigation Panel contains a 'Next >' button.



ChangeTracker: First step: select scans

3DSlicer

3D Slicer Version 3.6.2

File Edit View Window Help Feedback

ChangeTracker

Wizard

1/4. Define Scans

Select first and second scan of patient

Select Scan

1. Scan 2006-spgr.nrd

2. Scan 2007-spgr.nrd

Next >

Manipulate Slice Views

Manipulate 3D View

2006-spgr.nrd RAS: (98.8, -1.9, 131.3); Bg: Slice not shown.

S

Select baseline & follow-up studies:

Scan 1 = 2006-spgr

Scan 2 = 2007-spgr

Sagittal

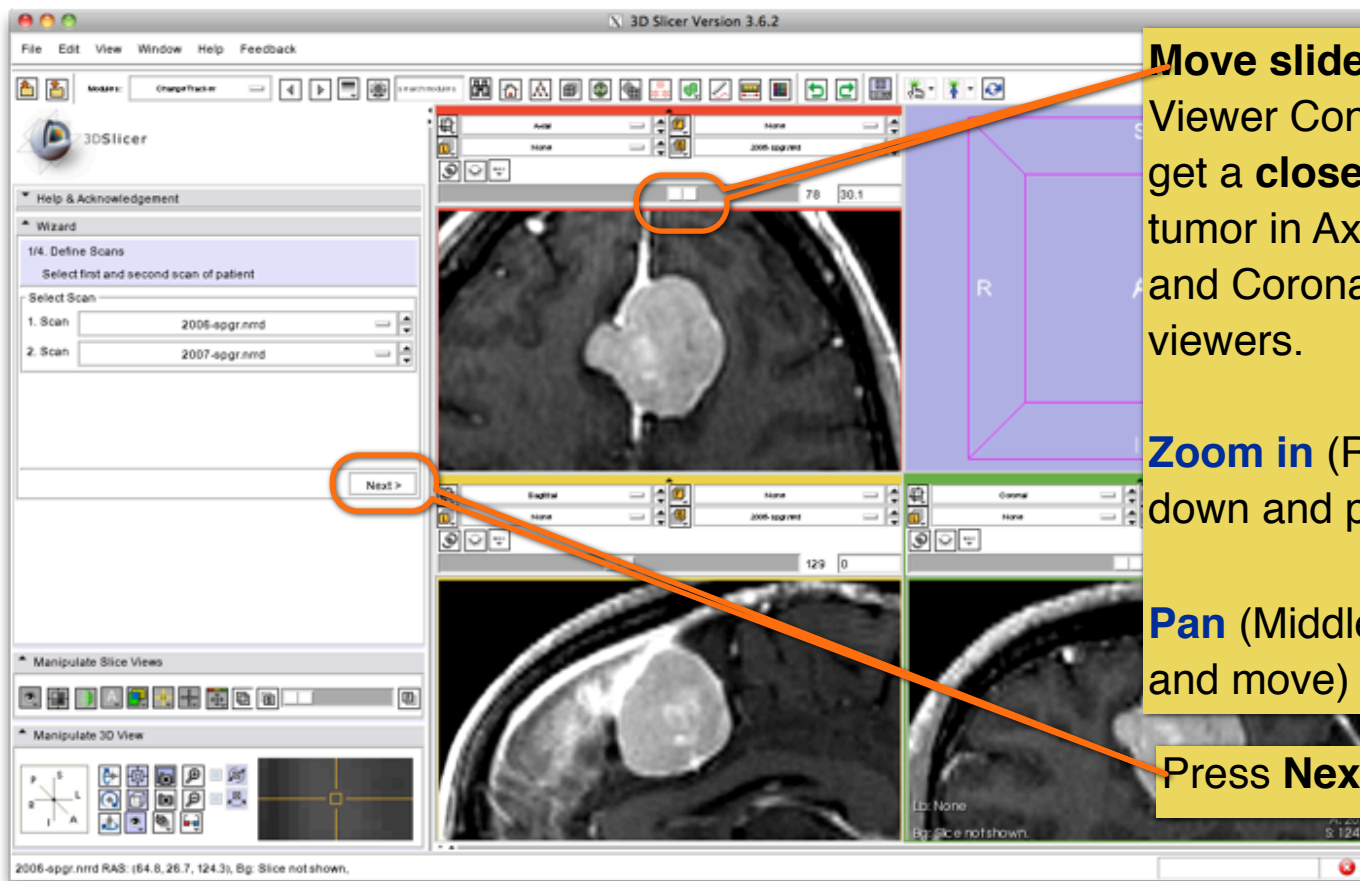
Coronal

Bg: 2006-spgr.nrd
None
None
Coronal
Sc: 0.25mm

Lr: None
Rr: 98.8
Ap: -1.9
Bt: Slice not shown
P: 131.3



ChangeTracker: inspect the tumor



Move sliders in Slice Viewer Control panels to get a **close-up view** of tumor in Axial, Sagittal and Coronal slice viewers.

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

Pan (Middle mouse down and move)

Press Next

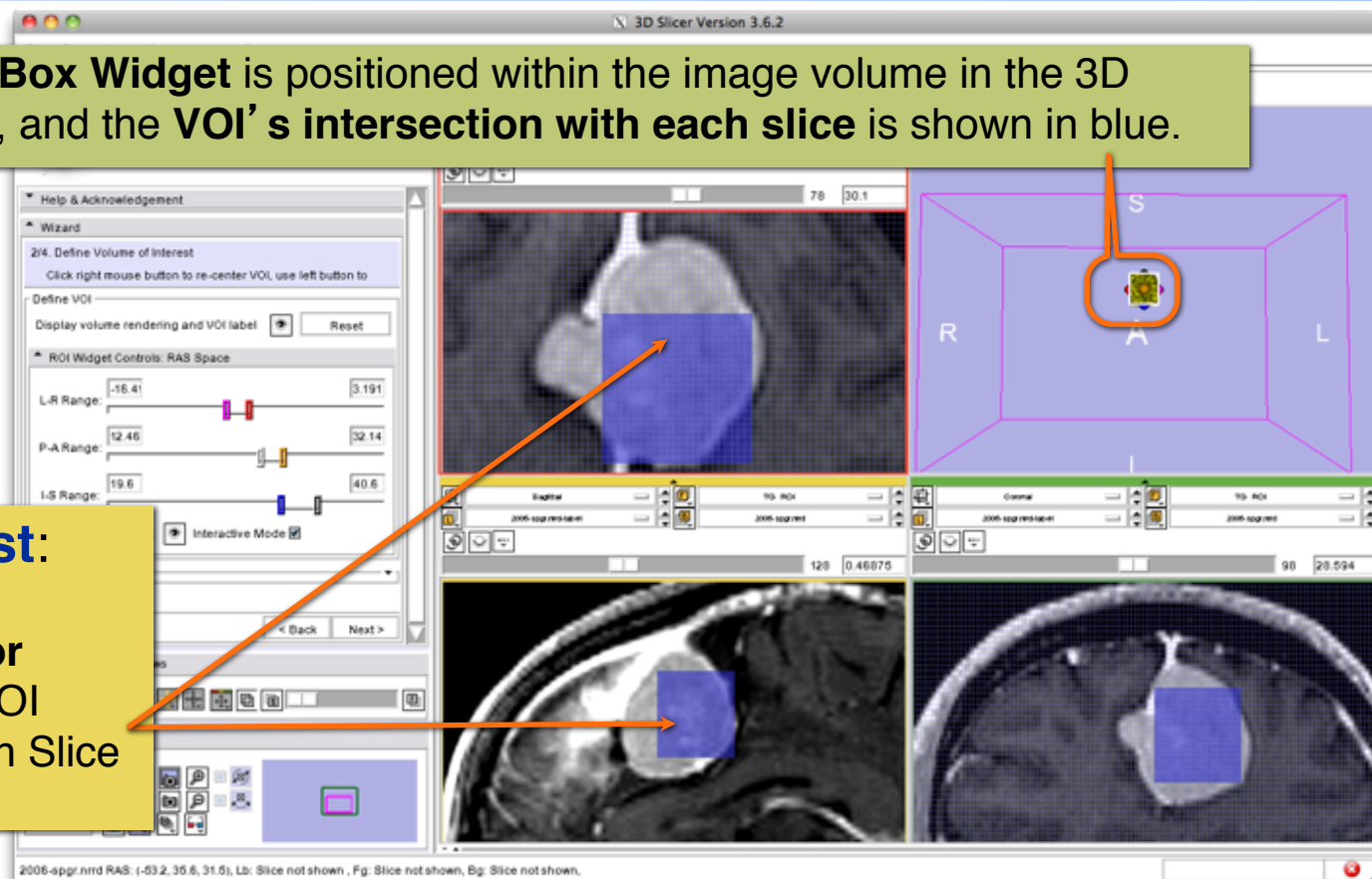


ChangeTracker: Step 2. Define a volume of interest

A **VOI Box Widget** is positioned within the image volume in the 3D viewer, and the **VOI's intersection with each slice** is shown in blue.

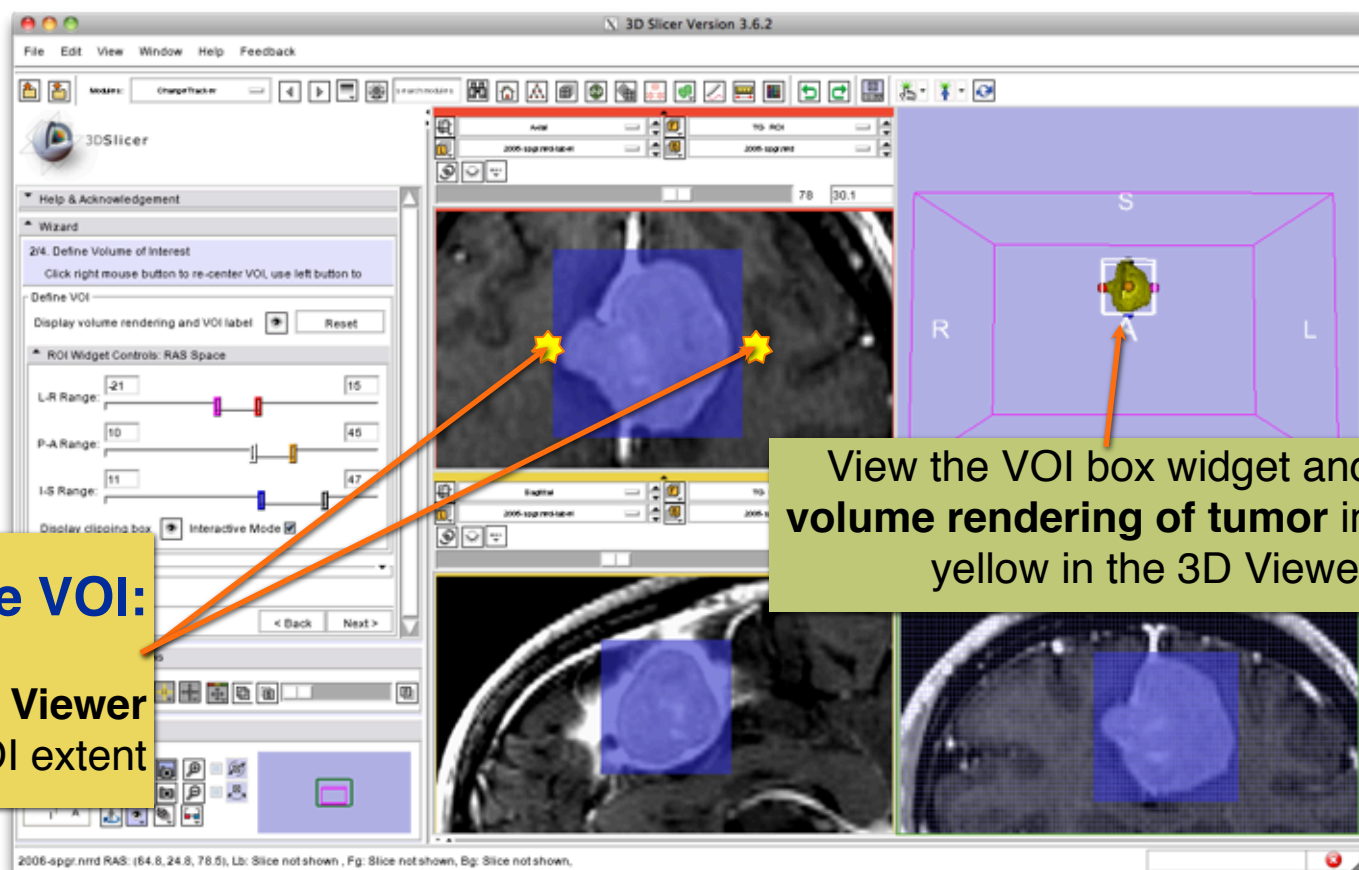
Center the VOI first:

Right click in the tumor center to position the VOI displayed in blue in each Slice Viewer.





