Analyze 15.0

USER'S GUIDE



© AnalyzeDirect, Inc. © Mayo Clinic Biomedical Imaging Resource

Analyze 15.0 User's Guide

Analyze 15.0 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 Analyze 15.0 are broad in scope, wide in scale and penetrating in impact.

Tutorial data

Example exercises are provided through out this user's guide. To work through these exercises, download the example data from https://analyzedirect.com/data/.

Analyze 15.0 User's Guide

- Analyze 15.0 Basics page 4
- Image Controls and Customization page 16
 - Input/Output page 32
 - Display page 88
 - Process page 164
 - Transform page 190
 - Segment page 269
 - Register page 477
 - Measure page 527

Analyze 15.0 Basics

The Analyze 15.0 workspace is the first operational window that appears when Analyze 15.0 is opened. The main window does not perform any imaging functions; rather, it coordinates all the modules within the Analyze 15.0 package and acts as a file manager for loaded data.

Once data is loaded into Analyze 15.0, it will appear in the tabbed workspace (1) as a thumbnail (2) in the workspace and is available to all of the modules (3). 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 Analyze 15.0 side menu.



Analyze 15.0 Modules

Analyze 15.0 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.



Provides direct loading and exporting of data for over 50 file formats



Display

Provides a powerful set of 2D and 3D image review and display tools



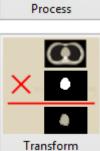
Process

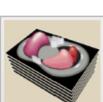
Facilitates image optimization, filtering and enhancement functions



Transform

Allows spatial and intensity transformations, mathematical processing and data reorientation.





Segment

Register

Measure

Provides sophisticated interactive tools for fast and precise region definition

Register

Segment

Provides multi-modality image fusion and image alignment of 2D, 3D and 4D data

Measure

Allows in-depth analysis with a suite of robust image measurement tools

5

Right Mouse Button Menu

The Analyze 15.0 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 (see Header Edit below) |
| 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 Analyze 15.0 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 Analyze 15.0 License Manager |
| Analyze 15.0 Update — Check to make sure the software is up to date; will also download and |
| install any necessary updates |
| Options — Configure Analyze 15.0 features, Object Map loading, and Window management |
| options (see Options below) |
| Help — Open the Analyze 15.0 User's Guide |
| Get Help — Open the AnalyzeDirect Support Page |
| |

About — View version, system and environment information

| Unload |
|--|
| Info |
| Rename |
| Edit Header |
| Duplicate |
| Append |
| Un-append |
| Select All |
| Invert Selected |
| |
| Arrange |
| Arrange Session Log |
| |
| Session Log |
| Session Log Current Directory |
| Session Log Current Directory License Manager |
| Session Log Current Directory License Manager Analyze Update |
| Session Log Current Directory License Manager Analyze Update Options |
| Session Log Current Directory License Manager Analyze Update Options User Guide |

Header Edit

When Edit Header is selected from the right-mouse menu, the Header Edit window will open. Header Edit enables the modification of the selected data's header information, including adding user defined fields or removing selected fields from the header. Header Edit is primarily used for adjusting dynamic range values, adding or correcting voxel dimension information, or modifying orientation (AVW image data only) for loaded volumes.

Exercise caution when modifying header files, as inconsistent values may cause unpredictable results. If used on non-AVW image data, Header Edit may not work.

the file..

| from | 🐋 Heade | r Edit - AnalyzePro | | | _ | | × |
|---|---------|---|--|-------------------------------------|----------------|-------------|------|
| ader ⁻ Edit | File | C:/temp/APRO/SIS | COM/BMA_SC_micro_CT.mmap | | | | |
| e ation, fields om the | Widt | h 615 | 10358.526367 | | _ | | ^ |
| y used alues, nension ntation ded | | MinimumDataValue = OriginalOrient = VoxelDepth = VoxelHeight = VoxelWidth = | AVW_TRANSVERSE 0.02 0.02 0.02 | | | | ~ |
| ing lues | Save | Find | Calculate Max/Min | | | Dor | ne |
| lts. | File - | opens a File selection | window enabling the selection | Depending on the type of f | ile selected t | the follo | wing |
| ta, | of a he | eader file (.hdr) to be | examined and/or modified. | fields are available, but sele | ction optior | ns may va | ary: |
| | DataT | ype - Displays the da | ta type of the selected file. | Save - Records all changes m | ade to the he | eader file | |
| | Choos | se from the drop-dow | n list to change the data type. | Calculate Max/Min – Calcula | ates and repo | orts the fi | le's |
| | Widtł | ı - Displays the image | width value. | maximum and minimum value | es. The follow | wing opti | ons |
| | Heigh | it - Displays the image | e height value. | are available: | | | |
| | Dept | 1 - Displays the numb | er of images in the volume | Ignore – Does not apply valu | es to header. | | |
| | Num | Vols - Displays the nu | mber of volumes contained in | Apply – Applies values to the | header. | | |

Done – Closes the Header Edit window.

Options

When Options is selected from the right-mouse menu, the Options window will open. The Options window allow users to enable and disable Analyze and Module Options.

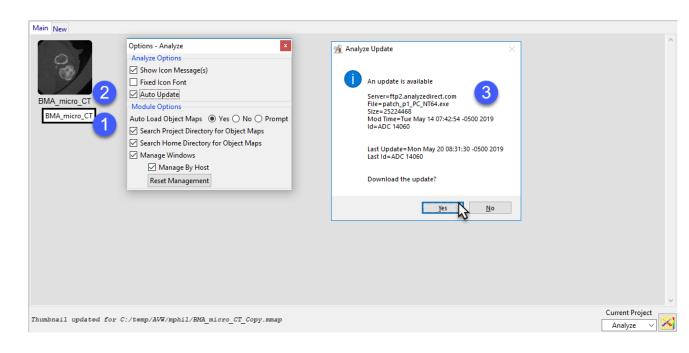
Analyze Options

Show Icon Message(s) – Enable or disable the display of pop-up messages returned when the mouse cursor is moved over a thumbnail in the workspace (1).

Fixed Icon Font – Enable or disable a default fixed icon font for loaded image data (2). **Auto Update** – Enable or disable Analyze 15.0 from automatically checking for updates when the software is opened (3). It is recommended that this option is enabled.

Module Options

Auto Load Object Maps - Determines whether Object Maps are automatically loaded (Yes), not loaded (No), or the user is prompted (Prompt) to load an object map when a module is opened.



Search Project Directory for Object Maps – Allows modules to search the current project directory for an object map when opened.

Search Home Directory for Object Maps - Allows modules to search the user's Home directory for an object map when opened.

Manage Windows - When enabled, Analyze and all modules remember the positions and size of each window.

Manage By Host – Stores separate window manOptionsagement information for each unique computer. This may be necessary if a user runs on more than one system and each system has different configurations (number of displays, display orient, and screen resolution).

Reset Management - Deletes the position and size information for the system resetting window management information.

Main Analyze 15.0 Window Actions and Quick Keys

Left click — Selects a file.

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

[Ctrl] + Left Mouse Click — Selects/deselects each file that has been clicked.

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

[Ctrl] + [Alt] + c — Recalculates the data sets minimum and maximum information.

[Shift] + [Ctrl] + [Alt] + p — Forces a patch update.

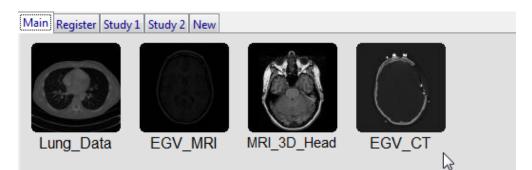
[Ctrl] + x — Duplicates selected file.

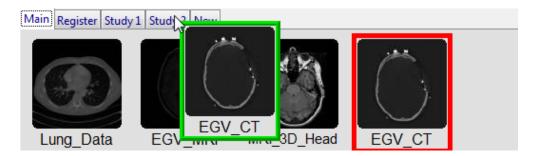
Double-clicking on a data set in the workspace restarts the last module used with that data. If there is not a module associated with the data, the Display module will open by default.

Workspace Tabs

The main Analyze 15.0 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.



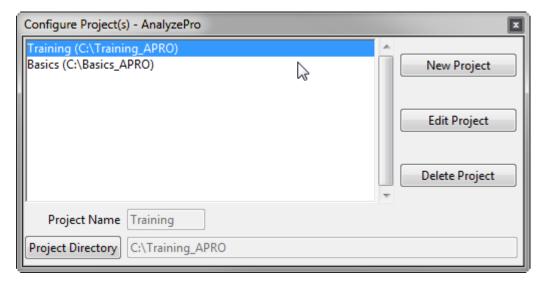


Projects

Workspaces can be organized into specific projects via the Current Project controls in the lower right of the Analyze 15.0 window. Analyze 15.0 creates a default workspace/ project from the computer username.

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

| Current Project | |
|-----------------|-------|
| Training 🔫 | \ge |



Creating a project

To create a new project, click on the Project Configuration button (1).

Next, click New Project (2).

Name the project (3) and then use the Project Directory button (4) to specify the location where the project will reside on disk. Note that this is the location where all data loaded into the project will be stored so ensure that the location has enough free disk space to handle the data you plan to load for the project. Also, it is recommended that the project be stored on a local disk and not on a network drive.

Click Create (5). The Project file will be created and now be available in the Current Project drop-down.

| nphil (C:\temp\AVW\mphil) | 2 |
|---------------------------------------|------------------------|
| Analyze (C:\temp\AVW\mphil) | New Project |
| | |
| | Edit Project |
| | |
| | Delete Project |
| Project Name Stroke | \checkmark |
| Project Directory C:\temp\AVW\Stroke\ | |
| (Note: Project Directory should be a | on a local hard drive) |
| Cancel | 5 Create |
| | |

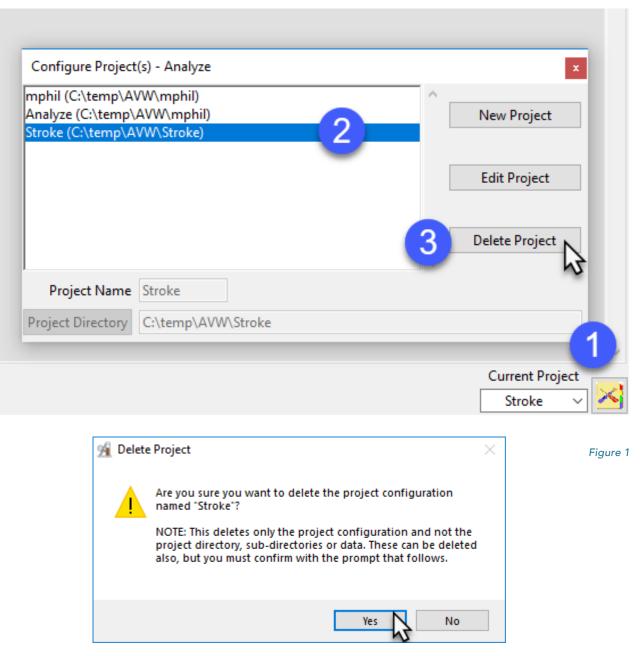
Deleting a project

Note, please exercise caution when deleting a project.

To delete a project, click the Project Configuration button (1).

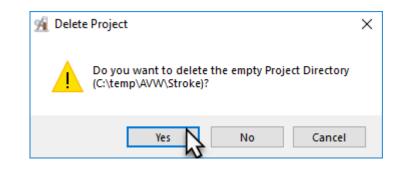
Select the Project you wish to delete (2) and then click delete (3).

A Delete Project file confirmation window will be returned. This window will ask you to confirm the deletion of the selected project file (Yes) or cancel the delete (No). Not that clicking Yes will only delete the project file of the selected project. This delete will not deleted the projects workspaces or loaded data. Select Yes to proceed with the deletion of the project.



Next, another Delete Project window will be returned. This window will allow users to delete (Yes), not delete (No), or Cancel the deletion of the project directory and data. Note that selecting Yes to delete the Project Directory will delete all workspaces, data, and other files associated with the project saved under the project file location. Select Yes to continue with the delete.

The selected project and all workspaces and data will be deleted.

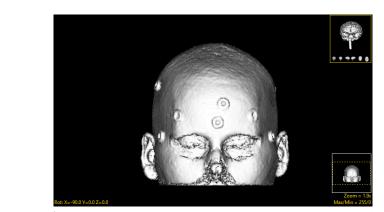


Object Maps

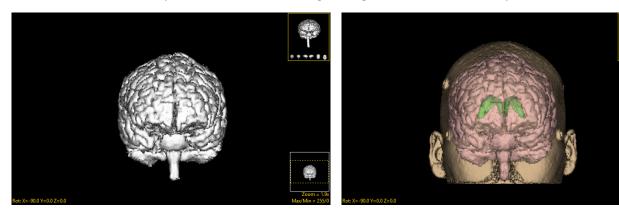
Analyze 15.0 uses a file called an object map to partition image data into groups of voxels within a segmentation component map. After creation of the object map through segmentation, it can be used to drive visualization, registration, surface generation and statistical analysis.

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



Original image



Grayscale segmentation

Object map segmentation

module. When the object map is loaded, the objects defined in it are overlaid on the image data. As can be seen in the above figures, grayscale segmentation destroys all voxels that are not part of the object of interest, whereas object maps preserve the original data by assigning the segmented voxels to objects.

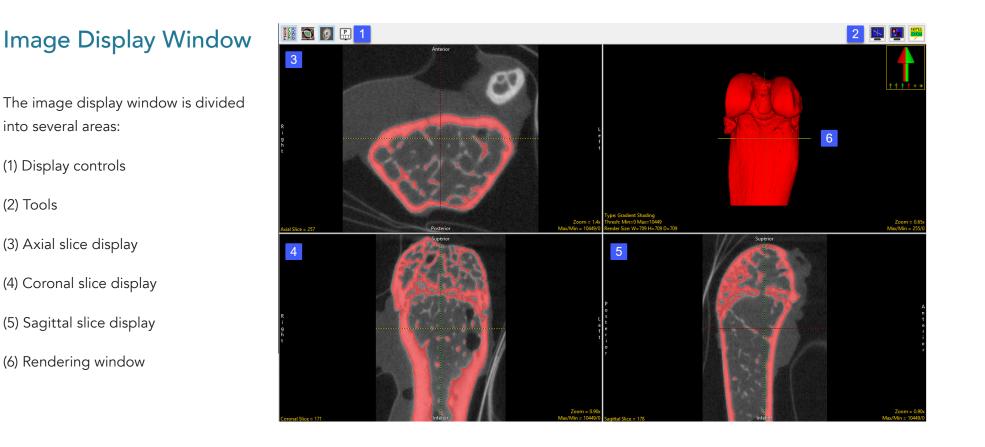
Image Display Controls and Customization

Introduction page 17

- Image Display Window page 17 Display Controls page 18
 - Tools page 19
 - Slice Display page 21
- Rendering Window and Tools page 28

Introduction

Analyze 15.0 provides common image display windows with interactive image controls across all modules. The following display options and controls are present in all sections of the software, but certain modules will contain additional functions. The implementation of the image display tools are similar for the Display, Transform, Segment, and Measure modules, implementation varies slightly for the Process and Register modules. For additional information on the Process and Register module display tools please refer to the Process and Register sections of this user's guide.



17

Display Controls

The Display Controls allow users to control and customize the layout of the display window.

Toggle All Orientations: Allows users to switch between the display of all three orthogonal displays (the axial, coronal and sagittal) to a single orientation display.

Toggle Oblique: Allows users to switch the oblique display window on and off.

Toggle Rendering: Allows users to switch the Render window on and off.

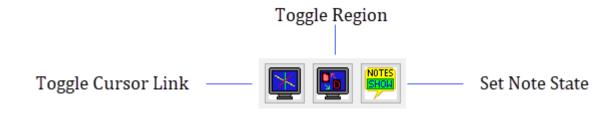
Controls Layout: This option allows users to control the layout of the display window. Choose to set the Axial as Primary, Coronal as Primary, Sagittal as Primary, Render as Primary or specify No Primary image (default option).



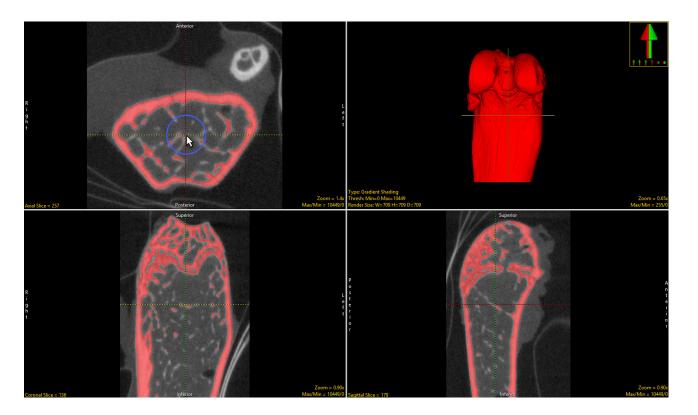


Tools

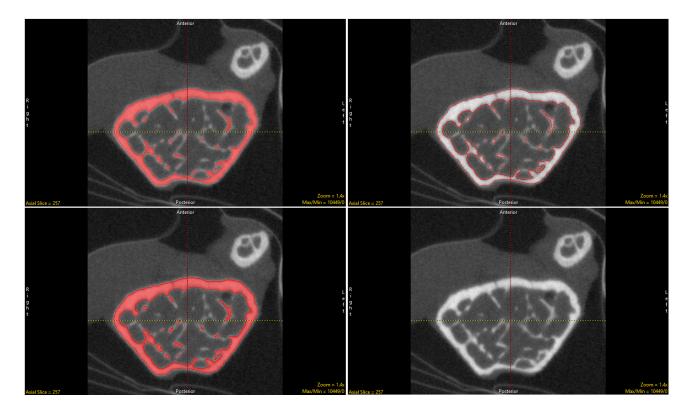
The Tools options in the upper lefthand corner of the Display Window, allow access to control tools for image navigation, display, and notation.



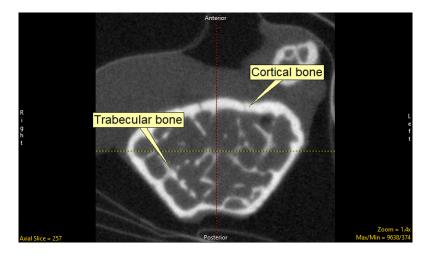
Toggle Cursor Link: Allows enabling and disabling of the Cursor Link tool. The Cursor Link tool allows users to interactively navigate through the image data. Moving the Cursor Link in any of the displays will interactively update the other displays. See the Cursor Link tool in the Slice Display and Render Window sections for additional information.



Toggle Region Display: The Toggle Region Display option allows users to quickly switch between the display of the overlaying regions on the slice displays. The display options are; Filled Regions, Region Edges, Both, and Regions Off. Note the keyboard shortcut to toggle regions displays is the t key.



Set Note State: Enables the Notes tool. The Notes tool allows users to annotate the 2D slice data or 3D rendering. Notes are automatically associated with the data set and can be displayed in other modules. Notes can be hidden or deleted at any time.

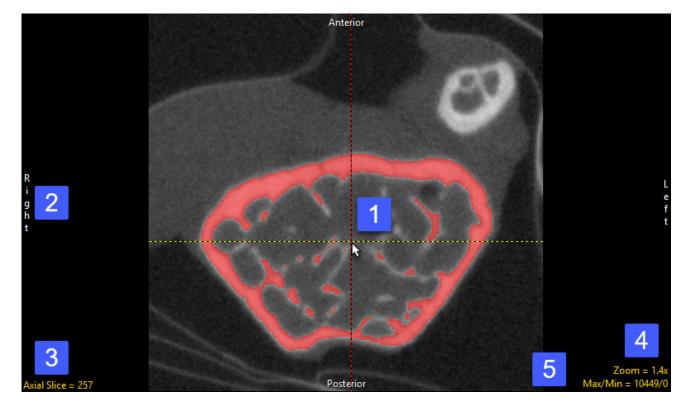


Slice Display

The Slice Display windows displays the 2D slice data in each of the three orthogonal orientations. In the default display mode the upper left window displays the axial orientation, the lower left the coronal orientation, and the lower right the sagittal orientation.

The Slice Display window includes several tools for viewing and navigating through the image data, these include:

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.



The Axial Slice Display window, showing 1) Cursor Link, 2) Orientation labels, 3) Slice tool, 4) Zoom tool, and 5) Max/Min tool.

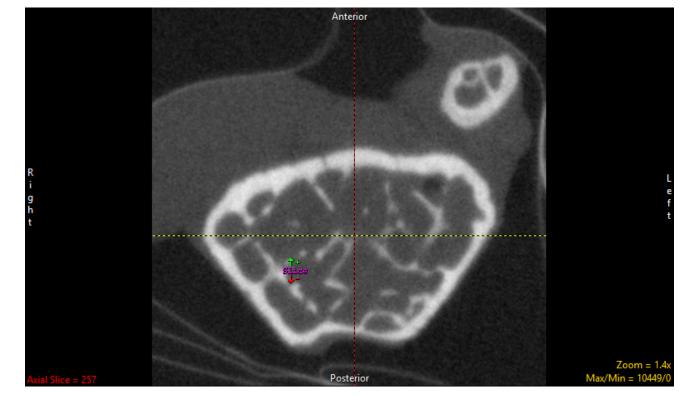
Arrow Keys: can also be used to move the linked cursor. The keys will move the linked cursor in the corresponding direction (up, down, left and right) for the active orientation.

Page Up and Down Keys: used to move through the slices in the active orientation.

Orientation Labels: displays helpful orientation labels. The labels can be abbreviated by right-clicking on them.

Slice Tool: Users can navigate through image slices using the slice tool. 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.

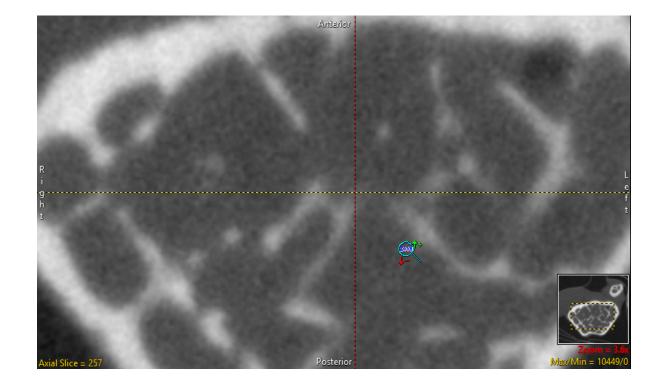
Users can quickly navigate to the First, Middle and Last slice by rightclicking the yellow Slice text. A specific slice number can be chosen by double-clicking the yellow Slice text and typing in the desired slice number.



Zoom Tool: Users can increase and decrease the display size of the data using the Zoom tool. 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.

Right-click on the Zoom tool to reveal additional options:

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 display of the data. The default is Bicubic (Input Driven). Users can switch to Linear (ID), Nearest Neighbor (Output Driven), Linear (OD), Bicubic and Windowed Sync.

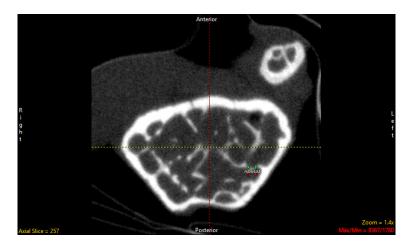
Zoom Center - Uses the center of the image to set as the zoom point.

Analyze 15.0 User's Guide

Pan tool: The Pan tool is automatically enabled when the Zoom size of the image is larger than the current window. Clicking in the tool allows users to Pan the zoomed area over the current display. To enable the Pan tool without zooming right-click on Zoom and select Options and then check Show Pan.

Show Transforms: Transforms (Flips and Rotations) can be enabled for the display window, providing the user with the ability to flip and rotate the image display. To enable transforms right-click on the Zoom tool and then choose Options > Show Transforms, select Enabled and then select Flips and/or Rotates.

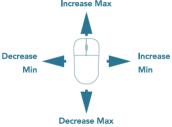
Max/Min tool: The Maximum and Minimum display intensities can be changed by clicking on the yellow Max/Min Tool at the bottom right corner of the image window. A cursor will return that allows the values to be manipulated. Hold down the left mouse button and move the mouse up/down or left/right.



To change only the Max value, 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 select the Max/Min option.

Right-click on the yellow Max/Min text to reveal the Preset Intensity options for the following list of modalities:



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.

Invert — When selected, inverts the display intensities in a single orientation. To change the intensity display from Max/Min to Window/ Level right click on the Max/Min tool and choose Options > Intensity Display and choose between Max/Min or Window/Level. Note that selecting the Change option provides you with the ability to chance the apply these changes to All Modules (default), This Module, or This Display Window only.

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 press enter or click outside the box.

Right Menu Options: Right-clicking in the Slice Display window reveals additional options.

Middle Button Action: Allows users to set the action of the middle mouse button. Choose from:

Change Slice (default) – Allows users to change the slice display by clicking the middle mouse button and moving the mouse forward, to move slice display forward, or backwards, to move the slice display backwards.

Change Zoom - Allows users to change the zoom display by clicking the middle mouse button and moving the mouse forward, to zoom in, or backwards to zoom out.

Change Intensity – allows max/min intensity values to be adjusted using the middle mouse button. Holding the middle mouse button and moving the mouse forward or backwards will adjust the maximum intensity value. Moving left and right will adjust the minimum intensity value.

Default - returns middle mouse button action back to the system default.

Annotate Changes – Enables and disables the annotations associated with changing slices, zoom, or intensities.

Mouse Wheel Action: Allows users to set the action of the middle mouse wheel. Choose from:

Change Slice (default) – Allows users to change the slice display by scrolling the middle mouse button forwards, to move slice display forward, or backwards, to move the slice display backwards.

| | Middle Button Action | ١. |
|---|----------------------------|----|
| | Mouse Wheel Action | Ł |
| | Copy to Clipboard | |
| ¥ | Isotropic | |
| ~ | Color Only Enabled Objects | |
| | Set Object Opacity (50%) | |
| | Label Enabled Objects | |
| ~ | Cursor Link | |
| ~ | Axis Labels | |
| | Border Ruler | |
| | Print | |
| | Reset | |

Max = 3071 Min = 1024

Mouse Wheel Action (continued):

Change Zoom – Allows users to zoom display by scrolling the middle mouse button forwards, to zoom in, or backwards, to zoom out.

Change Intensity Minimum – Allows users to adjust the minimum intensity value by scrolling the middle mouse wheel forwards or backwards.

Change Intensity Maximum - Allows users to adjust the maximum intensity value by scrolling the middle mouse wheel forwards or backwards.

Choose Middle Button Action – Allows users to scroll through the display tools (Slice, Zoom, or Intensity) for the Middle Button action. Selecting a tool will modify the action of the middle mouse button instantly.

Default - returns middle mouse button action back to the system default.

Annotate Changes – Enables and disables the annotations associated with changing slices, zoom, or intensities.

Other Right Menu Options:

Copy to Clipboard – Copies the current slice display to memory.

Isotropic - Active only for anisotropic data. Allows users to toggle between an isotropic or anisotropic display of the data.

Show Enabled Object Only- Available when Region Display is set to Both - Filled Regions and Region Edges. Ignores object Display Off setting.

Color Only Enables Objects – Available when Region Display is set to Filled Regions. The option allows users to enable the display of the object color overlay in the current orientation even if the display of the object is switched off in the Object Control Window. Option updates to Traces or Objects depending on the Region Display setting selected.

Trace Only Enabled Objects- Available in Segment only when Region Edges is enabled. See Segment for further information.

Copy to Clipboard ✓ Isotropic ✓ Color Only Enabled Objects Set Object Opacity (50%)

Middle Button Action

Mouse Wheel Action

- Label Enabled Objects
- Cursor Link
- Axis Labels
 Border Ruler

Print...

Reset

۲

Other Right Menu Options (continued):

Set Object Opacity (50%)- Allows users to adjust the alpha blend of the object color overlay on the grayscale image data. When enabled an Opacity slider is enabled below the current image allowing for interactive adjustment.

Label Enabled Objects – Allows users to enable/ disable the display of object names on the slice display. Note, the keyboard short cut to enable/disable labels is Shift + I.

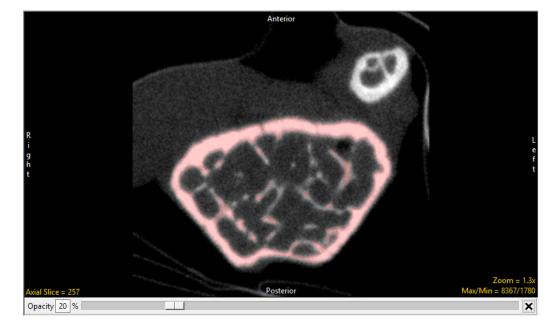
Cursor Link – Toggles the Cursor Link tool Off/On in the current display.

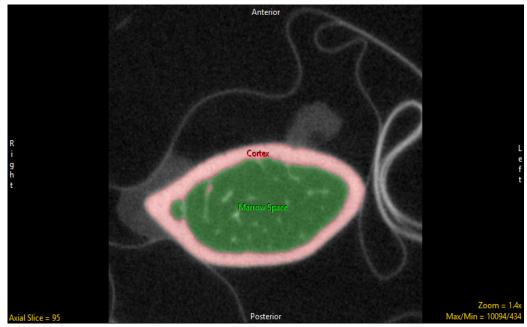
Axis Labels – Allows users to enable or disable the display of the axis labels on the perimeter of the slice display window.

Border Ruler – Enables/Disables the border ruler tool. Green hash marks represent 10mm increments, yellow represents 1mm increments, and blue represents 0.1mm increments.

Print – Sends capture of current slice display to printer.

Reset – Resets all options to default.





Rendering Window and Tools

The default upper right pane of the Image Display Window is the Rendering Window. This window displays a 3D rendering of the image volume

The Rendering Window includes several tools for viewing and navigating through the image data:

(1) Cursor Link tool

(2) Navigation Icon tool

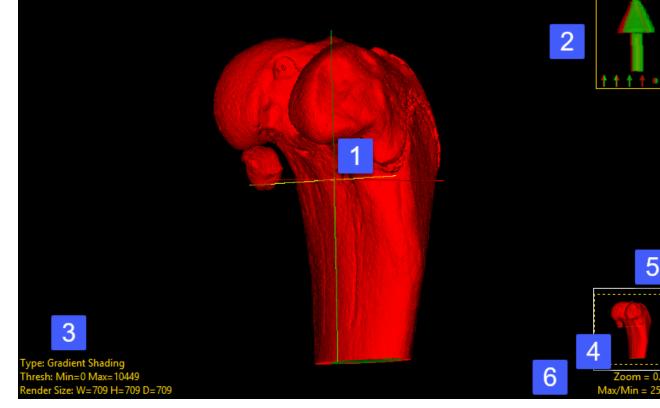
(3) Rotation tool

(4) Zoom tool

(5) Pan tool

(6) Max/Min tool

Cursor Link tool: As described in the Slice Display section above, the cursor link allows users to interactively navigate through the image data. The tool can be controlled from the 3D rendering or from any of the 2D orientations. Moving the tool on the



rendering will interactively update the orthogonal slice displays. The cursor link can be enabled or disabled using the Toggle Cursor Link button.

Navigation Icon tool — The Navigation Icon is a reference for the current orientation of the 3D image data, and also allows users to rotate the data or specify a standard view: front, back, top, bottom. To rotate the data, left-click on the Navigation Icon and hold the left mouse button down. The cursor will update to the

Rotation tool enabling

interactive rotation of the rendering viewpoint. Releasing the left mouse button will dismiss the rotate cursor.



Zoom tool: As with the Zoom tool for the 2D Slice Display, the Zoom tool in the Rendering Window allows users to increase and decrease the display size of the data. For more information refer to the Zoom tool description in the Slice Display section.

Pan tool: The Pan tool is automatically enabled when the Zoom size of the rendering is larger than the current window. Clicking in the tool allows users to Pan the zoomed area over the current display. To enable the Pan tool without zooming right-click on Zoom and select Options and then check Show Pan.'

Max/Min tool: The Maximum and Minimum display intensities for the rendering can be changed by clicking on the yellow Max/Min Tool at the bottom right corner of the 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.

Right Menu Options: Right-clicking in the Rendering Window reveals additional options. Most of these options, if available, are described in the Slice Display section, however, there are few additional configuration options specific to the Rendering window.

Middle Button Action: Allows users to set the action of the middle mouse button. See the Slice Display section for additional information.

Mouse Wheel Action: Allows users to set the action of the middle mouse wheel. See the Slice Display section for additional information.

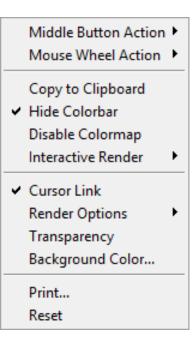
Copy to Clipboard: Copies the current rendering display to memory.

Hide Colorbar: Toggles the Colorbar Off/On in the current display.

Disable Colormap: Disables/Enables the Colormap in the current display.

Interactive Render: Allows users to selects between Reduced Quality (useful for interactive rotation of extremely large image volumes) and Full Quality.

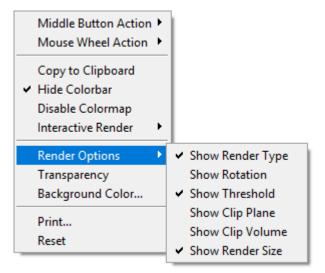
Cursor Link: Toggles the Cursor Link tool Off/On in the current display.



Render Options: Allows users to enable/disable the following rendering options:

Show Render Type: Allows users to view and change the rendering algorithm used to render the image data, choose from Depth Shading, Gradient Shading (default option), Volume Compositing, Maximum Intensity Projection, Summed Voxel Projection, Surface Projections, and Object Compositing. Double click on the Render Type option to cycle through the render types or right-click and choose a specific render type from the right mouse menu. For more information about render types and the render type specific options please refer to the 3D Rendering section of Display.

Show Rotation: Reports the current XYZ rotation angle coordinates. When selected, enables the rotate cursor. Right-click on the tool to choose from rotation default options; Front, Back, Left, Right, Top, and Bottom



Show Threshold: Displays the current Threshold maximum and minimum threshold values. Double clicking allows users to enter values. Right-click to specify Preset values or choose from Analyze Default, Calculated Max/Min, and DataType Max/Min.

Show Clip Plane: Enables the Clip Plane tool allowing users to specify the maximum and minimum depth along the ray path between which voxels are rendered. Clipping is particularly helpful when you need to observe the cross section of a 3D object.

Show Clip Volume: Enables the Clip Volume tool, allowing users to clip the volume with six clip planes (X low, X high, Y low, Y high, Z low, and Z high).

Show Render Size: Displays the current rendering size and allows the user to enter the rendering Width, Height, and Depth. Right click to choose from Default, Maximum Diagonal, Double Diagonal, Axial, Coronal, and Sagittal.

Right Menu Options (Continued):

Transparency: The Transparency option turns transparent rendering on or off. The transparency rendering mode is useful for visualizing objects contained within objects or objects with views obscured by other objects. Object opacity levels can be set using the Opacity options in the Object Control window.

Background Opacity: The Background Opacity option is only available when Transparency rendering is enabled. The option allows users to specify the background opacity for the transparency rendering.

Background Color: Allows users to set the color of the rendering background. The option opens a Color selection window enabling selection of desired color.

Print: Sends capture of current slice display to printer.

Reset: Resets all options to default.

| | Middle Button Action Mouse Wheel Action |) |
|---|--|-------|
| ~ | Copy to Clipboard Hide Colorbar Disable Colormap | |
| | Interactive Render | Þ |
| ~ | Cursor Link | |
| | Render Options | ۲ |
| | Transparency | |
| | Background Color | |
| | Print | |
| | Reset | |

Input/Output

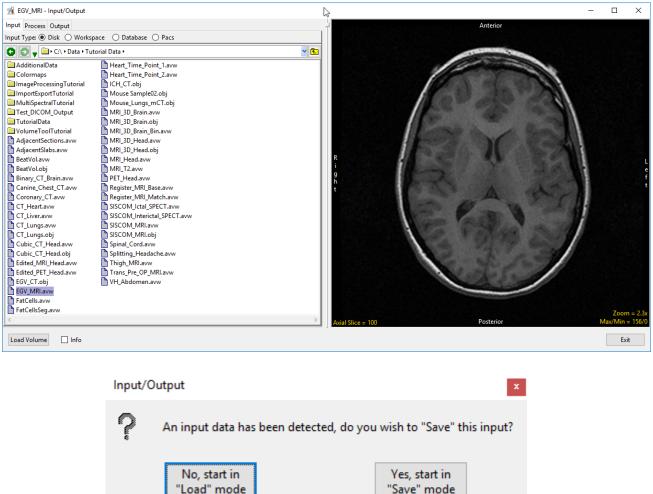
| | Introduction | page 33 |
|-----------------------------|---|--------------------|
| | Supported File Formats | page 34 |
| | The Input/Output Window | page 35 |
| | Input: Loading Data | page 37 |
| | Loading a Single File from Disk | page 37 |
| Loading Multiple 2D DIC | OM files as a 3D Volume from Disk | page 38 |
| Loading Multiple 2D Non-DIC | OM files as a 3D Volume from Disk | page 40 |
| Load | ing Multiple 3D Volumes from Disk | page 41 |
| Loading Multiple 3D Volu | mes as a 4D Multivolume from Disk | page 42 |
| | Loading Data From A Workspace | page 43 |
| Load | ding DICOM Data from a Database | page 44 |
| | Loading DICOM Data from a PACS | page 50 |
| | Process: Transforming Data | page 53 |
| | Organize | page 53 |
| | Intensities | page 56 |
| | Flip/Shift | page 65 |
| | Subregion | page 75 |
| | Cropping 4D Data | page 77 |
| | Resize | page 78 |
| | Pad/Orient | page 81 |
| | Output: Saving Data | page 85 |
| Ol | pening Input/Output in Save Mode | page 85 |
| | | |
| | Saving a Data Set | page 86 |
| | Saving a Data Set Storing Data in a Database | page 86 page 87 |
| 5 0 Uporto Guido | - | • |

Introduction

The Input/Output module centralizes the loading and saving of image data in Analyze 15.0. Input/Output supports the loading of 51 file formats including standard Analyze file formats, common radiological and neurological formats, vender specific file formats, 2D desktop publishing formats, and video formats (see table on next page).

The Input/Output module has two modes; Load mode and Save mode. Load mode is the default mode for the module while Save mode is enabled when a data set is selected in the workspace when Input/Output is opened.

If a data set is selected in the workspace when Input/Output is opened the module will prompt you to choose to start in Load mode or Save mode. Selecting Yes, will start the module in Save mode enabling the saving of the selected image.



| Formats | AnalyzeAVW | OBJMAP | AVW_VolumeFile | Analyzelmage(7.5) | AnalyzeScreen | UNKNOWN | DICOM | NIFTI | DJD | 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 | BMP | PostScript | SMIS | PNG | UMX | IMATRON | BIORAD | QUICKTIME | ITK | AVI | MPEG1 | VARIANFDF | VOX | VSI |
|-----------------|------------|------------------------|----------------|-------------------|---------------|---------|-------|-------|-----|-----------|-----|----------|---------|-----------|--------------|--------------|--------------|-----------|--------------|--------------|-----|--------------|-------|-----|-----|-----------|-----------|---------------|----------|------------------------|------------------------|-----------------------|-------------------|------------------------------|------------|------------|-------------------|-----------------|--------------|--------------|--------------|--------------|-----------|-----|--------------|----------|-----------|-----------------------|----------------------|
| Read | X | \times | X | X | X | X | X | X | X | X | X | X | X | X | X | | \mathbb{X} | | \mathbf{X} | \mathbb{X} | X | X | X | X | X | X | X | X | \times | $\left \right\rangle$ | \times | $\left \right\rangle$ | $\langle \rangle$ | $\langle \rangle$ | \Diamond | \bigcirc | | $\left \right>$ | \mathbf{i} | \mathbf{i} | \mathbf{X} | \mathbb{X} | X | X | \mathbb{X} | \times | \times | \times | \langle |
| Write | X | $\left \right\rangle$ | X | X | X | X | X | | X | X | | | | | | | | | X | \mathbb{X} | X | X | X | X | X | | | | X | | $\left \right\rangle$ | $\left \right $ | | | \langle | | $\langle \rangle$ | | X | \mathbf{i} | | | X | X | X | | | | |
| 2D | X | X | X | X | X | X | X | X | X | X | X | X | X | X | X | | \mathbb{X} | | \mathbb{X} | \mathbb{X} | X | \mathbb{X} | X | X | X | X | X | X | X | X | X | $\langle \rangle$ | $\langle \rangle$ | $\langle \rangle$ | \bigcirc | \bigcirc | \bigcirc | \land | \mathbb{N} | \searrow | \mathbb{X} | X | X | X | | | X | \times | $\left \right $ |
| 3D | X | X | X | Х | X | X | | X | | | X | X | | X | | | \setminus | | | | | | | | | | | | | X | | $\left \right\rangle$ | $\langle \rangle$ | $\left(\right)$ | | | | $\left \right>$ | | | X | \mathbb{X} | X | X | \mathbb{X} | \times | X | \times | \langle |
| 4D | X | X | | Х | | X | | X | | | X | X | | X | | | | X | | | | | | | | | | | | | | | | | | | | \setminus | | | X | | | X | | | | | $\left \right $ |
| Unsigned 8-bit | X | X | X | Х | X | X | X | X | X | X | X | X | | X | | | X | | \mathbf{X} | \mathbb{X} | X | X | X | X | X | | | | | X | \times | $\left \right\rangle$ | \bigwedge | $\langle \rangle$ | \bigcirc | \bigcirc | \bigcirc | \bigcirc | \mathbf{i} | \mathbf{i} | | X | X | X | | | X | \times | \langle |
| Signed 8-bit | X | | X | | | X | | X | | | | | | | | | | | | | | | | | X | | | | | | | | | | | | | | | | | | X | X | | | X | | |
| Unsigned 16-bit | X | | X | | | X | X | X | | | | | | | | | | | \setminus | | | | | | X | | | | | | | | | | | | | | | | | | | X | | | X | | $\overline{\langle}$ |
| Signed 16-bit | X | | X | Х | | X | X | X | | | X | X | X | X | X | \mathbb{X} | \mathbb{X} | | \mathbf{X} | | | | | | X | X | X | X | | X | | | $\langle \rangle$ | $\left\langle \right\rangle$ | | | | \setminus | | | X | \mathbb{X} | | X | | | \times | $\left \right\rangle$ | \langle |
| Unsigned 32-bit | X | | X | | | X | | Х | | | | | | | | | | | | | | | | | X | | | | | | | | | | | | | | | | | | | X | | | X | | |
| Signed 32-bit | X | | X | Х | | X | | Х | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | X | | | X | | |
| Float | X | | X | X | | X | | X | | | X | X | | Х | | | | | | | | | | | X | | | | | | | | | | | | | \setminus | | | | | | X | | | X | | $\overline{\langle}$ |
| Double | X | Í | ľ | | | X | | X | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Complex | X | | \times | X | | | | X | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| RGB | X | | X | X | X | X | X | X | X | X | | | | | | | | | \setminus | | | X | X | | X | | | | X | | | | | | \langle | \rangle | \land | | X | \mathbf{i} | | | X | | X | X | | | |

File Formats and Attributes Supported by Analyze 15.0

The Input/Output Window

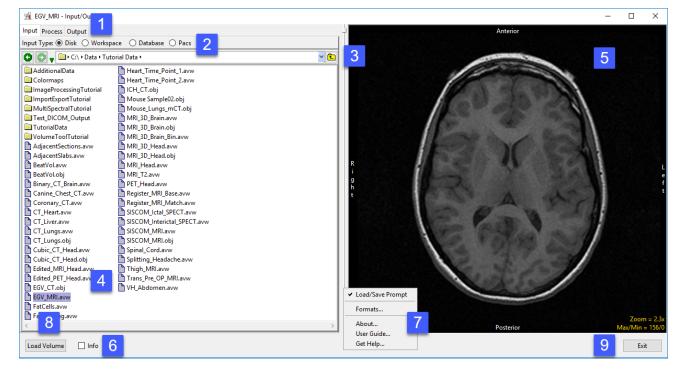
The Input/Output windows consists of the following nine sections:

1. Mode tabs: Allows user to select the mode for the Input/Output module from the following:

Input: Sets Input/Output to Load mode for loading data into Analyze.

Process: Provides tools for processing of image data, available for both load and save modes.

Output: Sets Input/Output to Save mode for exporting data from Analyze.



2. Input Types: Select the location to load data from or save data to.

Disk: Allows data to be selected and loaded from the system's local disks or network drives.

Workspace: Allows data to be selected and loaded from a workspace.

Database: Allows DICOM data to be imported into a database, selected and loaded into Analyze. For Save mode allows DICOM data to be stored in the database for export out of Analyze.

PACS: Allows for the configuration of Query/Retrieve (Q/R) of DICOM image data from PACS.

Analyze 15.0 User's Guide

3. Directory selector: Enables users to navigate to the location of the data to be loaded.

4. File selection area: Allows users to select the desired data sets for loading.

5. Image display: Provides a display for data review of the selected image file prior to loading.

6. Info option: When checked displays the header information for the selected file.

7. Right-mouse options:

Load/Save Prompt: Enable/Disable Load/Save Prompt (Figure 3.2)

Formats: Displays list of supported file formats and associated properties.

About - The About option opens the Analyze 15.0 About window. The About window provides detailed information about the system and the Analyze software. Selecting Done will close the About window.

User Guide - The User's Guide option opens this User Guide.

Get Help - Directs you to the AnalyzeDirect website support pages.

8. Load Volume: Loads the selected file into the current workspace.

9. Exit: Closes the Input/Output module.

| Properties Read 2D Unsigned 8-bit Signed 8-bit Write 3D Unsigned 16-bit Signed 32-bit 4D Unsigned 32-bit Signed 32-bit Float Double Complex RGB OBJMAP Analyzelmage(7.5) AnalyzeScreen JPG SunRaster CTI GE Advantage GESigna GESTARCAM INTERFILE TIFF PBM PGM PPM TARGA SiemensCT SIEMENSMAGVIS YUV ACRNEMA DICOM GIF ANIMATEDGIF PAPYRUS2 PAPYRUS3 SGIgb SGIbw BMP PostScript SMIS PNG QUICKTIME ITK AVI MPEG1 VSI VSI | 🕺 Supported Fo | rma | ts - Input/Ou | _ | |
|--|---|-----|--|------|--|
| AnalyzeAVW UNKNOWN AVW_VolumeFile OBJMAP AnalyzeImage(7.5) AnalyzeScreen JPG SunRaster CTI CTIECAT7 GE9800 GEADVANCE GE Advantage GESigna GESTARCAM INTERFILE TIFF PBM PGM PPM TARGA SiemensCT SIEMENSMAGVIS YUV ACRNEMA DICOM GIF ANIMATEDGIF PAPYRUS2 PAPYRUS3 SGlrgb SGIbw BMP VWD IMATRON BIORAD QUICKTIME ITK AVI MPEG1 VARIANFDF NIFTI | Write 3 | D | Unsigned 8-1 Unsigned 16 Unsigned 32 Float Complex | -bit | Signed 16-bit |
| OBJMAPAnalyzelmage(7.5)AnalyzeScreenJPGSunRasterCTICTIECAT7GE9800GEADVANCEGE AdvantageGESignaGESTARCAMINTERFILETIFFPBMPGMPPMTARGAXBMPICPICKERMRISiemensCTSIEMENSMAGVISYUVACRNEMADICOMGIFANIMATEDGIFPAPYRUS2PAPYRUS3SGIrgbSGIbwBMPPostScriptSMISPNGXWDIMATRONBIORADQUICKTIMEITKAVIMPEG1VARIANFDFNIFTI | _ | | | | |
| | OBJMAP JPG CTIECAT7 GE Advantage INTERFILE PGM XBM SiemensCT ACRNEMA ANIMATEDGIF SGIrgb PostScript XWD QUICKTIME | | Analyzelmage(7.5) SunRaster GE9800 GESigna TIFF PPM PIC SIEMENSMAGVIS DICOM PAPYRUS2 SGIbw SMIS IMATRON ITK | | AnalyzeScreen CTI GEADVANCE GESTARCAM PBM TARGA PICKERMRI YUV GIF PAPYRUS3 BMP PNG BIORAD AVI |

Input: Loading Data

Loading a Single File from Disk

Input type: Disk

To load a single 2D image, a 3D volume, or 4D multivolume into Analyze:

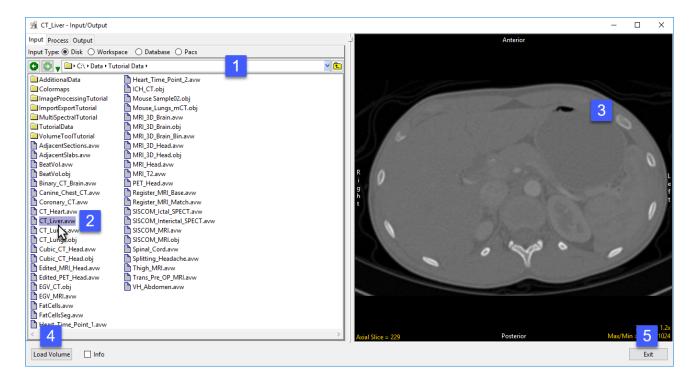
Open Input/Output.

Navigate to the data [1] and select the data set you want to load [2]. See table at beginning of this chapter for supported file formats.

Note that the data will be displayed. [3]

Click Load Volume [4] to load the data. The selected data set will be loaded into Analyze 15.0.

Click Exit [5] to close Input/Output.



Loading Multiple 2D DICOM Files as a 3D Volume from Disk

Input type: Disk

To load multiple 2D DICOM files as a single 3D volume from a folder on your system, Analyze provides an InMemory DICOM Database function. To generate the information needed to provide the necessary patient/study/series user interface for selecting DICOM volumes, do the following:

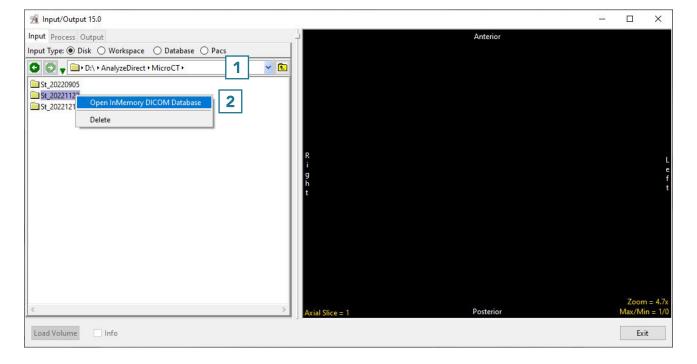
Open Input/Output.

Navigate to the directory that

contains the DICOM image folder. [1]

NOTE: Do NOT navigate into a folder that contains the DICOM image files (.dcm files). In the example figure above, the directory to navigate to is named "MicroCT", as this directory contains the DICOM image folders.

Next, perform a right-mouse click on a folder containing DICOM files (which in the example above is named "St_20221122") and select "Open InMemory DICOM Database". This quickly creates a temporary in-memory DICOM database which imports all the DICOM files found in the folder selected, including subfolders within.



Loading Multiple 2D DICOM Files as a 3D Volume from Disk (continued)

When the temporary in-memory database is created, the input type is automatically changed from Disk to Database [3].

Once the process is complete, the patient/study/series user interface is displayed [4].

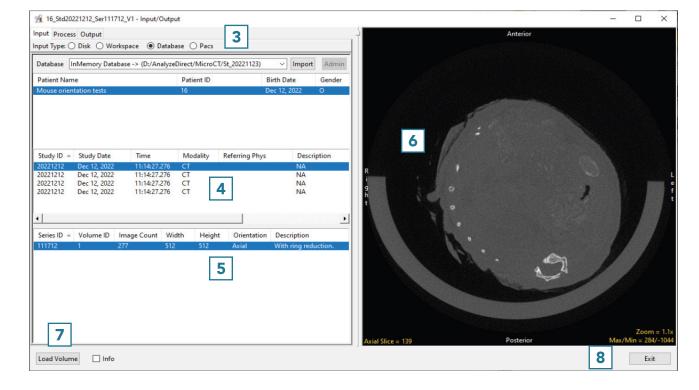
Any of the studies can be selected, and the series contained within a study will be displayed in the series pane [5].

Click on the desired volume within the series pane to see it displayed [6].

Click Load Volume [7] to load the desired series into Analyze as a single 3D volume.

Click Exit [8] to close Input/Output.

NOTE: For importing and loading of 2D DICOM files using a persistent DICOM database (rather than the temporary in-memory database method shown here), please refer to page 44.



Loading Multiple 2D Non-DICOM Files as a 3D Volume from Disk

JIEE00 - Input/Output

Input type: Disk

Frequently, scanner vendors do not support exporting data in a single 3D format and choose instead to export data as a series of 2D images such as TIFF or BMP. To load a series of 2D images into Analyze as a single 3D volume:

Open Input/Output.

Navigate to the series of 2D image files. [1]

To select a range of Image files, first

choose the first image in the series, then press the Shift key and finally select the last data set in the range [2]. Alternatively, select ctrl + a to select all files in the directory.

By default, all selected images will be treated as a single volume [3]. Other load options, such as loading a series of 2D images individually, are available from Process > Organize.

Click Load Volume [4] to load the data into the software as a single 3D volume.

Click Exit [5] to close Input/Output.

| M IIFF00 - Input/Output | | |
|--|--|----------------------|
| Input Process Output | Treating Multiple Images as Single Volume Other Options available in Process-> Organize | |
| Input Type: Disk Workspace Database Pacs | Other Options available in Process-> Organize | |
| 🕒 💽 🖕 🗀 • C:\ • Data • Tutorial Data • VolumeToolTutorial • | | |
| TIFF0000.tif TIFF0027.tif TIFF0054.tif TIFF0081.tif | TIFF0108.tif TIFF0135.tif TIF | |
| TIFF0001.tif TIFF0028.tif TIFF0055.tif TIFF0082.tif | TIFF0109.tif TIFF0136.tif TIF | |
| TIFF002.tif TIFF0029.tif TIFF0056.tif TIFF0083.tif | TIFF0110.tif TIFF0137.tif TIF | |
| TIFF0003.tif TIFF0030.tif TIFF0057.tif TIFF0084.tif | 🗅 TIFF0111.tif 🗋 TIFF0138.tif 🗋 TIF | |
| TIFF0004.tif TIFF0031.tif TIFF0058.tif TIFF0085.tif | TIFF0112.tif TIFF0139.tif TIF | |
| TIFF0005.tif TIFF0032.tif TIFF0059.tif TIFF0086.tif | TIFF0113.tif TIFF0140.tif TIF | |
| TIFF0006.tif TIFF0033.tif TIFF0060.tif TIFF0087.tif | TIFF0114.tif TIFF0141.tif TIF | |
| TIFF0007.tif TIFF0034.tif TIFF0061.tif TIFF0088.tif | TIFF0115.tif TIFF0142.tif TIF | |
| TIFF008.tif TIFF0035.tif TIFF0062.tif TIFF0089.tif | TIFF0116.tif TIFF0143.tif TIF | |
| TIFF0009.tif TIFF0036.tif TIFF0063.tif TIFF0090.tif | 🗅 TIFF0117.tif 🗋 TIFF0144.tif 🗋 TIF | |
| TIFF0010.tif TIFF0037.tif TIFF0064.tif TIFF0091.tif | TIFF0118.tif TIFF0145.tif TIF R | |
| TIFF0011.tif TIFF0038.tif TIFF0065.tif TIFF0092.tif | TIFF0119.tif TIFF0146.tif TIF | e |
| TIFF0012.tif TIFF0039.tif TIFF0066.tif TIFF0093.tif | | f |
| TIFF0013.tif TIFF0040.tif TIFF0067.tif TIFF0094.tif | ∠)121.tif L TIFF0148.tif L TIF t | t |
| TIFF0014.tif TIFF0041.tif TIFF0068.tif TIFF0095.tif | 🗖 TIFF0122.tif 🗋 TIFF0149.tif 🗋 TIF | |
| TIFF0015.tif TIFF0042.tif TIFF0069.tif TIFF0096.tif | 🗅 TIFF0123.tif 🕒 TIFF0150.tif 🕒 TIF | |
| TIFF0016.tif TIFF0043.tif TIFF0070.tif TIFF0097.tif | TIFF0124.tif TIFF0151.tif TIF | |
| TIFF0017.tif TIFF0044.tif TIFF0071.tif TIFF0098.tif | TIFF0125.tif TIFF0152.tif TIF | |
| TIFF0018.tif TIFF0045.tif TIFF0072.tif TIFF0099.tif | TIFF0126.tif TIFF0153.tif TIF | |
| TIFF0019.tif TIFF0046.tif TIFF0073.tif TIFF0100.tif | TIFF0127.tif TIFF0154.tif TIF | |
| TIFF0020.tif TIFF0047.tif TIFF0074.tif TIFF0101.tif | TIFF0128.tif TIFF0155.tif TIF | |
| TIFF0021.tif TIFF0048.tif TIFF0075.tif TIFF0102.tif | TIFF0129.tif TIFF0156.tif TIF | |
| TIFF0022.tif TIFF0049.tif TIFF0076.tif TIFF0103.tif | TIFF0130.tif TIFF0157.tif TIF | |
| TIFF0023.tif TIFF0050.tif TIFF0077.tif TIFF0104.tif | TIFF0131.tif TIFF0158.tif TIF | |
| TIFF0024.tif TIFF0051.tif TIFF0078.tif TIFF0105.tif | 🗅 TIFF0132.tif 🕒 TIFF0159.tif 🗋 TIF | |
| TIFF0025.tif TIFF0052.tif TIFF0079.tif TIFF0106.tif | TIFF0133.tif TIFF0160.tif | |
| TIFF0025.tif TIFF0053.tif TIFF0080.tif TIFF0107.tif | 🖿 TIFF0134.tif 🚹 TIFF0161.tif | 2.5x |
| < 4 | Axial Slice = 49 Posterior Max | x/ 5 ^{2.5x} |
| Load Volume | | Exit |

Loading Multiple 3D Volumes from Disk

MRI - Input/Output

Input Type:
Disk O Workspace O Database O Pacs

🗌 Info

Load Volume

Input Process Output

Input type: Disk

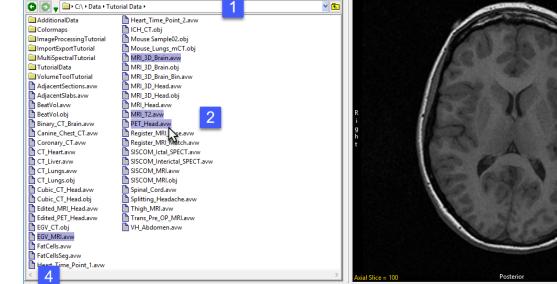
To load multiple 3-D volumes into the program simultaneously:

Open Input/Output. Navigate to the location of the image data. [1].

To select multiple data sets, hold down the Ctrl key and select each data set to load. [2].

If the data select has different properties (spatial dimensions, volume sizes, data types, etc.) the module will recognize this and treat the selected data sets as separate volumes [3]. Note that if the properties of the selected data sets are the same the module will default to load as a single multivolume. Click Load Volume to load all selected volumes.

Click Exit to close the module [4].



Exit

Loading Multiple 3D Volumes as a 4D Volume from Disk

Input type: Disk

Analyze 15.0 supports 4D image data sets or multivolumes. Multivolumes are data sets that that consist of multiple 3D volumes. Multivolume loading is automatically enabled when loading multiple volumes that have the same Voxel Dimensions and Datatype. To load a series of volumes as a multivolume:

Open Input/Output.

Navigate to the location of the image data. [1].

To select multiple data sets, hold down the Ctrl key and select each data set to load. [2].

As these data sets have the same

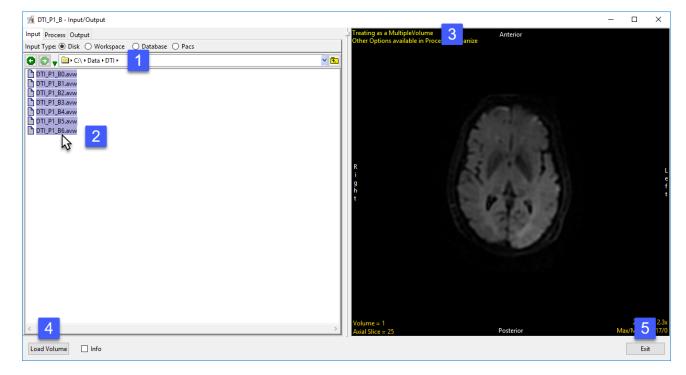
properties the module will default

to loading the data as a single

multivolume [3].

Click Load Volume to load all selected volumes [4].

Click Exit to close the module [5].

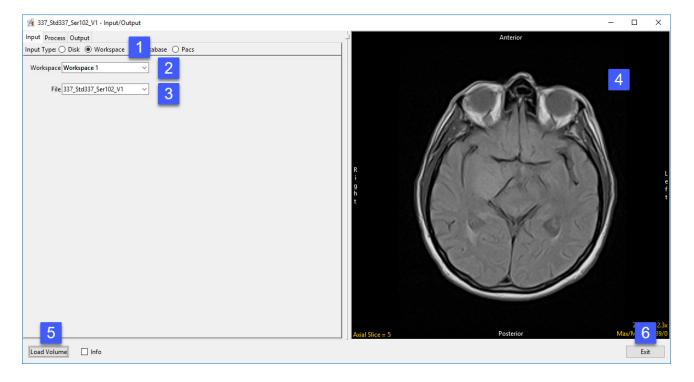


Loading Data From A Workspace

Input Type: Workspace

Input/Output supports the loading of image data from one workspace to another. To load data from a workspace into the current workspace (the workspace selected when Input/ Output was opened):

Open Input/Output. Use the Workspace drop-down menu to select a Workspace. [1]. Use the File drop-down menu to select a data set [2]. The selected data to be previewed in the Display window [3]. Click Load Volume to load the selected file to the current workspace [4]. Click Exit to close the module [5].



Loading DICOM Data from a Database

Input Type: Database

The Database input option is for the import of DICOM image data into Analyze 15.0. The Database option enables the indexing of collections of DICOM images through a local database file. To create a database and for DICOM data import:

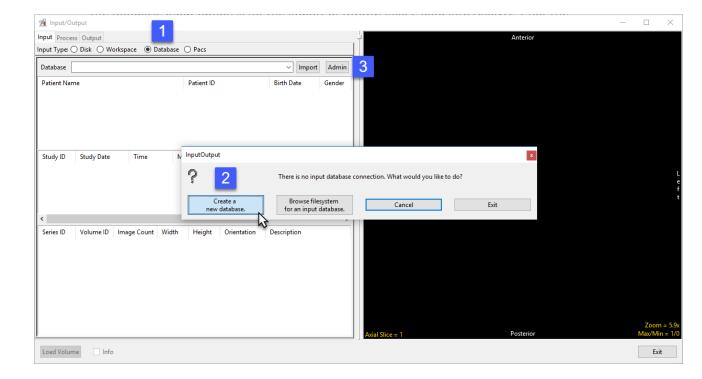
Open Input/Output.

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].



Note: If you have used previous versions of Analyze or AnalyzePro and have created DICOM databases you can use the 'Browse filesystem for an input database' to navigate to and select a .adb file. If this window is not returned or if this is not the first time you have opened the Database option, select Admin button [3] to open the Administer Databases window and create a new database.

The Administer Database(s) window will open.

Name the database [3] and set the location where the database will be saved. [4].

| Administer Database(s) | | x |
|--|---|--------------------|
| | ^ | Create Database |
| | | Configure Database |
| | ~ | Delete Database |
| Database Name Analyze 3 | | |
| Database Directory C:\Databases 4. | | |
| DICOM Communication O Enable Disable | | |
| Cancel | | Create |

Administer Database(s)

Enabling DICOM Communications (optional)

A DICOM receiver can be configured for the database. The receiver will run as a Windows service or Unix daemon and will actively listen on a specified port for DICOM image data to be pushed to it from PACS or any other DICOM node. 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.

Once configured on PACS you will be able to push DICOM image data from PACS to the Analyze 15.0 database. Note that if DICOM data is not being received after pushing from PACS you may need to open the port number for the Receiver on your system's firewall.

Click Create. [8].

| | ^ |
|-------------------------------------|-------------------|
| | Create Database |
| | |
| | Configure Databas |
| | |
| | Delete Database |
| 1 | ~ |
| Database Name Analyze | |
| Database Directory C:\Databases | |
| DICOM Communication Enable 5 able | |
| Receiver/STORESCP | 2 |
| Port: 8888 AET Name: Analyze_8888 | 0 |
| 6 7 | Create |

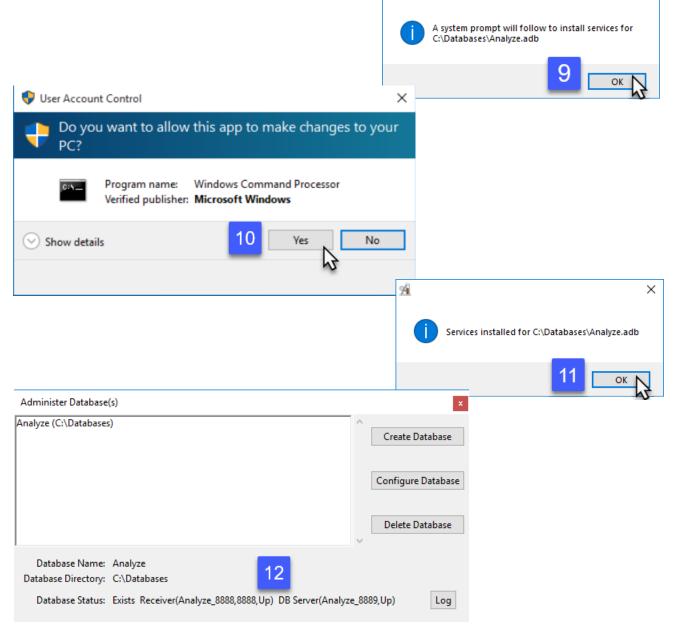
x

For Windows users an informational window will be returned informing your that a system prompt will follow to install services for the database. Click OK. [9]

In the Windows User Account Control prompt returned click Yes [10] to allow the program to install the receiver service.

Dismiss the service installed confirmation message by clicking OK [11].

Details about the receiver, as well as the associated database server, configured for the database are displayed at the bottom of the Administer Database(s) window [12]. Close the window.



94

Х

Importing Images

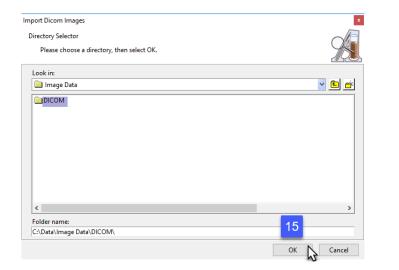
Once the Database is configured you can now start importing DICOM image data.

Click the Import button [13] or rightclick in the window and select Import DICOM Images. [14]

Use the Directory Selector to navigate to the location of the DICOM images to import and click OK. [15]

A window will open stating Import all DICOM files found below <the specified folder>; click Yes. [16]

| Database C:\Databases\Analyze.adb | | ✓ Import 13 n | | | |
|-----------------------------------|---|-------------------|-----------------------|-----------|-----------------|
| Patient Name | Patient ID Refresh Auto Refresh | Birth Date Gender | | | |
| Study ID Study Date Time | Mo Configure Columns Configure Filter Show Database Info Import Dicom Images Update DB | Description | R i 9 h t | | |
| < | | > | | | |
| Series ID Volume ID Image Count V | fidth Height Orientation | Description | | | |
| | | | Axial Slice = 1 | Posterior | Zoom Max/Min |





Loading **DICOM** Images

Once import is complete, the image data will be available in the database.

To load a DICOM volume, select the desired patient, study and series volume to see it displayed.

Click Load Volume [17] to load the desired series into Analyze 15.0.

NOTE: To load multiple 2D DICOM images as a 3D volume without using a persistent DICOM database, please refer to page 39.

| Database C | C:/Databases/Ar | nalyze.adb | | | | ~ Import | t Admin |
|--------------------|-----------------|-------------|-------|------------|----------------|----------------------|---------|
| Patient Nam | ie | | | Patient ID | | Birth Date | Gender |
| MR SIGN <u>A C</u> | ONTOUR 0.5T | | | 11 | | NA | F |
| MR SIGNA L) | X 1.0T | | | 337 | | NA | F |
| MR SIGNA L) | | | | 930 | | NA | F |
| MR SIGNA L) | | | | 28 | | NA | 0 |
| MR SIGNA PI | | | | 93 | | NA | м |
| MR dataset B | | | | reg2 | | Jan 01, 1911 | м |
| ULTRASOUN | ID GE | | | 000-00-000 | 00 | NA | F |
| Study ID 🔺 | Study Date | Time | Mo | dality F | Referring Phys | Description | |
| 11 | Apr 02, 1997 | 13:57:45 | MR | | MELOFF | e+1 MR BRA | IN |
| | | | | | | | |
| Serier ID a | Volume ID | Image Count | Width | Height | Orientation | Description | > |
| Series ID 🔺 | | Image Count | | Height | Orientation | Description | |
| Series ID × 200 | 1 | 18 | 256 | 256 | Axial | C5,1,4.5,0.7,1.1,0.0 | 85,108 |
| Series ID 🔺 | 1 | - | | - | | | 85,108 |
| Series ID × 200 | 1 | 18 | 256 | 256 | Axial | C5,1,4.5,0.7,1.1,0.0 | 85,108 |
| Series ID × 200 | 1 | 18 | 256 | 256 | Axial | C5,1,4.5,0.7,1.1,0.0 | 85,108 |
| Series ID × 200 | 1 | 18 | 256 | 256 | Axial | C5,1,4.5,0.7,1.1,0.0 | 85,108 |
| Series ID × 200 | 1 | 18 | 256 | 256 | Axial | C5,1,4.5,0.7,1.1,0.0 | 85,108 |
| Series ID × 200 | 1 | 18 | 256 | 256 | Axial | C5,1,4.5,0.7,1.1,0.0 | 85,108 |
| Series ID × 200 | 1 | 18 | 256 | 256 | Axial | C5,1,4.5,0.7,1.1,0.0 | 85,108 |
| Series ID × 200 | 1 | 18 | 256 | 256 | Axial | C5,1,4.5,0.7,1.1,0.0 | 85,108 |
| Series ID × 200 | 1 | 18 | 256 | 256 | Axial | C5,1,4.5,0.7,1.1,0.0 | 85,108 |
| Series ID × 200 | 1 | 18 | 256 | 256 | Axial | C5,1,4.5,0.7,1.1,0.0 | 85,108 |
| Series ID × 200 | 1 | 18 | 256 | 256 | Axial | C5,1,4.5,0.7,1.1,0.0 | 85,108 |

Loading DICOM Data from a PACS

Input Type: PACS

The PACS Input Type option allows users to configure Query and Retrieval of DICOM data from PACS. To set up communications to allow Query and Retrieval of DICOM data from PACS, first create a database, see previous section: Importing DICOM Data > Creating a Database, then:

Remote AET Configuration

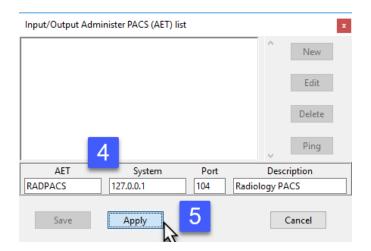
Open Input/Output.

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.

| 🔏 Input/Output | | | _ | |
|---|---|------------------------------------|-----------|-----------------------------|
| Input Process Output Input Type: O Disk O Workspace O Database Pacs Remote AET PACS/AET Query/Return AET LAPTOP-LBTHHAH2_MOVESCU System LAPTOP-LBTHHAH2 | | 2 | Anterior | |
| Query values Patient ID Study Date Find Clear Patients Name ID | Input/Output Administer PACS (AET) list | X New Edit Delete Ping | | |
| < Patient Study Series Study Series Series Series Study Series SeriesSeries Series | Save Apply | Cancel | Posterior | Zoom = 5.8 Max/Min = 1/0 |
| Retrieve Info | | | | Exit |



Loading DICOM Data from a PACS (continued)

The window will update and the PACS information will be available in the main window. [6].

Click Save to close the window [7].

Local Query/Retrieve AET Configuration

For Analyze 15.0 to successfully query and retrieve DICOM image data from PACS a local MOVESCU service needs to be configured.

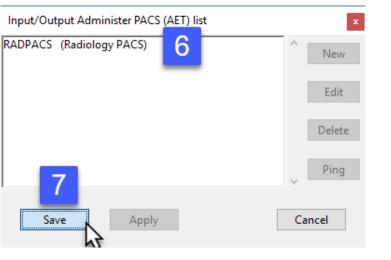
Under Query/Return AET click the Propertied button. [8]

In the window returned enter the Q/R AET.

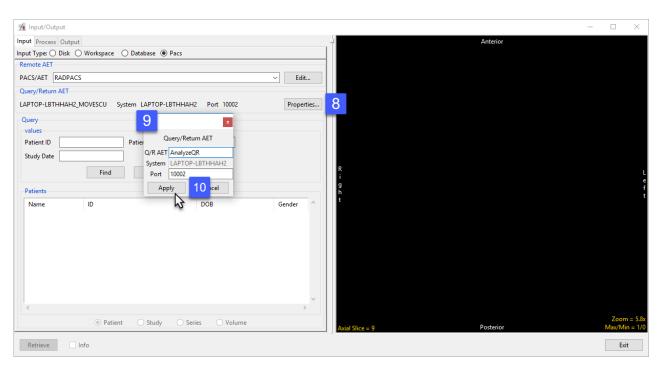
Note: The AET should not be over 16 alphanumeric characters.

Enter the Port number Q/R will use and then click Apply. [10]

Make a note of the Q/R AET and Port number. Your PACS administrator will need this information along with the systems IP address to configure Q/R on PACS.



Note: There may be additional configuration required on the PACS side by your PACS admin. Also, your systems Firewall may need to be configured to allow Inbound and Outbound communication for the Remote AET port and local Query/Return AET port prior to successful Q/R of DICOM image data from PACS.



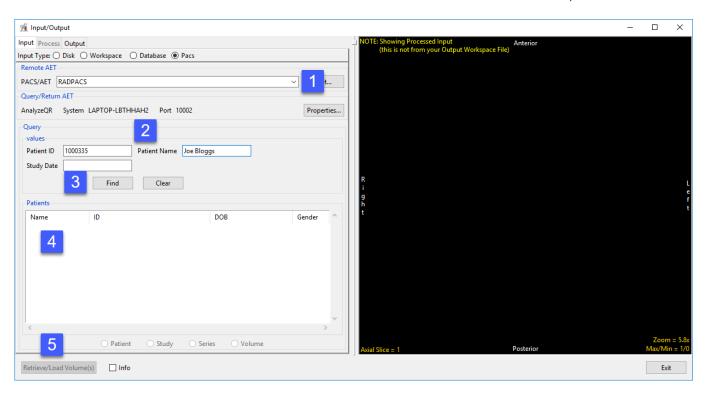
Loading DICOM Data from a PACS (continued)

Note: There may be additional configuration required on the PACS side by your PACS admin. Also, your systems firewall may need to be configured to allow Inbound and Outbound communication for the Remote AET port and local Query/Return AET port prior to successful Q/R of DICOM image data from PACS.

Querying and Retrieving DICOM data from PACS

To Query PACS, choose which PACS to query using the drop-down menu under Remote AET [1]. Under Query enter the Patient ID, Patient Name or Study Date [2] and click Find [3]. The relevant patient data will displayed under Patients. [4].

Select the patient and click Retrieve/Load Volume(s) [5] to load the selected data into the current workspace.



Process: Transforming Data

Spatial- and intensity-based transformations can be applied to the data while loading to or saving from Analyze 15.0. These transformation options are available from Input/Output > Process, once a data set is selected.

Organize

MultiVolume Override

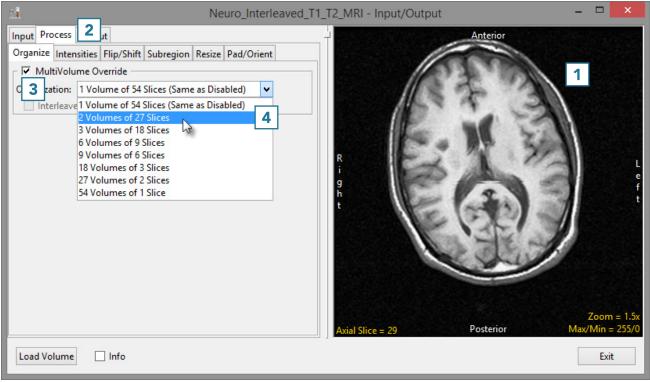
Sometimes image data may not be organized as expected. For example, two 3D data sets may be concatenated into a single 3D data set, requiring the data to be split into two volumes. Furthermore, the data may be interleaved. The MultiVolume Override options provide a utility to efficiently reorganize such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

Organize (continued)

- 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.

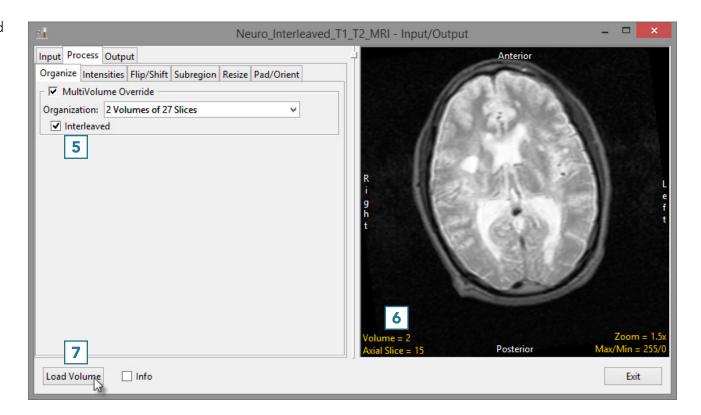
We know that in this example the 54-slice data set is comprised of a T1 and a T2 data set, each containing 27 slices. Select the appropriate option from the drop-down menu: 2 Volumes of 27 Slices [4].





Organize (continued)

- 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.



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

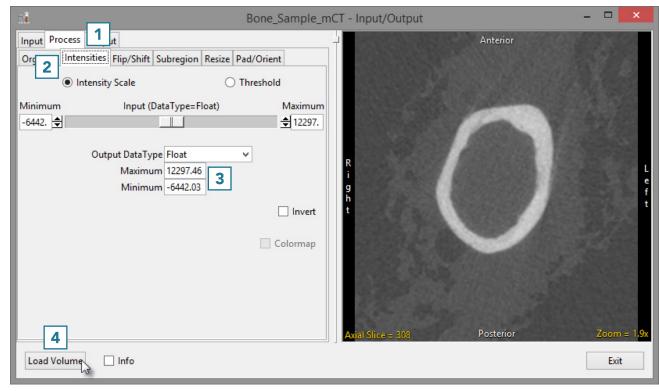
Changing the image data type can reduce the size of the data on disk. In this example, a microCT data set has a data type of Float. The size of the image data when loaded into AnalyzePro is 92.71 MB. Changing the data type to Signed 16-bit reduces the size of the data set by about 50% to 46.35 MB when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

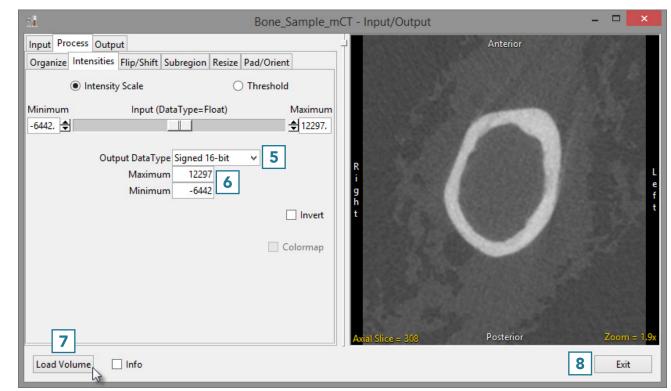
Analyze 15.0 User's Guide



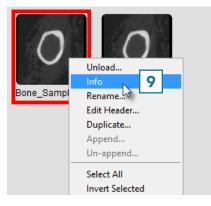
Download the Bone_Sample_mCT data set to follow along http://analyzedirect.com/data/



- 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].



- 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_mCTI Bone_Sample_mCT0 | Bone_Sample_mCT Bone_Sample_mCT0 |
|---|---|
| <pre>FileName=C:\temp\APRO\Michael\Bone_Sample_mCT.mmap DataType=AVW_FLOAT (32-bit float)</pre> | <pre>FileName=C:\temp\APRO\Michael\Bone_Sample_mCT0.mmap DataType=AVW_SIGNED_SHORT (16-bit signed)</pre> |
| Width=190 Height=208 Depth=615 | Width=190 Height=208 Depth=615 |
| NumVols=1 | NumVols=1 |
| Size=92.71 Mb | Size=46.35 Mb |
| <pre>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 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"</pre> | 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" |

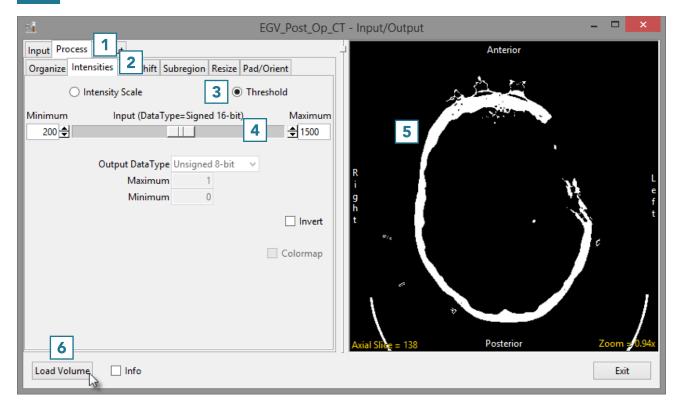
Threshold Scaling

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 Analyze.
- 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.



Info

Load Volume

EGV_Pre_Op_MRI - Input/Output -1 Input Process Anterior Organize Intensities Flip/Shift Subregion Resize Pad/Orient Intensity 2 O Threshold Minimum Input (DataType=Signed 16-bit) Maximum \$115 5 0 🗢 Output DataType Signed 16-bit ¥ Maximum 766 0 Minimum ឲ្យ ភ 4 Invert ÷ Colormap 3 Posterior Zoom = 1.5x Axial Slice = 100

Exit

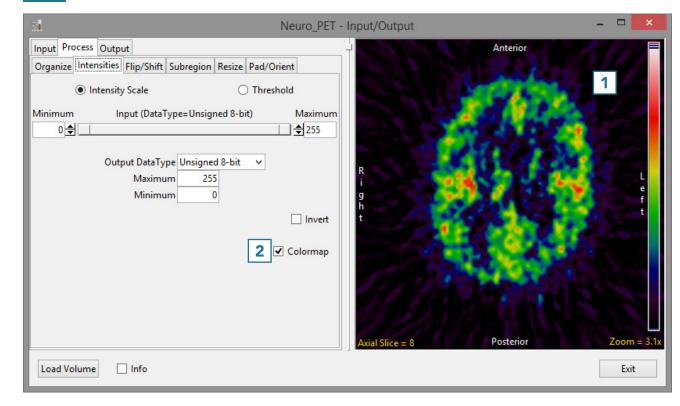
When loading a data set that has an associated colormap [1], the Colormap

checkbox will be selected [2].

Colormaps



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]

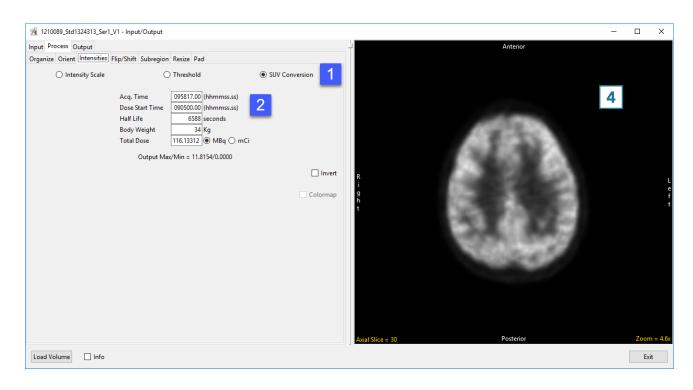
Note that the image display will update to show the grayscale data [4].

• To load the data, click Load Volume [5].

| Input Process Output Organize Intensities Flip/Shift Subregion Resize Pad/Orier Intensity Intensity Scale O Threshold | Anterior | 677. |
|---|---|--------------------------|
| Minimum Input (DataType=Unsigned 8-bit) | A Maximum €255 R i g | 4 L e |
| 3 C Load Volume Info | Invert h colormapi Axial Slice = 8 Posterior | t Zoom = 3.0x Exit |

Standard Uptake Value Conversion

The Standard Uptake Value (SUV) in PET data is defined as the ratio of activity in tissue per millimeter to the activity in the injected dose per patient body weight. When PET data is loaded into Analyze via the Input/ Output Database a new Intensity option 'SUV Conversion' appears, [1] the scale factors present in the DICOM header information with the PET data are used to automatically scale the data into units of activity per millimeter. [2] Any sampling of the PET data conducted in Analyze, such as ROI analysis, will provide values in this calibrated range.



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.

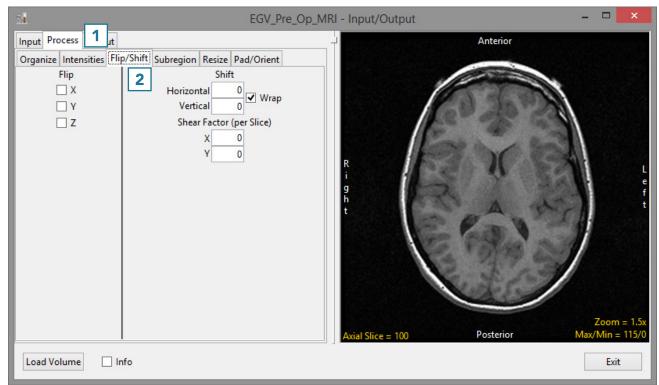
Once a flip checkbox is selected, the flip will be applied to the data and the display panel can be used to review. Unchecking the option will undo the flip. Flipping the data in only the X or Y direction will create a mirror image. If this is not the desired result, the data can be flipped in both the 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/

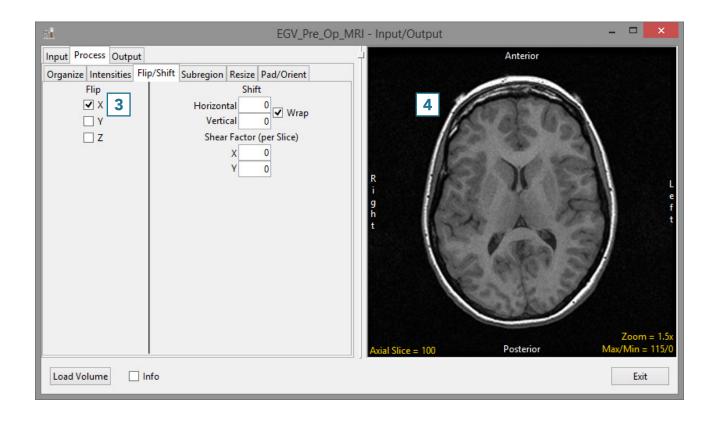
| Axis | OUTCOME |
|------|--|
| Х | Flips data horizontally, rotating about the vertical (Y) axis. |
| Y | Flips data vertically, rotating about the horizontal (X) axis. |
| Z | Changes the order of the slice data. |



Flip/Shift (continued)

• Check the X Flip option [3].

Note the update to the data [4].



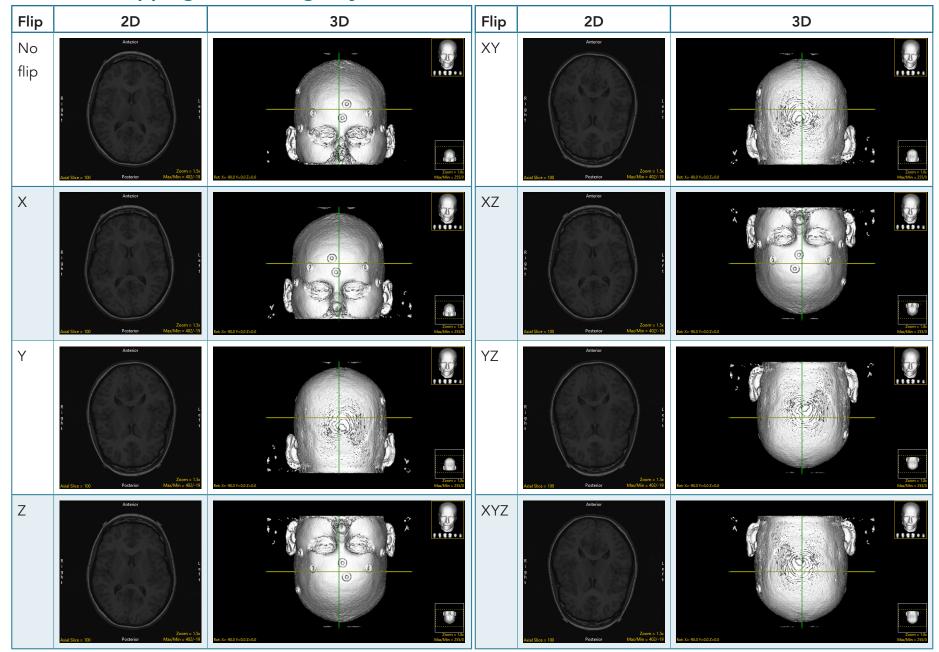
Flip/Shift (continued)

• Check the Y Flip option [5].

Note the update to the data [6].

• To load the data, click the Load Volume button [7].

| 24 | EGV_Pre_Op_MRI - Input/Out | iput – 🗆 🗙 |
|-----------------------------|---|--|
| Flip ✓ X ✓ Y 5 ☐ Z | Vertical 0 Vrap Shear Factor (per Slice) X 0 Y 0 R i g h t t | Anterior 6 6 6 7 8 8 10 15 15 10 10 15 15 15 15 15 15 15 15 15 15 |
| Load Volume In | 0 | Exit |



Results of Flipping Data Along Any Combination of Axes

Analyze 15.0 User's Guide

© AnalyzeDirect, Inc.

Flip/Shift (continued)

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/



Flip/Shift (continued)

• 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].



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 |

Flip/Shift (continued)

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

| - 54 | Neuro_MRI_S | Sagittal - Input/Output | - 🗆 🗙 |
|---|---|--|--|
| Input Process Output Organize Intensities Fli Intensities Compared Intensities Fli Intensities Intensities Fli Intensities Fli | p/Shift Subregion Resize Pad/Orient Shift Horizontal Vertical 30 Shear Factor (per Slice) X 0 Y 0 | P o s t e f o s t e f o s t e f o s t e f o s t e f o s t e f o s t e f o s t e f o s t f o s o s f o s f o s f o s f o s f o s f o s f o s f o s f o s o s f o s f o s s s o s o s o s o s o s o s o s o s o s o | And the second sec |
| Load Volume | nfo | | Exit |

Flip/Shift (continued)

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



Flip/Shift (continued)

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. Analyze 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.

Subregion

Cropping Data

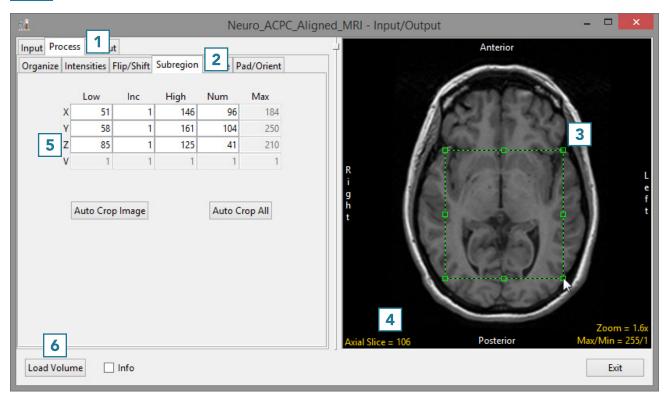
The Subregion tool in Input/Output > Process can be used to reduce the size of a data set without the need to interpolate the original voxel data. The tool can also be used to crop data to a specific region of interest.

Subregion (continued)

- 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 the 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/



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/



Resize

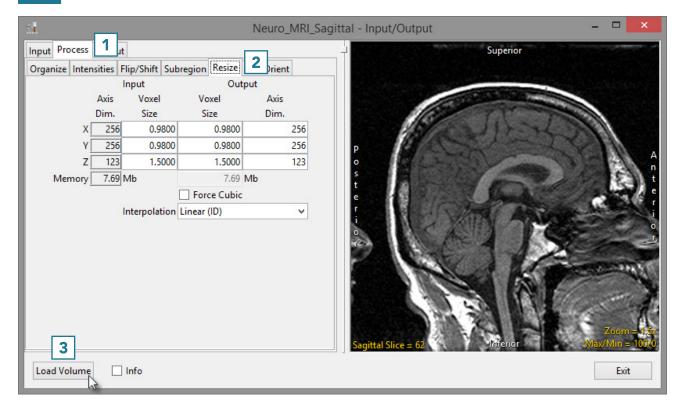
Resize can be used to resample image data. If data is acquired with anisotropic (non-cubic) voxels, resize can be used to resample the data to create an isotropic (cubic) data set.

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.



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



Resize (continued)

• 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.



Resize (continued)

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.

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.

Pad/Orient

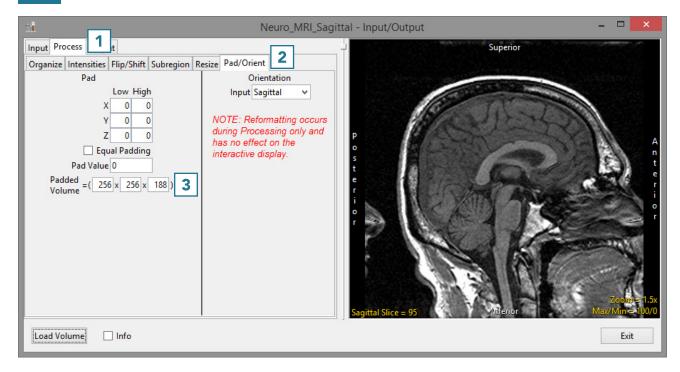
Padding Data

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].

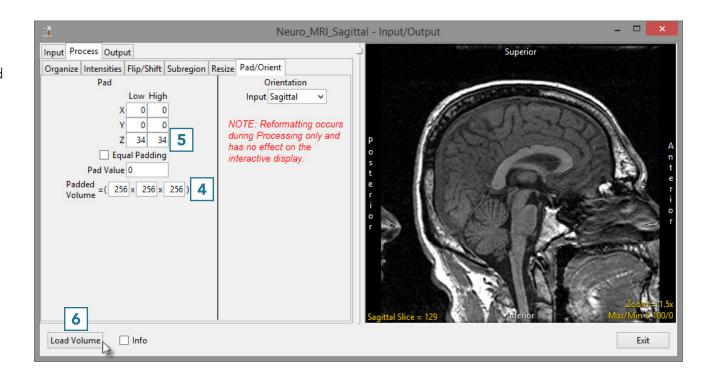


Download the Neuro_MRI_Sagittal data set to follow along http://analyzedirect.com/data/



Pad/Orient (continued)

- 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.



Pad/Orient (continued)

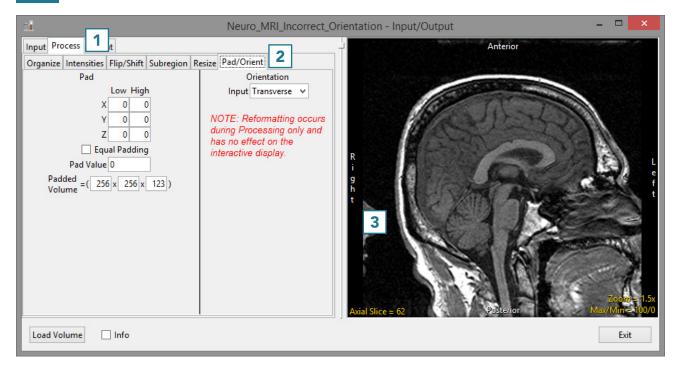
Correcting an Orientation Flag

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].





Pad/Orient (continued)

- 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 Analyze 15.0 as easily as it can be loaded into the program. Input/Output will open in Save mode when a data set is selected.

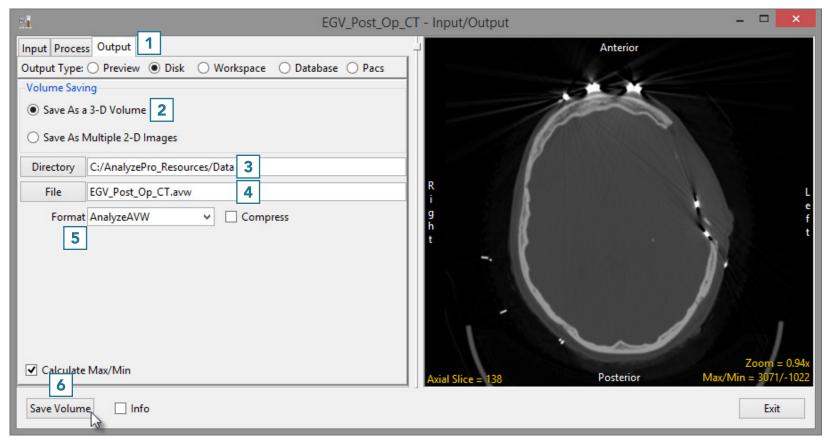
Opening Input/Output in Save Mode

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

| | | Input/Output |
|---|-----------------------------|--|
| ? | An input data has | peen detected, do you wish to "Save" this input? |
| | No, start in "Load" mode | Yes, start in "Save" mode |

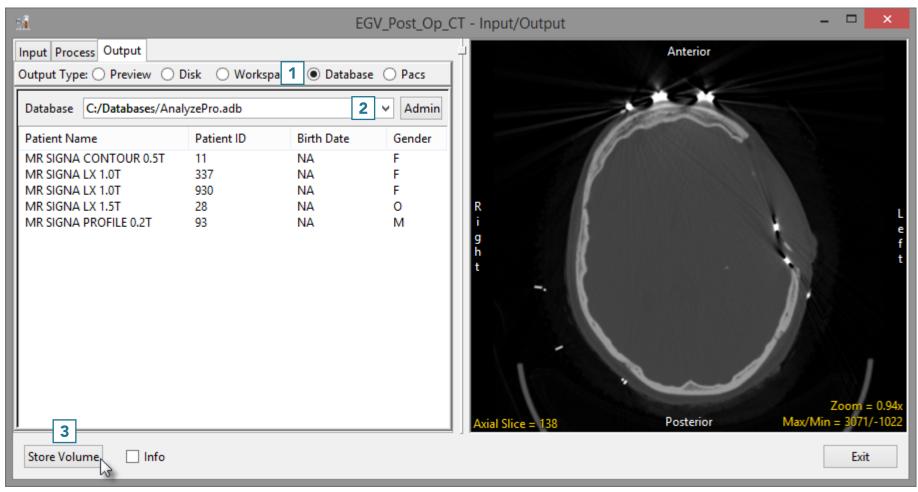
Saving a Data Set

- 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.
- 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.



