# AnalyzePro

## USER'S GUIDE

AnalyzeDirect

# AnalyzePro

## User's Guide

AnalyzePro is a robust research software for advanced biomedical imaging visualization, manipulation and measurement. It has been carefully designed to provide an intuitive and facile interface that allows full exploration of biomedical imaging data. The software features integrated modules that provide access to complementary tools for fully interactive multi-dimensional display, processing, segmentation, registration and measurement of biomedical imaging modalities including MRI, CT, PET, SPECT, ultrasound and digital microscopy. The applications of AnalyzePro are broad in scope, wide in scale and penetrating in impact.

# AnalyzePro

## User's Guide

# AnalyzePro Basics

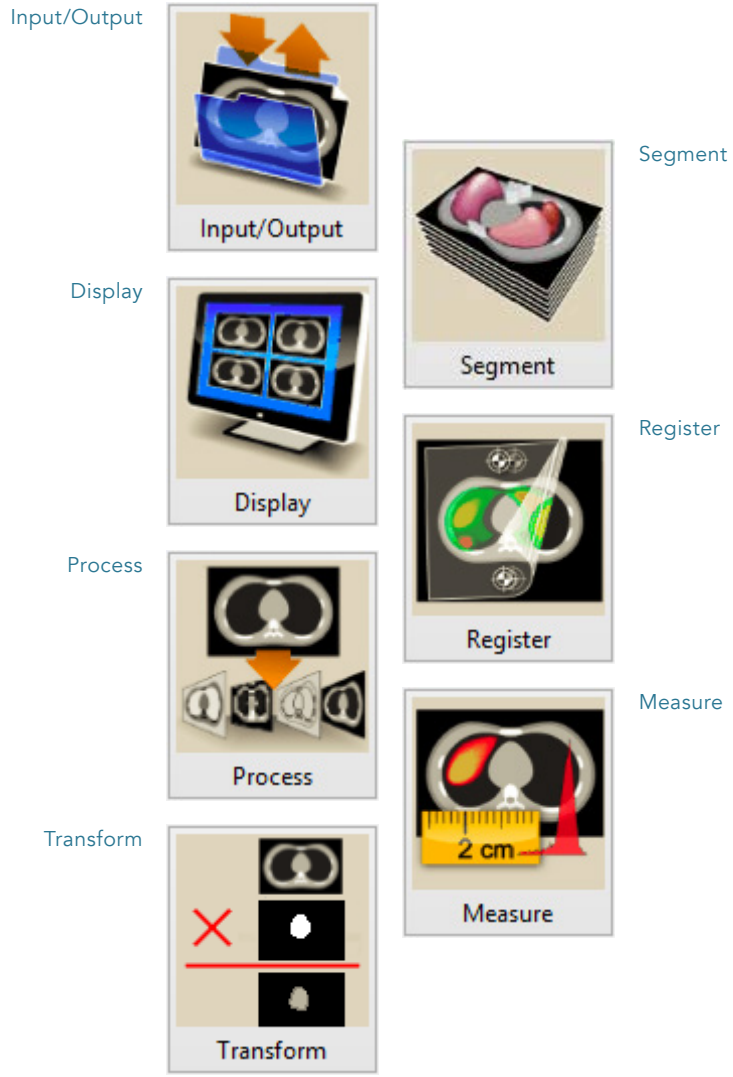
The AnalyzePro workspace is the first operational window that appears when AnalyzePro is opened. The main window does not perform any imaging functions; rather, it coordinates all the modules within the AnalyzePro package and acts as a file manager for loaded data.

Once data is loaded into AnalyzePro, it will appear as a thumbnail in the workspace and is available to all of the modules. To load data into a module, select the icon in the workspace (the thumbnail will appear framed in red when selected) and open the desired module from the AnalyzePro side menu.

# AnalyzePro Modules

AnalyzePro has been carefully designed to provide an intuitive and facile interface that significantly improves usability and performance.

The software features integrated modules that provide access to complementary tools for fully interactive multi-dimensional display, processing, segmentation, registration and measurement of image data.



# Right Mouse Button Menu

The AnalyzePro workspace includes additional options which can be accessed by right-clicking within the workspace. The menu provides the following options:

**Unload** — Unload selected data from the workspace
**Info** — Display the header information for a selected data set
**Rename** — Change the name of a selected data set
**Edit Header** — Modify the header information of a selected data set
**Duplicate** — Will duplicate the currently selected data set
**Append** — Append selected data
**Un-append** — Un-append 4D multi-volume data sets or RGB data sets
**Select All** — Select all data sets in the workspace
**Invert Selected** — Invert your selection of data in the workspace
**Arrange** — Arrange data sets by Name, Size or Modify Time
**Session Log** — Store information that might be useful to the AnalyzePro support team and software developers, should a problem ever arise with one of the modules
**Current Directory** — View and modify the Current Directory location
**License Manager** — Open the AnalyzePro License Manager
**AnalyzePro Update** — Check to make sure the software is up to date; will also download and install any necessary updates
**Options** — Switch on and off workspace features such as the PowerBar, and the pop-up icon names which are shown when the mouse cursor is moved over an image in the workspace
**User's Guide** — Open the AnalyzePro User's Guide
**Get Help** — Open the AnalyzeDirect Support Page
**About** — View version, system and environment information

# Main AnalyzePro Window Quick Keys

**[Ctrl] + a** — Selects all of the files in the workspace.

**[Ctrl] + Left Mouse Click or Middle Mouse Button** — Selects each file that has been clicked.

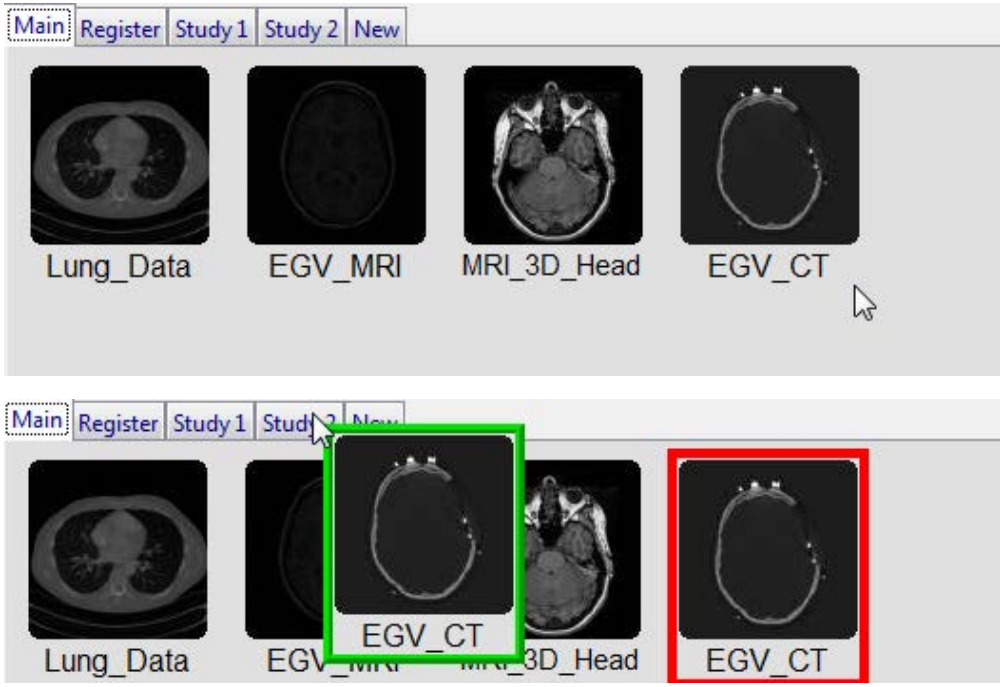
**[Shift] + Left Mouse Click** — Selects all files between first and last selections.

Double-clicking on a data set in the workspace restarts the last module used with that data. If there is not a module associated with the data, the Display module will open by default.

# Workspace Tabs

The main AnalyzePro Workspace can be partitioned into multiple workspaces using the tabs at the top of the main workspace, each of which can be given a name relevant to the task the workspace represents. To add a workspace, click New. To rename a tab, right-click the tab and select Rename.

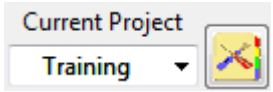
This permits efficient organization of loaded data sets into task-specific groups. Icons representing the loaded data sets can be manually organized in each workspace panel by dragging the icons to the desired location. Data sets can further be moved between workspaces by dragging to the tab associated with the workspace.

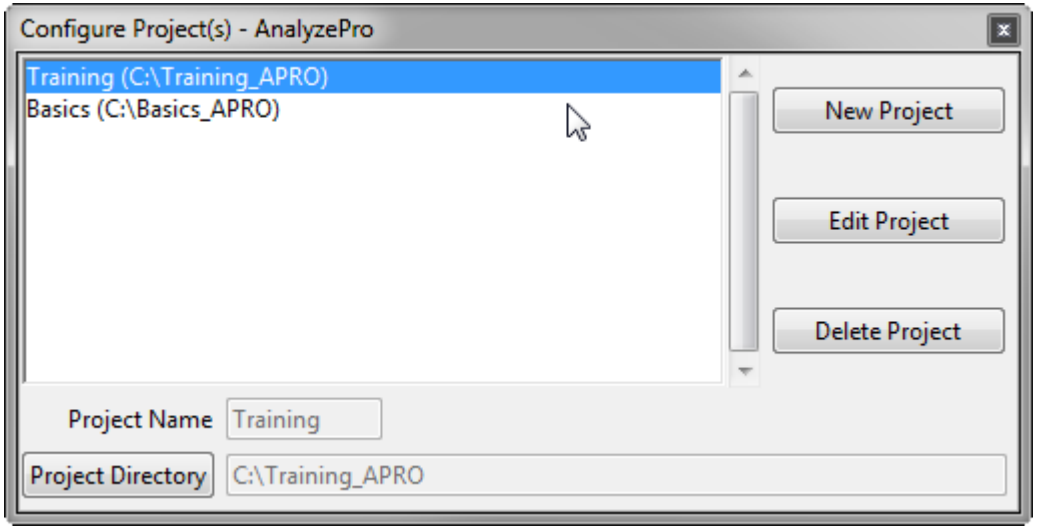


# Workspace Projects

Workspaces can be organized into specific projects via the Current Project controls in the lower right of the AnalyzePro window. AnalyzePro creates a default workspace/project from the computer username.

Projects can be added to a user-specific project list (click the workspace tool icon), with the workspace storage location for loaded images under the full control of the user.



# Image Controls
## and Customization

# Introduction

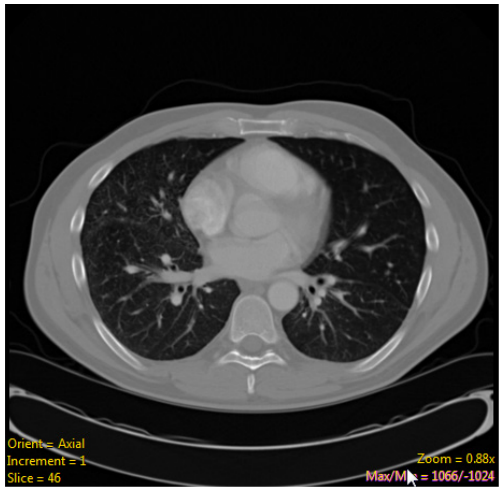
AnalyzePro provides consistent image display windows with interactive image controls. The following controls are present in all sections of the software, but certain modules will contain additional functions.

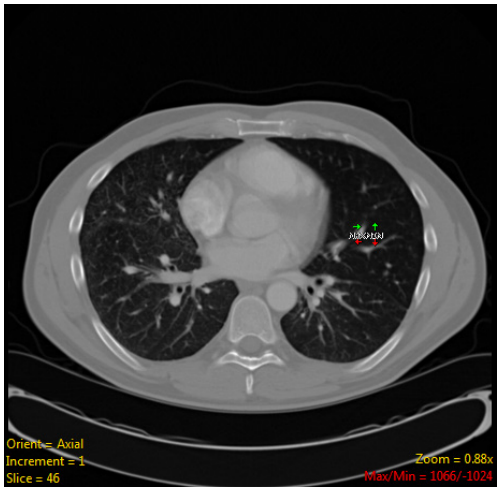
## Changing the Intensity Display of an Image

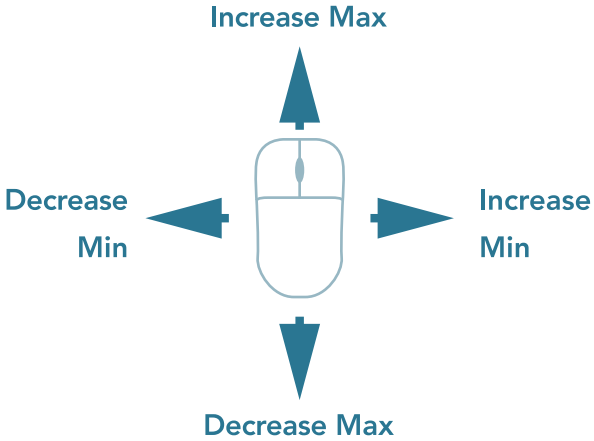
The Maximum and Minimum display intensities can be changed using the following methods:

**Max/Min Cursor** — Click the yellow Max/Min text at the bottom right corner of the image window. A cursor will return that allows the values to be manipulated. Hold down the left mouse button and move the mouse up/down or left/right. See the Max/Min graphic below to determine what value is changed for each direction.

If you want to change only the Max value, you can hold the Shift key while using the Max/Min cursor. The Min values can also be edited independently by holding the Ctrl key while moving the Max/Min cursor. Note [Shift] + Right Mouse Button can be used to adjust Max/Min in any window without having to first selecting Max/Min option.



**Preset Intensities** — Right-click the yellow Max/Min text. The following list of modalities and options will be returned:

**CT** — Soft Tissue, Chest, Abdomen/Pelvis, Lung, Brain, Bone, Head/Neck

**MR** — Brain T1, Brain T2, Sag T2, Head/Neck, Spine, Abdomen/Pelvis T1, Abdomen/Pelvis T2

**US** — Low Contrast, Medium Contrast, High Contrast

**Data** — Volume Max/Min, Image Max/Min, Range Max/Min

**User** — Declare specific Max/Min values with a label. Once a label is saved, it can be accessed within the user menu.

**Auto** — Automatically calculates the Max/Min voxel intensity for each slice. Note that the Max/Min values change from slice to slice as you scroll through.

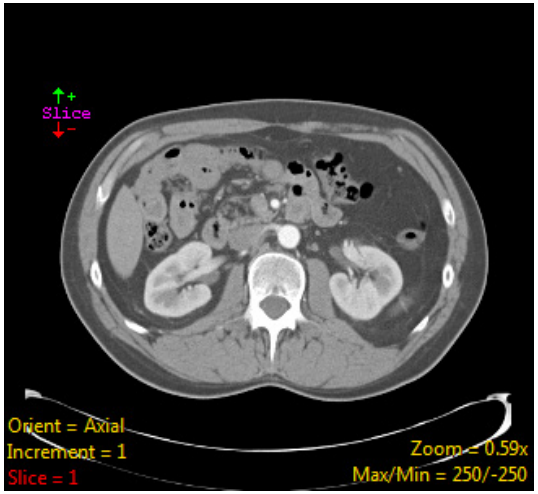
**Invert** — When selected, inverts the display intensities in a single orientation. To invert an entire data set, see Input/Output > Inverting Data or Transform > Intensity Transform > Invert.

**Manual Intensity Input** — Users can type in a Max/Min value by double clicking on the yellow Max/Min text. A box that contains editable fields will be returned. Input the desired values and hit enter or click outside the box. Max = 3071 Min = 1024

# Changing Image Slice

By default, users can navigate through the image slices using the following methods:

**Slice Cursor** — Click the yellow Slice text in the lower left hand corner of the image pane. An up/down slice cursor will appear. Hold down the left mouse button, and slide the cursor upward to move to a higher slice number and downward to move to a lower slice.

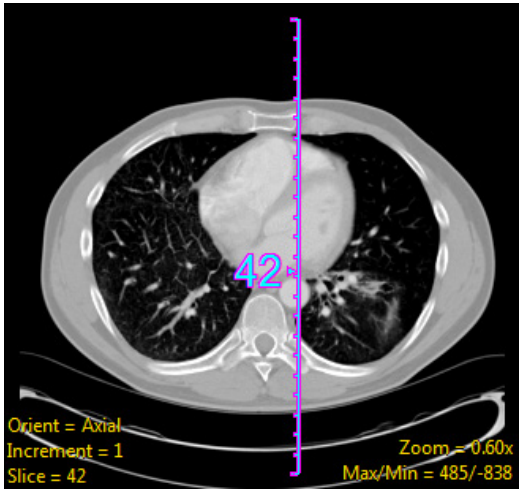



Users can quickly navigate to the First, Middle and Last slice by right-clicking the yellow Slice text. A specific slice number can be chosen by double-clicking the yellow Slice text and typing in the desired slice number.

**Keyboard** — Page Up and Page Down will will move forwards or backwards a page of images at a time during Multi-panel display mode in the Display module.

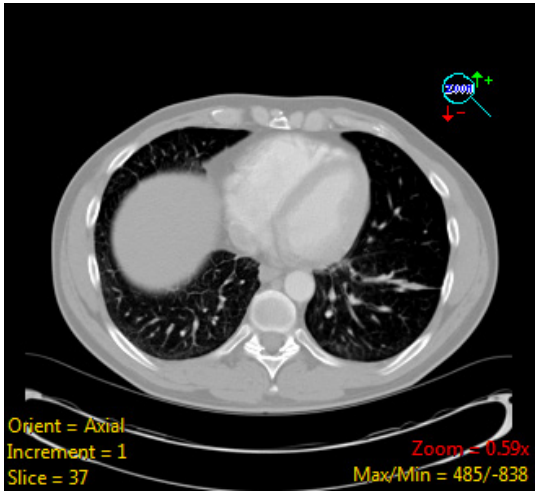
**Middle Mouse Wheel** — Increment one slice in the activated orientation by scrolling forward/backward using the middle mouse wheel.

**Middle Mouse Button Click** — Click and hold the middle mouse button to return a slice slider. Upward mouse movements will move to a higher slice and downward to a lower slice. Let go of the middle mouse button when the desired slice is reached. Note that the Middle Mouse Wheel and  Middle Mouse Button are user configurable and may have different defaults in different modules.



# Zoom

**Zoom Cursor** — Click on the yellow Zoom text in the bottom right corner of the image pane. A zoom cursor will be displayed. While clicking and holding the left mouse button, move the mouse upward to zoom in and downward to zoom out. Let go of the left mouse button when the desired zoom factor is reached.




**Zoom Presets** — Right-click the yellow Zoom text and the following options will appear:

- **Zoom levels** — 0.25x, 0.33x, 0.50x, 1.00x, 2.00x, 3.00x, 4.00x
- **Fit Window** — Uses a zoom factor that allows the data to fill the image pane.
- **Fit Width** — Uses a zoom factor that allows the data to fit the width of the image pane.
- **Fit Height** — Uses a zoom factor that allows the data to fit the height of the image pane.
- **Interpolation** — Allows the interpolation method to be changed for the data. The default is Bicubic (Input Driven). Users can switch to Linear (ID), Nearest Neighbor (Output Driven), Linear (OD), Bicubic and Windowed Sinc.

# Customization and Additional Display Options

**Orient** — Change the current orthogonal orientation of the image by left-clicking. Right-click to select the desired orientation from the menu.

**Middle Mouse Button Action** — Sets the middle mouse button action; reached by right-clicking in the image.

**Mouse Wheel Action** — Sets action for middle mouse scroll wheel action.

**Axis Labels** — Provides text labels for Right, Left, Anterior and Posterior.

**Copy to Clipboard** — Copies the current image to memory.

**Isotropic** — Switch between isotropic and anisotropic display for non-cubic data.

**Colormap** — Load or create a color map for the data.

**Cursor Link** — Enable or disable the linked cursor.

**Axis Labels** — Switch on/off the Axis labels.

**Border Ruler** — Enable or disable the border ruler tool.

**Reset** — Reset the image display.

# Input/Output

# Input: Loading Data

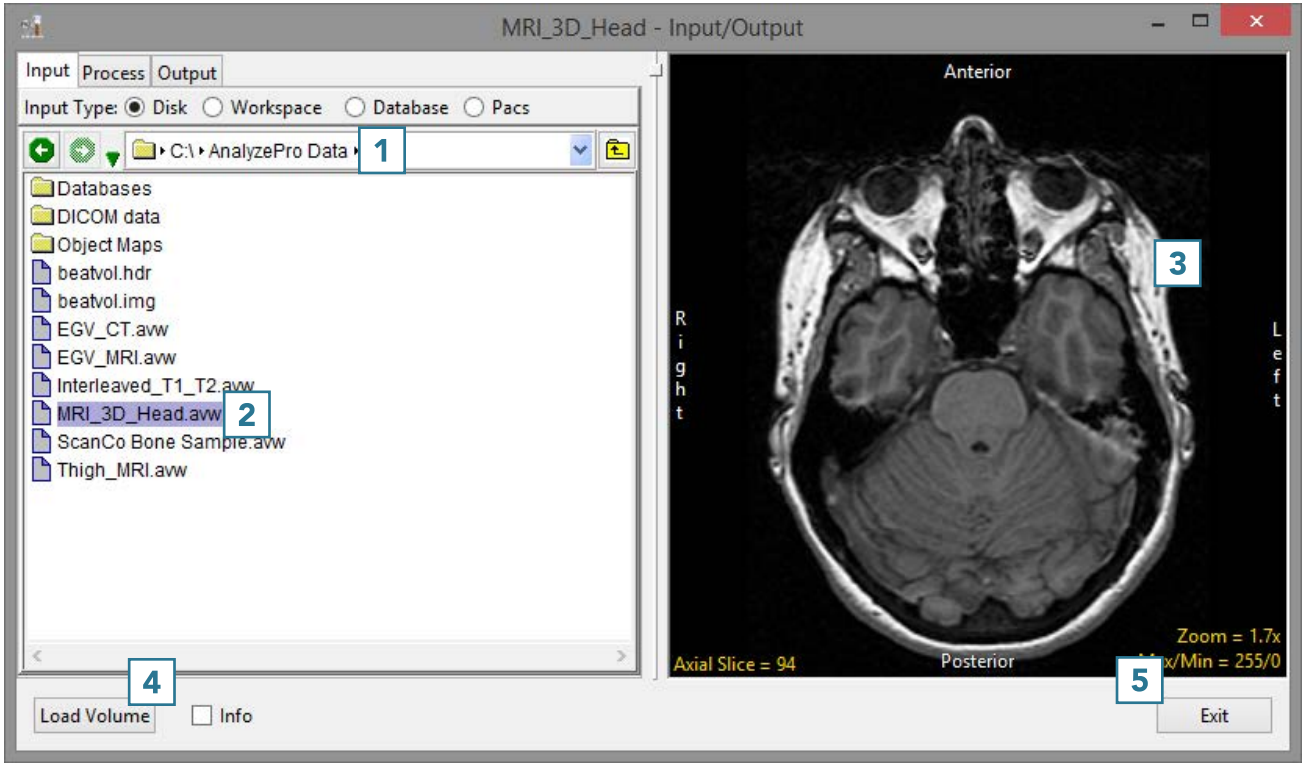
Data can be loaded into or saved out of AnalyzePro using Input/Output. Input/Output can also be used to transform image data while loading into or saving out of AnalyzePro.

## 1. Loading a Data Set

- Open Input/Output.
- Navigate to the data 1 and select the data set you want to load. 2 See Table 3.1 for supported file formats.

Note that the data will be displayed. 3

- Click Load Volume 4 to load the data.
- Click Exit 5 to close Input/Output.

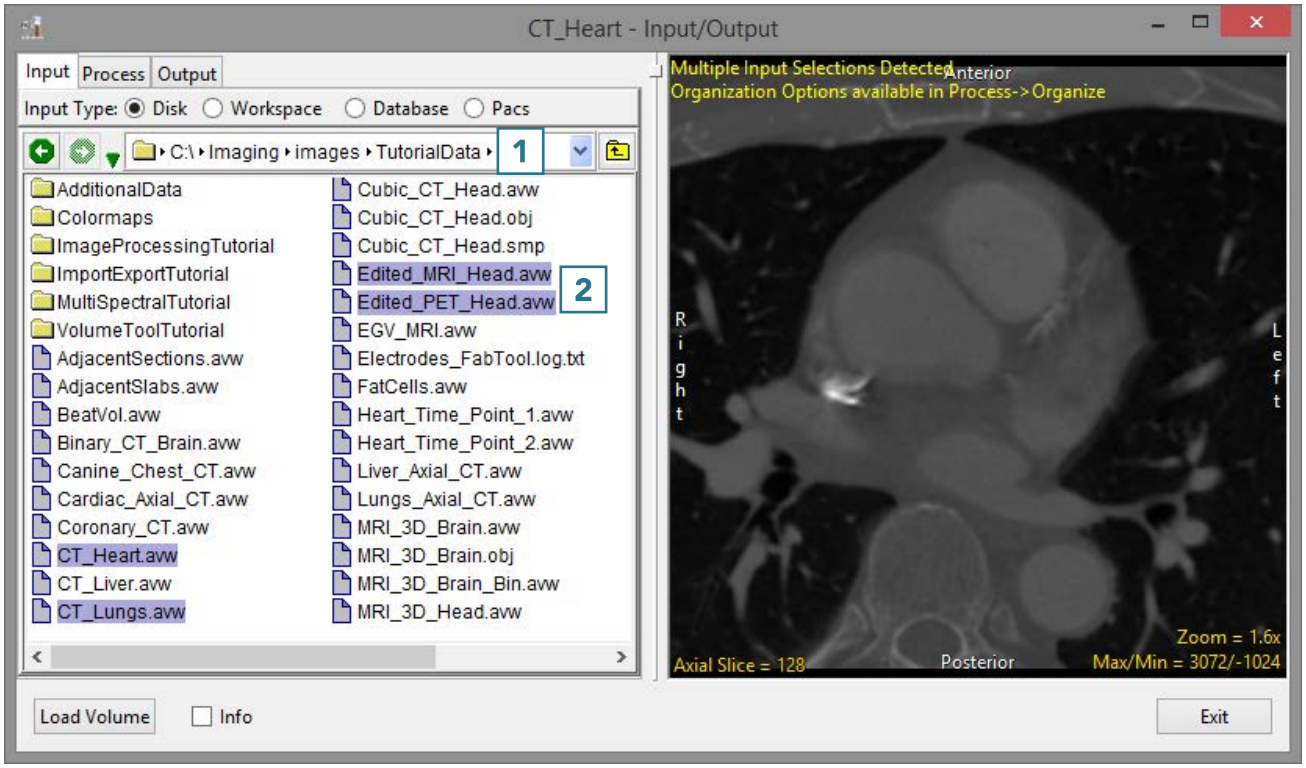


## Table 3.1: File Formats and Attributes Supported by AnalyzePro

| Formats | AnalyzeAVW | OBJMAP | AVW_VolumeFile | AnalyzeImage(7.5) | AnalyzeScreen | UNKNOWN | DICOM | NIFTI | JPG | SunRaster | CTI | CTIECAT7 | GE 9800 | GEADVANCE | GE Advantage | GESigna | GESTARCAM | INTERFILE | TIFF | PBM | PGM | PPM | TARGA | XBM | PIC | PICKERMRI | SiemensCT | SIEMENSMAGVIS | YUV | ACRNEMA | GIF | ANIMATEDGIF | PAPYRUS2 | PAPYRUS3 | SGIrgb | SGIlb | BMP | PostScript | SMIS | PNG | XWD | IMATRON | BIORAD | QUICKTIME | ITK | AVI | MPEG1 | VARIANFDF | vox | VSI |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Read | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X |
| Write | X | X | X | X | X | X | X | | X | X | | | | | | | | | X | X | X | X | X | X | X | | | | X | | X | X | | | X | | X | X | | | X | | | X | X | X | | | | |
| 2D | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | | | X | X | X |
| 3D | X | X | X | X | X | X | | X | | | X | X | | X | | | X | X | | | | | | | | | | | | X | | X | X | X | | | | | X | | | X | X | X | X | X | X | X | X | X |
| 4D | X | X | | X | | X | | X | | | X | X | | X | | | | X | | | | | | | | | | | | | | | | | | | | | X | | | X | | | X | | | | | X |
| Unsigned 8-bit | X | X | X | X | X | X | X | X | X | X | X | X | | X | | | X | X | X | X | X | X | X | X | X | | | | | X | X | X | X | X | X | X | X | X | X | X | X | | X | X | X | | | X | X | X | X |
| Signed 8-bit | X | | X | | | X | | X | | | | | | | | | | | | | | | | | X | | | | | | | | | | | | | | | | | | | X | X | | | X | | |
| Unsigned 16-bit | X | | X | | | X | X | X | | | | | | | | | | | X | | | | | | X | | | | | | | | | | | | | | | | | | | X | X | | | X | | X |
| Signed 16-bit | X | | X | X | | X | X | X | | | X | X | X | X | X | X | X | X | X | | | | | | X | X | X | X | | X | | | X | X | | | | | X | | | X | X | | X | | | X | X | X |
| Unsigned 32-bit | X | | X | | | X | | X | | | | | | | | | | | | | | | | | X | | | | | | | | | | | | | | | | | | | X | X | | | X | | |
| Signed 32-bit | X | | X | X | | X | | X | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | X | X | | | X | | |
| Float | X | | X | X | | X | | X | | | X | X | | X | | | | | | | | | | | X | | | | | | | | | | | | | X | | | | | | X | X | | | X | | X |
| Double | X | | | | | X | | X | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Complex | X | | X | X | | | | X | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| RGB | X | | X | X | X | X | X | X | X | X | | | | | | | | | X | | | X | X | | X | | | | X | | | | | | X | | X | X | | X | X | | | X | | X | X | | | | |

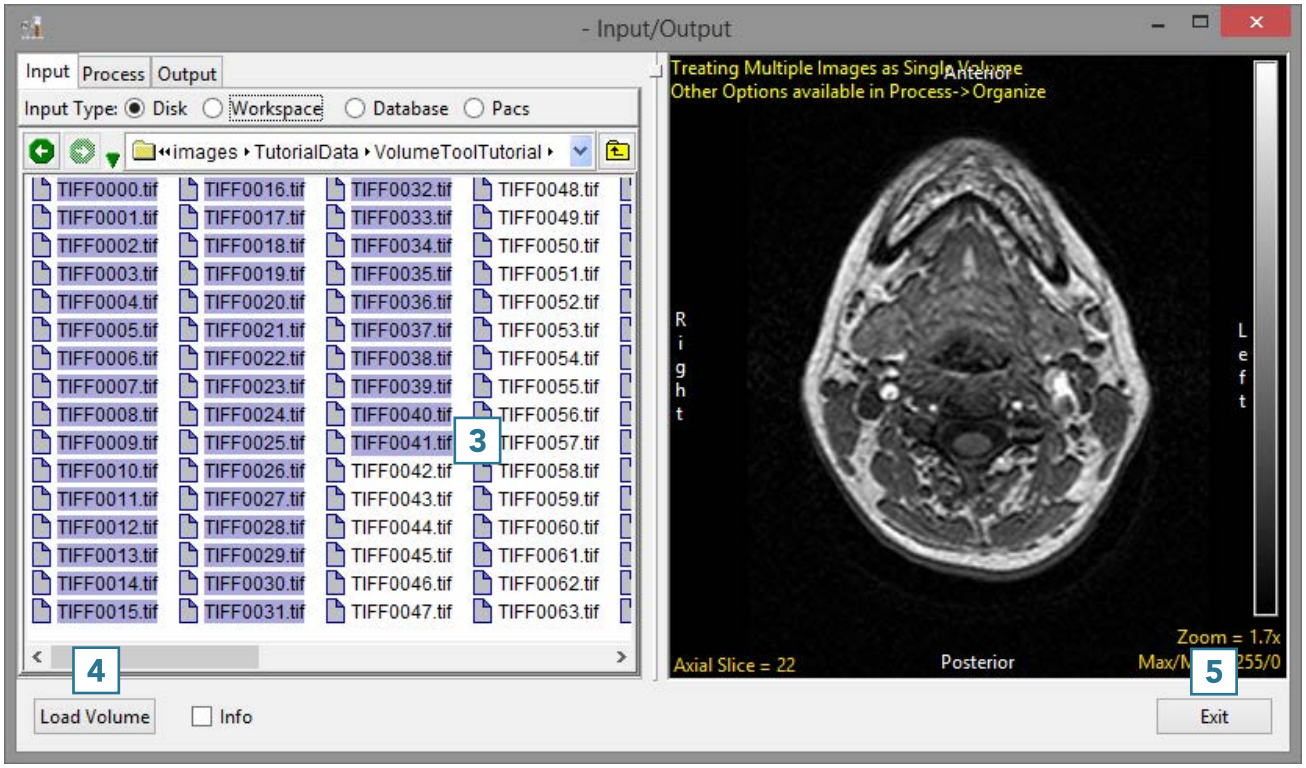
# 2. Loading Multiple Data Sets

- Open Input/Output.
- Navigate to the data sets. 1
- To select multiple data sets, hold down the Ctrl key and select each data set to load. 2



Alternatively, to select a range of data:

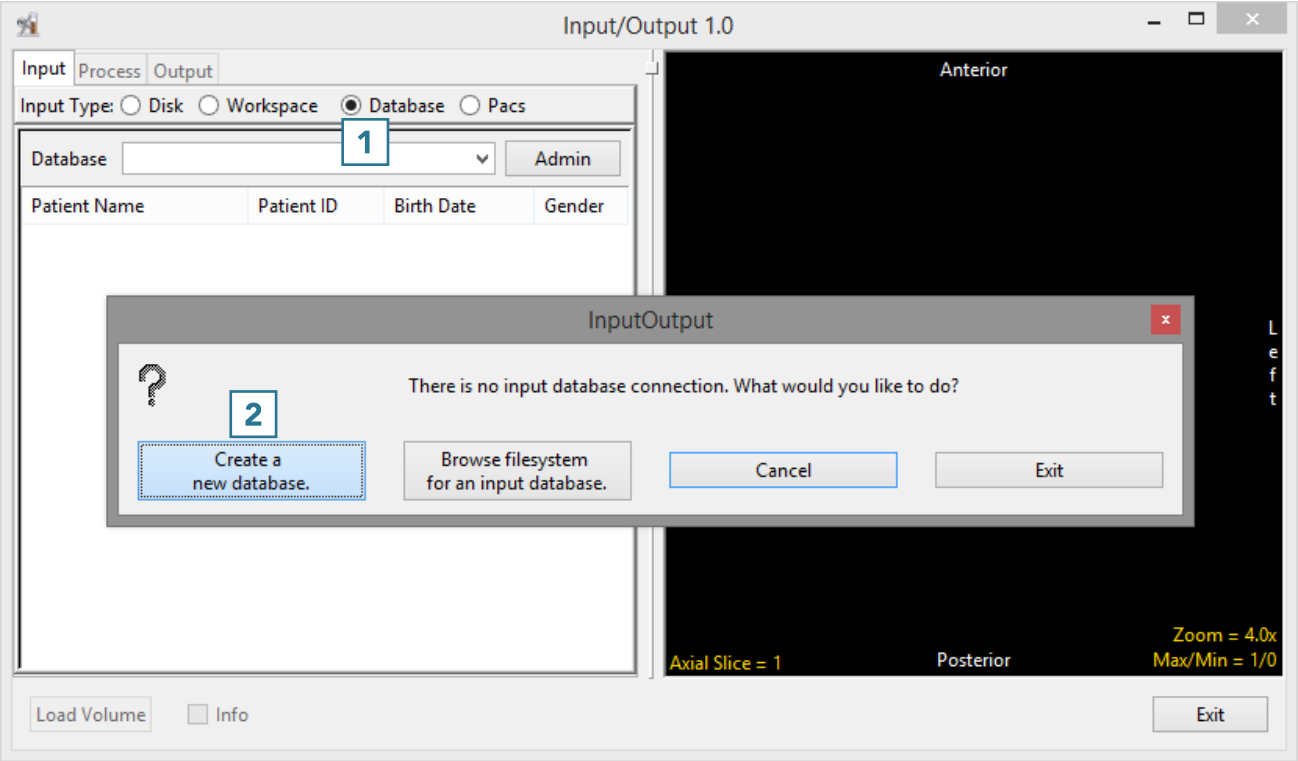
- Choose the first data set, then press the Shift key and finally select the last data set in the range. 3
- Click Load Volume 4 to load the data.
- Click Exit 5 to close Input/Output.



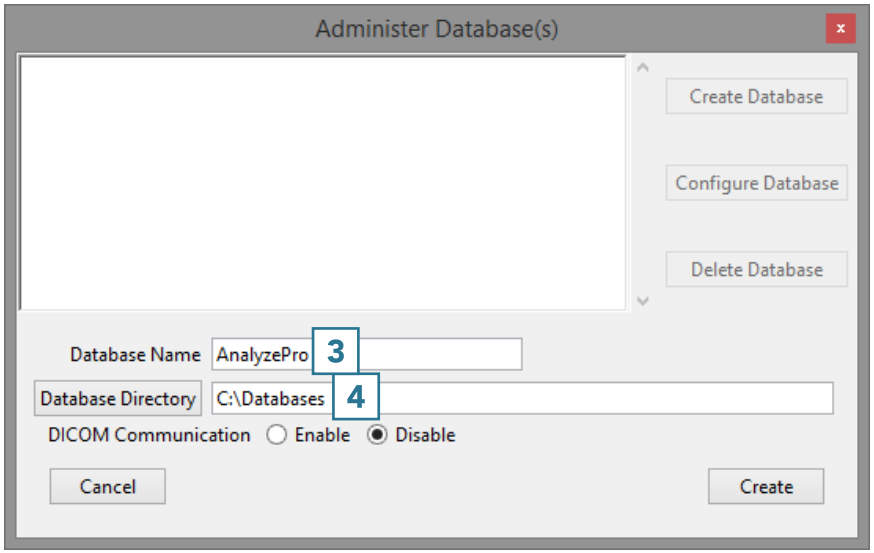
# 3. Importing DICOM Data

## Creating a Database

- Open Input/Output.
- Set Input Type to Database. 1
- The first time the Database option is selected, a window will be displayed, asking: 'There is no input database connection. What would you like to do?'
- Select Create a new database. 2



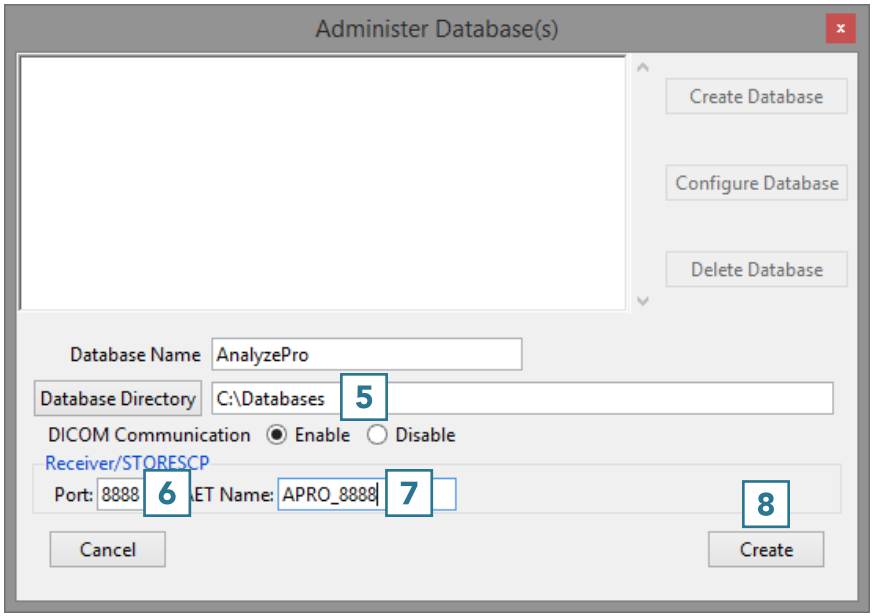
- The Administer Database(s) window will open.
- Name the database 3 and set the location where the database will be saved. 4



## Enabling DICOM Communications (optional)

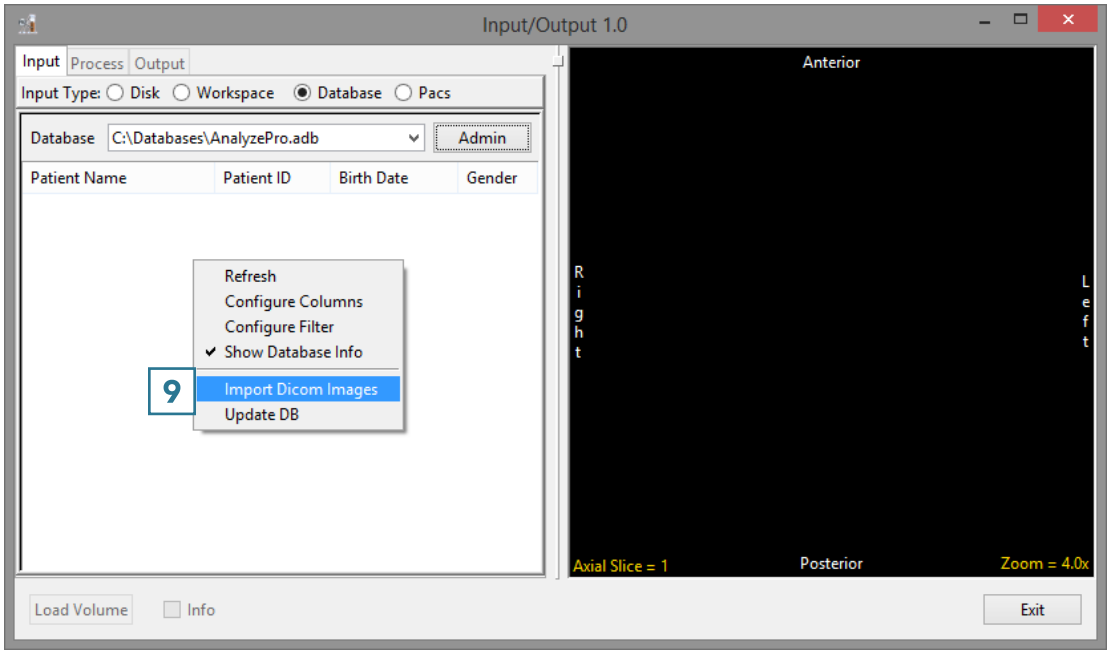
Setting up a receiver for the database will allow DICOM image data to be pushed from a PACS server to AnalyzePro. To set up a DICOM receiver:

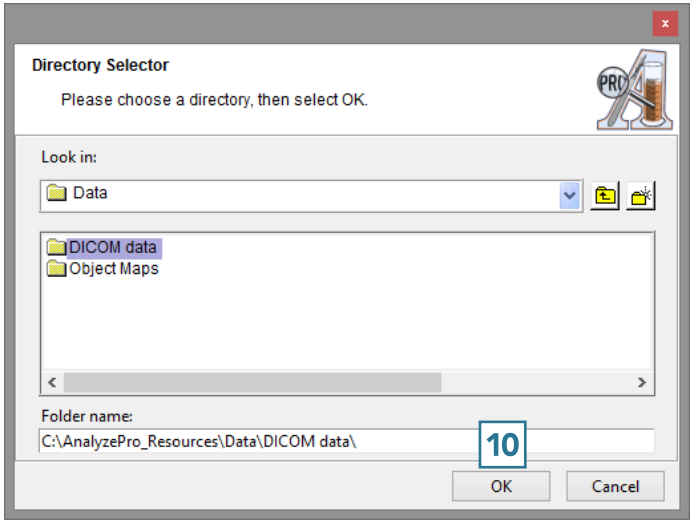
- Set the DICOM Communication to Enable. 5
- Set the Port number 6 and Application Entity Title (AET) Name. 7
  - Note that the AET Name should not go over 16 alphanumeric characters.
  - Make a note of the Port number and AET Name. Your PACS administrator will need this information along with the systems IP address to configure DICOM push from PACS.
- Click Create. 8



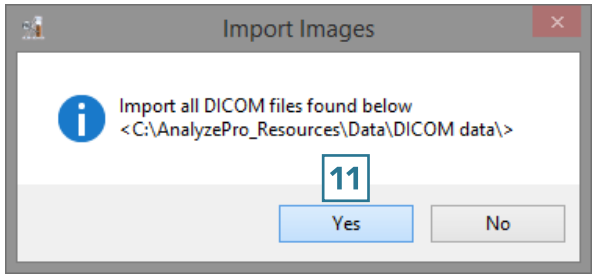
## Importing Images

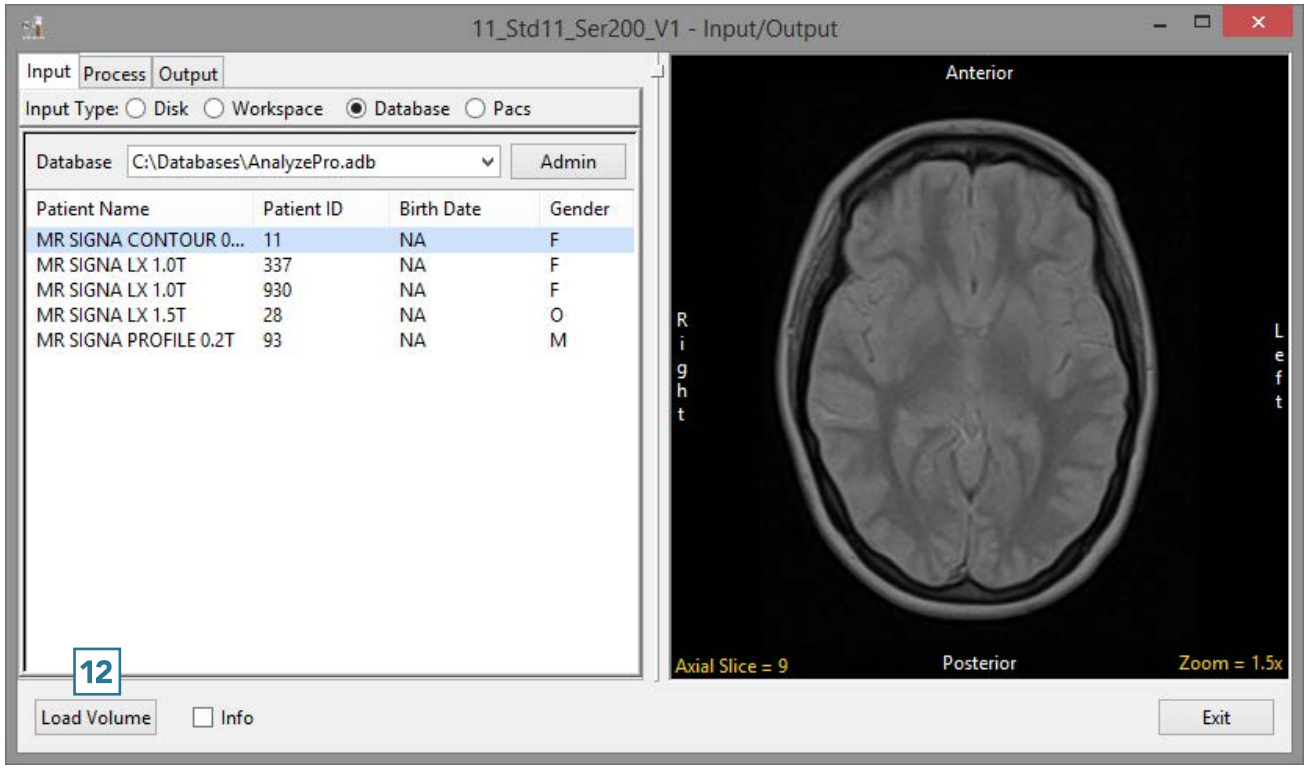
- Right-click in the window and select Import DICOM Images. 9
- Use the Directory Selector to navigate to the location of the DICOM images to import and click OK. 10



- A window will open stating Import all DICOM files found below <the specified folder>; click Yes. 11
- Once import is complete, the image data will be available in the database.
- To load a data set into AnalyzePro, select a data set and then click Load Volume. 12



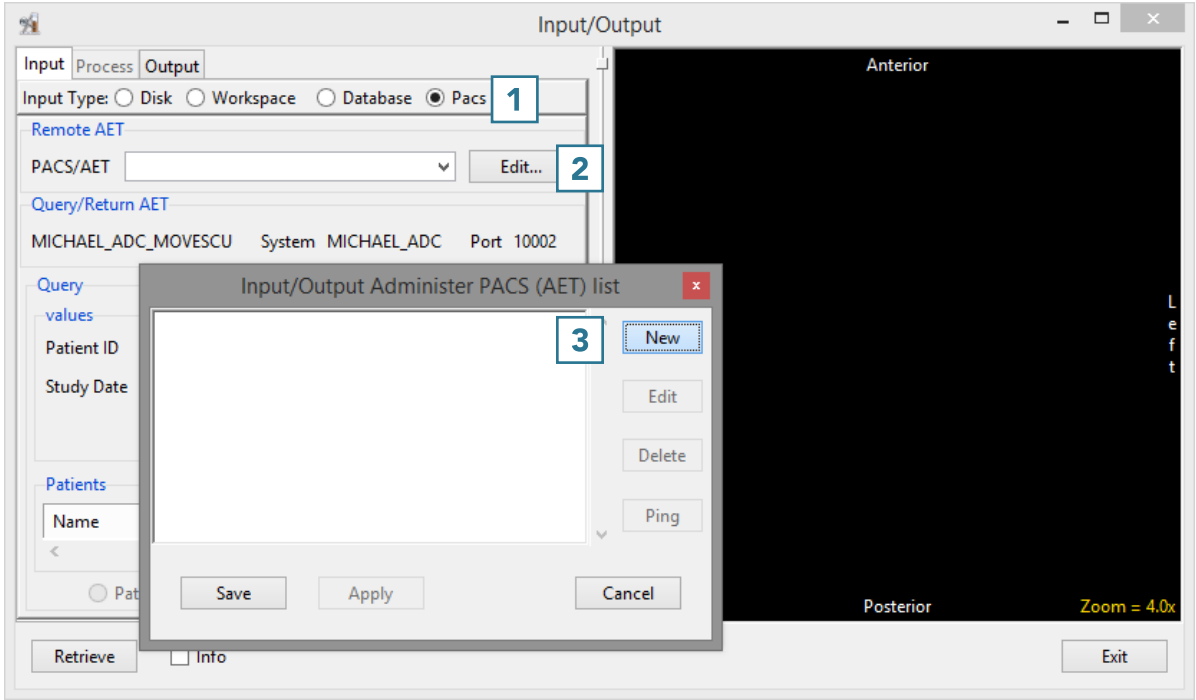



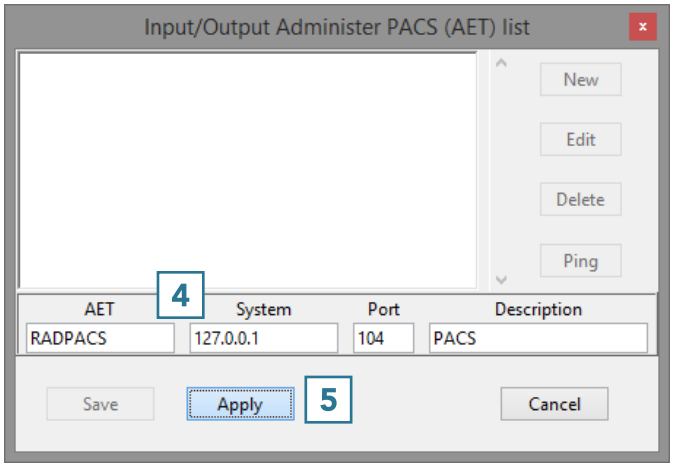
# 4. Configuring PACS Communications

To set up communications to allow Query and Retrieval of DICOM data from PACS, first create a database (see Creating a DICOM database), then open Input/Output.

- Set Input Type to PACS. 1
- Under Remote AET, click Edit. 2
- In the Input/Ouput Administer PACS (AET) list window that opens, click New. 3
- The window will update showing AET, System, Port, and Description fields. Enter the PACS information into these fields 4 and click Apply. 5

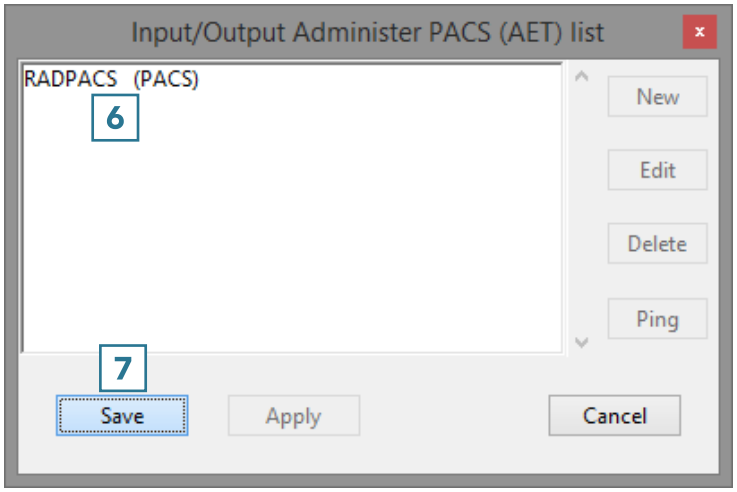
Note that you will need to contact your PACS administrator to obtain the relevant PACS information.



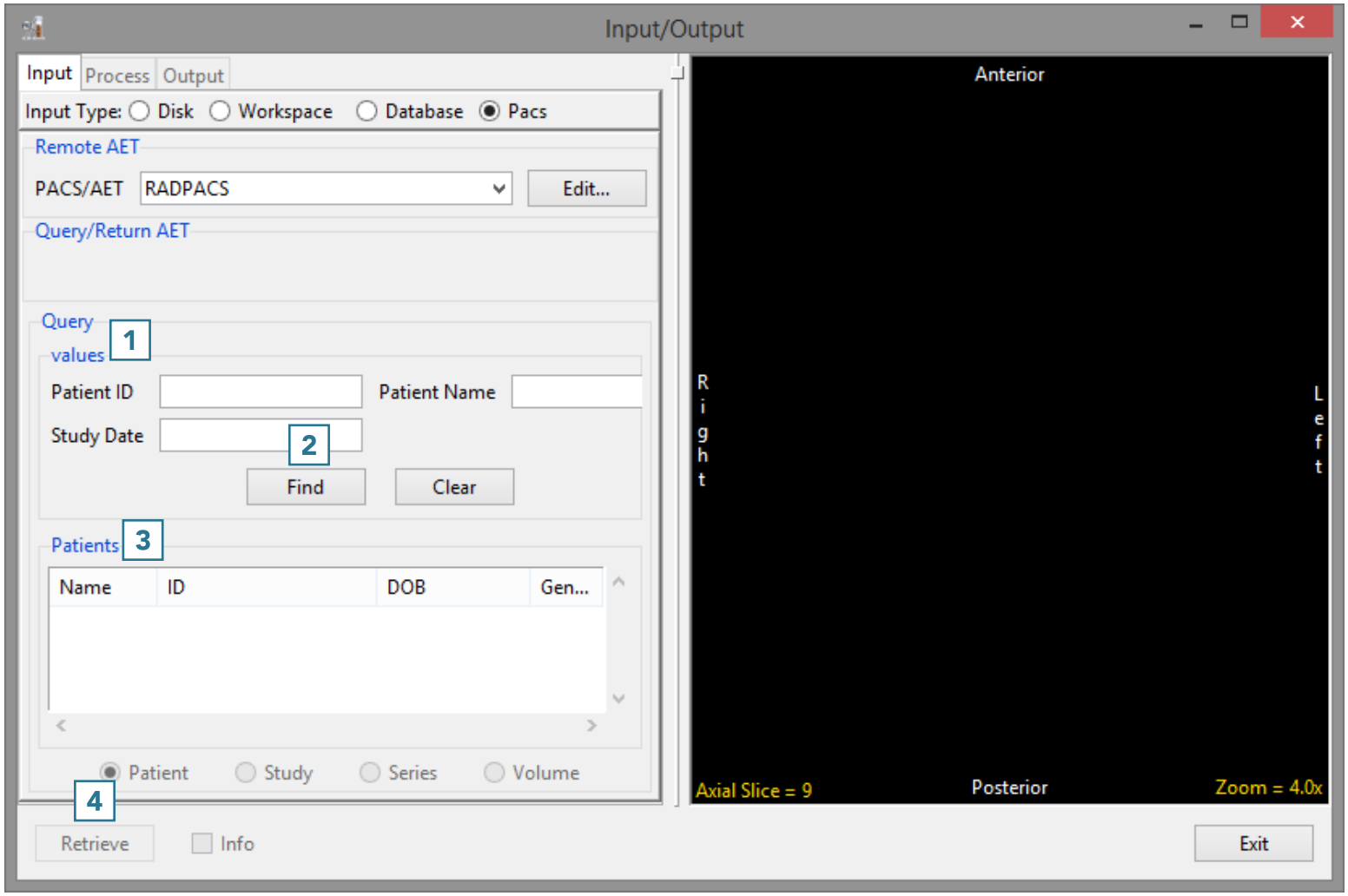



- The window will update and the PACS information will be available in the main window. 6
- Click Save to close the window. 7
- The PACS is now configured on the AnalyzePro side.

Note that there may be additional configuration required on the PACS side by your PACS admin.



- To Query the PACS, enter the Patient ID, Patient Name or Study Date 1 and click Find 2 or press [Enter].
- The relevant patient data will displayed under Patients. 3
- Select the patient and click Retrieve 4 to merge into the current database.



# Process: Transforming Data

Spatial- and intensity-based transformations can be applied to the data while loading to or saving from AnalyzePro. These transformation options are available from Input/Output > Process, once a data set is selected.

## 5. Organize

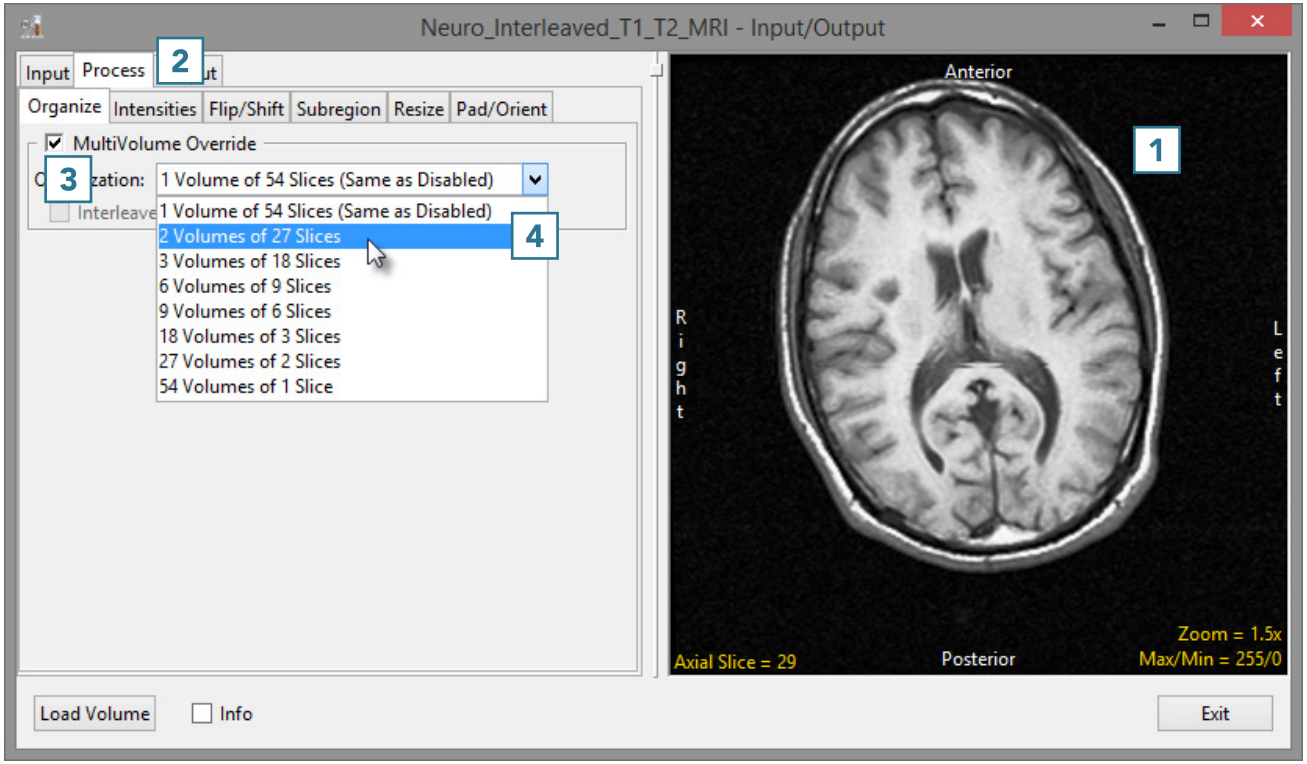
### MultiVolume Override

Sometimes image data may not be organized as expected. For example, two 3D data sets may be concatenated into a single 3D data set, requiring the data to be split into two volumes. Furthermore, the data may be interleaved. The MultiVolume Override options provide a utility to efficiently reorganize such problematic data while loading.

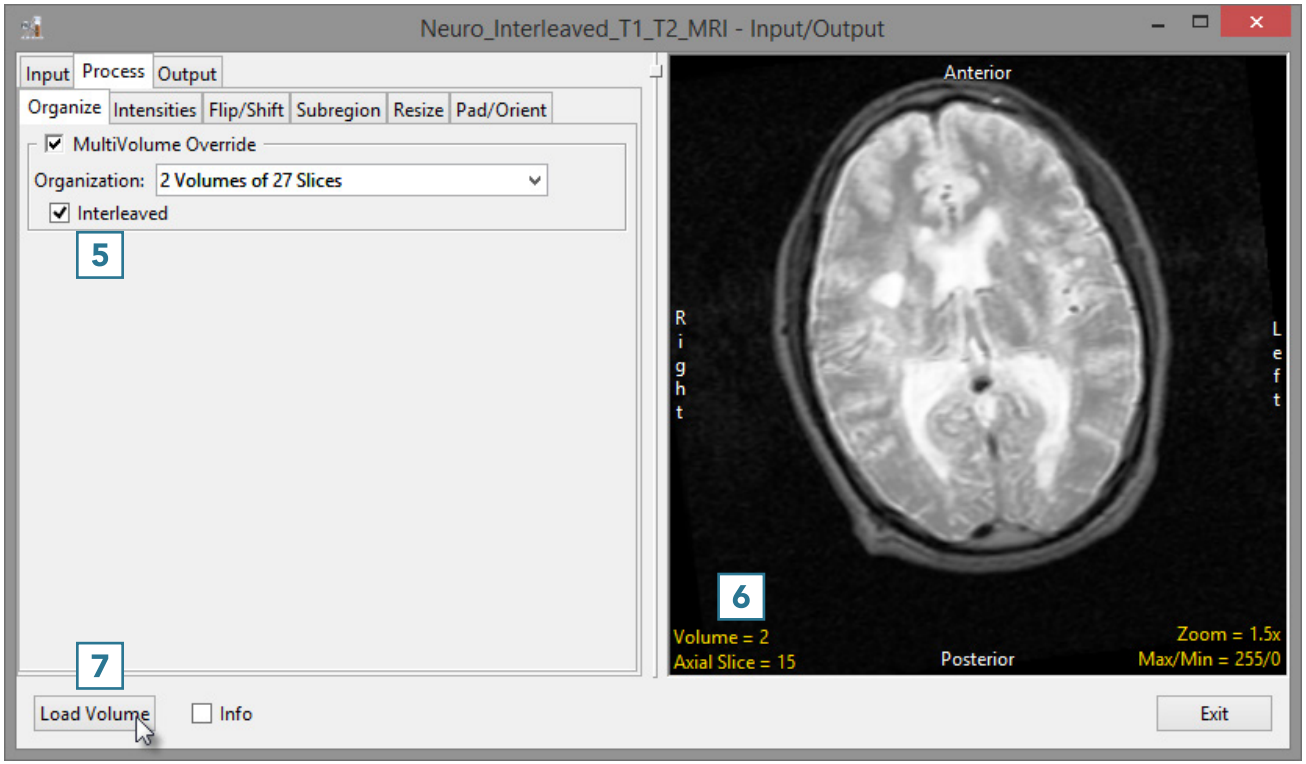
- Open the Input/Output module.
- Navigate to the data and select the data set you want to load and transform.
- Note that the data will be displayed. 1
- Select the Process tab. 2
- Under Organize, check the MultiVolume Override option. 3 All possible data reorganization options will be available from the drop-down menu.

We know that in this example the 54-slice data set is comprised of a T1 and a T2 data set, each containing 27 slices. Select the appropriate option from the drop-down menu: 2 Volumes of 27 Slices. 4

Download the Neuro_Interleaved_T1_2_MRI data set to follow along
http://analyzedirect.com/data/



- The data has now been changed from a single 3D data set containing 54 slices to a 4D multivolume made up of two 3D data sets, each containing 27 slices. Hold the cursor over the image and use the middle mouse wheel to scroll through the data. Note that in this example, the T1 and T2 image data is interleaved so the current volume will alternate between T1 and T2 slices.
- To correct for the interleaved image data, check the Interleaved option. 5
- Scroll through the image data for volume 1. This will now display only the T1 image data.
- Use the Volume option 6 to change to volume 2 and scroll through the data. Only T2 image data will be displayed.
- Click Load Volume 7 to load the corrected image data.



# 6. Intensities

The Intensities option allows for intensity scaling or threshold-based manipulations to be applied to the data.

## Intensity Scaling

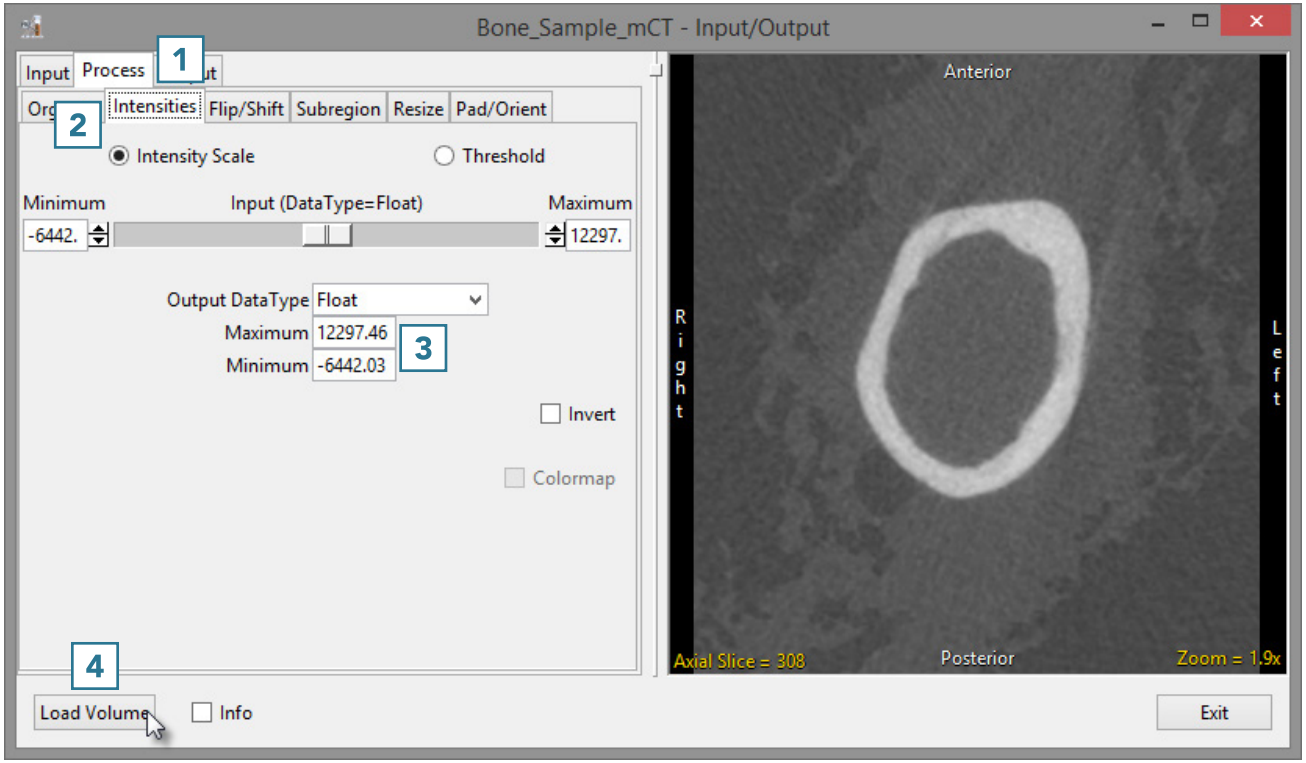
Intensity scaling allows for the adjustment of the voxel value information in the data. Image data can be scaled by adjusting the output Data Type. Values can also be linearly scaled using the Input Maximum and Minimum scale options.

## Modifying Image Data Type

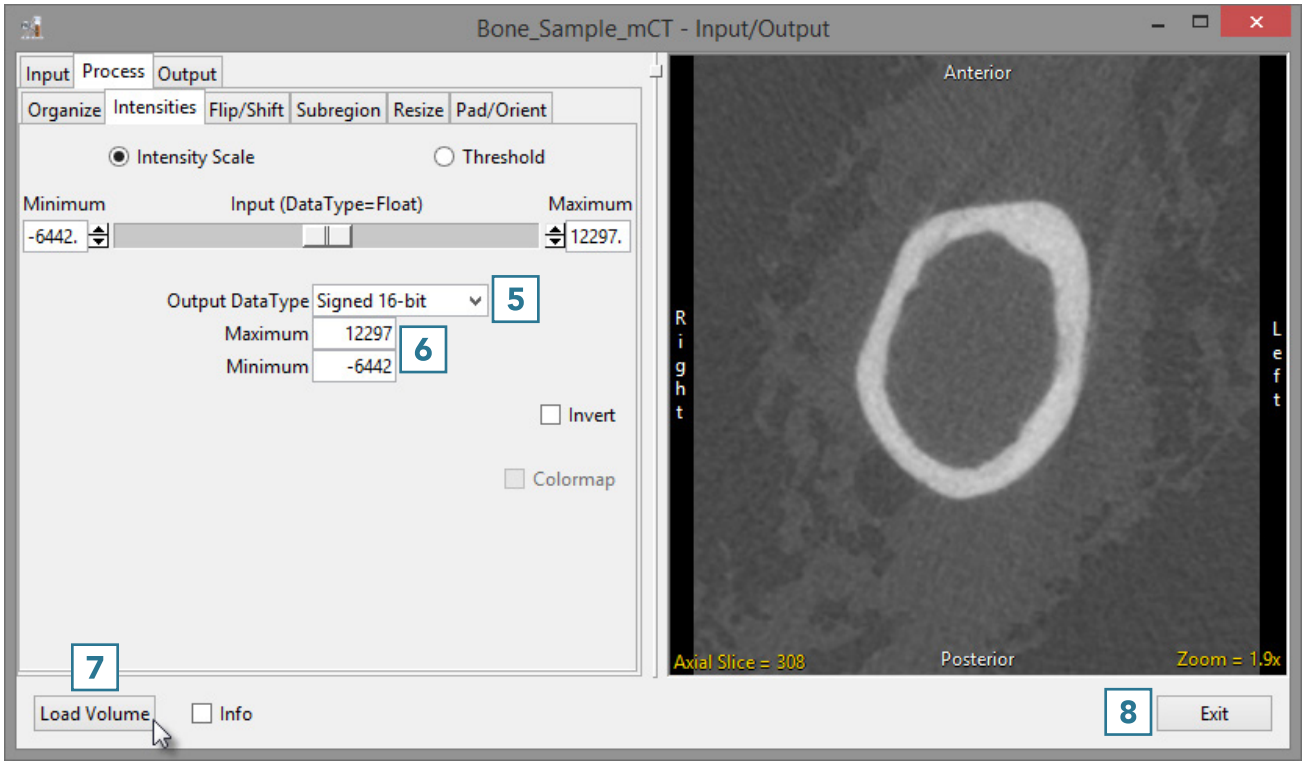
Changing the image data type can reduce the size of the data on disk. In this example, a microCT data set has a data type of Float. The size of the image data when loaded into AnalyzePro is 92.71 MB. Changing the data type to Signed 16-bit reduces the size of the data set by about 50% to 46.35 MB when loaded.

- Open Input/Output.
- Navigate to and select the data set you wish to load and transform.
- Select Process 1 and Intensities. 2
- Make a note of the Input Maximum and Minimum values. 3
- Select Load Volume. 4 This will load the volume to the workspace as a Float data set.

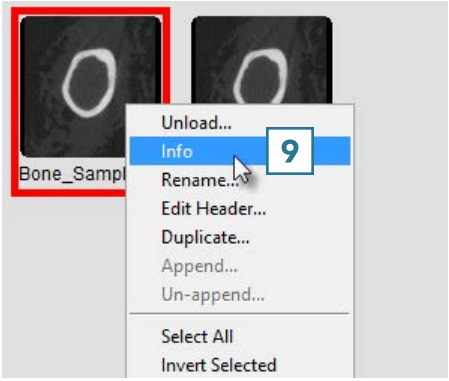
Download the Bone_Sample_mCT data set to follow along http://analyzedirect.com/data/



- Set the Output DataType to Signed 16-bit. 5
- Enter the Output Maximum and Minimum values 6 by copying the input maximum and minimum values and rounding to the nearest whole number.
- Select Load Volume 7 and select Create New when prompted.
- Exit Input/Output. 8



- In the AnalyzePro window, right-click on the first data set and select Info. 9 Repeat for the second data set.
- In the info panel beneath the data, note the size of the original and scaled data set.




Bone_Sample_mCT | Bone_Sample_mCT0

```
FileName=C:\temp\APRO\Michael\Bone_Sample_mCT.mmap
DataType=AVW_FLOAT (32-bit float)

Width=190
Height=208
Depth=615

NumVols=1

Size=92.71 Mb

Info:
        0002|0002="1.2.840.10008.5.1.4.1.1.2"
        0002|0003="2.16.756.5.23.5050.67.3003.3.2014
        0002|0010="1.2.840.10008.1.2.1"
        0002|0012="2.16.756.5.23.1.2"
        0002|0013="SCANCO_V1.2a"
        0008|0008="ORIGINAL\PRIMARY\AXIAL"
        0008|0016="1.2.840.10008.5.1.4.1.1.2"
        0008|0018="2.16.756.5.23.5050.67.3003.3.2014
        0008|0020="20140107"
        0008|0021="20140107"
        0008|0023="20140107"
```

Bone_Sample_mCT | Bone_Sample_mCT0

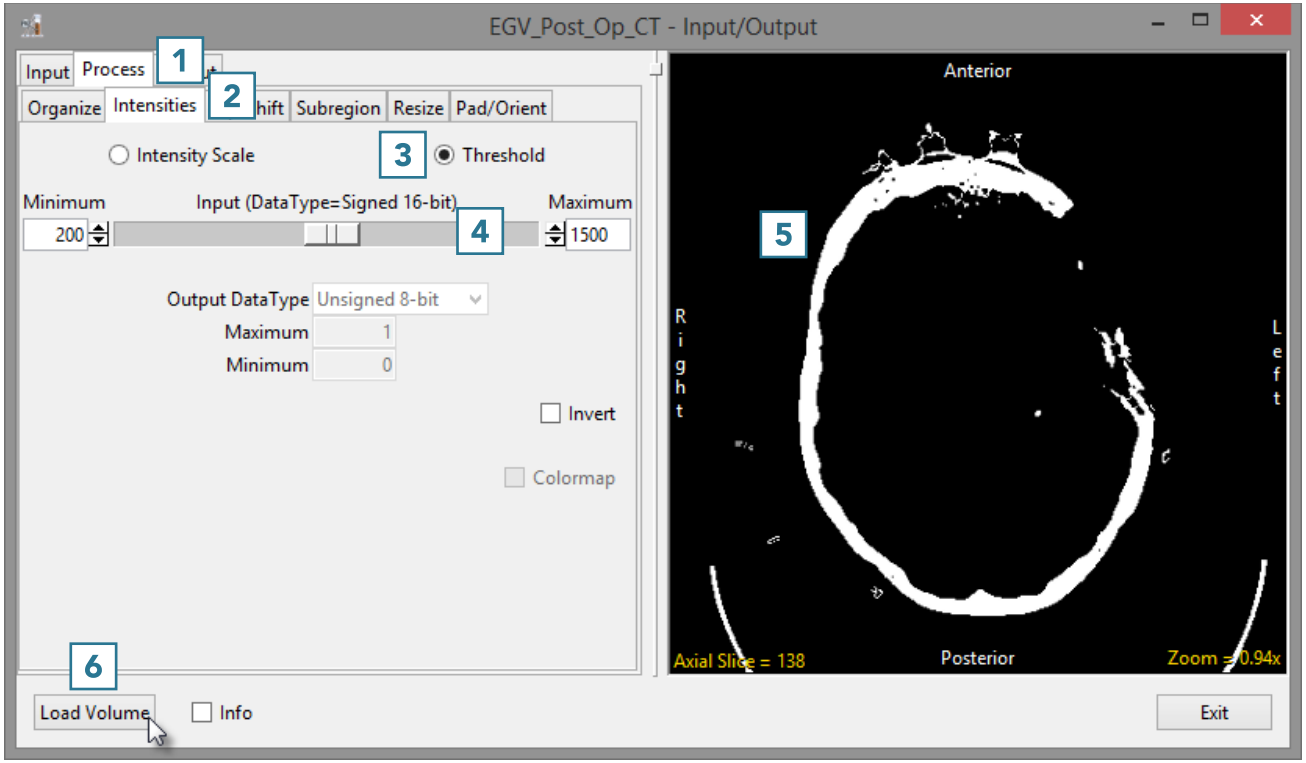
```
FileName=C:\temp\APRO\Michael\Bone_Sample_mCT0.mmap
DataType=AVW_SIGNED_SHORT (16-bit signed)

Width=190
Height=208
Depth=615

NumVols=1

Size=46.35 Mb

Info:
        0002|0002="1.2.840.10008.5.1.4.1.1.2"
        0002|0003="2.16.756.5.23.5050.67.3003.3.2014
        0002|0010="1.2.840.10008.1.2.1"
        0002|0012="2.16.756.5.23.1.2"
        0002|0013="SCANCO_V1.2a"
        0008|0008="ORIGINAL\PRIMARY\AXIAL"
        0008|0016="1.2.840.10008.5.1.4.1.1.2"
        0008|0018="2.16.756.5.23.5050.67.3003.3.2014
        0008|0020="20140107"
        0008|0021="20140107"
        0008|0023="20140107"
```

## Threshold Scaling

Threshold scaling allows a range of voxels from the input volume to be loaded as a binary data set. All voxels greater than or equal to the Input Minimum and less than or equal to the Input Maximum are set to 1. All other voxels are set to 0.

- Open Input/Output.
- Navigate to and select the data set to which you want to apply a threshold scaling.
- Select Process 1 and Intensities. 2
- Check the Threshold option. 3
- Use the Input sliders to set the threshold minimum and maximum. 4
- Note the image display will update, showing a binary image for the selected voxels. 5
- Click Load Volume 6 to load the binary volume.

Download the EGV_Post_Op_CT data set to follow along http://analyzedirect.com/data/



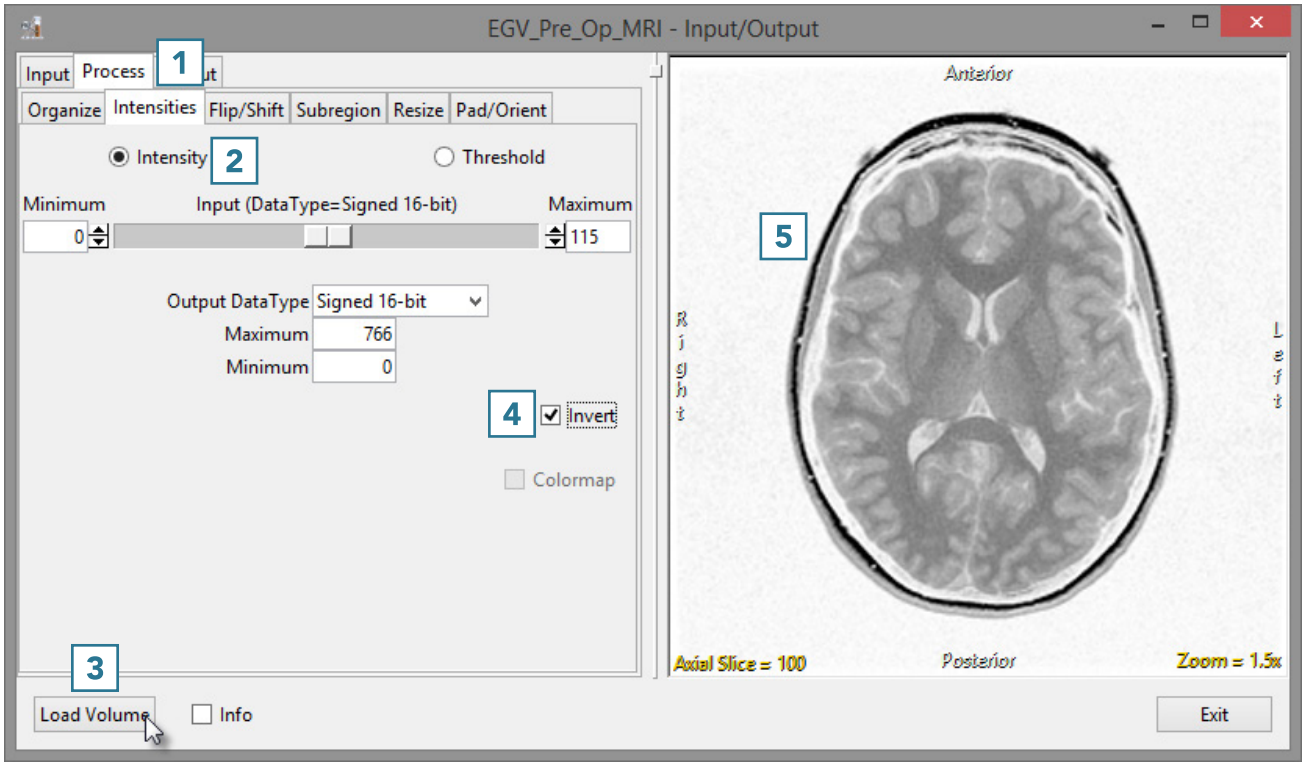
## Inverting Data

For certain applications, such as the segmentation of the thalamus, it is beneficial to view an inverted copy of the image data alongside the original grayscale data to improve visualization of the thalamus. Reviewing the original and inverted image data aids with manual delineation of the structure.

- Open Input/Output.
- Navigate to and select the data set you want to invert.
- Select Process 1 and Intensity. 2
- Select Load Volume 3 to load the data into AnalyzePro.
- Next, check the Invert option. 4 Note that the display of the data will update. 5
- Click Load Volume 3 and select Create New.

A grayscale and inverted version of the data are now available for use within the program. These two data sets can be simultaneously loaded into Segment.

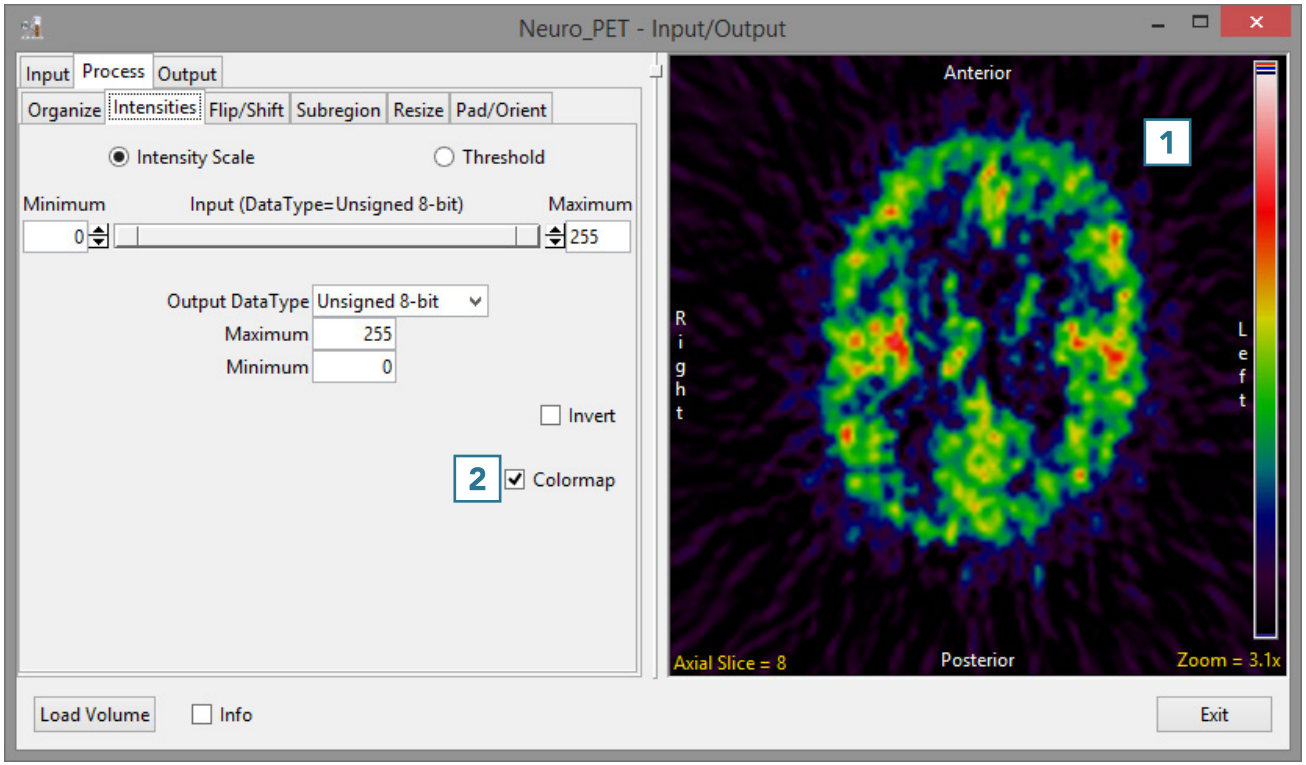
Download the EGV_Pre_Op_MRI data set to follow along http://analyzedirect.com/data/



## Colormaps

When loading a data set that has an associated colormap, 1 the Colormap checkbox will be selected. 2

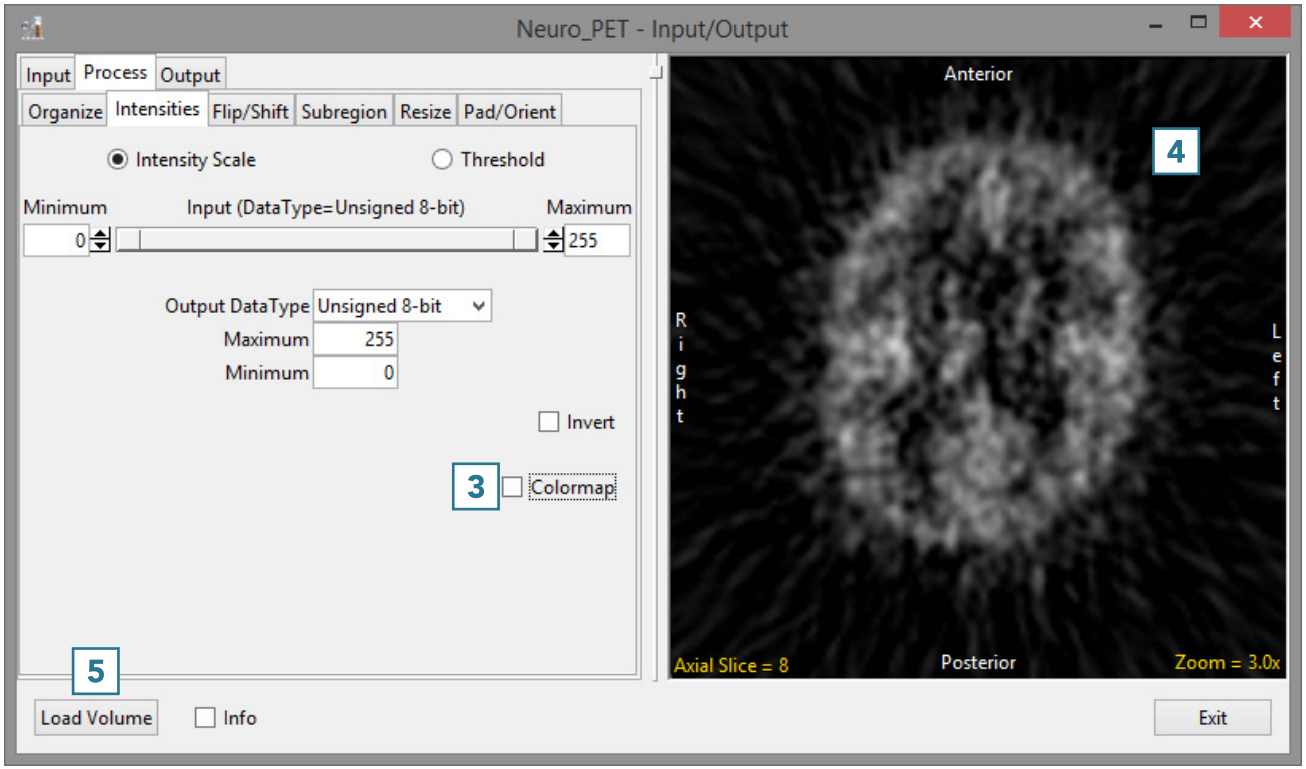
Download the Neuro_PET data set to follow along
http://analyzedirect.com/data/



- To load the grayscale data without the associated .lkup colormap file, uncheck the Colormap checkbox. 3

Note that the image display will update to show the grayscale data. 4

- To load the data, click Load Volume. 5



# 7. Flip/Shift

## Data Flipping

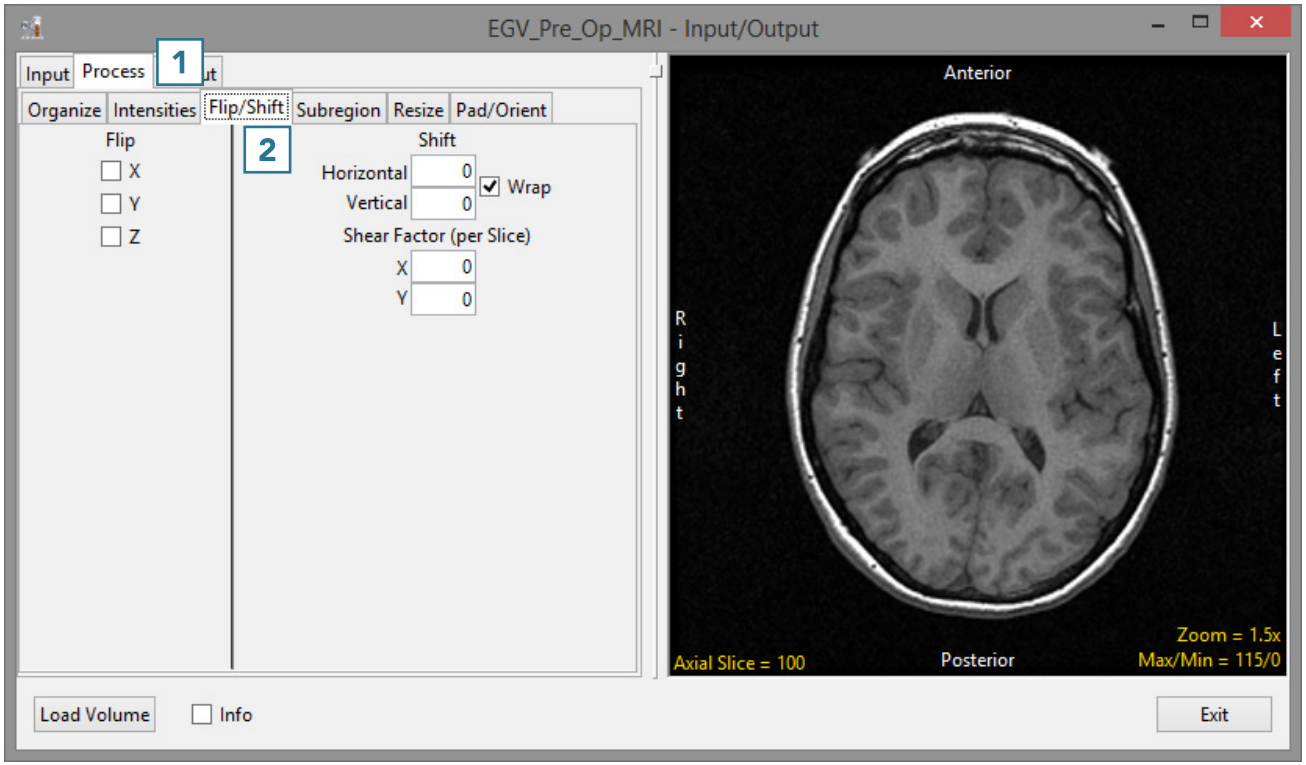
It may be necessary to flip data in order to orient it correctly. The Flip/Shift > Flip options allow users to flip data along any single axis or combination of axes.

Once a flip checkbox is selected, the flip will be applied to the data and the display panel can be used to review. Unchecking the option will undo the flip. Flipping the data in only the X or Y direction will create a mirror image. If this is not the desired result, the data can be flipped in both the X and Y directions at once to prevent a mirror image from being created. To apply a flip:

- Open Input/Output.
- Navigate to and select the data set to be flipped and loaded.
- Select Process 1 and Flip/Shift. 2

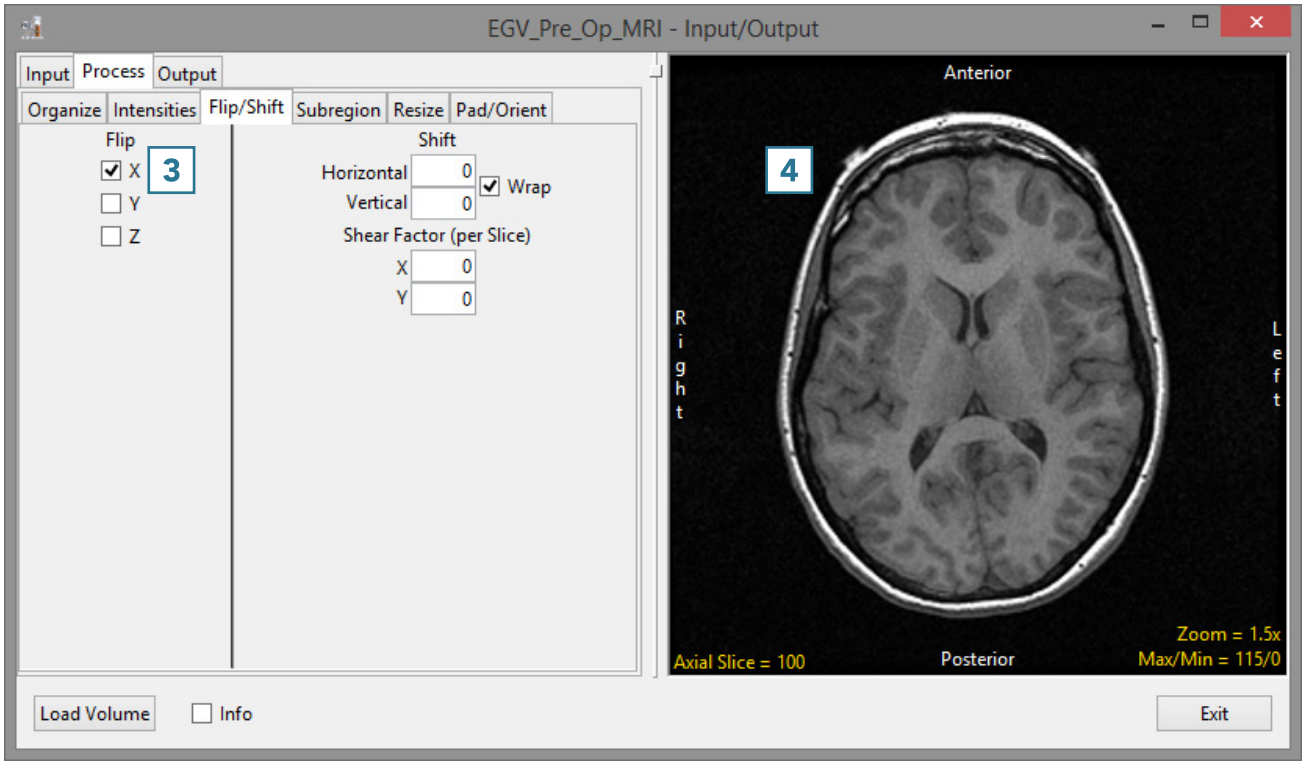
Download the EGV_Pre_Op_MRI data set to follow along http://analyzedirect.com/data/

| Axis | OUTCOME |
|---|---|
| X | Flips data horizontally, rotating about the vertical (Y) axis. |
| Y | Flips data vertically, rotating about the horizontal (X) axis. |
| Z | Changes the order of the slice data. |



- Check the X Flip option. 3

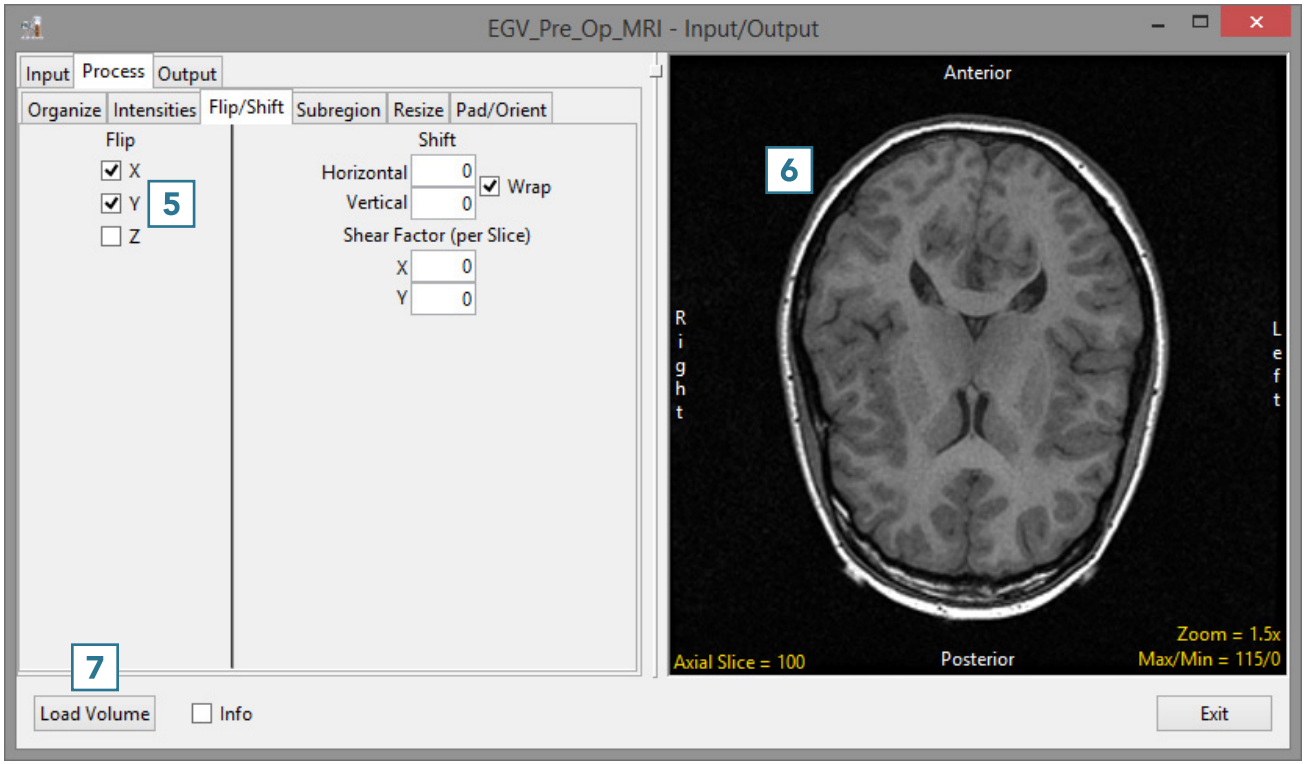
Note the update to the data. 4



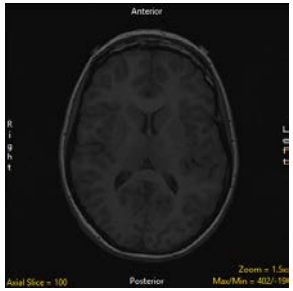
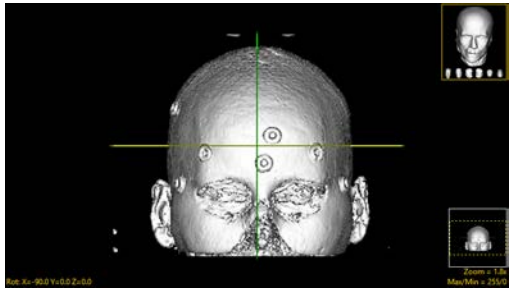
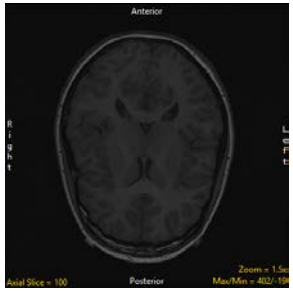
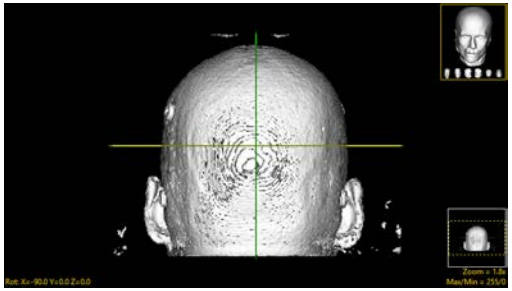
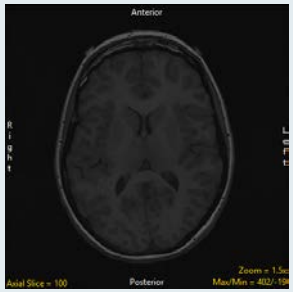
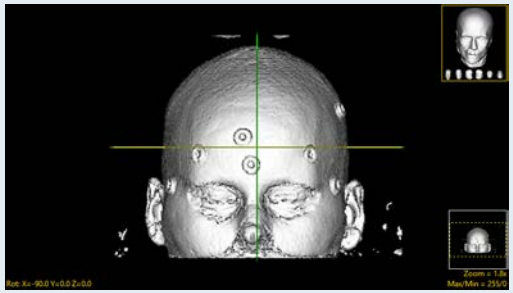
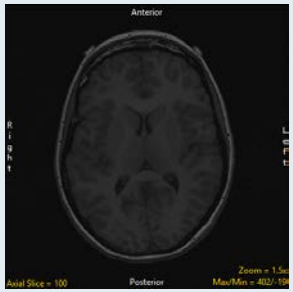
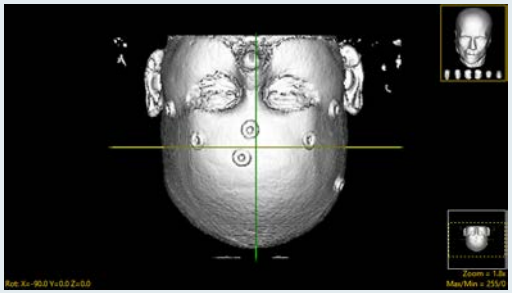
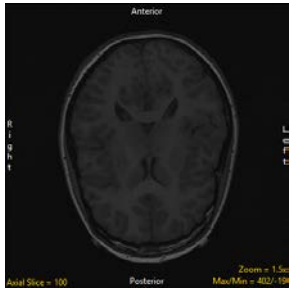
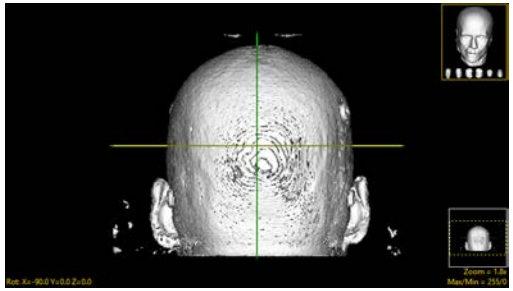
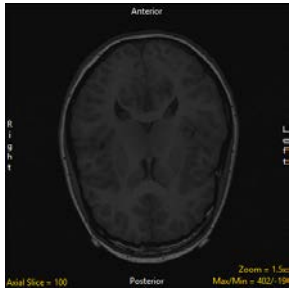
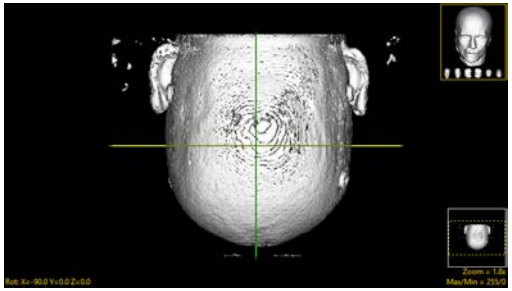
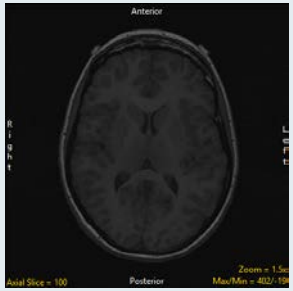
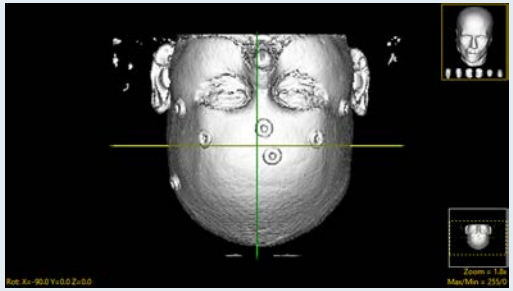
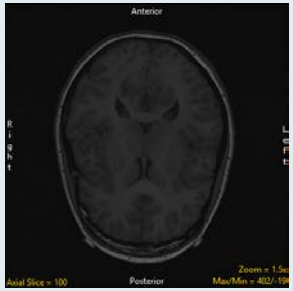
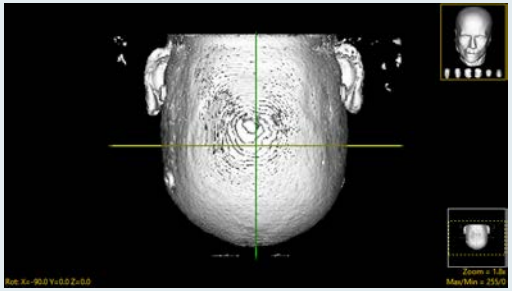
- Check the Y Flip option. 5

Note the update to the data. 6

- To load the data, click the Load Volume button. 7



## Table 3.2: Results of Flipping Data Along Any Combination of Axes

| Flip | 2D | 3D | Flip | 2D | 3D |
|---|---|---|---|---|---|
| No flip |  |  | XY |  |  |
| X |  |  | XZ |  |  |
| Y |  |  | YZ |  |  |
| Z |  |  | XYZ |  |  |

## Shifting Data

The shift option allows data to be shifted horizontally or vertically. Data shift may be necessary to correct for slice wraparound. In this example, the front slices of a sagittally-acquired MRI data set have wrapped around to the posterior side of the data set 1 and there are slices from the inferior side of the volume that have wrapped around to the superior side of the volume. 2

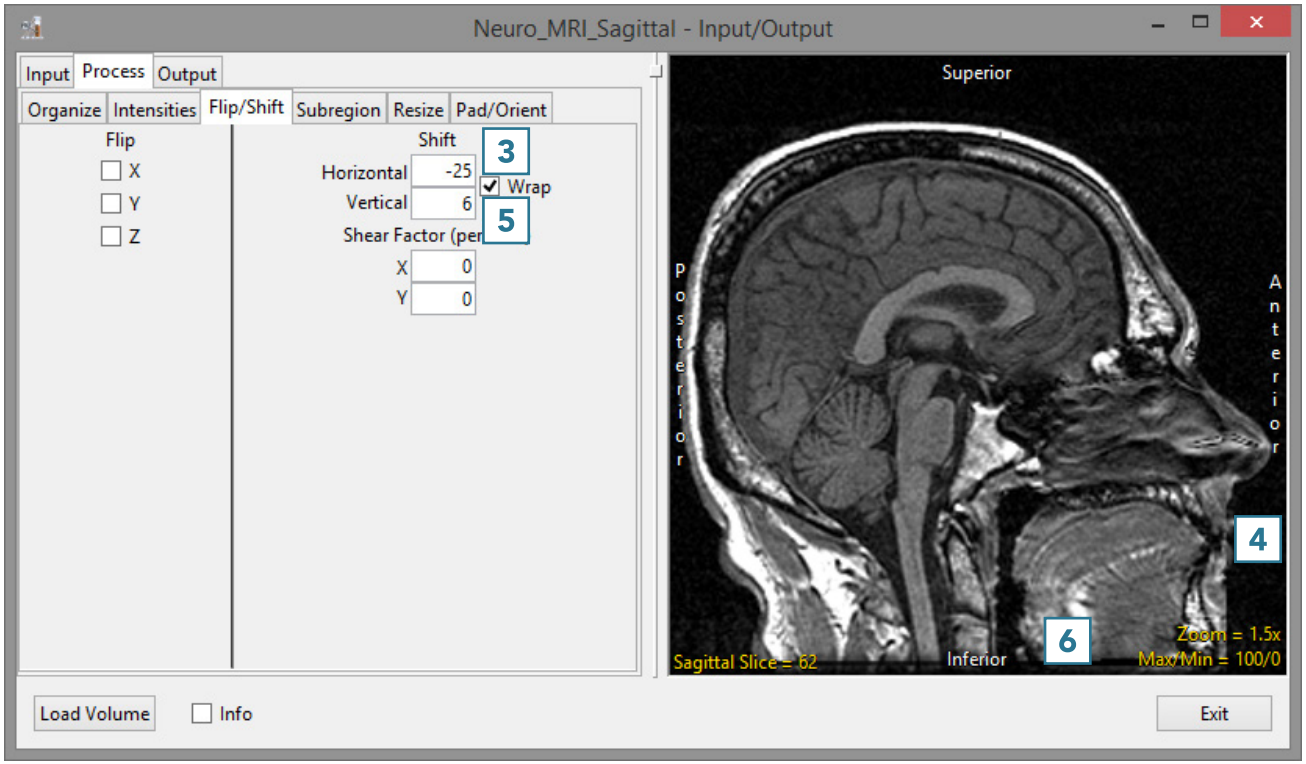
Download the Neuro_MRI_Sagittal data set to follow along http://analyzedirect.com/data/

- To correct for the horizontal shift in slices, enter -25 in the Horizontal Shift field. 3

Note that the data will be shifted back 25 slices. The last 25 slices will automatically wrap around from the posterior side of the data set to the anterior side of the data set. 4

- To correct for the vertical shift in slices, enter 6 in the Vertical Shift field. 5

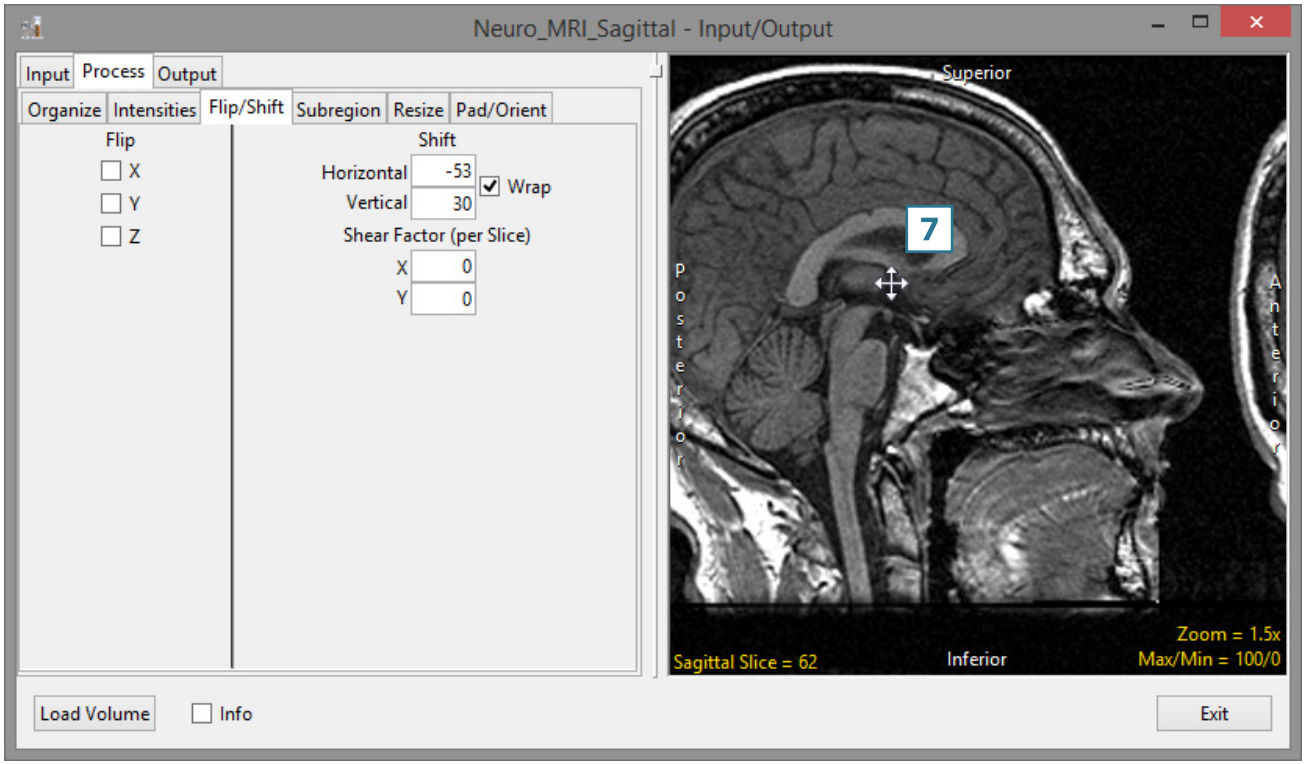
Note that the data will be shifted up 6 slices. The top 6 superior slices will automatically wrap around to the inferior side of the data set, since the Wrap checkbox is checked. 6



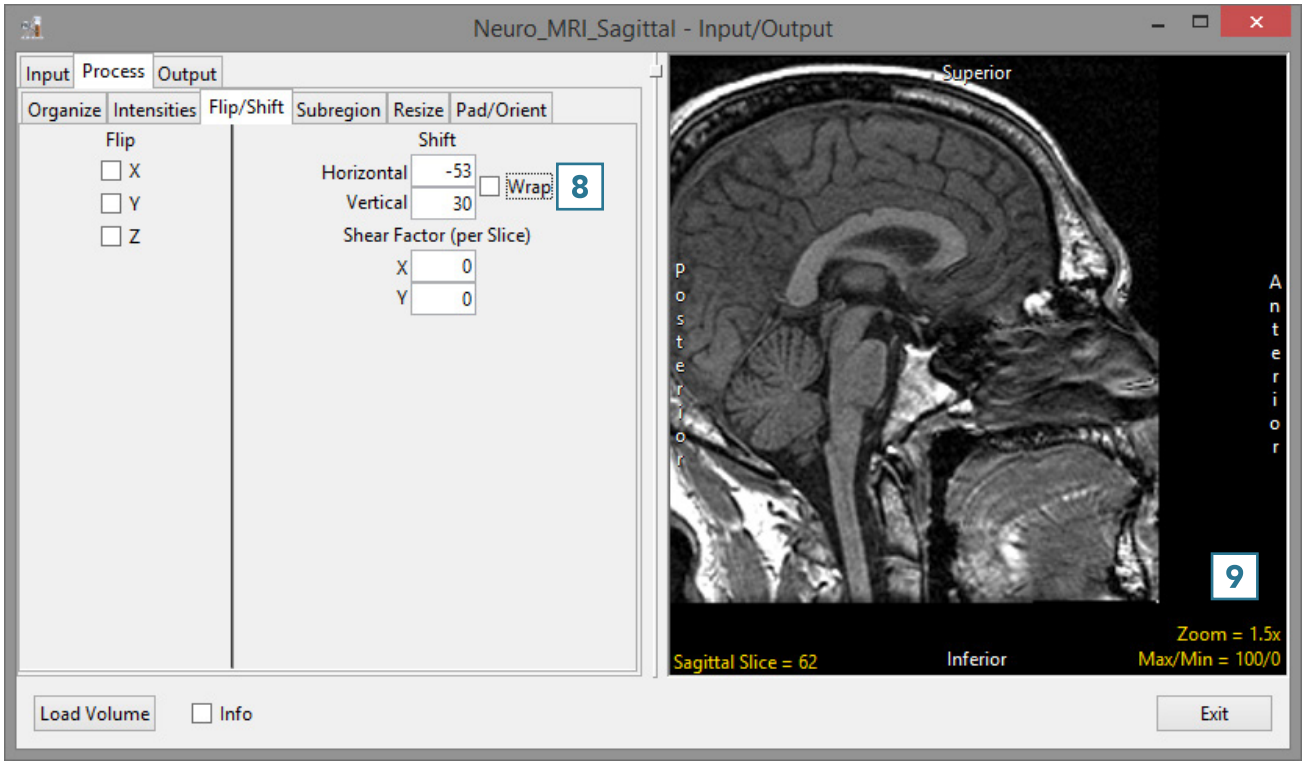
## Table 3.3: Shift Options Quick Reference

| Shift | Axial | Coronal | Sagittal |
|---|---|---|---|
| Horizontal + | To left | To left | To anterior |
| Horizontal - | To right | To right | To posterior |
| Vertical + | To anterior | To superior | To superior |
| Vertical - | To posterior | To inferior | To inferior |

- To shift data interactively, click on the image data. Note that the cursor will update; drag the data to a new location. 7



- Unchecking the Wrap checkbox 8 will prevent slices from being wrapped. 9



## Shear Factor Correction

Sometimes CT images are acquired with the gantry tilted obliquely (non-orthogonally) relative to the direction of the table movement. If the volume is constructed by stacking the image slices, the volume will appear sheared or skewed. AnalyzePro will automatically detect and apply the gantry tilt shear correction and the appropriate shear factor values will be populated in Shear Factor (per slice) fields. If desired, the Shear Factor (per slice) values can be manually entered.

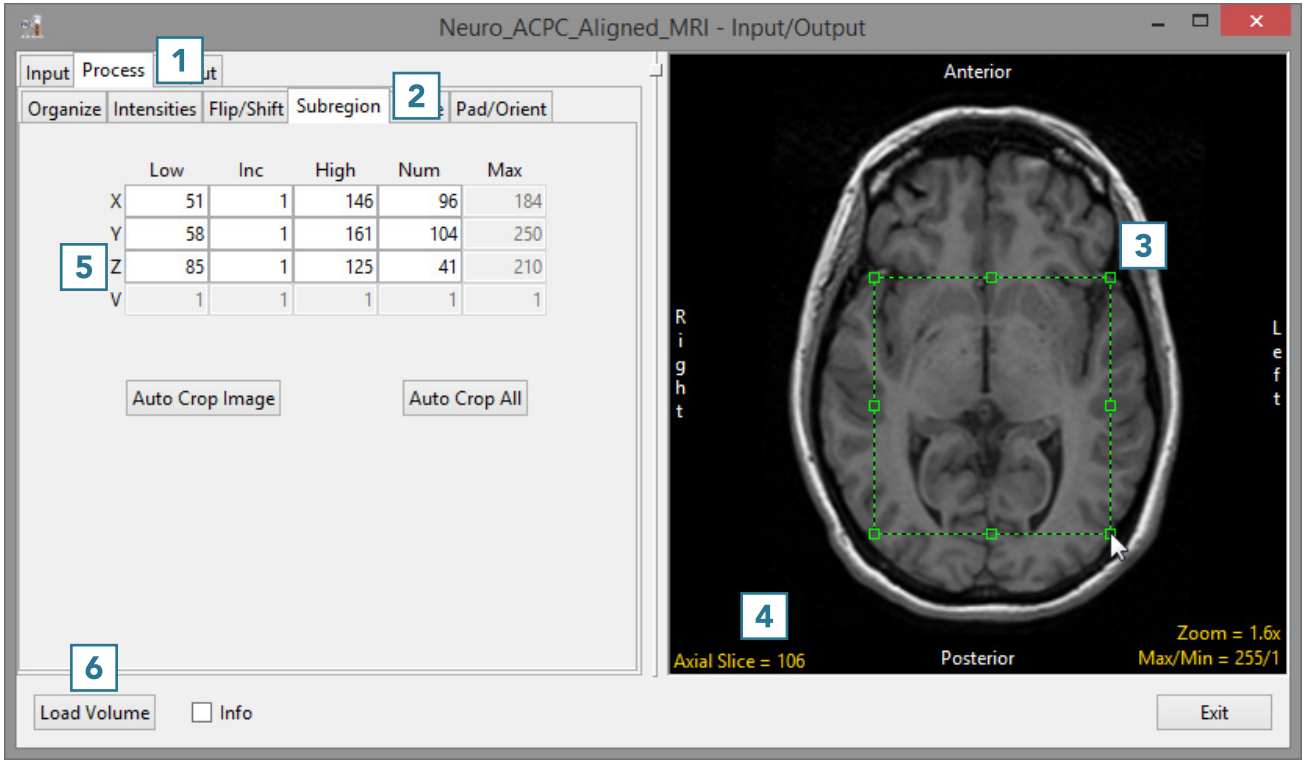
# 8. Subregion

## Cropping Data

The Subregion tool in Input/Output > Process can be used to reduce the size of a data set without the need to interpolate the original voxel data. The tool can also be used to crop data to a specific region of interest, which may be beneficial for certain applications, such as hippocampal segmentation.

