Signa® MR/i with Signa Select™ (ASP2) Learning and Reference Guide Volume 4: Post-Processing and Analysis

2292264-100 Rev. 0 (03/01)

Medical Device Directive

These products conform with the requirements of council directive 93/42/EEC concerning medical devices, when they bear the following CE Mark of Conformity:

CE 0459

This equipment generates, uses, and can radiate radio frequency energy. The equipment may cause radio frequency interference with other medical and non-medical devices and radio communications. To provide reasonable protection against such interference, the:

GE Signa MR/*i* Systems

comply with emissions limits for (Group 2, Class A) Medical Devices as stated in EN 60601-1-2. However, there is no guarantee that interference will not occur in a particular installation.

If this equipment is found to cause interference (which may be determined by turning the equipment on and off), the user (or qualified service personnel) should attempt to correct the problem by one or more of the following measure(s):

- reorient or relocate the affected device(s);
- increase the separation between the equipment and the affected device;
- power the equipment from a source different from that of the affected device; and/or
- consult the point of purchase or service representative for further suggestions.

The manufacturer is not responsible for any interference caused by using interconnect cables that are not recommended or by unauthorized changes or modifications to this equipment. Unauthorized changes or modifications could void the user's authority to operate the equipment.

Do not use devices that transmit RF Signals (**cellular phones**, transceivers, or radio controlled products) in the vicinity of this equipment as they may cause performance outside the published specifications. Keep the power to these types of devices turned off when near this equipment.

The medical staff in charge of this equipment is required to instruct technicians, patients, and other people who may be around this equipment to fully comply with the above requirement.

Immunity/Emissions Exceptions: Note the exceptions from the EMC test results. Check with the business EMC engineer for this information.

In accordance with the international safety standard IEC 601-1, this system is a Class I device, acceptable for Continous Operation, having ordignary protection against ingress of water with type B applied parts and is not for use in the presence of flammable anesthetics.

CAUTION: User to call or contact the local authorities for disposal of the MR System at the end of its useful life.

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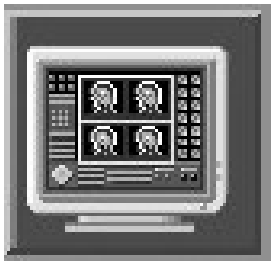
Chapter 1

Sharpening and Smoothing Images with ClariView

Where Am I?



Introduction

This chapter explains the ClariView™ image filtering process. ClariView is a post-processing feature that filters MR and MRA images to improve signal-to-noise, contrast, and edge sharpness. ClariView is used to smooth and sharpen images. This chapter gives you the step-by-step instructions for:

- Enhancing Images with Smoothing, Sharpening, and MRA Algorithms

In addition, this chapter answers the following questions:

1. When do I use ClariView?
2. How do I pick a filter in ClariView?
3. How do I save images with ClariView?
4. How are images be annotated with ClariView?

Something to Think About...

- Image filtering does not improve the diagnostic quality of the image.
- ClariView is available for images with a maximum image display matrix of 512 x 512.
- ClariView is NOT available for:
  - 0.2T, 0.5T, or 3.0T images
  - Screen saved images
  - 64 X 64, 128 x 128, or 1024 x 1024 matrix images
  - CT or DICOM images
  - 3D surface images
- Individual images are saved as a series.
- The system saves a maximum of nine filtered series. If you want to filter more than nine times, delete one or more filtered series. A new filter can be selected at anytime EXCEPT while the filtering process is running.
- Previewing temporarily assigns a new series number.
- A previewed image does not use the same window/level as the original image.

About... Sharpening and Smoothing Images in ClariView

This section presents the concepts necessary to successfully complete image filtering using the ClariView process. Specifically, you need to understand:

- The Purpose and Benefits of Image Enhancement
- Series Assignment in the Browser
- The ClariView Window

The Purpose and Benefits of Image Enhancement

The ClariView feature filters MR images to improve apparent signal to noise, contrast, and edge sharpness. ClariView makes the image more aesthetically pleasing, but does not improve the diagnostic quality of the image.

Any ClariView filter may be applied to any image. You may want to use preview first, and apply a few different filters to pick the filter that works best for that image.

Smoothing algorithms are used to remove graininess from high resolution and low signal images. Grainy images such as 512 x 512 matrix head, abdomen, or extremities would be good candidates for ClariView's smoothing algorithm. Filters D through I use a smoothing algorithm.

Sharpening algorithms help define structural edges in images with high signal and low noise. Filters A through C use a sharpening algorithm.

Filter J is used for filtering MRA (Magnetic Resonance Angiography) images, and can be applied to either the source images or the MIP (Maximum Intensity Pixel) images. The MRA-MIP filter smooths the vascular structures without introducing any black lines and provides good vessel delineation.

NOTE: If you plan to apply ClariView filters to the images, and you have used PPS, do not complete the exam when finished scanning. Post-processing functions must be done before the exam is completed in PPS. First click the **[End Exam]** button, then click the **[Defer]** button. Apply the ClariView filters. Then complete the exam by clicking **PPS** from the Browser menu bar, and click the **[Complete]** button to complete the exam.

The following table lists the different algorithms and gives a description of each.

- The following table gives a detailed description of the filter functions and suggested application.

Filter Name	***Filter Description and Use***
A	*Sharpen with very little smoothing*. This is an overall sharpening filter with very little smoothing. Used for high signal and very low noise 256 x 256 images. Candidate images include heads, abdomens, and extremities.
B	*Sharpen with little smoothing*. This is an overall sharpening filter with little smoothing.This filter enhances structural edges. Used for high signal and low noise 256 x 256 images. Candidate images include axial heads, cervical spines, lumbar spines (small FOV), abdomens, and extremities.
C	*Sharpen with smoothing.* This is an overall sharpening filter with smoothing. This filter enhances structural edges and suppresses noise. Extremity images would be good candidates.
D	*Smoothing with sharpening*. This filter has an equal blend of smoothing and sharpening. This filter enhances structural edges and suppresses noise. Candidate images include 512 x 512 head and extremity images.

Filter Name	***Filter Description and Use***
E	*Smoothing with little sharpening*. This filter produces more smoothing while sharpening a little to suppress noise. This filter provides some edge enhancement of structural edges. Candidate images include 512 x 512 head, abdomen, and extremity images.
F	*High smoothing with very little sharpening*. This filter produces smoothing and very little sharpening. This filter suppresses noise and provides smoother structural edges. Candidate images include high resolution and low signal images.
G	*High smoothing with some sharpening*. This filter produces both smoothing and sharpening. This filter suppresses noise and provides smoother regions but sharper structural edges. Used for high resolution and low signal images.
H	*High smoothing and sharpening*. This filter suppresses noise and provides smoother regions and sharper structural edges. Used for high resolution and low signal images.
I	*512 Spine*. This filter produces smoothing while maintaining structural edge definition without blurring. Used for 512 x 512 spine images with a large FOV.
J	*MRA-MIP*. This filter produces smoothing of vascular structures without introducing black lines and provides good vessel definition. Used for Maximum Intensity Projections (MIP) from MR Angiography (MRA) studies.

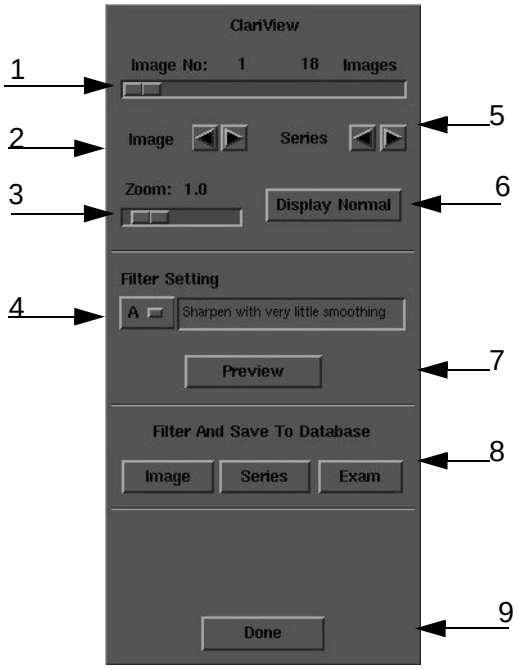
Series Assignment in the Browser

The filtered (enhanced) images created by the ClariView feature are saved to a new series. The unenhanced images remain in the original series in the Browser, while the new, filtered, series receives a new series number.

After filtering, the new series number is a multiple of 100 plus the original series' number. For example, if series 4 is filtered, the new series is 104; if series 4 is filtered again, it becomes series 204. Once a ClariView filter has been applied to an image or series, it is annotated in the series description in the Browser.

NOTE: If ClariView has been applied to an image, the annotation appears in the lower left corner of the film following the pulse sequence annotation, as FL:A-J where A-J is the applied filters. This annotation indicates that this is a filtered image and may not be of diagnostic quality.

The ClariView Window



ClariView

- 1 - Image Slider. Click and drag right or left to select a different image to preview.
- 2 - Image selector. Click to move to the next or prior image.
- 3 - Zoom. Click and drag right or left to select a zoom (magnification) factor and apply to the image.
- 4 - Filter setting selector. Click and drag to the desired filter setting. The filter description text box is to the right of this button.

- 5 - Series selector. Click to move to the next or prior series.
- 6 - **[Display Normal]**. Click this button to return the image to its original form (no filters) and normal size.
- 7 - **[Preview]**. Click to preview the filtered image without saving it. Previewing temporarily assigns a new series number.
- 8 - Filter and Save to Database area. Use the buttons in this area to apply the selected filter to an entire exam, series, or image, and to save the new, filtered images. The system counts the number of images or series completed during the filtering process. This count is shown in the area above the **[Done]** button.
- 9 - **[Done]**. Click this button to close and exit the ClariView window.

Something to Think About...

- A message window appears after ClariView is closed, stating **"ClariView failed**.**"** ClariView worked, so ignore the error message.

How to Sharpen and Smooth Images using ClariView

This section provides the step-by-step instructions for applying ClariView. Specifically, it describes how to:

- Enhance Images with the Smoothing, Sharpening, and MRA Algorithms
  - ° Reboot During a ClariView Procedure

Enhance Images with Smoothing, Sharpening, and MRA Algorithms

The ClariView feature filters MR images to make them more aesthetically pleasing. These filters have varying combinations of smoothing and sharpening.

ClariView smoothing algorithms remove graininess from high resolution and low signal images.

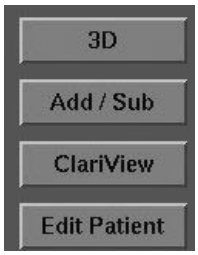
ClariView sharpening algorithms provide edge enhancement.

The MRA-MIP filter smooths the vascular structures without introducing any black lines and provides good vessel delineation. You can apply the MRA algorithm to either the source images or to the MIP images.

The process is the same for applying a smoothing, sharpening, or MRA filter. This section gives you step-by-step instructions for the ClariView process.

1. Click the **Display Desktop** icon from the control panel.

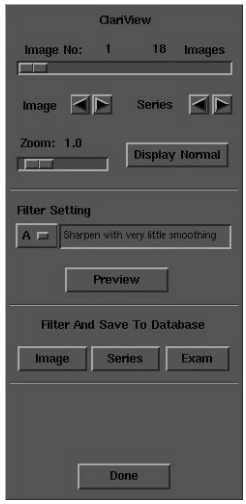
2. From the Browser, select the exam, series, or images you want to filter.
   - ClariView filters the entire exam, series, or any number of images you select.
   - To filter a subset of images in a series, select them before selecting ClariView.
3. Click **[ClariView]**, found on the right side of the Browser.



In Brief: Enhance with Smoothing, Sharpening, and MRA Algorithms

1. Click the **Display Desktop** icon.
2. Select from the patient list the exam, series, or image(s) to filter.
3. Click **[ClariView]**.
4. Select the image using the Image Slider.
5. Click **[Filter]** and drag to select filter. Select MRA-MIP for MRA images.
6. Click **[Preview]**.
7. Repeat steps 5-6 to preview with other filters. Repeat steps 4-6 to preview new images with selected filter(s).
8. When ready to save filtered images go to the Filter and Save to Database area. Click **[Image]**, **[Series]** or **[Exam]**.
9. Click **[Done]** to exit ClariView.
10. Filtered images are now listed in the Browser.

The ClariView window is displayed.



ClariView

4. Select the desired image to view, preview, or filter using the Image Slider.
5. Select the desired filter by clicking **[Filter]** and dragging to the desired choice.

ClariView/Filter

- The default setting is filter **A**.
- Filters **A-C** are sharpening filters and filters **D-I** are smoothing filters. The filters have a varying combination of both types of enhancements.
- **J** - is the MRA-MIP filter. Select for filtering MRA images.
- The filter description text box can be edited (up to 35 characters) and is saved with system shutdowns. For example, you can edit a specific filter for a particular exam; this helps to maintain consistency when filtering.
- To edit the text box, select the filter, place cursor in the box to the right, and type in the desired text.

6. Click **[Preview]** to view the current image with the selected filter.

ClariView/Preview

- A previewed image is NOT be saved to the Browser.

7. Repeat steps 6-7 to preview original image with other filters.
   - Repeat steps 5-7 to preview new images with the selected filter.

8. When ready to save the filtered images, go to the Filter and Save to Database area.

ClariView/Filter and Save to Database

   a) Click **[Image]** to save the current image with the selected filter.

   b) Click **[Series]** to save the entire series with the selected filter. If a subset of a series' images is selected, then only these images are saved with the selected filter.

   c) Click **[Exam]** to save the current exam with the selected filter.

9. Click **[Done]** to exit the ClariView window and return to the Browser.

ClariView/Done

- **[Done]** is not available while filtering is active.
- The filtered images are now be listed in the Browser.

NOTE: While the system is filtering the images, all other filter options are invalid except for **[Stop]**; clicking **[Stop]** stops the filtering process at any time.

- ° Any images processed prior to clicking **[Stop]** are saved to a new series.
- ° Click **[OK]** to confirm stopping the ClariView process.

- For filtering processes that exceed 5 minutes, a message displays the estimated filtering time.

Something to Think About...

- A message window appears after ClariView is closed, stating **"ClariView failed."** ClariView worked, so ignore the error message.

Enhance Images with Smoothing, Sharpening and MRA Algorithms

Reboot During the ClariView Procedure

When swapping between ClariView (Display Desktop) and ScanRx Desktop, you may need to reboot in order to continue with the ClariView procedure. An example situation and steps to reboot are as follows:

Sample Situation

a) The Viewer is open.

b) Click **[ClariView]**.

c) Filter the first series.

d) Click the **ScanRx Desktop** icon while ClariView is still open.

e) Return to the **Display Desktop** and filter the second series.

f) Click **ScanRx Desktop** icon again while ClariView is still open.

g) Return to the **Display Desktop** and the following happens to ClariView:

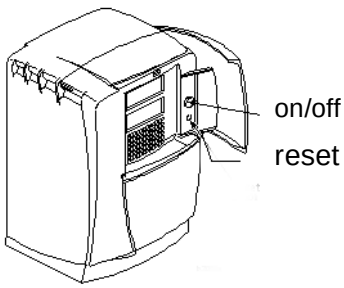
- The ClariView menu is not visible.
- The ClariView image window is up and is overlaid on the Viewer.

h) Press **Alt** + **F3** keys at the same time and switch between the Viewer and the Browser.

i) ClariView cannot be reopened or closed.

Rebooting Procedure

1. The system must be rebooted to continue. Open the door of the Octane computer.



In Brief: Reboot During the ClariView Procedure

1. Open the door of the Octane.
2. Press Reset.
3. Type **`signa`**.
4. Type **`adw2.0`**.

2. Press the reset button.

   Message appears requesting you hit any key to restart.

3. Press any **Key** on the keyboard.

   The system comes up with the Login/Password window.

4. At login type **`signa,`** using lowercase letters and press **Enter**.

5. At password, type **`adw2.0,`** using lowercase letters and press **Enter**.

NOTE: A message appears stating *Do not interact with the system until this message disappears.* You should not use the mouse or keyboard until this message disappears.

Volume 4

Chapter 2

Editing Patient Information

Where Am I?

Introduction

This chapter explains the process for editing patient information. Editing allows you to correct improperly entered patient information (i.e. wrong patient id) and you can add information that was previously unavailable at the time the patient data was entered into the system. This chapter contains the step-by-step instructions to:

- Edit the Patient Data
- View the Patient Log

In addition, this chapter answers the following questions:

1. What information can I change?
2. How do I change the patient information?

About... Edit Patient Information

This section presents the concepts necessary to successfully complete the edit process. Once the patient information data is edited, a new exam is created that replaces the old exam. If the original exam resides on archival media or another workstation, you will want to remove it to avoid confusion or duplicate exam numbers. Before editing patient data, you need to understand the following concepts:

- Data Available for Edits
  - Annotation of an Edited Exam
- The Edit Patient Data Window
- The Edit Log

Data Available for Edits

You can edit almost all of the patient information that was entered on the Patient Information area. The patient weight and exam number cannot be edited. The following is a list of conditions that must be met before an exam can be edited.

- The edits must be done on the same operator's console as the original information was entered.
- Only one exam number can be selected.
- There is sufficient disk space.
- The exam is NOT active and the exam edit time limit of two weeks has not expired.
- You **cannot** edit patient data when the following conditions exist:
  - The exam is "locked," which means the exam is
    - On the archive, network, or film queues.
    - Displayed in the Viewer or MiniViewer.
    - Still in scan mode (End Exam has not yet been selected).
    - Still reconstructing.

- The exam has not been created on that system, i.e. Hospital name, System ID, or Host ID do not match that of system on which you are trying to edit patient data.
- The exam is too “old.” This parameter is set under Guided Install>Edit Patient Data. Fourteen days is the default.
- The images are not in DICOM format.
- You have started the edit process and the number of images in the exam changes before the data updates. This could happen if you start to edit the patient data, then enter the Add/Subtract function and add images to the exam. When the edits are accepted an error message appears, you should exit the edit function and try again.

Something to Think About...

- You can edit the patient data on an exam containing a 3D model, however, the 3D model series will not be part of the new exam. If you select a 3D series, the edit process exits with an error.
- To avoid possible confusion with duplicate exam numbers, it is suggested that you edit the data before archiving, networking, or filming the exam.

CAUTION: **If your facility has purchased the ConnectPro feature and the patient information you are editing originated from the HIS/RIS Worklist Browser, the patient information at the local operator’s console will NOT match the patient information in HIS/RIS. Although it is NOT recommended to edit patient information gathered from the HIS/RIS, the Connect Pro feature does NOT lock the exam from being edited.**

Something to Think About...

- All network and archive copies of the original exam are NOT automatically removed and should be replaced with the new exam.
    - Copies of the exam may have been produced with Auto Network, Auto Archive, and Auto Film.
- All filmed copies of the exam should be replaced.
- If previous edits have been made, all edits should be made to the latest version of the exam.
- All images and post processing (screen saves, reformat, 3D surface) should be done before editing. All images created after the edit do NOT contain the edited information.
- When exams are sorted by date in the Display or Image Management Browsers and multiple versions of the exam are in the database, exams with the e+ annotation sort with the latest version appearing first. This is reversed for exams with the e- annotation, the most recent version sorts last.

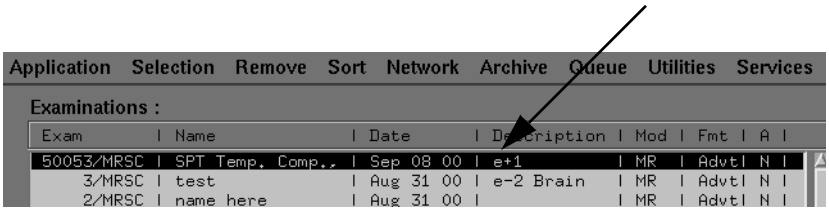
Annotation of an Edited Exam

Edited exams have specific annotation indicating that the patient data has been updated. This annotation is displayed in the Examination lists of the Display and Image Management Browsers, and in the Exam Description text box of the Series or Exam Text Page.

An edited exam is annotated with:

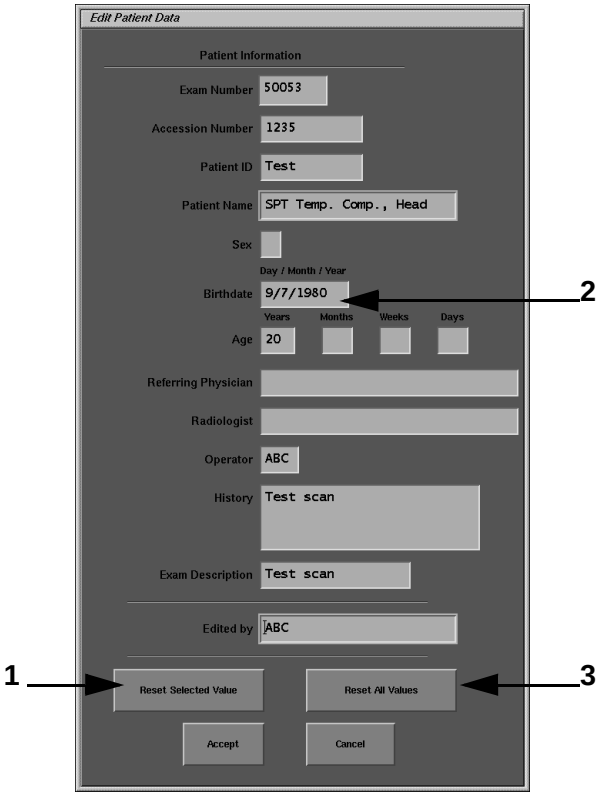
- A prefix (e).
- A + (plus) or - (minus) sign to indicate that the exam's date and time has been increased or decreased. The system determines the + or - by the time of day the exam number was edited. Any original exam that is edited after 11:55PM of the date the scan was completed has a - (minus) sign.
- The number of times the data was edited. For example, e+3, for data that was edited three times.

NOTE: The total number of edits allowed is 300.



The Edit Patient Data Window

You can edit or update data using the Edit Patient Data window. If the text box is empty, place the cursor in the in the text box, click, and type in the new data. If the text box already contains data, place your cursor in the text box and select the text you want to change. Once the text is selected, either press Delete (on the keyboard) or immediately begin typing in new data. If you make an error you can reset the individual text box or all the text boxes using the **[Reset Selected Value]** (**1**) or **[Reset All Values]** (**3**) buttons.



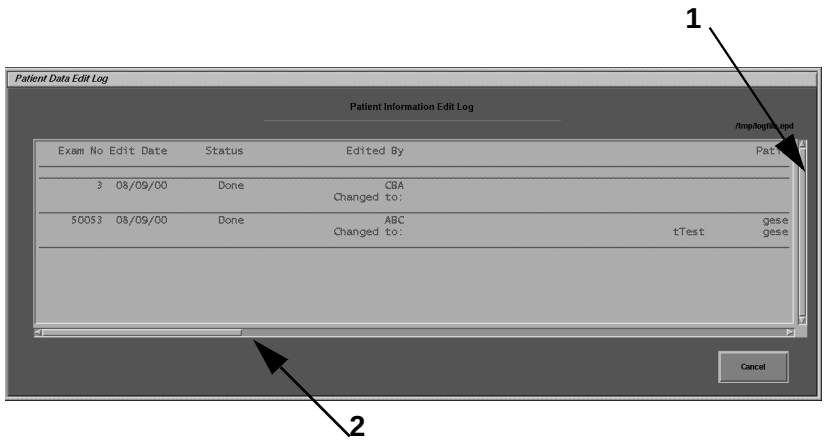
Something to Think About...

- The Exam Number text box is the ONLY text box displayed that CANNOT be edited. The patient weight is not displayed and therefore cannot be edited.
- When entering data in the Birthdate text box (**1**) the month, day, and year can be separated by a dash (-), slash (/), comma (,), or period (.). The year must contain four digits (1999).

The Edit Log

The Patient Information Edit Log is a list of all patients whose information has been edited. Each log file is composed of two rows and each exam entry is separated by a line. The top row contains the original information and the bottom row contains the new information. The log lists the same exam as many times as it is edited.

Vertical and horizontal sliders allow you to completely view the log. The vertical (**1**) slider views the list of the exams that have been edited, while the horizontal (**2**) slider allows you to view the changes made to individual text boxes in that exam. You must use the horizontal slider to view the text box edits because the log does not entirely fit on the viewing screen.



How to Edit Patient Information

This section provides the step-by-step instructions for editing patient information, including how to:

- Edit the Patient Data
- View the Patient Log

Edit the Patient Data

In Brief: Edit the Patient Data

1. Click the **Display Desktop** icon.
2. Select the exam to edit.
3. Click **[Edit Patient]**.
4. Click **[Edit Patient Data]**.
5. Caution message appears, click **[Accept]**.
6. Enter information to be edited, press **Enter** or left click to move about the window. Use **Delete** key to erase.
7. Enter the editor's initials.
8. Click **[Accept]** go to step 9, or **[Cancel]** go to step 10.
9. Click **[Accept]** at the confirmation message.
10. Click **[Accept]** or **[Cancel]**.

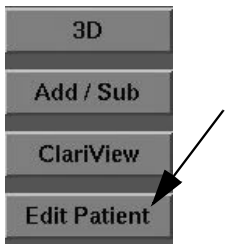
Use this procedure to change the information entered about a patient. For example, editing allows you to correct a wrongly entered patient ID number and add information that was previously unavailable.

Something to Think About...

- Be aware that the certain conditions must be met in order to successfully complete the edit process. These conditions are described in more detail in the About... section of this chapter.

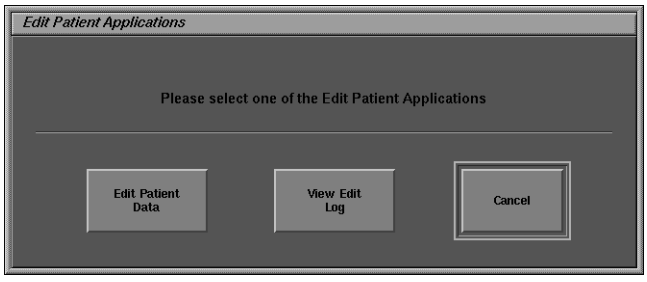
1. Click the **Display Desktop** icon from the control panel.

2. From the Browser, select the exam to be edited.
3. Click **[Edit Patient]**.



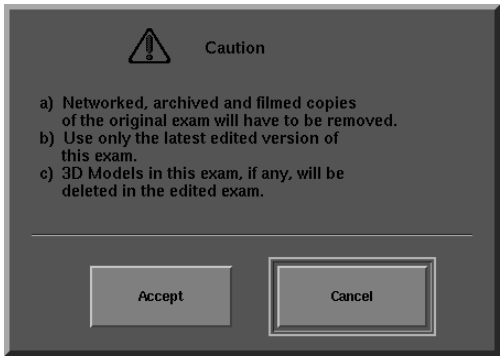
The Edit Patient Applications window appears.

4. Click **[Edit Patient Data]** to get to the Patient Information area.
   - Clicking **[Cancel]** exits you from the Edit Patient Data function.



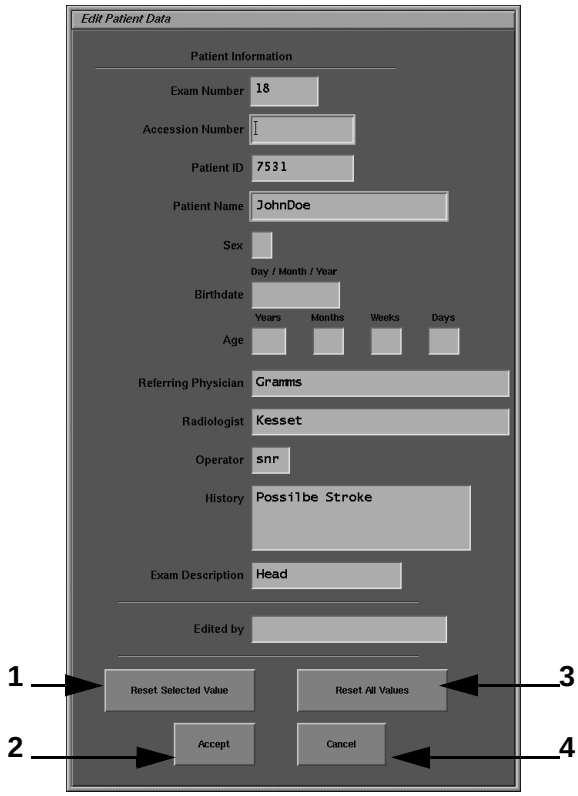
CAUTION: A caution message appears reminding you of the precautions you should follow.

- All network and archive copies of the original exam are NOT automatically removed and replaced with the new exam.
- All filmed copies of the original exam should be replaced.
- If there have been previous edits to this exam, all edits should be made to the most recent version of the exam.
- 3D Models in this exam are deleted in the edited exam.



5. Click **[Accept]** to continue or **[Cancel]** to exit the Edit Patient Data process.

   The Edit Patient Data window appears.

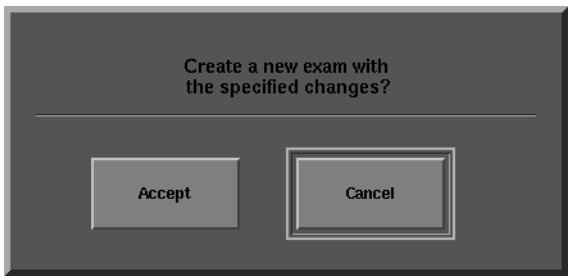


6. Press the **Enter** key on the keyboard or click to move around this window and make (type in) the changes. The **Delete** key must be used to erase highlighted text.
   - If you make a mistake you can:
     - Click **[Reset Selected Values]** (**1**) to reset the changed values to the previous values in the active (highlighted) text box.
     - Click **[Reset All Values]** (**3**) to reset all the changed values to the previous values.

7. Enter three characters in the **Edited by** text text box. You must enter data in this text box.

8. Click **[Accept]** (**2**) to save the changes. A confirmation message appears. Go to step 9.
   - Clicking **[Cancel]** (**4**) exits without saving the changes. A confirmation message appears. Go to step 10.

A confirmation message appears asking you to confirm or discard the creation of a new exam.



9. Click **[Accept]** on the confirmation message to start the saving process and create a new exam with the changes incorporated.
   - Clicking **[Cancel]** on the confirmation message returns you to the Edit Patient Data window without saving the changes and a new exam is NOT created.

Something to Think About...

- A status window appears if **[Accept]** was selected on the confirmation message window. This window remains open providing the edit save status as a percentage of completed. Depending on the size of the exam, it may take several minutes for the edit to complete.
- The edited exam is labeled with an “e+1” in the description area of the Browser. The “e” indicates that the exam has been edited; the “+1” indicates how many times the exam has been edited.

10. If **[Cancel]** was selected at step 8 do one of the following:
    - Click **[Accept]** to exit and discard the change and exit the Edit Patient Data window.
    - Click **[Cancel]** to exit you from the confirmation message but allows you to stay in the Edit Patient Data window.

View the Patient Log

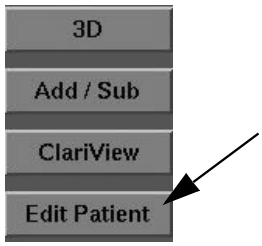
In Brief: View the Patient Log

1. Click the **Display Desktop** icon.
2. Click **[Edit Patient]**.
3. Click **[View Edit Log]**.
4. Click and drag sliders to view the Patient Information Edit Log.
5. Click **[Cancel]**.

The Patient Information Edit Log is a list of all exams that have been edited. The Patient Information Edit Log is for viewing purposes only and CANNOT be used for editing the patient data.

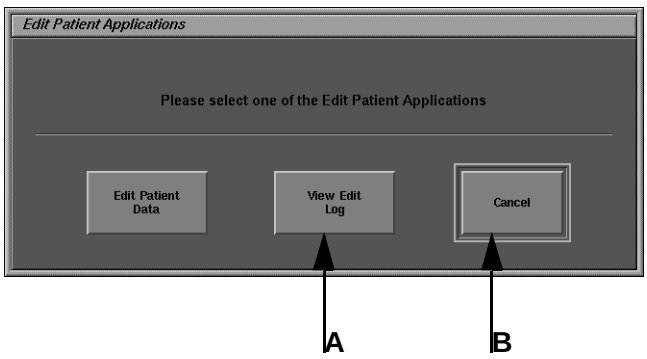
1. Click the **Display Desktop** icon from the control panel.

2. From the Browser, click **[Edit Patient]**.

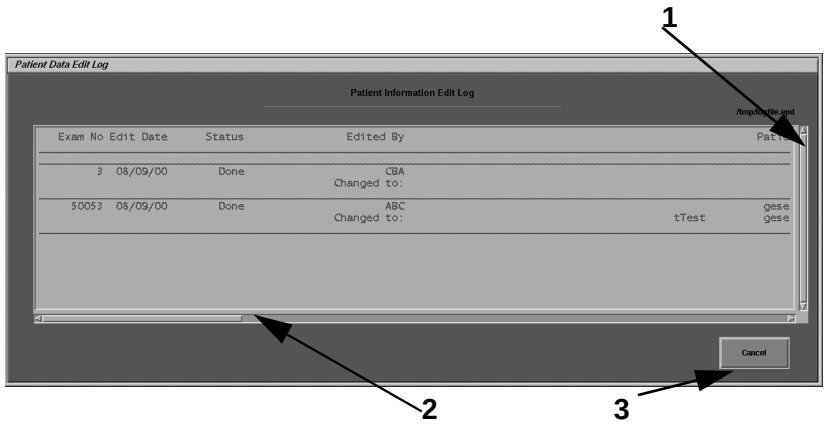


The Edit Patient Applications window appears.

3. Click **[View Edit Log]** (**A**) to view the Patient Information Edit Log.
   - Click **[Cancel]** (**B**) to exit without viewing the Patient Information Edit Log.



4. Click and drag on the vertical (**1**) and horizontal (**2**) sliders to view the entire the Patient Information Edit Log.



5. Click **[Cancel]** (**3**) to exit from the Patient Information Edit Log.

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Volume 4

Chapter 3

Combining Images

Where Am I?

Introduction

This chapter explains image combination, including addition, subtraction, pixel extraction, and binding processes. These processes allows you to perform various operations on one or two sets of images selected and place the resulting images in a new series. This chapter contains the step-by-step instructions to help you learn how to:

- Add One or Two Sets of Images
- Subtract Two Images Within the Same Set or Two Sets of Images
- Extract the Minimum or Maximum Pixels from One Set of Images
- Extract the Minimum or Maximum Pixels from Two Sets of Images
- Bind Images

In addition, this chapter answers the following questions:

1. What functions can be performed with the addition/subtraction application?
2. What are the effects of addition and subtraction?
3. What is binding?
4. What is image combination?
5. What is minimum and maximum pixel extraction?
6. What is the Ratio slider?

About... Combining Images

This section presents the concepts necessary to successfully complete image combination using various processes. Specifically, you need to understand:

- Image Combination
  - Image Addition
  - Image Subtraction
  - Maximum Pixel Extraction
  - Minimum Pixel Extraction
  - Binding Images
- Image Combination Window
  - Saving a Series
  - Sliding the Ratio Bar
  - Accepting Negative Pixels

Image Combination

The Image Combination function allows you to perform various operations on one or two sets of images selected on the Browser and place the resulting images in a new series.

The following functions are available with Image Combination:

- Image Addition
- Image Subtraction
- Maximum Pixel Value Extraction
- Minimum Pixel Value Extraction
- Image Binding

Something to Think About...

- One or two sets of images must be selected.
- If only one set is selected, each operation performed produces one resulting image.
- If two sets are selected, images in the two sets are paired according to physical location in the patient's body. Unpaired images in either set are ignored. Each operation performed produces one resulting image per pair.

Image Addition

Image Addition creates a new series by adding the corresponding signal intensity values pixel by pixel from one or two sets of images.

There are two types of image addition possible:

- Addition performed on one set of images, where the signal intensity values of all images are added, pixel by pixel, and then divided by the number of images in the set. The resulting image is an average of all the signal intensity values.
- Addition performed on two sets of images, where the images are paired by location and signal intensity values are added pixel by pixel. A weighting factor can be used by adjusting the ratio slider bar described later in this chapter.

The order of set selection does not matter for addition unless a weighting factor is used. For example, (100 + 300) and

(300 + 100) both yield the same result of 400 because of the commutative property of addition.

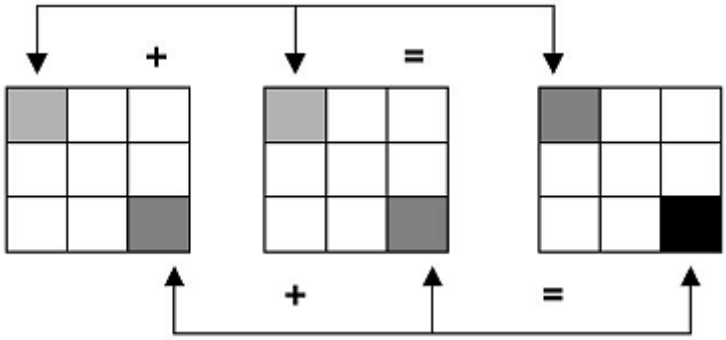


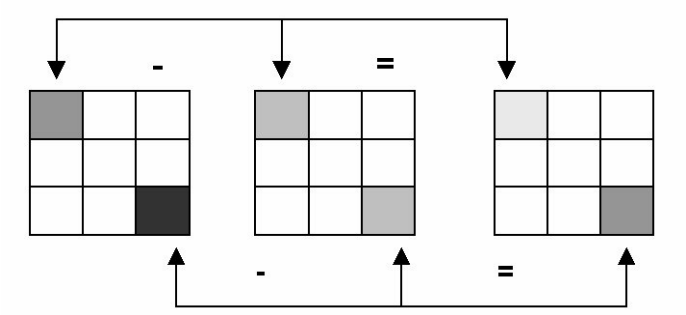
Image Subtraction

Image Subtraction creates a new series by subtracting the corresponding signal intensity values, pixel by pixel, from two sets of images. The two sets can be images from the same series, or images from two different series.

Two types of image subtraction are possible:

- Subtraction performed on two images within the same set, where the signal intensity values of the second image are subtracted, pixel by pixel, from the signal intensity values of the first image.
- Subtraction performed on two sets of images, where the images are paired by location, and the signal intensity values of the second set of images are subtracted, pixel by pixel, from the first set of images. A weighting factor can be used by adjusting the ratio slider bar discussed later in this chapter.

The set selection order for subtraction is important. For example, (100 - 300) and (300 - 100) do not yield the same result because the commutative property does not apply to subtraction. Otherwise, negative pixel values are set to zero, unless you explicitly accept them during the subtraction process.

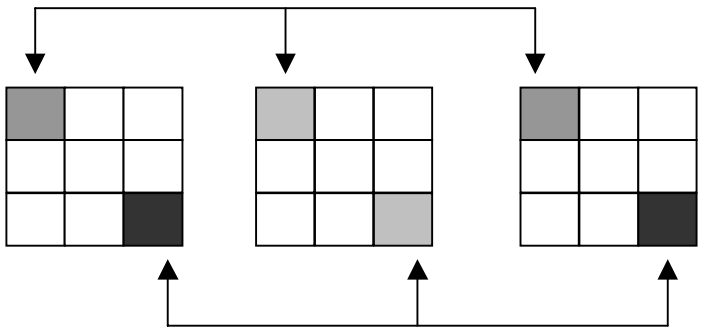


Maximum Pixel Extraction

The maximum pixel value extraction function finds the highest corresponding signal intensity value, pixel by pixel.

There are two types of maximum pixel value extraction:

- Extraction performed on one set of images, where the highest signal intensity value is selected, pixel by pixel, from among all images.
- Extraction performed on two sets of images, where the images are paired by location, and the highest signal intensity value is selected, pixel by pixel, between the two images.

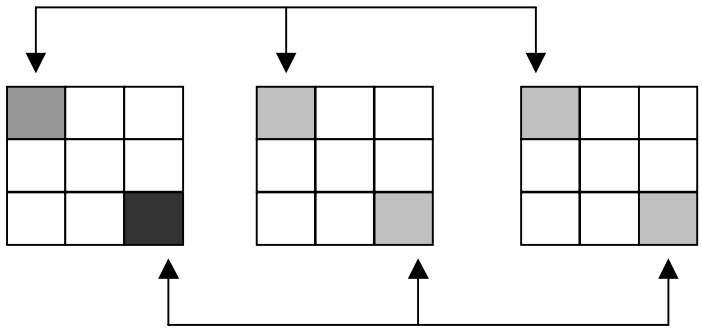


Minimum Pixel Extraction

The minimum pixel value extraction function finds the lowest corresponding signal intensity value, pixel by pixel.

There are two types of minimum pixel value extraction:

- Extraction performed on one set of images, where the lowest signal intensity value is selected, pixel by pixel, from among all images.
- Extraction performed on two sets of images, where the images are paired by location, and the lowest signal intensity value is selected, pixel by pixel, between the two images.



Binding Images

Binding creates a new series set that consists of copies of images from one or more existing series.

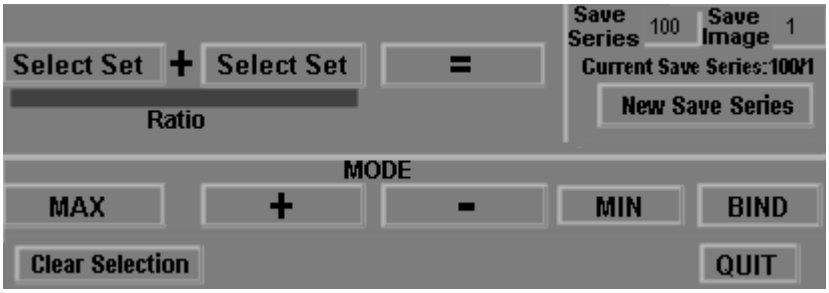
For example, series 2 with 10 images can be “bound” to series 4 with 15 images to create a new series with 25 images.

Image Combination Window

When you select the **[Add/Sub]** button from the Browser (or Viewer), the Image Combination window opens.

Functions in this window allow you to add, subtract, extract, or bind one or two sets of images and place the resulting images in a new series.

The following figure shows the Image Combination window.



Saving a Series

To differentiate combined or processed images from others in an exam, the resulting images are assigned a series number and starting image number by the Current Save Series indicator in the upper right hand corner of the Image Combination window. By default, images resulting from subsequent operations are added onto the end of the same series.

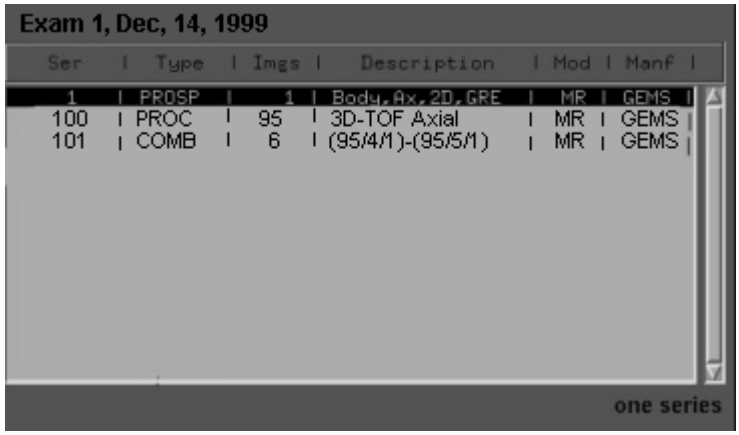
To place images resulting from subsequent operations into a new series, you must select the **[New Save Series]** button.

This increments the save series number by one and displays the **Save Series** and **Save Image** text boxes in the upper right corner of the Image Combination window. The numbers in these two text boxes can be accepted or the **Delete** and **Backspace** keys can be used to delete them, and the desired numbers can be entered in the text box.