Storing Data in a Database

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



Storing Data in a Database (continued)

- 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.

| | Edit DICOM tags | |
|----------------------|----------------------------------|---|
| Patient | | |
| ID (0010,00 | 20) 500 | |
| Name (0010,00 | 10) Joe Bloggs | |
| DOB (0010,00 | 30) | Ш |
| Gender (0010,00 | 40) M ~ | |
| Study | | |
| ID (0020,00 | 10) | |
| Description (0008,10 | 30) | |
| Date (0008,00 | 20) | |
| Accession (0008,00 | 150) | |
| Modalty (0008,00 | • • • | Ш |
| Portion (0008,00 | | |
| ✓ (0020,00 | 0d) Make New Study Instance UID | |
| Series | | |
| ID (0020,00 | 11) | |
| Orientation 🖲 Axia | I 🔿 Coronal 🔿 Sagittal | |
| Description (0008,10 | 3e) | |
| Procname (0008,10 | 30) | |
| ✓ (0020,00 | 0e) Make New Series Instance UID | |
| Other Tags | | |
| (gggg,eeee) | | |
| | | |
| Apply Tags and C | ontinue Clear Add Tag Cancel | |
| | | |

Edit/Add Dicom tags

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 <u>Configuring PACS Communications</u>.

| 54 | EGV_Post_Op_ | CT - Input/Output – 🗖 🗙 |
|--|---|--|
| Input Process Output | | Anterior |
| Output Type: O Preview O Disk | k 🔿 Workspace 💿 Database 🔿 Pacs | |
| Database C:/Databases/Analyze | ePro.adb 🗸 Admin | |
| Joe Bloggs 5 MR SIGNA CONTOUR 0.5T MR SIGNA LX 1.0T MR SIGNA LX 1.0T MR SIGNA LX 1.5T MR SIGNA PROFILE 0.2T | Patient ID Birth Date Gender 500 NA Refresh Configure Columns Configure Filter 28 93 Show Database Info Delete Patient Anonymize Patient Import Dicom Images Update DB Export Patient 6 Send Patient ► | R i g h t Axial Slice = 138 Posterior Com = 0.94x Max/Min = 3071/-1022 |
| Store Volume 🗌 Info | | Exit |

Display

| Introduction | page 90 |
|-------------------------------------|----------|
| Display Module Interface | page 91 |
| Menu | page 92 |
| Tools | page 97 |
| Display Area | page 97 |
| Display Configurations | page 97 |
| Multiple Panels | page 98 |
| All Orientations | page 99 |
| Single Image | page 101 |
| Oblique | page 102 |
| Colormaps | page 104 |
| Primary Panel | page 110 |
| 3D Images | page 111 |
| Intersecting Sections | page 112 |
| Cube Sections | page 114 |
| Wire Grid | page 115 |
| Render | page 116 |
| The Display Module Rendering Window | page 117 |
| Additional Rendering Controls | page 125 |

| Display Rendering Types | page 126 |
|------------------------------|----------|
| Depth Shading | page 127 |
| Gradient Shading | page 128 |
| Volume Compositing | page 129 |
| Maximum Intensity Projection | page 133 |
| Summed Voxel Projection | page 134 |
| Surface Projection | page 135 |
| Object Compositing | page 136 |
| Parametric Mapping | page 147 |
| Sequence Tool | page 149 |
| Perspective Tool | page 160 |
| | |
| | |

Introduction

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

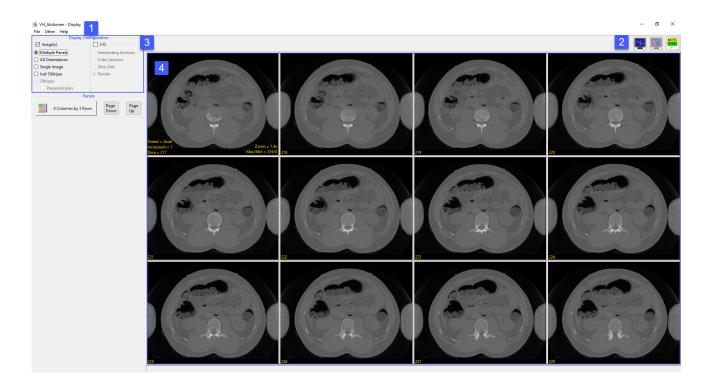
The 2D display options allow for the display of the image data in any or all orthogonal planes and also provides the ability to review data in any oblique plane.

The 3D tools provide a variety of display representations for three-dimensional image data sets. Display uses ray casting algorithms to rapidly generate volume rendered displays of two classes; Transmission displays (Projections) and Reflections displays (Surface).

Display Module Interface

The Display Module interface is divided into the following areas: [1] Menu, [2] Tools, [3] Display Configurations, and [4] Display Area.

Each of these Display Module Interface areas are now described:



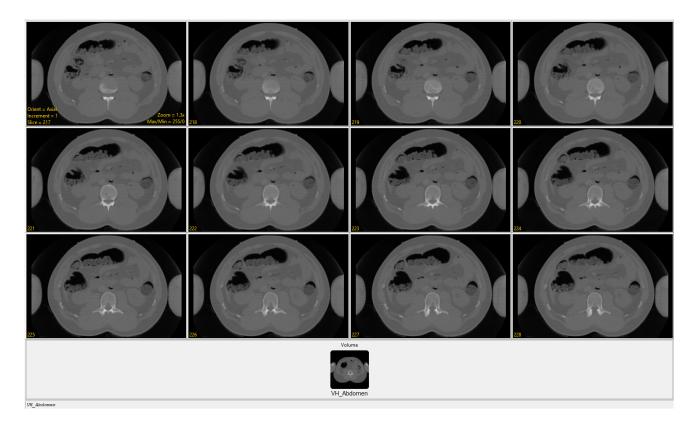
Menu

The Menu provides access to the File, Options, and Help menus.

File

The File menu allows users to load and save object maps for the loaded data set. The File options include:

Input Output Ports: Displays a Volume area at the bottom of the Display module window. This area facilitates the dragging and dropping of image data into the module.



Load Object Map: When selected opens a Load Object Map window allowing users to navigate to, select and load an object map file. The following options are available:

- Current Directory: Takes user to the current directory, the current directory is set by right-clicking in the main Analyze 15.0 window and then choosing Current Directory from the menu. See section 1. Analyze Basics for additional information.
- Workspace Directory: Takes user to the current Workspace directory.
- Home Directory: Takes user to the user's Home directory.
- Cancel Load: Cancels the load of the object map.

Save Object Map: When selected opens a Save Object Map window allowing users to navigate to name the object map and select a location to save the object map file.

Save Object Map As: Allows users to save a copy of the current object map without overwriting the original object map file.

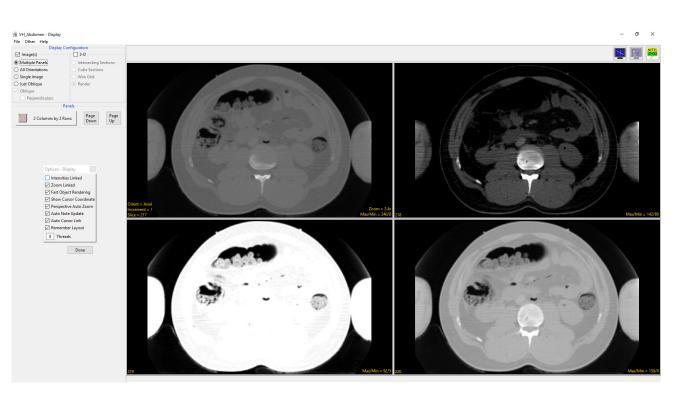
Unload Object Map: Unloads the loaded object map

Exit: Closes the module

Options

When selected opens the Options menu providing access to Module configuration options, including:

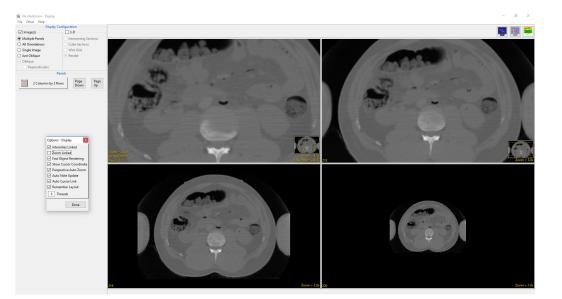
Intensities Linked: Allows users to enable or disable linked intensity adjustment. When linked any adjustment an images intensity display will be applied to all grayscale slices displayed. When disabled image intensities can be adjusted individually.

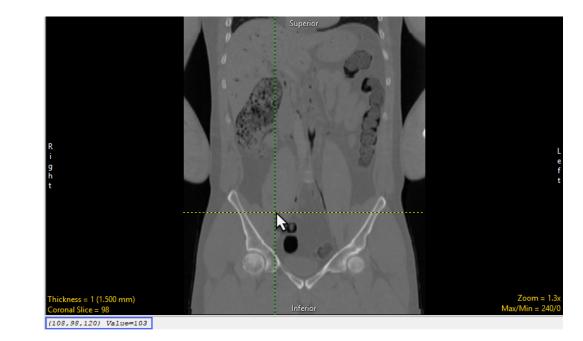


Zoom Linked: Allows users to enable or disable linked zooming. When linked any zoom in/out on an image is applied to all images. When disabled images can be displayed at different zoom levels.

Fast Object Rendering: Enables/ Disabled Fast Object Rendering

Show Cursor Coordinates: Allows users to Enable/Disable the display of the linked cursor coordinates and voxel grayscale value displayed in the lower left-hand corner of the display window.



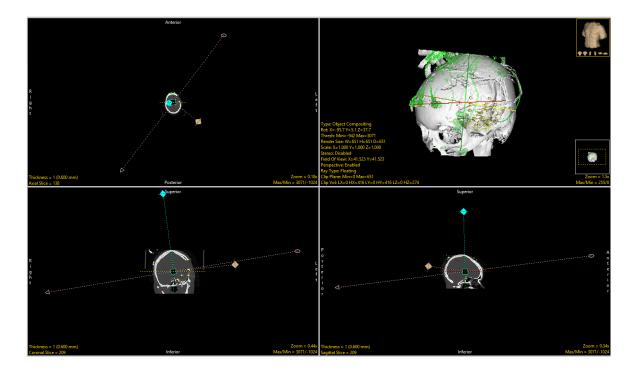


Perspective Auto Zoom: The

Perspective Auto Zoom function is used with the Perspective tool. When this option is enabled the orthogonal view will automatically zoom out so the user can see all camera control points.

Auto Note Update: Allows the Auto Note Update option to be enabled or disabled.

Auto Cursor Link: Allows the Auto Cursor Link option to be enabled or disabled.



Remember Layout: When enabled the module will remember changes made to the layout and will open with this layout in the future. When disabled the module will open with the default layout.

Threads: Allows users to specify the number of threads used in a multi-threaded rendering process. By default, the number of threads is set to the number of processors on the system.

Help

The Help menu provides users with quick access to help resources including:.

About: View version, system and environment information.

Users Guide: Opens the Analyze 15.0 User's Guide.

Get Help: Opens the AnalyzeDirect Support Page.

Analyze 15.0 User's Guide

96

Tools

The Tools options provide access to the Toggle Cursor Link, Toggle Region Display and the Set Note State tools. For further information on these tools please refer to section 2. Image Display, Controls and Customization.

Display Area

The Display Area provides access to various display windows and tools, a description of these tools can be found in section 2. Image Display, Controls and Customization. However, the Display module offers additional display functionality not found in other modules. These tools are described in the following Display Configurations sections.

Display Configurations

The Display Configuration area allows users to review data in 2D or 3D in the Display Area. The default setting when Display is first opened is for the Image(s) check box to be checked which enables the data to be displayed in an array of 2D images. When the 3D checkbox is checked, a 3D display window is added to the current display. A myriad of different display options are offered through Display Configurations which are now described:

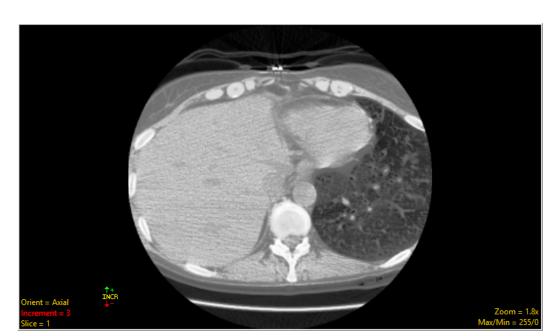
Multiple Panels

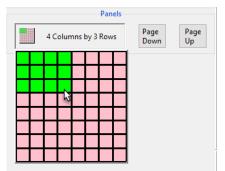
When Display is first opened, the Image(s) checkbox is selcted by default and the data set will be shown as a panel of sections from a single orthogonal orientation. The number of panels shown can be controlled using the Columns/Rows button and using the Page Down and Page Up buttons to change the number of slices shown. In the lower left-hand corner of the first image there are additional display controls tools. These are Orient, Increment, and Slice.

Orient: The Orient tool allows users to switch to switch between any of the three orthogonal orientations; Axial, Coronal, or Sagittal. Left click on the Orient tool to cycle through the orthogonal displays or right-click and choose the desired display option from the menu.

Increment: The Increment tool allows users to specify the interval used to determine the next image to be displayed. Click the yellow Increment text, the cursor will update to display an up/down INCR cursor. Hold down the left mouse button and slide the cursor upward to increase the increment value and downward to decrease the increment value.

Slice: Users can navigate through image slices using the slice tool. 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





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.

Thickness: Note that in the lower left-hand corner of each orthogonal display there is a Thickness option. The Thickness tool allows users to modify the orthogonal display from one to many slices, displaying a slab of slices in which the average, maximum intensity projection (MIP), weighted maximum intensity projection (weighted MIP), minimum intensity projection (MinIP) or weighted minimum intensity projection (weighted MIP), and decrease review time.

To adjust display thickness, click the yellow Thickness text, the cursor will update to display an up/down THICK cursor. Hold down the left mouse button, and slide the cursor upward to increase the thickness value and downward to decrease the thickness value. Users can also right-click and select thickness options calculated based on the data sets volume.

Thick Type: When the display thickness is increased the Thick Type option is displayed above the Thickness option. Left click on the Thick Type text to toggle through the Thick Type options or right-click and choose the desired option from the menu. The Thick Type options are shown on the following table:

| Thick Type | Description |
|----------------|---|
| Average | Average intensity projection displays data using the average values for all voxels in the volume and the thick type value for slice integration. This setting can be useful for viewing projections of noisy images, or for simulating a slice thickness other than what was scanned. |
| MIP | Maximum intensity projection displays data using only the highest values for each voxel of the volume and the thick type value for slice integration. |
| Weighted MIP | After the highest values of each voxel has been determined to be the maximum voxel along the ray path, its value is weighted by the percentage of its distance along the ray path. |
| MinIP | Minimum intensity projection displays data using only the lowest values for each voxel of the volume and the thick type value for slice integration. This slab mode is particularly useful when looking at air or fluid in smaller slabs of slices. |
| Weighted MinIP | After the minimum values of each voxel have been determined to be the minimum voxel along the ray path, its value is weighted by the percentage of its distance along the ray path. |

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. This is the default display option for loaded movie files.

In addition to the Thickness, Orient, and Slice display options (discussed earlier) there are video controls for image review, these include:

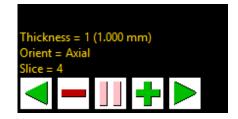
Play Reversed: Reverses the direction of the display. Clicking on the tool button again increases the display speed.

Display previous image: When selected displays to previous image.

Pause: Pauses the display of the images, to continue click on the pause or play button.

Display Next Image: When selected displays the next image.

Play: Begins the display of the images. Clicking on the tool button again increases the display speed.



Right-clicking on the controls provides access to additional options including options to change the video controls button size, the option to add a delay between the display of images, and an option to automatically reverse display of images at the end.

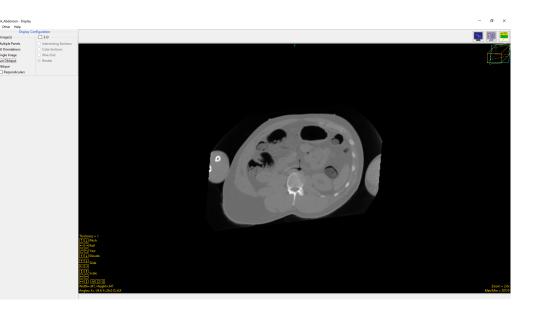
Oblique

The Oblique option is only available for the All Orientations and Single Image Image(s) and all 3-D display configurations. When the Oblique option is checked [1] it enables the display of a new Oblique window [2] allowing for the creation of any arbitrary plane using the Fly tool controls in the Oblique window [3] or by adjusting the blue Oblique Reference Lines enabled on the three orthogonal displays [4]. For further information on using the Fly tools or the Oblique Reference Lines to create oblique images please refer to section 6. Transform.

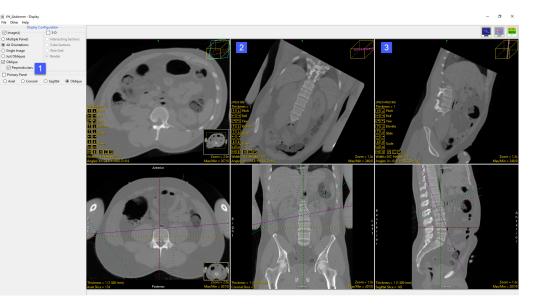


Additional 2D image display parameters are enabled including:

Just Oblique: When selected displays just the oblique image.



Perpendiculars: When this option is checked [1] additional oblique windows are displayed. [2] [3] These oblique displays are perpendicular to the first oblique image and allow for additional manipulations.



Colormaps

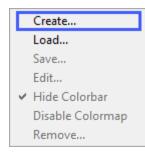
The Display module provides users with the ability to create or load a colormap over the grayscale image data. Options for creating, loading, saving, editing, hiding, disabling, and removing colormaps are available from the right mouse menu for any of the 2D image displays.

Right-click on 2D slice display and choose Colormap, a submenu for Colormaps will be displayed.

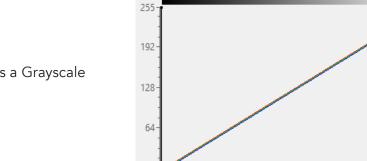
Create: When selected opens the Create Colormap window.

- Color Cells: allows you to specify the number of color cells to be used in the creation of the color map.
- Type: Allows you to specify the type of color map to be created, choosing from the following:



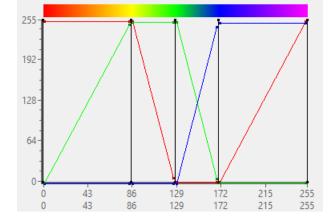


| Create Colormap | |
|-----------------|--|
| Color Cells 256 | |
| ⊖ Grayscale | |
| Type 🖲 Rainbow | |
| O Random | |
| Create | |

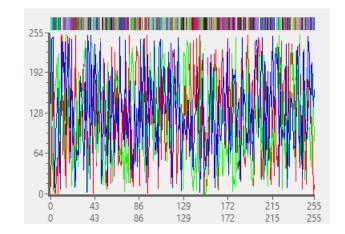


• Grayscale: Creates a Grayscale colormap.

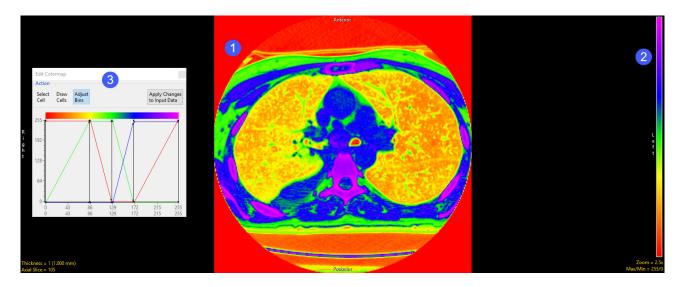
• Rainbow: Creates a Rainbow colormap.



• Random: Creates a Random colormap

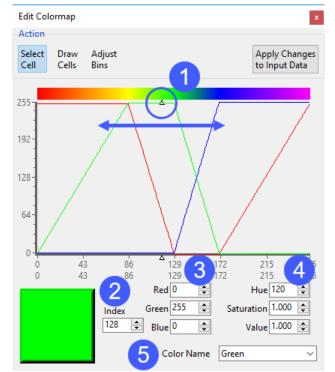


 Create: When selected creates colormap from specified color cells and type. The colormap is applied to the displayed image data (1), a color bar is displayed (2), and the Edit Color Map Window (3) is returned. When the Edit Colormap window opens the following options are available.

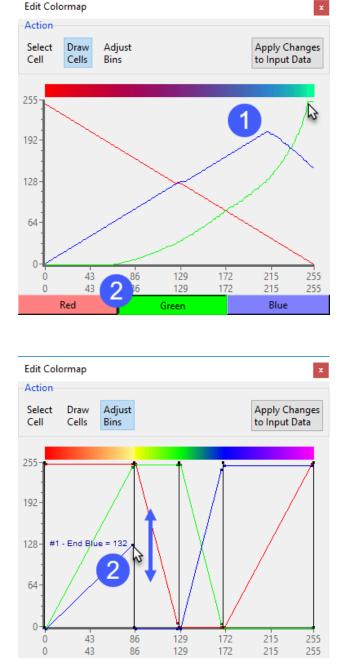


Action

- Select Cell: Allows users to modify the color of a specific color cell in the colormap.
 - Use the Index selection arrow
 (1) or the Index field (2) to select a color cell.
 - Adjust the color cell color using the RGB input fields (3), the HSV input fields (4), or the Color Name drop-down (5).



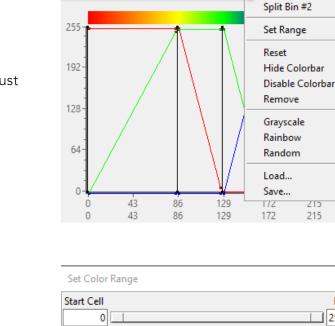
- Draw Cells: When selected allows users to draw color channels on the interface (1). Color channels can be enabled/disabled by clicking on the color buttons at the bottom of the window (2).
- Adjust Bins: Allows users to interactively manipulate bins and the color ranges of bins. Adjust Bins is the default selection.
 - Bins are indicated by the black vertical lines on the color map plot. To adjust a bin range, select the black control point at the top of the vertical black bin line (1) and move the line to the left or right to increase or decrease the bin range.
 - The Red, Green, and Blue color channels can be adjusted for each bin. Each color channel has a Start point and an End point. To adjust select the start or end point (2) for a color channel and move it up or down to adjust.





• Apply Changes to Input Data: must be selected in order to apply the colormap to the image data. If not selected before closing the Edit Colormap window or adjusting the slice display all work on the colormap will be lost.

- Right mouse menu options: Right-clicking in the colormap plot display will reveal additional options depending on the current Action selected. These options include: .
 - Delete Bin: When selected deletes the current Bin (available for Adjust Bin Action only).
 - Split Bin: When selected splits the current Bin into two bins (available for Adjust Bin Action only).
 - Set Range: Opens the Set Color Range window allowing users to specify the color for a range of color cells.
 - Start Cell: Specify the starting color cell.
 - End Cell: Specify the ending color cell.
 - Set Cell Range to:
 - Single Color: Select a single color for the color cell range.
 - Fade Between To Colors: Allows users to specify two colors to fade between for the specified color cell range
 - Start Color: Specify the Starting color. When Single Color is selected this is the only option.
 - End Color: Specify the Ending color.
 - OK: Closes the Set Range window.
 - Apply: Applies the edits to the colormap.



Adjust

Bins

Edit Colormap

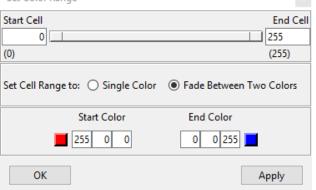
Draw

Cells

Action

Select

Cell



255

255

Apply Changes

Delete Bin #2

Analyze 15.0 User's Guide

- Reset: Resets the colormap.
- Hide Colorbar: Disables/Enables the colorbar on the display of the 2D image
- Display Colorbar: Disables the colormap on the grayscale image data. To enable the colormap again right-click on the grayscale data and choose Colormap and then uncheck Disable Colormap.
- Remove: Removes colormap from the image data.
- Grayscale: Sets the colormap to a grayscale colormap
- Rainbow: Sets the colormap to a Rainbow colormap
- Random: Sets the colormap to a Random colormap
- Load: Load an existing colormap (.lkup) file (see Load).
- Save: Save the current colormamp (.lkup) file.

Load: Allows users to navigate to and load an existing colormap .lkup file. A selection of predefined colormaps can be downloaded from analyzedirect.com/data

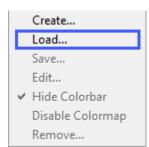
Save: Saves the current colormap .lkup file.

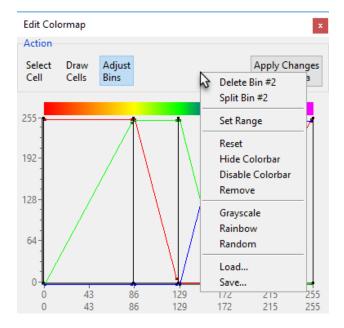
Edit: Opens the Edit Colormap window.

Hide Colorbar: Disables/Enables the colorbar on the display of the 2D image

Display Colorbar: Disables the colormap on the grayscale image data. To enable the colormap again right-click on the grayscale data and choose Colormap and then uncheck Disable Colormap.

Remove: Removes the colormap from the image data.





Primary Panel

The primary panel option allows any of the display images to be set as the primary image.

9 VH_Abdomen

Image(s Multiple Panel

) Single Imag

Primary Pan

Obligu

File Other Hel

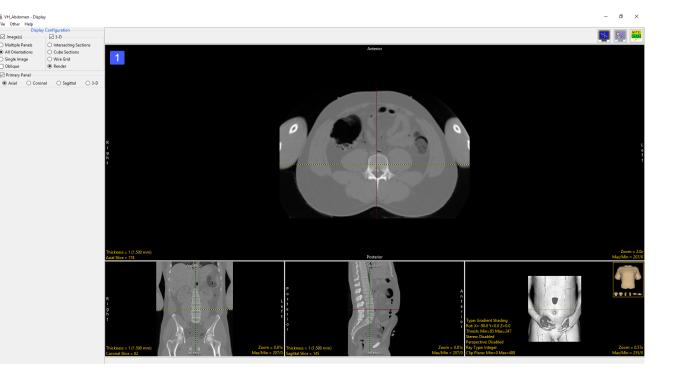
Axial: Makes the axial image the primary image. [1]

Coronal: Makes the coronal image the primary image.

Sagittal: Makes the sagittal image the primary image.

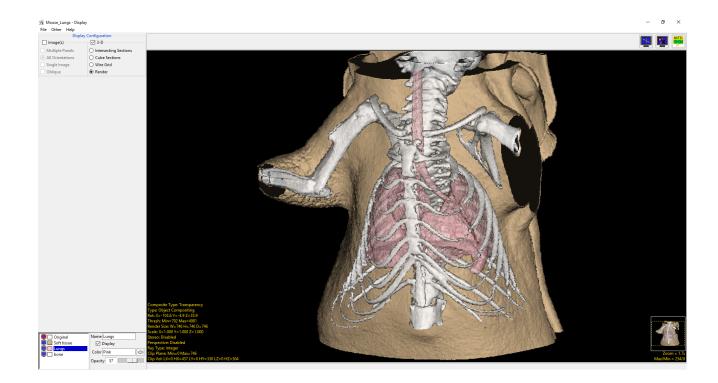
Oblique: Available when the Oblique option is selected. Makes the oblique image the primary image.

3-D: Makes the current selected 3-D display the primary image.



3D Images

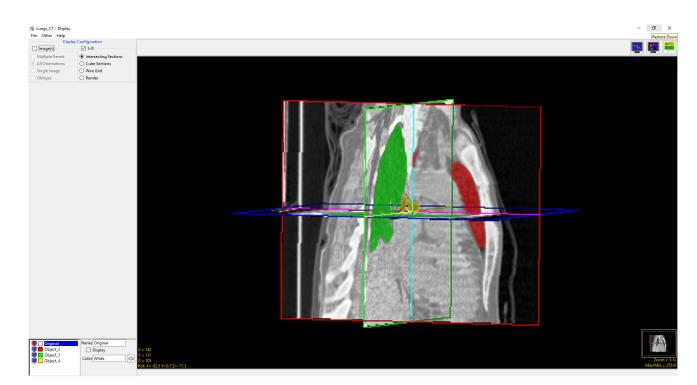
The 3D checkbox adds a three dimensional display window to the current collection of displays and enables the selection of the type of 3D visualization depicted in the 3D display window.



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.

In the lower left-hand corner of the Intersecting Sections display window are the Intersecting Sections navigation controls.



X: Controls the Sagittal (XZ) slice viewed in the display. Left click the X control option and the cursor will update. Hold down the left mouse button and slide the cursor up to increase and down to decrease the X value. Users can also right-click and select First, Middle, or Last.

Y: Controls the Coronal (YZ) slice viewed in the display. Left click the Y control option and the cursor will update. Hold down the left mouse button and slide the cursor up to increase and down to decrease the Y value. Users can also right-click and select First, Middle, or Last.

Z: Controls the Axial (XY) slice viewed in the display. Left click the Z control option and the cursor will update. Hold down the left mouse button and slide the cursor up to increase and down to decrease the Z value. Users can also right-click and select First, Middle, or Last.

112

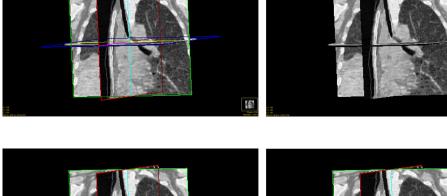
X/Y/Z Right-click options: The three slice display controls also provide the following configuration options by right-clicking:

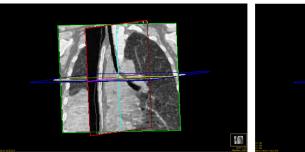
- Show (X, Y, or Z): Allows users to enable and disable the current slice orientation display.
- **Color Edges:** Allows users to enables and disable the color edges around the slice displays.
- Show Hidden Edges: Only available when Color Edges is enabled. Allows users to enable and disable hidden edges of the slice displays.

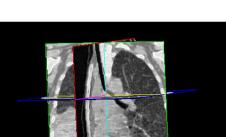
Rot: The Rotation tool, reports the current XYZ rotation angle coordinates. When selected, enables the rotate cursor. Right-click on the tool to choose from rotation default options; Front, Back, Left, Right, Top, Bottom and Angled.

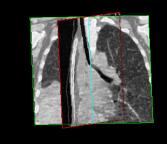
Right menu options:

- Copy to clipboard: Saves the current Intersecting Section image to memory. This can be pasted (Ctrl + v) into the Analyze 15.0 workspace, to be saved out of the software, or pasted into any other application.
- Save Intersecting Sections: When selected saves a recording of the Intersecting Section display to the current Analyze 15.0 workspace.





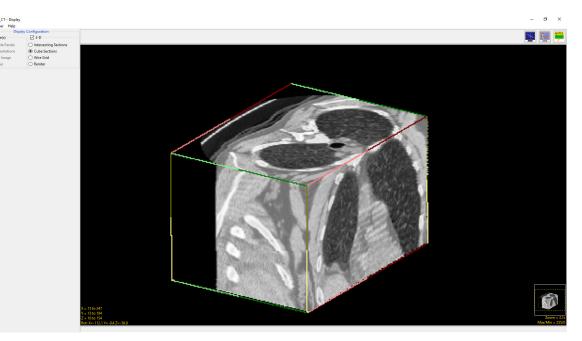




Cube Sections

Cube Sections 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. The following navigation controls are in the lower lefthand corner of the display window:

X: Controls the Sagittal (XZ) slices viewed in the display. Left click on the X control to update the cursor. Hold down the left mouse button and slide the cursor up/down to increase/decrease the minimum X value and left/right to increase/



decrease the maximum X value. Users can also right-click and select Full, 10 %, 25 %, or 33 %.

Y: Controls the Coronal (YZ) slice viewed in the display. Left click on the Y control to update the cursor. Hold down the left mouse button and slide the cursor up/down increase/decrease the minimum Y value and left/right to increase/decrease the maximum Y value. Users can also right-click and select Full, 10 %, 25 %, or 33 %.

Z: Controls the Axial (XY) slice viewed in the display. Left click on the Z control to update the cursor. Hold down the left mouse button and slide the cursor up/down to increase/decrease the minimum Z value and left/right to increase/decrease the maximum Z value. Users can also right-click and select Full, 10 %, 25%, or 33%.

X/Y/Z Right-click option: Color Edges - Allows users to enables and disable the color edges around the Cube Sections display.

Rot: The Rotation tool, reports the current XYZ rotation angle coordinates. When selected, enables the rotate cursor. Right-click on the tool to choose from rotation default options; Front, Back, Left, Right, Top, Bottom and Angled.

Right menu options: Copy to clipboard: copies the current Cube Section image. Save Cube Sections: saves display to the Workspace.

Analyze 15.0 User's Guide

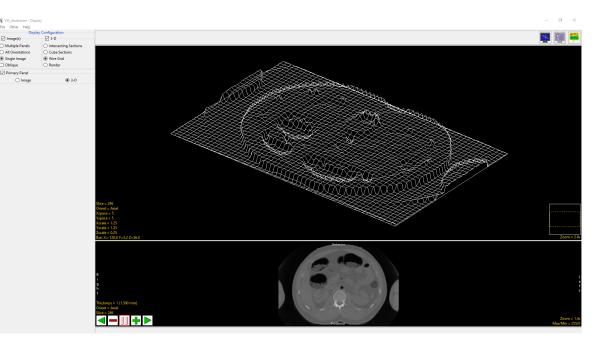
Wire Grid

Wire Grid generates and displays a plot of the current slice intensities. Options available are:

Slice: Allows navigation through slices data.

Orient: Allows change of display orientation.

Spacing: Allows different sampling of points in the slice for the wire grid display. Small values result in fine sampling and large values result in coarse sampling. Values in the range of 5 - 10 are a recommended starting point.



Xspace: Adjusts the row increment determining which rows of the slice are sampled for the display of the wire grid.

Yspace: Adjusts the column increment determining which rows of the column are sampled for the display of the wire grid.

Scale: Scale allows for the specification of the display size of the wire grid. The default values are 1. for X and Y and 0.1 for Z.

Xscale: Specifies the x scale used to determine the width of the wire grid.

Yscale: Specifies the y scale used to determine the width of the wire grid.

Zscale: Specifies the z scale used to determine the width of the wire grid.

Rot: The Rotation tool allows users to rotate the display of the wire grid.

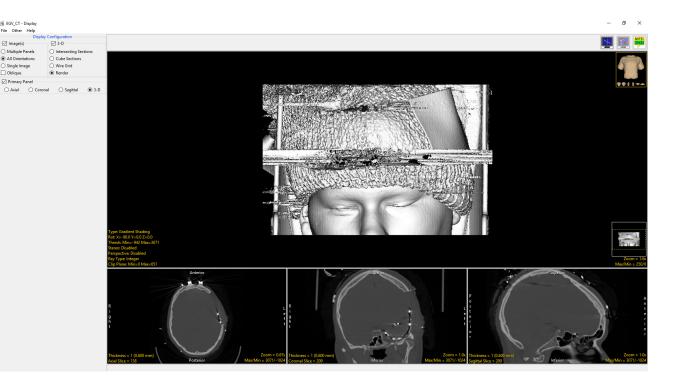
Right mouse menu options: *Copy to clipboard:* Saves the current wire grid image to memory. This can be pasted (Ctrl + v) into the Analyze 15.0 workspace, to be saved out of the software, or pasted into any other application. *Save Wire Grid:* When selected saves a recording of the Wire Grid display to the current Analyze 15.0 workspace.

115

Render

The Render option enables a 3D volume rendering in the 3D display window. Display uses ray casting algorithms to rapidly generate volume rendered displays of two classes; Transmission displays (Projections) and Reflections displays (Surface).

Transmission displays (Projections): Models the image voxels as light emitters and do not involve explicit surface detection. A display pixel's value is computed as a function of the ray passing through the entire volume.



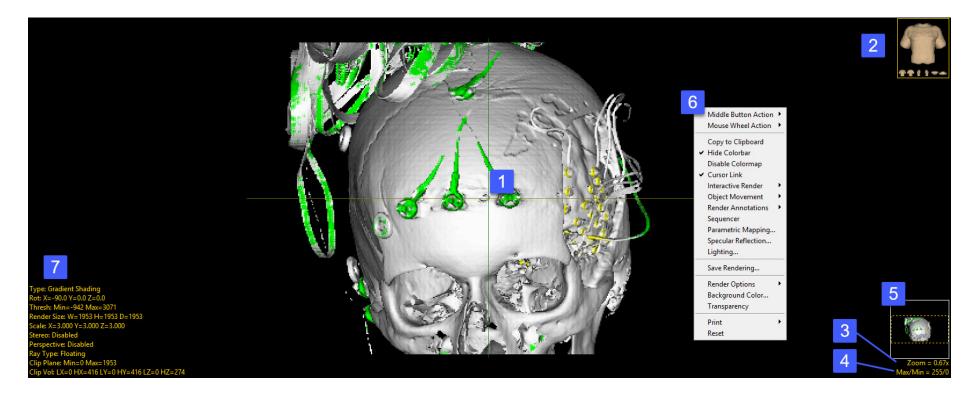
Reflection displays (Surface): Models the image voxels as light reflectors and require the detection of surfaces within the volume. The basic reflection algorithms consider the first voxel encountered by the ray which is within the threshold parameters to be the surface voxels to be rendered. The algorithms differ in how the detected surface voxels are rendered on the screen.

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 the rotation angle.

116

The Display Module Render Window

While the tools available for the slice and render display windows are covered in section 2. Image Display, Controls and Customization of this user's guide, the render window in Display has some additional features that are only available to users from the Display module. These features will be reviewed in more detail in this section of the guide.



The display module render window is comprised of several elements and tools: 1) the cursor link tool, 2) the navigation tool, 3) the zoom tool, 4) the pan tool, 5) the max/min intensity adjustment tools, 6) the right mouse menu options, and 7) additional rendering controls.

The Cursor Link: The cursor link allows users to interactively navigate through the image data. The tool is only enabled if the All Orientations, Single Image, or Oblique Image display configurations are enabled, otherwise to the Cursor Link tool is disabled. The Cursor Link tool can be controlled from the 3D rendering or from any of the 2D orientations. Moving the tool on the rendering will interactively update the orthogonal slice displays. The cursor linked can be enabled or disabled using the Toggle Cursor Link button.

The Navigation tool: The Navigation Icon is not just a reference for the current orientation of the 3D image data, the tool also allows users to rotate the data or specify a standard view; front, back, left, right, top, bottom. To rotate the data, left-click on the Navigation Icon and hold the left mouse button down. The cursor will update to the rotate cursor enabling interactive rotation of the rendering viewpoint. Releasing the left mouse button will dismiss the rotate cursor.

The Zoom tool: The Zoom tool in the Rendering Window allows users to increase and decrease the display size of the data. For more information refer to the Zoom tool description in section 2. Image Display, Controls and Customization.

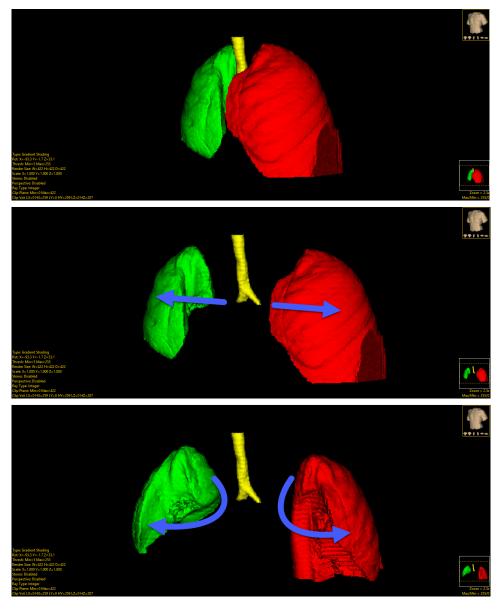
The Pan tool: The Pan tool is automatically enabled when the Zoom size of the image is larger than the current window. Clicking in the tool allows users to Pan the zoomed area over the current display.

The Max/Min Intensity Adjustment tool: The Maximum and Minimum display intensities for the rendering can be changed by clicking on the yellow Max/Min Tool at the bottom right corner of the 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.

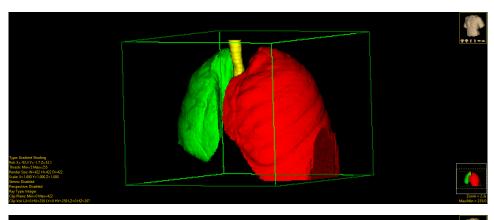
Right Menu Options: Right-clicking in the Rendering Window reveals additional options. Most of these options, if available, are covered in the Slice Display section, however, there are few additional configuration options specific to the Rendering window.

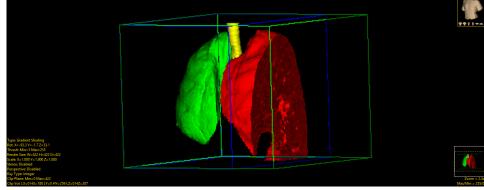
- Middle Button Action: Allows action setting of the middle mouse button. See the Slice Display section for additional information.
- Mouse Wheel Action: Allows action setting of the middle mouse wheel. See the Slice Display section for additional information.

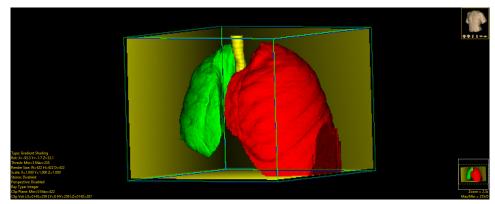
- **Copy to Clipboard:** Copies the current rendering display to memory.
- **Hide Colorbar:** Allows users to hide or show the colorbar when available.
- **Disable Colormap:** Allows users to enable or disable the colormap when available.
- **Cursor Link:** Toggles the Cursor Link tool Off/On in the current display.
- Interactive Render: Allows users to selects between Reduced Quality (useful for interactive rotation of extremely large image volumes) and Full Quality.
- **Object Movement:** Object Movement allows users to manipulate the location of disabled objects.
 - Disabled disable object movements.
 - Translation allows X, Y, and Z translations to be applied to the selected object.
 - Rotation allows X, Y, and Z rotations to be applied to the selected object.



- Reset 'Object-x' Movements rests all translations and rotations for the current object.
- Reset All Movements rests all translations and rotations for all objects.
- Render Annotations
 - Volume Edges when selected draws the volume edges on the rendered image.
 - Clips Edges when selected draws the clip edges on the rendered image.
 - Back Drop When selected displays a shaded backdrop in the rendered images.
 - Color Allows users to change the color of the Volume Edges, Clip Edges, or Background Render Annotations, when enabled.
- **Sequencer** allows users to enable the Sequencer tool for movie creation (see Sequencer for further information.)







- **Parametric Mapping** Allows creation of renderings with related parametric maps. When the option is selected the Parametric Mapping window opens.
 - Workspace allows users to select the workspace containing the related volume to be used for parametric mapping.
 - File allows users to select the volume to be used for parametric mapping.
 - Enable Parametric Mapping: Toggles On and Off the mapping of the related volume on the rendered surface.

| Parametric M | lapping - Display | x |
|--------------|--------------------------|---|
| Workspace | 1ain ~ | |
| File S | ISCOM_Activation_Map 🗸 🔮 | |
| 🗹 Enable Pa | arametric Mapping | |
| 0.65 | Mapping Factor 0.65 | |
| | Map Transparency Value | |



- Mapping Factor: Allows users to adjust the contribution of the related volume when combining the rendering of the input volumes. Increasing the mapping factor provides a clearer display of the related volume.
- Map Transparency Value: Allows users to adjust the transparency value of the related volume.

Right Menu Options (continued):

- **Specular Reflection:** The Specular Reflection rendering option is available for the Gradient Shading, Transparency and Volume Compositing render types. When the option is selected the Specular Reflection window opens.
 - Specular Reflection Choose from Off or On to determine whether Specular Reflection is used to render the volume. Specular Reflection causes the highlights on the shiny surface (1).
 - Factor Specifies the percentage of the shading that is done in Specular, 0.00 to 1.00. The rest of the shading is flat shaded.

| Specular Reflection - Display | | × |
|-------------------------------|------|------|
| Specular Reflection 🔿 Off 🔘 🤇 | Dn | |
| Factor 0.29 | | 0.29 |
| Exponent | 14.8 | |
| | | 14.8 |



• Exponent - Controls the falloff rate of the shading. For example, a shiny surface has a high falloff rate, giving a small bright spot. A more diffuse surface, has a much lower falloff rate, and thus a lower exponent.

- Lighting: The Lighting options allows users to specifying the location of the light source used in reflective renderings. This option is available for the Gradient Shading, Transparency and Volume Compositing render types. When selected a Lighting window opens providing the following options:
 - Horizontal Specifies the horizontal angle (azimuth) of the light source (in degrees) with respect to the viewpoint.
 - Vertical Specifies the vertical angle (elevation) of the light source (in degrees) with respect to the viewpoint.
 - Brightness – Specifies the brightness of the light source with respect to the viewpoint.
- **Save Rendering** saves the current rendering to the Analyze workspace.
- Render Options Allows users to enable/disable additional rendering options, these include:
 - Show Render Type Allows users to view and change the rendering algorithm used to render the image data, choose from Depth Shading, Gradient Shading (default option), Volume Compositing, Maximum Intensity Projection, Summed Voxel Projection, Surface Projections, and Object Compositing. Double click on the Render Type option to cycle through the render types or right-click and choose a specific render type from the right mouse menu. For more information about render types and the render type specific options please refer to the 3D Rendering section of Display.
 - Show Rotation Reports the current XYZ rotation angle coordinates. When selected, enables the rotate cursor. Right-click on the tool to choose from rotation default options; Front, Back, Left, Right, Top, and Bottom.

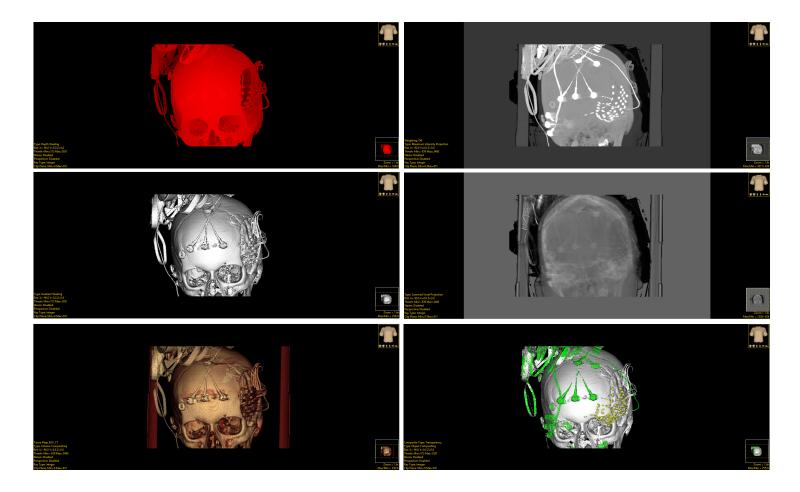
| Lighting - Display | | × |
|--------------------|-------|---|
| Horizontal | | |
| | 0 | |
| | | 0 |
| Vertical | | |
| | 0 | |
| | | 0 |
| Brightness | | |
| | | |
| | Reset | |

- Show Threshold: Displays the current Threshold maximum and minimum threshold values. Double clicking allows users to enter values. Right click to specify Preset values or choose from Analyze Default, Calculated Max/Min, and DataType Max/Min.
- Show Clip Plane: Enables the Clip Plane tool allowing users to specify the maximum and minimum depth along the ray path between which voxels are rendered. Clipping is particularly helpful when you need to observe the cross section of a 3D object.
- Show Clip Volume: Enables the Clip Volume tool, allowing users to clip the volume with six clip planes (X low, X high, Y low, Y high, Z low, and Z high).
- Show Render Size: Displays the current rendering size and allows the user to enter the rendering Width, Height, and Depth. Right click to choose from Default, Maximum Diagonal, Double Diagonal, Axial, Coronal, and Sagittal.
- **Background Color** allows users to set the color of the rendering background. The option opens a Color selection window enabling selection of desired color.
- **Transparency** The Transparency option turns transparent rendering on or off. The transparency rendering mode is useful for visualizing objects contained within objects or objects with views obscured by other objects. Object opacity levels can be set using the Opacity options in the Object Control window.
- **Background Opacity** The Background Opacity option is only available when Transparency rendering is enabled. The option allows users to specify the background opacity for the transparency rendering.
- **Print** Sends capture of current slice display to printer.
- **Reset** Resets all options to default.

Additional Rendering Controls

The additional rendering controls provide access to tools and rendering options only accessible from the Display module:

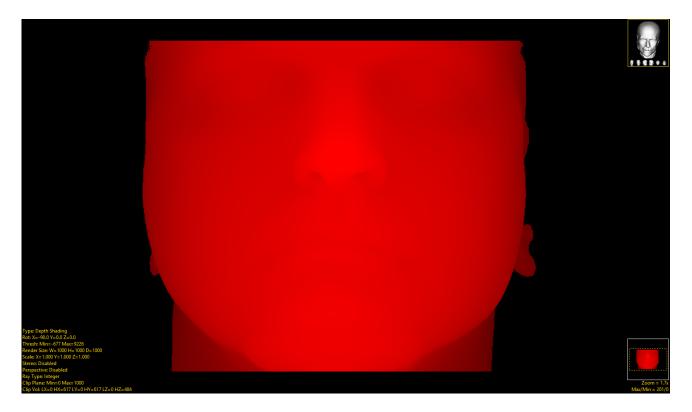
Type: Allows users to select which type of rendering algorithm to use to create the 3D rendering of the image data. The following Render Type options are available: Depth Shading, Gradient Shading, Volume Compositing, Maximum Intensity Projection, Summed Voxel Projection, Surface Projection, and Object Compositing. Each type is displayed below and summarized in the table that follows.



| 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. |

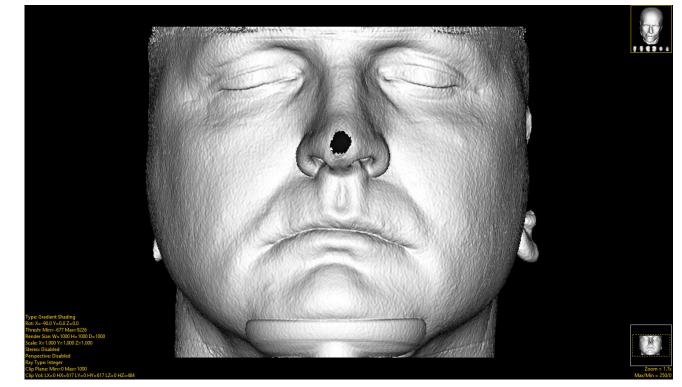
Depth Shading

In 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

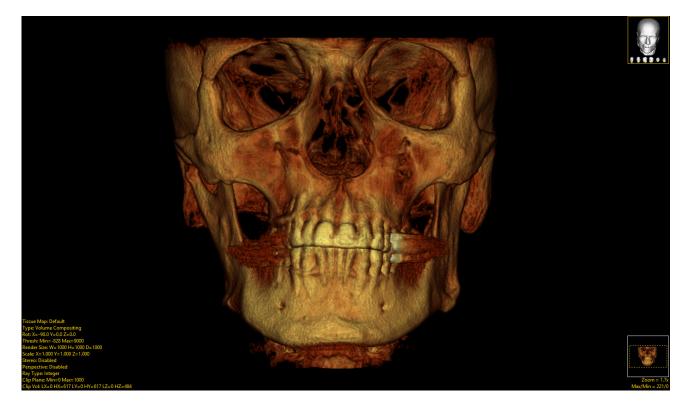
In Gradient Shading the grayscale gradient vector is computed using a 3D neighborhood about the surface voxel. The value projected at each output location is the dot product of the gradient vector and an independently specified light source vector. This simulates the appearance of a reflective surface under uniformfield illumination.



Volume Compositing

Volume Compositing (also know as 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 an Alpha map created via the Tissue Map window.

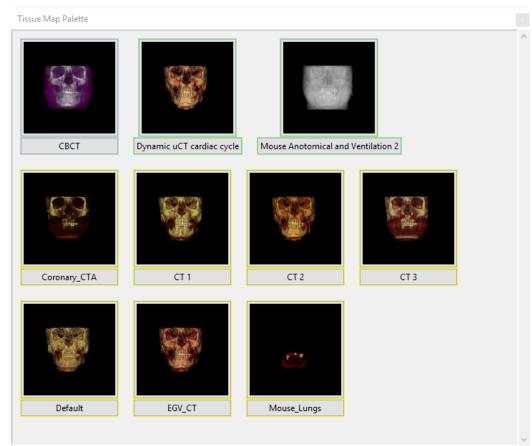
 Tissue Map: When the Volume Compositing render option is selected the Tissue Map option is automatically displayed above the Type option. A default tissue map loaded is loaded and used to render the image data. Tissue Map Right Click options are as follows:



Volume Compositing (continued)

Right Click Options

- Data Tissue Maps: Allows users to select any tissue maps previously created and saved for this data type.
- User Tissue Maps: Allows users to select any tissue maps they may have previously created and saved.
- System Tissue Maps: Allows users to select any system tissue maps created, saved and shared by other users. Also allows access to the tissue maps distributed with the program.
- Palette: Opens the Tissue Map Palette. This window provides a preview of the current data with all available Data, User, and System Tissue Maps. Double click on any of the preview icons to apply that tissue map to the image data.
- Browse: Allows users to browse the system for tissue maps.

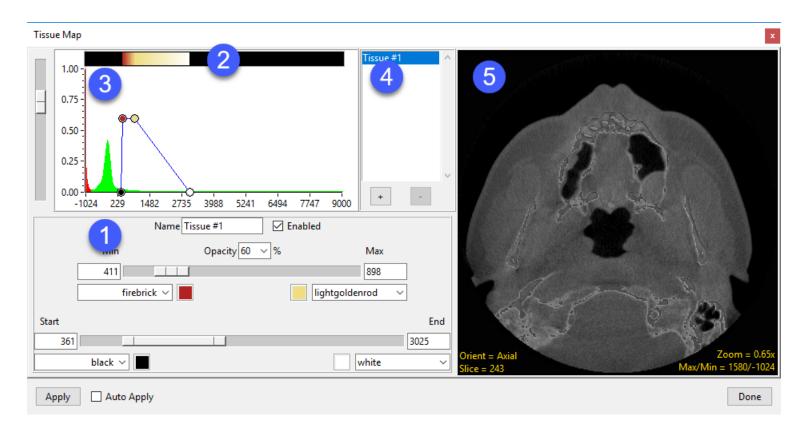


Volume Compositing (continued)

Right Click Options (continued)

• Edit: Opens the Tissue Map tool. Double-clicking on the Tissue Map text will also open this tool.

The Tissue Map tool - provides an interface to allow users to create or edit tissue maps by choosing color and opacity (alpha) values for tissue maps. The tool consists of: 1) The parameters area, 2) the colorbar, 3) the parameter display, 4) the tissue list, and 5) the image map.



Volume Compositing (continued)

The Tissue Map tool (continued)

(1) The Parameters Area: The parameters area allows users to assign color and opacity values to ranges of voxels based on intensity.

- To set a range of voxels for the tissue map use the Start/End and Min/ Max controls.
- To assign a color to each parameter use the color assignment dropdown menu or click on the color selector next to the drop-down menu.
- To adjust the selected tissue opacity level use the opacity drop-down menu.

(2) The Colorbar: Displays the tissue maps color bar.

(3) The Parameter Display: Displays an interactive graphical representation of the tissue map parameters over a plot of the image histogram.

(4) The Tissue List: Displays the current tissues within the tissue map. • To add a tissue, click the '+' key. To remove a tissue, select a tissue and then click the '-' key.

(5) The Image Map: The image map area previews the tissue map parameters on the current 2D image.



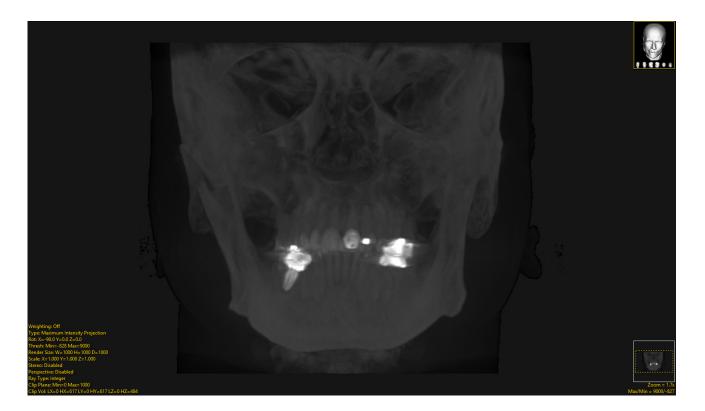
Analyze 15.0 User's Guide

Maximum Intensity Projection

In Maximum Intenstiy Projection the maximum voxel intensity along the ray path is used.

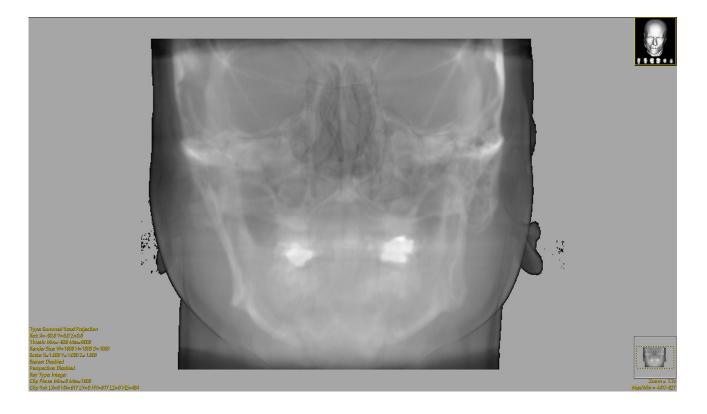
Weighting: On/Off - MIP Weighting enables the specification of performance of weighting.

- Off: This is the default state; no weighting is applied.
- On: When selected weighting is applied. Before the value of the voxel is compared to see if it is the maximum voxel, its value is weighted by the percentage of its distance along the ray path.



Summed Voxel Projection

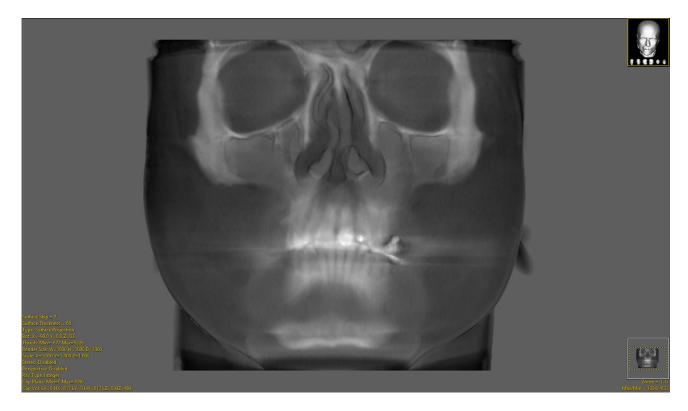
In Summed Voxel Projection the average of all voxels along the ray path is used.



Surface Projection

In 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.

- Surface Skip: Indicates the number of voxels to skip once a renderable voxel has been detected, before summing of the thickness begins.
- **Surface Thickness**: Specifies the maximum thickness for the rendered surface.

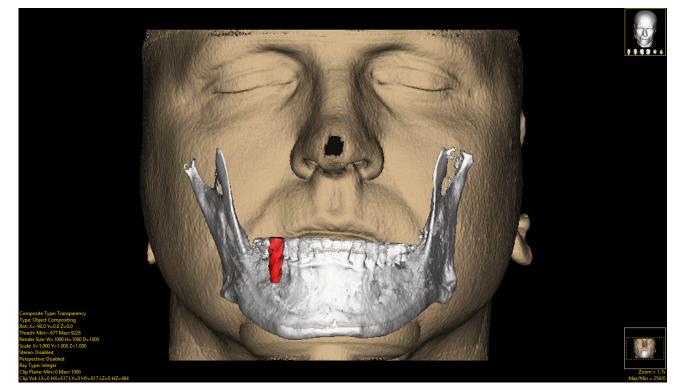


Object Compositing

Object Compositing is available only when an object map is loaded with the data set. This rendering option produces 24-bit color renderings where the voxel mapping along each ray path is controlled by the Composite Type yellow text.

Composite Type: The following composite type options are available.

 Transparency - Opacity, Thickness and Color parameters for each object are used to determine the contribution of each visible object voxel along the ray path.

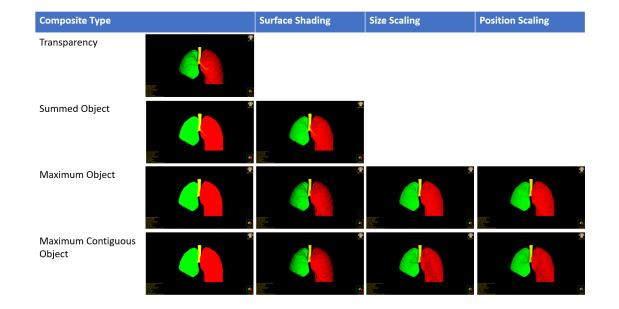


- Summed Object The object color contributions for each visible voxel along the ray path are summed and then divided by the total.
- Maximum Object The object which contributes the maximum number of voxels along each ray path is rendered.
- Maximum Contiguous Object The object which contributes the longest contiguous span of voxels along each ray path is rendered.

Object Compositing (continued)

Object Compositing Options: Surface Shading, Size Scaling, and Position Scaling options are available for certain composite types. These options are not available for Transparency. Size and Position Scaling are available for Maximum Contiguous Object methods.

- Surface Shading: Adds gradient-based surface shading to the output rendering when this option is enabled.
- Size Scaling: The count of voxels belonging to the rendered objects is used to weight the rendered contribution of that object along the ray. Larger counts will be brighter, fewer will be darker. This provides further visual information in the rendering with respect to the relative size of the object along the ray.
- Position Scaling: The output rendering weighted by the relative position of the first voxel rendered for the object along the ray path. This provides visual cues to show relative object position, with closer objects being brighter than those occuring later down the ray path.



Object Compositing (continued)

Rot: Reports the current XYZ rotation angle coordinates. When selected, enables the rotate cursor. Right-click on the tool to choose from rotation default options; Front, Back, Left, Right, Top, Bottom and Angled.

Thresh: The Threshold option displays the current Threshold maximum and minimum values. Editing the threshold values can be useful to eliminate noise, airspace, or tissue when an object map has not been loaded.



- Clicking the yellow Thresh text will update the cursor to an up/down/left/right Threshold (TRESH) cursor. Hold down the left mouse button and slide the cursor forward to increase the minimum threshold value and backwards to decrease it. Slide the cursor right to increase the maximum threshold value and left to decrease the maximum threshold value.
- Double clicking the yellow Thresh text allows users to enter minimum and maximum threshold values.
- Right-click to specify Preset values or choose from Analyze Default, Calculated Max/Min, and DataType Max/Min.

Analyze 15.0 User's Guide

Object Compositing (continued)

Render Size: The Render Size option allows users to specify various rendering size attributes. The options include:

- Width: Specifies the display width for the rendered image.
- Height: Specifies the display height for the rendered image.
- Depth: Specifies the depth for the rendered image.

Right click options:

- Default: Sets the width and height to the largest input volume axis. Depth is set to the maximum diagonal (Square Root of the sum of the squares of each input axis).
- Maximum Diagonal: Sets the width, height and depth to the maximum diagonal.
- Double Diagonal: Sets the width, height and depth to double the diagonal size.
- Axial: Sets the width and height to the volume's width and height. The depth is set to the maximum width-depth or height-depth diagonal.
- Coronal: Sets the width and height to the volume's width and depth. The depth is set to the maximum width-height or height-depth diagonal.
- Sagittal: Sets the width and height to the volume's height and depth. The depth is set to the maximum width-height or width-depth diagonal.

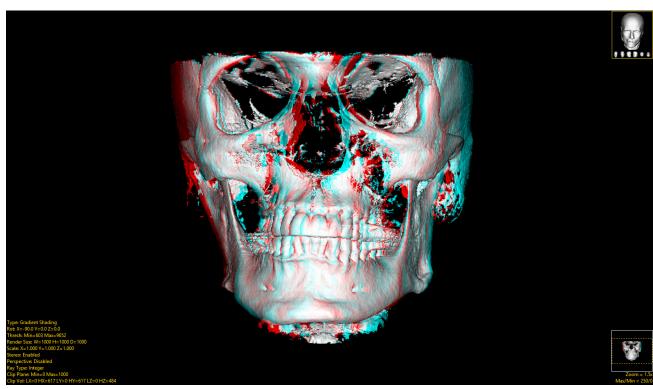
Object Compositing (continued)

Scale: Enables the specification of scaling factors to be applied to the inputs during the rendering process specifying the size of the rendered space. The following options are available:

- X: Specifies the X scale factor used to render the X axis, defining the render width.
- Y: Specifies the Y scale factor used to render the Y axis, defining the render depth.
- Z: Specifies the Z scale factor used to render the Z axis, defining the render height.

Stereo: The Stereo option allows users to generate stereo pairs of the current rendered image. To enable stereo pairs renderings, click on the yellow Stereo text or right click and check the Stereo option. The following right-click options are available:

- Red-Blue: Generates a rendering for use with "Red-Blue" glasses.
- Red-Green: Generates a rendering for use with "Red-Green" glasses.
- Red-Blue: Generates a rendering for use with "Red-Blue" glasses.



Object Compositing (continued)

Stereo (continued)

- Red-Green: Generates a rendering for use with "Red-Green" glasses.
- Cross Fusion: Generates a rendering for use without glasses. The viewer uses a technique of crossing their eyes, looking at the left image with the right eye and vice-versa.
- Interlaced: Generates a rendering where every other line comes from each view point. Viewing of this type usually requires an interlaced monitor and special glasses which trigger on each frames display.
- Disparity: Specifies the angle between the viewpoints. Half for each view point.
- Reverse Left/Right: When selected, swaps the viewpoints.
- Separation: Available only for Cross Fusion, this value specifies the number of voxels which separate the two centers of the two renderings.

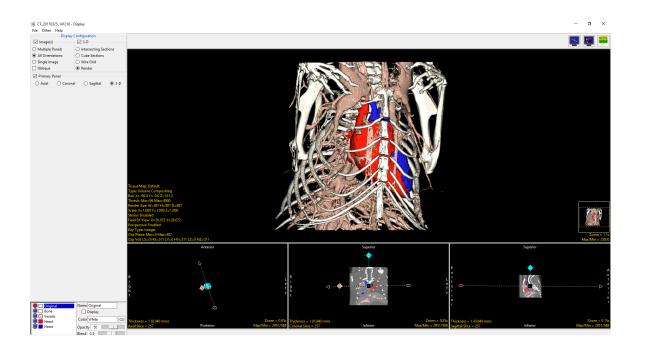
Perspective: The Perspective rendering tool allows users to create perspective renderings of the image data based on eye/camera and look at viewpoints. The tool can also be used in conjunction with the Sequence tool to create fly-thru movies. Clicking on the yellow Perspective text enables Perspective rendering. See the Perspective tool for further information on perspective rendering and movie generation.

- Right Click Options
 - Perspective: Enable or disable perspective rendering.
 - Perspective Ray Type: Allows users to choose between a floating point or integer ray type for perspective rendering. See Ray Type for further information.

Object Compositing (Continued)

Perspective (continued)

• Field Of View: The Field Of View (FOV) option allows users to specify the FOV for generating perspective renderings. Click the yellow Field Of View text and move the cursor right to increase the FOV, making the rendering appear smaller. Move the cursor left to decrease the FOV and the rendering appear larger. Double-clicking the yellow Field Of View text allows users to manually enter FOV parameters. Rightclicking on the Field Of View text provides access to the following options:



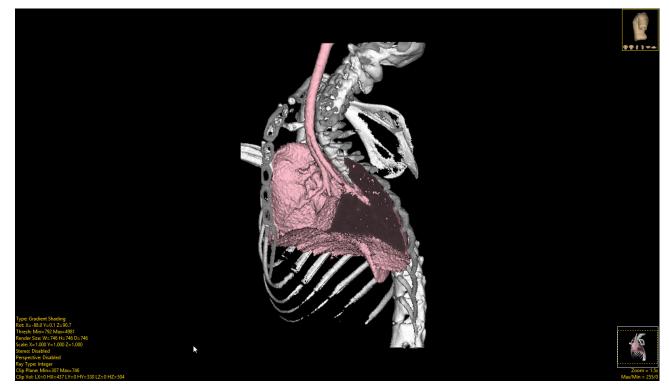
- Maintain Aspect: The Maintain Aspect option allows users to disable and enable aspect maintenance. Disabling the Maintain Aspect option allows users to specify different X and Y FOV parameters, allowing for the creation of a non-proportional rendering.
- Default: Sets the FOV to the default value, approximately a XY FOV value of 25.
- Zoom In: When selected decreases FOV, approximately a XY FOV value of 12.5.
- Zoom Out: When selected increases the FOV, approximately a XY FOV value of 50.
- Zoom Way Out: When selected increases the FOV, approximately a XY FOV value of 70.

Analyze 15.0 User's Guide

Object Compositing (Continued)

Ray Type: The Ray Type option allows users to switch the ray indexing type from Integer to Float. Switching to float will improve rendering, however, the best results will typically be seen with anisotropic data.

Clip Plane: The Clip Plane tool allows users to specify the maximum and minimum depth along the ray between which voxels are processed for inclusion in the rendered image. Voxels outside the depth range are ignored.



Clicking on the yellow Clip Plane text will update the cursor to display a CLIP cursor. Hold down the left mouse button and slide the cursor upwards to increase the Minimum clip value, backwards to decrease the value. Slide the cursor left to decrease the Maximum clip value and right to increase the Maximum clip value. Double click on the Clip Plane text to manually enter the minimum and maximum clip values

Right click options:

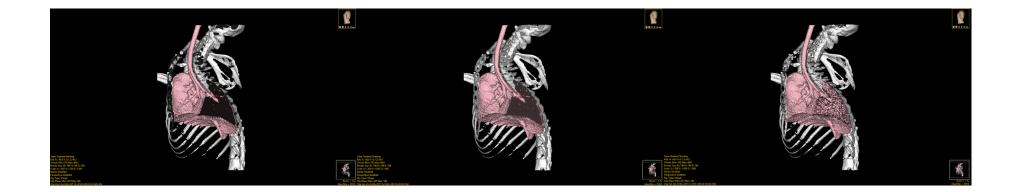
- Half way: When selected sets the minimum clip value to halfway through the data set.
- Reset: Resets the minimum and maximum clip values.

Analyze 15.0 User's Guide

Object Compositing (Continued)

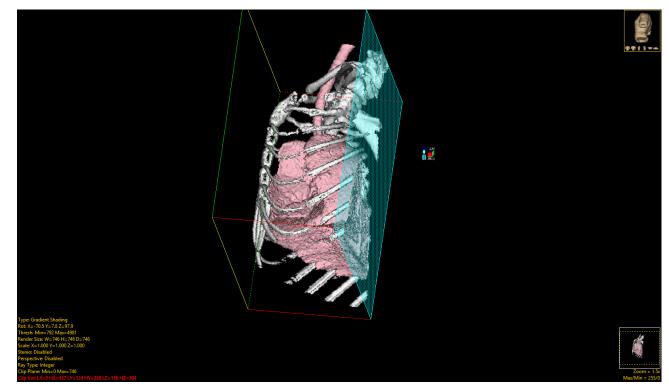
Clip Plane Right Click Options (cont): Clip Shading: The Clip Shading option specifies the type of shading used, choose from:

- Depth: Specifies that a value based only on depth is used to create the shaded pixel.
- Actual: Specifies that the gray scale value of the intersected voxel is used.
- Gradients: Specifies that the voxel along the ray path, just before the intersected voxel, is temporarily set to the input volume minimum intensity value and the gradient shading is calculated.



Object Compositing (Continued)

Clip Vol: The Clip Volume tool allows users to specify a sub-volume of the data to be rendered based on the X, Y, Z coordinates of the volume. Clicking on the yellow Clip Vol text will update the cursor to display a CLIP cursor and volume edges will appear around the rendered image. Click on the volume edges to toggle through the planes to clip, choosing from Low X, High X, Low Y, High Y, Low Z and High Z.



Hold down the left mouse button and slide the cursor upwards to increase the plane value, backwards to decrease the value.

Double click the text to manually enter the volume sub-volume parameters:

- LX: Low X, specifies the low X value.
- HX: High X, specifies the high X value.
- LY: Lox Y, specifies the low Y value.

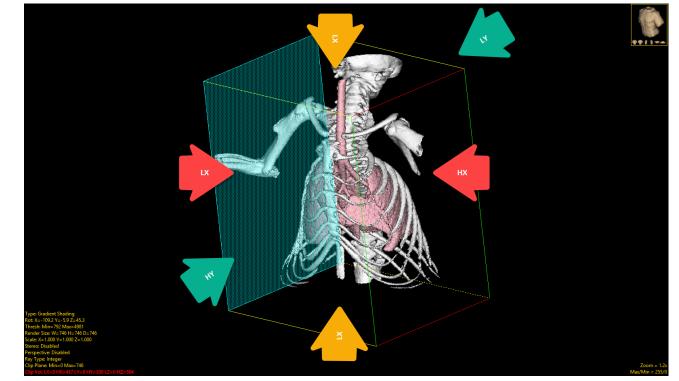
Object Compositing (Continued)

Clip Vol (continued):

- HY: High Y, specifies the high Y value.
- LZ: Low Z, specifies the low Z value.
- HZ: High Z, specifies the high Z value.

Clip Vol Right Click Options:

• Reset: Resets the minimum and maximum clip values.

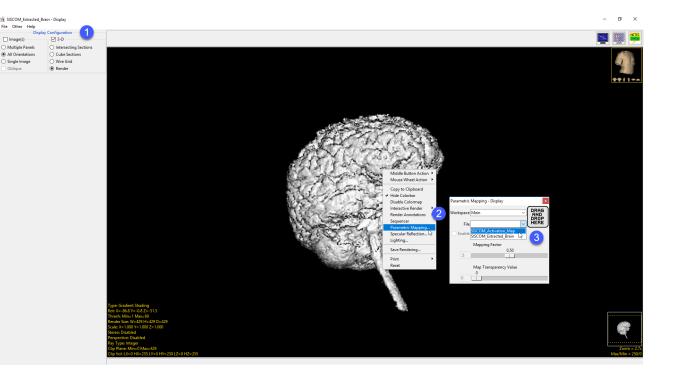


- Clip Shading: The Clip Shading option specifies the type of shading used. Choose from the following options:
 - Depth: Specifies that a value based only on depth is used to create the shaded pixel.
 - Actual: Specifies that the gray scale value of the intersected voxel is used.
 - Gradients: Specifies that the voxel along the ray path, just before the intersected voxel, is temporarily set to the input volume minimum intensity value and the gradient shading is calculated.

Parametric Mapping

The Parametric Mapping functionality provides users with the ability to blend the rendering of two image data sets. This is useful for displaying renderings of functional data with structural data. A related data set is loaded via the Parametric Mapping window available from the right mouse menu in the Render window. The related image must be registered with the base data set beforehand in order for it to be used as a parametric input volume.

Download the MRI_Brain.avw and the PET_Brain.avw to follow along from



https://analyzedirect.com/data. Use the Input/Output module to load both the MRI_Brain.avw and the PET_Brain.avw data sets. Select the MRI_Brain data set and then open Display. In Display set the Display Configuration to 3-D and choose the Render option (1). Uncheck the Image(s) option.

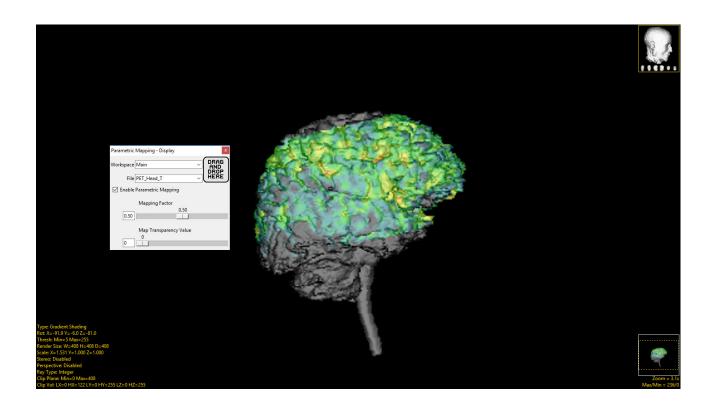
Change the orientation of the brain to right using the Navigation icon (2). Right-click in the Render window and choose Parametric Mapping from the menu options (3).

In the Parametric Mapping window choose the PET_Brain data set from the File drop down (4). If the data resides in another Workspace select that workspace using the Workspace drop down. Alternatively, drag-and-drop the related image from the workspace onto the Parametric Mapping window.

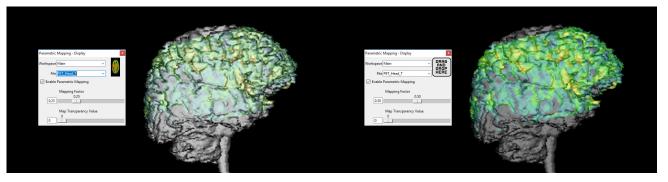
147

Parametric Mapping (Continued)

The Parametric rendering will be displayed.



Adjust the Mapping Factor and observe the effect on the rendering.



Sequence Tool

Creating a Basic Movie

The Sequence tool provides users with an intuitive interface to quickly create impressive movies of the rendered image data.

Download the Mouse_Lungs.avw data set to follow along, from https:// analyzedirect.com/data.•

Use the Input/Output module to load the Mouse_Lungs.avw.

Select the Mouse_Lungs data set and then open Display.



In Display set the Display Configuration to 3-D and choose the Render option. Uncheck the Image(s) option. (1)

Right-click in the Render window and select Sequencer from the menu (2). The Sequencer tool will be displayed below the rendering. (3)

Click the Add Key Frame button (4) to add a starting key frame to the sequencer (5).

Double-click the Yellow Thresh text in the lower left-hand corner of the Render window and change the minimum value to 2200 (6). Note the updated rendering. (7).

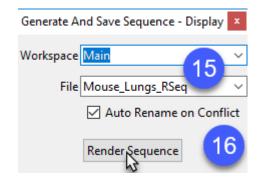
Click the Add Key Frame button (8) to add a new key frame to the sequencer (9).

Left click the Transition button (10) between the key frames to open the Transition parameters window (11), here set the number of Frame(s) to 30 (12). predection de scane ve de de sc

Click the Preview Sequence button (13) to preview the movie.

To save the movie to the Analyze workspace select Generate and Save. (14).

In the Window returned name the movie (15) and then select Render Sequence (16). The movie file will be saved to the workspace. Use the Input/Output module to save the movie out of the software as an .AVI, QuickTime, or Animated GIF.



Creating a Rotational Movie

Download the Mouse_Lungs.avw and the Mouse_Lungs.obj files to follow along, from https://analyzedirect.com/ data

Use the Input/Output module to load the Mouse_Lungs.avw.

Select the Mouse_Lungs data set and then open Display.

Select File > Load Object Map and load the Mouse_Lungs.obj.

In Display set the Display Configuration to 3-D and choose

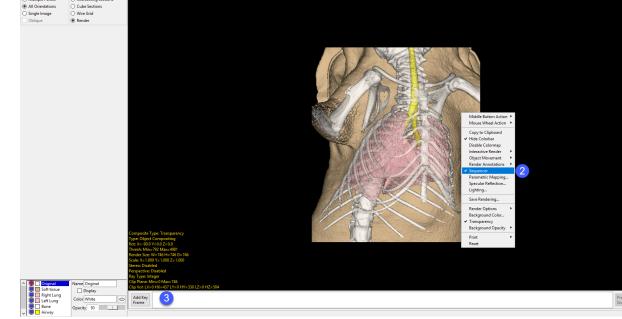
the Render option (1). Uncheck the Image(s) option.

Right-click on the Rendering and then choose Transparency from the menu.

After Transparency has been applied right click again and select the Sequencer option (2).

9 Mouse Lungs - Displ

The Sequencer tool will be displayed below the rendering (3)



To create a simple rotational movie, click the Add Key Frame button (4) twice to add two key frames to the sequencer (5).

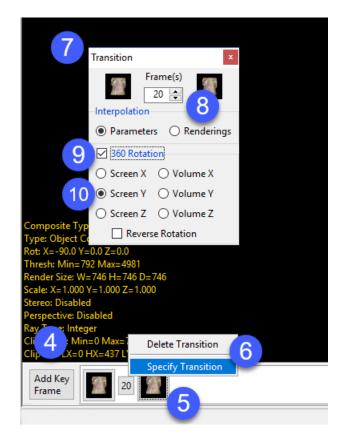
Left click the Transition button between the key frames (6) to open the Transition parameters window (7).

In the Transition window set the number of Frames to 20 (8), next check the 360 Rotation option (9) and then select Screen Y (10).

Select the Preview Sequence button to review the movie (11).

To save the movie to the Analyze workspace select Generate and Save. (12)

In the Window returned, name the movie and then select Render Sequence. The movie file will be saved to the workspace. Use the Input/Output module to save the movie out of the software as an .AVI, QuickTime, or Animated GIF.





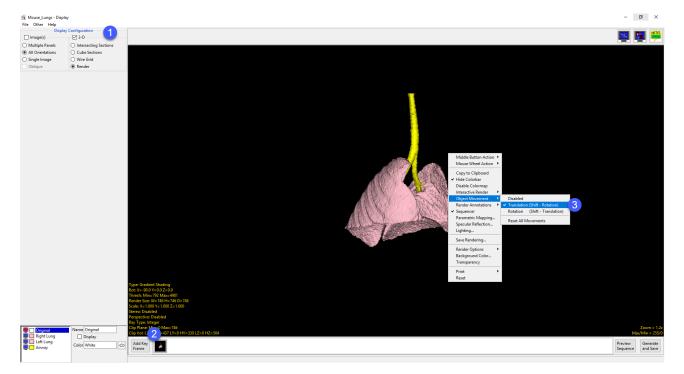
Enhanced Movie Making: Object Movement and Rotation

Download the Mouse_Lungs.avw and the Mouse_Lungs_2.obj files to follow along, from https://analyzedirect.com/ data

Use the Input/Output module to load the Mouse_Lungs.avw.

Select the Mouse_Lungs data set and then open Display.

Select File > Load Object Map and load the Mouse_Lungs_2.obj.



In Display set the Display Configuration to 3-D and choose the Render option (1). Uncheck the Image(s) option.

Right click in the Render window and select the Sequencer option.

The Sequencer tool will be displayed below the rendering, click the Add Key Frame button (2) to add a starting key frame to the sequencer.

Next, right-click on the in the Render window and choose Object Movement > Translation (3).

Click on the left lung object to select it and then drag it to the right (4). When complete click Add Key Frame (5).

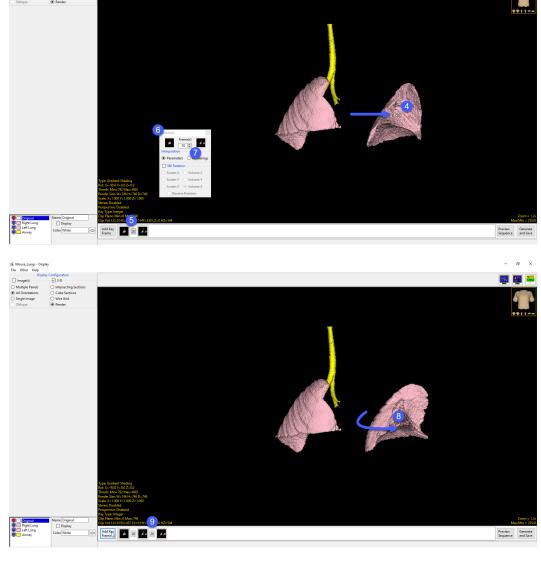
Click Transition button between the two key frames to open the Transition parameters window (6), set the Frame(s) to 20.

Click Preview Sequence to preview the movie so far.

Next, press the Shift key and then select the left lung, the Object Transformation will be changed from a translation to a rotation, rotate the left lung (8).

When complete click Add Key Frame, note that the transition is automatically set to 20 frames (9).

Click Preview Sequence to preview the movie so far.



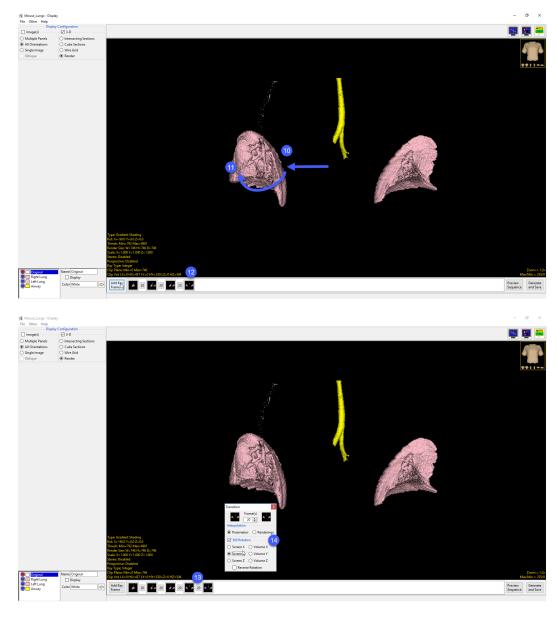
154

Next, let's perform the translation and rotation on the right lung in one key frame. Click on the right lung object to select it and then drag it to the left. (10) Press the Shift key and select the right lung again, rotate the right lung (11).

When complete click Add Key Frame, again the transition is automatically set to 20 frames (12).

Click Preview Sequence to preview the movie so far. The movie will show the left lung moving out the right side followed by a rotation, next the left lung will move out to the left side while performing a rotation.

Now let's add a rotation. Click the Add Key Frame button again to add a new key frame, click on the Transition button added before the last key frame (13). In the Transition window check the 360 Rotation option and choose Screen Y (14).



To end the movie, let's have all objects move back to their original positions. You could achieve this by right-clicking on the Render window and choosing Object Movement > Reset All Movements. However, in this case we will copy the first key frame and paste it to the end of the sequence we have generated.

Right-click on the first key frame and choose Copy from the menu (15).

Right-click at the end of the sequence and choose Paste (16) to paste a copy of the first key frame and the end (17). This provides a nice movie that starts and ends with the all objects in the same position, important for when looping the movie for a presentation.

Preview the movie and then use the Generate and Save option to save a copy to the workspace.

9 Mouse Lunas - Displ

Explore the other rendering options to help enhance your movies, for example use the Scale option to give the effect of zooming in or out of your rendered image and use the Clip Plane or Clip Volume options to clip into the data.

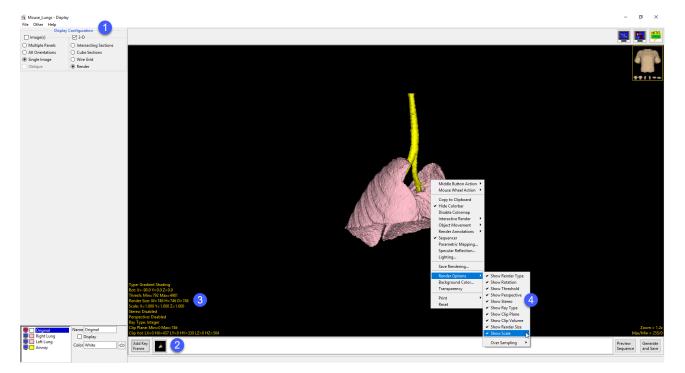
Enhanced Movie Making: Zooming and Clipping

Download the Mouse_Lungs.avw and the Mouse_Lungs_2.obj files to follow along, from https://analyzedirect.com/ data

Use the Input/Output module to load the Mouse_Lungs.avw.

Select the Mouse_Lungs data set and then open Display.

Select File > Load Object Map and load the Mouse_Lungs_2.obj.



In Display set the Display Configuration to 3-D and choose the Render option (1). Uncheck the Image(s) option.

Right click in the Render window and select the Sequencer option.

The Sequencer tool will be displayed below the rendering, click the Add Key Frame button (2) to add a starting key frame to the sequencer.

If the additional rendering options are not visible in the lower left hand corner of the Render window (3) enable the options by right-clicking in the Render window and then choosing Render Options from the menu, check the Show Scale and Show Clip Plane options, but feel free to enable all options (4).

Double click the yellow Scale text and change the X, Y, and Z Scale values to 2.2 (5). Note that the rending display size will increase.

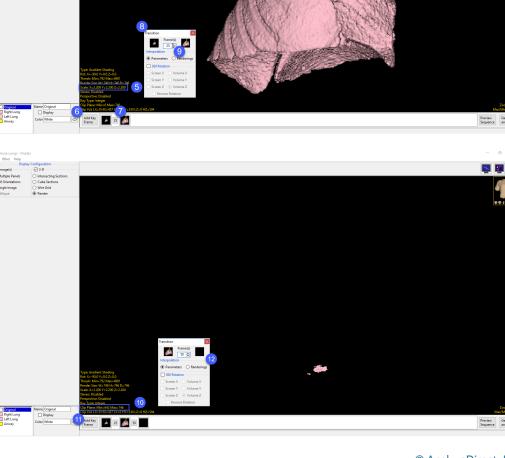
Click Add Key Frame (6) to add a new key frame to the sequence.

Click the Transition button (7), in the Transition parameters window (8) set Frame(s) to 25 (9).

Double click the yellow Clip Plane text and change the Min value to 642. (10) Note that the rendering display will be clipped.

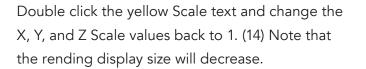
Click Add Key Frame (11) to add a new key frame to the sequence.

Click the Transition button and increase the number of Frame(s) to 50 (12).



Double click the yellow Clip Plane text and change the Min value back to 1. (13) Note that the rending display will update.

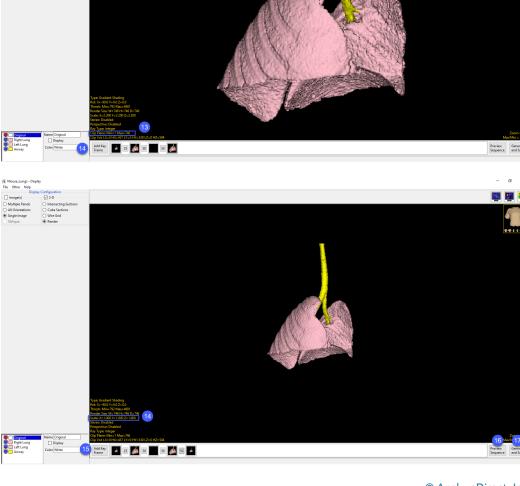
Click Add Key Frame (14) to add the new key frame to the sequence.



Click Add Key Frame (15) to add the new key frame to the sequence.

Click Preview Sequence (16) to preview the movie.

Click Generate and Save (17) to save the movie to the workspace.



Perspective Tool

The Perspective Tool provides users with another option to create powerful and interesting movies from their rendered image data.

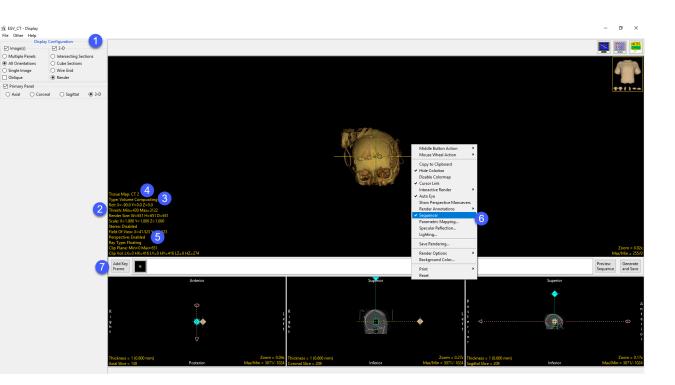
Download the EGV_CT.avw data set to follow along, from https:// analyzedirect.com/data.

Use the Input/Output module to load the EGV_CT.avw.

Select the EGV_CT data set and then open Display.

In Display check both the Image(s) and 3-D Display Configuration

options. Make sure to choose All Orientations and Render.



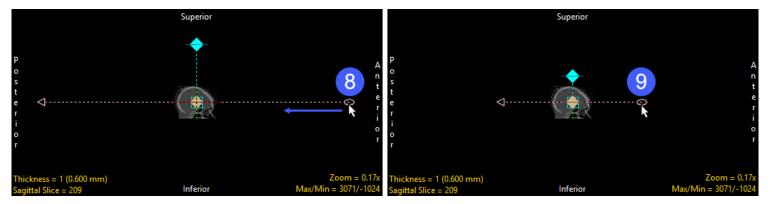
From the Render options in the lower left-hand corner double click on the yellow Thresh text and change the Min value to 430. (2) Note if the Render options are not available right click in the Render window and choose Render Options, enable all the options.

Right click on Type and select Volume Compositing. (3) Then right click on Tissue Map and choose System Tissue Maps > CT 2 (4).

Enable the Perspective tool by clicking on the Perspective option changing it from disabled to enabled. (5) Note that the three orthogonal views will update to display interactive camera and look at points. Right click in the Render window and choose Sequencer (6) to enable to sequencer below the Render window. Click Add Key Frame to add a starting key frame to the sequencer (7).

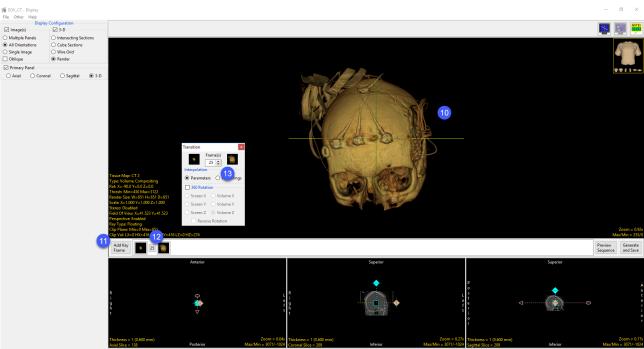
Analyze 15.0 User's Guide

Perspective Tool (continued)



In the Sagittal orientation click on the perspective camera point (round icon) (8) and move it to the left (9).

Oblique

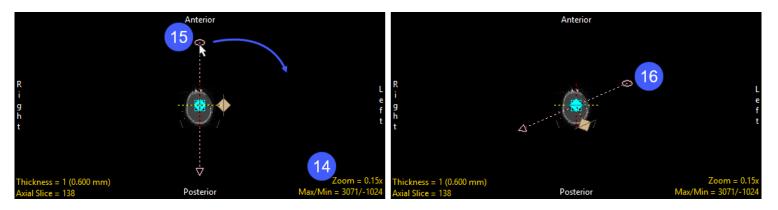


Note the update to the rendering (10).

Click the Add Key Frame button (11) to add the new key frame to the sequence. Click the Transition button (12) and set the Frame(s) to 25 (13).

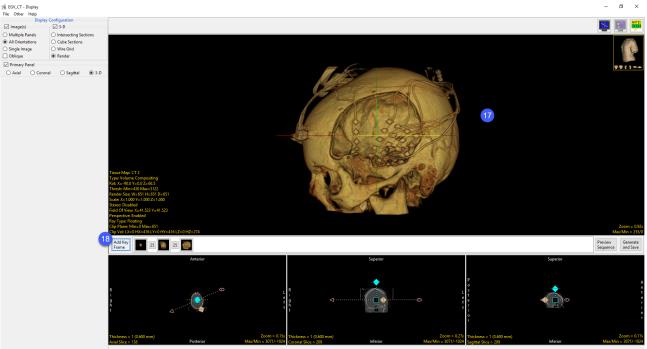
Perspective Tool (continued)

In the Axial orientation, zoom in to view the display clearer. (14). Select the perspective Camera point (15) and move it clockwise (16).



Image(s)

Oblique

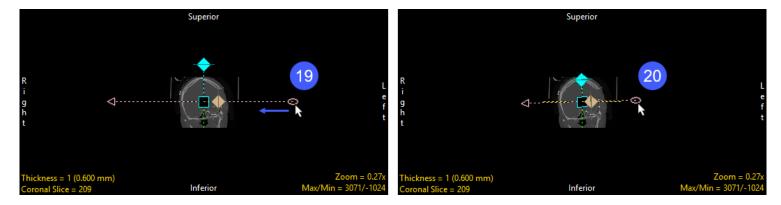


Note the update to the rendering (17).

Click the Add Key Frame button (18) to add the new key frame to the sequence.

