



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

a teaching affiliate of  
Harvard Medical School

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# Data Loading and 3D Visualization

Sonia Pujol, Ph.D., Harvard Medical School

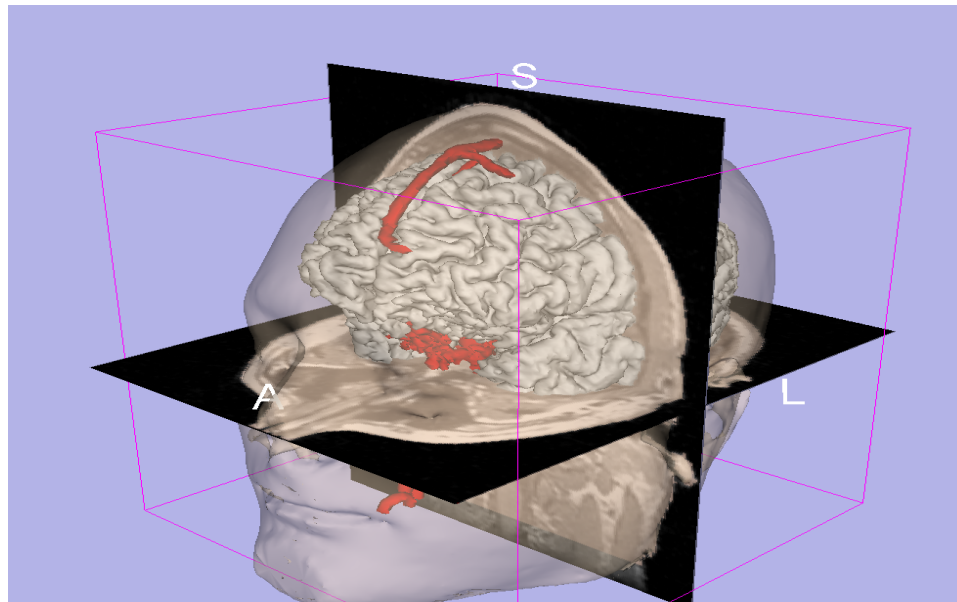
Director of Training, National Alliance for Medical Image Computing



# 3D Visualization of the Anatomy

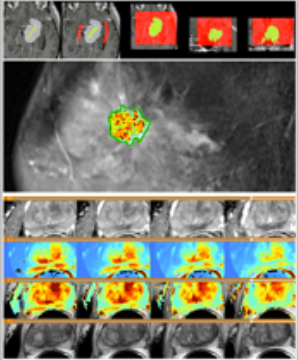
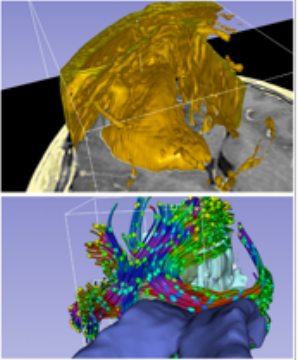
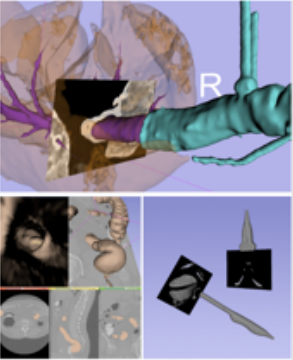

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Following this tutorial, you will be able to **load and visualize volumes** within Slicer4, and to **interact in 3D** with structural images and models of the anatomy.





# 3DSlicer

Powerful processing.	Streamlined interface.	Extensible platform.
 A grid of images showing various medical image processing techniques, including segmentation of a brain tumor and registration of two brain slices.	 A 3D visualization of a brain model, showing a yellow translucent surface and internal structures.	 A 3D visualization of a hand model, showing a purple translucent surface and internal structures.
 <p><b>3D Slicer</b> version 4.0</p>	<p><a href="http://www.slicer.org">www.slicer.org</a></p>	

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

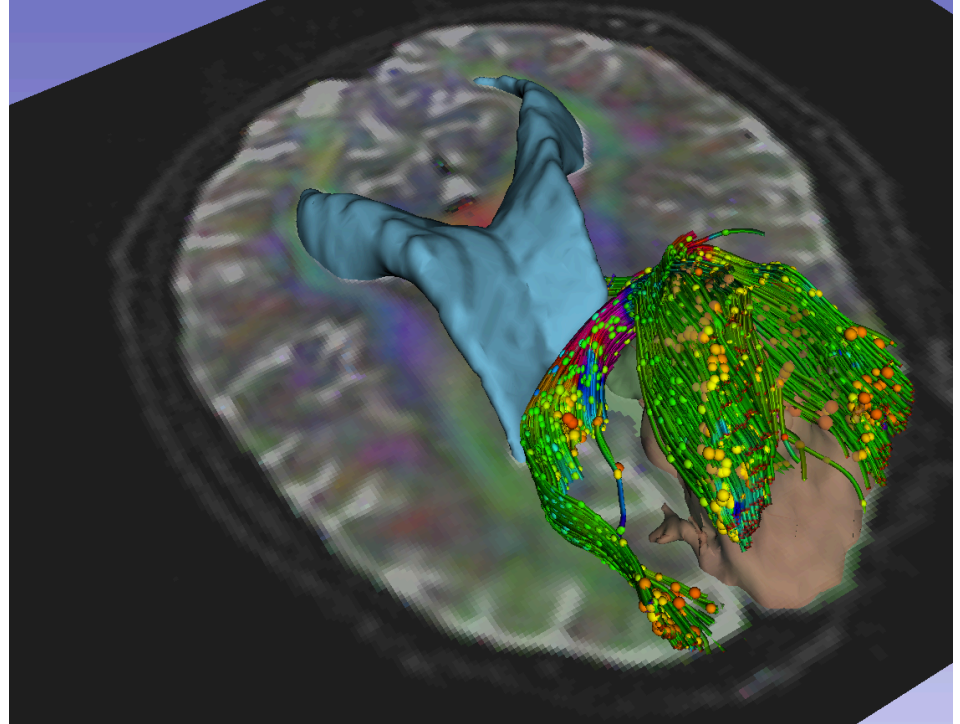
3DSlicer is a **multi-institutional effort** supported by the **National Institute of Health**.



# 3DSlicer

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- An **end-user application** for image analysis
- 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





3DSlicer version 4.1 is a multi-platform software running on **Windows, Linux, and Mac OSX.**



## Disclaimer

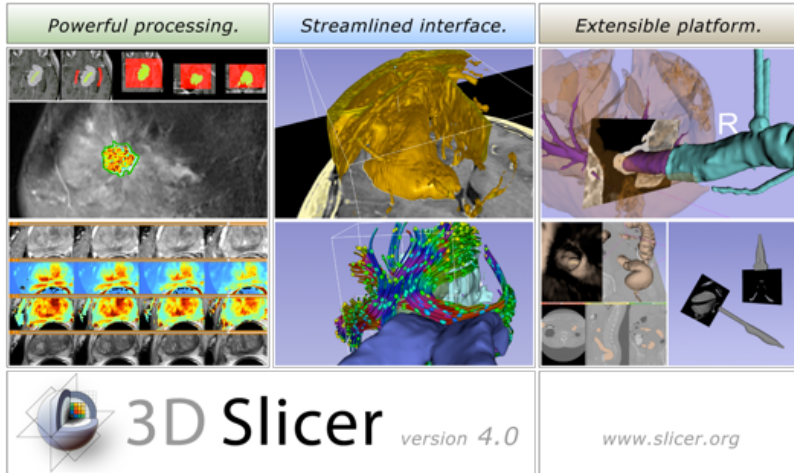
It is the responsibility of the user of 3DSlicer to comply with both the terms of the license and with the applicable laws, regulations and rules. **Slicer is a tool for research, and is not FDA approved.**





# 3DSlicer History

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



# NA-MIC and NAC



## National Alliance for Medical Image Computing

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

McGraw-Hill Custom Search Search

### NA-MIC Wiki

#### General

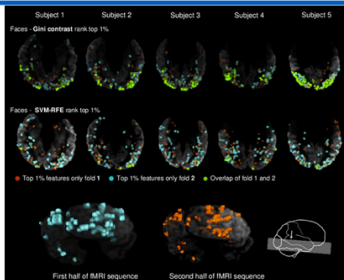
- Overview
- Organization
- Contact Us

#### Center Components

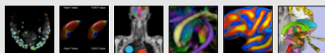
- Algorithms
- Engineering
- Diving Biological Projects
- Collaboration Grants

#### Resources

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



Detecting Stable Distributed Patterns of Brain Activation using Gini Contrast [Read more...](#)



1 of 23 Photos

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

Supported by the National Institutes of Health, [Roadmap Initiative](#).

Information about collaborating with NA-MIC is available [on our wiki](#).



### 97th Scientific Assembly and Annual Meeting

November 27 - December 2, McCormick Place, Chicago.

[Read more...](#)

[NEWS ARCHIVE](#)



## Neuroimage Analysis Center

"understanding the human brain through imaging"

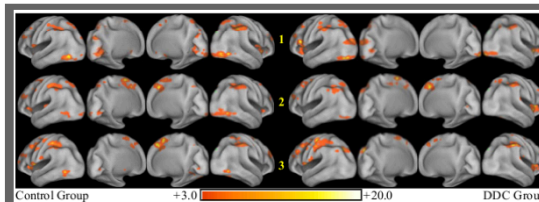
Google Custom Search

### About the NAC

- Overview
- Organization
- Research Cores
- Collaborations

### Resources

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



### State-space Models of Mental Processes from fMRI

Spatial Activity Maps. The average t-score maps of the two groups (voxel-wise group average divided by group std. dev.) are displayed on an inflated brain-surface (left lateral-posterior, left medial-posterior, right medial-posterior and right lateral-posterior). Each row shows the maps for one phase of the task and values 1-3 have been masked out for clarity.

[More...](#)

[Featured Image Archive](#)

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

The NAC is a major research center supported by the National Center for Research Resources (NCRR), a component of the National Institutes of Health.



P.I. Ron Kikinis, M.D.

Slide 8





# Slicer: Behind the scenes

Safari File Edit View History Bookmarks Window Help  
CDash - Slicer4  
http://www.cdash.org/Slicer4/index.php?project=Slicer4  
namic Google weather Slicer Countway Yahoo! eCommons dtl\_review  
RSNA 2011 - NAMIC CDash - Slicer4  
Login All Dashboards  
Slicer4  
Dashboard Calendar Previous Current Project  
WARNING: This CDash instance is running the bleeding edge svn trunk CDash code, and is updated frequently. You  
1 file changed by 1 author as of Sunday, November 27 2011 - 22:00 EST

**Nightly-Packages**

Site	Build Name	Update			Configure			Build		
		Files	Error	Warn	Error	Warn	Error	Warn	Pass	
factory-win7.kitware	Windows7-VS2010-32bits-QT4.7.1-PythonQt-With-Tcl-CLI-Release	0	0	0	2 <sup>0</sup>	0	2 <sup>0</sup>	107		
factory-mac-64bits.kitware	SnowLeopard-g++4.2.1-64bits-QT4.7-PythonQt-With-Tcl-CLI-Release	1	0	0	0	0	14 <sup>0</sup>	3		
factory-ubuntu-64bits.kitware	Linux-g++4.4.3-64bits-QT4.7-PythonQt-With-Tcl-CLI-Release	1	0	0	0	0	13 <sup>0</sup>	3		
factory-win7.kitware	Windows7-VS2008-64bits-QT4.7.1-PythonQt-With-Tcl-CLI-Release	0	0	0	0	0	1000 <sup>0</sup>	223		
factory-win7.kitware	Windows7-VS2008-32bits-QT4.7.1-PythonQt-With-Tcl-CLI-Release	1	0	0	0	0	1000 <sup>0</sup>	226		

**Nightly**

Site	Build Name	Update			Configure			Build			Test			Build Time
		Files	Error	Warn	Error	Warn	Error	Warn	Not Run	Fail	Pass			
whitecube.kitware	SnowLeopard-gcc4.2.1-QT4.7.0-PythonQt-With-Tcl-Release	1	0	0	27	0	190	0	96	391		11 hours ago		
youpi.sci.utah.edu	OpenSuse-c++4.5.0-64bits-QT4.6.3-PythonQt-With-Tcl-NoCLI-Release	0	0	0	0	0	15	0	304	6		11 hours ago		
eris.kitware	Linux-g++4.4-QT4.6.3-PythonQt-CLI-Release	1	0	0	0	0	15 <sup>0</sup>	2	36 <sup>0</sup>	451 <sup>0</sup>		3 hours ago		
factory-ubuntu-64bits.kitware	Linux-g++4.4.3-QT4.7-PythonQt-With-Tcl-CLI-Valgrind-Release	0	0	0	0	0	13 <sup>0</sup>	3	27 <sup>0</sup>	460 <sup>0</sup>		11 hours ago		
factory-ubuntu-64bits.kitware	Linux-g++4.4.3-64bits-QT4.7-PythonQt-With-Tcl-NoCLI-Coverage-Release	0	0	0	0	0	12 <sup>0</sup>	2	23 <sup>0</sup>	287 <sup>0</sup>		11 hours ago		
sagarmatha.kitware	Linux-g++4.3.3-QT4.7-PythonQt-With-Tcl-NoCLI-Release	0	0	0	0	0	12 <sup>0</sup>	2	22	288		12 hours ago		

**Continuous**

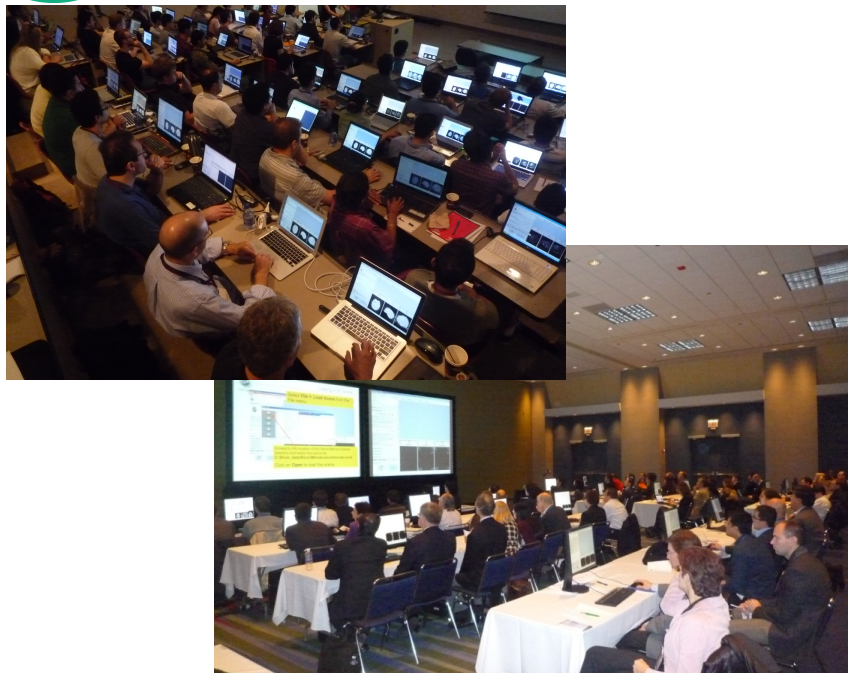
Site	Build Name	Update			Configure			Build			Test			Build Time
		Files	Error	Warn	Error	Warn	Error	Warn	Not Run	Fail	Pass			
youpi.sci.utah.edu	OpenSuse-c++4.5.0-64bits-QT4.6.3-PythonQt-With-Tcl-NoCLI-Release	2	0	0	0	0	0	0	304	6		1 hour ago		

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



# Slicer Training

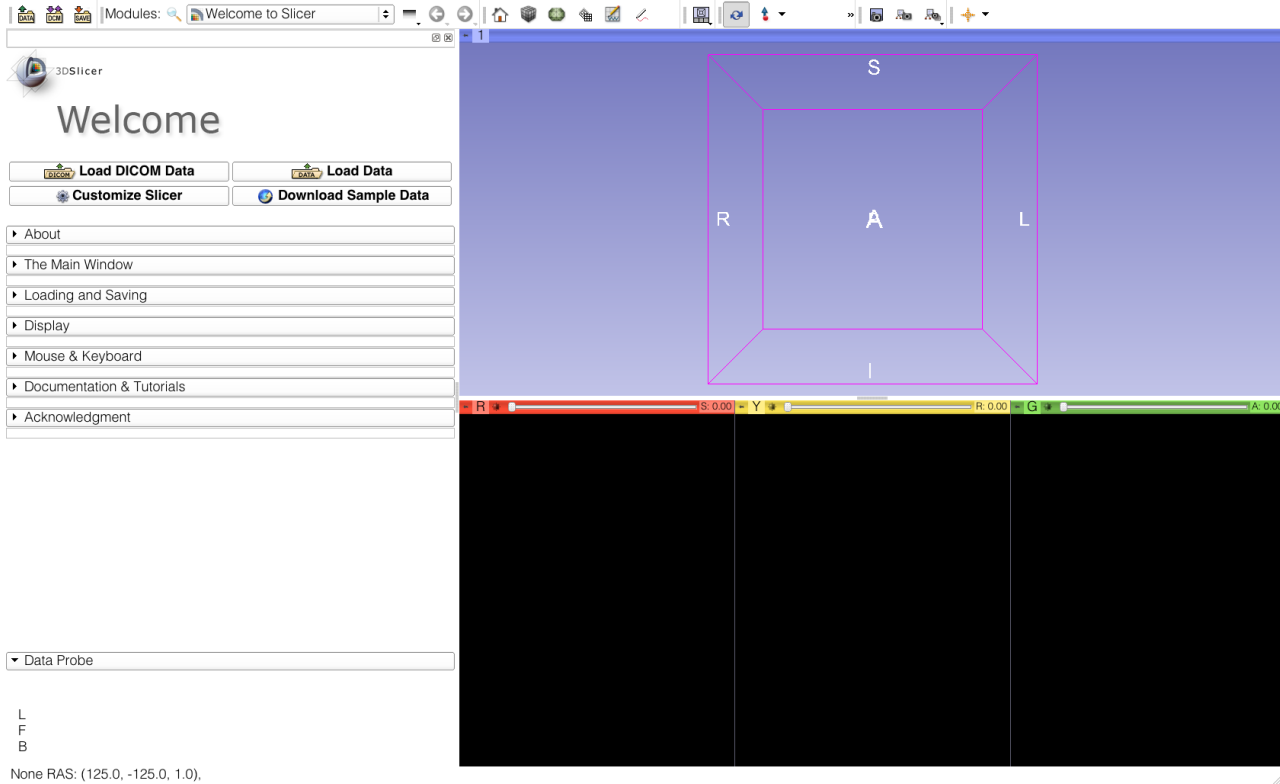
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- Hands-on training workshops at national and international venues (MICCAI, SfN, OHBM, RNSA..)
- >2,000 clinicians, clinical researchers and scientists trained since 2005

