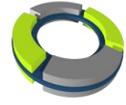




**Cedars-Sinai Medical Center**  
Department of Medicine  
Artificial Intelligence in Medicine Program



# AutoRecon

## Reference Manual

Version 2013.1

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Installation of Cedars-Sinai Cardiac Suite on vendor workstations is only to be performed by an authorized service engineer or applications specialist.

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## 1. Introduction

AutoRecon is an interactive application for the automatic or manual processing of one or more data sets. AutoRecon applies validated rules to processing and reorienting the ventricle while reducing the number of decisions required when processing data sets, which allows for consistent and reproducible results. The amount of automation and processing options provided by AutoRecon depends upon the data set selected. Depending on our workstation, the program may be available standalone or integrated directly within QGS+QPS.

### Automatic processing

AutoRecon provides the following options for automatically processing cardiac data sets:

- **Auto All:** Automatically determines the reconstruction limits, reconstructs, and reorients the cardiac datasets and creates the short axis, horizontal long axis, and vertical long axis data sets.
- **Auto Recon:** Automatically determines the reconstruction limits and reconstructs the cardiac data sets to generate the transverse data sets.
- **Auto Reorient:** Automatically reorients the cardiac transverse data sets. If the data sets have not been reconstructed, AutoRecon reconstructs the data sets automatically prior to reorientation.

AutoRecon also performs the following functions when automatically processing cardiac data sets:

- Identifies the left ventricle surface.
- Automatically corrects for motion (only if motion correction type is set to **Auto**)
- Fits the left ventricular surface to an ellipsoid.
- Reconstructs the transverse data set using filtered back projection reconstruction or iterative reconstruction with an unmodified ramp filter.
- Applies a smoothing filter (only if prefilter is selected) to the projection data set prior to creating the transverse data set.
- Vertically orients the long axis of the ellipsoid.

### Manual Processing

When processing non-cardiac SPECT data sets, you may manually position the reconstruction limit lines and choose the **Reconstruct** command to reconstruct the transverse data sets. You can reorient the reconstructed data sets by displaying the **Reorient** window, and then positioning the Azimuth and Elevation lines to the desired location.

AutoRecon provides the following manual processing features:

- Manual processing of one or more cardiac SPECT or gated SPECT data sets.
- Manual processing of one or more Brain, Bone, Liver or other SPECT data sets.
- Adjust the filter settings applied to reconstructed images.
- Create Transverse data sets using the *Reconstruct* command.
- *Reorient* reconstructed transverse data sets by manually positioning the Azimuth and Elevation lines.
- Motion correction for all SPECT data sets.

## 2. Tutorial

AutoRecon is available both in standalone and integrated (within QGS+QPS) formats. The following workflows will guide you through the processing steps for both scenarios.

### 2.1. Workflow for standalone AutoRECON

A typical AutoRecon sequence for a cardiac data set might proceed as follows:

1. Select appropriate datasets and launch AutoRecon.
2. Select *Auto All* to automatically process the data set.
3. Review appropriate pages (i.e. Reconstruct, Reorient, Motion, etc...) to ensure satisfactory adjustments were made by automatic processing. Make manual adjustments if necessary.
4. Navigate to the Save page.
5. Make appropriate file selections and click *Save*.
6. Click *Exit* to exit AutoRecon.

### 2.2. Patient Example

#### 2.2.1. File Selection

AutoRecon can be used to process cardiac, brain, or other (bone, liver, etc...) SPECT data sets with the following matrix sizes:

- 64 x 64 x 8
- 64 x 64 x 16
- 128 x 128 x 8

- 128 x 128 x 16

One or more SPECT data set(s) can be selected and batch processed as a group by choosing the **Auto All, Auto Recon, or Auto Reorient**. After processing the first data set, AutoRecon automatically proceeds to the remaining data sets and processes them without any further user interaction. Batch processing should be limited to data sets with similar characteristics such as matrix size, acquisition camera, etc.

For the purposes of this example, we'll assume to have selected standard Rest/Gated-stress single isotope raw projection data sets for the patient "**Abnormal, Study**".

### 2.2.2. Launching AutoRecon

AutoRecon can be launched by selecting the desired data set(s) and clicking the **AutoRecon** icon as shown in **Figure 1**.

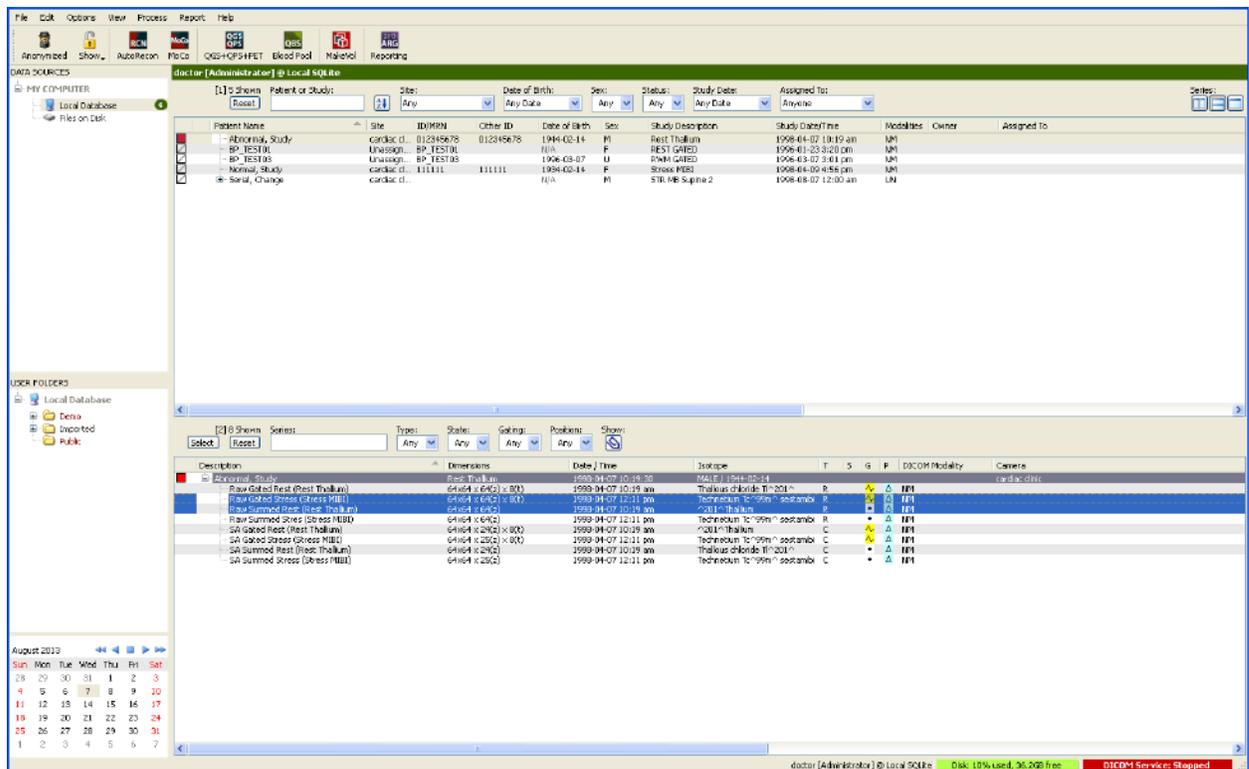


Figure 1

AutoRecon, in its standard configuration, will launch in a separate window with the Reconstruct page indicator and the Cardiac, Dual, Gated and Summed toggles highlighted (**Figure 2**). The Reconstruct page displays both the rest and stress data sets simultaneously. When processing a single data set, the left half of the AutoRecon screen displays the Reconstruct page and the right half

of the screen can display the Reorient, Filter, Motion, More, Save or Defaults screen. The name of the folder (generally, a patient name) and that of the data file are displayed in the horizontal section that also contains the color scales (Figure 2.1).

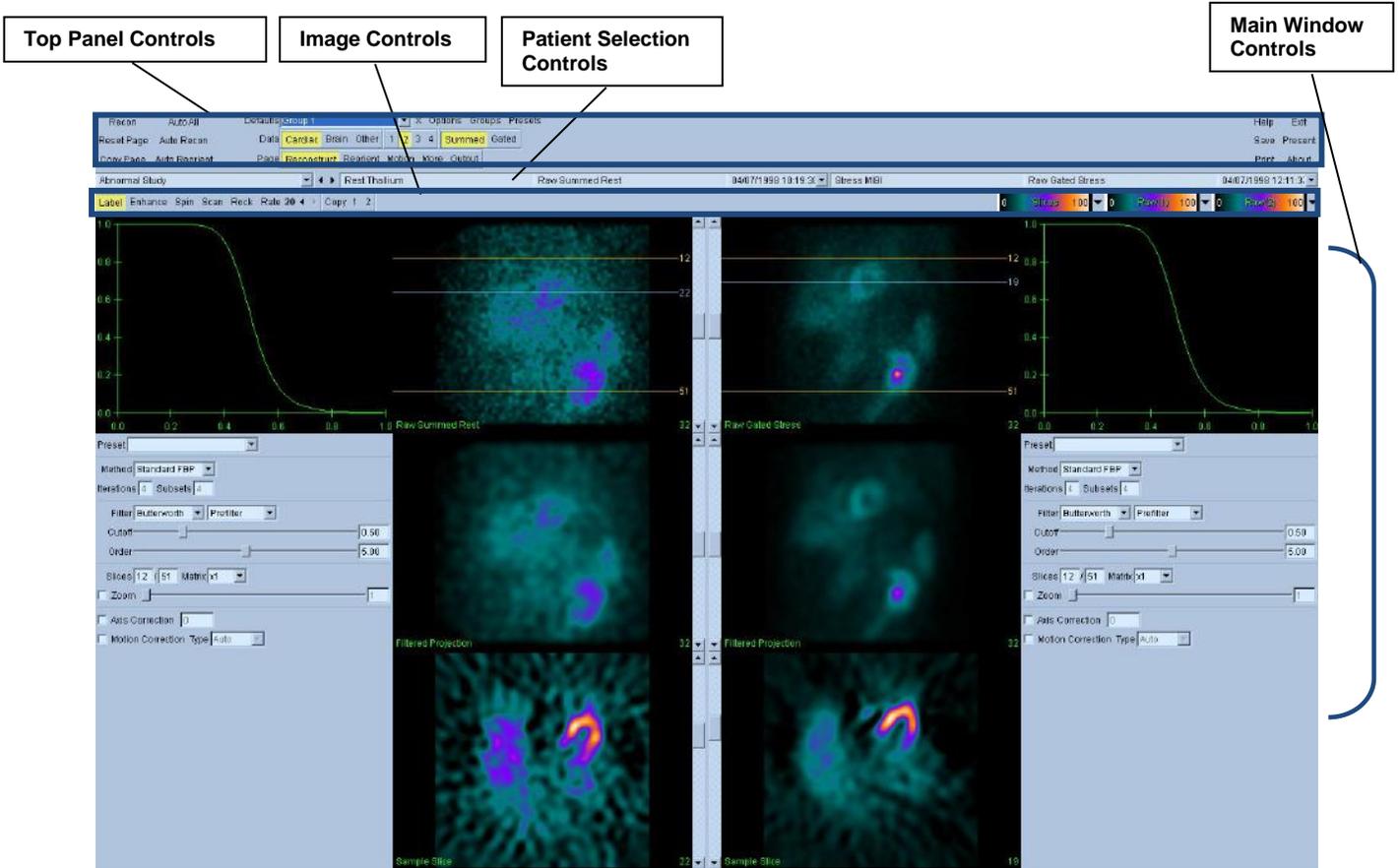


Figure 2



Figure 2.1

After displaying the Reconstruct page, utilize one of the following processing options:

- Click **Auto All** to automatically reconstruct and reorient the unprocessed cardiac data sets and create the transverse, short axis, horizontal long axis, and vertical long axis data sets. AutoRecon will automatically perform the following functions for all loaded dataset(s):

- Determine the reconstruction limits.
  - If motion correction type is set to **Auto**, the cardiac region will be evaluated and corrected for motion artifact.
  - Generate the transverse data set(s).
  - Reorient and reconstruct the short axis, vertical long axis, and horizontal long axis slices.
- Click **Auto Recon** to automatically generate the cardiac SPECT or gated SPECT transverse data set. AutoRecon will automatically perform the following functions for all loaded dataset(s):
    - Determine the reconstruction limits and generate the transverse data sets. However, AutoRecon will not automatically advance to the Reorient window.

**Note:** When **Auto Recon** is used with the Auto Motion Correction option selected, the study is corrected for motion artifacts within the yellow reconstruction lines in the projection viewport only.

- Click **Auto Reorient** to automatically reorient the cardiac SPECT or gated SPECT transverse data set. If you have not reconstructed the transverse data set, **Auto Reorient** will automatically reconstruct the data set prior to reorienting it.
- Manually process the study by following these steps:
  - Ensure that you have selected the appropriate data buttons and Defaults (**Figure 2.2 - Data Buttons**). Use the **Cardiac** Data button for Cardiac data sets, **Brain** for brain data sets, etc. Certain options, such as **Summed** and **Unsummed**, require pre-requisites, **Cardiac** and **Gated** options, before they can be used.