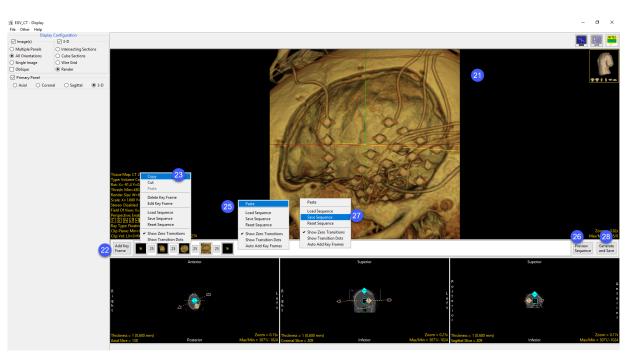
Perspective Tool (continued)

In the Coronal orientation click on the perspective camera point (19) and move it left, closer to the image data (20).



Note the update to the rendering (21). Click the Add Key Frame button (22) to add the new key frame to the sequence. Right click on the first frame and choose Copy (23). At the end of the sequence right click and choose Paste. (25) The movie will now start and end at the same point.

Preview the movie (26). If you wish to save the movie sequence to apply to another data set, right-click in the Sequencer and choose Save Sequence. (27). To save the movie to the workspace select Generate and Save (28).



Process

| Introduction | page 165 |
|---|----------------------------------|
| Spatial Filters | page 166 |
| Applying a Filter to a Data Set | page 169 |
| Morphology | page 172 |
| Available Morphological Operations | page 173 |
| Applying Morphological Operators to Data | page 174 |
| Histogram | page 180 |
| | page loo |
| Histogram Operations | page 181 |
| - | |
| Histogram Operations | page 181 |
| Histogram Operations Histogram Flatten | page 181 page 182 |
| Histogram Operations Histogram Flatten Histogram Preserve | page 181 page 182 page 184 |

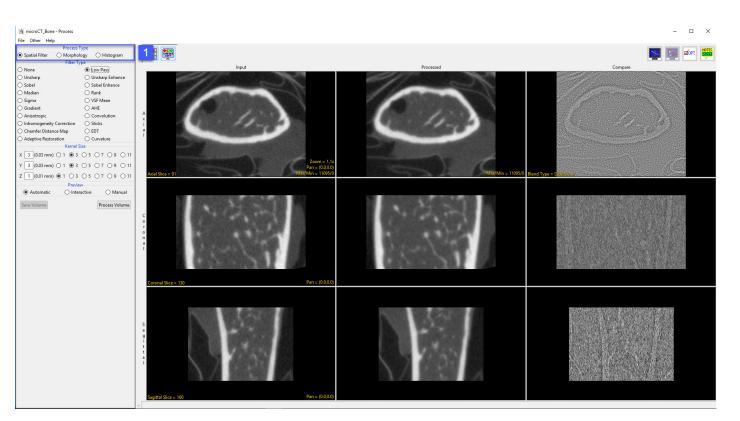
Introduction

The Process module provides access to image enhancement tools that allow data to be refined, such that image features can be seen easier or detection of regions is improved during segmentation.

There are three main process functions [1] available:

Spatial Filters - for the filtering of image data to reduce image noise or increase contrast between structures of interest.

Morphology - mathematical segmentation operations for the pre-processing of image data for segmentation.



Histogram - for the modification of the image histogram to enhance image quality or enhance features.

All of 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 σ \ddagger |
| VSF Mean | smoothes noise while preserving edges | replaces the value x of each voxel with the average value of voxels in the |
| | and thin lines | 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 ${\rm I_i}$ * global mean / local mean, where ${\rm I_i}$ 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.

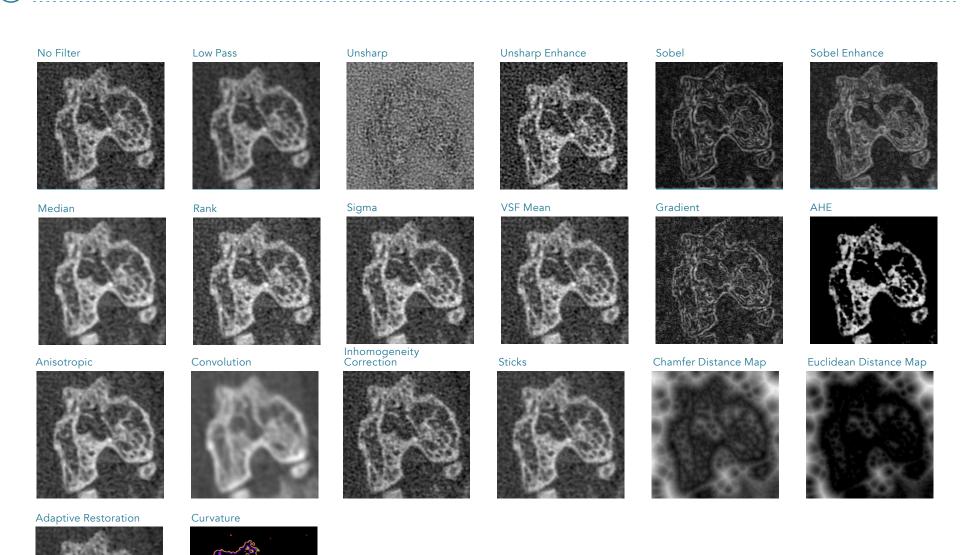
†The kernel size determines the number of voxels whose values are ranked, e.g. a 3 X 3 X 3 kernel has 27 voxels, a 5 X 5 X 5 kernel has 125 voxels and a 7 X 7 X 7 kernel has 343 voxels. The larger the kernel size, the more computationally intensive this filter becomes. It is recommended to use a smaller 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 ± 2σ range, the voxel in question will not be changed. Sigma (σ) 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.

IIA 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.



Applying a Filter to a Data Set

🐋 Analyze 15.0

Download the microCT_Bone.avw data set to follow along, from https://analyzedirect.com/data.

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

Use the Input/Output module to load the microCT_Bone.avw data set into the software.

Select the data set [1] and open Process [2].



đ

<u>(</u>) ا

•

Applying a Filter to a Data Set (continued)

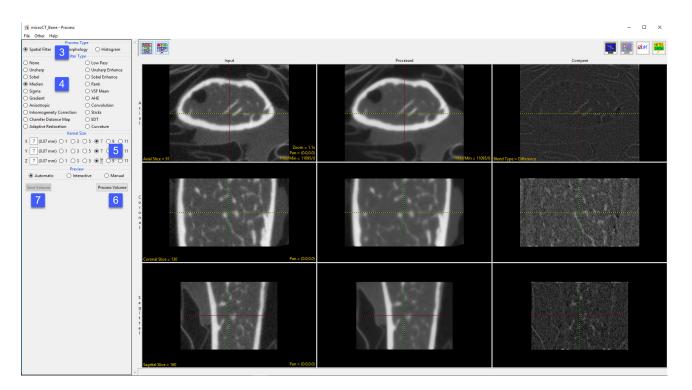
Choose Spatial Filter as the Process Type [3].

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.

Click Process Volume [6].

Once the processing is complete, the Save Volume button will become available. Click Save Volume [7].



Applying a Filter to a Data Set (continued)

Save Volume - Process

In the Save Volume window, choose to replace the input data set with the processed data set, or to create a new data set [8].

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 [9]. Create a new workspace volume containing the processed data.
 Workspace Main
 File microCT_Bone_Med
 Replace Input Volume with Processed Volume
 Save Volume
 10

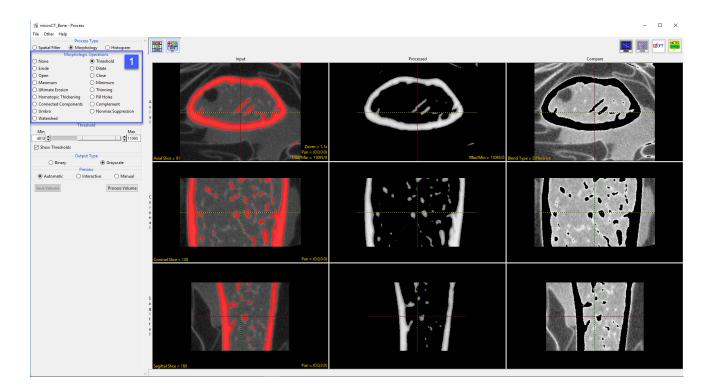
Replace contents of 'microCT_Bone' with the processed data.

Click Save Volume [10].

Morphology

A number of morphologic operations are available [1], and these are described in the table on the next page.

These operations can be performed on the entire volume or on selected objects if an object map is loaded.



Available Morphological Operations

| Morphologic Operation | Description | Method |
|-----------------------|---|---|
| Threshold | isolates structures defined by a difference in | sets voxels between and equal to the specified maximum and minimum to 1 and all |
| | intensity | other voxels to 0 |
| Erode | peels a layer from the outer edge of large | retains voxels in inner areas of the object, as determined by the structuring element |
| | objects and deletes small objects | 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 | performs successive erosions on the object until the last erosion before the |
| | components | components would disappear |
| Thinning | thins an object in binary or grayscale | thins the object based on the number of iterations specified, using template matching |
| 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 |

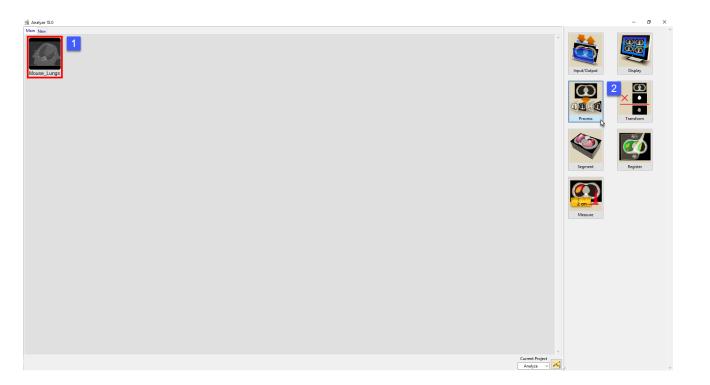
Applying Morphological Operators to Data

Download the Mouse_Lungs.avw data set to follow along, from https://analyzedirect.com/data.

This exercise will show how to apply a series of morphological operations to a data set to isolate an object of Interest while removing as much unwanted tissue as possible. This will prepare the data for further analysis. In this example we will isolate the lungs from a preclinical micro-CT data set by using various morphological operations including thresholding, eroding, and opens.

Use the Input/Output module to load the Mouse_Lungs.avw data set into the software.

Select the data set [1] and open Process [2].



File Other Help

) Erode

Oper Maxim O Ultimate Ero

Connected C Umbra Watershee

Show Threshold

Automati

ave Volum

8

O Binar

Min 1105 🜲

The first step in this process is to eliminate the background noise.

Choose Morphology as the Process Type [3].

Choose the Threshold option as the Morphological Operation [4].

Set the Minimum Threshold level to 1105 [5]. Note that this will eliminate the background single.

Set the Output Type to Grayscale [6].

Next, click Process Volume [7].

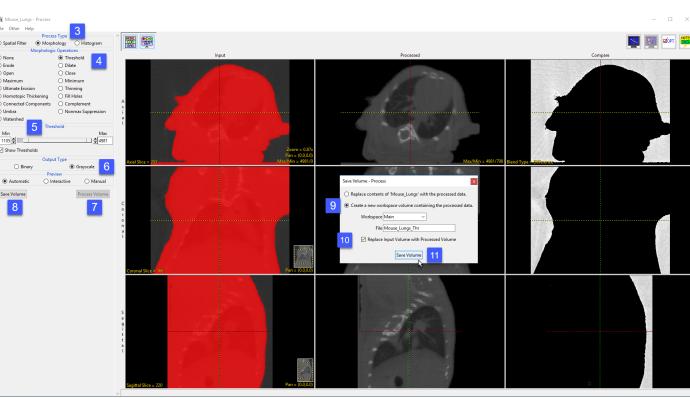
When processing is complete click Save Volume [8].

In the Save Volume window ensure the 'Create a new workspace volume containing the processed data.' option is selected [9].

Also, ensure the 'Replace Input Volume with Processed Volume' option is checked [10].

Click Save Volume [11]. The processed data will be saved as a new volume in the workspace and will also be set as the Input Volume for Process.

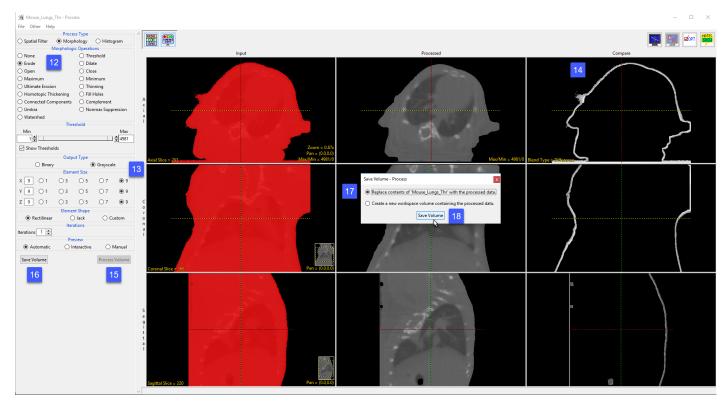




The next step is to remove a layer of voxels from the outer surface of the body. This step is completed in order to prevent these voxels from being included when we use thresholding in the next step to isolate the lungs.

Select the Erode option from the Morphological Operations menu [12].

Set the Element Size to 9 by 9 by 9 [13]. The voxels that will be eroded from the data can be seen in the Compare column [14].



Next, click Process Volume [15] and when processing is complete click Save Volume [16].

This time in the Save Volume window check the 'Replace contents of 'Mouse_Lung_Thr' with processed data.' option [17]. This will overwrite the volume and prevent an additional volume being written to the workspace.

Click Save Volume [18]. The processed data will be saved over the input volume and also be set as the Input volume.

Now we will use Thresholding to isolate the lung parenchyma.

Choose the Threshold option from the Morphological Operation menu [19].

Set the Minimum Threshold level to 1 and the Maximum Threshold level to 1639 [20].

Note that this threshold range will isolate the lungs [21].

Next, click Process Volume and when processing is complete click Save Volume.

In the Save Volume window leave the option set to

'Replace contents of 'Mouse_Lung_Thr' with processed data.'

Click Save Volume [22]. The processed data will be saved over the input volume and be set as the Input.



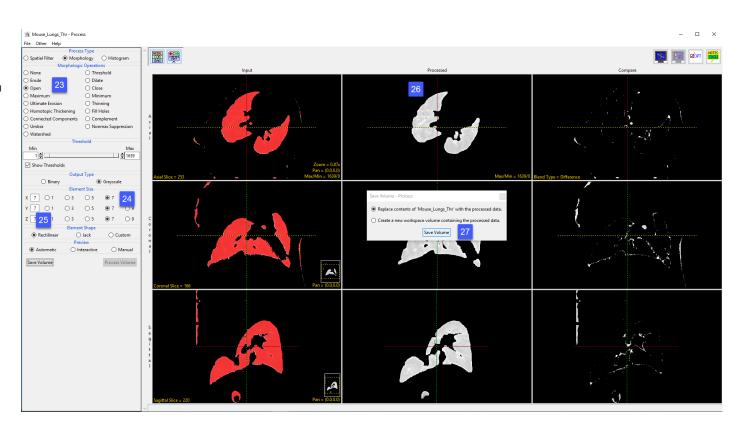
© AnalyzeDirect, Inc.

The final step to process this data set is to conduct a morphological Open operation on the image data. An Open operation is an erode followed by a dilation. The erode will take away layers, removing areas of noise. The dilate operation will then add back layers of voxels removed from the lung.

Set the Morphological Operation to Open [23]. Set the Element Size to 7 by 7

Ensure the Element Shape is

by 7 [24].



set to Rectilinear [25]. Note the preview of the final isolated lung data set [26].

Next, click Process Volume and when processing is complete click Save Volume.

In the Save Volume window leave the option set to 'Replace contents of 'Mouse_Lung_Thr' with processed data.'

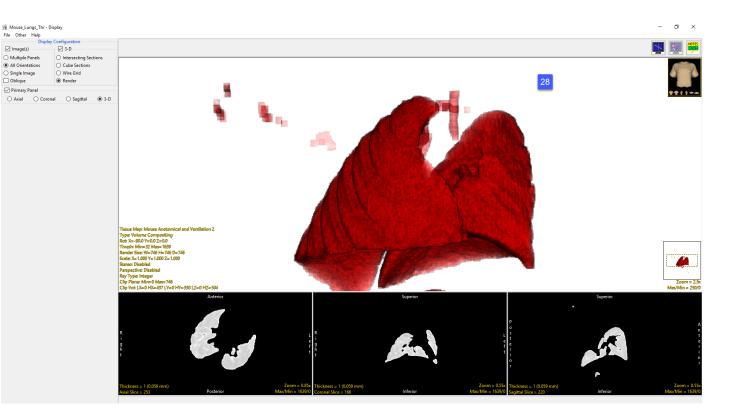
Click Save Volume [27]. The processed data will be saved over the input volume and be set as the Input.

Close the Process module.

Applying Morphological Operators to Data (continued)

Select the processed image data 'Mouse_Lung_Thr' from the workspace and view it using the Display module [28].

In four easy steps we have isolated the lungs with a minimal amount of surrounding noise. This data is ready for visualization, volume measurement, or further segmentation.



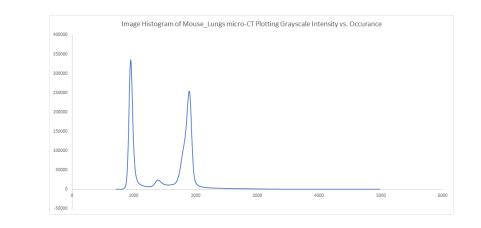
Histogram

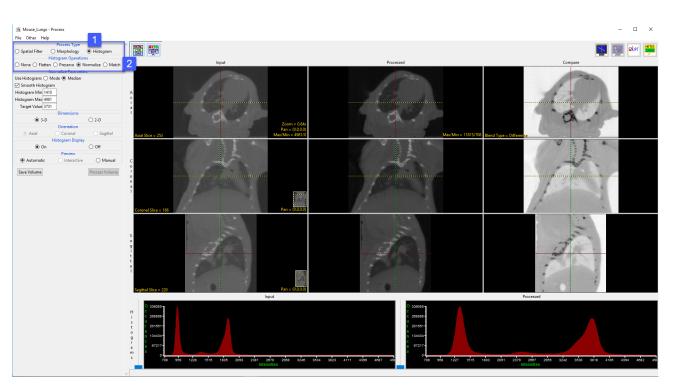
The histogram of an image is a function that relates the number of pixels in the image to the range of brightness values of those pixels. This can be expressed in a 2-D graph, plotting brightness vs. number of pixels.

The Histogram Process Type [1] allows users to perform the manipulations to alter the shape of the gray level histogram of an image to reduce noise, enhance contrast, or detect edges.

The Histogram Operations [2] available are:

- Flatten (also known as equalization)
- Preserve
- Normalize
- Match





Histogram Operations

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 |

Histogram Flatten

The histogram flattening function allows users to attempt to produce an even distribution of voxels across the gray scale range specified by the Output Range minimum and maximum. A volume which has roughly equal numbers of voxels at every gray scale value will tend to exhibit maximal contrast across the entire gray scale range. Original grayscale values may be brightened, darkened, and or binned together to affect the flattening procedure.

In this exercise we will apply the histogram flattening function to Cubic CT Head data set and observe the effects.





Download the Cubic_CT_Head.avw data set to follow along from http://analyzedirect.com/data

Load the Cubic_CT_Head.avw into Analyze using the Input/Output module.

Select the Cubic_CT_Head data set from the workspace [1] and open Process [2].

ø

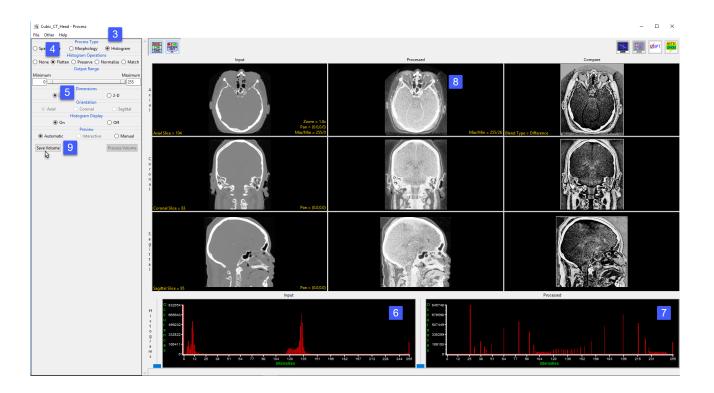
Histogram Flatten (continued)

Select the Process Type Histogram [3].

Set the Histogram Operation to Flatten [4].

Leave the Output Range Minimum set to 0 and Maximum set to 255 [5].

Note the input histogram [6] and the flattened output histogram [7]. The histogram flattening function has evenly distributed the range of voxels from the input volume across the grayscale range of the output volume.



Review the enhanced processed data set [8]. Additional structure in the brain can be seen in the processed image that is not visible with the current Max/Min levels set for the input volume.

Click Save Volume [9] to save the processed image data to the workspace.

Histogram Preserve

The histogram preserve function provides a utility for feature enhancement with in the input data set. The function works by mapping a broad grayscale range into a narrow range in a statistically optimal manner. For example, this function may be used to map 16384 gray level bins of a 16-bit image into 256 bins of an 8-bit image. The ideal distribution would place 1/256 of the total pixels in each of the 256 bins.

In the exercise we will demonstrate how to use the histogram preserve function to map the histogram of a 16-bit CT cardiac data set to an 8-bit data set and review the resulting





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

Load the CT_Heart.avw into Analyze using the Input/Output module.

Select the CT_Heart.avw data set from the workspace [1] and open Process [2].

ø

Histogram Preserve (continued)

Select the Process Type Histogram [1].

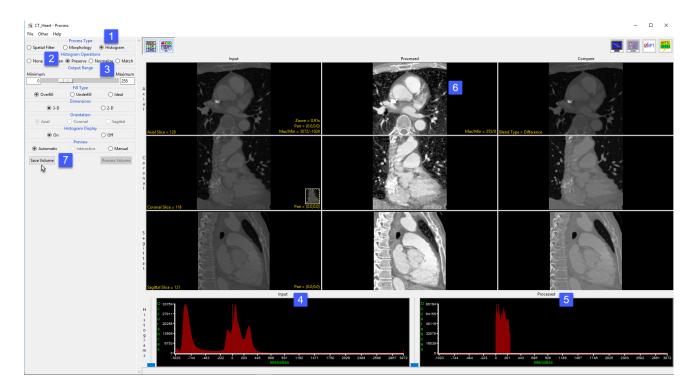
Set the Histogram Operation to Preserve [2].

Set the Output Range Minimum to 0 and the Maximum to 255 [3].

Note the input histogram [4] and the processed output histogram [5]. The histogram preserve function has mapped the entire range of the signed 16-bit input data set (-1024 to 3072) to the range of an unsigned 8-bit data set (0-255).

Review the enhanced processed data set [6].

Click Save Volume [7] to save the processed image data to the workspace.



Histogram Normalization

Histogram Normalization forces the Gaussian parameters of the image histogram (mean or mode) to specified values.

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.

Download the two data sets SISCOM_Ictal_SPECT.avw and SISCOM_Interictal_SPECT.avw from http://analyzedirect.com/data and load both datasets into the Analyze workspace using Input/Output. Select the SISCOM_Ictal_SPECT.avw data set from the 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]. Note the update to the processed histogram [4] and processed data set [5]. Setting the target value of each data set to the same value will allow comparison between the two.

Click Save Volume [6].

Analyze 15.0 User's Guide

Histogram Normalization (continued)

In the Save Volume window, choose to replace the input volume with the process volume [17] or create a new workspace volume [7].

Name the file, if creating a new workspace volume [8].

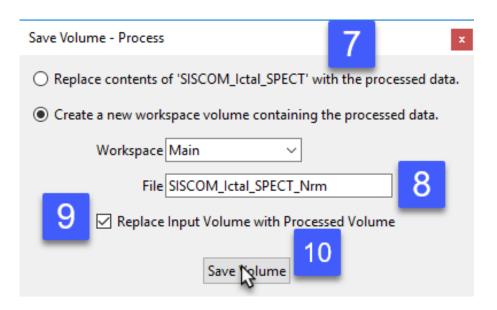
If you want to process the volume further, choose to replace the input volume with the process volume [9].

Click Save Volume to apply the changes [10].

Repeat these steps for the second data set, SISCOM_Interictal_ SPECT.avw.

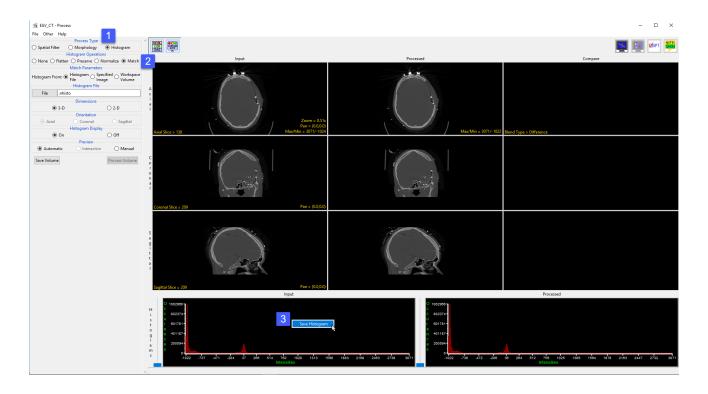
The two new volumes you have created have been normalized to the same value,

so equivalent numbers in the images now indicate levels of metabolic activity. The data sets can be subtracted to create a difference map or otherwise quantitatively compared.



Histogram Match

Histogram matching matches the intensity distribution of a volume to a histogram. The function forces the histogram of the input volume to match the grayscale distribution of the specified histogram file from another data set. Volumes of the same subject should have the same general distribution of gray levels, even though the parameters of a particular volume (exposure, brightness, contrast) may vary widely. Histogram matching may be used to normalize the absolute grayscale values of a set of volumes to a selected optimal example.



The goal of this exercise is to match the histograms of two data sets acquired for the same subject. Download the EGV_CT.avw and EGV_MRI. avw datasets from http://analyzedirect.com/data to follow along.

Load the two data sets into Analyze using the Input/Output module. Select the EGV_CT data set and open Process.

Set the Process Type to Histogram [1] and select the Match Histogram Operations option [2].

Right-click on the Input histogram and choose Save Histogram [3]. Save the histogram file to the Desktop. Close the Process module.

Analyze 15.0 User's Guide

Histogram Match (continued)

Select the EGV_MRI data set and open Process.

Set the Process Type to Histogram and select the Match Histogram Operations option.

Click the File button under Histogram File [4] and then navigate to and select the .nhisto file saved for the EGV_CT data set and then click open.

The histogram will be applied to the data set. Note the change in the processed histogram [5] and the processed MRI data [6].

Click Save Volume to saved the processed data to the workspace.



Transform

| | Introduction | page 192 |
|------------|-----------------------------------|----------|
| | Spatial Transforms | page 193 |
| | Pad | page 194 |
| | Subregion | page 197 |
| | Resize | page 201 |
| | Interpolation Types | page 204 |
| | Shift | page 206 |
| Correctin | g Wraparound Using the Shift Tool | page 207 |
| | Flip | page 210 |
| | Flipping Data | page 210 |
| | Apply Matrix | page 212 |
| | AC-PC Alignment of Brain Data | page 215 |
| | Data Reorientation | page 225 |
| | Follow Path | page 228 |
| | Reslicing Data along the Trachea | page 229 |
| | Intensity Transforms | page 233 |
| | Threshold | page 234 |
| Creating a | Binary Data Set with Thresholding | page 234 |

| | Intensity Scale | page 237 |
|------------|-----------------------------------|----------|
| | Modifying Image Data Type | page 238 |
| | Invert | page 240 |
| | Inverting Data | page 240 |
| | RGB Channel Manipulation | page 243 |
| | Creating an RGB Data Set | page 244 |
| | Image Calculator | page 246 |
| | Calculator Keypad | page 247 |
| | Calculator Canvas | page 248 |
| | Button Tool | page 249 |
| | Creating a Difference Map | page 250 |
| | Image Algebra | page 253 |
| | Formula Parser | page 254 |
| | Variables | page 259 |
| Applying a | Binary Mask to a Grayscale Volume | page 261 |
| | Image Repair | page 264 |
| | Repairing an Image | page 266 |



Introduction

There are several types of transformations that can be applied to data: **spatial transformations** such as cropping, resizing or flipping; **intensity transformations** such as thresholding, intensity scaling and inversion; and **custom transformations** using mathematical operators with image calculator/image algebra and image repair. All of this functionality is housed in the Transform module under five transformation tabs: [1]

- M CT_20110325_141216 - 🐳 🚺 🕀 -0.62710 -0.76066 0.167704 11.53679 0.838140 -5.20613 0.519018 21.18117 0.0 1.0 Save Mate n Type: O Nearest Neighbor O Linea Cubic Spline O Windowed Sinc fin: 🔿 DataType (0) Data Minimim (0) O User Specified 0 Apply Matrix Redo
- 1. Spatial Transforms
- 2. Intensity Transforms
- 3. Image Calculator
- 4. Image Algebra
- 5. Image Repair

Spatial Transforms

The Spatial Transforms tab [1] provides access to all the spatial transformation tools within Analyze including:

- Pad
- Subregion
- Resize
- Shift
- Flip
- Apply Matrix
- Follow Path

Many of the functions available in this section are also available in Input/Output under the Process tab, however, the implementation of these transformation tools within Transform take advantage of the new intuitive interface making data manipulation easier and quicker.



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. The options for this tool are as follows:

Pad: The padding options allow users to pad a data set. Padding places the Input volume in a larger output volume at the position specified by the padding values. The pad values specify the X, Y, and Z input volume starting and ending position in the output volume. The following padding options are available:

- · X Low: The X Low field allows users to apply padding to the starting X position for the data set.
- X High: The X high field allows users to apply padding to the ending X position for the data set.
- **Y Low:** The Y Low field allows users to apply padding to the starting Y position for the data set.
- Y High: field allows users to apply padding to the ending Y position for the data set.
- · **Z Low:** field allows users to apply padding to the starting Z position for the data set.
- **Z High:** field allows users to apply padding to the ending Z position for the data set.

Equal Padding: When the Equal Padding option is enabled a pad value entered in any of the pad fields will be applied to all fields, applying the same number of slices to each side of the volume.

Pad Value: The Pad Value option allows users to assign a specific grayscale value to be assigned to the padded regions in the output volume.

Padded Volume: The Padded Volume option allows users to specify the output dimensions of the volume.

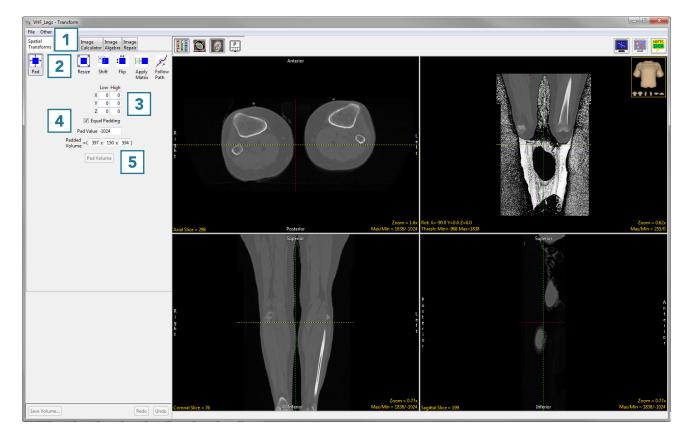
Pad Volume: Pads the input data based on the Pad parameters specified by the user.

Using the Pad Tool

Here we use the Pad tool to add blank slices around the original data set.

To follow along, download the data set VHF_Legs from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the data set to pad 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.

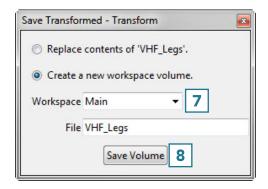


- To change the intensity value of the added slices, change the Pad Value [4].
- To set the padded volume dimensions, change the numbers in the appropriate boxes [5] and the low and high number of slices in each dimension will update automatically.

Using the Pad Tool (continued)

- 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.

| | Low | High |
|-------------------------|--------|------|
| Х | 0 | 0 |
| Y | 123 | 124 |
| Z | 0 | 0 |
| 🔲 Equ | al Pad | ding |
| Pad Value | -1024 | |
| Padded Volume =(397 | x 39 | 97 x |
| Pad V | olume | 6 |



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. Available options are as follows:

Subregion: The subregion matrix provides users with an interface to specify the starting (Low) and ending (High) crop points in each orientation (X, Y, Z, and V). Users can also specify increment (Inc) and Number (Num) of slices to crop. The subregion matrix will update when subregions are defined using the interactive cropping tool from the slice display.

- X: The X row allows users to specify column attributes for cropping data. Column attributes are automatically updated to reflect changes when modified.
 - · Low: Low allows users to specify the first column of pixels to be loaded.
 - · Inc: The increment options allows users to specify increments between the first column of pixels from each image to be loaded.
 - High: High allows users to specify the last column of pixels to be loaded.
 - Num: Number allows users to enter the number of columns for each image to be loaded.
 - Max: The Max field reports the maximum number of columns to be loaded. Note that this field is not editable.
- Y: The Y row allows users to specify the row attributes for cropping data. Row attributes are automatically updated to reflect changes when modified.
 - $\cdot\,$ Low: Low allows users to specify the first row of pixels to be loaded.
 - · Inc: The increment options allows users to specify increments between the first row of pixels from each image to be loaded.
 - High: High allows users to specify the last row of pixels to be loaded.
 - Num: Number allows users to enter the number of rows for each image to be loaded.
 - Max: The Max field reports the maximum number of rows to be loaded. Note that this field is not editable.
- Z: The Z row allows users to specify the slice attributes for cropping data. Slice attributes are automatically updated to reflect changes when modified.
 - · Low: Low allows users to specify the first slice to be loaded.
 - · Inc: The increment options allows users to specify increments between slices.
 - High: High allows users to specify the last slice to be loaded.

Subregion Options (continued)

Subregion > Z (Continued):

- \cdot Num: Number allows users to enter the number of slices to be loaded.
- Max: The Max field reports the maximum number of slices to be loaded. Note that this field is not editable.
- **Z: Only enabled when a multivolume is selected.** The V row allows users to specify the volume attributes for cropping data. Volume attributes are automatically updated to reflect changes when modified.
 - · Low: Low allows users to specify the first volume to be loaded.
 - · Inc: The increment options allows users to specify increments between volumes.
 - **High:** High allows users to specify the last volume to be loaded.
 - Num: Number allows users to enter the number of volumes to be loaded.
 - Max: The Max field reports the maximum number of volumes to be loaded. Note that this field is not editable.

Auto Crop: The Auto Crop tool will automatically calculate the minimum enclosing area to crop image data in the selected orientation. Auto crop will remove empty space around data. This is a useful utility for removing black background slices or automatically cropping binary data. The following options are available:

- Orientation: Allows users to select the orientation to be used to calculate the minimum enclosing area. Choose from; Axial, Coronal, or Sagittal.
- Slice(s): Allows users to auto crop the current slice or all slices in the current orientation.
- **Crop:** Initiates the auto crop process.

Extract Sub Volume: Extracts the sub volume utilizing the parameters specified in the subregion matrix.

Using the Subregion Tool

Here we will use the Subregion tool can be used to crop a data set to a specific region of interest.

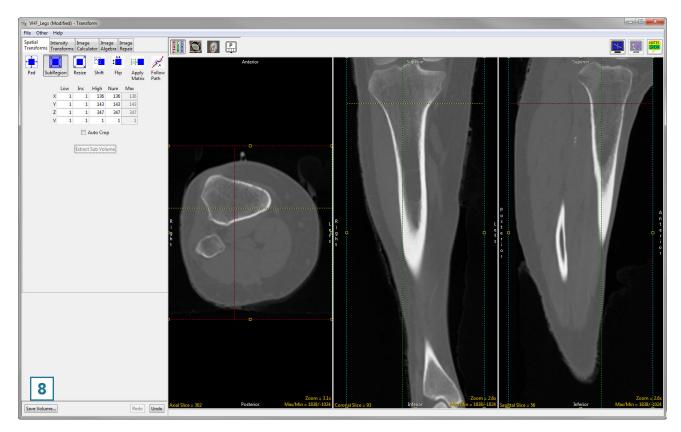
To follow along, download the data set VHF_Legs from analyzedirect.com/data and load into Analyze using Input/Output.

- 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].

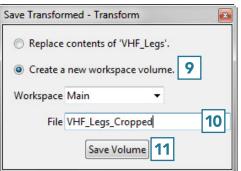


Using the Subregion Tool (continued)

• Click Save Volume [8] to save the cropped data set.

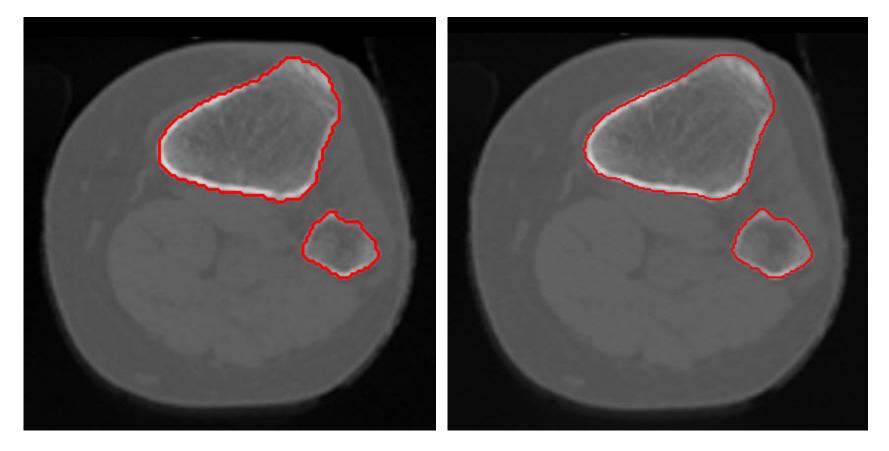


- To retain the original volume, choose to create a new workspace volume [9] and rename [10].
- Click Save Volume [11].
- Close Transform.



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

Resize Options

Resize: The resize tool allows users to perform tri-linear interpolation or voxel replication/sampling to resize a volume to a specific size. The interpolation parameters indicate the type of resize operation to perform. The following options are available:

Input: Displays the volume and voxel parameters of the input volume.

Axis Dim: Reports the voxel dimensions of the input volume:

• **X**, **Y**, **Z**: Displays the X, Y or Z dimension of the input volume.

Memory: Displays the size (memory usage) of the input volume.

Voxel Size: Reports the voxel size of the input volume. Note that the input X, Y, and Z values can be adjusted to accurately report the voxel size for the input volume.

• X, Y, Z: Displays the voxel width, height or distance between the slices of the input volume.

Output:

Voxel Size: Allows users to adjust the voxel size for the output volume. Note, when Force Cubic is selected, the individual X, Y, and Z fields are disabled leaving one value specifying the voxel size for X, Y, and Z in the output volume. When a voxel size is changed, the axis dimensions and memory usage are automatically calculated and updated to reflect the change.

· X, Y, Z: Allows users to specify the voxel width, height or distance between the slices for the output volume.

Memory: Reports the size (memory usage) for the output volume.

Axis Dim: The output axis dimensions display the voxel dimensions for the output volume. When a value is changed, the voxel size and memory usage are automatically calculated and updated to reflect the change.

• X, Y, Z: Specifies the X, Y or Z dimension of the output slice.

Force Cubic: When enabled, forces the output volumes voxel size to be cubic. This is useful when resizing anisotropic data to be isotropic.

Interpolate: Choose from Nearest Neighbor (ID), Linear (ID), Nearest Neighbor (OD), Linear (OD), Cubic Spline, Windowed Sinc or Shape Based to specify the interpolation method to use. See Table 6.1 for a full description of Interpolation Types.

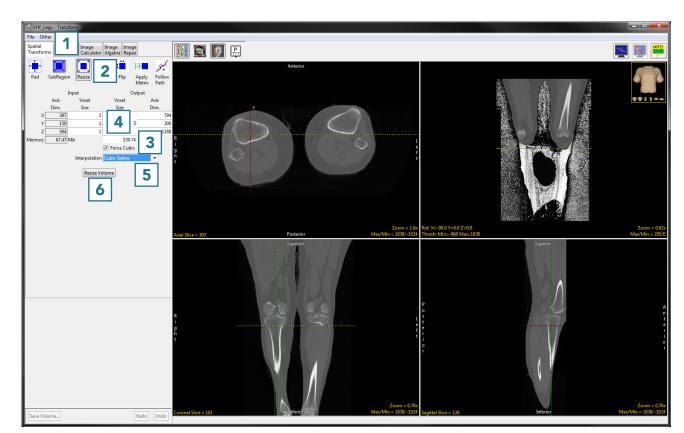
Using the Resize Tool

To follow along, download the data set VHF_Legs from analyzedirect.com/data and load into Analyze using Input/Output.

- 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 the table on the following page for different interpolation types.

• Click Resize Volume [6] to resample the data set.



Using the Resize Tool (continued)

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.

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.

Using the Resize Tool (continued)

• 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.

| Save Transformed - Transform | | |
|---------------------------------|---|--|
| Replace contents of 'VHF_Legs'. | | |
| Oreate a new workspace volume. | | |
| Workspace Main 🔹 | | |
| File VHF_Legs_Resampled | 9 | |
| Save Volume 10 | | |

Shift

The Shift tool can be used to shift data horizontally or vertically. This may be necessary to correct wraparound artifacts. Available options are as follows:

Shift: Allows users to enter the number of voxels to shift data in the X, Y, or Z:

- X: Entering a number will apply a positive x shift (shift to the left). Entering a negative number will apply a negative x shift (shift to the right).
- Y: Entering a number will apply a positive y shift (shift forward). Entering a negative number will apply a negative y shift (shift backward).
- Z: Entering a number will apply a positive z shift (shift up). Entering a negative number will apply a negative y shift (shift down).
- · Wrap: Allows users to specify if shifted voxels will wrap around when shifting.

Shift Volume: Applies the specified shift.

Shear: The Shear option allows users to apply horizontal and vertical shear correction in the Axial, Coronal, or Sagittal orientation. Note that Analyze automatically identifies and corrects for shear when loading data (see Shear Factor Correction in the Input/Output section of this manual).

- **Orient:** Choose from Axial, Coronal, or Sagittal.
- Horizontal: Allows users to specify the horizontal correction value for the selected orientation.
- Vertical: Allows users to specify the vertical correction value for the selected orientation.

Shear Volume: Applies the specified shear correction parameters.

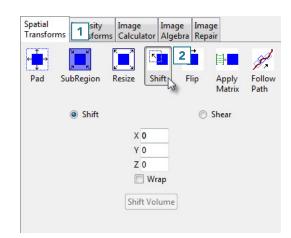
Using the Shift Tool

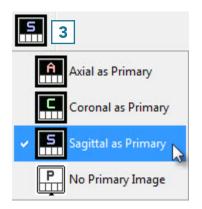
Correcting Wraparound Using the Shift Tool

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

To follow along, download the data set MRI_Head.avw from analyzedirect.com/data and load into Analyze using Input/Output.

- 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].

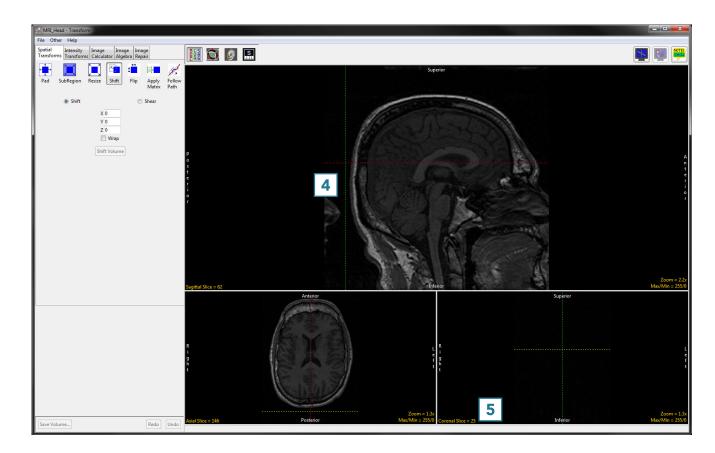




Using the Shift Tool (continued)

- 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 the table below to determine the correct sign and direction of the desired shift.

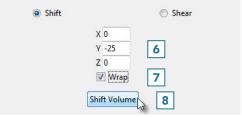


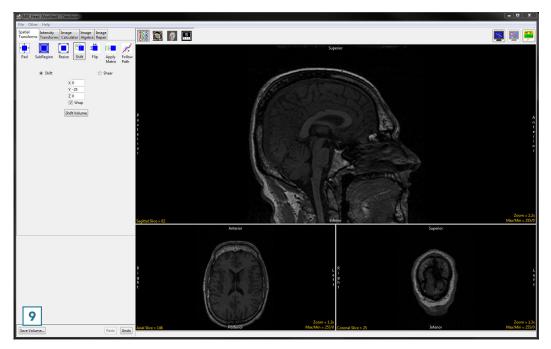
Shift Parameters

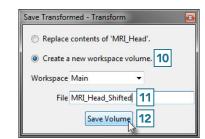
| | Axial | | Coronal | | Sagittal | |
|-----------|-------|------|---------|------|----------|------|
| Parameter | + | - | + | - | + | - |
| Х | right | left | right | left | | |
| Y | up | down | | | right | left |
| Z | | | up | down | up | down |

Using the Shift Tool (continued)

- 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

In some cases, 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, according to the following parameters.

Flip Parameters

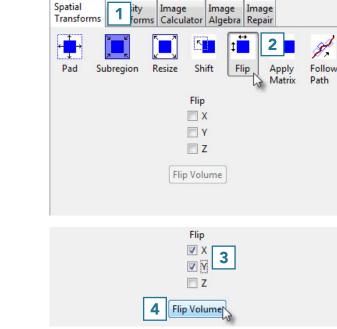
| Axis | Outcome |
|------|---|
| Х | flips data horizontally about the vertical (Y) axis |
| Y | flips data vertically about the horizontal (X) axis |
| Z | reverses the order of the slices |

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.

Flipping Data

To follow along, download the data set VHF_Legs from analyzedirect.com/data and load into Analyze using Input/Output.

- 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.

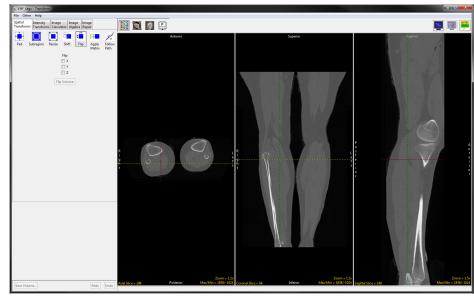


Flip (continued)

• Here, the data set before and after the X-Y flip is shown. 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.



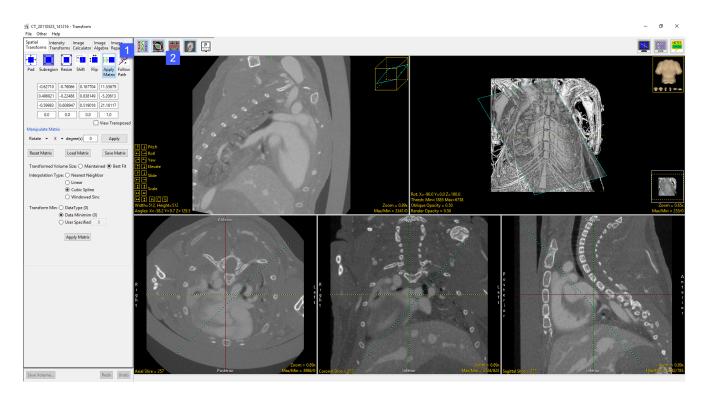




Apply Matrix

The Apply Matrix tool [1] when used in conjunction with the Oblique tool [2], 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 4x4 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. The AC-PC line (anterior commissure - posterior commissure line) also known as the bicommissural line, has been adopted as a standard by the neuroimaging community, and in most instances is the reference plane for axial imaging in everyday scanning.



Apply Matrix Options

Matrix: The matrix tool enables specification, application, loading, and saving of transformation matrices. The matrix displays a 4 x 4 the identity matrix for the data and will update to a transformation matrix when manipulations are made to the matrix. Adjustments can be made directly in any of the matrix fields; however, this is not recommended, instead use the manipulate matrix tools or the Obliques Window to adjust.

• View Transposed: When selected, inverts the transformation matrix.

Manipulate Matrix: Allows users to manipulate the transformation matrix. The following options are available:

- Rotate: Rotates the transformation matrix. Users can select to rotate the X, Y, and Z degree of rotation. The rotation is applied to the X axis first, then the Y axis, and finally the z axis.
 - X, Y, Z: Specifies that the transformation matrix will be rotated about the X, Y or Z axes.
 - **Degrees:** Specifies the degree of rotation.

Translate: Allows users to apply translations. Translations are applied to the X, Y, and Z.

- X, Y, Z: Specifies that the transformation matrix will be translated in X, Y or Z.
- **Voxels:** Specifies the number of voxels to translate.

Scale: Modifies the transformation matrix by a specified scale factor.

- **X, Y, Z:** Specifies that the transformation matrix will be scaled in X, Y or Z.
- Factor: Specifies the scale factor.

Identity: Sets the transformation matrix to the identity matrix.

Invert: Inverts the transformation matrix.

Apply: When selected, applies the specified manipulations options to the transformation matrix.

Apply Matrix Options (continue)

Reset Matrix: Resets the Matrix.

Load Matrix: Allows users to load previously saved matrix files.

Save Matrix: Allows users to save the current matrix file.

Isotropic Scaling: When anisotropic (non-cubic) data is loaded into Transform it is automatically scaled to isotropic (cubic) voxels. The Isotropic Scaling option will be enabled and set to Yes.

- Yes: This is the default option. Anisotropic data is automatically resampled to be isotropic. This enables the application of any transformation, as detailed above, and allows for the generation of a transformed volume in the isotropic space. The saved volume will have spatially correct, transformed voxels.
- No: Disables anisotropic resampling, please note that this is not recommended. Users should only select this option if they wish to save out anisotropic data, however, the transformed spatial voxel size will not be known and users will be prompted to remove the voxel spatial information from the header or copy the original isotropic voxel size from the input volume when saving the data.

Transformed Volume Size: Allows users to choose between Best Fit or Maintained to specify if the saved volume should be resize to best fit the data (recommended) or if it should maintain the original volume dimensions.

Interpolation Type: Allows users to specify the interpolation type to be used when transforming the data. Choose from Nearest Neighbor, Linear, Cubic Spline, or Windowed Sinc.

Transform Min: Allows users to select the grayscale value of additional/new background voxels. Choose between; Data Type, Data Minimum, or User Specified.

Apply Matrix: When selected, applies the specified transformation matrix to the image data.

Using the Apply Matrix Tool

AC-PC Alignment of Brain Data

In this exercise we will use the tools available in the Transform module to align an MRI scan of the brain along the AC-PC axis.

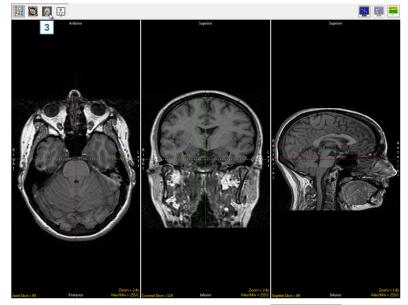
To follow along, download the data set MRI_Head.avw from analyzedirect.com/data and load into Analyze using Input/Output.

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

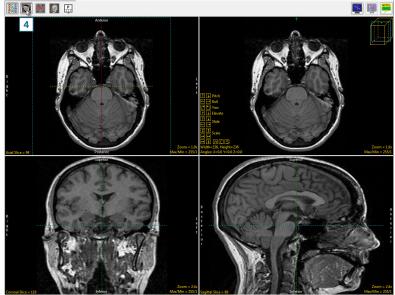
| Spatial Transforms | 1 sity | Image S Calcula | Image tor Algeb | | - | |
|-------------------------------|------------|--------------------|--------------------|---------|-----------------|----------------|
| | | | N | ‡ | | 2 |
| Pad Su | ibregion | Resize | Shift | Flip | Apply Matrix | Follow Path |
| | 1.0 | 0.0 | 0.0 | | 0.0 | |
| | 0.0 | 1.0 | 0.0 | | 0.0 | |
| | 0.0 | 0.0 | 1.0 | | 0.0 | |
| | 0.0 | 0.0 | 0.0 | | L.O | |
| Martin | March 1 | | | E | View T | ransposed |
| Manipulate Rotate | | ▼ degr | ee(s) 0 | | Appl | y |
| Reset N | 1atrix | Loa | d Matrix | | Save M | atrix |
| Tran | sformed V | olume Siz | e: 🔘 Main | ntained | Best F | it |
| Inter | polation T | ype: 🔘 N | earest Nei | ghbor | | |
| 🔘 Linear | | | | | | |
| Oubic Spline | | | | | | |
| | | © W | /indowed S | Sinc | | |
| Transform Min: 🔘 DataType (0) | | | | | | |
| | | | Minimim | (1) | | |
| | | O User | Specified | 1 | | |
| | | App | y Matrix | | | |

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.



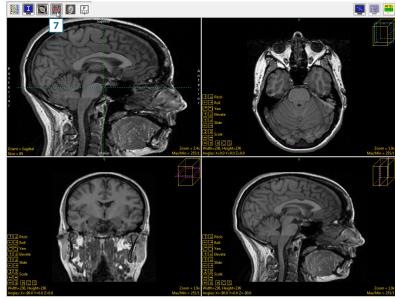
• Switch on the oblique [4]. Now, the oblique and the three orthogonal views are shown.



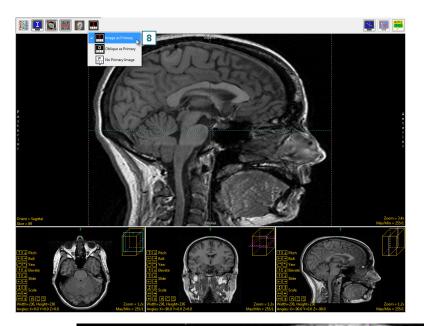
- Toggle the orthogonal orientations to a single image [5].
- Set this image to the sagittal view by clicking twice on the Orient parameter [6].
- Now the sagittal orientation and the oblique image are shown.



• Switch on the perpendicular images [7].



 The AC-PC line will be defined on the sagittal view, so doubleclick the sagittal image or select Image as Primary in the dropdown menu [8].



reget & Septed to the set of the

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].



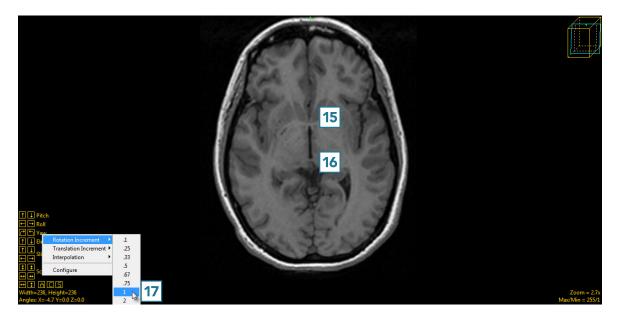
• To set the oblique plane to be parallel, rather than perpendicular, to the AC-PC plane, right-click on one of the perpendicular axis endpoints and set the Matrix to Create to Parallel [13].



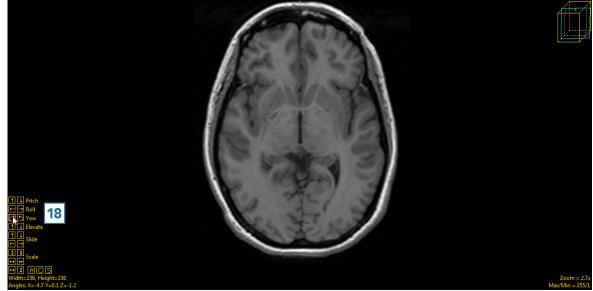
- Now the main oblique image (the leftmost of the three) is an AC-PC aligned axial image [14].
- Double-click this image to make it the primary image.



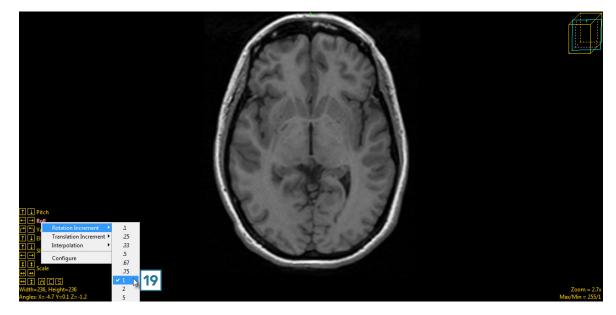
- The AC [15] and PC [16] can both be seen on the same oblique slice, indicating good AC-PC alignment.
- To adjust vertical alignment of the data set, right-click Yaw and set the Rotation Increment to 1 [17].



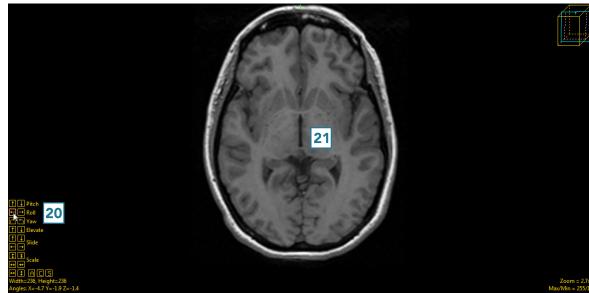
 Use the left and right Yaw buttons to align the data set vertically [18]. The increment can be made even smaller to make smaller adjustments as needed.



 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].



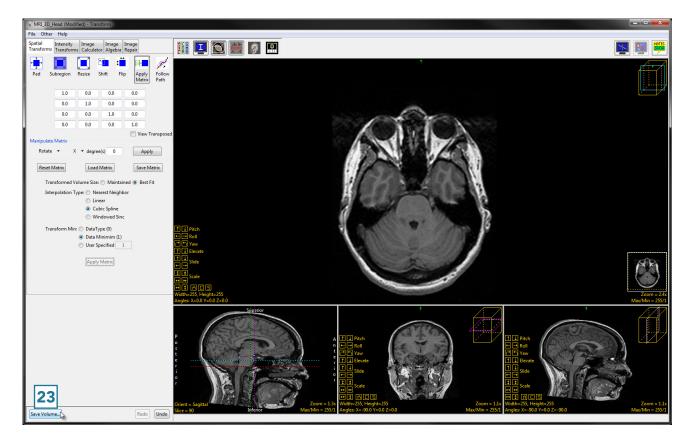
 Click on the left and right roll buttons [20] to adjust the data set until the anatomical structures appear symmetrical [21].



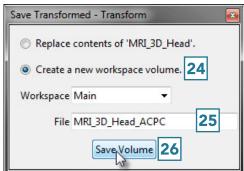
• Click Apply Matrix [22] to apply the transformation.

| ← Pad | Subregion | Resize | Shift Fl | ip Appl | Follow |
|----------|--|-------------|-------------|-----------|--------------|
| | - | | | Matr | |
| | 0.999238 | 0.020560 | -0.03315 | 0.106856 | |
| | -0.01745 | 0.995657 | 0.091437 | 19.57691 | |
| | 0.034894 | -0.09078 | 0.995258 | -21.9265 | |
| | 0.0 | 0.0 | 0.0 | 1.0 | |
| Maninul | ate Matrix | | | Viev | v Transposed |
| | | . ▼ degree | e(s) 0 | A | oply |
| Т | et Matrix Transformed V nterpolation T | olume Size: | | ined 🖲 Be | Matrix |
| | | 🔘 Lin | ear | | |
| | | | bic Spline | | |
| | | © Wi | ndowed Sin | c | |
| Т | ransform Min | : 🔘 DataTy | /pe (0) | | |
| | | Oata N | Ainimim (1) | | |
| | | O User S | pecified | 1 | |
| | | Apply | Matrix 22 | 2 | |

• 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.



Data Reorientation

The Apply Matrix option can be used to reorient data. An example of this can be found when using the Analyze Bone Microarchitecture Analysis (BMA) Add-On, which requires that the input bone specimens are orientated into a specific orientation [1] as a prerequisite for bone tissue classification and measurement. The Oblique reorientation tools and Apply Matrix option in Transform provide the tools necessary to successfully re-orientate the image data for analysis.



In this exercise we will use the tools available in the Transform module to correctly orient a micro-CT bone data set for processing in the BMA add-on module.

To follow along, download the data set BMA_PE_micro_CT.avw from analyzedirect.com/data

Load the data into Analyze using Input/Output.

Select the data set from the Analyze workspace and open Transform.

In Transform select the Spatial Transforms tab [2] and then choose the Apply Matrix option [3]. Click the Toggle Oblique button [4] to enable to Oblique window [5].

Note, if your display does not look like that shown in the screenshot, right-click on the Controls Layout icon and choose Default Display Layout, this will return you to the standard 4 window display showing the axial, coronal, sagittal, and render displays. Now click the Toggle Oblique button. Right-click in the coronal window and select the Perpendicular Axis tool (6). <complex-block><complex-block><complex-block>

Use the Perpendicular Axis tool (red and black dashed line) [7] to define a line down the center of the bone to be analyzed. Do this by repositioning the ends of the line. In this example this is done on the coronal window. An oblique plane (shown by the blue and black dashed line) [8] will be defined perpendicular to the red and black line.



The plane will need to be adjusted in the sagittal view [9].

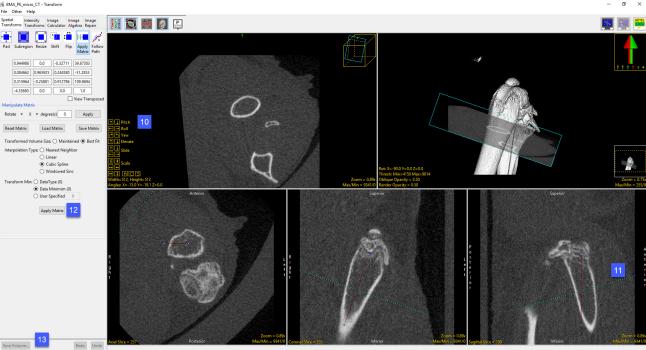
To do this, use the Pitch buttons in the oblique window [10] to manipulate the blue line until it is perpendicular to the long axis of the bone in the sagittal window. [11]. Note that in this example the axis (shown in blue and black on the sagittal image) should be pitched slightly upwards. This is achieved using the Pitch Up button.

To apply the transformation to the data set click the Apply Matrix button. [12]

Once the transformation is complete the data can be saved to the workspace by clicking the Save Volume button. [13]

In the Save Tranformed window returned choose the 'Create a new workspace volume' option and then append '_reformatted' to the original file name. Finally click Save Volume. The reformatted data set will be saved to the workspace.





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. Available options include the following.

Path coordinates: Users can interactively define path coordinates by clicking on and of the orthogonal display images.

- · Load: Allows users to load a previously defined set of path coordinates.
- · Save: Allows users to save the current path coordinates.
- **Reset:** Resets the current path coordinates.

Intermediate Point(s): Allows users to enable or disable the automatic intermediate points are created between users defined points:

- **None:** No intermediate points will be created.
- · Linear: Intermediate points will be created by linear interpolation between user defined points.
- Spine: Intermediate points will be created by spline interpolation between user defined points.

Image Width: Allows users to define the width of the generated path images.

Image Height: Allows users to define the height of the generated path images.

Interpolation Type: Allows users to specify the interpolation type to be used when creating the path images. Choose from Nearest Neighbor, Bilinear, Cubic Spline, or Windowed Sinc.

Workspace: The workspace drop down allows users to specify which workspace the path image sequence will be saved to.

File: File allows users to specify the name of the path sequence.

Preview Images: Will display a preview of the path sequence.

Generate Images: Will save the path sequence to the selected workspace with the specified file name.

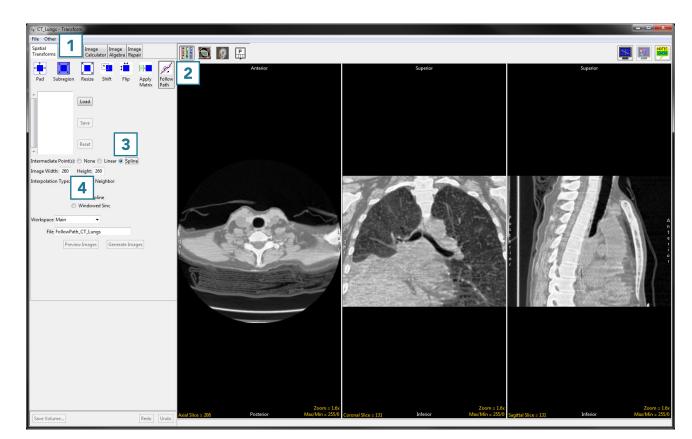
Using the Follow Path Tool

Reslicing Data Along the Trachea

A good example for the use of the Follow Path tools involves reslicing data along the centerline of the trachea, using lung data from CT.

To follow along, download the CT_Lungs data set from analyzedirect.com/data and load into Analyze using Input/Output.

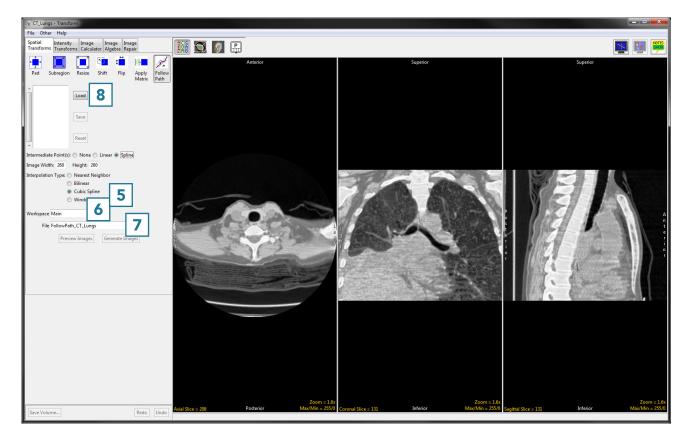
- Select the data set to reslice along a path of points and open Transform. Navigate to Spatial Transforms [1] and select the Follow Path tool [2].
- Choose a method of connecting the points: none, linear, or spline
 [3]. Spline creates the smoothest transition between slices, so that will be selected 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.

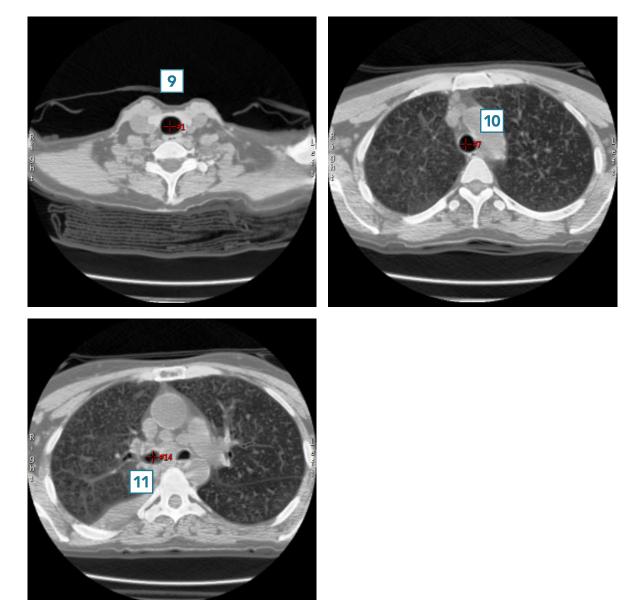
Using the Follow Path Tool (continued)

- The interpolation type [5] can be set to nearest neighbor, bilinear, cubic spline or windowed sinc. For more information on interpolation types, see the table shown earlier in the Resize section.
- 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.



Using the Follow Path Tool (continued)

- 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].



Using the Follow Path Tool (continued)

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

| Spatial Transforms | Intensity Transforms | Image Calculator | Image Algebra | Image Repair | |
|--|--|---------------------------|------------------|-----------------|----------------------------|
| Pad Su | Jbregion F | Resize Sh | ift Fl | | pply Follow Patrix Path |
| ▲ 128 158 20 130 155 12 130 153 17 129 149 10 128 148 12 128 145 14 124 141 12 123 138 12 121 135 12 ↓ 119 132 12 | 87 L 76 52 54 S 86 25 19 R | ave | | IVI | atrix <u>Patri</u> |
| Intermediate Image Width Interpolation | Point(s): 260 He Type: Bi O Bi | ight: 260 earest Neigh | bor | Spline | |
| Workspace M | | T_Lungs | Generate | : Images | 12 |
| | | | | | |

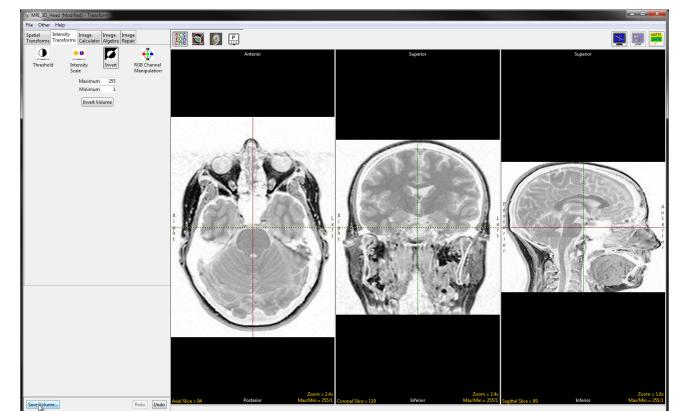
232

Intensity Transforms

The Intensity Transforms tab allows access to tools that enable image intensity values to be adjusted. These would be used, for example, to make an image easier to process or to highlight certain objects within the image. The Intensity Transforms available in Analyze include:

- Threshold
- Intensity Scaling
- Inversion
- RGB channel manipulation

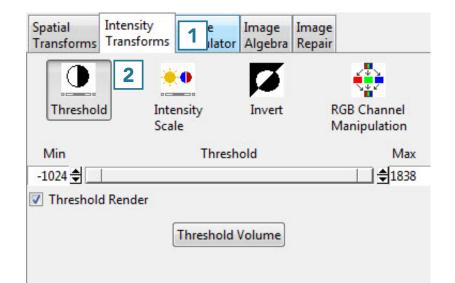
Many of the functions available in this section are also available in Input/ Output under the Process>Intensities tab.



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. Available options include the following:

Threshold slider: The Threshold double-ended slider bar allows users



to specify a range of threshold values using the minimum and maximum ends of the threshold slider. Selecting the minimum end of the slider and moving it to the right will increase the minimum threshold value, moving it to the left will decrease the minimum value.

Threshold Render: Enables and disables the 3D threshold preview. It is recommended to disable this option for large data sets.

Threshold Volume: Threshold the volume data based on the minimum and maximum threshold range set using the threshold slider.

Creating a Binary Data Set with Thresholding

To follow along, download the VHF_Legs data set from analyzedirect.com/data and load into Analyze using Input/Output.

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

Analyze 15.0 User's Guide

Using the Threshold Tool (continued)

- 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.



Using the Threshold Tool (continued)

• 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 [9].
- Rename [10] and click Save Volume [11].
- Close Transform.

| Save Transformed - Transform | | |
|---------------------------------|--|--|
| Replace contents of 'VHF_Legs'. | | |
| Create a new workspace volume. | | |
| Workspace Main 👻 | | |
| File VHF_Legs_Binary 9 | | |
| Save Volume 10 | | |

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.

Available options include the following:

Input: Reports the input data type and minimum and maximum intensity values.

- **DataType:** Display the input data's data type.
- **Maximum:** Displays the input data's maximum intensity value. Note, this value can be adjusted to accurately report the maximum value in the input volume.
- **Minimum:** Displays the input data's minimum intensity value. Note, this value can be adjusted to accurately report the minimum value in the input volume.

Output: Allows users to adjust the output data type and minimum and maximum intensity values. The following options are available:

- **DataType:** The DataType drop down menu allows users to select from the available data types, including; unsigned 8-bit, signed 8-bit, unsigned 16-bit, signed 16-bit, unsigned 32-bit, signed 32-bit, Float, RGB, and Double.
- **Maximum:** Displays the output data's maximum intensity value. This value can be adjusted.
- **Minimum:** Displays the output data's minimum intensity value. This value can be adjusted.

Intensity Scale Volume: Scales the data based on the intensity scaling parameters set.

Using the Intensity Scale Tool

Modifying Image Data Type

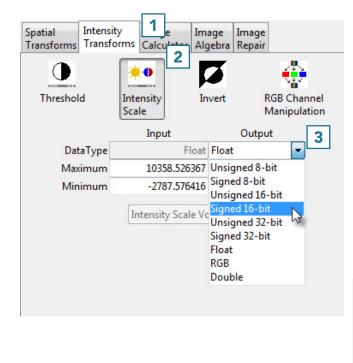
Changing the data type can reduce the size of the data on disk. In this example, a microCT data set has a data type of Float and the size of the image data is 92.71 MB. Changing the data type to signed 16-bit reduces the size of the data set by about 50% to 46.35 MB without having a significant effect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

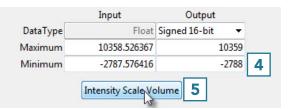
To follow along, download the Bone_Sample_mCT data set from analyzedirect.com/data and load into Analyze using Input/Output.

- 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].

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.





Using the Intensity Scale Tool (continued)

• Click Save Volume [6] to save the scaled data set.

nsity Image Image Image nsforms Calculator Algebra Repair ٠ 7 RGB Channe Manipulatio DataT ianed 16-bit 1035 Maximu -2788 Minimu -2788 Intensity Scale Volume Zoom = 0 Max/Min = 2 6 Redo Undo Save Volume...

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

| Save Transformed - Transform | | | | |
|--|-------------|------------|---|--|
| Replace contents of 'Bone_Sample_mCT'. | | | | |
| Oreate a new workspace volume. 7 | | | | |
| Workspace N | 1ain | • | | |
| File B | one_Sample_ | mCT_Scaled | 8 | |
| Save Volume 9 | | | | |

Invert

For certain segmentation and visualization applications, it is beneficial to view an inverted copy of the image data alongside the original grayscale data. Available Options are as follows:

Maximum: Allows users to specify the maximum intensity value for the inverted data set.

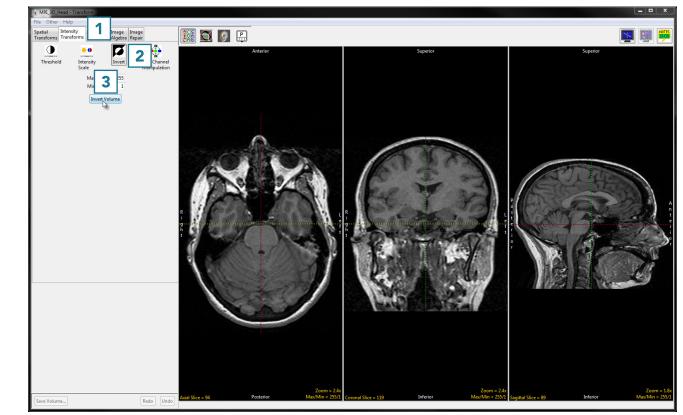
Minimum: Allows users to specify the minimum intensity value for the inverted data set.

Invert: When selected inverts the image data.

Inverting Data

To follow along, download the MRI_3D_Head data set from analyzedirect.com/data and load into Analyze using Input/Output.

- 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.



Using the Invert Tool (continued)

• Click Save Volume [4] to save the inverted data set.

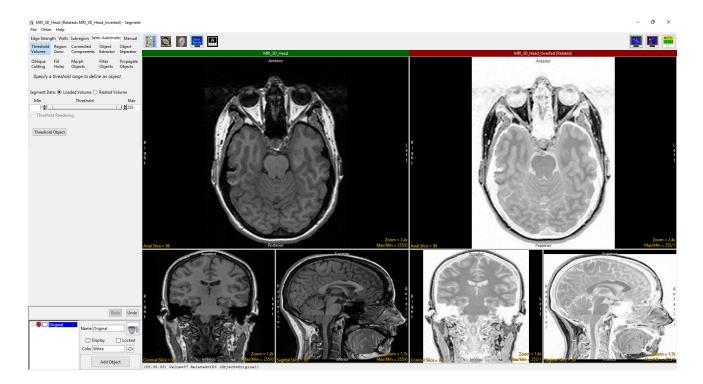


- In the Save Transformed window, choose to create a new workspace volume [5].
- Rename [6] and click Save Volume [7].
- Close Transform.

| Save Transformed - Transform | | | | |
|------------------------------------|-------------------------|--|--|--|
| Replace contents of 'MRI_3D_Head'. | | | | |
| Oreate a | new workspace volume. 5 | | | |
| Workspace | Main 🔻 | | | |
| File | MRI_3D_Head_Inverted 6 | | | |
| | Save Volume 7 | | | |

Using the Invert Tool (continued)

- The inverse version of the input data can be useful for delineation of objects during segmentation. As the Segment module supports dual inputs, select the original MRI_3D_Head data set from the workspace and with the Ctrl key selected click on the inverted version just created, MRI_3D_ Head_Inverted, and open Segment.
- Either input can be used for the segmentation of brain structures.



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:

Conversions from 24-bit Options

| Option | Description |
|-------------------|--|
| Grayscale Formula | Converts the RGB values to an 8-bit grayscale image using the following formula: |
| | 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 |
| Red Channel | Specifies that only the 8-bit red channel is used for conversion |
| Green Channel | Specifies that only the 8-bit green channel is used for conversion |
| Blue Channel | Specifies that only the 8-bit blue channel is used for conversion |

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. Uses the following options: Object Color: Creates a color image displaying object color overlaid on voxels that are |
| | part of the selected objects in the object map. All other non-object voxels are removed from the image; Enhanced Object Color: |
| | This option is the same as the Object Color option but with enhanced (brighter) object color; Object Color Only: Creates a colored |
| | image representation of the grayscale image data with solid colored objects overlaid; Object with Edges: Creates a colored image |
| | of the grayscale data overlaid with object boundaries; Object Edges Only: Creates a colored image of object boundaries only; • |
| | Show All Objects: Uses all objects for the colored image; Enabled Objects Only: Uses only enabled objects for the colored |
| | image; Color Enabled Only: Uses only color enabled objects for the colored image. |
| Combine Channel(s) | Combines the red, green and blue channels into a 24-bit color image |
| Convert Image | Initiates the conversion process using the parameters set. |

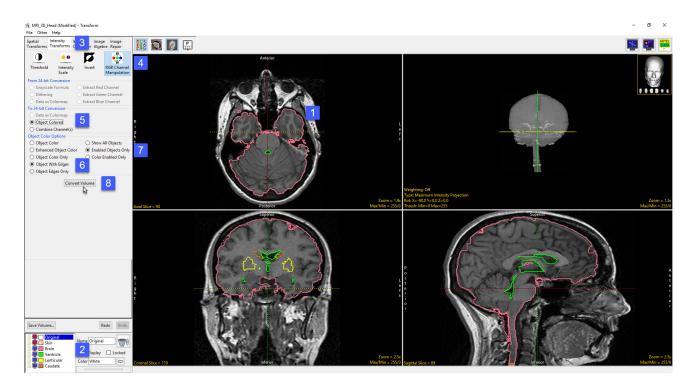
RGB Channel Manipulation (continued)

Creating an RGB Data Set

Creating an RGB dataset by fusing a grayscale input volume with its associated object map can provide a useful reference image.

To follow along, download the MRI_3D_Head.avw and MRI_3D_ Head.obj data sets from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the MRI-3D_Head data set and open Transform.
- In Transform select File > Load Object Map and load the MRI_3D_Head.obj. The object map will be overlaid on the grayscale image data [1].



- In the Object control window switch Off the display of the skin object and then switch On the display of the Lenticular and Caudate objects [2].
- Select the Intensity Transformation tab [3] and then select the RGB Channel Manipulation option [4].
- Under the To 24-bit Conversion select the Object Colored option [5].
- The Object Color Options will be displayed below. Select Object With Edges [6] and then select Enabled Objects Only [7]
- Click Convert Volume [8].

RGB Channel Manipulation (continued)

- Once the transformation is complete save the new RGB data set to the workspace using the Save Volume button [9].
- The image data can be saved out of Analyze using the Input/Output module.

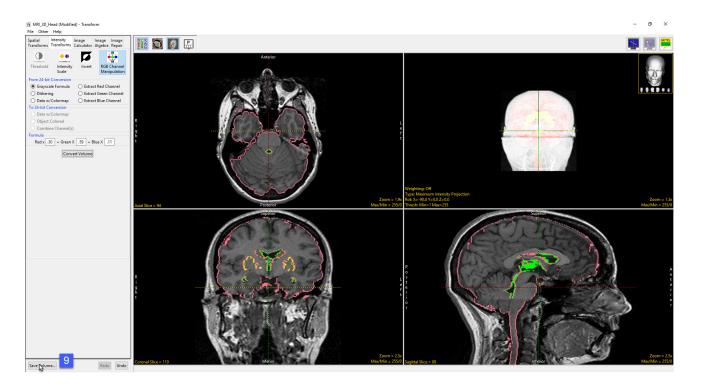


Image Calculator

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.

The Image Calculator interface provides a keypad [1] allowing users to input functions to the calculator's scrollable canvas [2]. The canvas displaying input data, applied functions, and results. Users can also right click on the canvas to access the Buttons Tool to add additional functions to the keypad [3]. Image Calculator also provides the standard image display area [4] for data review.



Calculator Keypad

M CT_20110325_141216 - Transform File Other Help Spatial Intensity Image Image Image Transforms Calculator Algebra Rep Image Imag S 📩 🖉 🗄 5 . Apply Follow Matrix Path -0.62710 -0.76066 0.167704 11.53679 0.496921 -0.22488 0.838149 -5.20613 -0.59983 0.608947 0.519018 21.18117 0.0 0.0 0.0 1.0 View Transpose Rotate 💌 degree(s) 0 Appl Reset Matrix

*The modulo operation finds the remainder after division of one number by another.

There are also two drop-down menus available above the keys; Deg and Auto.

Deg: Sets the trigonometric input to Degrees, Radians, or Gradians.

Auto: The Auto drop-down menu specifies how volume data will be handled during operations that may cause data overflow, for example the multiplication of two signed 16-bit data sets. The default setting, Auto, ensures that the volume data will be automatically promoted up to the next appropriate data type. In the case of the multiplication of two signed 16-bit data sets the resulting data set would have a data type of signed 32-bit. All other options will fix the calculator to work only in that data type. This means that overflow and wrapping may occur. In some instances, the data type of the volume generated may not be the type selected due to the operation and may require a specific output datatype, for example the extraction of a red channel from an RGB data set. The following data types options are available:

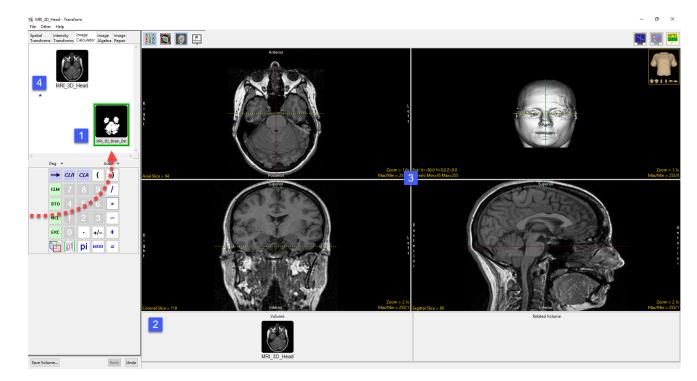
| Unsigned 8-bit | Signed 8-bit | Unsigned 16-bit |
|----------------|------------------|-----------------|
| Signed 16-bit. | Unsigned 32-bit. | Signed 32-bit. |
| Float | RGB | Complex |

By default, the keypad provides access to the following functions:

Calculator Canvas

Data is loaded into the Image Calculator interface if a data set is selected when Transform is opened. Image Calculator also accepts image data via drag-and-drop from the workspace onto the calculator canvas [1], onto the Volume input port [2] when File > Input/Output Ports is enabled, or onto any of the display windows [3].

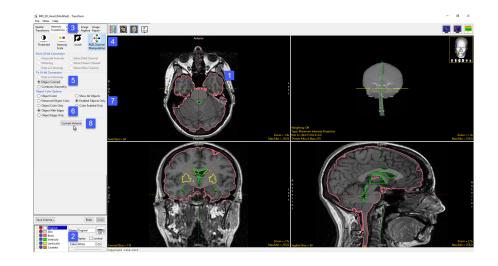
The calculator canvas also accepts matrix files loaded from disk and functions from the keypad [4].



Button Tool

Additional functions can be added to the calculator keypad. To add more functions to the keypad right click in the calculator canvas and select Buttons to open the Button Tool [1].

To add a function drag the function button from the Palette to the Key Pad [2]. The function will be automatically added to the calculator keypad [3].





The following additional functions are available:

- ** Convert rectangular coordinates (x,y) to polar (r,0), computes magnitude r
- *** Convert rectangular coordinates (x,y) to polar (r,0), computes phase 0

Analyze 15.0 User's Guide

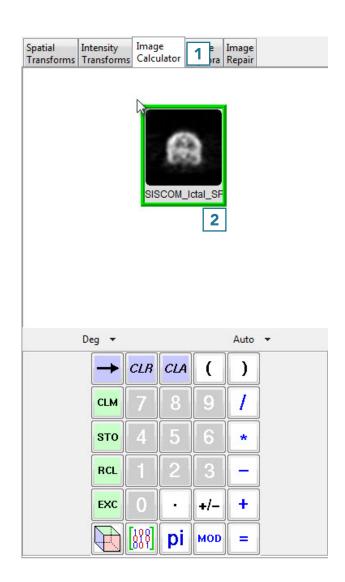
Creating a Difference Map

A good example of Image Calculator use is in the creation of a difference map between ictal and interictal SPECT data sets, typically acquired in the study of epileptic seizures. These difference maps can be used to study regions of hypo- and hyperperfusion.

To follow along, download the SISCOM_Ictal_SPECT_Nrm and SISCOM_Interictal_SPECT_Coregistered_Nrm data sets from analyzedirect.com/data and load into Analyze using Input/ Output.

The SPECT data inputs for this exercise have already been registered and normalized so that they can be compared.

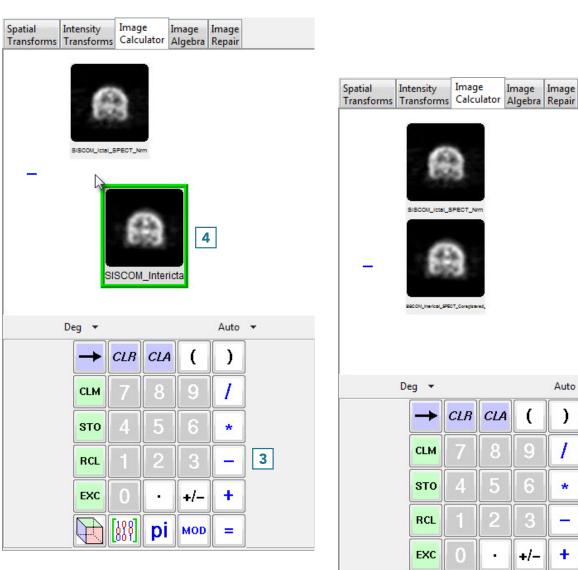
- Open Transform and navigate to Image Calculator [1].
- Drag and drop the ictal data set into the calculator window [2].

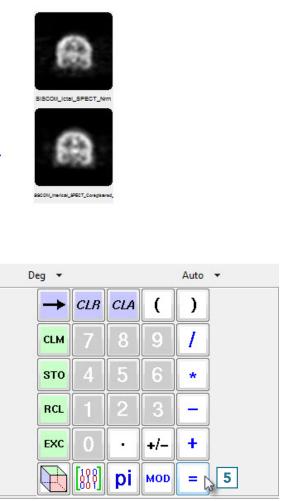


Creating a Difference Map (continued)

- 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.





Image

Image Image

Intensity

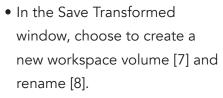
Creating a Difference Map (continued)

Spatial

Intensity Image

Image Image

• Click Save Volume [6] to save the difference map.



- Click Save Volume [9].
- Close Transform.

The difference map is now saved to the Analyze Workspace and is available for use in other modules.

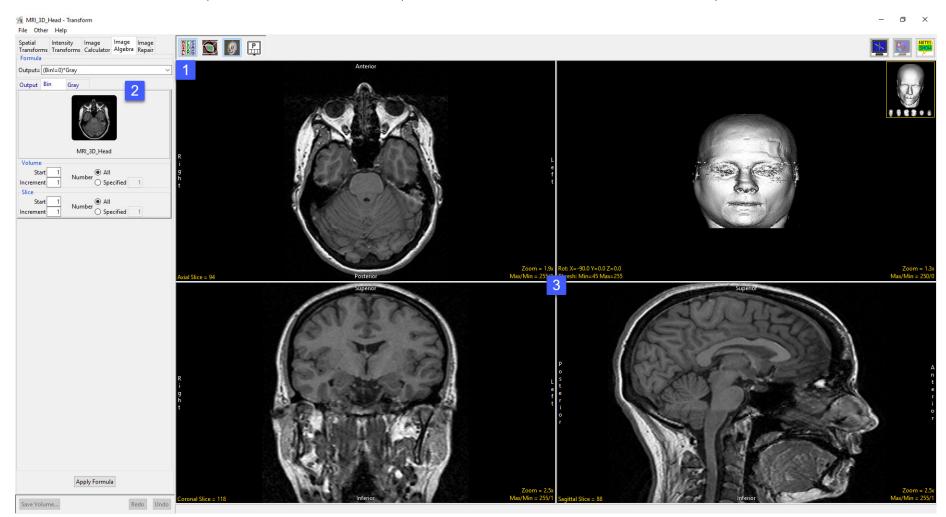
| siscol, Job, SRECT, Ven | | | | | | |
|-------------------------|------|----------------|-----|-----|------|---|
| | | | | | | |
| D | eg 🔻 | | | | Auto | - |
| | - | CLR | CLA | (|) | |
| | CLM | 7 | 8 | 9 | 1 | |
| | вто | 4 | 5 | 6 | * | |
| | RCL | 1 | 2 | 3 | - | |
| EXC 0 · +/- + | | | | | | |
| | | [<u></u> 888] | pi | MOD | = | |
| | | | | | | |
| | | | | | | |

| Save Transformed - Trans | sform | | | | |
|---|-----------------------|--|--|--|--|
| Replace contents of 'SISCOM_Interictal_SPECT_Coregistered_Nrm'. | | | | | |
| Oreate a new works | pace volume. 7 | | | | |
| Workspace | Workspace 5 | | | | |
| File Difference_Map 8 | | | | | |
| Save Volume 9 | | | | | |

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.

The Image Algebra interface provides access to a Formula parser [1], variable tabs [2], and the standard display area [3].



Analyze 15.0 User's Guide

Formula Parser

The Formula field allows users to enter a formula to process image data, alternatively users can choose from a list of predefined formulas.

A formula may be as simple as Output=Input, which copies a file, or as complex as to contain up to 1000 variables and 1000 constants. When entering complex formulas parenthesis should be used literally to group mathematical operations.

The following operators are supported; +, -, *, /, (), <, >, <= ,>= , ==, !=

| Symbol | Name | Meaning/Definition | Example | |
|--------|--------------------|--|--|--|
| = | Equals sign | Equality; is equal to, equals | Output = Input Copies a file | |
| != | Equality operator: | Not equal to operator; is not equal | Output = (Input!=145)*Input | |
| | Inequality | to, does not equal. Returns true if | Removes voxels equal to 145 from the image. '(Input!=145)' assigns all voxels not equal to 145 to 1 and | |
| | | the operands to not have the same | all voxels equal to 145 to 0. '*Input' then multiples the resulting binary image with the original grayscale | |
| | | value; otherwise, it returns false. | image, all voxels assigned to 1 are kept while all voxels assigned to 0 are removed from the final image. | |
| == | Equality operator: | Equal to operator returns true (1) | Output = (Mask==0)*Volume | |
| | Equality | if both operands have the same | Inverts the binary mask input image so all voxels set to 1 are removed from the final image while all voxels | |
| | | value; otherwise it returns false (0). | set to 0 are kept. Normally when multiplying a grayscale and binary the voxels set to 1 in the binary mask | |
| | | | are kept while the voxels set to 0 are removed. 'Mask==0' keeps all the voxels in the binary image with | |
| | | | a value of 0. '*Volume' multiples the (inverted) binary image with the grayscale images, the resulting | |
| | | | grayscale image contains the voxels that were set to 0 in the binary image. | |
| < | Strict inequality | Less than | Output = (Input<155)*128 | |
| | | | In this formula if the voxel intensity value is less than 155, TRUE(1) is returned and these voxels are | |
| | | | assigned an intensity value of 128, else False(0) is returned and the result is 0 and the original grayscale | |
| | | | value is preserved. '(Input<155)' assigns all voxels less than 145 to 1 and all other voxels to 0. '*128' then | |
| | | | assigns all voxels with a value of TRUE(1) an intensity value of 128. | |

| Symbol | Name | Meaning/Definition | Example |
|--------|-------------------|-----------------------------------|--|
| > | Strict inequality | Greater than | Output = (Input>45)*Input |
| | | | Keeps all voxels greater than 145 (146 and higher) in the image and removes all other |
| | | | voxels. '(Input>145)' assigns all voxels greater than 145 to 1 and all other voxels to 0. |
| | | | '*Input' then multiples the resulting binary image with the original grayscale image, all |
| | | | voxels assigned to 1 are kept while all voxels assigned to 0 are removed from the final |
| | | | image. |
| <= | Inequality | Less than or equal to | Output = (Input<=145)*Input |
| | | | Keeps all voxels equal to and less than 145 in the image and removes all other voxels. |
| >= | Inequality | Greater than or equal to | Output = (Input>=145)*Input |
| | | | Keeps all voxels equal to and greater than 145 in the image and removes all other voxels. |
| + | Plus sign | Addition | Output = File1 + File2 |
| | | | Adds two files. Summing data is for useful for averaging data for noise reduction. |
| - | Minus sign | Subtraction | Output = File1 – File2 |
| | | | Subtracts File2 from File1. Subtraction is useful for creating a difference image or |
| | | | removing background noise. |
| * | Asterisk | Multiplication | Output = Binary*Grayscale |
| | | | Multiplies two data sets, in this example the binary image is multiplied by a greyscale |
| | | | image. All voxels in the binary mask equal to 1 will be kept in the resulting greyscale |
| | | | image while all voxels with a value of 0 will be removed. Useful for masking data. |
| 1 | Division slash | Division | Output = (File1+File2)/2 |
| | | | Averages 2 data sets. Useful for averaging images to reduce noise. |
| () | Parentheses | Calculate expression inside first | Output = (Input-intercept)/slope |
| | | | Scales image data based on the slope and intercept values from a linear regression line. |
| | | | Useful for rescaling CT data to HU's or BMD units. '(Input-intercept)' minuses the intercept |
| | | | value from the input value prior to dividing by the slope '/slope'. |

Application examples:

Data Normalization: Output=(input-(min(input)))/(max(input))-(min(input))

Scaling data to a phantom: Output = (Input-#intercept#)/#slope#

Masking data and setting the excluded voxels to a specific intensity value: Output=(Mask==0)*Volume+(Mask==1)*#value#

The following functions are supported:

| Function | Notes |
|----------------------|--|
| sqrt(equation) | Equation can be a variable or a constant. |
| log(equation) | Equation can be a variable or a constant. |
| exp(equation) | Equation can be a variable or a constant. |
| count() | Returns the output slice number. |
| max(variable) | Returns the maximum value. |
| min(variable) | Returns the minimum value. |
| avg(variable) | Returns the average value. |
| abs(variable) | Returns absolute value. |
| int(variable) | Converts to integer, truncating floating point values. |
| float(variable) | Converts to floating point values. |
| xpos() | Returns the x position in the input image. |
| ypos() | Returns the y position in the input image. |
| ADDTOT(num_add, inc) | Returns the sum of the added images as a floating point image. |
| ADDAVG(num_add, inc) | Returns the result of the added and averaged images. |
| RED(variable) | Returns the red portion of the RGB image if the variable specifies an RGB image or an image with a colormap. |
| GREEN(variable) | Returns the green portion of the RGB image if the variable specifies an RGB image or an image with a colormap. |
| BLUE(variable) | Returns the blue portion of the RGB image if the variable specifies an RGB image or an image with a colormap. |

Note: ADDTOT() and ADDAVG() are specialized functions that allow large groups of images to be summed or averaged. Unlike other functions which use a single image as input, these functions allow for multiple image inputs, with a single output image generated. The options in the variables menu all users to specify which input image is passed to a function. With these functions, the values specified in the variables menu specify only the starting slice for a group of images. num_add specifies the total number of images to add together, and inc specifies the increment between these images. Special status messages are generated when these functions are executed. Review these messages carefully if you experience problems accomplishing the desired total and averaging functions.

Additional information when defining formulas:

- Surrounding variables with #'s, will cause prompting for the information that is to be put in the formula in place of the variables.
- Variable names must begin with an alpha character and have no more than 15 alphanumeric characters.
- <,>,<=,>=,==,!= are boolean operators that can be used in user specified formulas. The following is an example showing the use of boolean operators:

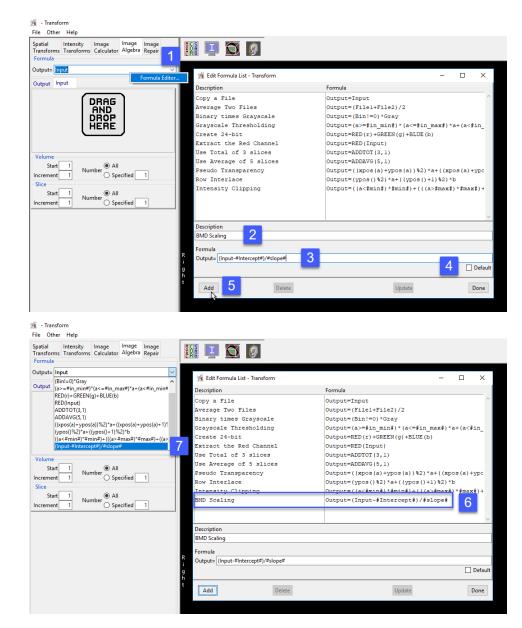
There are several useful formulas preloaded, as detailed in the table below.

| 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) |

Adding Formulas

To add your own formula to the list of formulas available from the formula drop down menu, do the following.