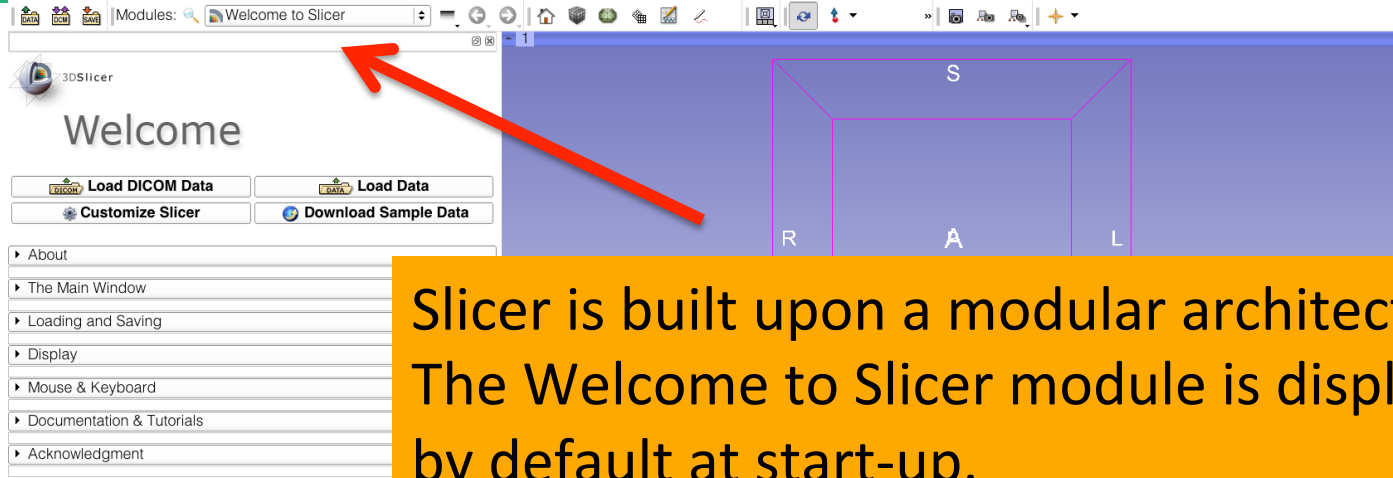


# 3DSlicer version 4.1





# Welcome to Slicer4

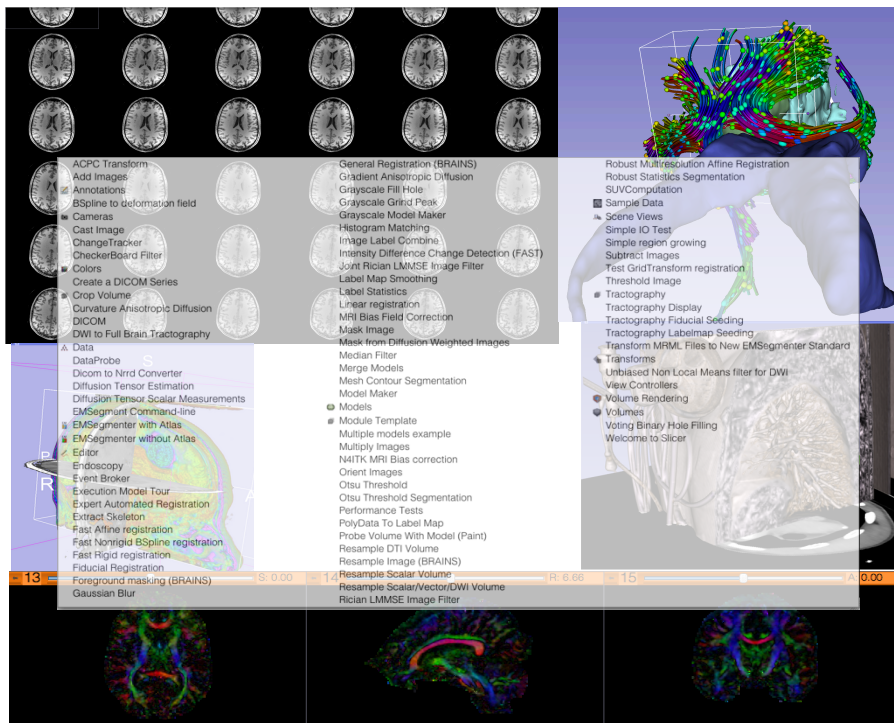


Slicer is built upon a modular architecture. The Welcome to Slicer module is displayed by default at start-up. Click on Welcome to Slicer to display the 103 modules of Slicer in the Modules menu





# Welcome to Slicer4



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



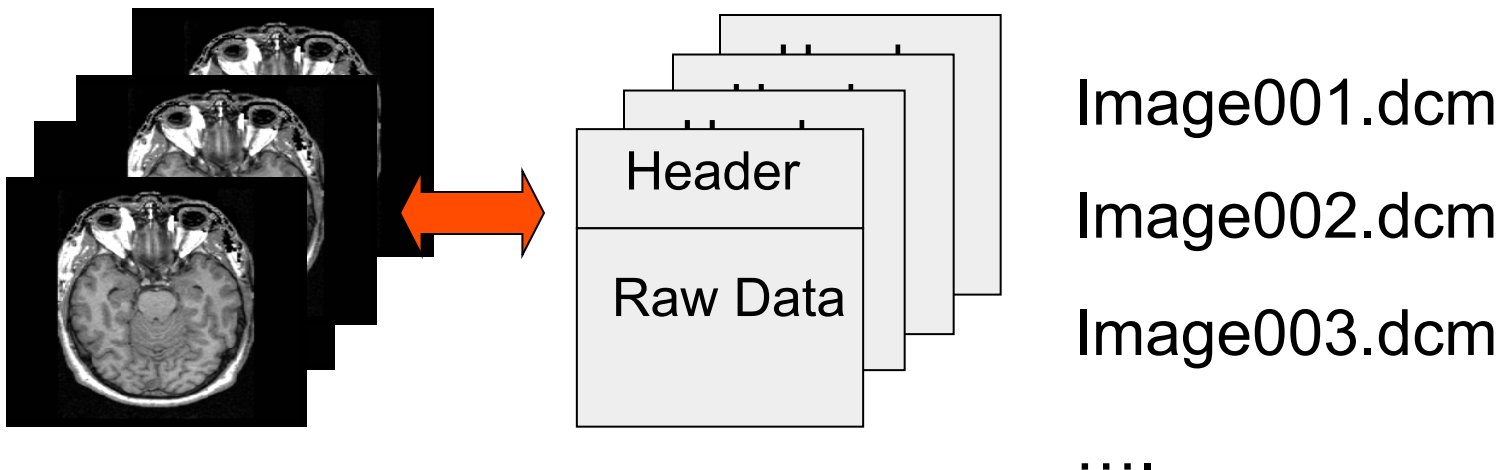
# **PART 1: LOADING AN MR VOLUME**



# The DICOM 3.0 File Format

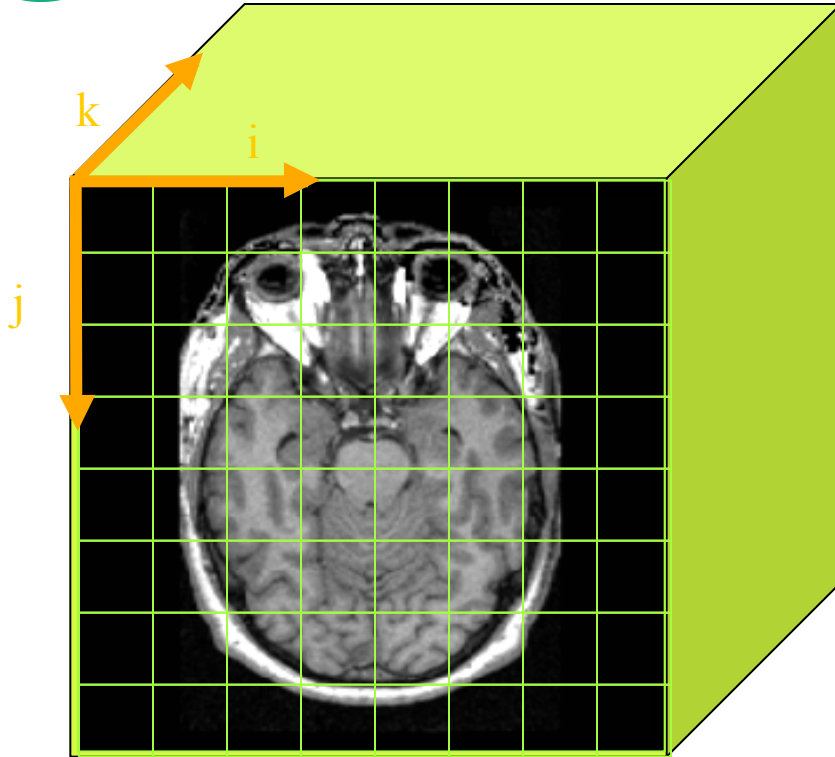
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Most radiological imaging equipment produce images in DICOM file format (‘.dcm files’)





# Data Representation

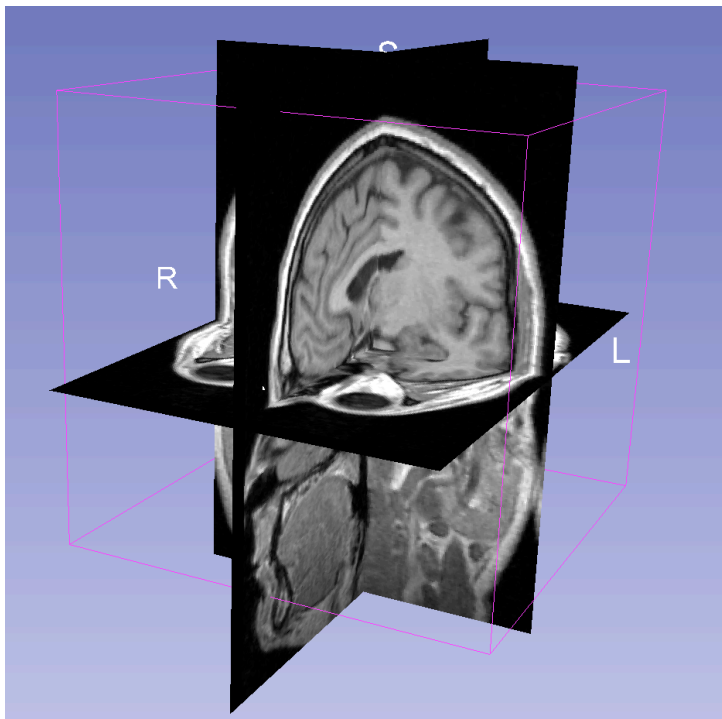


- The result of a volumetric acquisition is a **3D volume of data** related to the patient.
- The 3D raster dataset is sampled on a discrete grid with elements called **voxels** which contain the **signal intensity**.





# Tutorial Dataset



- The tutorial dataset is an MR scan of the brain of a healthy subject.
- The data in the **Nrrd** file format, part of the NA-MIC open-source toolkit
- DICOM data can be converted in Nrrd using the module '**DICOM to NRRD Converter**' in Slicer.

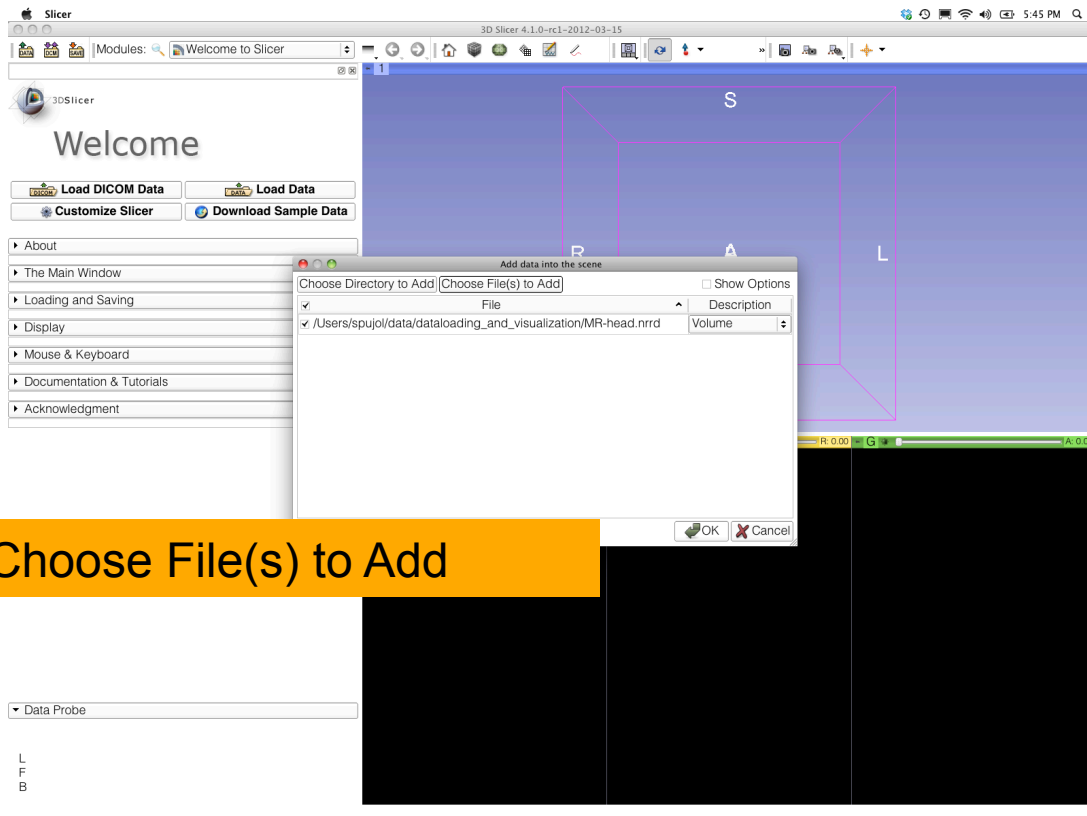


# Slicer4

A screenshot of the Slicer4 software interface. The window title is '3DSlicer' and the active module is 'Welcome to Slicer'. The interface is divided into a left sidebar and a main central area. The sidebar contains a 'Welcome' heading, four buttons: 'Load DICOM Data', 'Load Data', 'Customize Slicer', and 'Download Sample Data', and a list of menu items including 'About', 'The Main Window', 'Loading and Saving', 'Display', 'Mouse &amp; Keyboard', 'Documentation &amp; Tutorials', and 'Acknowledgment'. At the bottom of the sidebar, there is a 'Data Probe' dropdown menu and a small coordinate display showing 'None RAS: (125.0, -125.0, 1.0)'. The main central area is a large 3D view window, currently showing a blue background with a pink wireframe box labeled 'S'. A large yellow rectangular overlay is positioned in the center-right of the 3D view, containing the text 'Click on Load Data in the Slicer Welcome module' in bold black font. The top of the window features a standard toolbar with various icons for file operations and navigation.



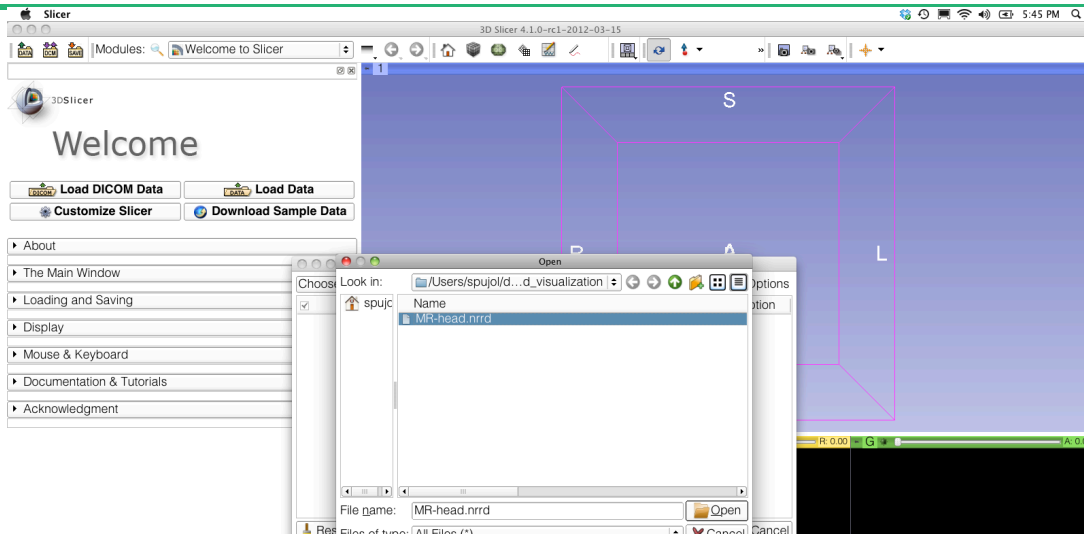
# Loading a volume



Click on Choose File(s) to Add



# Loading a volume

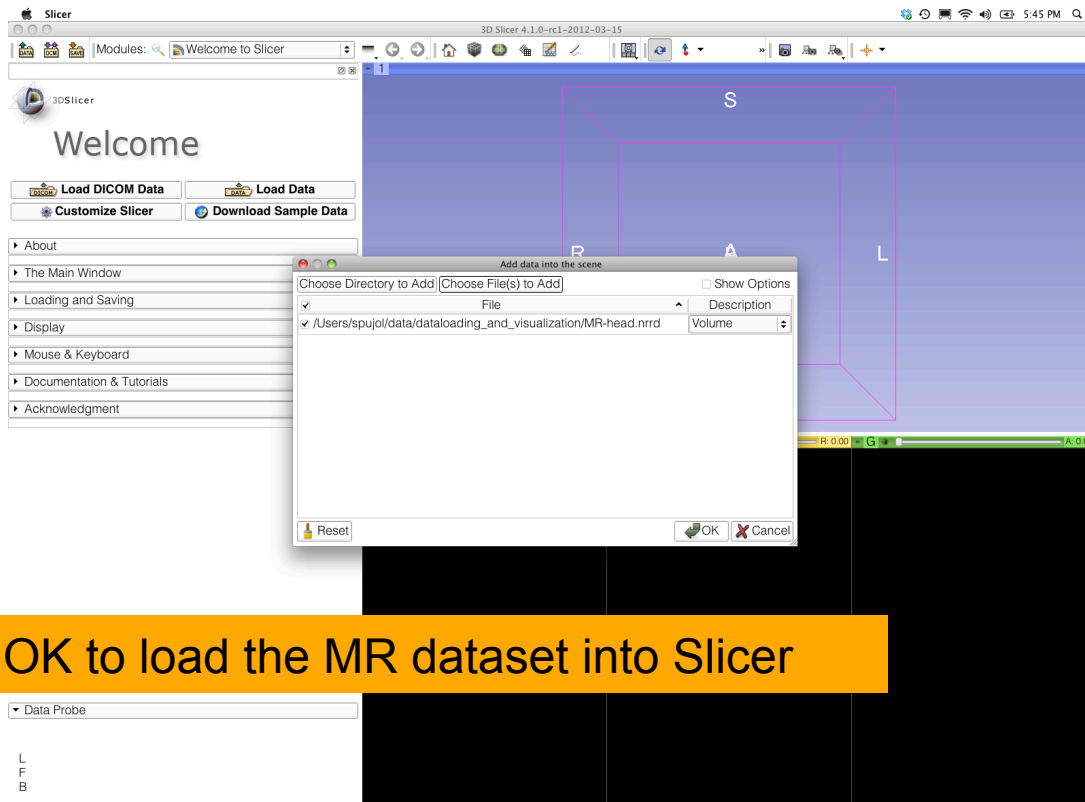


Browse to the location of the Visualization directory and select the file **MR-head.nrrd**