The series resulting from image combination operations are distinguished from other series in the Browser via one of the following two indicators in the Browser series list “Type” column:

- “PROC” appears in the Browser series list “Type” column if the images in the series are the result of processing pairs of images having identical locations in the patient’s body.
- “COMB” appears in the “Type” column if the images in the series are the result of a combination of images having different locations in the patient’s body.

The following figure displays the Browser series list.



Something to Think About...

- When Add/Sub is performed, the resulting images are annotated with the day on which the addition/subtraction was performed. To view the date on which the exam was performed, refer to the original image set.
- Since “PROC” series contain images resulting from processing pairs of images having identical locations in the patient’s body, such series can be used like any other series of acquisition images, i.e., geometric measurements, reformatting, 3D reconstruction, etc.

CAUTION: Since “COMB” series contain images resulting from a combination of images from different locations in the patient’s body, the absolute anatomical coordinates accompanying these series (shown both in the Browser and on the displayed images) are not accurate. Only relative geometric measurements (i.e. distance, angle or area) are accurate.

Sliding the Ratio Bar

The Ratio slider is available during addition and subtraction when both Select Set buttons are selected.

- Sliding the Ratio bar to the left increases the pixel weighting of the image (or images) on the left (first) image set.
- Sliding the Ratio bar to the right increases the pixel weighting of the image (or images) on the right (second) image set.
- The Ratio slider defaults to the middle to apply equal weighting.

NOTE: The pixel weighting can be adjusted on only one set of images, not both.

Accepting Negative Pixels

The Accept Negative Pixels option allows negative pixel values in the resulting images. If this function is not enabled, all negative pixel values are set to zero.

This operation is useful on pre and post contrast studies of the same slice location.

How to Combine Images

This section provides the step-by-step instructions on combining images. Specifically, it describes how to:

- Add One or Two Sets of Images
- Subtract Two Images Within the Same Set or Two Sets of Images
- Extract the Minimum or Maximum Pixels
  - One Set of Images
  - Two Sets of Images
- Bind Images
- Post Process Three Station Runoffs
  - Subtractions
  - Acquire Collapsed Images with IVI
  - Bind Multiple Series into a Single Series

Add One or Two Sets of Images

In Brief: Add One or Two Sets of Images

1. Click **Display Desktop**.
2. Click **[Add/Sub]**.
3. Select the desired images on the Browser images list.
4. Click the left **[Select Set]**. If you are adding two sets of images, select the second set of images and select the right most **[Select Set]**.
5. Click **[New Save Series]**.
6. Click **[+]**.
7. Click **[=]**.

This procedure defines how to perform image addition between one or two sets of images. This type of addition adds the image intensity values, pixel by pixel, of all pairs of images between the two selected sets corresponding to the same physical location in the patient's body. Follow this procedure to add one or two sets of images.

1. Click **Display Desktop**.

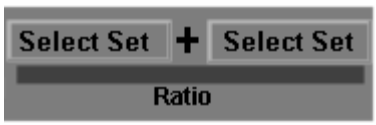
   - Located on the desktop control panel.
   - The Browser appears.

2. Click **[Add/Sub]**.

   - Located on the right column of the Browser.
   - The Image Combination window appears.

3. Select the desired images on the Browser images list.

4. Click the left **[Select Set]**.
   - Defines the first image set.
   - If you are adding two sets of images, select the second set of images and select the right most **[Select Set]**.



     ° Defines the second image set.

   - By default, equal weighting is applied to the two pixels in each pair, but you can change the weighting via sliding the Ratio bar. In all cases, for normalization purposes, each resulting pixel value is divided by two.

5. Click **[New Save Series]**.

- The images save in the Browser in a new series.
- If you do not select this option, the images save in the current saved series.

6. Click **[+]**.

- Selects the addition mode.

7. Click **[=]**.

- Performs the operation and generates the new images.
- The new series appears in the Browser when the function is complete.

Subtract Two Images Within the Same Set or Two Sets of Images

In Brief: Subtract Two Images Within the Same Set or Two Sets of Images

1. Click **Display Desktop**.
2. Click **[Add/Sub]**.
3. Click **[Clear Selection]**.
4. Do one of the following:
   - If you are subtracting two images within the same set, select the images and select the left most **[Select Set]**.
   - If you are subtracting two sets of images, select the image set you wish to use and select the left most **[Select Set]**. Repeat for second set, selecting right most **[Select Set]**.
5. Click **[New Save Series]**.
6. Click **[Accept Negative Pixels]**.
7. Click **[-]**.
8. Click **[=]**.

The following procedure defines image subtraction between images within one or two sets. This type of subtraction subtracts the image intensity values, pixel by pixel, of the second image or image set selected in the Browser. Follow this procedure to perform image subtraction on images within the same set or in two sets.

1. Click **Display Desktop**.

   - Located on the desktop control panel.
   - The Browser appears.

2. Click **[Add/Sub]**.

   - Located on the right column of the Browser.
   - The Image Combination window appears.

3. Click **[Clear Selection]**.

   - Clears the selection and insures that both Select Set button selections have no prior values.

4. Do one of the following:
   - If you are subtracting two images within the same set, select the two images you wish to use from the Browser, and select the left most **[Select Set]**.
   - If you are subtracting two sets of images, select the image set you wish to use and select the left most **[Select Set]**. Repeat for the second set, this time selecting the right most **[Select Set]**.

5. Click **[New Save Series]**.

   - The images save in a new series in the Browser.
   - If you do not select this option, the images save in the current saved series.

6. Click **[Accept Negative Pixels]**.

   - Allows negative pixel values in the resulting images.
     - If this function is not enabled, all negative pixel values are set to zero.

7. Click **[-]**.

   - Selects the image subtraction mode.

8. Click **[=]**.

   - Performs the operation and generates the new images.
   - The new series appears in the Browser when the function is complete.

Extract Minimum or Maximum Pixel Values

One Set of Images

In Brief: Extract the Minimum or Maximum Pixels From One Set of Images

1. Click **Display Desktop**.
2. Click **[Add/Sub]**.
3. Click **[Clear Selection]**.
4. Select the desired images on the Browser and click the left **[Select Set]**.
5. Click **[New Save Series]**.
6. Click **[Min]** or **[Max]**.
7. Click **[=]**.

The following set of steps defines how to find the minimum or maximum pixel value extraction on one image set. Depending upon your selection, this type of extraction finds the minimum or maximum pixel intensity, pixel by pixel, from among the images selected. To perform this operation:

1. Click **Display Desktop**.

   - Located on the desktop control panel.
   - The Browser appears.

2. Click **[Add/Sub]**.

   - Located on the right column of the Browser.
   - The Image Combination window appears.

3. Click **[Clear Selection]**.

   - Clears the selection and insures that both Select Set button selections have no prior values.

4. Select the desired images on the Browser and click the left **[Select Set]**.
   - Defines the set of images.

5. Click **[New Save Series]**.

   - The images save in a new series in the Browser.
   - If you do not select this option, the images save in the current saved series.

6. Click **[Min]** or **[Max]**.
   - Click **[Min]** to select the minimum pixel value extraction mode.

   - Click **[Max]** to select the maximum pixel value extraction mode.

7. Click **[=]**.

   - Performs the operation and generates the new images.
   - The new series appears in the Browser when image extraction is complete.

Extract Minimum or Maximum Pixel Values

Two Sets of Images

In Brief: Extract the Minimum or Maximum Pixels from Two Sets of Images

1. Click **Display Desktop**.
2. Click **[Add/Sub]**.
3. Click **[Clear Selection]**.
4. Select the first set of images on the Display Browser and click on the left **[Select Set]**.
5. Select the second set of images on the Browser, and click the right **[Select Set]**.
6. Click **[New Save Series]**.
7. Click **[Min]** or **[Max]**.
8. Click **[=]**.

The following set of steps defines how to find the minimum or maximum pixel values extraction between two sets of images. This type of extraction finds the minimum or maximum pixel intensity values, pixel by pixel, of all pairs of images between the two selected sets corresponding to the same physical location in the patient's body. To perform this operation:

1. Click **Display Desktop**.

   - Located on the desktop control panel.
   - The Browser appears.

2. Click **[Add/Sub]**.

   - Located on the right column of the Browser.
   - The Image Combination window appears.

3. Click **[Clear Selection]**.

   - Clears the selection and insures both Select Set button selections have no prior values.

4. Select the first set of images on the Browser and click on the left **[Select Set]**.
   - Defines the first image set.
5. Select the second set of images to extract from the Browser, and click the right **[Select Set]**.
   - Defines the second image set.
6. Click **[New Save Series]**.

   - The images save in a new series in the Browser.

- If you do not choose this option the images save in the current saved series.

7. Click **[Min]** or **[Max]**.
   - Click **[Min]** to select the minimum pixel value extraction mode.

   - Click **[Max]** to select the maximum pixel value extraction mode.

8. Click **[=]**.

   - Performs the operation and generates the new images.
   - The new series appears in the Browser when image extraction is complete.

Bind Images

In Brief: Bind Images

1. Click **Display Desktop**.
2. Click **[Add/Sub]**.
3. Click **[Clear Selection]**.
4. Select the desired set of images on the Browser and click left **[Select Set]**.
5. Select the desired set of images on the Browser and click the right **[Select Set]**.
6. Click **[New Save Series]**.
7. Click **[Bind]**.
8. Click **[=]**.

This procedure defines how to bind images together. You can create a new series that consists of copies of selected images from one or more existing series. Follow these steps to bind images together.

1. Click **Display Desktop**.

   - Located on the desktop control panel.
   - The Browser appears.

2. Click **[Add/Sub]**.

   - Located on the right hand column of the Browser.
   - The Image Combination window appears.

3. Click **[Clear Selection]**.

   - Clears the selection and insures both Select Set button selections have no prior values.

4. Select the desired set of images on the Browser and click the left **[Select Set]**.
   - Defines the first image set.
5. Select the desired set of images to bind on the Browser and click the right **[Select Set]**.
   - Defines The second image set.
6. Click **[New Save Series]**.

   - The images save in a new series in the Browser.
   - If you do not choose this option, the images save in the current saved series.

7. Click **[Bind]**.

- The Bind button selects the series binding mode.

8. Click **[=]**.

- Performs the operation and generates the new images.
- The new series appears in the Browser when the binding is complete.

NOTE: You can concatenate copies of images from other series to the end of the new series by following the same procedure, being sure to set up the New Save Series values correctly prior to clicking the **[=]** button.

In Brief: Subtraction of Three Station Runoffs

1. Click **Display Desktop**.
2. Select the arterial images from the upper station.
3. Click **[Add/Sub]**.
4. Click **[-]**.
5. Click left **[Select Set]**.
6. Select the mask images from the upper station.
7. Click right **[Select Set]**.
8. Click **[Accept Negative Pixels]**.
9. Click **[=]**.
10. Click **[Clear Selection]**.
11. Click **[New Save Series]**.
12. Select the arterial images from the middle station.
13. Click left **[Select Set]**.
14. Select the mask images from the middle station.
15. Click right **[Select Set]**.
16. Click **[Accept Negative Pixels]**.
17. Click **[=]**.
18. Click **[Clear Selection]**.
19. Click **[New Save Series].**
20. Select the arterial images from the lower station.
21. Click the left **[Select Set]**.

Post Process Three Station Runoffs

Subtractions

After performing a three station runoff with bolus chasing using SmartStep, it is possible to merge the top, middle, and bottom images together for filming. It involves three separate steps of instructions to follow. The first step involves subtracting the arterial images from the mask images. The second step involves acquiring a collapsed image projection with the use of IVI. The last step is binding them into one series which also aligns the three stations for filming. To perform the first function of subtracting the runoffs, follow these steps.

1. Click **Display Desktop**.

   - Located on the desktop control panel.
   - The Browser appears.

2. Select the arterial images from the upper station.
   - Click on the first image of the upper station in the Browser image list, press **Shift**, and click on the last image in the upper station.

3. Click **[Add/Sub]**.

   - Located on the right hand column of the Browser.
   - The Image Combination window appears.

4. Click **[-]**.

   - Selects the subtraction mode.

5. Click the left **[Select Set]**.

   - Defines the upper station arterial images as the first image set.

6. Select the mask images from the upper station in the Browser image list.
   - Click on the first image of the mask upper station in the Browser list, press **shift**, and click on the last image in the mask upper station.
7. Click the right **[Select Set]**.
   - Defines the upper station mask images as the second image set.
8. Click **[Accept Negative Pixels]**.

   - Allows negative pixel values in the resulting images.
     - If not enabled, all negative pixel values are set to zero.
9. Click **[=]**.

   - Performs the subtraction operation and generates the new images.
   - The subtraction images from the upper station are series 100.
10. Click **[Clear Selection]**.

   - Clears the selection and insures both Select Set button selections have no prior values to create new values for the middle station image subtractions.
11. Click **[New Save Series]**.

   - Saves in a new series and increments your middle station runoff to series 101.
12. Select the arterial images from the middle station.
   - Click on the first image of the middle station in the Browser image list, press **Shift**, and click on the last image in the middle station.

In Brief: Subtraction Continued

22. Select the mask images from the from the lower station in the Browser image list.

23. Click right **[Select Set]**.

24. Click **[Accept Negative Pixels]**.

25. Click **[=]**.

13. Click the left **[Select Set]**.
    - Defines the middle station arterial images as the first image set.
14. Select the mask images from the middle station in the Browser image list.
    - Click on the first image of the mask middle station in the Browser image list, press **Shift**, and click on the last image in the mask middle station.
15. Click the right **[Select Set]**.
    - Defines the middle station mask images as the second image set.
16. Click **[Accept Negative Pixels]**.
    - Allows negative pixel values in the resulting images.
      - If not enabled, all negative pixel values are set to zero.
17. Click **[=]**.
    - Performs the subtraction operation and generates the new images.
    - The subtraction images from the middle station is series 101.
18. Click **[Clear Selection]**.
    - Clears the selection and insures both Select Set button selections have no prior values to create new values for the lower station image subtractions.
19. Click **[New Save Series]**.
    - Saves a new series and increments your lower station runoff to series 102.
20. Select the arterial images from the lower station.
    - Click on the first image of the lower station in the Browser list, press **Shift**, and click on the last image in the lower station.
21. Click the left **[Select Set]**.
    - Defines the lower station arterial images as the first image set.

22. Select the mask images from the lower station in the Browser image list.
    - Click on the first image of the mask lower station in the Browser list, press **Shift**, and click on the last image in the mask lower station.
23. Click the right **[Select Set]**.
    - Defines the lower station mask images as the second image set.
24. Click **[Accept Negative Pixels]**.
    - Allows negative pixel values in the resulting images.
        - If not enabled, all negative pixel values are set to zero.
25. Click **[=]**.
    - Performs the subtraction operation and generates the new images.
    - The subtraction images from the lower station is series 102.
    - The three new series (100, 101, and 102) appear in the Browser when subtraction is complete.

NOTE: Proceed to step 2, acquiring collapsed image, with IVI.

In Brief: Acquire Collapsed Images with IVI

1. Select the upper station subtraction series.
2. Click **[IVI]**.
3. Right-click the collapsed image and select **[Save Image]**.
4. Select **File > New Model**.
5. Select the middle station subtraction series.
6. Click **[Load Slices]**.
7. Right-click the collapsed image and select **Save Image**.
8. Select **[File] > New Model**.
9. Select the lower station subtraction series.
10. Click **[Load Slices]**.
11. Right-click on the collapsed image and select **Save Image**.
12. Select **[File] > Quit**.

Post Process Three Station Runoffs

Acquire Collapsed Images with IVI

To perform the second step, acquiring collapsed images with IVI for three station runoffs, use the following procedure.

1. Select the upper station subtraction series.
   - The upper station subtraction images is series 100 in the Browser series list.
2. Click **[IVI]**.

   - Located on the right hand column of the Browser.
   - The Interactive Vascular Imaging (IVI) software package launches.
3. Right-click the collapsed image and select **Save Image**.
   - The collapsed image is in the upper left corner.
   - The new saved image is listed in your Browser series list as a “PJN” series.
4. Select **File > New Model**.
   - Selecting a new model gives you the ability to obtain the middle station images.
5. Select the middle station subtraction images
   - The middle station subtraction images is series 101 in the Browser series list.
6. Click **[Load Slices]**.
7. Right-click the collapsed image and select **Save Image**.
   - The collapsed image is in the upper left corner.
   - The new saved image is listed in your Browser series list as a “PJN” series.
8. Select **File > New Model**.
   - Selecting a new model gives you the ability to obtain the lower station images.
9. Select the lower station subtraction series.
   - The lower station subtraction series is series 102 in the Browser series list.

- Click **[Load Slices]**.

10. Right-click on the collapsed image and select **Save Image**.
    - The collapsed image is the image in the upper left corner.
    - The new saved image is listed in your Browser series list as a “PJN” series.
11. Select **File > Quit**.
    - Exits the IVI program.
    - There are three PJN series in your Browser series list.

NOTE: You may now proceed to step 3 to bind multiple series into a single series.

In Brief: Bind Multiple Series

1. Select the upper station PJN series.
2. Click **[Add/Sub]**.
3. Click **[New Save Series]**.
4. Change series 100 to series 103.
5. Click **[Bind]**.
6. Click the left **[Select Set]**.
7. Select the middle station PJN series.
8. Click the right **[Select Set]**.
9. Click **[=]**.
10. Click **[Clear Selection]**.
11. Click **[New Save Series]**.
12. Change the series number to 104.
13. Select all the images from binded series 103.
14. Click left **[Select Set]**.
15. Select the lower station PJN series.
16. Click right **[Select Set]**.
17. Click **[=]**.
18. Click **[Quit]**.
19. Select series 104.
20. Click **[Viewer]**.
21. Type **`format 3 1`** and press **Enter**.
22. Film the images.

Post Process Three Station Runoffs

Bind Multiple Series into a Single Series

To perform the third step, binding multiple series into a single series for three station runoffs, use the following procedure.

1. Select the upper station PJN series.
   - Click the first PJN series (100) in the Browser series list.
2. Click **[Add/Sub]**.
   - Located on the right hand column of the Display Browser.
   - The Image Combination window appears.
3. Click **[New Save Series]**.
   - Series 100 is the default number.
4. Change series 100 to series 103.
   - Clicking New Save Series multiple times increases the series number.
5. Click **[Bind]**.
   - Selects the series binding mode.
6. Click the left **[Select Set]**.
   - Defines the first image set.
7. Select the middle station PJN series.
   - Click the second PJN series (101) in the Browser series list.
8. Click the right **[Select Set]**.
   - Defines the second set of images.
9. Click **[=]**.
   - Performs the operation and generates the new images.
10. Click **[Clear Selection]**.
    - Clears the selection and insures that Select Set button selections have no prior values.

11. Click **[New Save Series]**.

12. Change the series number to 104.

    - Clicking New Save Series multiple times increases the series number.

13. Select all the images from binded series 103.

    - Click series 103 in the Browser series list.

14. Click the left **[Select Set]**.

    - Defines the first set of images.

15. Select the lower station PJN series.

    - Click on the third PJN series (102) in the Browser series list.

16. Click the right **[Select Set]**.

    - Defines the second set of images.

17. Click **[=]**.

    - Performs the operation and generates the new images.

18. Click **[Quit]**.

    - Exits Add/Sub program and closes the Image Combination window.

19. Select series 104 in the Browser series list.

20. Click **[Viewer]**.

    - Located on the right hand column of the Browser.

21. Type **`format 3 1`** and press **Enter** in the accelerator line.

    - The accelerator line is a command text box located in the lower left corner of your Viewer.

22. Film the images.

    - Select a one on one film composer format and press the **F3** key to film the images.

The following picture is a sample of what you should have created using the Post Processing Three Station Runoff steps.

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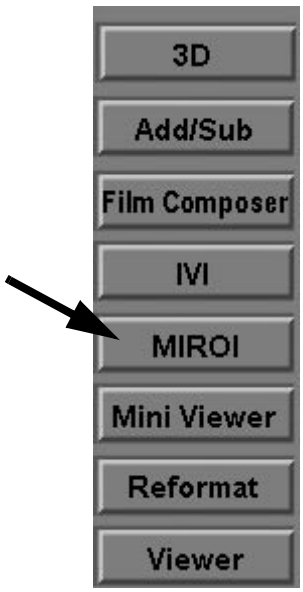
Chapter 4

Defining a Region of Interest with MIROI

Where Am I?



Introduction

This chapter explains the MIROI (Multiple Image Region of Interest) process. MIROI allows you to view signal intensity values over time. It contains the step-by-step instructions to help you learn how to:

- Load Image Data into MIROI
- View a Single Pixel Curve
- View a Curve of more than a Single Pixel
- View a Curve Representing the Pixels within a ROI
- Change the Scale of the Graph's Vertical Axis
- List Signal Intensity Values
- Display a Histogram
- Save the Graph Display

In addition, this chapter answers the following questions:

1. What is a multiple image region of interest?
2. What is the MIROI layout?
3. How do you manipulate an image?
4. How do you manipulate a graph?

About... MIROI

This section presents the concepts necessary to successfully complete the MIROI process. Specifically, you need to understand:

- MIROI Basics
- MIROI Layout
- MIROI Tool Panel
  - Load Series
  - Draw ROI
  - Single and Multi-Voxel ROI Cursor
  - Cursor ROI
  - aA Icon
  - Window/Level Presets
  - Rotate Icons
  - Film Composer
  - Get Protocol/Delete Protocol
  - Browser
  - Help Menu
  - Quit
- Manipulating the Image
  - Show/Hide
  - Smooth/No Smooth
  - Display Normal
  - Save View
  - Movie
- Manipulating the Graph
  - Set X Unit
  - Set Y Unit
  - List Values
  - Histogram
  - Save View
  - Create Annotation
  - Show Deviation

MIROI Basics

The Multiple Image Region of Interest (MIROI) tool is analysis software that allows you to graphically analyze signal intensity values within a defined area of interest on numerous images. This tool is useful for graphing a change in contrast enhancement over time through a defined area.

MIROI requires multiple images from a single series with the same scan plane, image center, and pixel size. The image set must be time ordered, but the images are not required to be equally spaced in time. For example, the trigger delay time for multi-phase images does not have to be equally spaced. Computed images, such as, screen saved, reformatted, or projection images may not be used.

Once valid images are acquired, MIROI displays the information in a graph that plots the change in signal intensity over time. This graph is called a time-intensity curve. The images and graphs can be saved and printed on film.

- Signal intensity is plotted on the y-axis.
- Time is plotted on the x-axis.

Curves are displayed as the ROIs are defined. Up to twenty curves may be displayed at one time on a single plot. If more than 20 ROIs are identified, only the 20 most recently defined ROIs are displayed and plotted. Total dataset size is a function of available memory and image matrix size.

Applications for using MIROI include contrast injection studies to determine the acquisition delay for contrast angios. It can also be used to determine peak flow velocity for vascular studies by finding the correct trigger delay for gated 2D TOF studies.

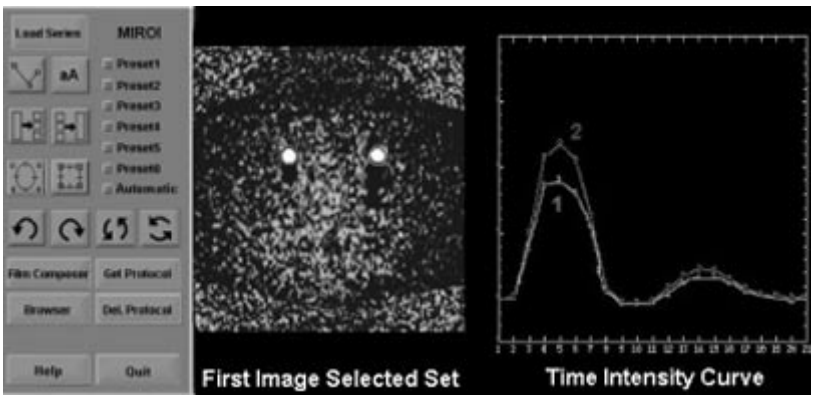
NOTE: The operator workstation's main Viewer, 3D Analysis Package, Reformat, IVI, and ClariView must be closed or stopped before MIROI can be opened.

MIROI Layout

MIROI is selected from the right column of the Browser on the Display Desktop.

NOTE: If you have purchased the FuncTool optional software package, it replaces MIROI with the **[FuncTool]** button and MIROI functions are then accessed through FuncTool.

MIROI opens, displaying the MIROI tool panel, the first image in the selected set, and the time-intensity curve (TIC).



MIROI Window

The curve in the graph represents the change in pixel value for the pixel under the cursor in all of the images.

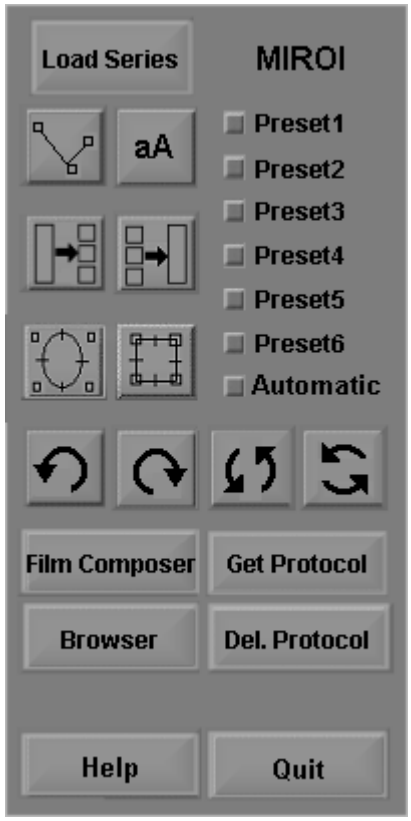
A curve can be displayed for:

- A single pixel
- 2 to 25 pixels
- An area defined by an ROI

The time-intensity curve can be changed to a list of signal intensity values or a histogram.

MIROI Tool Panel

The MIROI tool panel displays to the left of the image window.



MIROI Tool Panel

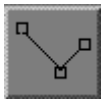
The tool panel contains all of the necessary buttons to perform the processes in MIROI.

Load Series

A selected series from the Browser is loaded into MIROI for processing when the **[Load Series]** button is selected. MIROI can accept up to 1,024 images. The first series selected is automatically loaded when MIROI is launched from the Browser. Subsequent selected series must be loaded into MIROI by using the **[Load Series]** button.

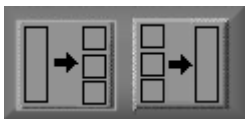
Draw ROI

You have the ability to draw your own ROI by clicking the **Draw ROI** icon, then holding down the shift key on the keyboard and clicking.



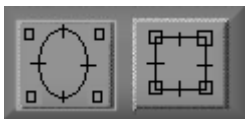
Single and Multi-Voxel ROI Cursor

The following icons allow you to change the cursor between a single ROI to a multi-voxel ROI and from multiple voxels to a single voxel ROI. Changing the ROI cursor is useful when performing multi-voxel spectroscopy.



Cursor ROI

The cursor ROI icons place an ellipse or square ROI on the image. The ROI statistics are also displayed. Once the ROI is displayed, it can be resized by clicking on one of the four boxes and dragging to desired size.



aA Icon

You have the ability to annotate your images in MIROI by the **aA** icon. Annotation is helpful to clearly label your images.

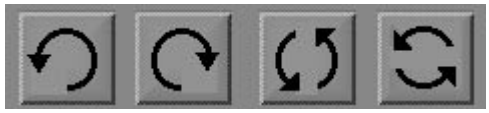
Window/Level Presets

Predefined Window/Level values can be applied to an image by selecting a preset value from the tool panel. The preset

selections are defined using the **[User Pref]** button in the Viewer.

Rotate Icons

The following **Rotate** icons are used to rotate or flip the displayed image superior, inferior, left, right, anterior, or posterior. The system annotations are immediately updated on the image.



Film Composer

The Film Composer can be launched in MIROI by clicking the **[Film Composer]** button in the lower right corner of the tool panel.

NOTE: For additional information on the film composer, refer to the chapter Filming Images, Volume 1.

Get Protocol/Delete Protocol

The protocol buttons are used when performing selected FuncTool operations to retrieve a defined protocol or to delete an existing protocol from the system.

Browser

The **[Browser]** button on the tool panel allows access to the main Browser for viewing exams.

Help Menu

The **[Help]** button gives access to a Help menu. This menu provides a quick reference of commonly used commands for manipulating and saving views and graphs. This is a toggle button which opens and closes the Help menu.

The following table describes the options found in the Help menu.

Keyboard Command	***Function***
F1	Films Image
F2	Films page
F5	Saves difference image
Copy (**CTRL+C**)	Copies the ROI
Paste (**CTRL+V**)	Pastes the ROI
Cut (**CTRL+X**)	Deletes the ROI
Shift	Adds the ROI
Alt/Meta	Density mask ROI
Space	Rescales the graph

Keyboard Command	Function
H	Displays the histogram
S	Saves screen view
W	Automatic width/level

Quit

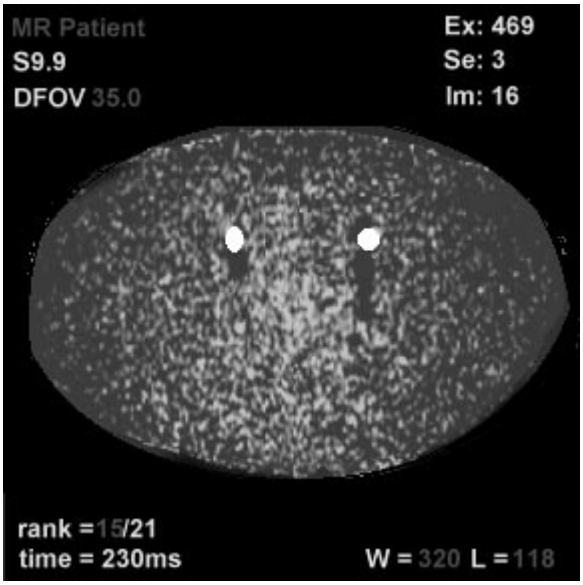
The **[Quit]** button closes the MIROI window and returns you to the Browser.

Manipulating the Image

The following table displays the image parameters that appear red (or underlined), indicating that they may be changed via the mouse button functions.

Image Parameter	Description
DFOV	The display field of view of the image.
rank = 15/16	The image number of the image displayed out of the total number of images.
W/L	The window and level settings.

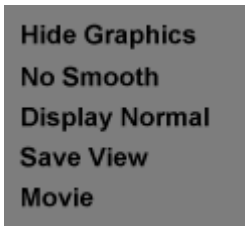
Note the changeable parameters in the figure below.



The changeable numbers displayed in red on the image in MIROI window can be changed by doing one of the following:

- Clicking the mouse button to increase the number in increments of one.
- Middle-clicking on the mouse button to change the cursor to an arrow ⇔, then dragging the mouse left or right to decrease or increase the number numerically.

The following functions are all accessed by placing the cursor over the image displayed, then right-clicking and dragging mouse button to select the feature.



- Show/Hide
- Smooth/No Smooth
- Display Normal
- Save View
- Movie

Show/Hide

Annotation and graphic ROIs can be hidden or shown the on the image by toggling the Show/Hide function. This key is not available until you place annotation or a ROI on the image.

Smooth/No Smooth

The images in MIROI can be filtered by selecting Smooth. This function toggles between Smooth and No Smooth to select or turn off the image filtering feature.

Display Normal

In MIROI, the image can be flipped or rotated in different directions in the image viewer. The image can be restored to its normal orientation by the Display Normal selection.

Save View

Save View creates a screen save of the image displayed. The images selected for a save view are stored with an image type of "ssave" and can be accessed only through the Browser.

Movie

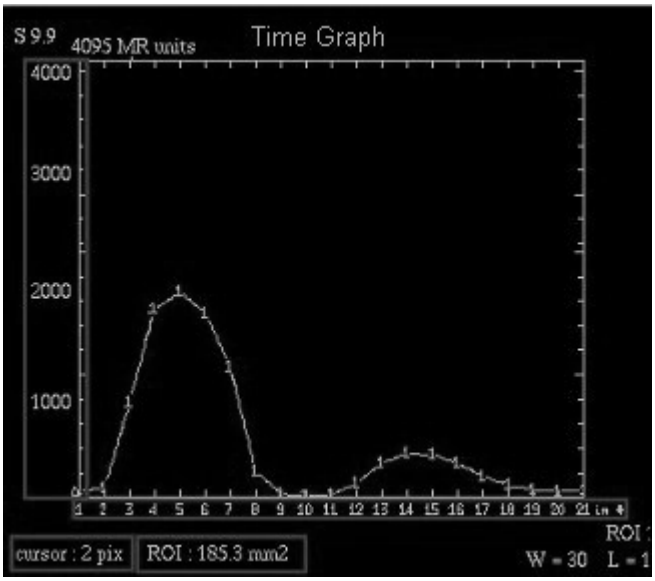
Selecting Movie launches the Movie window for cine display.

Manipulating the Graph

A graph is viewed in MIROI by placing the cursor or ROI on the image. The graph displays in the viewport to the right of the image representing the change in pixel(s) value for the pixel under the cursor for each image in the data set.

- The numbers on the y-axis represent MR units.
- The numbers on the x-axis represent pixel intensity values in parts per million (ppm).

The following figure represents a time graph that displays to the right of the image in the MIROI window.



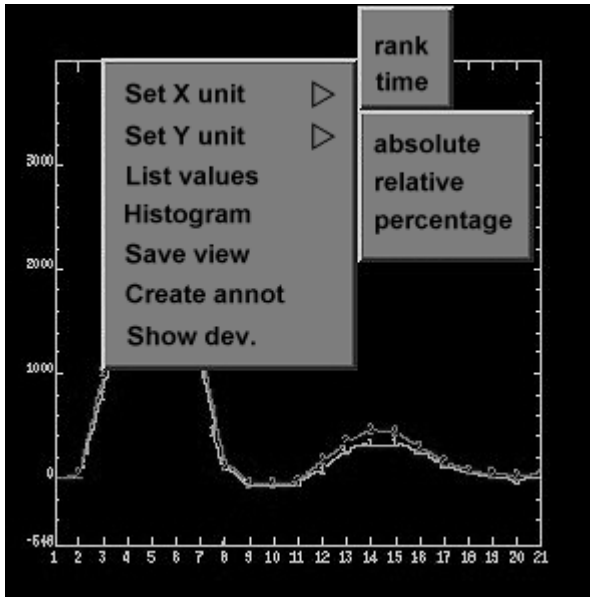
The y and x-axis scales have changeable numbers displayed in red (or underlined) on the graph in MIROI window. They can be changed by doing one of the following:

- Clicking the mouse button to increase the number in increments of one.
- Middle-clicking on the mouse button to change the cursor to an arrow ⇔, then dragging the mouse left or right to decrease or increase the number numerically.

The following functions are all accessed by placing the cursor over the graph displayed, then right-clicking and dragging the mouse button to select the feature.

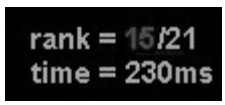
- Set X Unit
- Set Y Unit
- List Values
- Histogram
- Save View
- Create Annotation
- Show Deviation

The selections overlay the graph on the right side of the image window.



Set X Unit

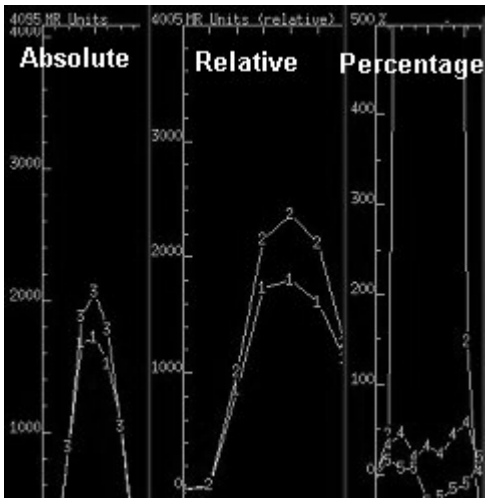
The Set X unit function allows you to toggles the x-axis of the curve between image time and image rank. Rank is defined as a set of images taken at a location. Rank 1 (the first set of images taken at the first location) is the default image set loaded when first entering MIROI. The time is represented in milliseconds.



Set Y Unit

The Set Y unit function allows you to toggle the unit of measurement for the y-axis of the curve between the pixels real value and a normalized value. The normalized scale sets the y-axis zero point to the ROI pixel value of slice number one.

The difference between absolute, relative, and percentage may be visualized vertically along the side of the time graph. This option is located in the **Set Y unit** selection as a sub menu.



List Values/Time Graph

Selecting **List values** displays the values of the current curve in a table. The voxel intensity changes may be listed by Rank (image number) or Time (trigger delay). Either Rank or Time can be selected in the **Set X unit** sub menu. Time graph returns the curve to its usual display.

The following figure demonstrates the list values of the current curve in a table.

Rank	ROI 01 AVG	ROI 02 AVG
im #	MR Unit	MR Unit
1	0.0	0.0
2	14.8	27.8
3	722.7	838.1
4	1475.0	1840.9
5	1606.2	2041.5
6	1442.3	1758.3
7	1005.0	1016.2
8	149.0	84.4
9	-28.5	-49.0
10	-40.9	-48.6
11	-33.8	-27.9
12	66.9	138.1
13	226.4	284.8
14	300.2	378.4
15	294.5	354.5
16	227.2	237.8
17	113.6	131.1
18	44.6	50.5
19	6.0	24.2
20	-10.5	9.4
21	6.5	22.0

Time	ROI 01 AVG	ROI 02 AVG
ms	%	%
0	0.0	0.0
48	24.6	44.7
96	1200.5	1346.9
144	2450.1	2958.7
192	2668.0	3281.0
240	2395.7	2825.8
288	1669.4	1633.2
336	247.5	135.6
384	-47.4	-78.8
432	-68.0	-78.1
480	-56.2	-44.8
528	111.1	222.0
576	376.1	457.7
624	498.6	608.1
672	489.3	569.8
720	377.4	382.2
768	188.7	210.7
816	74.1	81.2
864	9.9	38.8
912	-17.5	15.1
960	10.8	35.3

Histogram

Selecting **Histogram** displays the data in a histogram format. An alternative is to type "**H**" from the keyboard.

Save View

Save view allows you to screen save the curve or time graph. An alternative is to type **"S"** from the keyboard.

Create/Hide Annotation

Creating annotation allows you to type annotation on the graph. Select the hide annotation feature to temporarily hide the annotation on the graph.

Show Deviation

Selecting **Show Dev.** displays the deviation or measure of variability according to pixel values within the plotted ROI.

How to Define a MIROI

This section provides the step-by-step instructions for performing MIROI. Specifically, it describes how to:

- Load the Image Set Into MIROI
- View a Single Pixel Curve
- View a Curve of More Than a Single Pixel
- View a Curve Representing the Pixels Within A ROI
- Change The Scale of the Graph's Vertical Axis
- List Signal Intensity Values
- Display a Histogram
- Save the Graph Display

Load the Image Set Into MIROI

In Brief: Load the Image Set Into MIROI

1. Click **Display Desktop.**
2. Select the images on the Display Browser.
3. Click **[MIROI]**.

Use the following procedure to load images into MIROI:

1. Click **Display Desktop**.
2. Select the images on the Display Browser.
   - You can do this by clicking and dragging over a range of images for multiple images.
   - Click on one image for a single image.
   - Press the **Ctrl** key and select images.
3. Click **[MIROI]**.
   - Located on the right column of the Browser.
   - Launches the MIROI software.

NOTE: If the FuncTool software is installed on your system, MIROI is contained within FuncTool.

View A Single Pixel Curve

Use this procedure to view a single pixel curve.

1. To view a curve from a single pixel, position the mouse cursor on the image over the area of interest and press the **SPACEBAR** on the keyboard to scale curve.
   - The graph curve appears to the right of the image.

In Brief: View A Single Pixel Curve

1. Position the mouse cursor on the image and press the **SPACEBAR** on the keyboard.

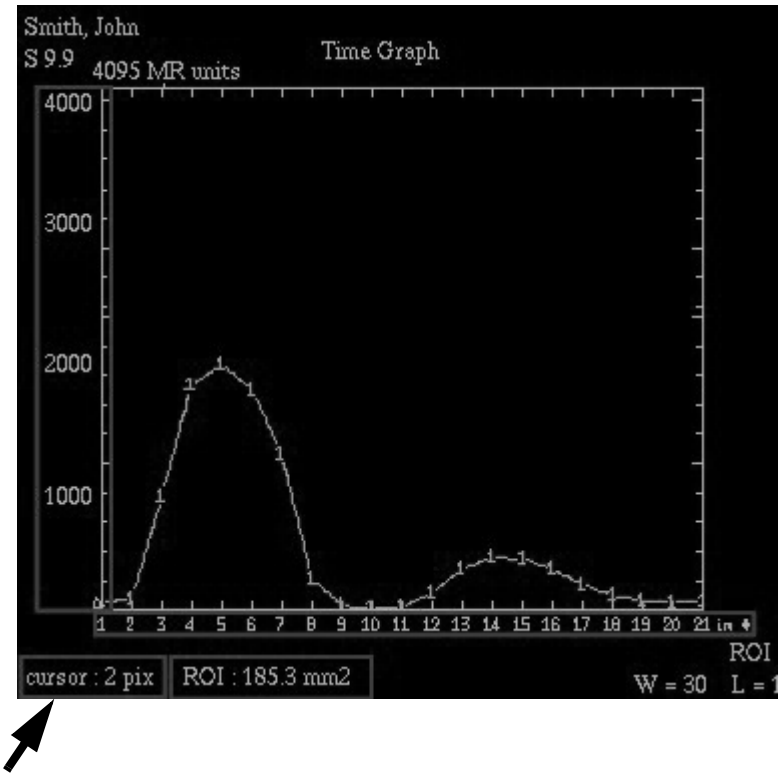
View a Curve of More than a Single Pixel

In Brief: View a Curve of More than a Single Pixel

1. Place the cursor on the number 1 in the lower left corner of your graph viewer.
2. Middle-click and drag to the right.
3. View the new curve.

Use this procedure to view a curve of more than a single pixel.

1. Place the cursor on the number adjacent to the word “cursor” in the lower left corner of your graph viewer.

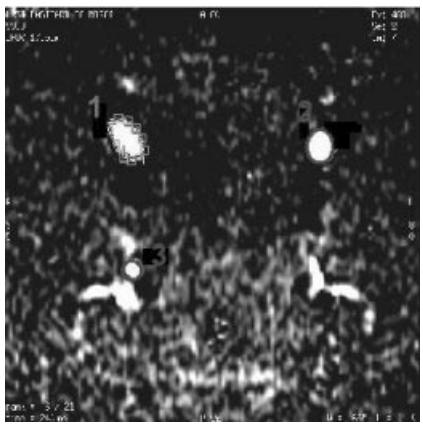


2. Middle-click (the cursor becomes ⇔) and drag it to the right.
   - The number one increases as the cursor is dragged right.
     - The maximum number is 25. At this point, the cursor itself widens in size to cover the area in pixels that was selected.
   - Middle-click and dragging to the left decreases the number.
3. View the new curve.

View a Curve Representing the Pixels within an ROI

Use this procedure to create an ROI and to view the curve representing pixels within an ROI. This feature is useful when calculating a trigger delay for gated TOF runoffs for each femoral artery.

1. Place your mouse cursor where the ROI drawing is to begin.
2. Press the **Shift** key on your keyboard, then click once.
3. While continuing to hold down the **Shift** key, move the cursor to the next point and click again.
   - A line connecting the first point to the second point is drawn.
4. Move to the next position and click again until the ROI is completed.
   - Once ROI is complete, there is a closed circle around the region of interest.