- Open Input/Output.
- Navigate to and select the data set you want to crop.
- Select Process 1 and Subregion. 2
- To crop the data, click on the green box 3 in the display panel and adjust to the desired position.
- To define the crop in the Z range, click on the Slice option. 4 With your left mouse button held down, move the mouse up or down to navigate through the slice data. You can also use the scroll wheel to move through the slice data. When you reach the lower limit for the crop, enter the slice number in the Z Low box. 5 Enter the upper limit slice number in the Z High box.
- Click Load Volume to load the cropped data. 6

Download the Neuro_ACPC_Aligned_MRI data set to follow along
http://analyzedirect.com/data/

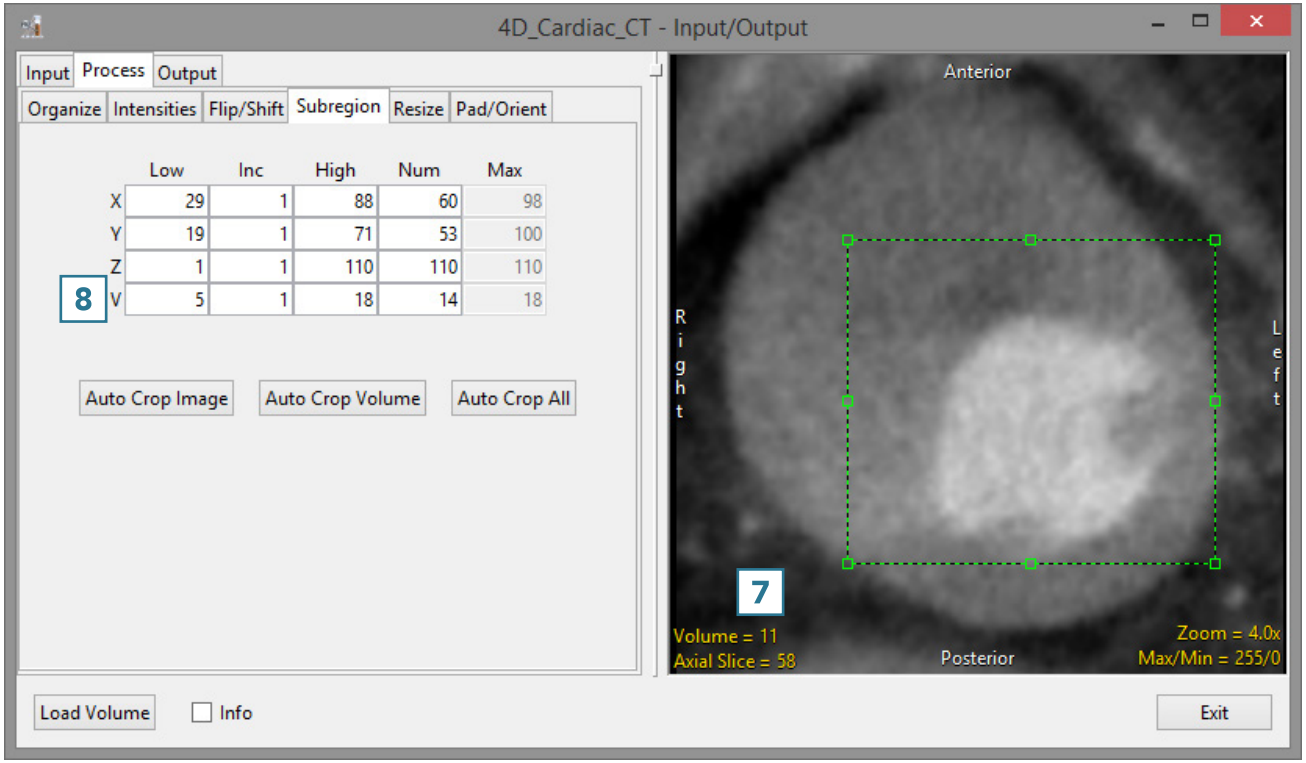


# 9. Cropping 4D Data

4D image data can also be cropped to remove time points from the data prior to loading. When a 4D data set is selected, a fourth dimension V (volume) will be enabled. 7 To crop a 4D data set:

- Select the Volume option 7 and use the cursor to navigate through the volumes in the data, just like you would use the Slice option to navigate through the slices in a single volume.
- Determine the volumes you want to remove from the multivolume and enter the corresponding lower and upper volume limits in the V Low and/or V High boxes. 8

Download the 4D_Cardiac_CT data set to follow along http://analyzedirect.com/data/



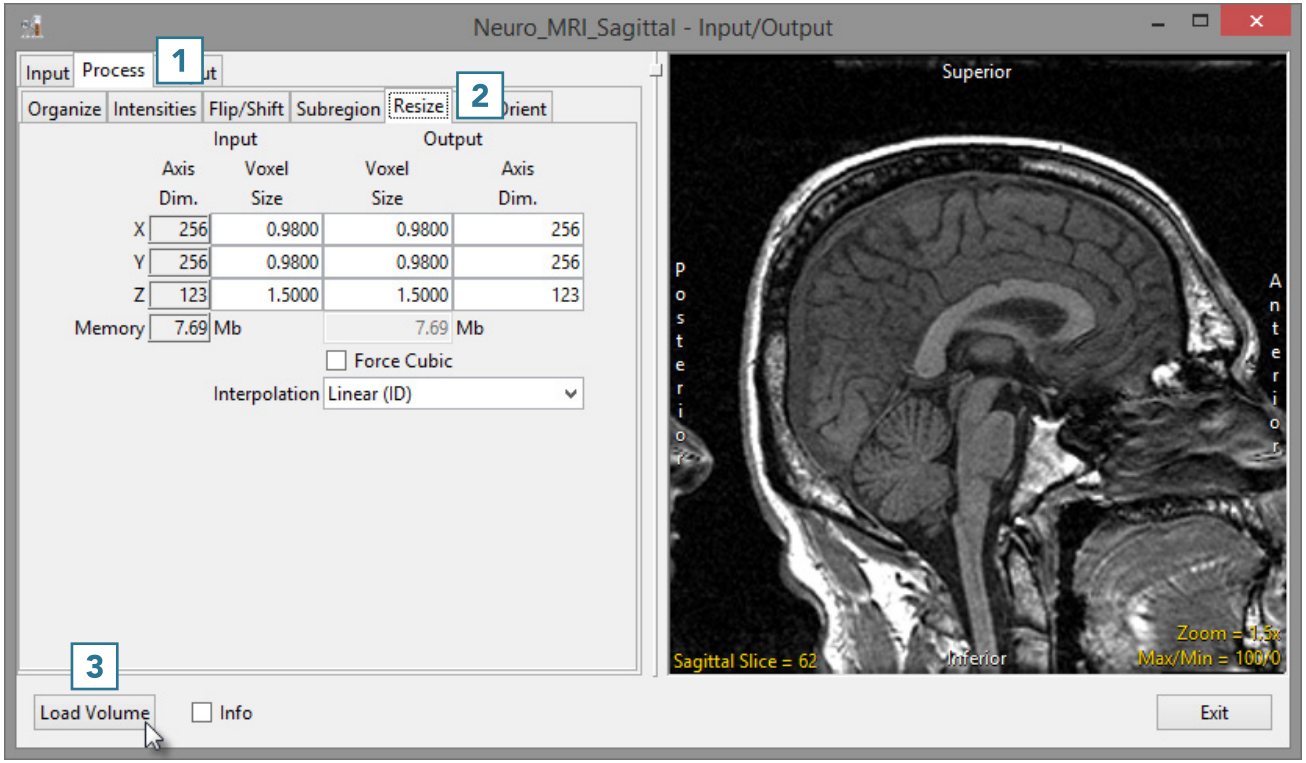
# 10. Resize

Resize can be used to resample image data. If data is acquired with anisotropic (non-cubic) voxels, resize can be used to resample the data to create an isotropic (cubic) data set.

Download the Neuro_MRI_Sagittal data set to follow along http://analyzedirect.com/data/

## Resampling Anisotropic Data

- Open Input/Output.
- Navigate to and select the data set to be resampled.
- Select Process 1 and Resize. 2
- Click Load Volume 3 to load the data set without resampling.



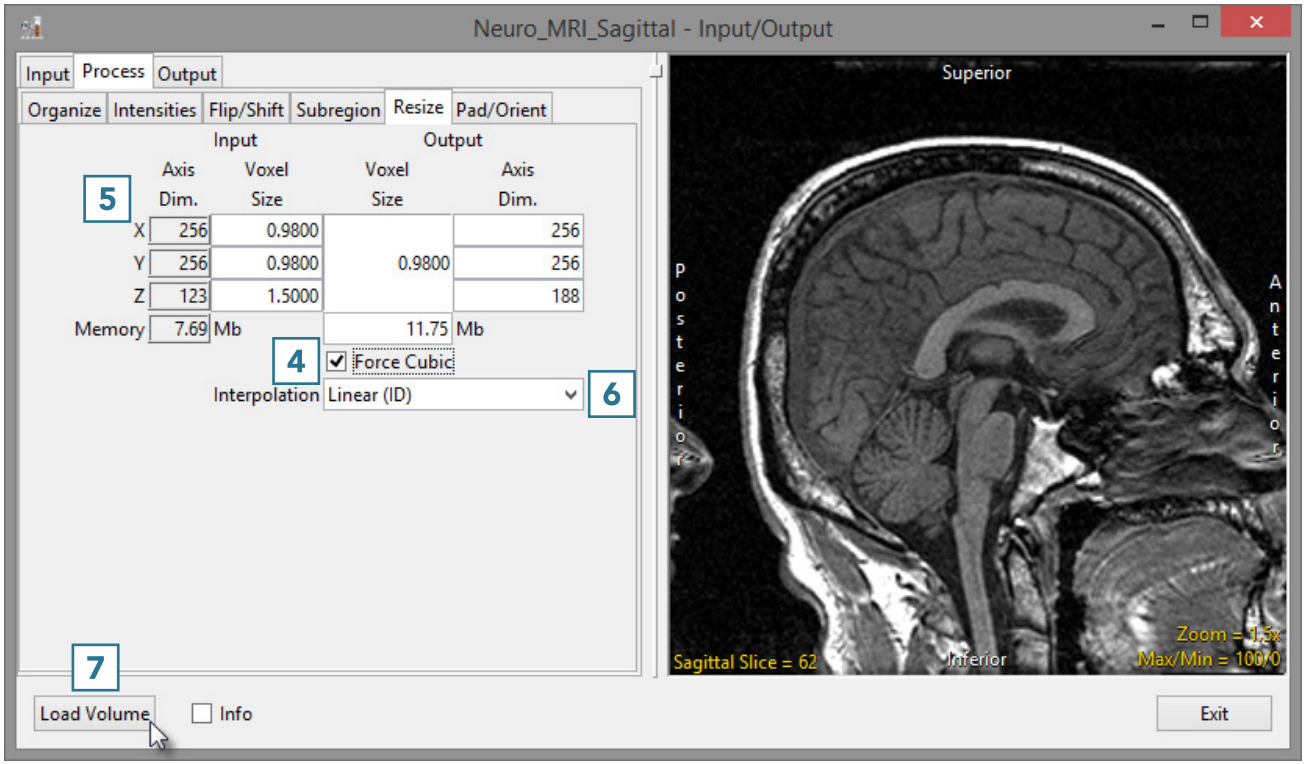
- Check the Force Cubic checkbox. 4

Note the input and output voxel size and the input and output axis dimensions. 5 The data has been resampled at the highest spatial resolution (0.98). The Z dimension which originally had a voxel size of 1.5 has now been resliced to 0.98. To accommodate this, the number of slices in the Z dimension has increased from 123 to 188 (123*1.5/0.98 = 188).

- The interpolation option used to create the new slice data can be selected from the interpolation drop-down menu. 6

For information about various interpolation types, see Table 3.4 or 6.1.

- Click Load Volume 7 and select Create New. Compare both the original and resampled data sets using Display.



Each interpolation type is either input driven (ID) or output driven (OD).

Input driven interpolation algorithms process each voxel in the input volume and map each input voxel into the output space. The actual interpolation takes place in the output space, given the projected contributions of each input voxel into that space. Input driven algorithms will always use every voxel in the input volume as part of the interpolation process.

Output driven algorithms step through each voxel in the output data set and find the corresponding set of voxels in the input data set that map into the output. The interpolation of voxels takes place in the input space, depending on the type of interpolation selected. Output driven algorithms are more common in image processing as they guarantee that every voxel in the output data set will be filled with an interpolated value.

## Table 3.4: Interpolation Types

| Interpolation Type | Description |
|---|---|
| Nearest Neighbor* | selects the value of the closest voxel to which the interpolation resampling maps |
| Linear* | applies a linear interpolation of grayscale intensity based on the distance of neighboring voxels from the interpolated voxel |
| Cubic Spline** | uses a cubic spline function to determine interpolated value |
| Windowed Sinc** | uses windowed sinc function sin(x)/x to determine interpolated value |
| Shape Based | only available for binary data; calculates Euclidean distance, then performs linear interpolation between distance images |

*The Nearest Neighbor and Linear interpolation types can be specified as ID or OD.

**The Cubic Spline and Windowed Sinc interpolation types are both OD. Since they use higher-order functions, they account for more neighboring voxels and thus may provide a better estimate for the interpolated value. These algorithms are also more compute-intensive.

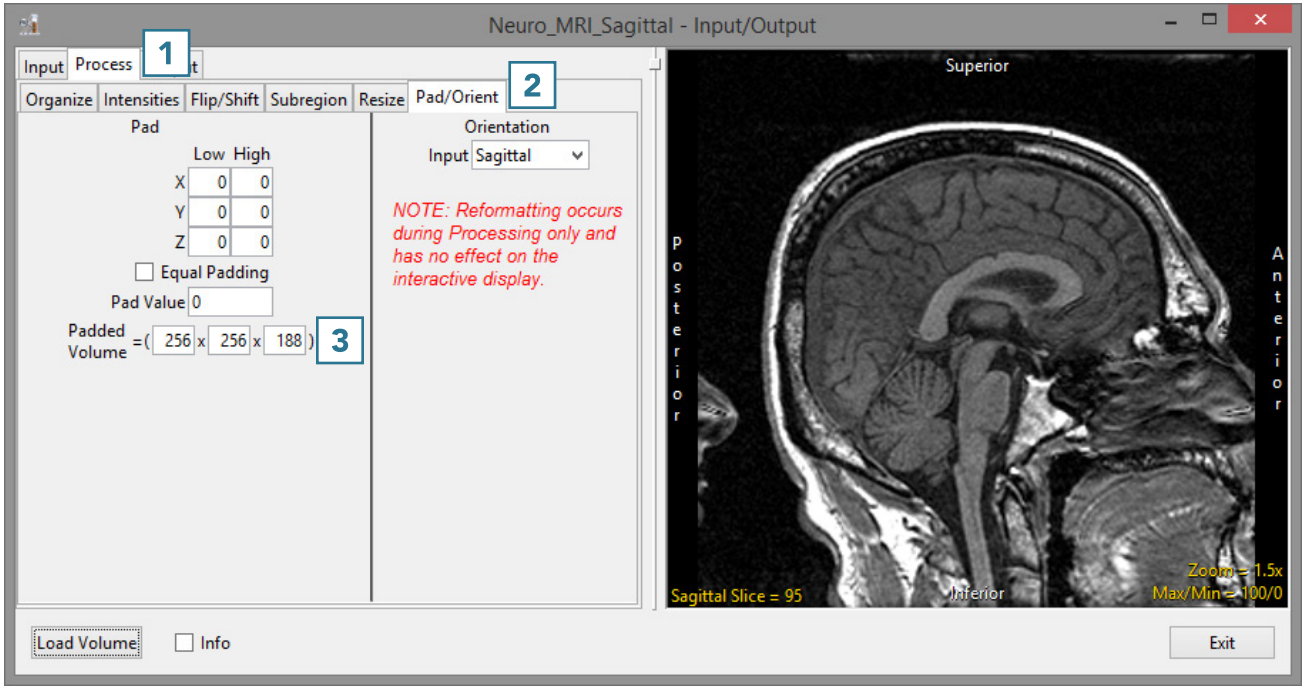
# 11. Pad/Orient

## Padding Data

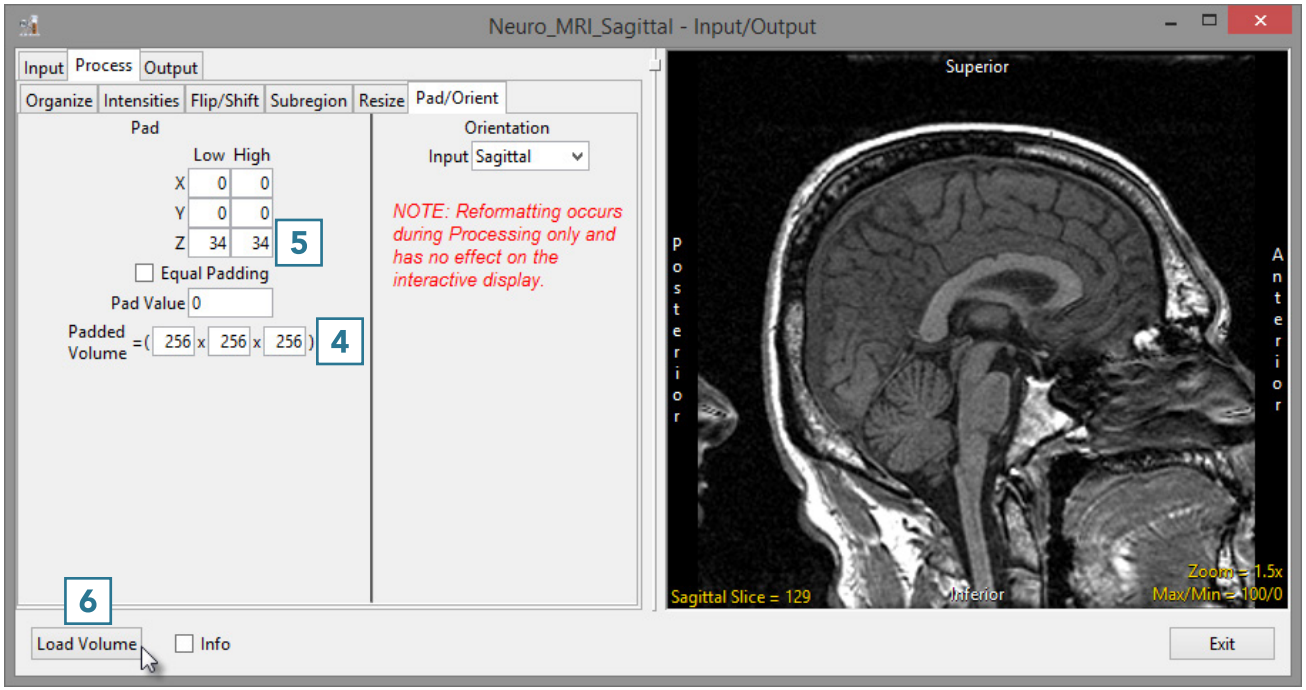
The Pad/Orient option can be used to pad image data. This may be necessary to create a data set with certain dimensions or to make a data set isovolumetric (equal number of slices in each orientation).

- Open Input/Output.
- Navigate to and select the data set to be padded.
- Select Process 1 and Pad/Orient. 2
- Note the slice dimensions for the data are reported in the Padded Volume fields. 3

Download the Neuro_MRI_Sagittal data set to follow along http://analyzedirect.com/data/



- To make the data set isovolumetric, update the appropriate Padded Volume field. 4 The Pad tool will try to apply an equal number of slices to pad the data in the pad axis. 5
- Users can also choose to pad all slices to either the Low or High field for the appropriate axis.
- Click Load Volume 6 to load the data.



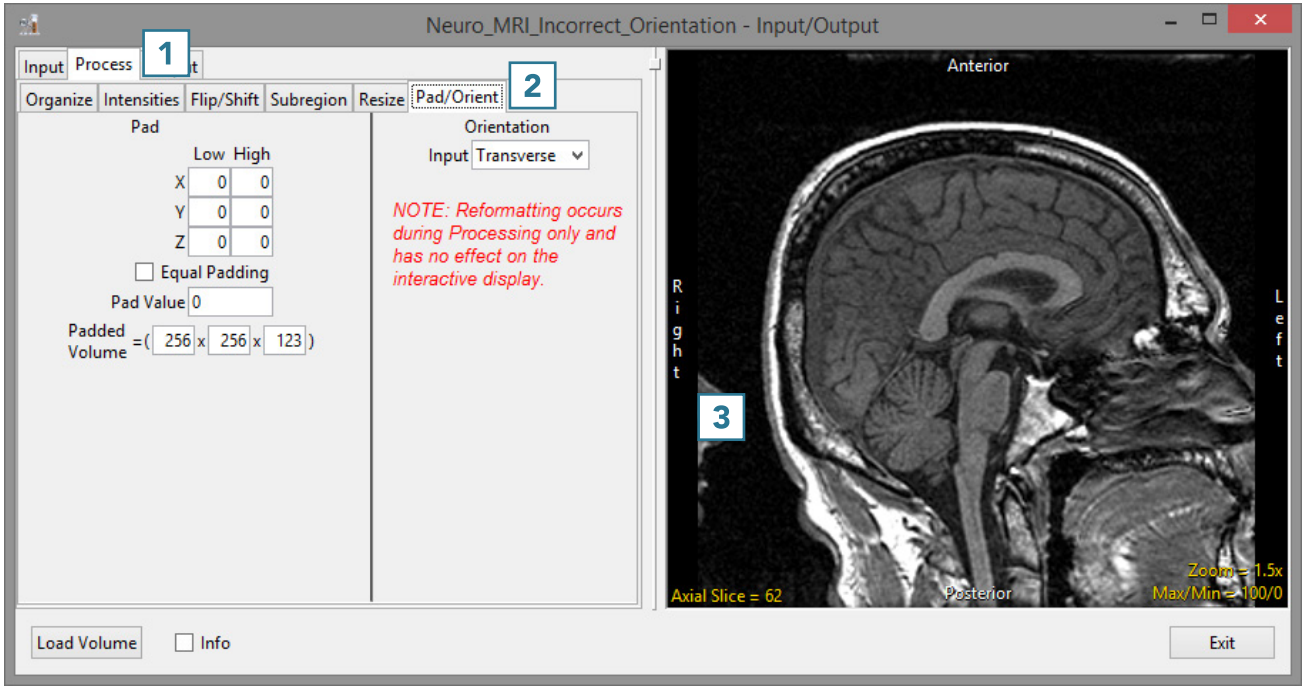
## Correcting an Orientation Flag

If a data set is loaded with an incorrect orientation flag, it will not orient correctly in other AnalyzePro modules. The Orientation option can be used to correct this.

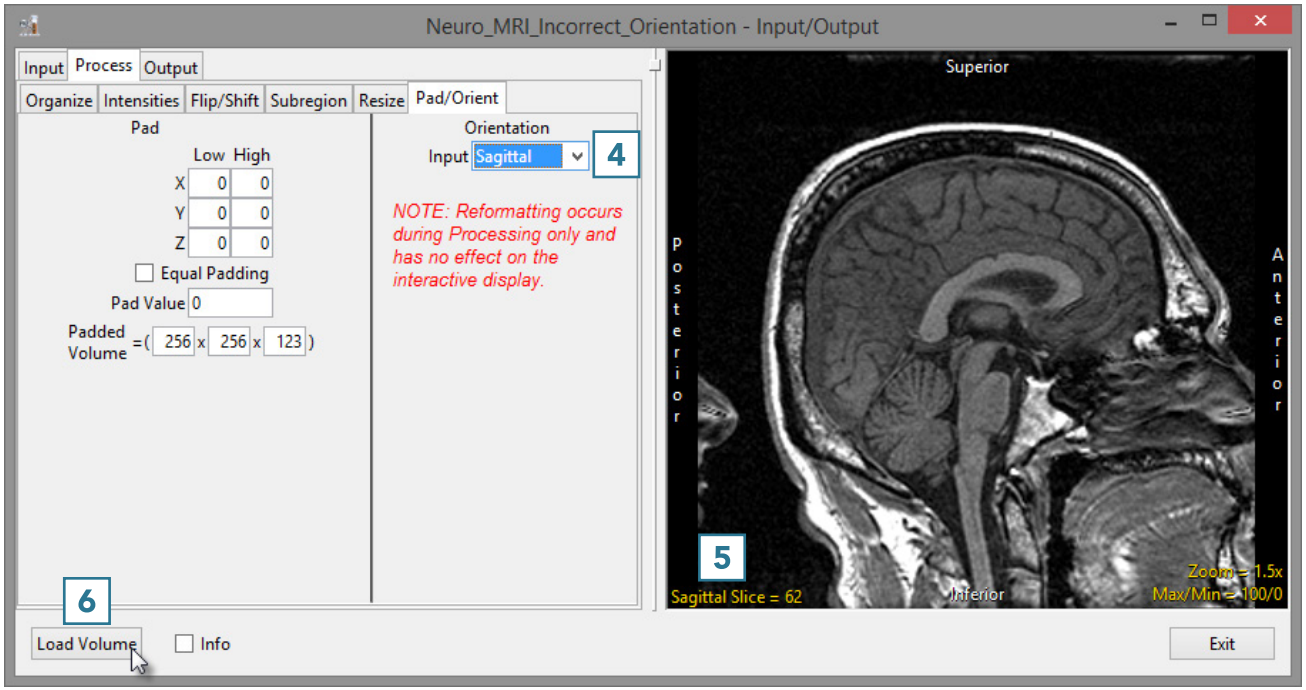
- Open Input/Output.
- Navigate to and select the data set to be padded.
- Select Process 1 and Pad/Orient. 2

Note that the orientation of this sagittally-acquired data set is marked as axial. 3

**Download the Neuro_MRI_Incorrect_Orientation data set to follow along http://analyzedirect.com/data/**

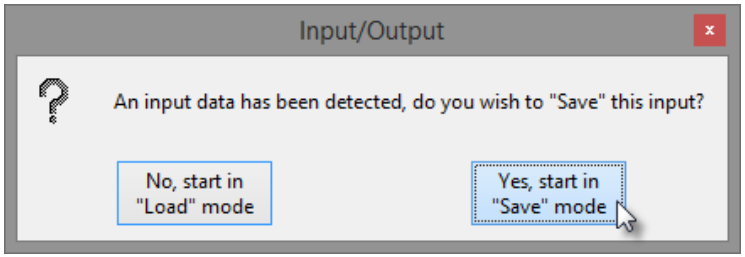


- To correct this, set the Orientation Input option to Sagittal. 4
- Note that the axis labels in the preview are corrected. 5
- Click Load Volume 6 to load the data.



# Output: Saving Data

Data can be exported from AnalyzePro as easily as it can be loaded into the program. Input/Output will open in Save mode when a data set is selected.

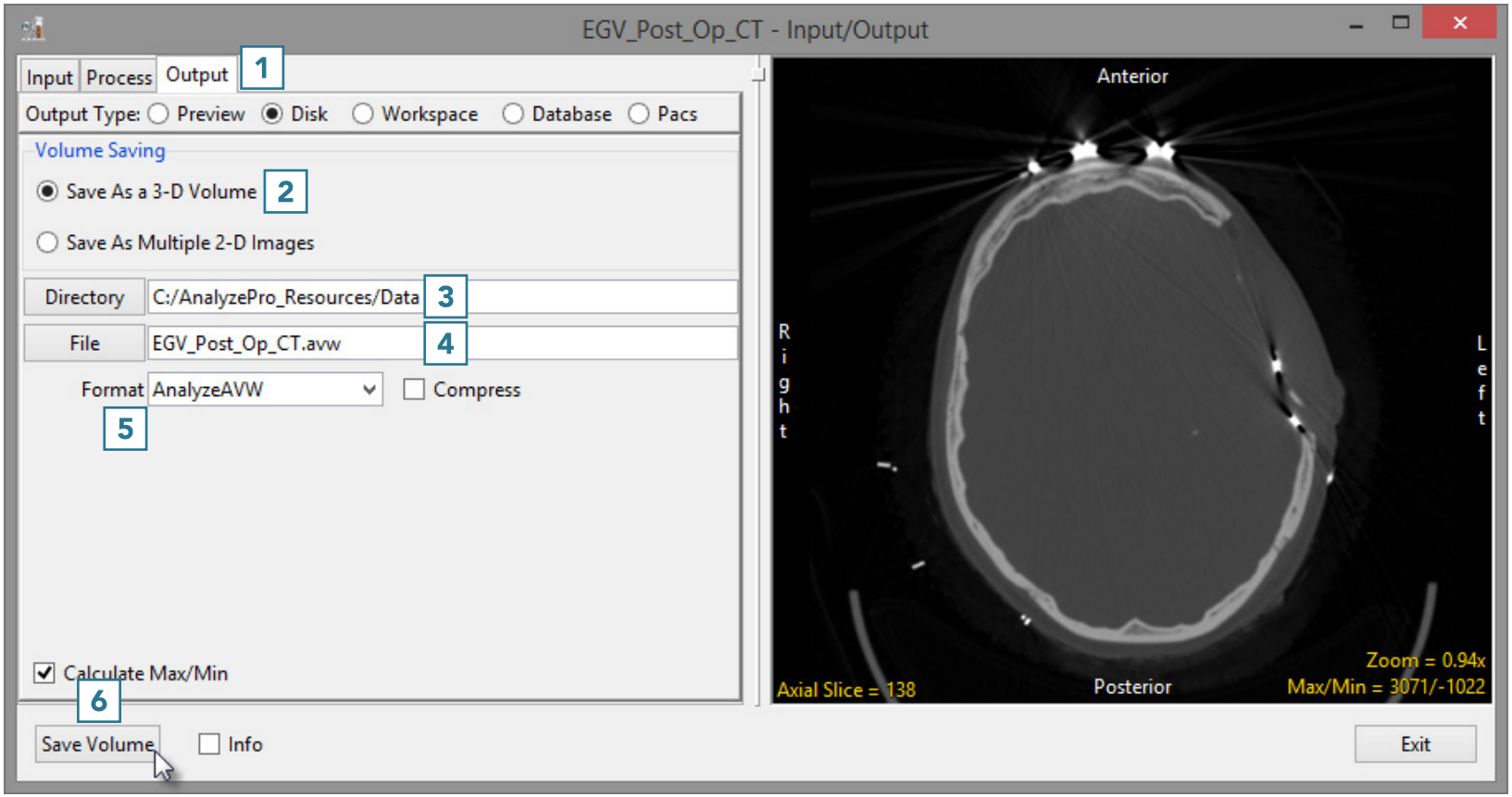



## 12. Opening Input/Output in Save Mode

- Select a data set and open Input/Output.
- A window will open, prompting you to open in Load or Save mode. Select Save mode.

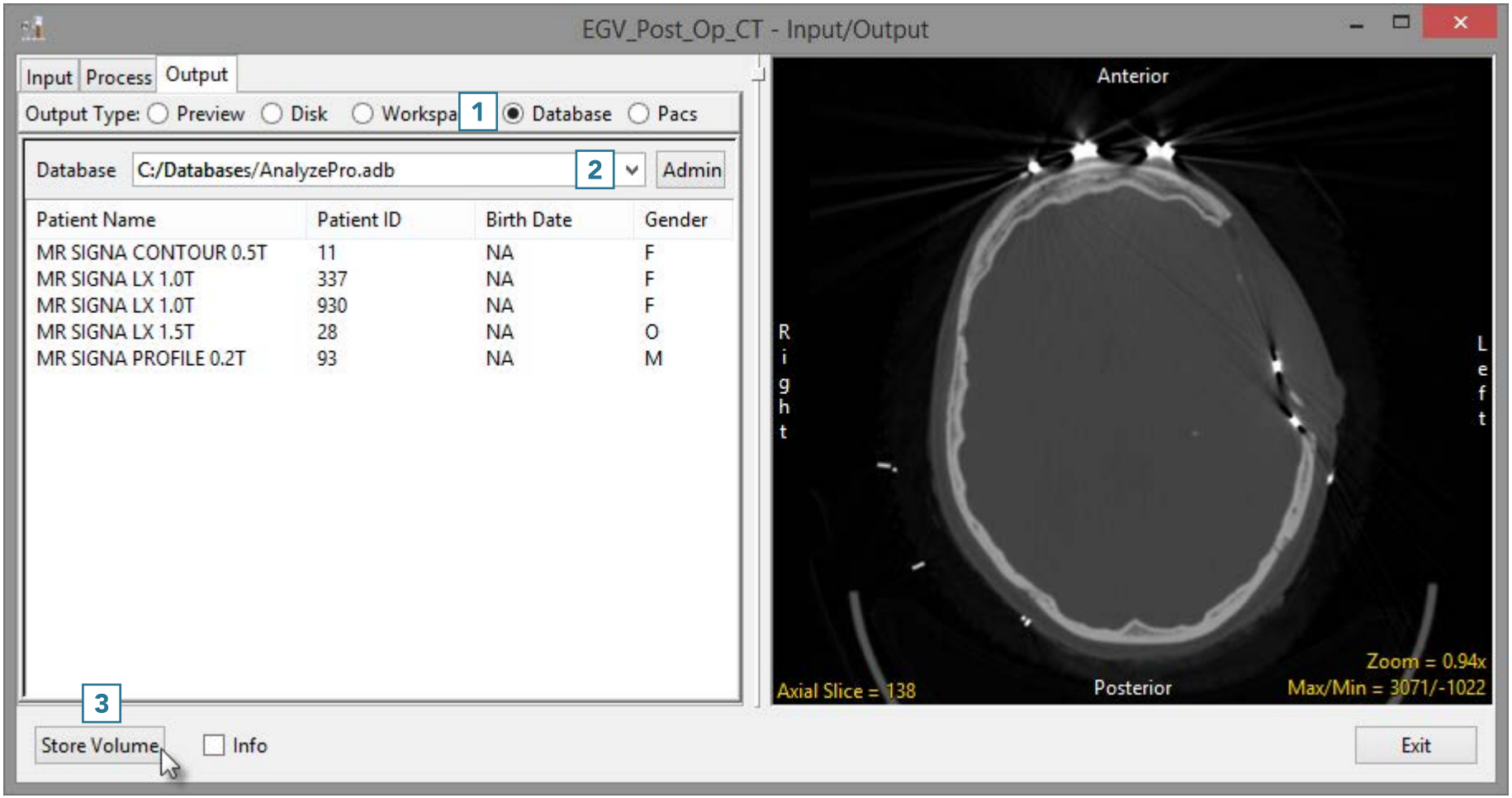
# 13. Saving a Data Set

- Input/Output will open with Output selected and the Output Type set to Disk. 1
- Choose to save the data as a 3D Volume 2 (default) or as multiple 2D images. The selection will determine the formats you can select for saving the data (see Table 3.1).
- Use Directory 3 to select the location where you will be saving the data.
- Use File 4 to rename the data.
- Use Format 5 to specify the file format for the saved data.
- Select Save Volume to save the data.

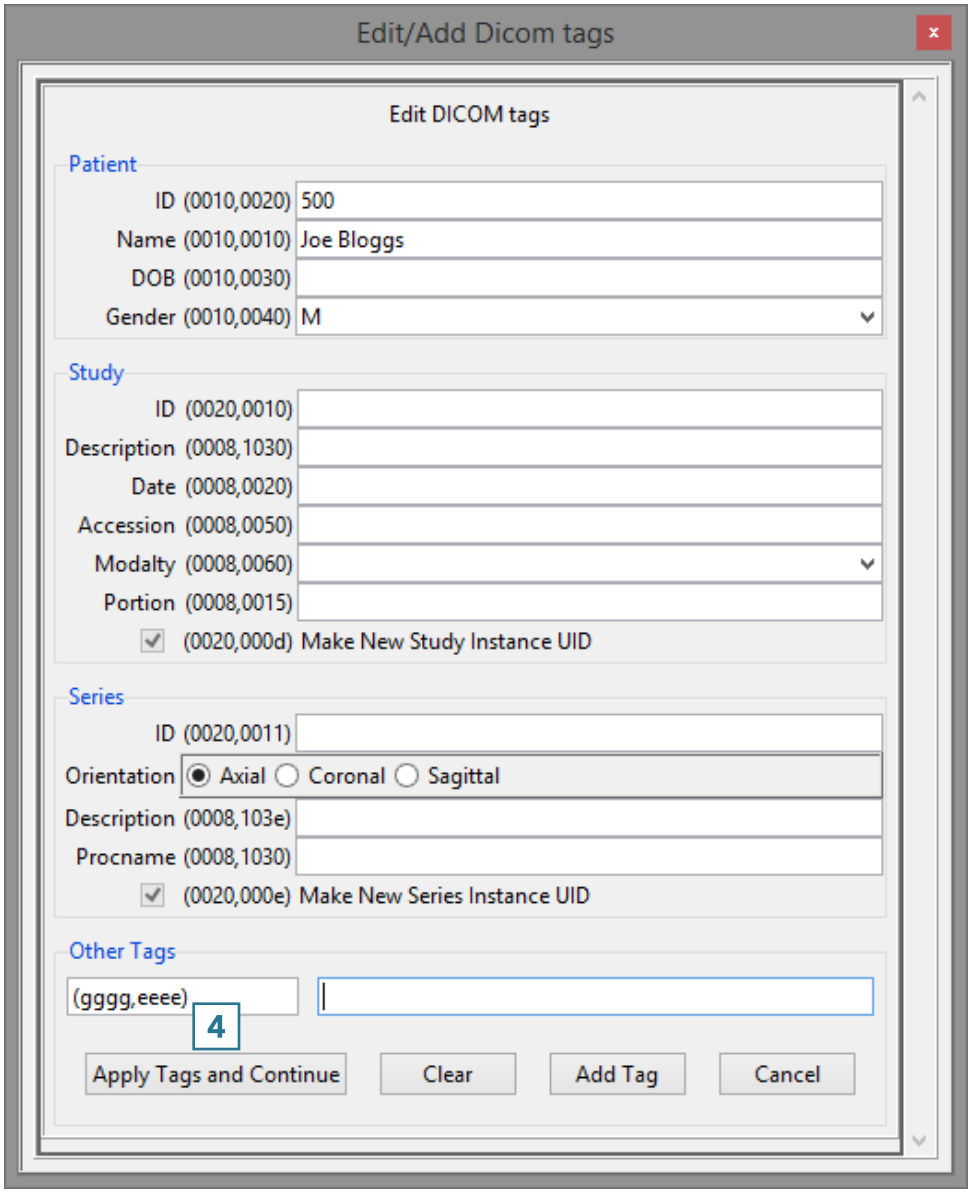


# 14. Storing Data in a Database

- Select the Database option. 1
- If required, select a database from the drop-down. 2
- Click Store Volume. 3

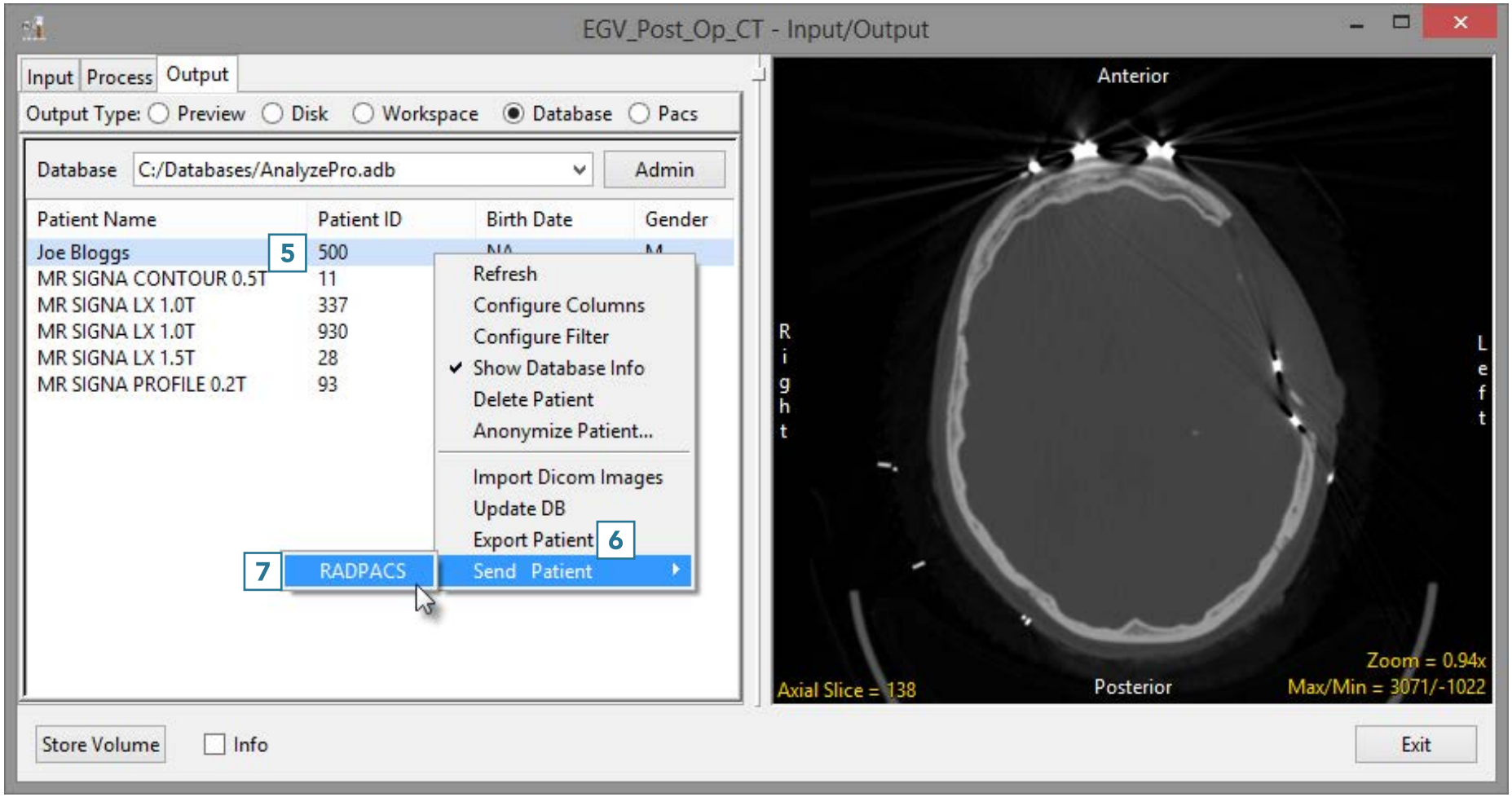


- The Edit/Add DICOM tags window will open. Use this tool to add or edit any DICOM tag information.
- Click Apply Tags and Continue. 4
- The data will be exported to and merged into the database.



# 15. Sending Data to PACS

- Right-click on the data to send to PACS. 5
- Select Send Patient 6 and choose the PACS AET where you want to send the data. 7
- To configure PACS, see Configuring PACS Communications.



# Display

# Introduction

The Display module allows image data to be reviewed interactively in 2D and 3D.

- Select the dataset from the main AnalyzePro workspace and click the Display module.

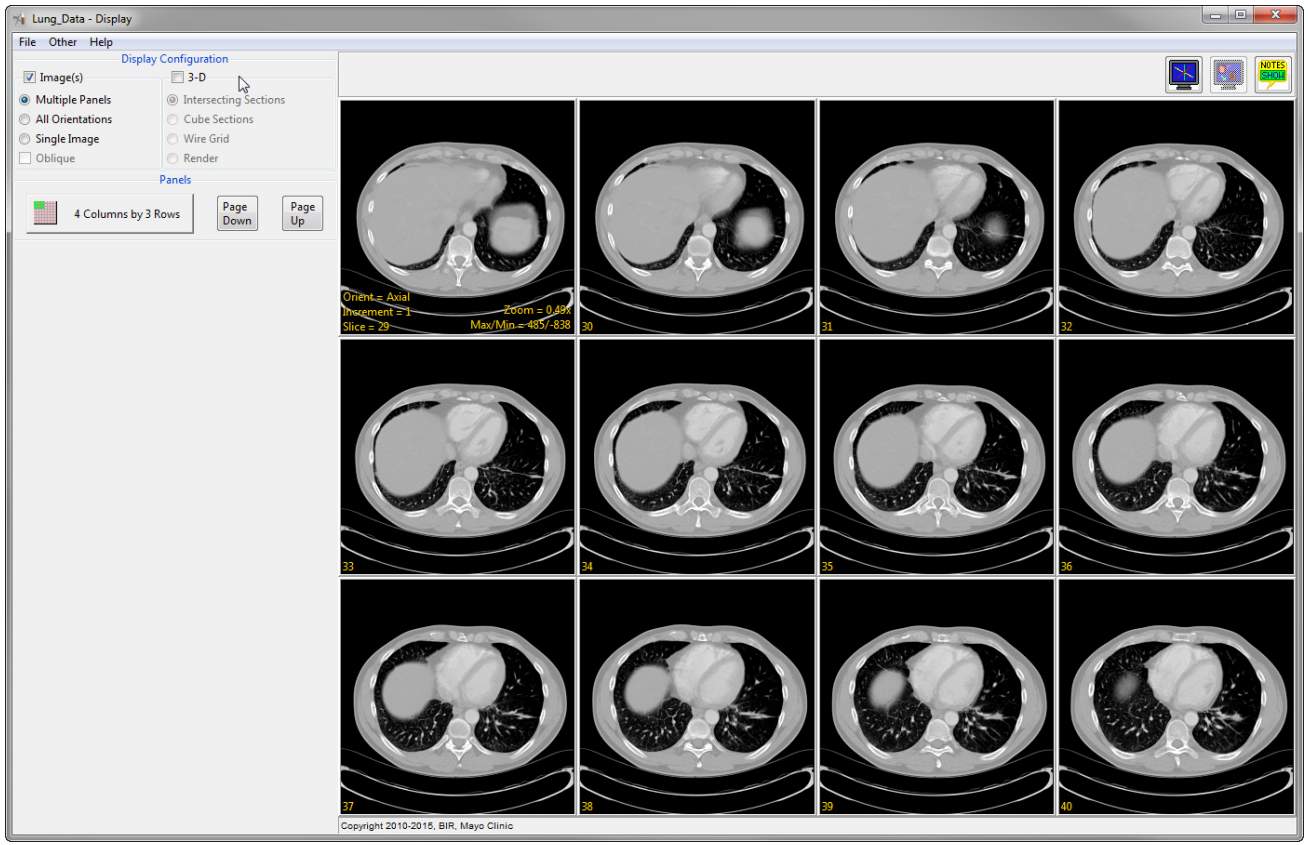
# 2D Images

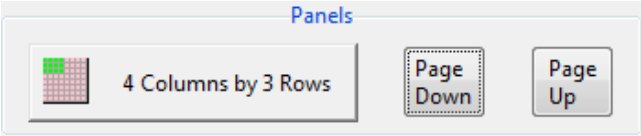
## Multiple Panels

When Display is first opened, the data set will be shown as a panel of sections from a single orthogonal orientation.

- The number of panels shown can be controlled using the Columns/ Rows button. Use the Page Up/ Page Down keys to change the slices shown.

**Download the Lung_Data data set to follow along http://analyzedirect.com/data/**

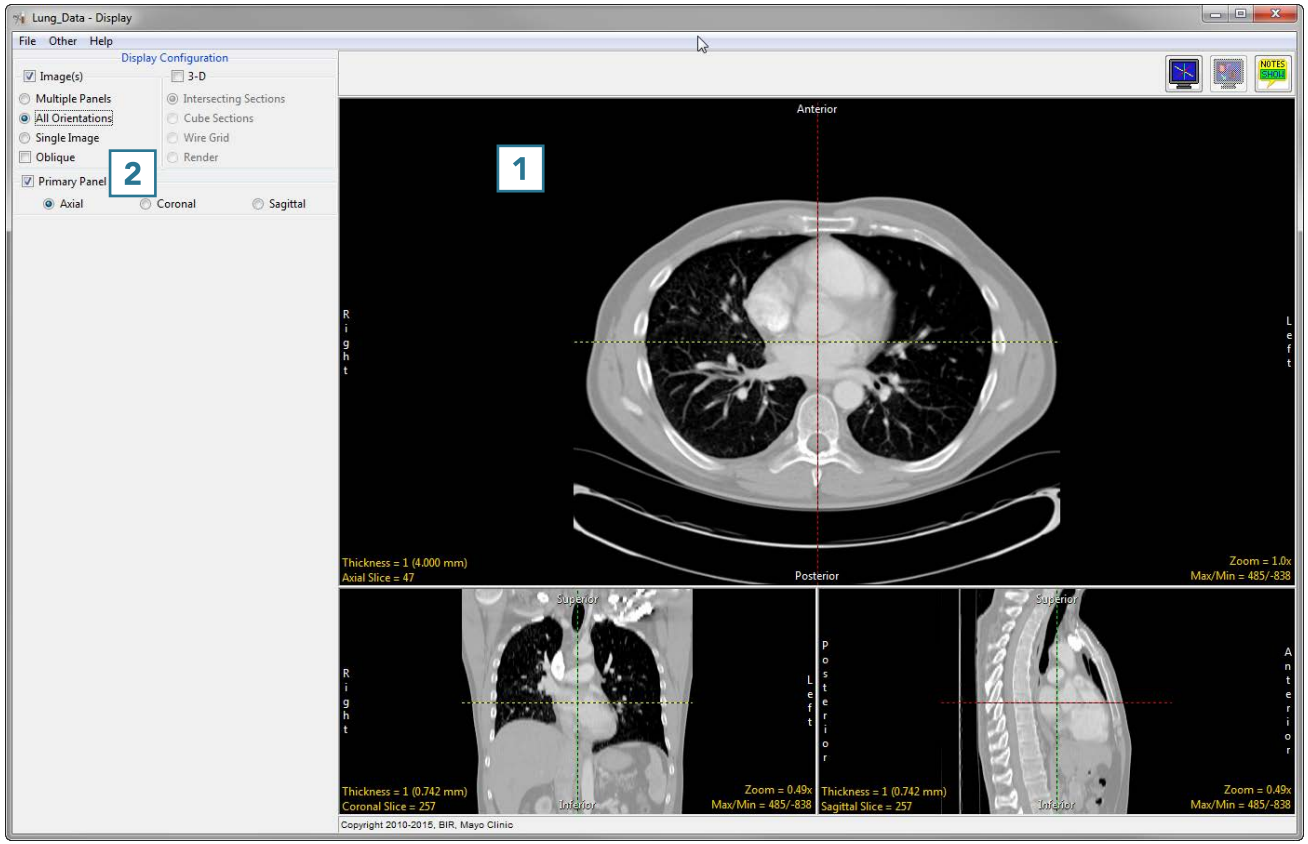



Note: AnalyzePro will remember the most recent display settings when you exit and reopen modules.

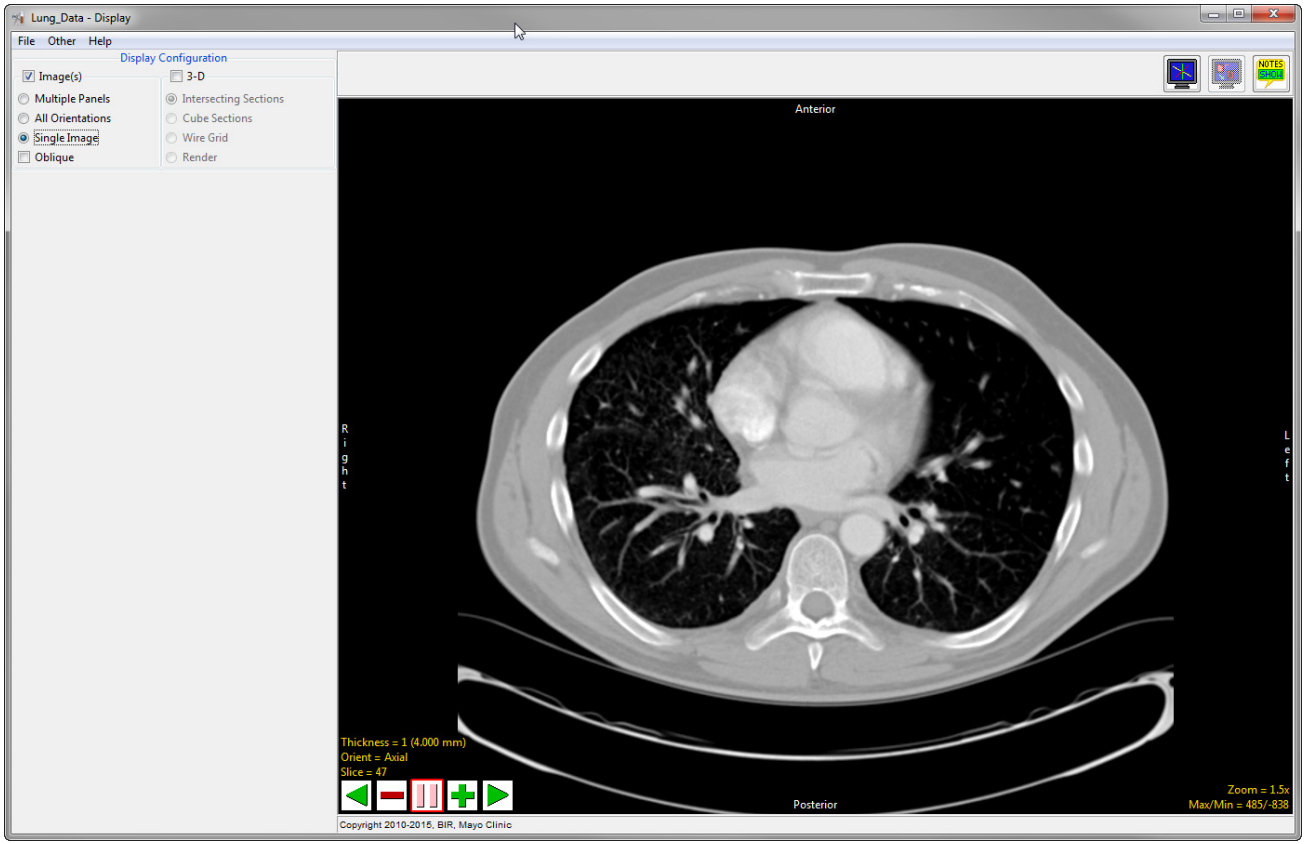
# All Orientations

Images can be shown as a 3-panel display depicting all orthogonal orientations using the All Orientations option. In this view, the larger Primary Panel 1 can be set to any of the orthogonal orientations by selecting the radio buttons under Primary Panel options 2 or by double-clicking the desired image.



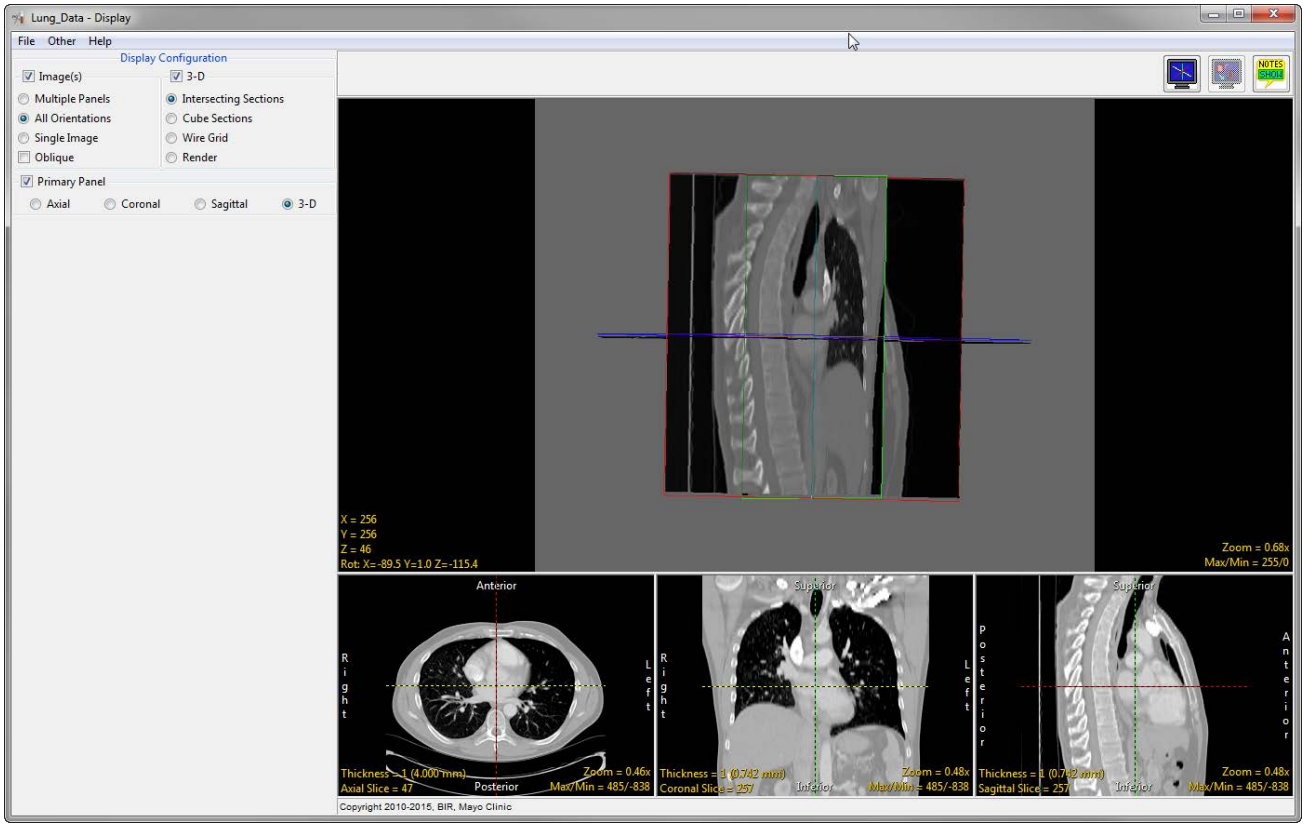
# Single Image

The Single Image option shows an image from a single orthogonal orientation, with sequential image display options shown as buttons in the lower left of the image display. Note this is the default mode if a movie file is loaded.



# 3D Images

The 3D checkbox adds a 3D display window to the current collection of displays and enables the selection of the type of 3D visualization depicted in the 3D display window.

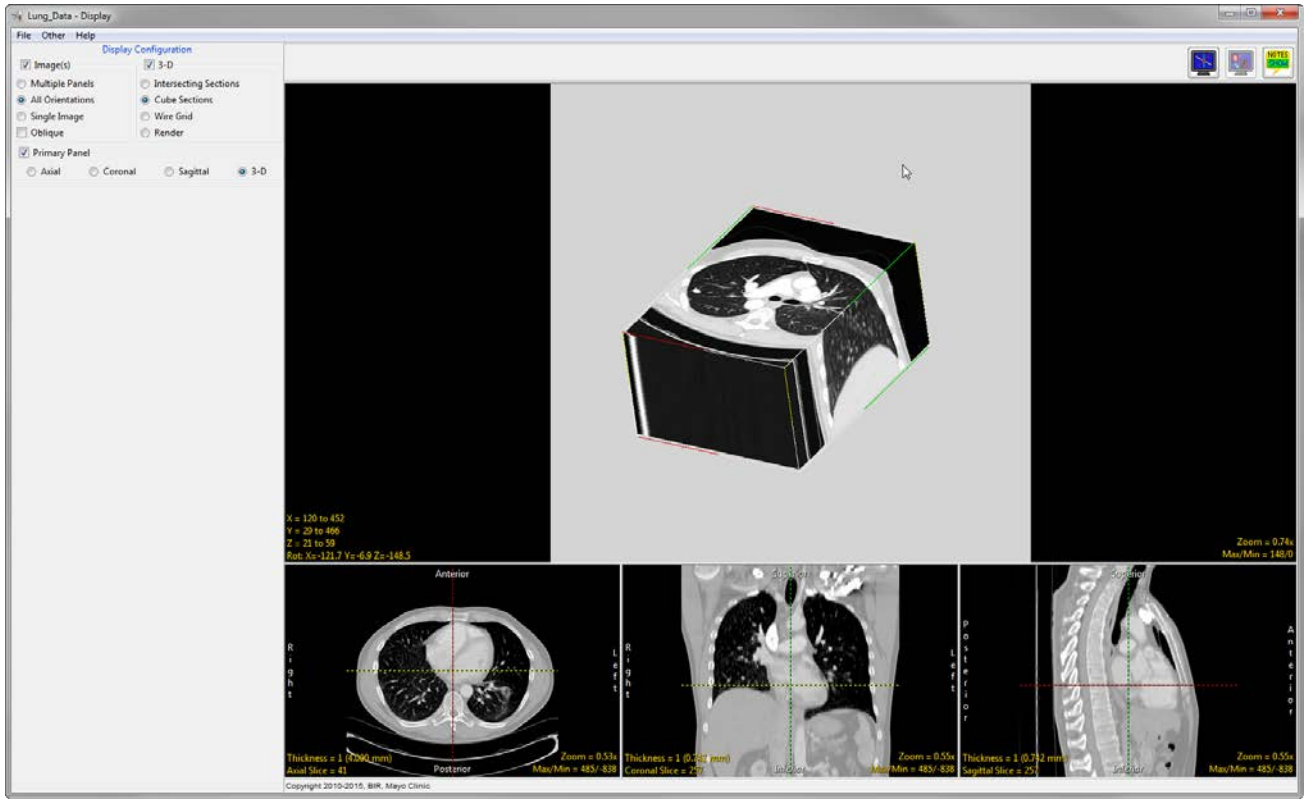



## Intersecting Sections

The Intersecting Sections option displays a 3D data set via orthogonal section displays. Intersecting Sections shows three slices that can be controlled using the X/Y/Z values in the image display or interactively selected by choosing the planes in the intersecting sections display.

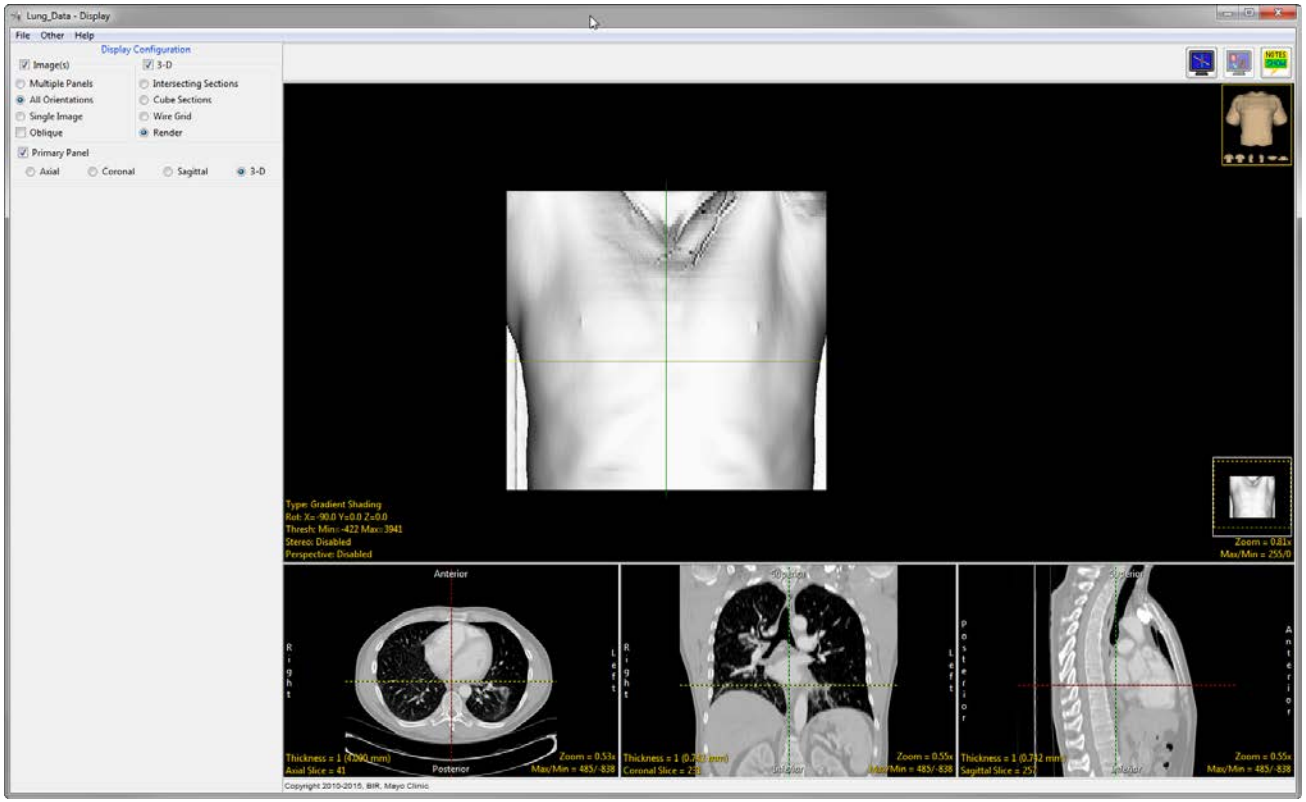
# Cube Sections

The Cube Sections option shows images on the face of a cube representing the data set, with controls to select the slices numerically in the window or by interactively grabbing an image on the cube.

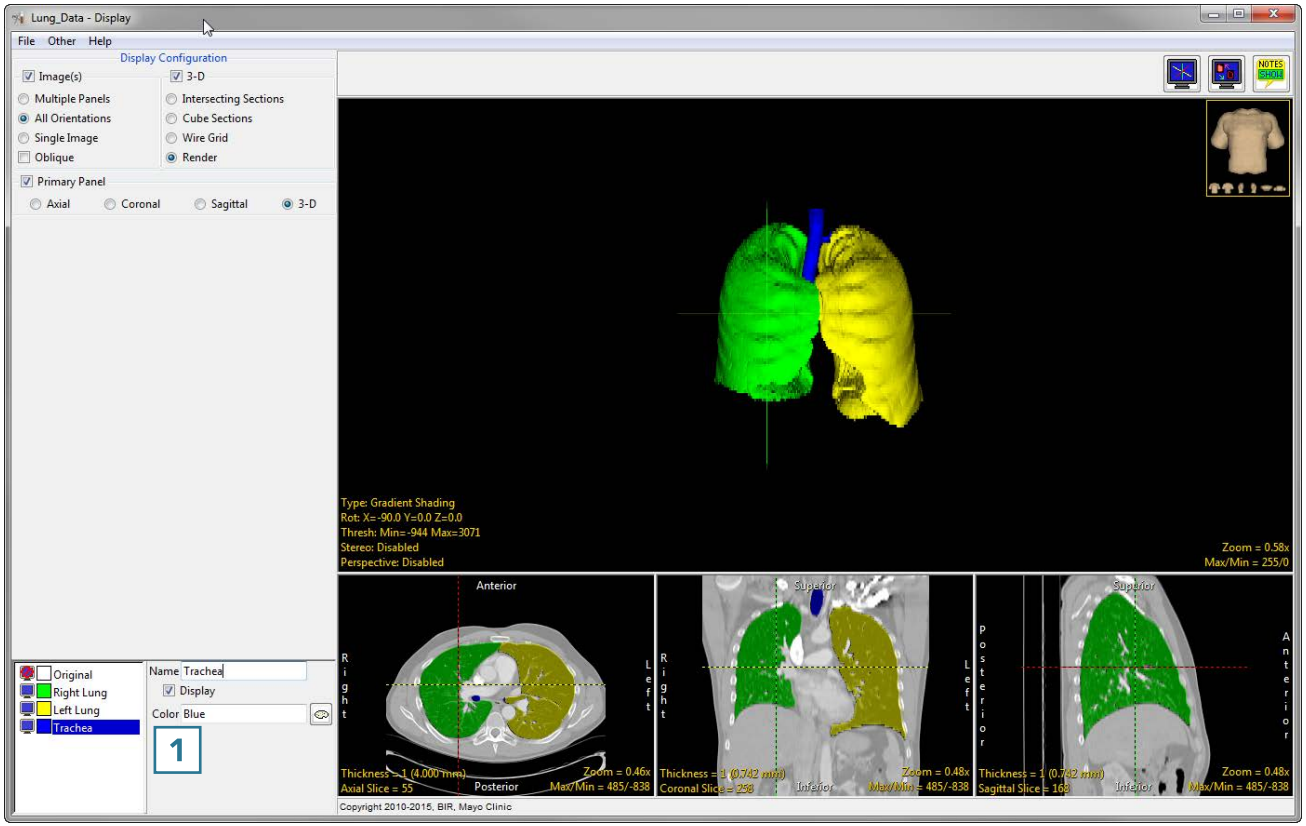


# Render

The Render option enables a 3D volume rendering in the 3D display window. By default, a voxel gradient shaded rendering is shown, with controls for threshold selection and rotation angle. Clicking and dragging the rendering with the middle mouse button controls rotation angle.

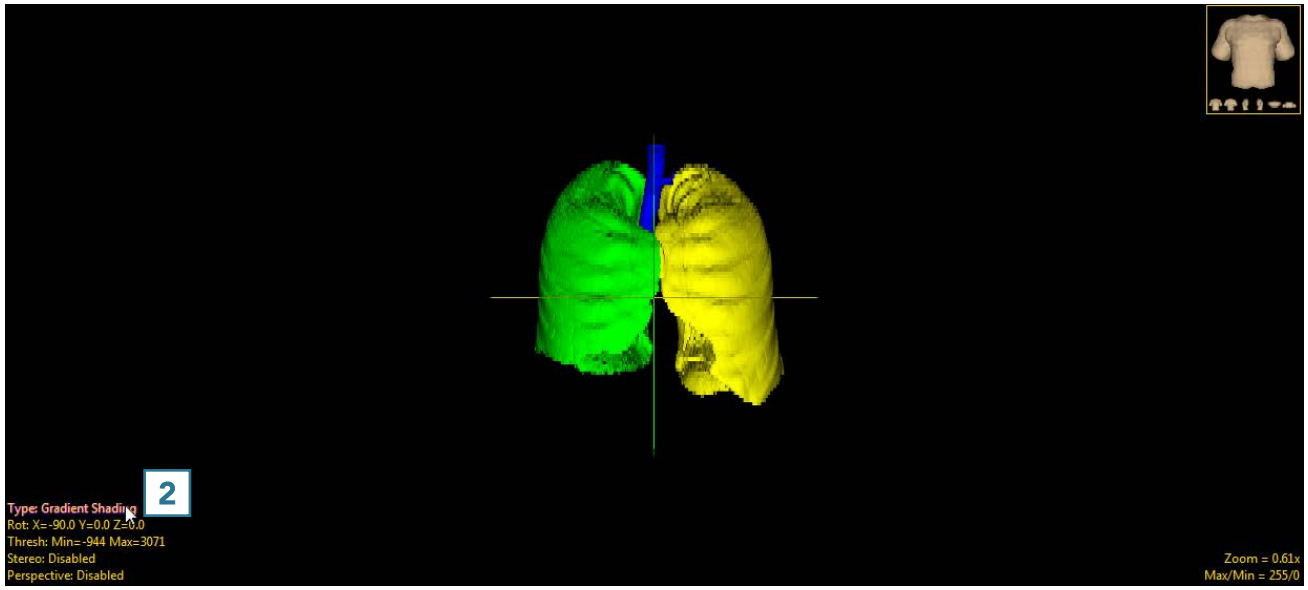


If an object map was assigned to the volume or loaded using File > Load Object Map, all images will be displayed with the associated objects. The controls 1 for the object map name, colors and visibility will be available at the bottom left of the module window.



Alternative 3D render types can be selected by clicking the Type 2 text in the bottom left corner.

For more information about Render Types, refer to Table 4.1: Display Rendering Types.



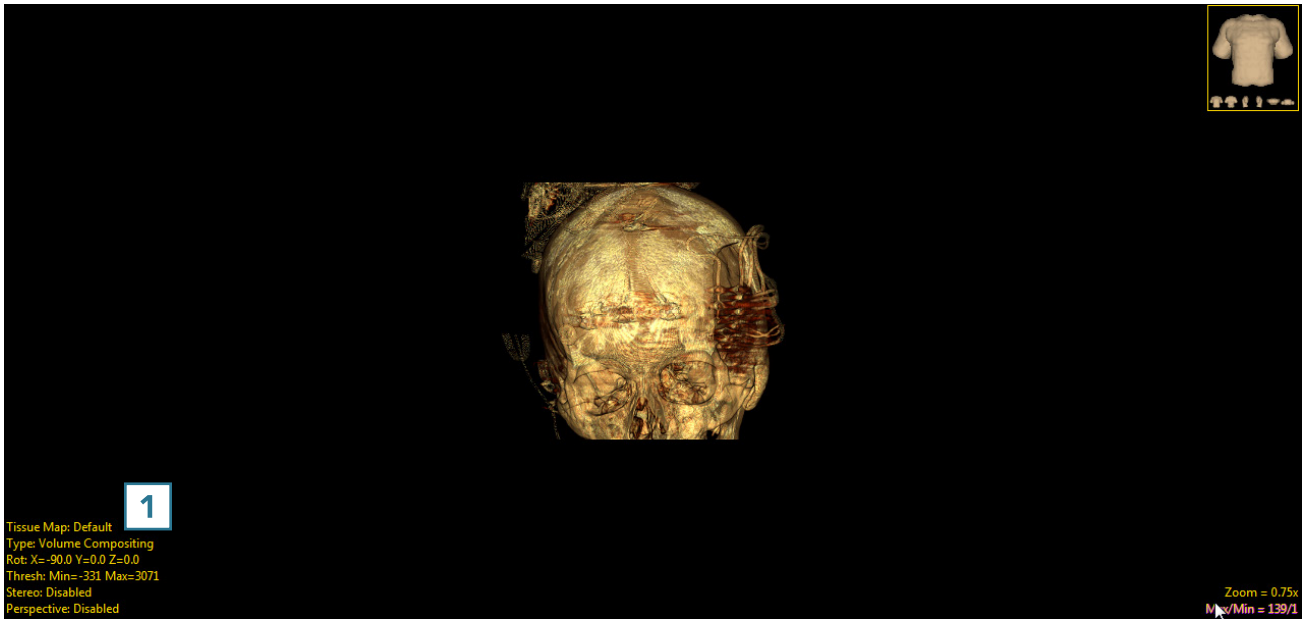
## Table 4.1: Display Rendering Types

| Render Type | Description |
|---|---|
| Depth Shading | The value of each output pixel is a function of depth only. The depth of the first renderable voxel found along the ray path is used to determine the brightness of that voxel. Closer voxels will appear brighter than more distant voxels. |
| Gradient Shading (Default) | The grayscale gradient vector is computed using a 3D neighborhood about the surface voxel. The value projected at each output location is the dot product of the gradient vector and an independently specified light source vector. This simulates the appearance of a reflective surface under uniform-field illumination. |
| Volume Compositing | Volumetric compositing integrates the gradient-shaded value of all voxels along the ray path. The contribution of each gradient-shaded voxel value is weighted by color and opacity values. The color and opacity information for each intensity is specified using the Alpha map window. |
| Maximum Intensity Projection | The maximum voxel intensity along the ray path is used. |
| Summed Voxel Projection | The average of all voxels along the ray path is used. |
| Surface Projection | The algorithm searches down the ray for a voxel that is within the current threshold range. Then, it skips the first S voxels along the ray, where S is specified by the Surface Skip value. Last, it returns the average of the next T values, where T is specified by the Surface Thickness. The surface projection rendering can be limited to enabled objects if an object map is loaded. |
| Object Compositing | Available only when an object map is loaded with the data set. Produces 24-bit color renderings where the voxel mapping along each ray path is controlled by the Composite Type yellow text. |

# 1. Tissue Maps

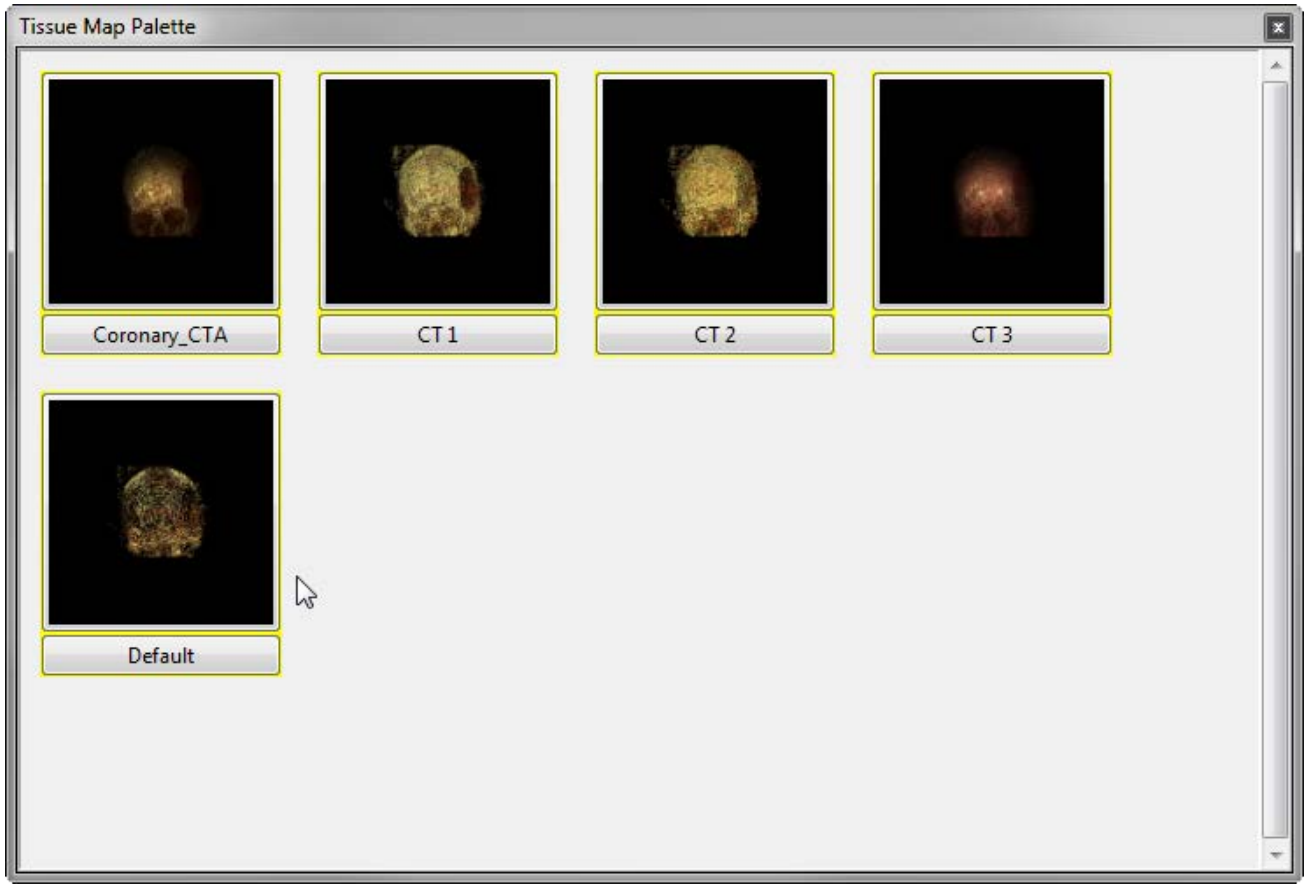
Each rendering type will have specific visual attributes and some will have additional type-specific controls. For example, the following exercise uses the Volume Compositing Render type with a tissue map.

- In the render pane, right-click the yellow Type text and select Volume Compositing.
- The render type will be changed and the data will be displayed using a default tissue map.
- Click the yellow Max/Min text and use the cursor to adjust the intensities, if necessary.
- Right-clicking on the yellow Tissue Map text 1 will provide a menu that contains several options.



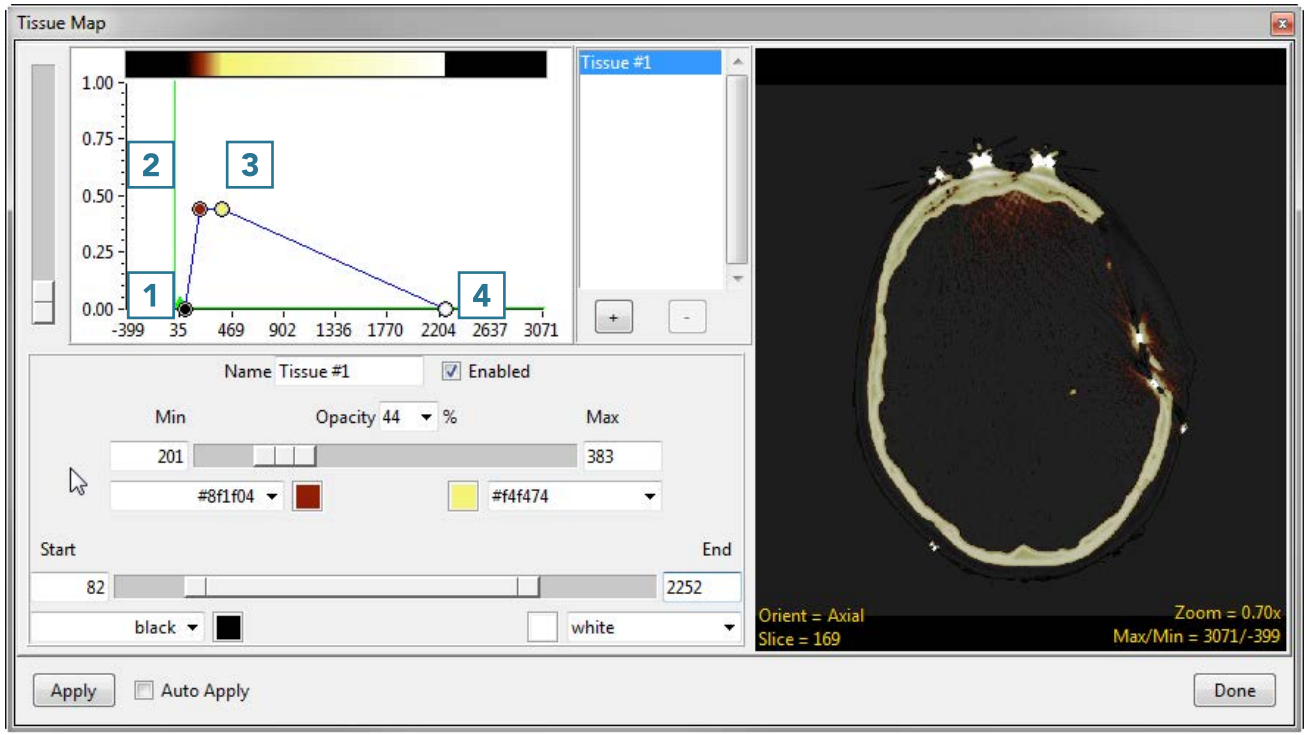
# Select Palette

A number of existing tissue maps can be quickly selected using System Tissue Maps. Alternatively, selecting Palette will return a window with thumbnail previews of each tissue.

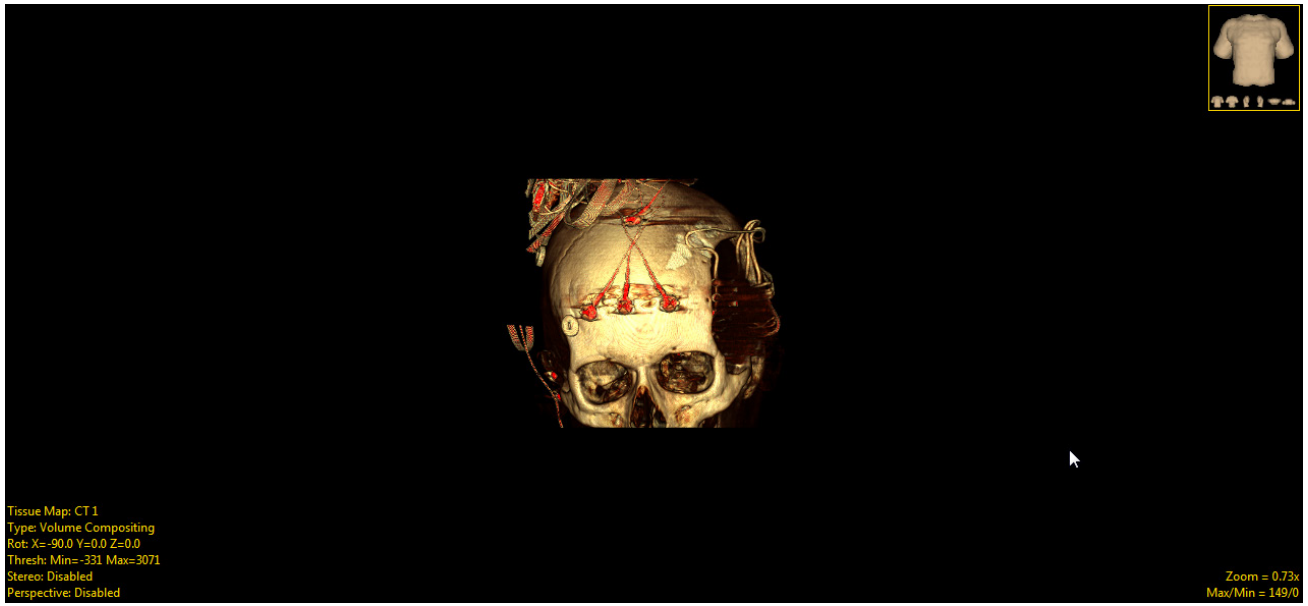


Customized tissue maps can be generated using the Edit option within the options panel. A Tissue Map tool will open that provides four control points to manipulate which voxel values are mapped to specific colors and to adjust opacity.

- Start: 1 The starting voxel value within the volume mapped to a specific color (chosen from the color drop-down menu).
- Min: 2 The minimum voxel value within the volume that will be mapped to a specific color.
- Max: 3 The maximum voxel value within the volume that will be mapped to a specific color.
- End: 4 The ending voxel value within the volume mapped to a specific color.



Additional tissues can be added by clicking the + button. Once you are satisfied with the tissue map, click Apply. The tissue map can be saved by right-clicking within the point graph and then selecting Save Tissue Map.



# Process

# Introduction

There are three main process functions available: Spatial Filters, Morphology and Histogram. These functions are used to prepare data for further segmentation and analysis.

# Spatial Filters

There are 19 different spatial filters that can be applied to a data set. These are described in the table below. A filter can be applied to the entire volume or to selected objects if an object map is loaded.

| Filter Type | Description | Method |
|---|---|---|
| Low Pass | dampens noise, smoothes volume | replaces the value of each voxel with the average value of the neighborhood* |
| Unsharp | eliminates homogeneous regions, highlights edges and noise | subtracts a low pass filtered volume from the original volume |
| Unsharp Enhance | combines unsharp with original volume | adds an unsharp filtered volume to the original volume |
| Sobel | highlights edges | performs a classic edge detection filter |
| Sobel Enhance | combines Sobel with original volume | adds a Sobel filtered volume to the original volume |
| Median | dampens noise, smoothes volume | replaces the value of each voxel with the average value of the neighborhood* |
| Rank | generic rank filter | orders all the values of voxels in the neighborhood* and returns the value corresponding to the rank in the ordered list† |
| Sigma | smoothes noise while preserving edges and thin lines | replaces the value x of each voxel with the average value of voxels in the neighborhood* having values of $x \pm 2\sigma$ ‡ |
| VSF Mean | smoothes noise while preserving edges and thin lines | replaces the value x of each voxel with the average value of voxels in the neighborhood§ having values of $x \pm \sigma$ |
| Gradient | highlights edges | replaces the value of each voxel with the maximum absolute difference between its value and that of its orthogonal neighbors |

| Filter Type | Description | Method |
|---|---|---|
| AHE | enhances contrast for viewing (not for measurement) | adjusts voxel values based on histogram of a localized region¶ |
| Anisotropic | reduces noise while preserving edges | performs 2D affine, unbiased or biased anisotropic diffusion for the number of iterations and time per iterationll specified |
| Convolution | smoothes noise, resulting in a blurry image | performs spatial convolution of volume with user-supplied point spread function |
| Inhomogeneity Correction | corrects low-frequency grayscale gradients | replaces voxel intensity with $I_i$ * global mean / local mean, where $I_i$ is the input voxel intensity |
| Sticks | suppresses noise while enhancing thin edges | applies directional masks and determines output based on Type parameter |
| Chamfer Distance Map | creates a map that may be used for shape recognition | calculates Chamfer distance of each voxel to nearest nonzero voxel |
| Euclidean Distance Transform | creates a map that may be used for shape recognition | calculates Euclidean distance of each voxel to nearest nonzero voxel |
| Adaptive Restoration | reduces noise using an adaptive method | degrades image by constant-power additive noise, then applies a low pass filter |
| Curvature | creates a map of instantaneous local surface curvature | sums binary voxel values in the 26-connected neighborhood of each voxel to give a curvature value from 0-26 |

*The neighborhood around each voxel is defined by the kernel dimensions selected in the Kernel Size options.

†The kernel size determines the number of voxels whose values are ranked, e.g. a 3 X 3 X 3 kernel has 27 voxels, a 5 X 5 X 5 kernel has 125 voxels and a 7 X 7 X 7 kernel has 343 voxels. The larger the kernel size, the more computationally intensive this filter becomes. It is recommended to use a smaller kernel size such as 3 X 3 X 3. In a 3 X 3 X 3 kernel, a rank of 1 would return the minimum value, a rank of 14 would return the median value and a rank of 27 would return the maximum value.

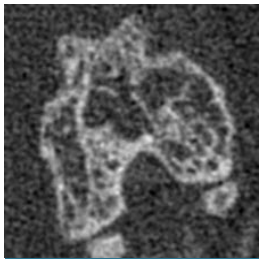
‡If fewer than 9% of the voxels in the kernel fall within the $x \pm 2\sigma$ range, the voxel in question will not be changed. Sigma ($\sigma$) is defined using the text box or slider bar.

§The circular neighborhood around each voxel is specified by the Ring parameter.

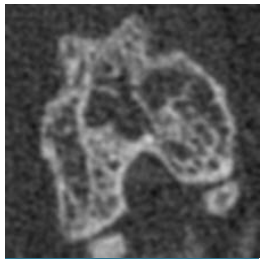
¶Clip Fraction — Specifies the limit of contribution of any given grayscale value, reducing the enhancement of noise in the resulting image or volume. This method is particularly effective for images which have subtle detail in both very bright and very dim regions of the image. It may also be used to expand the dynamic range of grayscale in a region which has subtle but significant changes.

||A value of 0.25 is recommended for general use and will be used as the default if the supplied value is zero or negative. However, a value of 0.10 or less is required to guarantee stable behavior. The lower value will require more iterations but should be used if absolutely correct results are essential. This option is only available when Type is set to Affine.

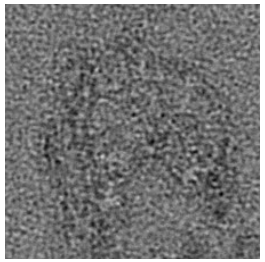
No Filter



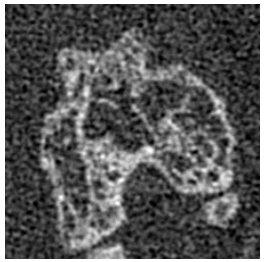
Low Pass



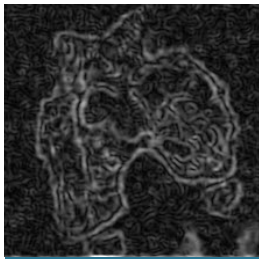
Unsharp



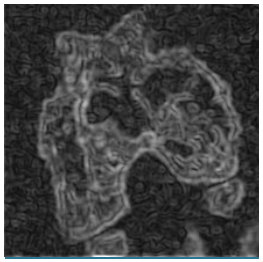
Unsharp Enhance



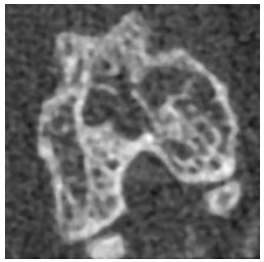
Sobel



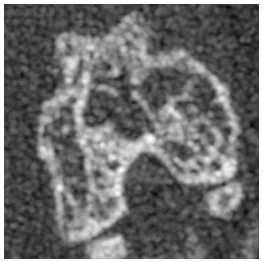
Sobel Enhance



Median

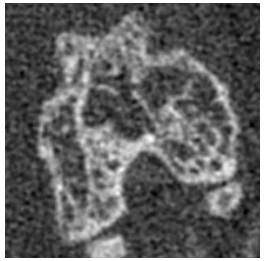


Rank

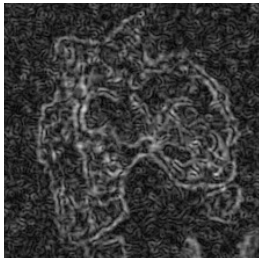


Sigma

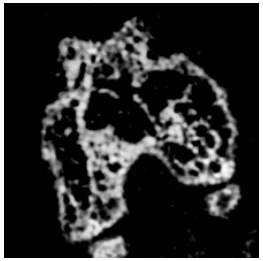
VSF Mean



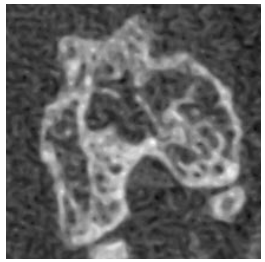
Gradient



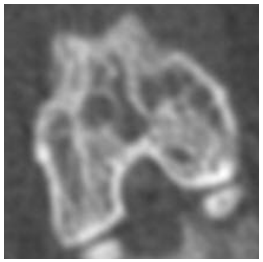
AHE



Anisotropic

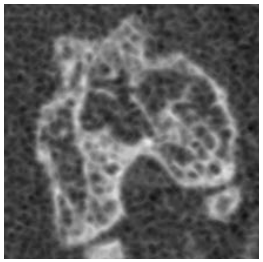


Convolution

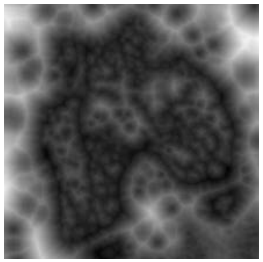


Inhomogeneity Correction

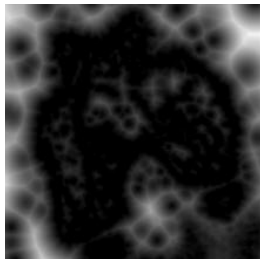
Sticks



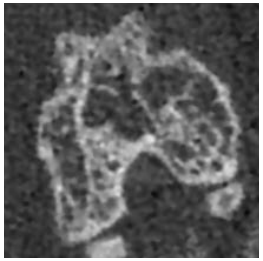
Chamfer Distance Map



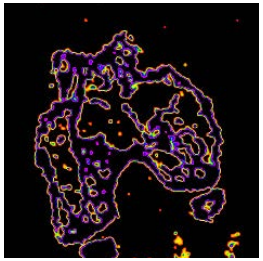
Euclidean Distance Map



Adaptive Restoration



Curvature



# 1. Applying a Filter to a Data Set

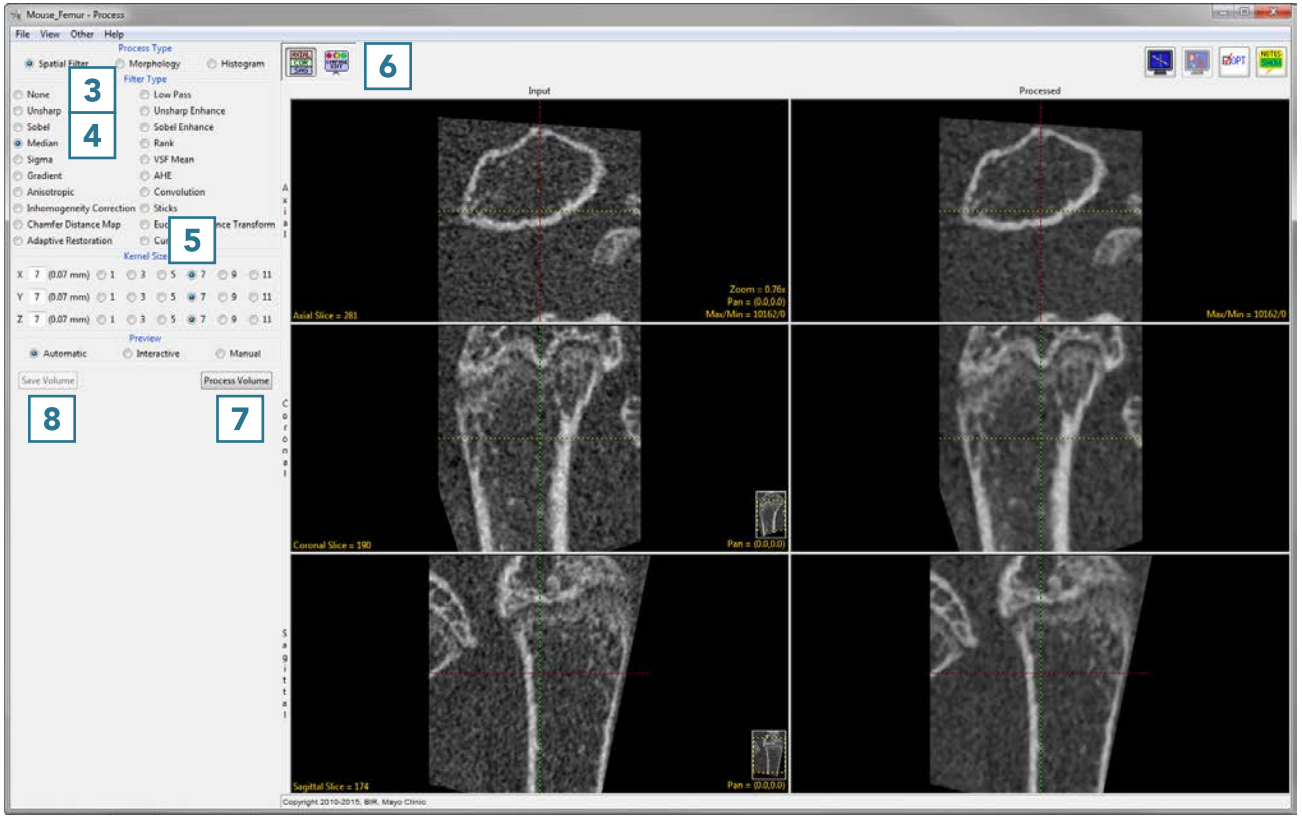
This exercise will show how to apply a median filter to a microCT bone data set.

- Select the data set in the AnalyzePro workspace 1 and open Process. 2

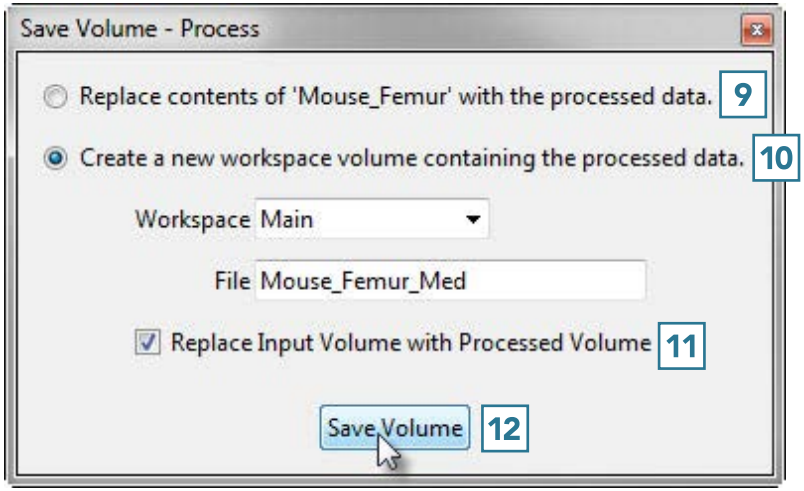
Download the Mouse_Femur data set to follow along http://analyzedirect.com/data/

- Choose Spatial Filter as the Process Type. 3
- Choose a Filter Type. 4 Low Pass and Median filters are commonly used to smooth noisy data.
- Set the Kernel Size in the X, Y and Z dimensions. 5 A kernel size of 7 X 7 X 7 is often used for microCT data acquired using a PerkinElmer scanner.
- To toggle the Compare view, use the Compare Diff button. 6


- Click Process Volume. 7
- Once the processing is complete, the Save Volume button will become available. Click Save Volume. 8



- In the Save Volume window, choose to replace the input data set with the processed data set 9 or to create a new data set. 10
- The new data set can be saved in any workspace in the current project and renamed in the File checkbox. Check the Replace Input Volume with Processed Volume box if you want to further process the processed volume. 11
- Click Save Volume. 12



# Morphology

A number of morphologic operations are available, as described in the table below. These operations can be performed on the entire volume or on selected objects if an object map is loaded.

| Morphologic Operation | Description | Method |
|---|---|---|
| Threshold | isolates structures defined by a difference in intensity | sets voxels between and equal to the specified maximum and minimum to 1 and all other voxels to 0 |
| Erode | peels a layer from the outer edge of large objects and deletes small objects | retains voxels in inner areas of the object, as determined by the structuring element dimensions and shape |
| Dilate | expands small objects in a binary volume | adds voxels to outer areas of the object, as determined by the structuring element dimensions and shape |
| Open | removes small objects and breaks isthmuses | erosion followed by dilation |
| Close | fills thin gulfs and small holes | dilation followed by erosion |
| Maximum | emphasizes high-intensity regions | grayscale equivalent of binary dilation |
| Minimum | emphasizes low-intensity regions | grayscale equivalent of binary erosion |
| Ultimate Erosion | shows the last voxels remaining of disconnected components | performs successive erosions on the object until the last erosion before the components would disappear |
| Thinning | thins an object in binary or grayscale | thins the object based on the number of iterations specified, using template matching |

| Morphologic Operation | Description | Method |
|---|---|---|
| Homotopic Thickening | thickens an object in binary or grayscale | thickens the object based on the number of iterations specified |
| Fill Holes | fills holes in a volume | fills holes in 2D or 3D, based on the connectivity value chosen |
| Connected Components | finds connected regions in a volume | performs a 2D or 3D connected component analysis |
| Complement | generates inverse of an image | generates the binary or grayscale complement of the image |
| Umbra | darkens the image | decreases the intensity value of all voxels by the specified intensity cutoff value |
| Nonmax Suppression | shows voxels of highest intensity | sets voxels which are not at a local maximum to zero |
| Watershed | performs classic watershed operation | thresholds a binary volume, performs repeated erosions, sets voxels to erosion level and connects components |

# Histogram

The available histogram operations are Flatten, Preserve, Normalize and Match. These operations can be performed on the entire volume or on selected objects if an object map is loaded.

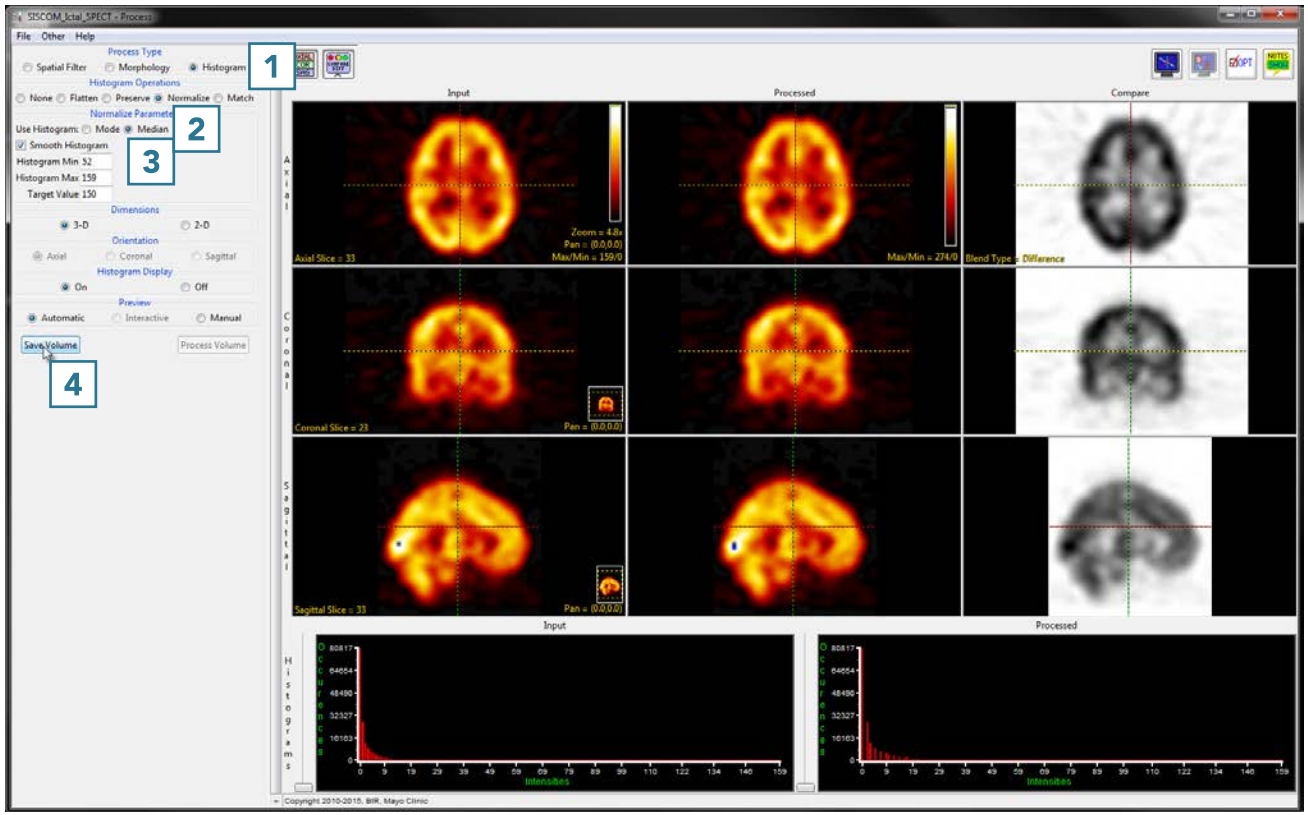
| Histogram Operation | Description | Method |
|---|---|---|
| Flatten | maximizes contrast | evenly distributes voxels across the specified intensity output range |
| Preserve | brightens image while preserving contrast | maps the input intensity range onto a narrower output range in a statistically optimal manner |
| Normalize | allows comparison of data sets | forces the mean or mode of the histogram to specified values |
| Match | allows comparison of data sets | matches the intensity distribution to a loaded histogram file or the histogram of another volume |

# 2. Histogram Normalization

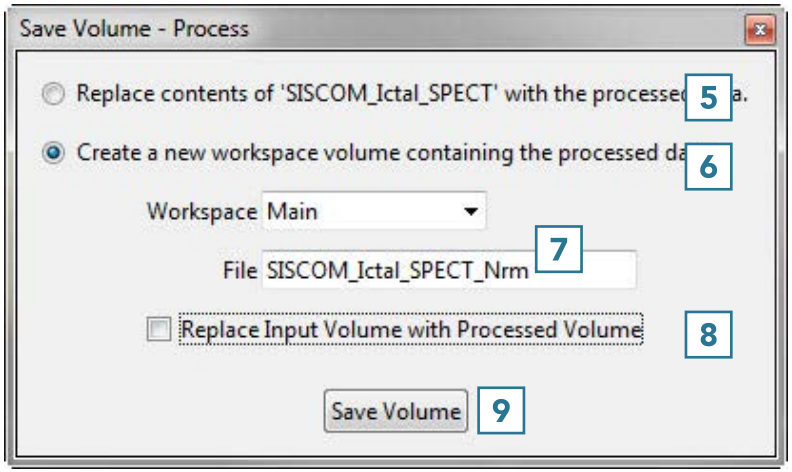
This exercise will show how to normalize the histogram of two functional data sets to the same median value so that they can be compared to each other.

- Select the first data set in the main workspace and open Process.
- Set the process type to Histogram 1 and choose Normalize 2 as the histogram operation.
- Set the parameters to use the histogram median and a target value of 150. 3
- Setting the target value of each data set to the same value will allow comparison between the two.
- Click Save Volume. 4

**Download the SISCOM_Ictal_SPECT and SISCOM_Interictal_SPECT data sets to follow along http://analyzedirect.com/data/**



- In the Save Volume window, choose to replace the input volume with the process volume 5 or create a new workspace volume. 6
- Name the file, if creating a new workspace volume. 7
- If you want to process the volume further, choose to replace the input volume with the process volume. 8
- Click Save Volume to apply the changes. 9




Repeat these steps with the other data set. Once both data sets are normalized to the same median value, they can be subtracted to create a difference map or otherwise quantitatively compared.

# Transform

# Introduction

There are several types of transformations that can be applied to data: spatial transformationss such as cropping, resizing or flipping; intensity transformations such as thresholding, intensity scaling and inversion; custom transformations using mathematical operators with image calculator/image algebra and image repair.

# Spatial Transforms

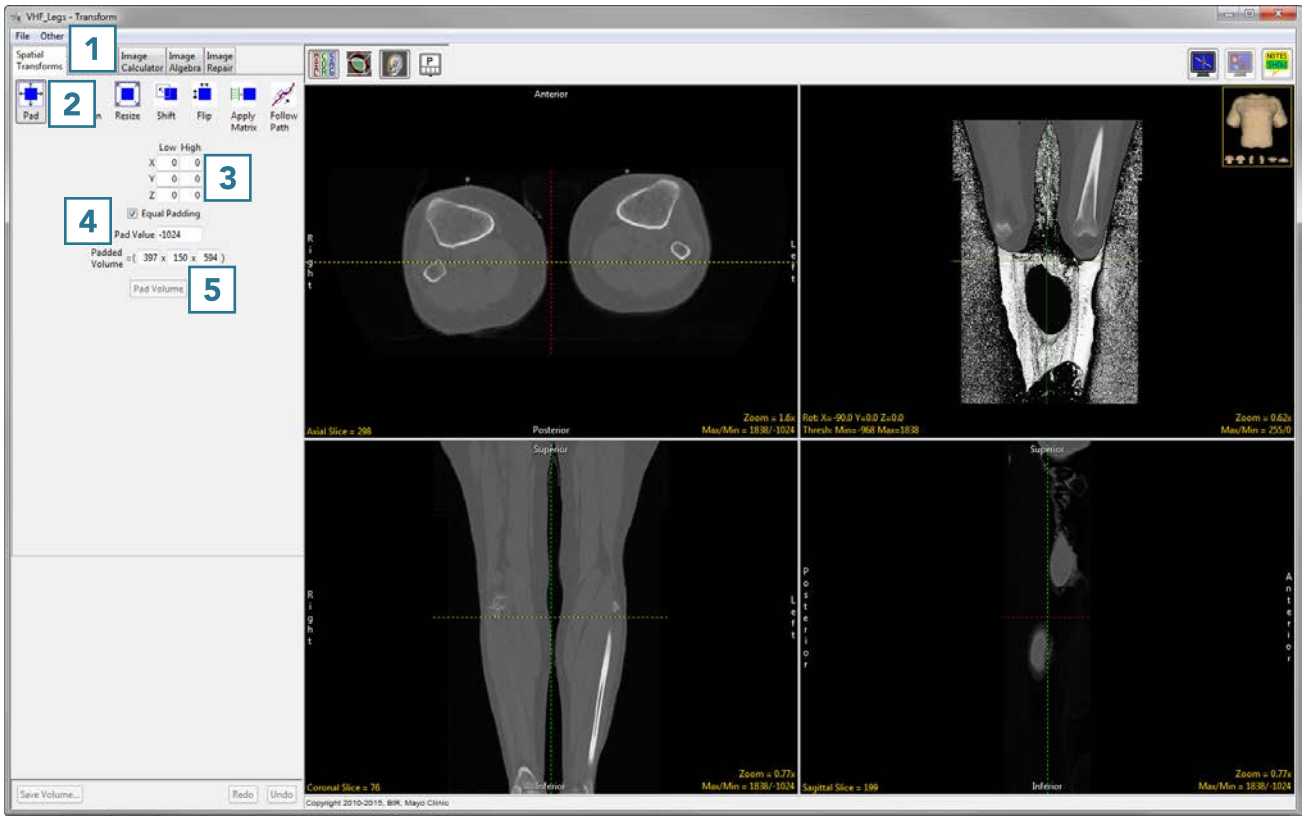
Many of the functions available in this section are also available in Input/Output under the Process tab.

## Pad

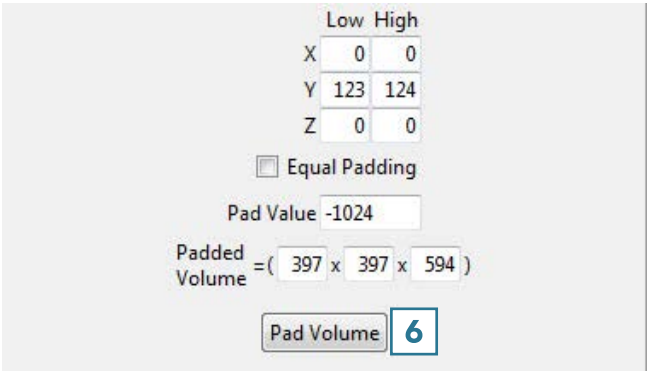
The Pad tool can be used to add blank slices around the original data set. This may be necessary to create a data set with certain dimensions or with the same number of slices in each dimension.

- Select the data set to crop and open Transform. Navigate to Spatial Transforms 1 and select the Pad tool. 2
- To add a given number of slices to the low or high end of the data set in any dimension, type the number of slices to be added in the appropriate boxes 3 and the padded volume dimensions will be updated.
- To change the intensity value of the added slices, change the Pad Value. 4
- To set the padded volume dimensions, change the numbers in the appropriate boxes 5 and the low and high number of slices in each dimension will update automatically.

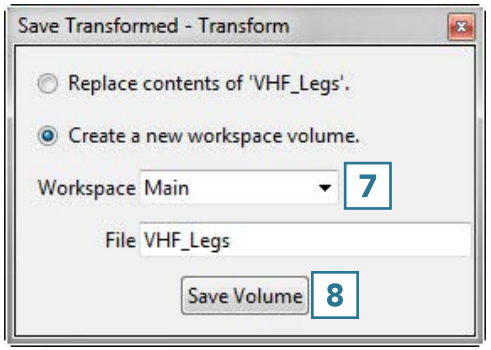
**Download the VHF_Legs data set to follow along http://analyzedirect.com/data/**



- Once the dimensions have been changed from the original dimensions, the Pad Volume button will update.
- Click Pad Volume to apply the changes. 6



- Click the Save Volume button to save the padded volume to the workspace. To retain the original volume, choose to create a new workspace volume 7 and click Save Volume. 8
- Close Transform.

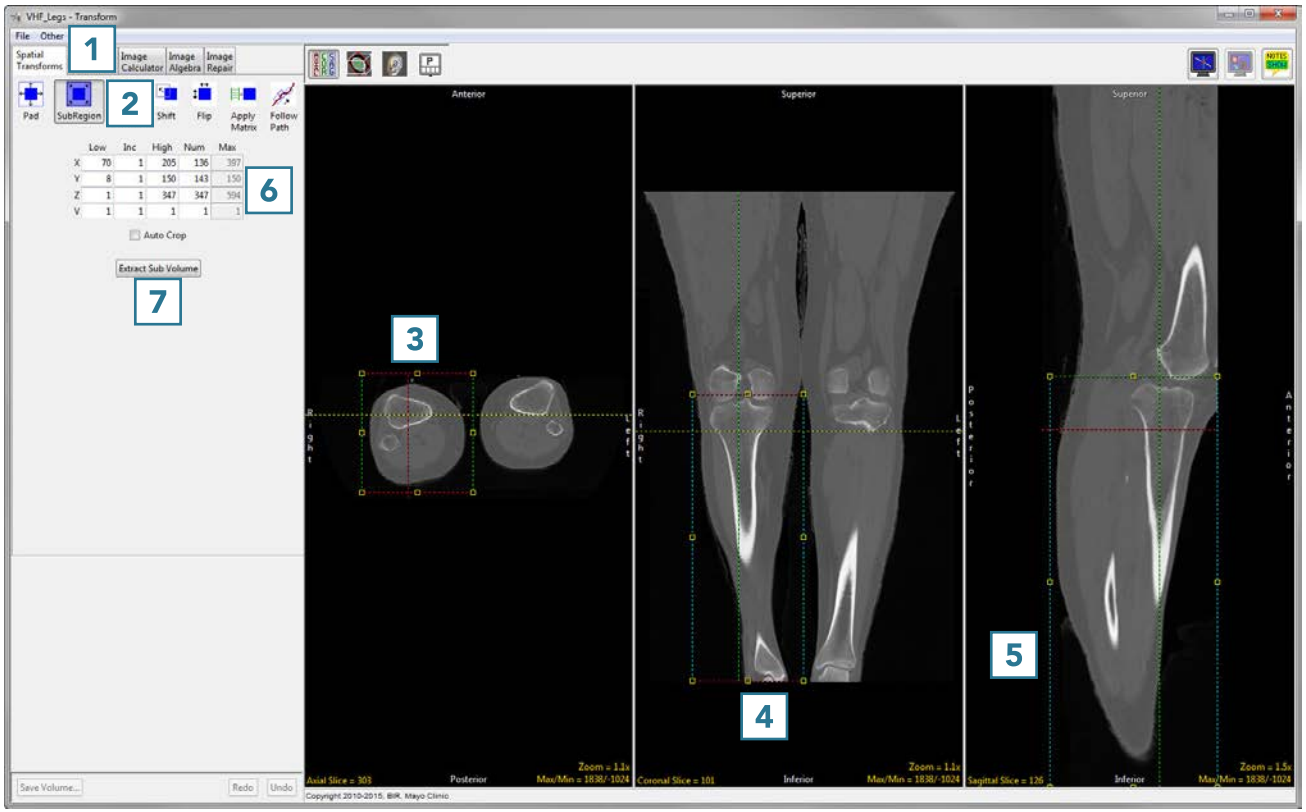


# Subregion

The Subregion tool can be used to reduce the size of a data set without interpolating within the original data, or to crop to a specific region of interest.

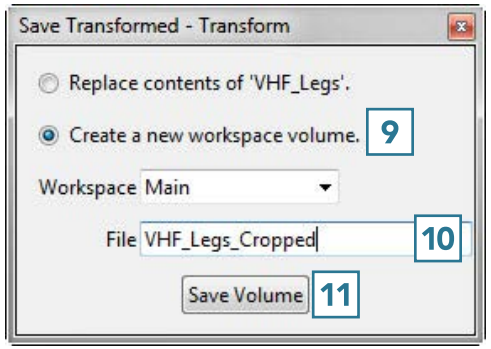
- Select the data set to crop and open Transform. Navigate to Spatial Transforms 1 and select the Subregion tool. 2
- Use the control points to set the cropped region in the axial, 3 coronal 4 and sagittal 5 orientations. Scroll through the slices to ensure the region is correct throughout the data set.
- To set the cropped region to specific slice numbers, use the input boxes. 6
- Click Extract Sub Volume to perform the crop. 7

Download the VHF_Legs data set to follow along
http://analyzedirect.com/data/



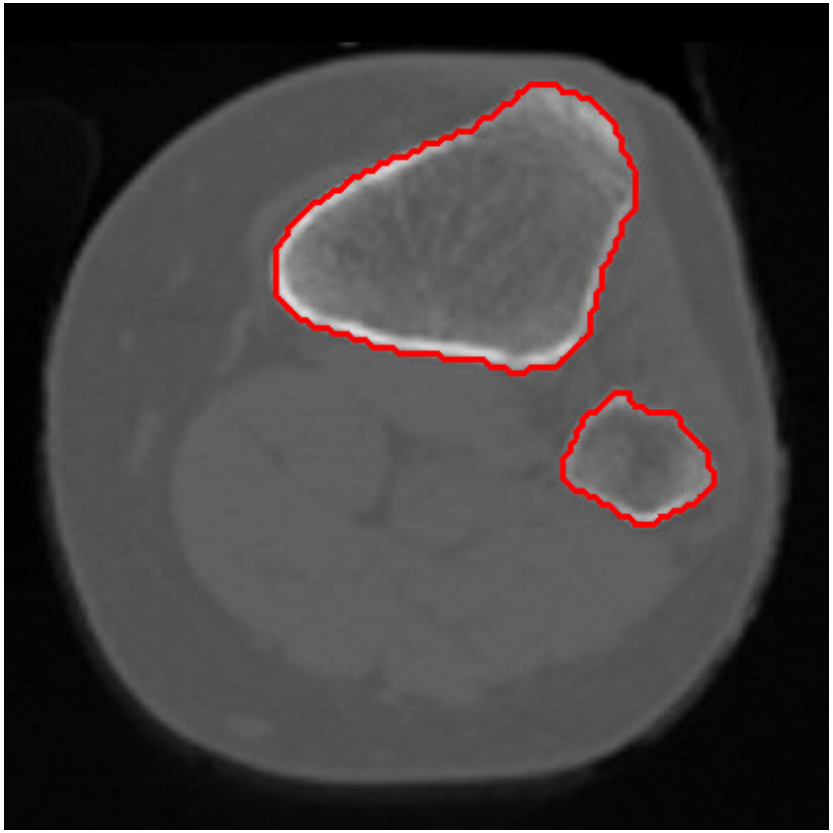
- Click Save Volume **8** to save the cropped data set.

- To retain the original volume, choose to create a new workspace volume 9 and rename. 10
- Click Save Volume. 11
- Close Transform.

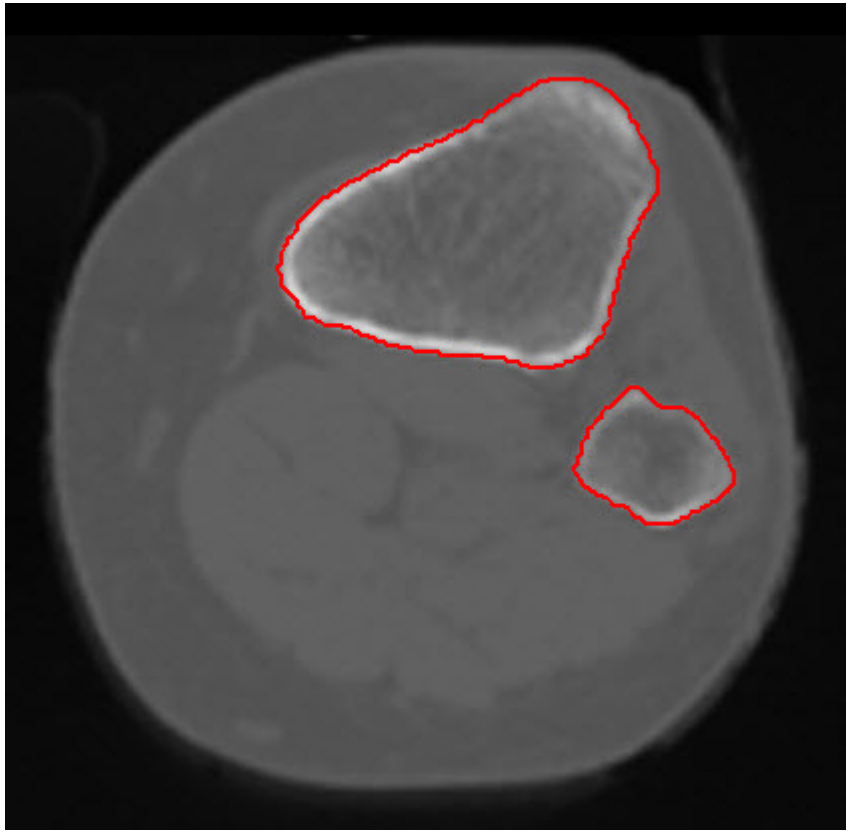


# Resize

The Resize tool can be used to resample image data. If data is acquired with anisotropic (non-cubic) voxels, the Resize tool can be used to resample the data to create an isotropic (cubic) data set. Occasionally data with a relatively large voxel size can be segmented more smoothly if resampled to a smaller voxel size. This will not change the resolution of the data but allows for a smoother definition of regions during segmentation.



Original Voxel Size



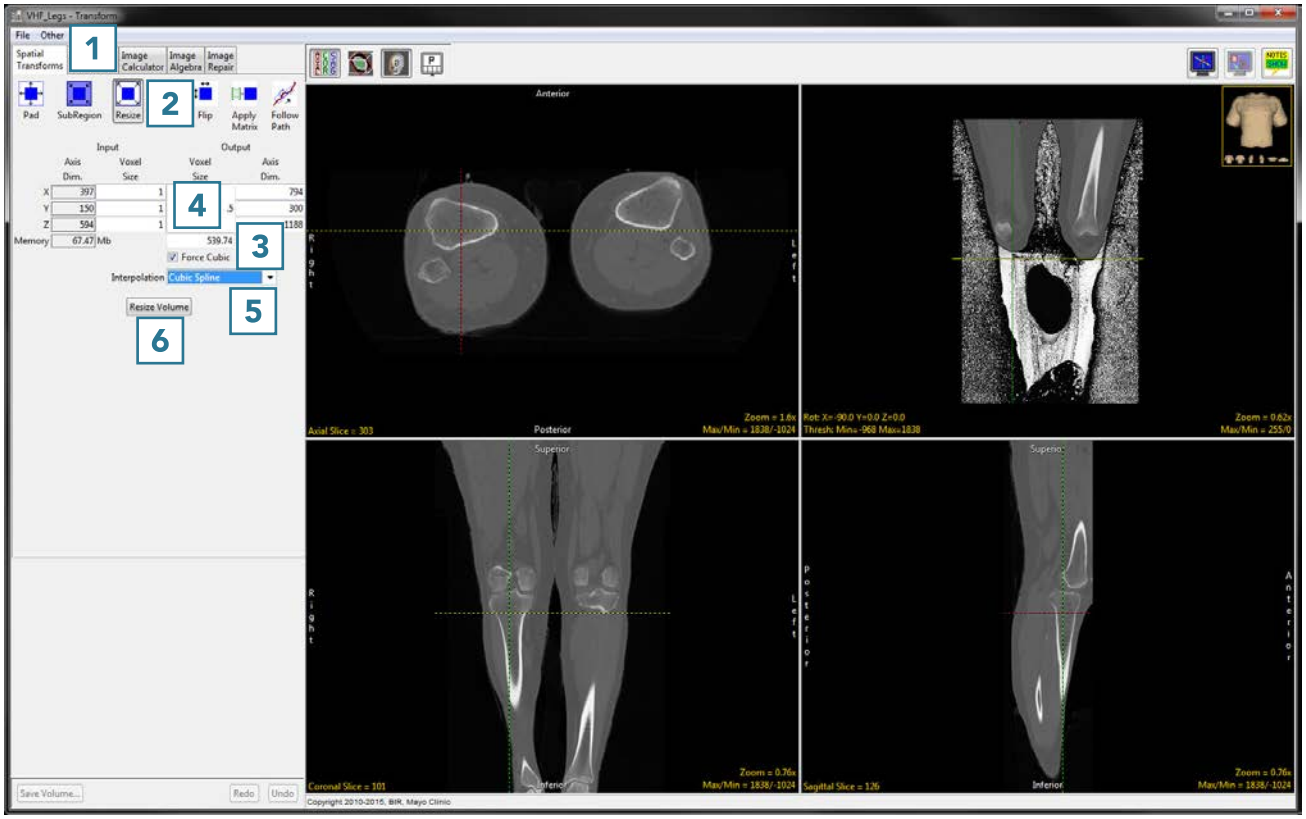
Resampled Voxel Size

- Select the data set to resize and open Transform. Navigate to Spatial Transforms 1 and select the Resize tool. 2
- Check the Force Cubic checkbox to interpolate between anisotropic voxels, 3 set the new voxel size 4 and choose an interpolation type. 5

See Table 3.4 or 6.1 for different interpolation types.

- Click Resize Volume 6 to resample the data set.

