# Analyze 12.0
# Training Guide

AnalyzeDirect

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# Introduction

Welcome to the Analyze 12.0 Essential Training Guide. This document provides an overview of Analyze 12.0 core functionality through exercises that guide new users step-by-step through basic and advanced Analyze procedures. A fully comprehensive overview of all Analyze 12.0 module functionality can be found in the User's Guide and Tutorials located under the Help menu within the software. If you have not installed Analyze 12.0, please refer to the Analyze 12.0 Installation Instructions provided with the software.

## Installing Tutorial Data

In order to work through the Essential Training Guide exercises and Analyze Tutorials, you need to install the tutorial data from the Resources CD. To install the tutorial data:

1. Insert the **Analyze Resources CD** into your computer.

2. Open **Analyze 12.0** and choose **Help > Tutorials.**

3. Click **Install Tutorial Data** at the bottom of the Tutorials window. Note, if the tutorial data has already been insatlled this button will not appear.

4. In the window returned, specify the path to the tutorial data, for example **D:\TutorialData** (where D:\ is equal to your CD-ROM drive)

5. Click **Install**. All of the tutorial data will be copied from the Resources disk to the **$:\BIR\images\TutorialData** folder (where $ is the install directory, e.g. C:\ on a windows system).

## Quick Reference

Button Reference: Displays PowerBar button or tool button referenced in that exercise step. The button will be next to the step that it refers to. Often, the step only mentions the file path, but the button is displayed as a shortcut. Example:

 Open the **DICOM Tool** (**File > DICOM Tool)**.

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# Analyze Basics

## The Main Analyze Window

The main Analyze window is the first operational window that appears when Analyze is opened. The main Analyze window does not perform any imaging functions, but it does coordinate all the modules within the Analyze package and acts as a file manager for loaded data. It consists of three major components: the Analyze workspace, where all of the loaded data, represented as icons, are managed; the Analyze menu, where individual Analyze modules are selected; and the Analyze PowerBar, which provides icon-based shortcuts to the most frequently used Analyze modules.

Analyze Menu ——
Power Bar ——
Tabbed Analyze
Workspace ——
Image Data Icon ——
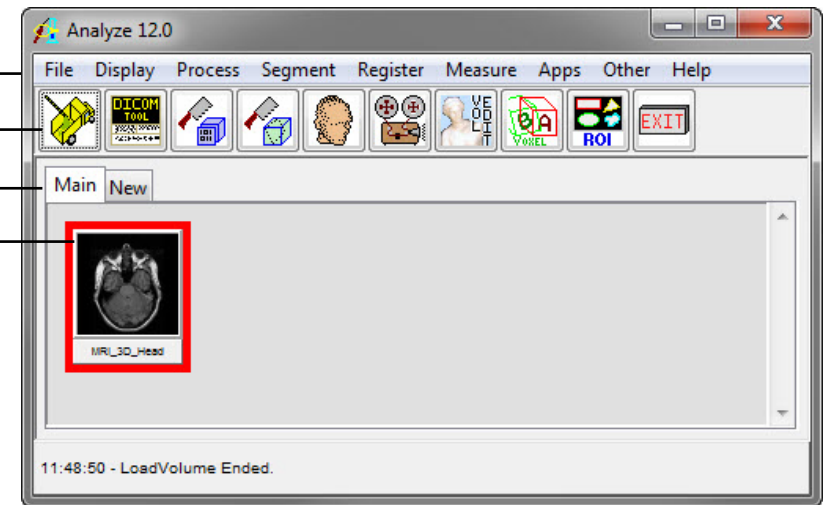
## Loading Data into Analyze

Image data is loaded into Analyze using one of the load modules (Load, Load As, DICOM Tool, or Import/Export) from the 'File' menu in the main Analyze window. Most of the individual Analyze modules also support data loading directly within the module (File > Load within the module).

To load DICOM data, use the DICOM module; for more information on how to use this module, please refer to Exercises 1-2 of this Guide.

To load all other data into Analyze, refer to Exercises 3-6 of this Guide.

The tutorial data used in the Essential Training Guide exercises can be loaded into Analyze using the Load module (File > Load). It is assumed that the data was installed to $:\BIR\images\TutorialData (where $ is the install directory, e.g. C:\ on a Windows system) according to the "Installing Tutorial Data" instructions on page 6.

# Analyze Basics

## The Analyze Workspace

Once data is loaded into Analyze it will appear as an icon in the Analyze workspace and is available to all of the modules in the Analyze package. To load data into a module, select the image icon in the Analyze workspace (the icon will appear framed in red when selected) and open the desired module from the Analyze menu or PowerBar. If multiple icons are selected at the time the module is opened, one of the two actions will occur:

1. If the opened module supports or requires multiple volumes, the volumes are used in the order selected.

2. If multiple loaded volumes are not supported, then multiple instances of the module are invoked.

## Right Mouse Button Menu

The Analyze workspace is an area with additional options. When the right mouse button is clicked in the workspace, a menu will appear. The menu provides the following options:

- **Unload**: Unload selected data from the Analyze 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

- **Append:** Append selected data

- **Unappend:** Unappend 4D multi-volume data sets, or RGB data sets

- **Select All:** Select all data sets in the Analyze workspace

- **Invert Selected:** Invert your selection of data in the Analyze workspace

- **Arrange:** Arrange data sets by Name, Size or Modify Time

- **Current Directory:** View and modify the Current Directory location

- **Workspace Directory:** View and modify the Workspace Directory Location

- **Session Log:** Stores information that might be useful to the Analyze support team and software developers, should a problem ever arise with one of the modules.

## Main Analyze Window Quick Keys

- **<Ctrl><a>** Selects all of the files in the workspace.

- **<Shift><Left Mouse Click>** Selects all files between first and shifted selections.

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

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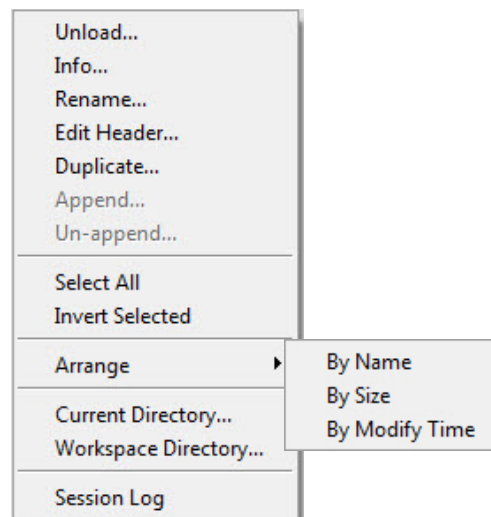
# Analyze Basics

## The Analyze Menu

The **File** menu contains the modules that are used to input and output data, as well as the standard 'Save', 'Save As' and 'Exit' options.

### Display

Multiplanar Sections
Oblique Sections
Volume Compare
Volume Render
Surface Render
Virtual Endoscopy
Movie

### Process

Image Calculator
Image Algebra
Image Repair
Histogram Ops
Spatial Filters
Filter Designer
3-D FFT

### Segment

Image Edit
Volume Edit
Morphology
Watershed
Multispectral Classification
Object Extractor
Surface Extractor

### Register

2-D Registration
2-D Non-rigid Registration
Point to Surface
3-D Surface Registration
3-D Voxel Registration
3-D Non-rigid Registration

### Measure

Line Profile
Region of Interest
Stereology
Object Counter
Tree Analysis

### Apps

SISCOM
Mayo 3-D Brain Atlas*
DTI*
BMA*
T2 Projection*
Volume Metrics*

*These modules require the purchase of an additional license

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# Analyze Basics

## The Analyze Menu

Additional items available in the Analyze menu include:

The **Other** menu contains utilities and modules for configuration and resource monitoring.

- **Resources:** The Resource Monitor assists in maintaining system resources at a level that does not impede proper execution of Analyze. The resources being monitored and displayed are Swap space, Workspace, and user specified directory Disk space. For all three, the Resource Monitor reports the amount of space used, space available or free, and total capacity.

- **PowerBar Editor:** the PowerBar Editor is an option that appears in all Analyze modules that contain PowerBar options.

- **Options:** The Options item allows you to switch on and off workspace features such as the PowerBar, and the pop-up icon names which are shown when the mouse cursor is moved over an image in the workspace. You can also configure Add-On modules to be switched on or off.

- **AppDefaults Editor:** The AppDefaults Editor provides several tools for managing and changing defaults or user preferences for the Analyze workspace and specific Analyze modules. For further information about the AppDefaults Editor please reference the User's Guide (**Help > User's Guide**).

The **Help** menu provides access to several important Analyze resources:

- **User's Guide:** Provides detailed information on each Analyze module.

- **Tip of the Day:** Can be set to display an Analyze "tip" each time Analyze is opened.

- **Tutorials:** Tutorial exercises covering some of the main Analyze functions. Note, you must have selected to install the Tutorials during initial Analyze installation.

- **Analyze Update:** Checks to make sure Analyze is up-to-date, also will download and install any necessary updates.

- **Online Support:** Provides a direct link to the AnalyzeDirect Support home page.

- **Analyze Demos:** Provides a direct link to a list of Help Movies

- **Copyrights:** Documentation of Analyze Copyrights.

- **About:** Provides version, system, and environment information.

# Analyze Basics

## Main Analyze PowerBar

Directly below the menu bar in the main Analyze window you will find the PowerBar of icons. The icons on this main Analyze PowerBar provide shortcuts to the most commonly used Analyze modules. By default, the main Analyze PowerBar contains icons for:

**Load As, DICOM Tool, Multiplanar Sections, Oblique Sections, Volume Render, Movie, Volume Edit, 3D Voxel Registration, Region of Interest, and Exit.**

## Module-Specific PowerBars

In addition to the main Analyze window, you can also find a **PowerBar** in each Analyze module. The icons included on the PowerBar of each Analyze module provide shortcuts to the most commonly used tools and options within that specific module.

## PowerBar Editor - Customizing PowerBars

Customizing Analyze PowerBars is a quick and easy way to streamline your work flows and routine processes. To customize the PowerBar displayed within any Analyze window, you can use the **PowerBar Editor** found under the window's 'Other' menu (**Other > PowerBar Editor**).

Using the PowerBar Editor, you can:

- **Add/Remove PowerBar icons**: To add an icon to the PowerBar, select it in the PowerBar Editor list (selected icons appear highlighted in black). To remove an icon, deselect it in the PowerBar Editor list.

- **Change the order of PowerBar icons:** With the PowerBar Editor open, drag-and-drop an icon on the PowerBar to a new location.

- **Create additional PowerBars:** To create multiple PowerBars for the main Analyze window or an Analyze module, click the New button in the PowerBar Editor and then select the desired icons for the new PowerBar. You can scroll through the PowerBars using the up/down arrow buttons added to the far left of the PowerBar.

- Be sure to press **Save** in the PowerBar Editor if you wish to keep your PowerBar changes for future sessions. Otherwise, changes will be lost upon exiting the Analyze module, or Analyze.

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**Analyze 12.0:** Essential Training Guide

# Loading Data into Analyze

**Analyze**Direct

# DICOM Tool: Quick Configuration

The DICOM Tool expands DICOM support in Analyze, enabling the indexing of collections of DICOM images through a local database file. This exercise will demonstrate how to create a database and then how to import DICOM data into the database. *Note: If you are a previous BirPacs user please contact support@analyzedirect.com for instructions on migrating your database to the DICOM Tool.*

1. Open the **DICOM Tool** (**File > DICOM Tool**).

2. The DICOM Tool will detect that there is no database present; a dialog box will be returned asking you if you would like to create a new database or browse for an existing database, click **Create a new local database**.

   *note*   If this is not the first time you have accessed the DICOM Tool, you can access the Create New Image Database window by selecting File > Create Database.

3. The **Create New Image Database** window (Figure 1) allows you to specify a database name and file system directory, configure a DICOM receiver for the database (optional), configure a database server (optional), and specify the source of initial DICOM images (optional).

4. The **Local Database Name** will default to 'SystemName_PortNumber'; change the Local Database Name to TEST_5679.

5. On your system's local disk create a folder called '**AnalyzeDB**' ($:/AnalyzeDB)

6. Click the **Local Database Directory** button in the Create New Image Database window.

7. In the Browse for Folder window returned navigate to the location of the new '**AnalyzeDB**' folder ($:/AnalyzeDB), select the folder, and click **OK**. You have now specified the location of your local database.

8. To create the local database click the **Create Local Database** button.
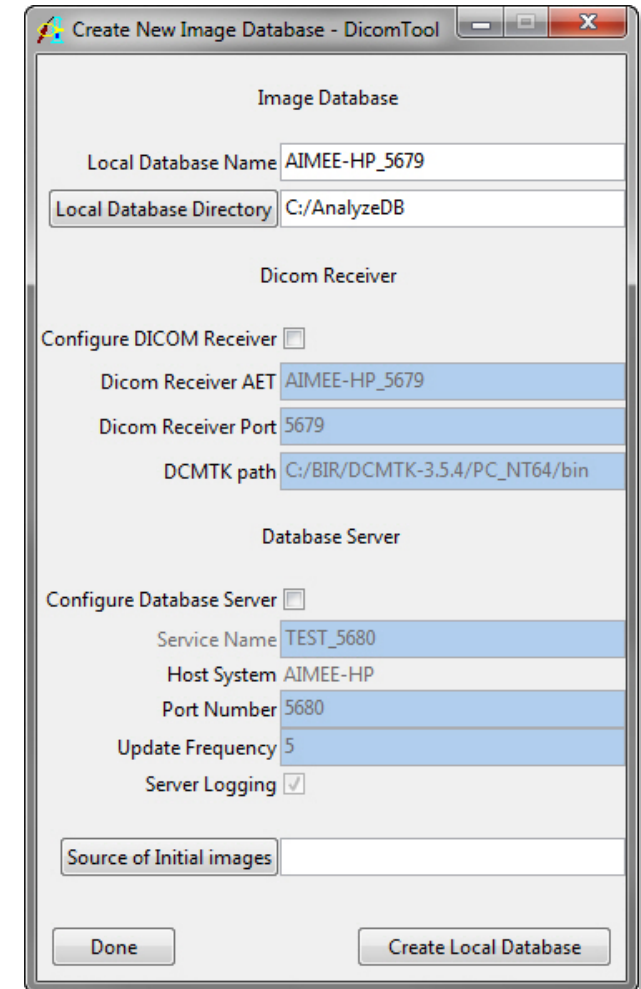
Figure 1

# DICOM Tool: Quick Configuration

9. Once the database has been created a dialog box will be returned stating 'All Done', click **OK**.

10. To import DICOM data into the DICOM Tool right-click anywhere in the white space and select **Import DICOM Images** from the menu (Figure 2). Alternatively, select **File > Import DICOM Images**.

11. In the (Browse for Folder) window returned navigate to and select the folder **$:\BIR\images\TutorialData\ImportExportTutorial**, then click OK.

12. A dialog box will be returned asking you to confirm that you would like to 'Import all DICOM files found below <C:/BIR/images/TutorialData/ImportExportTutorial>', click **Yes** to confirm.

13. All 121 DICOM images contained within the folder will be copied into the database. The DICOM Tool will automatically sort and index the data by patient, study, series, and volume.

14. Data can be selected and viewed in the DICOM Tool (Figure 3). To load a selected data set into the Analyze workspace click **Load Volume**; if you wish to resize or resample the data click **Load As**, this will load the selected data into the Load As module (see exercise 4 for instructions on how to use the Load As module).



Figure 2



Figure 3

# DICOM Tool: Advanced

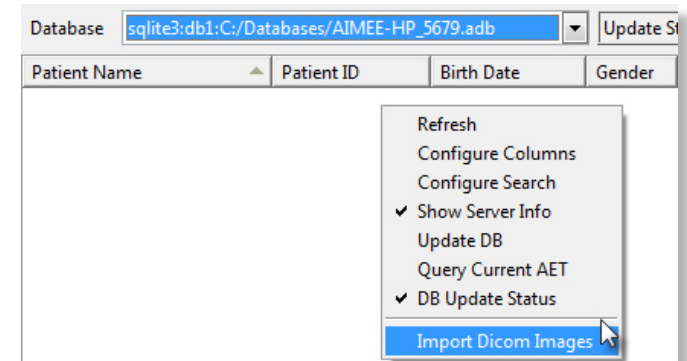The DICOM Tool expands DICOM support in Analyze, enabling the indexing of collections of DICOM images through a local database file. With the DICOM Tool, databases can be created, updated, and shared with other users with file system access to the images and the database file. This exercise will demonstrate how to create a database, configure a DICOM receiver and Database sender and then how to import DICOM data into the database. *Note: If you are a previous BirPacs user please contact support@analyzedirect.com for instructions on migrating your database to the DICOM Tool.*

1. Open the **DICOM Tool** (**File > DICOM Tool**).

2. If you have already completed Exercise 1, choose **File > Create Database**. If the DICOM Tool detects that no database is present, a dialog box will be returned asking you if you would like to create a new database or browse for an existing database, click **Create a new local database**.

## Specification of the Database Name and Directory

3. In the **Create New Image Database** window you can specify the database name and file system directory, specify a DICOM receiver for the database (optional), specify database server (optional), and specify the source of initial DICOM images (optional).

4. The **Local Database Name** will default to 'SystemName_PortNumber'; change the Local Database Name to **TEST2_5679**.

   *note*   Any name can be chosen for the local database, however when creating multiple databases, following a coherent naming convention will simplify database management.

5. The **Local Database Directory** option enables you to specify the directory on your system in which the database and all of the DICOM images will be stored.

   i. On your system's local disk create a folder called '**AnalyzeDB**' ($:/AnalyzeDB). Note that if you have completed exercise 1, **DICOM Tool - Quick Configuration**, this folder should already exist.

   ii. Once the directory has been created, click Local Database Directory in the Create New Image Database window, and navigate to the location of the new 'AnalyzeDB' folder ($:/AnalyzeDB).

   iii. Select the folder and click OK. You have now specified the location of your database.



Figure 1

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# DICOM Tool: Advanced

## Specification of a DICOM Receiver (optional)

6. The Configure DICOM Receiver option allows you to configure a DICOM receiver for the database. This step is optional, if you do not want to configure the receiver please move on to step 8, otherwise check the Configure DICOM Receiver option.

7. DICOM Receiver configuration requires three key pieces of information: the Receiver AET, the Receiver Port on the local system, and the directory where the DCMTK executable programs are installed.

   i. **DICOM Receiver AET**: By default is set to 'SystemName_PortNumber'. To reflect the receiver's connection to the database defined in step 4, change the DICOM Receiver AET to **TEST2_5679**.

   ii. **DICOM Receiver Port**: Specifies the TCP/IP port number on which the DICOM Receiver listens for connections to receive messages. For this exercise, the DICOM Receiver Port can remain **5679**.

   iii. **DCMTK Path**: The DCMTK executable files are automatically installed with Analyze in the **$:\BIR\DCMTK-3.5.4\$System_Type$\bin** directory (where $System_Type$ is your system platform, e.g. PC_NT) and the DCMTK Path will point to this directory by default. However, if Analyze is being run from a network rather than local installation, the DCMTK files should be installed locally and this path should point there.

# DICOM Tool: Advanced

## Specification of a Database Server (optional)

8. The Configure Database Server option allows you to configure an optional database server to manage automatic updates and multiple client access to the database over a network. The database server is a dedicated process attached to one database and accessible by system name and port number. It responds to connection requests, SQL statements, and requests for images, and polls the image storage area for newly received images to register. Configuring and installing a database server is very similar to configuring the DICOM receiver. This step is optional, if you do not want to configure the database server please move on to step 10, otherwise check the Configure Database Server option.

9. The Database Server fields are used to configure the database server process that controls access to the database.

   i. **Service Name**: The name by which the servicer is identified, for this exercise use **TEST2_5679**.

   *note* On Windows systems this becomes the name of the Windows Service; on UNIX systems it is used to name the daemon script which starts, stops and checks server status.

   ii. **Host System**: Identifies the system name this program is running on. You can create servers to run on your system, and any server should be attached to a database local file system.

   iii. **Port Number**: Specifies the port number client systems will use to connect to server. It cannot be the same port as the one used by the DICOM receiver (STORESCP). For this exercise set the port to **5680**.

   iv. **Update Frequency**: Specifies the interval in minutes at which the server will poll the image storage directory to see if the DICOM receiver has deposited images to be in the database. For this exercise, you can leave this set to **5**.

   v. **Server Logging**: Creates a log file of the database server for diagnostics.

*tip* It is recommend using a closely related port number so they can be easily remembered; e.g., if the receiver is running at port n, run that database server at port n+1.

# DICOM Tool: Advanced

## Specification of the Source of Initial Images (optional)

10. The **Source of Initial Images** option allows you to specify a directory containing DICOM images; click **Source of Initial Images**.

11. In the Browse for Folder window returned, navigate to the **$:\BIR\images\TutorialData** directory, select the **ImportExportTutorial** folder, and click **OK**.

## Creating the Database Server

12. To create the local database, click **Create Database Server**. Note, creating a Database Server requires administrative privileges; a dialog box will automatically be returned stating that you will receive a prompt from your operating system, click **OK**. You will then need to enter the administrator password.

13. The DICOM Tool will now copy the DICOM images from the initial source to the location (if selected) specified in step 5. The data will automatically be sorted and indexed by patient, study, series, and volume.

14. Once the process is complete, the Create New Image Database window will automatically be dismissed and the data will now be available in the DICOM Tool (figure 2).

## Viewing and Loading Data

15. Data can be selected from the Patient information panel in the DICOM Tool.

16. Select the data set with the 'Patient Name' **MR SIGNA LX 1.0T** and 'Patient ID' **337**. The data set will be highlighted, note the other information panels will automatically update with relevant Study, Series, and Volume information (when available).

17. Note there are two data sets available for selection in the Series information panel below. Select **Series 102**.
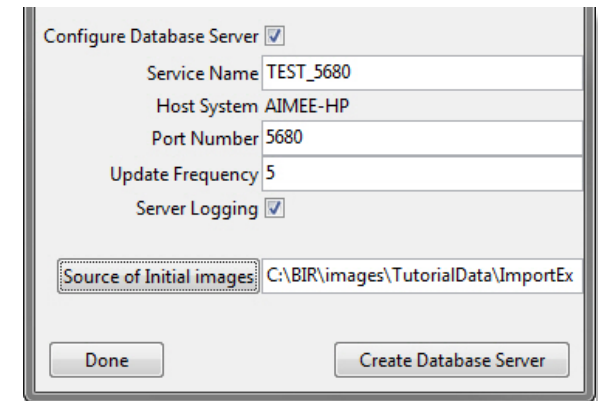
Figure 2

# DICOM Tool: Advanced

18. Review the data slice-by-slice by using the Slice Number slider bar under the image display.

19. Right-click on the image display to open the Intensity window (figure 3). Here you can change the intensity display of the image; use the slider bar to take the Maximum intensity level down to 500. The image display will interactively update. Click Done to dismiss the Intensity window.

20. To load this data set into the Analyze workspace, click Load Volume. The data set will automatically load into the Analyze workspace.

## Other DICOM Tool Options

21. Move the cursor over any of the information panels and right-click. The menu returned provides most of the options available for management of the images in the DICOM database, these options include:

  **Refresh**: Deselects any selected data and refreshes the data

  **Configure Columns**: Configure the column properties for the data display

  **Configure Search**: Focus the scope of the displayed data with an information search

  **Show Server Info**: Enable/disable display of recent databases and remote AETs

  **Update DB**: Register any recently received unregistered images in the database

  **Query Current AET**: Perform query retrieve on remote AET to retrieve images

  **DB Update Status**: Enable/disable display of Database Update Status

  **Import DICOM Images**: Copy and register images from the file system to the database

  **Load Patient**: Load patient data from files

  **Export Patient**: Export patient data to files

  **Delete Patient**: Delete the patient data from the database

  **Send Patient**: Send patient data to listening server

  **Anonymize Patient**: Anonymize the patient information (only available from the patient pane)


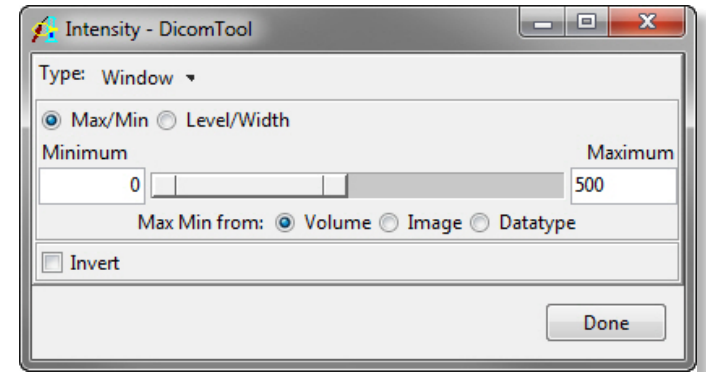
Figure 3

note    If you wish to resize or resample the data use the Load As button option, this will load the selected data into the Load As module (see exercise 4 for instructions on how to use the Load As module).

22. On your system's local disk create a folder called '**test_ export**' ($:/test_export).

23. Select the 'Patient Name' **MR dataset Brain** and then right-click and select the **Export Patient** option (figure 4).

24. In the (Browse for Folder) window returned, navigate to the new '**test_export**' directory, then click **OK**. The DICOM images will be exported out to this directory.

25. Now navigate to the '**test_export**' directory on your system's local disk; note the file names have changed to new DICOM UIDs.

26. In the DICOM Tool, with **MR data set Brain** still selected, right-click and select the Delete Patient option.

27. A dialog box will be returned asking you to confirm that this is what you want to do, click **Yes**. A delete confirmation window will be returned, click **OK** to dismiss it.

28. To import this data back into the DICOM Tool right-click in any of the information panels and select the **Import DICOM Images** option. In the window returned navigate to and select the 'test_export' directory on your system disk, then click **OK**.

29. You will be asked if you would like to 'Import all DICOM files found below <$:/test_export >', click **Yes** to import these images back into the database. The data will be automatically sorted and imported into the DICOM Tool database, and the data set will appear in the Patient information panel.

30. Close the DICOM module before proceeding to the next exercise.
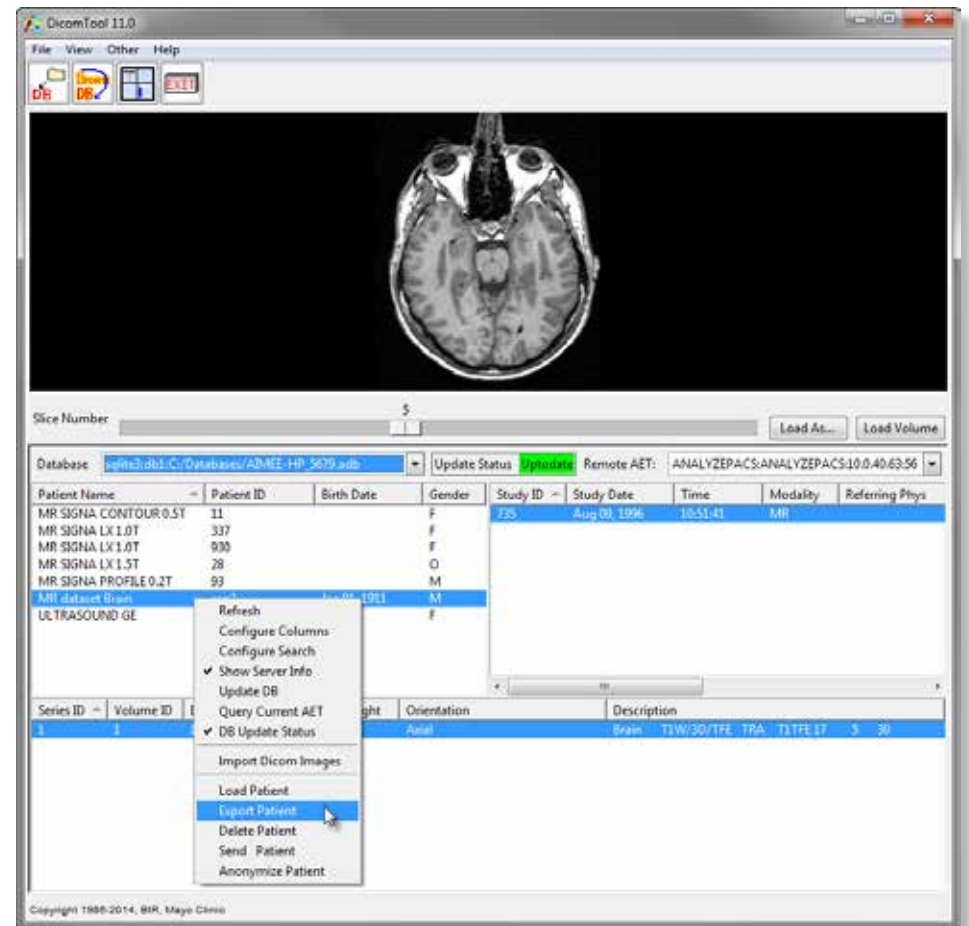


Figure 4

*tip* Multiple databases can be created for the DICOM Tool, so multiple DICOM receivers can be configured for the tool; you can select different databases from the Local Databases drop-down menu option.

# Switching on Support for Additional Formats

Analyze supports over 45 different file formats. By default, only the most common formats are enabled. The Import/Export module's External Libraries tool can be used to enable and disable these formats. This exercise will show you how to use the External Libraries tool to switch on support for additional formats.

1. Open the **Import/Export** module (**File > Import/Export**).

2. To view the file formats currently supported in Analyze, choose **Help > Formats**.

3. File formats currently supported are listed in the bottom '**Formats**' section of the Supported Formats window (figure 1). When a format is selected, the associated properties will automatically become checked in the '**Properties**' section of the window. Experiment by checking several different formats and noting their properties. Click **Done** to dismiss the window.

4. Open the **External Libraries** tool (**Tools > External Libraries**).

5. The External Libraries tool provides a graphical interface listing all formats supported by Analyze (figure 2). The green and red status indicators note whether a format is currently '**Loaded**' (L) and '**Configured**' (C) - green indicating yes and red indicating no.

6. If you wish to switch on support for a specific file format (for example, PICKERMRI), click on the format in the External Libraries tool. A Configure 'X' Format window will be returned (where 'X' is equal to the selected format) (figure 3).

7. In the Configure 'X' Format window, click **Load Now** to change the 'Currently Loaded' status to a green **Yes**.

> *note* Users running multiple operating systems need to configure support for each file format for each operating system. The 'Platforms' option allows the format to be configured for all operating systems (ALL) or for a specific operating system (SPECIFIED).
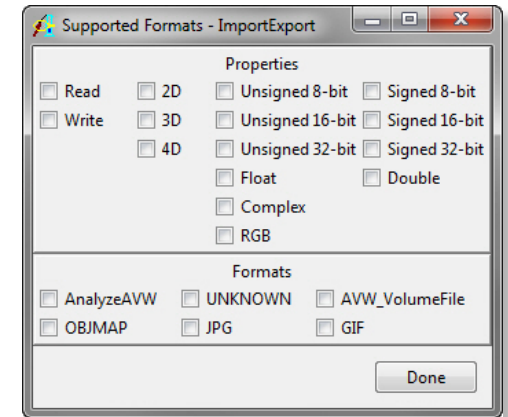
Figure 1

Figure 3

Figure 2

AnalyzeDirect
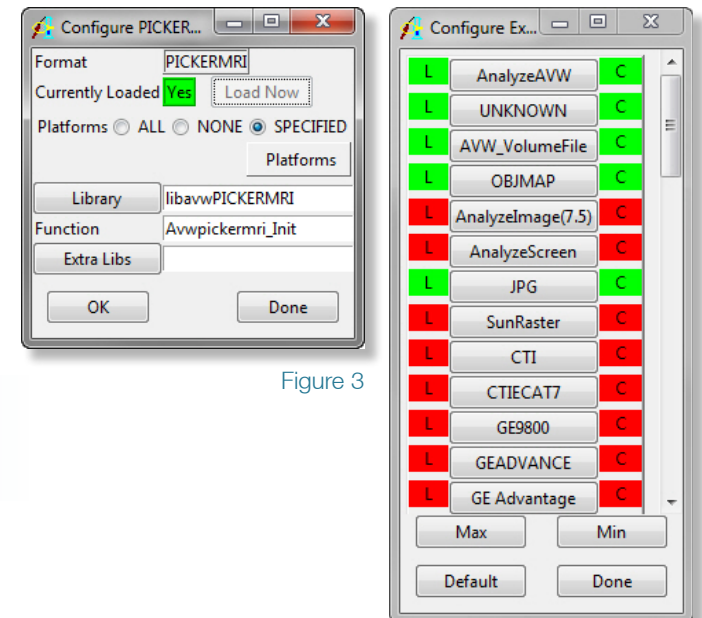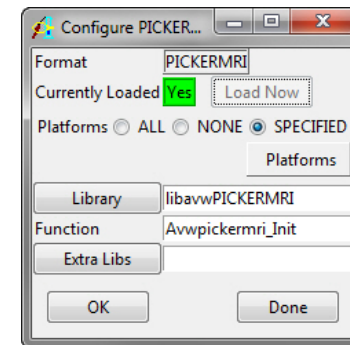
# Switching on Support for Additional Formats

Exercise 3

8. Click **OK**. A dialog box will be returned stating that your 'EXTEND.conf' file will be updated, click **OK** (figure 4). The format is now supported by Analyze.

9. If you would like to load and configure all supported formats for your system, click **Max** in the External Libraries tool. All image file formats will now be supported by Analyze. The 'L' and 'C' status indicators will appear green next time you open Import/Export and the External Libraries tool (figure 5).

*note* Each file format enabled increases the amount of memory used by your system; it also increases the time taken for a module to open. However, this is typically only an issue on older systems or systems where memory resources are scarce.

10. Click **Done** to close the External Libraries tool.

11. Close the Import/Export module before proceeding to the next exercise.

Figure 4

Figure 5

# Supported File Formats

## Analyze

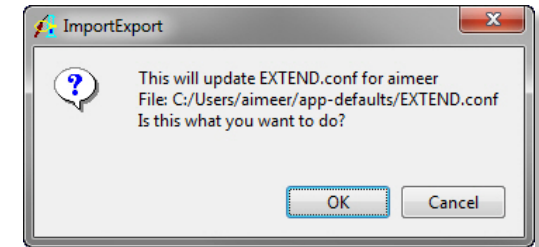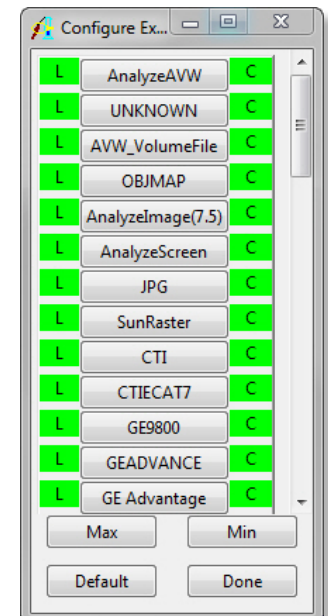| | |
|---|---|
| AnalyzeAVW | used internally for memory mapping, supports all data types, 2D, 3D, and 4D. |
| UNKNOWN | enables reading raw binary data into images, and exporting image data as raw. |
| Volume File | enables lists of 2D files to be used as 3D entity |
| OBJMAP | enables object maps to be treated as regular imgs |
| AnalyzeImg | old Analyze 7.5 format, i.e. .hdr/.img pairs |
| AnalyzeScrn | old Analyze 7.5 format of old Screen Edit program |

## Raster

| | |
|---|---|
| BMP | Microsoft Windows Bitmap |
| GIF | a common color indexed format |
| JPG | common format featuring lossy compression |
| PBM | ascii and binary formats used in Portable Bitmap Library |
| PGM | grayscale Portable Bitmap Library |
| PPM | 24 bit Color Portable Bitmap Library |
| PIC | format used by Softimage |
| PNG | Portable Network Graphics |
| PS | output to a PostScript raster dump |
| SGI | format used by Silicon Graphics |
| SUNRASTER | format used by Sun Microsystems |
| TARGA | a common color format |
| TIFF | tagged information file format, a common format |
| XBM | an ascii 'c programming language' format used by the X Windows system |
| XWD X | Windows dump |

## Standard Radiological File Formats

| | |
|---|---|
| DICOM | the standard medical image file format based on Mallincrodt ctn_3_0_3. |
| ACR/NEMA | precursor to DICOM |
| PAPYRUS2 3D | extensions to DICOM from OSIRIS |
| PAPYRUS3 3D | extensions to DICOM from OSIRIS |
| NIfTI | Neuroimaging file format |

## Video

| | |
|---|---|
| QUICKTIME | common movie format |
| YUV | single frame color video format |
| AVI | video format used by Microsoft Windows |
| MPEG1 | standard movie format |

## Vendor-Specific Radiological File Formats

| | |
|---|---|
| GE9800 | older CT format |
| GEADVANCE | Advance, nulcear medicine format |
| GEADVANTAGE | format for CT and MRI |
| GESIGNA | older MRI format Signa 4.x |
| GESTARCAM | older PET format |
| INTERFILE | a standard format for nuclear medicine |
| PICKER MRI | old MRI format used by Picker |
| SIEMENSCT | old Siemens CT format Somatom DR3 |
| SIEMENSMAGVIS | Siemens Magnetom Vision (MRI format) |
| CTI | PET format used by CTI, early version of ECAT7 |
| 7CTI | PET format used by CTI; CTIECAT7 |
| IMATRON | proprietary CT format |
| SMIS | proprietary MRI format |
| BRUCKER MRI | proprietary MRI format |
| BIO RAD | proprietary format |
| VARIAN FDF | Varian MRI format |

# Load As: Loading & Resizing Anisotropic Data

Scanner acquired data is rarely isotropic (cubic) which means that the voxel width, height, and/or depth have different sizes (most often a different slice thickness than the in-plane resolution). This exercise will demonstrate how to load an anisotropic (non-cubic) volume image with the same resolution as when acquired, and then load it again to resize the volume image to create an isotropically sampled volume (cubic) for further use in Analyze.

1.  Open the **Load As** module (**File > Load As**).

2.  Click **File** and navigate to and select the **MRI_Head.avw** data set in the **$:\BIR\images\TutorialData** directory.

3.  Uncheck the **Auto Exit After Load** option and click **Load**. The data will be loaded into the Analyze workspace as it was acquired (anisotropic).

4.  To load the data as isotropic (cubic), select the **Resize** tab (figure 1).

5.  Check the **Force Cubic** option and click **Load**; Select 'Create New' and the data will be resampled at the cubic resolution and then loaded. The highest spatial resolution in the acquired volume image is used as the cubic resolution for resampling.

6.  Two volumes are now loaded into the Analyze workspace, '**MRI_Head**' and '**MRI_Head0**'. The latter volume is the cubic volume. To examine the effects of this isotropic sampling, proceed to **Exercise 8: Multiplanar Sections**.

7.  If a specific cubic voxel resolution is desired, the voxel size can be changed. To set the output voxel dimension to 1.5 mm, enter 1.5 in the **Output Voxel Size** field and press <Enter>. Notice that the 'Output Axis Dimensions' and 'Memory' fields automatically adjust when the voxel dimension is changed.

8.  It is also possible to set a specific dimension for the resulting volume image. For example, if you wanted an output volume with an X dimension of 200, enter **200** in the **Output X Axis Dimension** field and press <**Enter**>. Again, the other parameters will automatically adjust.

9.  You may encounter data sets that are too large to be accommodated by the computer on which you are running (usually due to memory limitations), particularly at the resampled cubic resolution. Specifying a maximum memory size while the Force Cubic option is checked forces each parameter to adjust to the largest value possible that still fits within the specified memory size. Enter **16** into the **Output Memory Mb** field [G].

10. Close all windows related to the Load As module before proceeding to the next exercise.
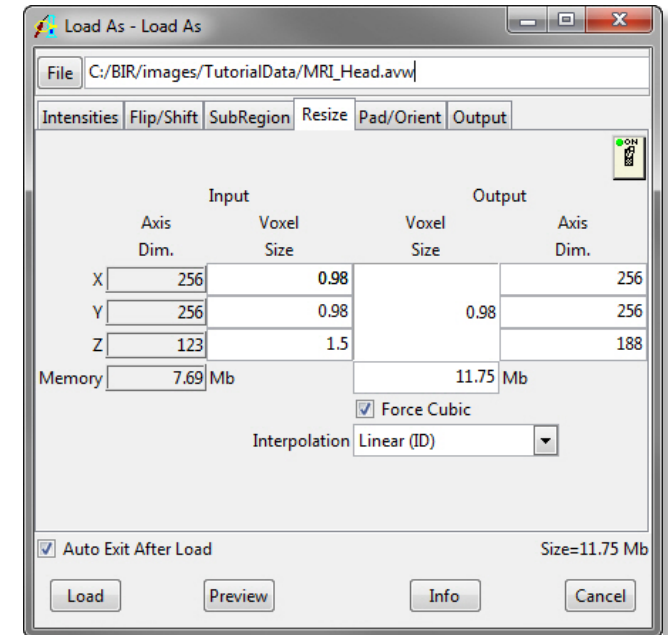


Figure 1

AnalyzeDirect

# Import/Export: Converting Raw Data to Images

Occasionally it is necessary to import raw data or image data of an unknown file format into Analyze. Such data can be imported if pixels are uncompressed and in contiguous images within the file. The Raw Data tool provides several interactive options to view data as images, ASCII strings, or as the actual binary values of bytes and words. Data can be directly loaded into Analyze or converted into Analyze format image files. Most image file formats consist of some initial header information describing the image(s) and the actual image data. This exercise will demonstrate how to convert raw data from a scanner, which currently has no direct file format support in Analyze.

1.  Open the **Import/Export** module (**File > Import/Export**).

2.  Open the **Raw Data** tool (**Tools > Raw Data**).

3.  With the **Files** tab selected, click the **File** button under 'Input' (figure 1).

4.  In the **Import/Export – Input File** window returned navigate to the **$:\BIR\ images\ TutorialData\ImportExportTutorial** directory and select the file **UNKNOWN1**.

5.  Select the **Image Parameters** tab (figure 2).

6.  For this exercise, assume that we know that this file contains one 256 x 256 image, a signed 16-bit integer. An image of this size requires 131072 bytes of storage (256 x 256 x 2), however the file size is 137210 bytes. This indicates that there is an additional 6138 bytes of header information present. This needs to be skipped to get to the first byte of image data. Finally, we know that the 16-bit image data in the file is stored in Big-Endian byte format.

7.  To accommodate this, set the following parameters:

    *   **Byte Offset: 6138**  (or check 'Auto Offset' to compute this automatically)

    *   **Width: 256**

    *   **Height: 256**

    *   **Data Type: signed 16-bit**

    *   **Byte Swap: Pairs** (this only needs to be set on a little-endian architecture, i.e., PC-based systems)
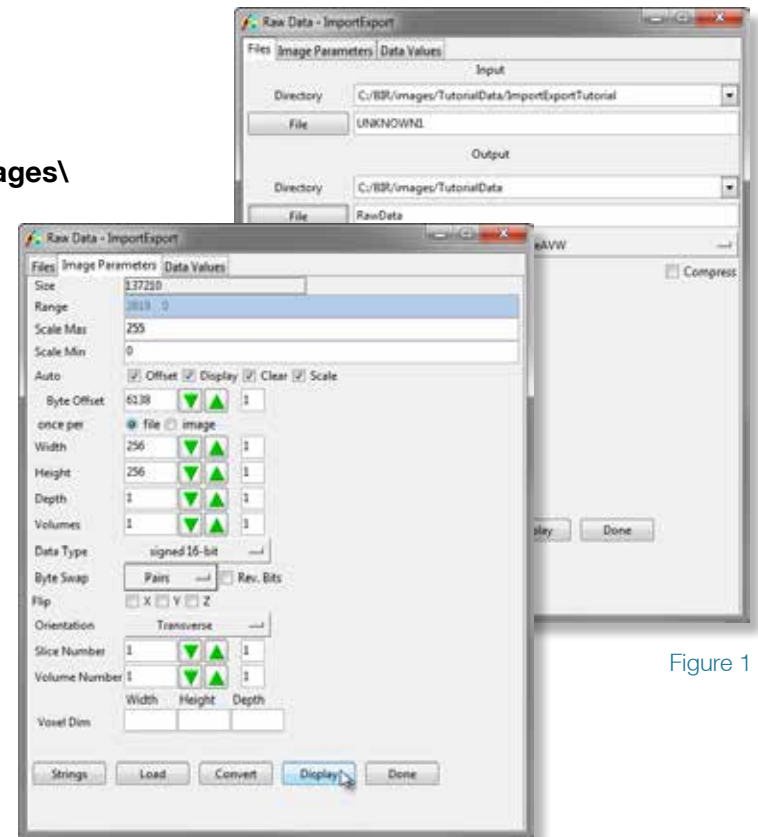
Figure 1

Figure 2

AnalyzeDirect

8. Check the following **Auto** options:

   - **Display**: Image display will update anytime a control parameter is changed.

   - **Clear**: Image display is cleared before a new image is displayed.

   - **Scale**: Data is automatically scaled from its entire dynamic range to 8-bits for display.

9. Click **Display** to view the current image in the main Import/Export window (figure 3).

10. Click **Load** in the Raw Data tool to load the image specified in the file into the Analyze workspace.

11. Experiment with the display effects by changing the image parameters to incorrect values, use the up and down arrow buttons found next to the Width and Height fields.

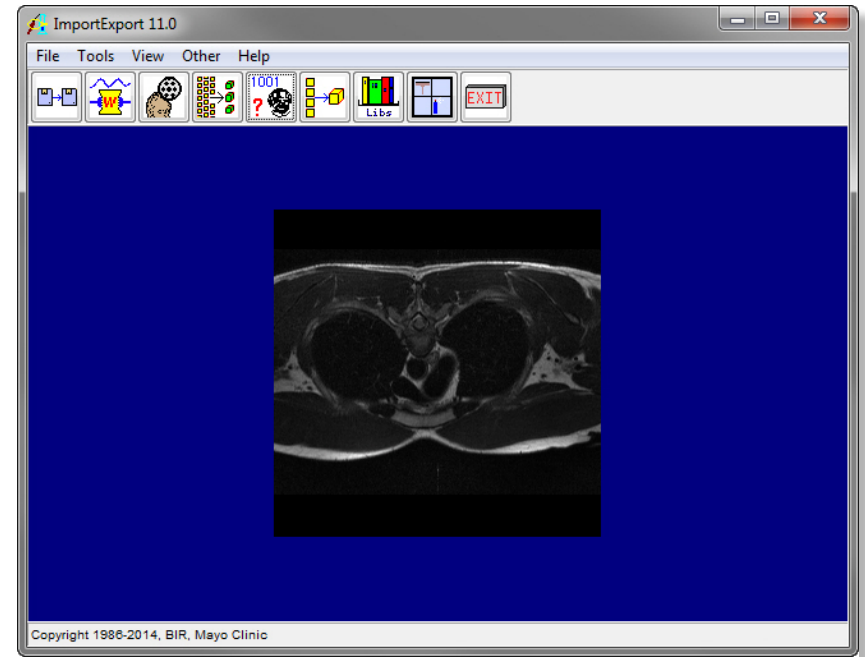12. Click **Done** to close the Raw Data tool.



Figure 3

# Import/Export: Volume Tool

Most medical image formats do not support 3-D directly, since each slice in a study is written to a separate file. The Volume Tool provides a way to create a pseudo format for handling groups of 2-D files as a single 3-D entity. Analyze uses the AVW_VolumeFile, or volume file (.vol), as a way to organize a list of 2-D files into a 3-D volume. The files must contain images of the same size and data type. This exercise will show you how to use the Volume Tool to create a volume file from a list of 2-D TIFF files.

1.  Open the **Import/Export** module (**File > Import/Export**).

2.  Open the **Volume Tool** (**Tools > Volume Tool**).

3.  In the Volume Tool, click **Wild Cards**.

4.  In the window returned (figure 1), click Directory and navigate to **$:\BIR\ images\ TutorialData\VolumeToolTutorial** - the directory containing the 2-D TIFF data for this exercise.

5.  The Filter field is set to * by default so everything in the directory is selected. As this directory only contains TIFF data specific to the data set we wish to load, leave the filter as is.

6.  Click **Apply**. The TIFF files will now be copied to the Volume Tool (figure 2).

7.  In the Volume Tool, click **Verify** to ensure that all the slices selected are the same size and data type.

8.  A dialog box (figure 3) will be returned upon successful verification stating 'Verify Succeeds'; click **Continue**.

9.  Click Save and save the volume file as **TIFF_Head.vol** in the **$:\BIR\images\ TutorialData** directory.

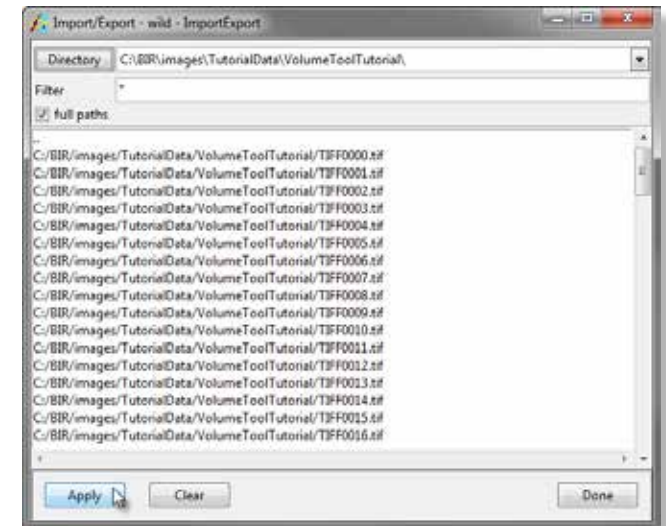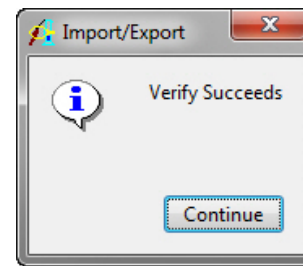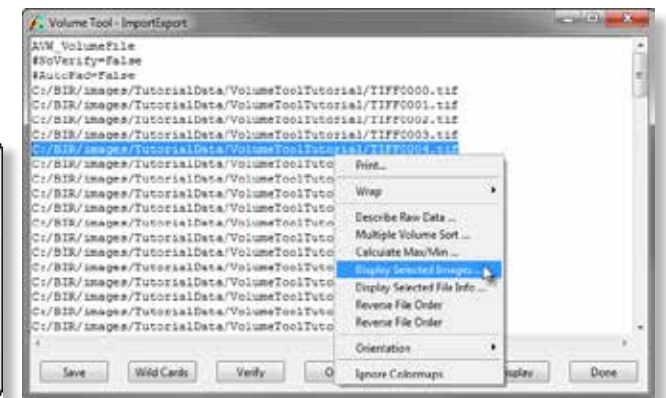10. Close the Import/Export module before proceeding to the next exercise.


Figure 1


Figure 3


Figure 2

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# Saving Data Out of Analyze

At some point it will become necessary for you to save your data out of Analyze. This exercise will demonstrate how to do this using the Save module.

1. Select a data set from the Analyze workspace. If there is no data loaded, load **MRI_3D_Head.avw** from the **$:\BIR\images\TutorialData** directory.

2. Open the **Save** module (**File > Save**).

3. Click **File** and navigate to the directory where you would like to save the data set and specify a name. Click **Save** to return to the main module window.

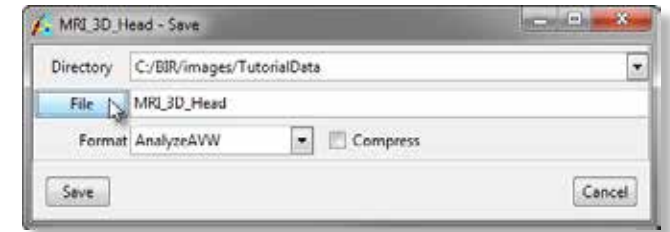4. Use the **Format** drop-down menu to specify the format in which you wish to save the data set.



Figure 1

> *note*  Only formats enabled in the external libraries tool will be available. To switch on support for additional formats, please refer to Exercise 3: Switching on Support for Additional Formats.

5. Click **Save** to save the data set and close the Save module.

> *tip*  You can also save your data out of Analyze using the Save As module. The Save As module provides the same tools as the Load As module, allowing you to resize, change orientation, sub-region, and perform other manipulations on your data while saving it out of Analyze.

AnalyzeDirect

**Analyze 12.0: Essential Training Guide**

# Display and Visualization

AnalyzeDirect

# Multiplanar Sections

The Multiplanar Sections module allows the user to quickly and easily view image data in the plane of acquisition or in any naturally orthogonal plane. The module contains several tools for easy two-dimensional display, and has the capacity to load volumes, load object maps, select orthogonal orientations, and perform intensity windowing or thresholding.

1. Load the **MRI_Head.avw** data set from the **$:\BIR\images\TutorialData** directory. The data set may already be available in the Analyze workspace if you have completed **Exercise 4: Loading and Resizing Anisotropic Data**.

2. Open the **Multiplanar Sections** module (**Display > Multiplanar Sections**).

3. Press the **Display Section(s)** PowerBar button or choose **Generate > Display Section(s).** This will begin a sequential display of the data, the display may be stopped at any time by clicking anywhere in the main Multiplanar Sections window (figure 1).

4. Since MRI_Head.avw was acquired in the sagittal orientation, this is the default orientation for display purposes. The display orientation can be changed to display images in a transverse, coronal, or sagittal orientation. Use the **Orientation** PowerBar buttons to change the display orientation or open the Orientation window (**Generate > Orientation**).

5. To specify a particular slice to view or to begin the sequential display from, open the **Slice** window (**Generate > Slice**). Use the 'Slice' slider bar to set the specific slice.
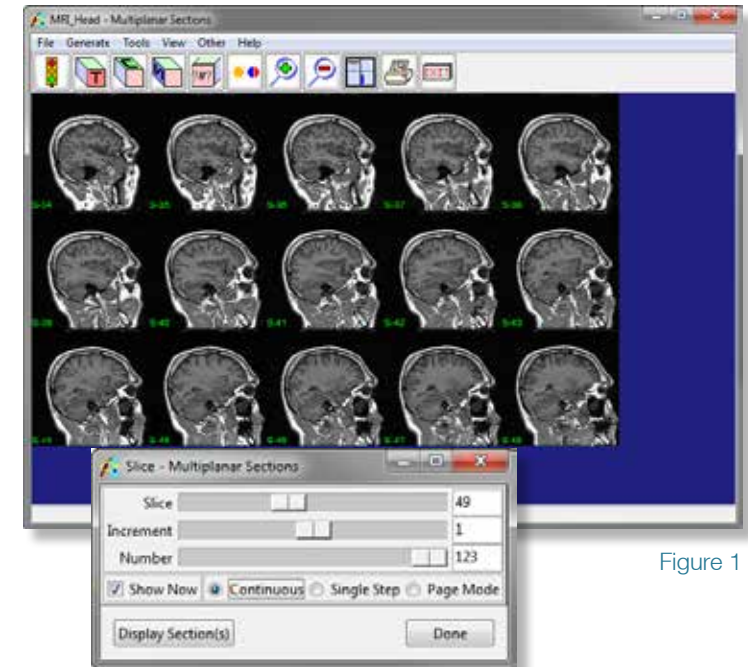
## Scan Tool

6. The **Scan Tool** (**Tools > Scan**) provides an interface for slice-by-slice review. Click either of the green 'play' arrows to start a sequential display of slices, or use the + and - buttons to move one slice at a time. The slider bar can also be used to move through the slices.

Figure 1

---

*tip*  The Slice window also contains three display options: Continuous, Single Step, and Page Mode. 'Continuous' sets the display mode to display the slices in a continuous stream. 'Single Step' turns off the continuous display of slices, when Display Section(s) is selected only one slice is displayed. 'Page Mode' sets the display mode to display a page of slices at a time when Display Section(s) is selected.

*note*  Since MRI_Head.avw is anisotropic, images will appear "squashed" in the coronal and transverse orientations. The resized data set MRI_Head0 created in exercise 4, Loading and Resizing Anisotropic data, will display normally in all three orientations.

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# Multiplanar Sections

## Intersecting Sections Tool

7.  Open the **Intersecting Sections** tool (**Tools > Intersecting Sections**). The Intersecting Sections tool provides an interactive display of intersecting orthogonal sections.

8.  To change the angle at which the intersecting sections are viewed, use the **View Angle X**, **Y**, and **Z** slider bars. The view angle can also be changed by clicking in the image display and dragging the image to a new view.

9.  Use the **Slice X**, **Y**, and **Z** slider bars to manipulate the intersecting orthogonal sections. The 'X' slider bar controls the sagittal slice displayed, 'Y' the coronal, and 'Z' the transverse; the slider bar and intersecting sections are also color-coded. The image display will interactively update, allowing the user to navigate through the interior of the data set.

10. The scale of each plane can also be changed using the **Scale X**, **Y**, and **Z** slider bars. To increase the scale of all planes in proportion to each other, uncheck the Individual Axis option; one Scale slider bar will replace the three slider bars, use this to increase and decrease the image size.

11. Right-click on the image display and choose **Auto Save**. Now, repeat some of the maneuvers described above; when you are finished, right-click again and uncheck the Auto Save option. The maneuvers performed have been recorded and saved to the Analyze workspace. The file can be reviewed with the **Movie** module (**Display > Movie**).
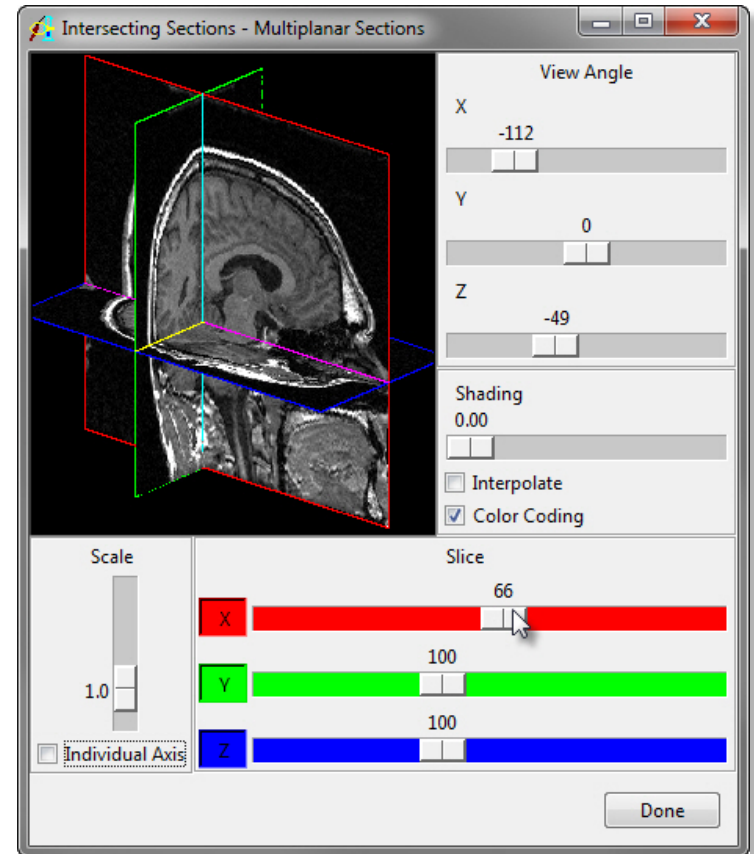


Figure 2

AnalyzeDirect

# Multiplanar Sections

## Cube Sections Tool

12. Open the **Cube Sections Tool** (**Tools > Cube Sections**). The Cube Sections tool provides an interactive display of orthogonal sections in a three-dimensional viewing cube.

13. The **View Angle** and **Scale** options for the Cube Sections tool may be changed as described for the Intersecting Sections tool.

14. Planes can be interactively sliced away in the three orthogonal orientations to reveal interior sections of the cube with the **Subregion X**, **Y**, and **Z** double-ended slider bars. As with the Intersecting Sections tool, 'X' controls the sagittal orientation slices displayed, 'Y' the coronal, and 'Z' the transverse; the slider bars and cube sides are also color-coded.

15. After subregioning the data set, right-click on the image display and choose **Extract Sub-volume**. The subregioned data set will be saved to the Analyze workspace.

