



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



# QGS+QPS

## Automatic Quantification

## Reference Manual

Version 2013.1

**Options: ARG, QPET, PlusPack20, AutoRecon, Fusion, Coronary Tree**

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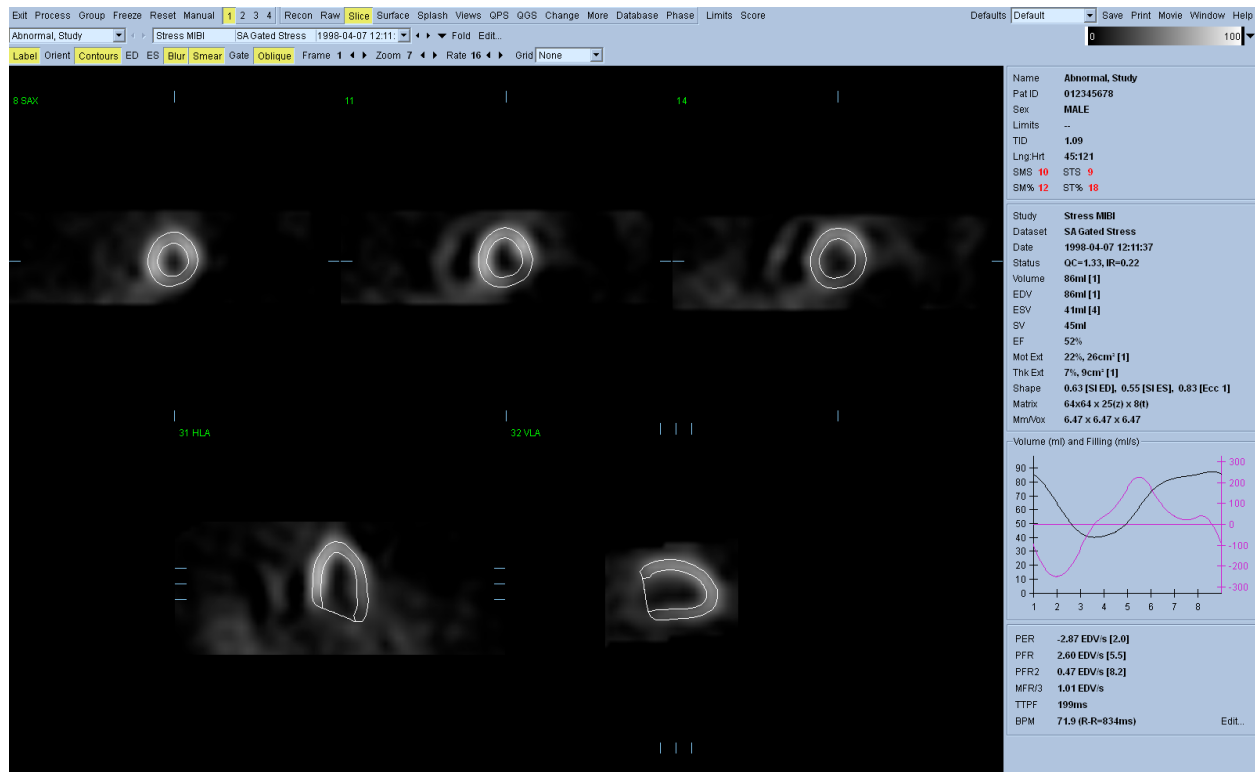
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# 1 Introduction



QGS+QPS (Automatic Quantitation) is an application for the automatic segmentation, quantification, analysis, and display of SPECT/PET myocardial perfusion studies. It is designed to assist the clinician in making an accurate, reproducible, and consistent assessment of LV function and perfusion. It works with any study consisting of gated, dynamic, and static (ungated) short axis, transverse, projection (raw), or screen capture dataset types, and has specialized support for a variety of acquisition and processing protocols including:

- SPECT/PET function.
- SPECT/PET perfusion.
- SPECT/PET viability.
- Stress/rest/delayed/attenuation corrected/reversibility.
- Dynamic PET/Coronary Flow Reserve and Absolute Blood Flow.
- Serial perfusion.
- Sestamibi/thallium.
- Rubidium/FDG.
- Male/female.
- Supine/prone.

Core functionality includes:

- Automatic generation of left ventricle (LV) inner and outer surfaces and valve plane from LV short axis perfusion SPECT/PET data, with optional manual intervention.
- Display of short axis datasets (up to 4 simultaneously), projection datasets (up to 16 simultaneously), and screen captures. Display formats include planar, orthogonal slice sets, surfaces, parametric surfaces, and polar maps.
- Functional metrics including LV volume/time curve, ED (end-diastolic) volume, ES (end-systolic) volume, SV (stroke volume), and EF (ejection fraction).
- Diastolic function metrics including PER (peak emptying rate), PFR (peak filling rate), PFR<sub>2</sub> (secondary peak filling rate), MFR/3 (mean filling rate over the first third of the ES to ED phase), and TTPF (time to peak filling from ES).
- Global and regional determination of motion and thickening abnormalities using normal limits.
- Segmental motion and thickening scores based on a 17- or 20-segment, multi-point scale, with corresponding summed scores: SMS (summed motion score), STS (summed thickening score), SM% (summed motion percent), and ST% (summed thickening percent).
- Global and regional determination of perfusion defects and defect reversibility using isotope- and gender-specific normal limits.
- Segmental perfusion scores (stress, rest, and reversibility) based on a 17- or 20-segment, multi-point scale, with corresponding summed scores: SSS (summed stress score), SRS (summed rest score), SDS (summed difference score), SS% (summed stress percent), SR% (summed rest percent), SD% (summed difference percent) and QS (quality score measure of segmentation).
- Optional generation of optimal perfusion normal limits from studies of only low-likelihood normal patients (30-40 cases per gender).

Extended workflow functionality, optimizing clinical efficiency and utility, includes:

- Integration of ARG (Automatic Report Generator) providing the ability within QGS+QPS to create, edit, sign, review, archive, and share customizable, consistency-checked, reports.
- Storage of all generated results in a separate review file.
- Application defaults, for rapidly switching QGS+QPS between custom configurations for different protocols, cameras, clinicians, etc.
- PowerPoint generation, for saving the application data, results, and settings in a format suitable for launching from within Microsoft PowerPoint.

Extended analysis functionality, providing further perspectives on the data, includes:

- Global metrics including TID (transient ischemic dilation), LHR (lung heart ratio), LV chamber volume, mid-myocardial surface area, shape index, and eccentricity.

- Motion frozen processing to generate ungated SPECT/PET datasets from gated ones by warping multiple frames into the end-diastolic frame.
- Global and regional phase analysis of mid-myocardial motion and myocardial thickening.
- Change processing for direct quantification of perfusion changes between two datasets through 3D elastic registration and count normalization.
- Prone-supine processing for quantification of perfusion on prone datasets as well as combined quantification of prone/supine datasets.
- A new method for quality control of LV MPS contours makes detection of failures in LV segmentation completely automated for objective and reproducible processing.

Extended modality functionality, enabling the analysis and display of alternative modalities, includes:

- SPECT/PET viability quantification to assess myocardial hibernation.
- Fused display of SPECT/PET/CT/CTA slices in three orthogonal planes.
- Automatic image co-registration of stand-alone coronary CTA and MPS images obtained on separate scanners.
- Review of coronary vessels, previously segmented and labeled from CT Angiography (CTA), fused with LV surfaces.
- PET Absolute Blood Flow and Coronary Flow Reserve quantification.
- Transverse processing for the quantification and display of transverse datasets.

### 1.1 Integration enhancements

On a number of platforms, QGS+QPS will better integrate with the host software. This covers dataset access, printing support as well as file output support.

### 1.2 Important Note

Because this application is licensed to a number of equipment manufacturers, the appearance of the screen may vary depending on the platform on which it is executed. The screen captures included in this manual may therefore vary slightly from what is observed on a given system. Similarly, features may vary as not all vendors provide support for all features of the software.

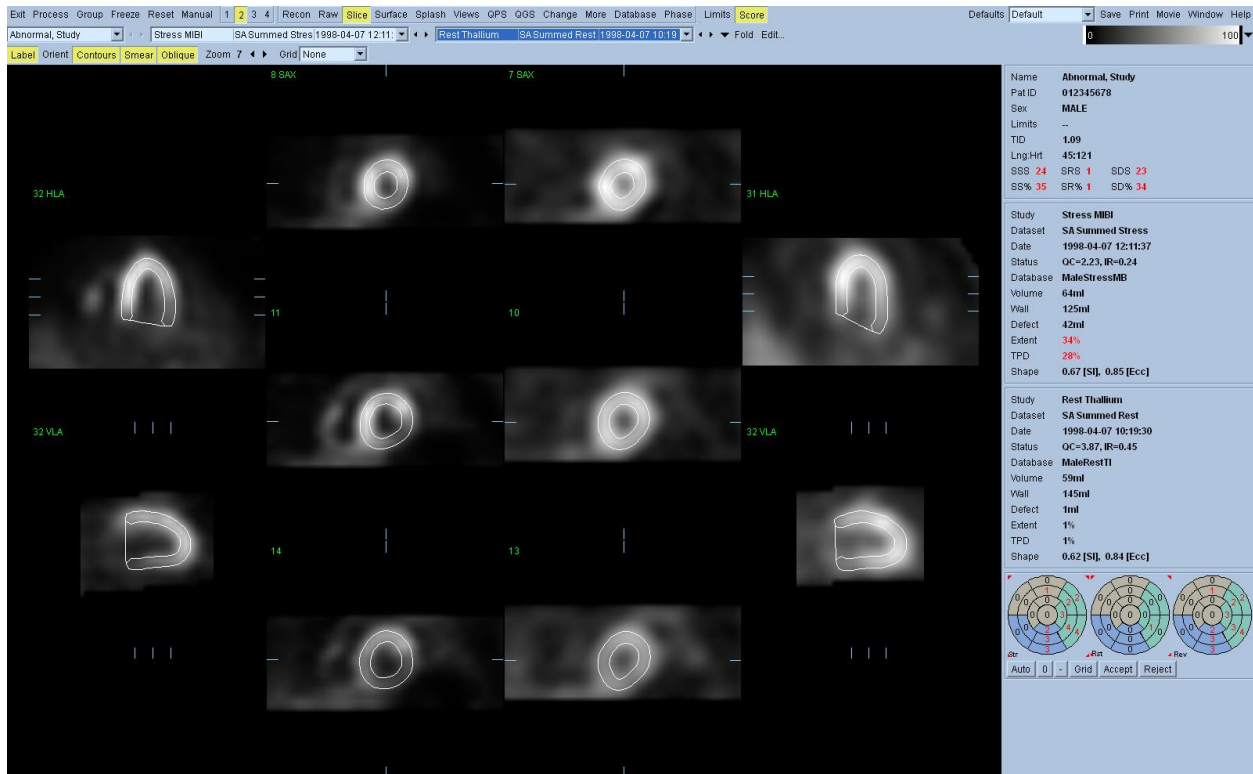
### 1.3 Warnings and Precautions

- Evaluate reconstructed datasets for proper reconstruction and reorientation before using QGS+QPS, and make sure that you correct for motion and other artifacts. Failure to perform any necessary corrections may result in misleading data, which may lead to misdiagnosis.
- Make sure that any output that you intend to use for interpretation is saved or exported in a lossless format (e.g., DICOM SC for snapshots saved to the database; TIFF or PNG for screen captures saved to a folder on a local drive). Output saved or exported in a lossy

format may not include all information necessary for a diagnosis; interpretation using non-diagnostic output may therefore lead to misdiagnosis.

- Make sure that any hardcopy output that you intend to use for interpretation is of diagnostic quality. Output of non-diagnostic quality may not include all information necessary for a diagnosis; interpretation using non-diagnostic output may therefore lead to misdiagnosis.
- Make sure that any cine output that you intend to use for interpretation is saved using a lossless AVI codec (coder-decoder). Output saved using a lossy codec may not include all information necessary for a diagnosis; interpretation using non-diagnostic output may therefore lead to misdiagnosis.
- Make sure that placement of the heart and lung ROIs is accurate, and verify that these ROIs are over the proper organs. Inaccurate heart and lung ROIs can result in incorrect computation of quantitative data, which can lead to misdiagnosis.
- Make sure that the placement of the LV contours is correct, and verify that these contours accurately reflect the myocardial wall limits. Inaccurate ventricular contours can result in incorrect computation of quantitative data, which can lead to misdiagnosis.
- Although QGS+QPS allows you great freedom in manipulating databases, you must take great care when doing so. Only the proper personnel should attempt this; if you are not knowledgeable about working with these databases, find someone who is. Using databases that contain conflicting or incompatible patient data may lead to misdiagnosis.
- You must verify correct contour creation. If contours appear too long, too short, or do not encompass the myocardium, you must manually adjust and save them. Incorrect contours generated for the normal limits population degrade the quantification results when applied to clinical studies, which may lead to misdiagnosis.
- You must verify that the correct TID is selected when loading a serial study with multiple stress and rest datasets from different dates since the TID selection can affect the QPS scores.
- When using batch processing (processing of multiple studies within one QGS+QPS session), manually selecting a normals limit applies that limit to all the studies that are loaded in the session.

## 2 Interface



The QGS+QPS main window consists of:

- Controls, in a horizontal pane spanning the top edge, control how the study is processed and displayed.
- Pages, in the rectangular area beneath the controls, for providing a series of alternative perspectives on the data and processed results. Only one can be displayed at a time.
- The info box, in a vertical pane beneath the controls and to the right of the pages, for displaying study information and statistics.

The intent is to give as much space as possible to displaying data while still providing quick access to commonly used controls.

### 2.1 Main Controls

The main controls for the application are:

<b>Exit</b>	Exits the program.
<b>Process</b>	Processes all studies and datasets, automatically segmenting and quantifying.
<b>Group</b>	Simultaneously solves the left ventricular geometry for all of the available datasets within a study.
<b>Freeze</b>	Using the motion frozen algorithm creates a perfusion (summed) dataset using the function (gated) dataset.

<b>Reset</b>	Deletes processed results from the current dataset(s).
<b>Manual</b>	Toggles manual mode. In cases where fully automatic processing fails or is suboptimal, manual mode can be used to provide guidance to the LV and lung/heart segmentation algorithms.
<b>1 2 3 4</b>	Selects the number of datasets to simultaneously display. For side-by-side evaluation of multiple datasets (e.g. stress/rest) or frames (e.g. ED/ES).
<b>Recon Raw Slice Surface Splash Views QGSResults QPSResults QPC Change Fusion Kinetic snapshot More Database Phase</b>	Selects the current page, with each page providing an alternative perspective on the data and processed results.
<b>Limits</b>	Brings up the perfusion normal limits selection dialog.
<b>Score</b>	Toggles the segmental scores window.
<b>Report</b>	Toggles the ARG (Automatic Report Generator) panel.
<b>Defaults Button</b>	Brings up the application defaults editor for creating, editing, and managing application defaults.
<b>Defaults Menu</b>	To the right of the defaults button, for quickly selecting and applying a set of application defaults.
<b>Save</b>	Saves the processed results and manual overrides to the clinical database for archiving and review.
<b>Print</b>	Prints the current screen either to the image database, as an image file (TIFF, JPEG, etc.), or to a system-defined printer.
<b>Movie</b>	Saves a movie of the current dataset to the image database (if supported) or as a movie file (AVI or DICOM MFSC, if supported).
<b>Window</b>	Launches secondary windows for the same instance of QGS+QPS
<b>Help</b>	Launches application reference guides.
<b>About</b>	Brings up version and copyright information.



### 3 Tutorial

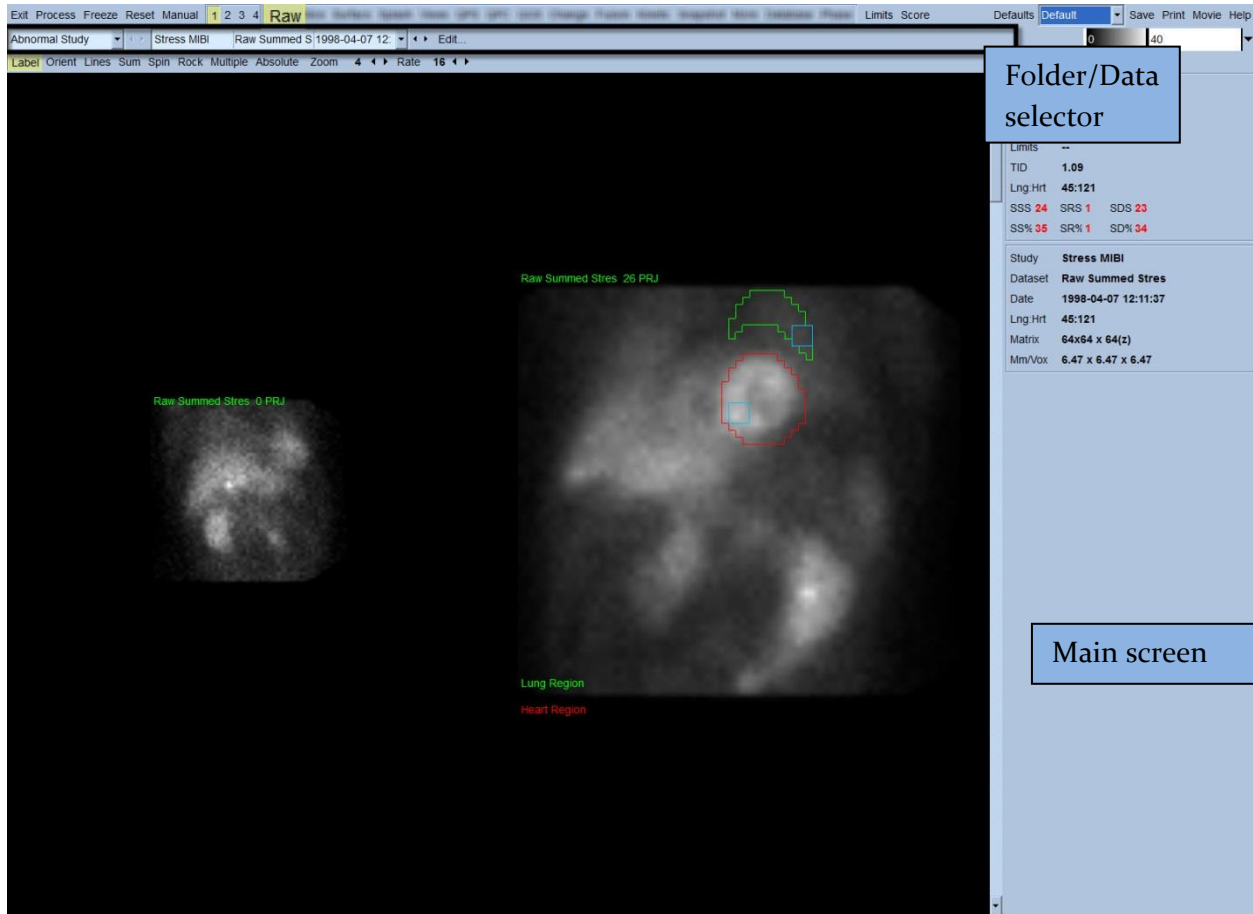
This tutorial guides you through processing and analyzing a sample SPECT study that indicates significant evidence of coronary artery disease (Abnormal Study).