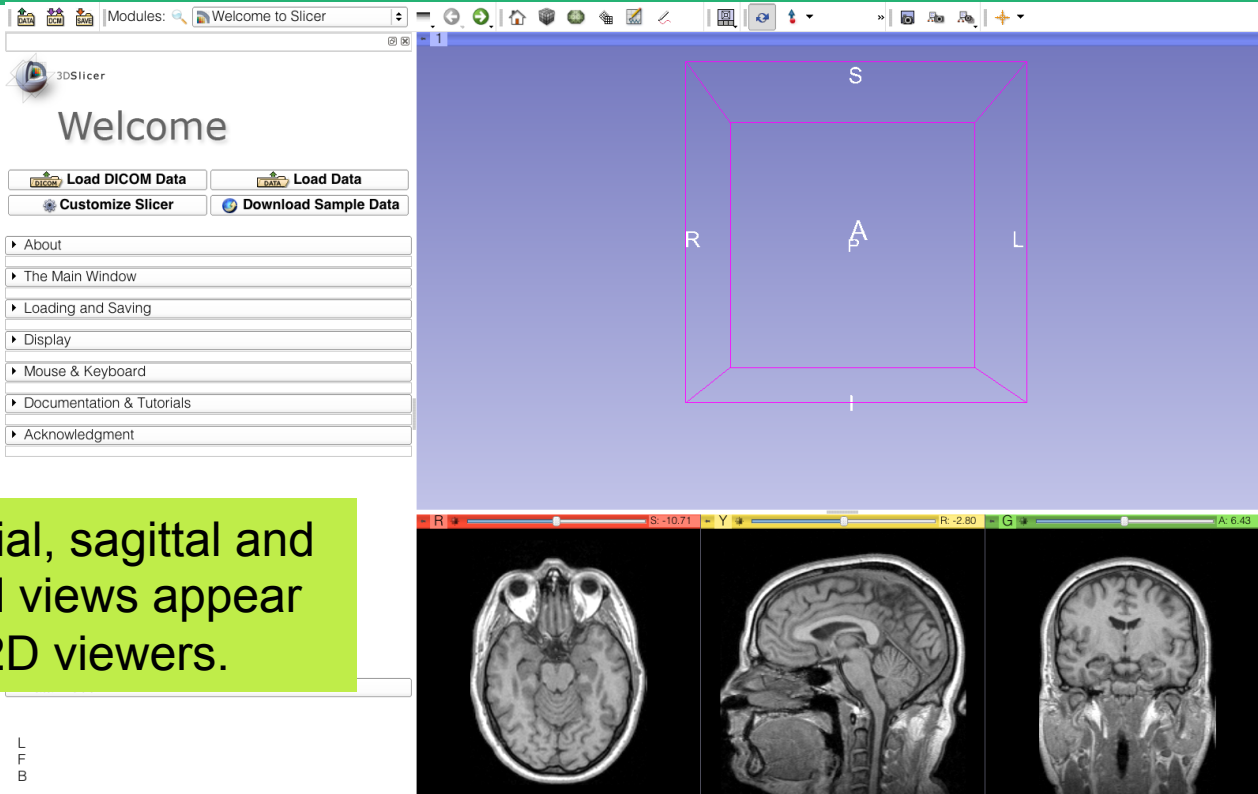
# Loading a volume



Click on OK to load the MR dataset into Slicer



# Loading a volume

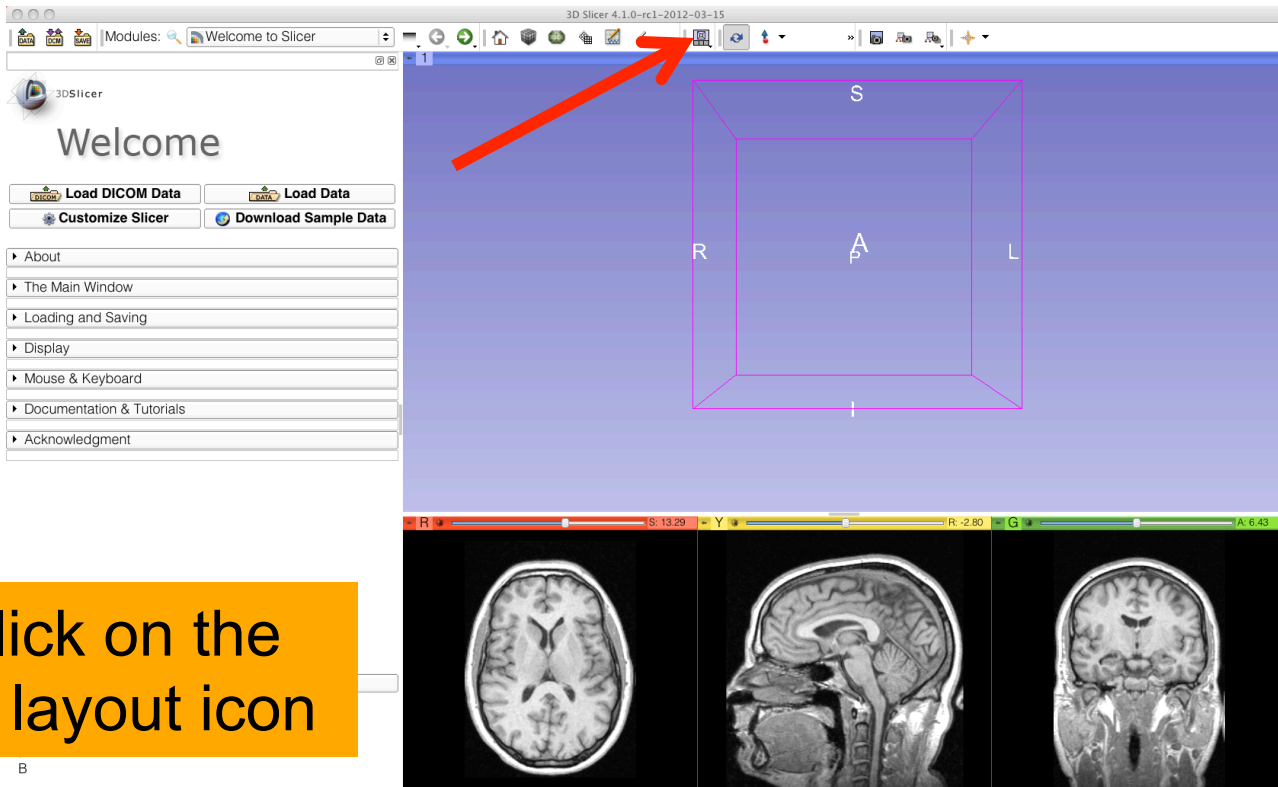


The axial, sagittal and coronal views appear in the 2D viewers.

L  
F  
B



# Loading a volume

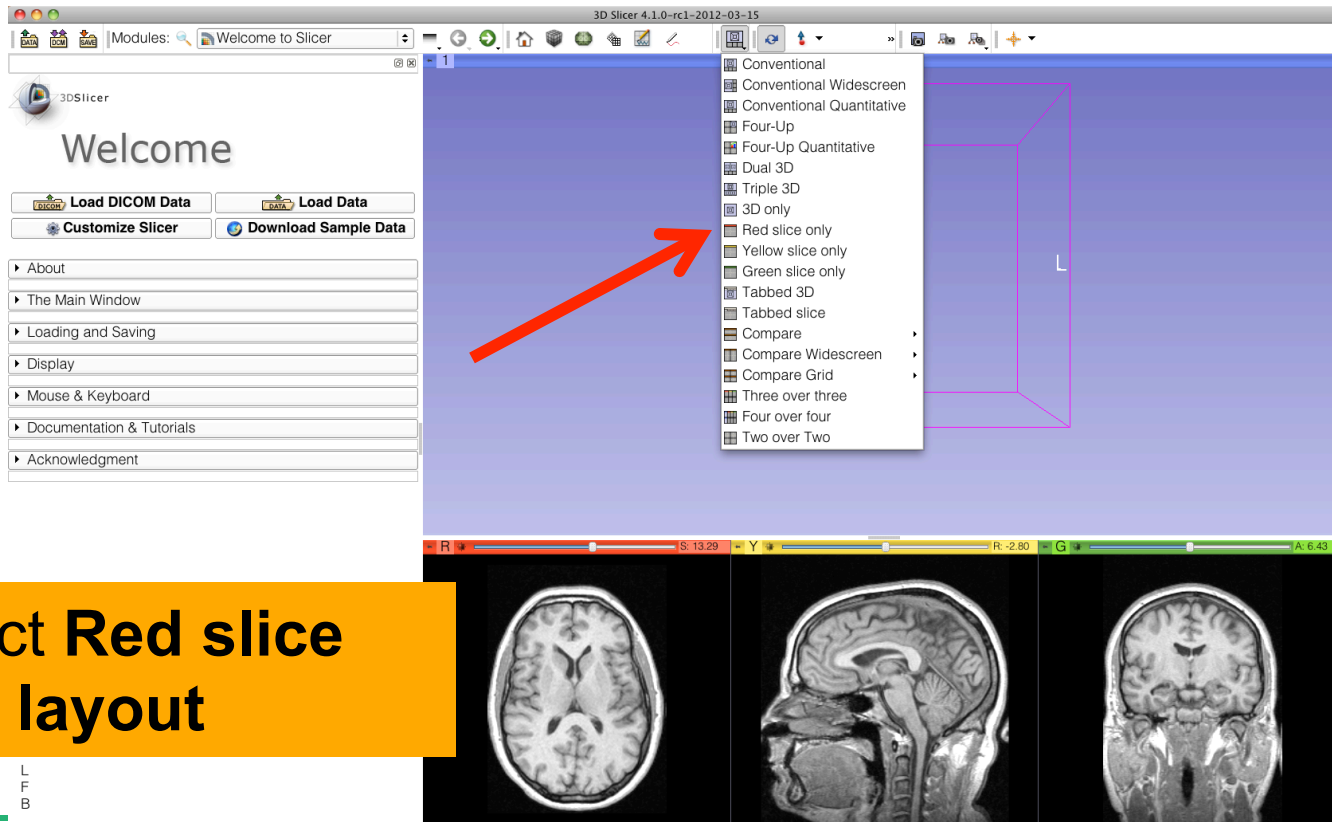


Left-click on the Slicer layout icon

B



# Loading a volume



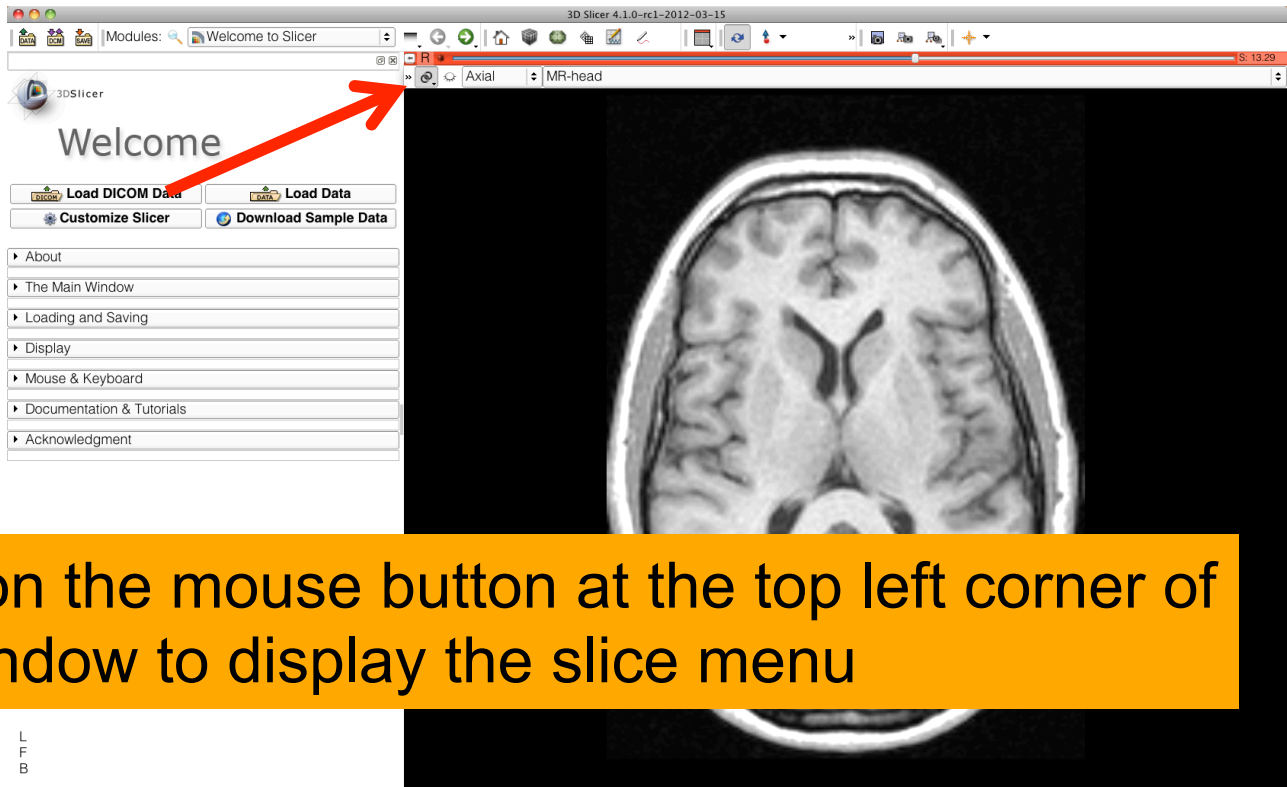
Select Red slice only layout

L  
F  
B





# Loading a volume

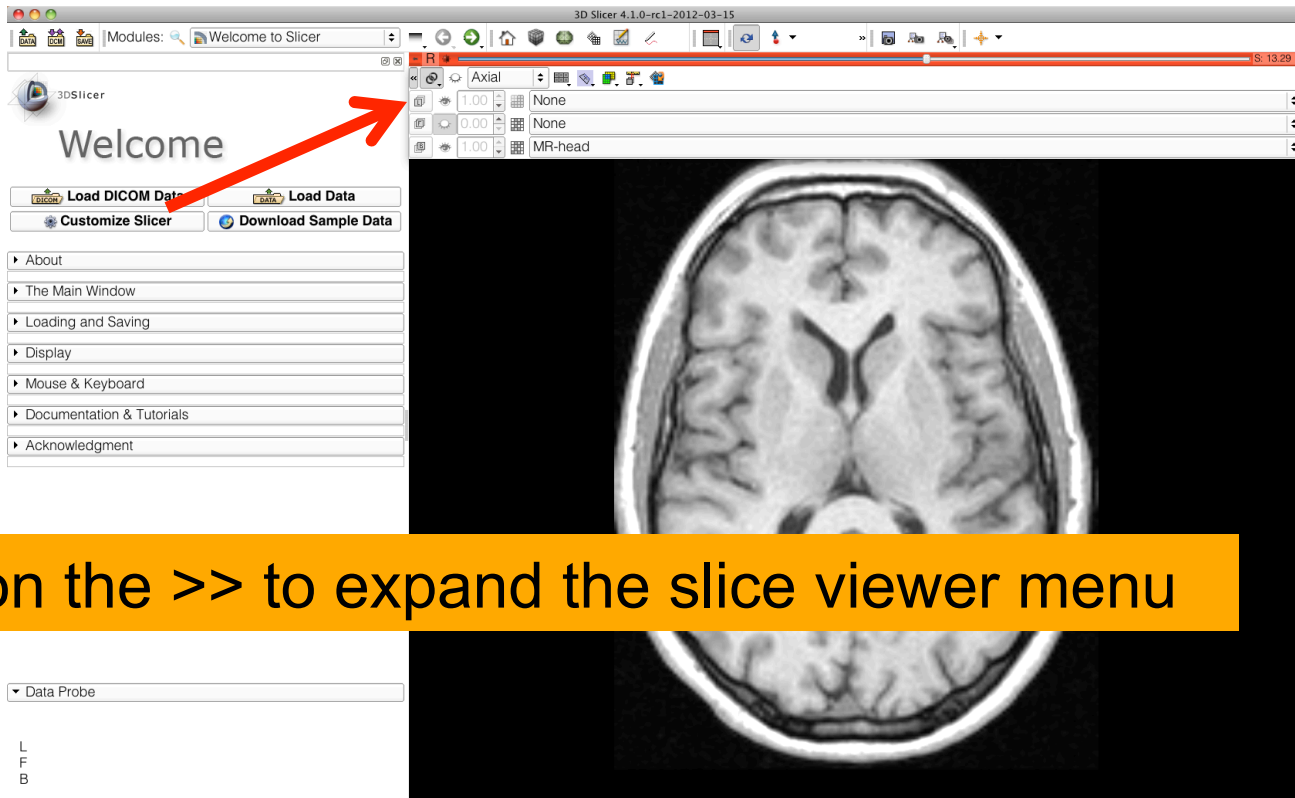


Position the mouse button at the top left corner of the window to display the slice menu

L  
F  
B

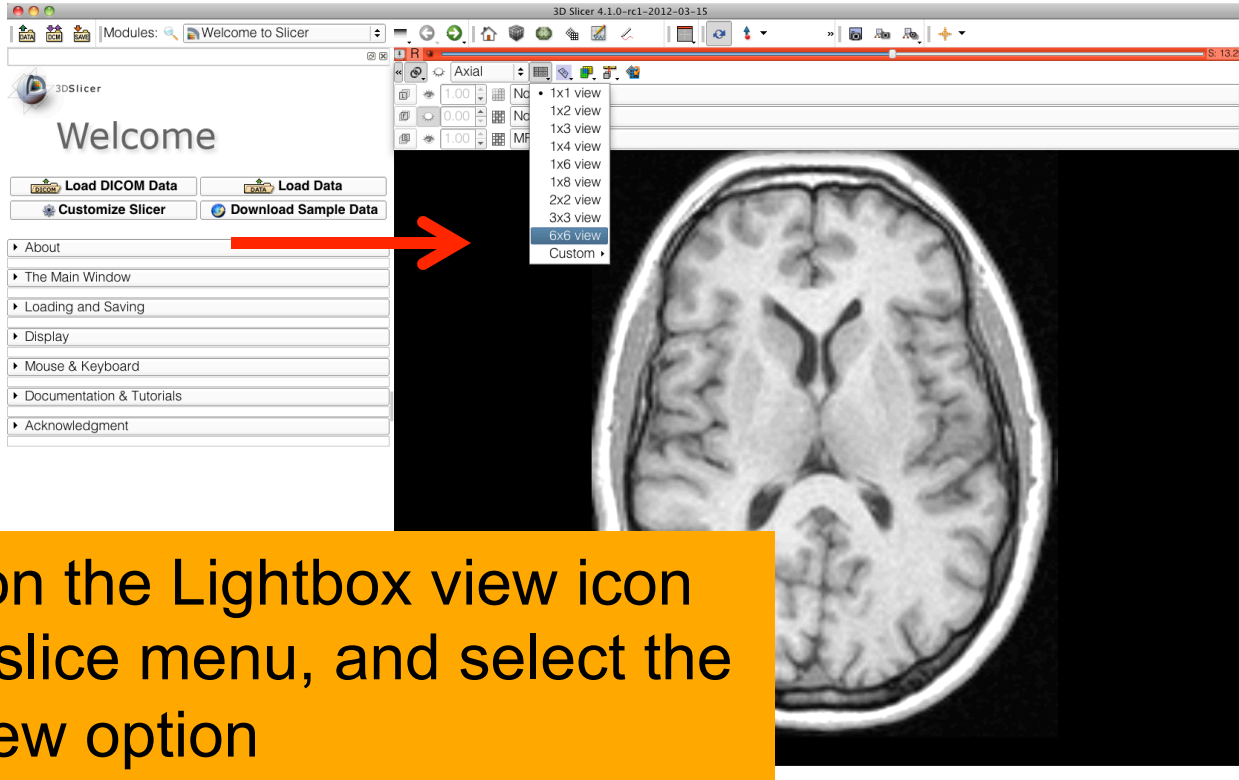


# Loading a volume





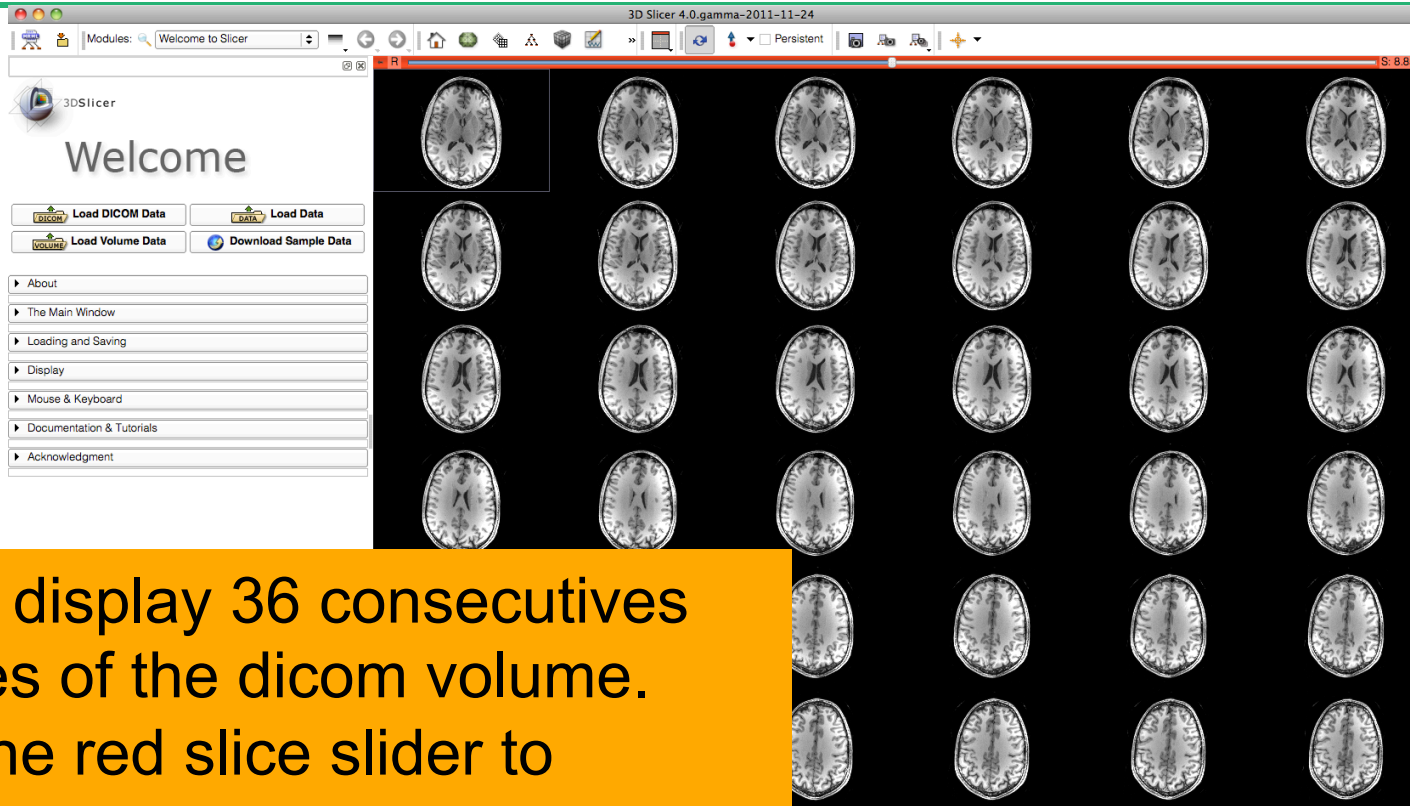
# Loading a volume



Click on the Lightbox view icon in the slice menu, and select the 6x6 view option



