Analyze 10.0
Essential Training Guide

Table of Contents

Table of Contents

Table of Contents

Analyze 10.0

Getting Started

Introduction

Welcome to the Analyze 10.0 Essential Training Guide. This document provides an overview of Analyze 10.0 core functionality through 56 exercises that guide new users step-by-step through basic and advanced Analyze procedures. A fully comprehensive overview of all Analyze 10.0 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 10.0, please refer to the Analyze 10.0 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 10.0** and choose **Help > Tutorials.**

3. Click **Install Tutorial Data** at the bottom of the Tutorials window. Note, if the tutorial data has already been installed 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**).

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
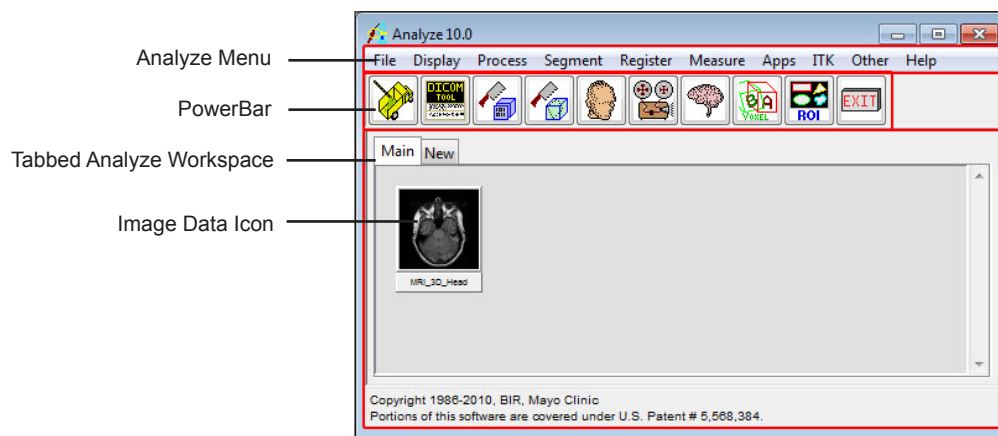
Loading Data into Analyze

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.

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.

note | To select multiple data sets hold down the <Ctrl> key while making selections with the mouse. Alternatively use the left mouse button to select the first data set and the middle button (if available) to select additional data sets.

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.
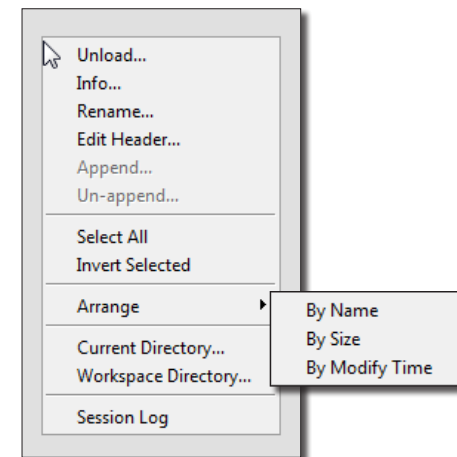
Main Analyze Window Quick Keys

<**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.

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.

The **Display** menu contains the Analyze modules that involve the display, visualization, and manipulation of image data:
- Multiplanar Sections
- Oblique Sections
- Volume Compare
- Volume Render
- Surface Render
- Virtual Endoscopy
- Movie

The **Process** menu contains the Analyze modules that are used for processing and classifying image data:
- Image Calculator
- Image Algebra
- Histogram Ops
- Spatial Filters
- Filter Designer
- 3-D FFT

The **Segment** menu provides facilities for image segmentation:
- Image Edit
- Morphology
- Watershed
- Multispectral Classification
- Object Extractor
- Surface Extractor

The **Register** menu contains all of the Analyze tools for image registration:
- 2-D Registration
- 2-D Non-rigid Registration
- Point to Surface
- 3-D Surface Registration
- 3-D Voxel Registration
- 3-D Non-rigid Registration

The **Measure** menu contains an extensive selection of measurement modules:
- Line Profile
- Region of Interest
- Stereology
- Object Counter
- Tree Analysis

The **Apps** menu option contains add-on modules available for Analyze:
- SISCOM
- Mayo 3-D Brain Atlas*
- DTI*
- T2 Projection*
- Volume Metrics*

The **ITK** menu contains modules that provide access to the Insight Toolkit (ITK):
- Filter
- Segment 2-D
- Segment 3-D
- Registration

*These modules require the purchase of an additional license

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.

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, Object Extractor, 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 [**A**], 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** [**B**]: 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 [**C**] 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 [**D**].
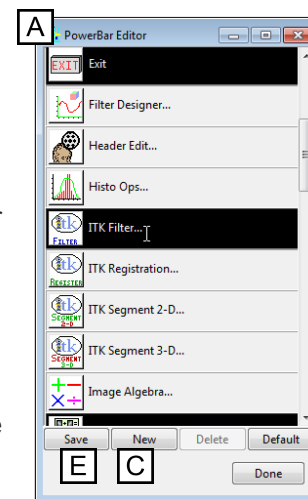
note | Be sure to press Save [E] in the PowerBar Editor if you wish to keep your PowerBar changes for future sessions. Otherwise, changes will be lost upon existing the Analyze module, or Analyze.
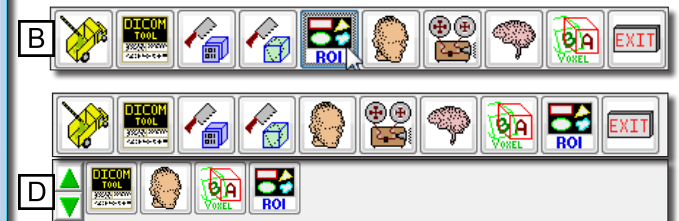
Analyze 10.0

Loading Data
Into Analyze

Exercise 1 : 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'; chance the Local Database Name to **TEST_5679** [**A**].

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 [**B**].

8. To create the local database click the **Create Local Database** button [**C**].

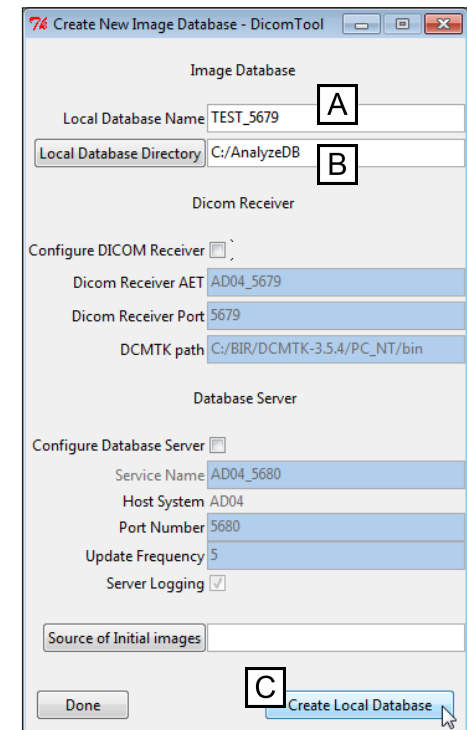9. Once the database has been created a dialog box will be returned stating 'All Done', click **OK**.

Figure 1

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** [**D**]; 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).
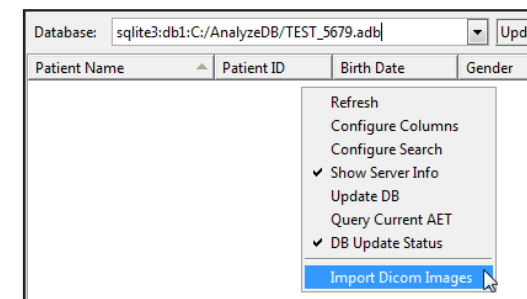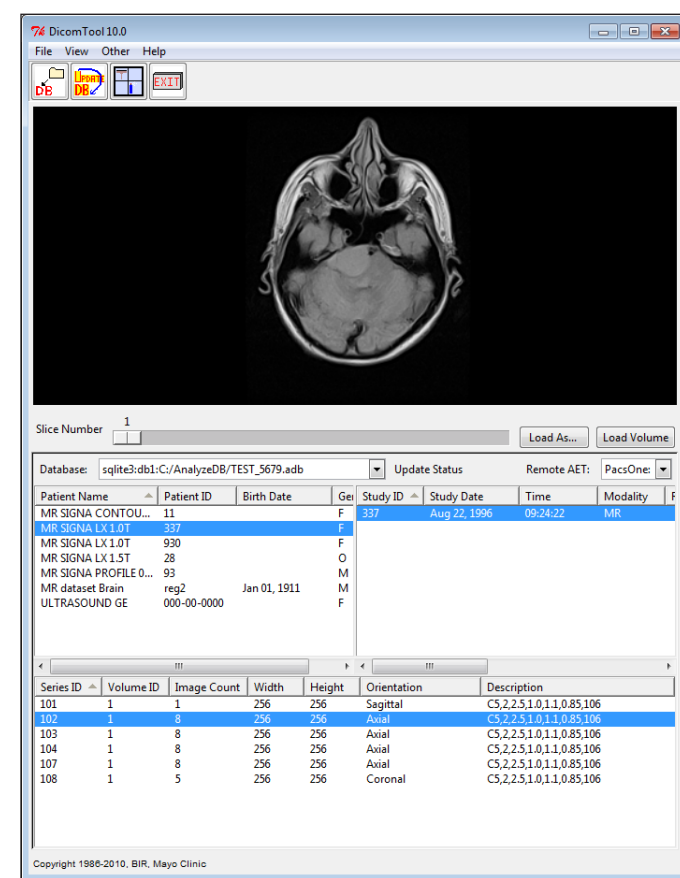

Figure 2

Figure 3

Exercise 2 : 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 BirPac user please contact support@analyzedirect.com for instructions on migrating your database to 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** [A] 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.
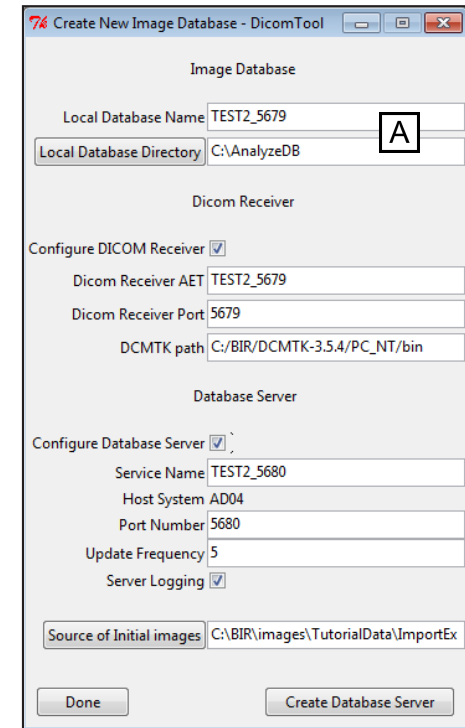
Figure 1

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 [**B**].

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 **$:\BIR\DCMTK-3.5\$System_Type$\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.

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 [C].

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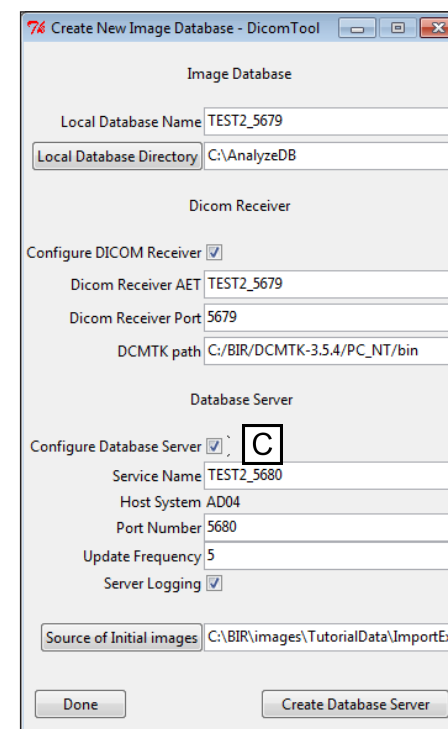
tip | It is recommend using a closely related port number so they can be easily remembered; e.g., if the receiver is running at port n, run that database server at port n+1.

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** [**D**].

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** [**E**]. 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 [**F**] 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 [**G**] below. Select **Series 102**.
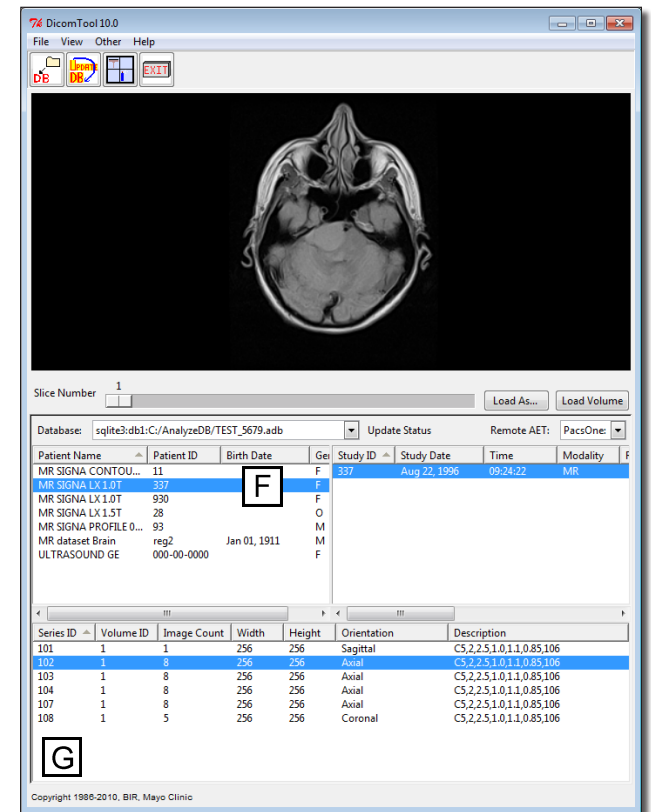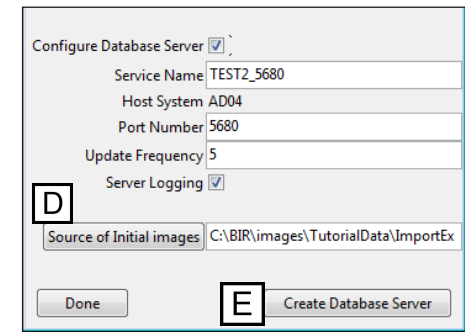
Figure 2

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)
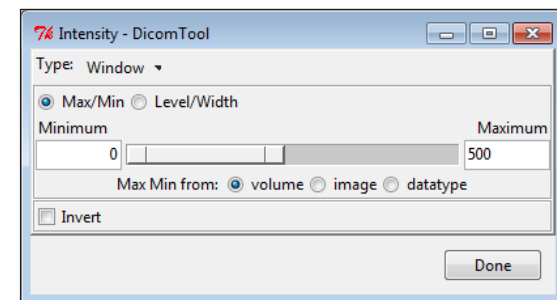

Figure 3

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 and 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.

> *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.

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

Figure 4

Exercise 3 : 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).
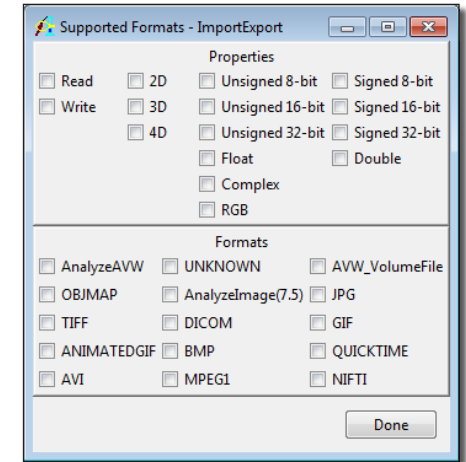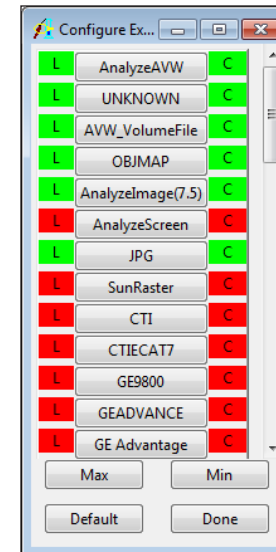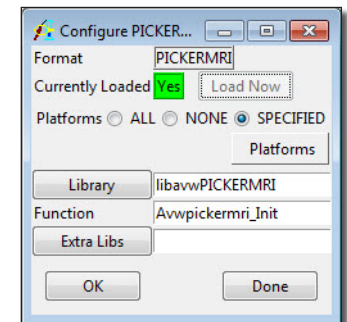
Figure 1

Figure 2

Figure 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 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.

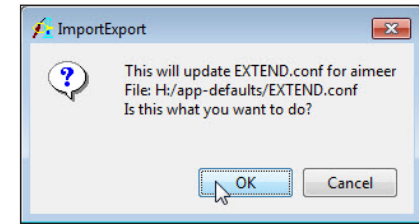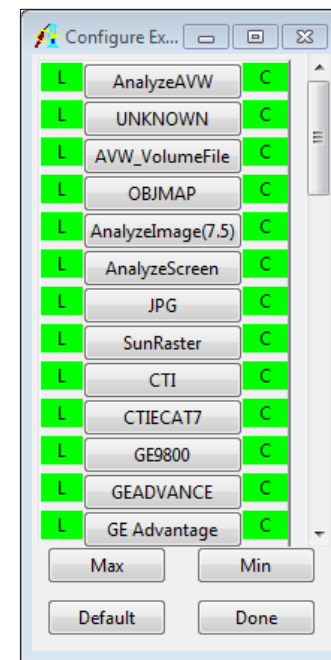11. Close the Import/Export module before proceeding to the next exercise.

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.
VolumeFile	enables lists of 2D files to be used as a 3D entity
OBJMAP	enables object maps to be treated as regular images
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 Protable 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

Video

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

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

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

Exercise 4 : Load As Loading and Resizing Anisotropic

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** [**A**] 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 [**B**] 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 [**C**] (figure 1).

5. Check the **Force Cubic** option [**D**] and click **Load**; 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 [**E**] 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 [**F**] 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.
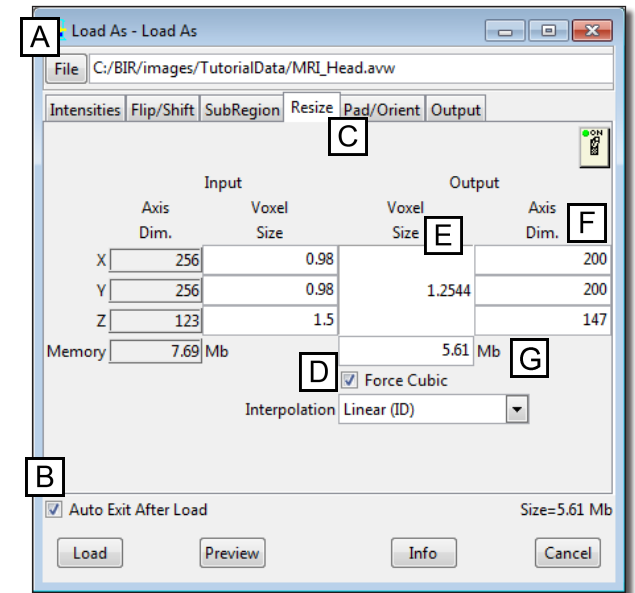

Figure 1

Exercise 5 : Import/Export Converting Raw Data into 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** [A](or check 'Auto Offset' to compute this automatically)
    *   **Width: 256** [B]
    *   **Height: 256** [C]
    *   **Data Type: signed 16-bit** [D]
    *   **Byte Swap: Pairs** (this only needs to be set on a little-endian architecture, i.e., PC-based systems) [E]

Figure 1

Figure 2

8. Check the following **Auto** options [**F**]:
   • **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.
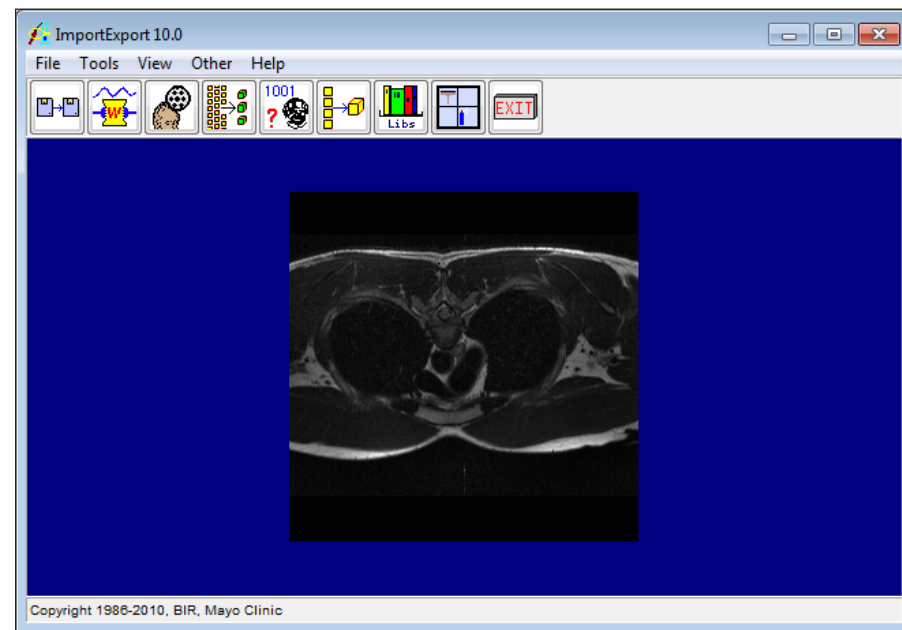
Figure 3

Exercise 6 : 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.

> tip | The volume file saved can now be loaded into Analyze using the Load or Load As modules. Alternatively you can load the volume file directly into the Analyze workspace from the Volume tool by clicking 'Load'.
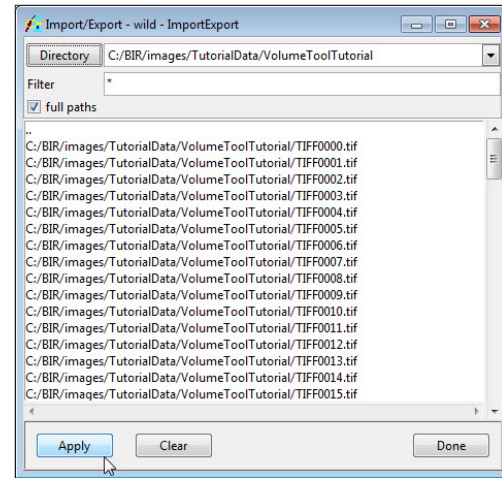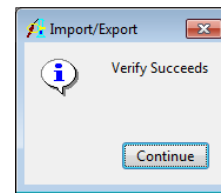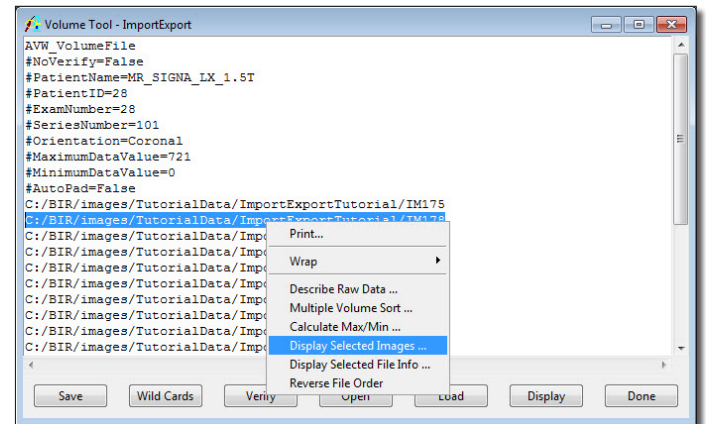
Figure 1

Figure 3

Figure 2

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

Exercise 7 : 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_ Head.avw** from the **$:\BIR\images\TutorialData** directory.

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

Figure 1

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.

> *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.
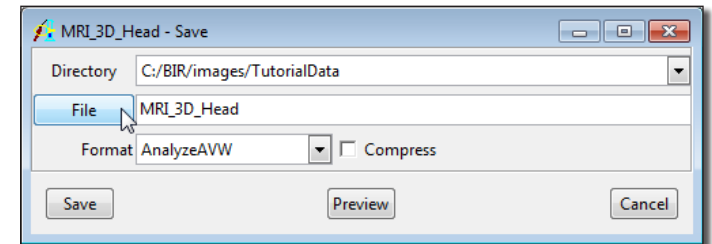
Analyze 10.0

Display & Visualization

Exercise 8 : 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.
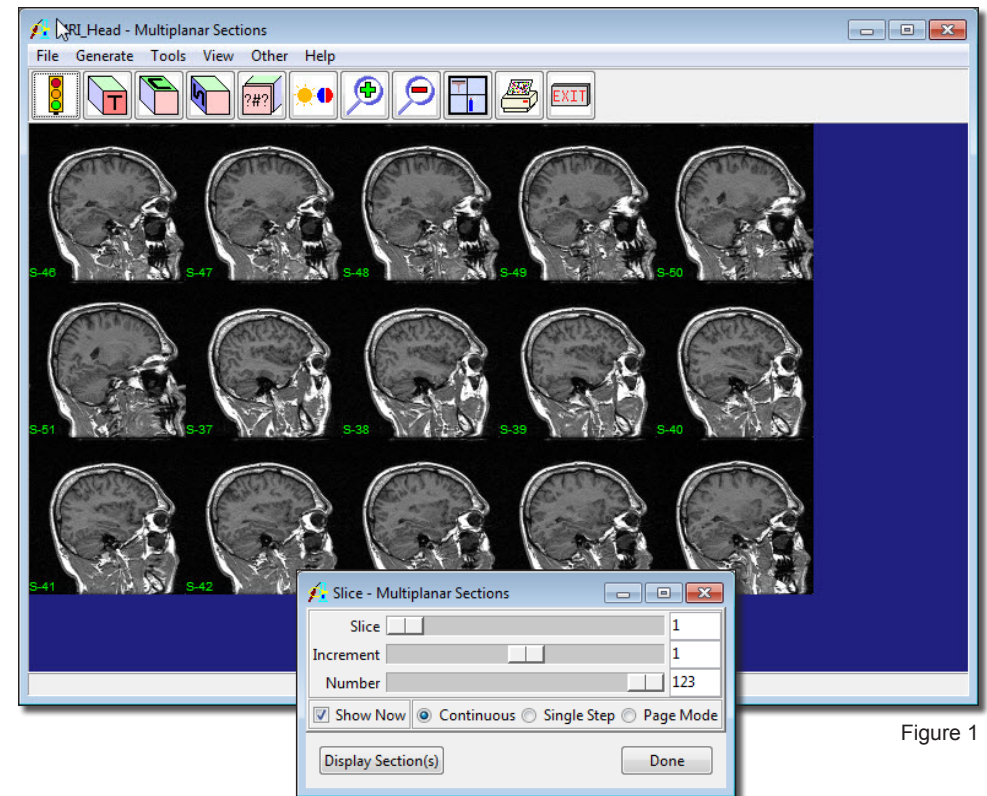

Figure 1

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.

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.

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 [**A**]. The view angle can also be changed by clicking in the image display [**B**] and dragging the image to a new view.

9.   Use the **Slice X**, **Y**, and **Z** slider bars [**C**] 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 [**D**] 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**).
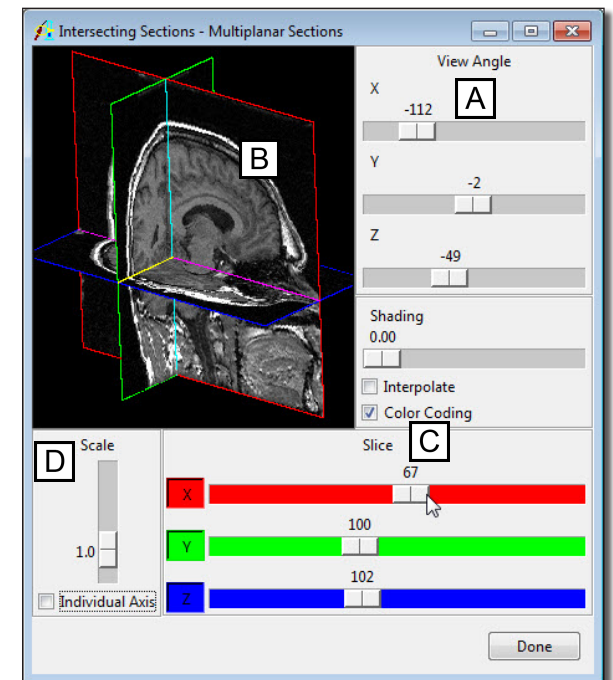

Figure 2

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** [A] and **Scale** [B] 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 revel interior sections of the cube with the **Subregion X**, **Y**, and **Z** double-ended slider bars [C]. 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

Additional Task
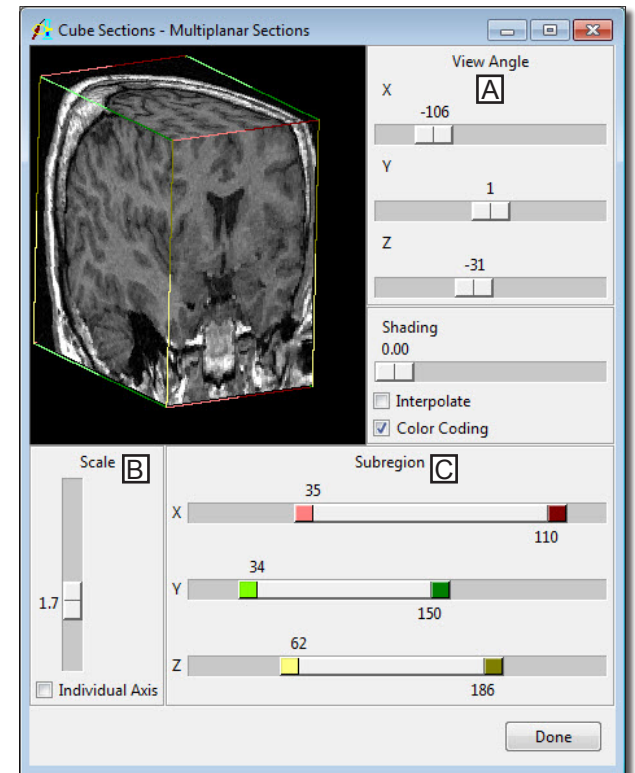
1. Creating a Grayscale Data Set with Color Overlaid Objects

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.

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 acceptation 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 date (figure 2).

5. Open the **Intensity** option (**View > Intensity**). In the Intensities window, review each of the Object Color modes by selecting each from the 'Mode' drop down menu.
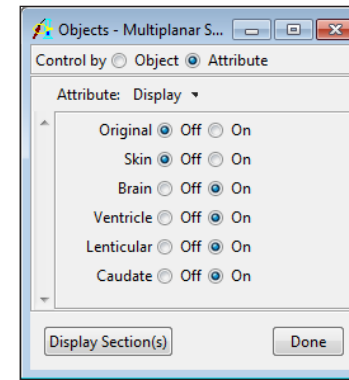
Figure 1
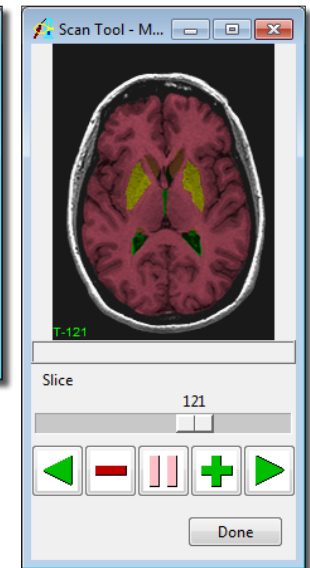
Figure 2
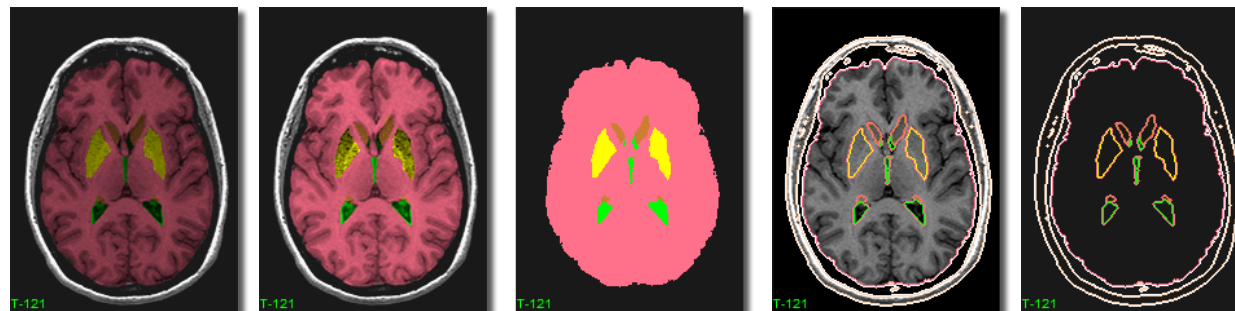
| Windowed Object | Local Max/Min | Object Only | Color Edges | Edges Only |

Figure 3

Additional Task

1. Creating a Grayscale Data Set with Color Overlaid Objects

6. Change the '**Mode**' back to '**Windowed Object**'.

    > *note* | If you have reviewed the data set using the Display Sections option, make sure you use the *Generate > Slice* option to set the slice number back to 1.

