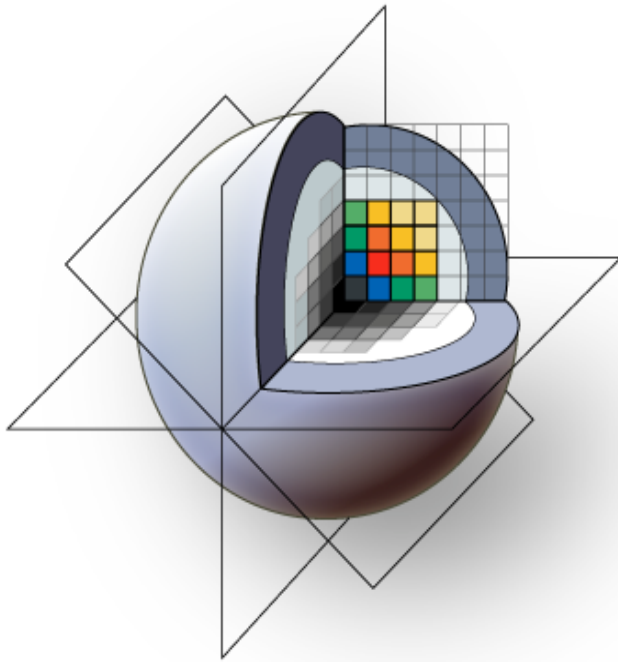




## *Slicer3 Training Compendium*

---

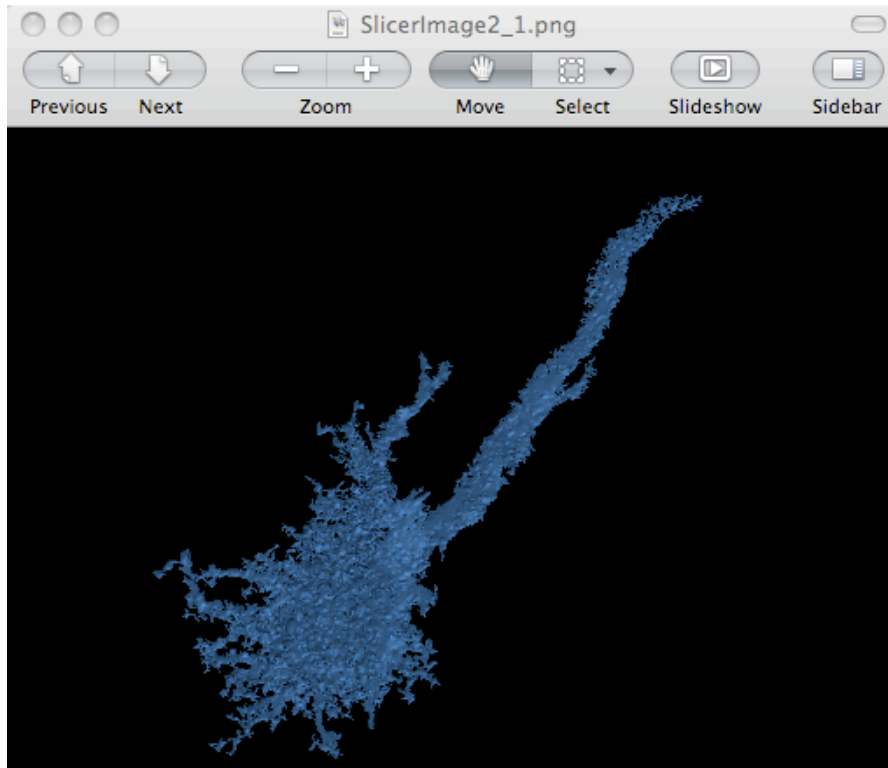
# Introduction to the Use of Slicer in Confocal Microscopy





# *Learning Objective*

---



Guiding you step by step through the process of loading confocal microscopy data, working with that data, and creating a 3D model for visualization.



# *Prerequisites*

---

This tutorial assumes that you have already completed the tutorial **Data Loading and Visualization**. Tutorials for **Slicer3** are available at the following location:

- **Slicer3** tutorials

<http://www.na-mic.org/Wiki/index.php/Slicer3.2:Training>

- At least 300 MB free disk space



# Materials

---

This tutorial requires the installation of the **Slicer3** software and the tutorial dataset. They are available at the following locations:

- **Slicer3** download page (***Slicer 3.4***)

<http://www.slicer.org/pages/Downloads/>

- Tutorial dataset (***Data from CCDB***)

<http://ccdb.ucsd.edu>

**Disclaimer:** *It is the responsibility of the user of Slicer to comply with both the terms of the license and with the applicable laws, regulations, and rules.*





# Overview

---

<b>Section 1 (Basic Slicer Operations)</b>	slide 6
Downloading Sample Data	slides 7-12
Loading data, layout and visualization	slides 13-28
Basic Editing (Editor module)	slides 29-36
<b>Section 2 (Model Building)</b>	slide 37
Downloading Sample Data	slides 38-42
Setup for Model Building	slides 43-46
Basic Model Building	slides 47-63
Model Building: Otsu Segmentation	slides 64-80
Saving Your Work	slides 81-82
Conclusion and Acknowledgements	slides 83-84

---



---

# *Basic Data Handling and Visualization*

**Note: this section uses a larger dataset**



# Downloading Sample Data

The Cell Centered Database (CCDB) is a web accessible database for high resolution 2D, 3D and 4D data from light and electron microscopy, including correlated imaging.

<http://ccdb.ucsd.edu>

The screenshot shows the Cell Centered Database website. The browser address bar displays <http://ccdb.ucsd.edu/index.shtml>. The website header includes the text "CELL CENTERED DATABASE™" and "National Center for Microscopy and Imaging Research" with the CCDB logo. Below the header is a row of five 3D microscopy images. The main content area features three columns: "2D & 4D Data", "Data Management", and "Knowledge Engineering". The "Data Management" section includes a "NEW RELEASE" section about MyCCDB. The "Knowledge Engineering" section includes a "SAO" section about the Subcellular Anatomy Ontology. At the bottom, a footer contains copyright information: "© 2002-2008 The Regents of the University of California. All rights reserved. Updated December 2008" and links for "User agreement", "Privacy Notice", "Copyright", and "Contact us".



# Downloading Sample Data

CELL CENTERED DATABASE™  
National Center for Microscopy and Imaging Research

MyCCDB coming soon!

Search CCDB

Purkinje

**Resources**  
Pacific Daylight Time  
La Jolla, CA, USA  
Data Display - Available  
Data Download - Available  
Image Display - Available  
Animation Display - Available

**Features**  
About  
Data  
Developer's Page  
Gallery  
Dictionary  
Links  
Publications  
Tools  
Help

**Sponsors**  
CRBS  
NBCR  
NCMIR  
NCRN  
NIBIB  
NIDA  
NIGMS  
NIMH  
UCSD

**2D, 3D & 4D Data**  
The Cell Centered Database (CCDB) is a web accessible database for high resolution 2D, 3D and 4D data from light and electron microscopy, including correlated imaging. Techniques range from wide field mosaics taken with multiphoton microscopy to 3D reconstructions of cellular ultrastructure using electron tomography...[\(more\)](#)

**DATA SPOTLIGHT**  
**Detailed geometry of membrane systems mediating cardiomyocyte excitability**  
CCDB has just released two 3D electron tomography data sets from a newly published study of the geometry of membrane systems mediating excitability in cardiac myocytes. [\(more\)](#)

**Data Management**  
The CCDB is developing "MyCCDB" for comprehensive management of 2D, 3D, and 4D light and electron microscopy data through a secure web portal. With an account to MyCCDB, users can manage their own data through the web using the CCDB's powerful search and display capabilities...[\(more\)](#)

**NEW RELEASE**  
MyCCDB will provide a personalized secure web-based portal for accessing, uploading and managing data through the CCDB. We are in the process of building the customized interface. In the meanwhile, you are free to preview MyCCDB through NCMIR's Telescience portal.

**Knowledge Engineering**  
The CCDB is participating in several large scale information projects to develop and utilize ontologies and spatial reference systems for data mining and data federation. The CCDB is utilizing ontologies to link data across scales and modalities. Additional details may be found by visiting the [NIF](#) and [SenseLab](#)...[\(more\)](#)

**SAO**  
We have developed the Subcellular Anatomy Ontology (SAO) for the nervous system to provide a formal ontology to describe structures from the dimensional range known as the "mesoscale," encompassing cellular and subcellular structure, supracellular domains, and macromolecules. [\(more\)](#)

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[User agreement](#) | [Privacy Notice](#) | [Copyright](#) | [Contact us](#)

- 1) Enter Search Term: Purkinje
- 2) Select 'Go'



# Downloading Sample Data

CELL CENTERED DATABASE™  
National Center for Microscopy and Imaging Research

Data | Search | Gallery | Dictionary | Publications | Tools | MyCCDB | Data Download | Help

Home • Search result for **Purkinje** (Total: 15 records - Modify search)  
1 2 Next

ID	Cell type	Structure	MP type	Thumbnails		
				Raw image	Reconstruction	Segmentation
<input type="checkbox"/> 2	Purkinje neuron	dendritic tree	confocal			
<input type="checkbox"/> 3	Purkinje neuron	dendritic tree	confocal			
<input type="checkbox"/> 4	Purkinje neuron	dendritic tree	confocal			
<input type="checkbox"/> 6	Purkinje neuron		confocal			
<input type="checkbox"/> 7	Purkinje neuron		confocal			
<input type="checkbox"/> 13	Purkinje neuron	spiny dendrite	IVEM			

Go to "http://ccdb.ucsd.edu/sand/main?event=displayRecon&mpid=13&pl=y"

1) Select Purkinje Cell with ID 2



# Downloading Sample Data

CELL CENTERED DATABASE™  
National Center for Microscopy and Imaging Research

Data | Search | Gallery | Dictionary | Publications | Tools | MyCCDB | Data Download | Help

Home • Search result • ALXP • Summary Information

**Data Set Information**  
Summary  
Details  
All information  
View metadata (pdf)  
Download metadata (pdf)  
Get ADOBE® READER®  
Project  
Specimen preparation  
Microscopy product  
Imaging product type  
Specimen description  
Imaging parameters  
2D Image  
Reconstruction  
Segmentation  
Links to...  
SenseLab  
New Search  
Search home  
Keyword  Go  
Accession #  Go  
Project ID  Go  
New!  
If you want to search for some keywords in a detail info. page, just simply highlight the keywords, right click over the selected text and click "Search CCDB"

**2D Image** **Reconstruction** **Segmentation** **Map Location**

Add to MyLabBench Download dataset Show project tree

**Summary Information**  
Microscopy product ID: 2  
Image basename: ALXP

Summary	
Project ID	P0001
Leader	Maryann Martone ( <a href="#">Other projects</a> )
Collaborators	Eric Bushong
Project Description	NeuroLucida tracing of filled Purkinje neurons
Experiment Purpose	To develop a canonical Purkinje neuron
Species	rat
System	central nervous system
Organ	brain
Region	cerebellum
Cell type	Purkinje neuron
Structure	dendritic tree
Product Type	optical section series
Instrument	BioRad.MRC.1024.Confocal

1) Select 'Download dataset'



# Downloading Sample Data

The screenshot shows the Cell Centered Database (CCDB) website. The browser address bar displays the URL: <http://ccdb.ucsd.edu/sand/main?selectedID=2&actionName=addAProductToMLBAndDow>. The page header includes the CCDB logo and the text "National Center for Microscopy and Imaging Research". A navigation menu contains links for Data, Search, Gallery, Dictionary, Publications, Tools, MyCCDB, Data Download, and Help. The main content area is divided into two sections: "New Search" and "Terms & Conditions".

**New Search**

Search home

Keyword  Go

Accession #  Go

Project ID  Go

**New!**  
If you want to search for some keywords in a detail info. page, just simply highlight the keywords, right click over the selected text and click "Search CCDB"

**Browse Products**

- All records (Data statistics)
- Filled cells
- Protein localization
- Correlated light microscopy & electron microscopy
- Electron tomography
- Brain mosaics
- Most recently released!

**Current Session**

- Back to search result
- View MyLabBench

**Terms & Conditions**

Please provide a valid email address. You will receive an email notification when there is any modification or update to the dataset you chose to download.

Your valid email address  (Required)

Your title & name  (Required)

Your institute name  (Required)

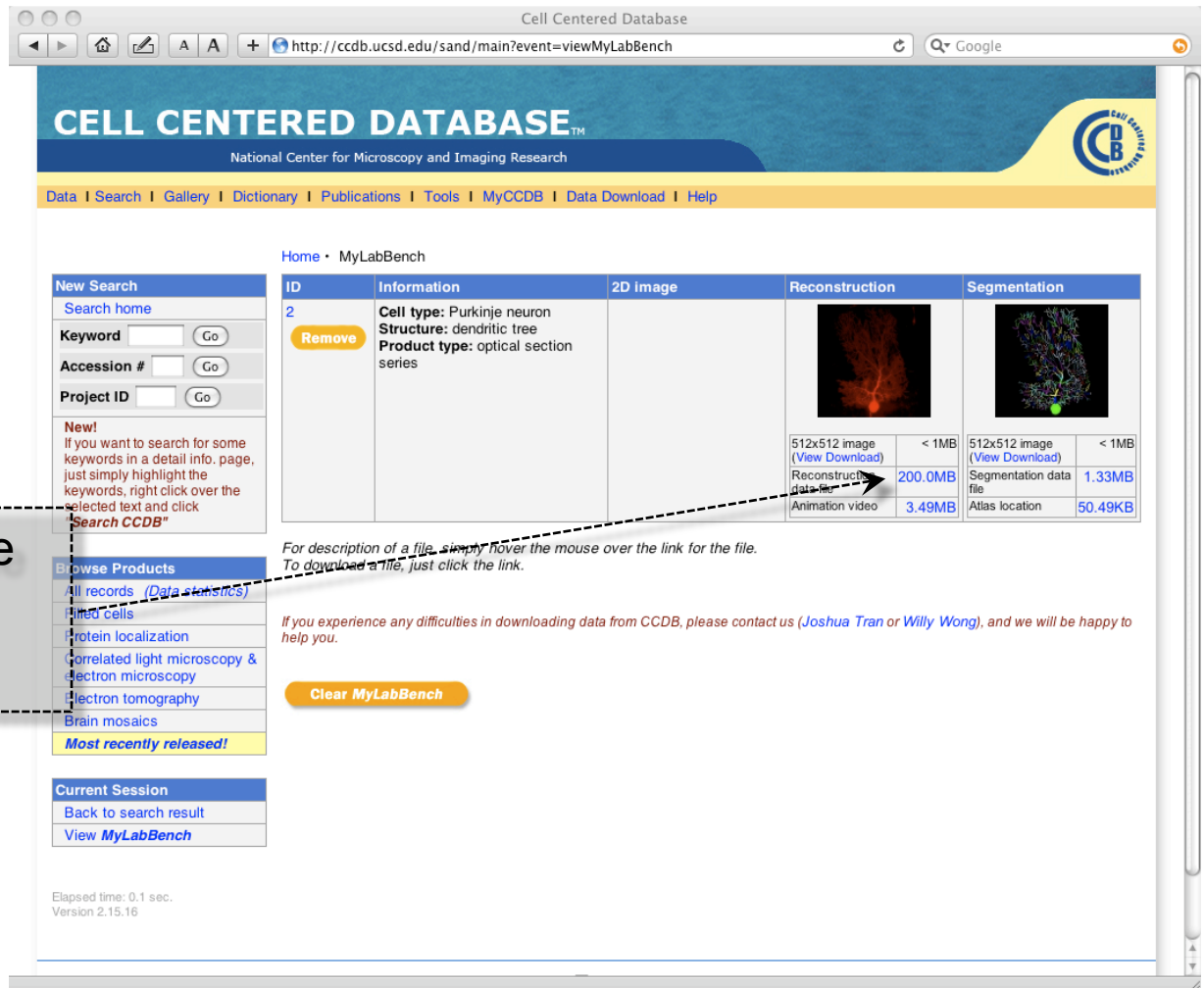
By clicking on the following button, I agree to all of the [terms and conditions](#).

1) Enter required information to receive updates

2) Select 'Continue'



# Downloading Sample Data



Cell Centered Database  
<http://ccdb.ucsd.edu/sand/main?event=viewMyLabBench> Google

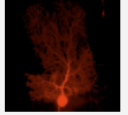
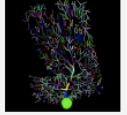
**CELL CENTERED DATABASE™**  
 National Center for Microscopy and Imaging Research

Data | Search | Gallery | Dictionary | Publications | Tools | MyCCDB | Data Download | Help

Home • MyLabBench

**New Search**  
 Search home  
 Keyword  Go  
 Accession #  Go  
 Project ID  Go

**New!**  
 If you want to search for some keywords in a detail info. page, just simply highlight the keywords, right click over the selected text and click "Search CCDB"

ID	Information	2D Image	Reconstruction	Segmentation
2	Cell type: Purkinje neuron Structure: dendritic tree Product type: optical section series <a href="#">Remove</a>		 512x512 image (View Download) < 1MB Reconstruction data file <b>200.0MB</b> Animation video 3.49MB	 512x512 image (View Download) < 1MB Segmentation data file 1.33MB Atlas location 50.49KB

For description of a file, simply hover the mouse over the link for the file. To download a file, just click the link.

If you experience any difficulties in downloading data from CCDB, please contact us ([Joshua Tran](#) or [Willy Wong](#)), and we will be happy to help you.

[Clear MyLabBench](#)

**Browse Products**  
 All records (Data streams)  
 Fused cells  
 Protein localization  
 Correlated light microscopy & electron microscopy  
 Electron tomography  
 Brain mosaics  
 Most recently released!

**Current Session**  
 Back to search result  
 View MyLabBench

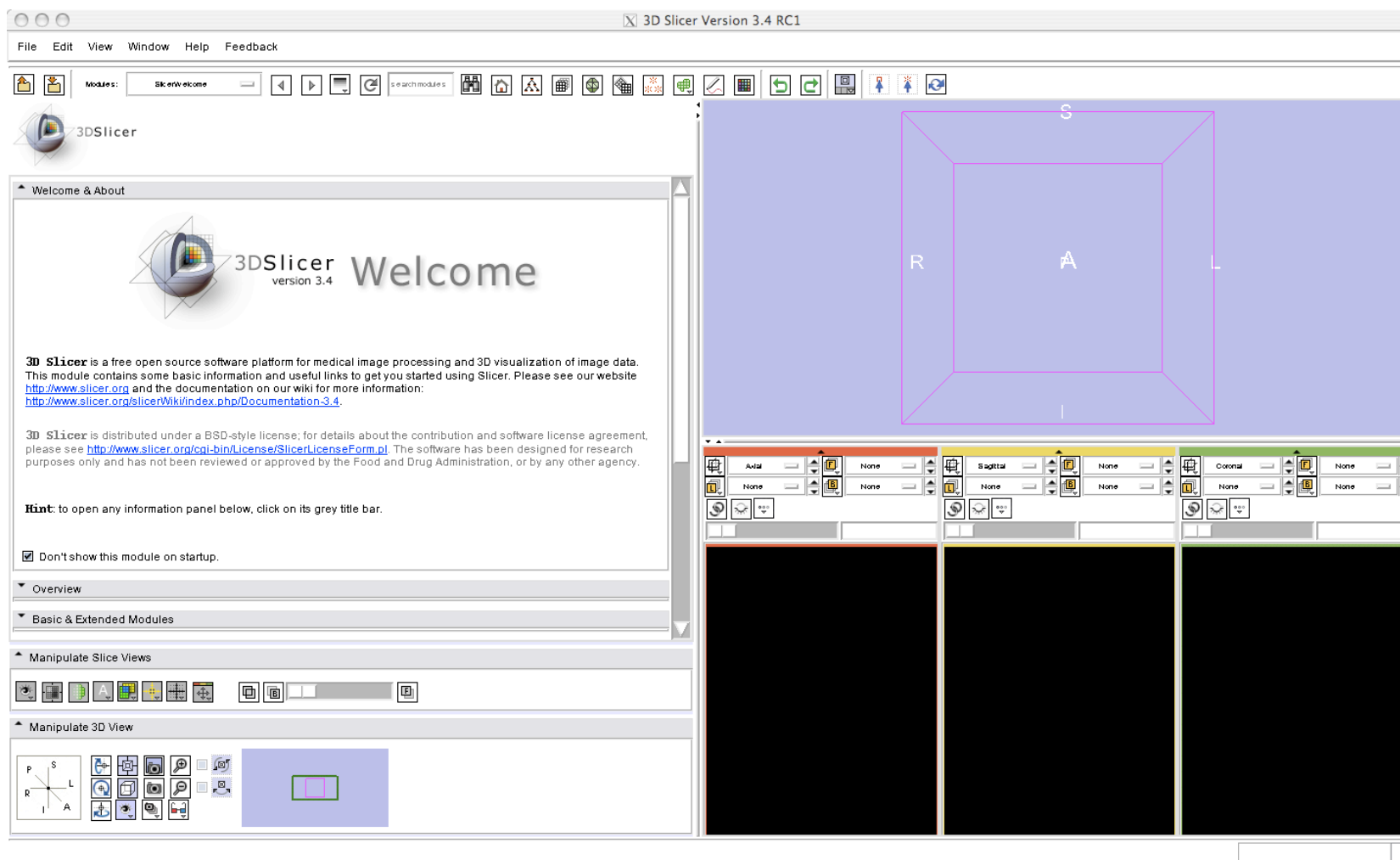
Elapsed time: 0.1 sec.  
 Version 2.15.16

1) Download data file by selecting '200.0MB'





# Launch Slicer





# Open Purkinje Cell Data

3D Slicer Version 3.4 RC1

File Edit View Window Help Feedback

Modules: SlicerWelcome

3DSlicer

Welcome & About

3D Slicer is a free open source software platform. This module contains some basic information and documentation on <http://www.slicer.org> and the documentation on <http://www.slicer.org/slicerWiki/index.php/Documentation>. 3D Slicer is distributed under a BSD-style license. Please see <http://www.slicer.org/copyright/license/> for purposes only and has not been reviewed or approved.

Hint: to open any information panel below, click on the corresponding icon.

Don't show this module on startup.

Overview

Basic & Extended Modules

Manipulate Slice Views

Load Scene... Ctrl-O

Import Scene...

Add Data... Ctrl-A

Add Volume...

Add Transform...