ChangeTracker: Step 2. Define a volume of interest



Next, resize the VOI:
Left click in any Slice Viewer to change the VOI extent

View the VOI box widget and volume rendering of tumor in yellow in the 3D Viewer



ChangeTracker: Step 2. Define a volume of interest

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

Wizard

2/4. Define Volume of Interest

Click right mouse button to re-center VOI, use left button to

Define VOI

Display volume rendering and VOI label Reset

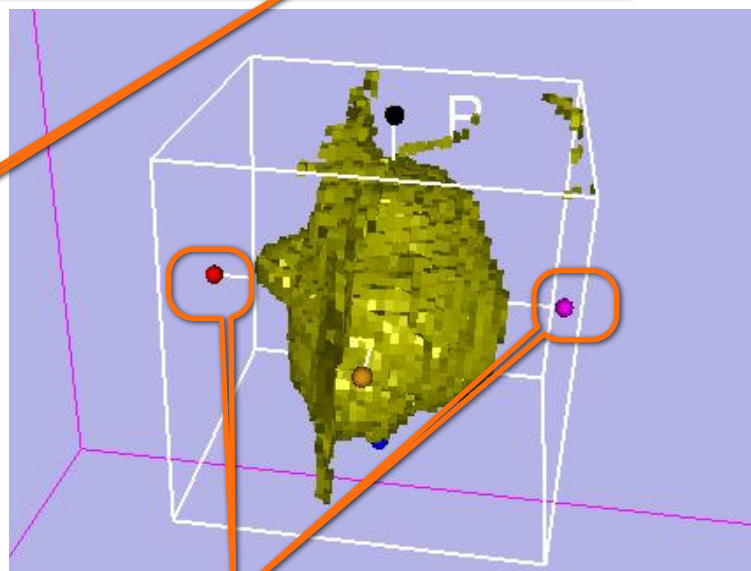
ROI Widget Controls: RAS Space

L-R Range:

P-A Range:

I-S Range:

Display clipping box Interactive Mode



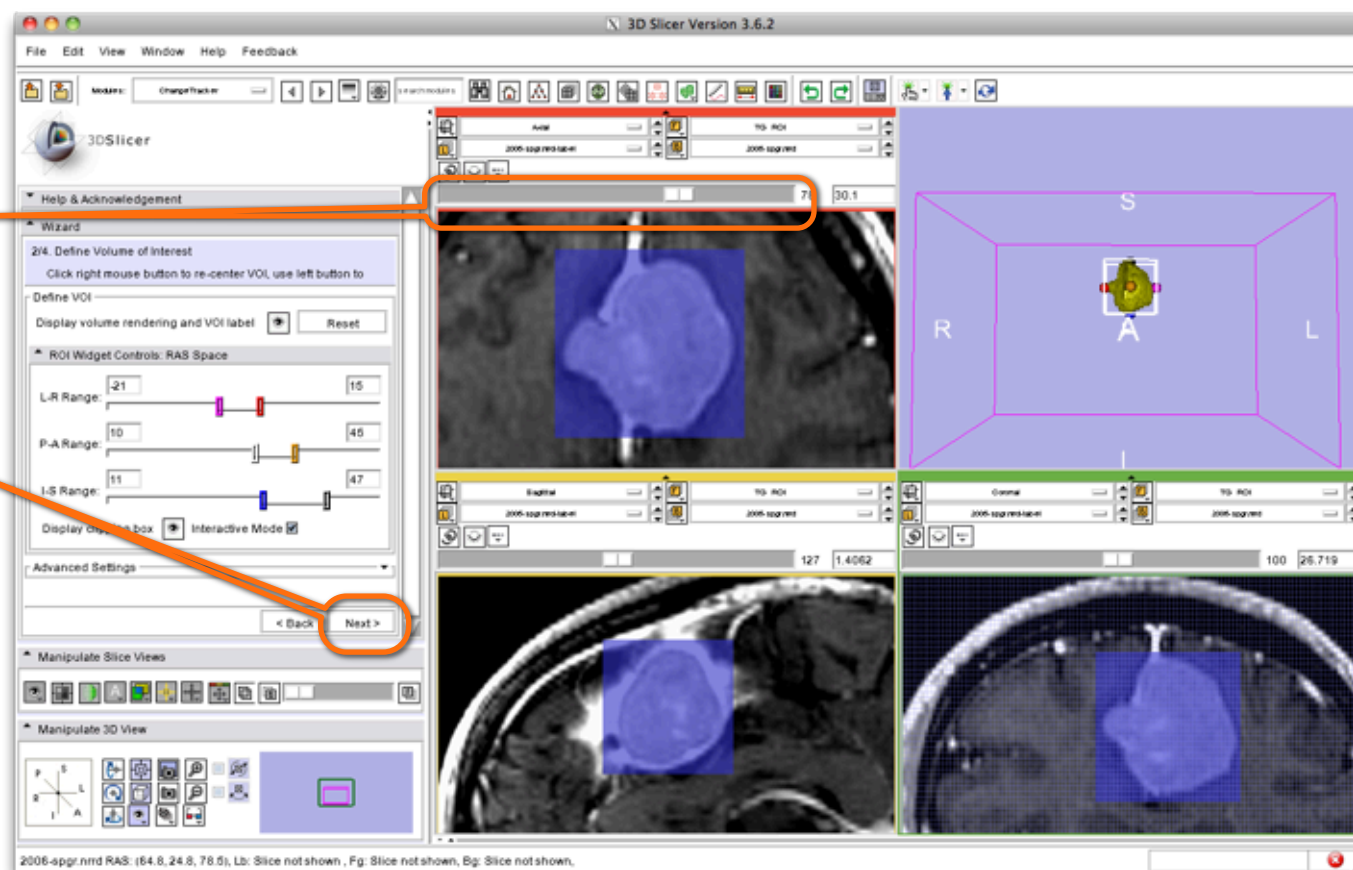
Note: VOI Widget range sliders are **color-coded** to match VOI box Widget handles in 3D Viewer



ChangeTracker: Step 2. Define a volume of interest

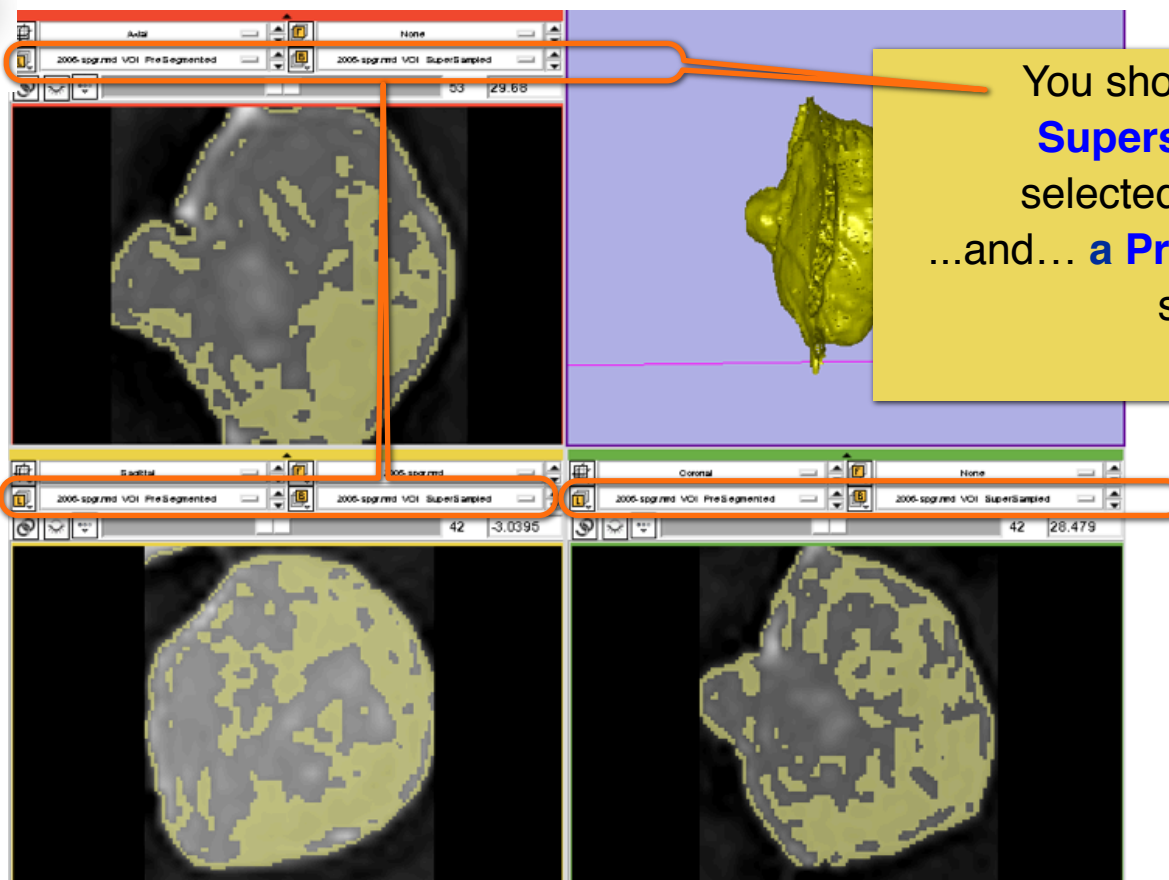
Scroll through slices
to ensure that tumor
boundaries are included
in the VOI.

Click Next





ChangeTracker: Step 3. Segment the tumor



You should see a volume called a **Supersampled VOI from scan1** selected in the **background** layer ...and... a **PreSegmented label map** selected in the **label** layer.



ChangeTracker: Step 3. Segment the tumor

The screenshot displays the 3D Slicer Version 3.6.2 interface. The 'ChangeTracker' wizard is active, showing step 3/4: 'Identify Tumor in First Scan'. The 'Identify Tumor' section has a 'Threshold' range slider set from 105 to 232, which is highlighted with an orange circle. The '3D Viewer' shows a 3D model of the segmented tumor in light yellow. The 'Slice Viewers' show axial, sagittal, and coronal slices with the segmentation overlay in light yellow. The 'Advanced Settings' section is expanded, and the 'Manipulate 3D View' section is visible at the bottom.