16. Click **Done** to close the Cube Sections tool.

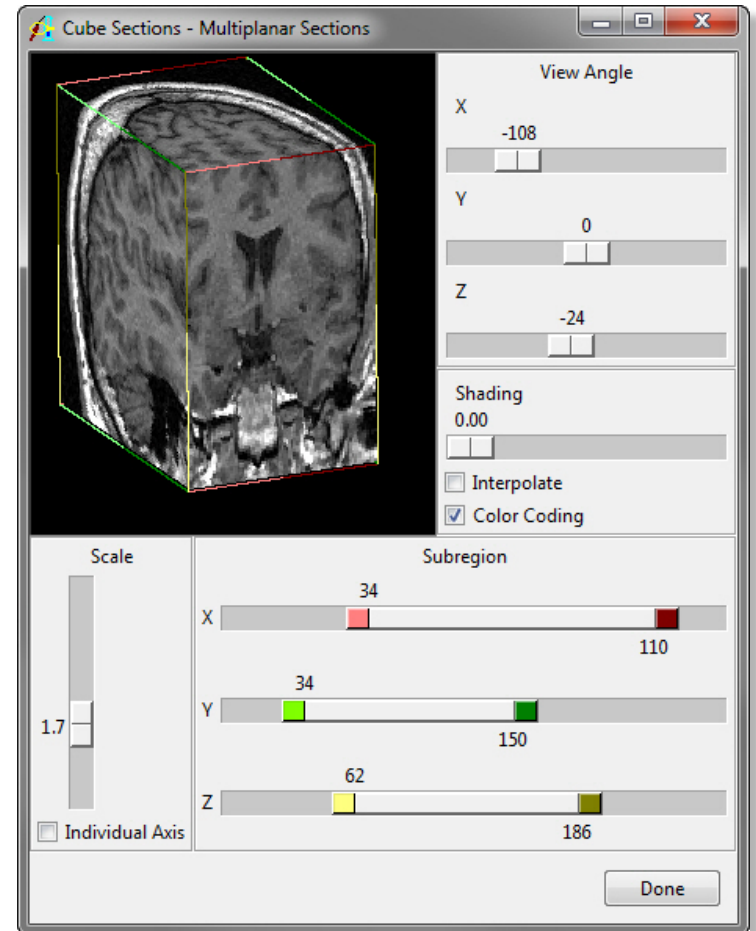17. Close the Multiplanar Sections module before proceeding to the Additional Task.



Figure 3

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# Multiplanar Sections: *Adding Color Overlay*

The ability to create a grayscale image overlaid with colored objects, also known as an Intensified Volume, can be useful. This exercise will demonstrate how to achieve this using the Multiplanar Sections module.

## Creating a Grayscale Data Set with Color Overlaid Objects

1. Select the **MRI_3D_Head** data set in the Analyze workspace and then open the Multiplanar Sections module (**Display > Multiplanar Sections**).

2. Choose **File > Load Object Map** and load the **MRI_3D_Head.obj** object map from the **$:\BIR\images\TutorialData** directory.

3. When the object map loads the Objects window will automatically open (figure 1). In the Objects window do the following:

   - Set '**Control by**' to '**Attribute**'

   - Set the Display of all objects to '**On**' with the exception of the Original and Skin objects.

4. Open the **Scan Tool** (**Tools > Scan**) and use the slice slider to review the display of the image data (figure 2).

5. Open the **Intensity** option (**View > Intensities**). In the Intensities window, review each of the Object Color modes by selecting each from the 'Mode' drop down menu.
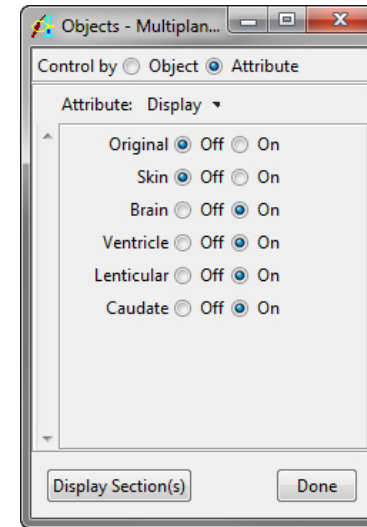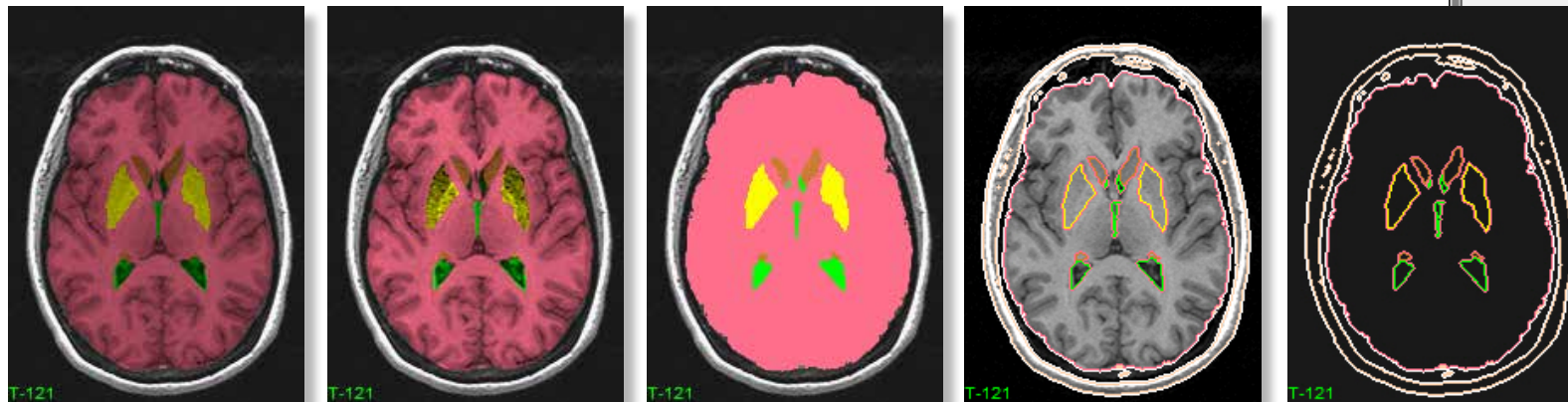


Figure 1



Figure 2



| Windowed Object | Local Max/Min | Object Only | Color Edges | Edges Only |

Figure 3

AnalyzeDirect

# Oblique Sections: Oblique Resizing of Volumes

Sometimes a particular structure of interest within a data set is not aligned with the orthogonal axes of the 3-D volume. The Oblique Sections module interactively generates any arbitrary plane through a data set and allows reformatting of a series or the entire data set. This exercise will demonstrate how to create an obliquely resampled data set for further analysis with Analyze.

1. Load the **Canine_Chest_CT.avw** data set from the **$:\BIR\images\ TutorialData** directory.

2. Open the **Oblique Sections** module (**Display > Oblique Sections**).

3. Open the **Fly** tool (**Generate > Fly**).

4. Use the Fly tool (figure 1) to rotate the current oblique plane from the transverse orientation to the sagittal orientation:

   v. Click the **Roll Right** button nine times to rotate the oblique plane into the sagittal orientation. The **Fly Value** defaults to **10**, so for each selection of 'Roll Right', the plane is rotated by 10 degrees (90 total).

   vi. Given that the view of this sagittal orientation is as if the body was in a prone position, click the **Yaw Counter Clockwise** button nine times to rotate the body upright. This is a right lateral view of the chest.

   vii. If a left lateral view is desired, click the **Roll Left** button to complete a roll of the oblique plane by 180 degrees (select the button 18 times). Note that the plane appears to rotate through the data set, passing from a right lateral view to a left lateral view.

8. Reset the oblique plane to the central transverse slice by selecting the '**T**' Cube at the bottom of the Fly tool.

*tip*   The 'Fly Value' [B] can be changed to make incrementally larger or smaller changes when performing manipulations (e.g. set the 'Fly Value' to 180 and press 'Roll Left' once to rotate 180 degrees).
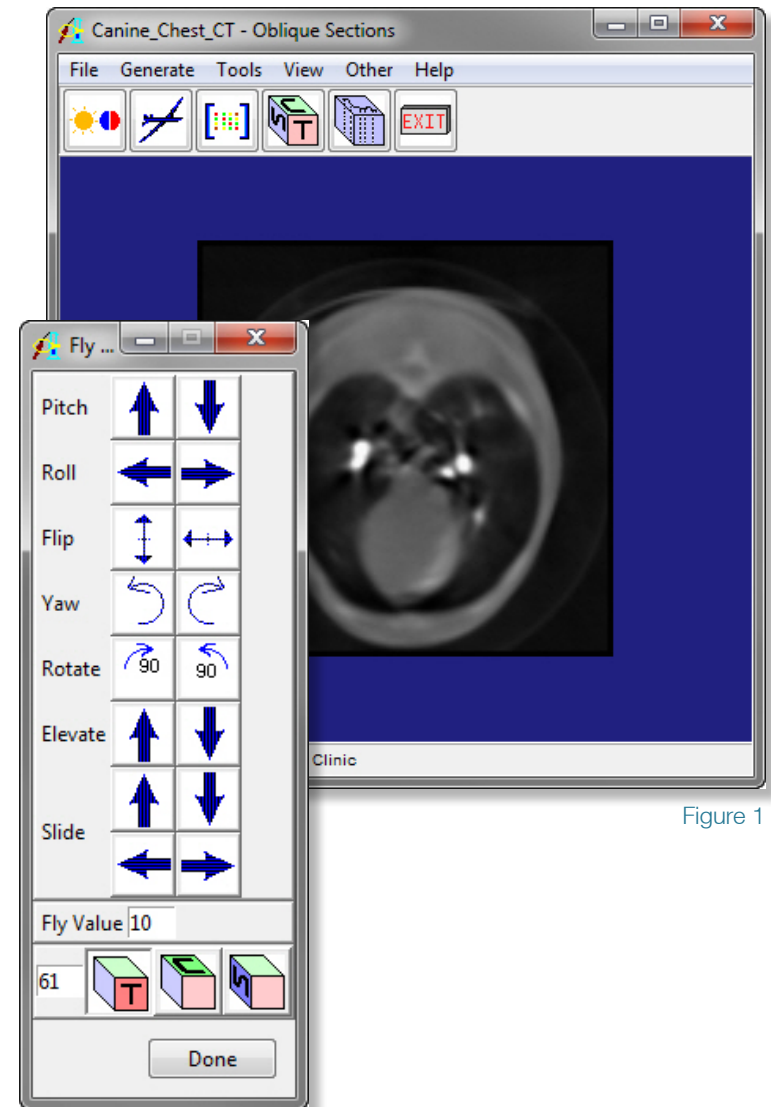


Figure 1

AnalyzeDirect

9. Open the **Matrix Tool** (**Tools > Matrix**) to display the current transformation matrix that reflects this 3-D orientation (figure 2).

10. Now, complete the "fly" maneuvers as given above to rotate from the transverse orientation to the sagittal orientation again. Note the changes in the transformation matrix in the Matrix tool as these maneuvers are carried out. This demonstrates that the oblique plane manipulation is represented as a full 3-D transformation, with resampling of the data occurring based on the respective 3-D transformation as given in the matrix.

11. Use the **Fly** tool to select an arbitrary oblique orientation of your choice. For example, click the Roll Right button three times, then the **Yaw Clockwise** button four times.

12. To save the data set in this oblique orientation, choose **File > Output**.

13. In the **Output** window, set **Destination** to **Workspace** and change **Name** to **xxx_myoblique** (where 'xxx' are your initials) (figure 3).

14. To resample the entire data set, set Method to **Reformat Entire Volume**. Since this is an oblique orientation, the resampling space for the new data set may need to be larger than the original, so by default the **Change to best fit data** option is selected to output a large enough data set to capture all transformed voxels.

15. Click **Generate Slices**. The resampled data set is now saved to the Analyze workspace.

16. Close the Oblique Sections module before proceeding to the Additional Task.

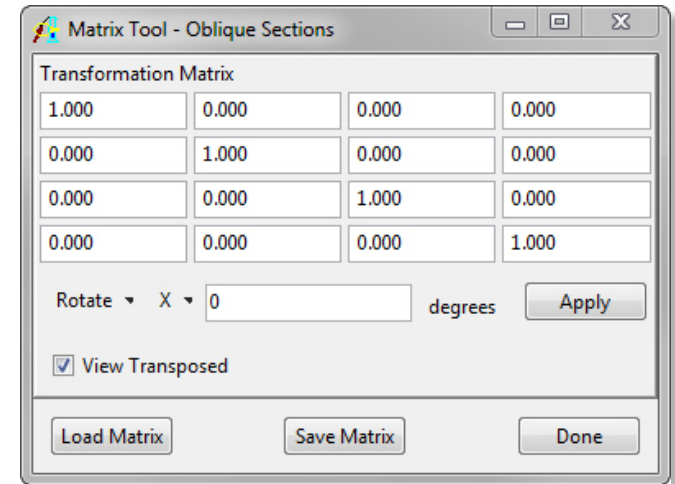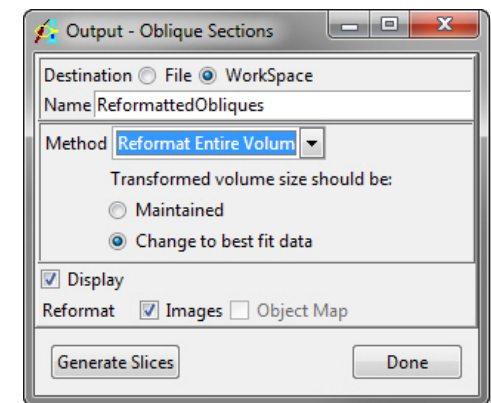17. To view your new reformatted data set, open it with the Multiplanar Sections module.

Figure 2

Figure 3

# Oblique Sections: *Grid Align*

The Grid Align tools provide users with the ability to interactively reorientate image data using a grid overlay on the current oblique **slice, this** allows for easy reorientation with reference to structures in the slice. The grid allows for reorientation via translation and yaw of the oblique slice. This task will demonstrate how to reorientate data using the tool.

1. Load the **MRI_3D_Head.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Oblique Sections** module (**Display > Oblique Sections**).

3. Open the **Fly** tool (**Generate > Fly**). Use the Fly tool to set the display orientation to Sagittal by clicking on the S-cube.

4. Next select **Generate > Grid Align** to apply the grid overlay to the current slice.

## Translation:

- Click to select a point near the center of the grid axis (anywhere within the 36 center boxes).
- While holding the mouse button down, move your cursor so that the center intersection of the grid is moved to the new desired location, in this example the middle of the cerebellum.
- Release the mouse button. The image will be translated with the selected region as the new center point.
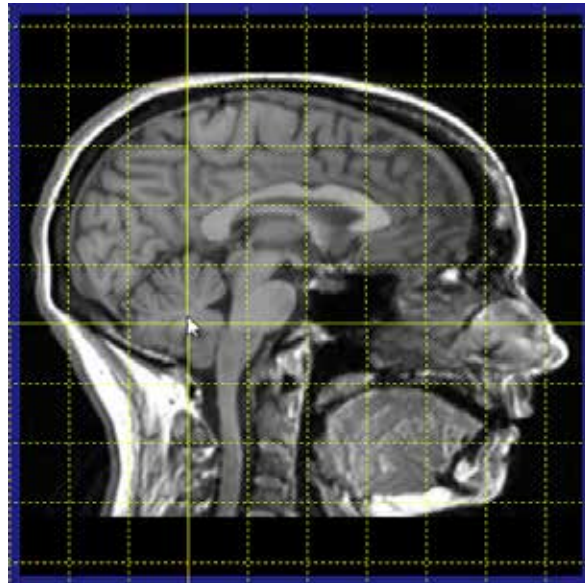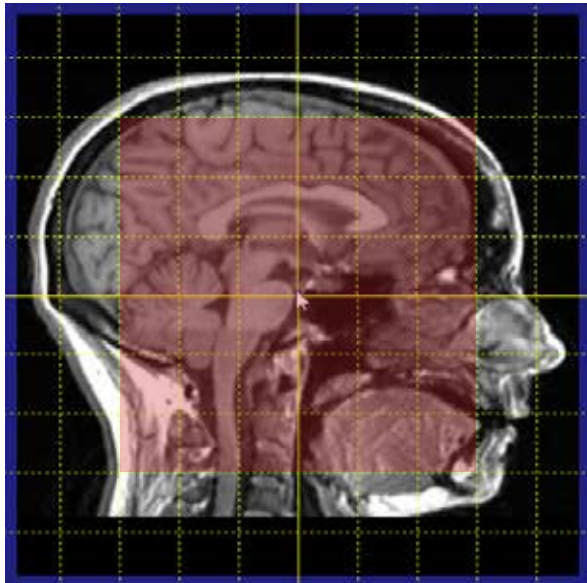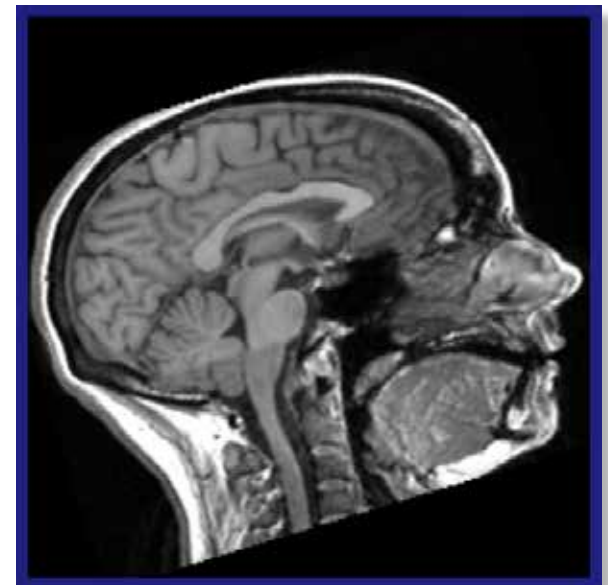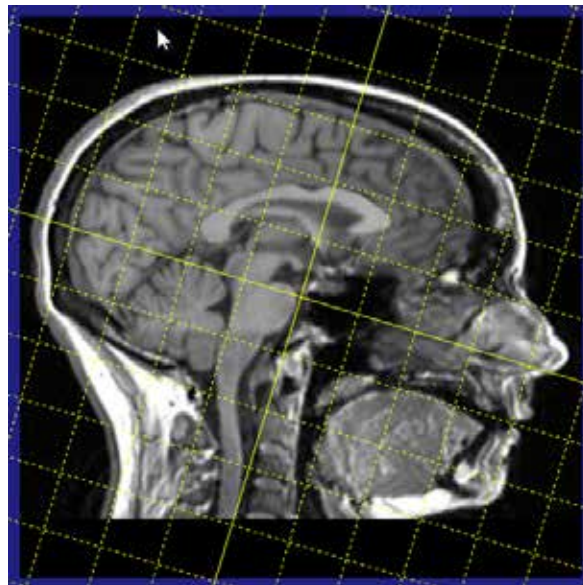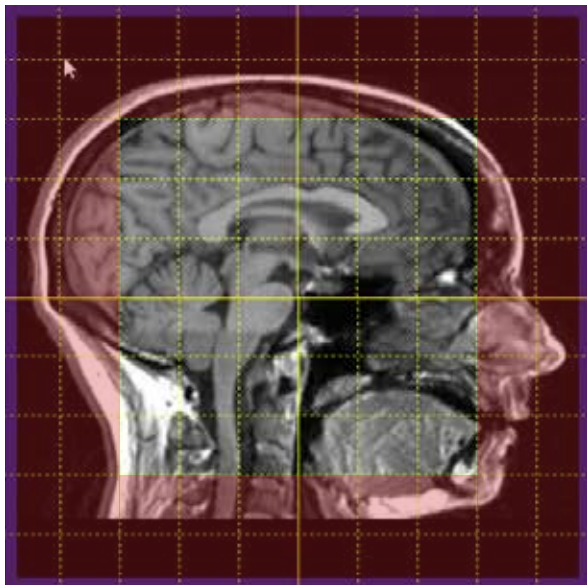
# Oblique Sections: *Grid Align*

5.   Click on the **S-Cube** in the Fly tool to reset the image display.

## Yaw

6.   Click to select anywhere towards the outside of the grid (anywhere not within the 36 center boxes).

7.   While holding the mouse button down, move your cursor to rotate the grid about the center axis, in this example, aligning a grid line along the brain stem.

8.   Release the mouse button to apply the **Yaw** reorientation to the image.

9.   Close all Oblique Sections windows before proceeding to the next exercise.

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# Oblique Sections: Manual AC-PC Realignment

This exercise will review additional manual realignment tools available in the Oblique Sections module. The exercise will explain how to use these tools by demonstrating how to realign the brain along the AC-PC. Please note that the Mayo 3D Brain Atlas add-on provides an interactive AC-PC based alignment tool for realignment of volume image data to the Talairach-Tournoux coordinate and proportional grid system, for more information please review the Mayo 3D Brain Atlas exercise.

1. Load the **MRI_3D_Head.avw** data set from the **$:\BIR\images\ TutorialData** directory. Then open the **Oblique Sections** module (**Display > Oblique Sections**).

2. Once the Oblique Sections module is open, select the **Orthogonals** (**Tools > Orthogonals**).

3. In the Orthogonals window (figure 1), move to the mid-sagittal slice where the AC and PC can be identified using the slider bar under the sagittal display pane. It may be helpful to increase the display size of the sagittal slice. To do this, right-click on the pane and select the **Size** option.

4. At the bottom of the Orthogonal window, select the **Interactive Perp Axis** option to turn on the interactive generation of the perpendicular axis and the perpendicular oblique.

5. Now, on the sagittal image, move your cursor to either the AC or PC points and select this point with your mouse button. Hold the mouse button down as you drag the line from this point to the other AC or PC point. Release the mouse button when the other point has been selected.

6. This provides the AC-PC axis and generates an oblique image, which is perpendicular to the midpoint of this axis - essentially a coronal image.

7. The **Perpendicular Axis** window automatically opens (figure 2). This will allow you to note the coordinates of the AC and PC points (Point 1 and Point 2) if desired.

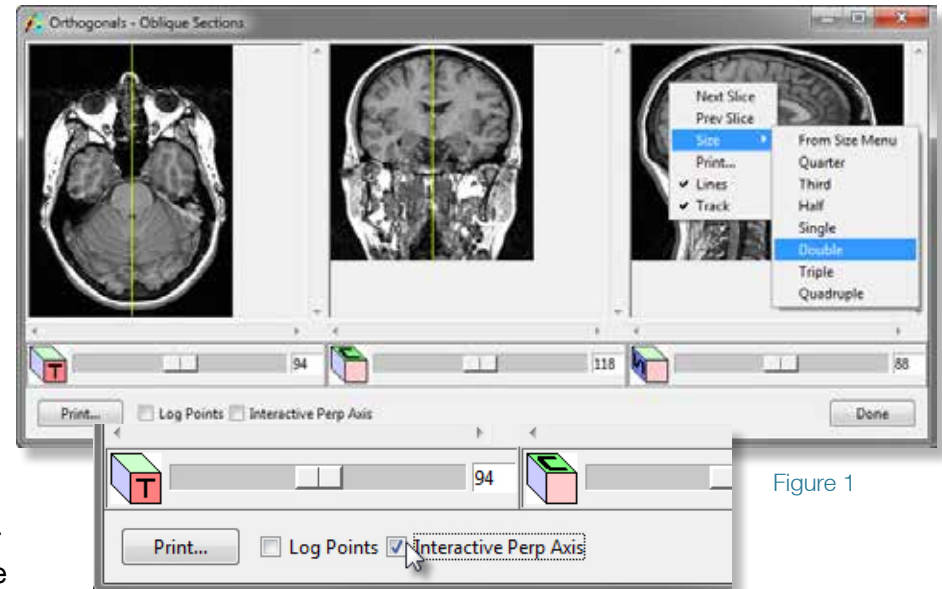8. Open the **Fly** tool from the Generate menu in the main Oblique Sections window (**Generate > Fly**).
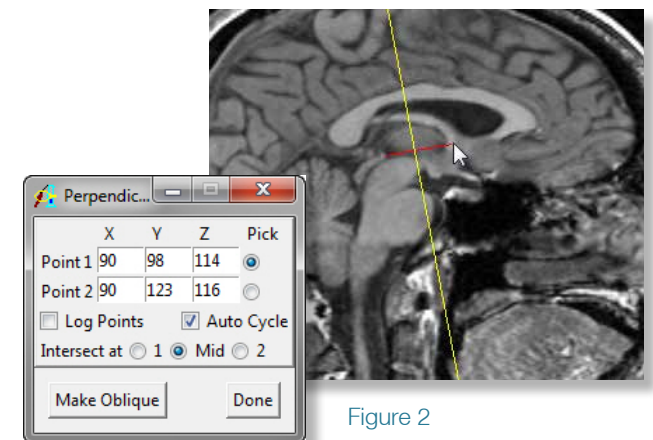


Figure 1



Figure 2

AnalyzeDirect

# Oblique Sections: Manual AC-PC Realignment

9. Change the **Fly Value** to **90** (figure 3), and do a Pitch maneuver. This 90 degree pitch places the current oblique image in the plane of the AC-PC line.

   *note*   The anterior part of the brain should be at the top of the oblique image. If it is not, then you can do two more 90 degree pitch maneuvers to flip this oblique plane around 180 degrees.

10. Now change the **Fly Value** to a smaller value (e.g. 1 to 5 degrees).

11. Viewing the main oblique image, you can use the **Roll** and **Yaw** maneuvers to attempt to accommodate brain symmetry in this oblique plane. This is an entirely visual process and shouldn't require much manipulation. Note that you may have to do other smaller manipulations along the way to adjust for the volume being tilted slightly, but you can do this at any time.

12. When satisfied with this 'transverse-oblique' along the AC-PC plane, select **File > Output**.

13. Change the **Method** to **Reformat Entire Volume** to generate the output volume at this new orientation. The option is available to reformat back into the original volume size (Maintained), or new output volume that can hold the entire span of the rotated original volume (Change to best fit data).

14. Select **Generate Slices** to save the AC-PC aligned volume to the Analyze workspace.

15. Close the Oblique Sections module before proceeding to the next exercise.
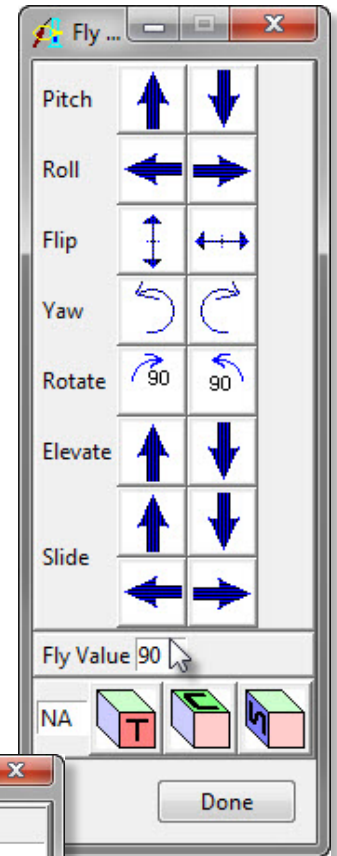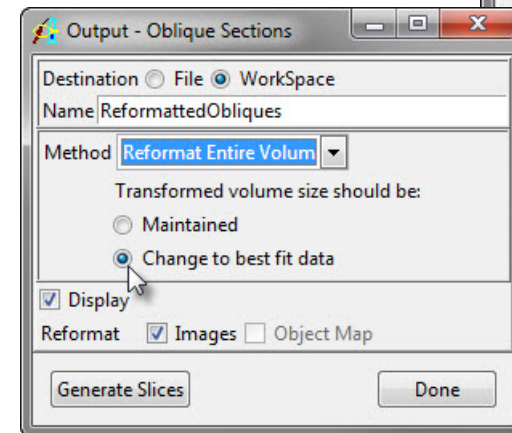
Figure 3

Figure 4

AnalyzeDirect

# Volume Compare

The Volume Compare module provides the ability to compare data sets images that have the same spatial resolution. This exercise will provide an overview of the module.

1. Load the **MRI_3D_Head.avw** and **MRI_3D_Brain.avw** data sets from the **$:\BIR\images\TutorialData** directory. Select both data sets, **MRI_3D_Head.avw** first and **MRI_3D_Brain.avw** second.

2. Open the **Volume Compare** module (**Display > Volume Compare**).

3. Open the **Blend** window, select **Yellow-Cyan**. Click on any of the images and drag your cursor to move through the image display. Alternatively, use the arrow keys and the page up, page down keys to move through the data.

4. From the File menu, select **Load First Object Map** and load the **MRI_3D_Head.obj**.

5. Next, load the **MRI_3D_Brain.obj** object map for the second volume (**File > Load Second Object Map**).

6. Use the crosshairs to navigate through the data (figure 2).

7. Double click in any pane to log points. To save the Point Log, click **Save** (figure 3).

8. To save the Fused Volume, select **File > Save Fused**.

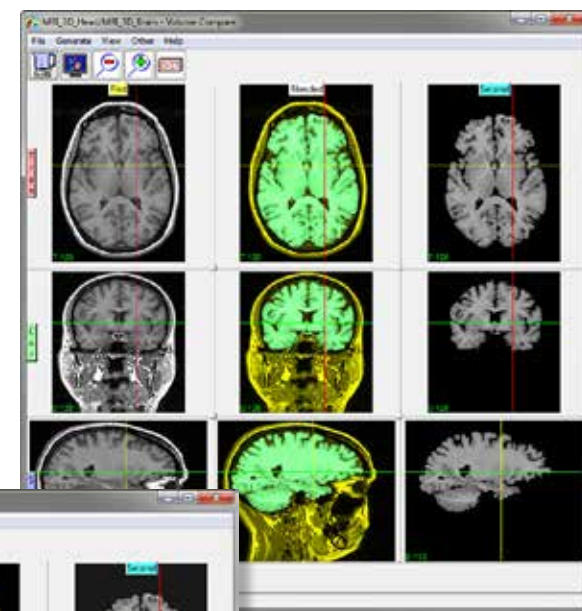9. 9. Close the Volume Compare module before proceeding to the next exercise.
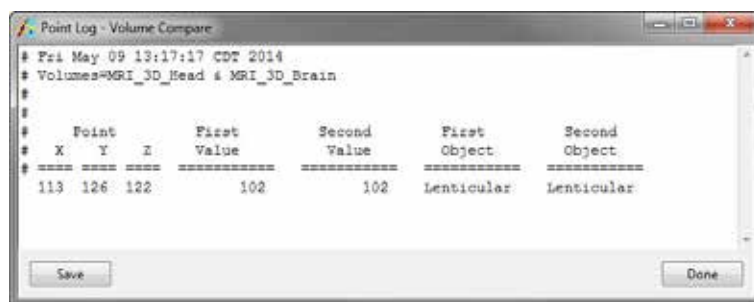

Figure 1


Figure 2


Figure 3

# Volume Render: Basic Rendering Controls

The Volume Render module provides a variety of display representations for three-dimensional image data sets. Also provided in the module are tools for volume image editing and measurement. This exercise will demonstrate the different control parameters involved in the process of volume rendering. This includes demonstrating various rendering algorithms that are part of the suite of techniques used to render volume images with Analyze.

1. Load the **Cubic_CT_Head.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Volume Render** module (**Display > Volume Render**).

3. Press the **Render** PowerBar button or choose **Generate > Render**.

4. Open the **Preview** window (**Generate > Preview**).

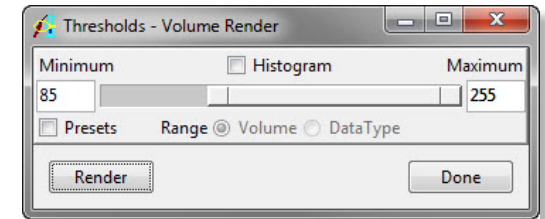5. To rotate the image data in this window, click and drag the mouse.

## Thresholding Data

6. Open the **Thresholds** window (**Generate > Thresholds**).

7. Set the **Threshold Minimum** to **85** (figure 1) - all voxels with a value less than 85 are now removed from view.

8. The resulting image can be seen in the Preview window (figure 2). Click **Render** to display the rendering in the main Volume Render window.

9. Now, set the **Threshold Minimum** to **145**—all voxels with a value less than 145 are now removed from view. Click **Render**.
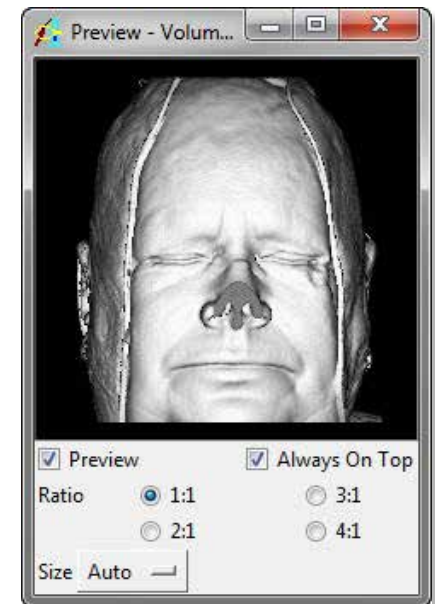


Figure 1



Figure 2

AnalyzeDirect

# Volume Render: Basic Rendering Controls

## Rendering Algorithms

10. Open the **Render Types** window (Generate > Render Type) (figure 3).

11. Experiment with the rendering algorithms.

12. Select the **Depth Shading** option. View the rendering in the Preview window. Click **Render** to display the rendering in the main Volume Render window.

    *note*   When working with anisotropic data, the 'Interpolated Rays' option may help to improve the quality of the rendering.

13. Select the **Volume Compositing** option. View the rendering in the Preview window. Click **Render** to display the rendering in the main Volume Render window (figure 7). For more information on the Volume Compositing Tissue Map Type Specific option, please review exercise 13, **Volume Render – Tissue Map Tool**.

14. Select the **Maximum Intensity Projection** option. Click **Render** to display the rendering in the main Volume Render window.

15. Select the **Summed Voxel Projection** option and click **Render.**

16. Select the **Surface Projection** option. Set the **Threshold Minimum** back to **145** in the Thresholds window, then click **Render**. This render type is more effective with different input data, but the effect can be seen using the current surface.

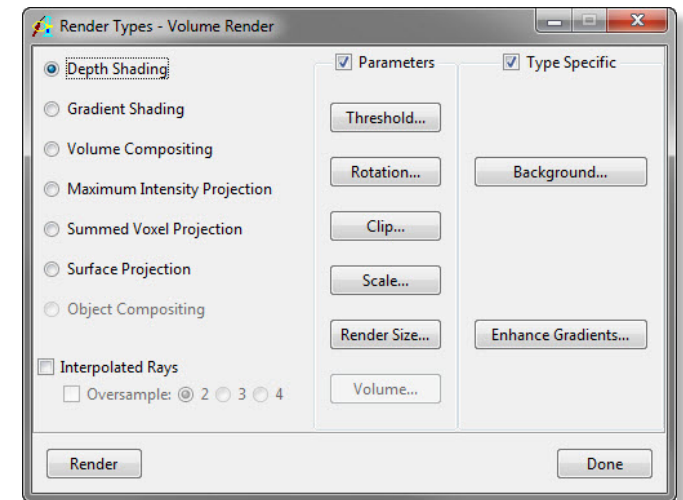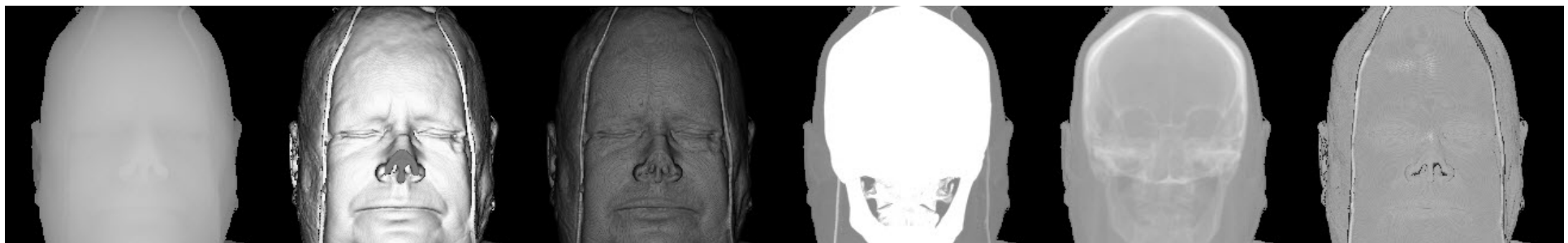17. Select **Gradient Shading** before moving to the next section.

Figure 3

*note*   Additional parameters for each render type are available in the Render Types window. Upon clicking on each Render Type, notice that type specific parameters will either become enabled or disabled depending on whether the parameter is supported.

| Depth Shading | Gradient Shading | Volume Compositing | Maximum Intensity Projection | Summed Voxel Projection | Surface Projection |

# Volume Render: Basic Rendering Controls

## Clip Tool

18. Open the Clip tool from the **Render Type** window or from (**Generate > Clip**).

19. The Clip tool (figure 5) allows a subregion of the volume to be rendered. Experiment with the **Clip Plane** and **Clip Volume** parameters.

20. Click **Done** to close the Clip tool.

21. Close all windows related to the Volume Render module before moving onto the next exercise.
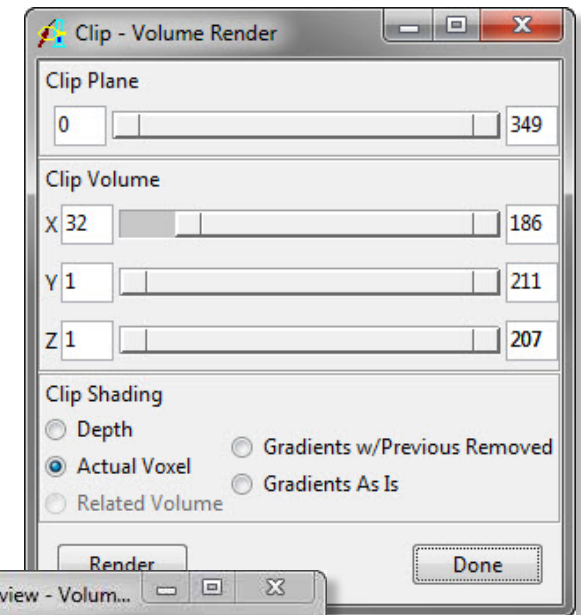


Figurre 5



Figure 6

AnalyzeDirect

# Volume Render: Advanced Rendering Controls

Adding the ability to control specific objects in the rendering process provides incredible power and versatility in the creation of unique visualizations. In Analyze, this is possible with the use of object maps. Object maps are special image files that are used in Analyze to partition and identify structures as belonging to a particular segmented object. Voxels in the volume image correspond directly, on a one-to-one basis, with a voxel in the object map, whose value assigns the voxel to a particular segmented object. Each of the objects within the object map can be controlled and manipulated independently. This exercise will begin to explore the power of object control in creating 3-D visualizations, but will only "scratch the surface" of the endless possibilities for exploration of this 3-D visualization space.

1. Load the **Cubic_CT_Head.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. 2. Open the **Volume Render** module (**Display > Volume Render**).

## Defining Objects in an Object Map

3. Choose **File > Create Object Map**. The **Objects** window will automatically be returned; dismiss the window for now by clicking **Done**.

4. Open the **Threshold Tool** (**Tools > Manipulate > Threshold**) (figure 1).
   - Set the **Minimum Threshold** to **85**.
   - Set **Change** to **Object Map**.
   - Set **Defined Object** to **\*\*\*New\*\*\*.**
   - Click **Threshold Volume** to define a new object. Note all voxels from **85** to **255** will be defined as a new object, 'Object_2'.
   - Click **Done** to close the Threshold Tool.

5. Open the **Preview** window (**Generate > Preview**) to interactively review your changes.

6. Click **Render** to display the rendering in the main Volume Render window (figure 2).

7. In the main Volume Render window, open the **Thresholds** window (**Generate > Thresholds**). Set the **Threshold Minimum** to **145** and click Render.
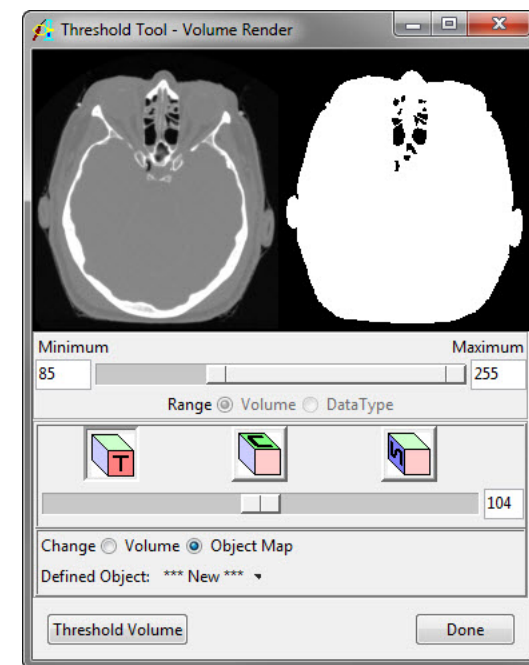


Figure 1



Figure 2

8. Open the **Connect Tool** (**Tools > Manipulate > Connect**).

- Change the **Connect Method** to **Connected Components**.

- Set to **Keep the '3' Largest Objects**.

- Click **Label Components**. The three largest objects will automatically be identified and labeled as new objects (figure 3).
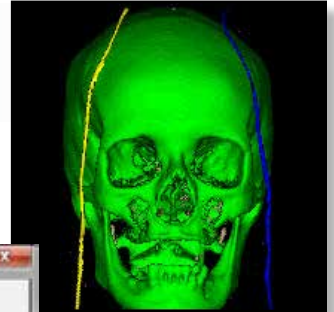
- Click **Done** to close the Connect Tool.

## Manipulating Objects

9. In the **Objects** window (View > Objects) (figure 4), click **Reassign Object(s)**.

10. In the window returned (figure 5), select: **BlueObject** from the Reassign from list. From the drop down menu to the right select: **YellowObject**. Click **Apply** and then **OK** to dismiss the window. Note the update in the Preview window.

11. Click **Remove Unused** in the **Objects** window to remove 'BlueObject'. Click **OK** in the dialog box returned.

12. Select the **GreenObject** from the Object drop-down menu. Then change the following attributes:

- Name: **Bone**
- Color: **white**
- Shades: **32**

13. Select the **YellowObject** from the Object drop-down menu. Then change the following attributes:

- Name: **Rope**
- Color: **red**
- Shades: **8**

14. Click **Render**.

15. In the **Thresholds** window (**Generate > Thresholds**), set the **Threshold Minimum** to **5**.

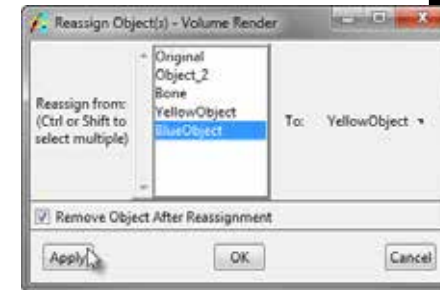16. Return to the Objects window and set **Control by** to **Attribute**.

note    Up to 255 different objects can be defined in an object map.


Figure 3


Figure 4


Figure 5

17. Set the **Display** attribute to **Off** for the **Original** object. Then, click **Render**.

18. Open the **Render Types** window (**Generate > Render Type**). Select the **Object Compositing** option, then open the **Object Mapping** window, (**Generate > Type Specific > Object Mapping**).

19. Select the **Transparency** render type (figure 6) and click **Render** to view the effects.

20. A variety of object attributes can be controlled in the Objects window. Set **Attribute** to **Opacity** by selecting it from the drop-down menu. Change the **Bone** object to **1** (opaque). Click **Render** (figure 7).
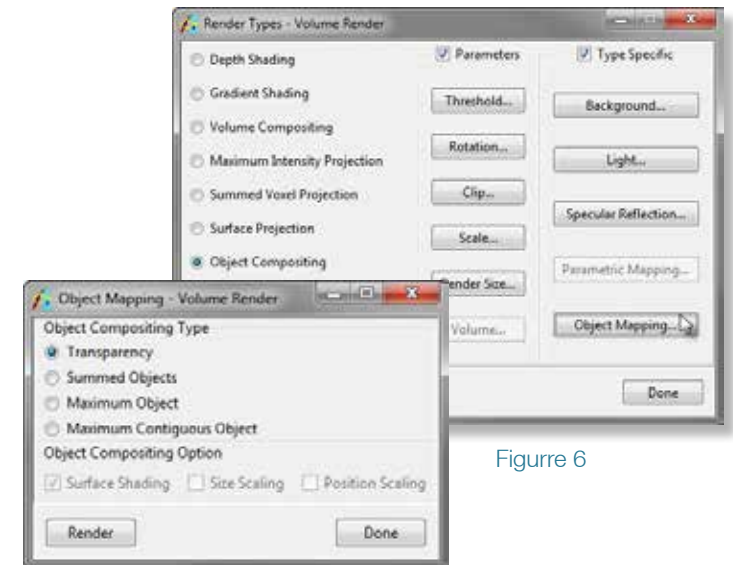
## Saving an Object Map

21. Object maps can be saved for review or use at a later time, or to load into another Analyze module; choose **File > Save Object Map** to save the object map.

22. Name the file **Cubic_CT_Head_xxx.obj** (where 'xxx' are your initials) and specify a location to save the file, then click **Save** (object maps are saved as .obj files).

23. Close the Volume Render module before proceeding to the next exercise.

Figurre 6

Figure 7

# Volume Render: Tissue Map Tool

The Tissue Map tool provides a control interface that allows for the creation of unique visualizations. This exercise will demonstrate how to use the tool to generate visualizations of different tissues.

1. Load the **CT_Heart.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Volume Render** module (**Display > Volume Render**).

3. Open the **Render Types** window (**Generate > Render Type**).

4. Select the **Volume Compositing** render type (figure 1). Then open the Tissue Map tool by clicking the **Tissue Map** button.

5. A tissue map is a mapping of the voxel values within a volume to a given color and opacity. The Tissue Map tool provides several control options to aide in the creation of a tissue map for a volume.

6. The Tissue Map tool provides four control "points" to manipulate which voxel values are mapped to specific colors and opacity (figure 2).
   - **Start**: The starting voxel value within the volume mapped to a specific color (chosen from the color drop-down menu) with 0% opacity.

   - **Min:** The minimum voxel value within the volume that will be mapped to a specific color and set opacity (e.g. 44%).

   - **Max:** The maximum voxel value within the volume that will be mapped to a specific color and set opacity (e.g. 44%).

   - **End:** The ending voxel value within the volume mapped to a specific color with 0% opacity.

7. Click **Render** to view the rendering with the default parameters (displayed in the main Volume Render window).
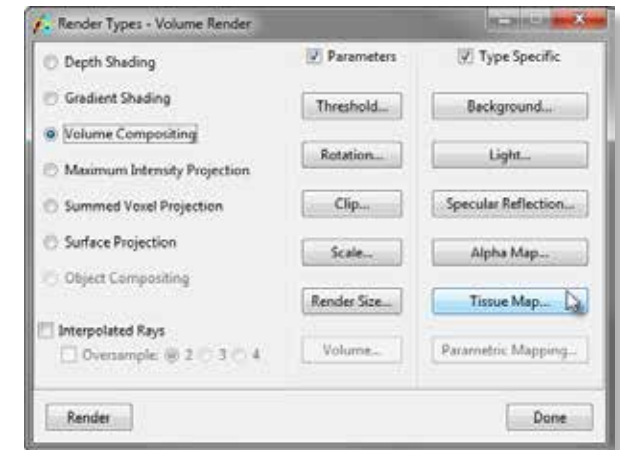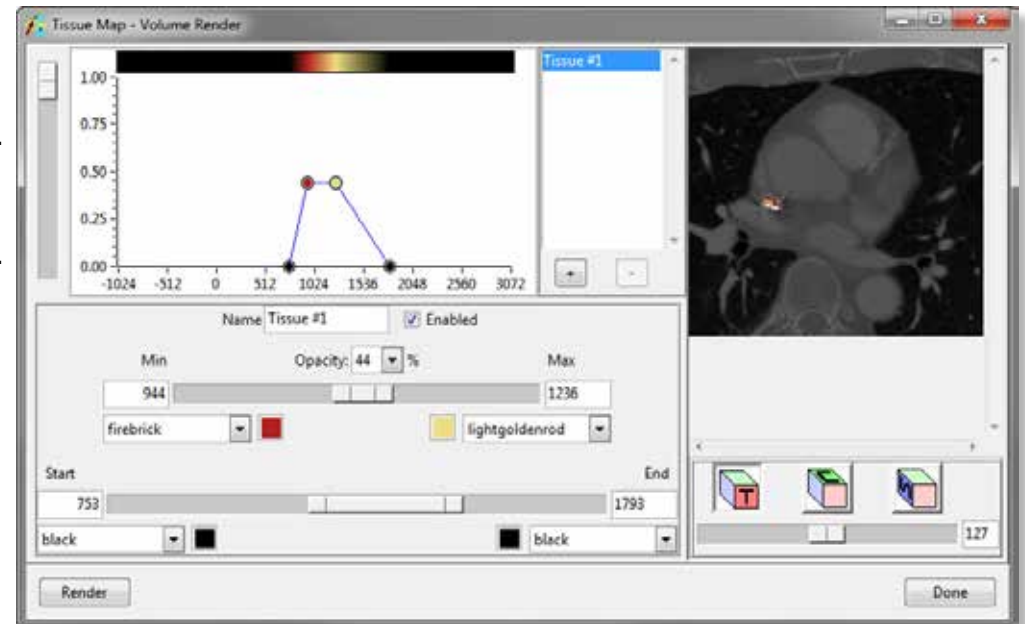


Figure 1



Figure 2

AnalyzeDirect

8. Use the slider bars, or type the numbers in the appropriate text box in the Tissue Map tool to set the following (figure 3):

   - **Start: 157**

   - **Min: 200**

   - **Max: 500**

   - **End: 3072**

9. Select **60** from the **Opacity** drop-down menu. Click **Render** to view the effect of the changes (figure 4).

10. Now, experiment by moving the control points in the graphical display. Click **Render** as desired.

11. Right-click in the graphical display and select **Show Histogram**; the volume histogram will be calculated and displayed. This option may help determine voxel values associated with tissues.

12. Several default tissue maps are also available, rightclick in the graphical display and choose **Default Tissue Maps > CT2**; once loaded, click **Render** (figure 5).

13. Experiment with adding a second tissue to the tissue map by clicking the **+** button to the right of the graphical display. Click Render as desired to see the effect.

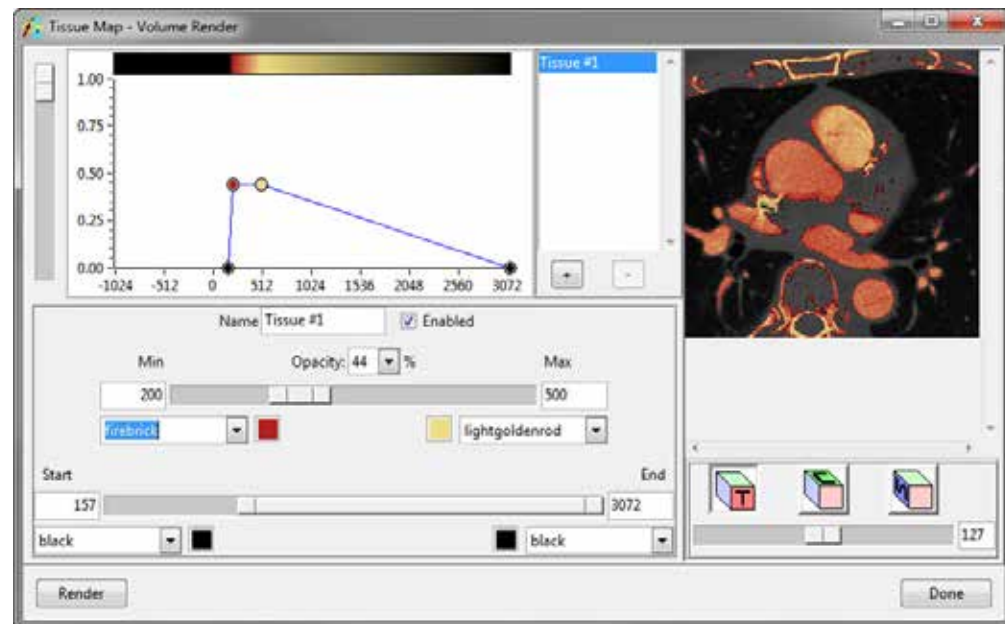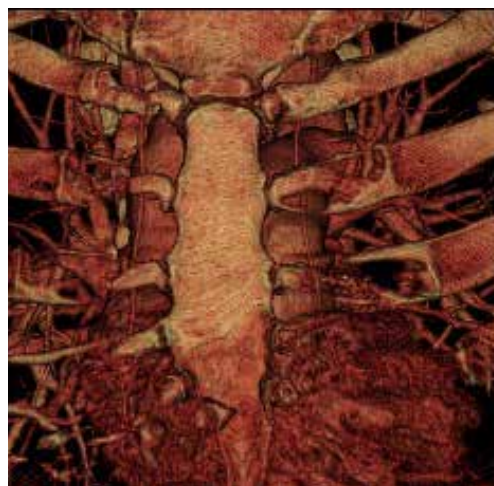14. Close the Volume Render module before proceeding to the next exercise.



Figure 3



Figure 4



Figure 5

# Volume Render: Movie Making

The Volume Render module contains a number of tools for movie generation. This exercise will introduce the Sequence tool. While complicated movies can be created, the goal of this exercise is to demonstrate how to generate a quick, simple movie. For more information, please review the Movie Making with Volume Render Tutorial after you have completed this exercise. The tutorial can be accessed from the Help menu in the main Analyze workspace.

1. Load the **Cubic_CT_Head.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Volume Render** module (**Display > Volume Render**).

3. Choose **File > Save Renderings** (figure 1).

4. In the Save Renderings window, check the **Save After Each Render** option and change **Name** to **MyTestMovie**. The movie that is generated will automatically be saved to the Analyze workspace as 'MyTestMovie'.

5. Click **Done** to dismiss the Save Renderings window.


Figure 1

6. Open the **Sequence** tool (**Generate > Sequence**).

7. By default, the 'sequence' already has one action, 'Z Rotation'. To modify the action click **Modify**, and then click on the red '**Z Rotation**' action (figure 2). The Action window will automatically be returned.

8. For the first part of this movie, we will threshold the data set to show the structure of interest, in this case the head. If you have completed Volume Render exercises 11 and 12, you will know that in order to view the head in this data set, we need to increase the threshold minimum to 85.

9. In the **Action** window, set the following parameters (figure 3):

- **Action Name: Threshold**

- **Number of Frames: 36**, the default frame display is 12 frames per second.

- **Persistent:** Checking the 'Persistent' option will ensure that the minimum threshold parameter set in this action will be retained for the rest of the movie. If not checked, the threshold minimum will be reset after the action is completed.

- **Parameter: Threshold**
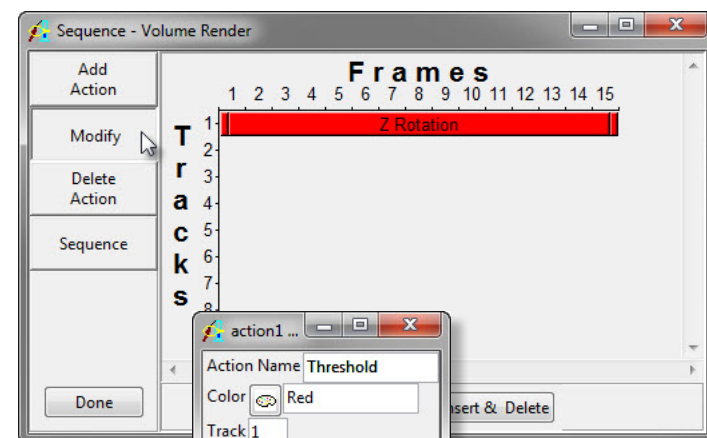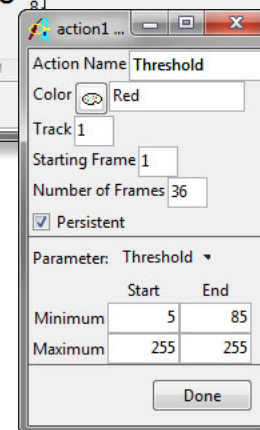
- **End Minimum: 85**


Figure 2


Figure 3

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# Volume Render: Movie Making

10. To preview the movie with the new action, first open the **Preview** window (**Generate > Preview**).

11. Now, in the Sequence tool, click **Sequence**. Then, click **Make Sequence** (figure 4).

12. A dialog box will be returned asking if you would like to 'Preview' or 'Make the Sequence', click **Preview the Sequence**. The movie will now be played in the Preview window.

*note*   The 'Preview the Sequence' option is only available when the Preview window is open. If the Preview window is not open, the dialog box will not be returned after clicking 'Make Sequence', instead the sequence will automatically be generated.

13. Add another action to the movie. Click **Add Action** and place the new action on Track 2 in Frame 36; this will be directly under the last frame of the 'Threshold' action (figure 5).

14. Once the new action has been added, click **Modify** and then click on the new action to open the Action window.

15. We will now add a rotation to the movie. Set the following parameters for the new action:

- **Action Name: Rotation**

- **Number of Frames: 60**

- **Parameter: Rotation**

- **End Z: 720** (2 rotations, 360=1 rotation)

16. Click **Done** to dismiss the window.

17. Review the movie. Click **Sequence**, and then, with the Preview window open, click **Make Sequence**.

18. In the dialog box returned, click **Preview the Sequence**. The movie playing in the Preview window should show the data set being thresholded to the head, followed by two quick rotations about the Z-axis.
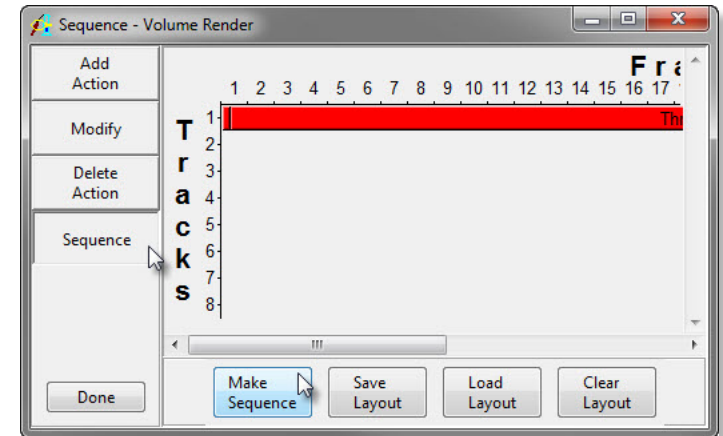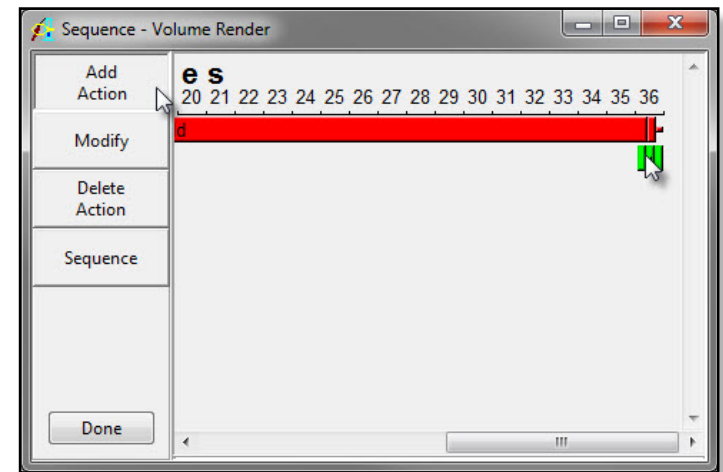


Figure 4



Figure 5

*note*   To slow the rotation of the data set, simply add more frames in the Action window (e.g. Change Number of Frames from 60 to 120), or only show one rotation by changing the End Z value to 360 from 720.

AnalyzeDirect

# Volume Render: Movie Making

19. To generate the movie, click **Sequence** again. This time, after clicking **Make Sequence**, choose **Make the Sequence** from the dialog box returned.

20. As the sequence is generated, each frame will be displayed in the main Volume Render window. Each frame is also being written to a movie file called 'MyTestMovie' in the Analyze workspace (specified earlier in the Save Renderings window).

21. Once sequence generation is complete, close the Volume Render module.

22. In the Analyze workspace, select the MyTestMovie file and review it using the **Movie** module (**Display > Movie**). (figure 6)

23. To save the movie out of Analyze, choose **File > Save** in the Analyze window. Choose a movie file format (AVI, QuickTime, or AnimatedGIF) from the **Format** dropdown menu before clicking Save.