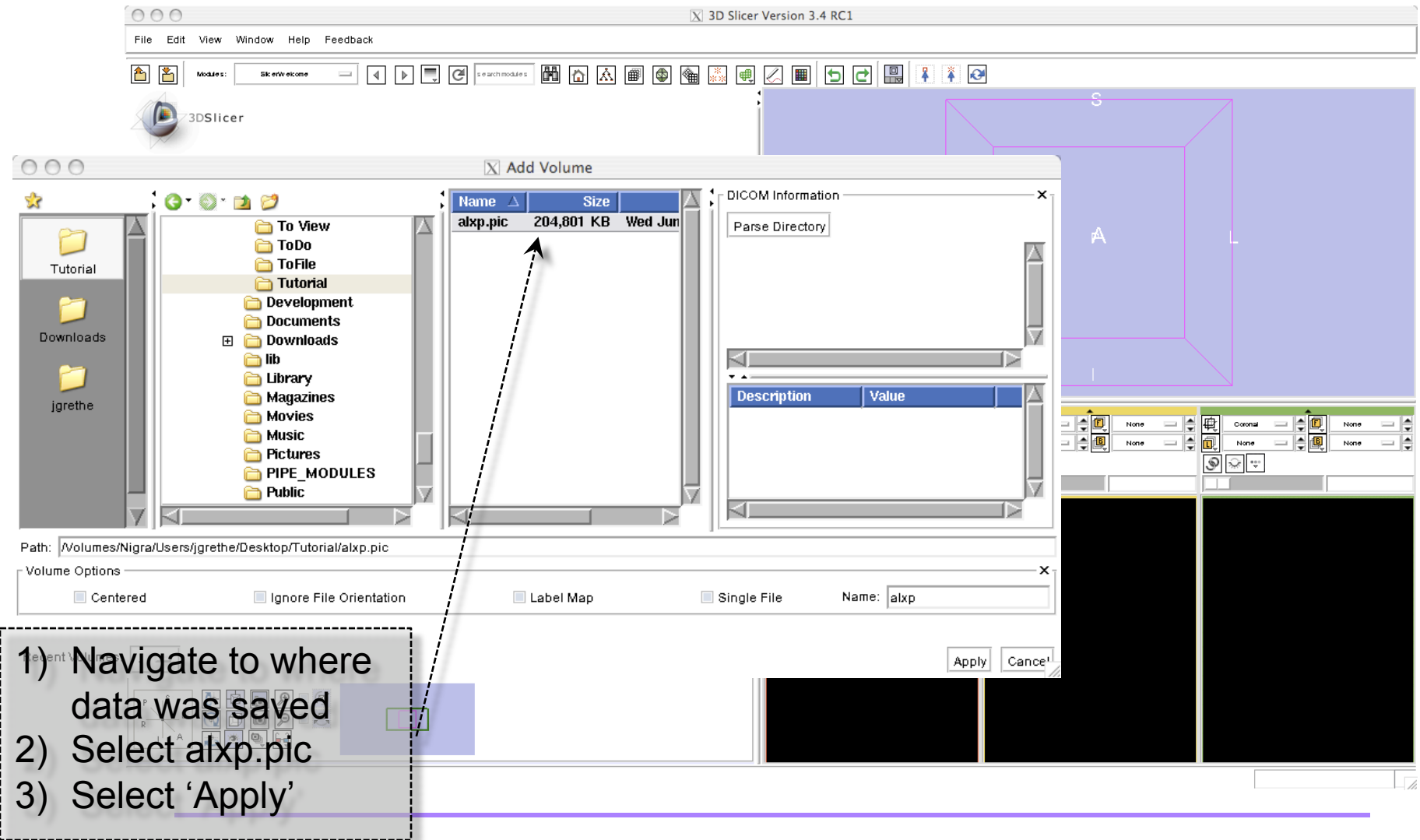
Save Ctrl-S

Close Scene Ctrl-W

Exit

1) Select 'Add Volume' from the 'File' menu

# Open Purkinje Cell Data



3D Slicer Version 3.4 RC1

File Edit View Window Help Feedback

Modules: Skip Welcome

3DSlicer

Add Volume

Name	Size	Modified
alxp.pic	204,801 KB	Wed Jun

DICOM Information

Parse Directory

Description	Value

Path: /Volumes/Nigra/Users/jgrethe/Desktop/Tutorial/alxp.pic

Volume Options

Centered  Ignore File Orientation  Label Map  Single File Name: alxp

Apply Cancel

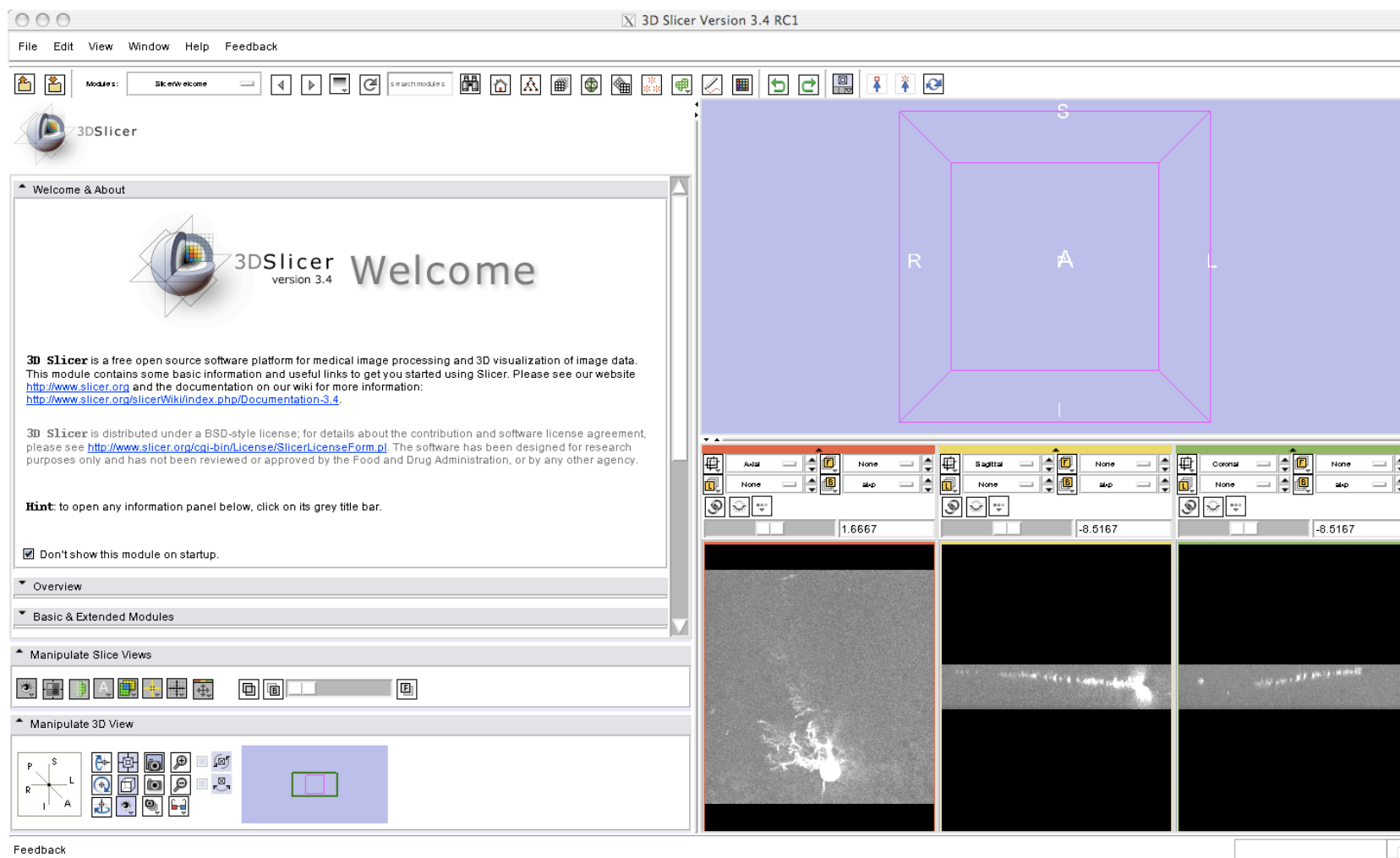
1) Navigate to where data was saved

2) Select alxp.pic

3) Select 'Apply'



# Setup Slicer Layout

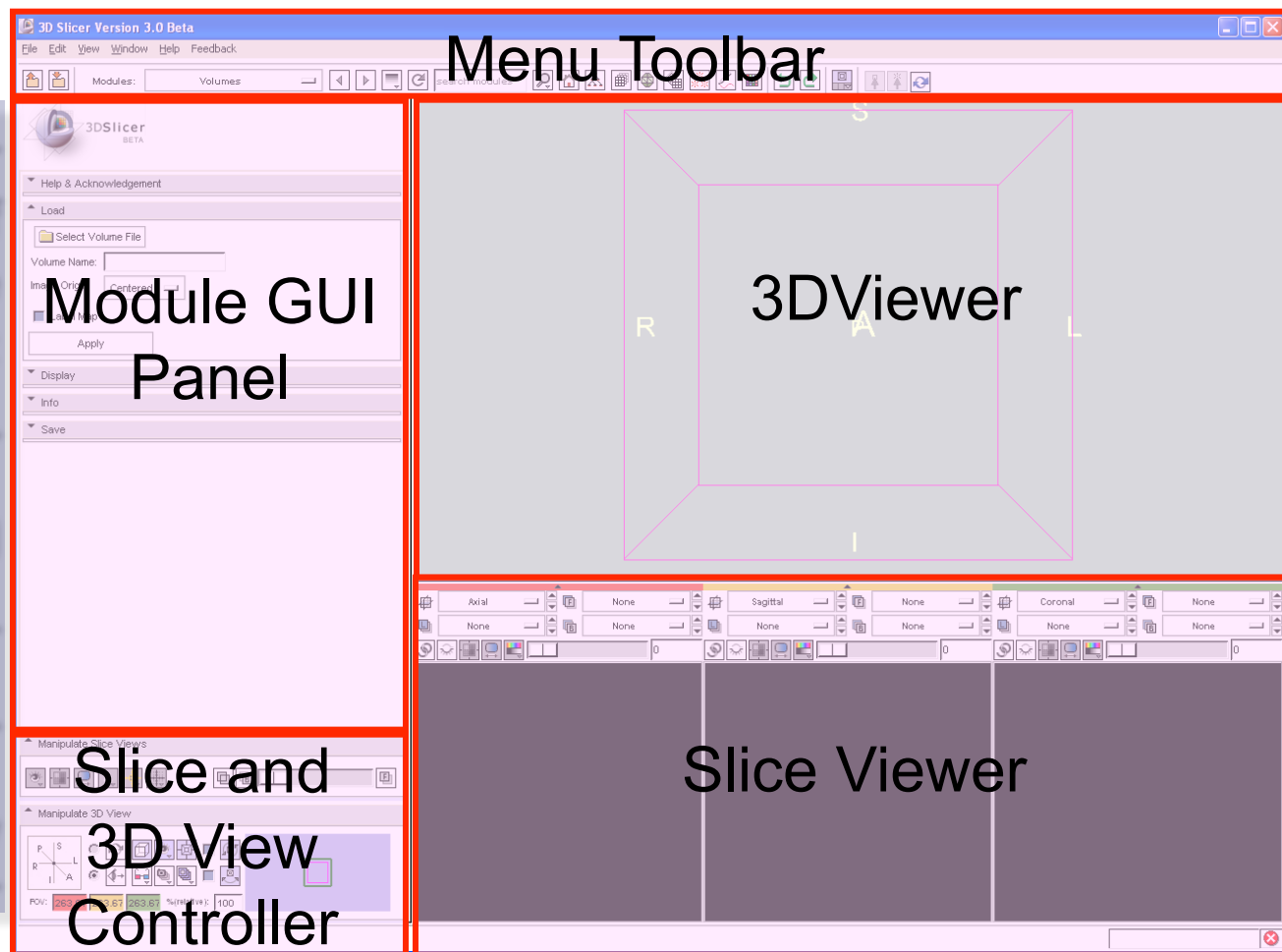




# Slicer GUI Layout

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





# Setup Slicer Layout

The screenshot shows the 3D Slicer software interface. The title bar reads "3D Slicer Version 3.4 RC1". The menu bar includes "File", "Edit", "View", "Window", "Help", and "Feedback". The toolbar contains various icons for file operations and navigation. A "Welcome & About" panel is open, displaying the 3DSlicer logo and version 3.4. Below the logo, it says "Welcome" and provides information about the software. A dashed box highlights two instructions:

- 1) Slicer provides many layouts
- 2) For this tutorial select the 'Four-up' layout

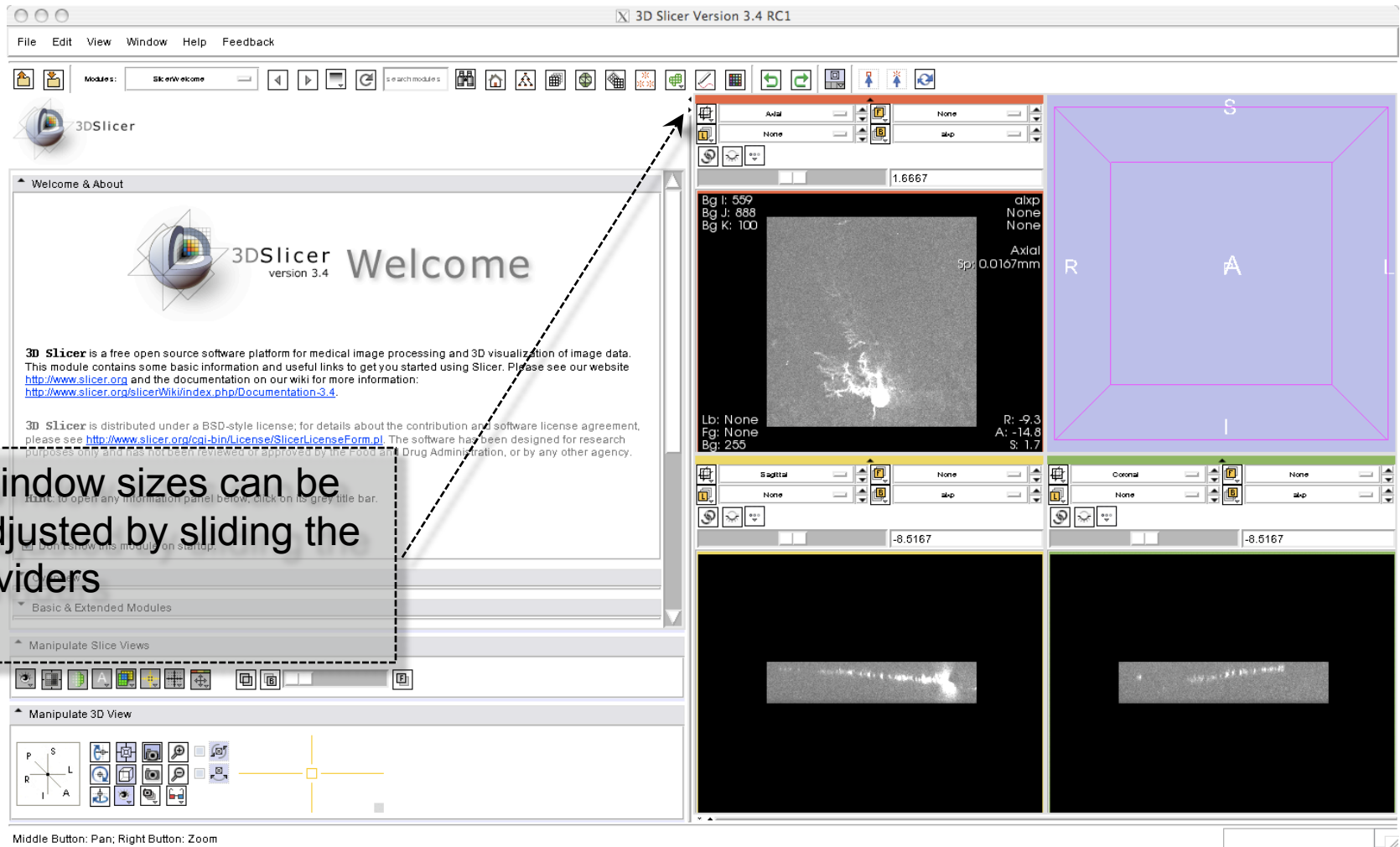
The main 3D view area is currently empty, with a dashed box indicating where the layout menu is being accessed. The layout menu is open, showing several options:

- Conventional layout
- Four-up layout** (highlighted)
- 3D only layout
- Red slice only layout
- Yellow slice only layout
- Green slice only layout
- Tabbed 3D layout
- Tabbed slice layout
- Compare layout

Below the layout menu, there are two toggle options: "Toggle GUI panel visibility" and "Toggle GUI panel L/R". A "close" button is at the bottom of the menu.