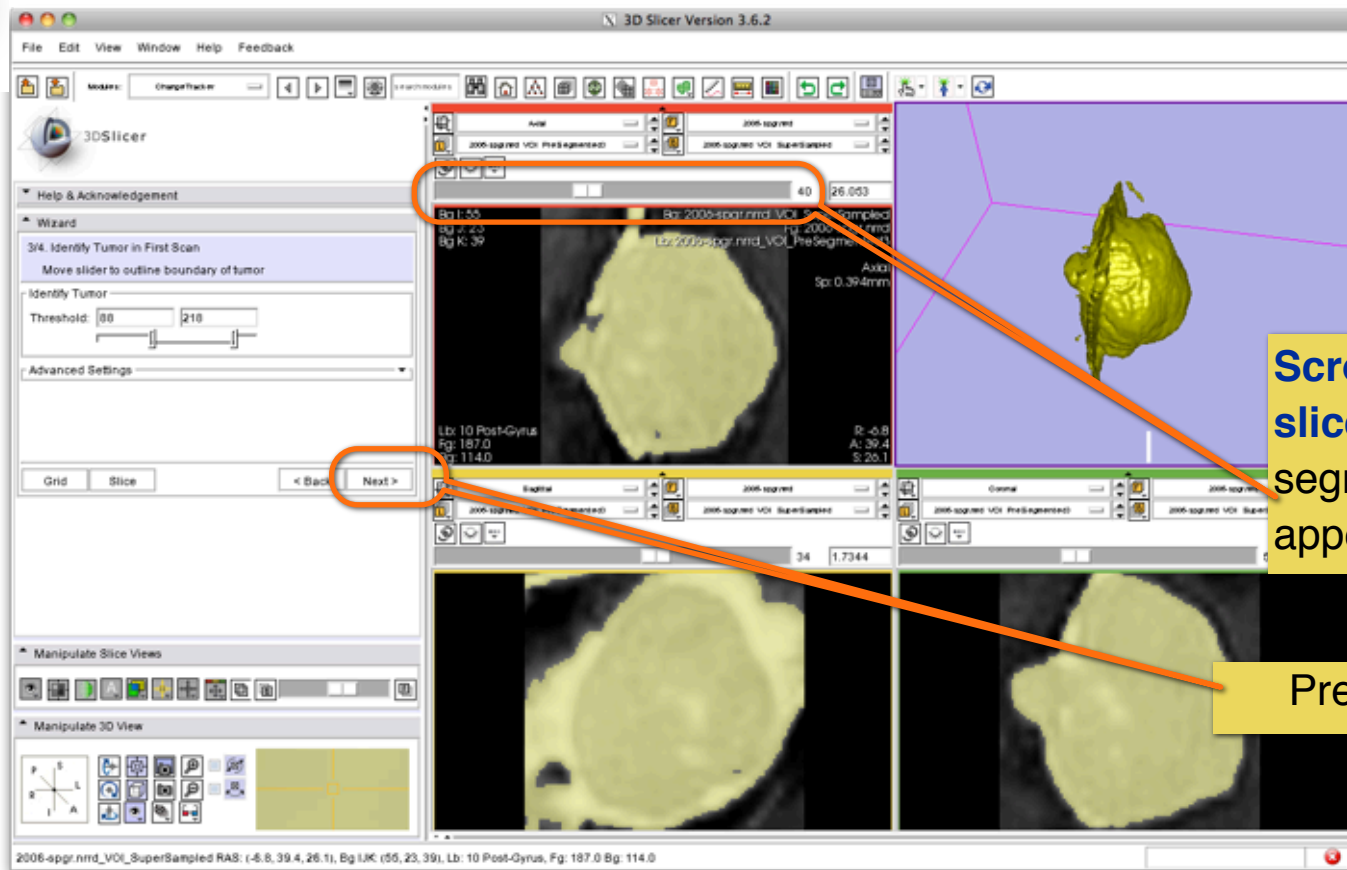
3D Viewer shows model of tumor

Slice Viewers show VOI with current segmentation overlay in light yellow

Modify the segmentation by moving threshold range slider



ChangeTracker: Step 3. Segment the tumor



Scroll through the slices until the segmentation appears optimal.

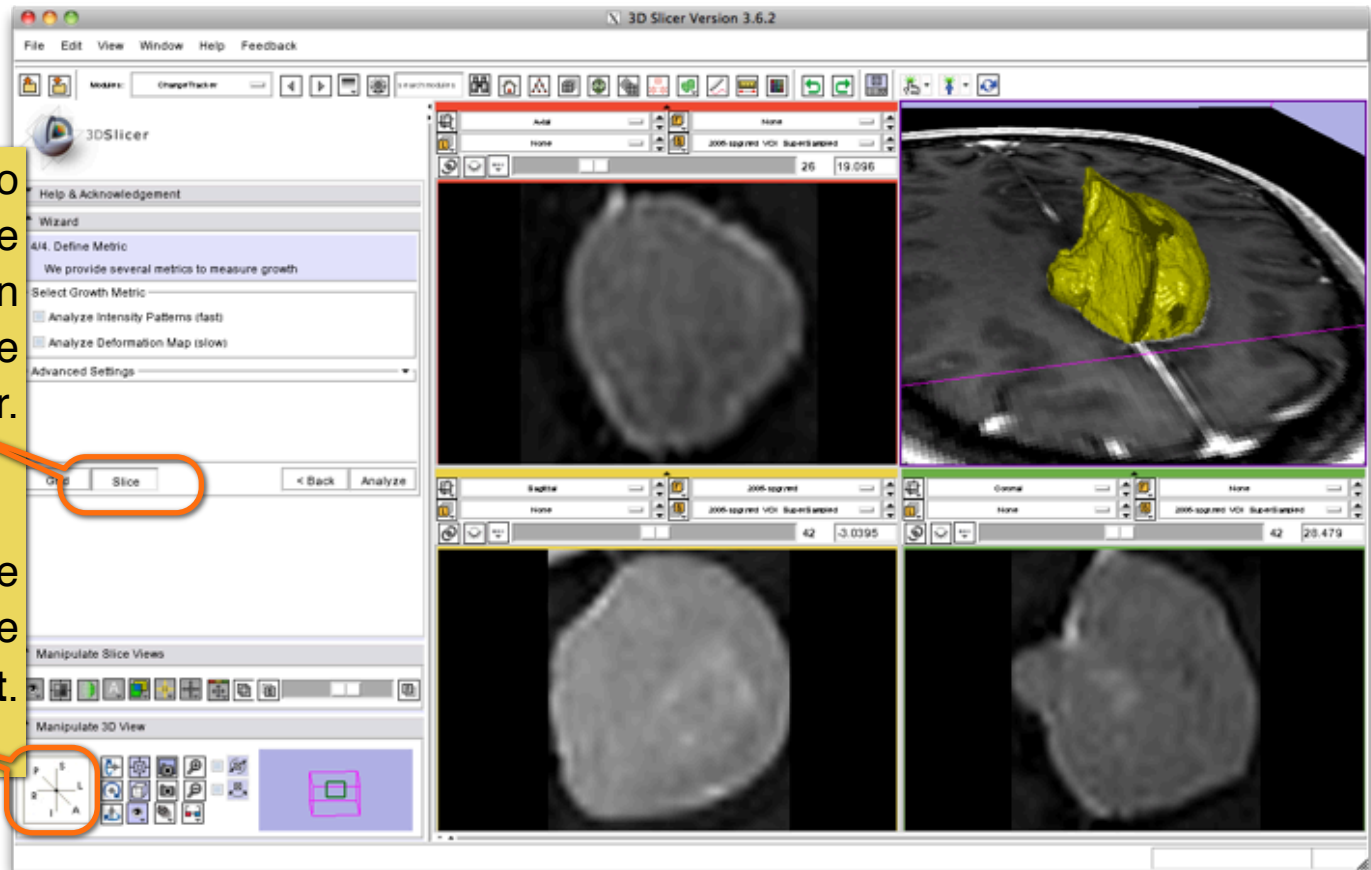
Press Next.



ChangeTracker: Final step: Select Metric for change detection

Press the **Slice** option to view the volume rendered segmentation with the axial slice together.

If you need to reset the 3D View, try using the **Axis Navigator Widget**.



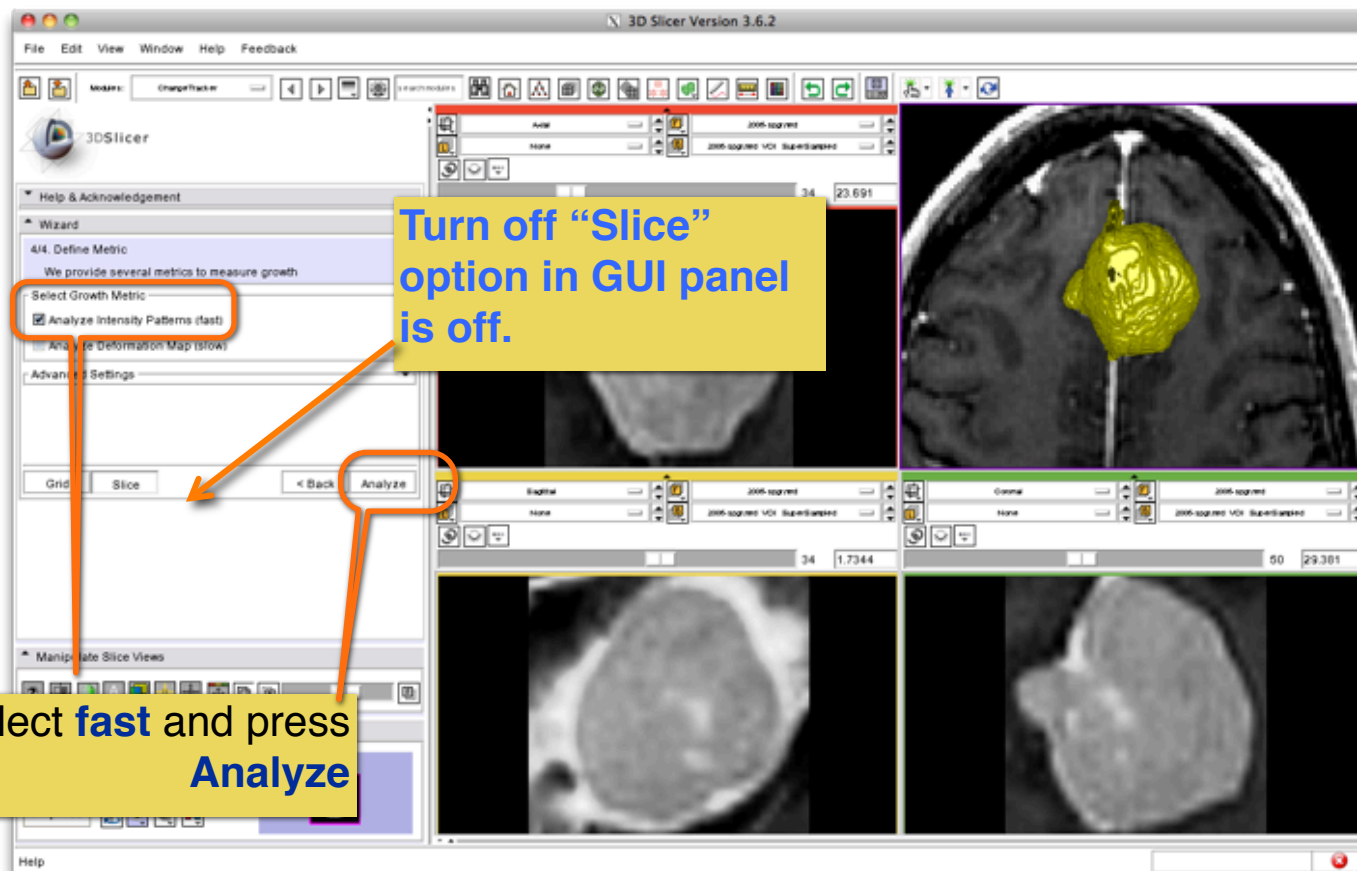


ChangeTracker: Final step: Select Metric

Metric Options:

Detect change by analyzing **intensity pattern (fast)**

Measure change by analyzing **deformation map (slow)**

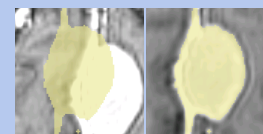




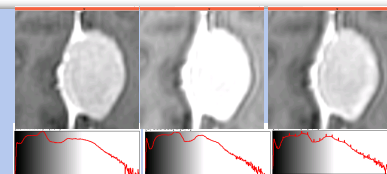
ChangeTracker: Algorithm details

Konukoglu *et al.* ,“Monitoring Slowly Evolving Tumors”, ISBI, 2008

Register Scan1 & Scan2 (baseline and follow-up)
(**preserve volume**)



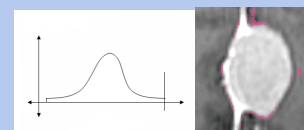
Normalize intensities



Using **segmentation** and **difference image**, compute **probability density function** of dormant tissue