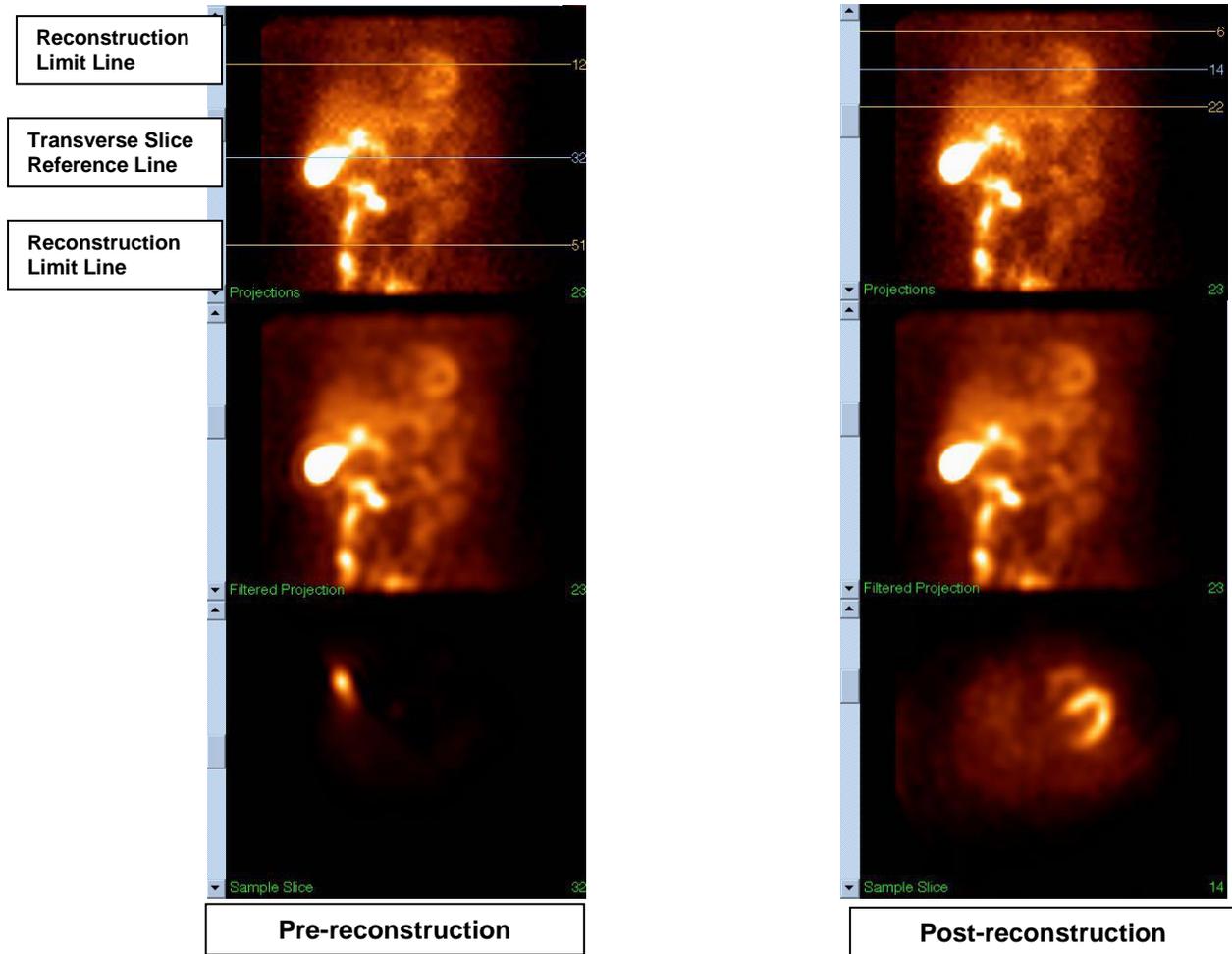
Note: The selected Data button must be appropriate for the displayed data set to properly specify the orientation of the transverse data set displayed in the Transverse viewport.



**Figure 2.2 - Data Buttons**

- Make appropriate selection in the Motion Correction menu. The options are:
  - **Auto:** Use for Cardiac data sets to have AutoRecon automatically locate the heart, evaluate for motion artifact, and make the appropriate corrections/adjustments.
  - **Manual:** Use for all SPECT data sets. AutoRecon imports any manual corrections from the Motion page and uses it for reconstruction.

- Using the left mouse button, drag the reconstruction limit lines to the desired position, and then click **Reconstruct** to manually create the cardiac (Brain or Other) transverse data. The upper and lower reconstruction limits should enclose the left ventricle symmetrically and be placed less than 5 pixels from the ventricle ( **Figure 2.3**). Care should be taken to ensure the reconstruction limits do not clip the left ventricle.



**Figure 2.3**

- Click the **Reorient** button to display the Reorient page.
  - Cardiac reorientation is accurately determined once the following occurs:
    - The reoriented left ventricle is visible in the Short Axis, Vertical Long Axis, and Horizontal Long Axis viewports.
    - Visual agreement with the placement and orientation of the Azimuth and Elevation lines in the Transverse and Sagittal viewports.
    - The short axis data appears circular, vertical long axis data appears horizontal, and horizontal long axis data appears vertical in their respective viewports.

Shows an accurately reoriented left ventricle. **Figure 3** shows an accurately reoriented left ventricle.

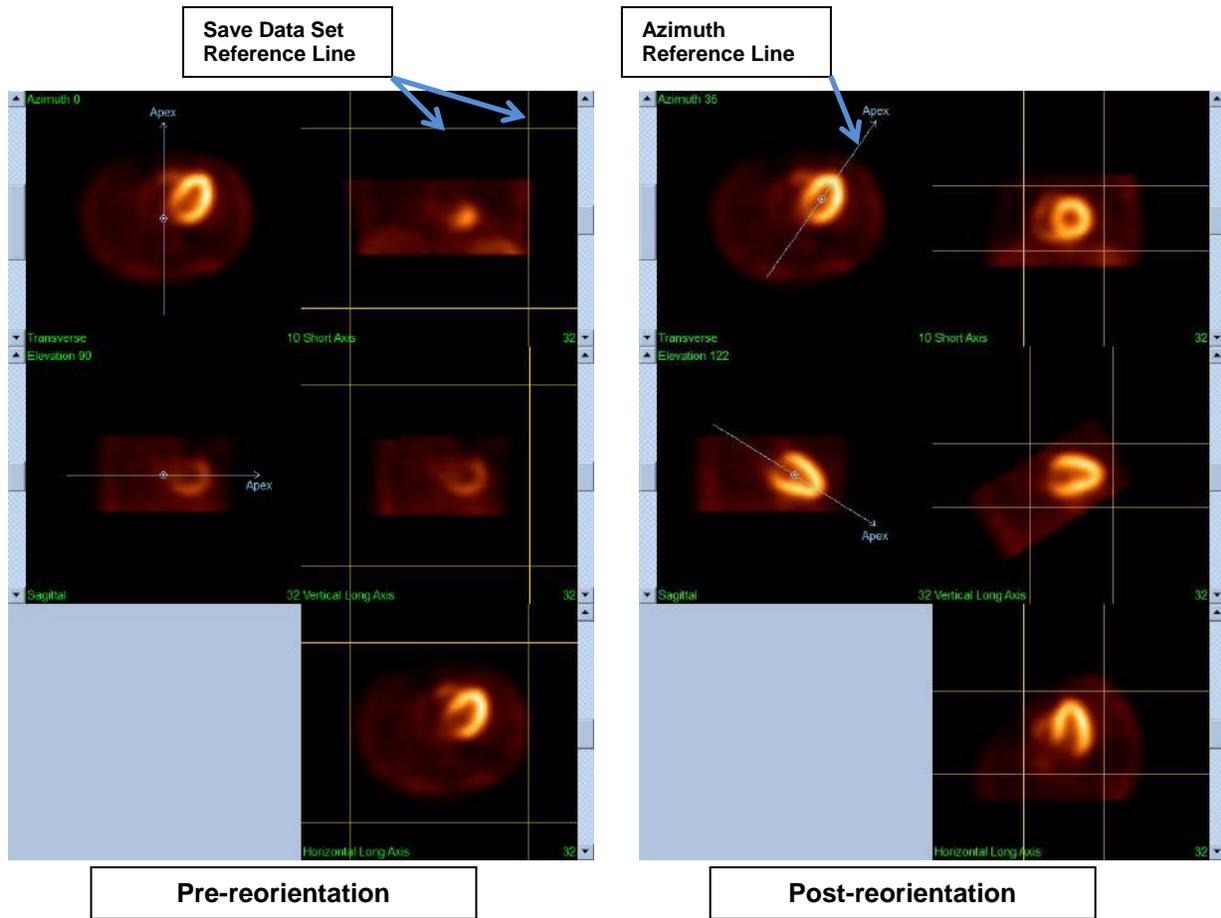


Figure 3

- If necessary, manually reorient the ventricle and reposition the save data set reference lines.
  - Drag the circle on the Azimuth or Elevation reference line to the center of the ventricle.
  - Drag the ends of the Azimuth or Elevation reference line in the direction that you want to orient the ventricle.
  - Drag the save data set reference lines to the desired position. The reference lines should be close to the ventricle, but should not clip the ventricle.
- Click **Output** to display the Save window (**Figure 4**).
  - Check the radio boxes for each data set that should be saved.
  - Verify that the View IDs are accurate.

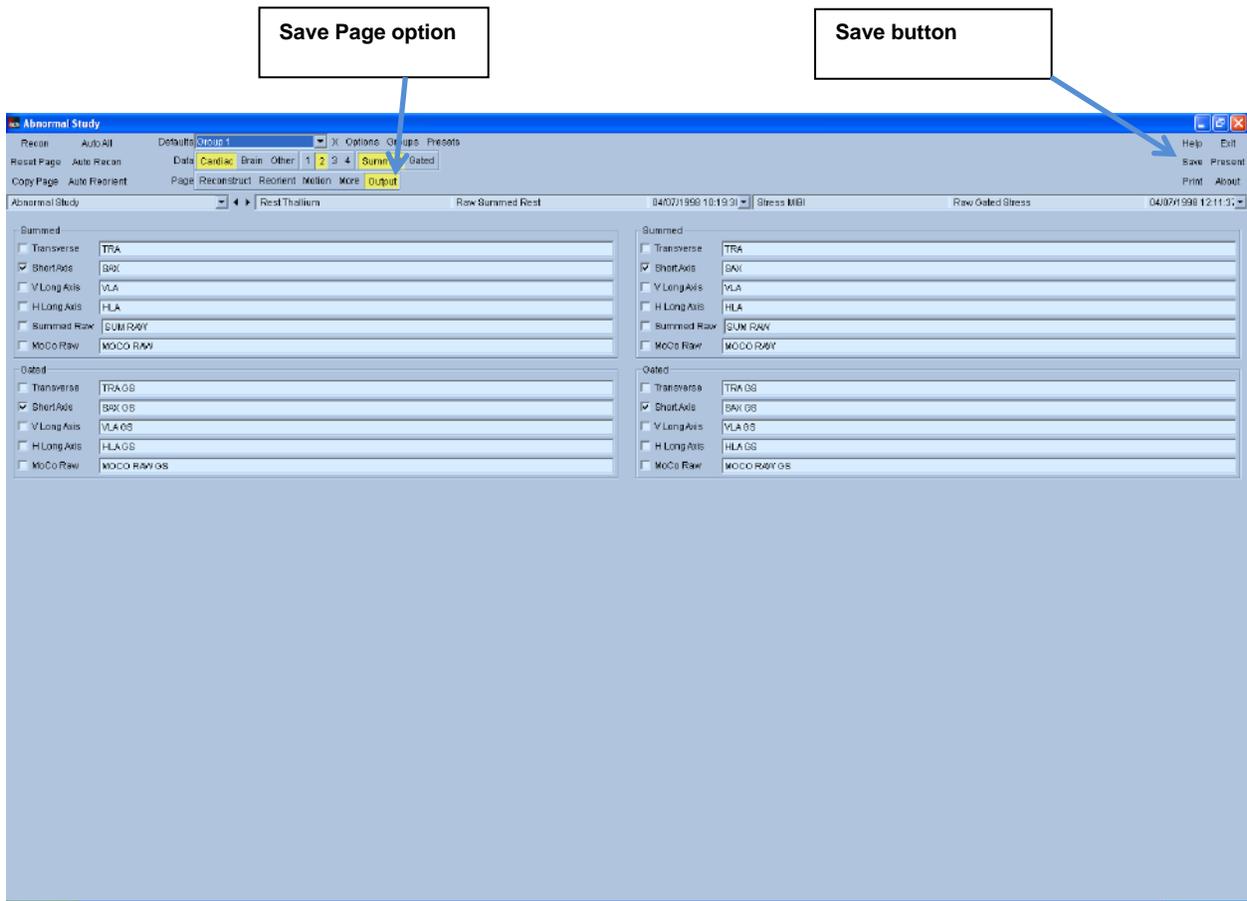


Figure 4

- Click the *Save* button to save the data sets.
- Click *Exit* to exit AutoRecon.