7. Next select **File > Output Intensified**. A message will be returned (figure 4), select '**Continue**'.

8. A new Intensified Volume will be saved to the Analyze Workspace.

9. Close the Multiplanar Sections module before proceeding to the next exercise.

Output Intensified - Multiplanar Sections

Output Intensified uses the settings specified in the Slice, Orientation and Intensity windows to create an Intensfied Volume in the Analyze Workspace.

Continue   Cancel
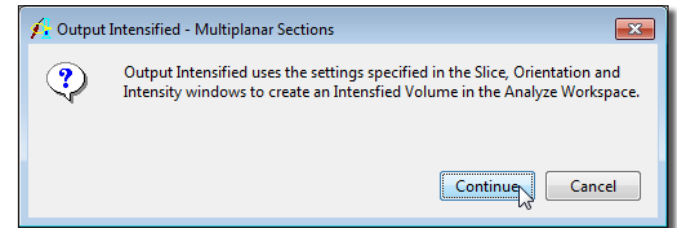
Figure 4

Exercise 9 : 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:

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

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

   iii. If a left lateral view is desired, click the **Roll Left** button [**D**] 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.

   > 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).

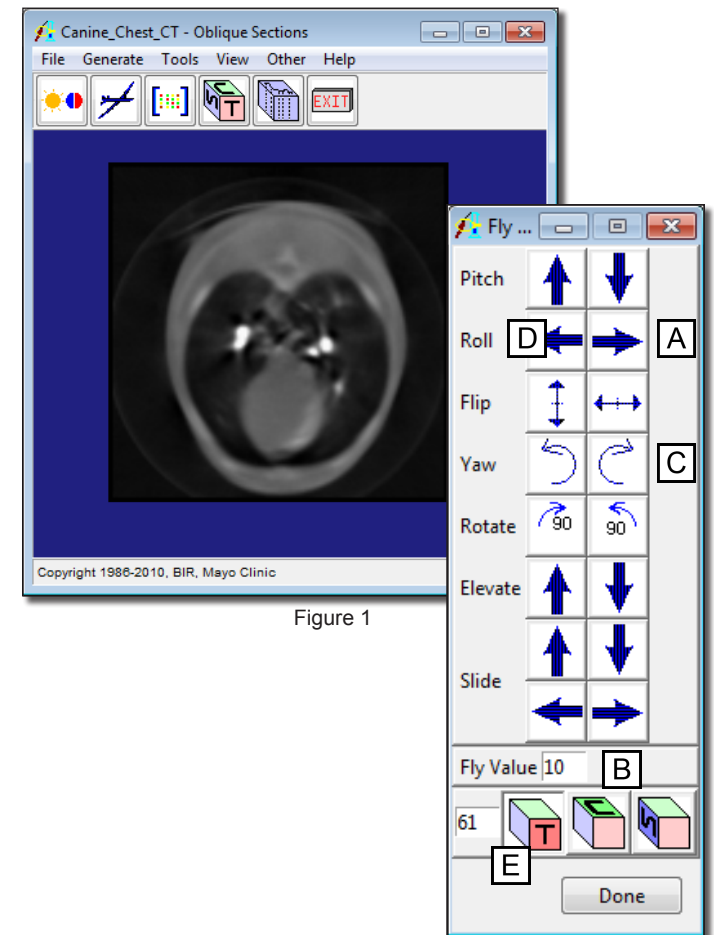4. Reset the oblique plane to the central transverse slice by selecting the 'T' Cube at the bottom of the Fly tool [**E**].

Figure 1

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

6. 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.

7. 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.

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

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

10. 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.

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

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

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

Figure 2

Figure 3

Additional Task
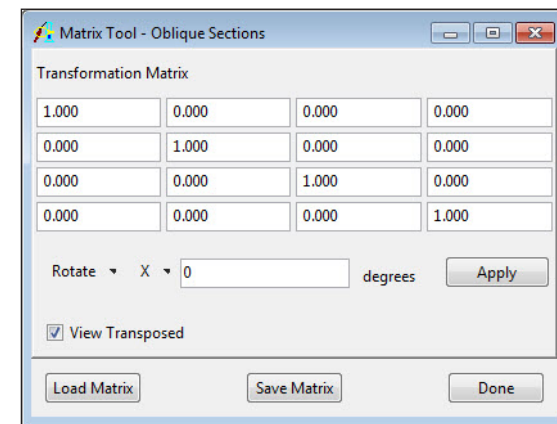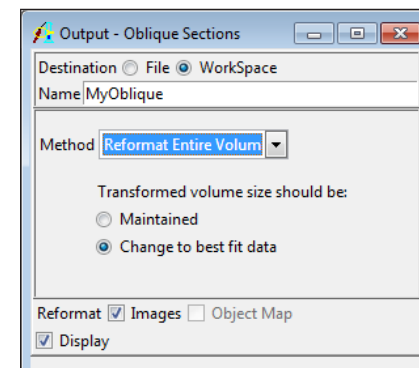
1. Grid Align Tool

The new Grid Align tools provides users with the ability to interactively reorientate image data using a gird 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). [A]
*   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. [B]
*   Release the mouse button. The image will be translated with the selected region as the new center point. [C]

Additional Task
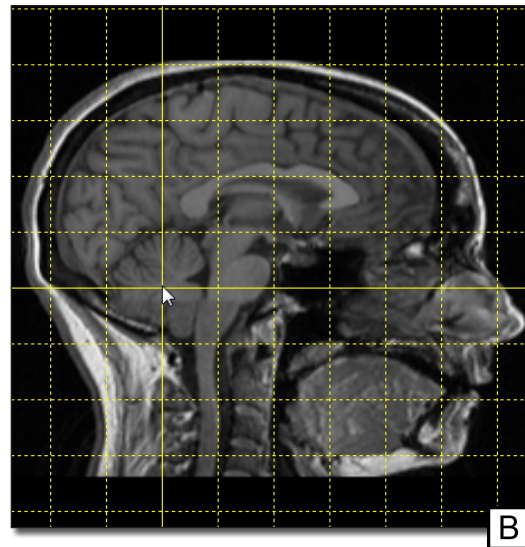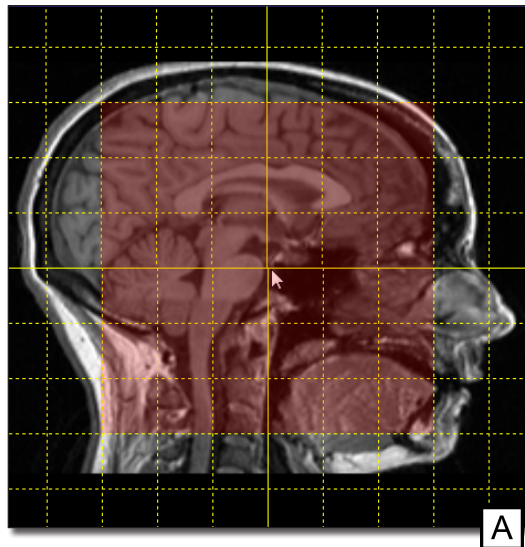
1. Grid Align Tool

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

Yaw:
- Click to select anywhere towards the outside of the grid (anywhere not within the 36 center boxes). [A]
- 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. [B]
- Release the mouse button to apply the Yaw reorientation to the image. [C]

A | B | C
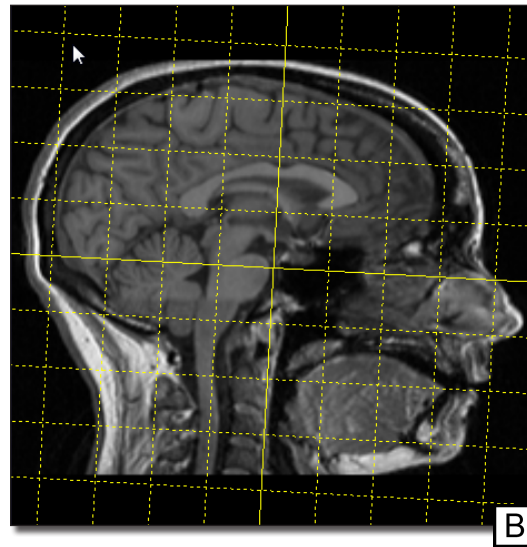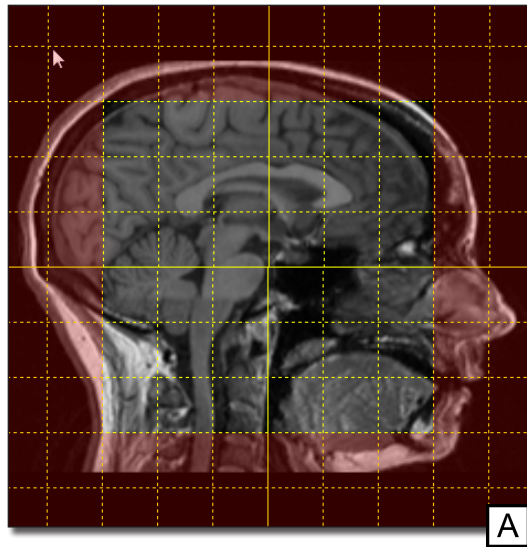
6.   Close all Oblique Sections windows before proceeding to the next exercise.

Exercise 10 : 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 [**A**]. 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 [**B**].
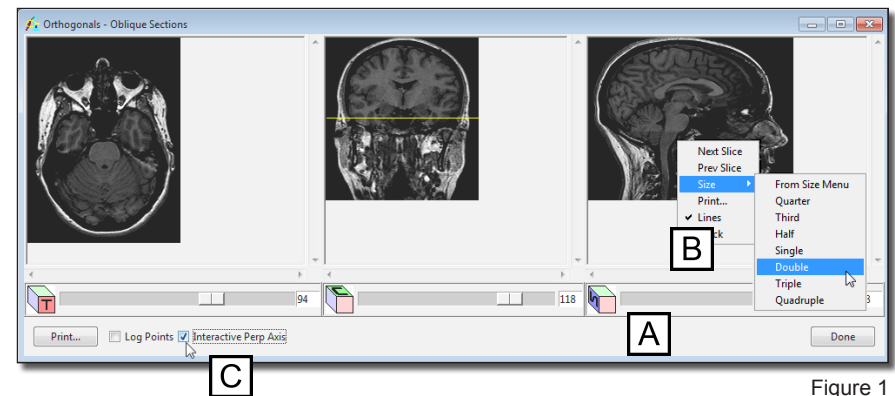
Figure 1

4. At the bottom of the Orthogonal window, select the **Interactive Perp Axis** option [**C**] 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 [**D**].

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**).
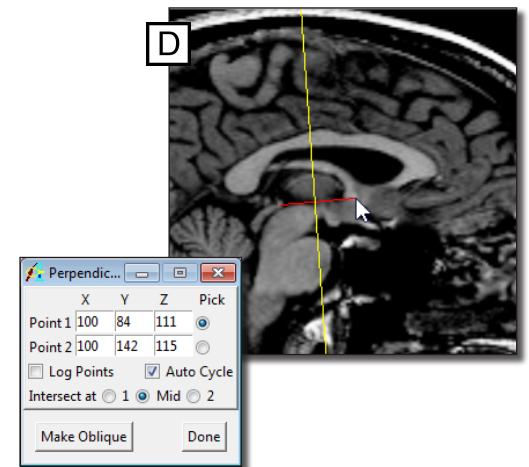

Figure 2

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.

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

> 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.

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. It is up to you to reformat this 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.
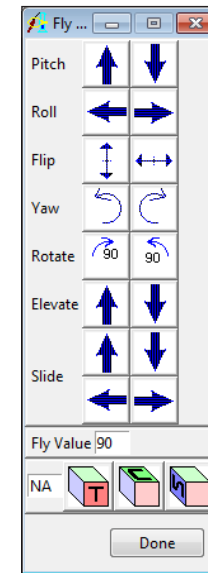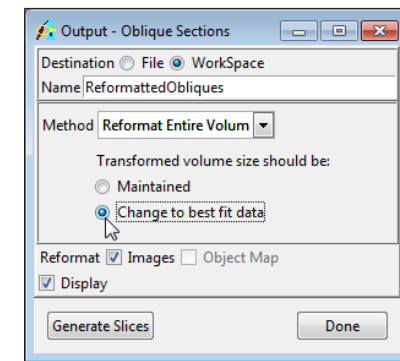
Figure 3

Figure 4

Exercise 11 : 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. Close the Volume Compare module before proceeding to the next exercise.
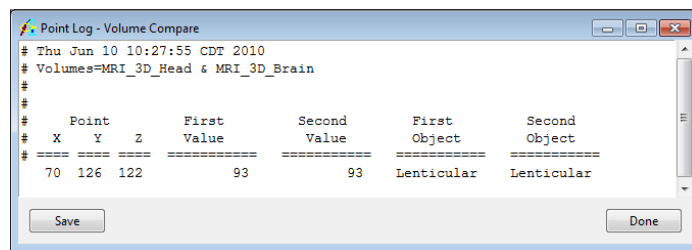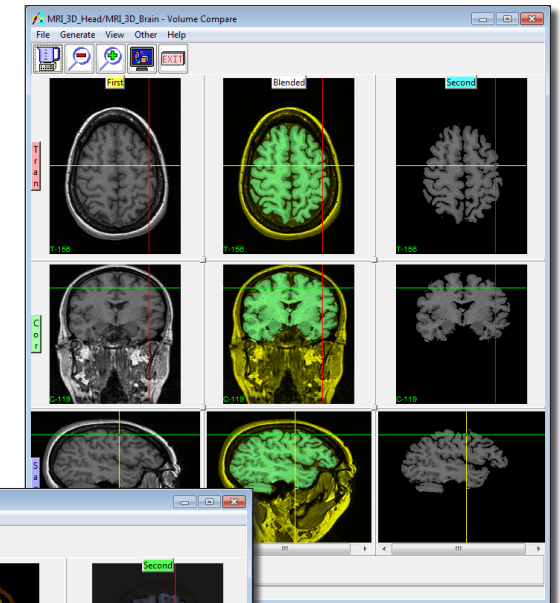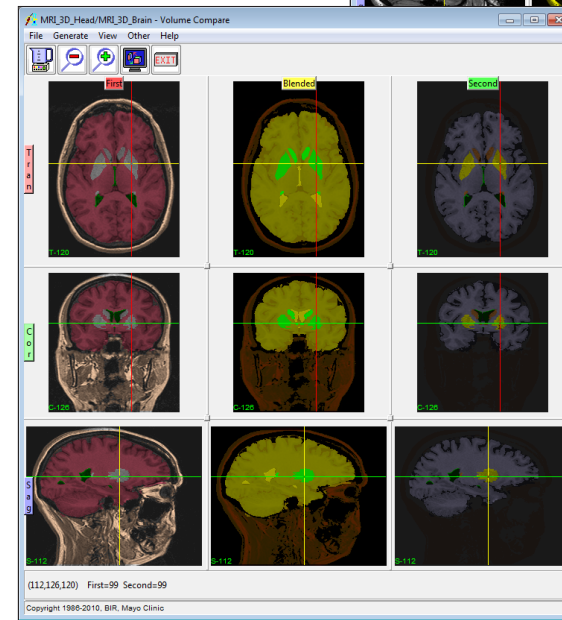
Figure 1

Figure 2

Figure 3

Exercise 12 : 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**).

Thresholding Data

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

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

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

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

Controlling the Rotation Parameters

9. Open the **Rotation** window (**Generate > Rotation**).

10. The **Volume Absolute** option is selected by default (figure 3); use the **X**, **Y**, and **Z** slider bars to change the rendering view. Click **Render** as desired.

11. Select the **Screen Relative** and **Volume Relative** options and compare the different rotation methods available. The 'Screen Relative' option specifies that the rotation of the volume be performed relative to the current screen axis, while the 'Volume
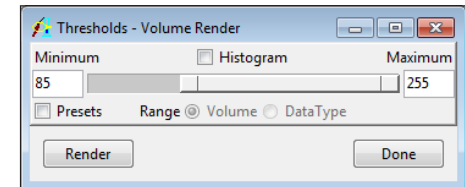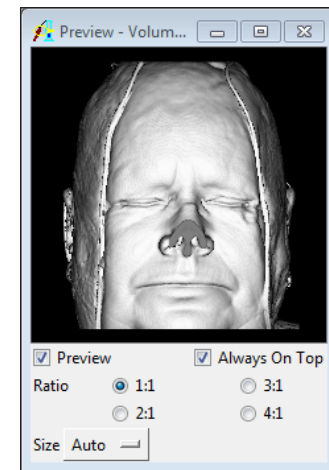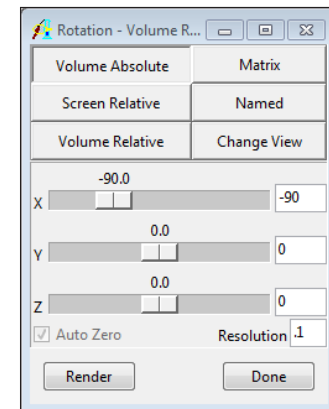
Figure 1

Figure 2

Figure 3

Relative' option specifies that the rotation be performed relative to the current position of the volume axis.

12. Look at the **Matrix** option, but adjustment is not recommended.

13. Experiment with the **Named** option views.

14. Select the **Change View** option and use the arrows to manipulate the rendering view (figure 4). Alternatively, you can click and drag the rendering to a new angle in the image display.

> note | As the rendering is moved, only the originally viewable voxels are interactively re-rendered, providing visual cues to the movement and orientation of the image. Upon release of the mouse button, the full image is rendered at the new orientation.

15. When you are familiar with all of the rotation options, select the **Front** view from the **Named** option and click **Render**.

16. Click **Done** to dismiss the Rotation window.
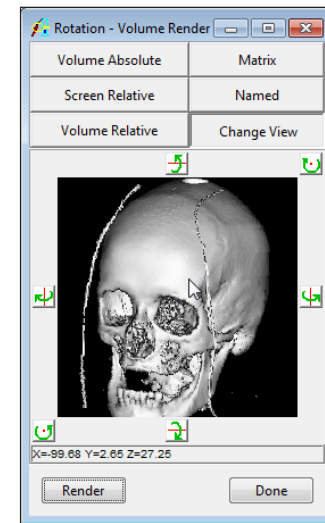
Figure 4

Rendering Algorithms

17. Open the **Render Types** window (**Generate > Render Type**) (figure 5).

18. Experiment with the rendering algorithms. (See Note below).

19. Select the **Depth Shading** option. View the rendering in the Preview window. Click **Render** to display the rendering in the main Volume Render window (figure 6).

20. 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.

> note | Additional parameters for each render type are available from the Type Specific sub-menu (Generate > Type Specific), explanation of all of these additional options is beyond the scope of this exercise, but more information can be found in the User's Guide (Help > User's Guide).
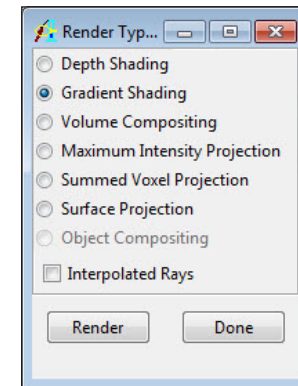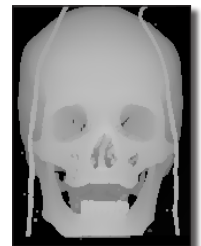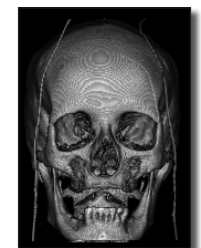
Figure 6

Figure 5

Figure 7

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

    • This render type is normally used with vascular data where the signal is enhanced (usually using contrast), but the dense bone in this data set also shows up well. Try the MIP Weighting option available from with the Type Specific sub-menu (**Generate > Type Specific > MIP Weighting**). The 'Before' weighting option works very well with this input data (figure 8).

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

    • If the threshold minimum is still set to 145, the Summed Voxel Projection algorithm is actually only adding and averaging the voxels corresponding to bone, ignoring all soft tissue. In most cases, whenever you use the Summed Voxel or Maximum Intensity Projections render types, you may want to set the threshold range to the complete range of the input data.

    • In the **Thresholds** window (**Generate > Thresholds**) change the Threshold **Minimum** to **0** and click **Render**. Notice that now the Summed Voxel Projection rendering looks like a re-projection X-ray (a Digitally Reconstructed Radiograph – DRR) (figure 9).

23. 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 (figure 10).

24. Select **Gradient Shading** and click **Done** to dismiss the Render Types window.

The Clip Tool

25. Open the **Clip tool** (**Generate > Clip**).

26. The Clip tool (figure 11) allows a subregion of the volume to be rendered. Experiment with the **Clip Plane** and **Clip Volume** parameters.

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

28. Close all windows related to the Volume Render module before moving onto the next exercise.
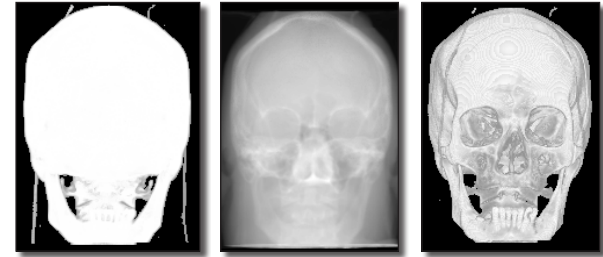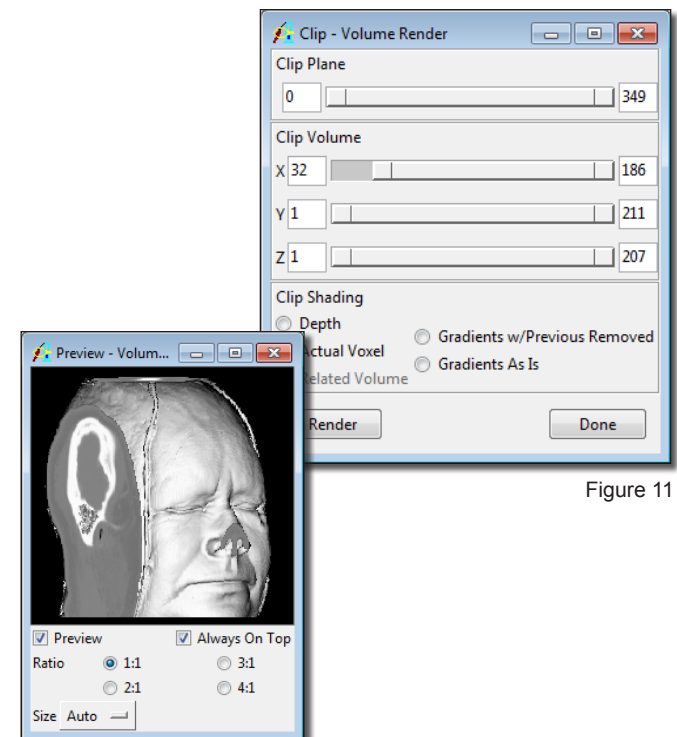
Figure 8   Figure 9   Figure 10

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

Figure 11

Figure 12

Exercise 13 : 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. Open the **Volume Render** module (**Display > Volume Render**).

> Defining Objects in an Object Map

Figure 1

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** [**A**].
    - Set **Change** to **Object Map** [**B**].
    - Set **Defined Object** to *****New***** [**C**].
    - Click **Threshold Volume** to define a new object. Note all voxels from 85 to 255 will be defined as a new object, 'Object_2'.
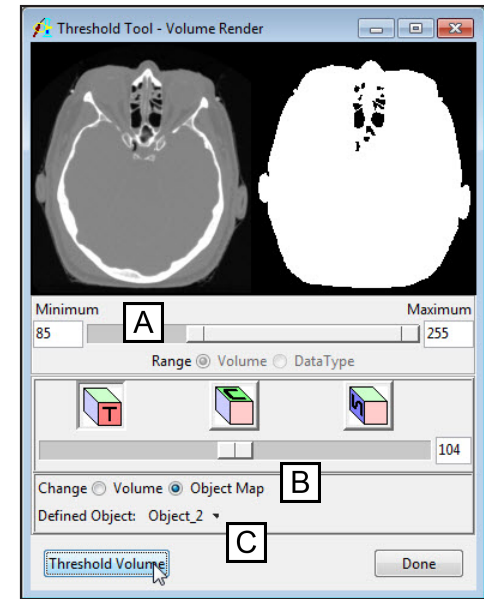   - Click **Done** to close the Threshold Tool.

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

6. Open the **Objects** window (**View > Objects**). Select **Object _2** (if it is not already selected) from the **Object** drop-down menu. Change the following attributes for Object_2:

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

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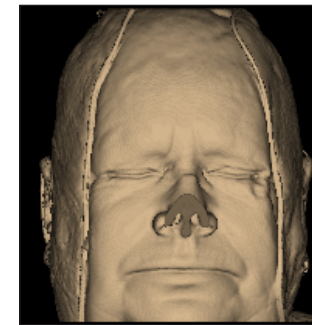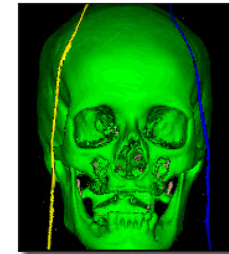

Figure 2

9. 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.

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

Figure 3

Manipulating Objects

10. In the **Objects** window (**View > Objects**) (figure 4), click **Reassign Object(s)** [**A**].

11. 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.

12. Click **Remove Unused** [**B**] in the Objects window to remove '**BlueObject**'. Click **OK** in the dialog box returned.

13. Select the **GreenObject** from the **Object** drop-down menu. Then change the following attributes:
    * **Name: Bone**
    * **Color: white**
    * **Shades: 32**

14. Select the **YellowObject** from the **Object** drop-down menu. Then change the following attributes:
    * **Name: Rope**
    * **Color: red**
    * **Shades: 8**

15. Click **Render**.

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

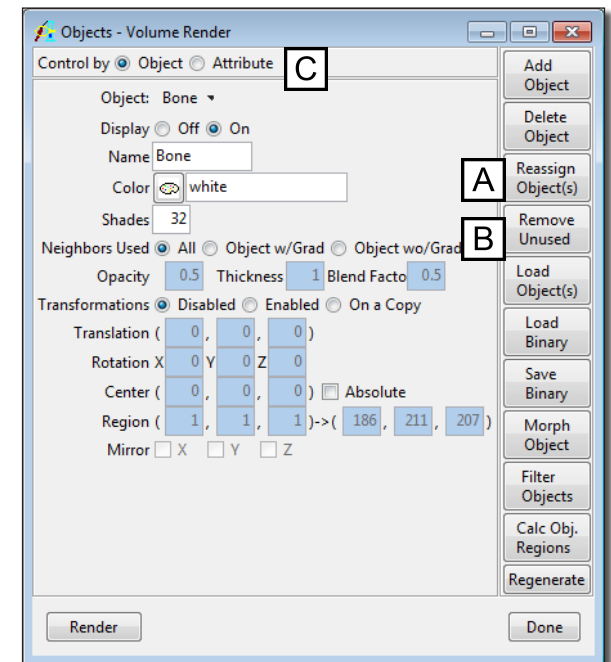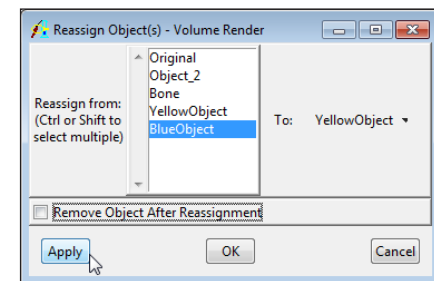17. Return to the **Objects** window and set **Control by** to **Attribute** [**C**].

Figure 4

Figure 5

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

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

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

21. 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

22. 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.

23. 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).

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

note The Object Mapping is only available if the Object Compositing option is selected. The Transparency render type is only available when an object map has been loaded or created.
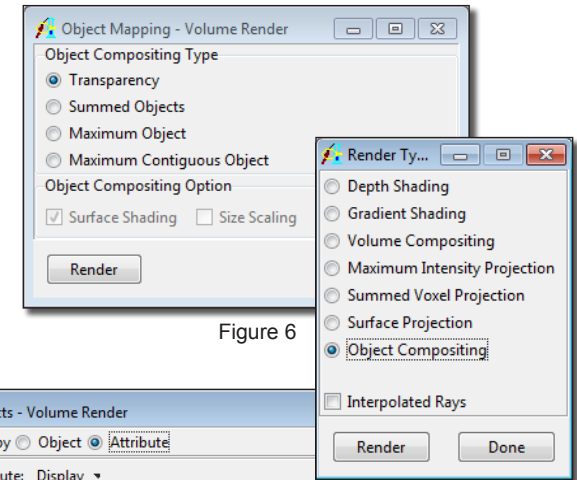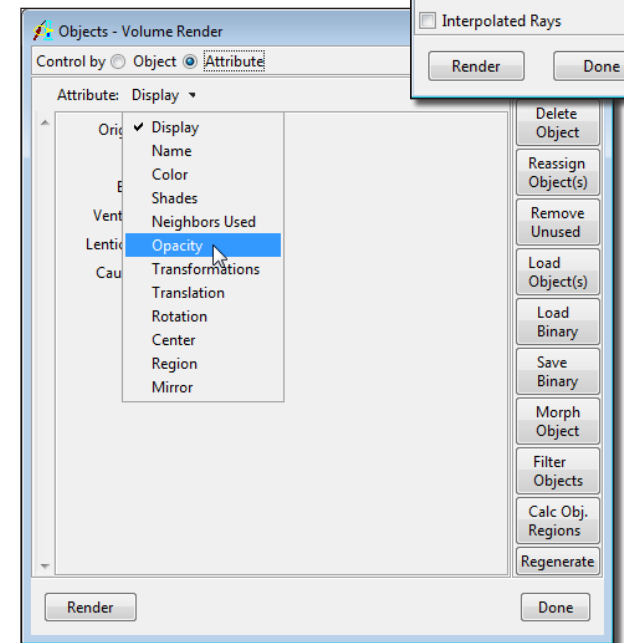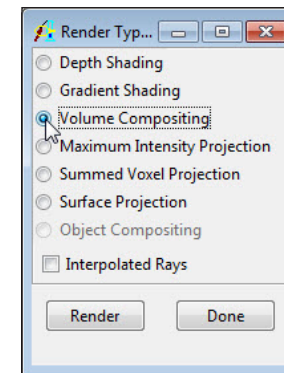
Figure 6

Figure 7

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). Click **Render**, then click **Done** to dismiss the window.

5. Open the **Tissue Map** tool (**Generate > Type Specific > Tissue Map**).

6. 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.

7. The Tissue Map tool provides four control "points" to manipulate which voxel values are mapped to specific colors and opacity (figure 2).
    - **Start** [A]: The starting voxel value within the volume mapped to a specific color (chosen from the color drop-down menu) with 0% opacity.
    - **Min** [B]: The minimum voxel value within the volume that will be mapped to a specific color and set opacity (e.g. 44%).
    - **Max** [C]: The maximum voxel value within the volume that will be mapped to a specific color and set opacity (e.g. 44%).
    - **End** [D]: The ending voxel value within the volume mapped to a specific color with 0% opacity.