5. To edit or move an ROI, click along any edge of the ROI.
   - The ROI changes color and the points along the ROI border are clearly visible.
   - Click and drag a point to resize the ROI.
   - Click and drag along the border to move the ROI.
6. View the curve.
   - The curve represents the pixel value changes for all the pixels in the ROI.
   - While the cursor is within the graph with curves from any ROI, two lines (one horizontal and one vertical) appear

In Brief: View a Curve Representing The Pixels within a ROI

1. Place your mouse cursor where the ROI drawing is to begin.
2. Press the **Shift** key, then click.
3. While continuing to hold down the **Shift** key, move the cursor to the next point and click again.
4. Move to the next position and click again until the ROI is completed.
5. To edit or move an ROI, click along any edge of the ROI.
6. View the curve.

along the individual time points, and a relative pixel value for the ROI displays.

- To draw subsequent ROIs, click anywhere within the image except on the current ROI.
  - This de-selects the current ROI and turns its color from green to purple.
  - Now draw the next ROI in the same way as the first.

NOTE: You cannot add an ROI if you have selected Hide Graphics from the context menu.

Change the Scale of the Graph's Vertical Axis (Signal Intensity)

Use this procedure to change the scale of the graph's vertical axis.

1. Place the cursor over the top or bottom value (displayed in red text) and do one of the following:
   - Click to increase the value.
   - Right-click to decrease the value.
   - Middle-click (the cursor changes to ⇔) and drag left or right to increase or decrease the value.
2. Press the **Spacebar** to auto scale the graph.
   - This places the points in the middle of the scale.

In Brief: Change the Scale of the Graph's Vertical Axis (Signal Intensity)

1. Click on the top or bottom red value on the vertical scale.
2. Press the **Spacebar** to auto scale the graph.

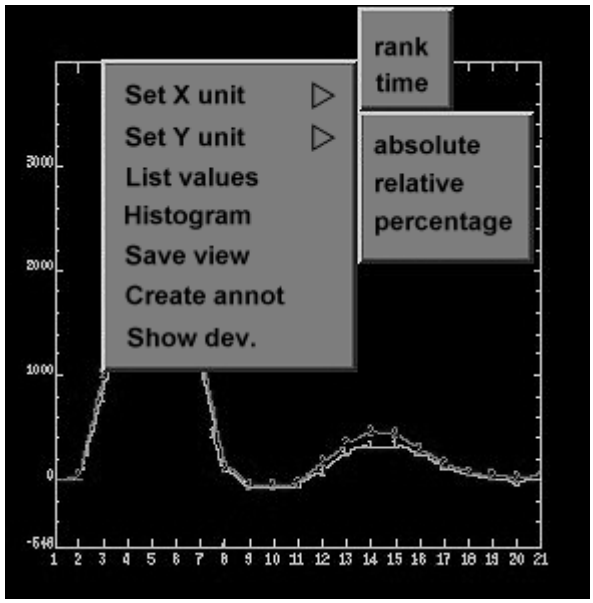
List Signal Intensity Values

In Brief: List Signal Intensity Values

1. Position the cursor on the graph.
2. Right-click and select **List values** > **rank** or **time**.

Use this procedure to change the curve graph to a list of the actual signal intensity values.

1. Position the cursor on the graph.
2. Right-click and select **List Values** > **rank** or **time**.
   - A sub menu appears overlying the graph.



   - Rank lists the values by image number.
   - Time lists the values by trigger delay.
     - This feature is helpful for calculating trigger delay for gated 2D TOF studies.

Rank	ROI 01 AVG	ROI 02 AVG
im #	MR Unit	MR Unit
1	0.0	0.0
2	14.8	27.8
3	722.7	838.1
4	1475.0	1840.9
5	1606.2	2041.5
6	1442.3	1758.3
7	1005.0	1016.2
8	149.0	84.4
9	-28.5	-49.0
10	-40.9	-48.6
11	-33.8	-27.9
12	66.9	138.1
13	226.4	284.8
14	300.2	378.4
15	294.5	354.5
16	227.2	237.8
17	113.6	131.1
18	44.6	50.5
19	6.0	24.2
20	-10.5	9.4
21	6.5	22.0

Time	ROI 01 AVG	ROI 02 AVG
ms	%	%
0	0.0	0.0
48	24.6	44.7
96	1200.5	1346.9
144	2450.1	2958.7
192	2668.0	3281.0
240	2395.7	2825.8
288	1669.4	1633.2
336	247.5	135.6
384	-47.4	-78.8
432	-68.0	-78.1
480	-56.2	-44.8
528	111.1	222.0
576	376.1	457.7
624	498.6	608.1
672	489.3	569.8
720	377.4	382.2
768	188.7	210.7
816	74.1	81.2
864	9.9	38.8
912	-17.5	15.1
960	10.8	35.3

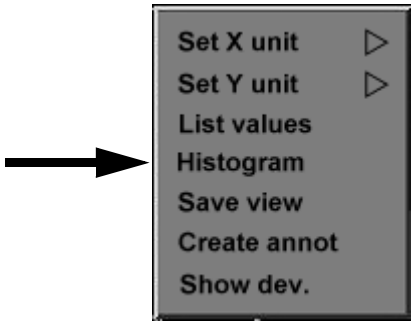
Display a Histogram

In Brief: Display a Histogram

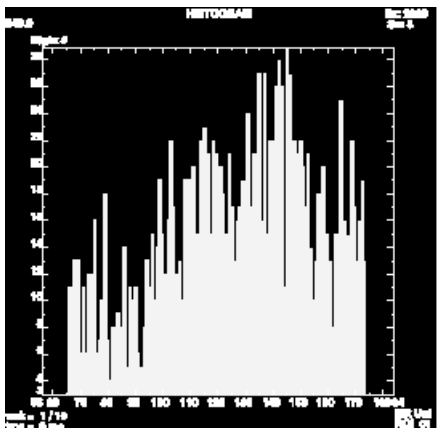
1. Select a curve or ROI
2. Right-click and select **Histogram**.

Use this procedure to display a histogram of the signal intensity values.

1. Select a curve on the graph or an ROI on the image.
2. Right-click and select **Histogram**.



- A Histogram displaying signal intensity values replaces the graph curve.



MIROI / Histogram

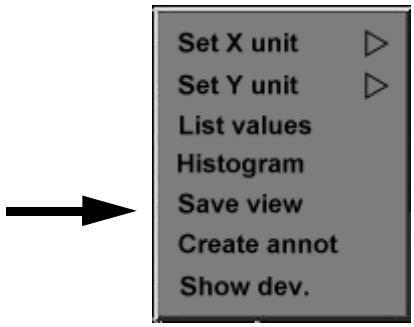
Save the Graph Display

In Brief: Save the Graph Display

1. Position the mouse cursor on the graph.
2. Right-click and select **Save view**.

Use this procedure to save your graph display.

1. Position the mouse cursor on the graph.
2. Right-click and select **Save view**.



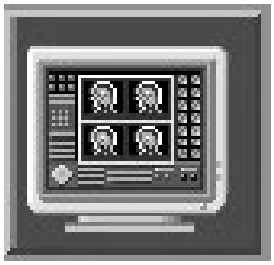
- Saves the graph for later viewing and archiving.
- The image is stored with an image type of "ssave".

Volume 4

Chapter 5

Creating Vascular Projections - IVI

Where Am I?



Introduction

This chapter explains the Interactive Vascular Imaging (IVI) process. This post-processing tool is focuses on the creation of vascular projection images. The Vascular Display Package, or Interactive Vascular Imaging, creates projection images from a 2D stack or 3D volume of Magnetic Resonance Angiography (MRA) images and allows you to view the data from different angles.

IVI uses a ray tracing technique called Maximum Intensity Pixel (MIP) to create projection images.

IVI allows you to modify the volume of interest to remove competing structures, such as fat, to improve the vascular images.

This chapter contains the step-by-step instructions to:

- Select a Valid Image Set
- Modify the Volume of Interest
- Rotate the MIP Image
- Define a Batch Projection Series

In addition, this chapter answers the following questions:

1. What types of image sets can be processed with IVI?
2. What is a MIP projection?
3. How are MIP projections generated?
4. What effect does threshold have on the volume?
5. What effect does scalpel have on the volume?
6. What are the applications?

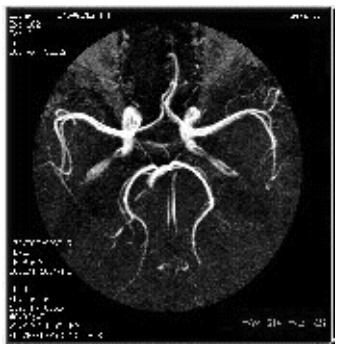
About... IVI

This section presents the concepts necessary to successfully complete the IVI (Interactive Vascular Imaging) process. Specifically you need to understand:

- Valid Image Sets
- MIP Projections
- IVI Layout
- Threshold
- Scalpel
- Applications

Valid Image Sets

A valid image set must use a white-blood technique for MIP. A TOF (Time of Flight) or PC (Phase Contrast) pulse sequence can be used to obtain white blood images. Vascular pulse sequences of 2D or 3D, and fast imaging can be used.



All images must have the same orthogonal scan plane, image center, and pixel size. Oblique images, Add/Sub images, and Reformat images can be loaded into IVI. Screen saved images are not allowed.

The range of images loaded for IVI post processing must not contain two images at the same location.

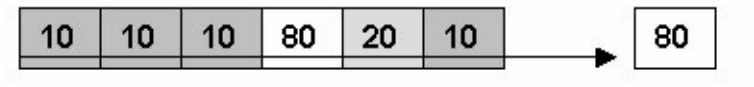
Isometric voxels (cube shaped) and overlapping slices improve the quality of IVI projection images. The FOV (Field of View), the matrix size, and the slice thickness affect the voxel size. The formula to determine the voxel size is: FOV / matrix = slice thickness. For example, an image with a 256 x 256 matrix, a

26cm FOV, and a 1 mm slice thickness results in an isometric voxel. The imaging option Square Pixel may help to maintain an isometric voxel especially when using a phase FOV less than one.

MIP Projections

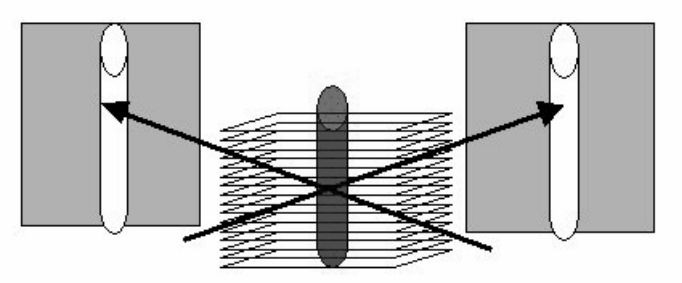
Maximum Intensity Pixel (MIP) projection traces a ray or angle through a stack of 2D images or a 3D image volume. The highest pixel intensity along the ray is projected or displayed in the resulting image.

In white blood images, the vascular structures typically have high signal intensity values and project into the created image.



- Along the ray (which is traced through these pixels, the highest pixel value 80) projects into the image.

Rays can be traced through the 2D stack or 3D volume at different angles.



Something to Think About...

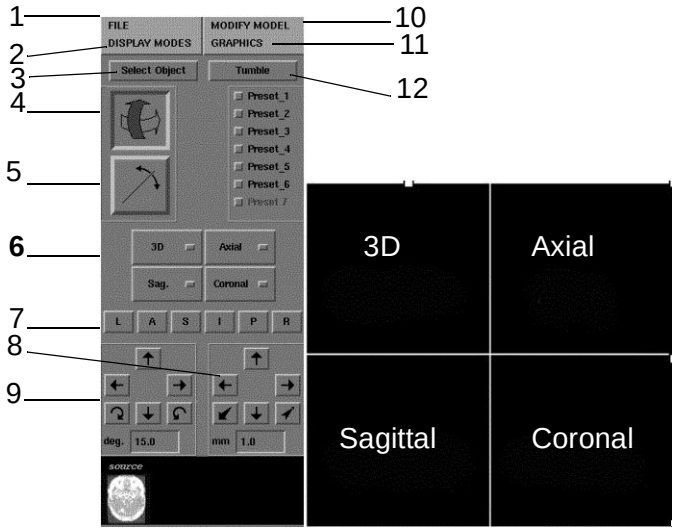
- The time stamp on IVI images correspond to the time of the landmark, not the time the source images were acquired.

Layout

IVI has a window and displays four viewports:

- The 3D MIP view displays in the upper-left viewport.
- An axial reformat view displays in the upper-right viewport.
- A sagittal reformat view displays in the lower-left viewport.
- A coronal reformat view displays in the lower-right viewport.

The viewport layout can be changed using the View Buttons on the tool panel or the active annotation on the image.



- **1 - File**. The following options are displayed when **File** is selected.
    - **Rebuild** - Allows you to rebuild the 3D volume using a different protocol.
    - **Load Model** - Allows you to load a saved “3D” model selected on the Browser.
    - **Save Model** - Allows you to save a 3D model. Saved 3D models appear on the Browser in the series list with the mention “3DOBJ” in the Type column of the list.
    - **New Model** - Allows you to close all windows and return to the Browser to select a new set of images. Once a new image is selected, select **Build Model > MR Angio**.

- **Film Composer** - Allows you to call up the Film Composer window in the lower right corner of the monitor.
- **About IVI...** - Tells you what version (software level) of IVI is on your system. Select About IVI..., note the version of IVI, and click the **[OK]** button to close the About IVI... window.
- **Quit** - Exits IVI.

- **2** - **Display Modes**. The following options are displayed when Display Modes is selected.
  - **Set Batch/Movie Loop** - Allows you to prescribe a film batch consisting of a sequence of reconstructed images or allows you to set up and run a “movie” loop via the Batch Filming/Movies window.
  - **Identify mm./slices** - Allows you to set up slice cross reference markings and/or a graduated ruler scale via the Identify mm./slices window.
  - **Cursor Lock** - Allows you to restrict 3D cursor movement to the trace (the trace must be present) or restrict 3D cursor movement to the x-axis or y-axis, via the Cursor Lock window.
  - **Display/Actions Defaults** - Allows you to set graphics (traces and cursor) display, cursor style, and annotation visibility via the Display/Actions Defaults window.
  - **Filming Setup** - Allows you to set whether the cursor is shown or hidden on saved images and the default film size, via the Filming Setup window.
  - **Color / Light / Window** - Sets density window to linear or negative via the Color / Light / Window window.
- **3** - **Select Object**. When you click this button, the object defined by the current cursor position is selected and all the other objects not directly connected to it are deleted from the view.
- **4** - **Tilt/Rotate Mode Select**. When you click this icon, the mouse can be used to tilt and rotate the image via the on-screen trackball. This feature is used for viewing purposes only; these rotated images are not be saved for future use.

- **5** - **Oblique Mode Select**. When you click this icon, the mouse can be used to move and rotate plane traces of reformatted views (oblique or baseline reformatted) on all views except curved, histogram, cross section, or profile views.This is used for viewing purposes only; these rotated images are not be saved for future use.
- **6** - **View** buttons. Click on the button of the corresponding viewport and then select the desired orientation to change the plane (or select **No View** to close viewport).
- **7** - **View Planes**. When you click one of the **[View Planes]** buttons, the 3D object returns to one of the standard baseline views (**L**eft, **A**nterior, **S**uperior, **I**nferior, **P**osterior and **R**ight).
- **8** - **Movement Increment**.
    - Selecting **mm** allows you to apply a specific amount of movement to the image. The increment size is changed in millimeters by moving the mouse pointer into this text box, delete the existing value by pressing the **Backspace** key, and enter the desired increment value from the keyboard. Click on an arrow button above to move the image by the millimeters entered, and move in the direction indicated by the arrow on the button.
- **9** - **Rotation Increment**.
    - Selecting **deg.** allows you to apply a specific degree of rotation to the image. The increment size in degrees is changed by moving the mouse pointer into this text box, delete the existing value by pressing the **Backspace** key, and enter the desired value from the keyboard. Click on an arrow button to the rotate by the number of degrees entered and rotate in the direction indicated by the arrow. Rotation is possible only on a 3D or Oblique view.
- **10** - **Modify Model**. The following options are displayed when **Modify Model** is selected.
    - **Threshold/VOI** - Allows you to adjust the upper and lower pixel level thresholds and apply scalpel cuts via the Threshold/VOI window.
    - **SAVS/Paintbrush** - Not applicable for IVI.
    - **Advanced Processing** - Not applicable for IVI.

- **Filter Floaters** - Allows you to set the size threshold for filtering floaters via the Filter Floaters window.
- **Undo** - Allows you to undo the last operation performed.

Something to Think About...

- The possibility of undoing the last operation is permanently lost if the selection of the views on which the last operation was performed is changed.

- **11** - **Graphics**. The following options are displayed when Graphics is selected.
  - **Distance** - Allows you to measure the distance along a trace via the Graphics window. The distance is displayed real-time in the Graphics window.
  - **Angle** - Allows you to measure the angle between two segments of a trace via the Graphics window.
  - **Area** - Allows you to measure the area defined by a closed trace via the Graphics window.
  - **User Annot / Trace** - Allows you to enter and edit text annotation via the Graphics window.
- **12** - **Tumble**. Clicking the **[Tumble]** button creates a short movie loop that provides a slight rocking movement to the 3D Model. The purpose is to enhance the depth perception of the object. Click the **[Tumble]** button again to resume normal display of the MIP image.

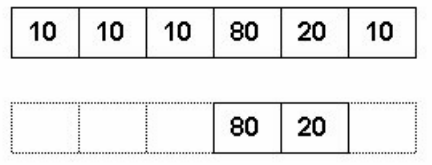
Threshold

The threshold determines the range of signal intensity values included for display in the volume of interest. Threshold is accessed by selecting **Modify Model** and then selecting **Threshold/VOI**.

The volume of interest can be modified by adjusting the threshold, provided the signal intensity values of the undesired structures differ from those of the structures of interest.

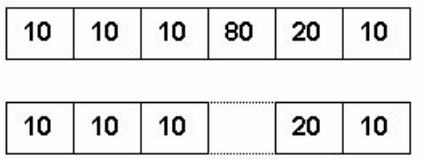
A minimum threshold displays pixels whose signal intensity value is equal to or greater than the selected value. Any pixels

with a signal intensity less than the selected value are removed from the volume.



- With a minimum threshold of 20, pixels with values less than 20 are removed from the volume.

A maximum threshold displays pixels whose signal intensity value is equal to or less than the selected value. Any pixels with a signal intensity greater than the selected value are removed from the volume.



- With a maximum threshold of 20, pixels with values greater than 20 are removed from the volume.

A range threshold can also be used to set both a minimum and a maximum signal intensity limit.

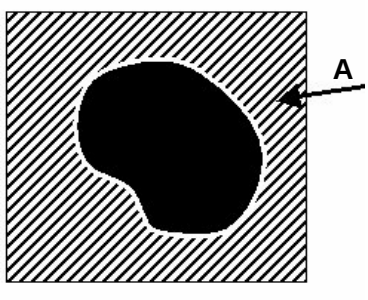
Scalpel

The volume of interest can also be modified by cutting away undesired structures using the scalpel feature.

Scalpel is used when physical distance separates structures.

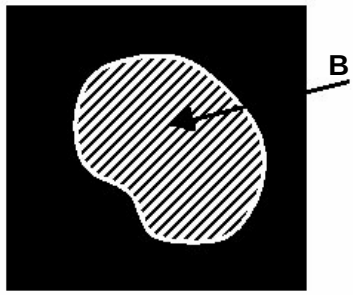
The scalpel defines the cut line. The area outside, inside, or along the trace created by the scalpel can be removed.

- Outside the trace removes the area outside of the trace.



A - Shows the area removed from the volume of interest.

- Inside the trace removes the area inside of the trace.



B - Shows the area removed from the volume of interest.

How to Create Vascular Projections Using IVI

This section provides the step-by-step instructions for Creating Vascular Projections using the IVI process. IVI is used to generate projection images at different angles through a 2D stack or a 3D volume of white-blood MRA images.

Specifically, it describes how to:

- Select the Image Set
- Modify the Volume of Interest (VOI)
  - Using Scalpel
  - Using Threshold
- Rotate the MIP Image
- Define a Batch Projection Series

Select the Image Set

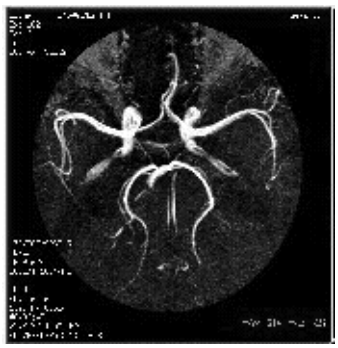
In Brief: Select the Image Set

1. Click the **Display Desktop** icon.
2. Highlight the exam and series on the Browser.
3. Check the image locations and deselect any duplicates.
4. Click **[IVI]**.

It is important to select only the images that meet the prerequisites to create the Vascular Projections using IVI.

1. Click the **Display Desktop** icon from the control panel.

2. From the Browser, highlight the exam and series to use for the creation of IVI Projection images.
   - These are the prerequisites:
     - A white-blood technique must have been used to acquire the images. MR Angiogram images are created by repeatedly exciting a predefined volume of anatomy until the stationary tissue is partially saturated and the signal from the tissue is suppressed. Blood flowing into the predefined volume of anatomy is not saturated but fully magnetized by the main magnetic field and yields a stronger signal. In the resulting image, the blood appears bright and the stationary tissue is suppressed.



     - All images must have the same scan plane, image center, and pixel size. Oblique images may used; although all images must have the same obliquity. (Screen Save images cannot be used.)
     - The range of images selected must not contain two images at the same location.

3. Click and drag to select images to load for IVI. Check the locations of all images selected, and deselect all duplicates at the same location. If you press the **Ctrl** (control) key while scrolling through the images, you are able to select only those images you want to use for IVI. Or, you can make your first image selection, hold the **Shift** key and make your last image selection, and all images in-between are selected.
4. Click **[IVI]** from the Browser.

Browser

In Brief: Modify the Volume of Interest Using Scalpel

1. Follow the steps for Selecting the Image Set.
2. Make the viewport with the 3D MIP primary.
3. Close the remaining viewports.
4. Select the prescription plane.
5. Select **Modify Model > Threshold/VOI**.
6. Select **Display Modes > Display / Actions Defaults**.
7. Click **Free Hand Trace [On]** or **[Off]**.
8. Click **[Close]**.
9. Place cursor at start of trace.
10. Press **Shift** to move red cursor to start point.
11. Press **Shift**, click and hold to draw trace, or click and release repeatedly.
12. Select Cut Mode, inside, outside, or along trace.
13. Click **[Apply Cut]**.
14. Click **[Clear Trace]** or **[Undo]**.

Modify the Volume of Interest Using Scalpel

Modifying the volume of interest process allows you to remove unwanted structures, such as fat, from the volume of interest and determine if the unwanted structures differ by physical distance or by signal intensity. Depending on how the structures differ determines which method to use to modify the volume of interest.

- Use scalpel to remove undesired structures that are physically separate (physical distance) from the volume of interest.
- Use threshold to remove undesired structures that differ by signal intensity. Do not use threshold if the signal intensity values do not differ.

NOTE: Please read the instructions for both Scalpel and Threshold carefully. They are different procedures and give different results.

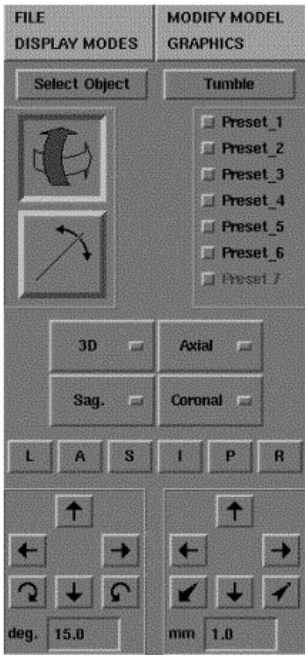
- Threshold and Scalpel may both be applied to the same IVI image to remove unwanted structures.

The following are step-by-step instructions how to remove unwanted structures from the volume of interest.

1. Follow the steps to Select the Image Set, as described previously.
   - Once you click **[IVI]** the images begin to load.

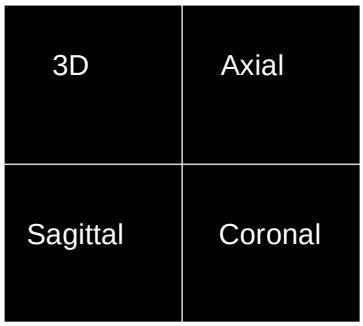
Browser

The IVI window appears.



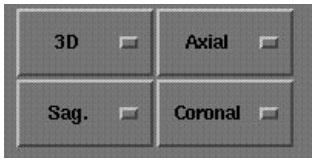
IVI window

2. Click on the 3D viewport, in the upper left view, to activate it as the primary view.



Viewer Display

3. Close the Axial, Sagittal and Coronal viewports to decrease the processing time. Click Axial, Sagittal, and Coronal **[View Type]** in the middle of the IVI window and then click No View. Although closing these viewports is optional, you may want to leave them open to use as a reference.



IVI window

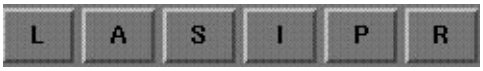
In Brief: Modify the Volume of Interest Using Scalpel

14. If necessary, change prescription plane and repeat steps 9-13. Go to step 15 if plane change is NOT needed.

15. Click **[Close]** from the Threshold/VOI window.

16. Select **File > Quit**. To rotate images, Do Not Exit. See Rotating the MIP Image or Defining a Batch Projection Series.

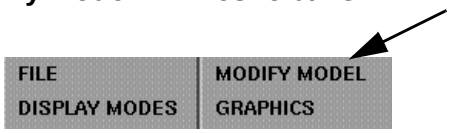
4. To change the prescription plane (plane of the IVI image), click **[L,A,S,I,P,S, or I]** found on the IVI window. Clicking one of these at any time changes the prescription plane.



IVI window

- L=Left View
- A=Anterior View
- S=Superior View
- I=Inferior View
- P=Posterior View
- R=Right View

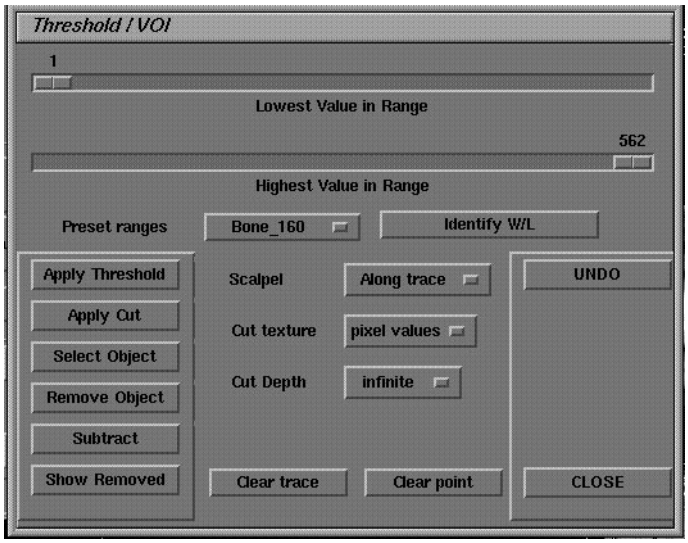
5. Select **Modify Model** > **Threshold/VOI**.



IVI window

The Threshold/VOI window appears.

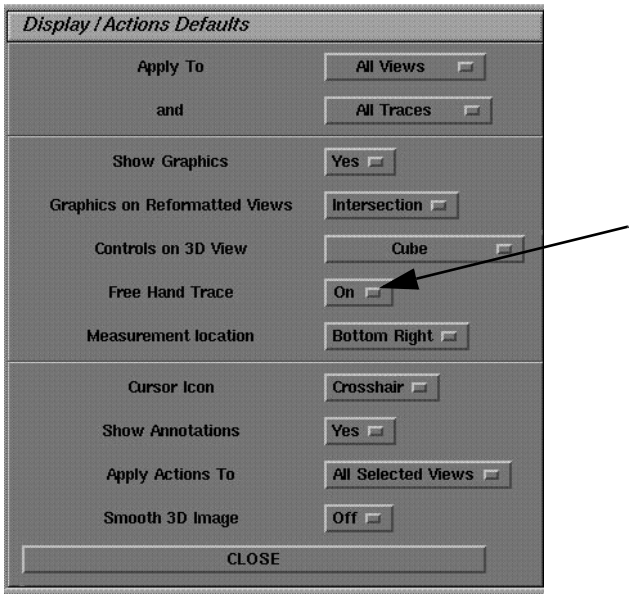
- Hint: Click and drag along the border of the Threshold/VOI window to move into one of the closed viewports.



Modify Model /Threshold / VOI window

6. To set the trace mode, select **Display Modes** located on the IVI window and then select **Display/Actions Defaults**.
   - You only need to do this step to change the default; this makes your selection the default.

   The Display/Actions Defaults window appears.



Display Modes / Display / Actions Defaults

7. Select the trace mode (arrow) of your choice:
   - Click **[On]** to turn on free trace mode.
   - Click **[Off]** to turn on segment trace mode.

NOTE: See the chapter Reformat for more information about Free Hand Trace.

8. Click **[Close]** to exit from this window.

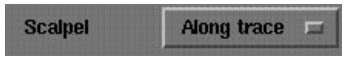
9. On the 3D MIP image in view, position the cursor at the starting point of your trace.

10. Press the **Shift** key, click and hold the left mouse click and do one of the following:
    - If using Free Hand Trace, drag the cursor around the region of interest to trace the cut line.
    - If using Segment Trace, click and release to deposit points around the region of interest, thereby tracing the cut line. Note the following:
      - While pressing the **Alt** key, click and drag any anchor located on the trace to the desired location.

Repeat this process to make necessary edits. The trace updates once the mouse is released.

- Repeatedly pressing the **D** key deletes a series of the most recently deposited points.

11. From the Threshold window, select the cut mode. Click the button to the right of **Scalpel,** and then select the desired cut mode.



Threshold / VOI window

- The cut mode choices are:
  - **Inside trace** - removes area inside of the trace.
  - **Outside trace** - removes the area outside of the trace.
  - **Along trace** - removes the area of the trace (along the cutline).

12. Click **[Apply Cut]** to remove the undesired area.

Threshold / VOI window

13. If satisfied, click **[Clear trace]**.

Threshold / VOI window

- If not satisfied, click **[Undo]** and start over.

Threshold / VOI window

14. If necessary, change the prescription plane (click one of the buttons as shown below to change plane) and repeat steps 9-14.

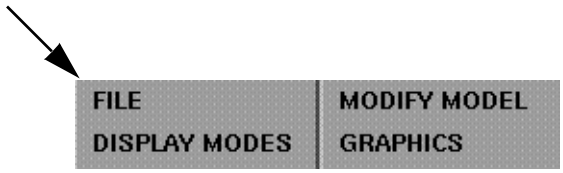
IVI window

- If a plane change is NOT needed go to step 16.

15. Click **[Close]** to exit from the Threshold/VOI window.

NOTE: The images that have threshold applied are NOT saved for future viewing or rotations. Go to the section Rotating the MIP Image for the steps to rotate images and Defining a Batch Projection Series to save your images.

16. If the images do not need saving or filming, exit the IVI window. Select **File > Quit**.



IVI window

In Brief: Modify the Volume of Interest Using Threshold

1. Follow the steps to Select the Image Set.
2. Make the viewport with the 3D MIP primary.
3. Close the remaining viewports.
4. Click on the prescription plane.
5. Select **Modify Model > Threshold/VOI**.
6. Select Threshold Values.
7. Click **[Apply Threshold]** (or **[Undo]** or **[Cancel Identity]** if necessary).
8. If needed, change plane and repeat steps 6-7.
9. Click **[Close]** to exit Threshold/VOI.
10. To rotate images, go to the section Rotating the MIP Image or Defining a Batch Projection Series.
11. Select **File > Quit**.

Modify the Volume of Interest

Modify the Volume of Interest Using Threshold

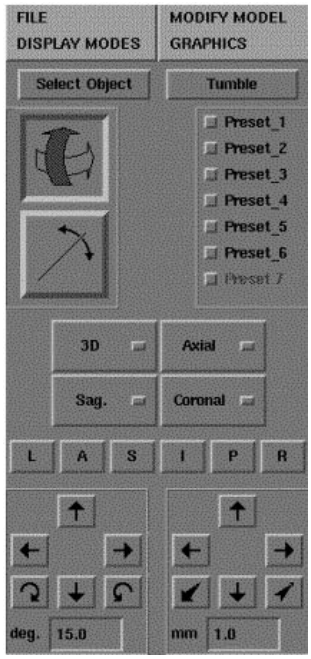
Use threshold to remove undesired structures that differ by signal intensity. Do not use threshold if the signal intensity values do not differ.

The following lists the instructions, step-by-step, to remove unwanted structures from the volume of interest using Threshold.

1. Follow the steps to Select the Image Set, as described previously.
   - Once you click **[IVI]** the images begin to load.

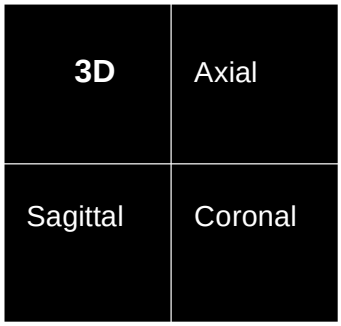
Browser

The IVI window appears.



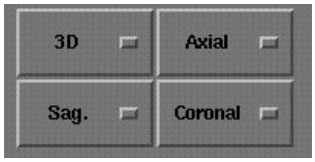
IVI window

2. Click on the 3D viewport to activate it as the primary view.



Viewer Display

3. Close the Axial, Sagittal and Coronal viewports to decrease the processing time. Click Axial, Sagittal, and Coronal **[View Type]** in the middle of the IVI window and drag to No View. Although closing these viewports is optional, you may want to leave them open to use as a reference.



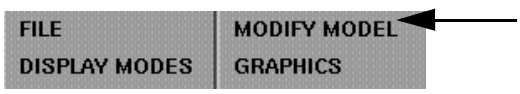
IVI window

4. To change the prescription plane (plane of the IVI image), click **[L, A, S, I, P, S, or R]** on the IVI window. Clicking one of these at any time changes the prescription plane.

IVI window

- **L**=Left View
- **A**=Anterior View
- **S**=Superior View
- **I**=Inferior View
- **P**=Posterior View
- **R**=Right View

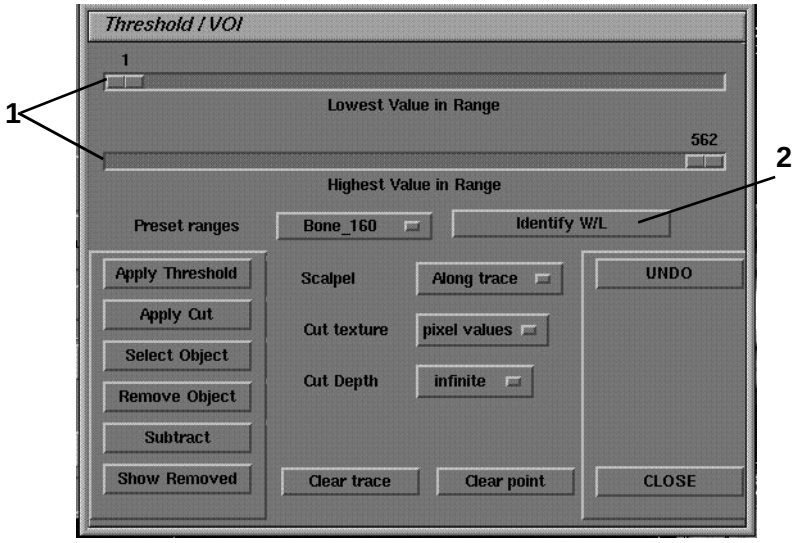
5. Select **Modify Model > Threshold /VOI**.



IVI window

- Hint: Drag the Threshold/VOI window to the upper right hand corner of the viewer.

The Threshold/VOI window appears.

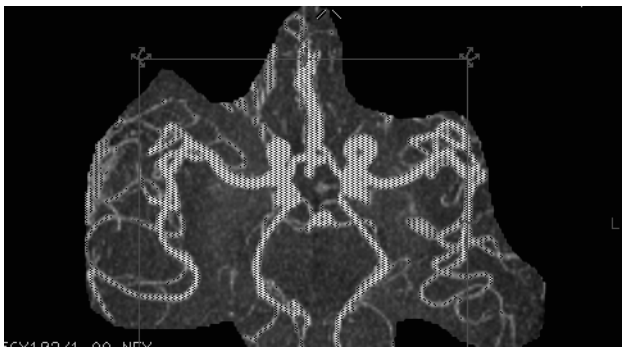


Threshold / VOI window

6. Click and drag on either slider (**1**) at the top portion of the Threshold/VOI window to adjust the threshold range.
   - Or, you can place the cursor to the right or left of the current slider position and click once to change the value by one.

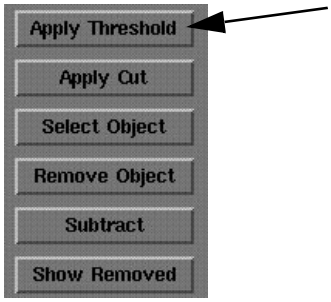
Threshold / VOI window

NOTE: When the Threshold Range adjustment sliders are being moved, the “Identify W/L” (**2**) function is automatically activated, and allows you to visualize, in real-time, the parts of the new object that will be kept. Everything that is green (or hash marked on a Black/White window) remains. Below is an example of an image with the “Identify W/L” function active.



Viewer Display

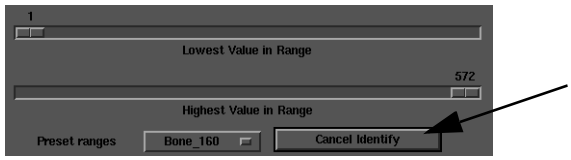
7. Once the new values are set, click **[Apply Threshold]**. The new object is displayed and the **[Identify W/L]** function is automatically turned off.



Threshold / VOI window

- The image may “move” in the Viewer. To correct, place the cursor in the Viewer, right click and drag to **center on Object**.
- Clicking **[Undo]** removes the last threshold applied to the image.

- Click **[Cancel Identify]** removes the shading that was applied to the image using the threshold values. Cancel Identify on the Threshold window and toggles between Cancel Identify and Identify W/L.



Threshold / VOI window

8. If necessary, change the prescription plane (clicking one of the buttons shown below changes the plane) and repeat steps 6-7.

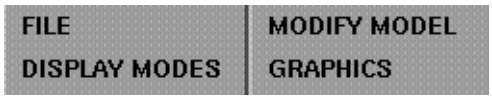
IVI window

- L=Left View
- A=Anterior View
- S=Superior View
- I=Inferior View
- P=Posterior View
- R=Right View

9. Click **[Close]** to exit from the Threshold/VOI window.

NOTE: These images that have the threshold applied are NOT saved for future viewing or rotations. Go to the section Rotating the MIP Image for the steps to rotate images and Defining a Batch Projection Series to save your images.

10. If the images do not need saving or filming, exit the IVI window by selecting **File > Quit**.



IVI window

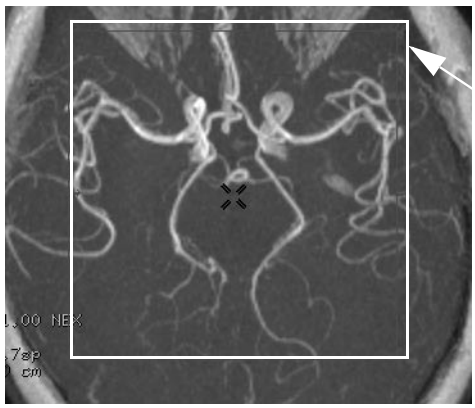
Rotate the MIP Images

Once you have created and modified the MIP image, most times you want to view these images from different angles. There are three different ways in which to rotate the MIP image: Interactive, Explicit, and Batch Projection. This section discusses Interactive and Explicit; Batch Projection is discussed in the next section. Interactive is similar to a “real-time” view and Explicit allows you to program exactly which angles (views) you want.

Something to Think About...

- The time stamp on IVI images correspond to the time of the landmark, not the time the source images were acquired.

1. Have a MIP image displayed in Viewer.
   - If a MIP is not displayed, follow the steps from the previous sections Select the Image Set and Modify the Volume of Interest.
2. To rotate Interactively, click and drag one of the corner points of the “on-screen” trackball (the square box displayed in the viewport).



Viewer Display

- The direction of the drag determines the direction of the rotation.
- Releasing the mouse stops the rotation.
- These images are NOT saved for future review or filming. (Refer to the section Defining a Batch Projection Series for information on saving and filming rotated images.)

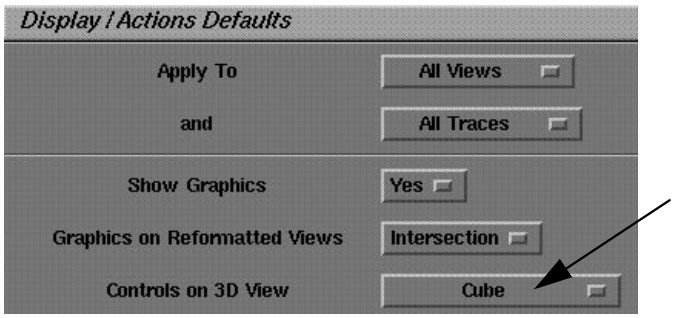
In Brief: Rotate the MIP Image

1. Have a MIP image in Viewer.
2. To rotate Interactively, click and drag on corner of “on-screen trackball.” Stop the drag to stop the rotation.
3. To rotate Explicitly, determine method mm or deg.
4. Enter the values in the appropriate text box of the IVI window.
5. Click arrow in IVI window to rotate.
6. Stop clicking on arrow to stop rotation.
7. Select **File > Quit**.

- Place the cursor in the image, NOT on the “on-screen trackball,” right click and then left-click **[Save Image]** to save this image on the Browser.

NOTE: The larger the data set, the slower the images rotate.

° To change the default for the “on-screen” trackball, select **Display Modes > Display/Action Defaults** and click the button next to the **Controls on 3D View**, to toggle between **Handle** and **Cube**.

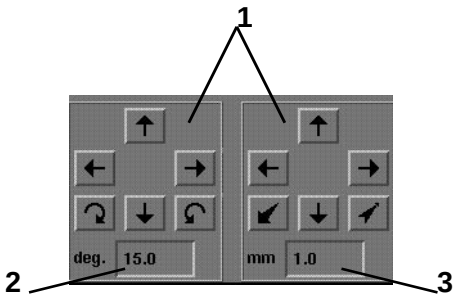


Display Modes / Display / Actions Defaults

° Click and drag the corners of the “on-screen trackball” to rotate with Handle or click and drag the sides of the “on-screen trackball” to rotate with Cube.

° Click **[Close]** to exit from the Display/Actions Defaults window.

3. To rotate Explicitly, first determine the mode: Degrees (deg.) or Millimeters (mm).



IVI window

4. Enter the value in the text box next to deg. (**2**) for the angle of rotation.

- Or, enter the value in the text box next to mm (**3**) for the millimeters of movement.

5. Click the appropriate arrow (**1**) in the direction you want to rotate.
   - Each time the arrow is clicked, the image rotates by the set angle or millimeters.
6. Stop clicking the arrow to stop the rotation.
   - The same number of clicks, on the opposite arrow, brings the image back to its original position.

NOTE: These images are NOT be saved for future viewing or filming. (Refer to the section Defining a Batch Projection Series for information on saving and filming rotated images.)