## 2.3. Workflow for integrated AutoRECON (within QGS+QPS)

A typical AutoRecon sequence for a cardiac data set might proceed as follows:

1. Select appropriate RAW projection datasets and launch QGS+QPS (with the AutoRECON option enabled).
2. Navigate to the **Recon** page within QGS+QPS.
3. Select **Auto All** to automatically process the data set.
4. Review appropriate pages (i.e. Reconstruct, Reorient, Motion, etc...) to ensure satisfactory adjustments were made by automatic processing. Make manual adjustments if necessary.
5. Once satisfied, click **Accept** to finalize the adjustments.
6. Navigate to the QGS+QPS pages and review the appropriate quantitative results.
7. Click **Save** and click **Save All** (saves all loaded patients) or **Save Current** (saves current patient) from the reconstructed tab of the save dialog. This will save the constructed volume files back to the database.
8. Once finished, click **Exit**.

For the purposes of this example, we'll assume to have selected standard Rest/Gated-stress raw projection data sets for the patient "**Abnormal, Study**".

### 2.3.1. Launching QGS+QPS with AutoRecon

QGS+QPS can be launched by selecting the desired data set(s) and clicking the **QGS+QPS** shown in below Figure.

The screenshot displays the 'doctor' software interface. At the top, a menu bar includes File, Edit, Options, View, Process, Report, and Help. Below the menu is a toolbar with icons for 'QGS+QPS+PET', 'Blood Pool', 'Reorient', and 'Reporting'. A red arrow points to the 'QGS+QPS+PET' icon. The main window is titled 'doctor [Staff Physician] @ Local SQLite' and contains a table of patient data. The table has columns for Patient Name, Site, ID(MRN), Other ID, Date of Birth, Sex, Study Description, Study Date/Time, Modalities, Owner, and Assigned To. The data rows are:

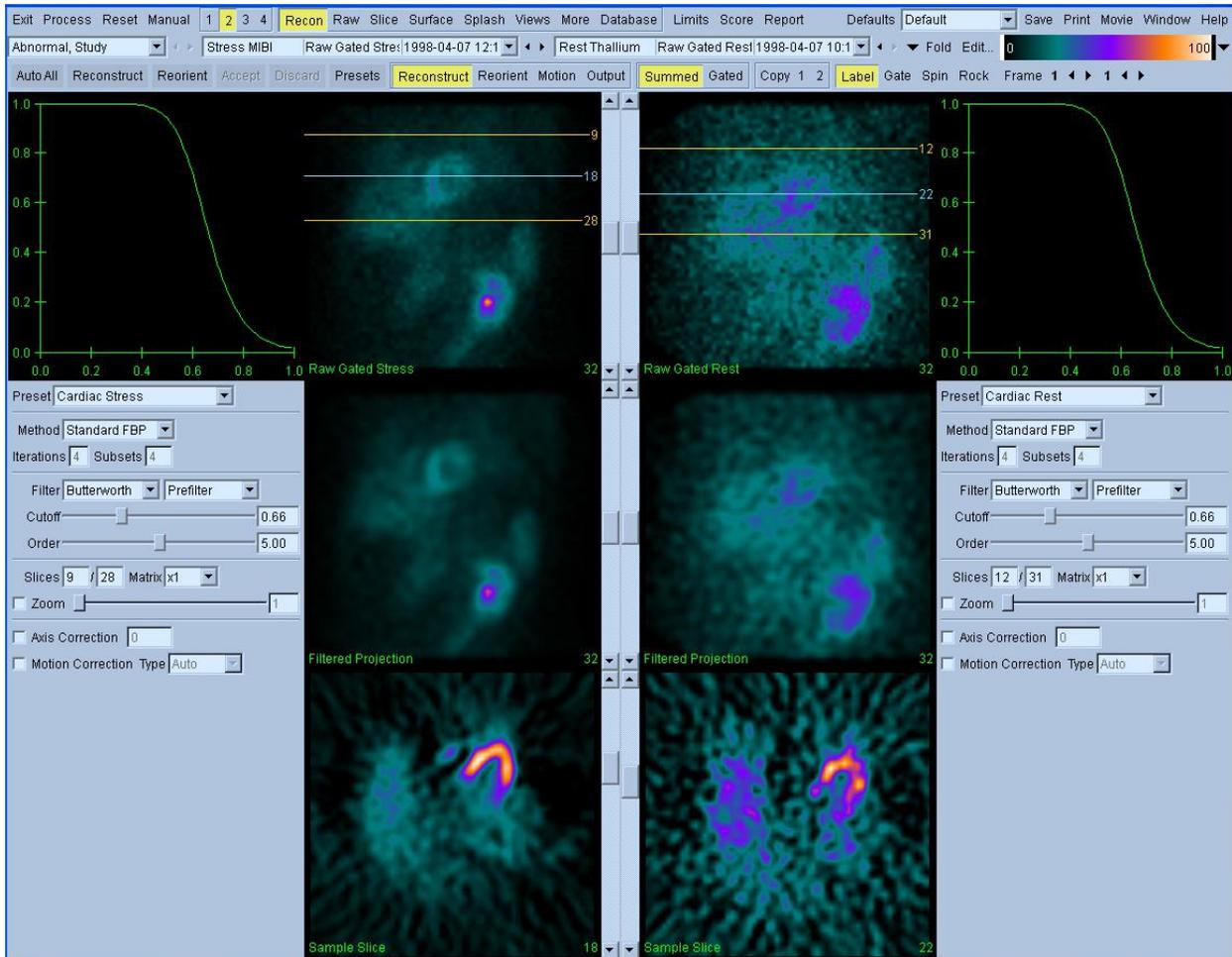
| Patient Name   | Site       | ID(MRN)   | Other ID  | Date of Birth | Sex | Study Description | Study Date/Time     | Modalities | Owner | Assigned To |
|----------------|------------|-----------|-----------|---------------|-----|-------------------|---------------------|------------|-------|-------------|
| Abnormal_Study | cardiology | 012265278 | 012265278 | 1944-02-14    | M   | Rest Thallium     | 1998-04-07 10:19 am | NM         |       |             |
| BP_TEST01      | Unassign.  | BP_TEST01 | 1111      | 1944-02-14    | F   | REST GATED        | 1998-03-23 3:23 pm  | NM         |       |             |
| BP_TEST03      | Unassign.  | BP_TEST03 |           | 1998-03-07    | U   | PHYS GATED        | 1998-03-07 3:51 pm  | NM         |       |             |
| Normal_Study   | Unassign.  | 1111111   |           | 1994-02-14    | F   | Stress PET        | 1998-04-09 4:56 pm  | NM         |       |             |

Below the patient table is a section for 'SERIES' with a table showing details for the selected 'Abnormal\_Study' series:

| Description                     | Dimensions           | Date / Time         | Isotope                | T | S | G | P | DICOM Modality | Camera     |
|---------------------------------|----------------------|---------------------|------------------------|---|---|---|---|----------------|------------|
| Abnormal_Study                  | Rest Thallium        | 1998-04-07 10:19:33 | THAL / 2044-02-14      |   |   |   |   |                | cardiology |
| Rest Gated Rest (Rest Thallium) | 64x64 x 64(2) x 8(2) | 1998-04-07 10:19 am | Thallium 201Tl 201Tl   | R |   |   |   | NM             |            |
| Rest Gated Stress (Stress PET)  | 64x64 x 64(2) x 8(2) | 1998-04-07 12:11 pm | Technetium 99mTc 99mTc | R |   |   |   | NM             |            |

At the bottom left, there is a calendar for August 2015. The status bar at the bottom indicates 'doctor [Staff Physician] @ Local SQLite', 'Disk: 9% used, 36.428 free', and 'DICOM Services Stopped'.

Clicking on the **Recon** page within QGS+QPS to access the integrated AutoRecon program. In its standard configuration, AutoRecon will launch with the Reconstruct page indicator and Summed toggles highlighted. The Reconstruct page is able to display both the rest and stress data sets simultaneously. When processing a single data set, the left half of the AutoRecon screen displays the Reconstruct page and the right half of the screen can display the Reorient or Motion screens. The name of the folder (generally, a patient name) and that of the data file are displayed in the horizontal section that also contains the color scales.



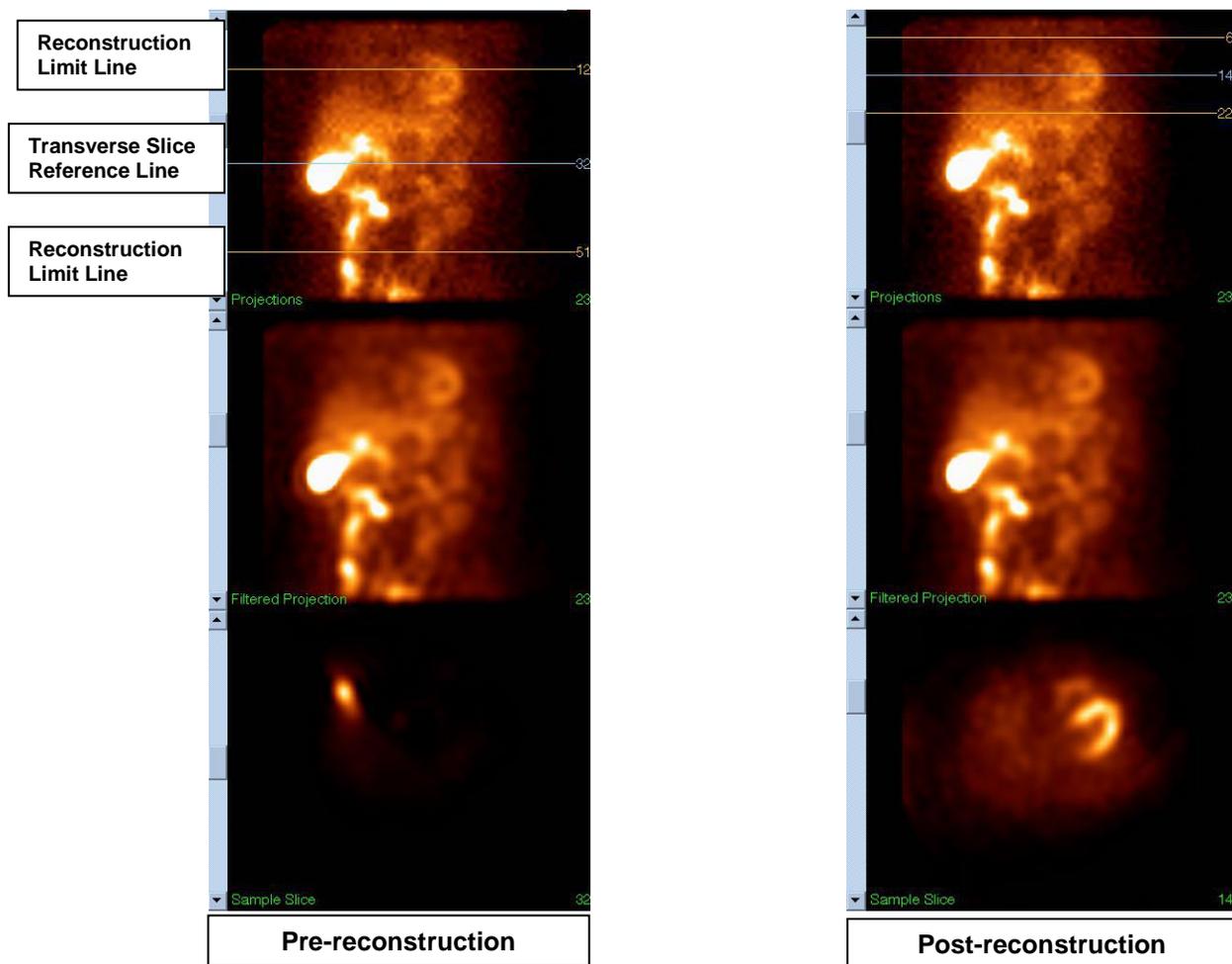
After displaying the Reconstruct page, utilize one of the following processing options:

- Click **Auto All** to automatically reconstruct and reorient the unprocessed cardiac data sets and create the transverse, short axis, horizontal long axis, and vertical long axis data sets. AutoRecon will automatically perform the following functions for all loaded dataset(s):
  - Determine the reconstruction limits.
  - If motion correction type is set to **Auto**, the cardiac region will be evaluated and corrected for motion artifact.
  - Generate the transverse data set(s).