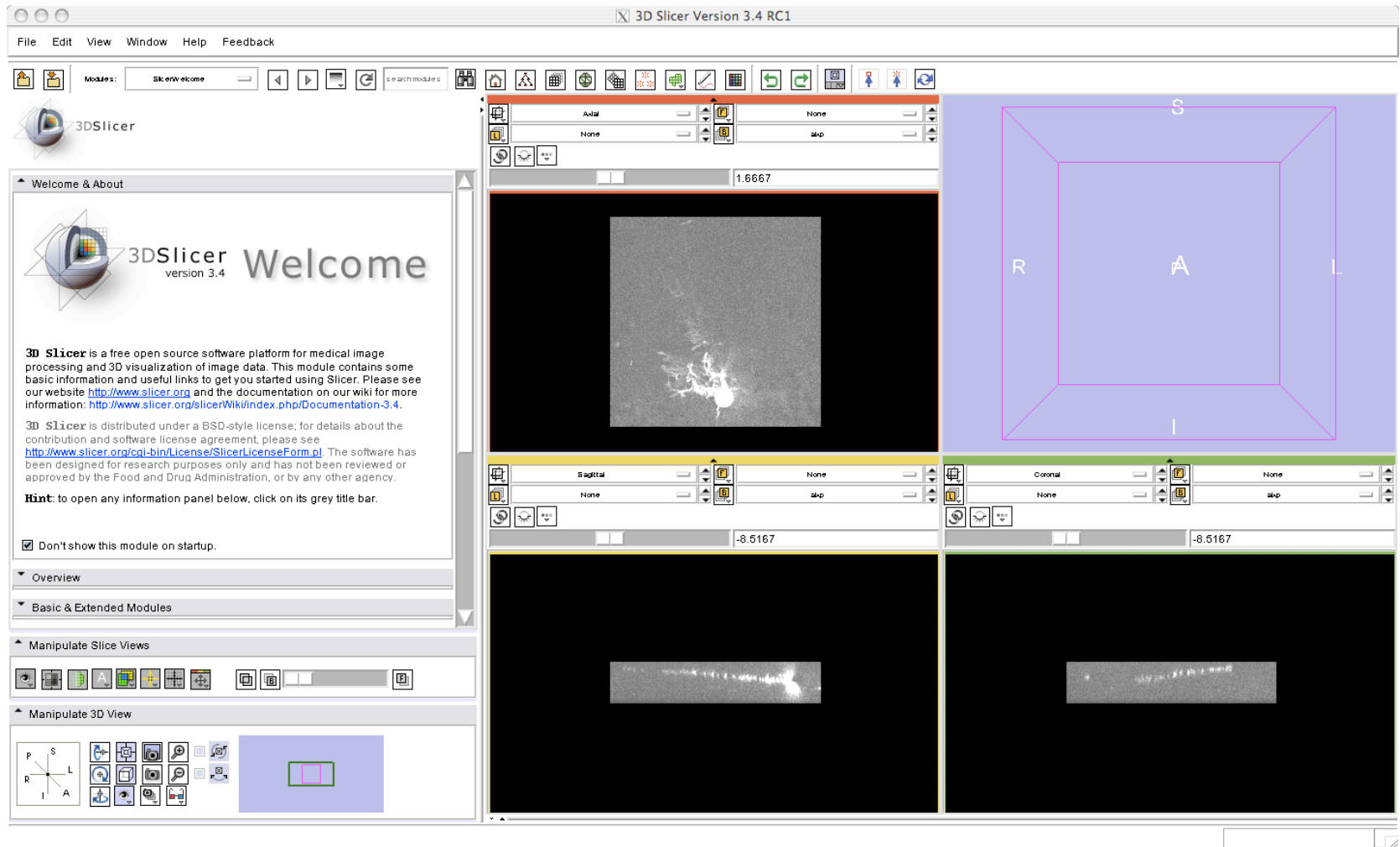


# Setup Slicer Layout





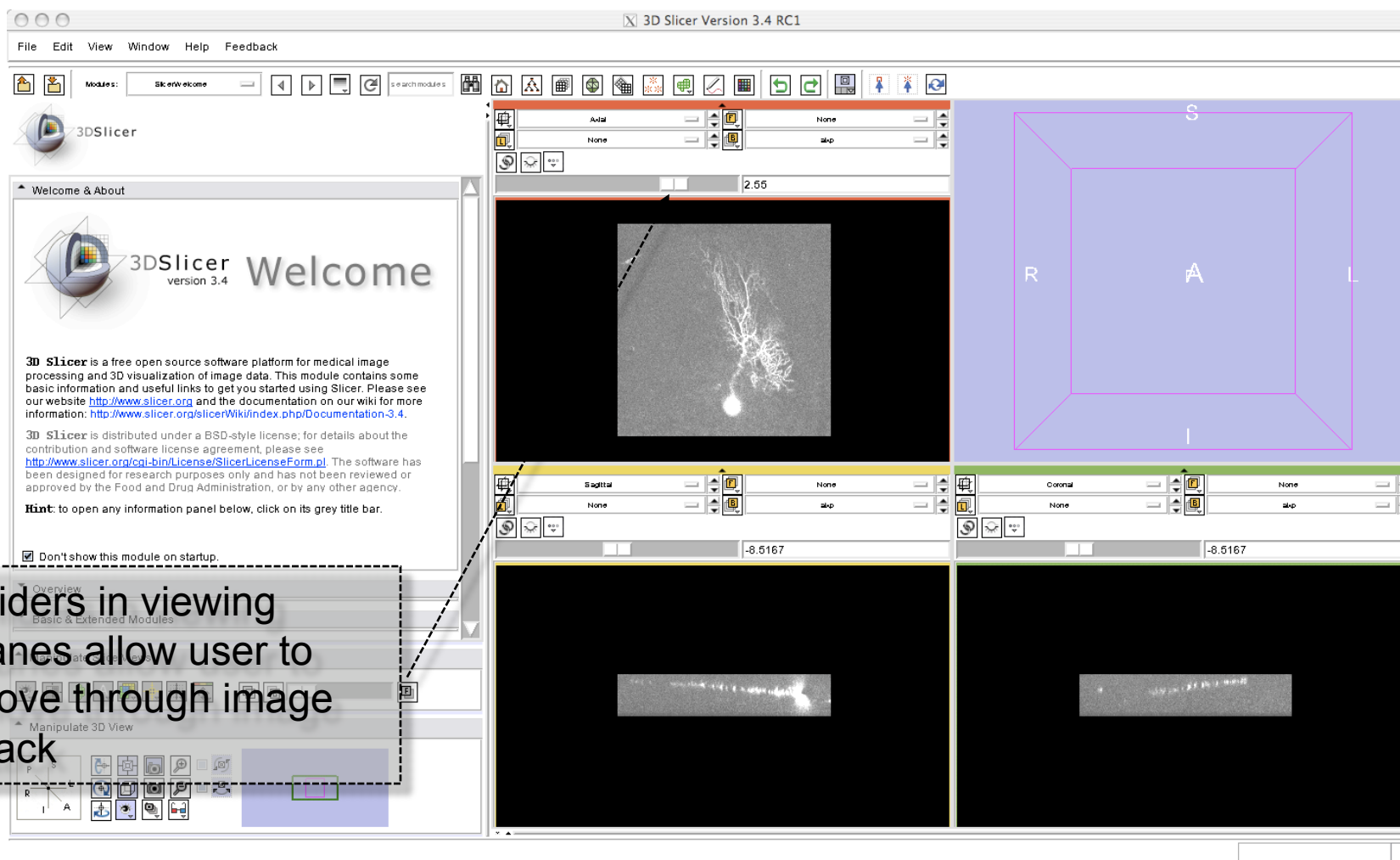
# Completed Slicer Layout Setup





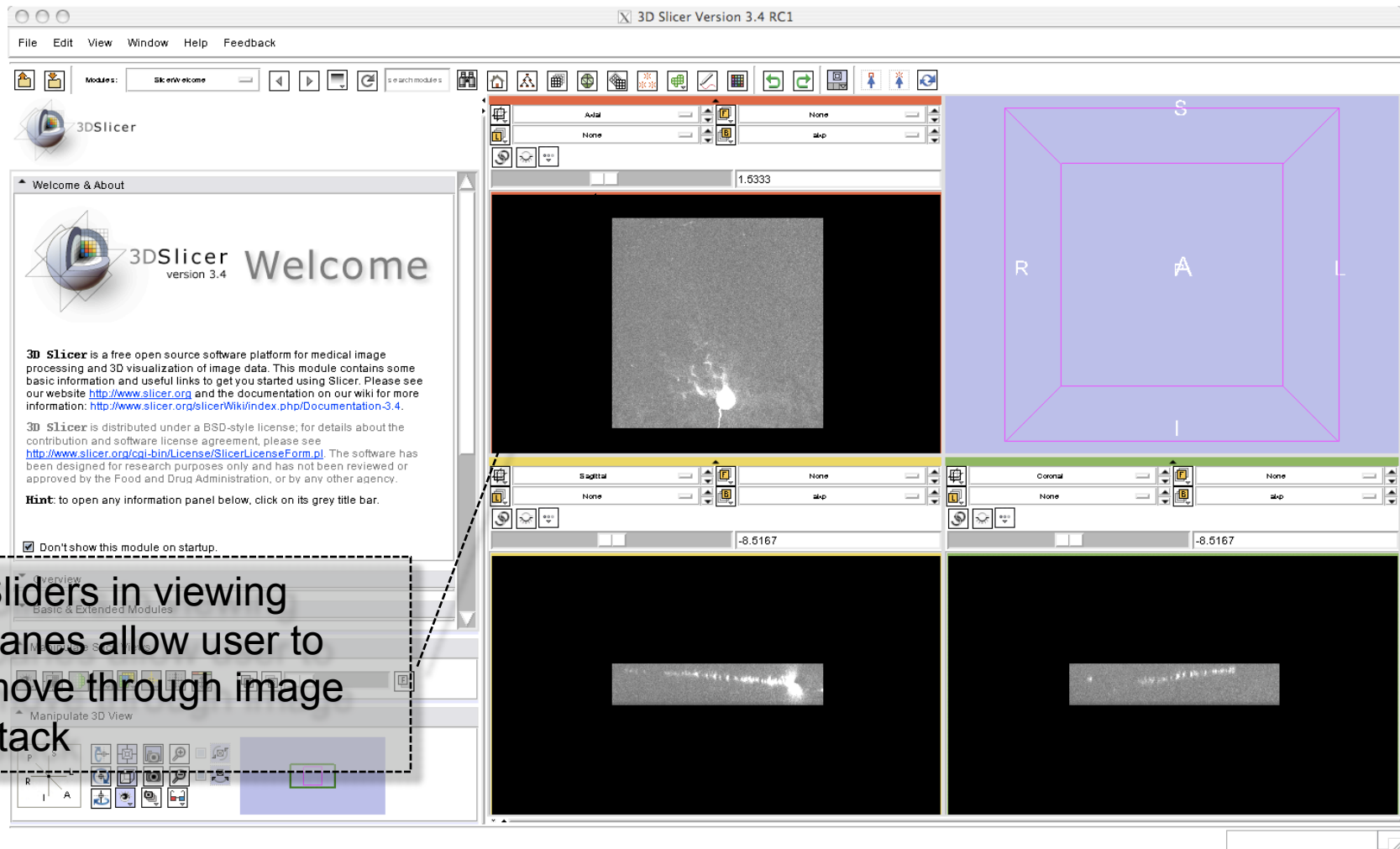


# Viewing Confocal Slices



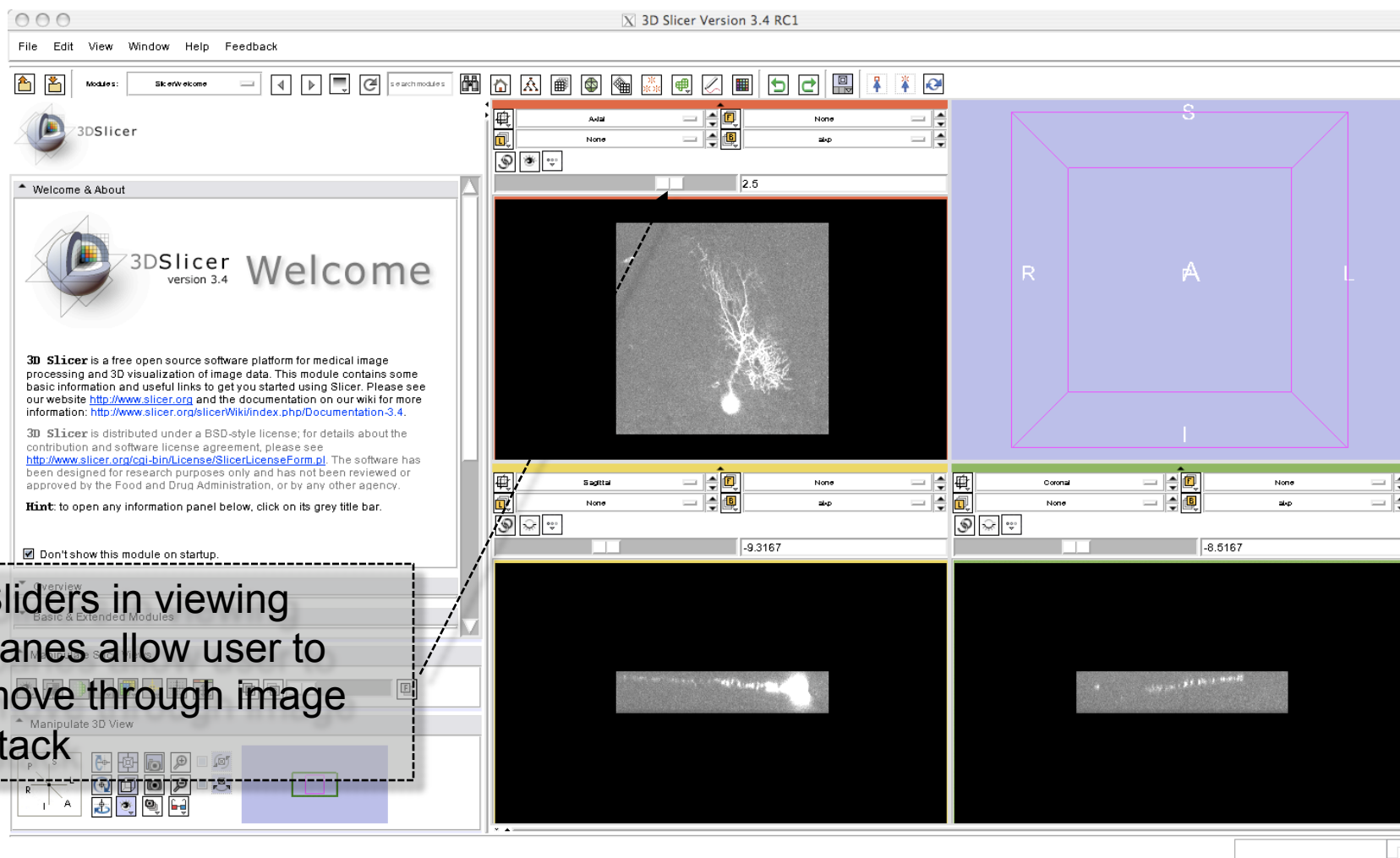


# Viewing Confocal Slices





# Viewing Confocal Slices

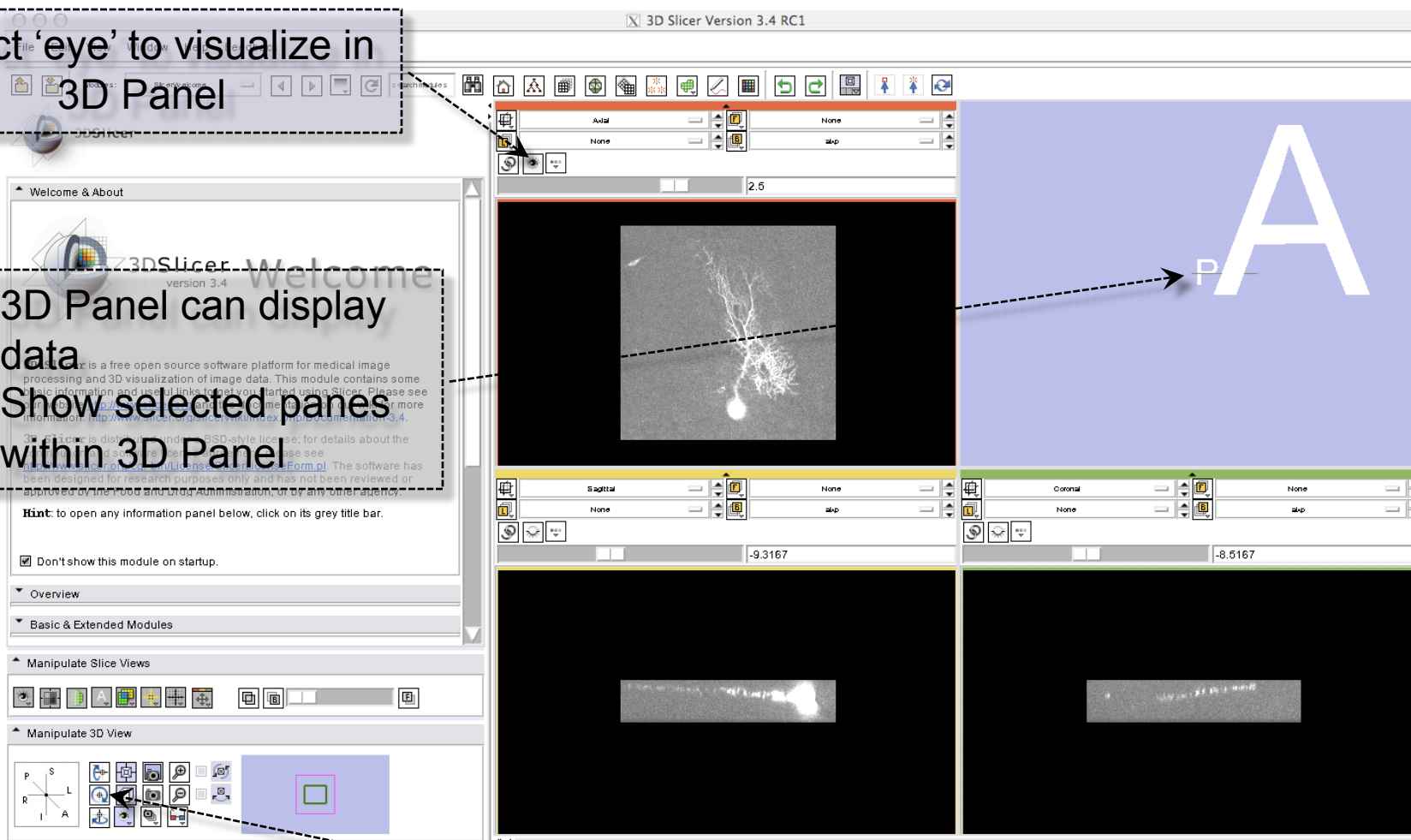




# Basic Viewing in 3D Panel

Select 'eye' to visualize in 3D Panel

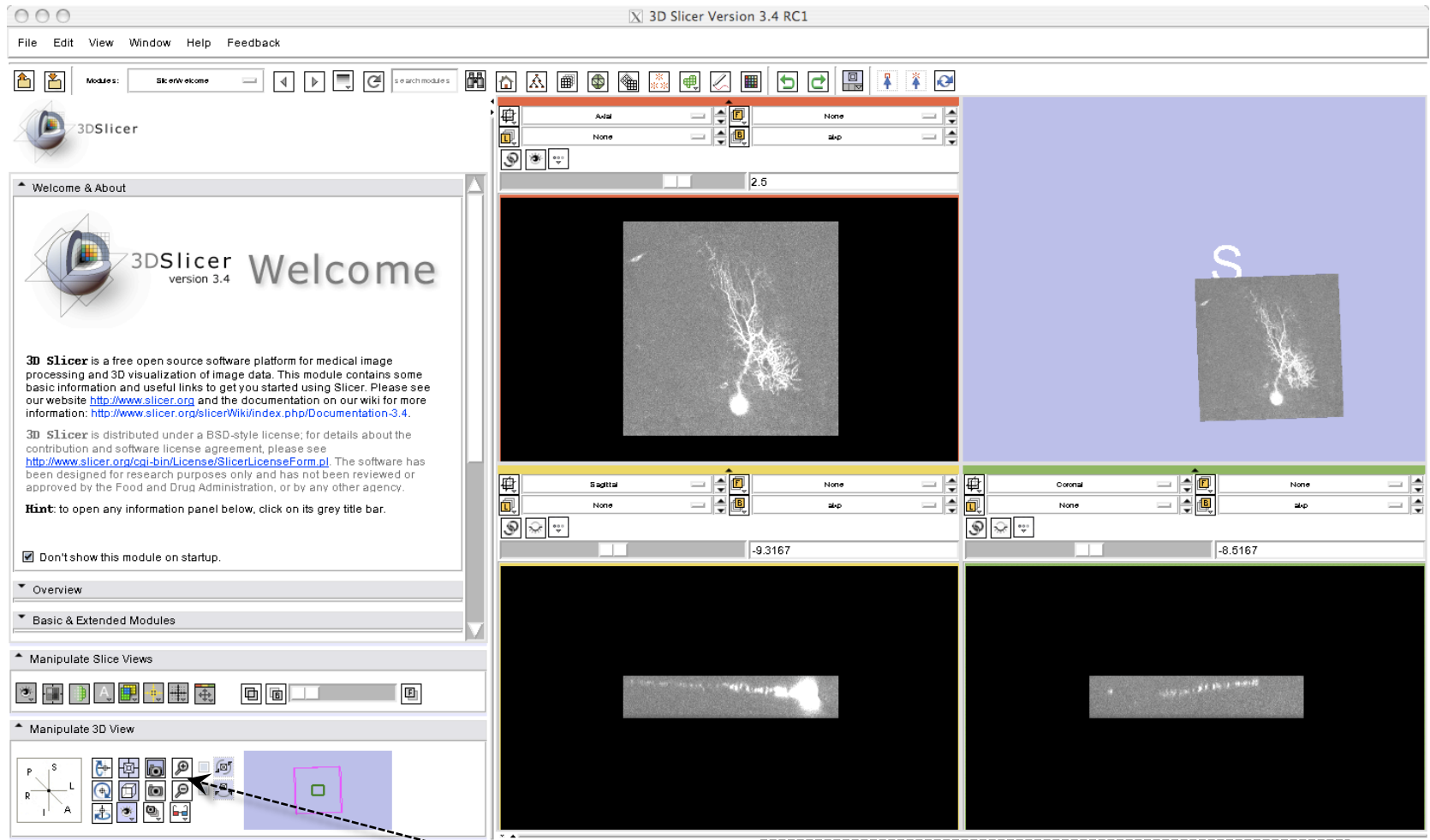
- 1) 3D Panel can display data
- 2) Show selected panes within 3D Panel



Rotate 3D view via rotation buttons or by clicking and dragging in 3D panel



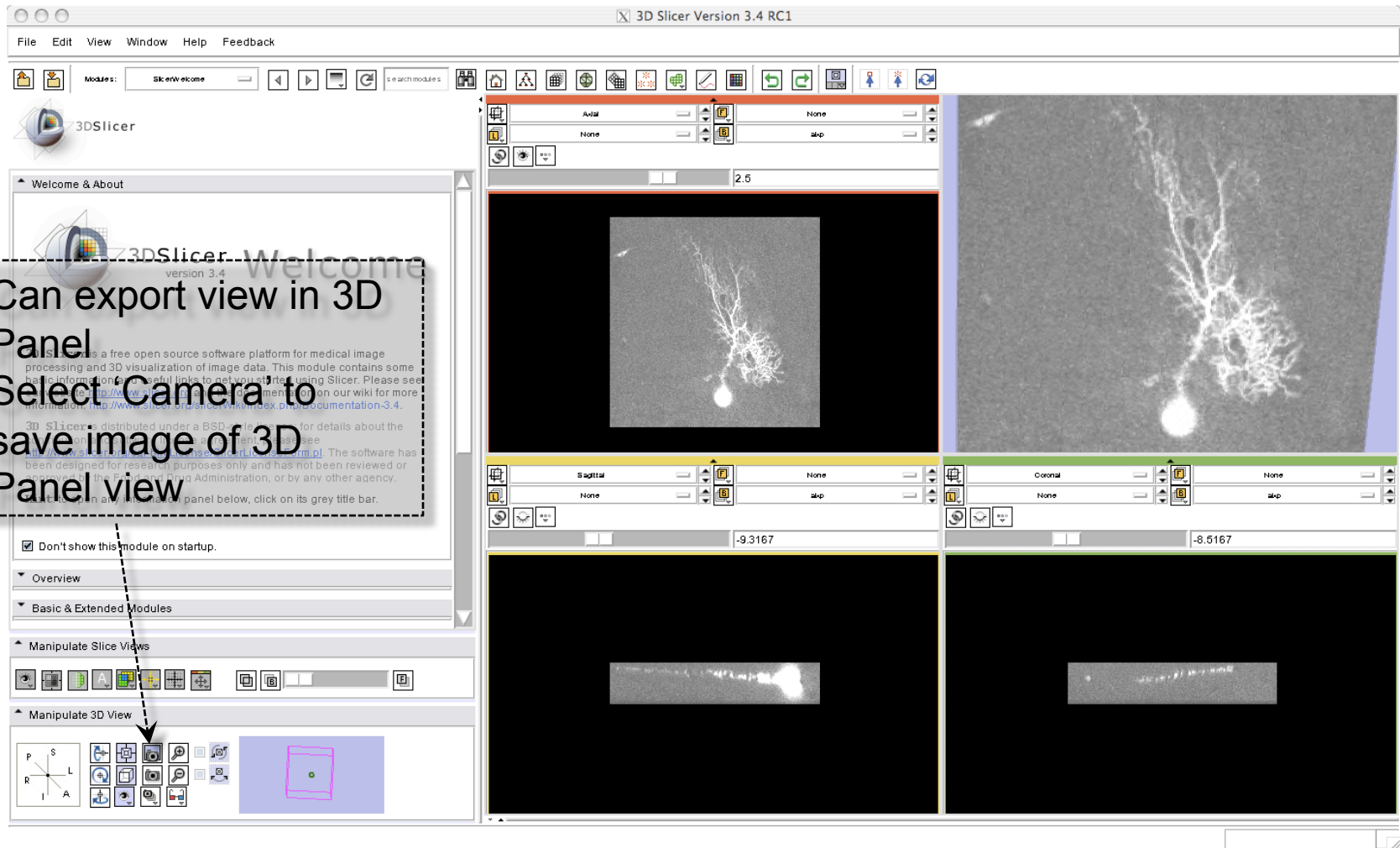
# Basic Viewing in 3D Panel



Zoom 3D view via zoom buttons or by clicking in 3D panel



# Basic Viewing in 3D Panel







# Basic Viewing in 3D Panel

The screenshot shows the 3D Slicer software interface. The main window displays a 3D model of a brain scan. A 'Screen Capture Options' dialog box is open, showing the following settings:

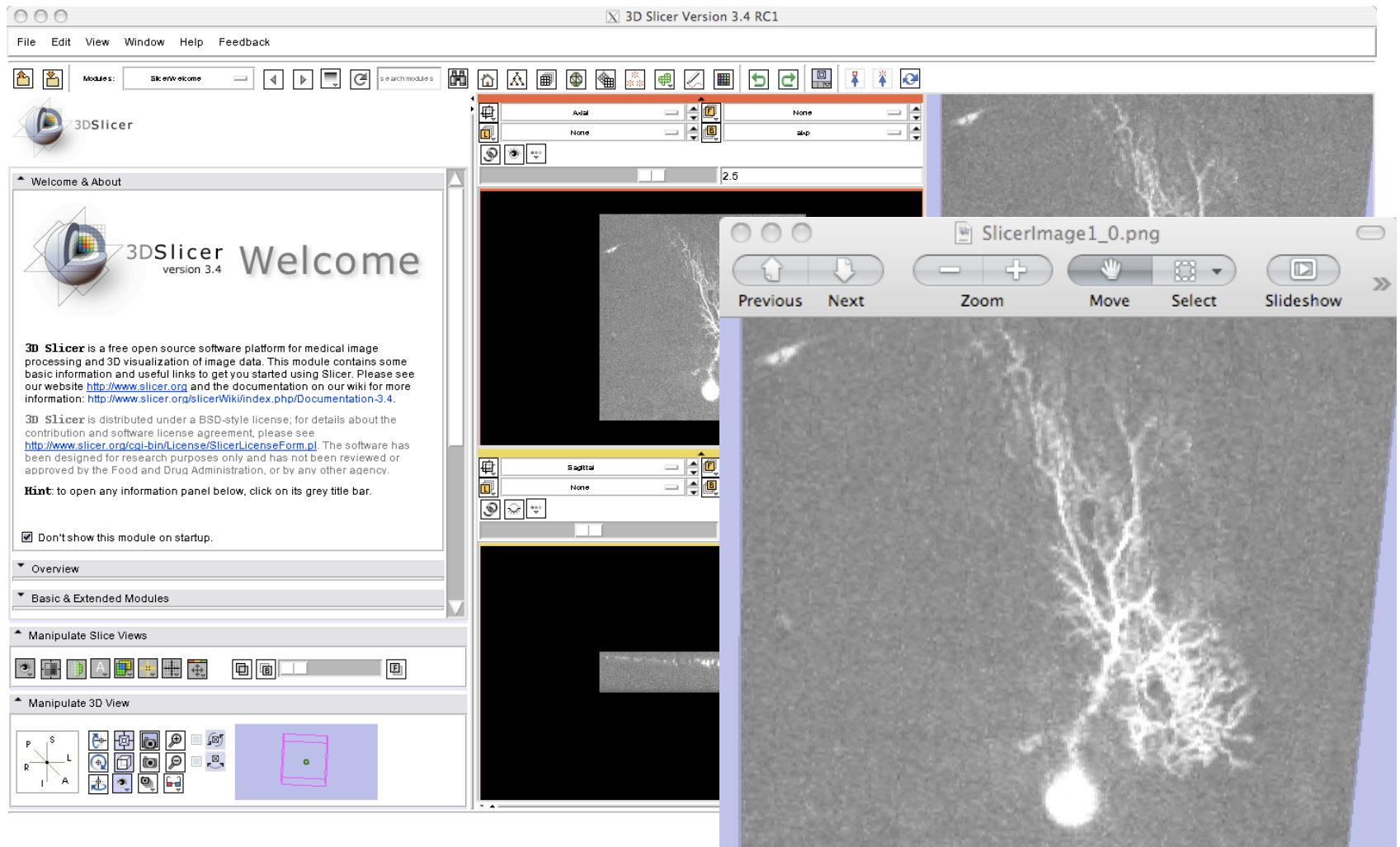
- Directory / folder: /Volumes/Nigra/Users/jgrethe/Desktop/Tutorial
- Image name: SlicerImage1
- Image version number: 0
- Image scale: 1
- Choose Format: .png
- Overwrite existing any files

Buttons for 'Close' and 'Capture' are visible at the bottom of the dialog box.

1) Save file in desired location

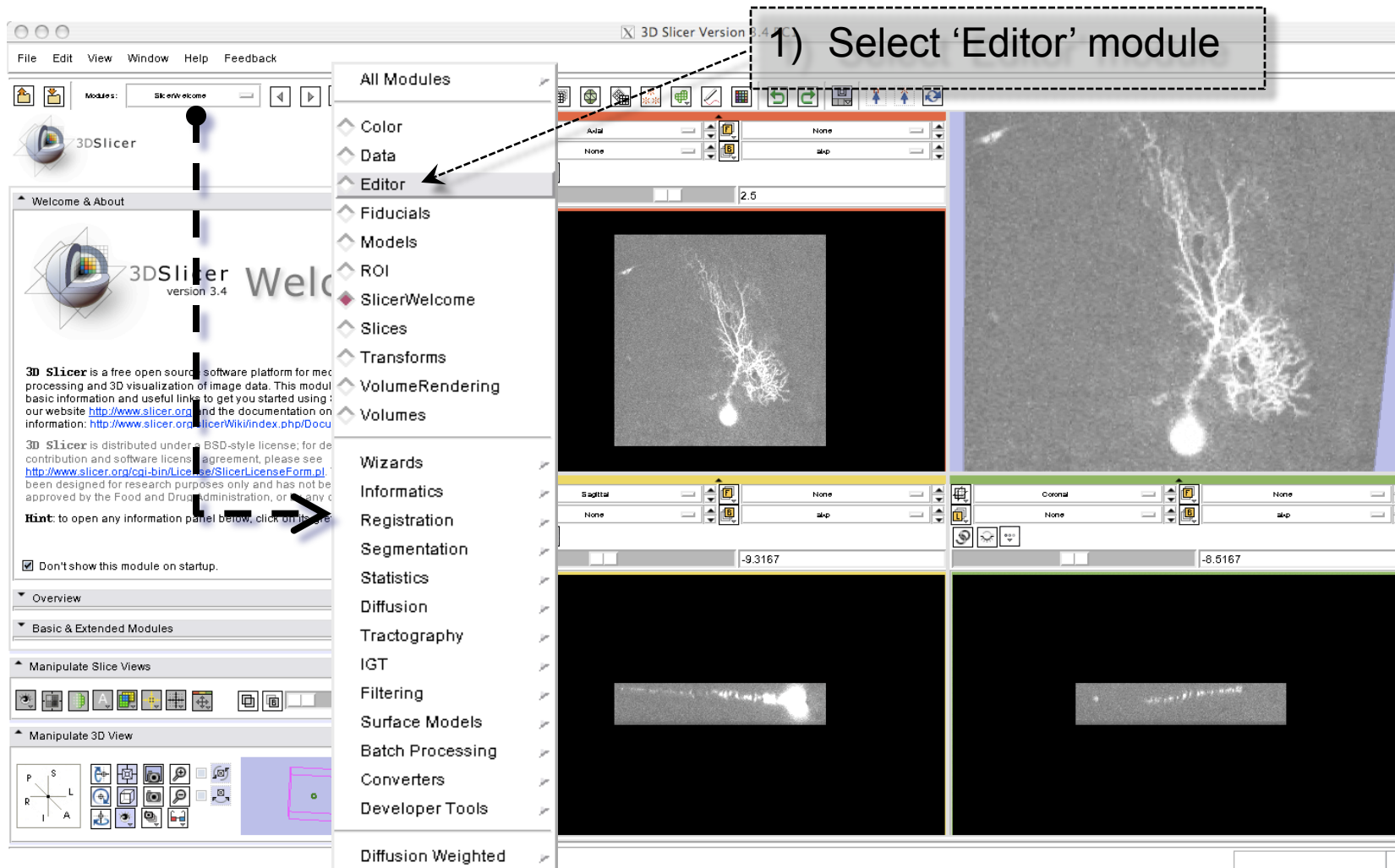


# Basic Viewing in 3D Panel





# Editing Module



1) Select 'Editor' module

All Modules

- Color
- Data
- Editor
- Fiducials
- Models
- ROI
- SlicerWelcome
- Slices
- Transforms
- VolumeRendering
- Volumes

Wizards

- Informatics
- Registration
- Segmentation
- Statistics
- Diffusion
- Tractography
- IGT
- Filtering
- Surface Models
- Batch Processing
- Converters
- Developer Tools
- Diffusion Weighted

3D Slicer version 3.4

3D Slicer is a free open source software platform for medical image processing and 3D visualization of image data. This module provides basic information and useful links to get you started using our website <http://www.slicer.org> and the documentation on our website: <http://www.slicer.org/wiki/index.php/Documentation>

3D Slicer is distributed under a BSD-style license; for details on the contribution and software license agreement, please see <http://www.slicer.org/cgi-bin/licenses/Slicer-licenseForm.pl>. It has been designed for research purposes only and has not been approved by the Food and Drug Administration, or any other regulatory agency.

Hint: to open any information panel below, click on the arrow icon.

Don't show this module on startup.