- Right click in the Formula field [1].
- In the Edit Formula List window returned enter a description for your formula [2].
- Next, enter the formula [3]. Remember to surround variables with #'s to make them imputable.
- Uncheck the Default option [4], unless you wish your formula to be the default formula that appears in the formula bar when Image Algebra is selected.
- Click Add [5].
- The formula will be added to the list [6] and will be selectable from the formula drop down menu [7].
- Apply Formula: Applies the formula to the image data.
- Save Volume: Opens the Save Transform window



Variables

Variables are dynamically generated when a formula is created or selected. The entries allow for the specification and/or modification of data values and parameters. Should a parameter fail to be provided and a default value cannot be determined, the formula parser will prompt the user for the value. The following options are available (depending on the current formula):

Output: allows for the specification of the output image attributes. The following options are available:

- Volume: The volume field enables specification of the volume attributes for the output file ٠
 - · Start: Specifies the starting volume number for the output file.
 - · Increment: Specifies the increment used between volumes for the output file.
- Slice: The slice field enables specification of the slice attributes for the output file. •
 - · Start: Specifies the starting slice number in the output volume for each volume processed.
 - · Increment: Specifies the increment between slices for the output volume.
 - · Slice(s) Per Volume: Specifies the number of slices in each output volume. Options are: Same: When selected, in number of slices in the first input file is used as the number of slices in the output file; Specified: When selected specification of the number of slices in the output file.
- DataType: Specifies the data type of the output file. Users can choose from a list of available data types, including; unsigned 8-bit, • signed 8-bit, unsigned 16-bit, signed 16-bit, unsigned 32-bit, signed 32-bit, float, RGB, and double.
 - · Rounding: When enabled, floating values are converted to integers by rounding to the nearest integer, otherwise the number will be truncation at the decimal point. This option has no effect if the calculated value is an integer or the Output Datatype is float.
- Max/Min: Specifies the method used to set the maximum and minimum values for the output file. The following options are available: ٠
 - · Copy: Specifies that the maximum and minimum values are copied from the input file.
 - · Calculate: Specifies that the maximum and minimum values are calculated for every slice processed.
 - Full Range: Specifies that the maximum and minimum are set to the full range possible for the current data type.

| Rounding | Calculate | |
|----------------|--------------|--|
| | 🔿 Full Range | |
| | | |
| | | |
| | | |
| | | |
| | | |
| cted, indicate | es that the | |
| lected, enab | oles the | |
| | | |
| | | |
| luding: unsig | med 8 bit | |

Image Image

Same

Max/Min Settings Copy

Calculate

O Specified 512

Spatial

Formula Output= Input

Volume Start Increment

Slice Start

Increment

DataType

Signed 16-bit

Output Input

Intensity Image Transforms Transforms Calculator Algebra Repair

Slice(s) Per Volume

Variables (continued)

Variable: The variable parameters, named assigned from the variable defined in the formula, allows for the specification of the variable (e.g. Input) volume attributes. The following options are available:

- Volume: The Volume field enables specification of the volume attributes for the variable volume.
 - · Start: Specifies the starting volume number for the variable volume.
 - Increment: Specifies the increment used between volumes for the variable volume.
 - Number: Choose from the following to specify the number of volumes to be processed:

All: Specifies that all volumes in the variable volume will be processed; *Specified:* Indicates the number of volumes in the variable volume to be processed.

- Slice: The slice field enables specification of the slice attributes for the variable volume.
 - Start: Specifies the starting slice number in the variable volume for each volume processed.
 - Increment: Specifies the increment between slices for the variable volume.
 - Number: Choose from the following to specify the number of slices to be processed: <u>All</u>: Specifies that all slices in the variable volume will be processed; *Specified*: Indicates the number of slices in the variable volume to be processed.

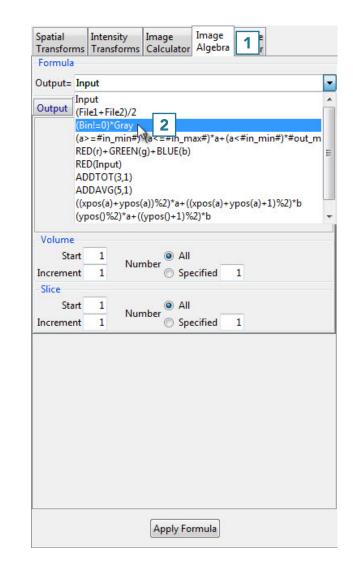
| | Intensity Transforms | lmage Calculator | lmage Algebra | lmage Repair | |
|--------------------|-------------------------|---------------------|------------------|-----------------|---|
| Output= In | put | | | | ~ |
| Output In | put | | | | |
| | | | | | |
| Volume | EGV_MRI | | | | |
| Start Increment | 1 1 Nur | nber 🔘 All 🔾 Spe | cified | 1 | |
| Start Increment | 1 1 Nur | nber 🔘 All 🔾 Spe | cified | 1 | |

Applying a Binary Mask to a Grayscale Volume

A good example of Image Algebra use involves multiplying 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.

To follow along, download the MRI_3D_Head and MRI_3D_Head_Bin data sets from analyzedirect.com/data and load into Analyze using Input/Output.

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



Applying a Binary Mask to a Grayscale Volume (continued)

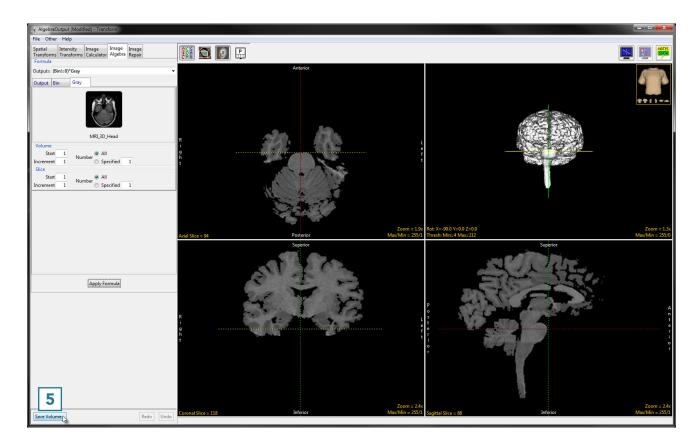
- The input variables will appear as tabs labeled with the variable names.
- Drag and drop the binary data set into the designated space on the Bin tab [3].
- Do the same with the grayscale data set on the Gray tab.

• Once both data sets are loaded into Image Algebra, click the Apply Formula button [4]

| Formula | |
|--|---|
| Output= (Bin!=0)*Gray | |
| Output Bin Gray | |
| Volume Start 1 Number @ All Increment 1 Number @ All Slice Start 1 Number @ All Increment 1 Number @ All Increment 1 Specified 1 | Formula Output = (Bin!=0)*Gray Output Bin Gray Image: Start 1 Start 1 Number Image: Start 1 Number Specified 1 Start 1 Number All Increment 1 Number All Start 1 Number Specified 1 |
| Apply Formula | |
| | 4Apply_Formula |

Applying a Binary Mask to a Grayscale Volume (continued)

- 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.

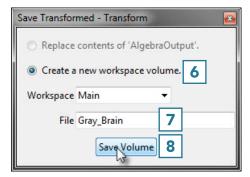
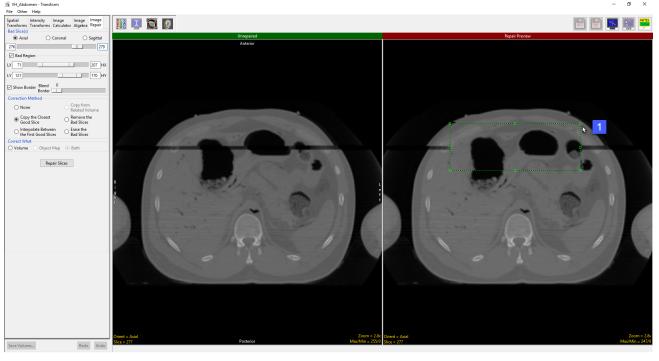


Image Repair

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. Available options are as follows:

Bad Slice(s): This option allows users to specify a range of bad slices or an area of corrupt data.



Axial, Coronal, Sagittal: Allows a range of slices to be selected in the Axial, Coronal or Sagittal orientations.

Slider: The Bad Slices(s) double-ended slider allows users to specify a range of bad slices in the selected orientation.

Bad Region: Enables the specification of a region in the image data to repair. The region is defined by the following options:

- \cdot LX: Specifies the lowest X coordinate of the bad region.
- $\cdot\,$ HX: Specifies the highest X coordinate of the bad region.
- $\cdot\,$ LY: Specifies the lowest Y coordinate of the bad region.
- $\cdot\,$ HY: Specifies the highest Y coordinate of the bad region.

Alternately, users can use the green selection area shown on the Repair Region image to define the region to repair [1].

Analyze 15.0 User's Guide

Image Repair Options

Bad Region (continued)

- · Show Border: Displays a rectangular box around the region defined by the Bad Region X and Y parameters.
- Blend Border: The blend border options allows for the specification of a region around the bad region where the corrected image information is slowly blended with the current image intensities. Move the slider button to adjust the Blend border size. Set this value to zero if no transition area is desired.

Correction Method: Allows users to select an appropriate correction methodology. Select from the following options:

- · None: No correction will occur.
- · Copy the Closest Good Slice: Copies all the pixel values from the closet non-bad image.
- Interpolate Between the First Good Slice: Use Linear interpolation to calculate a replacement slice for each bad slice. The value of
 each voxel is computed using information for each of the good slices on each side of the bad slices. The percentage of each image
 uses is calculated based on the distance from the bad slice to each good slice.
- Copy from Related Volume: Only available if a related volume is loaded. This option copies all pixel values from the related volume.
 Commonly used with a mirrored and registered copy of the input volume to symmetric features in regions.
- Remove the Bad slices: The slices are removed and the slices after the last bad slice are shifted to the area removed. This option leave blanks in the last few images for the selected orientation.
- \cdot Erase the Bad Slices: The selected range of bad slices are just set to the minimum data type value.

Correct What: The correct what options allows user to correct the original image data (Volume), a loaded object map (Object Map), or both the original image data and object map (Both).

Repair Slices: Applies the selected correction method to range of the bad slices, or regions within those slices.

Repairing an Image

Here we will repair an image that has a series of corrupt slices.

Repairing an Image

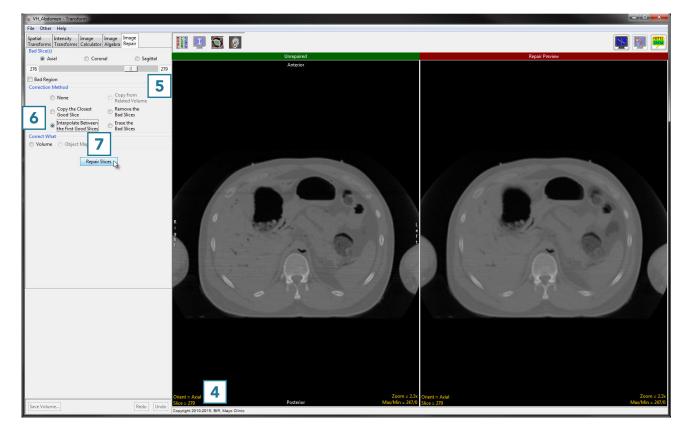
To follow along, download the VH_Abdomen data set from analyzedirect.com/data and load into Analyze using Input/Output.

- 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].



Repairing an Image (continued)

- 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.



Repairing an Image (continued)

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.

| Save Transformed - Transform | | | | |
|-----------------------------------|-------------|-----------|--------|---|
| Replace contents of 'VH_Abdomen'. | | | | |
| O Replace | contents of | VII_ADUO | men . | |
| Oreate a new workspace volume. 10 | | | | |
| | | | | |
| Workspace | Main | • | | |
| File | VH_Abdome | en_Correc | ted 11 | _ |
| | | | | |
| Save Volume 12 | | | | |
| | 15 | i | | |

Segment

| | Introduction | page 272 |
|---------------------------------|--|---|
| | Object Maps | page 273 |
| | Segment Module Interface | page 274 |
| | Menu | page 275 |
| | Display Controls | page 279 |
| | Tools | page 290 |
| | Object Controls Window | page 295 |
| | Orthogonal Image Display | page 305 |
| | Rendering Window | page 306 |
| | Segmentations Tools | page 307 |
| | Edge Strength | page 308 |
| | Walls | page 315 |
| | | |
| | Subregion | page 323 |
| | Subregion Semi-Automatic Tools | page 323 page 327 |
| | - | |
| Th | Semi-Automatic Tools | page 327 |
| Th | Semi-Automatic Tools Threshold Volume | page 327 page 328 |
| | Semi-Automatic Tools Threshold Volume reshold Volume and Segmentation | page 327 page 328 page 334 |
| 3 | Semi-Automatic Tools Threshold Volume reshold Volume and Segmentation Region Grow | page 327 page 328 <i>page 334</i> page 337 |
| 3 | Semi-Automatic Tools Threshold Volume reshold Volume and Segmentation Region Grow D Segmentation with Region Grow | page 327 page 328 page 334 page 337 page 340 |
| 3 2 | Semi-Automatic Tools Threshold Volume reshold Volume and Segmentation Region Grow D Segmentation with Region Grow D Segmentation with Region Grow | page 327 page 328 page 334 page 337 page 340 page 344 |
| 3 2 | Semi-Automatic Tools Threshold Volume reshold Volume and Segmentation Region Grow D Segmentation with Region Grow D Segmentation with Region Grow Connected Components | page 327 page 328 page 334 page 337 page 340 page 344 page 346 |
| 3 2 menting Multiple Obje | Semi-Automatic Tools Threshold Volume reshold Volume and Segmentation Region Grow D Segmentation with Region Grow D Segmentation with Region Grow Connected Components | page 327 page 328 page 334 page 337 page 340 page 344 page 346 page 349 |

Segmentation of Multiple Objects Using Object Extractor page 355

Segmenting Multiple O

| 0 | - | ~ |
|---|---|---|
| 2 | / | υ |

| Object Separator page | ge | 32/ |
|-----------------------|----|-----|
|-----------------------|----|-----|

- Separating Objects page 359
 - Oblique Cutting page 361
- Editing Objects via Oblique Cutting page 363
 - Fill Holes page 367
 - Filling Holes in Objects page 368
 - Using Fill Holes for Segmentation page 370
 - Morph Objects page 372
- Using Morphological Operations to Improve Segmentation page 375
 - Filter Objects page 378
 - Using Filter Objects to Improve Segmentation page 380
 - Propagate Objects page 382
 - Using Propagate Objects page 384

Manual Tools page 385

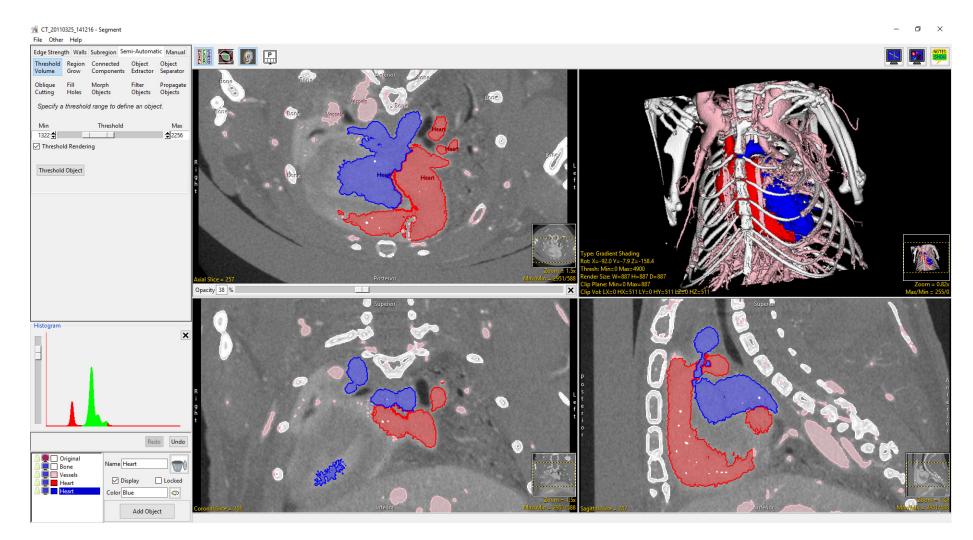
- Freehand Draw page 386
- Using Freehand Draw to Define a 2D Region page 388
- Using Freehand Draw to Define a Single Shape on a 2D Slice page 390
 - Using Freehand Draw to Define a Single Shape in 3D page 391
 - Using Freehand Draw to Paint Regions of Interest page 393
 - Manual Trace page 396
 - Manual Contour Tracing and Editing page 399
 - Manual Trace and Auto Advance page 401
 - Auto Trace page 403
 - Using Auto Trace to Define a 2D Region of Interest page 409
 - Polygon Trace page 412

| Region Definition and Regi | on Modification with Polygon Trace | page 414 |
|--|--|---|
| | Spline Trace | page 418 |
| Using Spline | Trace to Define a Region of Interest | page 420 |
| | Smart Trace | page 421 |
| | Smart Trace Region Definition | page 423 |
| | Reassign Object | page 425 |
| | Reassigning Objects | page 426 |
| | Nudge Edit | page 431 |
| Editing | g Object Borders using Nudge Edit | page 432 |
| Using the Nu | ıdge Edit Tool with Locked Objects | page 435 |
| | Divide Regions | page 436 |
| | Grid Division of an Object | page 437 |
| | Radial Division of an Object | page 439 |
| | | |
| Dividing Regions Between Borde | rs – Interpolating Between Objects | page 441 |
| | rs – Interpolating Between Objects ers – Interpolating Within an Object | page 441 page 443 |
| | | , _ |
| | ers – Interpolating Within an Object | page 443 |
| | ers – Interpolating Within an Object Adjust Regions | page 443 page 445 |
| | ers – Interpolating Within an Object Adjust Regions Using the Adjust Regions Tool | page 443 page 445 page 446 |
| Dividing Regions Between Borde | ers – Interpolating Within an Object Adjust Regions Using the Adjust Regions Tool Fabricate Shape(s) | page 443 page 445 page 446 page 452 |
| Dividing Regions Between Borde | ers – Interpolating Within an Object Adjust Regions Using the Adjust Regions Tool Fabricate Shape(s) Using Fabricate Shape(s) | page 443 page 445 page 446 page 452 page 456 |
| Dividing Regions Between Borde | ers – Interpolating Within an Object Adjust Regions Using the Adjust Regions Tool Fabricate Shape(s) Using Fabricate Shape(s) a Text File using Fabricate Shape(s) | page 443 page 445 page 446 page 452 page 456 page 462 |
| Dividing Regions Between Borde | ers – Interpolating Within an Object Adjust Regions Using the Adjust Regions Tool Fabricate Shape(s) Using Fabricate Shape(s) a Text File using Fabricate Shape(s) Manual Tools for 3D Editing | page 443 page 445 page 446 page 452 page 456 page 462 page 464 |
| Dividing Regions Between Borde | ers – Interpolating Within an Object Adjust Regions Using the Adjust Regions Tool Fabricate Shape(s) Using Fabricate Shape(s) a Text File using Fabricate Shape(s) Manual Tools for 3D Editing Dual Input Segmentation | page 443 page 445 page 446 page 452 page 456 page 462 page 464 page 467 |
| Dividing Regions Between Borde Creating Objects from Gener | ers – Interpolating Within an Object Adjust Regions Using the Adjust Regions Tool Fabricate Shape(s) Using Fabricate Shape(s) a Text File using Fabricate Shape(s) Manual Tools for 3D Editing Dual Input Segmentation 4D Segmentation | page 443 page 445 page 446 page 452 page 456 page 462 page 464 page 467 page 469 |

271

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.



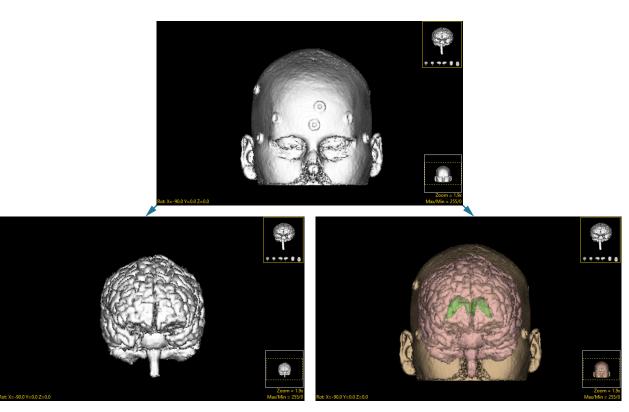
Object Maps

Analyze 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



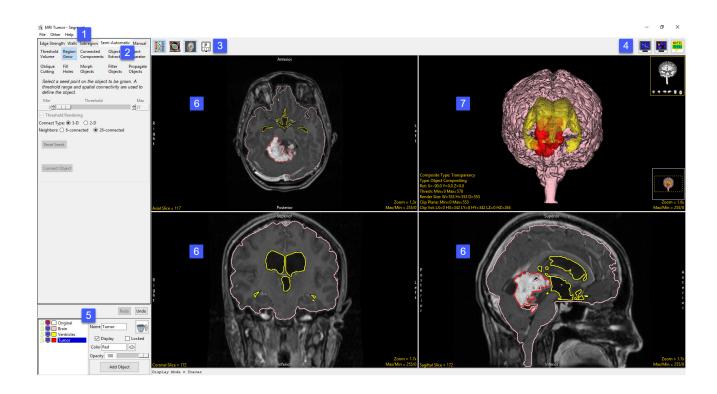
Grayscale segmentation destroys all voxels that are not part of the object of interest.

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

Segment Module Interface

The Segment Module interface is divided into the following areas: [1] Menu, [2] Segmentation Options, [3] Display Controls, [4] Tools, [5] Object Control Window, [6] Orthogonal Image Display, and [7] Rendering Window.

Each of the Segment Module Interface areas are now described:



Menu

The Menu provides access to the File, Options and Help menus.

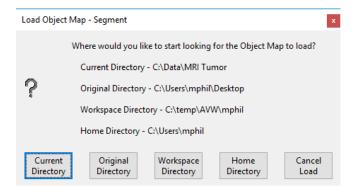
File

The File menu allows users to load and save object maps for the loaded data set. The File options include:

Input/Output Ports: Displays a Volume area at the bottom of the Segment module window. This area facilitates the dragging and dropping of image data into the module and the loading of a related image data set, see Dual Input Segmentation for additional information.

Load Object Map: When selected opens a Load Object Map window allowing users to navigate to, select and load an object map file. The following options are available:

- Current Directory: Takes user to the current directory, the current directory is set by right-clicking in the main Analyze 15.0 window and then choosing Current Directory from the menu. See section 1. Analyze Basics for additional information.
- Workspace Directory: Takes user to the current Workspace directory.
- Home Directory: Takes user to the user's Home directory.
- Cancel Load: Cancels the load of the object map.



Menu (continued)

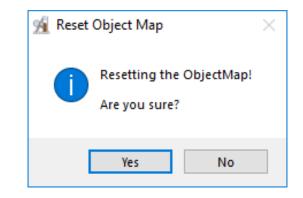
Save Object Map: When selected opens a Save Object Map window allowing users to navigate to name the object map and select a location to save the object map file.

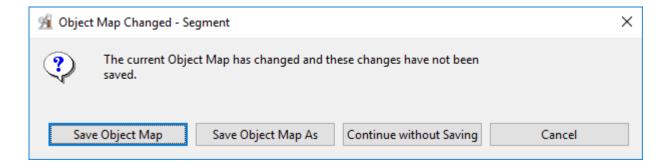
Save Object Map As: Allows users to save a copy of the current object map without overwriting the original object map file.

Reset Object Map: Resets the current loaded object map, deleting all defined objects. When this option is selected a prompt will be returned asking you to confirm the reset. Select 'Yes' to continue or 'No' to cancel.

If the object map has not been saved or changes to an object map have not been saved when the Rest Object Map option is selected an Object Map Changed prompt will be returned providing the opportunity to save the object map.

Exit: Closes the module





Menu (continued)

Other

The other menu provides access to additional module options and configuration of the tools area.

Options: When selected opens the Options menu providing access to Module configuration options, including:

- Intensities Linked: Allows users to enable or disable linked intensity adjustment. When linked any adjustment an images intensity display will be applied to all grayscale slices displayed. When disabled image intensities can be adjusted individually.
- Fast Object Rendering: Enables/Disabled Fast Object Rendering.
- Show Cursor Coordinates: Allows users to Enable/Disable the display of the linked cursor coordinates and voxel grayscale value displayed in the lower left-hand corner of the display window.
- Auto Note Update: Allows the Auto Note Update option to be enabled or disabled.
- Auto Cursor Link: Allows the Auto Cursor Link option to be enabled or disabled.
- Remember Layout: When enabled the module will remember changes made to the layout and will open with this layout in the future. When disabled the module will open with the default layout.
- Threads: Allows users to specify the number of threads used in a multi-threaded rendering process. By default, the number of threads is set to the number of processors on the system.

Menu (continued)

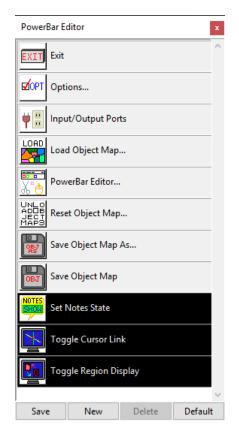
Powerbar Editor

When selected opens the PowerBar editor allowing users to add additional shortcut buttons to the tools area of the Segment window. Add or remove the following shortcut buttons form the tools area: 1) Exit, 2) Options, 3) Input/Output, 4) Load Object Map, 5) PowerBar Editor, 6) Reset Object Map, 7) Save Object Map As, 8) Save Object Map, 9) Set Note Stat, 10) Toggle Cursor Link, 11) Toggle Region Display.

Help

The Help menu provides users with quick access to help resources including:

- About: View version, system and environment information.
- Users Guide: Opens the Analyze 15.0 User's Guide.
- Get Help: Opens the AnalyzeDirect Support Page.



Display Controls

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.

3 1 Control Layout 2 1 2 3 3 4 2 4 1 </td

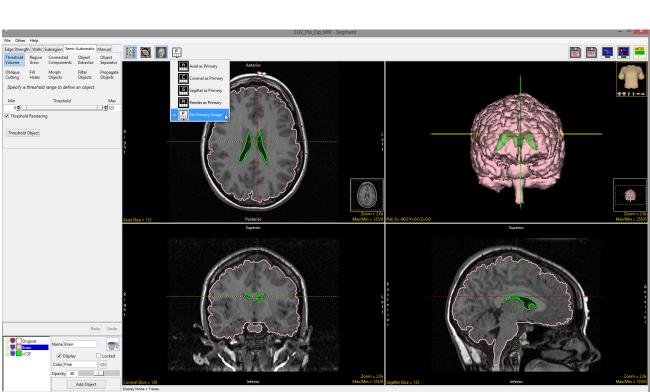
Control Layout

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.

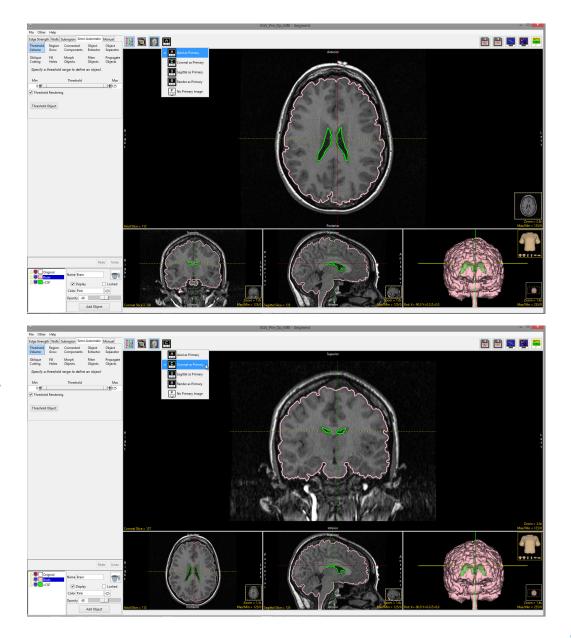
No Primary Image: This is the default selection.

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

© AnalyzeDirect, Inc.



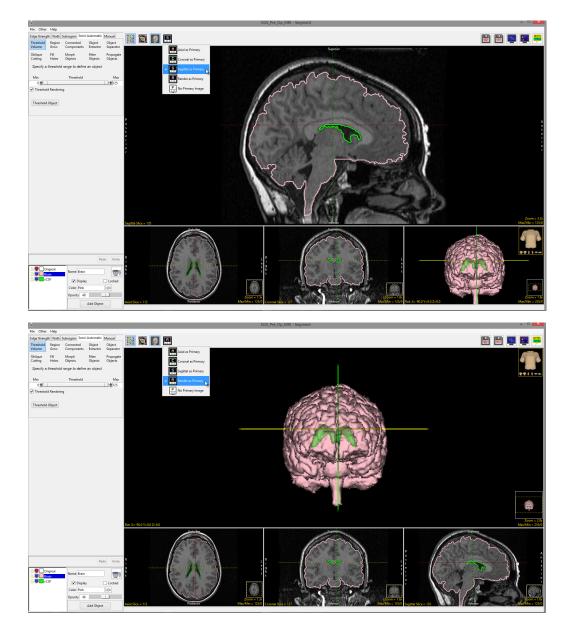
Axial as Primary: Focuses the display on the axial image. The coronal, sagittal and rendering windows are displayed below the axial window.



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

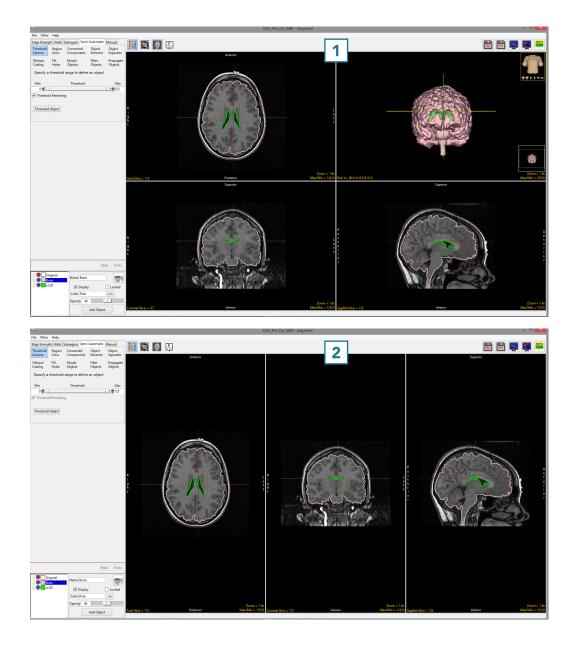
Sagittal as Primary: Focuses the display on the sagittal image. The axial, coronal and rendering windows are displayed below the sagittal window.

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



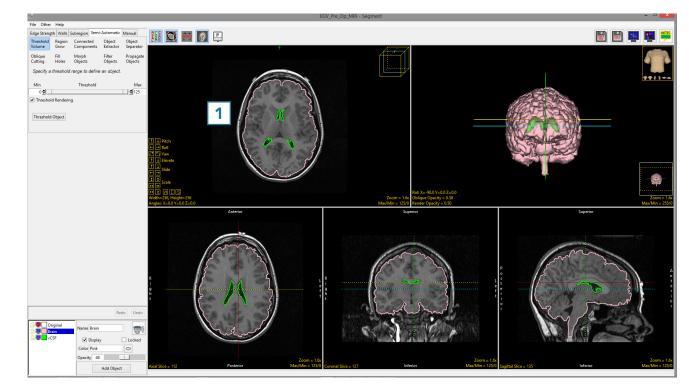
Toggle Rendering

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.

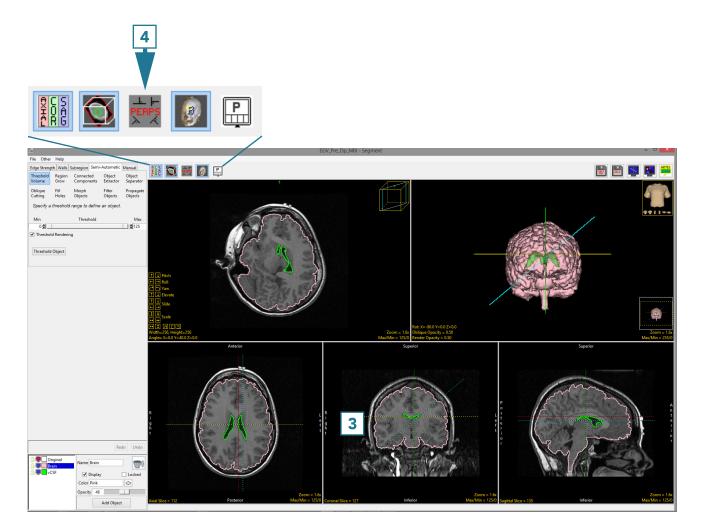


The oblique window provides users with the ability to create any arbitrary oblique plane on the fly, using the control tools [2] in the oblique window.



The oblique image can also be generated using the blue oblique reference line that appears in all of the other enabled windows [3].

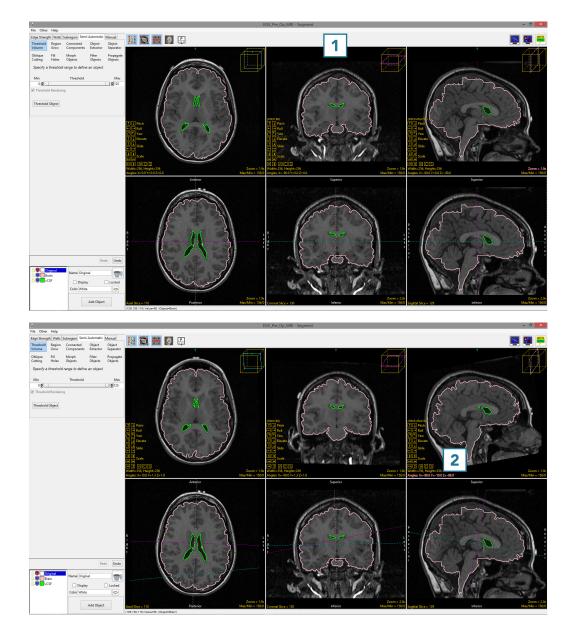
When the oblique image is enabled, an additional option becomes available: Toggle Perpendicular [4].



Toggle Perpendicular

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

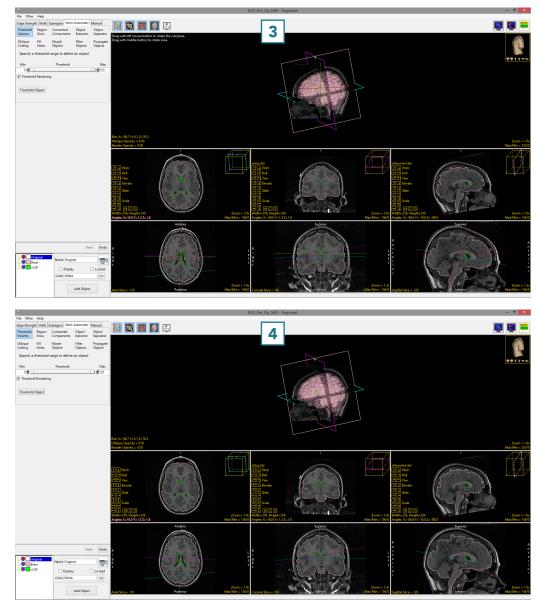
The control tools [2] can be used to manipulate each orientation to aid users with the generation of the desired oblique plane.



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.

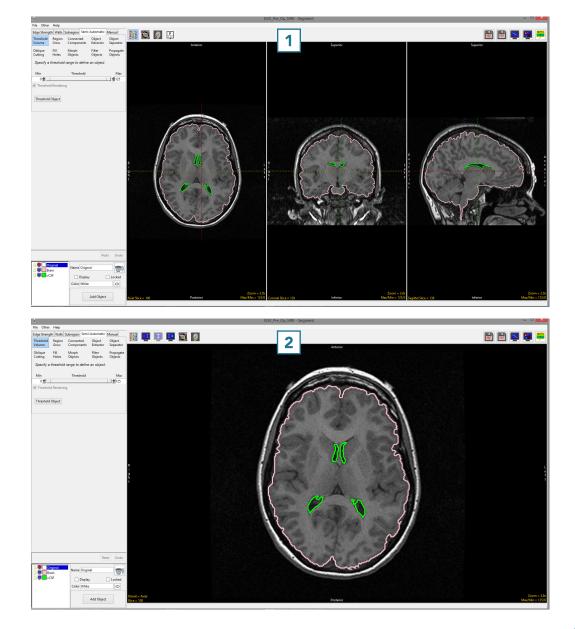
For more information about creating oblique planes, refer to the <u>Apply</u> <u>Matrix exercise</u> in the Transform section.



Display Controls (continued)

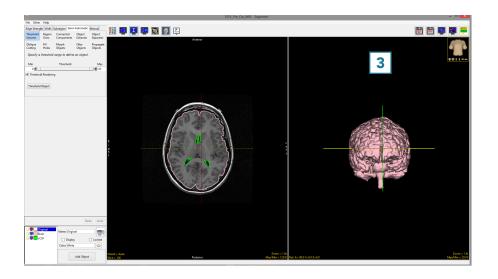
Toggle All Orientations

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].

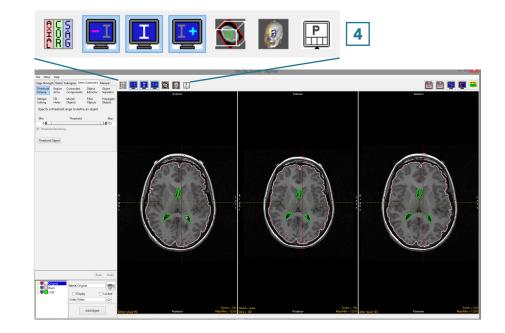


Display Controls (continued)

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



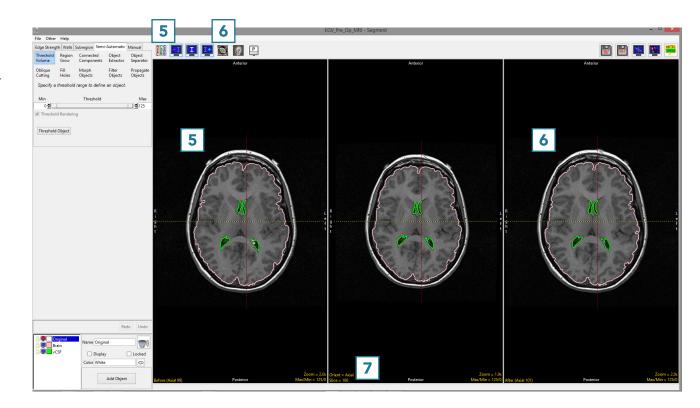
options are enabled [4].



When display is toggled to single display mode, additional display

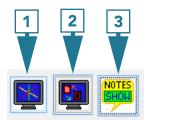
Display Controls (continued)

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.



Tools

The Tools options in the top right hand corner of the Segment Module Interface, provide access to the Cursor Link, Toggle Region Display and the Set Note State tools.





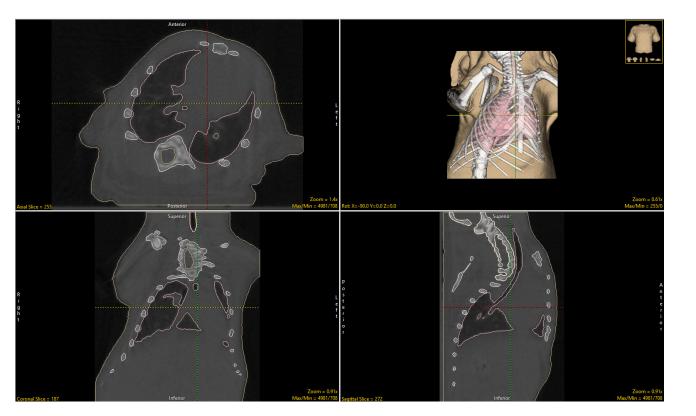
Cursor Link

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.

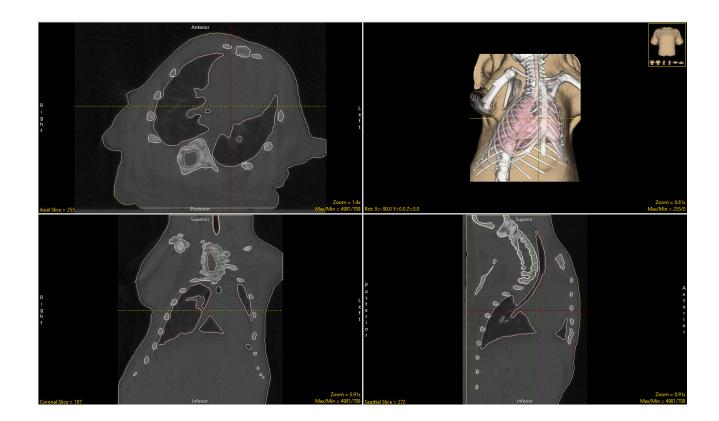


Toggle Region Display

Users have the option to change the display of objects on the 2D slices. Users can cycle through the various object display options using



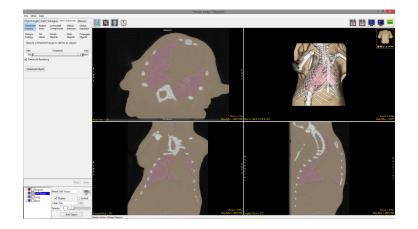
the Toggle Region Display button or using the t key.



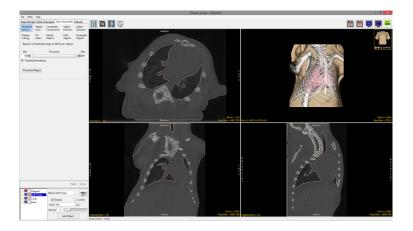
© AnalyzeDirect, Inc.

There are four object display options:

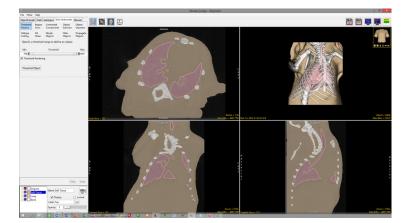
Filled Regions



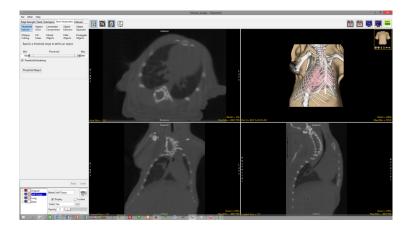
Edges



Filled Regions with Edges



Off



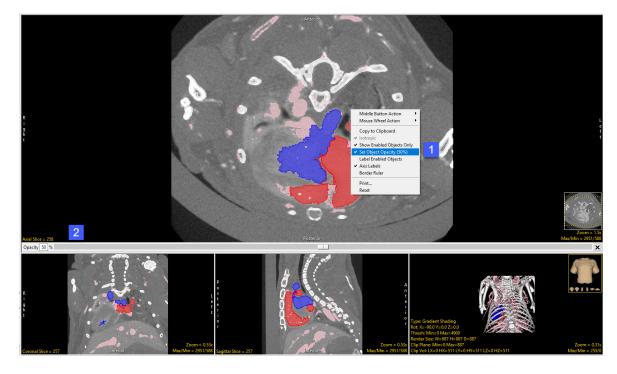
Analyze 15.0 User's Guide

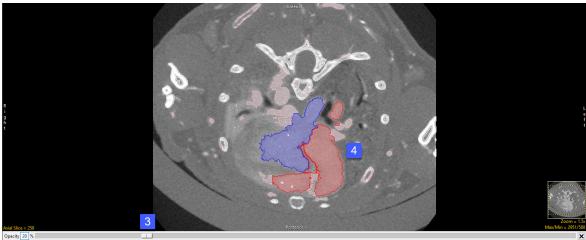
2D Object Opacity Display: It is possible to change object color alpha blend for the display of objects on the 2D slice data for the filled regions and filled regions with edges object display options. Adjusting the alpha blend allows users to visualize underlaying grayscale data while still seeing which voxels are assigned to objects.

To adjust the alpha blend right-click on any of the 2D slices displays and then choose the Set Object Opacity [1] option to enable it.

An Opacity slide will appear below the slice display window [2] allowing users to adjust the alpha blend of the objects on the image data. The default opacity value is 50%.

Use the slider to reduce the object opacity value [3] and review the effect [4].





Notes

The Notes tool in Analyze 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).

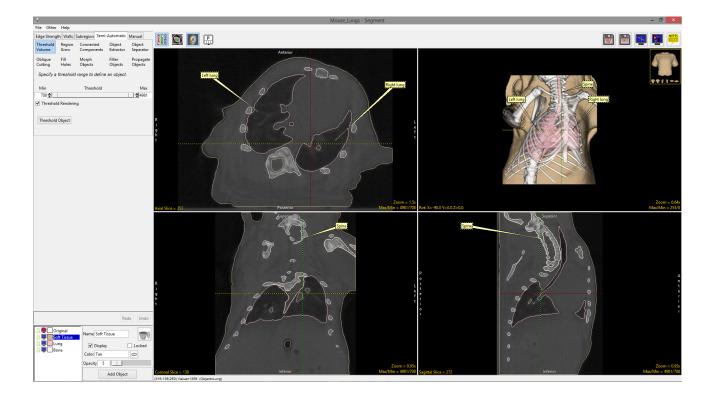


Allows users to make and edit notes.



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.



Object Controls Window

The Object Controls window allows users to add objects to the current object map. It also allows users to edit object properties. The Object Controls window provides users with the following object control options, functions, and productivity tools:

Add Object

The Add Object button [1] allows users to add new objects to the object map. Objects are show in the object list [2].

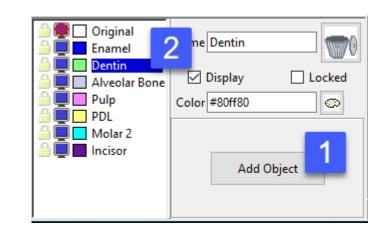
Name

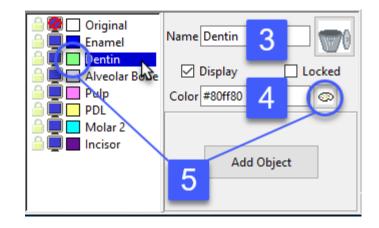
The Name field [3] in the object attributes area allows users to modify the assigned object name to something applicable for the segmented object.

Color

Object color can be updated by entering the color name (e.g. Gray) or the hex color code (e.g. #808080) in the Color field. [4]

Object colors can also be interactively selected using an object color palette. To open the Color palette, click on the palette icon [5] next to the Color field or the colored square next to the object name in the object list.





The Color selection palette [6] will open, select a basic color or use the color selector to choose a color. Color HSL and RGB values can also be input.

Display

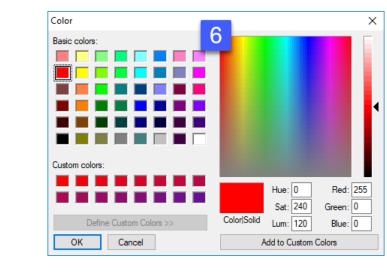
The Display attribute for an object controls if the object is visible or not on the 2D slice displays and 3D rendering. To disable and enable the display of an object use the Display checkbox [7] in the object attribute are or click the screen icon next [8] to the object in the object list.

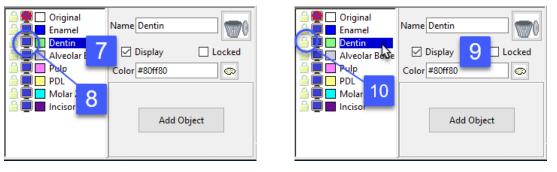
Object Lock

Object locking provides the ability to lock objects preventing the voxels assigned to the locked object from being edited. This is a

powerful tool to aide segmentation, as 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. However, 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.

Objects can be locked and unlocked by checking the Locked checkbox [9] in the object attribute area or by clicking the lock icon [10] for the object in the object list.





Opacity

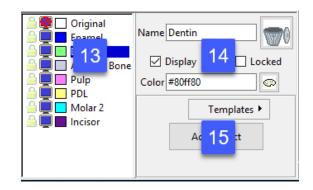
The Opacity option [11] is only available when the Transparency option is enabled. To enable the option right-click on the rendering and choosing Transparency form the menu. Adjusting object opacity levels allows users to enhance the rendered display of objects. Object opacity can be manipulated by using the opacity slider or by entering a value in the text field.

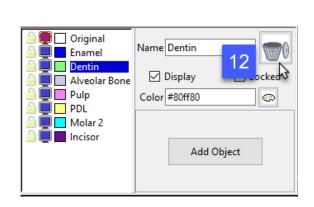
Delete

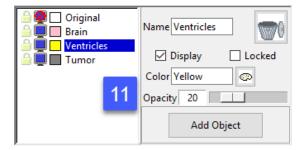
The delete button [12] allows users to remove objects form the object map. Voxels assigned to an object that is deleted are reassigned back to the Original object and the object is removed from the object list.

Right Mouse Menus

There are several right mouse menu options in the object controls window, and these menus are accessible by right-clicking in the object list [13], the object attribute area [14], and the area around the Add Object button. [15]







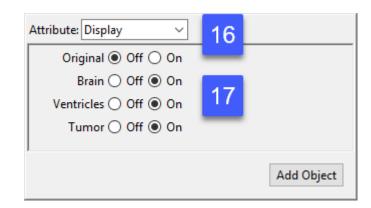
Object List Right Mouse Menu

Right click in the object list area to access additional object functionality from the right mouse context menu. These options include:

Control By: The Control By option allows users to set the control of object attributes by objects or by attribute. When set to Object users can modify all object attributes for a single object. When set to Attribute users can modify the selected attribute for all objects:

 Objects: Objects is the default control by option, displaying a list of objects. Attributes for each object can be edited in the object attribute area for each object.

| Control By | • |
|------------------|---|
| Remove Unused | |
| Reorder Objects | |
| Reassign Objects | |
| Recalc Objects | |
| Load Objects | |
| Load Binary | |
| Save Binary | |
| Save Grayscale | |
| Apply Edits | |
| Load Surface | |
| Extract Surfaces | |
| | |
| | |



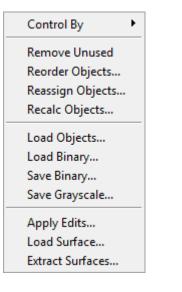
Attributes: When the Attributes option is selected the object list area updates providing an attribute drop down menu [16]. Users can select any of the object attributes to enable or disable for all the objects in the object map [17]. The attribute options include; Display, Lock, Name, Color, Shades, Neighbors Used, and Opacity. Controlling by Attribute is extremely useful when you need to modify attribute values for many objects. Right-clicking in the object area provides access to additional selection options to enable or disable attributes including All, None, and Invert.

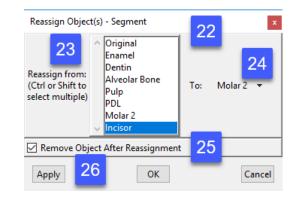
Analyze 15.0 User's Guide

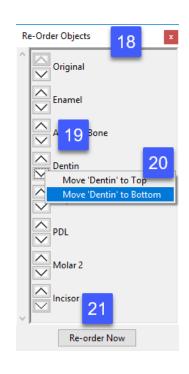
Remove Unused: allows users to quickly delete any object in the object list that doesn't have a voxel assigned to it. A helpful option for object map clean-up.

Reorder Objects: allows users to reorder objects in the object list. When selected a Reorder Objects window opens [18]. Objects can be moved up or down in the object list using the arrow keys next to the object [19]. Right-clicking on an object allows you to move the object to the top or bottom of the object list [20]. To apply changes in object order click the Re-order button [21].

Reassign Objects: Selecting the reassign object option will open the Reassign Object(s) window enabling the reassignment of one or many objects to another. Select the object to reassign from the 'Reassign From' list [23] then set







the object to reassign to from the 'To' drop down list. [24] Check or uncheck the Remove Object After Reassignment check box [25] and then click Apply. [26] All voxels assigned to the objects selected in the 'Reassign From' list will be assigned to the object in the 'To' list.

Recalc Objects: When this option is selected the module calculates and sets the minimum enclosing 3-D region for each object.

Load Objects: allows users to load objects from another object map into the current object map. For example, electrodes segmented from a CT data set could be loaded onto a brain object in a co-registered MRI data set. To use, right-click on the object list area and then choose Load Objects from the menu. In the window returned navigate to and select the object map that contains the object(s) you wish to load. Once select a Load Object(s) window [27] will open. Check the objects you wish to load [28] and then click Load Selected [29].

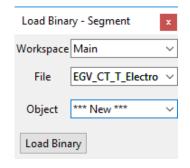
Please note, loaded objects will overwrite voxels assigned to other objects so consider the order that objects are loaded. For example, loading a hippocampus object into an object map that contains the whole brain would work fine, however, loading the whole brain into an object map that contains the hippocampus would not work, as the hippocampus object would be overwrote by the brain object.

Load Binary: allows users to create objects using a binary image. For example, electrodes segmented from a CT data set saved to the workspace as a binary image could be loaded onto a brain object in a co-registered MRI data set. The following options are available:

- o Workspace: Select the workspace that contains the binary image to load.
- o File: Select the binary image file.
- o Object: Choose the object to create from the binary image input.

To use, right-click on the object list area and then choose Load Binary from the menu. In the Load Binary window returned use the Workspace menu option to select the workspace that contains the binary image. Next use the File option to select the binary image from the workspace. Finally, use the Object drop-down menu to set the object the binary image will create, by default the option is set to ***New***, however, any object in the object map can be selected. Finally, click Load Binary.

Control By Load Object(s) - Segment Select Object(s) to Load Remove Unused Reorder Objects... 1) Original 2) Electrodes Reassign Objects... Recalc Objects... 28 Load Objects... Load Binary... Save Binary... Save Grayscale... Apply Edits... Load Surface... Re-define Only Renderable Extract Surfaces... Load Selected Cancel



Save Binary: allows users to save any object in the object map out to the selected workspace as a binary image, the voxels part of the object will be saved as 1's while every other voxel will be saved as a zero. The following options are available:

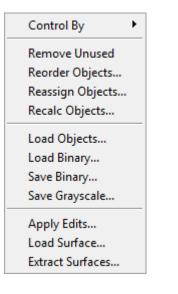
- o Object: Chose the object to save.
- o Workspace: Select the workspace to save the binary image to.
- o File: Name the file.
- o Save Binary: Initiates the save process.

Save Greyscale: allows users to save any object in the object map out to the selected workspace as a grayscale image, with all voxels not part of the object removed from the image (set to the background). The following options are available:

o Object: Chose the object to save.

o Workspace: Select the workspace to save the greyscale image to.

- o File: Name the file.
- o Save Greyscale: Initiates the save process.



| Save Binary - Segment 🔹 | | | | | |
|-------------------------|---------------|-----------|--|--|--|
| Object | Brain | ~ | | | |
| Workspace | Main | ~ | | | |
| File | EGV_MRI_Brain | | | | |
| | | Overwrite | | | |
| Save Binary | | | | | |

| Save Grayscale - Segment | | | | |
|--------------------------|-----------|--|--|--|
| Object Brain | ~ | | | |
| Workspace Main | ~ | | | |
| File EGV_MRI_Brain | | | | |
| | Overwrite | | | |
| Save Grayscale | | | | |

Apply Edits: allows users to change the voxel grayscale values in the image for any object in the object list, including the original object. To use, right-click on the object list area and then choose Apply Edits from the menu. In the Apply Object Edits to Volume window returned [30] select the object(s) to edit [31] and then use the drop-down menu to choose the type of edit to apply. The following options are available:

- Set to Value: Allows users to select a single greyscale value that all voxels represented by the object will be assigned to.
- Intensity Scale Values: Provides users with the ability to the range of the grayscale values by adjusting the minimum and maximum values.
- Random Value: Assigns voxel values to a random value. The Random value maximum and minimum range defaults to volumes maximum and minimum, but these values can be edited by the user.
- Gaussian Value: Assigns voxel values within the object to be assigned to a Gaussian Value. Mu and Sigma values are calculated automatically, but can be updated by the user.

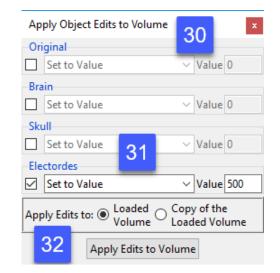
Assign the desired value(s). Choose to Apply the edits to the Loaded Volume or a Copy of the Loaded Volume (recommended) and then click the Apply Edits to Volume button [32] to update the data set.

Load Surface: Allows users to load related .stl or .pogo surface files for the data set.

Extract Surface: The Extract Surface option allows users to generate and save surface files from objects. For instructions on how to use this option please refer to the Generating Surface Files from Objects section of this guide.

Analyze 15.0 User's Guide





© AnalyzeDirect, Inc.

The Object Attribute Area Right Mouse Menu

Right click in the object attribute area to access additional object functionality from the right mouse context menu. These options include:

Control By: The Control By option allows users to set the control of object attributes by objects or by attribute. For a full description please see the Control By section in the Object List Right Mouse Menu Options section above.

Neighbors: The Neighbors option allows users to specify which voxels are used to calculate the gradient for image rendering. Changing the neighbors option can help improve the display of rendered objects especially with anisotropic data sets or with objects loaded from related data sets. The following options define the neighbors used:

- All: Specifies that all voxels, no matter which object they belong to are used.
- Object w/Gradient: The object with gradient specifies that only the grayscale values of neighboring voxels which belong to the same objects are used.
- Object wo/Gradient: The object without gradient specifies that only neighboring voxels which belong to the same object are used. The grayscale value of the voxels are ignored, with gradient computations applied to the object map itself (binary surface rendering).
- Object Smoothed: This option is similar to object without gradient option, however, instead of using only the neighboring voxels belonging to the same object to calculate the shading, the neighboring voxels within a5x5x5 region around the voxels of interest are used. A weighting factor is applied so that the closest neighbors have twice the contribution as those twice as far away.

Shades: The Shades options allows users to set the number of shades used for the object. Users can choose from; 1, 16, 32, 50, 64, and 256.

Control By
Neighbors
Shades

The Add Object Area Right Mouse Menu

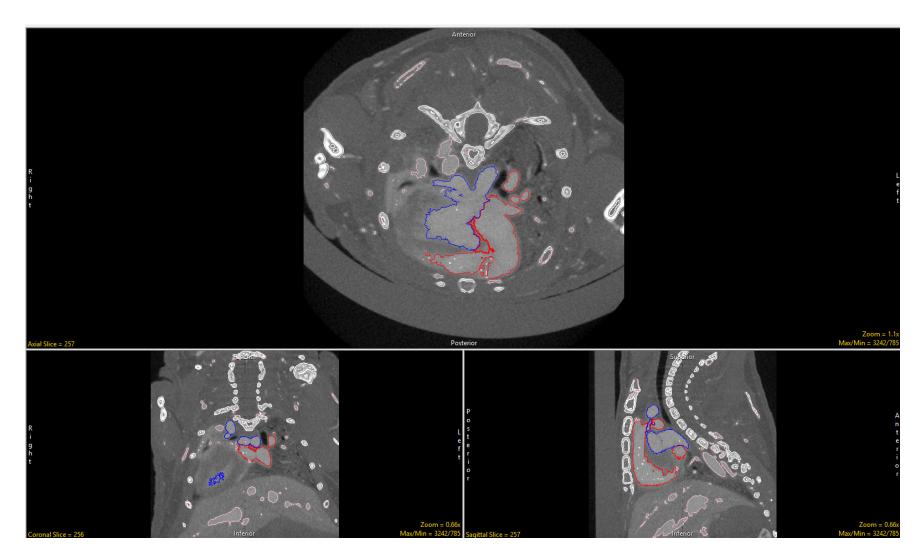
Right click in the Add Object area provides access to the Templates option. The Templates option allows users to create object templates for object maps, this option is especially useful when users create the same object maps containing the same objects for multiple volumes. It is also helpful for object maps that contain may objects. To use this option, create a list of objects specifying object names, colors, and any other attributes and then right-click and choose Templates > Save Templates. Choose to save for the Current User or All Users and then name the template. Click Save.

| Save Template | | | | | | |
|------------------------------------|--------|--|--|--|--|--|
| Save for: Current User All Users | | | | | | |
| Template Name Brain | | | | | | |
| Save | Cancel | | | | | |

To load an object template right click in the Add Object area and then select the template. User specific templates (Current User) are shown at the top of the window while system templates (All Users) are shown in the middle. Once the template is selected the objects specified in the template will be loaded to the object list. Note that these are just empty objects, templates will not save any kind of segmented object region.

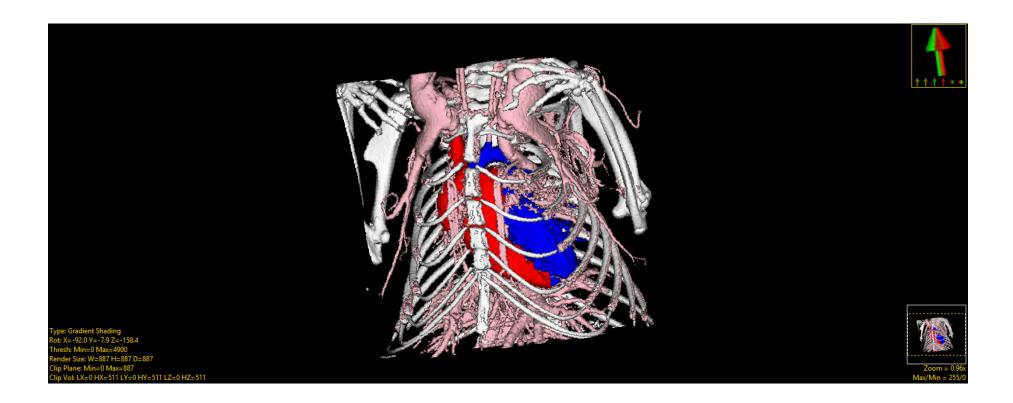
Orthogonal Image Display

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 the Display section of The Analyze User's Guide.



Renedering Window

The Rendering Window provides an interactive 3D display of the segmented image data. For more information about the render window, refer to the Display section of The Analyze User's Guide.



Segmentation Tools

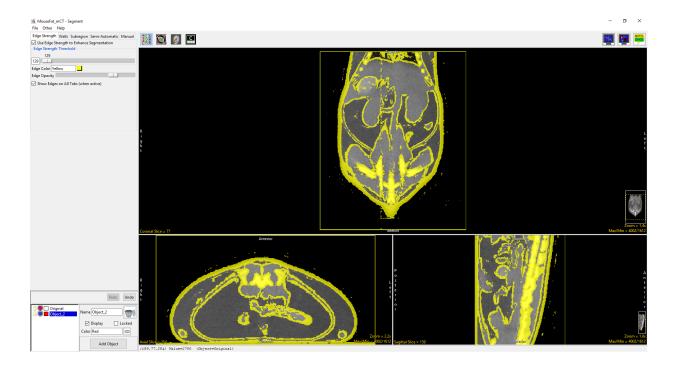
The segmentation options are provided in five tabs:

- 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 now be described.

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 with a definable edge color and form boundaries around structures. The boundaries act as limits, restricting semi-automatic segmentation operations. The following controls are available:



Use Edge Strength to Enhance Segmentation: When this option is checked the Edge Strength option is enabled for the image data, a 3 by 3 by 3 Sobel filter is applied to the volume and the Edge Strength Threshold slider and additional options are enabled.

Edge Strength Threshold: This slicer defines the upper threshold value for the Sobel filtered gradient volume. When the left mouse button is used to drag the slider, all of the voxels with gradient values less than or equal to the threshold value are highlighted. Semi-automated segmentation algorithms are applied to the voxels within the threshold range.

Edge Color and Edge Opacity: Allows users to specify the color and adjust the opacity display of the edge overlay on the image data.

Show Edges on All Tabs (when active): maintains the display of the edges on the image data when moving to different segment tabs.

Analyze 15.0 User's Guide

Using Edge Strength

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

To follow along, download the data set CT_Heart from analyzedirect.com/data and load into Analyze using Input/Output.

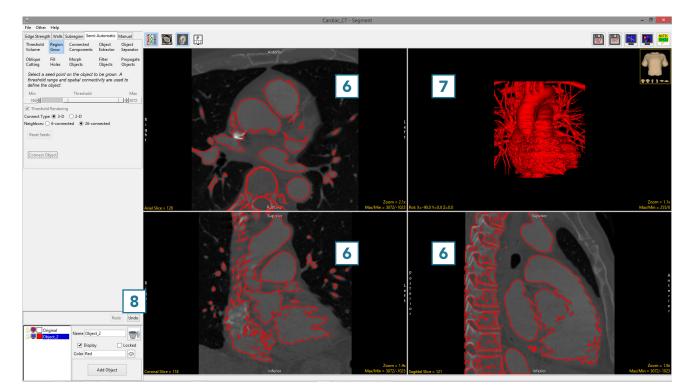
- Select the data set and open Segment.
- Select Semi-Automatic [1], and choose Region Grow [2].
- Click on the image data to set a seed point [3]. The seed point should be in the object you would like to isolate.
- Set the threshold Min/Max values to define the object [4] and click Connect Object [5].



- 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 [8].

• Click Undo.

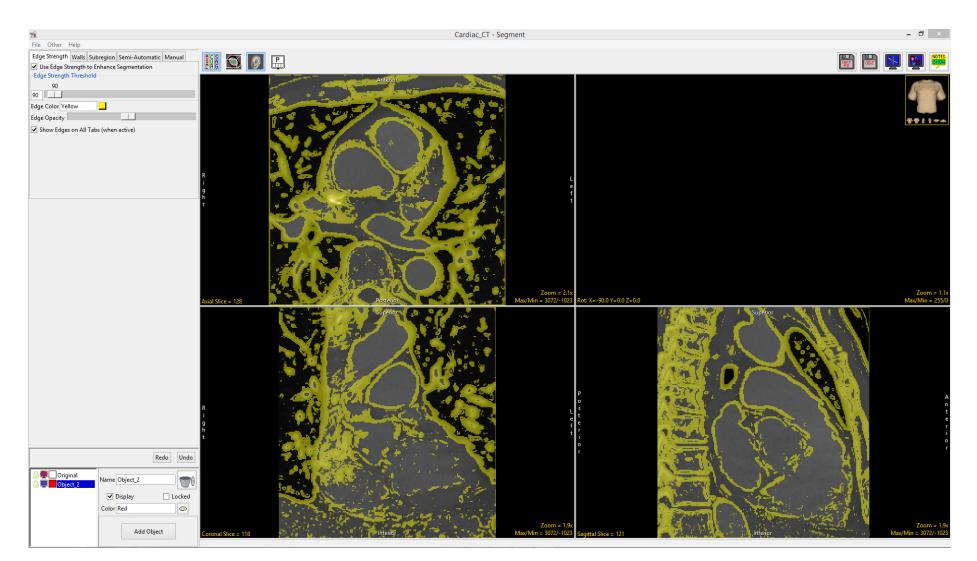


Now we will repeat this segmentation using edge strength to separate the heart from the rest of the data set.

- 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].

| Edge Strength | 9 | Subregion | Semi-Automat | ic Manual | | | |
|------------------|--|------------|--------------|-----------|--|--|--|
| ✓ Use Edge Stre | Use Edge Strength to Enhance Segmentation 10 | | | | | | |
| Edge Strength | Thres | hold | L | | | | |
| 90 | - | | | | | | |
| 90 1' | 1 | | - | | | | |
| Edge Color Yello | w | 1 2 | | | | | |
| Edge Opacity | | | 14 | | | | |
| Show Edges | on All | Tabs (when | active) | | | | |
| 13 | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |

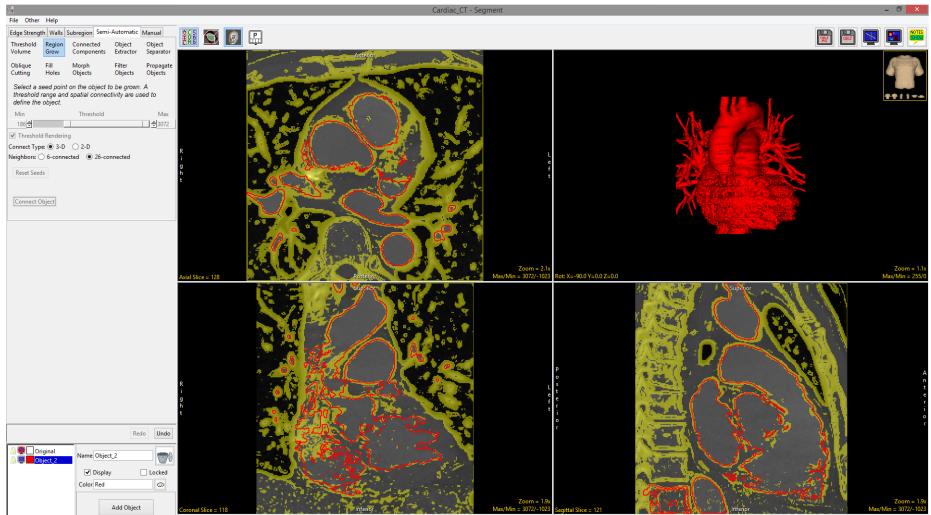
The edges detected on this data set using the Edge Strength algorithm with an edge strength threshold of 90 are shown overlaid on the data below.



- 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].

| Edge Strength | Walls | Subregion | Semi-Automatic | | Manual | |
|--|----------------|------------------|--|--|----------------------|----|
| Threshold Volume | Region Grow | | Connected Object Components Extractor | | Object Separator | |
| Oblique Cutting | Fill Holes | Morph Objects | | | Propagate Objects | |
| Select a seed point on the object to be grown. A threshold range and spatial connectivity are used to define the object. | | | | | | |
| Min | Min Threshold | | | | М | ax |
| 186 🚖 📃 🔤 🗍 🖨 3072 | | | | | 72 | |
| ✓ Threshold Rendering | | | | | | |
| Connect Type: 3-D 2-D | | | | | | |
| Neighbors: O 6-connected | | | | | | |
| Reset Seeds | | | | | | |
| Connect Object | | | | | | |

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.

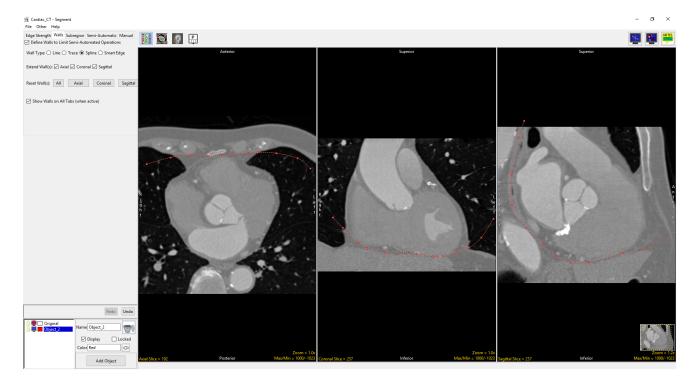


SEGMENT > WALLS

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.

The Walls option allows users to define traces which are used to limit the extent of an object. Separate walls can be created in each orientation, the wall defined in one orientation is not reflected in the other orientations. Traces defined on slices are linearly interpolated within each orientation reducing user interaction time, so that a trace defined on slice 10 and a trace defined on slice 50 are automatically interpolated between so the user doesn't have to define the wall on each slice between. The interpolated traces are designated by a dashed green line, while the user defined traces appear as a dashed red line.



Walls are used with the Threshold Volume, Region Grow, Connected Components, Object Extractor and Object Separator Semi-Automatic tools. Walls can also be used in conjunction with the Edge Strength and Subregion tools.

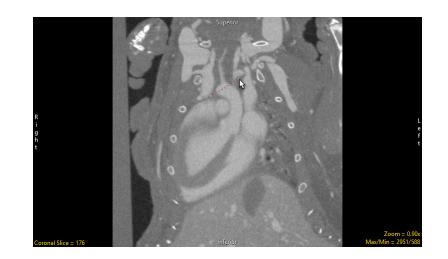
Walls Tab Options

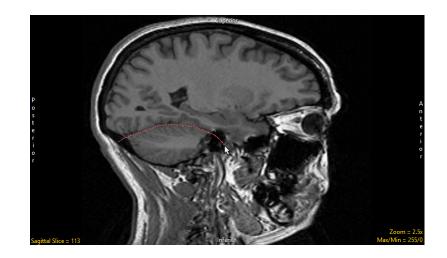
The Walls tab provide the following option:

Define Walls to Limit Semi-Automated Operations: When checked enables wall definition options allowing users to define walls on the image data.

Wall Type: Allows users to select the wall definition mode, the options include:

- Line: The line option allows users to define a straight-line wall on the image data.
- Trace: Allows user to define a freehand wall on the image data
- Spline: The Spline option allows users to define a curved wall.
 Splines are flexible curve traces with movable control points that are useful for creating smooth walls.



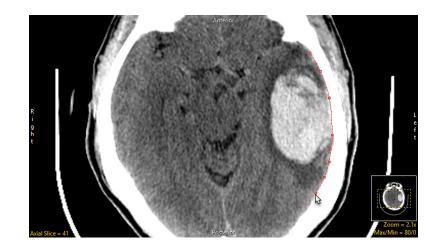


Walls Tab Options (continued)

- Smart Edge: The smart edge option detects regions of high rate of change of voxel intensity (gradient) that represent edges, smart edge snaps to the edges of these regions.
- Sensitivity: The sensitivity of the smart edge can be adjusted using the slider or the mouse scroll wheel. The lower the value the less sensitive the tool is, the higher the value the more sensitive the tool is.

Extend Wall(s): Specifies if the wall is extended beyond the first and last user defined wall in each orientation.

Reset Wall(s): Allows the user to reset the defined walls in any or all orientations.



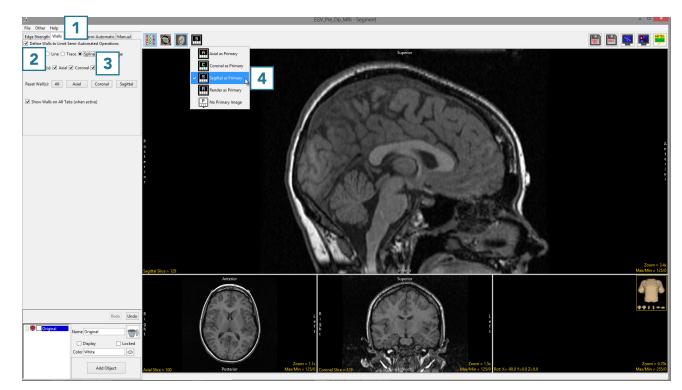


Using Walls

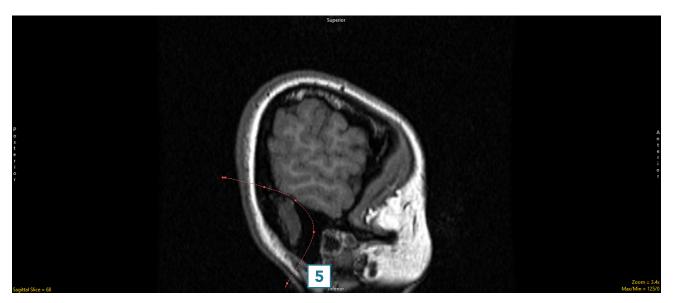
Here we will use the Walls functionality to segment the cerebellum from the rest of the brain parenchyma in a head MRI dataset.

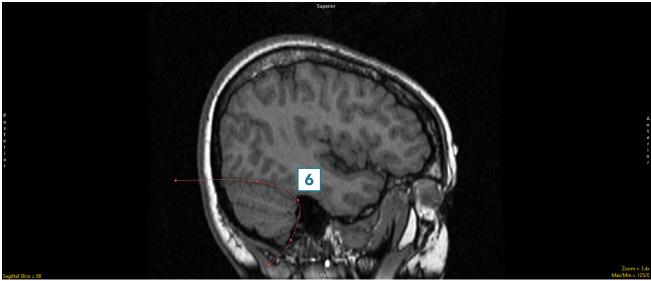
To follow along, download the data set EGV_MRI from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the 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].



- 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.

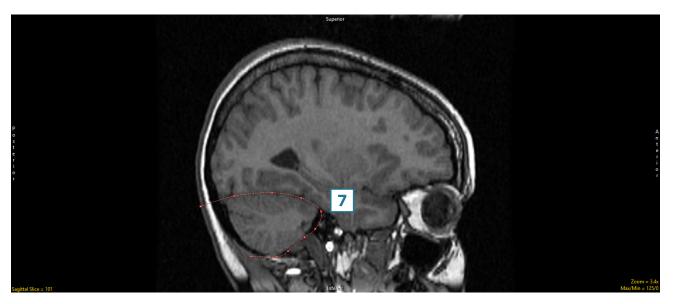


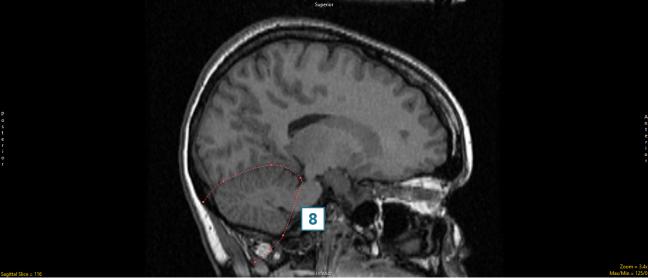


 Once the cerebellum is no longer well defined by the wall, redefine the wall on that slice. The wall will be interpolated between all slices on which it is defined. When finished, scroll through the slices to ensure that the cerebellum is well defined by the wall.

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].

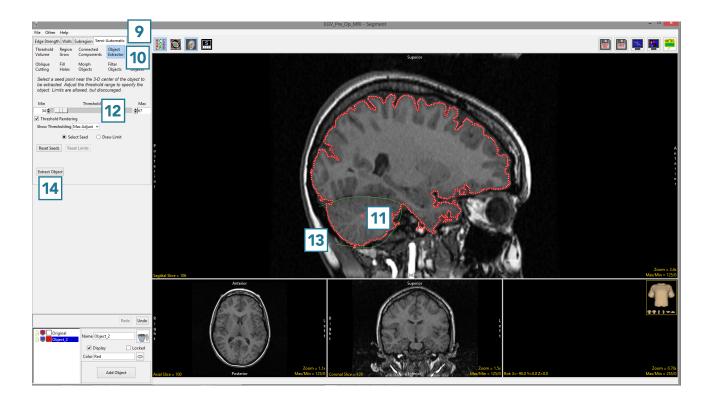




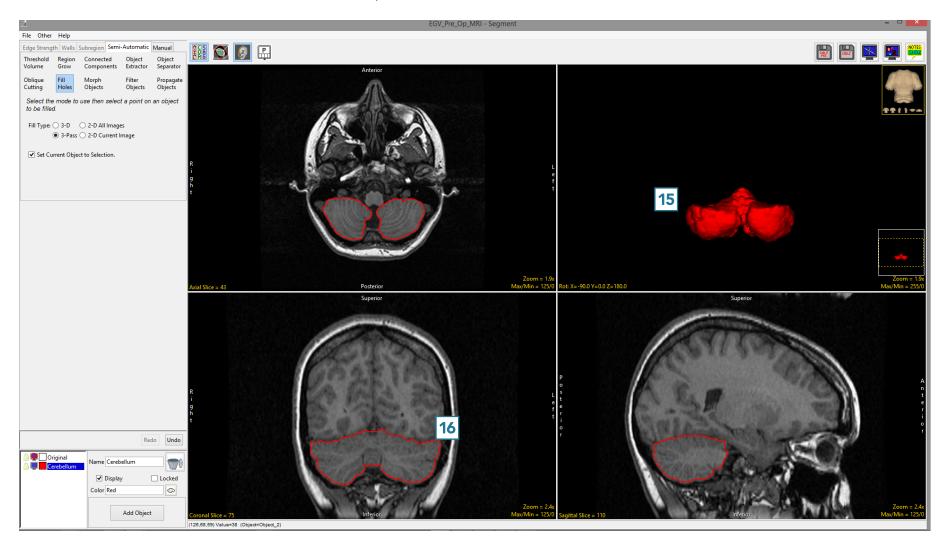
- Once the cerebellum boundary is defined in three dimensions by the wall, select the Semi-Automatic tab [9] and choose Object Extractor [10].
- Click in the cerebellum on a sagittal slice to set a seed point [11].
- Adjust the maximum and minimum threshold values [12] until the auto trace defines the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

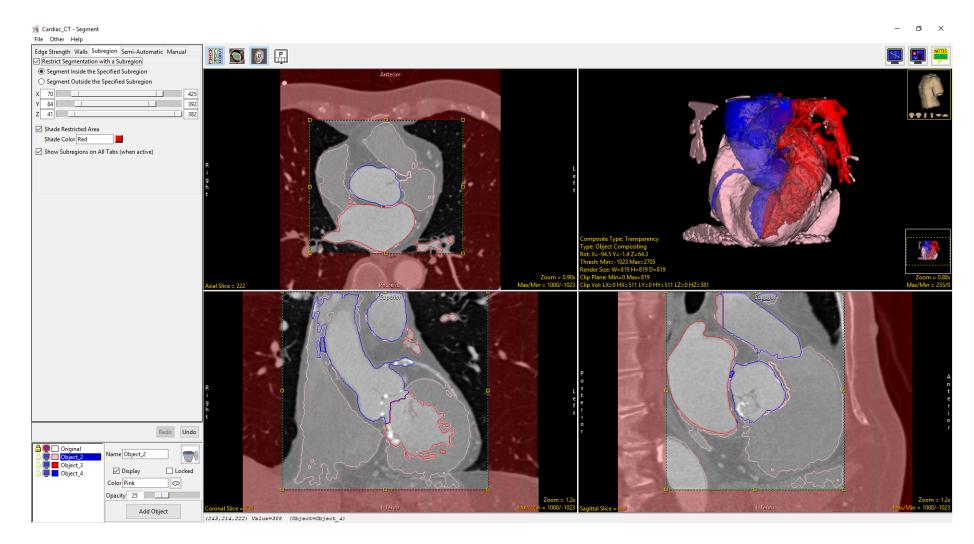


- The cerebellum will be isolated and displayed in 3D.
- Once segmentation is complete, the structure will be rendered [15] and overlaid on the slice data [16].
- Save your work by selecting File > Save Object Map.



Subregion

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



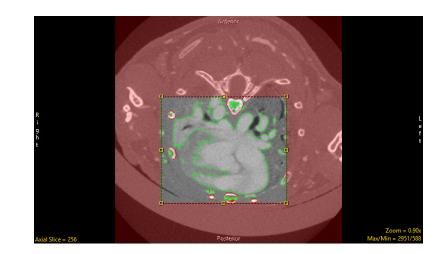
Subregion Options

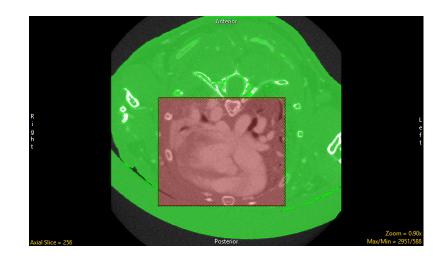
Subregion can be used with the Threshold Volume, Region Grow, Connected Components, Object Extractor and Object Separator Semi-Automatic tools. Subregion can also be used in conjunction with the Edge Strength and Wall tools.

Restrict Segmentation with a

Subregion: When checked enables subregion restriction of semiautomatic and manual segmentation tools. The following options are available:

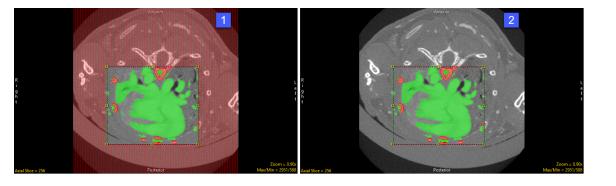
- Segment Inside the Specified Subregion: Allows users to segment within the specified subregion.
- Segment Outside the Specified Subregion: Allows users to segment outside the specified subregion.

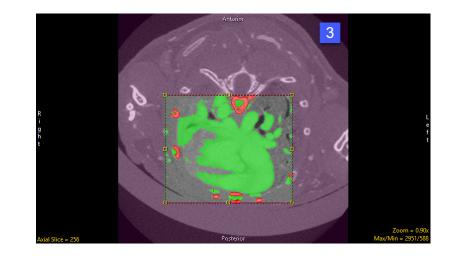




Subregion Options (continued)

- X Slider: Allows users to define the extent of the subregion in the X orientation.
- Y Slider: Allows users to define the extent of the subregion in the Y orientation.
- Z Slider: Allows users to define the extent of the subregion in the Z orientation.
- Shade Restricted Area: Allows users to switch on shading [1] for the restricted area or switch off shading [2] for the restricted area.
- Shade Color: Allows users to change the color of the restricted area [3] by typing a color in the color field area or by selecting a color using the color section option.
- Segment Outside the Specified Subregion: Allows users to segment outside the specified subregion.
- Shade Color: Allows users to change the color of the restricted area [3] by typing a color in the color field area or by selecting a color using the color section option.



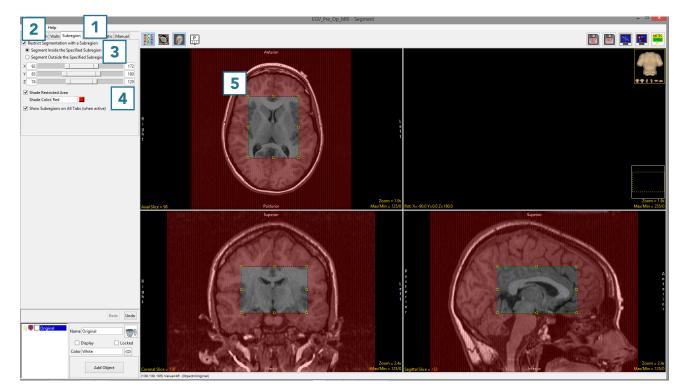


Setting a Subregion

Here we will set a Subregion to protect and limit the region when segmenting with other tools.

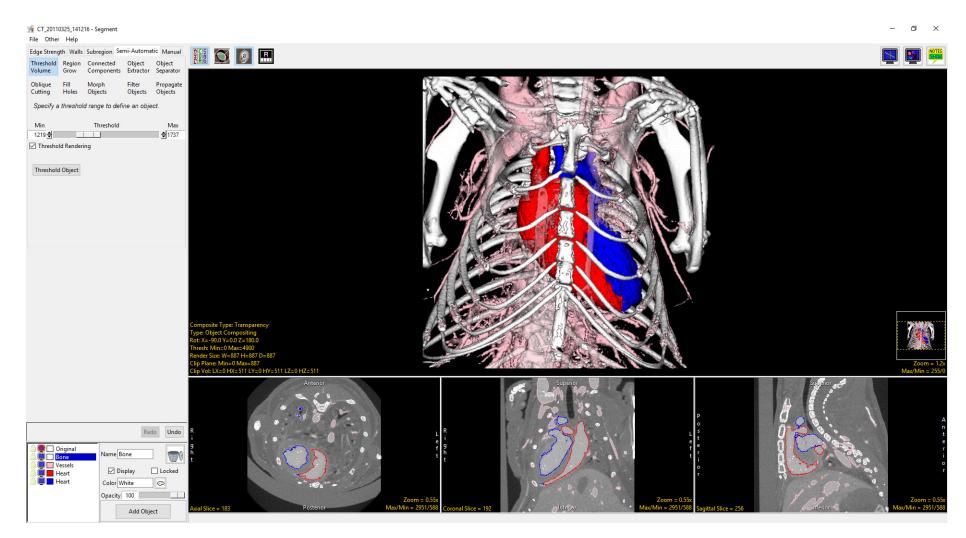
To follow along, download the data set EGV_MRI from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the 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.



Semi-Automatic Tools

The Semi-Automatic tab provides access to many useful tools for interactive, efficient segmentation of objects. These tools include simple 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.



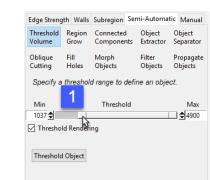
Threshold Volume

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.



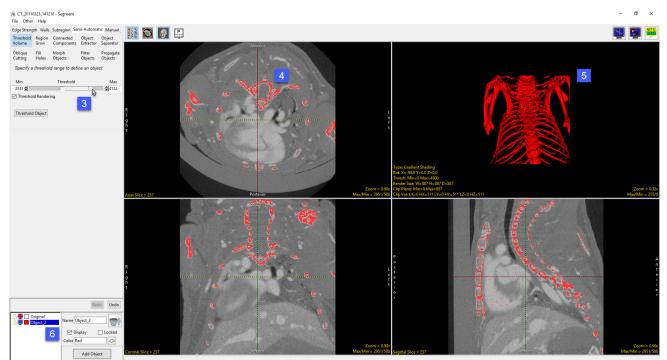
Threshold Volume Options

Threshold Slider: The Threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slider. Selecting the minimum end of the slider [1] and moving it to the right will increase the minimum threshold value, moving it to the left will decrease the minimum value. Selecting the maximum side of the slider [2] and moving it to the left will decrease the maximum threshold value, moving the slider to the right will increase the maximum value. Voxel with values outside the range are ignored and not include as part of the current object.



| Edge Strengt | th Walls | Subregion | Ser | ni-Automat | ic Manual |
|---------------------|----------------|-----------------------|---------------|---------------------|----------------------|
| Threshold Volume | Region Grow | Connected Componer | | Object Extractor | Object Separator |
| Oblique Cutting | Fill Holes | Morph Objects | | Filter Objects | Propagate Objects |
| Specify a | threshole | d range to d | defii | ne an obje | ct. |
| | | | | | |
| Min | | Thresho | ld | | Max |
| Min 1037 🔷 | | Thresho | ld | | Max |
| 1037 🚖 | d Renderi | -14 | ld | | |
| | d Renderi | -14 | 1d 2 | | |
| 1037 🚖 | | -14 | ^{Id} | | |

When adjusting the minimum or maximum threshold range [3] an interactive preview showing the range of selected voxels will be displayed overlaid on the grayscale data [4], a 3D display of the voxels will also be displayed in the render window. [5] The color of the previewed voxels will match the color of the object you currently have selected. [6]



Holding the Alt key while dragging either the minimum or maximum end of the slider allows for smaller adjustment of the value allowing users to fine tune selections. Clicking in the trough to either side of the minimum or maximum end of the slider [7] will advance the value by 1. Shift-click will decrease the value by 1.

Min and **Max:** The minimum and maximum input field allows users to manually enter the minimum or maximum threshold value. There are also arrow up and down buttons the right of the input field to increase or decrease the currently value by 1.

Threshold Rendering: This option allows users to disable and enable to 3D preview of the selected voxel range. It is recommended to disable this option by unchecking the checkbox when working with large data sets.

Threshold Object: Assigns the voxels in the selected range to the current object.

Right click options: Right clicking on the Threshold slider provides users with access to the following options:

Presets: The Presets option allows users to define threshold values for specific structures or objects of interest. This is particularly useful for those users who routinely segment the same structures from their image data.

| Threshold Volume | Region Grow | Connected Components | Object Extractor | Object Separator | | | | | |
|---------------------|--|-------------------------|---------------------|----------------------|--|--|--|--|--|
| Oblique Cutting | Fill Holes | Morph Objects | Filter Objects | Propagate Objects | | | | | |
| Specify a | threshol | d range to defii | ne an obje | ct. | | | | | |
| Min | | Threshold | | Max | | | | | |
| _ | 1037 € ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ | | | | | | | | |
| Threshold | l Object | | | | | | | | |
| | | | | | | | | | |

Edge Strength Walls Subregion Semi-Automatic Manual

| Name | Min | Max | Depend | Туре | Dependancies | Action | Order |
|--------------|------|-------|--------|------|--------------|--------|----------------|
| Dentin | 750 | 1649 | Any | ~ | | Delete | |
| Enamel | 1650 | 3000 | Any | ~ | | Delete | |
| Alveolar Bon | 1000 | 10000 | Any | ~ | | Delete | \land \lor |
| | | | Any | ~ | | Add | |

Right click options (continued)

Presets (continued): When the Edit Presets Thresholds window opens, the following options are available:

- Name: Allows users to enter the name for preset
- Min: Enter the minimum threshold value for the preset
- Max: Enter the maximum threshold value for the preset
- Depend Type: Allows users to set dependencies for presets. This option allows users to set multiple presets but only the presets that meet the dependencies requirements are displayed for the current data. In the example screenshot two sets of segmentation presets

| Name | Min | Max | Depend Type | | Dependancies | Action | Order |
|------------|------|-------|-------------------|---|-----------------|--------|----------------|
| Dentin | 750 | 1649 | Any | ~ | | Delete | |
| Enamel | 1650 | 3000 | Any | ~ | | Delete | \land |
| Bone | 1000 | 10000 | Any | ~ | | Delete | \land |
| Ortho_ST | 85 | 1000 | Volume Dimensions | ~ | 450 x 450 x 224 | Delete | \land |
| Ortho_Musc | 95 | 230 | Volume Dimensions | ~ | 450 x 450 x 224 | Delete | \land |
| Ortho_Bone | -43 | 96 | Volume Dimensions | ~ | 450 x 450 x 224 | Delete | \land \lor |
| | | | Any | ~ | | Add | |

have been defined. The first three presets are for a dental segmentation application. The second three presets are for a muscle segmentation application. As the first three presets Depend Type is set to Any, these presets will be available for any data set loaded into the Segment module. However, the latter three presets have a Depend Type set to Volume Dimension and the Dependency set to a volume size of 450 by 450 by 224, these presets will only be available for data sets loaded into Segment of this size. The following Depend Types are available:

Module: Defaults can be set for specific modules, for example presets to segment image data can be set to only appear when the data is opened with Segment, presets for rendering set to appear only when data is opened with Display.

Volume Name: The preset will only display if the volume name meets dependency criteria.

Volume Data Type: The preset will only display if the volume data type meets the dependency criteria.

Volume Dimensions: The preset will only display if the volume data type meets the dependency criteria.

Any: Default option. The preset will be displayed.

Right click options (continued) Presets (continued):

- Dependencies: Allows users to specify the dependency criteria for the selected Depend Type.
- Action: Allows users to Add or Remove presets.
- Order: Allows users to change the order in which the presets are listed. As a general rule of thumb presets should be listed in the order they are used for segmentation.

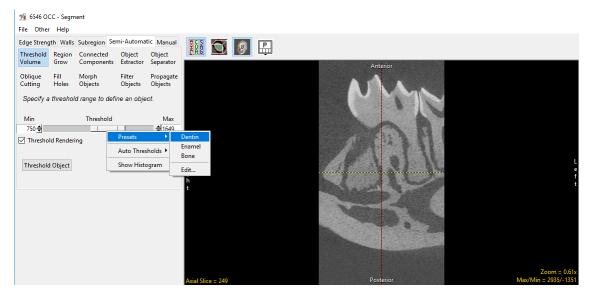
To define a set of presets do the following:

Right-click on the Threshold slider and choose Presets.

In the Presets window set the preset name, next enter the min and max threshold values, finally set a Depend Type and Dependency if desired. Click Add and either enter the next Preset or choose Save.

Once Presets are established, they can be accessed by simply right-clicking on the Threshold slider and choosing Presets and then the Preset name.

| | Ortho_ST | 85 | 1000 | Volume Dimensions | \sim | 450 x |
|-----------------|------------|-----|------|-------------------|--------|-------|
| | | | | | | |
| | Ortho_Musc | 95 | 230 | Volume Dimensions | \sim | 450 x |
| | | | | | | |
| | Ortho_Bone | -43 | 96 | Volume Dimensions | \sim | 450 x |
| re listed. As a | | | | | | |
| | | | | Any | \sim | |
| y are used for | | | | | | |
| | Save | | | | | |
| | | | | | | |
| | | | | | | |
| | | | | | | |
| | | | | | | |
| | | | | | | |
| | | | | | | |
| | | | | | | |
| | | | | | | |



| Edit Preset T | hesholds | | | | | | × |
|---------------|----------|-------|-------------------|---|-----------------|--------|---------------|
| Name | Min | Max | Depend Type | | Dependancies | Action | Order |
| Dentin | 750 | 1649 | Any | ~ | | Delete | |
| Enamel | 1650 | 3000 | Any | ~ | | Delete | \wedge |
| Bone | 1000 | 10000 | Any | ~ | | Delete | \wedge |
| Ortho_ST | 85 | 1000 | Volume Dimensions | × | 450 x 450 x 224 | Delete | \wedge |
| Ortho_Musc | 95 | 230 | Volume Dimensions | ~ | 450 x 450 x 224 | Delete | $\wedge \lor$ |
| Ortho_Bone | -43 | 96 | Volume Dimensions | ~ | 450 x 450 x 224 | Delete | |
| | | | Any | ~ | | Add | |
| Save | | | | | | | |

© AnalyzeDirect, Inc.

Right click options (continued)

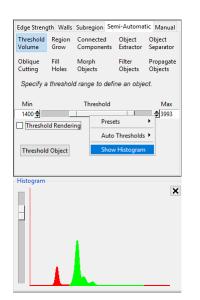
Auto Thresholds: The auto thresholds option allows users to compute up to 6 automatically computed threshold to specify the number of automatic thresholds computed. Selecting a threshold value will set the minimum threshold to that value.

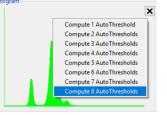
Show/Hide Histogram: When selected, calculates and displays the volume histogram below the Threshold Volume options.

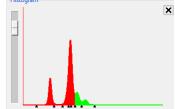
When the threshold minimum and maximum values are adjusted the voxels within the selected range display as green on the histogram while the voxels out of range are displayed in red. Adjusting the scale bar to the left side of the histogram display will increase or decrease the scale the histogram.