**Download the VHF_Legs data set to follow along http://analyzedirect.com/data/**



Each interpolation type is either input driven (ID) or output driven (OD).

Input driven interpolation algorithms process each voxel in the input volume and map each input voxel into the output space. The actual interpolation takes place in the output space, given the projected contributions of each input voxel into that space. Input driven algorithms will always use every voxel in the input volume as part of the interpolation process.

Output driven algorithms step through each voxel in the output data set and find the corresponding set of voxels in the input data set that map into the output. The interpolation of voxels takes place in the input space, depending on the type of interpolation selected. Output driven algorithms are more common in image processing as they guarantee that every voxel in the output data set will be filled with an interpolated value.

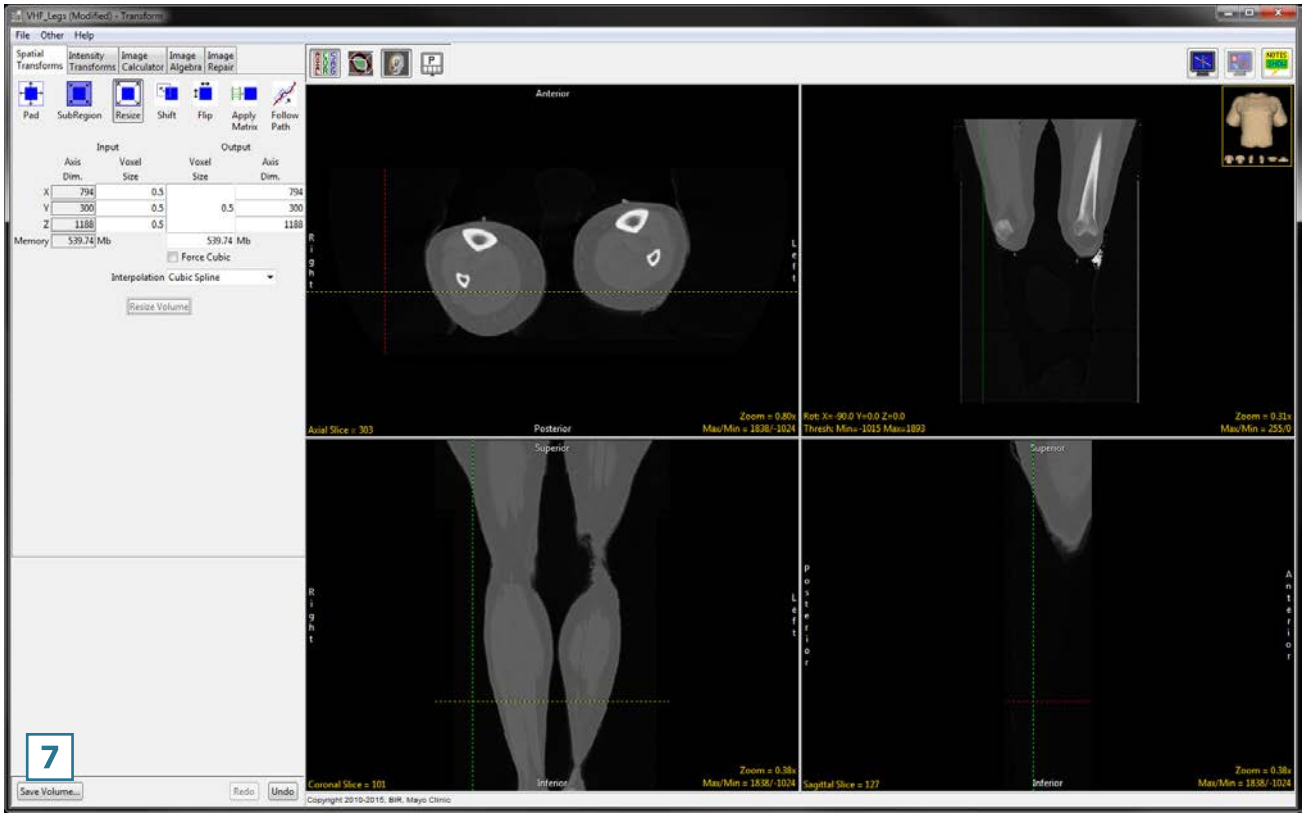
## Table 6.1: Interpolation Types

| Interpolation Type | Description |
|---|---|
| Nearest Neighbor* | selects the value of the closest voxel to which the interpolation resampling maps |
| Linear* | applies a linear interpolation of grayscale intensity based on the distance of neighboring voxels from the interpolated voxel |
| Cubic Spline** | uses a cubic spline function to determine interpolated value |
| Windowed Sinc** | uses windowed sinc function sin(x)/x to determine interpolated value |
| Shape Based | only available for binary data; calculates Euclidean distance, then performs linear interpolation between distance images |

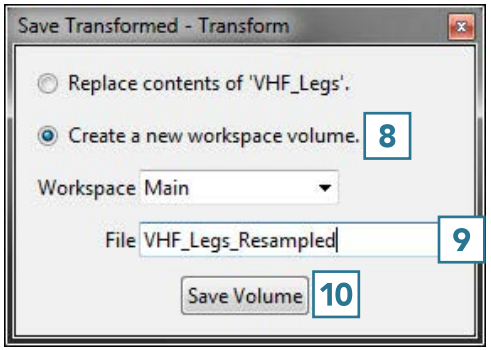
*The Nearest Neighbor and Linear interpolation types can be specified as ID or OD.

**The Cubic Spline and Windowed Sinc interpolation types are both OD. Since they use higher-order functions, they account for more neighboring voxels and thus may provide a better estimate for the interpolated value. These algorithms are also more compute-intensive.

- Click Save Volume **7** to save the resampled data set.



- To retain the original volume, choose to create a new workspace volume, 8 rename 9 then click Save Volume. 10
- Close Transform.



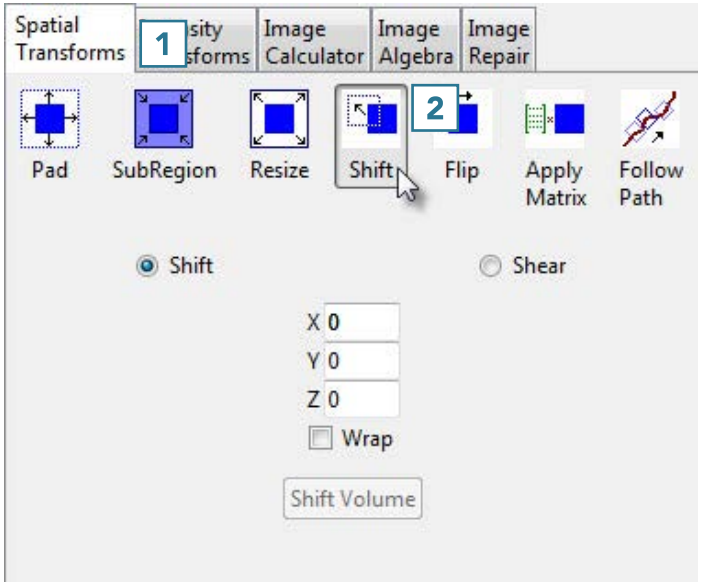
# Shift

The Shift tool can be used to shift data horizontally or vertically. This may be necessary to correct wraparound artifacts.

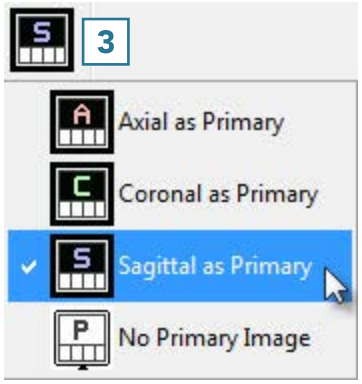
Download the MRI_Head data set to follow along http://analyzedirect.com/data/

## 1. Correcting Wraparound Using the Shift Tool

- Select the data set to shift and open Transform. Navigate to Spatial Transforms 1 and select the Shift tool. 2

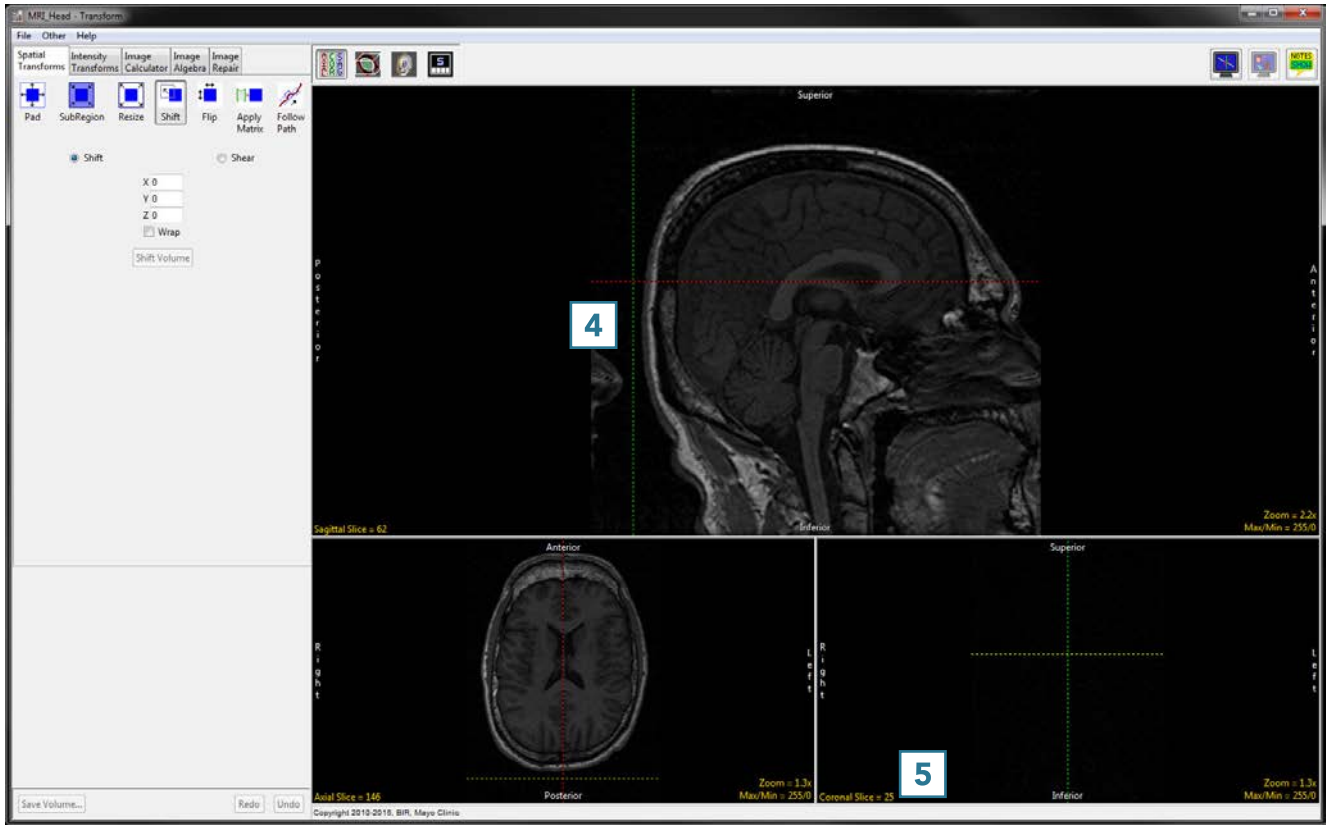


- This data set has a wraparound artifact which is visible in the sagittal view.
- Set sagittal as the primary view by double-clicking on the sagittal image or using the primary view menu. 3



- Use the linked cursor to determine the shift parameter value. 4
- In this data set, when the cursor is lined up with an appropriate break point in the sagittal view, the corresponding coronal slice number is 25. 5

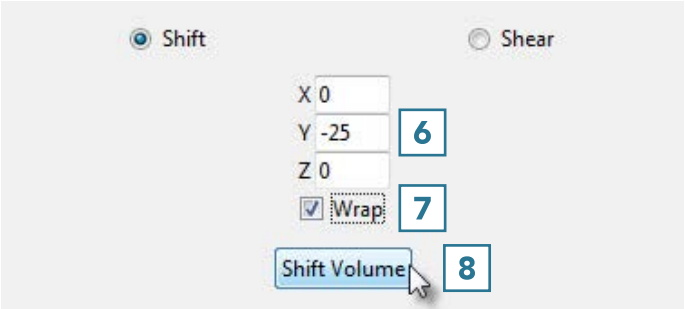
Refer to Table 6.2 to determine the correct sign and direction of the desired shift.



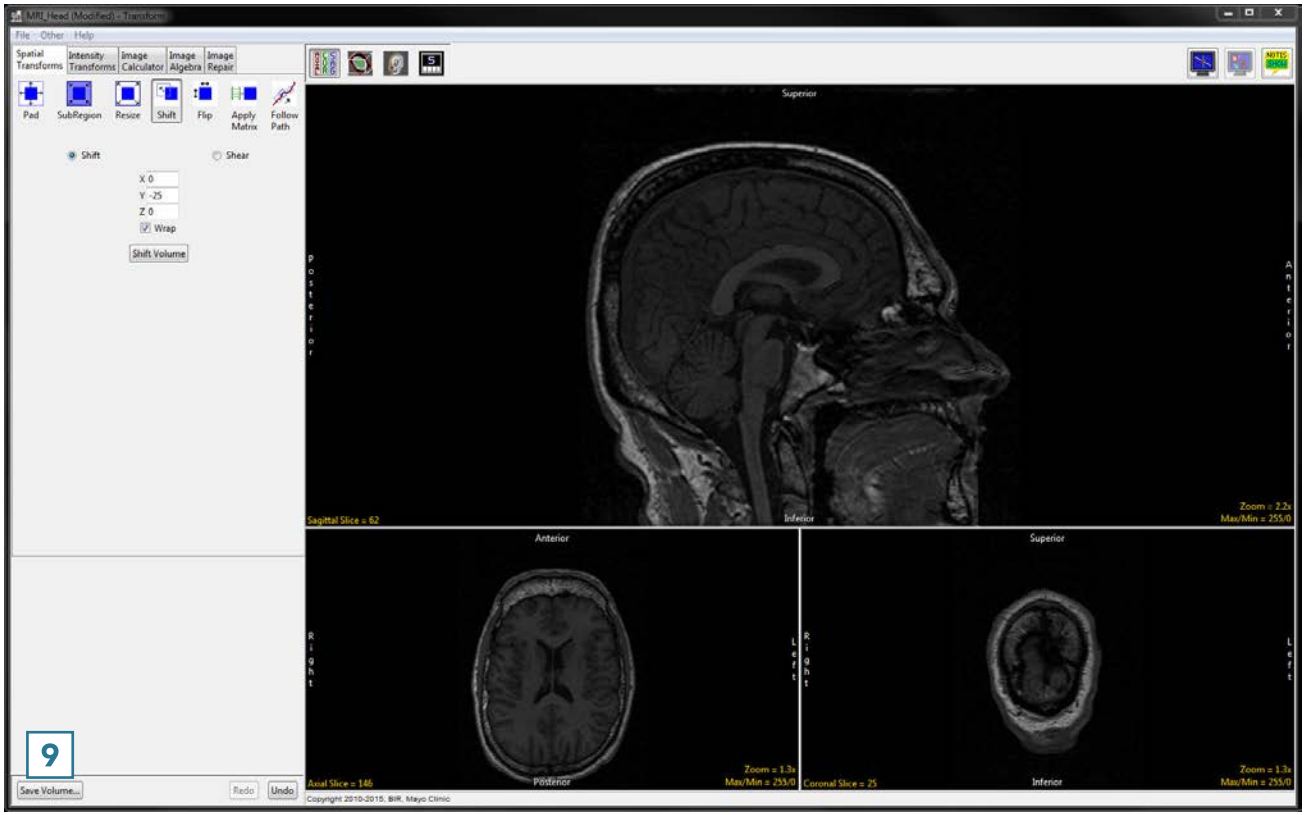
## Table 6.2: Shift Parameters

| | Axial | | Coronal | | Sagittal | |
|---|---|---|---|---|---|---|
| **Parameter** | **+** | **-** | **+** | **-** | **+** | **-** |
| X | right | left | right | left | | |
| Y | up | down | | | right | left |
| Z | | | up | down | up | down |

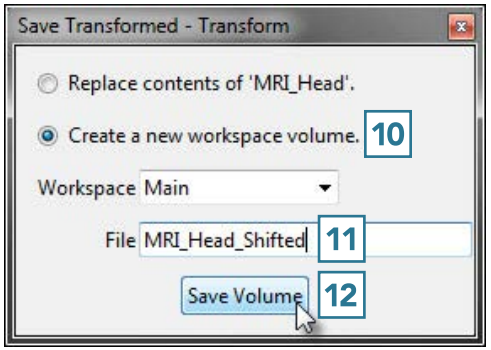
- Since we want to shift the sagittal image to the left, we will use a Y parameter of -25.
- Type this parameter value into the input box. 6
- Select the Wrap checkbox. 7
- Click Shift Volume to complete the shift. 8



- The data set will shift to the left by 25 slices and wrap those slices back around to connect with the rest of the head.
- Click Save Volume to save the shifted data set. 9



- In the Save Transformed window, choose to create a new workspace volume. 10
- Rename 11 and click Save Volume. 12
- Close Transform.



# Flip

It may be necessary to flip data in order to orient it correctly. The Flip tool allows users to flip data along any single axis or combination of axes.

## Table 6.3: Flip Parameters

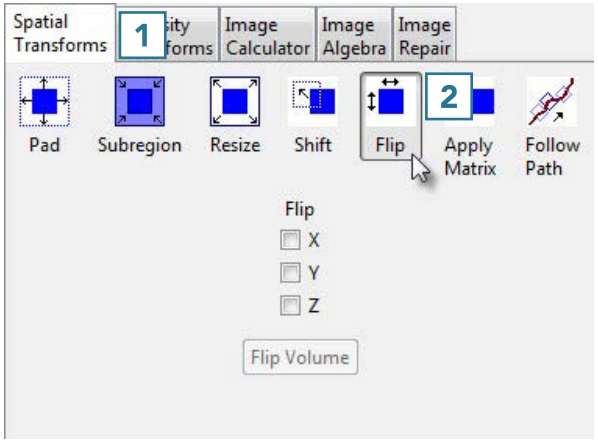
| Axis | Outcome |
|---|---|
| X | flips data horizontally about the vertical (Y) axis |
| Y | flips data vertically about the horizontal (X) axis |
| Z | reverses the order of the slices |

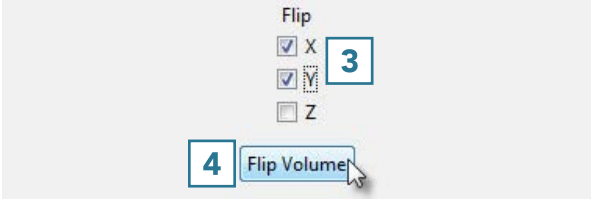
Flipping the data in only the X or Y direction will create a mirror image. If this is not the desired result, the data can be flipped in both the X and Y directions at once to prevent a mirror image from being created.

# 2. Flipping Data

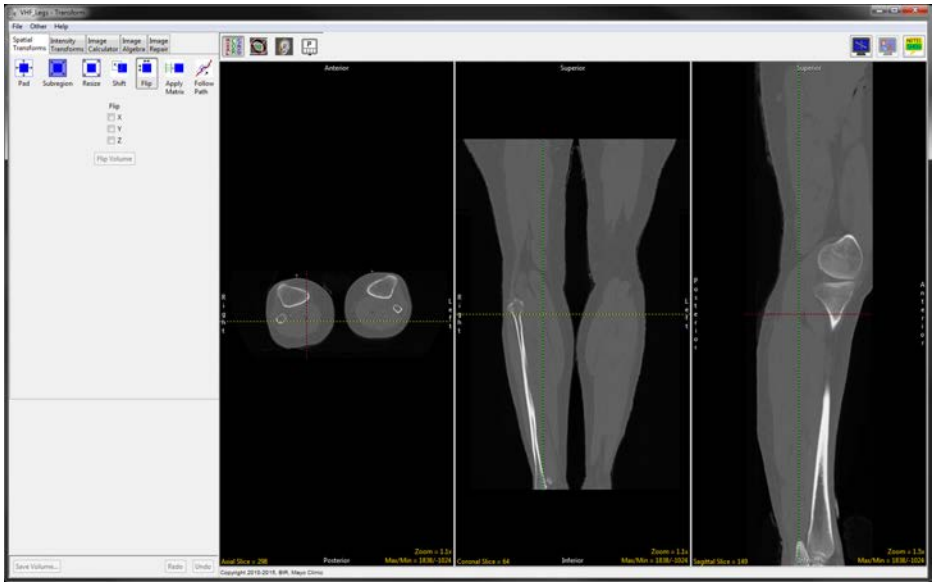
- Select the data set to flip and open Transform. Navigate to Spatial Transforms 1 and select the Flip tool. 2
- Select the checkboxes for the directions you wish to flip the data. 3 We will flip this data in the X and Y directions to avoid creating a mirror image.
- Click Flip Volume 4 to apply the flip.

Download the VHF_Legs data set to follow along http://analyzedirect.com/data/

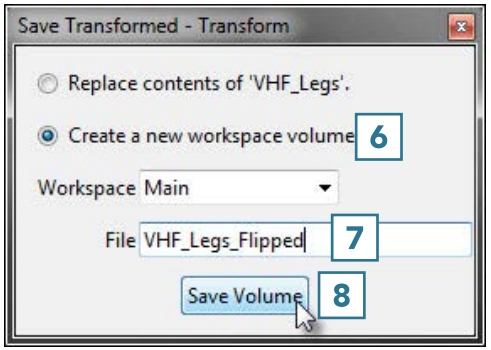


- The data set before and after the X-Y flip is shown below. Once the data is flipped, click Save Volume to save the flipped data set. **5**



- In the Save Transformed window, choose to create a new workspace volume. 6
- Rename 7 and click Save Volume. 8
- Close Transform.



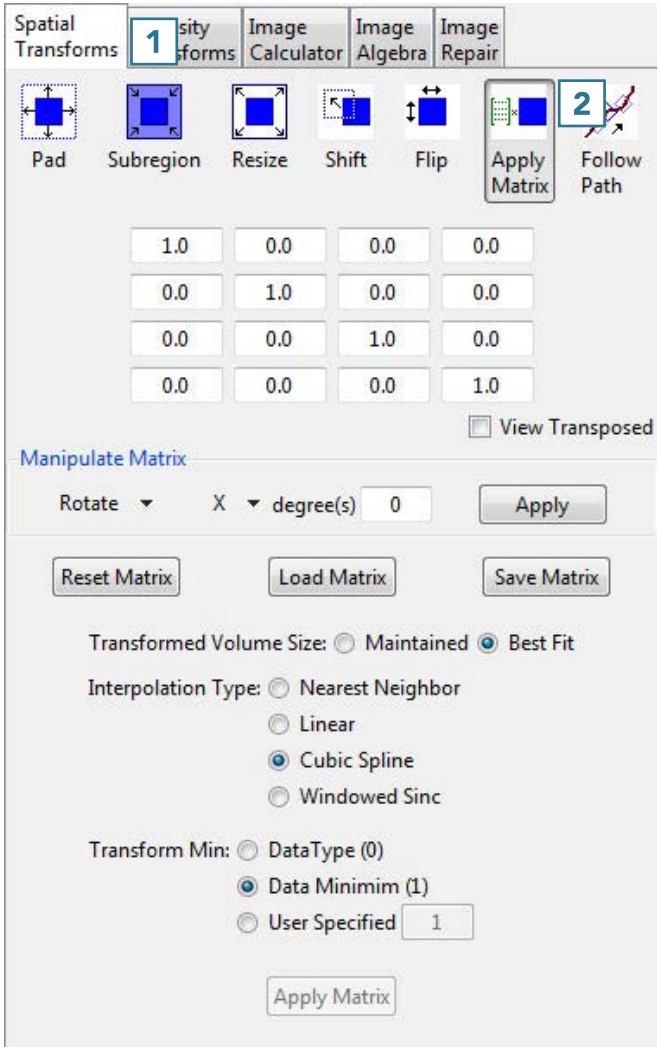
# Apply Matrix

The Apply Matrix tool can spatially transform a data set in many different ways, including rotation, translation and scaling (stretching or compressing) along any axis and inversion. In addition, any 4 X 4 matrix can be loaded into the tool to apply the same transformation to many data sets. Another prominent feature of this tool is the ability to output oblique data sets, such as AC-PC aligned brain data.

# 3. AC-PC Alignment of Brain Data

- Select the data set to align along the AC-PC axis and open Transform.
- Navigate to Spatial Transforms. 1
- Select the Apply Matrix tool. 2

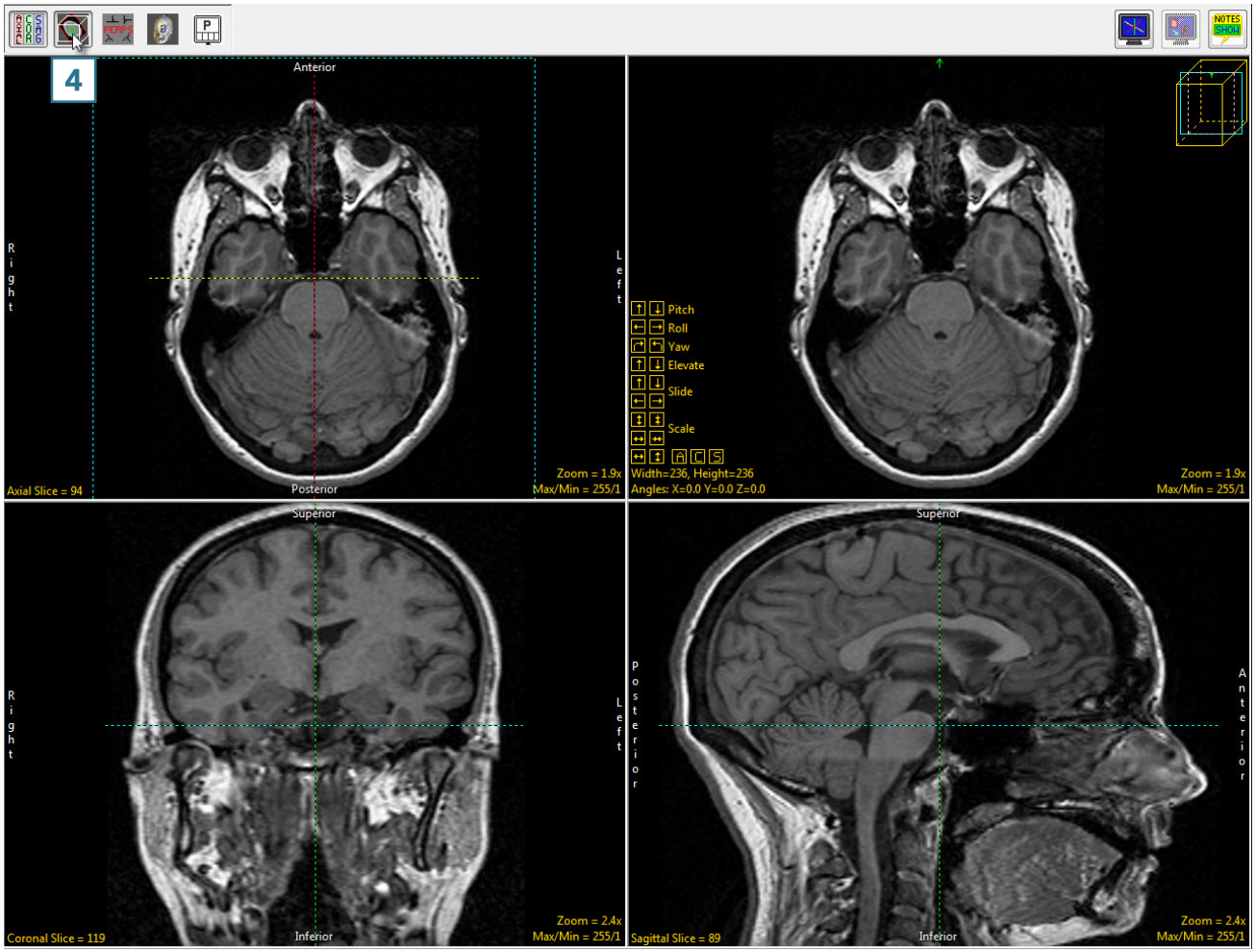
Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/



The optimal display settings for AC-PC alignment or any other manipulation of an oblique plane are as follows:

- Switch off the rendering 3 (unless an object map is loaded, which might help visualize the oblique). Now the three orthogonal views are shown.

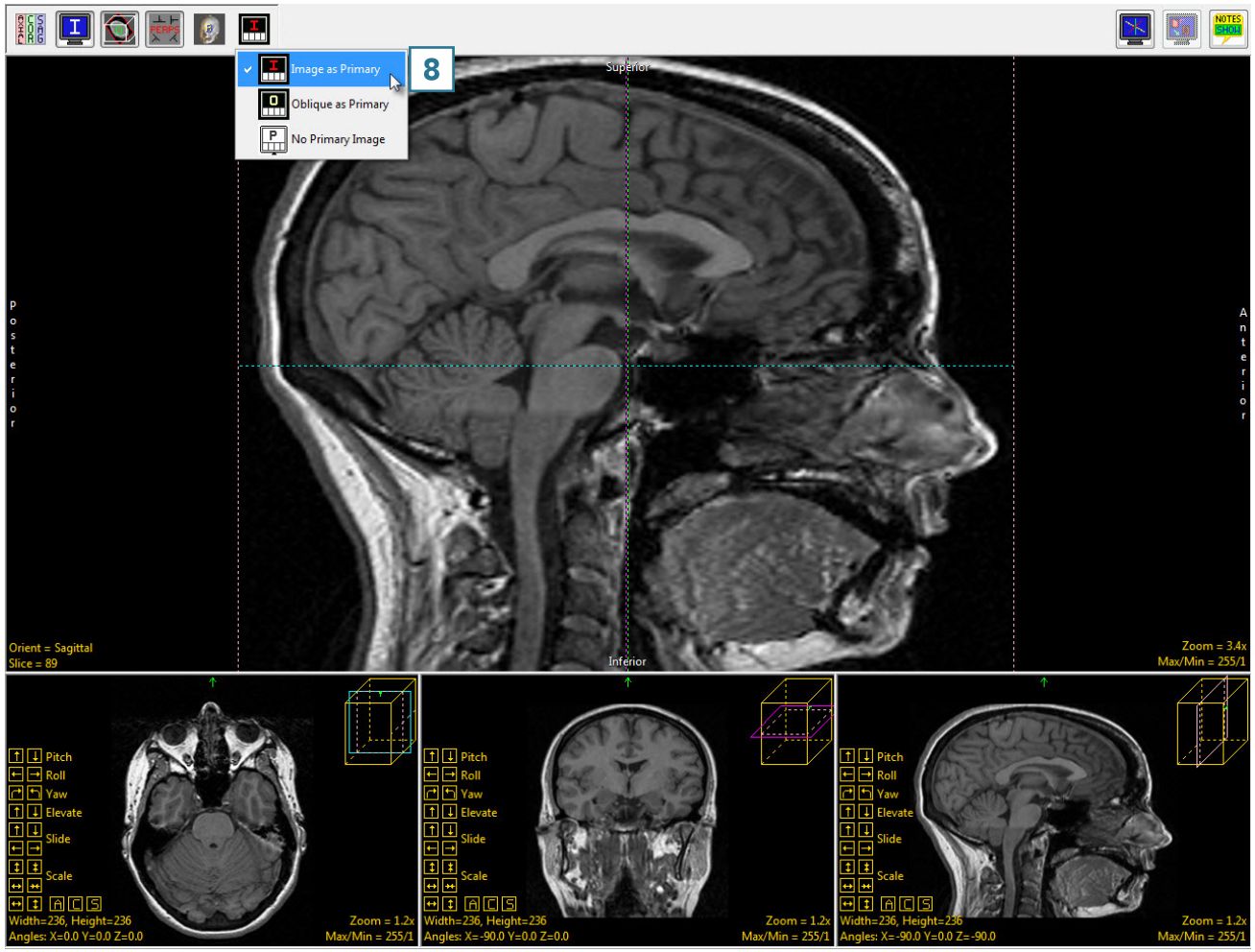
- Switch on the oblique. 4 Now, the oblique and the three orthogonal views are shown.



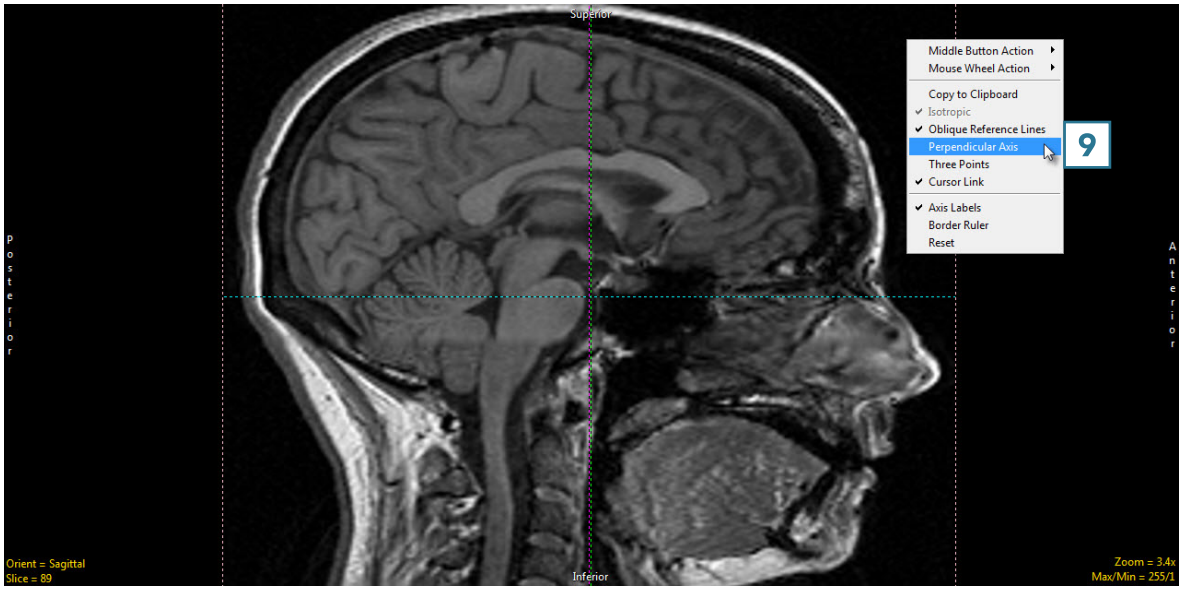
- Toggle the orthogonal orientations to a single image. 5
- Set this image to the sagittal view by clicking twice on the Orient parameter. 6
- Now the sagittal orientation and the oblique image are shown.

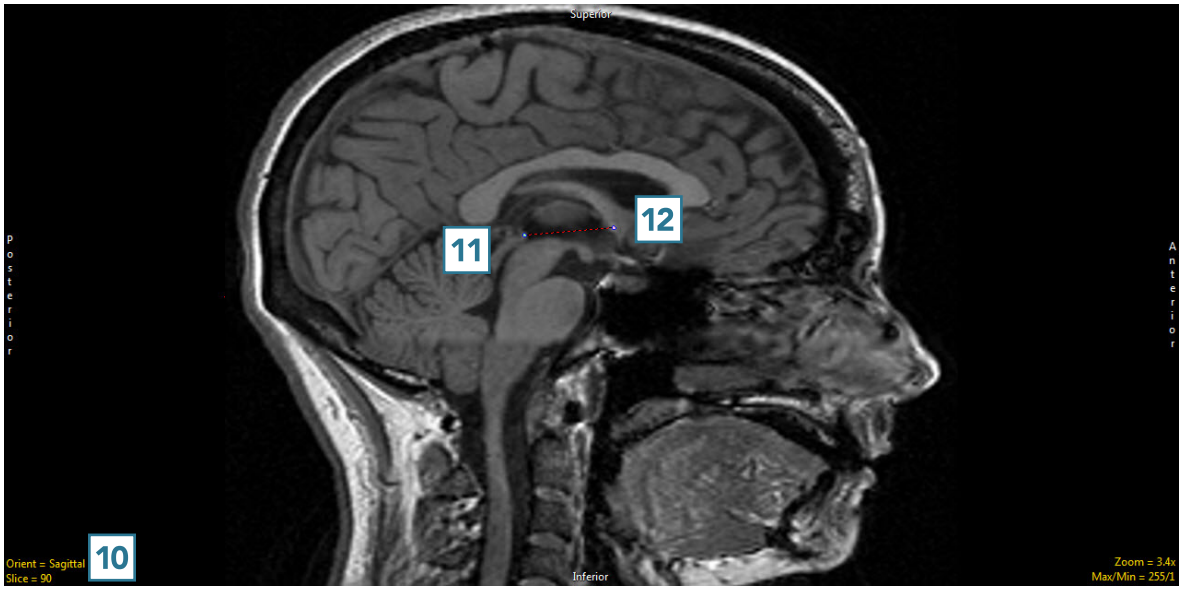
- Switch on the perpendicular images. 7

- The AC-PC line will be defined on the sagittal view, so double-click the sagittal image or select Image as Primary in the drop-down menu. 8

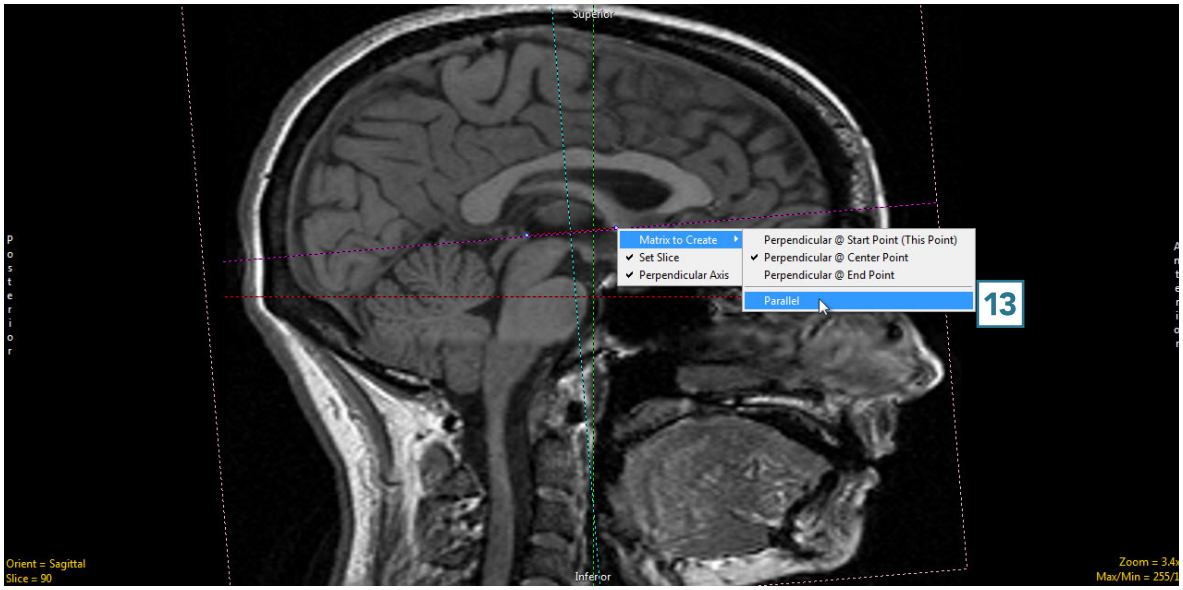


- Right-click on the sagittal image and select Perpendicular Axis 9 to turn on the perpendicular axis tool.
- Navigate to the mid-sagittal slice, which for this data set is slice 90. 10
- Drag the left endpoint of the perpendicular axis to the posterior commissure. 11
- Drag the right endpoint of the perpendicular axis to the anterior commissure. 12

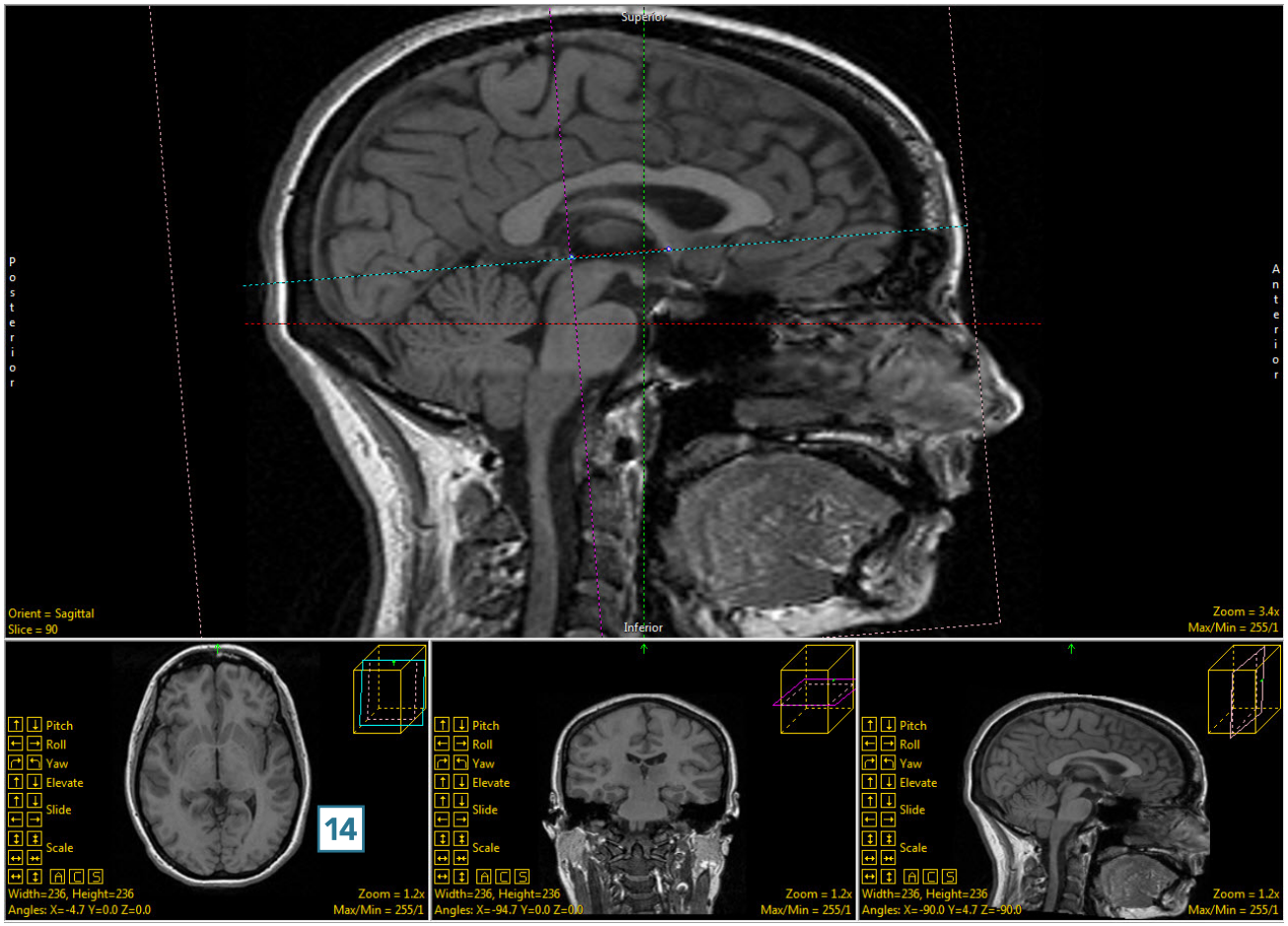


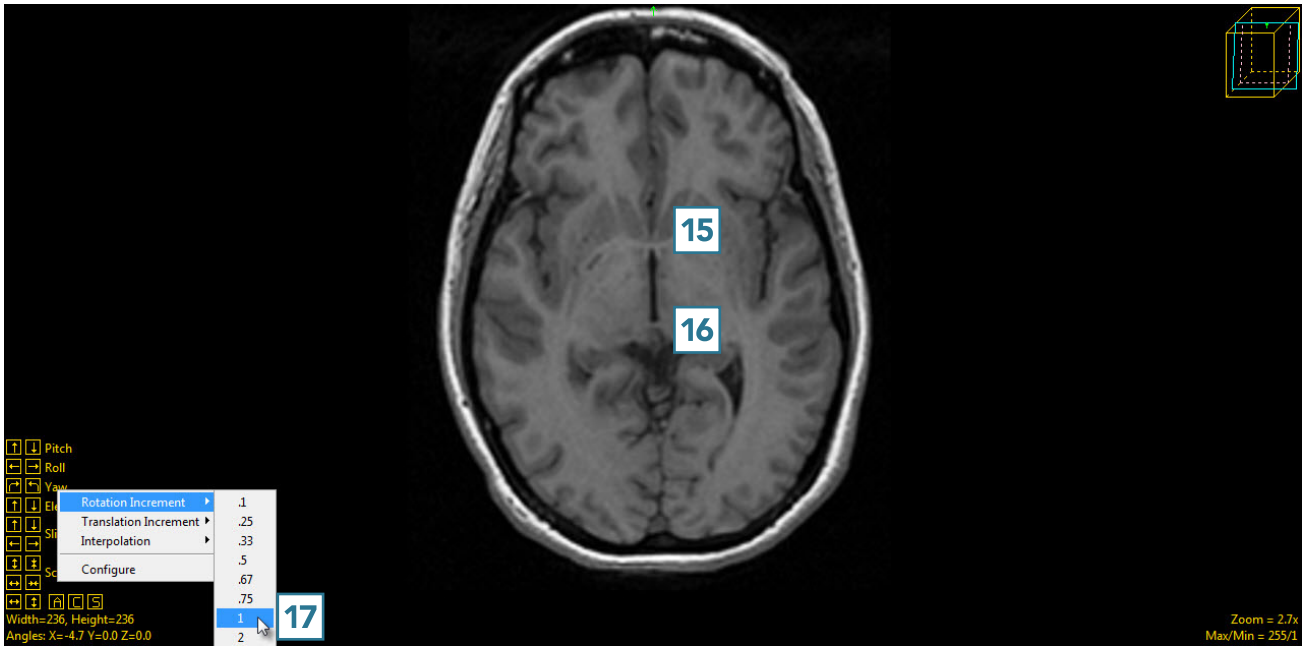
- To set the oblique plane to be parallel, rather than perpendicular, to the AC-PC plane, right-click on one of the perpendicular axis endpoints and set the Matrix to Create to Parallel. 13



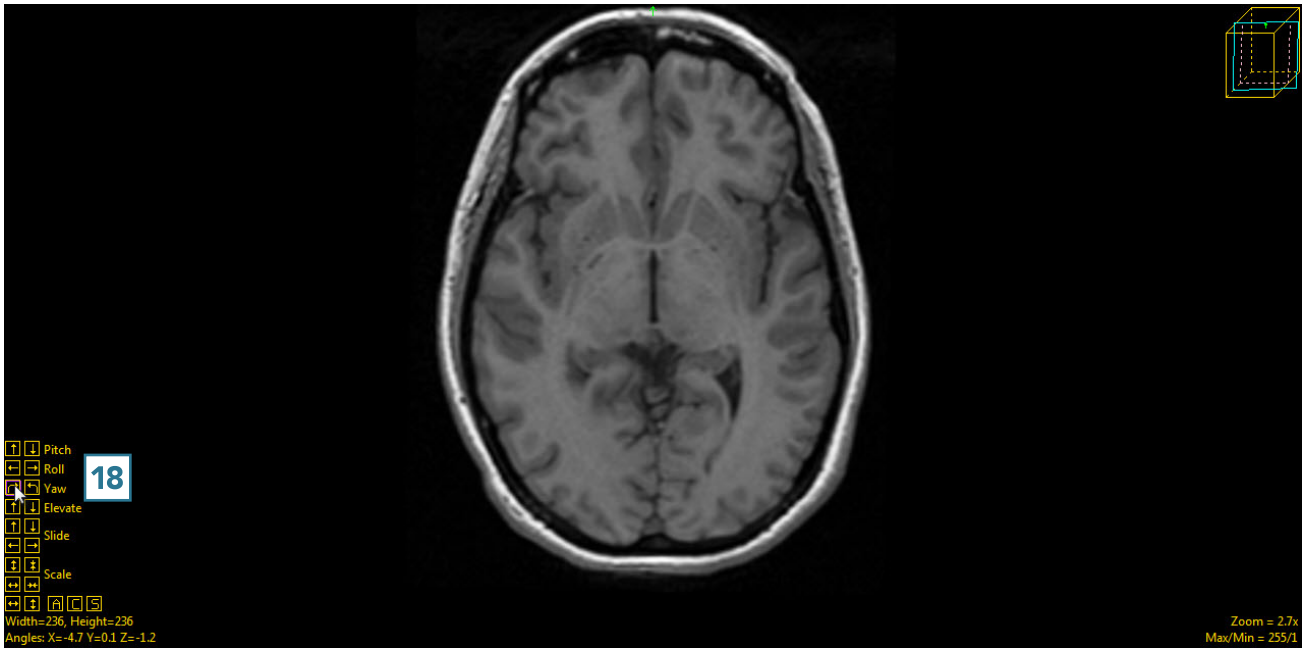
- Now the main oblique image (the leftmost of the three) is an AC-PC aligned axial image. 14
- Double-click this image to make it the primary image.



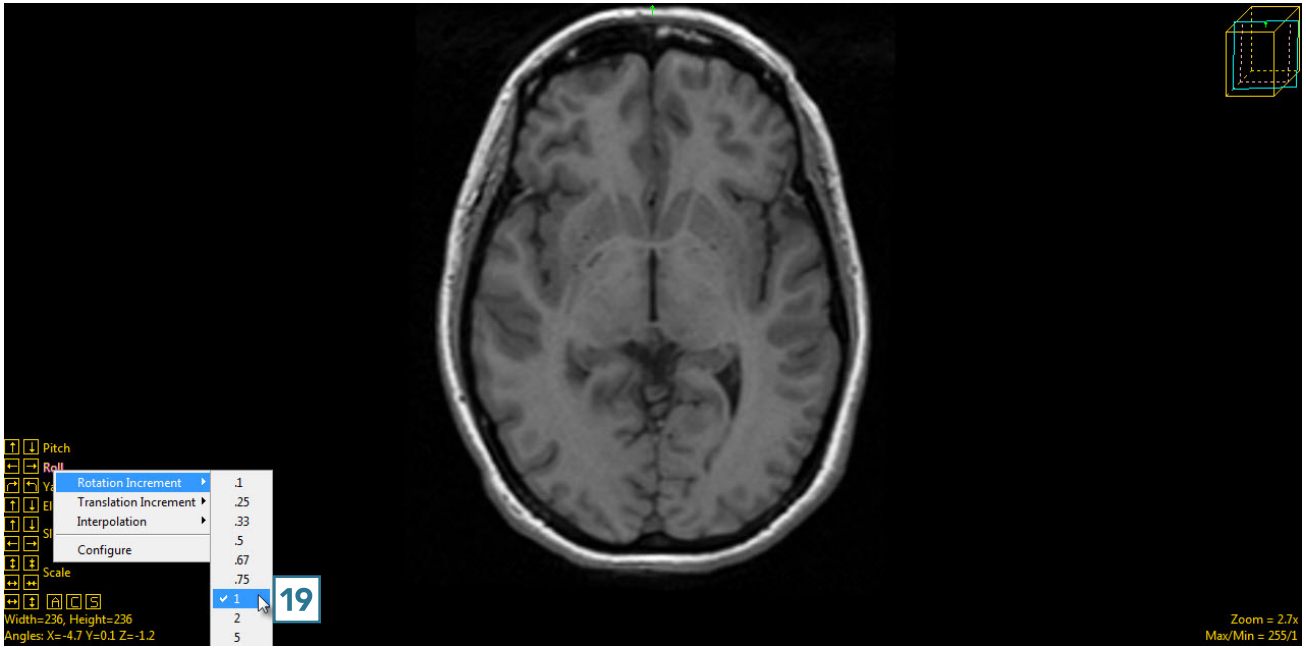
- The AC 15 and PC 16 can both be seen on the same oblique slice, indicating good AC-PC alignment.
- To adjust vertical alignment of the data set, right-click Yaw and set the Rotation Increment to 1. 17



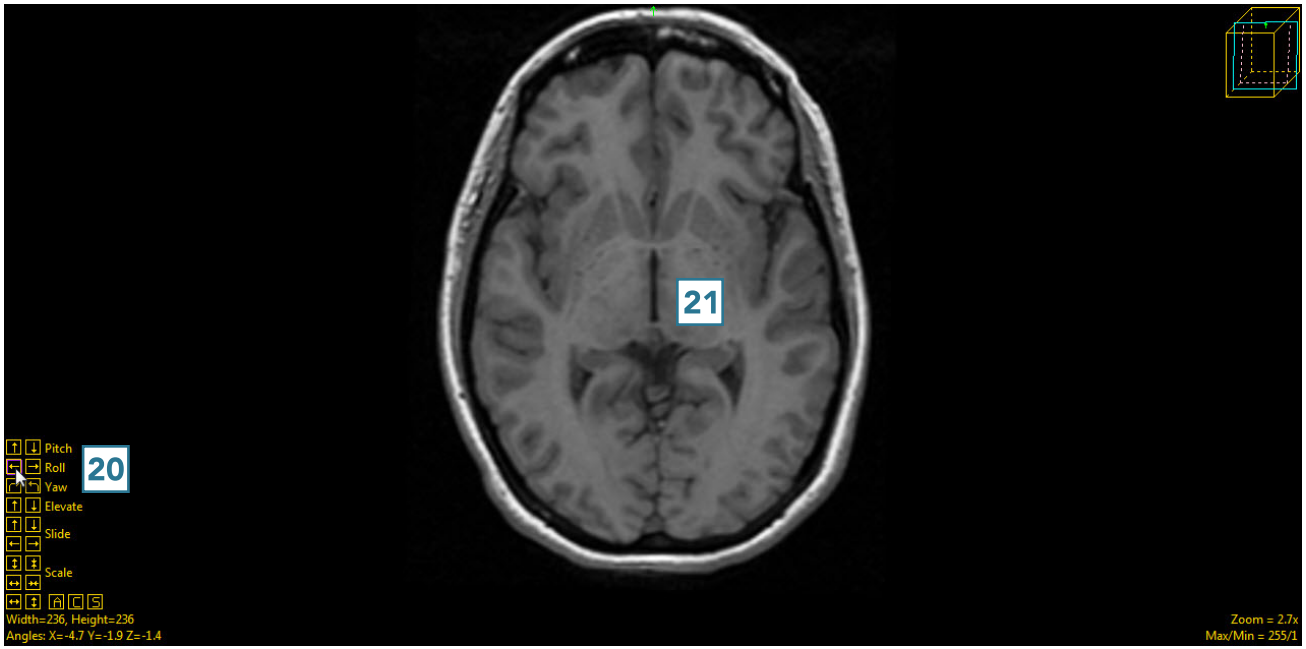
- Use the left and right Yaw buttons to align the data set vertically. 18 The increment can be made even smaller to make smaller adjustments as needed.



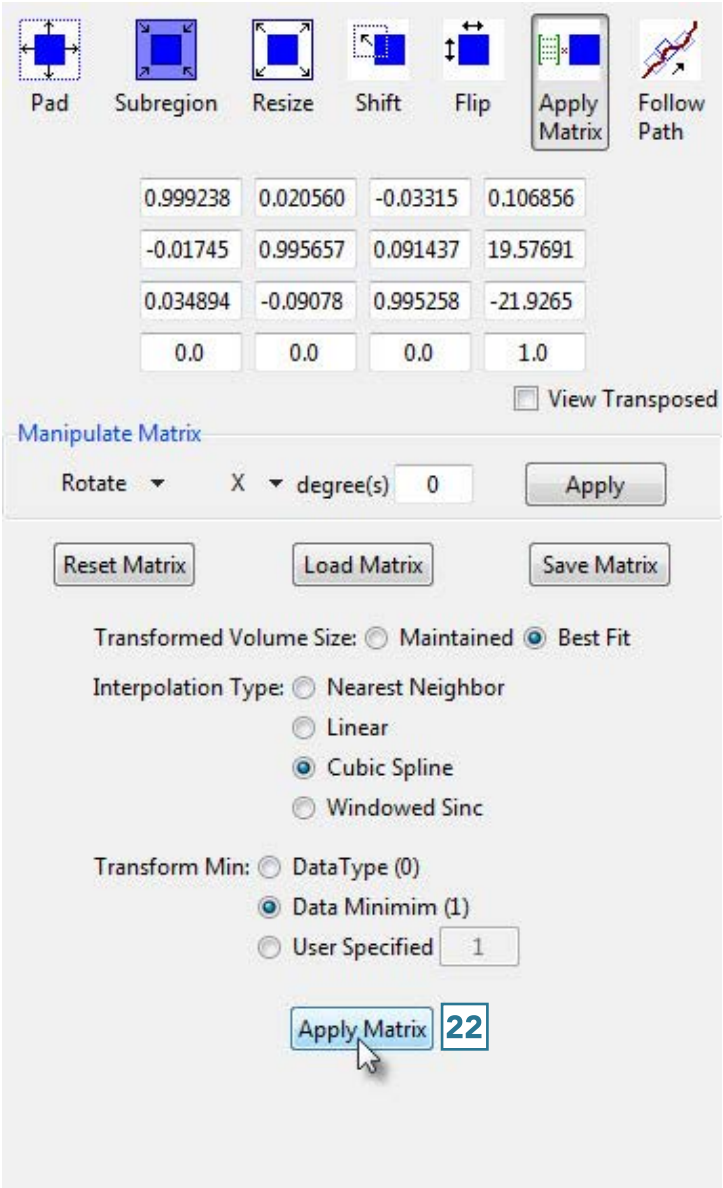
- The last adjustment to be made to the oblique plane will be done using the Roll function. Right-click on Roll and change the Rotation Increment to 1. 19



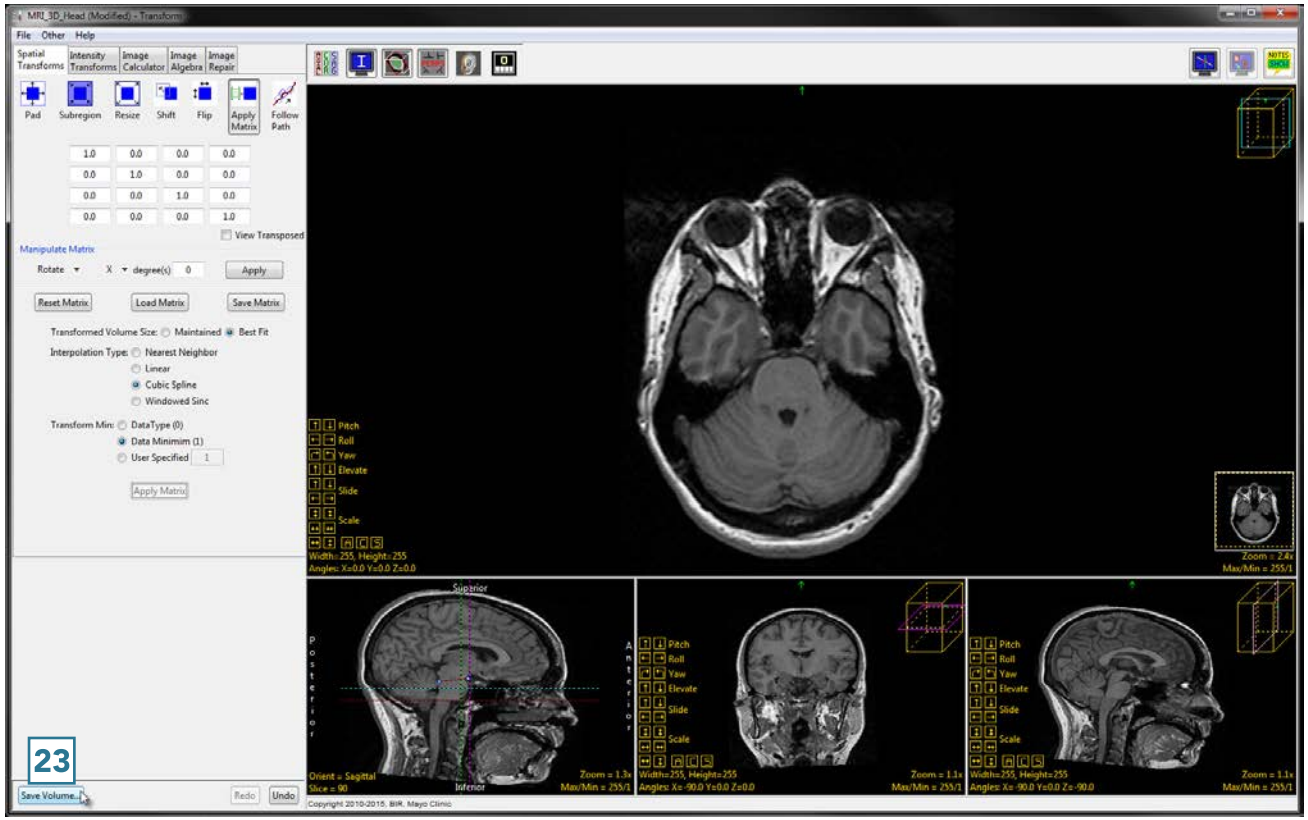
- Click on the left and right roll buttons 20 to adjust the data set until the anatomical structures appear symmetrical. 21



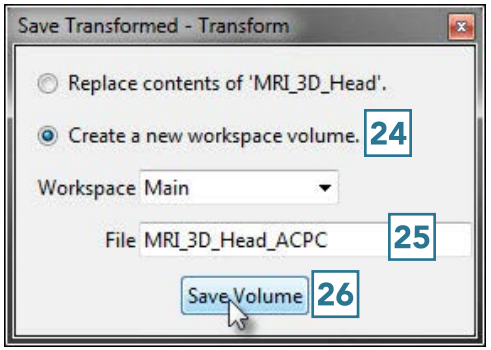
- Click Apply Matrix 22 to apply the transformation.



- Click Save Volume **23** to save the transformed data set.



- In the Save Transformed window, choose to create a new workspace volume. 24
- Rename 25 and click Save Volume. 26
- Close Transform.



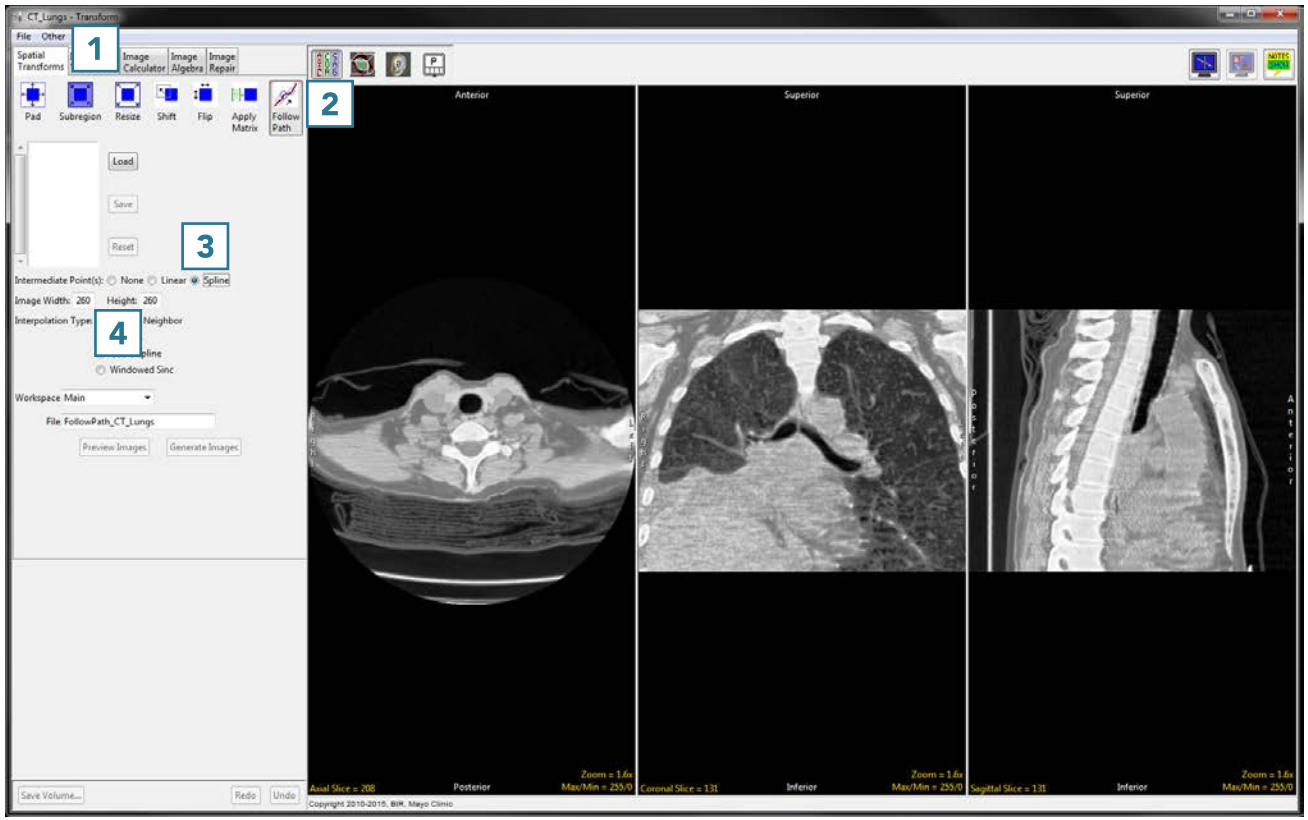
# Follow Path

The Follow Path tool is useful for reslicing a data set along the centerline of a vessel or airway. A series of points is chosen along a path in the data set, and the data is resliced perpendicular to the line created by these points.

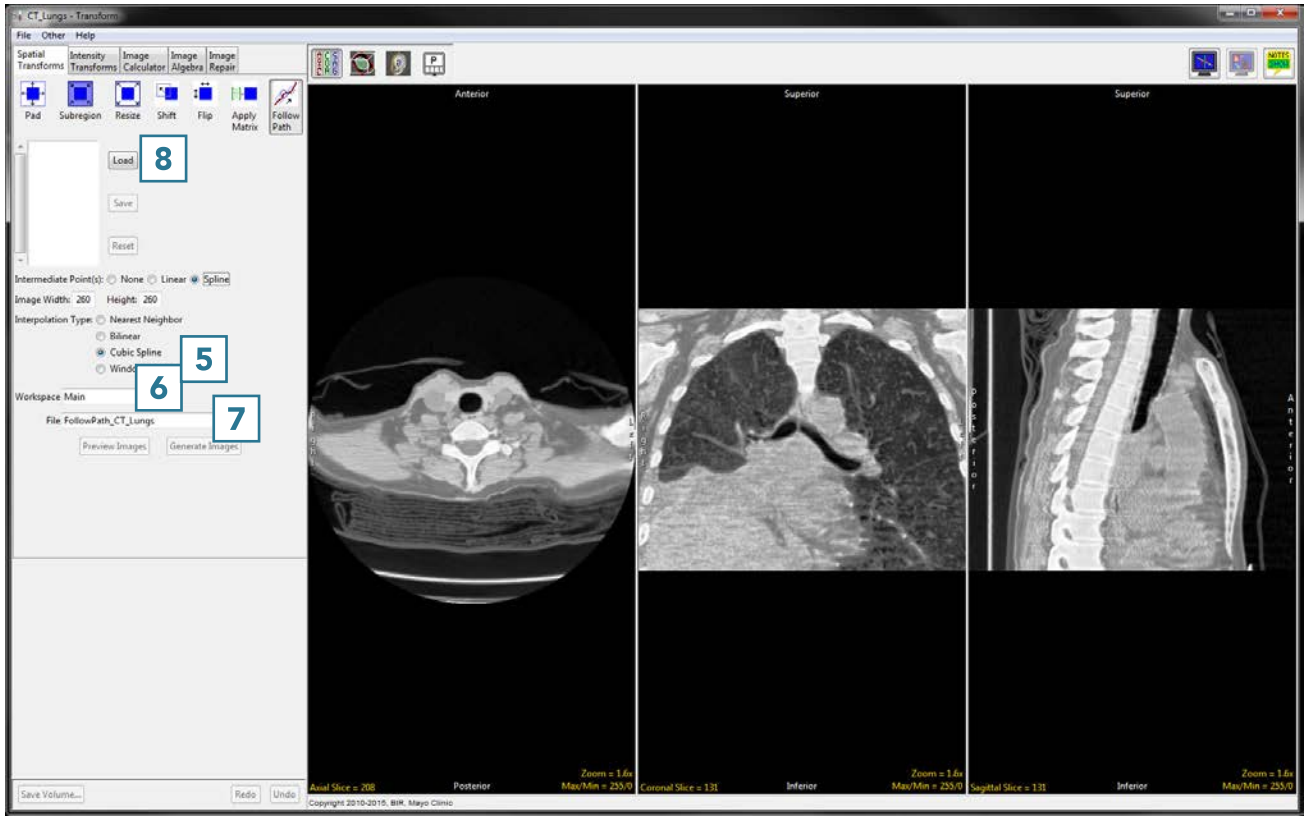
# 4. Reslicing Data along the Trachea

- Select the data set to reslice along a path of points and open Transform. Navigate to Spatial Transforms 1 and select the Follow Path tool. 2
- Choose a method of connecting the points: none, linear, or spline. 3 Spline creates the smoothest transition between slices, so that will be selected here.
- The image width and height 4 determine the dimensions of the output. If you are interested only in measuring the cross-sectional area of the structure on each slice, the image dimensions can be reduced from their original size.

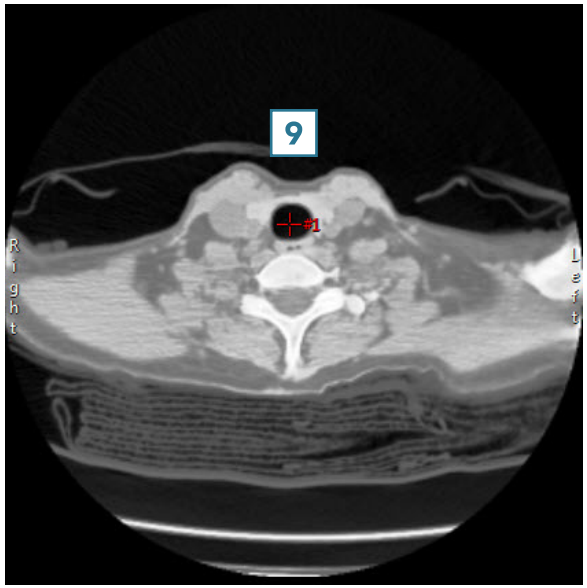
**Download the CT_Lungs data set to follow along http://analyzedirect.com/data/**

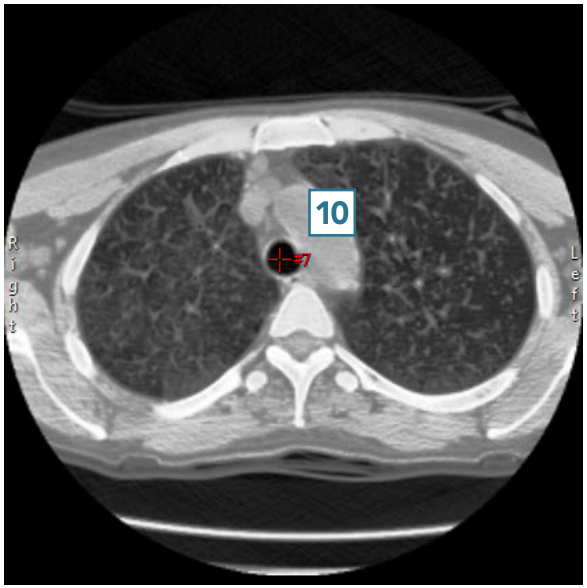


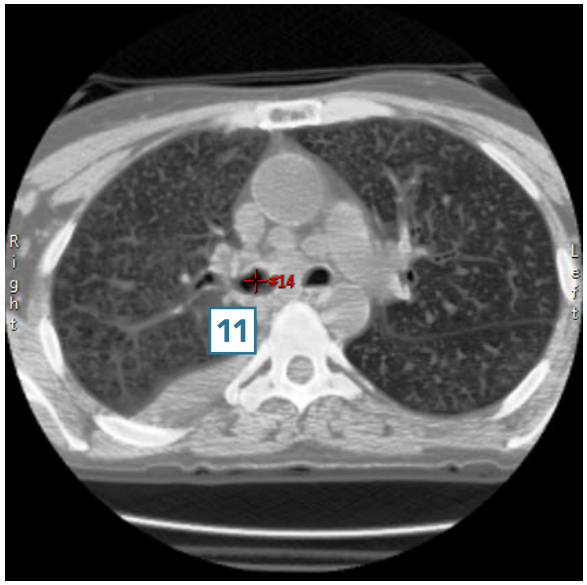
- The interpolation type 5 can be set to nearest neighbor, bilinear, cubic spline or windowed sinc. For more information on interpolation types, see Table 6.1.
- Choose a workspace 6 and output file name 7 for the resliced data set.
- Now it is time to choose the points. A previously saved set of points can be imported using the Load button. 8 Points can also be chosen by selecting them directly on the data set. Points can be chosen in any orthogonal image but must be chosen in order along a path.



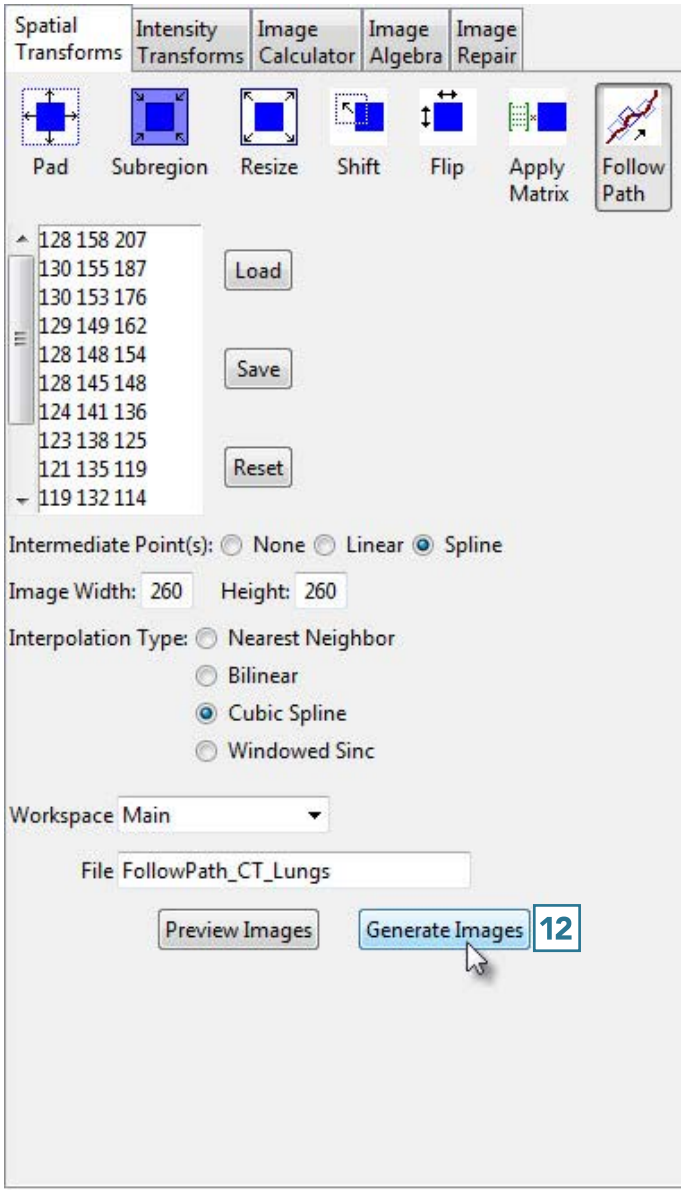
- Click in the trachea to set the first point. 9
- Scroll through the slices and continue to set points along the path 10 until reaching the last point of the desired path. 11



- Click Generate Images 12 to create the resliced data set and save it to the specified workspace.
- Close Transform.



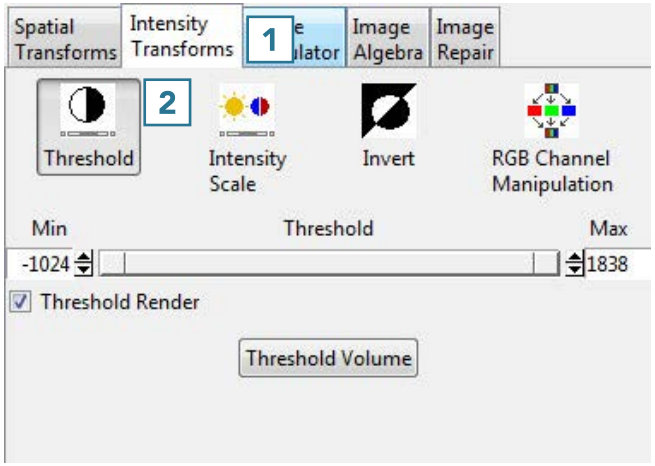
# Intensity Transforms

The Intensity Transforms available in AnalyzePro include thresholding, intensity scaling, inversion and RGB channel manipulation. Many of the functions available in this section are also available via Input/Output > Process > Intensities.

# Threshold

Threshold scaling allows a range of voxels from the input volume to be saved as a binary data set. All voxels greater than or equal to the threshold minimum and less than or equal to the threshold maximum are set to 1 and all other voxels are set to 0.

Download the VHF_Legs data set to follow along http://analyzedirect.com/data/



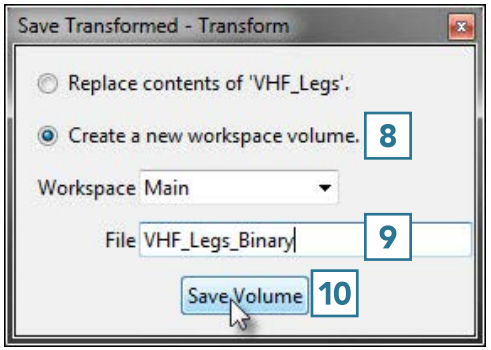

## 5. Creating a Binary Data Set with Thresholding

- Select the data set to threshold and open Transform. Navigate to Intensity Transforms 1 and select the Threshold tool. 2

- Use the sliders to set the threshold minimum and maximum, or type the values into the input boxes. 3
- While the slider is held down, the voxels defined by the given threshold range are highlighted in red in the orthogonal views. 4
- The rendering that will result from that threshold range is shown. 5
- Click Threshold Volume 6 to apply the global threshold.

- The result is a binary data set. Click Save Volume 7 to save this data set.

- In the Save Transformed window, choose to create a new workspace volume. 8
- Rename 9 and click Save Volume. 10
- Close Transform.



# Intensity Scale

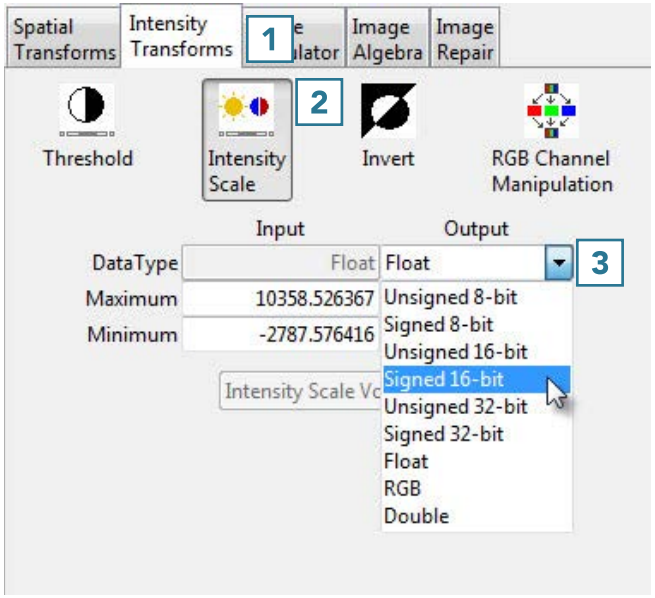
Intensity scaling allows for the adjustment of the voxel value information in the data. Image data can be scaled by adjusting the output data type.

# 6. Modifying Image Data Type

Changing the data type can reduce the size of the data on disk. In this example, a microCT data set has a data type of Float and the size of the image data is 92.71 MB. Changing the data type to signed 16-bit reduces the size of the data set by about 50% to 46.35 MB without having a significant effect on the voxel intensities.

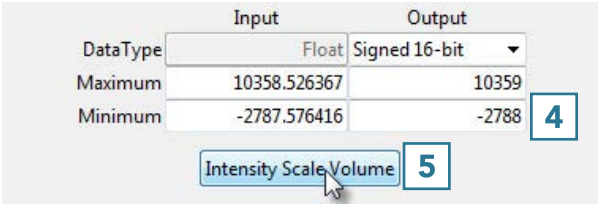
- Select the data set to scale and open Transform.
- Navigate to Intensity Transforms. 1
- Select the Intensity Scale tool. 2
- Select the Signed 16-bit data type from the Output drop-down menu. 3

Download the Bone_Sample_mCT data set to follow along http://analyzedirect.com/data/



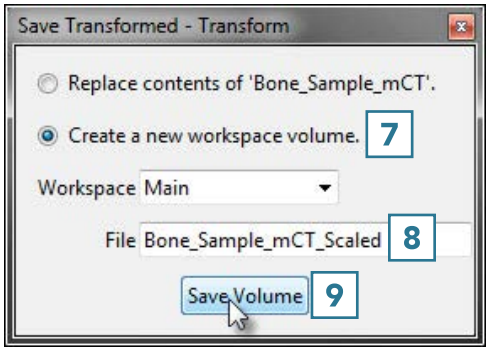
The maximum and minimum values will be set to the default values for the signed 16-bit data type.

- Change these values to match the maximum and minimum input values, rounding to the nearest whole number. 4
- Click Intensity Scale Volume 5 to apply the changes.



- Click Save Volume 6 to save the scaled data set.

- In the Save Transformed window, choose to create a new workspace volume. 7
- Rename the file. 8
- Click Save Volume. 9
- Close Transform.



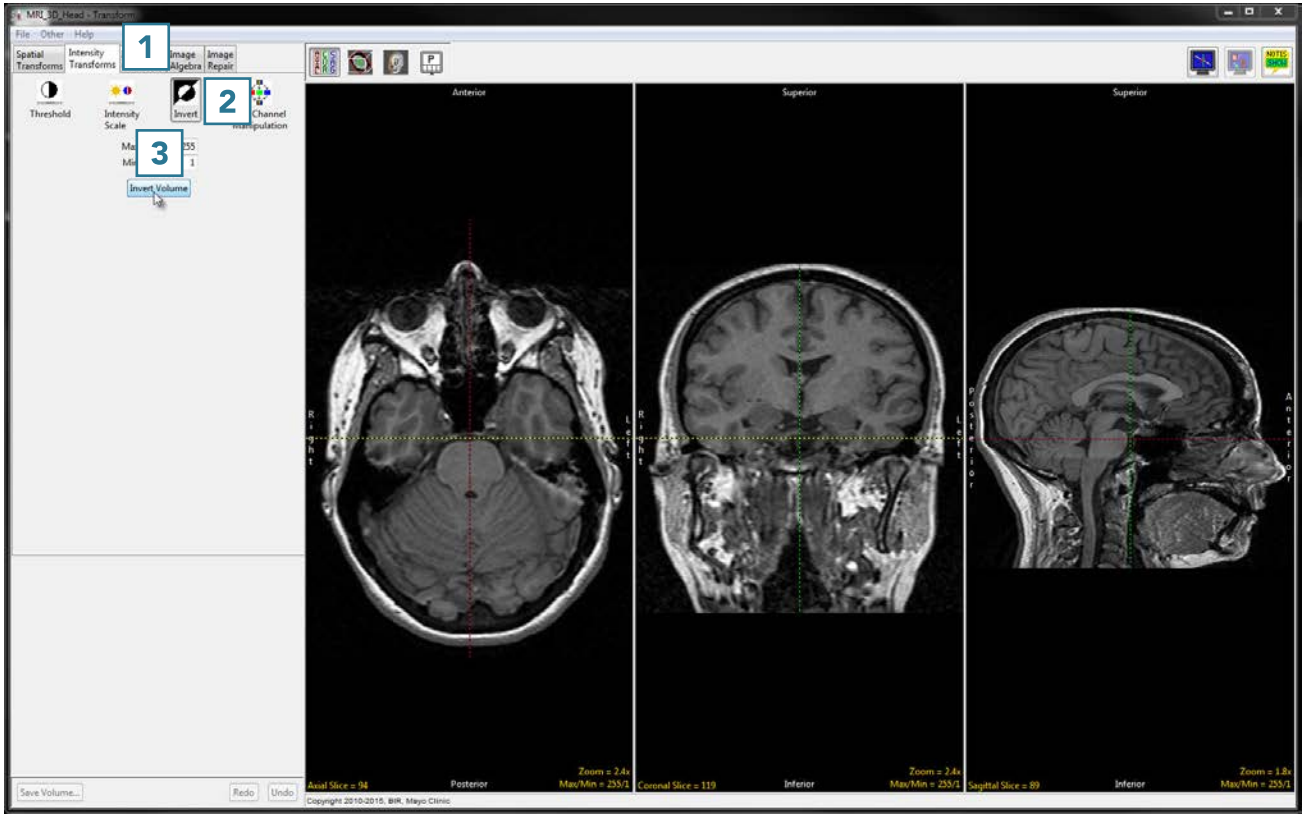
# Invert

For certain segmentation and visualization applications, it is beneficial to view an inverted copy of the image data alongside the original grayscale data.

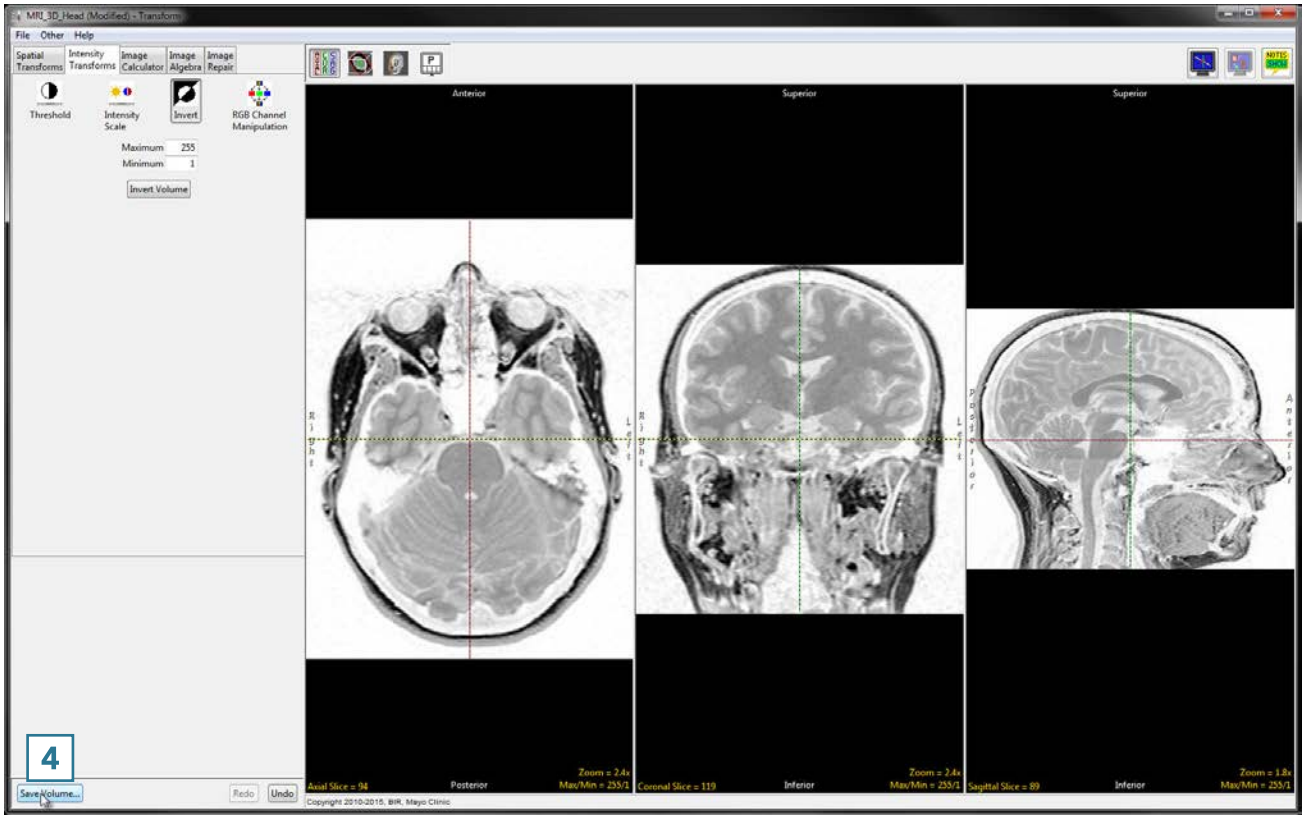
# 7. Inverting Data

- Select the data set to invert and open Transform.
- Navigate to Intensity Transforms. 1
- Select the Invert tool. 2
- Click Invert Volume 3 to apply the inversion.

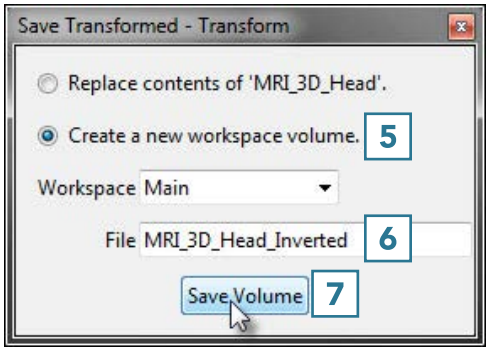
Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/



- Click Save Volume **4** to save the inverted data set.



- In the Save Transformed window, choose to create a new workspace volume. 5
- Rename 6 and click Save Volume. 7
- Close Transform.



# RGB Channel Manipulation

The RGB Channel Manipulation tool allows data to be converted to or from 24-bit color data.

If the input is a 24-bit color file, the following options are available:

## Table 6.4: Conversions from 24-bit Options

| Option | Description |
|---|---|
| Grayscale Formula | Converts the RGB values to an 8-bit grayscale image using the following formula:<br>gray_voxel = red_voxel*.3+green_voxel*.59+blue_voxel*.11 |
| Dithering | Converts the RGB values to 8-bit with a colormap. The number of color cells used is specified by the Number Of Colors value. |
| Data w/Colormap | Converts the RGB values to data with a colormap using the colors in the input data |
| Extract Red Channel | Specifies that only the 8-bit red channel is used |
| Extract Green Channel | Specifies that only the 8-bit green channel is used |
| Extract Blue Channel | Specifies that only the 8-bit blue channel is used |

Data can also be converted to a 24-bit color image using the following options.

## Table 6.5: Conversions to 24-bit Options

| Option | Description |
|---|---|
| Data w/Colormap | Converts a data set with a colormap loaded into a 24-bit color image |
| Object Colored | Uses a data set and an object map to make a 24-bit data set where all the voxels have been colored using colors and definitions in the object map |
| Combine Channel(s) | Combines the red, green and blue channels into a 24-bit color image |

# Image Calculator

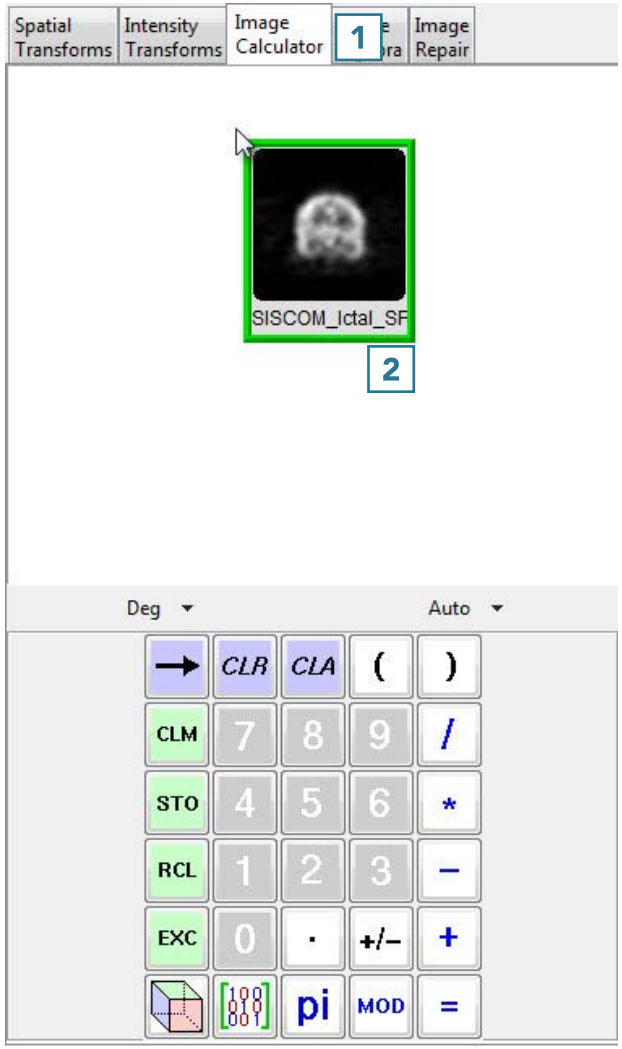
The Image Calculator tool allows many mathematical functions to be applied to volumes, matrices and constant numerical values, including basic arithmetic operations, trigonometric functions and logic operators.

# 8. Creating a Difference Map

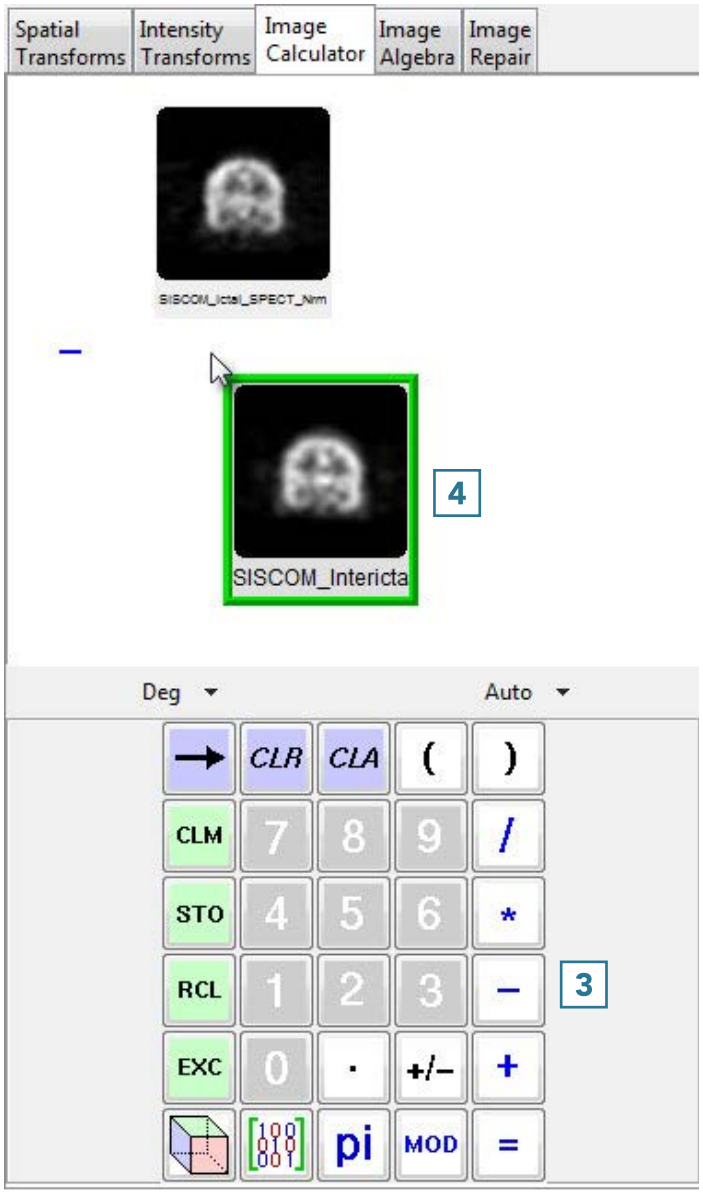
This exercise will show how to create a difference map showing the areas of higher blood flow to the brain during an epileptic seizure. Interictally (in a non-seizure state), many epilepsy patients exhibit hypoperfusion in the region of the seizure focus. Ictally (during seizure), radiotracers can be injected to produce an image of cerebral perfusion patterns. The difference map between the ictal and interictal SPECT data sets can be used to determine the region of increased activation during seizure.

- The SPECT data inputs for this exercise have already been registered and normalized so that they can be compared.
- Open Transform and navigate to Image Calculator. 1
- Drag and drop the ictal data set into the calculator window. 2

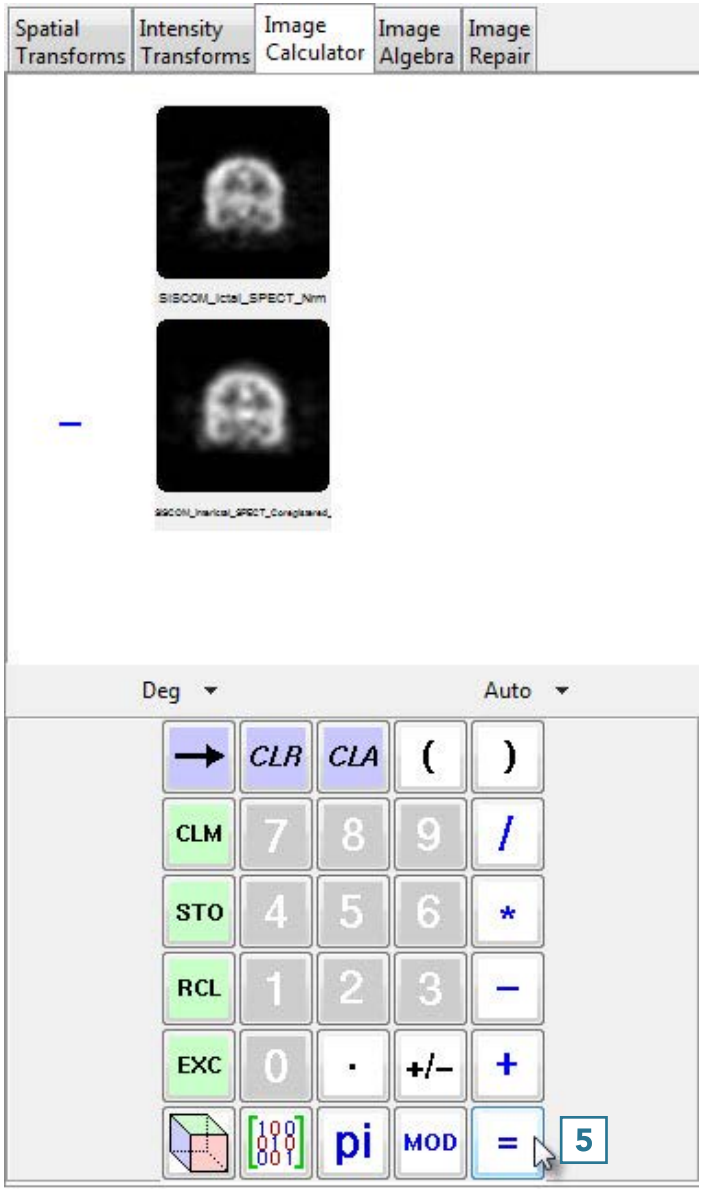
Download the SISCOM_Ictal_SPECT_Nrm and SISCOM_Interictal_SPECT_Coregistered_Nrm data sets to follow along http://analyzedirect.com/data/



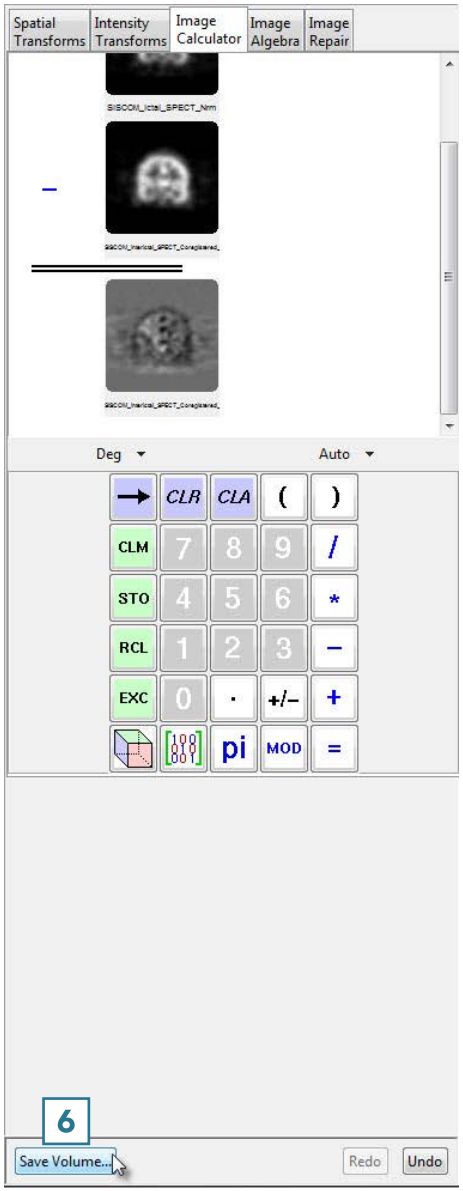
- Press the minus key. 3
- Drag and drop the interictal data set into the calculator window. 4



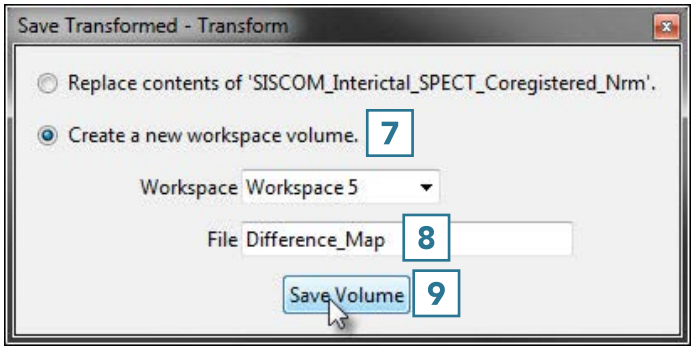
- Press the equals key 5 to complete the subtraction.



- Click Save Volume 6 to save the difference map.



- In the Save Transformed window, choose to create a new workspace volume 7 and rename. 8
- Click Save Volume. 9
- Close Transform.



# Image Algebra

Image Algebra performs mathematical operations on volumes and constant numerical values by means of an algebraic formula parser. There are several useful formulas preloaded, as detailed in the table below.

## Table 6.6: Preloaded Image Algebra Formulas

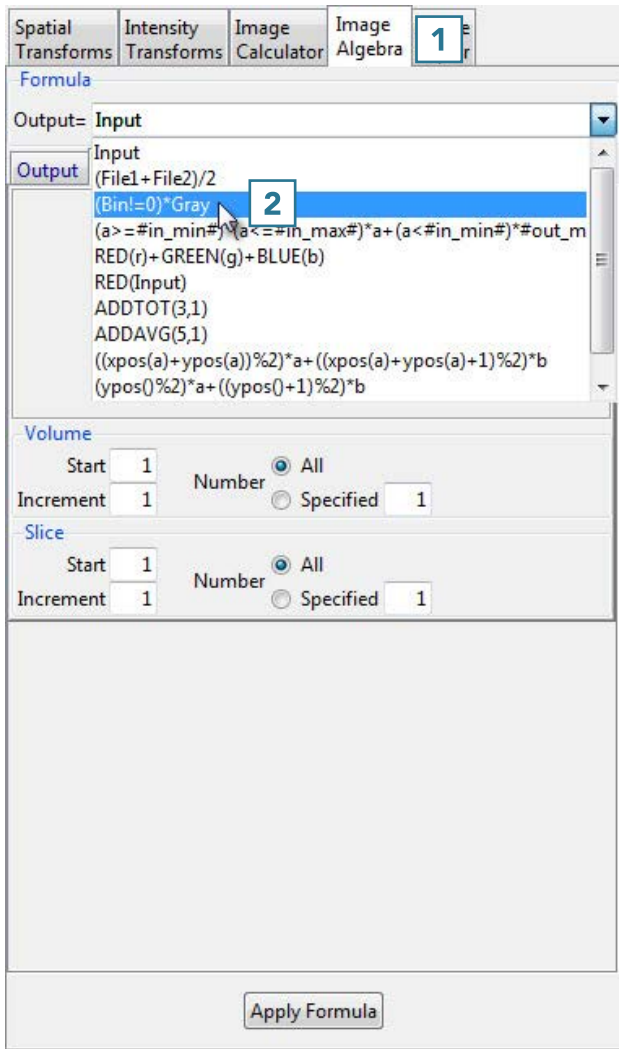
| Formula | Output= |
|---|---|
| Copy a File | Input |
| Average Two Files | (File1+File2)/2 |
| Binary times Grayscale | (Bin!=0)*Gray |
| Grayscale Thresholding | (a>=#in_min#)*(a<=#in_max#)*a+(a<#in_min#)*#out_min#+(a>#in_max#)*#out_max# |
| Create 24-bit | RED(r)+GREEN(g)+BLUE(b) |
| Extract the Red Channel | RED(Input) |
| Use Total of 3 slices | ADDTOT(3,1) |
| Use Average of 5 slices | ADDAVG(5,1) |
| Pseudo Transparency | ((xpos(a)+ypos(a))%2)*a+((xpos(a)+ypos(a)+1)%2)*b |
| Row Interlace | (ypos()%2)*a+((ypos()+1)%2)*b |
| Intensity Clipping | ((a<#min#)*#min#)+(((a>#max#)*#max#)+((a>=#min#)*(a<=#max#))*a) |

# 9. Applying a Binary Mask to a Grayscale Volume

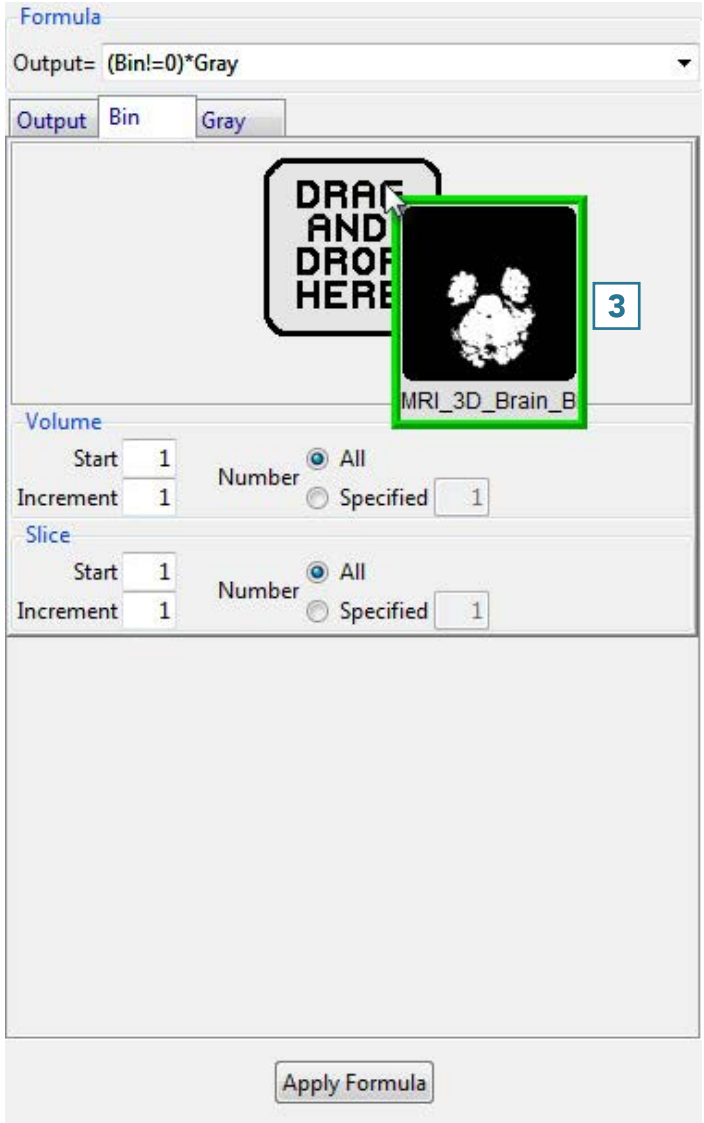
This exercise demonstrates how to multiply a grayscale data set with a binary data set. The binary brain will act as a mask; all voxels in the grayscale data set that fall within the binary mask will be kept, while the voxels that fall outside will be removed.

- Open Transform and navigate to Image Algebra. 1
- From the formula drop-down, select the third option down: (Bin!=0)*Gray. 2

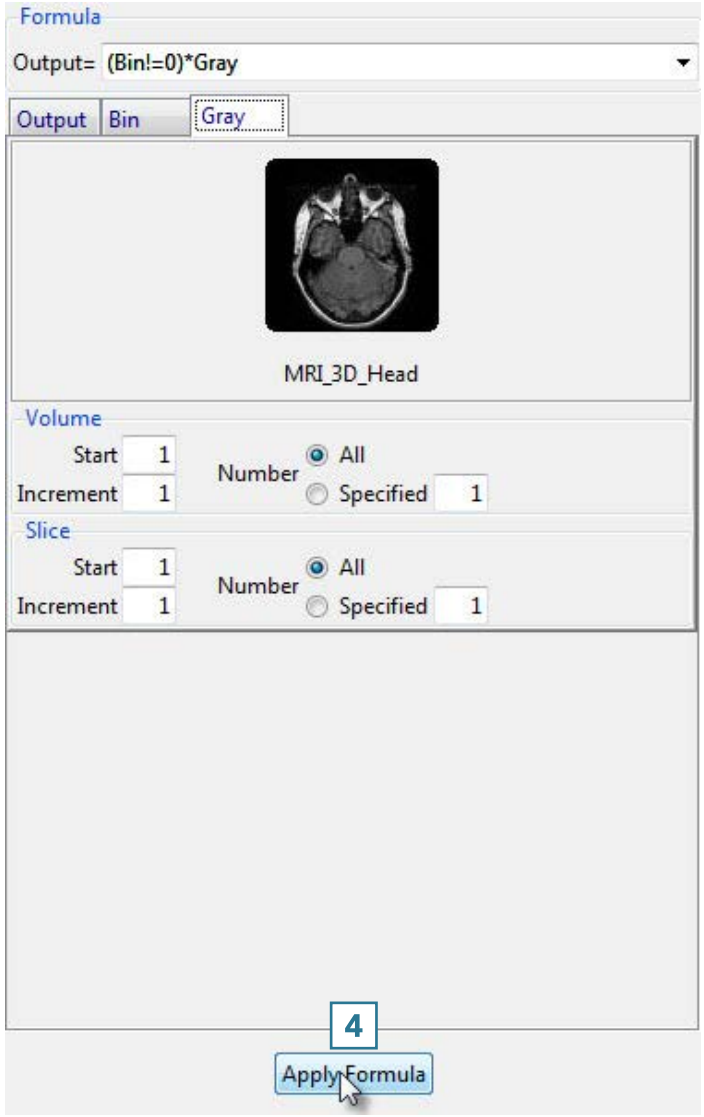
Download the MRI_3D_Head and MRI_3D_Brain_Bin data sets to follow along http://analyzedirect.com/data/



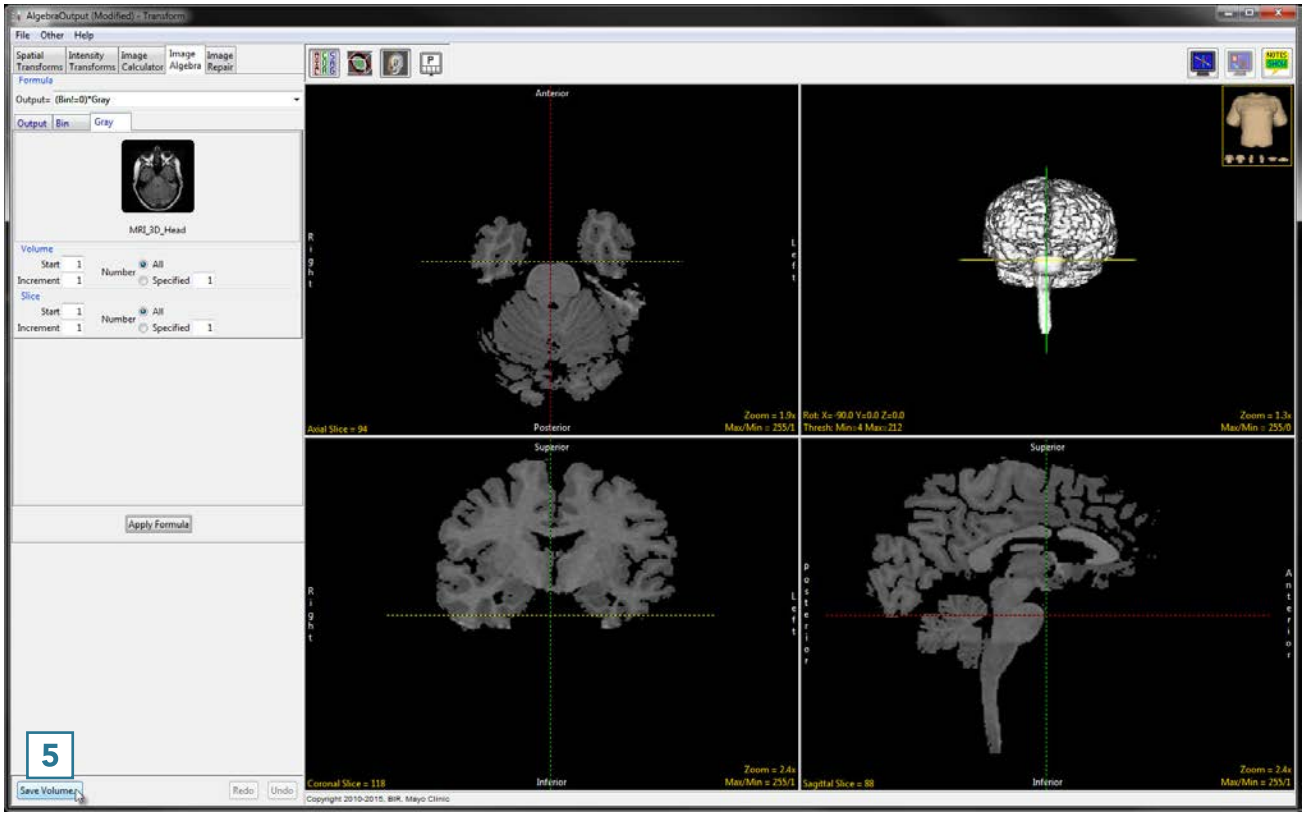
- The input variables will appear as tabs labeled with the variable names.
- Drag and drop the binary data set into the designated space on the Bin tab. 3
- Do the same with the grayscale data set on the Gray tab.



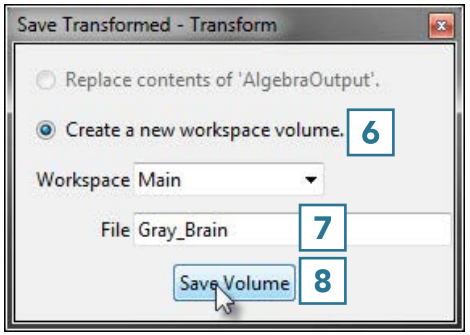
- Once both data sets are loaded into Image Algebra, click the Apply Formula button. **4**



- The result is shown to the right.
- Click Save Volume **5** to save the masked data set.



- In the Save Transformed window, choose to create a new workspace volume 6 and rename. 7
- Click Save Volume. 8
- Close Transform.



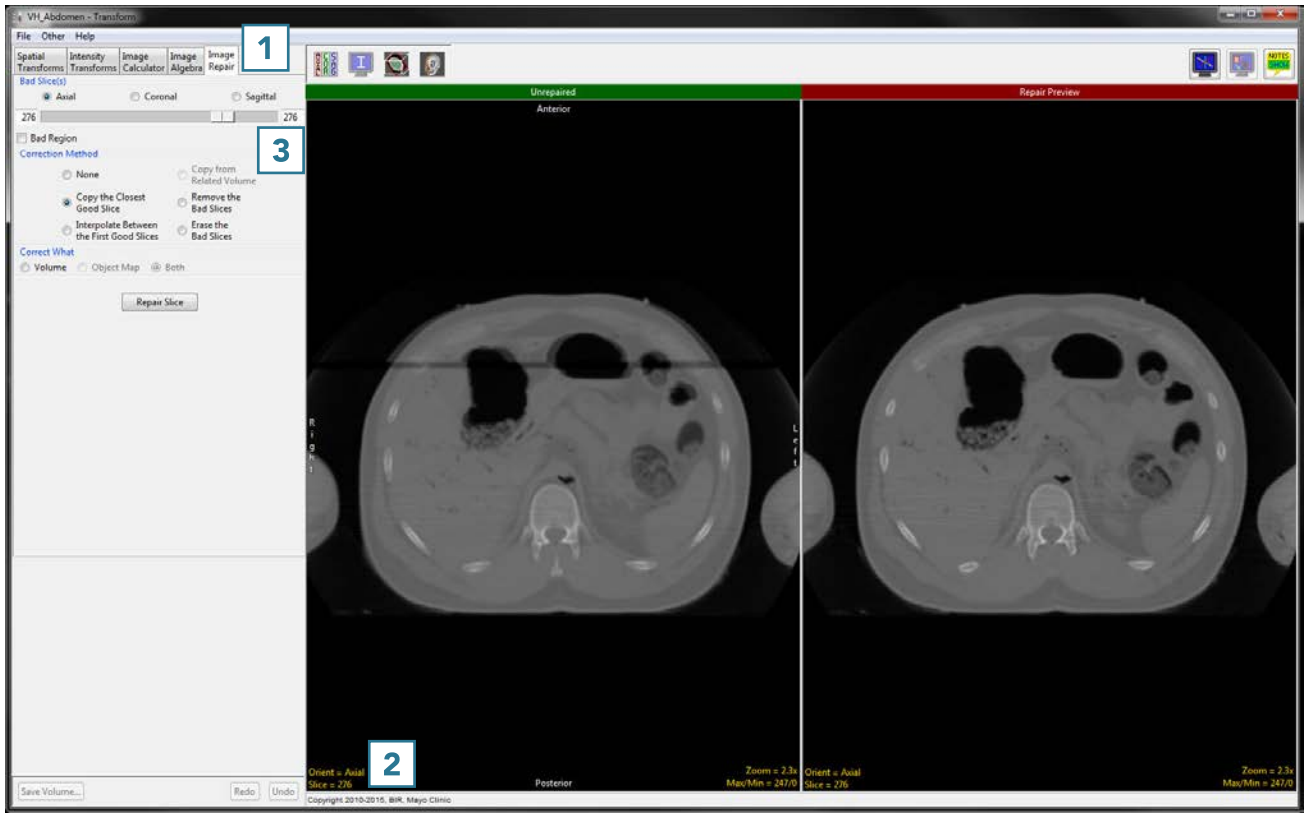
# Image Repair

The Image Repair tool includes the ability to designate bad slices or subregions that can be repaired by copying voxels from neighboring slices, interpolating across neighboring slices, copying from a related volume or removing bad regions from the volume. Subregion repair includes the ability to blend voxels at the edge of the region.

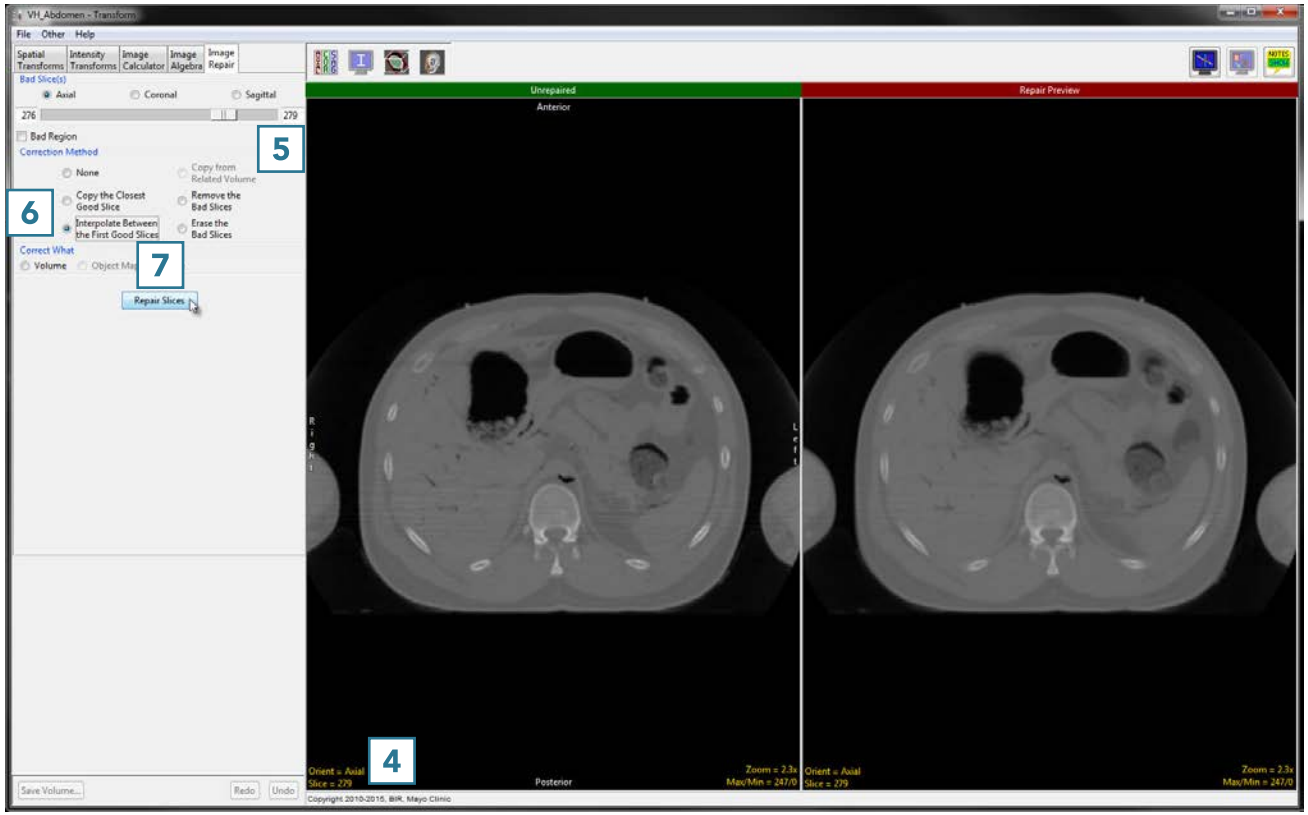
# 10. Repairing an Image

- Open Transform and navigate to Image Repair. 1
- Navigate to the first corrupt slice in the data set, which for this example is slice 276. 2
- Move the lower limit of the bad slices slider bar to 276. 3

**Download the VH_Abdomen data set to follow along http://analyzedirect.com/data/**

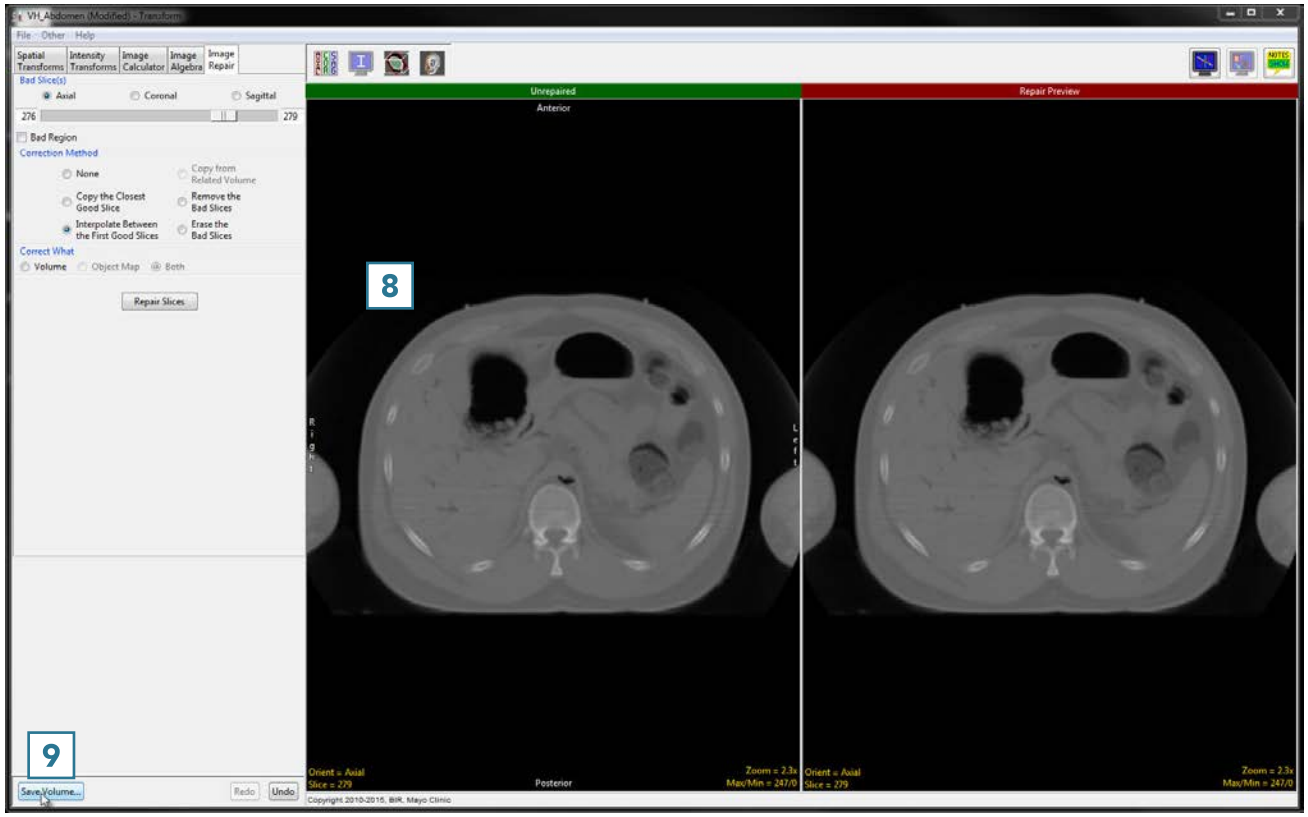


- Navigate to the last corrupt slice in the data set, which for this example is slice 279. 4
- Move the upper limit of the bad slices slider bar to 279. 5
- Set the correction method to Interpolate Between the First Good Slices. 6
- Click Repair Slices 7 to apply the correction.