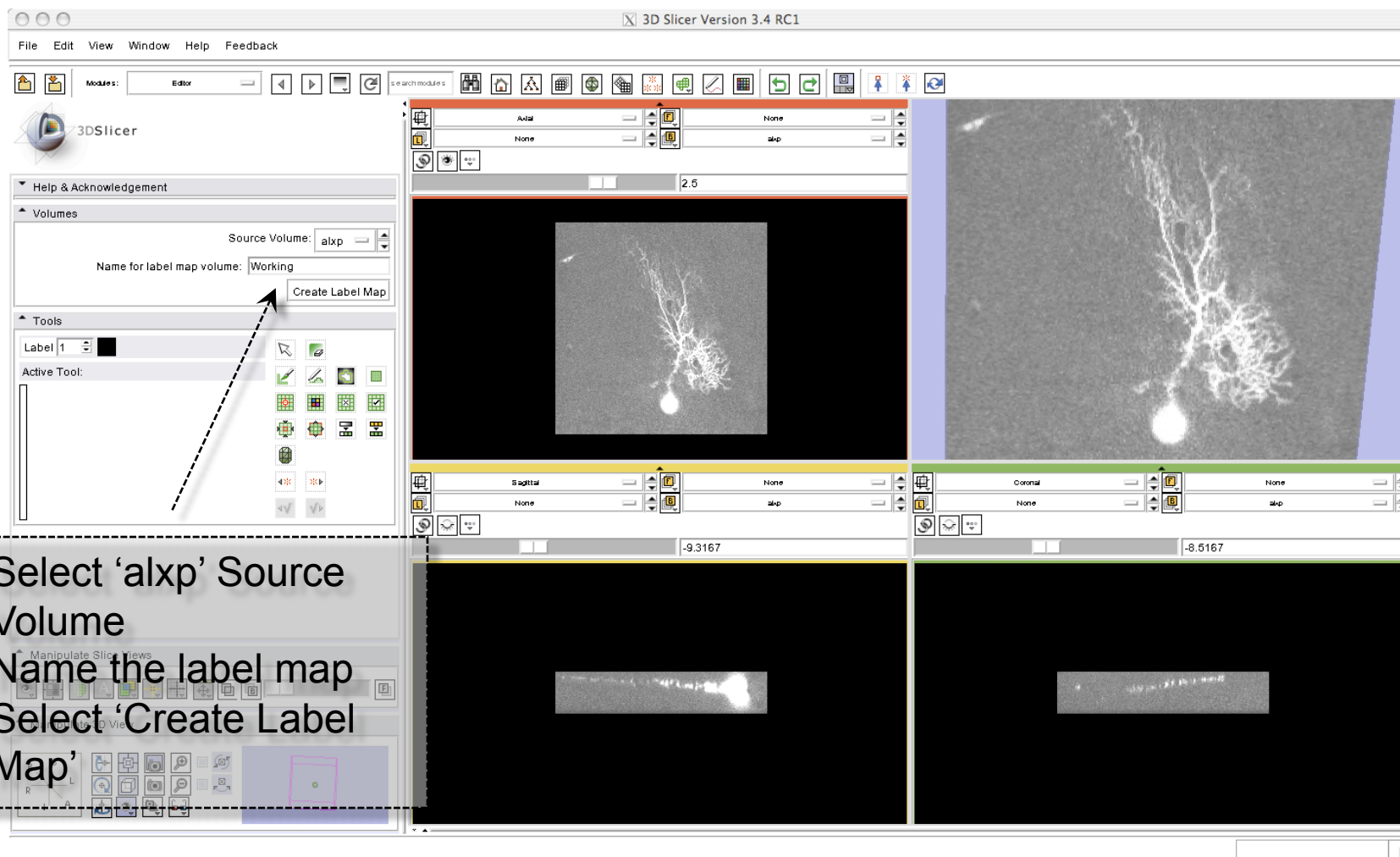
Overview

Basic & Extended Modules

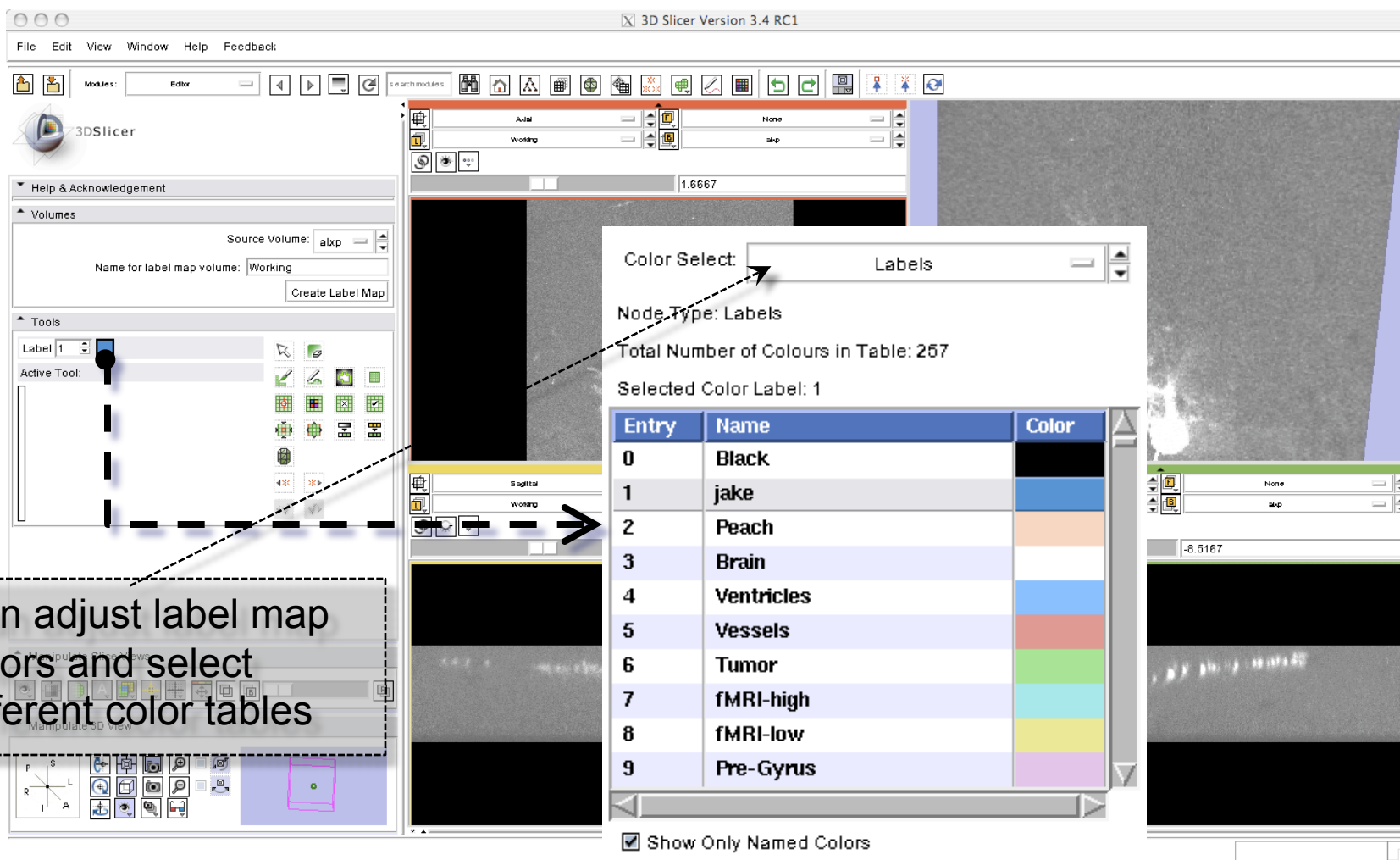
Manipulate Slice Views

Manipulate 3D View

# Creating A Label Map



# Adjusting Label Map Color



3D Slicer Version 3.4 RC1

File Edit View Window Help Feedback

Modules: Editor

3DSlicer

Help & Acknowledgement

Volumes

Source Volume: atxp

Name for label map volume: Working

Create Label Map

Tools

Label 1

Active Tool:

Color Select: Labels

Node Type: Labels

Total Number of Colours in Table: 257

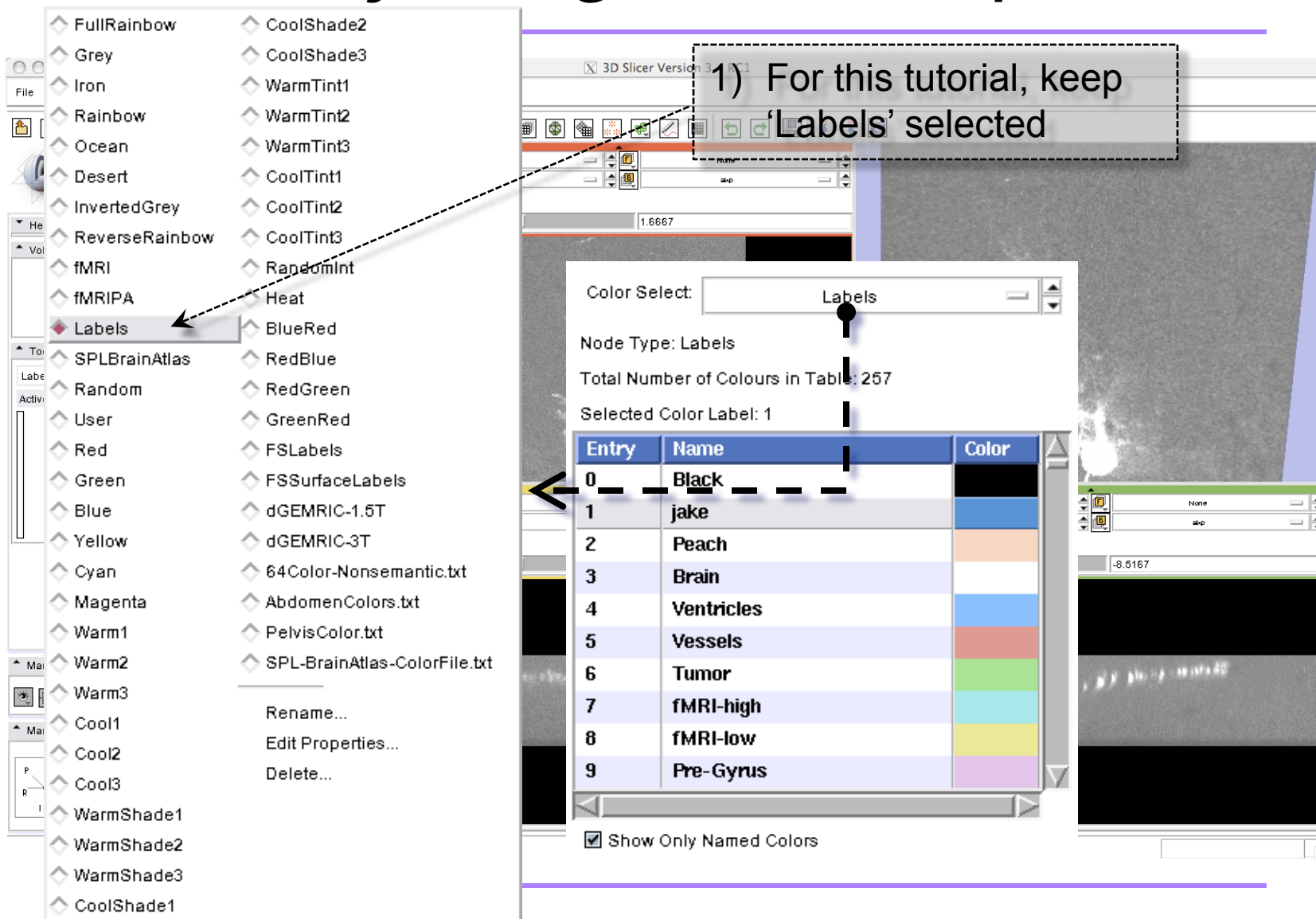
Selected Color Label: 1

Entry	Name	Color
0	Black	Black
1	jake	Blue
2	Peach	Orange
3	Brain	Light Blue
4	Ventricles	Light Blue
5	Vessels	Red
6	Tumor	Green
7	fMRI-high	Cyan
8	fMRI-low	Yellow
9	Pre-Gyrus	Purple

Show Only Named Colors

1) Can adjust label map colors and select different color tables

# Adjusting Label Map Color



1) For this tutorial, keep 'Labels' selected

Color Select: Labels

Node Type: Labels

Total Number of Colours in Table: 257

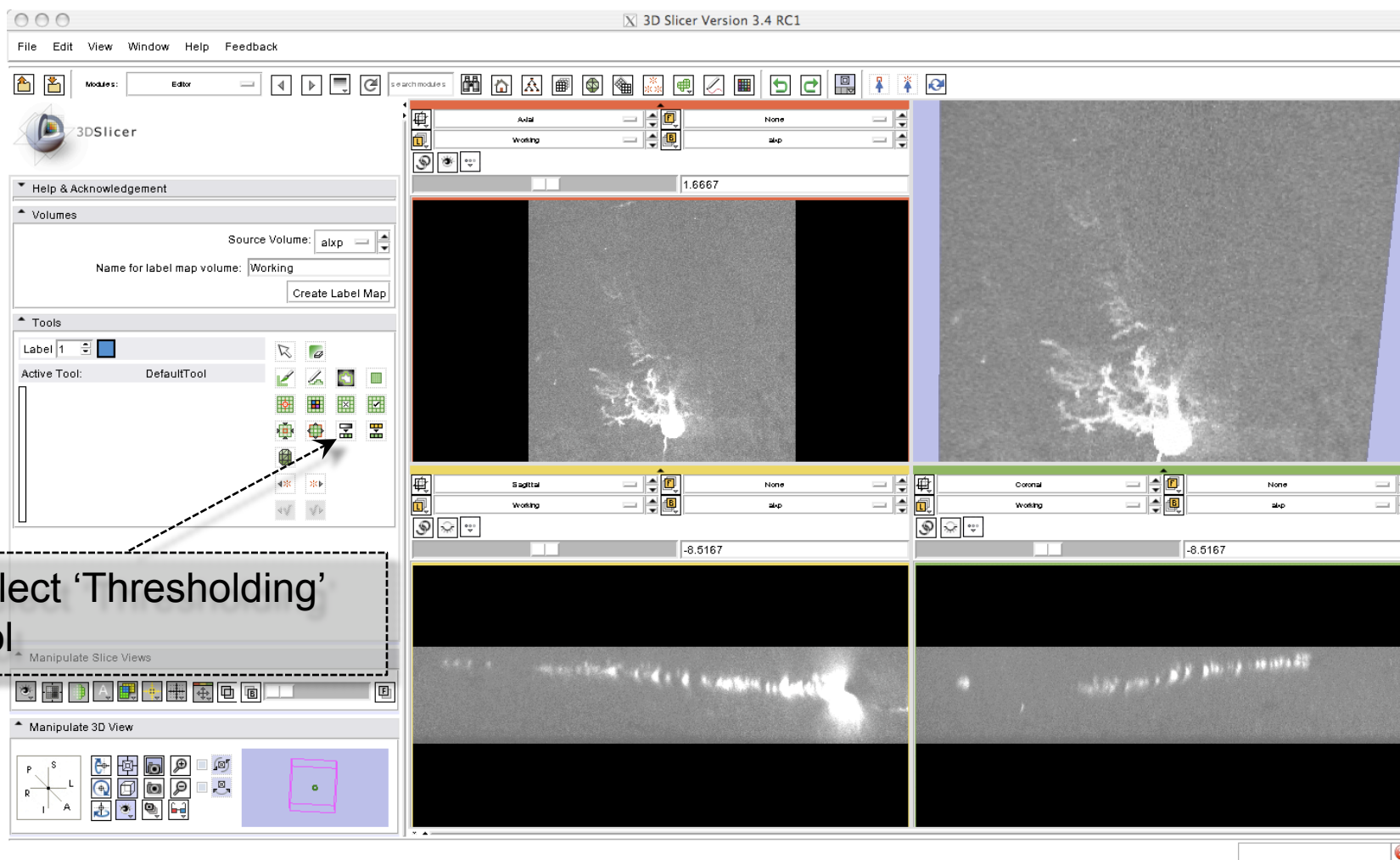
Selected Color Label: 1

Entry	Name	Color
0	Black	
1	jake	
2	Peach	
3	Brain	
4	Ventricles	
5	Vessels	
6	Tumor	
7	fMRI-high	
8	fMRI-low	
9	Pre-Gyrus	

Show Only Named Colors



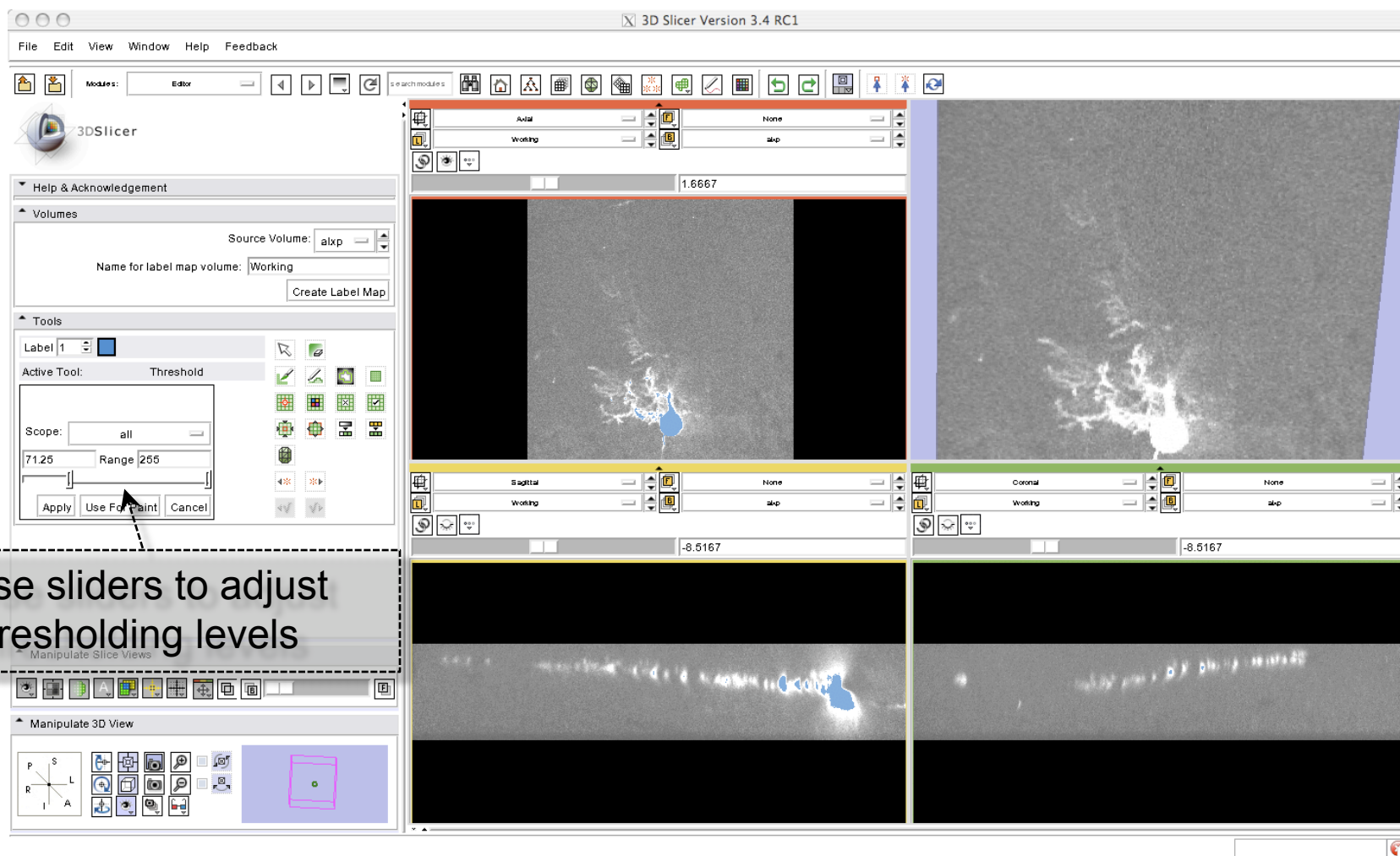
# Editing: Basic Thresholding







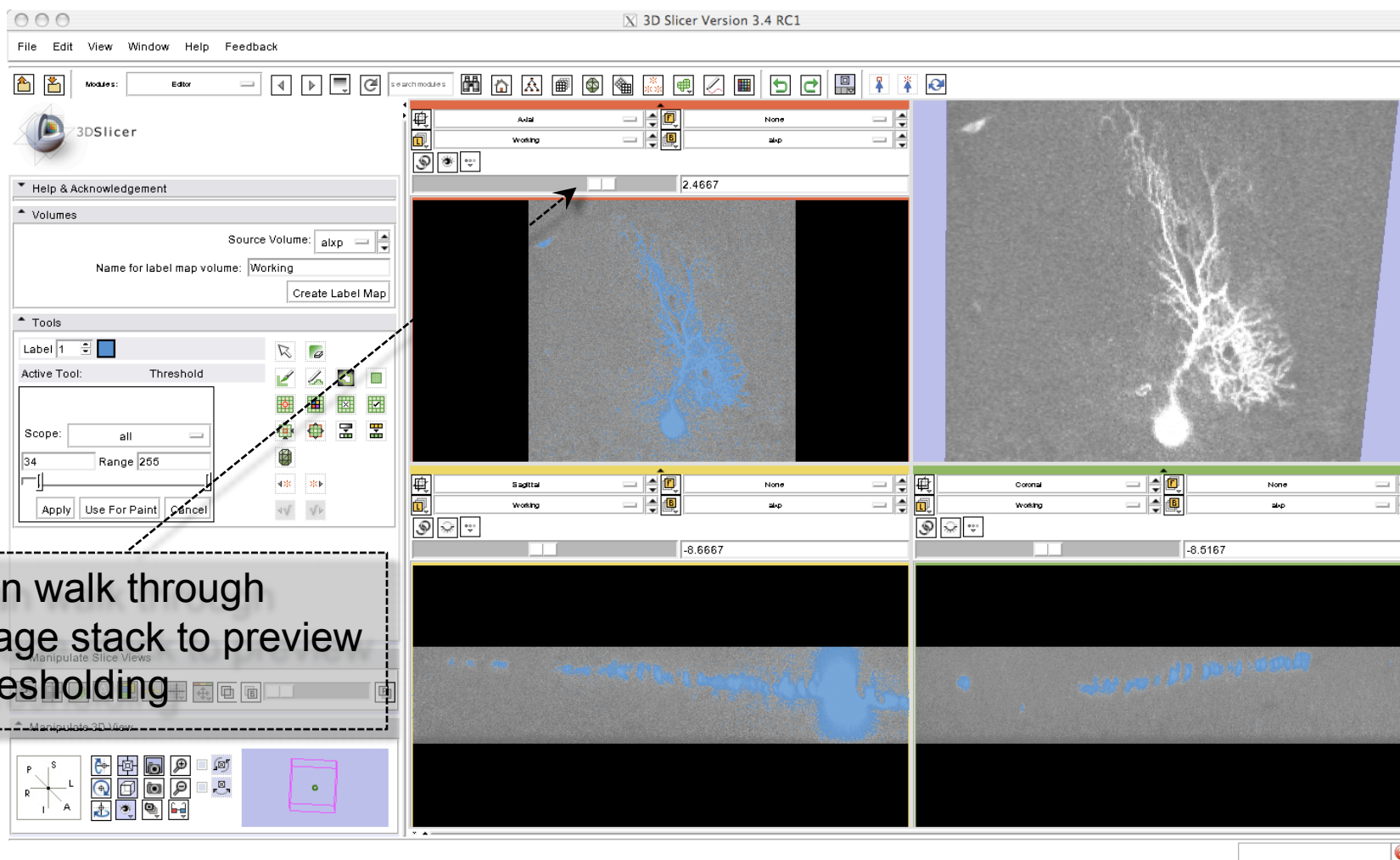
# Editing: Basic Thresholding



1) Use sliders to adjust thresholding levels



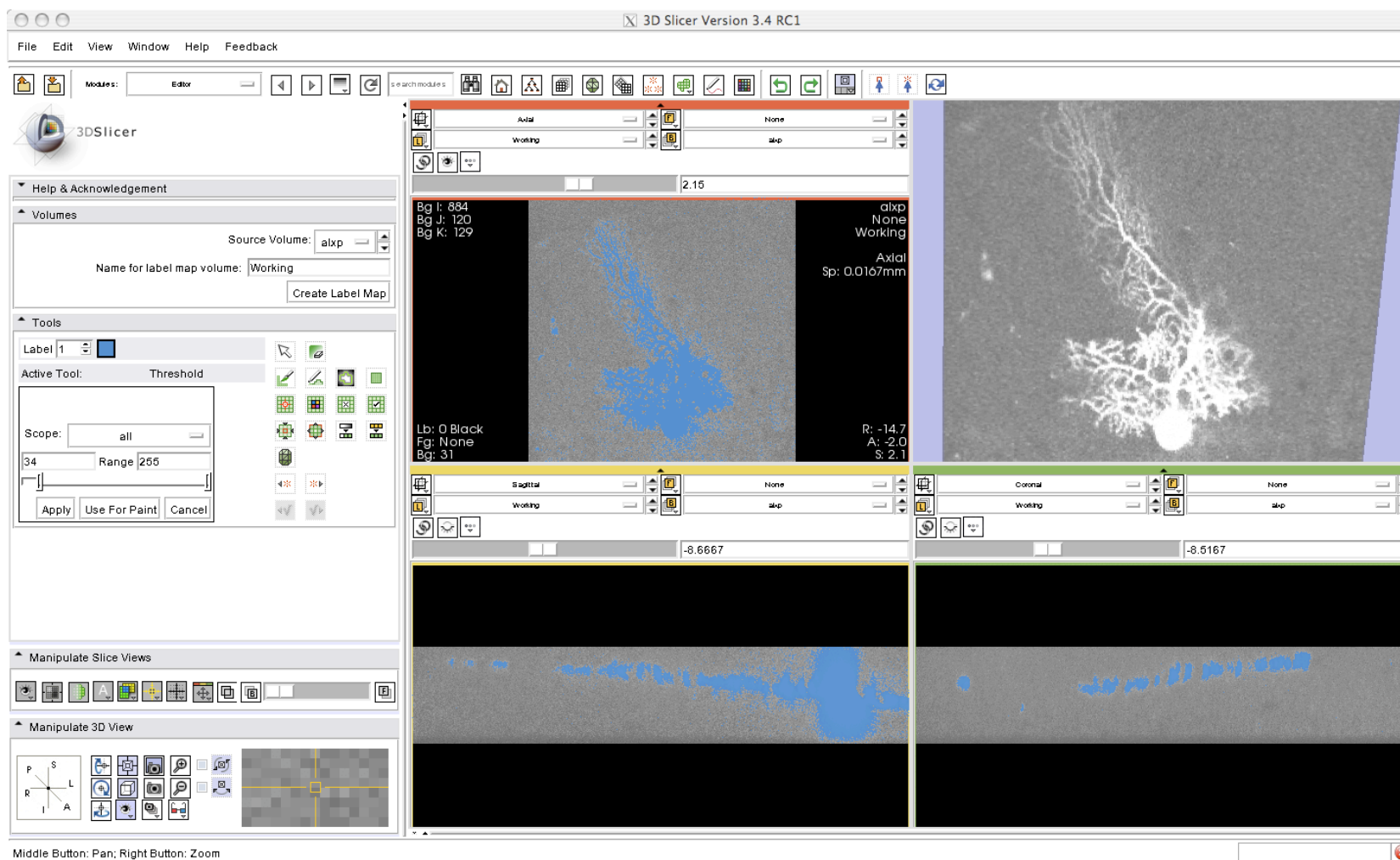
# Editing: Basic Thresholding



1) Can walk through image stack to preview thresholding



# Editing: Basic Thresholding







---

# *Model Building*

**Note: this section uses a smaller dataset so that computations can be completed in a reasonable time**



# Downloading Sample Data

The screenshot shows the Cell Centered Database website. The browser address bar displays 'http://ccdb.ucsd.edu/index.shtml'. The page header includes 'CELL CENTERED DATABASE™' and 'National Center for Microscopy and Imaging Research'. A search bar on the left contains the text 'astrocyte' and a 'Go' button. Below the search bar are sections for 'Resources', 'Features', and 'Sponsors'. The main content area is divided into three columns: '2D, 3D & 4D Data', 'Data Management', and 'Knowledge Engineering'. The footer contains copyright information and links for 'User agreement', 'Privacy Notice', 'Copyright', and 'Contact us'.