Right clicking on the histogram allows users to auto compute up to 8 threshold values for the image data. The thresholds are displayed as triangular buttons at the bottom of the histogram display, selecting a triangle will set the minimum threshold value.

9 CT_20110325_141216 - Segment File Other Help Edge Strength Walls Subregion Semi-Automatic Manual 🕤 👔 🖻 Region Connected Object Object Components Extractor Separator Oblique Filter Morph Propagate Cutting Holes Objects Objects Objects Specify a threshold range to define an object. Min Threshold Max 0 🔷 _] \$4900 Presets Threshold Rendering Compute One Compute Two Show Histogram **Threshold Object** Compute Three Compute Four 479 Compute Six 🕨 1263 1632 2148





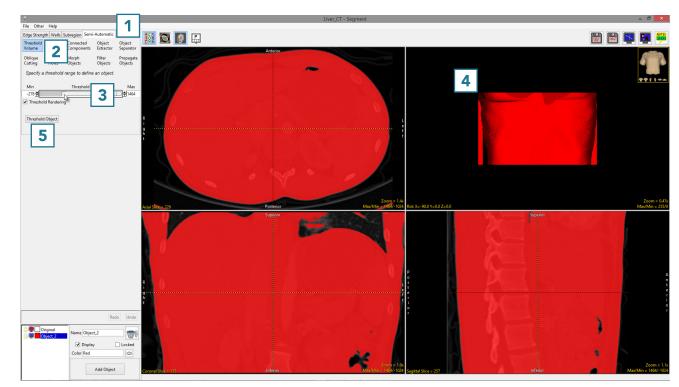


Threshold Volume Segmentation

Here we will use Threshold Volume to create a new object in a dataset.

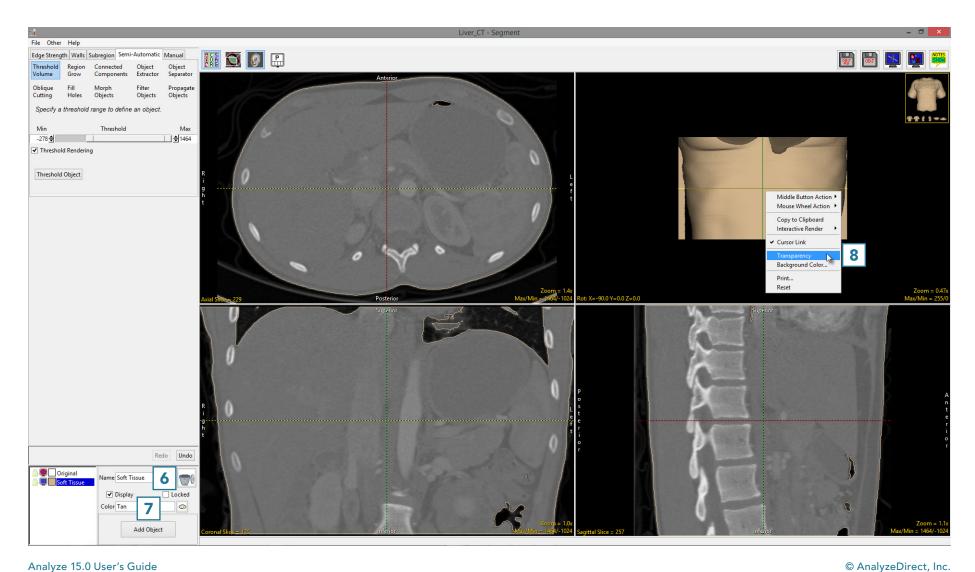
To follow along, download the data set CT_Liver from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the 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.



Threshold Volume Segmentation (continued)

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



Threshold Volume Segmentation (continued)

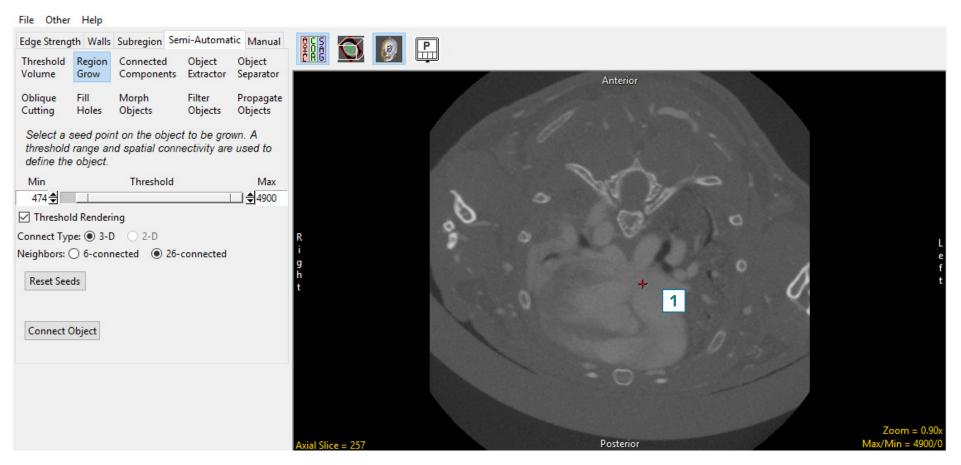
- Add a new object [9].
- Update the name [10] and color [11].
- Adjust the threshold range [12] so that the bone is displayed in the binary preview, then click Threshold Object [13].
- Note that the rendering [14] will update to display both objects. The bone is now fixed to visible, as the rendering 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.

To enable the Region Grow options, first a seed point must be set on the structure you wish to isolate [1]. Note, multiple seeds can be selected to facilitate the simultaneous segmentation of multiple objects as long as the objects have the same threshold properties, for example multiple disconnected bones.



Region Grow Options

When the seed is set the following options become available:

Threshold slider: The Threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slider. For a full description of the threshold slider please refer to the Threshold Volume section.

Min and **Max:** The minimum and maximum input field allows users to manually enter the minimum or maximum threshold value. There are also arrow up and down buttons the right of the input fields to increase or decrease the currently value by 1.

Threshold Rendering: Allows users to disable and enable to 3D preview of the selected voxel range. Disable this option by unchecking the checkbox when working with large data sets.

Connect Type: Determines if the connection type will be 3D or 2D.

3-D: Region grow will be applied to the (3D) volume.

2-D: Region grow will be limited to the current (2D) slice.

Neighbors: Allows users to select the number of neighboring voxels during the connection process. The options available depend on the connect type. For 3D, users can choose 6-connected or 26-connected. For 2D, 4-connected or 8-connected can be selected.

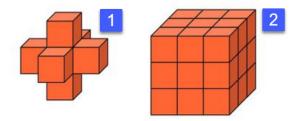
• 3D Neighbor options:

6-connected: Specifies that only 3-D neighbors are checked for connectivity during the region growing process. [1]

26-connected: Specifies that the entire 26-voxel neighborhood is checked for connectivity during the region growing process. [2]

File Other Help

| Edge Strengt | h Walls | Subregion | Semi- | Automati | c Manual | | |
|--|----------------|-----------------------|--------|----------|----------------------|--|--|
| Threshold Volume | Region Grow | Connected Componer | | - | Object Separator | | |
| Oblique Cutting | Fill Holes | Morph Objects | | | Propagate Objects | | |
| Select a seed point on the object to be grown. A threshold range and spatial connectivity are used to define the object. | | | | | | | |
| Min | | Thresho | ld | | Max | | |
| 474 🚔 | | | | | _ \$ 4900 | | |
| ✓ Threshold | d Renderi | ing | | | | | |
| Connect Typ | e: 🖲 3-D |) 🔿 2-D | | | | | |
| Neighbors: (| 6-conr | nected 💿 | 26-cor | nected | | | |
| Reset Seeds | | | | | | | |
| Connect O | bject | | | | | | |



Region Grow Options (continued)

• 2D Neighbor options:

4-connected: Specifies that only 2-D neighbors are checked for connectivity during the region growing process. [3]

8-connected: Specifies that the entire 8-voxel neighborhood is checked for connectivity during the region growing process. [4]

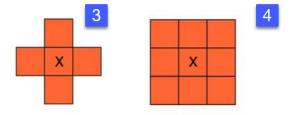
Reset Seeds: Resets the user defined seed(s). Seeds can also be deleted by right clicking on the seed and then selecting delete.

Connect Object: Initiates the connection process.

Threshold Slider right click options: Right clicking on the Threshold slider provides users with access to the following additional options; Presets, Auto Threshold, Show/Hide Histogram. For more information please refer to the Threshold Slider right click options in the Threshold Volume section.

Seed point right click options: Right clicking on a seed point provides the following options:

- **Style:** The style options allows users to change the of the seed point. Select from Dot, Crosshair (default), Arrow, and Diamond.
- Label: The label options allows user to enable and disable labels for seed points. Select from None (default), Number (useful when setting multiple seeds), and Tag.
- **Shadow:** Allows users to enable (default) or disable the shadow effect for the seed.
- **Delete:** Deletes selected seed point.



File Other Help

| Edge Strengt | th Walls | Subregion Ser | ni-Automat | ic Manual | | | |
|--|-------------------|-------------------------|---------------------|----------------------|--|--|--|
| Threshold Volume | Region Grow | Connected Components | Object Extractor | - | | | |
| Oblique Cutting | Fill Holes | Morph Objects | Filter Objects | Propagate Objects | | | |
| Select a seed point on the object to be grown. A threshold range and spatial connectivity are used to define the object. | | | | | | | |
| Min | Min Threshold Max | | | | | | |
| 474 🚔 | | | | _ €4900 | | | |
| Threshol | d Renderi | ng | | | | | |
| Connect Typ | e: 🖲 3-D |) 🔿 2-D | | | | | |
| Neighbors: (| 6-conn | ected 💿 26- | connected | | | | |
| Reset Seeds | | | | | | | |
| Connect C |)bject | | | | | | |

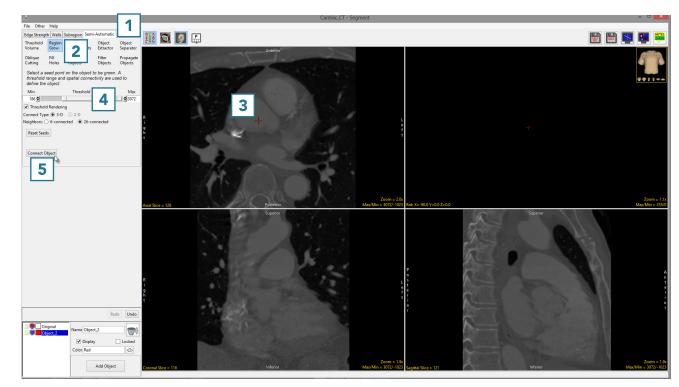
3D Segmentation with Region Grow

Here we will use Region Grow to segment a new object in a dataset.

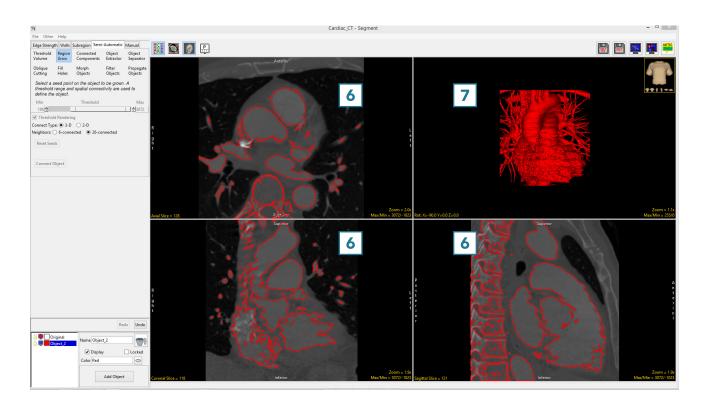
To follow along, download the data set CT_Heart from

analyzedirect.com/data and load into Analyze using Input/Output.

- Select the 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].



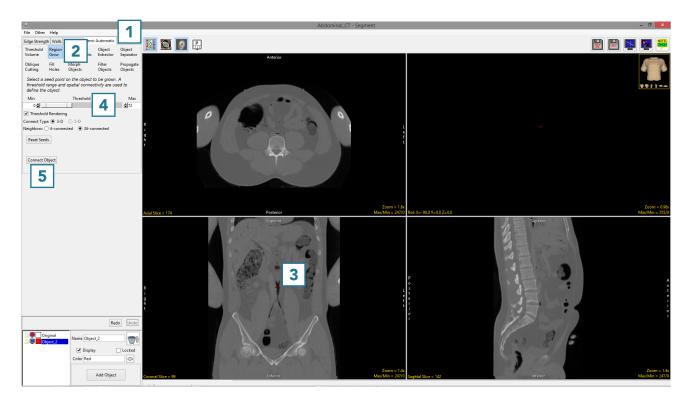
- The voxels fulfilling the seed point and threshold criteria for the region grow will be assigned to a new object.
- The segmented object is shown overlaid on the 2D slice data [6] and a 3D rendering [7] is displayed.



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.

To follow along, download the data set VH_Abdomen from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the 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].



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.



111 🖸 🚺 🗜

🔛 🔤 👱

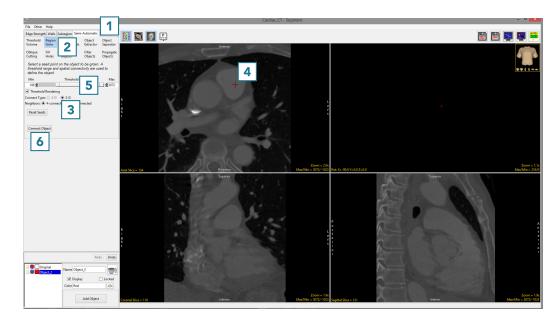
2D Segmentation with Region Grow

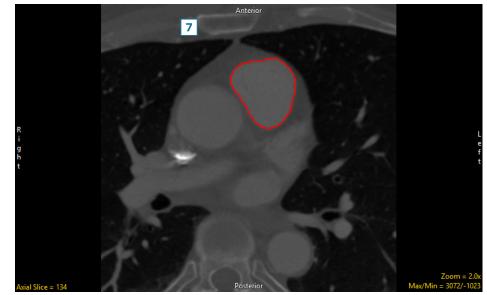
Region grow also provides the ability to limit the region to a single slice via the 2D Connect Type option.

To follow along, download the data set CT_Heart from analyzedirect.com/data and load into Analyze using Input/Output.

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

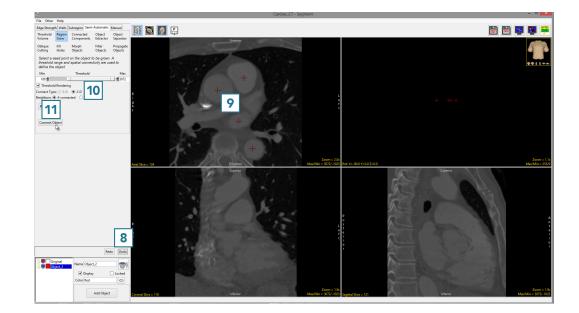
Analyze 15.0 User's Guide



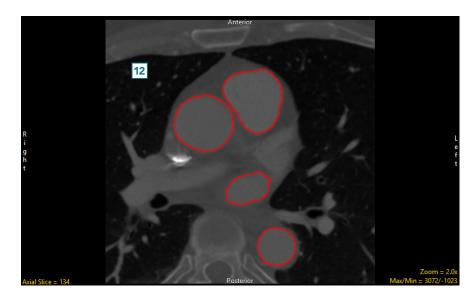


© AnalyzeDirect, Inc.

- 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].

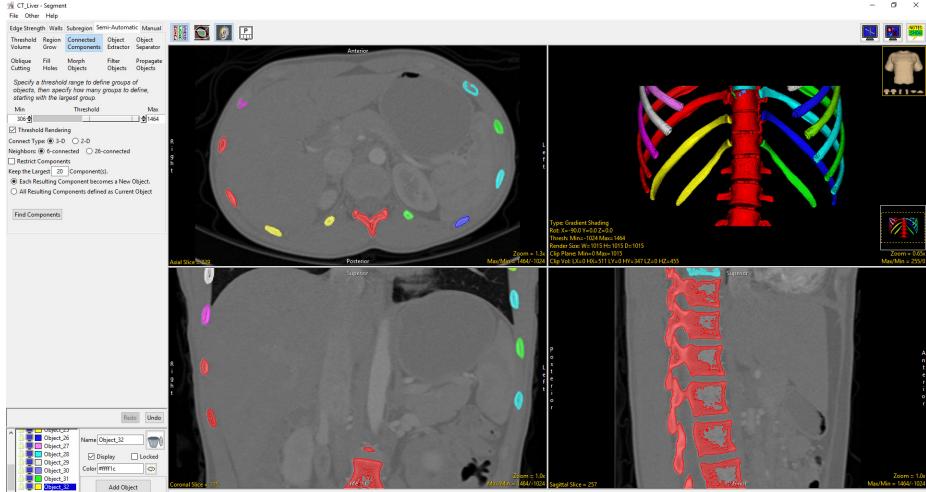


• All of the regions falling within the threshold criteria will be isolated in 2D [12].



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.



Display Mode = Traces & Colored Regions

Connected Components Options

The following Connected Components options are available:

Threshold slider: The Threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slider. For a full description of the threshold slider please refer to the Threshold Volume section.

Min and **Max:** The minimum and maximum input field allows users to manually enter the minimum or maximum threshold value. There are also arrow up and down buttons the right of the input fields to increase or decrease the currently value by 1.

Threshold Rendering: Allows users to disable and enable to 3D preview of the selected voxel range. Disable this option by unchecking the checkbox when working with large data sets.

Connect Type: Determines if the connection type will be 3D or 2D.

3-D: Region grow will be applied to the (3D) volume.

2-D: Region grow will be limited to the current (2D) slice.

Neighbors: Allows users to select the number of neighboring voxels during the connection process. The options available depend on the connect type. For 3D, users can choose 6-connected or 26-connected. For 2D, 4-connected or 8-connected can be selected. For a full description of the neighbor options refer to the Region Grow section.

| File | Other | Help |
|------|-------|-------|
| 1110 | oulei | ricip |

| Edge Streng | th Walls | Subregion | Se | mi-Automat | ic | Manual |
|---------------------|----------------|-----------------------|------|---------------------|----|--------------------|
| Threshold Volume | Region Grow | Connected Componer | | Object Extractor | | bject eparator |
| Oblique Cutting | Fill Holes | Morph Objects | | Filter Objects | | ropagate bjects |
| Specify a | threshold | d range to (| lefi | ine aroups i | of | |

Specify a threshold range to define groups of objects, then specify how many groups to define, starting with the largest group.

| Min | Threshold | Max |
|---------------------|-----------------------|---------------|
| 306 븆 | | 1464 |
| ✓ Threshold Renderi | ng | |
| Connect Type: 🔘 3-D | 0 🔿 2-D | |
| Neighbors: 🖲 6-conr | ected 🔘 26-conne | cted |
| Restrict Componer | nts | |
| Keep the Largest 20 | Component(s). | |
| Each Resulting Co | mponent becomes a l | New Object. |
| O All Resulting Com | ponents defined as Cu | urrent Object |
| | | |

Find Components

Connected Components Options (continued)

Restrict Components: When enabled displays a set of criteria that can be used to restrict the object segmentation resulting from the connected component analysis. Components with less than or more that the values entered in the x and y parameters will be ignored in the connected components analysis. These options specify that All Components must have:

- At least 'x' voxel(s), but no more than 'y' Voxels(s): Segmented components must have at least the minimum number of voxels in its structure as specified by 'x' and no more than the maximum number of voxels in its structure as specified by 'y'.
- Restrict Components

 All Components must have:

 At least
 1

 Voxel(s), but no more than
 13421772

 Voxel(s), but no more than
 512

 A Width of
 1

 Voxel(s), but no more than
 512

 Voxel(s), but
- A Width of 'x' voxel(s), but no more than 'y' Voxels(s): Segmented components must have a width of at least the minimum number of voxels as specified by 'x' and no more than the number of voxels as specified by 'y'.
- At Height of 'x' voxel(s), but no more than 'y' Voxels(s): Segmented components must have a height of at least the minimum number of voxels as specified by 'x' and no more than the number of voxels as specified by 'y'.
- At Depth of 'x' voxel(s), but no more than 'y' Voxels(s): Segmented components must have a depth of at least the minimum number of voxels as specified by 'x' and no more than the number of voxels as specified by 'y'.

Keep Largest X Component(s): Allows users to set the maximum number of objects to be kept in the connected component process.

Each Resulting Component becomes a New Object: When selected determines that each segmented component is assigned to its own object in the object map.

Each Resulting Component defined as Current Object: When selected determines that each segmented component is assigned to the current object selected in the object map.

Find Components: Initiates the connected components segmentation.

Analyze 15.0 User's Guide

Segmenting Multiple Objects Using Connected Components

Here we will use Connected Components to segment several objects in a dataset.

To follow along, download the data set CT_Liver from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the data set and open Segment.
- In the Object Control window click Add Object, name the object Bone and then make sure the object is selected [1].
- Select Semi-Automatic [2] and choose Connected Components [3].
- Set the threshold range [4] to isolate the spine and ribs. A minimum threshold value of 295 and a maximum of 1464 works well for this dataset.
- Set the number of components to keep to 14 [5]
- This time select the Each Resulting Component defined as Current Object option [6]. Now all 14 isolated components will be set to a single object.
- Click Find Components [7].
- The data will be thresholded and the largest groups of voxels specified will be identified and rendered as a single object [8].



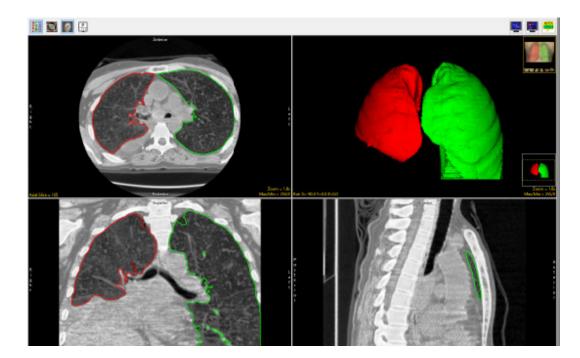
Object Extractor

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.



Object Extractor Options

As with the Region Grow tool, a seed point must be set on the structure you wish to segment [1] before the Object Extractor options are enabled. Note, multiple seeds can be selected for the simultaneous segmentation of multiple structures with the same threshold parameters, for example the segmentation of both the left and right lungs. When the seed is set the following options become available:

Threshold slider: The Threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and <complex-block>A here: spreight die here:

maximum ends of the threshold slider. For a full description of the threshold slider including right click options, please refer to the Threshold Volume section.

Min and **Max:** The minimum and maximum input field allows users to manually enter the minimum or maximum threshold value. There are also arrow up and down buttons the right of the input fields to increase or decrease the currently value by 1.

Threshold Rendering: This option allows users to disable and enable to 3D preview of the selected voxel range. It is recommended to disable this option by unchecking the checkbox when working with large data sets.

Object Extractor Options (continued)

Show Thresholding: When the minimum and maximum threshold values are selected the adjustment is previewed on the 2D slice data. By default, the Show Thresholding option is set to Max Adjust. Adjusting the minimum threshold value will display as a update of the outer boundaries of the object only {x} while adjusting the maximum will display as a filled preview. To enable the filled preview the following options are available.

Max Adjust: Only adjusting the maximum threshold level will preview with the filled region.

Min Adjust: Selecting Min Adjust will reverse the default preview display so that adjusting the minimum threshold value will show a filled region while adjusting the maximum threshold values will display the outer boundaries of the object only.

Any Adjust: Will set the filled preview display when adjusting either the minimum or maximum threshold value.

Never: Disables the filled preview display. Both minimum and maximum threshold adjustment will display the outer boundaries of the object only.

Select Seed: Switches to seed selection mode.

Draw Limit: Switches to limit definition mode. Allowing users to define limits on the image data to prevent the defined region from leaking into surrounding structures.

Reset Seeds: Resets the user defined seed(s). Note, you can delete a seed point by right-click on the seed and choosing Delete. Seeds can also by moved by left-clicking on the seed and then dragging to a new location.

Reset Limit: Resets all user defined limits.

Analyze 15.0 User's Guide

Extract Object: Initiates the Object Extraction segmentation process.

| Attraction of the second secon | 1991 1991 | Antoir | Leeft |
|--|--------------|--------|--------------|
| | Zoom = 0.90x | | Zoom = 0.90x |

| Edge Streng | th Walls | Subregion Ser | mi-Automa | tic Manual | | |
|--|----------------|--|-------------------|----------------------|--|--|
| Threshold Volume | Region Grow | Connected Object Components Extractor | | Object Separator | | |
| Oblique Cutting | Fill Holes | Morph Objects | Filter Objects | Propagate Objects | | |
| Select a seed point near the 3-D center of the object to be extracted. Adjust the threshold range to specify the object. Limits are allowed, but discouraged. | | | | | | |
| Min | | Threshold | | Max | | |
| 86 🚔 | | | | \$235 | | |
| Threshol | ld Renderi | ng | | | | |
| Show Thre | sholding | Max Adjust 🗸 | | | | |
| | Selection | tt Seed 🔿 🖸 |)raw Limit | | | |
| Reset See | ds Re | set Limits | | | | |
| Extract Ob | oject | | | | | |

File Other Help

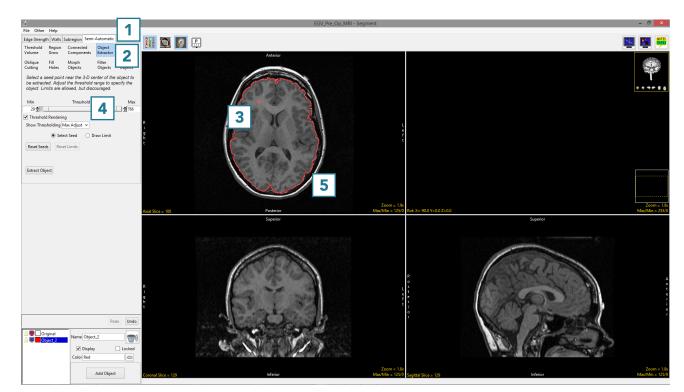
Segmentation of a Single Object Using Object Extractor

Here we will use Object Extrator to segment a single object in a dataset.

To follow along, download the data set EGV_MRI from

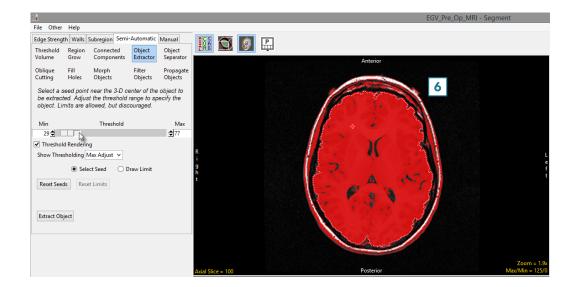
analyzedirect.com/data and load into Analyze using Input/Output.

- Select the 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].

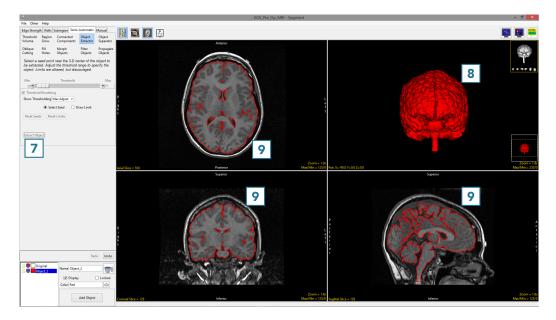


Segmentation of a Single Object Using Object Extractor (continued)

- 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.

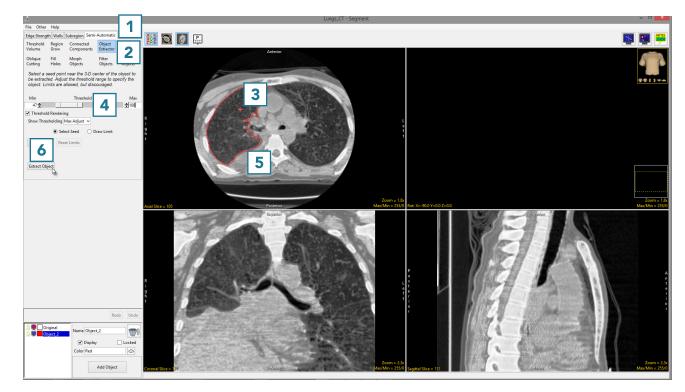


Segmentation of Multiple Objects Using Object Extractor

Here we will use Object Extrator to segment multiple objects in a dataset.

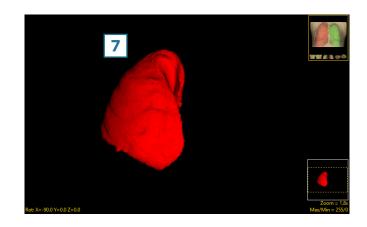
To follow along, download the data set CT_Lungs from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the 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]

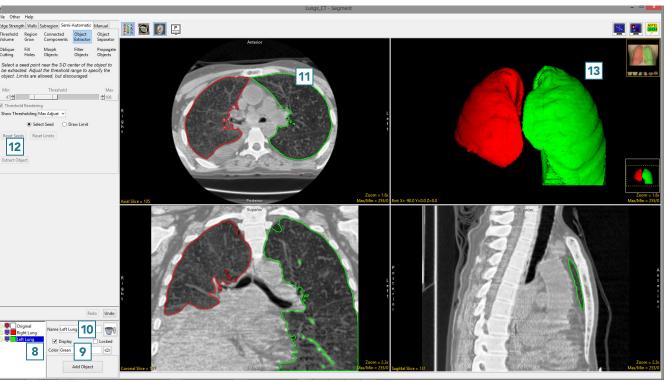


Segmentation of Multiple Objects Using Object Extractor (continued)

• Once the segmentation process is complete, the object will be rendered [7].

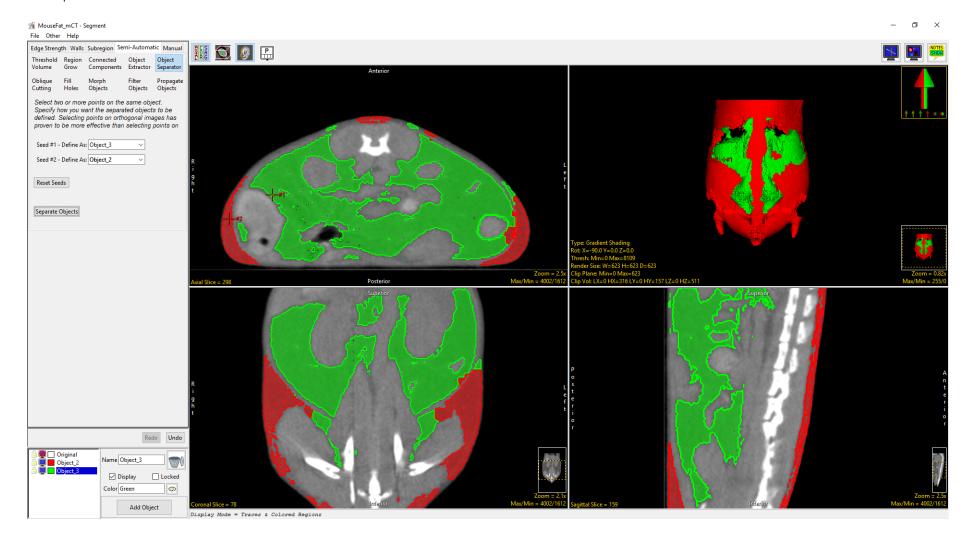


- Rename the object [8]. Add a new object [9] and rename [10].
- Set a seed point in the next object [11] and select Extract Object [12].
- Once the segmentation process is complete, the object will be rendered [13].
- Save your work by selecting File
 Save Object Map.



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. The purpose of the tool is to break objects into two or more objects. The tool requires a minimum of two seed points to be set.



```
357
```

Object Separator Options

The following Object Separator Options are available:

Seed #1 – Define As: This option is enabled when the first seed point location is set. By default this option is set to Current Object, that is the object currently selected in the object control window. Selecting the drop-down menu allows users to choose from; Current Object, Not Changed (the object that the seed voxel is already assigned to), New, and then any objects in the object list.

Seed #2 – Define As: This option is enabled when the second seed point location is set. By default this option is set to Not Changes, that is the object the seed point voxel is currently assigned to. Selecting the drop-down menu allows users to choose from; Current Object, Not Changed, New, and then any objects in the object list.

Reset Seeds: Deletes all defined seed points.

Separate Objects: Begins the Object Separator process.

Seed point right click options: Right clicking on a seed point provides the following options:

Style: The style options allows users to change the of the seed point. Select from Dot, Crosshair (default), Arrow, and Diamond.

- Label: The label options allows user to enable and disable labels for seed points. Select from None (default), Number (extremely useful when setting multiple seeds), and Tag.
- Shadow: Allows users to enable (default) or disable the shadow effect for the seed.

Delete: Deletes selected seed point.

| | Edge Strengt | th Walls | Subregion | Semi-Autom | atic Manual |
|--------|---|----------------|-----------------------|-------------------|----------------------|
| is | Threshold Volume | Region Grow | Connected Componer | | Object Separator |
| | Oblique Cutting | Fill Holes | Morph Objects | Filter Objects | Propagate Objects |
| ject | Select two or more points on the same object. Specify how you want the separated objects to be defined. Selecting points on orthogonal images has proven to be more effective than selecting points on | | | | |
| t this | Seed #1 - | Define As | Object_3 | ~ | |
| ing | Seed #2 - | Define As | Object_2 | ~ | |

File Other Help

| arate | Objects |
|-------|---------|
| | |

Reset Seeds

Sep

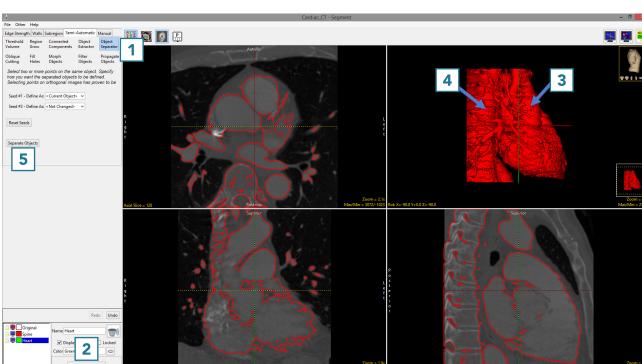
358

Separating Objects

Here we will use Object Separator to disconnect objects in a dataset.

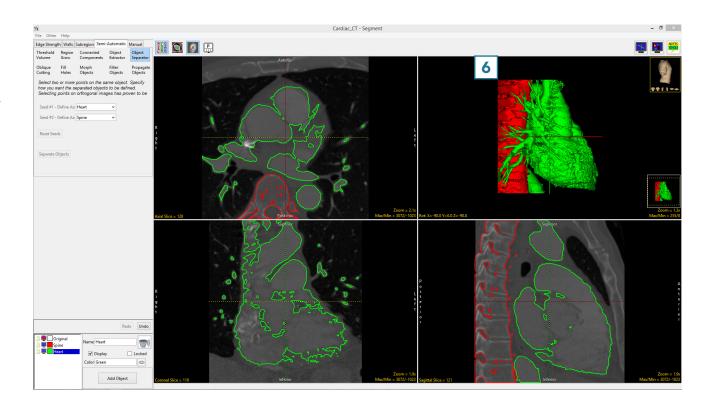
To follow along, download the data set CT Heart from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the 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.
- Reset Seed 5
- 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].



Separating Objects (continued)

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



Oblique Cutting

The Oblique Cutting tool enables the specification and display of an oblique cut plane in the volume image. The selected object can be split at the cut plane, with the smaller region after the split assigned to a different object as specified in the object control window. This tool is particular useful for splitting and reassigning vessels to new objects.

When the Oblique Cutting tool is selected the user must click on the image in the approximate location were the cut is to be placed, this can be done by clicking on the rendering or any of the orthogonal views. Once selected the Obliques window will open [1] and the oblique cut plane will be displayed on the rendering [2] and as a blue dashed line on the orthogonal displays. [3] The following Oblique Cutting options [4] will be made available:



Oblique Cutting Options

The following Oblique Cutting Options are available:

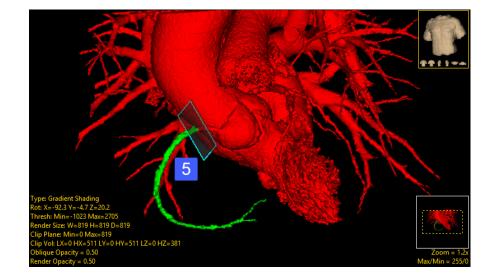
Cut: When the Cut option is clicked the selected object is split at the location of the oblique cut plane, the smaller object after the split is assigned to the object currently selected in the object window [5]. If the same object is selected a message will be returned stating 'Attempting to assign cut vein to itself'. [6] Click OK to dismiss the warning and then select or add a new object in the object control window.

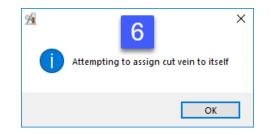
Cancel: Selecting cancels will cancel the Oblique Cut, the Oblique Cut options will no longer be available and then Oblique Cut Plane will be removed from the orthogonal slice displays.

Find Best: The Find Best option searches for the oblique image which contains the most circular representation of the selected object.

Recenter: Recenters the oblique plane. The center of the selected object on the oblique plane is computed. The oblique plane is then adjusted so that this computed center is displayed as the center in the oblique window.

Additional Options: The oblique cut plane can be adjusted by dragging an edge of the plane on the rendered image or by dragging the endpoints or center of the cut plane lines displayed on the orthogonal images.





Analyze 15.0 User's Guide

Oblique Cutting of Objects

Here we will use Oblique Cutting to specify and display an oblique cut plane in a dataset.

To follow along, download the data set Cardiac_CT from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the 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].



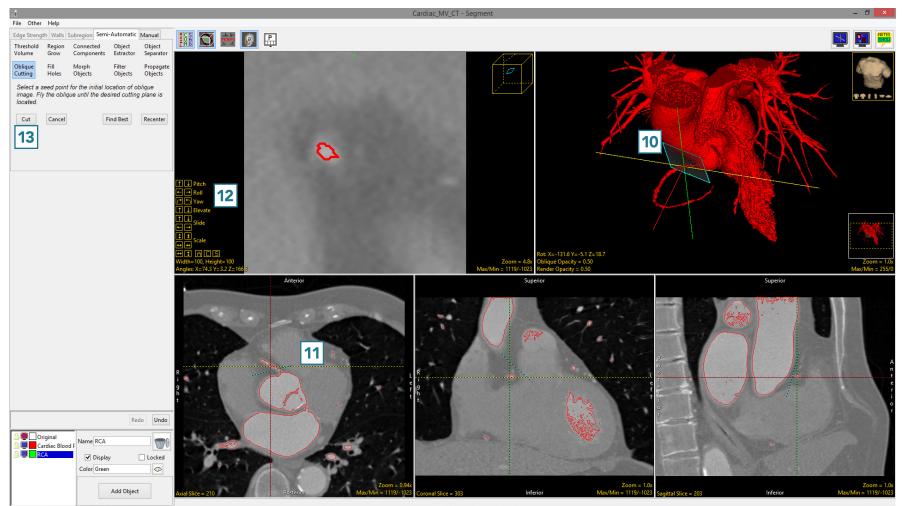
Oblique Cutting of Objects (continued)

- 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].



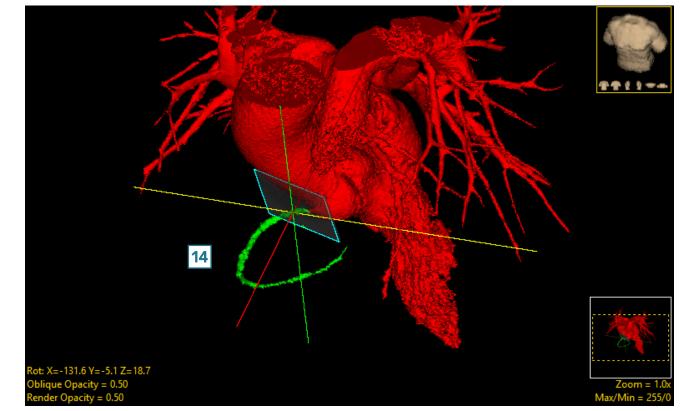
Oblique Cutting of Objects (continued)

- 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.



Oblique Cutting of Objects (continued)

- 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.



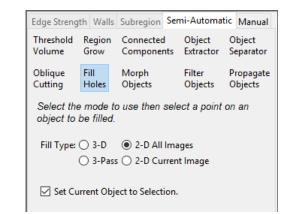
Fill Holes

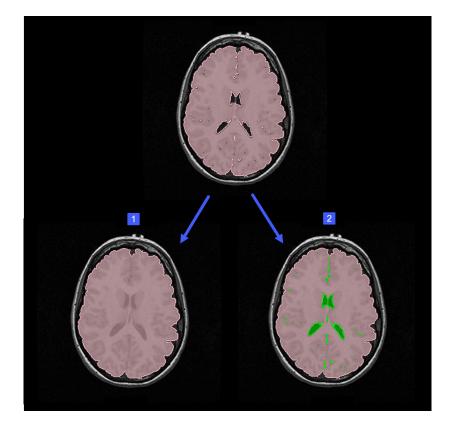
The Fill Holes function performs a flood-fill operation on the selected object. The operation reassigns voxels belonging to other objects to the selected object. The fill operation stops when it reaches the boundary of the object.

Fill Type: The fill type option allows users to select from the following fill type operations:

- 3-D: Fills three dimensional holes in the volume. This option is useful for filling small holes in the image data.
- 3-Pass: This option fills holes by process the volume, image by image in all three orthogonal directions.
- 2-D All Images: Conducts a 2D region fill on all 2D slices in the selected orientation.
- 2-D Current Image: Conducts a 2D region fill on the current 2D slice.

Set Current Object to Selection: Allows users to enable (default) or disable setting the filled region to the same object as being filled. Keep this option enabled if you wish to fill holes in an object and have them assigned to the same object [1], uncheck and disable this option if you wish to have the voxels that fill the holes in the object assigned to a different object, an object that is selected from the object list [2].





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.

To follow along, download the data set EGV_MRI from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the 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].

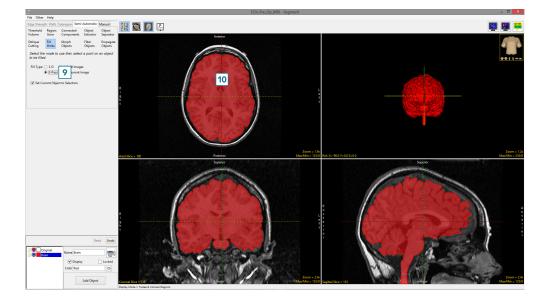


Filling Holes in Objects (continued)

- 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.

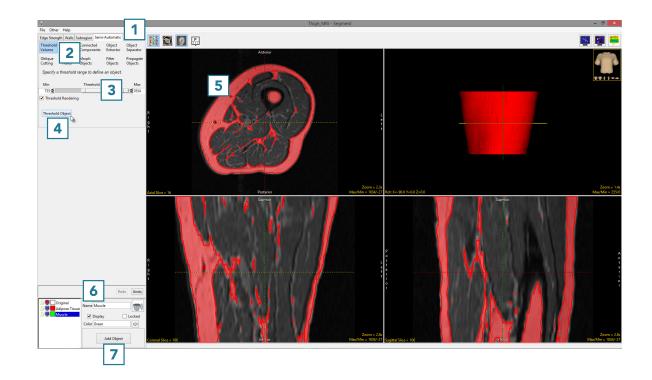


Using Fill Holes for Segmentation

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.

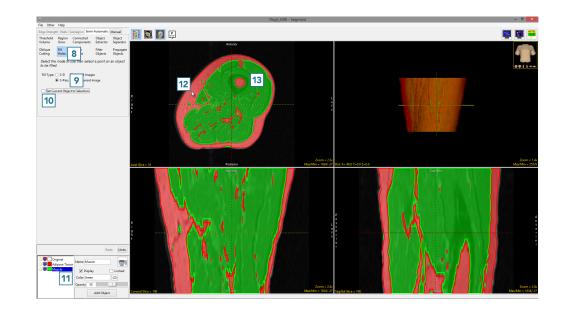
To follow along, download the data set Thigh_MRI from analyzedirect.com/data and load into Analyze using Input/Output.

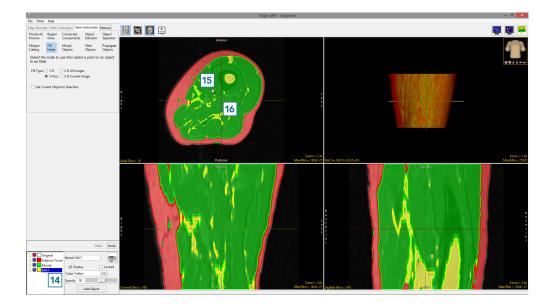
- Select the data set and open Segment.
- Select Semi-Automatic [1] and choose Threshold Volume [2].
- Set a threshold range [3] to globally segment the adipose tissue and click Threshold Object [4].
- The adipose tissue will be segmented [5].
- Rename the object [6], add a new object [7] and name it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



Using Fill Holes for Segmentation (continued)

- 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.



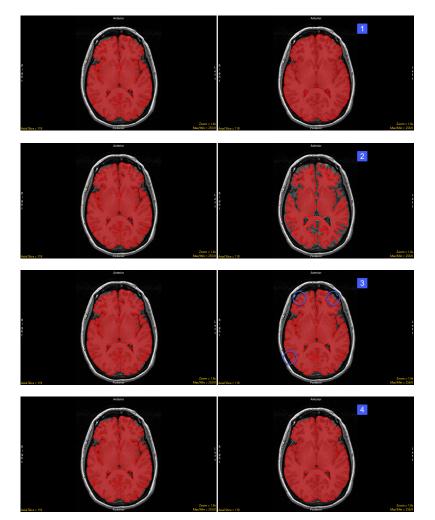


Morph Objects

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 <u>Morphology</u> tool in Process. The following Morph Objects options are available:

Operation: The operation drop-down menu allows users to select the morphological operation to perform. Choose from:

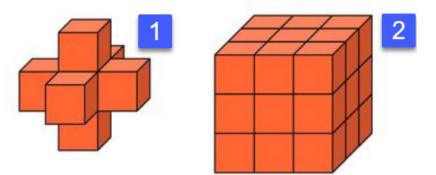
- Dilate: Adds a layer of voxels to an object, increasing the size of the object by increasing the objects boundaries while reducing the size of holes in the object [1].
- Erode: Removes a layer of voxels from an object, decreasing the size of the object by eroding the objects boundaries and increasing the size of holes in the object [2].
- Open: Performs an erode followed by a dilate [3]. In general, an open is less destructive than an erosion. The effect of the operation is to preserve voxels that have a similar shape to the structuring element, while removing other regions from the object. The effect on the image can be subtle as indicated in the image below.
- Close: Performs an dilate followed by a erode [4]. The close operation is similar to the dilate operation in that it tends to increase the object boundaries and shrink holes within the object. However, the close operation is less destructive of the original object boundary.



Morph Objects (continued)

Element Shape: Allows users to choose between a jack [1] or box [2] shaped element.

 Jack: A jack-shaped structuring element includes only the orthogonal elements to the center voxel of the structuring element. In a 3x3x3 jack-shaped structuring element, there are 7 voxels - one center voxel surrounded by the 6 orthogonal neighbors. The diagonal voxels are not part of this structuring element [1].



• Box: A rectilinear structuring element is a solid rectangle (or cube) of the given size in X, Y, and Z. For example, a 3x3x3 rectilinear structuring element is a 27-voxel cube - one center voxel surrounded by 26 orthogonal and diagonal voxels [2].

Element Size: The element size, sometimes referred to as kernel size, allows users to set the X, Y, and Z dimensions of the selected element shape that will be used in the chosen morphological operation.

- X: The X option allows users to specify the width of the structuring element. Select 1, 3, 5, 7, 9, or enter an odd numbered value into the text entry field.
- Y: The Y option allows users to specify the height of the structuring element. Select 1, 3, 5, 7, 9, or enter an odd numbered value into the text entry field.
- Z: The Z option allows users to specify the depth of the structuring element. Select 1, 3, 5, 7, 9, or enter an odd numbered value into the text entry field.

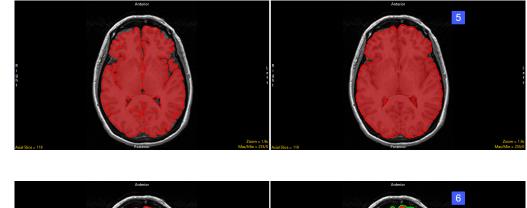
Note, to specify a 2D element set any of the dimensions to 1. A 3x3x3 jack-shaped structuring element will erode away or dilate (add) a single layer of voxels on the structure, a 5x5x5 structuring element will generally take away or add two voxels, etc.

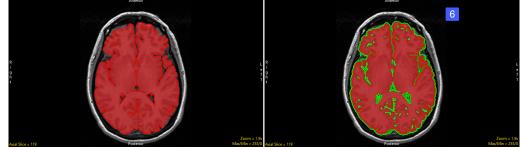
Morph Objects (continued)

Use Conditional Volume: The use conditional volume option is only available for the dilate operation. When selected the option allows a user to limit the dilation of the current object, conditioning the results with a volume selected from the workspace. The voxels that exist in the conditional volume define a 'mask' for voxels to be processed in the current volume. When selected the following options are available to choose the conditioning volume:

- Workspace: Allows the user to select the workspace that contains the conditional volume.
- Name: Allows user to select the volume to use as the conditional volume. Note volumes can be binary or grayscale.
- Drag and drop here: Allows users to select the conditional volume via drag-and-drop from the workspace.

Set Current Object to Selection: The Set Current Object to Selection option is only available for the dilate and close operations. The option allows users to enable (default) or disable setting the current object as the selected object for the output of the morphological operation, that is the voxels that will be added to the object once the dilate or close operation is complete. Keep this option enabled if you wish to assign the additional voxels to the same object [5], uncheck and disable this option if you wish to have assign the additional voxels to a different object, an object selected from the object list. [6]



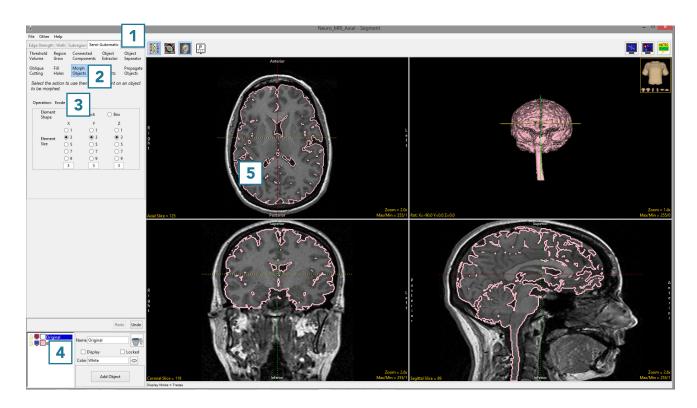


Using Morph Objects to Improve Segmentation

Here we will improve the segmentation of an object by applying rudimentary morphological operations to the object.

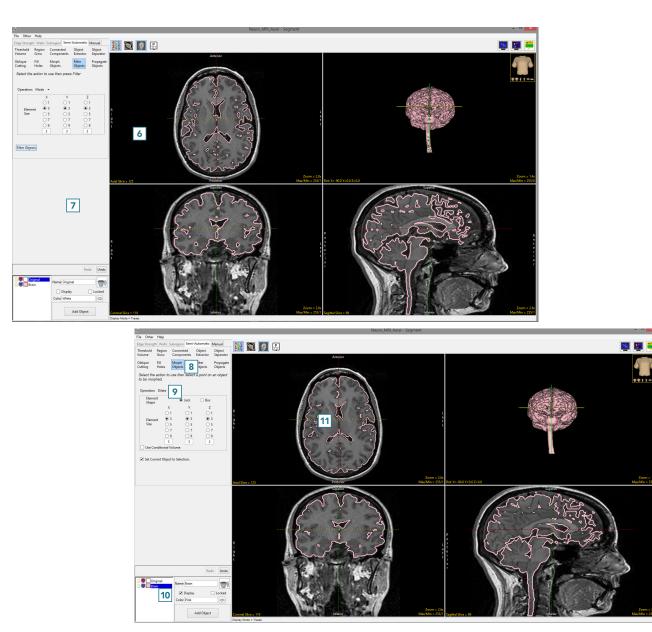
To follow along, download the data set MRI_3D_Head from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the 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.



Using Morph Objects to Improve Segmentation (continued)

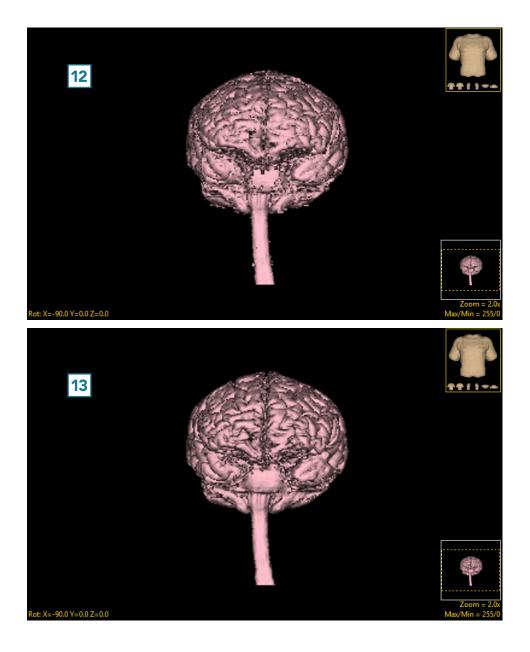
 Select Filter Objects [6] and apply a 3 X 3 X 3 Mode filter to the brain by clicking Filter Objects [7].



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

Using Morph Objects to Improve Segmentation (continued)

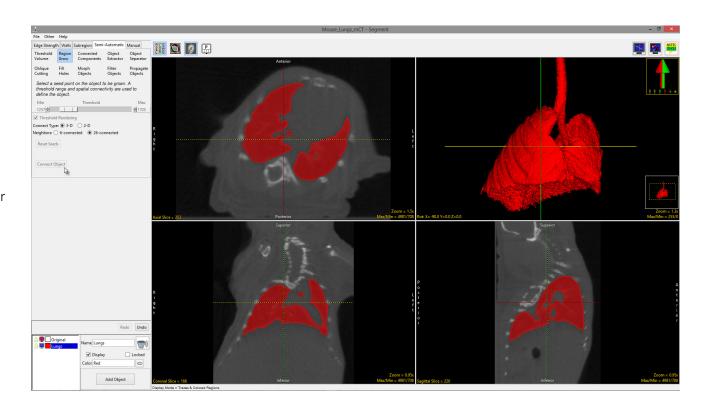
Note the difference between the pre [12] and post [13] processed brain objects.



Filter Objects

Filtering objects is a simple and intuitive way to reduce noise, fill small holes, and smooth object edges. Filtering objects reduces the amount of variation between the pixels (2D) or voxels (3D) that make up the object. The filtering process simply replaces each pixel or voxel with a function of itself and its neighbors, defined by the element size selected.

The filter is only applied to segmented objects and does not change the original data. If after attempting to segment a structure from a data set you decide that filtering the grayscale image data would improve the segmentation result refer to the Process module > Spatial Filters processing type to access all of the software's filtering options.



Filter Objects Options

Operation: Three filtering operations are available:

- Mode: The mode filter replaces the target voxel with the mode of the neighborhood of voxels specified by the element size. The value repeated most often is the mode.
- Median: Like the mode filter the median filter considers each voxel in the neighborhood specified by the element size to replace the target, however, instead of simply replacing the voxel with the mode of the neighboring voxel values, it replaces is with the median of those values. The median is calculated by first sorting all the voxel values into numerical order and then replacing the target voxel with the middle voxel value.
- Rank: Like the median filter the rank filter first sorts the values with in the neighborhood specified by the element size, numerically. However, the value used to replace the target voxel is dependent upon the rank value selected by the user using the Rank Slider.
 - Rank Slider: The slider allows users to specify of rank value used. The range of rank values is dependent on the neighborhood of voxels used for the filter, which is controlled by the element size. For example, in a 3x3x1 region the minimum rank value would be 1 while the maximum rank value would be 9. If the rank value was set to 6, the corresponding voxel value for that ranked voxel would by used to replace the target voxel.

Element Size: Allows users to set the X, Y, and Z dimensions of the rectilinear element to be used in the selected filtering operation.

- X: allows users to specify the width of the element. Select 1, 3, 5, 7, 9, or enter an odd numbered value into the text entry field.
- Y: allows users to specify the height of the element. Select 1, 3, 5, 7, 9, or enter an odd numbered value into the text entry field.
- Z: allows users to specify the depth of the element. Select 1, 3, 5, 7, 9, or enter an odd numbered value into the text entry field.

Filter Objects: Initiates object filtering. Note that object filtering does not honor object locking, and locked objects will be filtered. If any objects in the object list are locked a message will be returned stating that locked objects have been detected and object filtering does not honor locks. The option to cancel (No) or to continue (Yes) with the filtering operation will be given.

| Segme | ent | x | | | |
|-------|--|-----|--|--|--|
| ~ | Locked Objects have been detected and Object Filtering does not honor Locks. | | | | |
| 9 | Do you want to continue even though locked objects might change? | | | | |
| | No | Yes | | | |

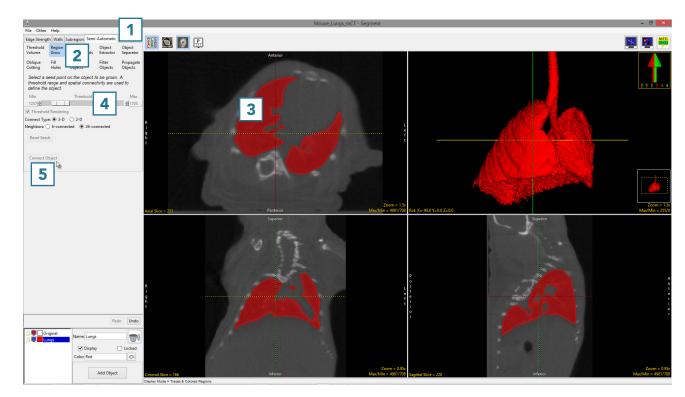
| Edge Strengt | h Walls | Subregio | n Sen | ni-Automa | atic Manual | | | | |
|--|----------------|------------------|--------------|---------------------|----------------------|--|--|--|--|
| Threshold Region Conr Volume Grow Com | | | | Object Extractor | Object Separator | | | | |
| • | | Morph Objects | | | Propagate Objects | | | | |
| Select the action to use then press Filter | | | | | | | | | |
| | | | | | | | | | |
| Operation: | Mode | - | | | | | | | |
| | ✓ Mode | | Y | ; | Z | | | | |
| | Median Rank | | 01 | ۲ |) 1 | | | | |
| Elemer | | ĸ | 3 ک | C | 3 | | | | |
| Size | 0 5 | | 05 | 0 |) 5 | | | | |
| | 07 | | \bigcirc 7 | 0 | 7 | | | | |
| | 0 9 | | 09 | C | 9 | | | | |
| | 3 | | 3 | | 1 | | | | |
| | | | | | | | | | |
| Filter Objects | | | | | | | | | |

Using Filter Objects to Improve Segmentation

Here we will improve the segmentation of an object by using Filter Objects.

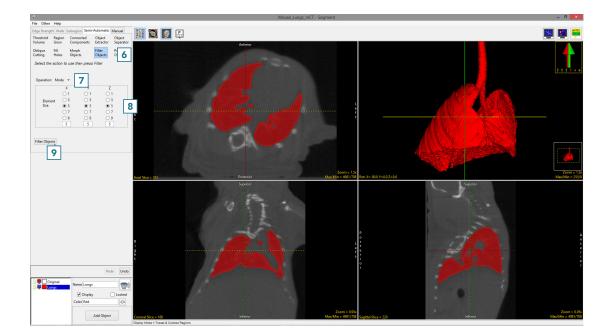
To follow along, download the data set Mouse_Lungs from analyzedirect. com/data and load into Analyze using Input/Output.

- 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].

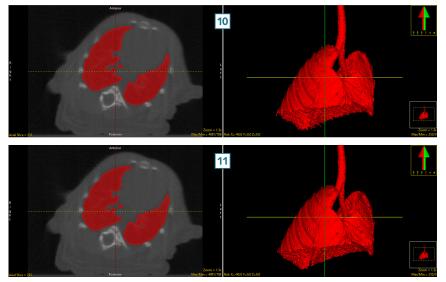


Using Filter Objects to Improve Segmentation (continued)

- 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 defines 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.

The following options are available:

Propagation Type: choose between propagating the current object (default) selected from the object list or all objects in the object list.

Axial: Select axial if the regions to propagate were defined in this orientation.

Coronal: Select coronal if the regions to propagate were defined in this orientation.

Sagittal: Select sagittal if the regions to propagate were defined in this orientation.

Smoothing: Enables a smoothing operation to be applied to the object(s) after propagation is completed.

Propagate Object: Initiates the region propagation process.





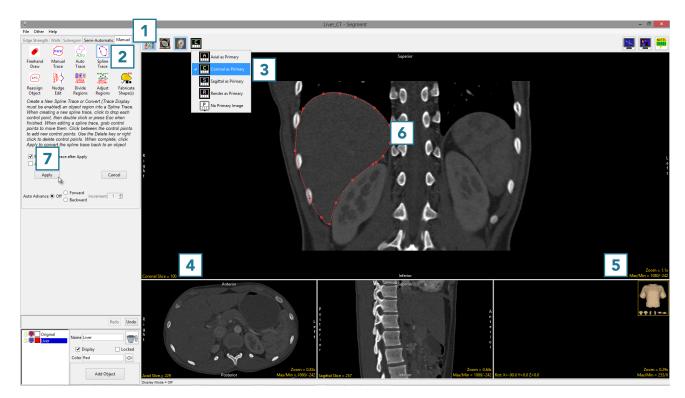
| Edge Strength | Walls | Subregion | Semi-/ | Automatic | Manual | | | | |
|---|---------------|------------------|-------------------------|-------------------|----------------------|--|--|--|--|
| Threshold Region Volume Grow | | | Connected Components | | Object Separator | | | | |
| | Fill Holes | Morph Objects | | Filter Objects | Propagate Objects | | | | |
| Select the Object to Propagate, specify the Propagation Options, then press Propagate. | | | | | | | | | |
| Propagation Type: Current Object All Objects | | | | | | | | | |
| Axial | | O Coro | 🔘 Coronal 💦 🔿 Sagitt | | al | | | | |
| Smoothing | | | | | | | | | |
| Propagate Object | | | | | | | | | |

Using Propagate Objects

Here we will extend the definition of a region using Propagate Objects.

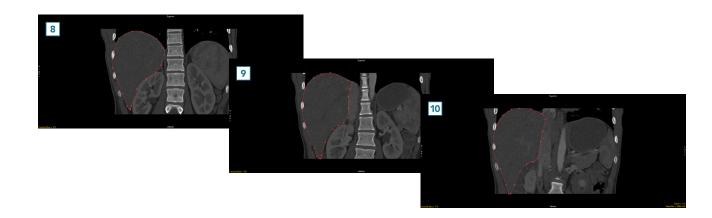
To follow along, download the data set CT_Liver from analyzedirect.com/ data and load into Analyze using Input/Output.

- Select the 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].

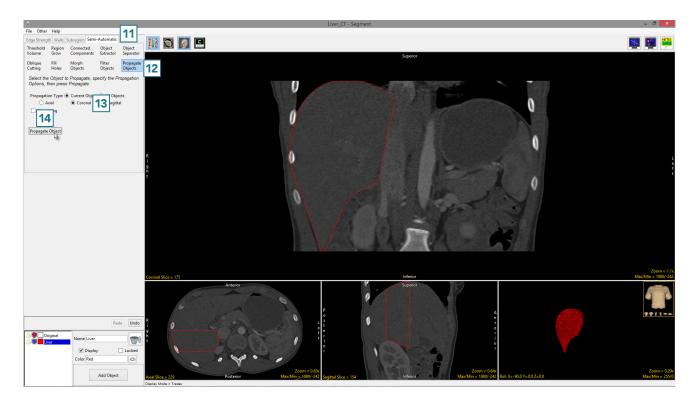


Using Propagate Objects (continued)

- 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.

The Manual Tools that will described in this section include the following:

- Freehand Draw
- Manual Trace
- Auto Trace
- Polygon Trace
- Spline Trace
- Smart Trace
- Reassign Object
- Nudge Edit
- Divide Regions
- Adjust Regions
- Fabricate Shape(s)

Freehand Draw

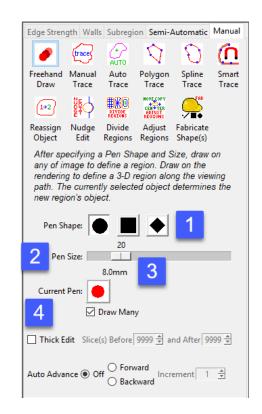
The Freehand Draw tool lets the user draw regions of interest directly onto the image data. The following options are available.

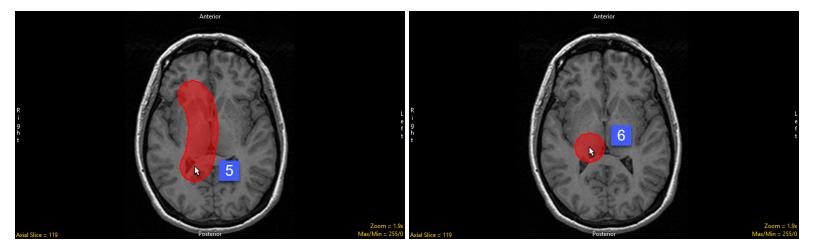
Pen Shape: The pen shape option [1] allows users to specify the shape of the pen for region definition, choose from Round, Square, or Diamond.

Pen Size: The pen size slider [2] provides users with the ability to adjust the size of the pen used for region definition. The pen size ranges from 1 to 100 pixels. Note that the real-world size of the pen is reported below the pen size slider [3].

Current Pen: The current pen icon [4] is a quick reference tool for users, displaying the selected pen shape, pen size, and object color of the selected object from the object list.

Draw Many: The draw many option allows users to enable (default) or disable the draw many option. Enable this option is you wish to draw a continuous region, [5] disable the option is you wish to draw a single region as defined by the pen shape, pen size, and selected object [6].





Analyze 15.0 User's Guide

© AnalyzeDirect, Inc.

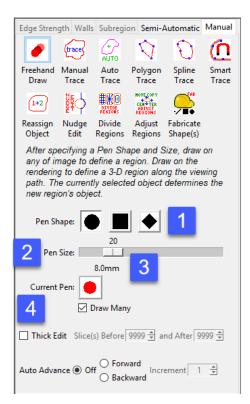
Freehand Draw (continued)

Thick Edit: The thick edit option allows users to apply edits (region definitions) defined on the current slice to other slices in the volume. When thick is enabled the following options are available:

- Slices(s) Before: Specifies the number of slices before the current slice in which to apply the edits.
- And After: Specifies the number of slices after the current slice in which to apply the edits.

Auto Advance: The auto advance option automatically moves users to a new slice, as defined by the auto advance options, once the current edit is defined. Note the auto advance will occur after the user releases the left mouse button and the edit is applied to the current slice. The auto advance option is a productivity tool allowing users to move through the image data without having to move the cursor from the current orientation window that regions are being defined on. The following options are available.

- Off: Off is the default option for auto advance. When off is selected auto advance is disabled.
- Forward: Specifies that auto advance will move forward through the image data (slice number increases).
- Backwards: Specifies that auto advance will move backwards through the image data (slice number decreases).
- Increment: Specifies the number of slices the auto advance will move forward or backwards.

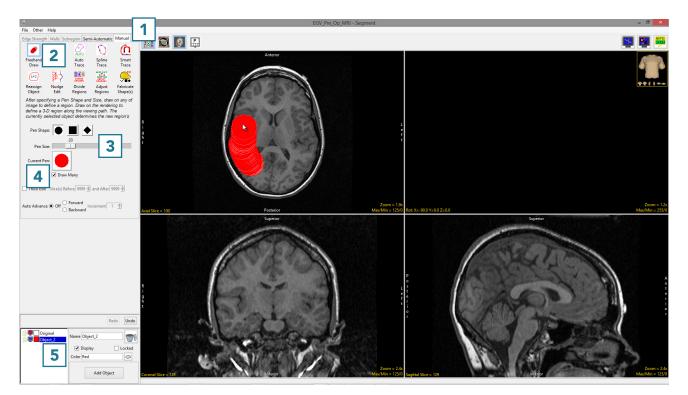


Using Freehand Draw to Define a 2D Region

Freehand Draw allows easy definition of 2D regions.

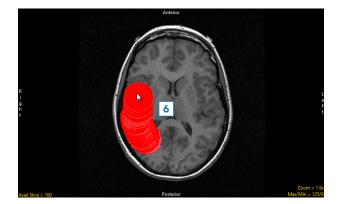
To follow along, download the data set EGV_MRI from analyzedirect. com/data and load into Analyze using Input/Output.

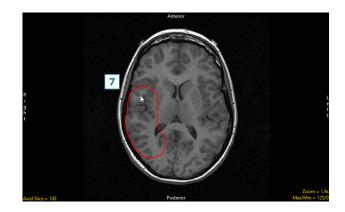
- Select the data set and open Segment.
- Select Manual [1] and choose Freehand Draw [2].
- Use the Pen Size slider to change the Pen Size to 20 [3].
- The Current Pen [4] will update to the color of the currently selected object [5].



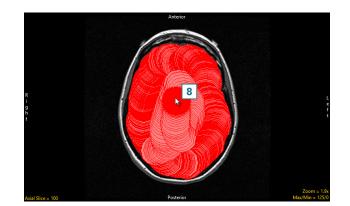
Using Freehand Draw to Define a 2D Region (continued)

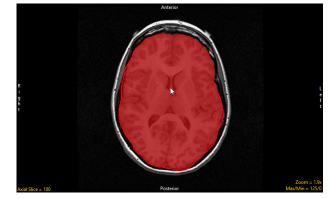
- Left-click on the image and drag the cursor to trace a region [6].
- Releasing the left mouse button will end the trace [7].





• Continue to define the brain using the pen tool [8].



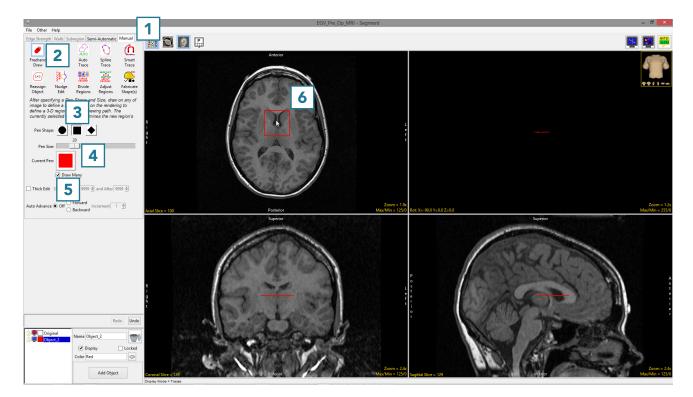


Using Freehand Draw to Define a Single Shape on a 2D Slice

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

To follow along, download the data set EGV_MRI from analyzedirect. com/data and load into Analyze using Input/Output.

- Select the 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.

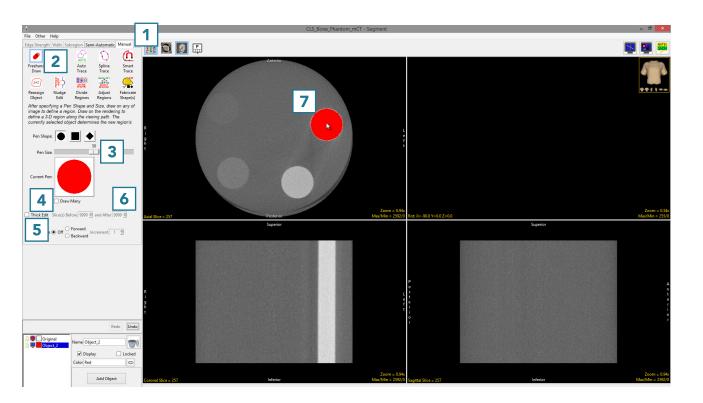


Using Freehand Draw to Define a Single Shape in 3D

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.

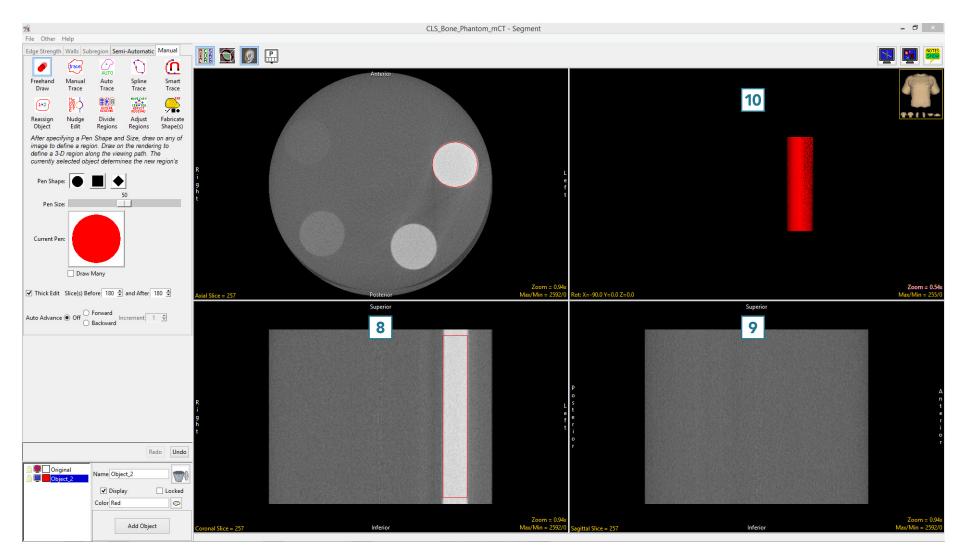
To follow along, download the data set CLS_Bone_Phantom from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the 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.



Using Freehand Draw to Define a Single Shape in 3D (continued)

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].

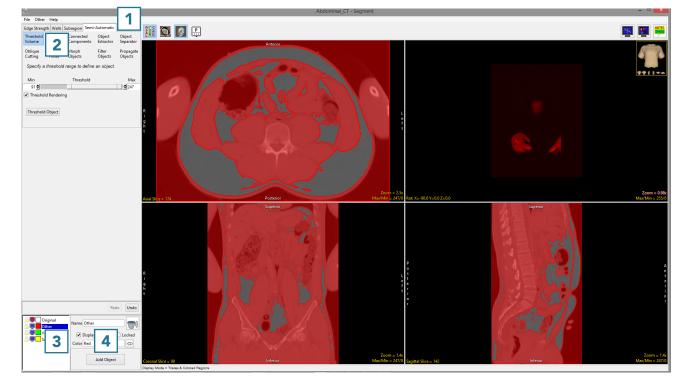


Using Freehand Draw to Paint Regions of Interest

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.

To follow along, download the data set VH_Abdomen.avw from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the data set and open Segment.
- Select Semi-Automatic [1] and choose Threshold Volume [2].

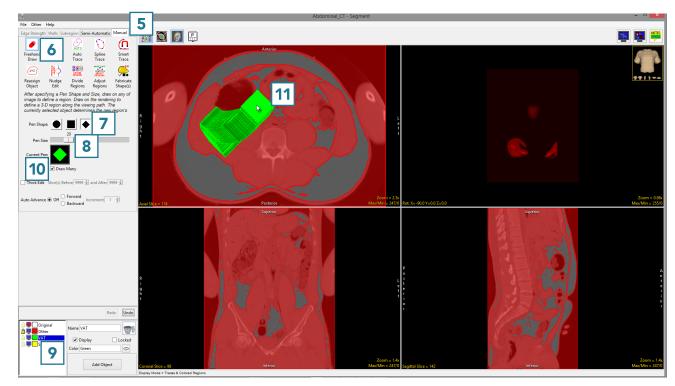


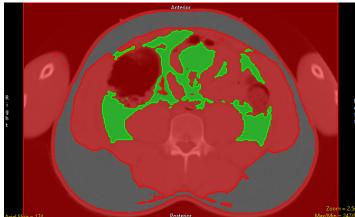
- Change the name of the current object to Other, then add two new objects: VAT (visceral adipose tissue) and SAT (subcutaneous adipose tissue) [3].Select the Other object and use global thresholding to assign voxels having intensity values of 0 to 81 and 91 to 247 to the Other object. This will assign 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.

Using Freehand Draw to Paint Regions of Interest (continued)

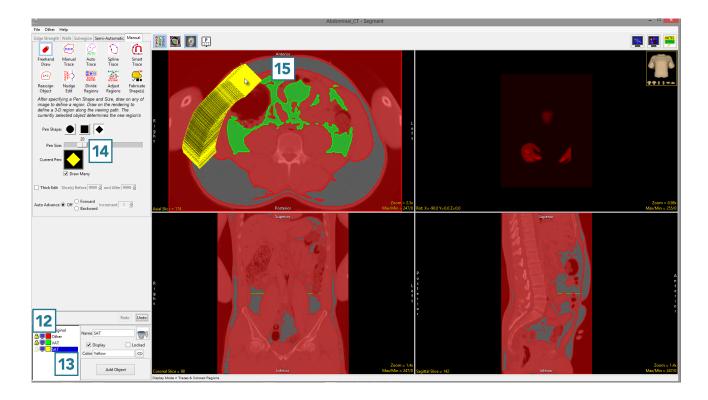
- Select Manual [5] and choose Freehand Draw [6].
- Set the Pen Shape to Diamond
 [7] and change the Pen Size to
 20 [8].
- Select the VAT object [9] and note that the Current Pen [10] will update to the color of the VAT object.
- Use the pen tool to draw over the VAT regions [11].



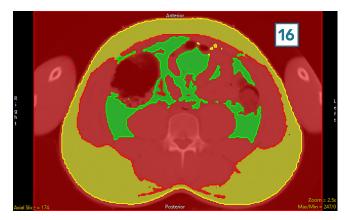


Using Freehand Draw to Paint Regions of Interest (continued)

- 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.

When the Manual Trace tool is selected the following options are available:

Thick Edit: The thick edit option allows users to apply edits (region definitions) defined on the current slice to other slices in the volume. When thick is enabled the following options are available:

- Slices(s) Before: Specifies the number of slices before the current slice in which to apply the edits.
- And After: Specifies the number of slices after the current slice in which to apply the edits.

Auto Advance: The auto advance option automatically moves users to a new slice, as defined by the auto advance options, once the current edit is defined. Note the auto advance will occur after the user releases the left mouse button and the edit is applied to the current slice. The auto advance option is a productivity tool allowing users to move through the image data without having to move the cursor from the current orientation window that regions are being defined on. The following options are available.

• Off: Off is the default option for auto advance. When off is selected auto advance is disabled.

Analyze 15.0 User's Guide

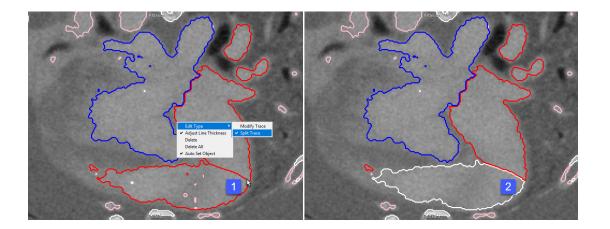
Manual Trace Options (continued)

Auto Advance (continued):

- Forward: Specifies that auto advance will move forward through the image data (slice number increases).
- Backwards: Specifies that auto advance will move backwards through the image data (slice number decreases).
- Increment: Specifies the number of slices the auto advance will move forward or backwards.

Right click options: Right clicking on a trace when Auto Trace is selected will provide access to the following additional editing options:

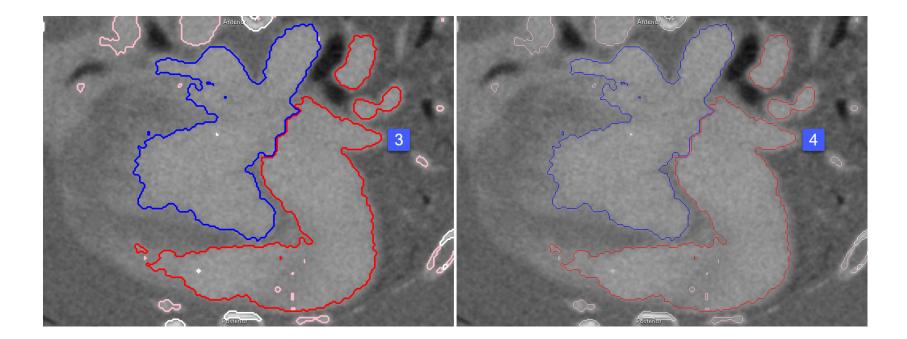
- Edit Type: Allows users to switch between the modify trace and split trace edit modes.
 - Modify Trace: The modify trace option is the default mode for manual trace editing. If the cursor is held over the boundary of an object when tracing begins the edit will apply to that object whose boundary is being modified, regardless of the object selected from the object list. If you wish to have edits applied to the object selected in the object list uncheck the Auto Set Object option. For more information on how to edit a trace refer to Manual Contour Tracing and Editing.
 - Split Trace: Split trace mode allows the current object to be edited [1] and split into two objects with the smaller section of the trace being assigned to the object selected in the object list. If the object selected is the same as the object being split the smaller section will be automatically assigned to a new object [2].



Manual Trace Options (continued)

Right click options (continued):

• Adjust Line Thickness: The adjust line thickness options allows users to switch the thickness display of the traced boundaries of objects. When enabled (default) traces appear thicker, [3] when disabled traces appear thinner. [4]



- Delete: Deletes selected region.
- Delete All: Deletes all regions on the slice.
- Auto Set Object: When enabled (default) edits made to object boundaries in Modify Trace mode are assigned to the object being edited. Unchecking the option will ensure boundary edits are assigned to the object selected in the object list.

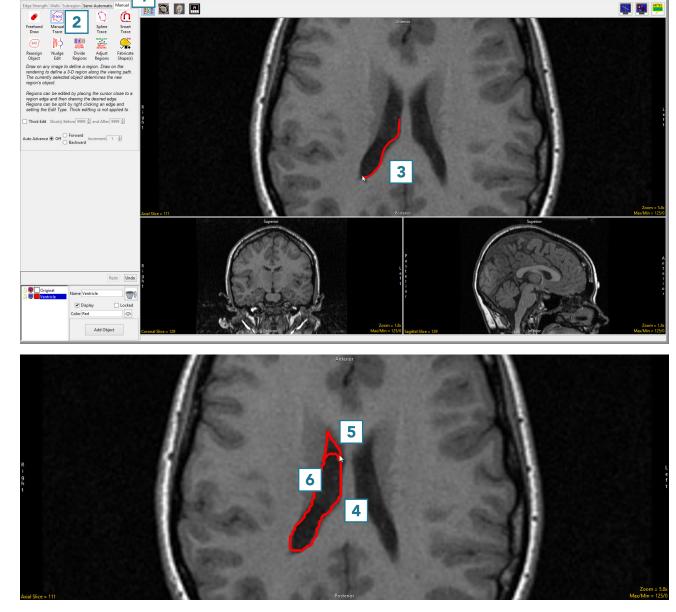
Analyze 15.0 User's Guide

Manual Contour Tracing and Editing

To perform contour tracing and editing using Manual Trace, use the following steps.

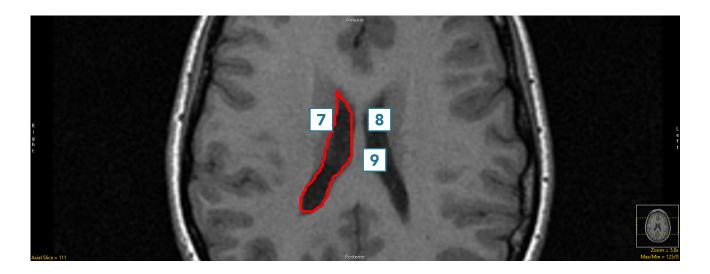
To follow along, download the data set MRI_3D_Head from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the 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].

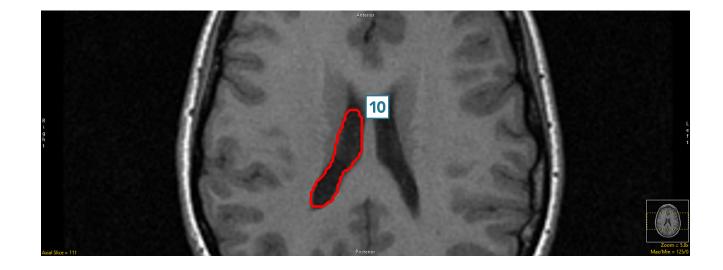


Manual Contour Tracing and Editing (continued)

- After clicking on the trace, 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].

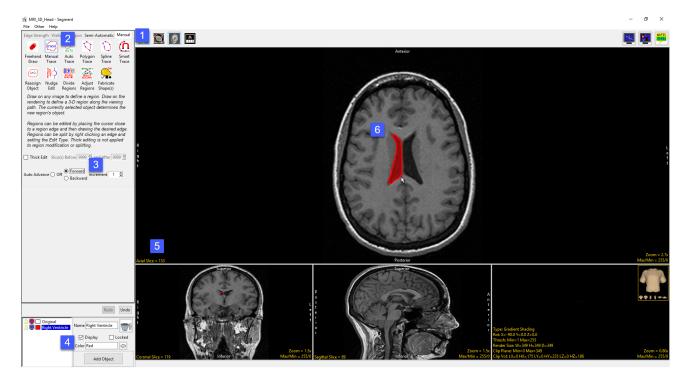


Manual Trace and Auto Advance

Here we will use the Auto Advance function of Manual Trace to automatically move forwards and backwards through image data as the region of interest is defined.

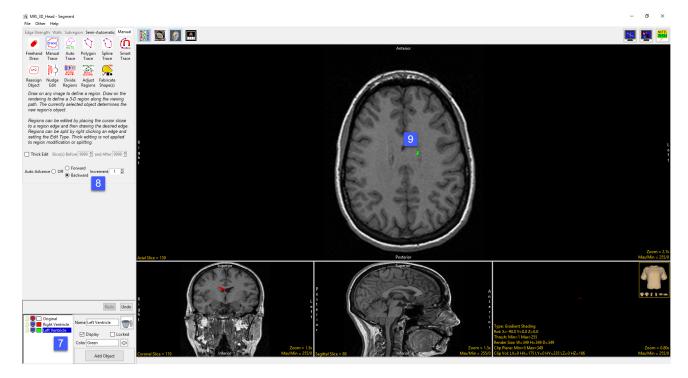
To follow along, download the data set MRI_3D_Head from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the data set and open Segment.
- Select Manual [1] and choose Manual Trace [2].
- Set Auto Advance to Forward [3].
- Add an object and name it Right Ventricle [4].
- Move to Axial slice 133 [5].
- Left click on the border of the right ventricle and trace the structure [6]. When complete release the left mouse button. The trace will be applied to this slice, and the next slice forward, slice 134, will appear.

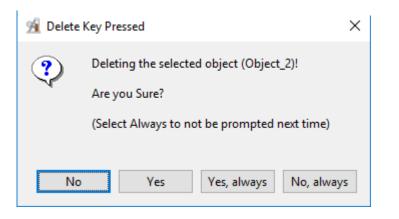


Manual Trace and Auto Advance (continued)

- Continue tracing the right ventricle in this manner until slice 139 is reached.
- At slice 139 add a new object and name it Left Ventricle [7]. Make sure the new object is selected.
- Change the Auto Advance option to Backward [8]
- Left click on the border of the left ventricle and trace the structure
 [9]. When complete release the left mouse button. The trace will be applied to slice 139 and slice
 138 will appear. Continue tracing the left ventricle until slice 133 is reached.



Tip: Object regions can be deleted by holding the cursor over the object and then pressing the delete key on your keyboard. Note that the first time you delete an object in this way for the current segmentation session you will be prompted on which action to take; don't delete (No), delete (Yes), delete and don't prompt this message in the future (Yes, always), don't delete and don't prompt this message in the future.



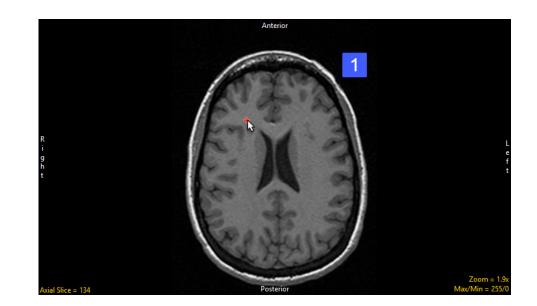
Auto Trace

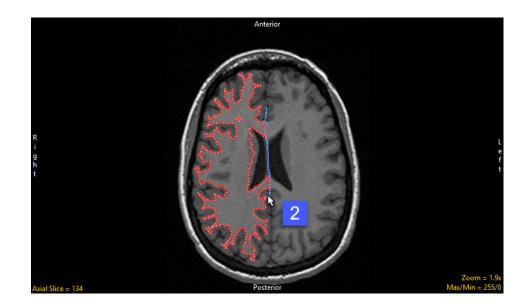
The Auto Trace tool enables the user to define and extract regions of interest from the image data using 2D seeded region growing. Region definition begins with a seed pixel, manually set by the user, on a structure of interest. Next, a threshold range is established by the user to define the boundary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

The following options are available:

Select Seed: The select seed mode is the default mode the Auto Trace tool will open in. Select seed allows users to set a seed point on the image data [1] to enable the Auto Trace tool options.

Draw Limit: The draw limit mode allows users to manually define limits on the image data to limit the auto trace region [2].

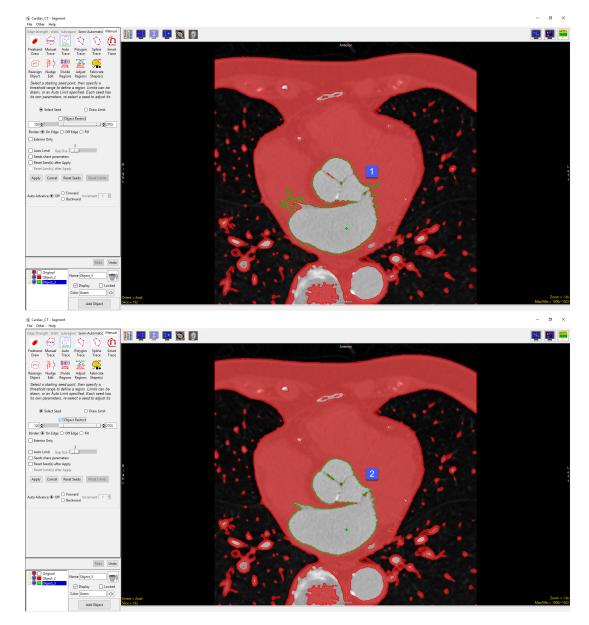




Object Restrict: The Object Restrict options allows users to restricts the definition of the current object with the boundaries of any established objects. When disabled traces are not limited by object boundaries [1]. However, when the option is enabled traces are restricted [2].

Threshold slider: The Threshold doubleended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slider. Minimum and Maximum values can be entered in the text entry fields while the arrow up and down keys to the right of the minimum and left of the maximum text entry fields can be used to increase or decrease values 1 point at a time. Click left and right of the text entry boxes

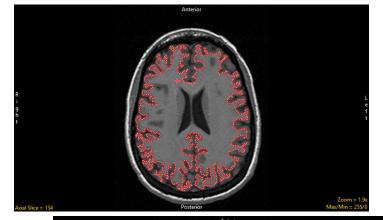
Tip: Clicking in the trough to either side of the minimum or maximum end of the slider will advance the value by 1. Shift-click will decrease the value by 1.

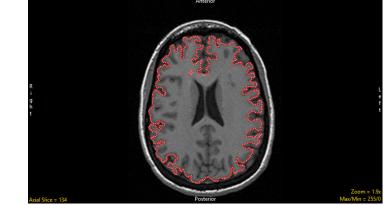


Right clicking options: Right clicking on the threshold slider will provide access to threshold presents. The Presets option allows users to select predefined thresholds or define new threshold values for specific areas of interest. For more information on Presets, including how to configure presents refer to the Threshold Volume.

Border: The Border options allows users to specify how the border of the trace will be displayed on the image, choose from:

- On Edge: The auto trace will be positioned exactly on the edge of the thresholded region (top image).
- Off Edge: The auto trace will be positioned one pixel off the edge of the thresholded region (middle image).
- Fill: The auto trace will display On Edge with a filled interior (bottom image).

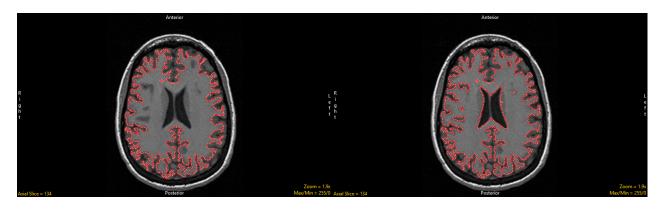


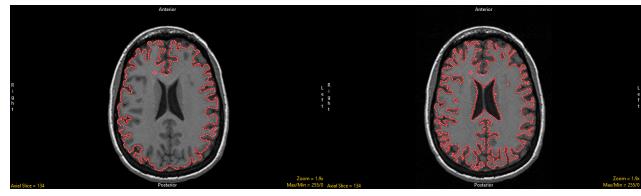


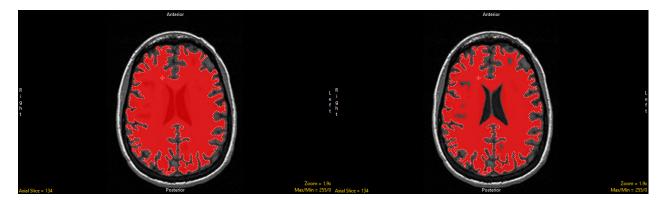


Exterior Only: The Exterior Only option allows users to enable (default) or disable the display of the exterior border only. Enable the option if you only wish to see the exterior borders of the trace, uncheck and disable the option if you wish to view the exterior and interior borders. The option is compatible for all Border displays.

- Top image: Exterior Only disabled with On Edge selected
- Middle Image: Exterior Only disabled with Off Edge selected
- Bottom image: Exterior Only disabled with On Fill selected







Auto Limit: The Auto Limit option applies a post processing step to the auto trace to eliminate thin portions of the auto trace. This option performs a morphologic open using the Gap Size value, defined by the user, to define the number of layers to be removed from the trace and then added back.

To use the option, after setting a seed point and appropriate threshold criteria to define a region [1], click the Auto Limit check box [2], then set the Gap Size using the slider, [3] review the impact on the defined region. [4] Note that the Gap Size of 0 is the same as having no Auto Limit set. This option helps eliminate the need for manually defining limits in some situations.



Seeds share parameters: The Seeds share parameters option allows users to enable or disable (default) seeds from sharing the same auto trace options including threshold range, border settings, auto limit, and object information. Enable this option if you wish to define multiple separate regions with the same parameters, keep this option disabled if you wish to define multiple separate regions with different parameters.

Reset Seed(s) after Apply: After applying the trace all seeds will be reset (deleted).

Reset Limit(s) after Apply: After applying the trace all limits will be reset (deleted).

Apply: Applies the trace to the slice.

Cancel: Cancels the Auto Trace, resets all defined seed points and limits.

Reset Seeds: Resets all seeds.

Reset Limits: Resets all limits.

Auto Advance: The auto advance option automatically moves users to a new slice, as defined by the auto advance options, once the current edit is defined. Note the auto advance will occur after the user releases the left mouse button and the edit is applied to the current slice. The auto advance option is a productivity tool allowing users to move through the image data without having to move the cursor from the current orientation window that regions are being defined on. The following options are available.

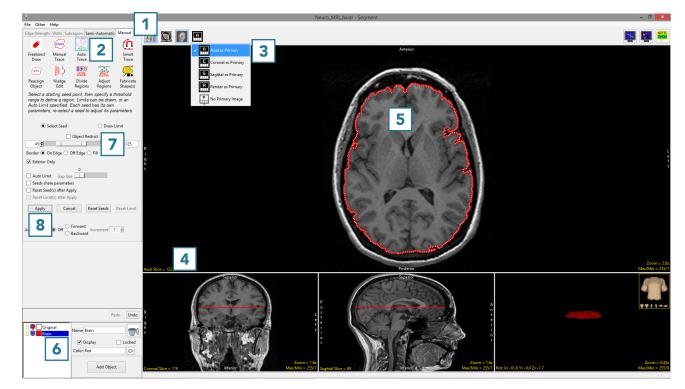
- Off: Off is the default option for auto advance. When off is selected auto advance is disabled.
- Forward: Specifies that auto advance will move forward through the image data (slice number increases).
- Backwards: Specifies that auto advance will move backwards through the image data (slice number decreases).
- Increment: Specifies the number of slices the auto advance will move forward or backwards.

Analyze 15.0 User's Guide

Using Auto Trace to Define a 2D Region of Interest

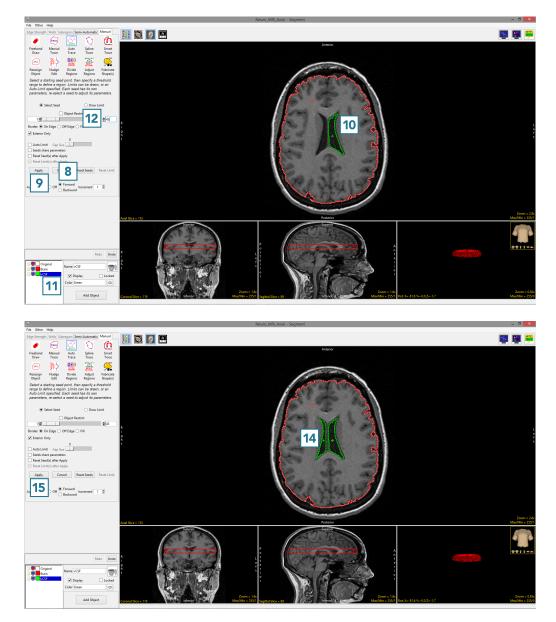
To follow along, download the data set MRI_3D_Head from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the 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.
- As the seed point and threshold range are carried forward, the brain will be redefined on this slice.