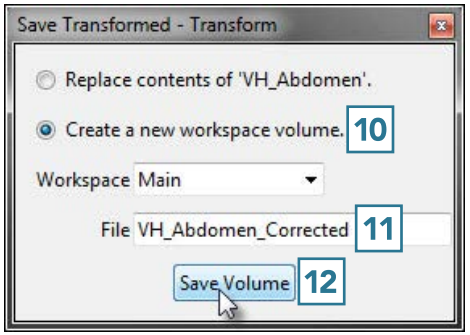


Note that the repaired version now appears on the left side of the window. 8

- Click Save Volume 9 to save the corrected data set.



- In the Save Transformed window, choose to create a new workspace volume 10 and rename. 11
- Click Save Volume. 12
- Close Transform.



# Segment

# Introduction

The goal of segmentation is to partition an image into regions, or objects, that are homogeneous with respect to one or more characteristics or features. Segmentation is a critically important tool for the processing of image data and is often the precursor to other applications such as measurement, visualization, surface-based registration and surface extraction.

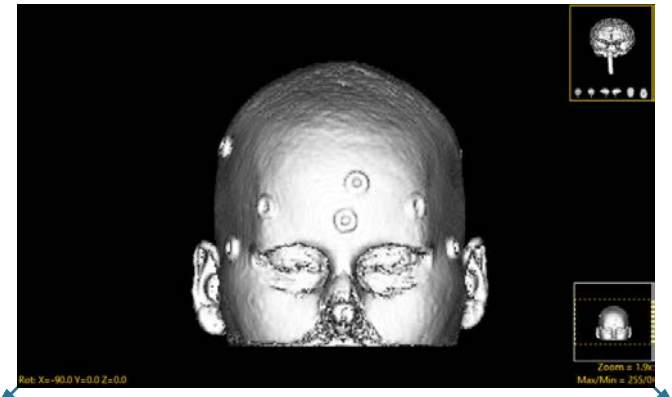
## Object Maps

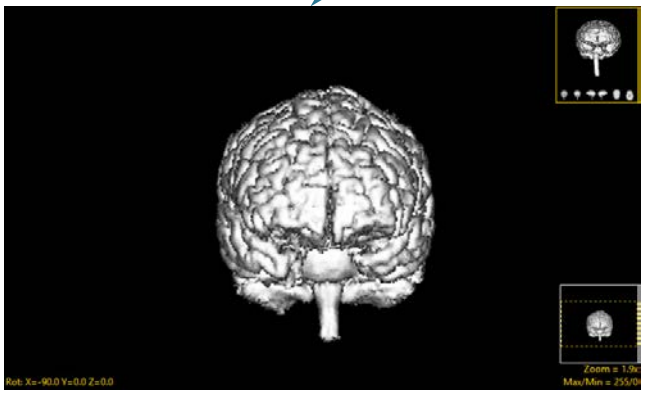
AnalyzePro uses a file called an object map to partition image data into groups of voxels within a segmentation component map. After creation of the object map through segmentation, it can be used to drive visualization, registration, surface generation and statistical analysis.

The object map is an associated volume with the same dimensions as the image data. Each voxel of the object map contains an 8-bit value which encodes it as belonging to 1 of 256 total possible objects. Every voxel in the data set is initially assigned to the first object (Original), leaving 255 additional objects that can be used for 2D region or 3D volume of interest definition.

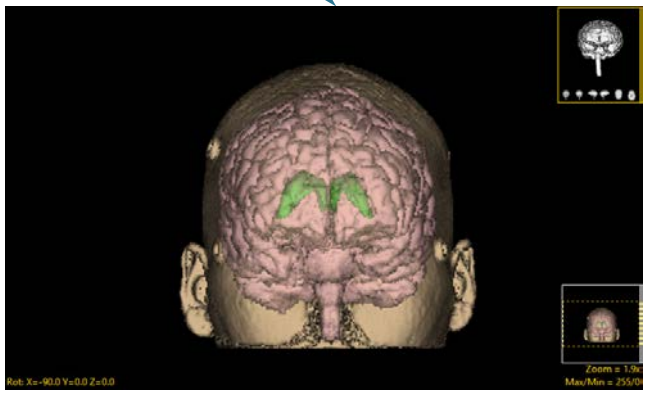
Object maps are loaded separately from the image data to which they are associated using the File > Load Object Map option in each functional module. When the object map is loaded, the objects defined in it are overlaid on the image data.

## Object Map Segmentation vs. Grayscale Segmentation



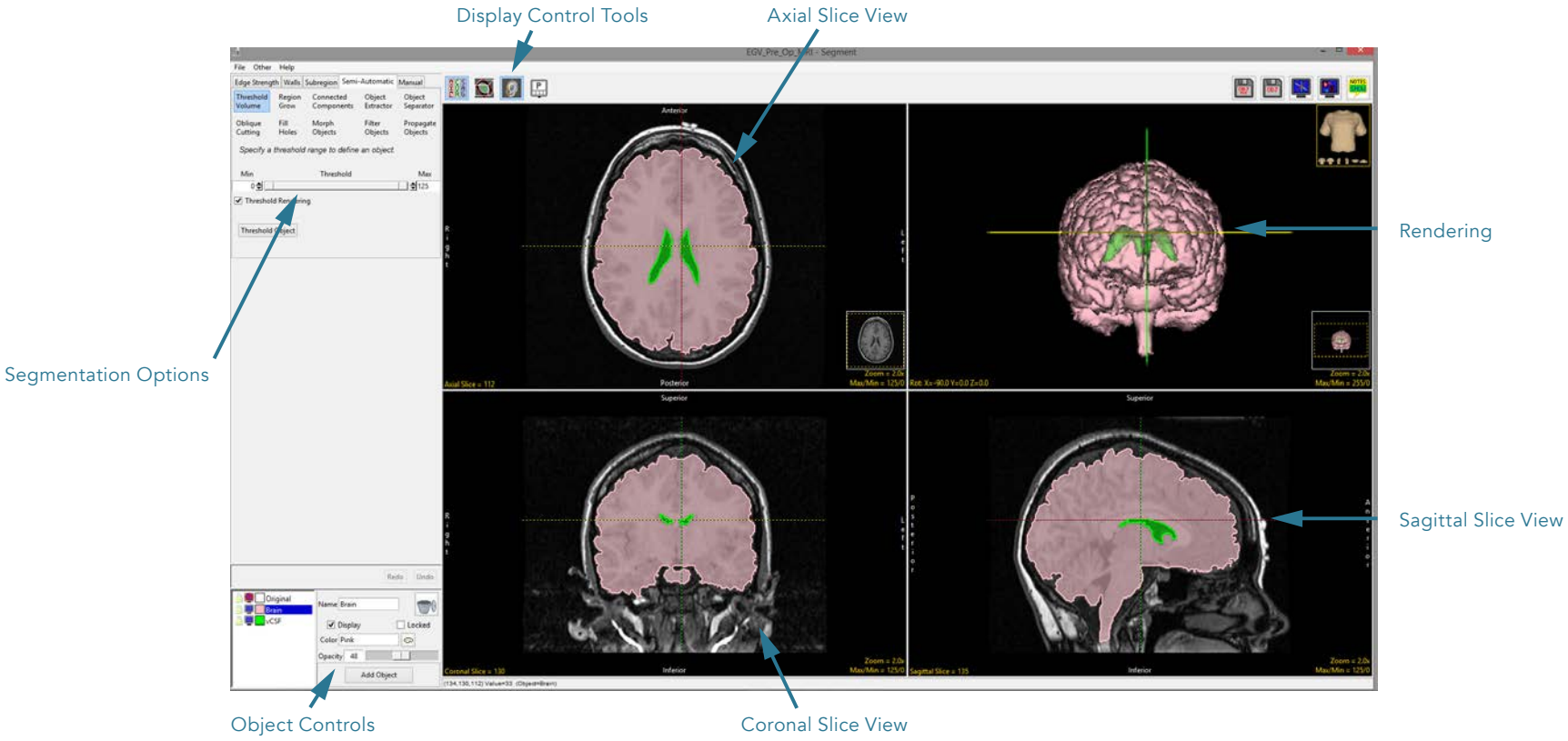


Grayscale segmentation destroys all voxels that are not part of the object of interest.



Object maps preserve the original data by assigning the segmented voxels to objects.

## Segment Overview



# Segmentation Options

The segmentation options are provided in five tabs:

- Edge Strength
- Walls
- Subregion
- Semi-Automatic
- Manual

These five tabs provide access to all the segmentation tools in Segment. The segmentation tools within each tab will be discussed in this section.

## Rendering

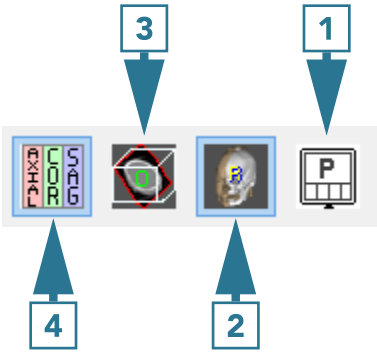
The render window provides an interactive 3D display of the segmented image data. For more information about the render window, refer to Display.

## Slice

The orthogonal slice display windows provide an interactive 2D review tool of the slice data in the axial, coronal and sagittal planes. For more information about the slice display windows, refer to Display.

## Display Control Tools

The Display Control tools allow users to control and customize the layout of the Segment display area. Some of these control options are unique to Segment.




1 Controls Layout

2 Toggle Rendering

3 Toggle Oblique

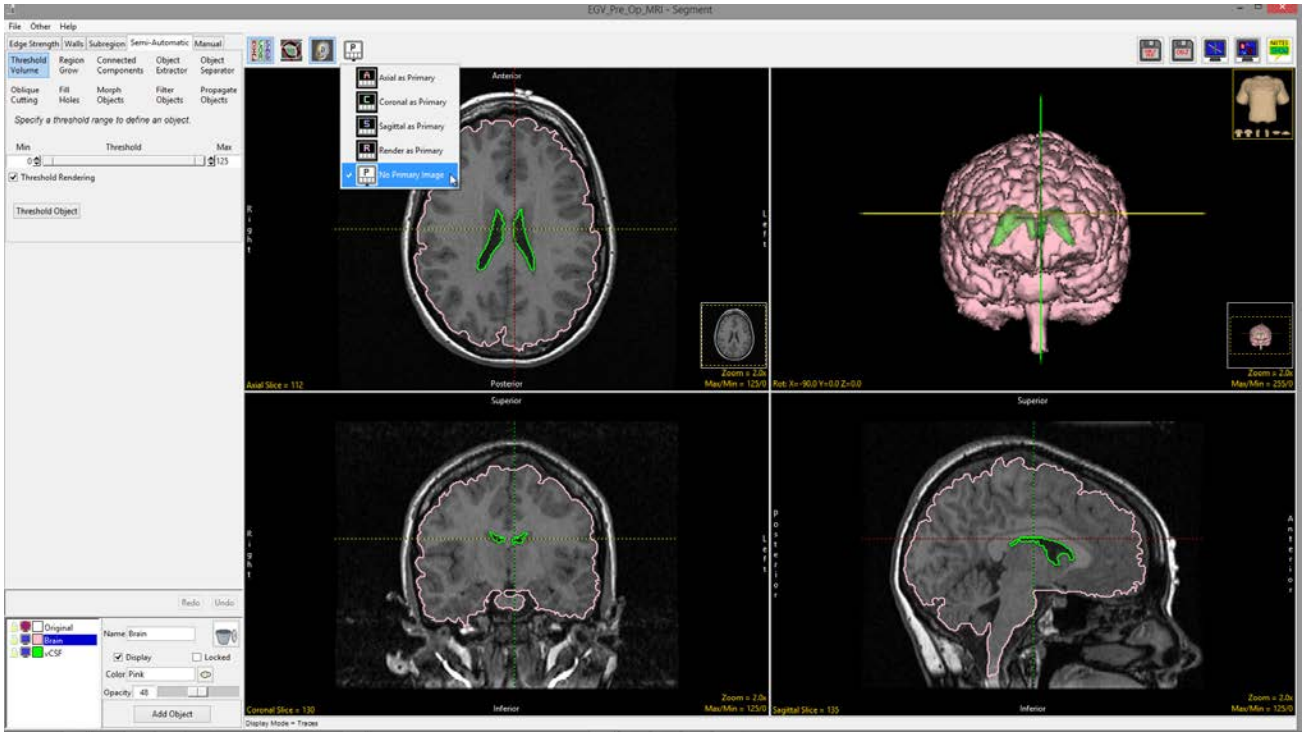
4 Toggle All Orientations

## Control Layout

This option allows users to control the layout of the display. Choose from Axial as Primary, Coronal as Primary, Sagittal as Primary, Render as Primary or No Primary image.

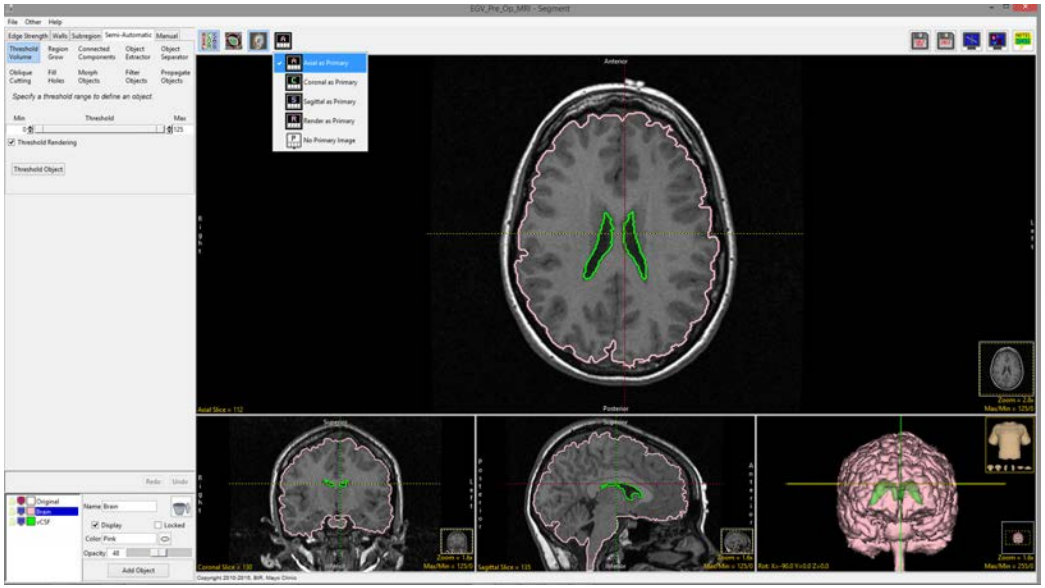
## No Primary Image

This is the default selection. This option displays the rendering and three orthogonal views in four equally sized windows.



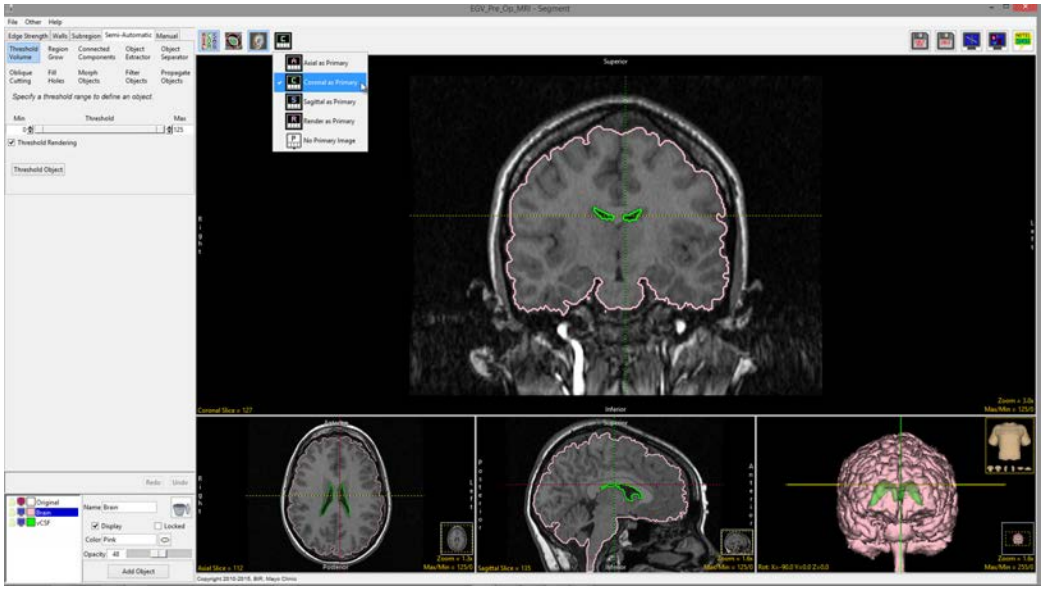
### Axial as Primary

Focuses the display on the axial image. The coronal, sagittal and rendering windows are displayed below the axial window.



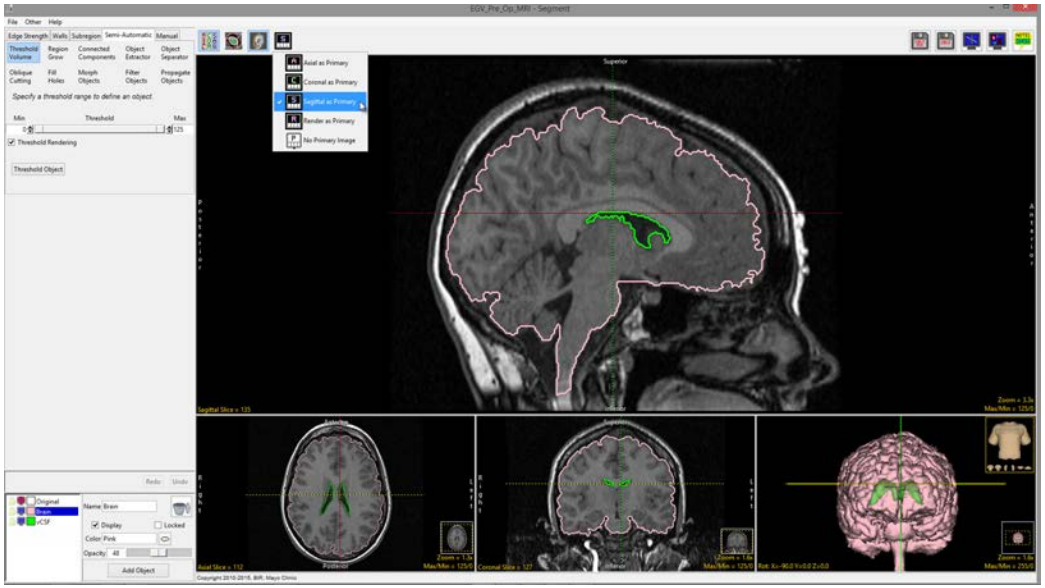
### Coronal as Primary

Focuses the display on the coronal image. The axial, sagittal and rendering windows are displayed below the coronal window.



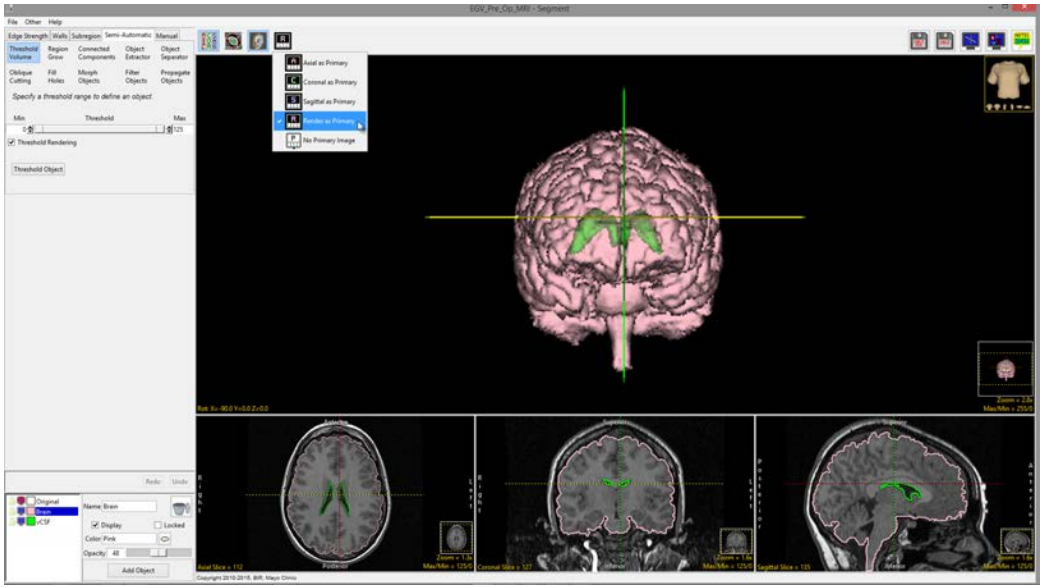
### Sagittal as Primary

Focuses the display on the sagittal image. The axial, coronal and rendering windows are displayed below the sagittal window.



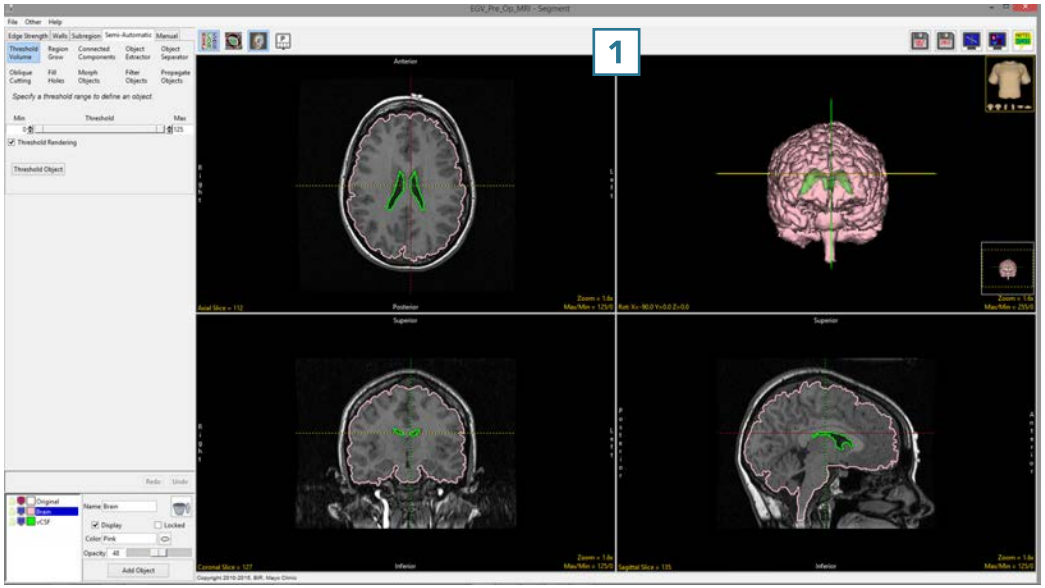
### Render as Primary

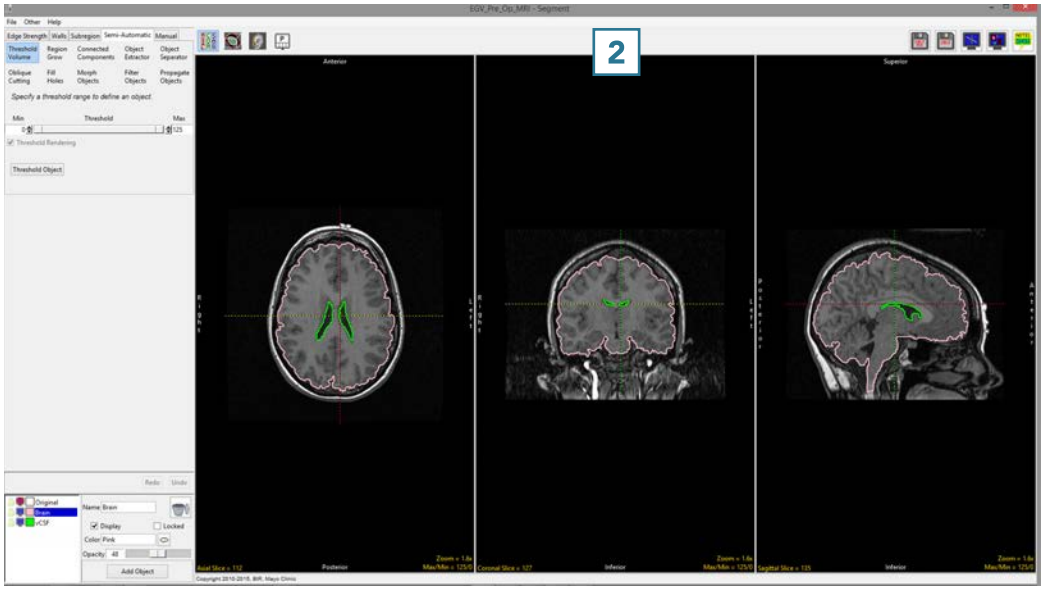
Focuses the display on the rendering. The axial, coronal and sagittal windows are displayed below the rendering.



## Toggle Rendering

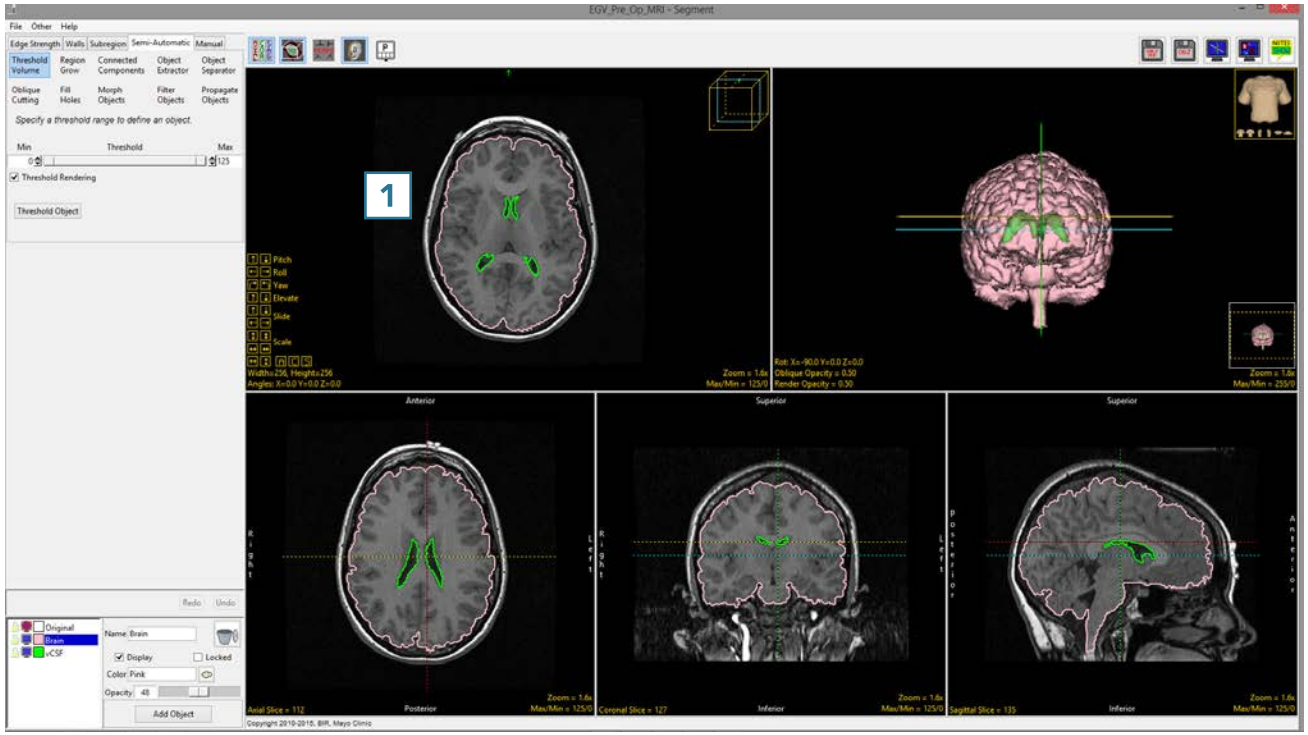
The Toggle Rendering options allows users to switch the Render window on 1 and off. 2



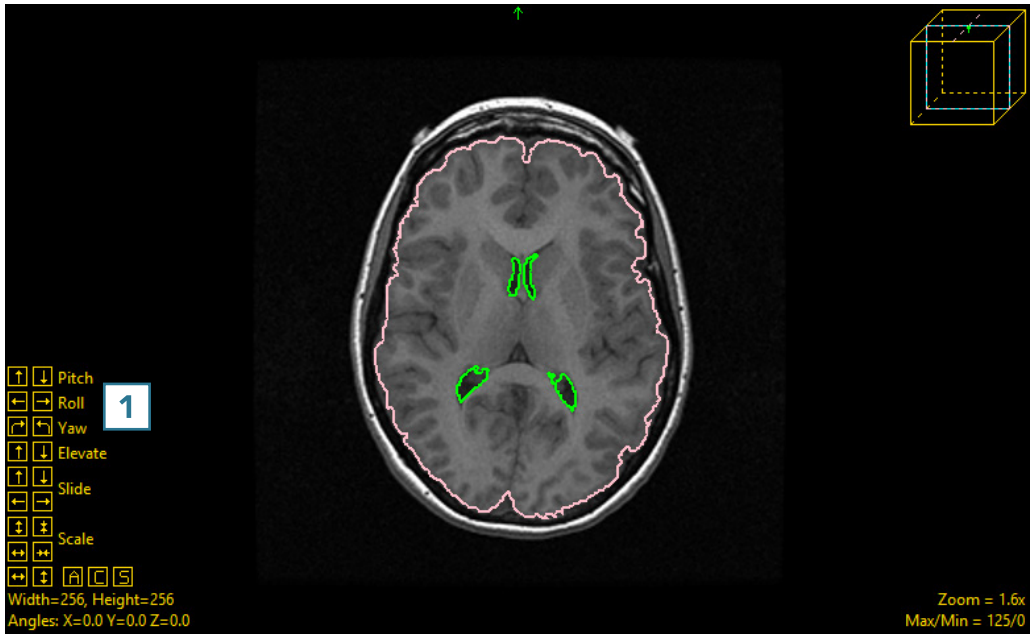



## Toggle Oblique

The Toggle Oblique option allows users to switch the oblique display window 1 on and off.

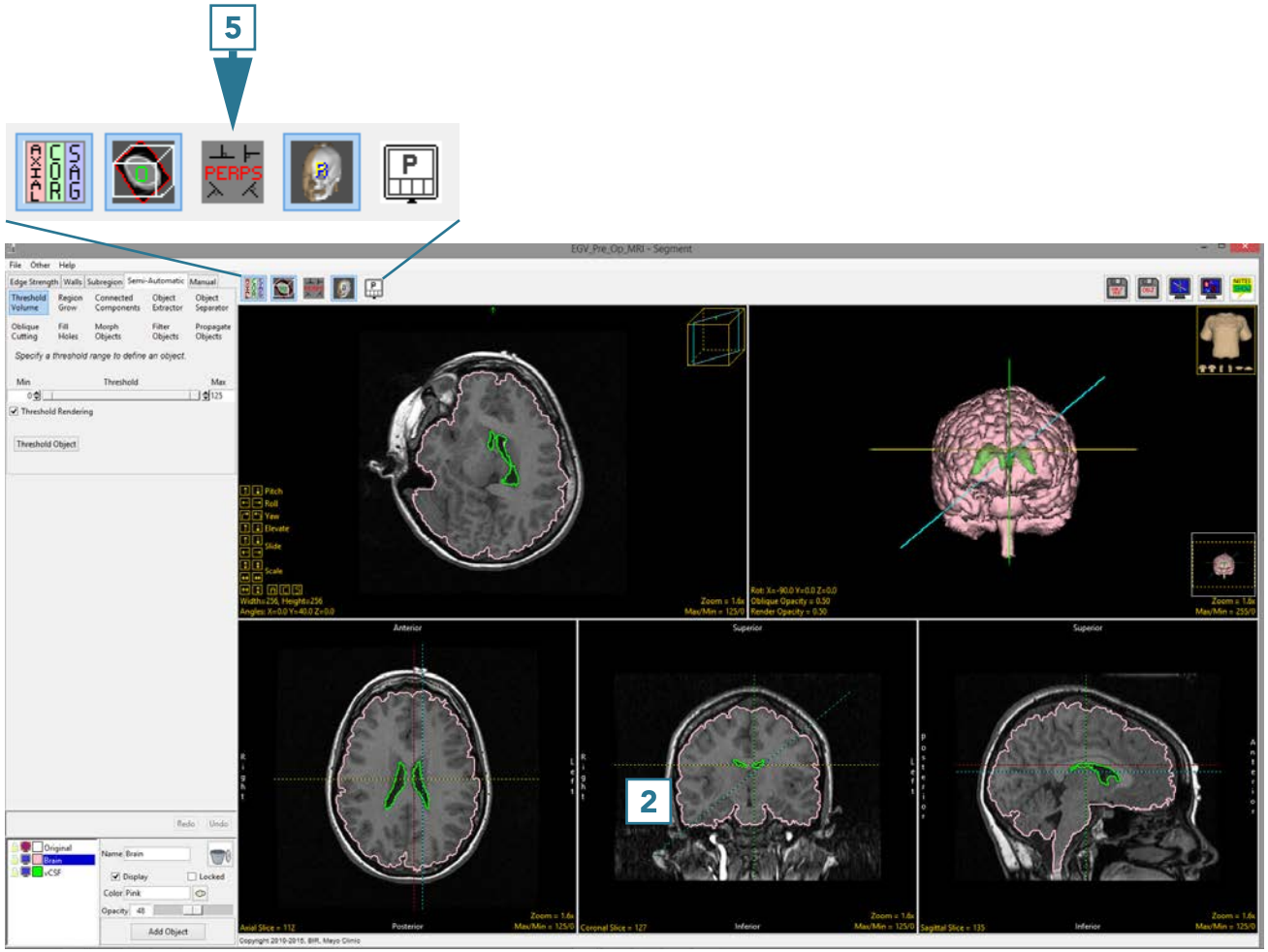


The oblique window provides users with the ability to create any arbitrary oblique plane on the fly, using the control tools in the oblique window. 1



The oblique image can also be generated using the blue oblique reference line that appears in all of the other enabled windows. 2

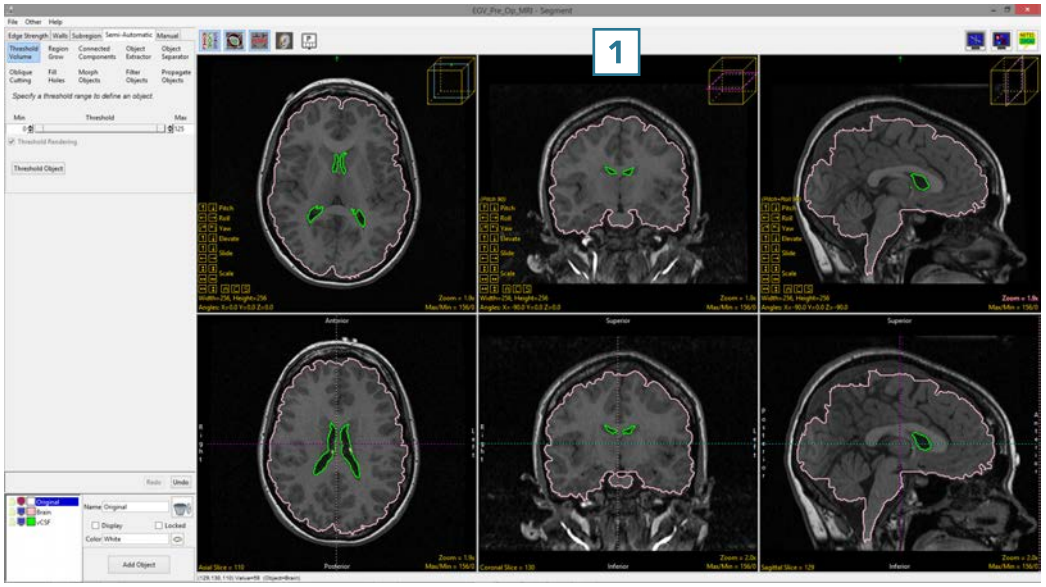
When the oblique image is enabled, an additional option becomes available: Toggle Perpendicular. 5

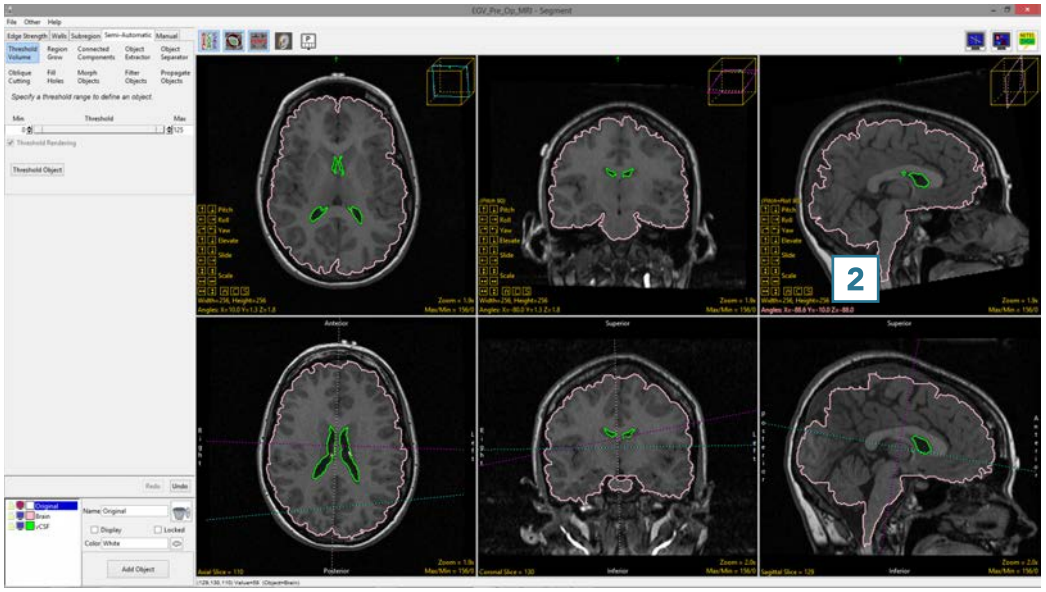


## Toggle Perpendicular

The Toggle Perpendicular window provides an oblique control window for each orientation. 1


The control tools 2 can be used to manipulate each orientation to aid users with the generation of the desired oblique plane.

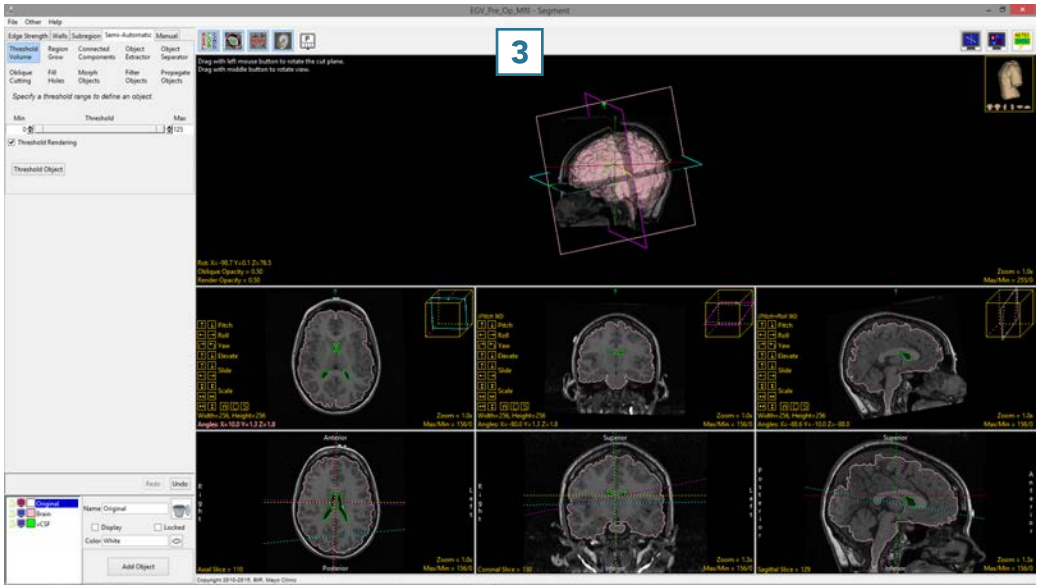


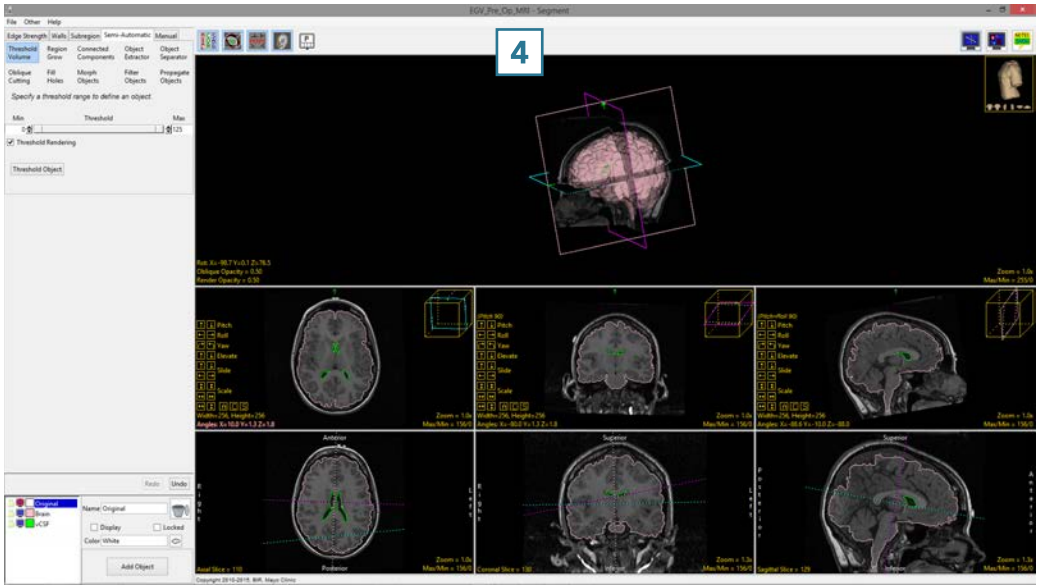



When enabled, the perpendicular displays can be viewed with the Rendering toggled on. 3 While this option is up to the user, some users find the oblique reference lines displayed on the 3D rendering helpful when manipulating the oblique plane in 2D.

Users may also find it useful to switch off the linked cursor tool 4 when using the oblique reference lines.

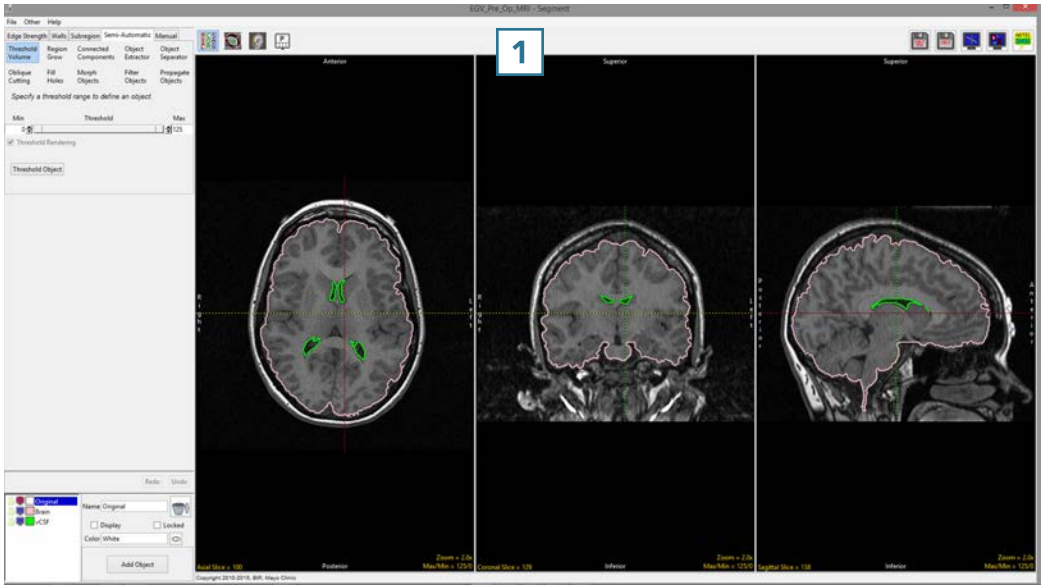
For more information about creating oblique planes, refer to the Apply Matrix exercise in the Transform section.

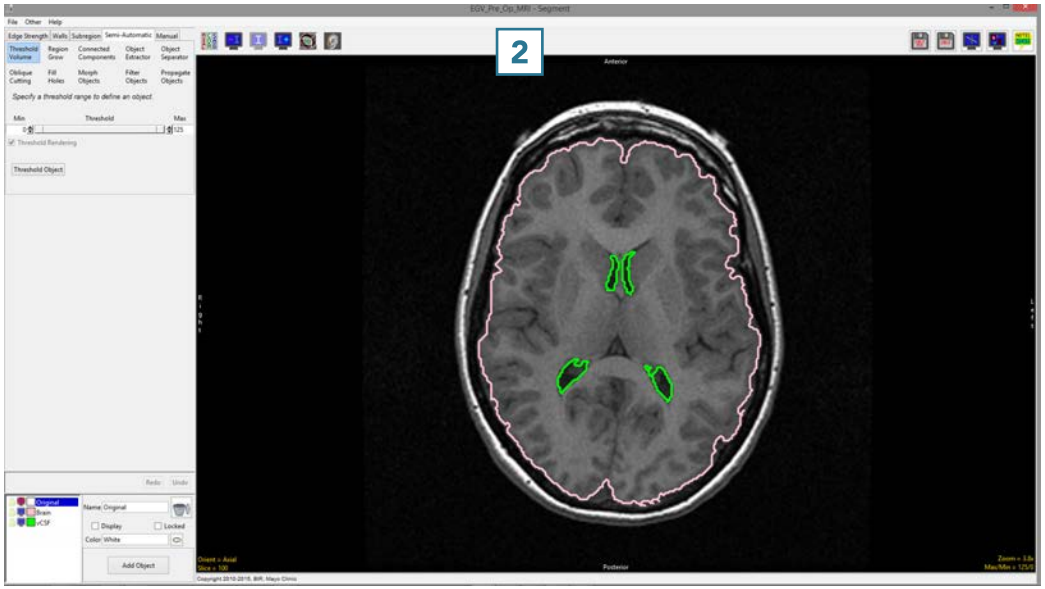


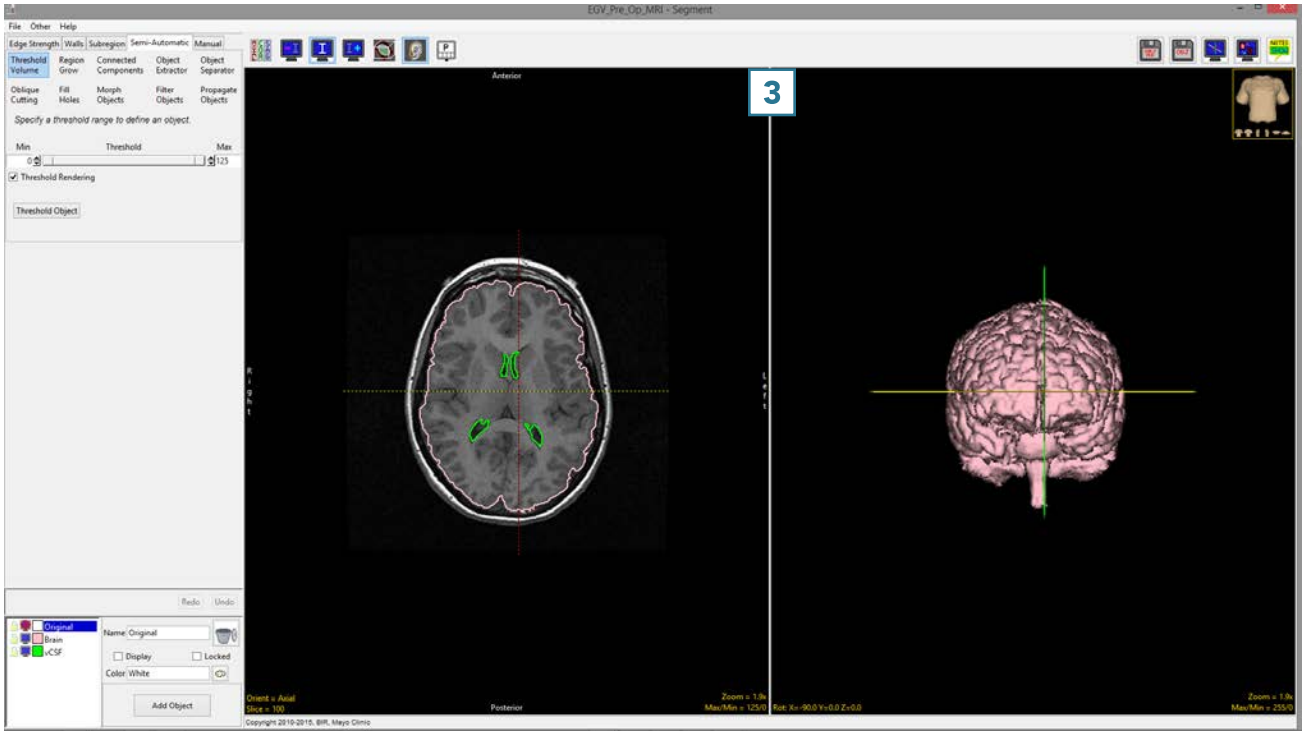
## Toggle All Orientations

The Toggle All Orientations option allows users to switch between the display of the axial, coronal and sagittal 1 windows to a single image window. 2

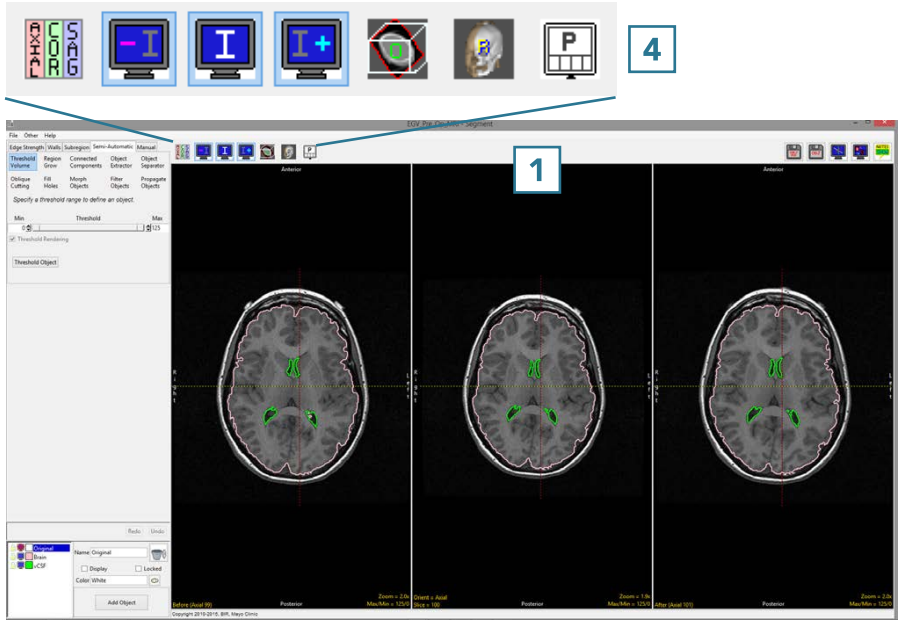


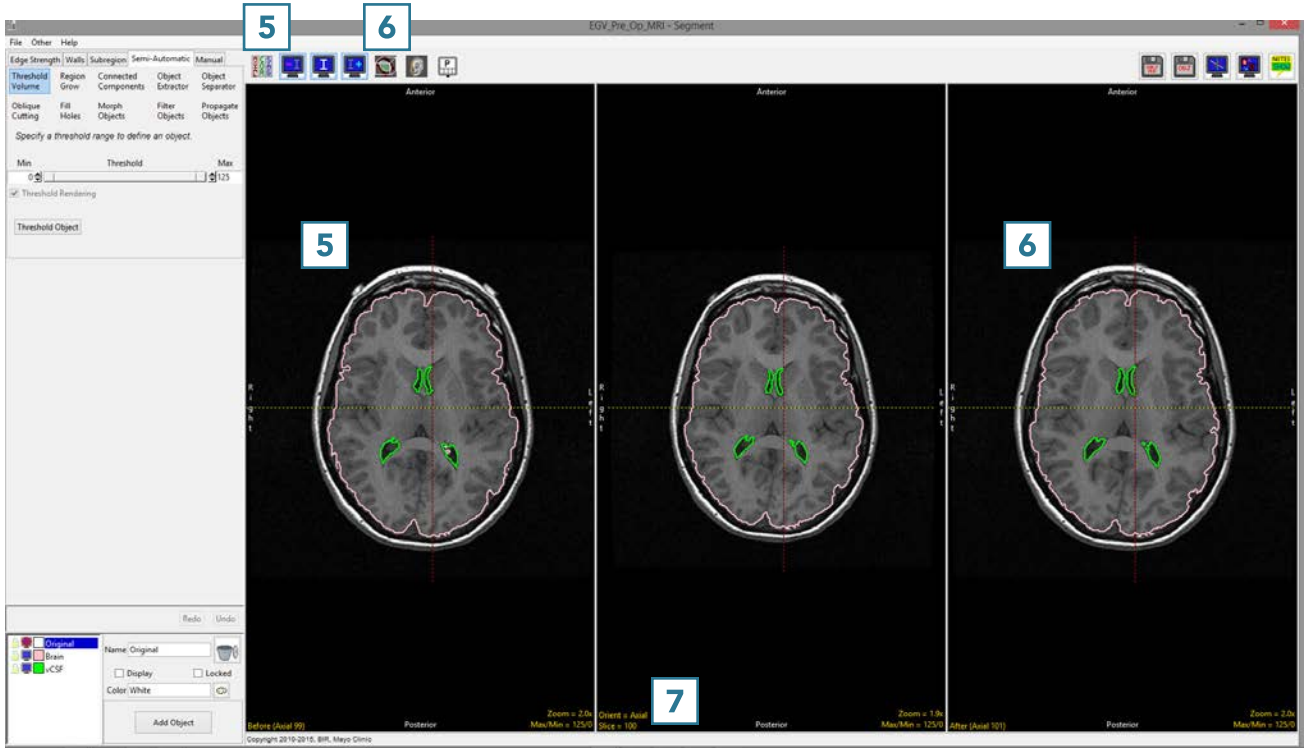
When the rendering is enabled, the 3D rendering will also be displayed. 3



When display is toggled to single display mode, 1 additional display options are enabled. 4



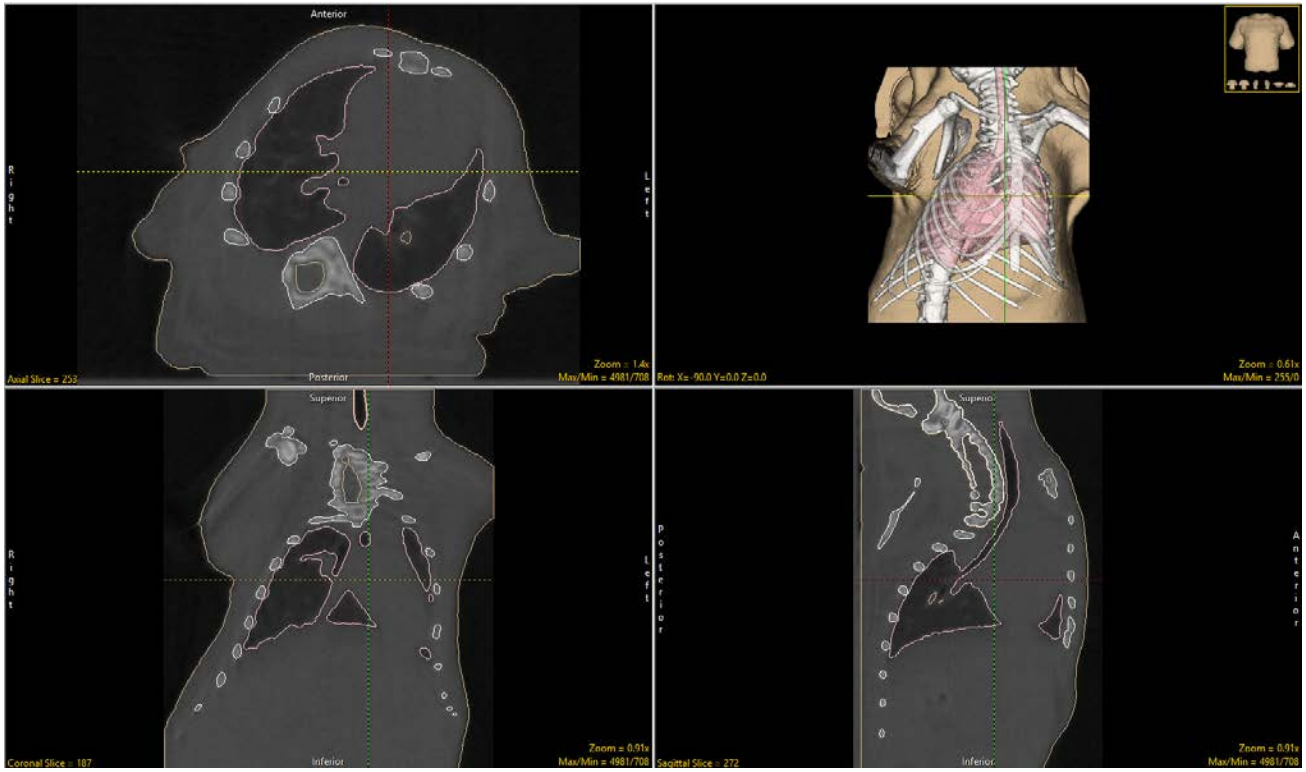
The additional options allow users to display the image before 5 and after 6 the current slice. To display another orientation, click on the Orient text 7 to cycle through the orthogonal orientation displays.



# Cursor Link

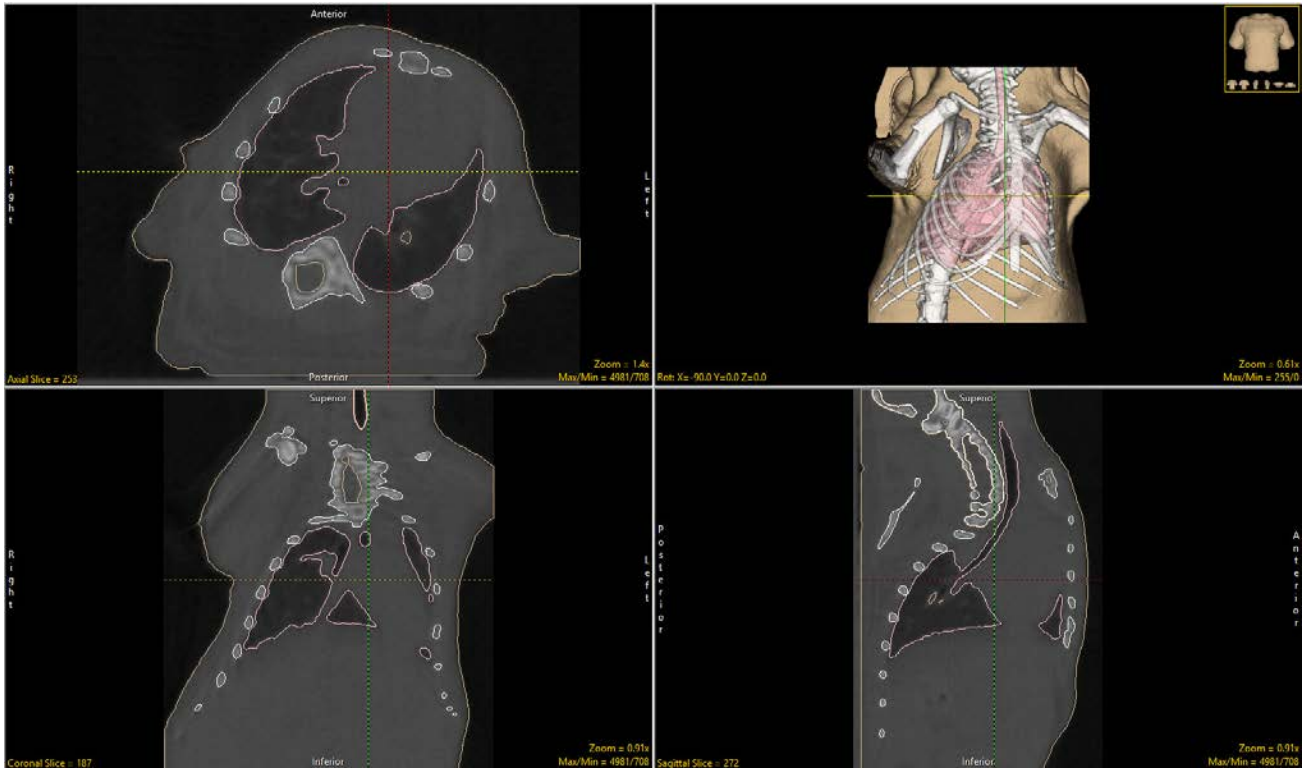
The cursor link allows users to interactively navigate through the image data. The tool can be controlled from any of the 2D orientations or from the 3D rendering. Moving the tool will interactively update the corresponding slice displays.

The linked cursor can be enabled or disabled using the Toggle Cursor Link button.



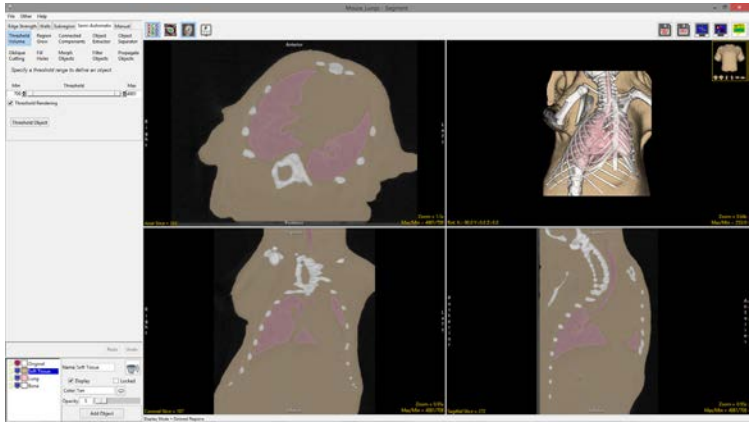
# Toggle Region Display

Users have the option to change the display of objects on the 2D slices. Users can cycle through the various object display options using the Toggle Region Display button or using the t key.

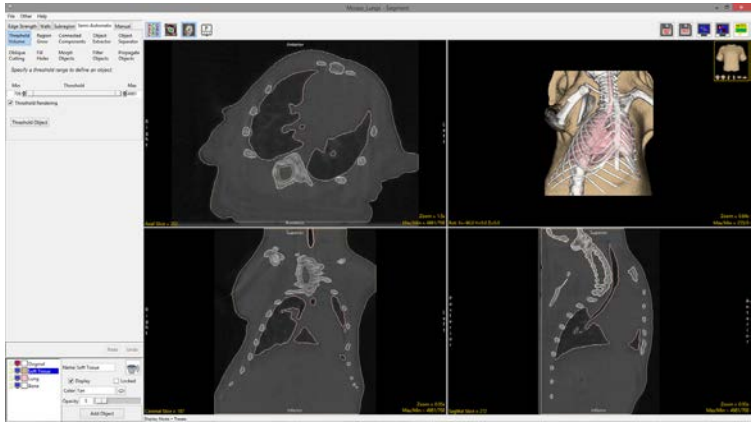


# There are four object display options:

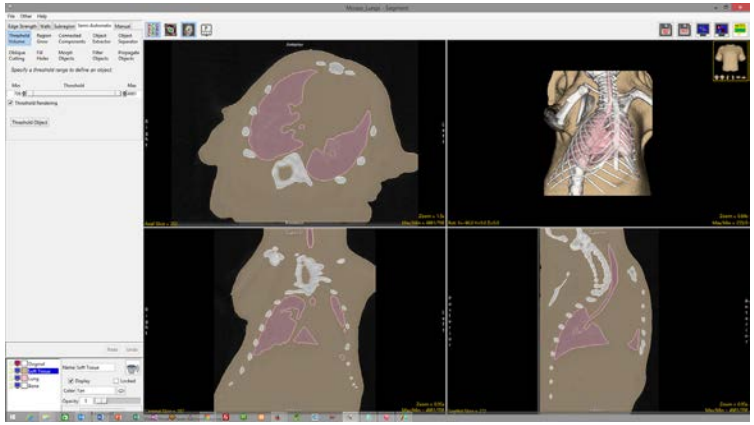
## Filled Regions



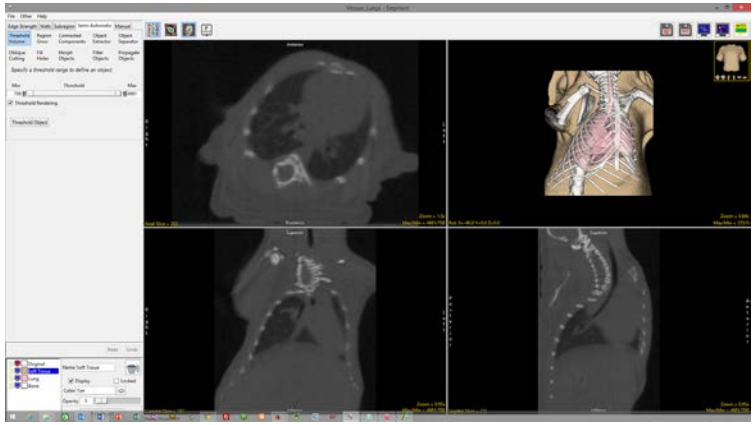
## Edges



## Both



## Off



# Notes

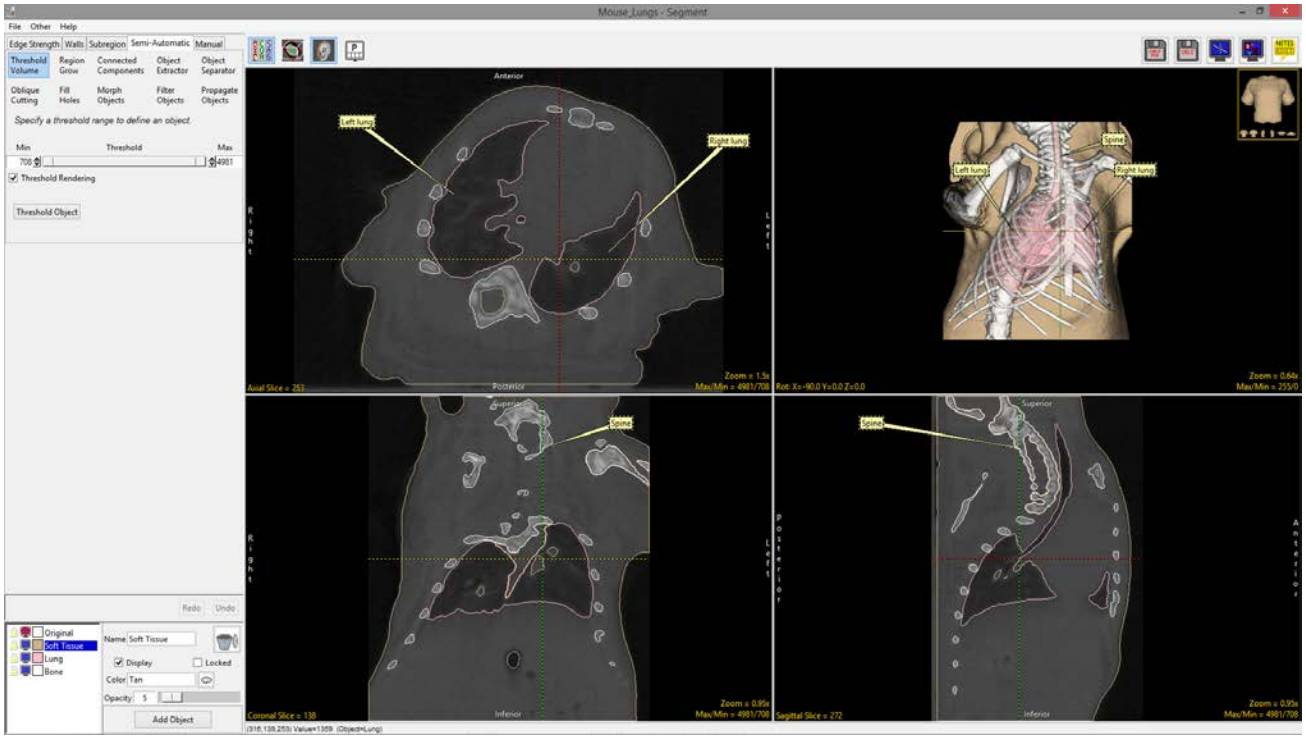
The Notes tool in AnalyzePro allows users to annotate image data in 2D or 3D. Notes will be associated with the data set and can be loaded into other modules. Notes can be hidden or deleted at any time.


Shows notes (default).


Allows users to make and edit notes.


Hides notes.

To annotate a data set using notes click on the Notes button in the toolbar. (Note that the Edit mode will be activated.) Click on any 2D slice or the 3D rendering to create a note.



### Save Object Map As

Allows users to save an object map as a new object map. This is helpful for creating copies of the original object map for editing.

### Save Object Map

Allows users to quickly save edits made to the current object map. This option will overwrite the loaded object map. Use caution when using Save Object Map.

## Object Controls

The AnalyzePro object controls allow users to edit object properties on the fly. The object control window allows users to edit the following object attributes:

The Name field 1 allows users to rename objects from the default assigned names.

The Color option 2 allows object color to be changed from the default color assigned to the object. The color can be edited by typing a color name in the text entry field or by selecting a color using the color picker, which can be reached by clicking the colored square next to the object name in the object list.

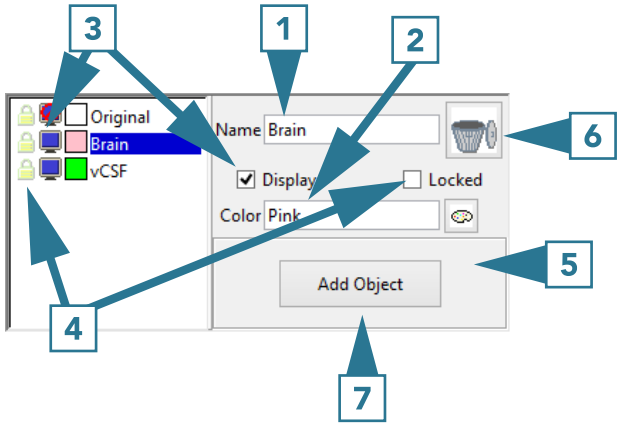
Object Display 3 can be switched on or off by checking or unchecking the Display checkbox or the monitor icon next to the object in the object list.

Object Lock 4 provides the ability to lock objects, which is a powerful segmentation technique. Locking an object protects objects from being written over. When an object is locked, the boundary of the object acts as a limit. This can be leveraged to help with the segmentation of objects that are spatially connected. Some semi-automatic tools do not observe locked objects. Before such a tool is used, a dialog box will appear notifying the user of this.

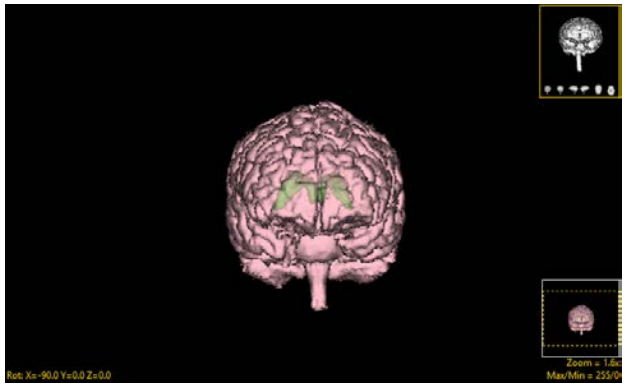
Opacity: 5 Right-clicking on the rendering and choosing Transparency allows the opacity of each object to be manipulated to enhance display of objects. Object opacity can be manipulated by using the opacity slider or by entering a value in the text field.

Delete 6 allows users to remove objects. Voxels assigned to an object that is deleted are reassigned back to the Original object.

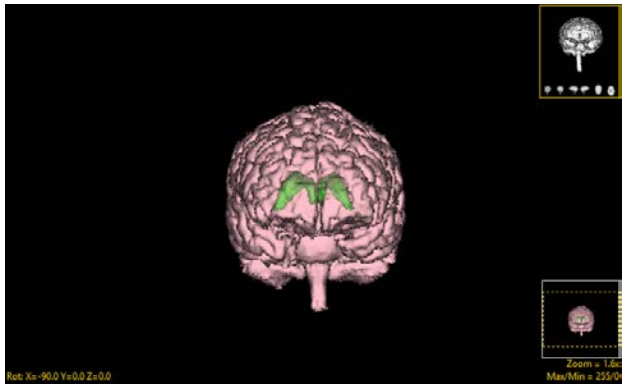
Add Object 7 button allows users to add new objects to the object map.



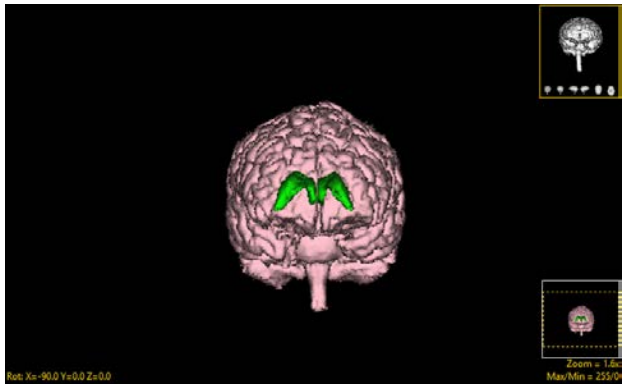
The effect of changing the opacity level of the brain parenchyma object.



70%



50%



5%

# Edge Strength

The Edge Strength option allows users to mask the input data with a set of enhanced gradients that act as limits aiding in the segmentation of structures. Edge strength works by applying a 3 X 3 X 3 Sobel filter to the image data, which can be interactively adjusted using the Edge Strength Threshold slider. All voxels with gradient values less than or equal to the selected threshold value are displayed in red and form boundaries around structures. The boundaries act as limits, restricting semi-automatic segmentation operations.

# 1. Using Edge Strength In Segmentation

First we will attempt to segment the heart from this CT data set without using edge strength.

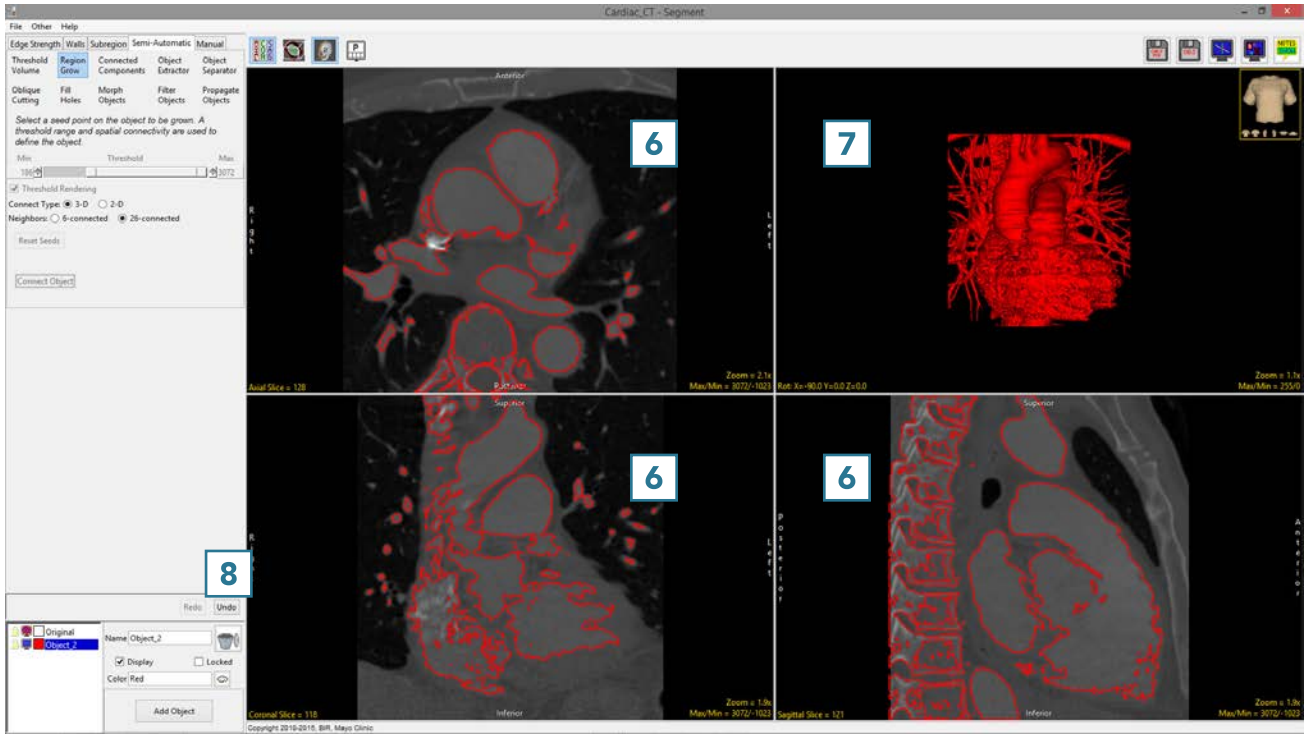
- Select a data set and open Segment.
- Select Semi-Automatic 1 and choose Region Grow. 2
- Click on the image data to set a seed point. 3 The seed point should be in the object you would like to isolate.
- Set the threshold Min/Max values to define the object 4 and click Connect Object. 5

**Download the CT_Heart data set to follow along http://analyzedirect.com/data/**

- The results of the region grow are shown below.
- The segmented object is shown overlaid on the 2D slice data 6 and a 3D representation 7 is displayed.

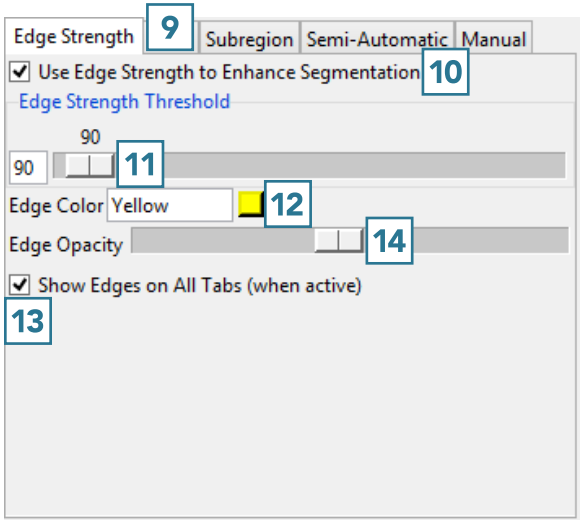
Note that both the heart and the spine have been assigned to Object_2.

- Click Undo.

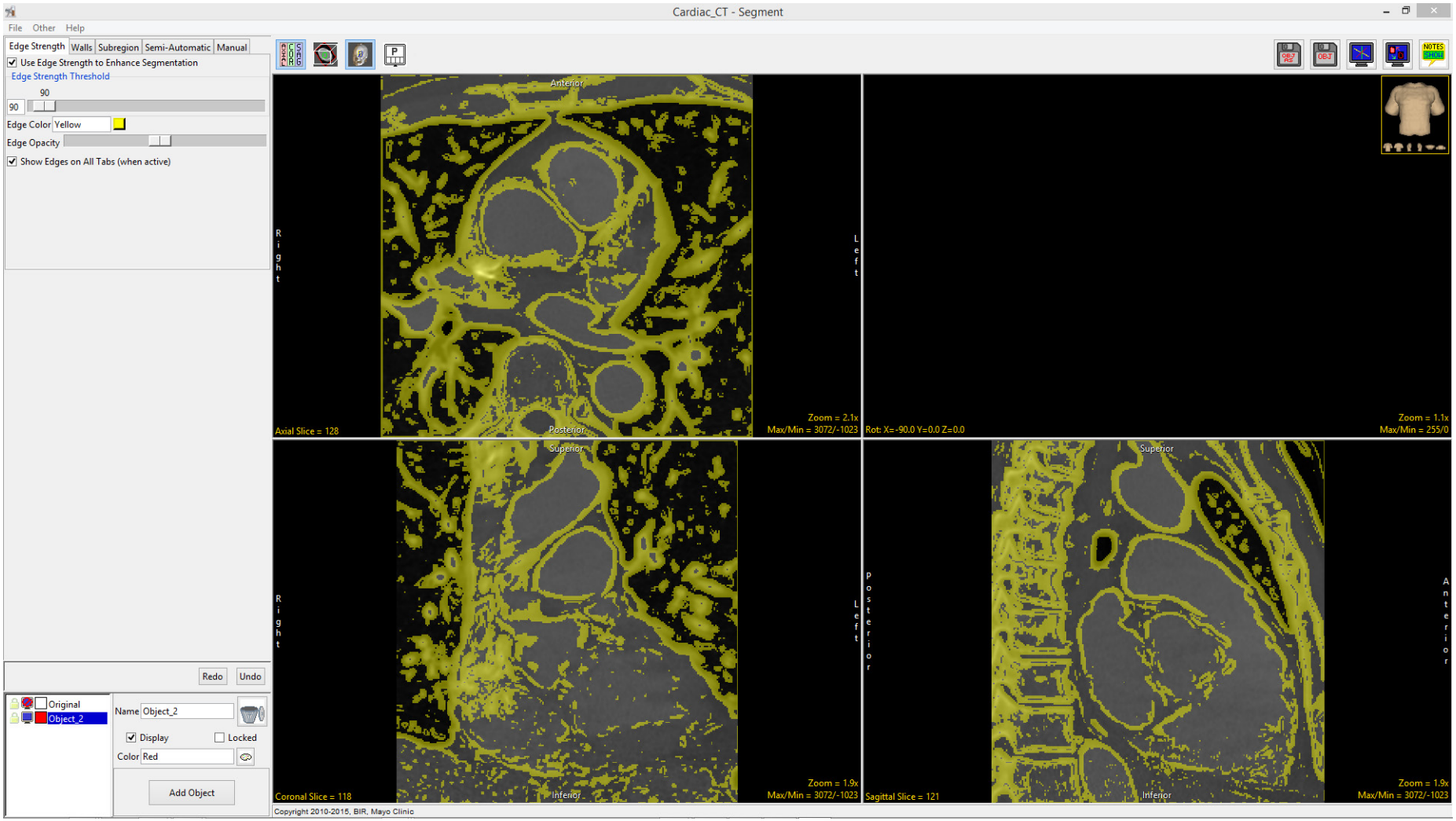


Now we will repeat this segmentation using edge strength to separate the heart from the rest of the data set.

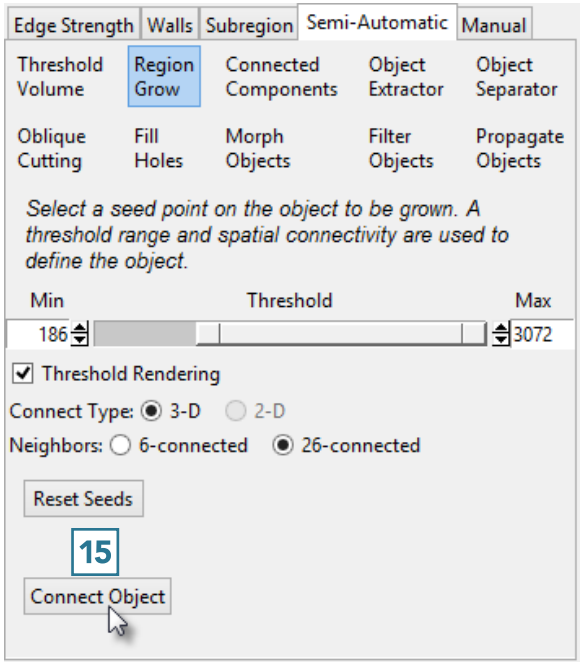
- Select Edge Strength 9 and check Use Edge Strength to Enhance Segmentation. 10
- Set the Edge Strength Threshold to 90. Note that this value will be different for each data set. In general, adjust the edge strength using the slider 11 until you find a suitable value. The edges will interactively update on the data set. Use the edge display to determine the suitable edge strength value.
- Optionally, change the color of the edge by entering the desired color in the text field or by using the color selector. 12
- When performing the segmentation, leave the Show Edges checkbox 13 selected. If required, reduce the Edge Opacity using the slider. 14



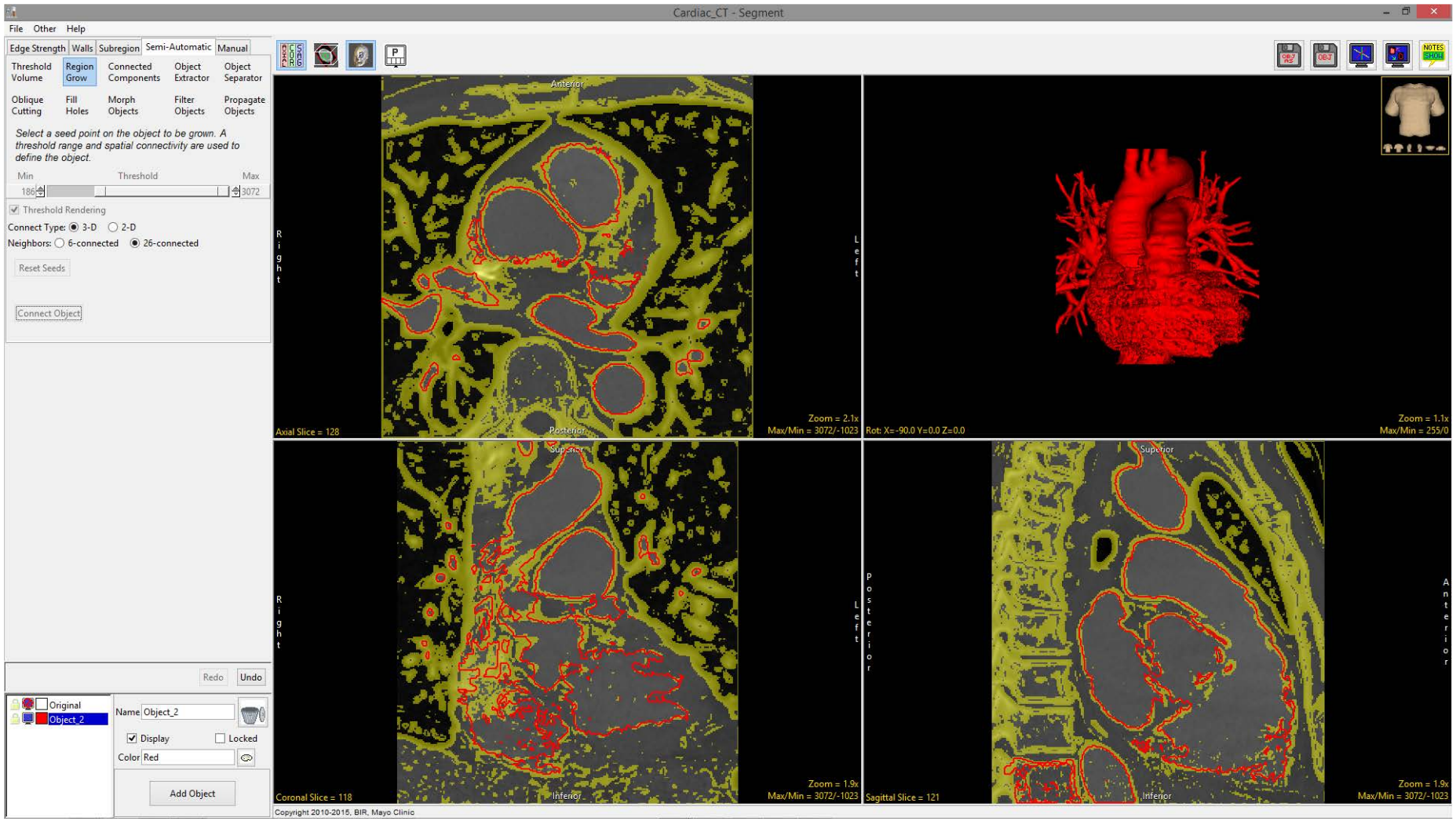
The edges detected on this data set using the Edge Strength algorithm with an edge strength threshold of 90 are shown overlaid on the data below.



- Repeat the segmentation. Select Semi-Automatic, then choose Region Grow.
- Click on the image data to set a seed point. The seed point should be in the object you would like to isolate.
- The Threshold Min/Max values should still be set to the previous values. If not, reset them to define the object and then click Connect Object. 15



Note that this time, only the heart was segmented. The Edge Strength technique prevented the region grow algorithm from including the spine in the object. Further segmentation can now be achieved with or without Edge Strength enabled. Select File > Save Object Map to save your work.



# Walls

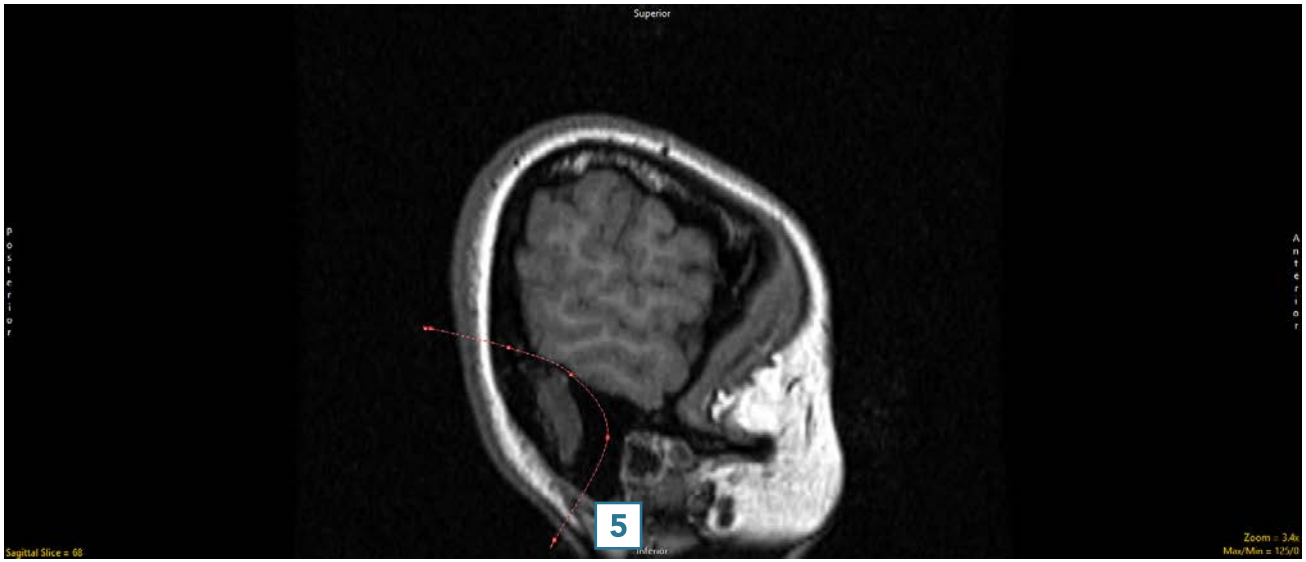
Segmenting structures of interest that are connected to surrounding anatomy with similar grayscale values can be challenging. The Walls option provides tools to create adaptable 3D limits to help make this process easier for the user. The Walls tool is useful for many segmentation applications, particularly isolating the cerebellum from the rest of the brain parenchyma or limiting the boundaries of a region grow operation to isolate blood pools from cardiac data.

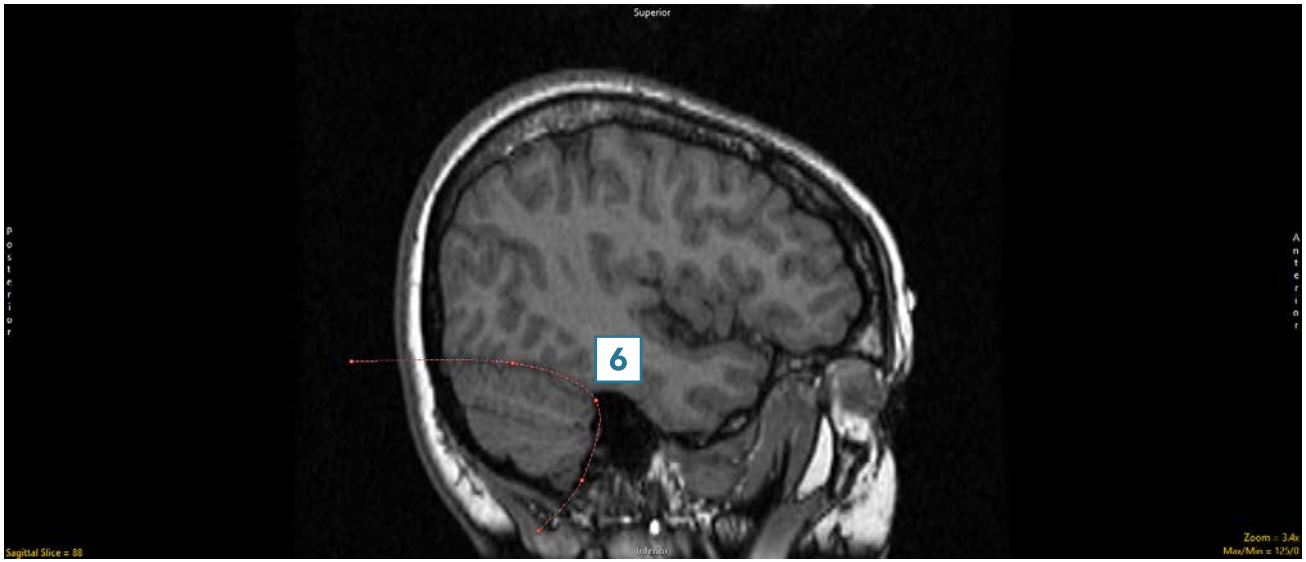
# 2. Using Walls with Semi-Automatic Segmentation

- Select a data set and open Segment.
- Select Walls 1 and check Define Walls to Limit Semi-Automated Operations. 2
- Set the Wall Type to Spline. 3
- Set the primary display to Sagittal. 4

Download the EGV_MRI data set to follow along
http://analyzedirect.com/data/

- Navigate through the sagittal slices to find the first slice that includes tissue belonging to the cerebellum. Draw a wall separating the cerebellum from the cerebrum on this slice.
- To draw a wall using the spline tool, left-click to set spline points which will connect into a smooth line. Double-click when defining the last spline point to set the spline. 5
- The spline points can be adjusted by left-clicking and dragging. Right-clicking on a spline point allows you to delete it or make other changes to the spline such as closing the spline or deleting the entire spline.
- Move forward through the sagittal slices and adjust the wall as required. 6
- The Wall can also be redrawn if necessary.

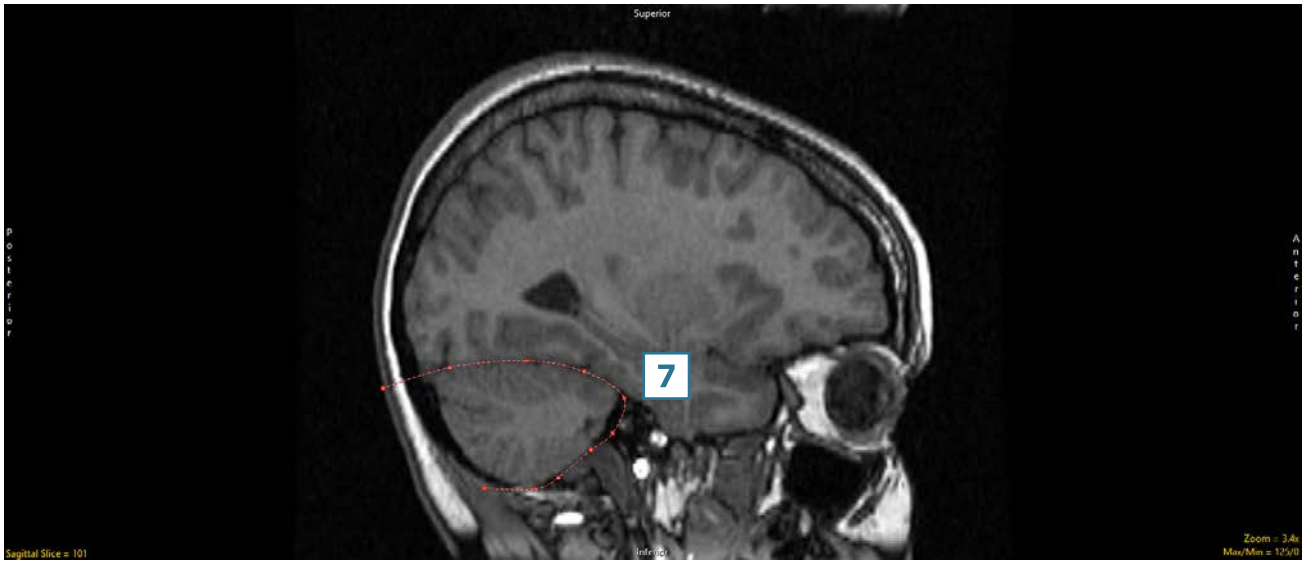


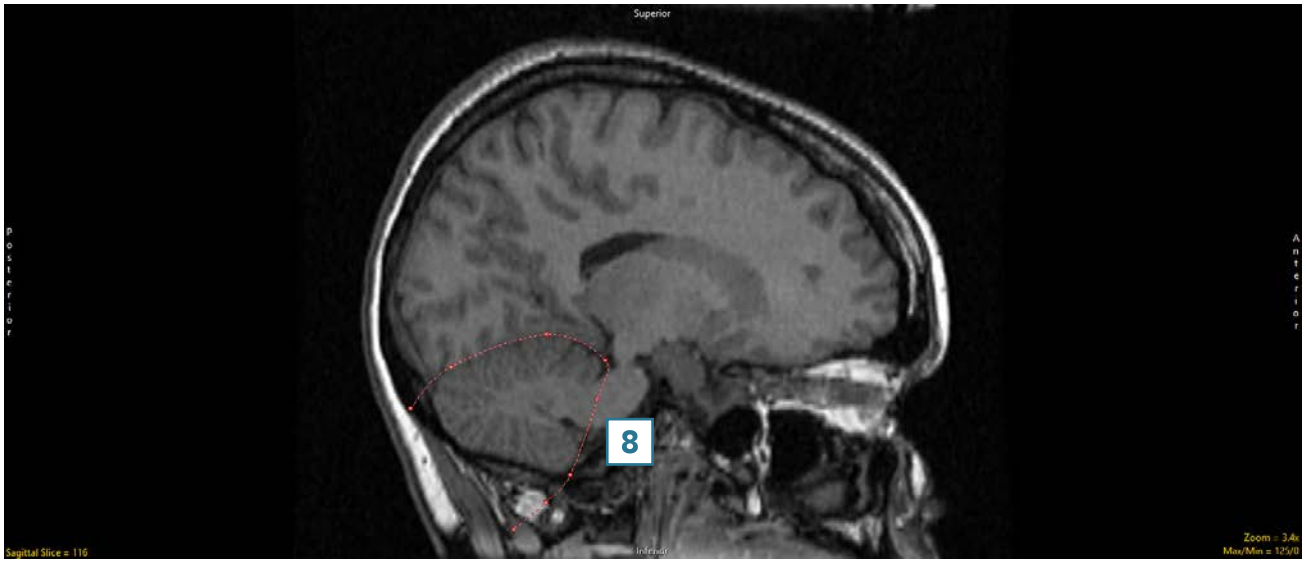



- Once the cerebellum is no longer well defined by the wall, redefine the wall on that slice. The wall will be interpolated between all slices on which it is defined. When finished, scroll through the slices to ensure that the cerebellum is well defined by the wall.

Note that walls can be set in multiple orientations. This is helpful when trying to isolate structures connected to several surrounding structures in all orientations. For example, it can be used when isolating the heart from the lungs, spine, sternum, etc. It can also be useful to define walls in the sagittal and coronal orientations to better segment the cerebellum.

- Continue to define walls around the cerebellum in the sagittal orientation. 7 8

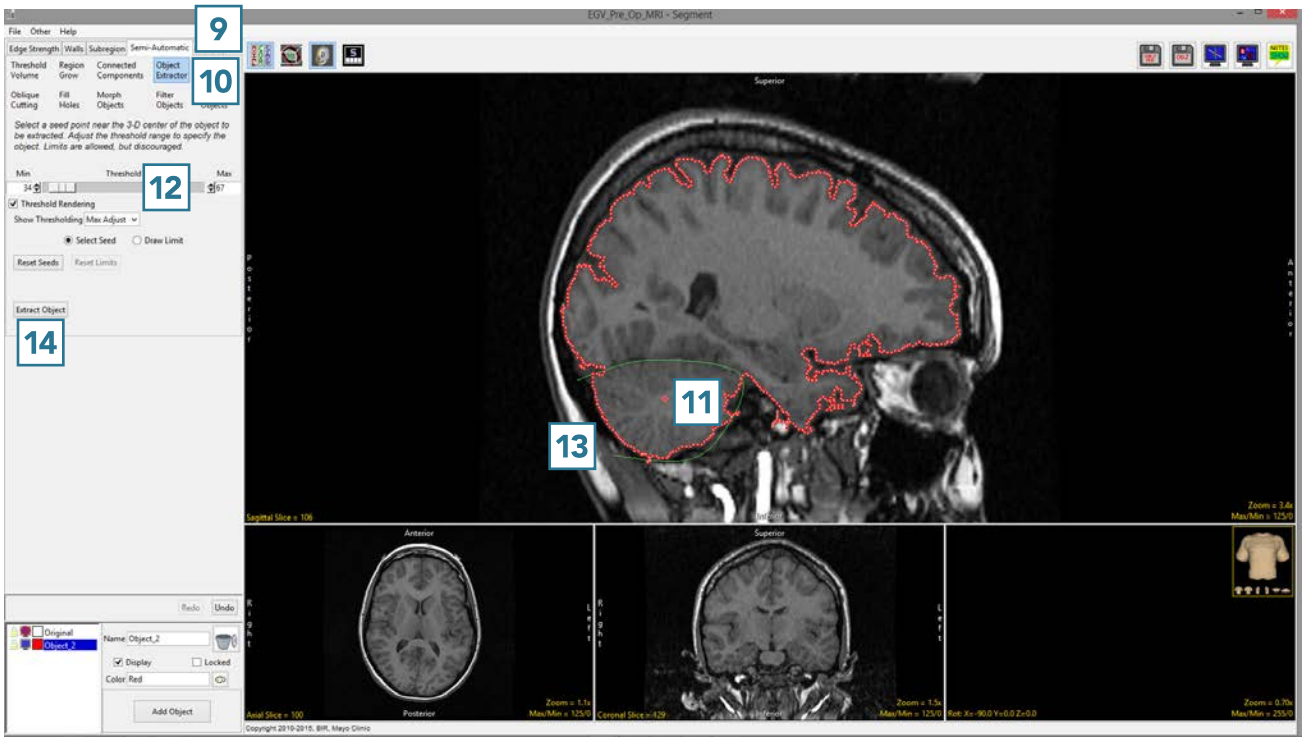


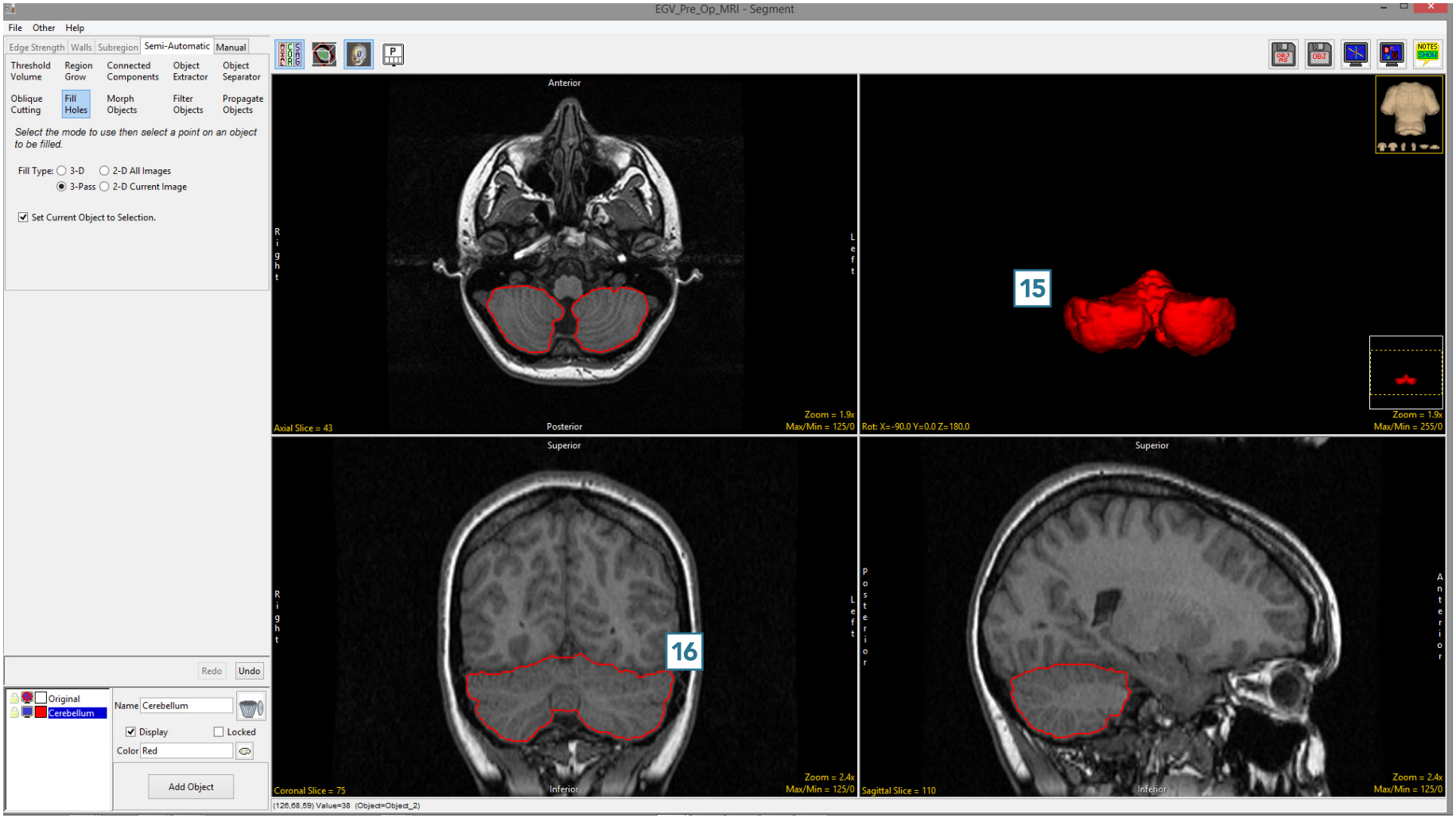
- Once the cerebellum boundary is defined in three dimensions by the wall, select the Semi-Automatic tab 9 and choose Object Extractor. 10
- Click in the cerebellum on a sagittal slice to set a seed point. 11
- Adjust the maximum and minimum threshold values 12 until the auto trace defines the object. 13

Note that while the entire brain will be defined, the walls will prevent the whole brain from being segmented and will confine the segmentation to the cerebellum.

- Click Extract Object. 14



- The cerebellum will be isolated and displayed in 3D.
- Once segmentation is complete, the structure will be rendered 15 and overlaid on the slice data. 16
- Save your work by selecting File > Save Object Map.



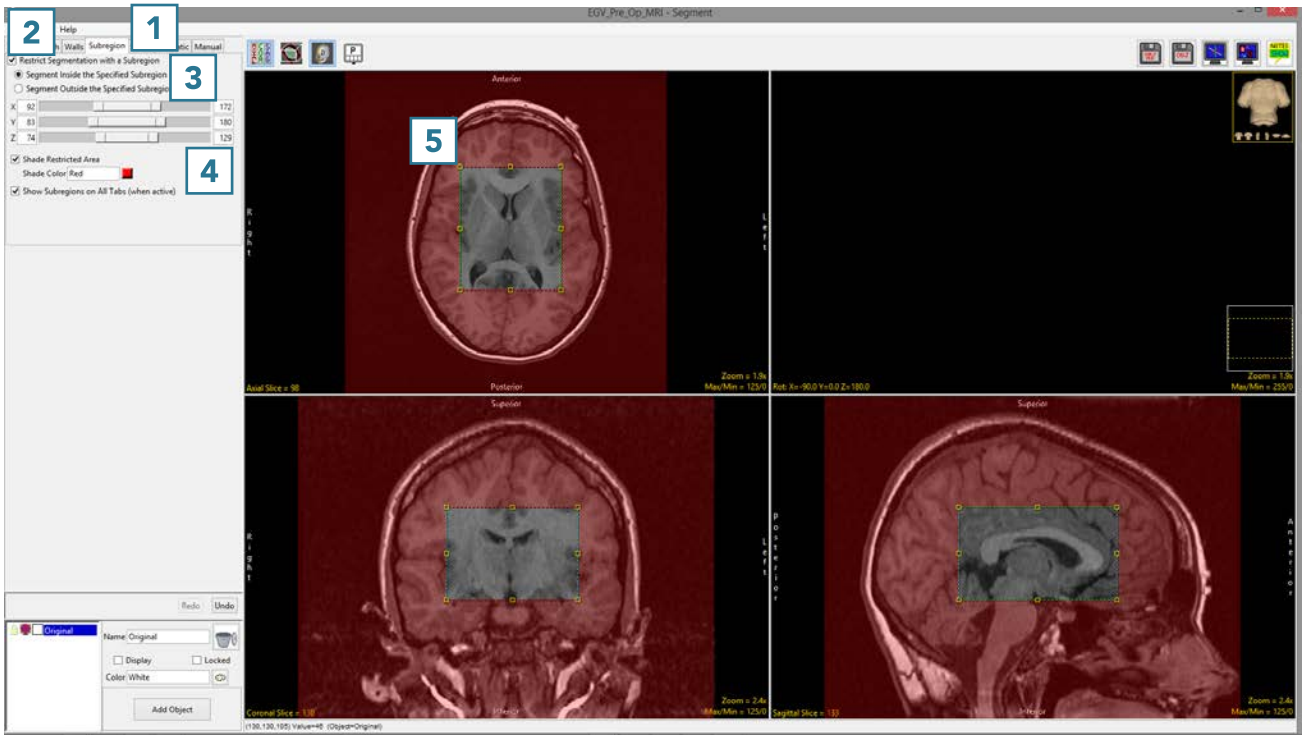
# Subregion

Subregion allows users to limit segmentation to a specific user-defined region. This tool is particularly useful when you would like to segment a structure of interest, such as the hippocampus, without having to crop the original image data.

# 3. Setting a Subregion

- Select a data set and open Segment.
- Select Subregion 1 and check the Restrict Segmentation with a Subregion checkbox. 2
- Choose to Segment Inside (default) or Outside the Subregion. 3
- Use the X, Y, Z sliders 4 or the yellow control points 5 to specify the Subregion in all orientations.
- The area in red will be protected as you move to the Semi-Automatic or Manual tools to segment regions of interest.

**Download the EGV_MRI data set to follow along http://analyzedirect.com/data/**



# Semi-Automatic Tools

The Semi-Automatic tab provides access to many useful tools for interactive, efficient segmentation of objects. These tools include simply segmentation options, such as threshold, to more advanced, semi-automated techniques like object extraction and object separation. The segmentation tools available also include those that use 3D spatial connectivity and include region growing and connected components.

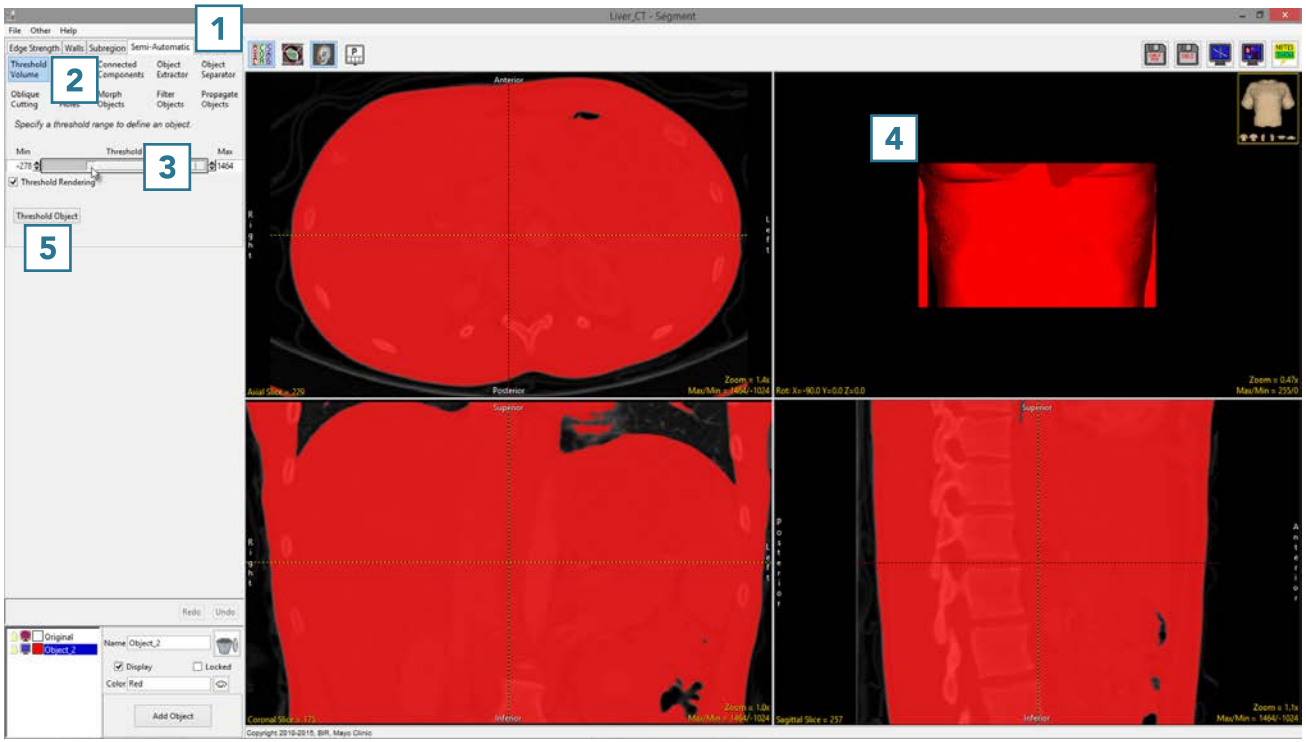
# Threshold Volume

Threshold segmentation allows a range of voxels from the input volume to be assigned to an object. All voxels greater than or equal to the threshold minimum and less than or equal to the threshold maximum are assigned to the object.

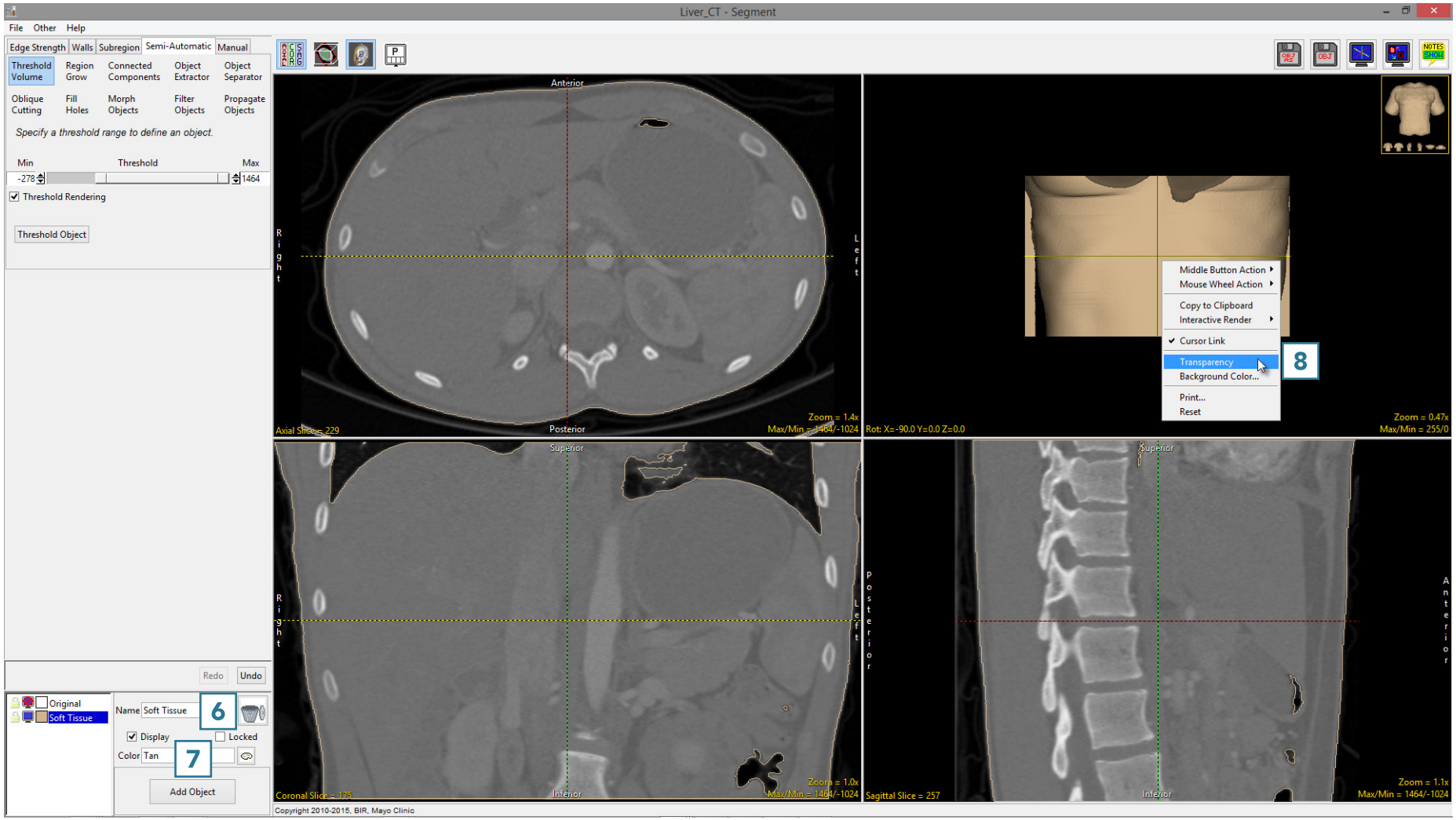
# 4. Threshold Volume and Segmentation

- Select a data set and open Segment.
- Select Semi-Automatic 1 and choose Threshold Volume. 2
- Use the Threshold slider 3 to adjust the voxel intensity range, so that the soft tissue is displayed in the binary mask preview. This data set is scaled to Hounsfield Units (HU), so the grayscale intensities represent HU. This may be used to isolate tissue with a known HU range. 4
- Click Threshold Object 5 to assign all selected voxels to the current object.

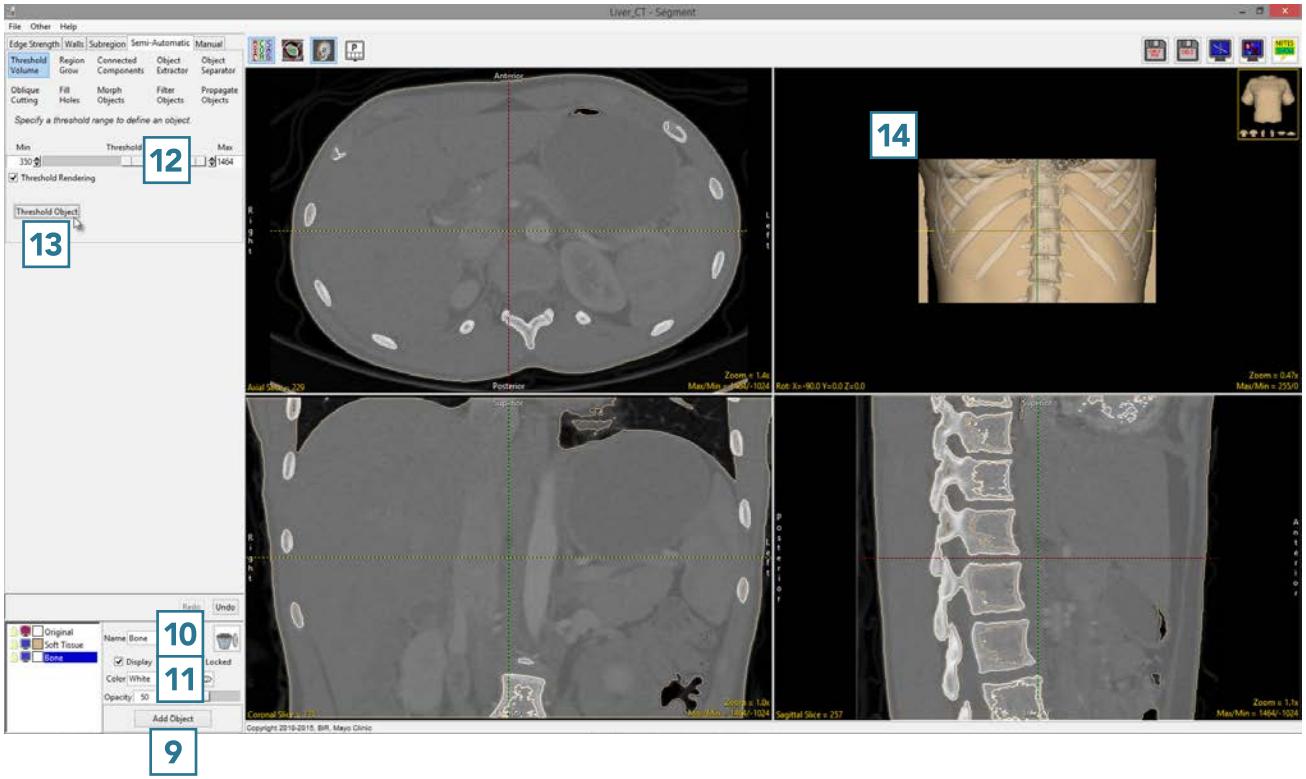
Download the CT_Liver data set to follow along
http://analyzedirect.com/data/



- Rename the object, 6 then change the color. 7
- Right-click on the rendering and select Transparency. 8



- Add a new object. 9
- Update the name 10 and color. 11
- Adjust the threshold range 12 so that the bone is displayed in the binary preview, then click Threshold Object. 13
- Note that the rendering 14 will update to display both objects. The bone is now fixed to visible, as the rendering transparency is enabled. 8
- Select File > Save Object Map to save your work.