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

Figure 1

The Tissue Map tool is **only** available with the Volume Compositing render type
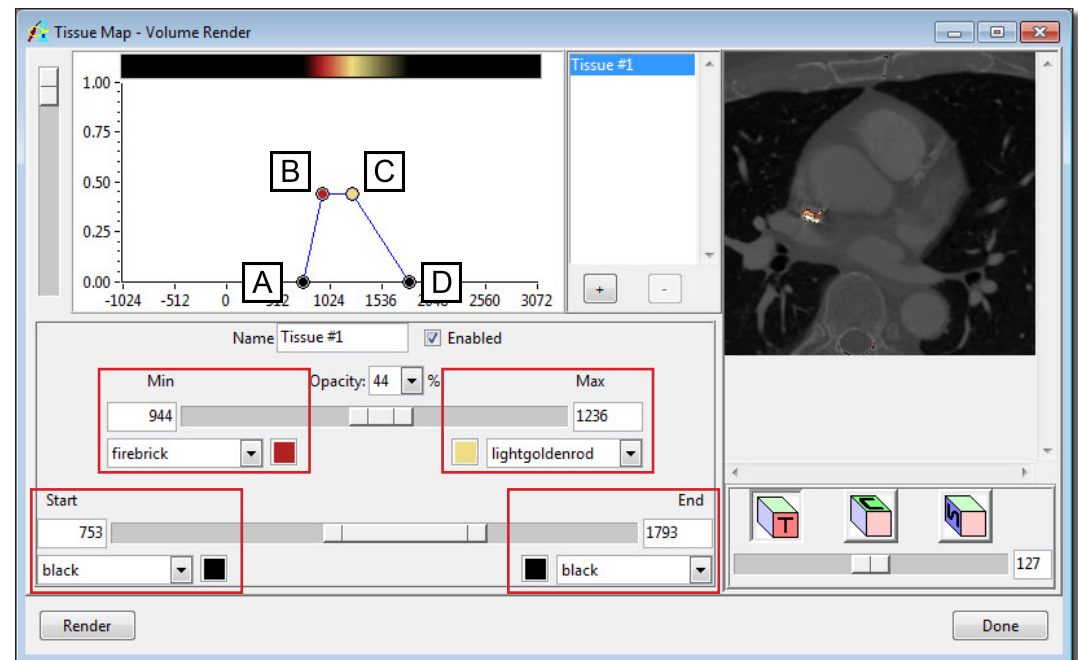

Figure 2

9. Use the slider bars [**A**] in the Tissue Map tool to set the following (figure 3):
    - **Start: 157**
    - **Min: 200**
    - **Max: 500**
    - **End: 3072**

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

11. Now, experiment by moving the control points in the graphical display [**C**]. Click **Render** as desired.

12. 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.

13. Several default tissue maps are also available, right-click in the graphical display and choose **Default Tissue Maps > CT1**; once loaded, click **Render** (figure 5).

Figure 3

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

15. Close the Volume Render module before proceeding to the next exercise.
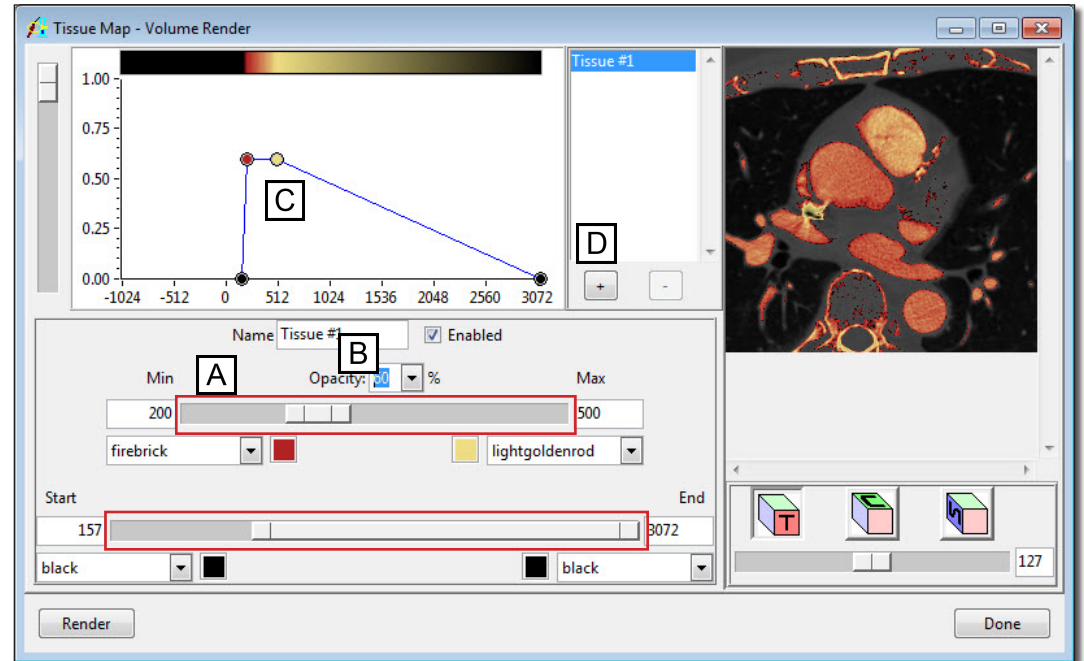
Figure 4   Figure 5

Exercise 15 : Volume Render Movie Making with the Sequence Tool

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.

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

7. By default, the 'sequence' already has one action, 'Z Rotation'. To modify the action click **Modify** [A], and then click on the red '**Z Rotation**' action [B] (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.
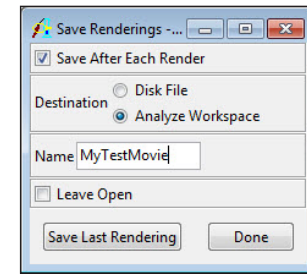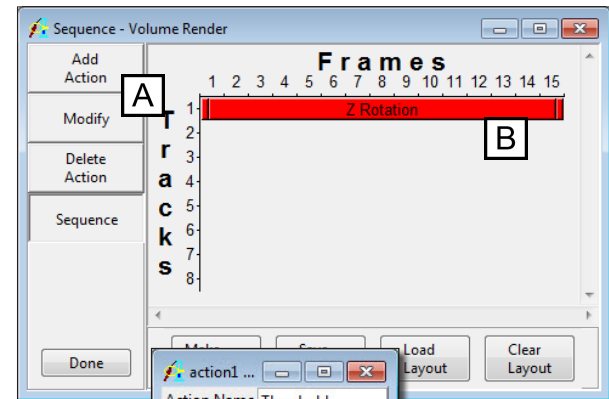   - **Parameter: Threshold**
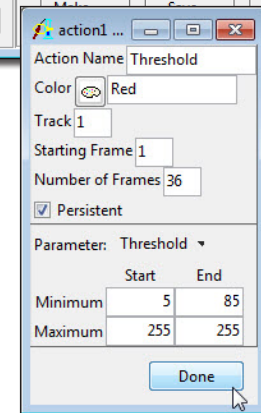   - **End Minimum: 85**

Figure 1

Figure 2

Figure 3

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

11. Now, in the Sequence tool, click **Sequence** [**C**]. Then, click **Make Sequence** [**D**] (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** [**E**] and place the new action on **Track 2** in **Frame 36** [**F**]; this will be directly under the last frame of the 'Threshold' action (figure 5).

14. Once the new action has been added, click **Modify** [**G**] 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.
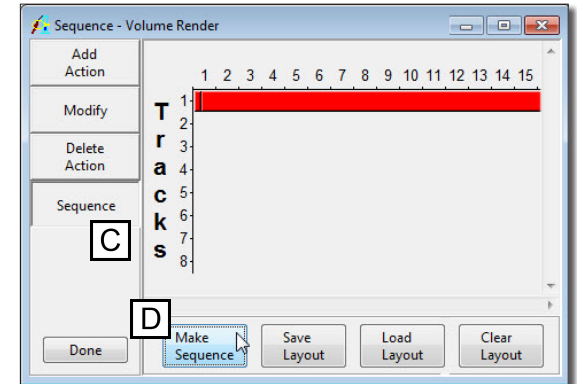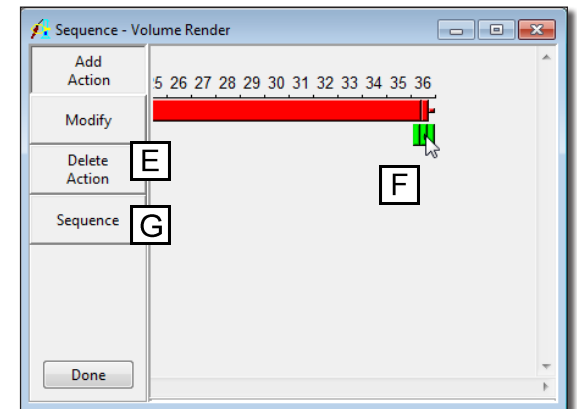

Figure 4

Figure 5

> tip | 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.

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** drop-down menu before clicking **Save**.

24. Close the Movie module before proceeding to the next exercise.
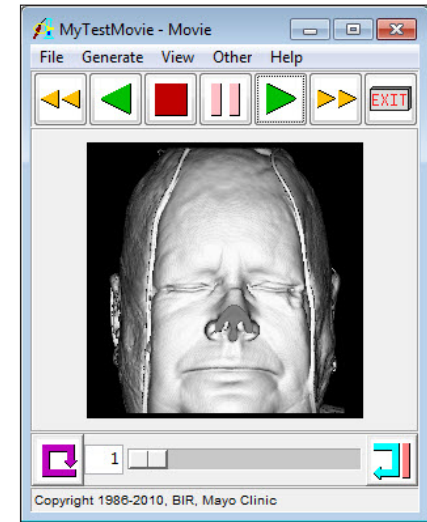
Figure 6

Exercise 16 : Volume Render Fix Tool

The Fix Tool provides the capability to correct for bad slices within a volume. The tool allows a variety of correction methods for missing or corrupt images that occur in a volume, including removing corrupt images, copying from an adjacent uncorrupted image, and interpolation from a range of uncorrupted images near the corrupt image. This exercise will demonstrate how to use the Fix Tool to correct for bad slices within a volume.

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

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

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

4. Now, open the **Thresholds** window (**Generate > Thresholds**).

5. Set the **Threshold Minimum** to **26**; the Preview window will interactively update (figure 1). Note the lines that appear in the image [**A**].

6. Open the **Ortho Sections tool** (**Tools > Display > Ortho Sections**).

7. In the Ortho Sections tool (figure 2), click on the line in the rendering seen in the top left pane [**B**]. The three orthogonal views will automatically update. Notice the corrupt image in the transverse orientation [**C**].

8. Click **Done** to close the Ortho Sections tool. Also close the Thresholds and Preview windows.
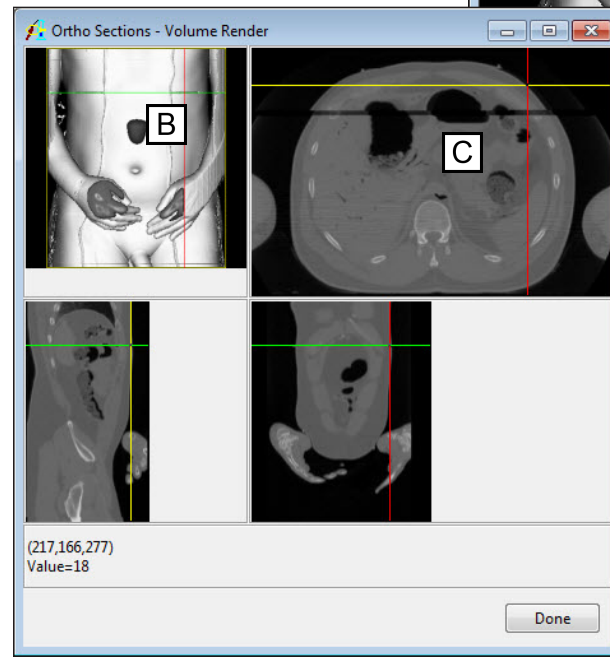
Figure 1

Figure 2

9. Open the **Fix Tool** (**Tools > Manipulate > Fix**).

10. In the Fix Tool (figure 3), use the **Displayed Slice** slider bar [**D**] to locate the first corrupt slice. Note that the first corrupt slice is slice 276.

11. In the **Bad Slice(s)** portion of the window, set **slice 276** as the **first bad slice** [**E**].

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

13. In the **Bad Slice(s)** portion of the window, set **slice 279** as the **last bad slice** [**F**].

14. Select **Interpolate Between the First Good Slice** for the correction method [**G**].

> note | This method uses linear interpolation to calculate a replacement slice for each bad slice. The value of each voxel is computed using information for each of the good slices on each side of the bad slices. The percentage of each image used is calculated based on the distance from the bad slice to each good slice.

15. Click **Fix 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'.

16. Click **Done** to close the Fix Tool.

17. In the main Volume Render window, press the **Render** PowerBar button or choose (**Generate > Render**). Note that the lines that appeared in the top of the image are no longer present (figure 4).

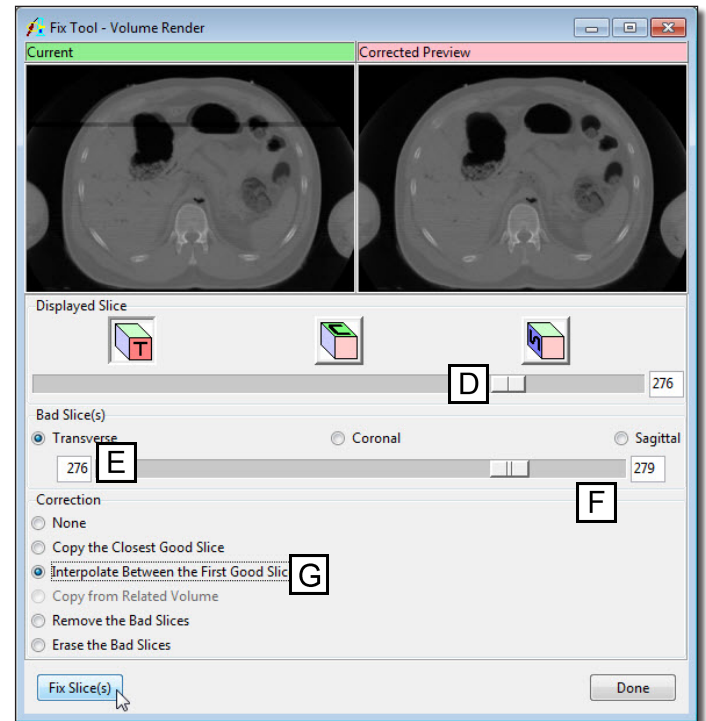18. Close the Volume Render module before proceeding to the additional task.

Figure 3

Figure 4

1. Copy from Related Volume Option

The option 'Copy from Related Volume' provides the ability to use a related volume as input for the Fix Tool, allowing images to be copied from the Related Volume to the Loaded Volume. To demonstrate the new fix option we will correct for the corrupt slices in the 'VH_Abdomen' data set, using the fixed slices from the 'VH_Abdomen0' data set.

1. Select the **VH_Abdomen** data set in the Analyze workspace and open the **Volume Render** module (**Display > Volume Render**).

2. In the main Volume Render window, choose **File > Input/Output Ports**. The VH_Abdomen data set icon will appear under the 'Volume' port.

3. In the Analyze workspace, select the fixed data set created in the main exercise, **VH_Abdomen0**.

4. Drag-and-drop **VH_Abdomen0** to the **Related Volume** port in the main Volume Render window (figure 5).

5. Open the **Fix Tool** (**Tools > Manipulate > Fix**).

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

7. Select **Copy from Related Volume** for the correction method.

8. Click **Fix Slice(s)**. Slices 276 through 279 will be copied from the related volume and replace the corrupt slices in the loaded volume. A dialog box will be returned, click **Change a Copy of the Loaded Volume**.

9. Click **Done** to close the Fix Tool.

10. In the main Volume Render window, press the **Render** PowerBar button or choose **Generate > Render**. Note that the lines that appeared in the top of the image are no longer present (see step 7 in the main exercise).

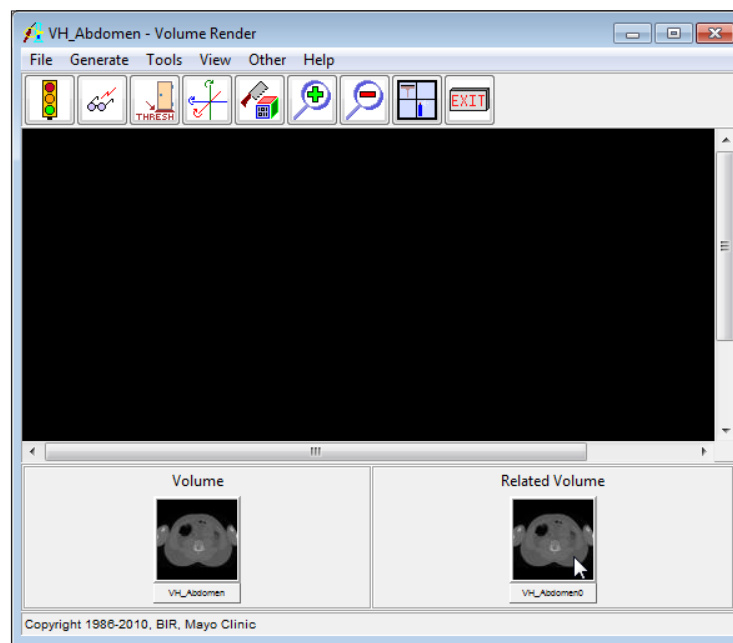11. Close the Volume Render module before proceeding to the next exercise.

Figure 1

Exercise 17 : Volume Render Creating a Merged Image

The Volume Render Merge Tool allows images generated with different render types to be merged into a single image providing users with the ability to create unique visualizations of their image data. This exercise will demonstrate how to use the Merge Tool to create a unique rendering of the brain and ventricles.

Creating the First Image

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

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

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

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

5. Open the **Rotation** window (**Generate > Rotation**). In the Rotation window select **Named** and then select **Right**. Note that after this point you will not be able to reposition the data.

6. Open the **Objects** window (**View > Objects**) and set the '**Control by**' option to '**Attribute**'. Set the **Display** attribute to **Off** for all objects except the Ventricle (figure 1).

7. Next we will use some of the additional rendering options to generate a rendering of the ventricle. Open the **Specular Reflection** tool and **Light** tool from the **Type Specific** menu (**Generate > Type Specific > **).

8. In the **Specular Reflection** tool set the following parameters (figure 2):
   • **Specular Reflection** to **On**
   • **Factor** to **0.32**
   • **Exponent** to **0.1**

9. Use the Light tool to brighten the image display by moving the Brightness slider to the right (figure 3).

10. Once these parameters are set, click the **Render** button in the main Volume Render window.
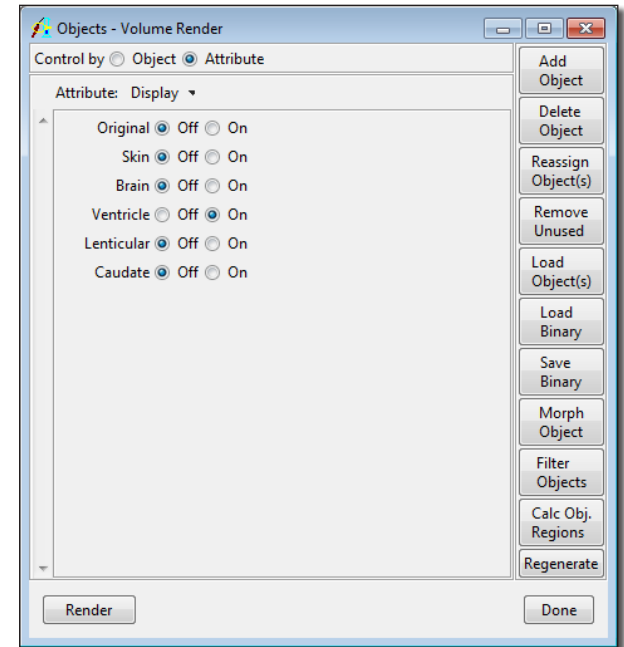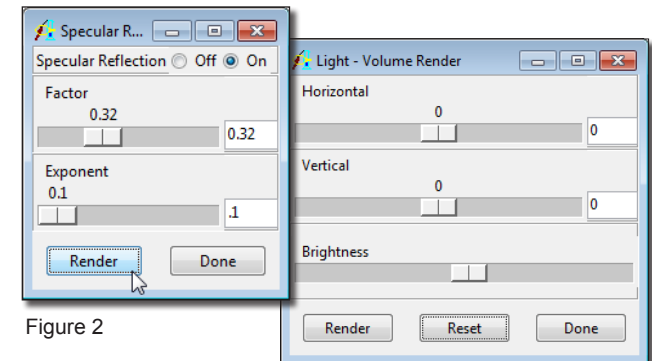
Figure 1

Figure 2

Figure 3

11. Next open the **Merge** tool from the Tools menu (**Tools > Display > Merge**).

12. The current rendering will be displayed in the 'Current' port. Click the '**Current to Previous**' button to copy the current rendering over to the 'Previous' port (figure 4).

   note | If you wish to return to this point at a later time, save the rendering by right-clicking in the 'Previous' port and select the 'Save Previous' option.

Creating the Second Image

13. In the **Objects** window, switch the display of the **Ventricle** to **Off** and the display of the **Brain** to **On**. Next, change the Attribute from **Display** to **Color** and change the Brain color from **Pink** to **White** (figure 5).

14. Open the **Render Type** window (**Generate > Render Type**) and set the **Render Type** to **Surface Projection** (figure 6).

15. Next, open the **Surface** option from the **Generate > Type Specific** menu. In the Surface option set **Skip** to **2** and **Thickness** to **6** (figure 7). Note the display of the brain from the Preview window.

16. Once these parameters have been set, click on the **Render** button in the main Volume Render workspace.
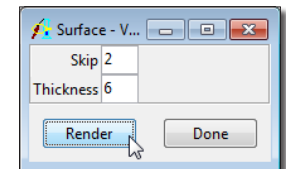
17. The 'Current' rendering in the Merge Tool will update.

Merging the Images

18. Right-click on the main image display window in the Merge Tool, set the Merge Type to Average (figure 8). Note the updated display. Right-click and set the Merge Type back to ZBuffer Depth.
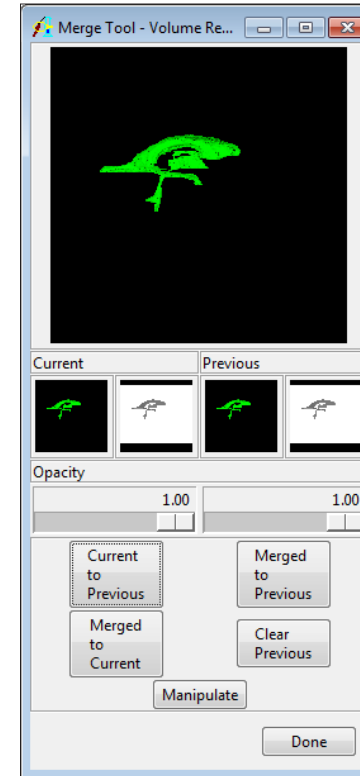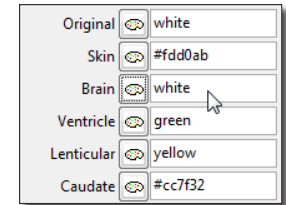
Figure 4
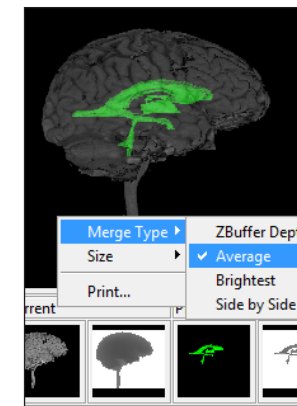

Figure 5

Figure 6

Figure 7

Figure 8

19. Decrease the 'Opacity' value of the current rendering by moving the Opacity slider bar under the current rendering to the left. An Opacity of 0.32 works well (figure 9).

20. Next, click the '**Merge to Current**' button.

21. To save the rendering, select **File > Save Renderings**. In the **Save Renderings** window, change the Name to 'Merged Image' and then click on the '**Save Last Rendering**' button.

22. The following window may be displayed (depending upon the render options you set).
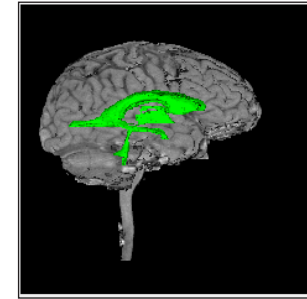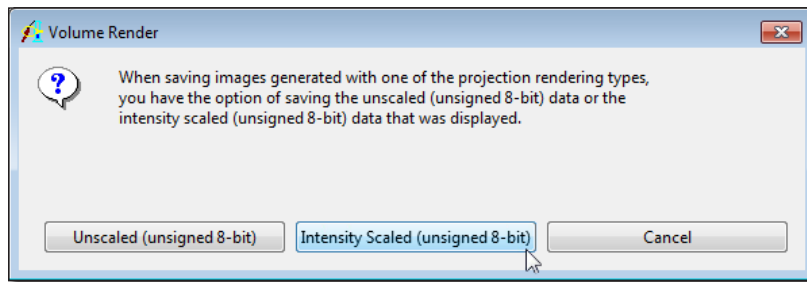
Figure 9

23. Select the '**Intensity Scaled (unsigned 8-bit)**' option. The rendering will be saved to the Analyze workspace and can be saved out of Analyze as a .jpg, .tiff, or .bmp using the Save module.

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

Exercise 18 : Volume Render Creating A High Definition 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).

5. Open the **Tissue Map** tool (**Generate > Type Specific > Tissue Map**). Right-click on the main tissue map panel and select Load Tissue Map, choose the CT 2 default tissue map.

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.
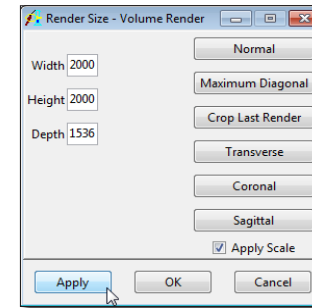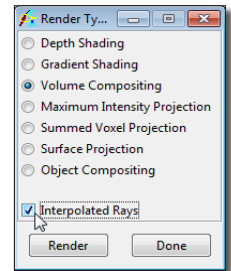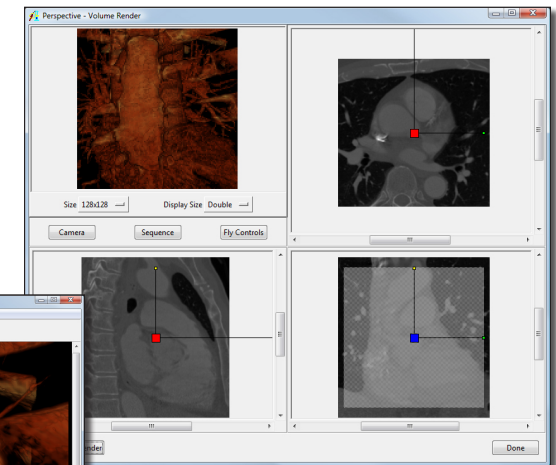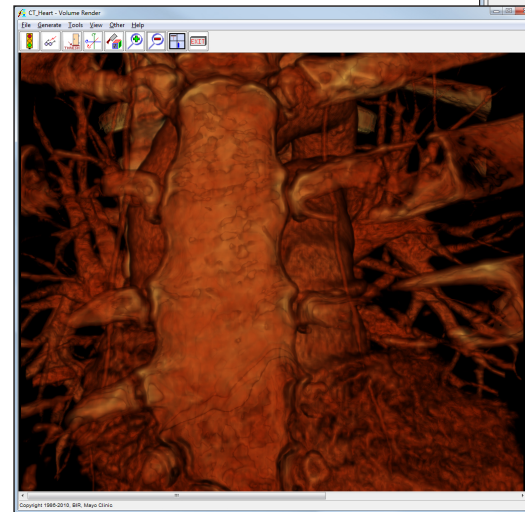

Figure 1

Figure 2

Figure 3

Exercise 19 : 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 sue 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.

   note | The SISCOM_4D_ActivityMap is a multivolume created using the SISCOM module. Each volume represents an activation map generated with a different activity standard deviation. Starting at 0.1 and increasing at a 0.1 intervals to 5.0

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. If necessary, use the **Rotation** window (**Generate > Rotation**) '**Change View**' option to maneuver the brain to a desirable orientation (figure 3).
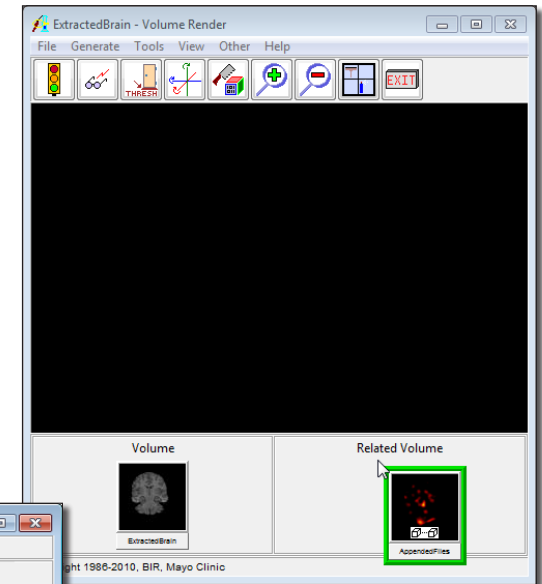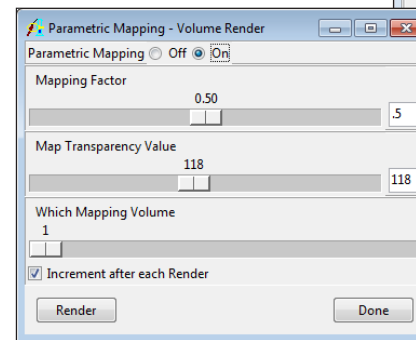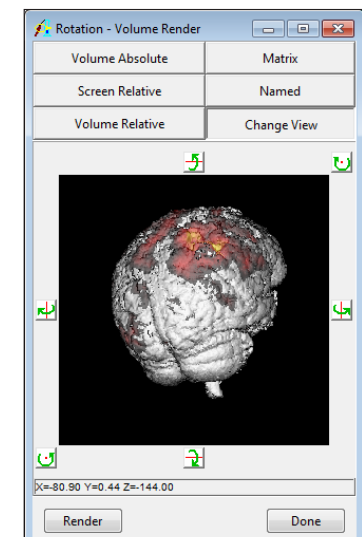
Figure 1

Figure 2

Figure 3

8. Review the effects of changing the **Mapping Factor** and **Map Transparency** 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).

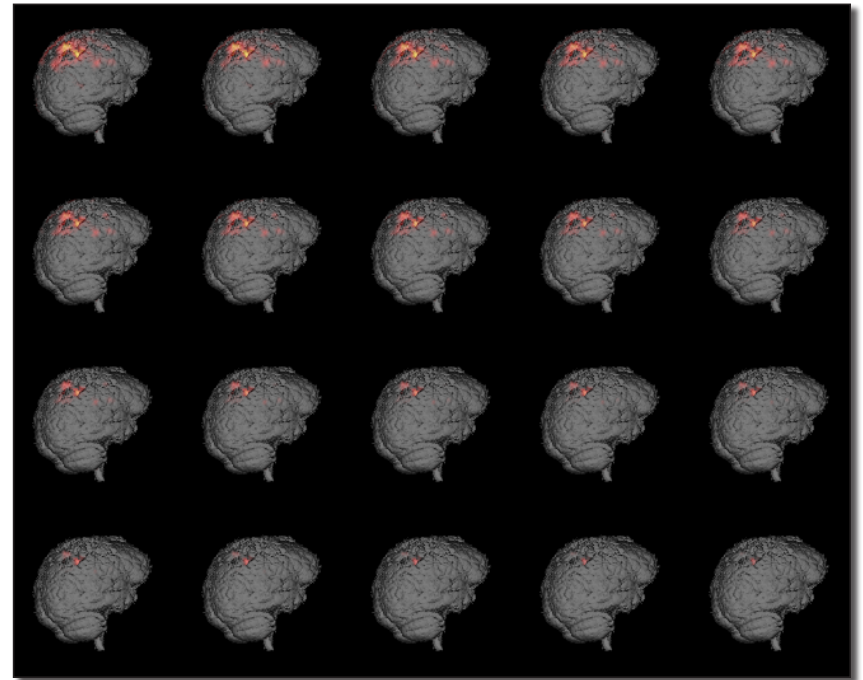10. Close the Volume Render module before proceeding to the next exercise.