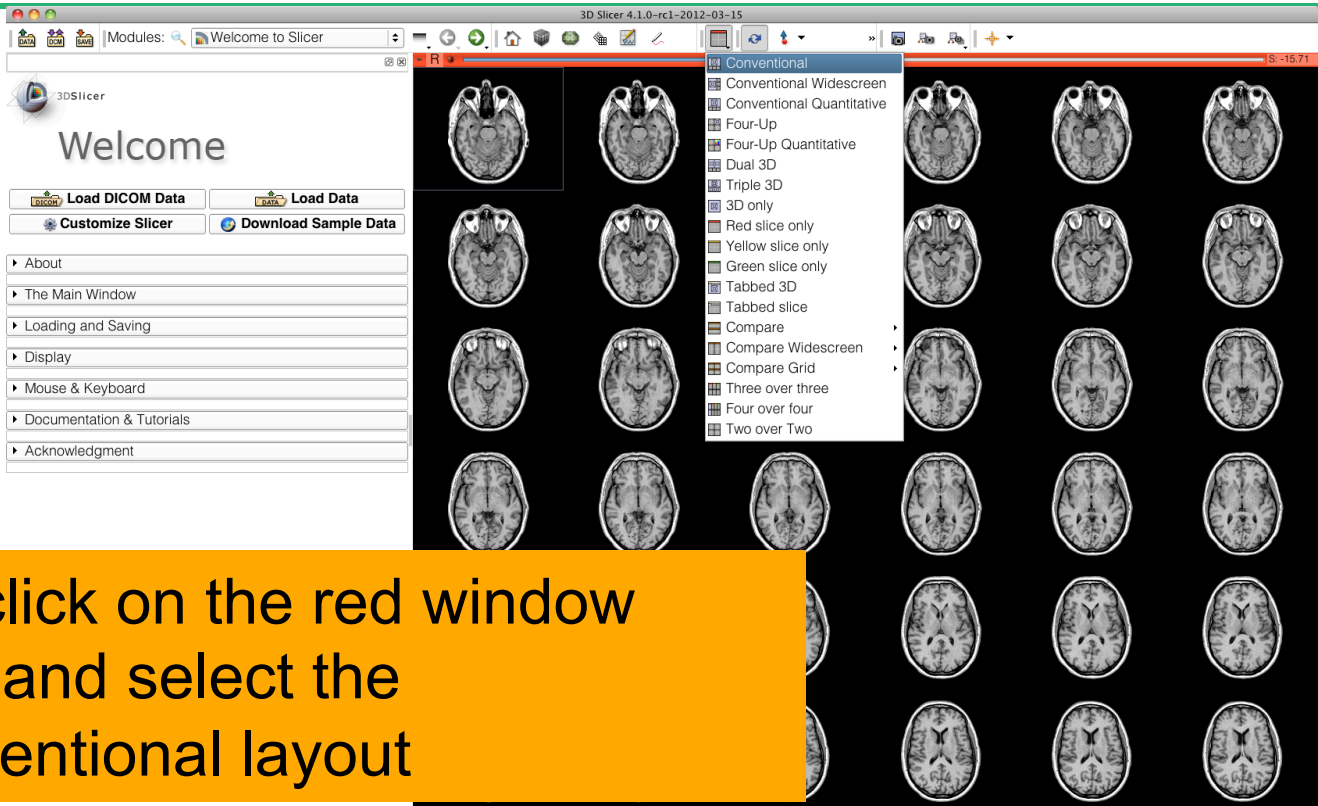
# Loading a volume



Slicer display 36 consecutives images of the dicom volume.  
Use the red slice slider to browse through the data



# Loading a volume



Left click on the red window icon, and select the Conventional layout

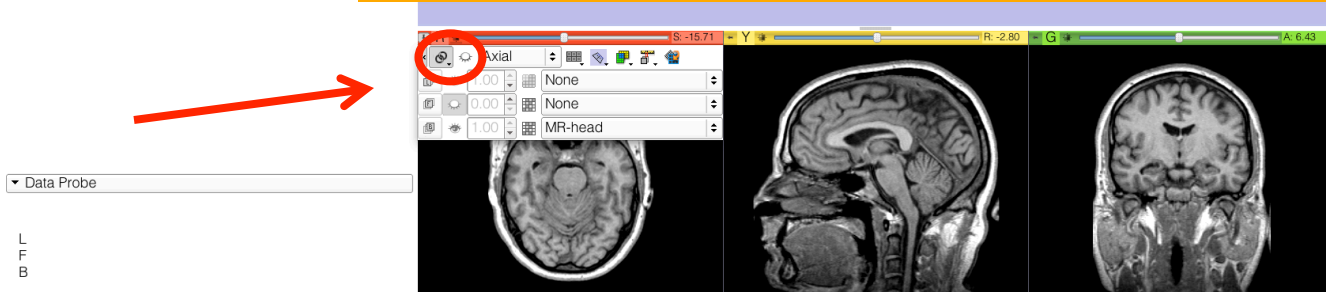
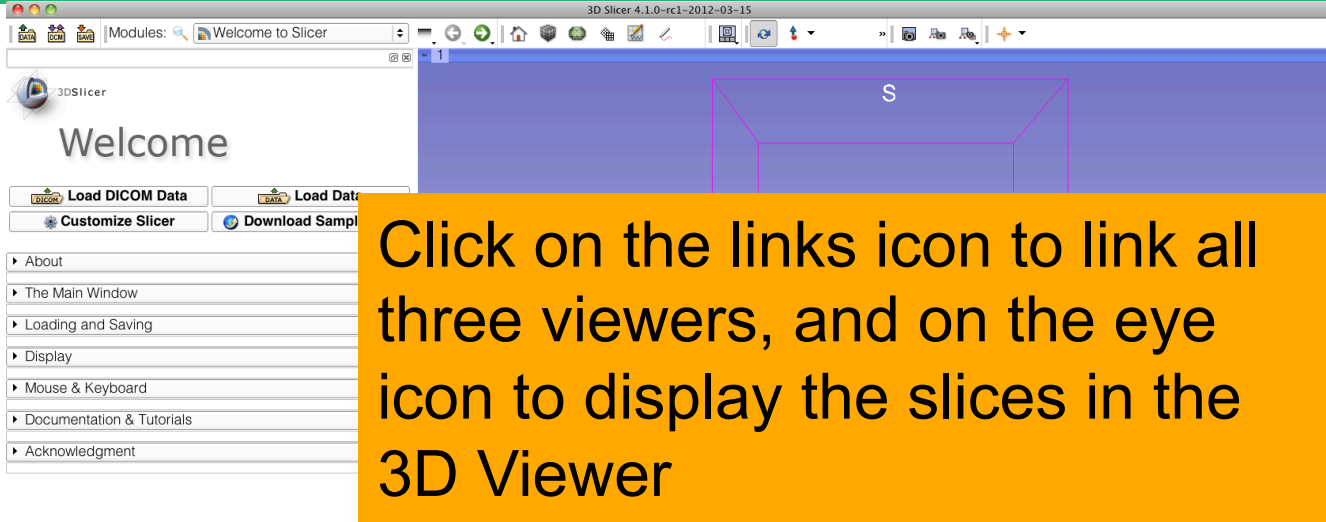


# Loading a volume

The screenshot shows the 3D Slicer software interface. On the left is a sidebar with a 'Welcome' message and several buttons: 'Load DICOM Data', 'Load Data', 'Customize Slicer', and 'Download Sample Data'. Below these are expandable menu items: 'About', 'The Main Window', 'Loading and Saving', 'Display', 'Mouse & Keyboard', 'Documentation & Tutorials', and 'Acknowledgment'. At the bottom left, there is a 'Data Probe' dropdown menu and 'L', 'F', 'B' orientation indicators. The main window is currently in a 1x1 view, showing a single MRI slice. A red arrow points to the 'Lightbox' view in the bottom-left corner of the main window, which displays a grid of 20 small MRI slices. A yellow text box with black text is overlaid on the main window, reading: 'Select the lightbox viewer in the red slice menu, and come back to 1x1 view'. The top of the window shows a standard Windows taskbar with various icons and the text 'Modules: Welcome to Slicer'.



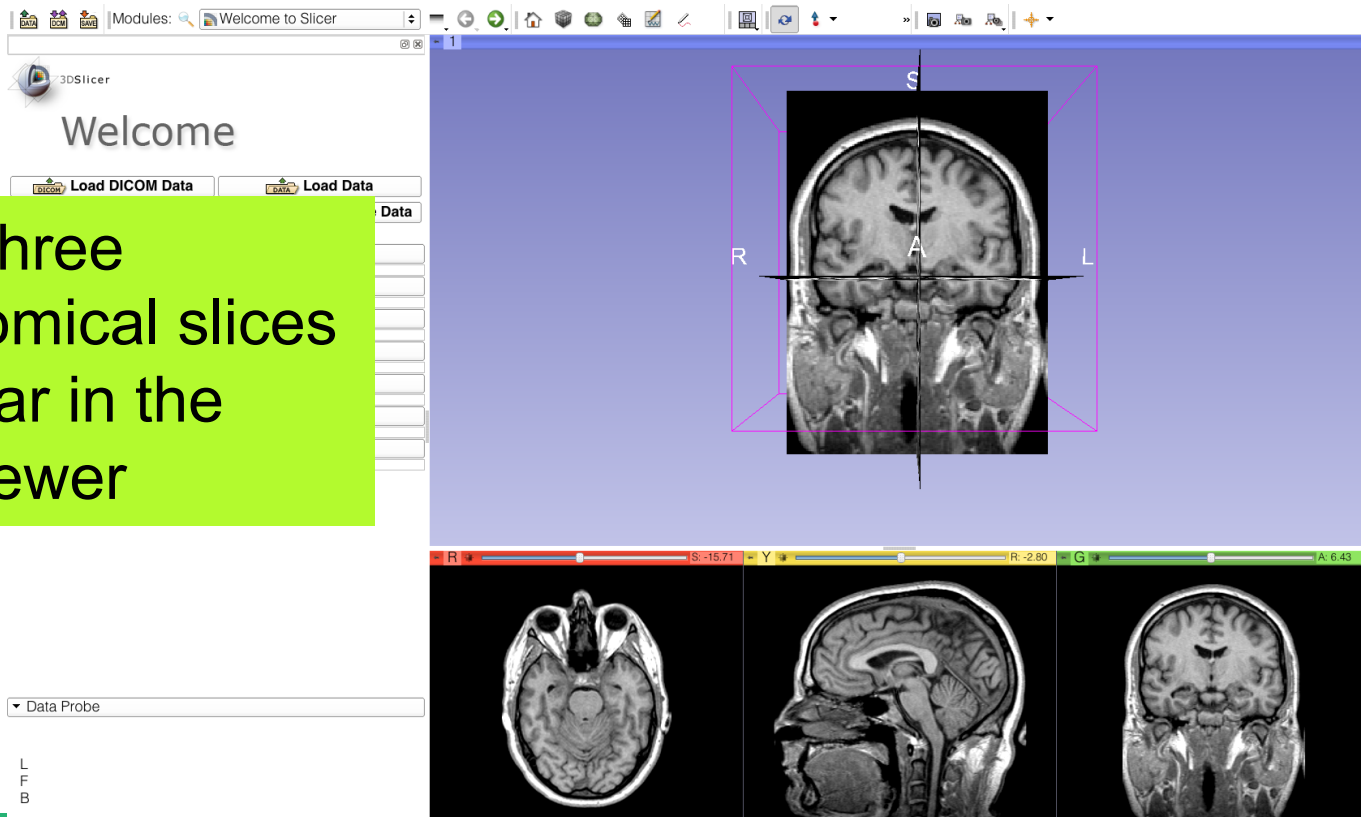
# Loading a volume





# Loading a volume

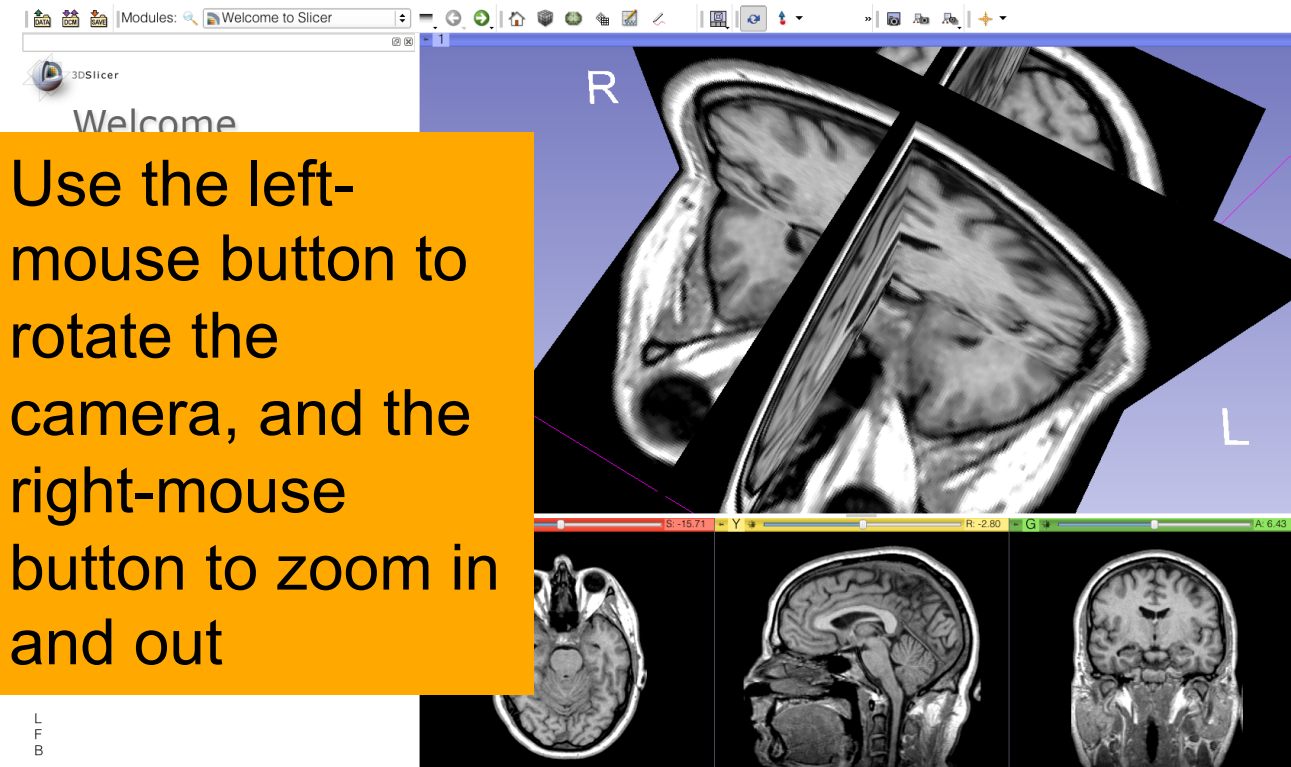
The three anatomical slices appear in the 3DViewer





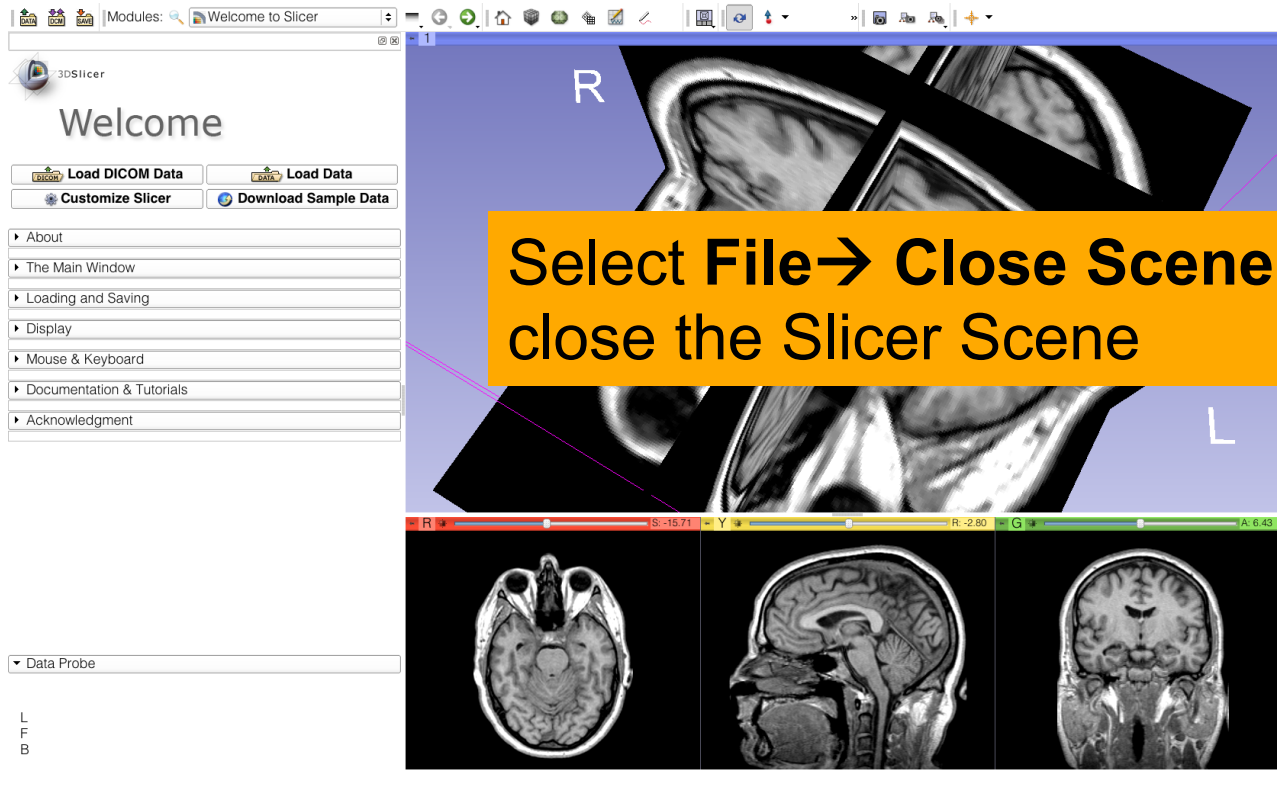


# Loading a DICOM volume



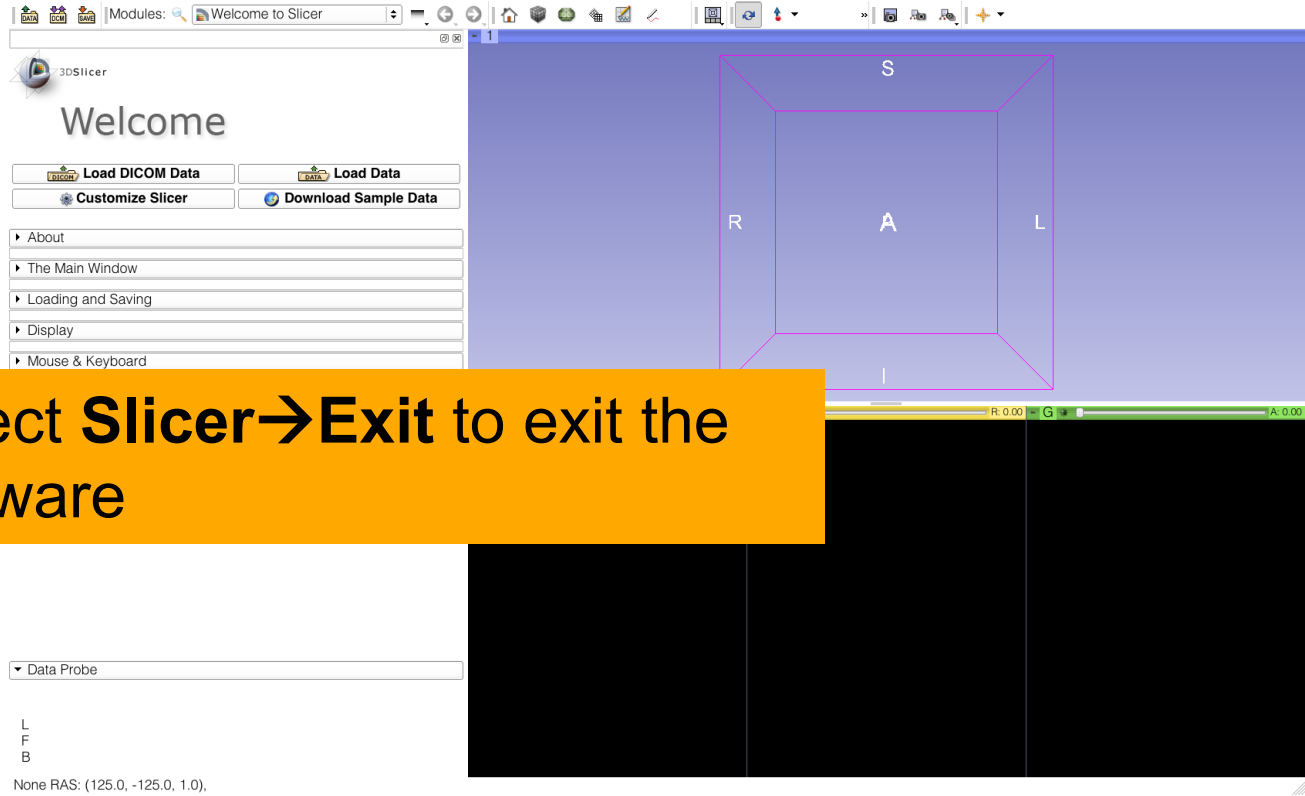


# Close the scene





# Exit Slicer



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



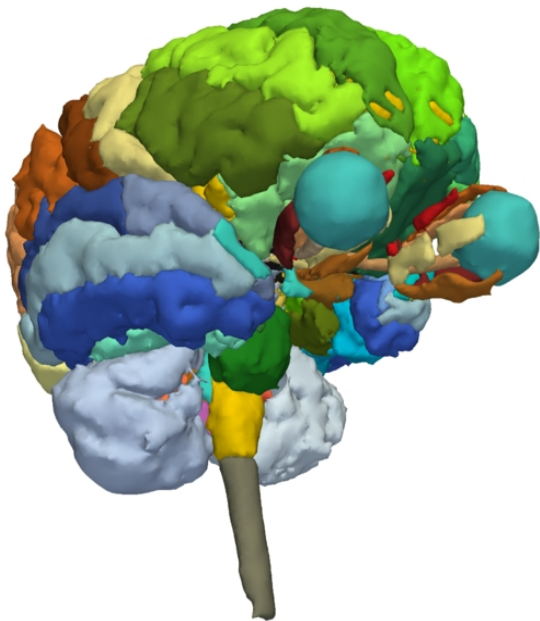
## Part 2:

3D visualization of surface models of the brain



# 3D Slicer Scene

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- A Slicer scene is a MRML file which contains a list of elements loaded into Slicer (volumes, models, fiducials...)
- The tutorial scene contains an MR scan of the brain and 3D surface models of anatomical structures.
- The tutorial data are part of the SPL-PNL Brain Atlas developed by Thalos et al.