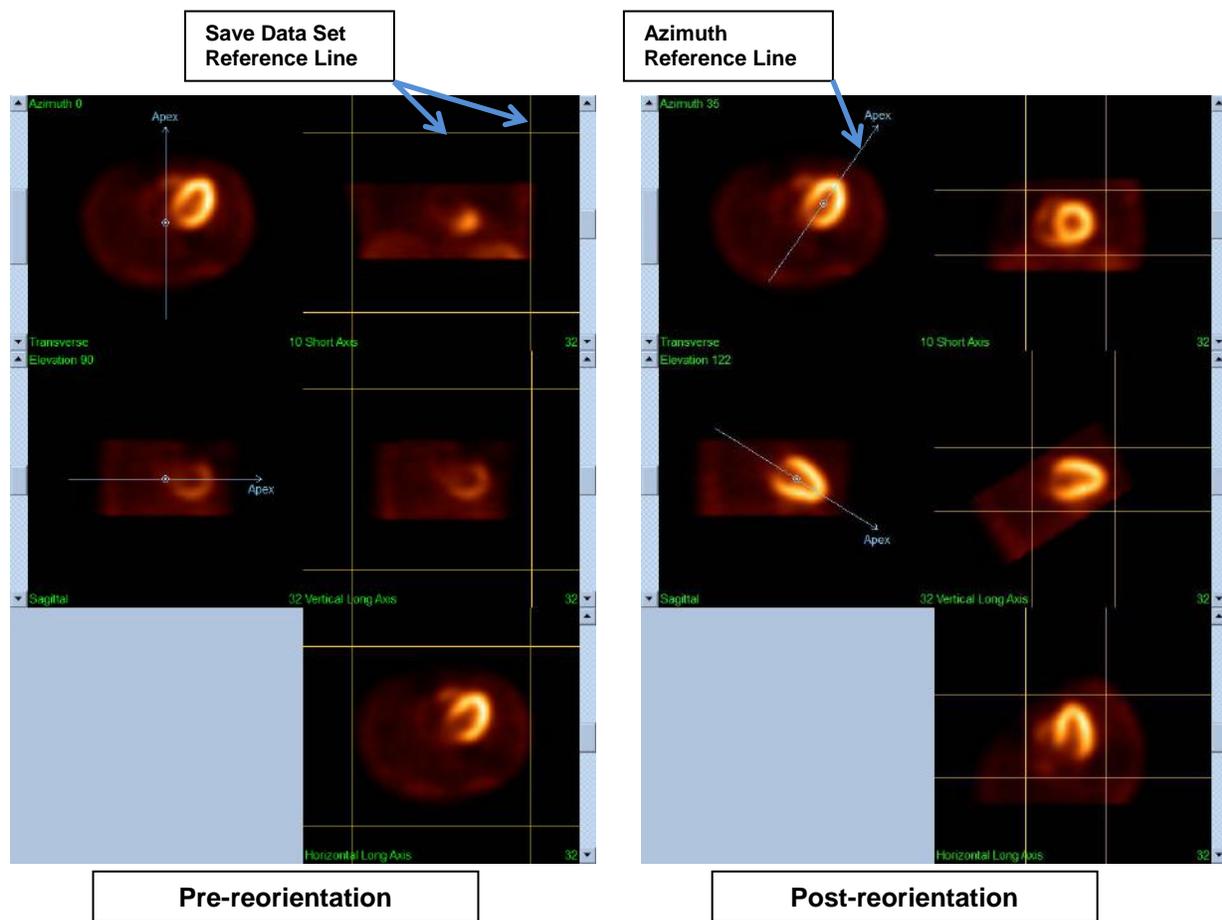
- Reorient and reconstruct the short axis, vertical long axis, and horizontal long axis slices.
- Click **Reconstruct** to automatically generate the cardiac SPECT or gated SPECT transverse data set. AutoRecon will automatically perform the following functions for all loaded dataset(s):
  - Determine the reconstruction limits and generate the transverse data sets. However, AutoRecon will not automatically advance to the Reorient window.

**Note:** When **Reconstruct** is used with the Auto Motion Correction option selected, the study is corrected for motion artifacts within the yellow reconstruction lines in the projection viewport only.

- Click **Reorient** to automatically reorient the cardiac SPECT or gated SPECT transverse data set. If you have not reconstructed the transverse data set, **Reorient** will automatically reconstruct the data set prior to reorienting it.
- Manually process the study by following these steps:
  - Ensure that you have selected the appropriate data buttons and Defaults.
  - Make appropriate selection in the Motion Correction drop-down menu. The options are:
    - **Auto:** Use for Cardiac data sets to have AutoRecon automatically locate the heart, evaluate for motion artifact, and make the appropriate corrections/adjustments.
    - **Manual:** Use for all SPECT data sets. AutoRecon imports any manual corrections from the Motion page and uses it for reconstruction.
  - Using the left mouse button, drag the reconstruction limit lines to the desired position and then click **Reconstruct** to manually create the cardiac transverse data. The upper and lower reconstruction limits should enclose the left ventricle symmetrically and be placed less than 5 pixels from the ventricle. Care should be taken to ensure the reconstruction limits do not clip the left ventricle.



- Click the *Reorient* page button to display the Reorient page.
  - Cardiac reorientation is accurately determined once the following occurs:
    - The reoriented left ventricle is visible in the Short Axis, Vertical Long Axis, and Horizontal Long Axis viewports.
    - Visual agreement with the placement and orientation of the Azimuth and Elevation lines in the Transverse and Sagittal viewports.
    - The short axis data appears circular, vertical long axis data appears horizontal, and horizontal long axis data appears vertical in their respective viewports. Shows an accurately reoriented left ventricle. The below figure shows an accurately reoriented left ventricle.



- If necessary, manually reorient the ventricle and reposition the save data set reference lines.
    - Drag the circle on the Azimuth or Elevation reference line to the center of the ventricle.
    - Drag the ends of the Azimuth or Elevation reference line in the direction that you want to orient the ventricle.
    - Drag the save data set reference lines to the desired position. The reference lines should be close to the ventricle, but should not clip the ventricle.
- Click **Accept** to accept finalize the adjustments.
- Click **Output** to display the Save window.
  - Check the radio boxes for each data set that should be saved.
  - Verify that the View IDs are accurate.



- Click the **Save** button to save the reconstructed volume data sets.
- Navigate to the desired QGS+QPS pages (Raw, Slice, Splash, etc...) to post-process volumes and review the quantitative results.

### 3. AutoRecon Controls

#### 3.1. Common Controls

This section describes controls common to multiple AutoRecon pages. The AutoRecon application contains the following 4 groups of controls (Figure 5):

- Top Panel Controls
- Patient Selection Controls
- Image Controls
- Main Window Controls

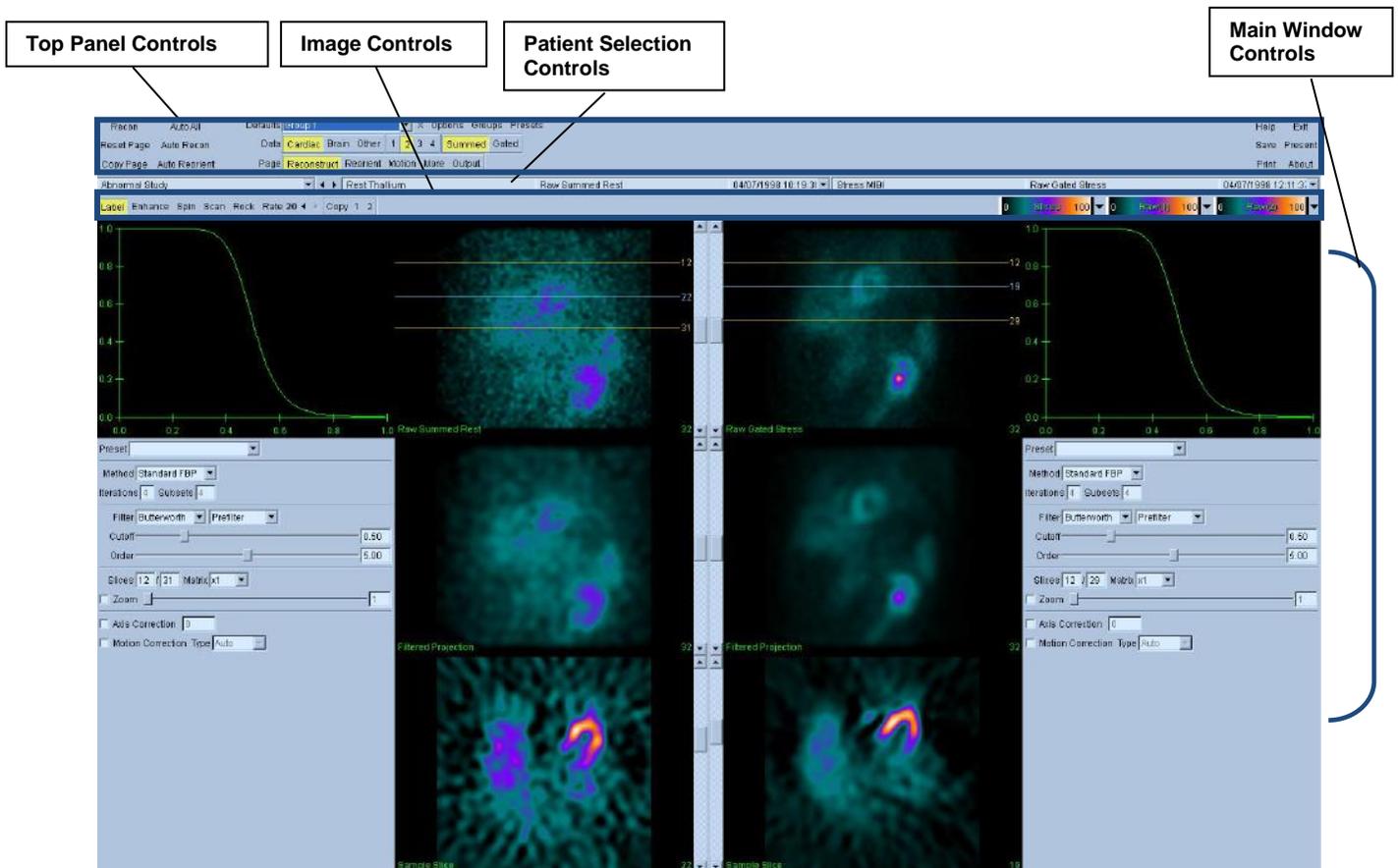


Figure 5

### 3.1.1. Top Panel Controls

The AutoRecon top panel controls ([Figure 5.1](#)) allow you to perform application functions such as selecting defaults files, saving files and formatting images. Most of these controls are accessible regardless of the currently displayed AutoRecon page with the following few exceptions:

- **Auto All, Auto Recon and Auto Reorient** are only displayed when the **Cardiac** Data button is selected.
- The **Summed** and **Unsummed** controls are displayed only when **Cardiac** and **Gated** are selected.

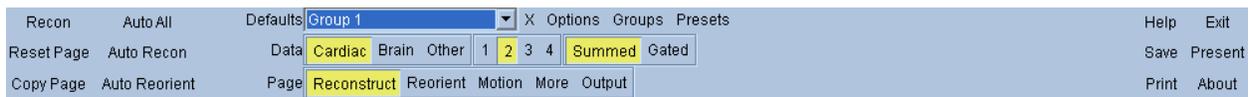


Figure 5.1

#### 3.1.1.1. Recon

**Recon** manually reconstructs the SPECT or gated SPECT data set. To manually process the loaded data set(s), define the reconstruction limits by dragging the upper and lower limit lines to the desired location. After positioning the limit lines, click **Recon** to generate the transverse slices. AutoRecon does not automatically advance to the **Reorient** page when using **Recon**.

Note: If **Auto** is selected for Motion correction Type, AutoRecon displays the **Motion** page after reconstructing the data set(s).

#### 3.1.1.2. Reset page

**Reset Page** restores the processed data set(s) and viewport settings to their initial values. **Reset Page** also removes any processed data set(s) that have not been saved.

#### 3.1.1.3. Copy Page

**Copy Page** copies the processing settings from one set of viewports to all other objects loaded in memory.

#### 3.1.1.4. Auto All

**Auto All** is available for cardiac data set(s) only. It automatically determines the reconstruction limits, reconstructs and reorients the data set(s). When using **Auto All**, AutoRecon generates the transverse slices, proceed automatically to the Reconstruct window and automatically reorients the ventricular volume.

Note: If **Auto** is selected for Motion correction Type, AutoRecon displays the **Motion** page after reconstructing the data set(s).

### 3.1.1.5. Auto Recon

**Auto Recon** is available for cardiac data sets only. It automatically determines the reconstruction limits and reconstructs the cardiac data set(s). When using **Auto Recon**, AutoRecon generates the transverse slices, but does not proceed to the Reorient page automatically.

Note: If **Auto** is selected for Motion correction Type, AutoRecon displays the **Motion** page after reconstructing the data set(s).

### 3.1.1.6. Auto Reorient

**Auto Reorient** is available for cardiac data sets only. It is used to automatically reorient cardiac data sets. If you have not reconstructed the data, **Auto Reorient** will automatically reconstruct and then reorient the data sets.

Note: If **Auto** is selected for Motion correction Type, AutoRecon displays the **Motion** page after reconstructing the data set(s).

### 3.1.1.7. Defaults

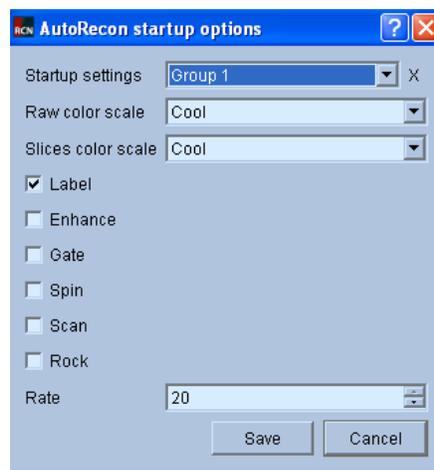
The **Defaults** field displays the name of the currently selected defaults file. You may load different defaults files by clicking on the drop down menu and selecting the desired defaults.