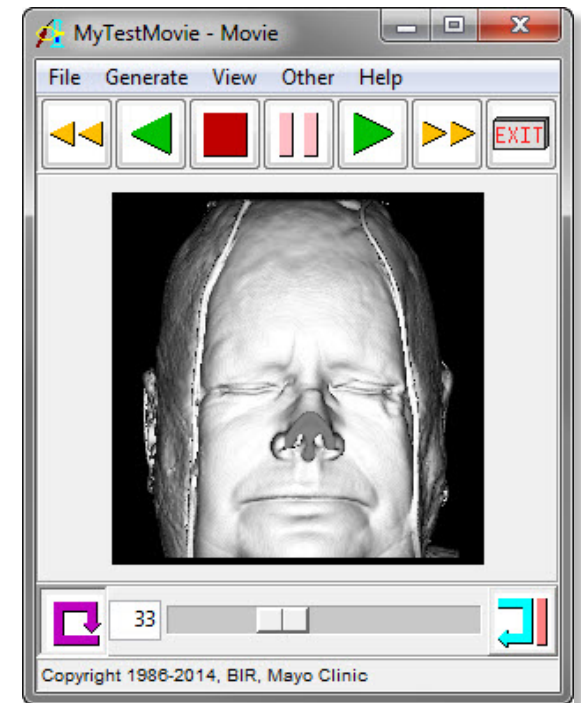24. Close the Movie module before proceeding to the next exercise.



Figurre 7

# Volume Render: High Def Volume Rendering

The Volume Render module allows for the generation of High Definition Volume Renderings. This exercise will demonstrate how to generate a high definition volume rendering using a CT data set with a Volume Composite with a tissue map overlay. Note the high definition volume renders can be generated with any of the rendering algorithms available in the Volume Render module.

1. Load the **CT_Heart.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Volume Render** module (**Display > Volume Render**).

3. Open the Render Size option from the Generate menu and change the Width and Height of the Render size to 2000x2000. Then click Apply (figure 1).

4. Open the **Render Type** window from the Generate menu and select **Volumetric Compositing**, check the Interpolated Rays option (figure 2).



Figure 1

5. Click the **Tissue Map** button to open the Tissue Map tool. Right-click on the main tissue map panel and select **Default Tissue Maps**, choose the **CT 2** default tissue map.



Figure 2

6. Now open the **Perspective Rendering** tool (**Tools > Display > Perspective**) and then click the Perspective Render button (figure 3). In Perspective mode, a ray is cast for every output pixel in the rendering. In this case 4 million (2000x2000) rays are cast through the current field of view (FOV) for the perspective geometry.

7. Note the Render Size controls the number of rays, and the FOV controls the space in the volume through which that number of rays is cast. It may take a little while to render depending on the volume size.

8. Once the rendering is complete, the HDVR will be displayed in the main Volume Render window.

9. To save the rendering, Select **File > Save Rendering**. Name the rendering HDVR and then click the **Save Last Rendering** button.

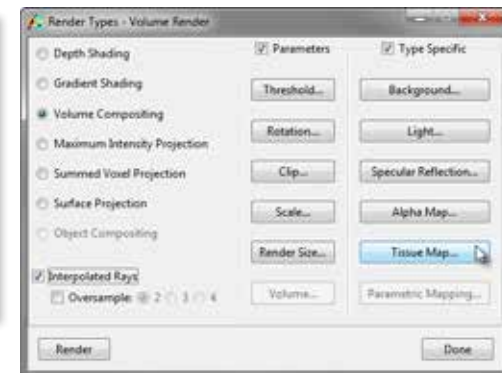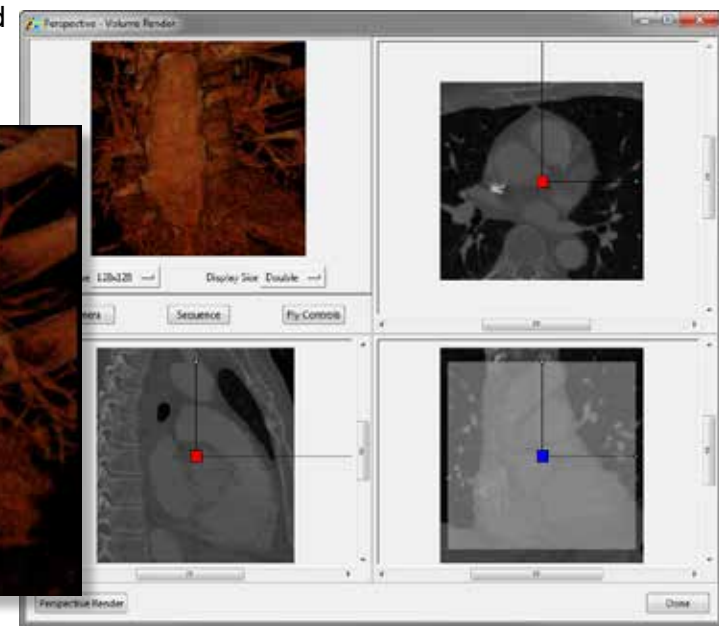10. Close the Volume Render module before proceeding to the next exercise.



Figure 3

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# Volume Render: Parametric Mapping

Volume Render provides the ability to generate parametric maps when a related volume is loaded and the render type is set to gradient shading. This exercise will demonstrate how to use the parametric mapping option.

1. Load the **SISCOM_Extracted_Brain.avw** and **SISCOM_4D_ActivityMap.avw** data set from the **$:\BIR\ images\TutorialData\AdditionalData** directory.

2. Open the **Volume Render** module (**Display > Volume Render**). In the Volume Render window, select **File > Input/Output Ports** (figure 1).

3. Drag-and-drop the **SISCOM_Extracted_Brain** file from the Analyze workspace into the Volume port. Next, drag-and-drop the **SISCOM_4D_ActivityMap** from the Analyze workspace into the **Related Volume** port.

4. Open the **Preview** window (**Generate > Preview**).

5. Open the **Parametric Mapping** window (**Generate > Type Specific > Parametric Mapping**).

6. In the Parametric Mapping window, set **Parametric Mapping** to **On** (figure 2).

7. Review the rendering in the Preview window. To rotate the image, drag and drop the rendering in Preview window (figure 3).

8. Review the effects of changing the **Mapping Factor** and **Map Transparency Value** options in the Parametric Mapping interactively in the Preview window.

9. To view the 4D multivolume over time, use the **Which Mapping Volume** option. Check **Increment after each Render**, then press **Render**, until you've made your way through the volumes (figure 4).
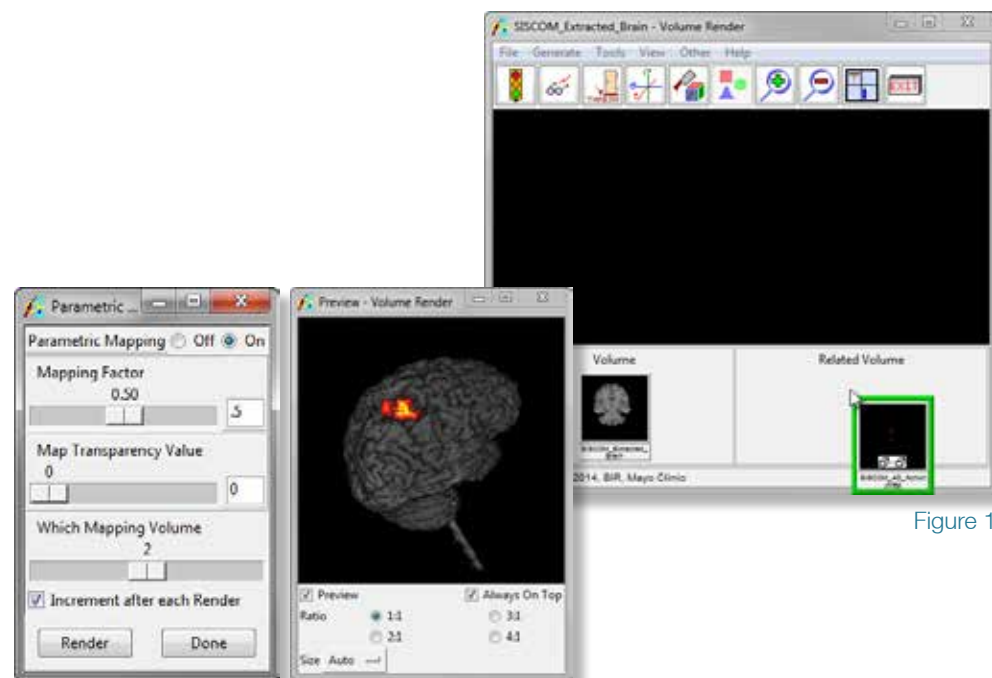
10. Close the Volume Render module before proceeding to the next exercise.
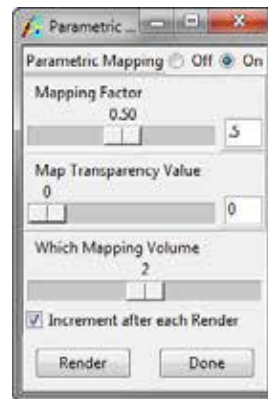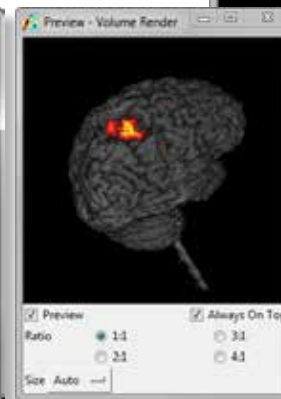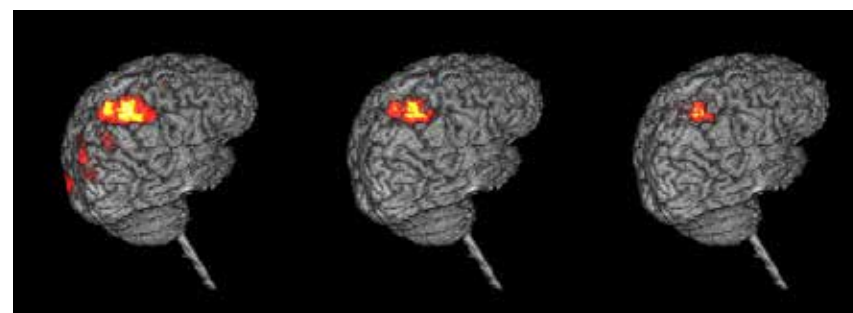


Figure 1



Figure 2



Figure 3



Figure 4

AnalyzeDirect
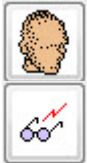
# Volume Render: Creating and Modifying Objects <span>Exercise 18</span>

Volume Render is a powerful display module. In the Volume Render module, you can use many different tools to create many different outcomes. This exercise will demonstrate an amalgamation of Volume Render tools, to create a desired display.

## Creating the Object Map

1. Load the **Coronary_CT.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Select the data set and open the **Volume Render** module (**Display > Volume Render**).

3. Open the **Toggle Preview** window (**Generate > Preview**).

4. Open the **Threshold** tool (**Tools > Manipulate > Threshold**). Use the slider bar to increase the minimum threshold, note that the preview in the Preview window updates interactively. Increase the threshold until you have thresholded the heart - **63** is a good minimum value for this data set.

5. In the **Threshold** tool, set **Change** to **Object Map**. Set **Define Object** to ***New***.

6. Now select the **Threshold Volume** button. Your object map now contains one object; the heart.

7. In the Threshold tool, increase the **Threshold Minimum** until you see only the vascular system surrounding the heart, a minimum value of **133** is good. Set Define Object to ***New***.

8. Select the **Threshold Volume** button again, Object_3 is created and contains only the vascular system (figure 2).

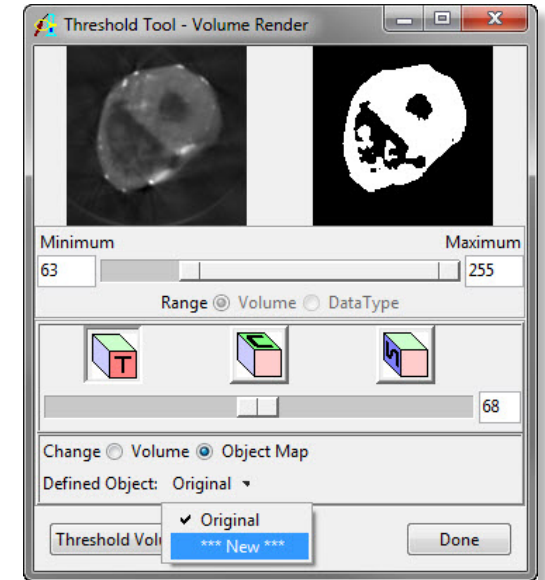9. Set the **Threshold Mimimum** to **1** and then close the **Threshold** tool.
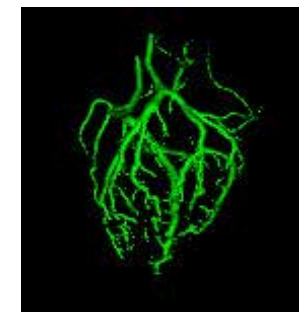
Figure 1

Figure 2

AnalyzeDirect

# Volume Render: Creating and Modifying Objects

## Modifying the Object Display Options

10. Open the **Objects** window (**View > Objects**), at the top of the window set **Control By** to **Attribute**. Set the display of the **Original** to **Off**, then select Render.

11. In the main Volume Render module, select **Generate > Render Type**. In the **Render Type** window returned, select **Object Compositing** and then hit **Render** (figure 3). The render will show both the heart and the vessels.

12. In the Objects window, select **Name** from the **Attribute** drop down menu and change the name of **Object_2** to **Heart**, and the name of **Object_3** to **Vessels**.

13. Now select **Color** from the **Attribute** drop down menu and change the color of the **Heart** to **Pink** and the color of the **Vessels** to **Red**. Note that you can just type the name and hit enter to change the color of the object.

14. Now select **Opacity** from the **Attribute** drop down menu and change the opacity of the **Heart** to **.02**. Change the thickness of the **Vessels** to **2** (figure 4). You will see the Preview window update (figure 4). To view the results in the main Volume Render module, hit **Render**.

15. Experiment with other settings and tools within the Volume Render module.

16. To save your object map, select **File > Save Object Map**.

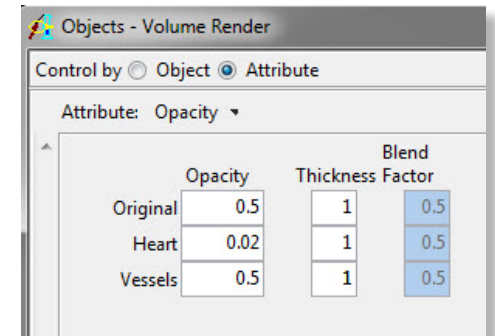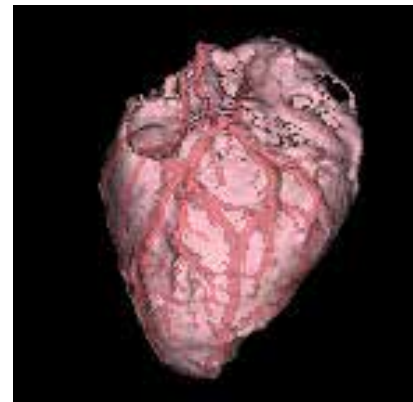17. Close the Volume Render module before proceeding to the next exercise.
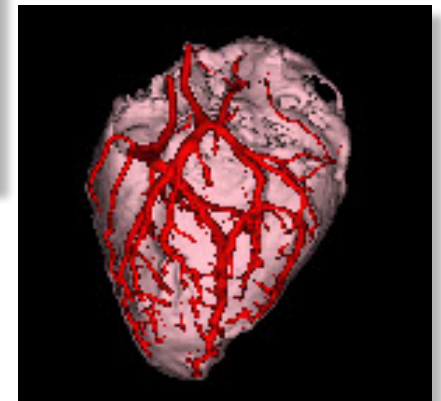
Figure 4

Figure 3

Figure 5

AnalyzeDirect

# Volume Render: Fabricate Tool

The Volume Render Fabricate Tool allows for the creation of objects from a text file with coordinates or by user defined coordinates. This exercise will demonstrate how to create objects from a predefined log file. The log file provides a list of the coordinates, the centroids of 61 electrodes from an electrode grid. Using the fabricate tool we will create an electrode object around each coordinate.

1. Load the **Trans_Pre_OP_MRI** and open it in the **Volume Render** module (**Display > Volume Render**).

2. Open the **Fabricate Tool** (**Tools > Manipulate > Fabricate**). Click the **Alt** button once and then click the File button (figure 1).

3. Navigate to the log file **Electrodes_FabTool.log** in the **C:/BIR/ Images/TutorialData** directory.

4. Adjust the **Radius** to **10.** This will define an electrodes object with a radius of 10 voxels. Set **Change** to **Object Map**, then from the **Defined Object** menu select **\*\*\*New\*\*\***.

5. Click **Create**.

6. From the main Volume Render window, open the **Preview** window (**Generate > Preview**). To rotate the image, click and drag the rendering in the Preview window.

7. Open the **Render Type** window (**Generate > Render Type**), select **Object Compositing**, the rendering is shown in figure 3.
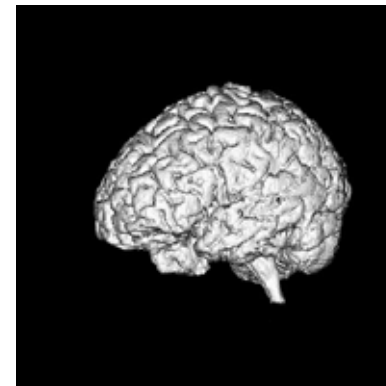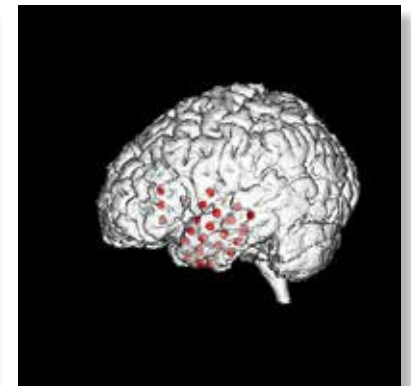

Figure 1


Figure 2


Figure 3

AnalyzeDirect

# Surface Render: Surface Maps

Surface Render provides a semi-automated interface for the conversion of object maps into surface maps using the Adapt/Deform algorithm.

1.  Load the **Cubic_CT_Head.avw** data set from the **$:\BIR\images\TutorialData** directory.

2.  Open the **Surface Render** module (**Display > Surface Render**).

3.  Choose **File > Load Object Map** and load the **Cubic_CT_Head** object map from the **$:\BIR\ images\TutorialData** directory.

4.  In the Objects window (**View > Objects**) returned, set **Control by** to **Attribute** and set the **Display** attribute to **Off** for the **Rope**, **Left Skin**, and **Skull** objects (figure 1).

5.  Choose **File > Create Surface Map**.

6.  In the **Surfaces** window (**View > Surfaces**) returned, click **From Object(s)**. A dialog box will be returned asking if you would like to create the surface map from all currently active objects, click **Yes**. The objects that have their 'Display' attribute set to 'On' (in the Objects window) will be tiled and a surface map generated.
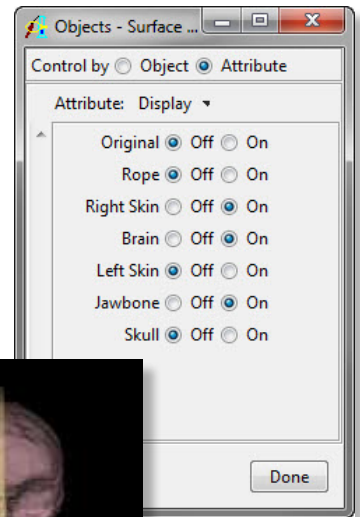
7.  Once the surface map is generated, click **Render** to display the results (figure 2).

8.  Choose **File > Load Surface Map** and load the **Cubic_CT_Head.smp** surface map from the **$:\BIR\images\TutorialData** directory.

9.  Click **Render** to display the results.

10. Open the **Camera** tool (**Generate > Camera**) and set **Sort** to **Front-Back** (figure 3). Click **Render** to display the results.

11. In the Surfaces window set **Control** by to **Attribute**. Choose **Shading** from the **Attribute** drop-down menu and change the shading of the **Right Skin** surface to **Gouraud**.

12. Click **Render**, note the changes in the rendering (figure 4). Experiment with the different shading options.

13. Choose **File > Save Surface Map** to save changes made to the surface map.

14. If you wish to export the surface map out of Analyze for use in another application, choose **File > Export Surface Map**. Surface maps can be exported out of the Surface Render module in the Inventor (.iv) or VRML (.vrml) surface description formats.

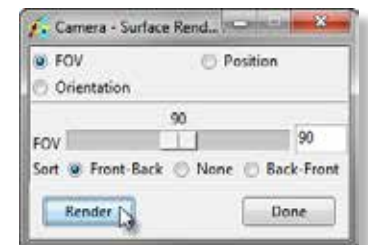15. Close the Surface Render module before proceeding to the next exercise.

Figure 1

Figure 2

Figure 3

AnalyzeDirect

# Virtual Endoscopy

Virtual Endoscopy is an important visualization application that results from the ability to create 3-D visualizations from a viewpoint inside of the body. This exercise will familiarize you with the Virtual Endoscopy module, demonstrating basic functionality and various methods of controlling the view.

1. Load the **CT_Lungs.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Virtual Endoscopy** module (**Display > Virtual Endoscopy**).

## Basic Controls

3. Position the cursor on the image display near the center of the trachea (the hole in the flat surface) and click once; this will be set as the new 'Look At' point and the 'Eye' position will advance (figure 1).

> *tip* The 'Eye' position advances toward the selected point based on settings in the View Parameters window.

4. Position the cursor on the flat surface outside of the trachea and **click once**.

5. The 'Back' PowerBar button can be used to reposition to previous locations; the 'Forward' PowerBar button will move to the next location if one has been defined. Press the **Back** button once.

6. Position the cursor over the center of the trachea and click several times to navigate into the trachea. Then, press the **Back** button until you return to the starting location.
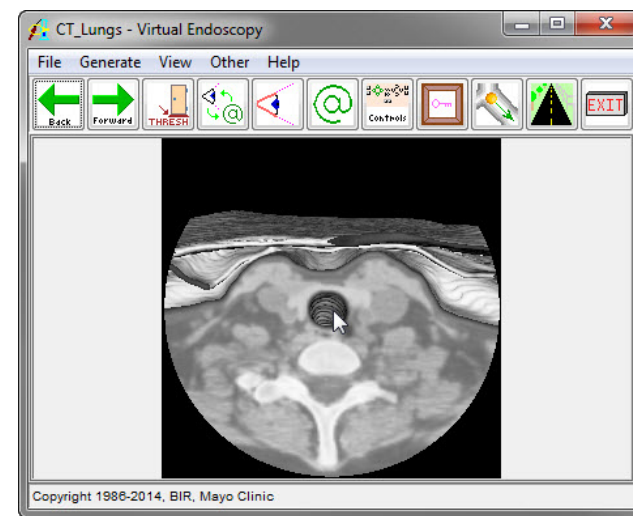
## Advanced Controls

7. Open the **View Parameters** window (**Generate > View Parameters**).

8. Set the **Move Percent** to **50**. Now, click again on the image display near the center of the trachea; note the effect of increasing the Move Percent (figure 2).

9. The View Parameters window (figure 3) also allows you to specify a location by typing in coordinates. Set the following coordinates:

   - **Eye**      X: 128      Y: 150      Z: 181
   - **Look At**  X: 125      Y: 142      Z: 120
   - **Up**       X: 0        Y: 1        Z: 0

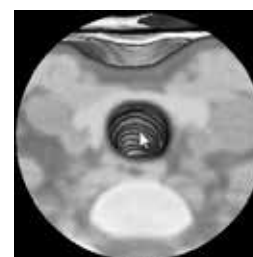10. Click **Render** in the View Parameters window to display the location of the coordinates (figure 4).
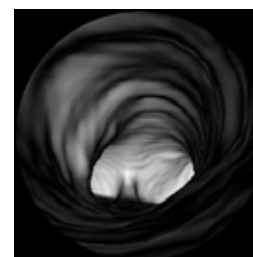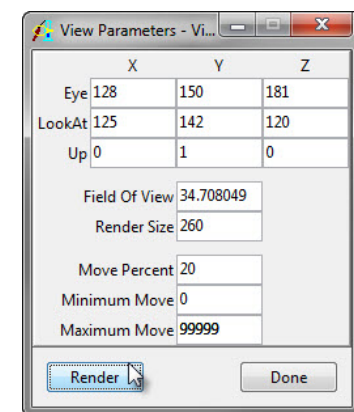

Figure 1


Figure 2


Figure 3


Figure 4

AnalyzeDirect

# Virtual Endoscopy

11. Reset **Move Percent** to **20** in the View Parameters window and click **Done** to dismiss the window.

12. Many times when an obvious entry location is not available, the 'Orthogonal Eye' and 'Look At' views are very useful. To enable these views, press the **Eye** and **Look At** PowerBar buttons or choose **View > Eye** and **View > Look At**. When enabled, three interactive panes become available (figure 5) on either side of the module window, displaying the transverse, coronal, and sagittal sections that intersect with the current 'Eye' position or 'Look At' point. A new 'Eye' position or 'Look At' point can be set by clicking in any of the orthogonal section panes.

*tip* The 'Eye' position advances toward the selected point based on settings in the View Parameters window (Generate > View Parameters).

13. Press the **Manual Controls** PowerBar button or choose **Generate > Manual Controls**. The Manual Controls will appear in the main module window, allowing you to select the translation or rotation actions, the increment, and point(s) to manipulate. To apply a manual action, click the **Render** button at the bottom of the main module window.

14. Use the interactive Orthogonal Eye/Look At panes and the Manual Control buttons to navigate down into the trachea until you reach the bifurcation of the airway.

15. Press the **Show Object** PowerBar button or choose **Generate > Show Object**. The Show Object window allows the 'Eye' position and 'Look At' direction to be manipulated on an exterior rendering. The rendering shows a circle indicating the 'Eye' position and an arrow for the 'Look At' direction (figure 6).

*note* Since the visualization is created by thresholding, you must be "inside" the object in order for it to be rendered.

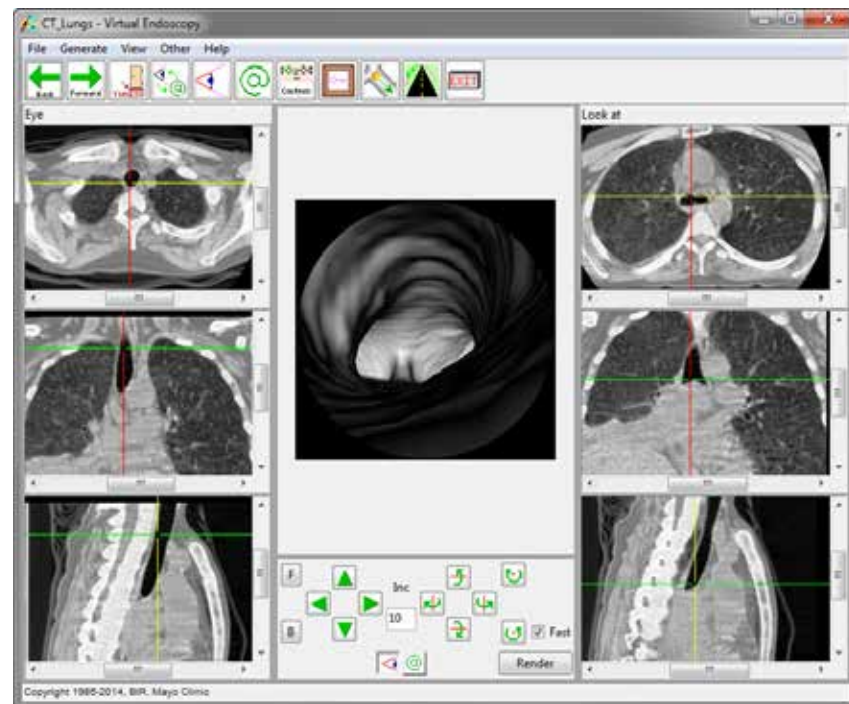16. Close all Virtual Endoscopy windows before proceeding to the next exercise.
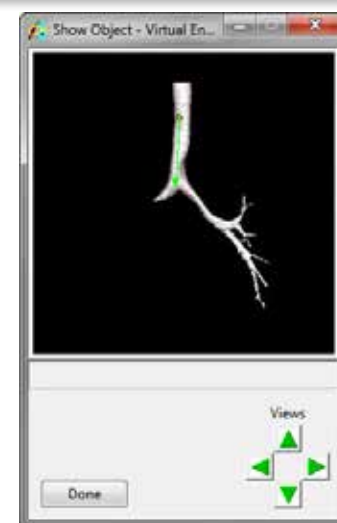


Figure 5



Figure 6

AnalyzeDirect

# Virtual Endoscopy: Movie Generation

The Virtual Endoscopy module provides an interactive interface for endoscopic visualization. Often the desired result of such an endoscopic exploration is a detailed endoscopic movie sequence along a specified 'fly-through' path. This exercise will demonstrate how to achieve this by defining a path using key frames then generating all endoscopic renderings along this path.

1. Load the **CT_Lungs.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Virtual Endoscopy** module (**Display > Virtual Endoscopy**).

3. Before beginning to record the movie, move closer to the trachea. Position the cursor near the center of the trachea and click three times to cause incremental movement towards the target.

4. Press the **Add Key Frame** PowerBar button or choose **Generate > Sequence > Add Key Frame** to specify the first key frame (this is where the movie will begin).

5. Move closer to the trachea by clicking three more times within the tracheal lumen (figure 1). After the movement towards the trachea has stopped, press the **Add Key Frame** button to add another key frame.

6. Choose **Generate > Sequence > Auto Key Frame**, this option causes any new viewpoint to automatically be added as a key frame.

7. Continue to click within the tracheal lumen and navigate down to the bifurcation of the airway (approximately 9 clicks) (figure 2).

8. When you reach the bifurcation of the airway, click in the left bronchus to reorient the viewpoint down that specific branch. Click several more times to traverse down the left bronchus.

9. When you have moved down the left bronchus (figure 3), choose **Generate > Sequence > Auto Key Frame** to turn off the Auto Add Key Frame option.

10. To save the sequence, choose **Generate > Sequence > Save Sequence**.

11. To generate a movie of the sequence, choose **Generate > Sequence > Generate Sequence**. The full sequence (defined by the key frames) will now be generated by the module; all endoscopic renderings will be generated along the defined path.

12. The fly-through movie will be available in the Analyze workspace and can be viewed with the **Movie** module (**Display > Movie**).


Figure 1


Figure 2


Figure 3

> *note* Rendering the endoscopic movie may take a few minutes depending upon your system and the size of the movie.
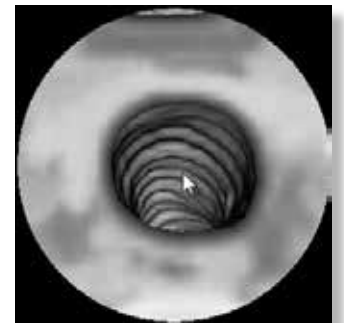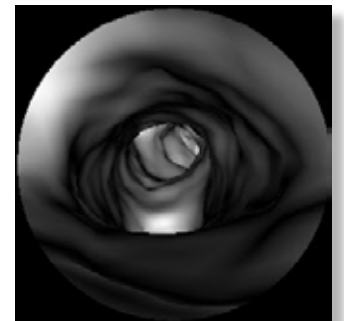
# Virtual Endoscopy: *Centerline Generation*

The Virtual Endoscopy module provides the ability to generate the centerline of an endoscopic structure using the current Eye and Look At points. Key frames are automatically generated between the two points and displayed in the Sequence Edit window once the centerline has been created, allowing an endoscopic sequence to be generated along the centerline, thus reducing the time taken to create fly-through movies. This task will show you how to create a centerline and generate the resulting endoscopic movie.

1. Load the **CT_Lungs.avw** data set from the **$:\BIR\images\ TutorialData** directory.

2. Open the **Virtual Endoscopy** module (**Display > Virtual Endoscopy**).

3. Position the cursor over the center of the trachea and click to navigate into the trachea. Clicking 12 times should position you midway into the trachea (figure 1).

4. Press the **Eye** and **Look At** PowerBar buttons to enable the Eye and Look At views. Then press the **Show Object** PowerBar button to open the **Show Object** window.

5. In the Show Object window, click on and drag the green arrow (the Look At point) to the end of the airway (figure 2).

6. Use the **Look At** panels to correct the Look At position, make sure that the Look At position is on the airway (figure 3).
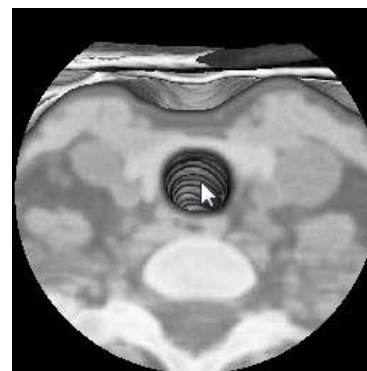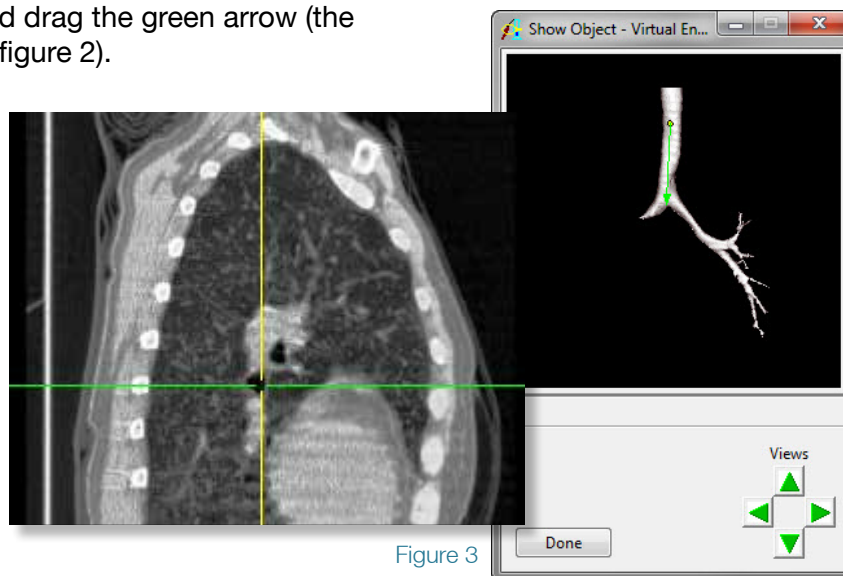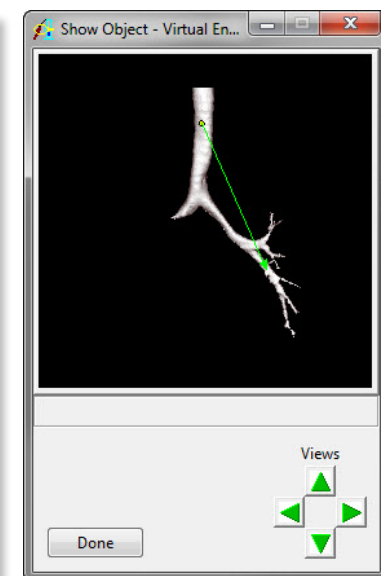

Figure 1


Figure 3


Figure 2

**AnalyzeDirect**

# Virtual Endoscopy: *Centerline Generation*

7. Next select **Generate > Generate Centerline.** The module will calculate the centerline between the current Eye and Look At points. Once calculated, the Sequence Edit tool will open displaying the automatically generated key frames, the centerline will be displayed in the Show Object window (figure 4).

note  If you do not have the Look At point centered exactly in the airway, you will receive an error when generating the centerline. If this happens, reposition your Look At point and try again.

8. To generate the endoscopic movie, select **Generate > Sequence > Generate Sequence**. The endoscopic movie based on the centerline will be generated and saved to the Analyze workspace.

9. Close all windows associated with the Virtual Endoscopy module before proceeding to the next Additional Task.
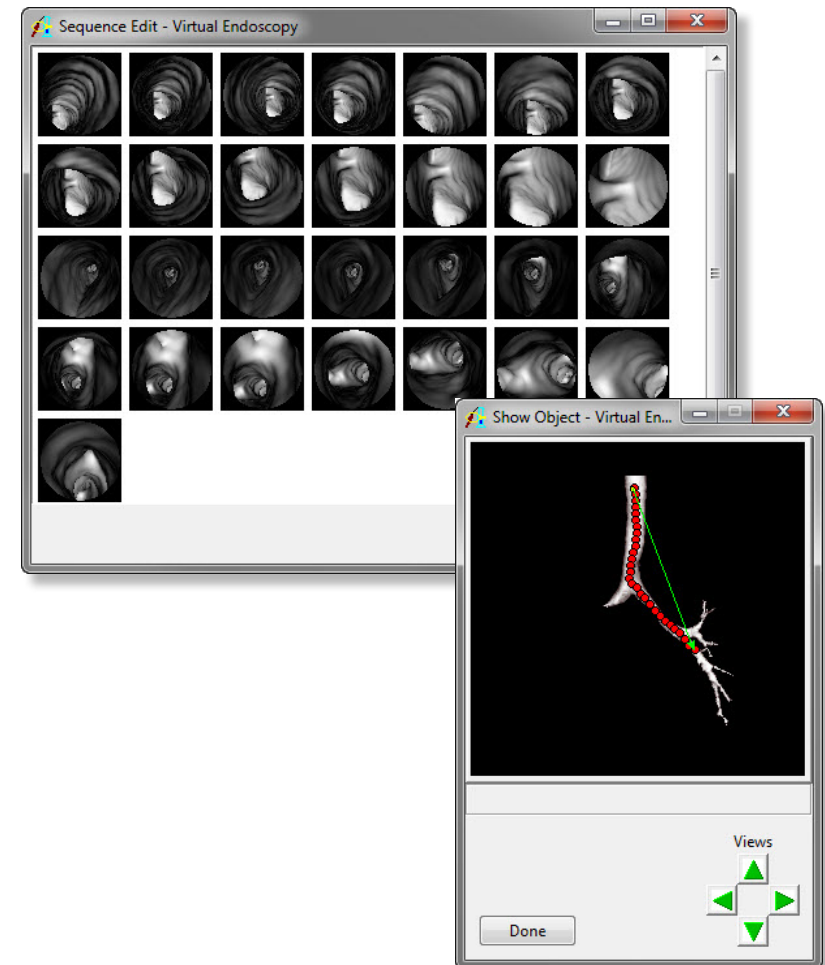


Figure 4

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**Analyze 12.0:** Essential Training Guide

# Process

# Image Calculator: Image Manipulation

This exercise will demonstrate how to use the Image Calculator module for rudimentary image processing and manipulation.

1. Load both the **MRI_3D_Head.avw** and **MRI_3D_Brain_Bin.avw** data sets from the **$:\BIR\ images\TutorialData** directory.

2. With the **MRI_3D_Head** data set selected in the Analyze workspace, open the **Image Calculator** module (**Process > Image Calculator**).

3. In the Image Calculator module, the MRI_3D_Head data set icon should appear in the white space above the calculator (figure 1).

4. Click the **Multiply** button on the calculator.

5. Drag-and-drop the **MRI_3D_Brain_Bin** data set from the Analyze workspace into the Image Calculator module (white space).

*note* In order to be able to drag-and-drop data sets from the Analyze workspace into the module, make sure that the Analyze window is not maximized to full window display.
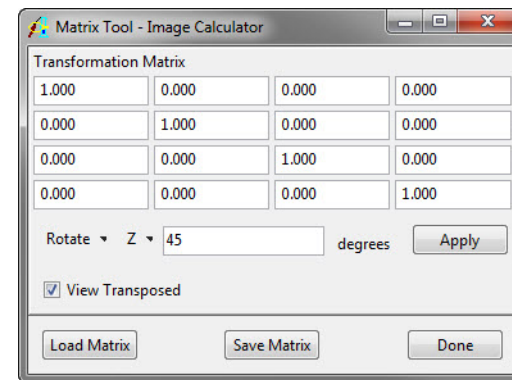
6. This first manipulation demonstrates how to multiply a grayscale data set with a binary data set. The binary brain will act as a mask; all voxels in the grayscale data set that fall within the binary mask will be kept, while the voxels that fall outside will be removed.

7. Click the **Equals** button on the calculator. A dialog box will be returned stating that the action modifies the loaded volume, click **Change a Copy of the Loaded Volume**.

8. The masked grayscale data will appear in the Image Calculator module; a copy will be automatically be saved to the Analyze workspace.

9. Click the **Multiply** button again.

10. Click the **Matrix** button on the calculator.

11. The Matrix Tool will open (figure 2); set to **Rotate** around the **Z-axis 45 degrees** and click **Apply**. Click **Done** to close the Matrix Tool.

12. Click the **Equals** button on the calculator. A Transformation window will be returned; use the default settings and click **Transform**.

13. The transformed data will appear in the Image Calculator module and the copy in the Analyze workspace will be updated.

Figure 1

Figure 2

# Image Calculator: Image Manipulation

14. Right-click on the calculator and choose **Buttons**; the Button Tool will open (figure 3).

15. The Button Tool includes a 'Palette' and 'Key Pad' (figure 3). To add a button to the main calculator, drag-and-drop it from the 'Palette' to the 'Key Pad' area of the Button Tool.

16. Click the **Flip** button that now appears on the calculator (figure 4).

17. In the Function Options window returned, check the **Flip X** option and click **Apply** (figure 5).

18. View the results by clicking the **Volume** button on the calculator.

19. A copy of the data set (as specified earlier) with the manipulations performed has automatically been saved to the Analyze workspace.

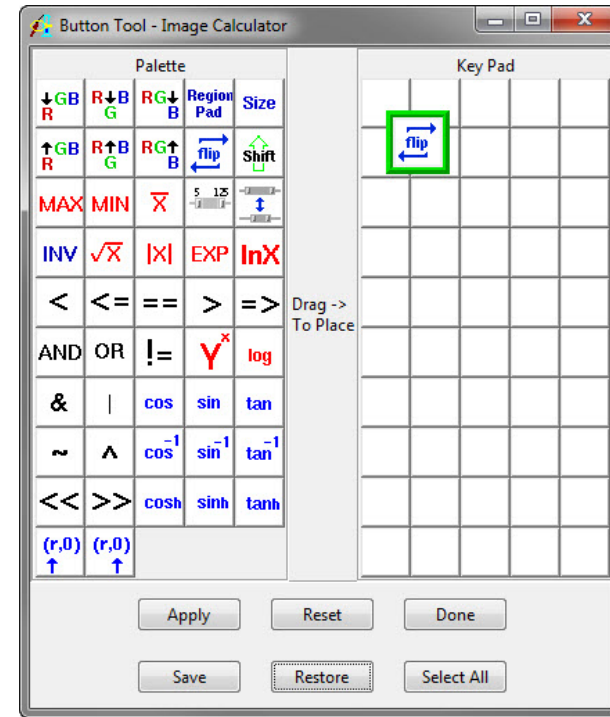20. Close the Image Calculator module before proceeding to the next exercise.
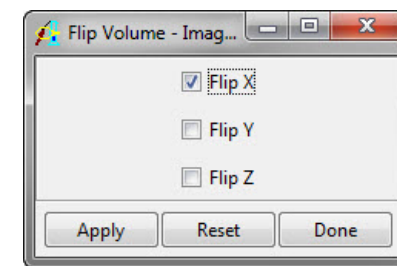


Figure 3



Figure 4



Figure 5

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# Image Calculator: SubRegion Data

The Image Calculator module performs mathematical operations on volumes, matrices and constant numerical values. The module also contains a number of processing functions including: subregioning (crop), flipping, resizing, shifting etc. This exercise will demonstrate how to use some of these additional processing tools to manipulate your data.

1. Load the **MRI_3D_Head.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Image Calculator** module (**Process > Image Calculator**).

3. In the Image Calculator module, right click on the white space and select **Buttons** from the menu options (figure 1).

Figure 1

4. In the **Button Tool**, select the **Region Pad** button from the palette on the left, and drag and drop it onto the Key Pad on the right.

5. After the Region Pad button has been moved to the Key Pad, hit **Apply**. The main Image Calculator key pad will be updated with the additional button option. Close the Button Tool.

Figure 2

6. Now drag and drop your data set from the Analyze workspace onto the Image Calculator process canvas (the white space). This will load the data set into the module and the volume will appear on the canvas.

7. Hit the **Region Pad** button, the Region Pad button's **Subregion-Pad Volume** window will be returned (figure 4).

8. In this window you can subregion the data by entering Low and High values for the X, Y and Z options.
   **X Low** - Specifies the first column of pixels from each slice to be loaded.
   **X High** - Specifies the column end point
   **Y Low** - Specifies the first row of pixels from each image to be loaded
   **Y High** - Specifies the row end point
   **Z Low** - Specifies the first slice from the selected volume to be loaded
   **Z High** - Specifies the slice endpoint
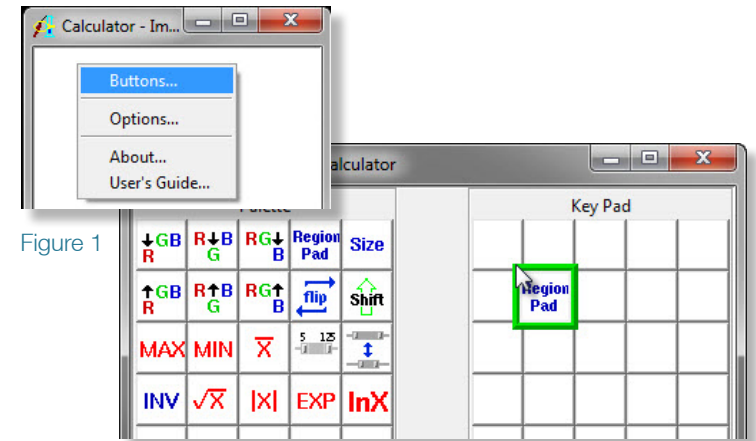
Figure 3    Figure 4

# Image Calculator: SubRegion Data

9. Click on the **Interactive** button in the Subregion window.



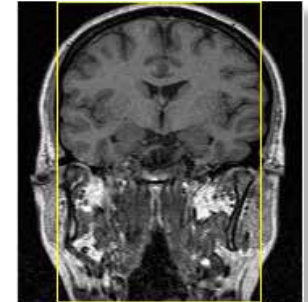**Example 1: Subregioning 50 slices in the X.**

- Set the **X Low** value to **25**
- Set the **X High** value to **162**



**Example 2: Subregioning 50 slices in the Y.**

- Set the **Y Low** value to **25**
- Set the **Y High** value to **211**
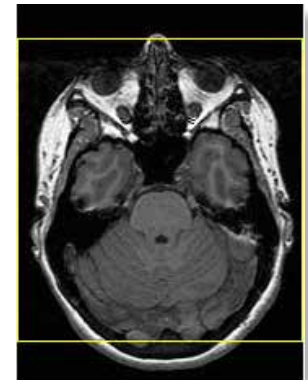


**Example 3: Subregioning 50 slices in the Z.**

- Set the **Z Low** value to **25**
- Set the **Z High** value to **151**
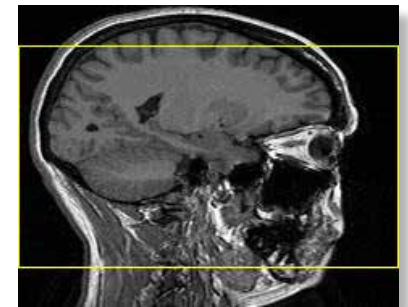
# Image Calculator: SubRegion Data

10. Now use the interactive tool to subregion. Use the tool to trace a bounding box around the area you wish to subregion.

- To define the box, simply click and drag the box on the image display.

- You can review and adjust the box in all three orthogonal orientations, by using the T, C, or S cube icons to change orientations.

- You can review your subregion on all slices prior to applying the subregion, use the slice slider bar to navigate through the volume.

11. A subregion defined in the Interactive tool automatically updates in the X,Y and Z high/low values in the Region Pad Function Option window. To apply a subregion to a data set, hit **Apply** in the Region Pad Function Option window.

12. When you Apply a subregion you will be asked if you would like to apply the changes to the Loaded or if you would like to Change a Copy of the Loaded Volume. Select **Change a Copy of the Loaded Volume**. The changes made to the copy of the data set will automatically be saved to the Analyze workspace.

13. Close all windows associated with Image Calculator before proceeding to the next exercise.
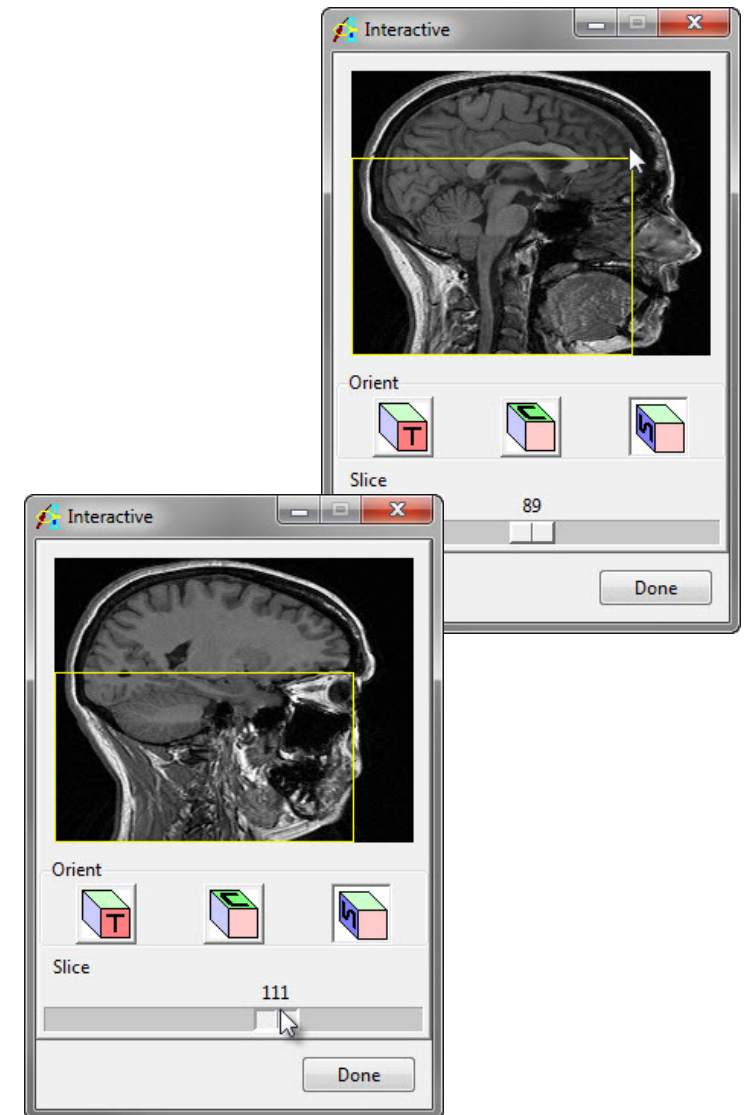
# Image Algebra: Formula for Image Manipulation

The Image Algebra module provides an algebraic formula parser, allowing both simple and complex algebraic operations (containing up to 1000 variables and 1000 constants) to be performed on image data. This exercise will demonstrate the use of common algebraic processing and other manipulations with the Image Algebra module.

1. Load the **Cubic_CT_Head.avw** data set from the **$:\BIR\images\ TutorialData** directory.

2. Deselect the Cubic_CT_Head data set in the Analyze workspace, and then open the **Image Algebra** module (**Process > Image Algebra**).

## Thresholding Data

3. You may remember from previous exercises (Volume Render 12 and 13), that the Cubic_CT_Head data set can be thresholded to 145 to show bone.

4. Enter the formula: **Output = (a > 145) * a**. Press <**Enter**> (figure 1)

5. Drag-and-drop the **Cubic_CT_Head** data set from the Analyze workspace into the Image Algebra module under variable '**a**'.

6. Click the **Output** button; in the Parameters window returned, set **Name** to **Bone**. Click **Done** to dismiss the window.

7. Click **Go** in the main Image Algebra window to begin processing.

8. Once processing is complete, right-click on the **Output** icon and select **Display** to examine the data with all voxels less than 145 removed (figure 2). Close the Display tool once the data has been reviewed.
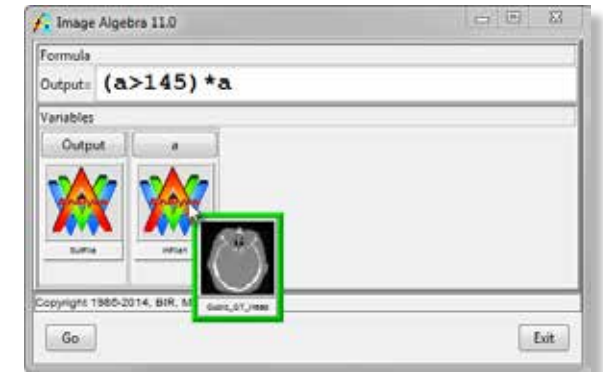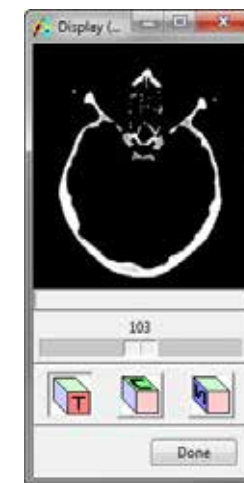
## Manipulating Data

9. In the Image Algebra module edit the formula: **Output = (a < 145) * a**. Press <**Enter**>. All voxels greater than 145 will now be removed from the data set.

note    The Image Algebra module remembers parameters from previous Image Algebra sessions. If the module detects parameters from a past session, it will prompt the user to remember or forget these settings.



Figure 1



Figure 2

AnalyzeDirect

10. Click the 'a' button to view the parameters for variable 'a' (figure 3). Click **Done** to dismiss the Parameters window.

11. Click the **Output** button and change **Name** to **NoBone**. Click **Done** to dismiss the window.

12. Click **Go** in the main Image Algebra window to begin processing.

13. Once processing is complete, right-click on the **Output** icon and select **Display** to examine the data with bone removed.

14. Now, try adding the bone back in with the new formula: **Output = (b >= 1) * b + (b < 1) * a**. Press <**Enter**> (figure 4).

15. Since we have reused the 'a' variable, the Image Algebra module will remember the data associated with it from the previous example. However, this is the first time the '**b**' variable has been specified, so drag-and-drop **NoBone** (from Output or the Analyze workspace) to the area under variable '**b**'.

16. Click the **Output** button and change **Name** to **BoneAdded**. Click **Done** to dismiss the window.

17. Click **Go** to process the new formula (figure 4).

18. Once processing is complete, right-click on the **Output** icon and select **Display** to examine the data with the bone added back.

19. Right-click in the formula field and explore some of the example formulas provided.

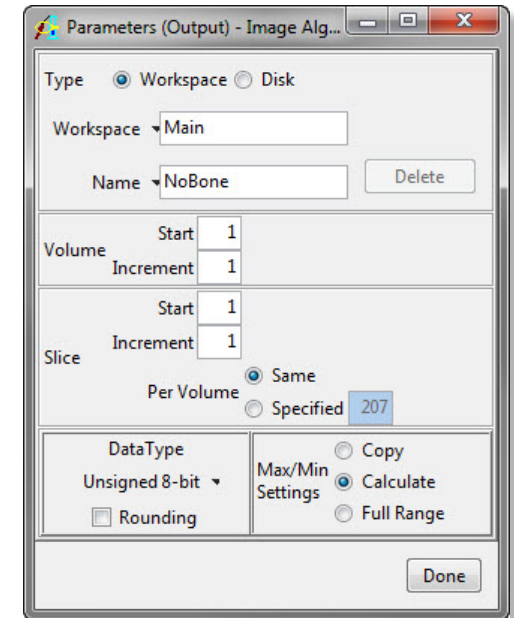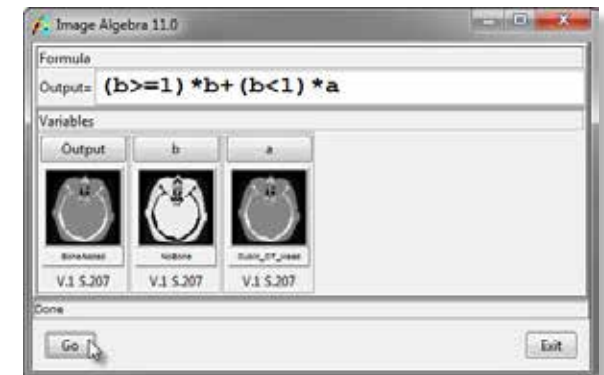20. Close the Image Algebra module before proceeding to the next exercise.



Figure 3



Figure 4

# Image Repair

The Image Repair module is a module that 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 removed from the volume. Subregion repair includes the ability to blend voxels at the edge of the region.

1. Load the **VH_Abdomen.avw** data set from the **$:\BIR\images\ TutorialData** directory.

2. Open the **Image Repair** module (**Process > Image Repair**).

3. In the Image Repair module (figure 1), use the Displayed Slice slider bar to locate the first corrupt slice. Note that the first corrupt slice is slice 276.

4. In the **Bad Slice(s)** portion of the window, set slice **276** as the first bad slice.

5. Now, use the Displayed Slice slider bar to locate the last corrupt slice. Note: the last corrupt slice is slice 279.

6. In the Bad Slice(s) portion of the window, set slice 279 as the last bad slice.

7. Select **Interpolate Between the First Good Slices** for the correction method.

8. Click **Repair Slice(s).** A dialog box will be returned, click **Change a Copy of the Loaded Volume**. The fix will now be applied to a copy of the data set; the fixed data set will be saved to the Analyze workspace as 'VH_Abdomen0'.

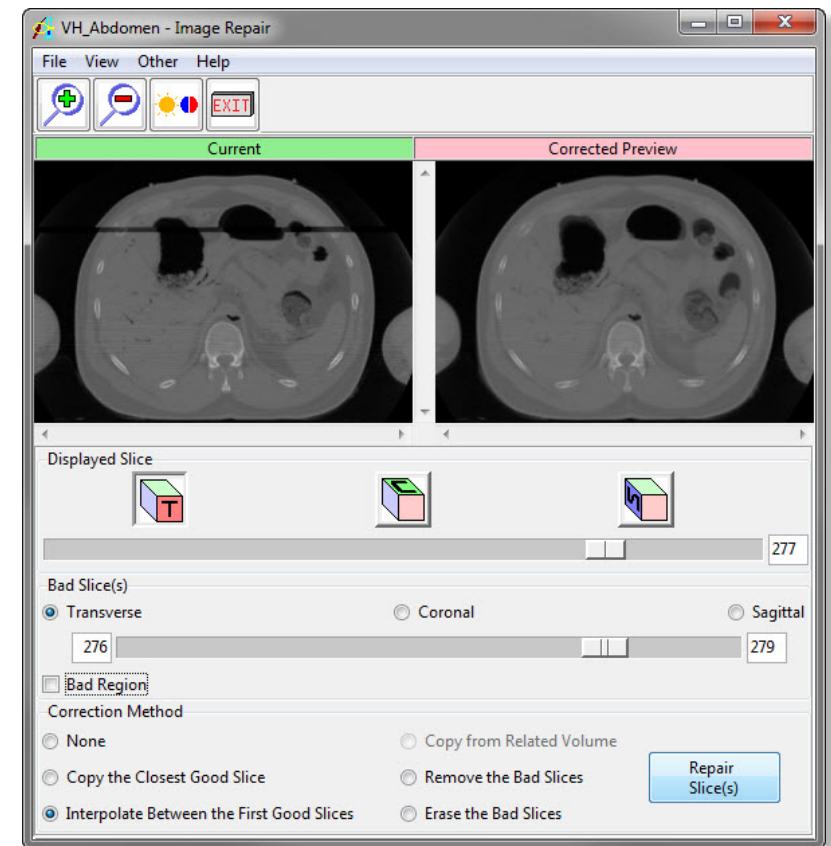9. Close the Image Repair module before proceeding to the next task.