Figure 4

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. The Objects window (**View > Objects**) will automatically be returned.

4. In the **Objects** window, 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**. The Surfaces window (**View > Surfaces**) will automatically be returned.

6. In the **Surfaces** window, 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).

   note | Where possible, the attributes of the surfaces in the surface map and the objects in the object map should have equivalent values.

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**.
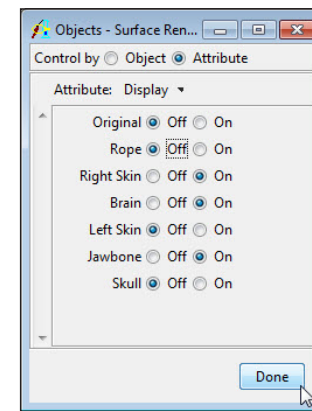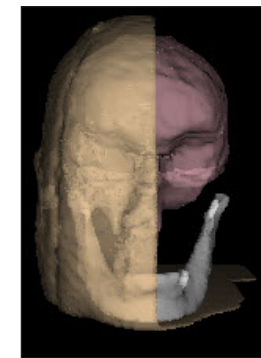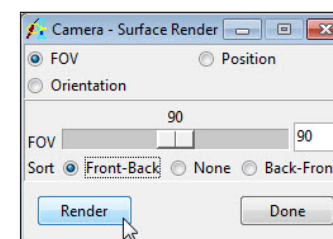

Figure 1

Figure 2

Figure 3

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. To learn about more surface rendering tools and options, complete the Additional Task.
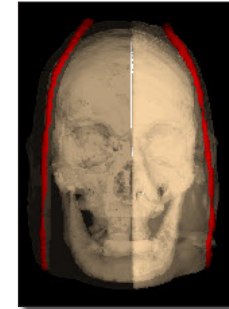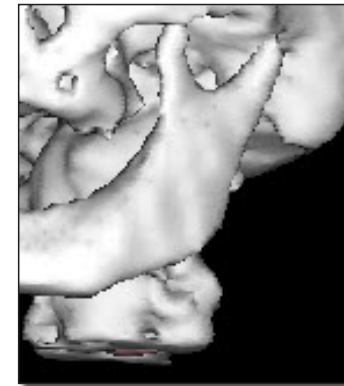
Figure 4

Additional Task

1. Advanced Visualization

1. Open the **Preview** window (**Generate > Preview**) to view changes prior to rendering.

2. In the **Camera tool** (**Generate > Camera**), set FOV to 60.

3. In the **Surfaces** window (**View > Surfaces**) select **Display** from the **Attribute** drop-down menu and set the **Rope**, **Right Skin**, and **Left Skin** surfaces to **Off**.

4. Choose **Transparency** from the **Attribute** drop-down menu, and set the **Skull and Jawbone** surfaces to **1.0**. Click **Render**.

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

6. With the **Volume Absolute** option selected, set **X: -64, Y: -3, Z: 37**. Then, click **Render**.

7. In the Camera tool select the **Position** option and set the **Z** position to **–300**. Click **Render** and note the changes in the rendering.

8. Now, set the **Position** coordinates to **X: 12, Y: 41, Z: -215**. Click **Render** and note the changes in the rendering (figure 5).

9. In the Rotation window, select the **Change View** option. Use the arrow buttons or click and drag the rendering to a new view in the image display.

10. Notice that each time the view is modified the image is re-rendered in the main module window. To prevent this, right-click on the 'Change View' image display and deselect **Regenerate on Release**.

11. Close all windows related to the module before proceeding to the next exercise.

Figure 5

Exercise 21 : Virtual Endoscopy Interactive Generation of Endoscopic Views

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

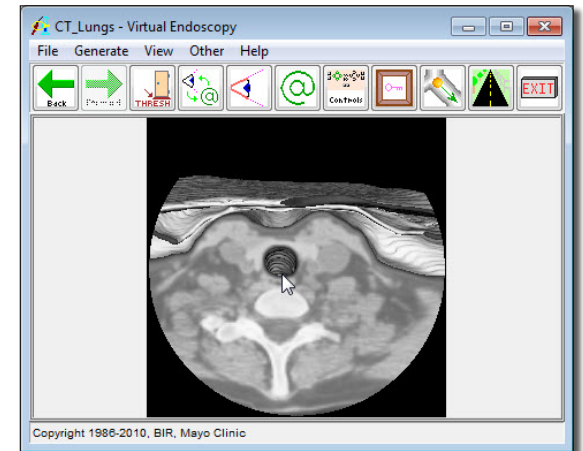10. Click **Render** in the View Parameters window to display the location of the coordinates (figure 4).
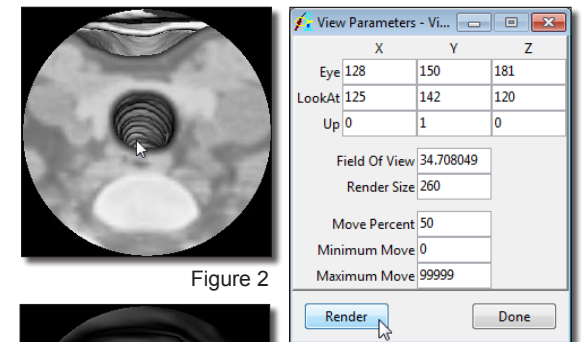

Figure 1

Figure 2

Figure 3

Figure 4

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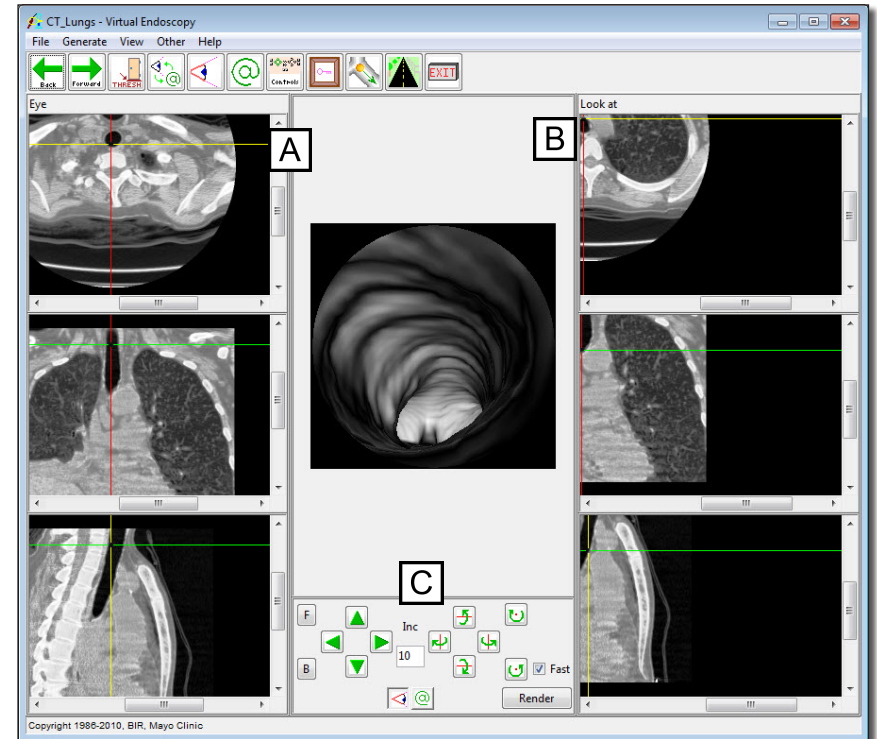
13. Press the **Manual Controls** PowerBar button or choose **Generate > Manual Controls**. The Manual Controls will appear in the main module window [**C**], allowing you to select the translation or rotation actions, the increment, and point(s) to manipulate. To apply a manual action, click the **Render**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

Figure 5

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.

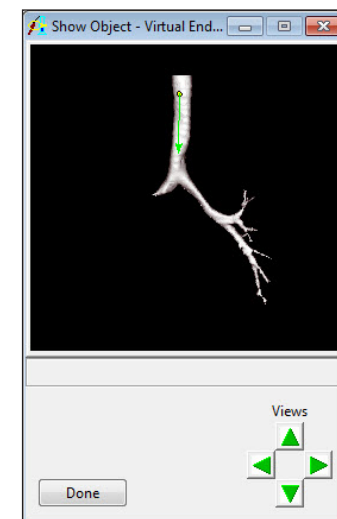16. Close all Virtual Endoscopy windows before proceeding to the next exercise.

Figure 6

Exercise 22 : Virtual Endoscopy Endoscopic 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 Add 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 Add 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**).
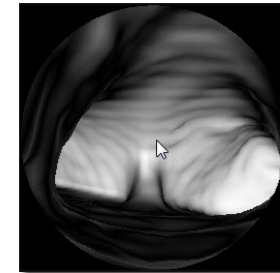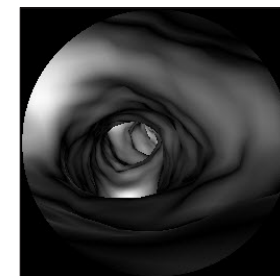

Figure 1

Figure 2

Figure 3

note | Rendering the endoscopic movie may take a few minutes depending upon your system and the size of the movie.

Additional Task

1. Advanced Maneuvers

1. After viewing your movie try recreating the movie adding these steps into the main exercise after **Step 7**.

2. When you reach the bifurcation of the airway, click in the right bronchus. Click two more times to move further into the bronchus (figure 1).

3. Press the **Back** PowerBar button three times, and then proceed down the left bronchus.

4. At the end of the left bronchus press the **Invert Positions** PowerBar button, then move back up through the left bronchus towards the trachea.

5. When you reach the trachea choose **Generate > Sequence > Auto Add Key** Frame to turn off the Auto Add Key Frame option.

6. Choose **Generate > Sequence > Generate Sequence** to generate the movie (figure 2).

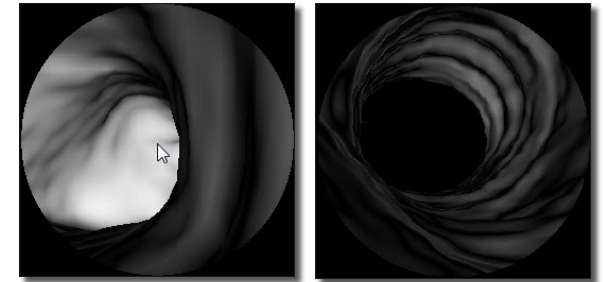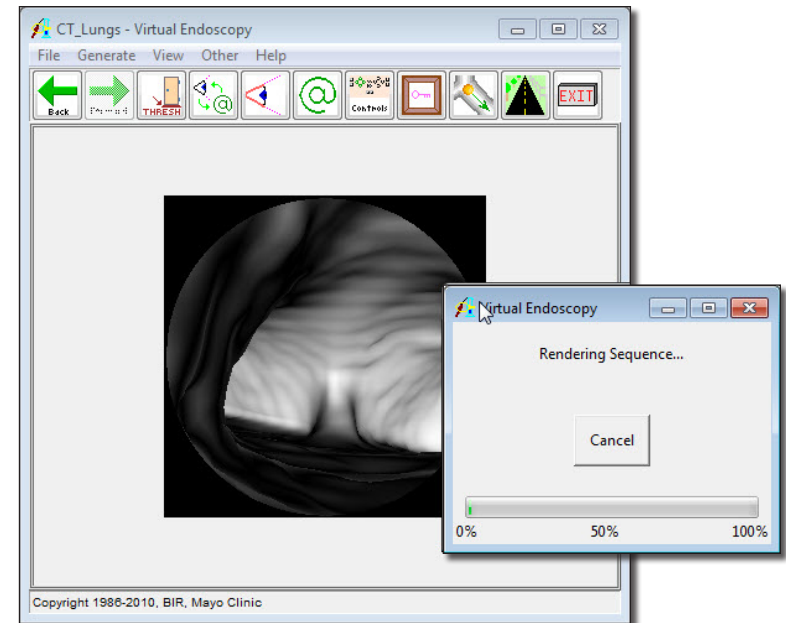7. Close the Virtual Endoscopy module before proceeding to the next Additional Task.

Figure 1

Figure 2

Additional Task

2. Generating a Centerline

The Virtual Endoscopy module provides that 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).
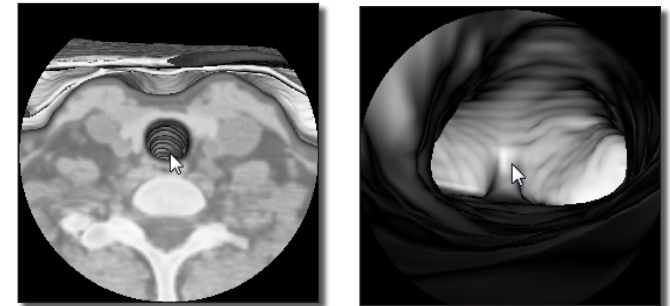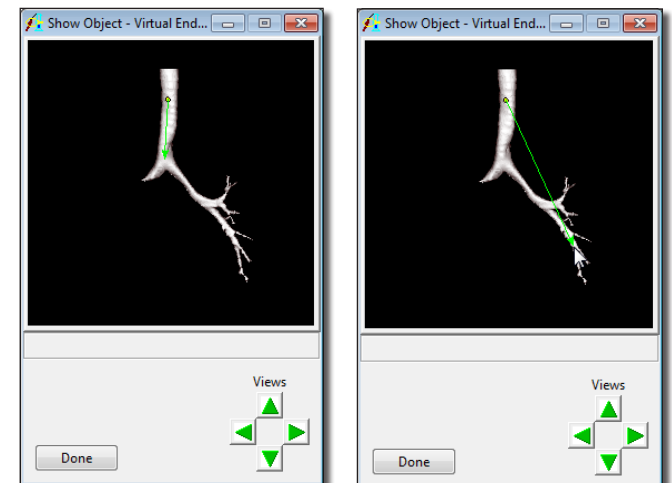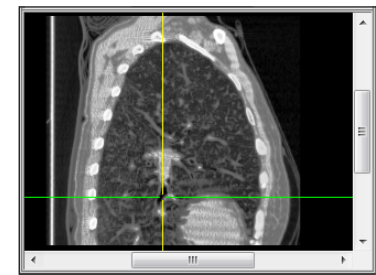

Figure 1

Figure 2

Figure 3

2. Generating a Centerline

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.
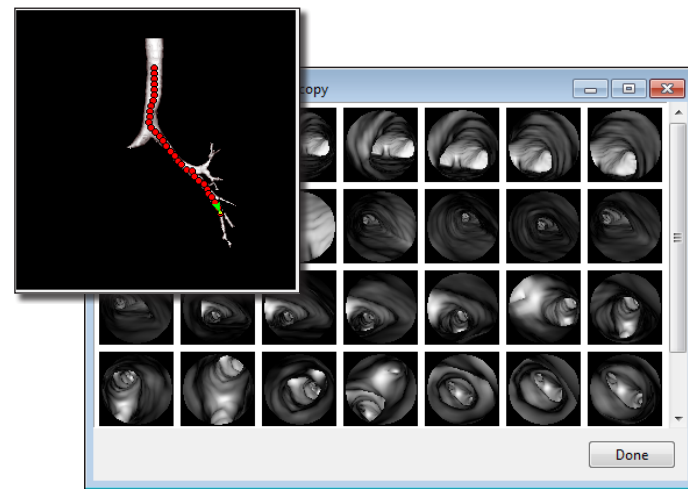

Figure 4

Additional Task

3. Adding Color to Endoscopic Movies

Movies generated in the Virtual Endoscopy module can be given a quick update by apply a color map using the Multiplanar Sections module.

1. Select the endoscopic fly-through movie from the Analyze workspace and open the **Multiplanar Sections** module **Display > Multiplanar Sections**.

2. Open the **Intensities** window **View > Intensities.**

3. In the **Intensities** window set **Type** to **Colormap**. Here you can generate your own custom color map or load an existing color map (figure 1). Load the **hot_ body.lkup** from the **C:\BIR\images\TutorialData\Colormaps** directory.

4. Once loaded, set **Range** to **Data Type** and then increase the **Max** value to **255**.

5. To review the movie, select the Display Sections button from the PowerBar (figure 2).

6. To save the color intensified movie, select **File > Output Intensified**. The color map will be applied to a copy of the movie and saved to the Analyze workspace.

7. Close all windows associated with the Virtual Endoscopy module before proceeding to the next exercise.
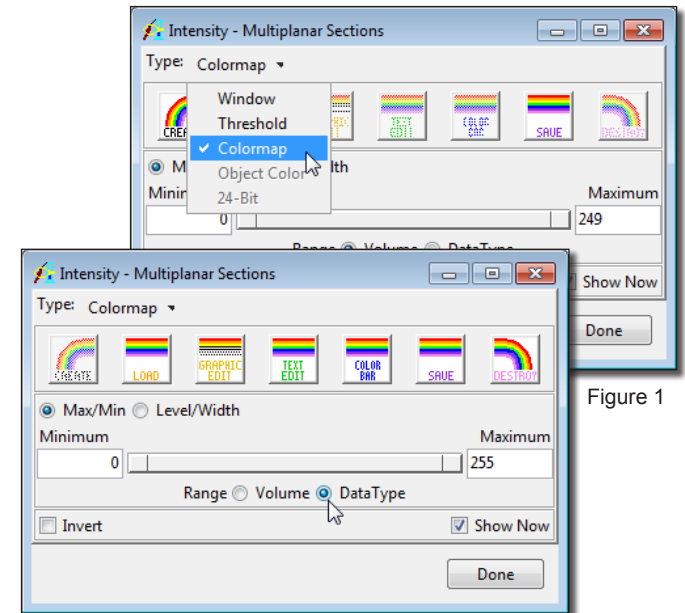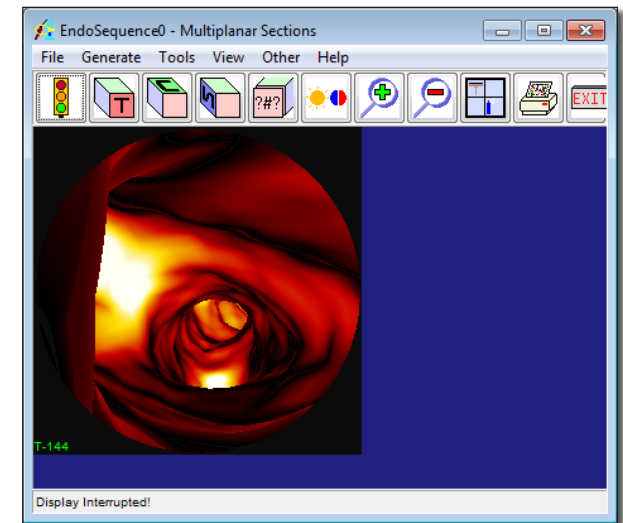
Figure 1

Figure 2

Exercise 23 : 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 [**A**] 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).

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 [**B**] 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 [**C**] 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.

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.
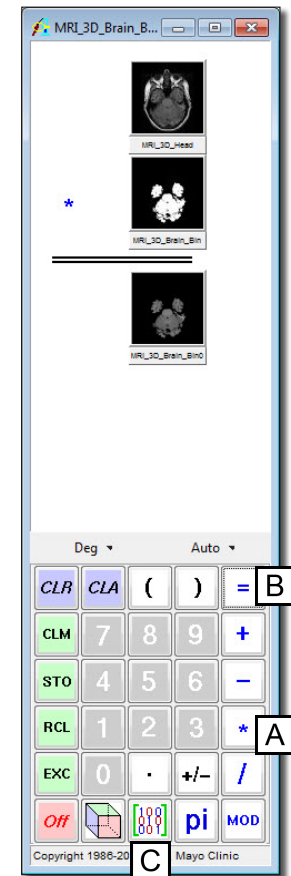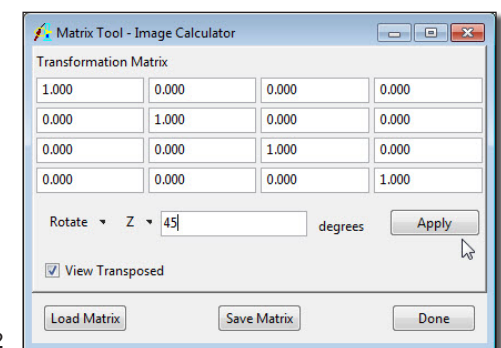
Figure 1

Figure 2

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 [**D**] 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 Tool** button [**E**] 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.
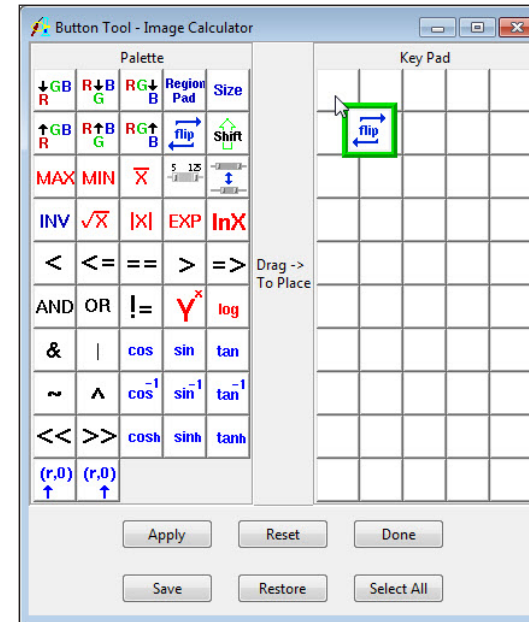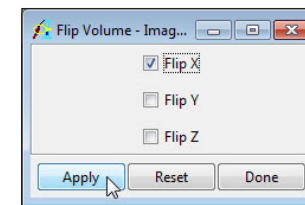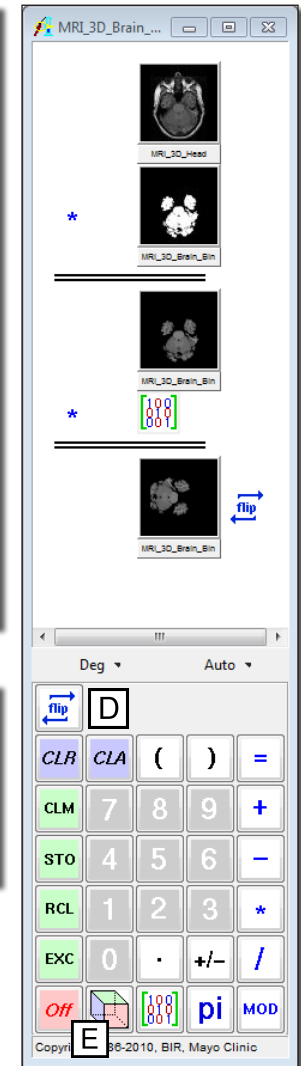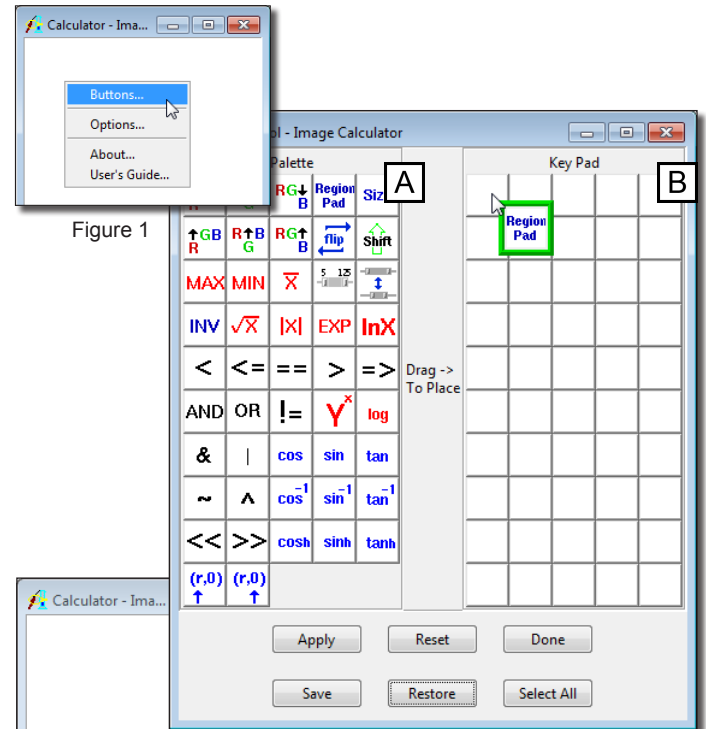

Figure 3

Figure 5

Figure 4

Exercise 24 : 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 [A] from the palette on the left, and drag and drop it onto the Key Pad [B] 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.

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 [C], the Region Pad buttons **Function Option** 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 2

Figure 3

Figure 4

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

Figure 5

Example 1: Subregioning 50 slices in the X.

   i.   Set the **X Low** value to **25**
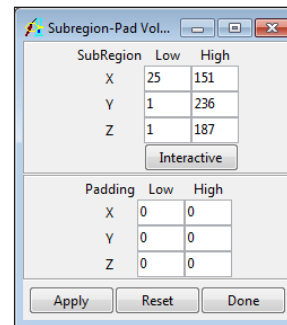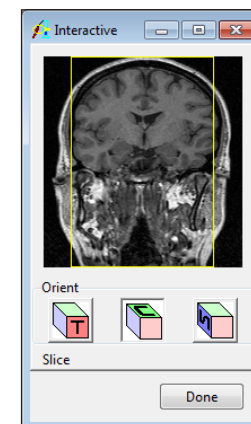
   ii.   Set the **X High** value to **151**

Example 2: Subregioning 50 slices in the Y.

   i.   Set the **Y Low** value to **25**

   ii.   Set the **Y High** value to **211**

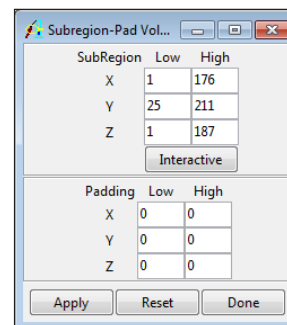Figure 6

Example 3: Subregioning 50 slices in the Z

   i.   Set the **Z Low** value to **25**
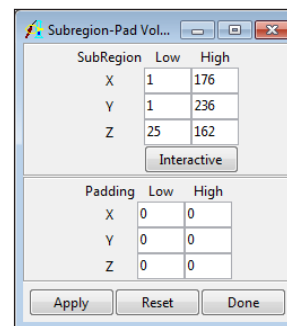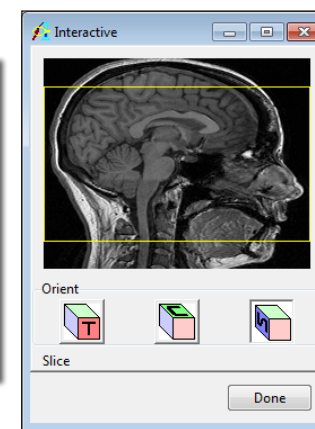
   ii.   Set the **Z High** value to **162**

Figure 7

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 [**A**].
    - 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 [**B**].

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.
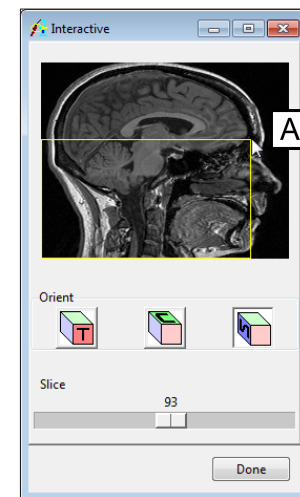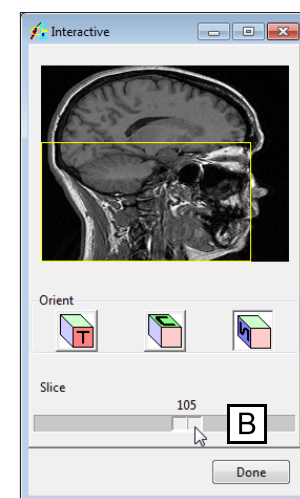

Figure 8

Figure 9

Exercise 25 : 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**).

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.

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

5. [**B**] 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 [**C**]; in the **Parameters** window returned, set **Name** to **Bone**. Click **Done** to dismiss the window.

7. Click **Go** [**D**] 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.

Figure 1

Figure 2

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.

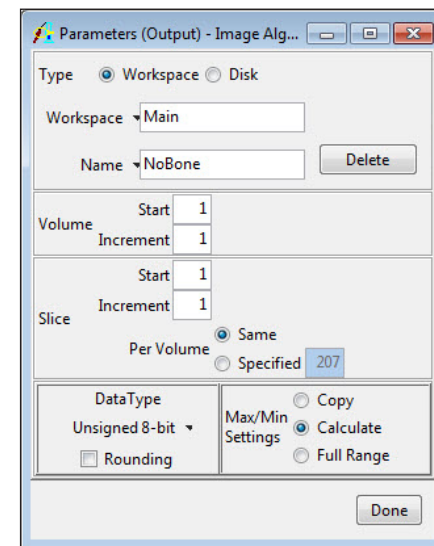20. Close the Image Algebra module before proceeding to the next exercise.
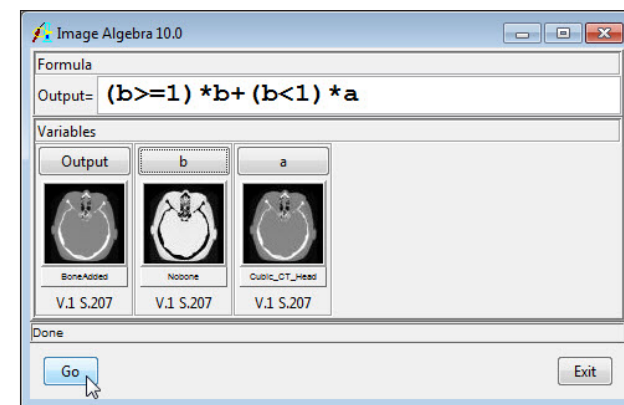

Figure 3

Figure 4

Exercise 26 : 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.