7. If you do not want to save or film the images, exit the IVI window by selecting **File > Quit**.

IVI window

In Brief: Define a Batch Projection

1. Have MIP image in Viewer.
2. Select **Display Modes > Set batch/Movie loop**.
3. Make the viewport with the MIP image primary.
4. Click **[Rotation]**.
5. Select the arrow for rotation direction.
6. Enter value for **Number of views** or enter value for **Angle between views**.
7. Select the **Output** mode.
8. Click **[Add Protocol]** to save protocol or **[Get Protocol]**.
9. Type in name for protocol, if appropriate.
10. Click **[OK]**.
11. Click **[Apply]**.
12. Set additional parameters.
13. Select **File > Quit**.

Rotate the MIP Images

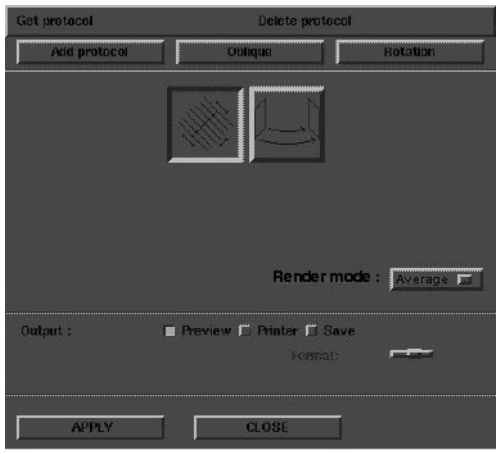
Define a Batch Projection Series

The Batch Projection method allows you view the MIP images rotating in a loop, similar to a movie. You can film, archive and view the images directly from Batch Projection. Also, for additional information about Batch Projection Filming and Movie Loop see the **Reformat** chapter.

1. Have a MIP image displayed in Viewer.
   - If a MIP is not displayed, follow the steps from the previous sections Select the Image Set and Modify the Volume of Interest.
2. From the IVI window, select **Display Modes > Set batch/Movie loop**.

IVI window/Display Modes

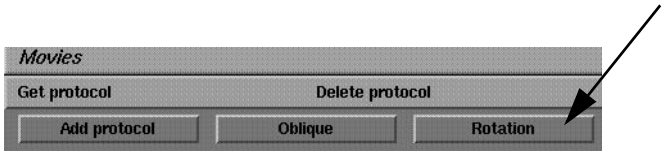
The Movies window appears.



Display Modes/Set batch/Movie loop

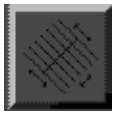
3. Click on a viewport to make it primary.

4. Click **[Rotation]** to view the images in a 180 degree rotation.



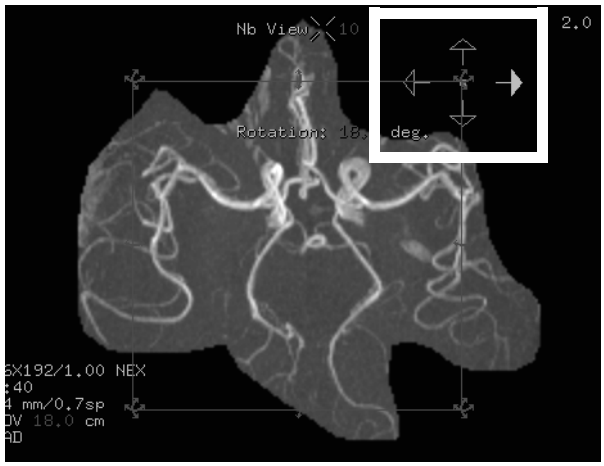
Set Batch / Movie Loop / Movie window

- Check that the **Graphics Rx** icon is selected on the Movies window.



Movies window / Graphics

5. On the viewport, click the arrow pointing in the desired rotation direction.



- The window/level may need to be adjusted to make the arrows visible.

Viewer

6. On the Movies window do one of the following:
   - Enter the number of views in the **Number of views** (**A**) text box and the **Angle between views** automatically adjusts for a 180° rotation.

- Or, enter the degrees of rotation in the **Angle between views** (**B**) text box and the **Number of views** automatically adjusts for a 180° rotation.

Movies window

7. Select one of the following **Output** modes:

Movies window

- Select **Preview** to simply view the images; these images are NOT saved to the Browser.
- Select **Printer** to send the images to the laser printer for film generation. For more detailed information, see the Reformat chapter.
- Select **Save** to send the images to the system disk. These images are saved to the Browser as a separate series and can be viewed, manipulated, and filmed via the Viewer or the Mini Viewer.

NOTE: **Preview** and **Save** CANNOT be selected at the same time.

8. Click **[Add Protocol]**, to save these parameters as a protocol.

Movies window

The Parameter window appears.

9. Type the name desired for this protocol in the text box.

Add Protocol/Parameter window

10. Click **[OK]** to save the protocol and close the Parameter window.

- To access this saved protocol, click **[Get Protocol]** and then click on this protocol.
- Click **[Cancel]** to close the Parameter window without saving the protocol.

Movies window

11. Click **[Apply]**. The system generates the rotational images.

Movies window

12. You can set additional parameters like Loop mode, and display speed during the display.

- Click **[Close]** to exit the Movies window.

13. To exit the IVI window, select **File > Quit**.

IVI window

In Brief: Rotate Using First and Last Image

1. Have a MIP image in Viewer.
2. Select **Display Modes > Set batch/Movie loop**.
3. Select first image for rotation.
4. Make the viewport with the first image primary.
5. Click the **Movie Mode** icon.
6. Click **[First View]**.
7. Choose one method:
   a) Enter value for **Number of views** or enter value for **Angle between views**. OR
   b) Enter value in degree text box and direction (arrow) for rotation.
8. Click **[Final View]**.
9. Select the **Output** mode.
10. Click **[Apply]**.
11. Select **File > Quit**.

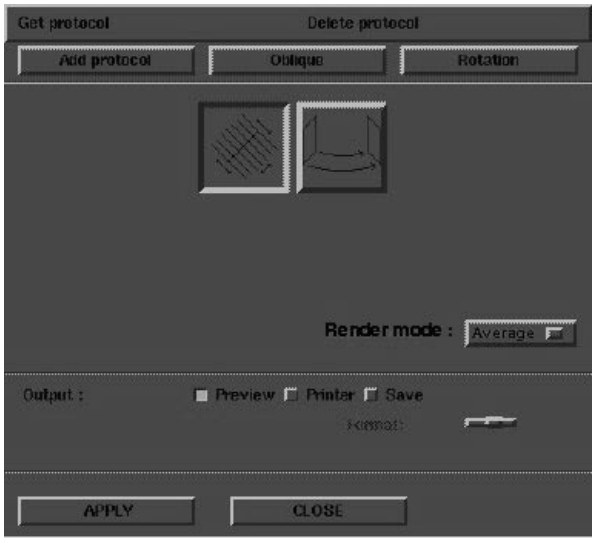
Rotate the MIP Images

Rotate Using First and Last Image

You may want to rotate the MIP images other than 180° as previously described. The following steps describe how to select the first and the last slice for the rotation, and to select specific degrees of rotation allowing for unique customizing of the rotation.

1. Have a MIP image displayed in Viewer.
   - If a MIP is not displayed, follow the steps from the previous sections Select the Image Set and Modify the Volume of Interest.
2. From the IVI window, select **Display Modes > Set batch/Movie loop**.

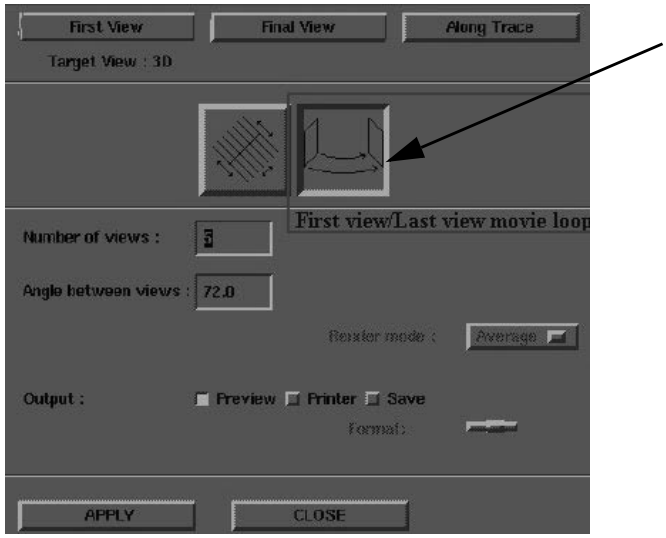
   The Movies window appears.



Display Modes/Set batch/Movie loop

3. Select the image desired as the first image of the rotation.
4. Click on a viewport to make it primary.

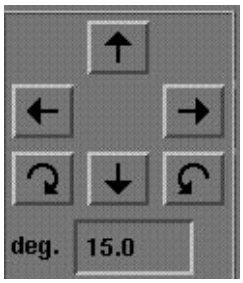
5. Click the **Movie Mode** icon to access the movie functions.



Movie Mode

6. Click **[First View]**.

7. Use one of the following methods to choose the angle of rotation and the number of images in the rotation:
   - Enter a value in either the **Number of views** text box or the **Angle between views** text box. The system automatically calculates the other value so that when the two values multiplied together equal 360°.
   - Select the degree of rotation by entering the desired value in the **degree** text box on the IVI window, and click the **arrow** (from the IVI window) to set the direction of rotation. Continue to click the arrow until you reach the desired last image for rotation.



IVI window

8. Click **[Final View]**.
9. Select one of the following **Output** modes:
   - **Preview** to view the images in rotation on the monitor, these images not saved,
   - **Printer** to print the rotated images, can only be used if an output device is connected to the system, or
   - **Save** to save the rotated images to the Browser.
10. Click **[Apply]** to start the rotation process.
    - If you selected **Preview** and achieved the desired rotation, you must repeat steps nine and ten, select **Save** and select **Apply**, to save these images to the Browser for future viewing and archiving.
    - To change the start location, end location, or rotation of images, repeat steps three through nine.
    - Click **[Close]** to exit the Movie Mode window.
11. To exit the IVI window, select **File > Quit**.

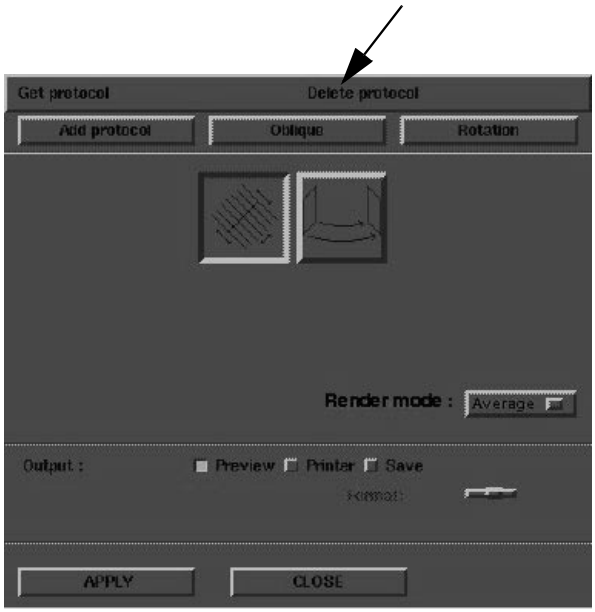
IVI window

NOTE: You can save images individually to the Browser by placing the cursor in the viewport, right-click and then left-click on **Save Image**. This method is useful if you selected the rotation or movement increment from the IVI window (step seven).

Delete an IVI Protocol

As the list of IVI protocols grow, you may wish to delete unused protocols. The following are step-by-step instructions to delete an IVI protocol.

1. Select **Display Modes > Set batch/Movie loop** to open the Movies window.



2. Click **[Delete Protocol]** (see above arrow) to display the list of stored protocols.
3. Select the protocol to be deleted, and a confirmation message apppears.

4. Click **[Yes]** if the correct protocol is named in the confirmation message.
   - Click **[No]** to exit the message window without any deletions.
5. Click **[Close]** to exit the Movies window.
6. Select **File > Quit**, to exit the IVI window.

In Brief: Delete an IVI Protocol

1. Select **Display Modes > Set batch/Movie loop**.
2. Click **[Delete Protocol]**.
3. Select the protocol to be deleted.
4. Click **[Yes]**.
5. Click **[Close]**.
6. Select **File > Quit**.

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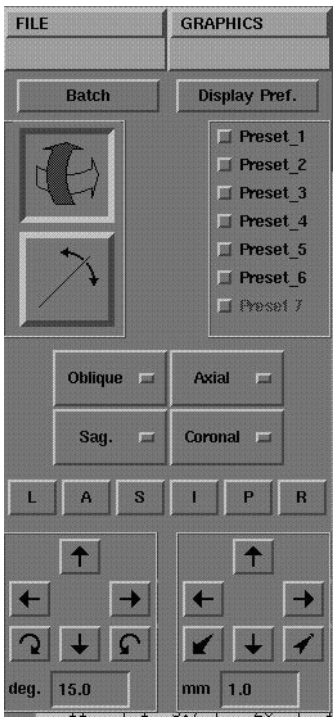
Volume 4

Post-Processing and Analysis

Chapter 6

Reformat

Where Am I?



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Introduction

This chapter explains the reformatting process. The reformat software application is designed to generate reformatted cut planes from the acquired images. It contains the step-by-step instructions to help you learn how to:

- Select the Image Set
- Move the Orthogonal View Locations
- Adjust the Oblique View Angle
- Define an Oblique Batch Series
- Define a Radial Batch Series
- Define a Curve
- Adjust the Plane Thickness and Rendering Mode in MPVR

In addition, this chapter answers the following questions:

1. What types of image sets can be processed with reformat?
2. What types of cursor controls are available?
3. What types of orientation guides are available?
4. What is a curved plane reformat?
5. What is a volume reformat?

About... Reformatting

This section presents the concepts necessary to successfully complete the Multi-planar Reformat and Multi-planar Volume Reformat process. Specifically you need to understand:

- Valid Image Sets
- Series/Image Selection
- Reformat Layout
  - Starting the Reformat Package
  - Plane Orientation Indicator
  - File Menu
  - Graphics Menu
  - Graphics Command Window
  - Tilt/Rotate Mode Select Button
  - Oblique Mode Select Button
  - Windowing Parameter Preset Buttons
  - View Type Buttons
  - Movement/Rotation Increment Buttons
  - Batch Command Window
  - Movie Loop Command Window
  - Previewing Command Window for Film Batch or Movie Loop
  - Identify mm. / Slices Command Window
  - Cursor Annotations Command Window
  - Display Graphics Options Command Window
  - Display Color Window Command
  - Display Film Command Window
  - On View Operations
- MPVR
- Applications for Reformat

Valid Image Set

The Reformat package allows a 2D stack or 3D volume of image data acquired in one plane to be cut and viewed in a different plane.

- For example, image data acquired in the axial plane can be reformatted and viewed in the coronal, sagittal, or oblique plane.

Acquired image data can also be reformatted and viewed along a curved plane or in a thicker plane than the original slice thickness.

It is not possible to perform reformatted cut plane reconstruction on just any set of images available on your MR system. Certain requirements must be fulfilled for the images to be eligible for use by the Reformat Package.

- All images must have the same orthogonal scan plane, image center, and pixel size. Screen saved images are not allowed.
- The range of images selected must not contain two images at the same location, and the inter-slice distance must not exceed 10 mm.
- Isometric voxels and overlapping slices improve the quality of reformat images.

NOTE: The physician is responsible for determining if the maximum inter-slice distance of 10 mm is acceptable for the exam.

The Reformat Package uses the FIRST selected image in the Browser as a basis for using/discarding the other images selected for reconstruction. For example, any images with a different matrix size, slice obliquity or C.T. gantry tilt from that of the first selected image in the Browser are discarded from the reconstruction process.

Something to Think About...

- Reformat selects a viewport with the same image plane (sagittal, axial, oblique, or coronal) that was used to create the protocol. If the protocol was created on a coronal image, it applies to a coronal image, if possible, regardless of which viewport you have selected. For example, assume the protocol was created on a coronal

image. If the you select an axial, sagittal or oblique view port (red line around viewport) and then select [Get Protocol], the protocol applies to a coronal viewport, if there is one available. If there is no coronal viewport available, the protocol applies to the user selected viewport.

- Create the protocol with the same plane that is used during the reformat session.

Series/Image Selection

Select the Display Desktop icon. Before starting the Reformat Package, you must first select the series or set of images (that meet the requirements, listed on the previous page) on the system Browser. You can do this by clicking and dragging over a range of images for multiple images or just clicking on one image for the whole series.

NOTE: If only one image is selected on the Browser, the entire series is used for cut plane reformation.

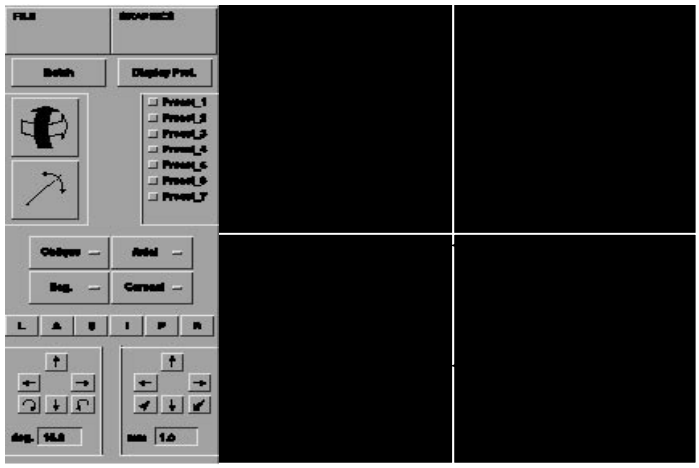
Reformat Layout

Starting the Reformat Package

Once you have selected the desired series or range of images on the Browser, click on the **[Reformat]** button in the Browser. The Reformat main command window with its default four-view display (Oblique, Axial, Sagittal and Coronal) pops up.

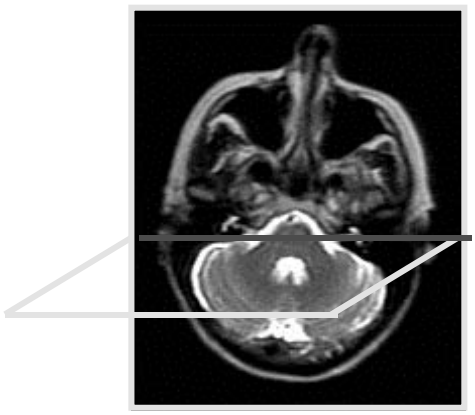
- The oblique reformat view is displayed in the upper-left quadrant.
- An axial reformat view displays in the upper-right quadrant.
- A sagittal reformat view displays in the lower-left quadrant.

- A coronal reformat view displays in the lower-right quadrant.



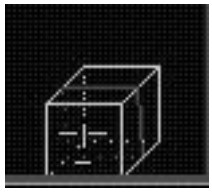
Plane Orientation Indicator

Reformat provides a plane orientation indicator in the lower right corner of each view. The indicator cross-references the reformatted plane to the original (acquisition) plane image.



The oblique plane orientation indicator is located in the lower right corner of a reformatted view during plane trace manipulation. It can be used to help you keep track of the plane trace being rotated or moved, with respect to the patient's body. This indicator consists of a cube with a stylized face including

nose, eyes and mouth. The slice plane is displayed inside the cube.



File Menu

Click left on **[File]**, the following options are displayed:

File Menu

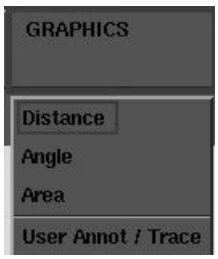
[New Model], allows you to close all windows and return to the Browser to select a new set of images for reformation. Once a new image set is selected, click on **[Load Slices]** and new reformatted images are displayed.

[Film Composer], allows you to call up the Film Composer window to the lower right corner of the monitor.

[Quit], exits the Reformat Package.

Graphics Menu

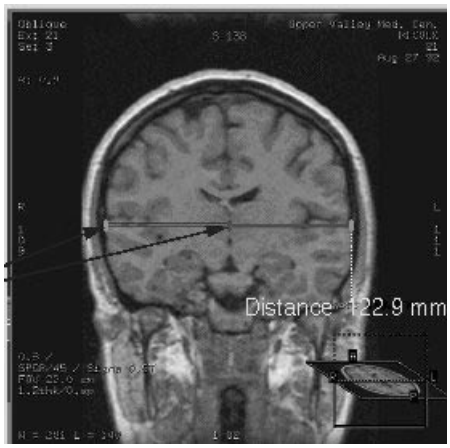
Click on the **[Graphics]** button**,** the following options are displayed:



Graphics Menu

[Distance], allows you to measure the distance along a two point trace. You can read the current Total Length and Last Segment Length of the trace in real time when you have the Graphics Command Window open.

To adjust the length and angle of the distance line, hold down **ALT** on keyboard then Click and drag on any Red or Green anchor then release the mouse at the desired location. Distance in millimeters updates upon mouse release.

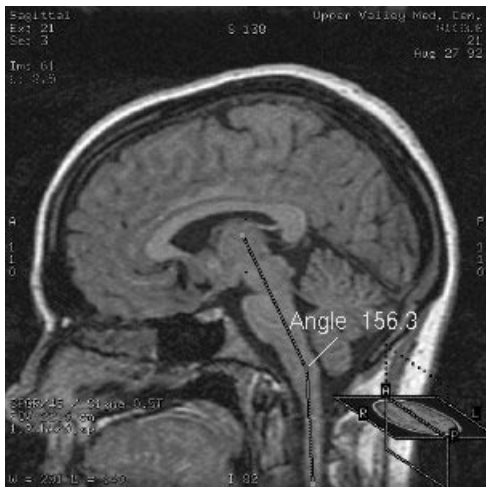


Distance Image

[Angle], results in an open three-point trace (i.e. two segment) appearing in the selected viewport, which you can edit using the various buttons available at the top of the command window.

You can read the Angle between the two segments of the trace in the Graphics command window which opens automatically

To adjust the length and angle of the distance line: Hold down the **ALT** on keyboard then Click and drag on any Red or Green anchor then release the mouse at the desired location.

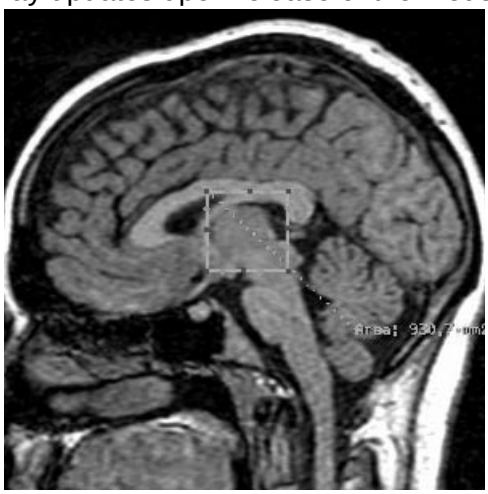


Angle Image

[Area], results in a closed four-point trace (i.e. polygon) appearing on the view which you can edit using the various buttons available at the top of the command window. You can read the Area inside the polygon in real time when you have the Graphics command window open.

To edit an ROI:

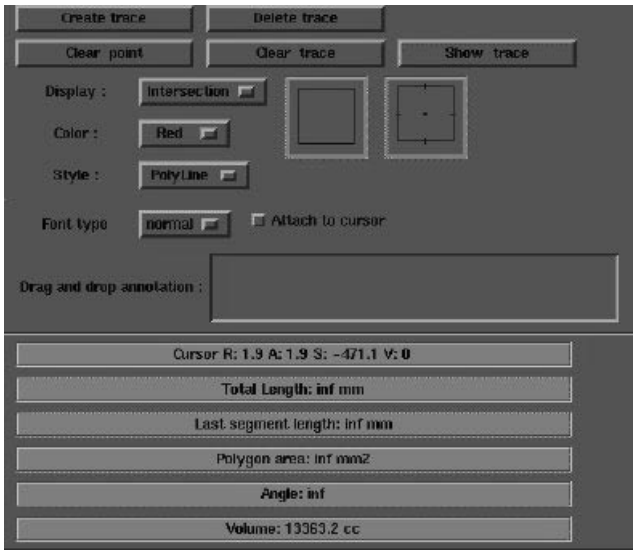
- Position the cursor in the viewport of interest. Press and hold the **ALT** Key.
- Click on any Red or Green anchor and drag it to a desired location.
- Area display updates upon release of the mouse.



Area Image

Graphics Command Window

[User Annot Trace], allows you to enter and edit text annotations via the Graphics command window.



Graphics Command Window

Create trace

This button is used to create a new freehand trace.

- Click left on the **[Create trace]** button. Press **SHIFT** key on keyboard and Click left mouse to create freehand trace.

Delete trace

This button is used to delete the current trace.

- Click on the **[Delete trace]** button.

NOTE: The deleted trace remains visible on unselected views, but disappears the next time the view is selected.

Clear point

This button is used to clear the last entered point from the trace.

- Click on the **[Clear point]** button to clear the last entered point from the trace.

Clear trace

This button is used to clear a new trace.

- Click on the **[Clear trace]** button. You can now create a new trace by pressing the **SHIFT** key and the left mouse button.

Show trace

This button is used to display the last trace when the **[Show Graphics]** button is set to **[No]** in the **[Display/Actions Defaults]** command window and/or if the **[Display]** button in the Graphics command window is set to **[Intersection]** for reformatted views.

- Click on the **[Show trace]** button.

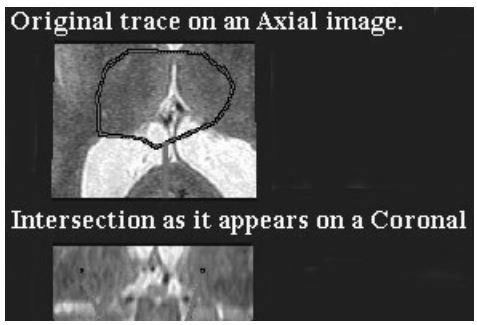
NOTE: This button has no effect if the **[Show Graphics]** button is set to **[Yes]** in the Display/Actions Defaults command window and, for reformatted views, the **[Display]** button in the Graphics command window is set to **[Projection]**.

Display

This button allows you to specify the way you want traces to be displayed on cut-plane views. It is a toggle button between **[Projection]** and **[Intersection]**.

- Choose **[Intersection]** if you want only a part of the traces that intersects the cut-plane to be displayed.
- Choose **[Projection]** if you want the projection of the entire trace to be superimposed on the cut-plane.

An option that displays an entire or partial trace on all viewports, except the viewport the original ROI was traced on.

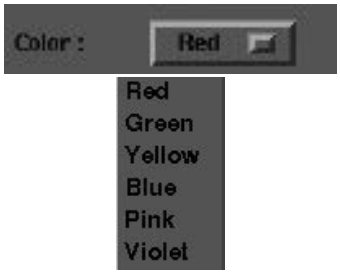


Intersection and Projection Image

Color

This button is used to change the color of the current trace.

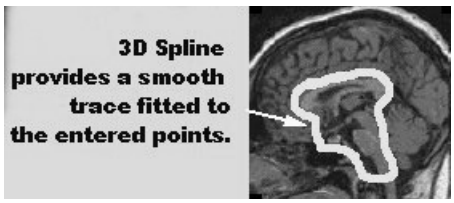
- Click on the **[Color]** button and select the desired color from the menu that pops up.



Style

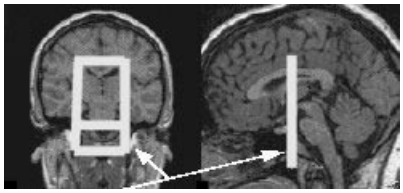
This button is used to choose different styles for the current trace, **[Polyline]**, **[3D Spline]**, **[2D Spline**] and **[Cylinder]**. Click on the **[Style]** button and select the desired trace style option from the menu that pops up by clicking again on it.

Polyline Image



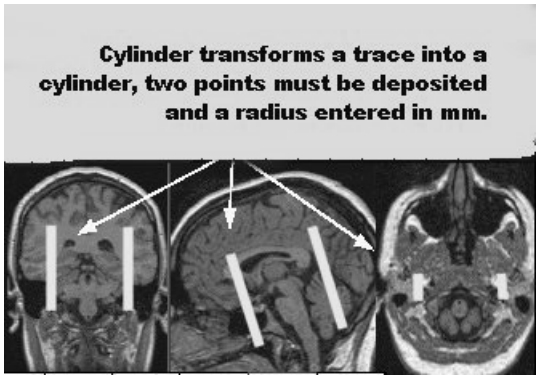
3D Spline Image

NOTE: Do not define too many points when using **[3D Spline]** style to avoid unpredictable behavior of the spline function.



2D Spline Image

[2D Spline] displays a smooth trace on reformatted slices. A Trans field width of the trace may be displayed on views other than the viewport the original trace was drawn on. The width of the trace is user dependent and selected from a pop-up menu.



Cylinder Image

Trace edit box

This box enables selecting a trace for editing.

- Click and hold left on the box, drag it to the desired trace on the image view and drop it.

Trace rotation and translation box

This box is used to rotate and translate a trace.

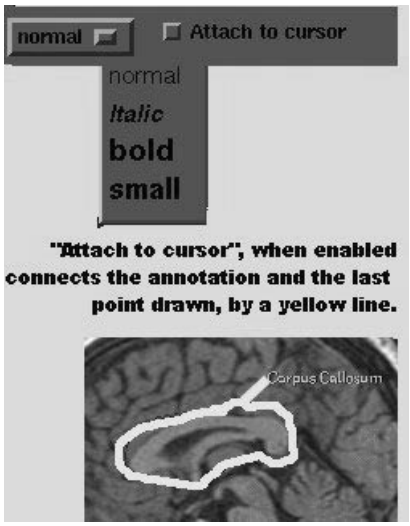
- Click and hold left on the box, drag it to the desired trace and drop it.
- A box with control handles (i.e. points) appears around the trace. Click and hold left on the center handle and drag to

translate the trace or click and hold left on the handles at the corners of the box and drag to rotate the trace.

Font type / Attach to Cursor

This button is used to choose the font type for annotations. The attach to cursor attaches the annotation to the trace with a yellow line.

- Click on the **[Font type]** button and select the desired font type **[normal]**, **[italic]**, **[bold]**, or **[small]** from the menu that pops up.



Attach to Cursor Image

- Click to activate the **[Attach to cursor]** button and again to deactivate it.

Drag and drop annotation

This text box is used to enter text for annotation anywhere on the view.

- Move the mouse pointer into the drag and drop annotation text box and enter the desired annotation text from the keyboard.
- Click/Hold on the text, drag to the approximate desired location on the viewport and release. The annotation appears on the view.
- To remove an annotation, Click/Hold on the annotation, drag off the view and release.

Cursor position display

This display provides the 3D cursor position and the associated voxel intensity in real time. The R, A, S and V values correspond to the **R**ight, **A**nterior, and **S**uperior cursor coordinates in mm, and the **V**oxel intensity, respectively.

Total Length display

This display provides the total trace length.

Last segment length display

This display provides the length of the last trace segment entered.

- Measurement accuracy is equal to the displayed length value + / - inter-slice distance.

Polygon area display

This display provides the area of the polygon defined by the trace. The area is calculated by projecting the trace onto the plane of the screen.

- If the trace endpoints are not connected, this area value is calculated as if a segment were joining the two trace endpoints.

- Measurement accuracy is equal to the displayed area value + / - (inter-slice distance)^2.

Angle display

This display provides the angle between two adjacent segments of the trace. The angle is always measured between the last two trace segments entered.

- The angle being measured is indicated on the trace by a small arc between the two segments.
- Measurement accuracy is equal to the displayed segments which are five times larger than the inter-slice distance. The accuracy improves with the length of the segments.

Volume display

This display provides the total volume of the 3D object. Following is a list of various factors to be considered to appreciate the accuracy of the volume measurement:

- Measurement accuracy is equal + / - the volume of the border layer.
- Measurement error is due to partial volume effects of the voxels making up the 3D object.
- The smoother the object the better the accuracy.
- The higher the image resolution (512 x 512 pixels as opposed to 256 x 256 pixels) the better the accuracy.
- The larger the object the better the accuracy. For example, if the volume measurement on a cube-shaped object displayed with a resolution of 256 x 256 pixels reads 1cm^3 , its true volume is between 0.729 and 1.342 cm^3 (-27.1%/+34.2%) whereas if the volume measurement on a cube-shaped object displayed with the same resolution reads 1000 cm^3, its true volume is between 970.3 and 1030.3 cm^3 (2.97%/+3.03%).

Measurement annotations

The Cursor, Total Length, Last segment length, Polygon area, Angle displays and Volume displays described in the paragraphs above can all be represented as moveable,

real-time updated, on-view annotations, attached to the trace by a “rubber band.” To do this:

- Click/Hold on the desired display, drag to the approximate desired location on the view and release. The measurement annotation appears on the view.
- Click/Hold on the measurement annotation and drag it to the exact desired location and release.
- To remove a measurement annotation, Click/Hold on it, drag off the view and release.

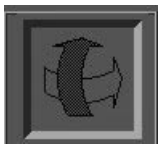
Close button

This button is used to close the Graphics command window.

- Click on the **[Close]** button to close the Graphics command menu.

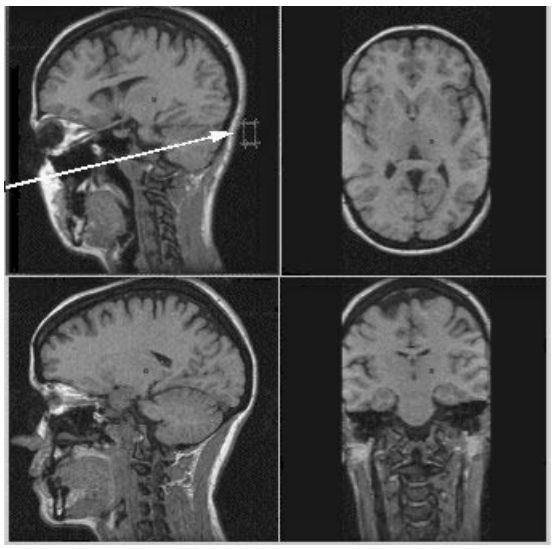
Tilt/Rotate Mode Select Button

Click left on the **[Tilt/Rotate Mode Select]** button, the mouse can be used to tilt and rotate the image via the on-screen trackball which appears on the oblique view when the Rotate icon is selected. The onscreen trackball cursor (red cube) can be used to rotate the oblique view by clicking and dragging on one of the four corner handles.



Tilt/Rotate Mode Button

The red dot cursor icon attaches to a pixel that may be represented in all 3 planes. The Oblique viewport may be rotated with the rotation handles.



Tilt/Rotate Mode Images

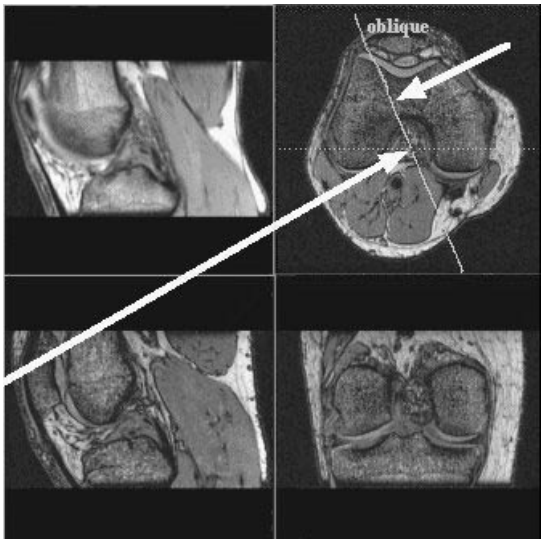
NOTE: Only the **[Tilt/Rotate Mode Select]** button OR the **[Oblique Mode Select]** button can be activated at a given moment.

Oblique Mode Select button

Click on the **[Oblique Mode Select]** button, the mouse can be used to move and rotate plane traces of reformatted views (oblique or baseline reformatted) on all views except curved, histogram, cross section or profile views.

Oblique Mode Button

Click on the red dot to move vertical, horizontal, and oblique reference lines. All viewports updates. Click on the solid yellow oblique line to change oblique viewport only.



Oblique Mode Images

NOTE: Only the **[Tilt/Rotate Mode Select]** button OR the **[Oblique Mode Select]** button can be activated at a given moment.

Windowing Parameter Preset buttons

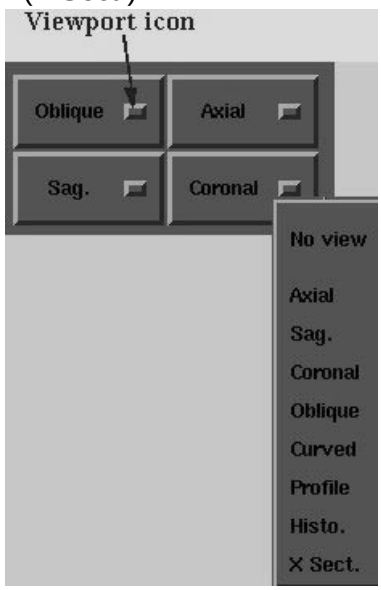
When you click left on one of the **[Windowing Parameter Preset]** buttons, or simply on the title next to it, the windowing parameters of the selected view(s) are set accordingly.

Presets

Preset Window / Levels may be set to the site preference. To change the Title and W/L values go to the Main viewer and open the User Prefs menu.

View Type buttons

Click on one of the four **[View Type]** buttons, a list of view type options appears. To activate viewport options, click on any viewport icon and make a selection from the pop-up menu. Orthogonal planes of Axial, Sagittal, and Coronal display, as well as the option of Oblique, Curved, Profile, Histogram (Histo) and Cross section (X Sect.).



Viewport Button Icons

[No View]

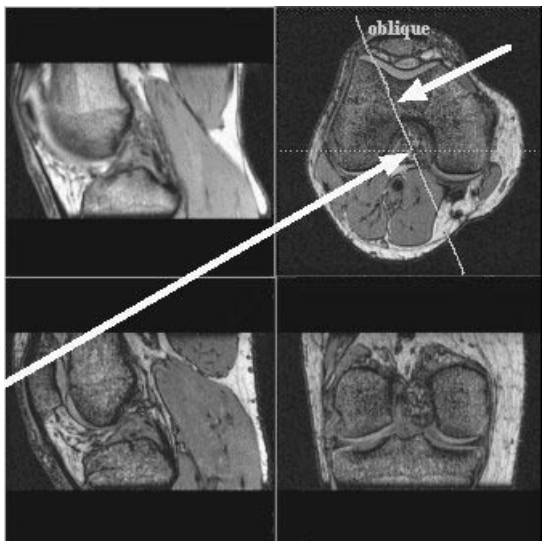
Selecting the **[No View]** , causes the corresponding viewport to disappear.

[Axial], [Sag], [Coronal]

Select one of these view types, and the corresponding views appear in that viewport.

[Oblique]

[Oblique] reformat allows the user to manipulate the oblique image in any position using the rotation handles, directional arrows, or viewplane buttons. To enable Oblique Reformation, an Oblique viewport must be opened.

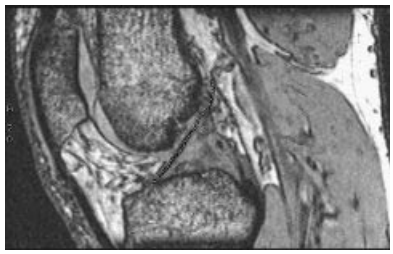


Oblique Reformatted Images

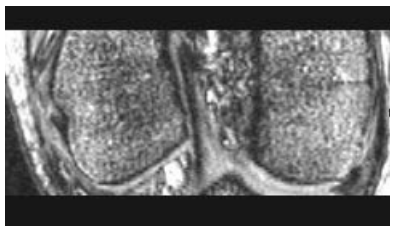
[Curved]

[Curved] reformat allows the user to trace a line, on an orthogonal image. This line may be in any direction or on any slice. An image is then created from that trace. To enable Curved Reformation, a Curved viewport must be opened. Press

the **SHIFT** key and click to deposit points along a line of interest. The curved viewport updates in real time.



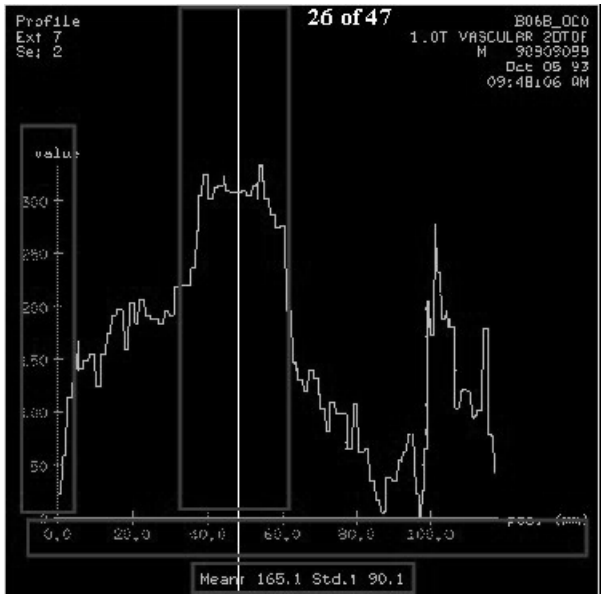
Curved Reformat Sagittal Viewport



Curved Viewport Outcome

[Profile]

A **[Profile]** view provides a gray scale along a trace.



Profile View

The profile displays the intensities of the pixels along the trace that you created.

The horizontal axis indicates the position in millimeters along the trace.

The vertical axis is the pixel intensity value of that position.

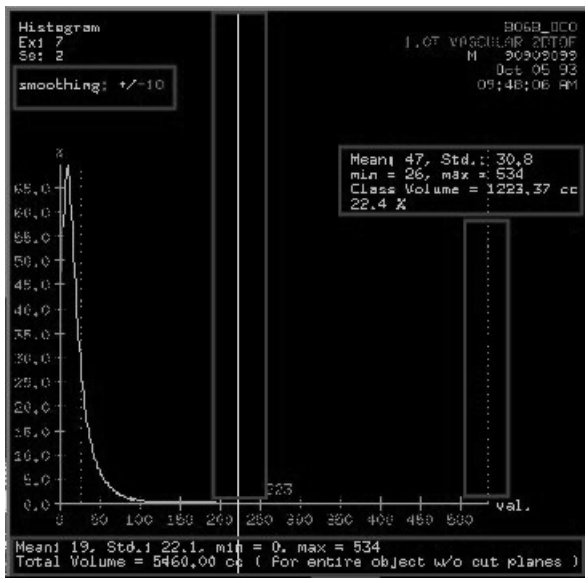
Mean is the average pixel intensity value along the trace.

Std. is the standard deviation of pixel intensity values along the trace.

The pixel intensity reference line provides a correspondence between the 3D cursor position along the trace.

[Histogram]

A volume **[Histogram]** view provides voxel intensity values, total object volume, and percentage of occurrence of each voxel intensity value in an object.



Histogram Screen

Smoothing annotation changes the vertical axis values and creates a smoothing effect on the histogram curve. The percentage of occurrence values are averaged and are attributed to the voxel intensity point.

- To change the value, move the mouse to the annotation value on the view (number are in red next to smoothing).
  - ° Click right to reduce the value by one, click left to increase the value by one, or click middle mouse and drag to change values.

The voxel volume information is for the object within the primary view only. The tolerance for error in the Total Volume

measurement is directly proportional to the surface area of the object.