Figure 1

# Image Repair: *Repair a Bad Region*

The 'Bad Region' option provides the user the ability to define only a selected region to be repaired. To demonstrate this option we will use the VH_Abdomen data set and repair only the corrupt regions.

1. Select the **VH_Abdomen** data set in the Analyze workspace and open the **Image Repair** module (**Process > Image Repair**).

2. As in the main exercise, set slice **276** as the first bad slice and slice **279** as the last bad slice.

3. Select the **Bad Region** option, the region boundaries and region sliders will appear.

4. Adjust the region sliders until just the corrupt area is defined (figure 1).

5. Try adjusting the **Blend Border** and **Correction Method**. Review the different results.

6. Click **Repair Slice(s)**. Slices 276 through 279 will be corrected according to the region and correction method. A dialog box will be returned, click **Change a Copy of the Loaded Volume**.

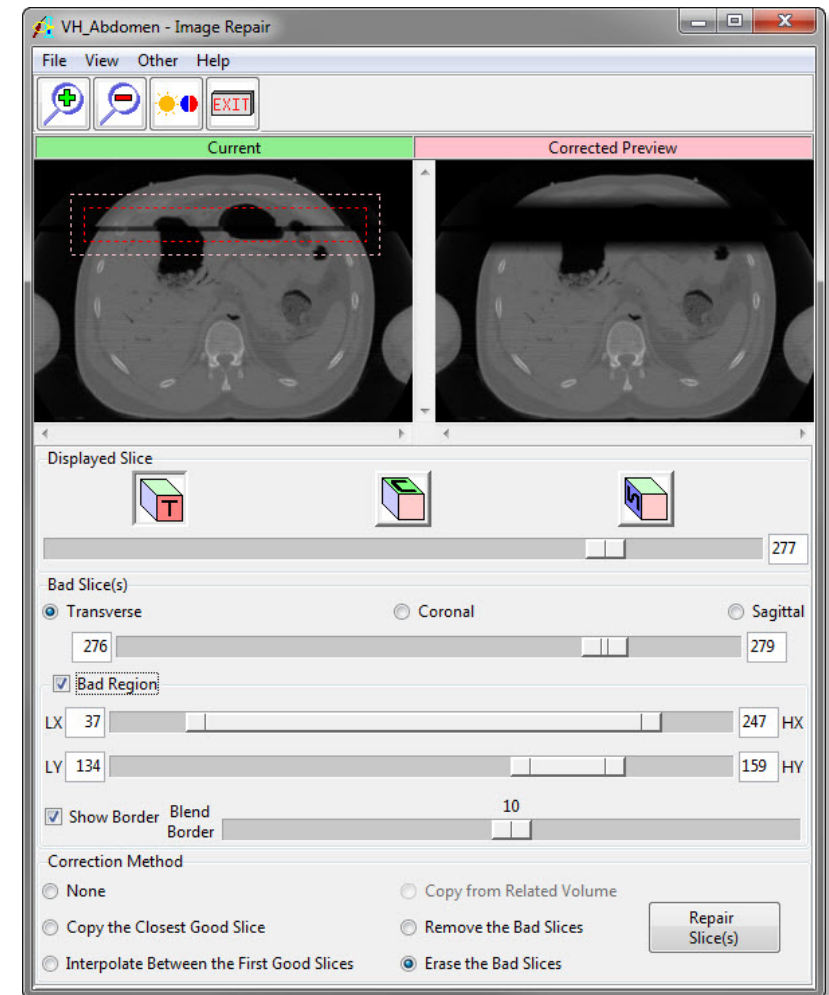7. Close the Image Repair module before proceeding to the next exercise.



Figure 1

# Histogram Operations: Histogram Normalization

The Histogram Operations module provides the ability to do histogram processing, such as histogram matching, flattening, and equalization (normalization). The goal of this exercise is to demonstrate how to normalize the histograms of SPECT images taken under different conditions.

1. Load both the **SISCOM_Ictal_SPECT.avw** and **SISCOM_Interictal_SPECT. avw** data sets from the **$:\BIR\images\TutorialData** directory.

2. With only the **SISCOM_Ictal_SPECT** data set selected in the Analyze workspace, open the Histogram Operations module (**Process > Histogram Ops**).

3. Open the **Function** window (**Generate > Function**).

4. In the Function window select Histogram Normalize and set the following parameters (figure 1):

   • **Use Histogram: Median**

   • **Target Value: 150**

   • **Image Display: Original and Filtered**

   • **Histogram Display: On**



Figure 1

5. Click **Filter**. An Input and Output Histogram will automatically be returned. The filtered result will be displayed in the main Histogram Operations window.

6. In the Function window change **Action** to **Memory** and click **Filter** again. A dialog box will be returned stating that the action modifies the loaded volume, click **Change a Copy of the Loaded Volume**.

7. Drag-and-drop the SISCOM_Interictal_SPECT data set from the Analyze workspace into the main Histogram Operations window.

8. Press the **Filter** PowerBar button. In the dialog box returned, click **Change a Copy of the Loaded Volume**.

9. 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 (figure 2). Additionally, both normalized volumes have automatically been saved to the Analyze workspace.

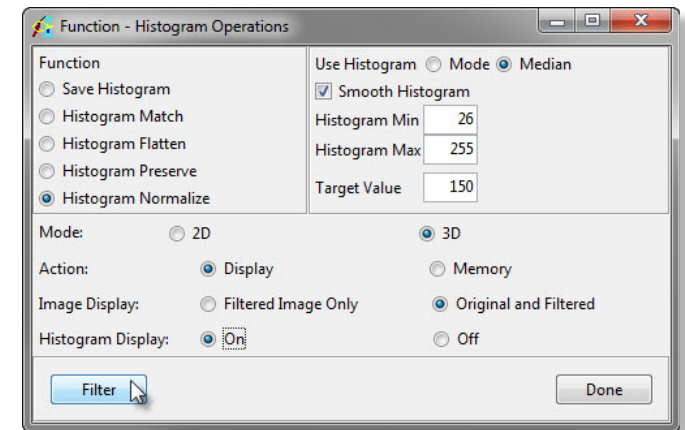10. Close the Histogram Operations module before proceeding to the next exercise.



Figure 2
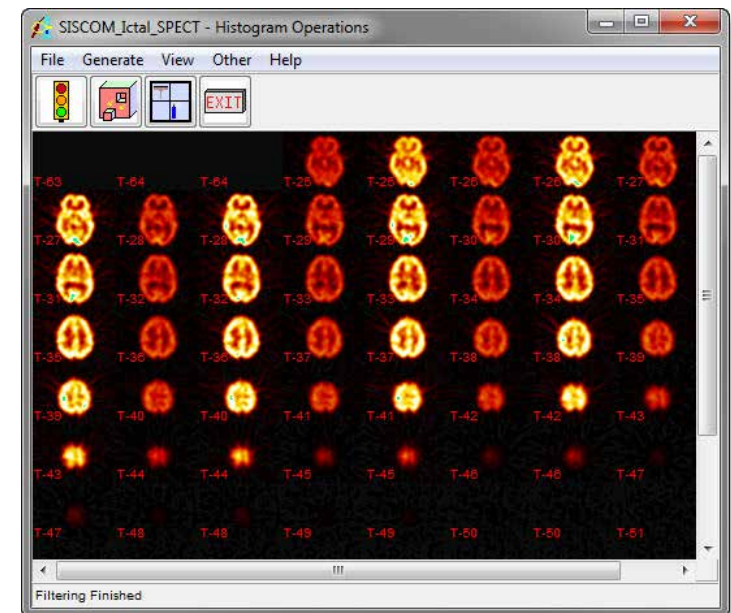
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# Spatial Filters

The Spatial Filters module enables the application of two-dimensional and three-dimensional filters to image data. This exercise will demonstrate how to apply a filter in the Spatial Filters module to your data.

1. Load the **MRI_3D_Head.avw** data set from the **$:\BIR\images\ TutorialData** directory.

2. Open the **Spatial Filters** module (**Process > Spatial Filters**).

3. Open the **Preview Options** window (**Generate > Preview Options**).

4. Select the **Loaded and Preview Volumes** option (figure 1). This will preview the original data set and a copy of the data set with any filter applied, side-by-side.

5. Open the **Filters** window (**Generate > Filters**).

6. In the Filters window, select the Low Pass filter by clicking the radio button next to the option (figure 2).

7. Now, click **Preview**. The original data set and the filtered data set will be displayed side-by-side in the main Spatial Filters window (figure 3), the filtered data set appears on the right.

8. Preview several other filters, noting the effect of each.

9. To apply a filter to the data set, click **Filter** in the Filters window. A dialog box will be returned stating that the action modifies the loaded volume, click **Change a Copy of the Loaded Volume**.

10. A filtered copy of your volume will be saved to the Analyze workspace.

11. Close the Spatial Filters module before proceeding to the next exercise.
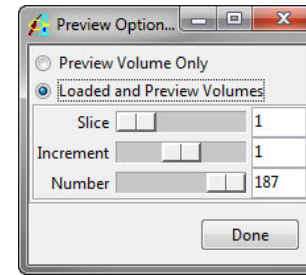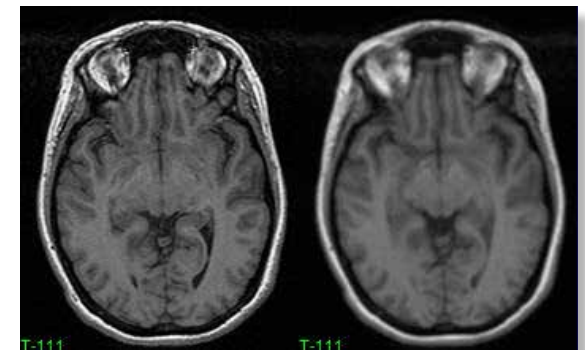


Figure 1



Figure 2



Figure 3

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# Filter Designer

The Filter Designer module is a general-purpose 2D image processing tool which performs convolution and deconvolution in the frequency domain using the Fast Fourier Transform (FFT). This exercise will demonstrate how to use the Filter Designer process functions available when a data set and it's associated Point Spread Function are loaded.

1. Load the **Chromosome_2D_512** and **Chromosome_2D_PSF** data sets from **C:\BIR\images\TutorialData\ImageProcessingTutorial**.

2. Select **Chromosome_2D_512** and open the **Filter Designer** module (figure 1) from the Process menu.

3. Drag and drop the PSF file from the workspace onto the **PSF input icon**.

4. Double-click on the Input icon to open the **Input Selector** window, and double click on the **Output** icon to open the **Output Viewer**.

5. The **Convolver** function has automatically been applied to the data. The Fourier transform of the selected section (slice) of the input volume is multiplied by the Fourier transform of the selected section (slice) of the PSF volume. The output is the inverse Fourier transform of the resulting spectrum.

6. Compare the input (figure 2) and output (figure 3) images.

7. Right-click on the Output icon and select '**Store This Section**' option. The output data set will be saved to the Analyze workspace. If desired the Filter and Spectrum generated by the process can also be saved in this manner.

8. Change the function to **Generate > Process > Cross Correlator**.

9. A cross correlation function of the selected section of the input volume with the selected section of the PSF volume will be generated.

10. Compare the input and output images.

11. Review the other functions available from the **Generate > Process** menu. Adjust the associated parameters to see the effect on the filtered image data.
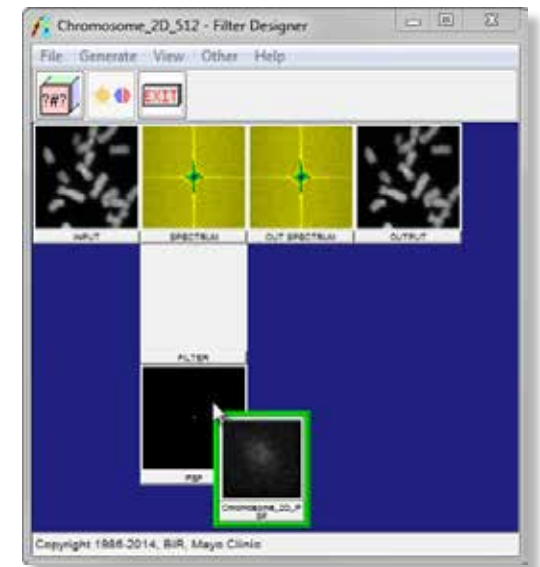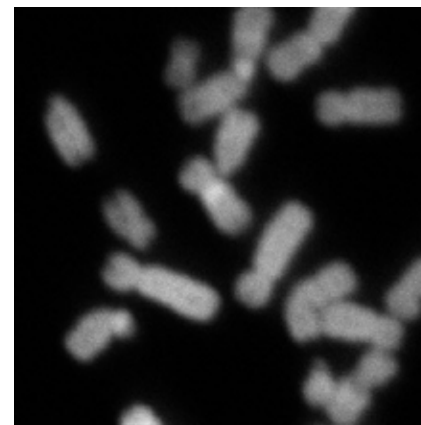


Figure 1
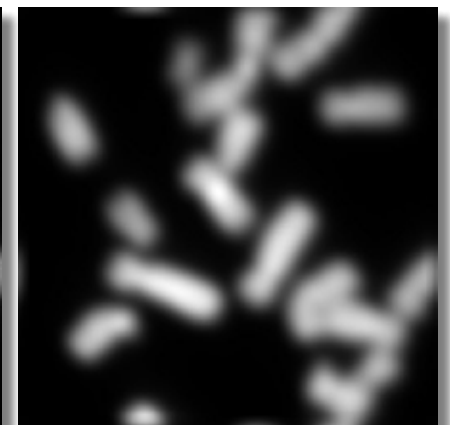


Figure 2: Convolver Input          Figure 3: Convolver Output

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# Filter Designer: *Defining Filters*

Filter Designer is a general-purpose 2D image processing tool, the module allows users to interactively define a representation of a frequency filter. This exercise will show you how to manually define filters to filter your image data.

1. Select **MRI_3D_Head** and open the **Filter Designer** module (**Process > Filter Designer**).

2. Set the **Slice** to **100** (**Generate > Slice**) (figure 1).

3. In the **Filter Designer** window draw a **Low Pass** filter (figure 2).

4. After releasing the mouse the filter will be applied to the current slice.

5. Double click on the **Output** image to view the effect of the low pass filter (figure 3).

6. Now in the Filter Designer window, define a High Pass filter (figure 4).

7. Note the update to the Output image (figure 5).

8. To save the current filtered image right-click on the output image and select **Store This Selection**. Set **Change a Copy of Image Data** when prompted. Slice 100 in the data set will be filtered.

9. To review the filtered data, open it with the Multiplanar Sections module. The filter has been applied to slice 100.
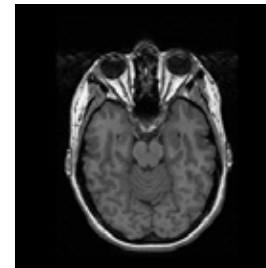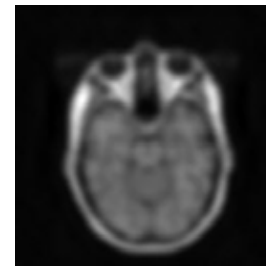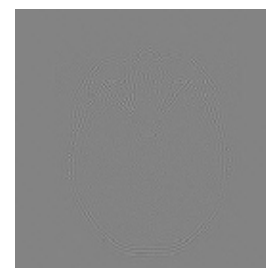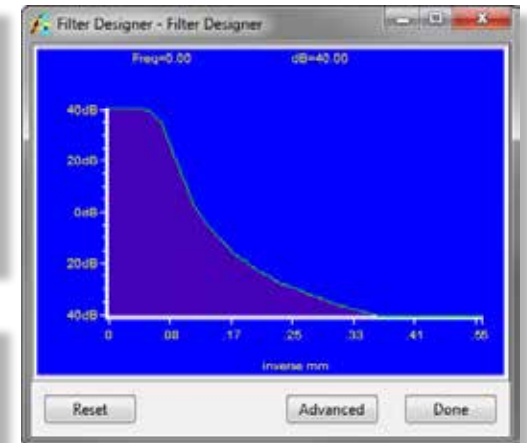


Figure 1



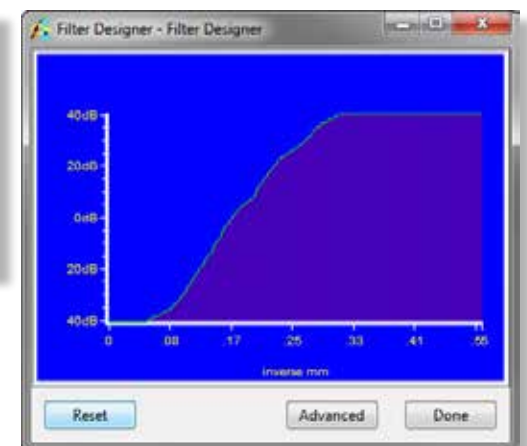Figure 2



Figure 3



Figure 5



Figure 4

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**Analyze 12.0:** Essential Training Guide

# Segmentation

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# Image Edit: Manual Segmentation

The Image Edit module provides a number of manual segmentation tools. This exercise will demonstrate how to segment grayscale data using the auto trace tool. For a full overview of all the segmentation tools in the module, please review the Image Edit tutorial available from the Help menu in the Analyze window.

1. Load the **MRI_3D_Head.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Image Edit** module (**Segment > Image Edit**).

3. Use the **Slice Slider** to move to **Slice 122**.

4. In the main Image Edit window, select the **Auto Trace** tool. Position the cursor near the center of the brain and click to set a seed point. The Image Edit window will automatically update to display Auto Trace parameters (figure 1).

5. Use the double-ended slider bar at the bottom of the window to adjust the threshold range until a reasonable trace of the brain is obtained. A threshold **minimum** of **34** and **maximum** of **129** works well for this data set.

6. Select the **Delayed Flood Fill** tool and place a fill point outside the auto-traced region (click on the background).

7. Select the **Auto Trace** tool again and click **Apply & Advance**.

8. A dialog box will be returned stating that the action modifies the loaded volume, click **Change a Copy of the Loaded Volume**. The area outside the trace will be highlighted in red, and then the next slice will appear in the image display (the slice number can be seen in the lower left corner of the image display).

9. Review the edited slice by opening the **Edit Review Tool** (**Tools > Edit Review**) (figure 2).

> *note* An edited version of the data set will be automatically saved to the Analyze workspace.
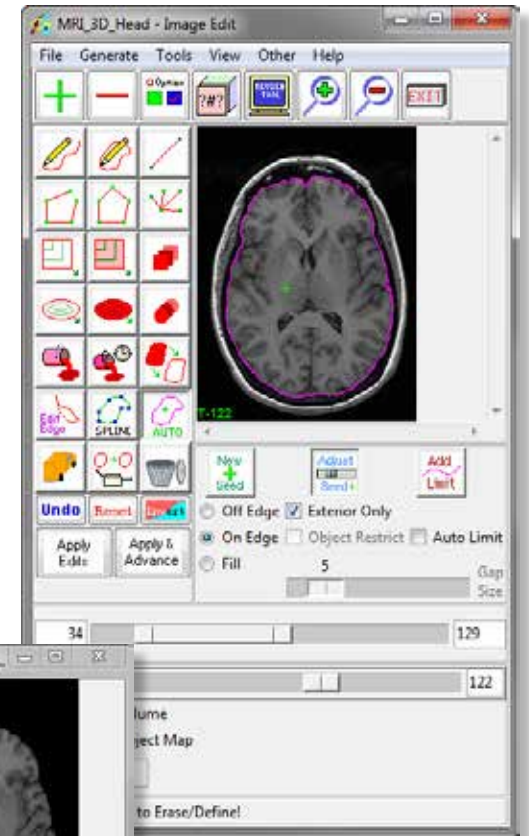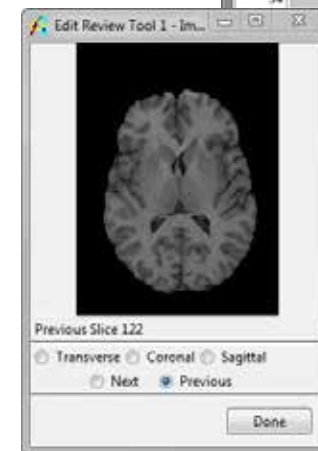
Figure 1

Figure 2

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# Image Edit: Manual Segmentation

10. In the main Image Edit window, you will notice that when the module advanced to slice 123 (step 8) the seed point and auto trace parameters set in step 5 were copied forward. The trace should have automatically adjusted to the brain on this slice. If not, the seed point may have been copied forward to an area outside the brain or to a voxel with a different grayscale value. Use the **Move** button and adjust the seed point.

11. If the trace needs no further adjustment and the Delayed Flood Fill point is still positioned outside the trace, click **Apply & Advance** and edit 19 more slices, finishing on **slice 142**.

12. In the Edit Review tool, change the orientation to **Coronal** and then **Sagittal**, note the slice edits in these orientations (figure 3).

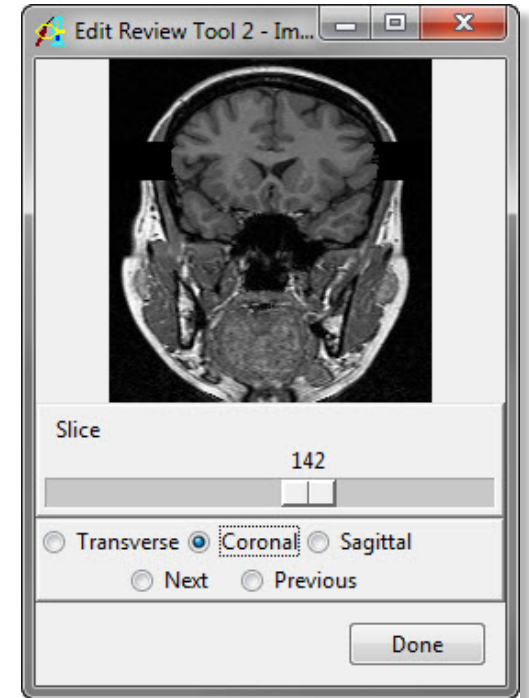13. Close all windows related to Image Edit before moving to the next exercise.



Figure 3

# Image Edit: Object Map Creation

As discussed in Exercise 13: Volume Render Advanced Controls, object maps are special image files that are used in Analyze to partition and identify structures as belonging to a particular segmented object. This exercise will demonstrate how to create an object map containing manually segmented objects.

1. Load the **MRI_3D_Head.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Image Edit** module (**Segment > Image Edit**).

3. Choose **File > Create Object Map**. The Objects window (**View > Objects**) will automatically be returned (figure 1).

4. Click **Add Object** to create a new empty object (Object_2).

5. Change **Name** from **Object_2** to **Brain**. Click **Done** to dismiss the Objects window.

6. Use the slider bar to move to **Slice 122**.

7. At the bottom of the main **Image Edit** window, set **Change** to **Object Map** and choose **Brain** from the **Defined Object** drop-down menu.

8. Select the **Auto Trace** tool; the Image Edit window will automatically update to display Auto Trace parameters (figure 2).

9. Position the cursor near the center of the brain and click to set a seed point. Use the double-ended slider bar at the bottom of the window to adjust the threshold range until a reasonable trace of the brain is obtained. A threshold **minimum** of **34** and **maximum** of **129** works well for this data set.

10. Select the **Delayed Flood Fill** tool and place a fill point inside the auto-traced region (click inside the region).

11. Select the **Auto Trace** tool again.

12. Click **Apply & Advance**. The next slice will appear in the image display (the slice number is displayed in the lower left corner).
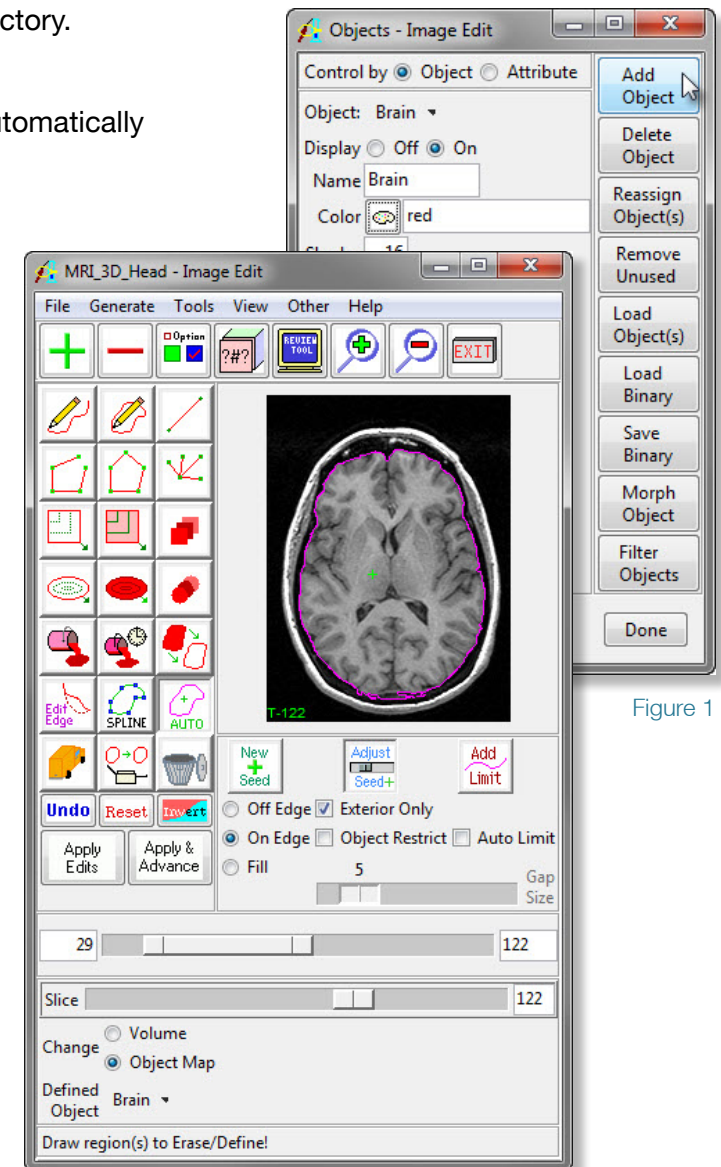
Figure 1

Figure 2

# Image Edit: Object Map Creation

13. View the edited object map by opening the **Edit Review Tool** (**Tools > Edit Review**).

> *note*  If you did not set the 'Change' option to Object Map (step 7) the defined region will appear black in the Edit Review tool.

14. Select the **Previous** option in the Edit Review tool. The change can also be viewed by selecting the **Coronal** option (figure 3).

15. With the **Auto Trace** tool selected, continue to segment slices by clicking **Apply & Advance** in the main Image Edit window. Segment the brain on **20 slices** (to slice 142).

> *note*  If the auto trace does not apply to a slice, or leaks to unwanted structures, try the following: 1) adjust the threshold range, 2) draw a limit after selecting the 'Add Limit' button, or 3) turn on the 'Auto Limit' option and adjust the 'Gap Size'. Additionally, the auto trace can be adjusted on a slice by moving the seed point with the 'Move' button selected.



Figure 3

16. To save the created object map for use in other Analyze modules, choose **File > Save Object Map**. Save the object map as **xxx_mybrain.obj** (where 'xxx' are your initials).
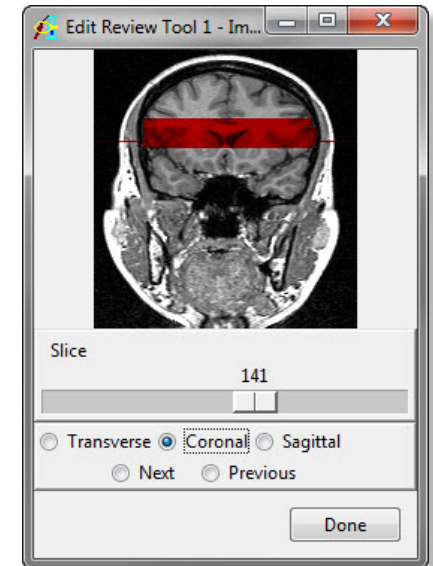
17. Close all windows before moving to the next exercise.

# Volume Edit

The Volume Edit module provides interactive segmentation tools for manual and semi-automated object definition of structures using an intuitive 3D interface. This exercise will provide an overview of how these tools can be used to interactively build an object map.

1. Select **MRI_3D_Head** from the Analyze Workspace, and open the Volume Edit module (**Segment > Volume Edit**).

2. Click the **Add Object** button to add a new object. Change the **Name** to **Skin** and **Color** to **Tan**.

3. Select the **Semi-Automatic** tab, and then select **Threshold**.

4. Adjust the threshold using the double-ended slider. Set the **Minimum Threshold** to **44** and the **Maximum Threshold** to **255**. Click the **Define Object** button.

5. The next step is to extract the brain. Select **Object Extractor**, and click the **Add Object** button, change the **Name** to **Brain** and **Color** to **Pink**. In the Transverse orientation, move to slice 135.

6. Click to set a seed point within the white matter (figure 2).

7. Adjust the **Minimum Threshold** to **48** and the **Maximum Threshold** to **141**. Click **Extract Object**.

*tip*   To toggle through intensity display options, press Ctrl+F9 on your keyboard. Review the options and decide which is most useful to you.
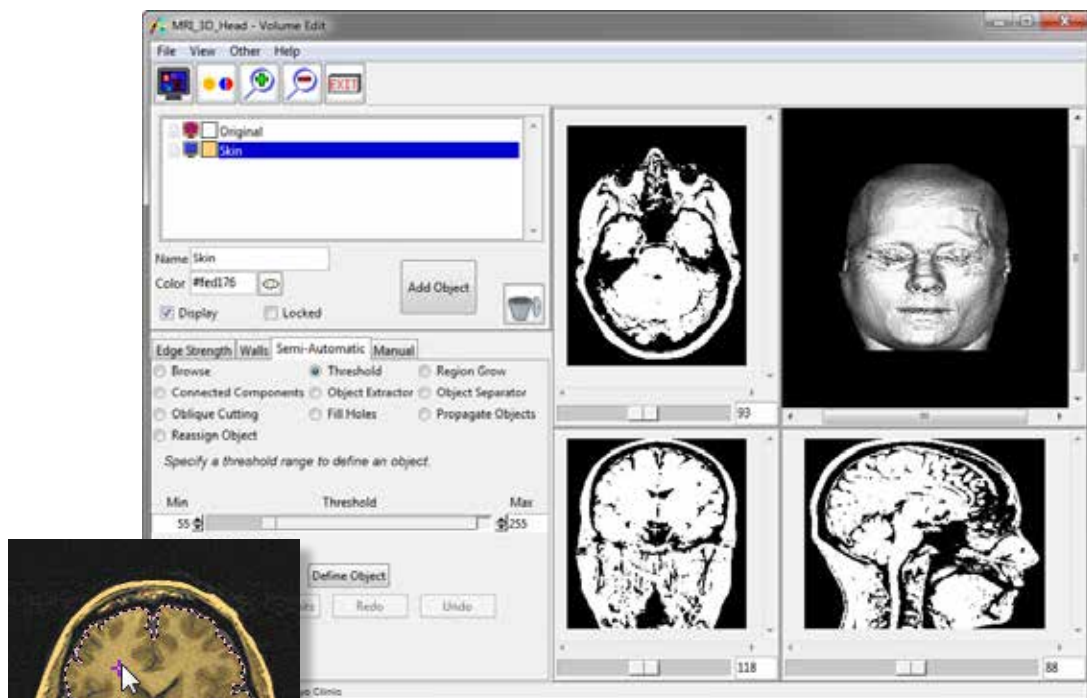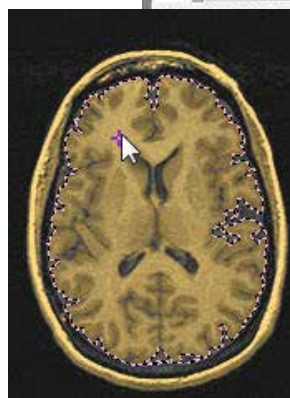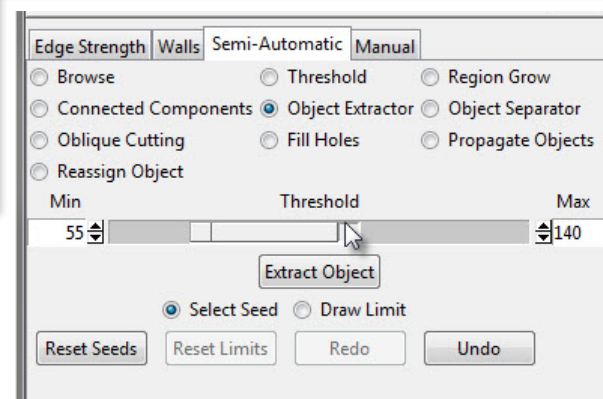


Figure 1



Figure 2



Figure 3

# Volume Edit

8. The brain will be extracted as the second object in the object map.

9. Once the brain object has been extracted, select the **Manual** tab.

10. To extract the ventricles, click the **Add Object** button. Change the **Name** to **Ventricles** and **Color** to **Green**. Select the **Auto Trace** tool.

11. Move to Transverse Slice **130** and set a seed point within the Ventricles.

12. Set the **Threshold Minimum** to **1** and the **Threshold Maximum** to **48** (figure 4). If there are unconnected regions that should belong to the same object, click to set additional seed points.

13. To automatically advance the seedpoints to the next slice, set **Auto Advance** to Forward, then click **Apply**.

14. Click the **Apply** button until the ventricles are defined. If needed, click the **Reset Seeds** button and click to place new seed points inside the ventricles (figure 5).

15. To review the segmentation on the rendering, right click on the render window and select **Transparency** (figure 6). To rotate the rendering, click and drag with the middle mouse button.

16. To save the created object map for use in other Analyze modules, choose **File > Save Object Map**. Close the Volume Edit module before proceeding to the next exercise.
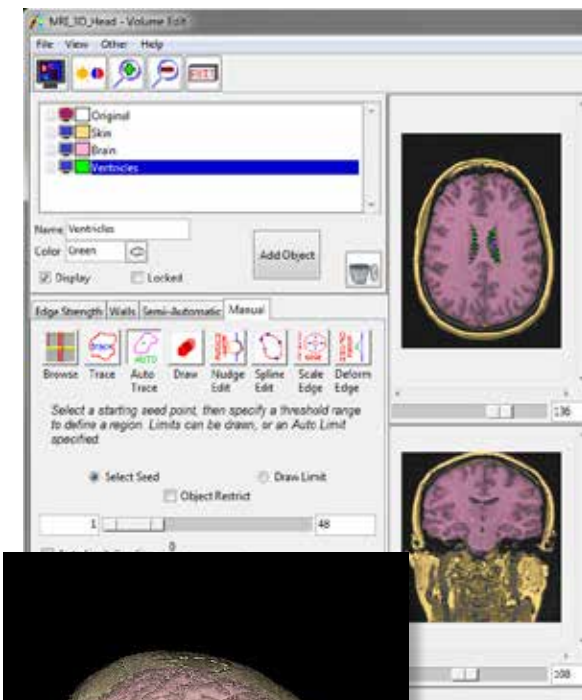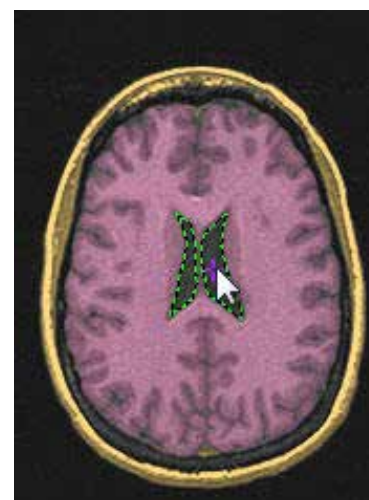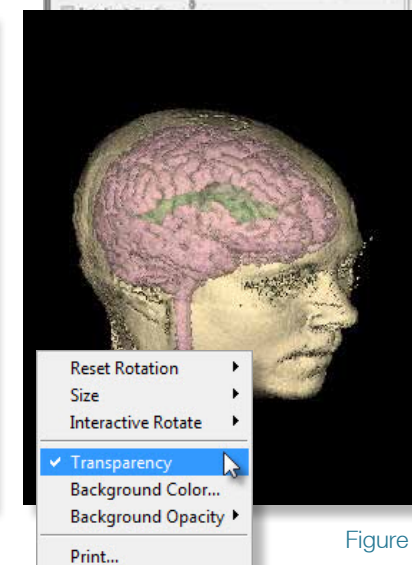
Figure 4

Figure 5

Figure 6

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# Volume Edit: Adipose Tissue Segmentation

In this exercise we will review the segmentation of visceral and subcutaneous adipose tissue to demonstrate key Volume Edit functionality including; Edge Strength, Region Growing, and Object Separation. However, this application is one approach used for the segmentation and separation of fat pads in mice.

1. Download the **CLS_MouseFat.avw** data set from **www.analyzedirect.com/data/CLS_MouseFat.zip**. Use **File > Load** to load the data into Analyze.

2. Use the **Process > Spatial Filters** module to apply a **3 x 3 x 3** median filter to the data set. See Exercise 27: **Spatial Filters** for instructions on applying a filter to a data set.

3. Next select the filtered data set (**CLS_MouseFat_Med**) and open **Segment > Volume Edit**.

4. Click the **Intensities** button and adjust the **Minimum** and **Maximum** intensity values to improve display of fat and abdominal wall.

5. From the **Edge Strength** tab check the '**Use Edge Strength**' option.

6. Set the **Edge Strength Threshold** to **63**. Note that the abdominal wall is shown in red (figure 1).

7. Next select the **Semi-Automatic** tab and choose the **Region Grow** option.

8. In the transverse orientation use the slider bar to move to slice **256**. Click intra-abdominal fat then set the **Threshold Minimum** to **2230** and the **Threshold Maximum** to **2540** (figure 2).

9. Click **Extract Object**.

10. Repeat to add any additional areas of adipose tissue.

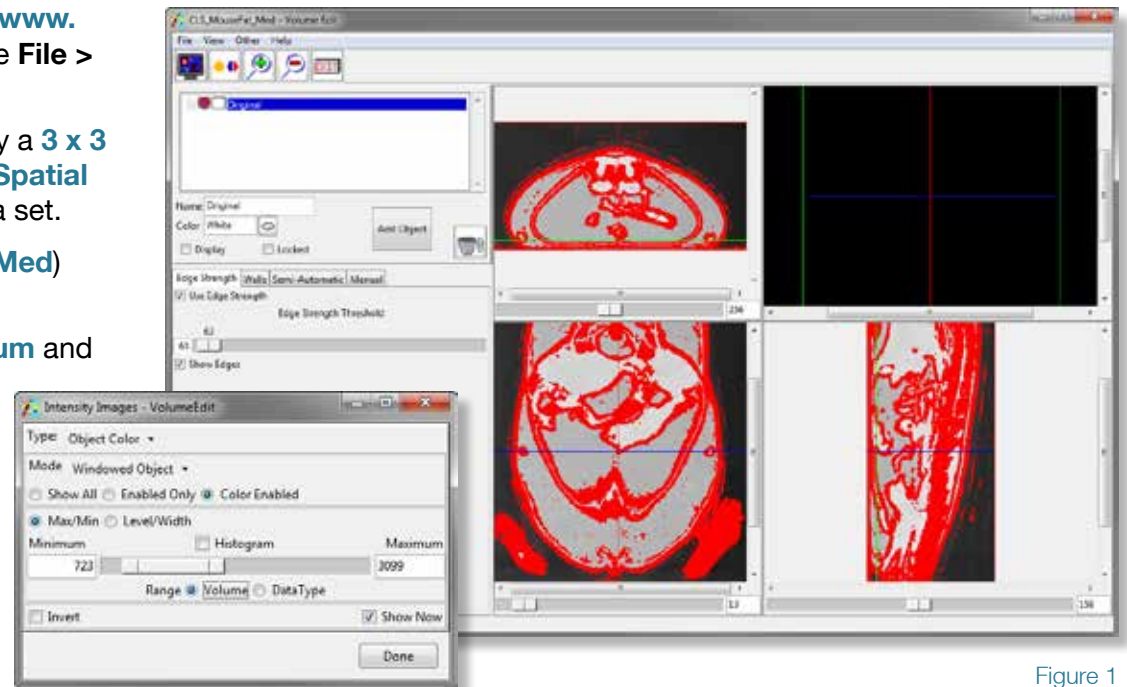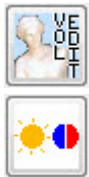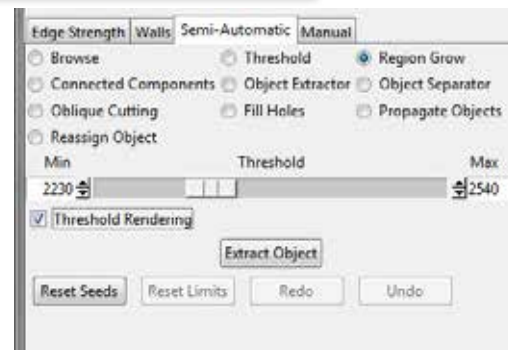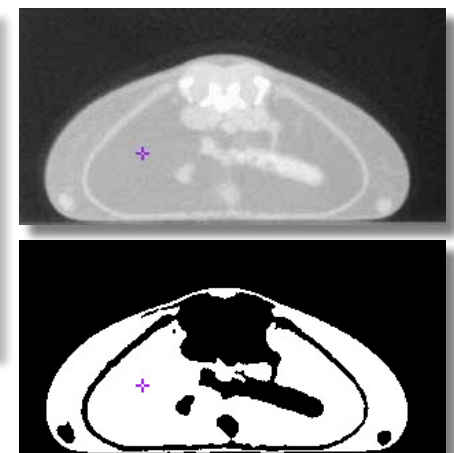11. In the **Objects** control panel rename **Object_2** to **VAT**



Figure 1



Figure 2



Figure 3

(Visceral Adipose Tissue).

12. Click **Add Object**, change the name of the new object to **SubQ** (Subcutaneous Adipose Tissue)

13. Select **Object Separator**. Click to set a seed point in a region of subcutaneous adipose tissue. Then click to set a second seed point in a region of visceral adipose tissue (figure 4).



Figure 4

14. Click **Separate**. The two regions of adipose tissue will be broken into their respective sub-compartments (figure 5).

15. Save the object map by selecting **File > Save Object Map**.

16. Note that the VAT and SubQ volumes can be sampled using the **Measure > Region of Interest** module. For more information please refer to exercise 51: Region of Interest - Measuring Objects in Object Maps.
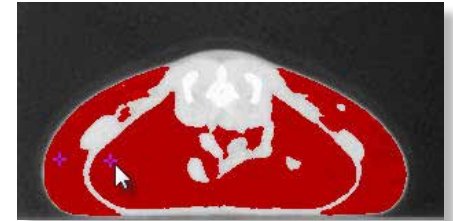
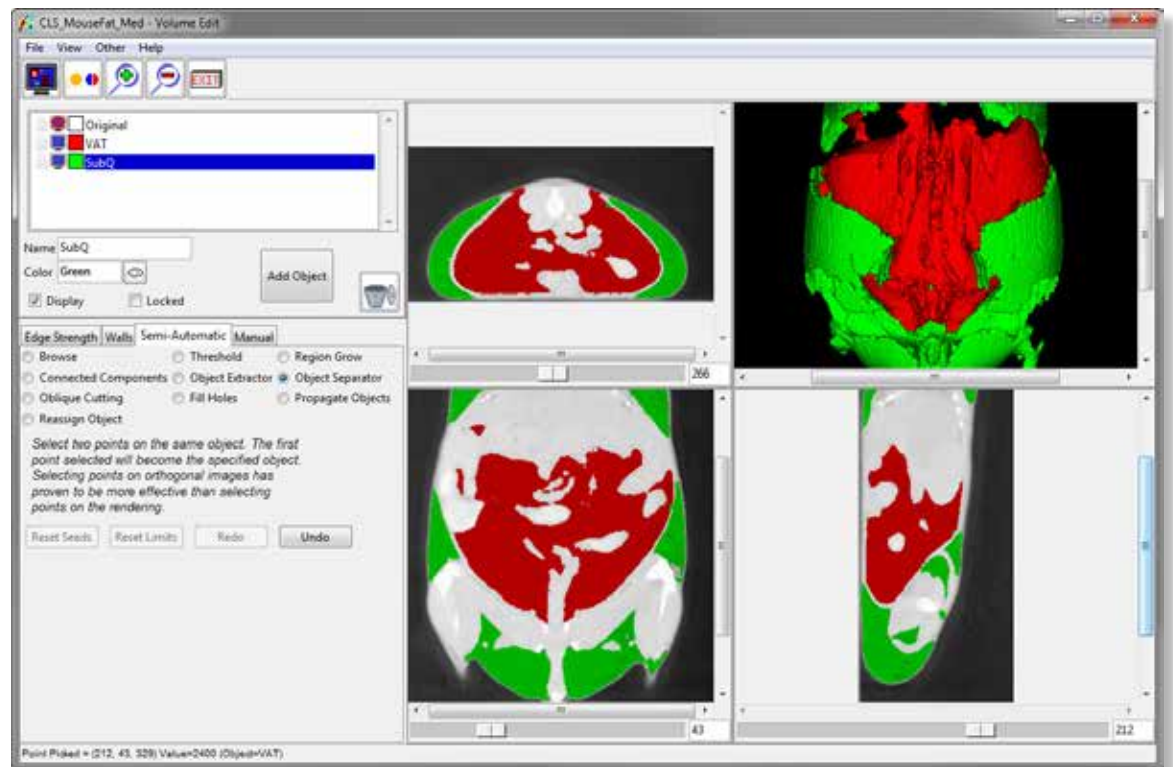17. Exit the Volume Edit module.



Figure 5

# Volume Edit: 4D Segmentation

Segmentation is often the precursor to other image analysis applications such as image measurement. Volume Edit provides a gamut of tools for a variety of segmentation tasks not only applicable to 2D-ROI and 3D-VOI measurement but also 4D-VOIs. In this exercise we will use the Volume Edit module to segment the left atrium in the heart using the Object Extractor tool over a series of 18 3-D volumes that span the entire cardiac cycle. The segmentation result can then be used for a number of applications such as calculation of blood volumes in the region over different stages of the cardiac cycle or cardiac ejection fraction.

1. Load the mouse dataset **BeatVol** from **$:\BIR\images\ TutorialData** directory.

2. Use **File > Load** to load the data set into Analyze.

3. Next select the **BeatVol** data set and open **Segment > Volume Edit**.

4. Note that there is an additional Volume control option. Use the Volume slider to navigate through all 18 volumes. Set the volume back to 1 when done.

5. The "Segment All Volumes" option will be checked by default, with this option checked the semi-automatic segmentation task performed on the currently selected volume will be propagated to each volume in the series.

6. Click on the **Semi-Automatic** tab and choose the Object Extractor option.

7. Set a seed point in the Left Atrium.  Set the **Min Threshold** to **154** and the **Max Threshold** to **255**, then click **Extract Object**. The Object will be segmented in all 18 volumes. Review the segmentation by moving through the Volume Slider.

8. Save the object map by selecting **File > Save Object Map**.
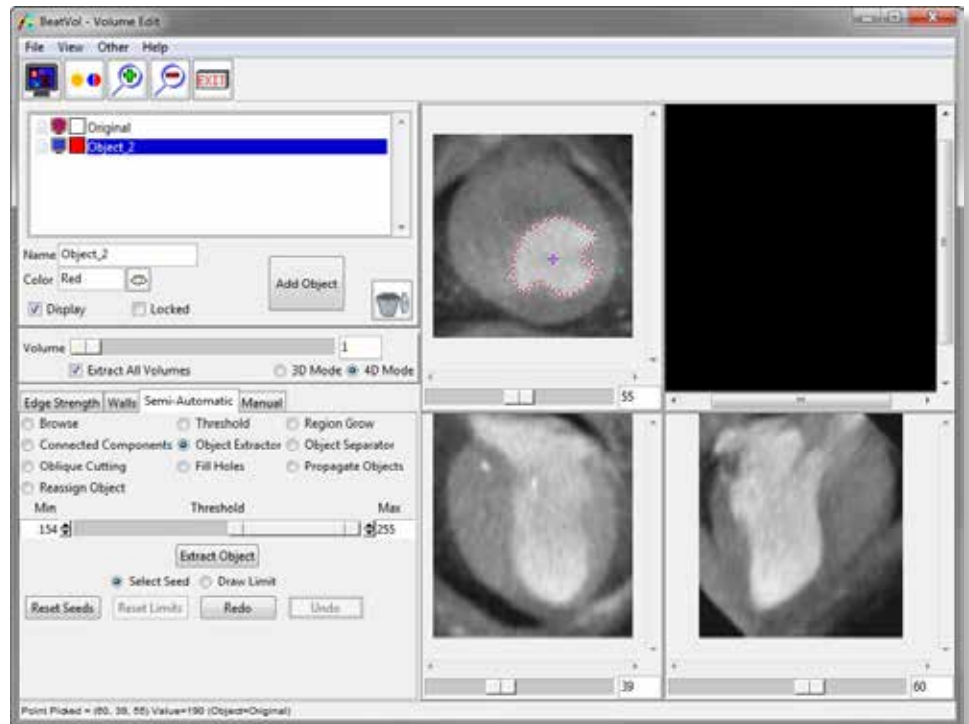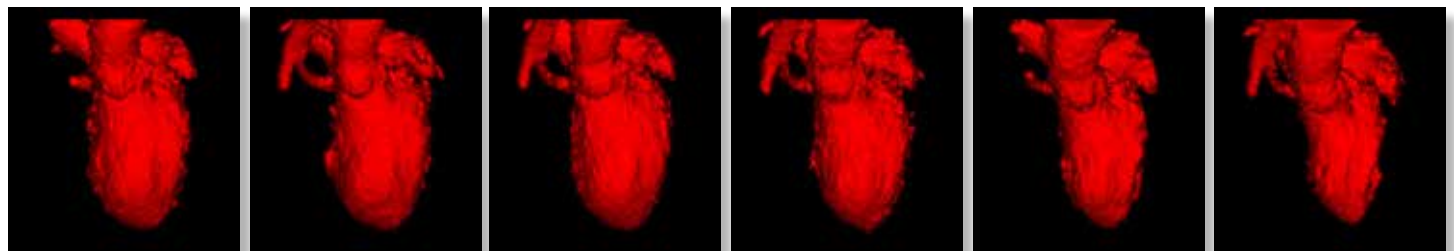
9. Exit the Volume Edit module.

Figure 1

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# Volume Edit: Cerebellum Segmentation

Segmenting structures from surrounding anatomy with a similar grayscale intensity can be difficult. This exercise will demostrate how to utilize the walls function in Volume Edit to make segmenting the cerebellum from the rest of the brain easier.

1. Load the **MRI_EGV_Brain.avw** from the the **$:\BIR\images\TutorialData** directory.

2. Select the data set and open **Segment > Volume Edit**.

3. Adjust the intensity range by opening **View > Intensities** and lowering the **Maximum value** to **80**.

4. Select the **Walls** tab, and check **Define walls to limit semi-automated operations**. In the options returned, set **Draw Walls** and **Spline** (figure 1).

5. In the Sagittal view navigate to slice **68**. Start setting spline points between the cerebellum and the rest of the brain. Click **Apply** on the Walls panel after completing a spline, or hit **A** on your keyboard to apply the spline.

*note* Always define walls in the same manner. For example if defining from the front to the back of the brain make sure all walls for defined in this way.

6. Move forward several slices and define another spline. Repeat across the brain (figure 2).
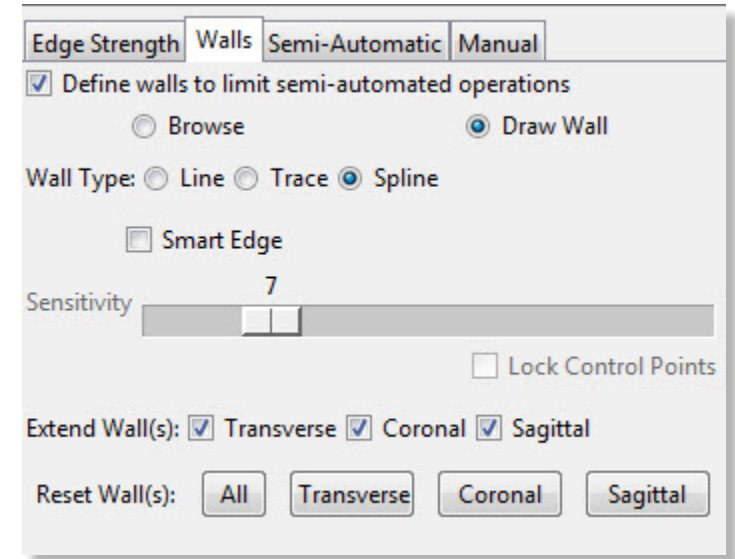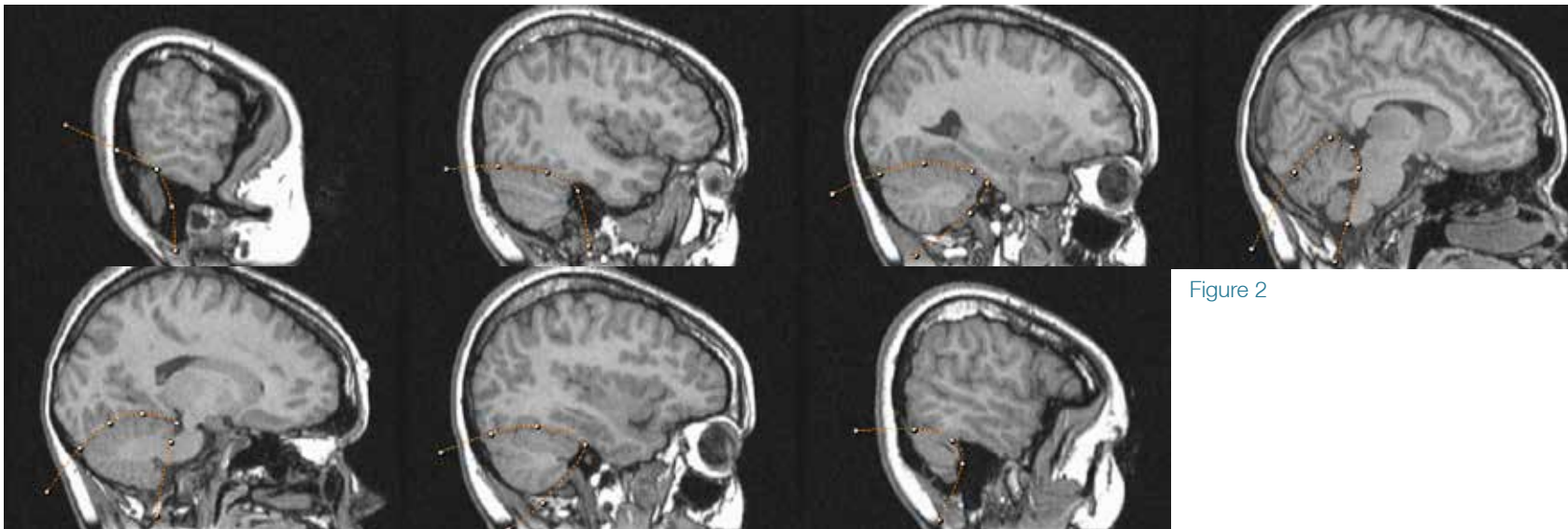


Figure 1



Figure 2

7. Once complete, move back through the slices and review the walls. Add new walls if needed.

8. Select the **Semi-Automatic** tab and select the **Object Extractor** option. Click in the cerebellum on a sagittal slice to set a seed point.

9. Select a min threshold of **30** and a max of **69** (figure 3). Click **Extract Object**.

10. Lock Object_2 and click **Add Object**. Set a seed point in the white matter on a spatially connected transverse slice, then click **Extract Object**.

11. Change the name of **Object_2** to **Cerebellum** and **Object_3** to **Brain**.

12. Save the Object Map (**File > Save Object Map**) and open in **Measure > Region of Interest** to make measurements of the Brain and Cerebellum objects.

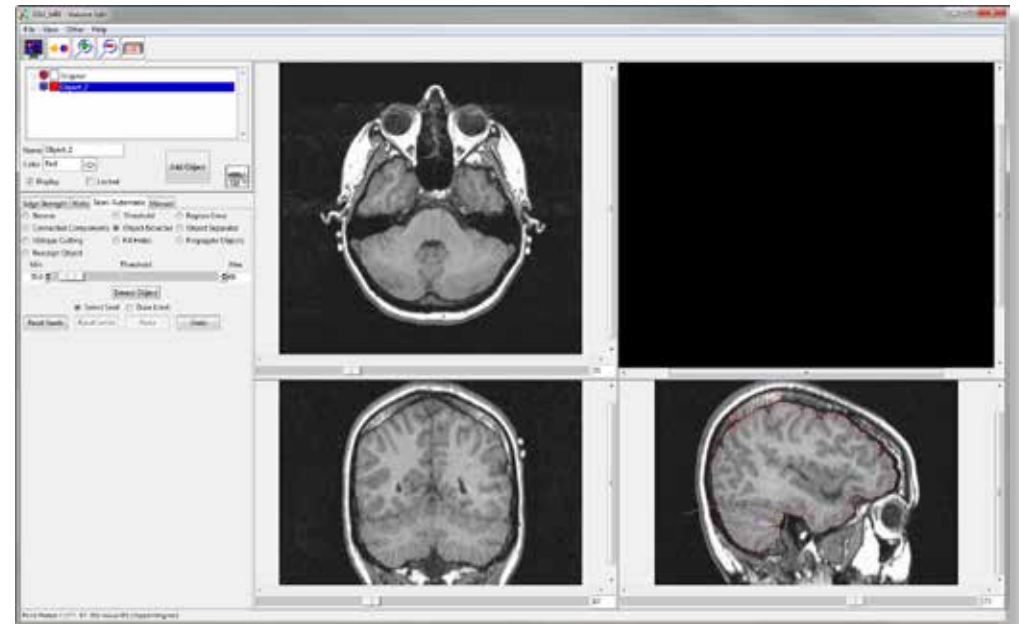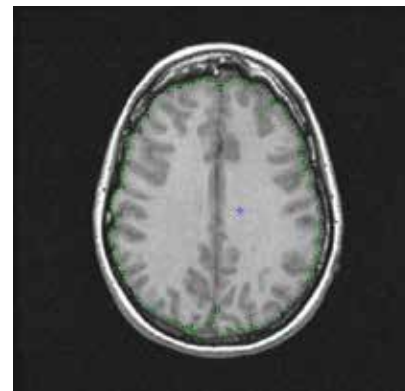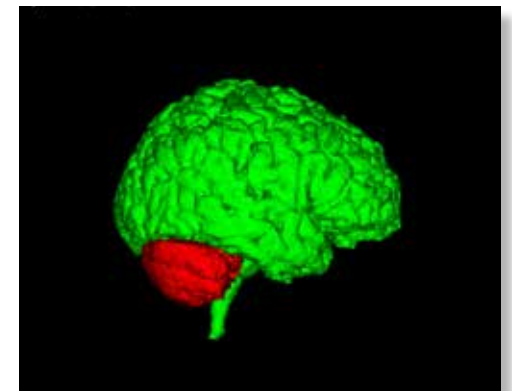13. Close the module before proceeding to the next exercise.



Figure 3



Figure 4



Figure 5

# Volume Edit: Lung Segmentation

In this exercise we will review lung segmentation from preclinical mouse data. We will cover additional segmentation and processing tools available in the module, including object separation and morphological operations dilation, erosion, and fill holes.

1. Download the mouse dataset **Mouse_Lungs** from **www. analyzedirect.com/data.**

2. Unzip the data and then use **File > Load** to load the Mouse data set into Analyze.

3. Next select **Process > Spatial Filters** to apply a **3 x 3 x 3** median filter to the data set. See Exercise 27: **Spatial Filters** for instructions on applying a filter to a data set.

4. Next select the filtered data set (**Mouse_Lungs_Med**) and open **Segment > Volume Edit**.

5. Click **Add Object**, change the name of the new object to **Lungs**.

6. Next select the **Semi-Automatic** tab and choose **Object Extractor** (figure 1).

7. Using the slider under the transverse image move to slice **210**, now click inside the lungs to set a seed point.

8. Use the threshold slider to define a threshold range with a **minimum** of **1200** and **maximum** of **1550** (figure 2). Then click the **Extract Object** button.

9. If necessary repeat the object extraction steps to add any missed regions to the Lung.

10. To separate the trachea from the lungs add a new object, click **Add Object** and name the object **Trachea&Bronchi** (figure 3).