QGS+QPS is able to quantify global and regional parameters of perfusion and function using one or more, gated or summed short axis data set. For perfusion analysis, typically two data sets - stress/rest, stress/redistribution, rest/redistribution, etc. are used. If possible, it is also advisable to select the related projection data set(s), so as to be able to assess acquisition artifacts at the earliest possible stage in the processing/analysis chain. For the purposes of this example, we'll assume to have selected the following files for the patient ABNORMAL STUDY:

Study	Dataset	Description
STRESS MIBI	Raw Summed Stress	(Summed stress projection image set)
STRESS MIBI	Raw Gated Stress	(Gated stress projection image set)
STRESS MIBI	SA Gated Stress	(Gated stress short axis image set)
STRESS MIBI	SA Summed Stress	(Summed stress short axis image set)
REST THALLIUM	Raw Summed Rest	(Summed rest projection image set)
REST THALLIUM	Raw Gated Rest	(Summed rest projection image set)
REST THALLIUM	SA Gated Rest	(Gated rest short axis image set)
REST THALLIUM	SA Summed Rest	(Summed rest short axis image set)

#### 3.1 Launching

Launching QGS+QPS in its standard configuration will bring up the Main screen as shown below with the *Raw* page indicator and the *Label* toggle highlighted. A representative projection image from the **Raw Summed Stress** dataset is shown, with the number to its left showing its order in the dataset. Left-clicking on *Label* toggles that number on and off. Left-clicking on and dragging the vertical black stripe rightmost in the scale will “saturate” the scale and make the LV visible in cases where strong extra cardiac activity exists.



The name of the Folder (generally, a patient name) and that of the projection data set are displayed in the horizontal section that also contains the data set selector, the data set editor and the color scale.

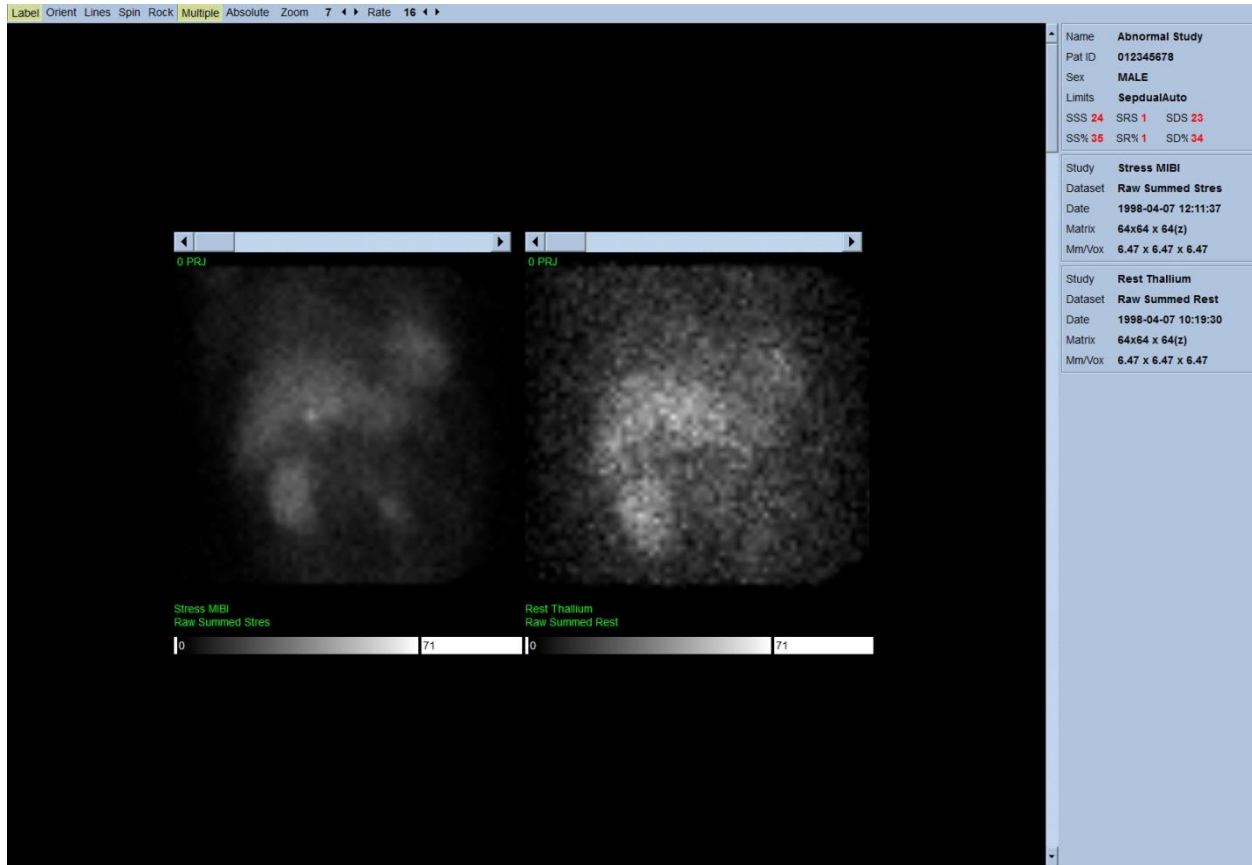


Left-clicking on the data set selector will bring up a pull-down menu listing all selected data sets as seen below, from which any projection data set can be chosen and displayed.

Stress MIBI	Raw Summed Stres	1998-04-07 12:11:37	Raw / NM / EM	Static	Stress	Supine	LHR
Rest Thallium	Raw Summed Rest	1998-04-07 10:19:30	Raw / NM / EM	Static	Rest	Supine	
Stress MIBI	Raw Gated Stress	1998-04-07 12:11:37	Raw / NM / EM	Gated	Stress	Supine	
Rest Thallium	Raw Gated Rest	1998-04-07 10:19:30	Raw / NM / EM	Gated	Rest	Supine	

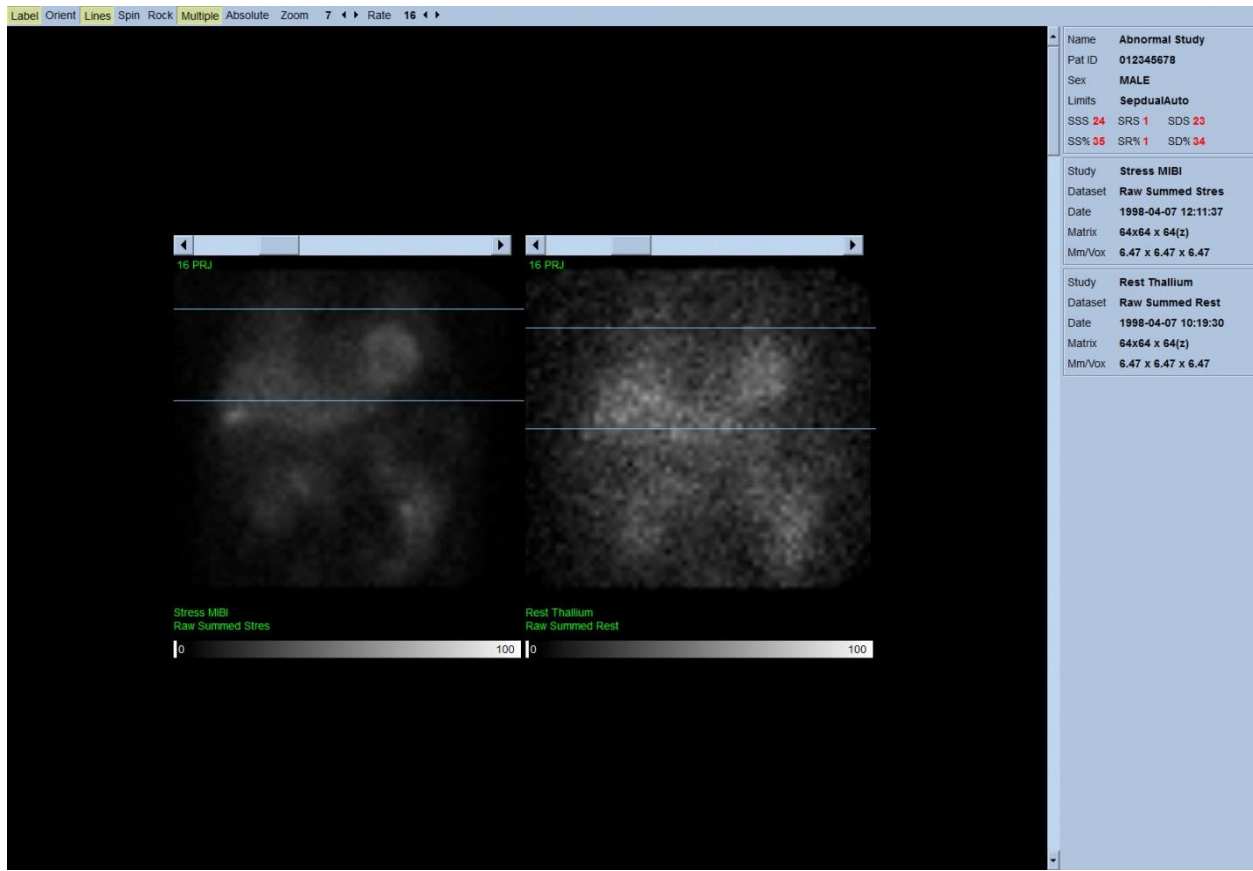
Two projection datasets (or more, when applicable) can be displayed side-by-side by left-clicking **Multiple** on the page control bar. While the color scale still acts on both images, an individual

color scale is also provided underneath each image. The number of controls on the page control bar is specific to the page selected on the Main screen toolbar.



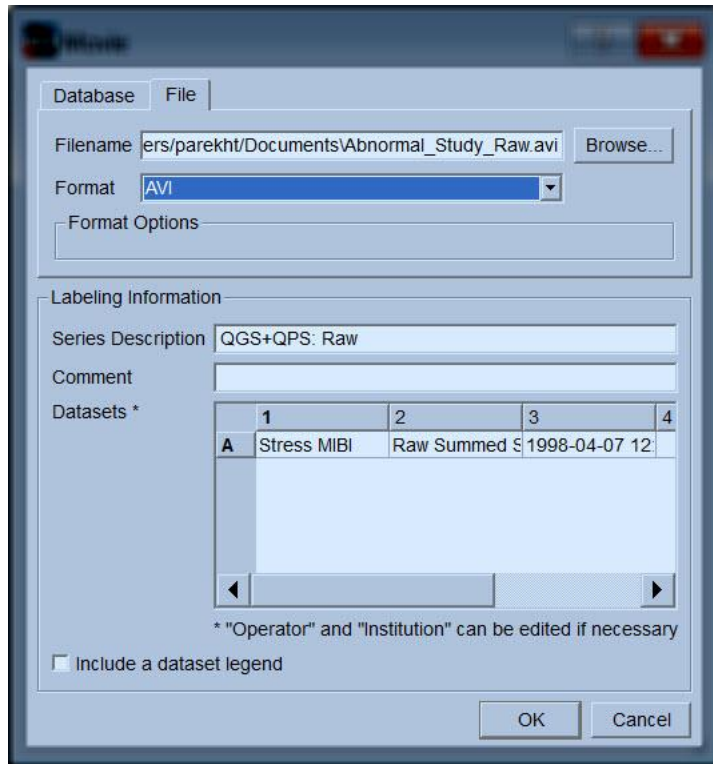
### 3.2 Reviewing the Rotating Projection Images

Clicking **Lines** toggle brings up two horizontal lines that should be manually positioned so that they tightly straddle the LV shown below. A continuous loop cine display of the projection data sets can then be started by clicking **Spin** (0 to 360 degrees continuous rotation). Clicking **Rock** toggle (in addition to the **Spin** toggle) will display an alternating cine (0 to 180 degrees and 180 to 0 degrees rotation). The cine speed can be adjusted by clicking the ◀ ▶ symbols on the right side of the **Rate** label. Any sudden movement of the LV's perceived boundaries towards or away from the lines should be noted, as should a uniform upward drift (upward creep of the heart, often associated with the diaphragm's return to its normal position soon after exercise). With dual detector cameras in the 90 degree configuration, upward creep may produce a sudden "jump" in correspondence of the middle of the projection data set, as can detector misalignment. Major motion may affect the quantitative parameters; if such motion is detected, it would be prudent to repeat the acquisition.



In addition to patient or organ motion, flickering (sudden variations in brightness between adjacent projections) can be assessed by reviewing the projections cine. Flickering is often an indication of gating errors, which are reflected in the ungated projection images when the latter are built through summation of the gated projection datasets.

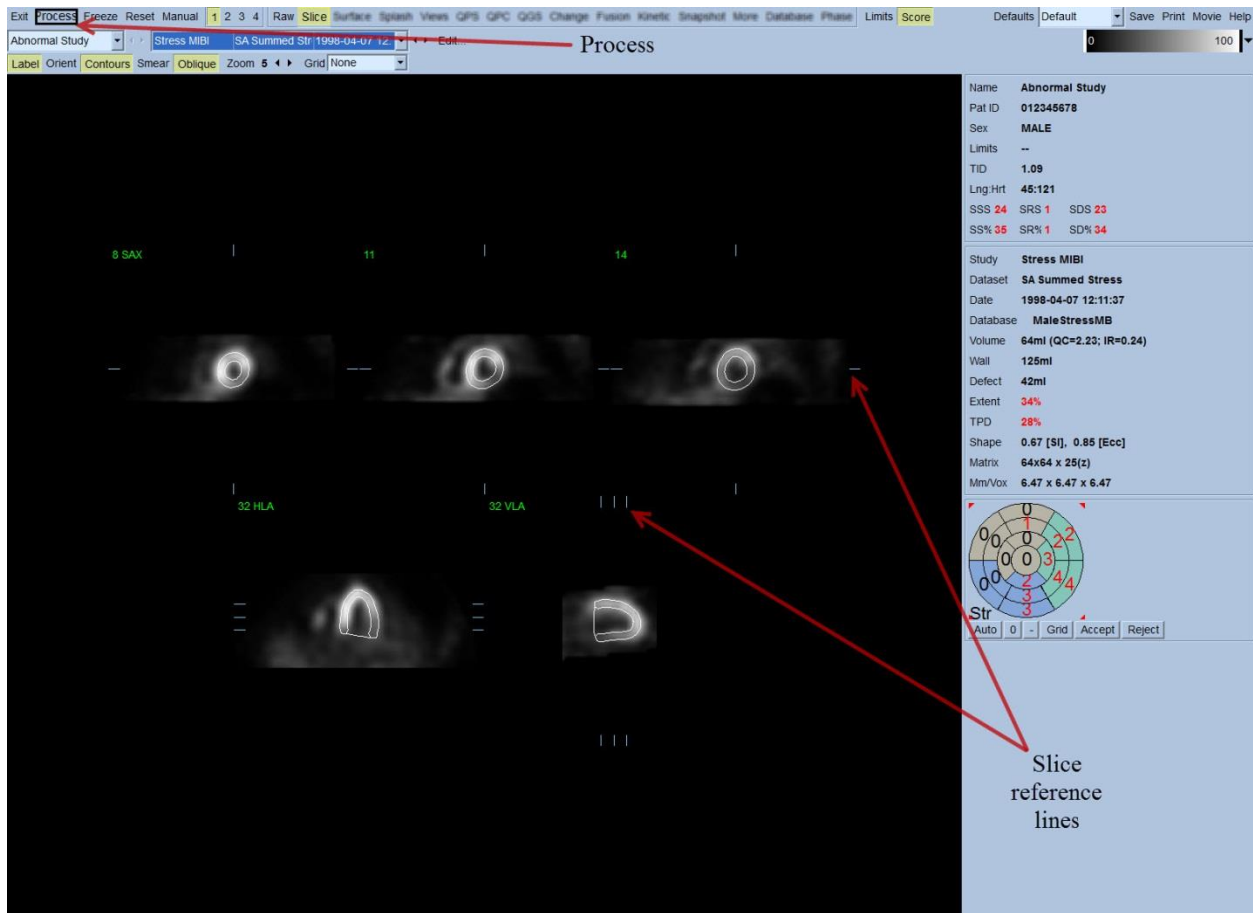
To generate a “movie” file of the raw data, click on the **Movie** button located on the global bar at the top right of the page to bring up the “movie” dialog box. Under the **File** tab page enter an appropriate path and file name for the newly created movie (AVI) file. Click **OK**.



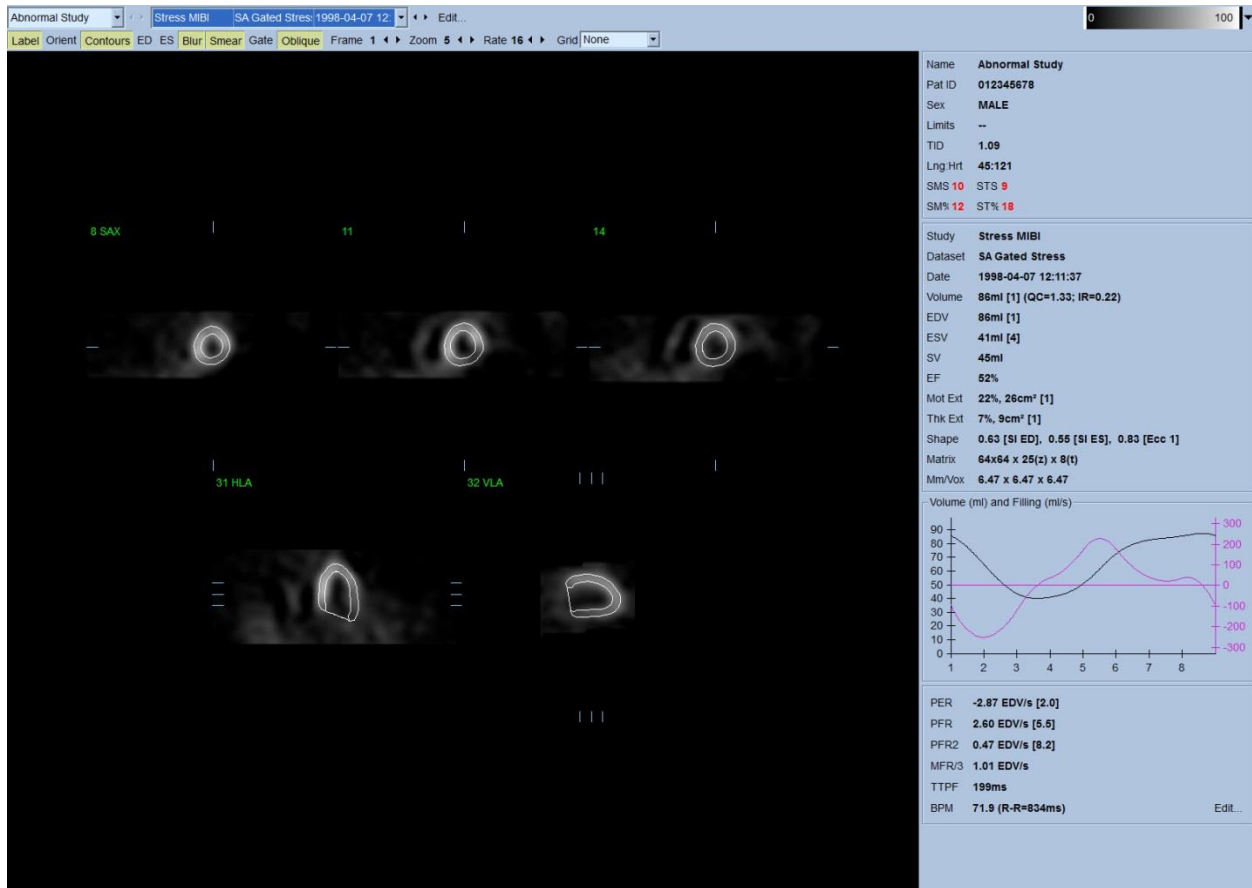
### 3.3 Processing the Images

Clicking on the *Slice* page indicator will highlight it and advance QGS+QPS to the *Slice* page view shown below. As a result, the SA Stress Gated data set or the Short Axis (SA) data set will be automatically selected and displayed. Five 2D images or “slices” are presented in standard ACC orientation, i.e., left to right = apex to base for three short axis images (top row), with the bottom row consisting of a horizontal and a vertical long axis image.