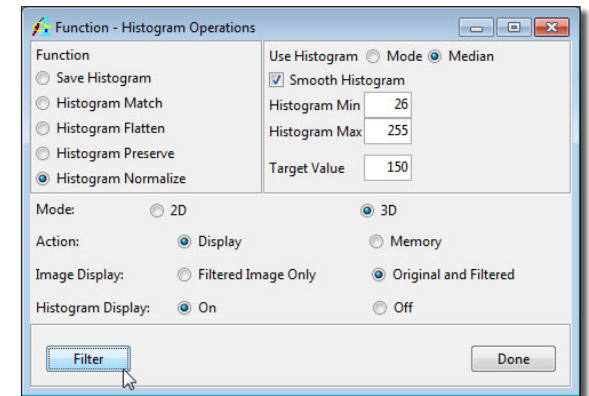10. Close the Histogram Operations module before proceeding to the next exercise.
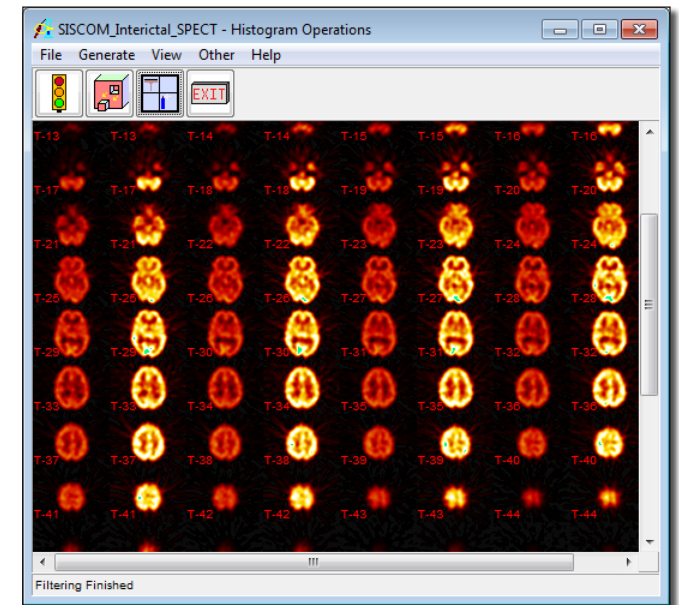

Figure 2

Exercise 27 : 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** [**A**]. 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** [**B**] 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.
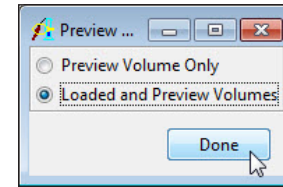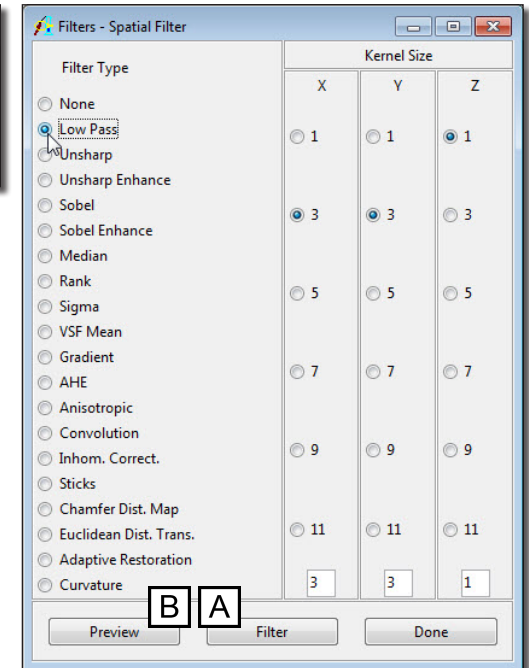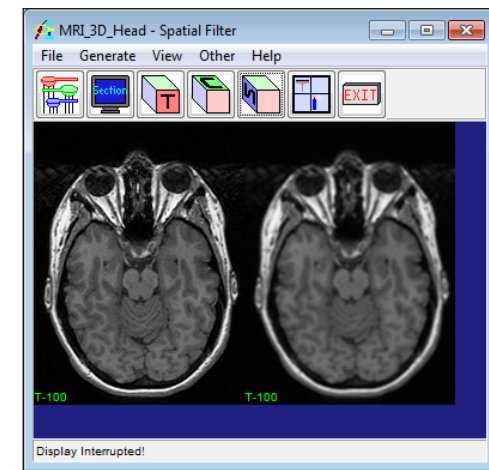
Figure 1

Figure 2

Figure 3

Analyze 10.0

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. Open the **Slice** window (**Generate > Slice**), and use the slider bar to move to **Slice 122**.

4. In the main Image Edit window, select the **Auto Trace** tool [**A**]. 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 [**B**] 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** [**C**].

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 [**D**]).

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

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

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.
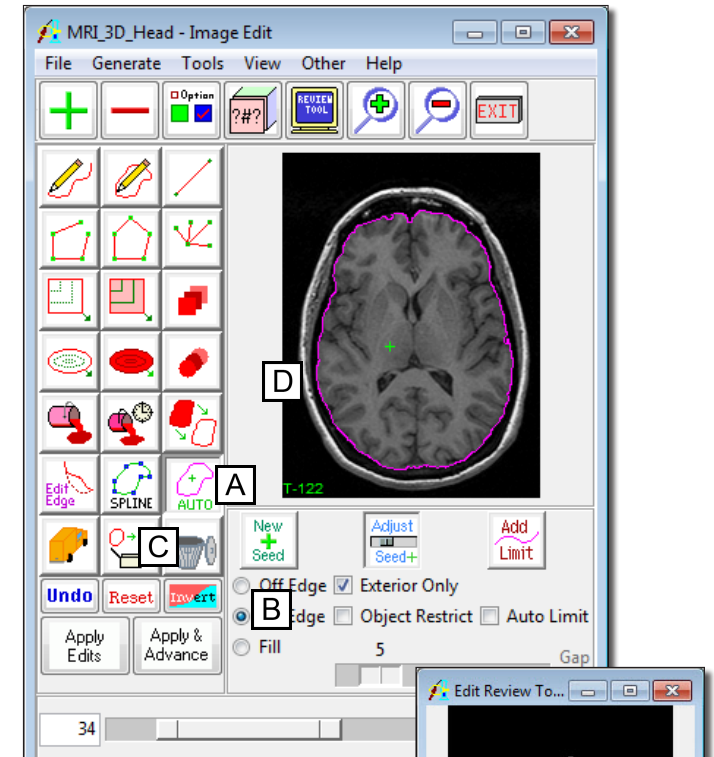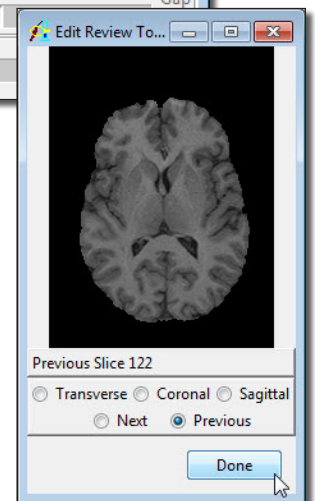
Figure 1

Figure 2

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. To create a rendering of the edited data complete the Additional Task.
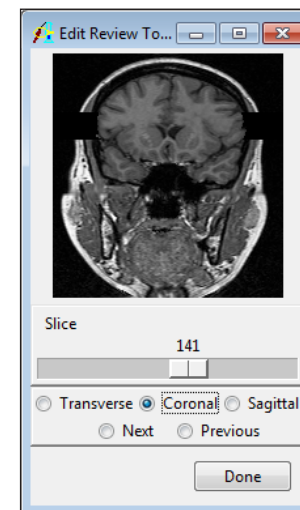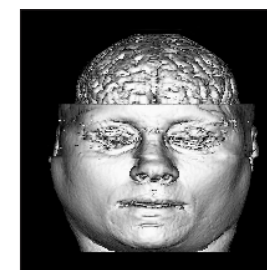
Figure 3

1. Rendering Segmented Data

Additional Task

1. Continue to segment the data set until approximately **slice 181** to remove the entire top of the head.

2. Close the Image Edit module.

3. Select the **MRI_3D_Head0** data set in the Analyze workspace and then open the **Volume Render** module (**Display > Volume Render**).

4. Open the **Thresholds** window (**Display > Thresholds**).

5. Set the **Minimum threshold** level to **50**, then click **Render**. The rendering will be displayed in the main Volume Render window (figure 4).

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

Figure 4

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** [**A**] to create a new empty object (Object_2).

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

6. Open the **Slice** window (**Generate > Slice**), and 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 [**C**].

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 [**D**] 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 [**E**]).

    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.
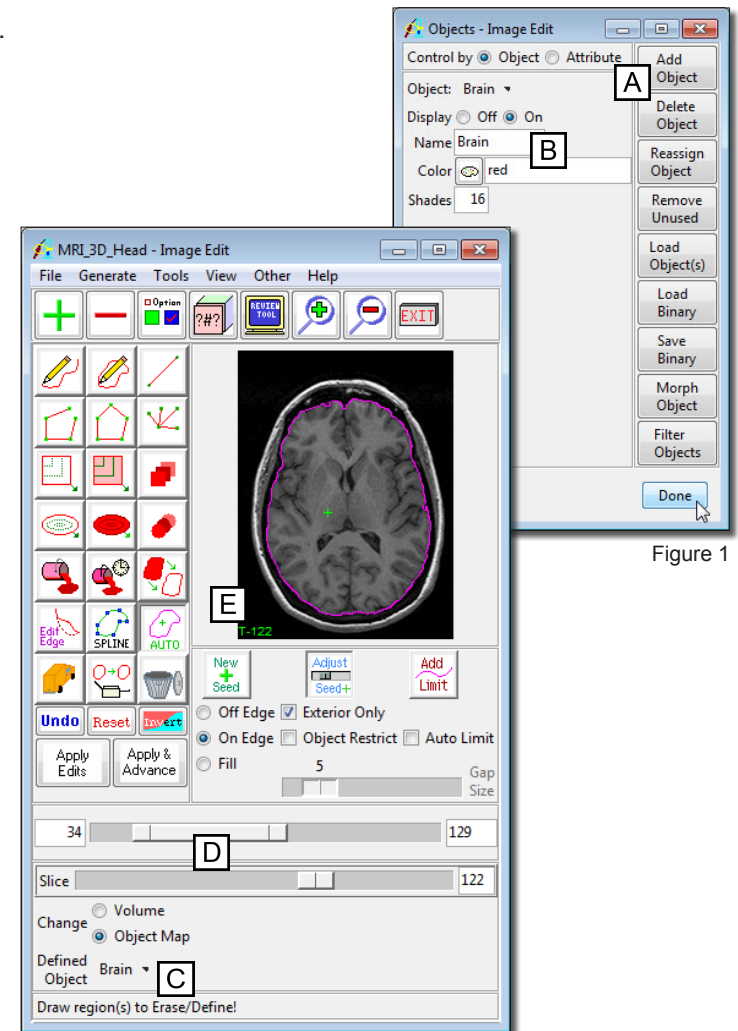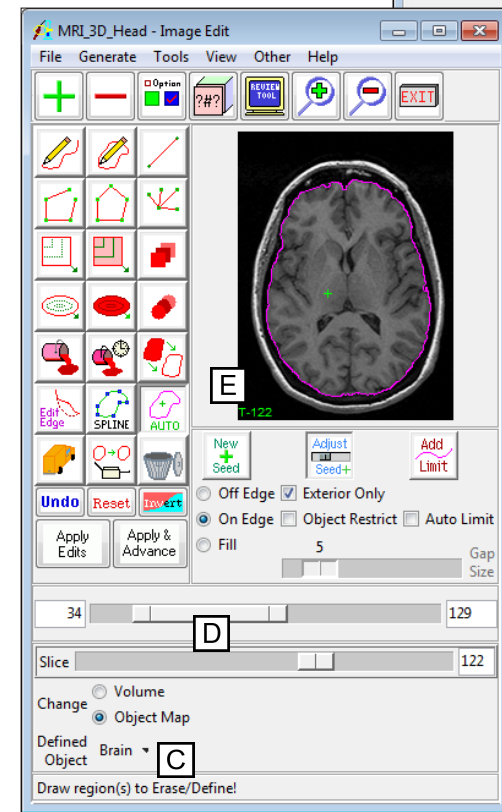
Figure 1

Figure 2

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

14. Select the **Previous** option in the Edit Review tool. The change can also be viewed by selecting the **Sagittal** option.

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).

> tip | 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.

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).
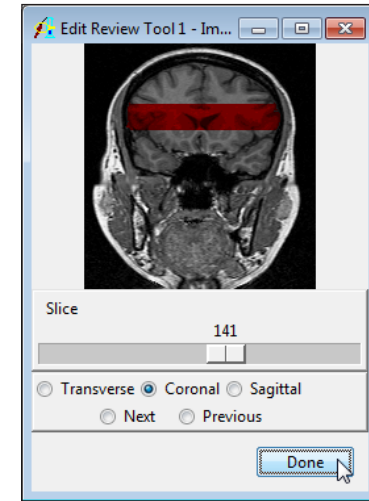
Figure 3

Additional Task

1. Viewing the Object Map in Volume Render

1. In the Analyze workspace, select the **MRI_3D_Head** data set and open the **Volume Render** module (**Display > Volume Render**).

2. Choose **File > Load Object Map** and load the **xxx_mybrain.obj** object map (saved earlier in step 16).

3. Open the **Objects** window (**View > Objects**). Set **Control by** to **Attribute** and set the **Display** attribute to **Off** for the **Original** object.

4. Click **Render**. You should see a rendering of the object you created in the Image Edit module.

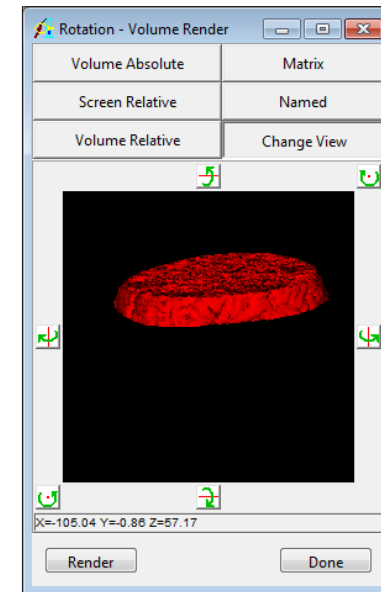5. Use the **Rotation** window (**Generate > Rotation**) to generate different views of the object (figure 2).

Figure 1

Exercise 30 : Morphology Morphological-Based Segmentation

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 [**A**]. 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 [**B**]. 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** [**C**]. Change **Max. No. of Components** to **1**. Click **Connect Volume**.

11. In the Step Editor window, click **Conditional Dilate** [**D**]. 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.
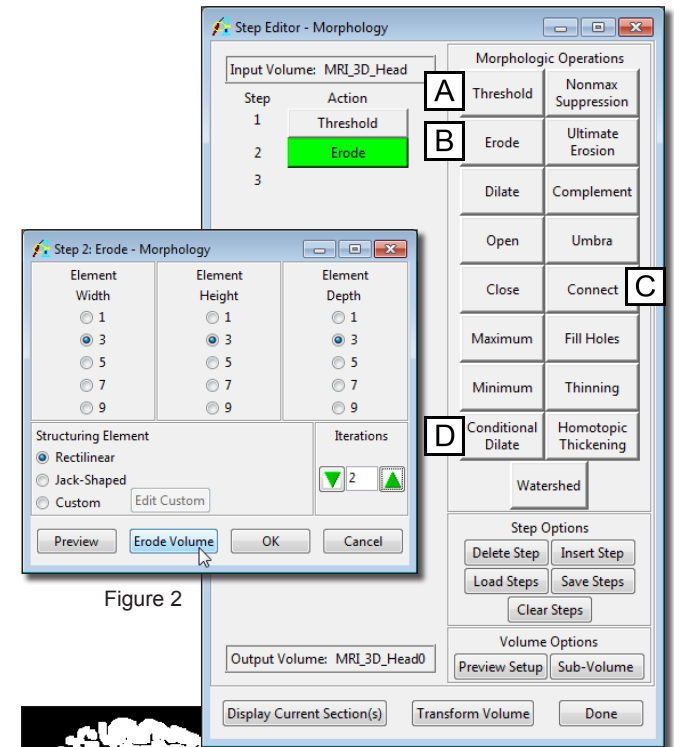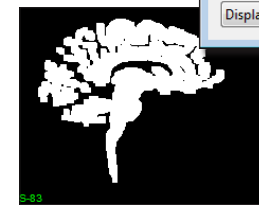
Figure 2

Figure 3

Figure 1

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.

Exercise 31 : 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 object, the masked volume, and 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.

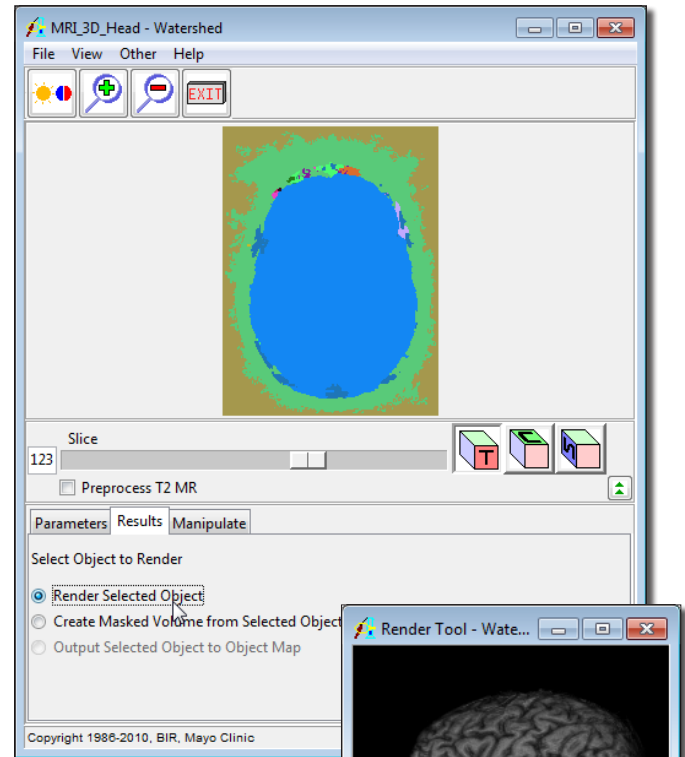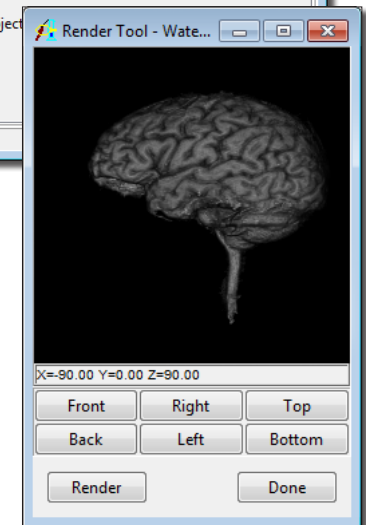11. Close all windows before proceeding to the next exercise.

Figure 1

Figure 2

Exercise 32 : 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.

    note | If you use the Load As module to load the data set into Analyze, select 'Single Multivolume' when prompted.

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 [**A**] 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 [**B**] next to the 'Slice' slider bar.

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. Select the **Curved Line** tool and define a small region of grey matter (peripheral brain tissue) as **class 2**. Make sure to choose 'class 2' from the **Classes** drop-down menu [**C**] before starting the trace. The paired values will show as green in the scattergram and in the image display.

    tip | To move a defined region hold <Shift> then click and drag the region to the desired location.
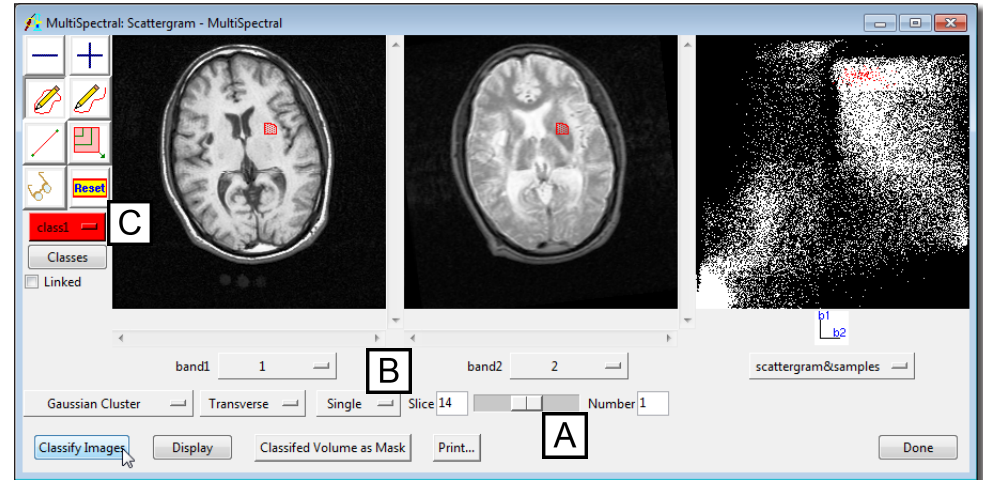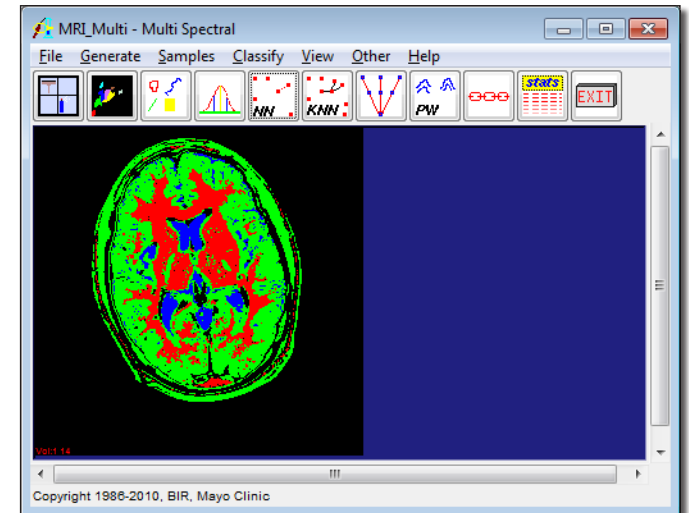
Figure 1

Figure 2

7. Select the **Closed Trace** tool and define a small region of cerebrospinal fluid (in the central ventricles) as **class 3**.

8. Click **Classify Images**. The Gaussian Scattergram Classifier window will automatically be returned (figure 3), click **Classify**. Click **Done** to dismiss the window.

9. 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 4).

10. 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.

11. Close the Multispectral Classification module before proceeding to the next exercise.
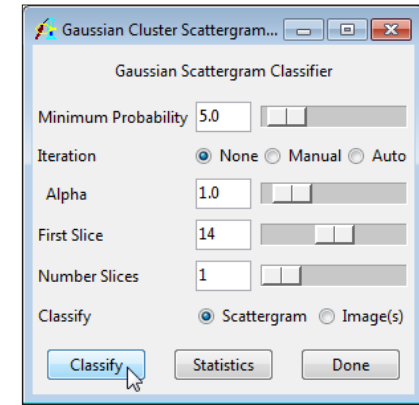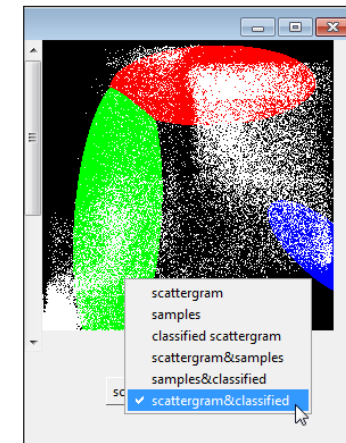

Figure 3

Figure 4

Exercise 33 : 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 the **Extract Options** 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 [**A**] now available to set the **Threshold Minimum** to **49** and the **Maximum** to **140**.

   note | Click the Clear Regs button [B] at any time to remove all traces and limit ranges. A new starting slice may also be defined if required by clicking the Target Slice button [C].

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

Additional Task

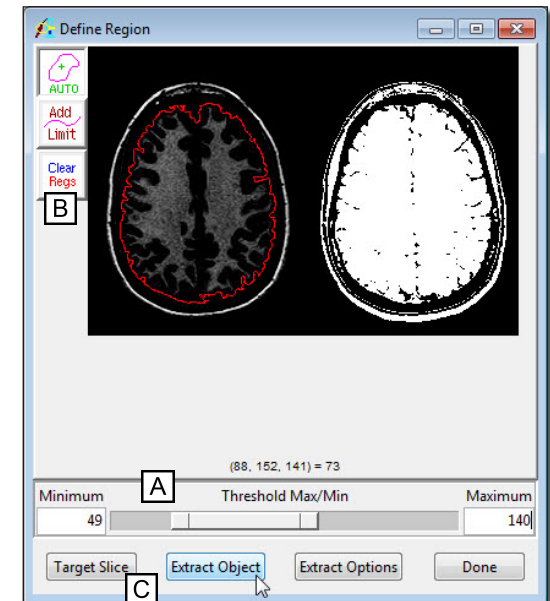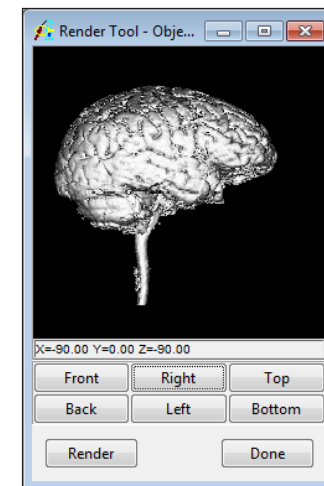### 1. Extract Options - Creating an Object Map

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 overlaid on the original image data in the main **Object Extractor** window (figure 3). The Render Tool will also automatically be returned, 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.
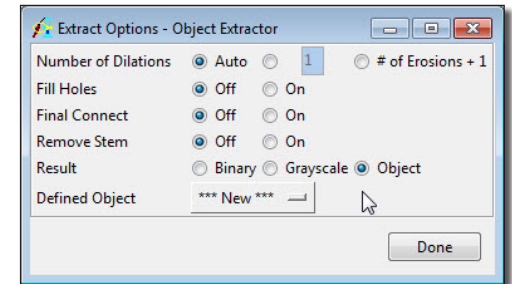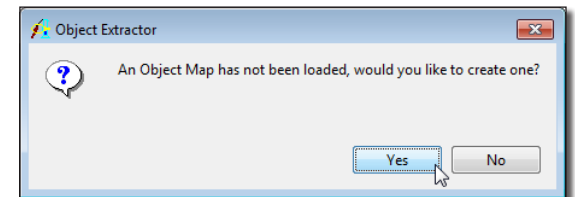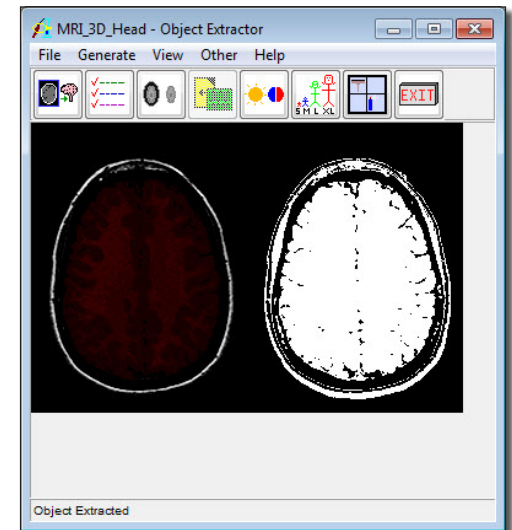

Figure 1

Figure 2

Figure 3

Additional Task

2. Extract Options - 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 in the Analyze workspace and then 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.

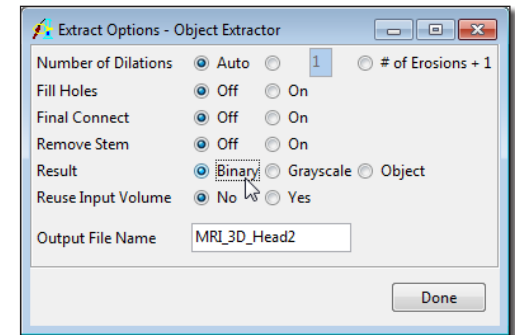7. Close the Object Extractor module before proceeding to the next Additional Task.

Figure 1

Additional Task

3. Extract Options - 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 in the Analyze workspace and then 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 brain with the brain stem removed will be displayed in the main Object Extractor window. The **Render Tool** will also automatically be returned (figure 2), 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.
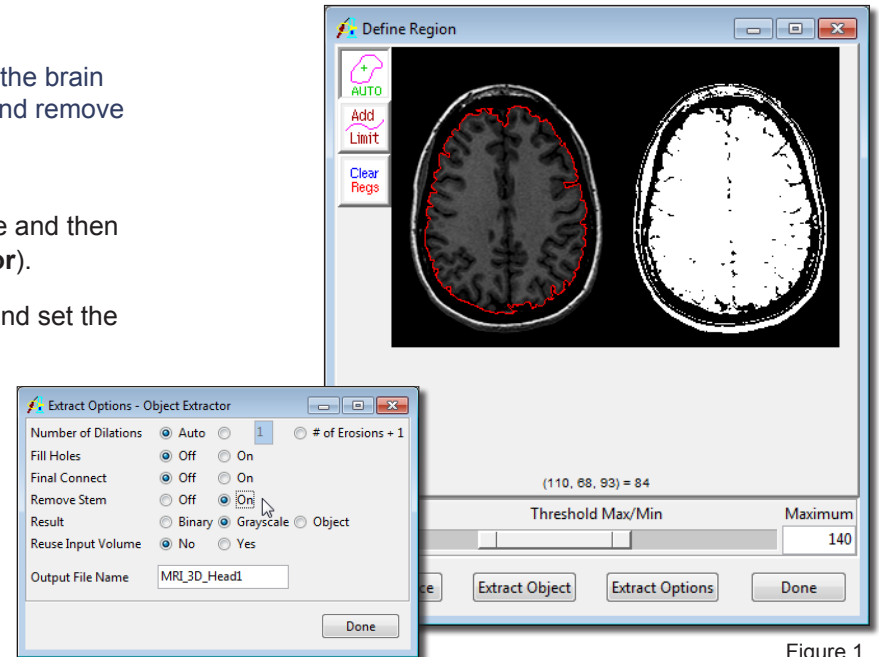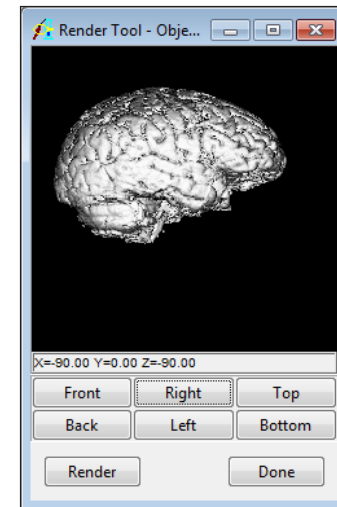
Figure 1

Figure 2

Exercise 34 : Object Extractor Extracting Multiple Objects

The Object Extractor module supports the creation of multi-object object maps. This exercise will demonstrate how to achieve this.

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 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 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 [**A**] 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 [**B**]. 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).
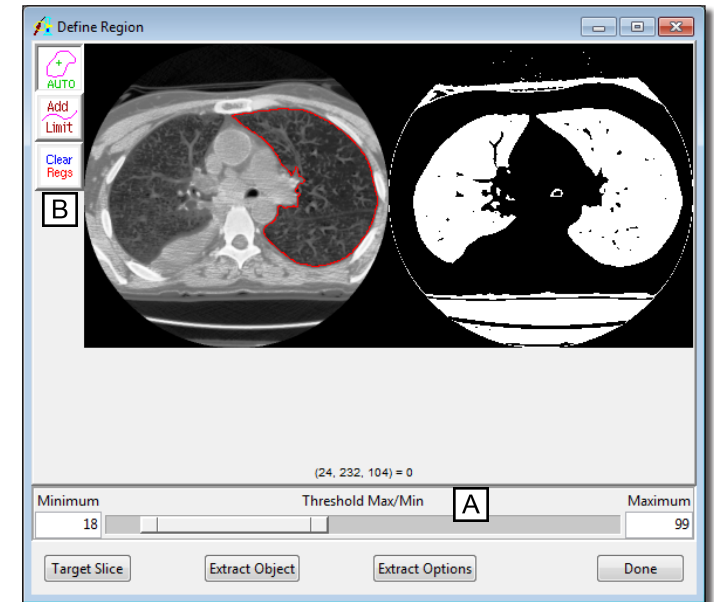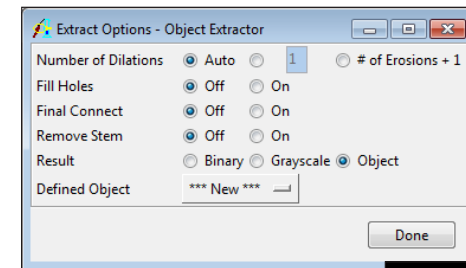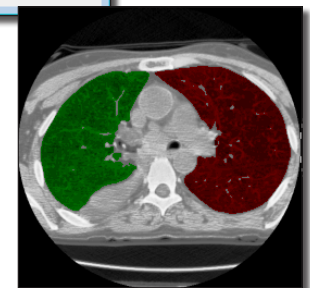

Figure 1

Figure 2

Figure 3

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.
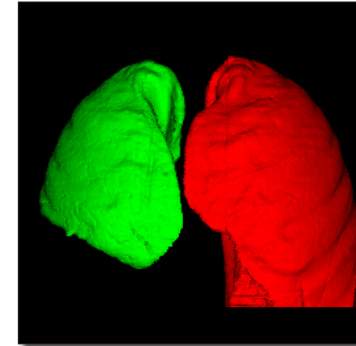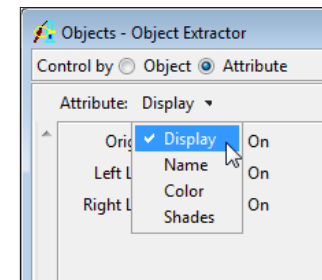

Figure 4

Figure 5

Exercise 35 : 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** [**A**] 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. 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** [**B**].