Figure 2

Figure 1



Figure 3

AnalyzeDirect
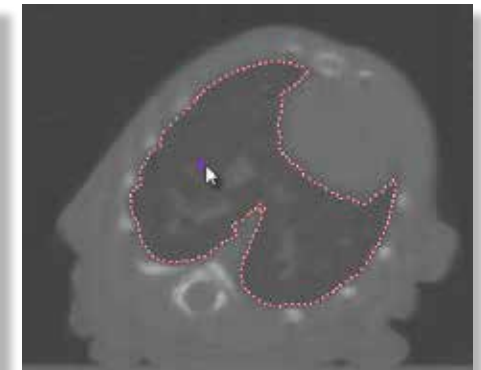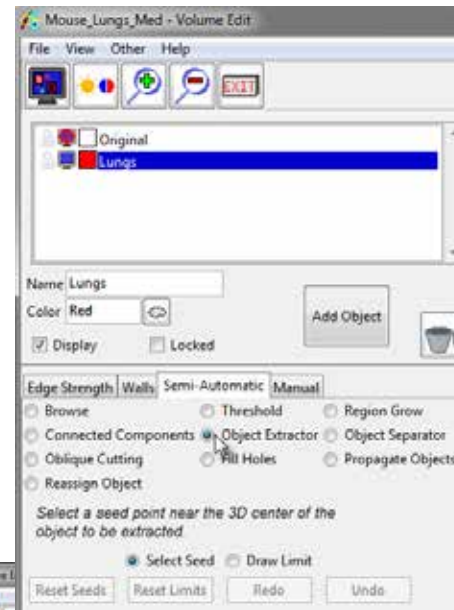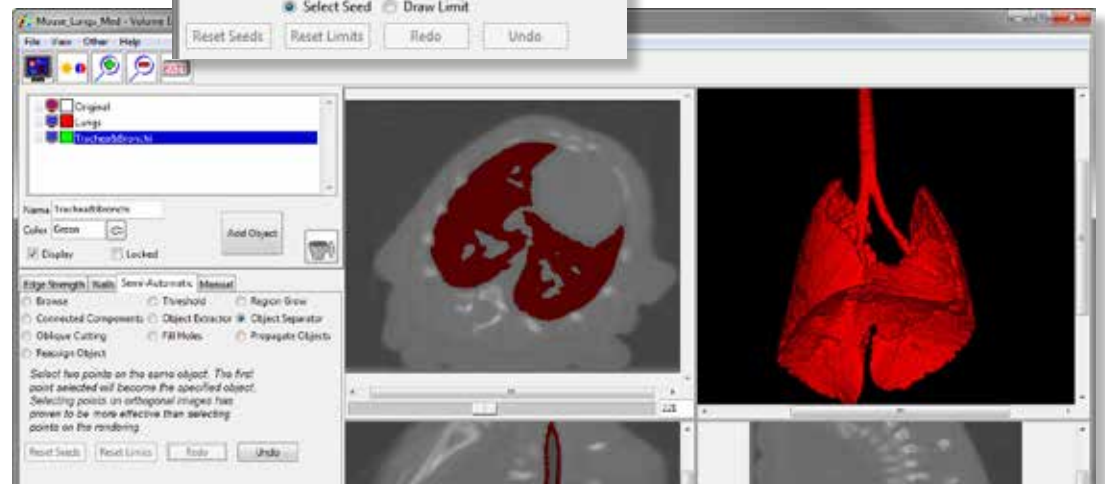
# Volume Edit: Lung Segmentation

11. Next select **Object Separator**. Click on the trachea to set a seed point then click on the lungs to set a second seed point. Note you can click on either the 3-D rendering or the 2-D slices. Next click '**Separate**'.

12. Review the separation results. Repeat the object separation steps to separate any remaining areas of the trachea from the lungs (figure 3).

13. Select the **Trachea&Bronchi** object in the Object list and then click the '**Delete**' button to remove the object.

14. To obtain a total lung volume measurement it may be necessary to fill any holes in the lungs. To do this use the morphological tools in the Objects window. Select **View > Objects**, set Object to Lungs and then click on the Morph Objects button.



Figure 3

15. In the Morph Objects window set the following parameters (figure 5):

    - **Objects** to **Lungs**
    - **Operation** to **Dilate**
    - **Element Shape** to **Jack**
    - **Element Size** to **5 by 5 by 5**
    - **Defined Object** to **Lungs**

16. Click **Morph**. The Lungs object will be dilated. Now, set the following parameters (figure 6):

    - **Objects** set to **Lungs**
    - **Operation** to **Fill Holes**
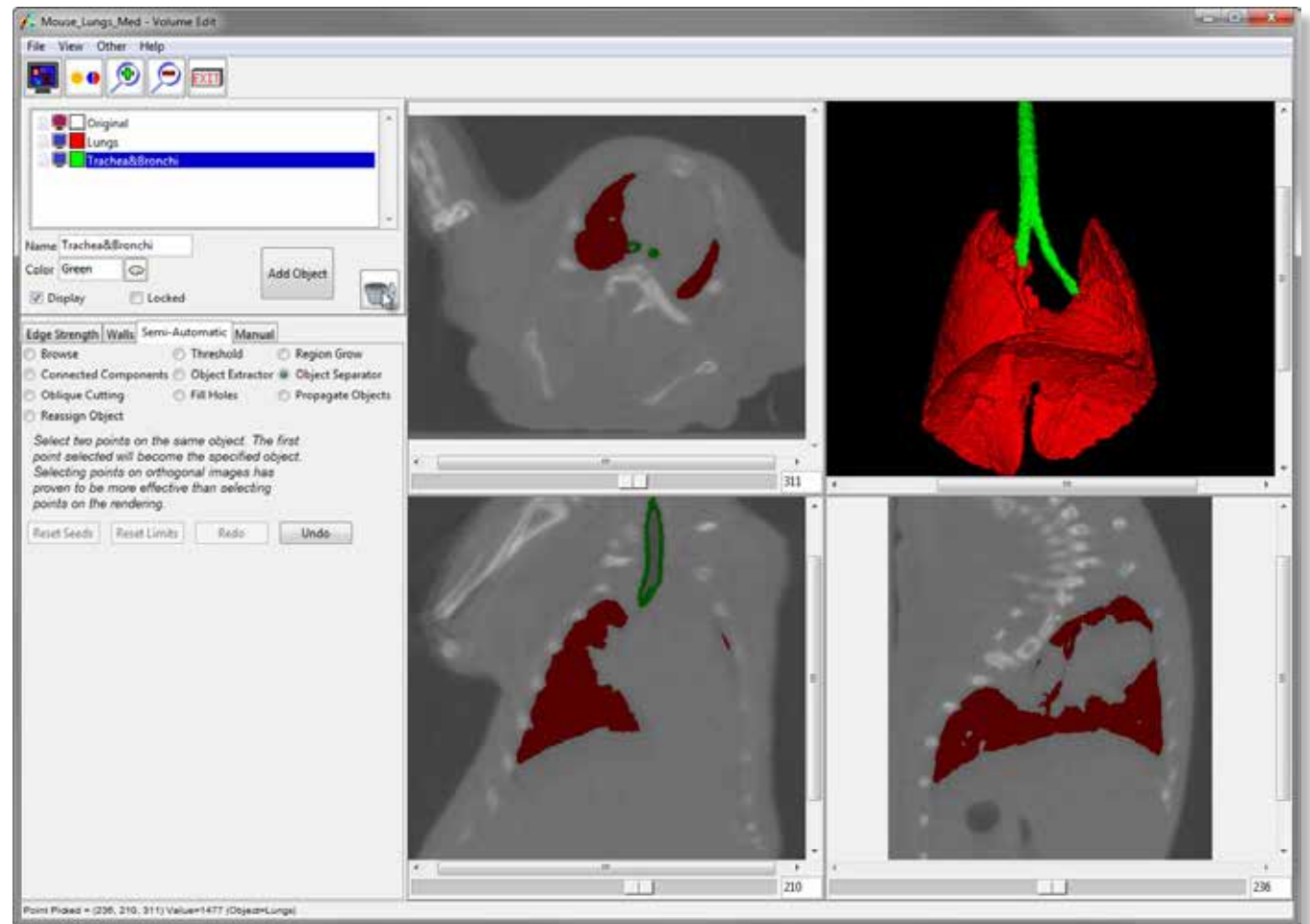    - **Fill Type** to **3 pass 2D; Transverse;** and **4-connected**
    - **Defined Object** to **Lungs**

17. Click **Morph**. The Lungs object will be filled.

18. Finally set (figure 7):

    - **Objects** to **Lungs**
    - **Operation** to **Erode**
    - **Element Shape** to **Jack**
    - **Element Size** to **5 by 5 by 5**
    - **Defined Object** to **Original**

19. Click **Morph**. The Lungs object will be eroded. Click **Done** to dismiss the Morph Objects window.

20. Save the object map by selecting **File > Save Object Map**.

21. Note that the lung volume can be measured using the **Measure > Region of Interest** module. For more information please refer to **Exercise 55: Region of Interest - Measuring Objects in Object Maps**.
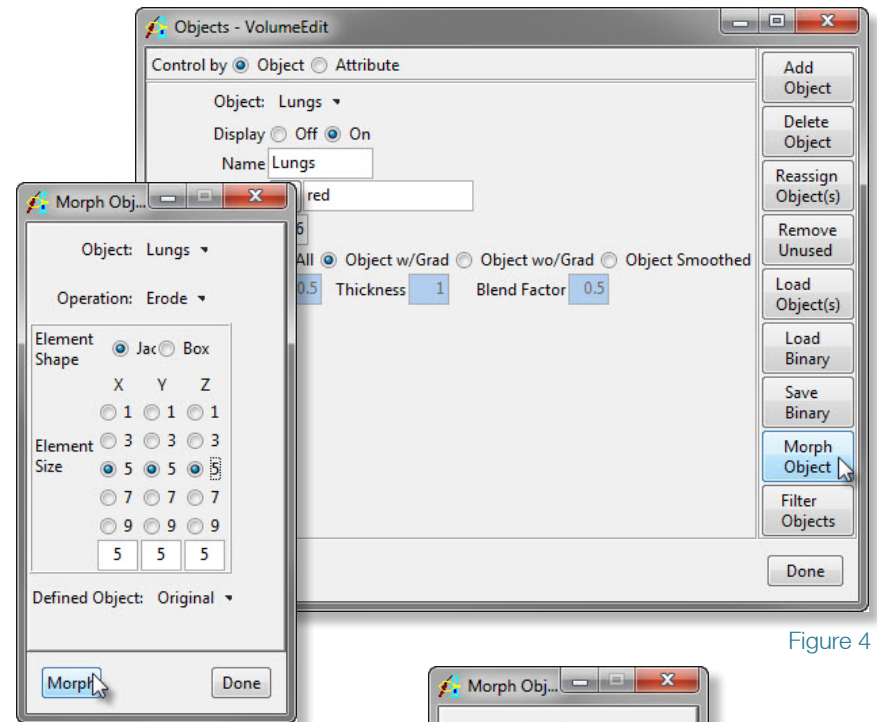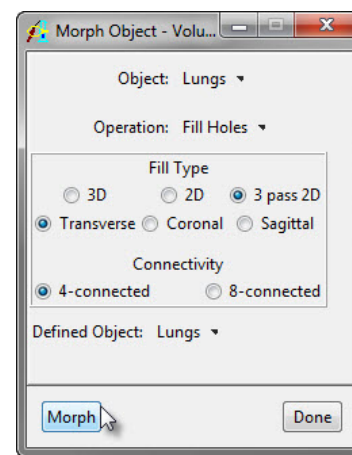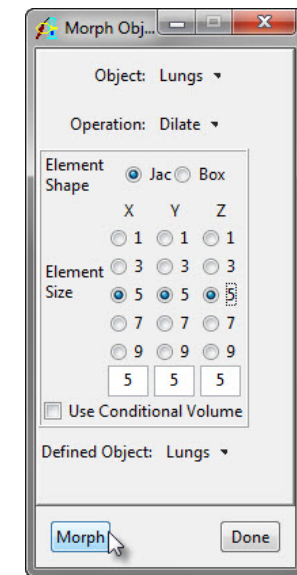
22. Exit the Volume Edit module.



Figure 4



Figure 5



Figure 6



Figure 7

# Volume Edit: Advanced Segmentation

In this exercise we will review some of the additional tools and options in the Volume Edit module designed to enhance your segmentation capabilities. The exercise will demonstrate the application of the Edge Strength and Walls tools to set 3D limits on the image data set. The exercise will then explore the Object Extractor, Object Separator, and Oblique Cutting options.

1. Download the **Cardiac_CT.avw** data set from **www.analyzedirect.com/data**. Unzip the file and then use **File > Load** to load the data set into Analyze.

2. Select the **Cardiac_CT** data set and open **Segment > Volume Edit**.

3. In the **Edge Strength** tab check the **Use Edge Strength.**

4. Set **Edge Strength Threshold** to **94** (figure 1). Note: The Edge Strength option allows users to mask the loaded volume with a threshold range of sobel filter gradients, aiding with the segmentation of objects.

5. Next select the **Walls** tab. Check **Define walls to limit semi-automated operations**. Now select **Draw Wall** and then set **Wall Type** to **Line** (figure 2).

6. Using the slice slider below the transverse image, move to slice **138**. Draw a line along the mitral valve between the left ventricle and left atrium (figure 3).

7. Now move to transverse slice **171**. Draw another line along the mitral valve (figure 4). Note: Using the transverse slice slider move back to slice 138. Note that the wall defined between slice 138 and 171 has interpolated between the two positions over the slices in between. This wall will act as a 3D limit across the volume aiding with segmentation of the data. Move back to slice 171 before proceeding.

8. In the object control panel click the **Add Object** button
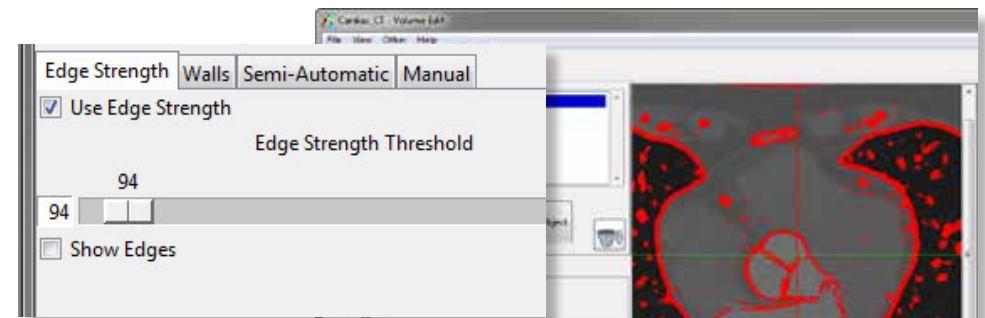

Figure 1
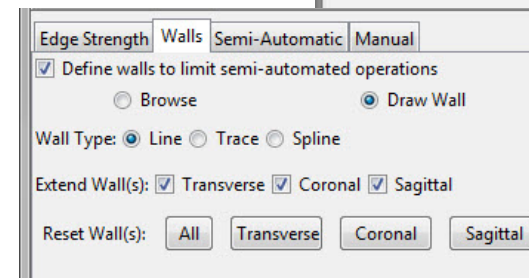

Figure 2
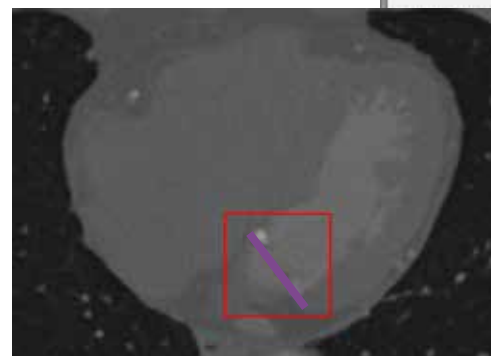

Figure 3
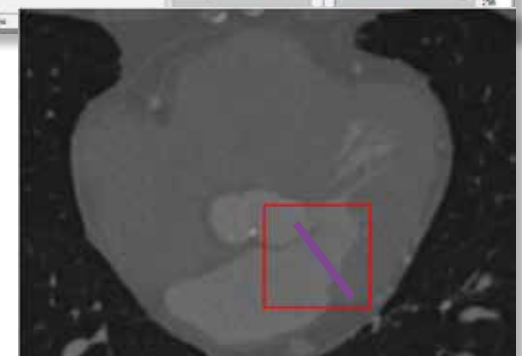

Figure 4

(figure 5).

9. Select the **Semi-Automatic** tab and choose the **Object Extractor** option.

10. Using the Sagittal slice slider move to slice **228**.

11. Click in the middle of the left atrium to set a seed point (figure 6). Set the following threshold range: **Minimum**: **235** and **Maximum**: **2213**.

12. Click **Extract Object** (figure 7). Note: The 3D limits specified by defining walls in the transverse orientation prevented the aorta from being included as part of this segmented object.

13. Click the **Add Object** button and move to transverse slice **262**.

14. Click in the middle of the aorta to set a seed point (figure 8).  Note: The module remembers the previous threshold range set (if the seed pixel value is within the threshold range) and will automatically populate the minimum and maximum threshold values.

15. Click **Extract Object** (figure 9).

16. To enable the transparency rendering view right-click on the rendering and select **Transparency**.

17. Click **Add Object**.
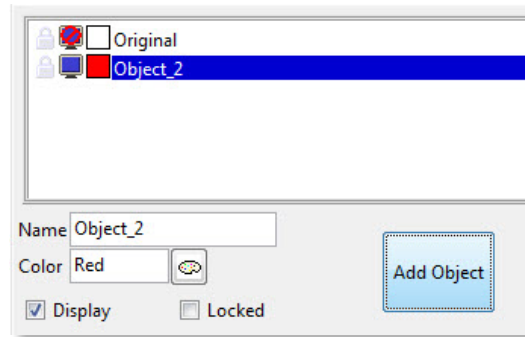

Figure 5
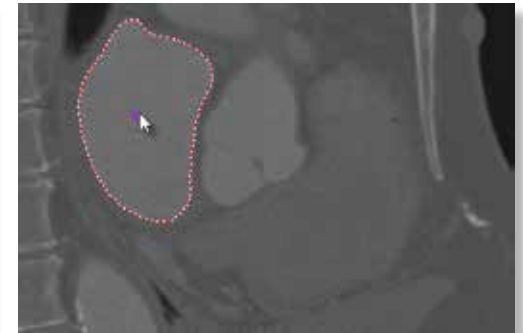

Figure 6
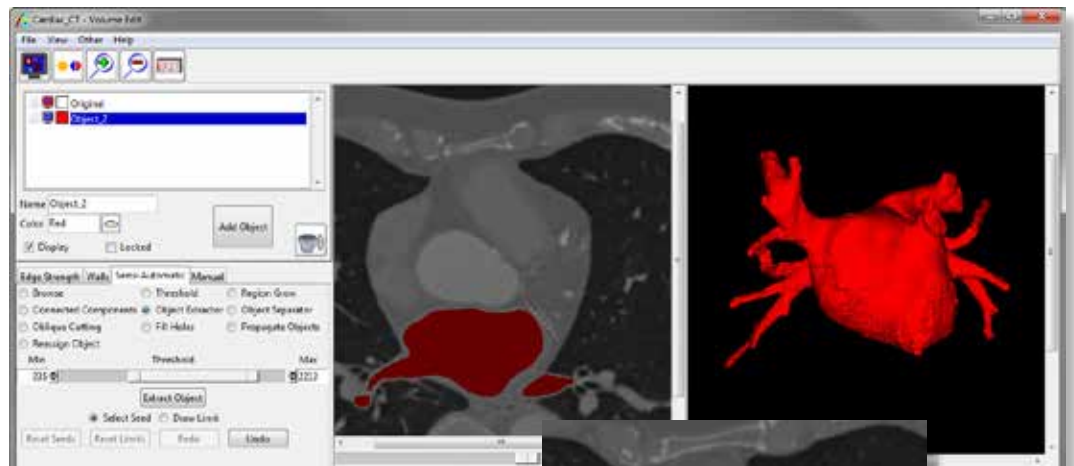

Figure 7
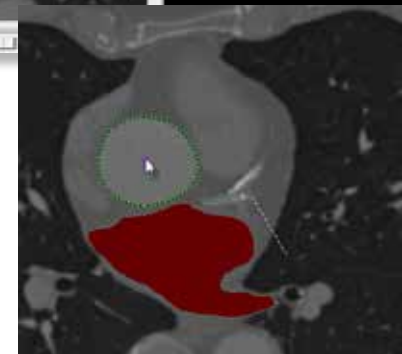

Figure 8

# Volume Edit: Advanced Segmentation

18. Next select the **Object Separator** option.

19. On the rendering click to set a seed point on the aorta.

20. Then set a second seed point on the left ventricle below the aortic valve.

21. Now click **Separate**. The aorta will be split into two objects (figure 10).

22. Click **Add Object**.

23. Now select the **Browse** tool. Using the middle mouse button (or the left-mouse button + CTRL key) rotate the rendering of the heart so you can clearly see the pulmonary vein.

24. Select the **Oblique Cutting** option and then click on the pulmonary vein. The Volume Edit interface will update to show the **Oblique Cutting** interface. Note: The oblique plane can be moved or rotated interactively using the orthogonal images or the rendering.

25. Right-click in the oblique image and select the **Dimensions/Increment** option. Set the **Width** to **50** and the **Height** to **50**, then click **Done**.

26. Click the **Cut** button in the manual control panel to separate the pulmonary vein into the new object (figure 11).

27. Click **Browse** to return to the regular Volume Edit interface.

28. Select **File > Save Object Map** to save your work.

29. Close the Volume Edit module.
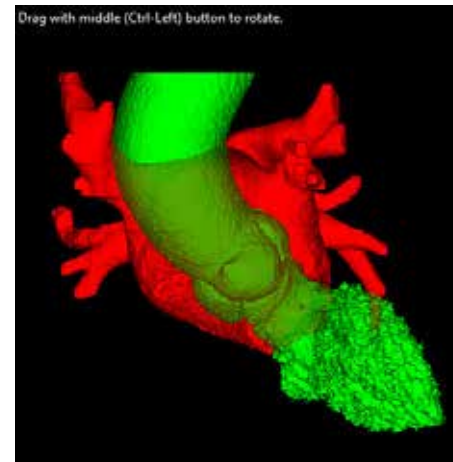


Figure 9
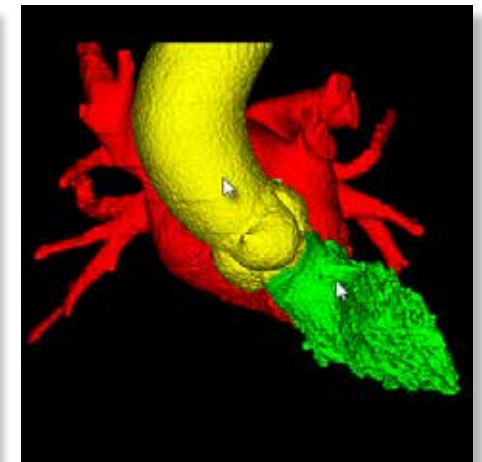


Figure 10
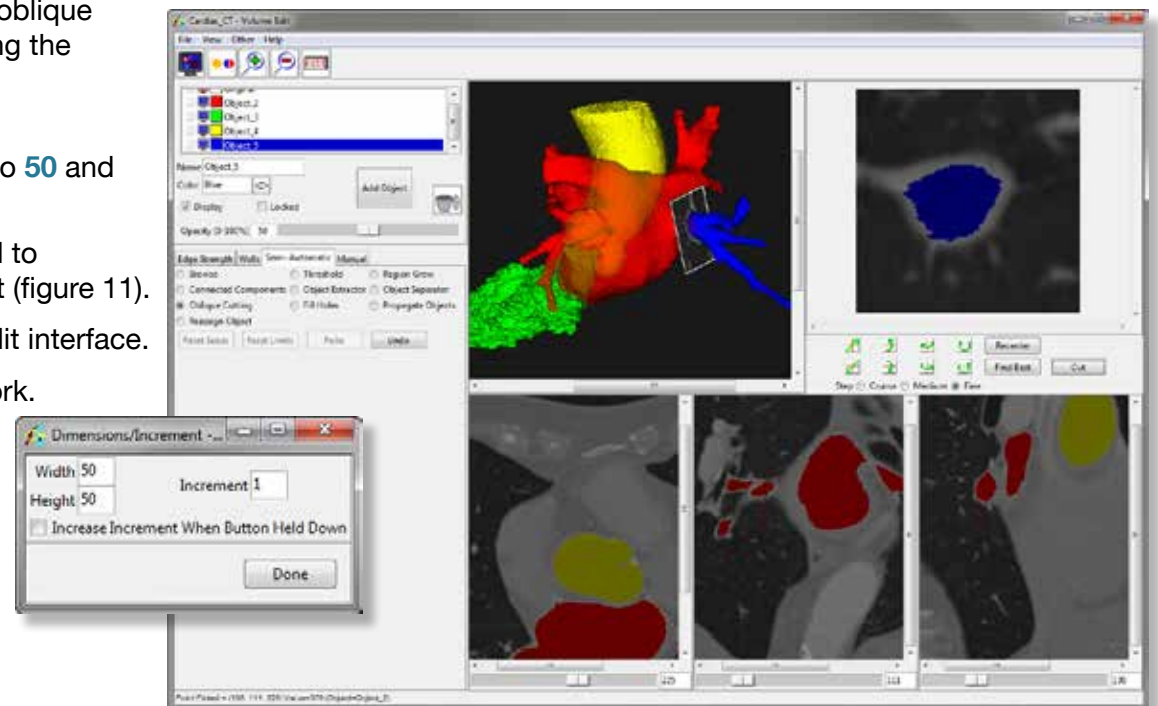


Figure 11

# Volume Edit: Liver Segmentation

Manual segmentation is often necessary when semi-automatic segmenation fails. While manual segmentation can be time consuming, Analyze has tools to speed up segmentation time. The propagate regions option uses shaped-based interpolation to extend the definition a region to slices on which it was not defined. For example, if the user defined a region on every third slice, the tool could be used to fill in the region on the slices in between.

1. Load the **CT_Liver.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Volume Edit** module (**Segment > Volume Edit**).

3. Click on the **Intensities** button and adjust the minimum and maximum intensities.

4. Use the slice slider bar underneath the Coronal view and navigate to slice 100

5. Select the manual tab and then the **Spline Edit** tool. Check the **Smart Edge** option and set the **Sensitivity** to **3**.

6. Begin clicking around the outside of the liver on the Coronal slice 100 (figure 1). Once finished double click to close the spline.

7. Once the spline has been closed and the points are correctly set, click **Apply**.

8. Navigate to Coronal slice **125**. Use spline edit to define the liver and click **Apply**.

9. Repeat the same process for Coronal slice **150** & **175** (figure 2).

*note*   - Control points can be moved using the middle mouse button (or <Shift> + Left mouse button).
   - To add a control point click with the left mouse button.
   - To delete a control point, right click on the control point and select "Delete Control Point".



Figure 1



Figure 2

**AnalyzeDirect**

# Volume Edit: Liver Segmentation

10. Select the **Semi Automatic** tab and click on the **Propagate Objects** option.

11. Set the **Propagation Type** to the **Current Object** and select **Coronal**.

12. Click **Propagate**.

13. The module will use shape-based interpolation to generate regions on the slices between the defined regions (figure 3).

14. Close the module before proceeding to the next exercise.



Figure 3

AnalyzeDirect

# Morphology

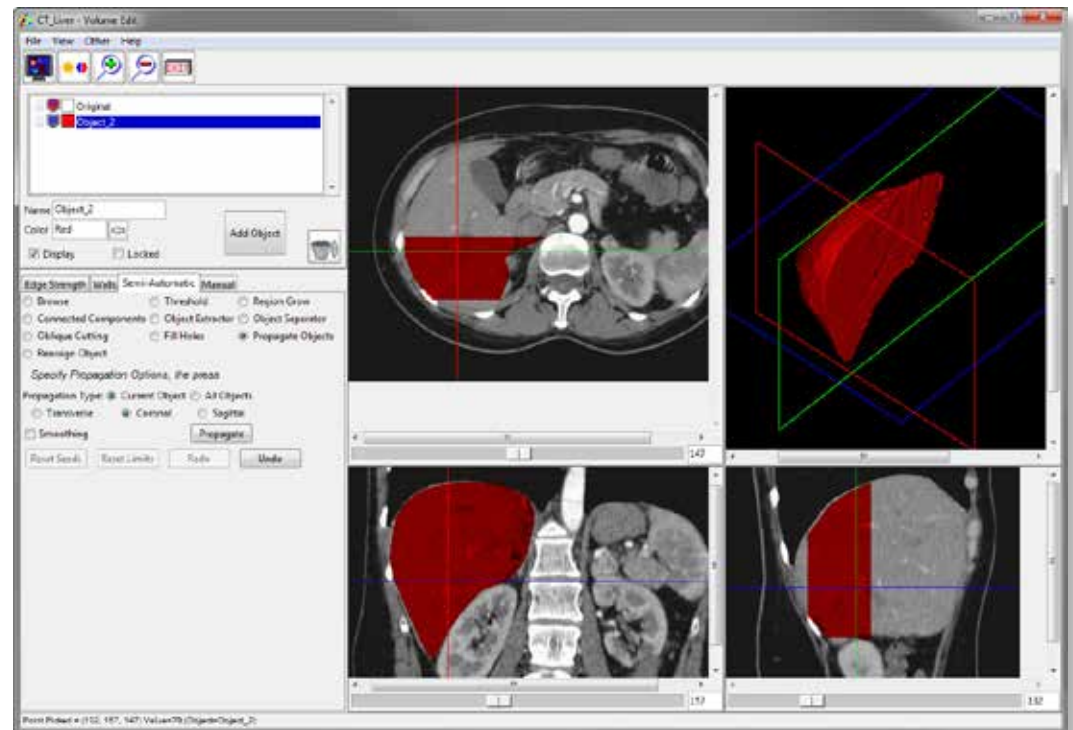The Morphology module applies 1-D, 2-D, or 3-D mathematical morphological transformations and object topology operations to a data set. This exercise will demonstrate the morphological segmentation tools available in the module by showing how to segment the brain from an MRI data set.

1. Load the **MRI_3D_Head.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Morphology** module (**Segment > Morphology**).

3. From the **Generate** menu, open the Slice tool. Move the slice slider to slice 130.

4. Open the **Step Editor** window (**Generate > Step Editor**) (figure 1).

5. Click the **Threshold** button. In the Step 1: Threshold window returned, set the **Threshold Min** to **65**. Click **Threshold Volume**. In the window returned, select **Change a Copy of the Loaded Volume**.

6. Select **Generate > Display Section(s) > Current** to review that data.

7. Select **File > Save Volume**. Save the volume as **MRI_3D_Head_bin**.

8. Click the **Erode** button. In the Step 2: Erode window, change the **Element Depth** to **3** and change the value **Iterations** to **2**. Click Erode Volume (figure 2).

9. In the Step Editor window, click **Transform Volume**. A dialogue box will be returned, select **Yes**.

10. Click **Connect**. Change **Max. No. of Components** to **1**. Click **Connect Volume**.

11. In the Step Editor window, click **Conditional Dilate**. In the Conditional window, change **Element Depth** to **3** and change **Iteration** to **1**. Next load the conditional volume by clicking the Volume button. Use the window returned to select the MRI_3D_ Head_bin.avw data set saved in step 7. Press the **Cond. Dilate Volume** button.

12. To view your segmentation, select **Generate > Display Section(s) > Current** (figure 3).

13. The binary segmentation is available in the Analyze workspace. To obtain a suitable volume for further analysis multiply the binary volume by the input grayscale volume using the Image Calculator or Image Algebra modules.

14. When you are finished reviewing, close all windows related to the Morphology module before proceeding to the next module.

*note* Notice the left side of the Step Editor window; as operations are selected from below the Morph Operations, the sequence of steps is maintained on the left.
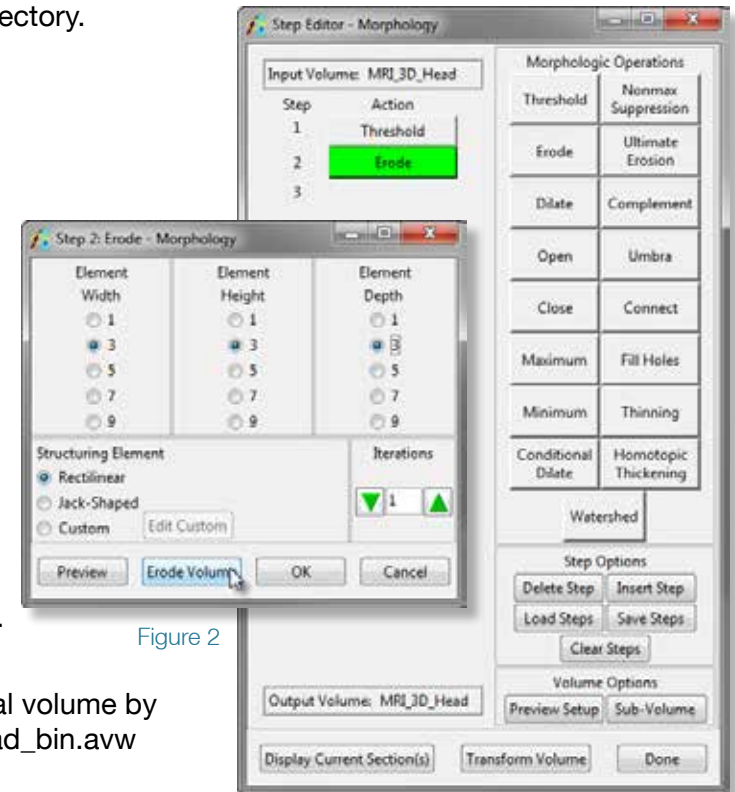


Figure 2



Figure 1



Figure 3

# Watershed: Automated Segmentation

The goal of this exercise is to demonstrate how to automatically strip the skull from in a T1- or T2-weighted MRI scan.

1. Load the **MRI_3D_Head.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Watershed** module (**Segment > Watershed**).

3. The Watershed module default parameters usually allow for a successful segmentation of the brain. Check the **Always Display** option and view the red pixels that define the 'Pre-Fill' level on different slices and orientations. Do not change the Pre-Fill Value (49).

4. Click **Watershed Segment Volume** to initialize the automatic segmentation.

5. After the automatic segmentation process has completed, the **Results** tab is automatically selected (figure 1). Each segmented object will appear as a different random color in the image display.

6. With the **Render Selected Object** option selected, click on the object that represents the brain in the image display.

7. The Render Tool will automatically be returned (figure 2), allowing you to review the segmented objects from difference orthogonal orientations. You can also click and drag the rendering to a new view in the Render Tool image display.

8. Select the **Create Masked Volume from Selected Object** option from the Results tab. Then, click again on the object that represents the brain. The Compare window that appears allows you to review the original and segmented volume side-by-side, slice-by-slice in different orthogonal views.

9. The File menu provides options to save the segmented volume, the masked volume, and create an object map of the segmented object.

10. Choose **File > Save Masked Volume**. In the window returned, set Destination to Analyze Workspace and then click **Save Volume**. The object clicked on in step 8 after selecting 'Create Masked Volume from Selected Object' will be saved to the Analyze workspace. Click **Done** to dismiss the Save Masked Volume window.

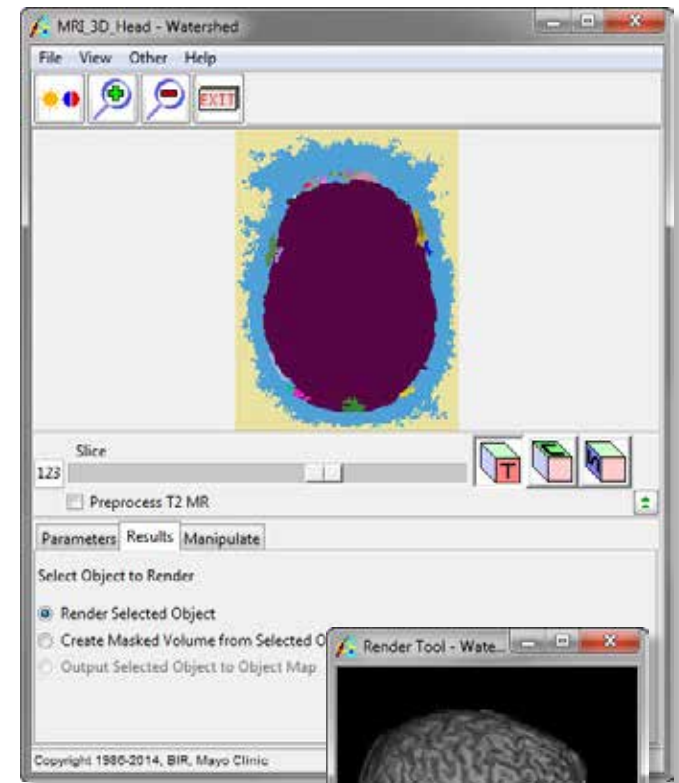11. Close all windows before proceeding to the next exercise.
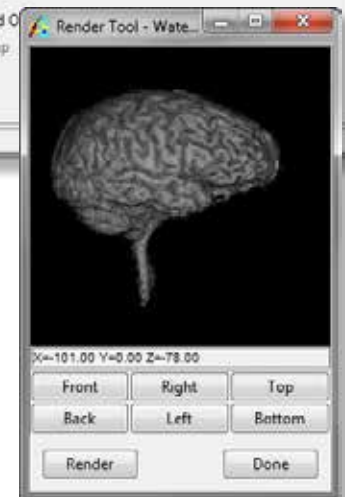


Figure 1



Figure 2

AnalyzeDirect

# Multispectral Classification

The goal of this exercise is to demonstrate the use of the Scattergram tool in the Multispectral Classification module to illustrate the various supervised classifiers in the multispectral measurement space.

1. Load the **MRI_multi.avw** data set from the **$:\BIR\images\TutorialData\ MultiSpectralTutorial** directory. This file contains a spatially co-registered MRI T1 and T2 volume of the same patient.

2. Open the **Multispectral Classification** module (**Segment > Multispectral Classification**).

3. Open the **Scattergram** window (**Samples > Scattergrams**).

4. In the Scattergram window (figure 1), move the **Slice** slider bar to slice 14. The T1 and T2 sections are displayed side-by-side along with the scattergram of the pixels. To increase the image display size, change **Single** to **Double** in the drop-down menu next to the 'Slice' slider bar.
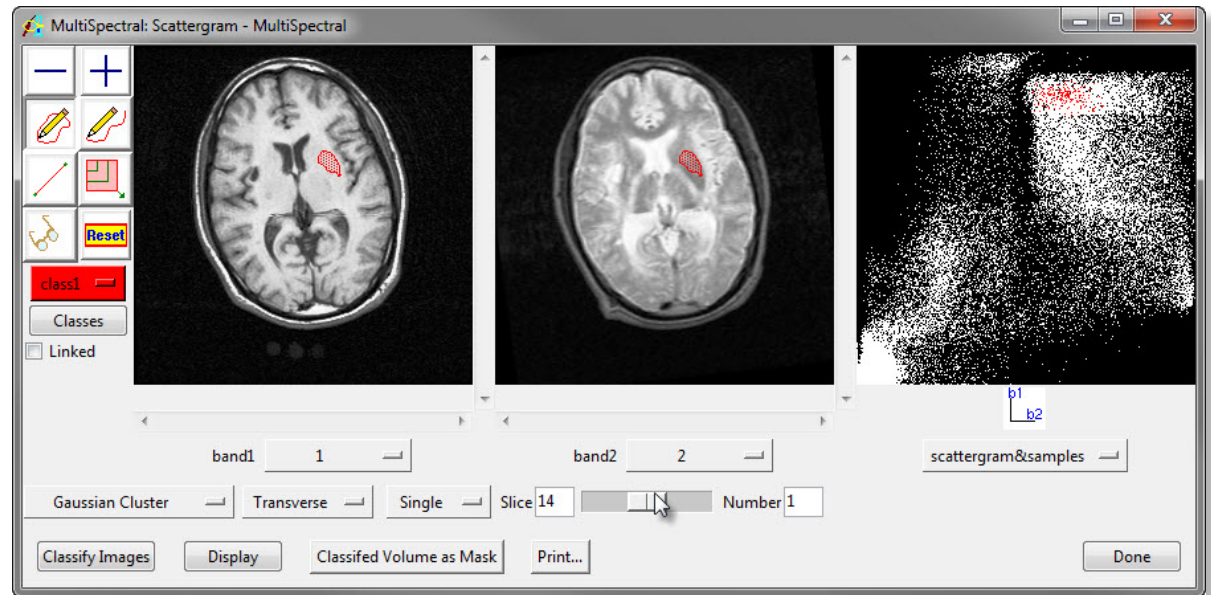


Figure 1

5. Select the **Closed Trace** tool and define a small region of white matter (central brain tissue) as class 1 by drawing on the image display. The paired values found in this region are colored red in the scattergram display and on the image displayed in the main Multispectral Classification window (figure 2).

6. Choose 'class 2' from the **Classes** drop-down menu before starting the trace. Select the **Curved Line** tool and define a small region of grey matter (peripheral brain tissue) as class 2. The paired values will show as green in the scattergram and in the image display.

7. Select the **Closed Trace** tool and define a small region of cerebrospinal fluid (in the central ventricles) as class 3.



Figure 2

AnalyzeDirect
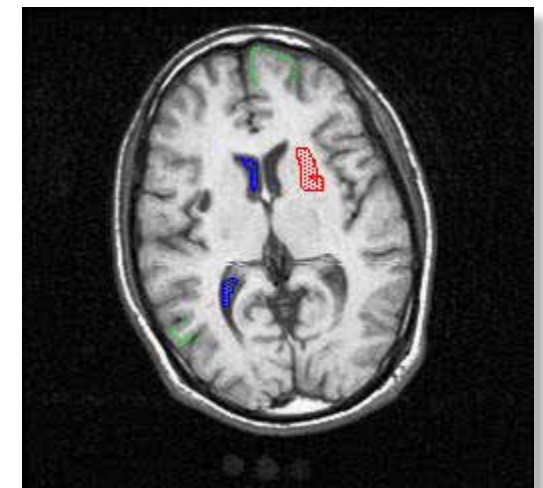
# Multispectral Classification

8. Click **Classify Images**. The Gaussian Scattergram Classifier window will automatically be returned (figure 3), click **Classify**. Click **Done** to dismiss the window.

9. In the main Multispectral Classification window, the classified image will be returned (figure 4).

10. Choose **Scattergram & Classified** from the drop-down menu below the far right pane of the Scattergram window to view the Gaussian class boundaries derived from the samples (figure 5).

11. By selecting classifiers other than 'Gaussian Cluster' in the Scattergram window before clicking Classify Images, other supervised classifiers can be demonstrated on the same samples.

12. Close the Multispectral Classification module before proceeding to the next exercise.

Figure 4

Figure 3

Figure 5

AnalyzeDirect

# Object Extractor: Automated Brain Segmentation

The Object Extractor module applies thresholding, morphology erosion and dilation, and region growing steps in an attempt to automatically segment an object within a volume. This exercise will demonstrate how to use this module.

1. Load the **MRI_3D_Head.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Object Extractor** module (**Segment > Object Extractor**).

3. Open the **Define Region** window (**Generate > Define Region**) to begin the segmentation process.

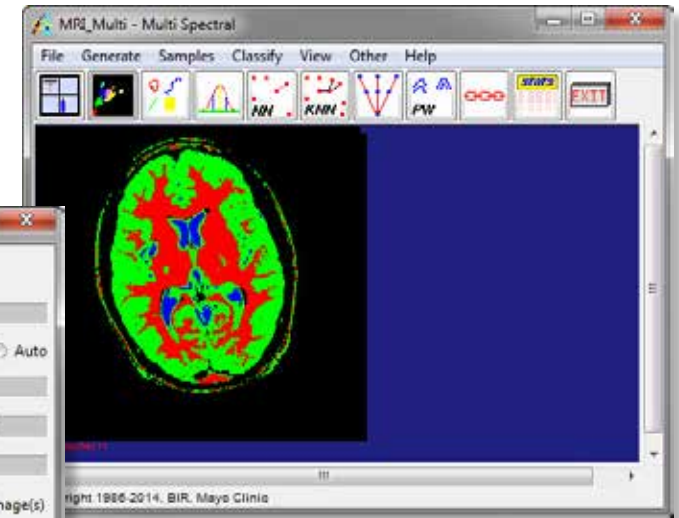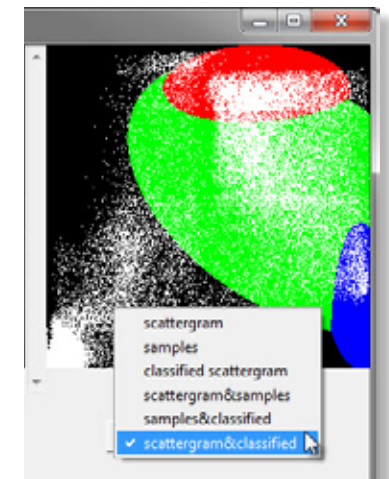4. To define an auto trace on any slice of the volume, first specify a starting slice using the 'Slice' slider bar. **Slice 141** is an excellent starting point for this data set. Note that the orientation can be changed using **Target Slice** directly below the slider bar.

5. In order to define a threshold range for the auto trace, a seed point must be set. Position the cursor near the center of the brain and click to set a seed point.

6. The Define Region window will automatically update (figure 1) to display auto trace parameters. Use the double-ended slider bar now available to set the **Threshold Minimum** to **49** and the **Maximum** to **140**.

7. Click **Extract Object** to start the object extraction process. The grayscale copy of the extracted object will automatically be saved to the Analyze workspace.

8. Once the process is complete, a rendering of the extracted object will be displayed in the main Object Extractor window. The **Render Tool** will also automatically be returned, allowing you to view the object from different orientations (figure 2).

9. The resulting extraction can be further examined in the Compare window (**Generate > Compare**). The Compare window will allow the user to compare the original and segmented volume slice-by-slice.

10. If the extraction is not satisfactory, the data may be re-segmented by clearing the regions in the Define Region window (**Generate > Define Region**) and selecting a new seed point and threshold range.

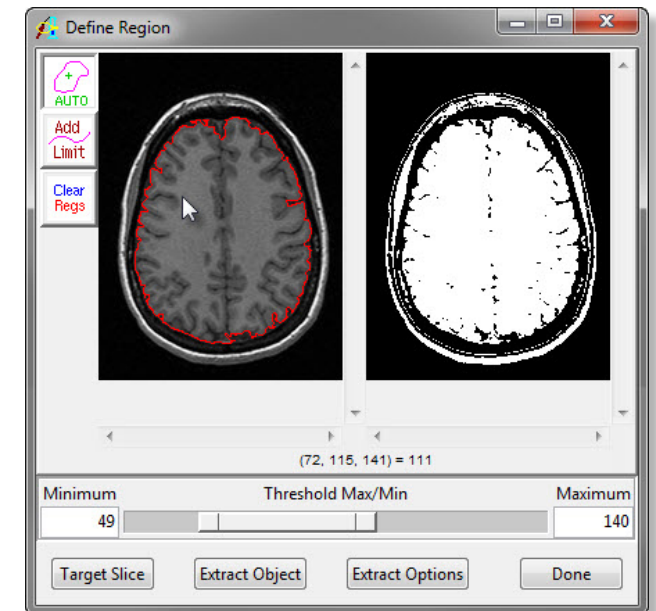11. Close the Object Extractor module before proceeding to the Additional Tasks.
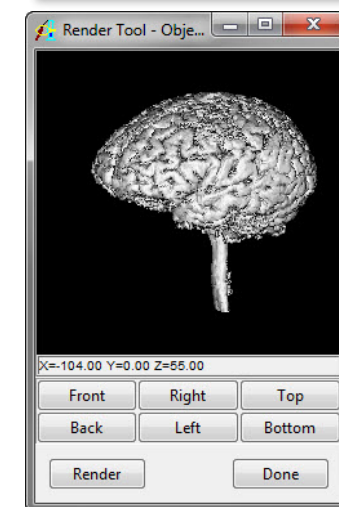


Figure 1



Figure 2

AnalyzeDirect

# Object Extractor: *Creating an Object Map*

As introduced in earlier exercises, an object map is a special image file used by Analyze to partition and identify structures as belonging to a particular segmented object. Voxels in the image volume correspond directly, on a one-to-one basis, with a voxel in the object map, whose value assigns the voxel to a particular segmented object. Since object map files can also be loaded into other Analyze modules, the same objects within an image volume can be referenced for a variety of purposes (see Exercise 47: Region of Interest Measuring Objects in Object Maps). This exercise will demonstrate how to create an object map in Object Extractor.

1. Select the **MRI_3D_Head.avw** data set loaded in the Analyze workspace and open the **Object Extractor** module (**Segment > Object Extractor**).

2. Open the **Define Region** window (**Generate > Define Region**) and set the **Target Slice** to **141**.

3. Click inside the brain to set a seed point. Set the **Threshold Minimum** to **49** and the **Maximum** to **140**.

4. Click **Extract Options** and set the **Result** to **Object** (figure 1). A dialog box will be returned asking if you would like to create an object map, click **Yes** (figure 2). Click **Done** to dismiss the **Extract Options** window.

5. In the Define Region window, click **Extract Object** to start the object extraction process.

6. Once the extraction process is complete the object will be displayed in the Render Tool (figure 3), allowing you to view the object from different orientations.

7. The object map will not be automatically saved, if you wish to save the object map choose **File > Save Object Map.**

8. Close the Object Extractor module. To learn how to create a binary object with the Object Extractor proceed to the next Additional Task.
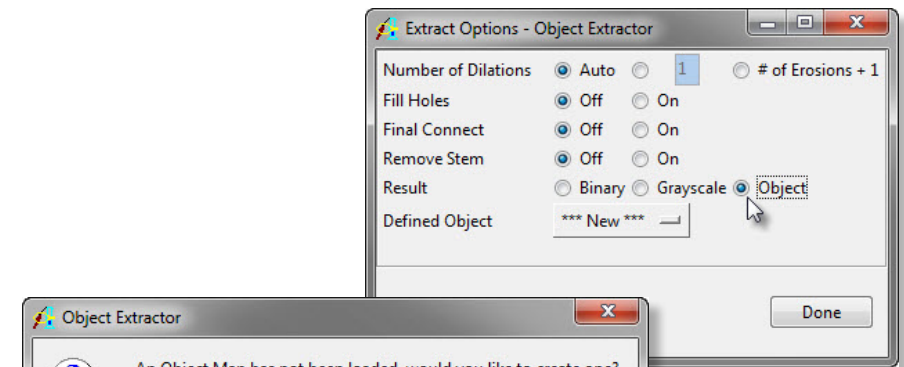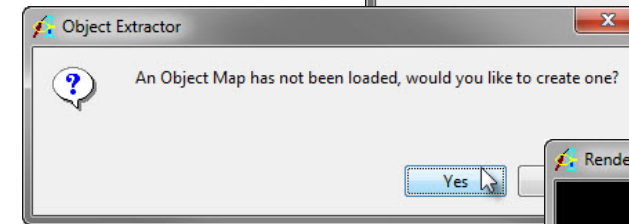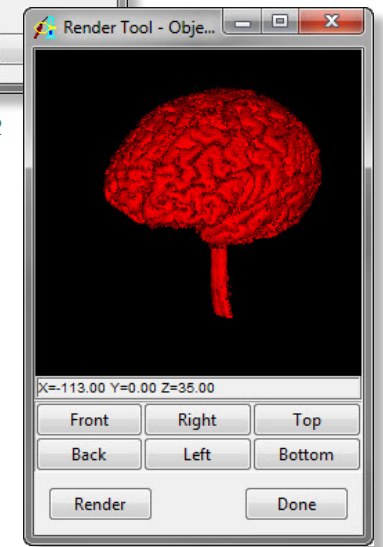
Figure 1

Figure 2

Figure 3

# Object Extractor: *Creating a Binary Object*

Occasionally it is necessary to save the segmented object as a binary object, as opposed to a grayscale object like in the first part of this exercise. This additional task will demonstrate how to achieve this.

1. Select the **MRI_3D_Head.avw** data set loaded in the Analyze workspace and open the **Object Extractor** module (**Segment > Object Extractor**).

2. Open the **Define Region** window (**Generate > Define Region**) and set the **Target Slice** to **141**.

3. Click inside the brain to set a seed point. Set the **Threshold Minimum** to **49** and the **Maximum** to **140**.

4. Click **Extract Options** and set the **Result** to **Binary** (figure 1). Click **Done** to dismiss the Extract Options window.

5. In the Define Region window, click **Extract Object** to start the object extraction process.

6. Once the process is complete, a rendering of the extracted object will be displayed in the main Object Extractor window. The Render Tool will automatically be returned again, allowing you to view the object from different orientations. The segmented binary brain will be automatically saved to the Analyze workspace and can now be used with any other Analyze module.

7. Close the Object Extractor module before proceeding to the next Additional Task.



Figure 1

AnalyzeDirect
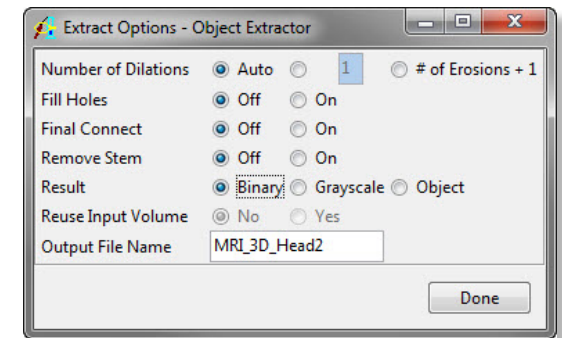
# Object Extractor: *Automatic Brain Stem Removal*

The Object Extractor module now provides the option to automatically remove the brain stem from your segmented brain. This task will demonstrate how to segment and remove the brain stem.

1. Select the **MRI_3D_Head.avw** data set loaded in the Analyze workspace and open the **Object Extractor** module (**Segment > Object Extractor**).

2. Open the **Define Region** window (**Generate > Define Region**) and set the **Target Slice** to **141**.

3. Click inside the brain to set a seed point. Set the **Threshold Minimum** to **49** and the **Maximum** to **140**.

4. Click **Extract Options** and set the **Remove Stem** option to **On** (figure 1). Click **Done** to dismiss the Extract Options window.

5. In the Define Region window, click **Extract Object** to start the object extraction process.

6. Once the process is complete, a rendering of the extracted object will be displayed in the main Object Extractor window. The Render Tool will automatically be returned again, allowing you to view the object from different orientations. The segmented grayscale brain will be automatically saved to the Analyze workspace and can now be used with any other Analyze module.

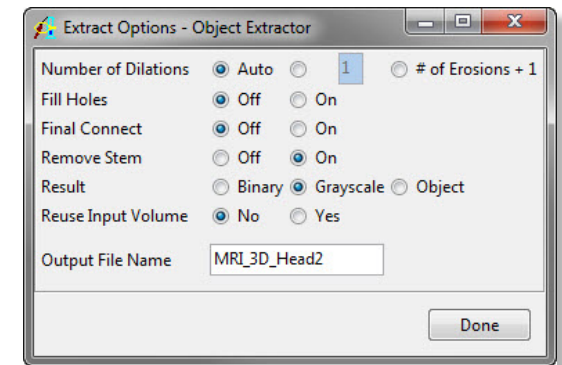7. Close the Object Extractor module before proceeding to the next exercise.
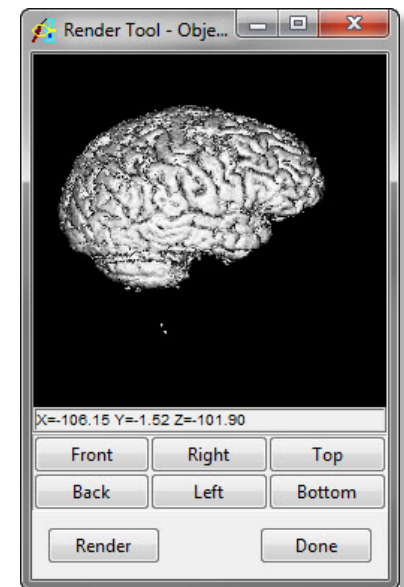


Figure 1



Figure 2

AnalyzeDirect

# Object Extractor: Extracting Multiple Objects

The Object Extractor module supports the creation of multi-object object maps. This exercise will demonstrate the segmentation and separation of the lungs.

1. Load the **CT_Lungs.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Object Extractor** module (**Segment > Object Extractor**).

3. Open the **Define Region** window (**Generate > Define Region**) to begin the segmantation process.

4. To define an auto trace on any slice of the volume, first specify a starting slice using the 'Slice' slider bar. Slice **104** is the default slice, and it is an good starting point for this data set.

5. Position the cursor near the center of the left lung and click to set a seed point.

6. The Define Region window will automatically update (figure 1) to display auto trace parameters. Use the double-ended slider bar now available to set the **Threshold Minimum** to **18** and the **Maximum** to **99**.

7. Click the **Extract Options** button, and set the **Result** to **Object** (figure 2), select **Yes** in the window returned.

8. In the Define Regions window, click **Extract Object** to start the object extraction process. The left lung will be extracted and saved as the object called 'Extracted'. The object will appear red.

9. Open the Define Regions window again, when opened click the **Clear Regions** button. Next, click in the right lung to set a seed point, set the **Threshold Minimum** to **18** and the **Maximum** to **104**.

10. Click **Extract Object** again. The right lung will be extracted and saved as the object called Extracted (2), the object will appear green. In the main Object Extractor module you will see both lungs (figure 3).



Figure 1



Figure 2



Figure 3

AnalyzeDirect

11. The render window will now display both lungs in 3D (figure 4).

12. To change the name and color of each object, go to the **Objects** window (**View > Objects**). Set **Control By** to **Attribute**, and from the drop down menu select the **Name** and **Color** attribute options (figure 5).

13. To save the object map for use in other modules, select **File > Save Object Map**.

14. Close all windows related to the Object Extractor module before proceeding to the next exercise.
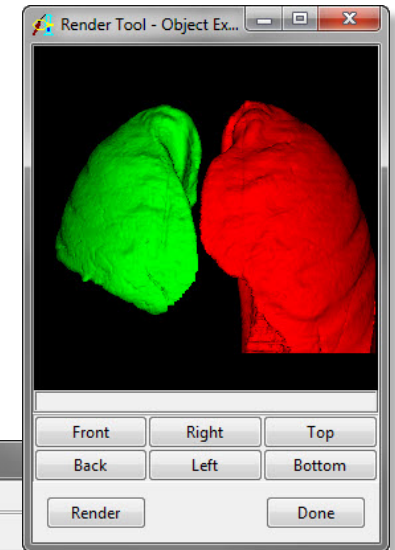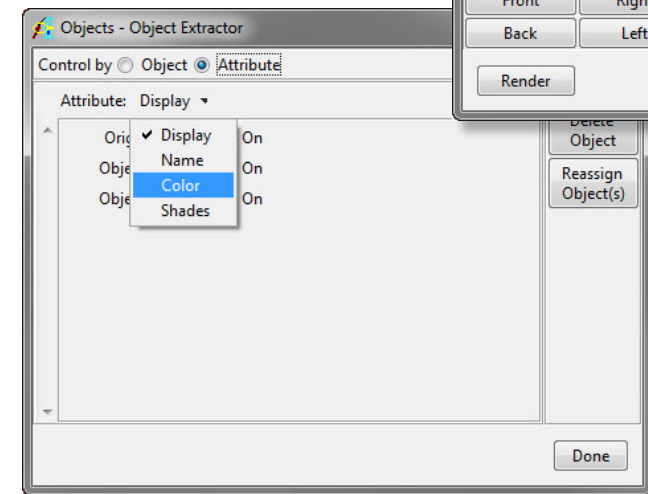
Figure 4

Figure 5

# Surface Extractor: Polygonal Surface Extraction

Polygonal surface extraction is the process of converting an object in the voxel-based volume to a representation of the surface of the object, expressed as sets of vertices and polygons. This conversion must optimally extract a representative surface, with as much detail as possible, but do so with as few vertices and polygons as possible. This exercise will use the Adapt/Deform algorithm to perform such an optimal surface extraction. Often this surface extraction is a precursor to using the surface with other applications, such as CAD/CAM modeling, rapid prototyping (model building), and finite element analysis.

1. Load the **MRI_3D_Head.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Surface Extractor** module (**Segment > Surface Extractor**).