Clicking the *Process* button will automatically apply the applicable algorithms to the data, segmenting the LV, calculating the endocardial and epicardial 3D surfaces and the valve plane, and determining all the global and regional quantitative cardiac parameters. The intersection of the 3D surfaces and the valve plane in the 2D slices planes are displayed as “contours” overlaid onto the five slices, which are now representative of equally spaced (short axis images) or mid-ventricular (long axis images) portions of the LV.



Moreover, all quantitative parameter fields in the right portion of the screen should now be filled with numeric values, in addition to the creation of time-volume and filling curves (for gated short axis datasets). We'll examine and discuss the quantitative measurements in more detail later.



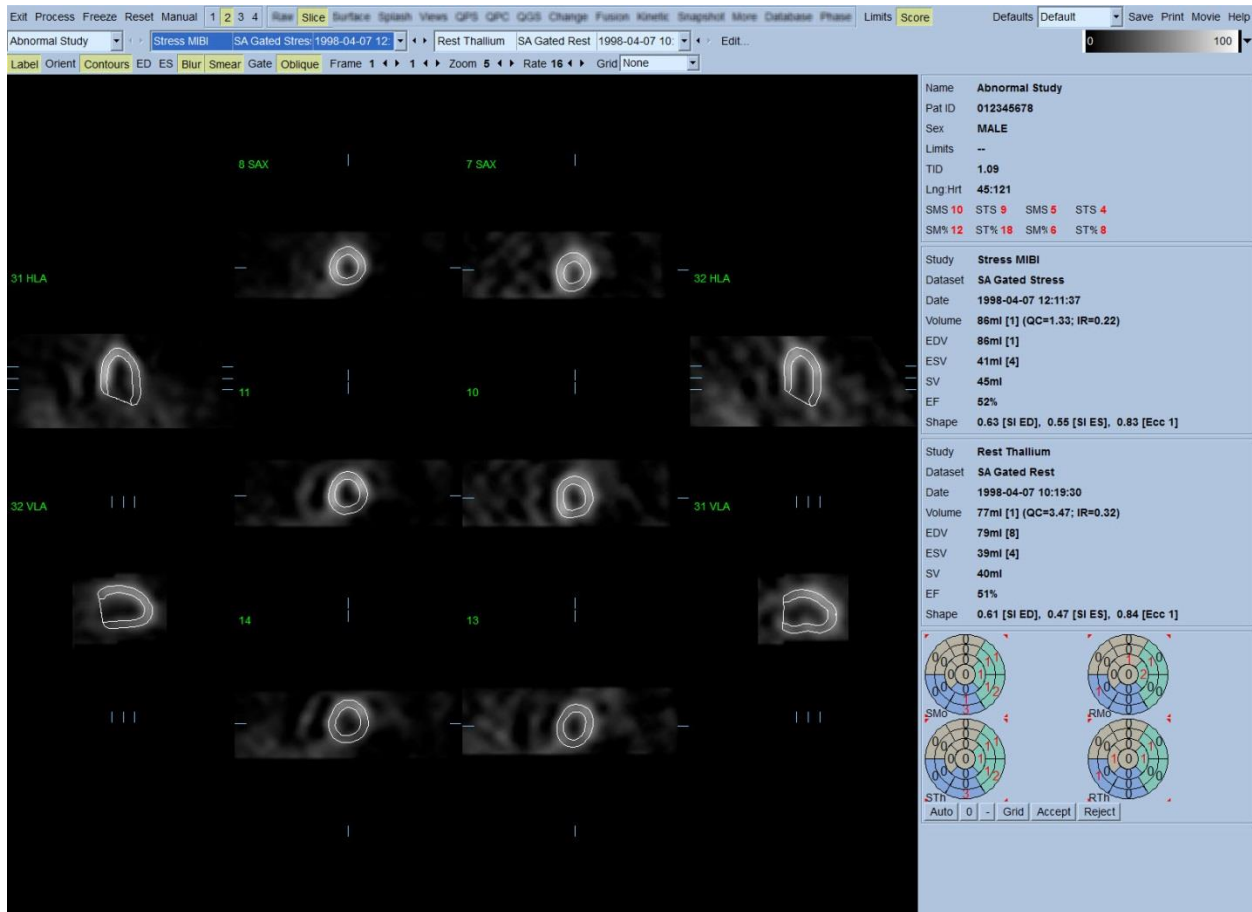
### Group Processing

Group processing allows for simultaneously solving left ventricular geometry for all of the available datasets. It allows the algorithms, in regions where structure cannot be definitively determined for one or more of the datasets, to make decisions that exploit all the available information and that do not introduce arbitrary inter-study inconsistencies. When **Group** is ON, datasets belonging to the same patient are processed as a “pair” (or, if more than two studies are involved, as a “group”).

### Checking the contours

Typically two major types of segmentation failures are observed in clinical practice, incorrect LV shape determination (Shape **QC**) and incorrect valve plane positioning (Intensity Ratio - **IR**). The new quality score (QS) feature aims to provide the user with a reliable contour quality feedback that issues a warning if the LV contours are incorrect and need manual adjustments. Refer to the Quality Score section of the manual for more details on this feature.

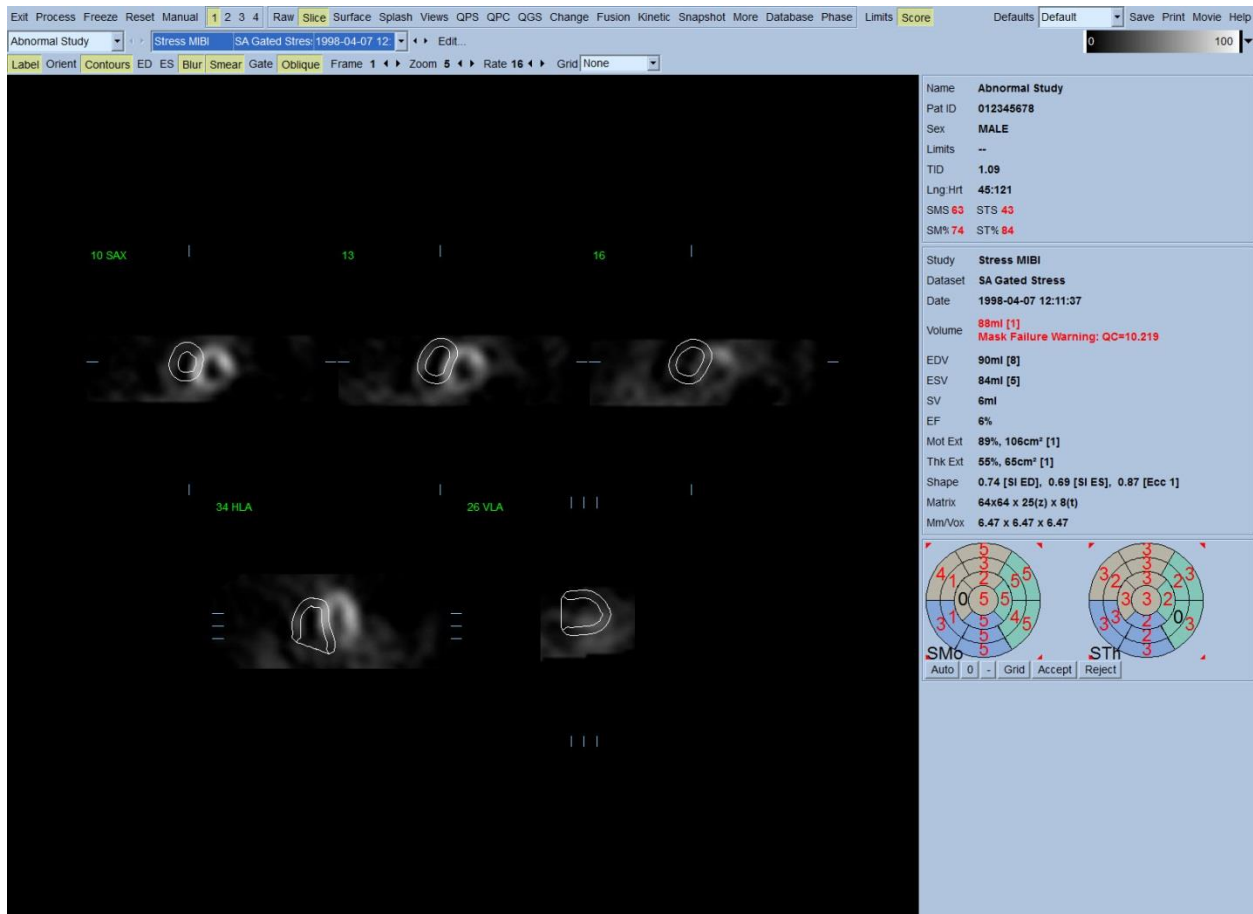
The location of the five slices displayed can be interactively adjusted by moving their corresponding slice reference lines in orthogonal views; however, in most patient studies this will not be necessary. Both the stress and the rest short axis datasets can be visualized by clicking the **2** (dual) buttons, which also splits the display in two as shown below. The stress images are displayed on the left half and the rest images on the right half of the display.



At this point, a visual check for obvious inaccuracies in the way the contours follow the LV must be performed. This will likely involve clicking the **Contours** toggle on and off, and possibly setting the images in motion (cine) by clicking the **Gate** toggle. Most major inaccuracies are due to the presence of extra cardiac activity, and will be immediately apparent from the display as seen below. In particular, one would expect to see the contours centered on a structure other than the LV, or see the contours “pulled away” from the LV to follow closely adjacent activity, especially in the inferior wall region. Both of these occurrences are extremely infrequent (0-5% in the published literature), and can be readily dealt with using the “Manual” option.

**⚠ CAUTION:** If a failure rate higher than 10% consistently occurs, there may be a systematic problem with the way the data is acquired, patient positioning (too high/too low) or other errors.





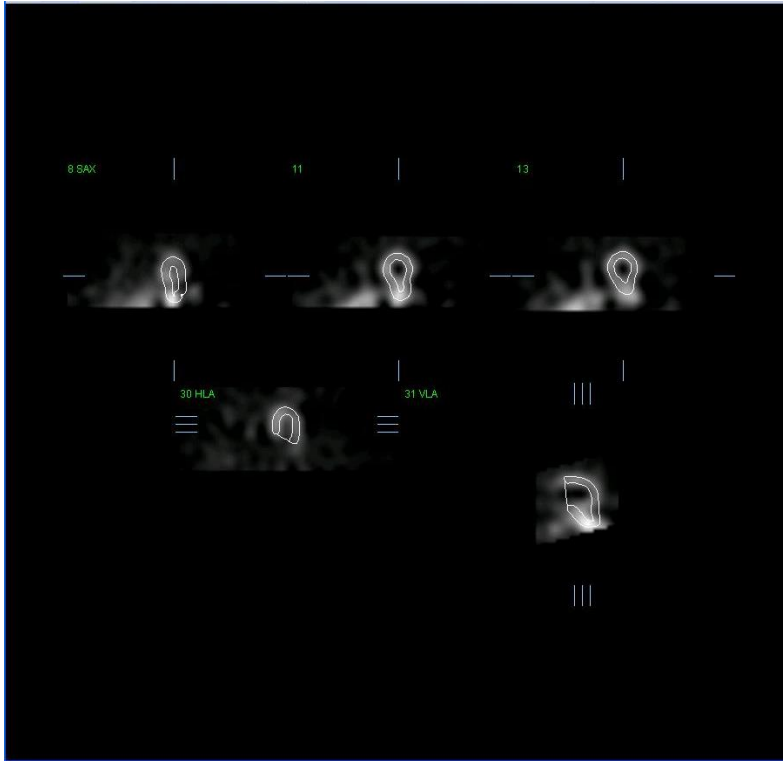
### Modifying the Contours (Manual Page)

Clicking the **Manual** toggle will bring up a modified version of the Slice page, with masking graphics superimposed upon the slices. It is possible to modify the shape and position of the masking graphics by left-clicking and dragging the masking graphic handles, small squares placed at various points on the masking graphics shown below. The mask should be shaped and positioned so that it encompasses the LV and excludes all extra cardiac activity. Before doing so, it may be advisable to toggle the incorrect contours off by clicking the **Contours** button. Clicking the **Mask** toggle and clicking the **Process** button will force the automatic algorithm to operate on the portion of the 3D image inside the mask, and new contours plus new quantitative measurements will be generated and displayed.

1. Position short axis crosshairs over LV center.  
 2. Position long axis line end-points over LV apex and base.  
 3. Position mask outside of LV.  
 4. Select Localize (limits initial LV search to mask) and then process.  
 5. If necessary, reprocess with Mask (disregards all counts outside of mask) and/or Constrain (locks LV apex and base).

Note that the segment positioned on the LV's long axis serves only as a reference. In cases where simple masking has not produced satisfactory contours as show below, one has the option of setting two exact locations through which the apical and basal portion of the contours must pass; this is done by clicking the **Constrain** toggle to highlight it, then clicking again on the **Process** button.

**⚠ CAUTION:** The “Constrain” option should not be used unless absolutely necessary, as it can greatly affect the reproducibility of the quantitative measurements. Please make sure the **Constrain** button is NOT highlighted when starting the masking process in the **Manual** page. One instance in which **Constrain** is used is when the valve plane is incorrectly identified and the stress and/or rest contours clearly exceed its location. This will typically result in a “ring” of artifactual hypoperfusion at the periphery of the perfusion polar map(s), not associated with a standard coronary territory.



### 3.4 Reviewing Gated SPECT images on the Slice page

An initial visual assessment of LV function can be performed by left-clicking the Gate toggle to display cine of the five slices while clicking the **Contours** toggle on and off. The cine speed can be adjusted by clicking the ◀ ▶ symbols on the right side of **Rate**. Moreover, a temporal and a spatial smoothing filter can be applied to the images by left-clicking the **Blur** and **Smear** toggles, respectively. This is especially useful to reduce statistical noise in low-counts images for visual assessment, and it will not affect the quantitative results.

Note: The “Blur” and “Smear” functions only affect image display. The QGS algorithms operate on the original, unsmoothed data regardless of Blur and Smear settings.

**i** **INFORMATION:** At Cedars-Sinai Medical Center (CSMC), a gray or thermal scale is typically used to assess motion, and a 10-point scale (Step10) is used to assess thickening. A comprehensive description of the CSMC segmental scoring method can be found in “*Berman D, Germano G. An approach to the interpretation and reporting of gated myocardial perfusion SPECT. In: G Germano and D Berman, eds. Clinical gated cardiac SPECT. Futura Publishing Company, Armonk; 1999:147-182.*” Essentially, images are scored based on a 20 or 17 segment model and a categorical scale of 0-5 (motion) or 0-3 (thickening).

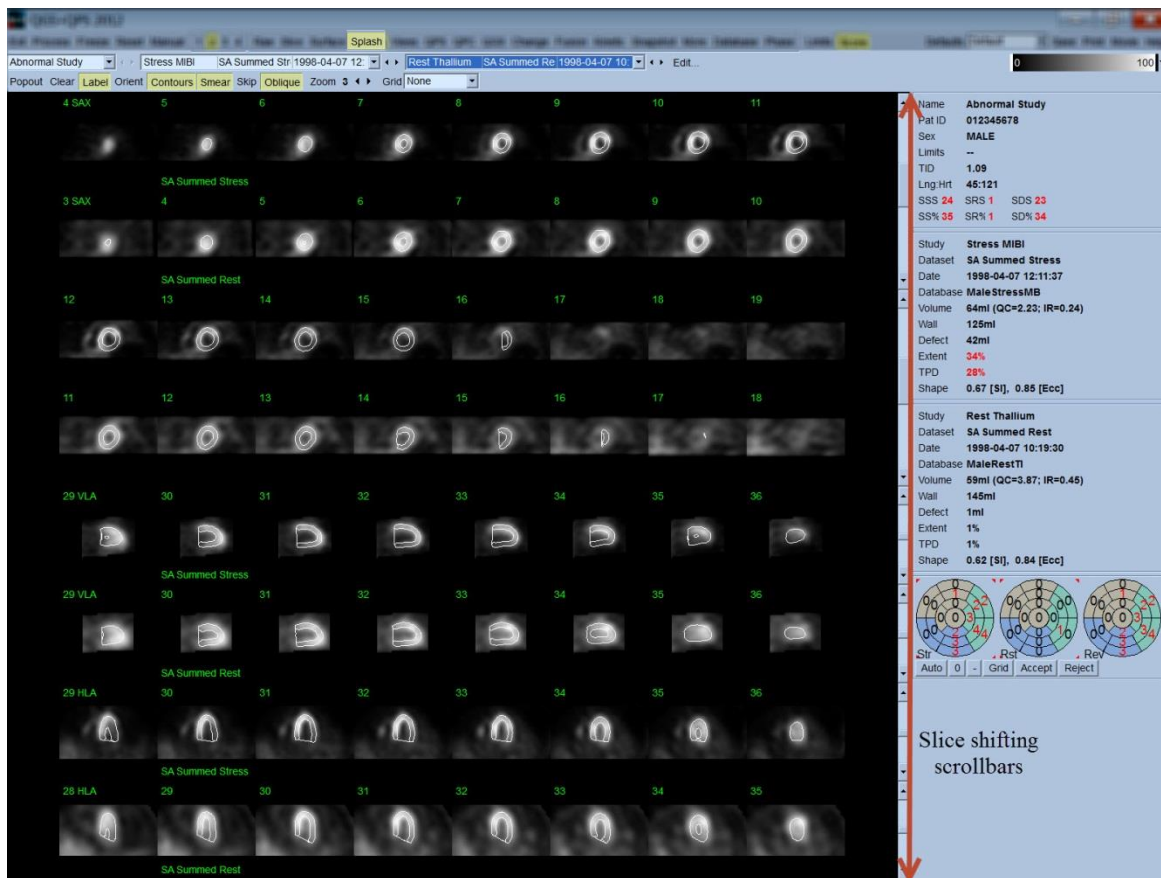
### 3.5 Reviewing Gated or Summed (un-gated) SPECT Images on the Splash page

Although the *Slice* page can be useful to make a quick initial determination of the presence and location of perfusion abnormalities, accurate perfusion assessment must precede from the entire

short axis datasets. Clicking on the **Splash** page indicator will bring up all the available short axis images, which (if the **z** button is on) will be displayed in interleaved fashion for the stress and the rest studies as show below. In essence, the first dataset to appear in the **Info** box will correspond to rows 1, 3, 5 and 7 of the display, the second dataset to rows 2, 4, 6 and 8. Stress and rest images are automatically chosen, and ought to be well aligned; to manual shifting of a dataset by one or more slice(s) can be achieved by clicking and dragging the appropriate scrollbars to the right of the images. Images (gated only) can be viewed simultaneously as cine by clicking the **Gate** toggle.