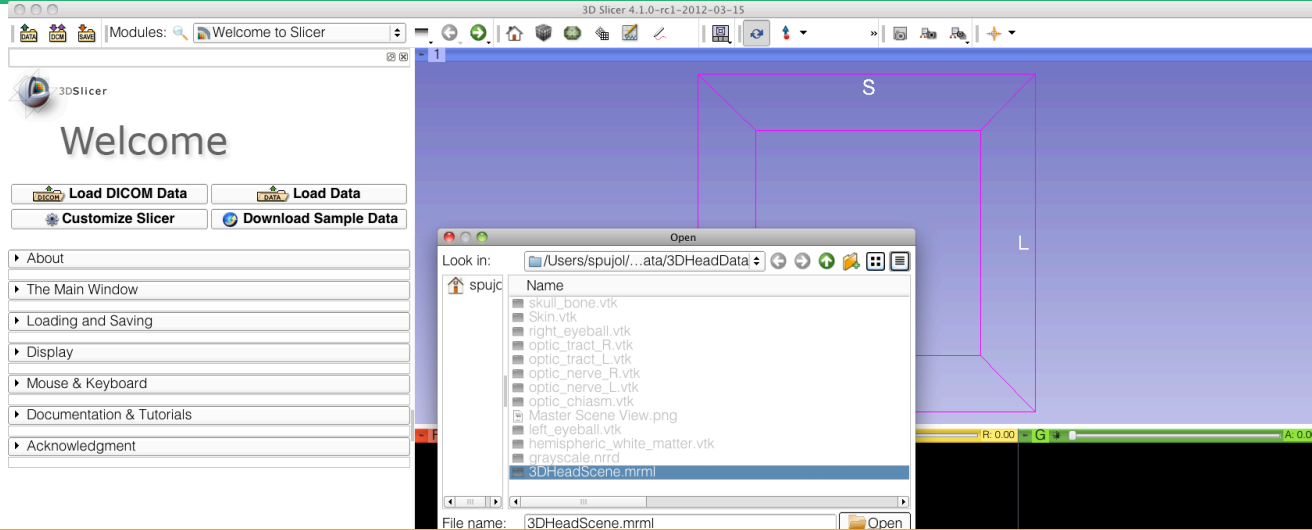
# Loading a Scene

A screenshot of the 3DSlicer software interface. The left sidebar shows the 'Welcome' screen with buttons for 'Load DICOM Data', 'Load Data', 'Customize Slicer', and 'Download Sample Data'. Below these are expandable menu items: 'About', 'The Main Window', 'Loading and Saving', 'Display', 'Mouse &amp; Keyboard', 'Documentation &amp; Tutorials', and 'Acknowledgment'. At the bottom of the sidebar, there is a 'Data Probe' dropdown menu and a coordinate system showing 'None RAS: (125.0, -125.0, 1.0)'. The main 3D view area is a blue cube with axes labeled 'S' (Superior), 'R' (Right), 'A' (Anterior), 'L' (Left), and 'I' (Inferior). A yellow text box is overlaid on the bottom right of the 3D view, containing the instruction: 'Select File → Load Scene from the main menu'. The top of the window shows a standard Windows-style menu bar with 'Modules' and a search bar.

**Select File → Load Scene  
from the main menu**



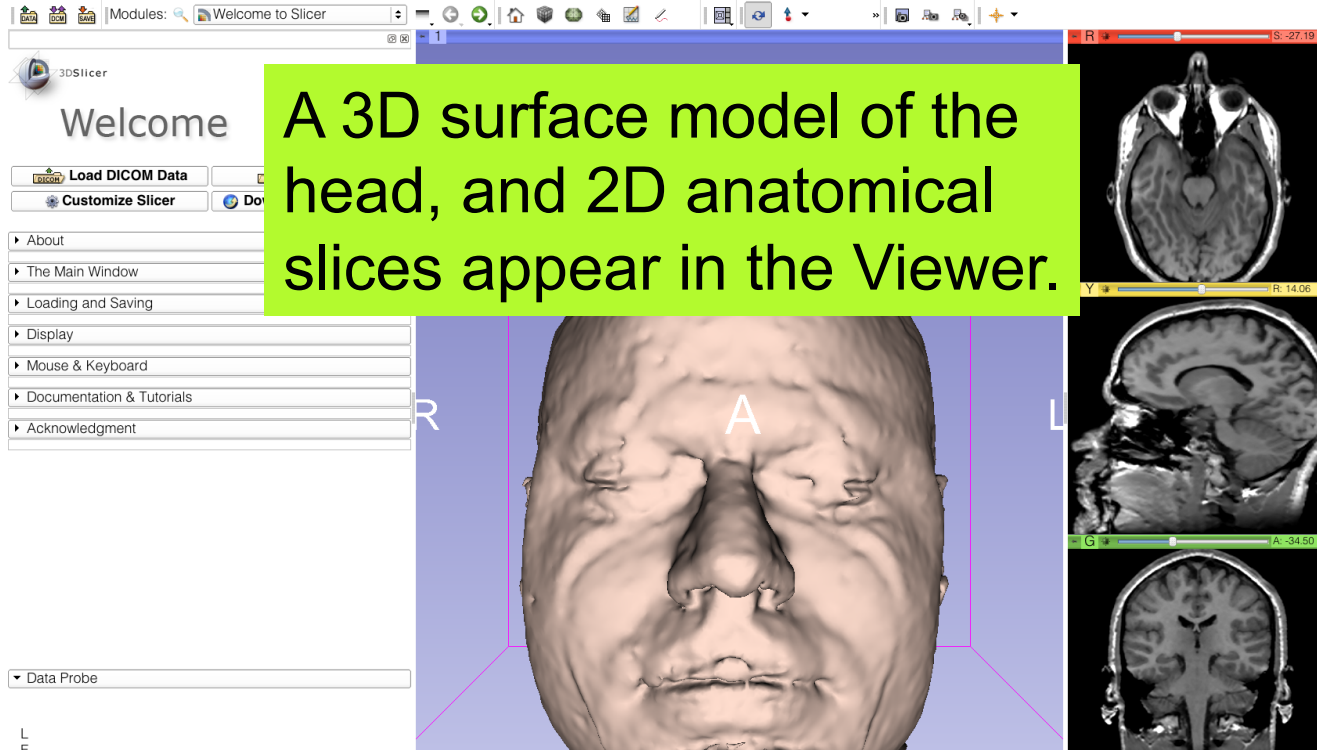
# Loading a Scene



Browse to the directory **3DHeadData**, located in the **3DVisualizationData** directory, select the file **3DHeadScene.mrml** and click on **Open**



# Loading the Slicer Scene

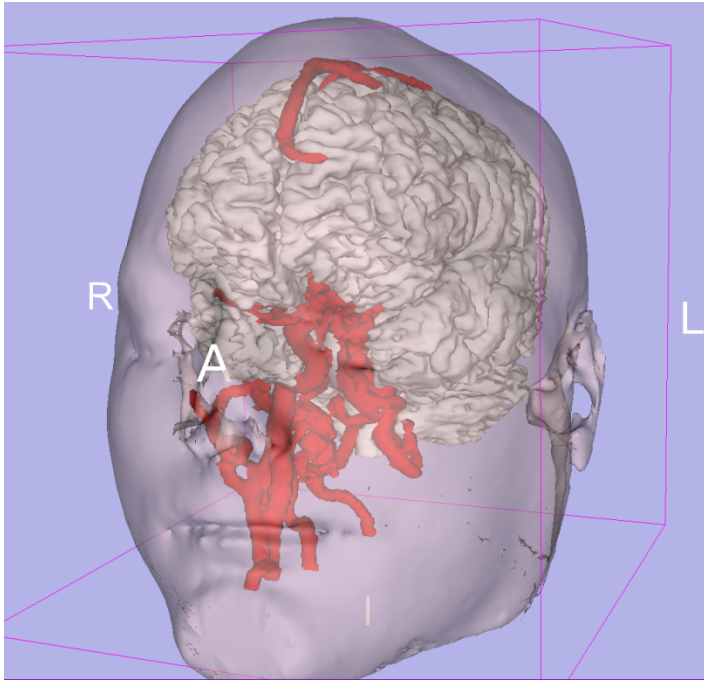






# 3D Surface Models

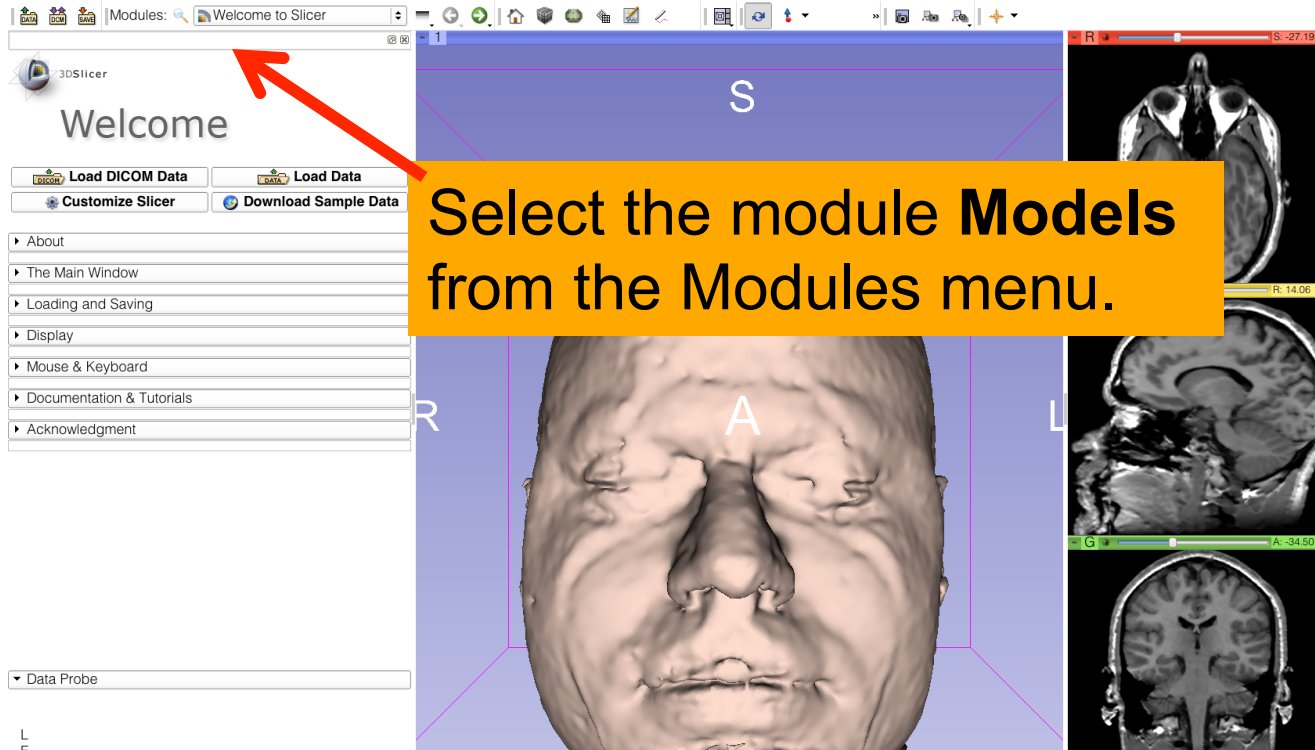
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- A **3D model** is a surface reconstruction of an anatomical structure.
- The model is a **triangular mesh** that approximates a surface from a 3D label map.
- The scalar values for surface models are integers which correspond to the **label** that had been assigned in the segmentation process.



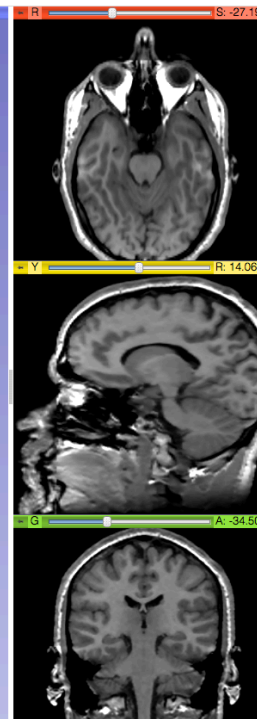
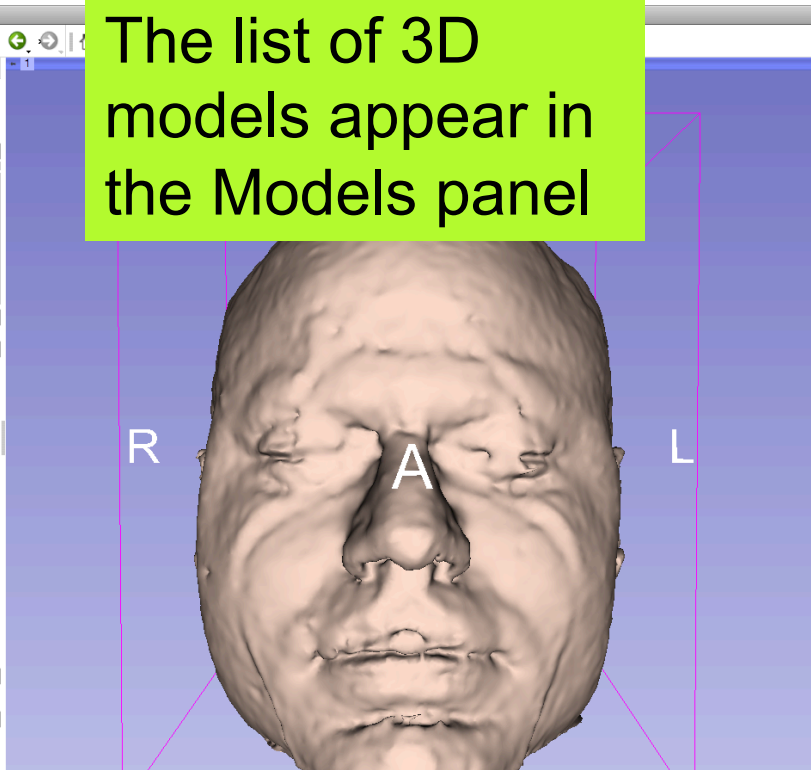
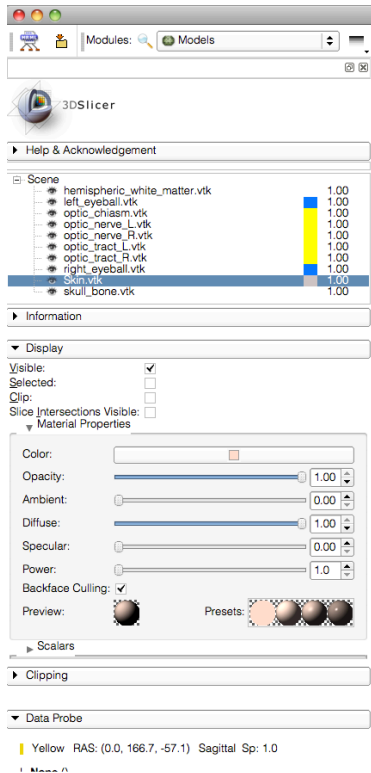
# Loading the Slicer Scene





# Models module

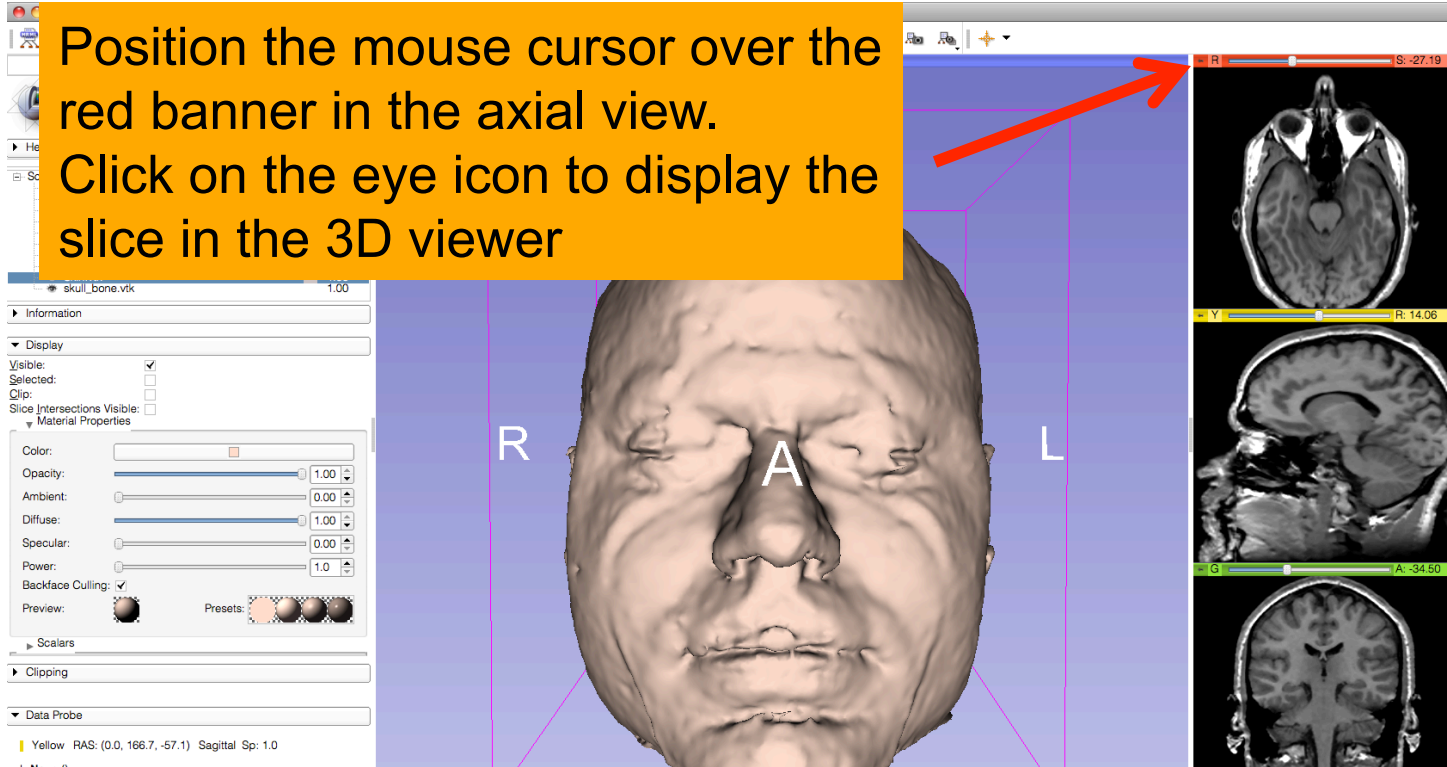
The list of 3D models appear in the Models panel





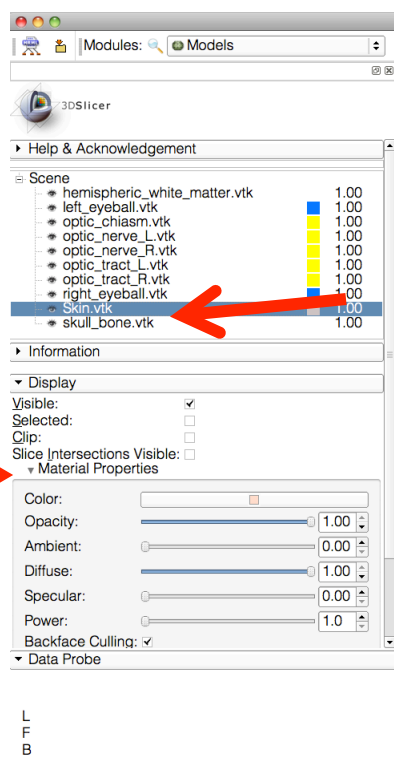
# 3D Visualization

Position the mouse cursor over the red banner in the axial view.  
Click on the eye icon to display the slice in the 3D viewer