3. Choose **File > Load Object Map** and load the **MRI_3D_Head.obj** object map.

4. Open the **Extraction Parameters** window (**Generate > Extraction**).

5. Click **Objects** at the top of the Extraction Parameters window (figure 1). In the window returned, leave the **Brain** set to **On** and set all other objects to **Off** (figure 2). Click **Done** to dismiss the window.

6. Create a polygonal surface of the 'Brain' object using the Adapt/Deform algorithm with the default parameters. With the **AdaptDeform** tab selected click **Extract**.

7. A dialog box will be returned stating the number of polygons generated. Note the number of polygons (approximately 37,258), then click Done.

8. To create a rendering of the surface model, choose **Generate > Render**. A surface map will automatically be created for the 'Brain' surface, and the **Surfaces** window returned. The rendering will be displayed in the main Surface Extractor window (figure 3).

9. In the Extraction Parameters window change the **Cube Edge Size** to **5** and rebuild the surface by clicking **Extract**. Note, the number of polygons generated (approximately 12,261), then click **Done**.

10. Choose **Generate > Render** to view the extracted surface with the new parameters (figure 4). Increasing the 'Cube Edge Size' will smooth the surface, reducing the number of voxels considered when generating the initial surface estimate, which reduces the polygon count.
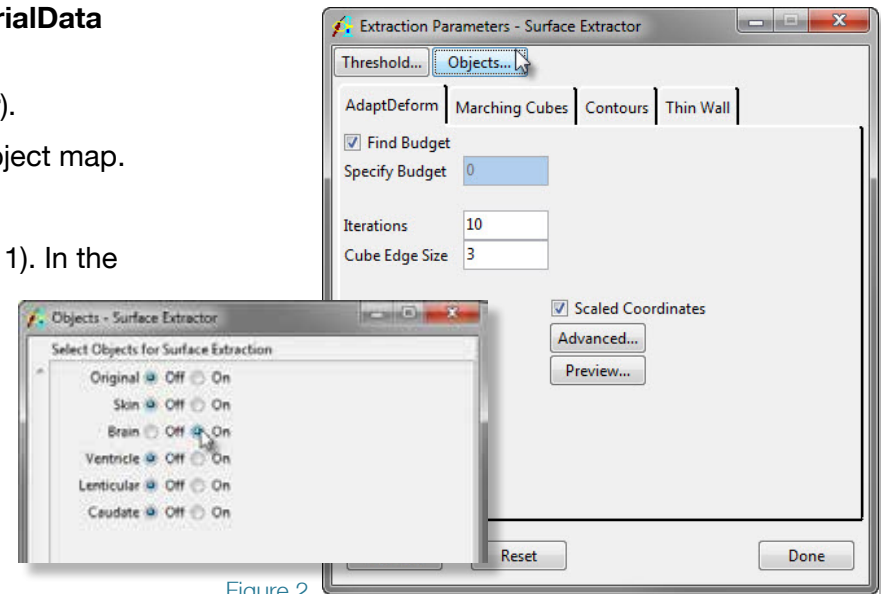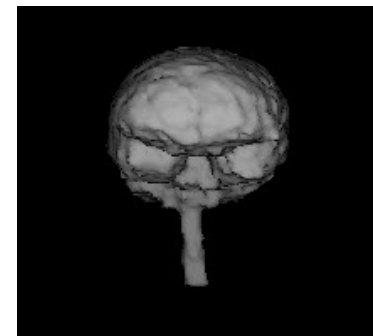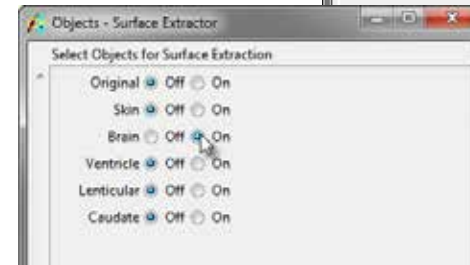
Figure 2

Figure 1

Figure 3

Figure 4

**Analyze**Direct

11. Click **Reset** in the Extraction Parameters window to restore the default parameters ('Cube Edge Size' of 3).

12. Click **Advanced** and change the **Time Step** to **0.5**. Click **Done** to dismiss the window.

13. Rebuild the surface by clicking **Extract** in the Extraction Parameters window. Note the number of polygons generated (approximately 37,258), then click **Done**.

14. Choose **Generate > Render** to view the extracted surface with the new parameters. Increasing the 'Time Step' causes the surface extraction to reach equilibrium faster, producing a smoother surface without altering the polygon count. When the opposite changes are made, the surface will conform to the voxel surface better, resulting in a rougher, more "voxelated" surface.

15. **Decreasing** the **Surface Force** and increasing the **Spring Constant** (also 'Advanced' options) smooths the surface without altering the polygonal count by forcing the polygons to bridge small variations in the voxel surface (the polygons' attraction to the surface is reduced and they become harder to bend).

16. Choose **File > Save Surface > To File** to save the extracted surface to disk.

17. In the Save Surface window returned (figure 6) you can select from the following surface description formats in the **Format** drop-down menu: Alias (.obj), Autocad (.dxf), Compressed Iges (.iges), Iges (.iges), Inventor (.iv), Patran (.out), Ply(.ply) Poly (.poly), 3D Systems (.stl), Binary 3D Systems (.stl), Vrml (.wrl).

18. Close the Surface Extractor module. To learn about extracting the surface of a binary data set, complete the following Additional Task.
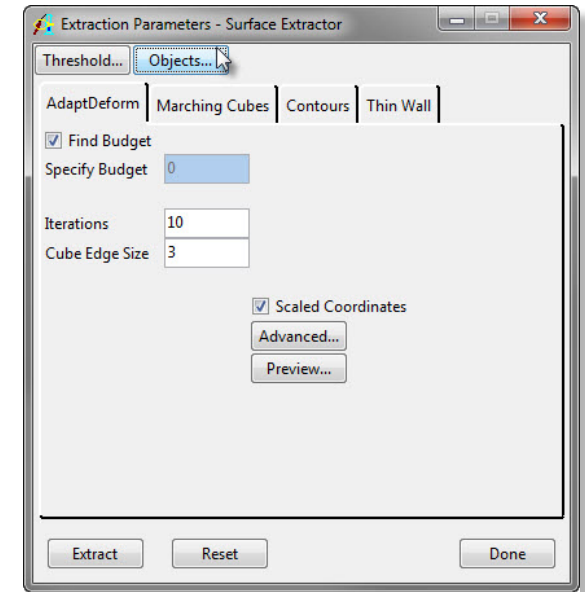
Figure 5
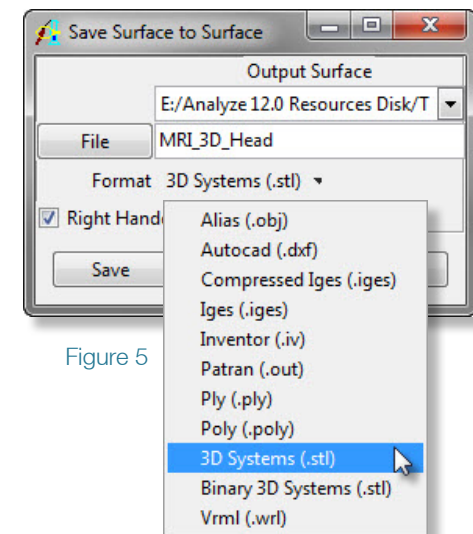
Figure 5

# Surface Extractor: *Extracting a Binary Data Set*

1. Load the **MRI_3D_Brain_Bin.avw** data set from the **$:\BIR\images\ TutorialData** directory.

2. Open the **Surface Extractor** module (**Segment > Surface Extractor**).

3. Open the **Extraction Parameters** window (**Generate > Extraction**).

4. With the **AdaptDeform** algorithm tab selected, click **Extract**.

5. Note the number of polygons generated (approximately 37,504) and choose **Generate > Render** to view the extracted surface (figure 1).

6. Close the Surface Extractor module before proceeding to the next exercise.
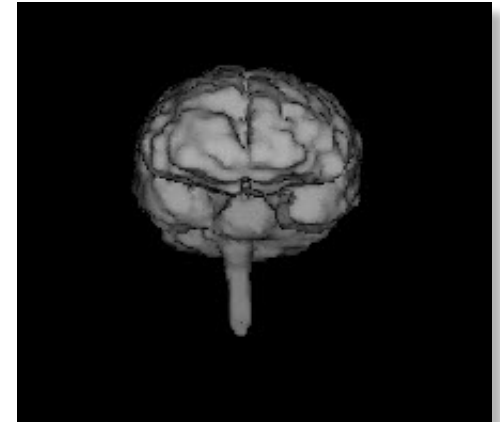


## Supported Surface File Formats

Figure 5

### Polygonal Formats

| | |
|---|---|
| Alias Wavefront | (.obj) Read and Write |
| Autocad | (.dxf) Read and Write |
| IGES | (.iges) Write only |
| Compressed IGES | (.iges) Write only |
| Inventor | (.iv) Write only |
| Patran | (.out) Write only |
| Poly | (.poly) Read and Write |
| Binary 3D Systems | (.stl) Raad and Write |
| VRML | (.wrl) Write only |

### Contour Formats

| | |
|---|---|
| HP 3D | (.hpgl) Write only |
| IGES | (.iges) Write only |
| Compressed IGES | (.iges) Write only |
| Pogo | (.slc) Read and Write |
| 3D Systems Stereolithography | (.slc) Read and Write |
| ASCII Columns | (.txt) Read and Write |

# Surface Extractor: Contour Surface Extraction

Contour surface extraction is the process of converting an object in the voxel-based volume to a representation of the surface of the object, expressed as a series of stacked contours. This surface extraction is a precursor to other applications, such as CAD/CAM modeling, rapid prototyping (model building), and finite element analysis. This exercise demonstrates how to use the Contours algorithm.

1. Load the **MRI_3D_Head.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Surface Extractor** module (**Segment > Surface Extractor**).

3. Choose **File > Load Object Map** and load the **MRI_3D_Head.obj** object map.

4. Open the **Extraction Parameters** window (Generate > Extraction).

5. Click **Objects** at the top of the Extraction Parameters window (figure 1). In the window returned, switch the **Ventricle** to **On** and set everything else **Off**. Click **Done** to dismiss the window.

6. Create a contour surface of the 'Ventricle' object using the **Contours** algorithm with the default parameters. Select the **Contours** tab and click **Extract**.

7. A dialog box will be returned stating the number of slices for which contours were generated. Note the number of slices used (60), then click Done.

8. To create a rendering of the extracted contour model, choose **Generate > Render**.

9. In the Extraction Parameters window, click **Advanced** in the 'Contours' tab. Check the **Subvolume Extraction** option and click **Done** to dismiss the window (figure 2).

10. Rebuild the contour surface by clicking **Extract** in the Extraction Parameters window. Note the number of slices used (108). This resamples and reformats the object and thus changes the number of slices.

11. Choose **Generate > Render** to create a rendering of the extracted contour model (figure 3).

12. Close the Surface Extractor module before proceeding to the next exercise.

Figure 1
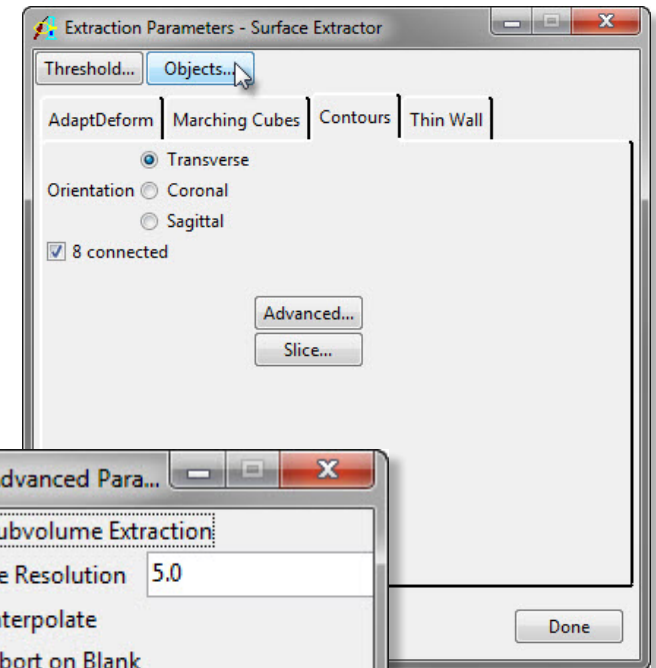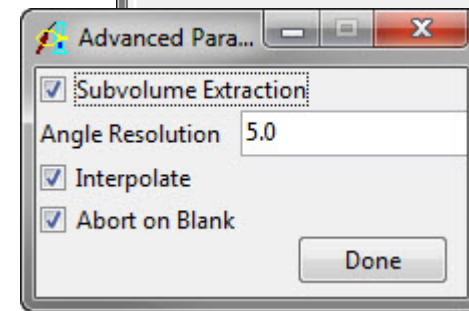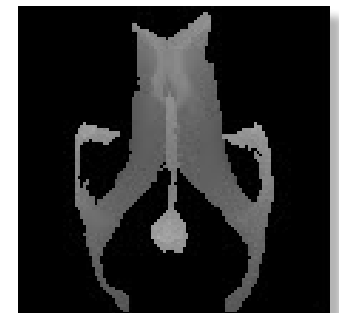
Figure 2

Figure 3

AnalyzeDirect

# Registration

# 2D Registration

The 2D Registration module determines geometric transformation parameters which can be used to align 2D images, section to section by matching common contours or by matching sections to a single base slice. This exercise will demonstrate how to do this using the 2D Registration module to align a series of misaligned 2D slices.

1. Load the **Spinal_Cord** data set from the **$:/BIR/images/TutorialData** folder.

2. Open the **2D Registration** module (**Register > 2D Registration**).

3. Open the **Cursor Link** Tool (**Tools > Cursor Link**).

4. Choose a **Blend** from the right-click menu in the upper right pane.

5. To review the data slice by slice, use the **Match Section** slider bar.

6. If required, slice data can be manually adjusted using the manual adjust control operations.

7. The **% Base Image** allows the combined image display (upper right pane) to fade between the base and match image.

8. Open the **Control** window (**Generate > Control**).

9. Choose between a **Sequential** or **Single** reference registration mode (figure 2):

   **Sequential**: each slice will register sequentially to its neighbor (ie slice 2 to slice 1, slice 3 to slice 2, etc.)
   **Single Reference**: will register each slice to a single base slice (defined with the To Section slider).

10. The **Register Section** and **Thru** slider bars allow users to determine a range of slices to be registered (ie slices 10-20 only).

11. Set the registration mode to **Sequential**, then click **Done**.
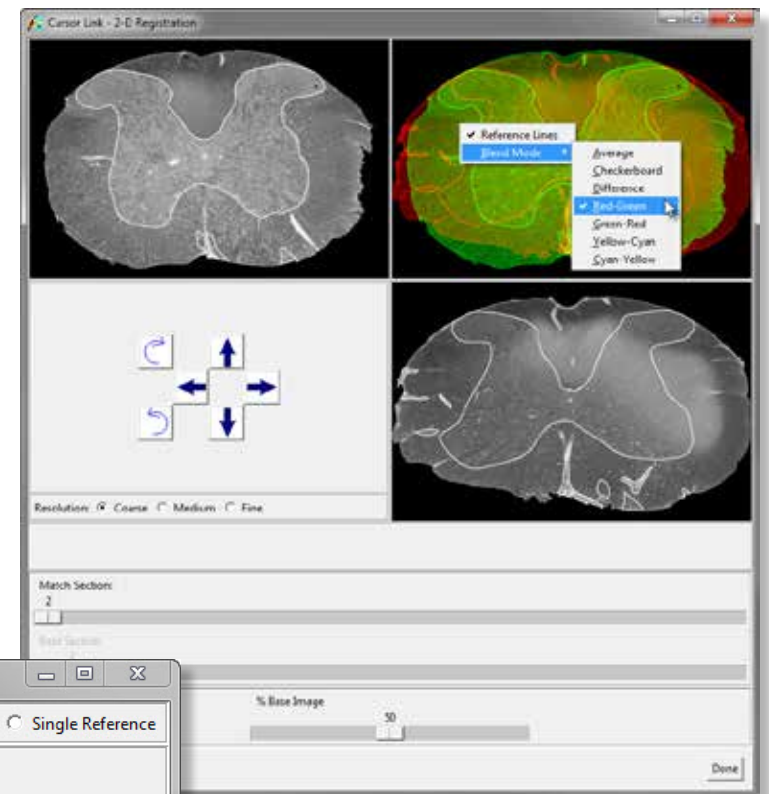
Figure 1

Figure 2

AnalyzeDirect
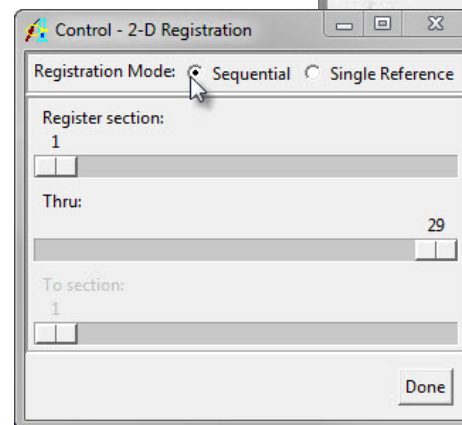
# 2D Registration

12. Open the **Voxel Match** window (**Generate > Voxel Match**), expand the **Threshold**, **Sample Region** and **Search Parameters** options (figure 3).

13. Check the **Show Thresholding** option the image, the cursor link tool will update converting the images to binary representations. Only voxels displayed as white will be considered for the registration.

14. Set the **Minimum threshold** value to **5** to eliminate background noise. Then uncheck the Show Thresholding option.

15. The Sample Region option will allow for defining a region to consider for registration. See the **X Minimum** to **69** and the **X Maximum** to **333**. Then set the **Y Minimum** to **33** and the **Y Maximum** to **237**. Reset the Min/Max X and Y values before proceeding. Note the region is defined on the blended and match image (figure 4).

16. The Search Parameters option allows users to adjust the X and Y Translation range, the Z Relation range and the X and Y Scaling range.

17. Click **Register**. Select **Generate > Transform Slices**, set the **Destination** to **Analyze Workspace**, then click **Go**. The data will be transformed and saved to the Analyze workspace.

18. Compare the input and output data sets to see the effect of the registration on the data.



Figure 3



Figure 4

AnalyzeDirect

# 2D Non-Rigid Registration

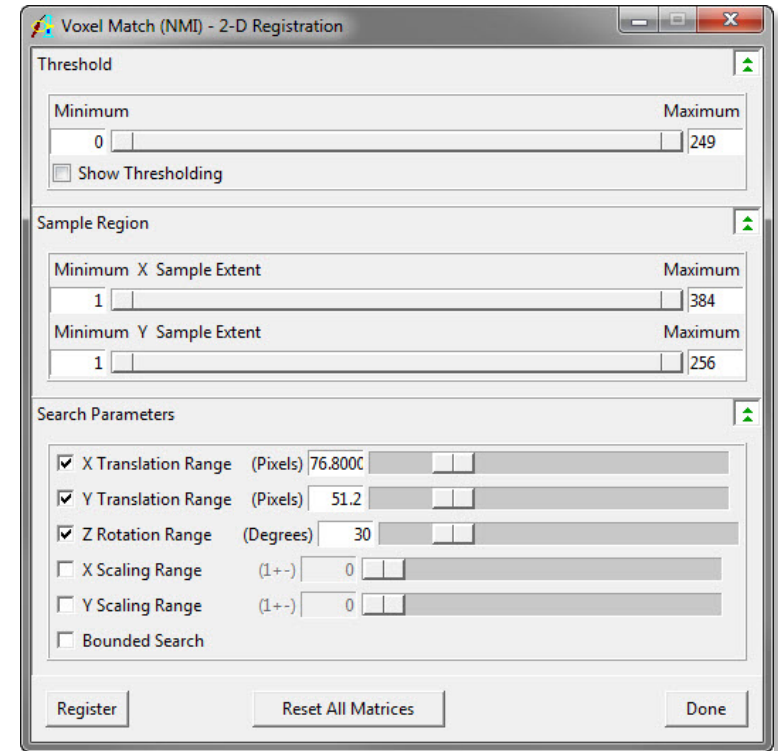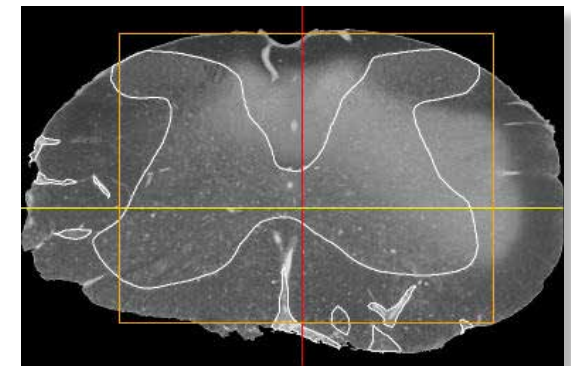The 2D Non-Rigid Registration module applies local Normalized Mutual Information (NMI) image registration in a grid of subregions. The optimized local registration transformations are then interpolated across the image to effect a continuous non-rigid transformation. This exercise will demonstrate how to register two adjacent sections to correct for the difference stretching forces each section has been subjected to.

1. Load the **AdjacentSections** data set from the **C:/BIR/images/TutorialData** folder.

2. Open the **2D Non-Rigid Registration** module (**Register > 2D Non-Rigid**).

3. Open the **Control Window** (**Generate > Control**) (figure 1). Two Registration Modes are provided, Sections or Slabs.

   - **Sections**: allows for each image to be non-rigidly registered to the next.

   - **Slabs**: registration will only be performed at Interfaces between slabs, during transformation the non-rigid transformation is relaxed through the slab.

4. Set the **Registration Mode** to **Sections**. You can now choose between a Sequential or Single Reference registration.

   - **Sequential**: specifies that each section will register sequentially to its neighbor.

   - **Single Reference**: will register each slice to one base slice, the To Section slider is used to select the base.

5. Select **Sequential** (figure 2). Do not close the **Control** window.

6. Open the **Cursor Link** tool (**Tools > Cursor Link**). The Cursor Link window displays two sections; the Base and Match, in their current registration, as well as the two sections overlaid. Right click in the overlay window and select a Blend option from the Blend Mode menu.
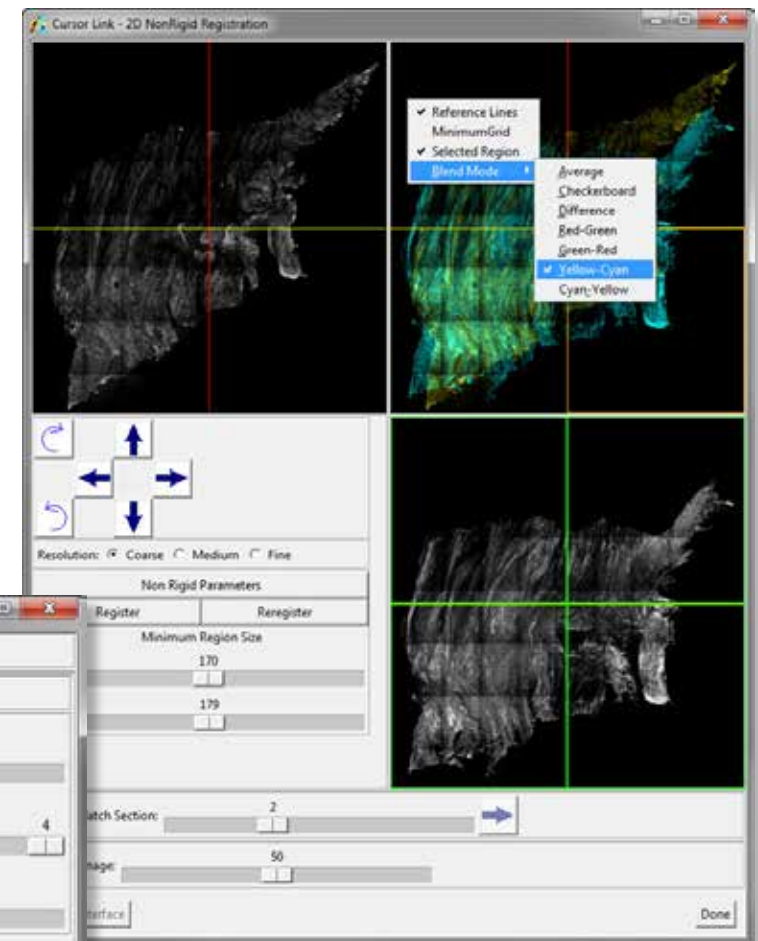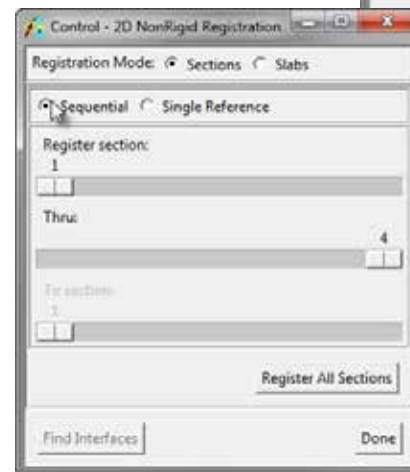


Figure 1



Figure 2

AnalyzeDirect

# 2D Non-Rigid Registration

7. By default, the Match section displays the current minimum region grid (the grid of subregions the local NMI is applied to), shown in green. Note there are 4 regions, to adjust the region size use the Minimum Region Size X and Y sliders To increase the number of regions from 4 to 9, set the **X slider** to **112** and the **Y slider** to **119**.

8. Note the orange box in the overlay window shows the current selected region. To switch this on in the Base and Match windows right-click and select the **Selected Region** option (figure 3).

9. Manual transformations and rotations can be applied to the current selected region in the Match image using the **Manual Adjustment** buttons. Because the regional displacements are interpolated across the image, some transformations may also affect adjacent areas of the image. The **Resolution** options (Coarse, Medium or Fine) below the Manual Adjustment buttons control the amount of displacement. Note, **Fine** resolution is a one pixel translation or one degree rotation, **Coarse** is approximately ten.

10. Click on the **Non Rigid Parameters** button.

11. In the Non-Rigid Match window (figure 4), review the following options:

    • **Threshold**: Check the Show Thresholding option and note the update in the image display as you adjust the threshold range. Only voxels displayed as white will be considered for the registration.

    • **Samples**: specifies the minimum and maximum sampling density.

    • **Process**: these options set limits of confidence on the registration procedure.

12. To Register the sections sequentially click the **Register All Sections** button in the Control window.

13. After registration is complete select **Generate > Transform Slices** from the main 2D Non-Rigid Registration window. In the **Transformation** window returned, set the **Destination** to **Analyze Workspace** and set the **Interpolation** option to **Linear** (default), next click **GO**. The transformed image data will be saved to the Analyze workspace.

14. Close the 2D Non-Rigid Registration module.


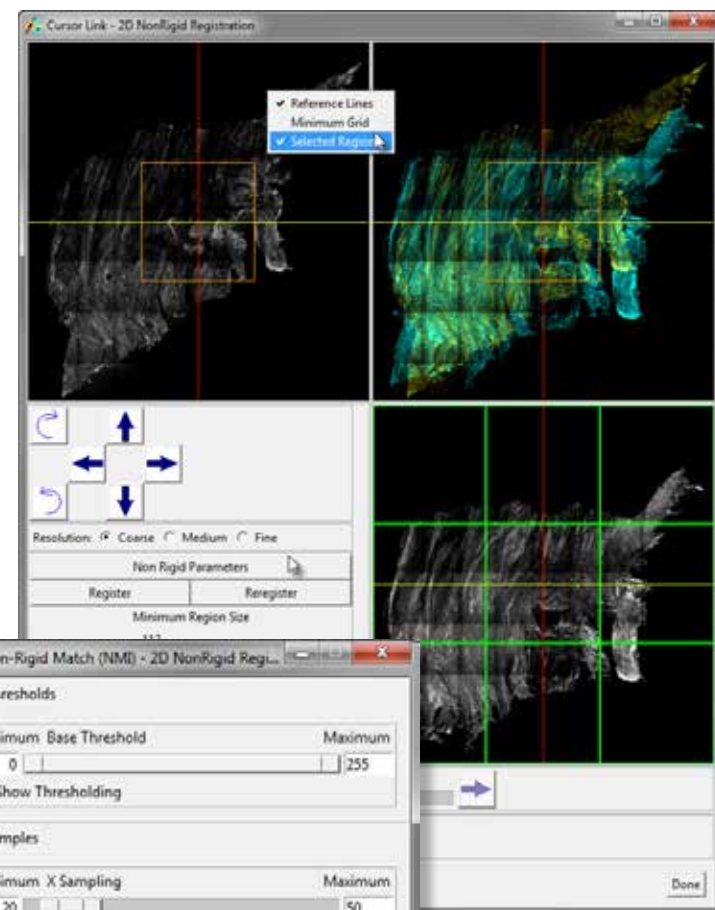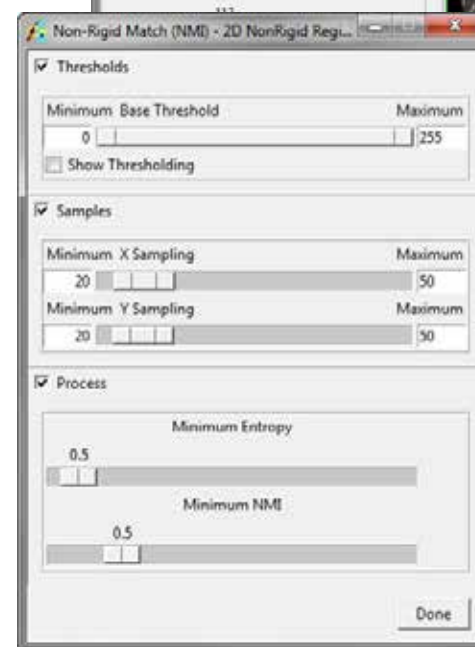
Figure 3



Figure 4

AnalyzeDirect

15. Review the original data and then the registered data (Match2D_out) using the Multiplanar Sections module. Observe the difference in the slice data between the two data sets, specifically slices 2 and 3 in the registered data set (figure 6).
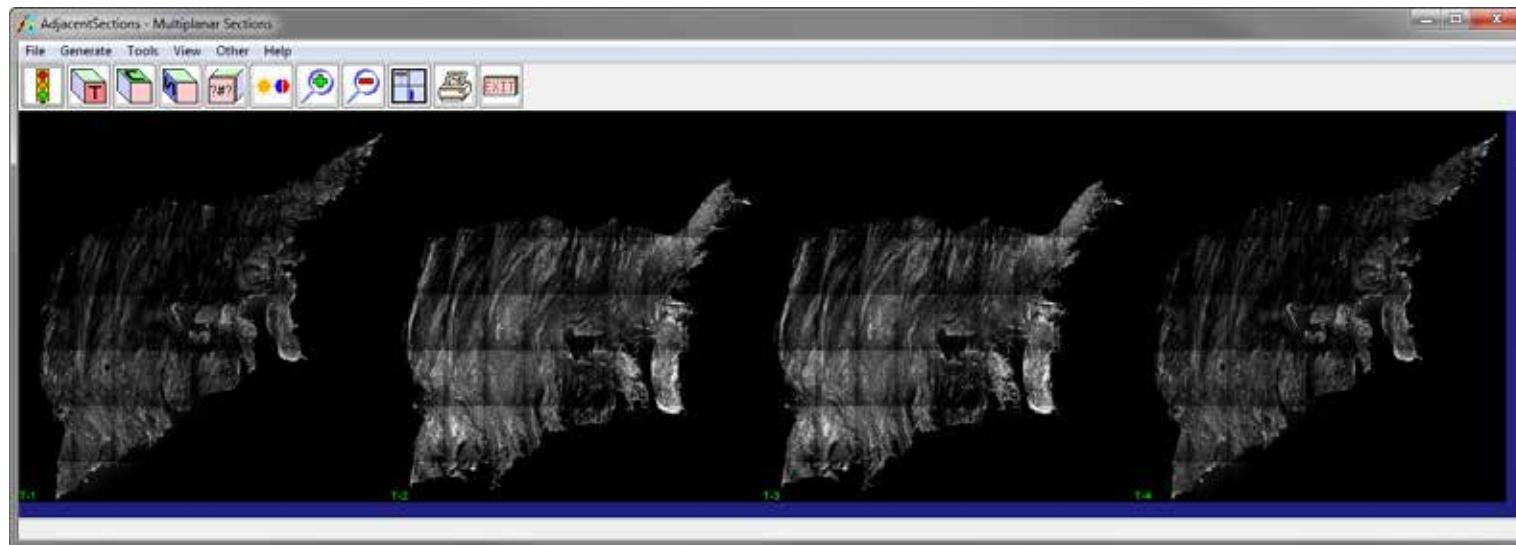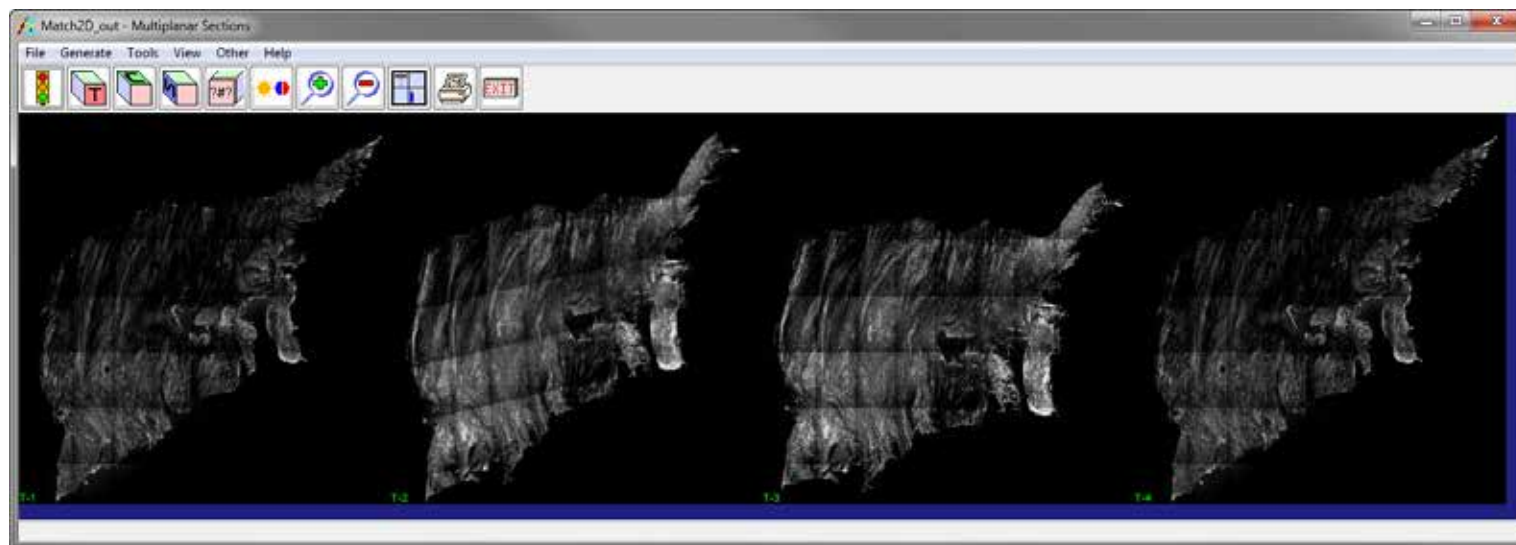


Figure 5



Figure 6

# 3D Surface Registration

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

1. Load the **Edited_MRI_Head.avw** and the **Edited_PET_Head.avw** data sets from the **$:\BIR\images\TutorialData** directory.

2. Select the **Edited_MRI_Head.avw** data set, then while holding down the <**Ctrl**> key, select the **Edited_PET_Head.avw** data set.

3. Open the **3-D Surface Registration** module (**Register > 3-D Surface**).

4. Select **File > Input/Output Ports** to view the import and output ports at the bottom of the main 3-D Surface Registration window. Make sure that Edited_ MRI_Head is the base volume, and Edited_PET_Head is the match volume.

5. Open the **Blend** window (**Generate > Blend**). Set the **Blend Type** to **Green-Red**.

6. Examine the combined images to determine if they need to be registered.

7. Select **Generate > Register** to register the two volumes.

8. Select **File > Save Transformed** and save the transformed PET to the Analyze workspace.

9. Close the 3-D Surface Registration module before proceeding to the next exercise.

AnalyzeDirect
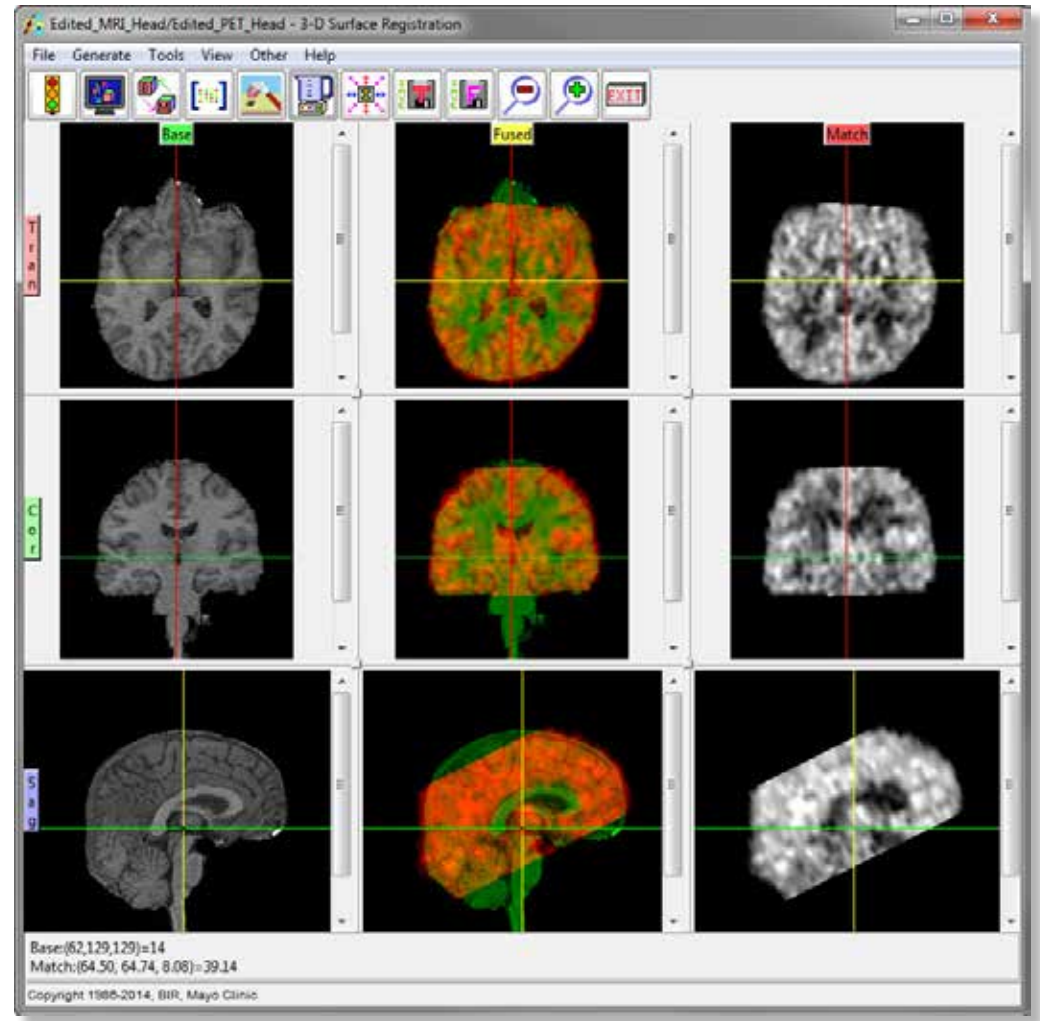
# 3D Voxel Registration

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

1. Load both the **MRI_Head.avw** and **PET_Head.avw** data sets from the **$:\BIR\ images\TutorialData** directory.

2. In the main Analyze workspace, first select the **MRI_Head** data set. Then, while holding down the <**Ctrl**> key, select the **PET_Head** data set (resulting in both being selected).

3. Open the **3-D Voxel Registration** module (**Register > 3-D Voxel**).

4. Choose File > Input/Output Ports to ensure that MRI_Head is assigned as the 'Base Volume' and PET_Head is assigned as the 'Match Volume'.

## Main Interface Features

5. The main interface contains nine image display panes (figure 1).

   - **First Column**: Displays the 'Base' volume (MRI_Head)

   - **Last Column**: Displays the 'Match' volume (PET_Head) pre-scaled to the size of the base volume

   - **Middle Column**: Displays the base and match volumes fused together

   - **Rows**: Display the volumes in the transverse, coronal, and sagittal orientations

6. By default, the volumes are displayed with cubic voxels. To turn off the cubic display press the **Toggle Cubic** PowerBar button. For this exercise leave cubic display on.
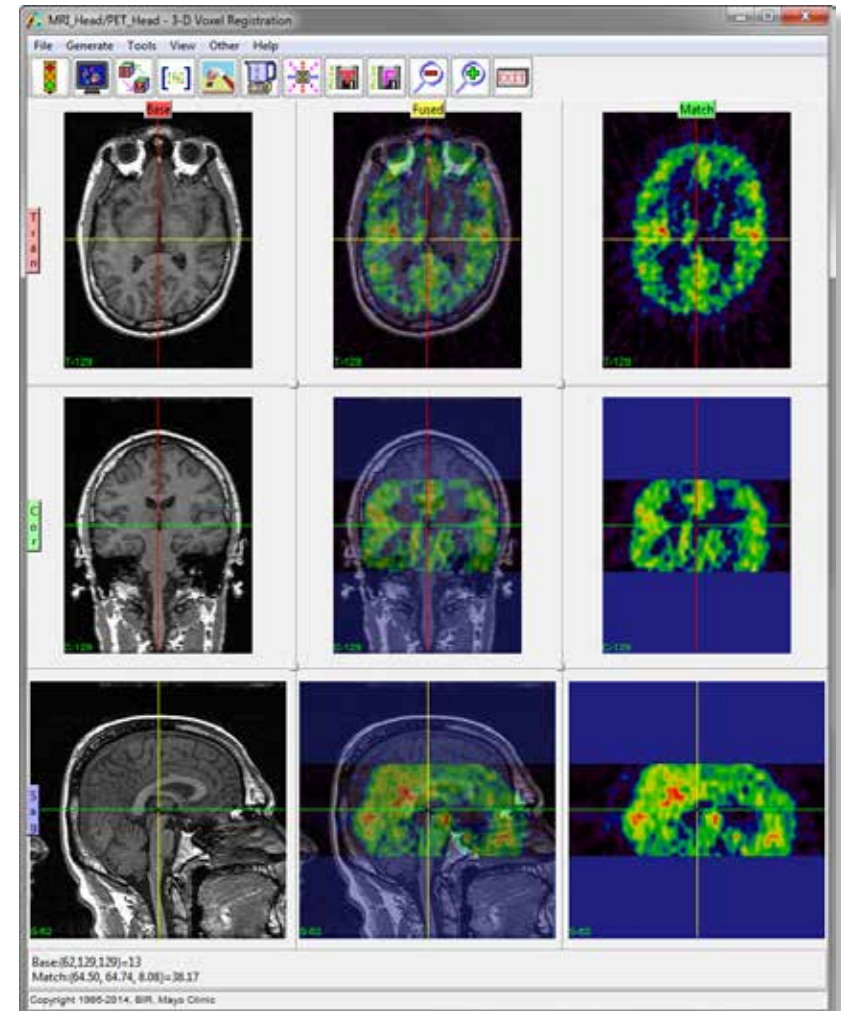


Figure 1

# 3D Voxel Registration

7. Open the **Blend** window (**Generate > Blend**). The Blend window provides different settings to help visually evaluate the registration. Experiment with the different blend options (figure 2) and then click **Done** to dismiss the window.

8. The crosshair in each of the image display panes can be used to move through the volumes. When the crosshair is moved in any of the panes, the other panes automatically update to display the same volume coordinate. Note, the base and match coordinates are reported at the bottom of the window.

9. Right-click on any of the image display panes to view options for controlling individual tiles, reference lines, image sizes, annotations, and interactivity.
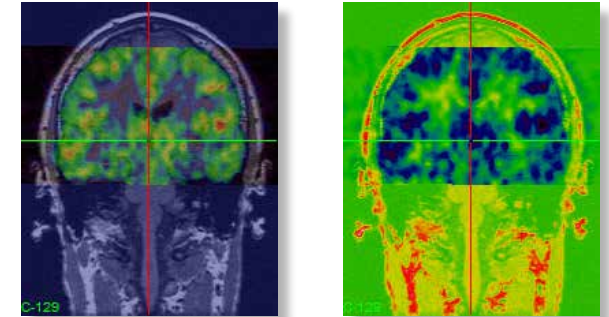
## Registration

10. For this exercise, no parameters need to be changed for a successful registration, the default settings are appropriate. Press the **Register** PowerBar button or choose **Generate > Register**.

11. After registration is complete you will see that the PET volume has been scaled, rotated, and translated to match exactly the sagittal MRI. To evaluate the registration, move the crosshair in any of the panes and change the 'Blend' type to 'Average'.

12. To view the current transformation matrix open the **Matrix Tool** (**Tools > Matrix**). You may manually enter rotations, translations, and scaling to the matrix by selecting an option and increment (figure 3). You may also save the current matrix as an ASCII floating-point file or load a previously saved matrix.

13. You may also use manual correction buttons in the **Manual** tool (**Tools > Manual**) to incrementally change the registration matrix. The buttons move the match volume section in the directions indicated, and then adjust the 3-D matrix depending upon the orientation selected.
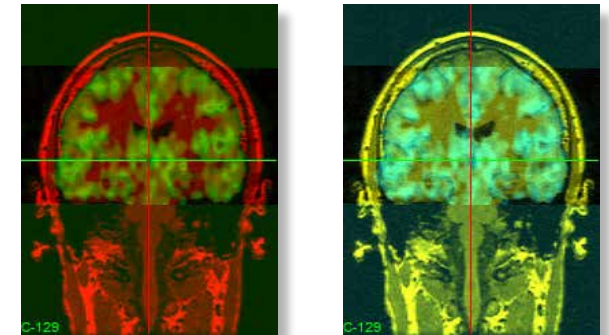


Figure 2
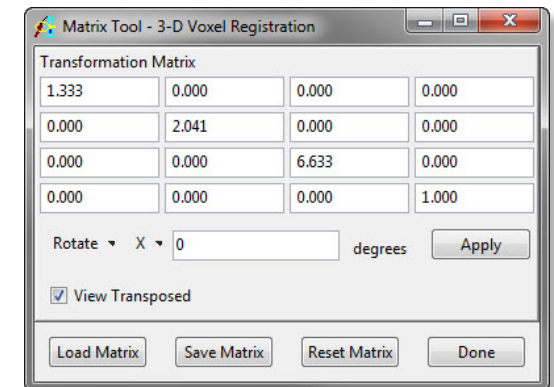


Figure 3

# 3D Voxel Registration

## Saving Transformed and Fused

14. To save a copy of the transformed match volume (PET_Head), choose **File > Save Transformed**; the transformed volume can be saved to disk or to the main Analyze workspace (figure 4).

15. To save the fused volume, choose **File > Save Fused**; the fused volume can be saved to disk or to the main Analyze workspace.

16. Close the 3-D Voxel Registration module before proceeding to the Additional Task.
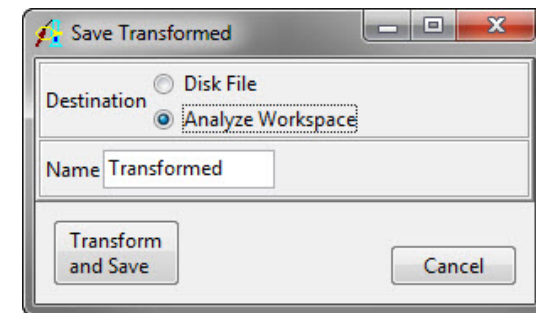
Figure 6

# 3D Voxel Registration: *Manual Scale Adjustment*

The Manual Registration tool in both the 3-D Voxel and Surface Registration modules now provides the ability for users to manually adjust the scale of the Match data prior to registration. This task will demonstrate how to access and use the new Adjust Scale tool.
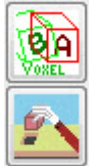
1. Select the **MRI_Head.avw** data set. Then while holding down the **<Ctrl>** key, select the **PET_Head.avw** data set (resulting in both being selected).

2. Open the **3-D Voxel Registration** module (**Register > 3-D Voxel**).

3. To access the **Adjust Scale** tool, open the **Manual Registration** tool from the Tools > Manual menu (figure 1). Check the **Adjust Scale** option, the Manual Registration tool will update with **X**, **Y**, and **Z** scale tools.

4. Adjust the scale of the Match data up and down in each orientation by click on the arrow up and arrow down keys. Note the display of the Match data each time the scale is adjusted.

5. Close all windows associated with the 3-D Voxel Registration module before proceeding to the next exercise.



Figure 1

AnalyzeDirect
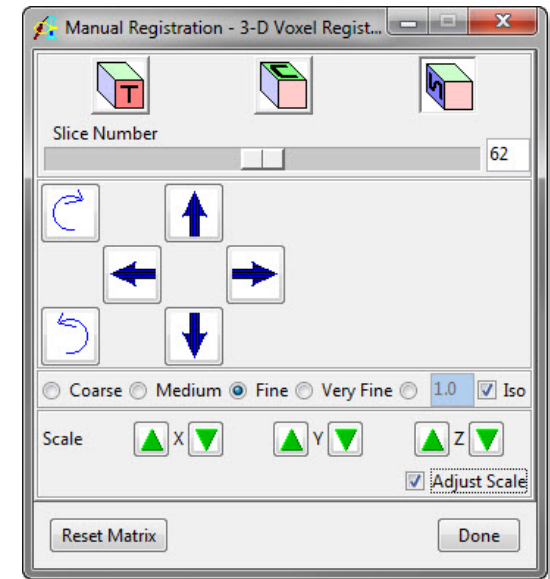
# 3D Voxel Registration: Mutual Information

This exercise will demonstrate how to adjust a 3-D registration starting position to achieve an optimal registration of two 3-D volume images.

1. Load both the **Register_MRI_Base.avw** and **Register_MRI_Match.avw** data sets from the **C:\BIR\images\TutorialData** directory.

2. In the Analyze workspace, first select the **Register_MRI_Base** data set. Then, while holding down <**Ctrl**> select the **Register_MRI_Match** data set (resulting in both being selected).

3. Open the **3-D Voxel Registration** module (**Register > 3-D Voxel**).

4. Choose **File > Input/Output Ports** to ensure that Register_MRI_Base is assigned as the 'Base Volume' and Register_MRI_Match is assigned as the 'Match Volume'.

5. Open the **Blend** window (**Generate > Blend**). Select the **Red-Green** blend and then click **Done**. The 'Red-Green' blend option will help evaluate the registration (figure 1).

6. Press the **Register** PowerBar button or choose **Generate > Register**.

7. Examine the center 'Fused' column of the main module window (figure 1). As you can see, the registration is not acceptable.



Figure 1

AnalyzeDirect
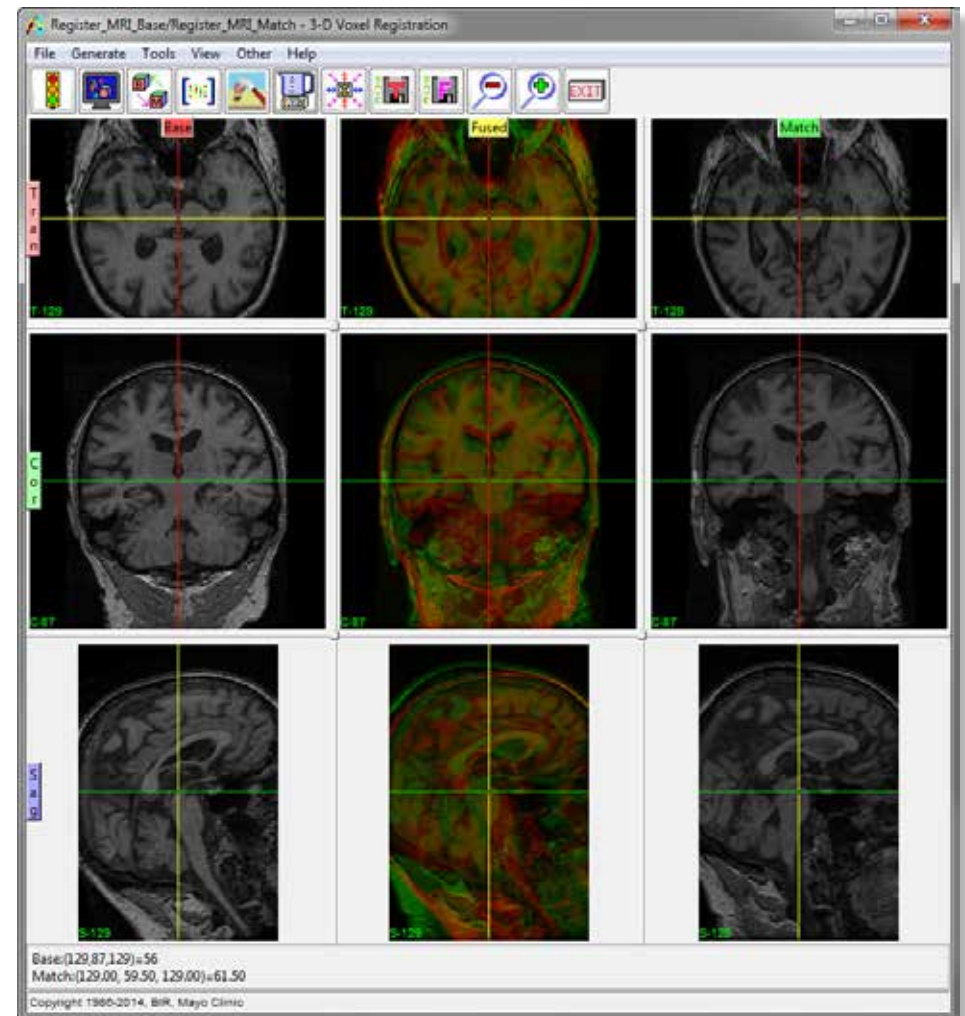
# 3D Voxel Registration: Mutual Information

## Manual Adjustment

8. Since the registration is not acceptable, manually adjust the starting point of the registration. Open the **Manual** tool (**Tools > Manual**).

9. Click **Reset Matrix** in the Manual tool (figure 2), this will reset the match volume to the original starting position.

10. Now, using the Manual tool options, move the match volume to a better starting position and press **Register**.

11. If the registration is still not acceptable, return to the Manual tool and click Reset Matrix again.

12. Now, select the **Coarse** adjustment option and press the **down** arrow button once.

13. Change the orientation from coronal to sagittal by selecting the **S-cube** and then press the right arrow button once.

14. Press **Register**. The volumes should now register correctly.

## Saving

15. To save the transformed match volume (Register_MRI_Match), choose **File > Save Transformed**; the transformed volume can be saved to disk or to the Analyze workspace.

16. To save the fused volume, choose **File > Save Fused**; the fused volume can be saved to disk or to the Analyze workspace (figure 3).

17. Close the 3-D Voxel Registration module before proceeding to the next exercise.
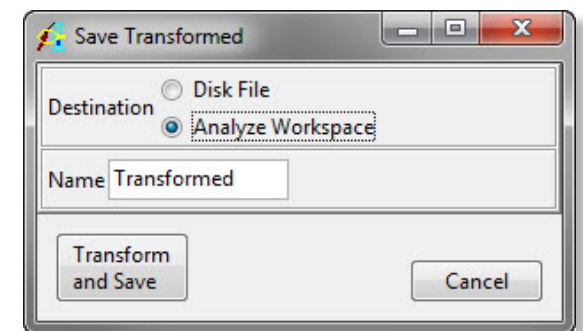
Figure 2

Figure 3

# 3D Non-Rigid Registration

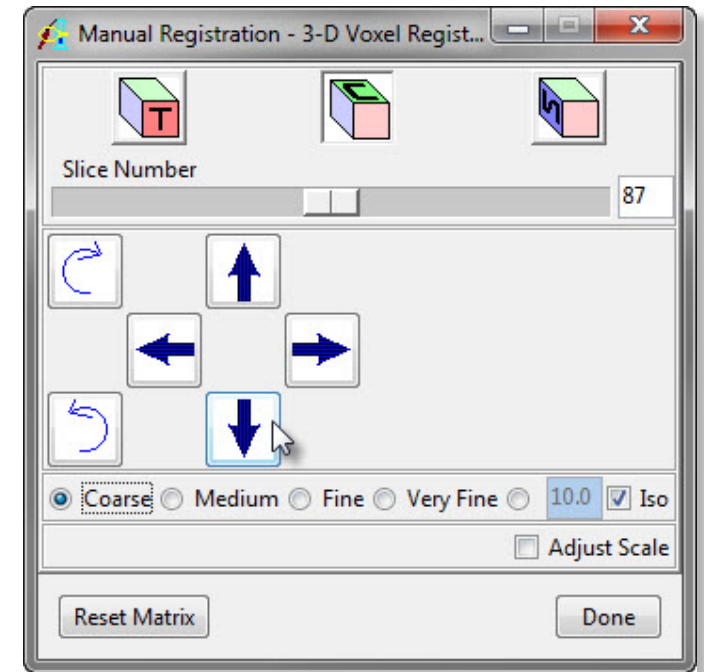Non-rigid registration allows for non-linear deformation in the registration transformation between volumes. This exercise will demonstrate how to use the 3D Non-Rigid Registration module.

1. Load both the **Heart_Time_Point_1.avw** and **Heart_Time_Point_2. avw** data sets from the **C:\BIR\images\TutorialData** directory.

2. In the Analyze workspace, first select the **Heart_Time_Point_1** data set. Then, while holding down <**Ctrl**> select the **Heart_Time_ Point_2** data set (resulting in both being selected).

3. Open the **3-D Non-Rigid Registration** module (**Register > 3-D Non-rigid**).

4. Choose **File > Input/Output Ports** to ensure that Heart_Time_ Point_1 is assigned as the 'Base Volume' and Heart_Time_Point_2 is assigned as the 'Match Volume' (figure 1).

5. To open the **Cursor Link** tool (figure 2), select **Tools > Cursor Link**. The cursor link will allow you to interactively review the data.

6. To change the orientation, open **View > Orientation**, select **Coronal**. To change the size of the data, select **View > Size**.

7. To set a blend mode, right click in the top-right display pane. Use the Section slider to navigate through the data.



Figure 1



Figure 2

AnalyzeDirect
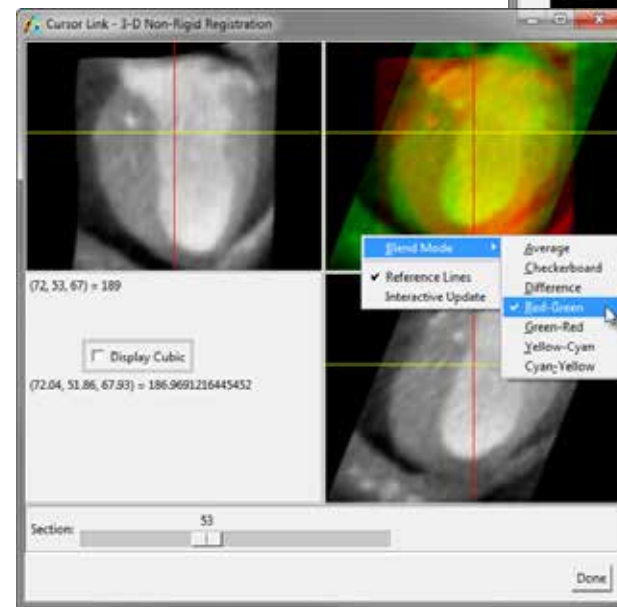
8. Open the **Generate > 3D Non-Rigid NMI** window. This window gives the following options:
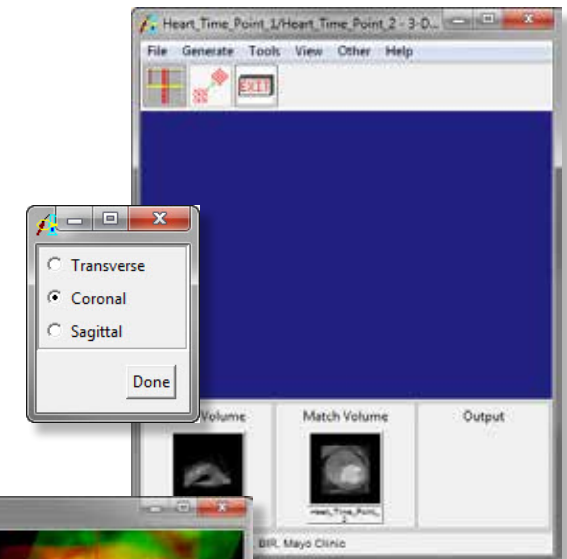
   - **Threshold**: specifies the clip values applied to the volumes before attempting registration. Check the Show Thresholding option and note the update in the Cursor Link image display as you adjust the threshold range, only voxels displayed in white will be considered for registration.