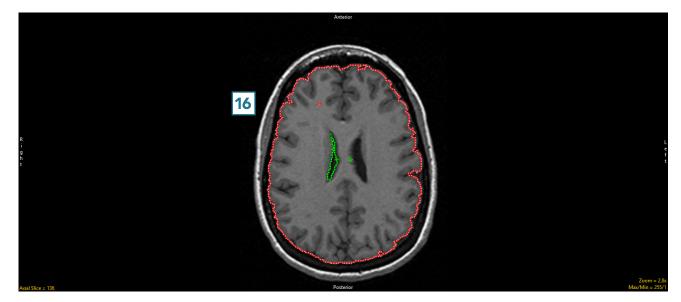
Using Auto Trace to Define a 2D Region of Interest (continued)

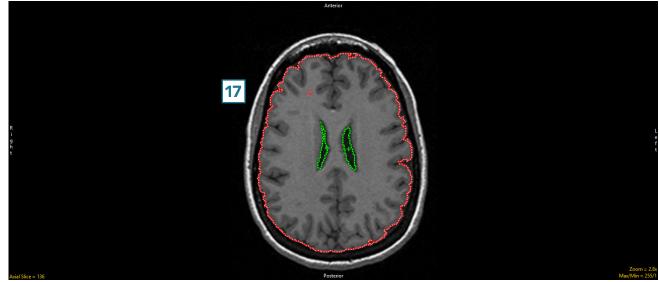
- Set the Auto Advance option to Forward [8] and click Apply [9]. The brain will be traced on this slice and the display will automatically move forward to slice 124.
- Continue to apply the auto trace to the brain up to slice 133. If the initial seed point is copied to a slice where it does not fall 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].



Using Auto Trace to Define a 2D Region of Interest (continued)

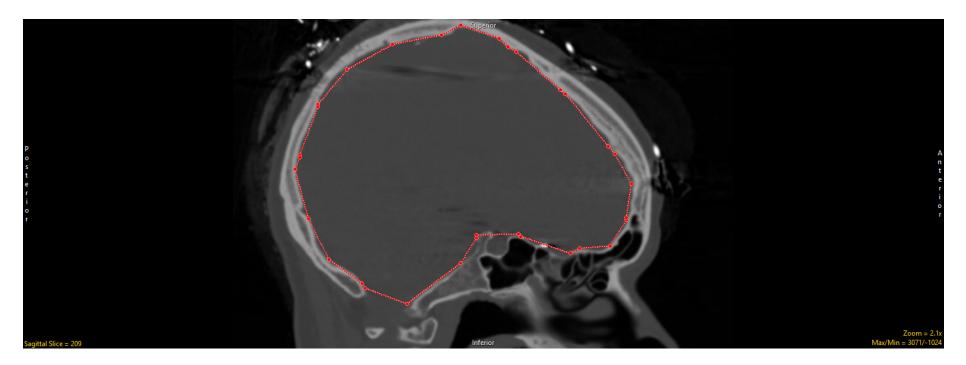
- Continue clicking Apply to trace the Brain and vCSF objects. If a seed point is copied to a location where it is no longer on the target object [16], move the seed point back onto the object [17] and continue to apply the auto trace.
- Stop defining objects at slice 137.
- Select File > Save Object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





Polygon Trace

The Polygon Trace tool enables the definition of a closed polygon region.



The following options are available:

Reset Polygon Trace after Apply: Resets (deletes) the polygon trace after the region is defined. Polygon traced regions are defined after the user double-clicks or presses the escape (Esc) key to close the trace ending the tracing process, the trace is applied when the Apply button is clicked, the 'A' key on your keyboard is pressed, the user right-clicks on the spline trace and selects Apply from the menu or the Auto Apply option is enabled.

Auto Apply: When selected the polygon trace is automatically applied once the user double-clicks or presses the escape key to close the trace.

Polygon Trace Options

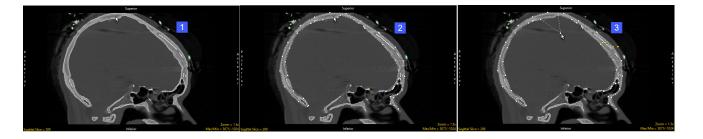
Auto Advance: The auto advance option automatically moves users to a new slice, as defined by the auto advance options, once the current edit is defined. Note the auto advance will occur after the user releases the left mouse button and the edit is applied to the current slice. The auto advance option is a productivity tool allowing users to move through the image data without having to move the cursor from the current orientation window that regions are being defined on. The following options are available.

- Off: Off is the default option for auto advance. When off is selected auto advance is disabled.
- Forward: Specifies that auto advance will move forward through the image data (slice number increases).
- Backwards: Specifies that auto advance will move backwards through the image data (slice number decreases).
- Increment: Specifies the number of slices the auto advance will move forward or backwards.

Right click options: Right clicking on the Polygon trace provides users with the following options:

- Apply: Applies the trace.
- Cancel: Cancels the trace, deleting the trace and controls points.
- Auto Apply on Control Point Adjust: This option is only available when Auto Apply is enabled and when editing a Polygon trace or trace converted to a Polygon. When selected any edits made to the Polygon will be automatically applied when a control point is moved.
- Delete Control Point: Deletes the control point the cursor if currently over.
- Delete Spline: Deletes the trace and controls points.

Note: Clicking on an object border [1] when the Polygon Trace is selected will convert the object region into a polygon [2] with adaptable control points [3].

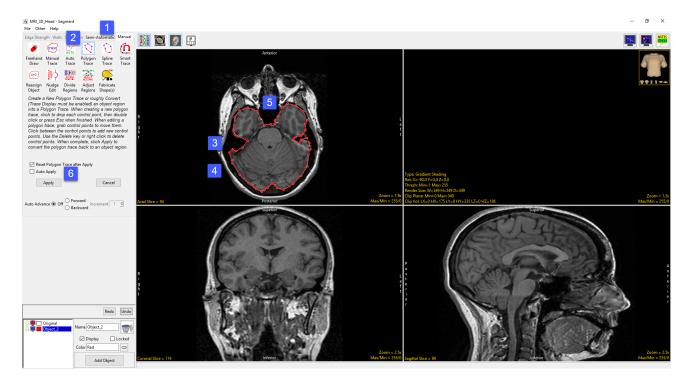


Region Definition and Region Modification with Polygon Trace

Here we will use the Polygon Trace tool to define a region of interest and then how to divide a region into subregions.

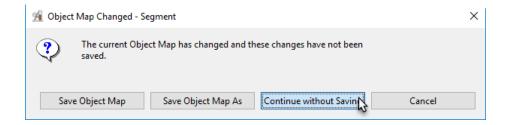
To follow along, download the data set MRI_3D_Head from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the data set and open Segment.
- Select Manual [1] and choose Polygon Trace [2].
- To define a Polygon trace around the brain in the axial image, left click on the image to set the first control point [3] and then move the cursor and left click again to set a second control point [4].
- Continue in defining the border or the brain in this manner until complete [5]. Double-click or press the Esc key to end tracing and then process Apply [6] to define the region.

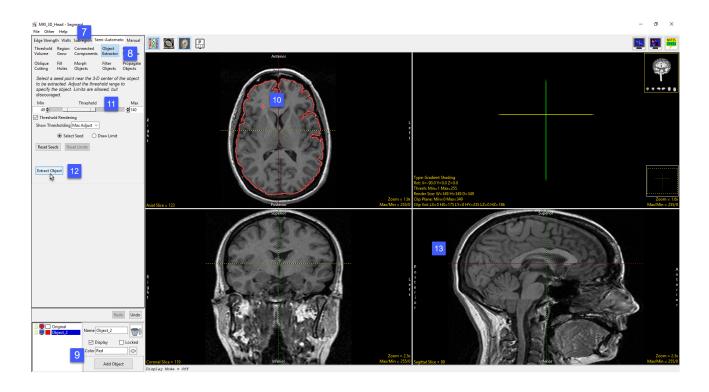


Region Definition and Region Modification with Polygon Trace (continued)

 Select File > Reset Object
 Map to delete the trace, select
 'Continue without Saving' when prompted.

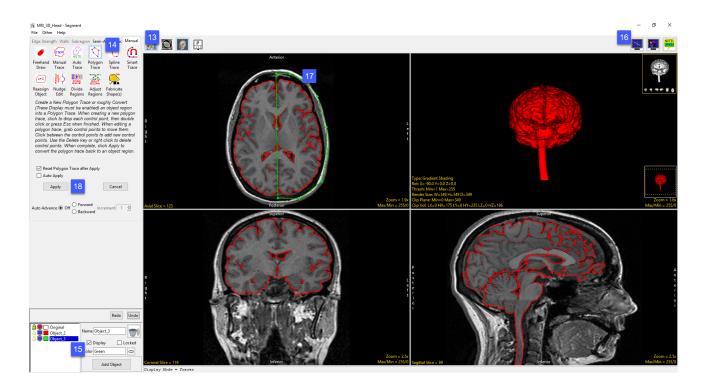


- Next, segment the brain in 3D using the Object Extractor. Select the Semi-Automatic tab [7] and then choose Object Extractor [8].
- Click Add Object [9] to add an object to the object list and then click in the white matter on axial slice 123 to set a seed point [10].
- In the Threshold option set the minimum threshold value to 49 and the maximum to 140 [11] and then click Extract Object [12].



Region Definition and Region Modification with Polygon Trace (continued)

- To subsegment a 2D region do the following. Select the Manual tab [13] and then choose the Polygon tool [14]. Lock the Original object and then add a new object to the object list [15].
- Switch off the Linked Cursor [16] and then use the Polygon tool to define the left hemisphere of the brain on axial slice 123, [17] and then click Apply [18].

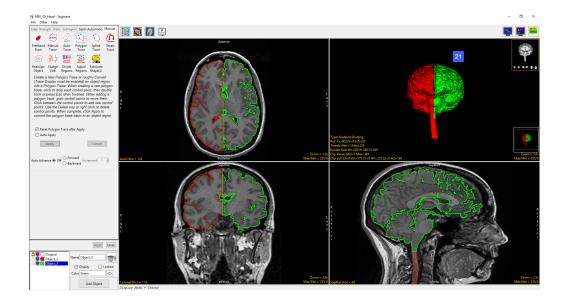


Region Definition and Region Modification with Polygon Trace (continued)

- The brain on slice 123 has been split into two objects representing the left and right hemisphere [18].
- The Polygon trace tool can also be used to edit 3D objects. To subsegment a 3D region define a Polygon trace over the left hemisphere of the brain in the Rendering window [19] and then click Apply [20].

<complex-block>

 All voxels not assigned to a locked object within the trace (and all voxels along the ray path) have be assigned to the selected object [21].



Spline Trace

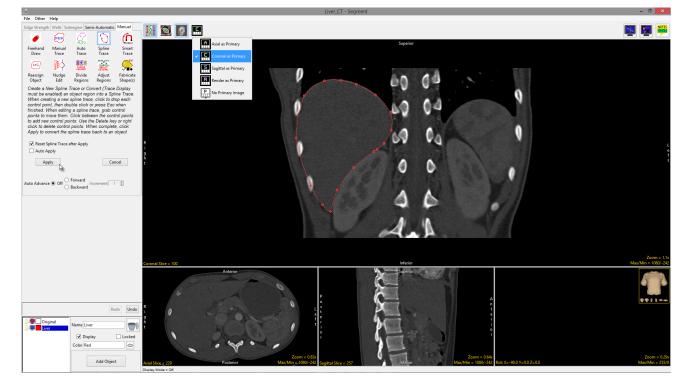
The Spline Trace tool allows users to define curved regions of interest. Splines are flexible curve traces with movable control points that are useful for creating smooth edge traces.

The available options are as follows:

Reset Spline Trace after Apply:

Resets (deletes) the spline trace after the region is defined. Spline traced regions are defined after the user double-clicks or presses the escape (Esc) key to close the trace ending the tracing process, the trace is applied when the Apply button is clicked, the 'A' key on your keyboard is pressed, the user right-clicks on the spline trace and selects Apply from the menu or the Auto Apply option is enabled.

Auto Apply: When selected the spline trace is automatically applied once the user double-clicks or presses the escape key to close the trace.



Spline Trace Options

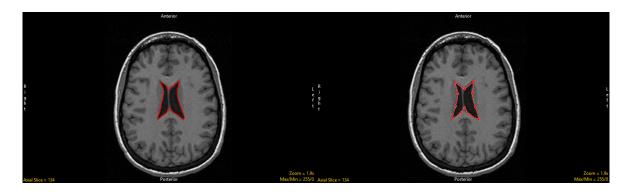
Auto Advance: The auto advance option automatically moves users to a new slice, as defined by the auto advance options, once the current edit is defined. Note the auto advance will occur after the user releases the left mouse button and the edit is applied to the current slice. The auto advance option is a productivity tool allowing users to move through the image data without having to move the cursor from the current orientation window that regions are being defined on. The following options are available.

- Off: Off is the default option for auto advance. When off is selected auto advance is disabled.
- Forward: Specifies that auto advance will move forward through the image data (slice number increases).
- Backwards: Specifies that auto advance will move backwards through the image data (slice number decreases).
- Increment: Specifies the number of slices the auto advance will move forward or backwards.

Right click options: Right clicking on the Spline trace provides users with the following options:

- Apply: Applies the trace.
- Cancel: Cancels the trace, deleting the trace and controls points.
- Auto Apply on Control Point Adjust: This option is only available when Auto Apply is enabled and when editing a Spline Trace or trace converted to a Spline Trace. When selected any edits made to the trace will be automatically applied when a control point is moved.
- Delete Control Point: Deletes the control point the cursor if currently over.
- Delete Spline: Deletes the trace and controls points.

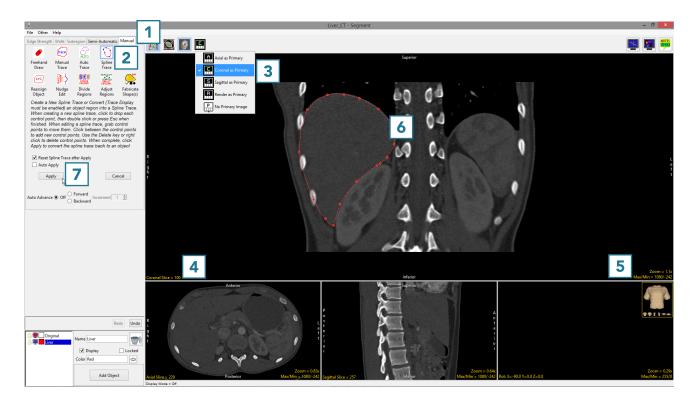
Note: Clicking on an object border when the Spline Trace is selected will convert the object region into a spline with adaptable control points.



© AnalyzeDirect, Inc.

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

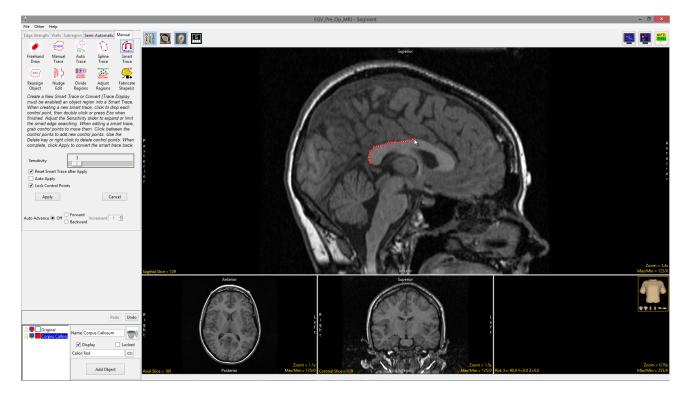
The Smart Trace tool detects regions of high rate of change of voxel intensity (gradient) representing edges. The tool snaps to the edges of these regions. The sensitivity of the smart edge can be adjusted using the slider or the mouse scroll wheel.

The following options are available:

Sensitivity: The sensitivity of the smart edge can be adjusted using the slider or the mouse scroll wheel. The lower the value the less sensitive the tool is, the higher the value the more sensitive the tool is.

Reset Smart Trace after Apply:

Resets (deletes) the smart trace after the region is defined. Smart trace regions are defined after the user double-clicks to close and end the tracing process and then pressing the Apply button, selecting the 'A' key on your keyboard, or having the Auto Apply option selected.



Auto Apply: When selected automatically applies the Smart Trace region.

Lock Control Points: Allows users to lock or unlock (default) the smart trace controls points. Unlocking the control points allows users to move the control points.

Auto Advance: The auto advance option automatically moves users to a new slice, as defined by the auto advance options, once the current edit is defined. Note the auto advance will occur after the user releases the left mouse button and the edit is applied to the current slice. The auto advance option is a productivity tool allowing users to move through the image data without having to move the cursor from the current orientation window that regions are being defined on. The following options are available.

- Off: Off is the default option for auto advance. When off is selected auto advance is disabled.
- Forward: Specifies that auto advance will move forward through the image data (slice number increases).
- Backwards: Specifies that auto advance will move backwards through the image data (slice number decreases).
- Increment: Specifies the number of slices the auto advance will move forward or backwards.

Right click options: Right clicking on the Smart Trace provides users with the following options:

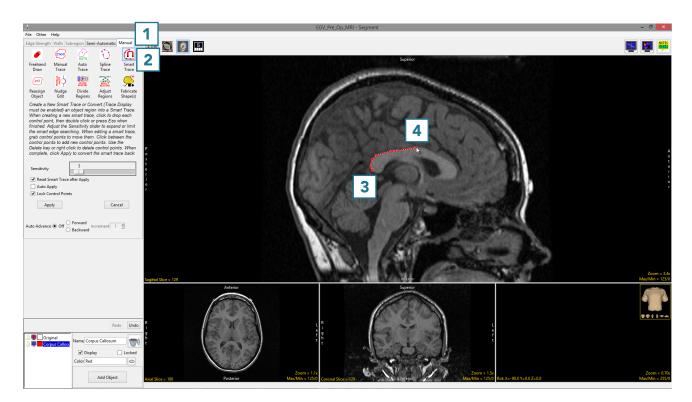
- Apply: Applies the trace.
- Cancel: Cancels the trace, deleting the trace and controls points.
- Auto Apply on Control Point Adjust: This option is only available when Auto Apply is enabled and when editing a Smart Trace or trace converted to a Smart Trace. When selected any edits made to the Smart Trace will be automatically applied when a control point is moved.
- Delete Control Point: Deletes the control point the cursor if currently over.
- Delete Spline: Deletes the trace and controls points.

Note: Clicking on an object border when the Smart Trace is selected will convert the object region into a Smart trace with adaptable control points.

Smart Trace Region Definition

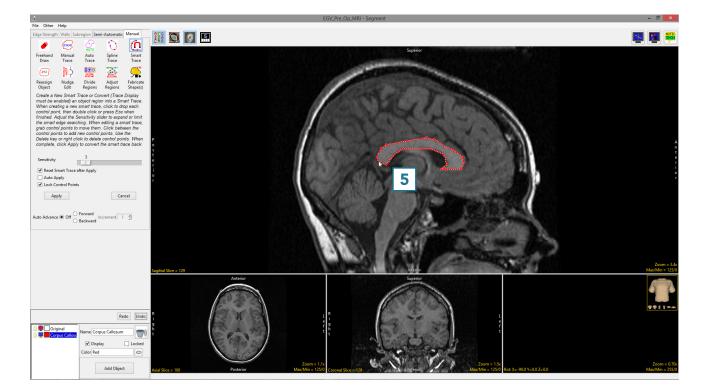
To follow along, download the data set MRI_3D_Head from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the 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.



Smart Trace Region Definition (continued)

- 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 the table below:

Reassignment Types

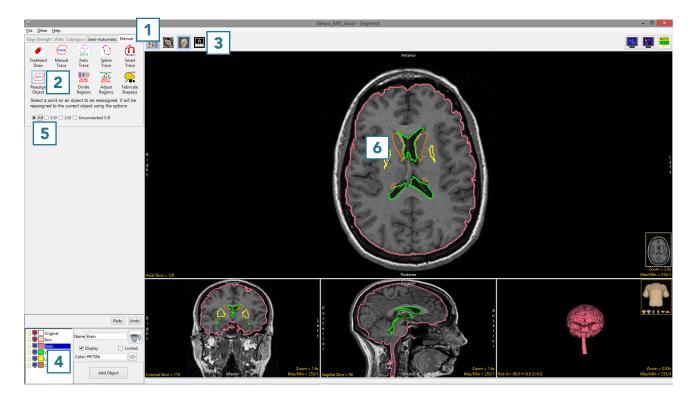
| Reassignment Type | Action |
|-------------------|---|
| All | All voxels in the selected object are reassigned to the current object |
| 3D | All voxels in the selected object that are connected in 3D to the seed pixel are reassigned to the current object |
| 2D | All voxels in the selected object 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 |

Reassigning Objects

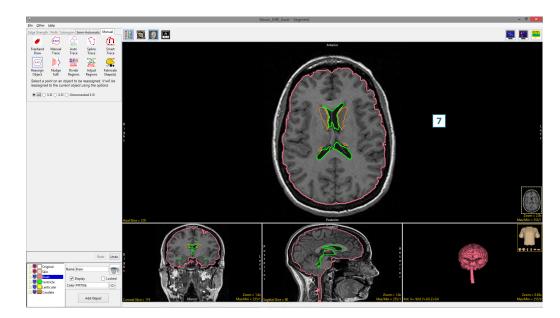
Here we will reassign the voxels of one object to another object.

To follow along, download the data set MRI_3D_Head from analyzedirect.com/data and load into Analyze using Input/Output.

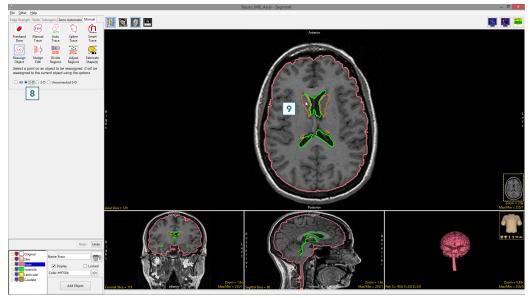
- Select the data set and open Segment.
- Use File > Load Object Map to load the corresponding object map.
- Select Manual [1] and choose Reassign Object [2].
- Set the primary display to axial [3] and move to axial slice 130.
- Switch the display of the Skin object off and switch on the display of the 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].



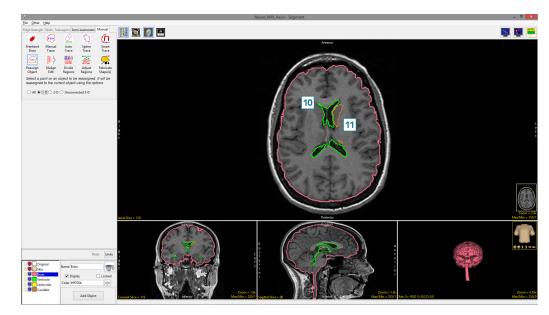
 Note that all the voxels of the Lenticular object have been reassigned to the Brain object [7].



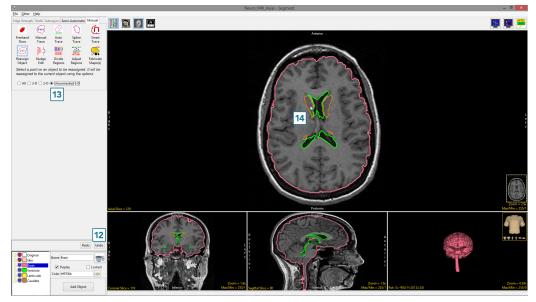
 Set the reassignment type to 3D [8] and click on the brown Caudate object on the right side of the brain [9].



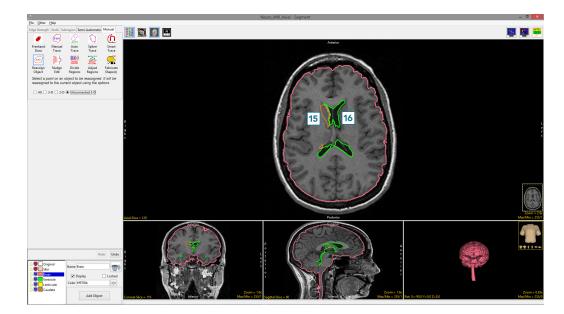
 Note that the all the voxels of the Caudate object connected to the seed pixel have been reassigned to the Brain object [10]. As the left caudate nucleus is not connected to the right caudate nucleus, that part of the object remains [11].



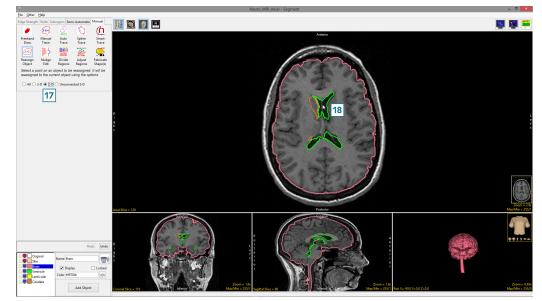
- Click Undo [12] and set the reassignment type to Unconnected 3D [13].
- Click on the brown Caudate object on the right side of the brain [14].



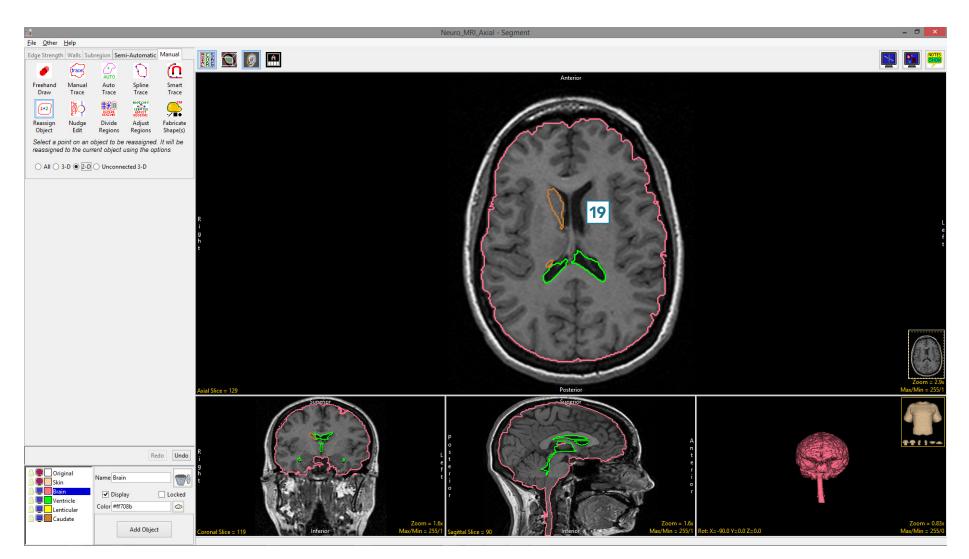
 Note that this time, all the voxels assigned to the Caudate object connected to the seed pixel have been kept [15] while those unconnected voxels representing the left caudate nucleus have been reassigned to the Brain object [16].



- 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. When Nudge Edit is selected the cursor mode will update to the Nudge Edit tool when an image is clicked on. Available options include:

Auto Advance: This option automatically moves users to a new slice as defined by the auto advance options, once the current edit is

defined. Note the auto advance will occur after the user releases the left mouse button and the edit is applied to the current slice. The auto advance option is a productivity tool allowing users to move through the image data without having to move the cursor from the current orientation window that regions are being defined on. The following options are available.

- Off: Off is the default option for auto advance. When off is selected auto advance is disabled.
- Forward: Specifies that auto advance will move forward through the image data (slice number increases).
- Backwards: Specifies that auto advance will move backwards through the image data (slice number decreases).
- Increment: Specifies the number of slices the auto advance will move forward or backwards.

Analyze 15.0 User's Guide

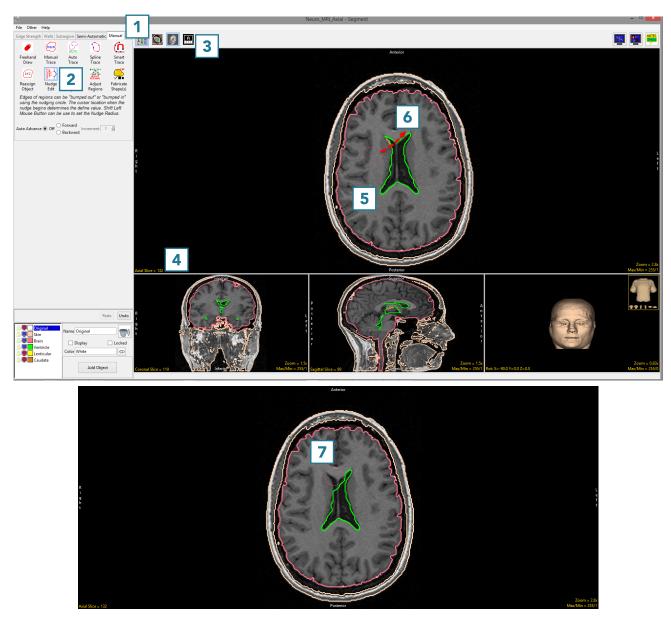
Editing Object Borders using Nudge Edit

To follow along, download the data set MRI_3D_Head from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the data set 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].

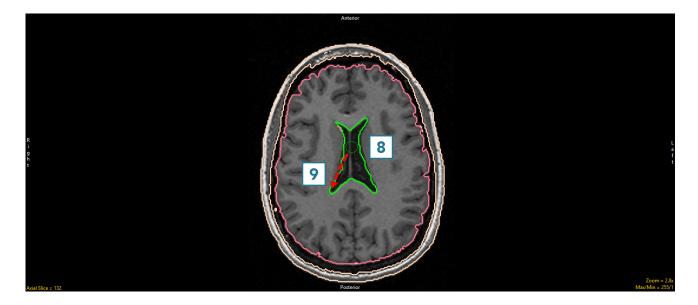
Note the color of the cursor will match the object being nudged.

- 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].

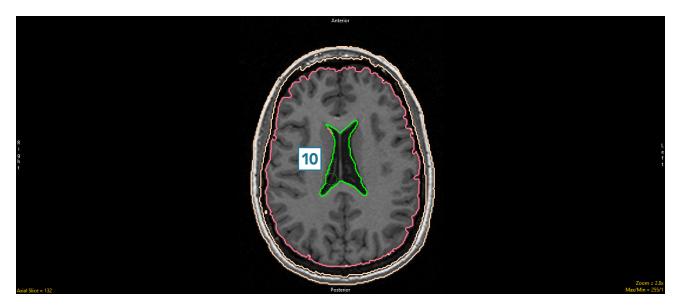


Editing Object Borders using Nudge Edit (continued)

- 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].



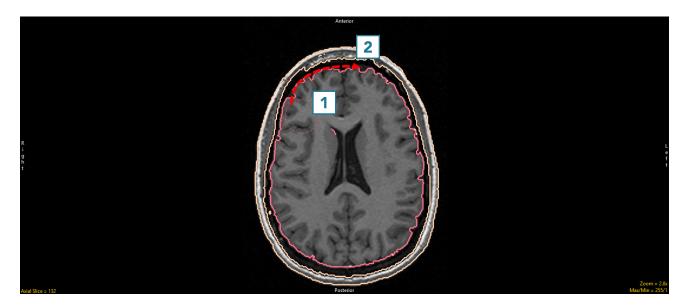
• The borders of the Brain and Ventricle objects will be updated as the cursor moves through [10].

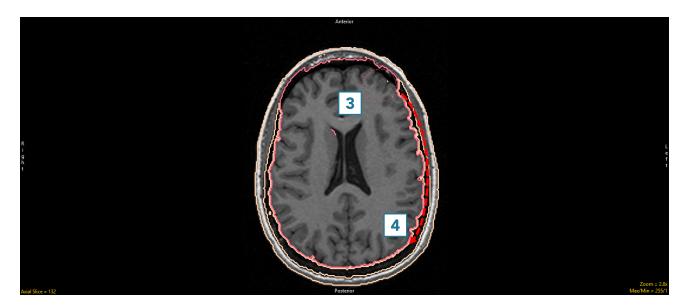


Using the Nudge Edit Tool with Locked Objects

The Nudge Edit Tool can also be used in conjunction with locked objects. When measuring the intracranial area on a certain slice, after reassigning the Ventricle object on this slice to the Brain object using Reassign Object, the Skin object can be locked and the brain object pushed out using the Nudge tool to the border of the skin object.

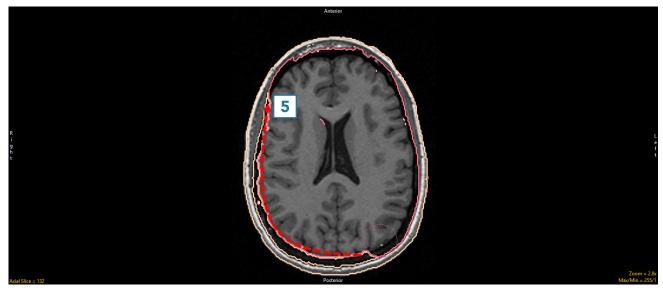
- Use Reassign Object to reassign the Ventricle object on Axial slice 132 to the Brain object.
- Lock the Skin object.
- Select the Nudge Edit tool.
- Click in the Brain [1] and move the Nudge Edit tool into the intracranial space [2] between the Brain and Skin objects.
- Note that the Brain object will be pushed into the intracranial space but not into the locked skin object [3].
- Continue moving the Nudge tool through the intracranial space [4].



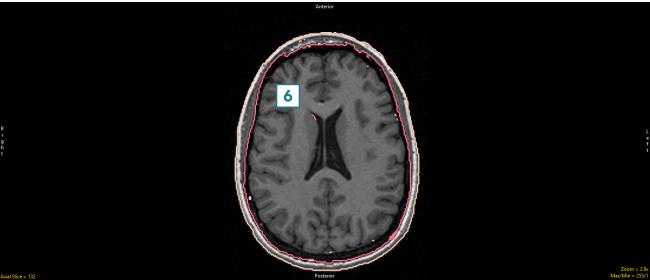


Using the Nudge Edit Tool with Locked Objects (continued)

 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 Edit 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.

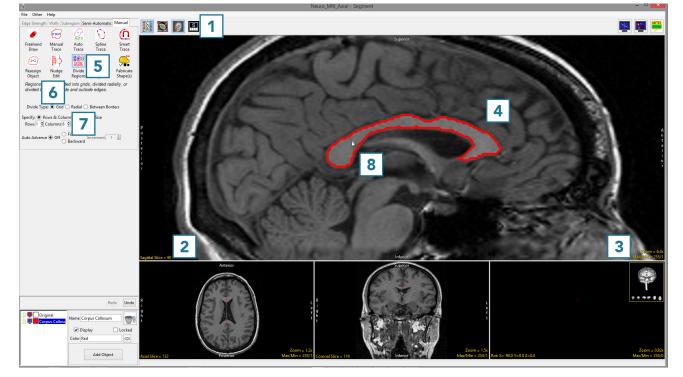
| Divide Type | Function | Example |
|-----------------|---|---------|
| Grid | Divides selected object into rectangles. Specify: Controls how the object will be divided by specifying between Rows and Columns or Region Size. Rows & Columns: specifies the number of rows and columns the object will be divided into. Region Size: specifies the size (in pixels) of the rectangle that will be used to divide the object. | |
| Radial | Radially divides selected object, splitting the object into pie wedges. Divisions: specifies the number of divisions the structure will be split into. Start Angle: specifies the starting angle of the first division. End Angle: disabled by default., but when enabled, specifies the ending angle for the radial division. | |
| Between Borders | Divides object into concentric shapes. Divisions: specifies the number of concentric divisions the structure will be split into between borders. Enter the number into the text entry box or use the arrow up/down keys to set number. | |

Grid Division of an Object

Grid division can be useful for subdividing structures into various anatomical substructures. Here we will perform a grid division of the corpus callosum (CC) on the mid-sagittal slice into its substructures.

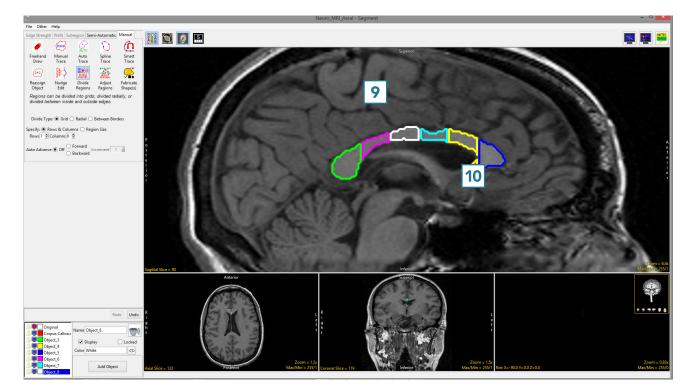
To follow along, download MRI_3D_Head from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the dataset 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].



Grid Division of an Object (continued)

- 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.

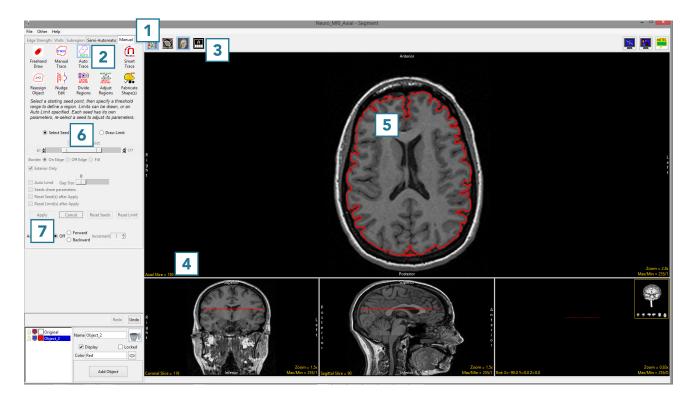


Radial Division of an Object

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

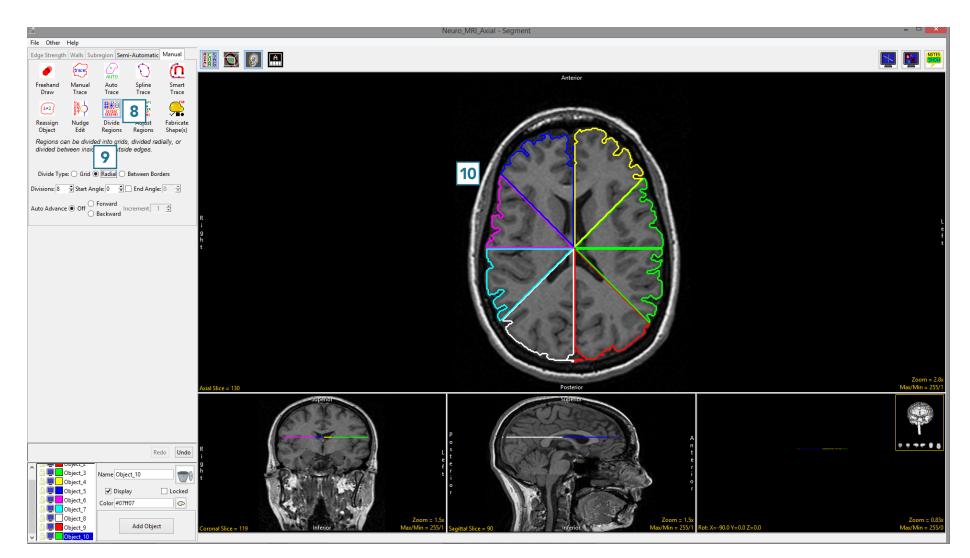
To follow along, download the data set MRI_3D_Head from analyzedirect.com/data and load into Analyze using Input/Output.

- 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.



Radial Division of an Object (continued)

- 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 – Interpolating Between Objects

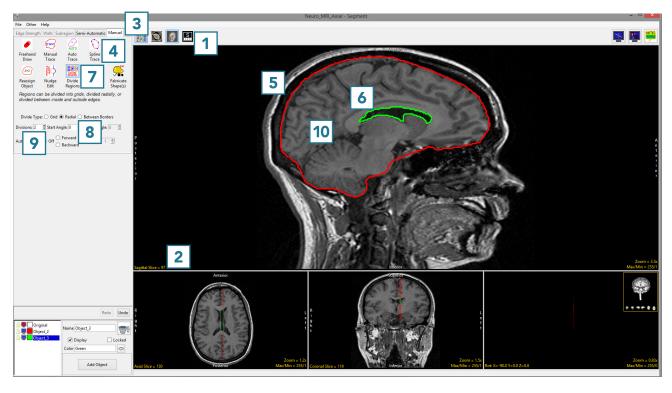
The Divide Regions Between Borders division type allows users to create a concentric set of objects. The tool will divide the area between an inner and outer border into the number of regions specified by the user, which is acheived by interpolating new borders between the inner and outer border.

To follow along, download the data set MRI_3D_Head from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the dataset 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].

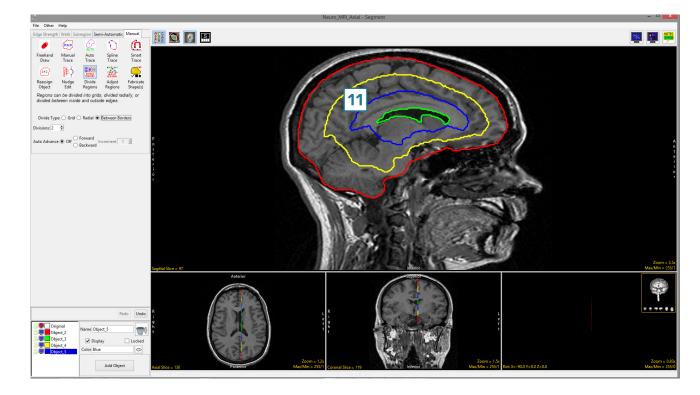
Analyze 15.0 User's Guide

• Click anywhere in the brain between the red brain border and the green ventricle border [10].



Dividing Regions Between Borders – Interpolating Between Objects (continued)

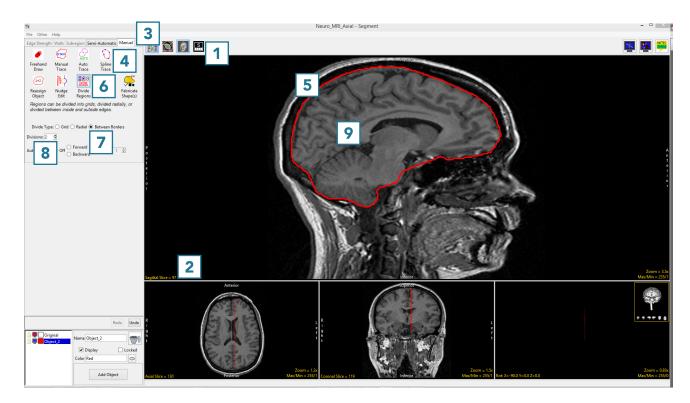
 2 new regions will be interpolated between the brain and ventricles [11].



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.

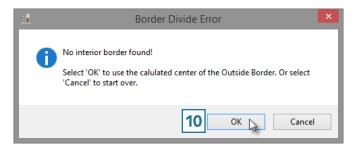
- Select MRI_3D_Head and open Segment.
- Set the primary display to Sagittal [1] and use Slice [2] to move to sagittal slice 96.
- Select Manual [3] and choose Spline [4].
- Use the Spline tool to define a region of interest around the brain [5].
- Select the Divide regions tool
 [6] and set the Divide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

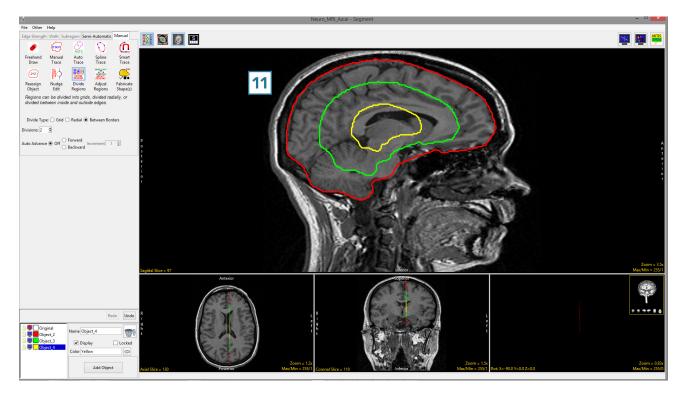


443

Dividing Regions Between Borders – Interpolating Within an Object (continued)

- 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. The adjust option provides users with the following region adjustment options:

Adjust Regions Methods and Functions

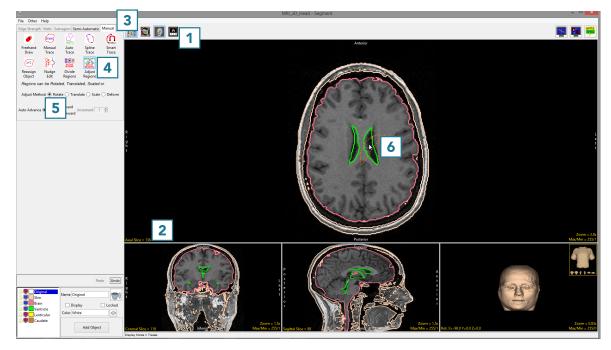
| Method | Function | | | | |
|-----------|---|--|--|--|--|
| Rotate | The Rotate option allows users to rotate a region. To rotate a region, left click on the region to select it, the region will be outlined with a dashed | | | | |
| | yellow and red line. With the left mouse button still pressed move the mouse up to rotate the region clockwise and down to rotate counterclockwise. | | | | |
| Translate | The Translate option allows users to translate a region left, right, up, or down. To translate a region, left click on the region to select it, the region will | | | | |
| | be outlined with a dashed yellow and red line. With the left mouse button still pressed move the mouse up, down, left, or right to move the region. | | | | |
| | The following options are also available for translate: | | | | |
| | With mouse movement: This is the default option and will allow the user to translate the selected region. | | | | |
| | A copy of the region: Allows users to translate a copy of the selected region. Choose from the following Copied Object options | | | | |
| | Same: Copied object is assigned to the same object as the selected object. | | | | |
| | Current: Copied object is assigned to the currently selected object from the object list. | | | | |
| | New: Copied object is assigned to a new object. | | | | |
| | Region so that its centered on brightest point: This option will shift the selected region so that the brightest pixel in the object is used as the new | | | | |
| | center point for the object. | | | | |
| Scale | The Scale option allows users to adjust the regions scale by increasing and decreasing it both horizontally and vertically. To scale a region, left click on | | | | |
| | the region to select it, the region will be outlined with a dashed yellow and red line. With the left mouse button still pressed move the mouse up and | | | | |
| | down to adjust the scale vertically or move the mouse left or right to adjust the scale horizontally. | | | | |
| Deform | The Deform option allows users to interactively deform regions. To apply a free transform deformation on a region, left click on the region to select it, | | | | |
| | the region will be outlined with a dashed yellow and red line. With the left mouse button still pressed move the mouse up or down and left or right to | | | | |
| | deform. | | | | |

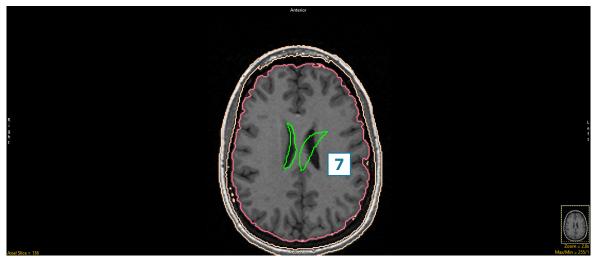
Using the Adjust Regions tool

Here we will rotate, translate, scale and deform objects using the Adjust Regions tool.

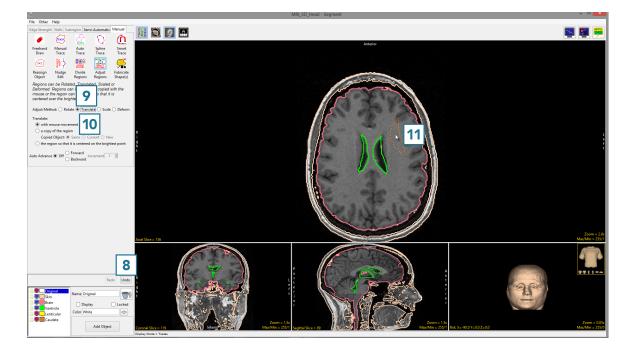
To follow along, download the data set MRI_3D_Head from analyzedirect.com/data and load into Analyze using Input/Output.

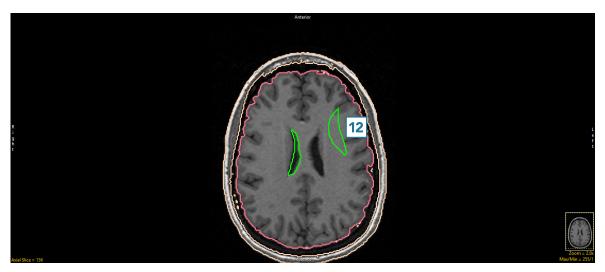
- Select the dataset and open Segment.
- Select File > Load Object Maps and load MRI_3D_Head.obj.
- Set the primary display to Axial [1] and move to Axial slice 136 [2].
- Select Manual [3] and choose Adjust Regions [4].
- Set the Adjust Method to Rotate [5].
- Click in an object to select it and move the mouse up or down to rotate the object [6].
- Release the mouse button to end the rotation and commit the rotation to the object [7].





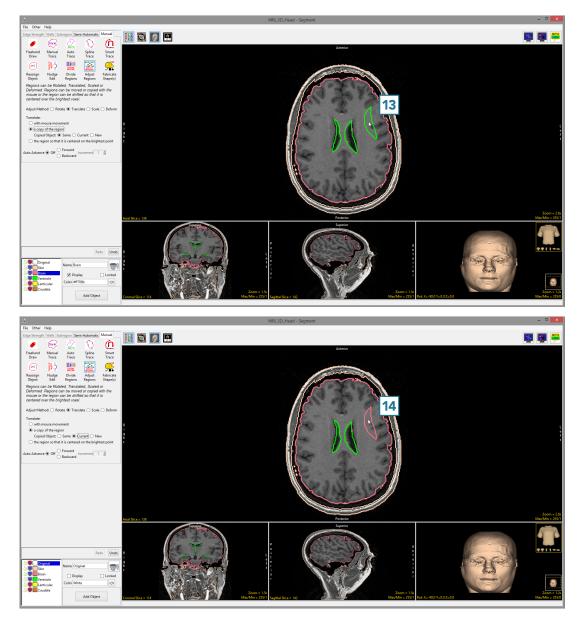
- Click Undo [8] and set the Adjust Method to Translate [9].
- With the Translate option set to with mouse movement [10], click in an object and drag to a new location [11].
- Release the mouse button to end the translation. The object will be moved to the new location [12].





- 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].

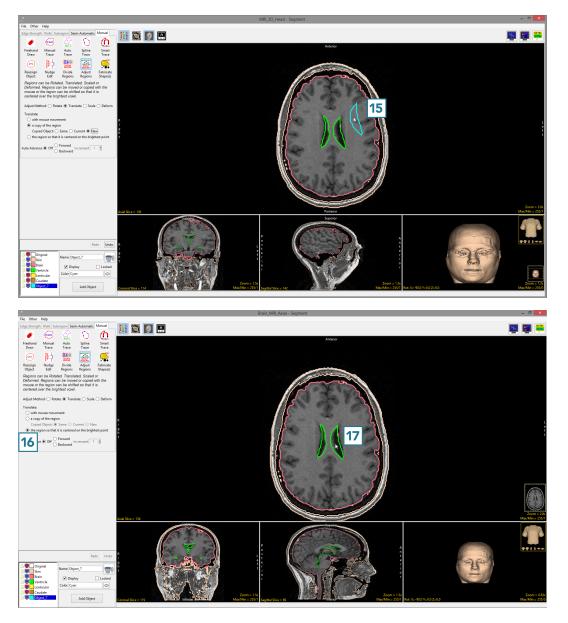
 Setting Copied Object to Current assigns voxels in the new region to the object currently selected in the Object Control window [14].



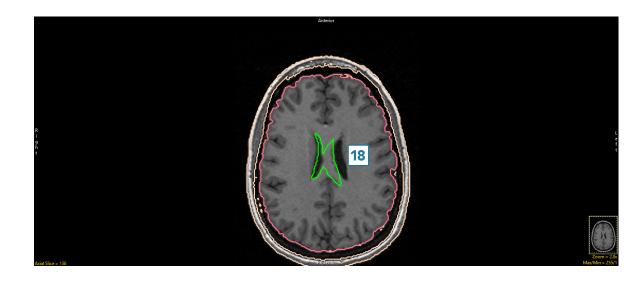
 Setting Copied Object to New assigns voxels in the new region to a new object [15].

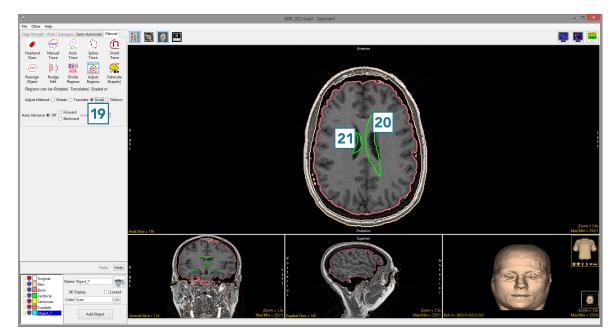
The Translate Adjust Method also allows users to Translate the region so that it is centered on the brightest point. With this option, the tool calculates the brightest pixel in the object and sets that as the the center of the object, translating the object appropriately.

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

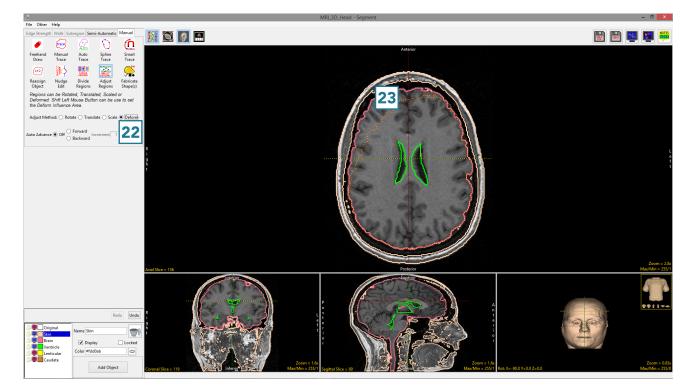


- The region will instantly be recentered around the brightest point in the object [18].
- Click Undo.
- Set the Adjust Method to Scale [19].
- Click in an object and move your mouse to increase the scale of the selected object [21].
- Moving the mouse up and down adjusts the scale in the vertical direction. 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 with 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.

The **Object to Create** option allow users to specify a set of parameters to create 2D or 3D objects within a data set.

Dimension: Allows users to choose to create a 2D or 3D object.

2-D: The following **Shape** options are available for 2D object creation:

Dot: The Dot option allows user to create a 1-pixel dot on any of the 2D images.

Square: The Square option allows users to create a 2D square on any of the 2D images.

Rectangle: The Rectangle option allows users to create a 2D rectangle on any of the 2D images.

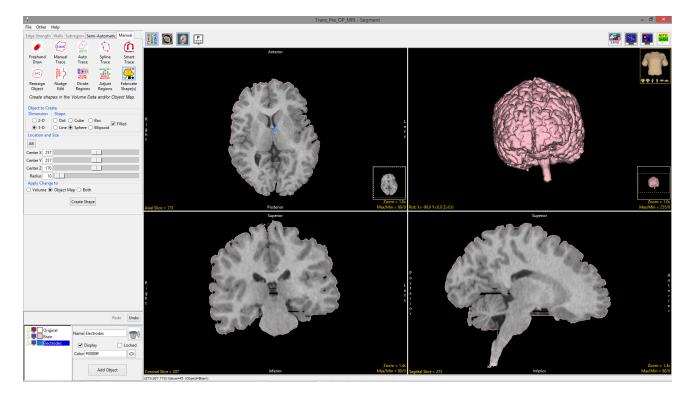
Line: The Line option allows users to create a 2D line on any of the 2D images.

Circle: The Circle option allows users to create a 2D circle on any of the 2D images.

Oval: The Oval option allows users to create a 2D oval on any of the 2D images.

Note the Filled option allows users to enable (default) or disable the application of a fill to the preview of the 2D region, the fill color will correspond to the color of the selected object. Fill is not available for Dot or Line shape options.

Analyze 15.0 User's Guide



Fabricate Shape(s) Options

Draw Slice: The Draw Slice options provide the ability to specify the orientation and slice the shape will be created on. Alternatively, the slice and orientation can be set by clicking on the desired slice in the desired orientation

- · 2-D Orient: Choose from Axial, Coronal, or Sagittal.
- · 2-D Slice: Use the slice slider or manually enter the slice number to create the object on for the selected orientation.

Location and Size: Provides the ability to specify the location and size of the shape being created. For any of the 2D shapes chosen (Dot, Square, Rectangle, Line, Circle, or Oval), the following shape dependent sub-options are enabled:

Dot Location and Size Options:

- Alt: Set the preferred way to define the size and location of the dot object. Press Alt to choose; pixels (default), real world distances, or X,Y coordinates (X,Y).
- X: Set the X location for the dot. Use the slider to set the value or manually enter the in the text entry box.
- Y: Set the Y location for the dot. Use the slider to set the value or manually enter the in the text entry box.

Square Location and Size Options:

- Alt: Set the preferred way to define the size and location of the square object. Press Alt to choose; pixels (default), real world distances, manually setting the X, Y coordinates for the lower left corner, using sliders to set the X, Y coordinates for the lower left corner, or manually setting the X, Y coordinates of the center of the square.
- · Center X: Set the X center location for the square. Use the slider to set the value or manually enter the in the text entry box.
- · Center Y: Set the Y center location for the square. Use the slider to set the value or manually enter the in the text entry box.
- Size: Set the size in pixels for the square. Use the slider to set the value or manually enter the in the text entry box. Alternatively, click on the square on the image and drag it to the desired size.

Object to Create > 2D > Location and Size (continued):

Rectangle Location and Size Options:

- Alt: Set the preferred way to define the size and location of the rectangle object. Press Alt to choose; pixels (default), real world distances, manually setting the lower left (X1, Y1) and upper right (X2, Y2) coordinates, using sliders to set X1, Y1, X2, and Y2, double-ended slides to specify the both the X and Y low and high values, or manually entering the lower left rectangle X and Y coordinates and the rectangle Width and Height values.
- · Center X: Set the X center location for the rectangle. Use the slider to set the value or manually enter the in the text entry box.
- · Center Y: Set the Y center location for the rectangle. Use the slider to set the value or manually enter the in the text entry box.
- Width: Set the width in pixels for the rectangle. Use the slider to set the value or manually enter the in the text entry box. Alternatively, select either vertical side of the rectangle on the image and drag it to the desired size.
- Height: Set the height in pixels for the rectangle. Use the slider to set the value or manually enter the in the text entry box. Alternatively, select either horizontal side of the rectangle on the image and drag it to the desired size.

Line Location and Size Options:

- Alt: Set the preferred way to define the size and location of the line object. Press Alt to choose; setting start X, Y and end X, Y points using sliders (default), double-ended sliders with pixel values, double-ended sliders with real world distances, or entering coordinates manually.
- Start X: Set the X start location for the line. Use the slider to set the value or manually enter the in the text entry box.
- Start Y: Set the Y start location for the line. Use the slider to set the value or manually enter the in the text entry box.
- End X: Set the X end location for the rectangle. Use the slider to set the value or manually enter the in the text entry box.
- · End Y: Set the Y end location for the rectangle. Use the slider to set the value or manually enter the in the text entry box.
- \cdot Note, users can also manually adjust the end points of the line and drag to the desired location.

Object to Create > 2D > Location and Size (continued):

Circle Location and Size Options:

- Alt: Set the preferred way to define the size and location of the circle object. Press Alt to choose; pixels (default), real world distances, or manually entering the center X, Y coordinates and circle radius.
- · Center X: Set the X center location for the circle. Use the slider to set the value or manually enter the in the text entry box.
- Center Y: Set the Y center location for the circle. Use the slider to set the value or manually enter the in the text entry box.
- Radius: Set the radius of the pixels for the circle. Use the slider to set the value or manually enter the in the text entry box.

Oval Location and Size Options:

- Alt: Set the preferred way to define the size and location of the oval object. Press Alt to choose; pixels (default), real world distances, manually entering the center X1, Y1 and X2, Y2 coordinates, using sliders to set the X1, Y1 and X2, Y2 coordinates, double-ended sliders to set both X/Y high/low values, or manually entering the lower left X and Y coordinates and the oval Width and Height
- · Center X: Set the X center location for the oval. Use the slider to set the value or manually enter the in the text entry box.
- · Center Y: Set the Y center location for the oval. Use the slider to set the value or manually enter the in the text entry box.
- Width: Set the width in pixels for the oval. Use the slider to set the value or manually enter the in the text entry box.
- Height: Set the height in pixels for the oval. Use the slider to set the value or manually enter the in the text entry box.

3-D: The following Shape options are available for 3D object creation:

Dot: The Dot option allows user to create a 1-pixel dot within the volume data.

Cube: The Cube option allows users to create a 3D cube within the volume data.

Box: The Box option allows users to create a 3D box within the volume data.

Line: The Line option allows users to create a 3D line within the volume data.

Sphere: The Sphere option allows users to create a sphere within the volume data.

Ellipsoid: The Ellipsoid option allows users to create an ellipsoid within the volume data.

Cylinder: The Cylinder option allows users to create a cylinder within the volume data.

Analyze 15.0 User's Guide

© AnalyzeDirect, Inc.

Object to Create > 3D (continued):

Note the Filled option allows users to enable (default) or disable the application of a fill to the preview of the 3D region, the fill color will correspond to the color of the selected object. Fill is not available for the Dot or Line shape options.

Location and Size: Provides the ability to specify the location and size of the shape being created. For any of the 3D shapes chosen (Dot, Cube, Box, Line, Sphere, or Ellipsoid), the following shape dependent sub-options are enabled:

Dot Location and Size Options:

- Alt: Set the preferred way to define the size and location of the dot object. Press Alt to choose; pixels (default), real world distances, text file input (see Creating Objects from a Text File for further information), or manually entering the X,Y, Z coordinates (X, Y, Z).
- X: Set the X location for the dot. Use the slider to set the value or manually enter the in the text entry box.
- Y: Set the Y location for the dot. Use the slider to set the value or manually enter the in the text entry box.
- · Z: Set the Z location for the dot. Use the slider to set the value or manually enter the in the text entry box.
- Note, users can click on any of the 2D images or the rendering to set the X, Y, Z coordinates for the dot.

Cube Location and Size Options:

- Alt: Set the preferred way to define the size and location of the cube object. Press Alt to choose; manually entering X, Y, Z center voxel coordinates and cube size (default), sliders to define the X, Y, Z, and size parameters of the cube, sliders with corresponding real world distances, text file input, or manually setting the X, Y, Z coordinates for the lower left front corner coordinate and cube size value.
- Center (X, Y, Z): Set the cube center voxel by entering the X, Y, Z coordinates of the center location for the cube. Alternatively, click and drag the 2D display of the cube in any orthogonal orientations to reposition.
- Size: Set the size in voxels for the square. Users can also click on the 2D display of the cube in any orientation and interactively increase or decrease the size of the cube in 3D.

Object to Create > 3D > Location and Size (continued):

Box Location and Size Options:

- Alt: Set the preferred way to define the size and location of the box object. Press Alt to choose; to use slides to enter X, Y, Z and Width, Height and Depth values in voxels for the box (default), manually entering X, Y, Z center and the box Width, Height and Depth values, using sliders to specify the X, Y, Z center values and Width, Height, and Depth values in real world coordinates, use a text file to specify the box parameters, manually specify the X1, Y1, Z1 and X2, Y2, and Z2 values to define the box, use sliders to determine the X1, Y1, Z1 and X2, Y2, and Z2 values, use double-ended sliders the X, Y, and Z upper and lower parameters, or manually enter coordinates for LX, LY, LZ and With, Height, and Depth values to define the box.
- Left (X): Set the X value for the box. Use the slider to set the value or manually enter the in the text entry box.
- Lower (Y): Set the Y value for the box. Use the slider to set the value or manually enter the in the text entry box.
- Front (Z): Set the Z value for the box. Use the slider to set the value or manually enter the in the text entry box.
- Width: Set the width value for the box. Use the slider to set the value or manually enter the in the text entry box.
- Height: Set the height value for the box. Use the slider to set the value or manually enter the in the text entry box.
- Depth: Set the depth value for the box. Use the slider to set the value or manually enter the in the text entry box.

Line Location and Size Options:

- Alt: Set the preferred way to define the size and location of the line object. Press Alt to choose; setting start X, Y, Z points for the line end points using double-ended slider bars, using double-ended slider bars mapped to real work distances, manually entering the XYZ coordinates for both end points, or using single sliders to specify the Start X, Start Y, Start Z, End X, End Y, and End Z coordinates.
- X, Y, Z Sliders: Use the double-ended slider bar to set the X, Y and Z values for each end point of the 3D line. Adjusting the lower end of the slider will adjust the X, Y or Z point location for the first end point of the line while adjusting the upper end of the slider will adjust the X, Y or Z point location for the second end point of the line.
- \cdot Note, line end point for the 3D line can be adjusted by selecting and moving the end points on any of the orthogonal images.

Object to Create > 3D > Location and Size (continued):

Sphere Location and Size Options:

- Alt: Set the preferred way to define the size and location of the sphere object. Press Alt to choose; to set sphere parameters in voxels using an X, Y, Z and Radius slider (default), to set sphere parameters in real world distances using an X, Y, Z and Radius slider (default), a text file to define a sphere(s), or manually enter the X, Y, Z and Radius parameters in voxels manually.
- · Center X: Set the X center location for the sphere. Use the slider to set the value or manually enter the in the text entry box.
- · Center Y: Set the Y center location for the sphere. Use the slider to set the value or manually enter the in the text entry box.
- Radius: Set the radius of the pixels for the sphere. Use the slider to set the value or manually enter the in the text entry box.

Ellipsoid Location and Size Options:

- Alt: Set the preferred way to define the size and location of the ellipsoid object. Press Alt to choose; to set ellipsoid parameters in voxels (default), real world distances, using a text file, manually entering the center X1, Y1, Z1 and X2, Y2, Z2 coordinates, using sliders to set the X1, Y1, Z1 and X2, Y2, Z2 coordinates, double-ended sliders to set both X, Y, and Z upper and lower values, or manually entering the lower left X, Y, Z coordinates and the ellipsoid Width, Height, and Depth values, use sliders to enter the X, Y, Z position information and Width, Height, and Depth values, or coordinates to specify the center X, Y, Z and values for ellipse Width, Height, and Depth.
- · Center X: Set the X center location for the ellipsoid. Use the slider to set the value or manually enter the in the text entry box.
- Center Y: Set the Y center location for the ellipsoid. Use the slider to set the value or manually enter the in the text entry box.
- · Center Z: Set the Z center location for the ellipsoid. Use the slider to set the value or manually enter the in the text entry box.
- Width: Set the width in pixels for the ellipsoid. Use the slider to set the value or manually enter the in the text entry box.
- Height: Set the height in pixels for the ellipsoid. Use the slider to set the value or manually enter the in the text entry box.
- · Depth: Set the depth in pixels for the ellipsoid. Use the slider to set the value or manually enter the in the text entry box.

Object to Create > 3D > Location and Size (continued):

Cylinder Location and Size Options:

- Alt: Set the preferred way to define the size and location of the cylinder object. Press Alt to choose; to set cylinder parameters in voxels (default), use real world distances, to use a text file, to manually entering the center X, Y, Z coordinates and input the radius and length values, or use sliders to input the Center X, Y, Z, Radius, and Length values.
- · Center X: Set the X center location for the cylinder. Use the slider to set the value or manually enter the in the text entry box.
- · Center Y: Set the Y center location for the cylinder. Use the slider to set the value or manually enter the in the text entry box.
- · Center Z: Set the Z center location for the cylinder. Use the slider to set the value or manually enter the in the text entry box.
- Radius: Set the radius in pixels for the cylinder. Use the slider to set the value or manually enter the in the text entry box.
- · Length: Set the length in pixels for the cylinder. Use the slider to set the value or manually enter the in the text entry box.
- · Axis: Choose which axis; X, Y, or Z (default) to orientate the length of the cylinder.

Apply changes to: Allows users to select the image volume, the object map, or both to defined the fabricated shape(s).

Volume: Applies the fabricated object to the grayscale image data.

- Set Volume Voxels to: Choose to assign greyscale voxel values as user defined Specified value, a Random Value, or a Gaussian Value.
 - · Specified value: Allows users to select a greyscale value that all voxels within the fabricated shape will be assigned to.
 - · Random Value: Assigns voxel values within the fabricated shape to editable random values from 1 to 255.
 - Gaussian Value: Assigns voxel values within the fabricated shape to a Gaussian Value. Default Mu and Sigma values are assigned at 128.0 and 25.6 respectively but can be updated by the user.
- **Object Map:** Allows users to assign the fabricated shape to the selected object in the object list.
- **Both:** Applies fabricated shape to both the Volume and Object Map (see above).

Create Shape: Initiates the Fabrication process.

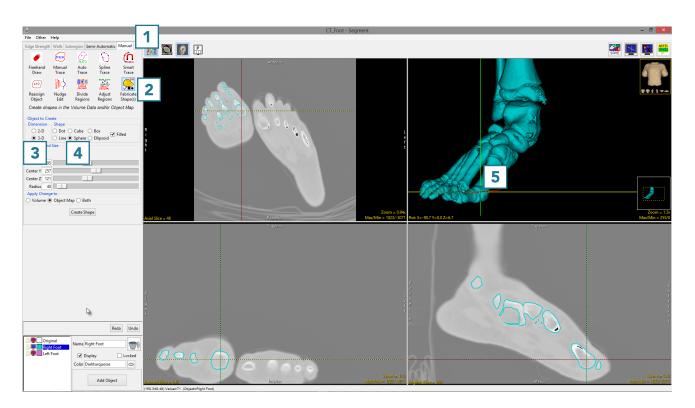
Analyze 15.0 User's Guide

Using Fabricate Shape(s)

Here we will use the Fabricate Shape(s) tool to create a 3D shape in a volume.

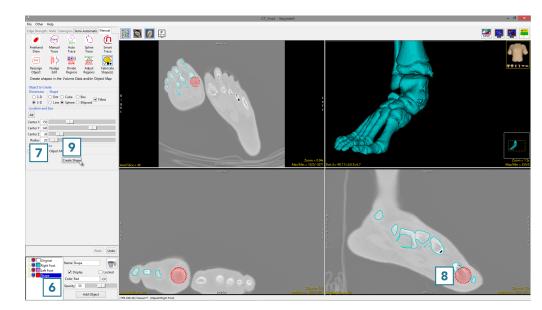
To follow along, download the data set CT_Foot from analyzedirect.com/ data and load into Analyze using Input/Output.

- Select the data set 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].

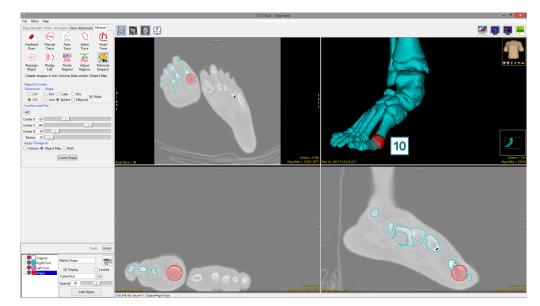


Using Fabricate Shape(s) (continued)

- 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. Rightclick on the rendering and select Transparency for a clearer view of the object in 3D [10].

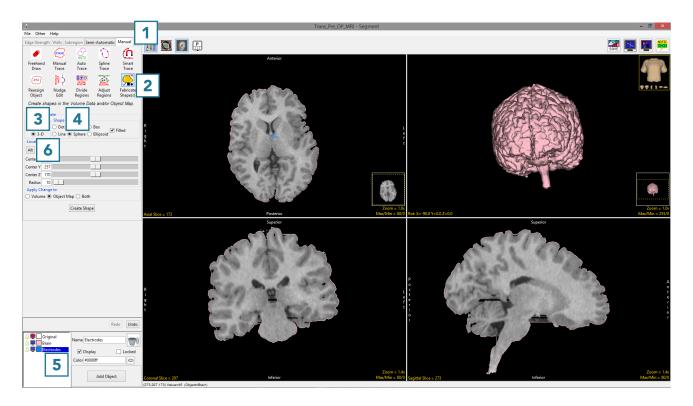


Creating Objects from a Text File using Fabricate Shape(s)

Here we will show how Fabricate Shape(s) can create objects defined in a text file.

To follow along, download the data set Trans_Pre_OP_MRI from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the data set 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.

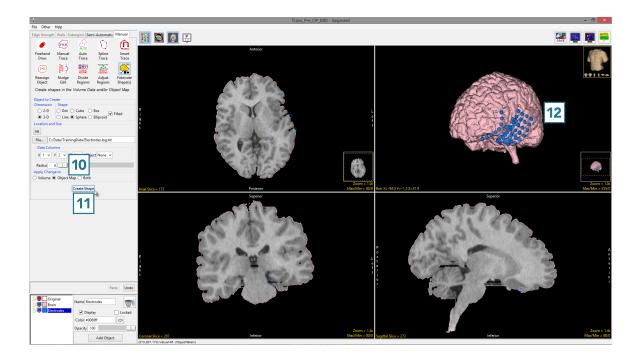


Creating Objects from a Text File using Fabricate Shape(s) (continued)

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

| 21 | | | | Fabricate | | | | × |
|---------------|----------------|-------------------|--------------------|--------------------|---------------|------|---|--------|
| Look in: | 📗 TrainingData | | ~ | G 🌶 📂 🖽 - | | | | |
| æ | Name | ^ | | Date modified | Туре | Size | | |
| 2 | | I_Multivolume | 10/3/2007 11:22 PM | Text Document | 1 KB | | | |
| Recent places | Electrode | is.log 8 | | 5/14/2015 11:09 AM | Text Document | 1 KB | | |
| | | | | | | | | |
| Desktop | | | | | | | | |
| <u></u> | | | | | | | | |
| Libraries | | | | | | | | |
| Libraries | | | | | | | | |
| | | | | | | | | |
| This PC | | | | | | | | |
| | | | | | | | | |
| | | | | | | | | 9 |
| Network | File name: | Electrodes.log | | | | | ~ | Open N |
| | Files of type: | Text File (*.txt) | 7 | | | | ~ | Cancel |
| | | row rise (1042) | | | | _ | • | |

- 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.

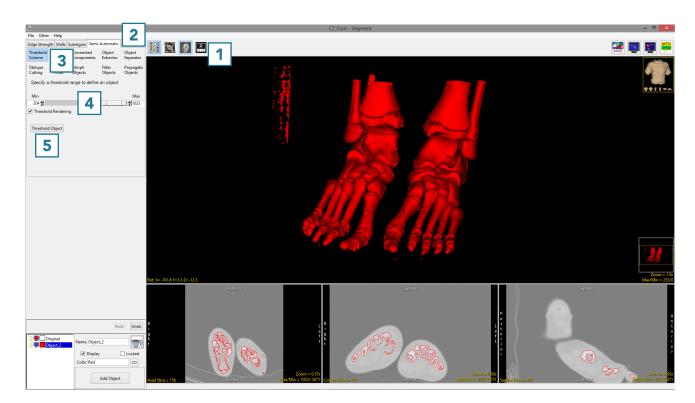


Manual Tools for 3D Editing

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.

To follow along, download the data set CT_Foot from analyzedirect.com/ data and load into Analyze using Input/Output.

- Select the data set 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].

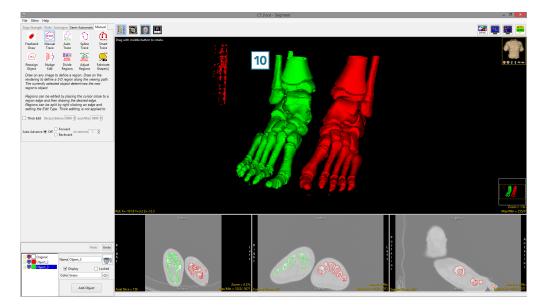


Manual Tools for 3D Editing (continued)

- 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].

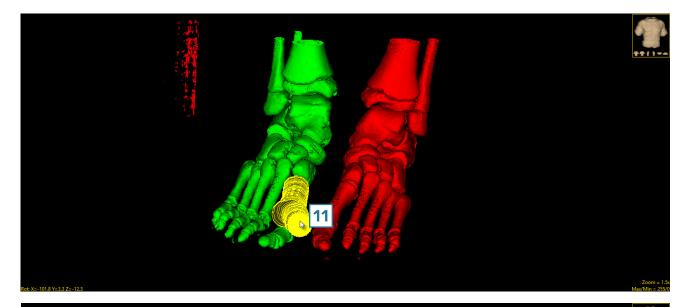


 Complete the trace and release the left mouse button. All voxels not assigned to the Original object within the trace will be assigned to the selected object [9].

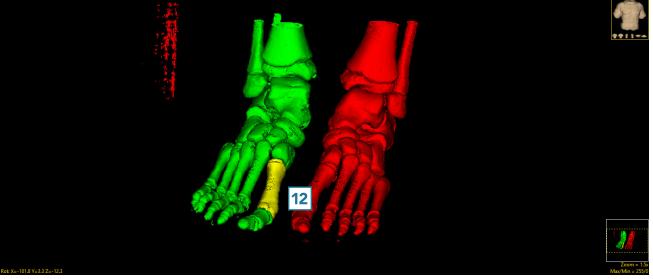


Manual Tools for 3D Editing (continued)

- Add a new object.
- Select the Freehand Draw trace and trace over one of the bones in the right foot [11].



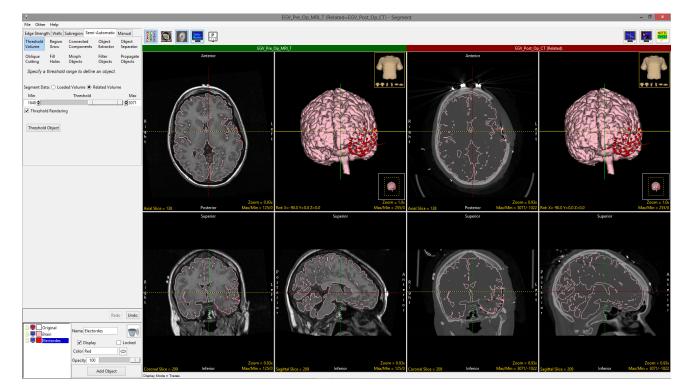
• Everything under the region will be assigned to the selected object [12].



Dual Input Segmentation

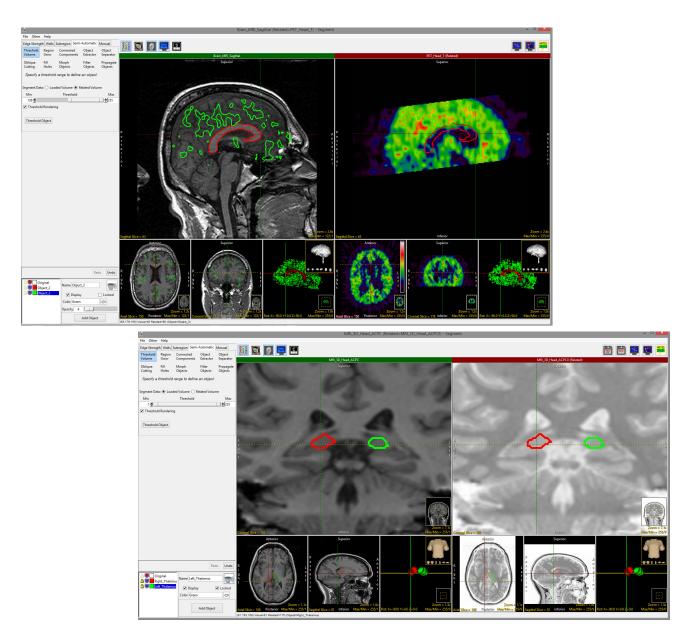
Segment allows users to load two registered input data sets. The ability to load related volumes is powerful and allows users to segment structures from either data set.

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



Dual Input Segmentation (continued)

 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.

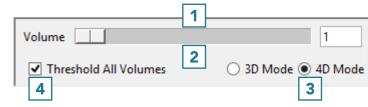


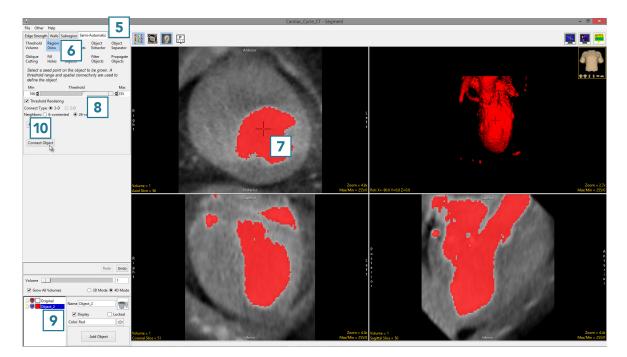
 Loading two copies of the same input data set allows users to adjust or invert intensity display values on the related volume. This can be leveraged to assist with the segmentation of brain structures such as the thalamus.

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. To follow along, download the multivolume data set 4D_Cardiac_CT.avw from analyzedirect.com/ data and load into Analyze using Input/Output.

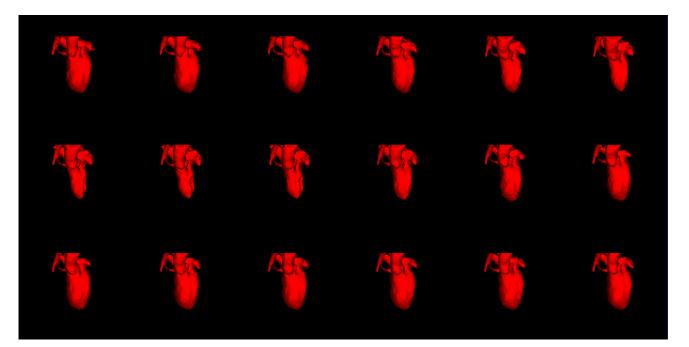
- Select the multivolume data set and open Segment.
- A Volume control window will be available above the object control window [1].
- The slider [2] allows users to navigate through the 3D volumes in the multivolume.
- The window also provides the user with options to create a 3D or 4D object map [3]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





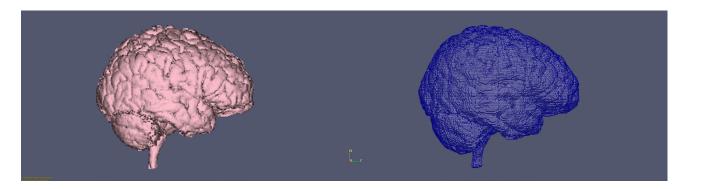
4D Segmentation (continued)

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

Surface generation offers users the ability to create and export surface files for 3D printing, additive manufacturing, and CAD applications. There is a fundamental transformation that needs to take place between the voxel-based volume image world and an explicit surface description file, for which Analyze provides several helpful algorithms.



Analyze provides the ability to efficiently and accurately extract and represent a surface from a specific object of interest, exporting this surface in several common surface description formats including STL (see table for a list of supported surface formats).

| Format | Extension |
|-----------------------------|-----------|
| Alias Wavefront | .obj |
| Autocad | .dxf |
| Compressed IGES | .iges |
| IGES | .iges |
| Inventor | .iv |
| Patran | .out |
| Ply | .ply |
| Poly | .poly |
| 3D Systems | .stl |
| Binary 3D Systems (default) | .stl |
| VRML | .wrl |

The key to surface generation is to use Analyze to accomplish a segmentation of the particular structure of interest from the volume image data, using any of the available tools provided with Segment, and then use the segmented object to drive the surface extraction process for the optimal definition and output of the surface data.

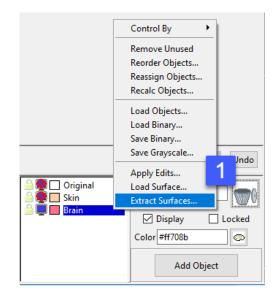
Analyze 15.0 User's Guide

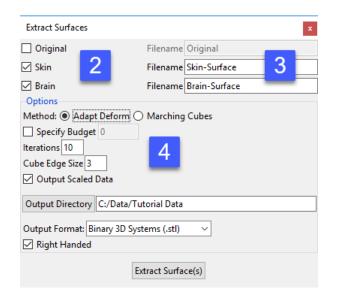
Surface Generation Options

The Segment module provides the mechanism to extract a surface description of segmented objects from volume image data via two unique Analyze-specific algorithms; Adapt Deform or Marching Cubes. Both Adapt Deform and Marching Cubes extract an optimal description of the surface with as few polygons as possible. Once extracted, the surface can be saved in many common surface description formats and imported into third party 3D printing program, CAD software, or rapid prototyping equipment.

Extract Surface: The Extract Surface window provides users with the interface to generate surface files. To access the window right click in the Object List and choose Extract Surface [1]. The following options are available:

- **Object:** The Object selection area allows users to select objects to generate surfaces for [2]. Note that multiple objects can be selected, each object will be exported to its own surface file. If users wish to combine objects in a single surface file objects either need to be combined prior to surface extraction using the Reassign Object function or combination needs to be conducted after export using a third-party application.
- **Filename:** Surface file names are specified in the Filename field. [3] This field becomes available once an object is selected.
- **Options:** The Options area allows users to specify the surface extraction method for surface generation. When a method is selected method specific options become available. User can choose between Adapt Deform and Marching Cubes:
 - Adapt Deform: The Adapt Deform algorithm (enabled by default) [4] specifies that the adaptive deformation algorithm will be used to generate the tiled surface.





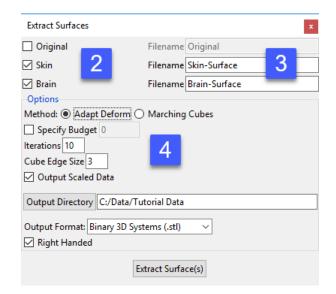
Surface Generation Options (continued)

- Options (continued)
 - Adapt Deform (continued): This algorithm is based on an adaptive mesh model; a discrete dynamic system constructed from a set of nodal masses that are interconnected by adjustable springs. This system is governed by a set of ordinary differential equations of motion (discrete Lagrange equations) that allow the system to evolve to equilibrium.

In the mass-spring model, the set of coupled equations are solved iteratively in time to update the position of the nodal masses until the masses reach an equilibrium position. For the purposes of surface reconstruction, the equilibrium positions of the nodal masses will approximate the surface of the object. The initial positions of the nodal masses are determined by creating a rough approximation of the surface using a surface tracking technique. A cubic grouping element is used to create a lower resolution version of the data set, which is then systematically triangulated to form the initial approximation of the surface. The following options are available:

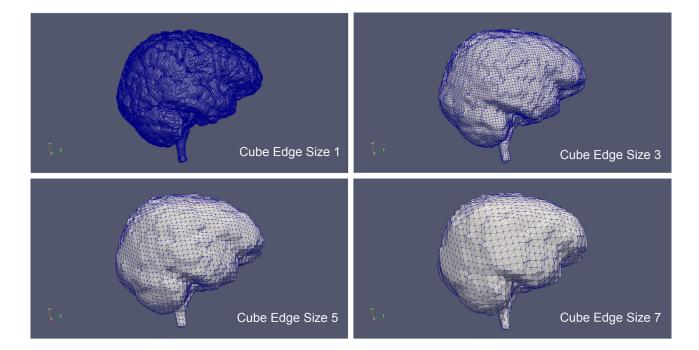
· Specify Budget: Allows users to specify the maximum number of polygons in the final surface.

- **Iterations:** Iterations allows the user to specify the number of iterations of the deformation process. While there are a maximum number of iterations beyond which there will be little or no improvement in the quality of the final surface, that point is highly dependent on the data.
- **Cube Edge Size:** The Cube Edge Size option allows users to adjust the length (in voxels) of a side the initial cubic grouping element. This grouping element is used to form the initial surface approximation. If the polygonal budget is set to 0, then smaller cubes will result in higher resolution surfaces, otherwise cube size should be inversely related to the polygonal budget in order to reduce the number of iterations required to reach equilibrium (small polygonal budgets require large cube sizes).



Surface Generation Options (continued)

- Options (continued)
 - Adapt Deform (continued): The effects of changing the cube edge size on the resulting surface can be seen in this image. The larger the cube edge size the smoother the generated surface is. Note, increasing the resolution (reducing cube edge size) increases the processing time and this is demonstrated by setting the 'Cube Edge Size' to '1'.

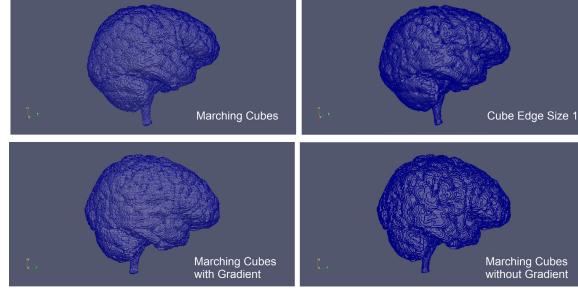


- In cases where a high resolution (Cube Edge Size of 1) is required, it is recommended that users use the Marching Cubes algorithm.
- Marching Cubes: The Marching Cubes option [5] specifies that the marching cubes algorithm will be used to generate the tiled surface. The algorithm processes the data in scan line order and calculates the polygonal vertices using linear interpolation.

| Extract Surfaces | | x |
|--|-------------|---------------|
| Original | Filename | Original |
| 🗹 Skin | Filename | Skin-Surface |
| 🗹 Brain | Filename | Brain-Surface |
| Method: O Adapt Deform Use Gradient Output Scaled Data | Marching | Cubes 5 |
| Output Directory C:/Data/Tut | torial Data | |
| Output Format: Binary 3D Syst ☑ Right Handed | ems (.stl) | ~ |
| Ext | tract Surfa | ce(s) |

Surface Generation Options (continued)

- Options (continued)
 - Marching Cubes (continued): As discussed in Adapt Deform if a surface file of the exact segmented object (a cube edge size of 1) is required, then Marching Cubes should be used. This will provide an accurate surface description, in a smaller file, in a fraction of the time of Adapt Deform.
 - Use Gradient: The Use Gradient option is enabled (checked) by default.
 - Checked: When enabled the algorithm will use the gradient information present in the voxel data to estimate surface position. This results in a smooth surface that may have a higher error estimate than the equivalent binary surface extraction.
 - Unchecked: When enabled the algorithm will ignore gradient information and generate a surface based on binary thresholding. This will produce a "voxelated" surface that minimizes the error between voxel surface and the reconstructed polygonal surface.
 - **Output Scaled Data:** When selected will scale the surface file into real world coordinates. When the surface coordinates will be scaled from voxel dimensions in the header information of the data to real world dimensions. This requires the VoxelWidth, VoxelHeight, and VoxelDepth parameters be set correctly in the volume's header information.
 - Output Directory: Allows users to specify the location where the generated surface files will be saved to.
 - · Output Format: Allows users to specify the format the generated surface files will be saved in (see previous table for formats)
 - **Right-handed:** For both the Adapt Deform and Marching Cubes extraction processes the surface files created will have a 3D lefthanded coordinate system. Checking the right-handed option will flip the surface file to a right-handed coordinate system.
 - Extract Surface(s): Initiates the surface generation and export routine. When completed a dialog box will be returned.



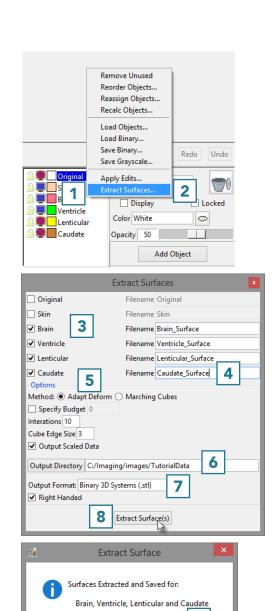
Generating Surface Files from a Selection of Objects

Here we will generate several surface files at once from objects we have previously segmented and which are contained in an object map.

To follow along, download the data set MRI_3D_Head from analyzedirect.com/data and load into Analyze using Input/Output.

- Select the data set 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].
- 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 confirming that the selected surfaces have been generated and saved. Click OK [9] to close the window.

The generated surfaces can now be retrieved from the output directory and used in other third party applications such as 3D printing, additive manufacturing, or computer aided design.



9 ок

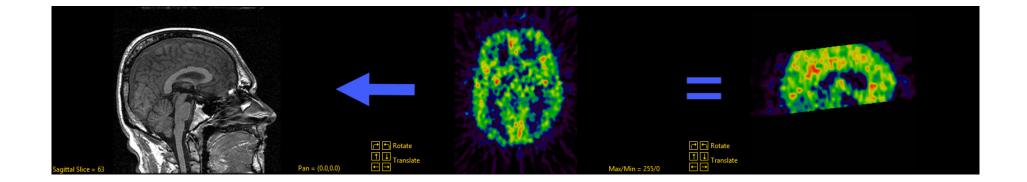
Register

| Introduction | page 478 |
|---|----------|
| Image Registration | page 478 |
| Image Fusion | page 479 |
| Transformation | page 479 |
| Register Volume Interface | page 480 |
| Menu | page 480 |
| Tools | page 484 |
| Display Area | page 484 |
| Registration Controls | page 495 |
| Registration Controls > 2D | page 498 |
| Registration Controls > 3D | page 507 |
| 3D Registration - Surface Alignment | page 514 |
| 3D Registration - Mutual Information | page 519 |
| Troubleshooting Registration Problems | page 521 |
| Not enough overlapping information between input data sets | page 522 |
| Background or artifact noise | page 524 |
| Adjusting the sample region to include or exclude regions in the match data | page 525 |

Introduction

Image Registration

The goal of image registration is to determine a spatial transformation that will bring into alignment separately acquired images of the same object. When accurately registered, each separate image will have the same coordinate system and same voxel size, a voxel in one image will represent the same physical location as the corresponding voxel in the other image. The registration process interpolates the registered images as they are resampled and/or reformatted during the registration process. For example, registration of an axial PET data set to a sagittal MRI data set results in the PET data being transformed (resampled and reformatted) into the sagittal MRI space.

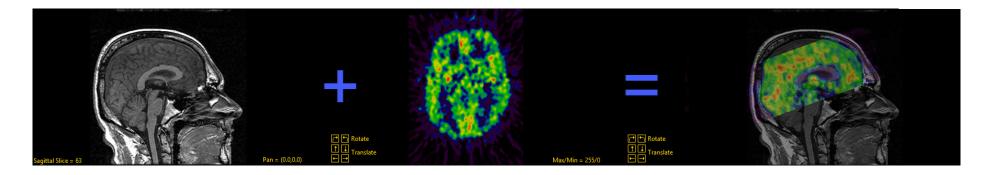


Registration is a prerequisite for several applications including; the display, segmentation, and analysis of structural and functional data, algebraic manipulation of image data (image addition, subtraction, multiplication, and division), the analysis of dynamic image data, and the fusion of data from multiple images.

Introduction (continued)

Image Fusion

Image fusion is the process of combining, into one image, the information from multiple registered images. For example, the registration of an axial PET to a sagittal MRI allows for the transformed PET image data to be superimposed upon the sagittal MRI and output as a single fused volume illustrating both structure and function.



Transformation

Transformation is the process of changing a match data set to align with the base data set using the parameters calculated during registration, these parameters include; translation, rotation, scaling, and shear.

Translation: A translation moves data to a different position. A 2D image can be moved left, right, up or down. A 3D volume can be moved left, right, up, down, backwards or forwards.

Rotation: Rotation rotates the data at a particular angle from its origin.

Scaling: Scaling changes the size of a data set. Scaling either expands or compresses the dimensions of the image data.

Shear: Shearing, sometimes referred to as skewing, is a transformation that slants the shape of the data.

Analyze 15.0 User's Guide

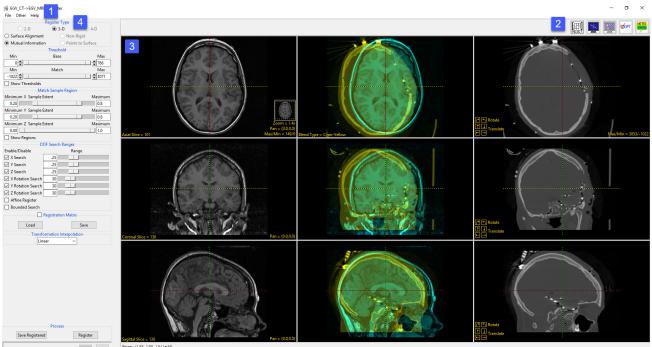
Register Module Interface

The register module is divided into several areas: 1) the menu, 2) tools, 3) the display area, and 4) the registration controls.

Menu

File: The File menu allows users to load the base and match data, load and save transformed object maps, and save transformed match data. The File options include:

 Input/Output: Displays a Volume area at the bottom of the Register module window. This area facilitates the dragging and dropping of image data into the module and the reversing of inputs via the Swap Inputs button.



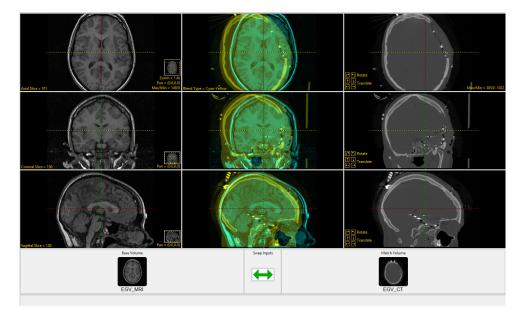
Base: (130,130,101)=39 Match: (211.34, 211.34, 140.34)=39.56

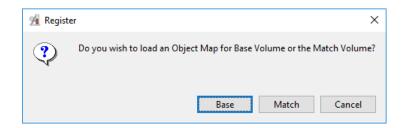
Menu (Continued)

File >Input/Output (continued):

Tip: Swapping inputs is useful when you register a match data set to a base data but need the base data set transformed into the space of the match data set. This situation can arise when you are unable to register image A to image B, but are able to register image B to image A.