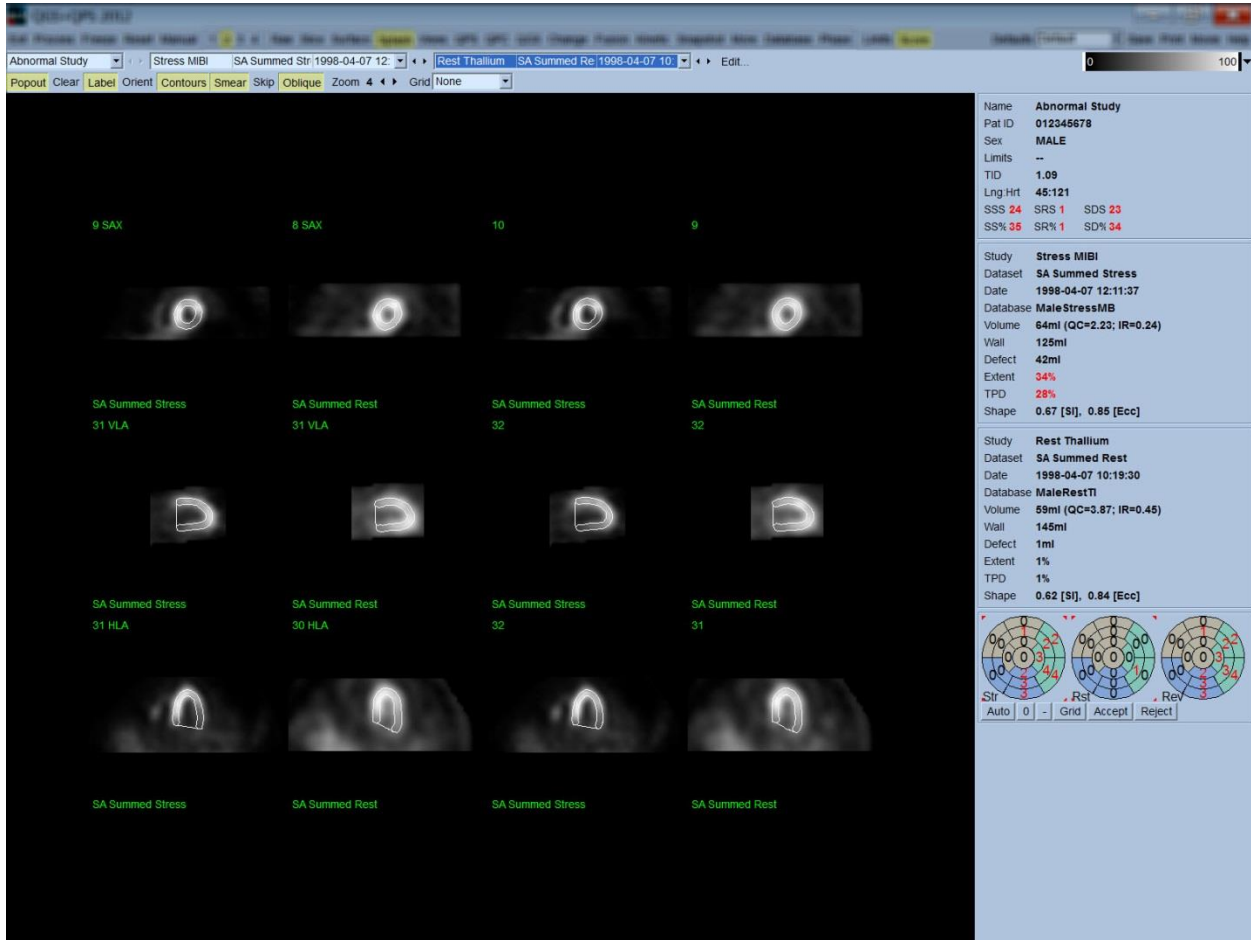
A spatial smoothing filter can be applied to the images by turning on the **Smear** toggle on the page control bar. This is especially useful to reduce statistical noise in low-counts images for visual assessment, and it will not affect the quantitative results.

Clicking on the dataset selector on the **Splash** page will bring up all the available short axis images. A spatial and/or temporal smoothing filter can be applied to the images by clicking the **Smear** and **Blur** (gated datasets only) toggles respectively. This is especially useful to reduce statistical noise in low-counts images for visual assessment, and it will not affect the quantitative results.



Optionally, key slices may be “blown up” for further review. This is achieved by right-clicking on the desired images to select/deselect them (the corners of the selected items are highlighted in

blue), then left-clicking on the **Popout** toggle on the page control bar. To de-select all the selected slices click **Clear**. The images below show four short axis, horizontal and vertical long axis images for each of the stress and rest data sets that can be displayed using the **Popout** toggle in the **Splash** page.



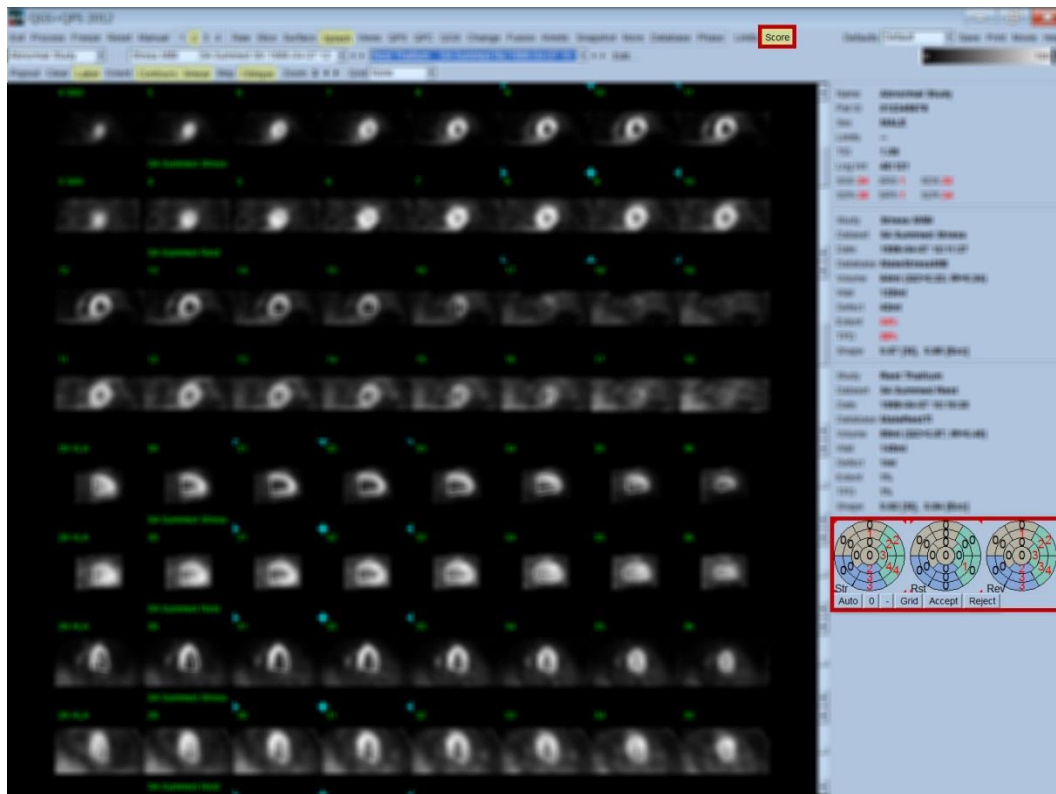
**i** **INFORMATION:** At Cedars-Sinai Medical Center (CSMC), a gray or thermal scale is typically used to assess perfusion. A comprehensive description of the CSMC segmental scoring method can be found in “*Berman D, Germano G. An approach to the interpretation and reporting of gated myocardial perfusion SPECT. In: G Germano and D Berman, eds. Clinical gated cardiac SPECT. Futura Publishing Company, Armonk; 1999:147-182.*”. Essentially, images are scored based on a 20 or 17 segment model and a categorical scale of 0-4 (0=normal to 4=absent perfusion).

## Using the Score Box

Clicking on the **Score** toggle will bring up the **Score Box** with its 20-segment or 17-segment polar maps with segment demarcation outlines for the stress, rest and difference portion of the study, shown below is a 20 segment score example. Each ring in these “categorical polar maps” is related to the displayed images as follows: apex to base = inner to outer rings.

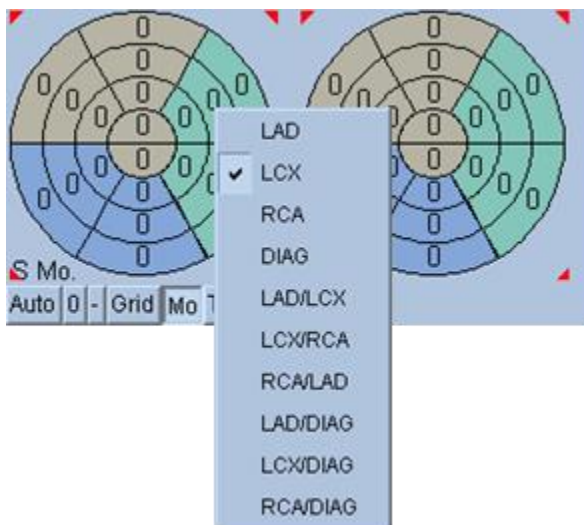
The display scheme aims at making it easier for the physician to identify the 20 (or 17) segments for which perfusion must be scored. Selecting the **Segments** option from the **Grid** pull-down menu on the page control bar will overlay demarcations onto the stress and rest images, clarifying which portion of which slice belongs to which segment. Alternating between the **Segments** and **None** options of the **Grid** pull-down menu facilitates the visual assessment of segmental scores, which can then be entered in the Score box to override automatic scoring, if so desired.

A universal set of normal limits is applied to all gated short axis datasets to automatically calculate motion and thickening scores for all segments, as well as the summed motion and thickening scores (SMS and STS), the percent summed motion and thickening scores (SM% and ST%) and the extent of motion and thickening abnormality (Mot Ext and Th Ext) expressed both as area in cm<sup>2</sup>, and as a percent of the mid-myocardial surface area. If any of the segmental scores is deemed inaccurate by the reviewing clinician, he/she can increase it or decrease it by left or right clicking on its numeric value in the box. SMS, STS, SM% and ST% will adjust automatically.



If the appropriate normal limits are preset for this patient, the program will automatically calculate perfusion scores for all segments, as well as the summed stress, rest and difference scores (SSS, SRS and SDS) and the corresponding summed percent scores (SS%, SR% and SD%) and the extent of perfusion abnormality. Otherwise, the normal limits database to apply to the dataset will have to be selected by clicking on the **Edit...** button, located next to the dataset selector, and selecting the appropriate limits file from the dropdown menu. The user selects one of the displayed normal limits selections in the dialog window and clicks **OK**. If any of the segmental scores is deemed inaccurate by the reviewing clinician, he/she can increase it or decrease it by left or right clicking on its numeric value on the respective score polar map. SSS, SRS, SDS, SS%, SR%, and SD% will adjust automatically.

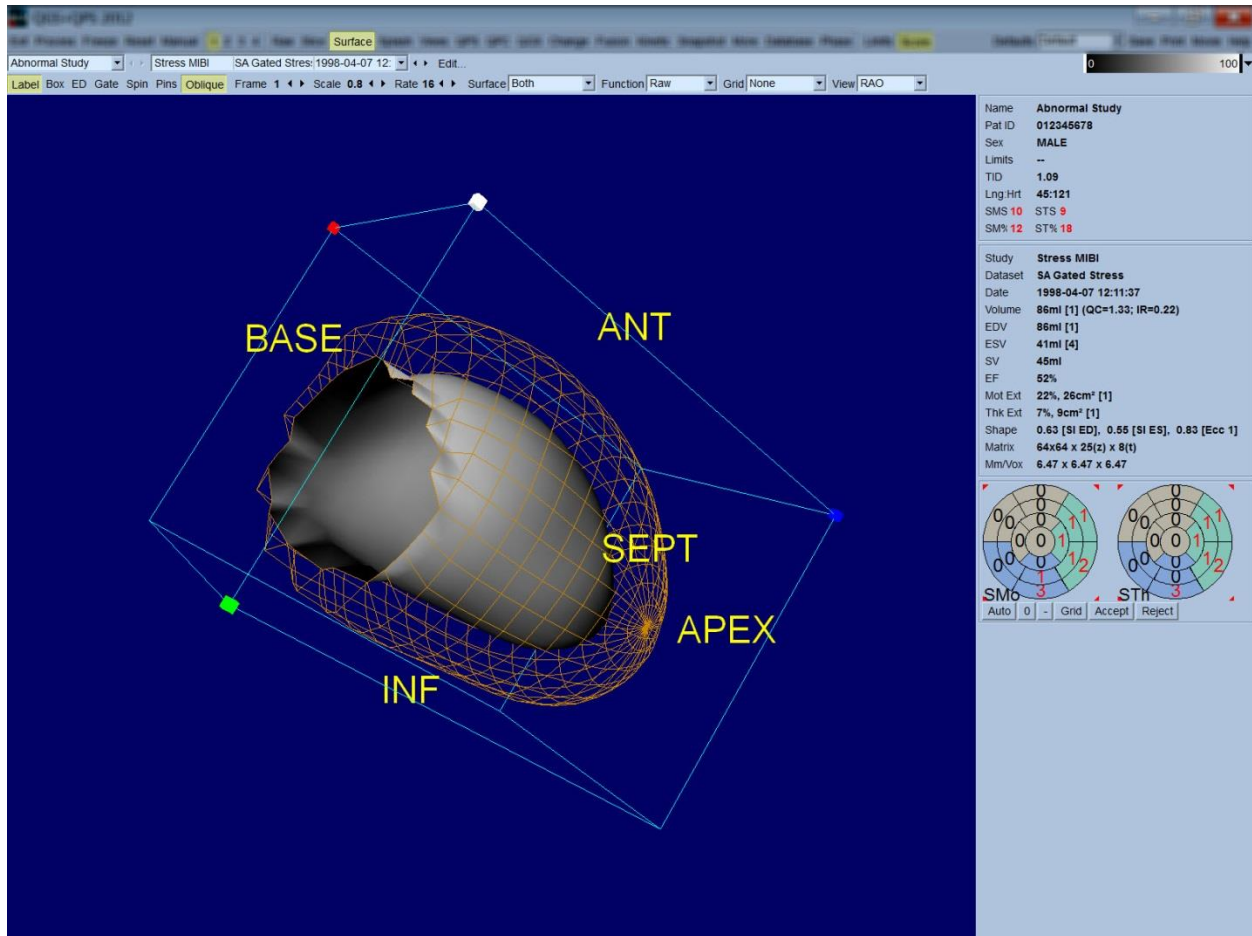
Note: The summed percent scores represent the summed scores normalized to the worst possible score obtainable in the model chosen (i.e., 80 for the 5-point, 20-segment model and 68 for the 5-point, 17-segment model), as described in Berman et al., JACC 2003;41(6):445A.



Scoring is further enhanced by the color coding of segments based on the coronary vessels supplying that segment. The Tan colored segments are assigned to the LAD, Green to the LCX, and Blue to the RCA. By default, the application will attempt to choose the coronary vessel based on the visual scores. This can be overwritten by right-clicking on a segment and selecting the appropriate vessel from the list of vessels. In some cases it is unclear to which vessel the defect belongs. When this occurs, select the abnormal segment in question and choose a combination of vessels. The **Auto** button will load the automatically generated scores.

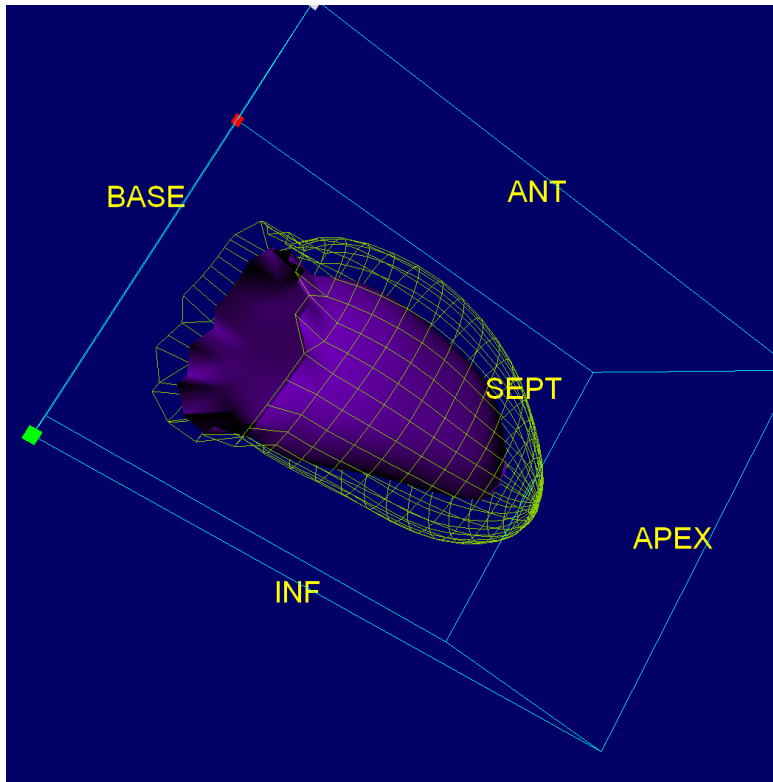
### 3.6 Reviewing SPECT Images in the Surface Page

Clicking on the **Surface** page indicator will bring up the **Surface** page shown below, a parametric representation of the LV, consisting of a wireframe surface (epicardium) and a shaded surface (endocardium). This type of display is not as useful for perfusion as it is for gated SPECT data, but can nevertheless aid in assessing LV size and shape. Clicking **Gate** allows cine display to follow the 3D endocardium and epicardium movement throughout the cardiac cycle, while clicking and dragging on the image will interactively and in real time position it to the observer's liking.