Set **threshold** for voxel-wise analysis

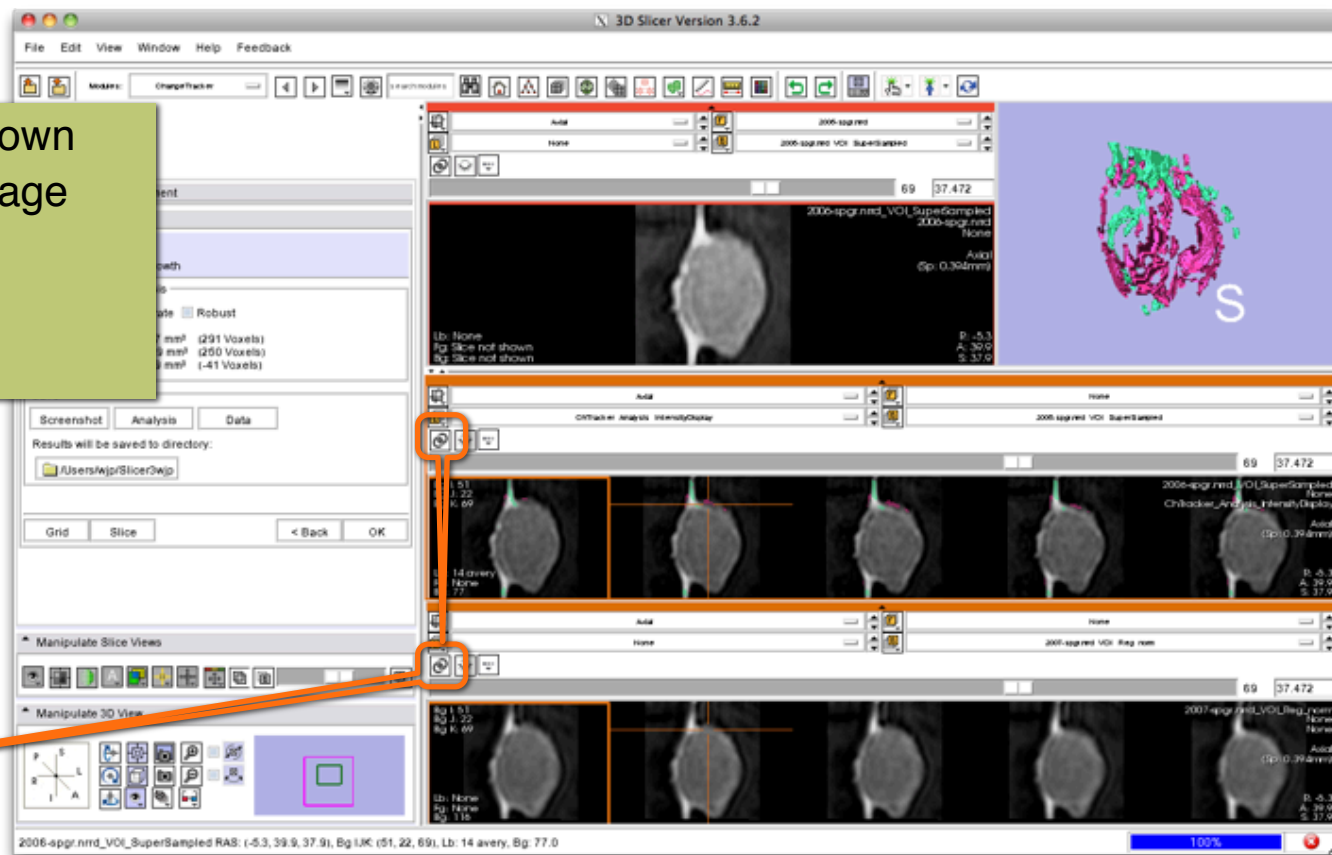




ChangeTracker: Results: change in pathology

Change in volume is shown overlaying the tumor image and in the 3D Viewer:
magenta = growth
green = shrinkage

Note: Analysis is displayed in the “Compare View” layout with linked control for the compare Viewers.

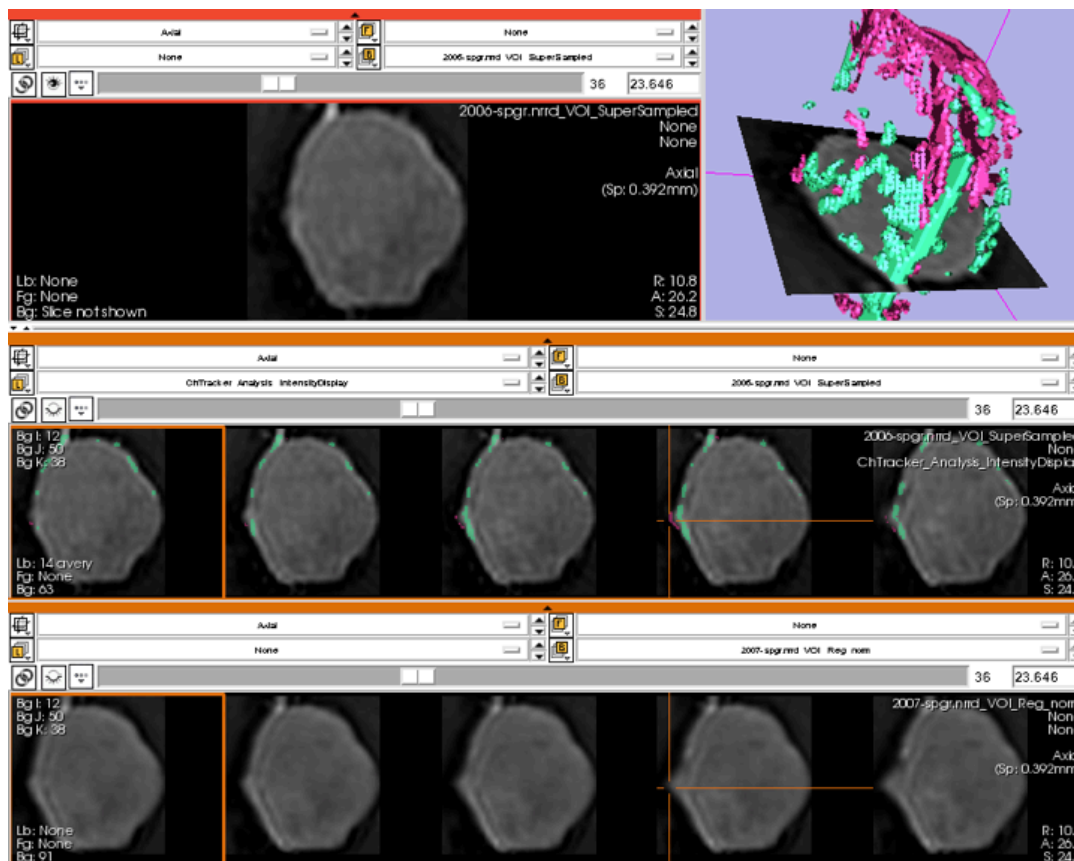




ChangeTracker: Results: change in pathology

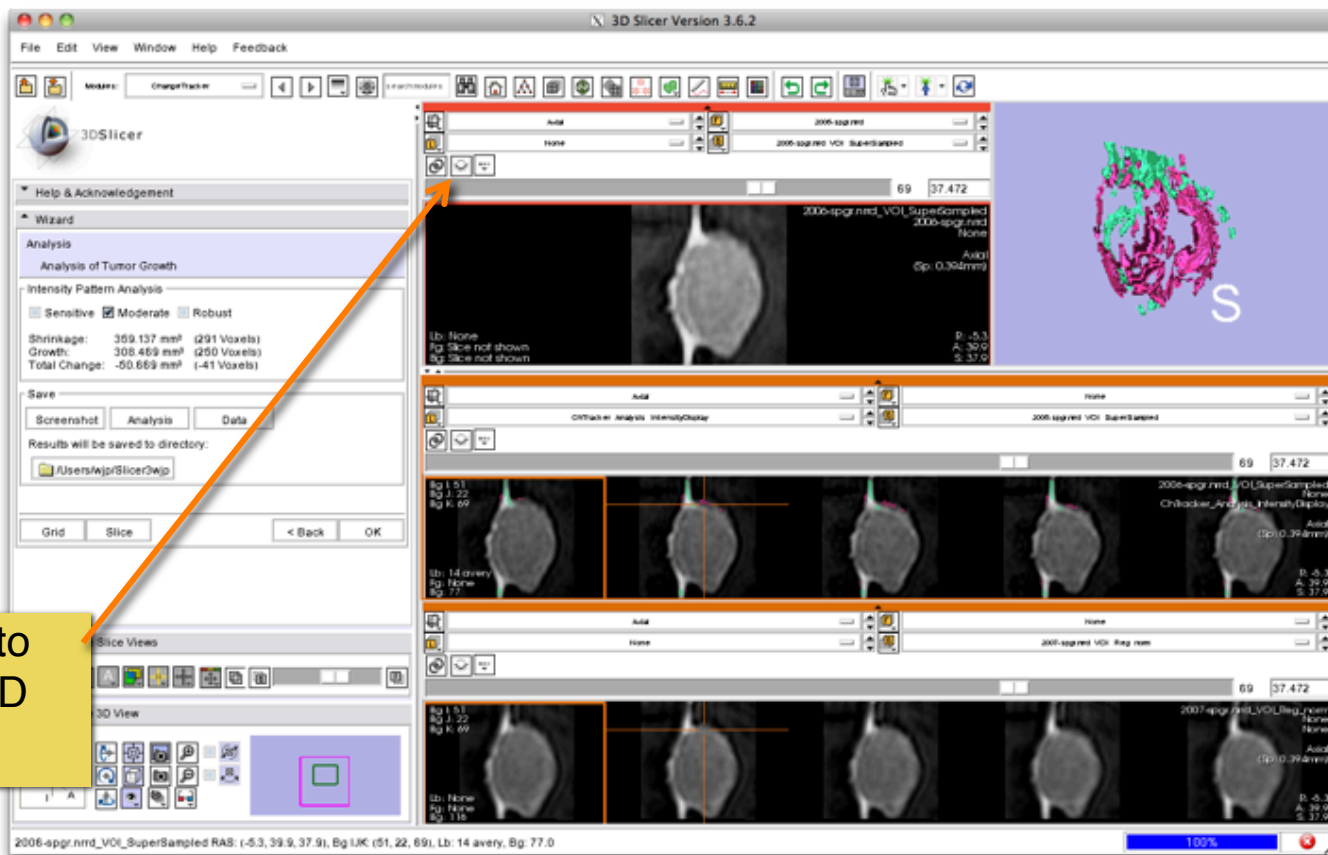
“Compare View” layout displays:


- Axial slice & 3D View
- Five corresponding consecutive slices for the VOI in Scan1 (**top row**), and
- in the Scan2 (**bottom row**).





ChangeTracker: Results: change in pathology

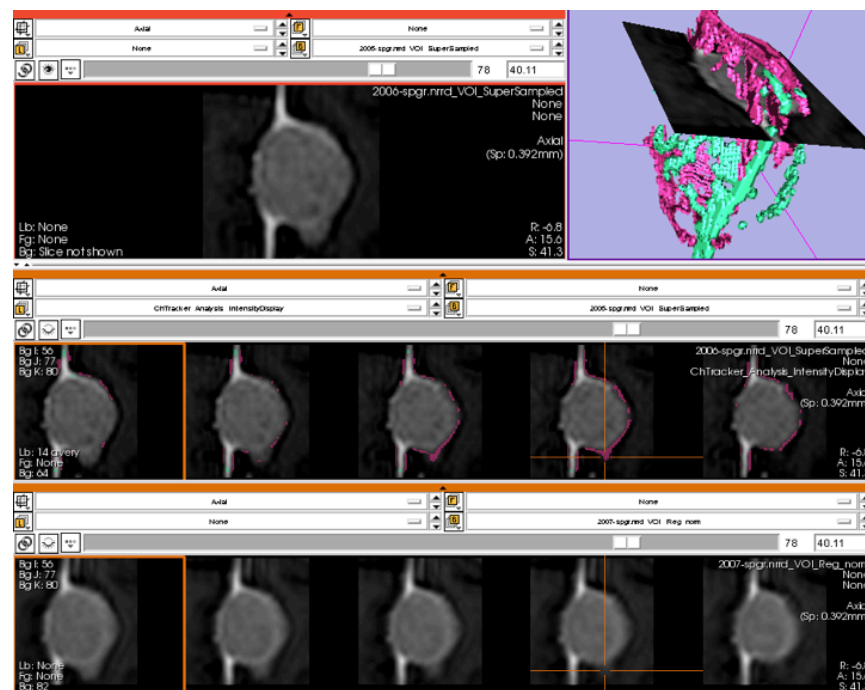
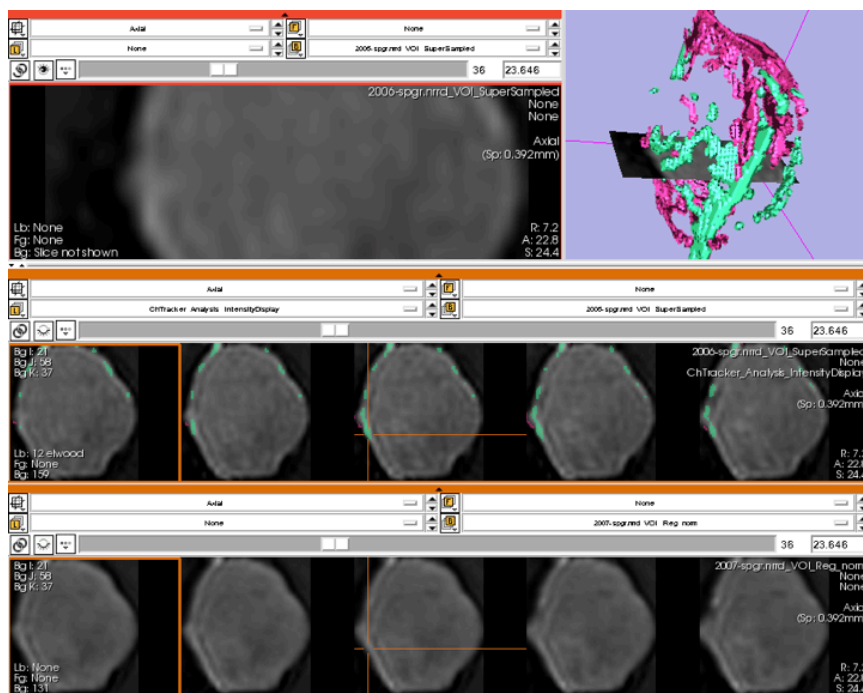


Select **visibility icon**  to **show axial slice** in the 3D Viewer.