- Load Object Map: Allows users to load an object map for the Base and/or Match volume. When selected a window will be returned prompting the user to specify which volume the object map should be loaded for. There is also the option to cancel the object map load. Once Base or Match is selected a Load Object Map window will open allowing users to navigate to, select, and load an object map file. The following options are available:
 - **Current Directory:** Takes user to the current directory, the current directory is set by rightclicking in the main Analyze 15.0 window and then choosing Current Directory from the menu.
 - **Workspace Directory:** Takes user to the current Workspace directory.
 - **Home Directory:** Takes user to the user's Home directory.
 - **Cancel Load:** Cancels load of the object map.





Menu (Continued)

File (continued):

- **Unload Object Map:** Allows users to unload the Base, Match, or both object maps. Users also have the option to cancel the object map unloading process.
- **Save Registered:** The Save Registered option allows users to save the transformed match data set, the fused image data, or the transformed match object map only available if a match object map was loaded.

When the Save Object Map option is selected users will be prompted to save the object map or cancel the save. When Save Object Map is selected a new window will open providing users with the option to overwrite the loaded object map (Yes) or to save as a new object map (No, I want to specify a name and location).

• **Exit:** Closes the module

Other: The other menu provides access to the Options and Powerbar editor menus.

Other > Options: When selected opens the Options menu providing access to Module configuration options, including:

- Intensities Linked: Allows users to enable or disable linked intensity adjustment. When linked any adjustment an images intensity display will be applied to all grayscale slices displayed. When disabled image intensities can be adjusted individually.
- Linked Pan: Allows users to enable (default) or disable linked image panning. Note that linked panning only applies to the current row of images. Disabling linked pan allows you to pan a single image at a time.

| ~ | r | |
|-----------------|--|---|
| | Base Match Both Cancel | |
| | | |
| | Save Registered × | |
| | Save Type: Transformed Fused Object Map | |
| | Workspace Main 🗸 | |
| | File EGV_CT_T | |
| | Save Transformed Cancel | |
| | | |
| | | |
| 🕺 Save ObjectMa | p - Register | × |
| You are | e sure you want to overwrite 'C:/Data/EGV/EGV_CT.obj'? | |
| | Ver No I want to sperify name and location Cancel | |

Do you wish to unload the Base Object Map, Match Object Map or Both?

頬 Register

?

Х

Menu (Continued)

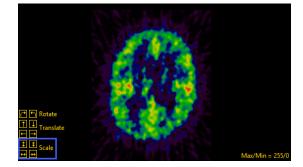
Other > Options (continued):

- Linked Zoom: Allows users to enable or disable linked zooming. The following options are available:
 - Both: Both is the default option, when selected any zoom in/out on an image is applied to all images for both input data sets.
 - · Row: Allows zooming to be applied to the current row of images.
 - · Column: Allows zooming to be applied to the current column of images.
- Linked Blend: The linked blend option allows for the enabling (default) and disabling of the same blend type to be applied to all fused images in the center column. Keep enabled if you wish to apply the same blend option to all fused images, disable if you wish to apply different blend options to the fused images.
- Adjust Scale: Allows users to enable or disable (default) the scale tool for the match data allowing for interactive image scaling.
- Auto Note Update: Allows the Auto Note Update option to be enabled or disabled.
- **Threads:** Allows users to specify the number of threads used in a multi-threaded rendering process. By default, the number of threads is set to the number of processors on the system.

Other > Powerbar Editor: Provides access to the Powerbar Editor allowing users to add and remove tools from the tools area. See the Powerbar Editor description in the Segment section for further information.

Help: The Help menu provides users with quick access to help resources including:

- **About:** View version, system and environment information.
- Users Guide: Opens the Analyze 15.0 User's Guide.
- **Get Help:** Opens the AnalyzeDirect Support Page.



Analyze 15.0 User's Guide

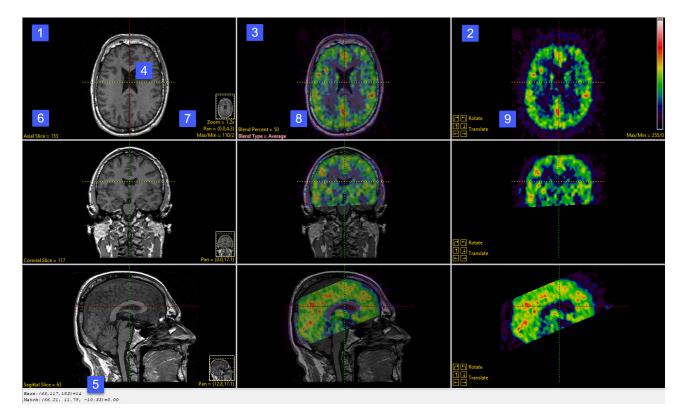
Tools

The Tools options provide access to the Toggle Cursor Link, Toggle Region Display and the Set Note State tools. For further information on these tools please refer to section 2. Image Display, Controls and Customization.

Reset Matrix: The reset matrix tool is unique to Register and allows users to reset the match data sets matrix at any time. To reset the match registration matrix simply click the Reset Matrix button.

Display Area

The Register display area consists of; 1) the base image display, 2) the match image display, 3) the fused image display, 4) the linked cursor tool, 5) linked cursor coordinates, 6) slice display tool, 7) image display controls, 8) blend type options, and 9) manual registration tools.



Display Area: The Register module display area is a nine-panel display divided into three columns and three rows; each column displays a different data set while each row displays a different orientation. The first column [1] displays the base data set, the third column [2] displays the match dataset, while the middle column [3] displays a fused image - a blended combination of the base and match data. The top row displays all three image data sets (base, fused, and match) in the axial orientation, the middle row displays all three data sets in the coronal orientation, and the bottom row displays all three data sets in the sagittal orientation.

The Cursor Link: The cursor link [4] allows users to interactively navigate through the input image data. The cursor linked tool can by adjusted in any of the nine display panels interactively updating all nine simultaneously. The linked cursor coordinates as well as the voxel intensity value for both the base and match volumes are displayed in the lower left-hand corner. [5] The cursor link can be enabled or disabled using the Toggle Cursor Link button.

The Slice Tool: Users can navigate through image slices using the slice tool. Click the yellow Slice text in the lower left-hand corner of the base axial, [6] coronal, or sagittal image display. 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.

Image Display Controls: Register provides users with access to the Zoom, Pan, and Max/Min tools [7].

Zoom Tool: Users can increase and decrease the display size of the data using ٠ the Zoom tool. Click on the yellow Zoom text in the bottom right corner of the

Pan = (0.0, 0.0)

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. For a full description of the Zoom tool including right mouse menu options please refer to the Zoom tool in Section 2. Image Display, Controls and Customization.

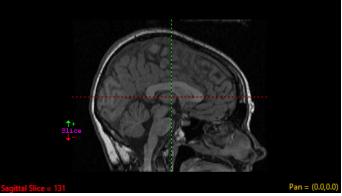
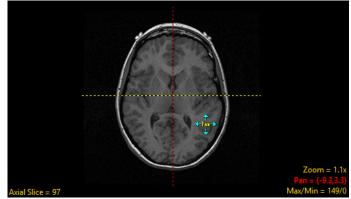
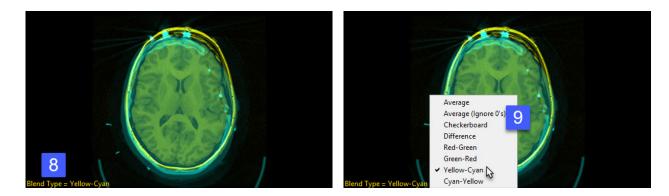


Image Display Controls > Zoom Tools (Continued): Note: Linked Zooming can be disabled, enabled, or enabled for just columns or rows. See the Other > Options menu description above for additional information.

- **The Pan tool:** The Pan tool is automatically enabled in Register. Click on the yellow Pan text in the bottom right corner of the axial, sagittal, or coronal base images. A pan cursor will be displayed. While clicking and holding the move the cursor to pan the image. Panning is linked for the selected row, to pan the current image only disable Linked Pan in the Other > Options menu for additional information see the Other > Options menu description above.
- Max/Min tool: The Max and Min display intensities of the base data set can be changed by clicking on the yellow Max/Min Tool at the bottom right corner of the axial base 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 to adjust the display. To change the intensity display of the match data, click on the yellow Max/Min Tool at the bottom right corner of the match image window. For a complete description on how to how values are changed with the Max/Min tool please Section 2. Image Display, Controls and Customization.



Blend Type Options: The blend type in the lower left-hand corner of the fused axial image [8] can be used to adjust the blended composition of the fused image. To adjust the blend type, left click on the yellow Blend Type text to toggle through the blend type options, alternately, right click on the yellow Blend Type text and choose a blend type from the menu [9].

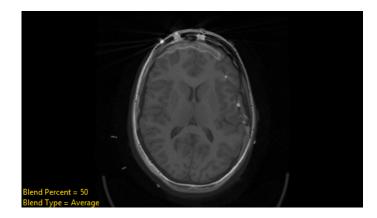


Blend Type Options (continued):

Blend type adjustment is helpful for the visual assessment and verifications of registration, especially when the base and match images are both grayscale [10]. Blend Type = Average

The following blend types are available:

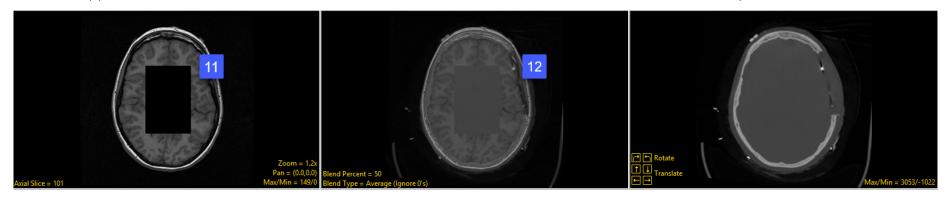
- **Average:** The Average blend option linearly interpolates the base and match images to form the fused image.
 - Blend Percent: The blend percent option is available when the Average blend type option is selected. The blend percent allows users to adjust the percent of the Base image used in the interpolation to form the fused image. The default blend percent is 50, lowering the percentage will lower the amount the base image displayed in the fused image, higher the percentage will increase the amount of the base image displayed in the fused image. Double-click on the yellow Blend Percent text to enter a percent value or right-click and choose a value from the menu.



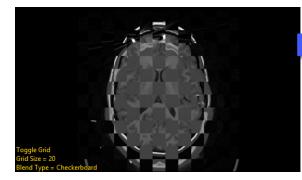
• Average (Ignore 0's): Like the Average blend option the Average (Ignore 0's) option linearly interpolates the base and match images to form the fused image, however, voxels with a value of 0 in the base image are not included when creating the fused image.

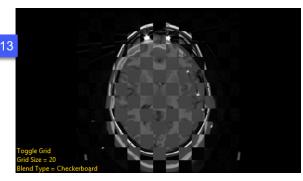
Blend Type Options > Average (Ignore 0's) (continued):

In the example here, a rectangular region has been removed from the base image and the voxel values set to 0 [11]. Instead of a black rectangle appearing in the fused image, these voxels are ignored and the voxels from the match image are displayed [12].



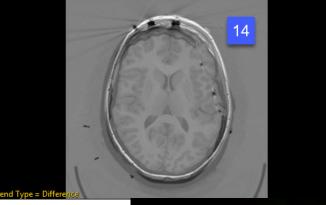
- **Blend Percent:** The blend percent option for the Average (Ignore 0's) blend options works and functions the same as the blend percent option for the Average blend option.
- **Checkerboard:** This function depicts the base and match volumes in a checkerboard pattern. The following options are available:
 - $\cdot\,$ Grid Size: Allows users to specify the size of squares used to create the checkerboard grid.
 - Toggle Grid: Switches the base and match volume inputs for the checkerboard squares [13].

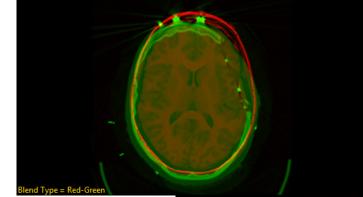


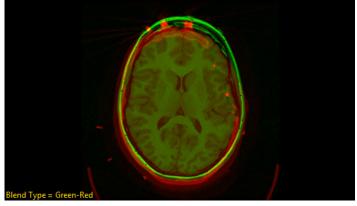


Blend Type Options (continued):

- **Difference:** The difference option subtracts the base volume from the match, directly showing the difference between volumes [14].
- Red-Green: The red-green blend option applies a red color overlay to the base volume and green color overlay to the match volume. Color blending is useful when the two volumes are both grayscale or from the same modality.
- **Green-Red:** The green-red blend option applies a green color overlay to the base volume and red color overlay to the match volume.



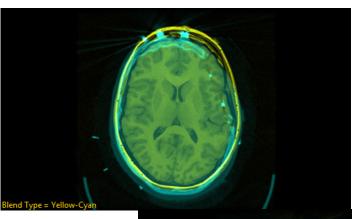


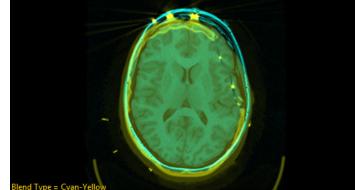


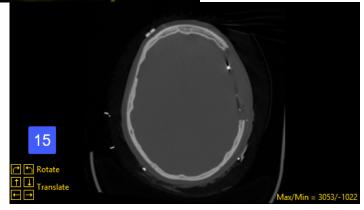
Blend Type Options (continued):

- Yellow-Cyan: The yellow-cyan blend option applies a yellow color overlay to the base volume and cyan color overlay to the match volume.
- **Cyan-Yellow:** The cyan-yellow blend option applies a cyan color overlay to the base volume and yellow color overlay to the match volume.

Manual Registration Tools: The manual registration tools [15] allow users to adjust the position of the match data set by translating or rotating the data in the axial, coronal, and sagittal orientations. When enabled users are also able to scale the match data manually in all orientations.

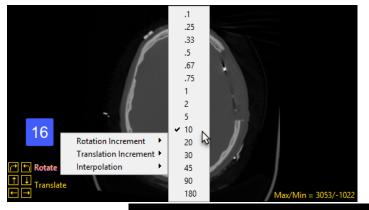


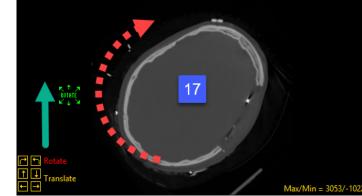


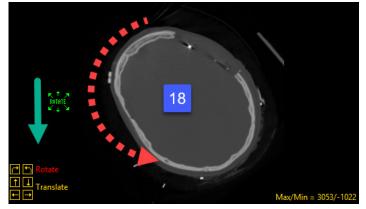


Manual Registration Tools (continued):

- Rotate: The rotate buttons allow users to incrementally rotate the image data clockwise or counterclockwise relative to the selected orientation. Left click either rotate button to rotate the data in that direction.
 - Rotate increment: The default number of pixels rotated at a time is 10, to adjust the number of degrees for each rotation left click on the yellow Rotate text and then choose Rotation Increment and then select for the options available [16].
 - Rotating with the mouse: Left click on the yellow Rotate text and a Rotate cursor will be displayed.
 While clicking and holding the left mouse button, move the mouse upward to rotate clockwise
 [17] and downward to rotate counterclockwise [18].



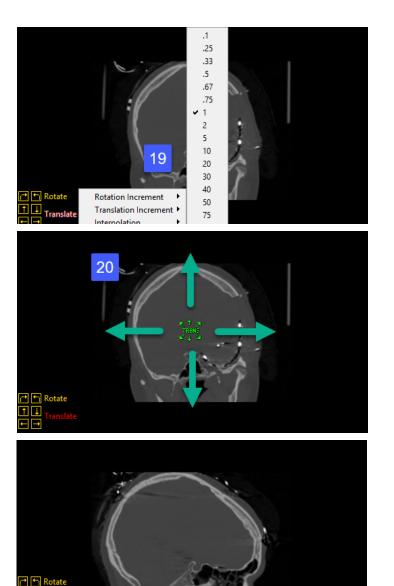




© AnalyzeDirect, Inc.

Manual Registration Tools (continued):

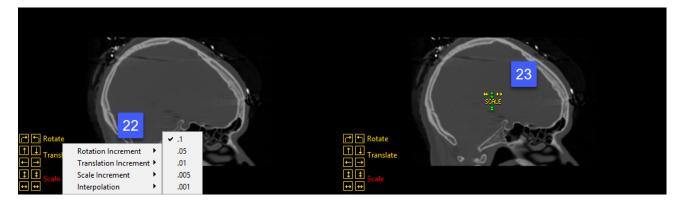
- **Translate:** The translate buttons allow users to incrementally translate the image data up or down or to the left or right, relative to the selected orientation. Left click any of the four translate buttons to translate the data in that direction.
 - Translate increment: The default number of pixels translated at a time is 1.
 To adjust the number of pixels for each translation left click on the yellow
 Translate text and then choose Translation Increment and then select for
 the options available [19].
 - Translating with the mouse: Left click on the image or click on the yellow Translate text and a Translate cursor will be displayed. Translation will mimic the movement of the mouse: while clicking and holding the left mouse button, move the mouse forward to translate the image up, backwards to translate the image down, right to move the translate the image right, and left to translate the image left [20]. Note, translation from the left mouse button is enabled by default, allowing translation of the match image data by clicking on it and moving the cursor. To disable this option right click in any of the Match display windows and uncheck the Left Drag to Translate option.
- Scale: The scale tools are not enabled by default; they can be enabled from the Other > Options menu. The scale buttons [21] allow users to incrementally translate the image data up or down or to the left or right, relative to the selected orientation. Left click any of the four translate buttons to translate the data in that direction.

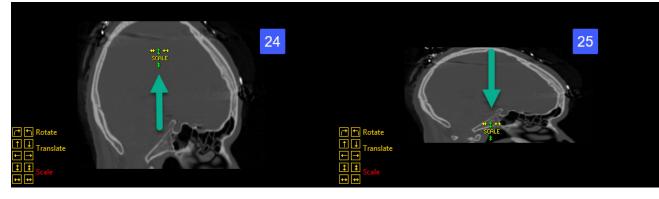


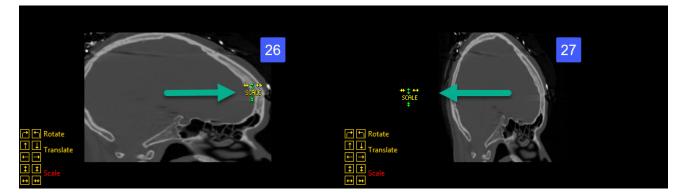
Manual Registration Tools > Scale (continued):

- Scale increment: To adjust the scale increment left click on the yellow Scale text and then choose Scale Increment (only available when scale is enabled) and then select for the options available [22].
- Scaling data with the mouse: To scale using your mouse, left click on yellow Scale text and a Scale cursor will be displayed [23]. While clicking and holding the left mouse button, move the mouse forward to increase the vertical scale [24], move the mouse backwards to decrease the vertical scale [25].

Move the cursor to the right to increase the horizontal scale [26], left to decrease the horizontal scale [27].



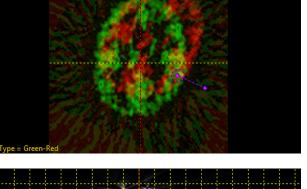


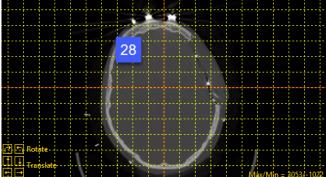


Manual Registration Tools Right Click Options: Right clicking on the manual registration tools provides access to the Rotation, Translation, and Scale Increment adjustment options. The right menu also provides access to an Interpolation option allowing users to select the following interpolation options for manual manipulation of the data; Nearest Neighbor, Linear, Bicubic (default), and Windowed Sync.

Display Area Right Mouse Options: The following additional options are available from the right mouse menu in the Register display area. Note that the options available depend on the column selected (Base, Fused, Match). The options include:

- Middle Button Action: Sets the action of the middle mouse button.
- **Rotate @ Point:** Only available in the Register module, this option allows users to select a specific point to use to rotate the match input around.
- Mouse While Action: Sets the action of the middle mouse wheel.
- · Copy to Clipboard: Copies the current slice display to memory.
- **Isotropic:** Active only for anisotropic data. Allows users to toggle between an isotropic or anisotropic display of the data.
- · Rotation Increment: Allows users to adjust the rotation increment (see Rotate Increment).
- · Translate Increment: Allows users to adjust the translation increment (see Translate Increment).
- · Scale Increment: Available when Scale is enabled. Allows users to adjust the scale increment (see Scale Increment).
- Matrix: The matrix option allows users to: *Load* a matrix file (*.mat file) for the match data set; *Save* the current matrix file; or *Reset*: the matrix file, selecting from Axial, Coronal, or Sagittal.
- Alignment Grid: When selected a grid displays over the current image providing a reference aid for match data realignment [28].
- Left Drag to Translate: Translation from the left mouse button is enabled by default, allowing users to translate the match image data by clicking on it and moving the cursor. To disable uncheck the option.
- · Reset: Resets all options to default. This option does not reset the matrix.





Registration Controls

The Registration Controls are found in the left hand column of the Register Module Interface.

Register Type

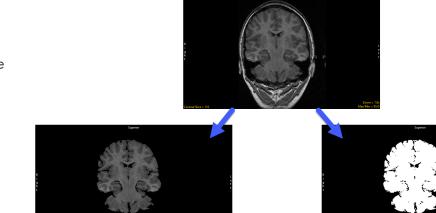
Register Type indicates the current dimensionality mode; 2-D, 3-D, or 4-D. This is set automatically by Register and is dependent upon the data selected. Choosing two single 2D slices or a single 3D volume will open the Register in 2-D mode, selecting two 3D volumes will open Register in 3-D mode. Note, if multivolumes are selected, additional volume controls became available under 3-D mode. See Volumes for additional information. The Register algorithm is selectable and users can choose between Surface Alignment or Mutual Information.

Surface Alignment

Surface alignment, also referred to as surface matching, is a geometry-based registration method. Surface alignment is fast and robust, even in the presence of image noise and incomplete overlap of the input image volumes.

Surface alignment tries to maximize the overlap between corresponding surfaces extracted from two image inputs. To use surface alignment both input volumes must contain common objects which need be explicitly segmented from the grayscale image data, for example the brain from an MRI data set saved as either a grayscale or binary image prior to use in Register.

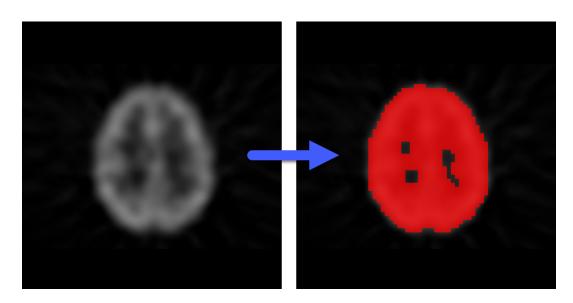
Alternatively, if the object is segmentable via thresholding (e.g. the brain from a SPECT image,) a surface can be defined interactively within Register using the threshold controls.



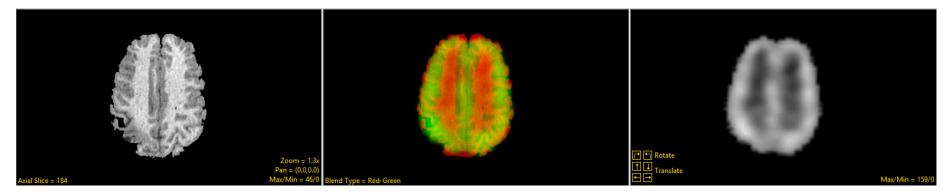
| 🕺 EGV_CT->EGV_MR | 1 | er | |
|--------------------|-----------|----------------|-----------|
| File Other Help | | | |
| | Register | Туре 4 | |
| 🔾 2-D | ۲ | I-D |) 4-D |
| Surface Alignment | i - | O Non-Rigid | |
| Mutual Information | n | O Points to Su | rface |
| | Thresh | old | |
| Min | Bas | e | Max |
| 0 🖨 💷 | | | 766 |
| Min | Mate | ch | Max |
| -1022 🖨 📃 | | | _] 🚔 3071 |
| Show Thresholds | | | |
| | | le Region | |
| Minimum X Sample | extent | | Maximum |
| 0.20 | | | 0.8 |
| Minimum Y Sample | extent | - | Maximum |
| 0.20 | | | 0.8 |
| Minimum Z Sample | extent | | Maximum |
| 0.00 | | | 1.0 |
| Show Regions | | | |
| | OF Search | - | |
| Enable/Disable | | Range | |
| X Search | .25 | | |
| Y Search | .25 | | |
| Z Search | .25 | | |
| X Rotation Search | 30 | | |
| V Rotation Search | 30 | | |
| Z Rotation Search | 30 | | |
| Affine Register | | | |
| Bounded Search | | | |
| | | | |

A surface is extracted from both the base object (base image) and the match object (match image). The base object is used to create a chamfer distance volume. This is a volume in which each voxel has a value equal to the number of single-voxel steps from that coordinate to the nearest point on the base surface. Surface points are defined as any non-zero-valued voxel with at least one zero-valued orthogonal neighbor in 3-D space.

For the match object surface points are defined as any non-zero-valued pixel with at least one



zero-valued orthogonal neighbor within the same slice. To evaluate the error at any orientation, the coordinates of the selected 'match surface' points are transformed into the space of the base image, and the chamfer volume voxel values at those coordinates are summed. If all the match surface coordinates land on the base surface, the sum is zero. The minima search algorithm is a variant of simulated annealing which searches for minima at randomly determined multiple starting orientations, researching promising minima at successively higher resolution until a best minima is found.



Analyze 15.0 User's Guide

Mutual information registration is proven to be effective for registering image data from different modalities. Mutual information seeks to align voxels whose values have common probabilities of being present in their respective image sets.

There are two components of the registration paradigm in Analyze:

1. The cost function used as the metric to judge when the volumes are in register.

2. The multiresolution search strategy used to find the global optimum of the cost function.

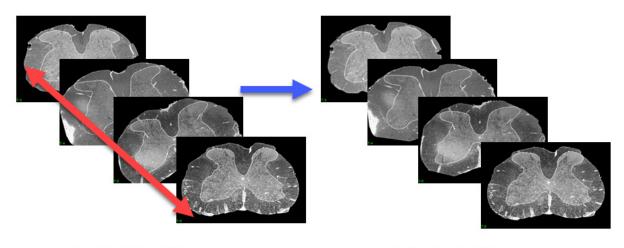
The mutual Information cost function is based on the individual and joint entropy measured from the voxel values in the base and match volumes. There needs to be enough overlap and mutually shared signal from common structures for a relationship to be found between the two volumes and for them to be successfully coregistered.

The mutual information algorithm determines the geometric transformation parameters used to spatially register the input data. The transformation parameters include both translation and rotation and scaling and shearing if enabled. The parameters are output in a homogeneous 4x4 matrix file. Image registration is achieved by transforming a volume using the transformation matrix.

| ment mation The olds Match S mple Extent mple Extent mple Extent s DOF Se | O Po reshold Base Match ample Reg t | 4 on-Rigid oints to Su jion | 4-D urface Max ↑ 766 Max ↑ 3071 Maximu 0.8 Maximu 0.8 Maximu 0.8 |
|--|---|---|---|
| ment mation The olds Match S mple Extent mple Extent mple Extent s DOF Se | 3-D N N Pc rreshold Base Match t t t | on-Rigid pints to Su | Max → 766 Max → 3071 Maximu 0.8 Maximu 0.8 Maximu |
| ment mation Th olds Match S mple Exten i mple Exten s DOF Se | NII Peareshold Base Match ample Reg t t | pints to Su | Max → 766 Max → 3071 Maximu 0.8 Maximu 0.8 Maximu |
| mation The olds Match S nple Exten nple Exten s DOF Se | O Pc areshold Base Match ample Rec t | pints to Su | Max |
| The second secon | meshold Base Match ample Reg t t | | Max |
| olds Match S nple Exten nple Exten nple Exten s DOF Se | Base Match ample Reg t t | gion | ➡ 766 Max ➡ 3071 ➡ 3071 ■ Maximu 0.8 Maximu 0.8 Maximu |
| olds Match S nple Exten i nple Exten s DOF Se | Match ample Reg t t | gion | ➡ 766 Max ➡ 3071 ➡ 3071 ■ Maximu 0.8 Maximu 0.8 Maximu |
| olds Match S nple Exten i nple Exten s DOF Se | ample Reg t t | gion | Max 3071 Maximu 0.8 Maximu 0.8 Maximu |
| olds Match S nple Exten i nple Exten s DOF Se | ample Reg t t | gion | Maximu 0.8 Maximu 0.8 Maximu 0.8 Maximu |
| Match S nple Extent nple Extent nple Extent s DOF Se | t t | gion | Maximu 0.8 Maximu 0.8 Maximu |
| Match S nple Extent nple Extent nple Extent s DOF Se | t t | gion | 0.8 Maximu 0.8 Maximu |
| nple Exteni I nple Exteni s DOF Se | t t | | 0.8 Maximu 0.8 Maximu |
| nple Exteni nple Exteni s DOF Se | t t | | 0.8 Maximu 0.8 Maximu |
| nple Exteni nple Exteni s DOF Se | t | | Maximu 0.8 Maximu |
| nple Exten s DOF Se | t | | 0.8 Maximu |
| nple Exten s DOF Se | | | Maximu |
| s DOF Se | | | |
| DOF Se | arch Rang | | |
| DOF Se | arch Rang | | 1.0 |
| | earch Kang | | |
| | | jes Range | |
| | 25 | Kange | |
| | 25 | | |
| | 25 | | |
| | _ | | |
| | _ | | |
| | | | |
| | 30 | | |
| | | | |
| rch | | | |
| - Regis | tration M | atrix | |
| 4 | | Save | |
| | | | - |
| | tion Interp | olation | |
| Linear | | ~ | |
| | earch er er rrch Regis | earch 30 er earch 30 er rch Registration M d ransformation Interp | earch 30 |

Registration Controls > 2D

2D registration determines the geometric transformation parameters to be used to align 2D images, slice-by-slice or matching a series of slices to a single base slice.



Unregistered stack of 2D images

Registered stack of 2D images

The following options are enabled/available with 2D registration:

2-D: The 2-D dimension mode is enabled when two 2D slices or a single 3D volume are loaded into Register.

Surface Alignment: Enables surface matching registration. The following options are available:

- **Threshold:** The Threshold double-ended slider bars for both the Base and Match data allows the end user to specify a range of threshold values to isolate common surfaces between the input images. Note, if common surfaces are not segmentable via thresholding the input data will need to be segmented prior to registration.
 - Base: The base threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slide for the base input data.

2-D > Surface Alignment > Threshold (continued):

- Match: The match threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slide for the match input data.
- Show Thresholds: When enabled displays a filled preview of the minimum/maximum threshold value set for base and match input data.

Registration Matrix: When enabled displays the 4 by 4 transformation matrix.

- Load: Load a matrix file (*.mat file) for the match data set.
- **Save:** Save the current matrix file.

Transformation Interpolation: The transformation interpolation option allows users to specify the interpolation type to be used when transforming the match data set. Users can choose from:

- **Nearest Neighbor:** Allows users to select the nearest neighbor option for interpolation. Nearest Neighbor works by selecting the value of the closest voxel to which the interpolation resampling maps. This interpolation option is generally the fastest of the four available interpolation options.
- Linear: Allows users to select the linear option for interpolation. The linear algorithm applies a linear interpolation of grayscale intensity based on the distance of neighboring voxels from the interpolated voxel.
- **Bicubic:** Bicubic is the default interpolation option. The Bicubic option uses a cubic spline function to determine interpolated value, resulting in a smoother image that preserves detail.
- Windowed Sinc: Allows users to select the Windowed Sinc option for interpolation. The algorithm uses the windowed sinc function sin(x)/x to determine the interpolated value.

Slices: This option is only available when a single 3D volume is selected for input for 2D registration. The slices sliders allow users to navigate through the base and match inputs.

- **Base:** The base slider controls the display of the base slice. This will also be the 2D slice used for registration.
- **Match:** The match slider controls the display of the match slice. This will be the slice registered to the base for single Matrix and Single Reference registration. See Process and Registration mode for information on other registration options.

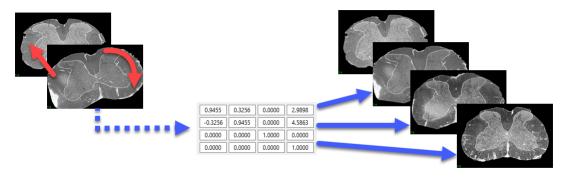
Process: The process controls allow users to register and save registration result, the following options are available.

- Save Registered: Allows users to save the transformed match image, the fused image, or the transformed object map (if applicable). See File > Save Registered at the being of this module section for a full description of the save options.
- **Register:** Initiates the slice-to-slice registration.
- **Register Pairs:** Only available when a single 3D volume is loaded. The register pairs option registered the current match slice to the current base slice. To adjust the select of the base or match slice input use the Slices sliders.
- Match Range: Only available when a single 3D volume is loaded. The match range slider allows users to specify a range of 2D match images to be registered to the base image.

Register Mode: Only available when a single 3D volume is loaded. The registration mode allows users to select from the following options:

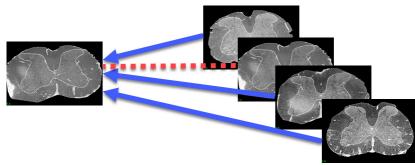
• **Single Matrix:** The single matrix option applies the transformation matrix created when registering the currently displayed match data set to the displayed base data to the range of match images selected using the match range slider. All images in the match range are transformed to the same single matrix.

Register Mode > Single Matrix (continued):



Single Matrix - the same transformation matrix is applied to all slices.

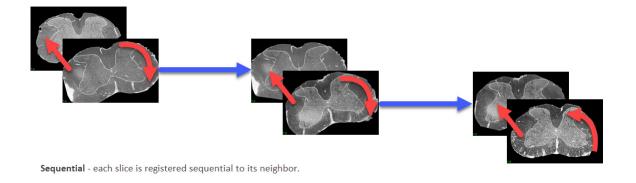
• **Single Reference:** The single reference option registers each of the match images specified in the match range, individually to the base image.



Single Reference - each slice is registered to a single base slice.

Register Mode (continued):

• **Sequential:** Performs a sequential match image to base image registration within the specified match range. For example, match image 2 to base image 1, then match image 3 to based image 2, etc.



• **Register Sequence:** Only available for the single reference and sequential register modes. When selected initiates registration.

Redo: Reverses your last undo action. Redo is only available after using Undo.

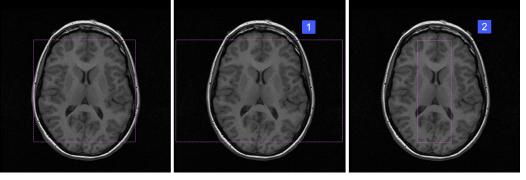
Undo: Reverses you last action. Can reverse more than one action.

Mutual Information enables mutual information-based registration. The following options are available:

- **Threshold:** The Threshold double-ended slider bars for both the Base and Match data allows the end user to specify a range of threshold values to consider for registration. The use of thresholding with mutual information-based registration is normally to remove background noise, artifact from implants, or other ranges of greyscale values from the data that could interfere with registration.
 - Base: The base threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slide for the base input data.
 - Match: The match threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slide for the match input data.
- **Show Thresholds:** When enabled displays a filled preview of the minimum or maximum threshold value set for base and match input data.

Match Sample Region: The match sample region slides allow users to increase or decrease the sampling density in the X, Y, and Z (if applicable).

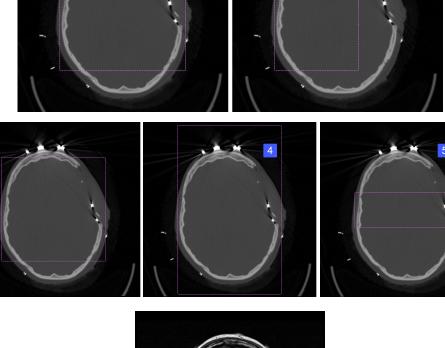
• Minimum X Sample Extent: Use the slider to specify the x sampling density. Decreasing the x minimum value and increasing the x maximum value will increase the minimum x sample range [1]. Increasing the x minimum value and decreasing the x maximum value will decrease the minimum x sample range [2].

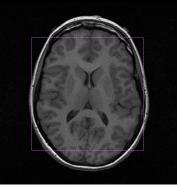


Match Sample Region (continued):

The minimum and maximum values can also be adjusted to select a specific x region or exclude a region that could interfere with registration [3].

- Y Sample Extent: As with the minimum X sample extent, users can use the minimum Y sample extent slider to specify the minimum y sampling density. Decreasing the y minimum value and increasing the y maximum value will increase the minimum y sample range [4]. Increasing the y minimum value and decreasing the y maximum value will decrease the minimum y sample range [5]. The minimum and maximum values can also be adjusted to select a specific y region or exclude a region that could interfere with registration.
- **Z Sample Extent:** Use the slider to specify the z sampling density.
- **Show Region:** Enables the display of the sample extent on the match image, showing the region as a purple and white dashed box.





DOF Search Ranges: The Degrees Of Freedom (DOF) search range allows users to adjust the default parameters set for registration.

- X Search: Allows users to adjust the maximum expected horizontal displacement (in either direction) of the match image in pixels.
- Y Search: Allows users to adjust the maximum expected vertical displacement (in either direction) of the match image in pixels.
- **Z Rotation Search:** Allows users to adjust the maximum expected rotation of the match image in degrees.
- Affine Register: Allows users to enable affine registration providing access to X and Y scale and shear search options:
 - X Scale Search: Adjust the maximum expected horizontal scaling difference between the match and base images
 - · Y Scale Search: Adjust the maximum expected vertical scaling difference between the match and base images
 - **X Shear in Y Search:** Adjust the level of x shear in the y search.
 - **Y Shear in X Search:** Adjust the level of y shear in the x search.
- **Bounded Search:** Limits the total number of search steps. The registration algorithm, while robust in most cases, can fail to converge in extremely low-information situations. This option avoids program hang-up in those situations, and seldom significantly affects typical solutions.

Registration Matrix: When enabled displays the 4 by 4 transformation matrix.

- · Load: Load a matrix file (*.mat file) for the match data set.
- **Save:** Save the current matrix file.

Transformation Interpolation: The transformation interpolation option allows users to specify the interpolation type to be used when transforming the match data set. Users can choose from:

• **Nearest Neighbor:** Allows users to select the nearest neighbor option for interpolation. Nearest Neighbor works by selecting the value of the closest voxel to which the interpolation resampling maps. This interpolation option is generally the fastest of the four available interpolation options.

Transformation Interpolation (continued):

- **Linear:** Allows users to select the linear option for interpolation. The linear algorithm applies a linear interpolation of grayscale intensity based on the distance of neighboring voxels from the interpolated voxel.
- **Bicubic:** Bicubic is the default interpolation option. The Bicubic option uses a cubic spline function to determine interpolated value, resulting in a smoother image that preserves detail.
- Windowed Sinc: Allows users to select the Windowed Sinc option for interpolation. The algorithm uses the windowed sinc function sin(x)/x to determine the interpolated value.

Slices: This option is only available when a single 3D volume is selected for input for 2D registration. The slices sliders allow users to navigate through the base and match inputs.

- Base: The base slider controls the display of the base slice. This will also be the 2D slice used for registration.
- **Match:** The match slider controls the display of the match slice. This will be the slice registered to the base for single Matrix and Single Reference registration. See Process and Registration mode for information on other registration options.

Process: The process controls allow users to register and save registration result, the following options are available.

- **Save Registered:** Allows users to save the transformed match image, the fused image, or the transformed object map (if applicable). See File > Save Registered at the being of this module section for a full description of the save options.
- **Register:** Initiates the slice-to-slice registration.
- **Register Pairs:** Only available when a single 3D volume is loaded. The register pairs option registered the current match slice to the current base slice. To adjust the select of the base or match slice input use the Slices sliders.
- **Match Range:** Only available when a single 3D volume is loaded. The match range slider allows users to specify a range of 2D match images to be registered to the base image.

Register Mode: Only available when a single 3D volume is loaded. The registration mode allows users to select from the following options:

• **Single Matrix:** Applies the transformation matrix created when registering the displayed match data set to the displayed base data to the images selected using the match range slider. All images in the match range are transformed to the same single matrix.

Register Mode (continued):

- **Single Reference:** This option registers each of the match images specified in the match range, individually to the base image.
- **Sequential:** Performs a sequential match image to base image registration within the specified match range. For example, match image 2 to base image 1, then match image 3 to based image 2, etc.
- **Register Sequence:** Only available for the single reference and sequential register modes. When selected initiates registration.

Redo: Reverses your last undo action. Redo is only available after using Undo.

Undo: Reverses you last action. Can reverse more than one action.

Registration Controls > 3D

The 3-D dimension mode is enabled when two 3D volumes or one or more multivolumes (4D data sets) are loaded into Register.

Surface Alignment: Enables 3D surface matching registration. The following options are available:

- **Threshold:** The Threshold double-ended slider bars for both the Base and Match data allows the end user to specify a range of threshold values to isolate common surfaces between the input images. Note, if common surfaces are not segmentable via thresholding the input data will need to be segmented prior to registration.
 - **Base:** The base threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slide for the base input data.
 - **Match:** The match threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slide for the match input data.

Show Thresholds: When enabled displays a filled preview of the minimum or maximum threshold value set for base and match input data.

Registration Matrix: When enabled displays the 4 by 4 transformation matrix.

- · Load: Load a matrix file (*.mat file) for the match data set.
- **Save:** Save the current matrix file.

Transformation Interpolation: The transformation interpolation option allows users to specify the interpolation type to be used when transforming the match data set. Users can choose from:

- **Nearest Neighbor:** Allows users to select the nearest neighbor option for interpolation. Nearest Neighbor works by selecting the value of the closest voxel to which the interpolation resampling maps. This interpolation option is generally the fastest of the four available interpolation options.
- **Linear:** Allows users to select the linear option for interpolation. The linear algorithm applies a linear interpolation of grayscale intensity based on the distance of neighboring voxels from the interpolated voxel.
- **Bicubic:** Bicubic is the default interpolation option. The Bicubic option uses a cubic spline function to determine interpolated value, resulting in a smoother image that preserves detail.
- Windowed Sinc: Allows users to select the Windowed Sinc option for interpolation. The algorithm uses the windowed sinc function sin(x)/x to determine the interpolated value.

Process: The process controls allow users to register and save registration result, the following options are available.

- Save Registered: Allows users to save the transformed match volume, fused volume, or the transformed object map (if applicable).
 See File > Save Registered at the being of this module section for a full description of the save options.
- **Register:** Initiates the 3D registration.
- **Register Pair:** Only available when the register mode is set to Single Reference or Sequential. Will initiate the registration of the current match volume to the current base volume.
- **Match Range:** Only available when one or more 4D multivolumes are loaded. The match range slider allows users to specify a range of 3D volumes in the 4D match multivolume to be registered to the base volume.

Register Mode: Only available when a single 4D volume is loaded. The registration mode allows users to select from the following options:

- **Single Matrix:** The single matrix option applies the transformation matrix created when registering the currently displayed match data set to the displayed base data to the range of match data sets selected using the match range slider. All volumes in the match range are transformed to the same single matrix.
- **Single Reference:** The single reference option registers each of the match volumes specified in the match range, individually to the base volume.
- **Sequential:** Performs a sequential match volume to base volume registration within the specified match range. For example, match volume 2 to base volume 1, then match volume 3 to based volume 2, etc.
- **Register Sequence:** Only available for the single reference and sequential register modes. When selected initiates sequential registration.

Redo: Reverses your last undo action. Redo is only available after using Undo.

Undo: Reverses you last action. Can reverse more than one action.

Volumes: This option is only available when one or more 4D multivolumes are selected for input for 3D registration. The Volume sliders allow users to navigate through the volumes in the match and/or base input multivolumes.

- **Base:** The base slider controls the display of the base volume. This will be the volume used for single matrix and single reference registration.
- **Match:** The match slider controls the display of the match volume. This will be the volume registered to the base for Single Matrix and Single Reference registration. See Process and Registration mode for information on other registration options.

Mutual Information: Enables 3D mutual information-based registration. The following options are available:

• **Threshold:** The Threshold double-ended slider bars for both Base and Match data allows specifification of a range of threshold values to consider for registration. The use of thresholding with mutual information-based registration is normally to remove background noise, artifact from implants, or other ranges of greyscale values from the data that could interfere with registration.

Analyze 15.0 User's Guide

Mutual Information > Threshold (continued): Enables 3D mutual information-based registration. The following options are available:

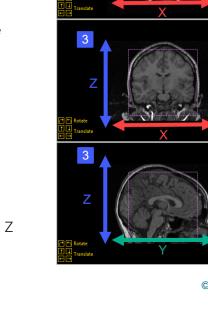
- **Base:** The base threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slide for the base input data.
- **Match:** The match threshold double-ended slider bar allows users to specify a range of threshold values using the minimum and maximum ends of the threshold slide for the match input data.
- Show Thresholds: When enabled displays a filled preview of the minimum or maximum threshold value set for base and match input data.

Match Sample Region: The match sample region slides allow users to increase or decrease the sampling density in the X, Y, and Z.

- X Sample Extent: Use the slider to specify the x sampling density. [1]
- Y Sample Extent: Use the slider to specify the Y sampling density. [2]
- · Z Sample Extent: Use the slider to specify the Z sampling density. [3]
- **Show Region:** Enables the display of the sample extent on the match image. The region will be shown as a purple and white dashed box.

DOF Search Ranges: The Degrees Of Freedom (DOF) search range allows users to adjust the default parameters set for registration.

- **X Search:** Allows users to adjust the x translation search step.
- **Y Search:** Allows users to adjust the y translation search step.
- **Z Search:** Allows users to adjust the z translation search step.
- **X Rotation Search:** Allows users to adjust the rotation about the x search step.
- **Y Rotation Search:** Allows users to adjust the rotation about the y search step.
- **Z Rotation Search:** Allows users to adjust the rotation about the z search step.
- **Affine Register:** Allows users to enable affine registration providing access to X, Y, and Z scale and shear search options:



DOF Search Ranges > Affine Register (continued):

- **X Scale Search:** Allows users to adjust the X scaling search parameter.
- **Y Scale Search:** Allows users to adjust the Y scaling search parameter.
- · **Z Scale Search:** Allows users to adjust the Z scaling search parameter.
- **X Shear in Z Search:** Allows users to adjust the level of x shear in the z search.
- **Y Shear in Z Search:** Allows users to adjust the level of y shear in the z search.
- **X Shear in Y Search:** Allows users to adjust the level of x shear in the y search.
- **Z Shear in Y Search:** Allows users to adjust the level of z shear in the y search.
- **Y Shear in X Search:** Allows users to adjust the level of y shear in the x search.
- **Z Shear in X Search:** Allows users to adjust the level of z shear in the x search.
- **Bounded Search:** Limits the total number of search steps. The registration algorithm, while robust in most cases, can fail to converge in extremely low-information situations. This option avoids program hang-up in those situations, and seldom significantly affects typical solutions.

Registration Matrix: When enabled displays the 4 by 4 transformation matrix.

- Load: Load a matrix file (*.mat file) for the match data set.
- **Save:** Save the current matrix file.

Transformation Interpolation: The transformation interpolation option allows users to specify the interpolation type to be used when transforming the match data set. Users can choose from:

- **Nearest Neighbor:** Allows users to select the nearest neighbor option for interpolation. Nearest Neighbor works by selecting the value of the closest voxel to which the interpolation resampling maps. This interpolation option is generally the fastest of the four available interpolation options.
- **Linear:** Allows users to select the linear option for interpolation. The linear algorithm applies a linear interpolation of grayscale intensity based on the distance of neighboring voxels from the interpolated voxel.

Transformation Interpolation (continued):

- **Bicubic:** Bicubic is the default interpolation option. The Bicubic option uses a cubic spline function to determine interpolated value, resulting in a smoother image that preserves detail.
- Windowed Sinc: Allows users to select the Windowed Sinc option for interpolation. The algorithm uses the windowed sinc function sin(x)/x to determine the interpolated value.

Process: The process controls allow users to register and save registration result, the following options are available.

- Save Registered: Allows users to save the transformed match volume, fused volume, or the transformed object map (if applicable).
 See File > Save Registered at the being of this module section for a full description of the save options.
- Register: Initiates the 3D registration.
- **Register Pair:** Only available when the register mode is set to Single Reference or Sequential. Will initiate the registration of the current match volume to the current base volume.
- **Match Range:** Only available when one or more 4D multivolumes are loaded. The match range slider allows users to specify a range of 3D volumes in the 4D match multivolume to be registered to the base volume.

Register Mode: Only available when a single 4D volume is loaded. The registration mode allows users to select from the following options:

- **Single Matrix:** The single matrix option applies the transformation matrix created when registering the currently displayed match data set to the displayed base data to the range of match data sets selected using the match range slider. All volumes in the match range are transformed to the same single matrix.
- **Single Reference:** The single reference option registers each of the match volumes specified in the match range, individually to the base volume.
- **Sequential:** Performs a sequential match volume to base volume registration within the specified match range. For example, match volume 2 to base volume 1, then match volume 3 to based volume 2, etc.
- **Register Sequence:** Only available for the single reference and sequential register modes. When selected initiates sequential registration.

Redo: Reverses your last undo action. Redo is only available after using Undo.

Undo: Reverses you last action. Can reverse more than one action.

Volumes: This option is only available when one or more 4D multivolumes are selected for input for 3D registration. The Volume sliders allow users to navigate through the volumes in the match and/or base input multivolumes.

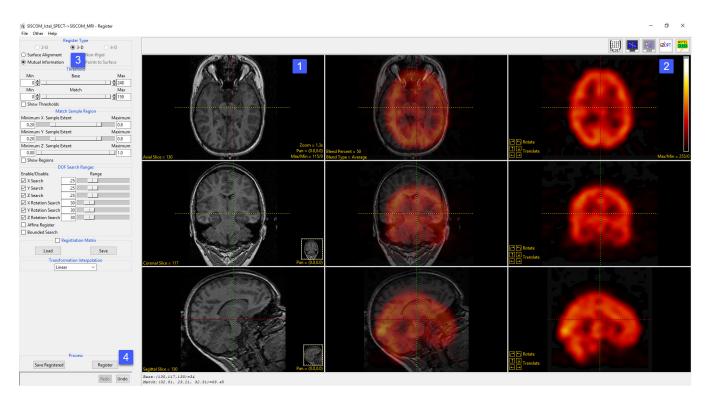
- **Base:** The base slider controls the display of the base volume. This will be the volume used for single matrix and single reference registration.
- **Match:** The match slider controls the display of the match volume. This will be the volume registered to the base for Single Matrix and Single Reference registration. See Process and Registration mode for information on other registration options.

3D Registration - Surface Alignment

Surface alignment is used to register image data that does not have enough or any mutual information, for example a functional SPECT scan and structural MRI scan. This exercise will provide the steps necessary to correctly register a SPECT scan and an MRI scan of the brain. However, first we will observe what happens when we try to register the image data set using Mutual Information.

To follow along, download data sets SISCOM_MRI.avw and SISCOM_Ictal_SPECT.avw from analyzedirect.com/data

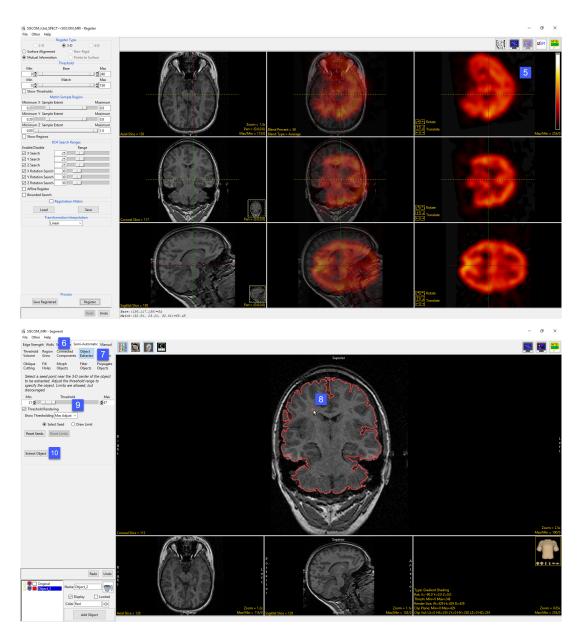
- Open Input/Output and load both the SISCOM_MRI.avw and SISCOM_Ictal_SPECT.avw data sets into Analyze.
- Once loaded select the SISCOM_MRI data set then press and hold the Ctrl button on your keyboard and select the SISCOM_Ictal_ SPECT data set and open Register. Note the order in which the data is selected is important. The first data set selected will be loaded
- as the base data set, in this example the MRI [1], while the second data set will be the match data set, in this example the SPECT [2].
- Set the Register Type to Mutual Information [3] and then click Register [4].



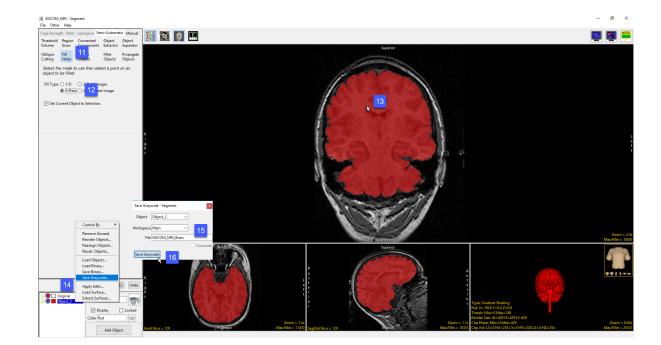
Due to the lack of mutual information between these two modalities the registration will fail. Note the incorrectly positioned SPECT [5] with respect to the MRI.

In order to facilitate successful registration of the MRI and SPECT data we need to establish surfaces for common objects in both data sets, this means the explicit segmentation of the brain from the MRI and SPECT data sets.

- Close the Register module.
- From the main Analyze window select the SISCOM_MRI data set and then open Segment.
- From the Semi-Automatic tab [6] select Object Extractor [7].
- On Coronal slice 115 click in the white matter to set a seed point [8]. Adjust the threshold range [9] to define the brain, a minimum value of 21 and a maximum value of 47 works well for this data set.
- Click Extract Object [10].



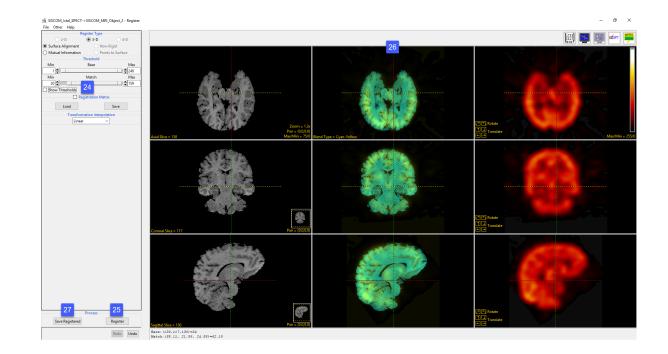
- After segmentation is complete notice that the brain object contains some minor holes. To correct for these holes, choose Fill Holes [11], set the Fill Type to 3-Pass [12], click on the brain object [13] to initiate the fill process.
- Once the fill process is complete the brain will no longer contain any holes. Right-click on the brain object in the object list and then choose Save Grayscale from the menu [14].



- In the Save Grayscale window retuned change the name of the output file to SISCOM_MRI_Brain [15] and click Save Grayscale [16]. A grayscale version of the segmented brain object will be saved to the workspace, this will provide the surface of the brain for surface alignment with the SPECT data set.
- Close Segment.
- As the brain surface in this SPECT data set can be easily isolated via thresholding in Register there is no need to segment the data set using Segment. However, if the SPECT image data contained extracranial signal that prevented a clear representation of the brain surface via thresholding the data set could be segmented to isolate the brain using Segment prior to use in Register.

- Select the SISCOM_MRI_Brain data set then press and hold the Ctrl button on your keyboard now select the SISCOM_Ictal_SPECT data set and open Register.
- Set the Register Type to Surface Alignment [17].
- If desired modify the blend type [18].
- Next click the Show Threshold check box [19].
- Note that all voxels for both the base and match data sets are currently selected. To exclude the background voxels from the base volume set the Base minimum threshold level to 1 [20] by entering the value in the text field or by adjusting the slider. Note the update on the base display [21], only the voxels within the red mask will be considered for registration.
- Adjust the threshold range for the match data set to remove the background voxels and all non-brain voxels. Set the minimum threshold value to 20 [22] by entering the value in the text field or by adjusting the slider. Note the update on the match display [23], the voxels within the red mask represent the brain and will provide the match surface to facilitate a successful registration.

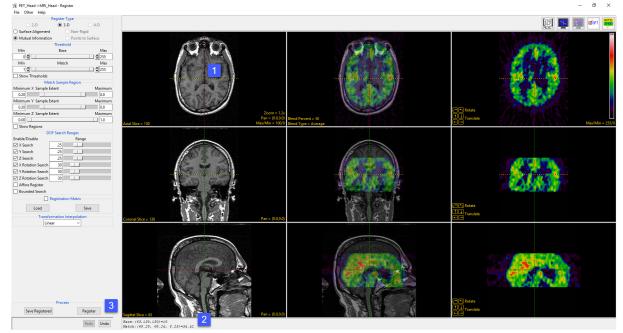
- Uncheck the Show Threshold option [24].
- To register the data click Register [25].
- After the registration is complete visually review the transformed and fused image data [26].
- Click Save Registered to save the Transformed SPECT data to the workspace and then close Register.



3D Registration - Mutual Information

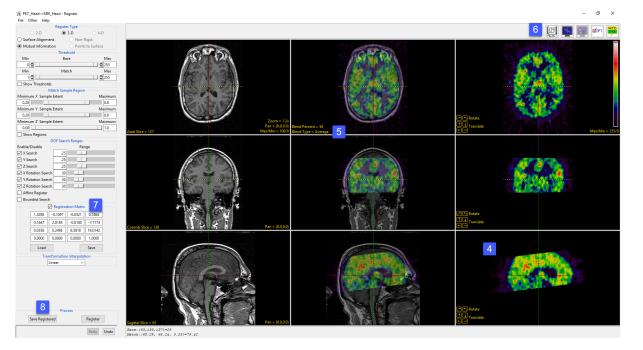
The goal of this exercise is to demonstrate how to apply mutual information to registration of image data from two different modalities, MRI and PET. The MRI data set is sagittal acquisition anisotropic (non-cubic) data set, while the PET data set is an axial acquisition with isotropic voxels, so not only are the image data sets different modalities they also have different volume and voxel dimensions and were acquired in different orientations. To view this information right-click on the data once loaded into Analyze and then choose Info, review the volume metadata in the tab at the bottom of the Analyze window. To follow along, download data sets MRI_Head.avw and PET_Head.avw from analyzedirect.com/data. Open Input/Output and load both the MRI_Head.avw and PET_ Head.avw data sets into Analyze.

- Select the MRI_Head data set and while holding down the Ctrl key, select the PET_Head data set and then open Register.
- 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. If the data was loaded incorrectly, click the Swap Inputs button to correct.
- The base MRI data set will display in the first column while the match PET data will display in the last column.
- At this point no registration has taken place, but the match data set has been correctly scaled to the base data set, displayed isotropically.
- The crosshair (linked cursor) [1] 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. Note that the base and match coordinates are reported at the bottom of the window [2].
- Click the Register button [3].



3D Registration - Mutual Information (continued)

- After registration is complete, you will see that the PET volume has been scaled, rotated and translated to match the sagittal MRI [4].
- If desired right-click the Blend Type yellow text in the fused axial image (middle upper panel) [5] and change the blend type.
- To evaluate the registration, move the crosshair in any of the panes. Note, if moving the crosshair in fused or match data you can unintentionally translate the data. If you do this click Undo to reverse the last action. To prevent this from happening again either right-click in a fused or match image and uncheck the 'Left Drag to Translate' option or simply control the crosshair maneuvers from the base volume only.
- 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 [6].
- To view the current transformation matrix, select the Registration Matrix box [7] 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 PET data set or fused MRI/PET data set, click Save Registered [8]. Select the Transformed Save Type, Workspace, File and then select Save Transformed.
- When finished close Register.



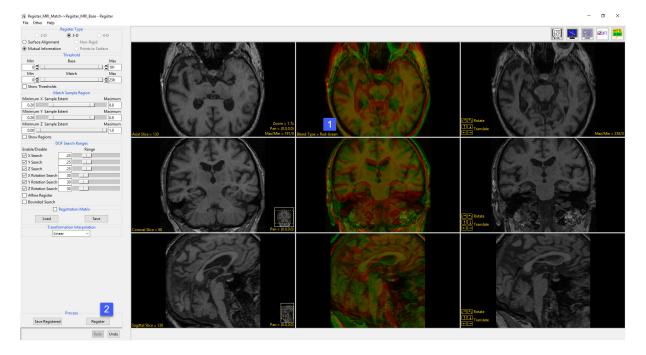
Troubleshooting Registration Problems

Sometime image registration will fail, fortunately the Register module provides several tools to help optimize conditions to achieve registration. Common problems include:

- • Not enough overlapping information between input data sets
- • Background or artifact noise
- • Adjusting the sample region to include/exclude regions in the match data

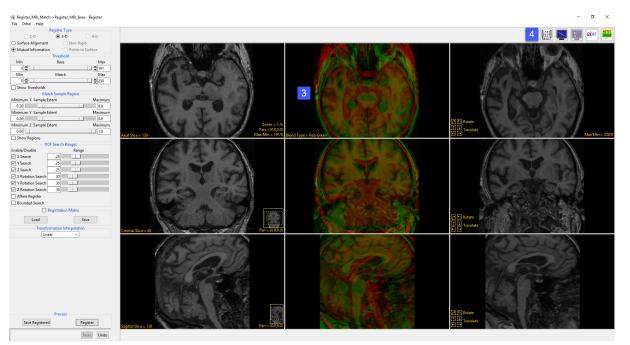
Not enough overlapping information between input data sets

- Download data sets Register_MRI_Base.avw and Register_MRI_Match.avw from analyzedirect.com/data to follow along.
- Use Input/Output to load the two data sets into Analyze. Select the Register_MRI_Base data set and while holding down the Ctrl key, select the Register_MRI_Match data set and then open Register.
- Select File > Input/Output Ports to view the input and output ports at the bottom of the Register window. Confirm that the Register_MRI_Base data set is assigned as the 'Base Volume' and Register_MRI_ Match data set is assigned as the 'Match Volume'. If the data is loaded incorrectly use the Swap Inputs option to correct.
- Use the Blend Type [1] to set a Red-Green blend for the fused image. The blend will help with visual assessment of the registration result as both the base and match data sets are grayscale.
- Press the Register button [2].

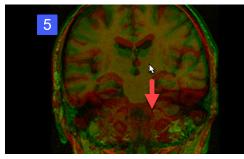


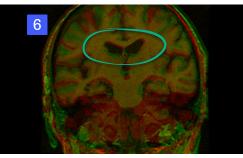
Not enough overlapping information between input data sets

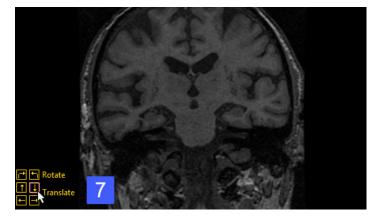
- Examine the Fused image data in the center column [3]. It is clear to see that the registration process failed. These image inputs do not have enough overlapping mutual information to facilitate a successful registration, however, the resolution to this issue is quite simple, the match data set needs to be manually adjusted so it has a new starting point closer to the base image.
- Since the registration is not acceptable click the Reset Matrix button [4].



- Left click on the coronal fused or match image and drag the data down slightly [5]. Release the mouse when the ventricles are aligned closer [6].
- Alternatively, use the down translation arrow [7] to move the coronal match image down 5 voxels.



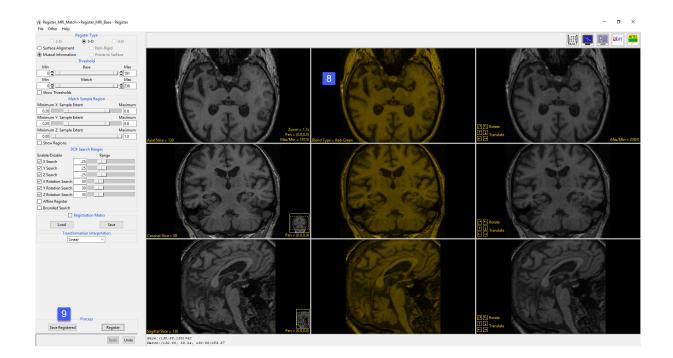




Analyze 15.0 User's Guide

Not enough overlapping information between input data sets (continued)

- Press the Register button.
- This time the image data will register correctly. Notice that the fused image will appear yellow [8] when aligned correctly. Use the Save Register [9] to save the transformed image data to the workspace.
- Note that when troubleshooting data you are experiencing problems with may need to make larger adjustments that could also include rotations and manipulations in all three orientations.
- Close Register.

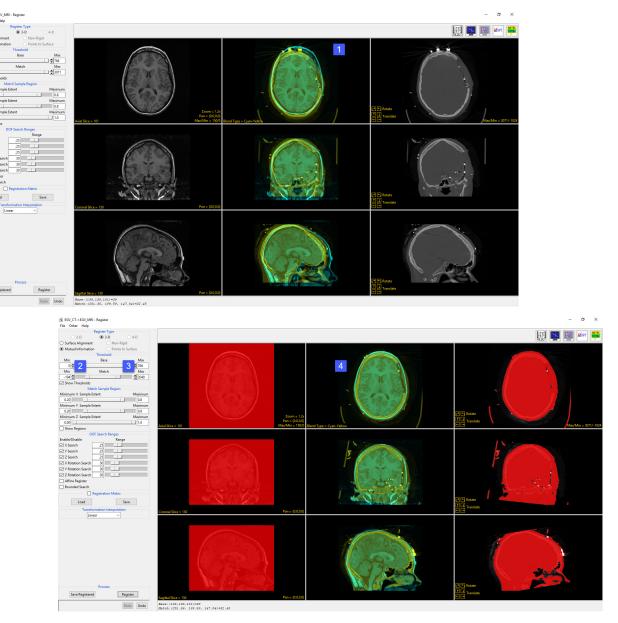


Background or artifact noise

Noise in the background of the image or from artifact in the image can prevent successful registration of image data.

In this example, registration of a postoperative CT to a pre-operative MRI fails due to the artifact from the electrodes in the CT data set [1].

However, simply setting a threshold range to exclude the voxels in the match data set that represent the electrodes, by decreasing the maximum threshold value [2], and the streak artifact from the electrodes, by increasing the minimum threshold value [3], allows for a successful registration [4].



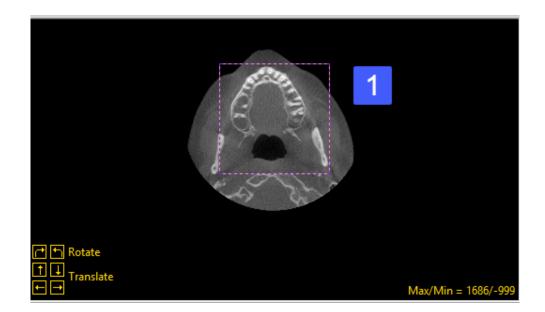
Analyze 15.0 User's Guide

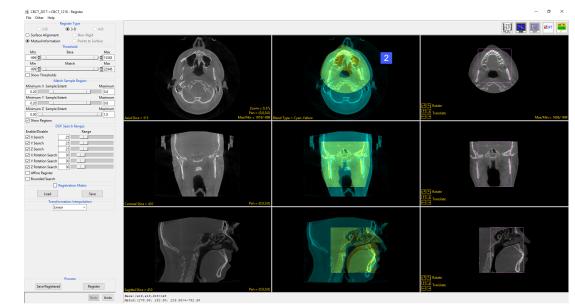
Adjusting the sample region to include or exclude regions in the match data

Registration can fail if not enough of the match data is considered for the registration. Registration can also fail if the match region considered for registration contains a region of large morphological change from the base data set, such as an implant in a postimplant data set. The match sample region allows users to adjust to match region considered for the registration, increasing or decreasing the match region as necessary.

The 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 [1] when the option is enabled.

In this example registration between a pre-procedure and post-procedure Cone Beam CT (CBCT) scans fails as the CBCT scans were acquired from different scanners with different parameters [2].





Adjusting the sample region to include or exclude regions in the match data (continued)

Adjustment of the match sample region to increase the X sample range [3] remedied the problem and allowed for successful registration of the image data [4].



Measure

| | Introduction | page 529 |
|--|-----------------------------------|----------|
| | Measure Module Interface | page 530 |
| | Menu | page 531 |
| | Measurement Tools | page 533 |
| Othe | er Measure Module Interface Areas | page 534 |
| 1-D Measurement Tools | | page 536 |
| | Sample Point(s) | page 536 |
| | Sample Line(s) | page 541 |
| Making Line Measurements using Sample Line(s) | | page 545 |
| Making FWHM Line Measurements using Sample Line(s) | | page 547 |
| Generating Line Profiles using Sample Line(s) | | page 549 |
| Making Line Measurements on the | 3D Rendering using Sample Line(s) | page 551 |
| | Sample Trace(s) | page 552 |
| | Sample Border(s) | page 554 |
| | Sample Angle(s) | page 557 |
| | Sample Two Lines | page 559 |
| | Sample Perpendicular Lines | page 561 |

| Sample 2-D Rectangle | page 563 |
|-------------------------|----------|
| Sample 2-D Oval | page 570 |
| Sample 2-D Closed Trace | page 572 |
| Selected Region | page 574 |
| Selected Object | page 576 |
| Enabled Objects | page 578 |
| Entire Image | page 585 |
| 3-D Measurement Tools | page 589 |
| Box | page 589 |
| | |

2-D Measurement Tools page 563

Selected Object page 593 Enabled Objects page 596

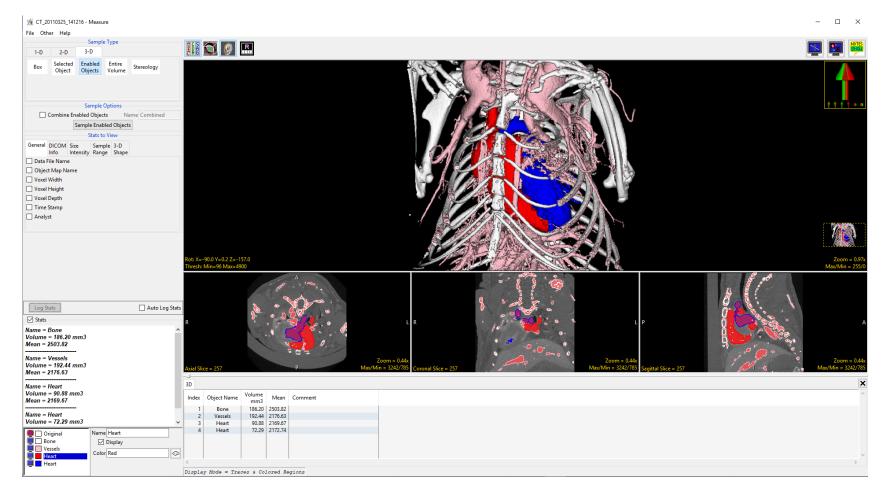
Entire Volume page 601

Stereology page 607

Sampling 4D Multivolumes using 3D Tools page 609

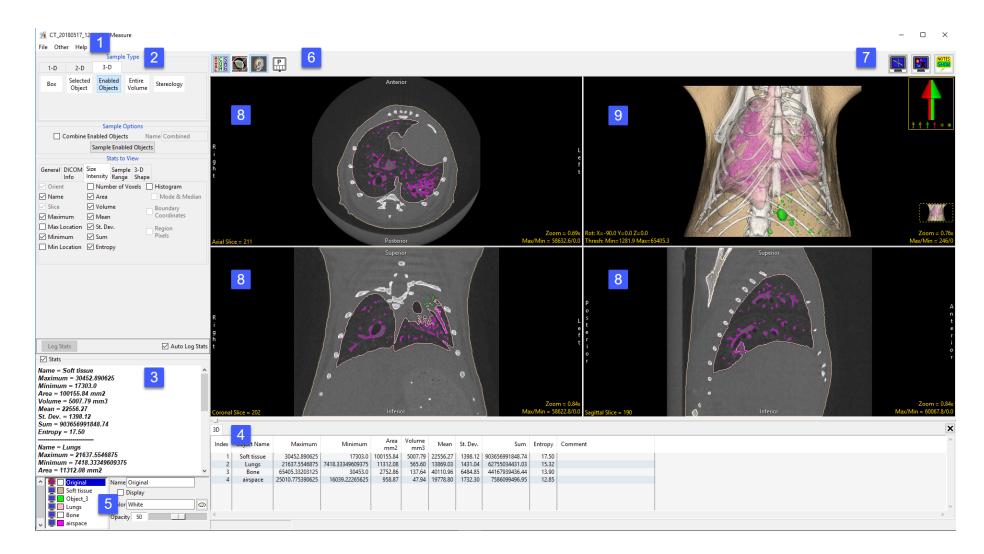
Introduction

The Analyze Measure module provides access to an array of measurement tools that allow users to sample their image data. 1D measurement tools are available for sampling and logging 3D positions of points, making line intensity and distances measures, or making angle measurements. 2D measurements tools allow users to interactively defined rectilinear or elliptical regions, sample freehanded traces of regions of interest, or sample regions or objects on images. Finally, 3D measurements tools allow users to sample loaded object maps to return spatial size measures, signal intensity information, or 3D shape characteristics.



Measure Module Interface

The measure module is divided into several areas: 1) the menu, 2) measurement tools, 3) stats display, 4) stats log, 5) the object control window, 6) display controls, 7) tools, 8) orthogonal image display, and 9) the rendering window. Each of these areas are now described.

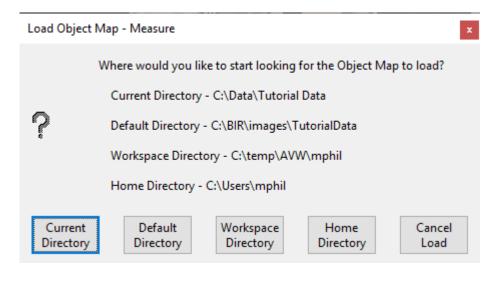


Menu

The Menu provides access to the File, Options and Help menus.

File: The File menu allows users to load and save object maps for the loaded data set. The File options include:

- **Input/Output Ports:** Displays a Volume area at the bottom of the Segment module window. This area facilitates the dragging and dropping of image data into the module and the loading of a related image data set, see Dual Input Segmentation for additional information.
- Load Object Map: When selected opens a Load Object Map window allowing users to navigate to, select and load an object map file. The following options are available:
 - **Current Directory:** Takes user to the current directory, the current directory is set by right-clicking in the main Analyze 15.0 window and then choosing Current Directory from the menu. See section 1. Analyze Basics for additional information.
 - · Workspace Directory: Takes user to the current Workspace directory.
 - Home Directory: Takes user to the user's Home directory.
 - Cancel Load: Cancels the load of the object map.
- Unload Object Map: Unloads the current object map
- **Exit:** Closes the module



Menu (continued)

Other: The other menu provides access to additional module options and configuration of the tools area.

- **Options:** When selected opens the Options menu providing access to Module configuration options, including:
 - Intensities Linked: Allows users to enable or disable linked intensity adjustment. When linked any adjustment an images intensity display will be applied to all grayscale slices displayed. When disabled image intensities can be adjusted individually.
 - · Fast Object Rendering: Enables/Disabled Fast Object Rendering.
 - **Show Cursor Coordinates:** Allows users to Enable/Disable the display of the linked cursor coordinates and voxel grayscale value displayed in the lower left-hand corner of the display window.
 - Auto Note Update: Allows the Auto Note Update option to be enabled or disabled.
 - Auto Cursor Link: Allows the Auto Cursor Link option to be enabled or disabled.
 - **Remember Layout:** When enabled the module will remember changes made to the layout and will open with this layout in the future. When disabled the module will open with the default layout.
 - **Decimal Places:** The Decimal Places options allows users to set the number of decimal places reported for measurements. By default the number of decimal places is set to 2.
 - **Threads:** Allows users to specify the number of threads used in a multi-threaded rendering process. By default, the number of threads is set to the number of processors on the system.
- PowerBar Editor: When selected opens the PowerBar editor allowing users to add additional shortcut buttons to the tools area of the Measure window. Add or remove the following shortcut buttons form the tools area: 1) Exit, 2) Options, 3) Input/Output, 4) Load Object Map, 5) PowerBar Editor, 6) Set Note Stat, 7) Toggle Cursor Link, 8) Toggle Region Display, and 9) Unload Object Map.
- Help: The Help menu provides users with quick access to help resources including:
 - **About:** View version, system and environment information.
 - · Users Guide: Opens the Analyze 15.0 User's Guide.
 - **Get Help:** Opens the AnalyzeDirect Support Page.

Measurement Tools

The measurement tools options are grouped into three tabs under Sample Type. These are:

1-D: The 1-D tab provides access to the following measurement tools:

- · Sample Point(s)
- · Sample Line(s)
- · Sample Trace(s)
- · Sample Border(s)
- · Sample Angle(s)
- $\cdot\,$ Sample Two Lines
- · Sample Perpendicular Lines

3-D: The 3-D tab provides access to the following measurement options:

- · Box
- · Selected Objects
- · Enabled Objects
- \cdot Entire Volume
- · Stereology

2-D: The 2-D tab provides access to the following sampling options:

- · Sample 2-D Rectangle
- · Sample 2-D Oval
- · Sample 2-D Closed Trace
- · Selected Region
- · Selected Object
- · Enabled Object
- · Entire Image

These three tabs provide access to all of the measurement tools in Measure. The measurement tools within each tab will be discussed in the Measurement Tools section of this guide.

Other Measure Module Interface Areas

Stats Display

The stats display area reports the select measurements. Measurements cannot be saved from this area (see Stats Log for saving out measurements), however, measurements can be copied and pasted from this area.

Stats Log

When the Auto Log Stats option is checked the Stats Log reporting the selected measurements will be displayed below the main image display area. The following right mouse menu options are available:

- Save Log: Allows users to save the log file as a .csv file.
- Clear Log: Clears all measurements from the current log file.
- **Dismiss Log:** Closes the log file.
- **Remove Last Entry:** Allows users to delete the last entry in the stats log.

Object Control Window

The Measure object controls window allows users to enable and disable the display of objects within the current object map. It also allows users to edit object properties including name, color, and opacity.

Display Controls

The Display Control tools allow users to control and customize the layout of the Measure display area. For further information on these tools please refer to the Image Display, Controls and Customization section of this User's Guide.

Other Measure Module Interface Areas (continued)

Tools

The Tools options provide access to the Toggle Cursor Link, Toggle Region Display and the Set Note State tools. For further information on these tools please refer to the Image Display, Controls and Customization section of this User's Guide.

Orthogonal Image Display

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 the Display section of this User's Guide.

The Rendering Window

The render window provides an interactive 3D display of the segmented image data. For more information about the render window, refer to the Display section of this User's Guide.

1-D Measurement Tools

1D measurements include points, lines, trace, angles, borders distances, 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. Note 1-D measurements (apart from Sample Border(s)) can be made on image data with or without a loaded object map. The 1-D tab provides access to the following measurement tools:

· Sample Point(s)

Sample Border(s)

- · Sample Line(s)
- · Sample Trace(s)

Sample Point(s)

The Sample Point(s) 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. The following options are available:

Sample Options: Provides users with access to the following point sampling options:

- · Name: Allows users to assign a name to the selected point when reported to the log file.
- · Persistent: When selected prevents previously selected points for being cleared from the image.
- **Clear:** Clears all points from the image.

Stats to View: The stats to view area allows users to enable and disable measurements and information reported to the stats log.

- **General:** Allows users to report information about the image data set including:
 - · Data File Name: Reports the data set name to the stats log.
 - · Object Map Name: Reports the object map name to the stats file.
 - Voxel Width: Reports the voxel width to the stats file.
 - · Voxel Height: Reports the voxel height to the stats file.
 - Voxel Depth: Reports the voxel depth to the stats file.

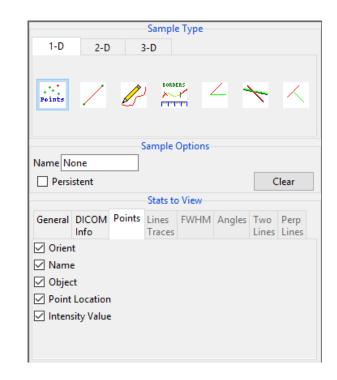
· Sample Angles

- \cdot Sample Two Lines
- · Sample Perpendicular Lines

Sample Point(s) (continued)

Stats to View > General (continued):

- **Time Stamp:** Reports the date and time of sampling to the stats file.
- Analyst: Reports the current user logged into the system to the stats file.
- **DICOM Info:** Only applicable for DICOM image data, allows users to report:
 - · Patient Name: Reports the patient name to the stats log.
 - Patient ID: Reports the patient ID to the stats log.
 - Birth Date: Reports the patient's date of birth to the stats log.
 - **Gender:** Reports the patient's gender to the stats log.
 - Weight: Reports the patient's weight to the stats log.
 - **Study ID:** Reports the study ID to the stats log.
 - **Study Date:** Reports the study date name to the stats log.
 - **Study Time:** Reports the study time to the stats log.
 - · Study Description: Reports the study description to the stats log.
 - · Series Number: Reports the series number to the stats log.
 - Series Description: Reports the series description to the stats log.
 - · Accession Number: Reports the accession number to the stats log.
 - Modality: Reports the modality to the stats log.
- **Points:** Provides users with the option to report the following point related information and measurements:
 - Orient: Reports the orientation the point was logged in. Options include; Axial, Coronal, Sagittal, Rendering, and Oblique.
 - **Name:** Reports the name.
 - · Object: Reports the object the point was logged on (if an object map is loaded).
 - Point Location: Reports the X, Y, Z location of the point.
 - Intensity Value: Reports the greyscale intensity value of the point.



Sampling Points using Sample Point(s)

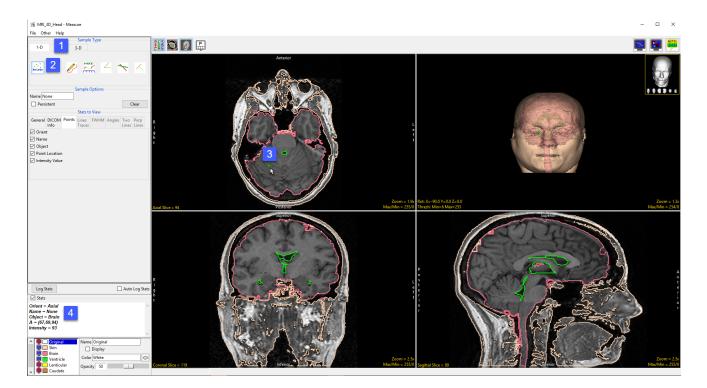
The Sample Point(s) tool can be used to sample landmarks for morphological applications.

Download the MRI_3D_Head.avw data set from analyzedirect.com/data to follow along.

To sample points, do the following:

- Open Input/Output and load MRI_3D_Head.avw into Analyze.
- 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].



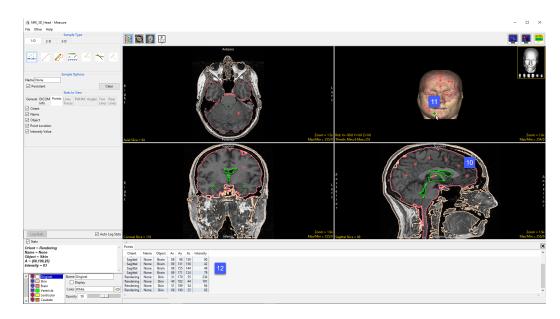
Sampling Points using Sample Point(s) (continued)

- 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].

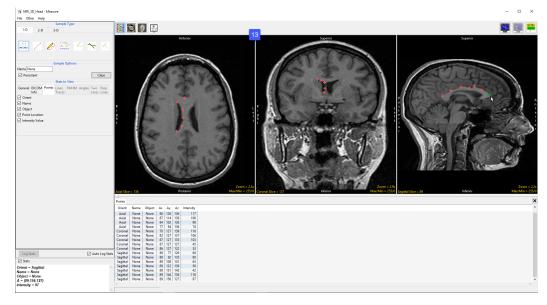


Sampling Points using Sample Point(s) (continued)

- 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].



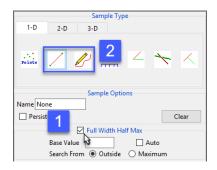
Sample Line(s)

The Sample Line(s) tool allows users to define a line on a 2D image or a 3D rendering. The tool will report distance measurements, line intensity profile and the coordinates of the line end points. The following configuration options are available:

Sample Options: Provides users with access to the following line sampling options:

- Name: Allows users to assign a name to the defined lines when reported to the log file.
- **Persistent:** When selected prevents previously defined lines for being cleared from the image.
- **Clear:** Clears all lines from the image.





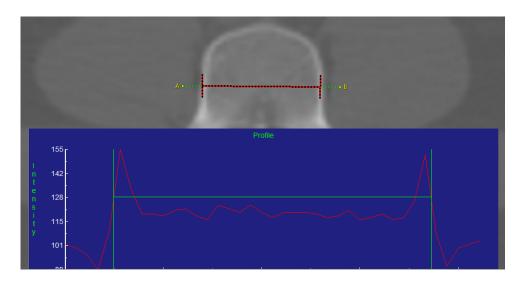
Full Width Half Max: The Full Width Half Max (FWHM) option can be enabled [1] for the Sample Line(s) and Sample Trace(s) tool [2]. Once enabled, Measure will automatically log FWHM

distance measurements [3] for defined lines [4] and traces.

Sample Line(s) Options (continued)

Full Width Half Max (continued):

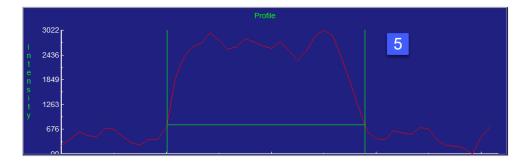
- **Base Value:** Allows users to specify the value used in the FWHM calculation.
- Auto: When enabled, the base value is automatically calculated by computing the mean of the nine-point neighborhoods around each endpoint of the line or trace
- **Search from:** Allows users to specify the search mode for FWHM measurement. The following options are available:
 - **Outside:** Specifies that search begins at the ends of the profiles.
 - **Maximum:** Specifies that search begins at the maximum value and proceeds to both the left and right for the two half max values.



The Full Width Half Max

To find the FWHM of the line profile [5] (the calculation of pixel intensities along straight lines and freehand traces on the images), the 'Half Max' value is first computed using the formula:

Half Max = ((Maximum Value – Base Value)/2 + Base Value)



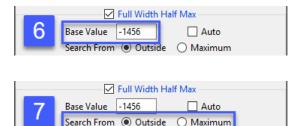
Sample Line(s) Options (continued)

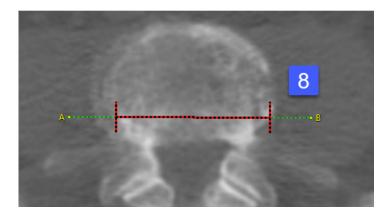
Full Width Half Max (continued):

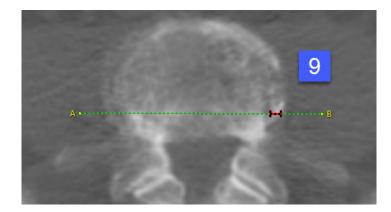
The 'Maximum Value' is the maximum intensity value of the line profile. The 'Base Value' is defined under the Full Width Half Max options [6]. The Base Value can be set to a specified value, or it can be set dynamically using the 'Auto' option. When the Auto option is selected, the Base Value is set to the mean intensity value of the nine-point neighborhoods surrounding each endpoint of the line. Once the Half Max value is known, Measure will search the line profile to see where that value is first crossed over on either side of the line maximum. The direction from which the module searches the line profile for the Half Max is determined by the 'Search From' option in under the Full Width Half Max options [7].

If the Search From option is set to 'Outside', then Measure will search for where the line intensity values cross over the Half Max value beginning at the outside of the profile and moving inwards. In this example, the FWHM will be defined by the closest voxel to either endpoint of the line with an intensity value greater than the Half Max value [8].

If Search From is set to 'Maximum', then Measure will search for where the line intensity values cross over the Half Max value beginning at the profile Maximum and moving outwards (to the right and left). In this example, the FWHM ends up being defined by the voxels closest to the line Maximum that have an intensity value less than the Half Max [9]. Once the FWHM of the line has been defined, Measure will compute the FWHM distance by taking the distance between the voxels on either side of the FWHM weighted by their relative value to the true Half Max value.







Analyze 15.0 User's Guide

Sample Line(s) Options (continued)

Stats to View

General: Allows reporting of general data parameters in the stats log file. See Sample Point(s) > Stats to View > General for full description.

DICOM Info: Allows reporting of DICOM tag information. See Sample Point(s) > Stats to View > DICOM Info for full description.

Line Traces:

- · Orient: Reports the orientation the line was defined in. Options include; Axial, Coronal, Sagittal, Rendering, and Oblique.
- Name: Reports the name.
- End Point Locations: Reports the X, Y, Z location of each line end point (A and B).
- · Maximum: Reports the maximum voxel intensity value along the line.
- · Minimum: Reports the minimum voxel intensity value along the line.
- · Mean: Reports the mean intensity value for the voxels along the line.
- · Standard Deviation: Reports the standard deviation.
- **Endpoint Distance:** The Endpoint Distance (or Distance as reports in the stats display) reports the linear distance from end point A to end point B. Note, even if this option is unchecked it will still be reported to the stats display area and stats log.
- **Curved Distance:** Reports the curvilinear distance between the endpoints. The curvilinear distance is an approximation based on the distance between the two 3-D surface endpoints.
- **Surface Distance:** The Surface Distance is only available for lines defined on the rendering. This option reports the surface distance of the line. The defined line is projected onto surface of the rendering and measured.
- **Profile:** Displays the line profile plot.

FWHM:

- Half Max: Reports the half max intensity value.
- Half Max Location: Reports the X, Y, Z location of both half max locations.
- · Maximum: Reports the maximum voxel intensity value along the line.
- Base Value: Reports the Base Value.
- · Distance: Reports the FWHM distance.

Analyze 15.0 User's Guide

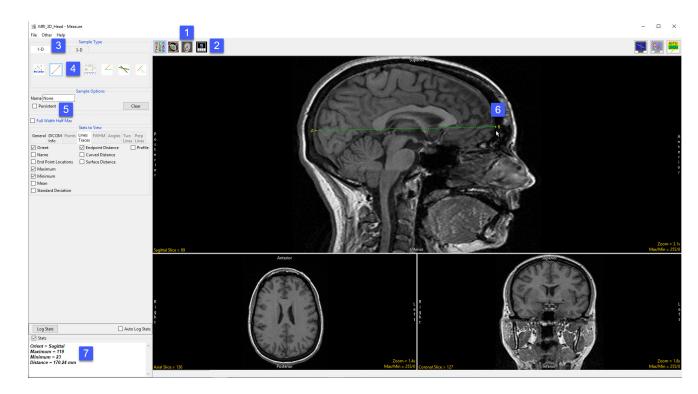
Making Line Measurements using Sample Line(s)

Here we use the Sample Line(s) tool to make line measurements.

Download the MRI_3D_Head.avw data set from analyzedirect.com/data to follow along.

To make a line measurement, do the following:

- Open Input/Output and load MRI_3D_Head.avw into Analyze.
- 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].
- If checked (enabled), uncheck Full Width Half Max [5].
- Define a line on a sagittal slice. [6] To draw a line position the cursor on the image and press the left mouse button to begin drawing. Release the button to end the line.
- The coordinates for the line endpoints (A and B) and the line distance are reported in the Stats review area [7].



Making Line Measurements using Sample Line(s) (continued)

- 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.

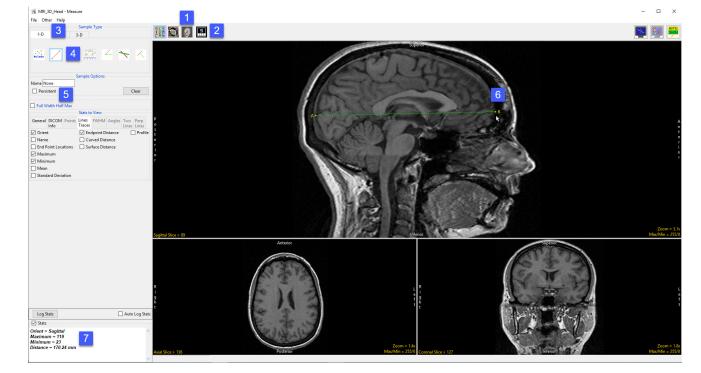


Generating Line Profiles using Sample Line(s)

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

Download the MRI_3D_Head.avw data set from analyzedirect.com/data to follow along.

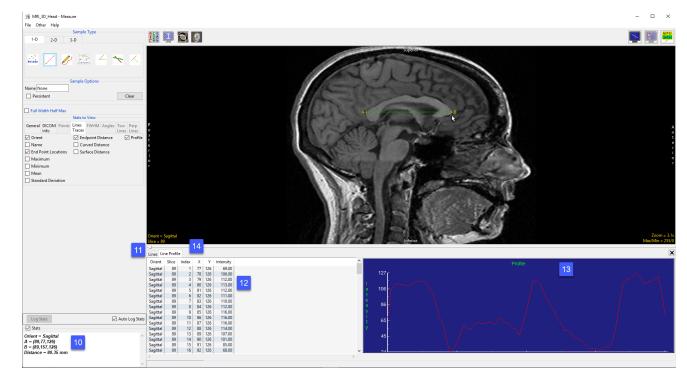
- Open Input/Output and load MRI_3D_Head.avw into Analyze.
- Select MRI_3D_Head and open Measure.
- Switch the display of the Rendering off [1] and toggle the display of all orientations off [2].



- Use the Orient option to switch to Sagittal [3].
- Select the 1D Sample Type [4]. Choose the Line tool [5].
- If enabled (checked), 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].

Generating Line Profiles using Sample Line(s) (continued)

- 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].



Making FWHM Line Measurements using Sample Line(s)

The Sample Line(s) 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. FWHM measurements can be useful when trying to make exact measurements on a structure when placing the end points accurately is difficult.

Download the VH_Abdomen.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load VH_Abdomen.avw into Analyze. Select VH_Abdomen and open Measure.
- Select the Sample Line(s) tool [1] from 1-D Sample Type.
- Define a line in the axial orientation to measure the distance from the right side of the vertebral body to the left side [2].
- Note the distance [3].

Analyze 15.0 User's Guide



Making FWHM Line Measurements using Sample Line(s) (continued)

- Placing the endpoints, point A and point B, exactly in the correct location to obtain an accurate measurement can be difficult.
- Click Clear [4] to reset the line.
- Check the Full Width Half Max checkbox [5] and check the Auto option to have the tool calculate the FWHM Base Value.
- Select the FWHM Stats to View tab [6] and make sure Distance
 [7] is selected, this will report the FWHM Distance in the stats display.



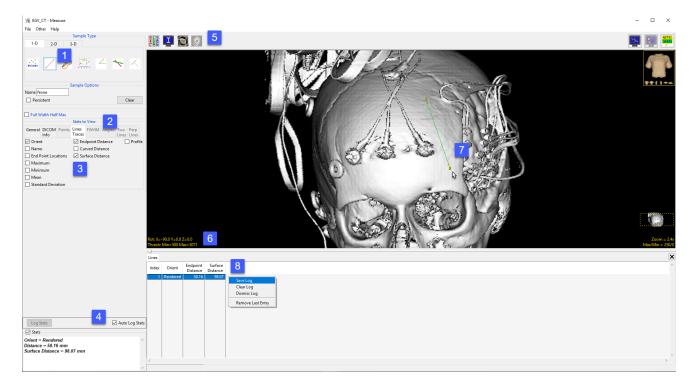
- In the axial orientation, define a line across the vertebral body, however, this time do not place the endpoints of the line exactly on each side of the vertebral body [8]. Note that the FWHM is overlaid in red on the line.
- Note the distance measurement in the stats display [9]. Even if the same distance measurements as before were obtained, FWHM is a quicker and easier method than trying to accurately place endpoints.

Making Line Measurements on the 3D Rendering using Sample Line(s)

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

Download the EG_CT.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load
 EG_CT.avw into Analyze. Select
 EG_CT and open Measure.
- Select the Sample Line(s) tool [1] from 1-D Sample Type.
- From Stats to View select the Line Traces tab [2].



- Ensure that both the Endpoint Distance and Surface Distance options are selected [3] and check Auto Log Stats [4].
- Use the Display control tools [5] to enable the display of the rendered image and switch off the display of the slice data.
- To view the skull, double-click on the yellow Thresh text in the lower left-hand corner and set the minimum value to 500 [6]. The skull will be displayed. Define a line on the skull [7].
- Note that both the straight line and surface distance have been reported to the stats log [8]. Note the difference in the measurements. Right-click to save the log.

Sample Trace(s)

The Sample Trace(s) tool provides all the functionality of the Sample Line(s) tool, while allowing the user to define a freehand trace. Available options are as follows:

Sample Options: Provides users with access to the following trace sampling options:

- Name: Allows users to assign a name to the defined trace when reported to the log file.
- **Persistent:** When selected prevents previously defined traces for being cleared from the image.
- **Clear:** Clears all traces from the image.

Full Width Half Max: The Full Width Half Max (FWHM) option can be enabled for the Sample Line(s) and Sample Trace(s) tool. For additional information refer to the FWHM description under Sample Line(s) tool.