- 1) Enter Search Term: Astrocyte
- 2) Select 'Go'



# Downloading Sample Data

Cell Centered Database

http://ccdb.ucsd.edu/sand/main?stype=lite&keyword=astrocyte&event=display&Submit

## CELL CENTERED DATABASE™

National Center for Microscopy and Imaging Research

[Data](#) | [Search](#) | [Gallery](#) | [Dictionary](#) | [Publications](#) | [Tools](#) | [MyCCDB](#) | [Data Download](#) | [Help](#)

Home • Search result for **astrocyte** (Total: 204 records - [Modify search](#))  
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 [Next](#)

ID	Cell type	Structure	MP type	Thumbnails		
				Raw image	Reconstruction	Segmentation
<input type="checkbox"/> 8	protoplasmic astrocyte		confocal			
<input type="checkbox"/> 9	protoplasmic astrocyte		confocal			
<input type="checkbox"/> 10	protoplasmic astrocyte		confocal			
<input type="checkbox"/> 11	protoplasmic astrocyte		confocal			
<input type="checkbox"/> 37	protoplasmic astrocyte		confocal			
<input type="checkbox"/> 38	protoplasmic astrocyte		confocal			

**1) Select Astrocyte with ID 8**

**New Search**  
[Search home](#)  
Keyword    
Accession #    
Project ID    
**New!**  
If you want to search for some keywords in a detail info. page, just simply highlight the keywords, right click over the selected text and click "Search CCDB"

**Browse Products**  
[All records \(Data statistics\)](#)  
[Filled cells](#)  
[Protein localization](#)  
[Correlated light microscopy & electron microscopy](#)  
[Electron tomography](#)  
[Brain mosaics](#)  
**Most recently released!**

**Current Session**  
[Back to search result](#)  
[View MyLabBench](#)

Elapsed time: 2.8 sec.  
Version 2.15.16



# Downloading Sample Data

The screenshot shows the Cell Centered Database (CCDB) website interface. The browser address bar displays the URL: <http://ccdb.ucsd.edu/sand/main?mpid=8&event=displaySum>. The page title is "CELL CENTERED DATABASE™" and the subtitle is "National Center for Microscopy and Imaging Research". The navigation menu includes: Data | Search | Gallery | Dictionary | Publications | Tools | MyCCDB | Data Download | Help.

The main content area shows search results for "e13hpc1c". The "Summary Information" section includes a "Download dataset" button, which is highlighted by a dashed box and an arrow pointing to it from a text box on the left. The "Summary" table below provides details about the project.

Summary	
Project ID	P1123
Leader	Maryann Martone ( <a href="#">Other projects</a> )
Collaborators	Diana Price and Andrea Thor
Project Description	Confocal images
Experiment Purpose	to obtain multi resolution data for CCDB
Species	rat
System	central nervous system
Organ	brain
Region	hippocampus
Cell type	protoplasmic <b>astrocyte</b>
Structure	
Product Type	optical section series
Instrument	Biorad Radiance 2000 Confocal

1) Select 'Download dataset'



# Downloading Sample Data

CELL CENTERED DATABASE™  
National Center for Microscopy and Imaging Research

Data | Search | Gallery | Dictionary | Publications | Tools | MyCCDB | Data Download | Help

Home · View MyLabBench · Terms & Conditions

**New Search**  
Search home  
Keyword  Go  
Accession #  Go  
Project ID  Go

**New!**  
If you want to search for some keywords in a detail info. page, just simply highlight the keywords, right click over the selected text and click "Search CCDB"

**Browse Products**  
All reports (Data statistics)  
Filled cells  
Protein localization  
Correlated light microscopy & electron microscopy  
Electron tomography  
Brain mosaics  
Most recently released!

**Current Session**  
Back to search result  
View MyLabBench

**Terms & Conditions**  
Please provide a valid email address. You will receive an email notification when there is any modification or update to the dataset you chose to download.

Your valid email address  (Required)  
Your title & name  (Required)  
Your institute name  (Required)

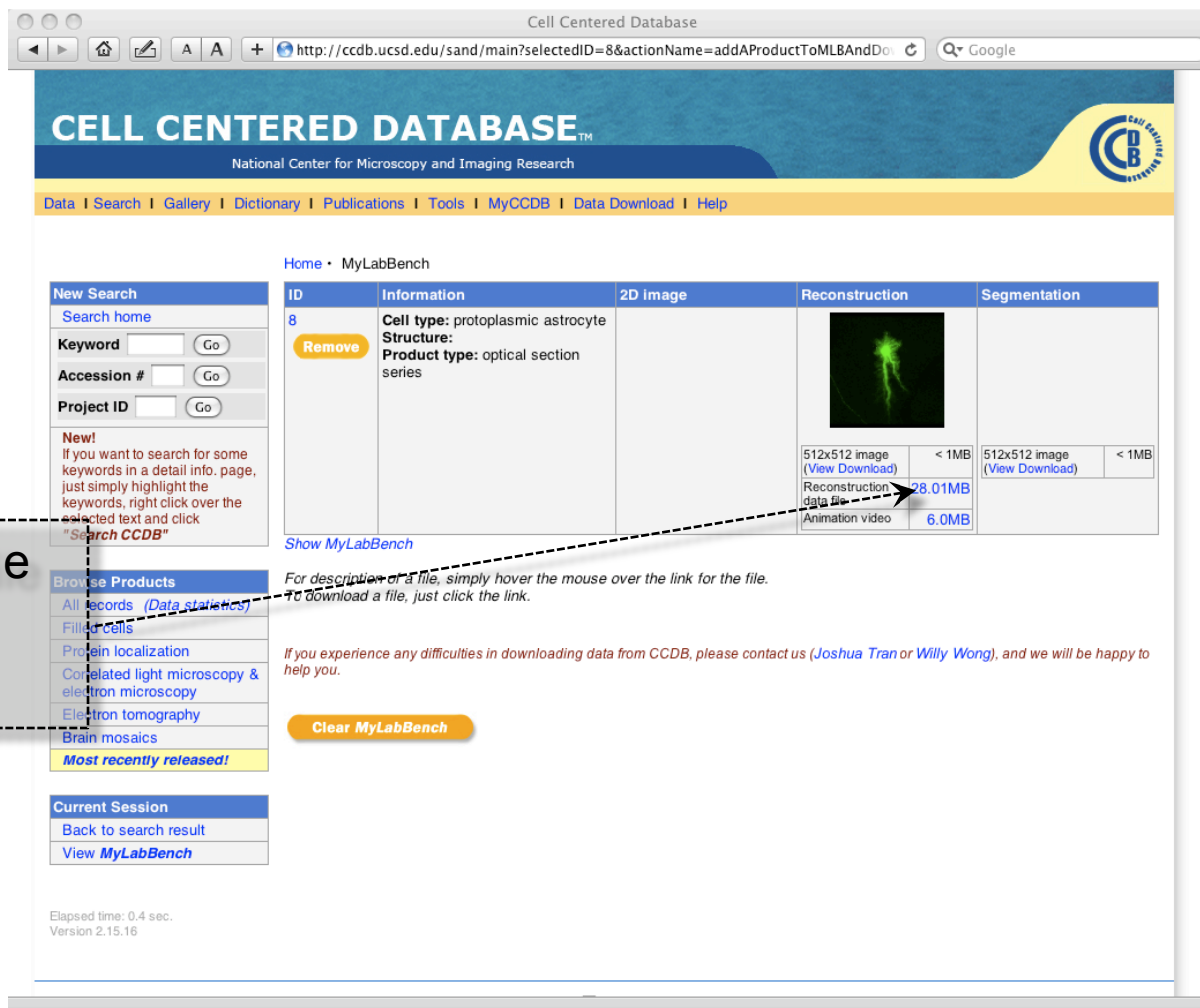
By clicking on the following button, I agree to all of the [terms and conditions](#).

Elapsed time: 0.0 sec.  
Version 2.15.16

1) Enter required information to receive updates

2) Select 'Continue'

# Downloading Sample Data



Cell Centered Database

http://ccdb.ucsd.edu/sand/main?selectedID=8&actionName=addAProductToMLBAndDo

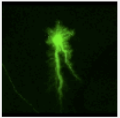
**CELL CENTERED DATABASE™**  
National Center for Microscopy and Imaging Research

Data | Search | Gallery | Dictionary | Publications | Tools | MyCCDB | Data Download | Help

Home · MyLabBench

**New Search**  
Search home  
Keyword  Go  
Accession #  Go  
Project ID  Go

**New!**  
If you want to search for some keywords in a detail info. page, just simply highlight the keywords, right click over the selected text and click "Search CCDB"

ID	Information	2D Image	Reconstruction	Segmentation
8	Cell type: protoplasmic astrocyte Structure: Product type: optical section series <a href="#">Remove</a>		 512x512 image (View Download) < 1MB <b>Reconstruction data file 28.01MB</b> Animation video 6.0MB	512x512 image (View Download) < 1MB

[Show MyLabBench](#)

For description of a file, simply hover the mouse over the link for the file. To download a file, just click the link.

If you experience any difficulties in downloading data from CCDB, please contact us (Joshua Tran or Willy Wong), and we will be happy to help you.

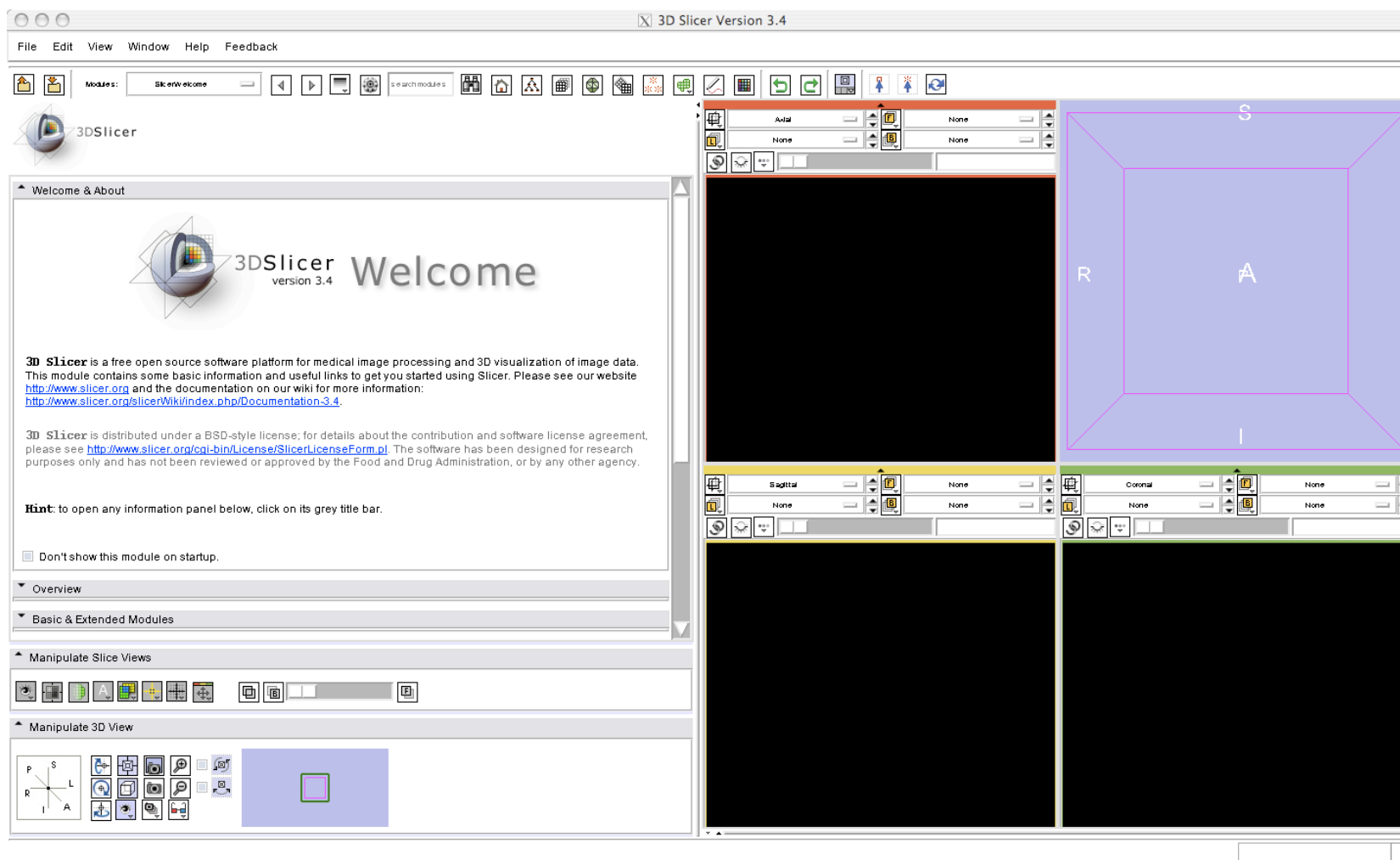
[Clear MyLabBench](#)

Elapsed time: 0.4 sec.  
Version 2.15.16

1) Download data file by selecting '28.01MB'



# Launch Slicer



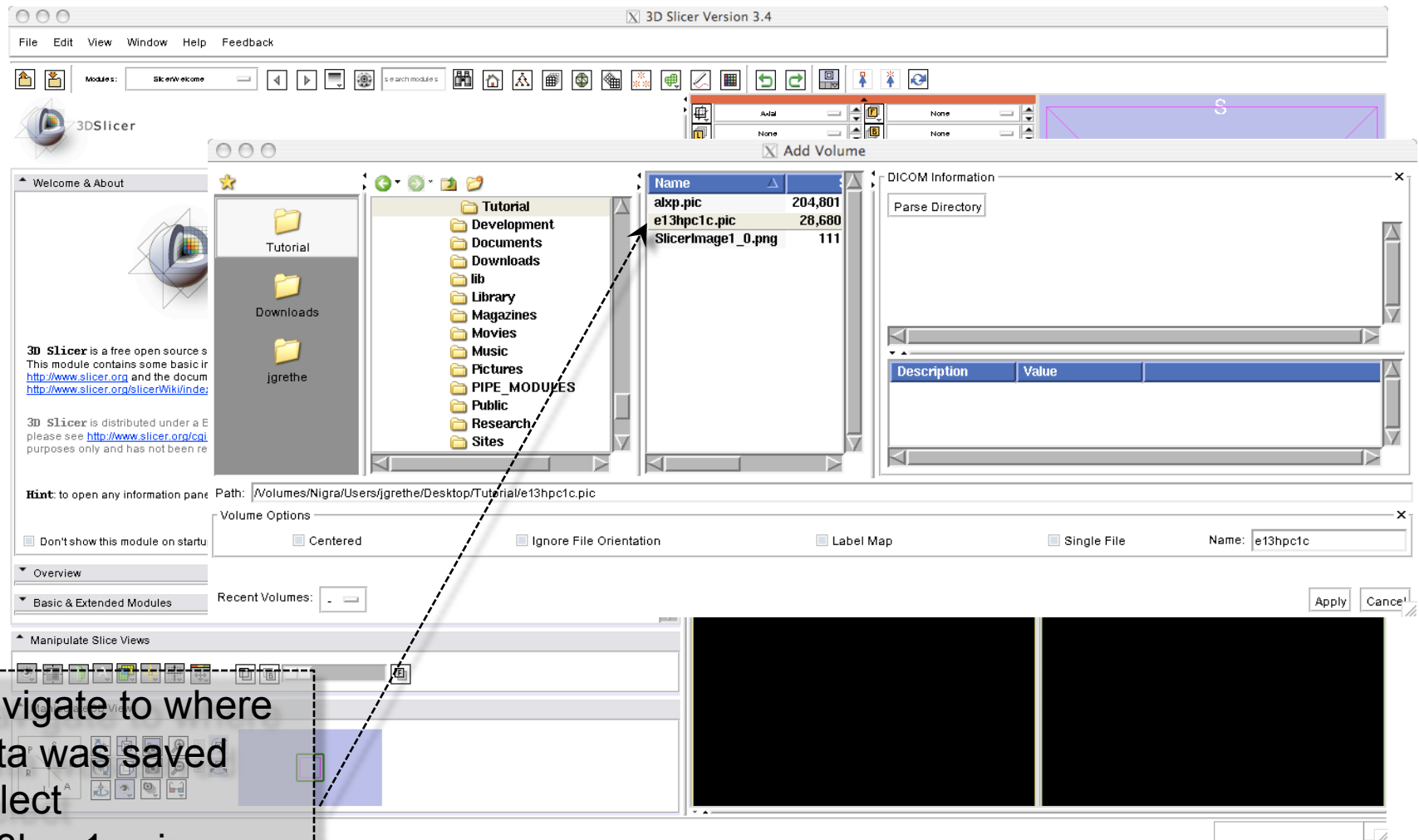


# Open Astrocyte Data

The screenshot shows the 3D Slicer 3.4 application window. The 'File' menu is open, displaying the following options: Load Scene... (Ctrl-O), Import Scene..., Add Data... (Ctrl-A), Add Volume... (highlighted), Add Transform..., Save (Ctrl-S), Close Scene (Ctrl-W), and Exit. A dashed arrow points from the 'Add Volume...' option in the menu to a callout box. The callout box contains the text: '1) Select 'Add Volume' from the File menu'. The main interface shows a 3D visualization area with a purple wireframe box, and various toolbars and panels are visible.



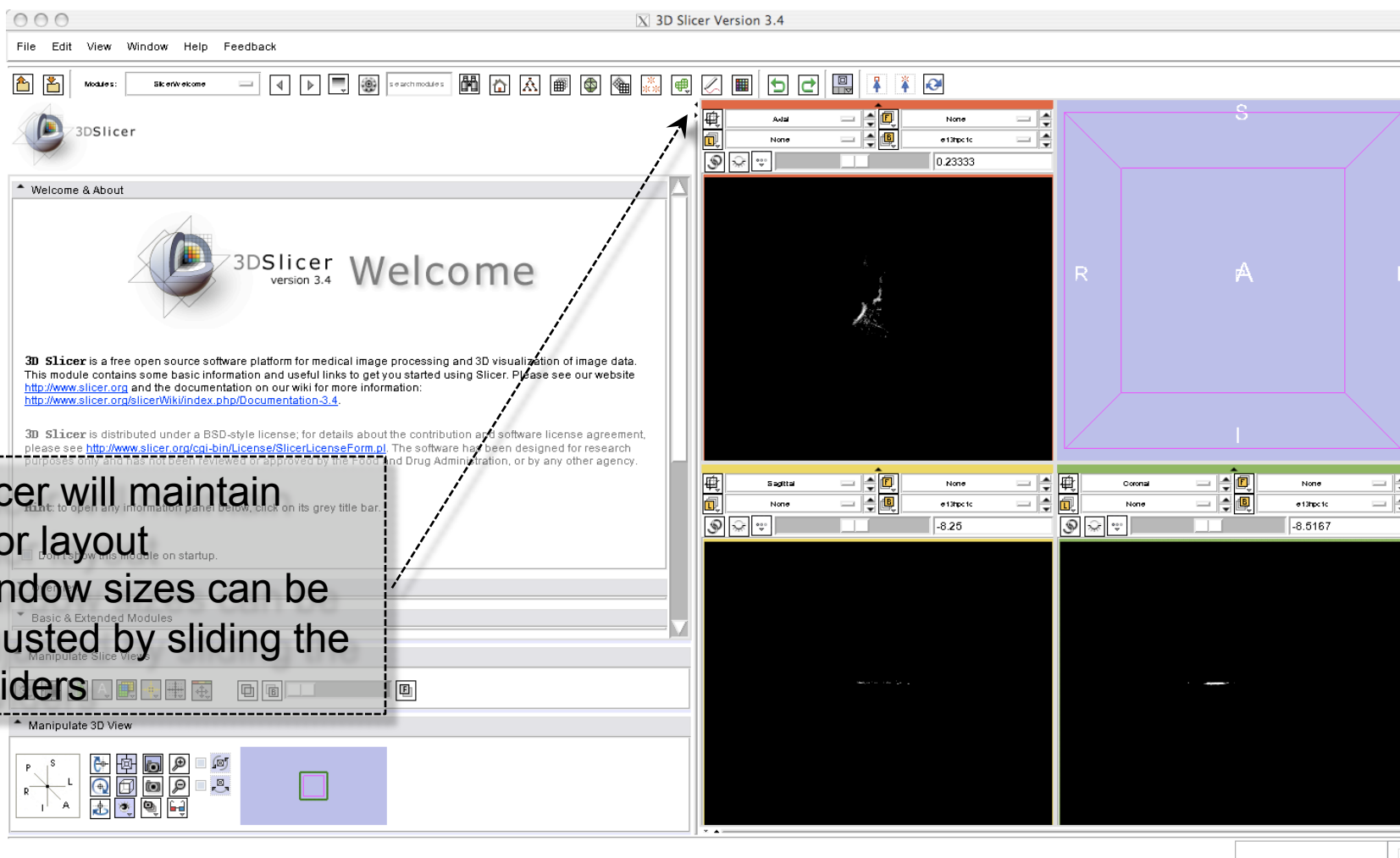
# Open Astrocyte Data



- 1) Navigate to where data was saved
- 2) Select e13hpc1c.pic
- 3) Select 'Apply'



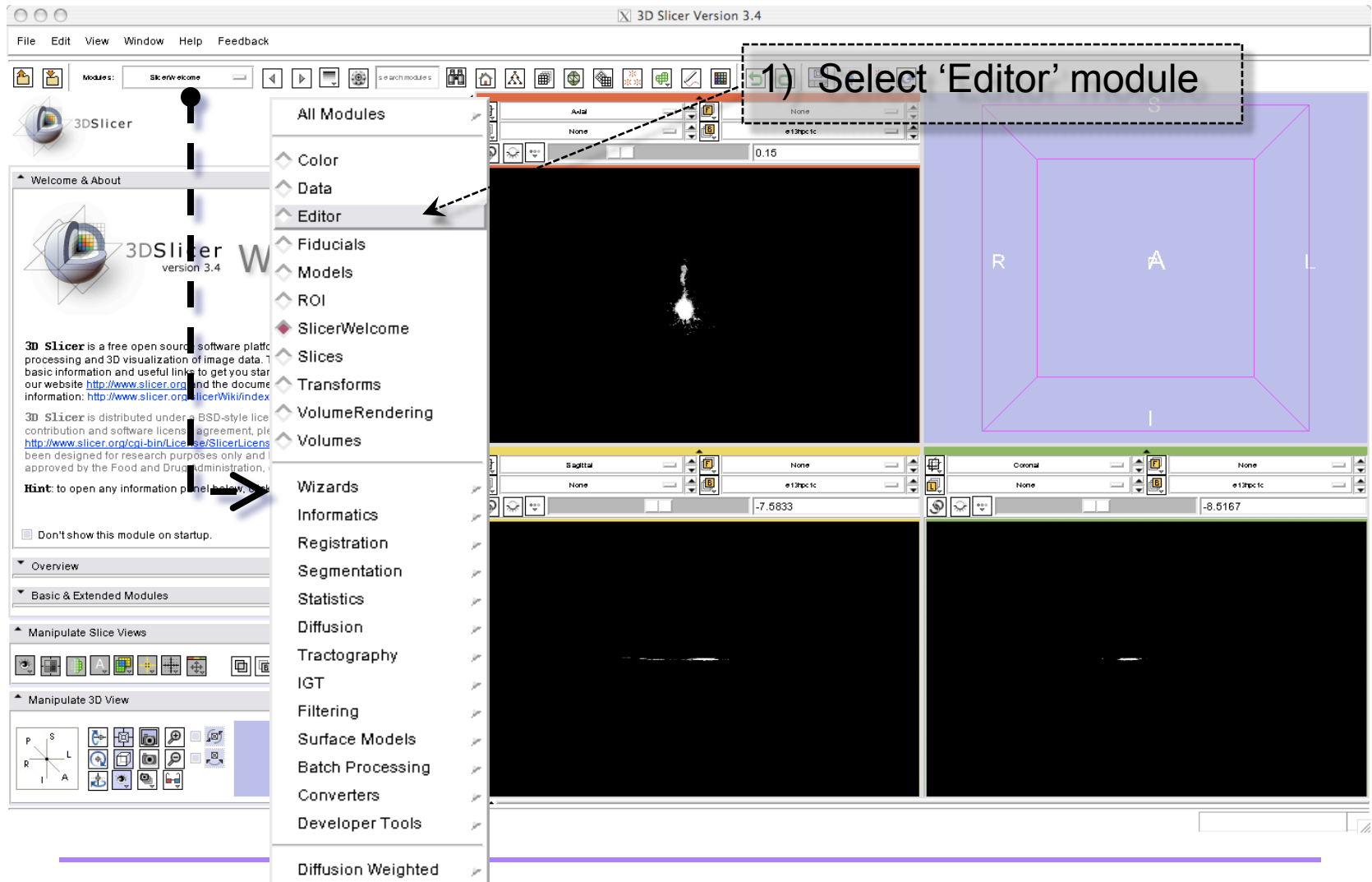
# Adjust Slicer Panels



- 1) Slicer will maintain prior layout
- 2) Window sizes can be adjusted by sliding the dividers



# Model Building: Threshold





# Model Building: Threshold

1) Select 'e13hpc1c' Source Volume

2) Name the label map

3) Select 'Create Label Map'