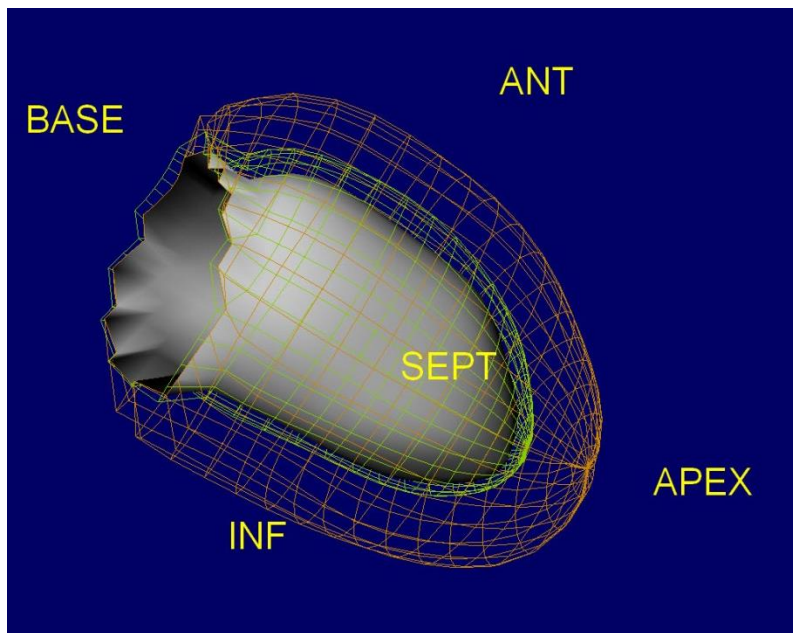


While myocardial thickening can be conceivably assessed from the epi-/endocardial display, it is easier to assess motion from a display containing the endocardium as well as its position at end-diastole. This is achieved by selecting the **Inner** option from the Surface pull-down menu, and clicking **ED** on the page control bar to highlight it. With this type of display and **Gate** toggle on, a good proxy for regional motion is how well the endocardium pulls away from its fixed position at end-diastole. All three surfaces can be displayed by selecting **Both** in the Surface pull-down menu.



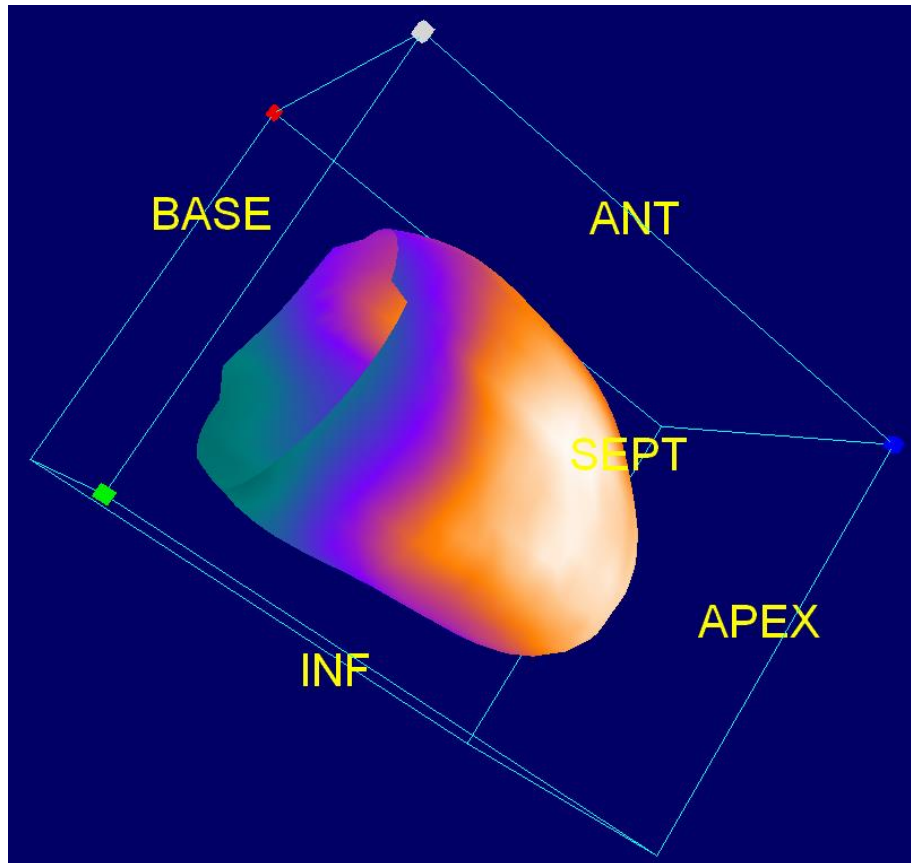


Endocardium with its position at ED



All 3 surfaces using Both option from the surface pull-down menu

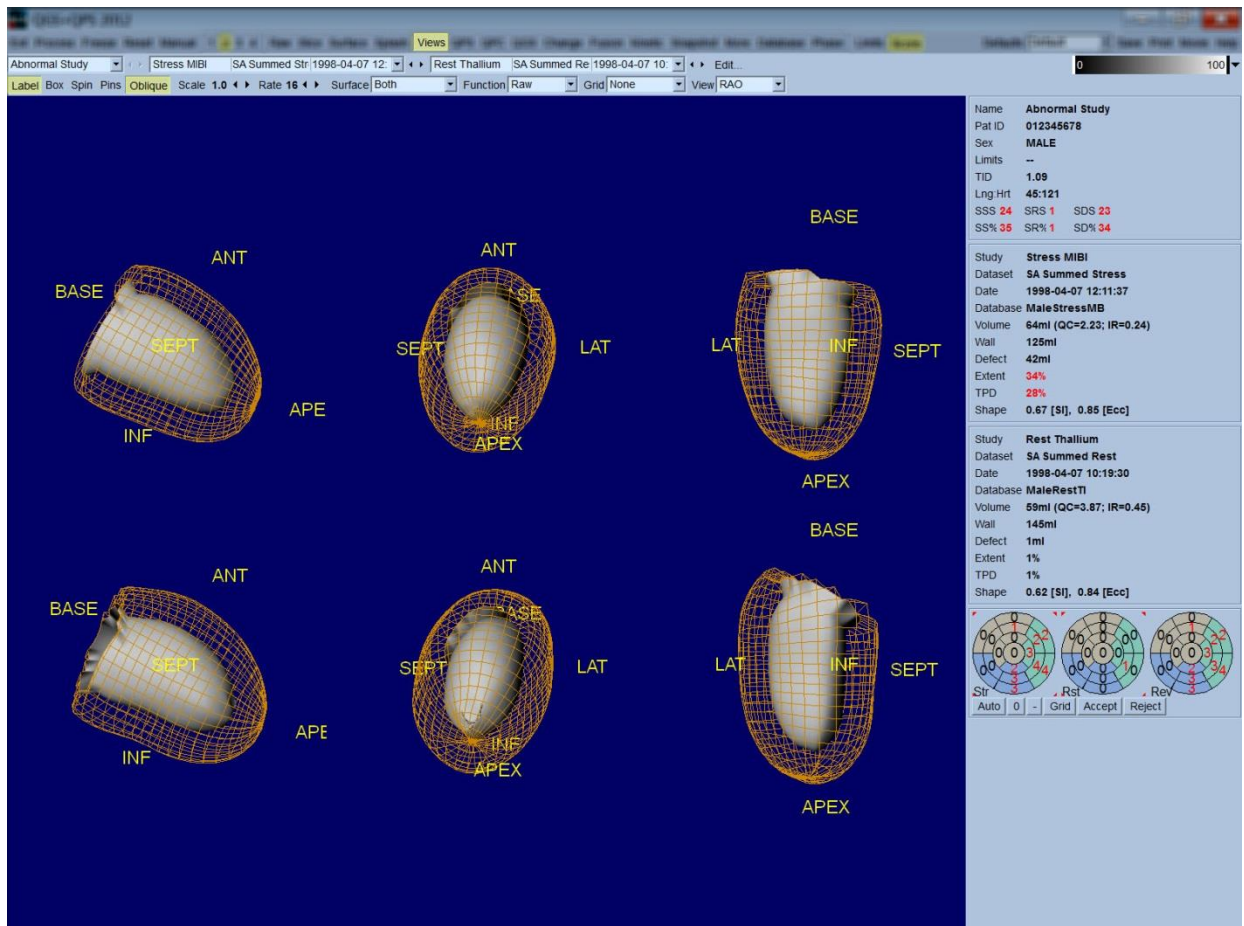
For function evaluation, the endocardial surface does not have counts mapped onto it, because it would make it harder to evaluate regional function in patients with large perfusion defects. If one wants to visualize the evolution of perfusion during the cardiac cycle, selecting the **Function** option from the Surface pull-down menu will display the mid-myocardial surface with maximal counts mapped onto it.



Mid-myocardial surface with maximal counts show using the Function option from the surface menu

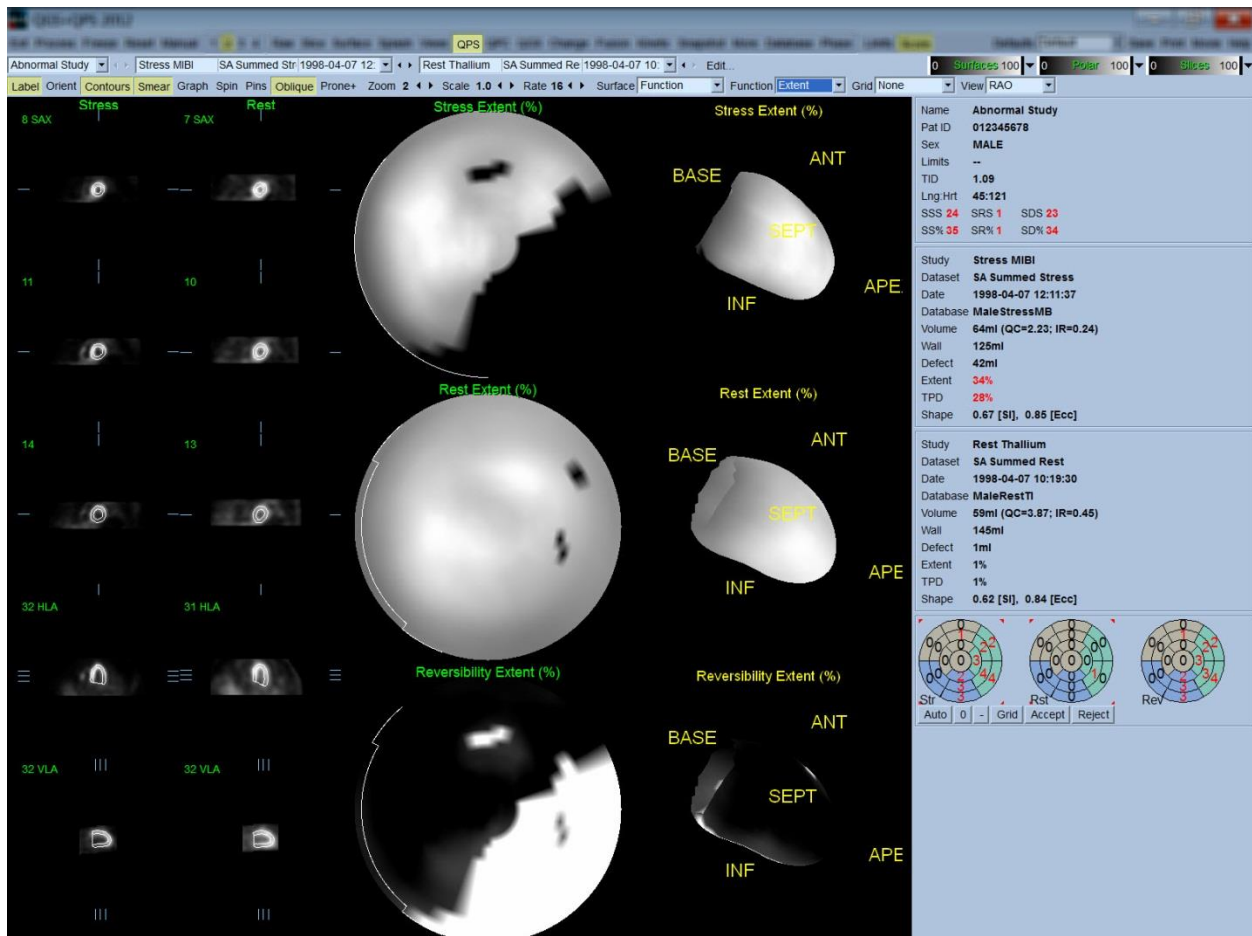
### 3.7 Reviewing gated SPECT images on the Views page

Clicking on the **Views** page indicator will bring up the **Views** page shown below, with six 3D viewports very similar to that in the **Surface** page. The main purpose of this page is to allow full coverage of the LV (albeit with smaller images compared to the one in the **Surface** page), and to facilitate comparison of stress and rest images by manipulating them in lockstep through left-clicking and dragging. Again, selecting the **Function** option from the **Surface** pull-down menu is recommended if perfusion needs to be assessed. For gated SA datasets the top row represents the end-diastolic views of the RAO, LAO and inferior orientations. The bottom row represents the same views and surfaces at end-systole. The images can be viewed as a cine display of the cardiac cycle by clicking the **Gate** toggle. If more than one dataset is selected, three orientations per dataset will be displayed and cined, with each column of images manipulable in lockstep by left-clicking and dragging.



### 3.8 Putting it All Together: the QPS Results Page

Clicking the **QPS** button in will bring up the QPS Results page, which aims at presenting, in synthetic format, all information related to the perfusion SPECT study for the patient. When available, two datasets are always displayed on the Results page (1, 3, and 4 display options are inactive). Clicking the **Score** toggle will replace the score box with either a table showing the amount of stress and rest defect extent and TPD as well as defect reversibility (**Graph** toggle off), or a bar graph showing percent stress defect extent and reversibility (**Graph** toggle on). If a screen capture is taken of this page with the **Contours** toggle off, the **Smear** toggle on and the **Extent** option selected from the **Function** pull-down menu, it would represent a good image to send the referring physician. The following rule is applied to all pixel based scores (TPD, extent and defect) and segment based scores (visual scores): whenever rest scores contain values that are higher on rest than on stress (when comparing stress/rest pair pixel by pixel or segment by segment); in these situations the rest segment or pixel will be assigned the stress score values.



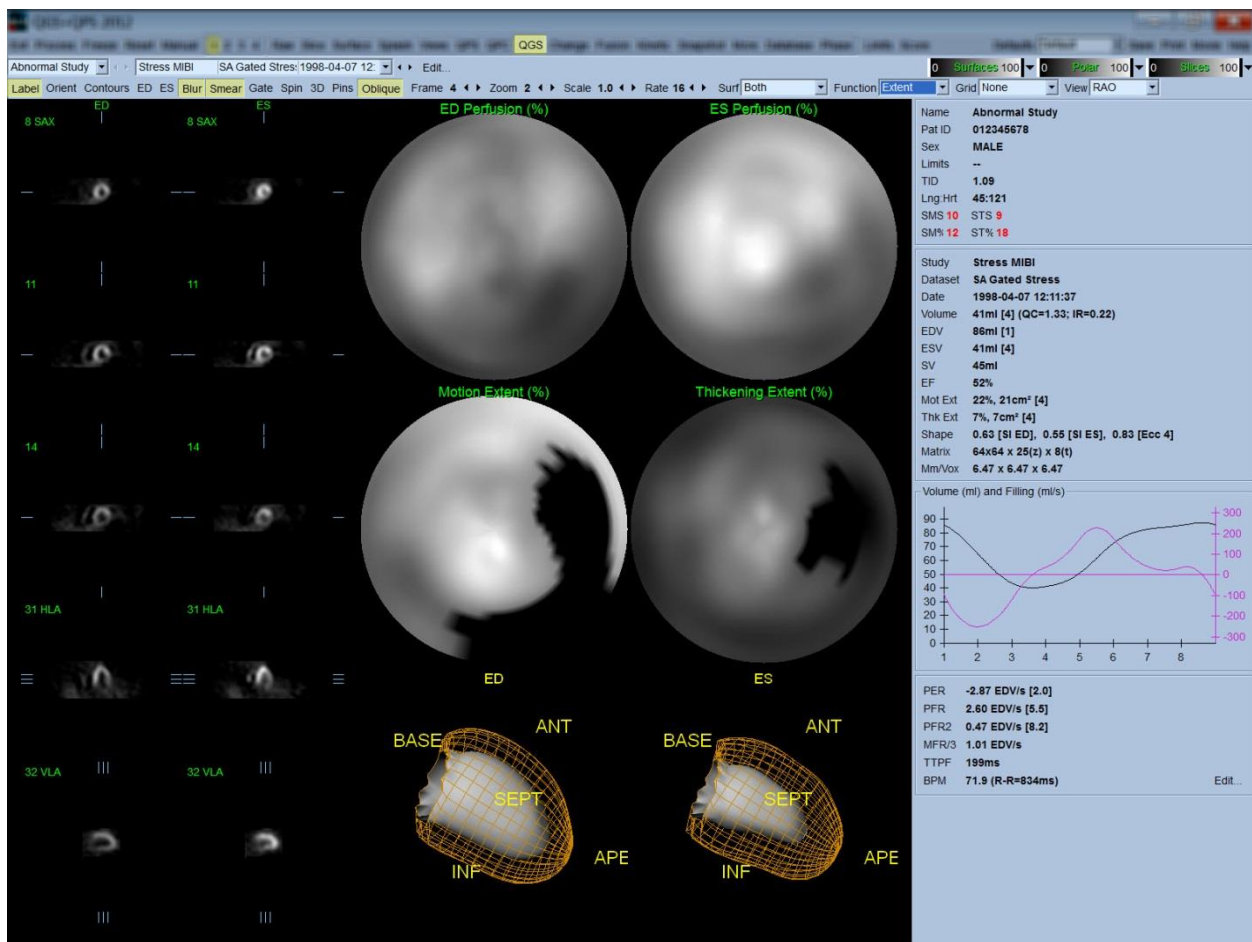
#### Assessing the Polar Maps

The results page provides three perfusion polar maps and three 3D parametric surfaces (stress, rest and reversibility). The **Function** pull-down menu contains the options **Raw**, **Severity**, and **Extent**, all of which apply to both 2D and 3D displays. A grid of 20 or 17 segments (**Segments**), 3

vascular territories (*Vessels*) or 5 regions (*Walls*) can be overlaid onto all polar maps and surfaces from the *Grid* pull-down menu. For polar maps, the numbers associated with the overlay represent the average value of the parameter measured by each map within the segment, territory or region in which they lie. Both stress and rest perfusion values are normalized to 100.