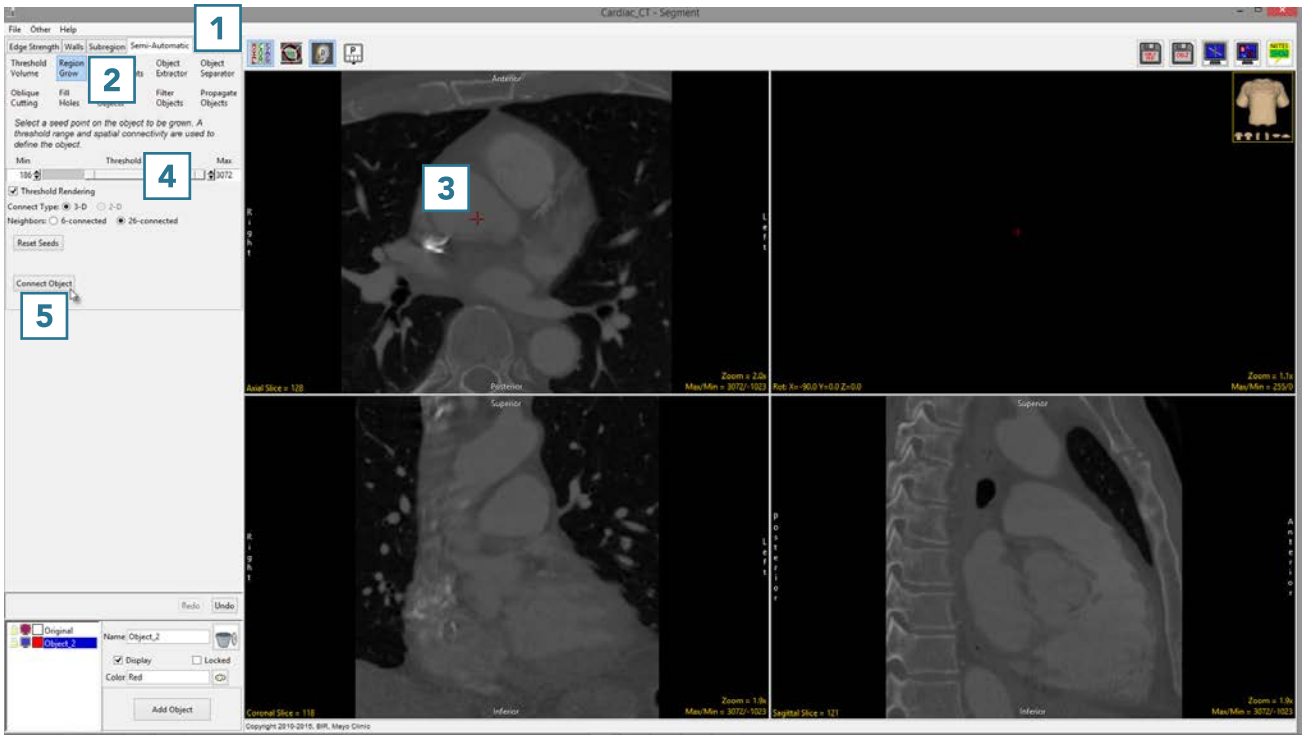
# Region Grow

Whereas threshold-based segmentation applies globally to all voxels in the volume, region growing can be used to limit the segmentation to voxels that are connected to a user-defined seed point which fall within a specified threshold range.

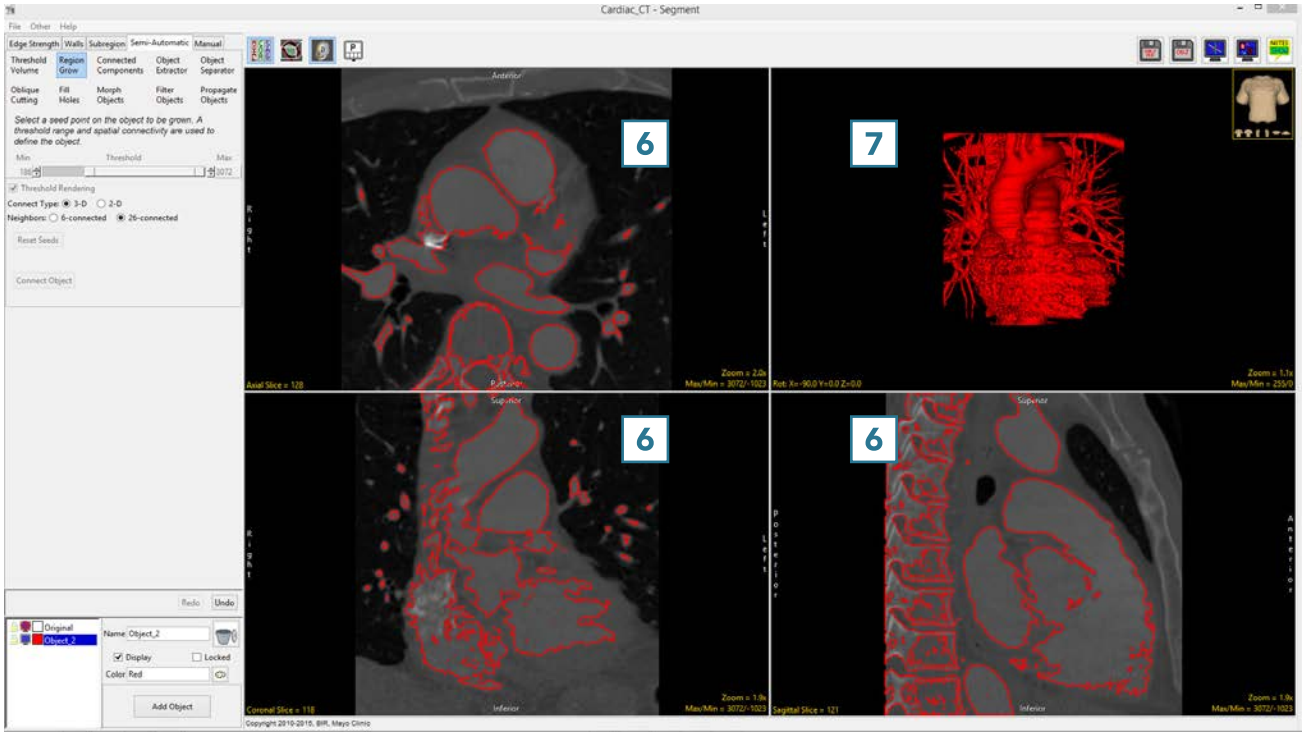
# 5. Segmentation with Region Grow

- Select a data set and open Segment.
- Select Semi-Automatic 1 and choose Region Grow. 2
- Click on the image data to set a seed point in the object you would like to isolate. 3
- Set the Threshold Min/Max values to define the object. 4
- Click Connect Object. 5

Download the CT_Heart data set to follow along http://analyzedirect.com/data/



- The voxels fulfilling the seed point and threshold criteria for the region grow will be assigned to a new object.
- The segmented object is shown overlaid on the 2D slice data 6 and a 3D rendering 7 is displayed.

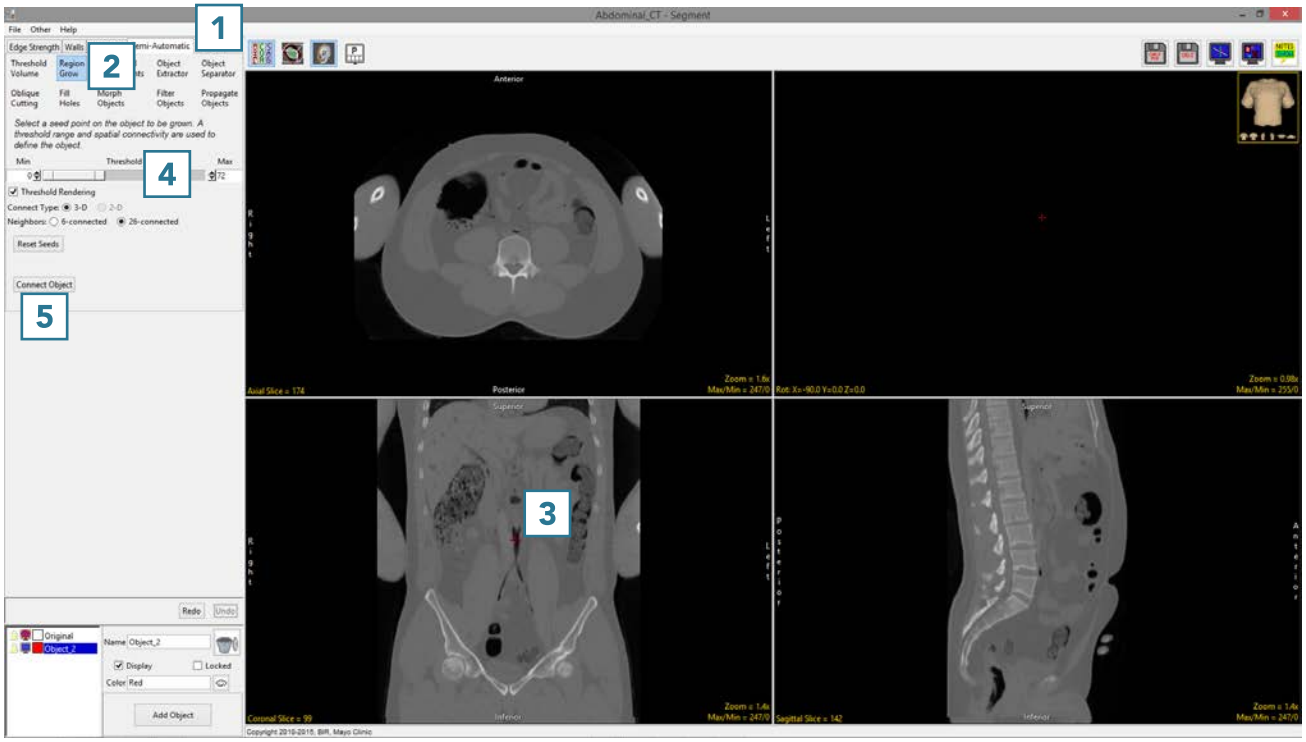


# 6. Adjusting Connected Neighbors

It may be necessary to adjust the number of neighbors used in order to limit the region grow. This will help prevent unwanted objects from being segmented with the target object.

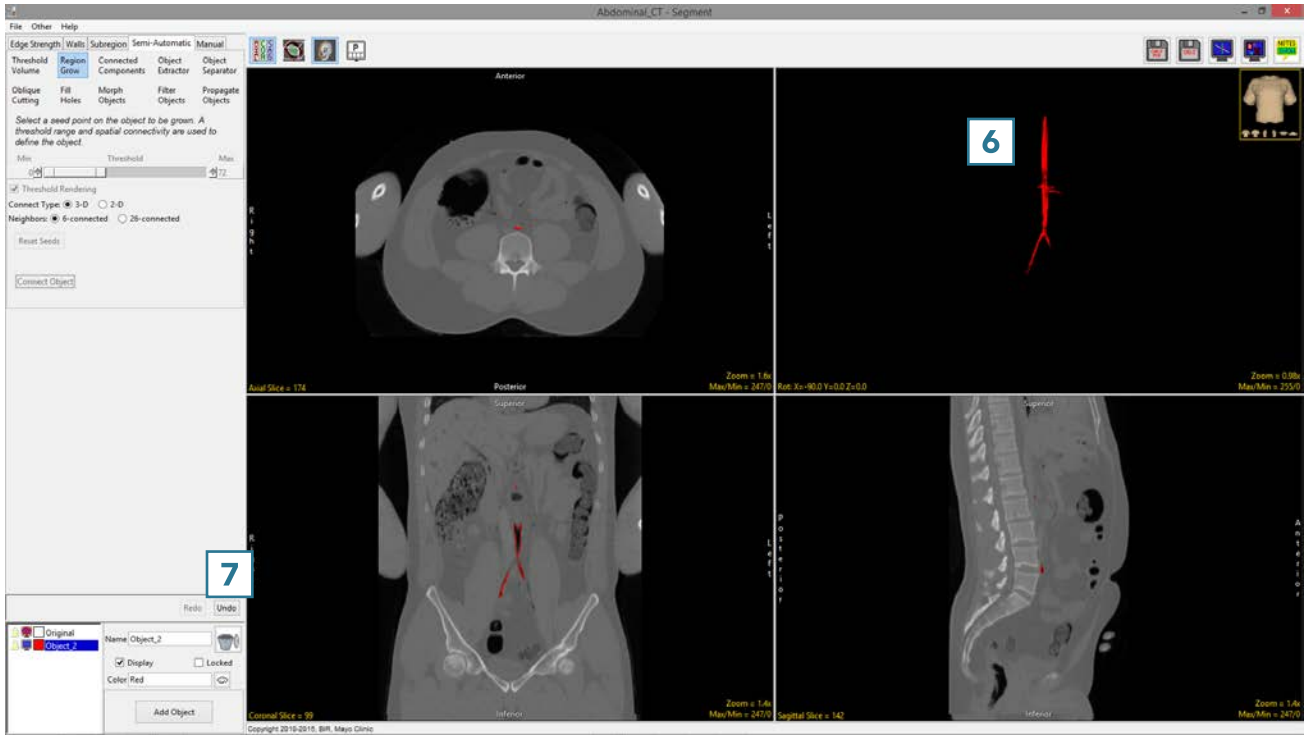
- Select a data set and open Segment.
- Select Semi-Automatic 1 and choose Region Grow. 2
- Click on the image data to set a seed point in the structure you would like to isolate. 3
- Set the Threshold Min/Max values to define the object 4 and click Connect Object. 5

Download the VH_Abdomen data set to follow along
http://analyzedirect.com/data/



Note that the segmentation of the abdominal aorta in the example, using the default 26-connected neighbors, also assigns part of the left lung into the object. 6

- Click Undo. 7



- Set the seed point, 8 set Neighbors to 6-connected, 9 and click Connect Object. 10

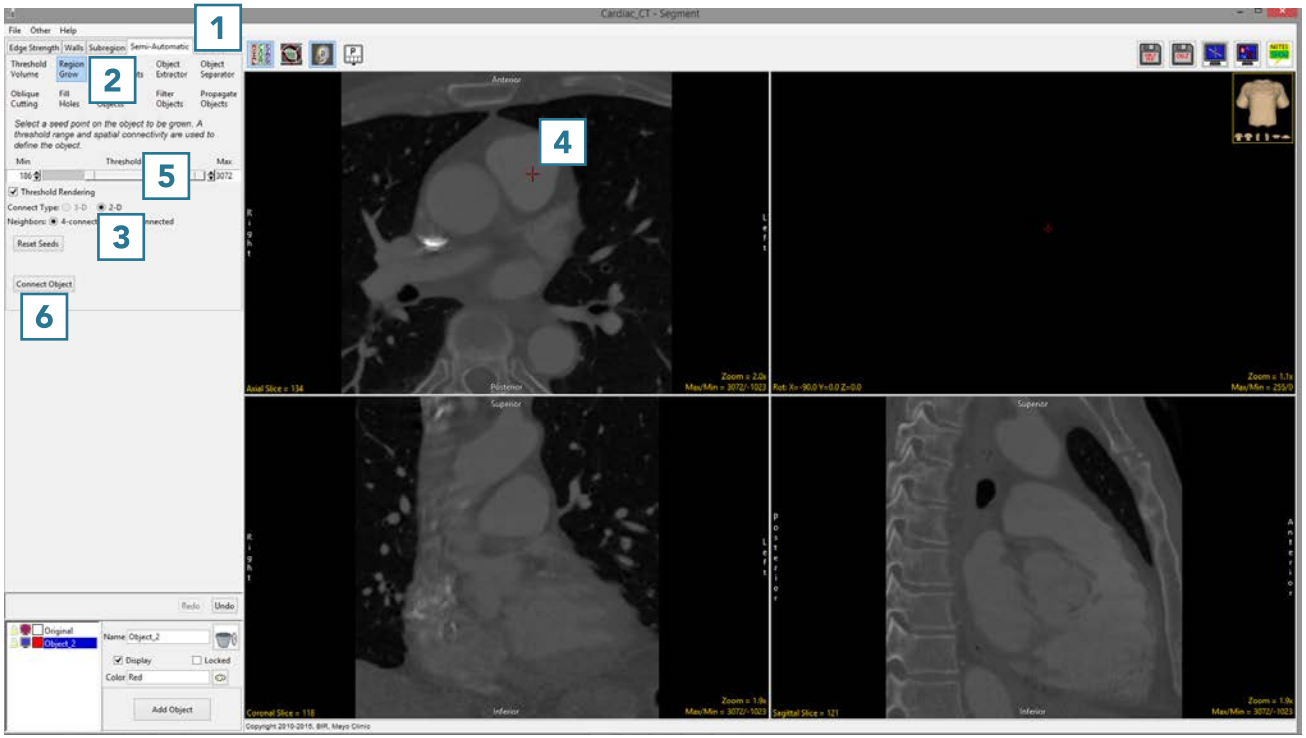
Note the segmentation result for the abdominal aorta 11 no longer contains part of the left lung.

# 7. 2D Region Grow

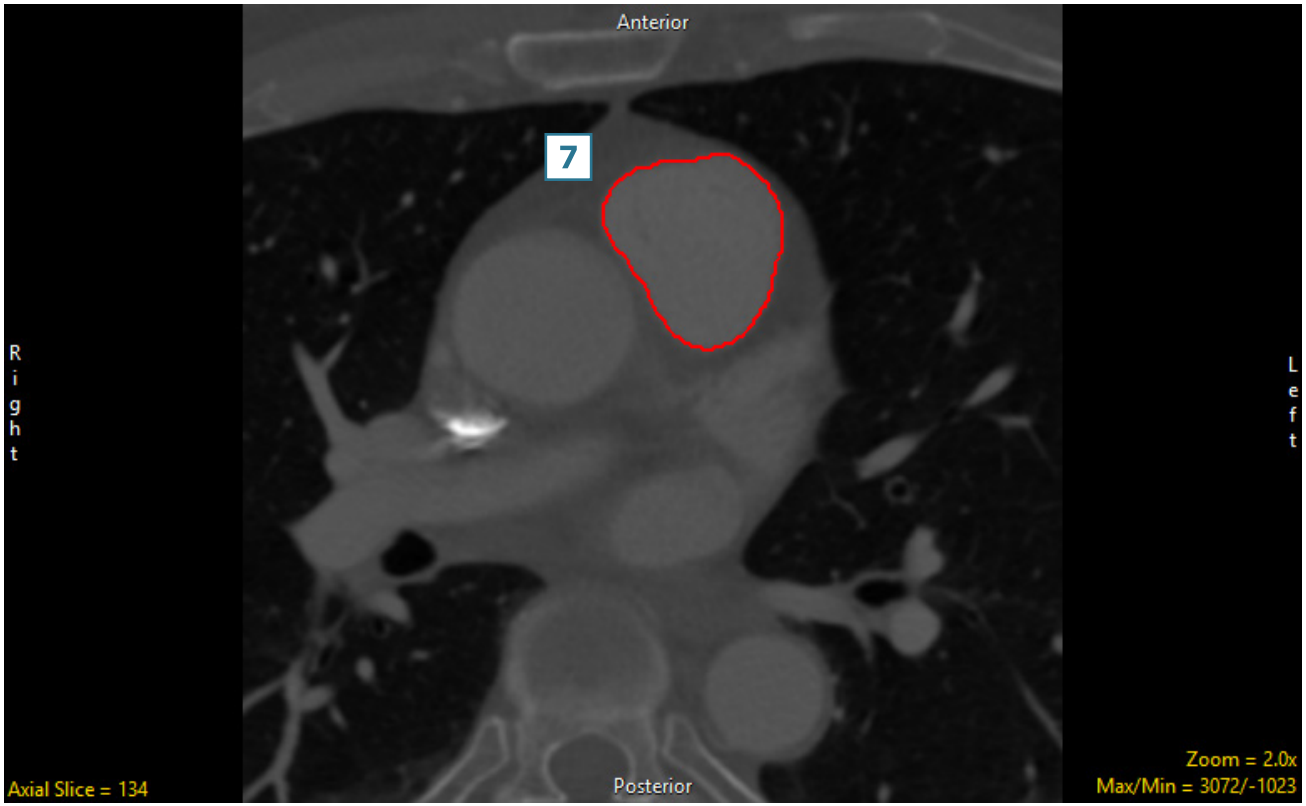
Region grow also provides the ability to limit the region to a single slice via the 2D Connect Type option.

- Select a data set and open Segment.
- Select Semi-Automatic, 1 choose Region Grow 2 and set the Connect Type to 2D. 3
- Click on the image data to set a seed point. 4 The seed point should be in the 2D structure you would like to isolate.
- Set the Threshold Min/Max values to define the object 5 and click Connect Object. 6

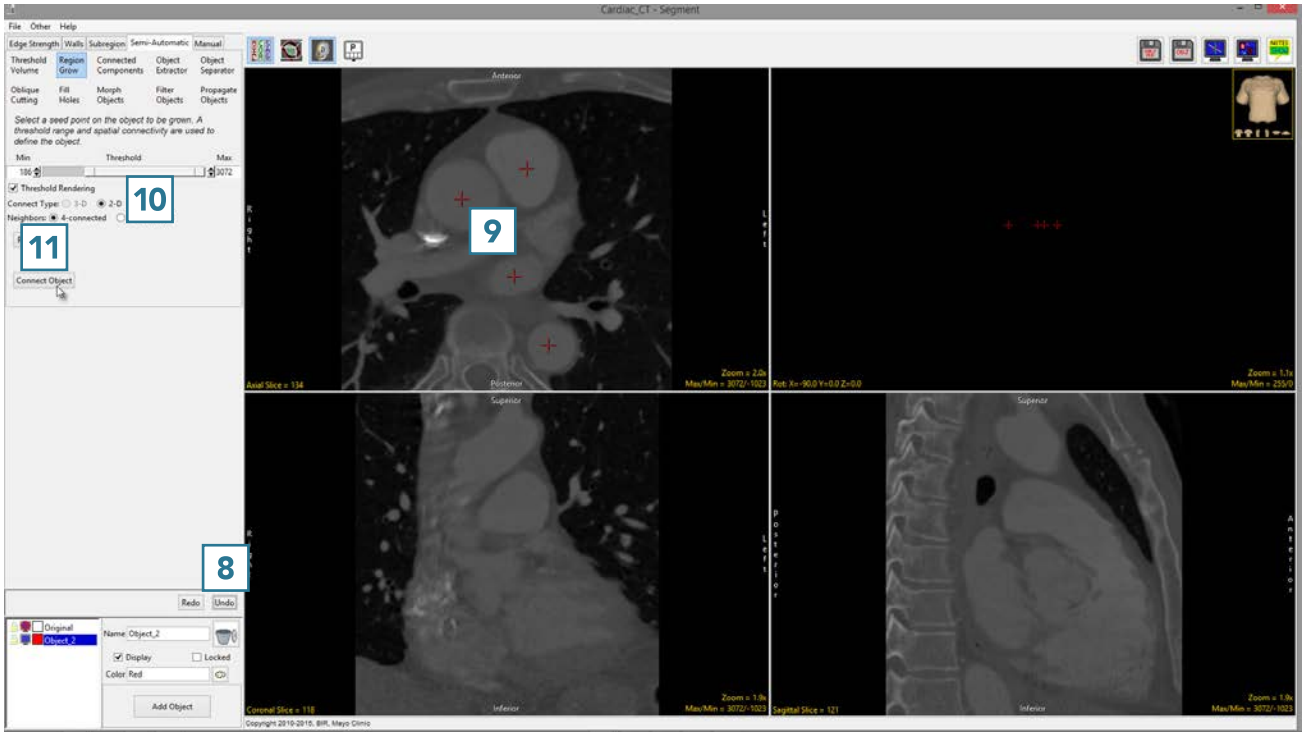
Download the CT_Heart data set to follow along http://analyzedirect.com/data/



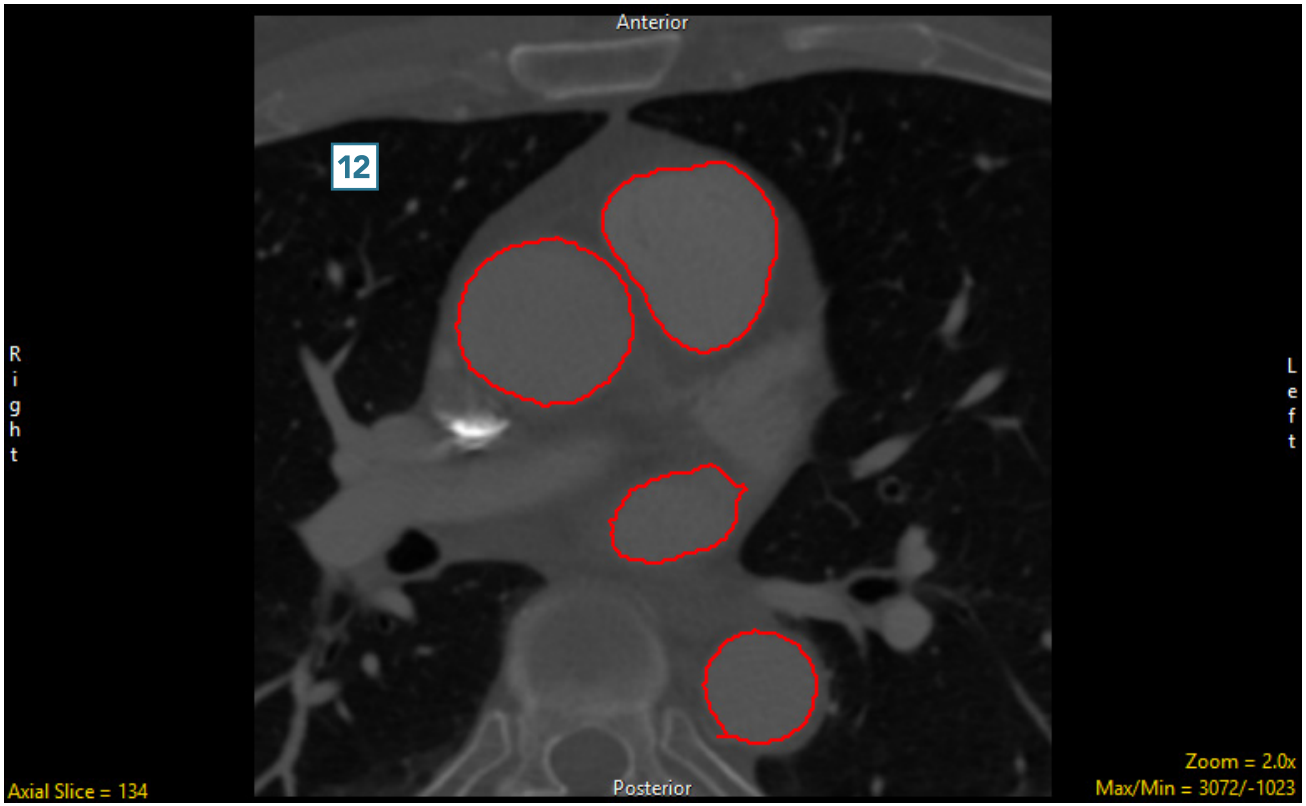
- The region will be isolated on the single slice. 7



- To segment multiple 2D regions, click Undo. 8
- Click on the image data to set multiple seed points on the regions you want to segment. 9
- Set the Threshold Min/Max values to define the object 10 and click Connect Object. 11



- All of the regions falling within the threshold criteria will be isolated in 2D. 12



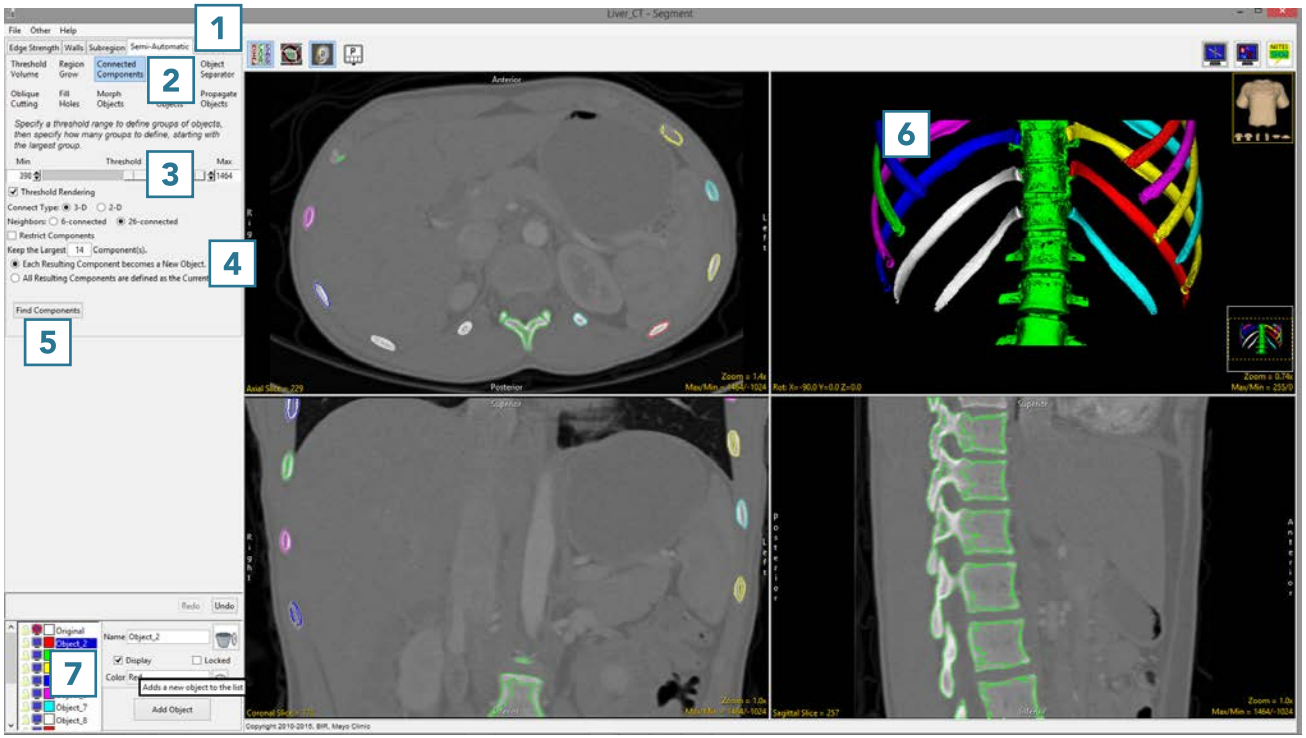
# Connected Components

The connected components tool allows users to identify groups of objects based on spatial connectivity and intensity range. This segmentation method finds groups of voxels within a user-specified intensity range and assigns spatially disconnected groups to independent objects. The number of objects identified is specified by the user, and objects are created in order of largest to smallest based on the number of connected voxels in each object.

# 8. Segmenting Multiple Objects Using Connected Components

- Select a data set and open Segment.
- Select Semi-Automatic 1 and choose Connected Components. 2
- Set the threshold range 3 to isolate a group of objects, such as spine and ribs.
- Set the number of components to keep to 14. 4
- Click Find Components.
- The data will be thresholded and the largest groups of voxels specified 5 will be identified and rendered. 6
- The objects will be listed in the object control window. 7

Download the CT_Liver data set to follow along
http://analyzedirect.com/data/



# Object Extractor

The Object Extractor tool enables the user to define and extract objects from image data using a combination of thresholding, region growing and morphological operations.

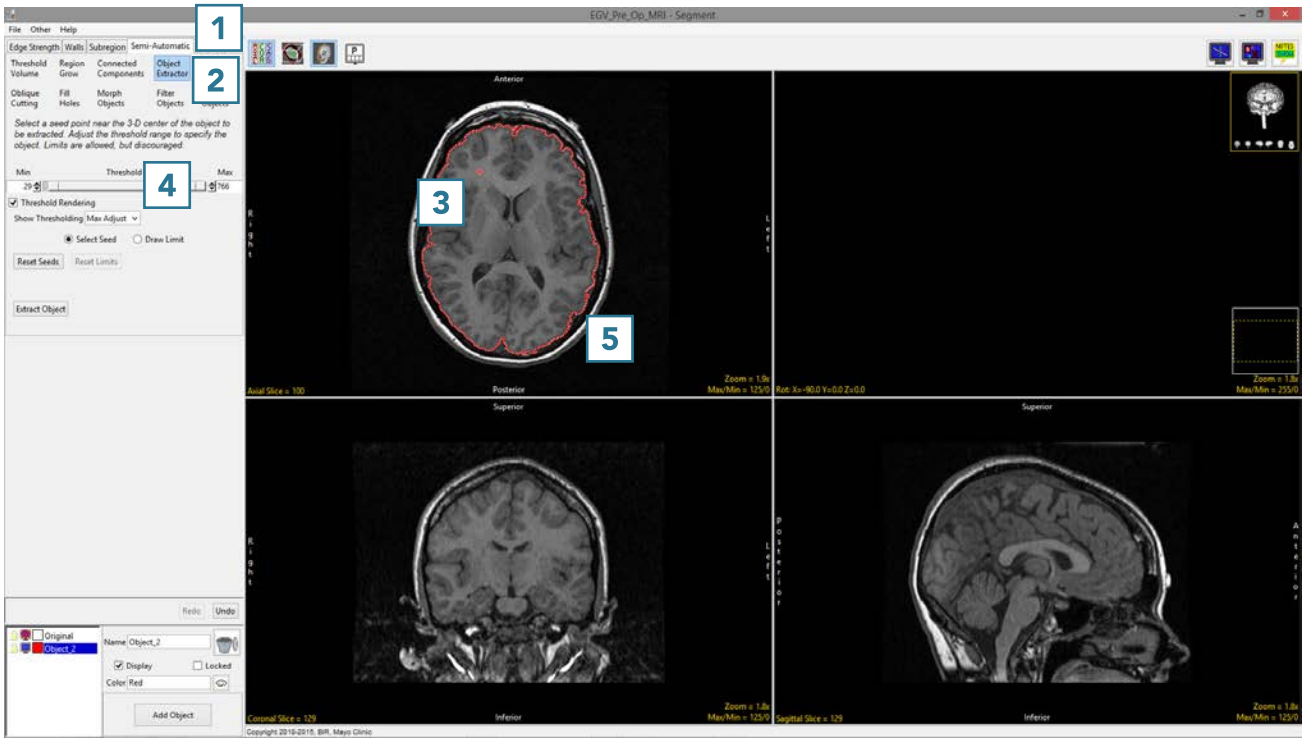
First, a seed point is manually set on a structure of interest. Next, a threshold range is established by the user to define the structure. The region defined by a given threshold range is shown on the 2D slice containing the seed point using a 2D auto trace mechanism. This region updates interactively as the threshold range is adjusted, allowing the user to determine the threshold range that properly defines the region of interest. The Object Extractor segmentation routine is ready to be started once the seed point and threshold range define the structure on the initial slice.

The algorithm first applies a global threshold to the data set, using the minimum and maximum values specified by the user. Next a 3D binary erosion is performed on the binary result of the global threshold. The erosion attempts to break connections between the target structure and neighboring regions which have similar intensity values. The erosion is followed by a 3D 6-neighbor region grow, which uses the initial seed point. The processed target slice on which the initial seed point was set is compared to the initial auto trace from the user-defined seed point and threshold range. The erosion and region growing steps are repeated until the set of voxels on the processed target slice are a subset of the initial auto trace. Next, the processed data is conditionally dilated until 99% of the voxels in the auto traced region on the processed target slice are recovered. Once the extraction process is complete, the resulting object is rendered and displayed over the 2D slice data.

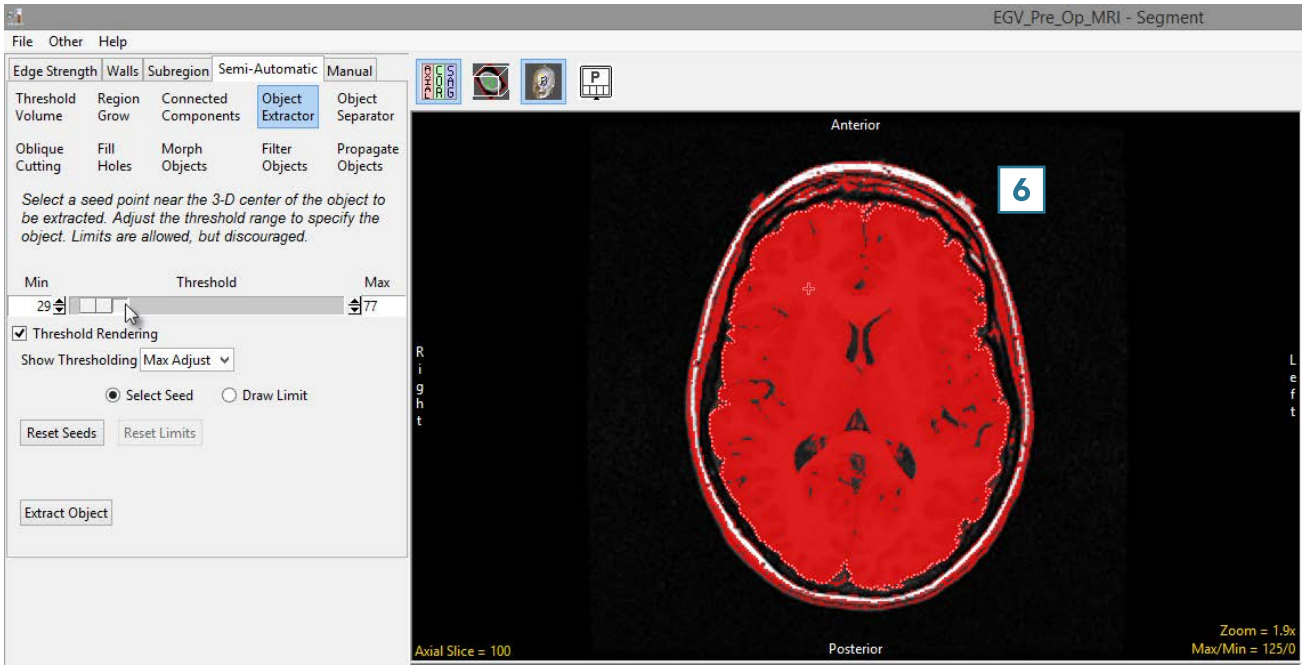
# 9. Segmentation of a Single Object Using Object Extractor

- Select a data set and open Segment.
- Select Semi-Automatic 1 and choose Object Extractor. 2
- Click on the image data to set a seed point in the object you would like to isolate. 3
- Adjust the minimum threshold value 4 until the auto trace defines the object. 5

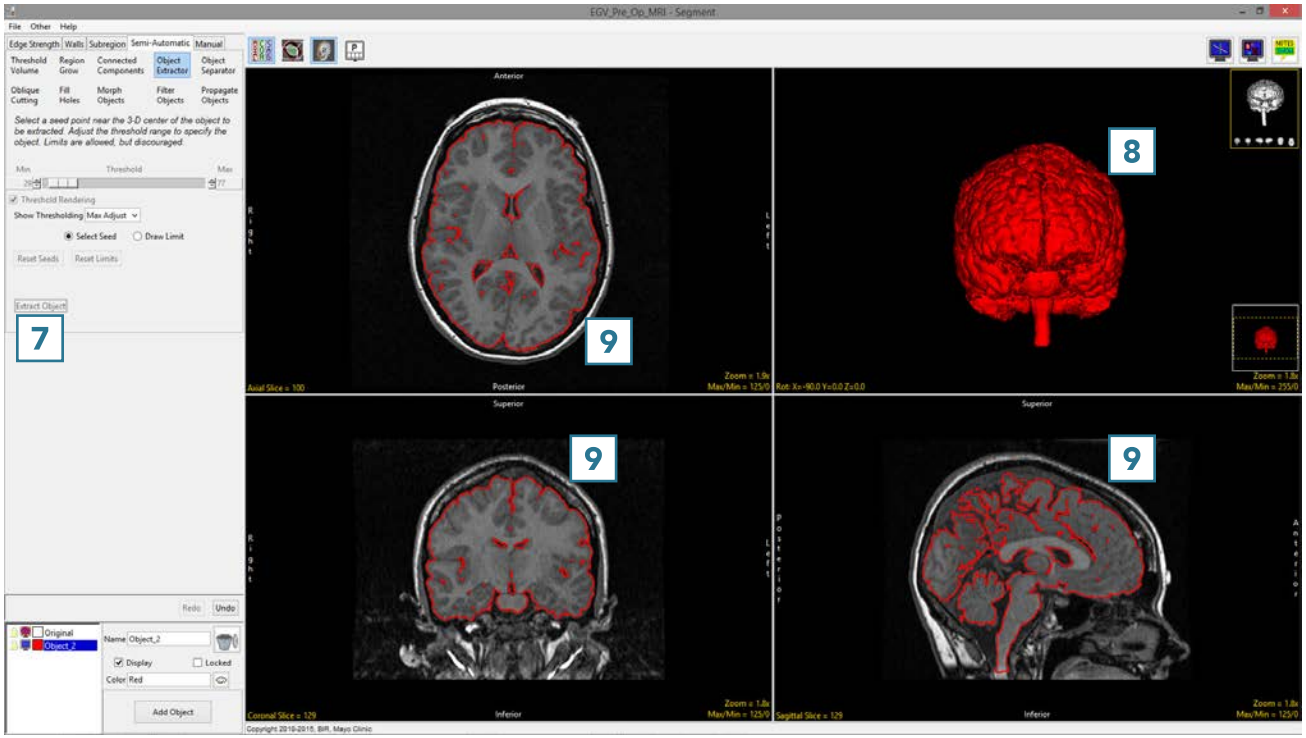
Download the EGV_MRI data set to follow along
http://analyzedirect.com/data/



- Adjust the maximum threshold level and note that the red binary mask will interactively update.
- Lower the maximum threshold value until holes start to appear in the red binary mask in the structures surrounding the brain, but not in the brain. 6



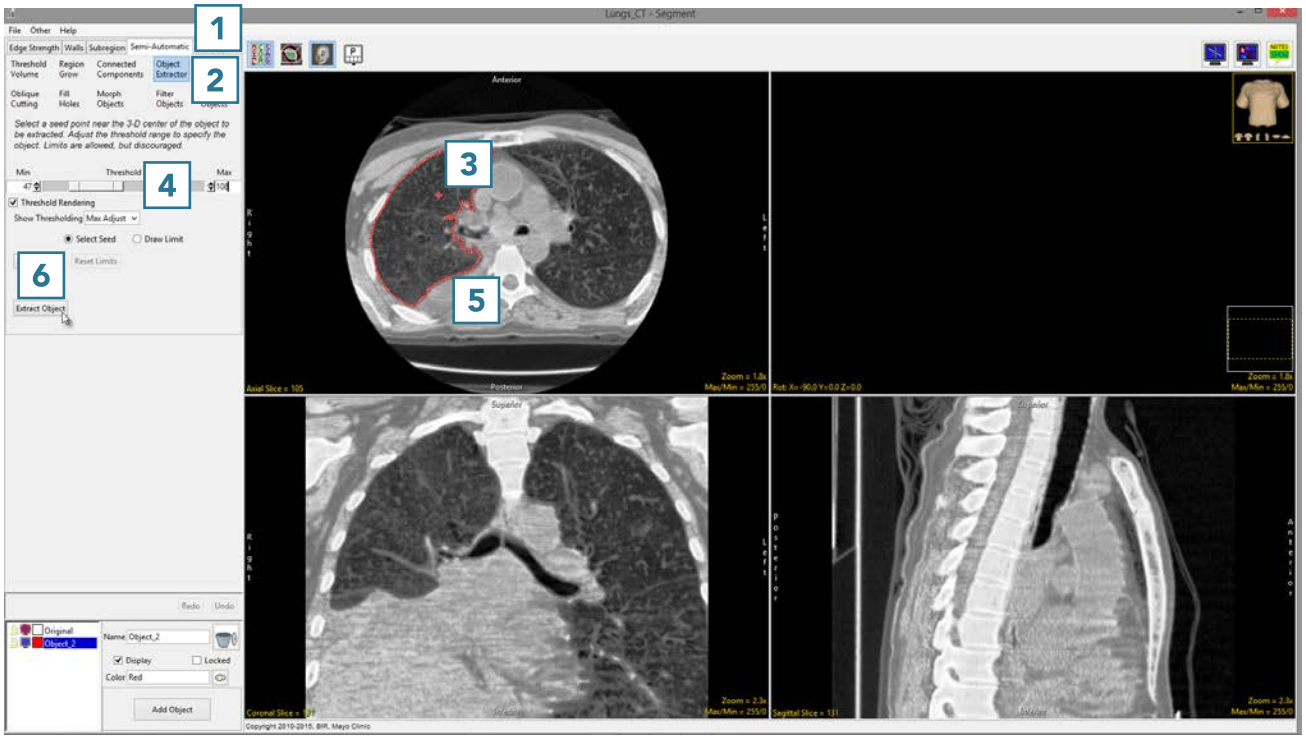
- Click Extract Object. 7
- Once segmentation is complete, the object map will be rendered 8 and overlaid on the slice data. 9
- Save your work by selecting File > Save Object Map.



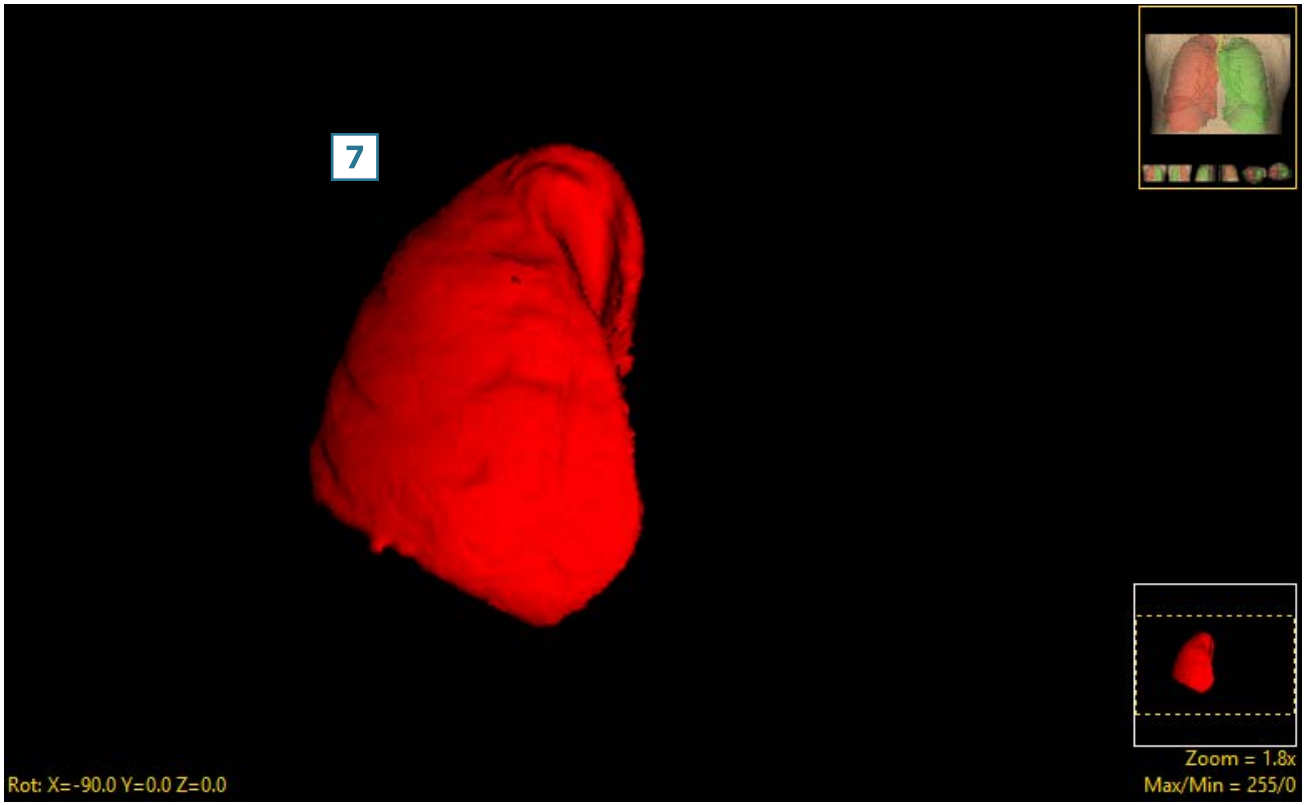
# 10. Segmentation of Multiple Objects Using Object Extractor

- Select a data set and open Segment.
- Select Semi-Automatic 1 and choose Object Extractor. 2
- Click on the image data to set a seed point in the object you would like to isolate. 3
- Adjust the minimum and maximum threshold values 4 until the auto trace defines the object. 5
- Select Extract Object. 6

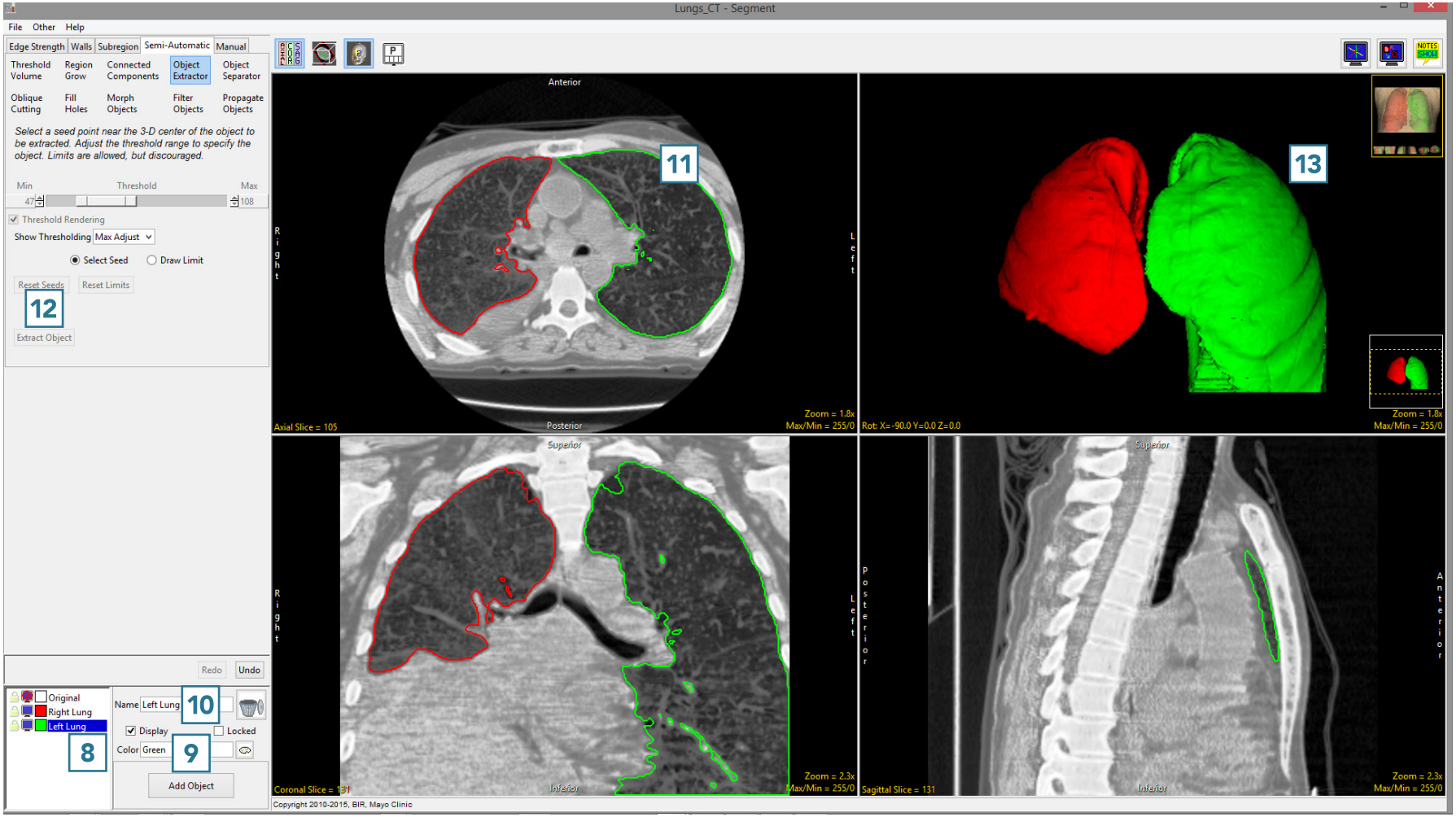
Download the CT_Lungs data set to follow along
http://analyzedirect.com/data/



- Once the segmentation process is complete, the object will be rendered. 7



- Rename the object. 8 Add a new object 9 and rename. 10
- Set a seed point in the next object 11 and select Extract Object. 12
- Once the segmentation process is complete, the object will be rendered. 13
- Save your work by selecting File > Save Object Map.



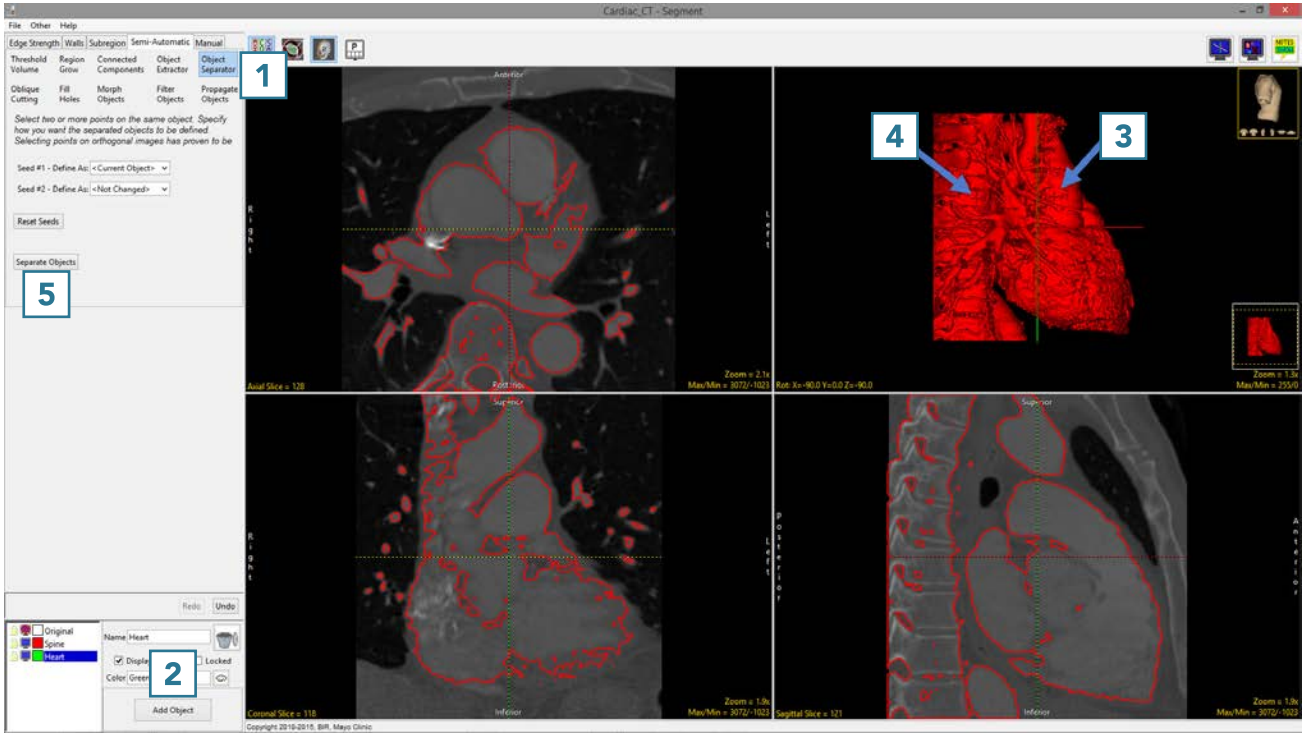
# Object Separator

The Object Separator tool uses morphologic erosion to break connections between objects based on user-defined seed points to specify objects to separate.

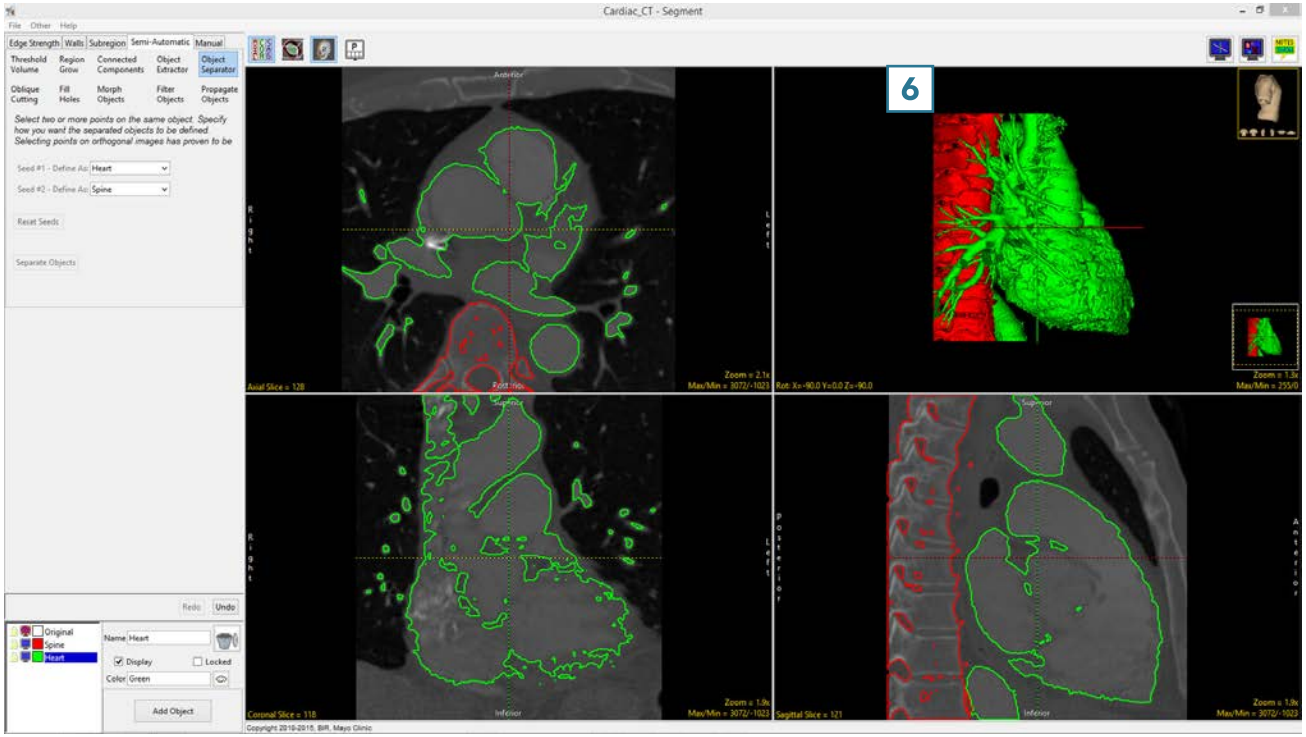
# 11. Separating Objects

- Select a data set and open Segment.
- Select Semi-Automatic and choose Region Grow.
- Click on the image data to set a seed point. The seed point should be in the object you would like to isolate.
- Set the Threshold Min/Max values to define the object and then click Connect Object.
- The structure will be isolated.
- Rotate the rendering to view the objects to disconnect.
- Select Object Separator 1 and click Add Object. 2
- Set a seed point on the first structure 3 and add a seed point to the second structure. 4 Object separator usually works best when the seed points are set in the orthogonal images.
- Click Separate Objects. 5

Download the CT_Heart data set to follow along
http://analyzedirect.com/data/



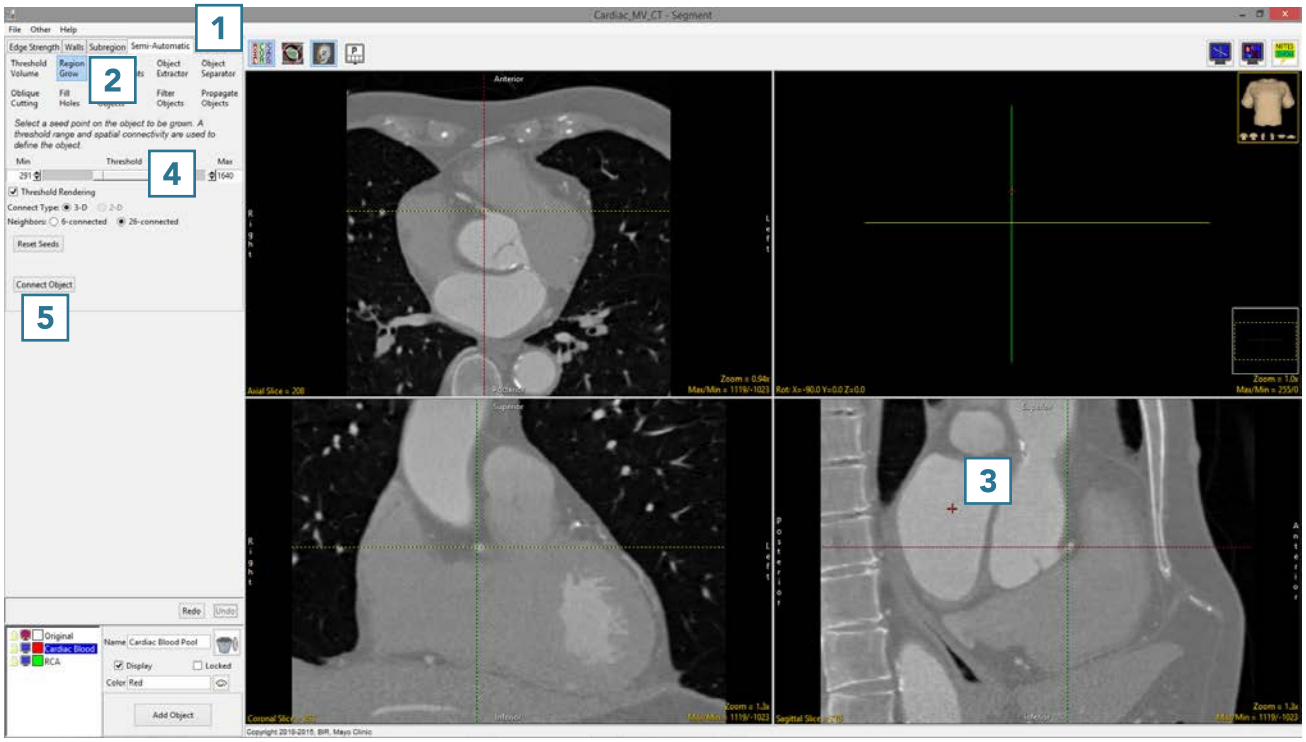
- The structures will be disconnected and assigned to different objects. 6
- Save your work by selecting File > Save Object Map.



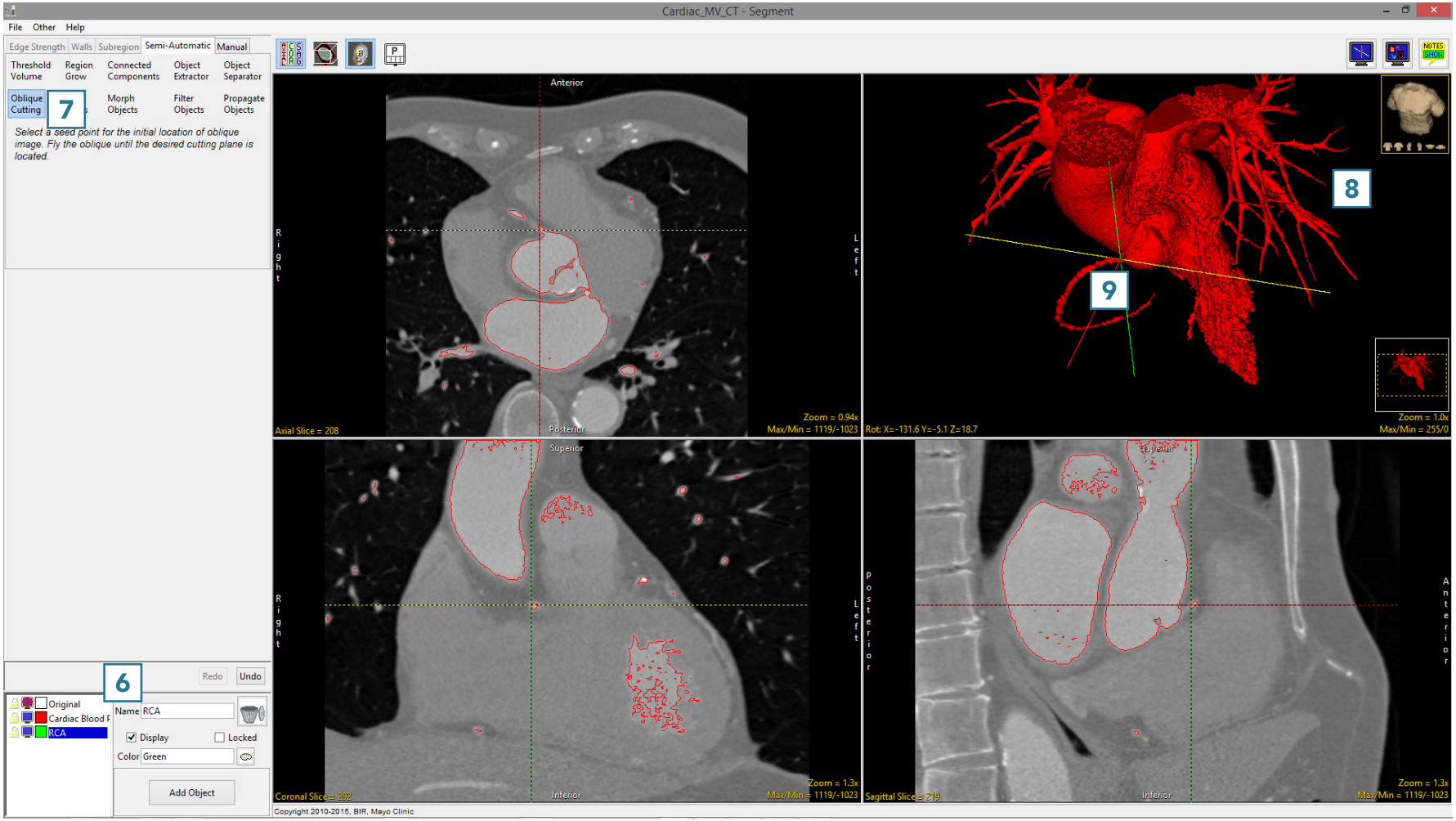
# 12. Editing Objects via Oblique Cutting

- Select a data set and open Segment.
- Select Semi-Automatic 1 and choose Region Grow. 2
- Set a seed point in the middle of the left atrium. 3
- Define a threshold range to describe the blood pool 4 and click Connect Object. 5

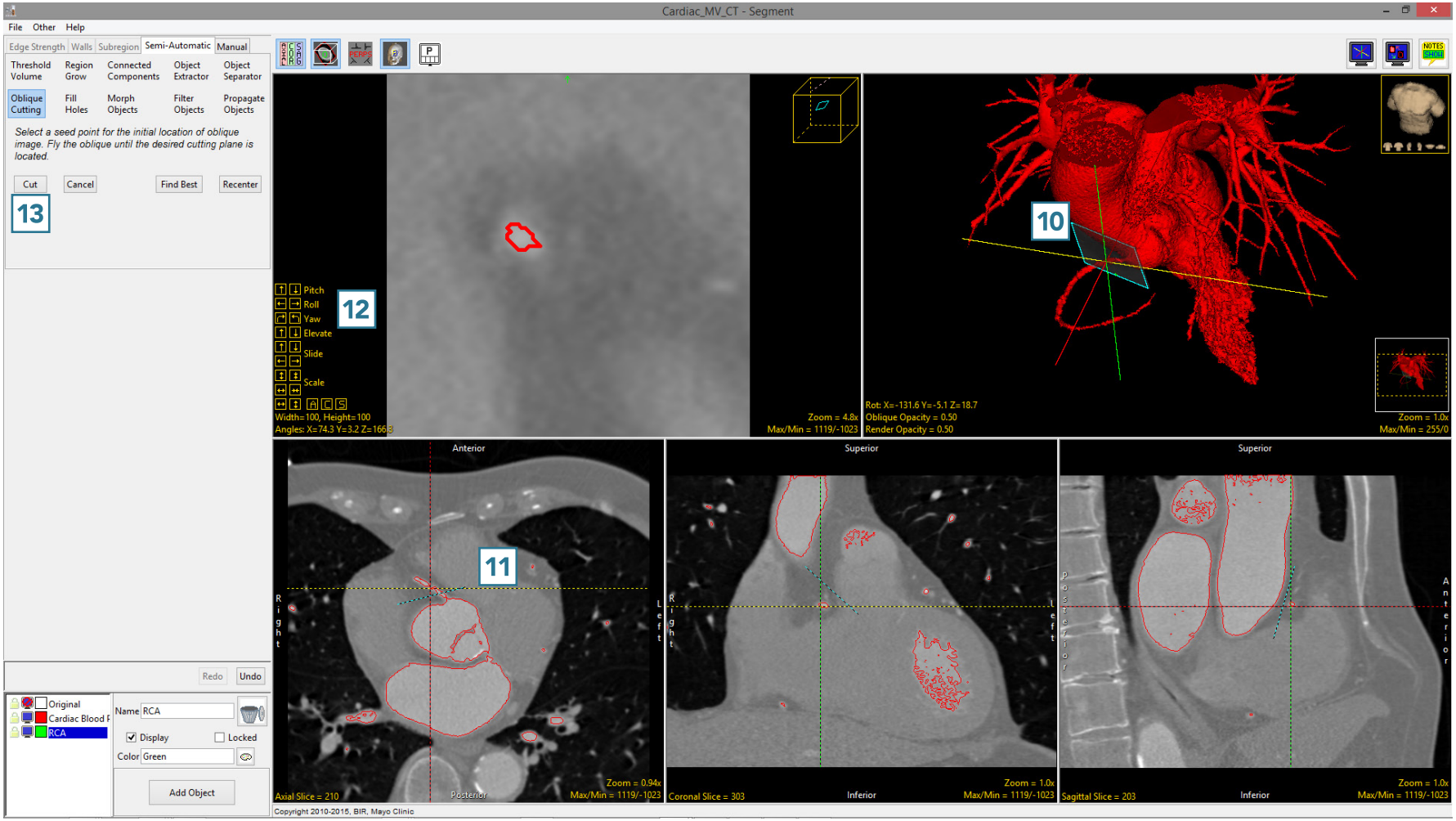
Download the Cardiac_CT data set to follow along
http://analyzedirect.com/data/



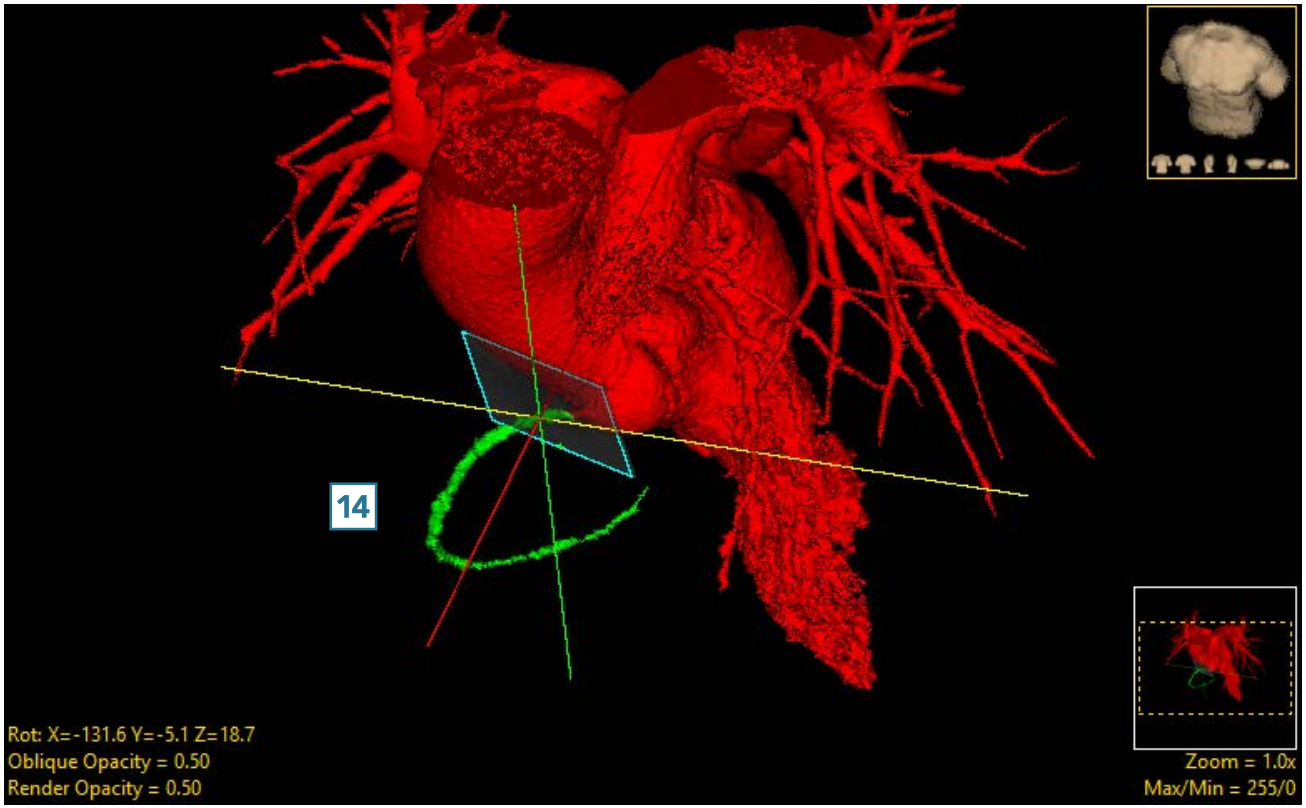
- Add a new object and name it RCA (right coronary artery). 6
- Select Oblique Cutting. 7
- Rotate the rendering of the heart so the RCA is visible. 8
- Move your cursor to the base of the RCA and click to set a seed point on the RCA. 9



- The Segment interface will update while the Oblique Cutting algorithm finds the best plane to cut the RCA from the main heart object.
- If the computed cut plane is not ideal you can adjust the plane interactively on the rendering 10 or on any of the slice displays. 11
- The navigation tools can also be used on the oblique image. 12
- Select Cut 13 to cut the data.



- The RCA will be separated from the main object and assigned to the RCA object. 14
- To return to the regular display, click on the Toggle Obliques button to switch off the display of the oblique image.
- Select File > Save Object Map to save your work.



# Fill Holes

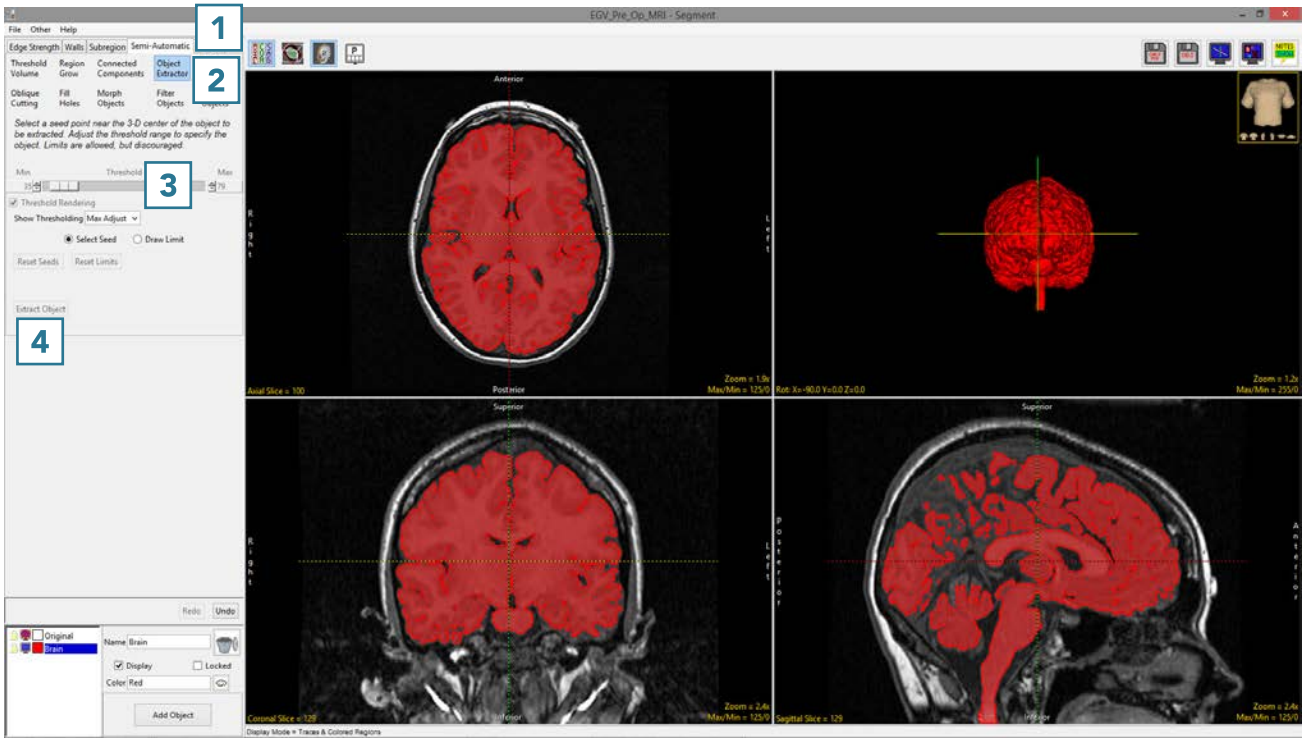
The fill holes function performs a flood-fill operation on the selected object. The operation reassigns voxels belonging to other objects to the selected object. The fill operation stops when it reaches the boundary of the object.

# 13. Filling Holes in Objects

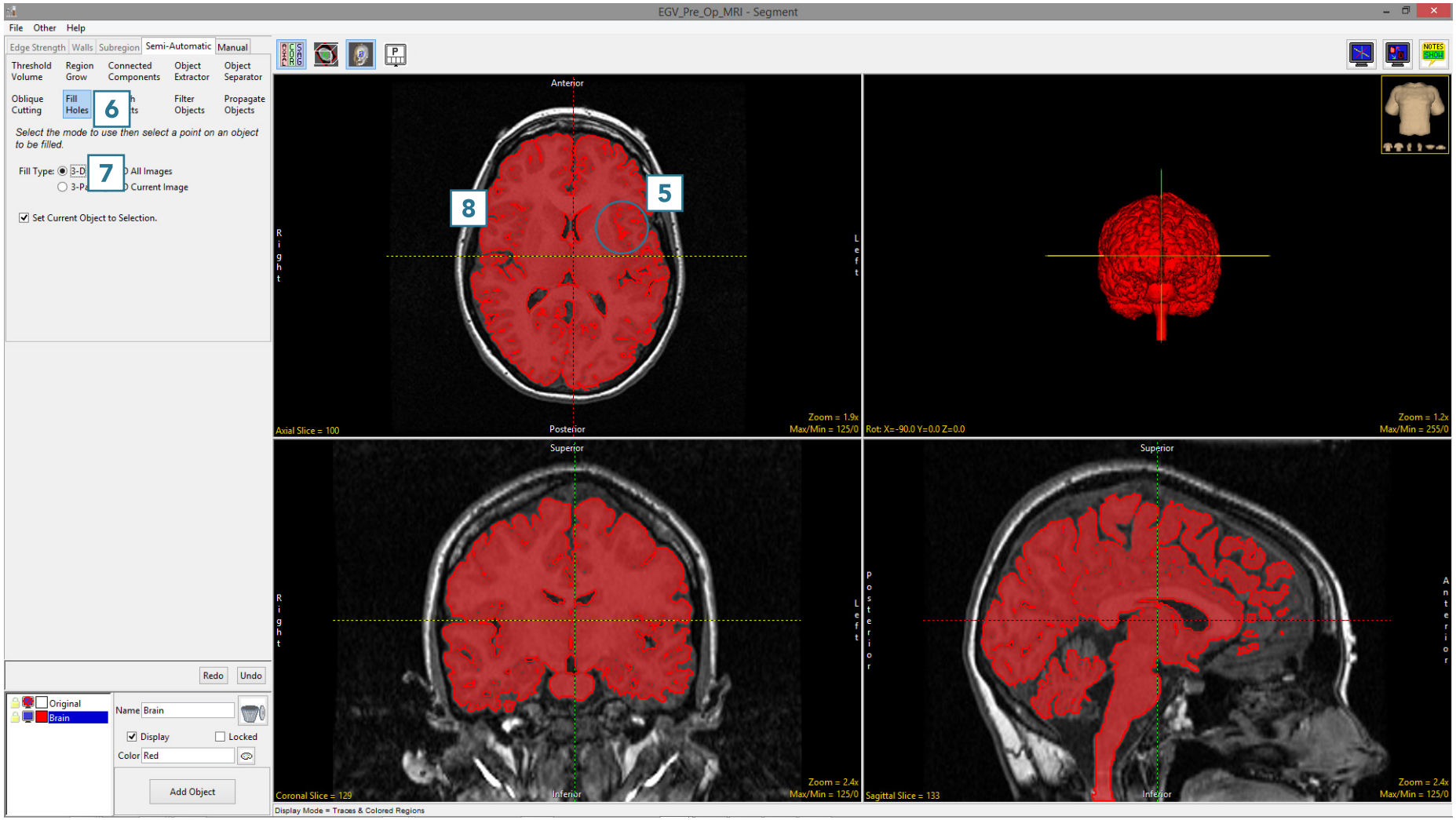
After the initial segmentation, an object may contain holes, which are voxels belonging to the Original object. To obtain an accurate volume measurement and to ensure the object is whole, it may be necessary to apply a fill holes operation on the object.

- Select a data set and open Segment.
- Select Semi-Automatic 1 and choose Object Extractor. 2
- Click on the image data to set a seed point.
- Adjust the minimum and maximum threshold values 3 to define the structure and select Extract Object. 4

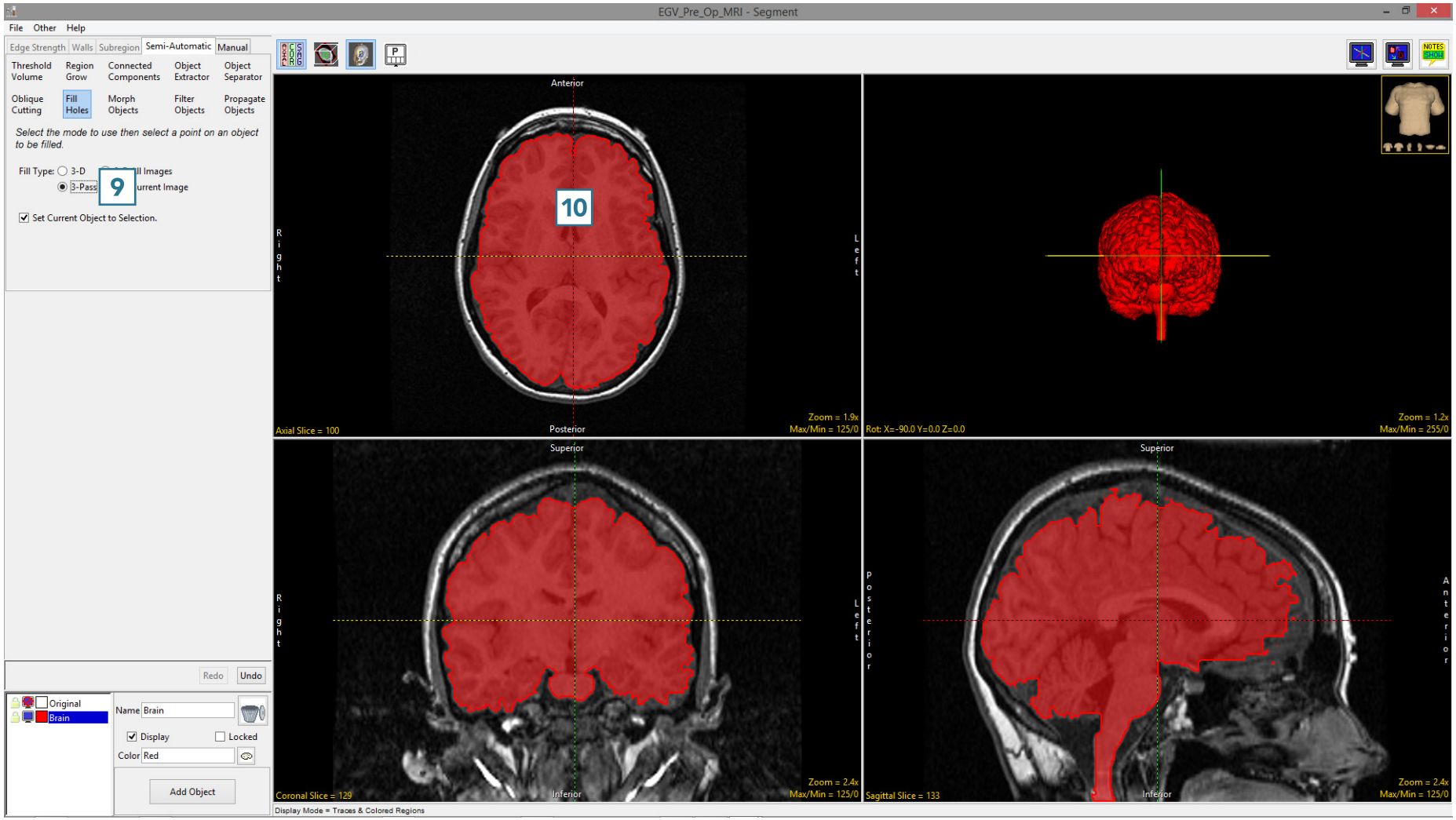
Download the EGV_MRI data set to follow along
http://analyzedirect.com/data/



- To remove small holes in the object 5 which are a result of the segmentation parameters, select Fill Holes. 6
- With the Fill Type set to 3D, 7 click on the object to fill smaller holes in the object. 8



- To fill larger holes, such as the ventricular CSF, use the 3-Pass Fill Type 9 and click on the brain. 10 All larger holes will be filled and assigned to the object.
- Select File > Save Object Map to save your work.

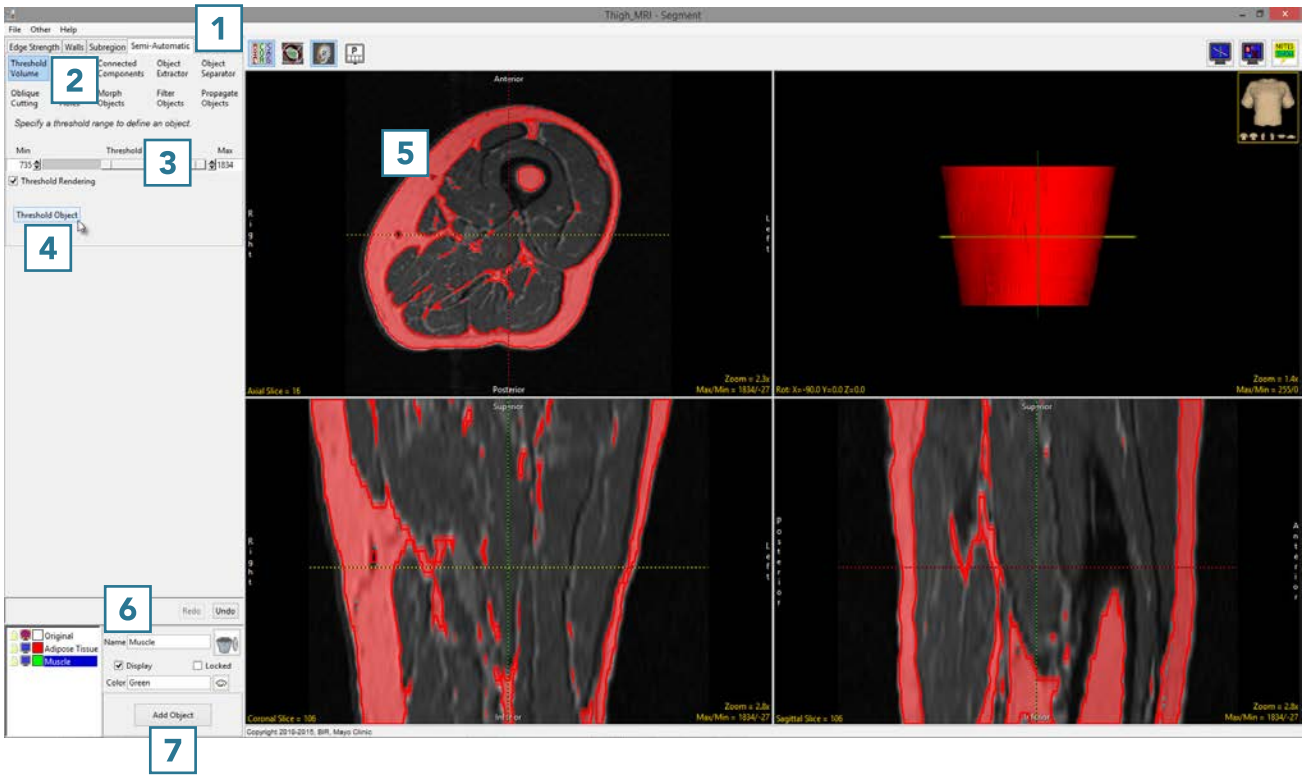


# 14. Using Fill Holes for Segmentation

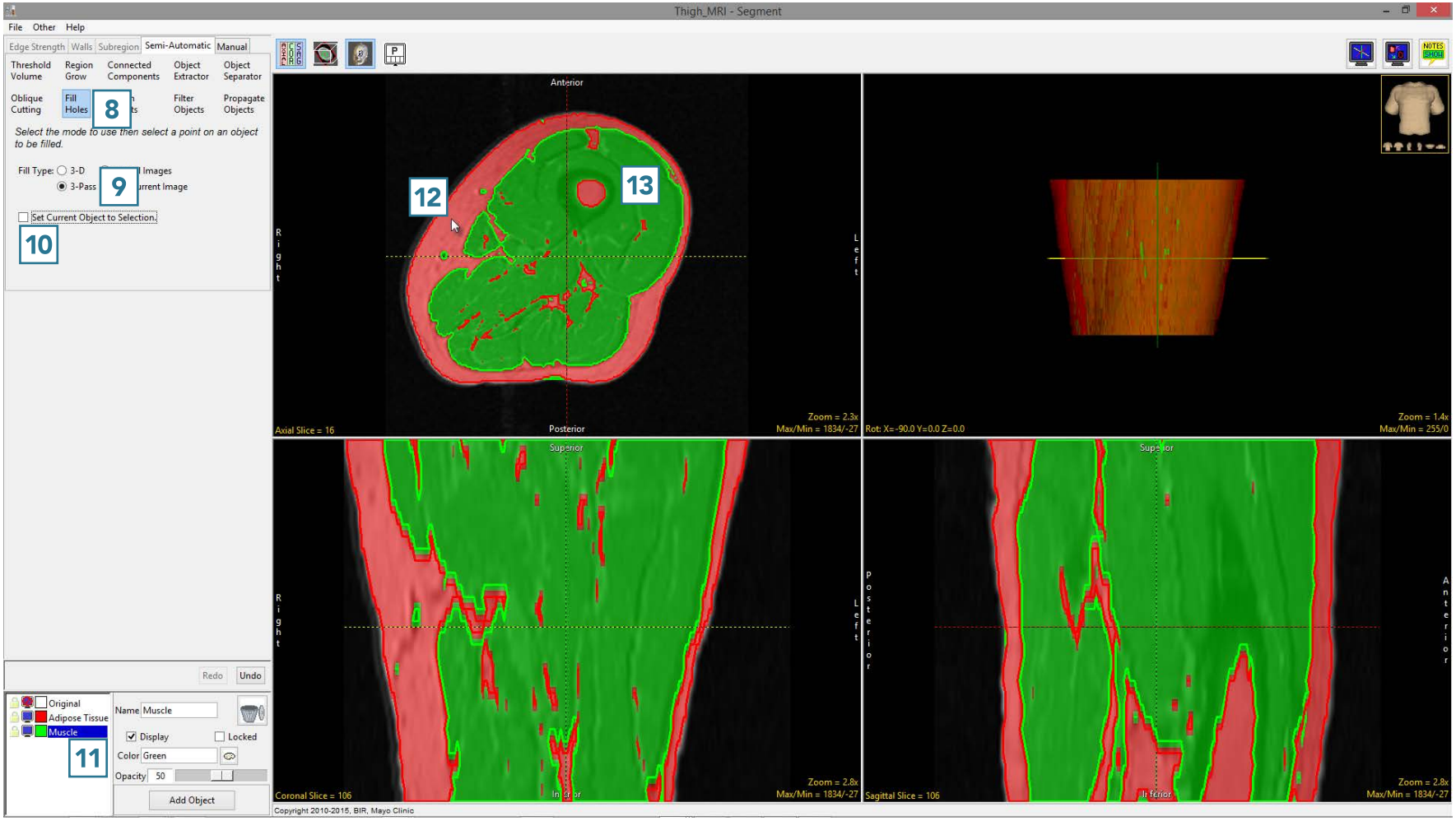
The fill holes option can also be used as a strategy to segment multiple objects. In this example we isolate the adipose tissue via threshold-based segmentation from a water-suppressed MRI data set. We will then use fill holes to create the muscle object and the intramuscular adipose tissue object.

- Select the data set and open Segment.
- Select Semi-Automatic 1 and choose Threshold Volume. 2
- Set a threshold range 3 to globally segment the adipose tissue and click Threshold Object. 4
- The adipose tissue will be segmented. 5
- Rename the object, 6 add a new object 7 and name the object Muscle.

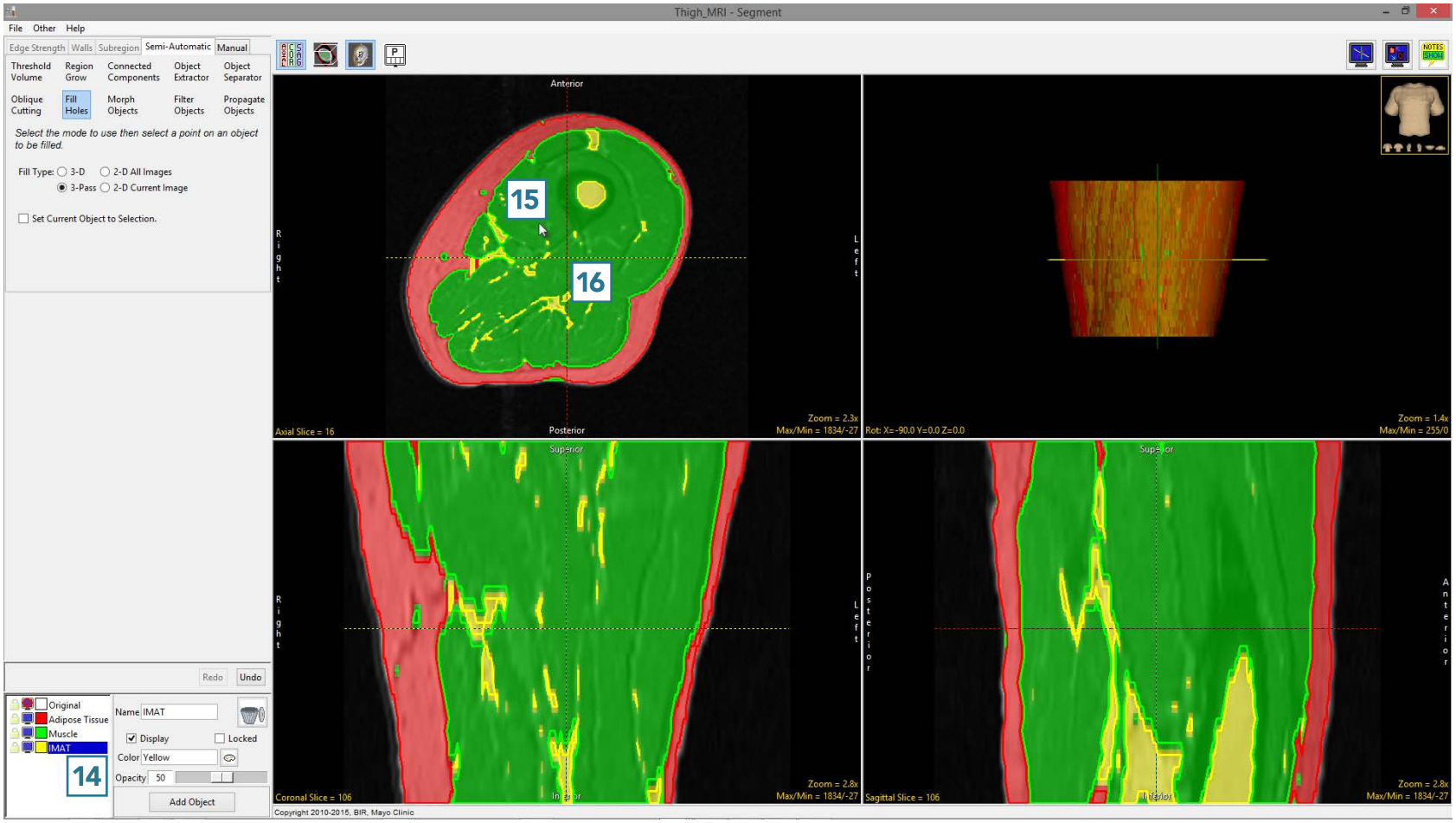
**Download the Thigh_MRI data set to follow along http://analyzedirect.com/data/**



- Select Fill Holes 8 and set the Fill Type to 3-Pass. 9
- Uncheck the Set Current Object to Selection 10 checkbox.
- Ensure that the Muscle object is selected 11 and click on the Adipose Tissue object. 12 The voxels inside the Adipose Tissue object currently assigned to the Original object will be reassigned to the Muscle object. 13



- To assign the voxels labeled as Adipose Tissue within the Muscle object to Intramuscular Adipose Tissue (IMAT).
- Add a new object 14 and name it IMAT.
- Click on the Muscle object to fill it. 15 The voxels inside the Muscle object currently assigned to the Adipose Tissue object will be filled and assigned to the IMAT object. 16
- Select File > Save Object Map to save your work.



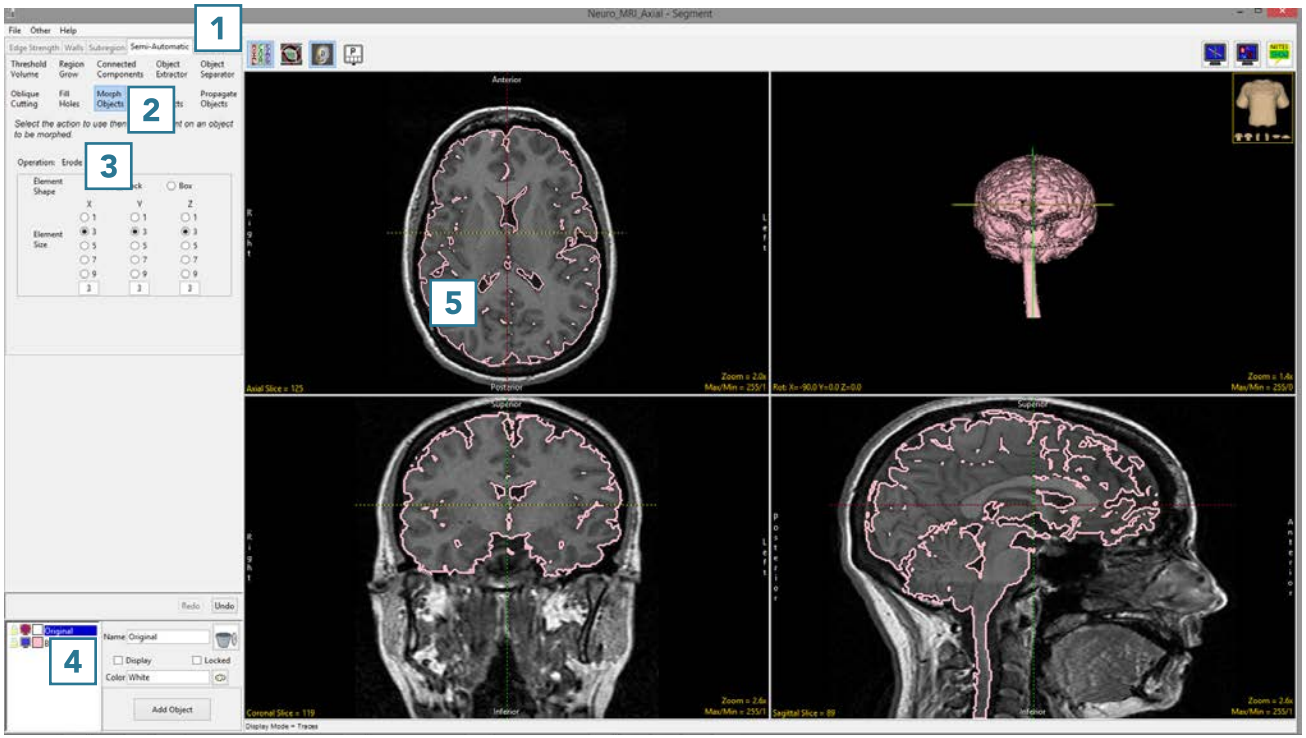
# Morph Objects

The Morph Objects option allows users to apply rudimentary morphological operations to objects. The operations available are dilate, erode, open and close. Additional morphological operations are accessible from the Morphology tool in Process.

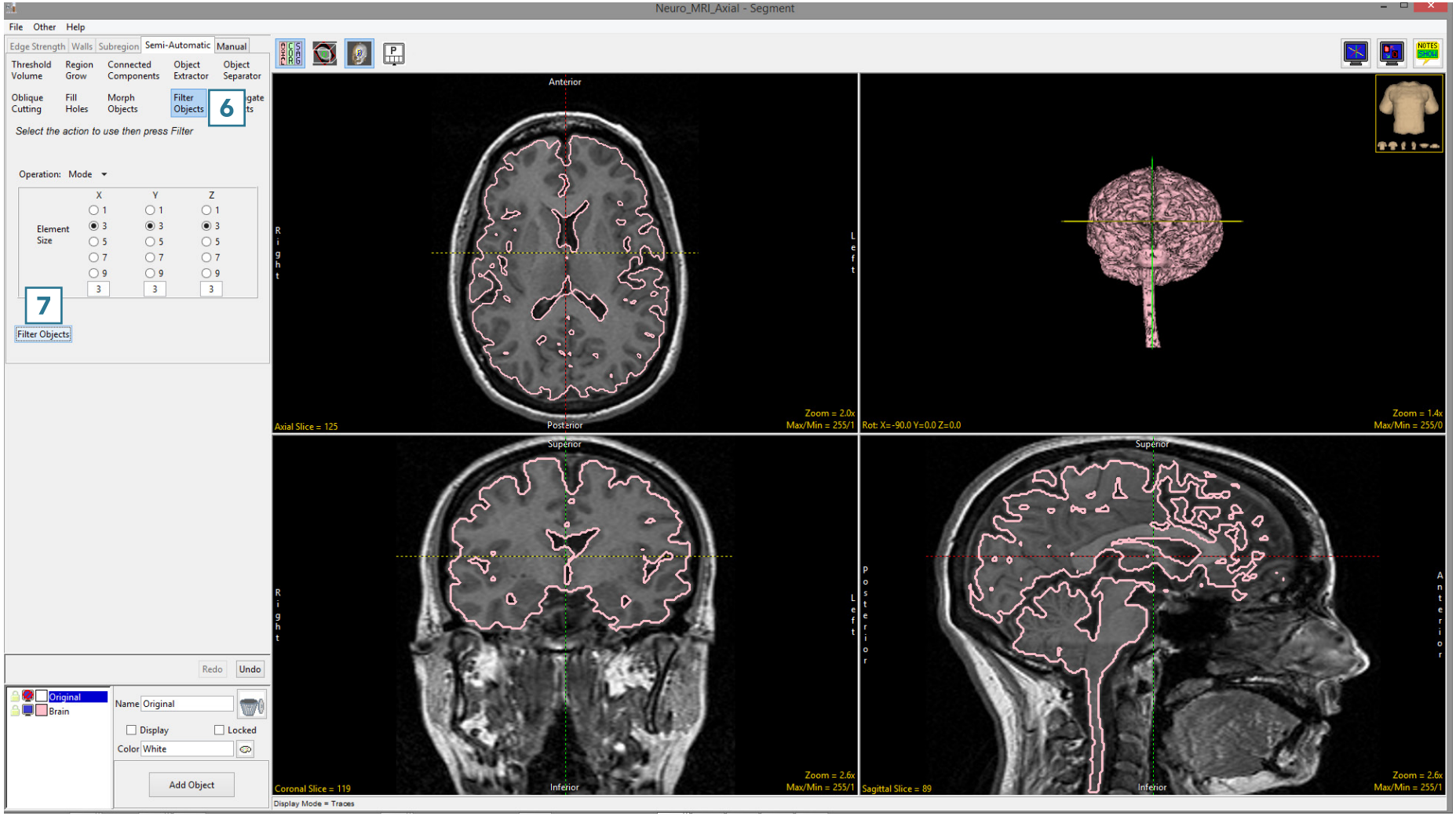
# 15. Using Morphological Operations to Improve Segmentation

- Select a data set and open Segment.
- Select Semi-Automatic 1 and choose Object Extractor.
- Click on the image data to set a seed point.
- Adjust the minimum and maximum threshold values to define the structure and select Extract Object.
- Once the object is segmented, rename and update the color.
- Choose Morph Object 2 and set Operation to Erode. 3
- Leave the element size set to 3 X 3 X 3.
- Set the target object to Original. 4 This will specify that any eroded voxels will be reassigned to the Original object.
- Now click on the brain 5 to initiate the erosion.

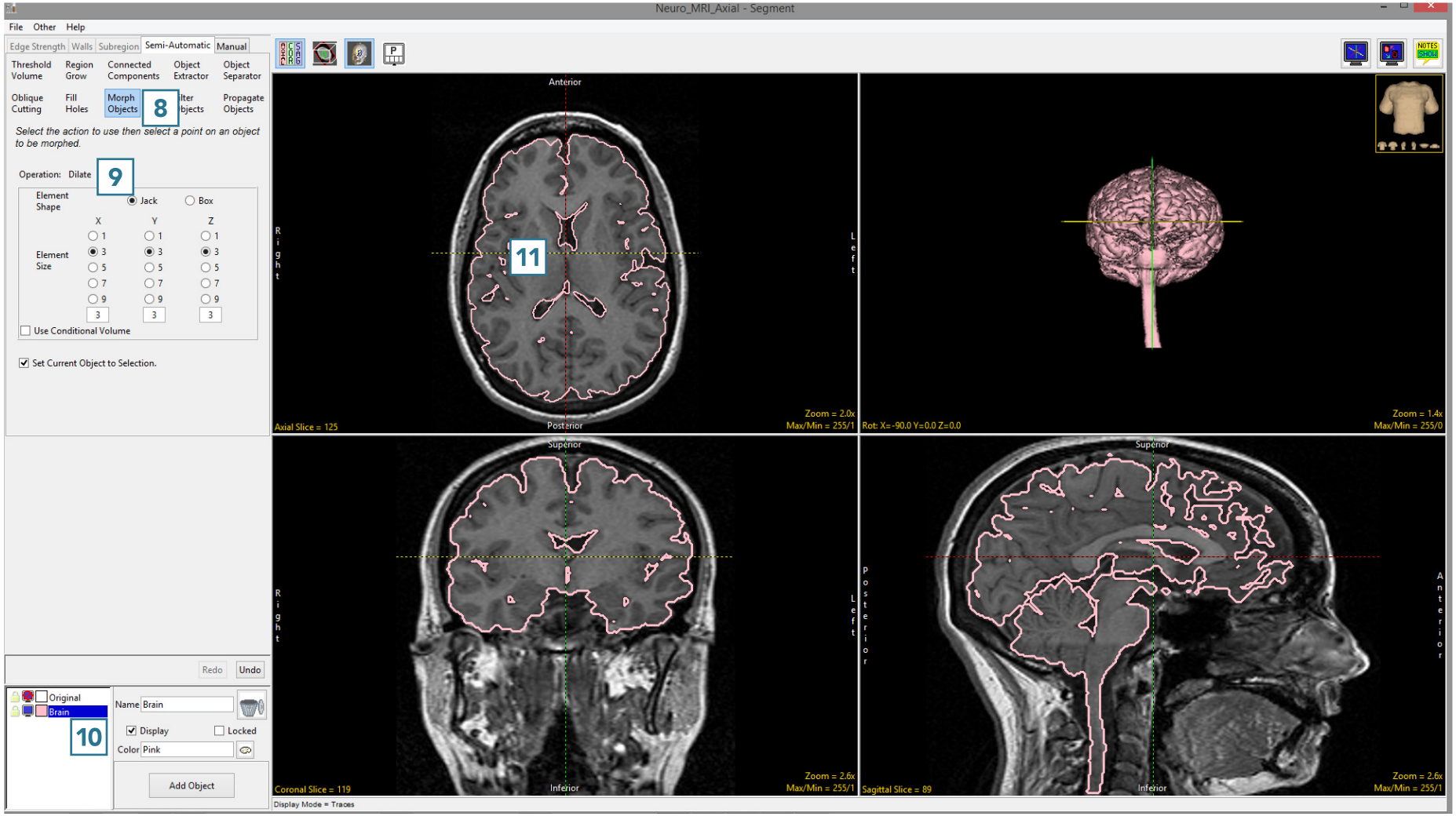
**Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/**



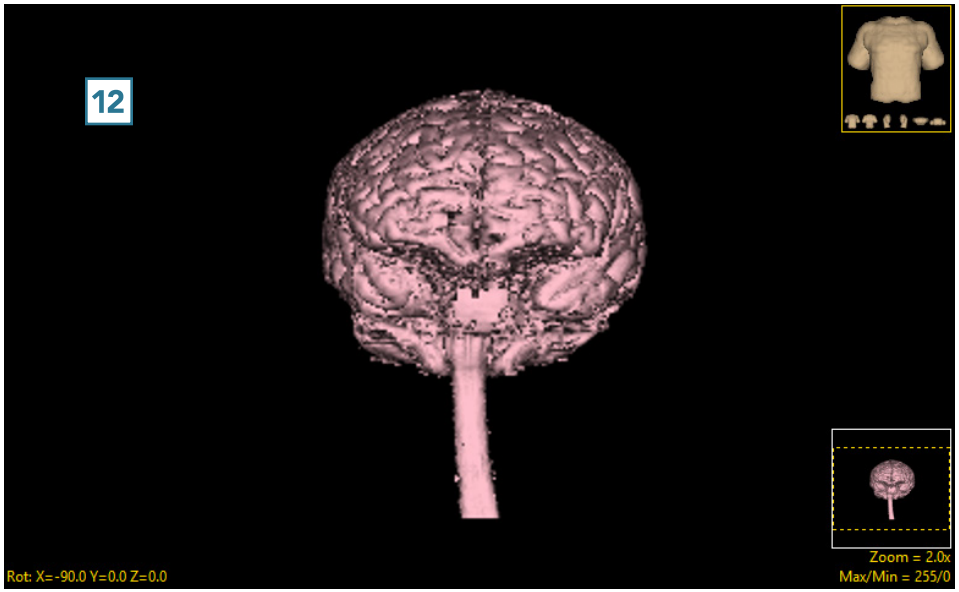
- Select Filter Objects 6 and apply a 3 X 3 X 3 Mode filter to the brain by clicking Filter Objects. 7

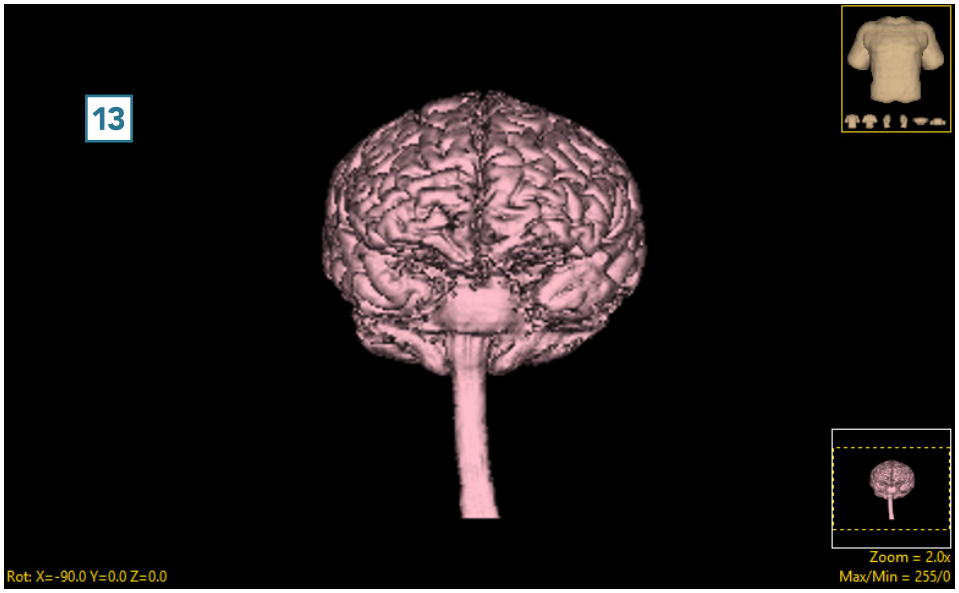


- Select Morph Objects 8 and set the Operation to Dilate. 9
- Select the Brain object 10 and click on the brain. 11



Note the difference between the pre 12 and post 13 processed brain objects.



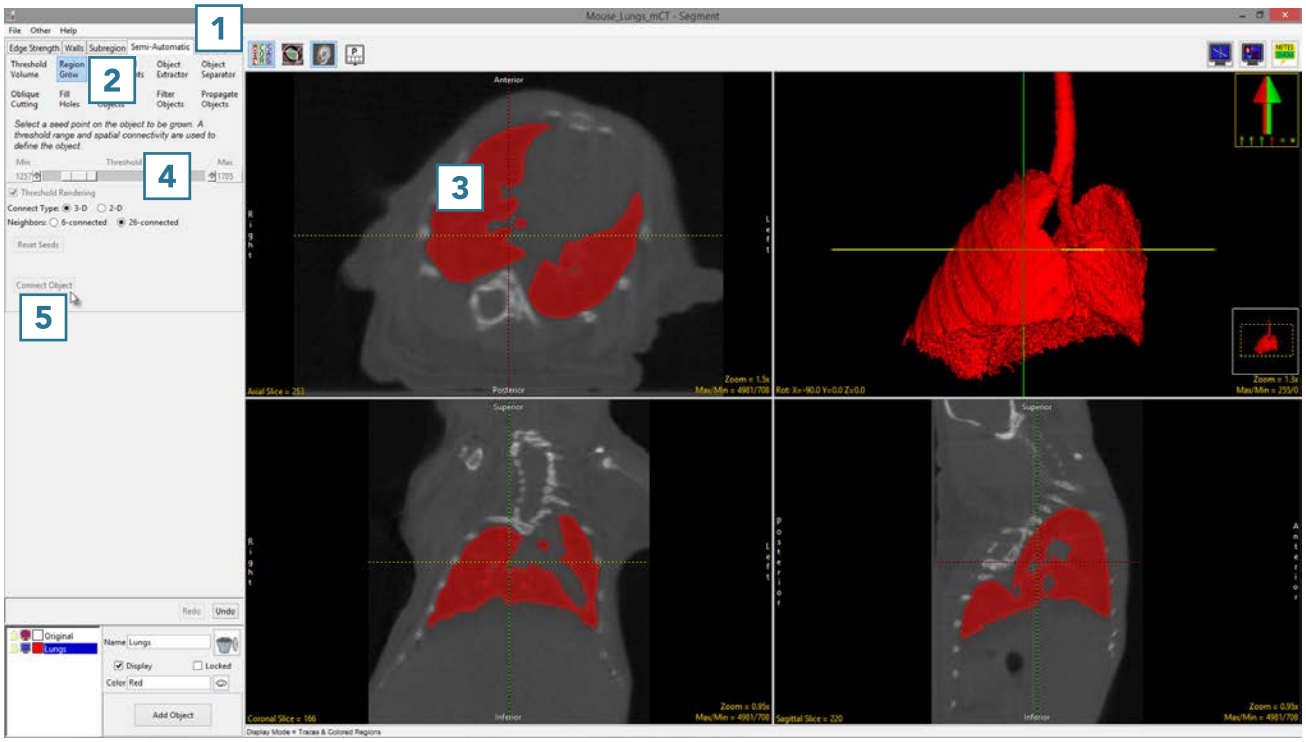



# Filter Objects

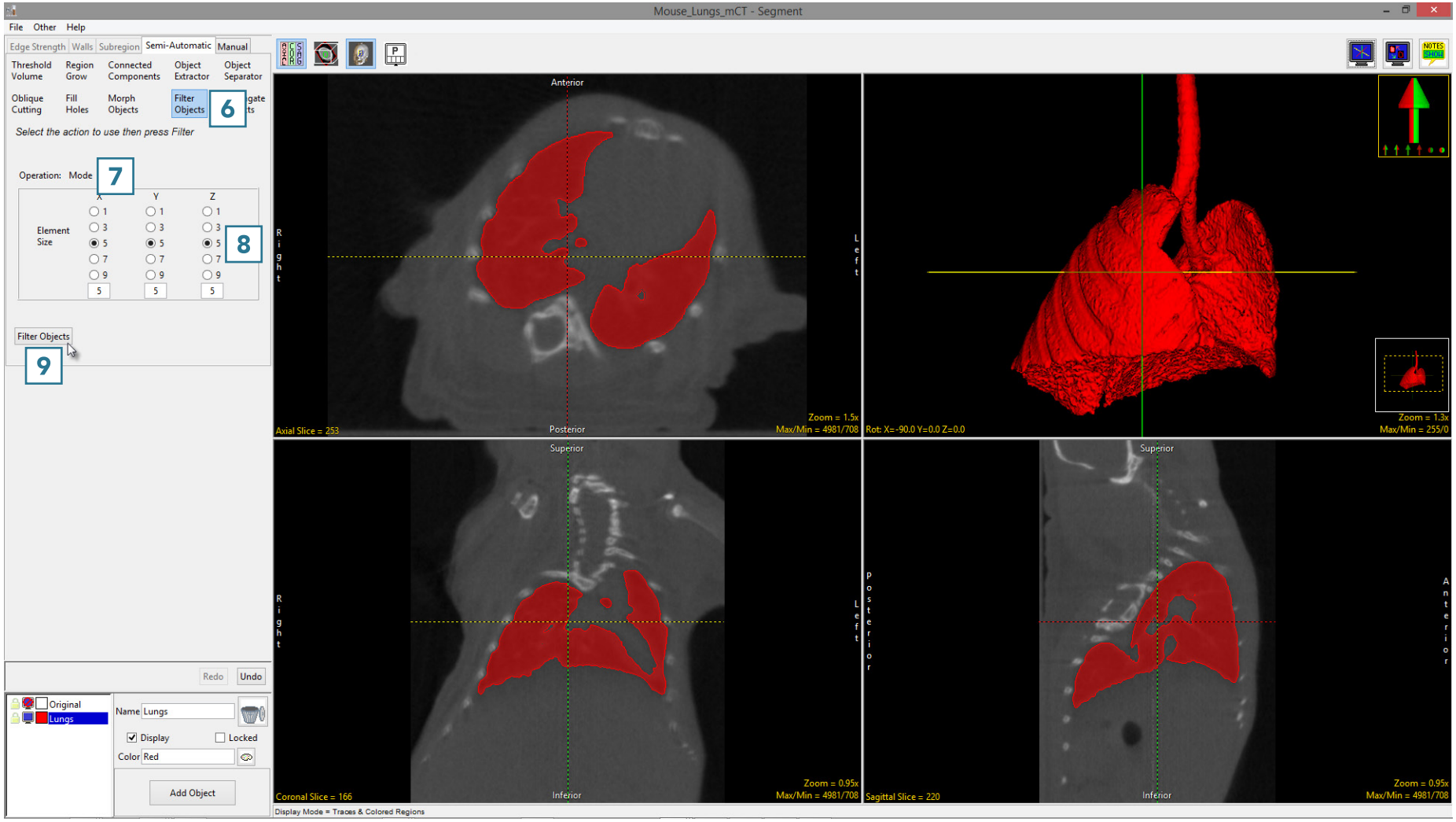
Filtering objects can reduce noise, fill small holes, and smooth edges. The filter is only applied to segmented objects and does not change the original data.

- Select the data set and open Segment.
- Select Semi-Automatic 1 and choose Region Grow. 2
- Set a seed point on the object you want to isolate 3 and set a threshold range 4 that describes the object.
- Click Connect Object. 5

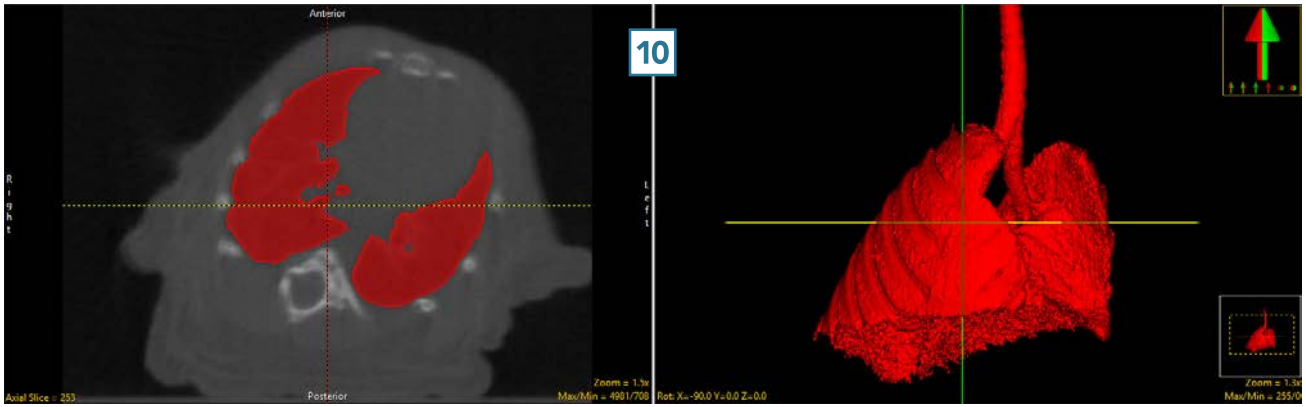
Download the Mouse_Lungs data set to follow along http://analyzedirect.com/data/

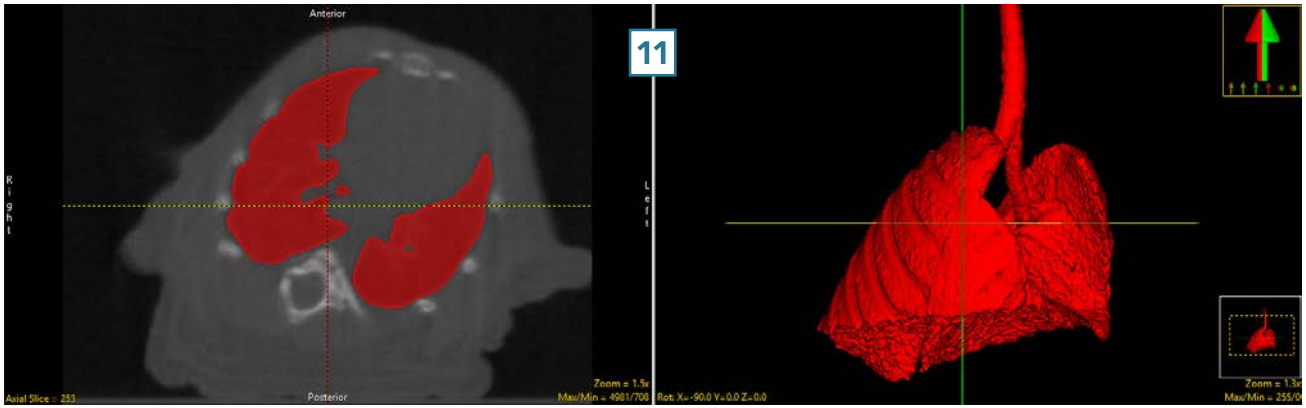


- Select Filter Objects. 6
- Set the Operation to Mode. 7
- Set the Element Size to 5 X 5 X 5 8 and select Filter Objects. 9



Note the difference in the 2D and 3D regions between the unfiltered 10 and filtered 11 segmentation results. Filtering has filled small holes, removed noise around the surface of the lung parenchyma and smoothed the contours of the segmentation.