- **Base Value:** Allows users to specify the value used in the FWHM calculation.
- **Auto:** When enabled, the base value is automatically calculated by computing the mean of the nine-point neighborhoods around each endpoint of the line or trace
- Search from: Allows users to specify the search mode for FWHM measurement. The following options are available:
- · Outside: Specifies that search begins at the ends of the profiles.
- Maximum: Specifies that search begins at the maximum value and proceeds to the left and right for the two half max values.

Stats to View

- General: Allows users to report general image data parameters in the stats log file. See General under Sample Point(s) > Stats to View for a full description of available options.
- DICOM Info: Allows users to report DICOM tag information if the data is in the DICOM format. See the DICOM Info under Sample Point(s)
 > Stats to View above for a full description of available options.
- Lines Traces: Allows users to report an array of information about the trace. See Lines Trace under Sample Lines(s) > Stats to View above for a full description of available options.
- **FWHM:** Allows report an array of information for Full Width Half Max measurements. See FWHM under Sample Lines(s) > Stats to View above for a full description of available options.

| | | | Sample | rype | | | | |
|--|---------------|--------|-----------------|-----------------|---------|----|------------------|-----|
| 1-D | 2-D | | 3-D | | | | | |
| Points | Ζ | ŀ | | ₩ / 4 | | 4 | $\boldsymbol{<}$ | |
| | | | Sample | Options | | | | |
| Name N | one | | | | | | | |
| Persi | stent | | | | | C | lear | |
| | | | ull Widt | h Half M | lax | | | |
| | Base V | alue 0 |) | 1 | Auto | | | |
| | Search | From | Outs | ide 🔘 | Maxim | um | | |
| | | | Stats to | View | | | | |
| General | DICOM Info | Points | Lines Traces | FWHM | Angles | | Perp Lines | |
| 🗹 Orien | t | | 🗹 End | dpoint Di | istance | |] Profi | ile |
| Name Curved Distance | | | | | | | | |
| End Point Locations Surface Distance | | | | | | | | |
| Maximum | | | | | | | | |
| 🗌 Minir | num | | | | | | | |
| Mean | | | | | | | | |
| C Stand | lard Devia | ation | | | | | | |

Analyze 15.0 User's Guide

Making Freehand Trace Measurements using Sample Trace(s)

Here we use the Sample Trace(s) tool to make freehand trace measurements.

Download the MRI_3D_Head.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load MRI_3D_Head.avw into Analyze. Select MRI_3D_Head and open Measure.
- Select the 1-D Sample Type [1] and choose Sample Trace(s) [2].
- Check any of the measurements required 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.



Sample Border(s)

The Sample Border(s) tool enables the measurement of a portion of an object's border. Note that an object map must be loaded in order to utilize this tool. The following user configuration options are available:

Sample Options: Provides users with access to the following border sampling option:

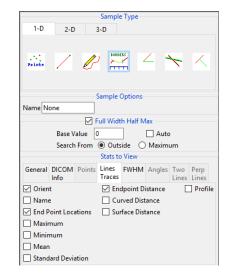
• **Name:** Allows users to assign a name to the region of the border being measured when reported to the log file.

Full Width Half Max: The Full Width Half Max option can be enabled for Sample Border(s), Sample Line(s) and Sample Trace(s) tool. For additional information refer to the FWHM description under Sample Line(s).

- **Base Value:** Allows users to specify the value used in the FWHM calculation.
- **Auto:** When enabled, the base value is automatically calculated by computing the mean of the nine-point neighborhoods around each endpoint of the line or trace
- Search from: Allows users to specify the search mode for FWHM measurement. The following options are available:
- · Outside: Specifies that search begins at the ends of the profiles.
- Maximum: Specifies that search begins at the maximum value and proceeds to the left and right for the two half max values.

Stats to View

- General: Allows users to report general image data parameters in the stats log file. See General under Sample Point(s) > Stats to View for a full description of available options.
- DICOM Info: Allows users to report DICOM tag information if the data is in the DICOM format. See the DICOM Info under Sample Point(s)
 > Stats to View above for a full description of available options.
- Lines Traces: Allows users to report an array of information about the trace. See Lines Trace under Sample Lines(s) > Stats to View above for a full description of available options.
- **FWHM:** Allows report an array of information for Full Width Half Max measurements. See FWHM under Sample Lines(s) > Stats to View above for a full description of available options.

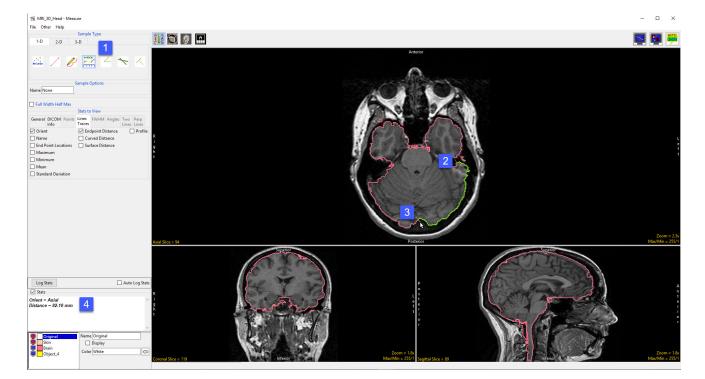


Making Border Measurements using Sample Border(s)

Here we use the Sample Border(s) tool to make border measurements.

Download the MRI_3D_Head.avw data set from analyzedirect.com/data to follow along.

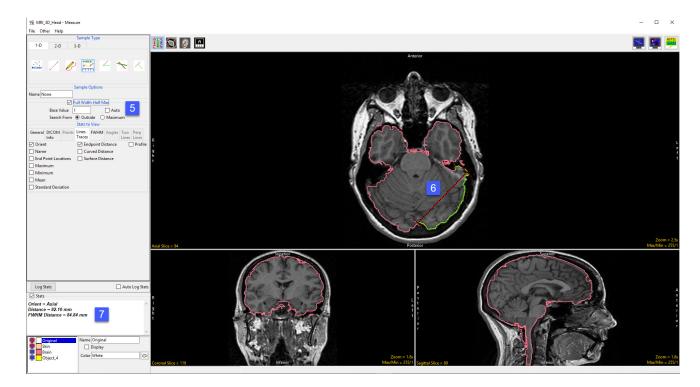
- Open Input/Output and load MRI_3D_Head.avw into Analyze.
 Select MRI_3D_Head and open Measure.
- Select File > Load Object Map and load the MRI_3D_Head.obj file.
- Select the Sample Border(s) tool
 [1] from 1-D Sample Type.



- To measure a length of an object border, move the cursor over the border and click to set the starting point [2] move the cursor to the where you wish to measure and click to set the end point [3].
- The distance measurement along the border will be reported in the stats display [4].

Making Border Measurements using Sample Border(s) (continued)

- To enable FWHM check the Full Width Half Max checkbox [5].
- Note that the FWHM is overlaid in red on the image display [6].
- The FWHM Distance will be reported in the stats display area
 [7]. If the FWHM distance is not displayed select the FWHM tab from Stats to View and select check the Distance option.



Sample Angle(s)

The Sample Angle(s) tool allows users to make distance measurements between points and angle measurements between defined lines. The following options are available:

Sample Options: Provides users with access to the following angle sampling options:

- · Name: Allows users to assign a name to the defined angle when reported to the log file.
- **Persistent:** When selected prevents previously defined angles for being cleared from the image.
- · Clear: Clears all angles from the image.

Stats to View

- General: Allows users to report general image data parameters in the stats log file. See General under Sample F ٠ a full description of available options.
- DICOM Info: Allows users to report DICOM tag information if the data is in the DICOM format. See the DICOM Info under Sample Point(s) ٠ > Stats to View above for a full description of available options.

Angles: The following angle measurement options are available:

- **Points:** Provides users with the option to report the following point related information and measurements: ٠
 - · Name: Reports the name entered in the Sample Options area for the angle measurement.
 - A: Reports the X, Y, Z coordinate location for point A of the angle measurement.
 - B: Reports the X, Y, Z coordinate location for point B of the angle measurement.
 - C: Reports the X, Y, Z coordinate location for point B of the angle measurement.
- **Distances:** Provides users with the option to report the following distance measurements: ۲
 - **AB:** Reports the distance between point A and point B.
 - BC: Reports the distance between point B and point C.
- Angles: Provides users with the option to report the following angle measurements:
 - **ABC 2-D:** Reports the 2D angle measurement.
 - ABC 3-D: Reports the 3D angle measurement.

| Name N | one | | Sample | Options | | | | | |
|-------------------|---------------|--------|-----------------|-----------|--------|---------|---------------|--|--|
| Persi | stent | | | | | C | lear | | |
| | | | Full Wid | th Half M | ax | | | | |
| | Base V | alue | 0 | | Auto | | | | |
| | Search | From | - | side 🔾 | Maximu | ım | | | |
| | | | Stats to | | | | | | |
| General | DICOM Info | Points | Lines Traces | | Angles | | Perp Lines | | |
| | oints | | Distan | ces | | Angle | s | | |
| Nam | e | _ | AB | | | ABC 2-D | | | |
| ☑ A ☑ B ☑ C | | E | 3C | | ABC | C 3-D | | | |
| | | | | | | | | | |

Sample Type

1-D

🗹 C

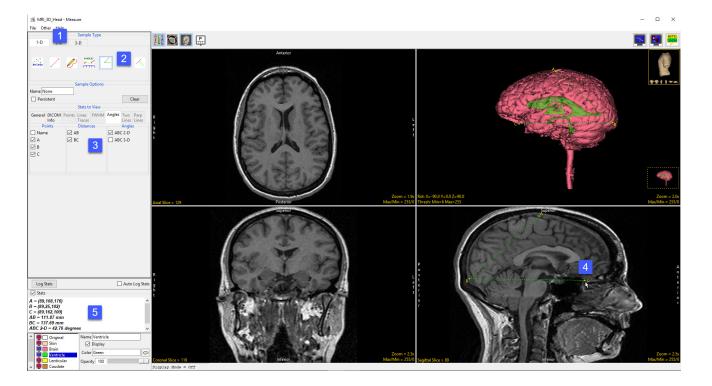
2-D 3-D

Making Angle Measurements using Sample Angle(s)

Here we use the Sample Angle(s) tool to make angle measurements.

Download the MRI_3D_Head.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load MRI_3D_Head.avw into Analyze.
 Select MRI_3D_Head and open Measure.
- Select File > Load Object Map and load the MRI_3D_Head.obj file.
- Select the 1D Sample Type [1]. Choose the Angles tool [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].



Sample Two Lines

Sample Type 1-D 2-D 3-D A RANDERS Sample Optic Name None Persisten Clear Full Width Half Max Auto Search From 💿 Outside 🔿 Maximum Stats to View General DICOM Points Lines FWHM Angles Two Perp Lines Lines Info Traces Points Distances Angles 🗌 Name AEC CEB B BED C BE DEA 🗹 🖸 CE **∠** E 🗹 DE

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

Sample Options: Provides users with access to the following sampling options:

- Name: Assigns a name to the defined set of two-line measurements when reported to the log file.
- **Persistent:** Prevents previously defined two-line measurements for being cleared from the image.
- · **Clear:** Clears all measurements from the image.

Stats to View

- General: Allows reporting of general data parameters in the stats log file. See General under Sample Point(s) > Stats to View.
- **DICOM Info:** Allows users to report DICOM tag information. See the DICOM Info under Sample Point(s) > Stats to View.

Two Lines:

- **Points:** Provides users with the option to report the following point related information and measurements:
 - Name: Reports the name entered in the Sample Options area for the two lines measurement.
 - A: Reports the X, Y, Z coordinate location for point A of the two line(s) tool.
 - B: Reports the X, Y, Z coordinate location for point B of the two line(s) tool.
 - C: Reports the X, Y, Z coordinate location for point C of the two line(s) tool.
 - D: Reports the X, Y, Z coordinate location for point D of the two line(s) tool.
 - E: Reports the X, Y, Z coordinate location for point E of the two line(s) tool.
- **Distances:** Provides users with the option to report the following distance measurements:
 - **AB:** Reports the distance between point A and point B.
 - \cdot **CD:** Reports the distance between point C and point D.
 - $\cdot\,$ AE: Reports the distance between point A and point E.

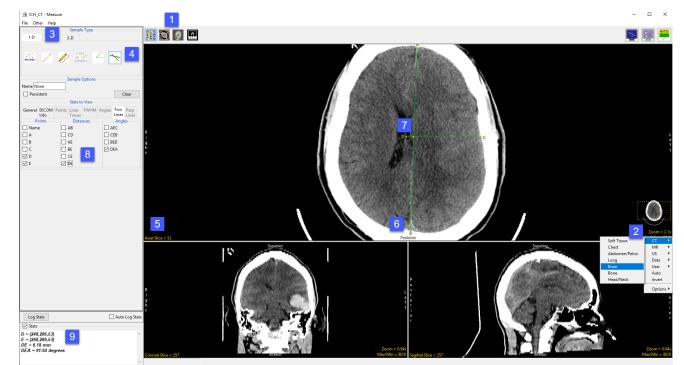
- $\cdot\,$ **BE:** Reports the distance between point B and point E.
- · CE: Reports the distance between point C and point E.
- **DE:** Reports the distance between point D and point E.
- Angles: Provides users with the option to report the following angle measurements:
 - **AEC:** Reports the 2D angle measurement for points A-E-C.
 - **CEB:** Reports the 2D angle measurement for points C-E-B.
- **BED:** Reports the 2D angle measurement for points B-E-D.
- · **DEA:** Reports the 2D angle measurement for points D-E-A.

559

Making Measurements using Sample Two Lines

Download the ICH_CT.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load
 ICH_CT.avw into Analyze. Select
 ICH_CT and open Measure.
- Use the display configuration tools to display the 3 ortho sections making axial view the primary [1].
- Right click on the Max/Min option and select CT > Brain. This will provide a better display of the brain structure in the CT data [2]. Select the 1D [3] Sample Type and choose Sample Two Lines [4].



- To measure the displacement of the septum pellucidum from the midline at the level of the foramen of Monro, find a suitable axial slice to make the measurement on. [5]
- 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 [6]. 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. [7] 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. [8] 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. [9]

Analyze 15.0 User's Guide

Sample Perpendicular Lines

The Sample Perpendicular Lines tools allows users to make point and distance measurements perpendicular to a defined line (points A and B).

Sample Options: Provides users with access to the following sampling options:

- · Name: Assigns a name to the perpendicular line measurements when reported to the log file.
- **Persistent:** Prevents previously defined perpendicular line measurements for being cleared.
- · Clear: Clears all perpendicular line measurements from the image.

Stats to View

- General: Allows users to report general image data parameters in the stats log file. See General under Sample Point(s) > Stats to View for a full description of available options.
- DICOM Info: Allows users to report DICOM tag information if the data is in the DICOM format. See the DICOM Info under Sample Point(s)
 > Stats to View above for a full description of available options.

Perp Lines:

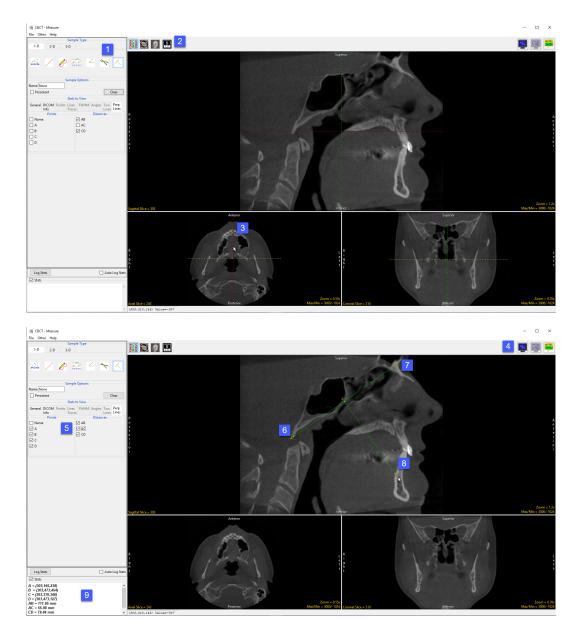
- Points: Provides users with the option to report the following point related information and measurements:
 - Name: Reports the name entered in the Sample Options area for the perpendicular line measurement.
 - A: Reports the X, Y, Z coordinate location for point A of the perpendicular line tool.
 - B: Reports the X, Y, Z coordinate location for point B of the perpendicular line tool.
 - C: Reports the X, Y, Z coordinate location for point C of the perpendicular line tool.
 - D: Reports the X, Y, Z coordinate location for point D of the perpendicular line tool.
- **Distances:** Provides users with the option to report the following distance measurements:
 - **AB:** Reports the distance between point A and point B.
 - AC: Reports the distance between point A and point C.
 - **CD:** Reports the distance between point C and point D.

| | | | Sampl | е Туре | | | |
|------------|--------|--------|-----------------|-------------|--------|-------|-----------------|
| 1-D | 2-0 | | 3-D | | | | |
| Points | / | Ŀ | 50M | 1 1 1 | | ~ | $\overline{\ }$ |
| | | | Sample | Options | | | |
| Name N | one | | | | | | |
| Persi | stent | | | | | C | lear |
| | | | ull Wid | th Half M | lax | | |
| | Base V | | | | Auto | | |
| | | | | side | _ | | |
| | Searci | FIOM | ~ | o View | Widxim | um | |
| c 1 | DICOL | n : . | | | | - | Dem |
| General | Info | Points | Lines Traces | FWHM | Angles | Lines | Perp Lines |
| | Point | s | | | Distan | | |
| 🗌 Nam | e | | E | AB | | | |
| 🖂 🗛 | | | E | AC | | | |
| 🖂 B | | | E | CD 🔽 | | | |
| ⊡ c | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |

Making Perpendicular Line Measurements using Sample Perpendicular Lines

The sample perpendicular lines tool is useful when making measurement perpendicular to specific landmarks in a data set. Download the CBCT.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load CBCT.avw into Analyze. Select CBCT and open Measure. Select the Sample Perpendicular Lines tool [1] from the 1-D Sample Type tab. Set the measure display so that all three orthogonal views are displayed with the Sagittal as the primary display [2].
- Adjust the Cursor Link tool in the axial [3] or coronal view to select a sagittal slice close to the mid-sagittal point. Toggle off the Cursor Link tool [4]. Enable all required Point and Distance measurements [5].
- Click on an area at the base of the skull [6] to set the first point (A) for the tool. Drag the second point B) to an area in the nasal bone [7]. The perpendicular line (points C and D) will appear halfway between points A and B. Drag point D to the mandible [8].
- The selected measurements will be reported to the stats display area [9]. Click Log Stats to log these measurements to a stats file that can be saved to disk.



2-D Measurement Tools

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.

2D measurements include measurements tools that can be used with or without object maps, these include; rectangular region of interest sampling, oval region of interest sampling, free trace region of interest sampling, and entire image sampling. The remaining three 2-D sampling options can only be used with an object map, these are; selected regions, selected object, and enabled object.

The 2-D tab provides access to the following measurement tools:

- · Sample 2-D Rectangle
- · Sample 2-D Oval
- · Sample 2-D Closed Trace

Sample 2-D Rectangle

The Sample 2-D Rectangle tool enables the drawing of a rectangle on the displayed image to define a region. To define a rectangular region left click on the image and then drag the cursor until the desired size and shape rectangle has been define. The following sampling options are available.

Sample Options: Provides users with access to the following 2-D Rectangle sampling options:

- · Name: Allows users to assign a name to the selected rectangle when reported to the log file.
- **Persistent:** When selected prevents previously defined rectangles for being cleared from the image.
- · Clear: Clears all rectangles from the image.

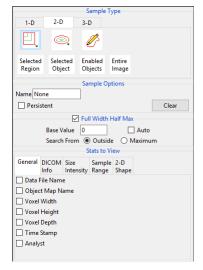
Stats to View: The stats to view area allows users to enable and disable measurements and information reported to the stats log.

Selected RegionSelected Object

- \cdot Enabled Object
- · Entire Image

Stats to View (continued):

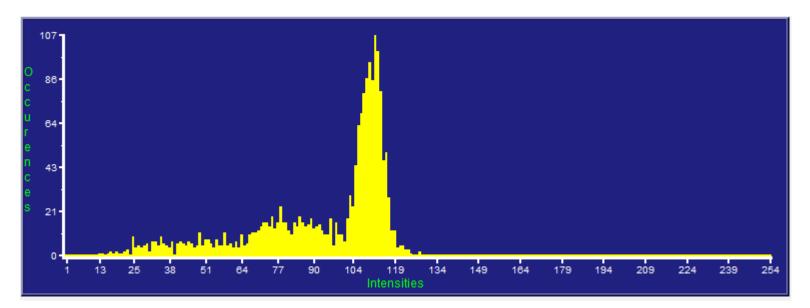
- **General:** Allows users to report general image data parameters in the stats log file. See General under Sample Point(s) > Stats to View for a full description of available options.
- **DICOM Info:** Allows users to report DICOM tag information if the data is in the DICOM format. See DICOM Info under Sample Point(s) > Stats to View above for a full description.
- **Size Intensity:** Allows users to report an array of size intensity information and measurements. The following options are available:
 - · Orient: Reports the orientation the region was defined in.
 - · Name: Reports the name entered in the Sample Options area for the region.
 - **Slice:** Reports the slice the region was defined on.
 - · Maximum: Reports the maximum voxel intensity in the region.
 - **Max Location:** Reports the location of the voxel with the maximum intensity value.
 - **Minimum:** Reports the minimum voxel intensity in the region.
 - · Min Location: Reports the location of the voxel with the minimum intensity value.
 - Number of Voxels: Reports the number of voxels in the defined region.
 - Area: Reports the area of the region using the formula: Area = number of voxels x voxel width x voxel height
 - **Volume:** Reports the volume of the region using the formula: Volume = number of voxels x voxel width x voxel height x voxel depth
 - Mean: Reports the mean intensity value of the voxels sampled in the region.
 - · St. Dev: Reports the standard deviation of the sampled voxels.
 - Sum: Reports the sum of the intensity values of the sampled voxels.
 - · Entropy: Reports the Shannon entropy of the sampled voxels.



Stats to View > Size Intensity (continued):

- Histogram: The histogram option reports plots the histogram of the region (intensities vs. occurrence) and reports relevant histogram information including:
- **Orient:** Reports the orientation the region was defined in.
- Slice: Reports the slice number the region was defined on.
- **Object:** Reports the object or region name.
- · Intensity: Reports all intensity values in the region.
- · Count: Reports the count of the intensity in the region
- Histogram Mode: Reports the Histogram Mode value.
- **Histogram Median:** Reports the Histogram Median value.

| Histogram | | 01:00 | 1.1 | C 1 | Histogram | Histogram |
|-----------|-------|--------|-----------|------------|-----------|-----------|
| Orient | Slice | Object | Intensity | Count | Mode | Median |
| Axial | 136 | Brain | 1.00 | 0 | 112.00 | 104.00 |
| Axial | 136 | Brain | 2.00 | 0 | | |
| Axial | 136 | Brain | 3.00 | 0 | | |
| Axial | 136 | Brain | 4.00 | 0 | | |
| Axial | 136 | Brain | 5.00 | 0 | | |
| Axial | 136 | Brain | 6.00 | 0 | | |
| Axial | 136 | Brain | 7.00 | 0 | | |
| Axial | 136 | Brain | 8.00 | 0 | | |
| Axial | 136 | Brain | 9.00 | 0 | | |
| Axial | 136 | Brain | 10.00 | 0 | | |
| Axial | 136 | Brain | 11.00 | 0 | | |
| Axial | 136 | Brain | 12.00 | 0 | | |
| Axial | 136 | Brain | 13.00 | 0 | | |
| Axial | 136 | Brain | 14.00 | 0 | | |
| Axial | 136 | Brain | 15.00 | 0 | | |
| < 1 | 100 | - · | 46.00 | - | | |



Stats to View > Size Intensity (continued):

- **Boundary Coordinates:** Reports the boundary (perimeter) coordinates of the region. Measurements include the following:
- · Index: Boundary pixel reference number.
- X: Reports the X position of the boundary coordinate.
- Y: Reports the Y position of the boundary coordinate.
- · **Slice:** Reports the slice position of the boundary coordinate.
- Orient: Reports the orientation the sampled region is defined in.
- Value: Reports the greyscale value of the boundary coordinate.
- · **Object:** Reports selected or enabled object when an object map is loaded.
- **Border:** Reports border thickness when an object map is loaded.
- **Region Pixels:** Reports information on all pixels that make up the defined region, measurements include:
- · Index: Region pixel reference number.
- X: Reports the X position of the pixel.
- Y: Reports the Y position of the pixel.
- Slice: Reports the slice position of the pixel.
- **Orient:** Reports the orientation the sampled region is defined in.
- · Value: Reports the greyscale value of the pixel.
- **Object:** Reports selected or enabled object when an object map is loaded.

| Bounda | ry Co | ordina | ates | | | | |
|--------|-------|--------|-------|--------|-------|--------|--------|
| Index | Х | Y | Slice | Orient | Value | Object | Border |
| 1 | 79 | 10 | 136 | Axial | 45 | Skin | 1 |
| 2 | 80 | 11 | 136 | Axial | 89 | Skin | 1 |
| 3 | 81 | 11 | 136 | Axial | 87 | Skin | 1 |
| 4 | 82 | 11 | 136 | Axial | 88 | Skin | 1 |
| 5 | 83 | 11 | 136 | Axial | 89 | Skin | 1 |
| 6 | 84 | 11 | 136 | Axial | 83 | Skin | 1 |
| 7 | 85 | 11 | 136 | Axial | 82 | Skin | 1 |
| 8 | 86 | 10 | 136 | Axial | 45 | Skin | 1 |
| 9 | 87 | 10 | 136 | Axial | 55 | Skin | 1 |
| 10 | 88 | 10 | 136 | Axial | 63 | Skin | 1 |
| 11 | 89 | 10 | 136 | Axial | 65 | Skin | 1 |
| 12 | 90 | 10 | 136 | Axial | 67 | Skin | 1 |
| 13 | 91 | 10 | 136 | Axial | 71 | Skin | 1 |
| 14 | 92 | 10 | 136 | Axial | 73 | Skin | 1 |
| 15 | 93 | 10 | 136 | Axial | 70 | Skin | 1 |

| Region | Pixels | | | | | |
|--------|--------|----|-------|--------|-------|--------|
| Index | Х | Y | Slice | Orient | Value | Object |
| 1 | 79 | 25 | 136 | Axial | 62 | Brain |
| 2 | 80 | 25 | 136 | Axial | 73 | Brain |
| 3 | 81 | 25 | 136 | Axial | 79 | Brain |
| 4 | 82 | 25 | 136 | Axial | 82 | Brain |
| 5 | 83 | 25 | 136 | Axial | 78 | Brain |
| 6 | 84 | 25 | 136 | Axial | 63 | Brain |
| 7 | 89 | 25 | 136 | Axial | 53 | Brain |
| 8 | 90 | 25 | 136 | Axial | 78 | Brain |
| 9 | 91 | 25 | 136 | Axial | 105 | Brain |
| 10 | 94 | 25 | 136 | Axial | 95 | Brain |
| 11 | 95 | 25 | 136 | Axial | 77 | Brain |
| 12 | 96 | 25 | 136 | Axial | 53 | Brain |

Stats to View (continued):

- **Sample Range:** Allows users to sample voxels within the defined region based on a minimum and maximum intensity range. The following options are available.
 - **Sample Range Slider:** The sample range slider allows users to define a minimum and maximum sample range based on the image histogram. Only voxels that meet the specified criteria will be sampled.
 - Range Min: Set the minimum for the sampling range.
 - **Range Max:** Set the maximum for the sampling range.
 - < Sample Min: Reports the number of voxels with an intensity value less than the specified minimum range value.
 - · > Sample Max: Reports the number of voxels with an intensity value greater than the specified maximum range value.
 - >= SMin & <= SMax: Reports the number of voxels with an intensity value equal to or greater than the sample minimum and equal to or less than the sample maximum.</p>
 - Mean in Range: Reports the mean intensity value of the voxels within the specified minimum and maximum sampling range.
 - STD in Range: Reports the standard deviation of the sampled voxels.
 - **Sum in Range:** Reports the sum of the intensity values of the sampled voxels within the defined range.
 - · Area in Range: Reports the area of the sampled voxels within the defined range.
 - · Volume in Range: Reports the volume of the sampled voxels within the defined range.
 - Brightness Area Product: Reports the Brightness Area Product for the sampled voxels. The value is calculated from the formula:
 (Mean in Range Min) * No. Pixels In Range.
- **2-D Shape:** All 2-D shape measurements assume the input image data will have square pixels and are in units of linear pixel-sides or square pixels as appropriate. The following options are available.
 - **MER Angle Resolution:** MER (Minimum Enclosing Rectangle) specifies the angle resolution to be used when searching for the Minimum Enclosing Rectangle.
 - **Perimeter:** Reports the perimeter of the region in pixel-sides and in calibrated voxel units.

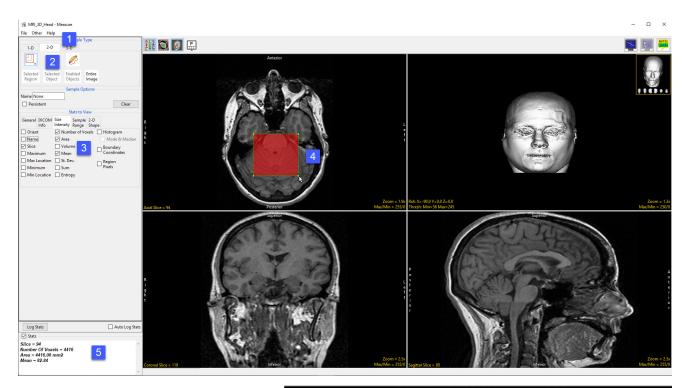
Stats to View > 2-D Shape (continued):

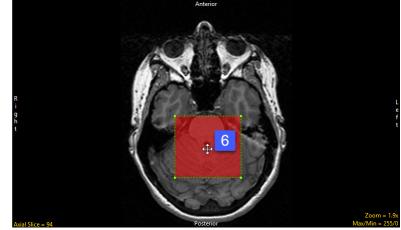
- **MER Angle:** Reports the angle of rotation in one-degree increments, at which the sides of the minimum enclosing Rectangle is parallel to the X and Y axes.
- **MER Area:** Reports the minimum enclosing rectangle.
- **MER Aspect Ratio:** Reports the short side of the minimum enclosing rectangle to the long side.
- **MER Coordinates:** Reports the coordinates of the four corners of the MER.
- **Rectangular Fit Factor:** Reports the ratio of the area of the region to the area of the minimum enclosing rectangle.
- **Circularity:** Reports the ratio of the perimeter squared of the region to the area of the region, (P²/A). This parameter takes on a minimum value of 4 pi for a circle.
- **Circ./(4*Pi):** Reports the circularity value divided by 4*Pi. This value should be 1 for a perfect circle.
- · Centroid: Reports the center gravity for the region.
- **Surface Voxels:** For use with the rendered image only. Reports the total number of voxels counted on the surface of the defined region.
- Surface Faces: For use with the rendered image only. Reports the total number of exposed faces for all surface voxels.
- Planar Area: For use with the rendered image only. Reports the count of 2-D pixels in the user defined area.
- **Surface Area:** For use with the rendered image only. Reports an estimate of the structures surface area within the defined region, computed by examining each surface voxel found via the tracking algorithm and assigning a surface area component for each voxel based on its non-surface neighbors.

Making 2D Rectangular Measurements using Sample 2-D Rectangle

Download the MRI_3D_Head.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load MRI_3D_Head.avw into Analyze. Select MRI_3D_Head and open Measure.
- Select File > Load Object Map and load the MRI_3D_Head.
 obj file. Select the 2D Sample
 Type [1] and choose Sample 2-D
 Rectangle(s) [2].
- In the Stats to View area check all required measurements [3] in the stats review area.
- Define a rectangle on the current axial slice [4].
- Selected measurements will be reported for the region in the stats review area [5]. Click Log Stats to return the stats to a log file that can be saved out of Analyze as a .csv file.
- Note, to move the rectangle, place the cursor in the center of the rectangle. When the cursor updates its shape [6] move the rectangle up, down, left, or right.





© AnalyzeDirect, Inc.

Sample 2-D Oval

The Sample 2-D Oval tools enabled the drawing of an oval on the displayed image to define a region for sampling. To define an oval region left click on the image and then drag the cursor until the desired size and shape oval has been define. The following sampling options are available:

Sample Options: Provides users with access to the following 2-D oval sampling options:

- Name: Allows users to assign a name to the selected oval when reported to the log file.
- Persistent: Prevents previously defined ovals for being cleared from the image.
- **Clear:** Clears all ovals from the image.

Stats to View: The stats to view area allows users to enable and disable measurements and information reported to the stats log.

- **General:** Allows users to report general image data parameters in the stats log file. See General under Sample Point(s) > Stats to View for a full description of available options.
- **DICOM Info:** Allows users to report DICOM tag information if the data is in the DICOM format. See DICOM Info under Sample Point(s) > Stats to View above for a full description of available options.
- Size Intensity: Allows users to report an array of size intensity information and measurements. Refer to the size Intensity description for Sample 2-D Rectangle for a description of all available options.
- **Sample Range:** Allows users to sample voxels within the defined region based on a minimum and maximum intensity range. Refer to the Sample Range description for Sample 2-D Rectangle for a description of all available options.
- **2-D Shape:** Allows users to report 2-D shape measurements for the defined region. Refer to the 2-D Shape description for Sample 2-D Rectangle for a description of all available options.

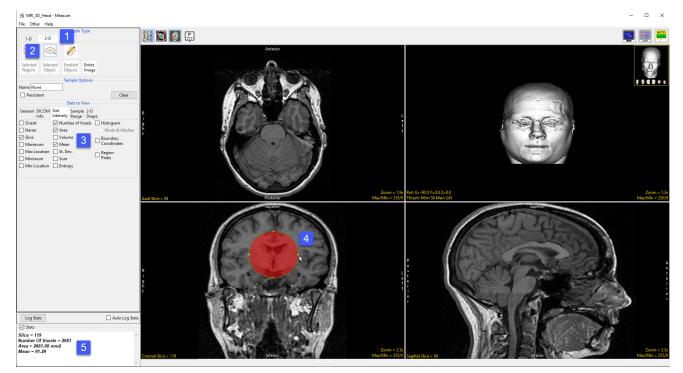
| | | | sample i | ype | | | | |
|--------------------|---------------|-------------------|-----------------|-----------------|--------|-------|--|--|
| 1-D | 2-D | 3- | D | | | | | |
| 믠 | | 2 | Ø | | | | | |
| Selected Region | Selec Obje | | abled | Entire Image | | | | |
| | | Sa | mple Op | tions | | | | |
| Name No | ne | | | | | | | |
| Persis | tent | | | | | Clear | | |
| | | 🗹 Fu | ll Width | Half Ma | x | | | |
| | Base V | alue 0 | | Г | Auto | | | |
| | Search | From |) Outsid | e () | Maximu | im | | |
| | | | Stats to V | iew | | | | |
| General | DICOM Info | Size Intensity | Sample Range | | | | | |
| 🗌 Data F | ile Nam | 2 | | | | | | |
| Object | Map Na | ame | | | | | | |
| Voxel Width | | | | | | | | |
| Voxel Height | | | | | | | | |
| Voxel | | | | | | | | |
| Time ! | | | | | | | | |
| Analy: | t | | | | | | | |
| | | | | | | | | |

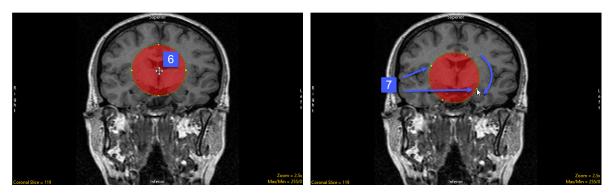
570

Making 2D Oval Measurements using Sample 2-D Oval

Download the MRI_3D_Head.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load MRI_3D_Head.avw into Analyze. Select MRI_3D_Head and open Measure.
- Select File > Load Object Map and load the MRI_3D_Head.obj file.
 Select the 2D Sample Type [1] and choose Sample 2-D Oval(s) [2]. In the Stats to View area check all required measurements [3] in the stats review area. Define a oval on the current coronal slice [4].
- Selected measurements will be reported for the region in the stats review area [5]. Click Log Stats to return the stats to a log file that can be saved out of Analyze as a .csv file. Note, to move the oval, place the cursor in the center of the oval. When the cursor updates its shape [6] move the oval up, down, left, or right. The oval can also be rotated using the either of the two larger green control points [7].





571

Sample 2-D Closed Trace

The Sample 2-D Closed Trace tools enable the drawing of a trace to define a region to sample on an image. When selected, position the cursor on the displayed slice, press and hold the left mouse button to draw a trace, release the mouse button to end the trace. The last point of the trace drawn is automatically connected to the first point of the trace. The following sampling options are available:

Sample Options: Provides users with access to the following 2-D closed trace sampling options:

- · Name: Assigns a name to the selected closed trace when reported to the log file.
- Persistent: Prevents previously defined closed traces for being cleared from the image.
- Clear: Clears all closed traces from the image.

Stats to View: The stats to view area allows users to enable and disable measurements and information reported to the stats log.

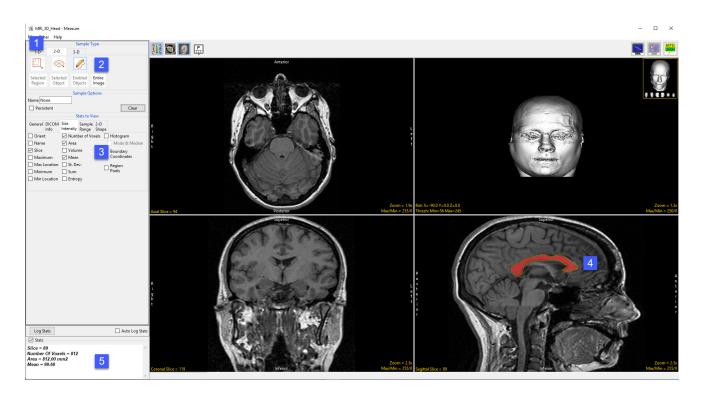
- **General:** Allows users to report general image data parameters in the stats log file. See General under Sample Point(s) > Stats to View for a full description of available options.
- DICOM Info: Allows users to report DICOM tag information if the data is in the DICOM format. See DICOM Info under Sample Point(s) > Stats to View above for a full description of available options.
- Size Intensity: Allows users to report an array of size intensity information and measurements. Refer to the size Intensity description for Sample 2-D Rectangle for a description of all available options.
- **Sample Range:** Allows users to sample voxels within the defined region based on a minimum and maximum intensity range. Refer to the Sample Range description for Sample 2-D Rectangle for a description of all available options.
- **2-D Shape:** Allows users to report 2-D shape measurements for the defined region. Refer to the 2-D Shape description for Sample 2-D Rectangle for a description of all available options.

| | | S | ample Ty | /pe | | | |
|--------------------|---------------|-------------------|-----------------|-----------------|--------|-----|-----|
| 1-D | 2-D | 3-1 | D | | | | |
| 旦 | | 2 | Ø | | | | |
| Selected Region | | | | Entire Image | | | |
| | | Sa | mple Opt | tions | | | |
| Name N | one | | | | | | |
| Persi | stent | | | | | Cle | ear |
| | | 🗹 Fu | ll Width H | lalf Ma | (| | |
| | Base V | alue 0 | | | Auto | | |
| | Search | From (| Outside | 0 | Aaximu | m | |
| | | S | tats to Vi | ew | | | |
| General | DICOM Info | Size Intensity | Sample Range | 2-D Shape | | | |
| 🗌 Data I | File Nam | e | | | | | |
| 🗌 Objec | t Map N | ame | | | | | |
| Voxel | Width | | | | | | |
| Voxel | - | | | | | | |
| Voxel | | | | | | | |
| Time | | | | | | | |
| Analy | st | | | | | | |
| | | | | | | | |

Making 2D Closed Trace Measurements using Sample 2-D Closed Trace

Download the MRI_3D_Head.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load MRI_3D_Head.avw into Analyze. Select MRI_3D_Head and open Measure.
- Select File > Load Object Map and load the MRI_3D_Head.obj file.
- Select the 2D Sample Type [1] and choose Sample 2-D Closed Trace [2].
- In the Stats to View area check all required measurements [3] in the stats review area.
- On the current sagittal slice define a trace around the corpus callosum [4].
- Selected measurements will be reported for the region in the stats review area [5].



Selected Region

The Selected Region option allows users to sample a region of an object on a 2D slice. An object map must be loaded for this sampling option to be available.

Sample Options: Provides users with access to the following selected region options:

• Name: Allows users to assign a name for the selected region when reported to the log file.

Stats to View: The stats to view area allows users to enable and disable measurements and information reported to the stats log.

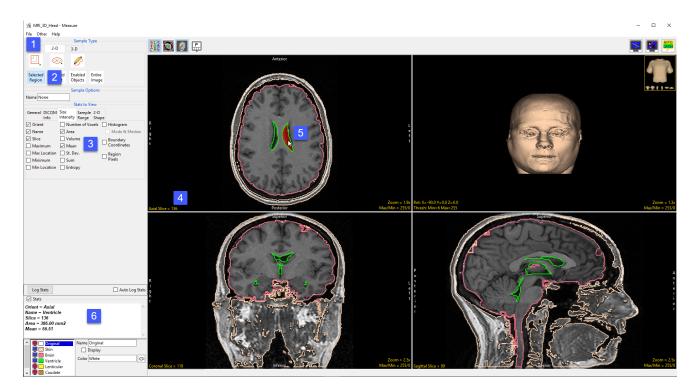
- **General:** Allows users to report general image data parameters in the stats log file. See General under Sample Point(s) > Stats to View for a full description of available options.
- DICOM Info: Allows users to report DICOM tag information if the data is in the DICOM format. See DICOM Info under Sample Point(s) > Stats to View above for a full description of available options.
- Size Intensity: Allows users to report an array of size intensity information and measurements. Refer to the size Intensity description for Sample 2-D Rectangle for a description of all available options.
- **Sample Range:** Allows users to sample voxels within the defined region based on a minimum and maximum intensity range. Refer to the Sample Range description for Sample 2-D Rectangle for a description of all available options.
- **2-D Shape:** Allows users to report 2-D shape measurements for the defined region. Refer to the 2-D Shape description for Sample 2-D Rectangle for a description of all available options.

| | | | Sample | Туре | | | |
|--------------------|---------|--------------|--------------------|-----------------|---------|--|--|
| 1-D | 2-D | | 3-D | | | | |
| Щ | | 2 | Ø | | | | |
| Selected Region | | | Enabled Objects | Entire Image | | | |
| | | | Sample (| Options | | | |
| Name N | one | | | | | | |
| | | \checkmark | Full Widt | h Half Ma | x | | |
| | Base V | alue | 0 |] [| Auto | | |
| | Search | From | Outs | ide 🔘 | Maximum | | |
| | | | Stats to | View | | | |
| General | | | | e 2-D Shape | 2 | | |
| 🗌 Data I | ile Nam | e | | | | | |
| 🗌 Objec | t Map N | ame | | | | | |
| Voxel | Width | | | | | | |
| Voxel Height | | | | | | | |
| Voxel Depth | | | | | | | |
| 🗌 Time | Stamp | | | | | | |
| 🗌 Analy | st | | | | | | |
| | | | | | | | |

Making Measurements using Selected Region

Download the MRI_3D_Head.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load MRI_3D_Head.avw into Analyze. Select MRI_3D_Head and open Measure.
- Select File > Load Object Map and load the MRI_3D_Head.obj file.
- Select the 2D Sample Type [1] and choose Selected Region [2].
- In the Stats to View area check all required measurements [3] in the stats review area.
- Move to axial slice 136 [4]. Click in the ventricle object on the left side to sample [5].
- Selected measurements will be reported for the region in the stats review area [6].



To sample all of the ventricle on this slice please refer to the Selected Object sampling type on the following pages.

Selected Object

The Selected Object option allows users to sample an object on a 2D slice. An object map must be loaded for this sampling option to be available.

Stats to View: The stats to view area allows users to enable and disable measurements and information reported to the stats log.

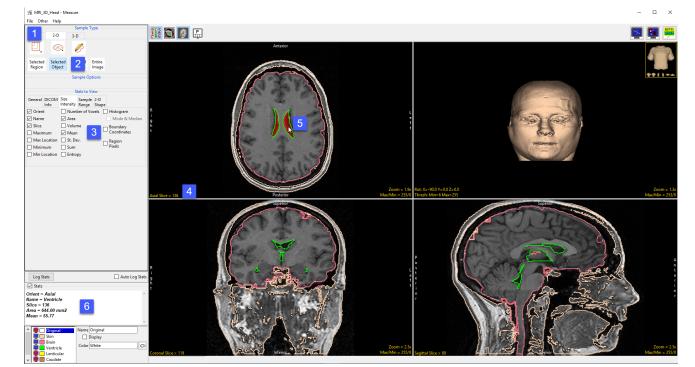
- **General:** Allows users to report general image data parameters in the stats log file. See General under Sample Point(s) > Stats to View for a full description of available options.
- DICOM Info: Allows users to report DICOM tag information if the data is in the DICOM format. See DICOM Info under Sample Point(s) > Stats to View above for a full description of available options.
- **Size Intensity:** Allows users to report an array of size intensity information and measurements. Refer to the size Intensity description for Sample 2-D Rectangle for a description of all available options.
- **Sample Range:** Allows users to sample voxels within the defined region based on a minimum and maximum intensity range. Refer to the Sample Range description for Sample 2-D Rectangle for a description of all available options.
- **2-D Shape:** Allows users to report 2-D shape measurements for the defined region. Refer to the 2-D Shape description for Sample 2-D Rectangle for a description of all available options.

| | | - | unpic i) | pc . | | | | | | | |
|--------------------|---------------|-------------------|-----------------|-----------------|---------|--|--|--|--|--|--|
| 1-D | 2-D | 3-1 | D | | | | | | | | |
| | | 2 | ß | | | | | | | | |
| Selected Region | Selec Obj | | | Entire Image | | | | | | | |
| | | Sa | mple Opt | tions | | | | | | | |
| | | | | | | | | | | | |
| | | Ful | ll Width H | lalf Ma | x | | | | | | |
| | Base V | alue 0 | | C | Auto | | | | | | |
| | Search | From (| | ~ | Maximum | | | | | | |
| | | S | tats to Vi | ew | | | | | | | |
| General | DICOM Info | Size Intensity | Sample Range | | | | | | | | |
| 🗌 Data F | ile Nam | e | | | | | | | | | |
| 🗌 Objec | t Map N | ame | | | | | | | | | |
| Voxel | Width | | | | | | | | | | |
| Voxel | - | | | | | | | | | | |
| Voxel | Voxel Depth | | | | | | | | | | |
| Time: | | | | | | | | | | | |
| Analy: | st | | | | | | | | | | |
| | | | | | | | | | | | |

Making Measurements using Selected Object

Download the MRI_3D_Head.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load MRI_3D_Head.avw into Analyze. Select MRI_3D_Head and open Measure.
- Select File > Load Object Map and load the MRI_3D_Head.obj file.
- Select the 2D Sample Type [1] and choose Selected Object [2].
- In the Stats to View area check all required measurements [3] in the stats review area.



- Move to axial slice 136 [4]. Click in the ventricle object on either the left or right side to sample [5]. Note that even though the two regions of the ventricle on this slice are spatially disconnected both are sampled as the sample type, selected object, will sample all voxels assigned to the selected object on the current 2D slice.
- Selected measurements will be reported for the region in the stats review area [6].

Enabled Objects

The Enabled Objects option allows sampling of all enabled objects (currently displayed) for the current slice, all slices, or a range of slices. An object map must be loaded for this option to be available.

Sample Options: Provides users the following sampling controls:

- **Orient:** Select the orientation to sample enabled objects in.
 - · Axial: Sets the sampling orientation to axial.
 - · **Coronal:** Sets the sampling orientation to coronal.
 - · Sagittal: Sets the sampling orientation to sagittal.
- **Slices:** Allows users to specify the slices sampled.
 - **Current Slice:** Samples the current displayed slice for the selected orientation.
 - · All Slices: Samples all slices in the selected orientation.
 - Slice Range: Samples the range of samples specified using the start and end slice fields for the selected orientation.
 - Start Slice: Allows users to set the starting slice for sampling. Slices before the start slice will not be sampled.
 - **End Slice:** Allows users to set the ending slice for sampling. Slices after the end slice will not be sampled.
 - · Combine Objects: Allows users to sum the measurements of the individually sampled objects.
 - · Name: Allows users to specify a name for the combined object measurements when reported to the stats log.
- Sample Enabled Objects: Initiates the sampling process.

Stats to View: The stats to view area allows users to enable and disable measurements and information reported to the stats log.

- General: Allows users to report general image data parameters in the stats log file (see General under Sample Point(s) > Stats to View.)
- DICOM Info: Allows users to report DICOM tag information (see DICOM Info under Sample Point(s) > Stats to View.)
- Size Intensity: Reports an array of size intensity information and measurements (see Size Intensity description for Sample 2-D Rectangle.)
- Sample Range: Samples voxels within a defined region based on a min/max intensity range (see Sample 2-D Rectangle > Sample Range.)
- **2-D Shape:** Reports 2-D shape measurements for the defined region (see Sample 2-D Rectangle > 2-D Shape.)



Analyze 15.0 User's Guide

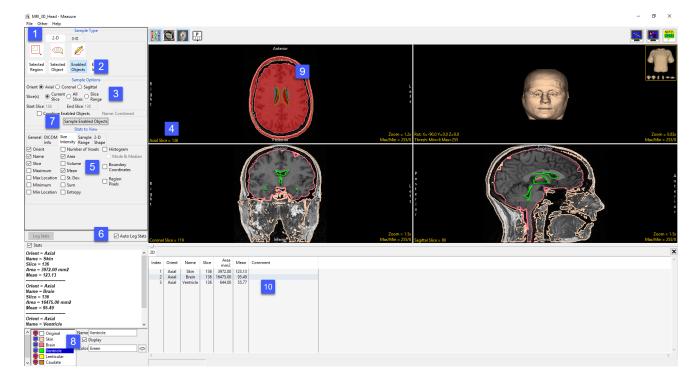
Sampling Objects using Enabled Objects

Download the MRI_3D_Head.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load MRI_3D_Head.avw into Analyze. Select MRI_3D_Head and open Measure.
- Select File > Load Object Map and load the MRI_3D_Head.obj file.
- Select the 2D Sample Type [1] and choose Enabled Objects [2].

Sampling the Current Slice

To sample all enabled objects for the current slice in a particular orientation, do the following:



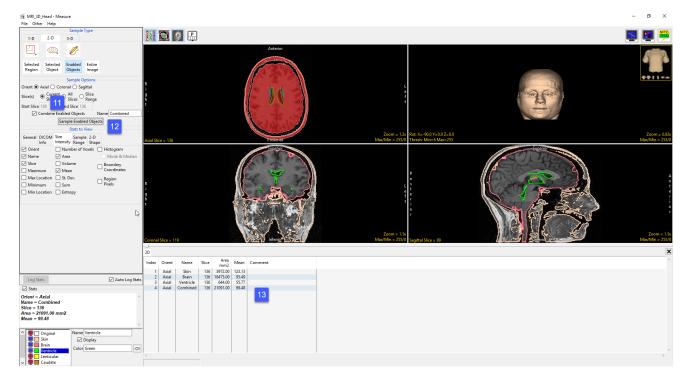
- Leave Orient set to Axial and Slice(s) set to Current [3]. This will sample the current axial slice when Sample Enabled Objects is selected. Change the axial slice to 136 [4].
- In the Stats to View area check all the measurements [5] to be reported. Check the Auto Log option [6].
- Click the Sampled Enabled Object button [7].
- All objects currently displayed [8] will be sampled. The sampled objects are displayed for the current slice in the current orientation [9].
- The selected measurements will be returned to the stats log for the current slice [10].

Analyze 15.0 User's Guide

Combining Objects for the Current Slice

To return summed measurements for the enabled objects, do the following: To return summed measurements for the enabled objects, do the following:

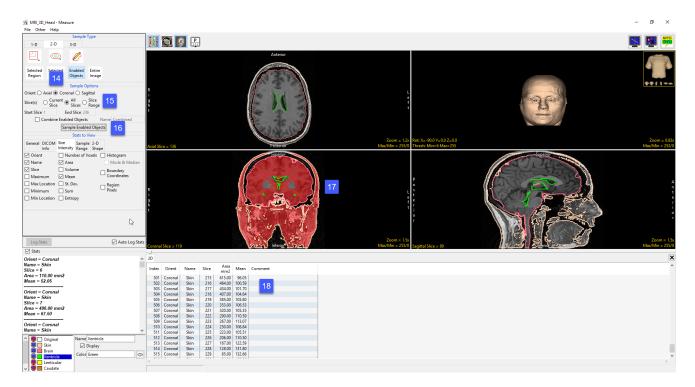
- Check the Combine Enabled
 Objects check box [11]. Leave the
 Name set to Combined.
- Click the Sampled Enabled Object button [12].
- All objects currently displayed will be sampled. The sampled objects are displayed in red in the current orientation. Measurements will be summed for the enabled objects (skin + brain + ventricles) and returned in a new row in the stats log [13].



Sampling All Slices

To sample all enabled objects for all slices in a particular orientation, do the following:

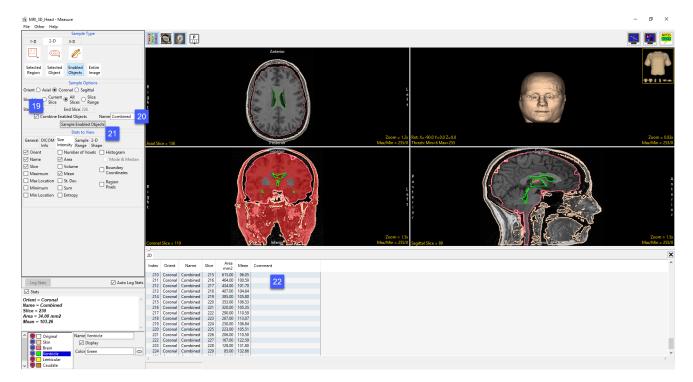
- Dismiss the stats log by clicking the x in the upper right-hand corner of the stats log.
- Set the Orient to Coronal [14] and set Slice(s) set to All Slices [15], these settings will allow you to sample all slices in the coronal orientation when Sampled Enabled Object is selected.
- Click the Sampled Enabled Object button [16].
- All objects currently displayed will be sampled. The sampled objects are displayed in red in the current orientation [17].
- Measurements will be returned to the stats log for the current slice [18].



Combining Objects when sampling All Slices

To return the individual object measurements summed in a single line entry in the stats log, do the following:

- Dismiss the stats log by clicking the x in the upper right-hand corner of the stats log.
- Check the Combine Enabled Objects check box [19].
- Leave the Name set to Combined [20].
- Click the Sampled Enabled Object button [21].
- All objects currently displayed will be sampled. The sampled objects are displayed in red in the current orientation. Measurements will be summed for the enabled objects and returned to the stats log for the current slice [22].



MRI_3D_Head - Measu

Sampling a Range of Slices

To sample a range of slices for all enabled objects in a specific orientation, do the following:

- Dismiss the previous stats log by clicking the x in the upper right-hand corner of the stats log.
- Next, uncheck the Combine Enabled Objects.
- Set the Orient to Sagittal [23] and set Slice(s) set to Slice Range [24].
- Set the Start Slice to 50 and the End Slice to 150 [25]. These settings will allow you to sample a range of slices, slice 50 to 150, in the sagittal orientation when Sampled Enabled Object is selected.
- File Other Help 111 🕥 👂 😐 2-D Sample 2-D Name Mode & N Boundary Coordinat Mean Max Location 🔲 St. De Region Pixels Min Location Entrop Log Stats Auto Log St Orient = Sagittal Name = Skin Slice = 50 Area = 12638.00 mm2 Mean = 124.41 Area mm2 Orient Name Slice Mean Comment
 mm2
 mm2
 mm2

 143
 5673.00
 128.111

 144
 9573.00
 122.61

 144
 5254.00
 81.07

 145
 9775.00
 125.86

 146
 9554.00
 188.86

 146
 4549.00
 80.07

 147
 9502.00
 130.99

 147
 4237.00
 19.63

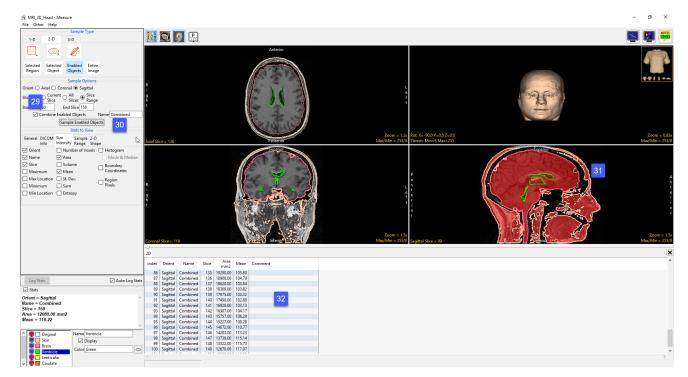
 148
 9246.00
 131.59
 Brain Skin Brain Skin Brain Skin Brain Skin Brain Skin Brain Skin Brain Orient – Sagitta Name – Brain Slice = 50 Area = 9763.00 mm Mean = 86.72 28 Orient = Sagittal Name = Skin 148 148 149 149 9346.00 131.55 Sagittal Sagittal Sagittal Sagittal Sagittal Sagittal 3976.00 78.55 9054.00 132.73 3616.00 77.83 D Display 150 150 8828.00 134.60 3252.00 77.46

- Click the Sampled Enabled Object button [26].
- All objects currently displayed will be sampled. The sampled objects are displayed in red in the current orientation [27].
- Measurements will be returned to the stats log for the enabled objects within the specified range of slices [28].

Combining Objects when Sampling a Range of Slices

To sum the object measurements in a single line entry in the stats log for a range of slices, do the following:

- Dismiss the stats log by clicking the x in the upper right-hand corner of the stats log.
- Check the Combine Enabled Objects check box [29].
- Leave the Name set to Combined [30].
- Click the Sampled Enabled Object button [31].
- All objects currently displayed will be sampled for the range of slices specified. The sampled objects are displayed in red in the current orientation. Measurements are summed for the enabled objects and returned to the stats log [32].



Entire Image

The Entire Image option allows users to sample measurements for the entire slice for the current slice, all slices, or a range of slices.

Sample Options: Provides users the following sampling controls:

- **Orient:** Select the orientation to sample enabled objects in.
 - · Axial: Sets the sampling orientation to axial.
 - · **Coronal:** Sets the sampling orientation to coronal.
 - · Sagittal: Sets the sampling orientation to sagittal.
- **Slices:** Allows users to specify the slices sampled.
 - **Current Slice:** Samples the current displayed slice for the selected orientation.
 - · All Slices: Samples all slices in the selected orientation.
 - **Slice Range:** Samples the range of samples specified using the start and end slice fields for the selected orientation.
 - **Start Slice:** Allows users to set the starting slice for sampling. Slices before the start slice will not be sampled.
 - **End Slice:** Allows users to set the ending slice for sampling. Slices after the end slice will not be sampled.
- Sample Entire Image: Initiates the sampling process.

Stats to View: The stats to view area allows users to enable and disable measurements and information reported to the stats log.

- General: Allows users to report general image data parameters in the stats log file (see General under Sample Point(s) > Stats to View.)
- DICOM Info: Allows users to report DICOM tag information (see DICOM Info under Sample Point(s) > Stats to View.)
- Size Intensity: Reports an array of size intensity information and measurements (see Size Intensity description for Sample 2-D Rectangle.)
- Sample Range: Samples voxels within a defined region based on a min/max intensity range (see Sample 2-D Rectangle > Sample Range.)
- 2-D Shape: Reports 2-D shape measurements for the defined region (see Sample 2-D Rectangle > 2-D Shape.)



Sampling the Entire Image

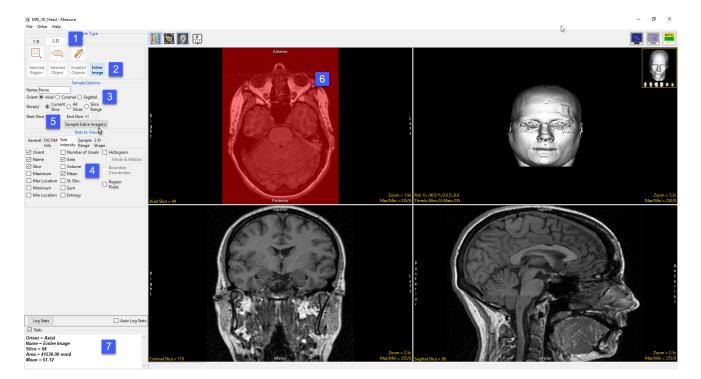
Download the MRI_3D_Head.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load MRI_3D_Head.avw into Analyze. Select MRI_3D_Head and open Measure.
- Select the 2D Sample Type [1] and choose Entire Image [2].

Sampling the Entire Current Slice

To sample the entire current slice, do the following:

- Leave Orient set to Axial and Slice(s) set to Current Slice [3]. This will sample the current axial slice when Sample Entire Image(s) is selected.
- In the Stats to View area check all the measurements [4] you would like returned.
- Click the Sample Entire Image(s) button [5].
- The current axial image will be sampled [6].
- The selected measurements will be returned to the stats review area [7].

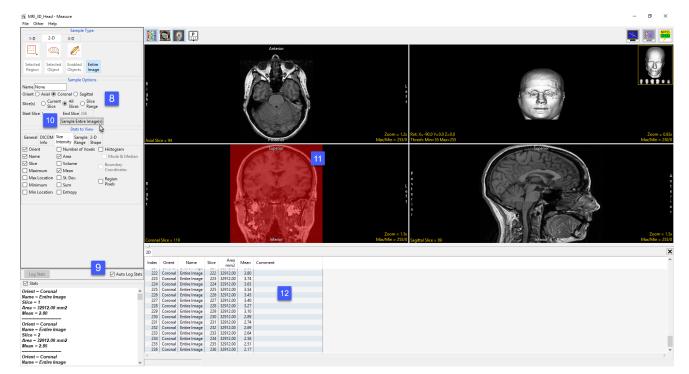


Sampling the Entire Image (continued)

Sampling the Entire Slice for All Slices

To sample the entire slice for all slices in the selected orientation, do the following:

- Set Orient to Coronal and then set Slice(s) to All Slices [8].
- Check the Auto Log Stats check box [9].
- Click the Sample Entire Image(s) button [10].
- All slices in the current orientation will be sampled [11].
- Measurements for each slice will be returned to the stats log [12].



Sampling the Entire Image (continued)

Sampling the Entire Slice for a **Range of Slices**

To sample the entire slice for a range of slices in the selected orientation. do the following:

- Dismiss the previous stats log by ٠ clicking the x in the upper righthand corner of the stats log.
- Next, set Orient to Sagittal and ٠ then set Slice(s) to Slice Range [13].
- Set the Start Slice to 50 and ۲ the End Slice to 150 [14]. These settings will allow you to sample a range of slices, slice 50 to 150, in the sagittal orientation.
- Click the Sample Entire Image(s) ٠ button [15].
- Only slices in the current range ٠ for the selected orientation will be sampled [16].
- Measurements will be returned to • the stats log [17].

| MRI_3D_Head - Measure | | | – a × |
|---|---|---|---------------------------------|
| File Other Help | | | |
| Sample Type 1-D 2-D 3-D | | | 💟 🕎 🏁 |
| 🖳 🔍 🌈 | Anterior | | |
| Selected Selected Enabled Entire Object Objects | | | 25 |
| Sample Options Name None | R | | |
| Orient O Axial O Coronal Sagittal | | | |
| Slice(s) Current All Slice Slice Slice Slice Carper 14 | | | |
| 15 Sample Entire Image(s) | | | |
| General DICOM Size Sample 2-D Info Intensity Range Shape | Axial Slice = 94 Pottenor | Zoom = 1.2x Asy/Min = 255/0 Thresh: Min=55 Max=255 | Zoom = 0.83x Max/Min = 250/0 |
| Orient Number of Voxels Histogram | Superior | Superior | |
| Name Area Mode & Median Slice Volume Boundary | | 16 | |
| Maximum Mean Coordinates Max Location St. Dev. Region | Ene the and | | A |
| Max Location St. Dev. Region Minimum Sum Min Location Entropy | | | n t |
| | | f | i |
| | | r | r |
| | | | 7 |
| | Coronal Slice = 119 Inferior N | Zoom a 1.5x Aav/Min = 255/0 Sagittal Slice = 89 Interior | Zoom = 1.5x Max/Min = 255/0 |
| | 20 | | × |
| Log Stats Auto Log Stats | Index Orient Name Slice Area mm2 Mean Comment 86 Sagittal Entrire Image 135 44132.00 50.75 | | |
| Log Stats Auto Log Stats | 87 Sagittal Entire Image 136 44132.00 49.32 88 Sagittal Entire Image 137 44132.00 48.23 | | |
| Orient = Sagittal | 89 Sagittal Entire Image 138 44132.00 47.45 90 Sagittal Entire Image 139 44132.00 46.41 | | |
| Name = Entire Image Slice = 50 | 91 Sagittal EntireImage 140 44132.00 45.11 | | |
| Area = 44132.00 mm2 | 92 Sagittal Entire Image 141 44132.00 43.99 93 Sagittal Entire Image 142 44132.00 43.16 | | |
| Mean = 58.95 | 94 Sagittal Entire Image 143 44132.00 42.51 95 Sagittal Entire Image 144 44132.00 41.92 | | |
| Orient = Sagittal Name = Entire Image | 96 Sagittal Entire Image 145 44132.00 41.39 | | |
| Slice - 51 | 97 Sagittal Entire Image 146 44132.00 40.99 98 Sagittal Entire Image 147 44132.00 40.38 | | |
| Area - 44132.00 mm2 Mean - 58.73 | 99 Sagittal Entire Image 148 44132.00 39.36 | | |
| | 100 Sagittal Entire Image 149 44132.00 38.12 | | ¥ |
| Orient = Sagittal Name = Entire Image | | | , |
| | | | |

3-D Measurement Tools

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. These options include; selected object and enabled object. The remaining three measurement options do not require an object map, these include; box, entire volume, and stereology.

The 3-D tab provides access to the following measurement tools:

 \cdot Box

Enabled Objects

· Stereology

· Selected Objects

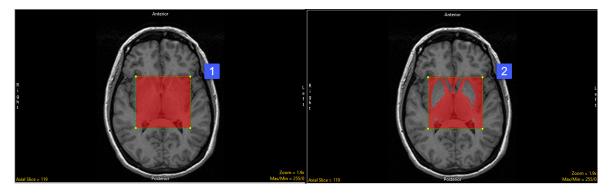
Entire Volume

Box

The Box tool enables users to interactively define and then sample a 3D box region of interest in the volume image data. The following sampling options are available.

Sample Options: Provides users with access to the following 3D Box sampling options:

- · Name: Allows users to assign a name to the selected box when reported to the log file.
- Sample Enabled Objects: This option is only available when an object map is loaded. When disabled (default) all voxels within the box will be sampled [1]. When enabled only voxels that form part of enabled objects within the box will be sampled [2].



Box Options (continued)

Stats to View: The stats to view area allows users to enable and disable measurements and information reported to the stats log.

- **General:** Allows users to report general image data parameters in the stats log file. See General under Sample Point(s) > Stats to View for a full description of available options.
- DICOM Info: Allows users to report DICOM tag information if the data is in the DICOM format. See DICOM Info under Sample Point(s) > Stats to View above for a full description of available options.
- **Size Intensity:** Allows users to report an array of size intensity information and measurements. Refer to the size Intensity description for Sample 2-D Rectangle for a description of all available options.

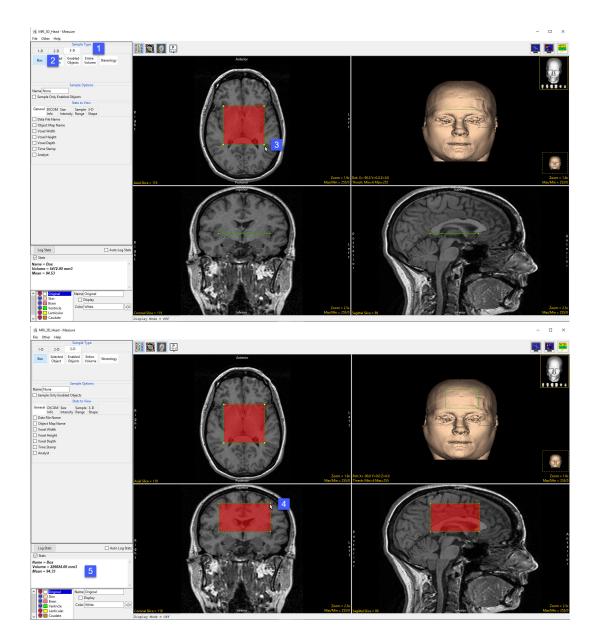


- **Sample Range:** Allows users to sample voxels within the defined region based on a minimum and maximum intensity range. Refer to the Sample Range description for Sample 2-D Rectangle for a description of all available options.
- **3-D Shape:** Allow users to measure the following 3-D shape measurements:
 - **MEB Angle Resolution:** MEB (Minimum Enclosing Brick) specifies the angle resolution to be used when searching for the Minimum Enclosing Brick.
 - Surface Area: The surface area option reports the estimated surface area for the sampled object.
 - **MEB Angles:** The MEB Angles option reports the orientation angles of the minimum enclosing brick around the object. The angle resolution is specified in the MEB Angle Resolution option.
 - **MEB Volume:** Reports the volume of the minimum enclosing brick.
 - **MEB Coordinates:** Reports the coordinates of the eight corners of the MEB.
 - Sphere Fit Factor: Reports the ratio: $SA_3 / (9V^2 * 4Pi)$ where 1 equals a perfect sphere.
 - · Bick Fit Factor: Reports the ratio: ObjectVolume/MEB_Volume where 1 equals a brick shaped object.
 - **Centroid:** Reports the center gravity for the object.

Making Measurements using Box

Download the MRI_3D_Head.avw data set from analyzedirect.com/data to follow along.

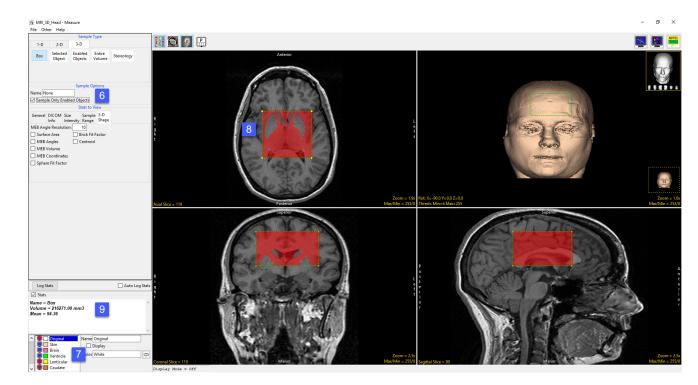
- Open Input/Output and load MRI_3D_Head. avw into Analyze. Select MRI_3D_Head and open Measure.
- Select File > Load Object Map and load the MRI_3D_Head.obj.
- Select the 3D Sample Type [1] and choose Box [2].
- To define a box first draw a rectangular region on one of the slices, in any orientation [3].
- In either of the other two orientations left click on a corner and then drag the cursor until the desired size and shape box is define [4].
- Selected measurements will be reported for the region in the stats review area [5]. Click Log Stats to return the stats to a log file that can be saved out of Analyze as a .csv file.



Making Measurements using Box (continued)

Making Box Measurements for Enabled Objects

- To sample only enabled objects within the box check the Sample Only Enabled Objects option [6].
- Only objects in the object list that are displayed [7] will be sampled [8].
- The stats review area will automatically update [9].



Selected Object

The Selected Object option allows users to sample an object within the 3D volume. An object map must be loaded for this sampling option to be available. The following sampling options are available:

Stats to View: The stats to view area allows users to enable and disable measurements and information reported to the stats log.

- **General:** Allows users to report general image data parameters in the stats log file (see General under Sample Point(s) > Stats to View.)
- DICOM Info: Allows users to report DICOM tag information (see DICOM Info under Sample Point(s) > Stats to View.)
- **Size Intensity:** Reports an array of size intensity information and measurements (see Size Intensity description for Sample 2-D Rectangle.)
- **Sample Range:** Samples voxels within a defined region based on a min/max intensity range (see Sample 2-D Rectangle > Sample Range.)
- 3-D Shape: Allow users to sample different 3-D shape-based measurement, see the 3-D Shape description under 3-D > Box for details on each of the 3-D shape measurements available.

| Sample Type | | | | | | | | | | |
|----------------|------------------|-------------------|-----------------|----------------|------------|--|--|--|--|--|
| 1-D | 2-D | 3-1 | D | | | | | | | |
| Box | Select Object | | | ntire olume | Stereology | | | | | |
| | | | | | | | | | | |
| Sample Options | | | | | | | | | | |
| | | | | | | | | | | |
| | | | | | | | | | | |
| | | 🗹 Ful | l Width H | lalf Max | | | | | | |
| | Base V | alue 0 | | | Auto | | | | | |
| | Search | From (| Outside | • O N | 1aximum | | | | | |
| | | S | tats to Vi | ew | | | | | | |
| General | DICOM Info | Size Intensity | Sample Range | | | | | | | |
| 🗌 Data I | File Nam | e | | | | | | | | |
| 🗌 Objec | t Map N | ame | | | | | | | | |
| Voxel Width | | | | | | | | | | |
| Voxel Height | | | | | | | | | | |
| Voxel Depth | | | | | | | | | | |
| Time | | | | | | | | | | |
| 🗌 🗌 Analy | st | | | | | | | | | |
| | | | | | | | | | | |

Making Measurements using Selected Object

Download the MRI_3D_Head.avw data set from analyzedirect.com/data to follow along.

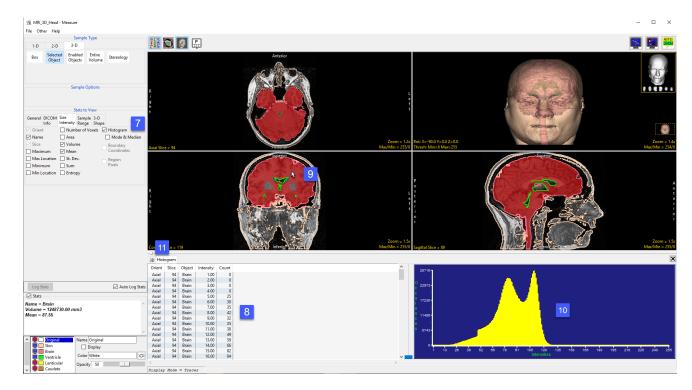
- Open Input/Output and load MRI_3D_Head.avw into Analyze. Select MRI_3D_Head and open Measure.
- Select File > Load Object Map and load the MRI_3D_Head.obj.
- Select the 3D Sample Type [1] and choose Selected Object [2].
- In the Stats to View area check the required measurements [3] to be sampled.
- Check Auto Log Stats [4].
- Click on the brain object in any of the three orthogonal slices [5].
- Selected measurements will be reported for the region in the stats log [6]. Right click to save the log to disk as a .csv file.



Making Measurements using Selected Object (continued)

Generating Histograms with Selected Object

- Check the Histogram checkbox [7].
- To generate the histogram statistics (intensity and count information) [8] click on the brain [9].
- The histogram for the sampled objects will be displayed below the display area [10] in a new Histogram tab [11] in front of the other statistics tabs.
- 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 rightclicking and selecting Save Log.

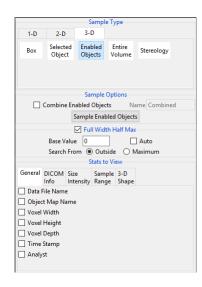


Enabled Object

The Enabled Object option allows users to sample all enabled objects (objects currently displayed) in the volume. An object map must be loaded for this sampling option to be available.

Sample Options: Provides users the following sampling controls:

- **Combine Objects:** Allows users to sum the measurements of the individually sampled objects.
 - **Name:** Allows users to specify a name for the combined object measurements when reported to the stats log.
- Sample Enabled Objects: Initiates the sampling process.



Stats to View: The stats to view area allows users to enable and disable measurements and information reported to the stats log.

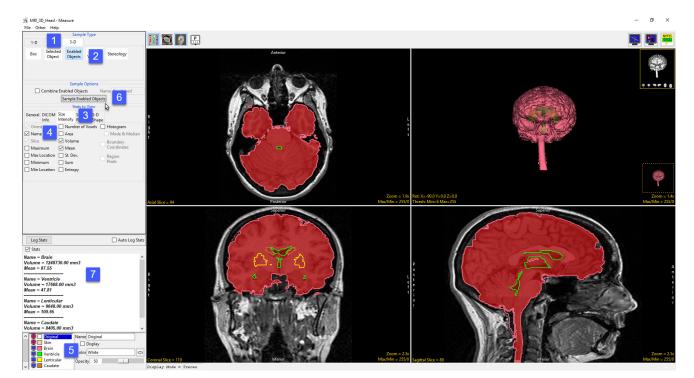
- General: Allows users to report general image data parameters in the stats log file (see General under Sample Point(s) > Stats to View.)
- **DICOM Info:** Allows users to report DICOM tag information (see DICOM Info under Sample Point(s) > Stats to View.)
- Size Intensity: Reports an array of size intensity information and measurements (see Size Intensity description for Sample 2-D Rectangle.)
- Sample Range: Samples voxels within a defined region based on a min/max intensity range (see Sample 2-D Rectangle > Sample Range.)
- **3-D Shape:** Allow users to sample different 3-D shape-based measurement, see the 3-D Shape description under 3-D > Box for details on each of the 3-D shape measurements available.

Making Measurements using Enabled Object

Sampling Enabled Objects

Download the MRI_3D_Head.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load MRI_3D_Head.avw into Analyze.
 Select MRI_3D_Head and open Measure.
- Select File > Load Object Map and load the MRI_3D_Head.obj.
- Select the 3D Sample Type [1] and choose Enabled Object [2].
- Select Size Intensity [3] and make sure that Name, Volume, and Mean are checked. Uncheck Area [4].

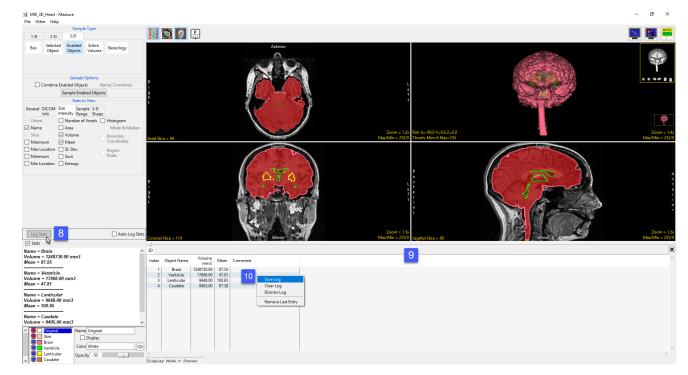


- Switch the display of the Skin object off [5] by clicking on the monitor icon next to the object in the object list.
- Switching the display of an object off disables the object so it won't be sampled. Switch on the Lenticular and Caudate objects.
- Click Sample Enabled Objects [6]. The selected measurements for the enabled objects will be reported to the stats review area [7].

Making Measurements using Enabled Object (continued)

Sampling Enabled Objects (continued)

- To report the selected measurements to a log file that can be saved from Measure, click the Log Stats button [8]. When clicked the button will become grayed out.
- The selected measurements for the enabled objects will be reported to a file below the image display area [9].
- To save the measurements log file, right-click in this area and select Save Log [10]. The log file will be saved as a .CSV file.



Making Measurements using Enabled Object (continued)

Using Enabled Objects to make Combined Measurements

- Check the Auto Log Stats checkbox [11].
- Next, check the Combine Enabled Objects checkbox [12].
- Name the combined result or leave the default name as Combined [13].
- Click Sample Enabled Objects [14].
- The combined measurements will be reported in the stats review area [15] and added to the log file.
- Checking additional measurement options [16] will automatically update in the stats review area with the selected measurement for the combined object [17].
- The measurements for the individual and combined objects will automatically update in the log [18].



Making Measurements using Enabled Object (continued)

Using Enabled Object to Generate a Combined Object Histogram

- Check the Histogram check box
 [18] and select Sample Enabled
 Objects [19].
- The histogram measurements will be reported [20] and the histogram plotted [21] in a new tab. Right-click to save the histogram log.



Entire Volume

The Entire Volume option allows users to sample measurements for the entire data set. The entire volume measurement option does not require an object map.

Sample Options: Provides users the following sampling controls:

• **Name:** Allows users to specify a name for the combined object measurements when reported to the stats log.

Stats to View: The stats to view area allows users to enable and disable measurements and information reported to the stats log.

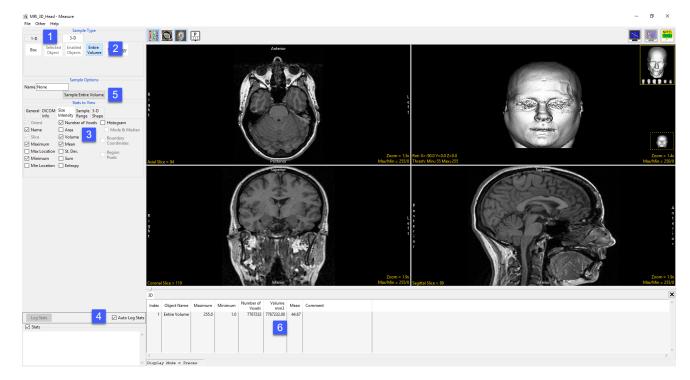
- **General:** Allows users to report general image data parameters in the stats log file (see General under Sample Point(s) > Stats to View.)
- **DICOM Info:** Allows users to report DICOM tag information (see DICOM Info under Sample Point(s) > Stats to View.)
- Size Intensity: Reports an array of size intensity information and measurements (see Size Intensity description for Sample 2-D Rectangle.)
- Sample Range: Samples voxels within a defined region based on a min/max intensity range (see Sample 2-D Rectangle > Sample Range.)
- **3-D Shape:** Allow users to sample different 3-D shape-based measurement, see the 3-D Shape description under 3-D > Box for details on each of the 3-D shape measurements available.

| | | S | ample Ty | /pe | | | | | |
|---|-----------------|--------|------------|----------------|------------|--|--|--|--|
| 1-D | 2-D | 3-1 | D | | | | | | |
| Box | Select Objec | | and a la | ntire olume | Stereology | | | | |
| | | | | | | | | | |
| | | Sa | mple Opt | tions | | | | | |
| Name N | one | | | | | | | | |
| | | Samp | le Entire | Volume | | | | | |
| | | 🗹 Ful | l Width H | lalf Ma | - (| | | | |
| | Base V | alue 0 | | | Auto | | | | |
| | Search | From |) Outside | 0 | Aaximum | | | | |
| | | S | tats to Vi | ew | | | | | |
| General DICOM Size Sample 3-D Info Intensity Range Shape | | | | | | | | | |
| 🗌 Data I | File Name | 2 | | | | | | | |
| 🗌 Objec | t Map Na | ime | | | | | | | |
| Voxel Width | | | | | | | | | |
| Voxel Height | | | | | | | | | |
| Voxel Depth | | | | | | | | | |
| Time Stamp | | | | | | | | | |
| Analy | | | | | | | | | |

Sampling the Entire Data Set using Entire Volume

Download the MRI_3D_Head.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load MRI_3D_Head.avw into Analyze. Select MRI_3D_Head and open Measure.
- Select File > Load Object Map and load the MRI_3D_Head.obj.
- Select the 3D Sample Type [1] and choose Entire Volume [2].
- Select Size Intensity [3] and make sure that Name, Volume and Mean are checked. Uncheck Area.
- Check Auto Log Stats [4] and click Sample Entire Volume [5].
- The selected stats for the entire volume will be reported in the Stats review area [6] and log file.



Stereology

The Stereology tool estimates volume and surface area using the stereological method of point counting. This method consists of overlaying images entirely with a randomly positioned and oriented systematic array of test points and counting the number of occasions on which a point lies within the feature of interest.

Stereology Options:

- **Estimate:** Choose from the following to determine the type of estimation to conduct:
 - · Volume Only: Specifies that only volume estimations will be made.
 - Volume & Surface Area: Specifies that both volume and surface area estimations will be made.
- Orient: Allows users to select the orientation to create the sampling grid in.

Slice:

- Start: Specifies the initial slice to be used for the grid. Enter the desired slice number in the text entry box.
- Incr: Specifies the interval of the slices used when generating the grid. Enter the desired increment in the text entry box.
- Number: Specifies the number of slices to be used for the grid. Enter the desired number in the text entry box.
- Spacing:
 - \cdot X: Allows users to the distance (in pixels) between grid elements in X.
 - Y: Allows users to the distance (in pixels) between grid elements in Y.
- **Start Position:** Choose from Random and Specified to specify whether the starting position is randomly selected or specified by the following options. When Random is selected the X Start Position, Y Start Position, and Angle text entry fields are disabled.
- **Random:** Generates a random grid.
- Specified:
 - Start X: Specifies the x position of the first grid element.
 - Start Y: Specifies the y position of the first grid element.
 - Angle: Specifies the angle used to position the grid on the image.



Stereology Options (continued)

Stereology Options (continued):

- **B/sqrt(A):** Specifies the value used in correcting the estimation of surface area. This value is determined during the estimation of the volume.
- Generate Grid: Generates the grid based on the parameters entered above.

Stats to View

- Stereology
 - · Volume:
 - **Points:** Reports the number of points selected.
 - **Volume:** Displays the current estimation of the specified volume.
 - **Coefficient of Error:** Specifies the current estimation of the error coefficient.
 - **Elliptical Error:** More accurate error estimate for objects which are unusually regular, close to an ellipsoidal shape.
 - · Surface Area
 - · X Intersection
 - · Y Intersection
 - · Z Intersection
 - **Surface Area:** Displays the current surface area estimation (in Surface Area mode only).
 - **B/sqrt(A):** Specifies the mean boundary length divided by the square root of the mean area of the sampled object on all the slices. This is computed in Surface Area Mode and improves Coefficient of Error Estimates.

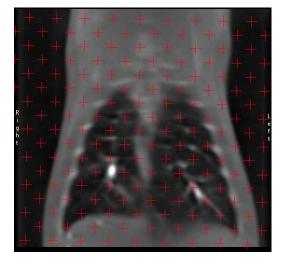
Right click options:

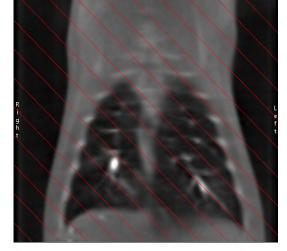
- **Copy Grid Forward:** Copies the current grid forward to the next grid slice. If points have been selected (green points) there selected state will be copied forward also.
- **Middle Button Action:** Allows users to set the action of the middle mouse button. See the Image Display, Controls and Customization section for a full description of this option.

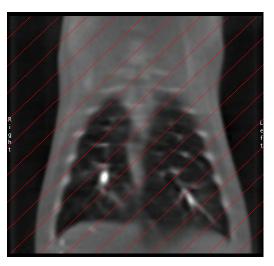
Stereology Options (continued)

Right Click Options (continued):

- **Mouse Wheel Action:** Allows users to set the action of the middle mouse wheel. See the Image Display, Controls and Customization section for a full description of this option.
- · Copy to Clipboard: Copies the current slice display to memory.
- · Isotropic: Active only for anisotropic data. Allows users to toggle between an isotropic or anisotropic display of the data.
- Show Active Slices Only: Allow users to automatically skip non-grid slices using the + or keys or the mouse scroll wheel.
- Show Grid: Toggles the display of the volume estimation grid when surface area is selected.
- Show X Lines: Toggles the display of the x lines for surface estimation when estimating surface area is active.
- Show Y Lines: Toggles the display of the y lines for surface estimation when estimating surface area is active.



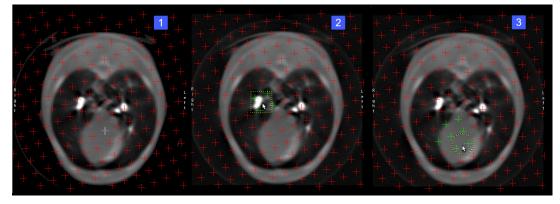




Stereology Options (continued)

Right Click Options (continued):

- **Toggle with 's' key:** When enabled allows users to toggle between Grid, X Lines, and Y Lines.
- Stereology Cursor: Allows users to change the shape of the cursor for selecting grid points. Users can choose from; Crosshair [1],
 - Rectangle [2], or Oval [3].



- Additional Cursor options: Additional options are available for the Rectangle and Oval cursors:
- **Rectangle Shape:** Choose from Square, Wide, or Tall.
- **Rectangle Size:** Tiny, Small, Medium, Large, Extra Large
- **Oval Shape:** Choose from Circular, Wide, or Tall.
- **Oval Size:** Tiny, Small, Medium, Large, Extra Large
- · Keyboard Shortcuts: The following keyboard shortcuts are available:
- **S:** Toggle through the cursor options.
- **X:** Toggle though cursor shape options.
- **Z:** Toggle through the cursor size options.

Axis Label: Allows users to enable or disable the display of the axis labels on the perimeter of the slice display window.

Border Ruler: Enables/Disables the boarder ruler tool.

Reset: Resets all options to default.

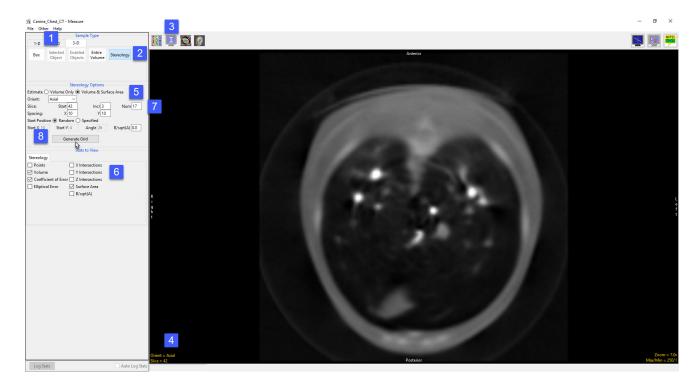
Analyze 15.0 User's Guide

Estimating Volume using Stereology

In this example we will use Stereology to estimate the volume of the heart in a CT data set.

Download the Canine_Chest_CT.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load Canine_Chest_CT.avw into Analyze. Select Canine_Chest_CT and open Measure.
- Select the 3D Sample Type [1] and choose Stereology [2].



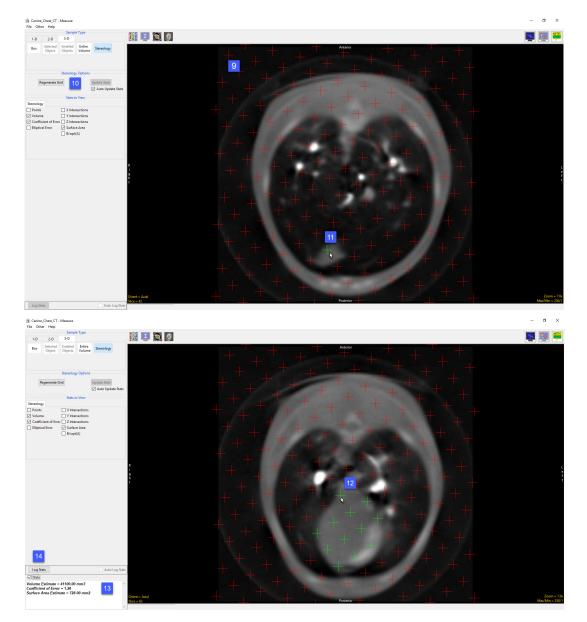
- Use the Display tools to configure the image display so that the rendering is disabled and only one orthogonal slice is displayed [3].
- Ensure the orientation is set to Axial and then move to slice 42 [4]. This is the first axial slice that the heart can be seen on.
- From Stereology Options set Estimate to Volume & Surface Area [5]. Notice that the surface area related measurement options become available in the Stats to View area [6].
- The heart first appears around axial slice 42 and remains visible until slice 94. To create a sampling grid that will encompass the heart set the Start Slice to 42. Using Stereology, it is not necessary to sample every slice, set the Grid Slide Increment to 3 and Number of Grid Slices to 17 [7].
- Click Generate Grid [8] to generate the sampling grid on the image.

Analyze 15.0 User's Guide

Estimating Volume using Stereology (continued)

- The grid will be overlaid on the image data.[9].
- The stereology options to generate the grid will no longer be visible, however, if you need to modify or recreate the grid click the Regenerate Grid button [10] and all options will be displayed.
- Move the cursor over to the image and click on any point that falls on the heart [11]. When completed press the + key on your keyboard to move to the next grid slice and repeat.
- As you continue to move through the data selecting points [12] the stats review area [13] will update with the measurements selected.
- When sampling is complete select Log Stats to log the measurements to a stats log that can be saved to disk as a .csv file.

Note: If Stereology is to be used for research study, it is necessary to validate the process for the study application. To validate a stereologic-based estimate of volume, segmentations of the structure of interest need to be established as gold standard volume measurements to which the stereologic estimates can be compared. These gold standard test volumes also provide the opportunity to establish best grid parameters to be used for the study.



Sampling 4D Multivolumes using 3D Tools

Measure can sample 4D image data. When 4D image data is loaded into Measure a volume slider is available allowing users to selected different volumes.

Download the 4D_Cardiac_CT.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load 4D_Cardiac_CT.avw into Analyze. Select 4D_Cardiac_CT and open Measure.
- Select File > Load Object Map and load 4D_Cardiac_CT.obj.

| % 4D_Cardiac_CT - Mea | asure | | | | | | | | | - 🗆 × |
|--|--|------------------|--|--|-----------|---|--|-----------------------------|---------|------------------------------|
| File Other Help | Sample Type 3-D | COR COR | S | P | | | | | | V 🖬 🛱 |
| General DICOM Size | ple Enabled Objects 6 Stats to View Sample 3-D ity Range Shape umber of Voxels Histogram | R i 9h t | | | Anterior | 3 | | | R | 1 |
| Name An An Slice ✓ Vo Maximum ✓ Me | lume 3 Boundary | Volum | e = 1 ice = 56 | | Posterior | | Zoom = 2.9x Rot: X=-90.0 Max/Min = 255/0 Thresh: Min= |) Y=0.0 Z=0.0 =5 Max=255 | | Zoom = 1.6 Max/Min = 254/ |
| Max Location St. Minimum Su Min Location En Log Stats Stats Stats Name = Blood Pool Volume = 33359.01 m ean = 192.62 | m Pieds | | e = 1 I Slice = 51 | | P C | | P L L L L L L L L L L L L L L L L L L L | e = 50 | A start | Zoom 2.5 Max/Mar. 253/ |
| Name = Blood Pool | | 3D | | | | | | | | > |
| Volume – 82962.49 m Mean – 192.32 | m3 | Index | Object Name | mms | | | | | | , |
| Name = Blood Pool Volume = 82629.29 m Mean = 192.12 | m3 | 4 5 6 7 | Blood Pool Blood Pool Blood Pool | 77482.47 191.14 69529.95 190.14 65072.48 189.30 62854.04 188.24 | 7 | | | | | |
| Name = Blood Pool Volume = 77482.47 m | m3 | × 10 | Blood Pool | 63146.88 187.83 65514.12 188.03 66307.15 187.83 | | | | | | |
| Volume | 1 | 11 12 13 | Blood Pool Blood Pool Blood Pool | 70446.45 190.2 73280.64 191.4 76406.88 192.4 78543.81 192.8 | | | | | | |
| Original Blood Pool | Name Original Display | 14 15 16 | Blood Pool Blood Pool | 79343.18 192.9 80087.14 193.3 | | | | | | |
| | Color White | Þ 17 | | 79799.84 192.6 80657.78 192.7 | | | | | | |
| | | < | | | | | | | | > |

- Select the 3D Sample Type [1] and choose Enabled Objects [2].
- Select Size Intensity [3] and check Name, Volume and Mean, and uncheck Area.
- Check Auto Log Stats [4] and check Sample All Volumes [5].
- Click Sample Enabled Objects [6].
- 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 [7]. Right click to save the log as a .CSV file.

Sampling 4D Multivolumes using 3D Tools (continued)

9 4D_Cardiac_CT - Measure

Measure can also generate 4D histograms from 4D image data. When 4D image data is loaded into Measure a volume slider is available allowing users to selected different volumes.

Download the 4D_Cardiac_CT.avw data set from analyzedirect.com/data to follow along.

- Open Input/Output and load 4D_Cardiac_CT.avw into Analyze. Select 4D_Cardiac_CT and open Measure.
- Select File > Load Object Map and load 4D_Cardiac_CT.obj
- File Other Help 1-D Mode & M Area Mean Max Location St. Dev 🗌 Sum Min Location Entrop Auto Log Sta Log Stats Stats Name = Blood Pool Volume = 83359.01 mm3 Mean = 192.82 Name = Blood Pool
 19.0
 returnsgram

 Intensity
 Count

 183.00
 2244

 184.00
 2268

 185.00
 2401

 186.00
 2403

 186.00
 2403

 186.00
 2404

 186.00
 2438

 189.00
 2449

 191.00
 2449

 191.00
 2449

 192.00
 2404

 193.00
 2332

 195.00
 2244

 196.00
 2332

 196.00
 2139

 196.00
 2139

 197.00
 1952
 Volume – 82962.49 mm3 Mean – 192.32 Name = Blood Pool Volume = 82629.29 mm3 Mean = 192.12 Name = Blood Pool Volume = 77482.47 mm3 Volume Sample All Vol Disp
- Select the 3D Sample Type [1] and choose Enabled Objects [2].
- Select Size Intensity [3] and ensure that Name, Volume and Mean, and Histogram are checked [4].
- Check Auto Log Stats [5] and check Sample All Volumes [6]. Click Sample Enabled Objects [7].
- The histogram measurements will be reported [8] and the histogram plotted [9] in a new tab.
- The volume slider [10] beneath the histogram stats allows review of histograms for all 3D volumes in the 4D multivolume.