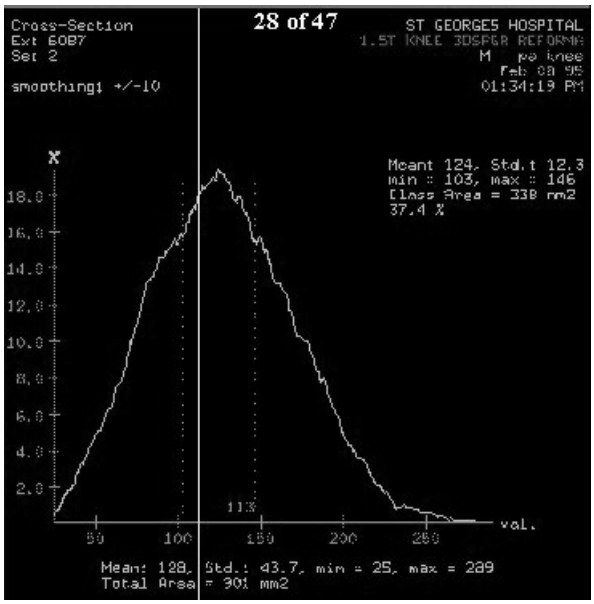
The Class Volume provides information about the Mean, Std. deviation, Minimum and Maximum pixel range, Volume in cc's, and percentage of occurrence of pixels within the boundary (green dotted) lines.

The voxel reference line position corresponds to the intensity of the voxel at the 3D cursor location in the object.

- To change the line position:
  - Either drag the line to the desired location, or press and hold the **SHIFT** key and Click/Drag the mouse left or right.

[X-Sect.]

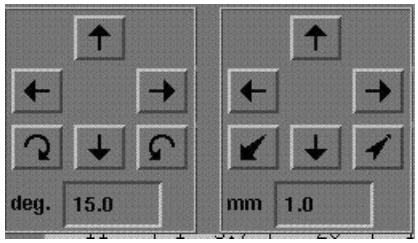
A cross-section Histogram view provides a percentage of occurrence of each pixel intensity value. In a user-defined area on a reformatted slice, pixel statistic values and area information is provided.



Cross-Section Histogram

Movement/Rotation Increment buttons

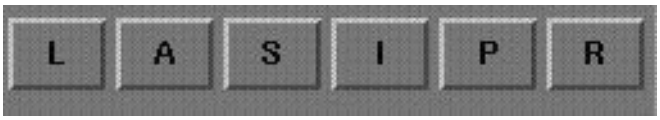
Click on one of the **[Movement/Rotation Increment]** buttons (one of the six buttons marked with an arrow), the selected view(s) rotate or the 3D cursor moves in the direction indicated by the arrow on the button. Rotation is possible only on a 3D or Oblique view.



- The increment size in deg. or mm. can be changed by moving the mouse pointer onto this text box, deleting the existing value by pressing the Backspace key, and entering the desired increment value from the keyboard.

Located directly above the increment rotation buttons is another way to manipulate and move the images to a desired plane.

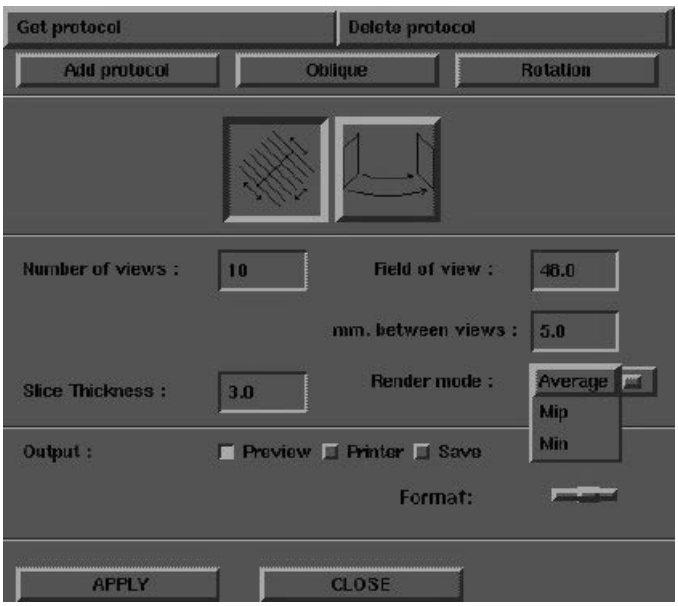
- L = Left or sagittal
- A = Anterior or coronal
- S = Superior
- I = Inferior or axial
- P = Posterior
- R = Right



Batch Command Window

This window is accessed via **[Batch]**. The Batch Filming/Movie Loop command window is used to set up one of the following:

- A film batch consisting of a sequence of oblique images.
- A “movie” loop on reformatted images.

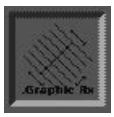


Set Batch/Movie Loop Command Window

[Batch filming mode]

The batch filming mode allows you to do several reformations at once, across the area of interest.

- Click on the **[Graphic Rx]** button in the Batch Filming/Movie Loop command window.



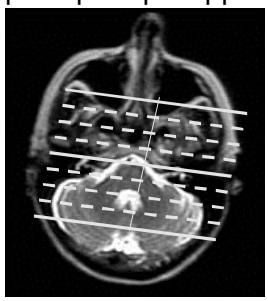
The buttons and parameters found in this command window during batch filming are described below:

Get Protocol

This menu allows the user to call up a previously stored set of batch filming prescription parameters for use or modification.

- Click on **[Get Protocol]** to open a list of available batch filming protocols and select one by clicking left on it.

The Batch Filming/Movie Loop command window now shows the parameters from the selected protocol and the corresponding prescription prompts appear on the primary view.



Delete Protocol

Delete protocol

This menu allows you to delete a previously stored set of batch filming prescription parameters.

- Click on **[Delete Protocol]** to open the list of available protocols.
- Select the protocol to be deleted by clicking on it.
- A small window pops up asking if you are sure you want to delete the protocol. Click on **[Yes]** to delete the protocol and click on **[No]** to cancel the delete operation.

Add Protocol

Add protocol

This button saves the current set of batch filming prescription parameters for future direct use via the **[Get Protocol]** menu.

- Click on the **[Add Protocol]** button.
- Type the desired name of the protocol in the small window that pops up.
- Click on **[OK]** (or press **ENTER**) to confirm saving of the protocol or on **[Cancel]** to abandon.

NOTE: The position and orientation of the prescription prompts on the view are saved in a protocol. This means when a protocol is later selected for use via the **[Get Protocol]** menu, the prescription prompts appears on the view in the same position with the same orientation. At that point, they can be either used directly or moved and oriented as desired.

Oblique

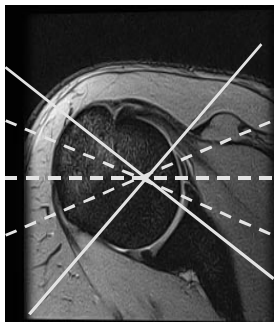
This button is used to prescribe a series of parallel oblique slices for batch filming.

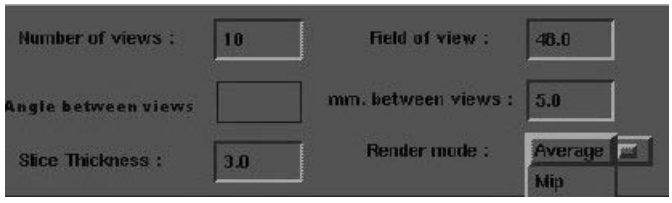
- Click on this button to select this prescription mode.
  - The parallel oblique prescription prompts appear on the primary view and the parameters that are specific to parallel oblique prescription become visible in the Batch Filming/Movie Loop command window.

Rotation

This button is used to prescribe a radial oblique batch on a primary axial, sagittal, coronal or oblique view.

- Click on this button to select this prescription mode.
  - The radial oblique prescription prompts appear on the primary view and the parameters that are specific to radial oblique prescription become visible in the Batch Filming/Movie Loop Command Window.





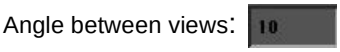
Number of Views

This text box is used to set the number of views (i.e. oblique slices) in the batch prescription.

- Move the mouse pointer into this text box, and delete the existing value by pressing the **BACKSPACE** key once for each digit to be deleted.
- Enter the desired number of views from the keyboard and press **ENTER**.

NOTE: For a parallel or (radial) oblique prescription, the number of cross-reference marks, the value of the Spacing (Rotation) annotation, the mm. between views (angle between views) text box are updated according to the value entered.

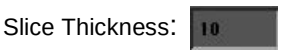
Angle between views text box (radial oblique prescriptions only)



This text box is used to set the rotation angle between views in a radial oblique prescription.

- Move the mouse pointer into this text box, and delete the existing value by pressing the **BACKSPACE** key once for each digit to be deleted.
- Enter the desired rotation angle, in degrees, from the keyboard and press **ENTER**.

Slice Thickness text box (parallel oblique prescriptions)



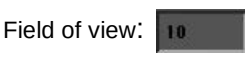
This text box is used, in an oblique prescription, to create oblique slices of a desired thickness.

- Move the mouse pointer into this text box, and delete the existing value by pressing the **BACKSPACE** key once for each digit to be deleted.
- Enter the desired slice thickness in mm, from the keyboard and press **ENTER**.

NOTE: To obtain the minimum slice thickness just enter zero.

If slice thickness is equal to two or more voxels, the **[Render mode]** button is activated. Select which rendering mode to be used on the slices. See “Render Mode Button” section.

Field of view



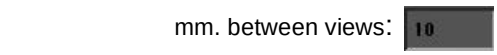
This text box is used to set the desired field of view for the batch being prescribed.

- Move the mouse pointer into this text box, and delete the existing value by pressing the **BACKSPACE** key once for each digit to be deleted.
- Enter the desired field of view value, in mm from the keyboard and press **ENTER**.

NOTE: A small field of view value effectively “zooms in” on the center of each prescribed image, whereas a high value “zooms out.”

NOTE: To facilitate subsequent on-film measurements, you may want to set the field of view to a value which is a simple, multiple or sub-multiple of the resulting image size on the film.

mm. between views text box (Parallel oblique prescriptions only)



This text box is used, in a parallel oblique prescription, to set the spacing between the slices in the prescription.

- Move the mouse pointer into this text box, delete the existing value by pressing the **BACKSPACE** key once for each digit to be deleted.
- Enter the desired distance, in mm, between slices and press **ENTER.**

NOTE: The spacing between the cross-reference marks, the value of the Spacing annotation and the Number of views text box are updated according to the value entered.

Render mode button (Oblique prescriptions - parallel and radial with thick slices only)

This button is used to set the rendering mode used to produce oblique slices when the Slice Thickness is set to a value corresponding to two or more voxels.

- Click/Hold on this button and select one of the options from the pull-down menu.
  - **[Average]** provides the average pixel intensity value of the slice taken along lines perpendicular to it.

- ° **[MIP]** provides the maximum pixel intensity value of the slice taken along lines perpendicular to it.
- ° **[Min]** provides the minimum pixel intensity value of the slice taken along lines perpendicular to it.

NOTE: The **[Render mode]** button is disabled when slice thickness is less than two voxels.

Output select buttons

These buttons are used to select the destination of the batch.

[Preview] is used to view the batch sequence on the monitor. No film output is generated. Its use excludes the use of the **[Printer]** and **[Save]** options. See “Previewing a film batch or movie loop” for more details about using this mode.

[Printer] is used to send the batch to the laser imager for film generation.

[Save] is used to store the batch in the data base. The batch subsequently appears in the Browser window as a new, separate series which can be viewed and manipulated via the Viewer or Mini Viewer application.

- Click on the desired button.
- Click on **[Apply]** to confirm the selection.

NOTE: The **[Printer]** button can only be activated if a hard copy output device is connected to the System.

Format

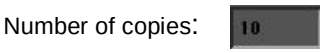
Click on this button to select the format for printing.

- Select Printer from the output select buttons to enable the **[Format]** button.
- Click on the **[Format]** button. A list of film formats appears for the batch.
  - ° The selected format (no. of rows x no. of columns), appears on the surface of the **[Format]** button.

NOTE: The list of available formats depends on the type of laser imager being used.

NOTE: The **[Format]** button is disabled when the **[Printer]** Output select button is not enabled.

Number of copies



This text box allows you to enter the number of copies of film you want. This text box is available only when the **[Printer]** Output select button is enabled.

- Move the mouse pointer into this text box, and delete the existing value by pressing the **BACKSPACE** key once for each digit to be deleted.
- Enter the desired number of copies from the keyboard and press **ENTER**.

Apply

This button is used to launch batch generation.

- Click on this button to launch batch generation.

NOTE: The batch is sent to the monitor, laser imager or data base depending on the choice of **[Output select]** buttons. (See Output select buttons for more information).

Close

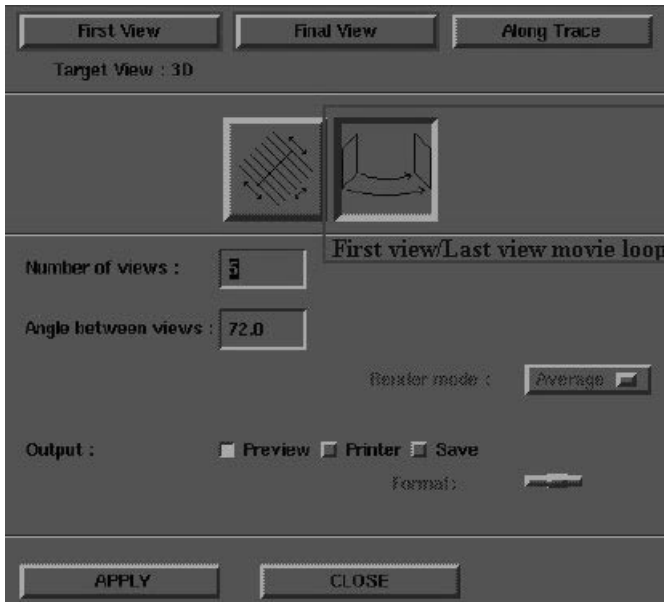
This button is used to close the Batch Filming/Movie Loop Command Window.

Click on the **[Close]** button to close the Batch Filming/Movie Loop Command Window.

Movie Loop Command Window

To set the Batch Filming/Movie Loop Command Window to the movie loop mode, click on the **[Movie Mode]** button.

The window appears as shown below.



Batch Movie / Loop Command Window

The various buttons and parameters in this command window during movie looping are described below.

First View

This button allows you to specify the first view to be used in the movie loop.

- Move and/or rotate the primary view to the desired first position using the viewplane buttons, directional arrows, or the on-screen rotational handles.
- Click on the **[First View]** button to enter the first view. The name of the first view appears on the upper left corner of the Batch Filming / Movie Loop Command Window; and the parameters that are specific to that

view type become visible in the Batch Filming / Movie Loop Command Window.

Final View

This button allows you to specify the final view to be used in the movie loop.

- Move and/or rotate the primary view to the final position.
- Click on the **[Final View]** button to enter the final view.

Number of views and Angle between views

These text boxes are used to specify either a desired number of images or an angle step size (or a distance step size for reformatted slices) between images.

- Move the mouse pointer into this text box, and delete the existing value by pressing the **BACKSPACE** key once for each digit to be deleted.
- Enter either the number of images (minimum possible number of images is five) or the angle step size in degrees (or distance step size in mm for reformatted slices) from the keyboard.

NOTE: The Angles between views text box appears only if the primary view is an oblique image.

Along Trace

This button allows you to generate a movie sequence of oblique slices along a trace. The use of this function is given below.

- Enter the desired trace in the usual way by pressing the **SHIFT** key and clicking on left mouse button.
- Select the oblique slice as primary view.
- Click on the **[Along Trace]** button.
- Click on **[Apply]** to execute the Movie Loop along the trace.

NOTE: To obtain a sequence of slices perpendicular to the trace, activate the cursor lock via: **[Display Pref]** > **[Cursor/Annot Tab] > [Cursor] > [Lock to Trace]** otherwise all slices are parallel to the slice defined via the **[First View]** button.

Output select buttons

These buttons are used to select the destination of the movie loop.

[Preview] is used to view the movie sequence on the monitor. No film output is generated. Its use excludes the use of the **[Printer]** and **[Save]** options. (See Previewing Command Window for Film Batch or Movie Loop for more details about using this mode).

[Printer] is used to send the batch to the laser imager for film generation.

[Save] is used to store the movie loop in the data base. The movie loop subsequently appears in the Browser window as a new, separate series which can be viewed and manipulated via the Viewer or Mini Viewer application.

- Click on the desired button.
- Click on **[Apply]** to confirm the selection.

NOTE: The **[Printer]** button can only be activated if a hard copy output device is connected to the System.

Format

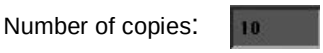
Click on this button to select the format for printing.

- Select Printer from the output select buttons to enable the **[Format]** button.
- Click on the **[Format]** button. A list of film formats appears for the batch.
    - The selected format (no. of rows x no. of columns), appears on the surface of the **[Format]** button.

NOTE: The list of available formats depends on the type of laser imager being used.

NOTE: The **[Format]** button is disabled when the **[Printer]** Output select button is not enabled.

Number of copies



This text box allows you to enter the number of copies of film you want. This text box is available only when the **[Printer]** Output select button is enabled.

- Move the mouse pointer into this text box, and delete the existing value by pressing the **BACKSPACE** key once for each digit to be deleted.
- Enter the desired number of copies from the keyboard and press **ENTER**.

Apply

This button is used to launch movie loop generation.

- Click on this button to launch movie loop generation.

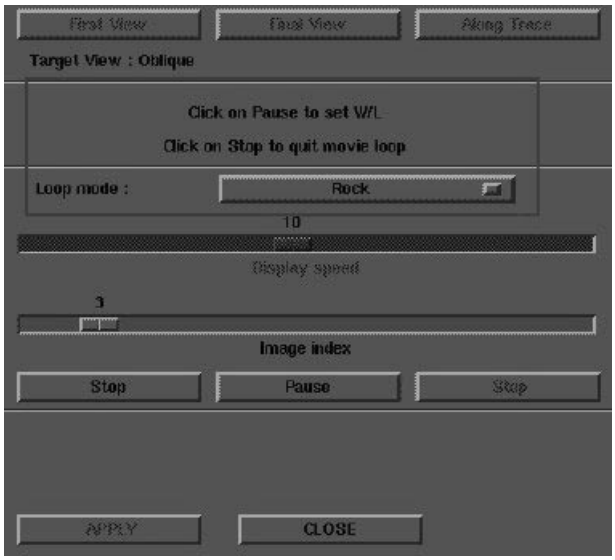
NOTE: The movie loop is sent to the monitor, laser imager or data base depending on the choice of **[Output select]** buttons. See “Output select buttons.”

Close

This button is used to close the Batch Filming/Movie Loop Command Window.

Click on the **[Close]** button to close the Batch Filming/Movie Loop Command Window.

Previewing Command Window for Film Batch or Movie Loop



Preview Command Window

When a movie loop or film batch is set up, the **[Preview]** button is activated and **[Apply]** button clicked on to launch it on-screen, the Batch Filming / Movie Loop Command Window appears as shown above.

The various buttons and parameters in this command window are described in the following pages:

Loop Mode

The **[Loop mode]** button allows the user to choose between two different preview loop display modes. This button is a toggle that goes between loop and rock.

The **[Loop]** mode is used for continuous forward display of the preview loop; when the last frame in the loop is reached the loop continues directly back to the first frame.

- Example: 1,2,3,4 1,2,3,4

The **[Rock]** mode is an alternating forward and reverse mode; when the last frame in the loop is reached, the preview loop goes in reverse until the first frame is reached, then the loop goes forward again, and so on.

- Example: 1,2,3,4,3,2,1

Display Speed

The Display speed slider allows you to adjust the preview loop frame rate.

- Hold left on the **[Display speed]** slider and drag left or right to obtain the desired display speed.

Or

- Place the mouse pointer to the right of the current slider position and click to increase the value by one, or place the mouse pointer to the left of the current slider position and click to decrease the value by one.

Image index

The image index slider allows you to freeze the preview loop and go to a desired frame in the loop.

- Place the mouse pointer to the right of the current slider position and click to increase the value by one, or place the mouse pointer to the left of the current slider position and click to decrease the value by one.

Stop

This button allows you to exit the Preview Display Mode and return to the normal Batch Filming / Movie Loop Command Window.

- Click on the **[Stop]** button to exit the Preview Display Mode and return to the normal Batch Filming / Movie Loop Command Window.

Pause / Restart

This button allows you to freeze the preview loop during viewing. This button is a toggle button that goes between Pause and Restart.

- Click on the **[Pause]** button to freeze the preview loop during viewing. The button becomes the **[Restart]** button.
- Click on the **[Restart]** button to continue displaying the preview loop. The button again becomes the **[Pause]** button.

Step

This button allows you to advance a frozen Preview Loop by one frame.

- Click on the **[Step]** button to advance a frozen Preview Loop by one frame.

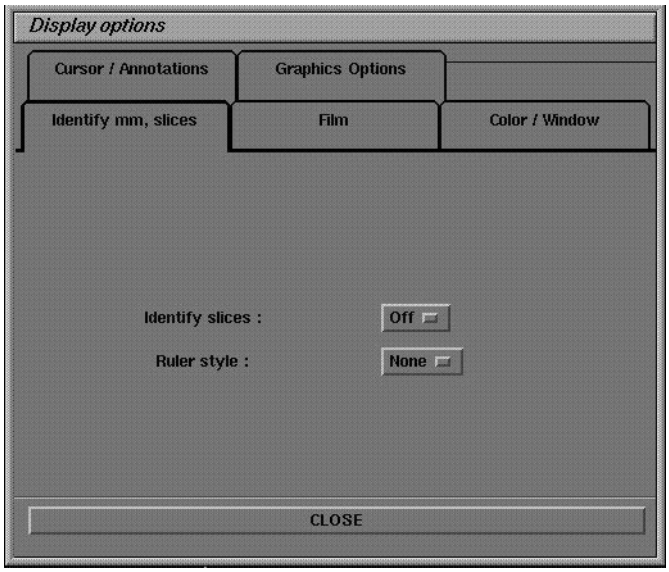
Close

This button is used to close the Batch Filming / Movie Loop command window.

- Click on the **[Close]** button to close the Batch Filming / Movie Loop Command Window.

Identify mm. / Slices Command Window

Access this window via: **[Display Pref.] > [Identify mm. / Slices]**



Identify mm. / Slices Command Window

The **[Identify mm. / Slices]** Command Window is used to set up slice cross reference markings and/or a graduated ruler scale on the view.

The buttons and parameters in this Command Window are described in the following pages.

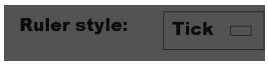
Identify slices

This toggle button allows you to turn slice cross reference markings on and off.

- Click on the **[Identify slices]** button and select **[On]** or **[Off]** from the menu that pops up.

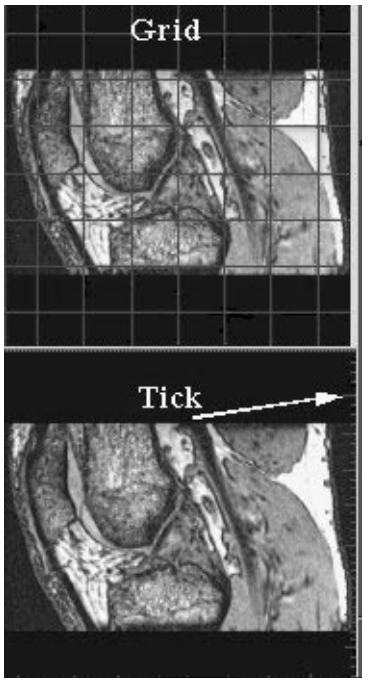
NOTE: Cross reference markings can only be visible if the original slices cut the view along a horizontal or vertical line.

Ruler style



This button sets the ruler style to one of three choices:

None, Tick or Grid.



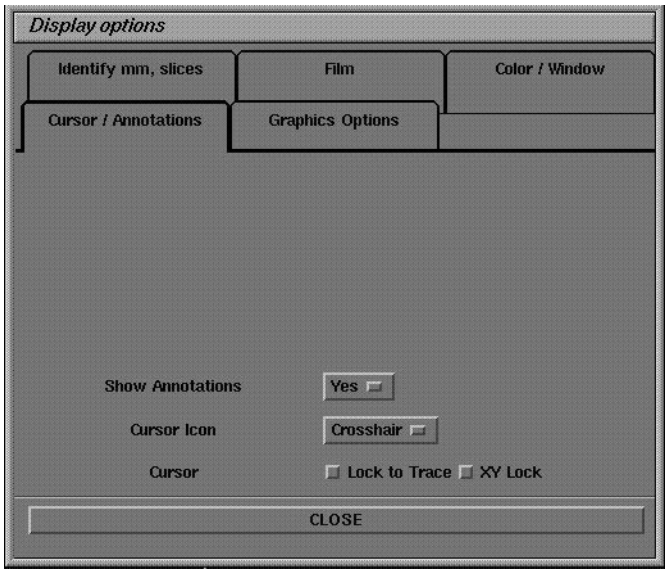
- Select a view as primary view and click on the **[Ruler style]** button and select the desired choice from the menu that pops up.
- Choose **[None]** for no ruler on the view, **[Grid]** for a grid on the entire view, or **[Tick]** for tick marks along the side of the view.

Close

This button is used to close the Identify mm./Slices Command Window.

Cursor / Annotations Command Window

Access via: **[Display Pref.]** > **[Cursor / Annotations]**



Cursor / Annotations Command Window

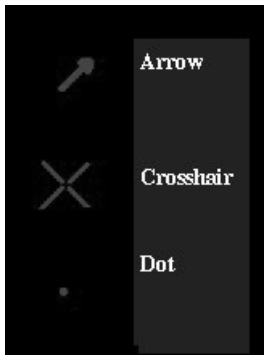
Show Annotations

This button allows you to specify whether or not all annotation is visible on all views.

- Click on the **[Show Annotations]** button and select **[Yes]** or **[No]** from the menu that pops up.

Cursor Icon

This button allows you to specify the 3D cursor style. This option gives you the choice of your cursor being a dot, arrow or crosshair.

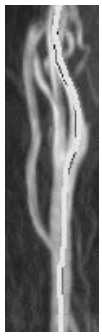


- Click on the **[Cursor Icon]** button and select the desired cursor style option (crosshair, arrow or dot) from the menu that pops up.

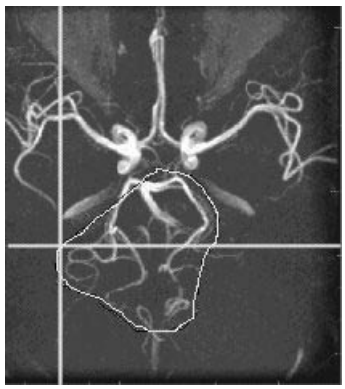
Cursor

The **[Cursor / Annotations]** Command Window is used to restrict 3D cursor movement to the current trace or to restrict 3D cursor movement to the X or Y axis.

- Click on the **[Lock to Trace]** button to enable restriction of the 3D cursor to the current trace. Click again on the same button to disable this restriction.



- Click on the **[XY Lock]** button to restrict 3D cursor movement to the X or Y axis.

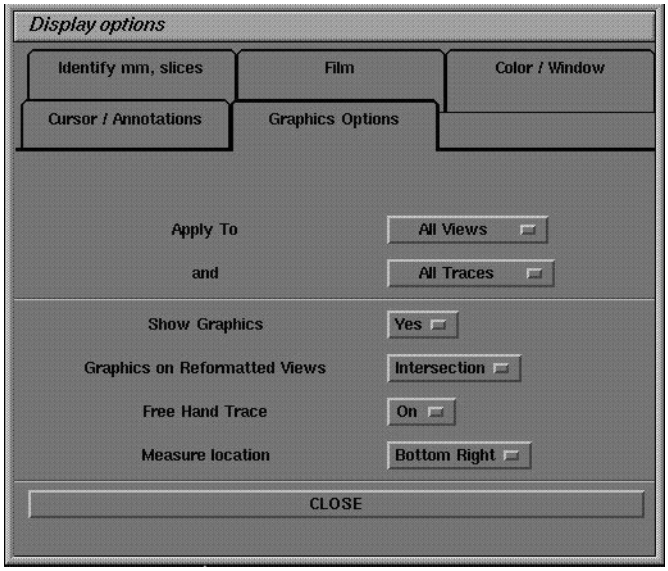


X and Y lines remain present throughout ROI tracing.

- Click on the **[Close]** button to close the Cursor Lock Command Window.

Display / Graphics Options Command Window

Access via: **[Display Pref.]** > **[Graphics Options]**



Display / Graphics Options Command Window

The Display/Graphics Options Defaults command window is used to set up the way graphics (trace) are displayed, free hand trace and measure location.

The various buttons and parameters in this command window are described below:

Apply to buttons

These buttons allow you to specify whether the **[Show Graphics]** button in this command window applies to all views and traces or only to selected ones.

- Click on the button and select the desired view(s) from the menu that pops up.

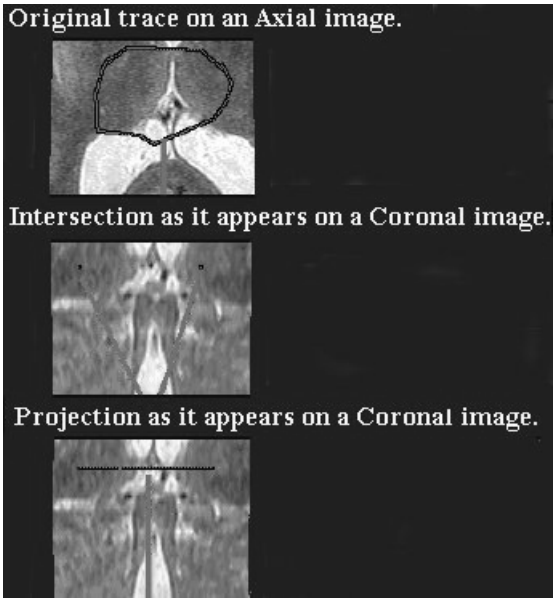
Show Graphics

This button allows you to turn the display of traces on and off.

- Click on the **[Show Graphics]** button and select **[Yes]** or **[No]** from the menu that pops up.

Graphics on Reformatted Views

This button allows you to specify the way traces should be displayed on cut plane views.



Intersection vs Projection

This button is a toggle button that allows you to choose either intersection or projection.

- Click on the **[Graphics on Reformatted Views]** button and select the desired option from the menu that pops up.
- Choose **[Intersection]** to display only the part of traces that intersects the cut-plane.
- Choose **[Projection]** to have the projection of the entire trace to be superimposed on the cut plane.

Free Hand Trace

This button allows you to choose a trace creation mode. It is a toggle that allows you either straight line segments or free hand drawing.

- Click on the **[Free Hand Trace]** button and select **[Off]** for straight segment trace creation, or select **[On]** for free hand trace creation.

Measure Location

This button allows you to choose the measure location.

- Click on the **[Measure Location]** button and select **[Mouse]** or **[Bottom right]**.

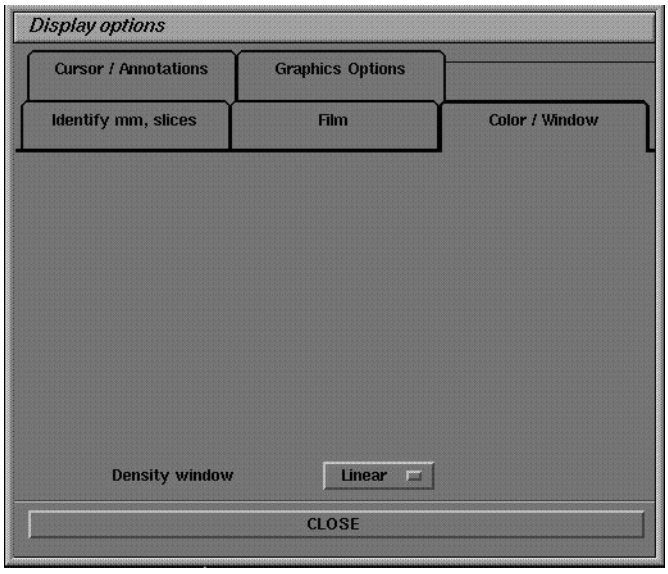
Close button

This button is used to close the **Display/Actions Defaults** Command Window.

- Click on the **[Close]** button to close the Display/Graphics Command Window.

Display / Color Window Command

Access via: **[Display Pref.]** > **[Color / Window]**



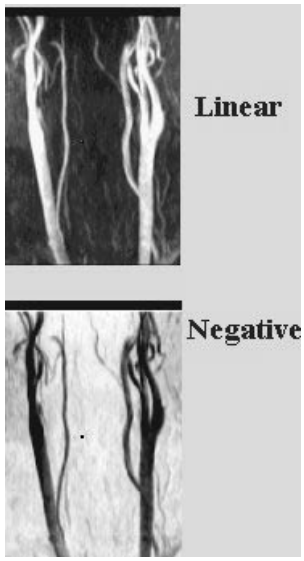
Color / Window Command

The Color / Window command is used to select a linear or negative density window.

The button and parameters in this command window are described below.

Density window

This button is used to select a linear (normal) or negative (inverse video) density window.



- Click on the **[Density Window]** button and select the desired option **[Linear]** or **[Negative]** from the menu that pops up.

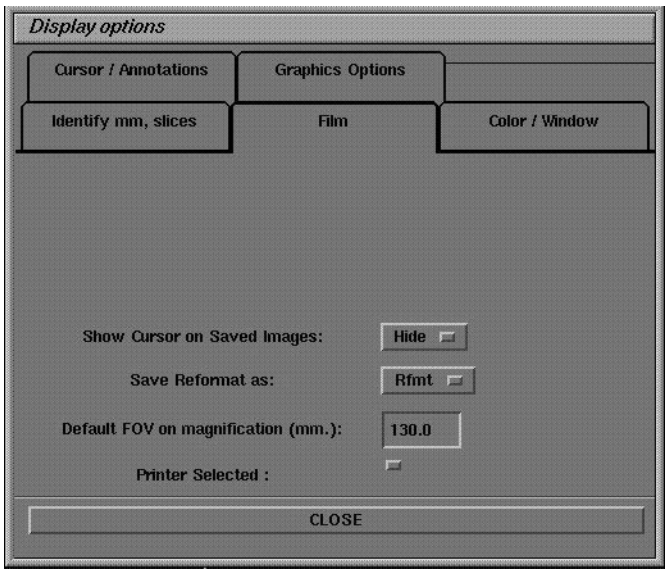
Close button

This button is used to close the **Display/Actions Defaults** Command Window.

- Click on the **[Close]** button to close the **Display/Actions Defaults** Command Window.

Display / Film Command Window

Access via: **[Display Pref.]** > **[Film]**:



The Filming Command Window is used to specify the default FOV on magnification and to determine whether or not the cursor is visible on saved images.

The various buttons and parameters in this command window are described below.

Show Cursor on Saved Images

This button is used to specify whether or not the cursor is visible on saved images.

- Click on the **[Show Cursor on Saved Images]** button and select either **[Show]** or **[Hide]** from the menu that pops up.

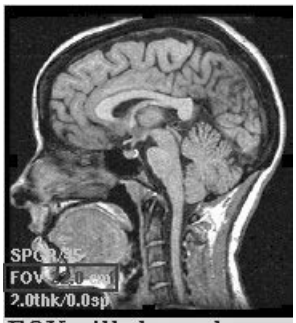
Save Reformat as

This button is used to specify whether or not the images you save are saved in the Browser as **Rfmt** or **ssave**.

- Click on the **[Save Reformat as]** button and select either **[Rfmt]** or **[ssave]** from the menu that pops up.

Default FOV on magnification (mm.)

This text box is used to specify the default FOV used when a magnification or reduction is performed.



FOV will change by 13 cm with the settings as displayed.

- Move the mouse pointer into this text box, delete the existing value by pressing the **BACKSPACE** key once for each digit to be deleted and enter the desired default FOV, in mm., from the keyboard.
- This value is important for facilitating distance measurements made directly on the film; when left/right is clicked on the FOV annotation, the resulting FOV is doubled/halved with respect to the default FOV value. Thus you can make measurements directly on the film and simply divide by the appropriate multiple of two to obtain the true distance.

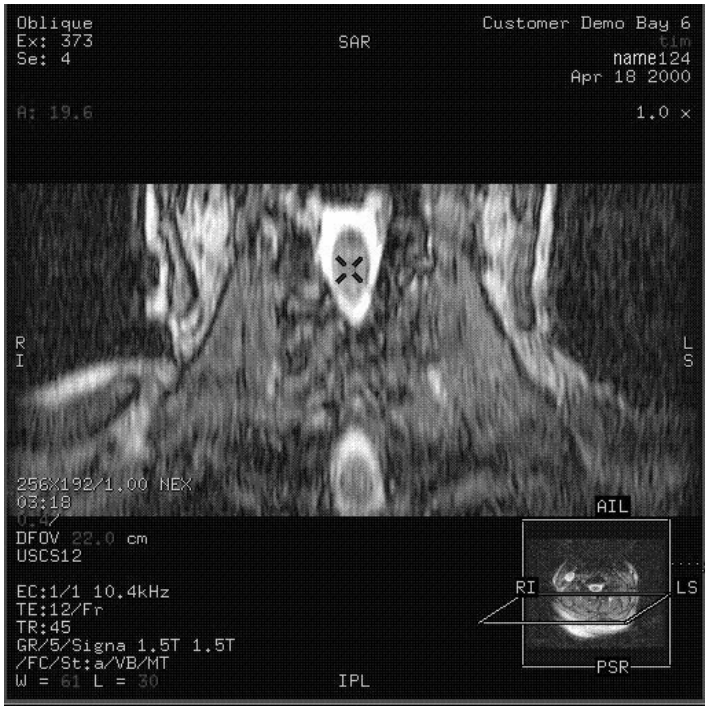
Printer Selected

This button allows you to choose a Printer for filming when in Reformat.

- Click on the **[Printer Selected]** button and select a filming destination from the menu that pops up.

On View Operations

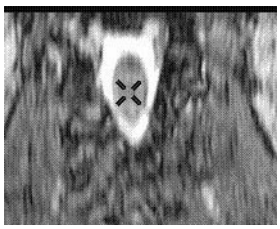
The details of all the operations that can be performed on views is outlined in the following pages. The figure below shows a view with the available annotations, indicators and controls that are described in this chapter.



Oblique Reformat View

The 3D Cursor

The 3D cursor provides 3D point identification on multiple views. The 3D cursor can appear as a crosshair, arrow or dot.



3D cursor with crosshair

NOTE: If, instead of a 3D cursor as described above, there are two perpendicular intersecting lines, this means that the **[XY Lock]** button has been activated in the **Cursor / Annotations** Command window, and the 3D cursor position is defined by the point of intersection of the two lines.

To move the 3D cursor (even if the XY Lock is activated), proceed as follows:

- Move the mouse pointer to the desired location on the view.
- Press and hold down the **SHIFT** key.
- As long as the **SHIFT** key is held down, the 3D cursor follows the mouse movements.
- When the 3D cursor is exactly where the user wants it release the **SHIFT** key to finish cursor movement.

OR

- An alternate method is to point precisely on the 3D cursor, Click/Hold on the cursor, and drag to the desired location and release. Because the defined point is three-dimensional, move the 3D cursor around on one view, the other views updates based on the changes in direction of the cursor.

OR

To move the 3D cursor by an exact amount, use the **[Movement/Rotation Increment Buttons]**.

- To center the 3D cursor in the 3D field of view, use the **[Reset pointer]** option in the Main On-View menu obtained by Click/Hold the right mouse button on the view.
- To see the numerical position of the cursor in real time, use the Graphics Command Window accessible via the File menu pull-down.
- To restrict cursor movement to a trace (the trace must be present), use the **[Lock Cursor to Trace]** button in the **Cursor / Annotations** Command Window which is accessible via the **Display Pref.** menu.

To restrict 3D cursor movement to the Xor Y axis, use the **[XY Lock]** button in the **Cursor Annotations** Command /Window accessible via the **Display Pref.** menu. The 3D cursor now appears as the intersection of a horizontal and vertical red line, which can be manipulated as follows:

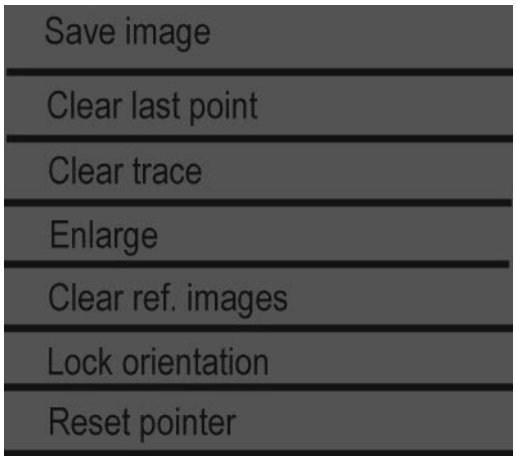
- Click/Hold left on the line you want to move.
- Drag the line to the desired position (the other line stays locked in place).
- Release left mouse.
- The 3D cursor is now at the new intersection of the two lines.
- To move the 3D cursor without restriction, press and Click/Hold on the point of intersection of the two lines and drag to the desired position.

NOTE: The 3D cursor can be either shown or hidden on saved images.

Main On-view Menu

This menu is accessed by Clicking/Holding right mouse anywhere on a view **except** on the trackball control points, the 3D cursor or any of the annotations.

The content of this menu depends on the view type and whether or not traces are present on the view. Only if there is a trace on the view **[Clear last point]** and **[Clear trace]** appear in the menu.



Click/Hold down right mouse on a view and the following options are displayed:

- **[Save image]** saves the view for future display in the Display Browser. The Reformat Package assigns a

name to the saved view that appears in the Display Browser.

- **[Clear last point]** exists only if a trace is present and allows the user to clear the last point entered on a trace.
- **[Clear trace]** exists only if a trace is present and allows the user to clear all points from the trace, enabling restart of trace entry.
- **[Enlarge]** (does not exist on Profile, Histogram or Cross Section Views), allows “zooming” in by a factor of two. This option then becomes **[Reset size]** for returning to the normal view.
- **[Clear ref. image]** removes the plane indicator in lower right corner of viewport.
- **[Lock orientation]** (oblique views only), allows lock view orientation (i.e. prevent rotation). This option then becomes **[Unlock orientation]** for restoring rotation ability.
- **[Reset pointer]** (does not exist on Profile, Histogram, Cross Section or Curved Views), allows centering of the 3D cursor in the 3D field of view.

Orientation Annotations

The orientation annotations appear above, below, to the left and to the right of the view. They indicate the orientation of the model with respect to the patient’s body (Left, Right, Superior, Inferior, Anterior and Posterior).

- When an orientation annotation is underlined (red on color monitors), you can click any mouse button on it and drag the mouse to orient the image. Release the mouse button to end the scroll operation.

Patient Name Annotation

The patient name annotation is located in the upper right corner of the view.

You can show or hide the patient name annotation as follows:

- Click/Hold right on the patient name annotation.
- Select **[Show]** or **[Hide]** from the menu that pops up.
- Release.

Window Level and Window Width Annotations

The window level and window width annotations (L and W, respectively) are located in the lower left corner of the view.

If the user wants windowing different from those provided by the **[Windowing Parameter Preset]** buttons in the main command window, adjust window level and width using the mouse as follows:

- Select the view(s) the user chooses to adjust.
- Move the mouse onto one of the selected views and Click/Hold the middle mouse button.
- Drag the mouse left or right to make the image brighter (window level reduced) or darker (window level increased), respectively. Release mouse when the desired window level is reached. The ***L*** annotation shows the new value.
- Drag the mouse left or right to make the image sharper (window width reduced) or smoother (window width increased), respectively. Release mouse when the desired window width is reached. The ***W*** annotation shows the new value.

Slice Annotation (Acquisition Views Only)

This annotation is located in the upper left corner of acquisition views. It can be used to “page” through the acquisition slices as described below.

- Point to the slice’s annotation number “Im: xx". Click to move up one slice or right to move down one slice. The slice annotation shows the new value.
- Point to the slice’s annotation number “Im: xx”. Hold down the middle mouse button and drag left to move continuously downward in the stack or drag right to move continuously upward in the stack. The slice annotation shows the new value.