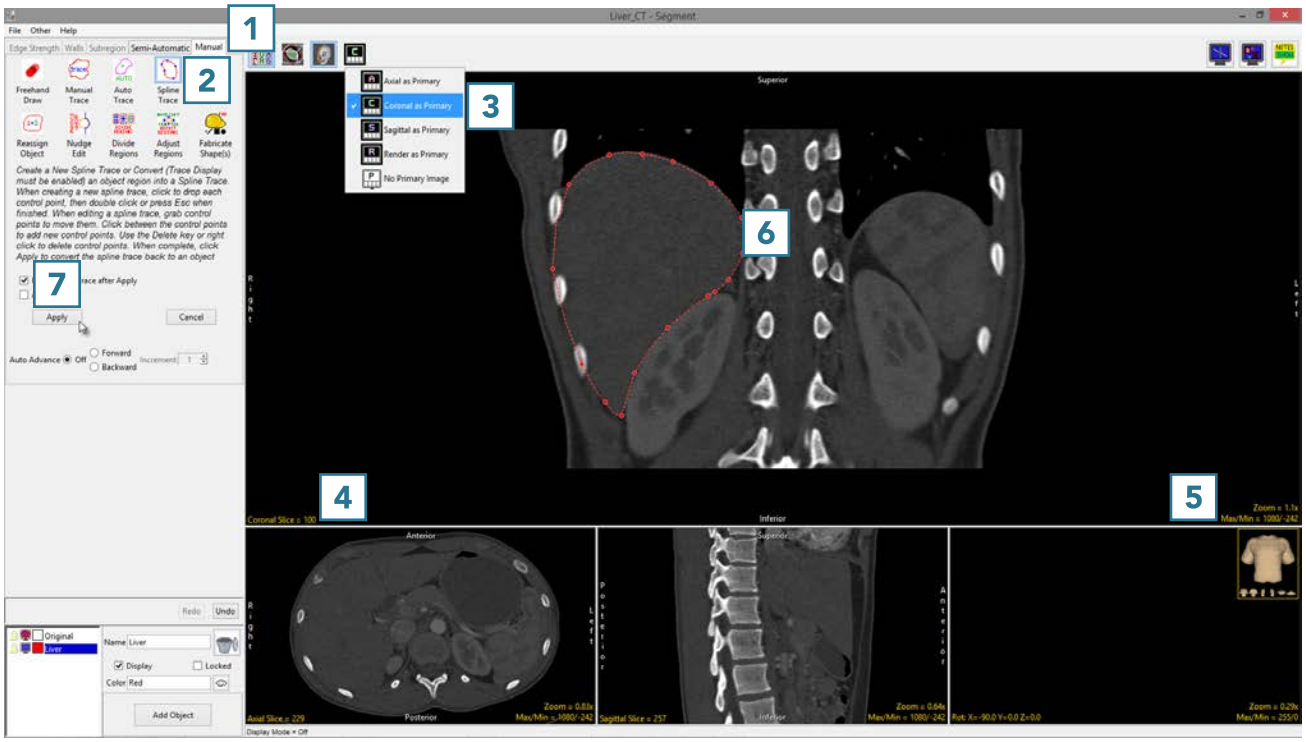
# Propagate Objects

The Propagate Objects tool uses shape-based interpolation to extend the definition of a region to slices of the volume on which it was not defined. For example, if the user defined a region on every fifth slice, this tool could be used to fill in the region on the skipped slices. The user must specify the direction in which objects are propagated by choosing the orthogonal orientation in which they were defined. A smoothing option is available which filters the objects to produce a smoother segmentation result.

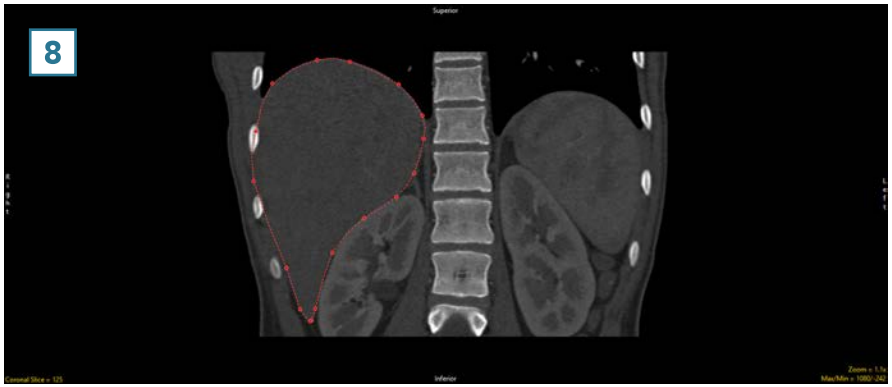
# 16. Propagate Objects

- Select a data set and open Segment.
- Select Manual 1 and choose Spline. 2
- Set the primary display to Coronal 3 and double-click on Slice 4 to move to coronal slice 100.
- Adjust the display intensity, 5 if desired.
- Trace a spline around the liver 6 and select Apply. 7

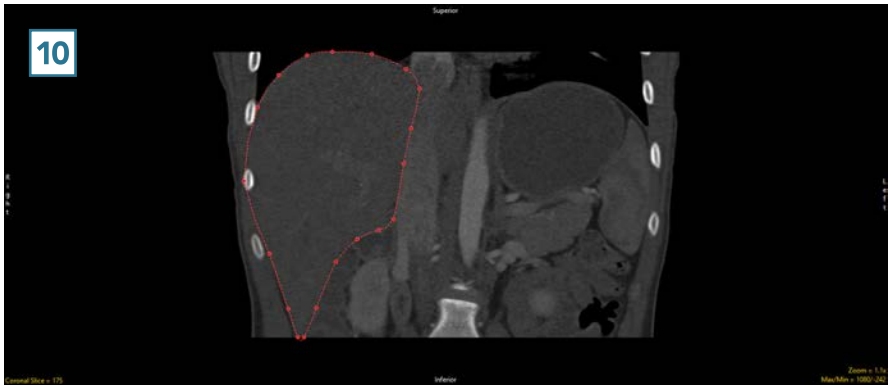
Download the CT_Liver data set to follow along http://analyzedirect.com/data/



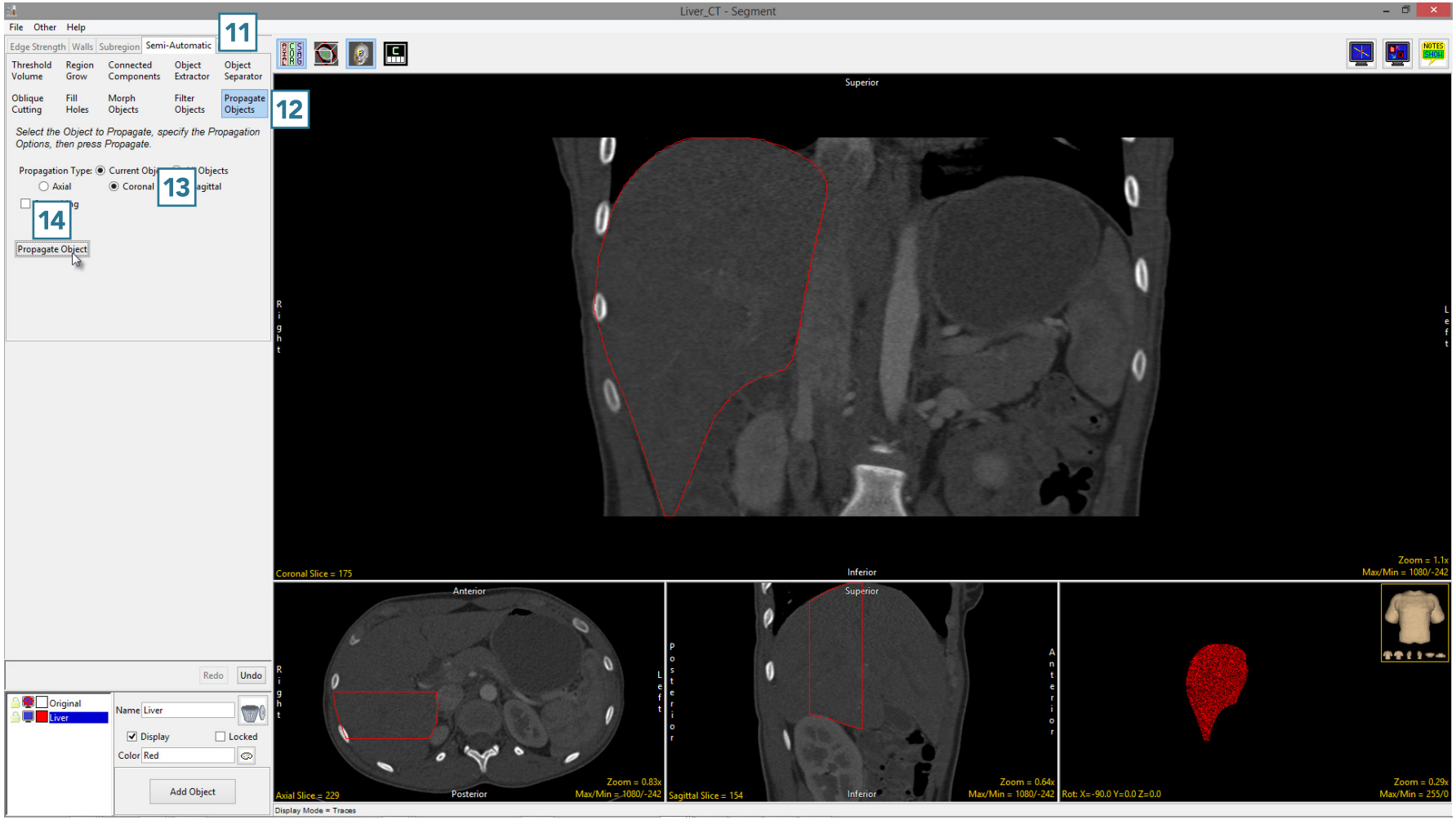
- Move to coronal slice 125 and trace the liver. 8
- Repeat on coronal slices 150 9 and 175. 10







- Select Semi-Automatic 11 and Propagate Objects. 12
- Set the propagation orientation to Coronal 13 and click Propagate Object. 14
- After the object propagation process is complete, the liver object will be defined from slice 100 to slice 175. The object can be reviewed in each orientation and the 3D rendering.



# Manual Tools

The Manual tab provides users with access to interactive segmentation tools for manual 2D slice-based segmentation. These tools allow users to define regions with precision while reducing the time required to perform manual segmentation.

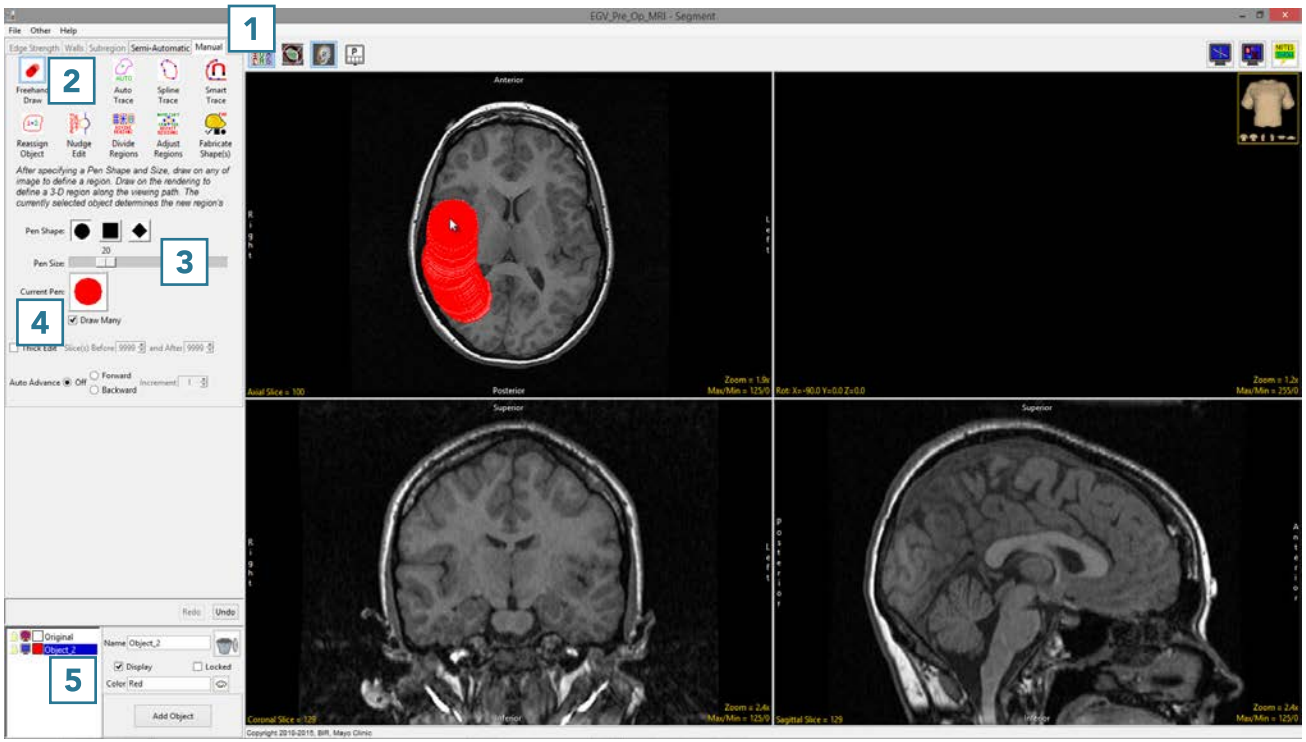
# Freehand Draw

The Freehand Draw tool lets the user draw regions of interest directly onto the image data. Three different Pen Shape options (circle, square, diamond) and a customizable Pen Size (from 1 to 100 pixels) are available.

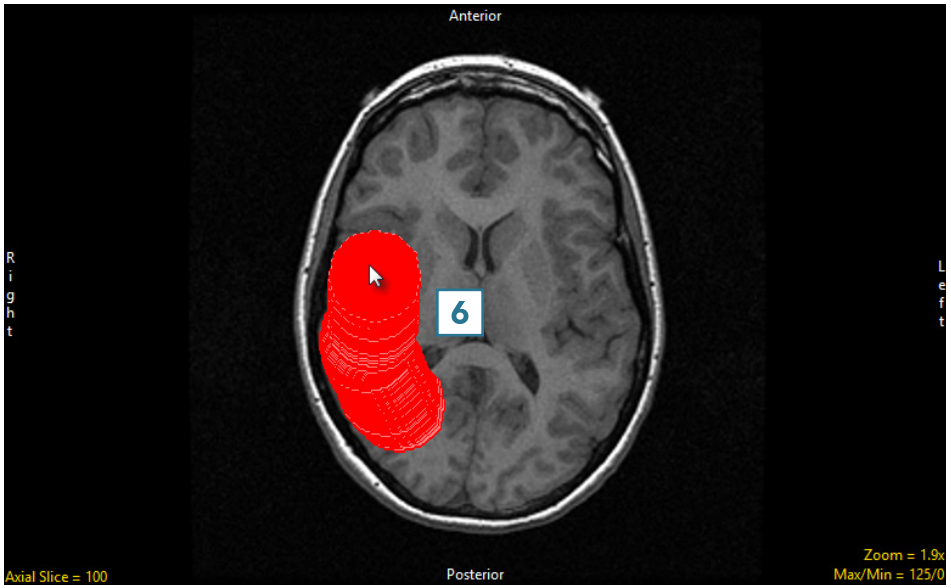
# 17. Using Freehand Draw to Define a 2D Region

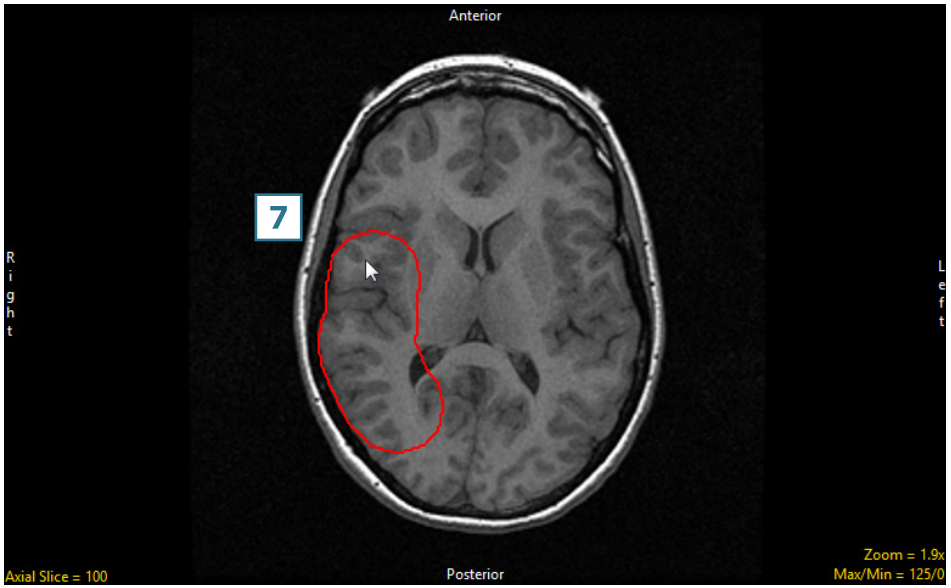
- Select a data set and open Segment.
- Select Manual 1 and choose Freehand Draw. 2
- Use the Pen Size slider to change the Pen Size to 20. 3
- The Current Pen 4 will update to the color of the currently selected object. 5

Download the EGV_MRI data set to follow along
http://analyzedirect.com/data/

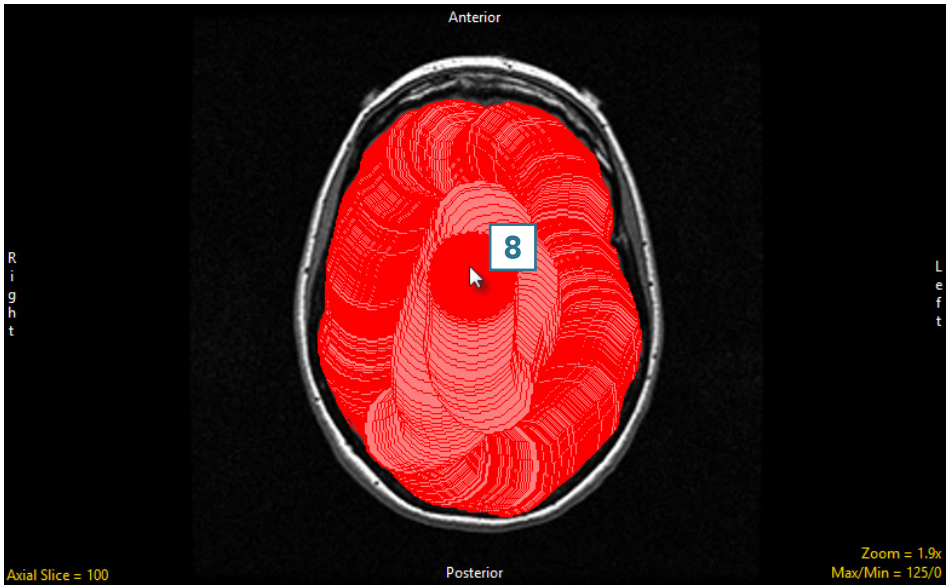


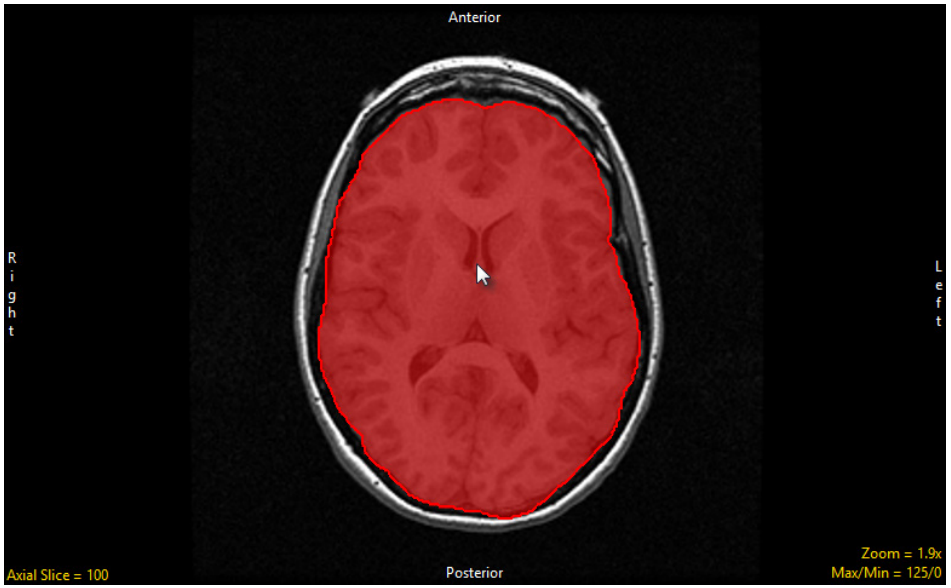
- Left-click on the image and drag the cursor to trace a region. 6
- Releasing the left mouse button will end the trace. 7



Continue to define the brain using the pen tool. 8



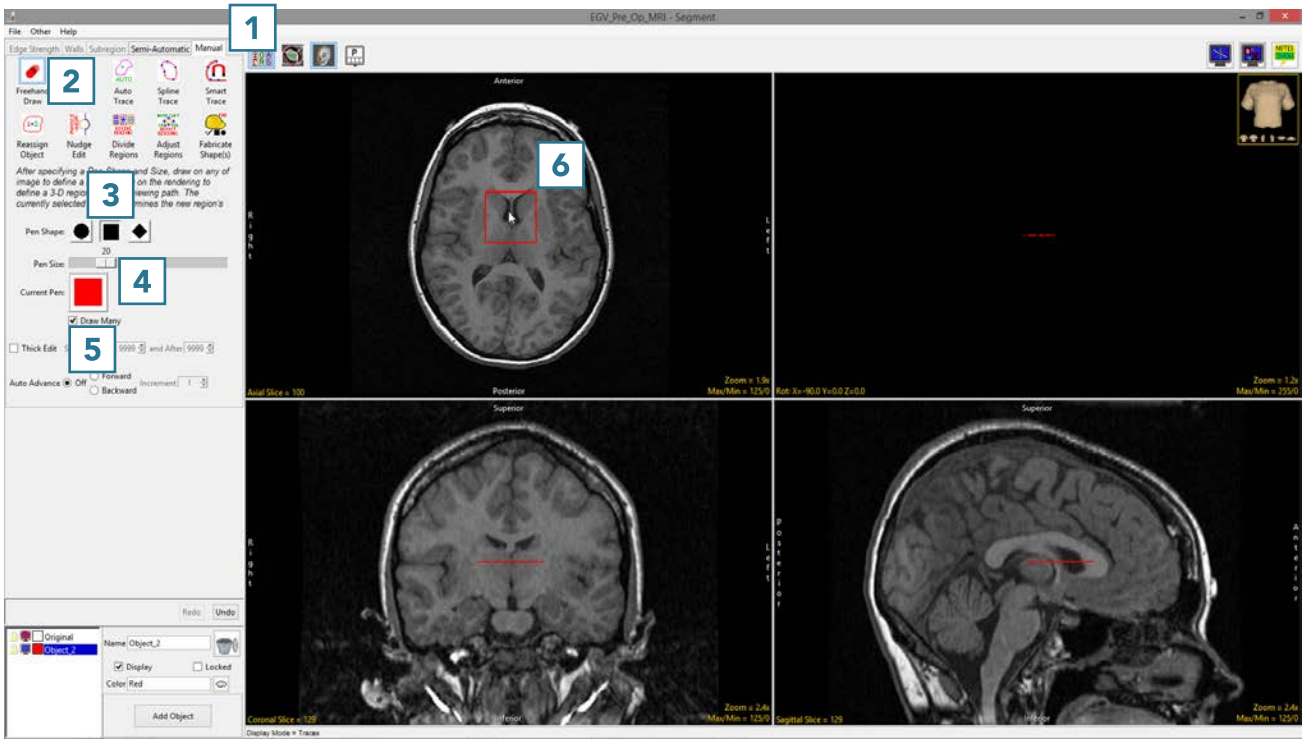



# 18. Using Freehand Draw to Define a Single Shape on a 2D Slice

The Freehand Draw tool allows users to define a single circle, square, or diamond.

- Select a data set and open Segment.
- Select Manual 1 and choose Freehand Draw. 2
- Set the Pen Shape to Square 3 and change the Pen Size to 25. 4
- Uncheck the Draw Many option. 5
- Click on the image to define a square. 6
- Additional squares can be defined by clicking on the slice again.

**Download the EGV_MRI data set to follow along http://analyzedirect.com/data/**

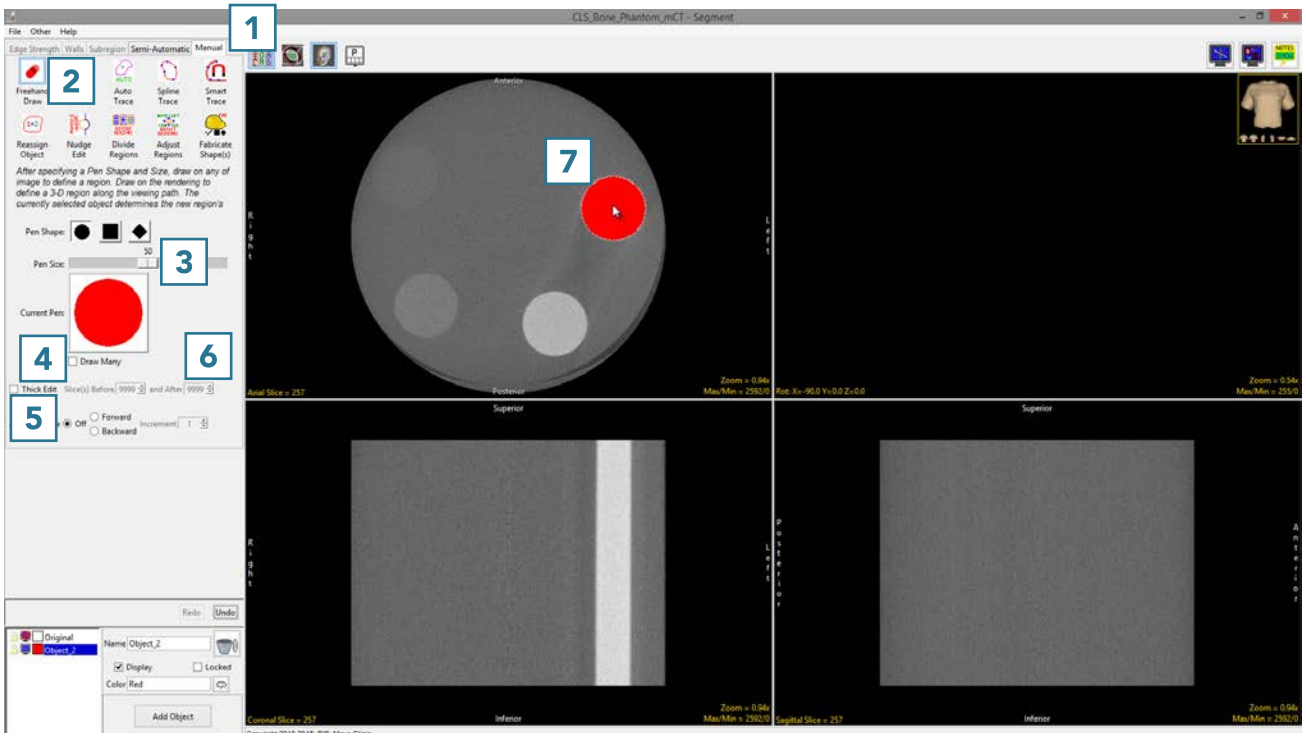


# 19. Using Freehand Draw to Define a Single Shape in 3D

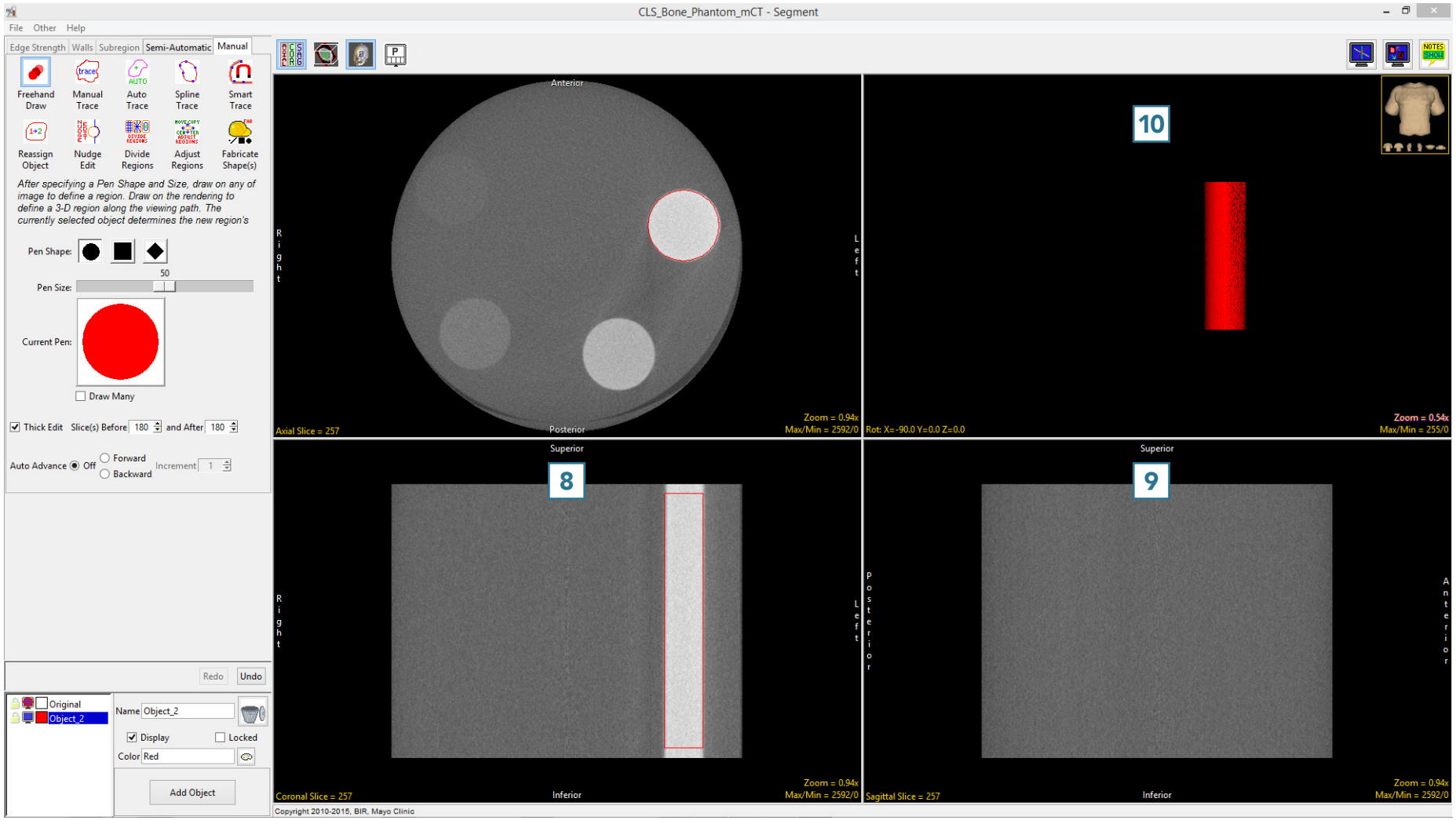
The Freehand Draw tool allows users to define a single shape (circle, square, or diamond) over many slices. This can be helpful when defining regions that are constant through the 3D volume.

- Select a data set and open Segment.
- Select Manual 1 and choose Freehand Draw. 2
- Change the Pen Size to 50 3 and uncheck the Draw Many option. 4
- Check the Thick Edit option. 5
- To define the phantom insert on multiple slices, use the Slice(s) Before and After options 6 to specify the extent of propagation of the 2D region through the data set. In this example, set both parameters to 180.
- Click on an insert 7 to define a region, and note that you can move the 2D region around. The region will not be defined until the left mouse button is released.

**Download the CLS_Bone_Phantom data set to follow along http://analyzedirect.com/data/**



Once the left mouse button is released the regions will be applied to the specified slices. Note the update in the coronal 8 and Sagittal 9 orientations and the 3D rendering. 10



# Painting Regions of Interest

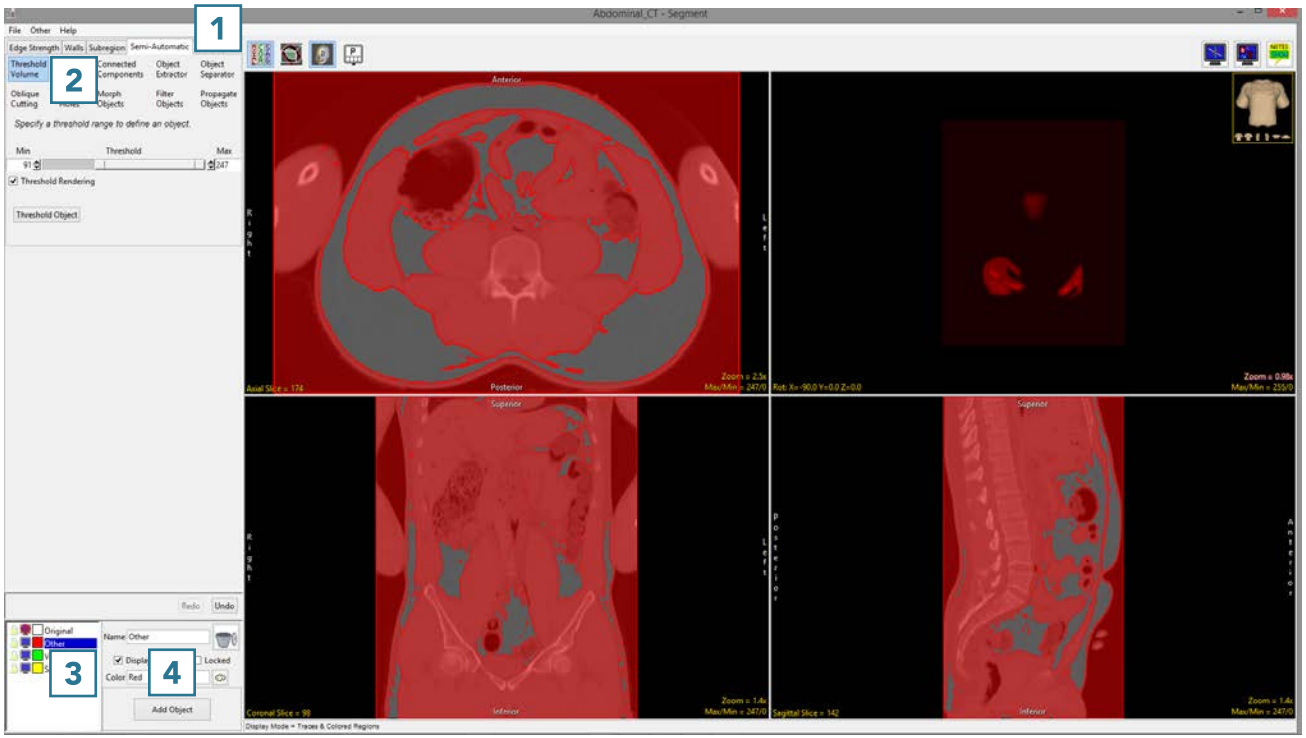
The Freehand Draw tool is particularly useful for manually defining or filling regions between locked objects, specifically when the region of interest is not easily segmentable but the surrounding tissue is.

# 20. Using Freehand Draw to Paint Regions of Interest

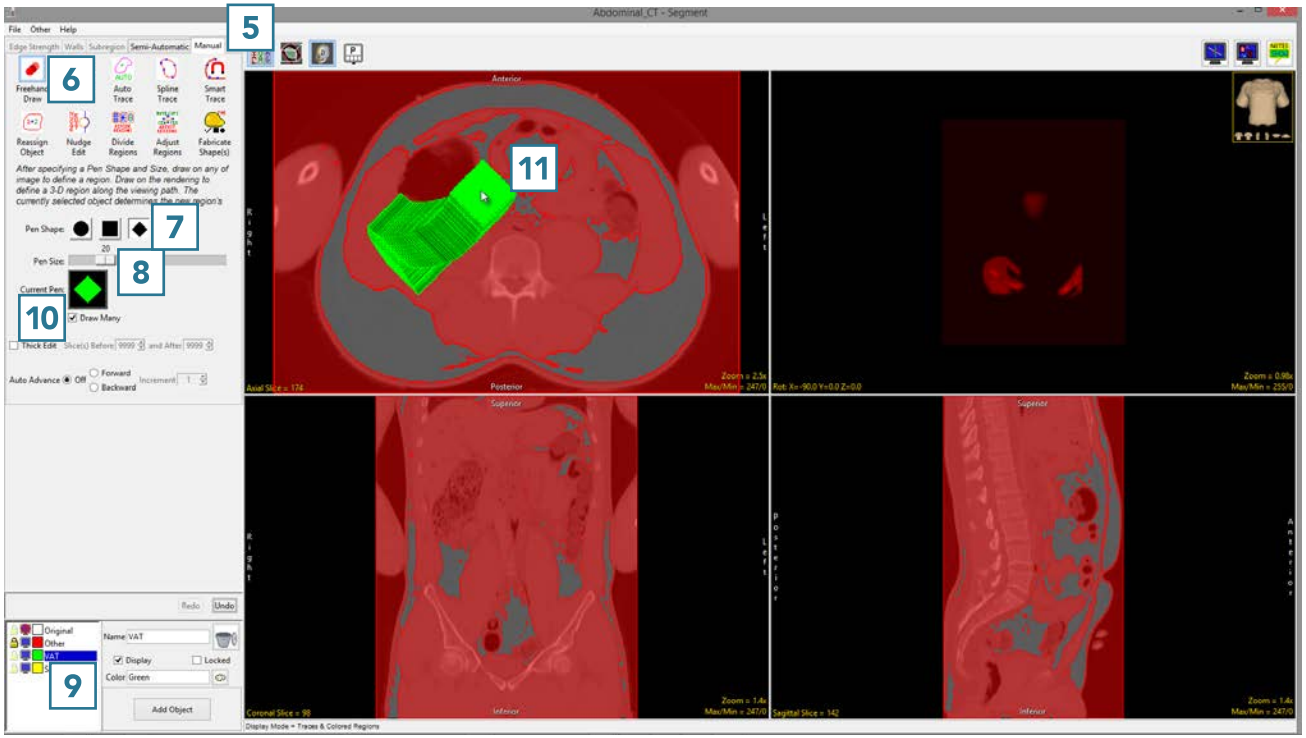
- Select a data set and open Segment.
- Select Semi-Automatic 1 and choose Threshold Volume. 2
- Change the name of the current object to Other, then add two new objects: VAT (visceral adipose tissue) and SAT (subcutaneous adipose tissue). 3
- Select the Other object and use global thresholding to assign voxels having intensity values of 0 to 81 and 91 to 247 to the Other object. This will assign all of the non-adipose tissue voxels to the Other object.
- Lock the Other object. 4

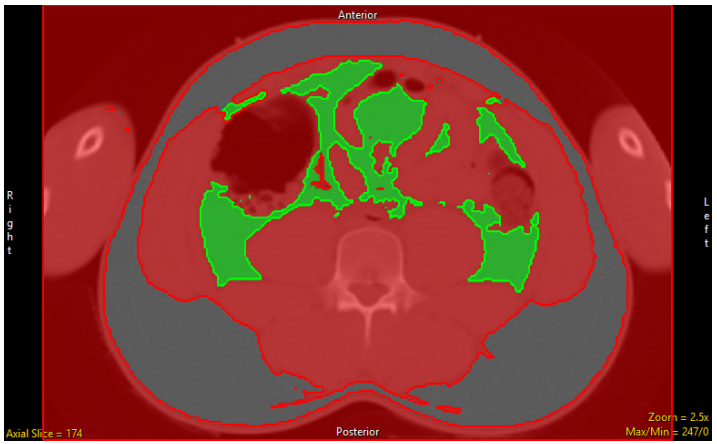
For more information on threshold-based segmentation, refer to Threshold Volume.

**Download the VH_Abdomen data set to follow along http://analyzedirect.com/data/**

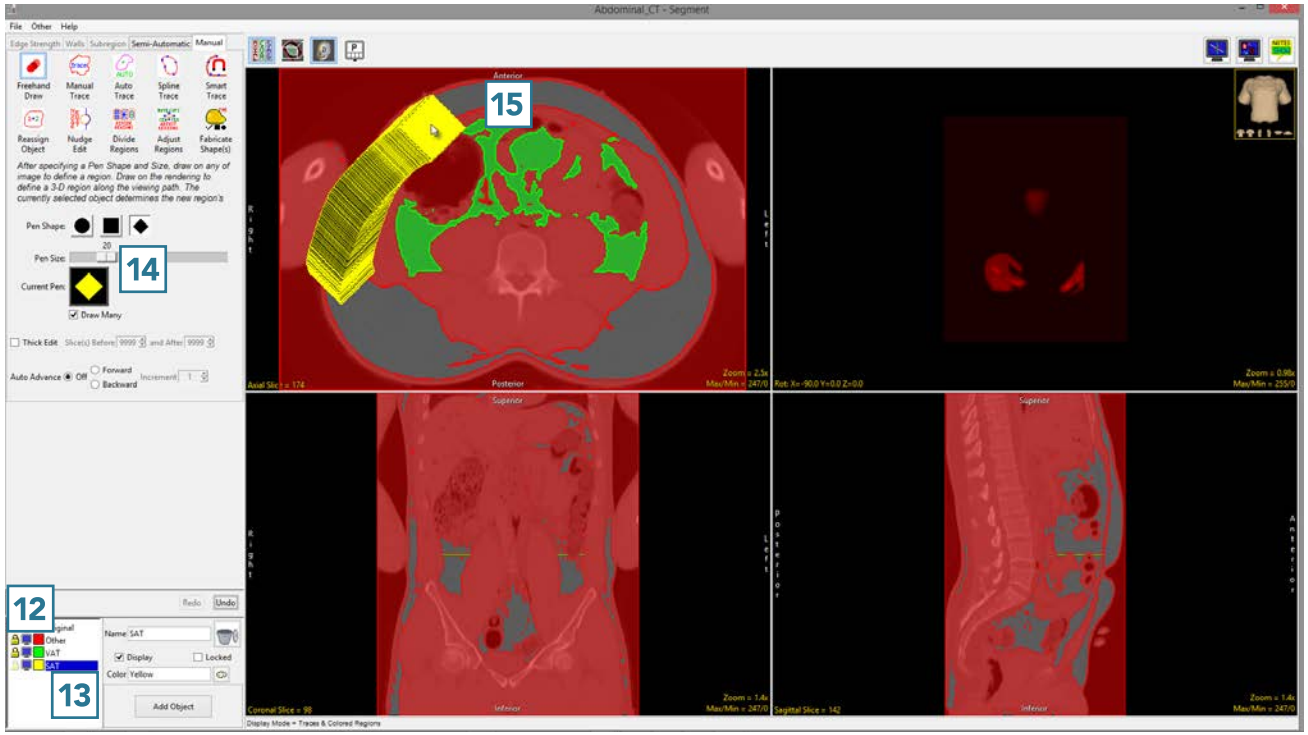


- Select Manual 5 and choose Freehand Draw. 6
- Set the Pen Shape to Diamond 7 and change the Pen Size to 20. 8
- Select the VAT object 9 and note that the Current Pen 10 will update to the color of the VAT object.
- Use the pen tool to draw over the VAT regions. 11

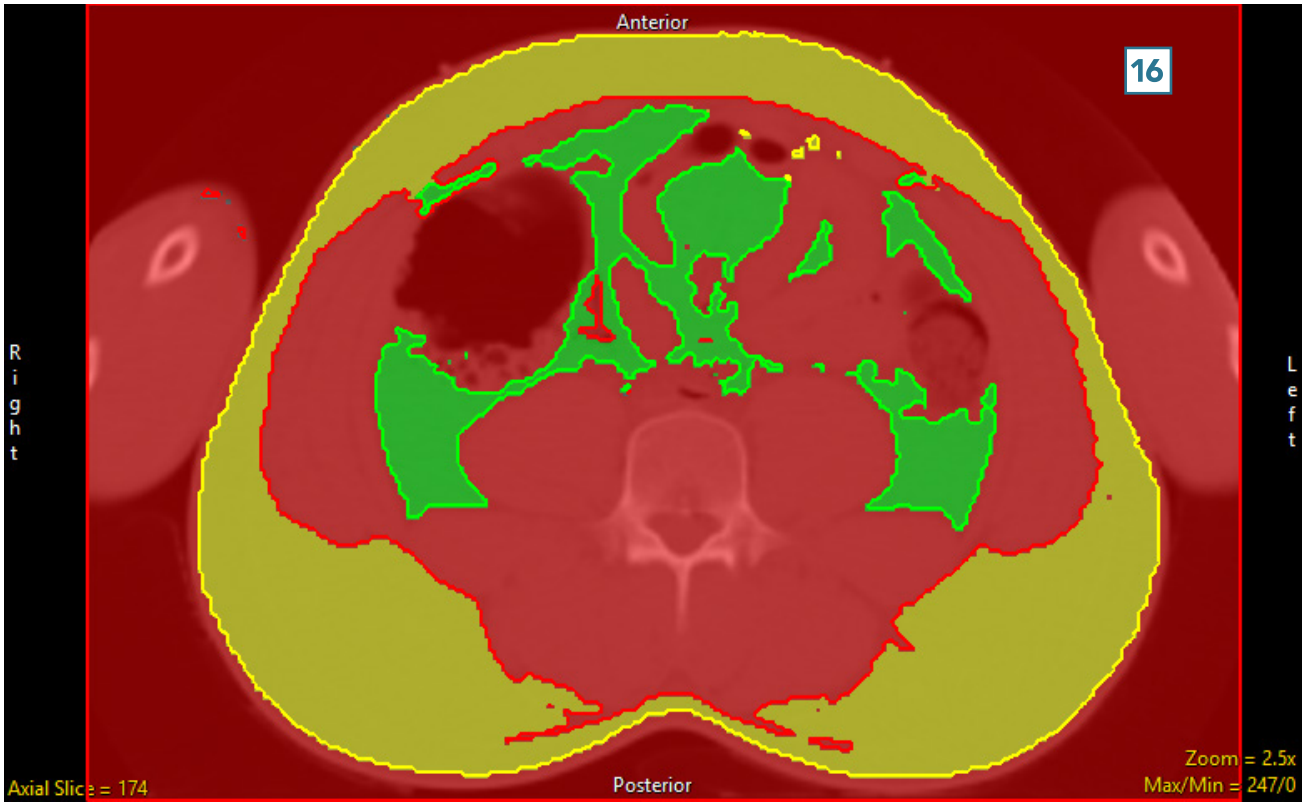


- Once the VAT region is defined, lock the VAT object 12 and select the SAT object. 13
- Increase the Pen Size to 30 14 and draw over the SAT regions. 15

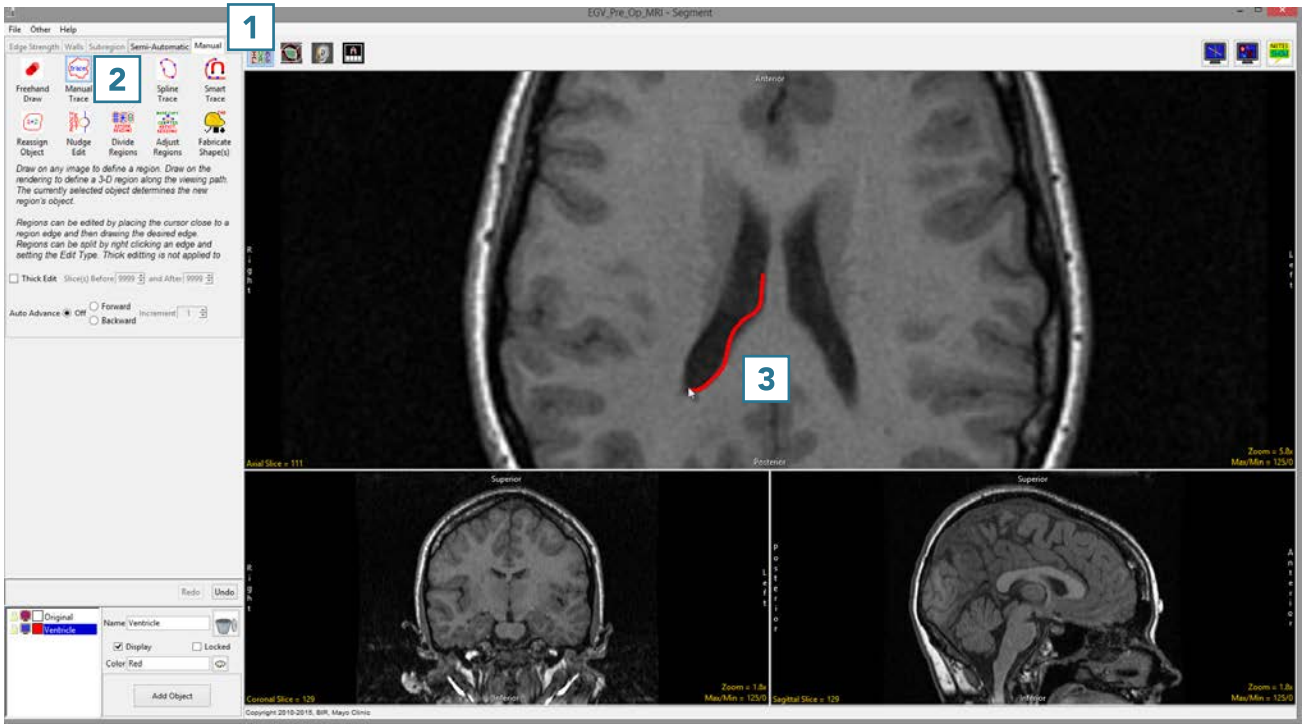


When finished, 16 use File > Save Object Map to save your work.



# Manual Trace

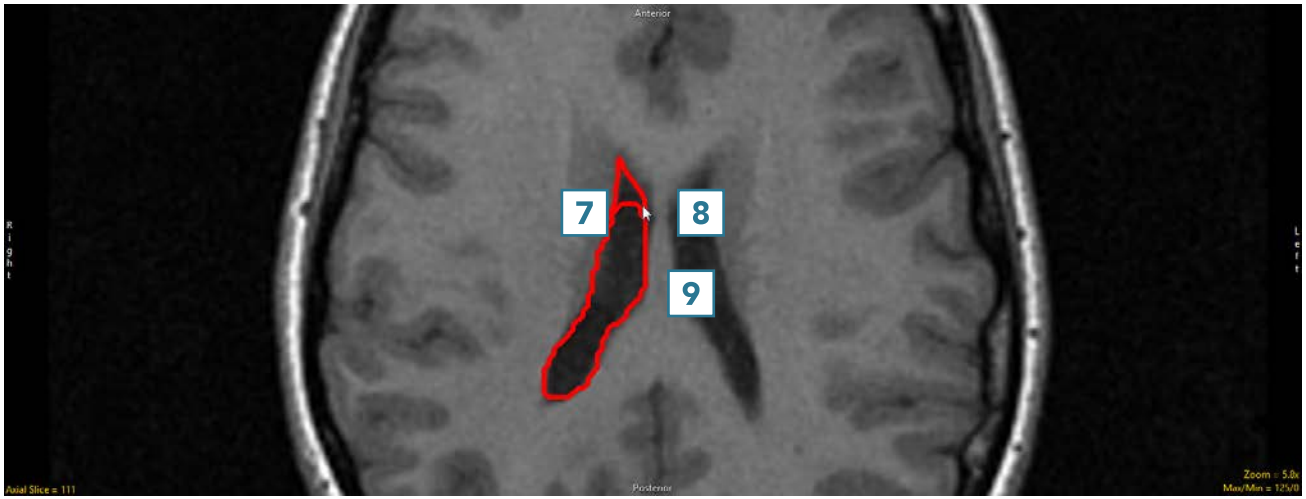
Like the Freehand Draw tool, the Manual Trace tool allows the user to draw regions of interest directly onto the image data. Manual tracing allows contours to be drawn around the edges of a region of interest.




## 21. Manual Contour Tracing and Editing

- Select a data set and open Segment.
- Select Manual 1 and choose Manual Trace. 2
- Left-click on a slice to begin tracing and move the cursor around the region you want to define. 3

- Release the left mouse button to complete the trace. 4
- To edit the trace and add pixels that may be missing, 5 click on the trace 6 and draw in the missing region. 7
- To edit the trace and remove additional pixels, 8 hover near the edge of the contour until the cursor changes to a + sign, then drag the cursor into the trace. 9

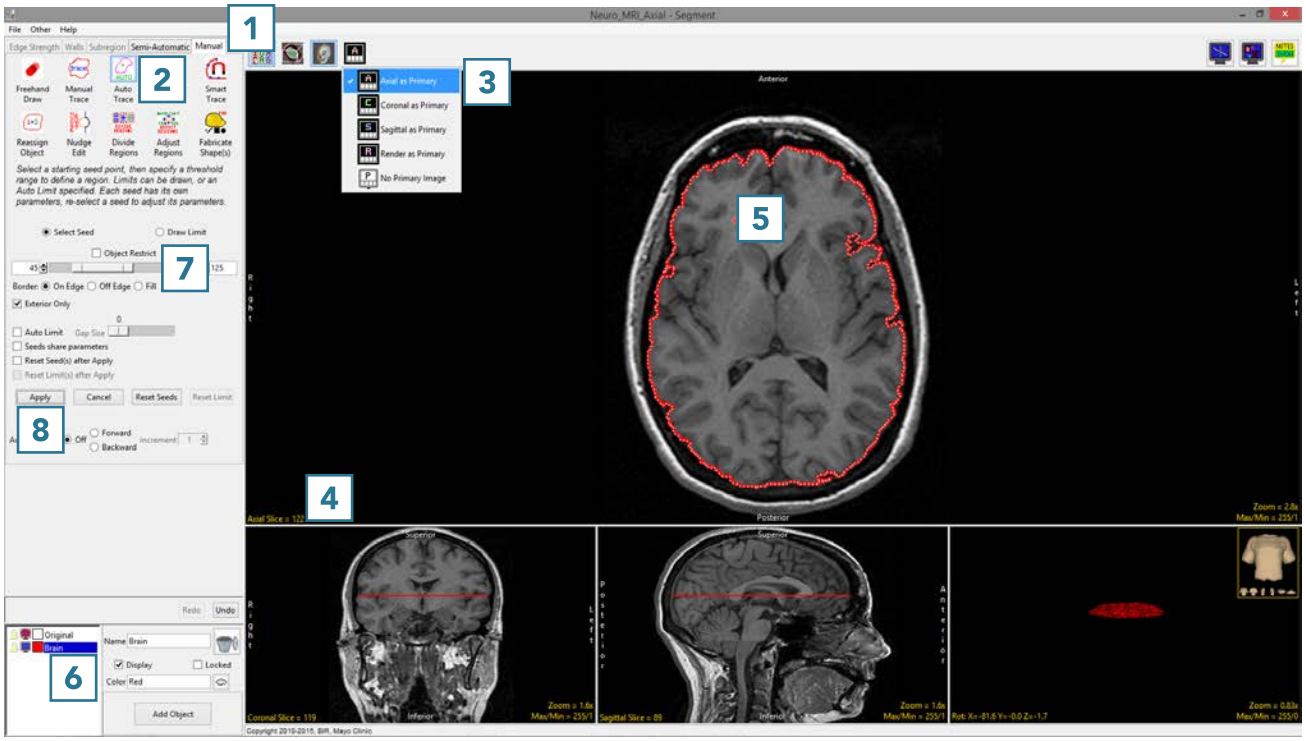
- Adjust the trace to remove the undesired pixels. 10

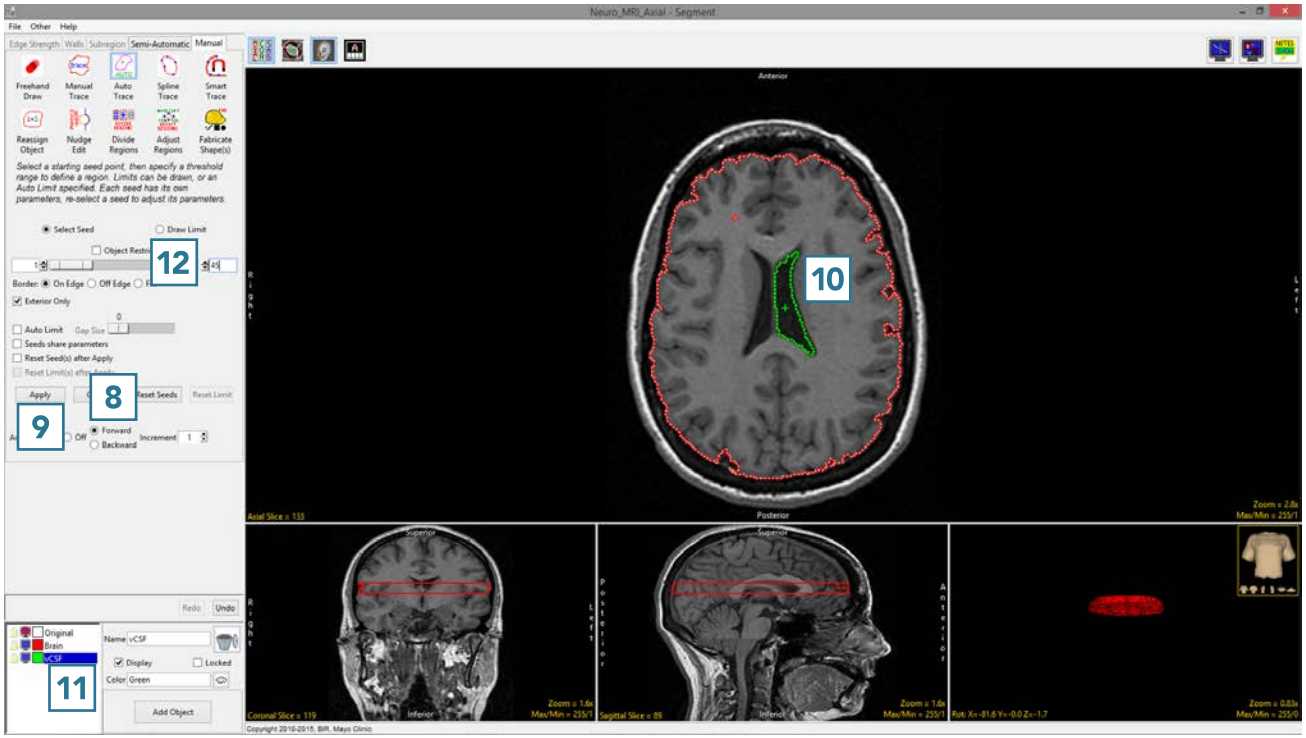
# Auto Trace

The Auto Trace tool enables the user to define and extract regions of interest from the image data using 2D seeded region growing. Region definition begins with a seed pixel, manually set by the user, on a structure of interest. Next, a threshold range is established by the user to define the boundary of the structure. The 2D region is defined by all the pixels in the threshold range that are connected to the seed pixel.

# 22. Using Auto Trace to Define a 2D Region of Interest

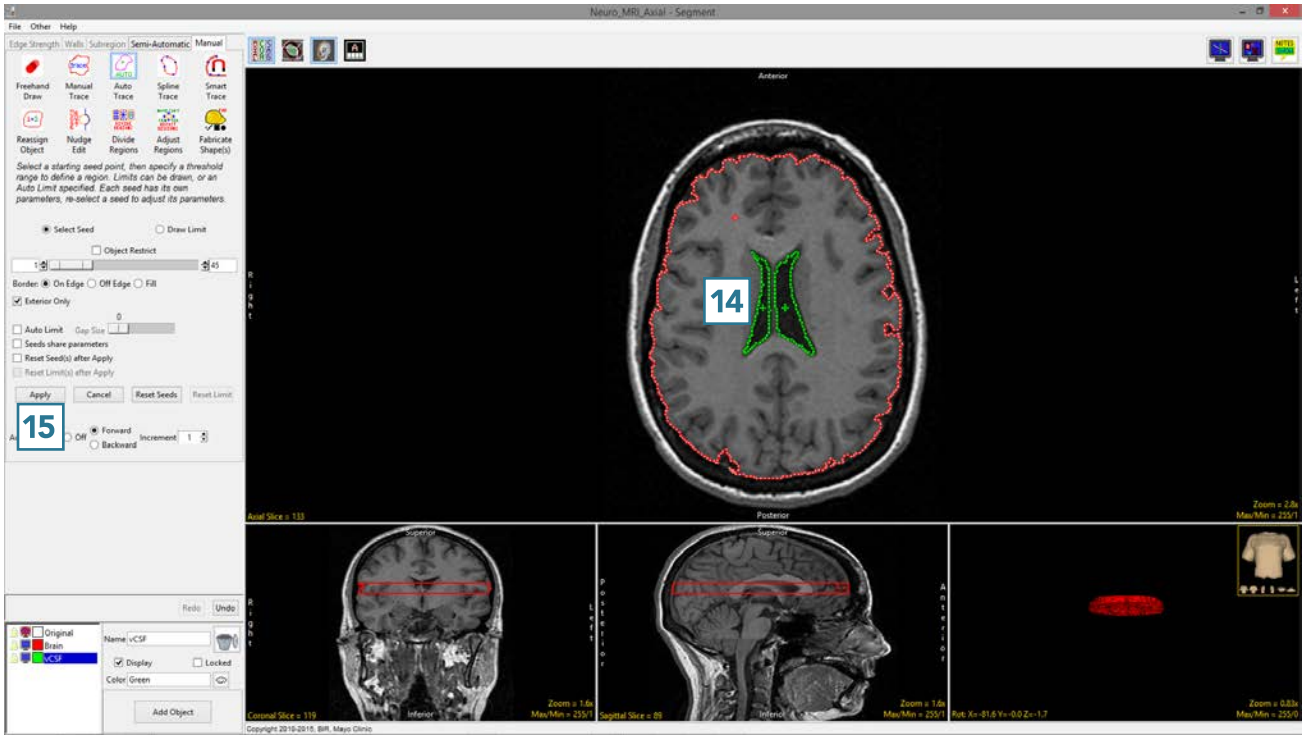
- Select a data set and open Segment.
- Select Manual 1 and choose Auto Trace. 2
- Set the primary display to Axial 3 and double-click Slice 4 to move to axial slice 122.
- Set a seed pixel in the white matter. 5
- Rename Object_2 to Brain 6 and then adjust the minimum and maximum threshold values 7 to define the brain.
- Click Apply 8 to trace the brain on this slice.



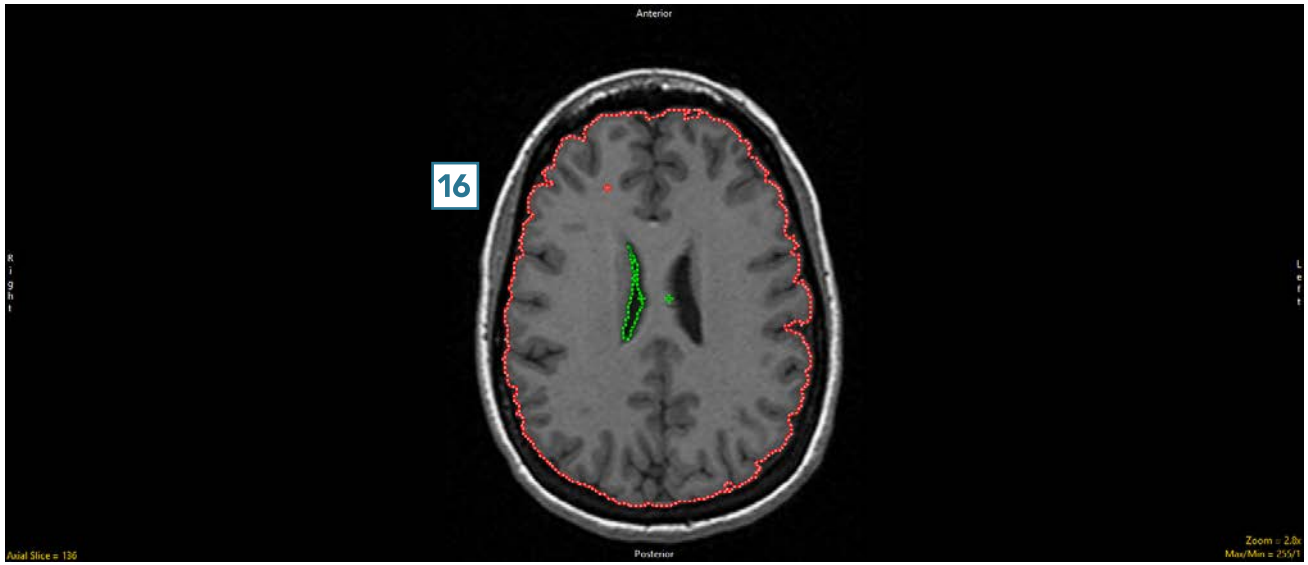


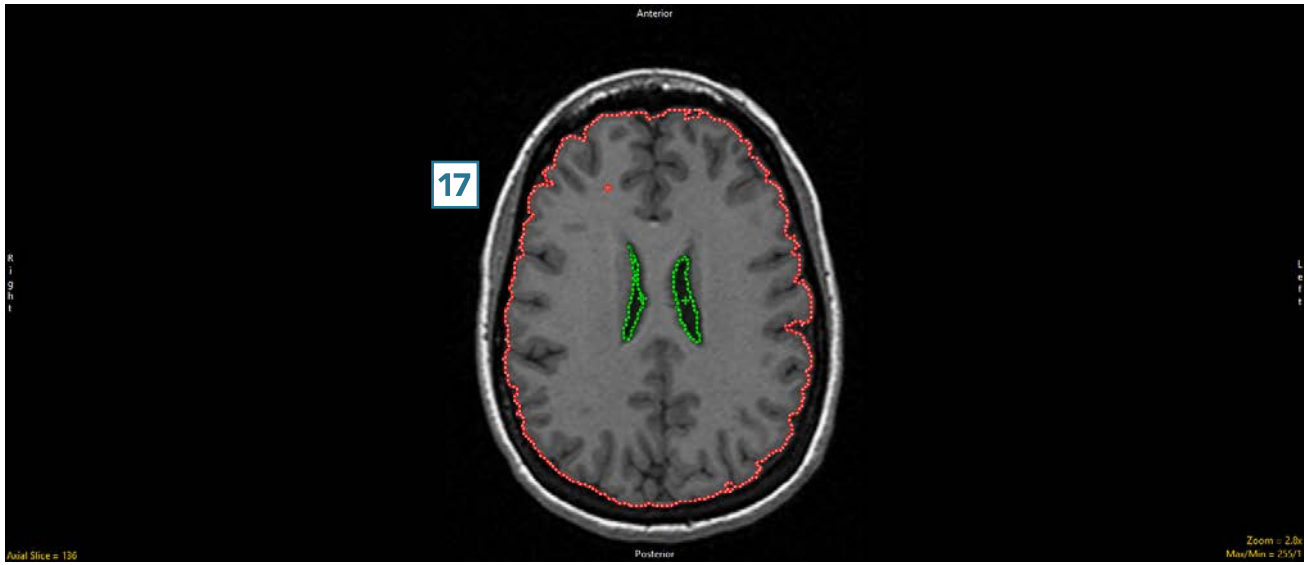

- Scroll forward to slice 123. The + key can also be used instead if your mouse has no scroll wheel.
- Since the seed point and threshold range are automatically carried forward, the brain will be redefined on this slice.
- Set the Auto Advance option to Forward **8** and click Apply. **9** The brain will be traced on this slice and the display will automatically move forward to slice 124.
- Continue to apply the auto trace to the brain up to slice 133. If the initial seed point is copied to a slice where it does not fall within the brain, reset the seed point and threshold range and click Apply to set a new auto trace on that slice.
- Click in the ventricular CSF to set a seed point. **10**
- Add a new Object and rename it vCSF. **11** Note that the second seed point will change color to match the color of the new object. Adjust the threshold range to define the vCSF object. **12**

- Set a second seed point to define the remaining vCSF 14 and click Apply. 15



- Continue clicking Apply to trace the Brain and vCSF objects. If a seed point is copied to a location where it is no longer on the target object, 16 move the seed point back onto the object 17 and continue to apply the auto trace.
- Stop defining objects at slice 137.
- Select File > Save Object Map to save your work.



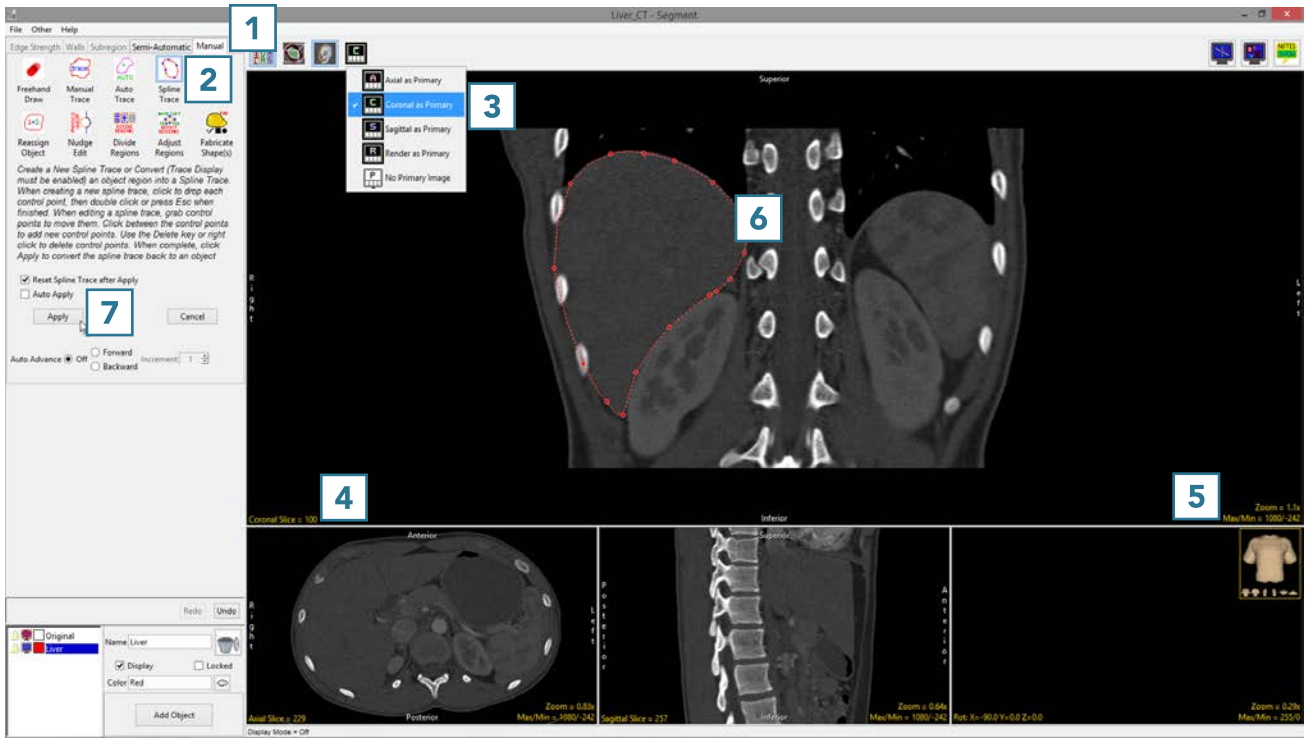



# Spline Trace

The Spline Trace tool allows users to define curved regions of interest. Splines are flexible curve traces with movable control points that are useful for creating smooth edge traces.

# 23. Using Spline Trace to Define a Region of Interest

- Select a data set and open Segment.
- Select Manual 1 and choose Spline Trace. 2
- Set the primary display to Coronal 3 and double-click Slice 4 to move to coronal slice 100.
- To begin drawing a spline, position the cursor on the image and left-click. 5 Reposition the cursor and left-click to continue drawing the spline around the object of interest. 6
- Double-click to end and close the spline.
- Note that control points can be moved. Click a control point, drag to a new location and the Spline will update.
- Select Apply 7 to apply the spline trace.
- Use File > Save Object Map to save your work.

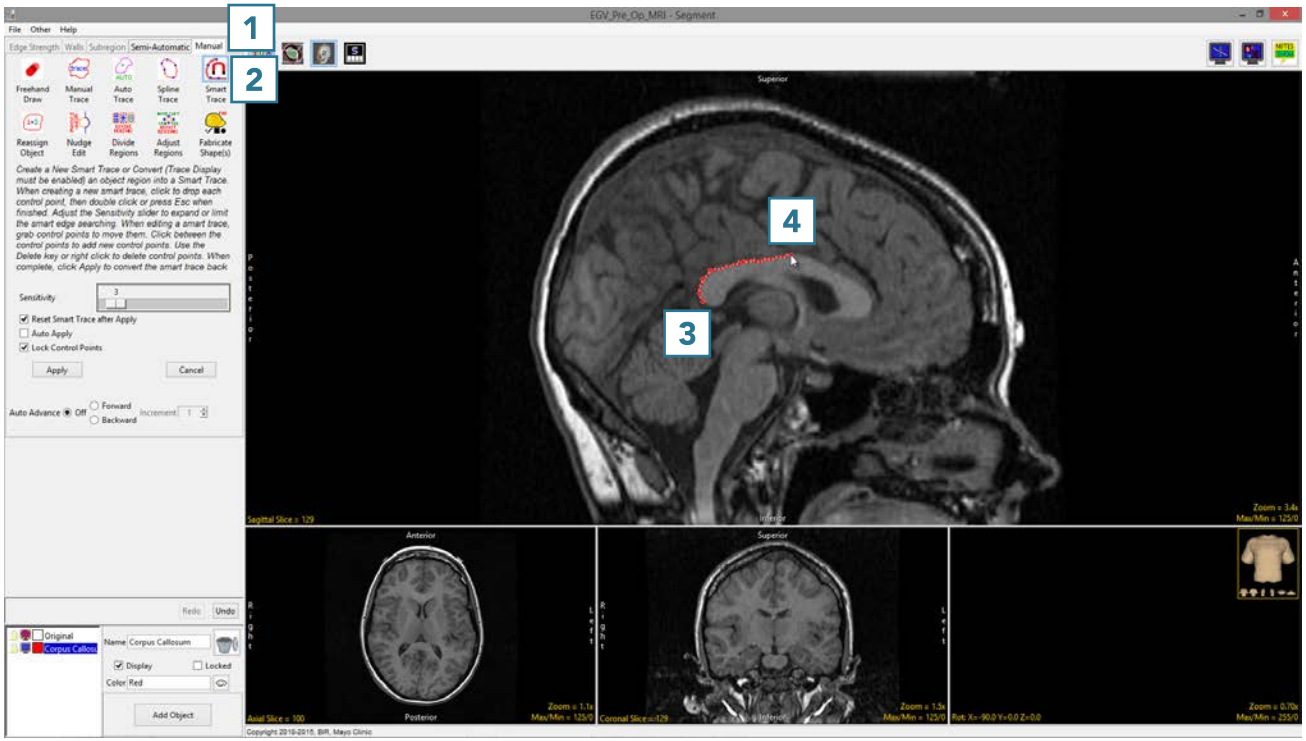


# Smart Trace

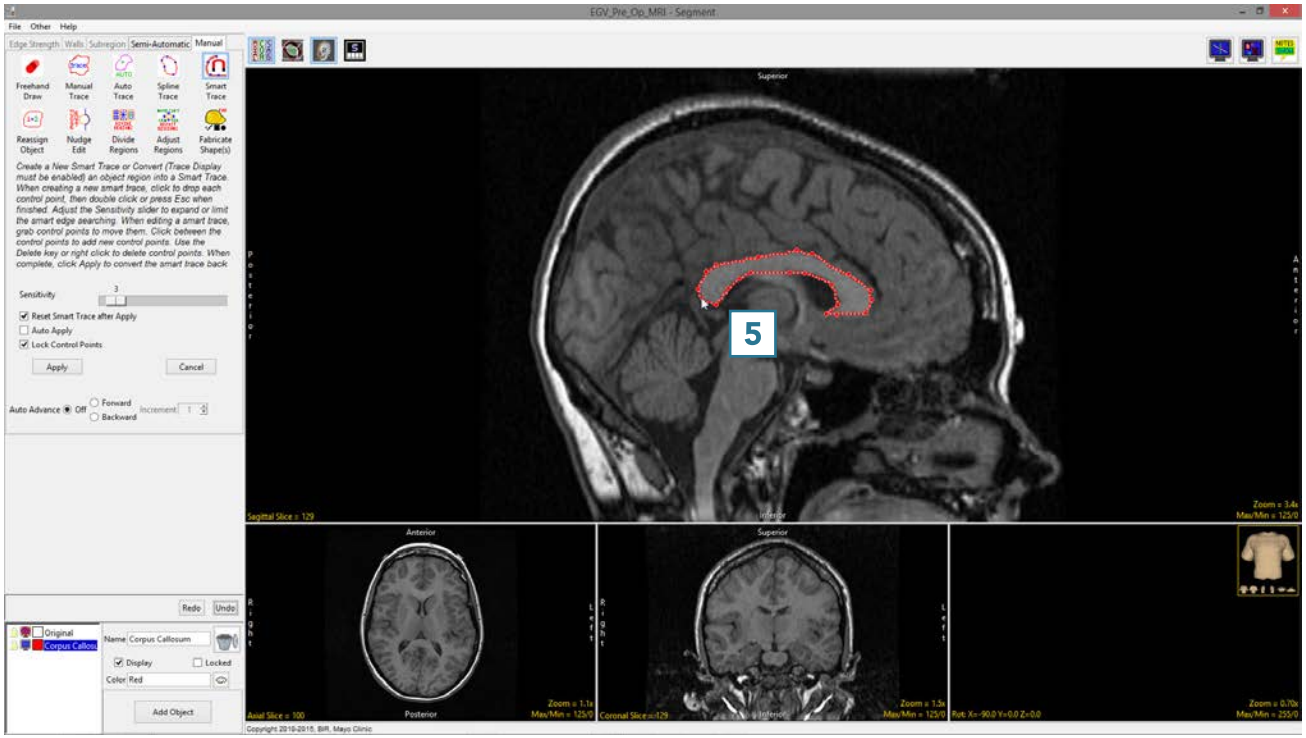
The Smart Trace tool detects regions of high rate of change of voxel intensity (gradient) representing edges. The tool snaps to the edges of these regions. The sensitivity of the smart edge can be adjusted using the slider or the mouse scroll wheel.

# 24. Smart Trace Region Definition

- Select a data set and open Segment.
- Select Manual 1 and choose Smart Trace. 2
- Left-click in the image to set the first control point. 3
- Move the cursor along the edge of the object and click to set additional control points. 4 To adjust the sensitivity of the smart edge, use the mouse scroll wheel. Scrolling up will increase the sensitivity and scrolling down will decrease sensitivity.



- When the trace is complete, double-click to close the spline. 5
- If needed, control points can be moved. Uncheck the Lock Control Points option, click on a control point and drag it to a new location. The Smart Trace will update.
- Control points can be deleted. Select a control point, right-click and select Delete Control Point.
- Select Apply or use the A key to apply the trace.
- Use File > Save Object Map to save your work.



# Reassign Object

The Reassign Object tool allows users to interactively reassign the voxels of one object to another object. First, select the object to which the voxels will be reassigned from the object control window. Then, select a reassignment type. Finally, to establish a seed pixel, click on the object to be reassigned. Object reassignment occurs immediately. Reassignment options are described in Table 7.1.

## Table 7.1: Reassignment Types

| Reassignment Type | Action |
|---|---|
| All | All voxels in the selected object are reassigned to the current object |
| 3D | All voxels in the selected object that are connected in 3D to the seed pixel are reassigned to the current object |
| 2D | All voxels in the selected object that are connected in 2D to the seed pixel are reassigned to the current object |
| Unconnected 3D | All voxels in the selected object that are not connected in 3D to the seed pixel are reassigned to the current object |

# 25. Reassigning Objects

- Select the data set and open Segment.
- Use File > Load Object Map to load the corresponding object map.
- Select Manual 1 and choose Reassign Object. 2
- Set the primary display to axial 3 and move to axial slice 130.
- Switch the display of the Skin object off and switch on the display of the Lenticular and Caudate objects. Select the Brain object and change the Opacity level of the Brain to 2. 4
- Set the reassignment type to All 5 and click on the yellow Lenticular object. 6

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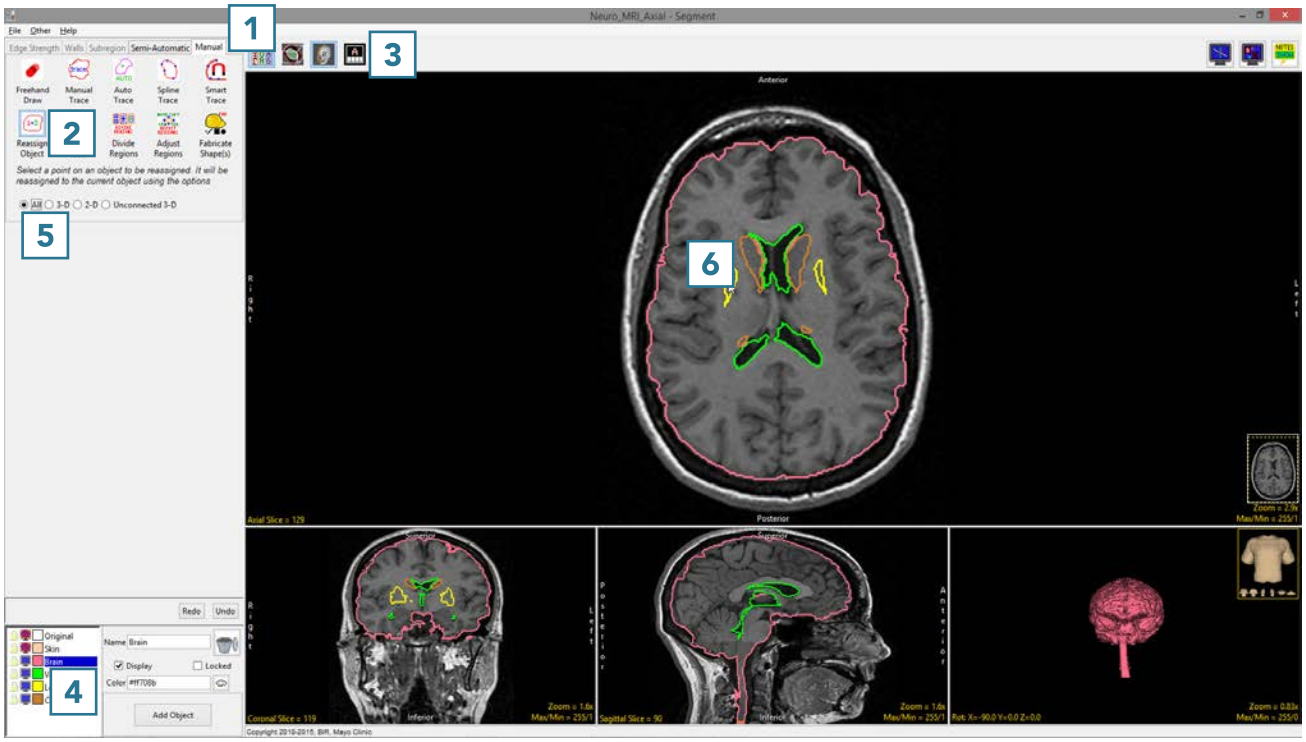
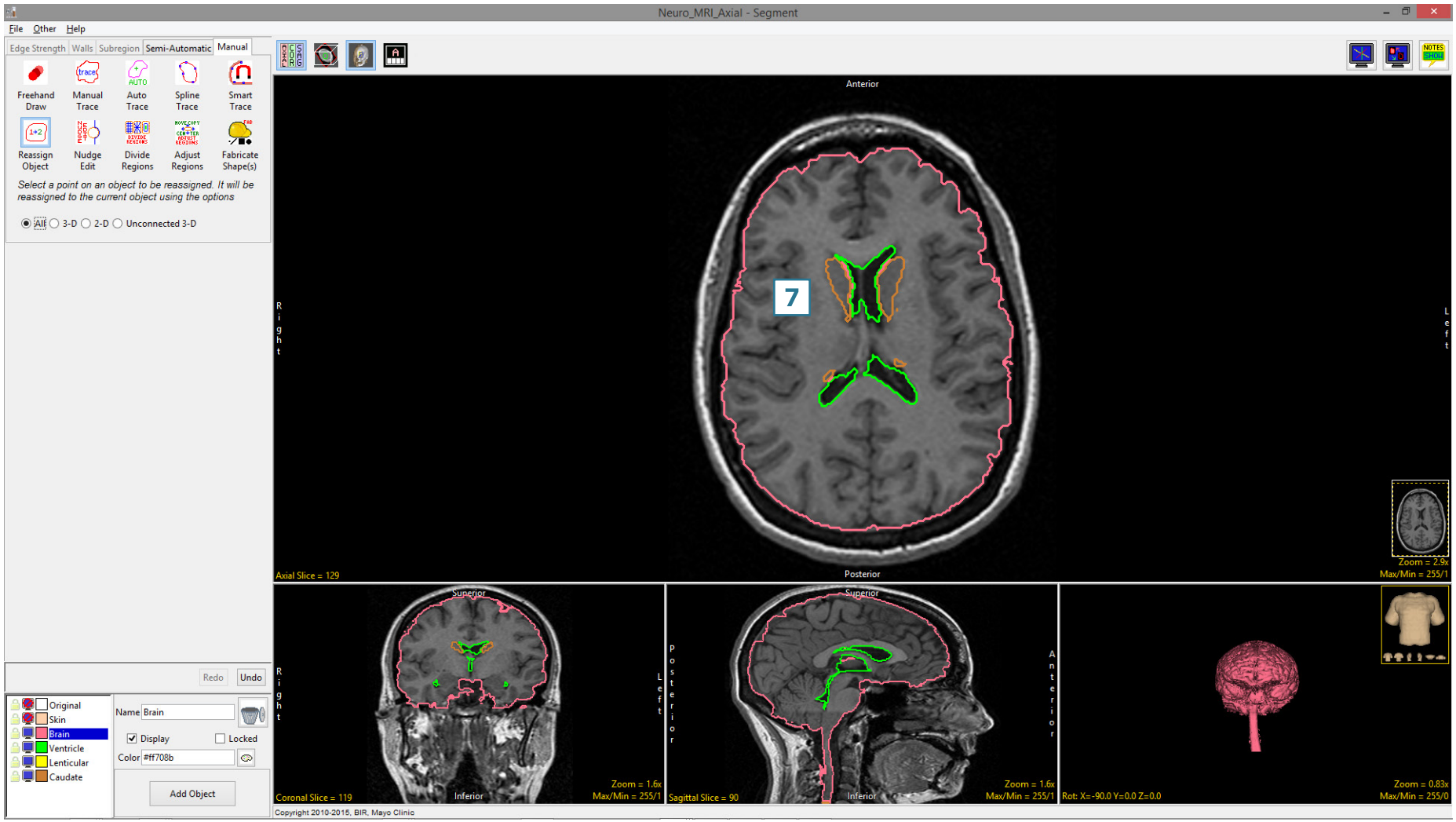
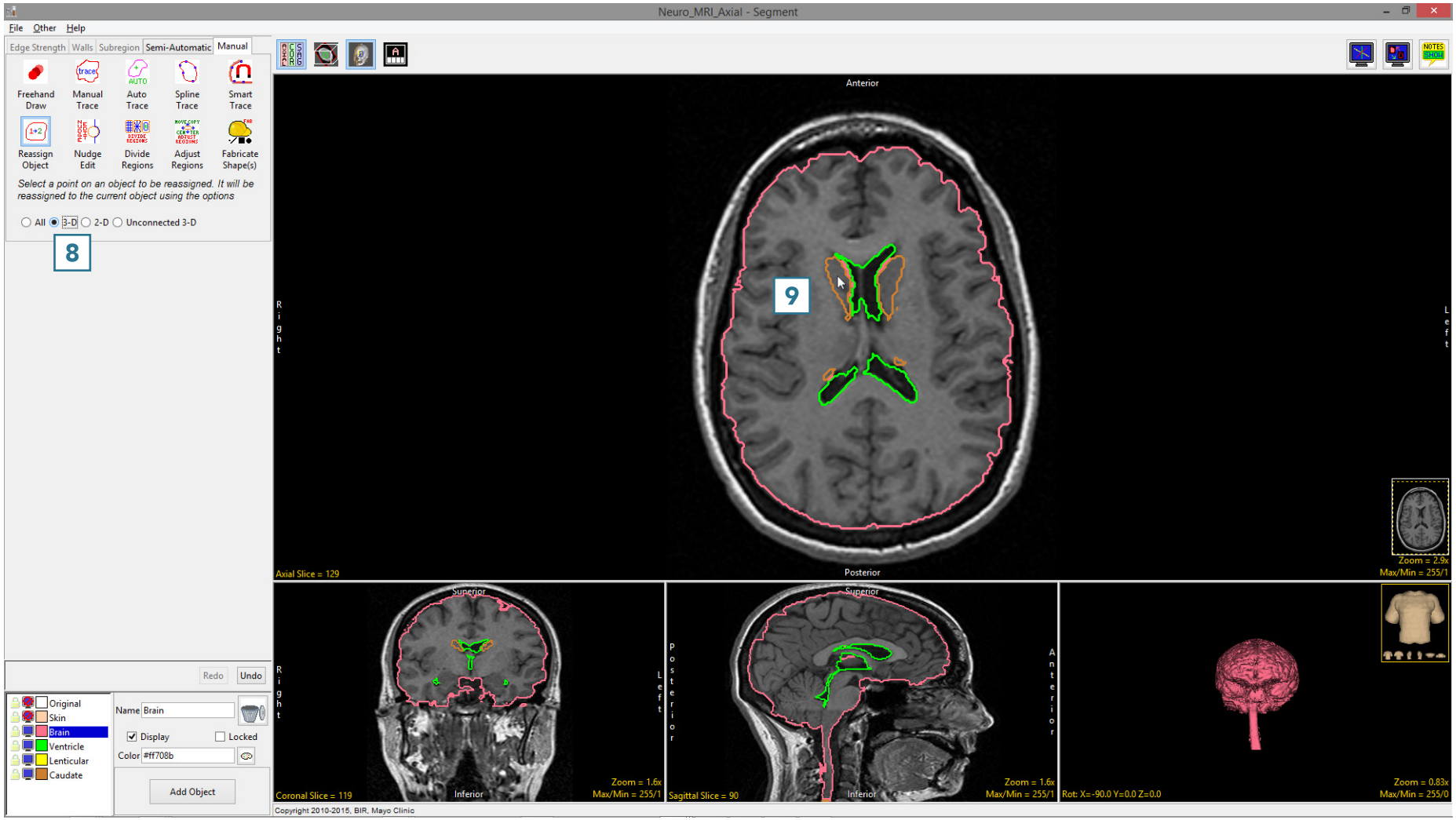


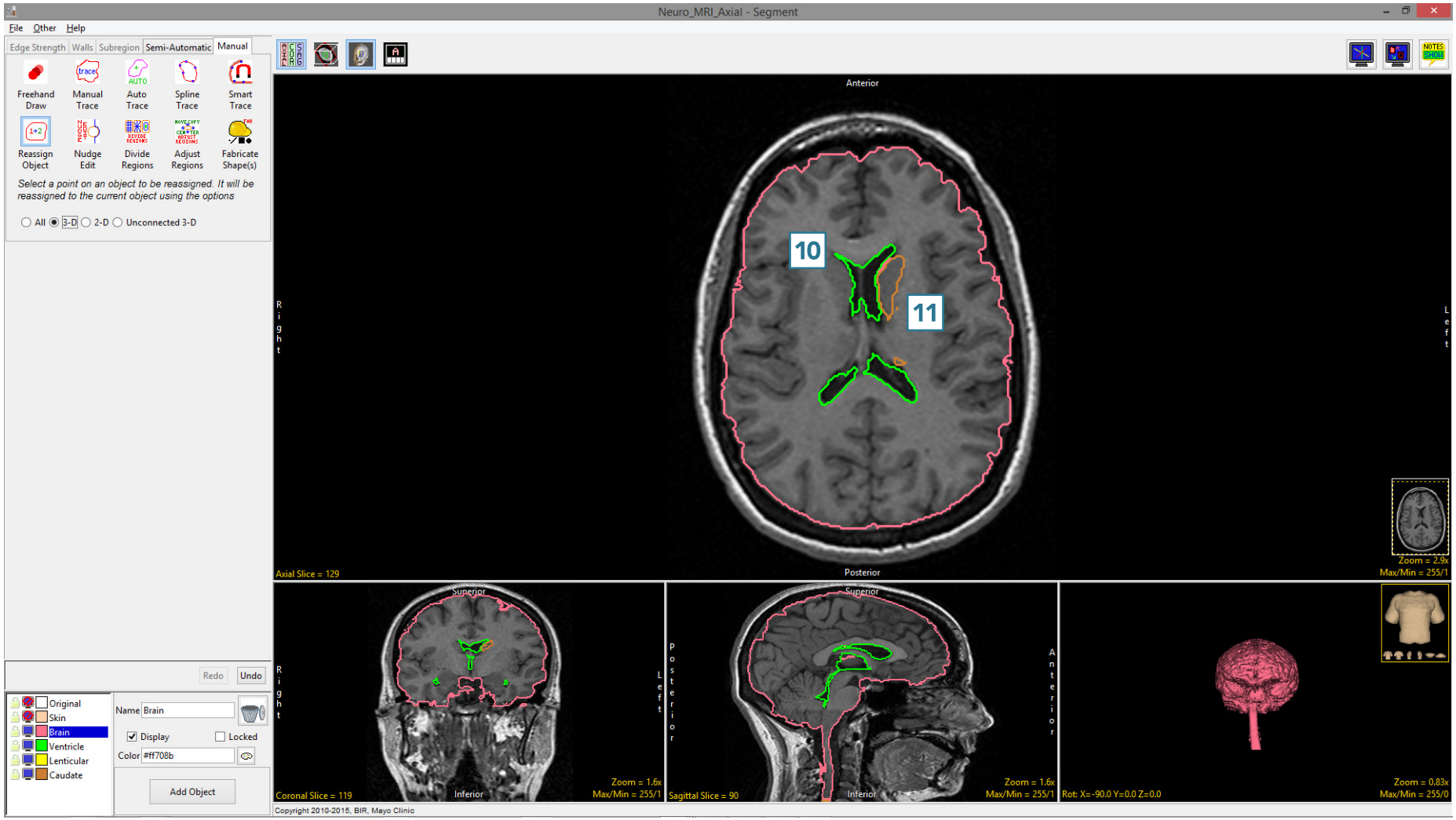
Note that all the voxels of the Lenticular object have been reassigned to the Brain object. 7



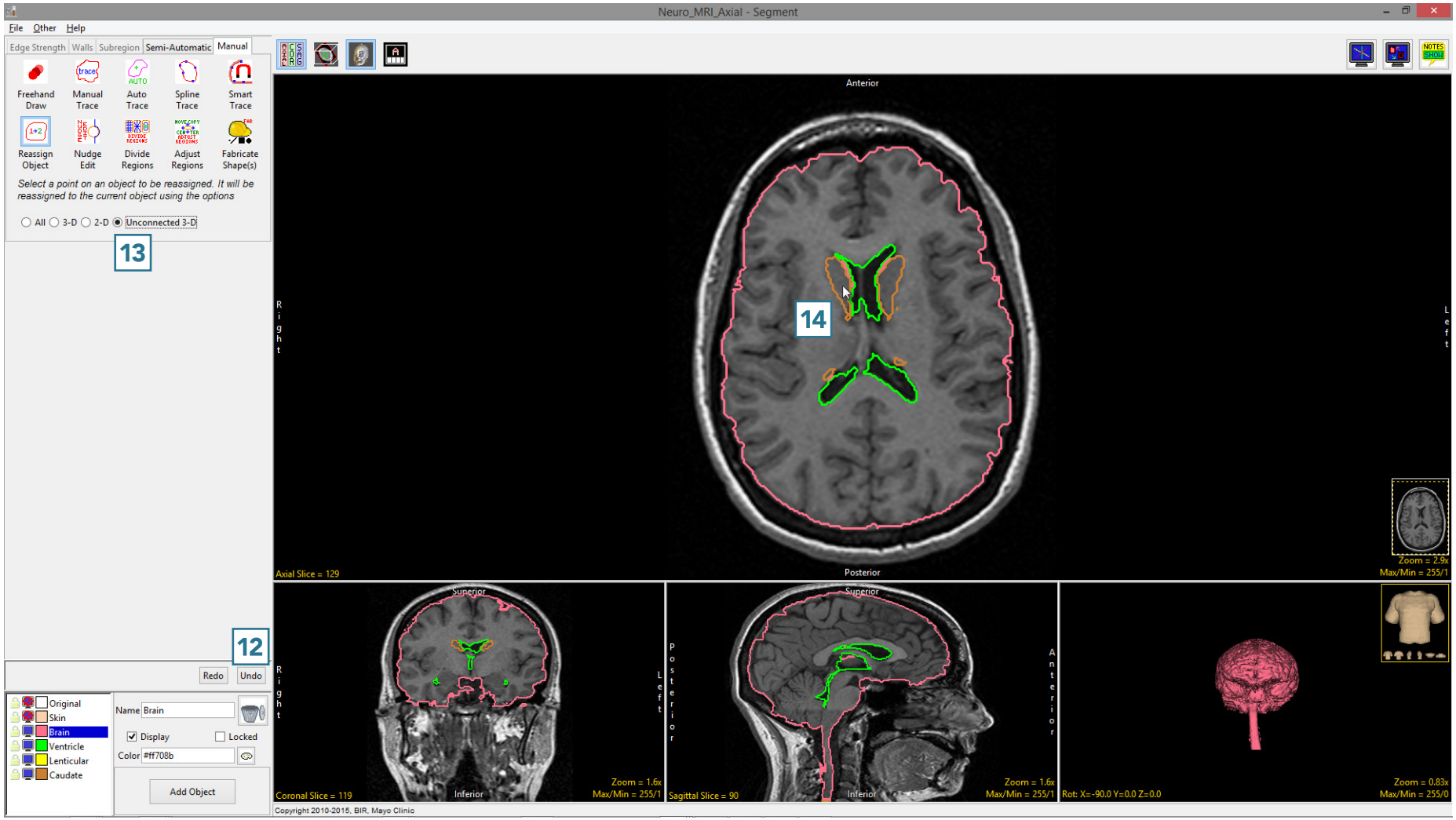
Set the reassignment type to 3D 8 and click on the brown Caudate object on the right side of the brain. 9



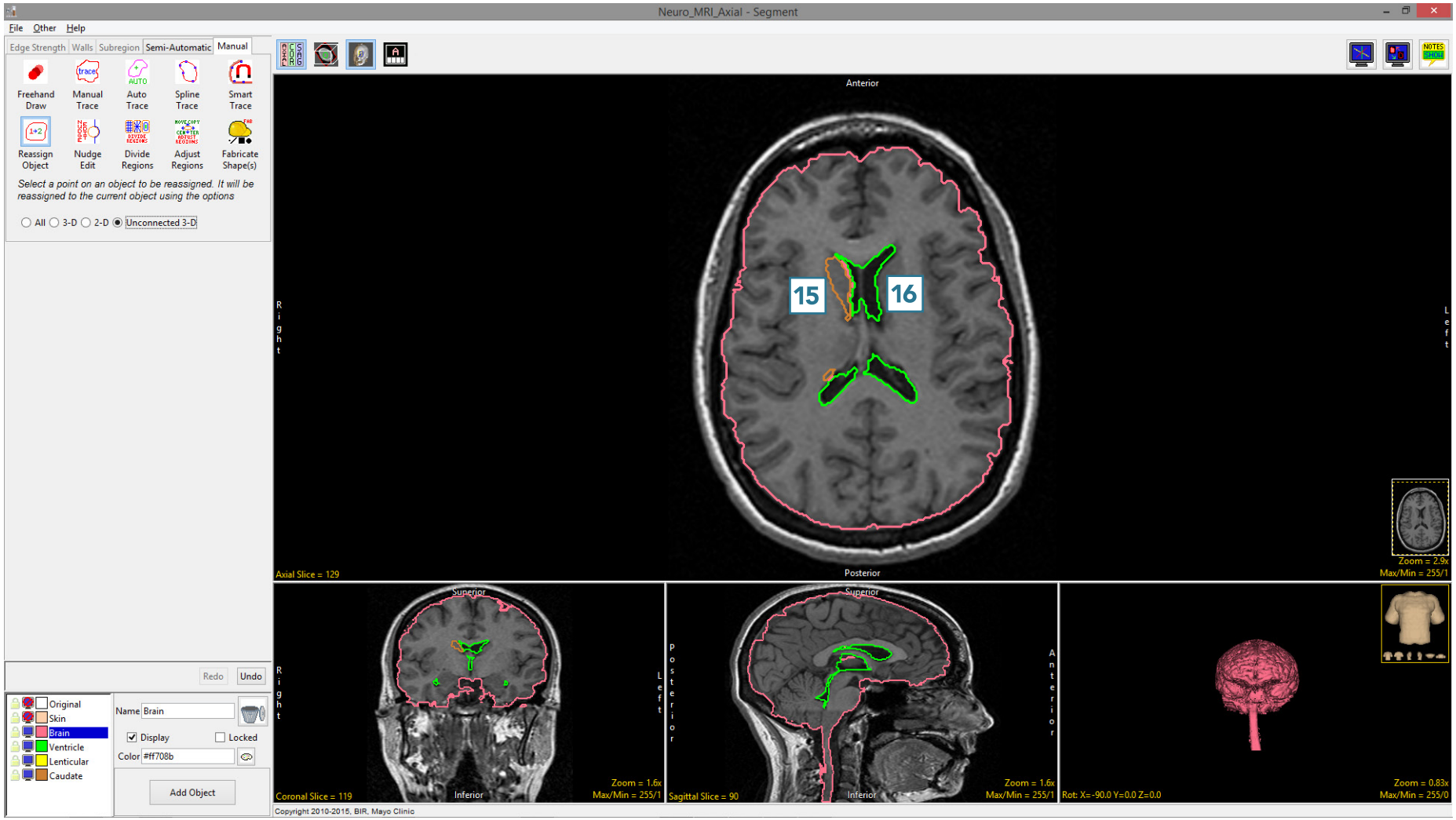
Note that the all the voxels of the Caudate object connected to the seed pixel have been reassigned to the Brain object. 10 As the left caudate nucleus is not connected to the right caudate nucleus, that part of the object remains. 11



- Click Undo 12 and set the reassignment type to Unconnected 3D. 13
- Click on the brown Caudate object on the right side of the brain. 14

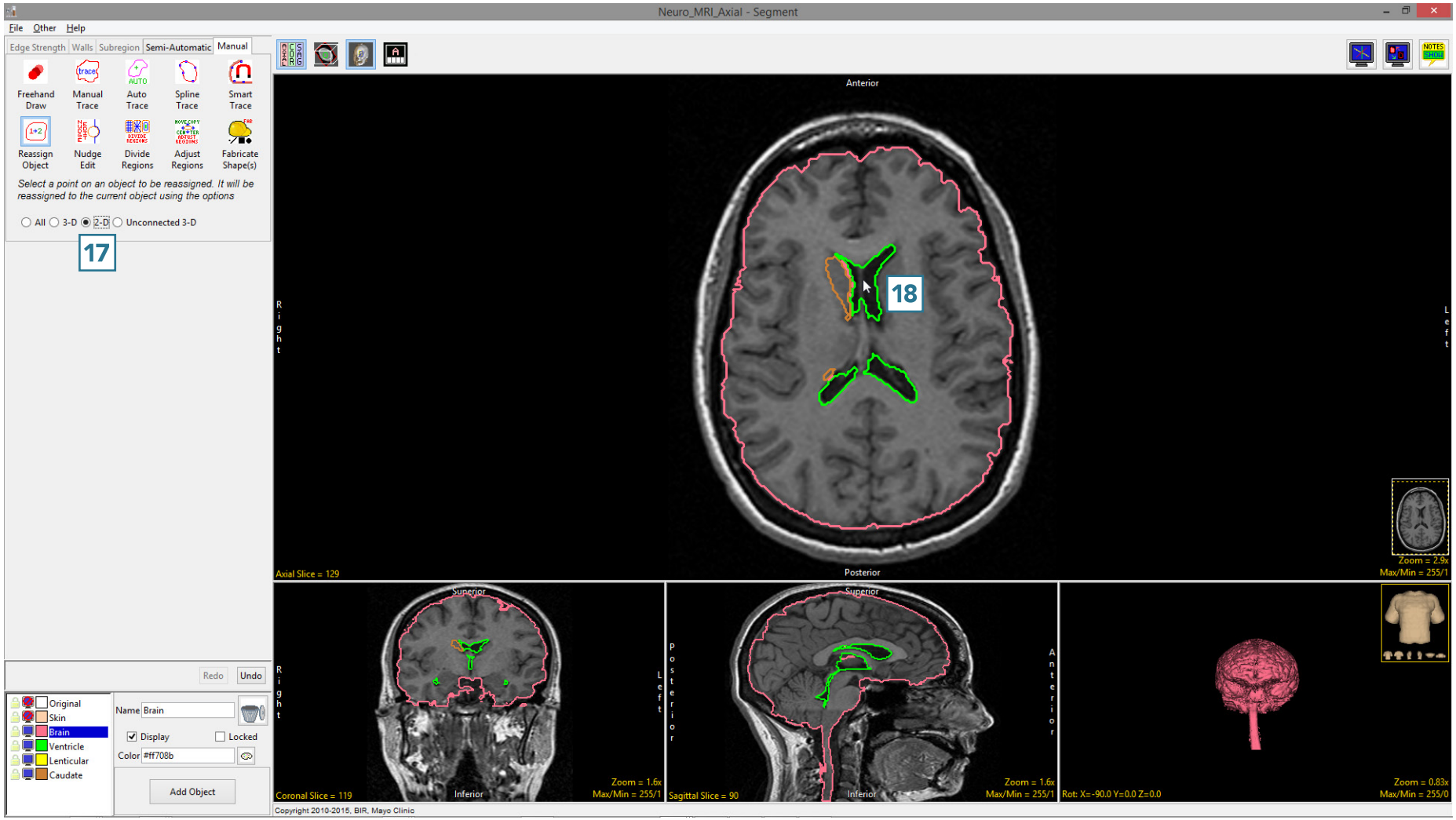


Note that this time, all the voxels assigned to the Caudate object connected to the seed pixel have been kept 15 while those unconnected voxels representing the left caudate nucleus have been reassigned to the Brain object. 16

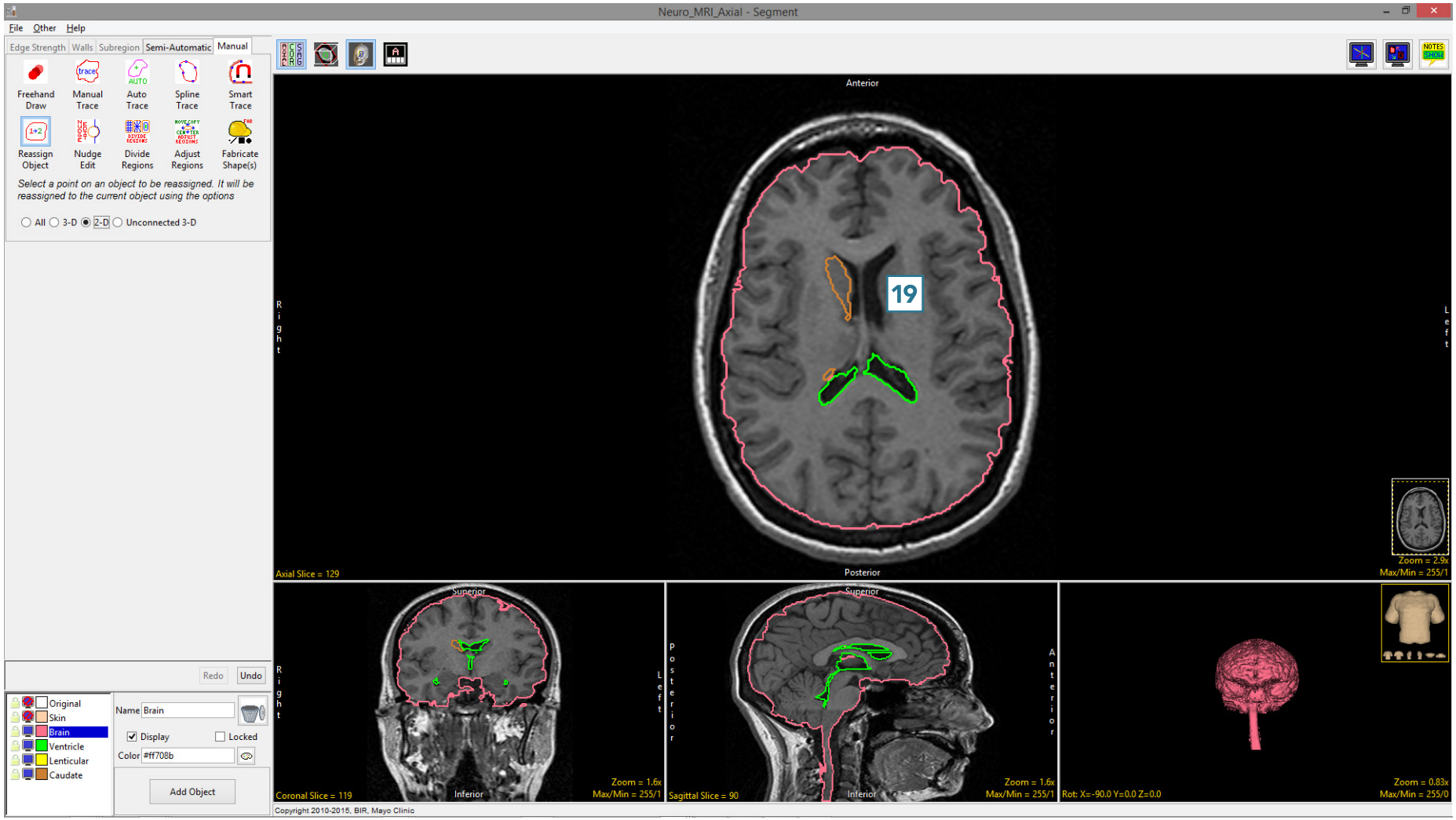


Note that for the All, 3D and Unconnected 3D reassignment types, seed points can be set on the 3D rendering.

- Set the reassignment type to 2D 17 and click on the anterior section of the green Ventricle object. 18



The voxels assigned to the Ventricle object, which are connected to the seed pixel only on this 2D slice have been reassigned to the Brain object. 19



# Nudge Edit

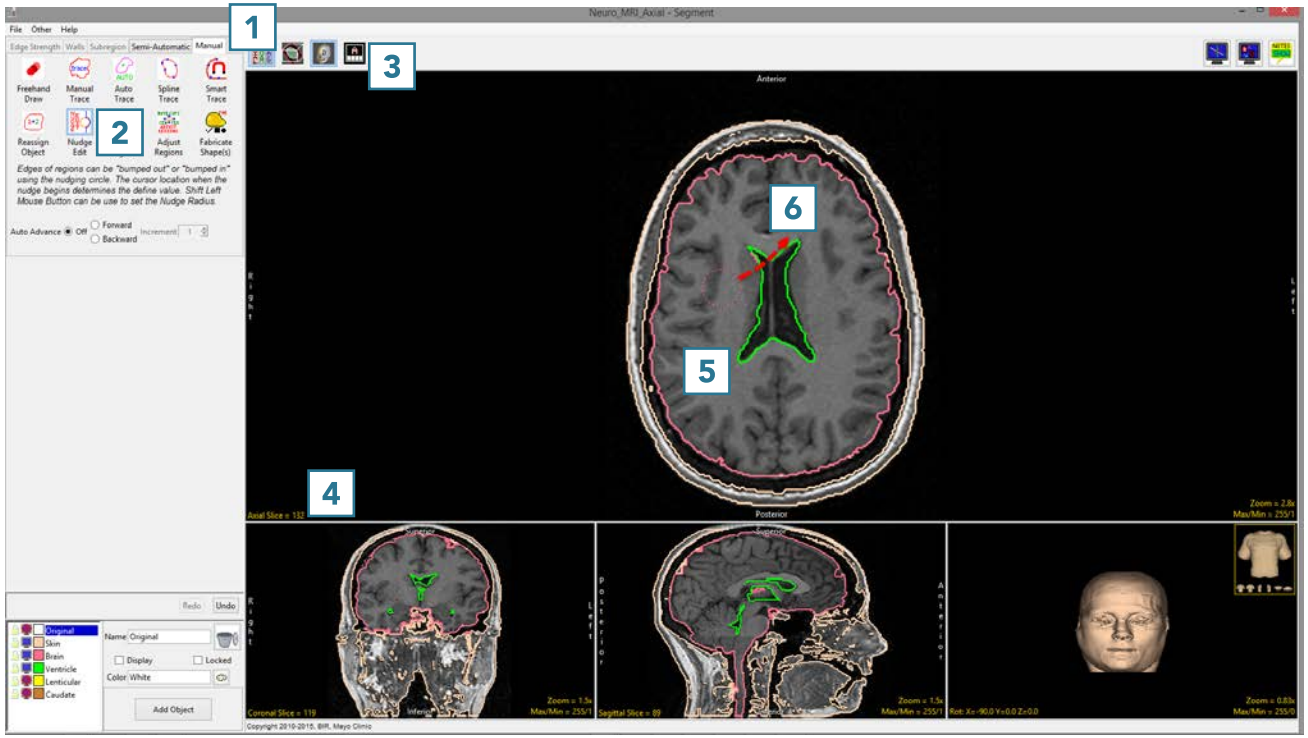
Nudge Edit enables users to manually edit borders of defined regions. The tool allows object borders to be pushed inwards or outwards using an adjustable circular cursor. The size of the cursor can be adjusted using the middle mouse button.

# 26. Editing Object Borders

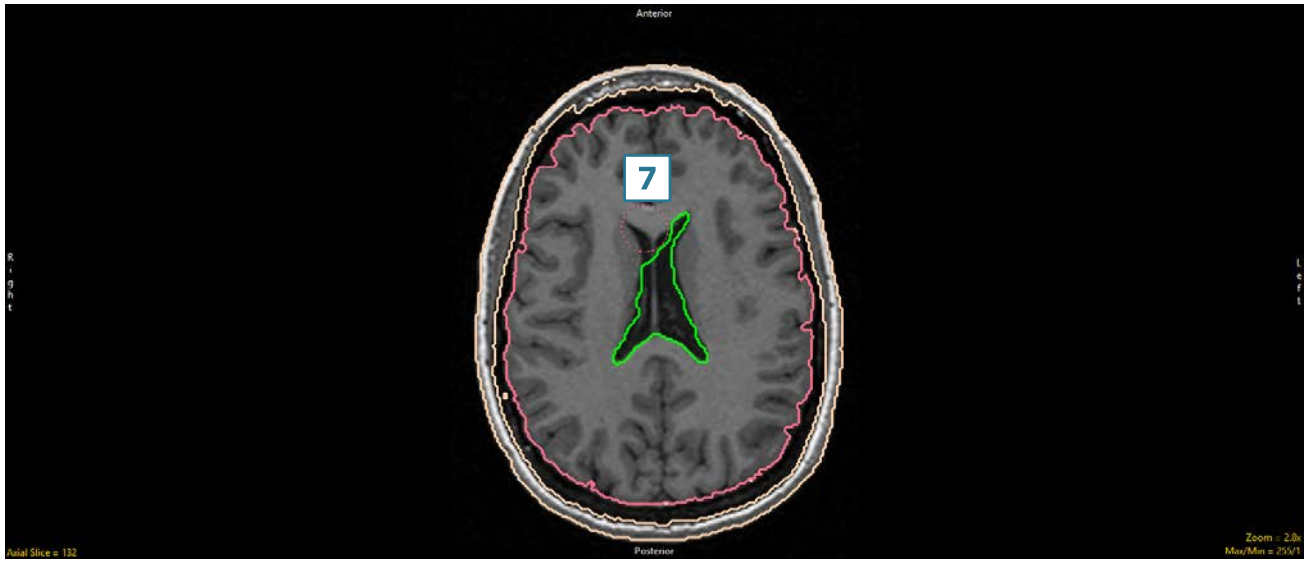
- Select MRI_3D_Head and open Segment.
- Select File > Load Object Maps and load MRI_3D_Head.obj.
- Select Manual, 1 then choose Nudge Edit. 2
- Set the primary display to Axial 3 and move to Axial slice 132. 4
- To edit the border of the Brain and Ventricle objects click in the brain. The circular nudge tool cursor will appear. 5

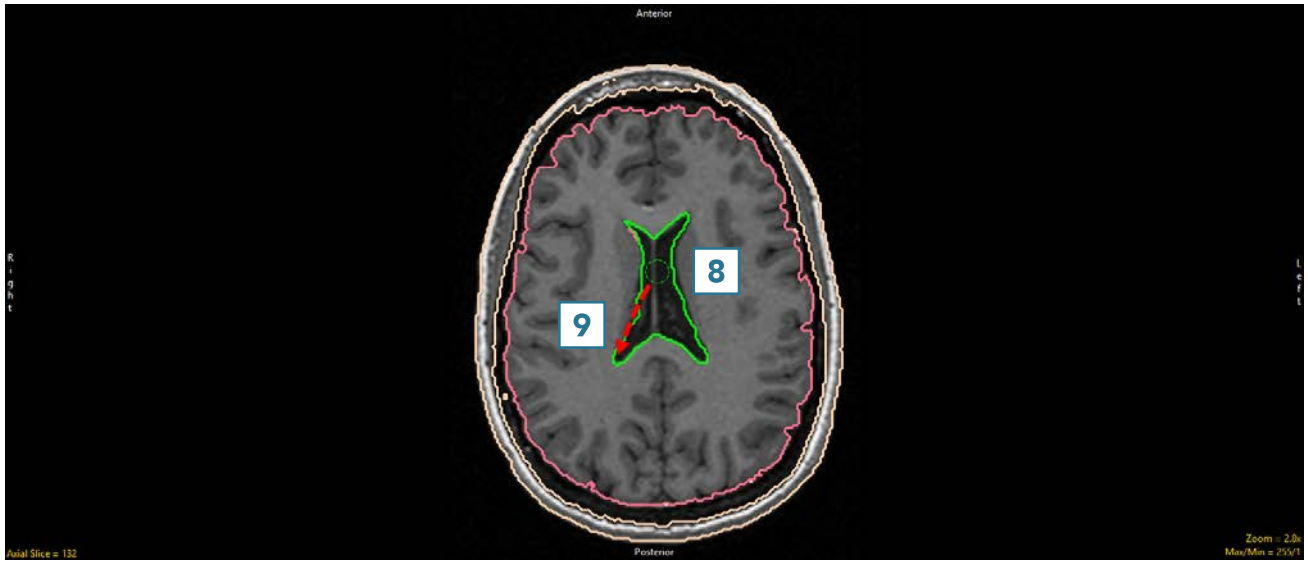
Note the color of the cursor will match the object being nudged.

- Move the cursor to edit the border. 6

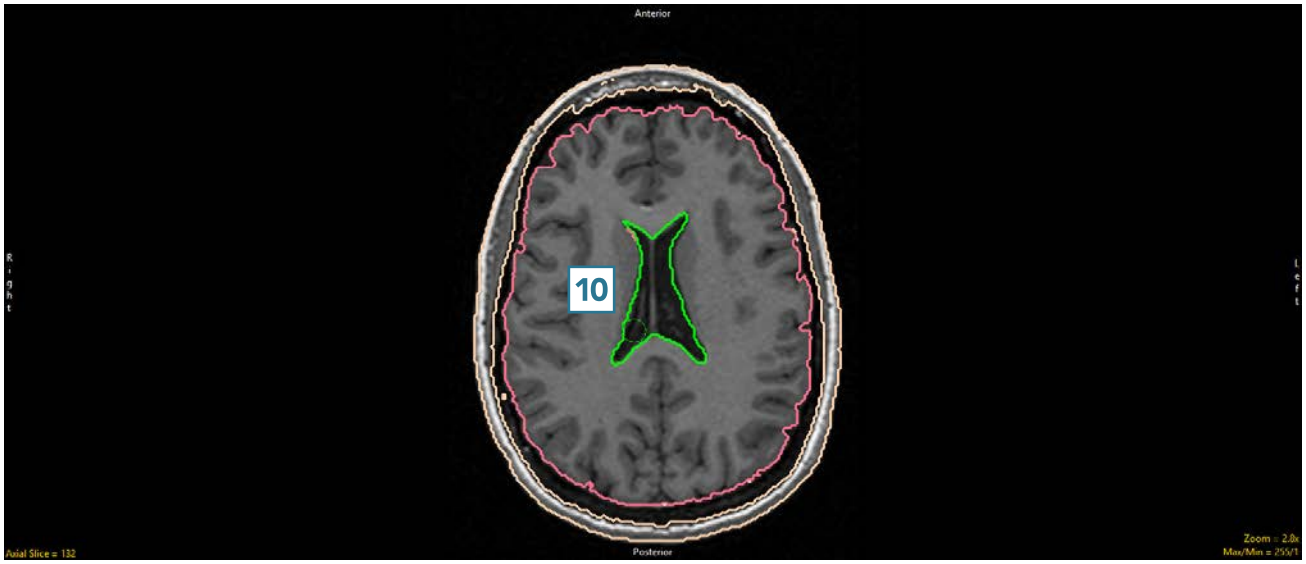


- The borders of the Brain and Ventricle objects will be updated as the cursor moves through. 7
- Click Undo.
- Using the middle mouse button, change the size of the cursor to 5, then click in the Ventricle object. 8 Push the border of the Ventricle object out to edit the object boundary. 9



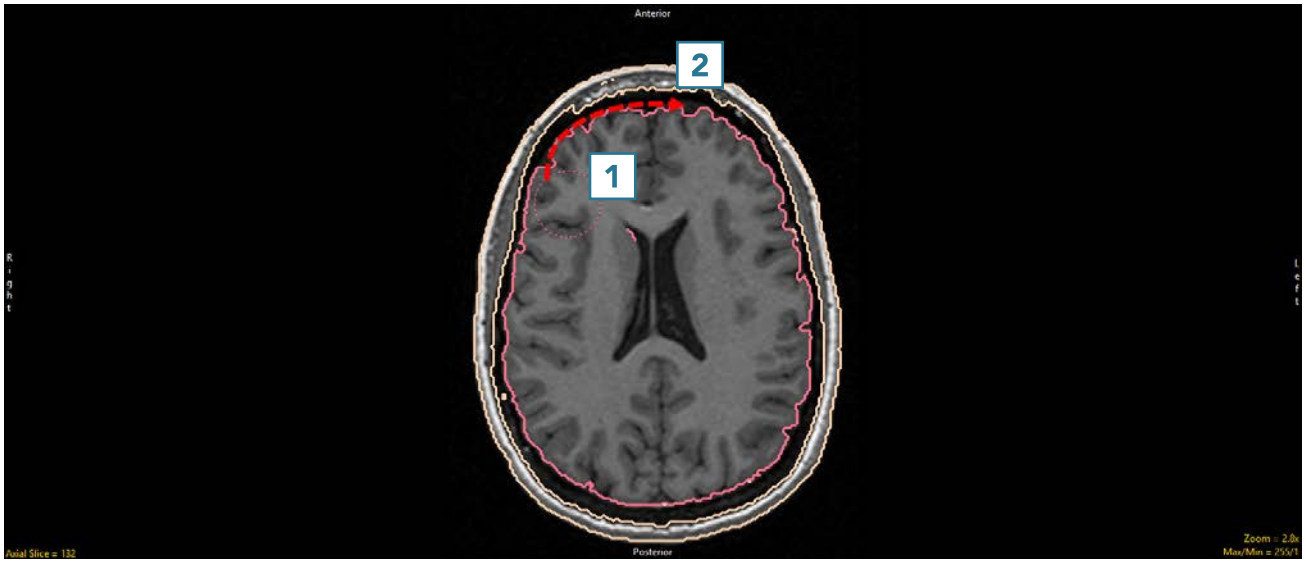



- The borders of the Brain and Ventricle objects will be updated as the cursor moves through. 10



# 27. Using the Nudge Tool with Locked Objects

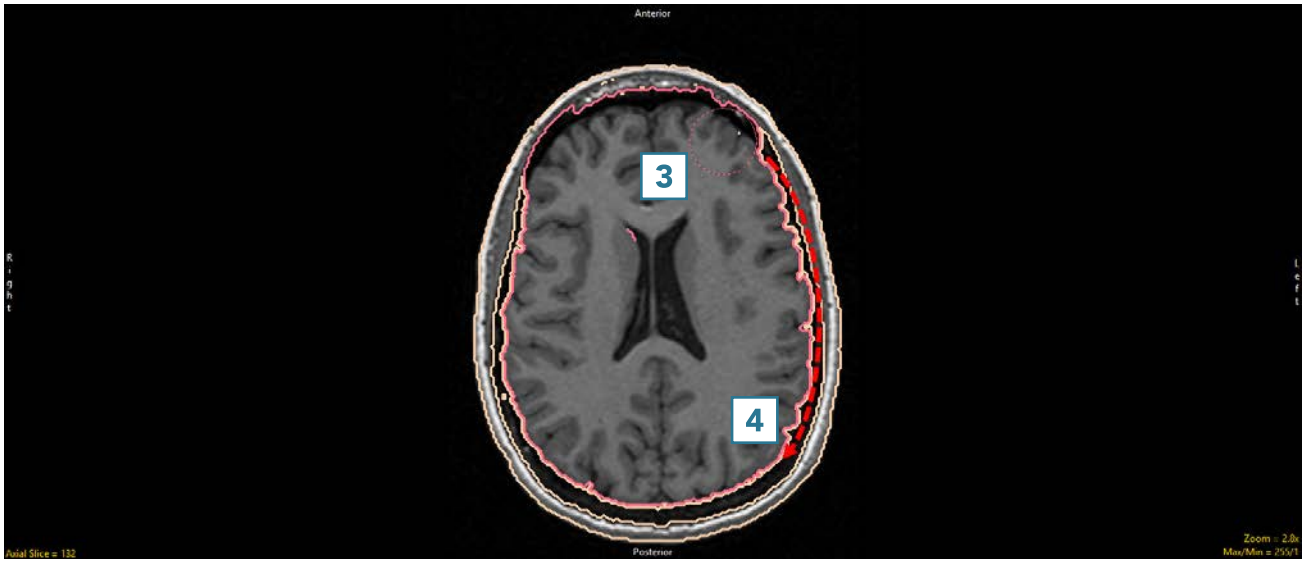
The Nudge Tool can also be used in conjunction with locked objects. For example, if a user decided that they wanted to measure the intracranial area on this slice, after reassigning the Ventricle object on this slice to the Brain object using the 2D object reassignment option (see the Reassign Object tool), the Skin object can be locked and the brain object pushed out using the Nudge tool to the border of the skin object.