ChangeTracker: Results: change in pathology

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

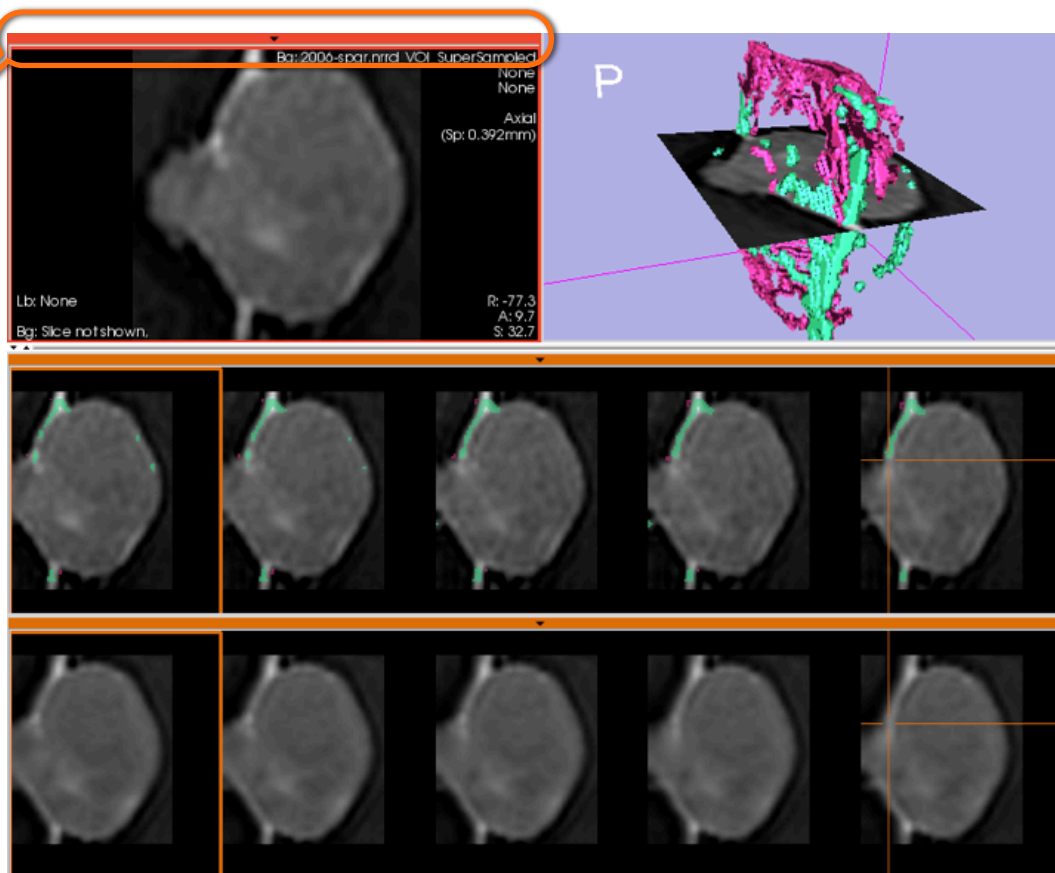




ChangeTracker: Exploring small volumetric changes

Click on the **colored bar** at the top of any Slice Viewer to show or hide the controls.

This allows more display space for viewing the image data.





ChangeTracker: Exploring small volumetric changes

Modify **sensitivity** of intensity pattern analysis

▼ Help & Acknowledgement

▲ Wizard

Analysis

Analysis of Tumor Growth

Intensity Pattern Analysis

Sensitive Moderate Robust

Shrinkage: 142.828 mm³ (116 Voxels)
Growth: 300.034 mm³ (243 Voxels)
Total Change: 157.206 mm³ (127 Voxels)

Save

Screenshot Analysis Data

Results will be saved to directory:

C:/Documents and Settings/wjp/Local Settings/Temp/Slicer3

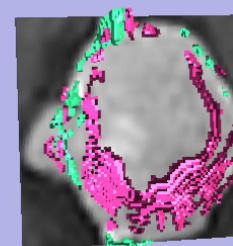
(You may need to twiddle the 3D viewer to see it update)

sensitive

Intensity Pattern Analysis

Sensitive Moderate Robust

Shrinkage: 243.458 mm³ (197 Voxels)
Growth: 327.234 mm³ (265 Voxels)
Total Change: 83.776 mm³ (68 Voxels)

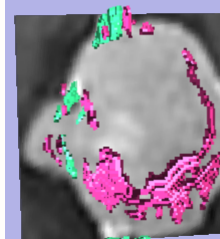


moderate

Intensity Pattern Analysis

Sensitive Moderate Robust

Shrinkage: 164.717 mm³ (133 Voxels)
Growth: 266.577 mm³ (216 Voxels)
Total Change: 101.860 mm³ (82 Voxels)

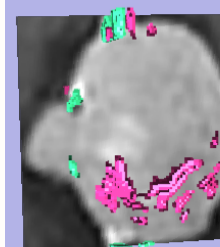


robust

Intensity Pattern Analysis

Sensitive Moderate Robust

Shrinkage: 116.475 mm³ (94 Voxels)
Growth: 186.418 mm³ (151 Voxels)
Total Change: 69.943 mm³ (56 Voxels)





ChangeTracker: Exploring small volumetric changes

Tested on Axial 3D SPGR T1 post Gadolinium scans (Voxel dimension: 0.94mm x 0.94mm x 1.20mm, FOV: 240mm, Matrix: 256 x 256).

Tumor boundary should be clear.

Only for contrast enhanced images.

Need homogenous enhancement across timepoints.

Not tested for tumors with changing necrosis.

Correspondence between Intensity-based and deformation mapping-based analyses should be checked.



ChangeTracker: exploring small volumetric changes

This tutorial demonstrated:

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

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

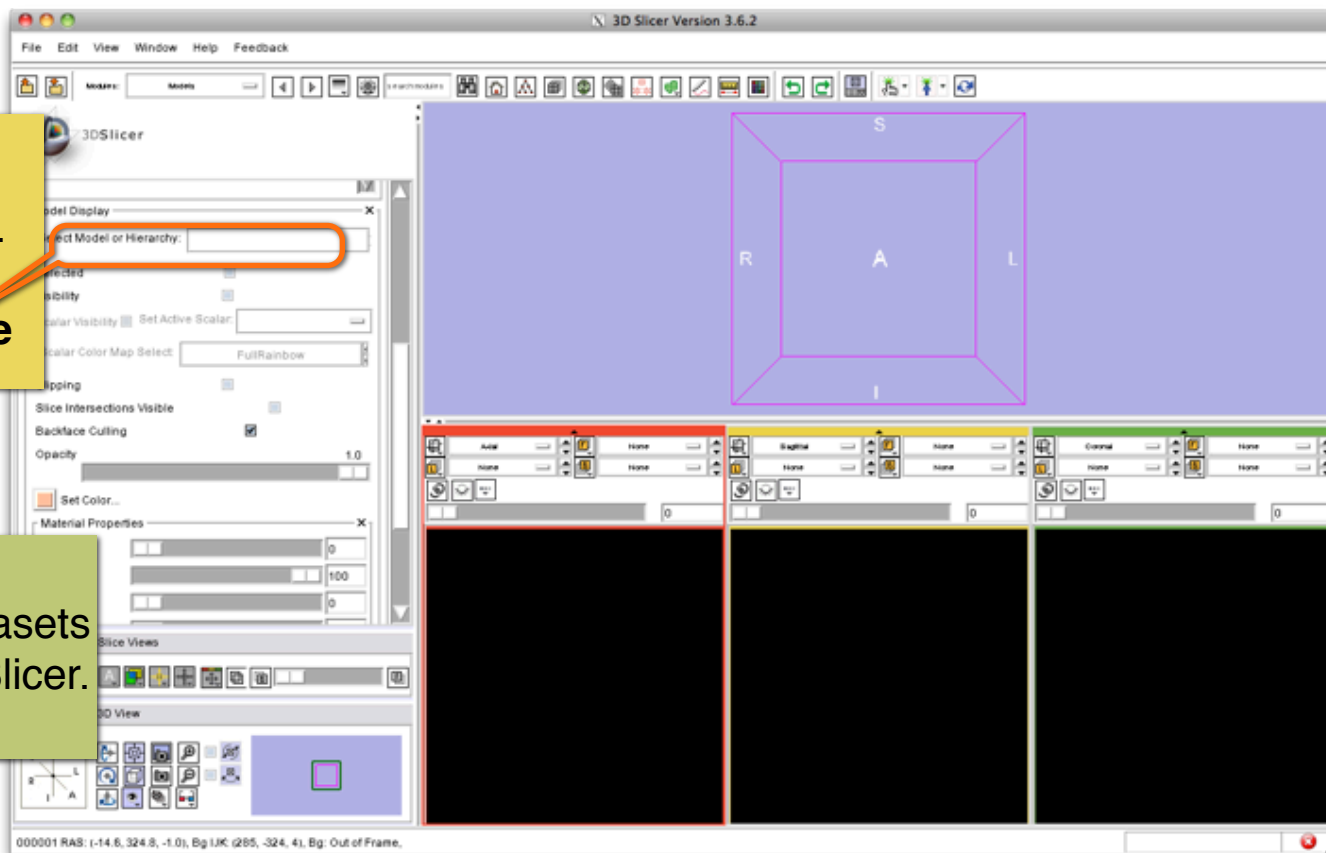


Clear the scene and its data.

Close the previous scene.

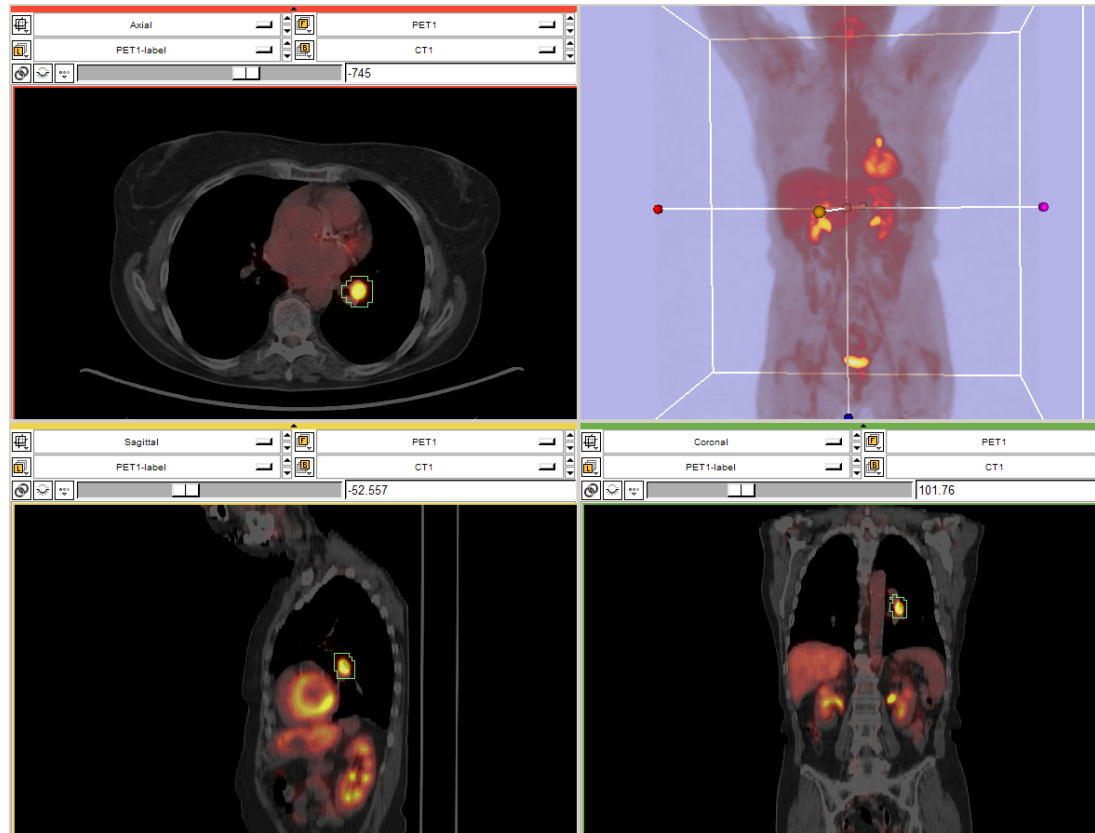
Select **File->Close Scene**

This removes any datasets previously loaded into Slicer.