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 2).

9. In the Extraction Parameters window change the **Cube Edge Size** [**C**] 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 3). 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.
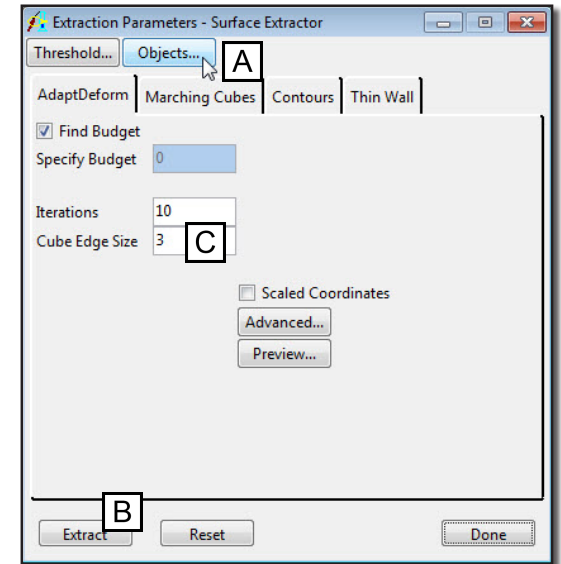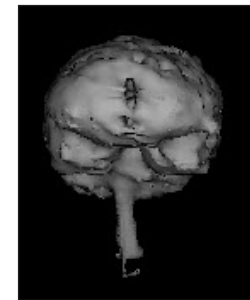

Figure 1

Figure 2

Figure 3

11. Click **Reset [D]** in the Extraction Parameters window to restore the default parameters ('Cube Edge Size' of 3).

12. Click **Advanced [E]** 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.

> note | Increasing the resolution increases the processing time, this is demonstrated by setting the 'Cube Edge Size' to '1'. In cases where a high resolution (Cube Edge Size of 1) is required, use the Marching Cubes algorithm.

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 polygon's attraction to the surface is reduced and they become harder to bend).

16. Press the **Save Surface** PowerBar button or choose **File > Save Surface > To File** to save the extracted surface to disk.

17. In the Save Surface window returned (figure 4) 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), 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.
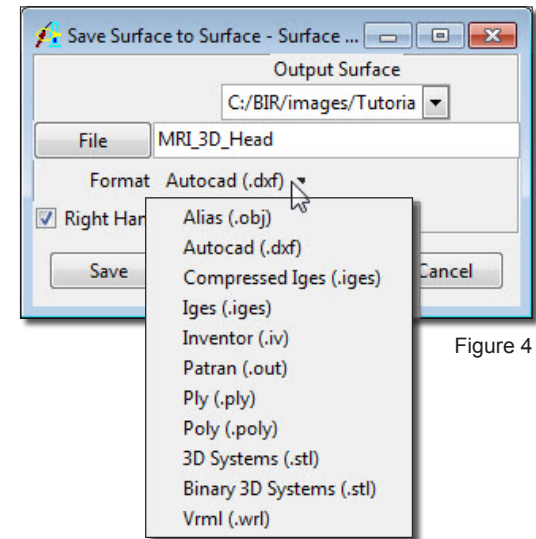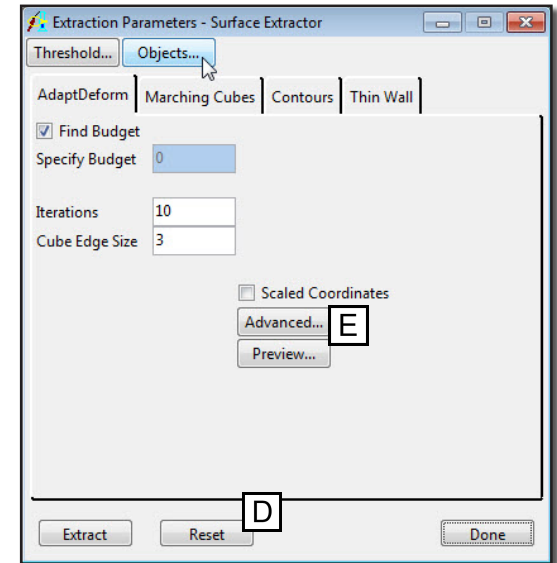
Figure 4

Additional Task

1. Extracting the Surface of 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).

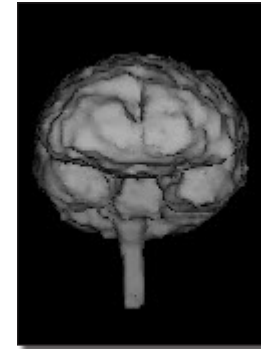6. Close the Surface Extractor module before proceeding to the next exercise.

Figure 1

Supported Surface File Formats

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

Exercise 36 : 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** [**A**] 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** [**B**] 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).

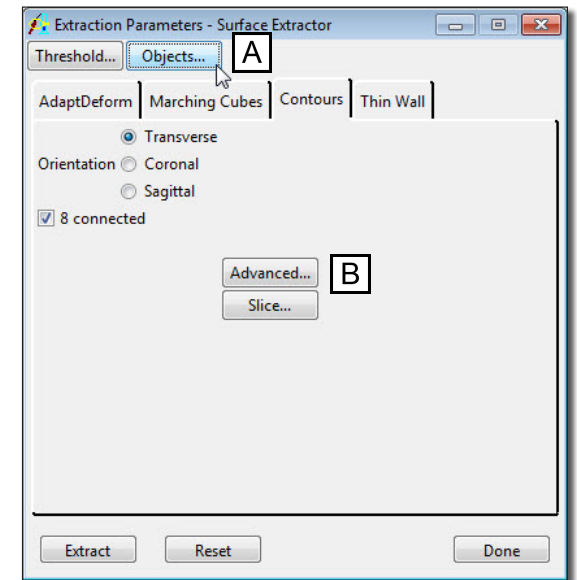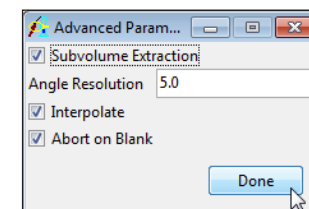12. Close the Surface Extractor module before proceeding to the next exercise.

Figure 1

Figure 2

Figure 3

Analyze 10.0

Registration

Exercise 37 : Registration 3-D 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.

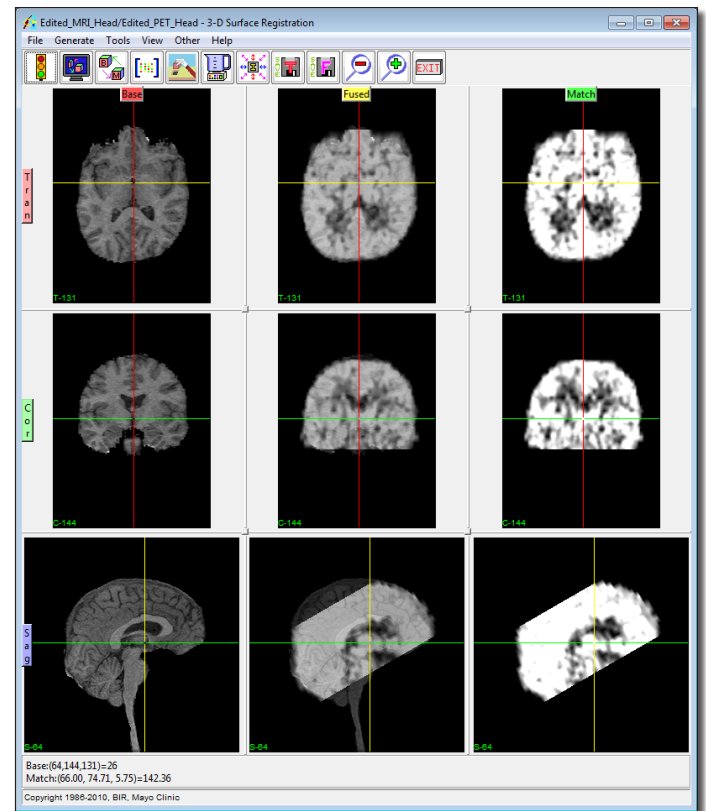9. Close the 3-D Surface Registration module before proceeding to the next exercise.

Figure 1

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.
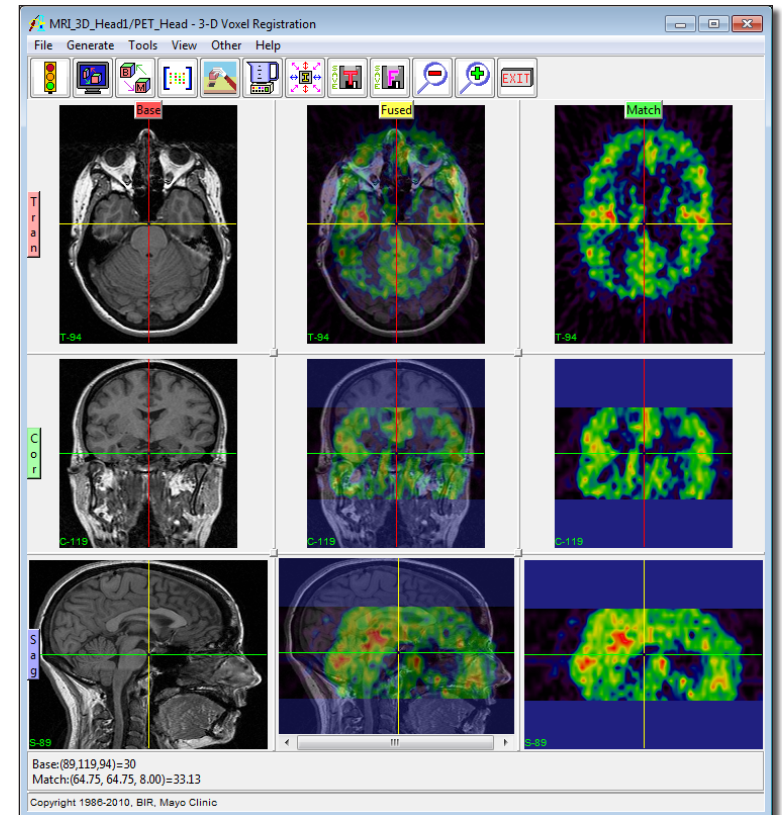

Figure 1

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.
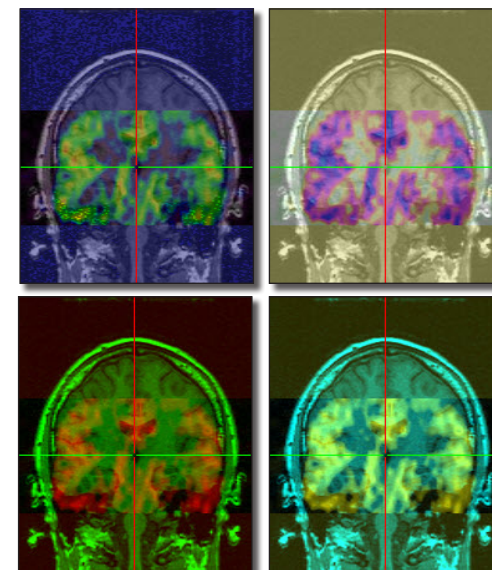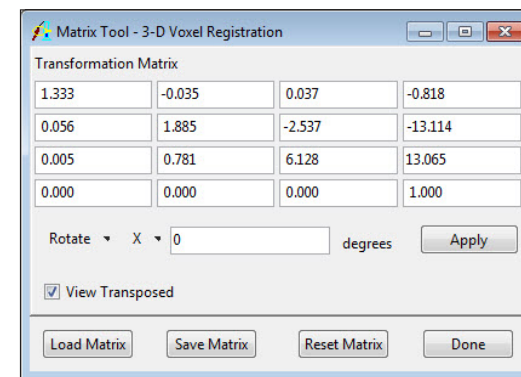
Figure 2

Figure 3

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.

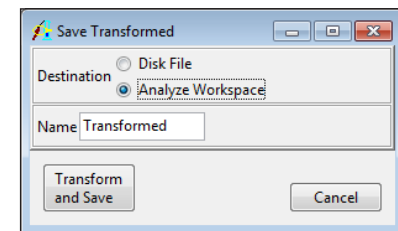16. Close the 3-D Voxel Registration module before proceeding to the Additional Task.

Figure 4

Additional Task

1. 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.
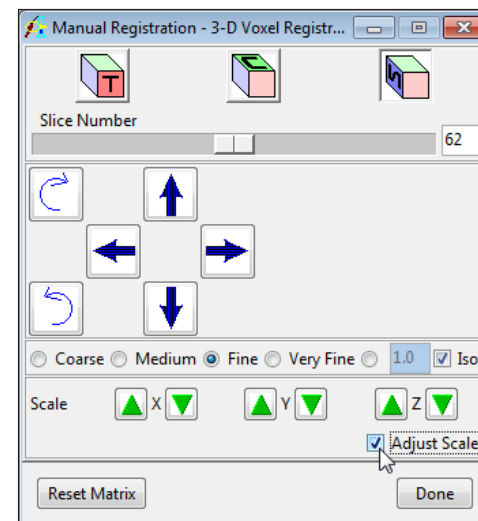
Figure 1

Exercise 39 : Image Registration Mutual Information Registration

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 **$:\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.

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.
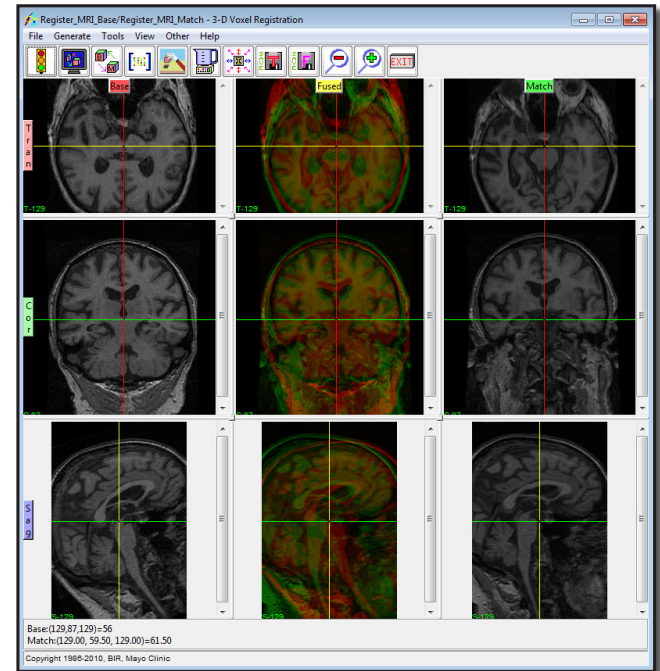
Manual Adjustment

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.
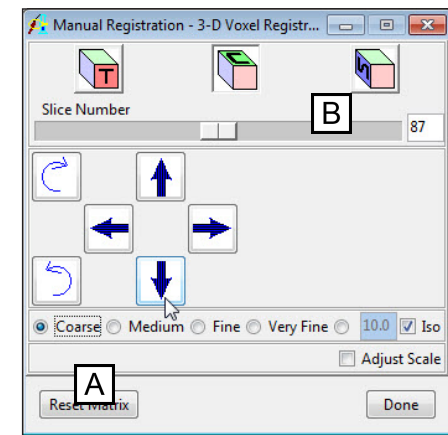

Figure 1

Figure 2

12. Now, select the **Coarse** adjustment option [**A**] and press the **down** arrow button once.

13. Change the orientation from coronal to sagittal by selecting the **S-cube** [**B**] and then press the **right** arrow button once.

14. Press **Register**. The volumes should now register correctly (figure 3).

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.

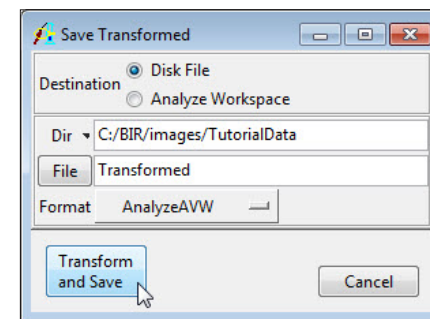17. Close the 3-D Voxel Registration module before proceeding to the next exercise.

Figure 3

Analyze 10.0
Measurement

Exercise 40 : Line Profile Calculating Image Intensities Along a Straight Line

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. Open the **Slice** window (**Generate > Slice**) to move through the volume image. Set the **Slice** to **97** and click **Done**.

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.

    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.
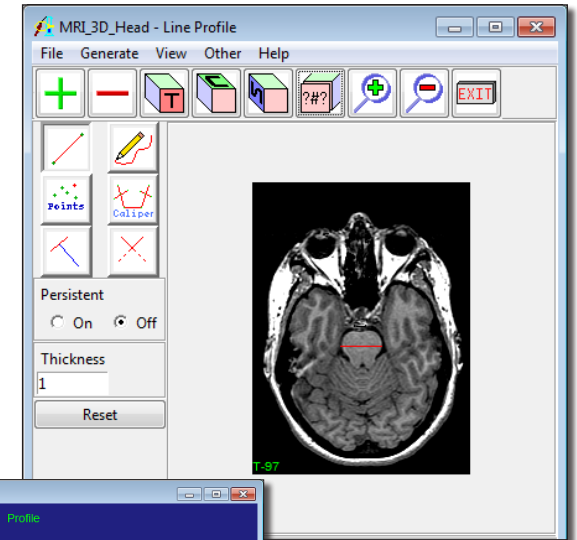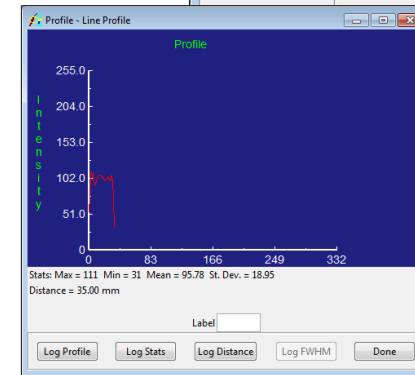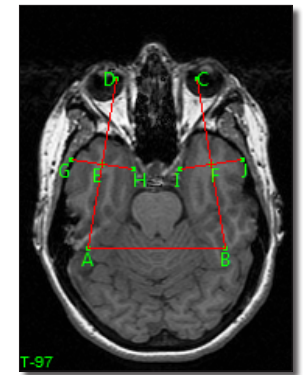
Figure 1

Figure 2

Figure 3

Additional Task

1. 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** (figure 4). 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.
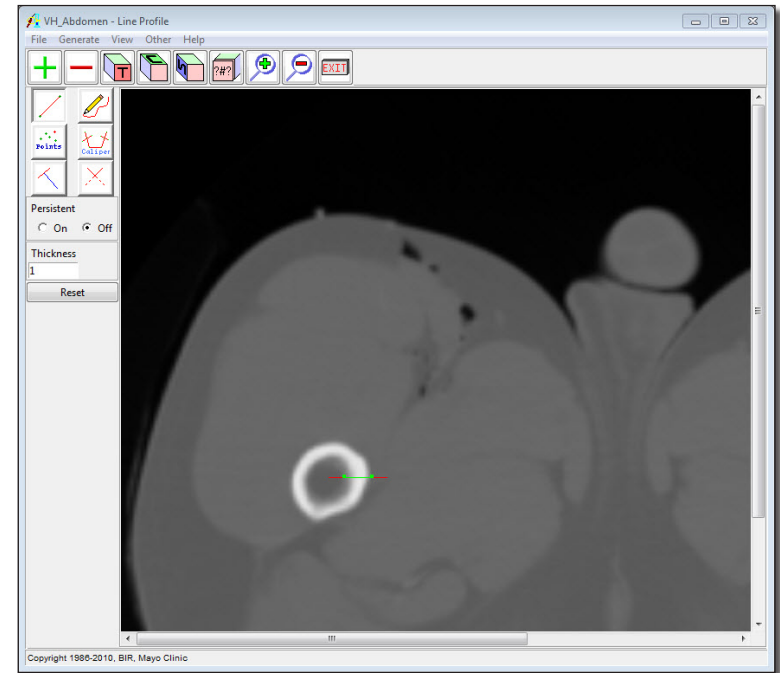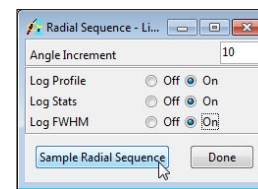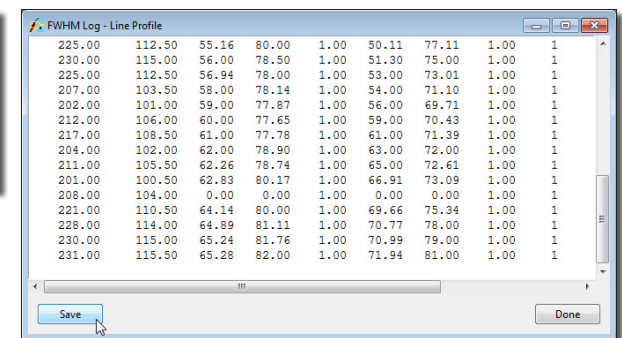
Figure 3

Figure 4

Figure 5

Exercise 41 : 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 the **Region of Interest** module (**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*** [**A**] at the bottom of the window (figure 1).

4. The buttons along the left side of the window control the definition of regions on the images [**B**]. The buttons below the image display allow you to modify the defined regions [**C**].

5. The first slice of the volume is automatically displayed when the ROI module is opened. You can move to a different slice using the **Show Next** and **Show Previous** Slice PowerBar buttons or by using the **Slice** slider bar [**D**]. The currently displayed slice number and orientation can always be seen in the lower left corner of the image display [**E**].

> *tip* | The + and - keyboard keys can also be use to move through the data set.

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 2).

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).

Figure 1

Figure 2

> *tip* | Holding the <Ctrl> key while sizing will force a square.

Oval Tool

9. Add a new region to slice 2 using the **Oval tool** (figure 3).

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 7. 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**.

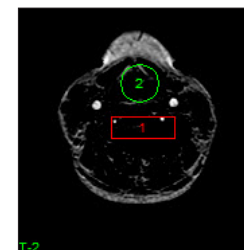12. Press the **Show Next Slice** PowerBar button to move to slice 4.

Figure 3

tip | Holding the <Ctrl> key while sizing will force a circle.

Polygon Tool

13. Since the 'Show Next Slice' button was pressed, and not the 'Copy Regions Forward' button, 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 5).

15. If after defining the region it is unsatisfactory, click the **Undo** button.

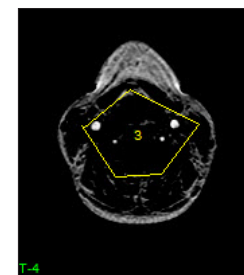16. Press **Show Next Slice** to move to slice 5.

Figure 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.

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 [**F**]. 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** [**G**] 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 [**H**]. 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.

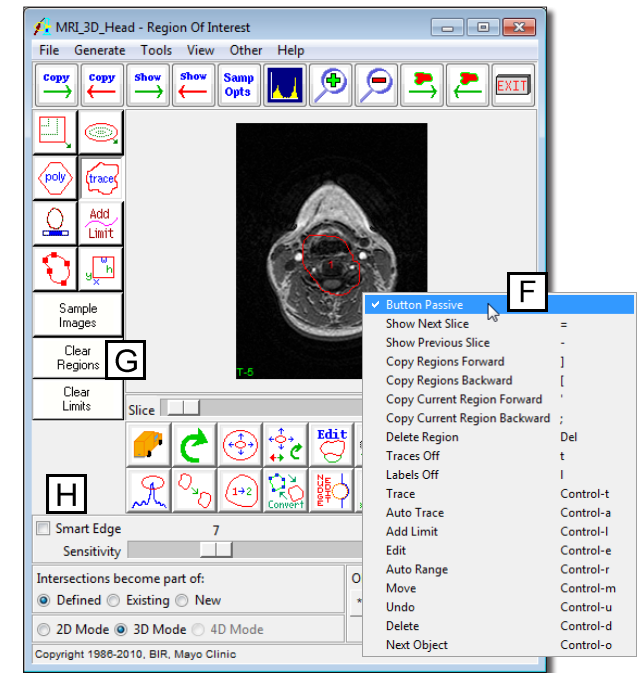22. Press **Show Next Slice** to move to slice 6.

Figure 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.

Additional Task

1. 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. Press **Show Next Slice** to 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 7).

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 7).

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 8).

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 9).

14. Close the Region of Interest module before proceeding to the next exercise.
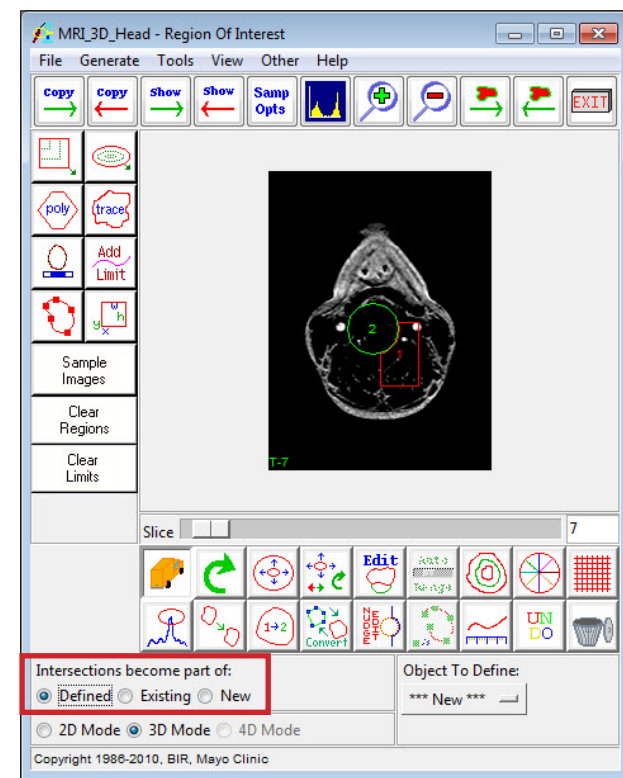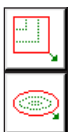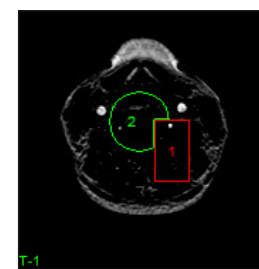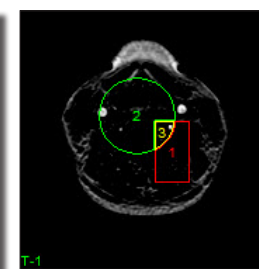

Figure 7

Figure 8

Figure 9

Exercise 42 : Region of Interest Defining Regions and Volume Measurements

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. The data set may be available in the Analyze workspace if you have completed Exercise 41: ROI Defining Regions.

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** [**A**] and the **threshold maximum** to **129** [**B**]. Then, click **Apply** [**C**]. 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.

note | You can change the image display size within the Size window (View > Size) or with the Magnifier PowerBar buttons.
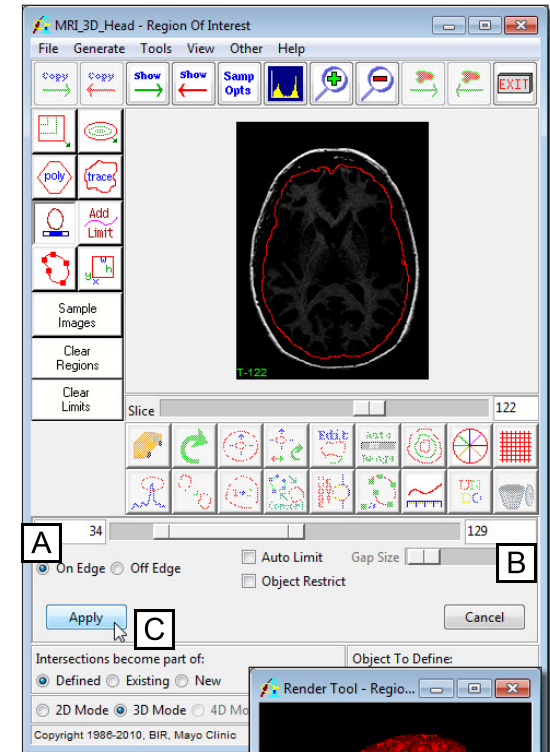
Figure 1

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.
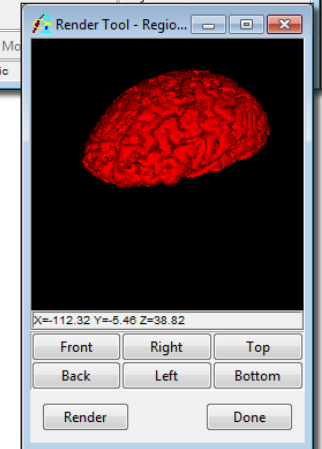
Figure 2

Measuring Regions

Samp Opts

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'.

18. In the Sample Options window, set **Sample** to **Slices Specified in Slice Menu.**

19. Open the **Slice** window (**Generate > Slice**) and set **Slice** to **122** (the first slice with the object) and **Number** to **59** (the number of slices after 122 on which the object appears) (figure 5).
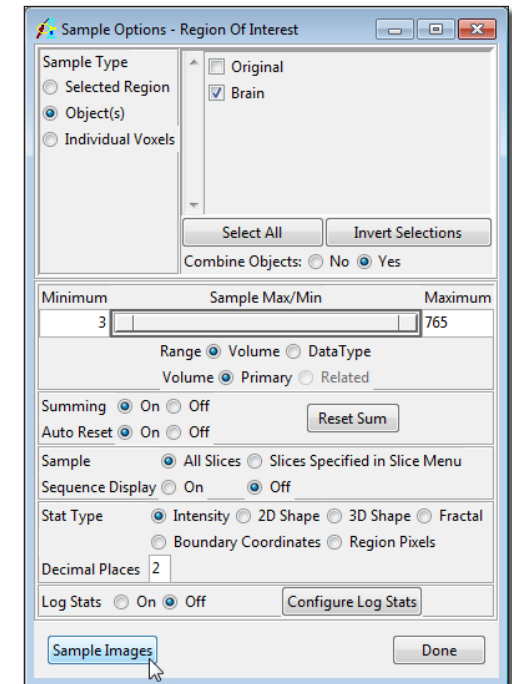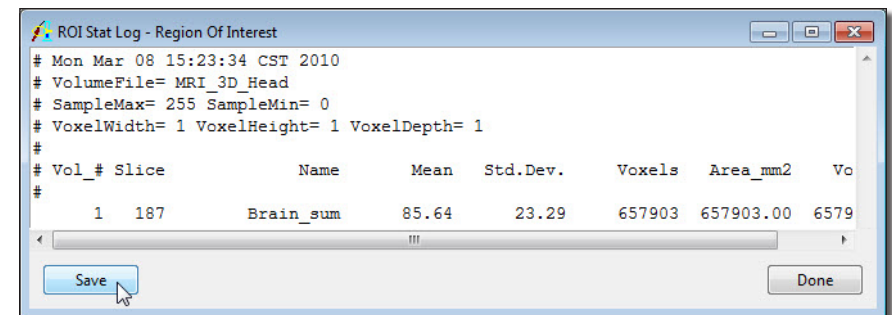
Figure 3

Figure 4

20. Click **Sample Images**. Only the slices specified in the Slice window will be sampled.

21. Experiment sampling the data with the different Stat Types available in the Sample Options window, for a full explanation of statistic types choose **Help > User's Guide** in the main ROI window.

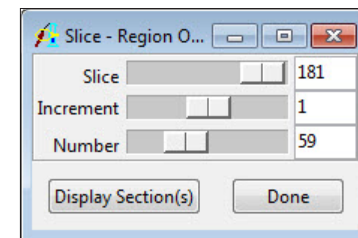22. To learn about editing regions complete the following Additional Task.