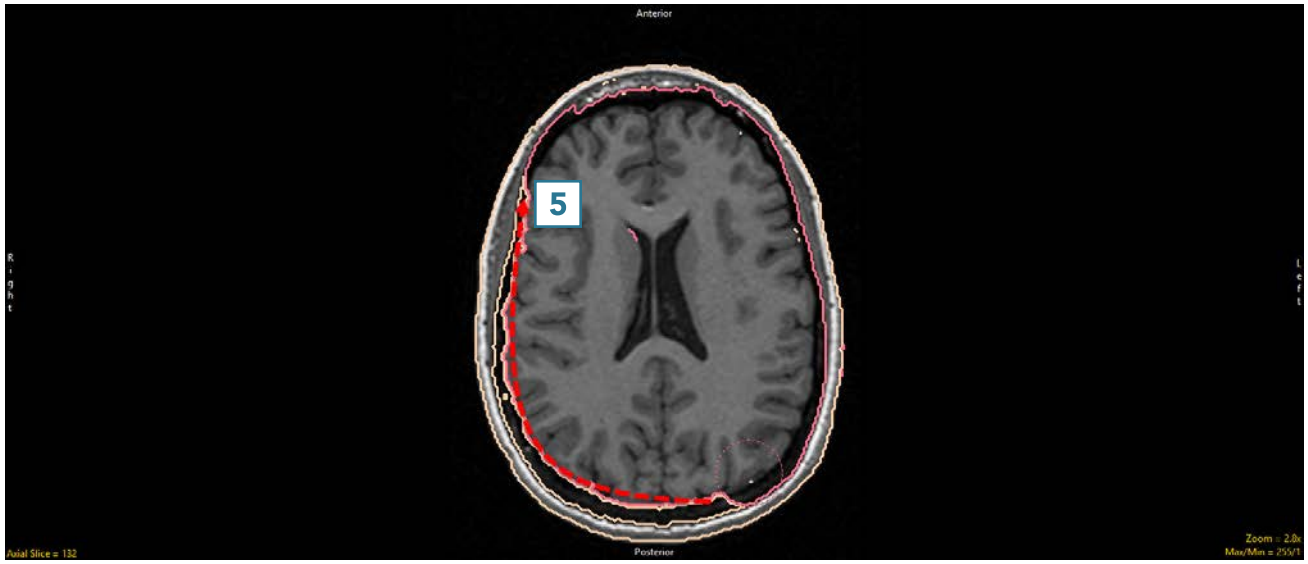

- Use the Reassign Object option to reassign the Ventricle object on Axial slice 132 to the Brain object.
- Lock the Skin object.
- Select the Nudge Edit tool.
- Click in the Brain 1 and move the Nudge tool into the intracranial space 2 between the Brain and Skin objects.

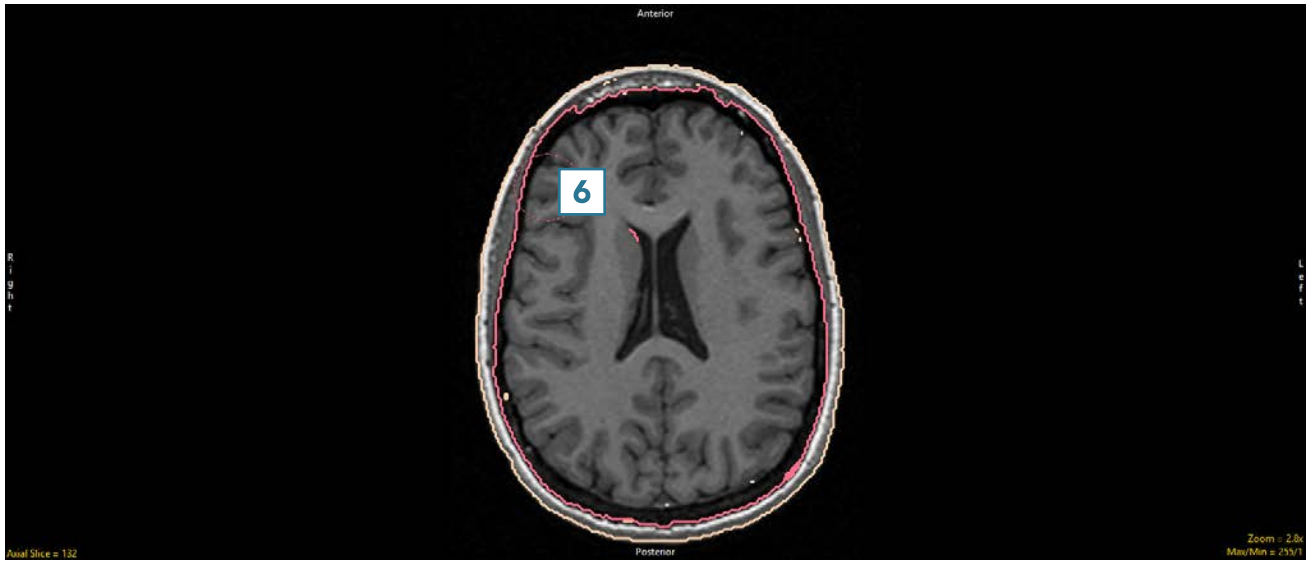
- Note that the Brain object will be pushed into the intracranial space but not into the locked skin object. 3
- Continue moving the Nudge tool through the intracranial space. 4

Note that if the cursor moves past the Skin object into the Original object, voxels in the Original object can still be added to the Brain object using the Nudge tool. To prevent this, lock the Original object as well.



- Continue moving through the intracranial space 5 to complete the edit. 6

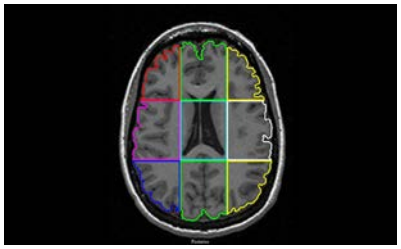
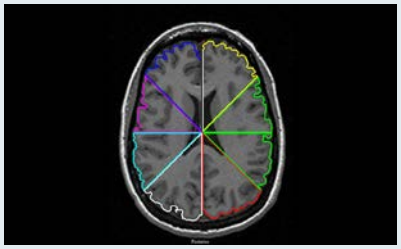
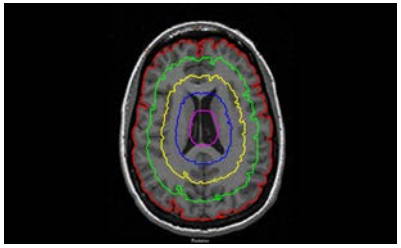


# Divide Regions

The Divide Regions tool allows users to divide objects into subdivisions based upon the division type selected. Users can choose between grid, radial or between borders.

## Table 7.2: Divide Regions

| Divide Type | Function | Example |
|---|---|---|
| Grid | Divides selected object into rectangles. |  |
| Radial | Radially divides selected object, splitting the object into pie wedges. |  |
| Between Borders | Divides object into concentric shapes. |  |

# 28. Grid Division of an Object

Grid division can be useful for subdividing structures into various anatomical substructures. For example, division of the corpus callosum (CC) on the mid-sagittal slice into its substructures is an important research methodology for assessment of the CC. A method for CC subdivision proposed by Witelson *et al*, "Hand and sex differences in the isthmus and genu of the human corpus callosum: a postmortem morphological study," provides an easy methodology for CC subdivision using AnalyzePro and has subsequently become the de facto standard for the procedure.

- Select MRI_3D_Head and open Segment.
- Set the primary display to Sagittal, 1 move to the mid-sagittal slice 2 and Zoom to the CC. 3
- Select Manual and use either Smart Trace or Auto Trace to define the CC on the mid-sagittal slice. 4
- Select Divide Regions. 5 Set the Divide Type to Grid. 6
- Set the Number of Rows to 1 and Columns to 6. 7
- Click in the CC. 8

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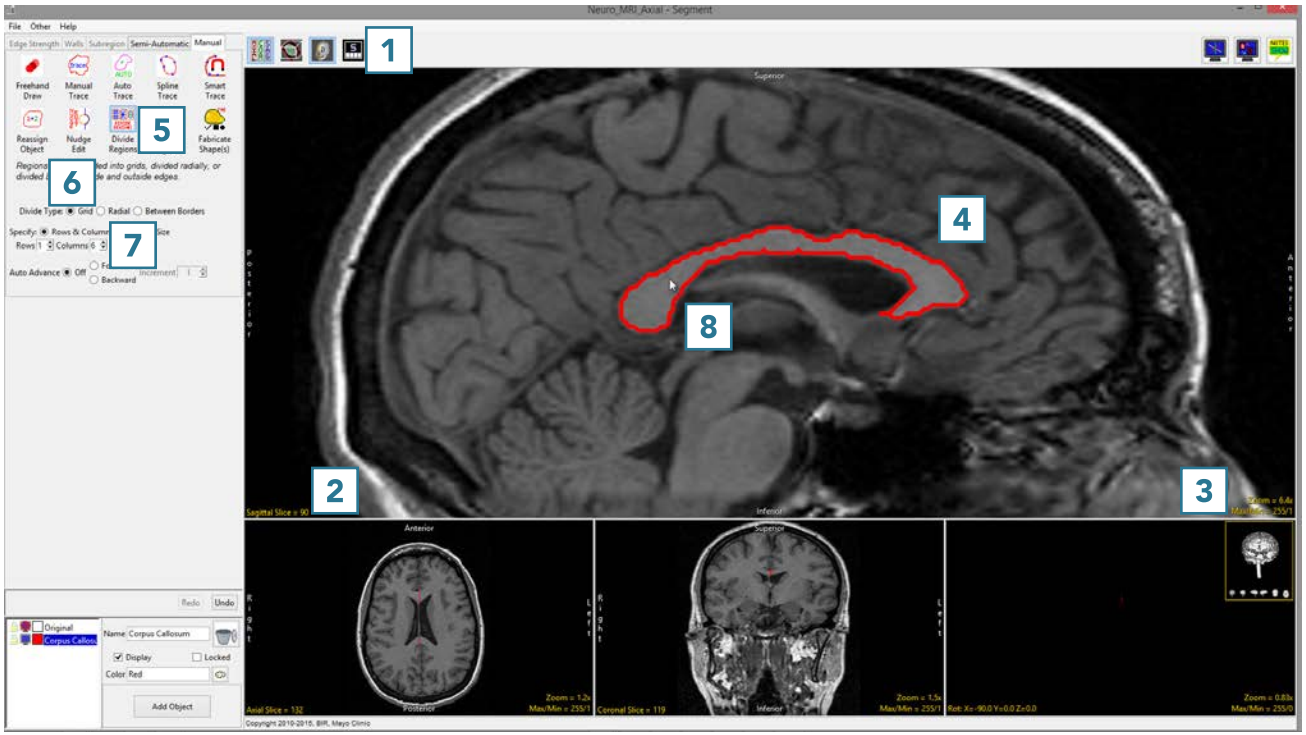
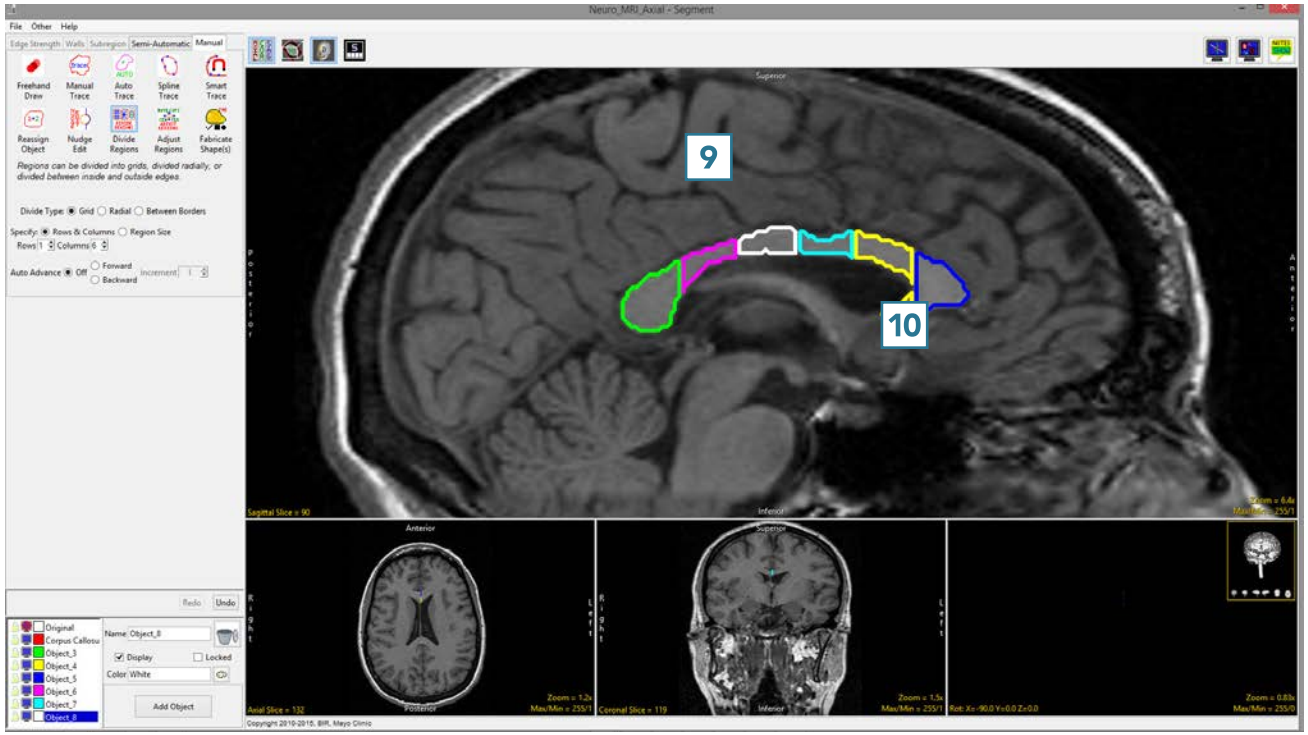


- The CC will be divided into 6 Subregions. 9
- Note that the Rostrum 10 will need to be assigned to a separate object. This can be achieved using the 2D reassignment option in the Reassign Object tool. Objects can be given the correct structural names (Splenium, Isthmus, Posterior Midbody, Anterior Midbody, Rostral Body, Genu and Rostrum) using the Object Control window.
- Use File > Save Object Map to save your work.

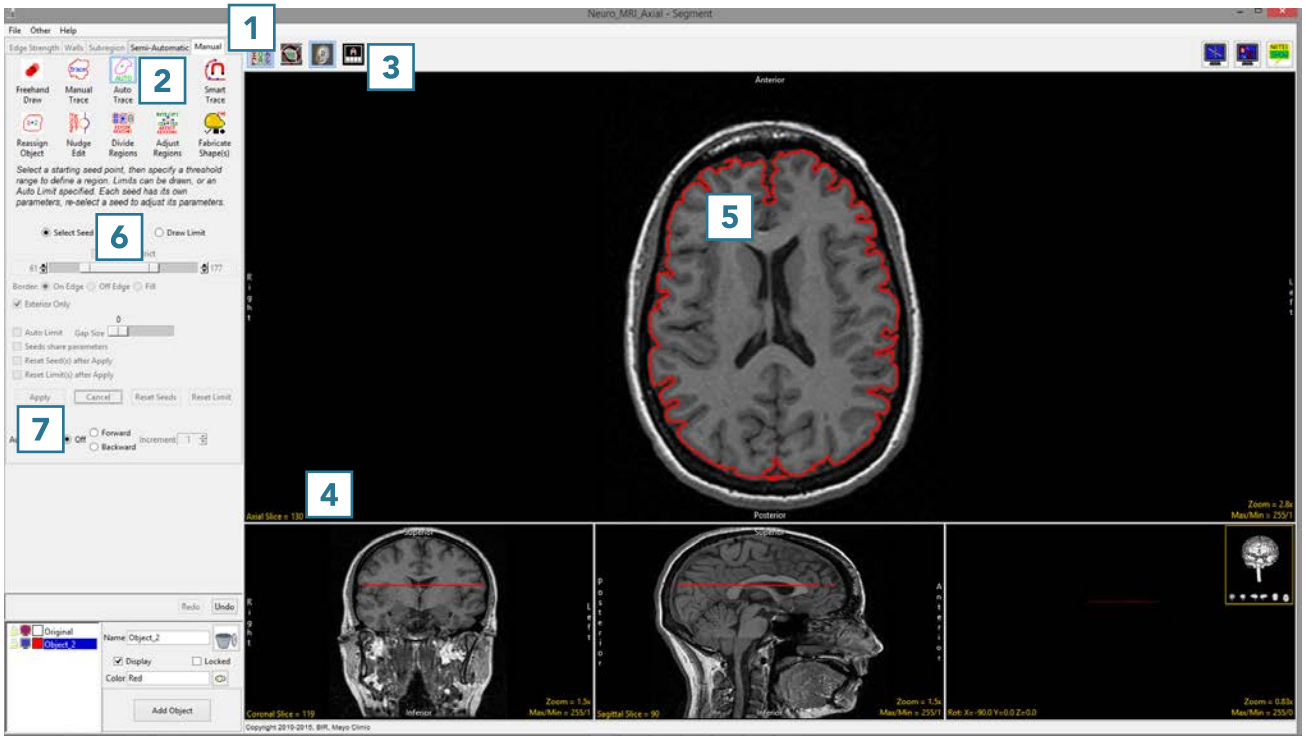


# 29. Radial Division of an Object

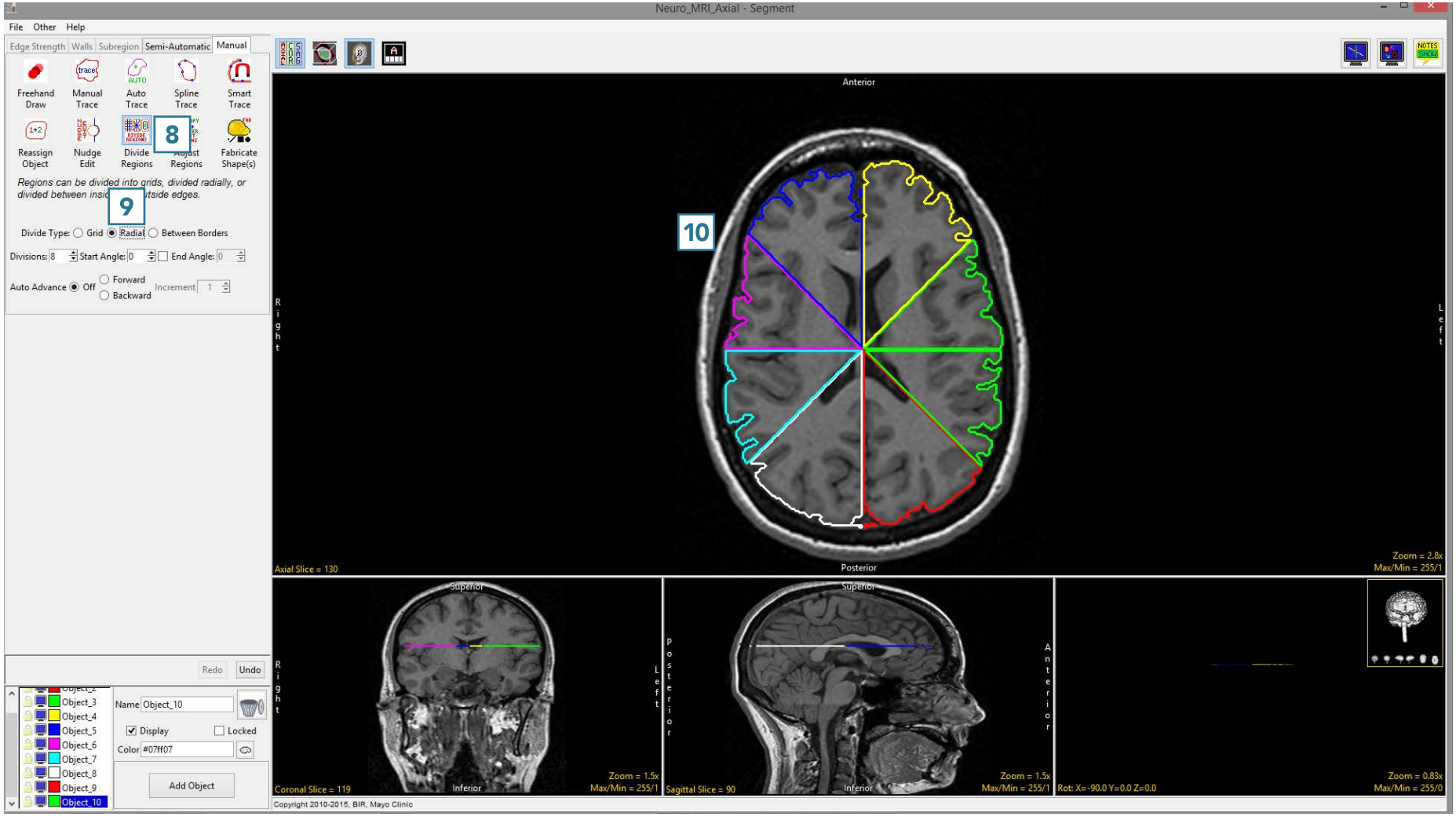
Like grid division, radial division of objects can be useful for subdividing structures into various substructures.

- Select MRI_3D_Head and open Segment.
- Select Manual 1 and choose Auto Trace. 2
- Set the primary display to Axial 3 and use Slice 4 to move to axial slice 130.
- Set a seed pixel in the white matter 5 and adjust the minimum and maximum threshold values 6 to define the brain. A min value of 45 and max value of 125 works well for this data set.
- Click Apply 7 to define the brain.

**Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/**



- Select the Divide Regions tool 8 and set the Divide Type to Radial. 9
- With Division set to 8, click anywhere in the brain to divide the object into 8 radial divisions. 10



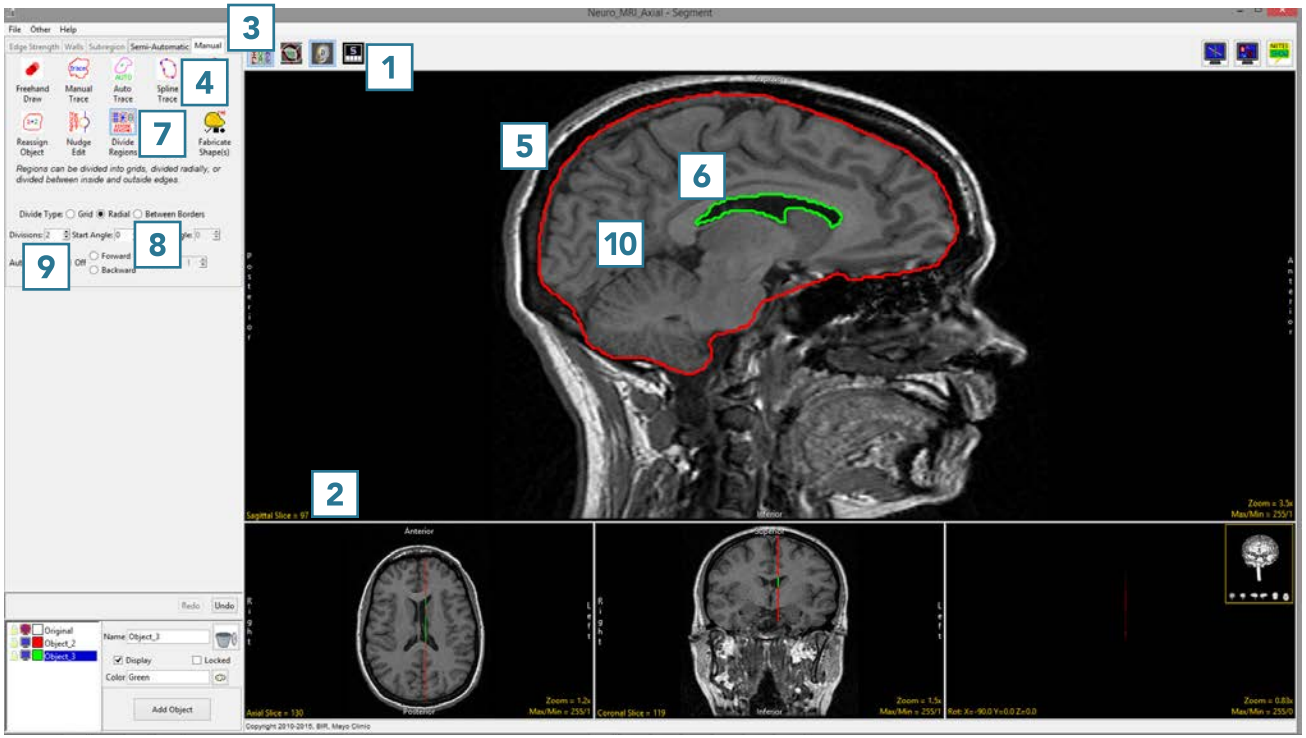
# Dividing Regions Between Borders

The Divide Regions Between Borders division type allows users to create a concentric set of objects. The tool will divide the area between an inner and outer border into the number of regions specified by the user, which is acheived by interpolating new borders between the inner and outer border.

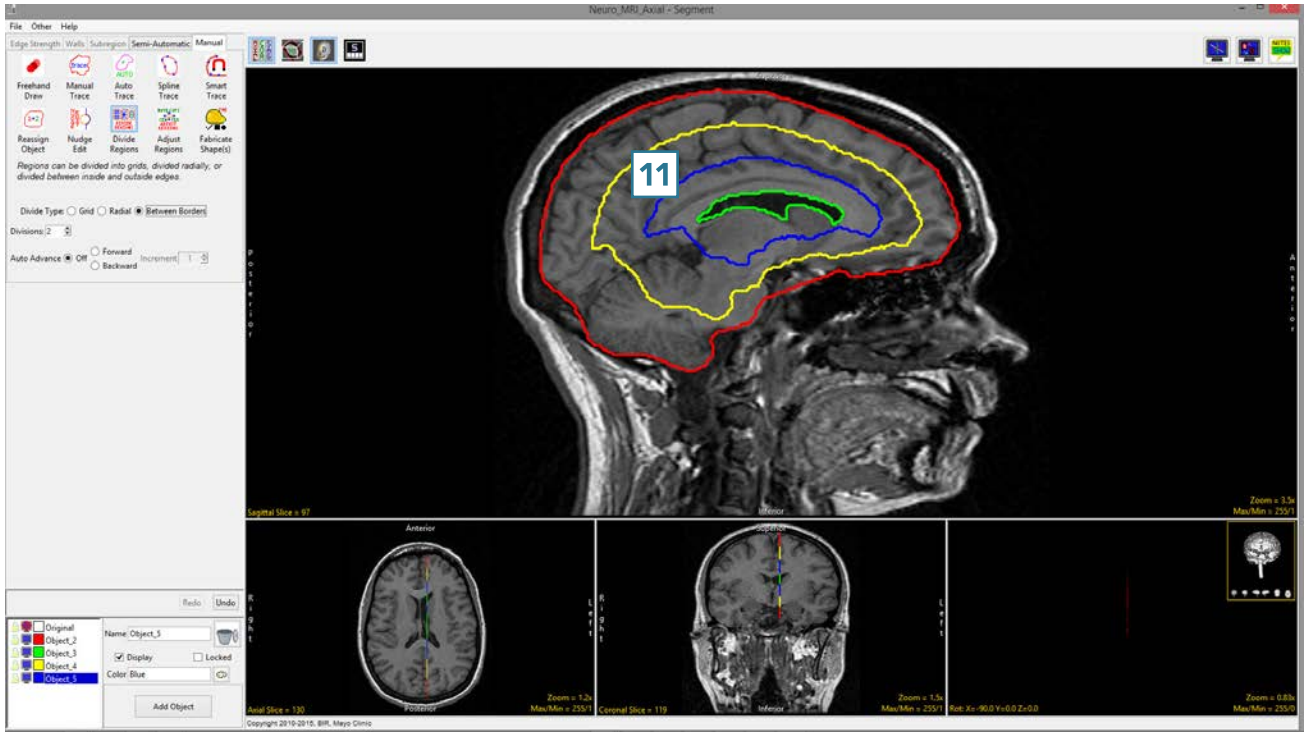
# 30. Dividing Regions Between Borders – Interpolating Between Objects

- Select MRI_3D_Head and open Segment.
- Set the primary display to Sagittal 1 and use Slice 2 to move to sagittal slice 96.
- Select Manual 3 and choose Spline. 4
- Use the Spline tool to define a region of interest around the brain. 5
- Add a new object and define a region of interest around the ventricles. 6
- Select the Divide Regions tool 7 and set the Divide Type to Between Borders. 8
- Set the Divisions to 2. 9
- Click anywhere in the brain between the red brain border and the green ventricle border. 10

**Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/**



- 2 new regions will be interpolated between the brain and ventricles. 11

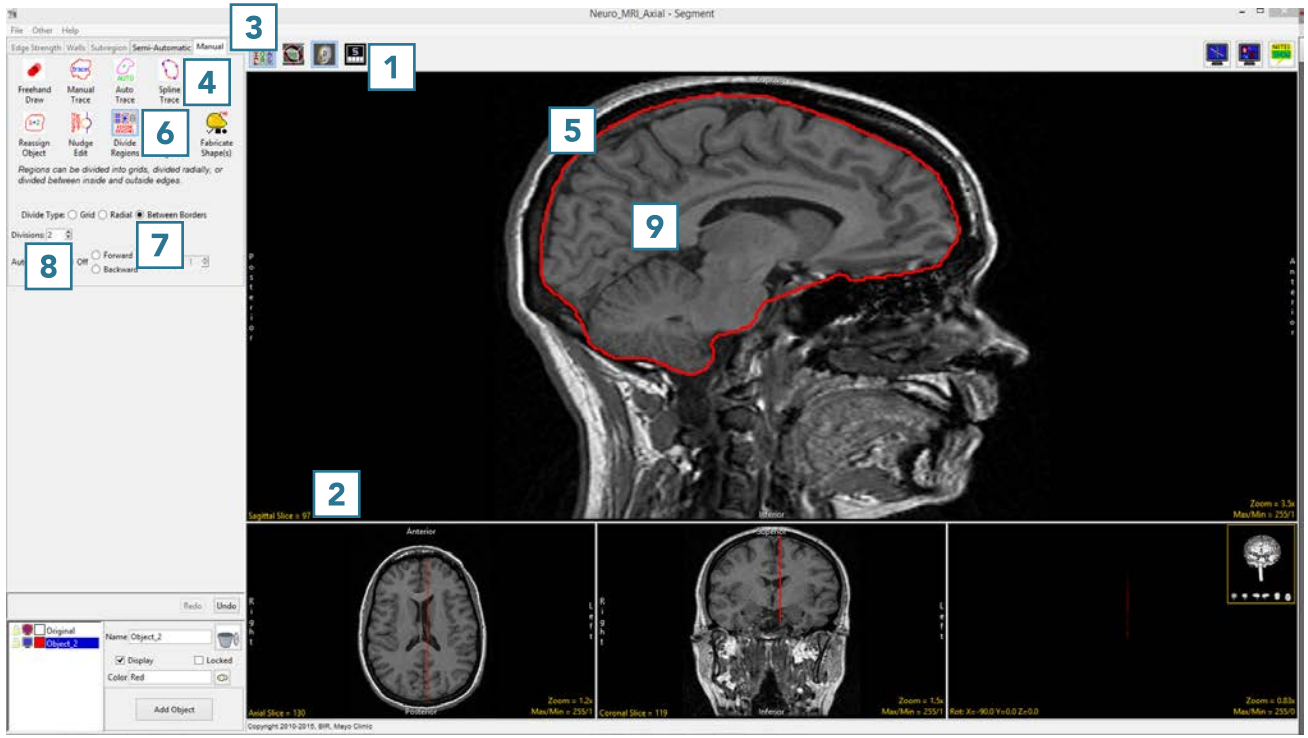


# 31. Dividing Regions Between Borders – Interpolating Within an Object

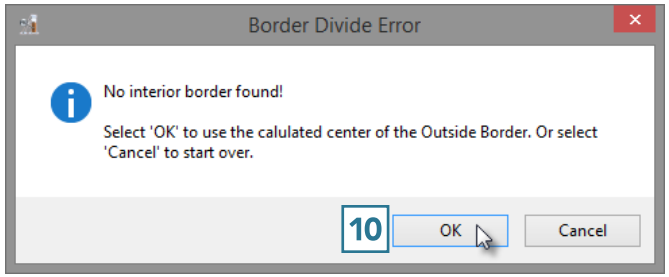
If there is no inner border defined when using the Divide Objects Between Border division type, the tool will calculate the center of the object and use this as an interpolation point, creating new interior object borders from the outer border.

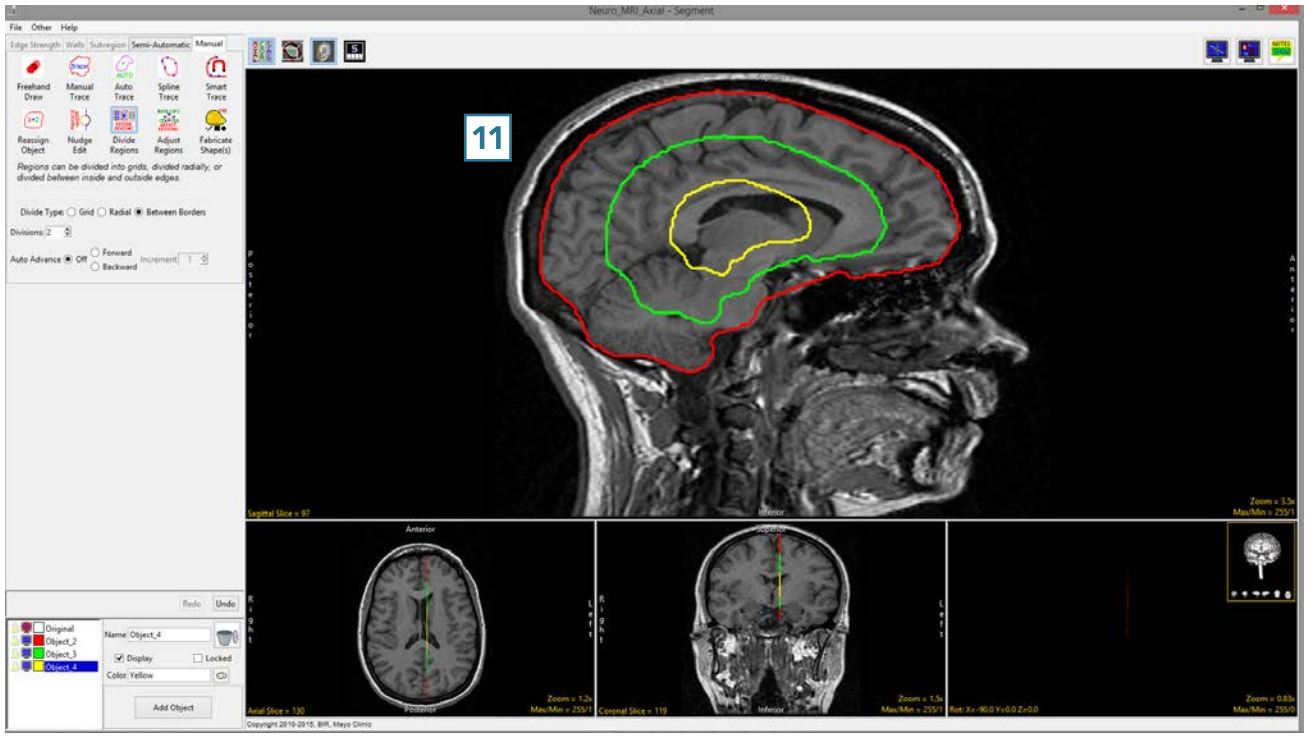
- Select MRI_3D_Head and open Segment.
- Set the primary display to Sagittal 1 and use Slice 2 to move to sagittal slice 96.
- Select Manual 3 and choose Spline. 4
- Use the Spline tool to define a region of interest around the brain. 5
- Select the Divide regions tool 6 and set the Divide Type to Between Borders. 7
- Set the Divisions to 2. 8 Click anywhere in the brain. 9

**Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/**



- The tool will detect that there is no interior border and return a Border Divide Error. Click OK 10 to enable the tool to use the center of the outside border as an interpolation point to substitute the interior border.
- The object will be subdivided into regions interpolated from the outer border and the new regions will look like smaller versions of the outer border. 11



# Adjust Regions

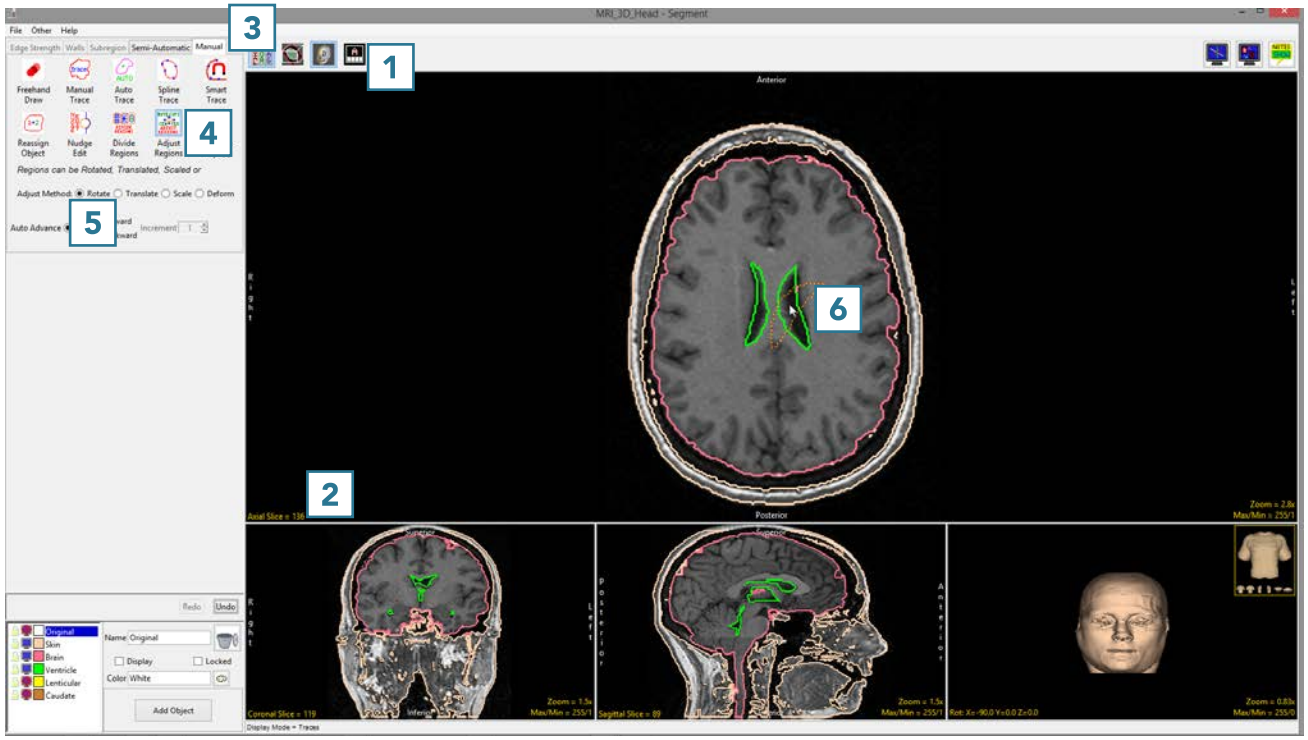
The Adjust Regions tool allows users to interactively manipulate regions. Users can rotate, translate, scale and deform objects.

## Table 7.3: Adjust Regions

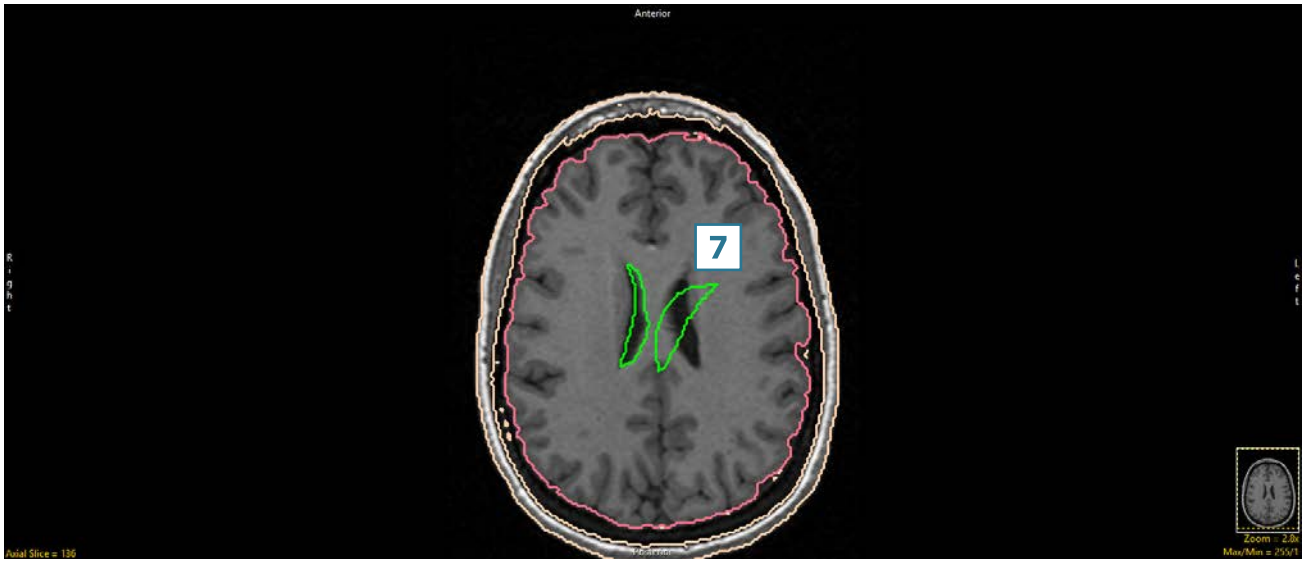
| Adjust Method | Function |
|---|---|
| Rotate | Rotates selected region clockwise or counterclockwise. |
| Translate | Translates selected region to a new location. Users can drag the region or a copy of the region to a new location. Objects can also be recentered around the brightest pixel in the object. |
| Scale | Increases or decreases the size of the region in the horizontal and/or vertical direction. |
| Deform | Deforms the selected object. |

- Select MRI_3D_Head and open Segment.
- Select File > Load Object Maps and load MRI_3D_Head.obj.
- Set the primary display to Axial 1 and move to Axial slice 136. 2
- Select Manual 3 and choose Adjust Regions. 4
- Set the Adjust Method to Rotate. 5
- Click in an object to select it and move the mouse up or down to rotate the object. 6

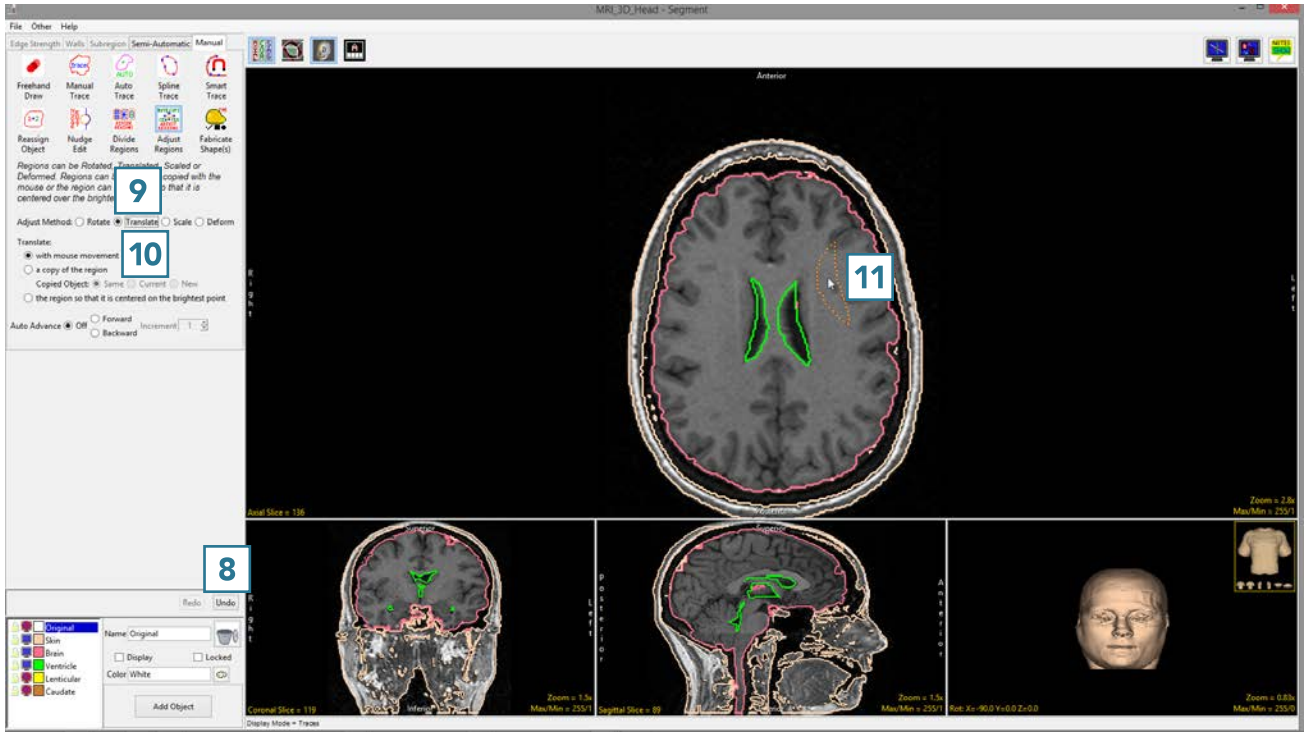
**Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/**



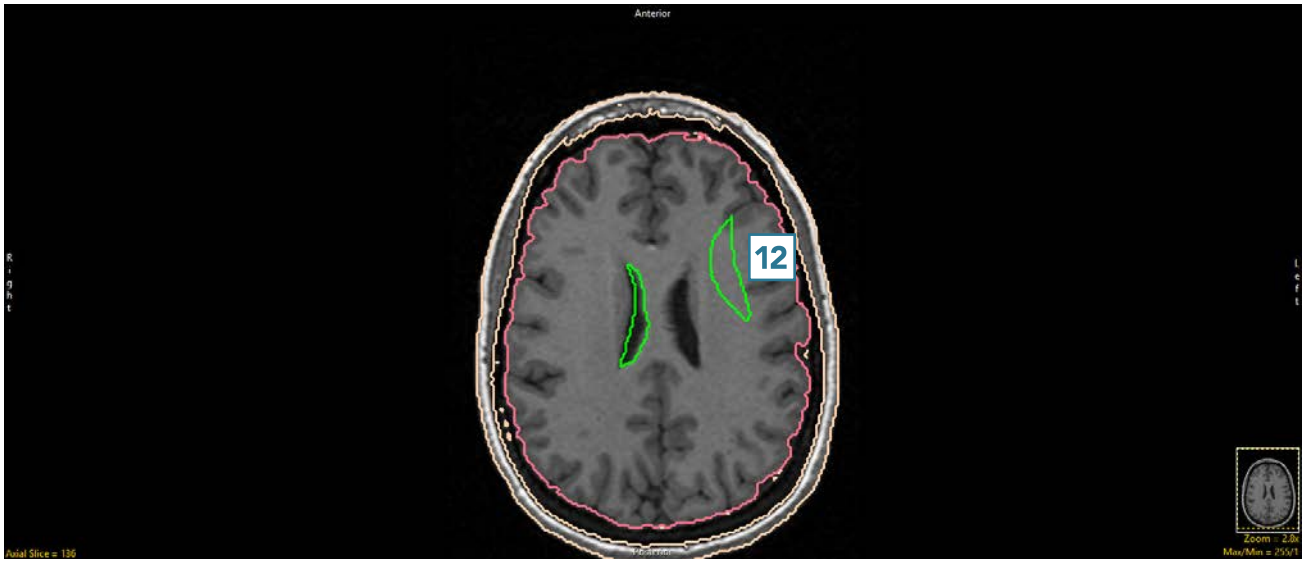
- Release the mouse button to end the rotation and commit the rotation to the object. 7



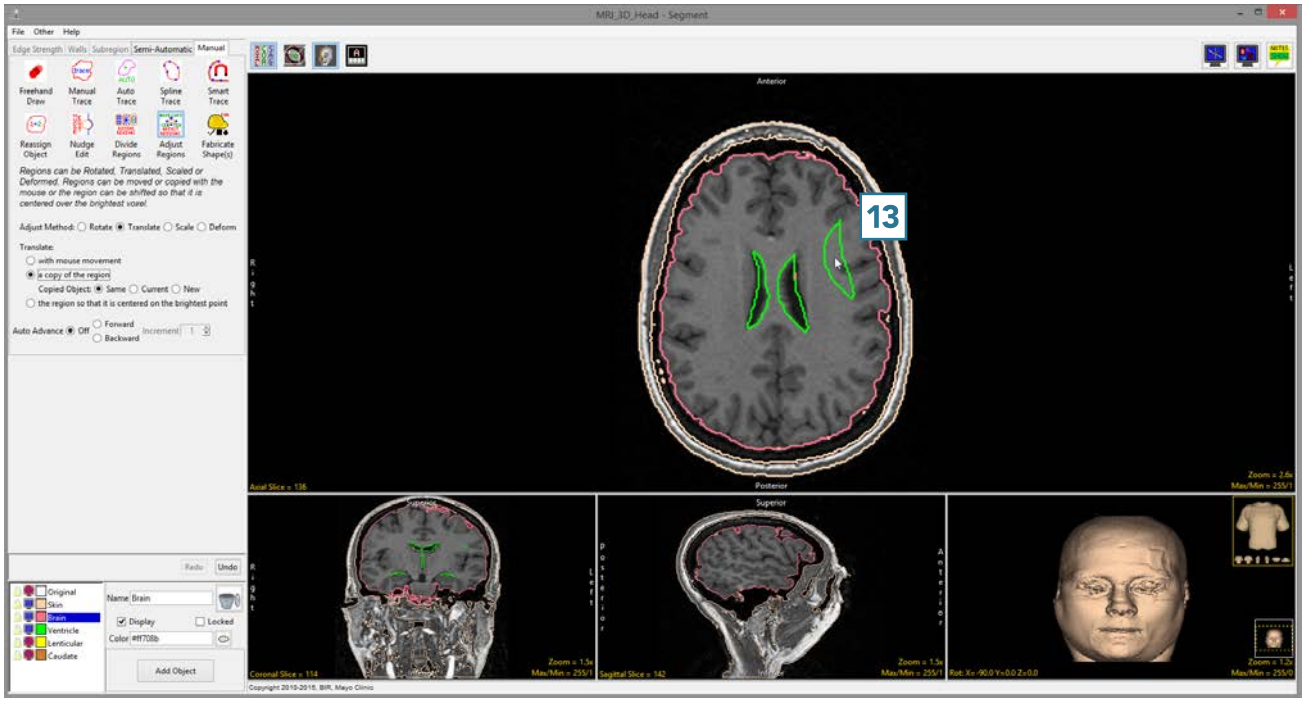
- Click Undo 8 and set the Adjust Method to Translate. 9
- With the Translate option set to with mouse movement, 10 click in an object and drag to a new location. 11



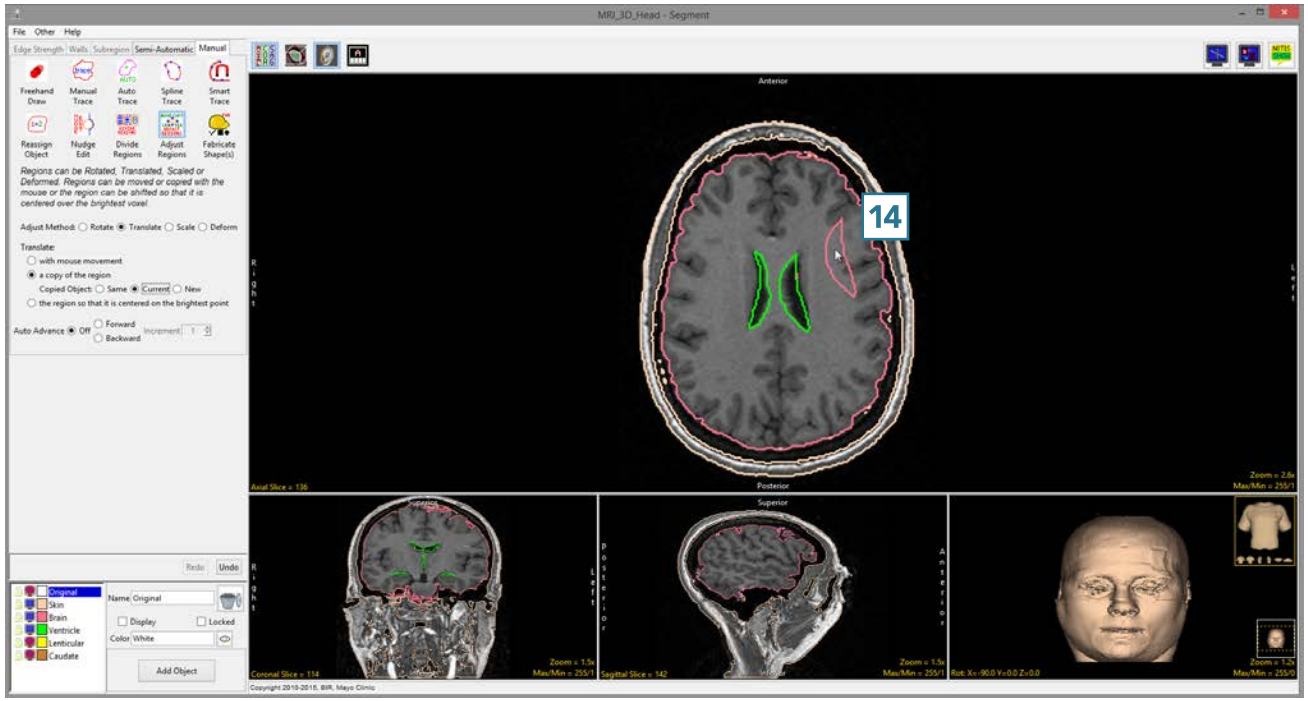
- Release the mouse button to end the translation. The object will be moved to the new location. 12



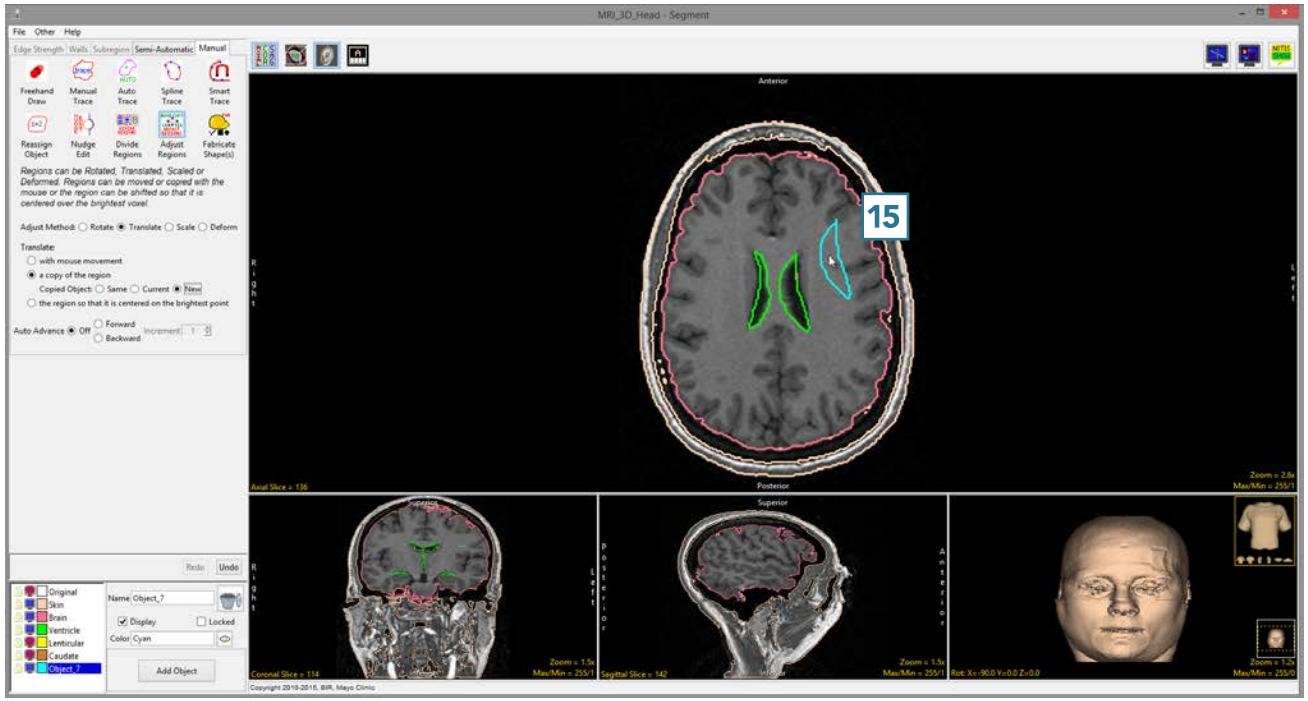
- Setting the Translate option to 'a copy of the region' will allow you to make a copy of the selected object and move to a new location.
- Setting Copied Object to Same assigns voxels in the new region to the same object as the parent region. 13



- Setting Copied Object to Current assigns voxels in the new region to the object currently selected in the Object Control window. 14

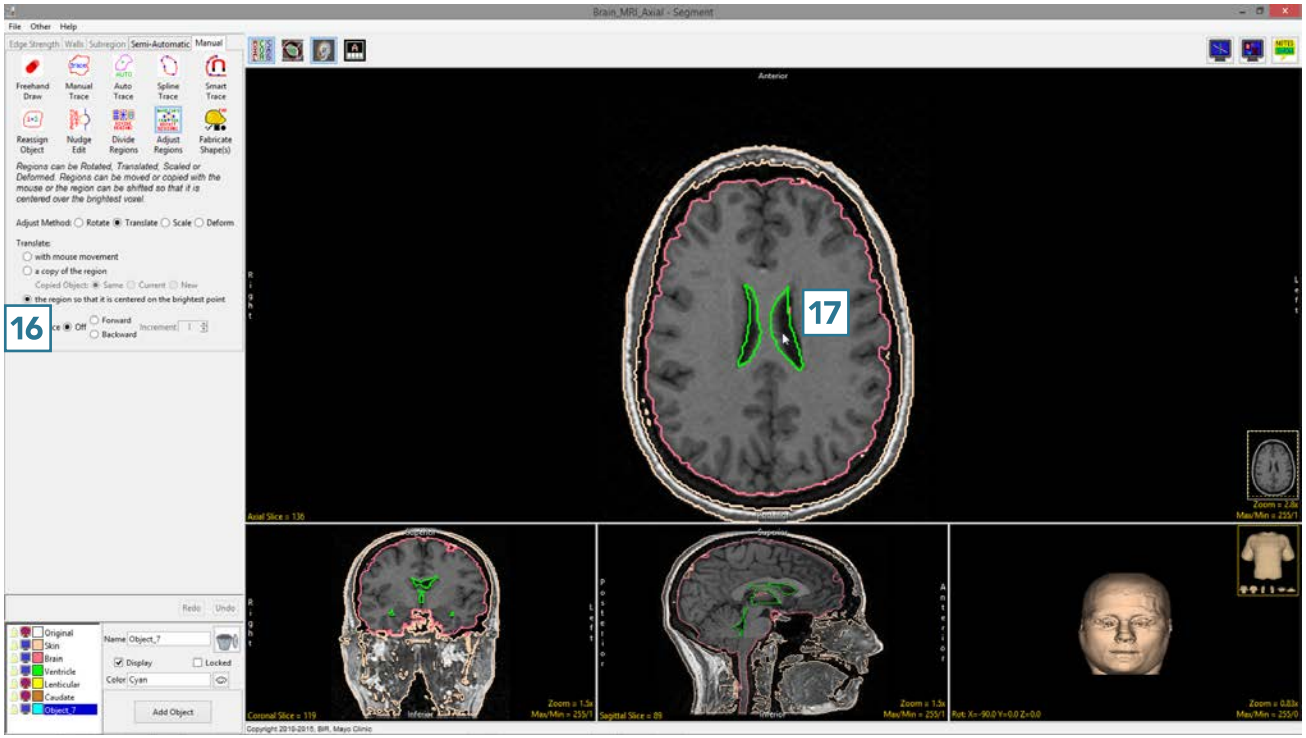


- Setting Copied Object to New assigns voxels in the new region to a new object. 15

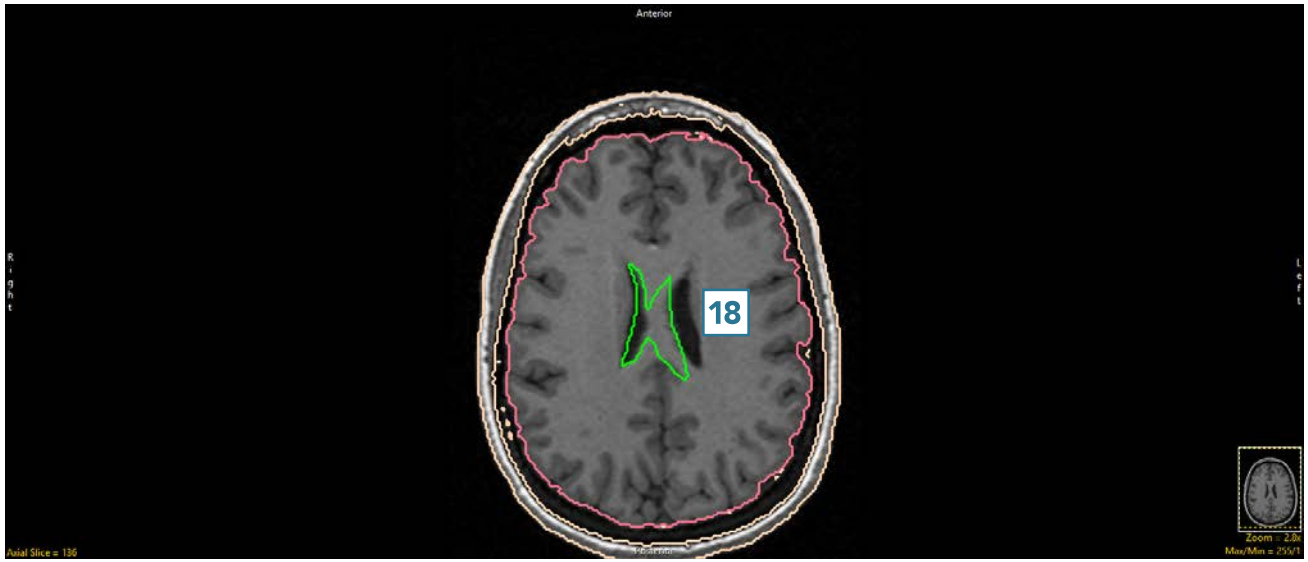


The Translate Adjust Method also allows users to Translate the region so that it is centered on the brightest point. With this option, the tool calculates the brightest pixel in the object and sets that as the the center of the object, translating the object appropriately.

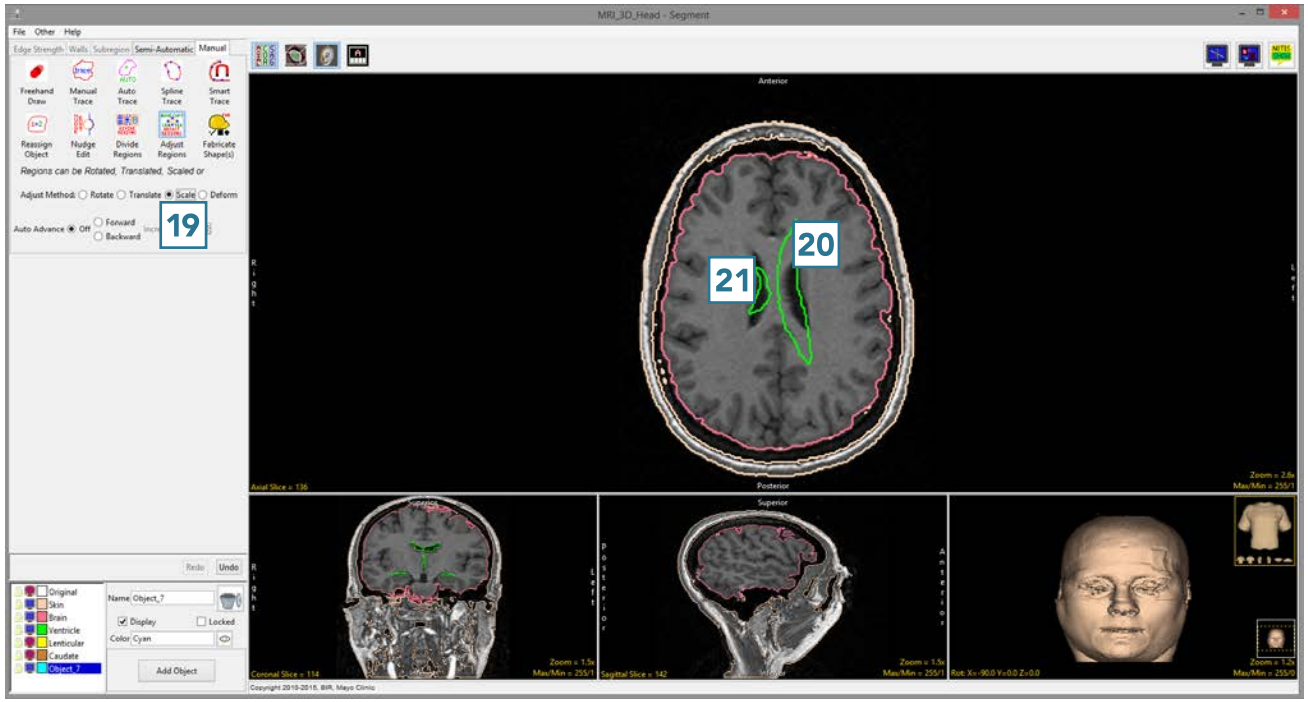
- Set the Translate method to the region so that it is centered on the brightest point. 16
- Click in an object. 17



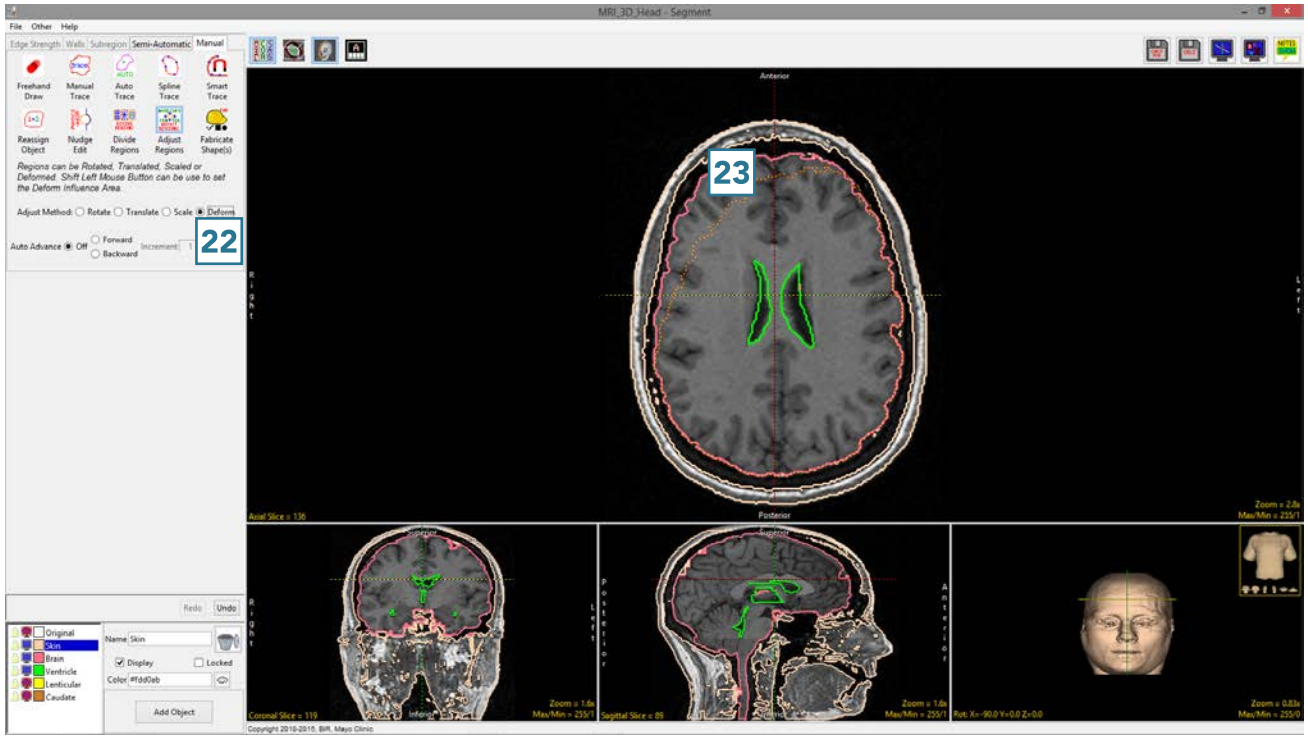
- The region will instantly be recentered around the brightest point in the object. 18



- Click Undo.
- Set the Adjust Method to Scale. 19
- Click in an object and move your mouse to increase the scale of the selected object. 20
- Moving the mouse up and down adjusts the scale in the vertical direction. Moving the mouse left and right adjusts the scale in the horizontal direction. Moving the mouse diagonally adjusts the scale of the object while preserving the shape. Release the button to commit the scale manipulation to the object.
- Click in an object and then move your mouse to decrease the scale of the selected object. 21
- Release the button to commit the scale manipulation to the object.



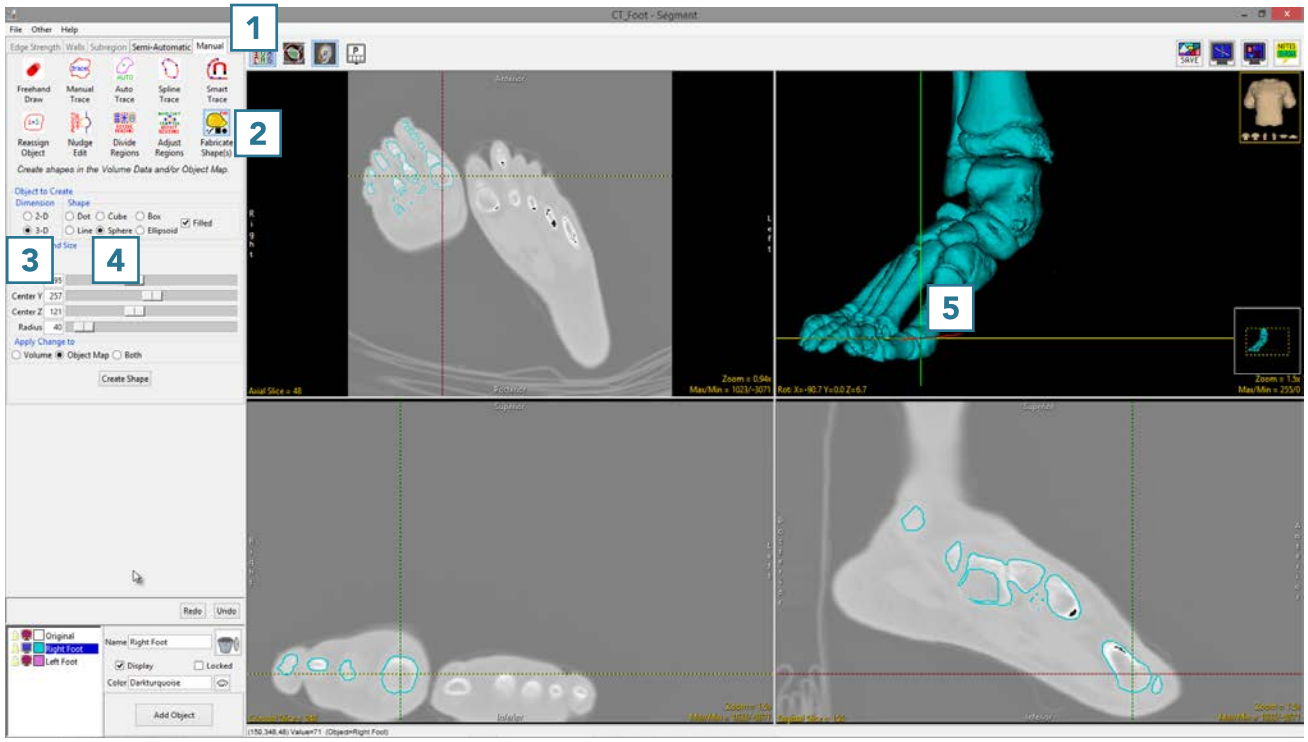
- Undo the previous manipulations.
- Set the Adjust Method to Deform. 22
- Click in an object and move your mouse to experiment w 23 the deformations available. [23] In this example the user is deforming the border of the brain object.
- Releasing the mouse button will apply the deformation to the object.



# Fabricate Shape(s)

The Fabricate Shape(s) tool allows users to create 2D and 3D objects in the object map or input grayscale data. The tool provides options for users to create shapes interactively or by loading a list of coordinates defined in a text file.

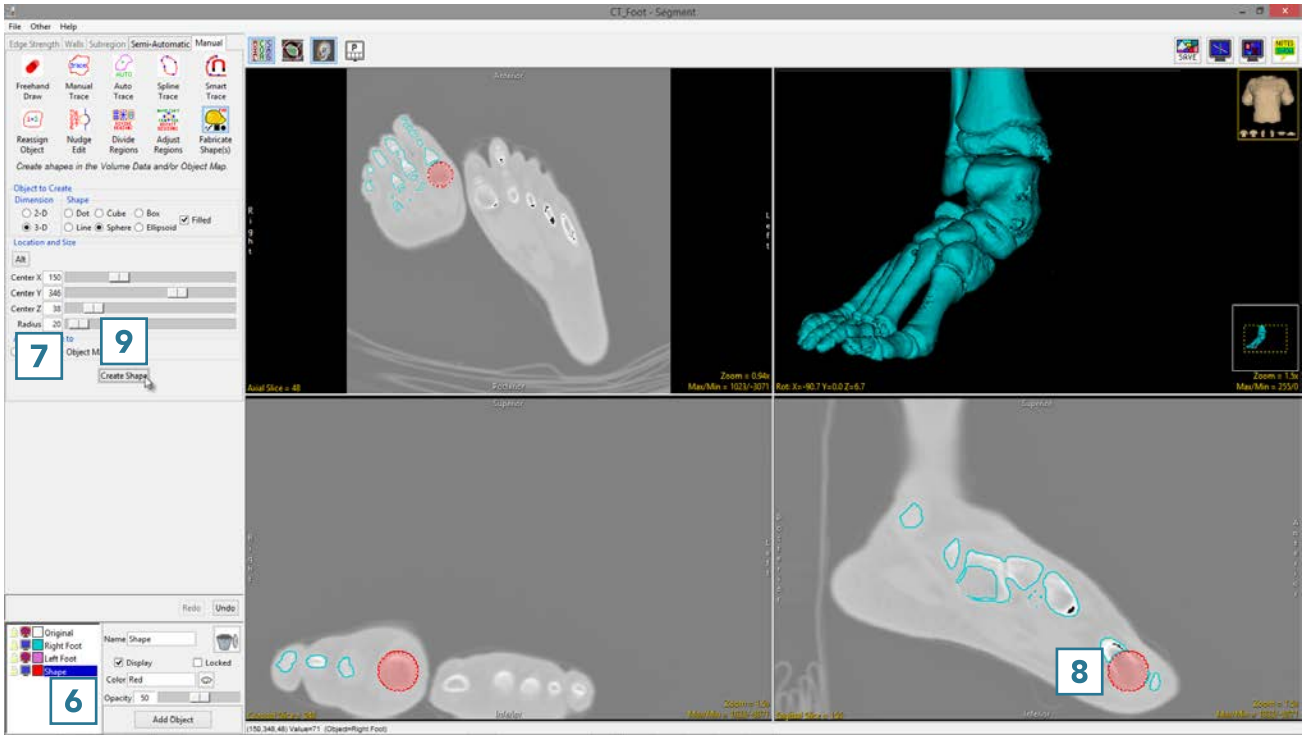
Download the CT_Foot data set to follow along
http://analyzedirect.com/data/



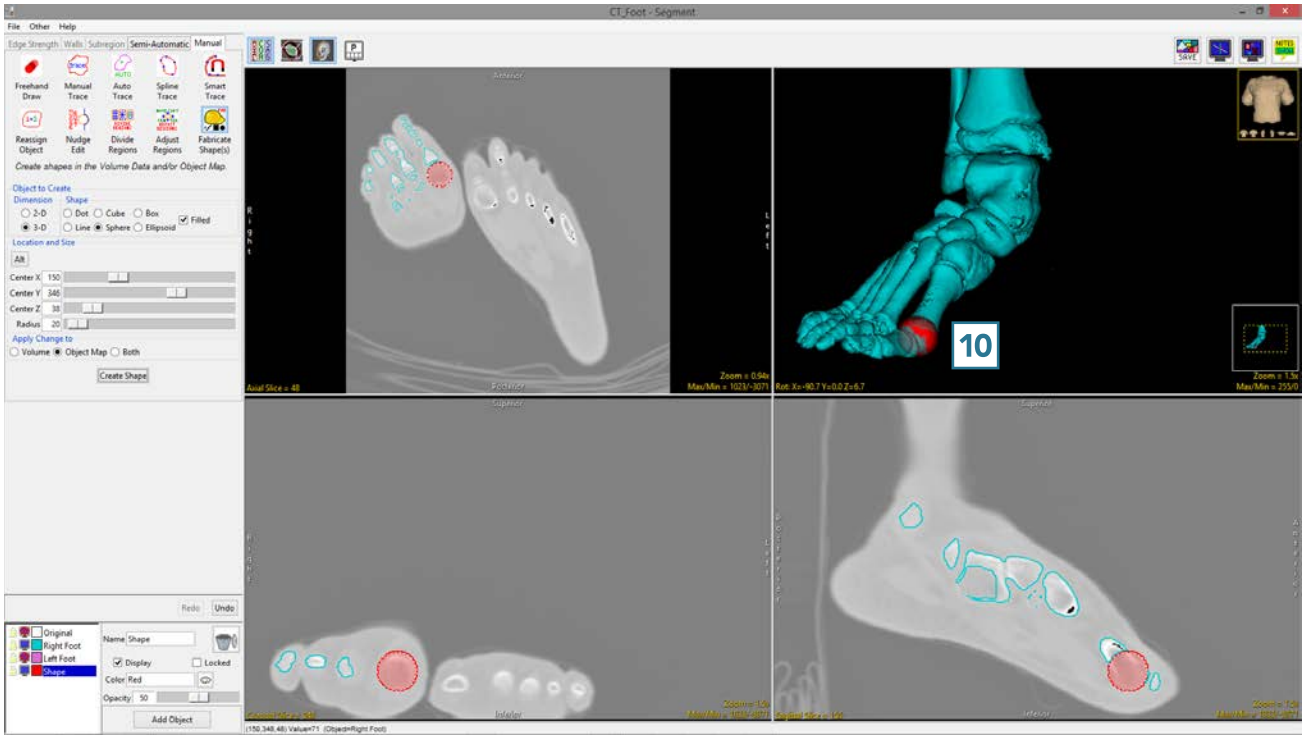

## 32. Creating a Shape

- Select CT_Foot and open Segment.
- Select File > Load Object Maps and load CT_Foot.obj.
- Select Manual 1 and choose Fabricate Shape(s). 2
- Set the Dimension to 3D 3 and set the Shape to Sphere. 4
- Use the linked cursor to navigate to the location where you would like to create the new shape. 5

- Add a new object, name it and assign a color. 6
- Change the Radius of the sphere 7 and drag the 2D shape template in any of the images to the location you where you want to create the shape. 8
- Select Create Shape. 9



- The shape will be created and added to the object map. Right-click on the rendering and select Transparency for a clearer view of the object in 3D. 10

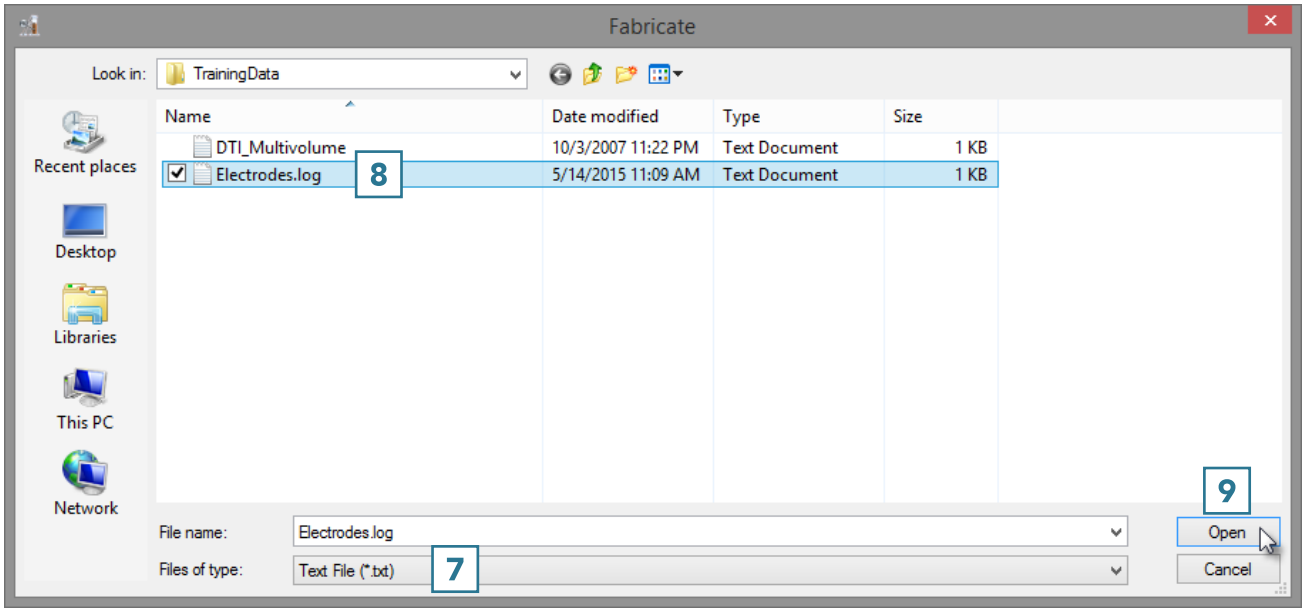


# 33. Creating Objects from a Text File

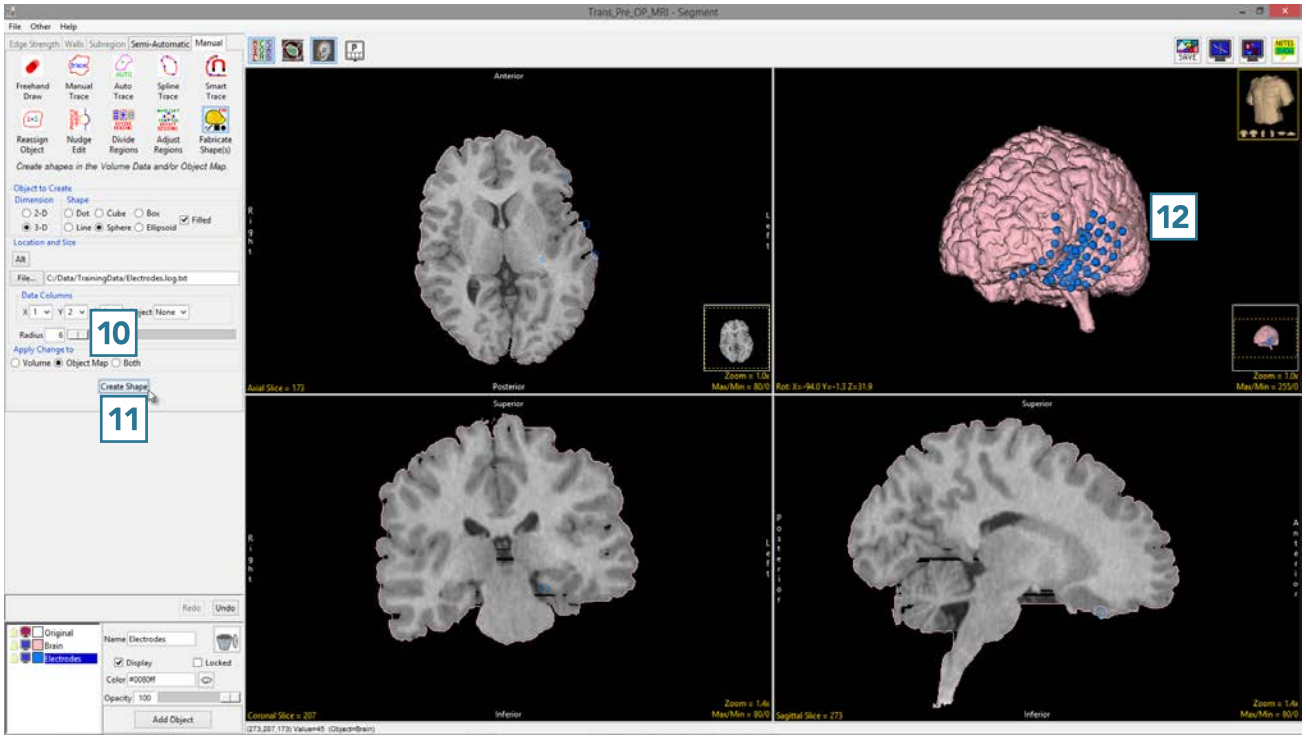
- Select Trans_Pre_OP_MRI and open Segment.
- Select File > Load Object Maps and load Trans_Pre_OP_MRI_brain.obj.
- Select Manual 1 and choose Fabricate Shape(s). 2
- Set the Dimension to 3D 3 and set the Shape to Sphere. 4
- Add a new object, name it Electrodes and assign a color to the object. 5
- Click on the Alt button 6 and select File.

**Download the Trans_Pre_OP_MRI data set to follow along http://analyzedirect.com/data/**

- In the window returned set Files of type to Text File (*.txt). 7
- Select Electrodes text file 8 and click Open. 9



- Set the Radius to 6 **10** and click Create Shape. **11**
- Once created, the new shapes will be added to the object map and can be viewed overlaid on the 2D images and in the 3D rendering. **12**
- Right-click on the rendering and select Transparency for a clearer view of the objects in 3D.
- Select File > Save Object Map and save your object map as Trans_Pre_OP_MRI_brain_and_electrodes.obj.



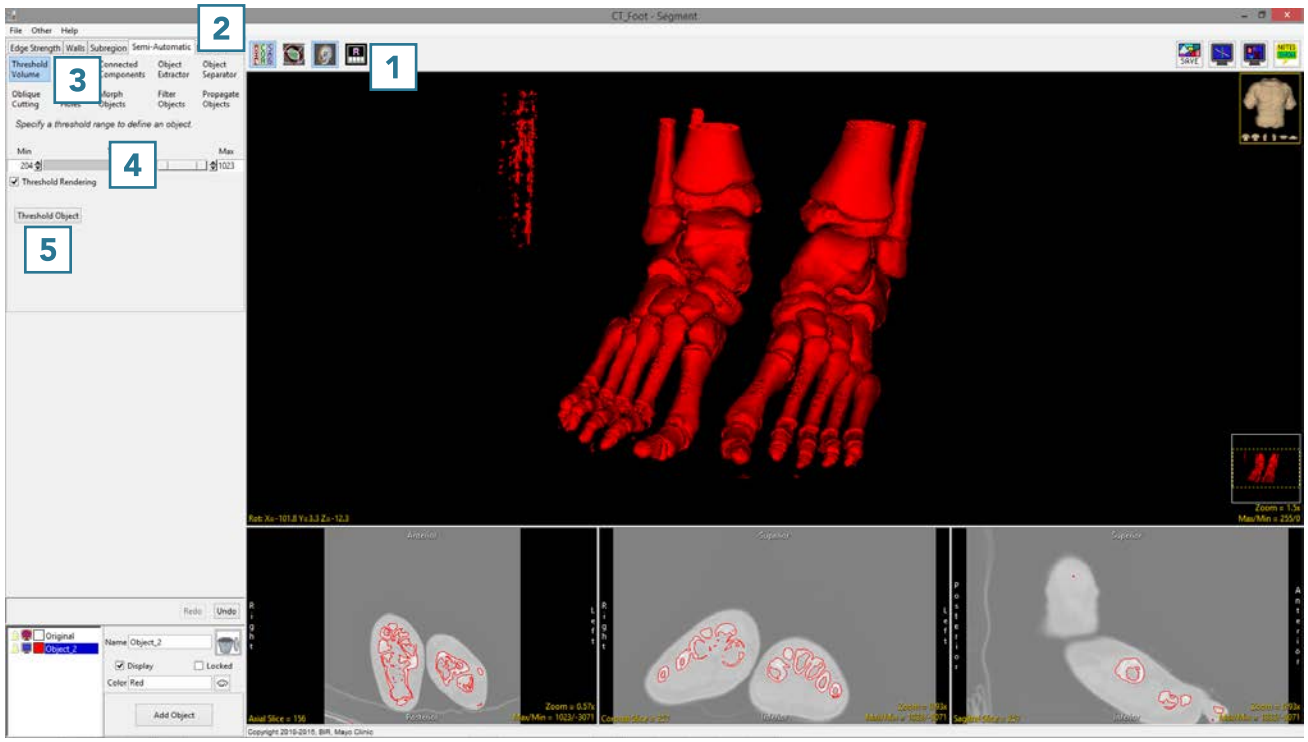
# Manual Tools for 3D Editing

Some of the manual tools have the capability to be used to edit objects in 3D. This is achieved by drawing directly on the 3D rendering.

Download the CT_Foot data set to follow along
http://analyzedirect.com/data/

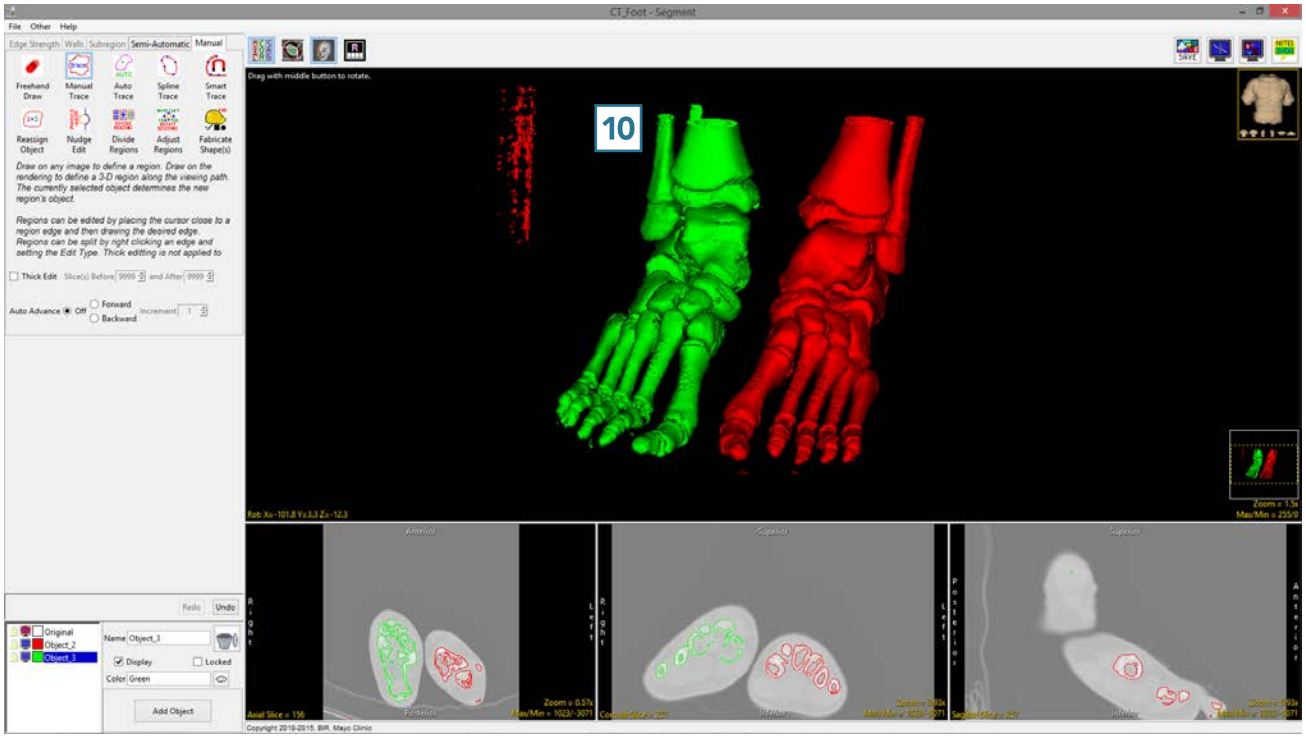
## 34. 2D Manual Trace Editing of Object Maps

- Select CT_Foot and open Segment.
- Set the primary display to Render. 1
- Select Semi-Automatic 2 and choose Threshold Volume. 3
- Set a Threshold range 4 to isolate the bones of both feet and click Threshold Object. 5



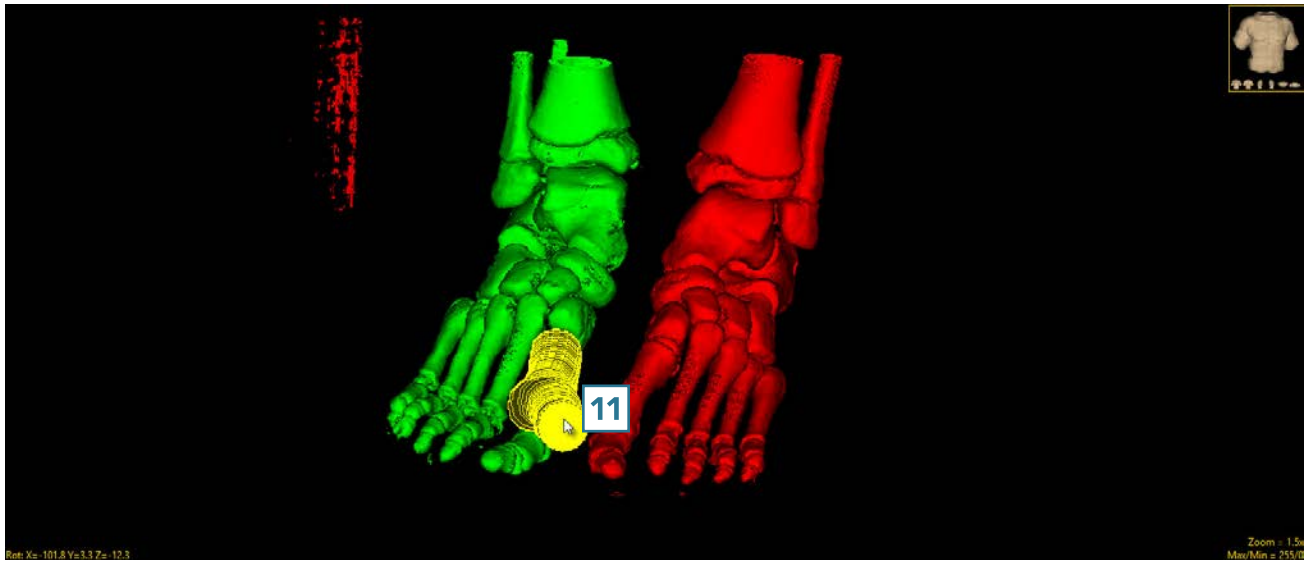
- Select Manual 6 and choose Manual Trace. 7
- Add a new object. 8
- Move the cursor to the Rendering and trace around the right foot. 9

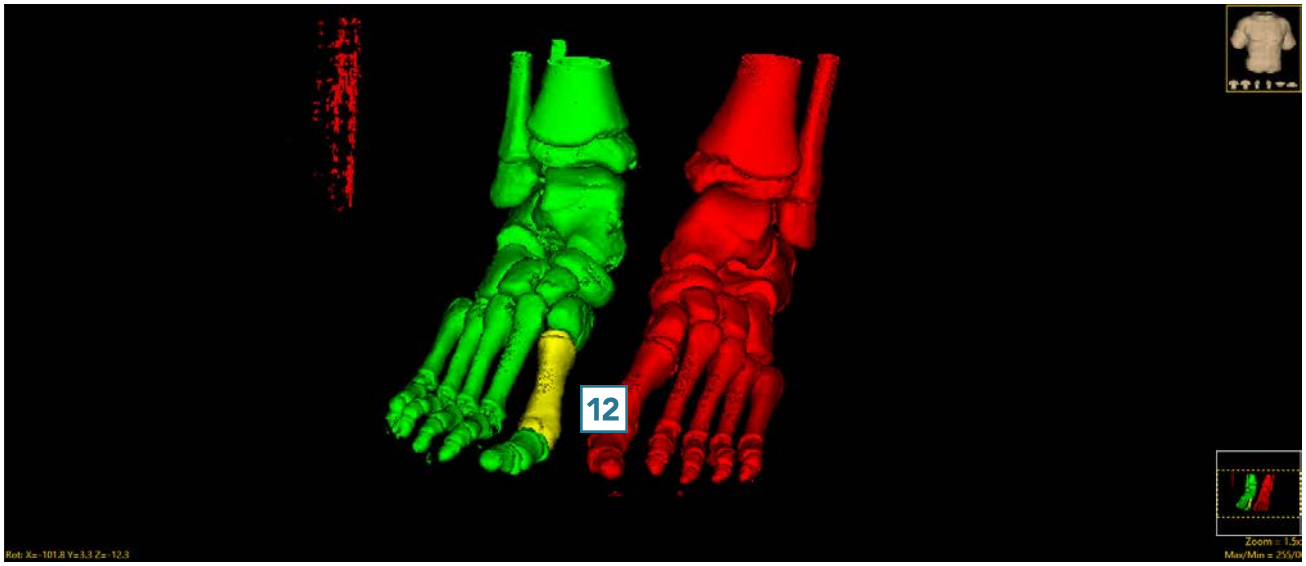
- Complete the trace and release the left mouse button. All voxels not assigned to the Original object within the trace will be assigned to the selected object. 10



# 35. 2D Freehand Draw Editing of Object Maps

- Add a new object.
- Select the Freehand Draw trace and trace over one of the bones in the right foot. 11
- Everything under the region will be assigned to the selected object. 12

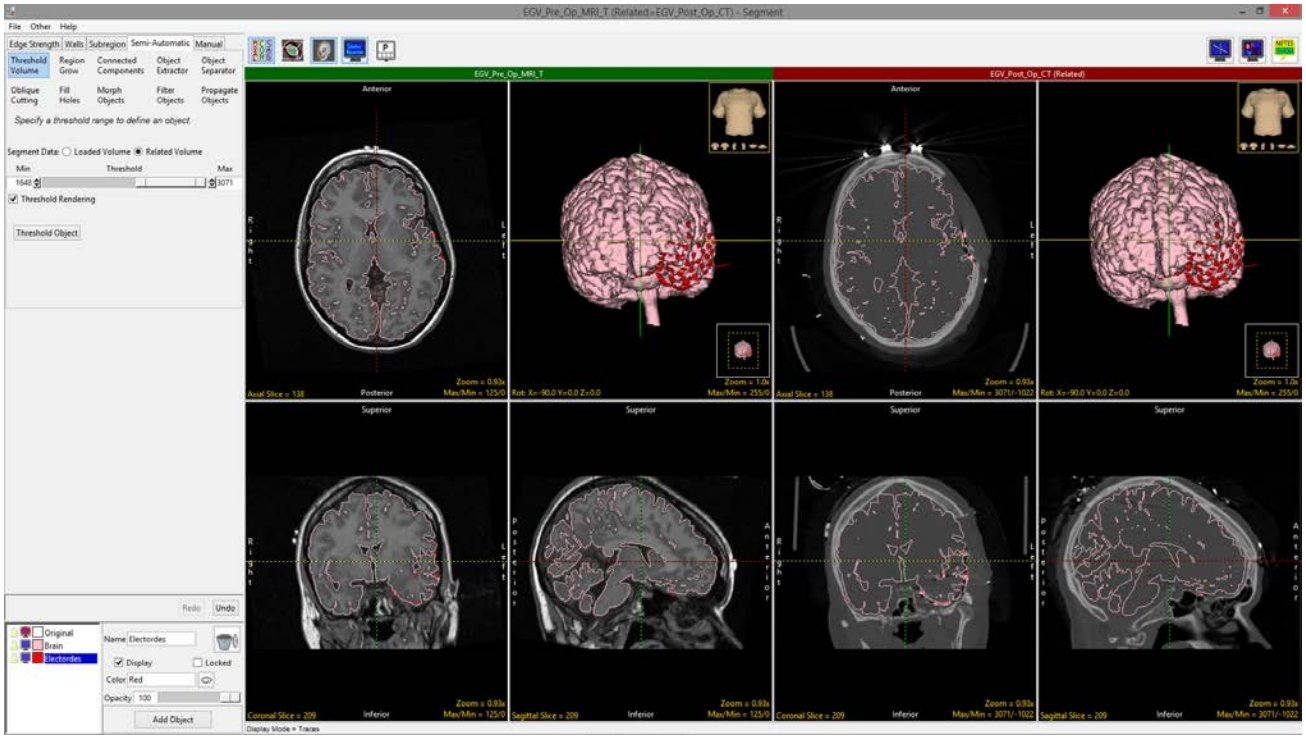


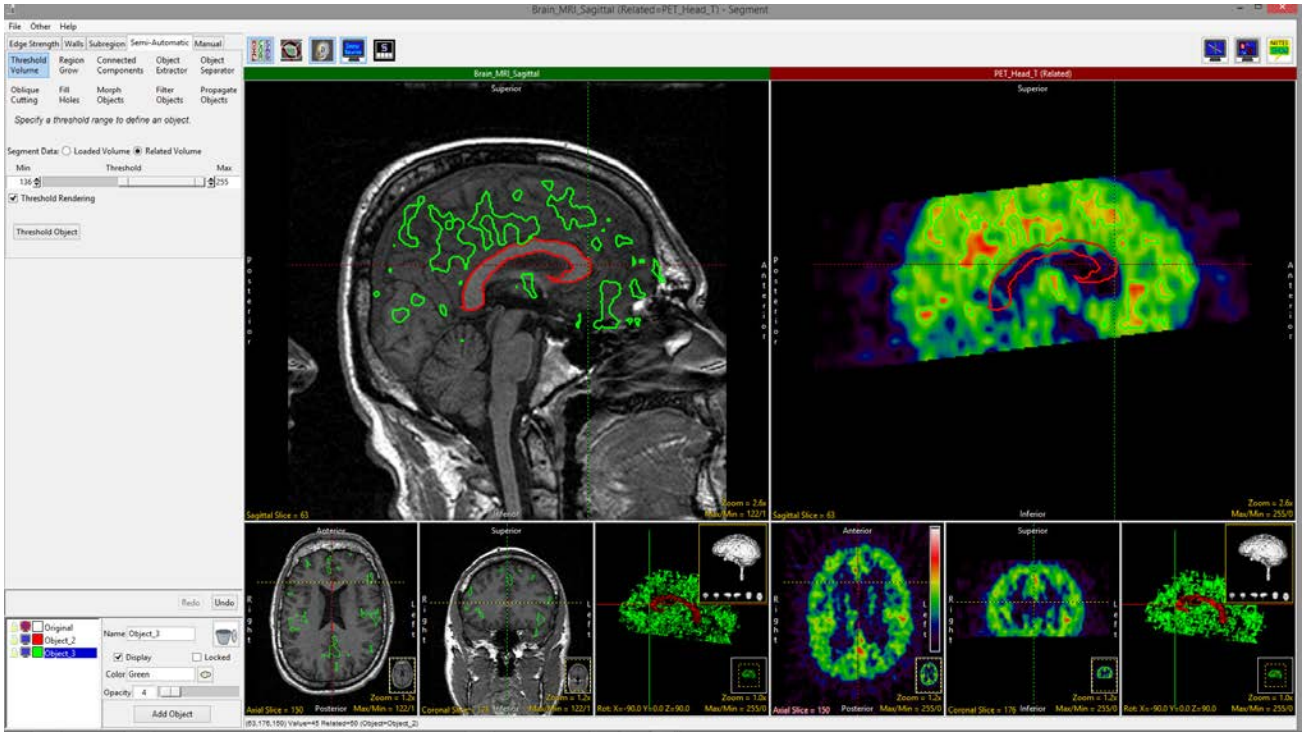
# Dual Input Segmentation

Segment allows users to load two registered input data sets. The ability to load related volumes is powerful and allows users to segment structures from either data set.

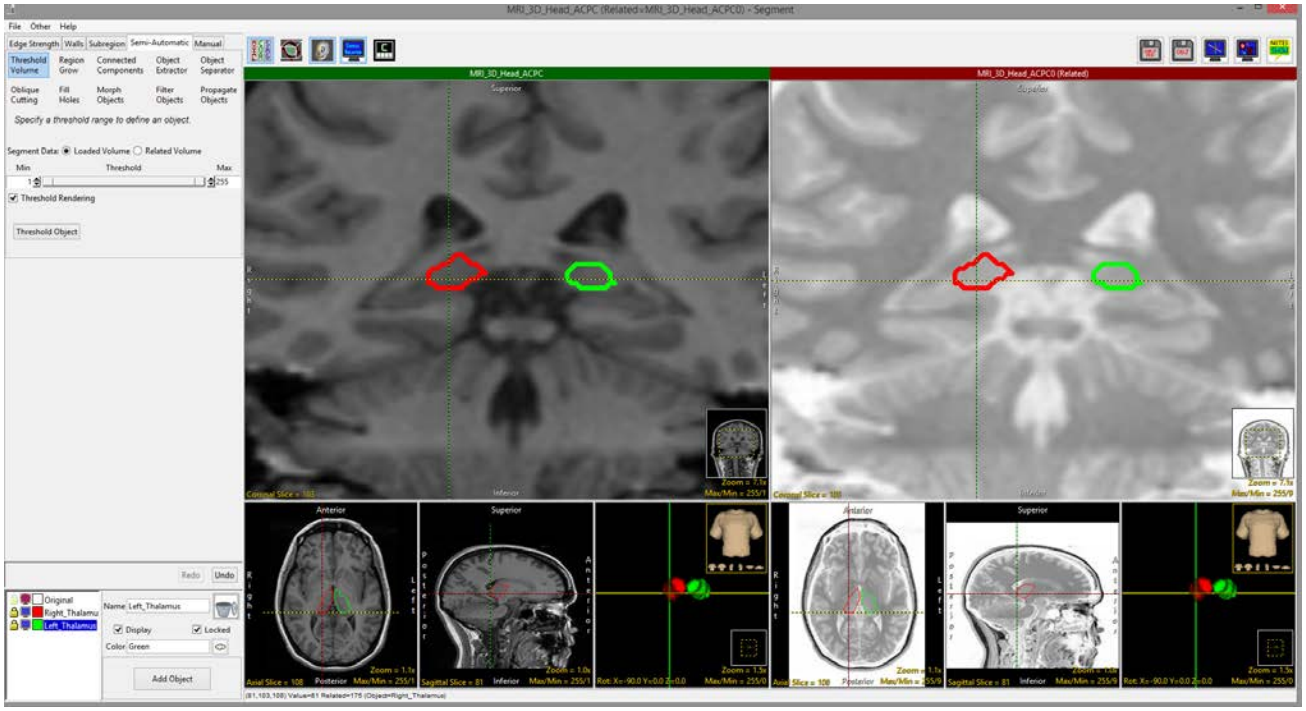
- Load registered pre-operative MRI and post-operative CT.
- Segment the brain from the MRI and electrodes from the CT.



- Load registered structural MRI and functional PET data. Structural regions can be delineated on the MRI and viewed on the PET, while regions of activity or uptake can be viewed on the functional data and displayed on the MRI.



- Loading two copies of the same input data set allows users to adjust or invert intensity display values on the related volume. This can be leveraged to assist with the segmentation of brain structures such as the thalamus.

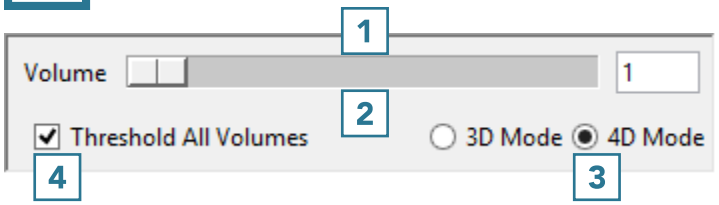


# 4D Segmentation

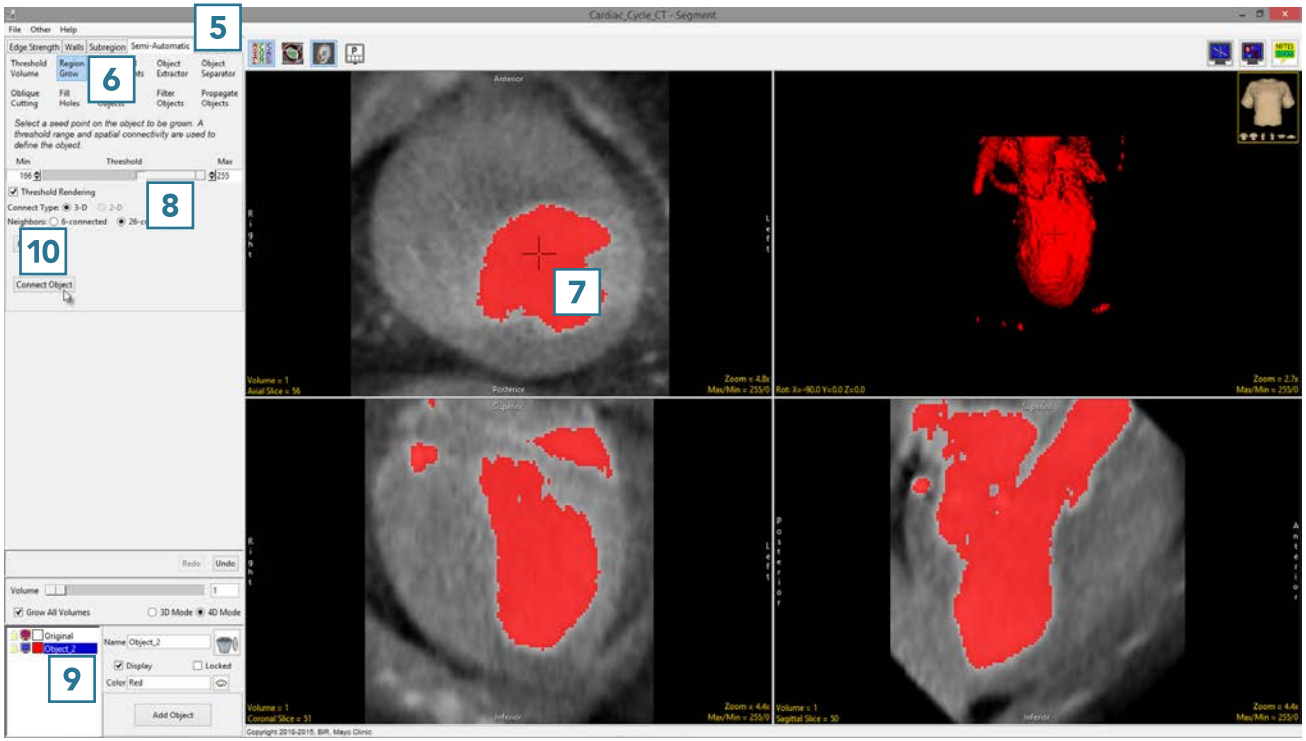
Segment supports 4D multivolumes. Users can use all of the segmentation tools to derive 2D, 3D, or 4D regions of interest. Segmentation using many of the Semi-Automatic tools can be configured to automatically propagate to the next 3D volume in the 4D multivolume as soon as the first segmentation is complete.

- Load the Cardiac Cycle CT data set into AnalyzePro.
- Select the multivolume and open Segment.
- A Volume control window will be available above the object control window. 1
- The slider 2 allows users to navigate through the 3D volumes in the multivolume.
- The window also provides the user with options to create a 3D or 4D object map 3 and to enable or disable the currently selected semi-automatic segmentation tool to be applied to all volumes in the multivolume. 4

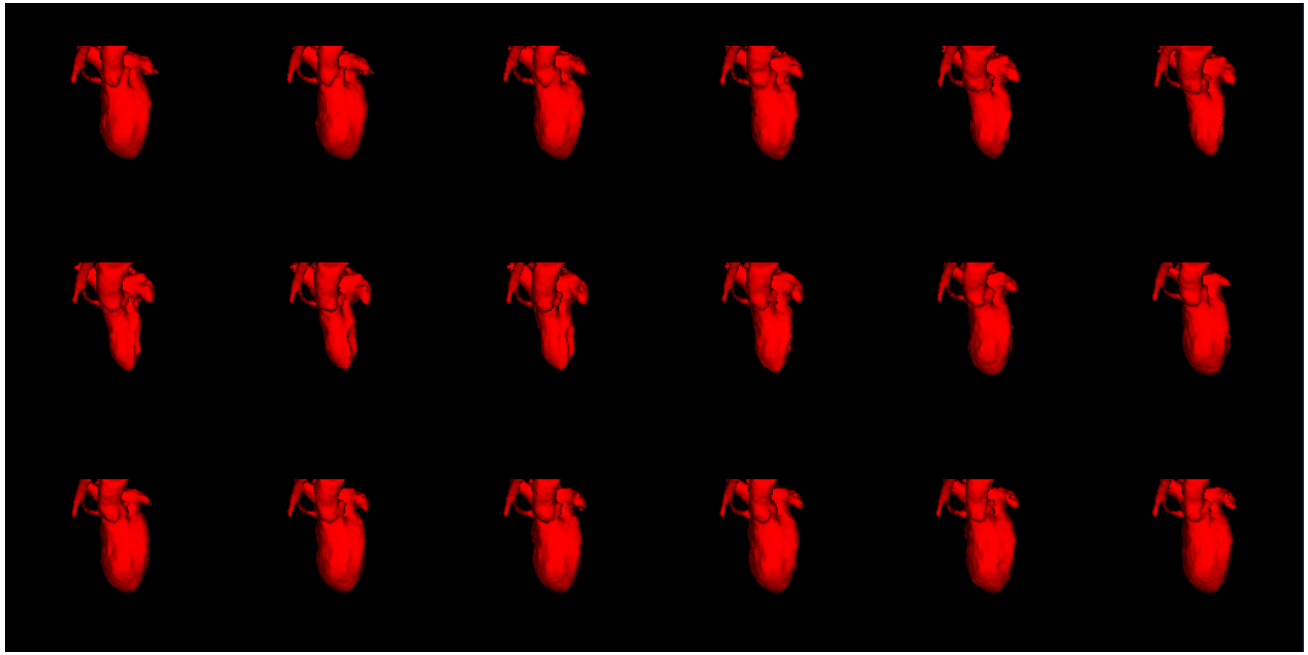
Download the Cardiac_Cycle_CT data set to follow along http://analyzedirect.com/data/



- Select Semi-Automatic 5 and choose Region Grow. 6
- Set a seed point in a blood pool 7 and set a threshold range to isolate the object of interest. 8
- Confirm mode is set to 4D and the Grow All Volumes option is checked. 9 Click Connect Object. 10



Segment will isolate the object from the first volume of the multivolume. After segmentation is complete, the parameters used to isolate the object from the first volume will be copied to the next volume and the blood pool will be segmented on the second volume. This will continue until all volumes have been processed. Use the volume slider to navigate through the multivolume to review the segmentation results.

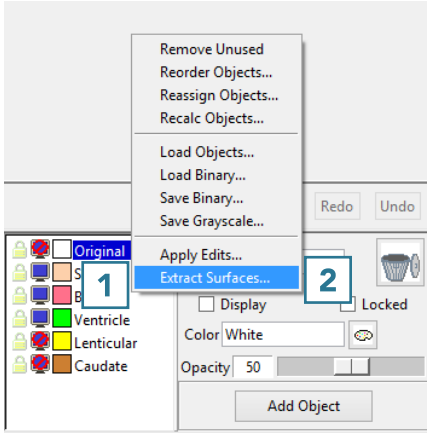


# Generating Surface Files from Objects

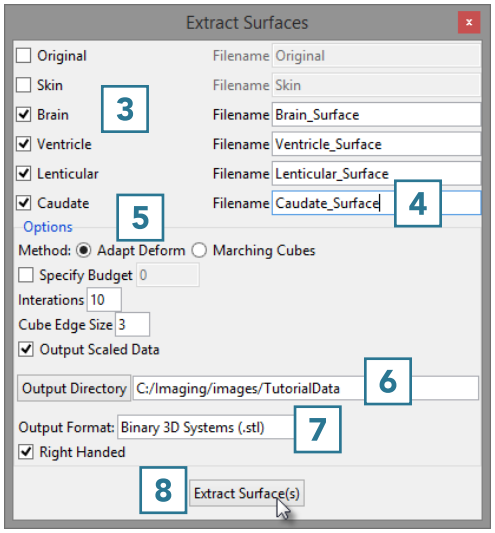
Segment provides users with the ability to export surface files for segmented structures.

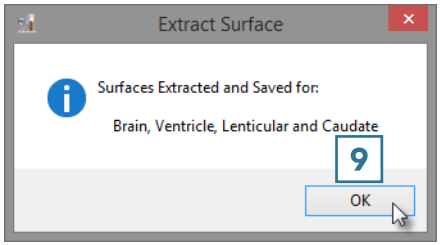
- Select MRI_3D_Head and open Segment.
- Select File > Load Object Maps and load MRI_3D_Head.obj.
- Right click on the object list 1 and select Extract Surface. 2

Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/



- Select the objects that you will use to generate a surface file. 3
- The output surface name will be the same as the object name. If desired, rename the output surface file name. 4
- Select the surface generation method. 5
- Set the Output Directory. 6
- Choose the ouput format. 7
- Click Extract Surface(s). 8
- When surface generation is complete a notification will be returned letting you know that the selected surfaces have been generated and saved. Click OK 9 to close the window.



# Register

# 3D Surface Alignment

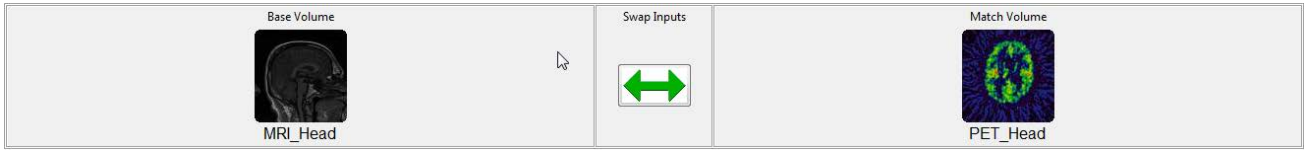
Surface matching is fast and robust, even in the presence of image noise and incomplete overlap of the image volumes. Both volumes must contain common objects, which must be explicitly segmented from the grayscale image data and saved as a grayscale or binary image. A surface is extracted from both a base object and a match object that are preprocessed from the base volume and match volume, respectively. This exercise will demonstrate how to achieve an optimal registration of two 3D volumes based on corresponding surfaces.

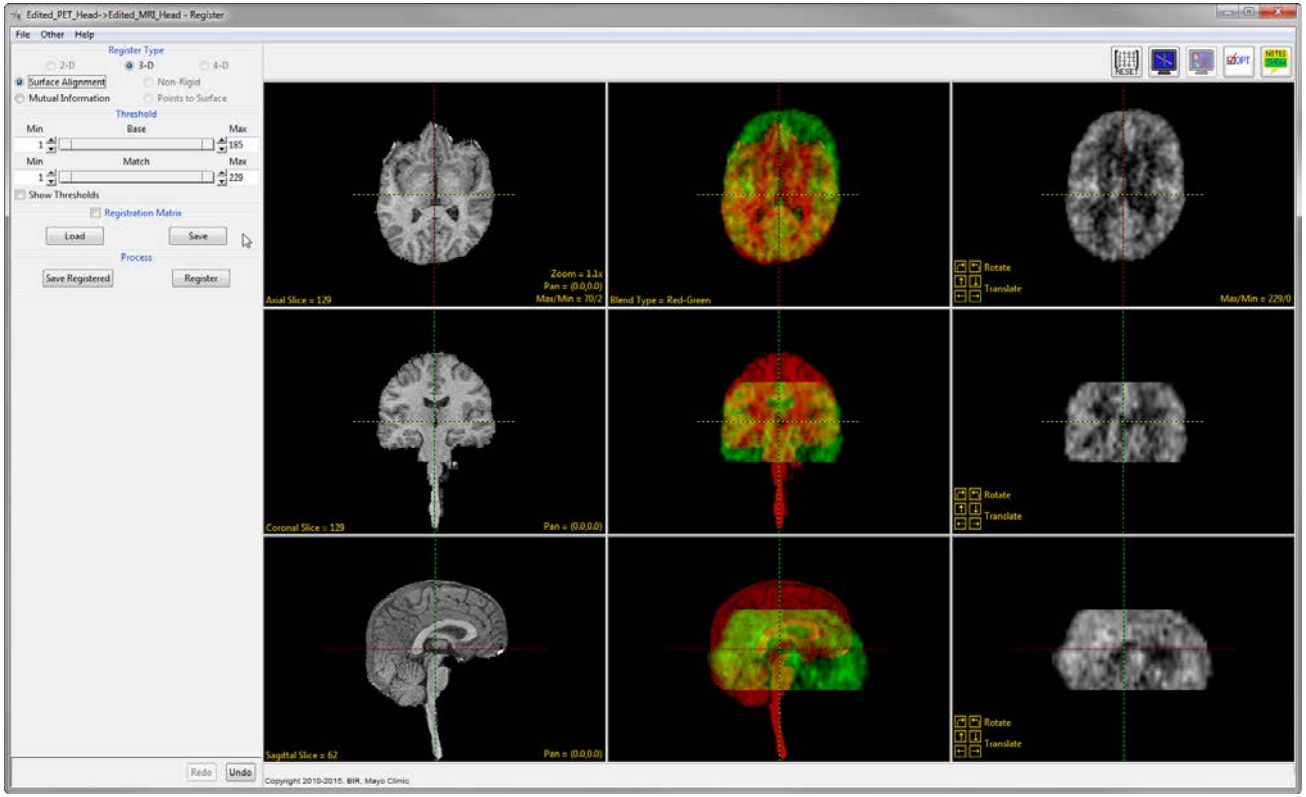
- Select the first data set (Edited_MRI_Head.avw), then while holding down the <Ctrl> key, select the second data set (Edited_PET_ Head.avw).