PET/CT Visualization and Analysis



Part III: *PET/CT Analysis using 3D Slicer*

Jeffrey Yap PhD
Ron Kikinis MD
Wendy Plesniak PhD

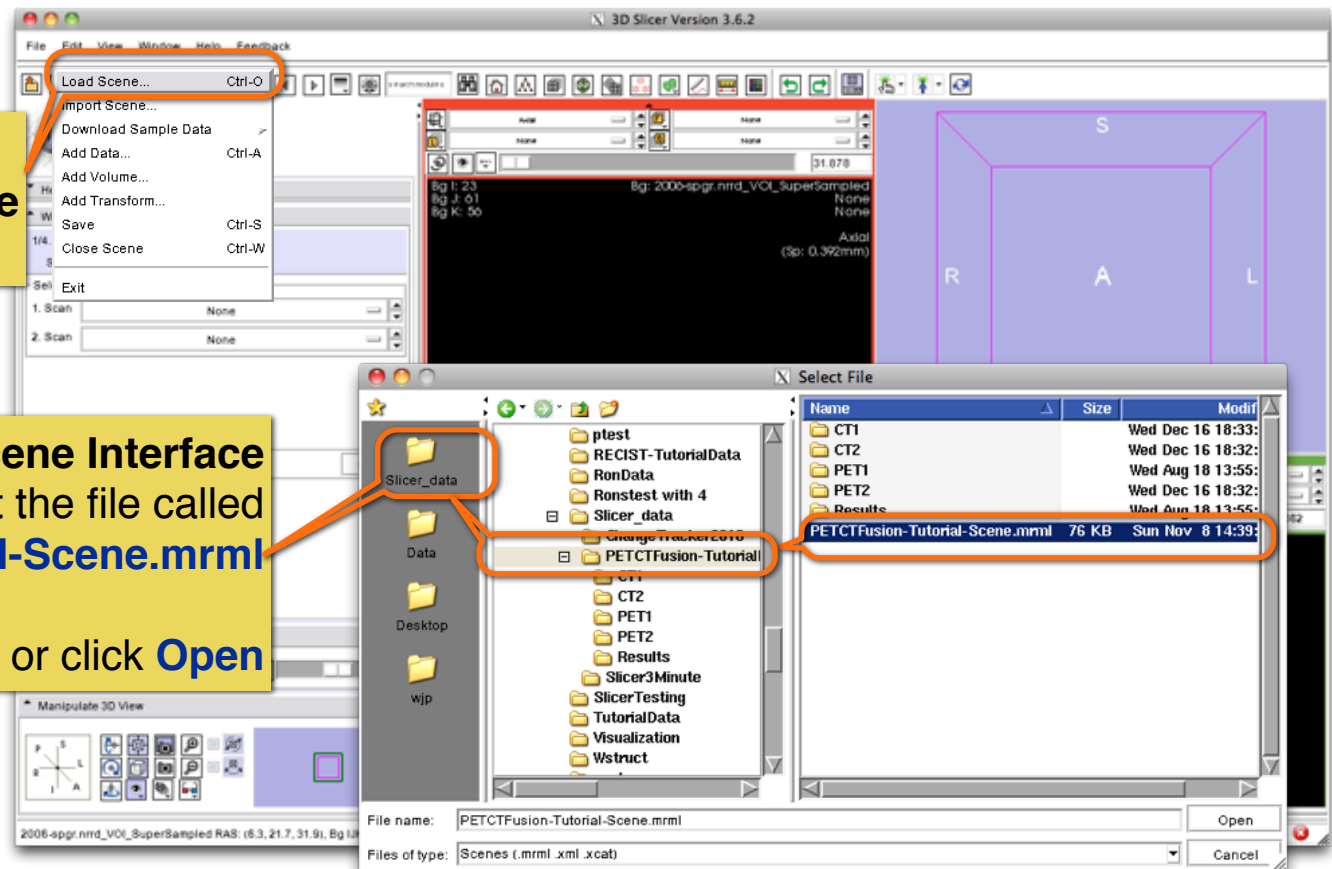


PET/CT Visualization and Analysis: Load the new scene

Select File->Load Scene

This raises the **Load Scene Interface**
select the file called
PETCTFusion-Tutorial-Scene.mrml

Double click the file, or click **Open**





PET/CT Visualization and Analysis: **About the data**

Non small cell lung cancer patient

Two PET studies: **baseline** acquired before treatment, and **follow-up** acquired 1 month after chemotherapy

Two non-diagnostic CT images are acquired without the use of contrast

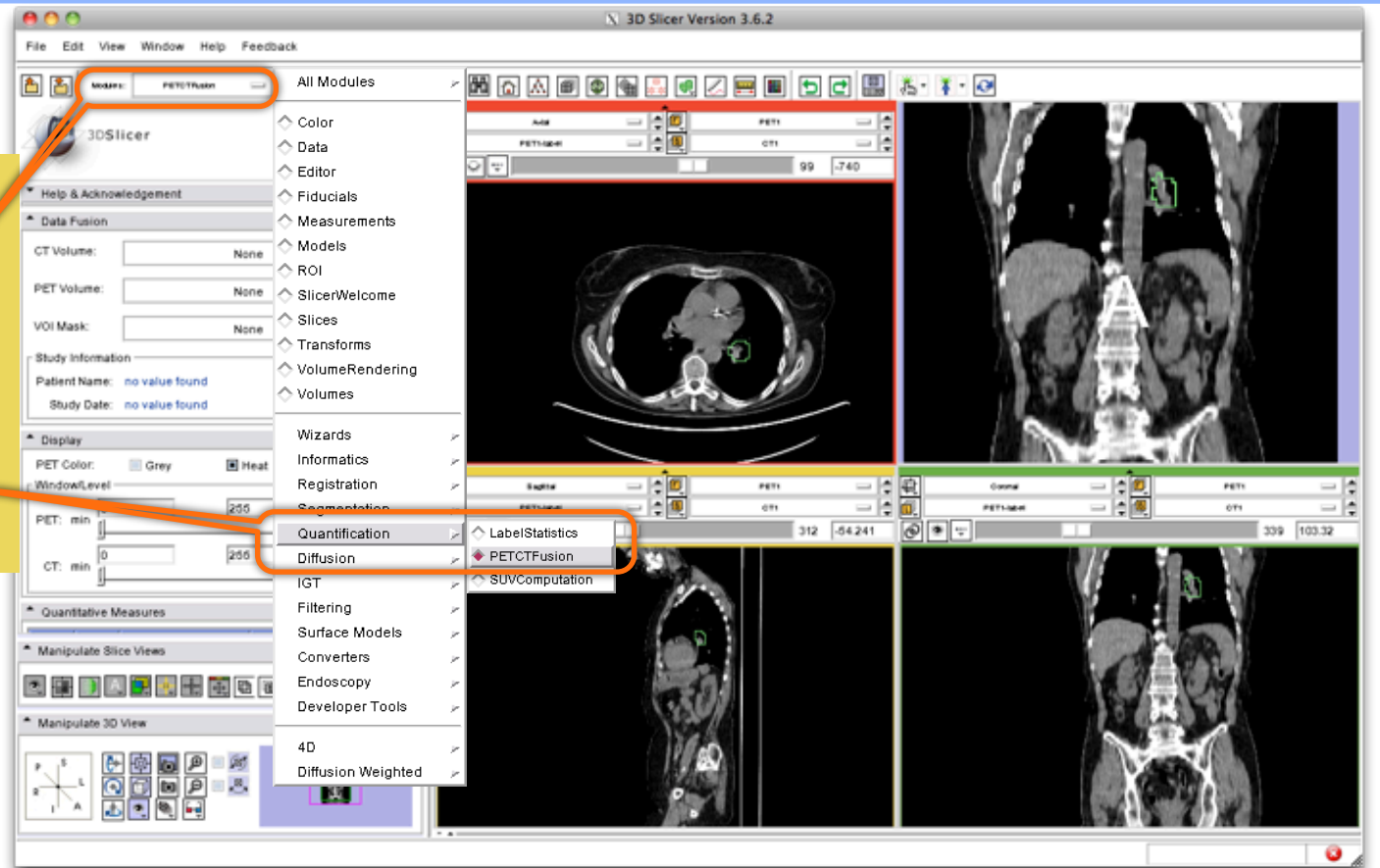
FDG-PET scans acquired 60 minutes after intravenous injection of approximately 20 mCi of ¹⁸F-FDG

Two VOIs have been created using Slicer's Editor Module.



PET/CT Visualization and Analysis: Open the PETCTFusion Module

Using the **Modules** Menubutton: Expose the menu and select the module called **PETCTFusion** under the **Quantification** category.





PET/CT Visualization and Analysis: **Select baseline study**

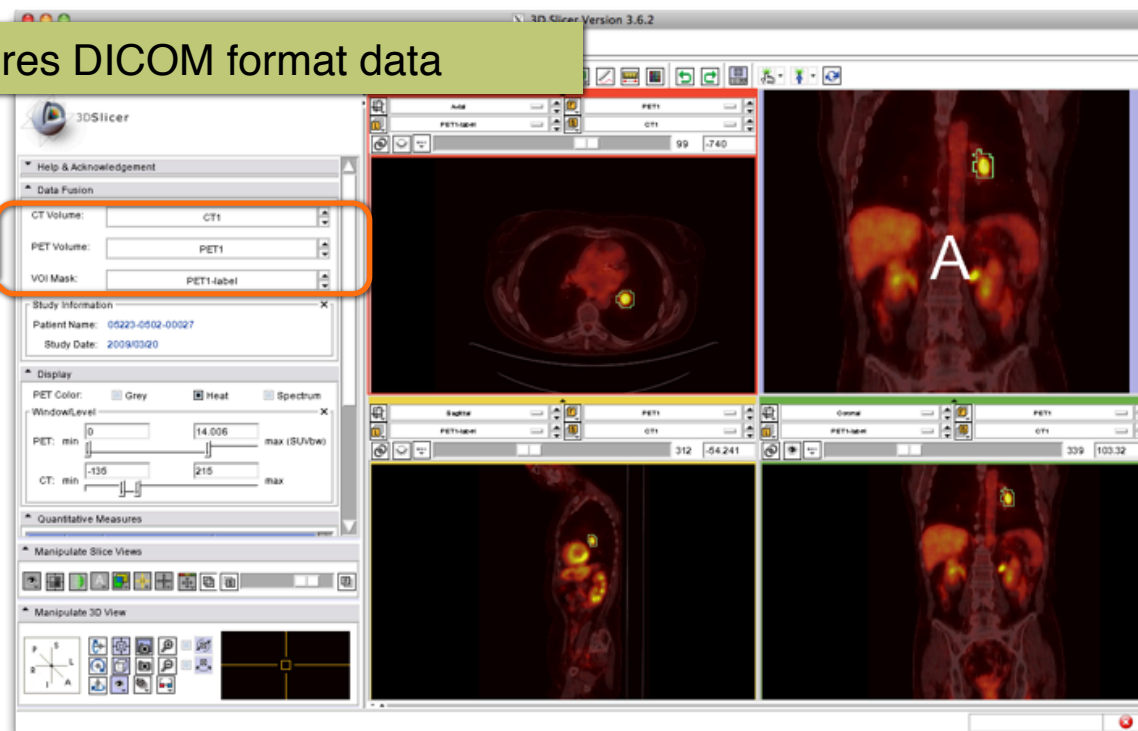
Note: Module requires DICOM format data

In the Data Fusion panel, select:

CT volume: CT1

PET volume: PET1

Tumor Mask: PET1-label



When the PET volume is selected, a “wait message” will be displayed while parameters are read from DICOM header.