### 3.9 Putting it all together: the QGS Results page

Clicking the *QGS* button will bring up the QGS Results page shown below, which aims at presenting, in synthetic format, all information related to the gated SPECT study in this patient. QGS Results page only supports single dataset mode (the *2*, *3* and *4* display mode buttons are inactive). Both the end-diastolic and end-systolic representative short axis slices and 3-D surfaces will be displayed and the latter can be cined by clicking *Gate*. Clicking the *Score* toggle off will replace the score box with a graph showing the time-volume curve (in black) and its derivative (filling curve), from which diastolic parameters are computed. The time-volume curve should be used to evaluate the existence of gating errors. If a screen capture is taken of this page with the *Contours* toggle off, the *Blur* and *Smear* toggles on and the *Extent* option selected from the *Function* pull-down menu, it would represent a good image to send the referring physician.

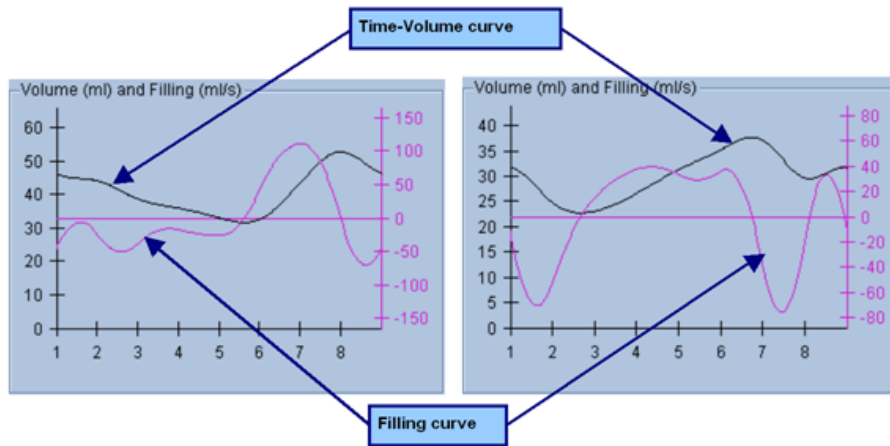


### Assessing the time-volume curve

A valid time-volume curve would be expected to have its minimum (end-systole) at frame 3 or 4, and its maximum (end-diastole) at frame 1 or 8 of a 8-frame gated acquisition. For a 16-frame gated acquisition, the minimum (end-systole) would be expected to be at frame 7 or 8 and its maximum (end-diastole) at frame 1 or 16. If major deviations from this expected behavior occur, the prudent assumption is that the gating was unsuccessful and the study needs to be repeated. Two examples of invalid time-volume curves are shown below.

It should be noted that any errors in the time-volume curve (gating errors) will be propagated to the filling curve, since the filling curve is the first derivative of the time-volume curve.

Note: In the time-volume curve graph, the volumetric value for interval 1 is also “appended” to the curve after interval 8 or 16, respectively, for 8-frame and 16-frame gated acquisitions.



### Assessing the Polar Maps

The QGS Results page provides two perfusion polar maps (at end-diastole and end-systole) and two function polar maps (regional motion and thickening). The **Function** pull-down menu contains the options **Raw**, **Extent** and **Severity**, all of which apply only to the function polar maps. Of those, only **Raw** is meaningful in the absence of motion/thickening normal limits. A grid of 20 or 17 segments (**Segments**), 3 vascular territories (**Vessels**) or 4 regions (**Walls**) can be overlaid onto all polar maps from the **Grid** pull-down menu: in every case, the numbers associated with the overlay represent the average value of the parameter measured by each map within the segment, territory or region in which they lie.

Mapping of the endocardial motion in the motion polar map follows a linear model from 0 mm to 10 mm. Motion greater than 10 mm is assumed to be = 10 mm (the scale "saturates" at 10 mm), while motion <0 mm (dyskinesia) is assumed to be = 0 mm. Likewise, thickening greater than 100% is assumed to be = 100% (the scale "saturates" at 100%), while thickening <0% (paradoxical thinning) is assumed to be = 0% in the thickening polar map. Unlike the motion map, which is "absolute" (millimeters), the thickening map is "relative" (thickness increase from end-diastole to end-systole).



**CAUTION:** While the presence of perfusion defects can be reasonably well assessed by “eyeballing” the perfusion polar maps, the same is not true of the motion and thickening maps! Indeed, it is well known that, even in normal patients, the septum typically moves less than the lateral wall (resulting in a “dark” area in the motion map), and the apex thickens more than the base (resulting in the “egg sunny-side-up” look of the thickening map). Function polar maps are best assessed by choosing the **Extent** option in the **Function** pull-down menu, which will black-out abnormal areas.

### **Pixel (Voxel) Size**

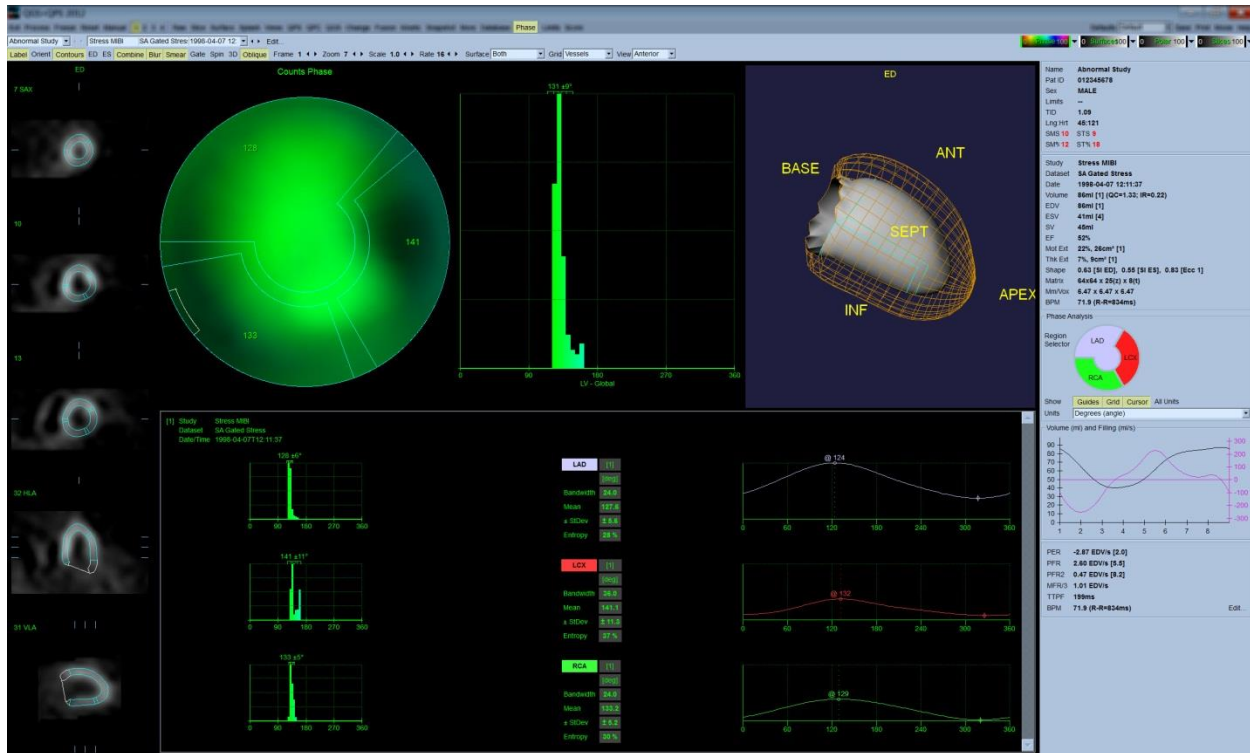
Area and volume measurements can be hampered by incorrect listing of the pixel size in the image header. This is usually not a problem with the LVEF, which is derived from a ratio of volumes. Similarly, perfusion measurements such as the absolute area of perfusion defects (but not the measurements of defects area as a percent of that of the LV!) can be hampered by incorrect listing of the pixel size in the image. Pixel size is usually automatically calculated by modern cameras, based on knowledge of field of view and zoom information. However, older cameras or "hybrid" systems (where one manufacturer's camera is interfaced to another manufacturer's computer) may not be set up to transfer pixel size information from the gantry, or may take a "standard" size (i.e., 1 cm) as default. In these cases, a correction factor should be manually calculated by imaging a known pattern (for example, two line sources separated by an exact distance), and counting the number of pixels between the lines' centroids in the reconstructed transaxial image. Key portions of an image header (including the pixel or voxel dimensions) can be viewed by selecting the **More** page.



**CAUTION:** One should be particularly wary of pixel sizes listed in the **More** page as integer numbers (0 and 1 being frequent occurrences), since they often indicate a transfer problem.

### **3.10 Phase Analysis**

To view global and regional phase information for gated studies, click the **Phase** page button. Global statistics will be displayed if the **Grid** toolbar setting is set to **None**. If a grid such as **Vessels** (shown below) is selected, statistics are shown for each region. Use the **Combine** toolbar toggle to switch between separate and combined phase and amplitude polar maps or parametric surfaces. The additional controls made available in the info box (right side of the application) control display options such as a real-time graph cursor or display units, and the polar map toggle allows the regional display to be restricted to certain regions only. In 2 dataset mode the time-activity curves are hidden to make room for another set of histograms, and in 3 or 4 dataset mode the regional displays are hidden completely. Please refer to the Phase Analysis chapter for additional information.



## 4 Viewing Images

QGS+QPS supports multiple image display formats including slices, surfaces, polar maps, and projections. The following controls are common to more than one image type, as appropriate:

<b>Label</b>	Toggles image labeling (slice numbers, surface labels, etc.).
<b>ED</b>	Toggles ED lock. When on, ED LV contours are displayed on every frame.
<b>ES</b>	Toggles ES lock. When on, ES LV contours are displayed on every frame.
<b>Gate</b>	Toggles temporal (inter-frame) cine.
<b>Frame</b>	Selects the gated frame to display.
<b>Rate</b>	Selects the cine speed.
<b>Grid</b>	Selects the grid mapping to use in defining how images should be divided into regions (ungated only).
<b>Function</b>	Selects which function type to display in polar maps and parametric surfaces.
<b>Oblique</b>	Toggles display of transverse datasets in short axis orientation.

The grid mappings are:

<b>Vessels</b>	LAD, LCX, RCA, DGA.
<b>Walls</b>	Apical, septal, lateral, superior, inferior.
<b>Segments</b>	17 (AHA) or 20 segments as defined by the active segmental score model.
<b>Groups</b>	Territories are defined by visual scores polar maps.



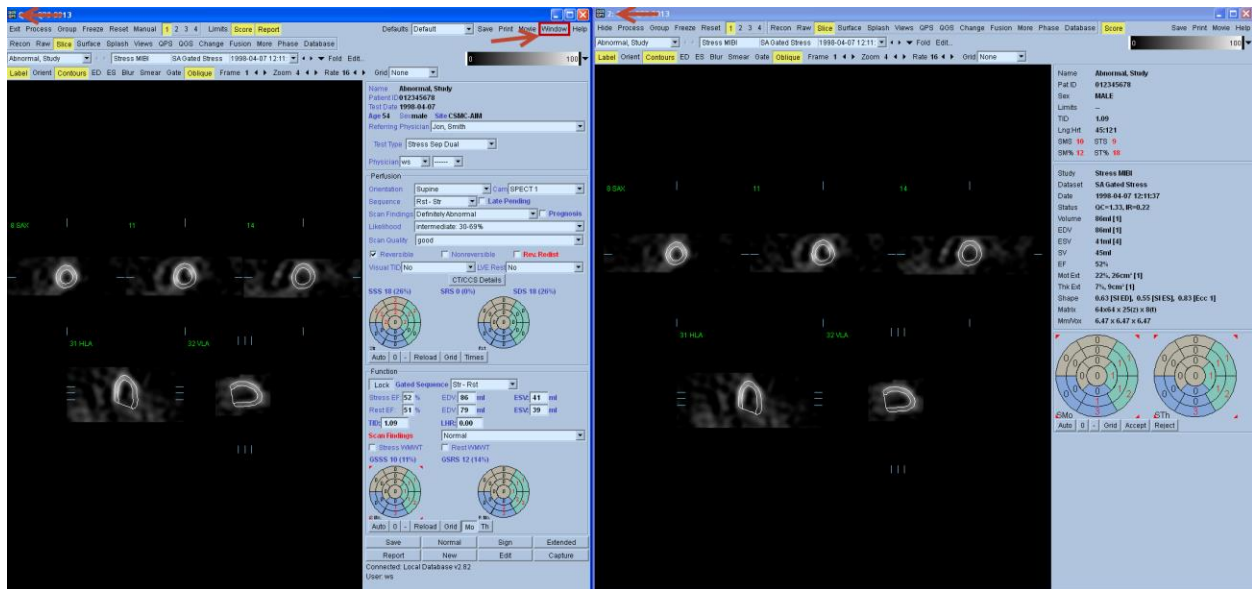
Note that grid mappings, while independent of the specific dataset to which they are applied, are defined in a way that is intended to be representative of most datasets.

The function types are:

<b>Raw</b>	Raw data, before any normal limits processing has been applied.
<b>Severity</b>	The data in terms of its difference from a normal value.
<b>Extent</b>	The data in terms of whether or not it falls within a normal range.
<b>Quant</b>	Displays discrete quantification based on the visual scoring scale (0-4) at the Pixel level.

#### 4.1 Multi-Monitor support

QGS+QPS supports unlimited number of displays, however, typically 2-4 monitor setups are most commonly used in clinical settings. Multiple windows of the same QGS+QPS instance may be launched using the **Window** button. All secondary windows operate in a synchronous manner with the primary window so that changes made to a study on the primary window are reflected on all secondary windows.



The title bar of the secondary windows will contain the instance number of that window. For example, the above image (right side) shows a 2 in its title bar.

Note: Reporting panel is only available from the primary window. Additionally, secondary windows can only be launched from the primary window. Closing the primary window will automatically close all secondary windows automatically.

## 4.2 Viewing Slices

Slices are 2D cuts from short axis and transverse datasets. Slice locations within datasets can be changed by dragging the corresponding slice reference lines in orthogonal views or, if labeling is turned off, anywhere in the viewports. Slices are displayed in the standard formats: short axis, vertical long axis, and horizontal long axis, transverse, sagittal, coronal. Rows and columns of a given slice format are always presented in standard order. From left to right or top to bottom:

<b>Short axis</b>	Apical to basal
<b>Horizontal long axis</b>	Inferior to superior
<b>Vertical long axis</b>	Septal to lateral
<b>Transverse</b>	Superior to inferior
<b>Sagittal</b>	Left to right
<b>Coronal</b>	Posterior to anterior

The slice specific controls are:

<b>Zoom</b>	Selects the slice zoom.
<b>Contours</b>	Toggles contour display, if processed results are available. Contours are the intersection of a given slice and the computed endocardial and epicardial surfaces.
<b>Blur</b>	Toggles temporal (inter-frame) smoothing. When on, a 1-2-1 smoothing kernel is applied across frames.
<b>Smear</b>	Toggles spatial (inter-slice) smoothing. When on, a 1-2-1 smoothing filter is applied across slices.

## 4.3 Viewing Surfaces

Surfaces are 3D surface rendered images of the processed LV. Surface viewpoints can be changed by dragging the image or by selecting one of the preset orientations.

<b>Scale</b>	Selects the surface image scale, normalized so that a scale of 1.0 fills most of the viewport.
<b>Box</b>	Toggles the surface display orientation box, each face of which corresponds to one of the orientation tags.
<b>Spin</b>	Toggles angular (inter-view) cine. When on, the surface rotates about the vertical axis.
<b>View</b>	Sets the display orientation. Choices are: anterior, lateral, inferior, septal, apical, basal, LAO, RAO, ECHO (the standard echocardiographic view). Note that the LAO and RAO viewpoints are intended to be representative, as specific short axis reorientation angles cannot in general be recovered.
<b>Surface</b>	Selects which wall surface to display (inner, outer, both, middle, counts). The counts selection displays the mid-myocardial surface with maximal counts mapped onto it for both gated and ungated datasets.
<b>Pins</b>	Toggles pin display, where parametric data is represented by lines extending from the surface with length proportional to magnitude.
<b>Vessels</b>	Toggles display of the coronary vessels, previously segmented and labeled.

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**Fuse** Registers the coronary vessels to its associated LV surface.

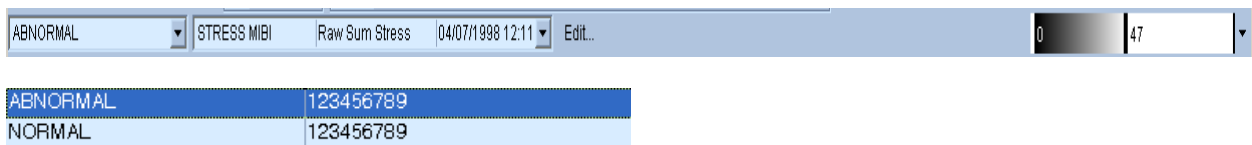
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#### 4.4 Viewing Polar Maps

Polar maps are 2D representations of the LV myocardium. The polar map to LV mapping is:

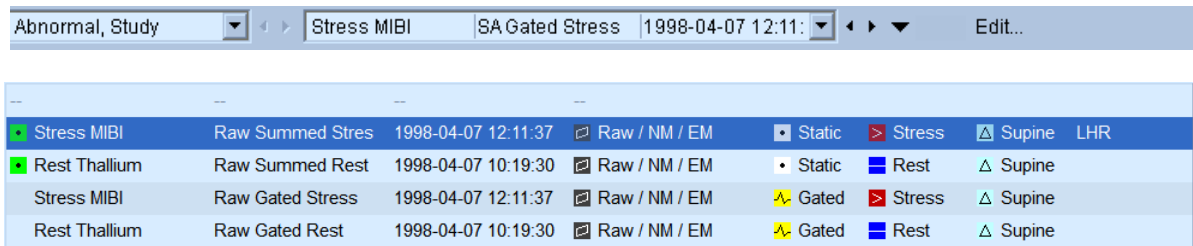
<b>Center</b>	Apical
<b>Left</b>	Septal
<b>Right</b>	Lateral
<b>Up</b>	Anterior
<b>Down</b>	Inferior

#### 4.5 Study Selector



The study selector selects the study to display, where each study is a collection of datasets.

#### 4.6 Dataset Selector



Each dataset selector selects a dataset to display from the current study. If more than one dataset is currently being displayed, then one dataset selector will be displayed per dataset with the leftmost dataset selector controlling the leftmost or topmost displayed dataset.

Predefined dataset layout options are available using the ▼ icon located next to the dataset selector.