# Model Building: Threshold

1) Select 'Thresholding' tool

2) Use sliders to adjust thresholding levels

3D Slicer Version 3.4

File Edit View Window Help Feedback

Modules: Editor

Source Volume: e13hpc1c

Name for label map volume: Threshold\_LM

Tools

Label 1

Active Tool: Threshold

Scope: all

100 Range 253

Apply Use For Paint Cancel

Enable Volume Check Points

Manipulate 3D View

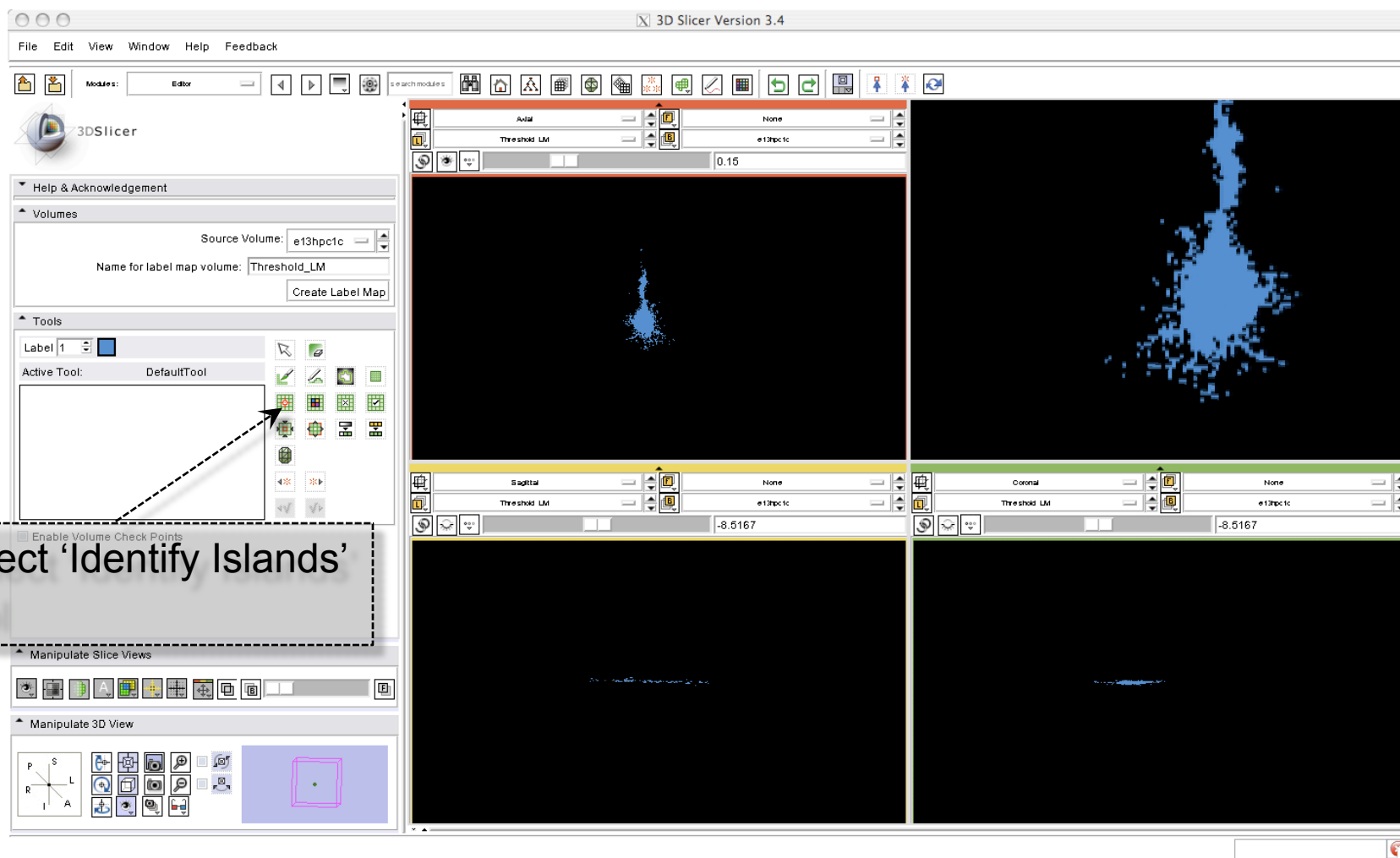
Axial None e13hpc1c 0.15

Sagittal None e13hpc1c -8.5167

Coronal None e13hpc1c -8.5167



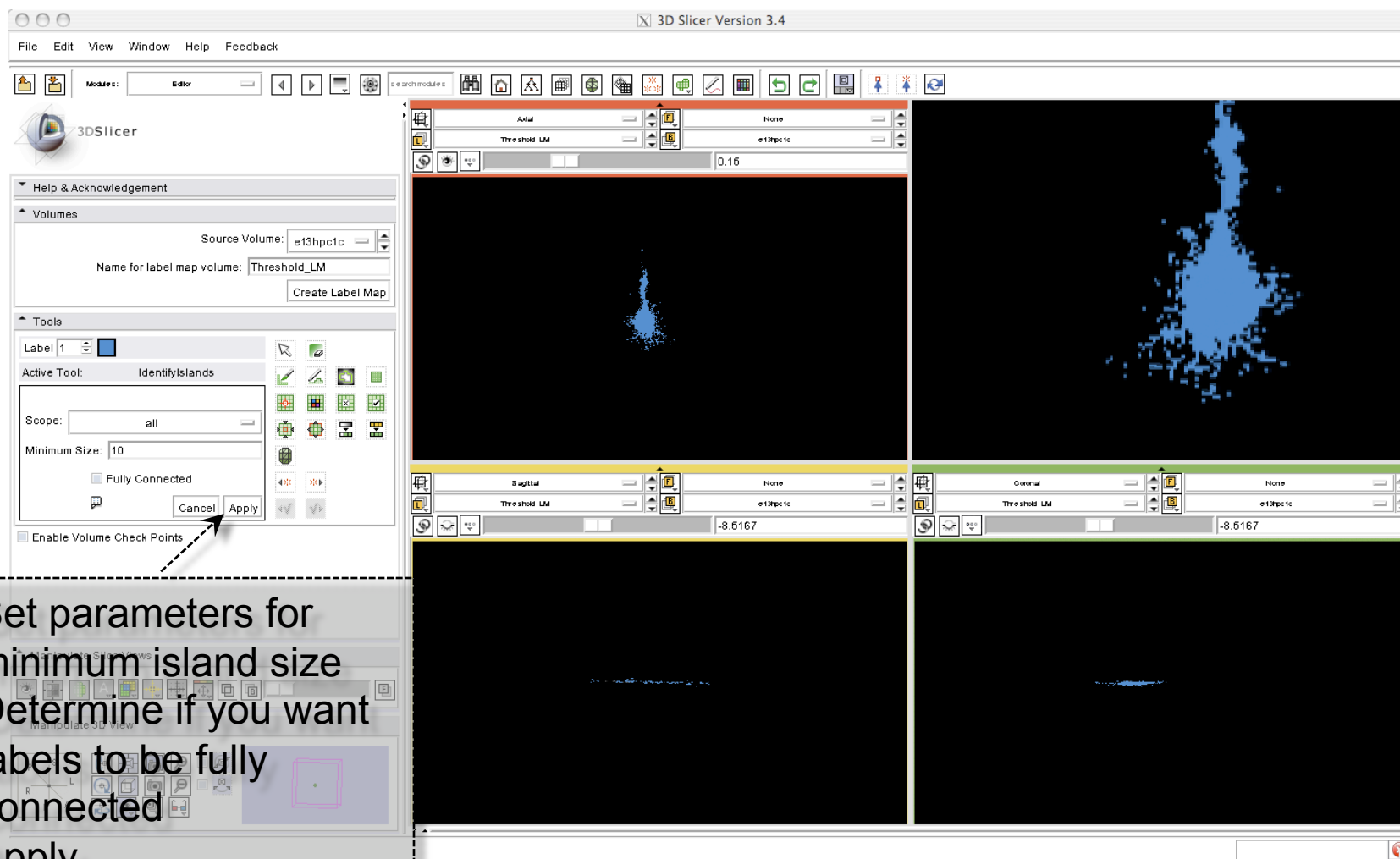
# Model Building: Threshold



1) Select 'Identify Islands' tool

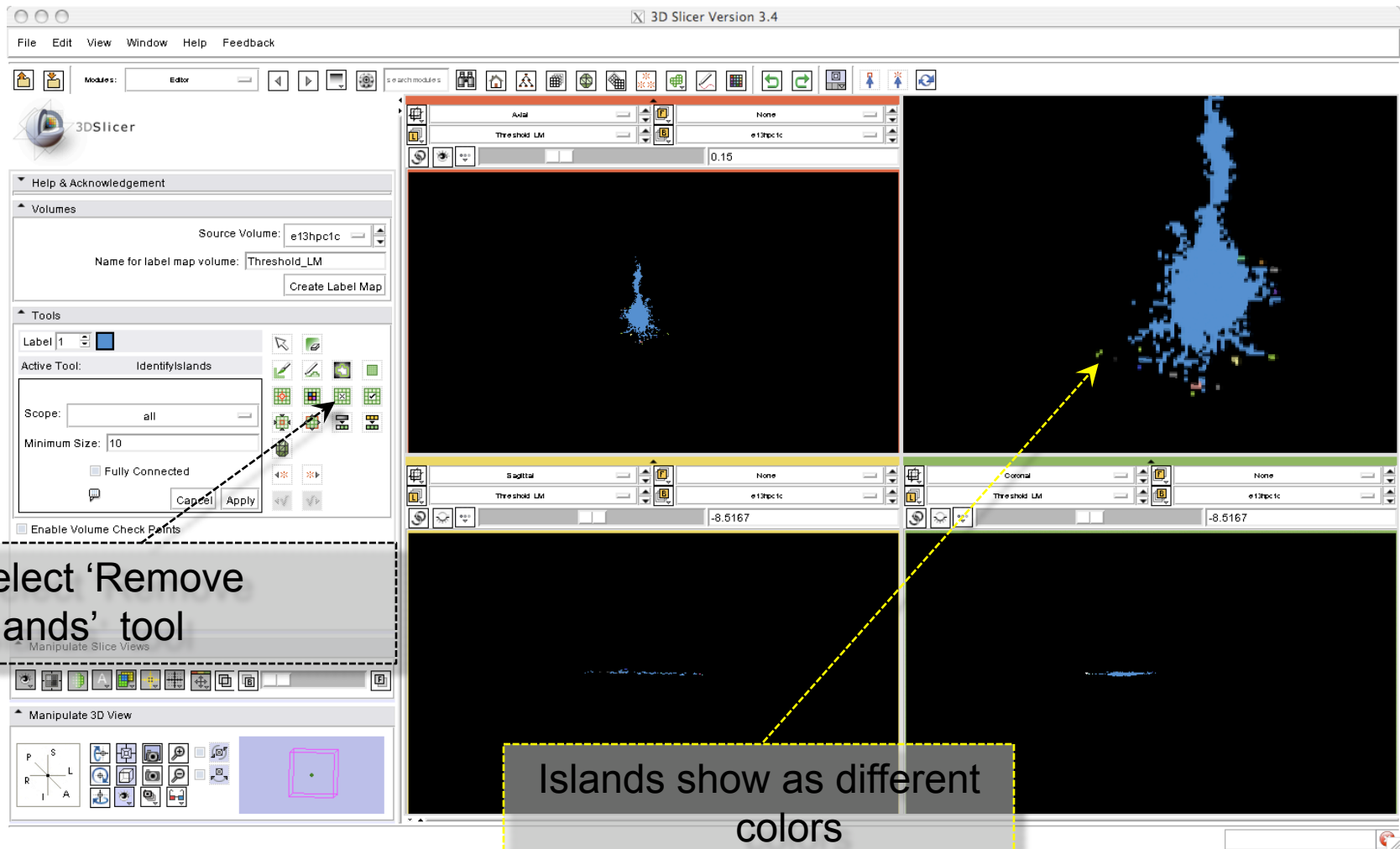


# Model Building: Threshold



- 1) Set parameters for minimum island size
- 2) Determine if you want labels to be fully connected
- 3) Apply

# Model Building: Threshold



The screenshot displays the 3D Slicer 3.4 interface. The top menu bar includes File, Edit, View, Window, Help, and Feedback. The main workspace is divided into three orthogonal views: Axial, Sagittal, and Coronal. Each view shows a thresholded volume (Threshold LM) with a value of 0.15. The volume is segmented into different colored regions (islands). A yellow dashed arrow points from a text box at the bottom to these colored regions.

On the left side, the 'Tools' panel is visible, showing the 'Identify Islands' tool selected. The 'Scope' is set to 'all' and the 'Minimum Size' is 10. A dashed arrow points from a text box to the 'Remove Islands' tool icon in this panel.

At the bottom left, a text box contains the instruction: "1) Select 'Remove Islands' tool".

At the bottom center, a text box contains the instruction: "Islands show as different colors".





# Model Building: Threshold

The screenshot displays the 3D Slicer 3.4 software interface. The main window is divided into several panels. On the left, the 'Tools' panel is active, showing the 'Remove Islands' tool. A dashed box highlights this tool with the text '1) Remove Islands'. Below it, another dashed box highlights the 'Model Builder Tool' with the text '2) Select 'Model Builder Tool''. The main 3D view area shows a blue segmented volume in three orthogonal planes: Axial, Sagittal, and Coronal. The 'Axial' view shows a threshold of 0.15, while the 'Sagittal' and 'Coronal' views show a threshold of -8.5167. The 'Model Builder Tool' is located in the bottom-left corner of the interface.



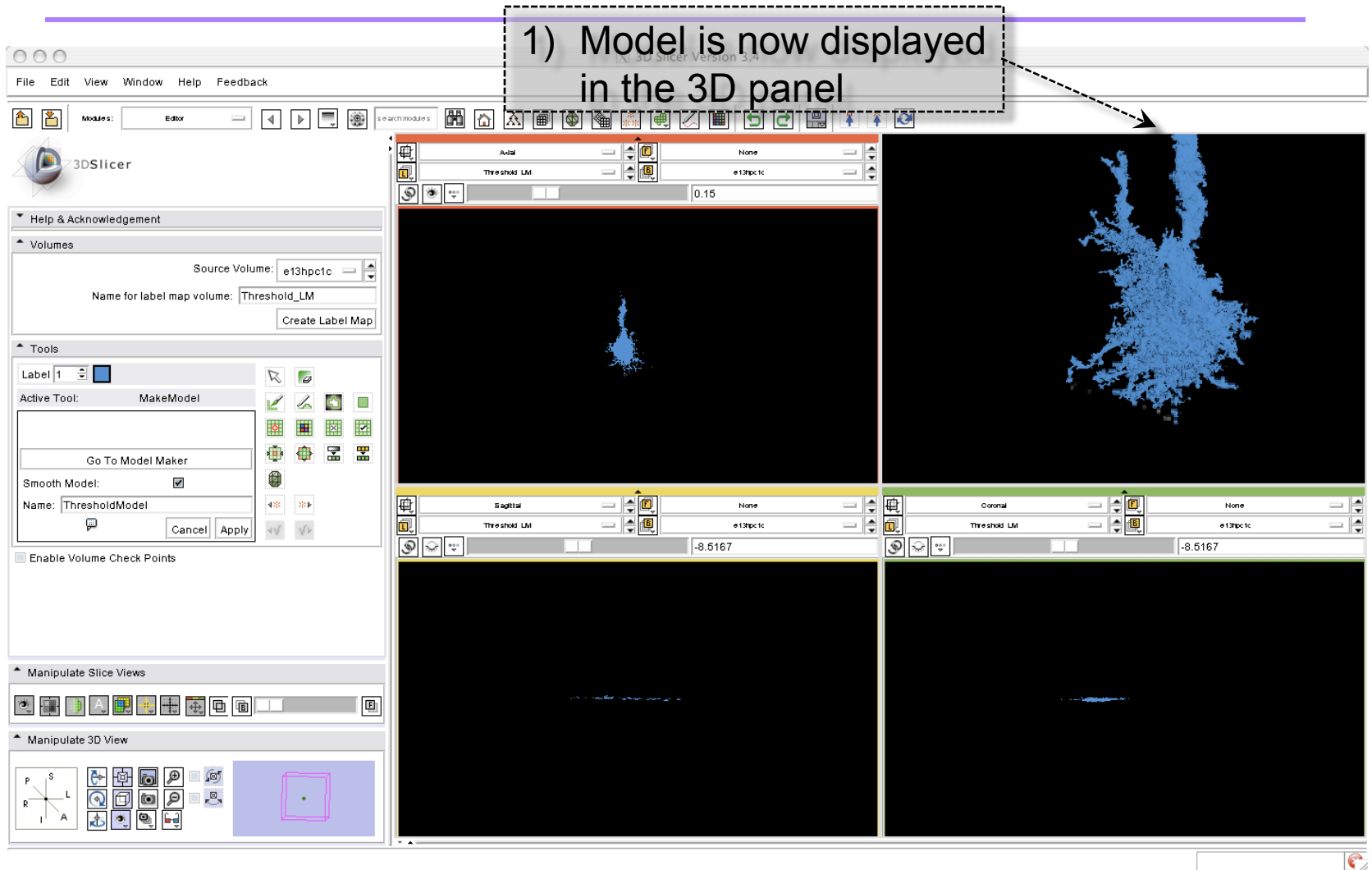
# Model Building: Threshold

The screenshot shows the 3D Slicer 3.4 interface. On the left, the 'Tools' panel is open, showing the 'MakeModel' tool. The 'Name' field is set to 'ThresholdModel'. The 'Apply' button is highlighted with a dashed box and an arrow pointing to it. The main 3D view shows a brain slice with a blue thresholded region. The 'Threshold LM' tool is active, and the 'Threshold' value is set to 0.15. The 'Sagittal' and 'Coronal' views are also visible, showing the same thresholded region.

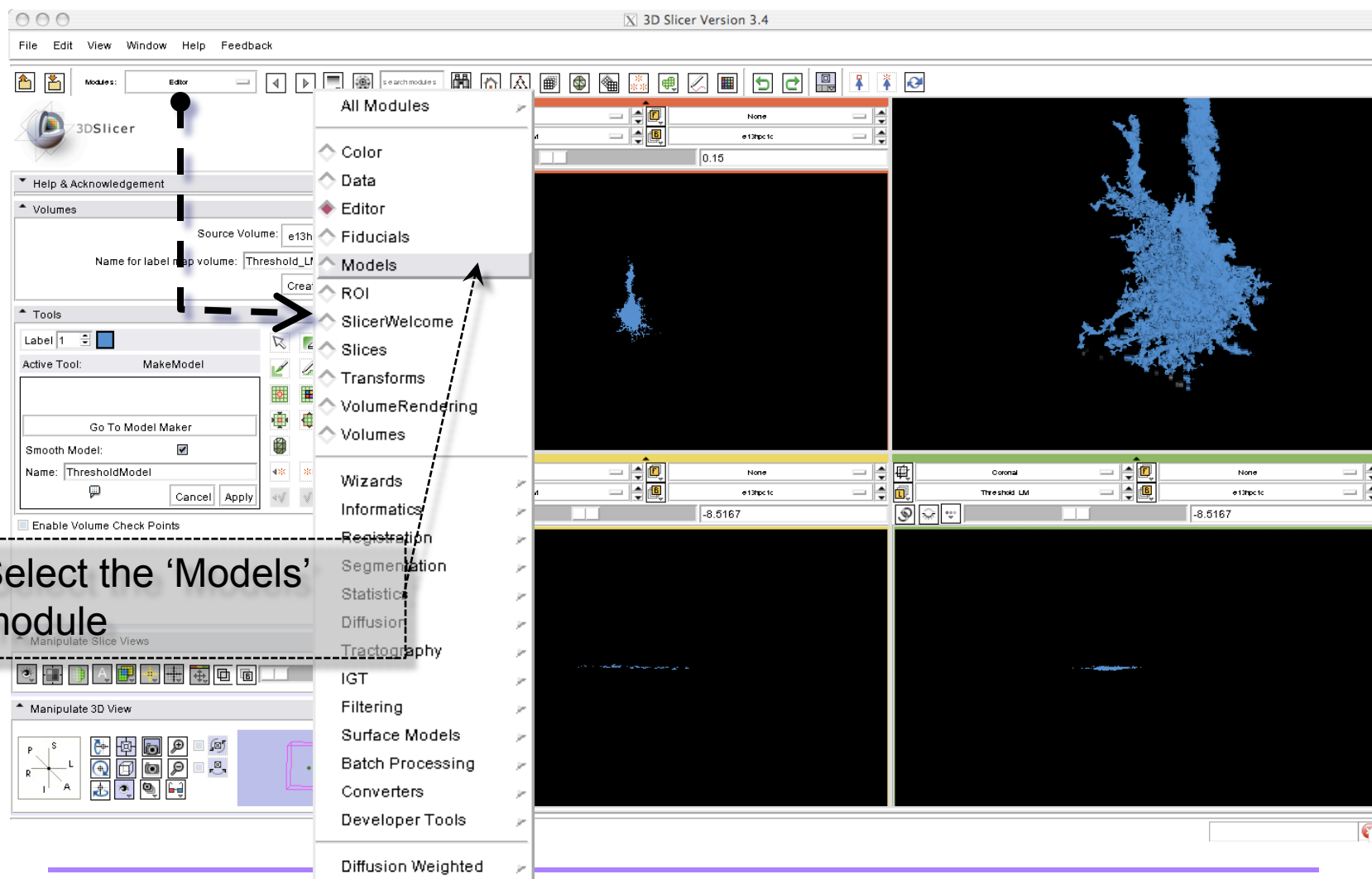
1) Name the model  
2) Generate model with defaults



# Model Building: Threshold



# Model Building: Threshold

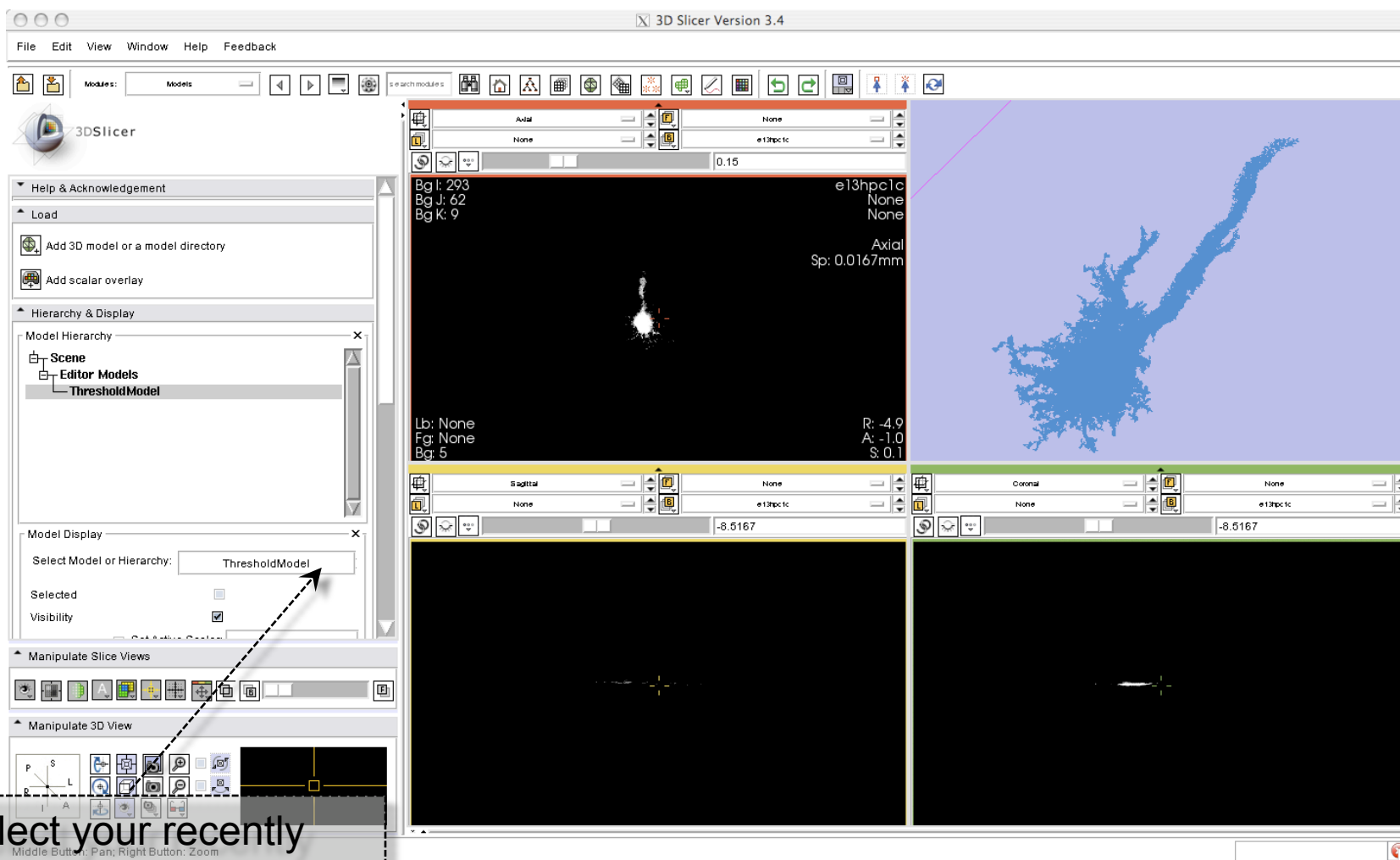


The screenshot displays the 3D Slicer 3.4 interface. The 'All Modules' list is open, and the 'Models' module is highlighted. A callout box with a dashed border contains the text '1) Select the 'Models' module'. The interface shows a 3D view of a brain slice with a blue thresholded region. The 'Tools' panel is visible, showing the 'MakeModel' tool. The 'Volumes' panel shows the source volume 'e13h' and the name for the label map volume 'Threshold\_LI'. The 'Slices' panel shows the 'Coronal' slice view with a threshold value of -8.5167.