   - **Minimum Region Size**: specifies the scales at which the registration is conducted.

   - **Samples**: defines the number of samples used in each region for which the Mutual Information cost function is evaluated.

   - **Process**: sets limits of confidence for the registration.

   - **Minimum Entropy**: specifies the minimum histogram entropy in a subregion in order to be registered.

   - **Minimum NMI**: specifies the minimum NMI value for a registration result to be considered valid.

9. Once you have defined your parameters in the 3D Non-Rigid NMI window, click **Register** to initiate the non-rigid registration process.

10. Once the registration is complete, review in the Cursor Link tool (figure 3).

11. To output the transformed match volume to the Analyze Workspace, select **Generate > Transform**.
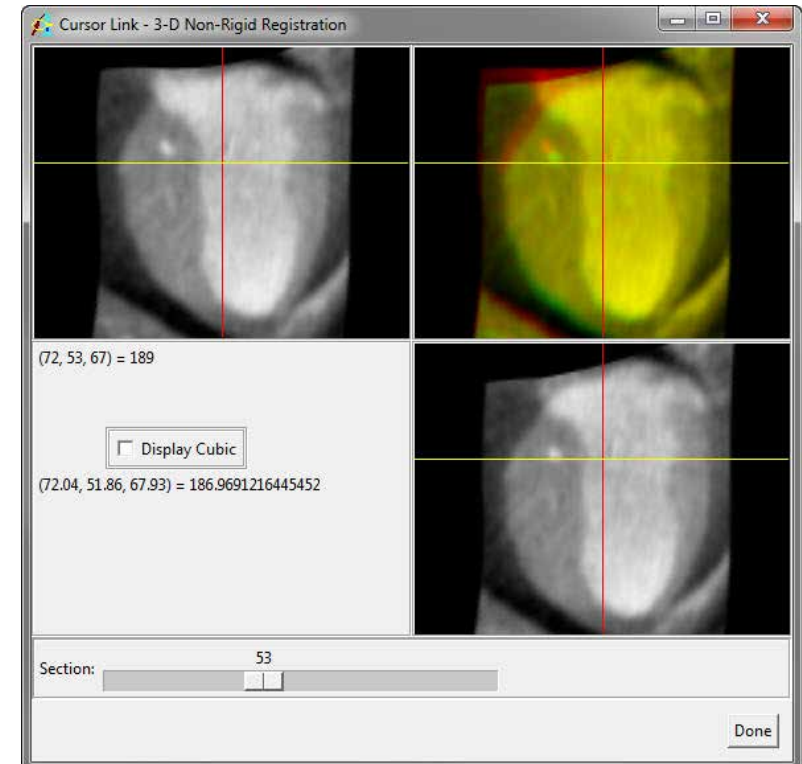
# 3D Non-Rigid Registration

12. Use the Volume Compare module to compare the original **Heart_Time_Point_1** and **Heart_Time_Point_2** data sets (figure 4). Then compare the original **Heart_Time_Point_1** and the transformed **Heart_Time_Point_2** data set (figure 5).
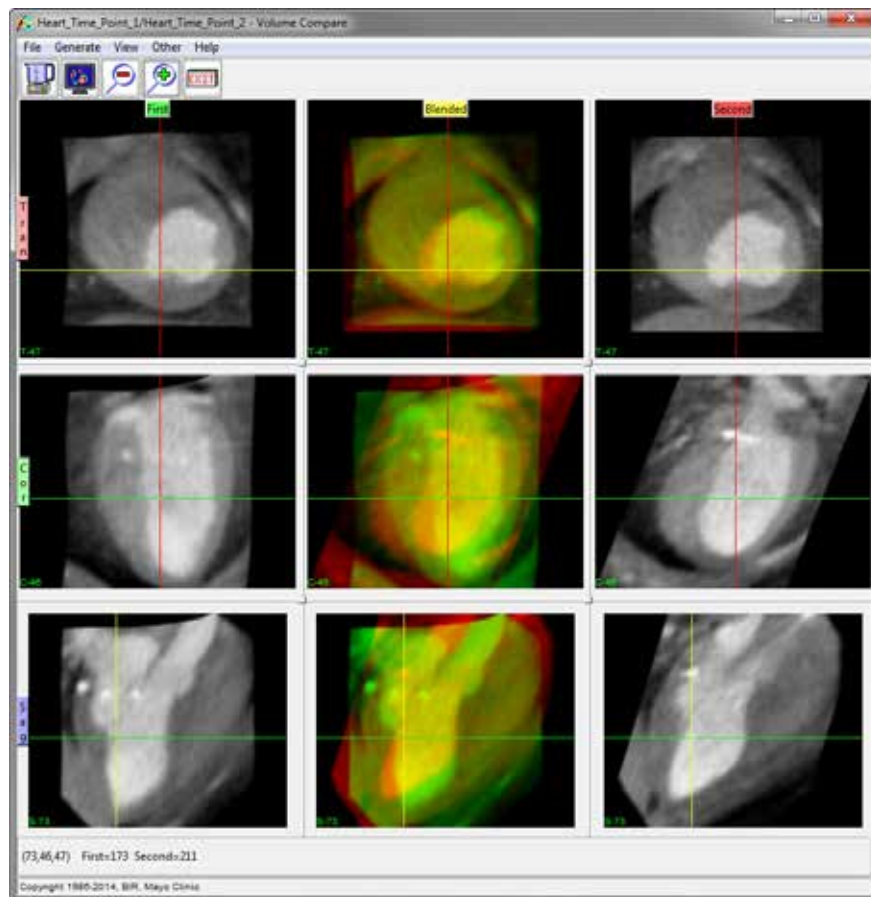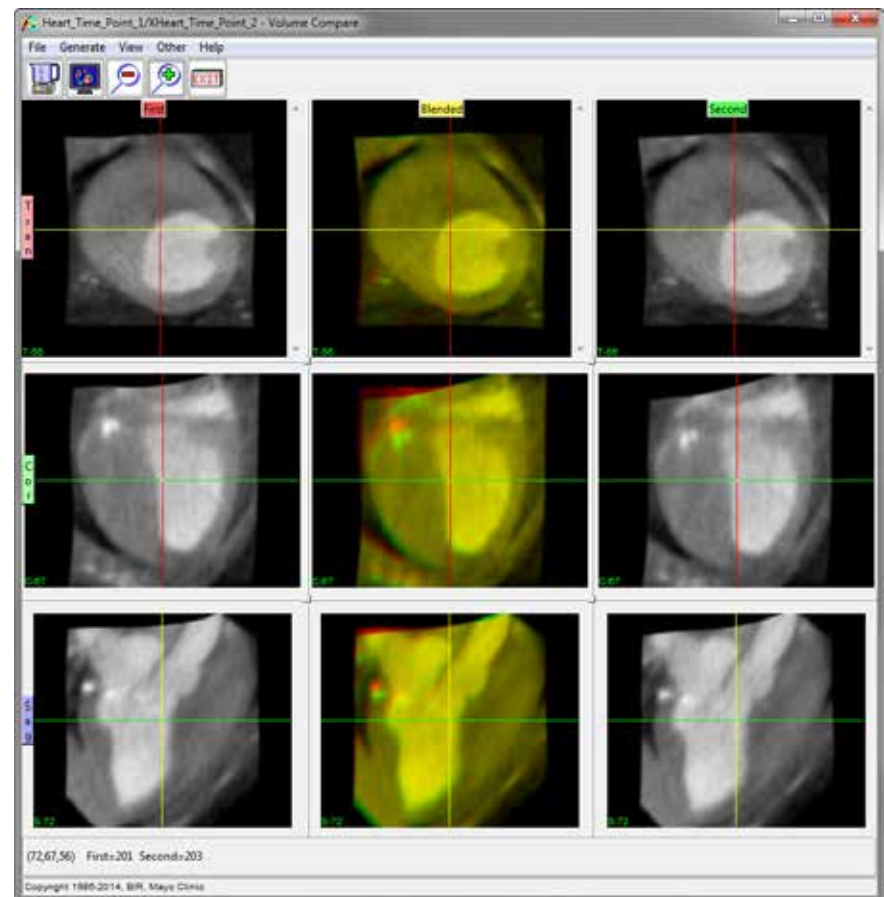


Figure 4



Figure 5

AnalyzeDirect

**Analyze 12.0:** Essential Training Guide

# Measurement

AnalyzeDirect

# Line Profile: Intensity-based Line Measurement

The Line Profile module enables calculation of image intensities along straight lines and freehand traces. Coordinate points and angle measurements can also be made. All measurements can be logged and saved to disk.

1. Load the **MRI_3D_Head.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Line Profile** module (**Measure > Line Profile**).

3. Use the slice slider to move to slice **97**.

4. To calculate the intensity values along a straight line in this slice, select the **Line** tool in the main Line Profile window (figure 1).

5. Position the cursor on the image and click to begin drawing. The **Sequence** window (**Generate > Sequence**) provides X and Y coordinate slider bars for precise positioning of lines.

6. The **Profile** window (figure 2) will automatically be returned when a line is drawn, displaying the intensity profile of the line. The Profile window allows profiles, statistics, distances, and FWHM (full width half max) measurements to be logged.

   *note*   To log FWHM, open the Profile Options window (Generate > Profile) and set 'Full Width Half Max' to 'On'.

7. Click **Log Profile** in the Profile window. To save the Line Profile Log as a .stats file for use in another application (such as Microsoft Excel), select **Save** in the Log window.

8. Select the **Trace** tool in the main Line Profile window to draw a freehand trace.

9. Select the **Caliper** tool (figure 3), an **Angle Measure** window will automatically be returned. The Caliper tool provides a series of repositionable points and lines, enabling measurement of user-specified angles and distances on a selected slice. The Angle Measure window will automatically update with any repositions.

10. Close the Line Profile module before proceeding to the Additional Task.

Figure 1

Figure 2          Figure 3

*tip*   If a structure of interest is in another orientation, choose Generate > Orientation to choose between transverse, coronal, and sagittal orientations, or define your own oblique orientation.

**AnalyzeDirect**
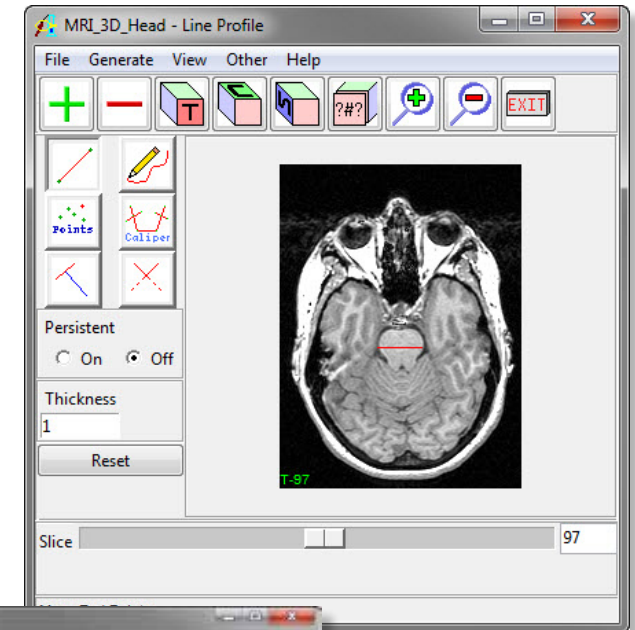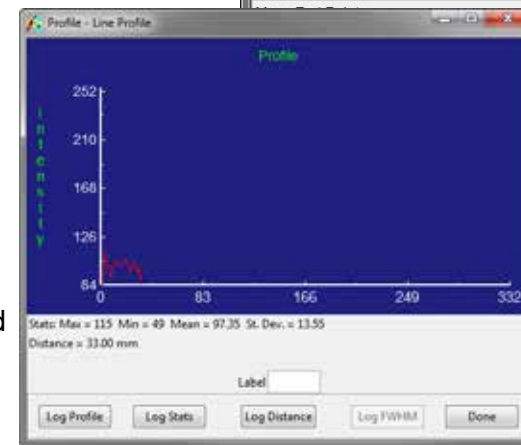
# Line Profile: *Radial Sequence Tool*

1. The **Radial Sequence** tool in the Line Profile module enables users to sample a radial sequence of profiles.

2. Load the **VH_Abdomen.avw** data set from the **$:\BIR\ images\TutorialData** directory.

3. Open the **Line Profile** module (**Measure > Line Profile**).

4. Open the **Profile Options** window (**Generate > Profile)** and set **Full Width Half Max** to **On**.

5. Select the **Line** tool and then draw a line starting in the middle of the right femur, finishing outside (figure 3).

6. Open the **Radial Sequence** tool (**Generate > Radial Sequence**).

7. Set the **Angle Increment** to **10**. When sampling a radial sequence the angle is incremented until a full 360 degrees from the starting position has been sampled.

8. Set **Log Profile**, **Log Stats**, and **Log FWHM** to **On**.

9. Click **Sample Radial Sequence**.

10. When the process has run, a Stats Log, Profile Log, and FWHM Log (figure 5) will be returned. To save any of the log files, right click and select **Save Log**.

11. Close the Line Profile module before proceeding to the next exercise.



Figure 4



Figure 5

# Region of Interest: Defining Regions

The Region of Interest module allows users to define and measure 3-D regions. This exercise will demonstrate how to use the tools in the module to define regions of interest within a volume image.
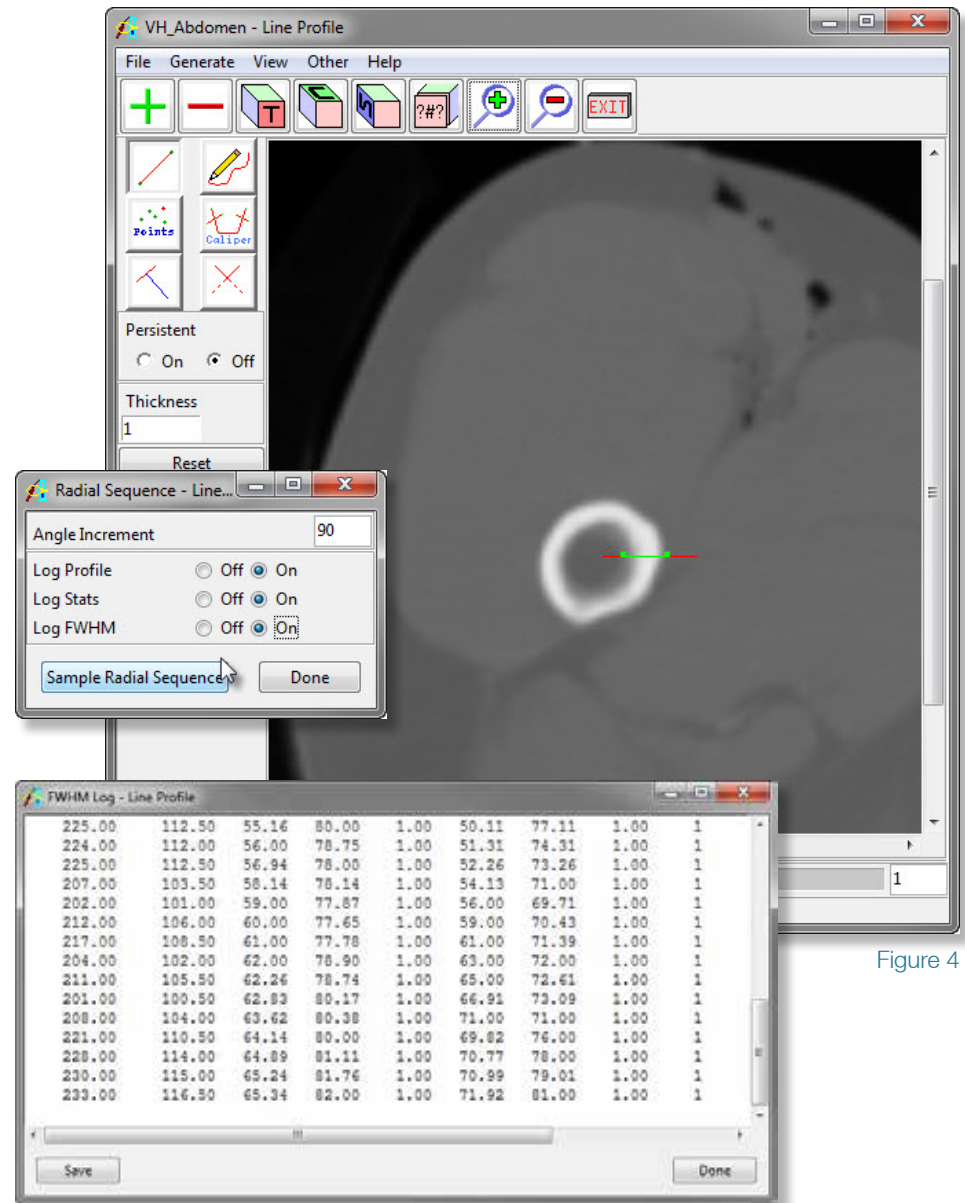
1. Load the **MRI_3D_Head.avw** data set from the **$:\BIR\images\ TutorialData** directory.

2. Open **Region of Interest** (**Measure > Region of Interest**).

## ROI Interface

3. When the module is opened, an object map is automatically created to store defined regions. To define a new region, make sure that the Object to Define: is set to ***New*** at the bottom of the window (figure 1).


Figure 3

4. The buttons along the left side of the window control the definition of regions on the images (figure 2). The buttons below the image display allow you to modify the defined regions (figure 3).

5. The first slice of the volume is automatically displayed when the ROI module is opened. You can move to a different slice by using the Slice slider bar or + and - on your keyboard. The currently displayed slice number and orientation can always be seen in the lower left corner of the image display.
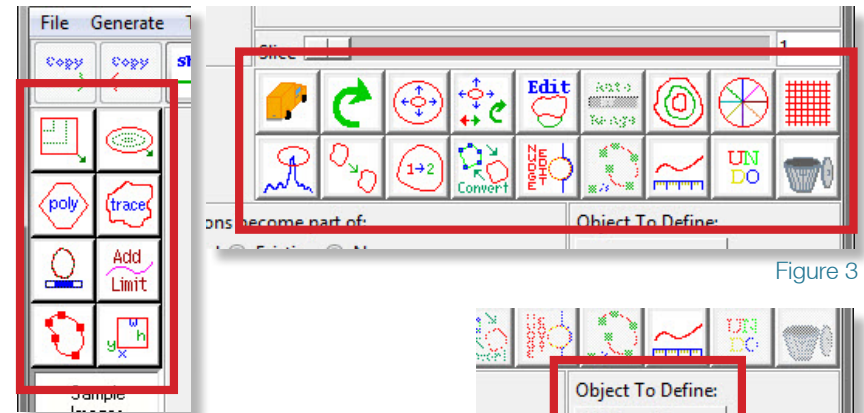

Figure 2
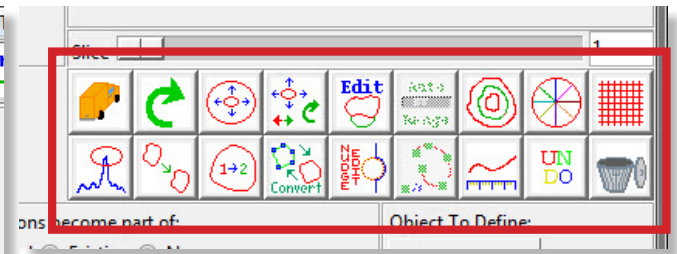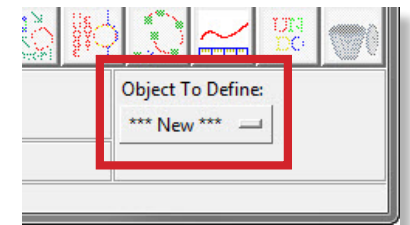

Figure 1

## Rectangle Tool

6. Define a rectangular region on slice 1 using the **Rectangle tool**. Position the cursor on the image display, then, click and drag the cursor out to size the rectangle, when you release the mouse button the new region '1.Object' will be created and added to the object map (figure 4).

7. Copy the region to the next slice (slice 2) by pressing the **Copy Regions Forward** PowerBar button once.

8. Regions can be modified using the buttons found below the image display. Select the **Move** button. Position the cursor near the region you wish to modify, then click and drag the cursor; any movement of the cursor will move the region. Also try using the **Rotate** and **Scale** buttons (found directly to the right of the Move button).

*tip* Holding the <Ctrl> key while sizing will force a square.


Figure 4

AnalyzeDirect
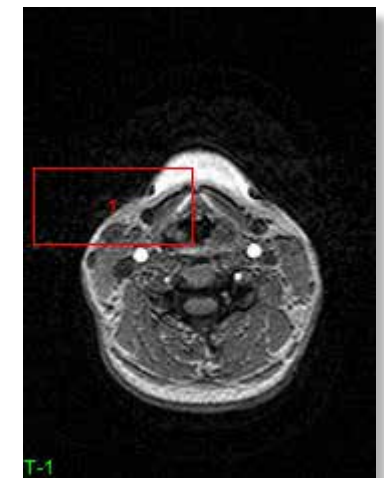
# Region of Interest: Defining Regions

## Oval Tool

9. Add a new region to slice 2 using the **Oval tool** (figure 5).

10. Press **Copy Regions Forward** to copy the regions to slice 3.

11. Select the **Move** button again. To move all regions on a slice simultaneously, hold the <**Ctrl**> key while moving the regions as described in step 8. When you release the mouse button, a dialog box will be returned asking if you would like to 'Move Regions in: This Slice Only, the Entire Object Map, or Cancel the move', click **This Slice Only**.

12. Move to slice 4.

## Polygon Tool

13. There are currently no regions defined on slice 4, define a region on slice 4 using the Polygon tool.

14. To begin defining the polygonal region, position the cursor on the image display and click once to set a starting point. Move the cursor outward to specify the length and direction of the first polygon side. To set a vertex and begin drawing another side, click once. Double-click to close the polygon (figure 6).

15. If after defining the region it is unsatisfactory, click the Undo button.

16. Move to slice 5.

## Manual Trace Tool

17. Define a region on slice 5 using the **Manual Trace** tool. Position your cursor on the image display, then click and hold the mouse button to begin drawing the trace, release the mouse button to end the trace. The last point of the trace will be automatically connected to the first point of the trace.
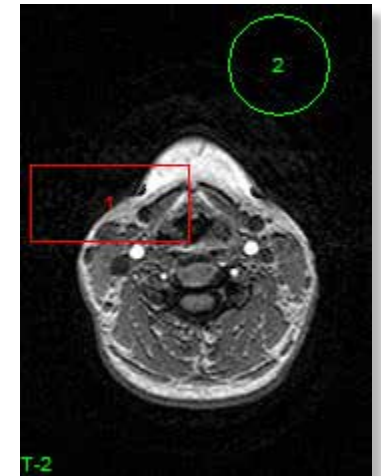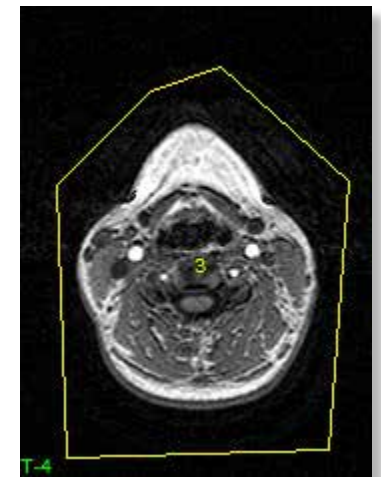


Figure 5



Figure 6

AnalyzeDirect

18. If you make a mistake while tracing, continue holding the mouse button down, and press the **<u>** keyboard key. The trace will slowly back up from the current position until the <u> key is released. Try this by drawing a line on the image, and while continuing to hold the mouse button down, press the <u> key. Once the trace has backed up half way, release the <u> key and continue your trace in a different direction.

19. To define a region without having to continuously hold down the mouse button, right-click on the image display and choose the **Button Passive** option. When 'Button Passive' is selected, simply click on the image display to begin the trace, and then click again when you are ready to end the trace and define the region. The 'Button Passive' option is available for all region definition tools.

20. Right-click and deselect the Button Passive option. Then, click **Clear Regions** on the left side of the window to clear all regions defined on this slice.

21. With the **Manual Trace** tool still selected, check the **Smart Edge** option. The 'Smart Edge' option searches for edges (areas of high gradient) when drawing a trace with the **Manual Trace** or **Spline** tools. Click once to begin a trace along an edge in the image display, letting 'Smart Edge' determine the path, click again to lock that portion of the trace. When the region of interest has been defined, double-click to end the trace. Uncheck the Smart Edge option.

22. Move to slice 6.

## Spline Tool

23. Define a new region on slice 6 using the **Spline** tool. The Spline tool enables the drawing of splines with moveable control points. Position the cursor on the image display and click once to begin drawing a spline, click once again to set a control point. When the region of interest has been defined, double-click to close the spline.

24. To modify the region with the spline control points, select the **Move** button and then drag any control point to a new location.
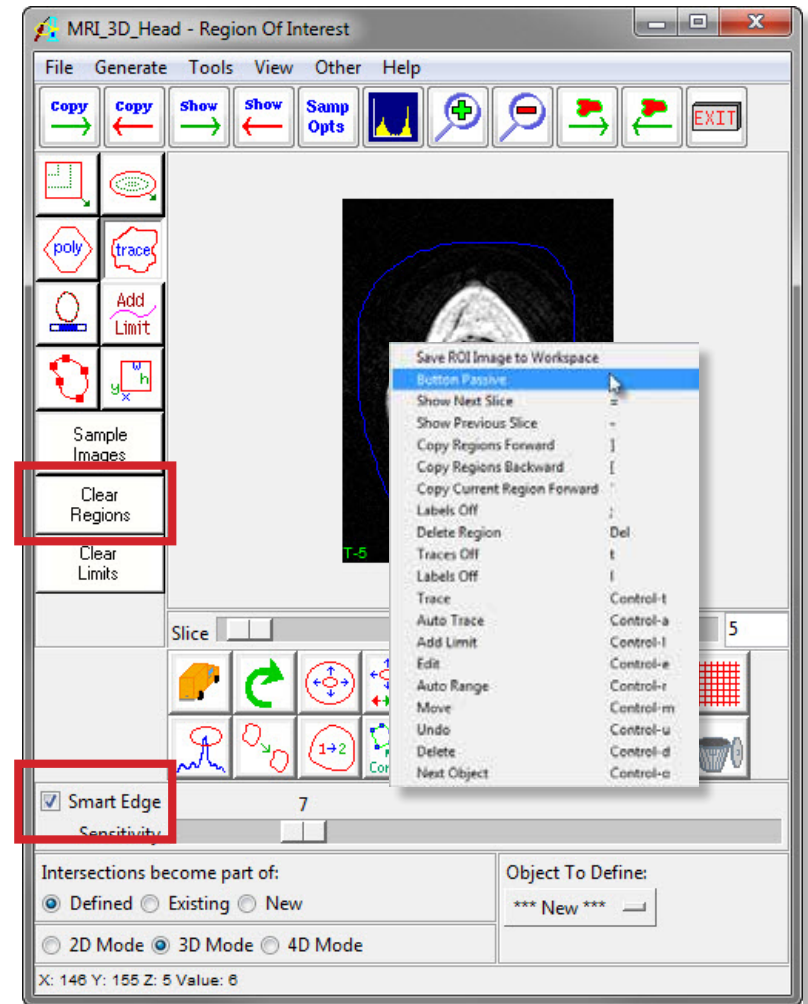


Figure 7

# Region of Interest: *Intersecting Regions*

1. When objects overlap, the resulting regions may not appear as expected. Since the object map is a one-to-one mapping of the voxels to an object, a voxel cannot be part of more than one object. The '**Intersections become part of**:' option (in the lower left hand corner) allows you to control how intersecting regions are handled.

2. Move to slice 7.

3. Choose **File > Reset Object Map** to clear all regions from the volume. In the dialog box returned, click **Continue without Saving**.

4. Ensure that **Intersections become part of:** is set to **Defined** (figure 8).

5. Select the **Rectangle** tool and define a region.

6. Now, select the **Oval** tool and define a region that overlaps the rectangle.

7. The intersecting area becomes part of the region being defined, 2.Object (figure 8).

8. Click **Undo** button and then set **Intersections become part of:** to **Existing**.

9. Select the **Oval** tool and again define a region that overlaps the rectangle.

10. The intersecting area now becomes part of the existing region, 1.Object (figure 9).

11. Click **Undo** and then set **Intersections become part of:** to **New**.

12. Select the **Oval** tool and again define a region that overlaps the rectangle.

13. The intersecting area now becomes a new region, 3.Object (figure 10).

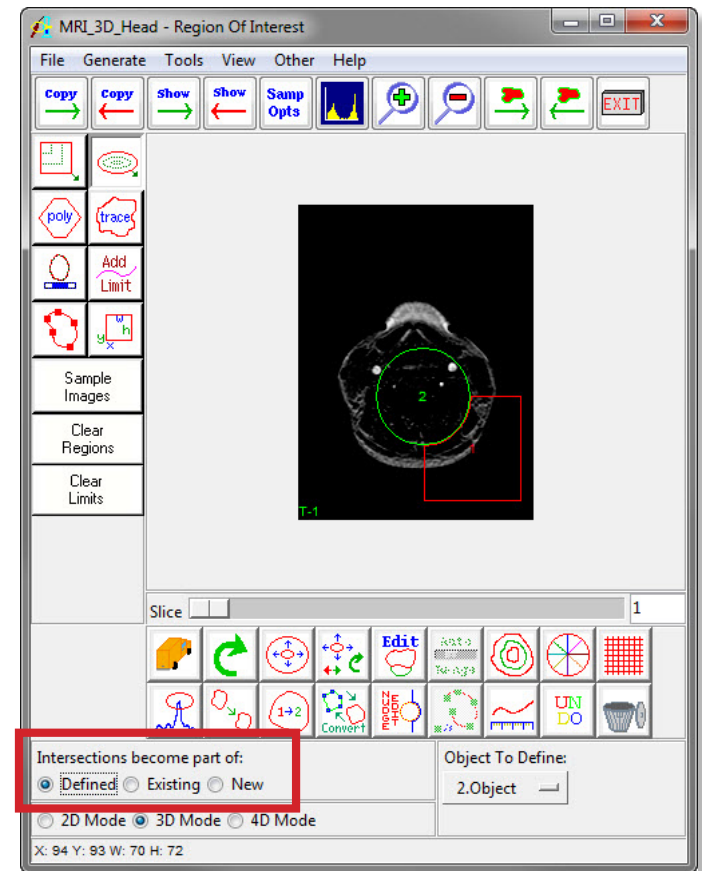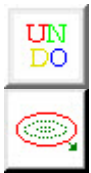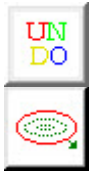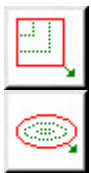14. Close the Region of Interest module before proceeding to the next exercise.



Figure 8
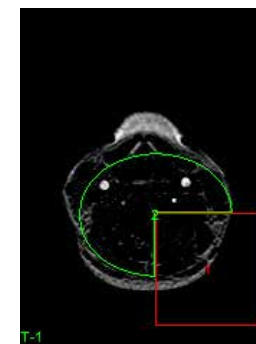


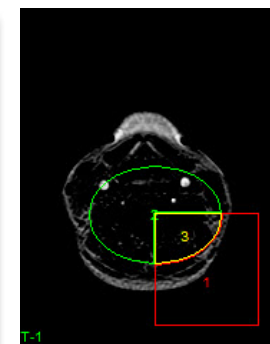Figure 9          Figure 10

# Region of Interest: Defining Regions

This exercise will demonstrate how to use more advance region definition tools in the Region of Interest module to define objects of interest within a 3-D volume image. The exercise will also show you how to measure these objects.

1. Load the **MRI_3D_Head.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Region of Interest** module (**Measure > Region of Interest**).

3. Using the slice slider below the image display, move to **Slice 122**.

4. In the main ROI window, select the **Auto Trace** tool.

5. Position the cursor near the center of the brain and click to set a seed point. The ROI window will automatically update once a seed point is set to display a double-ended slider bar (to specify a threshold range) and other Auto Trace parameters (figure 1).

6. Use the double-ended slider bar to set the **threshold minimum** to **34** and the **threshold maximum** to **129**. Then, click **Apply**. The double-ended slider bar will disappear and the new region will be named '1.Object'.

7. Press the **Copy Regions Forward** PowerBar button once. The auto trace will be copied to the next slice. Notice that the auto trace is recalculated for each slice based on the set threshold range.

8. Press **Copy Regions Forward** until the auto trace has been applied to all the remaining slices containing brain matter, (until approximately slice 181).

9. Once you have copied the region forward to the remaining slices, choose **Tools > Show Rendering** to open the **Render Tool** and view a 3-D rendering of the defined object (figure 2). Click **Done** to dismiss the window.

10. Open the **Objects** window (**View > Objects**). Select Object.1 from the Object drop-down menu and change **Name** of Object.1 to **Brain**. Click **Done** to dismiss the window.

Figure 1

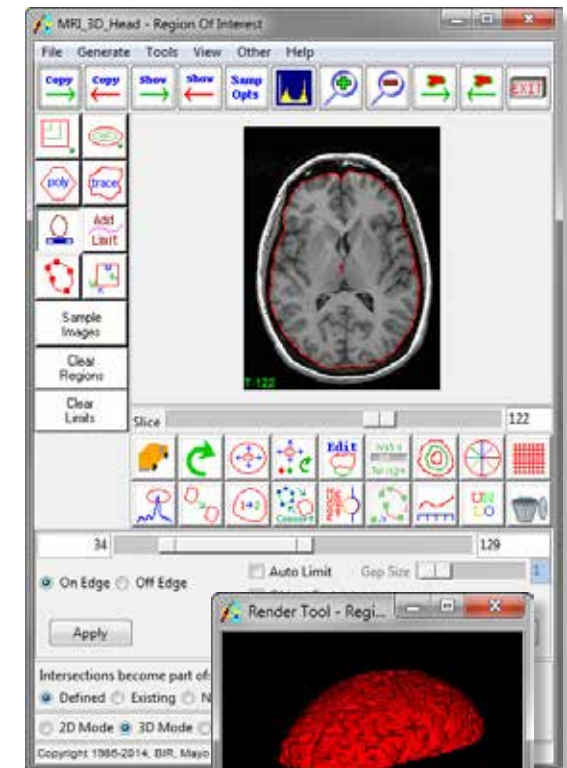*tip* If you placed your seed point towards the outside of the brain, it will eventually be copied forward to an area of a slice that does not contain the brain. Select the 'Move' button and move the seed point to the middle of the brain, then, continue to copy the region forward. To learn more about editing regions see the Additional Task at the end of the exercise.

Figure 3

**Analyze**Direct
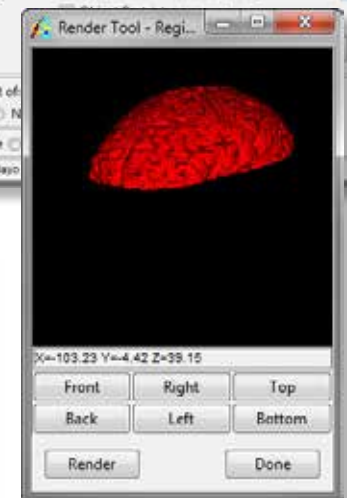
## Measuring Regions

11. Open the **Sample Options** window (**Generate > Sample Options**).

12. In the Sample Options window set the following (figure 3):

    - **Sample Type: Object(s), check the Brain object**

    - **Summing: On**

    - **Sample: All Slices**

    - **Sequence Display: Off**

    - **Log Stats: On**

13. Click **Configure Log Stats** to open the ROI Stats window. The ROI Stats window displays all statistics that can be returned for the 'Stat Type' selected in the Sample Options window (in this case the 'Intensity' Stat Type). All statistics with a check mark in the 'Log' box to the left will be reported in the ROI Stat Log when the defined object is sampled.

14. Click **Sample Images**. The module will now sample the defined object ('Brain').

15. The ROI Stat Log will automatically be returned, displaying the object statistics (figure 4). Click Done; in the dialog box returned click **Discard, then Exit**.

16. In the **Sample Options** window switch **Summing** to **Off** and **Sequence Display** to **On**.

17. Click **Sample Images** to sample the object again. This time each slice will be displayed as it is sampled as 'Sequence Display' is now set to 'On'. Notice the difference in time taken to sample the entire volume. The object statistics for each slice will be reported in the ROI Stat Log, as 'Summary' is set to 'Off'.
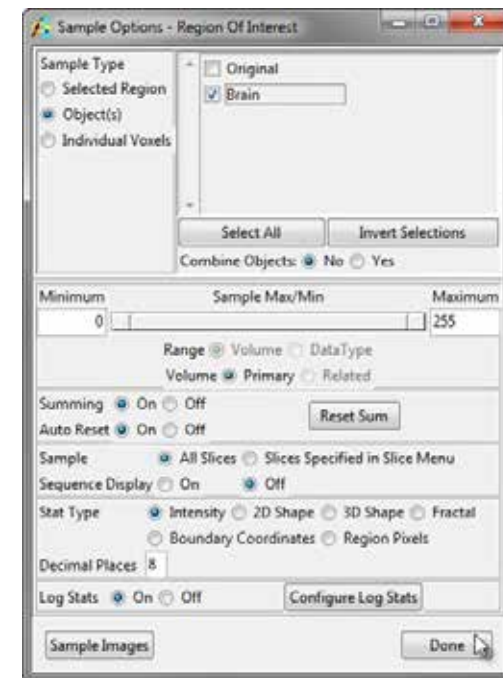


Figure 4
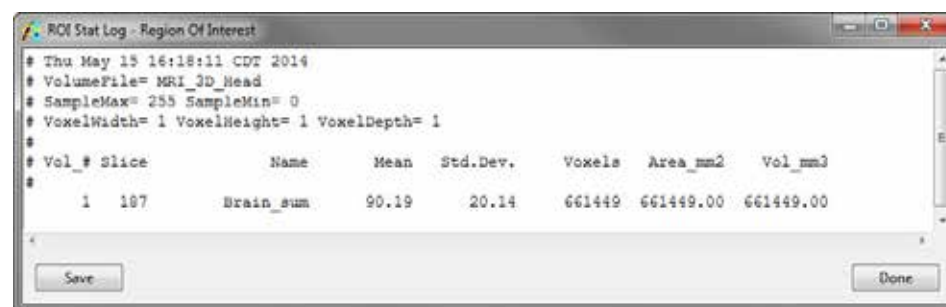


Figure 5

# Region of Interest: *Editing Regions*

1. Using the **Show Next** and **Show Previous Slice** PowerBar buttons, review the 'Brain' object (defined previously) slice-by-slice to determine if the auto trace leaked into other structures.

2. On slices where the auto trace leaked, select the **Edit Region** button and draw in the edge of the brain where the leak occurred. Areas beyond that edge will be removed from the object on that slice.

3. Next, use the slice slider below the image and move to slice **62**.

4. Ensure that the **Object to Define** is set to Brain (at the bottom of the ROI window). Then, trace the brain on slices 62-121 using the Auto Trace or another region definition tool.

5. Once you have traced the 'Brain' object on slices 66-121, choose **Tools > Show Rendering** to open the Render Tool and view a 3-D rendering of the define object (figure 1). Click **Done** to dismiss the window.

6. Open the **Sample Options** window (**Generate > Sample Options**) and set **Summing** back to **On** and **Sample** to **All Slices**.

7. Click **Sample Images** in the main ROI window to sample the 'Brain' object as it is defined on slices 66-181.

8. Choose **File > Save Object Map** to save the object map with the 'Brain' object.

9. Close the Region of Interest module before proceeding to the next exercise.



Figure 1

# Region of Interest: Measuring Regions

As well as allowing users to define and measure objects defined in the module the Region of Interest module also allows users to load and measure object maps created in other modules.

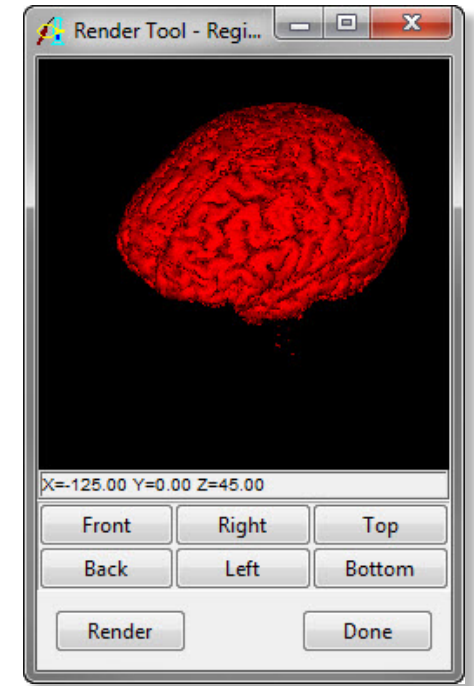1. Load the **MRI_3D_Head.avw** data set from the **$:\BIR\images\TutorialData** directory. The data set may be available in the Analyze workspace if you have completed exercise 45 or 46.

2. Open the **Region of Interest** module (**Measure > Region of Interest**).

3. Choose **File > Load Object Map** and load the **MRI_3D_Head.obj** object map from the **$:\BIR\images\TutorialData** directory.

4. Open the **Objects** window (**View > Objects**) and set **Control by** to **Attribute**.

5. Notice that this object map contains several objects. With the **Display** attribute selected, switch the **Lenticular** and **Caudate** objects to **On**.

6. Using the slice slider below the image display, navigate through the volume, the objects with the '**Display**' attribute set to '**On**' will be seen on the images (figure 1).

7. Open the **Sample Options** window (**Generate > Sample Options**).

8. In the Sample Options window set the following:

   - **Sample Type: Object(s), check Brain**
   - **Summing: On**
   - **Sample: All Slices**
   - **Sequence Display: Off**
   - **Log Stats: On**

9. Click the **Sample Images** button to sample the 'Brain' object.

10. The ROI Stat Log will automatically be returned, displaying the object statistics (figure 2). Note the volume given is only for the 'Brain' object, not the entire brain. To find the total volume of the brain you need to obtain the volume of the objects that make up the brain – in this exercise this includes the 'Brain', 'Ventricle', 'Lenticular', and 'Caudate' objects.
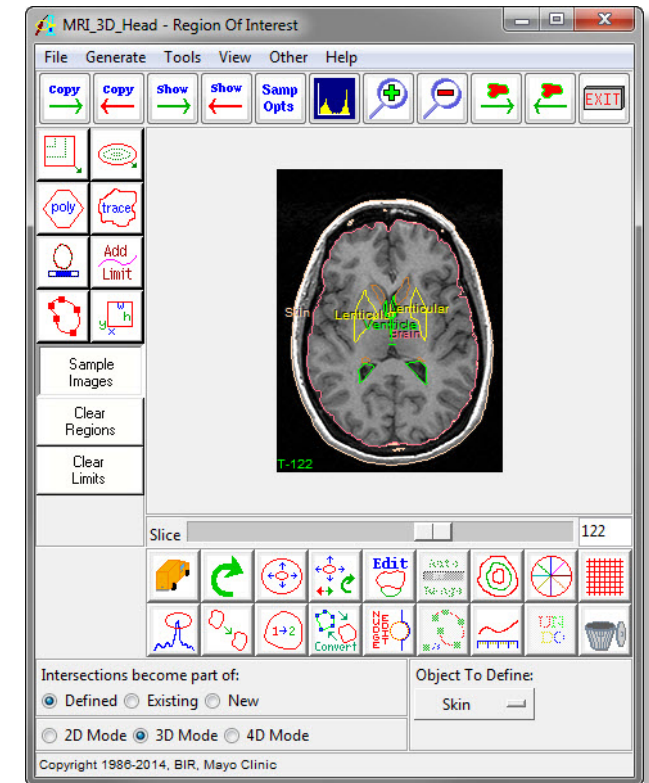


Figure 1



Figure 2

11. Click **Done** to close the ROI Stat Log; in the dialog box returned click **Discard, then Exit**.

12. In the Sample Options window, check the **Ventricle**, **Lenticular**, and **Caudate** objects (the 'Brain' object should already be checked).

13. Click **Sample Images** button. The individual volumes for each object will be returned to the ROI Stat Log. The sum of these volumes is the total brain volume.

14. To have the volume of the objects added together automatically for the total volume, set **Combine Objects** to **Yes** under the selection area.

15. Click **Sample Images**. The total brain volume will now be returned to the ROI Stat Log (figure 4).

16. Save the .stats file.
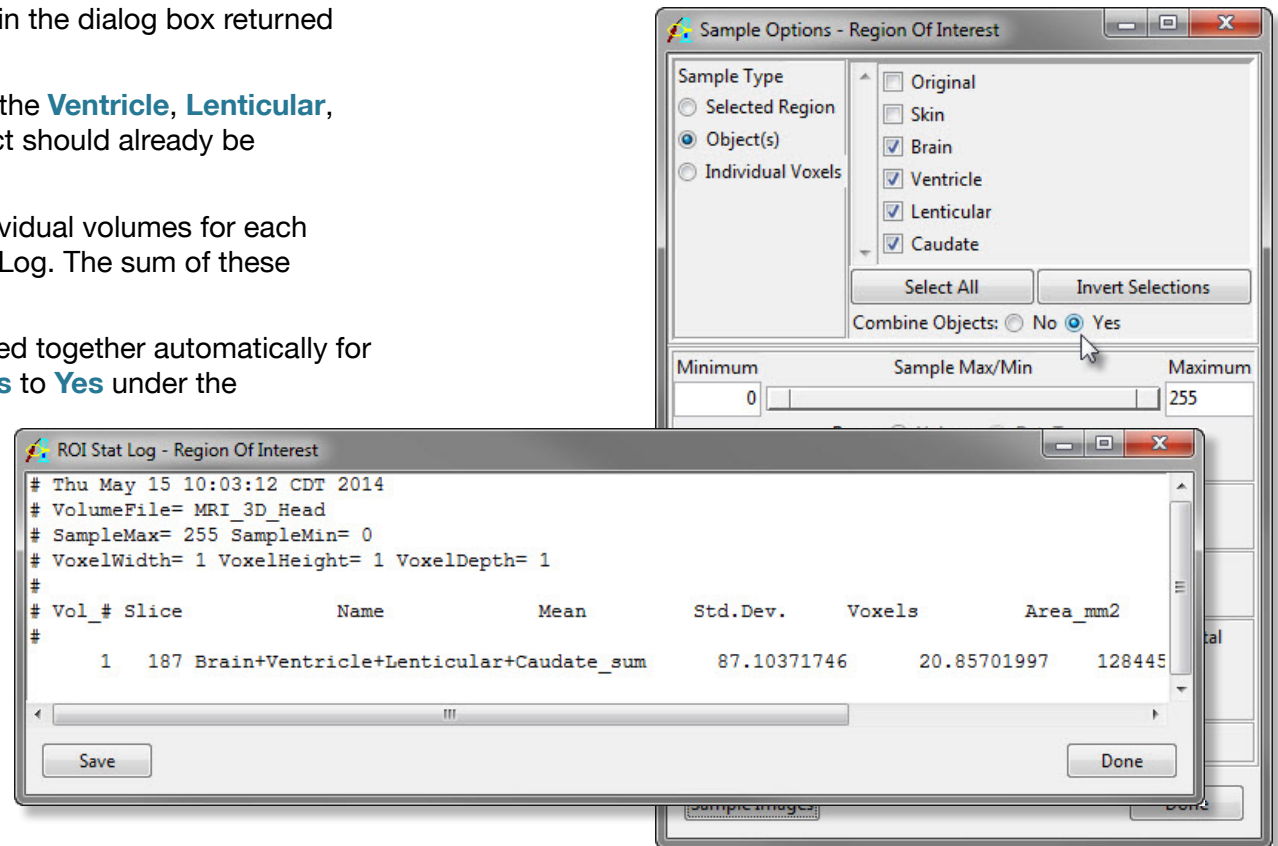


Figure 3

# Region of Interest: Histogram Analysis

This exercise will provide instructions on how to generate a histogram for an individual slice within a volume, an entire volume, and for a defined object.

## Sampling a Single Slice

1. Load the **MRI_3D_Head.avw** data set from the **$:\BIR\images\ TutorialData** directory.

2. Open the **Region of Interest** module (**Measure > Region of Interest**).

3. Use the slice slider directly below the image, and move to slice **97**.

4. Open the **Histograms** window (**Generate > Histograms**).

5. In the Histograms window, set **Histogram Display** to **On** and set **Log Histogram** to **On**.

6. In the main ROI window click on the image. The module will sample voxel intensity vs. occurrences. The results will be displayed as a histogram and saved to a Histogram Log file. The Histogram Log file can be saved by right-clicking in it and selecting **Save Log**.

7. Close all windows associated with the ROI module.

Figure 1

Figure 2

Figure 3

AnalyzeDirect
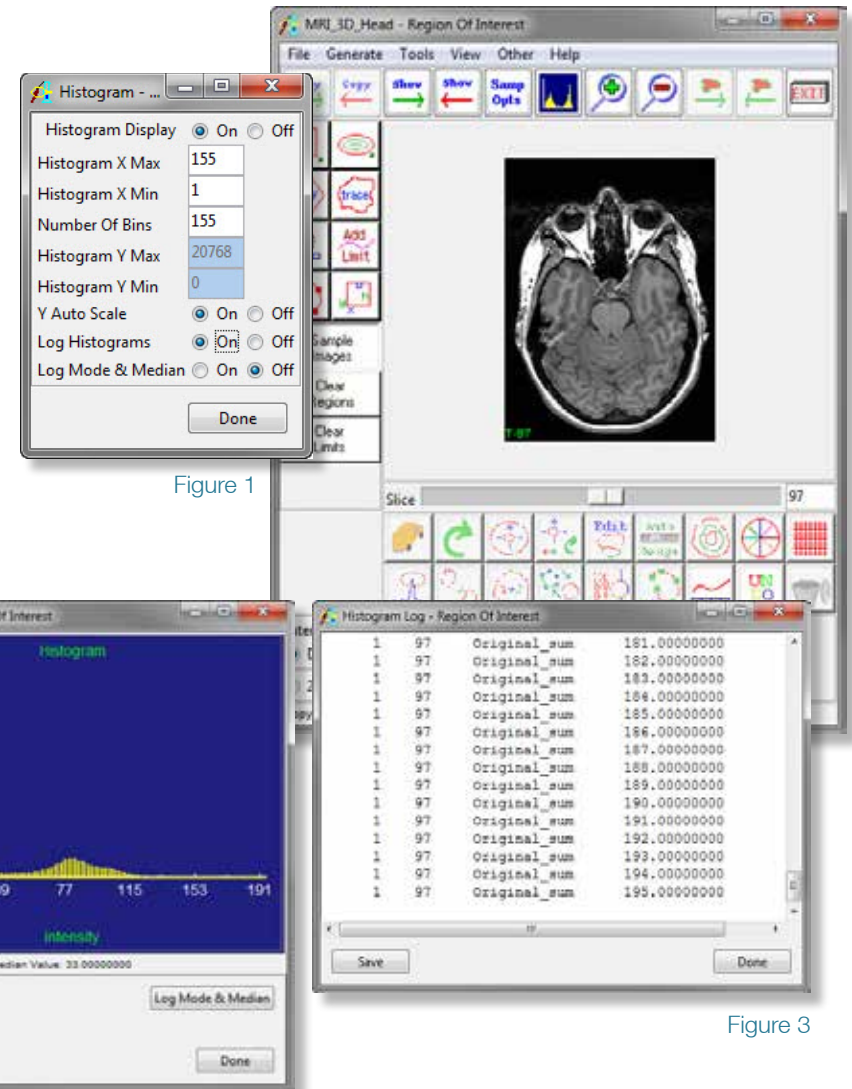
# Region of Interest: Histogram Analysis

## Sampling a Volume

1. Select the **MRI_3D_Head.avw** data set and open the **Region of Interest** module (**Measure > Region of Interest**).

2. In the Histograms window, set **Histogram Display** to **On** and set **Log Histogram** to **On.**

3. Next open the **Sample Options** window (**Generate > Sample Options**).

4. In the Sample Options window, set Summing to On and set Sample to All Slices (figure 4).

5. In the main ROI window click on the image display to start the sampling process. The module will sample voxel intensity vs. occurrences for the entire volume. The results will be displayed as a histogram and saved to a Histogram Log file (figure 5). The Histogram Log file can be saved out of Analyze by right-clicking in it and selecting **Save Log**.

*note*    If you want to sample all slices at the same time, but do not want to 'sum' the information, simply set Summing to Off, intensity vs. occurrence will be reported for each individual slice in the volume. For a quicker sampling time, set Sequence Display to Off.

6. Close all windows associated with the ROI module.

Figure 4

Figure 5

AnalyzeDirect

# Region of Interest: Histogram Analysis

## Sampling an Object

1.  Select the **MRI_3D_Head.avw** data set and open the **Region of Interest** module (**Measure > Region of Interest**).

2.  Select **File > Load Object Map** and load the **MRI_3D_Head.obj** from the **$:\BIR\images\TutorialData** directory.

3.  Open the **Histograms** window (**Generate > Histograms**).

4.  In the Histograms window, set **Histogram Display** to **On** and set **Log Histogram** to **On**.

5.  In the Sample Options window set the following (figure 7):

    *   **Sample Type: Object(s)**

    *   **Check only the Brain object**

    *   **Summing: On**

    *   **Sample: All Slices**

6.  Click on the **Sample Images** button to start the sampling process. The module will sample voxel intensity vs. occurrences for the brain object. The results will be displayed as a histogram, and also saved to a Histogram Log file (figure 7). The Histogram Log file can be saved out of Analyze by right-clicking in it and selecting **Save Log.**

7.  Close all windows associated with the ROI module.



Figure 6



Figure 7

AnalyzeDirect
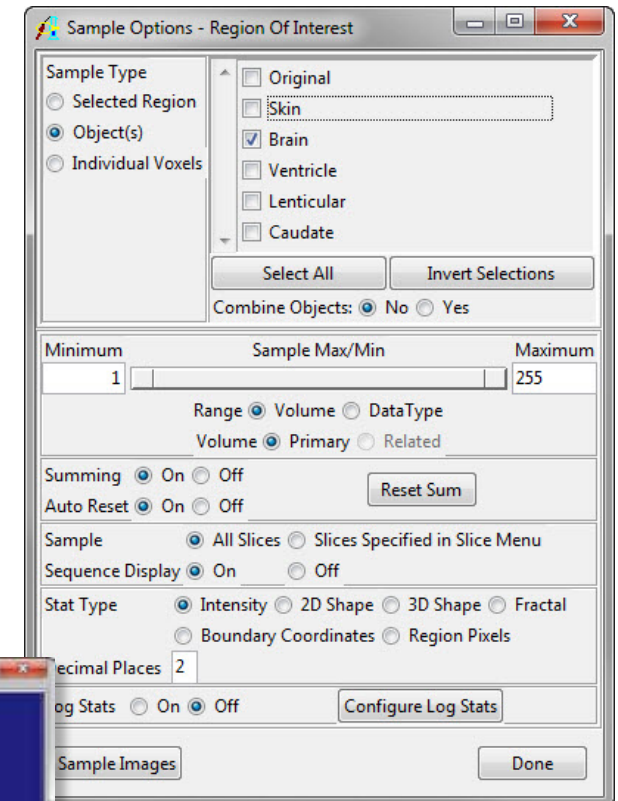
# Importing .stats files into Excel

ROI Stat Log files (.stats) and Histogram Log files (.hst) can be saved out of Analyze as text files. These text files can be imported into third party statistical applications such as Excel, for further statistical analysis. This exercise will demonstrate how to load a .stats file into Excel. Note that the process for loading a .hst file is identical.

1. Open **Excel**, then select **File > Open**.

2. In the Open window, select All Files (*.*) from the File Type drop menu.

3. Navigate to and open the .stats file.

4. The **Text Import Wizard** will appear.

5. In Step 1 of 3 Under **Original Data Type** select **Delimited** and click **Next** at the bottom of the screen.

6. In Step 2 of 3 of the Text Import Wizard, under the Delimiters select **Space**, and deselect any other options. Then click **Next**.

7. In Step 3 of 3, in the **Data Preview** section, simply click Finish at the bottom of the screen. Your stats file will now appear in an excel worksheet.

AnalyzeDirect
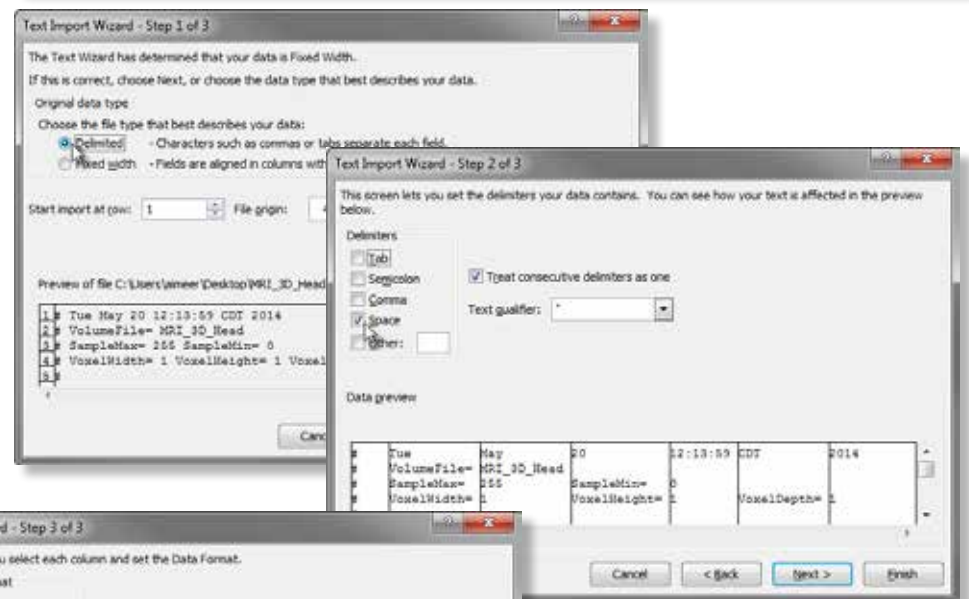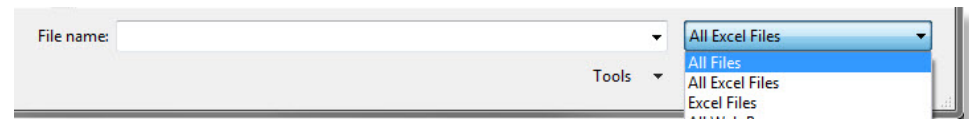
# Stereology: Estimating Volume

The Stereology module estimates volume and surface area using the stereological method of point counting. The point counting method consists of overlaying the 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.

1. Load the **Canine_Chest_CT.avw** data set from the **$:\BIR\images\ TutorialData** directory.

2. Open the **Stereology** module (**Measure > Stereology**).

3. The intensity scaling of the images must be changed so that they are viewable. Open the **Intensities** window (**View > Intensities**) and change the **Maximum** to **145**. Click **Done** to dismiss the window.

4. Open the **Grid Parameters** window (**Generate > Grid**) to set up a sampling grid that encompasses the heart (figure 1).

5. The heart first appears around slice **42** and remains visible until slice **94**. Set the **Starting Grid 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**.

6. Click **Generate Grid**. Then, click **Done** to dismiss the **Grid Parameters** window.

   *note*   Any name can be chosen for the local database, however when creating multiple databases, following a coherent naming convention will simplify database management.

7. In the main Stereology window, click in the image display and drag your cursor over all grid points that lie on the heart (figure 2). If points that are not on the heart are mistakenly selected, hold <**Shift**>, click and drag the cursor over to deselect them.