Figure 5

Additional Task

1. Editing Regions

Edit

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.

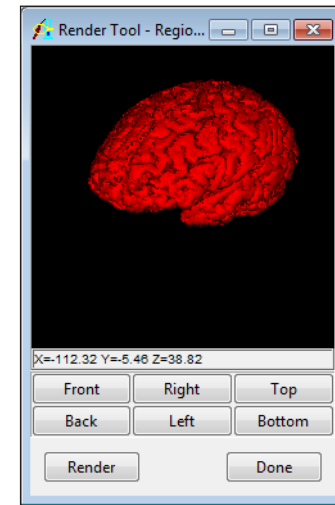9. Close the Region of Interest module before proceeding to the next exercise.

Figure 1

Exercise 43 : Region of Interest Measuring Objects in Object Maps

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** to **by Attribute**.

5. Notice that this object map contains several objects. With the **Display** attribute selected, switch the **Lenticular** and **Caudate** objects to **On**.

6. Open the **Slice** window (**Generate > Slice**) and 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.

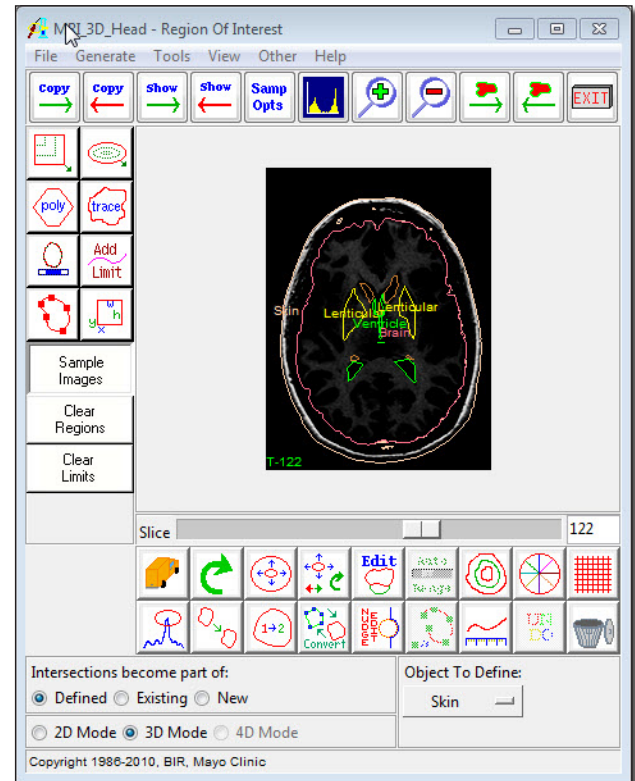11. Click **Done** to close the ROI Stat Log; in the dialog box returned click **Discard, then Exit**.
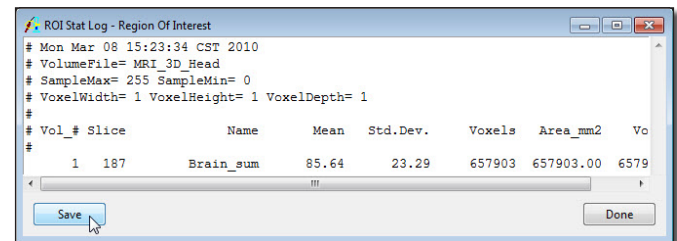

Figure 1

Figure 2

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 (figure 3).

15. Click **Sample Images**. The total brain volume will now be returned to the ROI Stat Log (figure 4)
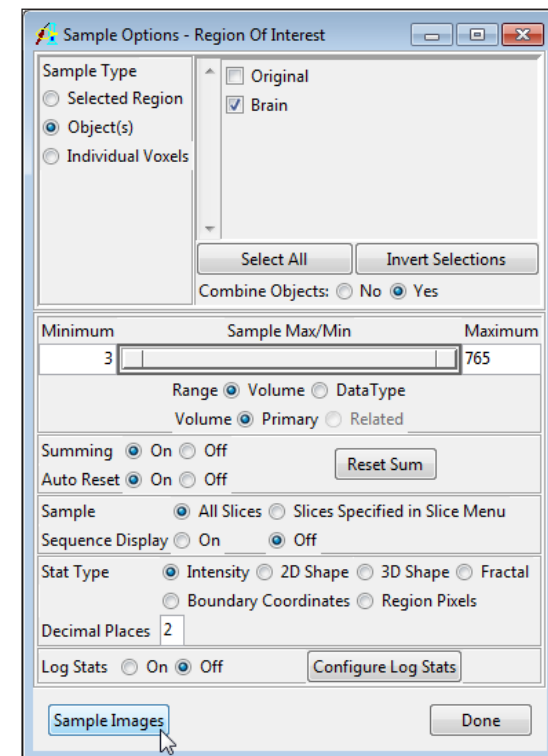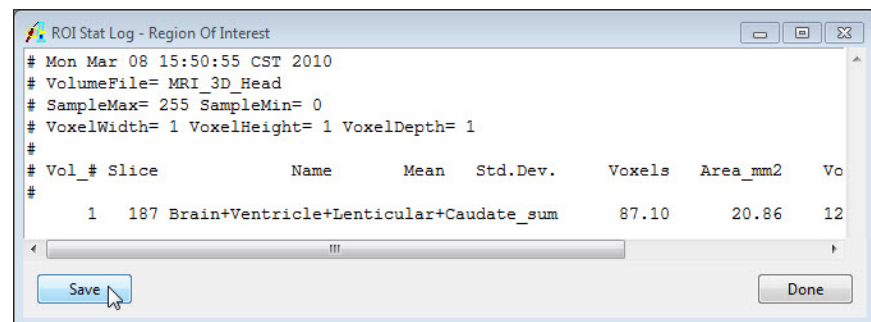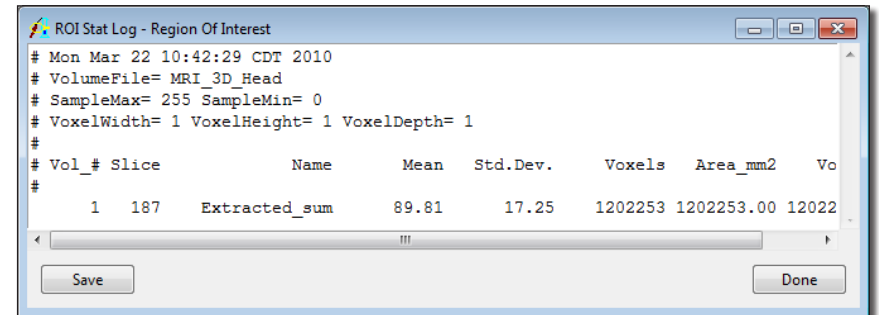

Figure 3

Figure 4

1. Volume Measurement - Manual vs. Automated Segmentation

Additional Task

1. Select **File > Load Object Map** and load the object map created in **Exercise 33: Object Extractor - Automated Segmentation**.

2. Follow steps 7-9 in the above exercise to calculate the volume of the 'Extracted' Brain object.

3. Compare the volume returned in the ROI Stat Log (figure 5) to that of the brain volume obtained in step 15.

4. Close the Region of Interest module before proceeding to the next exercise.

ROI Stat Log - Region Of Interest
```
# Mon Mar 22 10:42:29 CDT 2010
# VolumeFile= MRI_3D_Head
# SampleMax= 255 SampleMin= 0
# VoxelWidth= 1 VoxelHeight= 1 VoxelDepth= 1
#
# Vol_# Slice          Name        Mean    Std.Dev.    Voxels    Area_mm2    Vo
#
     1    187    Extracted_sum    89.81      17.25    1202253  1202253.00  12022
```
Save   Done

Figure 5

Exercise 44 : 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.

Figure 1

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 from the Measure menu (**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**.
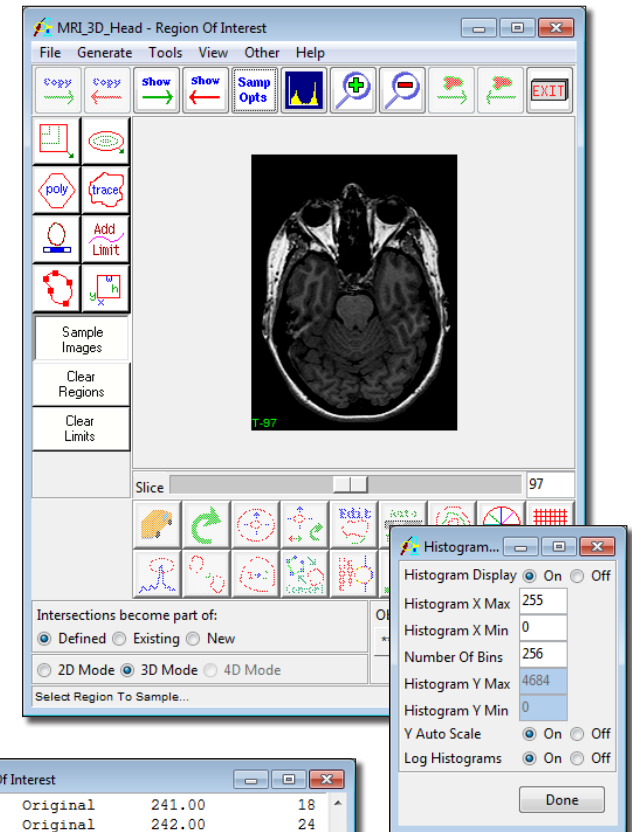
7. Close all windows associated with the ROI module.
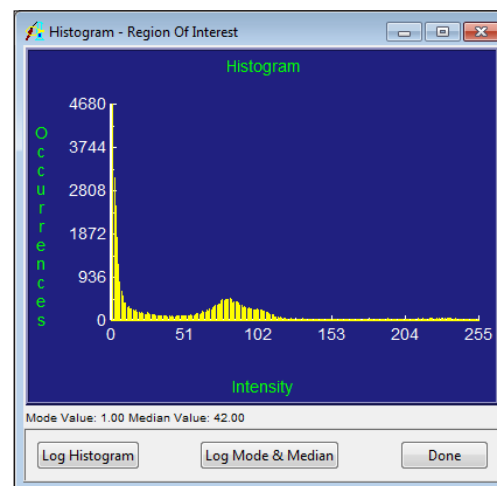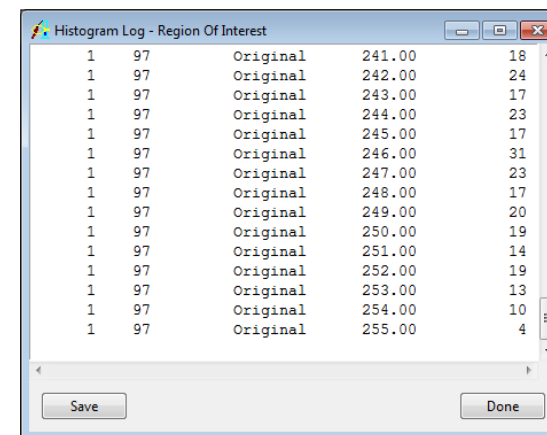

Figure 2

Figure 3

Sampling a Volume

1. Select the **MRI_3D_Head.avw** data set and open the **Region of Interest** module.

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

Sampling an Object

1. Select **MRI_3D_Head.avw** and open the **Region of Interest** module.

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

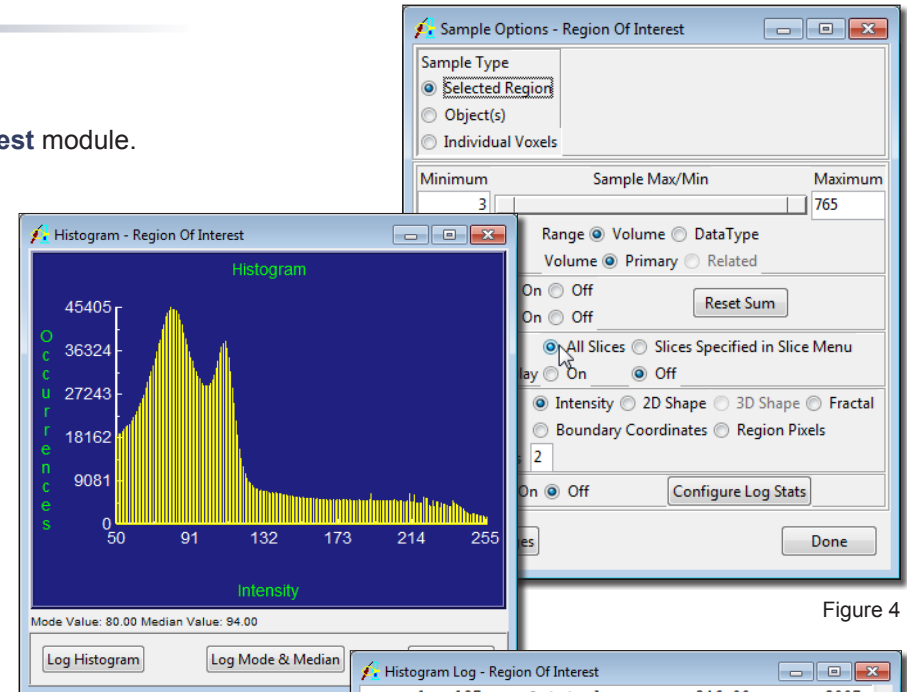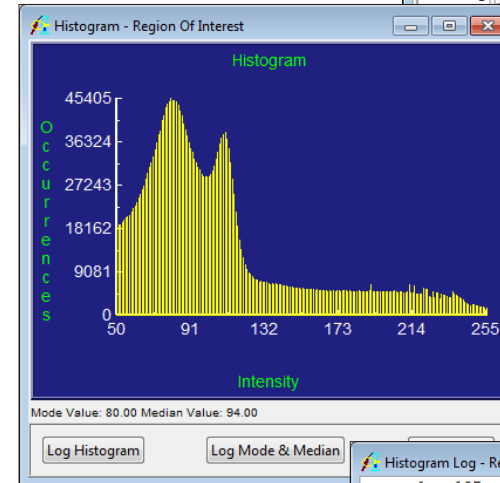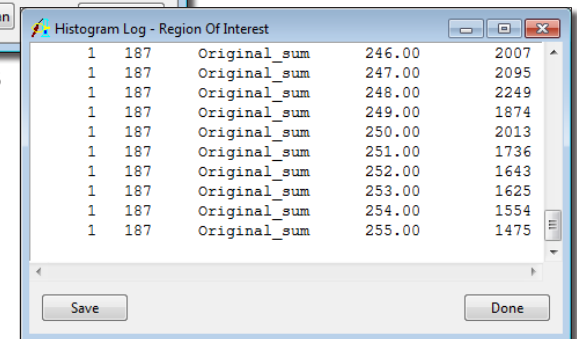3. Open the Histogram window (**Generate > Histogram**).

4. In the Histograms window set **Histogram Display** to **On** and set **Log Histogram** to **On**.

5. Next open the **Sample Options** window (**Generate > Sample Options**), and set the following parameters:

   - **Sample Type** to **Object(s)**
   - Uncheck all objects except the **Brain**
   - **Summing** to **On**
   - **Sample** to **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 before proceeding to the next exercise.
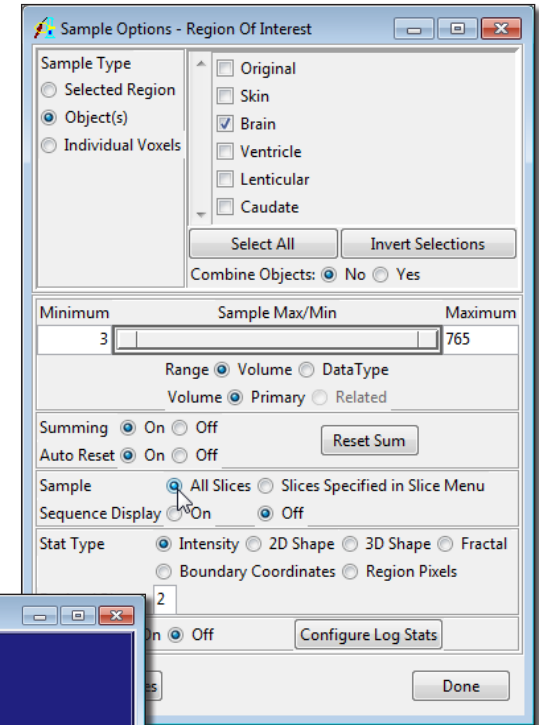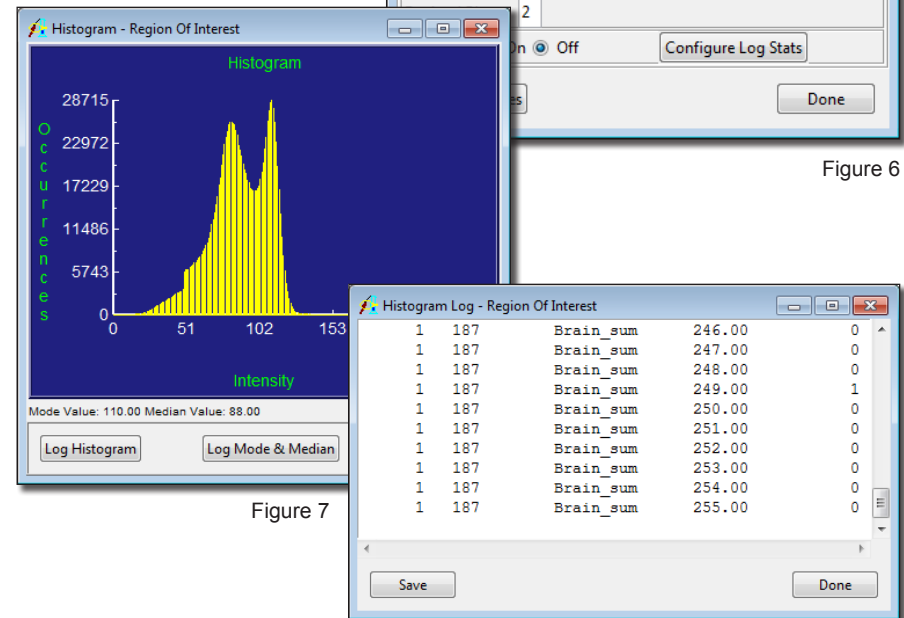

Figure 6

Figure 7

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. 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.
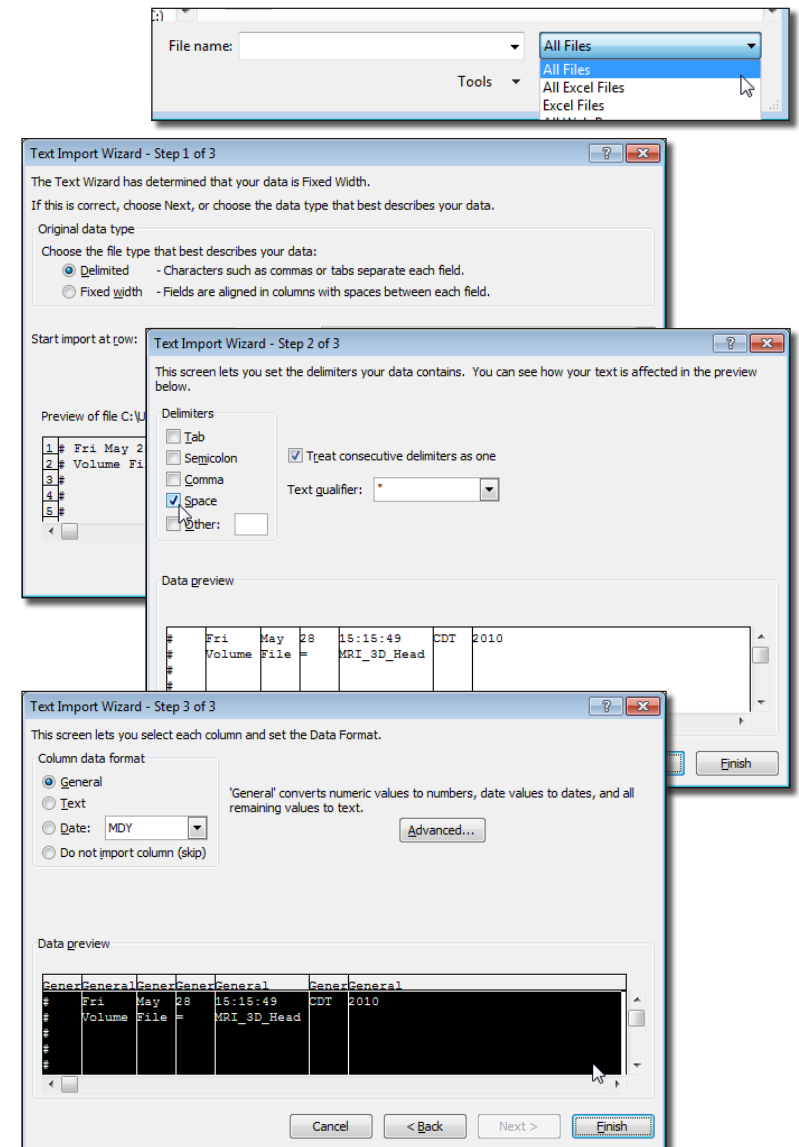
Exercise 46 : Stereology Estimating Volume

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).

| tip | Open the Size window (View > Size) to increase the size of the image display. |

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**.

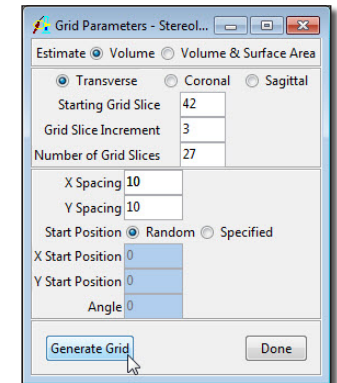6. Click **Generate Grid**. Then, click **Done** to dismiss the Grid Parameters window.

| tip | The Orthogonal tool (Tools > Orthogonal) shows the grid point location in the three orthogonal orientations and is helpful on points that are on or near the edge of the heart. |

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.

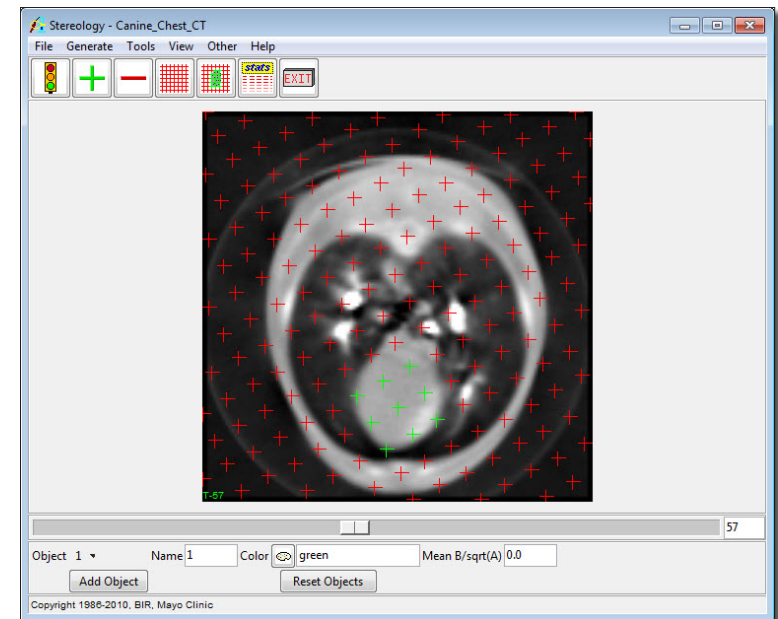10. Close the Stereology module before proceeding to the next exercise.

Figure 2

Exercise 47 : 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)**

   > *tip* | 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. Holding the <Ctrl> key 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).
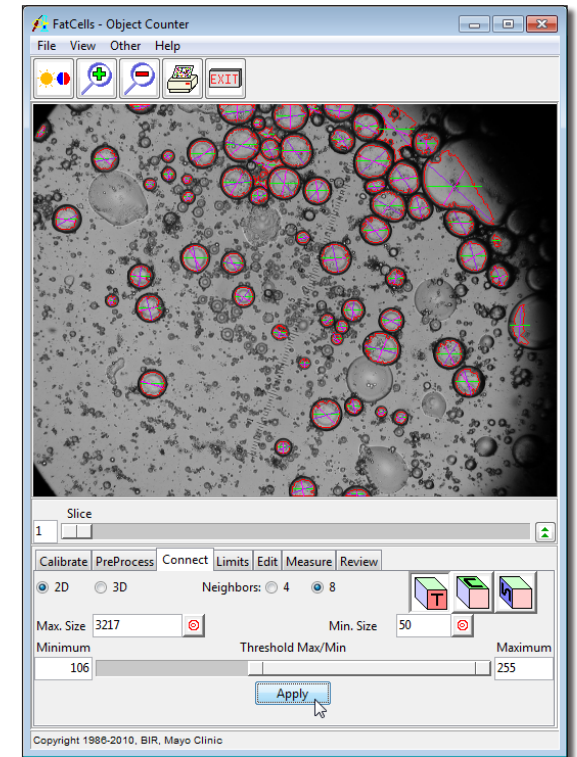

Figure 1

> *tip* | The 'Calibrate' tab provides the ability to determine the dimensions of pixels in an image. By drawing a line over a known distance in the image, such as on a ruler or structure of known size, the correct pixel dimensions can be established and the image can be calibrated for real-world measurements. Slice thickness can also be entered for 3D data.

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.
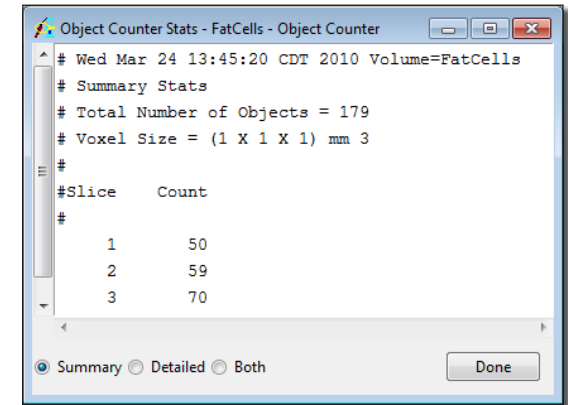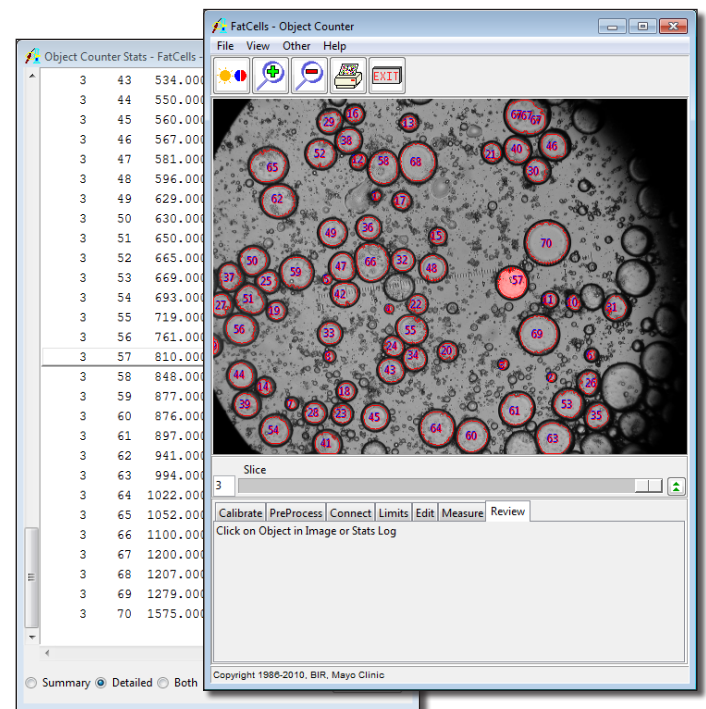

Figure 2

Figure 3

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

Figure 1

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

Figure 2

10. To view the trees generated in the extraction process, use the Tree drop-down menu [**A**] in the Tree Plot window. Select **Tree 2**.

11. Select all four of the **Views** buttons [**B**] to display the left, top, right and bottom views of the tree.

12. Check **Render** [**C**] 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.
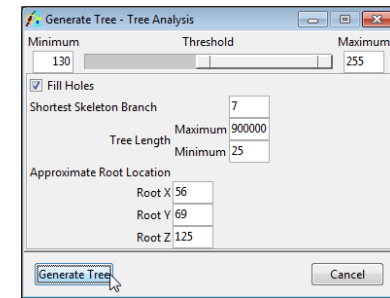
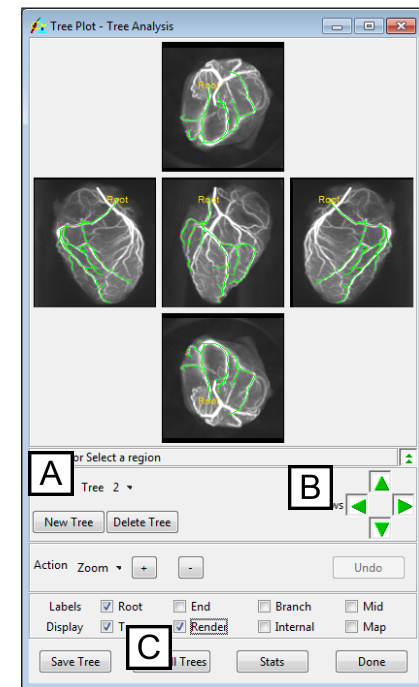13. Several of the Action options can also be used to manipulate the tree display. With **Action** set to **Zoom**, click the **+** and **-** buttons to increase or decrease the tree display size. To magnify a specific area in a tree, click and drag a rectangle over the area in any of the displayed views.

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**.

Figure 3

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.
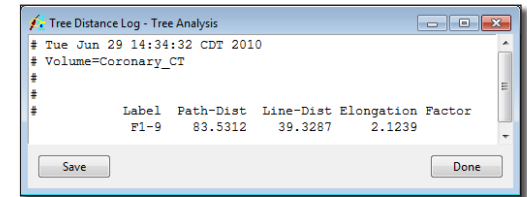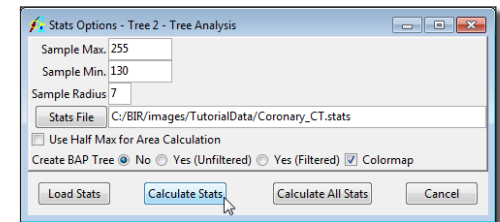

Figure 4

Figure 5

tip | When a point is selected in the 'Detailed' view, a BAP Plot will be returned and the point's branch will be highlighted in the Tree Plot window.

Additional Task

1. 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**) (figure 3).

5. Close the Tree Analysis and Movie modules before proceeding to the next exercise.
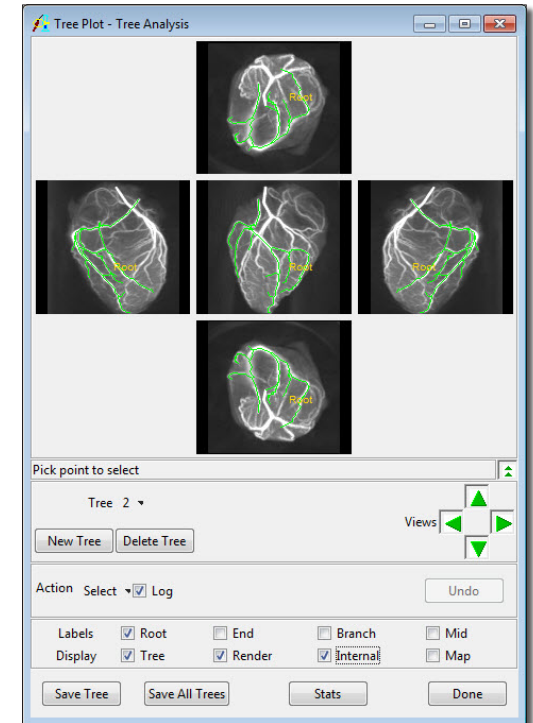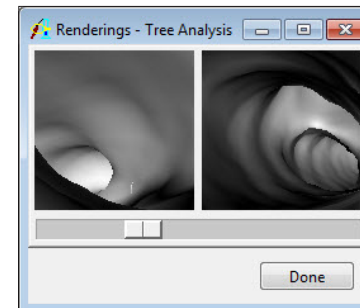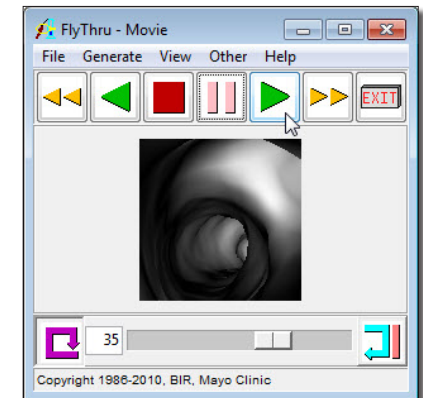

Figure 1

Figure 2

Figure 3

Analyze 10.0
Apps & Add-Ons

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 loaded 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 [**A**]. Note the change in the binary image.

   ii. Ensure that the Interictal Transformation Type is set to Linear [**B**].

   iii. Use the Activation Level slider bar to set the standard deviation to 2.0 [**C**].

   iv. Next, select the Register and Map button. The Register SPECT tool will automatically register, normalize, subtract, select the statistically significant voxels of activation, and output the activation map based on the parameters specified above. Note that the tool will update, displaying the Activation Map [**D**].