PET/CT Visualization and Analysis: Information displayed in “Layers”

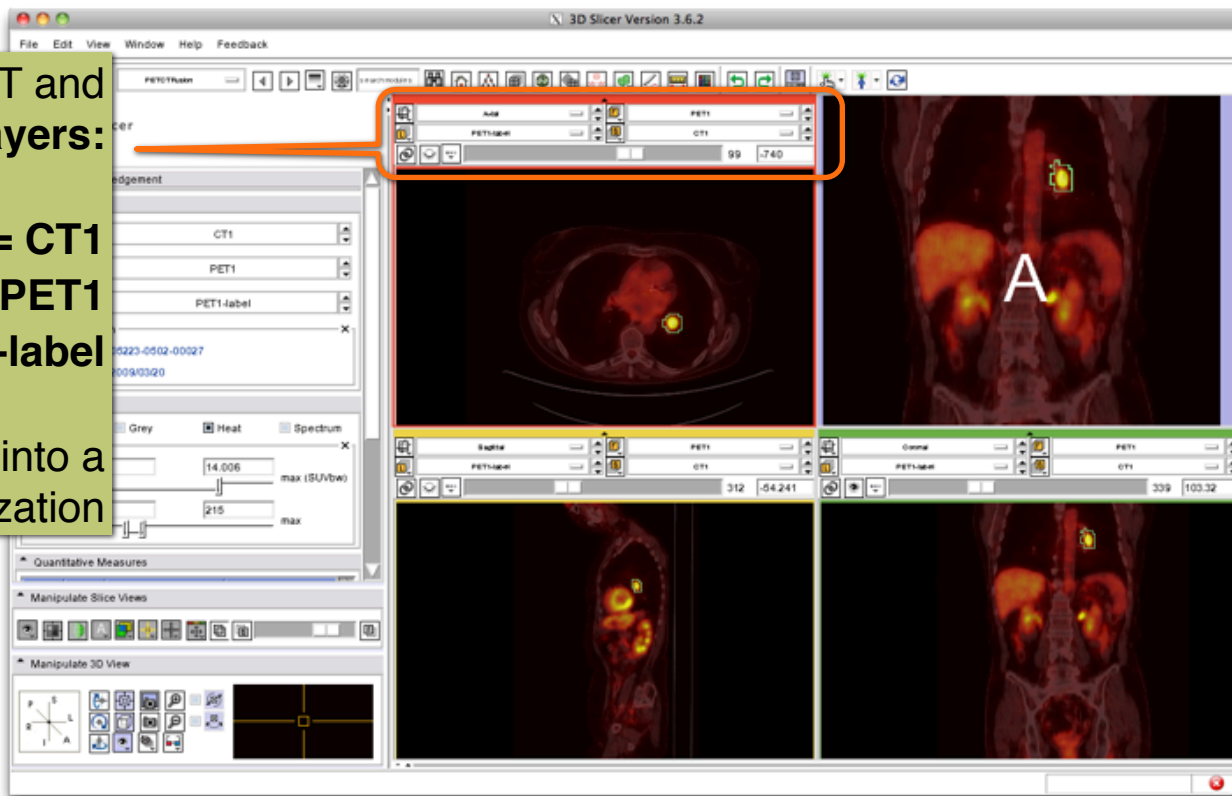
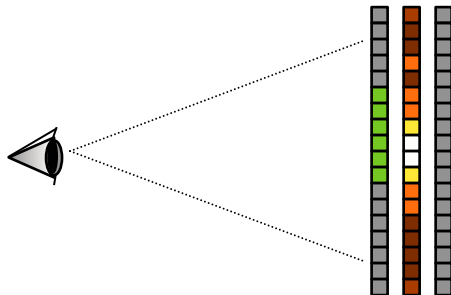
Note: this stacks the PET, CT and
VOI in three layers:

Background = CT1

Foreground = PET1

Overlay (Label) = PET1-label

where they can be blended into a
single visualization



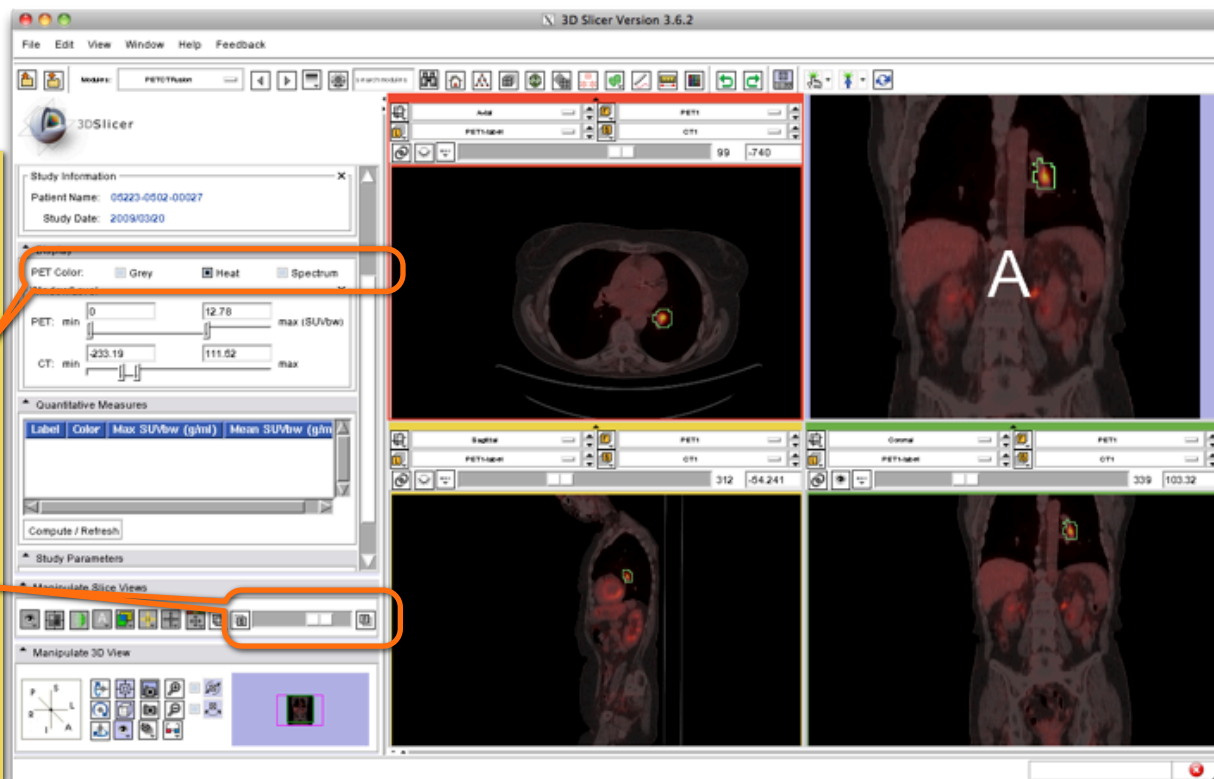


PET/CT Visualization and Analysis: Adjust display of the baseline study

In the Display Panel, **choose a colorization option** for the PET volume from among **Grey, Heat, or Spectrum**.

Adjust the **window and level** for CT1 and PET1 volumes.

Adjust the **Slices Fade Scale** to jointly display the datasets in the foreground and background layers.

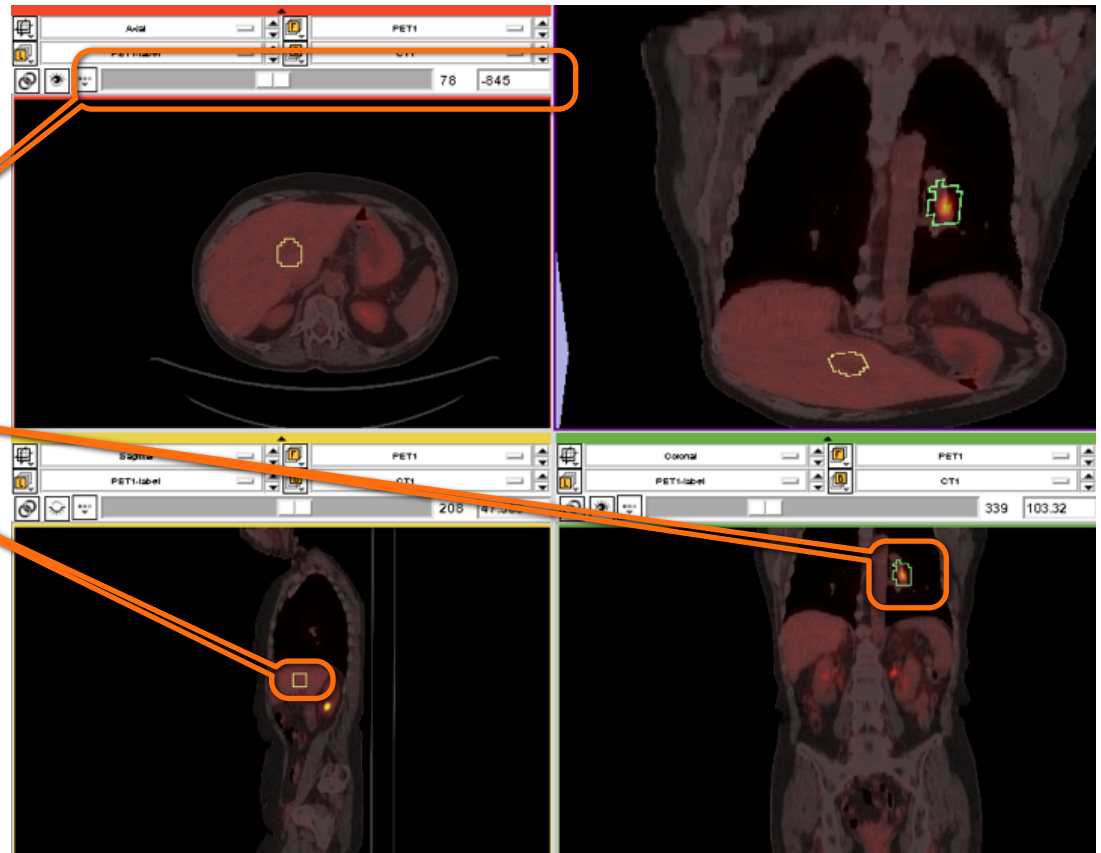




PET/CT Visualization and Analysis: Explore the visualization

Explore:
in the Slice Viewers, **scroll through the slices** to locate the green **Tumor label** and the yellow **Liver label**.

Note: (the yellow label is used only to demonstrate multiple-VOI functionality).





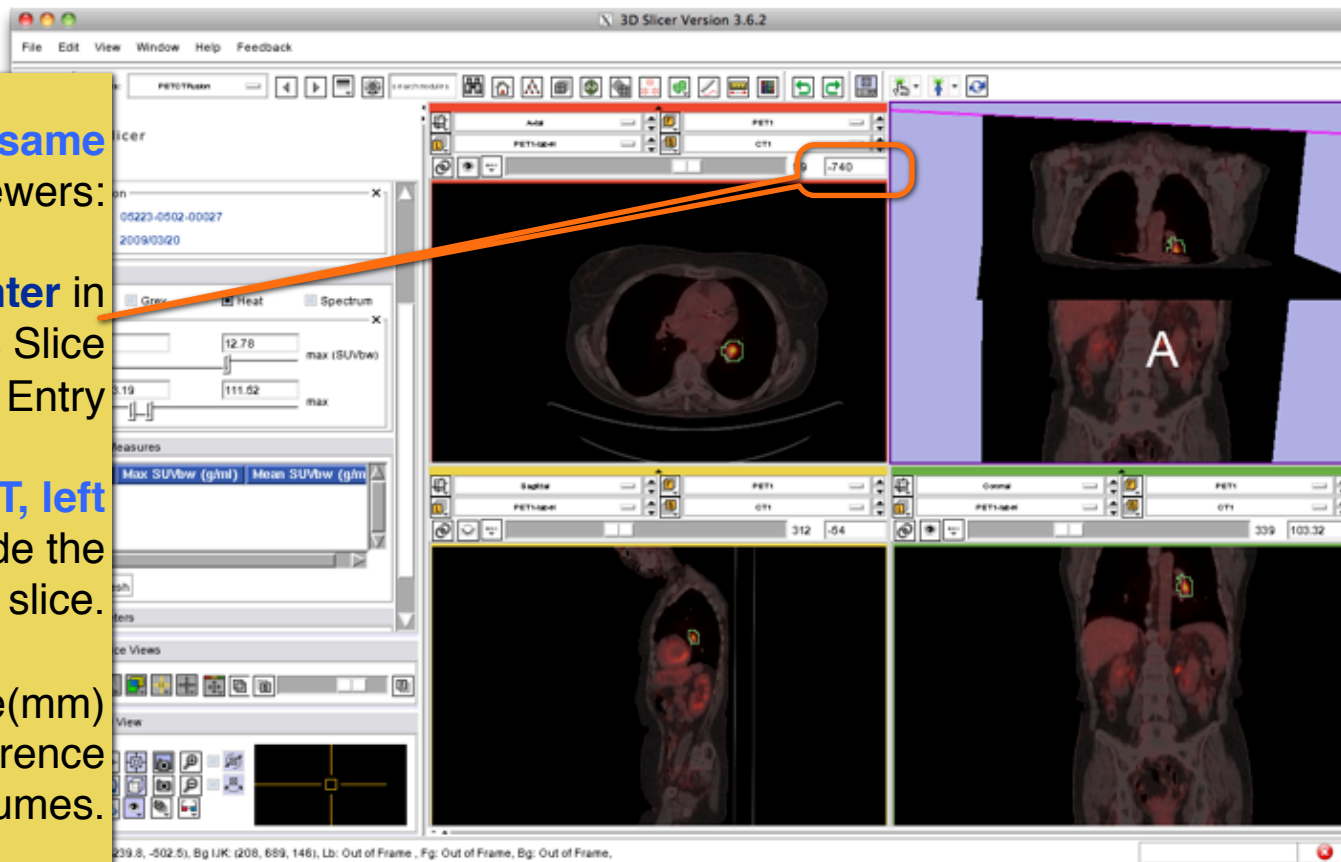
PET/CT Visualization and Analysis: View tumor in all slice viewers

Shortcut: To view the **same voxel** in all Slice Viewers:

Type **-740** and hit **enter** in the **Axial Slice Viewer's** Slice Number Entry

Then, hold down **SHIFT**, left **click and drag** inside the green VOI in the Axial slice.