1) Select the 'Models' module

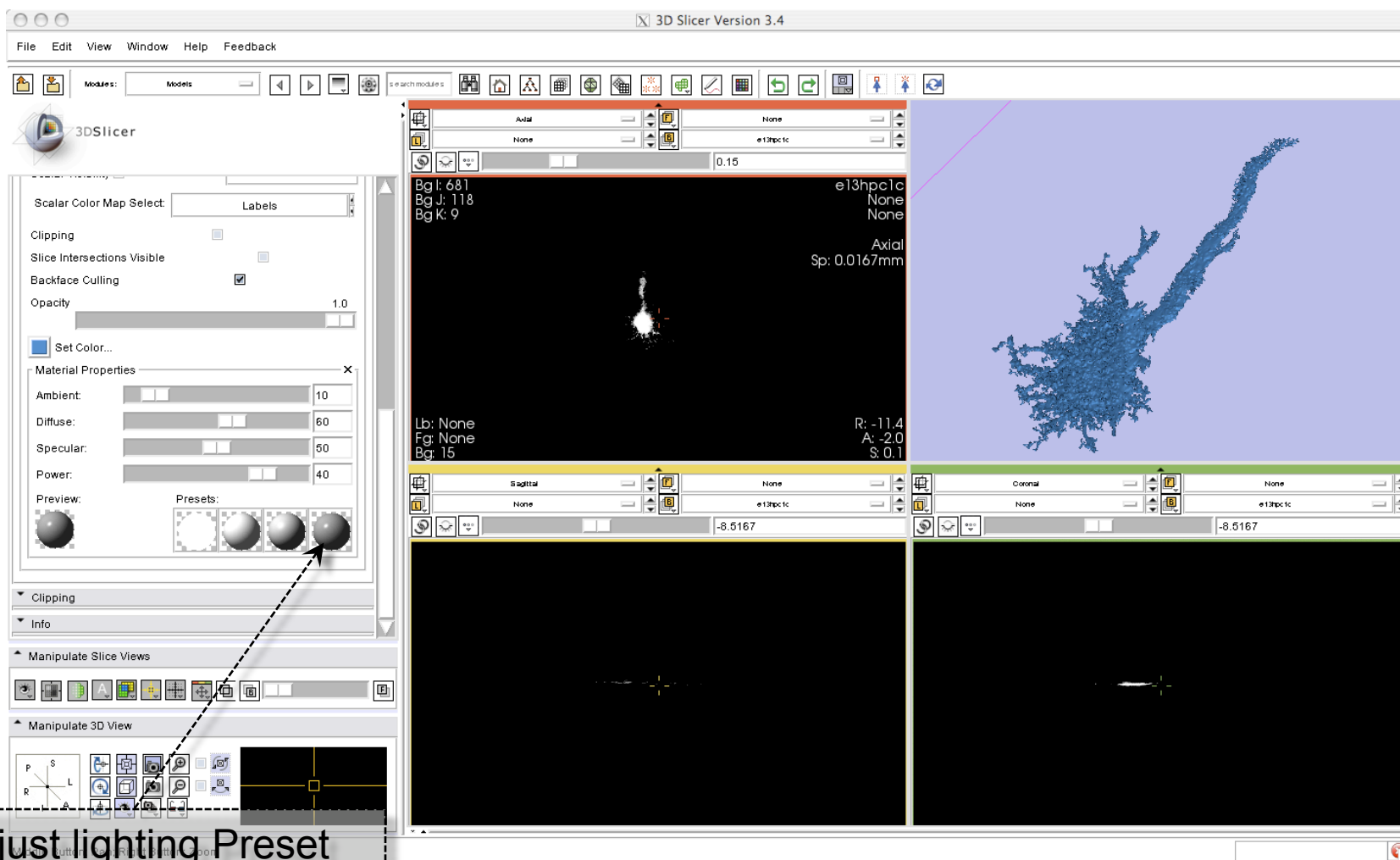


# Model Building: Threshold





# Model Building: Threshold





# Model Building: Threshold

1) Adjust opacity

The screenshot shows the 3D Slicer 3.4 interface. On the left, the Clipping panel is open, showing the Opacity slider set to 0.8. A dashed box highlights the '1) Adjust opacity' text and the Clipping panel. The main 3D view shows a blue 3D model of a brain slice. The Clipping panel also shows material properties: Ambient: 10, Diffuse: 60, Specular: 50, Power: 40. The Clipping panel also has a 'Manipulate Slice Views' section with icons for various slice views and a 'Manipulate 3D View' section with a navigation pad and icons for pan, zoom, and other view controls.

Middle Button: Pan; Right Button: Zoom





# Model Building: Threshold

1) Adjust 3D Panel view by removing cube, labels and setting background color

Material Properties

Ambient: 10  
Diffuse: 60  
Specular: 50  
Power: 40

Clipping

Info

Manipulate Slice Views

Manipulate 3D View

- Fiducial points
- Fiducial labels
- 3D cube
- 3D axis labels
- Light blue background
- Black background
- White background

close



# Model Building: Threshold

3D Slicer Version 3.4

File Edit View Window Help Feedback

Modules: Models

Scalar Color Map Select: Labels

Clipping

Slice Intersections Visible

Backface Culling

Opacity 0.8

1) With model completed – now export the view

Specular: 50

Power: 40

Preview:

Presets:

Manipulate Slice Views

Manipulate 3D View

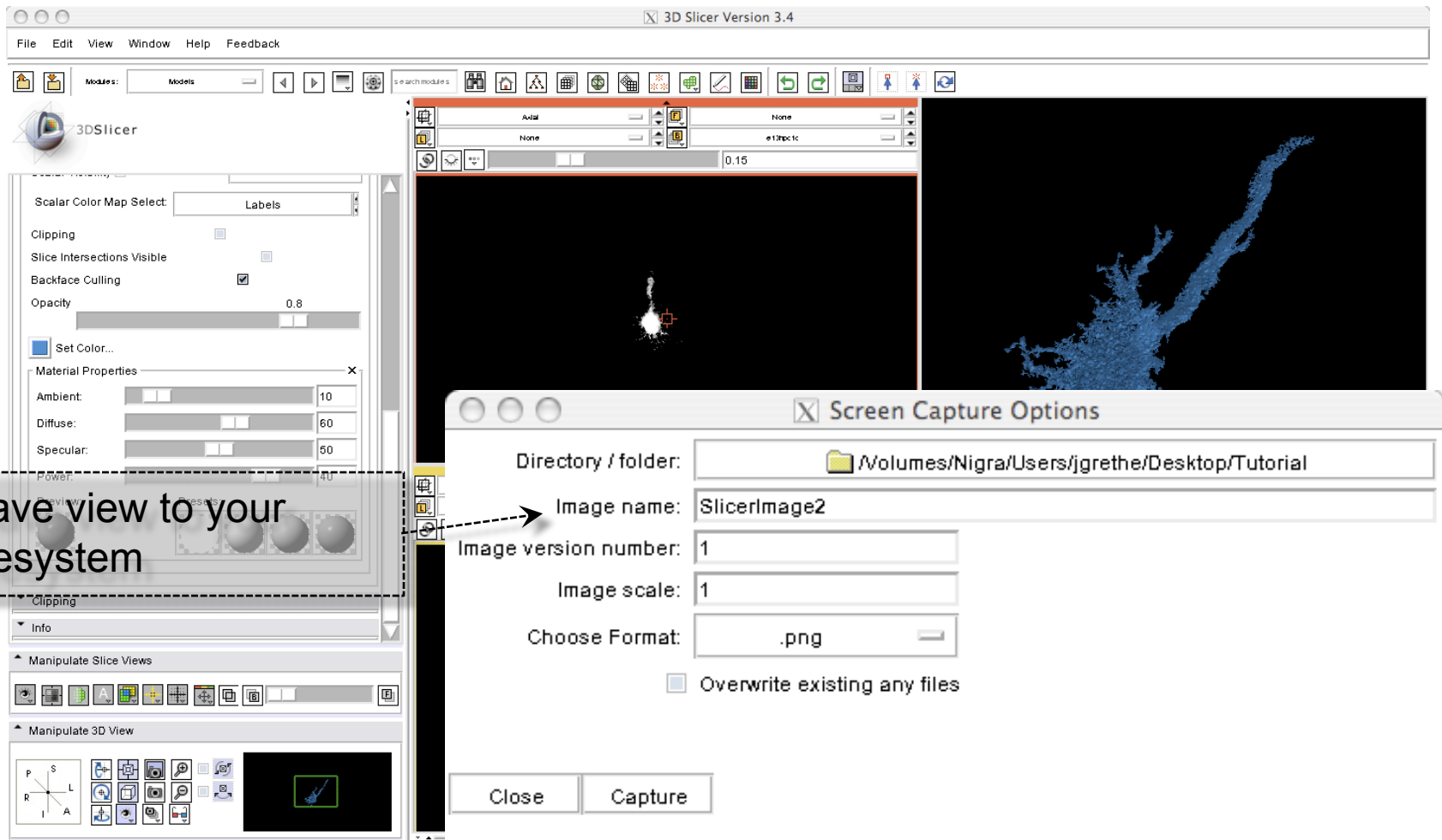
Avial None 0.15

Sagittal None -8.5167

Coronal None -8.5167



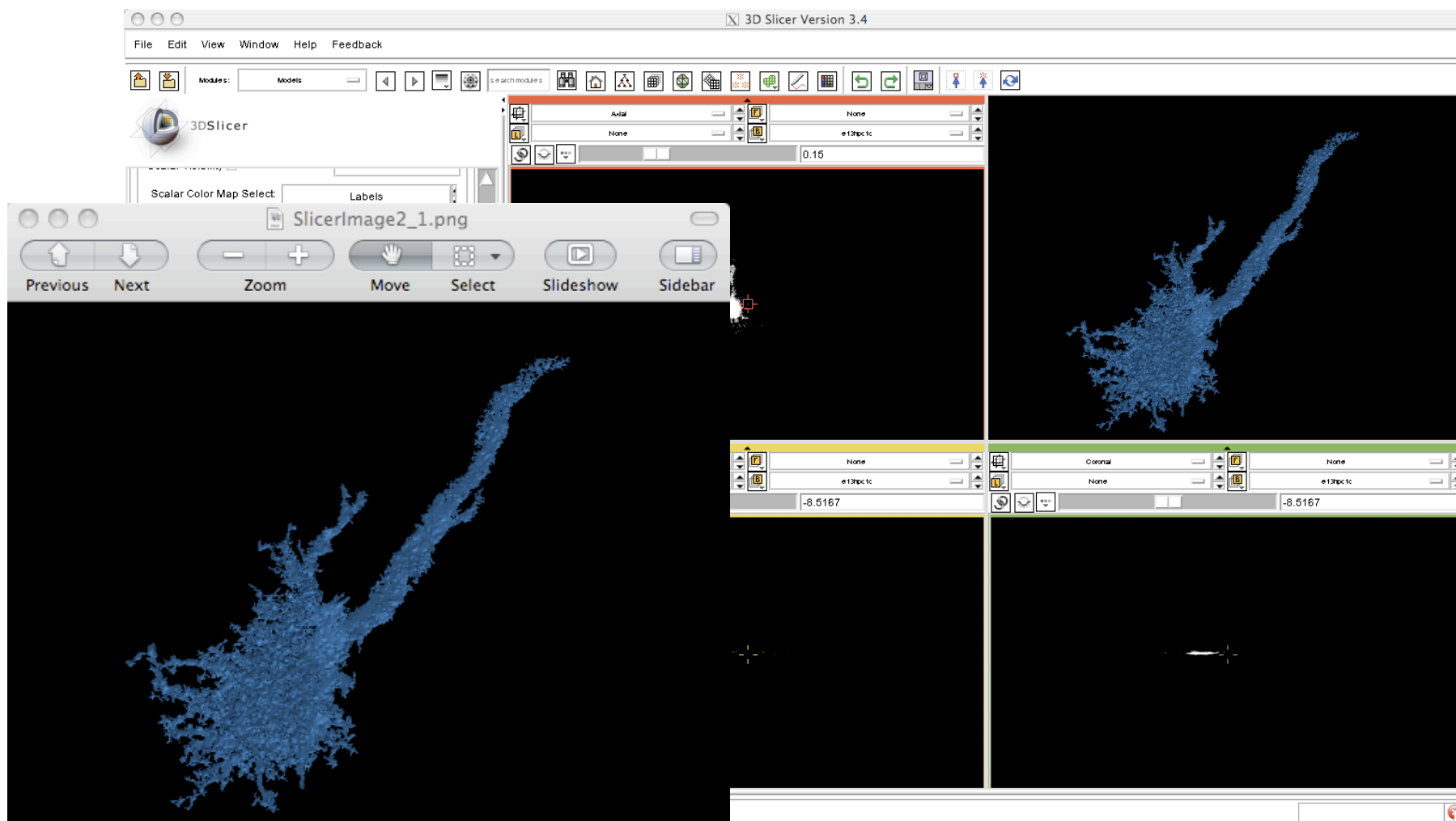
# Model Building: Threshold



1) Save view to your filesystem



# Completed Threshold Model Building





# *Model Building: Otsu Segmentation*

---

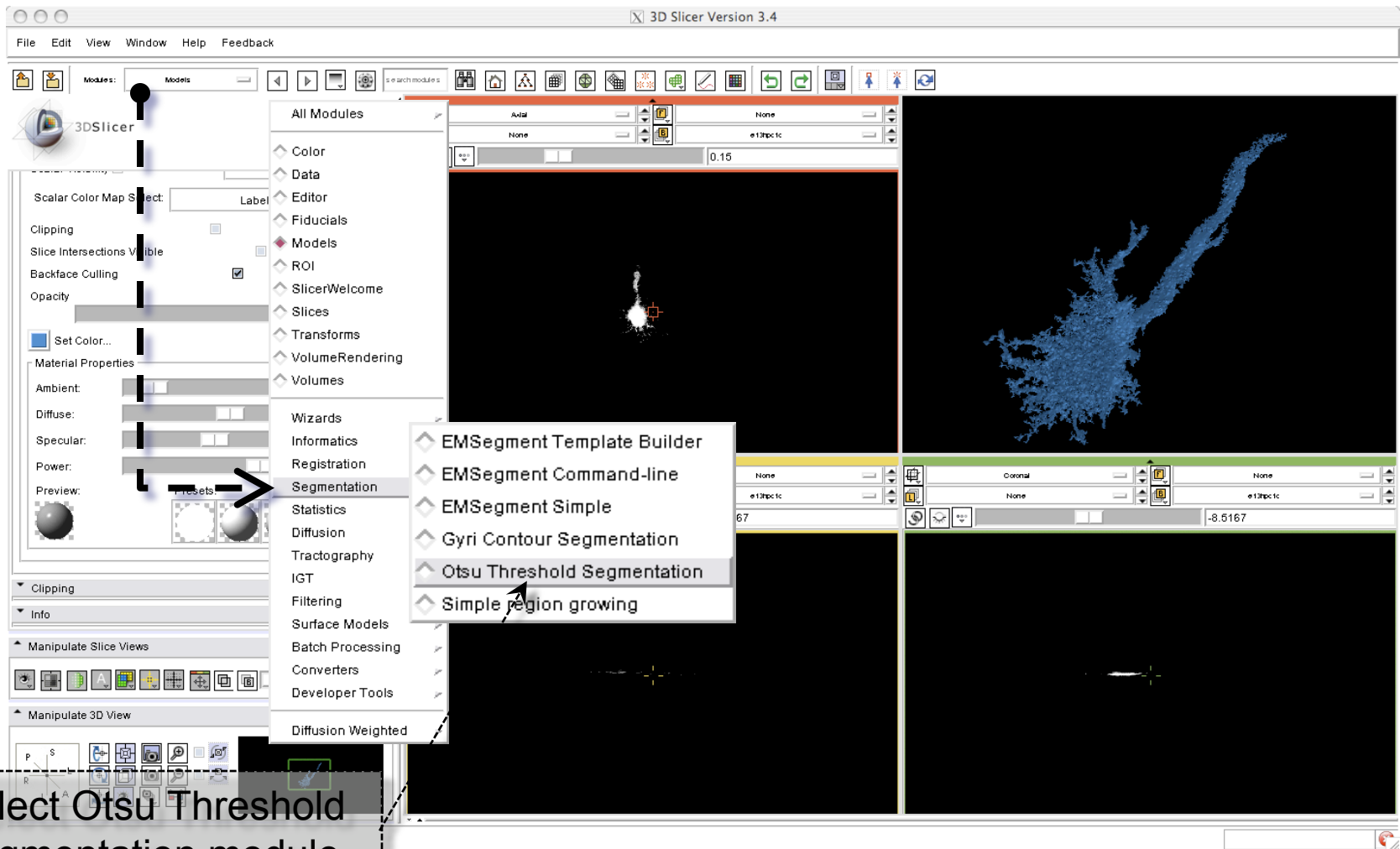
In computer vision and image processing, Otsu's method is used to automatically perform histogram shape-based image thresholding, or the reduction of a graylevel image to a binary image. The algorithm assumes that the image to be thresholded contains two classes of pixels (e.g. foreground and background) then calculates the optimum threshold separating those two classes so that their combined spread (intra-class variance) is minimal.

[http://en.wikipedia.org/wiki/Otsu's\\_method](http://en.wikipedia.org/wiki/Otsu's_method)

This section of the tutorial will demonstrate the use of Slicer Command Line Modules

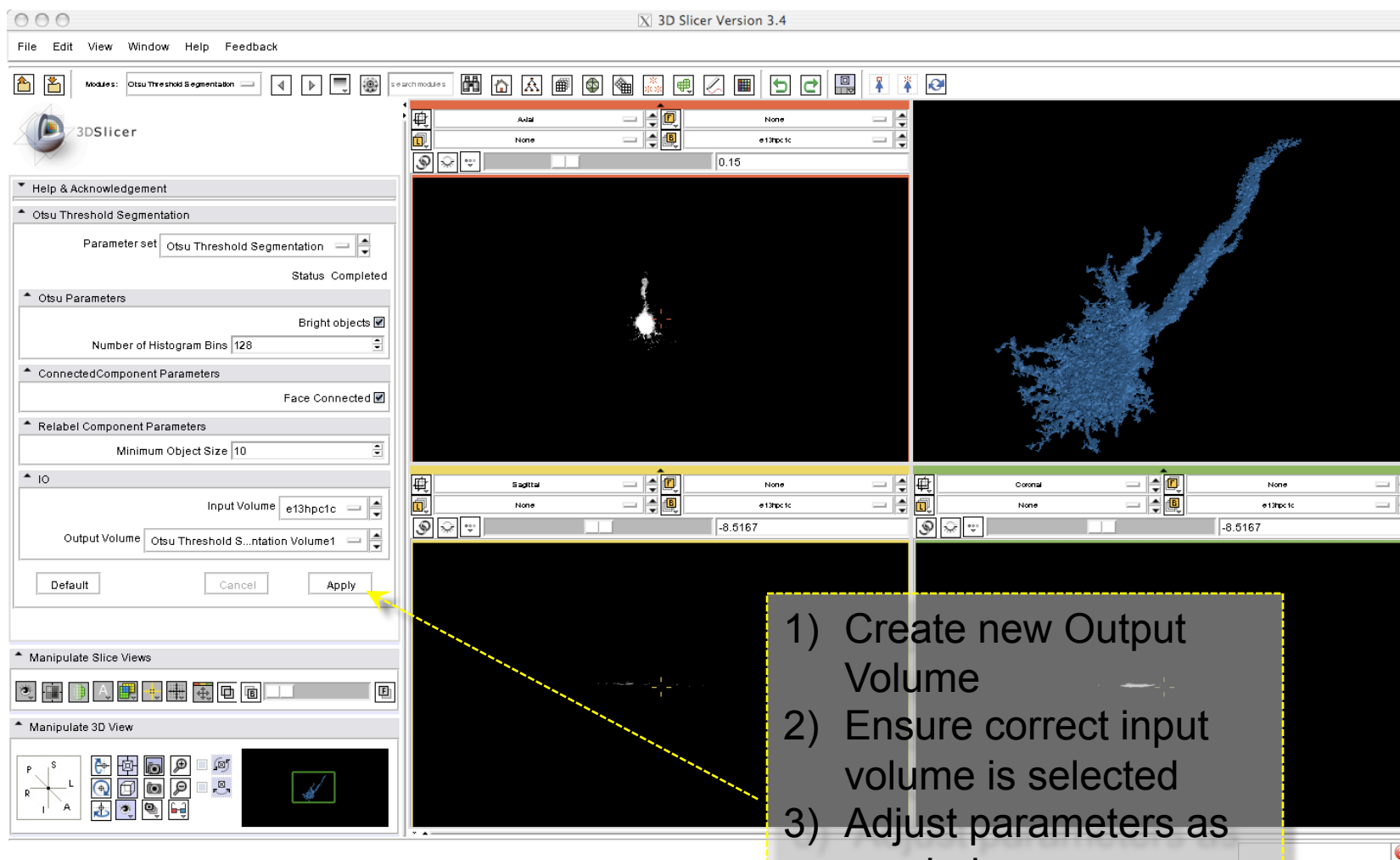


# Model Building: Otsu Segmentation





# Model Building: Otsu Segmentation







# Model Building: Otsu Segmentation

The screenshot displays the 3D Slicer 3.4 software interface. The main window is titled "3D Slicer Version 3.4" and shows the "Otsu Threshold Segmentation" module active. The left sidebar contains various toolbars, including "Help & Acknowledgement", "Otsu Threshold Segmentation" (with a parameter set of "Otsu Threshold Segmentation"), "Otsu Parameters" (with "Number of Histogram Bins" set to 128), "ConnectedComponent Parameters", "Relabel Component Parameters" (with "Minimum Object Size" set to 10), "IO", "Manipulate Slice Views", and "Manipulate 3D View". The top toolbar includes a search icon and a "1) Select 'Editor' module" annotation with a dashed box around the "Editor" icon. A dropdown menu is open, listing "All Modules" and various categories: Color, Data, Editor (highlighted with a dashed arrow), Fiducials, Models, ROI, SlicerWelcome, Slices, Transforms, VolumeRendering, Volumes, Wizards, Informatics, Registration, Segmentation, Statistics, Diffusion, Tractography, IGT, Filtering, Surface Models, Batch Processing, Converters, Developer Tools, and Diffusion Weighted. The main view area shows a 3D rendering of a segmented volume in blue, with a corresponding 2D slice view below it. The slice view shows a cross-section of the volume with a blue line representing the segmented structure. The slice view is labeled "Otsu Threshold Segmentation Volume 1" and has a value of -8.5167. The top right corner of the main view area shows a "0.23333" value.



# Model Building: Otsu Segmentation

3D Slicer Version 3.4

File Edit View Window Help Feedback

Modules: Editor

3DSlicer

Help & Acknowledgement

Volumes

Source Volume: Otsu Threshold Segmentation Volume1

Name for label map volume: Threshold\_Otsu

Create Label Map

Tools

Label 1

Active Tool: DefaultTool

4) Select label thresholding tool

1) Ensure Otsu source volume is selected

2) Name Otsu label map

3) Create label map for Otsu segmentation



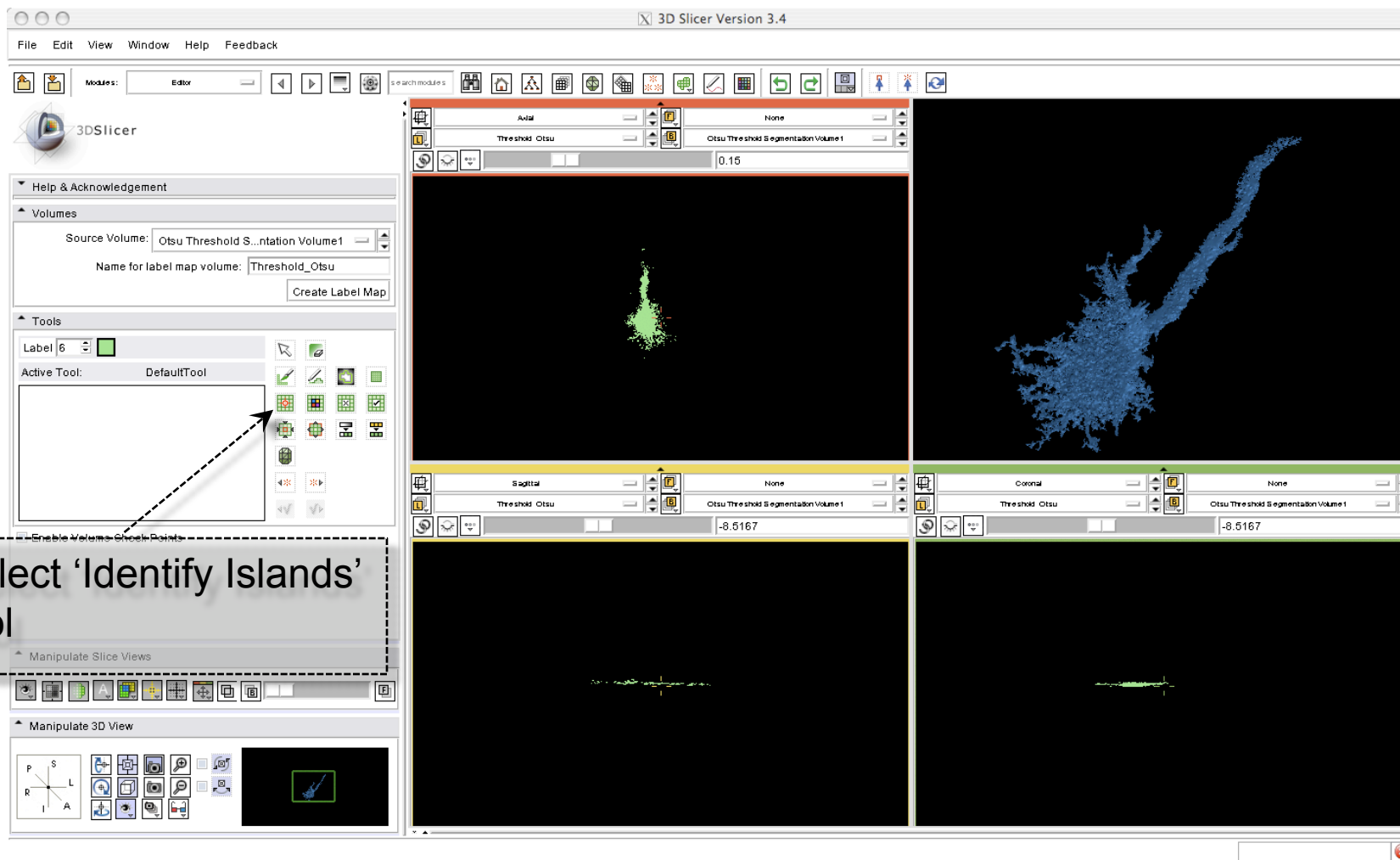
# Model Building: Otsu Segmentation

The screenshot shows the 3D Slicer 3.4 interface. The 'Threshold' tool is active, with the 'Scope' set to 'all' and the 'Range' set to '1' to '232'. The 'Label' is set to '6'. The 'Use For Paint' button is highlighted with a dashed arrow. The 3D view shows a segmented object in blue, with a corresponding label map in green. The 'Volumes' panel shows the source volume as 'Otsu Threshold Segmentation Volume1' and the name for the label map volume as 'Threshold\_Otsu'. The 'Tools' panel shows the 'Threshold' tool is active, with the 'Scope' set to 'all' and the 'Range' set to '1' to '232'. The 'Use For Paint' button is highlighted with a dashed arrow. The 3D view shows a segmented object in blue, with a corresponding label map in green. The 'Volumes' panel shows the source volume as 'Otsu Threshold Segmentation Volume1' and the name for the label map volume as 'Threshold\_Otsu'.