Field of View Annotation

This annotation is located in the lower left corner of the view. It can be used to “zoom” in or out on a view by a factor of two as described below.

- Point to the field of view annotation “FOV”. Click to half the current FOV, or Click right to double the current FOV. The annotation shows the new value.

OR

- Place your mouse over the FOV and depress your middle mouse and slide left or right and FOV changes in 1cm increments.

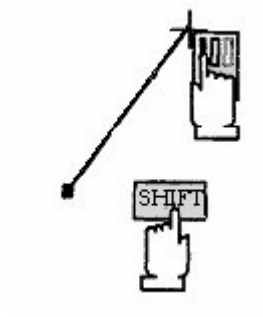
Creating and Editing Traces

Be aware that traces are 3D graphics and become part of the object in all non-icon views. This means that a trace can be created in one view and then edited in another view.

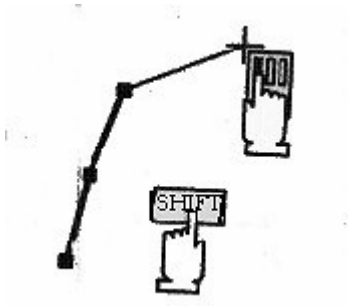
There are two types of traces that can be edited:

- **Segment trace** (define a series of points which the 3D Reformat Package connects together with straight line segments.
  - To create segment traces, first ensure that the **[Free Hand Trace]** button in the **[Display Pref. Menu]** and located under **[Graphics Options]** is set to **[Off]**.

° Holding the **SHIFT** key down, Click/Drag and release the mouse button at the first desired point.



° Still holding the **SHIFT** key down, Click/Drag and release mouse button at the next desired point. During dragging, a rubber band appears between the last point entered and the current mouse position.



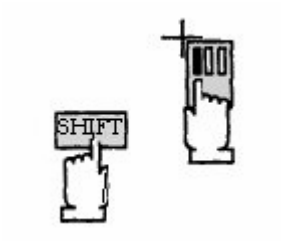
° To clear the last defined point, Click right on the view and select **[Clear last point]** from the Main on-view menu that pops up, or press **D** on the keyboard.

° To clear the entire trace and start again, Click right on the view and select **[Clear trace]** from the Main on-view menu that pops up, or press **Control+U** on the keyboard.

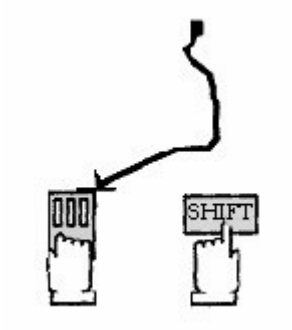
- **Free hand trace** (the trace follows mouse movement during creation).

  ° To create free hand traces, first ensure that the **[Free Hand Trace]** button in the **[Display Pref. Menu]** and located under **[Graphics Options]** is set to **[On]**.

- Holding the **SHIFT** key down, Click (do not hold) to activate tracing.



- Still holding the **SHIFT** key down, move the mouse to define the free hand trace.



- Release the **SHIFT** key to stop tracing. To restart tracing, again hold the **SHIFT** key down and Click (do not hold) left. (A straight line segment is drawn from the end of the trace to the current mouse pointer position.) Again, move the mouse to define your trace.
- To clear the last defined point, stop tracing by releasing the **SHIFT** key, then Click right on the view and select **[Clear last point]** from the Main on-view menu that pops up, or press **D** on the keyboard.
- To clear the entire trace and start again, stop tracing by releasing the **SHIFT** key, then Click right on the view and select **[Clear trace]** from the Main on-view menu that pops up, or press **Control+U** on the keyboard.

Editing Traces

To access the Drop to Edit box click left on **[File]** and select **[Graphics]**, and then select **[User Annot. / Trace]**. The **[Drop to Edit Box]** is shown below.

- Click/Hold on the **[Drop to edit]** box, Drag it onto the desired trace on the image view and drop it.
- Click on any of the points and Click on the defined point to be moved and drag to the new location.
- Release the left mouse button to enter the new point location.

NOTE: To quickly clear a point, Drag it to any other existing point and release left mouse button.

MPVR (Multi-Planer Volume Reformat)

Multi-planar volume reformat allows the adjustment of the reformat plane/slice thickness and rendering mode.

Reformat defaults to a one voxel thickness. MPVR allows the voxel thickness to be adjusted from 2 to 50 voxels.

MPVR allows the selection of rendering mode:

- Average provides the average pixel intensity of the reformat slice.
- MIP provides the maximum pixel intensity of the reformat slice. (brightest pixels)
- Min provides the minimum pixel intensity of the reformat slice. (darkest pixels)

MPVR defaults the rendering mode to Average.

Applications For Reformat

Reformat is used to display a 2D stack or 3D volume of image data in orthogonal, oblique and curved planes other than the original acquisition plane.

Use reformat to acquire in one plane but display and view in other planes.

Use reformat for anatomy that lies along complex or difficult angles to scan.

Use curved reformat for scoliosis spines and other anatomy that does not lie in a single plane.

Use MPVR for cholangiograms, myelograms, urograms and abdominal MRA.

How To Use Reformat

This section provides the step-by-step instructions for utilizing reformat. Specifically it describes how to:

- Select the Image Set
- Moving the Orthogonal View Locations
- Adjusting the Oblique View Angle
- Defining a Oblique Batch Series
- Defining a Radial Batch Series
- Defining a Curved Reformat View
- Adjusting the Plane Thickness and Rendering Mode with MPVR

Selecting the Image Set

Use this procedure to select the image data set.

1. Click the **[Display Desktop]** icon.

2. Highlight the series or range of images on the Display Browser. (A 3D sequence is recommended). Click/Drag for selected images.
3. Check the image locations and deselect any duplicates.
4. Click on **[Reformat]** to launch the software package.

In Brief: Selecting the Image Set

1. Click the **[Display Desktop]** icon.
2. Highlight the series or range of images on the Display Browser.
3. Check the image locations and deselect any duplicates.
4. Click on **[Reformat]** to launch the software package.

In Brief: Moving the Orthogonal View Locations

1. Position the mouse cursor over area of interest, and press **SHIFT** to move the 3D cursor to update the views.

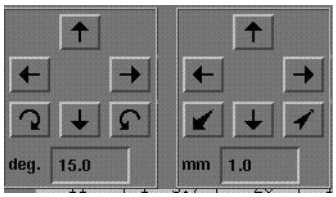
Moving the Orthogonal View Locations

The view location can be adjusted several ways:

1. Position the mouse cursor over area of interest, and press **SHIFT** key to move the 3D cursor to update the views.

OR

- Enter an increment value in the **mm. text box**, and Click the appropriate arrow.



OR

- Position the mouse cursor on the red slice location annotation.

  - ° Click left to increase.
  - ° Click right to decrease.
  - ° Click and hold down middle mouse, and drag right to increase or left to decrease.

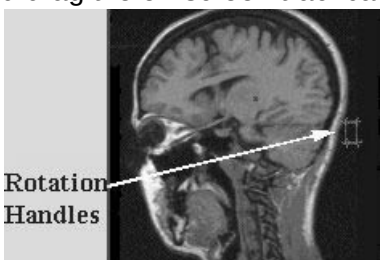
Adjusting the Oblique View Angle

The oblique reformat plane can be adjusted several ways:

1. To use the on screen trackball cursor, click the **[Tilt Rotate]** icon.

2. Position the mouse cursor on one of the corner handles of the on-screen trackball cursor.

3. Click/Hold and drag the on-screen trackball cursor.



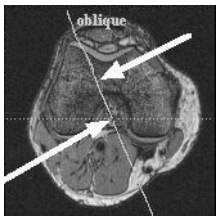
OR

To use the Oblique Mode Cursor

1. Click on the orthogonal image that you want to use to adjust the oblique plane.

2. Click the **[Oblique Mode]** icon.

3. Position the mouse cursor on the solid tilt line.



4. Click/Hold and drag the tilt cursor.

5. OR, enter a rotation value in the **degree increment text box** and Click the appropriate arrow.

In Brief: Adjusting the Oblique View Angle

1. Click the **[Tilt Rotate]** icon
2. Position the mouse cursor on one of the corner handles of the on-screen trackball cursor.
3. Click/Hold and drag the on-screen trackball cursor.

In Brief: Defining an Oblique Batch Series

1. Highlight the desired set of images.
2. Click on **[Reformat]**.
3. Select the viewport you wish to use to create the batch series.
4. Click **[Batch]** button**.**
5. Click **[Oblique]** button.
6. Click on the **[Graphic Prescription]** icon.
7. Click/Hold and drag one of the batch end markers to the start location.
8. Click/Hold and drag the other batch end marker to the end location.
9. Click/Hold and drag the slice center reference line to re-position the entire prescription.
10. Enter in text boxes:
    - Number of views.
    - Millimeter between views.
    - Slice thickness.
    - FOV
11. Select outputs.
12. Click **[Apply]**.

Defining an Oblique Batch Series

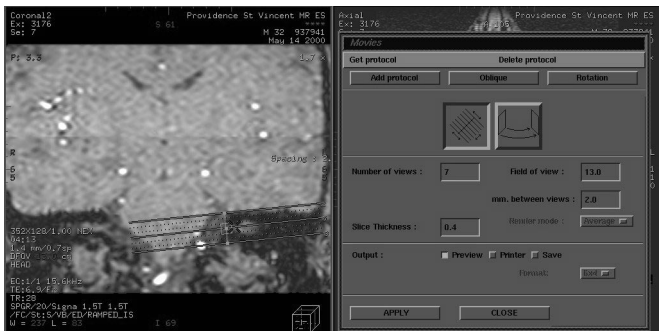
To define a entire set of batch reformations:

1. Highlight the desired set of images.
2. Click on **[Reformat]** to launch the Reformat Package.
3. Select the viewport you wish to use to create the batch series.
4. Click **[Batch]** button to activate the **Batch/Movie Loop Command Window**.

5. Click **[Oblique]** button.

6. Click on the **[Graphic Prescription]** icon. (This icon may already be selected).

7. To define the reformat locations, Click/Hold and drag one of the batch end markers to the start location.
8. Click/Hold and drag the other batch end marker to the end location.
9. Click/Hold and drag the slice center reference line to re-position the entire prescription.



10. Enter the appropriate values in the text boxes for:
    - Number of views. (number of slices)
    - Millimeter between views.
    - Slice thickness.
    - Field of view.
        - If the slice thickness is greater than one voxel, Click the **[Render mode]** button and select render mode type.
11. Select the output.
    - Click **[Printer]** to send the images to the laser camera.
    - Select the film format from the pull-down menu.
    - Click **[Save]** to send the images to the system disk as a new series.
12. Click **[Apply]**.

Defining A Radial Batch Series

In Brief: Defining A Radial Batch Series

1. Highlight the desired set of images.
2. Click on **[Reformat]**.
3. Select the viewport you wish to use create the batch series.
4. Click **[Batch]** button**.**
5. Click **[Rotation]** button.
6. Click on the **[Graphic Prescription]** icon.
7. Click/Hold and drag one of the batch end markers to the start location.
8. Click/Hold and drag the other batch end marker to the end location.
9. Click/Hold and drag the slice center reference line to re-position the entire prescription.
10. Enter in text boxes:
    - Number of views.
    - Degrees between views.
    - Slice thickness.
    - FOV
11. Select outputs.
12. Click **[Apply]**.

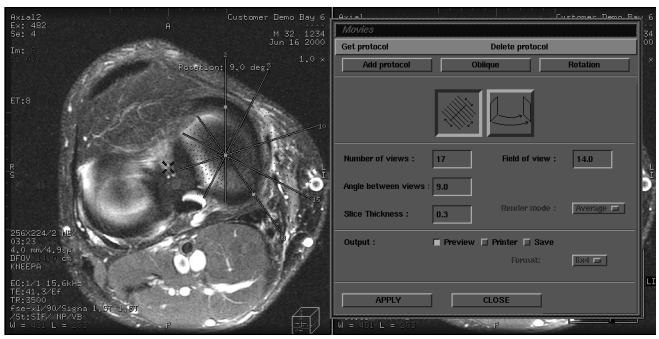
To define a entire set of radial reformations:

1. Highlight the desired set of images.
2. Click on **[Reformat]** to launch the Reformat Package.
3. Select the viewport you wish to use to create the radial batch series.
4. Click **[Batch]** button to activate the Batch/Movie Loop Command Window.

5. Click **[Rotation]** button.

6. Click on the **[Graphic Prescription]** icon. (This icon may already be selected).

7. To define the reformat locations, Click/Hold and drag one of the batch end markers to the start location.
8. Click/Hold and drag the other batch end marker to the end location.
9. Click/Hold and drag the slice center reference line to re-position the entire prescription.



10. Enter the appropriate values in the text box for:
    - Number of views. (number of slices)
    - Degrees between views.
    - Slice thickness.
    - Field of view.
        - If the slice thickness is greater than one voxel, click the **[Render mode]** button and select render mode type.
11. Select the output.
    - Click **[Printer]** to send the images to the laser camera.
    - Select the film format from the pull-down menu.
    - Click **[Save]** to send the images to the system disk as a new series.
12. Click **[Apply]**.

Defining a Curved Reformat View

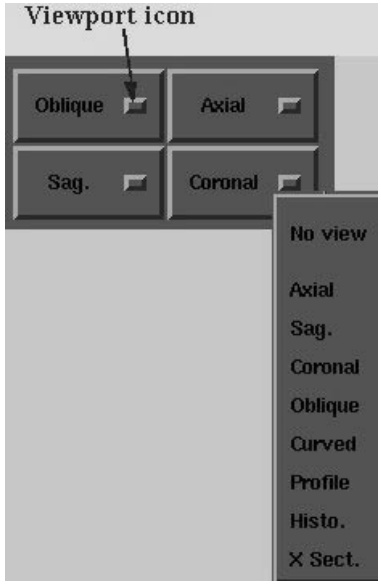
In Brief: Defining a Curved Reformat View

1. Highlight the desired set of images.
2. Click on **[Reformat]**.
3. Click on **[Oblique]** viewport button and from pull-down menu change to a **[Curved]** viewport.
4. Select the viewport you wish to use to create the curved reformat trace.
5. To define the curved plane, position the mouse cursor at the starting point on the desired image.
   - Press **SHIFT**, Click left and release to deposit the point.
   - Continue to press **SHIFT**, re-position cursor, Click left and release to deposit the next point.
6. The defined curved plane updates in the curved reformat viewport, (upper left viewport).

A curved reformat is useful to use on patients with scoliosis, optic nerves, and other anatomy that does not lie in a single plane.

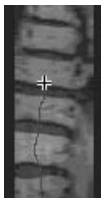
To define a curved reformat view:

1. Highlight the desired set of images.
2. Click on **[Reformat]** button to launch the Reformat Package.
3. Click on **[Oblique]** viewport button and from pull-down menu change to a **[Curved]** viewport.



4. Select the viewport you wish to use to create the curved reformat.

5. To define the curved plane, position the mouse cursor at the starting point on the desired image.
   - Press **SHIFT**, Click left and release to deposit the point.
   - Continue to press **SHIFT**, re-position cursor, Click left and release to deposit the next point.
   - Complete the definition of the curved plane.



6. The defined curved plane updates in the curved reformat viewport, (upper left viewport).

In Brief: Adjusting The Plane Thickness and Rendering Mode With MPVR

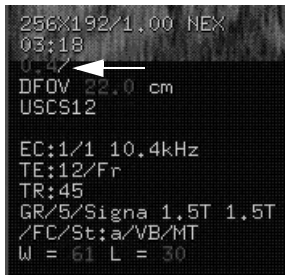
1. Highlight the desired set of images.
2. Click on **[Reformat]**.
3. Move the cursor into the Oblique viewport
4. Position the mouse cursor on the red slice thickness annotation.
5. Click the middle mouse and Drag to change the value in real-time.
6. Press **SPACEBAR.**
7. To adjust rendering mode position the mouse over the red rendering mode annotation and Click and hold down right mouse. A pull down menu appears to select rendering mode.
8. Press **SPACEBAR**.

Adjusting The Plane Thickness and Rendering Mode with MPVR

Multi-planar volume reformat allows the adjustment of the reformat plane slice thickness and rendering mode.

To adjust the plane thickness:

1. Highlight the desired set of images.
2. Click on **[Reformat]** to launch the Reformat Package.
3. Move the cursor into the Oblique viewport, which is now the MPVR viewport, (Oblique viewport if upper left view).
4. To adjust the voxel thickness, position the mouse cursor on the red slice thickness annotation. (See arrow below)



   - Click left to increase the thickness.
   - Click right to decrease the thickness.
   - Click the middle mouse and Drag the mouse to change the value in real-time.
5. Press **SPACEBAR** to execute the calculation.

To adjust the rendering mode:

6. Position the mouse cursor on the red rendering mode annotation on the MPVR image.
7. Click and Hold down right mouse. A pull down menu appears and you can drag to select a rendering mode.
   - Avg
   - mip
   - min ip
8. Press the **SPACEBAR** to execute the new rendering mode.
9. To return to a normal oblique image, change the slice thickness annotation to its minimum value.

Volume 4

Chapter 7

Creating 3D Models

Where Am I?

Introduction

The Three Dimensional (3D) Analysis option is a purchasable software application designed to generate reconstructed 3D volumes and reformatted cut planes on an MR series. The program allows you to build your own model or use a preset protocol such as MR Angio and MPVR (Multi-Projection Volume Reconstruction).

Images must meet certain requirements to be used in the 3D Analysis package:

- FOV (Field of View), matrix size, orientation, and display center must be the same for images in the set.
- Oblique acquisitions cannot be supported for right/left decubitus patient orientations.
- All images must be at different locations in the set.
- The set should include only axial, sagittal, coronal, or oblique images; other types of images such as screen saves, multi-slab, or multi-angle images are not supported.
- Interslice distance must be less than 10 mm.

3D Analysis uses the first selected image in the data set as a basis for using/discarding the other images selected for reconstruction. Any images having a matrix size or requirement different from that of the first selected image are discarded from the reconstruction process. Therefore, carefully choose the data set for 3D Analysis.

Access the 3D Analysis option from either the Browser or the **[Image Analysis]** button located on the Viewer. Detailed steps to perform the 3D Model can be found in the Advantage Windows User Guide on Volume Analysis, direction number 2221268.

Chapter 8

Analyzing Images with FuncTool

Where Am I?

FuncTool

Introduction

This chapter explains the process of analyzing images with FuncTool. It is a post-processing tool which has multiple functions. Some of the functions include post-processing techniques for Bold, Diffusion and Contrast Enhanced Imaging. This chapter contains key concepts as well as step-by-step instructions to help you learn how to:

- Display images within FuncTool
- Display graphs within FuncTool
- Create parametric images
- Adjust composite overlays
- Save images from FuncTool
- Film images from FuncTool
- Display 3D Focal CSI Images
- Create 3D Focal CSI Custom Protocols

NOTE: FuncTool is a purchasable post-processing option.

In addition, this chapter answers the following questions:

1. What types of image sets can be processed with FuncTool?
2. What are time-intensity curves?
3. What are algorithms?
4. What are parametric images?
5. What are the applications of FuncTool?
6. How are the viewports laid out in FuncTool for 3D Focal CSI images?

About... FuncTool

This section presents the concepts necessary to successfully complete the FuncTool Post-processing process. Specifically you need to understand:

- Description of FuncTool
- Valid Image Sets
- FuncTool Layout
- Algorithms
  - Correlation Coefficient
  - Positive Enhancement Integral
  - Negative Enhancement Integral
  - Mean Time to Enhance
  - Maximum Slope of Increase
  - Signal Enhancement Ratio
  - Maximum Difference Function
  - Difference Function
  - Average
  - Diffusion Coefficient
  - Exponential Diffusion Coefficient
  - Ratio (A-B)/(C-D)
  - MR Spectroscopy Protocols
- Applications
- 3D Focal CSI Viewport Layout
  - The Chemical Shift or Upper Left Viewport
  - The Spectral Grid or Upper Right Viewport
  - The Metabolite Image or Lower Left Viewport
  - The Reference or Lower Right Viewport

Description of FuncTool

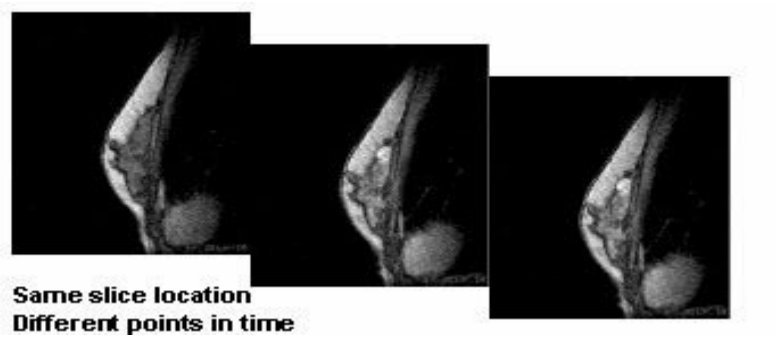
FuncTool is an optional image analysis software package, that processes dynamic image data to generate information with regard to changes in image intensity over time in the form of graphs and parametric images.

Valid Image Sets

A series of images must be acquired at the same scan location but at different moments in time, to be compatible with FuncTool. These series are called time-ordered or multi-phase series.

More specific, a valid image set must have the same scan plane, image center and pixel size. Up to 1024 images can be loaded from a single or multiple series. Signa LX, Signa Horizon, Signa Advantage, Signa Contour and Signa Profile images are all compatible, with a few exceptions; no screen save, reformatted or projection images are allowed.

Recommended pulse sequences are 2D GRE/SPGR, 2D fast GRE/SPGR, 3D GRE/SPGR, 3D fast GRE/SPGR and EPI.



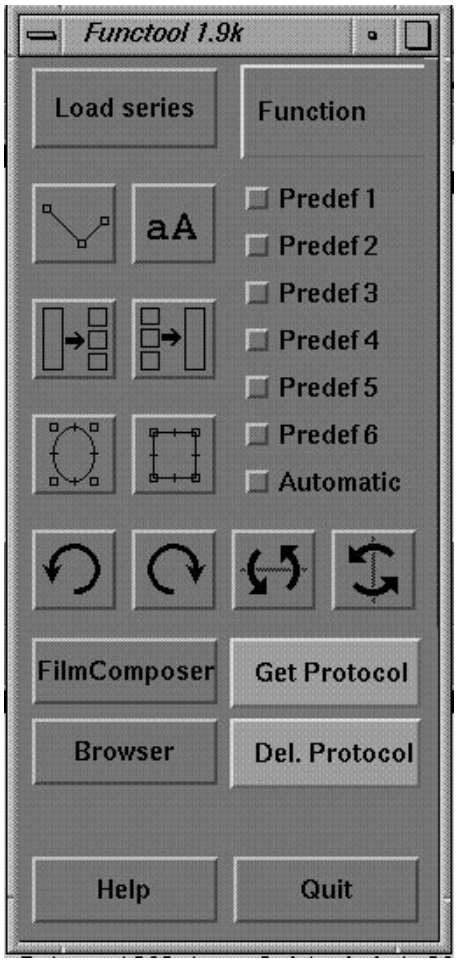
Something to Think About...

- A “time course” or “dynamic” data set is a time ordered acquisition with either a sequential change in scan time for each scan image or a trigger delay (multi-phase scan). The horizontal scale of a graph for such a data set represent time.
- A diffusion-weighted data set is an ordered acquisition with sequential changes in b-values. The horizontal scale of a graph for such a data set represent b-values.
- A MR spectroscopy data set is an ordered acquisition with sequential changes in frequency. The horizontal scale of a graph for such a data set represent parts per million (ppm values).

NOTE: You should be aware that for MR and CT data sets that do NOT contain multiple images for each location in the data set, graphs or function views generated are generally meaningless. If tried a message appears saying “Not a time series.”

FuncTool Layout

FuncTool is accessible from the Display Browser, on the right side of this screen. Initiating FuncTool from the Display Browser allows the Functool panel to display. This panel contains the selections for algorithms, protocols, ROI definition, W/L adjustment and film composer.



A brief description of the buttons are as followed:

- Load Series - 

Loads the selected series from the Display Browser into FuncTool.

- Function - 

Provides a list of algorithms used to create a parametric image.
  - When displaying the CSI data, the Function menu allows a number of choices. These choices differ from the

selections on the **[Get Protocol]** menu, because the Function menu selections cannot be modified and include no information concerning the definition of the protocols.

NOTE: A list of all algorithms and their functions are discussed in the next section.

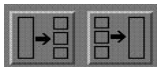
- Predefs - Is an area where seven previously saved window/level settings are.

NOTE: Predefs are the same as those set in the viewer.

- Annotate -  Creates user annotation on images within the FuncTool screen. Multiple areas of annotation can be added to an image and later deleted using the Copy, Paste or Cut special function key or Control-C (copy), Control-V (paste) or Control-X (cut) on the keyboard. To move an annotation to a different location on the screen, click, hold and drag the annotation with the left mouse to the desired location.

- Polygon/Spline -  Creates a polygon or spline region of interest. A polygon is a ROI with three or more straight sides. A Spline is the same polygon ROI with curved corner points.

NOTE: This is a toggle button which allows you to choose either a polygon or spline shape. The system defaults to first displaying the polygon. This button is inactive until the first side of the ROI is defined.

- Split ROI and Merge ROI -  Splits an ROI into multiple single-pixel ROIs, or restores the original ROI.

- ROI -  creates an ellipse or square region of interest (ROI) that's used to plot time intensity information

and perform statistical analysis on a specific region. ROI's may be cut, copied or pasted using the special function keys or the Control-X (cut), Control-C (copy), or Control-V (paste) options. The ROI calculates and displays in the lower left corner of the image, the following information:

- The area enclosed by the graphic in mm^2.
- The mean or average value of the pixels enclosed by the graphic.
- The standard deviation (DEV) of the pixel values enclosed by the graphic, which provides a measure of variability according to pixel values.
- The number of pixels for the cursor and the area calculated is displayed on the graph viewer.

Something to Think About...

- Before an ROI is defined, the cursor on the reference image reports a dynamic time curve and updates the graph and the value posted with each cursor movement. Press the **Shift** key to deposit an area of interest and freeze the time graph posted to the graph view.
- To draw subsequent ROI's click left anywhere within the image except on the current ROI. This effectively de-selects the current ROI and turn its color from green to purple. (If you have a color monitor.)
- Accuracy of on-view measurements - regardless of the zoom factor being used to view images, region of interest statistics are calculated based on the pixels from the original unzoomed image data.
- Accuracy with region of interest area graphics - area measurement accuracy using a region of interest graphic (rectangle, smooth curve, ellipse or free draw) is equal to the displayed are value +/- the circumference of the region multiplied by (image pixel size)^2/2. Mean and standard deviation values for the intensity of the pixels in the region are also affected by this accuracy. Region of interest statistics are based on the pixels inside the graphic defining the region.

- Rotate Buttons -  Changes the orientation of the images. Use the Rotate buttons to change the orientation of the images. To return to the original display, right-click on the image and select **[Display Normal]** from the shortcut menu. You cannot flip or rotate graphs.

Something to Think About...

- L, R, A, P image orientation annotations updates on the image.
- Does not flip or rotate the graphs.
- To return to image to normal orientation, right click, anywhere on the image, to select **[Display normal]** from the pop-up menu.

- Film Composer - 

Displays the film composer menu.

- Browser - 

Brings up the Browser menu, which list Exams, Series and images. This button can be used to select another series to replace the series currently loaded in FuncTool.

- Get Protocol - 

Displays a list of previously saved FuncTool protocols. From this menu you can load a protocol from the saved list.

- Del. Protocol - 

Displays a list of previously saved FuncTool protocols. From this menu you can delete protocols from the saved list.

- Help - 

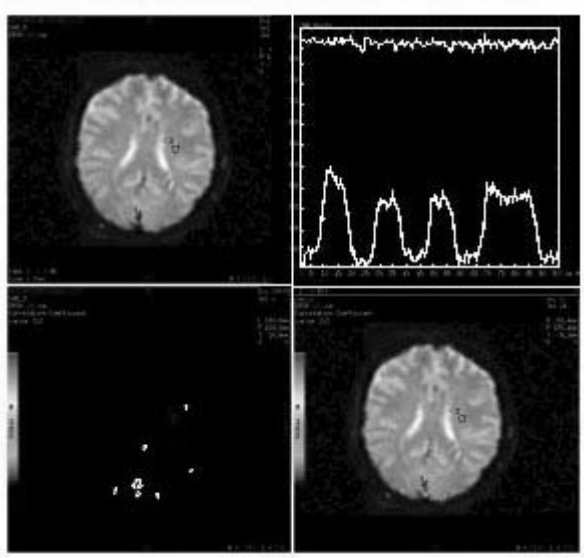
Provides a quick reference of commonly used commands.
  - Once **[Help]** is selected, the **[Function]** key changes to **[Function Help]** and only displays the list of algorithms. The Function menu is not operational until **[Help]** is toggled off.
  - Each **[Function]** algorithm and **[Get Protocol]** also contains a **[Help]** button. This button allows a pop-up window that contains information specific the function selected.

- Quit - 

Closes the FuncTool software. After closed the screen displays the Display Browser window.

The FuncTool viewer uses a four quadrant display:

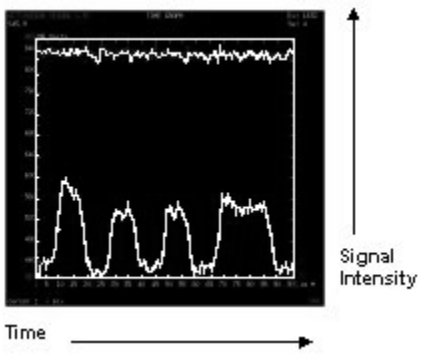
Reference Image Time Intensity Curve



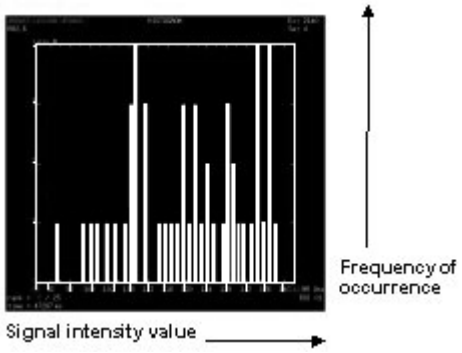
Parametric Image Composite Image

- A *reference image* is displayed in the upper-left quadrant. The number of reference images depends on the number of images in the time-ordered or multi-phase series.
- The *time-intensity curves* are displayed in the upper-right quadrant. They map the change in signal intensity over time and display the information as a graph, histogram or table.

  On a time graph, the time of occurrence is plotted on the x-axis and signal intensity is plotted on the y-axis. It represents the change in pixel values for the pixel under the cursor for every image in the data set.



On a histogram the signal intensity is plotted on the x-axis and the frequency of occurrence is plotted along the y-axis. The height of the bar is determined by frequency.



In a table the average signal intensity for a ROI is listed in MR unit values for each image.

- *Parametric images* are displayed in the lower-left quadrant. They emphasize the physiological information extracted from the signal intensity values. In a parametric image, the color scale (or gray scale) is based on calculated values.
- A *composite overlay* of the parametric image and a reference or anatomic image are displayed in the lower-right quadrant.

NOTE: Only the two upper views are initially displayed.

Algorithms

Algorithms are mathematical equations that are used to analyze the signal intensity values. They extract information about changes in the signal intensity values that the human eye cannot appreciate in the image. FuncTool algorithms are found by pressing the **[Function]** or **[Get Protocol]** key. Each algorithm has a separate function and meaning.

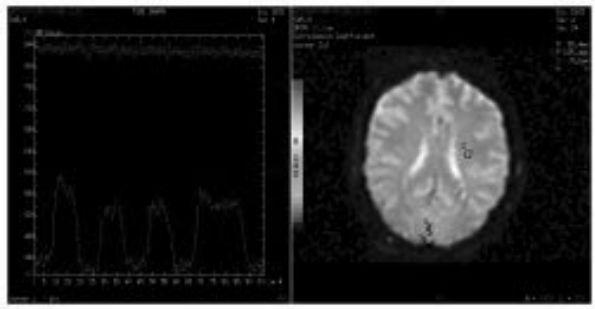
NOTE: Algorithms discussed are either found under the **[Function]** or **[Get Protocol]** buttons.

Correlation Coefficient

This algorithm is a relationship of the time course image intensity values to a user-specified “reference” function. It provides a pixel by pixel value that represents correlation of the time course data sets with a user-specified reference pattern.

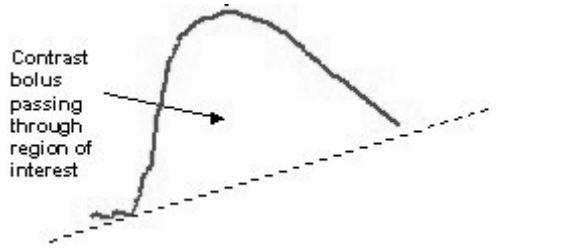
Applications for this algorithm may include a Blood Oxygen Level Dependent (BOLD), or task activation image set. A BOLD image sequence is typically a single shot, multiphase, GRE-EPI sequence with a limited number of slice locations and a high number of phases.

- During the acquisition, a task (stimulation) is performed on and off. Task activation or stimulation of an area of the brain increases the oxygen level which increases the T2* and resulting signal intensity. The type of task/stimulation depends on the area of the brain of interest.
- BOLD imaging is typically used in surgical planning to identify areas of task activities within the brain. It is also used for cognitive studies, psychiatric evaluation and treatment monitoring.



Positive Enhancement Integral

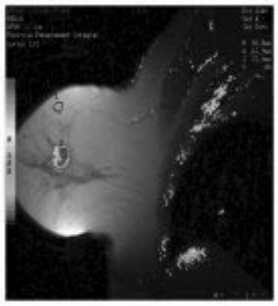
This algorithm displays pixels based on the amount of contrast that passed through the region(s) of interest. It is used to analyze dynamic contrast studies that capture T1 shortening effects of a contrast bolus. T1 shortening produces a positive enhancement or signal increase.



More specifically, it is time-course data acquired during the injection of an MR contrast agent, which may have image

intensity variations caused by changes in the magnetic resonance relaxation rate constant T1, resulting in positive enhancement. This function calculates the sum of the area underneath the time intensity curve within the user-specified range.

Applications for this algorithm may include contrast enhanced Breast imaging. Pulse sequences used are EPI, GRE, FGRE, SPGR or FSPGR.

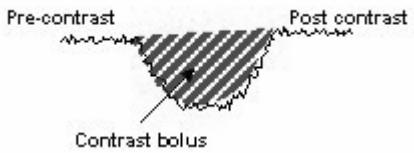


Positive Enhancement Integral display pixels based on variations in the volume of contrast.

NOTE: This algorithm is a predefined protocol not found under the function button.

Negative Enhancement Integral

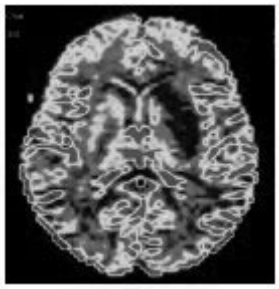
This algorithm displays pixels based on the amount of contrast that passed through the region(s) of interest. It is used to analyze dynamic susceptibility studies that capture the T2* shortening effects of a gadolinium bolus. T2* shortening produces a negative enhancement or signal decrease.



More specifically, it is time course data acquired during the injection of an MR contrast agent. This may have image intensity variations caused by changes in the magnetic resonance relaxation rate constant T2*, which result in a negative enhancement. This function calculates the sum of the area above the time intensity curve within the user specified range.

An application for this algorithm is dynamic susceptibility imaging (contrast enhanced imaging). This is typically used for stroke evaluation in conjunction with a diffusion sequence. Also

used to evaluate tumors (grade, recurrent and primary) and dementia. Pulse sequences used is a single shot, multi-phase SE-EPI pulse sequence acquired at 8-12 location with 30-40 phases.

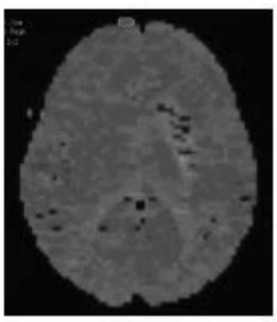


Negative Enhancement Integral images display pixels based on variations in the volume of contrast.

Mean Time to Enhance

This algorithm is used to analyze dynamic susceptibility and dynamic contrast studies and allows you to differentiate areas that reach peak contrast at different times. It displays pixels based on the time (from start) to peak contrast enhancement.

More specifically, for time-course data that exhibits a transient increase or decrease. The Mean Time to Enhance algorithm returns a value that characterizes the temporal position of the transient increase or decrease within the time-course. Transient increase or decreases that occur later in the time course have larger Mean Time to Enhance values and earlier increases or decreases have smaller first moment values.

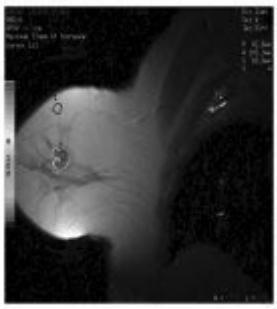


Mean Time to Enhance images display pixels based on variation in peak contrast times.

Maximum Slope of Increase

This algorithm is used to analyze dynamic contrast studies and allows you to differentiate areas based on the rapidity of contrast enhancement. Calculations done with the maximum slope of increase displays pixels based on the rate of contrast enhancement of uptake.

More specifically, with time-course data exhibiting a transient increase, the Maximum Slope of Increase algorithm returns a value that characterizes the maximum slope of increase. Transient increases that occur rapidly have larger maximum slope of increase values and those occurring gradually have smaller maximum slope of increase values.



Maximum Slope of Increase images display pixels based on variation in the slope or rate of contrast enhancement. Red indicates areas of steep slope or rapid uptake.

Signal Enhancement Ratio

This algorithm displays pixels based on a ratio value. The numerator of the ratio is the difference between the peak contrast and the pre-contrast. The denominator of the ratio is the difference between the post contrast and the pre-contrast.

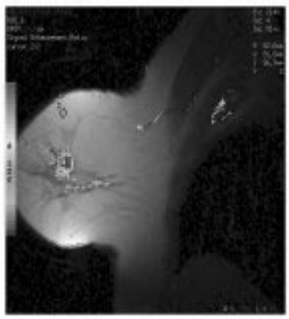
$$\frac{Smax - Spre}{Spost - Spre}$$

More specifically, with time-course data exhibiting a transient increase or decrease, the Signal Enhancement Ratio algorithm returns a value that characterizes the ratio between the above

mentioned Maximum Difference Function value and a user-specified value relative to the baseline in the time course data.

This ratio algorithm is used with dynamic contrast studies and allows you to differentiate areas where contrast enhancement is washed-out, sustained or still enhancing:

- Washed out Signal Enhancement Ratio > 1.1
- Sustained from 0.9 to < Signal Enhancement Ratio 1.1
- Enhancing Signal Enhancement Ratio < 0.9

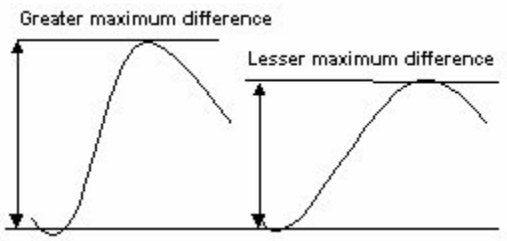


Signal Enhancement Ratio images display pixels based on contrast enhancement status. Red areas indicate wash-out.

NOTE: This algorithm is a predefined protocol not found under the function key.

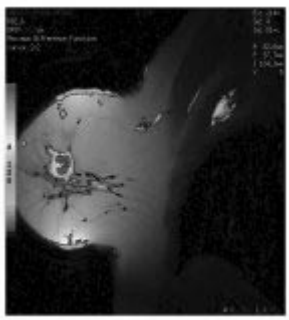
Maximum Difference Function

This algorithm displays pixels based on the difference between the minimum and maximum contrast enhancement. It is used to analyze dynamic contrast studies and allows you to differentiate areas that experience a greater difference between baseline and peak contrast enhancement.



More specifically, with time-course data exhibiting a transient increase or decrease, the Maximum Difference Function

algorithm returns a value that characterizes the difference between the maximum and the baseline values.



Max. Difference Function images display pixels based on variation between minimum and maximum contrast. Red indicates areas with greater differences.

NOTE: This algorithm is a predefined protocol not found under the function button.

Difference Function

This algorithm returns a value that characterizes the difference between the pixel value in the currently displayed image and the corresponding pixel value in the user specified reference image.

NOTE: This algorithm is a predefined protocol not found under the function button.

Average

This algorithm returns the average of the pixel values within a given image range. It is used in particular by the pre-defined protocols for MR spectroscopy.

By prefixing the image range with min, max, abs, log or dev, the algorithm can also be used to find the minimum, maximum or absolute pixel values in a given range, or their natural algorithm or standard deviation.

Diffusion Coefficient

This algorithm subtracts the T2 effects from diffusion-weighted images.

- In an isotropic diffusion-weighted image, restricted diffusion is bright and T2 “shine through” is also bright
- In a Diffusion Coefficient map, restricted diffusion is dark and T2 is isointense.
- This algorithm is found under the **[Function]** button.

Exponential Diffusion Coefficient

This algorithm removes T2 effects from diffusion-weighted images.

- In an Exponential Diffusion Coefficient map, restricted diffusion is bright (the same as a diffusion-weighted image), and T2 effects are isointense.
- This algorithm is found under the **[Get Protocol]** button.

Ratio (A-B)/(C-D)

This algorithm is used in a number of pre-defined protocols, that returns the value scale*(A-B)/(C-D), where A, B, C and D are image ranges and scale is a user defined scaling value. All parameters except A may be empty, so that it's possible to compute A, A-B, A/C or (A-B)/C. As in the Average algorithm, the image ranges can be prefixed with min, max, abs, log or dev.

MR Spectroscopy Protocols

This is a set of protocols used to compute and display metabolic maps from MR spectroscopy data. They show either the distribution of a metabolite (defined by its ppm range), or the ratio between two metabolites.

Pre-defined protocols are available for choline, creatine, N-acetyl and lactate lipid, and for the choline/creatine and choline/N-acetyl ratios.

NOTE: These predefined protocols are not found under the function button.

Applications

FuncTool is used to analyze images from task activation, dynamic susceptibility, dynamic contrast, and diffusion studies. Not all algorithms are used for all applications

- Task Activation studies use:
  - Correlation Coefficient.
- Dynamic susceptibility studies use:
  - Negative enhancement integral
  - Mean time to enhance
- Dynamic contrast studies use:
  - Positive enhancement integral

  - Mean time to enhance
  - Maximum slope of increase
  - Maximum difference function
  - Signal enhancement ratio
- Diffusion studies use:
  - Apparent diffusion coefficient
  - Exponential apparent diffusion coefficient
  - Ratio (A-B)/(C-D)
- MR spectroscopy studies use:
  - MR spectroscopy protocols

3D CSI Viewport Layout

Chemical Shift Images acquired with the Probe-P pulse sequence are displayed by selecting a display tool such as **[MIROI]** or **[Functool CSI]** from the Display Browser. Select the 3D CSI series from the Display Browser, a message window appears asking you to select a localizer. Select the localizer series that you used to prescribe the 3D CSI scan.

The initial display consists of five areas: the command window, and four display viewports. The chemical shift viewport appears in the upper left (UL), the spectral grid viewport in the upper right (UR), the metabolite image viewport in the lower left (LL), and the reference viewport in the lower right (LR). The chemical shift viewport defaults to No Smoothing.

NOTE: Whenever a protocol is selected from the **[Get Protocol]** menu, a Function parameters window is displayed over the bottom viewports.