8. When you are finished selecting points on the current slice, press the **Next Slice** PowerBar button to move to the next grid slice (specified earlier in the 'Grid Slice Increment' field) and select the appropriate points. Continue in this manner until all grid slices have been examined.

9. Open the **Statistics** window (**Generate > Statistics**) to view the estimated volume of the heart.

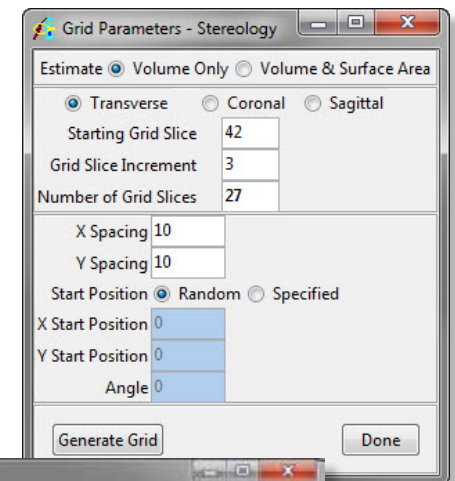10. Close the Stereology module before proceeding to the next exercise.
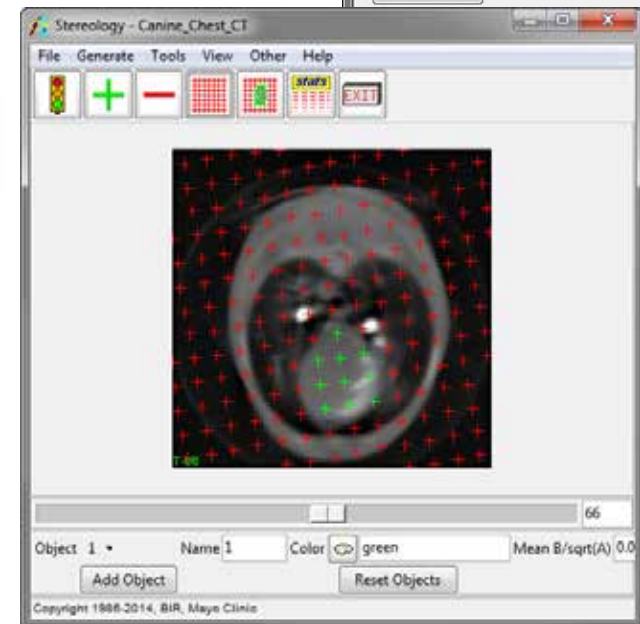


Figure 1



Figure 2

AnalyzeDirect

# Object Counter: Counting Cells

The Object Counter module allows a user to count the number of objects that occur on each slice of a loaded data set. The goal of this exercise is to count and measure cells from light microscopy data.

1. Load the **FatCells.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Object Counter** module (**Measure > Object Counter**).

3. Select the **PreProcess** tab. This tab allows for correction of intensity fall off near the edges of the image data by applying an Inhomogeneity Correction filter. Using the default settings, click **Apply**.

4. Select the **Connect** tab. This tab (figure 1) allows for the specification of region growing parameters used to segment objects, including whether the objects should be segmented in 2D or 3D (for this exercise, we will use 2D).

5. With 2D selected, set the following 'Connect' tab parameters:

   - **Max. Size: 3217**

   - **Min. Size: 50**

   - **Threshold Minimum: 106** (this will allow the cells to be separated from the background)

   *note*   The 'Max' and 'Min Size' parameters can be set by selecting the Interactive Size buttons next their respective text entry fields. Specify each by selecting either button and then drawing an ellipse around the largest/smallest object to be counted. Hold <Ctrl> while tracing forces the ellipse to be a circle.

6. Click **Apply**. All of the objects satisfying the size and threshold criteria will be identified and outlined in red on each slice of the volume.

7. Use the **Slice** slider bar to move through the slices in the data set. Return to slice 1 before proceeding to the next step.

8. Select the **Limits** tab. This tab allows interactive screening of segmented objects based on position and shape characteristics.

9. With the **Position** button selected, increase the **Y Min** to **11** using the arrow key found to the right. This will cause any objects with a Y coordinate less than 11 to be removed (objects along the bottom of the image display in the transverse orientation).
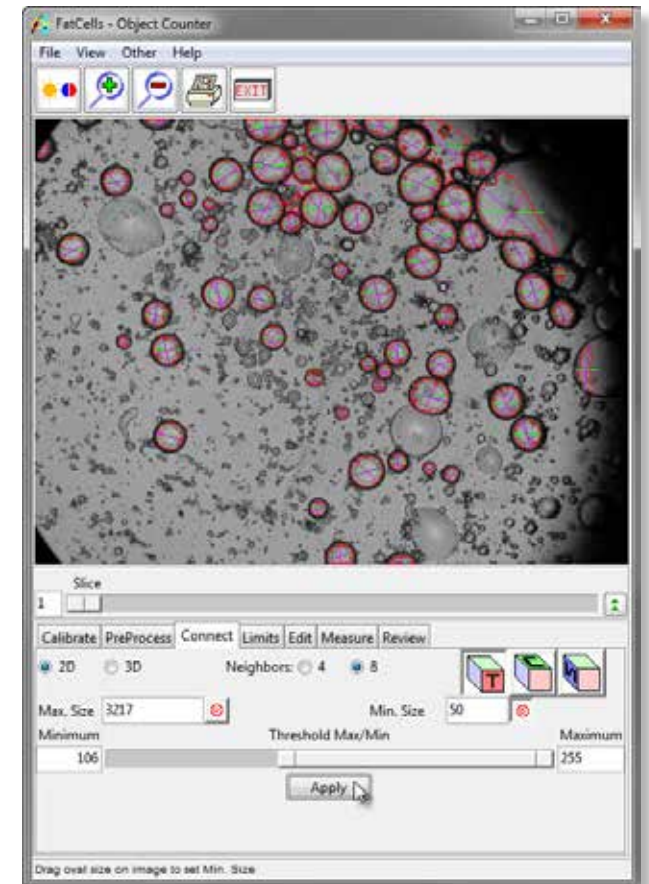


Figure 1

AnalyzeDirect

# Object Counter: Counting Cells

10. Reduce the **X Max** to **470** using the arrow key and observe the effect (seen along the right side of the image display).

11. By default, no shape screening is performed on the objects. Select the **Circularity** button, and check the **Restrict Circularity** option. Using the slider bar set the Circularity Maximum to 1.8.

12. Experiment with the effects of restricting Intensity, Diameter, Area, Perimeter, and Rectangularity.

13. Select the **Edit** tab. This tab allows objects to be added, deleted, and modified manually.

14. Select the **Measure** tab. This tab allows specification of the measurement statistics to be returned in the Object Counter Stats window.

15. To obtain a cell count on each slice click **Log Measurements** (without checking any of the options). The Object Counter Stats window will be returned, displaying a cell count for each slice (figure 2). Click **Done** to dismiss the window.

16. In the main Object Counter window select the **Measure** tab again. Check **Area** and then click **Log Measurements**. The Object Counter Stats window will be returned, displaying an object count for each slice and the average area of the objects on each slice.

17. To view the area for each individual object, select the **Detailed** option at the bottom of the Object Counter Stats window. When the 'Detailed' option is selected, click on any object in the Object Counter Stats window to highlight the object in the image display or vice versa (figure 3).

18. Experiment with other measurements available in the **Measure** tab.

19. Close the Object Counter module before proceeding to the next exercise.

*tip*   To save the Object Counter Stats as a .stats file for use in another application (such as Microsoft Excel), right-click in the window and select Save Log.
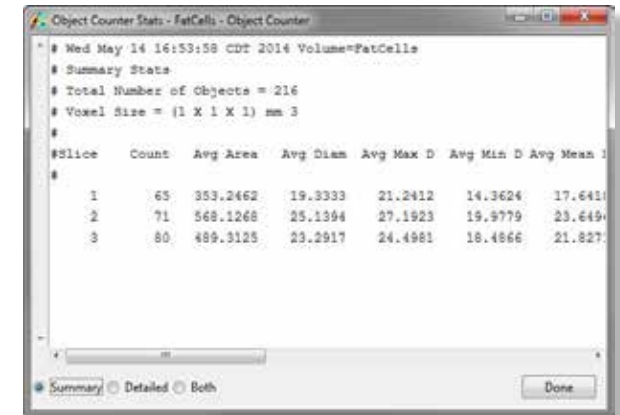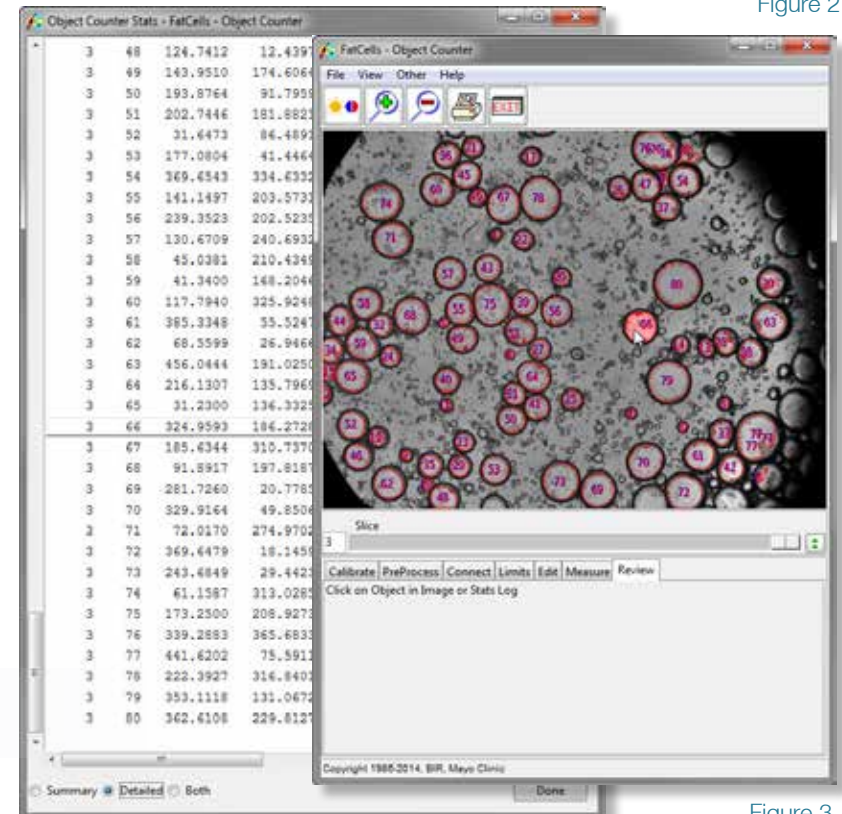
Figure 2

Figure 3

AnalyzeDirect

# Tree Analysis

The Tree Analysis module allows users to take an in-depth look at tree-like structures in medical images, such as coronary arteries. Branching angles, segment lengths, and cross sectional areas can all be measured with the module. This exercise will demonstrate how to use Tree Analysis to create, review, and sample a coronary tree.

## Tree Generation

1. Load the **Coronary_CT.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Open the **Tree Analysis** module (**Measure > Tree Analysis**).

3. Open the **Slice** window (**Generate > Slice**) and set **Slice** to **64**.

4. Open the **Generate Tree** window (**Generate > Generate Tree**).

5. Set the **Threshold Minimum** to **130** and **Maximum** to **255**.

6. Since the thinning algorithm used in the tree generation process is sensitive to holes within structures it is advised that the **Fill Holes** option always be left checked.

7. Leave the **Shortest Skeleton Branch** and the **Maximum/Minimum Tree Length** fields as their defaults.

8. Set the **Approximate Root Location** values to **X: 56, Y: 69, Z: 125**. Note that you can also set the Approximate Root Location by clicking in the main module window.

9. Click **Generate Tree**. The Tree Plot window will automatically be returned when the extraction is complete. The Tree Plot window can be used to view the trees generated and provides a number of tools for in-depth analysis of the structures.
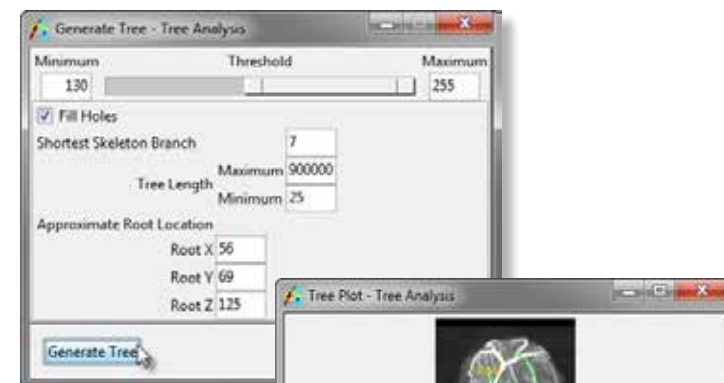
## Tree Display Options

10. To view the trees generated in the extraction process, use the Tree drop-down menu in the Tree Plot window. Select **Tree 2**.

11. Select all four of the **Views** buttons to display the left, top, right and bottom views of the tree.

12. Check **Render** from the **Display** options at the bottom of each window. A MIP rendering will be displayed behind each view of the trees. Experiment with the different Label and Display options.



Figure 1



Figure 2

AnalyzeDirect

# Tree Analysis

13. Several of the Action options can also be used to manipulate the tree display. With **Action** set to **Zoom**, click the + and - buttons to increase or decrease the tree display size. To magnify a specific area in a tree, click and drag a rectangle over the area in any of the displayed views.

14. Now, set **Action** to **Rotate**. Click in any of the views and drag the tree to a new rotation angle.

15. To return all views to their default display, right-click on any of the views and select **Reset**.

## Tree Manipulation

16. A new tree can be added by clicking the **New Tree** button. With **Action** set to **Add Point**, construct the new tree by drawing branches over the rendering in any of the views. The Add Point action can also be used to add branches to an existing tree.

17. An entire tree can also be deleted by selecting the **Delete Tree** button. Click **Undo** to recover deleted trees.

18. To only delete branches from a tree, set **Action** to **Delete Branch**. Click on a branch in any one of the views to delete it, all branches below it will also be removed from the tree.

19. Set **Action** to **Distance to Root** and check the Log option. Click on a point in the tree; the distance to the tree root from that point will be returned to a **Tree Distance Log** (figure 3).

20. Select **Stats** at the bottom of the Tree Plot window.

21. The Stats Option window returned allows specification of parameters used to calculate the various tree statistics (figure 4). The location where the resulting stats files are saved can also be set in this window. To calculate stats, press the Calculate Stats button.

22. The Tree Stats window (figure 5) displays the 'Summary' statistics for each branch of the tree. Select the 'Detailed' option from the bottom of the window to view statistics on each of the points in the branches.
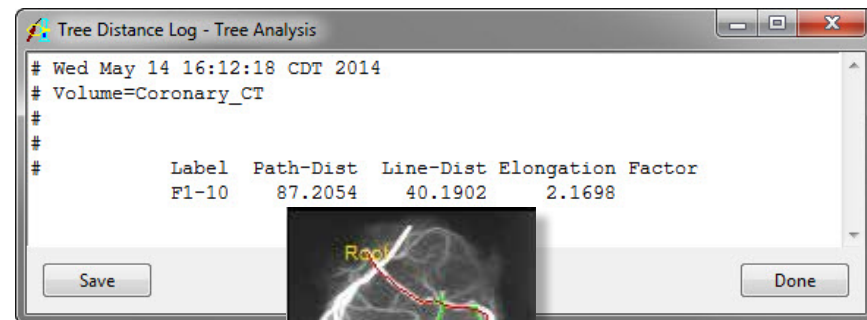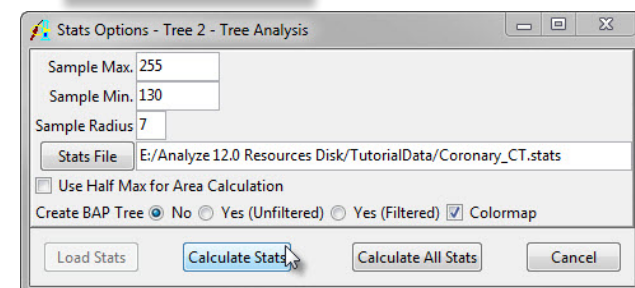


Figure 3



Figure 4



Figure 5

AnalyzeDirect
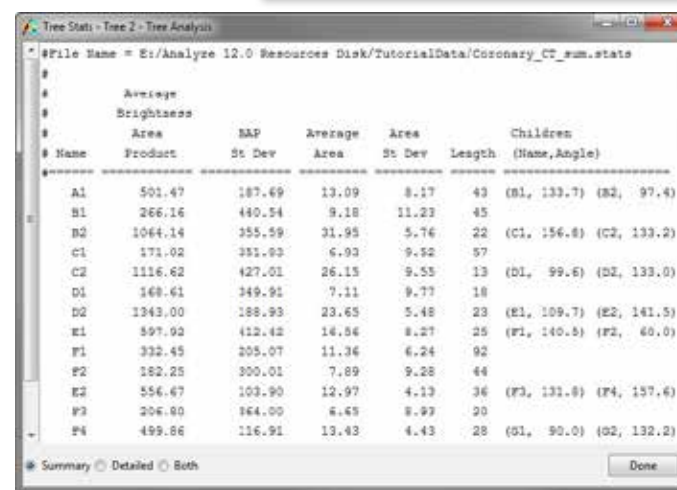
# Tree Analysis: *Generating a Fly-Through Movie*

1. Check **Internal** from the Display options in the Tree Plot window (figure 1).

2. Set **Action** to **Select** and click on the point in the tree from which you wish to begin your fly-through movie. The Renderings window will be returned.

3. By default, the Renderings window will display both fly-through sequence views: Away from Root on the left and Toward Root on the right (figure 2). Preview the sequence using the slider bar.

4. To generate the fly-through movie, right-click in the Renderings window and from the **Sequence** sub-menu, specify the direction of movement and the viewpoint for the movie. The movie will then automatically be saved to the main Analyze workspace and can be viewed with the Movie module (**Display > Movie**).

5. Close the Tree Analysis and Movie modules before proceeding to the next exercise.

Figure 1

Figure 2

AnalyzeDirect

# Apps & Add-Ons

**Analyze**Direct

# SISCOM *(Subtraction Ictal SPECT Co-registered to MRI)*

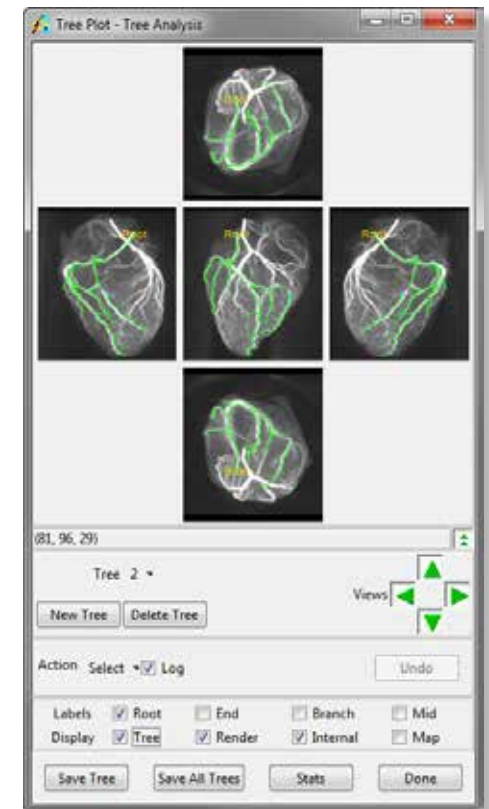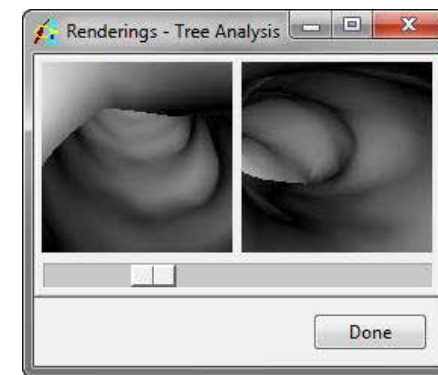Epilepsy Seizure Focus Localization with SISCOM (Subtraction Ictal SPECT CO-registered to MRI) automates the technique for advanced imaging of epilepsy patients that was developed with Analyze at the Mayo Foundation. This method uses a combination of SPECT and MRI imaging for improved diagnosis of areas of regional activation in the brain during a seizure. The SISCOM technique requires acquisition of ictal (during the seizure) and interictal (resting, or between seizures) SPECT images and an MRI volume spanning the entire brain. This exercise will demonstrate how to use the SISCOM module within Analyze.

1.  Load the data sets **SISCOM_Ictal_SPECT.avw**, **SISCOM_Interictal_SPECT.avw**, and **SISCOM_MRI.avw** from the **$:\BIR\images\TutorialData** directory.

2.  Select the data sets in the following order (hold down the <**CTRL**> key to select multiple data sets, or click using the middle mouse button):

    - **SISCOM_Ictal_SPECT.avw**

    - **SISCOM_Interictal_SPECT.avw**

    - **SISCOM_MRI.avw**

    Note the selection order: Ictal, Interictal, MRI. If the data is not selected in this order the SISCOM procedure will fail to run correctly.

3.  Open the **SISCOM** module (**Apps > SISCOM**).

4.  Open the **Register SPECT** option (**Process > Register SPECT**) to compute an activation map.
    i.   Set the Interictal SPECT minimum **Cerebral Activity Threshold** level to **75**. Note the change in the binary image.
    ii.  Ensure that the **Interictal Transformation Type** is set to **Linear**.
    iii. Use the **Activation Level** slider bar to set the standard deviation to 2.0.
    iv.  Next, select the **Register and Map** button. The Register SPECT tool will automatically register, normalize, subtract, select the statistically significantv oxels of activation, and output the activation map based on the parameters specified above. Note that the tool will update, displaying the Activation Map.

5.  Select **Next** to continue onto the next step of the SISCOM procedure, MRI brain extraction.
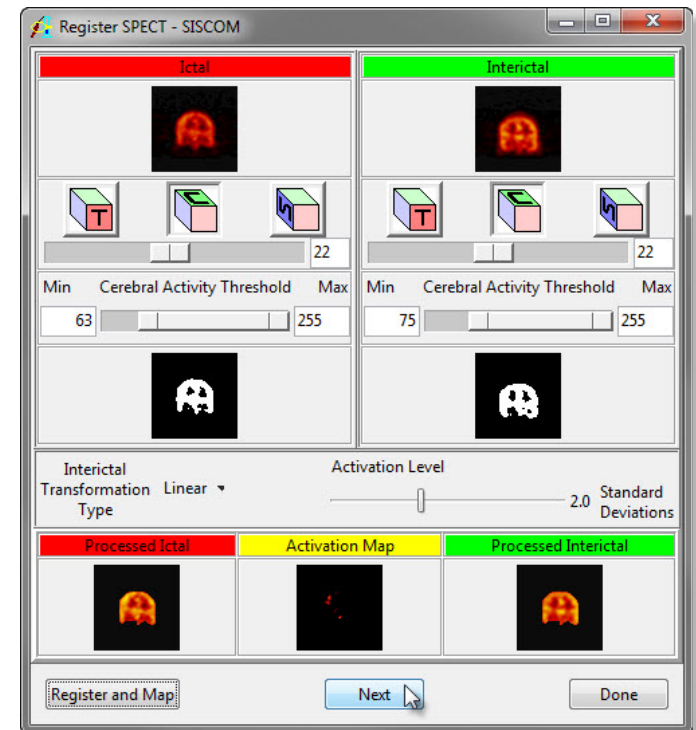


Figure 1

AnalyzeDirect

6. The Extract MRI Brain tool allows for segmentation of the brain for SPECT-MRI registration.

7. Right-click in the MRI data display window and select the Intensities option. In the Intensity (MRI) window returned, change the **Maximum** to **100** then click **Done** to close the Intensity Tool.

8. Use the slider bar to adjust the minimum and maximum threshold values to obtain the best definition of the cortical boundary as possible.

9. Select **Extract Brain** to segment the brain. After segmentation is complete, the extracted brain is automatically displayed in the Extract MRI Brain tool. The segmentation can be reviewed using the Slice slider bar (figure 2).

10. Select **Next** to continue to the next step, registration of the SPECT data sets to the MRI data sets.

11. The Fuse SPECT & MRI tool will automatically open and immediately run the Match Surfaces process, registering the SPECT data sets to the MRI data set and displaying the Activation Map overlaid on the MRI data set. The activation map and MRI can be reviewed using the orthogonal orientation buttons and the slice slider bar (figure 3).

12. Select **Fuse Volumes**. The activation map and MRI will be fused and automatically be saved to the Analyze workspace. Select **Done** to close the Fuse SPECT & MRI tool.
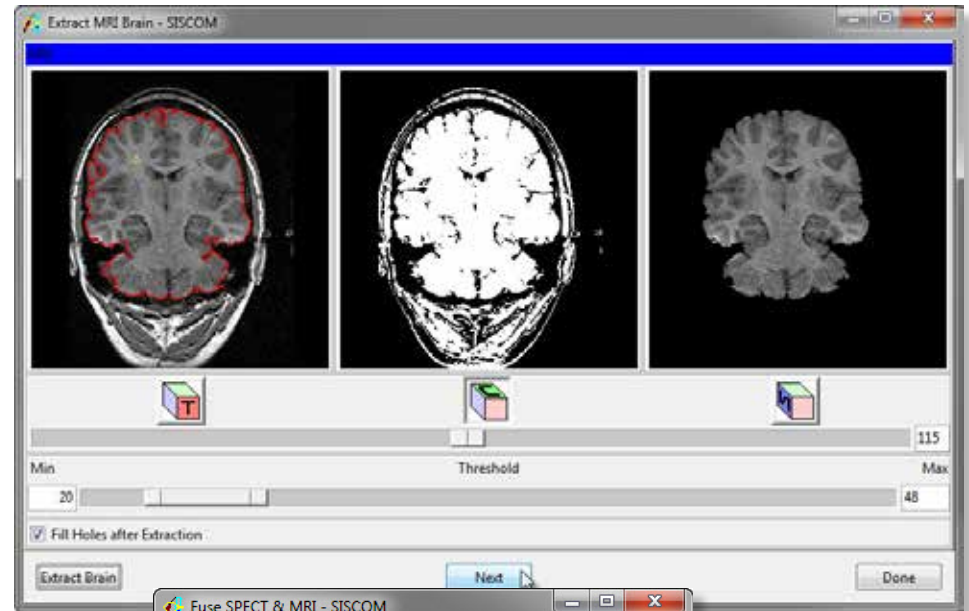


Figure 2
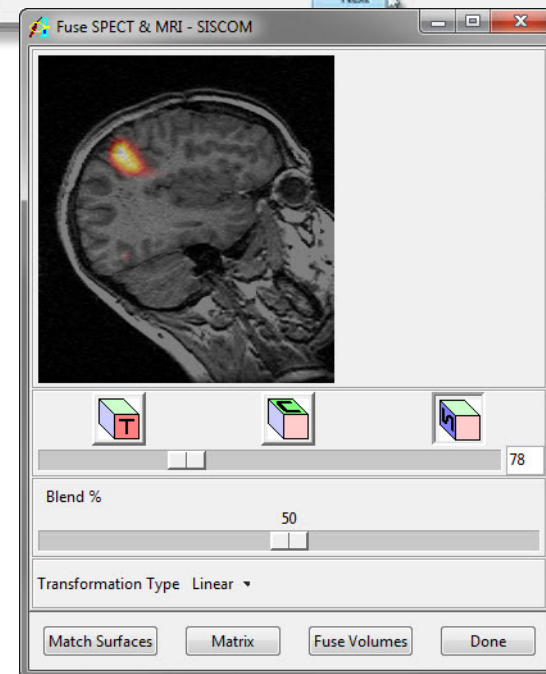


Figure 3

13. Select the **Compare Tool** option (**Process > Compare Tool**). The Compare Tool provides an interface for users to display and visually inspect the accuracy of the registration and fusion of the volumes created in the SISCOM process. Use the drop down menu options under each image to select the volumes to compare (figure 4). Select Done when review is complete.

14. Select the **Create Object Map** option from the **File** menu to generate an object map based on the areas of activation.

15. Select **Output Object Map**. The object map will be automatically saved to the location specified using the File option. The Render tool (figure 5) will automatically open, allowing for interactive review of the object map.

16. Close all windows related to the SISCOM module before proceeding to the next exercise.



Figure 4



Figure 5

# Mayo 3D Brain Atlas
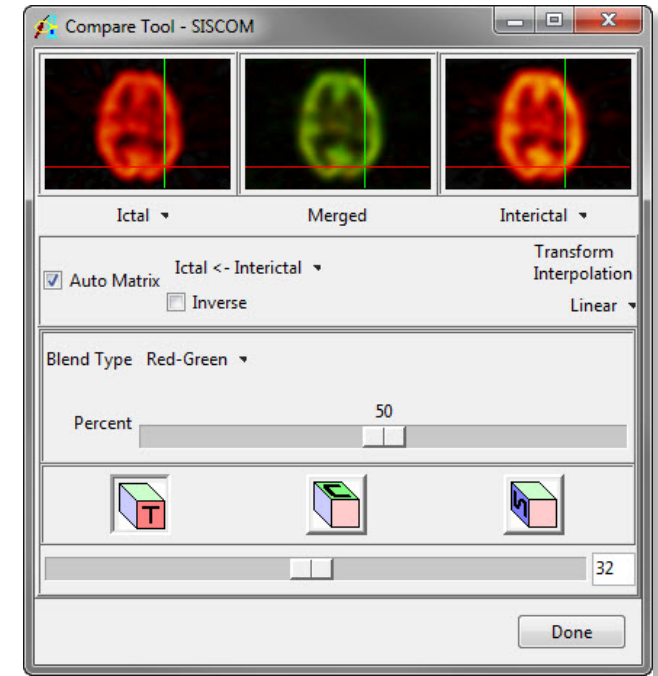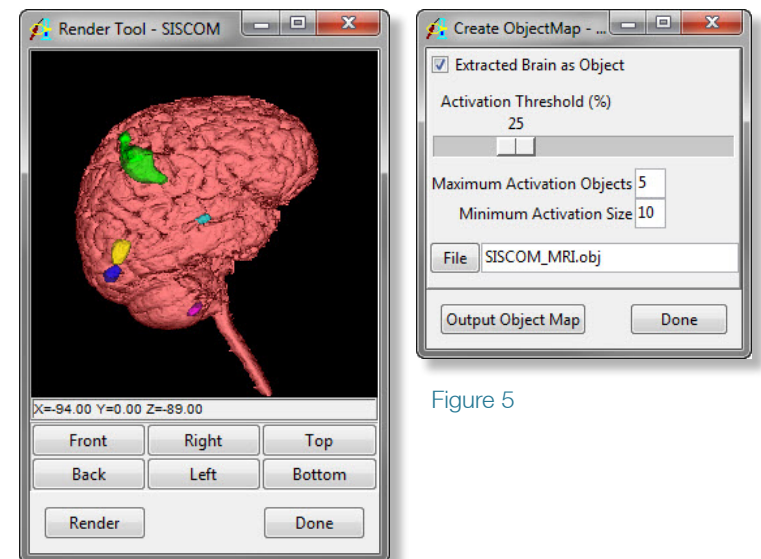
The Analyze Mayo 3D Brain Atlas add-on provides a unique 3D implementation of the Talairach anatomical atlas of the human brain. The Mayo 3D Brain Atlas add-on allows for 3D navigation of the atlas and interactive query and reporting of atlas-based coordinates in many common volumetric and neuroanatomical and neurofunctional frames of reference, including TT, MNI, SPM, FSL and ICBM coordinates. In addition, atlas-derived neuroanatomical regions can be output from the module and then utilized directly in many other Analyze modules. This exercise will demonstrate how to use the Mayo 3D Brain Atlas add-on.

1. Load the **MRI_3D_Head** data set from the **C:\BIR\images\TutorialData** directory.

2. Select the **MRI_3D_Head** data set then open the Mayo 3-D Brain Atlas module (**Apps > Mayo 3D Brain Atlas**).

3. The PowerBar buttons in the main Mayo 3D Brain Atlas window are set up in the sequence of operations performed. The first step to using the atlas is AC-PC based alignment of the loaded image data to the Talairach-Tournoux coordinate and proportional grid system.

4. Open the **Align AC-PC** window (**Tools > Align AC-PC**).

5. Use your cursor to move the **AC** and **PC** points to the appropriate location on the sagittal image. Enlarging the image may help to identify the AC and PC; right-click on the display and select **Size > Double**. Note that the left and right arrows and rotation buttons can be used to adjust the data set to correct for symmetry.

6. Select the AC point and move it to the appropriate location. The magnify window will automatically display helping you to determine the precise location of the AC (figure 1).

7. Select the PC point and move it to the appropriate location.

8. Select **Align AC-PC**. The image volume will realign to the AC-PC.

9. Select **Next** to open the **Extract Brain Tool**. A seed point and threshold range are automatically set by the Extract Brain Tool. These can be adjusted if necessary.

10. Check the **Fill Holes after Extraction** option and then select **Extract Brain**.

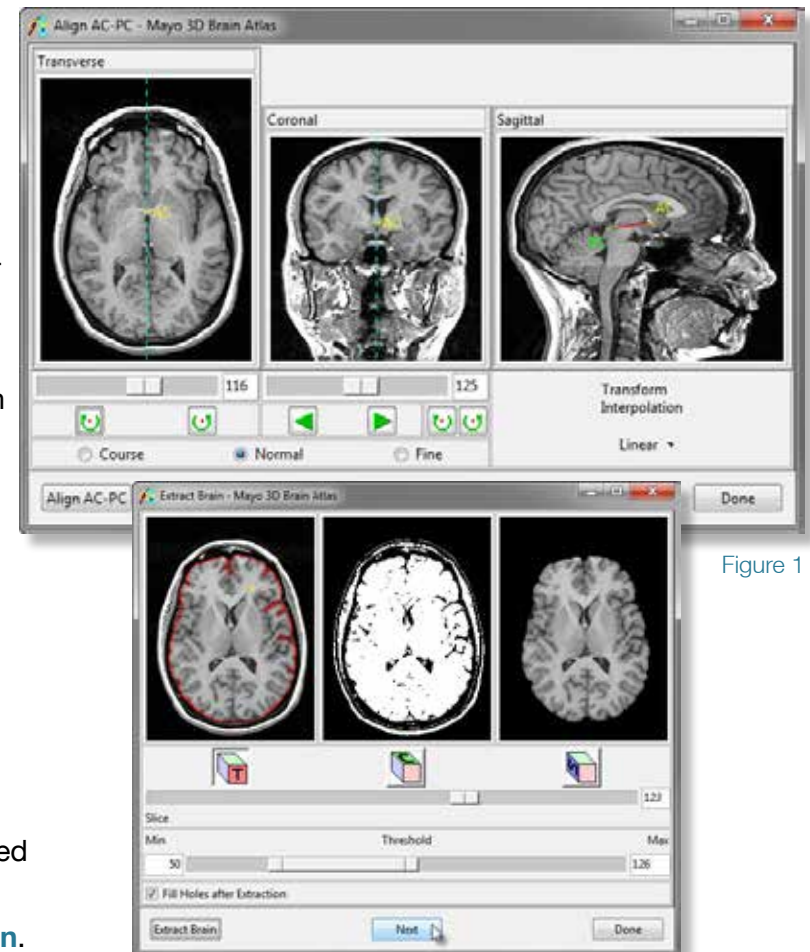11. The extracted brain can be reviewed using the **Slice** slider bar (figure 2).



Figure 1



Figure 2

AnalyzeDirect

# Mayo 3D Brain Atlas

12. Select **Next** to open the **Adjust Registration** tool (figure 3). If needed the atlas can be adjusted. Right-click in any of the orthogonal display panes and select **Restrict > None**. Note the right-click menu also provides options to display the loaded or extracted volume and increase the display size.

13. The grid can now be manipulated. Move the grid lines in any of the orthogonal displays to adjust the atlas. When you are finished making adjustments, right-click in any of the orthogonal displays and set **Restrict** back to **All**.

14. Move the yellow square marker in any of the orthogonal displays to move through the loaded volume. Note that when the marker is moved the name of the atlas region and the coordinates of the current marker point will appear in the lower left-hand corner of the window.

15. To query specific structures by coordinates, navigate back to the main module window and select the **Query Atlas** button from the PowerBar.

16. The **Adjust Registration** window and the **Query Atlas** window work together. The Query Atlas window will return the atlas structure and coordinates for the current location set in the Adjust Registration window.

17. In the Adjust Registration window, move the Yellow marker to a location you wish to query.

18. In the Query Atlas window click the **Query** button, the structure and location of the Yellow marker will be returned.

19. Check the **Query Range** option and set the **Range** to **5**. Click the **Query** button again. All structures with in a 5 voxel range will be reported in the query window (figure 4). Please note: The information returned can be saved as a text file by right-clicking in the Query window and selecting the **Save As** option.

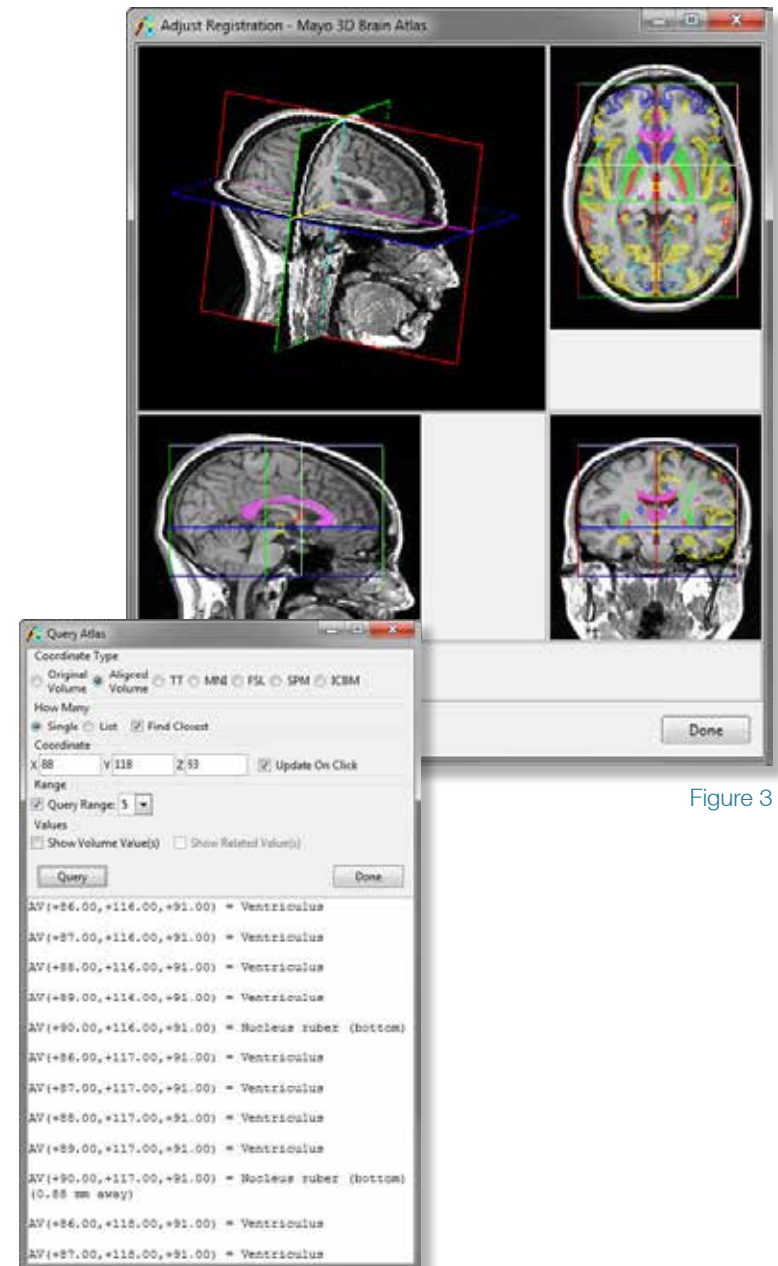20. Close the Query Atlas and Adjust Registration windows.



Figure 3



Figure 4

AnalyzeDirect

21. To save the atlas as an object map open the Generate Output window by clicking on the Output button in the PowerBar.

22. In the Generate Output window returned (figure 5), make sure the following options are set:
    - i. Set **Output What** to **Specified Atlas**
    - ii. Set **Space** to **Original Volume**
    - iii. Set **Which Atlas** to **Transverse**
    - iv. Set **Output As** to **Object Map**

23. Next change **Object(s)** to **Specified** and then click on the **List** button. The **Object List** window returned allows you to select only the objects you wish to output to the object map, click **Done** to close the window and then set **Object(s)** back to **All**.

24. Select Generate Output. The object map will be saved as '**AtlasOutput_MRI_3D_Head.obj**' in the specified directory.

25. Select Done in the Generate Output window and close the Mayo 3D Brain Atlas.

26. To review the Atlas object map created, select the **MRI_3D_Head** data set from the Analyze workplace and then open the Multiplanar sections module. Select **File > Load Object Map** and load the object map saved in step 23. Select the Traffic Signal icon to begin the sequence display of the data.

27. Close all windows before proceeding to the next exercise.
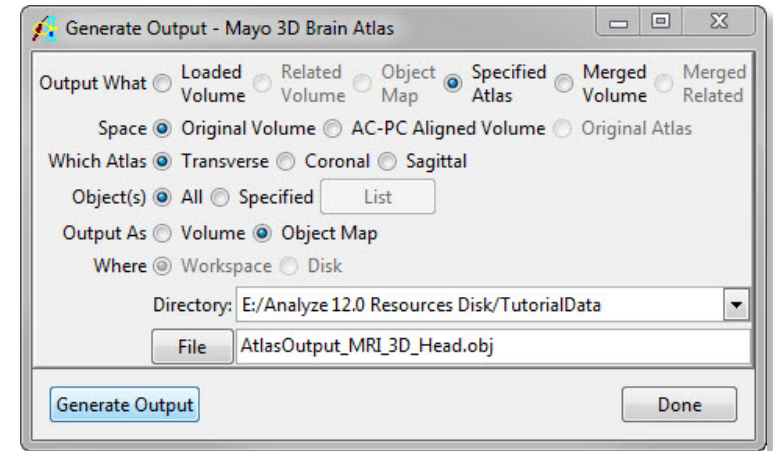


Figure 5

# Diffusion Tensor Imaging (DTI)

The Analyze MR Diffusion Tensor Imaging add-on computes and saves the primary diffusion maps from diffusion-encoded MRI data. The module also provides standard visualizations of DTI data and includes white fiber tracking and visualization (Tractography). This protocol will demonstrate how to compute DTI maps as well as compute and display fibers.

## Loading DTI data and Computing DTI Maps

1. To load in a series of DTI data open the **DICOM Tool** (**File > DICOM Tool**), then import the DICOM images (**File > Import Dicom Images**). Navigate to the folder containing the DTI data, and click **OK**. A dialogue window will be returned asking if you would like to import all DICOM files found below that directory, click **Yes**.

2. Select all the DTI files and click **Load Volume**. In the dialogue window returned, select **Create a 4D Multivolume**.

3. Once the volumes are loaded into the workspace, select the appended multivolume (Figure 1).

4. Open the **DTI** module (**Apps > DTI**), the module will open to the **Config** tab (figure 2).

5. Analyze will attempt to automatically load the gradient directions. If the gradient directions are not automatically loaded, click the **Load Gradient Directions** button and select a text file with the gradient directions already logged.

6. The data may require a flip along an axis.

7. Select the **Map Processing** tab.

8. Set a threshold so the background noise is set to white, any voxels displayed in white will not have map values computed (figure 3). Click **Compute DTI Maps**.
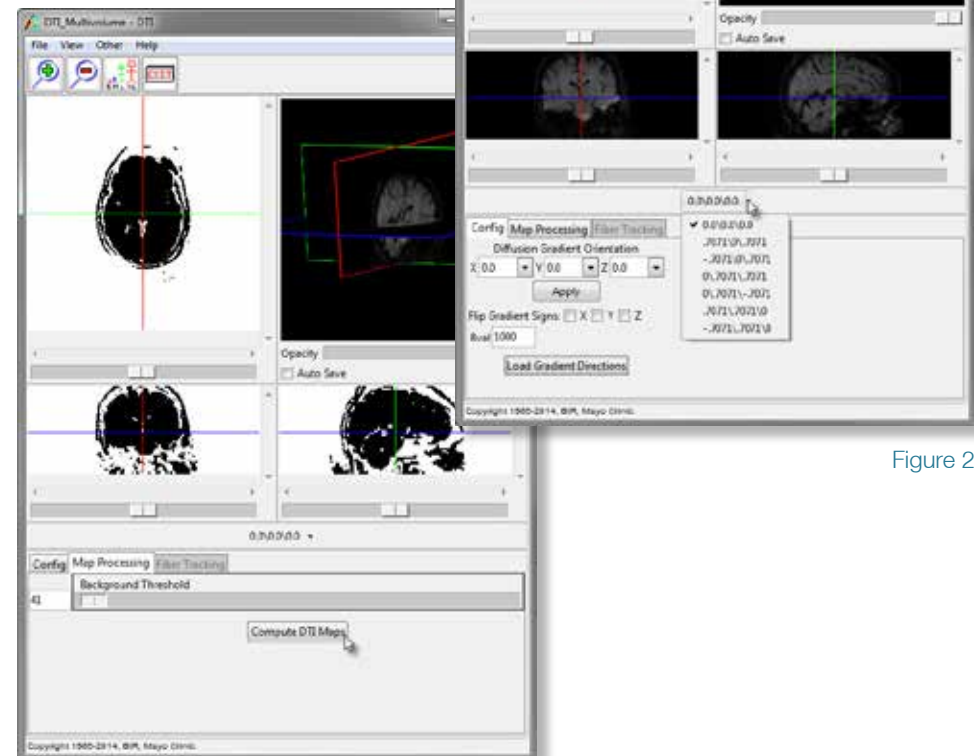
Figure 1

Figure 2

Figure 3

AnalyzeDirect

9.  After the DTI Maps have been computed, select **File > Save DTI Maps**. In the window returned, set the **Destination** to **Analyze Workspace** and click **Save Volume**.

10. All the DTI Maps will be output to the Analyze workspace.

11. To define a region of interest, select the **FA** map and the **EVCM**. Open the **Region of Interest** module (**Measure > Region of Interest**).

12. By moving the slice slider bar, select a slice that contains a region of interest. In this example, we will define the corpus callosum.

13. To begin defining, select the **Auto Trace** tool and set a seed point within the corpus callosum. A doubled ended threshold bar will be returned in the ROI window.

14. For this example, we set the **Minimum Threshold** to **143** and a **Maximum Threshold** of **237**. Click **Apply** to define this trace as an object.

15. Next, we will move to the next slice and set another object for the corpus callosum. Click to set a seed point within the region, and the threshold previously set should be automatically populated.

16. Click **Apply** to create a second object.

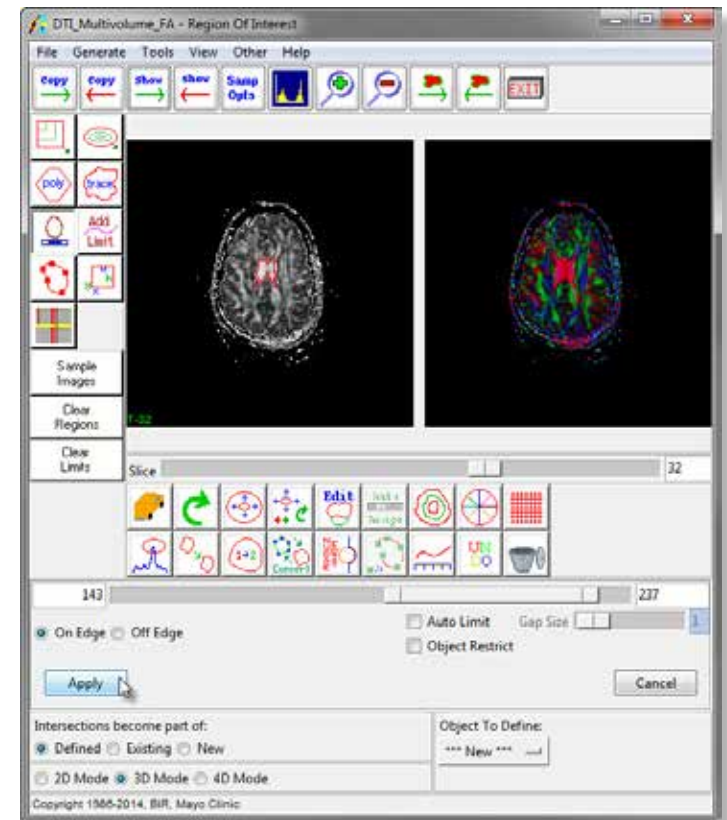17. Now that there are multiple objects defined, save the object map (**File > Save Object Map**).



Figure 4

18. Return to the DTI module and click on the **Fiber Tracking** tab. Click the **Load Object Map** button. Select the object map from the last section, and click **Open**. The two objects defined in the last section will be displayed.

19. Click the **Compute Fibers** button. Once the computation is complete, click the **Display Fibers** button.

20. In the display window, the fiber bundles are displayed (figure 5). You will see the fibers displayed in the object color they were assigned in the Region of Interest module. To zoom in or out on fiber bundles, hold the middle mouse button while moving the mouse forwards and backwards.

21. To rotate the fiber bundles, hold the left mouse button and move in the direction you wish to rotate.

22. To move the bundles within the window, hold the right mouse button and drag the bundles around the window.

23. To change the opacity of the image data, use the **Opacity** slider bar just below the window containing the fiber bundles.

24. Now under the **Boolean Operator**, select **AND**. Click **Display Fibers**. This operation will just show the fibers that are connected to Object 1 AND Object 2. The metrics of these fibers can be logged by clicking **Log Displayed Fiber Metrics**.

25. You can save these metrics out by clicking **Save** in the window returned. These metrics can then be imported into an excel spreadsheet.
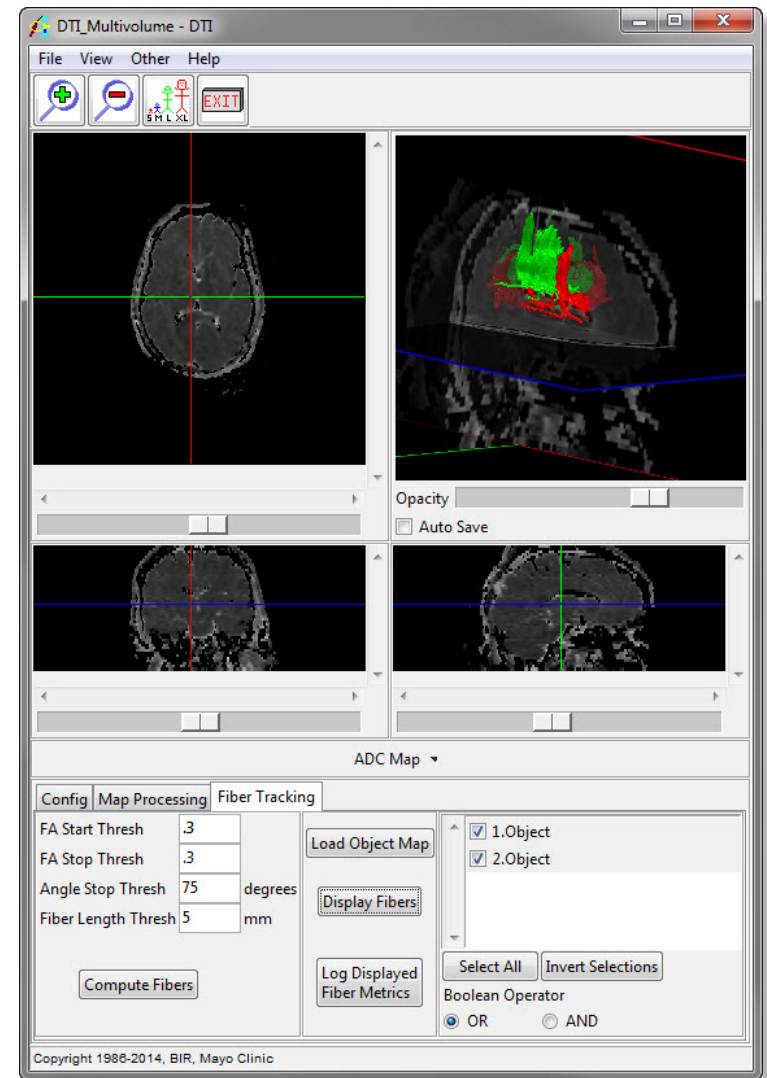


Figure 5

# T2 Projection

The MRI T2 Optimization Add-On provides the ability to enhance the relative contrast between different tissue types in T2 weighted MR images postacquistion. The add-on uses a piecewise non-linear intensity transformation based on prior knowledge. The prior knowledge is derived from training multiple post-processed data sets acquired at different relaxation (TR) and echo (TE) times. The transformation does not make any assumption on the pulse sequence parameters associated with the image to be projected. This exercise will demonstrate how to use the add-on to enhance a T2 MRI data set.

1. Load the **MRI_T2.avw** data set from the **$:\BIR\images\ TutorialData** directory.

2. Open the **T2 Projection** add-on (**Apps > T2 Projection**).

3. The input, or pre-enhanced, T2 data is displayed on the left side of the window, the post enhanced data is displayed on the right side.

4. Click **Show Forward**, until **Slice 15** is displayed.

5. The **Relaxation Time** (TR) can be adjusted by selecting a value from the TR (msec) drop-down menu. Select **1800**. Note that the post-enhanced display updates when a new value is selected.

6. Similarly, the **Echo Time** (**TE**) can be adjusted by selecting a value from the **TE** (msec) drop-down menu. Select **110**.

7. To save post-enhanced T2 select the **Create Projection** button. The projection will be saved to the Analyze workspace. Note the enhanced images are named according to the TR and TE values used. For example MRI_T2_1800-110.

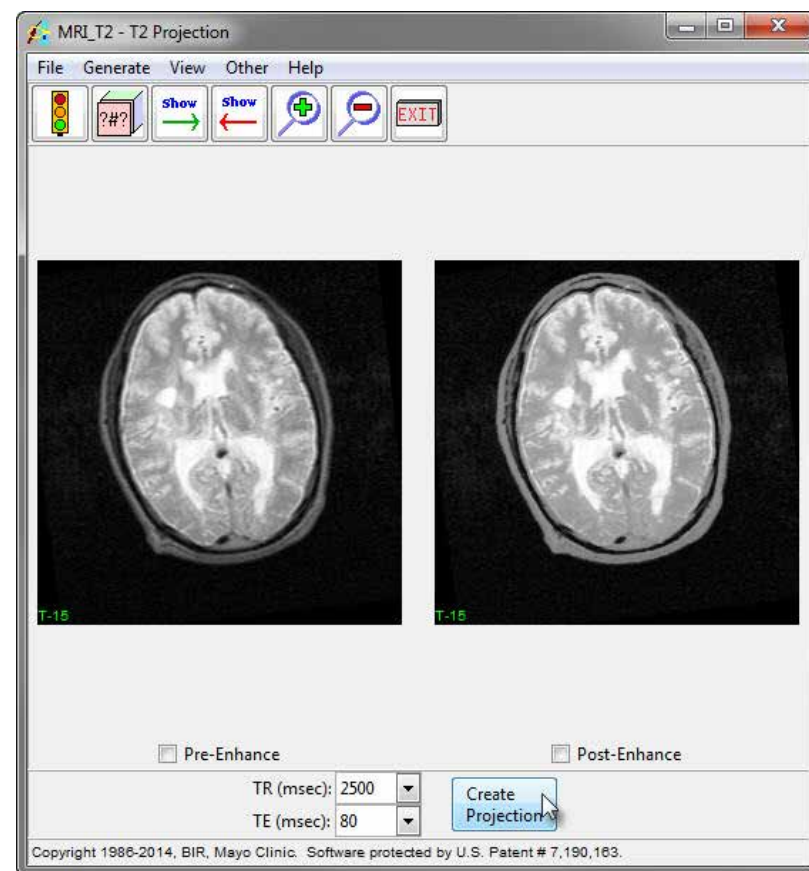8. Close all windows associated with the T2 Projection module before proceeding to the next exercise.



Figure 1

AnalyzeDirect

# Volume Metrics

The Volume Metrics Add-On provides tools to assess the quality of multiple associated volumes, allowing the creation of a set of statistics based on the type of metric chosen. The add-on can be used to assess the similarity of two co-registered three dimensional volumes using 15 parametric or 12 non-parametric similarity indices. The add-on can also be used to assess the concordance of different segmentation results with ground truth data using 47 popular binary similarity metrics. This exercise will demonstrate how to compute similarity metric values for two related data sets.

## Calculating and Logging Metrics

1. Load the **MRI_3D_Head.avw** and the **MRI_3D_Brain.avw** data sets from the **$:\BIR\images\TutorialData** directory.

2. With both volumes selected, open the **Volume Metrics** module (**Apps > Volume Metrics**). The first volume selected is the input volume, the second volume is the comparison volume.

3. To calculate all of the statistics for a specific metric option, select the **Metric Type**, then click the **Calculate Metrics** button. The metrics are calculated and displayed next to each Similarity Value.

4. To log the metrics in a log file, click on the **Log Metrics** button.

5. The **Volume Metrics Log** (figure 2) contains all of the metrics that are checked in the main window. To save the metrics log file to disk, right click in the log window and select **Save Log**.
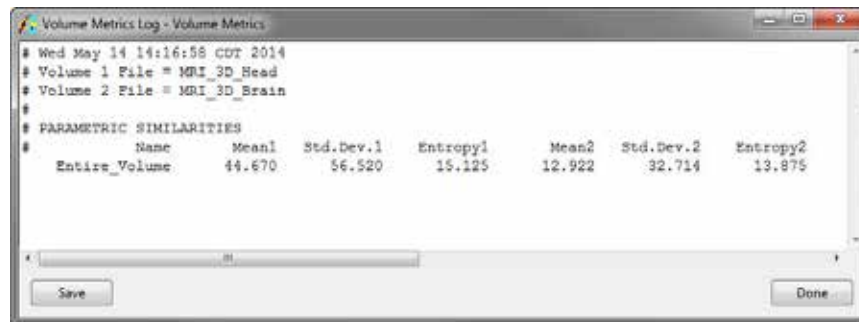
6. Click **Done** to close the log screen.
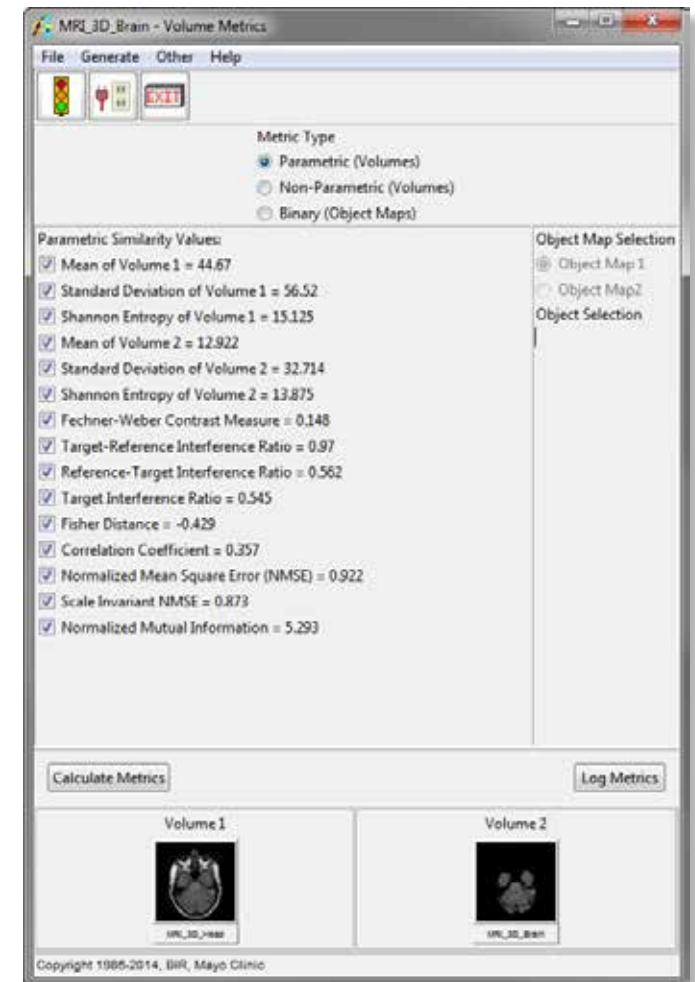


Figure 2



Figure 1