This displays the same(mm) position within the reference frame of all image volumes.





PET/CT Visualization and Analysis: Compute SUV for all VOIs in baseline

In the Quantitative Measures panel, click the **Compute/Refresh** button.

SUVmax and **SUVmean** for each VOI (represented by a different color in the label map) will be displayed in the table.

3D Slicer Version 3.6.2

Study Date: 2009/03/20

Display: PET Color: Grey Heat Spectrum Window/Level: PET: min 0 12.78 max (SUVbw) CT: min -233.19 111.02 max

Label	Color	Max SUVbw (g/ml)	Mean SUVbw (g/ml)
G	Green	8.019048	2.410203
B	Blue	3.638906	2.070964

Compute / Refresh

Processing label 8



PET/CT Visualization and Analysis: Compute SUV for all VOIs in baseline

Note these measurements for the tumor VOI, as we'll compare those from the follow-up study to them.

SUVmax(bw) = 8.02
SUVmean(bw) = 3.64

The screenshot shows the 3DSlicer software interface with a PET/CT scan. The 'Quantitative Measures' table is highlighted with an orange box and contains the following data:

Label	Color	Max SUVbw (g/ml)	Mean SUVbw (g/ml)
G	Green	8.019048	2.418283
B	Blue	3.638906	2.878964

The interface also shows various viewports: a central axial PET/CT slice, a coronal PET/CT slice labeled 'A', and a sagittal PET/CT slice. The status bar at the bottom indicates 'Processing label 8'.



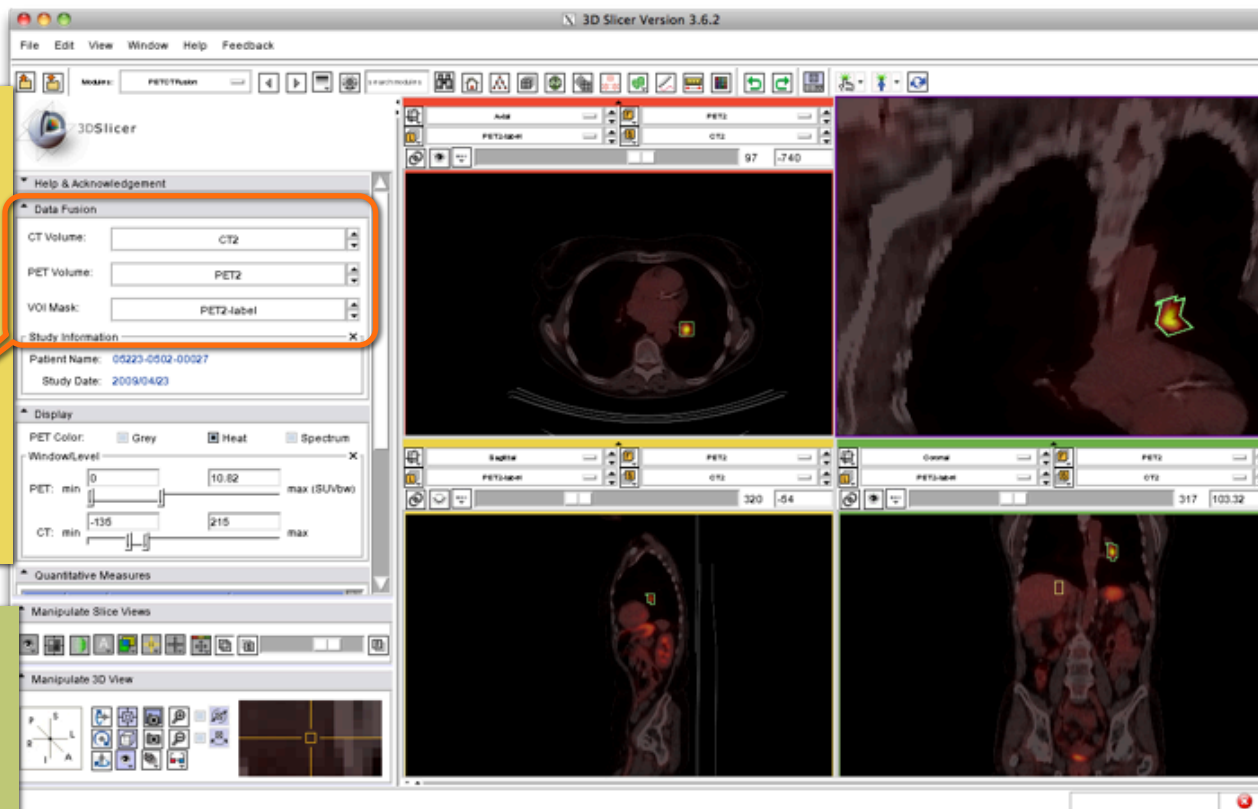
PET/CT Visualization and Analysis: Compute SUVbw for follow-up study

Look for **response to treatment** in the follow-up study:

In the **Data Fusion** panel, set:

CT volume = **CT2**,
PET volume = **PET2** and
Tumor Mask = **PET2-label**.

This dataset contains two **VOIs** that correspond to the segmentations the baseline study.

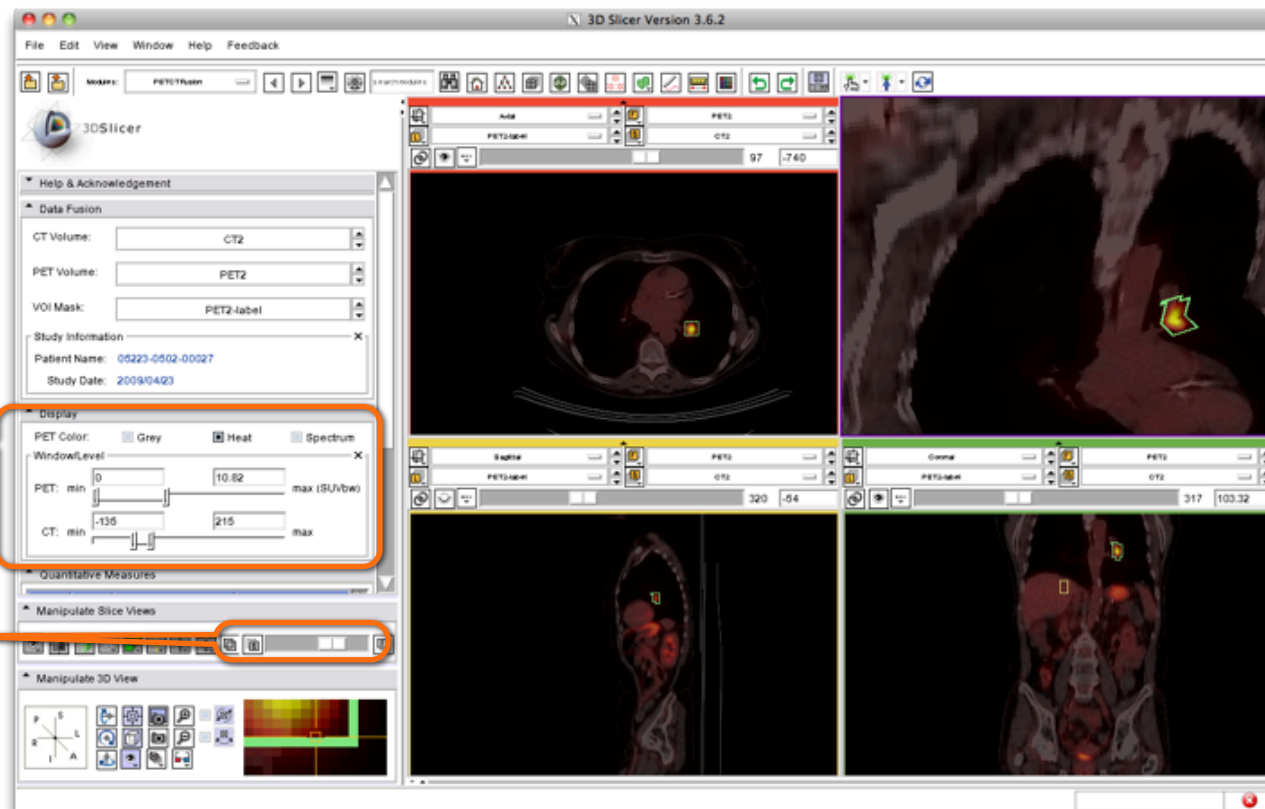




PET/CT Visualization and Analysis: **Modify display of the follow-up**

Adjust the **display** for the follow-up study.

You may want to adjust the **Slices Fade Slider** and manipulate the 3D View to refresh them.





PET/CT Visualization and Analysis: Compute SUVbw for follow-up

3DSlicer

Patient Name: 05223-0502-00027
Study Date: 2009/04/23

Display
PET Color: Grey Heat Spectrum
WindowLevel:
PET: min max (SUVbw)
CT: min max

Quantitative Measures

Label	Color	Max SUVbw (g/ml)	Mean SUVbw (g/ml)
G	Green	9.351174	3.033374
B	Yellow	3.224922	2.605969

Compute / Refresh

Study Parameters
Refresh SUV Attributes From DICOM

Manipulate Slice Views

Manipulate 3D View

CT2 RAS: (-54.0, 445.3, -590.0), Bg IJK: (319, -34, 126), Lb: 0 Black, Fg: 24.1 Bg: Out of Frame.

In the “Quantitative Measures” Panel:
select **Compute/Refresh** to compute SUVbw for the green Tumor volume (and yellow liver volume).



PET/CT Visualization and Analysis: **Assess response wrt this VOI**

Label	Color	Max SUVbw (g/ml)	Mean SUVbw
6	Green	8.019048	2.416263

Label	Color	Max SUVbw (g/ml)	Mean SUVbw
6	Green	9.351174	3.033374

Pre-Treatment Max SUVbw ~~8.0~~ g/ml

Post-Treatment Max SUVbw = 9.4 g/ml

+16.61% (SD)



PET/CT Visualization and Analysis: **Appropriate Use**

Still validating this module against performance of commercial systems.

Appropriate only for DICOM PET studies only

Not yet compatible with Philips datasets



Workshop Summary

This workshop has demonstrated:

- Basic scene loading and visualization using 3D Slicer
- Use of Slicer's ChangeTracker module to assess small changes in tumor size
- Workflow to make quantitative measurements of SUV (body weight) in Slicer's PETCTFusion module



Thank you and more information

Thank you for your attendance!

Tutorial Slides:

<http://www.na-mic.org/Wiki/index.php/File:Combined-RSNA2010-CTSA.pptx>

Tutorial Data:

<http://wiki.na-mic.org/Wiki/images/5/51/Slicer3MinuteDataset.zip>

<http://wiki.na-mic.org/Wiki/images/f/f8/RSNA-ChangeTracker-Tutorial-Data.zip>

<http://wiki.na-mic.org/Wiki/images/7/73/PETCTFusion-Tutorial-Data.zip>

Tutorial Software:

www.slicer.org/Downloads

More Information:

<http://www.slicer.org>



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THE HARVARD CLINICAL AND TRANSLATIONAL SCIENCE CENTER
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NIH U54EB005149



Brain Science Foundation



INRIA, France



Neuroimage Analysis Center (NAC)



National Center for Image-Guided Therapy (NCIGT)



Surgical Planning Laboratory, Brigham and Women's Hospital