### 3.1.1.8. Close

Clicking **X** will close the selected defaults file without applying any default settings to the data set. The **Defaults** field will revert back to none.

### 3.1.1.9. Options

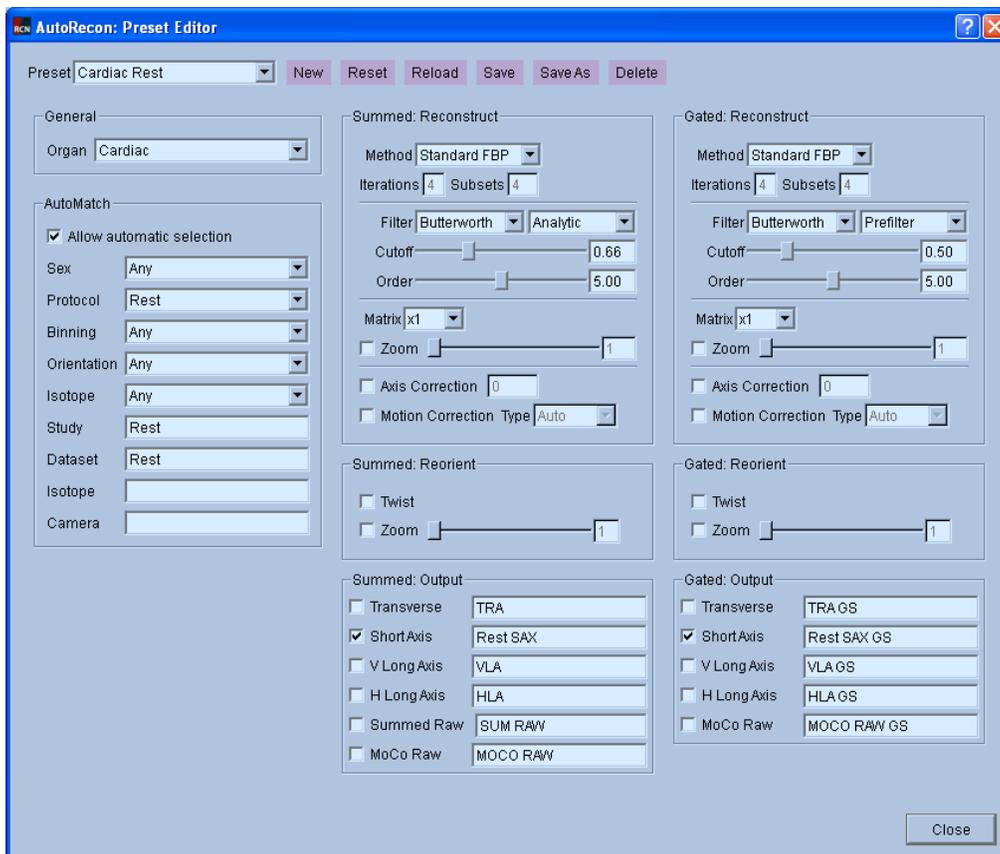
There are numerous start-up options that can be accessed using the **Options** button. These options are described below.



- **Startup settings:** Allows you to set the startup defaults preference of choice.
- **Raw color scale:** Allows you to set the startup color scale for raw projection images.
- **Slices color scale:** Allows you to set the startup color scale for slices.
- **Label:** Viewport labels are toggled ON when selected.
- **Enhance:** Enhance function is toggled ON when selected.
- **Gate:** Gate function is toggled ON when selected.
- **Spin:** Spin function is toggled ON when selected.
- **Scan:** Scan function is toggled ON when selected.
- **Rock:** Rock function is toggled ON when selected.
- **Rate:** Allows you to set the rate for the gating in frames per second.

### 3.1.1.10. Presets

The **Presets** dialog defines reconstruction parameters for a single dataset, plus auto match parameters for which datasets it should be applied to. The specific functions within **Presets** are described below.



### Universal controls

- **New:** Creates a new set of default presets.
- **Reset:** Resets the current set of defaults to factory settings.

- **Reload:** Reloads the current set of defaults from its last saved state.
- **Save:** Saves the current set of default presets.
- **Save As:** Saves the current set of defaults under a new name.
- **Delete:** Deletes the currently loaded presets.

### Auto match settings

These settings will allow the application to automatically match the default presets to the appropriate datasets.

- **Sex:** Select the gender that the preset should be limited to.
- **Protocol:** Select the appropriate protocol.
- **Binning:** Select the appropriate binning.
- **Orientation:** Select the patient orientation that the preset should be limited to.
- **Isotope:** Select the appropriate isotope for which the preset should be limited to.
- **Study:** The application will automatically associate any studies that contain the tags included in this field. For example, if **REST** is included in this field, any datasets containing the tag **REST** will be automatically associated with the preset defaults. The study field is the Procedure ID.
- **Dataset:** The application will automatically associate any studies that contain the tags included in this field. For example, if **REST** is included in this field, any datasets containing the tag **REST** will be automatically associated with the preset defaults. The study field is the View ID.
- **Isotope:** Enter the isotope tags that the application should use for auto matching.
- **Camera:** Enter the camera tags that the application should use for auto matching.

**NOTE:** The following guidelines can be used when entering the text strings for Proc ID and View ID.

- Use an asterisk (\*) as a wildcard in your entry. For example, you may want to display all of your stress and rest files using \*STR on one side, and \*RST on the other side of the display.
- Broaden your criteria by keeping it short. For example, enter -S to match any data sets that have this string. The blank space after -S is interpreted similar to an asterisk.
- To load all data sets, leave the Proc or View ID fields blank. All loaded data sets are displayed in the order in which they were selected.
- To specify the data sets for one window only, enter the Proc or View ID criteria on one side and the data sets that match that criteria will be displayed. Leave the Proc and View ID fields blank on the other side and the remaining data sets will be displayed there.
- 

### Reconstruction parameters

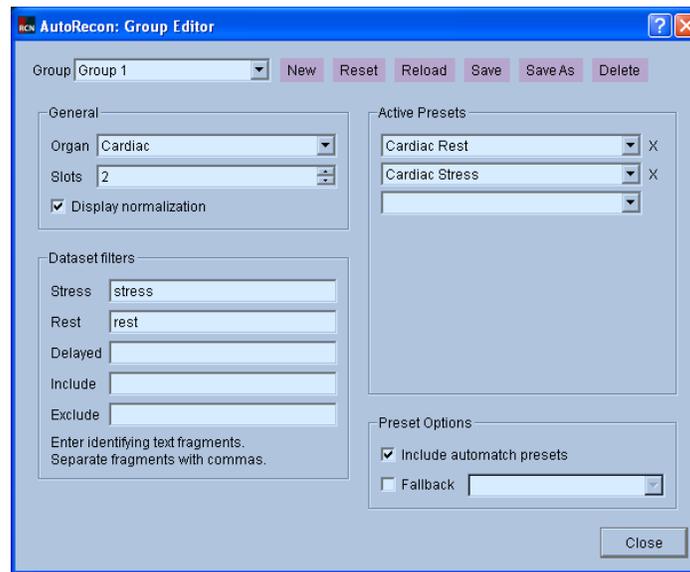
Reconstruction parameters for Summed (un-gated) and Gated datasets can be set using the options included under the reconstruction parameters.

## Output settings

These settings allow you select which processed volume files should be saved after pre-processing. Specific dataset labels may also be set for the desired datasets.

### 3.1.1.11. Groups

- This option allows you to define a group of *presets* to be considered for auto matching. There are also some protocol-specific parameters that can be set under the *Groups* option.



- **Organ**: Select the organ to which the group settings belong.
- **Slots**: Number of datasets to be simultaneously displayed.
- **Display normalization**: Sets the brightness on all images to a normalized level. This control finds the brightest pixel in the dataset volume, sets that pixel to 100%, and scales all pixels in the dataset from there.
- **Dataset filters**: These filters help the application automatically match the group defaults with the appropriate datasets.
- **Active presets**: Individual presets to be included in the group for auto matching.
- **Include auto match presets**: If no auto match was found with the active presets, the application also considers additional presets where 'allow automatic selection' is enabled.
- **Fallback preset**: As a last resort, the application can use the fallback preset if no other matches were found.

### 3.1.1.12. Data Buttons

The **Data** buttons (Figure 5.2) selection should correspond to the type of data set(s) being processed. This setting determines the orientation of the reconstructed data set(s) and the control options displayed on the AutoRecon windows.



Figure 5.2

- **Cardiac**: Used for SPECT and gated SPECT cardiac data sets. Enabling the **Cardiac** Data button displays the **Auto All**, **Auto Recon**, **Auto Reorient**, and the **Gated** options.
- **Brain**: Used for brain SPECT data sets.
- **Other**: Used for non-cardiac and non-brain SPECT data sets such as bone or liver studies.
- **1 2 3 4**: Useful for displaying multiple data sets simultaneously. For example, two cardiac data sets (Rest and Stress) can be displayed simultaneously.
- **Summed**: Used for the summed file of a gated SPECT data set.
- **Gated**: Used for gated SPECT data sets. The **Gated** button is only available when the **cardiac** data button is enabled. Enabling this option displays the **Summed** and **Unsummed** buttons

### 3.1.1.13. Page Buttons

The **Page** buttons (Figure 5.3) can be used to display the desired window.



Figure 5.3

- **Reconstruct**: Displays the reconstruct window that is used to reconstruct the unprocessed data set(s).
- **Reorient**: Displays the reorient window that is used to reorient the transverse data set(s).
- **Motion**: Displays the motion window that is used to evaluate the projection data set(s) for motion artifacts, and apply motion correction. The projection data set appears as a sonogram where the data set is displayed as a spiral. Presence of motion appears as a break in the spiral.
- **More**: Displays the **more** window that contains patient demographic data and information on the loaded data set(s).
- **Output**: Displays a window that can be used to determine what will be saved and also to modify the View IDs (if desired) when the **Save** button (top right of the screen) is selected.

### 3.1.1.14. Help

Clicking the **Help** button displays an online version of AutoRecon reference manual.

### 3.1.1.15. Save

After the current data set(s) is processed, the **Save** button can be used to save one or both data sets. The individual reconstructed data sets and the corresponding View IDs will be saved as they are defined in the save window.

### 3.1.1.16. Print

Used to print the currently displayed screen.

### 3.1.1.17. Exit

The **Exit** button is used to exit the AutoRecon application.

### 3.1.1.18. Present

This feature is a useful tool that allows saving a set of images and results along with a batch file. The batch file launches the AutoRecon application and loads the processed images. This is useful for showing case studies within a Microsoft PowerPoint presentation.

### 3.1.1.19. Snapshot

Used to print screen and save a copy of the screen as a snapshot.

## 3.1.2. Patient Selection Controls

The patient selection controls (**Figure 5.4**) will allow you to specify the data set displayed in each set of viewports.



Figure 5.4

- Patient selection menu: Click on the patient selection menu to display the list of selected data sets, and then click on the desired data set to display it in the viewports in the main area of the window.
- Arrows: Different data set can be selected by using the ◀▶ buttons.

## 3.1.3. Image Controls

The image control bar (**Figure 5.5**) contains controls for changing color maps, intensity and brightness. It also has additional functions that are described below.



**Figure 5.5**

- **Color Palette:** Clicking ▼ next to the appropriate color Palette displays a list of available color tables.
- **Background:** The background can be controlled by dragging the left edge of the color palette to the desired setting. Dragging it to the right increases the background level, and dragging it to the left decreases the background level. Increasing the background level will make low count areas less visible, whereas decreasing it will make the low count area within the image more visible. It lowers the threshold where the pixel values below the threshold are displayed as one color corresponding to the lowest value in the color table.
- **Brightness:** The image brightness can be controlled by dragging the right edge of the color palette to the desired setting. Dragging it to the left decrease the threshold where pixel values above the threshold are displayed as one color corresponding to the highest value in the color palette.

Note: Left clicking anywhere on the color palette slider will set the image brightness to that level. Dragging the slider with the left mouse button will move both the Background and Brightness sliders as a group.

- **Label:** Toggles the image labels within the viewports on and off.
- **Enhance:** Applies a spatial filter designed to enhance motion artifact visibility to the original and corrected projection sequences.
- **Spin:** This option will display the raw projection dataset in a cinematic format. It will sequentially display each frame for the loaded data set. The **Spin** button can be toggled on or off.
- **Scan:** Displays, Pixel by Pixel, reconstructed sample slice for the loaded image.
- **Rock:** Toggles the cine between selected frames.
- **Rate:** The rate arrow buttons can be used to change the rate of the cine display. This rate is measured in frames/second.
- **Copy:** Copies the reconstruction upper and lower limits and transverse slice limit line settings from the left to the right window or vice versa.

## 4. Main Window Controls

This section describes the controls that allow you to specify processing parameters. The available controls will vary depending on the type of data set(s) loaded and the page being displayed.

### 4.1. Reconstruct Page

The reconstruct page is used to reconstruct unprocessed data sets. It contains one or two sets of viewports and controls. The controls available on the Reconstruct page are described below.