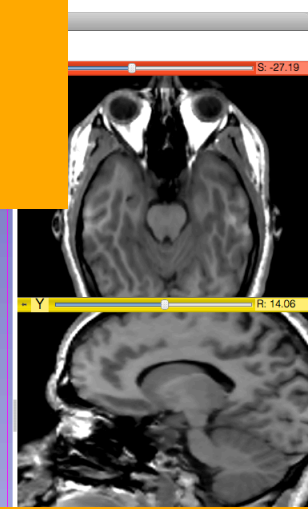
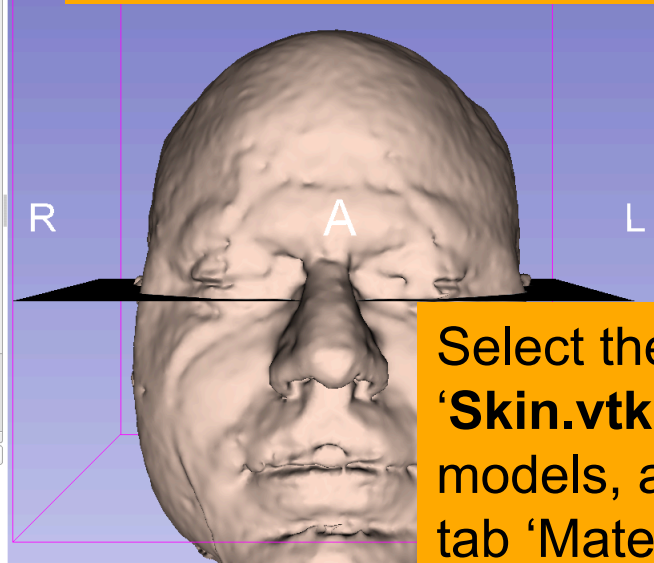




# 3D Visualization



Slice through the 3D model of the head using the axial slider

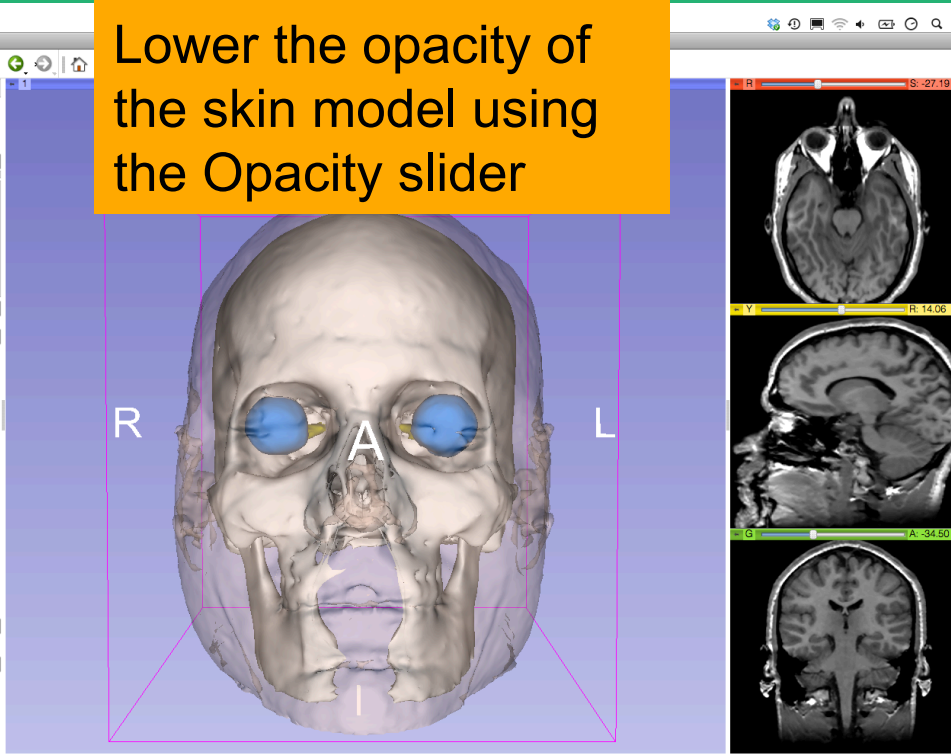
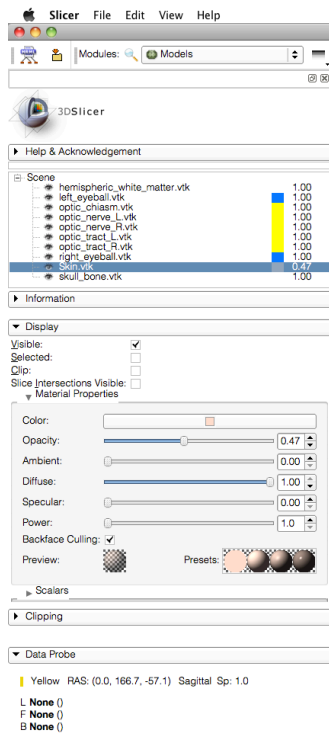


Select the model 'Skin.vtk' in the list of models, and expand the tab 'Material Properties' under 'Display'



# 3D Visualization

Lower the opacity of the skin model using the Opacity slider





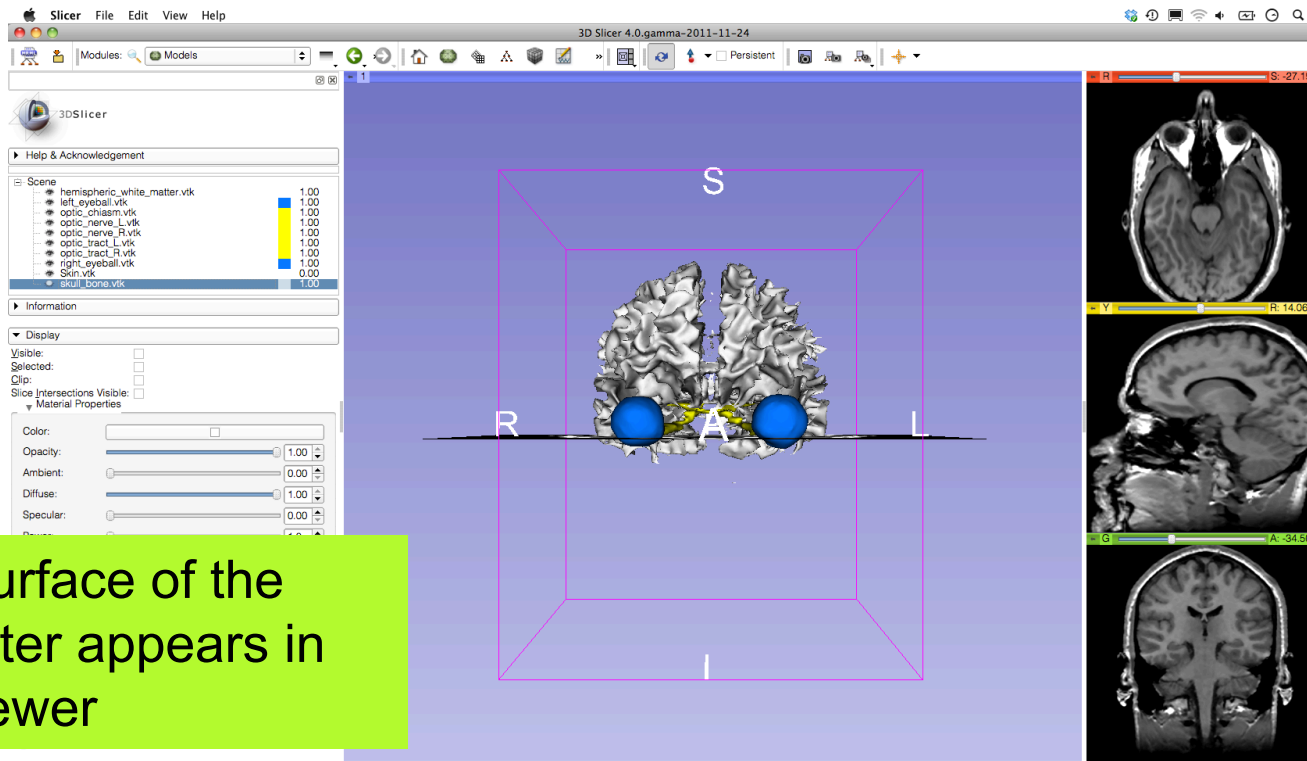
# 3D Visualization

Select the skull\_bone.vtk model, and turn off its visibility

The screenshot displays the 3D Slicer software interface. On the left, the 'Scene' panel lists several models, with 'skull\_bone.vtk' highlighted by a red arrow. Below it, the 'Information' panel shows the 'Visible' checkbox checked. The central 3D view shows a skull model with two blue spheres representing the eyes. To the right, three MRI slices are shown in axial, sagittal, and coronal views. The interface includes a 'Modules' menu at the top, a 'Help & Acknowledgement' section, and a 'Data Probe' section at the bottom left. The 3D view is labeled with 'R' (Right), 'L' (Left), and 'I' (Inferior).



# 3D Visualization

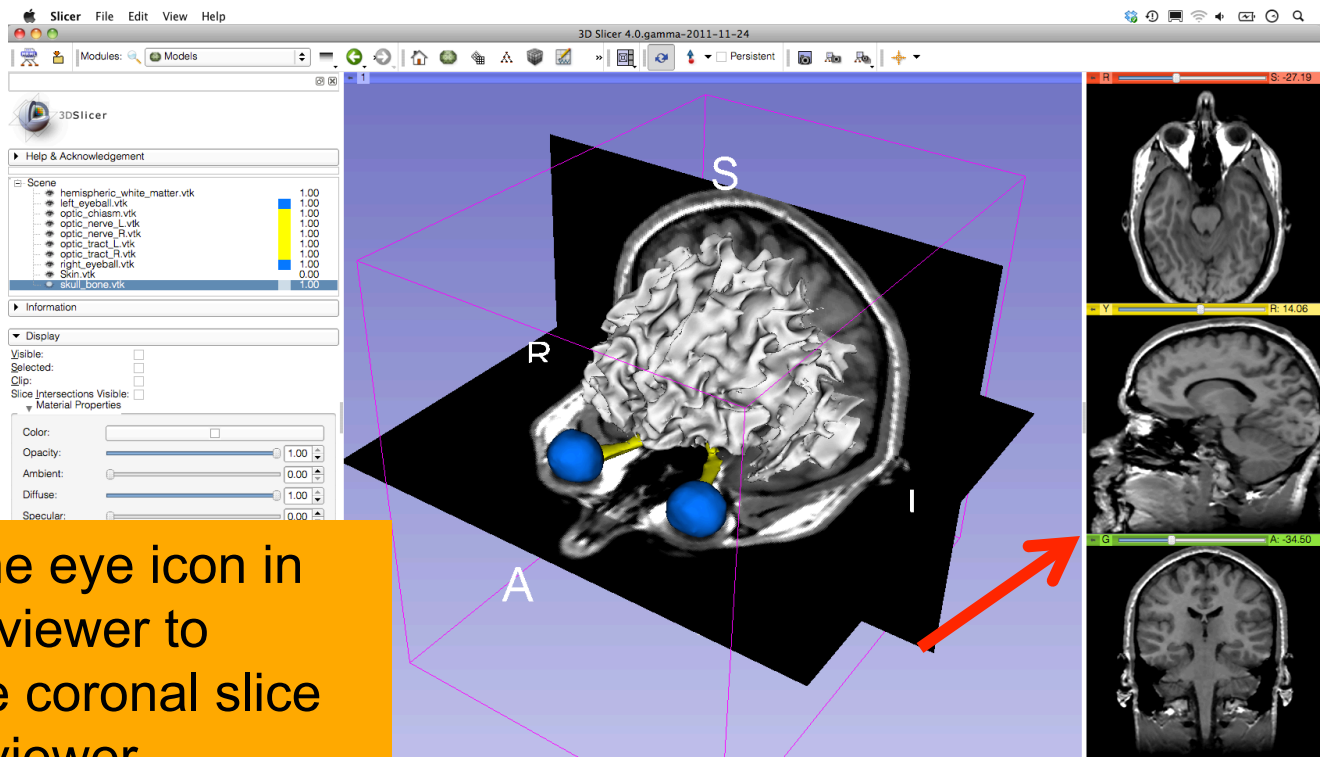


The 3D surface of the white matter appears in the 3D viewer





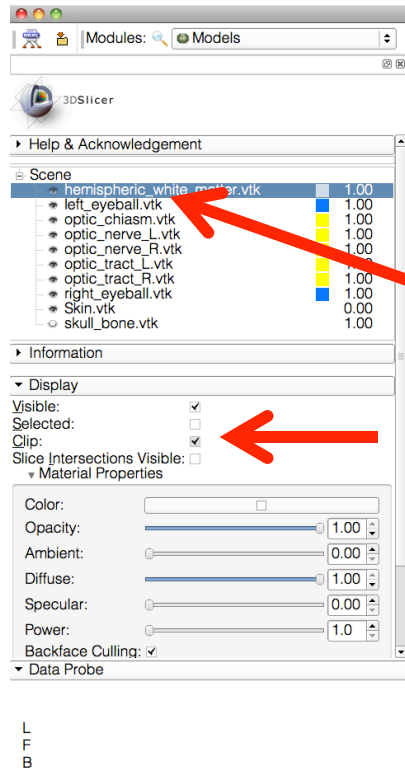
# 3D Visualization



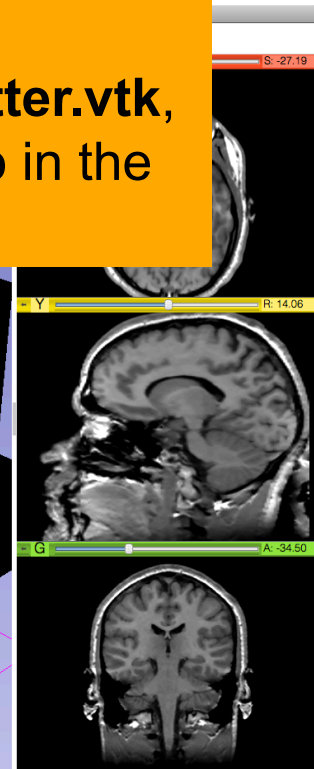
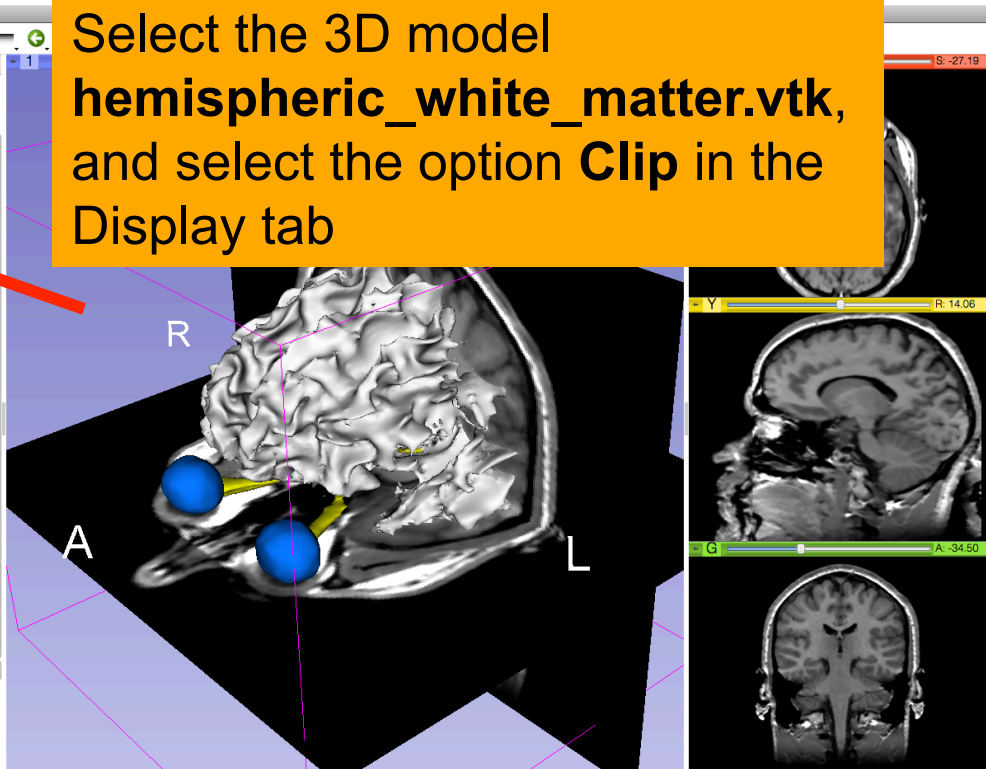
Click on the eye icon in the green viewer to display the coronal slice in the 3D viewer



# 3D Visualization



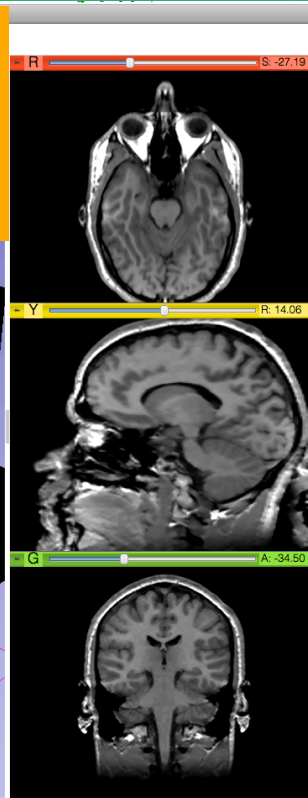
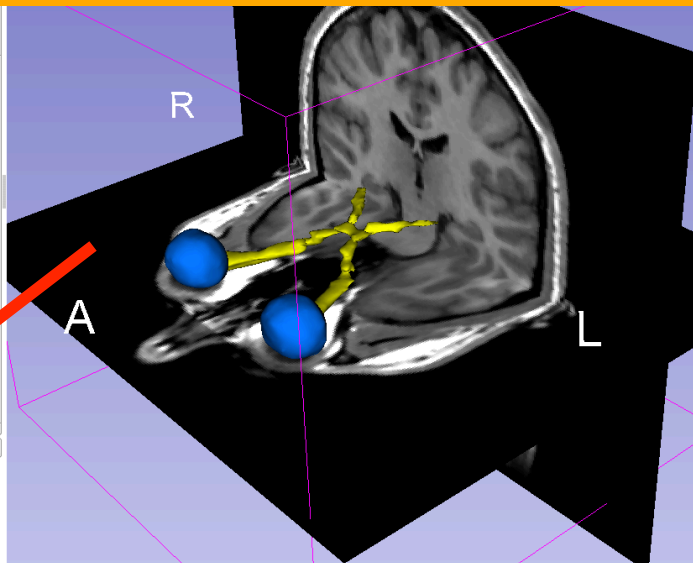
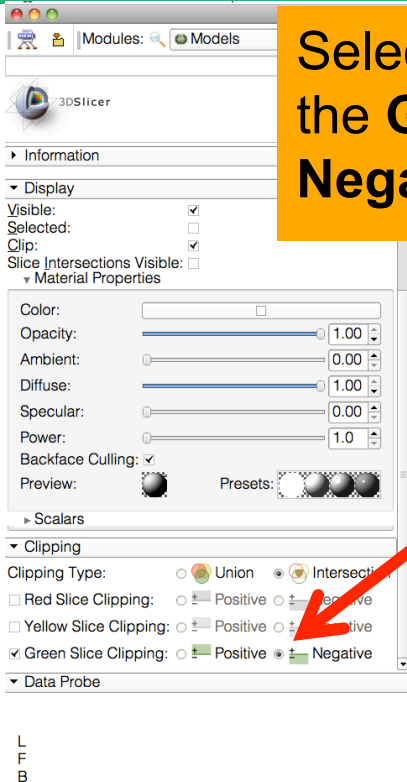
Select the 3D model **hemispheric\_white\_matter.vtk**, and select the option **Clip** in the Display tab





# 3D Visualization

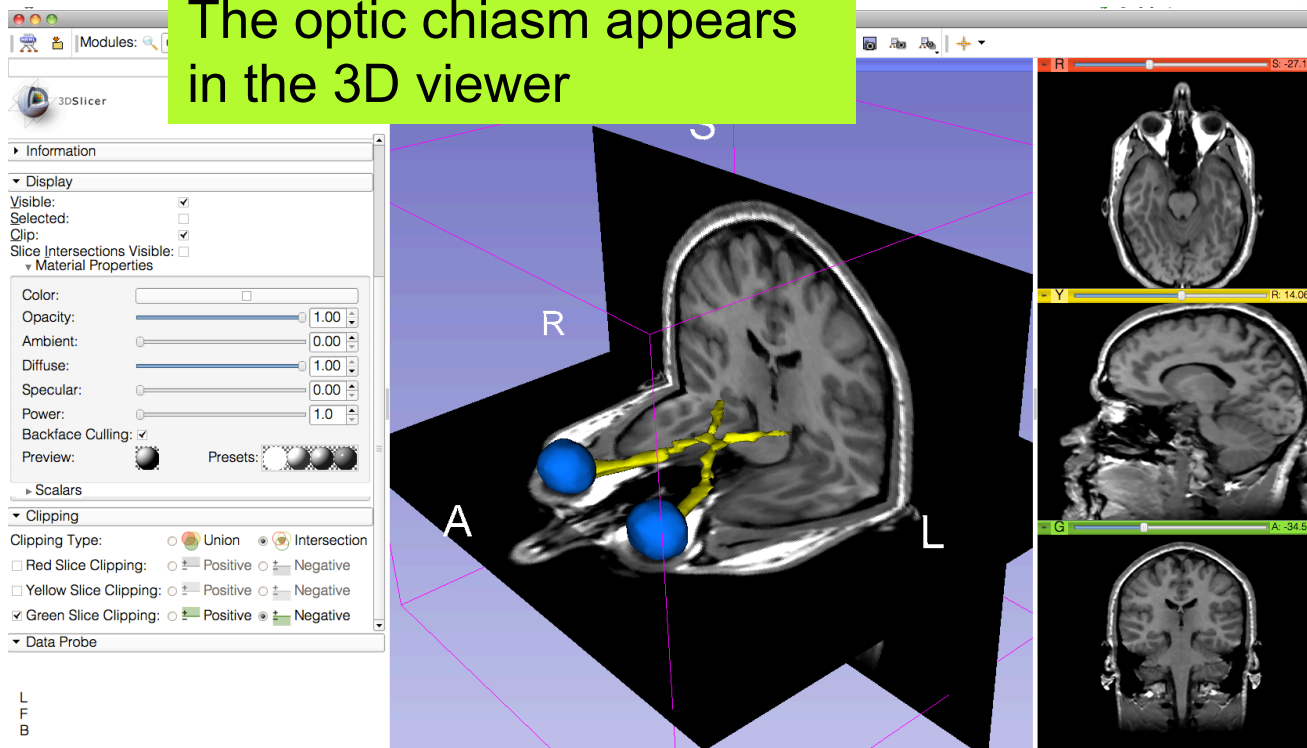
Select the tab Clipping, and set the **Green Slice Clipping** to **Negative Space**





# 3D Visualization

The optic chiasm appears in the 3D viewer





# 3D Visualization

The screenshot shows the 3D Slicer software interface. On the left, the 'Scene' panel lists several models, including 'hemispheric\_white'. Below it, the 'Information' panel is expanded to the 'Display' section. In this section, the 'Clip' checkbox is checked, and the 'Opacity' slider is set to 0.42. A red arrow points from the text box to this 'Clip' checkbox. The 'Clipping' section at the bottom shows 'Clipping Type' set to 'Intersection'. The main 3D view shows a brain model with blue eyes and a yellow crosshair. To the right, three orthogonal slice views (axial, sagittal, and coronal) are displayed. An orange text box is overlaid on the top part of the interface.