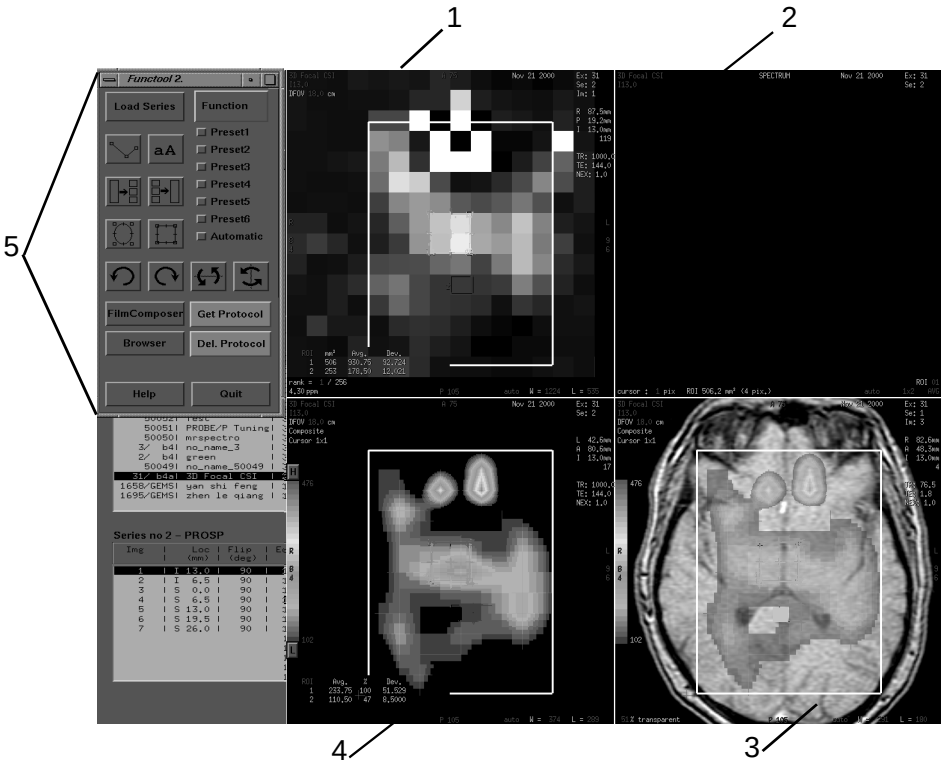


Figure 1: An example of the first areas displayed by the post-processing tool using a 3D CSI series.

1 - Chemical shift viewport (Upper Left-UL),
2 - Spectral grid viewport (Upper Right-UR),
3 - Reference viewport (Lower Right-LR),
4 - Metabolite image viewport (Lower Left-LL),
5 - Display command window.

Concepts, Applications, and Terminology

General features of the probe-P CSI display tool are described in this section. Features specific to each viewport are discussed later in this chapter.

Region-of-Interest (ROI) and Spectrum Colors

ROIs are outlined by a purple or a green line (Figure 2). A green ROI is the active ROI and usually has resizing and movement handles as part of the green outline. A purple ROI is inactive or deselected, and cannot be moved, resized, deleted, or copied.

An active ROI is deselected if you select another ROI from the command window. The active ROI is also deselected if you click anywhere on a viewport except on the cursor area, outline, on another ROI (in the UL, LL, and LR viewports), or spectrum (in the UR viewport). The same color code is used in the spectral grid (UR) viewport; purple corresponds to the spectra or information lists from inactive ROIs, and green to the spectrum or list from the active ROI. A third color – white – is used on the spectral grid (UR) viewport to distinguish the spectrum or list that corresponds to the current cursor location on any of the other viewports.

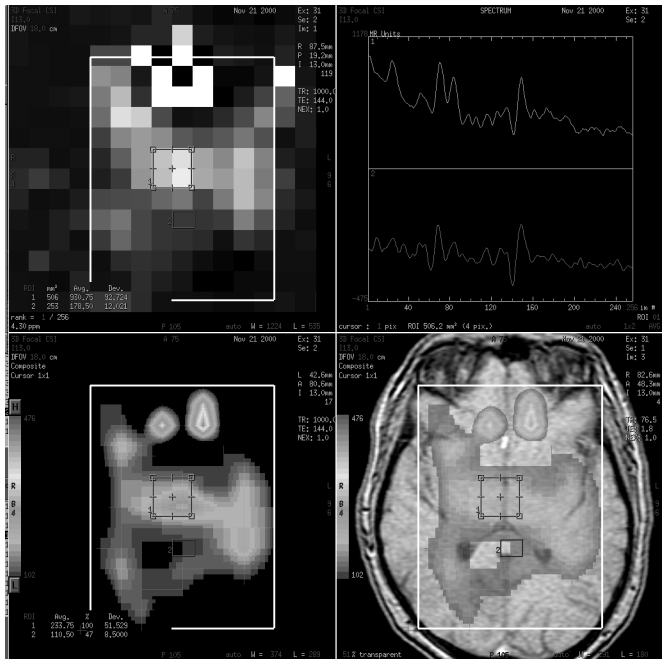


Figure 2: Demonstrates a typical Probe-P display with two ROIs, a reference image, and spectra.

Mouse use

The mouse buttons behave in a different manner when used in different areas of the viewports.

When clicked, or clicked and dragged over an active annotation (the red or bright white, alphanumeric characters in a viewport) the mouse buttons behave in a manner defined by, or consistent with the active annotation. Active annotations for each viewport are described later in the chapter.

When clicked in other areas of a viewport, the three mouse buttons behave in a fairly standard manner.

The left mouse button is used in combination with the cursor to select objects (e.g., a spectrum in the UR viewport or an ROI in any of the other three viewports), to drag or resize selected objects, to draw ROIs (when used with **Shift**), or to communicate a location to the display tool programs.

The middle mouse controls the viewport window width and level of the chemical shift (UL), of the metabolite image (LL), and the reference image (LR) viewports.

The right-click brings up viewport specific menus.

Keyboard use

The **arrow** keys can be used to increase or decrease items selected with the cursor – the behavior is identical to using the left and right mouse clicks, respectively.

You can use the **Ctrl-X**, **Ctrl-C**, and **Ctrl-V** key combinations to delete, copy, or paste an active (green) ROI. **Shift** is used with the left mouse button to draw an ROI.

You can use **Alt-F3** to raise and lower overlapping window on the desktop. For example, if you select **[Browser]** on the command window, the browser screen covers the display viewports and command window. To uncover the display viewports and command window, place the cursor anywhere on the Probe-P display tool and click **Alt-F3**. This key sequence can be used to raise and lower windows on any of the MR desktops.

Active annotations

Active annotations are the **red**, or **bright white** (on a black/white monitor), numbers, words, or acronyms displayed on the viewports (Figure 2). The active annotations respond or perform an action when the cursor is placed on the item and a mouse button is clicked, or clicked and dragged. You can increase or decrease active numbers by placing the cursor over the number, and clicking the left or right, respectively. Similarly, you can scroll the active numbers by clicking and dragging the middle button. You can also use the **left** and **right** cursor keys on the keyboard to increase or decrease a numeric value. Clicking on a red or bright white word allows you to change the display, or the location of a display. For example, to move the numeric lists that are displayed on the chemical shift, metabolite image, and reference viewports, click on the **ROI** active annotation and then drag and drop the list on another area of the viewport.

The **auto** active annotation automatically scales the display in a viewport. For the three viewports that display images or maps (UL, LL, and LR), clicking on **auto** automatically adjusts the window width and level of the displayed image/map. On the spectral grid (UR) viewport, selecting **auto** (or pressing the **Spacebar** on the keyboard) scales all spectra in that viewport to the active (green) spectrum. In this case, the maximum and minimum points in the active spectrum define the maximum and minimum spectrum display limits. A common scale allows you to compare and contrast signal intensities from several ROIs.

The **patient name**, displayed in red, or bright white, in the top left corner of each viewport, is an active annotation. Clicking the **patient name** displays a menu with the selection **[Hide patient name]**. The patient name region changes to ******** on all the viewports. You can redisplay the patient name by clicking the ******** and selecting **[Show patient name]**.

The **slice location**, displayed below the patient name, is an active annotation. You can page through the slice locations by clicking or clicking and dragging on this annotation. Multiple ROIs can be drawn on a slice or the slices of a 3D Focal CSI series. The ROIs are numbered sequentially in the order in which they are drawn on the slices.

Active annotations specific to each viewport are discussed later in this chapter.

Data smoothing conventions – The pixel smoothing feature that is a standard part of the MIROI or Functool software, should **not** be used with Probe-P maps. Keep the **"cursor: # pix" at 1.** Normally, the chemical shift images and metabolite maps in the three image views are displayed using simple pixel replication or smoothed using a bi-cubic smoothing algorithm. In addition, depending on the size of the cursor, a "regional" filter is applied to the images or maps. The size of the filtered region corresponds to the number of pixels used to define the cursor size. This means the information from 4, 9, 16, 25, 36, 49, 64, 81, or 100 neighboring pixels is smoothed. The number of pixels is given by the "cursor: # pix …" active annotation on the spectral grid viewport, or by the "cursor 1x1 …" display on the image viewports as shown in Figure 2. To avoid this "regional" data filter, set the cursor size active annotation to read "cursor: **1** pix …" on the spectral grid viewport. If you use any other cursor size, the numeric values corresponding to an ROI or pixel varies depending on the size of the cursor.

Image Pan/Zoom

Images or maps are displayed in three of the 4 viewports (Figure 2). Standard image annotations such as – DFOV, and A/P, R/L, and S/I that contain **red** or **bright white** numbers indicate that these are active annotations:

“DFOV **24.0** cm”, “A **120**”, “R **120**”, “L **120**”, and “P **120**”.

You can zoom by clicking on the DFOV **24.0** entry. You can pan the image by clicking and grabbing the **120**s. Zoomed, pixel replicated images with a split ROI are shown in (Figure 3). Select **[Display normal]** on the shortcut menus to undo the pan or zoom.

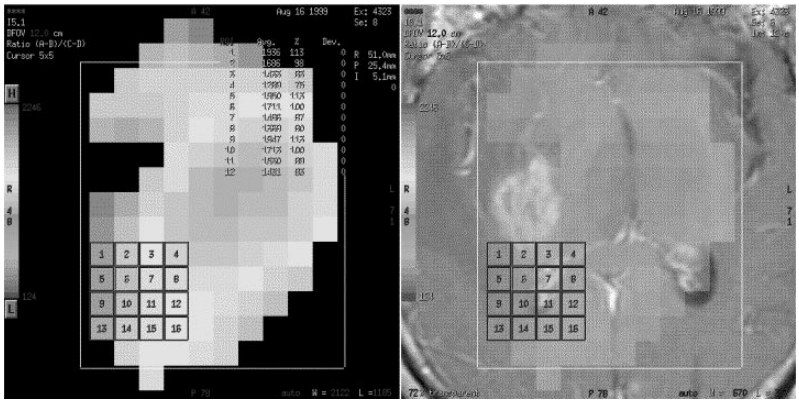


Figure 3: A zoomed display of a pixel replicated metabolite map and a split ROI.

Shortcut Menus

There are shortcut menus for each of the viewports with selections that allow you to modify the current and subsequent displays. Shortcut menus are accessed with a right-click anywhere on a viewport, except on an active (red or bright white) annotation, and drag and release on the desired option. The specific menus for each viewport are described later in this chapter.

Viewport Shortcut Menu Items

The following items may appear on the viewport shortcut menus.

You can toggle between **No smooth**/**Smooth**, **Hide**/**Show grid**, **Hide**/**Show Press ROI,** and **Show**/**Hide SAT bands** to show or hide these functions.

Feature	***Description***
Create Annotate	**Allows you to create annotation in the UL, LL, and LR viewports. Cursor must be in one of the 3 viewports.**
Color Ramps	**Allows you to change the color of the display. There are six choices: Rainbow (the default), Hot iron, Puh thallium, 3 colors, Gray levels, Inv. Rainbow (Inverted Rainbow).**
Display Normal	**Restores to the default image display if you have panned and/or zoomed the image. Window/level are not restored.**
Hide/Show graphics	**Must have cursor in viewport, selecting hides or shows graphics in that viewport only.**
Hide/Show grid	**Places the CSI acquisition grid over the image.**
Hide/Show PRESS ROI	**Hides or shows the voxel placement.**
Hide/Show SAT bands	**The graphically prescribed SAT bands are drawn on the reference image.**
Movie	**Allows you to view the chemical shift images, in the upper left viewport, in a movie mode, and allows you view the slices of the metabolite map in the lower left viewport, in a movie mode. Can use to check for patient motion.**
Save all	**Saves all the images of the series to the Display Browser as reformatted images.**
Save view	**Saves the current view to the patient data base as a screen save image in a separate series.**
Smooth/No Smooth	**Invokes a bi-cubic interpolation of the pixel data in the image, or a simple pixel replication, respectively.**

Table 1

The **Movie** option is available only in the upper left and lower left viewports. When selected a window opens allowing selection of movie display modes. Selecting Volume pages through the CSI slices or the metabolite slices, depending on

the viewport. Selecting Time highlights different signal intensities on the CSI image, and is only available on the chemical shift viewport. Rock and Loop are options for the sequence in which images are displayed. Rock alternates forward and reverse mode when the last image of the series is reached, for example: a series with four images displays 1, 2, 3, 4, 3, 2, 1. Loop is for continuous forward display of images, for example: a series with four slices displays 1, 2, 3, 4, 1, 2, 3, 4.

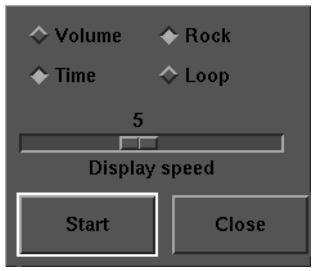


Figure 4: The Movies window.

The Chemical Shift or Upper Left (UL) Viewport

Individual chemical shift images, are displayed as non- zipped images, and are displayed in gray scale in this viewport. No smoothing is the default mode for displaying images in this viewport. The individual rank images can be used to characterize the homogeneity through the prescribed PRESS voxel, and the spatial variation of the water suppression. The rank is the number assigned to the image when the images are sorted by increasing time. Large variations in both appear as dark and light regions as in (Figure 5). Each rank image

corresponds to the spatial distribution of one of 256 equally spaced frequencies between 4.3 and 0.49 PPM.

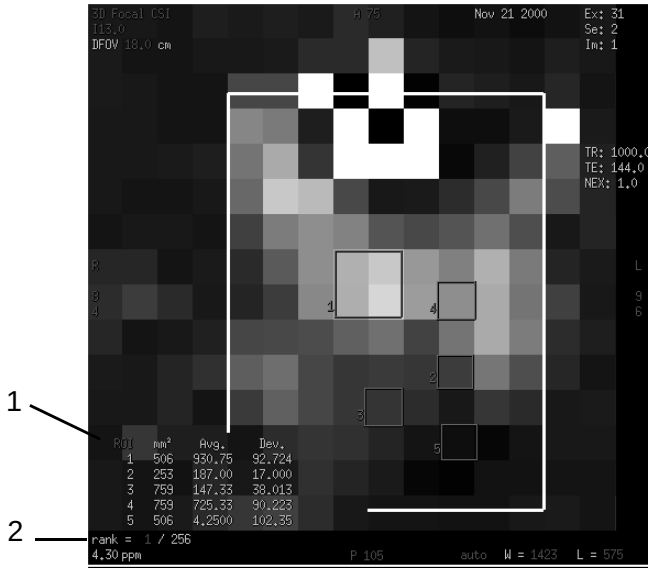


Figure 5: The chemical shift viewport, rank=1 display with five ROIs.

Initially, the first of the 256 chemical shift images is displayed, as indicated by the rank = **1** / 256 (2) entry displayed at the bottom left of the viewport. The rank number of the displayed chemical shift image is an active annotation and can be changed with the mouse buttons or the **arrow** keys. A right mouse click decreases the rank number and a left mouse click increases the number.

General information for each ROI is printed in this window. In the example (Figure 5), a column of ROI numbers (1) labeled "**ROI**", a column labeled "mm^2" which lists the area in millimeters for each ROI, and a column labeled "Avg." are displayed in the bottom left corner of the viewport. The average of the signals from the pixels in each ROI is listed in the "Avg." column. Depending on the selected metabolite a "Dev." column may appear showing the standard deviation. The ROI list can be moved to another part of the viewport by clicking and dragging the ROI label with the middle mouse.

The Chemical Shift Viewport Shortcut Menu

The default shortcut menu contains eight selections. Right-click in the upper left (UL) viewport to access this menu. Once an ROI, other graphic object, or annotation has been placed on the

viewport, other toggle items are added to the menu such as Hide/Show graphics and Hide/Show annotation.

Figure 6: Chemical shift viewport shortcut menu.

The Spectral Grid or Upper Right (UR) Viewport

One to at least 250 spectra can be displayed in this viewport; the initial display is blank. Three display colors are used for the spectra; green for the spectrum from the “active” ROI, purple for spectra from any other ROIs, and white for the spectrum corresponding to the cursor location when the cursor is used to select a spatial region on one of the image display viewports. The signal intensity for each of the 256 points in a spectrum can be listed for the spectra from 1- 8 ROIs (Figure 7). This list is accessed with a right-click in the spectral grid viewport and drag to select **List values**. You can click on the image number located at the top of the list (indicated by the red or bright white text) to scroll through the list. Left-click to increase and

right-click to decrease the image number. (For example, the “Rank im #,” number 65 in Figure 7.)

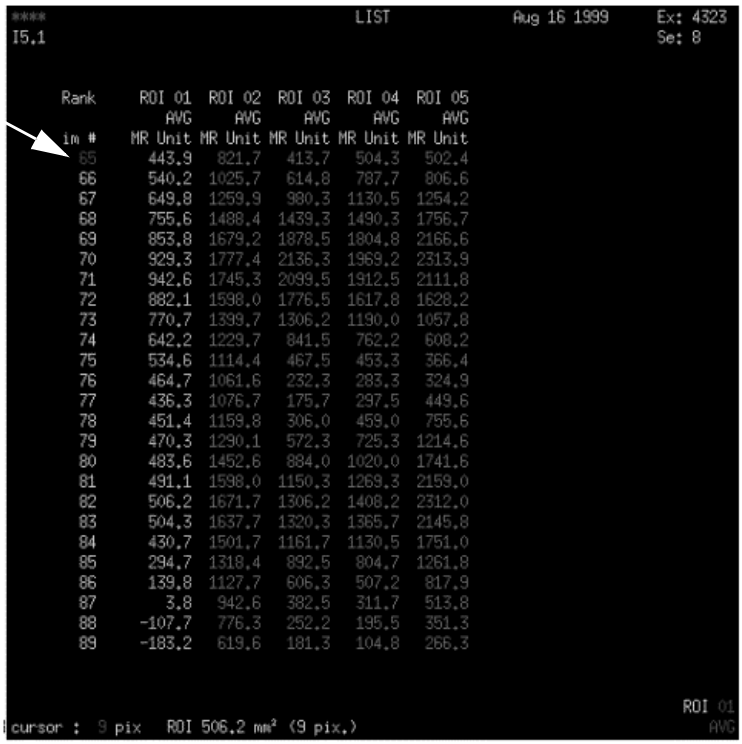


Figure 7: Spectral grid viewport with a list of signal intensities from five ROIs.

When you move the cursor on the spectrum or spectra displayed in the spectral grid viewport, two white lines intersect on the display and two numbers are displayed in white along the x- and y-axes (Figure 8). The x-axis number corresponds to the image rank number or to the PPM value of the chemical shift image (the 4.30 to 0.49 PPM region of the spectra is

displayed). The y-axis number corresponds to the signal intensity at the cursor location on the spectrum.

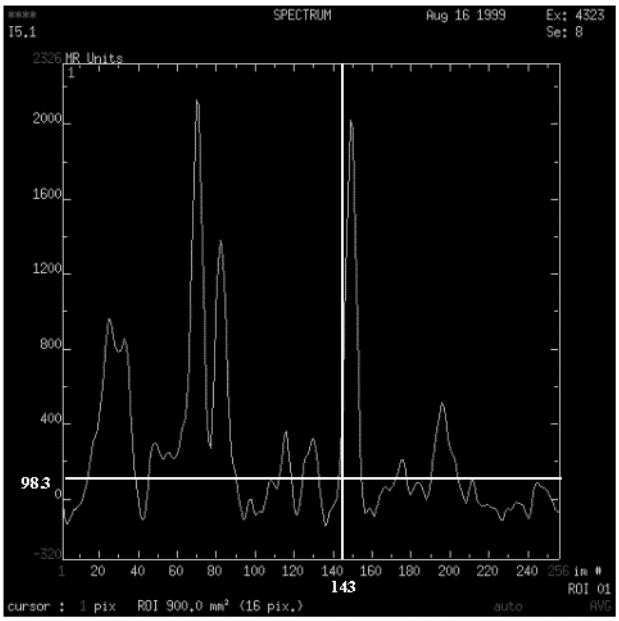


Figure 8: Using the cursor to display the signal intensity at a point in the spectrum.

You can also display the rank or complete chemical shift image in the chemical shift viewport (UL) for a given point in a spectrum by double clicking on a spectrum. For example, if you double click on the spectrum at point 143, the display in the chemical shift viewport changes to the 143rd rank or chemical shift image, and the UL display is “rank = 143 / 256”. The image number (im #) is the default for the x axis, to change, right-click

in the spectral grid viewport, drag to **Set x units** and select **ppm**.

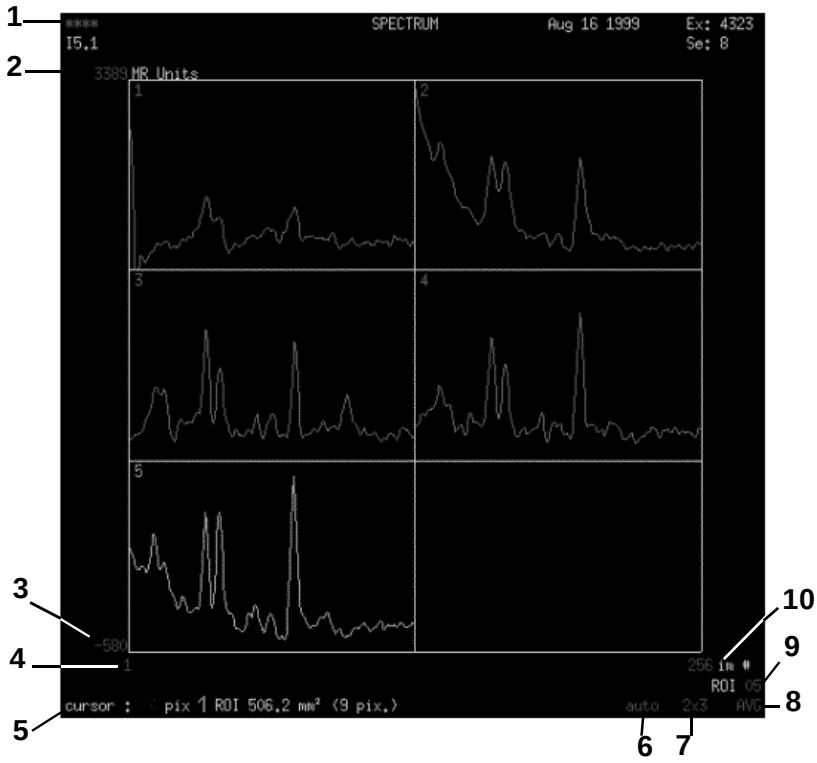


Figure 9: Spectra displayed in the spectral gird viewport.

Active annotations

There are ten active annotations in this viewport. In Figure 9, the active annotations, starting at the top left and moving down, are:

- (1) ******** – the patient name, which has been hidden in Figure 9.
- (2) **3389** – the current y-axis maximum value, used to scale the spectra.
- (3) **-580** – the current y-axis minimum value, used to scale the spectra.
- (4) **1** – the current x-axis starting image, used to zoom the spectra – units are points or rank image as shown in Figure 9, or PPM.
- (5) **cursor: 1 pix** – i.e., the number of pixels averaged to produce the cursor spectrum, and used to determine the extent of the cursor size smoothing region. **Set the value to one to avoid cursor size smoothing.**

- (6) **auto** – click to automatically scale the vertical spectra to the active spectrum (ROI) – pressing the **space bar** has the same effect. Select either an ROI or a specific spectrum in the UR viewport and click **auto**. The other spectra are vertically scaled to the selected ROI or spectrum.

- (7) **2x3** – click to toggle between the display of separate spectra, as shown in Figure 9, or to display the spectra superimposed on one frame, i.e., **1x1** (Figure 10).

- (8) **AVG** – click to toggle between the four spectrum display selections, AVG, MAX, MIN, and DEV (standard deviation) – these selections are explained later in the chapter.

- (9) **ROI 05** – indicates the active spectrum (ROI), click to change the active spectrum, clicking on the word “ROI” deselects the active spectrum (ROI).

- (10) **256 im #** – the current x-axis ending image, used to zoom the spectra – units are points or rank image as shown in Figure 9. If you set x units to PPM (using the shortcut menu, accessed with a right-click), the x (horizontal) scale changes to 4.30 - 0.49 ppm. With the cursor over the active annotation of 0.49, a right click increases this value and a left click decreases this value, the range is 0.49 - 4.29 ppm.

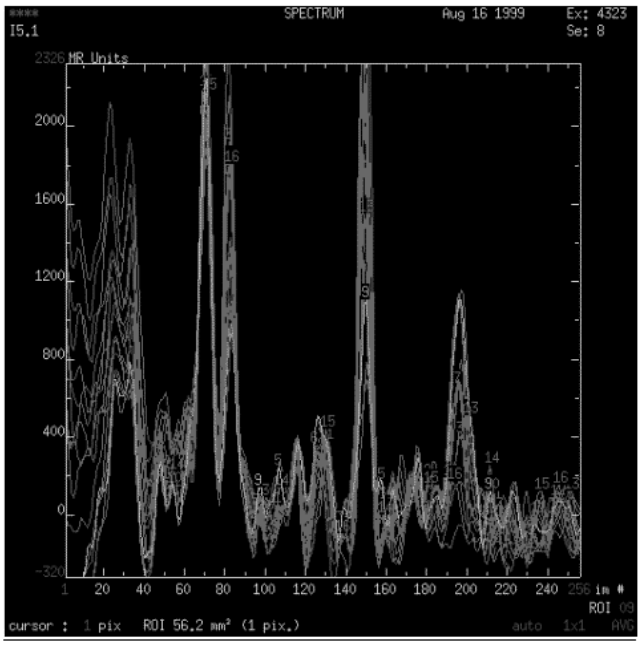


Figure 10: Superposition of 16 spectra in the spectral grid viewport.

Active Spectrum (ROI)

In the spectral grid viewport, to change the active spectrum (ROI) click on the spectrum, or click on the ROI active annotation. The active spectrum is always drawn in green.

Y-axis and Spectrum Scaling

Spectra can be scaled to fit the display window by clicking, or clicking and dragging the y-axis maximum and minimum active annotations. It is also possible to automatically scale the active spectrum to fit the display window or a frame by pressing the **Spacebar** on the keyboard, or clicking on the **auto** active annotation. If more than one spectrum is displayed, all spectra are scaled to the active spectrum (ROI) with these selections. Unless explicitly changed, the scale stays the same.

X-axis, Image Rank and the PPM Scale, and Spectrum Zooming

You can zoom the spectrum by clicking on the x-axis limits to select the region of the spectrum that you wish to display. Each spectrum consists of 256 points, one for each of the 256 Chemical Shift or rank images stored in a CSI data set. The spectra cover a frequency range from 4.30 to 0.49 PPM.

The PPM (parts-per-million) scale relates all resonant frequencies (peaks) to a standard frequency (i.e., on a Signa system to *in vivo* water at 4.7 PPM), and is independent of the field strength. At 1.5T, a change of 1.0 PPM corresponds to a change of approximately 64Hz. The N-acetyl groups resonate at 2.0 PPM, a frequency that is 2.7 PPM or 173Hz lower than the resonant frequency of the hydrogen atoms in the water molecule.

Unfortunately the resonant frequency of the hydrogen atoms in the water molecule is temperature dependent, while the resonant frequencies of the metabolites are relatively constant between 10-50°C. A water temperature change of one degree Celsius (1°C) corresponds to a frequency change of 0.6Hz (approximately 0.01 PPM). For example, the resonant frequency of water at 21°C is about 10Hz lower than the frequency of water at 37°C (body temperature). The PROBE/SVQ, probe SI, and 3D Focal CSI spectra are processed assuming tissue water resonates at 4.7 PPM, i.e., the tissues are at or near 37°C. When acquiring data from a

phantom at a temperature other than 37°C, the quantitative analysis program often fails, and/or the reconstructed spectrum may be shifted by the temperature dependent shift of the water resonance from 4.7 PPM.

Cursor Location Spectrum

The spectrum associated with the cursor location is the spectrum from one pixel, or an averaged value of the spectra from 4, 9, 16, 25, 36, 49, 64, 81, or 100 pixels. The number of pixels is selected by clicking on the cursor: # pix active annotation at the lower left of the viewport. The cursor spectrum is always displayed in white, and is always the last spectrum in a multi-spectrum display.

NOTE: Before displaying any metabolite or ratio maps, set the cursor value to one to avoid additional smoothing (based on the size of the cursor) of the maps.

Superimposed Spectra or Individual Spectra

In the initial or default display of multiple spectra - the 1x1 active annotation, (Figure 10) the spectra are superimposed on the display. The spectra are scaled to the maximum and the minimum values found in the set of selected spectra or to the last scale selected. Separate spectra, one for each ROI, are displayed in smaller individual frames for an NxN active annotation. In Figure 9, the five spectra are displayed as a 2x3 array, and the active annotation is 2x3.

Spectrum Average or Compression Techniques

The spectra or signal intensity lists can be displayed using one of 4 different methods to combine the data from more than one pixel. The four methods are:

- **AVG** - displays the average of the pixel values,
- **MAX** - displays the maximum pixel value for each point,
- **MIN** - displays the minimum pixel value for each point,
- **DEV** - displays the standard deviation for each point.

For spectra corresponding to a single pixel the AVG, MAX, and MIN methods produce identical spectra and intensity lists, and the DEV selection produces straight lines. Typically the default AVG selection should be used to display the spectra.

The Spectral Grid Viewport Shortcut Menu

This shortcut menu has several options and toggle options, that can be accessed with a right-click in this viewport. If an option is

selected, the menu contents change. The default shortcut menu and the sub-menu selections are:

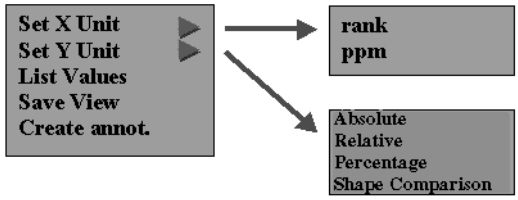


Figure 11: Spectral grid viewport shortcut menus.

If you place an ROI on one of the image viewports or you use Create annot., additional items are added to the shortcut menu as shown in Figure 12:

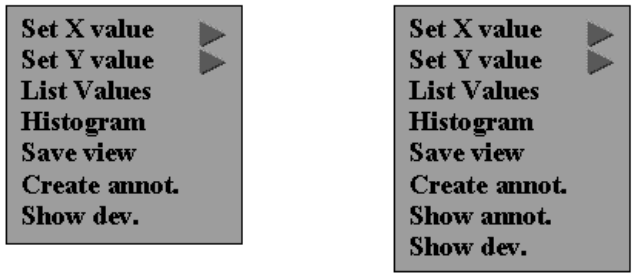


Figure 12: Expanded spectral grid viewport menus.

The toggle selections in the menu are: **List Values** and **Spectrum**, and **Show**/**Hide dev.** The **Show**/**Hide annot.** toggle selection only appears if you select **Create annot.**

- Under **Set X Unit** you have the option of choosing **rank** or **ppm**: Sets the x-axis unit label. The choices are points (image rank) or PPM (parts per million). Each spectrum consists of 256 points, one for each of the 256 chemical shift or rank images stored in a probe-P image. Each spectrum covers the range from 4.30 to 0.49 PPM.
- Under **Set Y Unit** you have the option of choosing **absolute**, **relative, percentage,** or **shape comparison**. For probe-P data display, always select **absolute** which plots the actual pixel values for each point. The other choices are meaningless for spectral data.
- **List Values** or **Spectrum**: Toggles between the spectrum display, and the display of a scrollable list of signal intensities (Figure 7) for each point in the spectrum.

Histogram: Displays a histogram of the data in an ROI. This selection is only available if an ROI has been placed on the images. If selected, the shortcut menu is reduced to three

selections, **Spectrum**, **List Values**, and **Save View** as shown in Figure 13, and the shortcut menu is limited to three selections until you select the **Spectrum** display again.

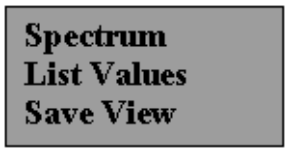


Figure 13: Spectral grid viewport menu if **Histogram** is selected.

- **Show dev.** or **Hide dev.**: Shows or hides the deviation or measure of variability of the plotted data.

The Metabolite Image or Lower Left (LL) Viewport

Average or Ratio metabolite maps corresponding to the protocols selected with **[Get Protocol]** or **[Function]** are displayed and manipulated in the lower left (LL) viewport. In the metabolite image viewport, the prescribed PRESS voxel is overlaid (the voxel is outlined in white) on the map as shown in Figure 14.

The metabolite maps are a combination of spatial and spectral signal intensity information. The maps are derived from the CSI rank images that can be viewed individually in gray scale in the chemical shift viewport. Average maps are created by combining/averaging several contiguous CSI images. The contiguous regions (see Table 2) correspond to the locations of the metabolite resonances or peaks.

Metabolite	***Image range***	***PPM***
Choline	**images 64..74**	**3.24 +/- 0.08 ppm**
Creatine	**images 78..88**	**3.02 +/- 0.08 ppm**
N-Acetyl	**images 143..154**	**2.02 +/- 0.08 ppm**
Lactate and Lipid	**images 183..222**	**0.9..1.5**
Startup	**images 50..200**	**3.5-1.33**
Composite	**images 64..222**	**0.9..3.32 ppm**

Table 2

Ratio maps are a simple extension of the average technique in which two different, contiguous sets of CSI rank images are separately combined, and then the two combined images are divided to produce a ratio map. In essence, a map corresponds to the spatial distribution of the signal intensity of a region of a spectrum, or of the ratio of signal intensities in two regions of a spectrum.

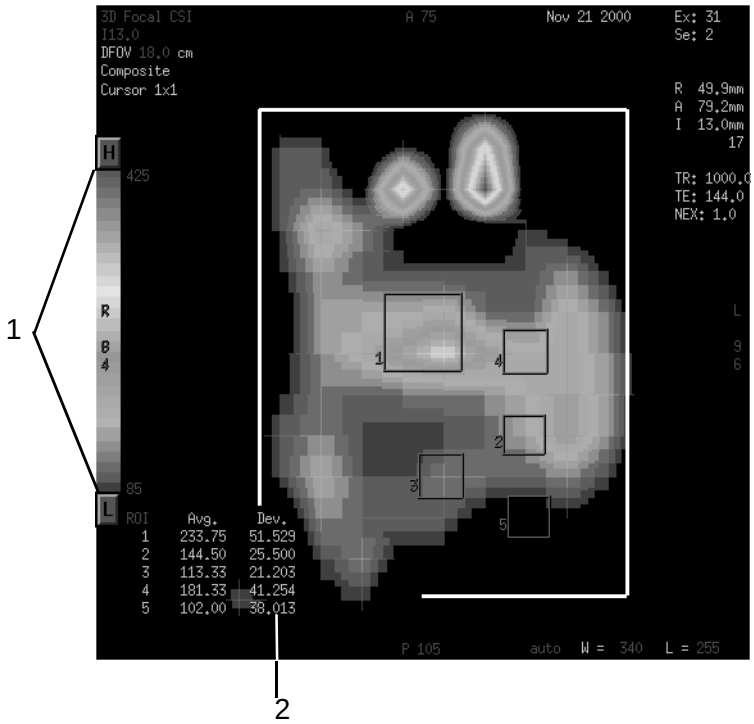


Figure 14: Metabolite image viewport display.

A numeric list of information appropriate to the current metabolite map or ratio map for each ROI is displayed on this viewport. The default location of the list is at the bottom left of the viewport. Click and drag the ROI text to move the listed information to another area of the viewport. In the example (Figure 14), ratios from five ROIs are listed. The “Dev.” column (2) displays the standard deviation of the selected metabolite. Depending on the metabolite chosen instead of “Dev.” a “%” column appears showing the relation of the individual ROI ratio values to the 100% value assigned to the active (green) ROI. The ratio for the active, fifth ROI is listed as 1082.2 (the actual value is 1.0822 which is scaled by 1000). The ratio for the fourth ROI is listed as 1555.5 which is 43% greater than the ratio from the active ROI.

Depending on the metabolite chosen instead of a “%” column you may be given a “Dev.” column displaying the standard deviation.

You can adjust the window width and level of the map by clicking and dragging the middle mouse, or by clicking on the active annotations at the bottom left of the viewport – “W = 340” or “L = 255” in Figure 14. The range of the color scale (1) at the left edge of the viewport is related to the window width (W) and window level (L) as:

colorscale maximum = W + L/2,

and

colorscale minimum = W – L/2.

You can adjust the colorscale maximum and minimum by clicking on the numbers at the top and bottom of the colorscale; 425 and 85 in Figure 14. If you select **[H]** at the top of the colorscale, those pixels in the map with an intensity larger than the maximum colorscale intensity are colored black. If you select **[L]** at the bottom of the colorscale, those pixels with an intensity less than the minimum colorscale intensity are colored blue. The **[H]** selection allows you to quickly see the maximum areas on any map.

If you change the display in the metabolite image viewport, e.g., if you zoom on the image or adjust the window width or level, the same changes or selections are applied to the metabolite map overlaid on the LR reference viewport.

The Metabolite Image Viewport Shortcut Menu

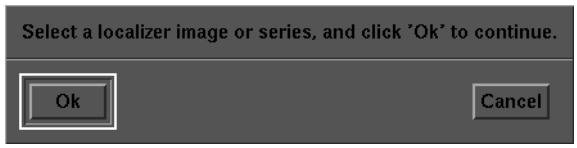
To access this menu, right-click in the viewport. The default shortcut menu contains four toggle selections – **No smooth**/**Smooth**, **Show**/**Hide grid**, **Hide**/**Show Press ROI**, and **Show**/**Hide SAT bands**. Once an ROI, any other graphic object, or annotation has been placed on the viewport, an additional toggle item is added, **Hide graphics** and **Show graphics** is added to the menu. Menu options selected in this viewport that affect the display of the map in the metabolite

image viewport have the same effect on the map overlaid on the reference viewport. The contents of the menu are:

Figure 15: Metabolite image viewport shortcut menu.

The Reference or Lower Right (LR) Viewport

Initially the display in the reference viewport consists of a metabolite map at a 50% transparency level overlaid on the localizer image currently displayed in the chemical shift viewport with the prescribed PRESS voxel outlined by a white line (Figure 1). When the display tool is launched a dialog box appears asking you to select a localizer image, highlight the localizer series from the Display Browser, the default is image three of the selected series.



This localizer reference image is displayed in the reference viewport, as shown in Figure 16.

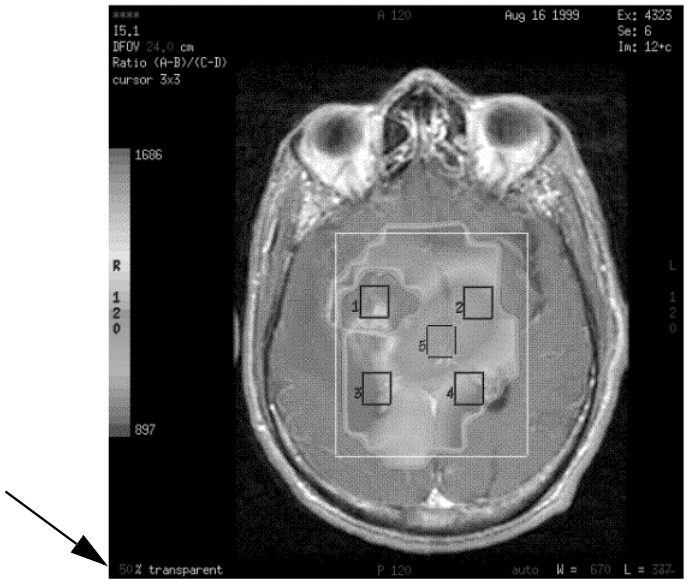


Figure 16: Reference viewport display with reference image.

You can adjust the transparency of the overlay by clicking on the 50% transparent (arrow) active annotation. You can adjust the window width and level of the localizer image by clicking and dragging the middle mouse.

The Reference Viewport Shortcut Menu

The default shortcut menu contains 10 selections. These selections are accessed with a right-click in the viewport. Once an ROI, any other graphic object, or annotation has been placed on the viewport, other menu options appear.

The contents of menu are:

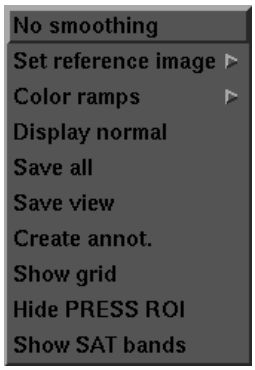


Figure 17: Reference viewport shortcut menu.

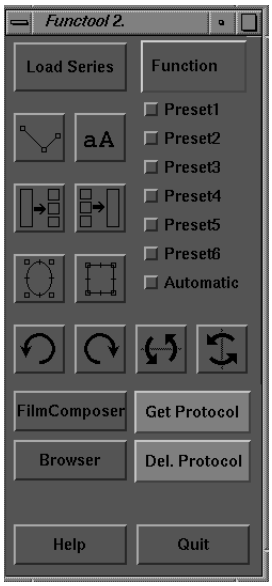
- **Set Reference Image** to display a selected image, or the original, default display. The shortcut options are **original** and **selection**.

The selection properties are:

- The default display in this viewport is a metabolite map at a 50% transparency level overlaid on the default image of the localizer series that you selected. Use **Set reference image** to display an image from a selected series, or the original CSI image with smoothing.
  - ° If you select **original,** the smoothed CSI image appears with a metabolite map overlay.
  - ° If you select **selection**, the localizer (selected) series, image three appears with a metabolite map overlay.

3D Focal CSI Display Tool Command Window

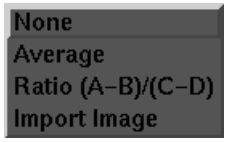
There are several different features of the command window that should be considered and require further explanation.



Function

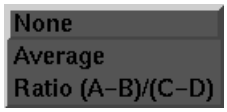
The Function menu allows a number of choices to display the CSI data. These choices differ from the selections on the **[Get Protocol]** menu, in that the Function menu selections cannot

be modified and include no information concerning the definition of the protocols.

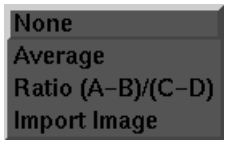


The Function menu selections opens to a set of metabolite selections.

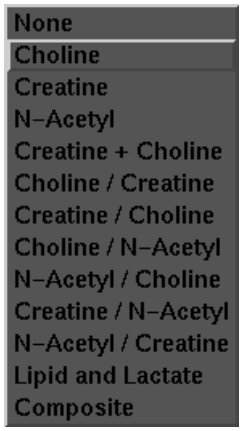
The General menu displays the following choices:



The Research menu displays the following choices:



The Spectroscopy menu displays the following choices:



The map of the metabolite or ratio of metabolites is displayed.

If you select a metabolite or ratio, such as Creatine/Choline a dialog box appears with the options for **[Compute]**, **[Save Protocol]**, **[Close]**, and **[Help]**.