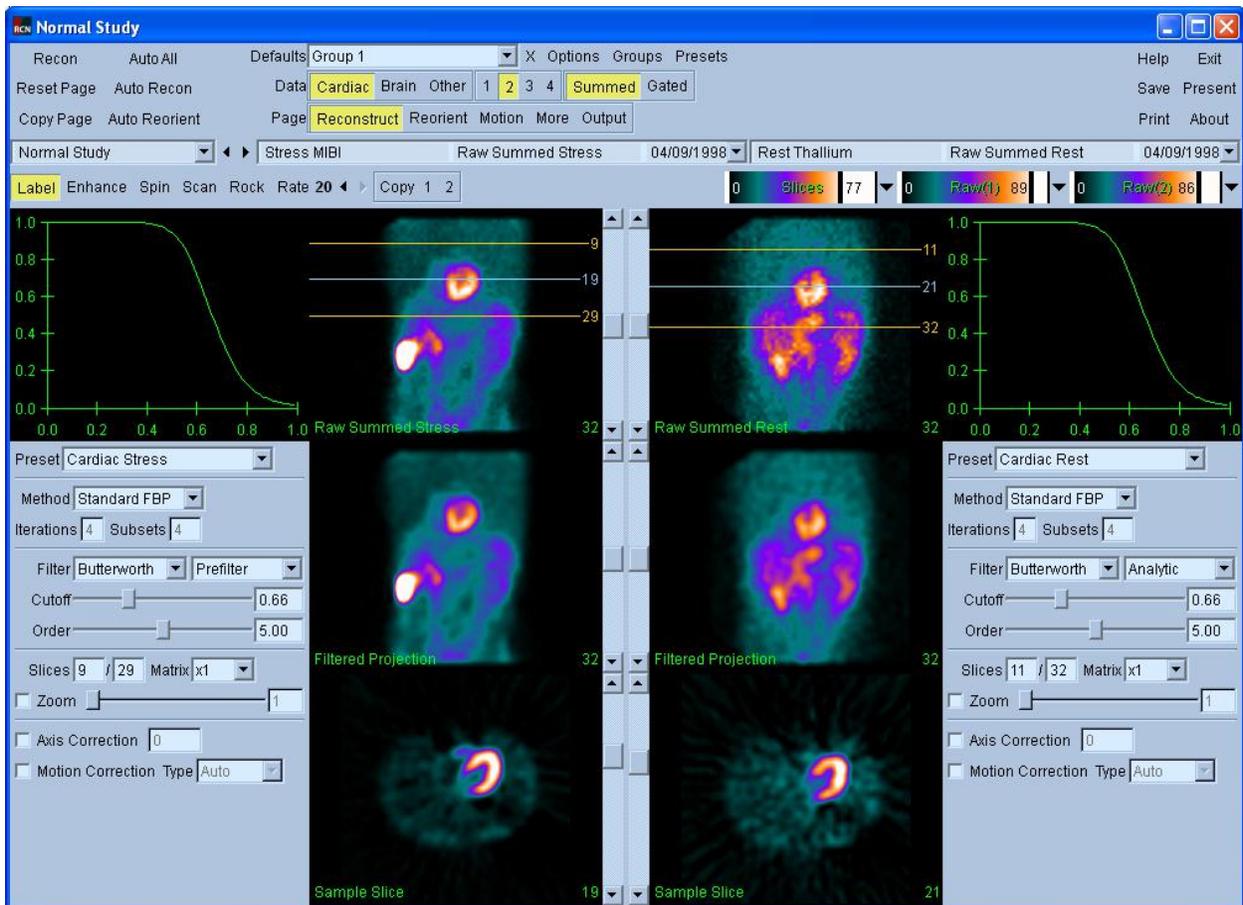


Figure 6

- Method: AutoRecon provides two reconstruction methods-Standard FBP and CS Iterative, for determining the transverse reconstruction parameters for the raw data sets. The control options available for each method are listed in the following table.

| Control           | FBP  | CS Iterative   |
|-------------------|--|--|
| Iterations        | N/A  | 12 iterations are recommended.   |
| Filter            | None, Butterworth, Gaussian, Hamming, Hanning, Parzen                                    | None, Butterworth, Gaussian, Hamming, Hanning, Parzen                                    |
| Filter - Y-Axis   | Off, Smooth, Analytic, Prefilter   | N/A  |
| Cutoff            | 0.1 – 2.0  | 0.1 – 2.0  |
| Order             | 0.0 – 10.0   | 0.0 – 10.0   |
| Slices            | First and Last Slice Numbers (corresponds to upper and lower reconstruction limit lines) | First and Last Slice Numbers (corresponds to upper and lower reconstruction limit lines) |
| Matrix            | Input matrix, 64, 128, 256   | Input matrix, 64, 128, 256   |
| Zoom              | 1.0 – 3.0  | N/A  |
| Axis Correction   | -5.0 – 5.0   | -5.0 – 5.0   |
| Motion Correction | Auto or Manual   | Auto or Manual   |

- **Iterations:** This control is only enabled if the selected method is Iterative. The number of iterations depends on your data and preferences.
- **Filter:** Filter allows you to select the filter applied to the data during reconstruction. Each filter modifies a ramp filter to smooth or enhance image details. Click on the filter option menu (Figure 6. 1) to display the list of available filters, and then select the desired filter.



Figure 6. 2

Depending on the selected Method, the Filter option menu contains combinations of the following filter options:

- **None:** No filter modifies the ramp filter applied to the data during reconstruction. This may produce sharp but noisy images.
- **Butterworth:** The Butterworth filter is a low pass filter that smoothes an image. You can control the smoothness by modifying the cutoff and order.

- **Gaussian**: The Gaussian filter can almost become any kind of filter (low pass, high pass, or band pass), with the shape of the filter being controlled by the cutoff frequency and the filter order.
- **Hamming**: The Hamming filter is a modified Hanning window with a more abrupt cutoff at the high frequency limit.
- **Hanning**: The Hanning filter a low pass filter that smoothes an image.
- **Parzen**: The Parzen filter is a filter with a linear fall off.

### Y Axis

The Y Axis filter determines the smoothing applied to the image. Y Axis filters can be applied to the reconstructed transverse data set or to the planar projection data set.

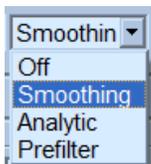


Figure 6. 3

The Y Axis option menu contains the following four options:

- **Off**: No smoothing is applied to the reconstructed or projection data set.
  - **Smoothing**: A 3 x 3 spatial filter is applied to each slice of the reconstructed data set.
  - **Analytic**: A filter based upon the settings in the Filters, Cutoff, and Order fields is applied to the reconstructed data set. The Analytic filter is a three-dimensional filter that smoothes the reconstructed data set in the x-, y-, and z-axis. Filter along the x-axis and y-axis smoothes the counts within each slice. Filtering along the z-axis smoothes the counts from slice to slice.
  - **Prefilter**: This is a smoothing filter used before reconstruction. This filter is used only with the standard FBP method.
- **Cutoff**: The Cutoff value determines the frequency that completely attenuates or produces a certain minimum attenuation of high frequency signals. Reducing the cutoff value smoothes the image by eliminating the high frequency signals. Increasing the cutoff value sharpens the image by retaining the high frequency signals. The scale value goes from 0.10 to 2.00. To increase or decrease the Cutoff value, click left on the slider and, while holding down the left mouse button, move the slider to the right or left.
  - **Order**: The Order value modifies the exponent that determines the rate at which a filter attenuates a signal. The filter order modifies the region where a filter goes from passing information to attenuating information. Decreasing the order widens the transition band, which decreases the attenuation rate of high frequency signals. Increasing the order narrows the

transition band, which increases the attenuation rate of high frequency signals. The scale value goes from 0.0 to 10.0. To increase or decrease the Order value, click left on the slider and, while holding down the left mouse button, move the slider to the right or left.

- **Slices:** Slices displays the Start Slice and End Slice of the reconstructed transverse data set. You can manually change the values in the Slices field by dragging the reconstruction limit lines with the mouse or by entering values directly into the text entry fields. Enter a value in the left Slices text entry field to specify the Start Slice. Enter a value in the right Slices text entry field to specify the Stop Slice.
- **Matrix:** The Matrix choices are only available if the chosen reconstruction method is Standard FBP. Matrix allows you to specify the matrix size of the reconstructed data sets. Left click on the Matrix option menu (Figure 6. 4) to display the list of available matrix sizes.

The x1 option creates a reconstructed data set that contains the same matrix size as the input data set. Selecting 64, 128, or 256 creates a reconstructed data set that contains the specified matrix size.

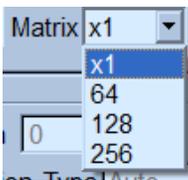


Figure 6. 5

- **Zoom:** The zoom option is only available if the chosen reconstruction method is Standard FBP. Zoom allows you to apply a zoom factor to the reconstructed data sets. AutoRecon applies the zoom factor to the reconstructed transverse data set. Short axis, horizontal long axis, and vertical long axis data sets created from this transverse data set are reconstructed using the same zoom factor. Reconstructing cardiac data sets using an increased zoom factor increases the ventricular size in the image matrix. The increased ventricular size may improve statistics when processing the zoomed short axis data sets with applications such as Cedars Quantitative Gated SPECT (QGS).
  - To create an off axis or zoomed reconstructed data set:
    - Left click on the zoom button to enable the Off Axis, Zoom, and Center options.
    - Specify a zoom factor for the reconstructed transverse data set by left clicking and dragging the zoom slider left to decrease or right to increase the zoom factor. As you increase the zoom factor, the displayed box decreases in size to show the reconstruction area (Figure 6. 6).

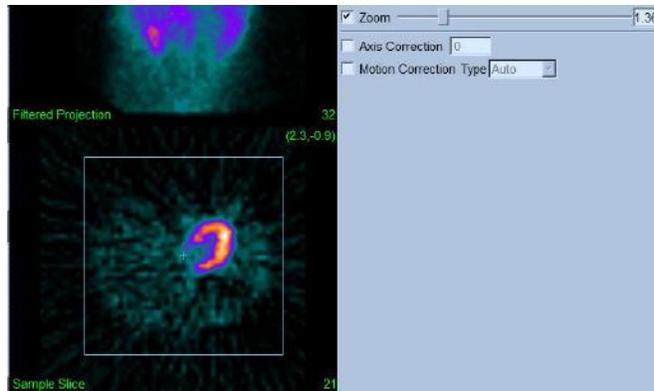


Figure 6.7

- For manual processing, drag the center point of the reconstruction to a new location within the Transverse Slice viewport.
  - Left click on the **Reconstruct** or on one of the automatic cardiac processing options to reconstruct the off axis, zoomed data set.
  
- **Axis Correction:** This option is only available if the chosen reconstruction method is Standard FBP. Axis Correction applies an axis of rotation correction to the reconstructed data sets. Left click on the Axis Correction toggle button to enable the option.
  
- **Motion Correction:** Select this button to apply motion correction to the reconstructed data set. If a Gated data set is selected, any correction made to a Summed file will automatically be made to the corresponding unsummed file. Your options are:
  - Auto: AutoRecon will automatically locate the heart, evaluate for motion artifact, and make the appropriate adjustments.
  - Manual: AutoRecon will import any manual corrections from the Motion Page and use it during the reconstruction to adjust for motion artifact.

## 4.2. Reorient Page

The Reorient window (Figure 6. 8) allows you to automatically or manually reorient cardiac SPECT data sets. When automatically processing cardiac SPECT data sets, left click on **Auto All** to reconstruct and reorient the data sets or left click on **Auto Reorient** to reorient the data sets. When processing non-cardiac SPECT data sets, no buttons appear in the upper-right corner of the window (or the upper-left corner if the Reorient window is displayed on the left).