Note that these data sets have been pre-segmented to common surfaces, in this case, the brain.

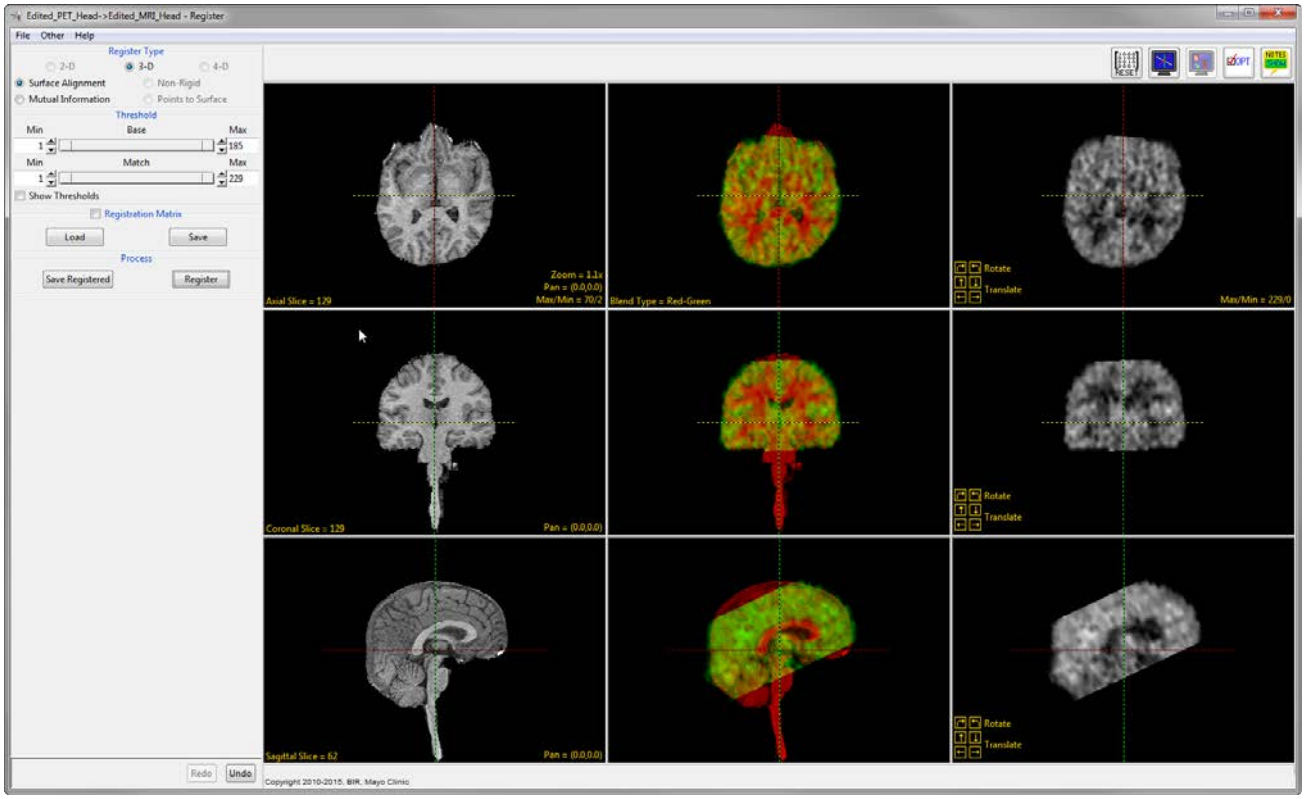
- Open Register.
- Select File > Input/Output Ports to view the input and output ports at the bottom of the main Register window. Make sure that Edited_ MRI_Head is the base volume, and Edited_PET_Head is the match volume.
- Select 3D and Surface Alignment from the Register Type options.

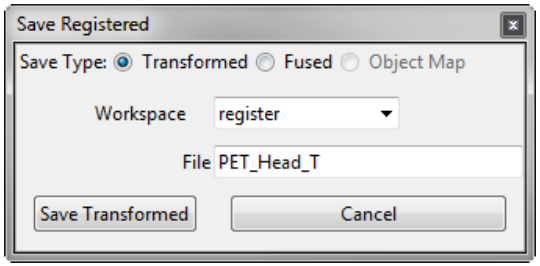
**Download the Edited_MRI_Head and Edited_PET_ Head data sets to follow along http://analyzedirect.com/data/**



- The interface contains nine image display panes.
  - First Column: Displays the Base volume.
  - Last Column: Displays the Match volume pre-scaled to the size of the base volume.
  - Middle Column: Displays the base and match volumes fused together.
  - Rows: Display the volumes in the axial, coronal and sagittal orientations.
- Examine the combined middle column to determine whether the volumes need to be registered.
- Click Register to register the two volumes.
- Click Save Registered to export the transformed PET data.
- Select the Transformed Save Type, Workspace, File and select Save Transformed.



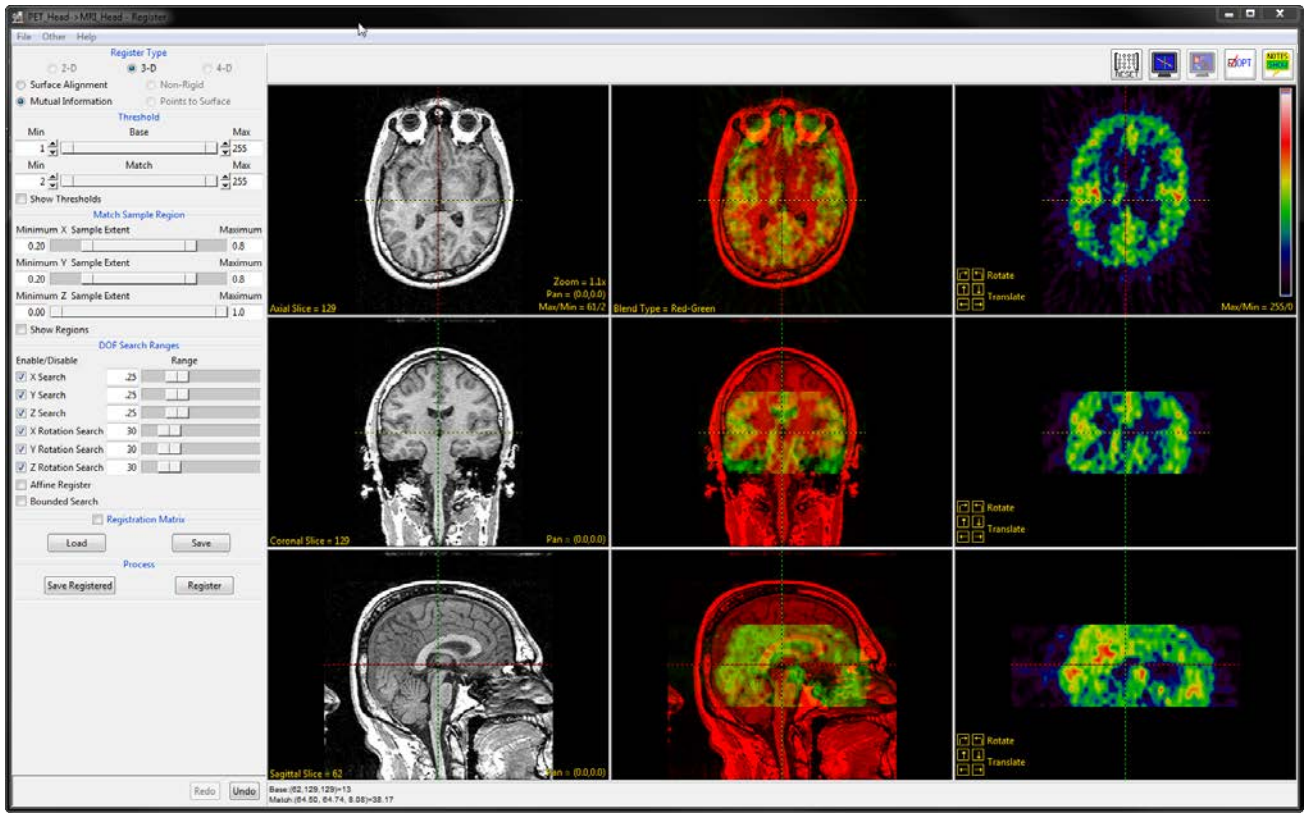
# 3D Mutual Information

The Mutual Information Register Type is an implementation of the Normalized Mutual Information algorithm and allows users to spatially register two volume images. Several unique and powerful algorithms allow the precise alignment of 3D data to be achieved, both quickly and efficiently. This exercise will demonstrate how to register two images of different modalities.

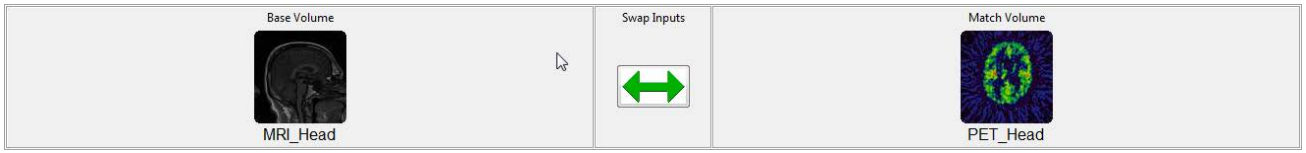
# Automatic Registration

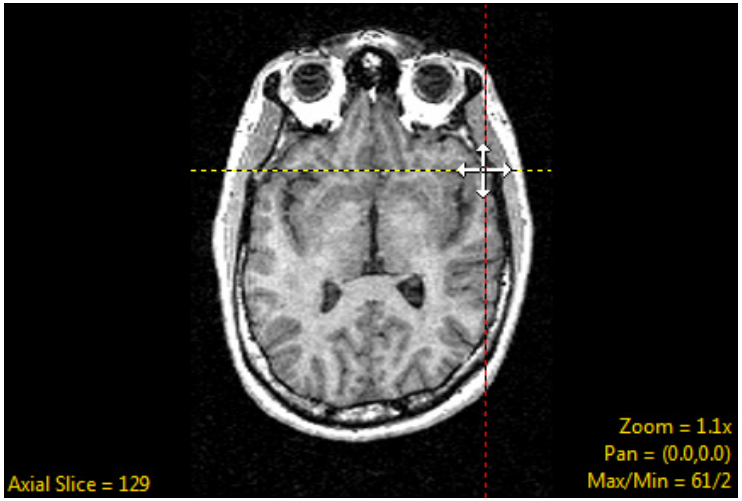
- Select the first data set (MRI_Head.avw), and while holding down the <Ctrl> key, select the second data set (PET_ Head.avw).
- Open Register.

**Download the MRI_Head and PET_ Head data sets to follow along http://analyzedirect.com/data/**



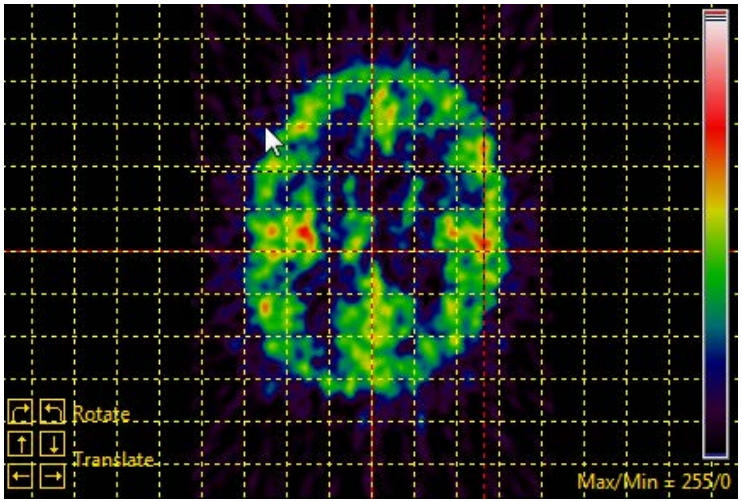
- Select File > Input/Output Ports to view the input and output ports at the bottom of the Register window. Make sure that MRI_Head is the base volume, and PET_Head is the match volume.
- The crosshair in each of the image display panes can be used to move through the volumes. When the crosshair is moved in any of the panes, the other panes automatically update to display the same volume coordinate.



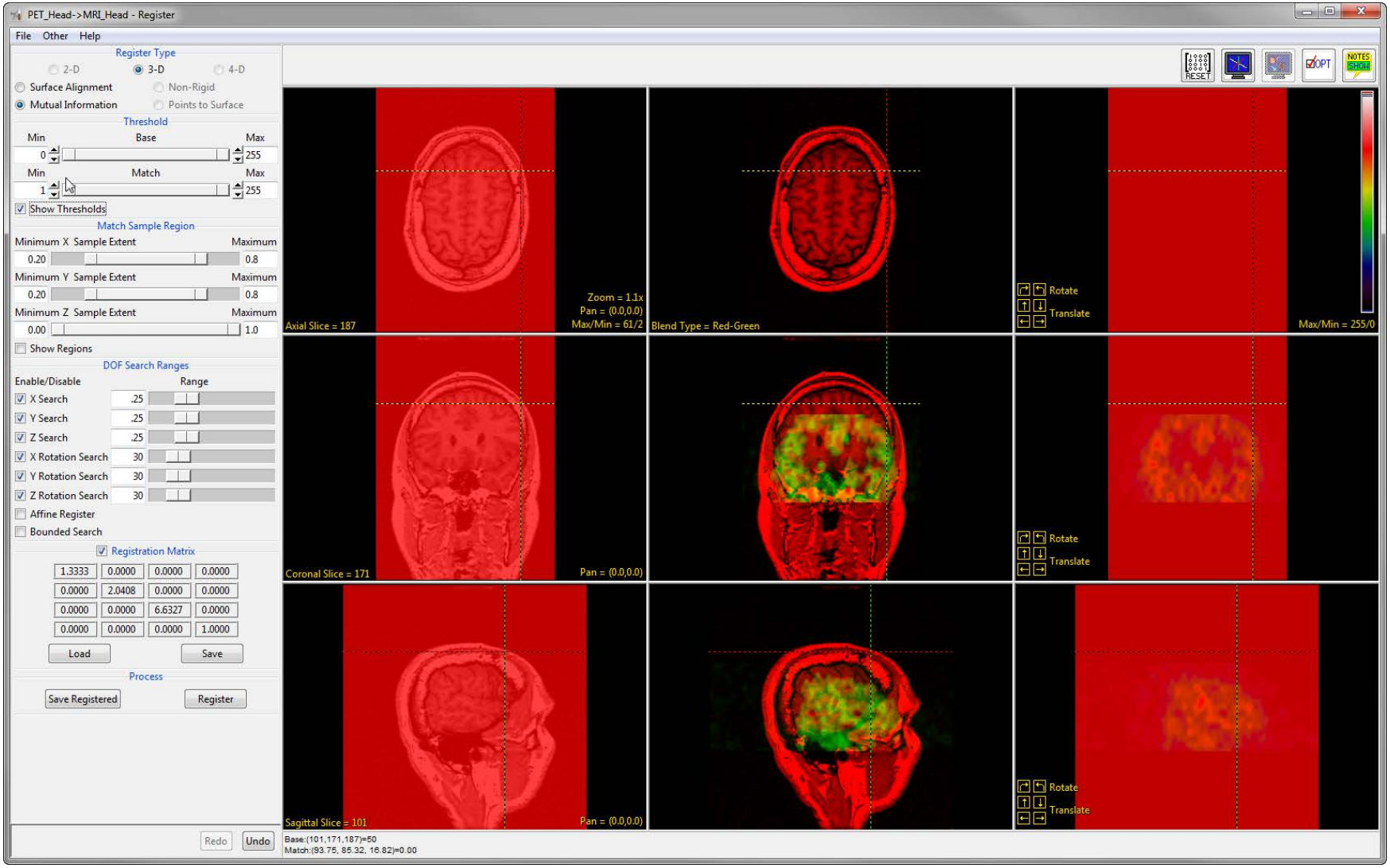




Note that the base and match coordinates are reported at the bottom of the window.

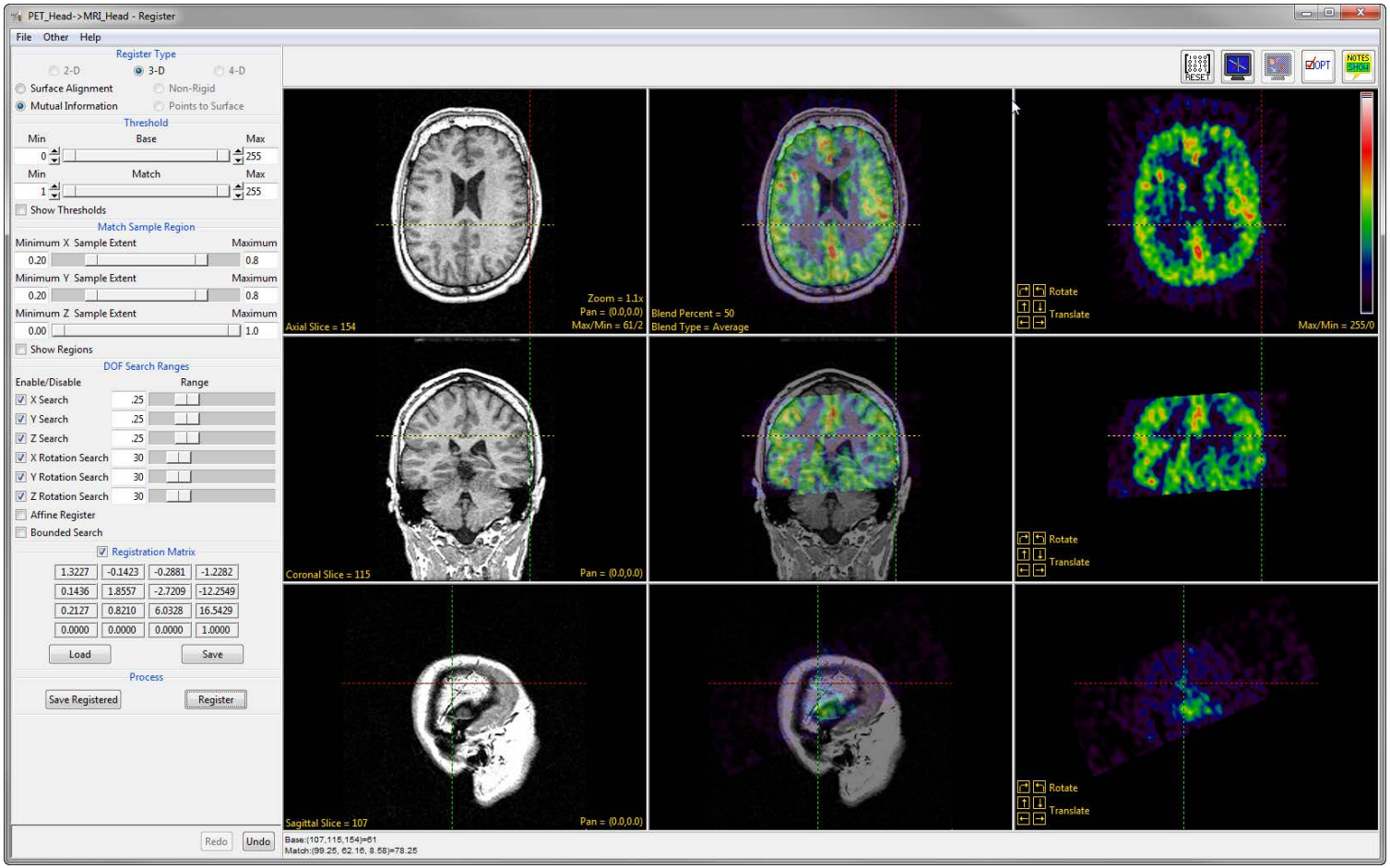
- Right-click on any of the image display panes in the last column to view several options such as adding an alignment grid.



- On the left tool bar under Threshold, check the Show Thresholds option and the image display will show a red overlay representing all voxels that will be considered for the registration. Set the Base Minimum to 0 and the Match Minimum to 1.

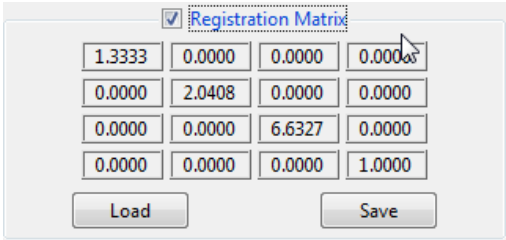


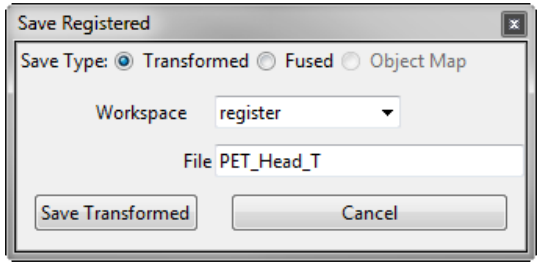
- Click the Register button.
- After registration is complete, you will see that the PET volume has been scaled, rotated and translated to match the sagittal MRI. Uncheck the Show Thresholds checkbox.
- Right-click the Blend Type yellow text in the middle upper panel and select Average.
- To evaluate the registration, move the crosshair in any of the panes.



- If the registration is not satisfactory, you can choose to undo the last action using the Undo button at the bottom of the left tool bar.


- If you want to reset the data back to the original matrix, use the Reset button in the top right of the register window.
- To view the current transformation matrix, select the Registration Matrix box on the left tool bar. This gives the option to save the current matrix as an ASCII floating-point file or load a previously saved matrix.
- To save a copy of the transformed or fused match volume (PET_Head), click Save Registered. Select the Transformed Save Type, Workspace, File and select Save Transformed.



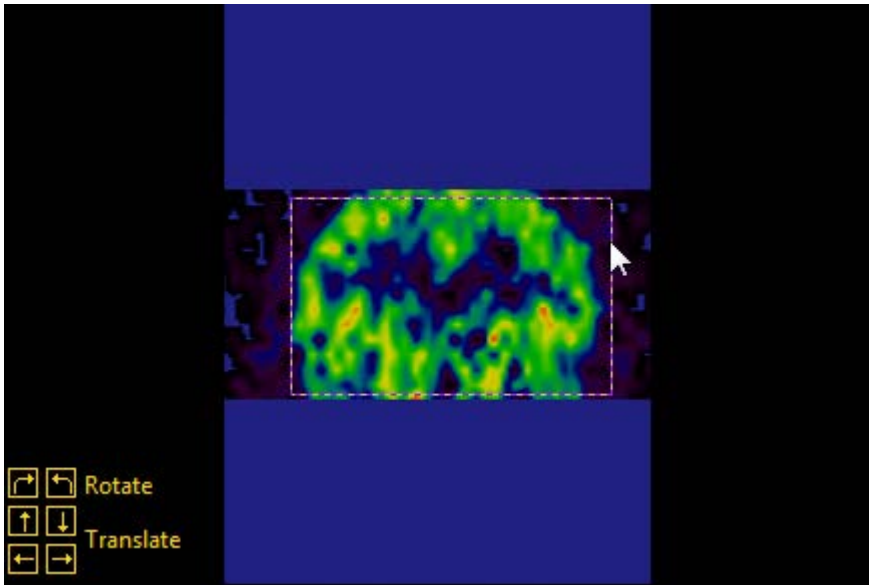



AnalyzePro also provides the ability to set a Match Sample Region and DOF Search Ranges.

Match Sample Region provides X, Y and Z sample extent sliders that define a specific spatial region used for registration. A dotted boundary line will appear on the right match image column.

The default region is optimal for MRI and CT volume images of the head. This tool can be useful for excluding excessive background or concentrating the registration on a specific region of interest.

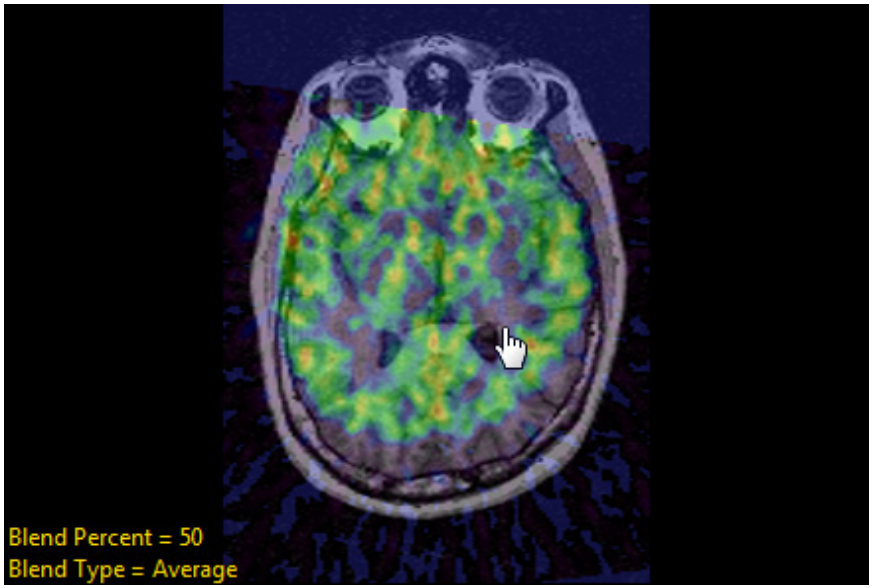
DOF Search Ranges allow you to set the number of degrees of freedom. Clicking the Affine Register checkbox enables the scale and shear transformations for a fully affine transform.

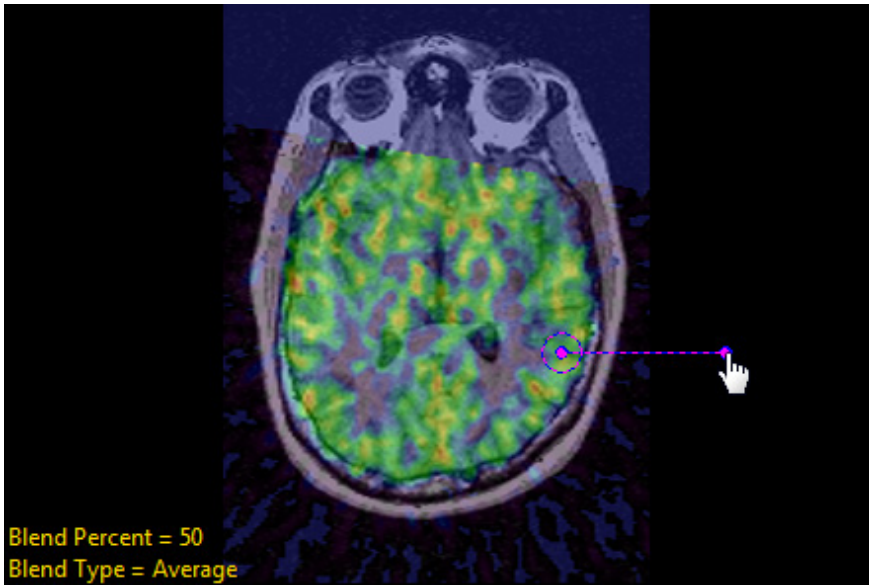


# Manual Registration

The Manual Registration controls provide the ability for users to manually register the match to the base volume. The left mouse button can be used to interactively translate the image within the middle fused and right match columns.

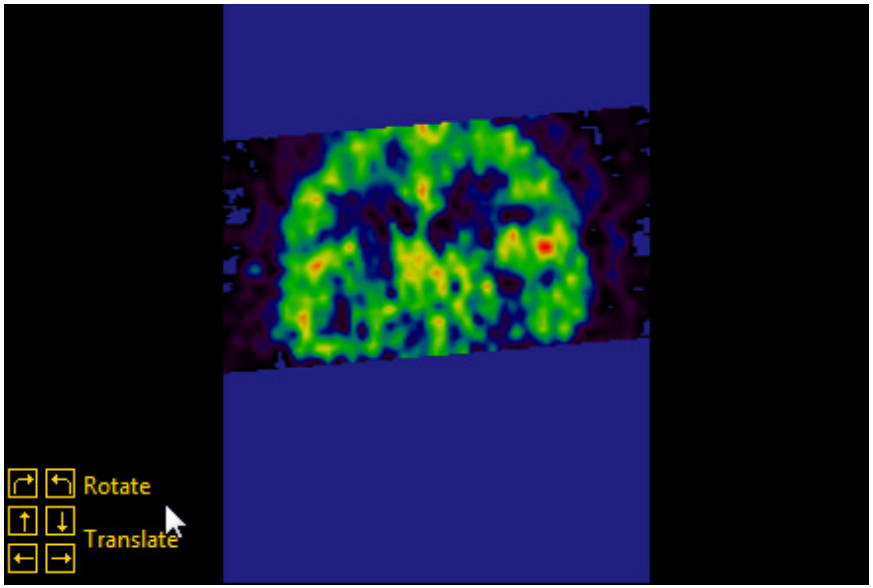
Interactive rotation of the image can be done by selecting the right mouse button menu and setting the middle mouse button action to rotation via the Rotate @ Point option. You can then hold the middle mouse button and a rotation control point will appear.



Rotation and Translation buttons are also present in the right match column. These buttons can be used for precise movements. The default increment is set to 1 but can be changed by right-clicking the control buttons and selecting Increment.

Once satisfied with the manual registration, you can save the registered match volume or invoke one of the automatic registration methods to refine the registration using the manual registration as an initial guess.



# Measure

# Introduction

The AnalyzePro Measure module provides access to all the measurement tools needed by users to sample their image data. No tools are provided for the definition of objects. Instead, Measure samples object maps defined using other modules, primarily Segment.

# 1D Measurements

1D measurements include points, lines, trace, angles, intersecting lines and perpendicular lines. Coordinates, signal values, linear distances, line profiles and angles can all be generated using Measure. Full Width Half Max (FWHM) parameters can also be set to control sampling.

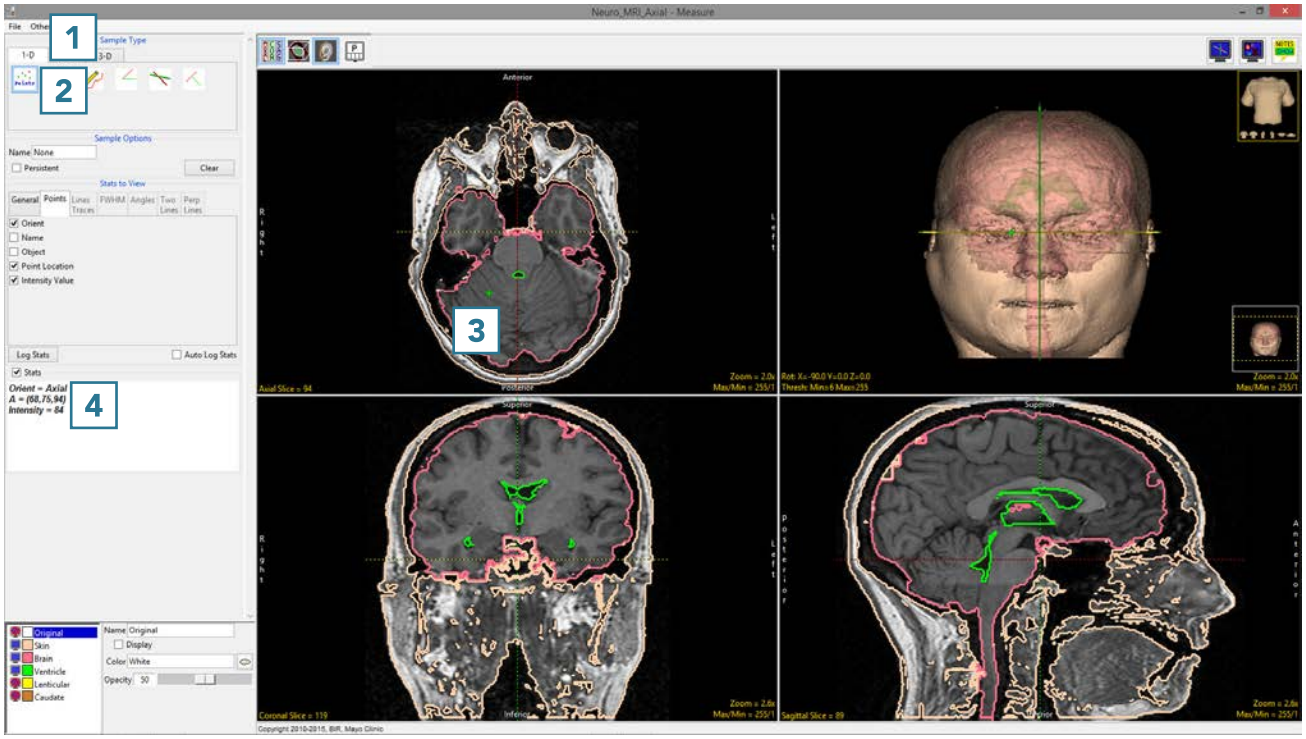
# 1. Sampling Points

The Points tool allows users to select points on the 2D image data or 3D rendering. The tool will report the coordinates and intensity value of the selected point.

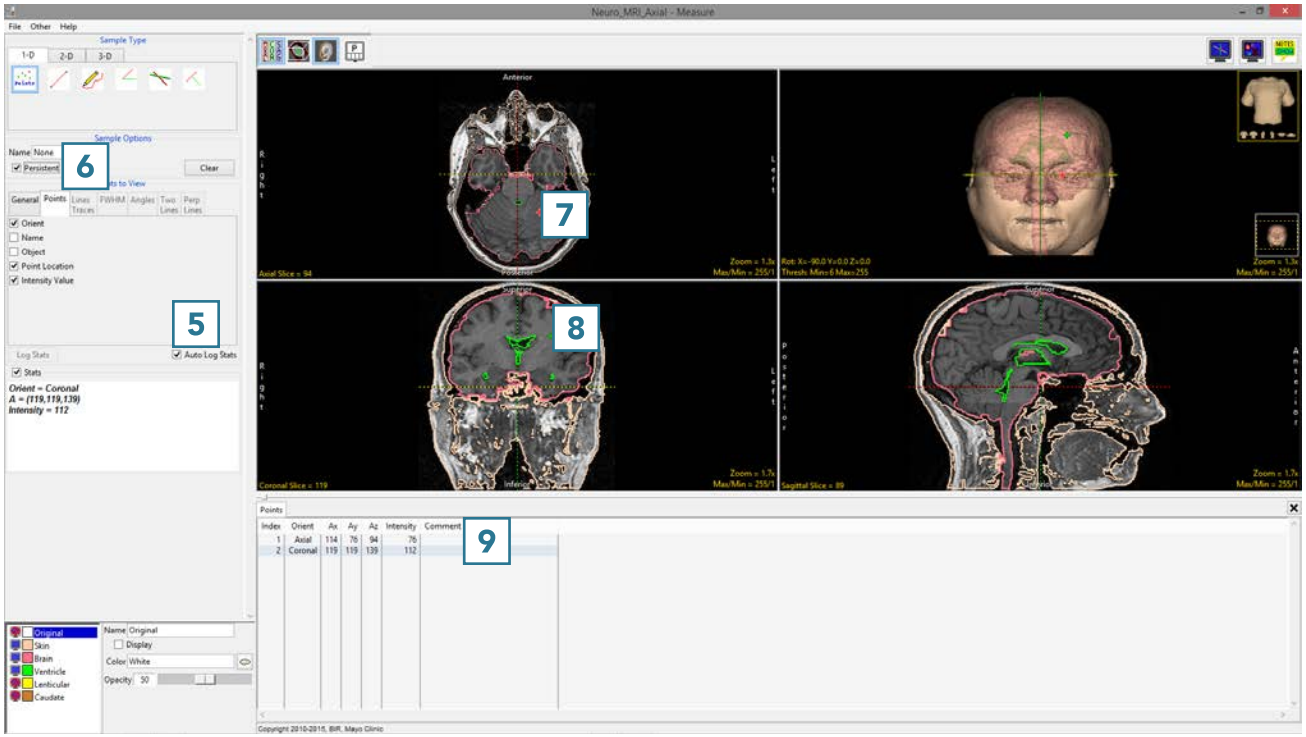
- Select MRI_3D_Head and open Measure.
- Select File > Load Object Maps and load MRI_3D_Head.obj.
- Select the 1D Sample Type 1 and choose Points. 2
- Click on the brain in the axial orientation 3 to set a point.

Note that the coordinates and intensity of the point will be reported in the Stats review area. 4

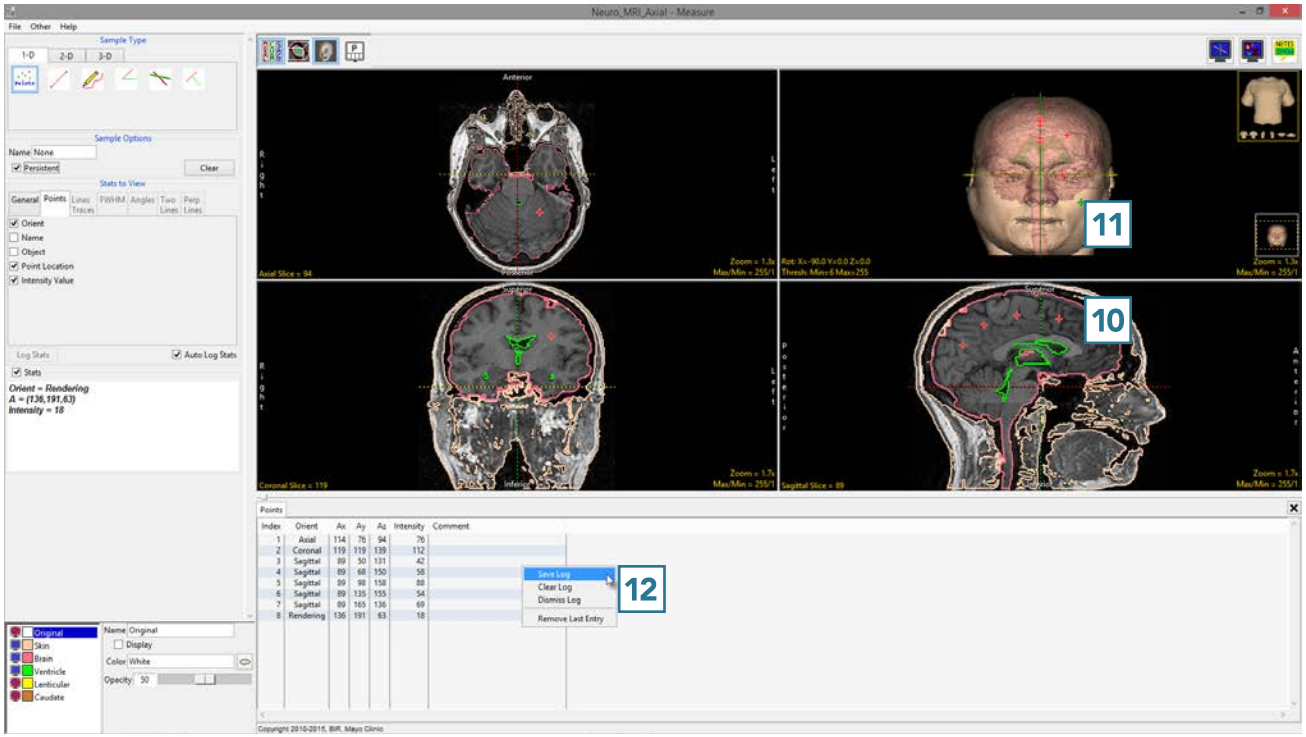
**Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/**



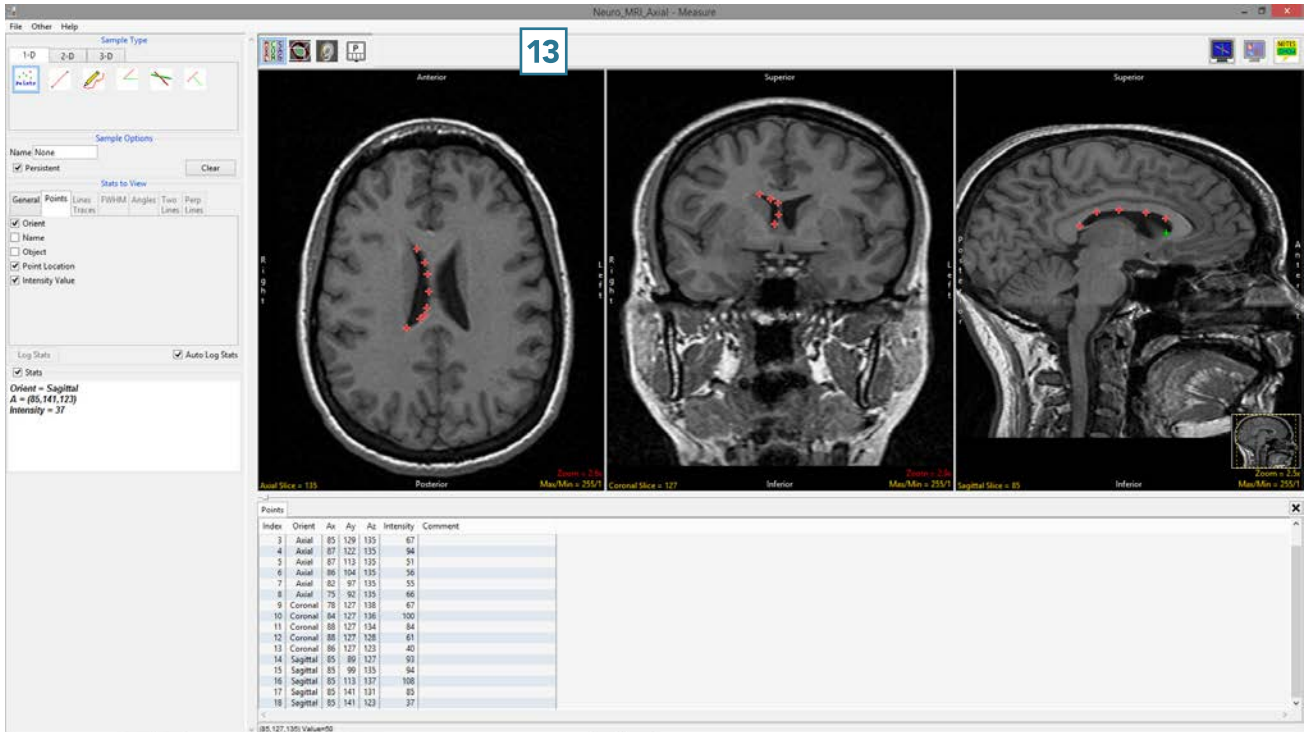
- Check the Auto Log Stats option. **5** Each point selected will now be saved to a measurement log.
- Check the Persistent checkbox. **6** This will prevent points from being cleared from the display when a new point is selected.
- Set a new point in the axial orientation **7** and set another point in the coronal orientation. **8** The current point will display as green, while previous points will change to red.
- The coordinates and intensity values will be reported in the log. **9**



- Set several new points in the sagittal orientation 10 and on the rendering. 11
- Right click on the log to save as a .CSV file. 12



Note that point sampling does not require an object map to be loaded. 13

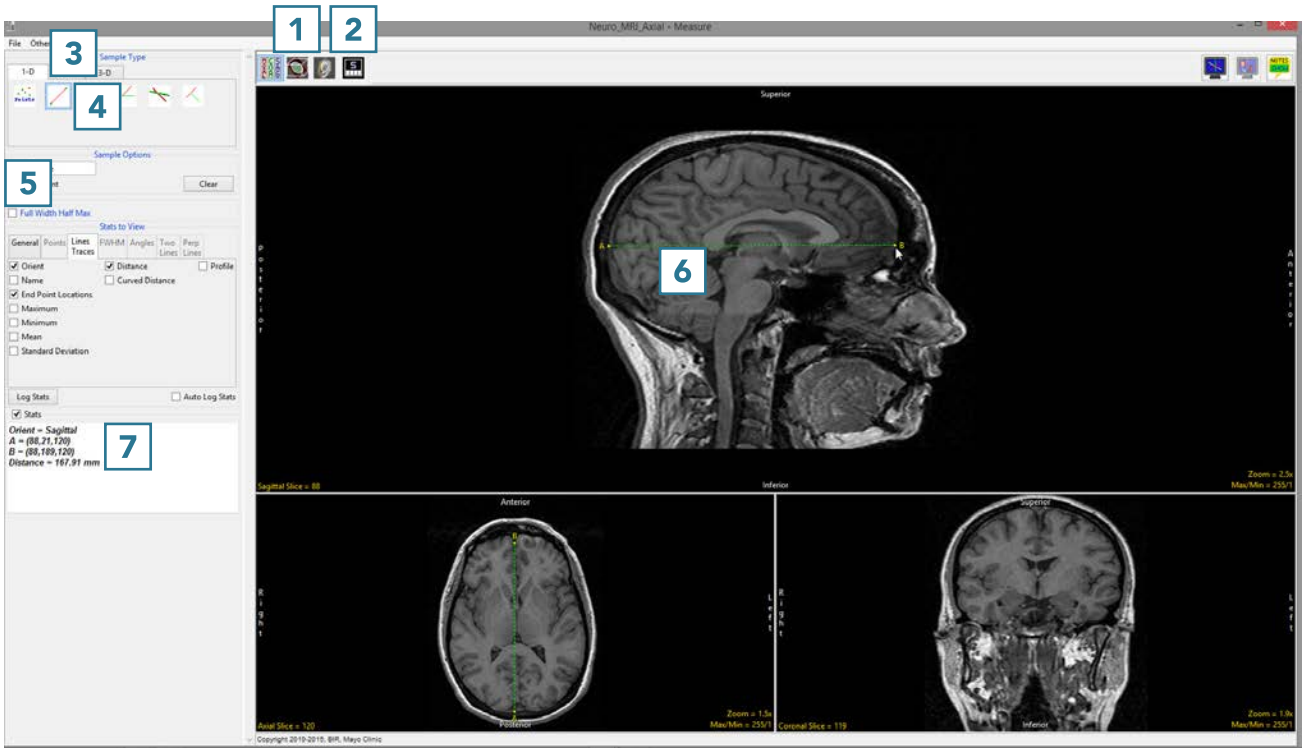


# 2. Making Line Measurements

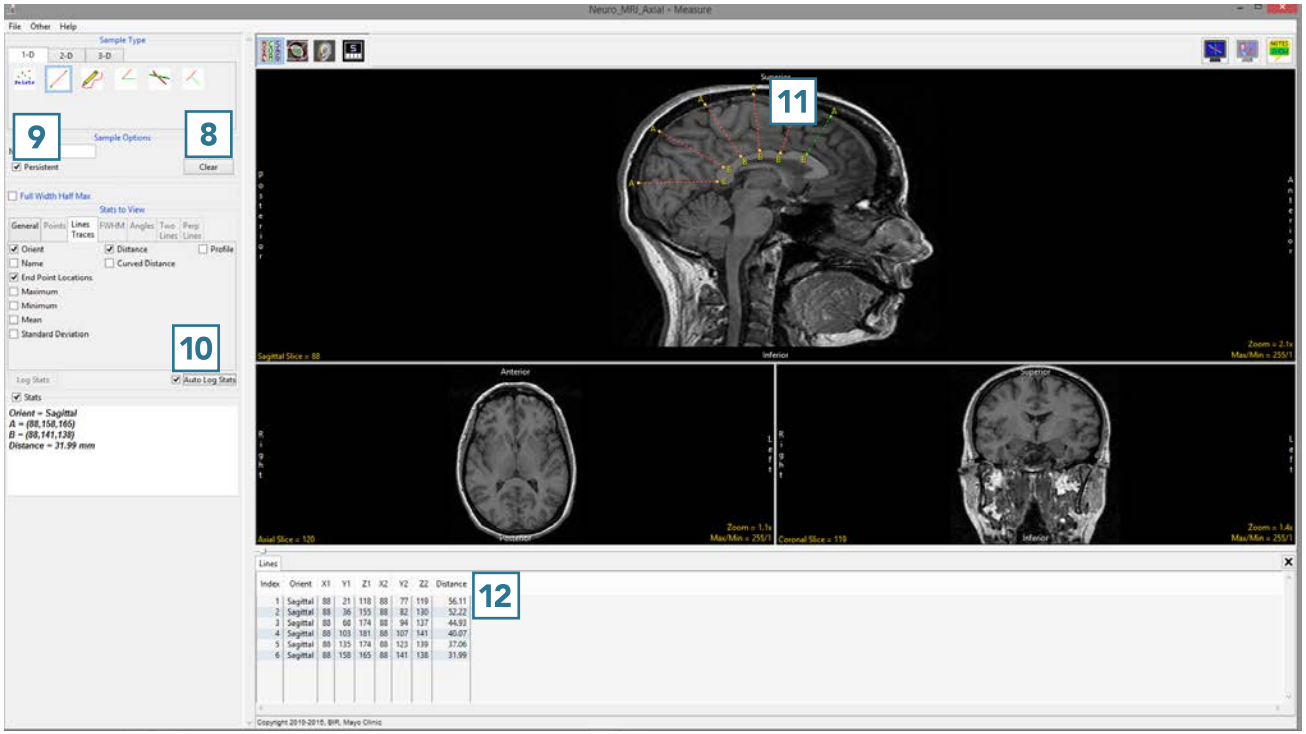
The Line tool allows users to define a line on a 2D image or the 3D rendering. The tool will report distance measurements, line intensity profile and the coordinates of the line end points.

- Select MRI_3D_Head and open Measure.
- Switch the display of the Rendering off 1 and set the primary display to Sagittal. 2
- Select the 1D Sample Type 3 and choose the Line tool. 4
- Uncheck Full Width Half Max. 5
- Define a line on a sagittal slice. 6
- The coordinates for the line endpoints (A and B) and the line distance are reported in the Stats review area. 7

**Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/**



- Press Clear 8 to reset.
- Check the Persistent 9 and Auto Log Stats checkboxes. 10
- Define several lines on the sagittal slice. 11
- The coordinates for the line endpoints (A and B) and the line distances are reported in the log. 12 Right click to save the log as a .CSV file.

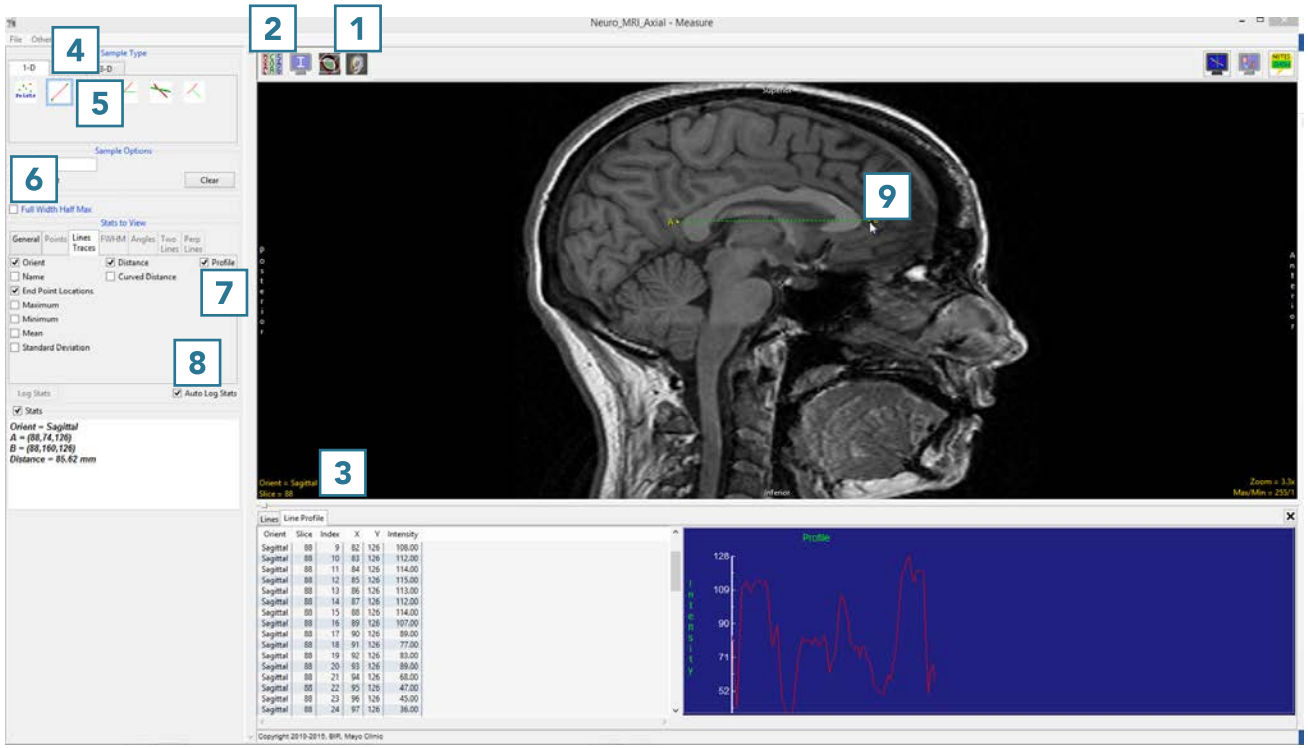


# 3. Generating Line Profiles

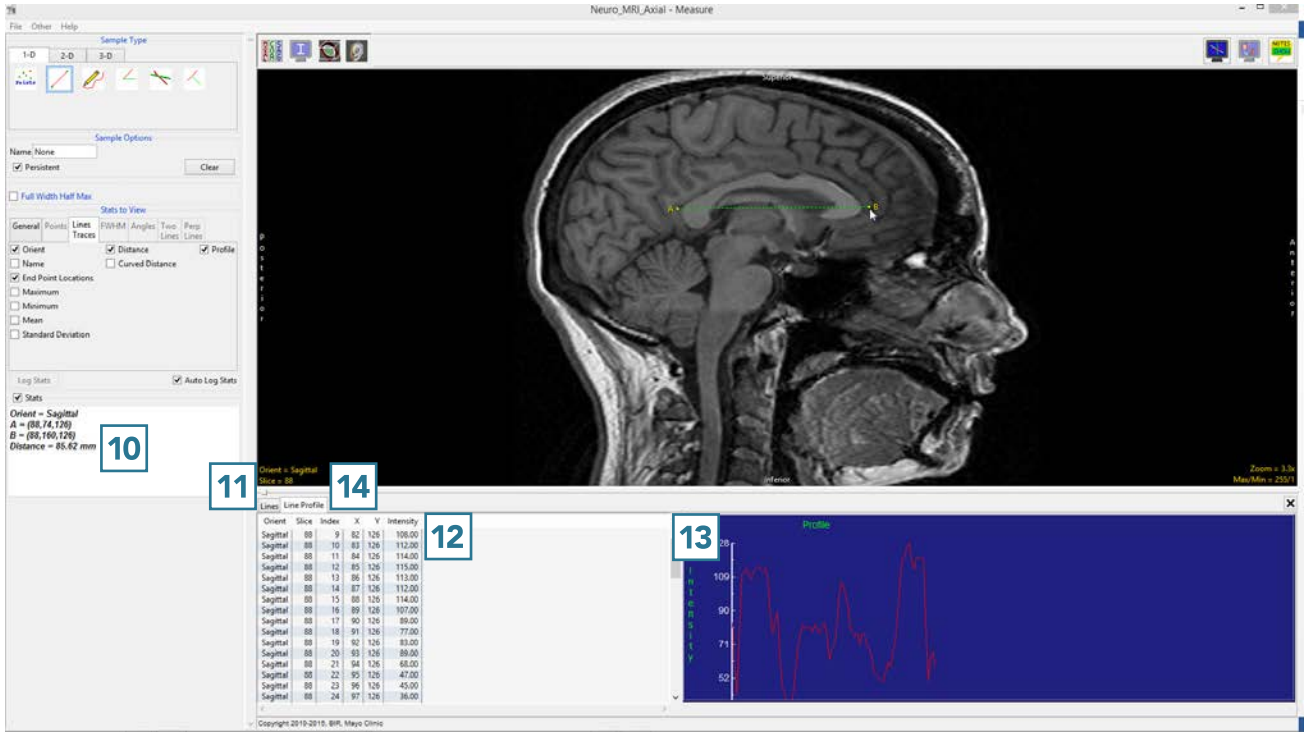
The Line tool allows users to sample and plot pixel intensity values for a defined line.

- Select MRI_3D_Head and open Measure.
- Switch the display of the Rendering off 1 and toggle the display of all orientations off. 2
- Use the Orient option to switch to Sagittal. 3
- Select the 1D Sample Type. 4 Choose the Line tool. 5
- Uncheck Full Width Half Max. 6
- Check the Profile option 7 and the Auto Log Stats checkbox. 8
- Define a line on a sagittal slice to measure the posterior to anterior distance of the corpus callosum. 9

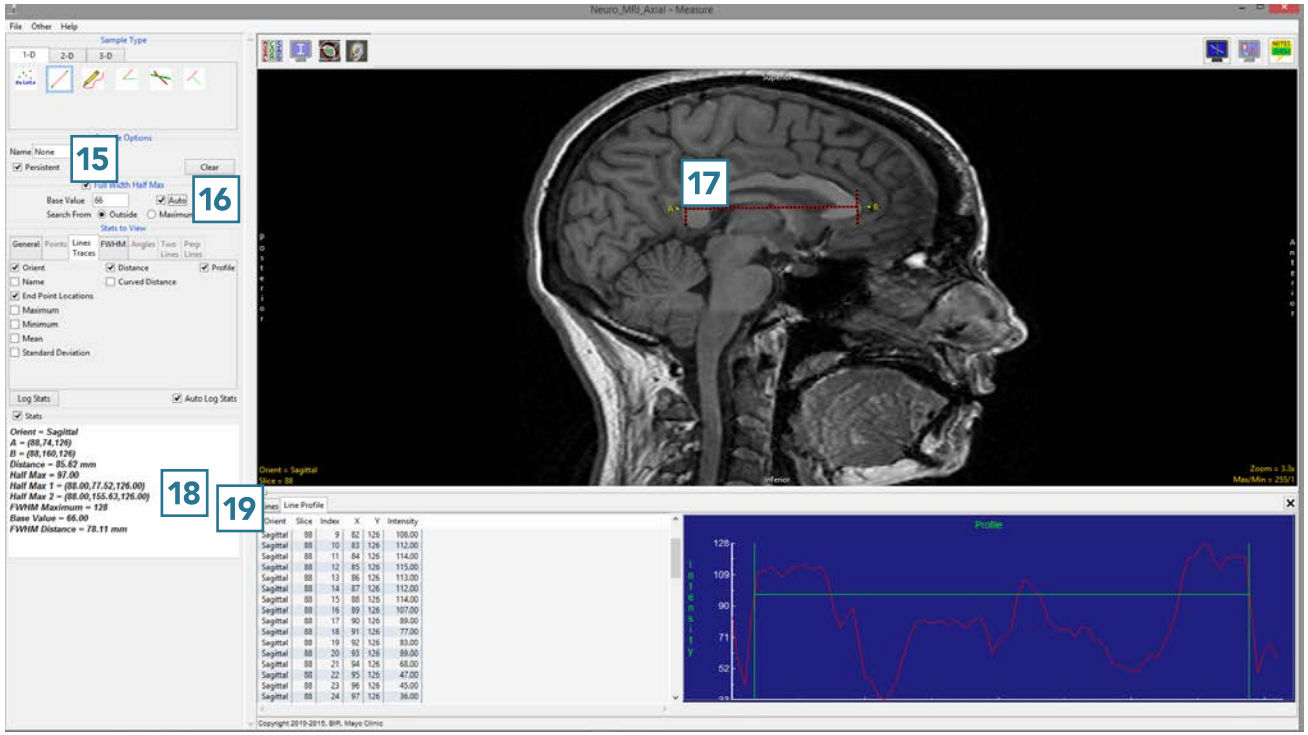
**Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/**



- The coordinates for the line endpoints (A and B) and the line distance are reported in the Stats review area 10 and in the Lines tab. 11
- The intensity profile of the defined line is logged 12 and plotted 13 in the Line Profile tab. 14



## Using FWHM to Aid with Line Measurements




The Line tool allows for measurement of FWHM (Full-Width, Half-Max) distance on a line that crosses a structure of sufficient contrast to produce edges which cross the half-max value, which represents half the difference between the minimum and maximum intensity values along the line.

- Check the Full Width Half Max checkbox 15 and check the Auto option to have the tool calculate the FWHM Base Value. 16
- Note that the FWHM is overlaid in red on the line. 17
- The Stats review area will update reporting the FWHM information. 18

Note any differences between the linear line distance value and the FWHM distance value. FWHM can help increase accuracy of such measurements.

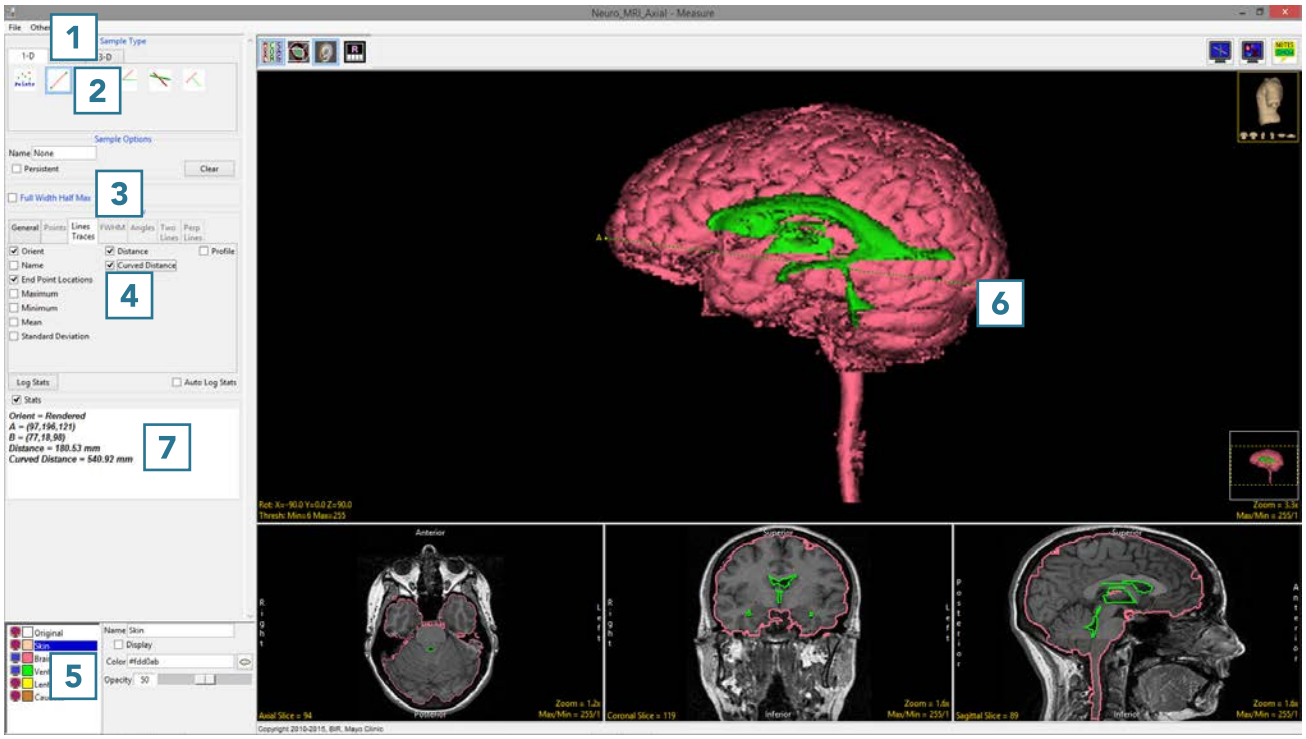
- FWHM measurements will also be reported in the Lines log. 19
- Right-click on the log to save as a .CSV file.

# 4. Making Line Measurements on the 3D Rendering

Like the Points tool, the Line tool can also be used to make measurements on the 3D rendering.

- Select MRI_3D_Head and open Measure.
- Select File > Load Object Maps and load MRI_3D_Head.obj.
- Select the 1D Sample Type 1 and choose Line. 2
- Uncheck Full Width Half Max. 3
- Under Line Traces check the Curved Distance option. 4
- Disable the Skin object. 5
- Define a line on the Rendering. 6
- The coordinates for the line endpoints (A and B) and both the linear and curved line distances are reported in the Stats review area. The curved distance represents the distance from A to B following the surface of the brain. 7

**Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/**

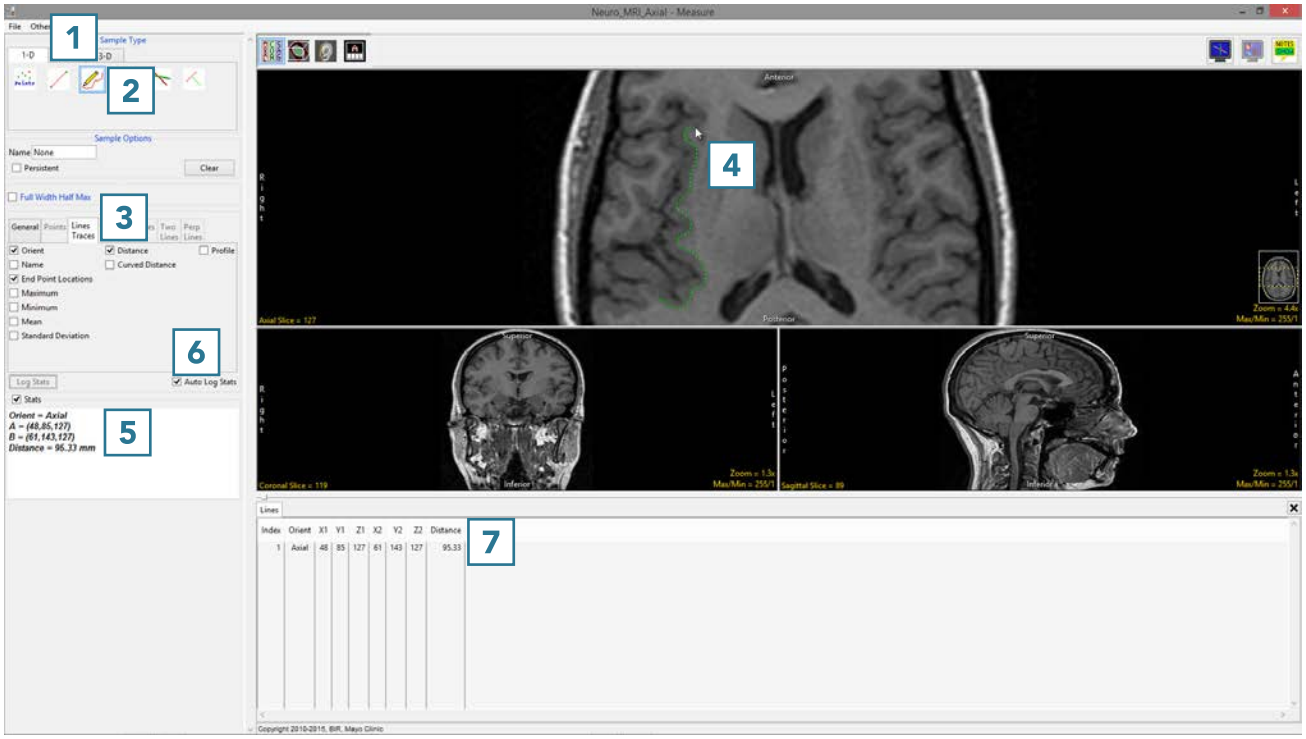


# 5. Making Freehand Trace Measurements

The Trace tool provides all the functionality of the Line tool, while allowing the user to define a curved trace.

- Select MRI_3D_Head and open Measure.
- Select the 1D Sample Type. 1
- Choose Sample Trace. 2
- Check any measurements you want to make from the Lines Traces tab. 3
- Define a freehand trace on the data. 4
- The measurements selected will be returned to the Stats review area 5 once tracing is completed.
- If the Auto Log Stats 6 checkbox is selected, the measurements will be added to the Lines log 7 which can be saved as a .CSV file.

**Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/**

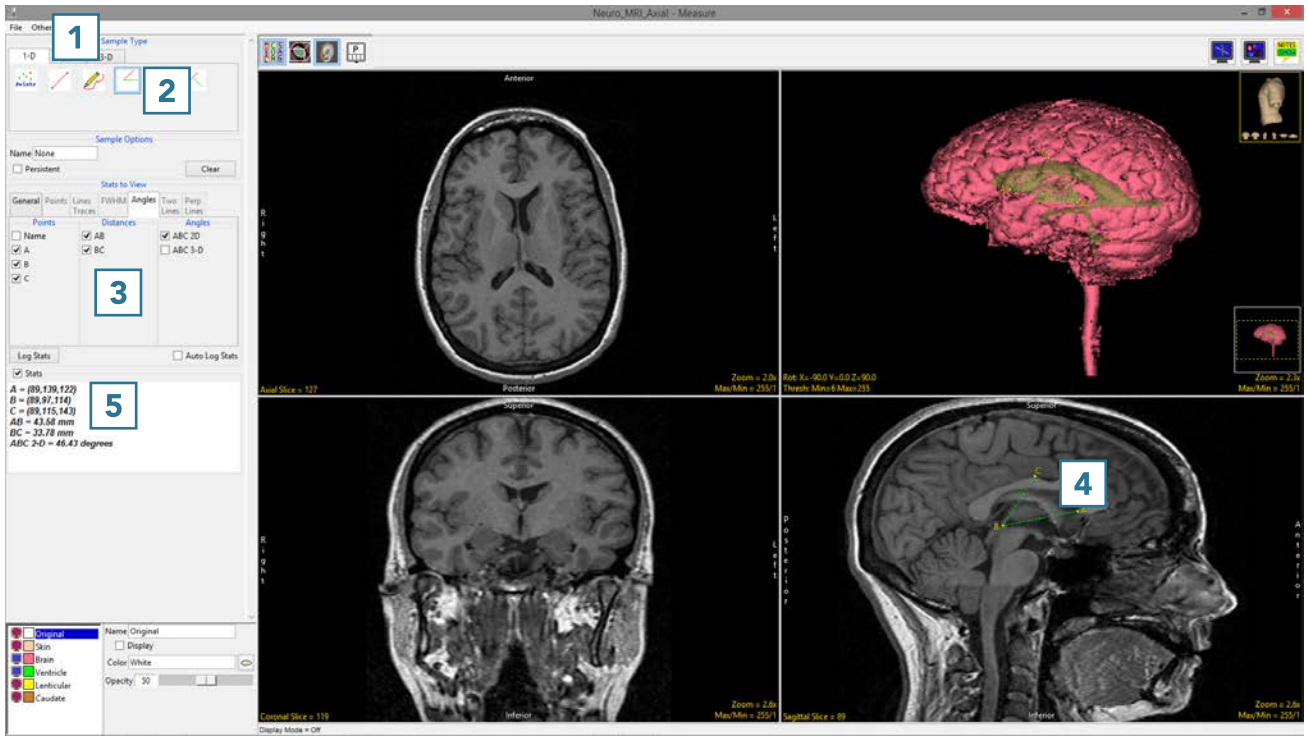


# 6. Making Angle Measurements

The Angles tool allows users to make distance measurements between points and angle measurements between defined lines.

- Select MRI_3D_Head and open Measure.
- Select File > Load Object Maps and load MRI_3D_Head.obj.
- Select the 1D Sample Type 1 and choose Angles. 2
- Check the Points, Distances, and Angles to be reported. 3
- Define the angles on any of the 2D slices or the 3D rendering. 4
- The selected measurements will be reported in the Stats review area. 5

**Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/**

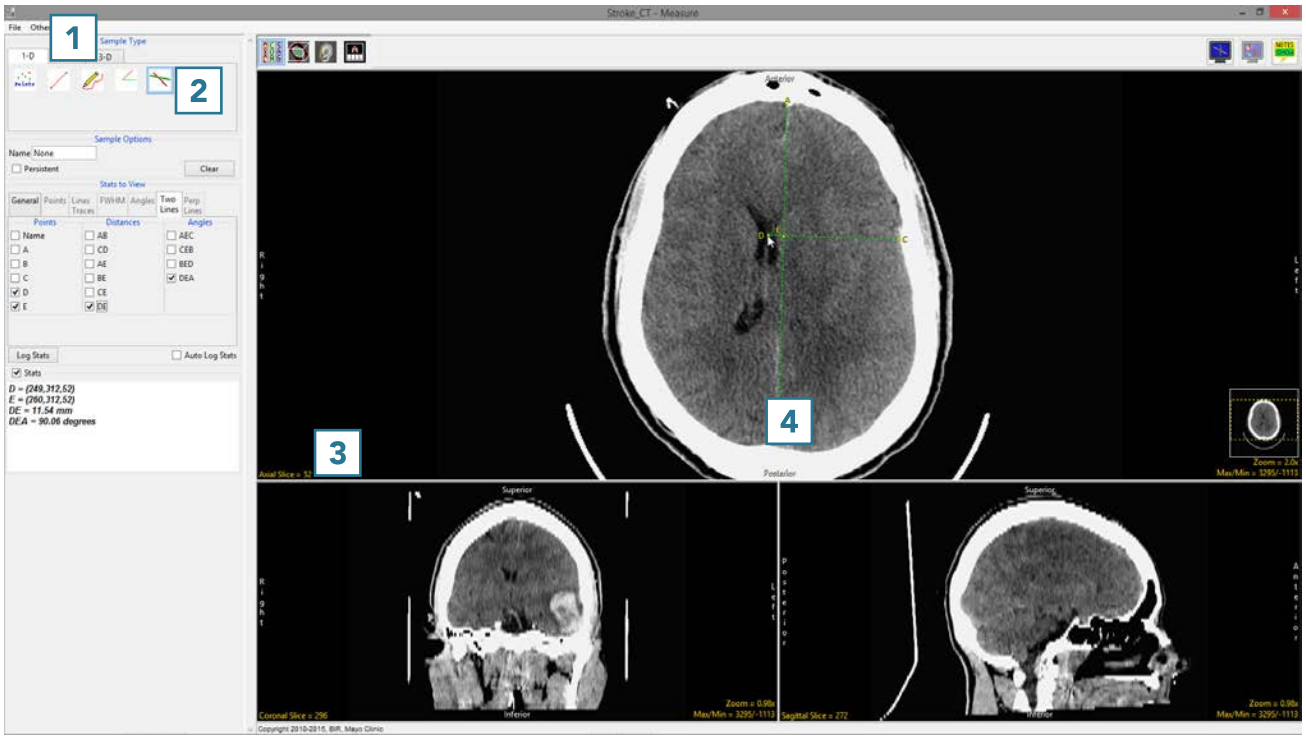


# 7. Making Distance Measurements with the Two Lines Tool

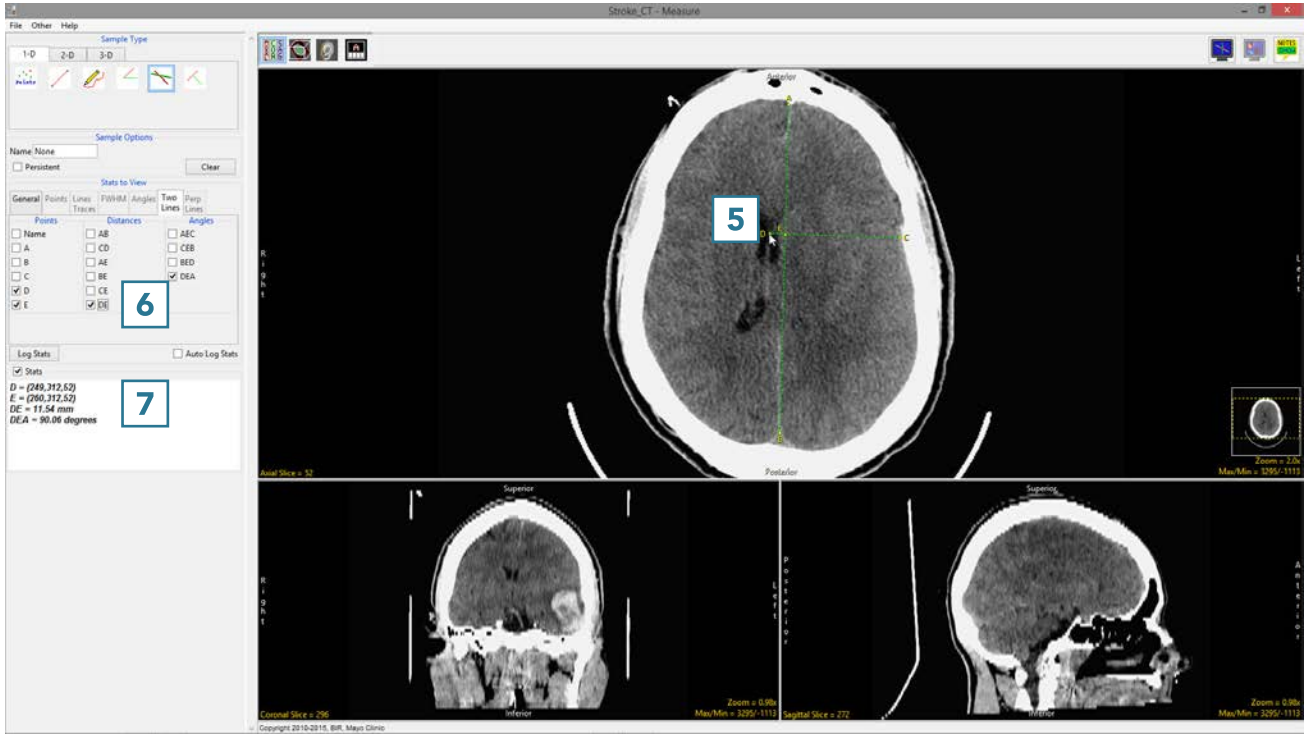
The Sample Two Lines tool provides users with an interactive tool for making line and angle measurements. The tool is useful for applications such as measuring midline shift in stroke CT images.

- Select a data set and open Measure.
- Select the 1D 1 Sample Type and choose Sample Two Lines. 2
- To measure the displacement of the septum pellucidum from the midline at the level of the foramen of Monro, set the primary display to Axial 3 and find a suitable slice.
- Click on the image to set the first point, A, and drag the end point of the first line, B, to the desired location. This is the midline. 4

**Download the Stroke_CT data set to follow along http://analyzedirect.com/data/**



- Once the midline is set, the next line will automatically appear. To define the second line, move point D perpendicular to the midline of the septum pellucidum. 5 Point C may need adjusting to make the second line perpendicular to the first.
- Check the Points, Distances, and any Angles you want to measure. 6 In this example, the midline shift measurement is between point D and point E. Reviewing angle DEA will confirm whether the second line is perpendicular to the first line. The angle should be 90 degrees.
- Measurements will be reported in the Stats review area. 7



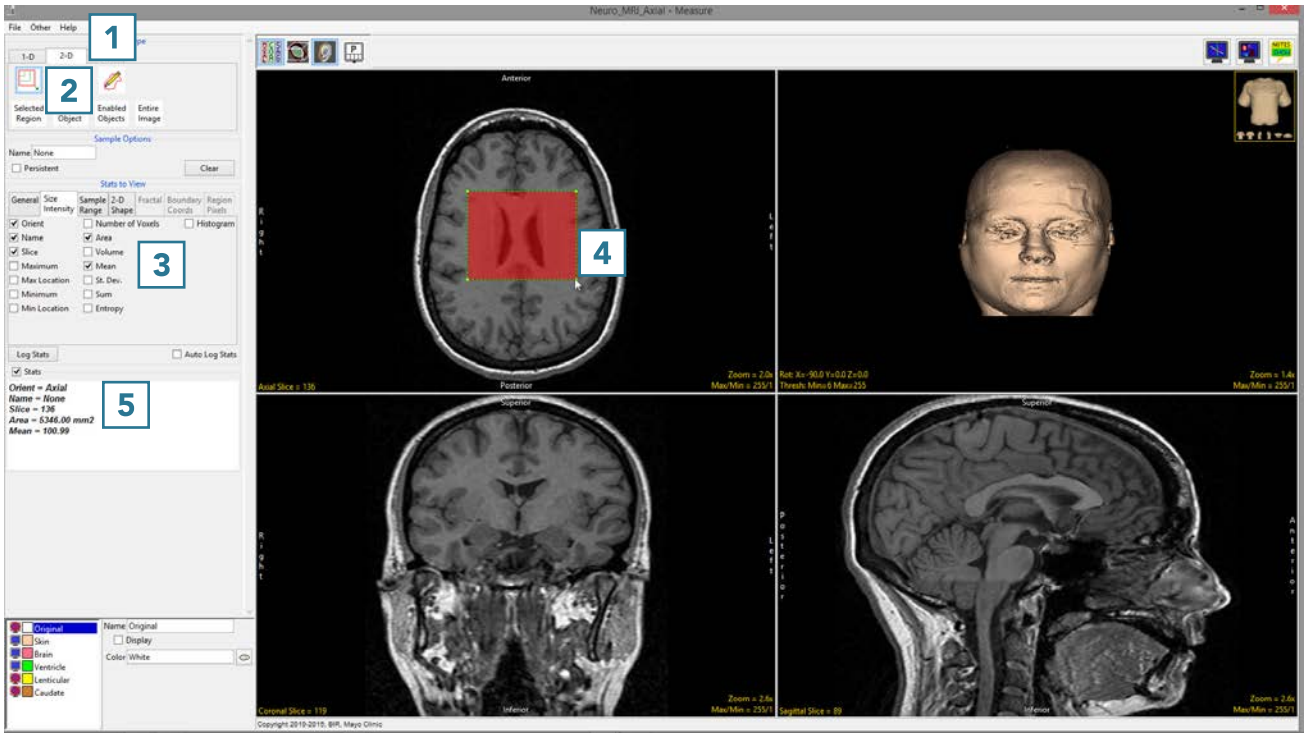
# 2D Measurements

The 2D sampling options in Measure allow users to derive measurements from interactively defined rectilinear or elliptical regions or from objects that exist on a specific slice. Measurement options available include spatial context measurements as well as signal value measurements, including Max/Min, mean, standard deviation, area, volume, 2D shape characteristics and more.

# 8. Making 2D Rectangular Measurements

- Select MRI_3D_Head and open Measure.
- Select File > Load Object Maps and load MRI_3D_Head.obj.
- Select the 2D Sample Type 1 and choose 2D Rectangles. 2
- Set the measurements you want to make. 3
- Define a rectangle on the data. 4
- Selected measurements will be reported for the region in the Stats review area. 5

Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/



# 9. Making 2D Oval Measurements

- Select the 2D Oval tool. 1
- Define an oval region to sample. 2
- Selected measurements will be reported for the region in the Stats review area. 3

Download the MRI_3D_Head data set to follow along
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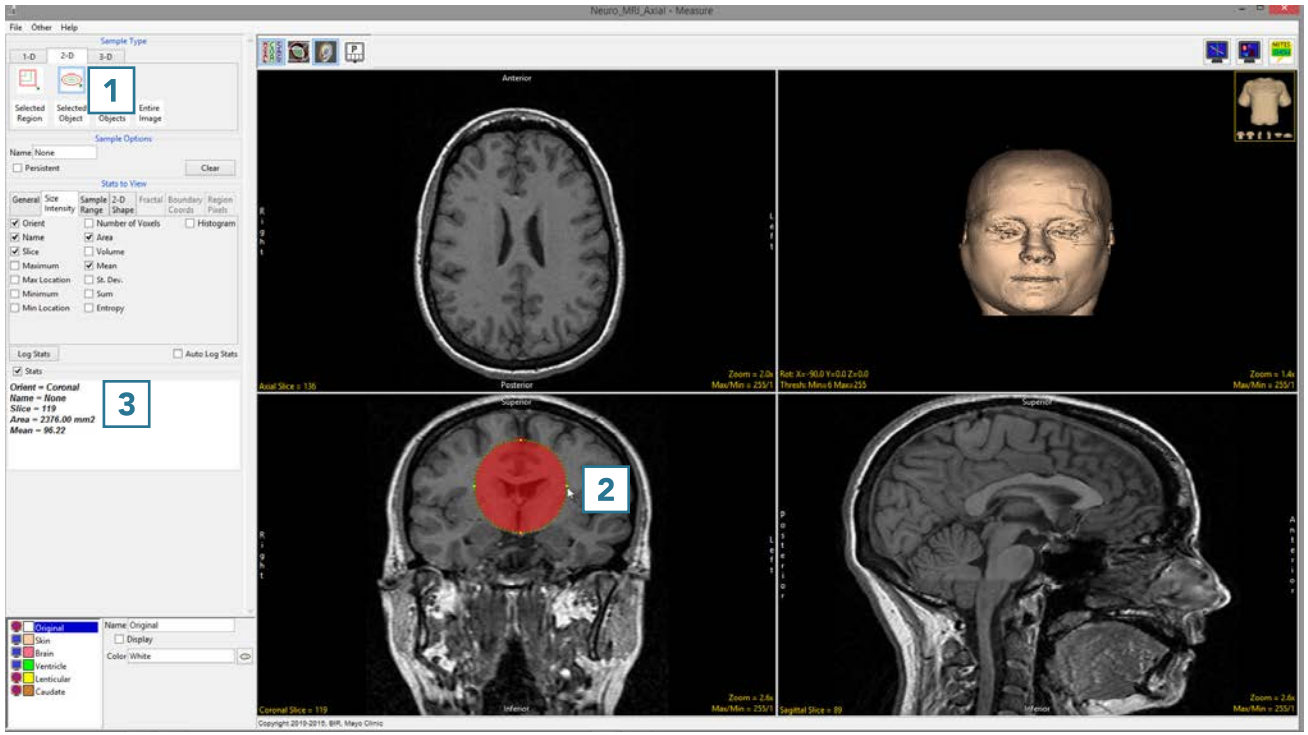

# 10. Making 2D Closed Trace Measurements

- Select the 2D Closed Trace tool. 1
- Define a region to sample. 2
- Selected measurements will be reported for the region in the Stats review area. 3

Download the MRI_3D_Head data set to follow along
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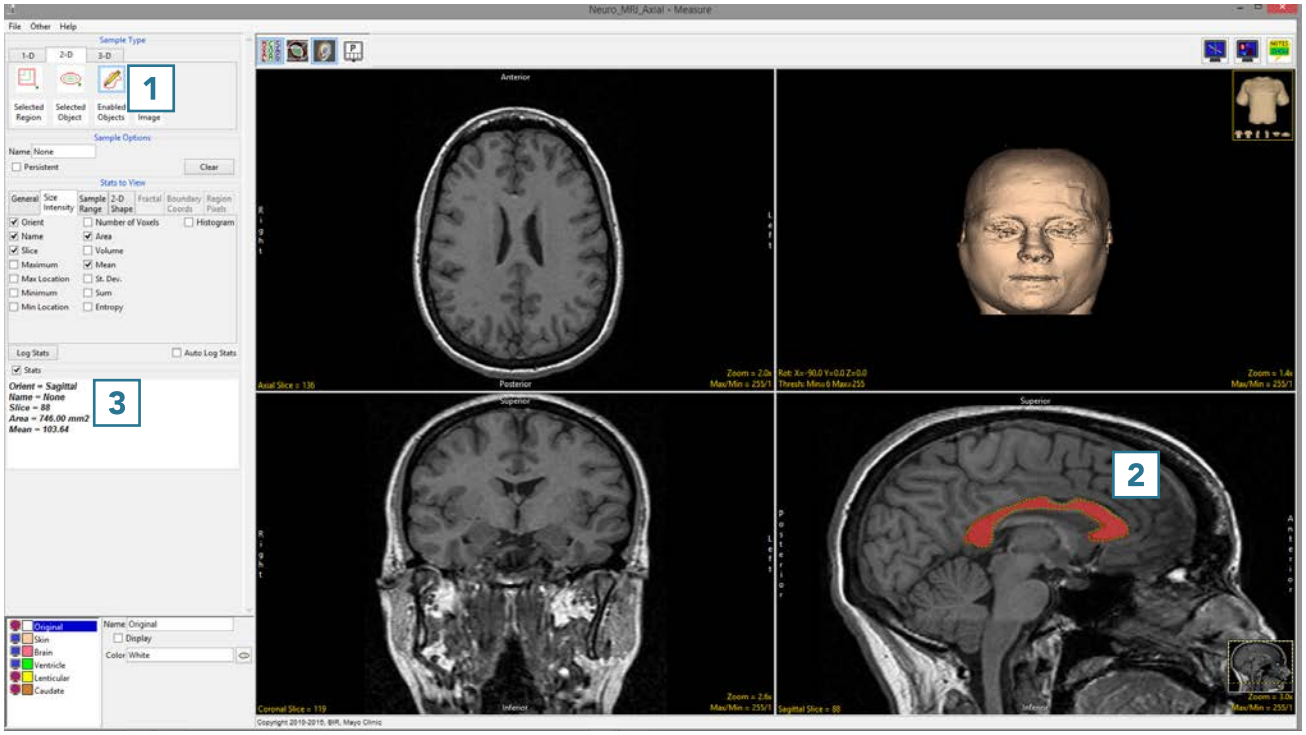
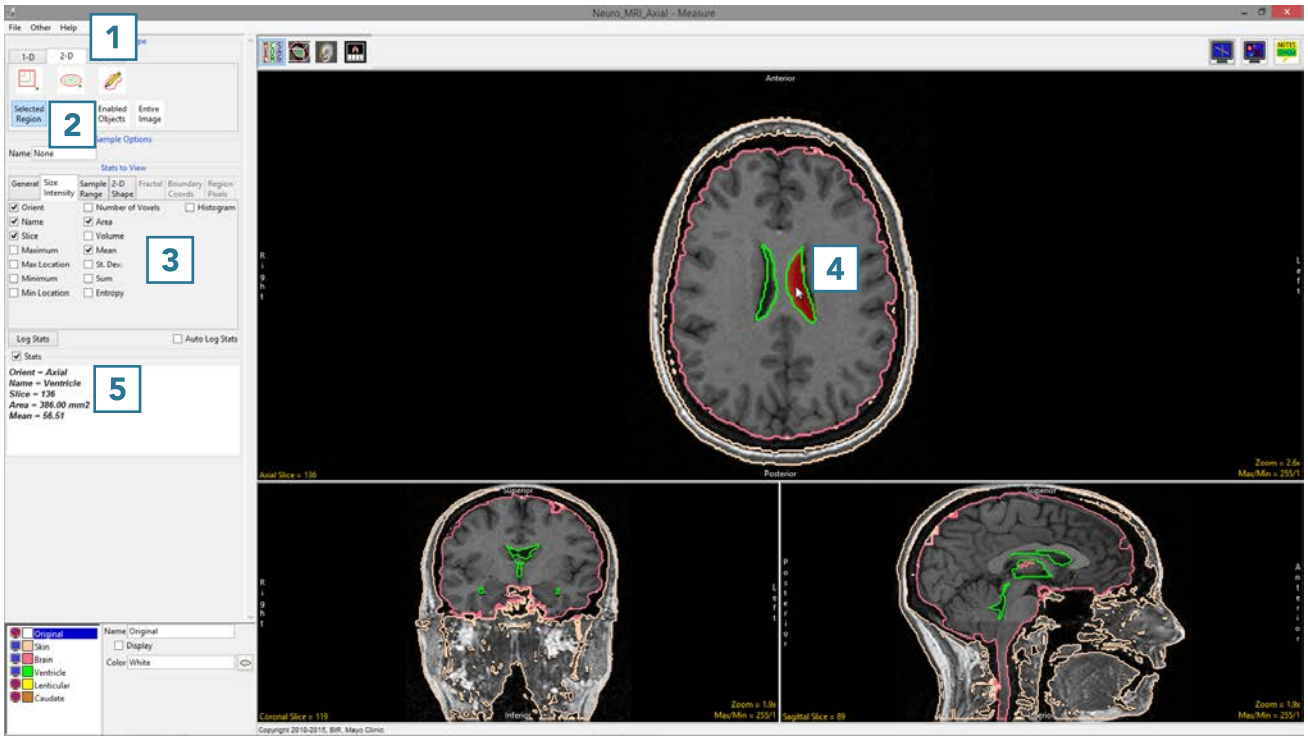


# Additional 2D Sampling Options

## Selected Region

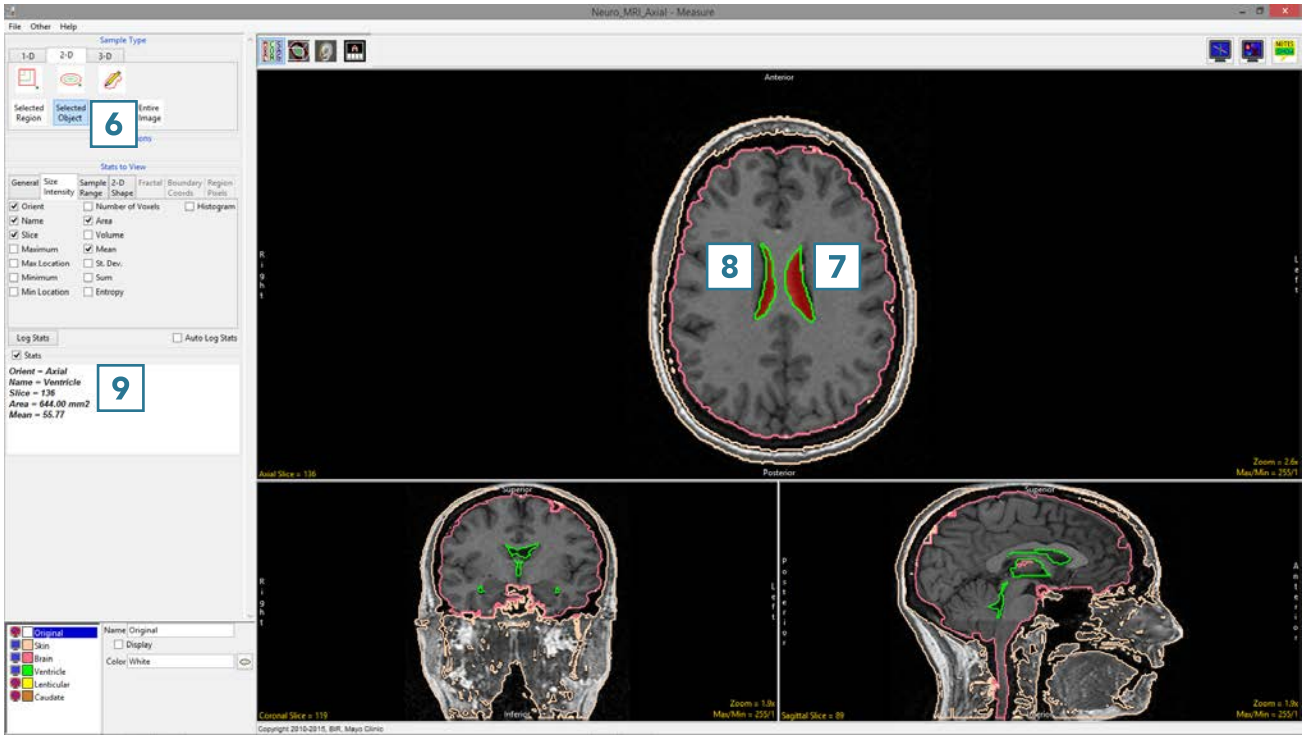
- Select MRI_3D_Head and open Measure.
- Select File > Load Object Maps and load MRI_3D_Head.obj.
- Select the 2D Sample Type. 1
- Choose Selected Regions. 2 Regions selected by clicking on the image will be sampled.
- Select the desired measurements 3 and click on a region. 4
- Selected measurements will be reported. 5

**Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/**



## Selected Object

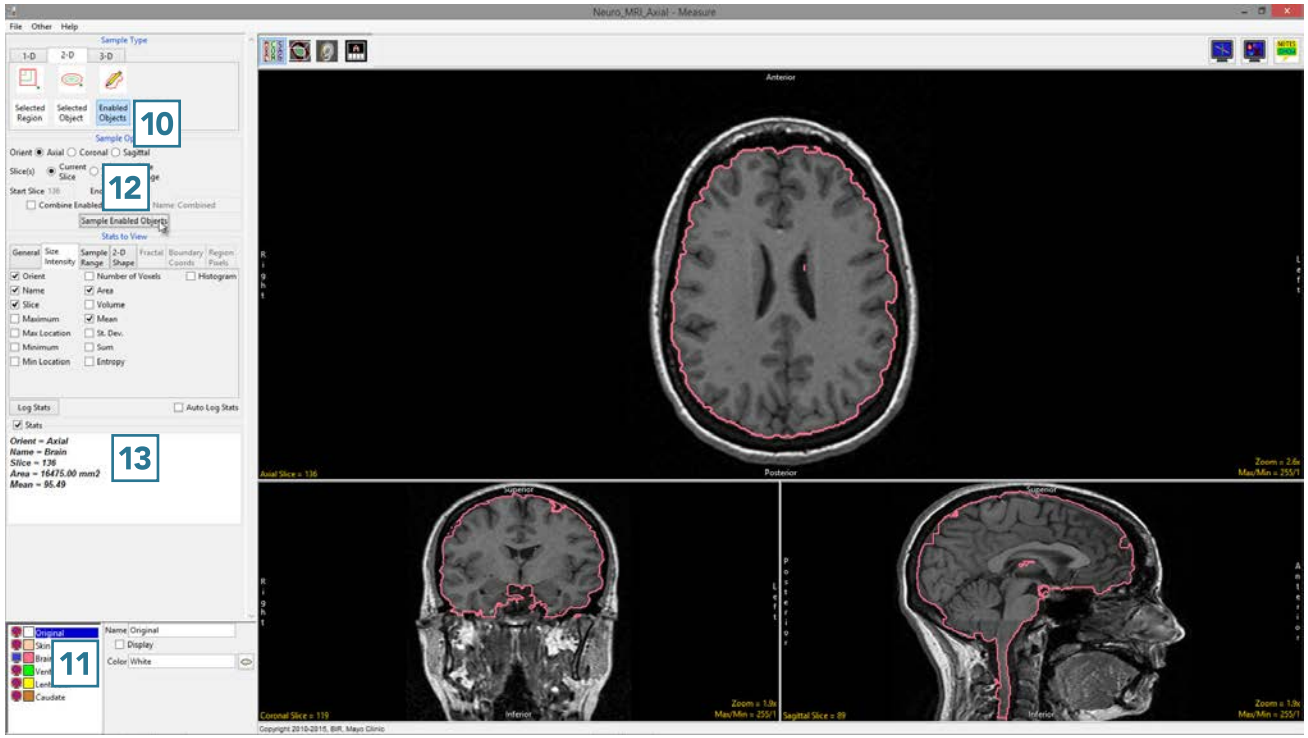
- Choose Selected Object. 6 All voxels representing the selected object (even if spatially disconnected on the slice) will be sampled.
- Click on a region. 7 In this example, the region of the ventricle on the left was selected. However all voxels assigned to the ventricle object are sampled. 8
- Selected measurements will be reported. 9



# Enabled Objects

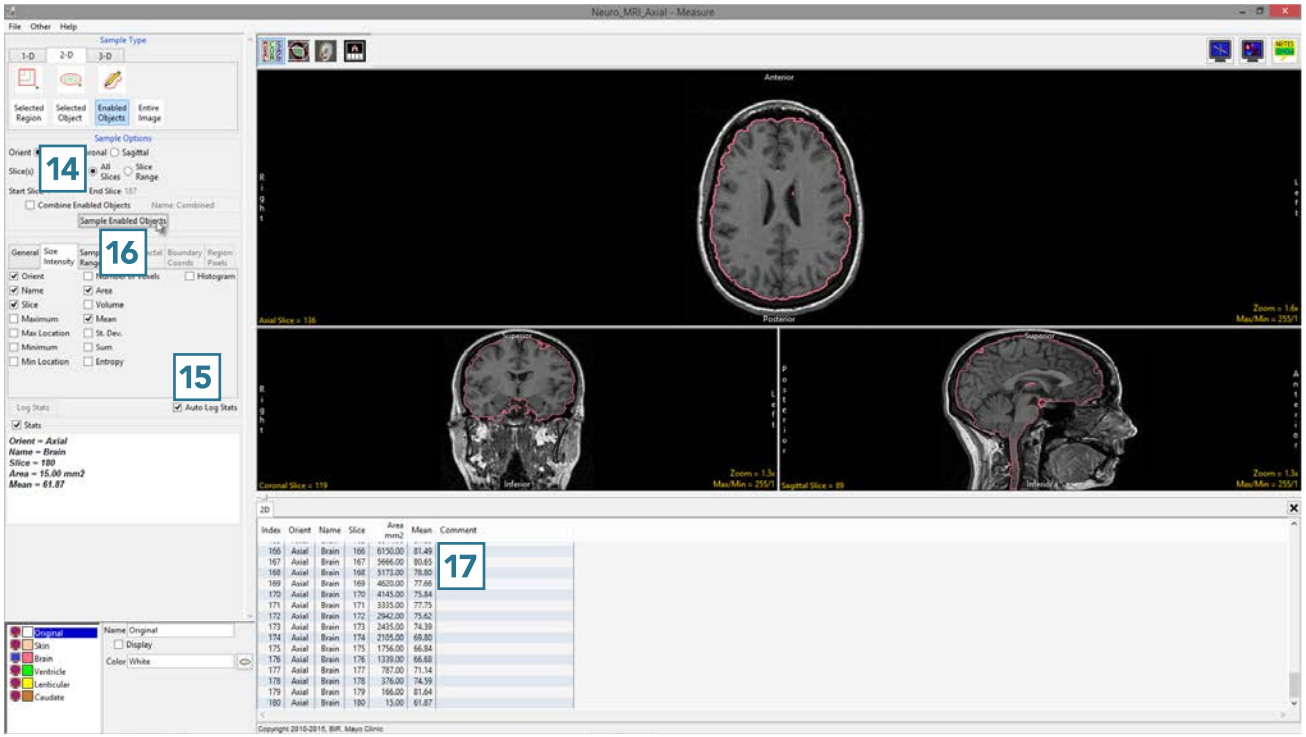
## Sampling the Current Slice

- Choose Enabled Objects. 10 Objects enabled in the Object control window will be sampled. Disable all objects apart from the Brain. 11
- Click the Sample Enabled Objects button. 12
- Selected measurements will be reported for the enabled object 13 for the current slice.



## Sampling All Slices

- Change Slices(s) to All Slices 14 and check the Auto Log Stats checkbox. 15
- Click the Sample Enabled Objects button. 16
- Selected measurements will be reported for the enabled object in the 2D log 17 and can be saved as a .CSV file.



## Sampling a Range of Slices

- Change the primary display to Sagittal. 18
- Disable the Brain object and enable the Ventricle object. 19
- Change Slices(s) to Slice Range. 20
- Set the Start Slice 21 to the first slice where the Ventricle object appears in the data, slice 54.
- Set the End Slice 22 to the last slice where the Ventricle object appears in the data, slice 126.
- Check the Auto Log Stats checkbox. 23
- Click the Sample Enabled Objects button. 24
- Measurements will be reported for the enabled object in the 2D log 25 and can be saved as a .CSV file.

# 3D Measurements

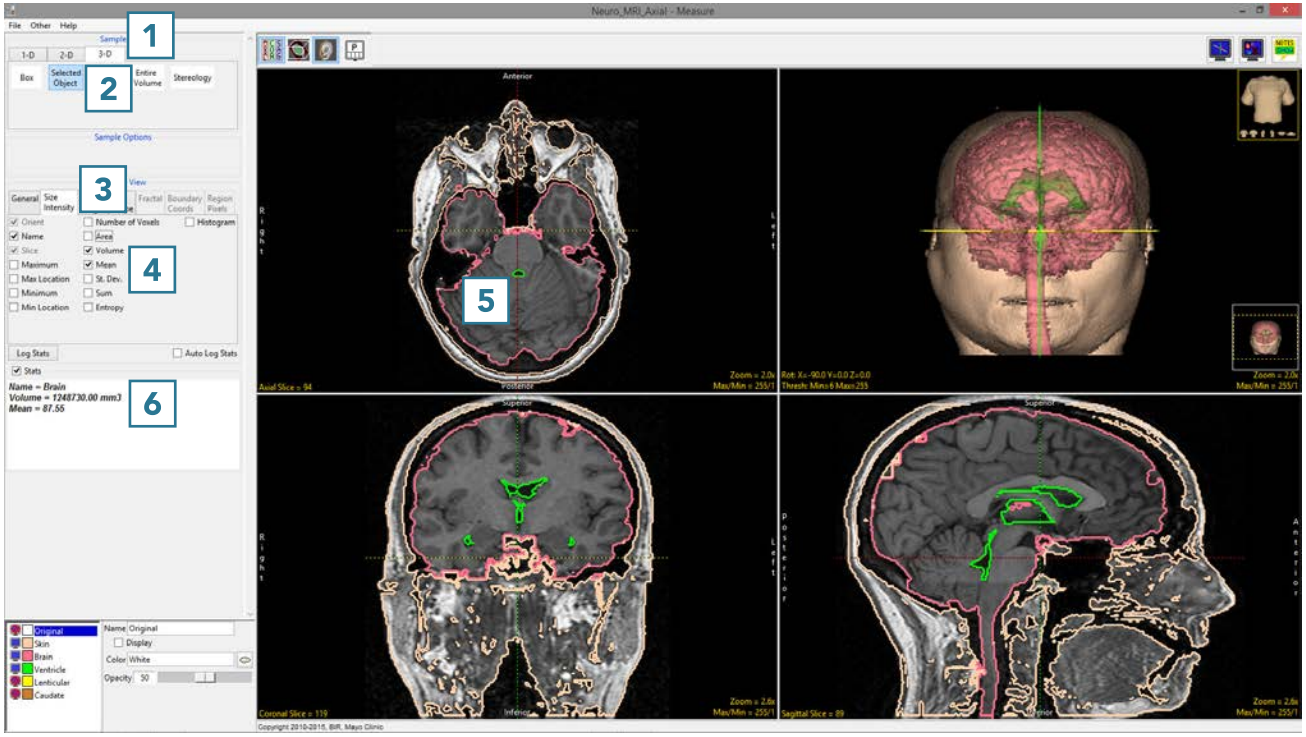
3D measurements are derived from the loaded object map for the data set. Spatial size, signal intensity information and 3D shape characteristics can be derived from an object or collection of objects.

# 11. Making Size and Intensity Measurements

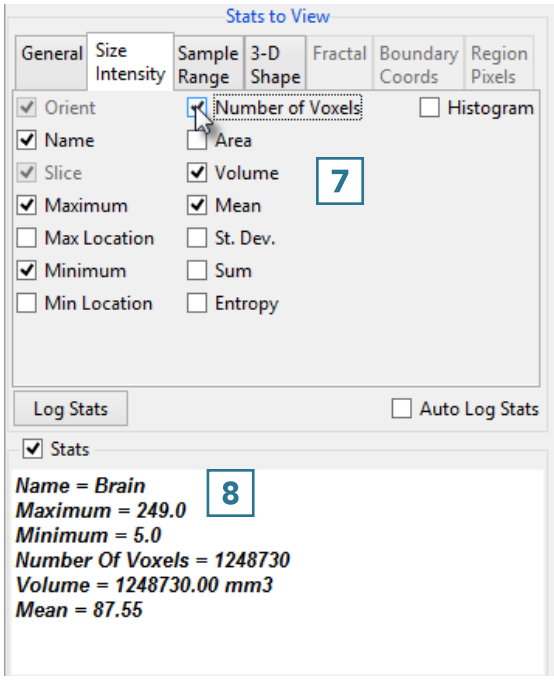
## Using Selected Objects to make a Volume Measurement

- Select MRI_3D_Head and open Measure.
- Select File > Load Object Maps and load MRI_3D_Head.obj.
- Select the 3D Sample Type 1 and choose Selected Object. 2
- Select Size Intensity 3 and make sure that Name, Volume and Mean are checked.
- Uncheck Area. 4
- Click on the brain. 5
- The selected measurements for the brain will be reported. 6

**Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/**



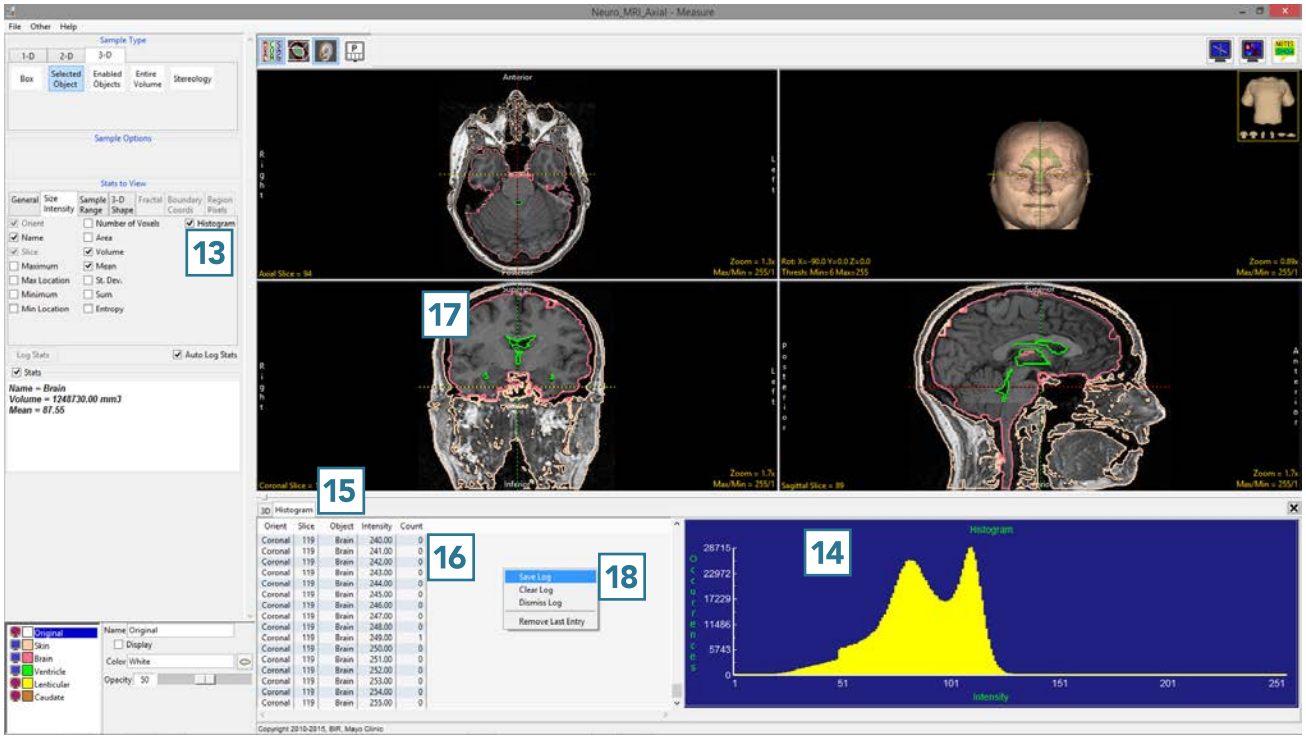
Checking additional measurement options 7 will automatically update the Stats area with the selected measurement. 8



- To report the selected measurements to a log file that can be saved from Measure, check the Auto Log Stats option 9 and click on the brain again. 10
- The selected measurements will be returned to a file below the image display area. 11
- To save the measurements log file, right-click in this area and select Save Log. 12 The log file will be saved as a .CSV file.

## Using Selected Objects to Generate a Histogram for an Object

- Check the Histogram checkbox. 13 The histogram for the sampled object will be displayed below the display area 14 in a new Histogram tab 15 in front of the other statistics tabs.
- To generate the histogram statistics (intensity and count information) 16 click on the brain. 17



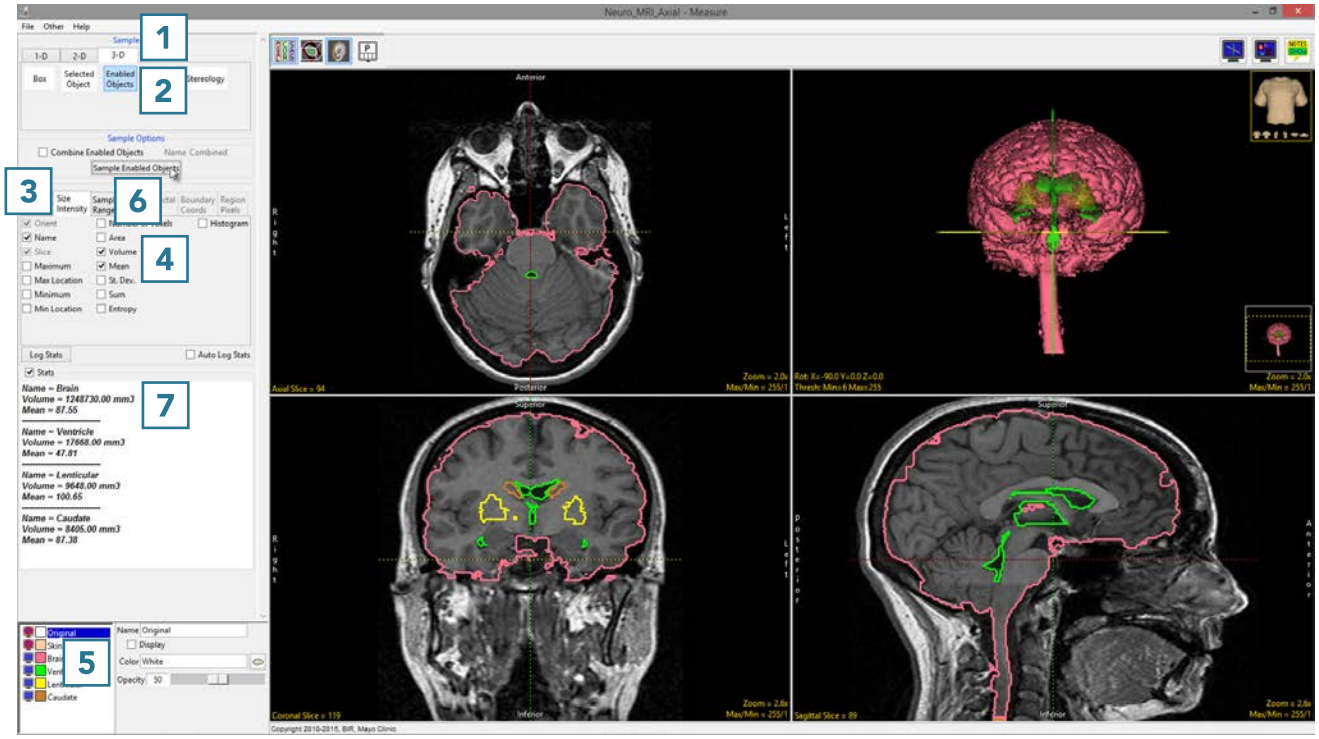

Note that objects with the view disabled can accidently be selected and sampled when using the Selected Object tool. Be aware when selecting an object to sample.

- The histogram information can be saved as a .CSV file by right-clicking and selecting Save Log. 18

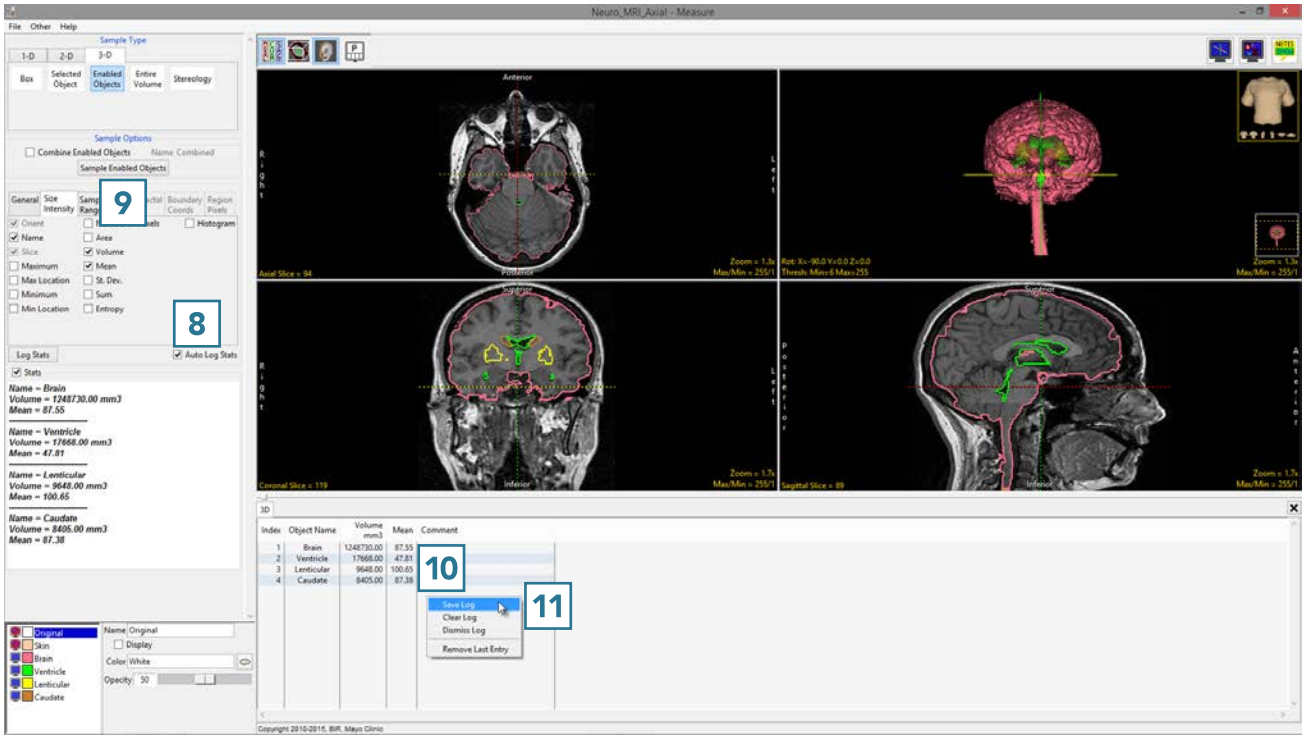
# 12. Using Enabled Objects to make Volume Measurements for Multiple Objects

- Select MRI_3D_Head and open Measure.
- Select File > Load Object Maps and load MRI_3D_Head.obj.
- Select the 3D Sample Type 1 and choose Enabled Objects. 2
- Select Size Intensity 3 and make sure that Name, Volume, and Mean are checked.
- Uncheck Area. 4
- Switch the display of the Skin object off 5 by clicking on the monitor icon next to the object in the object list.
- Switching the display of an object off disables the object so it won't be sampled. Switch on the Lenticular and Caudate objects.
- Click Sample Enabled Objects. 6 The selected measurements for the enabled objects will be reported. 7

Download the MRI_3D_Head data set to follow along
http://analyzedirect.com/data/



- To report the selected measurements to a log file that can be saved from Measure, check the Auto Log Stats option 8 and click Sample Enabled Objects. 9
- The selected measurements for the enabled objects will be returned to a file below the image display area. 10
- To save the measurements log file, right-click in this area and select Save Log. 11 The log file will be saved as a .CSV file.



# 13. Using Enabled Objects to make Combined Volume Measurements for Multiple Objects

- Check the Combine Enabled Objects checkbox. 1
- Name the combined result or leave with the default name Combined. 2
- Click Sample Enabled Objects. 3
- The combined measurements will be reported in the stats review area 4 and added to the log file. 5

- Checking additional measurement options 17 will automatically update in the Stats review area with the selected measurement for the combined object. 18
- The measurements for the individual and combined objects will automatically update in the log. 19

# 14. Using Enabled Objects to Generate a Combined Object Histogram

- Check the Histogram check box 1 and select Sample Enabled Objects. 2
- The histogram measurements will be reported 3 and the histogram plotted 4 in a new tab. Right-click to save the histogram log.

# 15. Sampling the Entire Data Set

Sometimes it is necessary to obtain statistics for the entire data set.

- Select MRI_3D_Head and open Measure.
- Select File > Load Object Maps and load MRI_3D_Head.obj.
- Select the 3D Sample Type. 1 Choose Entire Volume. 2
- Select Size Intensity 3 and make sure that Name, Volume and Mean are checked. Uncheck Area. 4
- Check Auto Log Stats 5 and click Sample Entire Volume. 6
- The selected stats for the entire volume will be reported in the Stats review area 7 and log file. 8

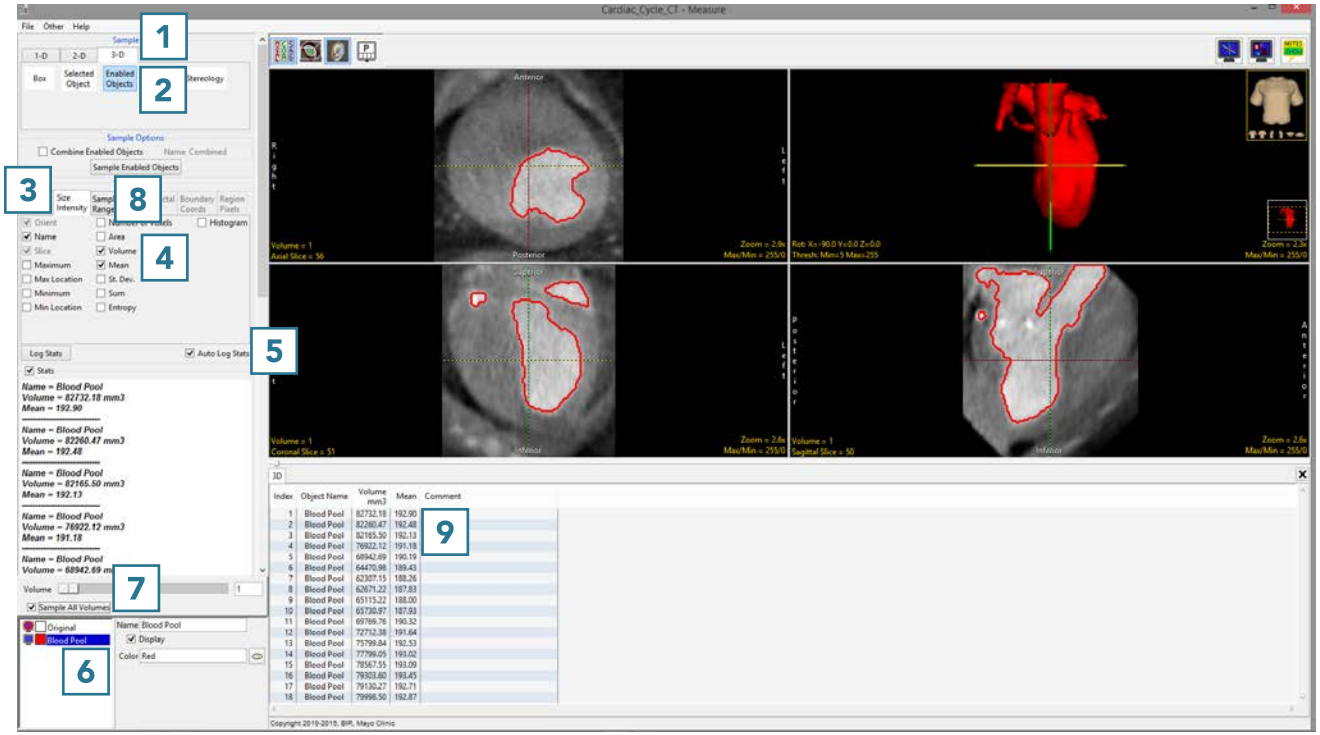
**Download the MRI_3D_Head data set to follow along http://analyzedirect.com/data/**

Technically, to sample stats for the entire volume, an object map is not required.

- Select MRI_3D_Head and open Measure.
- Select the 3D Sample Type 9 and choose Entire Volume. 10
- Select Size Intensity 11 and make sure that Name, Volume, and Mean are checked. Uncheck Area. [12 12
- Check Auto Log Stats 13 and click Sample Entire Volume. 14
- The selected stats for the entire volume will be reported in the Stats review area 15 and log file. 16

# 16. Measuring 4D Multivolumes

- Select 4D_Cardiac_Cycle and open Measure.
- Select File > Load Object Maps and load 4D_Cardiac_Cycle.obj.
- Select the 3D Sample Type 1
- Choose Enabled Objects. 2
- Select Size Intensity 3 and make sure that Name, Volume and Mean are checked.
- Uncheck Area. 4
- Check Auto Log Stats. 5
- Select the Blood Pool object from the object control window. 6
- Make sure Sample All Volumes is checked. 7
- Click Sample Enabled Objects. 8
- The total volume of the blood pool for each of the 18 3D volumes in the 4D multivolume will be reported in the 3D log. 9 Right click to save the log as a .CSV file.



# Table Index