- 1) Can adjust label color to be different from blue used before
- 2) Set proper parameters for label threshold (1 – max value)
- 3) Generate label map



# Model Building: Otsu Segmentation





# Model Building: Otsu Segmentation

3D Slicer Version 3.4

File Edit View Window Help Feedback

Modules: Editor

3DSlicer

Help & Acknowledgement

Volumes

Source Volume: Otsu Threshold Segmentation Volume1

Name for label map volume: Threshold\_Otsu

Create Label Map

Tools

Label: 6

Active Tool: Identify Islands

Scope: all

Minimum Size: 10

Fully Connected

Cancel Apply

Enable Volume Check Points

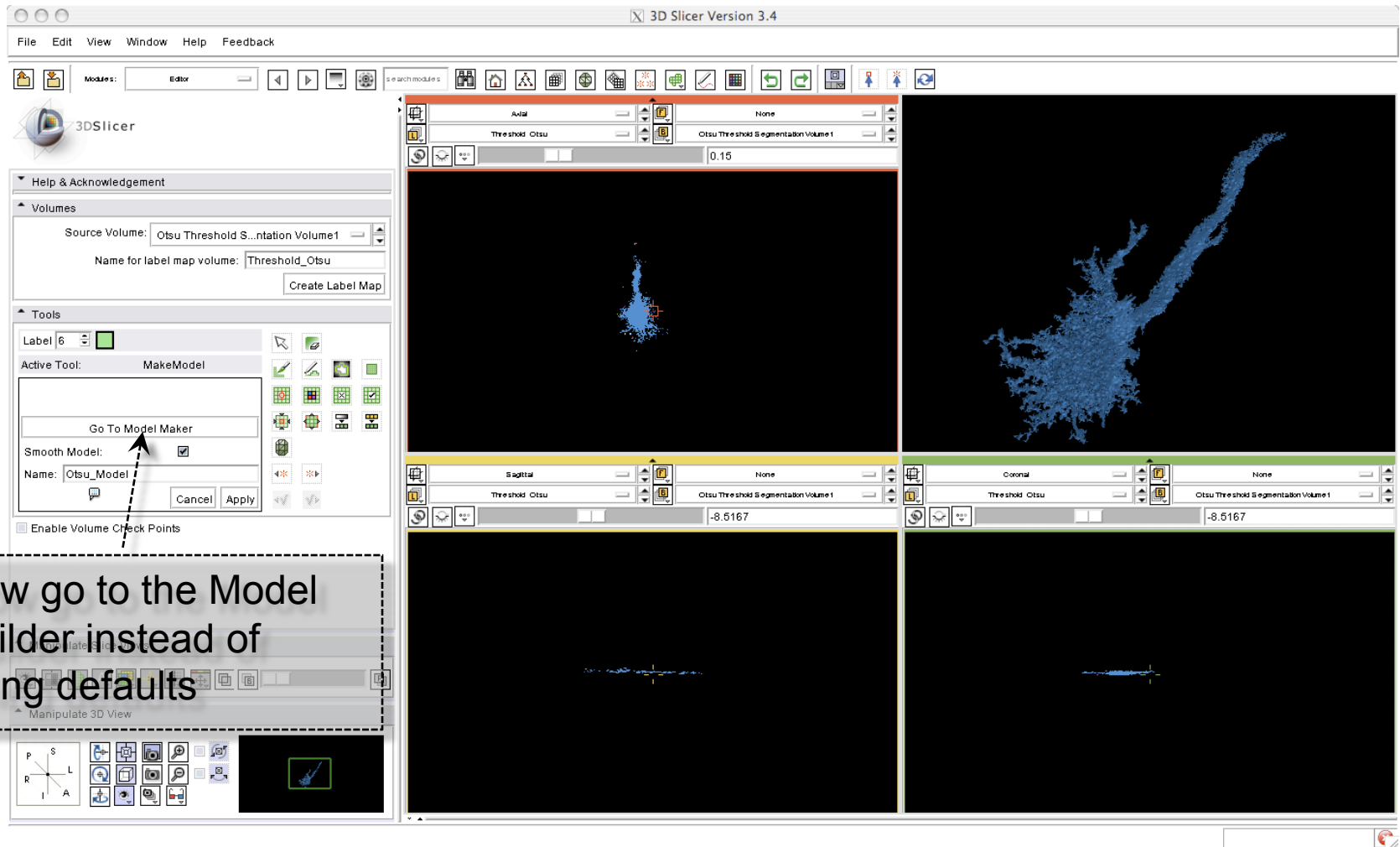
2) Select 'Model Builder' tool

1) Identify Islands as before

Middle Button: Pan; Right Button: Zoom



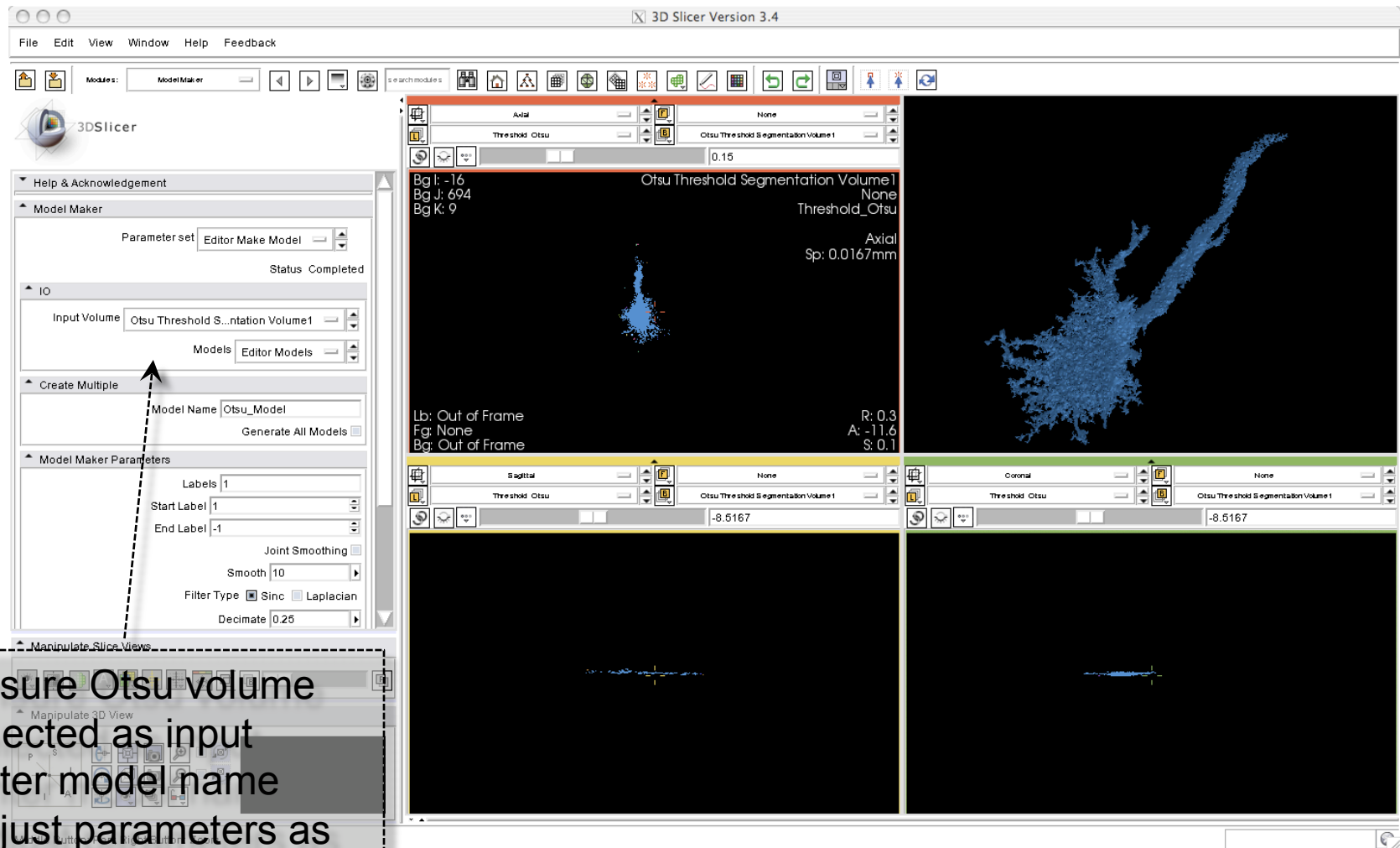
# Model Building: Otsu Segmentation



1) Now go to the Model Builder instead of using defaults



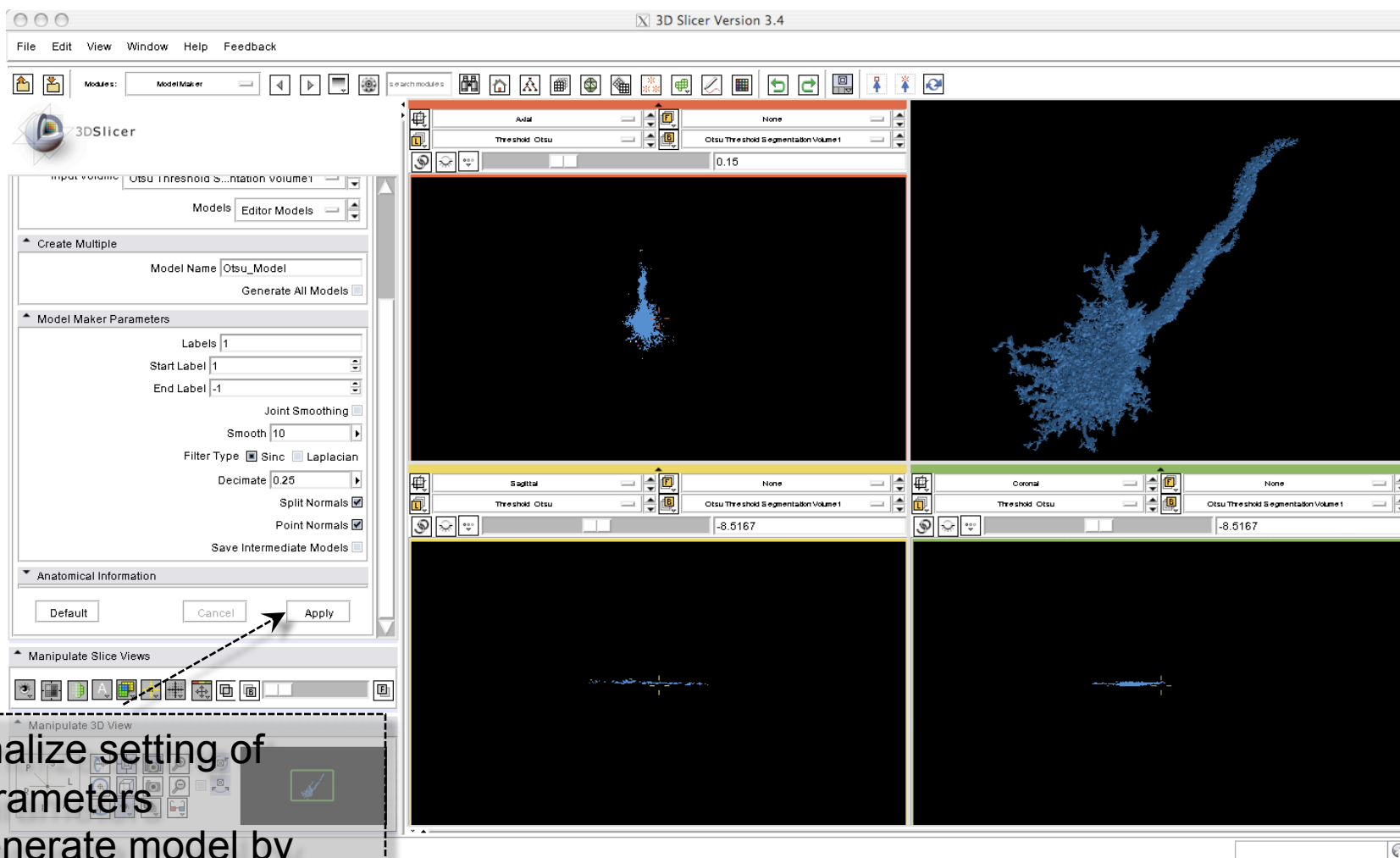
# Model Building: Otsu Segmentation







# Model Building: Otsu Segmentation



- 1) Finalize setting of parameters
- 2) Generate model by selecting 'Apply'



# Model Building: Otsu Segmentation

1) Select 'Data' module to manage which model to display

3D Slicer Version 3.4

File Edit View Window Help Feedback

Modules: Model Maker

All Modules

- Color
- Data
- Editor
- Fiducials
- Models
- ROI
- Slicer Welcome
- Slicer
- Slice
- Annotations
- Volume Rendering
- Wizards
- Informatics
- Registration
- Segmentation
- Statistics
- Diffusion
- Tractography
- IGT
- Filtering
- Surface Models
- Batch Processing
- Converters
- Developer Tools
- Diffusion Weighted

Input volume: Otsu Threshold Segmentation v1

Models Editor

Create Multiple

Model Name: Otsu\_Mod

General

Model Maker Parameters

Start Label: 1

Smooth: 1

Filter Type: Sin

Save Intermediate

Anatomical Information

Default Cancel

Manipulate Slice Views

Manipulate 3D View

3D View: Axial, None, Threshold: Otsu, Otsu Threshold Segmentation Volume 1, 0.15

Sagittal, None, Threshold: Otsu, Otsu Threshold Segmentation Volume 1, -8.5167

Coronal, None, Threshold: Otsu, Otsu Threshold Segmentation Volume 1, -8.5167



# Model Building: Otsu Segmentation

3D Slicer Version 3.4

File Edit View Window Help Feedback

Modules: Data

3DSlicer

Help & Acknowledgement

Display & Modify Scene

MRML Tree

- Scene
  - e13hpc1c
  - Threshold\_LM
  - Threshold\_Model
  - Otsu\_Threshold
  - Threshold\_Otsu
  - Otsu\_Model

Context Menu for Threshold\_Model:

- Cut Node
- Edit Properties...
- Toggle Visibility
- Delete Node

Display MRML ID's

MRML Node Inspector

Load & Add Scenes Or Individual Datasets

- Load new scene (close current)
- Add a scene (to current)

1) Toggle the visibility for the Threshold model off (right click on the model name to get menu)

Axial: Threshold: Otsu, Otsu Threshold Segmentation Volume 1, 0.15

Sagittal: Threshold: Otsu, Otsu Threshold Segmentation Volume 1, -8.5167

Coronal: Threshold: Otsu, Otsu Threshold Segmentation Volume 1, -8.5167

Coronal View Properties:

- Otsu Threshold Segmentation Volume 1
- None
- Threshold\_Otsu
- Coronal
- Sp: 0.0167mm
- Lb: Out of Frame
- Fg: None
- Bg: Out of Frame
- R: -2.3
- A: -8.5
- S: -1.7



# Model Building: Otsu Segmentation

The screenshot displays the 3D Slicer 3.4 interface. The MRML Tree on the left shows the following hierarchy:

- Scene
  - e13hpc1c
    - Threshold\_LM
    - ThresholdModel
    - Otsu Threshold Segmentation Volume1
    - Threshold\_Otsu
    - Otsu\_Model

The main view area shows four panels: Axial, Sagittal, Coronal, and a 3D view. The Axial view shows a blue segmented volume with a threshold of 0.15. The Sagittal view shows a blue segmented volume with a threshold of -8.5167. The Coronal view shows a blue segmented volume with a threshold of -8.5167. The 3D view shows a blue segmented volume.

1) Toggle the visibility for the Otsu model on (right click on the model name to get menu)



# Model Building: Otsu Segmentation

3D Slicer Version 3.4

File Edit View Window Help Feedback

Modules: Data

All Modules

- Color
- Data
- Editor
- Fiducials
- Models
- ROI
- SlicerWelcome
- Slices
- Transforms
- VolumeRendering
- Volumes

MRML Tree

- Scene
  - e13hpc1c
    - Threshold\_LM
    - ThresholdModel
    - Otsu Threshold Segmentation Volume
    - Threshold\_Otsu
    - Otsu\_Model

1) Select 'Models' module to adjust model rendering

Display MRML ID's

Manipulate Slice Views

Manipulate 3D View

Avial: None, Otsu Threshold Segmentation Volume 1, 0.15

Sagittal: None, Otsu Threshold Segmentation Volume 1, -8.5167

Coronal: None, Otsu Threshold Segmentation Volume 1, -8.5167



# Model Building: Otsu Segmentation

3D Slicer Version 3.4

File Edit View Window Help Feedback

Modules: Models

3DSlicer

Help & Acknowledgement

Load

- Add 3D model or a model directory
- Add scalar overlay

Hierarchy & Display

Model Hierarchy

- Scene
  - Editor Models
    - ThresholdModel
      - Otsu\_Model**

Model Display

Select Model or Hierarchy: Otsu\_Model

Selected

1) Ensure Otsu model is selected

Manipulate 3D View

Axial: Threshold Otsu, Otsu Threshold Segmentation Volume 1, 0.15

Sagittal: Threshold Otsu, Otsu Threshold Segmentation Volume 1, -8.5167

Coronal: Threshold Otsu, Otsu Threshold Segmentation Volume 1, -8.5167



# Model Building: Otsu Segmentation

3D Slicer Version 3.4

File Edit View Window Help Feedback

Modules: Models

Scalar Color Map Select: FullRainbow

Clipping

Slice Intersections Visible

Backface Culling

Opacity 0.8

Set Color...

Material Properties

Ambient: 20

Diffuse: 60

Specular: 50

Power: 40

Preview: Presets:

Clipping

Info

Multiple Views

Manipulate 3D View

Middle Button: Pan; Right Button: Zoom

Axial

None

Threshold Otsu

Otsu Threshold Segmentation Volume 1

0.15

Otsu Threshold Segmentation Volume 1

None

Threshold\_Otsu

Axial

Sp: 0.0167mm

Lb: Out of Frame

R: 0.1

Fg: None

A: -4.3

Bg: Out of Frame

S: 0.1

Sagittal

None

Threshold Otsu

Otsu Threshold Segmentation Volume 1

-8.5167

Coronal

None

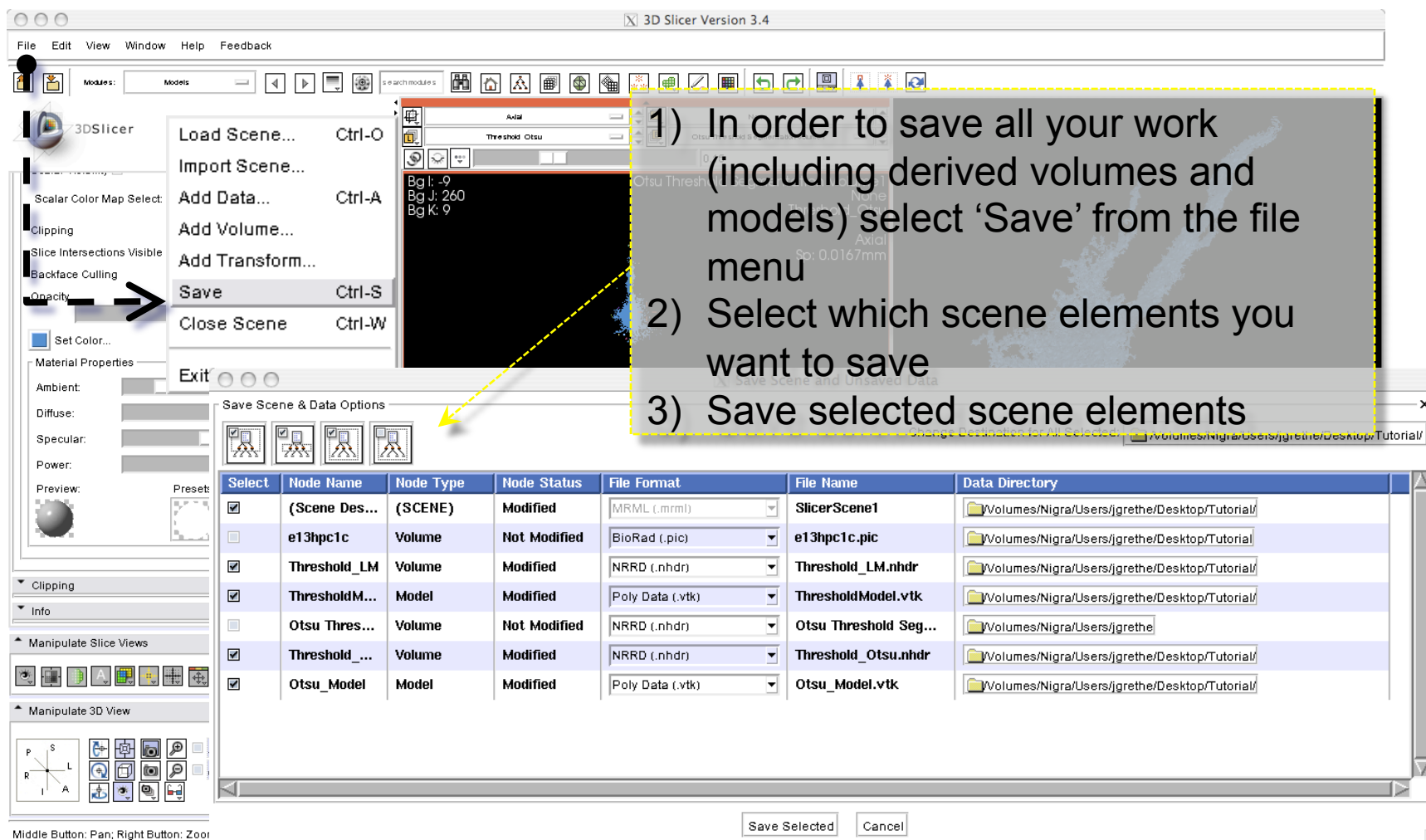
Threshold Otsu

Otsu Threshold Segmentation Volume 1

-8.5167

1) Adjusting lighting presets and opacity and other parameters as needed

# Saving Your Work



3D Slicer Version 3.4

File Edit View Window Help Feedback

Modules: Models

Load Scene... Ctrl-O  
 Import Scene...  
 Add Data... Ctrl-A  
 Add Volume...  
 Add Transform...  
 Save Ctrl-S  
 Close Scene Ctrl-W  
 Exit

1) In order to save all your work (including derived volumes and models) select 'Save' from the file menu  
 2) Select which scene elements you want to save  
 3) Save selected scene elements

Save Scene & Data Options

Select	Node Name	Node Type	Node Status	File Format	File Name	Data Directory
<input checked="" type="checkbox"/>	(Scene Des...	(SCENE)	Modified	MRML (.mrm)	SlicerScene1	Volumes/Nigra/Users/jgrethe/Desktop/Tutorial/
<input type="checkbox"/>	e13hpc1c	Volume	Not Modified	BioRad (.pic)	e13hpc1c.pic	Volumes/Nigra/Users/jgrethe/Desktop/Tutorial/
<input checked="" type="checkbox"/>	Threshold_LM	Volume	Modified	NRRD (.nhdr)	Threshold_LM.nhdr	Volumes/Nigra/Users/jgrethe/Desktop/Tutorial/
<input checked="" type="checkbox"/>	ThresholdM...	Model	Modified	Poly Data (.vtk)	ThresholdModel.vtk	Volumes/Nigra/Users/jgrethe/Desktop/Tutorial/
<input type="checkbox"/>	Otsu Thres...	Volume	Not Modified	NRRD (.nhdr)	Otsu Threshold Seg...	Volumes/Nigra/Users/jgrethe/
<input checked="" type="checkbox"/>	Threshold_...	Volume	Modified	NRRD (.nhdr)	Threshold_Otsu.nhdr	Volumes/Nigra/Users/jgrethe/Desktop/Tutorial/
<input checked="" type="checkbox"/>	Otsu_Model	Model	Modified	Poly Data (.vtk)	Otsu_Model.vtk	Volumes/Nigra/Users/jgrethe/Desktop/Tutorial/

Save Selected Cancel

Middle Button: Pan; Right Button: Zoom





# Saving Your Work

The screenshot shows a file explorer window titled 'Tutorial'. The left sidebar contains navigation options: DEVICES (Pallidum, Nigra), SHARED, PLACES, and SEARCH FOR (Today, Yesterday, Past Week, All Images, All Movies, All Documents). The main pane displays a list of files with columns for Name, Date Modified, Size, and Kind. The file 'SlicerScene1.mrml' is selected and highlighted. A dashed box with an arrow points to this file, containing the following text:

- 1) Scene information is saved in a mrml file.
- 2) Scene elements saved as separate files

Name	Date Modified	Size	Kind
alxp.pic	Today	200 MB	Radiance
e13hpc1c.pic	Today	28 MB	Radiance
Otsu_Model.vtk	Today	11.1 MB	Document
SlicerImage1_0.png	Today	112 KB	Portable Network Graphics image
SlicerImage2_0.png	Today	36 KB	Portable Network Graphics image
SlicerImage2_1.png	Today	56 KB	Portable Network Graphics image
SlicerScene1.mrml	Today	20 KB	Document
TempWrite	Today	--	Folder
Threshold_LM.nhdr	Today	4 KB	Document
Threshold_LM.raw.gz	Today	88 KB	gzip compressed archive
Threshold_Otsu.nhdr	Today	4 KB	Document
Threshold_Otsu.raw.gz	Today	56 KB	gzip compressed archive
ThresholdModel.vtk	Today	7.4 MB	Document



# *Conclusion*

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- This training module should have provided you with information needed to build models from varying confocal microscopy data
- Slicer provides an intuitive graphical user interface to interact with the data
- Open-source environment and open-access data used in this tutorial



# *Acknowledgements*

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