Figure 1

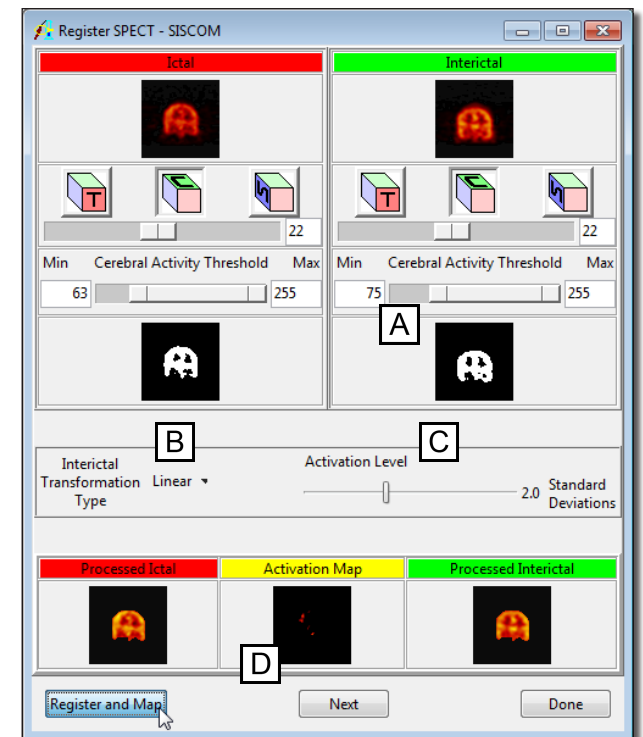5. Select **Next** to continue onto the next step of the SISCOM procedure, MRI brain extraction.

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 **101** 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. In this case, the threshold values do not need to be adjusted.

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. Also close the Extract MRI Brain and Register SPECT tools.
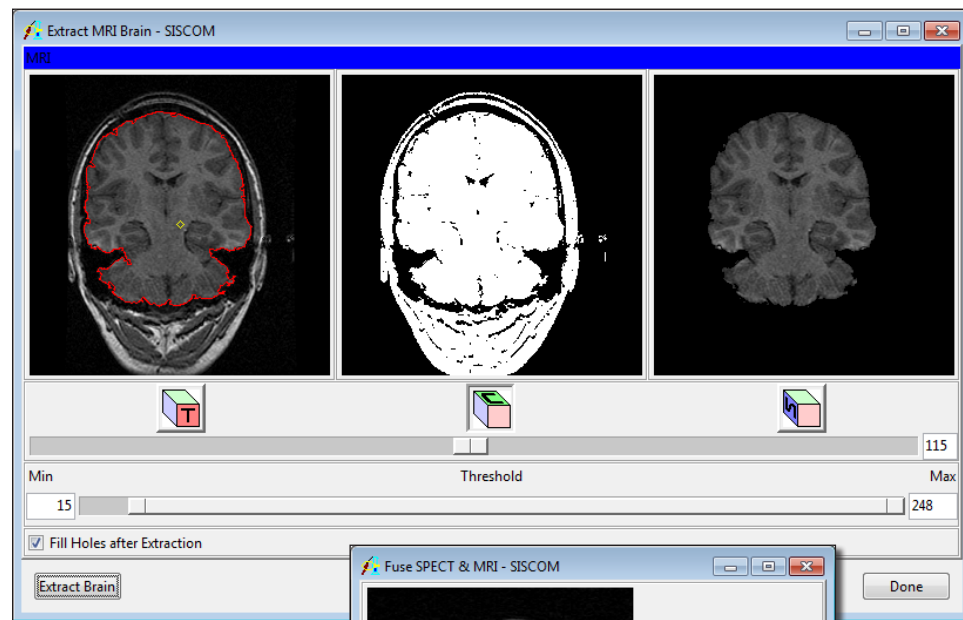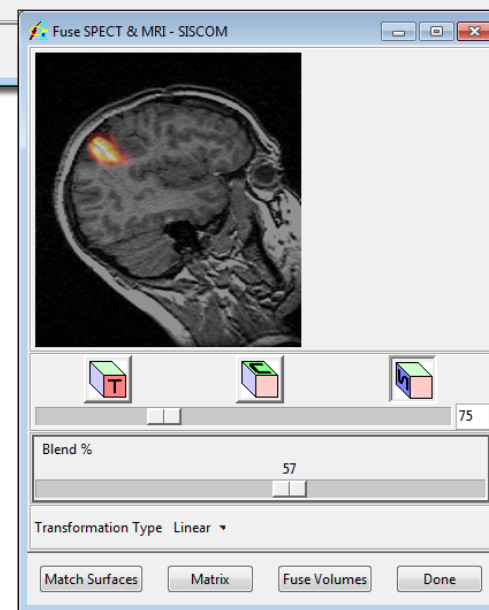

Figure 2

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 [**A**] 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.
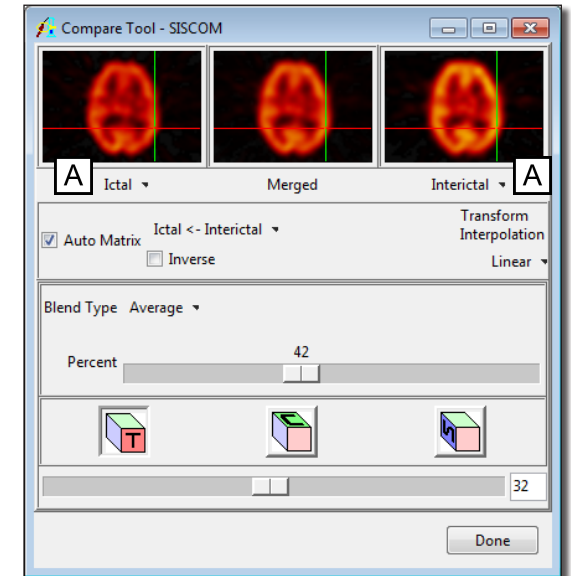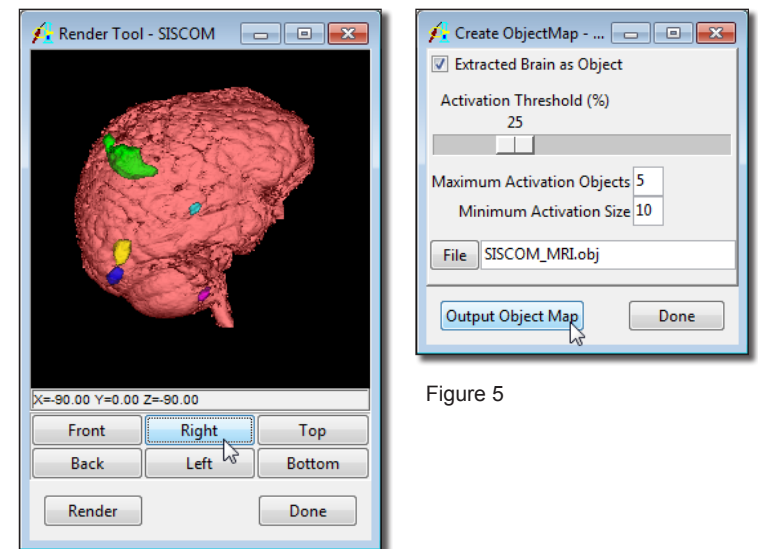

Figure 4

Figure 5

Exercise 50 : 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.avw** data set from the **$:\BIR\images\TutorialData** directory.

2. Select the **MRI_3D_Head.avw** 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**.

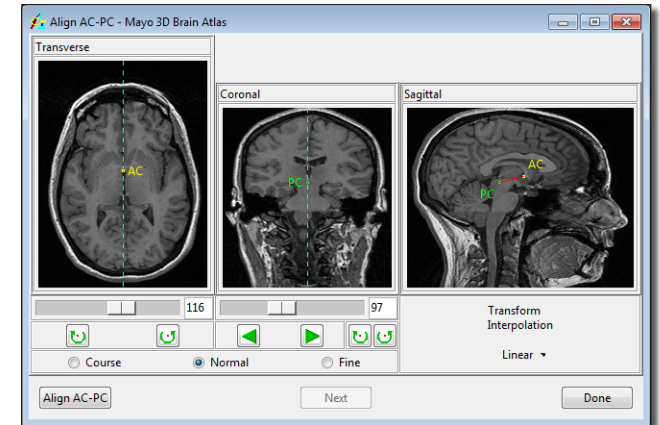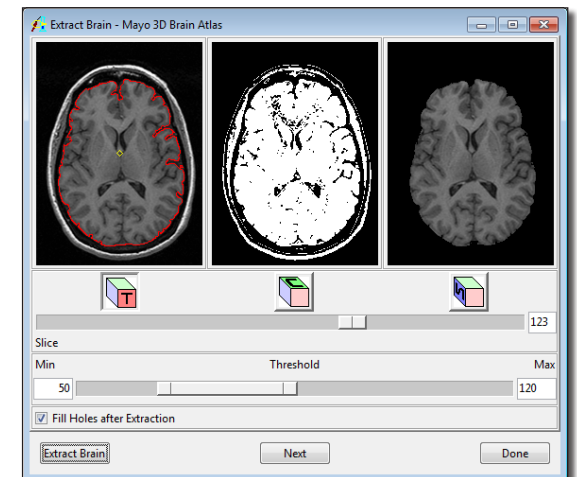11. The extracted brain can be reviewed using the **Slice** slider bar (figure 2).

Figure 1

Figure 2

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.

21. To save the atlas as an object map open the **Generate Output** window by clicking on the **Output** button in the PowerBar.
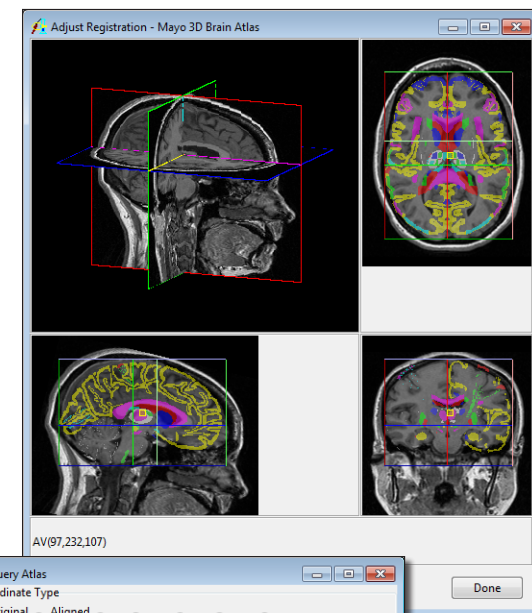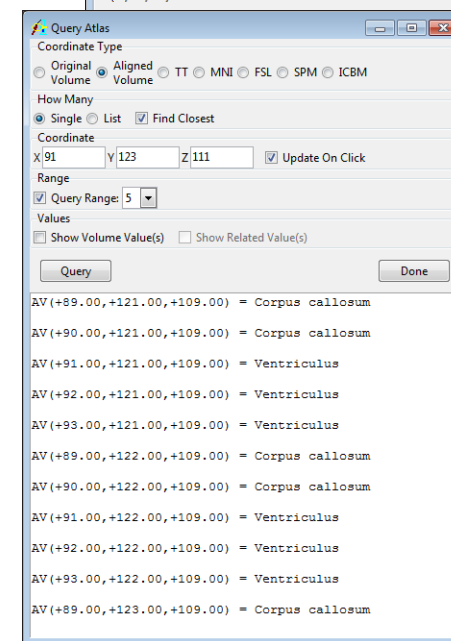

Figure 3

Figure 4

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.

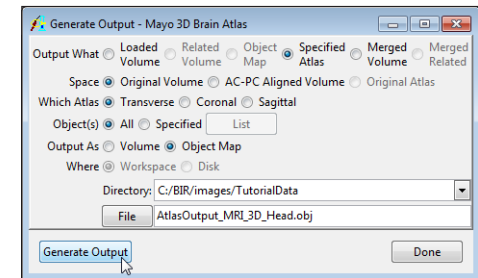27. Close all windows before proceeding to the next exercise.

Figure 5

Exercise 51 : 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 post-acquistion. The add-on uses a piecewise non-linear intensity transformation based on priori 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

Exercise 52 : 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**).

3. To calculate all of the statistics for a specific metric option, select the Metric Type [**A**], then click the **Calculate Metrics** button [**B**]. The metrics are calculated and displayed next to each Similarity Value [**C**].

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.

7. Close all of the windows associated with Volume Metrics before proceeding to the next exercise.
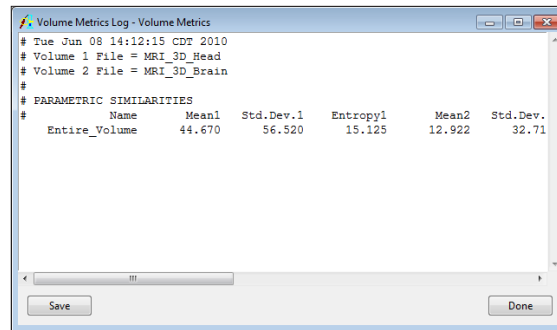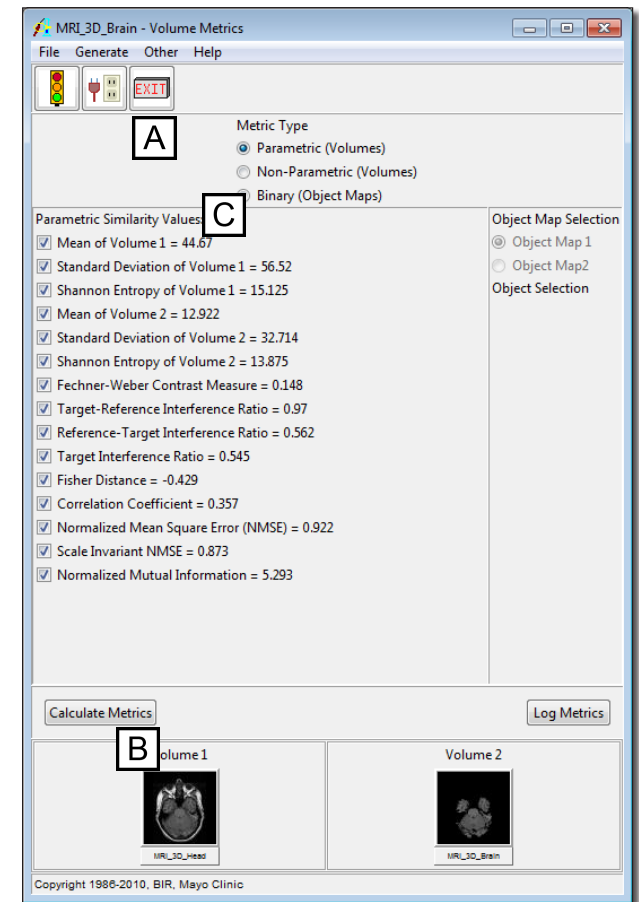

Figure 2

Figure 1

note | Volume 1 is the input volume, while Volume 2 is the comparison volume.

Analyze 10.0
ITK

Exercise 53 : ITK Filters

The ITK Filters module enables the application of ITK smoothing, edge-detection, and feature-extraction filters to image data. This exercise will demonstrate how to apply a filter in the ITK Filters module to your data.

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

2. Open the **ITK Filters** module (**ITK > Filter**).

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

4. Select the **Loaded and Preview Volumes** option. 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 **Bilateral** filter (figure 1).

7. Use the **Slice** slider bar to determine which slice you would like to preview the filter on; set to **Slice 128**.

8. Now, click **Preview**. The main module window will display the filtered slice on the left and original slice on the right (figure 2)

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

10. To apply a filter to the data set, simply 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**.

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

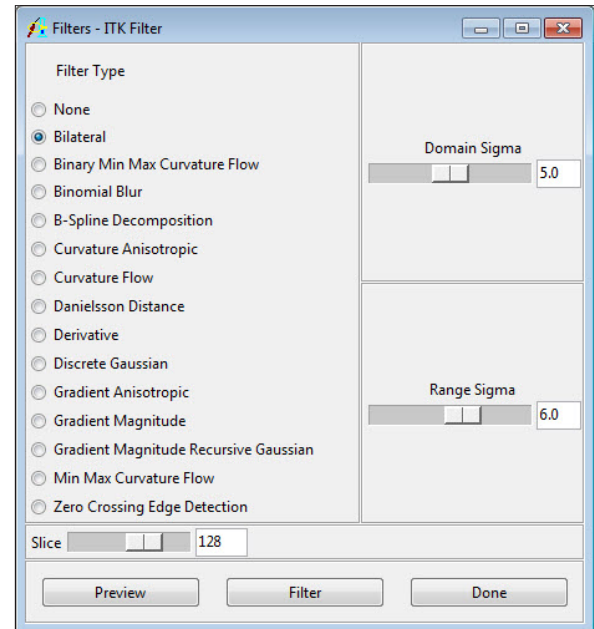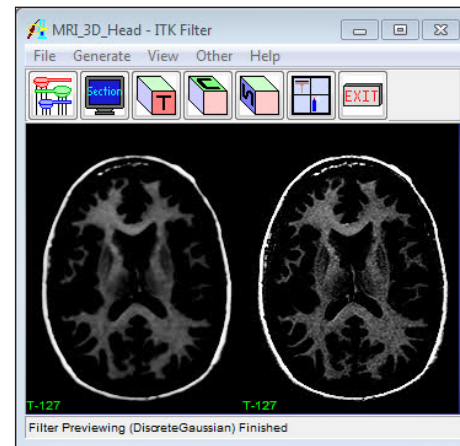12. Close the ITK Filters module before proceeding to the next exercise.

Figure 1

Figure 2

The ITK Segment 2-D module provides an interactive framework for applying sequential processing steps using ITK functions for segmentation of sets of 2-D slices based on region growing and level set methods. This exercise will demonstrate how to use the ITK Segment 2-D module.

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

2. Open the **ITK Segment 2-D** module (**ITK > Segment 2-D**).

3. Use the **Slice** slider bar to move to slice **133**, make sure that the image is displayed in the transverse orientation (select the T cube).

4. The **SubRegion** tab allows the user to limit segmentation to a specific region, helping decrease processing time. Check the **Use SubRegion** option and set the following values (figure 1):
    - **X: 63 and 120**
    - **Y: 78 and 152**
    - **Z: 1 and 187**

5. Select the **Smooth** tab. This tab provides several different methods for reducing noise on images. Select the **Gradient Anisotropic Diffusion** type and click the **Default** button.

6. Select the **Edge** tab. This tab provides methods for generating gradient images required for some seed- and mask-based segmentation algorithms. Select the **Gradient Magnitude** edge type.

7. Select the **Seed Based** tab. This tab provides different methods for performing seed-based segmentation on the current volume. Select the **Fast Marching** type.

8. Click once inside of the left ventricle to set a seed point. The right side will no longer be selected, set a second seed point by clicking once inside of the right ventricle (figure 2). Seed points can be reset by right clicking on the image display and selecting Reset Seed(s).

9. Select the **Mask Based** tab. This tab provides options to enhance features found in the 'Seed Based' tab. Select the **Shape Detection** type and set the **Alpha** value to **-2.1**.
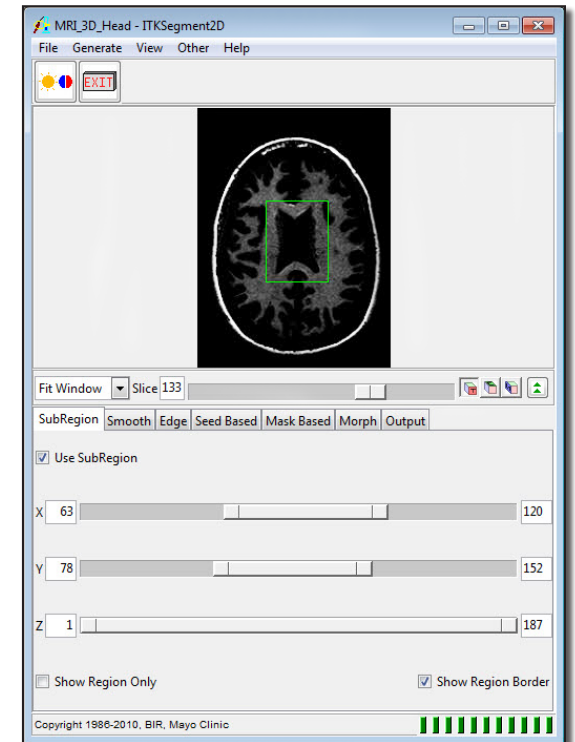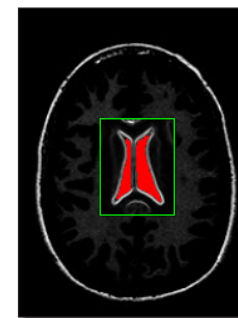

Figure 1

Figure 2

10. At this point, we have exhausted our enhanced ITK functionality, but there are still some built in post-processing steps that can be performed.

11. Select the **Morph** tab. This tab allows a number of post-processing steps, for example filling of small holes that still appear in the segmentation. Select the **4-connected** Fill Holes option.

12. Select the **Output** tab. This tab provides a number of output parameters. Change the output type to **Binary**. If you wish to save this slice, click **Save Slice** (figure 3). The 'Process Volume' button does apply all steps to the entire volume, but a more successful 3-D segmentation can be performed in the ITK Segment 3-D module (exercise 41).

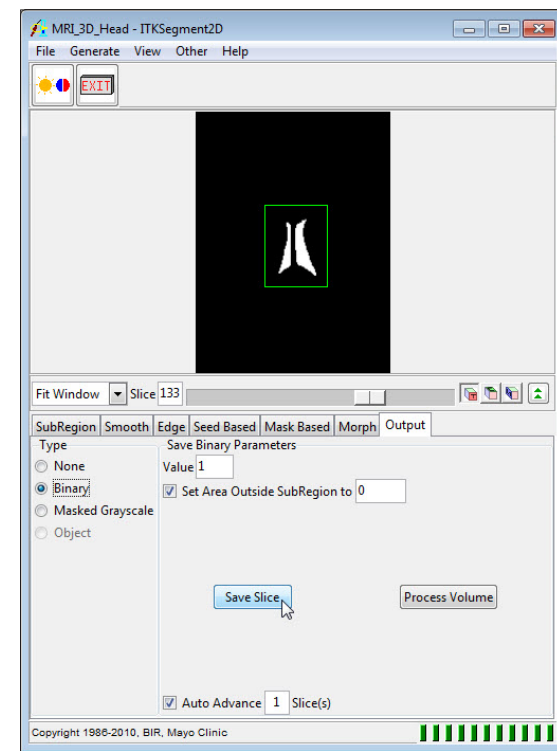13. Close the ITK Segment 2-D module before proceeding to the next exercise.

Figure 3

The ITK Segment 3-D module provides a framework for 3-D segmentation using ITK algorithms. This exercise will demonstrate how to use the ITK Segment 3-D module.

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

2. Open the **ITK Segment 3-D** module (**ITK > Segment 3-D**).

   | tip | The module displays the data set in all three orthogonal orientations. To update the display click on one of the display panes and move the cursor—the other two orientations will interactively update. |

3. Select the **SubRegion** tab (figure 1). Check the Use SubRegion option and set the following values:
   - **X: 51** and **127**
   - **Y: 36** and **162**
   - **Z: 86** and **144**

4. The subregion can also be specified interactively in the image display with the mouse when the **Adjust Subregion** button (found directly below the image display) is selected. Click **Extract SubRegion**.

5. Select the **Smooth** tab. Select the **Gradient Anisotropic Diffusion** type, and change the **Time Step** value to **0.0625**. Click **Smooth Volume**.

6. Select the **Edge** tab. Select the **Gradient Magnitude** edge type and then click **Detect Edge**.

7. Select the **Seed Based** tab and select the **Fast Marching** algorithm type.

8. Select the **New Seed** button (directly below the image display), and click to set a seed point in each ventricle.

9. Click **Seed Segment** to apply the seed-based segmentation.
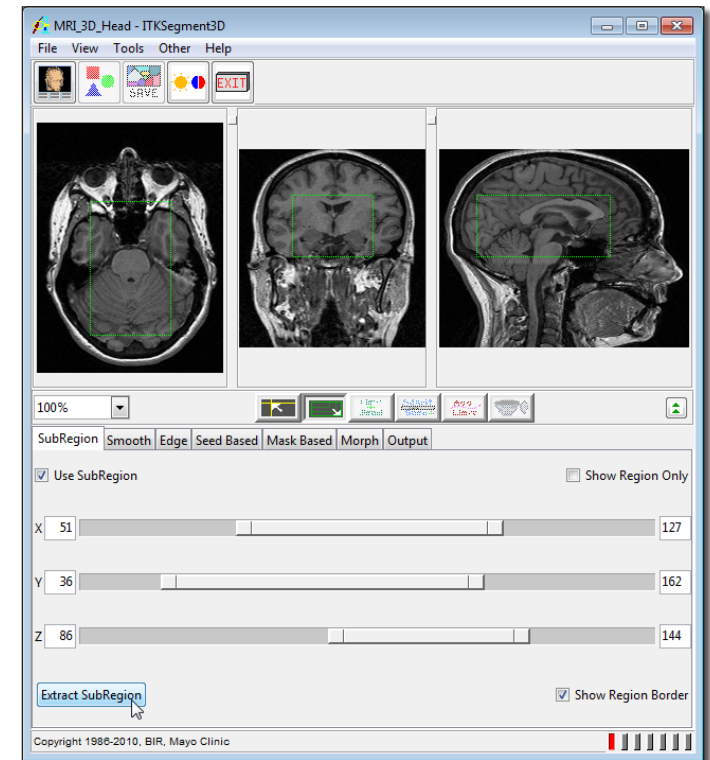

Figure 1

10. You can review the results of the segmentation with the **Render Tool** (**Tools > Render**). Click and drag the rendering to rotate it, or click the direction buttons to quickly change views (figure 2). You can leave this tool open, it will update as we modify our segmentation.

11. Select the **Mask Based** tab. Select the Shape Detection type and set the following and then click Mask Segment.

12. Select the **Morph** tab and choose the **Dilate** option and the **3-pass 2D Fill Holes** option.

13. Click **Apply Morphology**.

14. Select the **Output** tab for options to output the segmentation results.

15. Choose the **Binary** option and click **Output Volume** to create a binary mask of our segmented volume in the Analyze workspace (figure 3).

16. Also try selecting the **Masked Grayscale** option, and use the **Output Volume** button to output the resulting volume in the Analyze workspace.

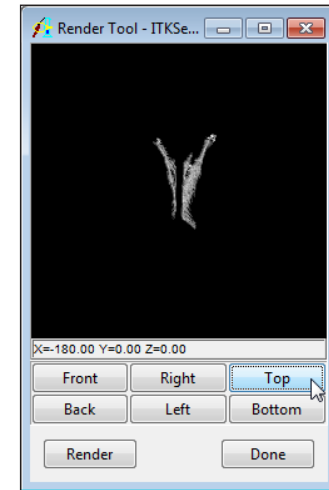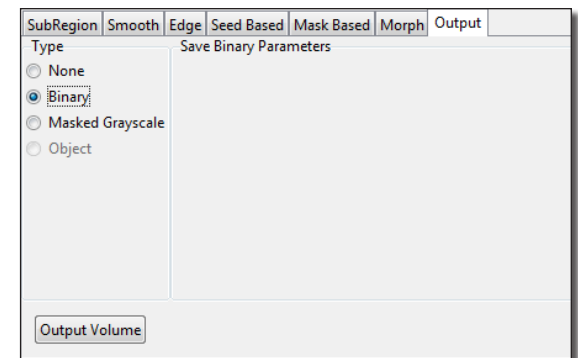17. Close the ITK Segment 3-D module before proceeding to the next exercise.

Figure 2

Figure 3

Exercise 56 : ITK Registration

The ITK Registration module functions the same as the Analyze 3-D Registration modules with the exception of ITK function specific parameters. The exercise will provide an overview of the module.

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

2. Next open the **Load As** module (**File > Load As**). Navigate to and select the **Register_MRI_Match.avw** data set from the **$:\BIR\images\TutorialData** directory. Select the **Resize** tab and check the **Force Cubic** option. Click **Load**.

3. Select the **Register_MRI_Base.avw** data set. Then, while holding down the <**Ctrl**> key, select the **Register_MRI_Match.avw** data set (resulting in both being selected).

4. Open the **ITK Registration** module (**ITK > Registration**).

5. Open the **Blend** window (**Generate > Blend**) and set the Blend Option to **Red-Green** (figure 1).

6. Press the **Register** PowerBar button or choose **Generate > Register**.

7. After registration is complete, evaluate the registration by moving the crosshair in any of the panes to navigate through the image data.

8. If you are satisfied with the registration, save a copy of the transformed match volume (Register_MRI_Match), choose **File > Save Transformed**. The transformed volume can be saved to disk or to the Analyze workspace.

9. If you are unsatisfied with the registration, reset by selecting the Reset Matrix button in the **Manual Registration** tool (**Tools > Manual Registration**). Adjusting the Match position manually and the ITK Registration Parameters (**Generate > Parameters**) (figure 2). For more information about the ITK Registration Parameters, please refer to the ITK Users Guide (www.itk.org/ItkSoftwareGuide.pdf).

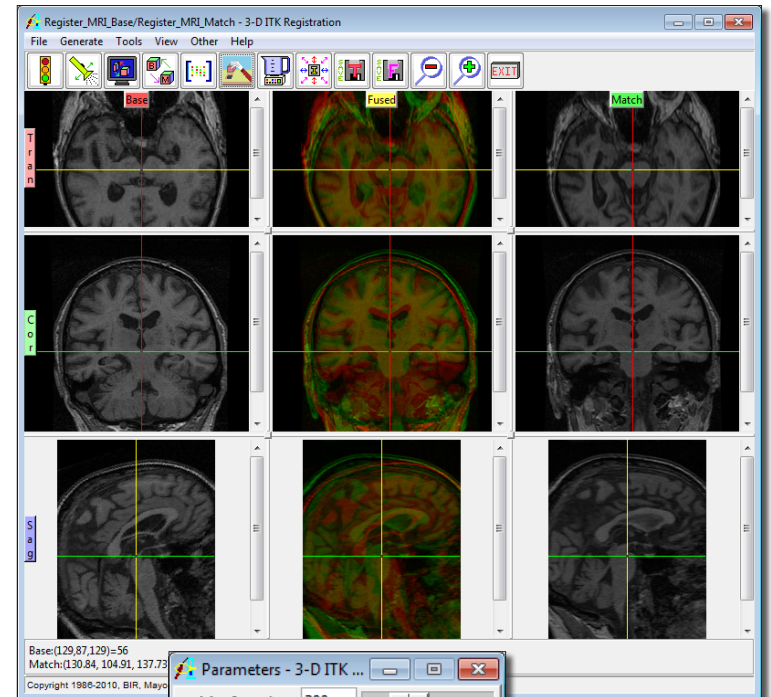10. Close the ITK Registration module.

Figure 1

Figure 2