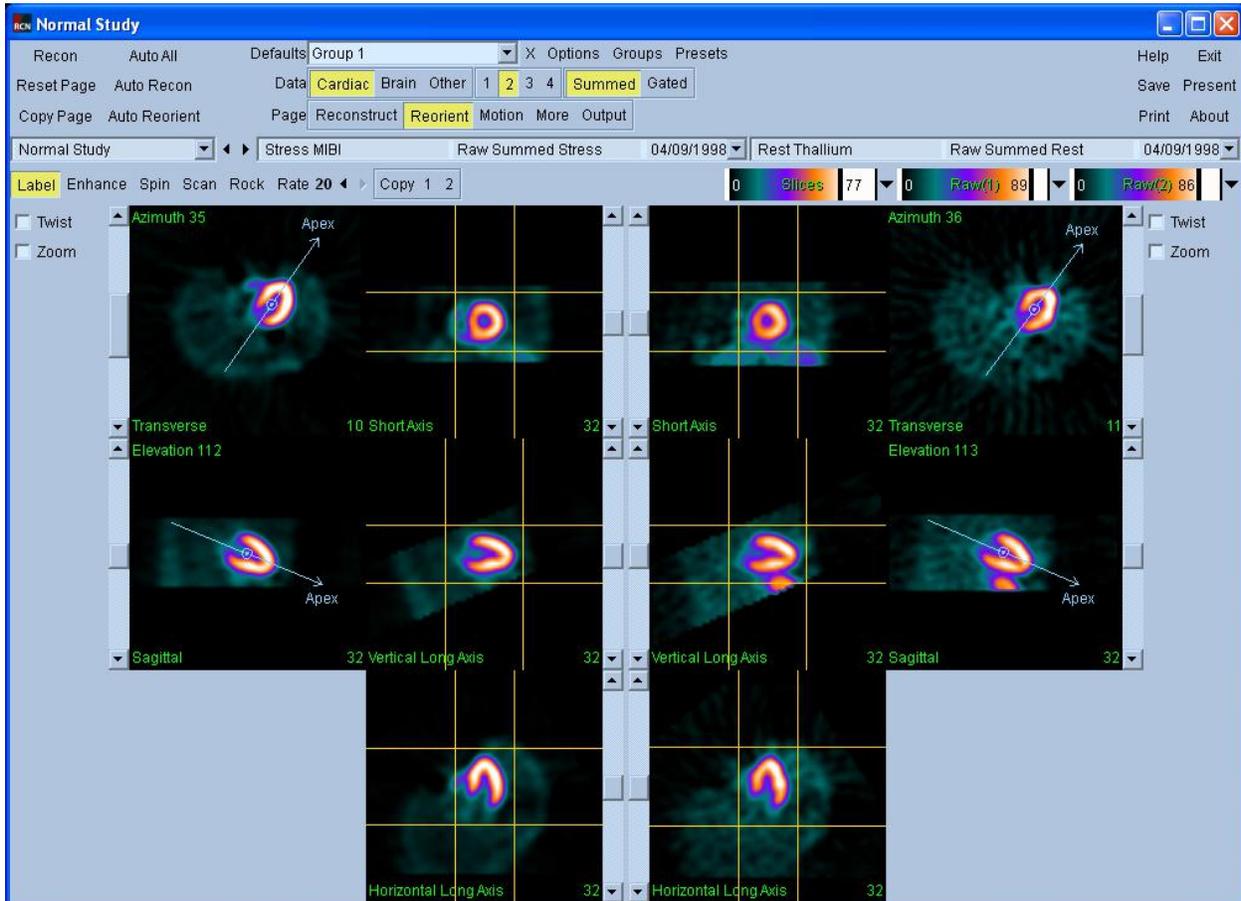


Figure 6. 9

- **Twist:** When you select this button a third viewport is displayed below the Azimuth and Elevation viewports. This viewport is used to control the axial tilt orientation of the displayed organ.
- **Zoom:** Select this button to change the zoom factor applied to the reoriented short axis and long axis images. Left click on the button and move the slider to the right to zoom in to the area of the display that is bounded by the reference lines. The range of the zoom is 1.0 to 3.0 and is displayed next to the Zoom label as the slider is adjusted.

### 4.2.1. Reorienting Data Sets

The Reorient window contains Azimuth and Elevation reference lines that you drag or rotate. If the Twist option is enabled, a third viewport is displayed below the Azimuth and Elevation viewports and an axial tilt reference line is displayed. The orientation of the reference lines determines the orientation of the reconstructed data sets.

- To manually reorient the organ of interest:
  1. If needed, enable Twist by left clicking and selecting the check box next to Twist. This will display the Twist viewport.
  2. Position the desired reference line in the organ of interest by dragging the circle in the middle of the Azimuth, Elevation, or Axial Tilt (Twist) reference line to the center of the organ of interest.
  3. Orient the desired reference line along the organ of interest by dragging the ends of the Azimuth, Elevation, or Axial Title reference lines in the direction that you want to orient the organ of interest. When positioning the reference lines, allow sufficient space between the reference lines and organ of interest so that you do not clip the organ of interest.

### 4.3. Motion Page

MoCo (Cedars-Sinai Motion Correction) is an application for the automatic and manual correction of SPECT acquisition motion artifacts (Figure 6.9). Pattern matching and segmentation algorithms are used in conjunction to minimize motion error metrics over the set of acquired projections; the resulting motion corrected projections are then presented to the operator for validation or modification. MoCo is constructed from the following components:

|                         |  |
|-------------------------|--|
| <b>Viewport Display</b> | Images and results display   |
| <b>Color Control</b>    | Selects current color scale and intensity mapping.                         |
| <b>Dataset Selector</b> | Selects the currently displayed dataset.                                   |
| <b>Viewport Control</b> | Controls display of viewports  |
| <b>MoCo Control</b>     | Controls automatic and manual motion correction processing and validation. |

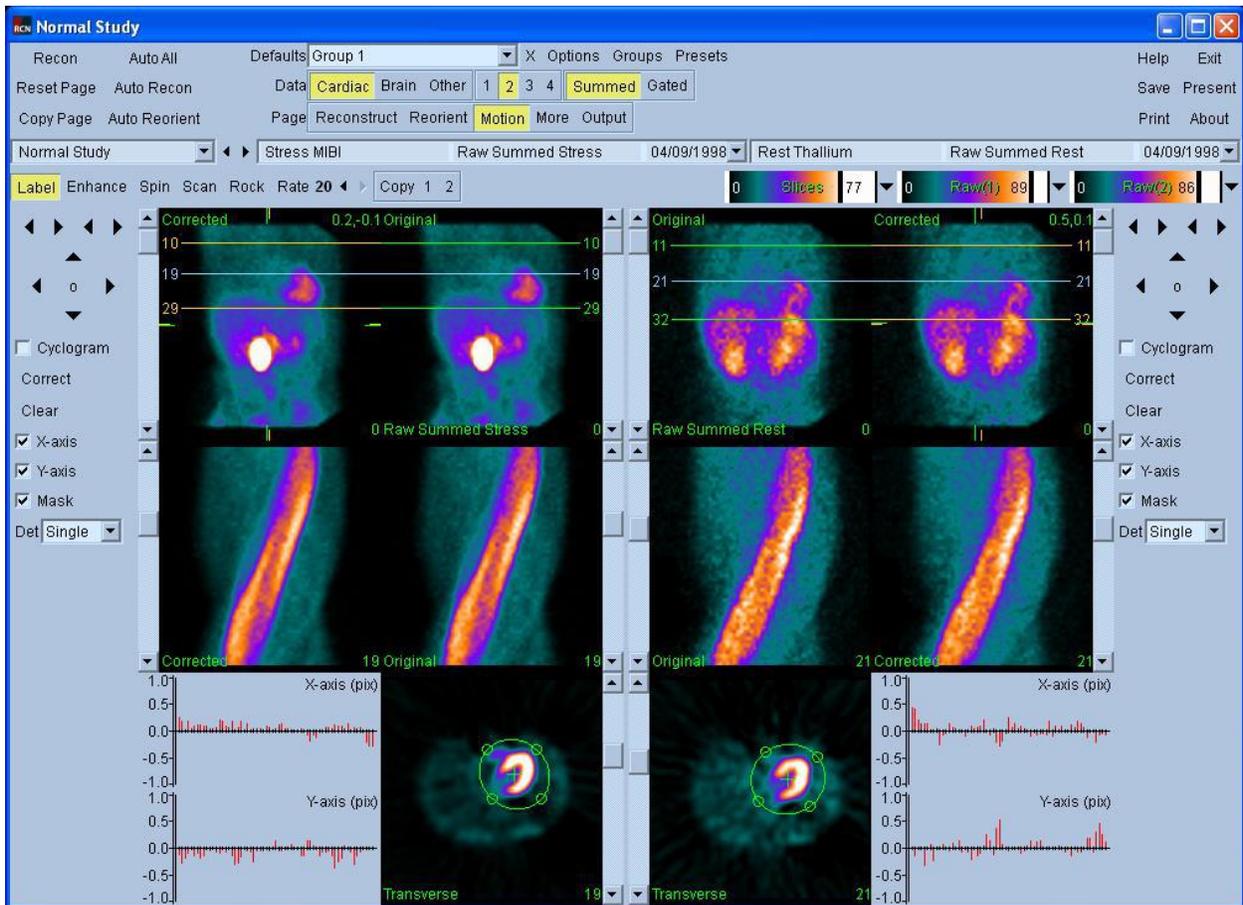
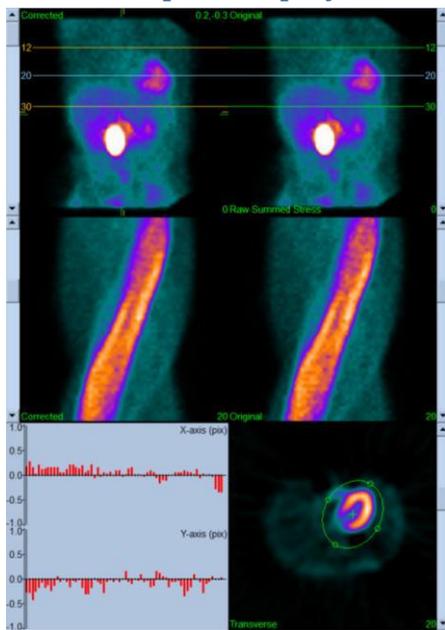


Figure 6.9

### 4.3.1. Viewport Display



The interface, which does not include externally accessible exit or save functionality as it is intended primarily to be embedded in a containing application, is constructed from the following components:

|                                      |   |
|--------------------------------------|---|
| <b>Original Projection Viewport</b>  | Displays a single projection from the uncorrected dataset. The current projection is selected by its corresponding scrollbar; horizontal motion reference lines are moved by dragging.  |
| <b>Corrected Projection Viewport</b> | Displays a single projection from the corrected dataset. The current projection is selected by its corresponding scrollbar; horizontal motion reference lines are moved by dragging. The motion correction x and y axis offsets are also displayed. |
| <b>Original Sinogram Viewport</b>    | Displays a single sinogram from the uncorrected dataset. The current sinogram is selected by dragging the sinogram reference line in the corresponding projection viewport.   |
| <b>Corrected Sinogram Viewport</b>   | Displays a single sinogram from the corrected dataset. The current sinogram is selected by dragging the sinogram reference line in the corresponding projection viewport.   |
| <b>X-axis Motion Graph</b>           | Displays the current x-axis motion correction offsets.  |
| <b>Y-axis Motion Graph</b>           | Displays the current y-axis motion correction offsets.  |
| <b>Motion Cursor</b>                 | Manually selects the x and y axis motion correction offsets. Also selects the current projections for the Original and Corrected Projection Viewports.  |
| <b>Mask</b>                          | Optional tool used to specify the region of interest.   |

### 4.3.2. Color Control



Two color scales exist: **Raw** controls most images which include the projections, sinograms and cyclogram displays. **Slices** controls the single slice displays, which is only available when Mask or Cyclogram is selected.

The Color Control is used to select the current color scale and intensity mapping. The color scale is selected by clicking on the color scale option menu and choosing from the ensuing list of available color scales. The intensity mapping is set using two parameters, the lower and upper levels, either of which can range from 0 to 100 percent. They together specify that portion of a dataset's dynamic range that is to be mapped onto the full color scale.

The lower and upper levels of the intensity mapping, represented with the lower and upper level bars, can be set through the color scale viewport, which supports the following interactions:

- Left drag either level bar to move it.
- Left drag any other point on the viewport to move both level bars simultaneously.
- Middle click or drag any point on the viewport to move the closer level bar to that point.
- Double left click anywhere in the viewport to reset the level bars to 0 and 100.

The following features are also provided through the option menu:

|                  |  |
|------------------|--|
| <b>Reset</b>     | Resets lower and upper levels.   |
| <b>Invert</b>    | Toggles the sense of the lower and upper levels.                       |
| <b>Step</b>      | Toggles color scale discretization.                                    |
| <b>Gamma</b>     | Toggles display of color scale gamma control.                          |
| <b>Expand</b>    | Toggles dynamic range expansion of lower and upper levels.             |
| <b>Normalize</b> | Toggles automatic dataset normalization based on segmentation results. |

### 4.3.3. Dataset Selector



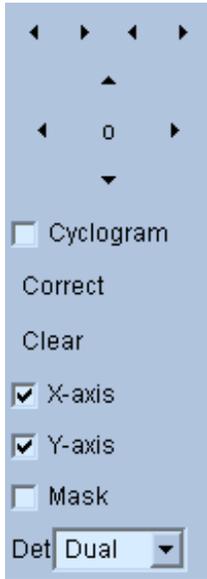
At start up the application is passed a list of one or more datasets as input. The dataset selector selects from this list the current dataset, i.e. the dataset to be viewed. It allows the user to page through the datasets by clicking the arrow buttons. In addition, the user can jump directly to a dataset by clicking on the dataset option menu; this pops up a list of available datasets from which the desired dataset can be selected. Multiple patients may be loaded at once for batch processing.