- **Compute** - Clicking allows the changes that you make to the parameters on the panel are invoked by clicking **[Compute]**. Whenever you click **[Compute]** the protocol title on the Function parameters panel, the function view,

and the composite view is changed to the generic “Average” or “Ratio (A-B)/(C-D)”.

- **Save Protocol** - Clicking allows you to save the metabolite or ratio as a protocol that can be stored and recalled for future use. Enter the name of the new protocol in the entry text box on this panel. To accept, and create the new protocol, click **[OK]**. Click **[Cancel]** to leave the “Save protocol” panel without creating the new protocol. User created protocols can be deleted at any time by clicking **[Del. Protocol]** on the Main Control Panel.
- **Close** - Allows you to exit from the Function parameters dialog box. Generally you would only use **[Close]**.
- **Help** - Clicking **[Help]** enlarges the Function parameters panel to include an explanation of the protocol, simple algorithmic information, and definitions of the parameters. **Help** allows viewing of the absolute value for the selected metabolite or ratio. This value cannot be changed, it is for viewing only.

Selecting a protocol from the **[Function]** menu, a Function parameters window (Figure 18) appears over the lower two viewports. No input lines are displayed on these windows and the selected protocols cannot be modified.

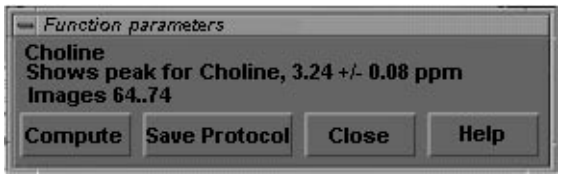
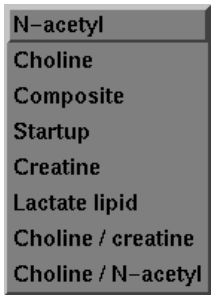


Figure 18: The Function parameters window appears.

Get Protocol

Selecting **[Get Protocol]** displays the metabolite map or metabolite ratio map using the pre-defined spectral regions to calculate the metabolite or ratio maps.



The following is brief description of the protocols:

- **N-acetyl** – displays the averaged, absolute pixel values from CSI image 143 through image 154 as a metabolite map,
- **Choline** – displays the averaged, absolute pixel values from CSI image 64 through image 74 as a metabolite map,
- **Composite** – displays the averaged, absolute pixel values from CSI image 64 through image 222 as a metabolite map,
- **Startup** – displays the averaged, absolute pixel values over the region 50-200. This is a good picture of the excited ROI.
- **Creatine** – displays the averaged, absolute pixel values from CSI image 78 through image 88 as a metabolite map,
- **Lactate lipid** – displays the averaged, absolute pixel values from CSI image 183 through image 222 as a metabolite map,
- **Choline/creatine** – displays a map of the ratio of the choline, 64 -74 region, to the creatine, 78 – 88 region,
- **Choline/N-acetyl** – displays a map of the ratio of the N-acetyl, 143 – 154 region, to the choline, 64 – 74 region.

Selecting a protocol from the **[Get Protocol]** menu on the command window, a Function parameters window, specific to the protocol, is displayed. Windows similar to those seen in Figures 19 and 20 appear. You can modify these windows, although the startup and composite windows cannot be modified. The Function parameters window for the Average metabolite maps of N-acetyl, choline, creatine, and lactate-lipid regions is fairly simple, with one input parameter line that defines the metabolite region and combining method (Figure 19).

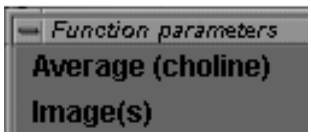


Figure 19: Function parameters window for the Average (choline) protocol.

If you select one of the Ratio (A-B)/(C-D) map protocols from the **[Get Protocol]** menu, a more complex window (Figure 20), is displayed. For the pre-defined choline/creatine and N-acetyl/choline ratio protocols, four of the 6 input parameter

lines are used to define 2 spectral regions, a threshold factor, and a scale factor.

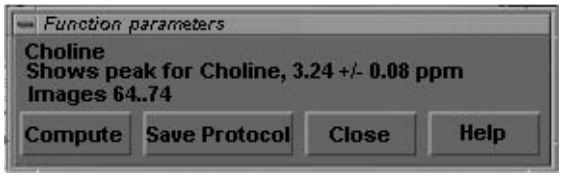


Figure 20: Function parameters window for the Ratio (choline/N-acetyl) protocol.

Both Average and Ratio (A-B)/(C-D) Function parameters windows contain four (4) selectable buttons. The four buttons shown in Figure 19 or 20 are labeled; **[Compute]**, **[Save Protocol]**, **[Close]**, and **[Help]**. Typically, you would only use **[Close]** to close the window.

- **[Help]** enlarges the Function parameters window to include an explanation of the protocol, simple algorithmic information, and definitions of the parameters.
- Changes made to the parameters in the input parameters text boxes are invoked by selecting **[Compute]**. Whenever you click **[Compute]** the protocol title on the Function parameters window, the metabolite image viewport, and the reference viewport is changed to the generic Average or Ratio (A-B)/(C-D).
- To save the changes for future use, click **[Save Protocol]**. Enter the name of the new protocol in the text box. Selecting **[OK]** creates and saves the new protocol.
  - Selecting **[Cancel]** leaves the Save protocol window without creating the new protocol. User created protocols can be deleted at any time by selecting **[Del. Protocol]** on the command window and drag to the protocol to delete.
- Click **[Close]** to close the window.

The Function parameters window for the Ratio (A-B)/(C-D) (choline/N-acetyl) protocol displayed in Figure 20 is the basis for all of the spectroscopy Function parameters windows. The Average (choline) example in Figure 19 is a simplified version of the ratio window.

In addition to the four selectable buttons, the window has six input parameter text boxes:

- The first four text boxes, labeled **Image(s) A**, **Image(s) B**, **Image(s) C**, and **Image(s) D**, specify an image or a range of images used in the protocol calculations. The values

returned by the pre-defined protocols are the scaled values of A, or A/C. It is possible to return the values of A, A – B, A/C, (A – B)/C, or (A – B)/(C – D), depending on which input parameter text boxes are left empty. For example, to return the simple ratio A/C, the B and D input parameter text boxes are left empty as shown in Figure 20. Clearly the Image(s) A input parameter text box can not be empty.

- The fifth text box specifies a pixel value **Threshold** used to suppress background noise or spurious signals. The threshold value is compared to the value of the denominator C or (C – D); whenever the denominator is less than the threshold value, the ratio is set to zero, and appears as a black pixel in the ratio map.
- The last parameter text box defines a **Scale** factor. A scale factor of 1000 is recommended to minimize round-off and integer truncation artifacts. For example, a scale factor of 1000 means that ratio values like 1.432 or 0.789 are listed in the metabolite image viewport as 1432 and 789, respectively. Using a smaller scale factor, in most cases, reduces the number of digits in the ratio. For example, scale factors of 100, 10, and 1 would scale the 1.432 value as 143, 14, and 1, respectively. Scale factors other than 1, 10, 100, or 1000 makes either visual or simple arithmetic comparisons of the spectra and ratio values difficult and are not recommended.

The general Ratio (A-B)/(C-D) algorithm uses the threshold and scale factors to return a value for each pixel in the ratio map according to the general equations:

if Threshold $\leq$ (C – D) then,

Pixel Value = Scale * (A – B) / (C – D),

or if Threshold > (C – D),

Pixel Value = 0.0 (the pixel is set to black on the ratio map).

The **Image(s)** input parameters can be a single image **N**, or a range of images **N..M**. For spectra this means either a single point, or a range of points in the spectra, respectively. There are also five, 3 letter input parameter prefixes that can be used to modify the combination of the points in the given region of the spectrum during a calculation:

- **abs N..M** – returns the average of the absolute values of the pixels in the range,

- **min N..M** – returns the minimum pixel value from the range,
- **max N..M** – returns the maximum pixel value from the range,
- **log N..M** – returns the average of the natural logarithms of the pixels in the range,
- **dev N..M** – returns the standard deviation of the pixels in the range.

The input entry text boxes in the pre-defined protocols for the four metabolite maps, and two metabolite ratio maps are all of the form **abs N..M**. Image or spectral regions are defined for three chemical species (N-acetyl groups, choline, and creatine), and a region containing the two chemical species lactate and lipid. The startup and composite protocols combine the signals from most of the spectral region.

The choline, creatine, and N-acetyl regions are used to define the input parameter entries for the choline/creatine, and the choline/N-acetyl ratio maps. Using the Function parameters window for the choline/N-acetyl Ratio map in Figure 20 as an example, the absolute values of the signal intensities for the chemical shift images 64 through 74 (**Image(s) A = abs 64..74**) are divided by the absolute values of the signal intensities of the chemical shift images 143 through 154 (**Image(s) C = abs 143..154**) using a threshold value of **2000**. The quotient is multiplied by the **1000** scale factor.

NOTE: A scale factor should be a multiple of 10.

The ratio map for with this protocol is calculated using the equation:

Pixel value = 1000 * (abs 64..74) / (abs 143..154)

where any value of **(abs 143..154) <2000** is set to zero.

Region of Interest

To place an ROI on the chemical shift, metabolite image, and reference viewports click either **[square ROI]** or **[ellipse ROI]**. A green (active) ROI is drawn at the center of the three image viewports. The ROI can be moved or resized by clicking on the resizing and movement handles on the ROI – the handles are only present on an active ROI. Alternatively, you can select **Shift**, left-click and drag to draw an ROI.

Once an ROI has been placed on the viewports, it can be split or divided to display the reconstructed CSI pixels contained within the ROI as shown in Figure 3. To split the ROI, select

[split ROI]. To return to the merged or single ROI, click **[merge ROI]**. Note that an ROI of any shape – rectangle, ellipse, or freely drawn – is composed of the square, reconstructed CSI pixels. By selecting **[split ROI]** you can always see which CSI pixels contribute to the ROI, and to the numeric information displayed or listed for the ROI. Once the ROI has been split it is possible to move and delete the individual CSI pixels.

Hints

Using Numeric Data Lists

To insure that the numeric data from an ROI that is listed on one of the 3 image viewports is consistent and reproducible, always set the cursor size active annotation on the spectral grid viewport to read “cursor: **1** pix …” (arrow Figure 21). The cursor size is also indicated by the “cursor 3x3 …” (circled Figure 22) annotation near the top left corner of the metabolite image and reference viewports. Using a value other than one invokes an additional pixel smoothing algorithm for the metabolite and ratio maps that varies with the cursor size.

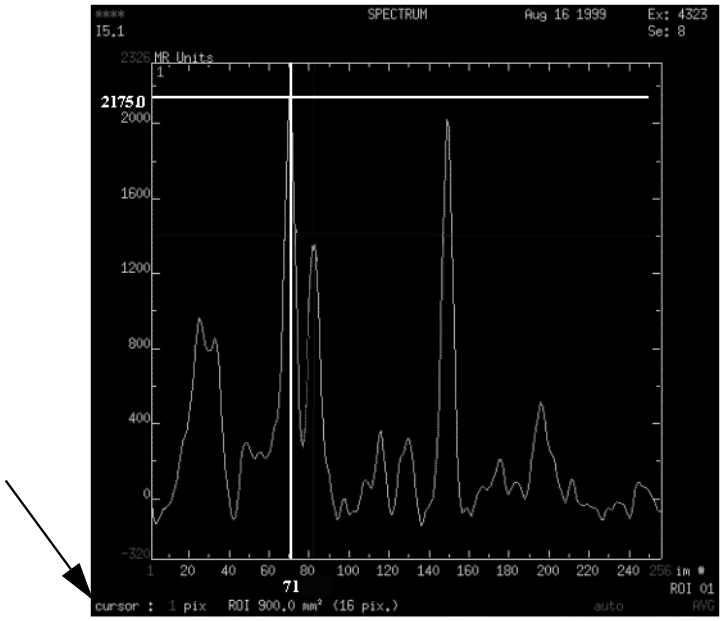


Figure 21: Solid White=choline peak maximum.

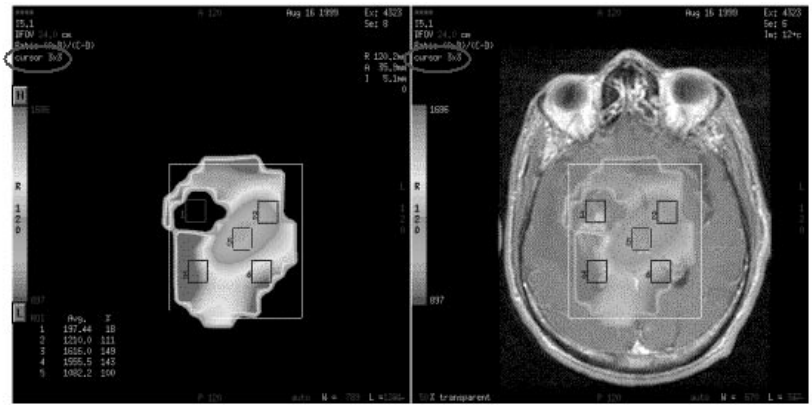


Figure 22: Metabolite image and reference viewports with nine (3x3) pixel cursor smoothing.

Metabolite and Ratio Maps with Sharp Edges

Occasionally the metabolite and ratio maps terminate with a sharp edge. The sharp edges are often an artifact of the cursor size smoothing algorithm noted just above. To avoid these artifacts always set the cursor size active annotation on the spectral grid viewport to read “**cursor: 1 pix …**”.

Saving and Filming Images

For more information regarding filming images see, Volume 1, Chapter 10.

When saving images in FuncTool there are two things you should remember:

- Right mouse click on the image and drag to **Save View**.
- Images do not save in color. Data set must be re-processed through FuncTool to display color.

How to Post Process Images with FuncTool

This section provides the step-by-step instructions describing how to:

- Display Valid Image Sets
- Display Various Graphs
- Create Parametric Images
  - Function Algorithm
  - Protocol Algorithm
- Adjust the Composite Overlay
- Display 3D Focal CSI Images
- Create a Custom 3D Focal CSI Protocol

Display Valid Image Sets

Use this procedure to load and display valid image date sets into FuncTool. You should already be familar with basic mouse functions before attempting this section.

To perform this and other tasks in this section you should have already acquired your valid image sets by using the GE pre-defined protocols listed in their appropriate sections.

1. Click on the **[Display Desktop]** icon.
2. Select the patient on the exam Display Browser. Then select the series you wish to load into FuncTool.
3. Click on **[FuncTool]**, located on the right side of the Display Browser screen. The selected series loads into FuncTool.

NOTE: The series automatically loads the mid-line slice of the series.

- If you desire another location to be displayed, place cursor on the red location annotation on the reference image and click with the left mouse to decrease location or the right mouse to increase the image location.
- If you desire another phase/rank image to be displayed, place the cursor on the red rank annotation on the reference image and click with the left mouse to increase image phase/rank or click with the right mouse to decrease image phase/rank.

4. You can window and level the image to your preference, by using the middle mouse button.

Display the Graphs

After a valid data image set has been loaded into FuncTool you may want to display different graphs. To do this the steps are as follows:

1. Identify an area on the image you wish to concentrate on.

NOTE: If you place your cursor on this area a time intensity curve appears in the graph section. Whenever you move the cursor a new graph curve appears. This curve graph is not set until you place an ROI.

2. Define your area of interest by using an ROI. To do this click the **[Elliptical ROI]** or **[Square ROI]**.

3. Size and position the ROI over the area of interest. Once sized and positioned, tap the **Space bar** to scale and display time intensity curve.
4. To display the time intensity curve in time units. Position the cursor on the time-intensity curve in the upper right quadrant, right click and drag to **Set X-axis,** and select **Time**.
5. To display the time intensity curve in image number. Position the cursor on the time-intensity curve in the upper right quadrant, right click and drag to **Set X-axis,** and select **Rank**.
6. To display a histogram instead of a time-intensity curve. Position the cursor on the time-intensity curve in the upper right quadrant, right click, and drag to **Histogram**.

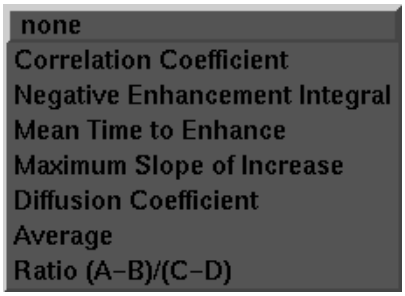
Create Parametric Images

Function Algorithms

To create a parametric image using algorithms located under the Function button.

1. Click the **[Function]** 

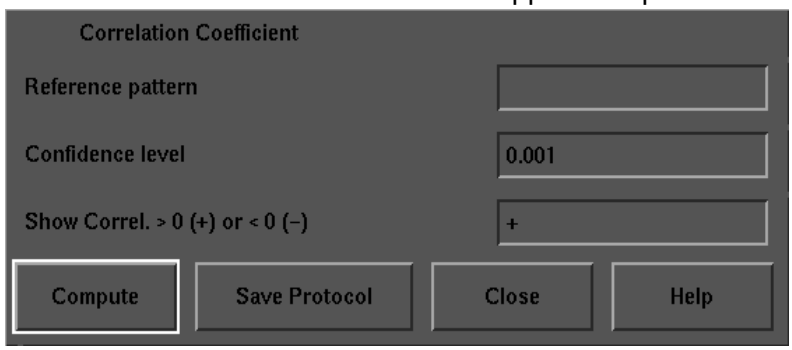
button. The function menu appears.



2. Click the desired algorithm.

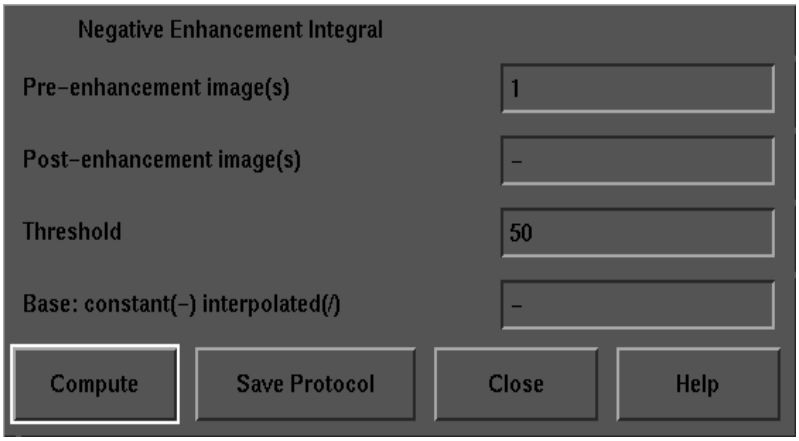
   ° Select **Correlation Coefficient** for task activation.

   The Correlation Coefficient menu appears. Input



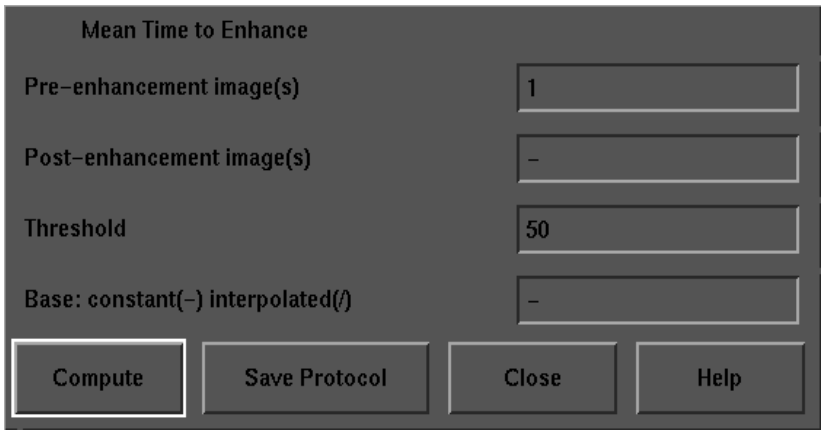
   parameters: Reference pattern is a sequence of numbers indicating the task or activity repeat cycle. For example you might input `(-1 9 -1 9)` this means to skip image 1 in the set of 10 images look at remaining 9 images. (Image 1 is commonly known as the flash image and is not needed in the data set.) Confidence Level is the statistical confidence chosen to threshold the display of the parametric image. The lower the confidence level, the higher degree of statistical confidence. Show Correlation is generally set to '+', so that all correlations greater than '0' are displayed.

° Select **Negative Enhancement Integral** for dynamic susceptibility. When this menu appears, input the values



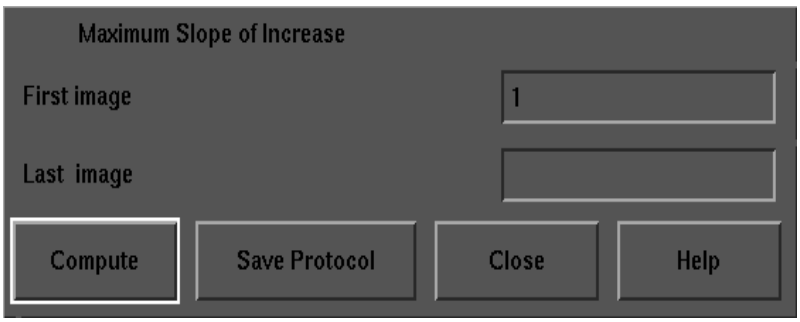
requested. Threshold default is 50. Base default is constant.

° Select **Mean Time to Enhance** for dynamic susceptibility or dynamic contrast. When this menu appears, input the

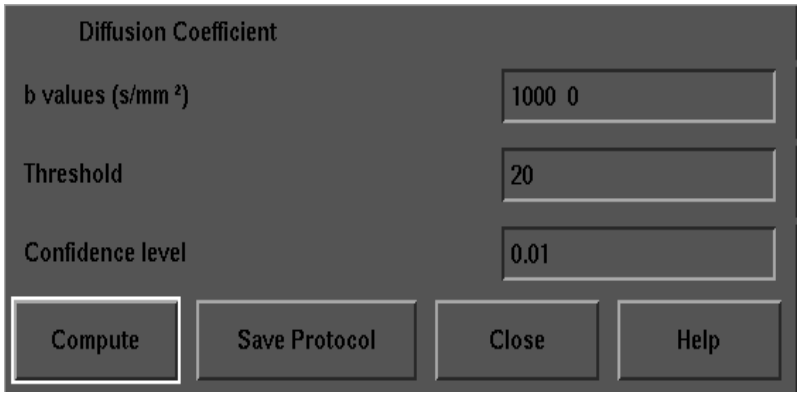


values requested. Threshold default is 50. Base default is constant.

° Select **Maximum Slope of Increase** for dynamic contrast. Input the requested imaging parameters.

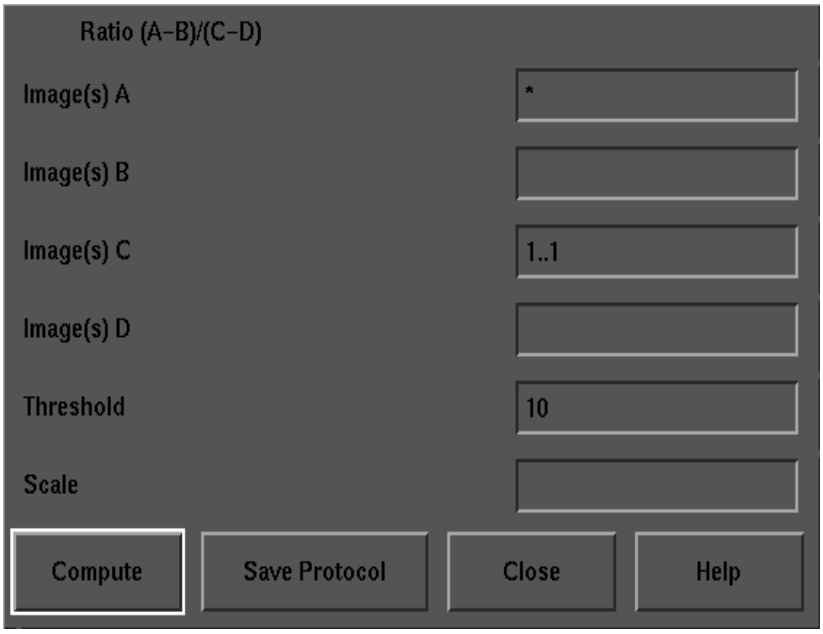


° Select **Diffusion Coefficient** for maps for diffusion. Input



parameters requested. B value should be what was set in scan prescription. Confidence level default is `0.01`.

° Select **Ratio (A-B)/(C-D)** for maps for diffusion. Input the



values requested. Image ranges and numbers can be used for values.

3. Now click **[Compute]** to process the values. A parametric image appears in the lower left quadrant and composite overlay image in the lower right quadrant.
4. The parametric image color scale defaults to rainbow, if you choose to change this scale, right click over the parametric image and drag to **color ramp**. Select the desired ramp.

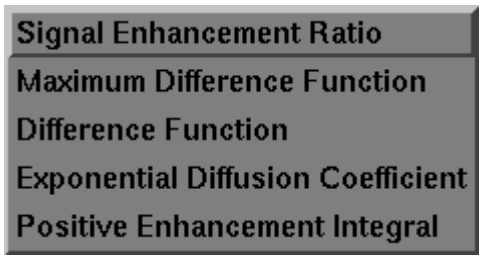
Create Parametric Images

Protocol Algorithms

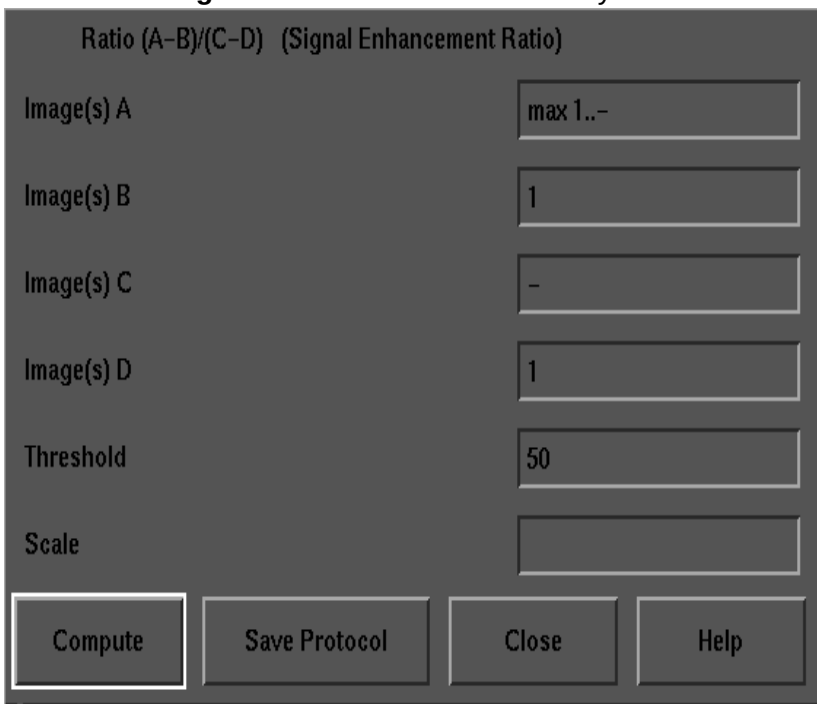
To create a parametric image using algorithms located under the Get Protocol button.

1. Click the **[Get Protocol]** 

button. The menu appears.

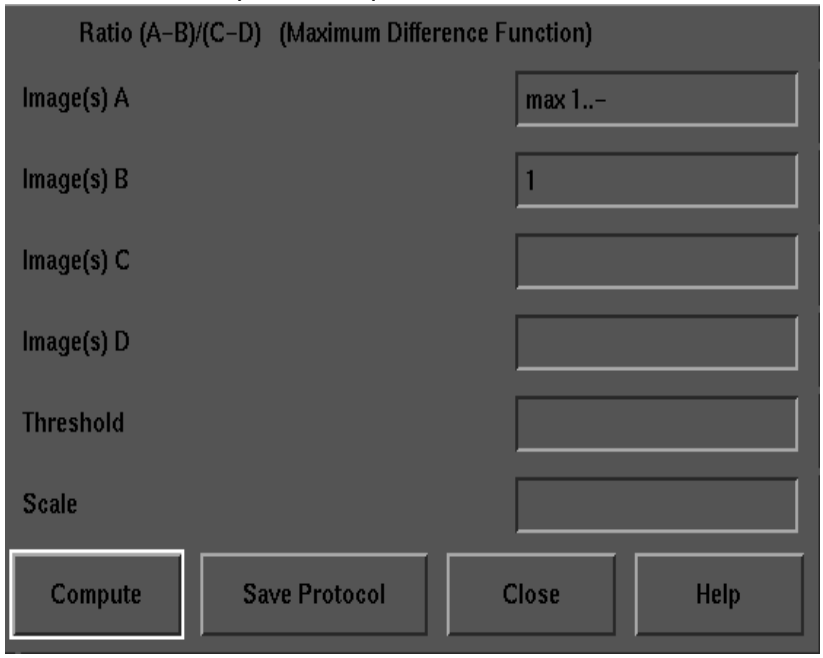


2. Click the desired protocol algorithm.
   - Select **Signal Enhancement Ratio** for dynamic contrast.



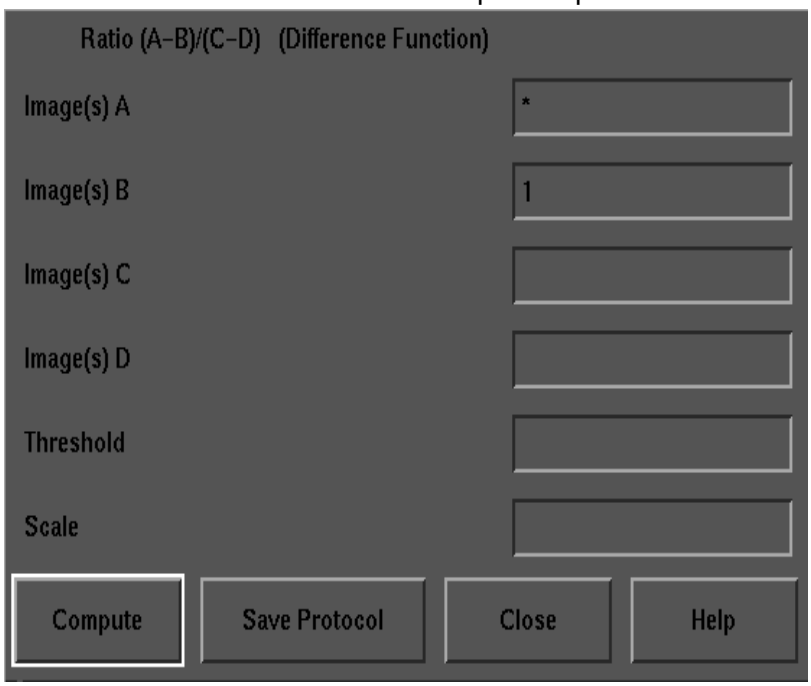
Input the parameters values. It is recommended you use default values. A = max. 1, B = first pre-enhancement image, C = last post-enhancement image, and D = same input value as B.

° Select **Maximum Difference Function** for dynamic contrast. Input the requested values, recommended as



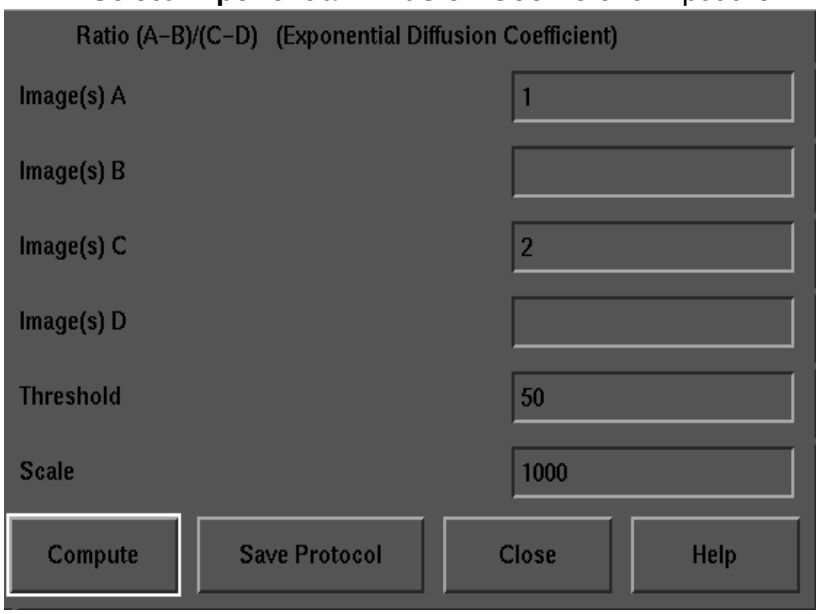
default values.

° Select **Difference Function**. Input the parameters



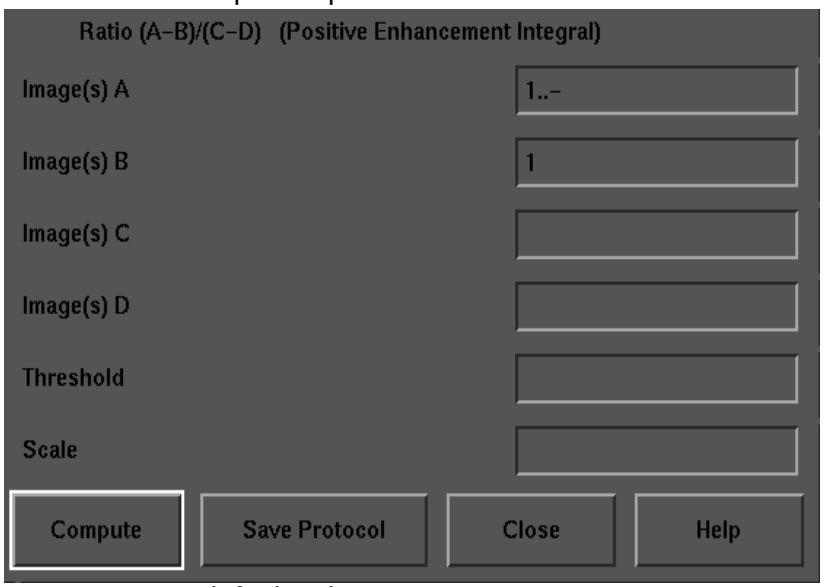
values. It is recommended you use default values.

° Select **Exponential Diffusion Coefficient**. Input the



parameters values. It is recommended you use default values. A = 1, B = none, C = 2, threshold 50, and scale 1000.

° Select **Positive Enhancement Integral** for dynamic contrast. Input the parameters values. It is recommended



you use default values.

3. Click **[Compute]** to process the values. A parametric image appears in the lower left quadrant and composite overlay image in the lower right quadrant.
4. The parametric image color scale defaults to rainbow If you choose to change this scale, right click on the parametric image and drag to **[color ramp]**. Select the desired ramp.

Adjust the Composite Overlay

You can change the image used for the composite image in the lower right quadrant.

1. Click the **[Browser]** 

button. This returns you to the display desktop.
2. Select the series and the image you want to display the overlay on, from the Display Browser.
3. Press **[Alt]** and **[F3]** at the same time to return to the FuncTool viewer.
4. Place the cursor in the lower right quadrant.
5. Right click and drag to **[Set Reference Image]**. Drag to **[Selection]** to display the selected image.

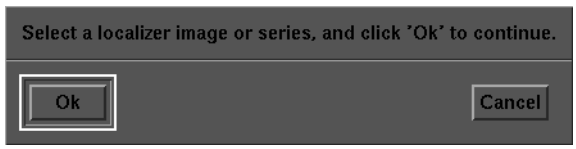
Display 3D Focal CSI Images

In Brief: Display 3D Focal CSI Images

1. Select a 3D Focal CSI series.
2. Select and launch the display tool software.
3. Select an appropriate localizer series/image and click **[Ok]**.
4. Click **[Get Protocol]** and select a metabolite.
   a) **A right-click in the viewport allows selection of saving one or all images.**
   b) Repeat steps one through four if needed, or continue with steps five through ten.
5. Select an ROI.
6. Click and drag one of the square handles to size the ROI.
7. Click the center of the active ROI and drag to move to desired position.
8. Place the cursor in the spectral grid viewport and press the **Spacebar** to scale.

Use this procedure to display the 3D Focal CSI images that you obtained during scanning. The prerequisites for display are a valid image set of 3D Focal CSI images and a display tool such as Functool CSI or MIROI. Software versions below Functool 2.0 are not able to accommodate the 3D Focal CSI images.

1. Select a 3D Focal CSI series from the Display Browser.
2. Click the display tool, **[Functool CSI]** for example, to launch the display software.
   - When the display tool is launched a dialog box appears asking you to select a localizer image. Highlight the localizer series from the Display Browser. The default is image three of the selected series.



3. Select an appropriate localizer series/image from the Display Browser and click **[Ok]**.
   - The display tool command window appears on the left and four viewports appear to the right. The upper left (UL) viewport displays a chemical shift image, the upper right (UR) is for displaying spectra (blank until an ROI is selected), the lower left (LL) displays a metabolite map, and the lower right (LR) displays a metabolite map overlaid on a reference image.

NOTE: The image in the UL, LL, and LR viewports default to the first image of the selected CSI series.

   - The viewports default to the reference of metabolites, you must select from the **[Get Protocol]** menu to select a different metabolite. See step 4.
   - Click **[Cancel]** to discontinue display.

4. Click **[Get Protocol]** and drag to select a metabolite display protocol from the menu. This displays the metabolite map and the map overlay. The protocol menu provides the following metabolite map selections:
   - N-acetyl
   - Choline
   - Composite

- Startup
- Creatine
- Lactate Lipid
- Choline/creatine
- Choline/N-acetyl

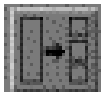
a) If desired, a right-click in the viewport displays a shortcut menu that allows selection of saving one or all images for later viewing from the Display Browser.

b) You can stop here, repeat steps one through four if needed, or continue with steps five through ten to select specific ROIs and obtain metabolite information for those areas.

5. Select one of the following ROIs from the display tool command window:
   - Elliptical for a circular ROI
   - Square for a square ROI
   - Spline for a spline ROI, and draw the ROI

NOTE: The ROI is drawn on the three image viewports.

6. Click and drag one of the square handles to size the ROI.
7. Click the center of the active ROI and drag to move to desired position.
8. Place the cursor in the spectral grid viewport and press the **Spacebar** to scale the grid to fit the viewport.
9. To place multiple ROIs on the viewports do one of the following:
   - Click on the ROI in the viewport to make inactive, then select the ellipse, square, or polygon/spline. Repeat as needed, remember to make the active ROI inactive.
   - To split an ROI, select the ROI to make it active and click **[Split ROI]**.



In Brief: Display 3D Focal CSI Images

9. To place multiple ROIs:
   - Click the ellipse, square, or polygon/spline. Repeat as needed. **OR**
   - Select the ROI to make it active and click **[Split ROI]**.
10. With the crosshair in upper right viewport, right-click, drag to **X Unit** and select **ppm**.
11. Set the active annotation **cursor: # pix**, in the upper right viewport, to one.

NOTE: You can page through the slices and place multiple ROIs on any of the slices. The ROIs are numbered consecutively (even if ROIs are placed on multiple slices). The maximum number of ROIs on one image is 12. For more than 12 ROIs, the new data replaces the data of previous ROIs. For example, ROI number 13 data replaces the data for ROI number one, ROI number 14 data replaces the data for ROI number two, and so on. All the ROIs are still seen on the viewport, just the data is missing. You can view the data for all the ROIs with a right-click in the UR viewport and click **List Values**.

10. With the crosshair still remaining in the upper right viewport, right-click to view a shortcut menu. Drag to **X Unit** and select **ppm** (parts per million). This displays the ppm scale below the spectrum which designates the chemical address of each metabolite.

11. In the upper right viewport the active annotation **cursor: # pix** should be one. To change the number (#) click, or click and drag left/right on the cursor number. Setting the value to one avoids cursor size smoothing.

NOTE: At anytime, you have the option to split the ROI, or merge the ROI by selecting the icon from the display tool command window.

Create a Custom 3D Focal CSI Protocol

The following step-by-step instructions teach you how to create site specific 3D Focal CSI display protocols. As a simple example, this task creates a protocol to display a ratio map and ROI ratio lists that correspond to the maximum of one metabolite (choline) divided by the maximum of the another metabolite (creatine) with reasonable Scale and Threshold values.

1. Have a valid 3D Focal CSI data set with the display tool launched.
2. Click **[Get Protocol]**.
3. Select a metabolite ratio protocol.
   - The Function parameters window appears.
4. Determine the maximum for the desired metabolite peaks using the cursor in the spectral grid view.
   - In the example shown in Figure 23, the solid white lines indicate that the maximum choline signal appears at point **71**, and the dotted white lines show that the maximum creatine value occurs at point **82**. In actual practice, the maximum value for the creatine peak would be determined using solid white lines too, but for this illustration dotted white lines are used.

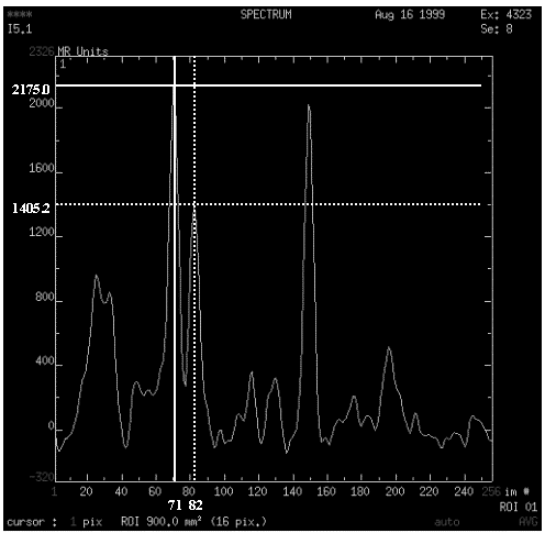


Figure 23: Spectral grid viewport. Solid White=choline peak maximum. Dotted white=creatine maximum.

In Brief: Create a Custom 3D Focal Protocol

1. Select a 3D Focal CSI series.
2. Click **[Get Protocol]**.
3. Select a metabolite ratio protocol.
4. Determine the maximum for the desired metabolite peaks using the cursor in the spectral grid view.
5. In the **Image(s) A** text box, enter **abs 71**.
6. In the **Image(s) C** text box, enter **abs 82**.
7. Change the **Threshold** text box value to **500**.
8. If needed, change the **Scale** text box value to **1000**.
9. Click **[Compute]**.
10. Make any changes to the Threshold value required to create a pleasing ratio map, and to the Scale value.

In Brief: Create a Custom 3D Focal Protocol

11. Click **[Save Protocol]** to save.
12. Enter a name and click **[OK]**.

5. In the **Image(s) A** input parameter text box, enter **abs 71**, the point value of the first metabolite.
6. In the **Image(s) C** input parameter text box, enter **abs 82**, the point value of the second metabolite.
   - Leave the Image(s) B and Image(s) D input parameter text boxes empty.
7. In the **Threshold** text box, change to an initial value of **500**.
8. If needed, in the **Scale** text box, change the value to **1000**.
9. Click **[Compute]** to compute and display the new Ratio map.
10. Make any changes to the **Threshold** value required to create a pleasing ratio map, and to the **Scale** value to produce reasonable ratio values.
    - For example, setting the **Threshold** value to 500 may produce a map with spurious signals outside of the prescribed PRESS voxel, in that case you would increase the value. If on the other hand the map is black, the threshold is too large and should be reduced.
11. Click **[Save Protocol]** to save this new protocol.
12. When prompted for the new name, enter a suitable name, for example, Cho/Cr MAX, and click **[OK]**.
    - The new protocol appears on the **[Get Protocol]** menu, and remains there until deleted.

Symbols

Numerics

A

B

C

D

E

F

G

H

I

N

O

P

Q

R

S

T

U

V

W

X

Y

Z