Uncheck the option clipping and lower the opacity of the White Matter surface



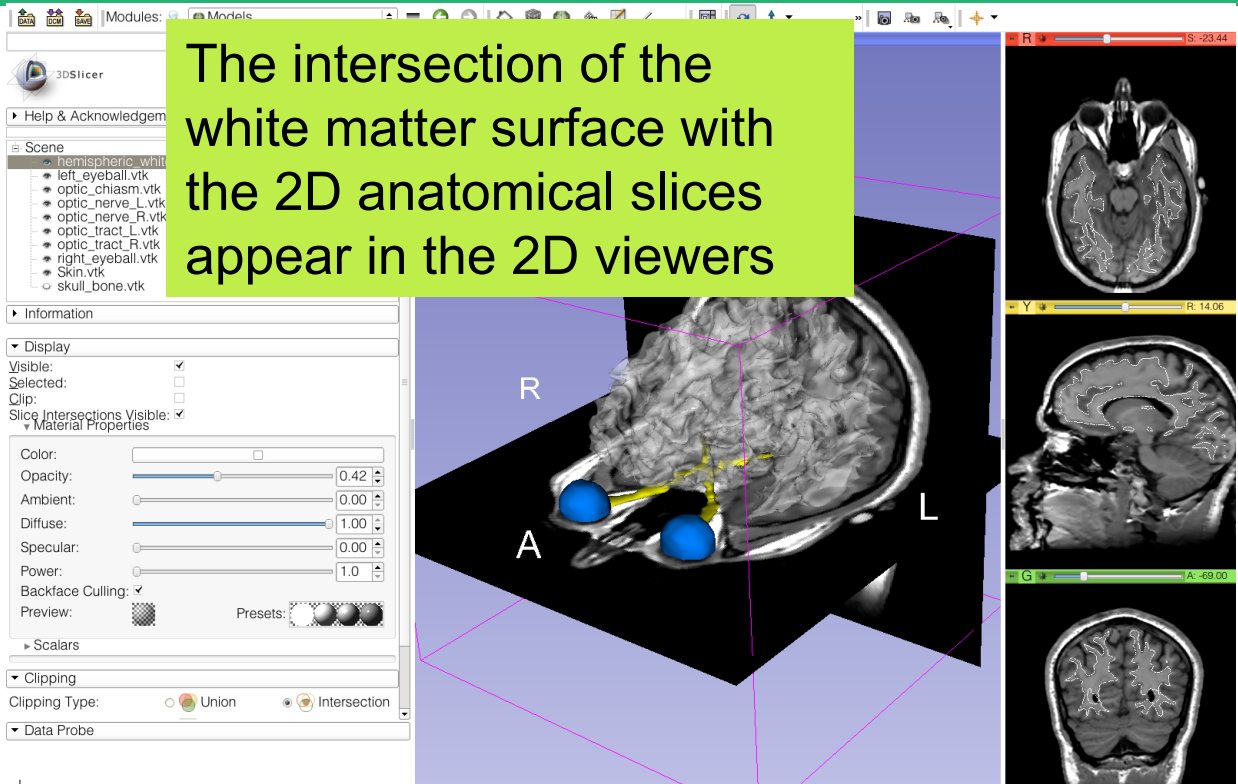
# 3D Visualization

The screenshot shows the 3D Slicer software interface. On the left, the 'Scene' panel lists several models, including 'hemispheric\_white'. Below it, the 'Information' panel is expanded to show 'Display' properties. A red arrow points to the 'Clip' checkbox, which is currently checked. The 'Opacity' slider is set to 0.42. To the right, a large 3D view shows a brain model with blue eyes and a yellow crosshair. The 'Clipping' panel at the bottom shows 'Clipping Type' set to 'Intersection'. On the far right, three axial, sagittal, and coronal slice views of the brain are displayed.

Uncheck the option clipping and lower the opacity of the White Matter surface



# 3D Visualization





# 3D Visualization

Select Conventional Layout from the layout manager, and turn off the visibility of the coronal slice in the green viewer.

The screenshot shows the 3D Slicer software interface. The main window displays a 3D model of a human head with a brain slice highlighted in yellow. The model is labeled with 'R' (Right), 'L' (Left), and 'A' (Anterior). To the right of the main view are three smaller views: an axial slice (top, labeled 'R'), a sagittal slice (middle, labeled 'Y'), and a coronal slice (bottom, labeled 'G'). The coronal slice is highlighted with a green border. The interface includes a scene list on the left, a display properties panel on the left, and a clipping panel at the bottom.

**Scene List:**

- hemispheric\_whit
- left\_eyeball.vtk
- optic\_chiasm.vtk
- optic\_nerve\_L.vtk
- optic\_nerve\_R.vtk
- optic\_tract\_L.vtk
- optic\_tract\_R.vtk
- right\_eyeball.vtk
- Skin.vtk
- skull\_bone.vtk

**Display Properties:**

- Visible:
- Selected:
- Clip:
- Slice Intersections Visible:
- Material Properties:
- Color:
- Opacity: 0.42
- Ambient: 0.00
- Diffuse: 1.00
- Specular: 0.00
- Power: 1.0
- Backface Culling:
- Preview:

**Clipping:**

- Clipping Type:  Union  Intersection

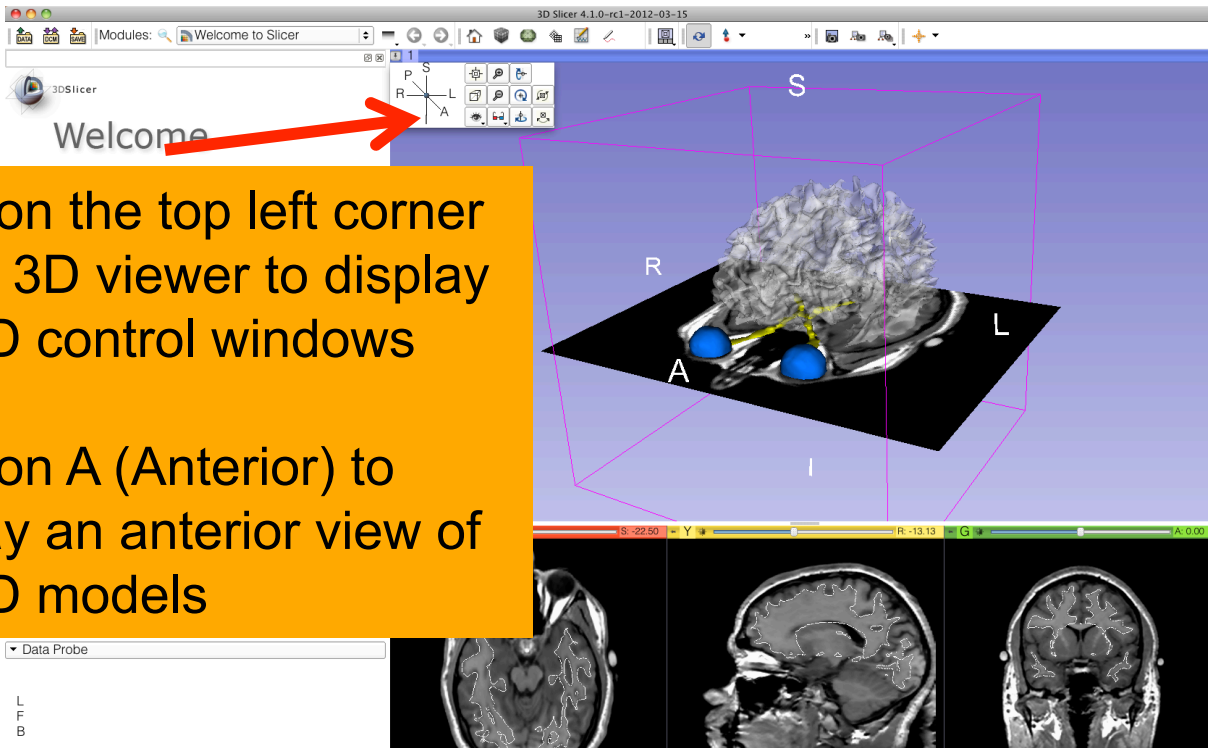
**Data Probe:**

-





# 3D Visualization

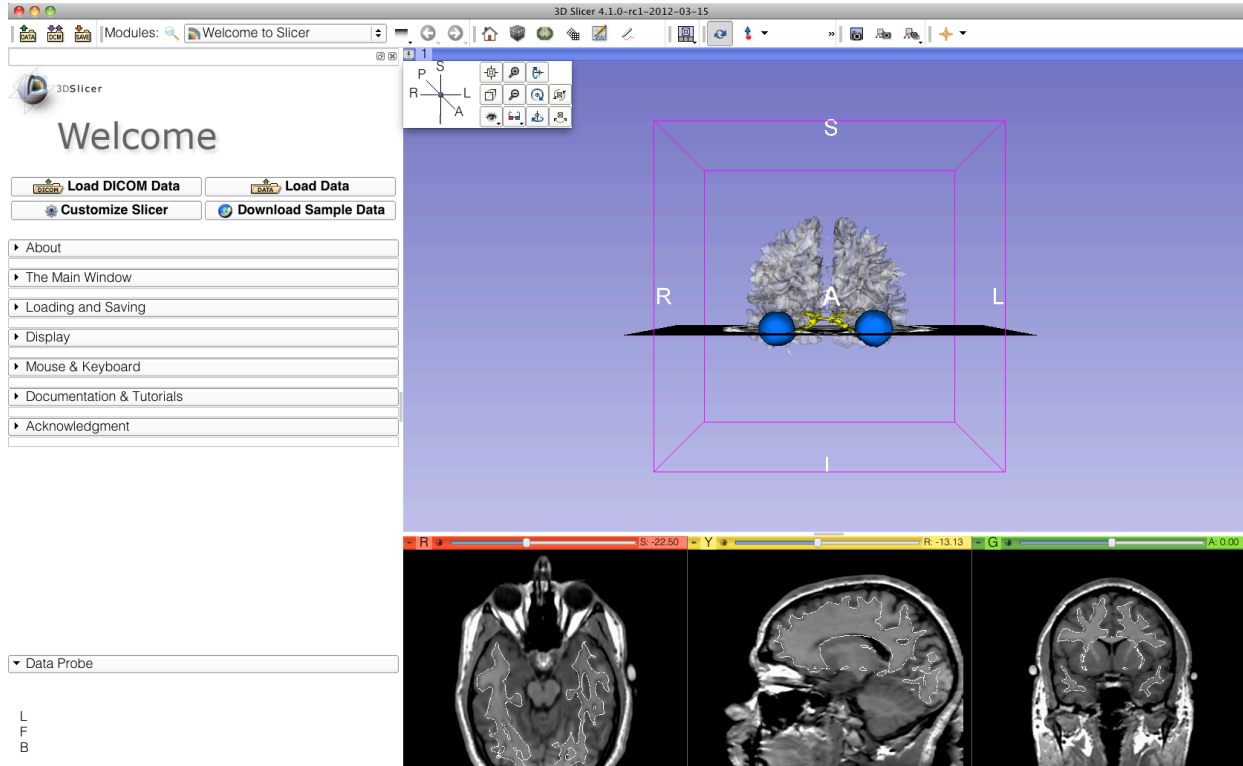


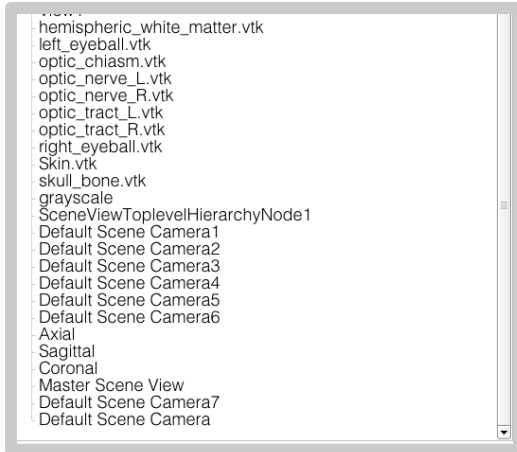
Click on the top left corner of the 3D viewer to display the 3D control windows