#### 4.3.4. Viewport Control

Label Enhance Spin Scan Rock Rate 20 ◀ ▶

|                |   |
|----------------|---|
| <b>Label</b>   | Enables viewport labeling including slice and projection numbers and motion reference lines.                                |
| <b>Enhance</b> | Applies a spatial filter designed to enhance motion artifact visibility to the original and corrected projection sequences. |
| <b>Spin</b>    | Toggles projection cine.  |
| <b>Scan</b>    | Toggles the sinogram cine.  |
| <b>Rock</b>    | Toggles bi-directional projection cine for sub 360° acquisitions (with spin also enabled).                                  |
| <b>Rate</b>    | Selects the cine and scan speeds.   |

### 4.3.5. MoCo Control



The MoCo Control is used to control automatic and manual motion correction processing and validation. The following controls are available:

|                  |  |
|------------------|--|
| <b>Cyclogram</b> | Enables cyclogram display mode. When enabled the sinogram viewports are replaced with their corresponding cyclogram viewports. A cyclogram is constructed by compositing the set of vertical strips defined by the intersection of each projection in the projection sequence with a plane constrained to be perpendicular to the projection and to the transverse plane and further constrained to intersect a user specified point in the transverse plane. A cyclogram accentuates horizontal (x-axis) motion artifacts in a manner analogous to a sinogram's accentuation of vertical (y-axis) motion. |
| <b>Correct</b>   | Initiate automatic or semi-automatic motion correction.  |
| <b>Clear</b>     | Reset all motion correction offsets to zero.   |
| <b>X-axis</b>    | Enable x-axis motion correction.   |
| <b>Y-axis</b>    | Enable y-axis motion correction.   |
| <b>Mask</b>      | Enable masking mode. When enabled an additional transverse slice viewport is enabled allowing the user to define a transverse volume delimited by an ellipse and lower and upper slice bounds upon which the motion correction algorithm should focus its efforts.   |
| <b>Det</b>       | Selects the number detector heads, permitting differing constraints to be used by the motion correction algorithm based on the camera geometry.  |

### 4.3.6. Automatically correcting for Motion

To automatically motion correct data sets, select the Auto motion correction option in the Reconstruction window and proceed with data set reconstruction. After reconstructing the data sets, the Motion window is displayed. The reference and corrected projection data sets are displayed in Cine mode so that you can observe for corrections in motion. Analyze the reference and corrected sinograms and the original and corrected projection view ports to verify that any motion artifact has been accurately corrected.

### 4.3.7. Manually correction for Motion

To correct for motion, step through each slice in the reference viewport, move the image up or down as needed to align the images, and reconstruct the image for motion correction.

The following steps can be executed to manually correct a data set for motion:

1. Analyze the sinogram, cyclogram, or the cine display of the projection data set to determine if the study contains a motion artifact. To help accentuate motion artifact, click on *Enhance* and analyze the cine display of the projection data set. With Enhance enabled, the pixel count difference between frames is displayed. Therefore, regions of increased motion are displayed as brighter regions.
2. Align the three horizontal reference bars in the reference viewport with a constant point of reference. Align the top reference bar with the superior ventricular surface, the bottom reference bar with the inferior ventricular surface and the middle reference bar with the mid-ventricular cavity (Figure 6.10). The reference bars will move to the same position in the Corrected viewport. These reference lines can be used as a visual cue when checking for presence of motion.

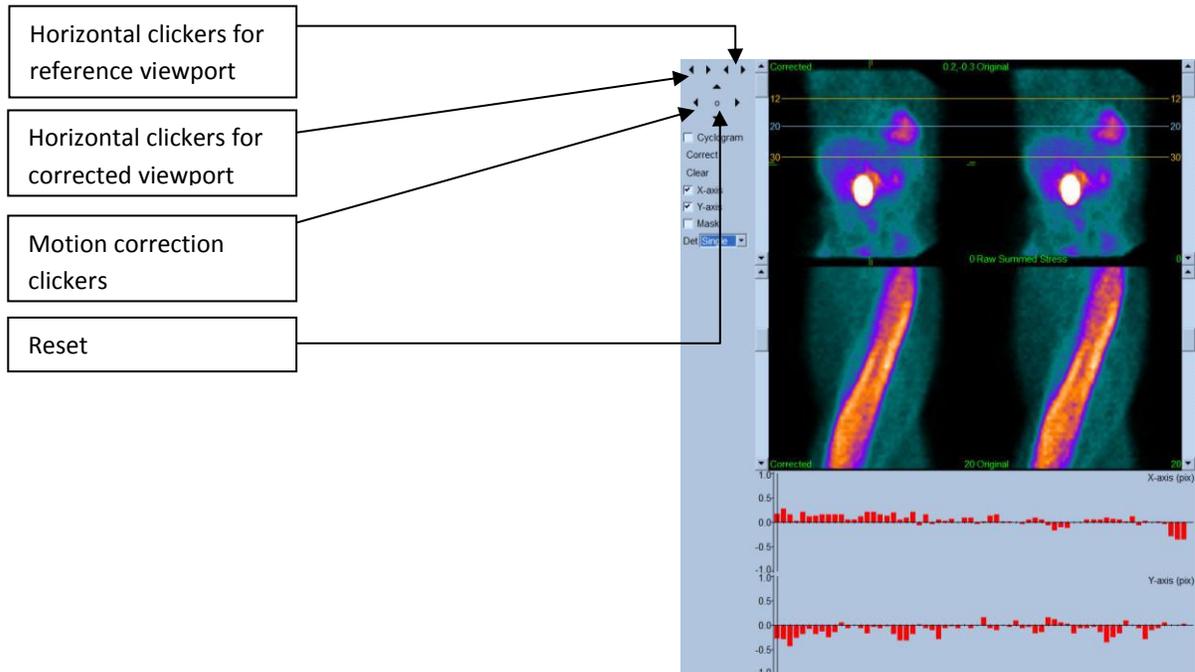


Figure 6.10

3. Step through the slices until an image needing correction is reached.
4. Left click on the motion correction clickers for the corrected viewport to move the image vertically or horizontally 0.1 pixel per click. When needed, left click on the reset button to return to the original settings. A red bar will appear in the graph viewport, which give a visual representation of the slices that have been motion-corrected, magnitude of motion correction (in pixels), and in what direction.
5. Ensure that motion corrected images are displayed in the projection viewports on the Reconstruct page.
6. Reconstruct using *Auto Recon* or *Auto All* to produce the motion-corrected transverse data set.

#### 4.4. More Page

The more page displays patient demographic and data set information for the currently displayed data sets (Figure 6.11).

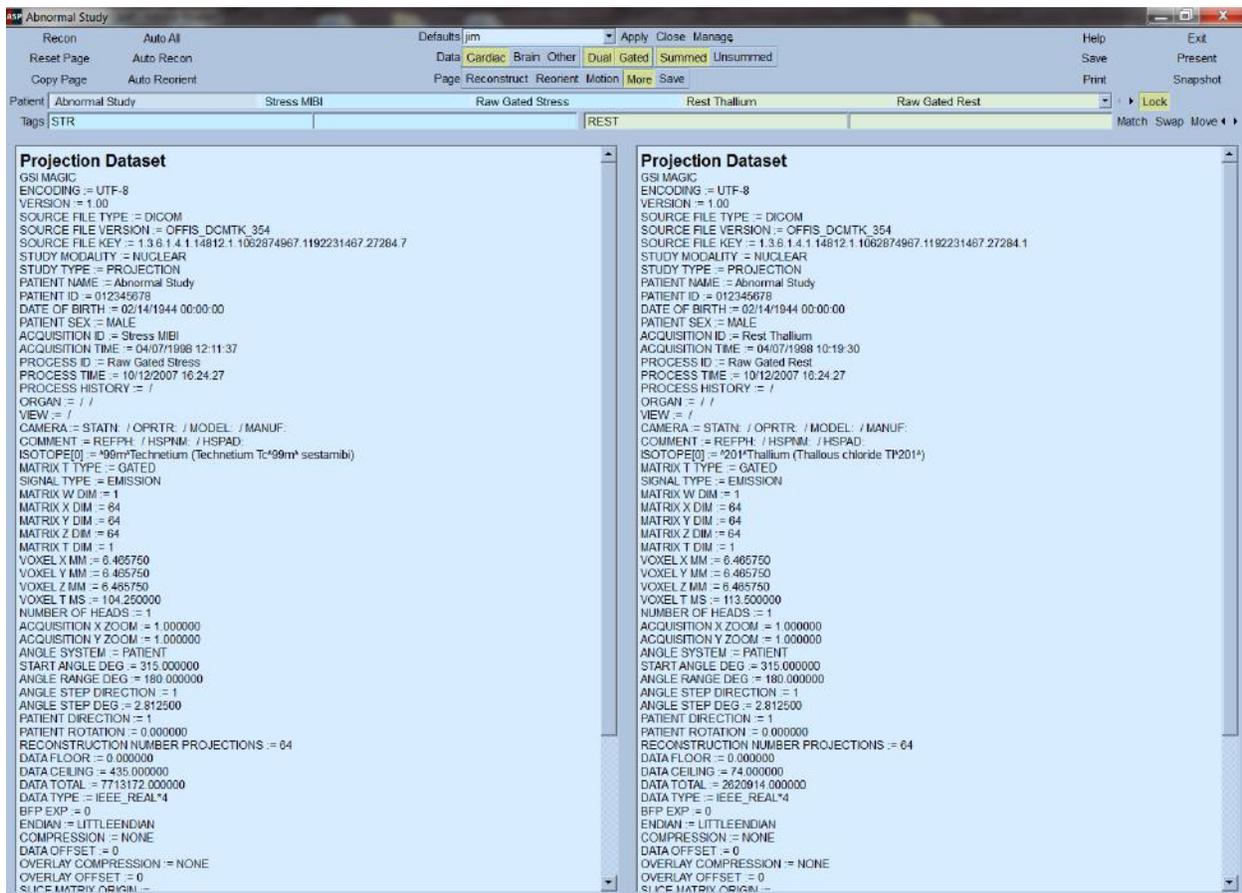


Figure 6.11

## 4.5. Output Page

- The **Output** window is used to save reconstructed volume files. It also allows for modifying the View IDs before the data sets are saved. All of the information selected or entered in the Save window determines what will be saved when the **Save**, at the right side of the Top Panel controls, is selected.

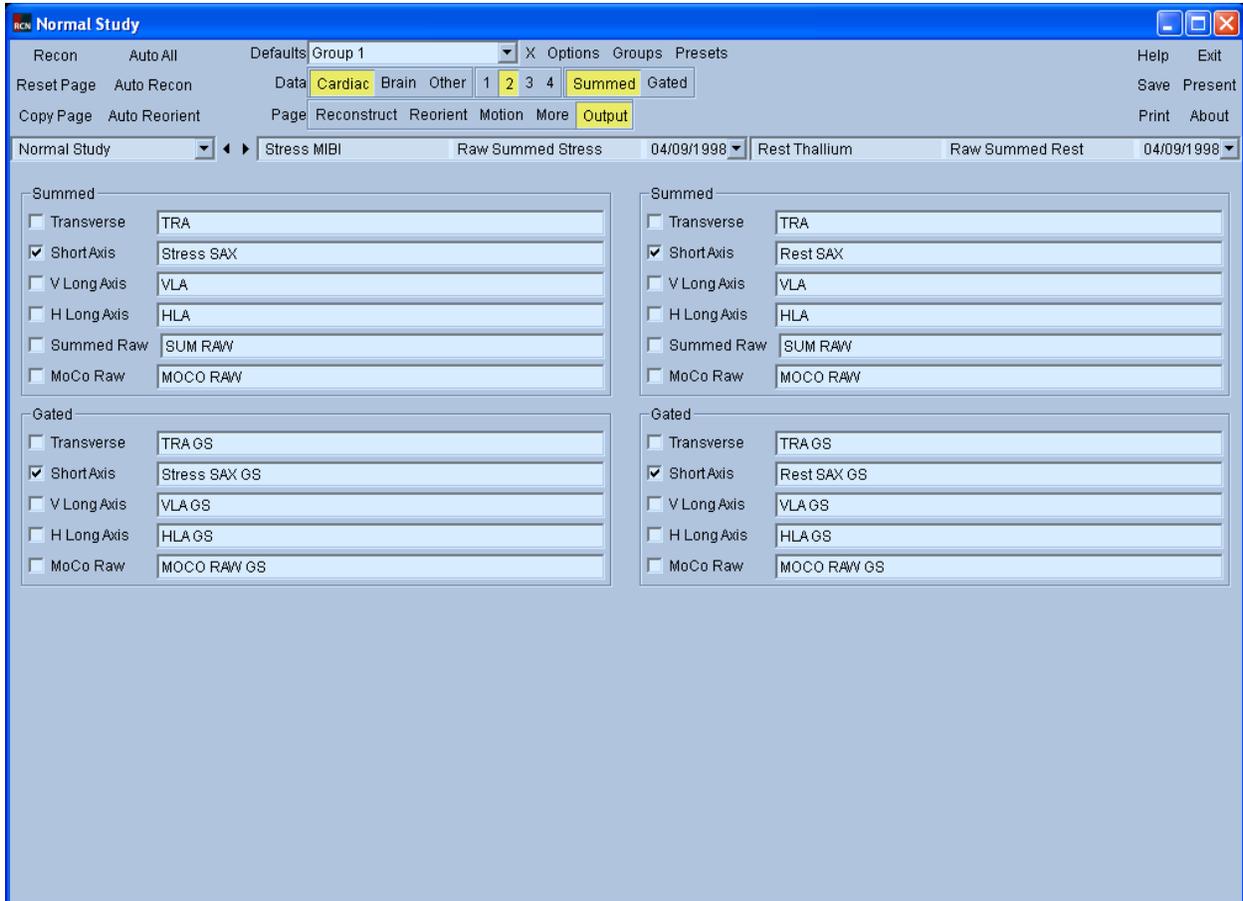


Figure 6.12

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