Click on A (Anterior) to display an anterior view of the 3D models



# 3D Visualization



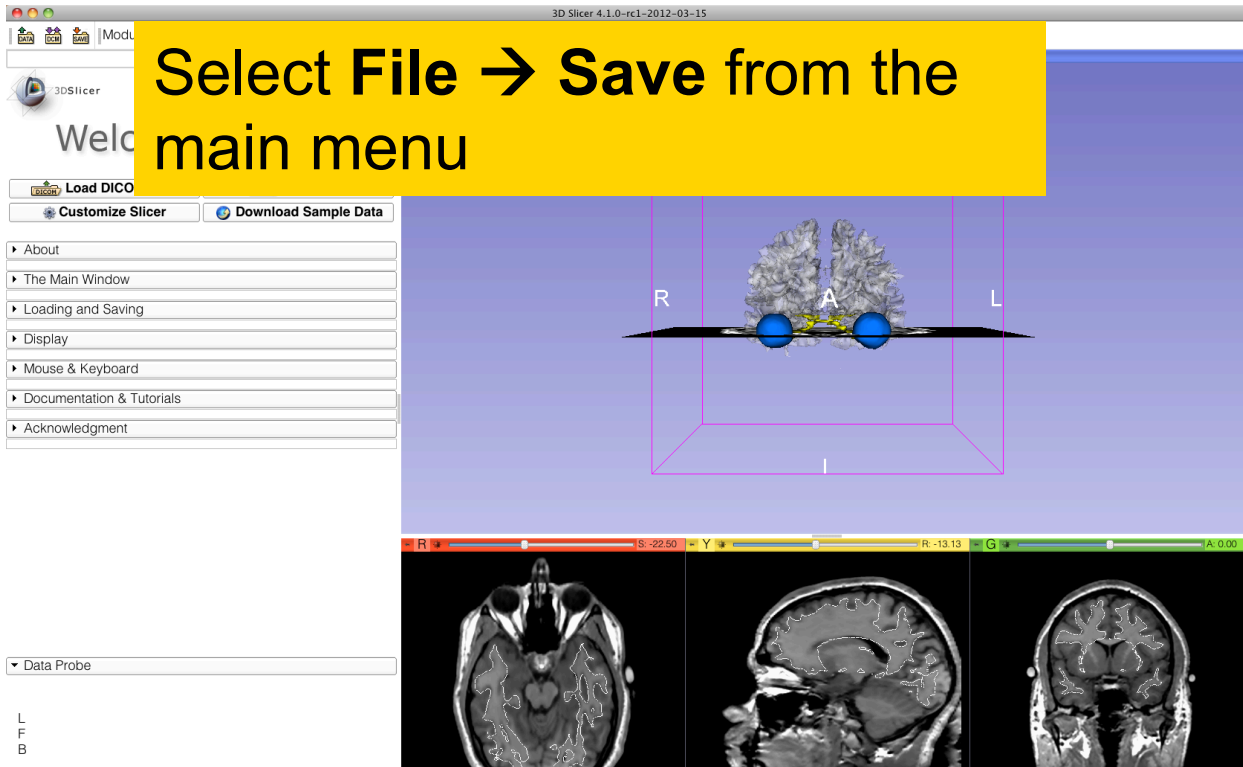


## Part 3:

# Saving a scene

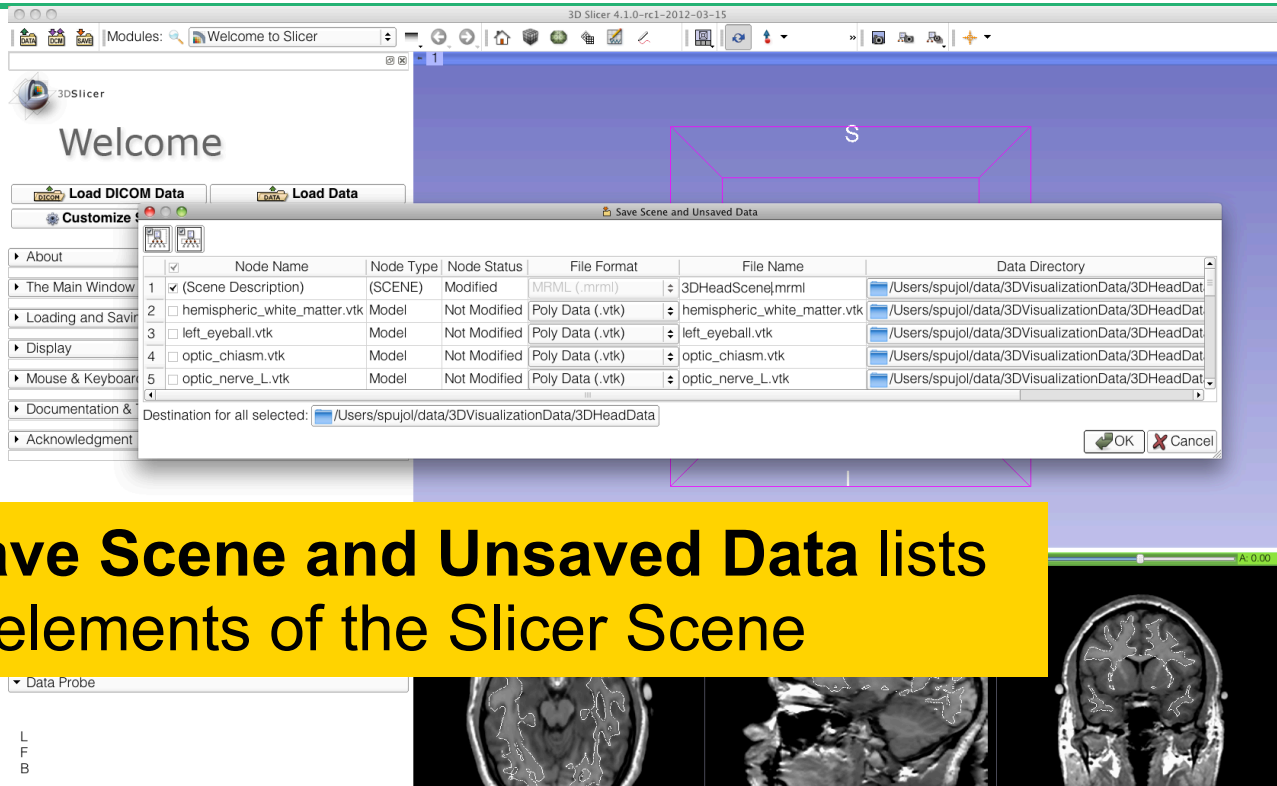


# Saving a Scene





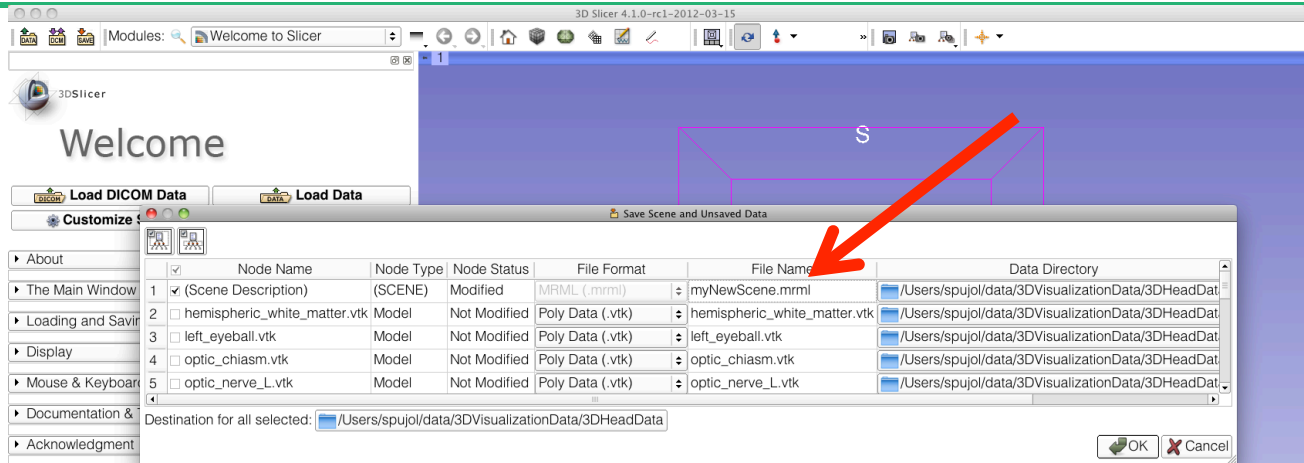
# Saving a Scene



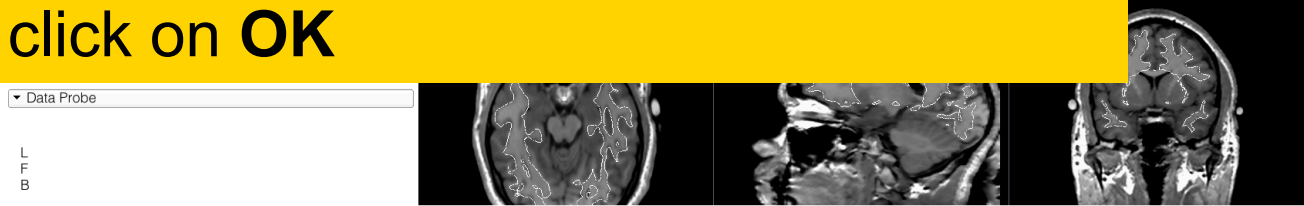
**The Save Scene and Unsaved Data lists all the elements of the Slicer Scene**



# Saving a Scene

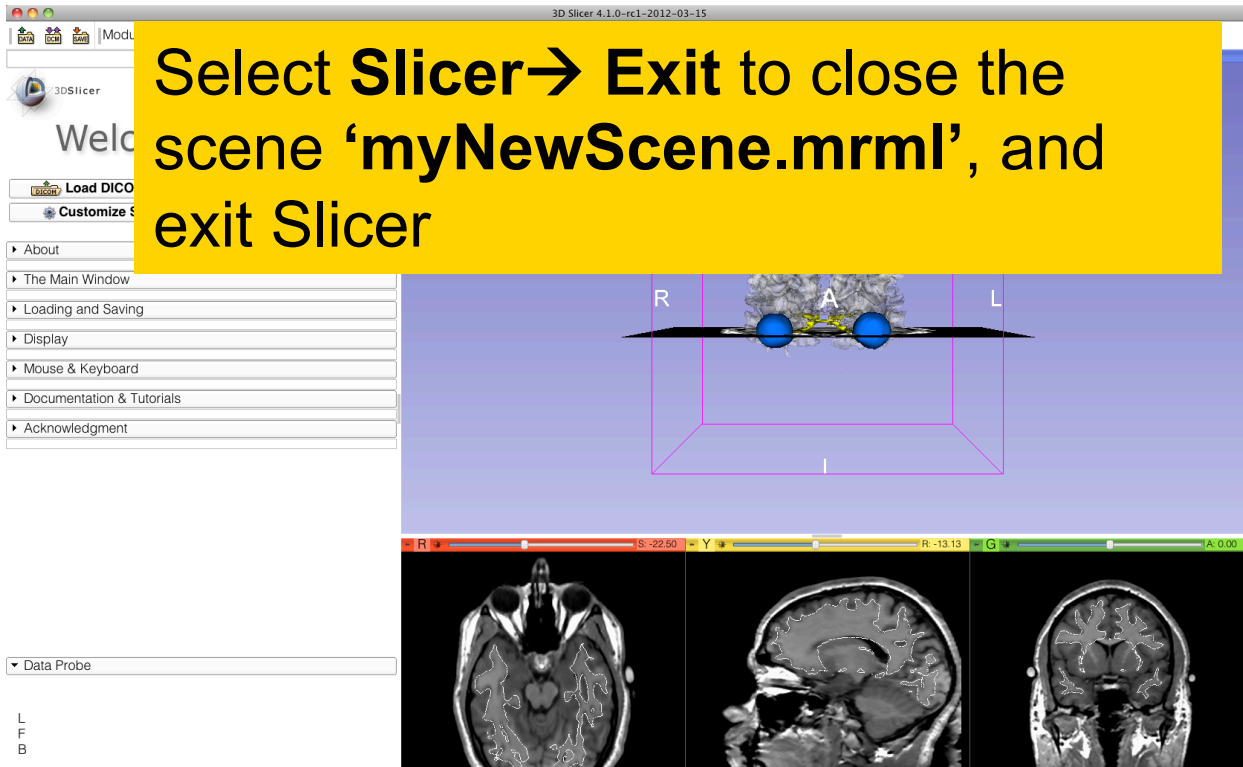


Rename the scene **myNewScene.mrml** and click on **OK**





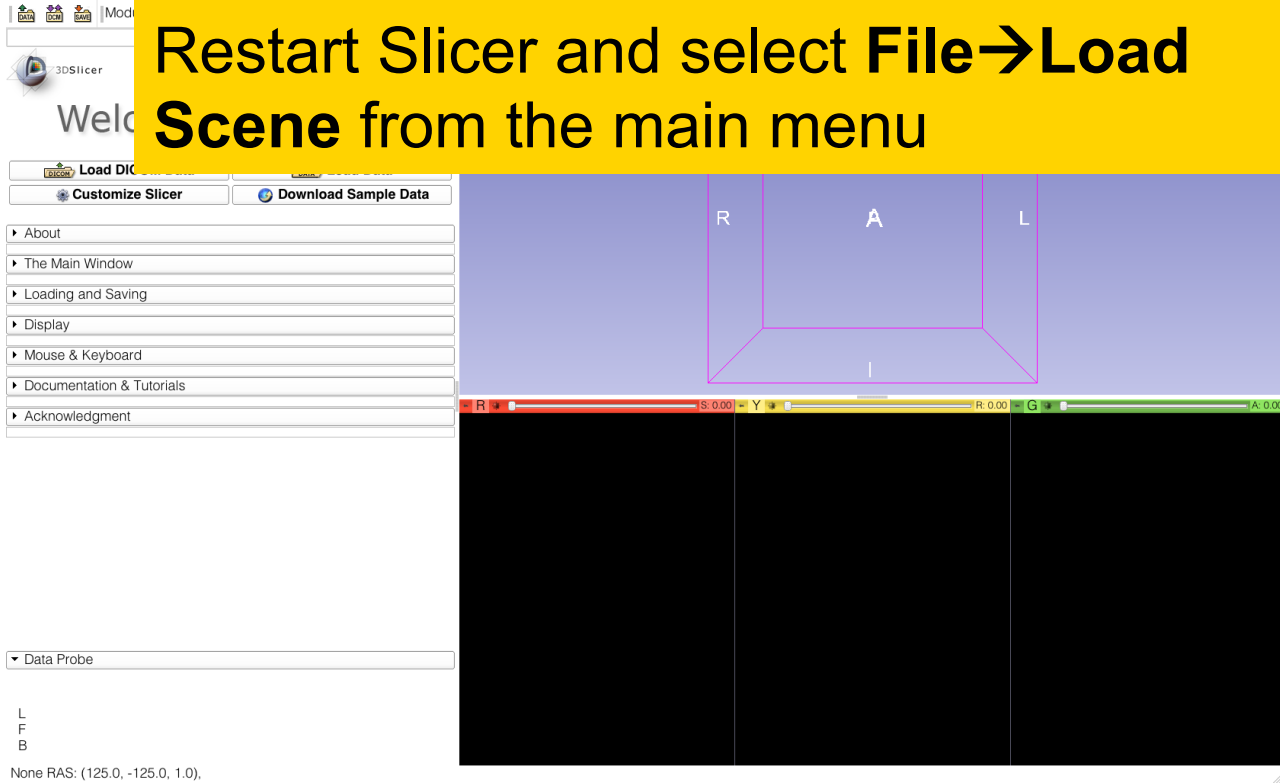
# Saving a Scene





# Scene Restore

Restart Slicer and select **File**→**Load Scene** from the main menu

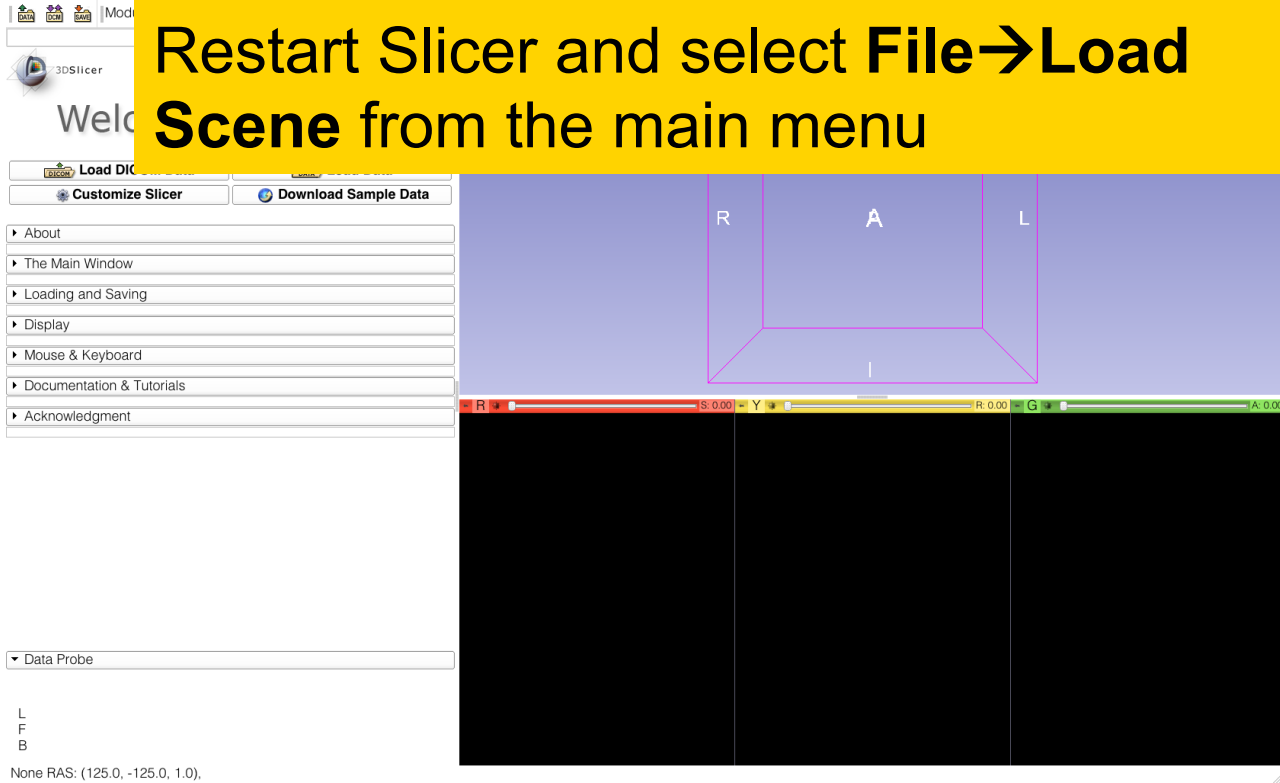






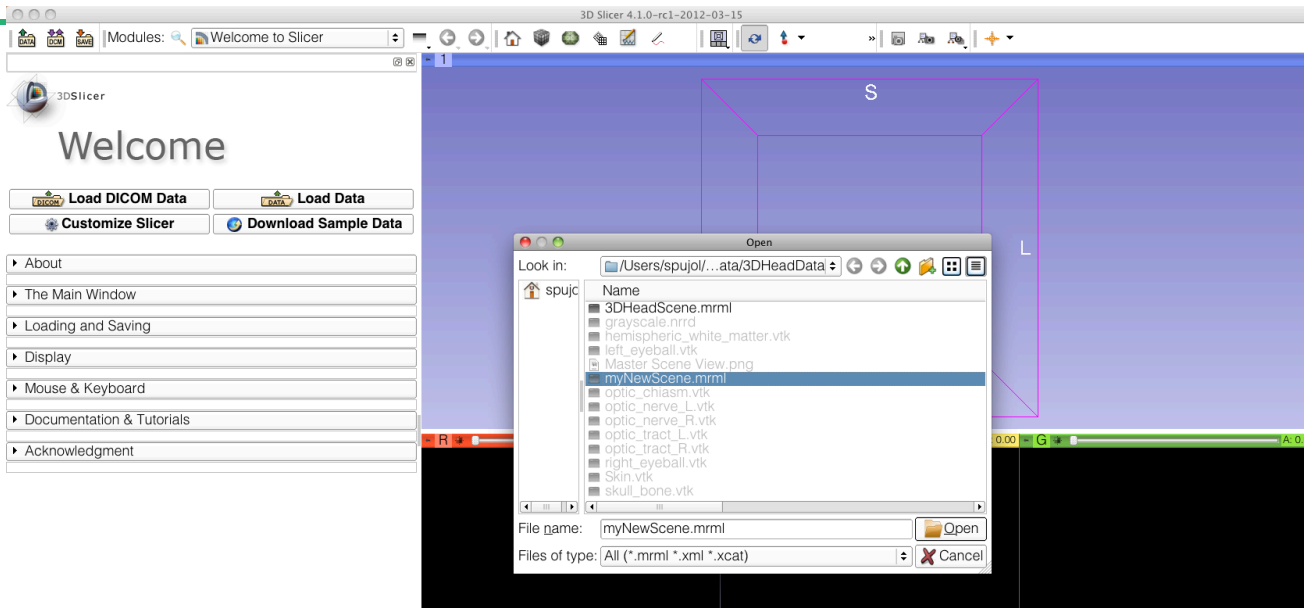
# Scene Restore

Restart Slicer and select **File**→**Load Scene** from the main menu





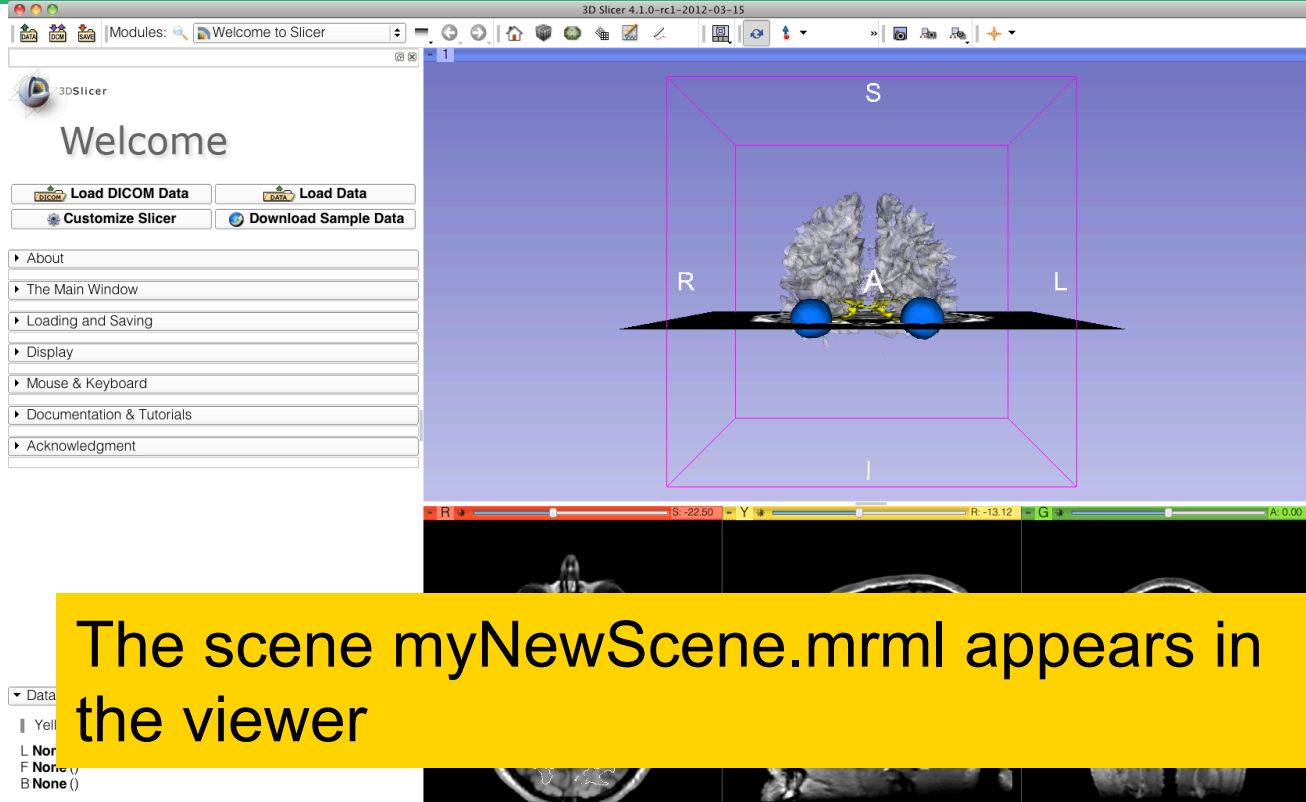
# Scene Restore



Browse to the directory where you copied the scene, select the file **myNewScene.mrml** and click on **Open**



# Scene Restore

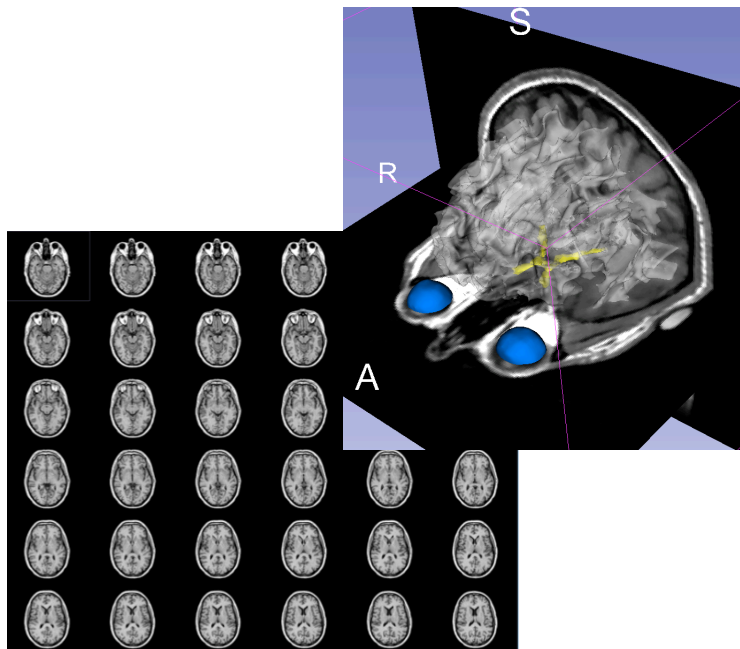


The scene myNewScene.mrml appears in the viewer



# Conclusion

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This tutorial guided you through the basics of data loading and interactive 3D visualization of volumes and 3D surface models in Slicer4.

Contact: [spujol@bwh.harvard.edu](mailto:spujol@bwh.harvard.edu)



# Slicer Community

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- [www.slicer.org](http://www.slicer.org)
- Mailing lists:  
[slicer-user@bwh.harvard.edu](mailto:slicer-user@bwh.harvard.edu)  
[slicer-devel@bwh.harvard.edu](mailto:slicer-devel@bwh.harvard.edu)



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