## 4.7 Dataset Editor

Dataset Editor

Patient

Name	ID	DOB	Sex
Abnormal Study	012345678	1944-02-14 00:00:00	Male

Datasets

Study	Dataset	Date	Isotope	Orientation	Type	Dimensions	Active	Stress	Rest	LHR	AttC	Database	
Stress MIBI	Raw Summed Stres	1998-04-07 12:11:37	Tc-99m	Supine	Raw / NM / EM	64x64 x 64(z)	Active	Stress	Rest	LHR	AttC		
Rest Thallium	Raw Summed Rest	1998-04-07 10:19:30	Tl-201	Supine	Raw / NM / EM	64x64 x 64(z)	Active	Stress	Rest	LHR	AttC		
Stress MIBI	Raw Gated Stress	1998-04-07 12:11:37	Tc-99m	Supine	Raw / NM / EM	64x64 x 64(z) x 8(t)	Active	Stress	Rest	LHR	AttC		
Rest Thallium	Raw Gated Rest	1998-04-07 10:19:30	Tl-201	Supine	Raw / NM / EM	64x64 x 64(z) x 8(t)	Active	Stress	Rest	LHR	AttC		
Stress MIBI	SA Summed Stress	1998-04-07 12:11:37	Tc-99m	Supine	ShortAx / NM / EM	64x64 x 25(z)	Active	Stress	Rest	Via	TID	AttC	FlipZ MaleStressMB <Auto>
Rest Thallium	SA Summed Rest	1998-04-07 10:19:30	Tl-201	Supine	ShortAx / NM / EM	64x64 x 24(z)	Active	Stress	Rest	Via	TID	AttC	FlipZ MaleRestTl <Auto>
Stress MIBI	SA Gated Stress	1998-04-07 12:11:37	Tc-99m	Supine	ShortAx / NM / EM	64x64 x 25(z) x 8(t)	Active	Stress	Rest	Via	AttC	FlipZ	
Rest Thallium	SA Gated Rest	1998-04-07 10:19:30	Tl-201	Supine	ShortAx / NM / EM	64x64 x 24(z) x 8(t)	Active	Stress	Rest	Via	AttC	FlipZ	

Unknown attributes are highlighted in red. Change as appropriate, limits last.

OK Cancel

Many QGS+QPS algorithms and displays require the correct categorization of datasets in order to work correctly. In cases where automatic categorization did not work, either because dataset fields were empty or because they did not match the criteria specified in the application defaults, the dataset editor can be used to correctly re-categorize. It is accessed by the **Edit** button to the right of the dataset selector and allows for changes to the following fields:

<b>Sex</b>	Patient sex (can only be set for the patient, not for individual datasets).
<b>Isotope</b>	The imaging radiopharmaceutical's isotope.
<b>Orientation</b>	Patient acquisition orientation.
<b>Type</b>	Short Axis or Transverse
<b>Active</b>	Enables the dataset to be processed and displayed.
<b>Stress</b>	Stress dataset.
<b>Rest</b>	Rest dataset.
<b>Via</b>	Viability (not always available).
<b>4Hour</b>	4 hour (delayed) dataset (option only available when using with Automated Report Generator).
<b>Late</b>	24 hour or later dataset (option only available when using with Automated Report Generator).
<b>Primary/TID</b>	The default datasets to be used in reversibility computations.
<b>LHR</b>	Dataset to be used for Lung/Heart ratio or Lung:Heart max counts.
<b>AttC</b>	Attenuation corrected.
<b>FlipZ</b>	Inverts image by 180 degrees on its Z-axis (useful for processing legacy data).
<b>Database</b>	The perfusion normal limits database to be applied.

Select **OK** to accept changes, **Cancel** to discard. If the limits field is incorrect, before changing it first try to correct any other incorrectly assigned fields, as this should lead to the limits field being correctly reassigned.

## 4.8 Color Scale Control



The color scale control selects the current color scale and color scale mapping for displayed images. The color scale mapping is defined by its lower and upper level bars, both of which can range from 0 to 100 percent, and which together specify the portion of a dataset's dynamic range that is mapped onto the full color scale. Depending on the page being displayed, there may be more than one color scale control, for example: one for surfaces, one for polar maps, and one for slices.

To change the current color scale, click the color scale down arrow and select from the drop down menu.

To change the lower and upper level bars, the color scale viewport supports these actions:

- 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 options are also available through the drop down menu:

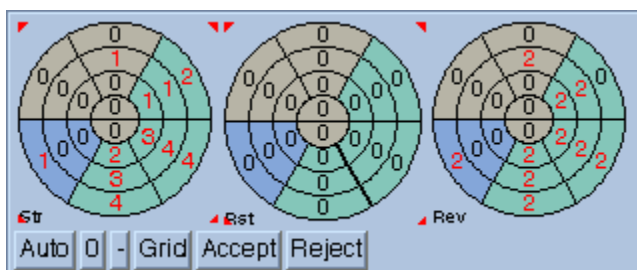
---

<b>Reset</b>	Resets lower and upper levels to 0 and 100%.
--------------	--

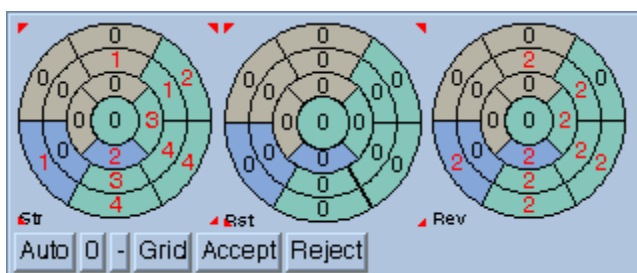
---

<b>Invert</b>	Toggles the sense of the lower and upper levels, flipping the color scale.
<b>Step</b>	Toggles color scale discretization, making the color scale stepped.
<b>Gamma</b>	Toggles display of the gamma control, which can be used to brighten or darken the color scale.
<b>Expand</b>	Toggles dynamic range expansion of lower and upper levels, so that the entire image may be represented using only a portion of the color scale.
<b>Split</b>	Toggles individual dataset color scale controls. Available only on pages with multiple datasets displayed.
<b>Normalize</b>	Toggles automatic dataset normalization based on segmentation results.

## 4.9 Score Box



Score box in 20 segment mode.



Score box in 17 segment mode.

The score box is used to display and edit segmental scores, in either 17 (AHA) or 20 segment format, for function and perfusion assessment. The segmental scores, each of which can range from 0 to 4 for perfusion, 0 to 5 for motion, and 0 to 3 for thickening, are displayed as numbers in standard polar map format and can be changed by left, right or middle clicking. Additionally, when two ungated datasets are being displayed, the reversibility (difference) polar map is computed and displayed to the right of the perfusion maps.

The score box controls are:

<b>Auto</b>	Automatically generates scores from normal limits and processed results.
<b>o</b>	Sets scores to zero.
<b>-</b>	Sets scores to unread.
<b>Accept</b>	Accepts scores, protecting them from further updates during processing.
<b>Reject</b>	Rejects scores, allowing further updates during processing.
<b>Grid</b>	Toggles grid display mode. When on, segmental scores are displayed in a rectangular grid.

The polar map labels are:

<b>Str</b>	Stress perfusion
<b>Rst</b>	Rest perfusion
<b>Rev</b>	Reversibility perfusion
<b>SMo</b>	Stress motion
<b>STh</b>	Stress thickening
<b>RMo</b>	Rest motion
<b>RTh</b>	Rest thickening

The grid display mode labels are:

<b>An</b>	Anterior
<b>AS</b>	Anteroseptal
<b>IS</b>	Inferoseptal
<b>In</b>	Inferior
<b>IL</b>	Inferolateral
<b>AL</b>	Anterolateral

Scores can be copied from one polar score map to another by clicking in the blue area bounded by the red corner triangles and dragging to another map. Similarly, in grid mode click in the red box and drag to another red box.

## Info Box

The info box displays panels of information for the displayed patient, study, and datasets, with the exact format depending on the dataset type (projection, short axis, etc.), number of datasets being displayed, and current page (raw, slice, etc.). When multiple datasets are displayed the topmost dataset panel corresponds to the leftmost dataset selector.

The patient panel fields may include:

<b>Name</b>	Patient name
<b>Pat ID</b>	Patient ID
<b>Sex</b>	Patient sex

The study panel fields may include:

<b>Limits</b>	The selected perfusion normal limits
<b>TID</b>	Transient ischemic dilation
<b>LHR</b>	Lung heart ratio
<b>Or</b>	Or
<b>Lng:Hrt</b>	Lung:Heart max counts
<b>SSS</b>	Summed stress score
<b>SRS</b>	Summed rest score
<b>SDS</b>	Summed difference score
<b>SS%</b>	Percent summed stress score
<b>SR%</b>	Percent summed rest score
<b>SD%</b>	Percent summed difference score
<b>SMS</b>	Summed motion score
<b>STS</b>	Summed thickening score
<b>SM%</b>	Summed motion percent
<b>ST%</b>	Summed thickening percent

The segmental summed scores display depends on the datasets being displayed. Perfusion scores are displayed for summed datasets, Motion and Thickening scores are displayed for gated datasets.

The dataset panel fields may include:

<b>Study</b>	Acquisition ID.
<b>Dataset</b>	Dataset ID.
<b>Date</b>	Date (and time, if available) of the acquisition.

<b>Name</b>	<b>Abnormal, Study</b>		
<b>Pat ID</b>	<b>012345678</b>		
<b>Sex</b>	<b>MALE</b>		
<b>Limits</b>	<b>SeptdualAuto</b>		
<b>TID</b>	<b>1.09</b>		
<b>Lng:Hrt</b>	<b>45:121</b>		
<b>SSS</b>	<b>25</b>	<b>SRS 1</b>	<b>SDS 24</b>
<b>SS%</b>	<b>31</b>	<b>SR% 1</b>	<b>SD% 30</b>
<b>Study</b>	<b>Stress MIBI</b>		
<b>Dataset</b>	<b>SA Summed Stress</b>		
<b>Date</b>	<b>1998-04-07 12:11:37</b>		
<b>Status</b>	<b>QC=2.23, IR=0.24</b>		
<b>Database</b>	<b>MaleStressMB</b>		
<b>Volume</b>	<b>64ml</b>		
<b>Wall</b>	<b>125ml</b>		
<b>Defect</b>	<b>42ml</b>		
<b>Extent</b>	<b>34%</b>		
<b>TPD</b>	<b>28%</b>		
<b>Shape</b>	<b>0.67 [SI], 0.85 [Ecc]</b>		
<b>Study</b>	<b>Rest Thallium</b>		
<b>Dataset</b>	<b>SA Summed Rest</b>		
<b>Date</b>	<b>1998-04-07 10:19:30</b>		
<b>Status</b>	<b>QC=3.87, IR=0.45</b>		
<b>Database</b>	<b>MaleRestTI</b>		
<b>Volume</b>	<b>59ml</b>		
<b>Wall</b>	<b>145ml</b>		
<b>Defect</b>	<b>1ml</b>		
<b>Extent</b>	<b>1%</b>		
<b>TPD</b>	<b>1%</b>		
<b>Shape</b>	<b>0.62 [SI], 0.84 [Ecc]</b>		



<b>Status</b>	Segmental quality score displayed as QC (Shape quality score) and IR (Intensity ratio around valve plane). A warning message is displayed if the shape QC score value is outside of the predefined normal threshold. <b>Manual</b> will be displayed if manual processing is applied to the dataset. <b>Saved</b> will be displayed if a results file is saved for the study.
<b>Volume</b>	LV chamber volume in ml for the current frame.
<b>EDV</b>	LV chamber volume in ml at end-diastole.
<b>ESV</b>	LV chamber volume in ml at end-systole.
<b>SV</b>	Stroke volume in ml.
<b>EF</b>	Ejection fraction in %.
<b>Area</b>	Mid-myocardial surface area in cm <sup>2</sup> for the current frame.
<b>Defect</b>	Global perfusion defect area in cm <sup>2</sup> or ml.
<b>Extent</b>	Perfusion defect area as percent of the mid-myocardial surface area.
<b>TPD</b>	Total perfusion deficit.
<b>Mot Ext</b>	Motion abnormality area in cm <sup>2</sup> and as percent of the mid-myocardial surface area.
<b>Thk Ext</b>	Thickening abnormality area in cm <sup>2</sup> and as percent of the mid-myocardial surface area.
<b>Eccentricity</b>	LV eccentricity for the current frame, a measure of elongation that varies from 0 (sphere) to 1 (line).
<b>Shape</b>	LV shape index for ED and ES and eccentricity for the current frame. Eccentricity is a measure of the elongation, and varies from 0 (sphere) to 1 (line). Shape index is the ratio between the maximum dimension of the LV in all short-axis planes and the length of the mid-ventricular long axis.
<b>Matrix</b>	Dataset dimensions in voxels.
<b>Mm/Vox</b>	Voxel dimensions in mm.

The diastolic function panel contains the volume/time and filling/time curves and the following statistics:

<b>PER</b>	Peak emptying rate.
<b>PFR</b>	Peak filling rate.
<b>PFR<sub>2</sub></b>	Secondary peak filling rate.
<b>BPM</b>	Heart rate in heart beats per minute (if available).
<b>MFR/3</b>	Mean filling rate over the first third of the end-systolic to end-diastolic phase.
<b>TTPF</b>	Time to peak filling from end-systole.

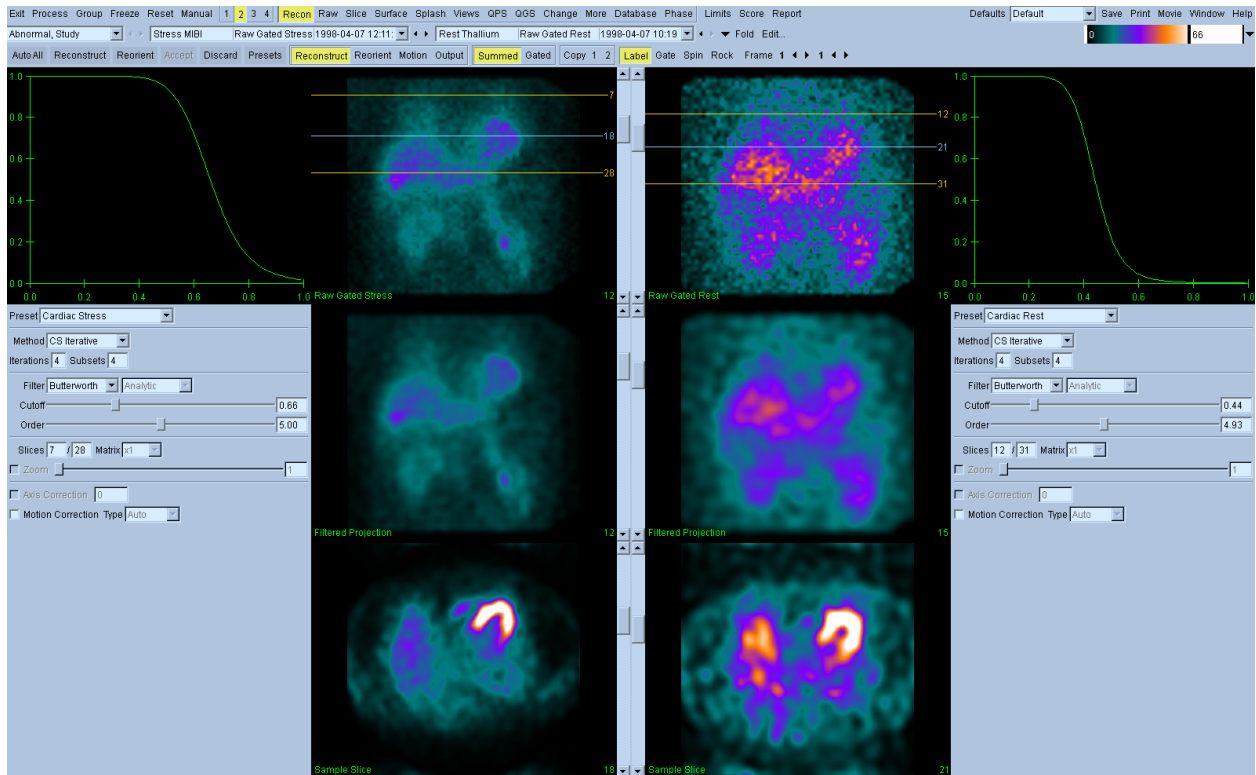
## 5 Pages

The pages are the central focus of QGS+QPS, with each one providing a different perspective on the input data and processed results. The controls available for each page vary depending on the currently selected defaults file. In all windows except **Snapshot** and **More**, images for each dataset appear in the image display panel and patient statistics appear on the right side of the window. When two or more datasets appear, you can adjust the number of images and the

amount of demographic information for each dataset to fit the space available. The following pages may be available on your workstation:

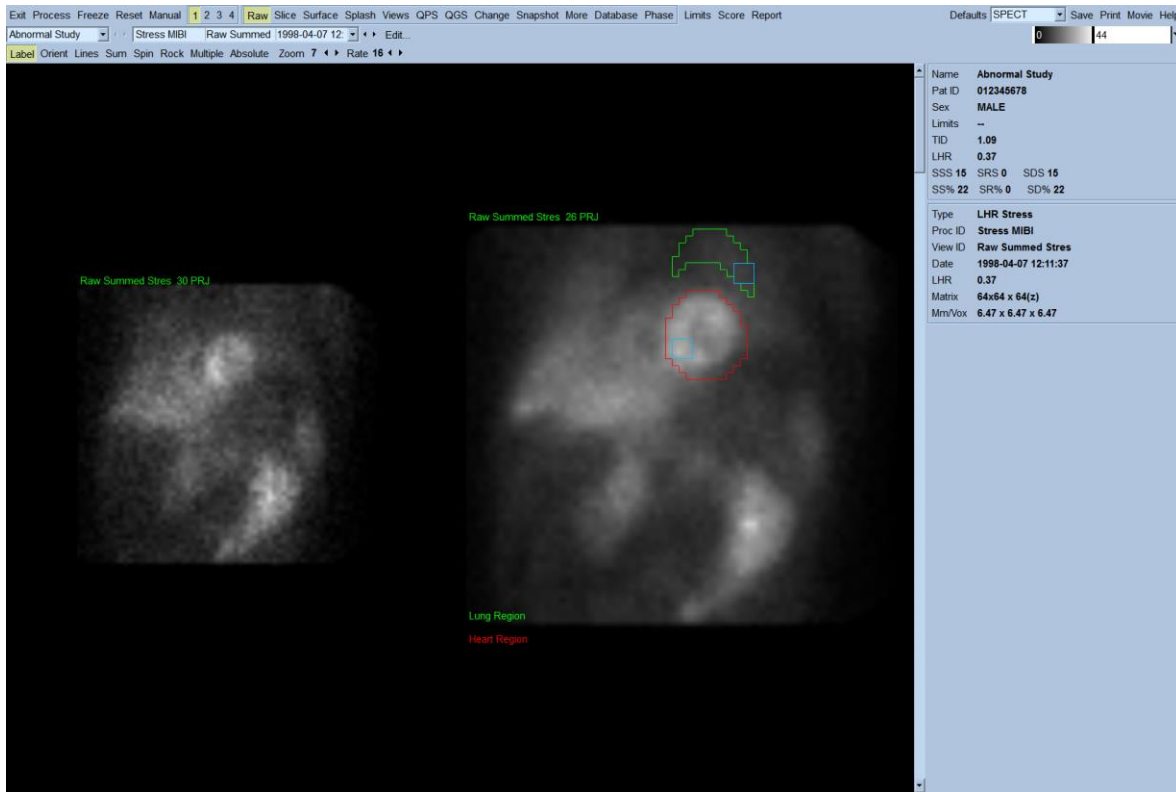
<b>Recon</b>	Displays the reconstruction & motion correction options.
<b>Raw</b>	Displays projection datasets and lung heart ratio analysis regions, can be used for quality control and review.
<b>Slice</b>	The slice page displays each dataset as a set of five large slices (three short axis, one vertical long axis, and one horizontal long axis), automatically or interactively selected, and can be used to examine features in detail. It is well suited for assessing motion and thickening.
<b>Surface</b>	Displays each processed dataset as a single large 3D image of the LV surfaces, and can be used to interactively visualize features and their spatial relations to each other.
<b>Splash</b>	Displays each dataset as multiple rows of small slices (one or two rows of short axis, one of vertical long axis, one of horizontal long axis), automatically or interactively selected. The corresponding LV surface contours can also be displayed. It is well suited for assessing function.
<b>Views</b>	Displays each processed dataset as one or two rows of small 3D images of the LV surfaces, (for a single gated dataset, one at ED and one initially at ES), and can be used to interactively visualize features and their spatial relations to each other.
<b>QPS</b>	Displays an overview of processed results and perfusion analysis for one or two datasets, using slices, surfaces, polar maps, graphs, charts, and tables.
<b>QPC</b>	Quantitative assessment of hibernating myocardium in SPECT/PET studies.
<b>QGS</b>	Displays an overview of processed results and functional analysis for a single dataset, using slices, surfaces, polar maps, graphs, and tables.
<b>Change</b>	Direct quantification of perfusion changes between two datasets.
<b>Fusion</b>	Fused review of SPECT/PET/CT/CTA slices in three orthogonal planes.
<b>Kinetic</b>	Displays processed dynamic PET datasets. Results include Myocardial Blood Flow (MBF), Coronary Flow Reserve (CFR), Spill-over Fraction (SF), etc.
<b>Snapshot</b>	Displays screen captures.
<b>More</b>	Displays demographic data from each image dataset header, and can be used to confirm that all relevant fields are filled appropriately.
<b>Database</b>	Allows the user to generate normal databases and limits for perfusion.
<b>Phase</b>	Enables phase analysis of LV mid-myocardial motion and myocardial thickening.

## 5.1 Recon Page



AutoRecon is an interactive application for the automatic or manual processing (motion correction, reconstruction, reorientation, filtering, etc...) of one or more raw datasets. AutoRecon applies validated rules to processing and reorienting the ventricle while reducing the number of decisions required when processing datasets, which allows for consistent and reproducible results. The amount of automation and processing options provided by AutoRecon depends upon the dataset selected. Refer to the AutoRecon reference manual for more details.

## 5.2 Raw Page



The raw page displays projection datasets and lung heart ratio analysis regions, and can be used for quality control and review. Projections are displayed on the left, while the lung and heart regions are displayed to the right on the summed subset of projections from which they were derived. These regions may be modified by entering manual mode from the raw page.

The default sort criteria for loading projection data are (in order of decreasing precedence):

1. Non-gated > gated
2. LHR > non-LHR
3. Stress > rest > neither

The page-specific controls are:

<b>Lines</b>	Toggles motion reference lines.
<b>Sum</b>	Toggles frame summation for ungated display of gated datasets.
<b>Spin</b>	Toggles projection cine.
<b>Rock</b>	Toggles bi-directional projection cine for sub 360° acquisitions (with spin also enabled).
<b>Multiple</b>	Toggles multiple mode. When on, as many datasets as can fit on the screen are displayed.

---

**Absolute** Toggles absolute normalization. When on, all datasets are scaled to the same maximum value, taken across all projection datasets in the study.

---

**Use the Raw page to:**

- Review the projection datasets in Spin mode (with or without lines toggled on) to look for patient motion.
- View and verify the accuracy of the bounding boxes and the regions of interest (ROIs) used for Lung and Heart computations.

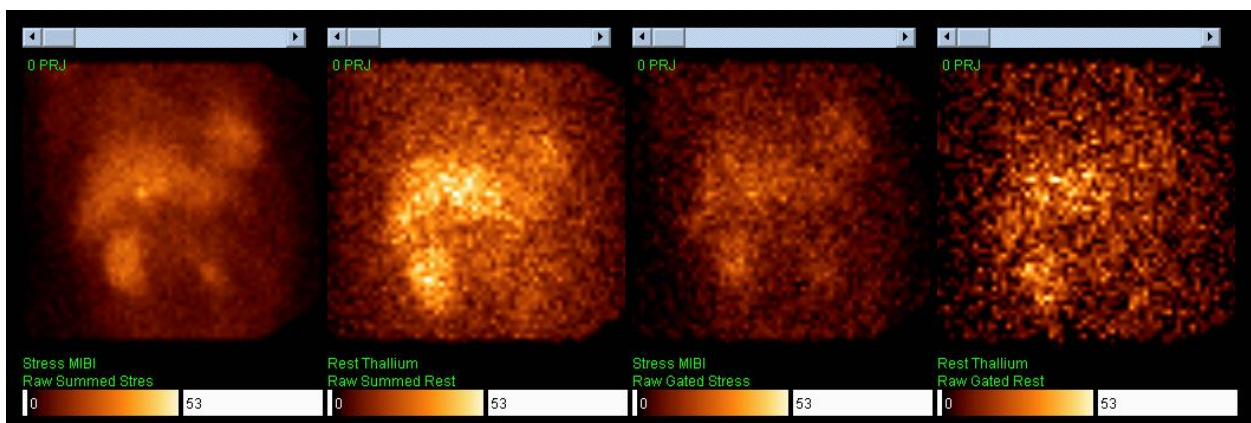
QGS+QPS uses the areas within these ROIs to calculate the Lung/Heart ratio. The ROIs are not created until you process the datasets by clicking **Process**.

Make sure that placement of the heart and lung ROIs is accurate and verify that these ROIs are over the proper organs. Inaccurate heart and lung ROIs can result in incorrect computation of quantitative data, which can lead to misdiagnosis. Manual adjustments to the ROIs can be made by clicking **Manual**.

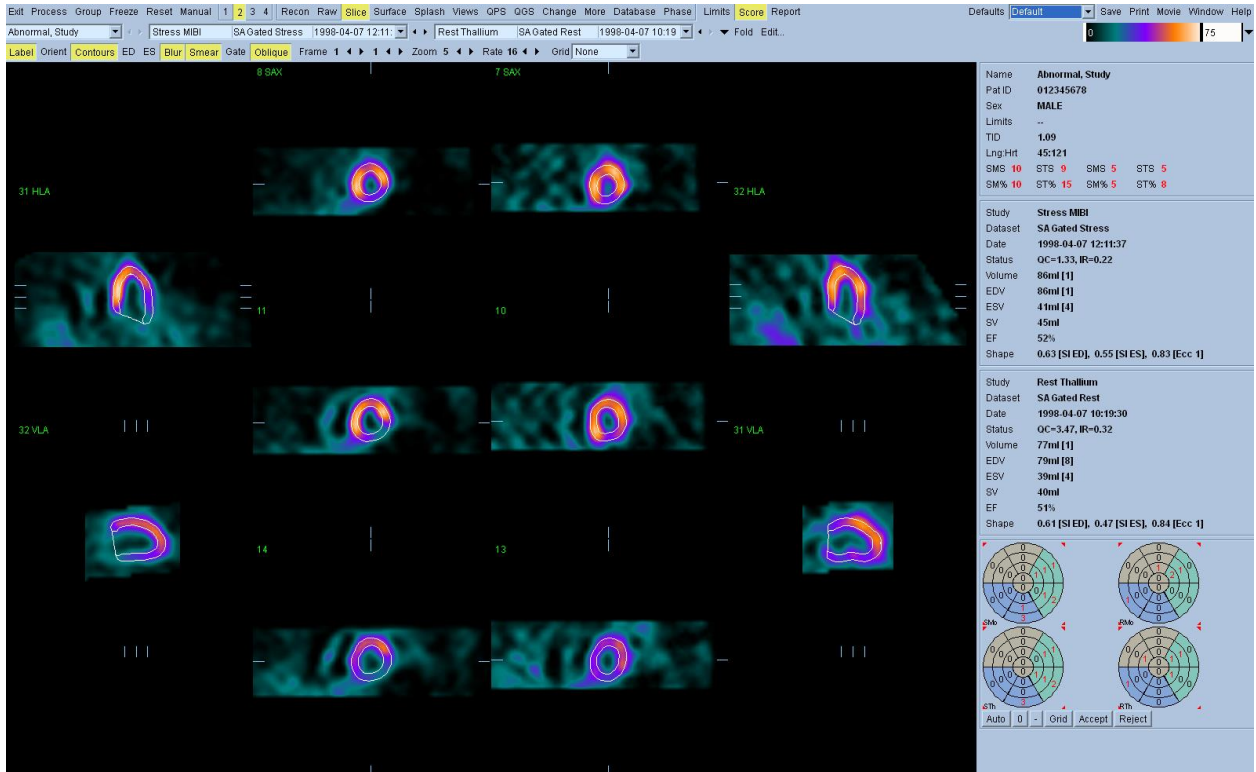
**Displaying Multiple Datasets**

Click **Multiple** to display all of the raw projection datasets for the currently selected patient. Each viewport has its own brightness control.

Click **Absolute** to toggle on absolute normalization. When on, all datasets are scaled to the same maximum value, which is taken across all projection datasets in the study.



## 5.3 Slice Page



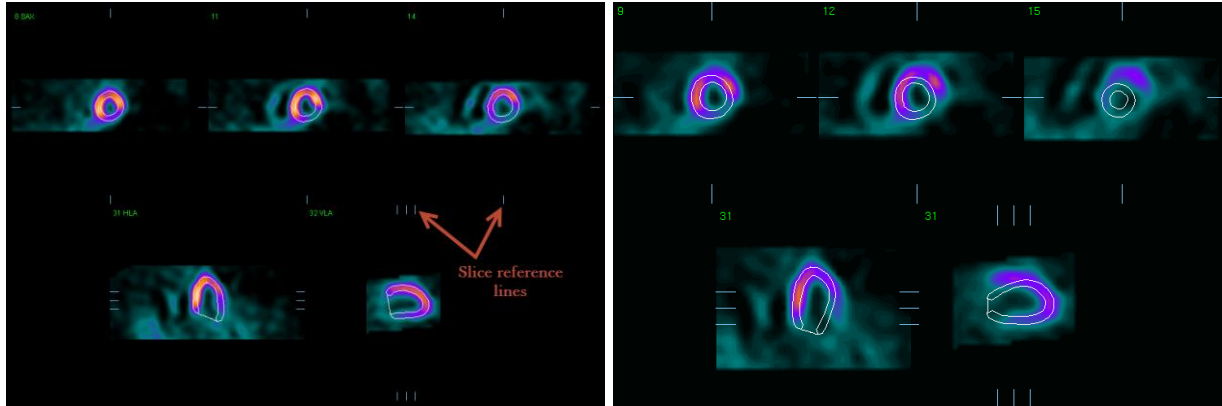
The slice page displays five viewports per dataset (three short axis, one vertical long axis, and one horizontal long axis) that are automatically or interactively selected. Once the study is processed, the slice page displays the statistics and superimposes the contours on the reference images (if the **Contours** toggle is on).

Use the **Slice** window to:

- Verify the accuracy of the contours for SAX datasets.
- Select and analyze various SAX slices.
- Verify that you have a gated or summed stress and rest dataset.

### Contour QA using the slice page

With the **Contours** toggle on, verify that the superimposed contours are appropriately placed. The below images show correct (left) and incorrect (right) contours. Use the reference lines within the respective viewports to cycle through all of the slices.



### Slice segmentation

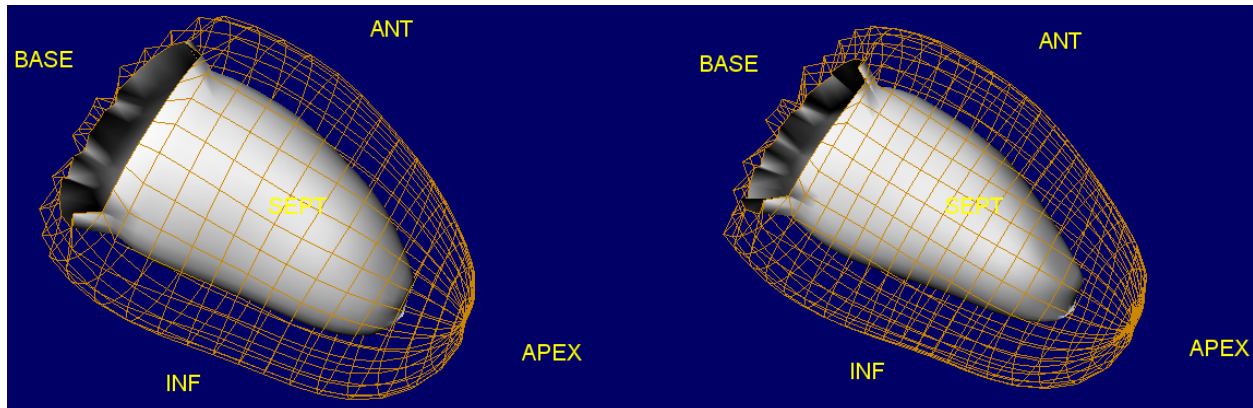
Each region on the **Visual Score** polarmap corresponds to one of four segment colors on the **Segments** overlay as follows:

Make sure **Segments** is selected from the **Grid** drop-down menu. The segment colors are most visible when using the grayscale color map.

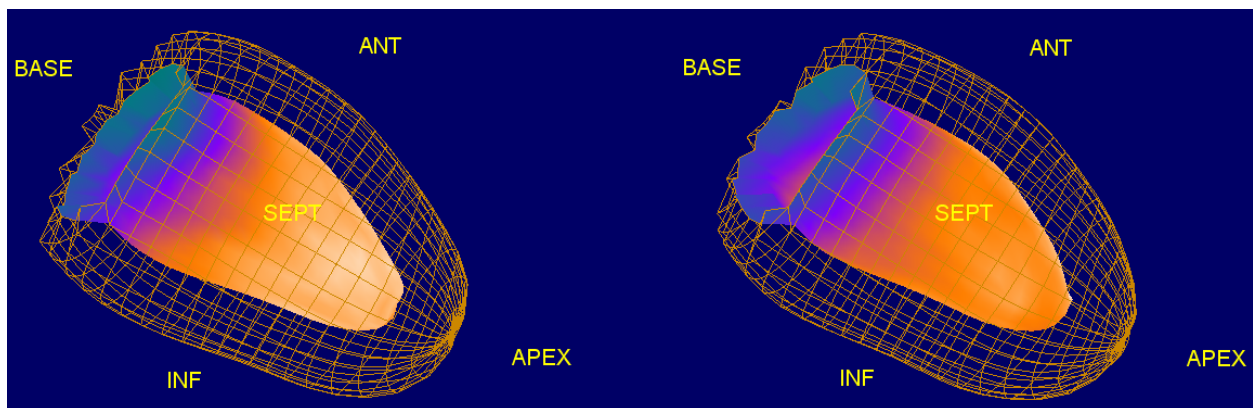
- Region 1 (Red): Apical
- Region 2 (Orange): Mid-ventricular towards the apex
- Region 3 (Yellow): Mid-ventricular towards the base
- Region 4 (Green): Basal



## 5.4 Surface Page



3D viewports with 2 gated (function) datasets selected. Both option is selected from the Surface menu.



3D viewports with 2 summed (perfusion) datasets selected. Func/Both option is selected from the Surface menu.

The surface page displays each processed dataset as a single large 3D image of the LV surfaces, and can be used to interactively visualize features and their spatial relations to each other. The 3D images may be used to evaluate ventricular wall motion. To evaluate perfusion, select **Function**, **Func/Both** or **Func/Outer** from the surface drop down menu.

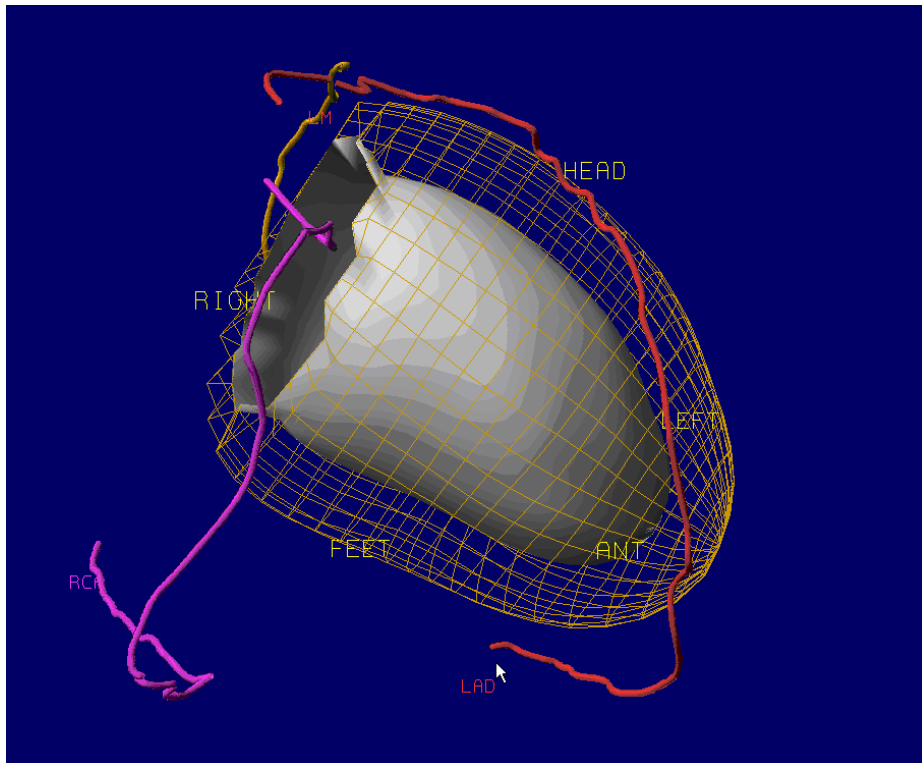
### Orientation

Orientation of the 3D images on the **Surface** page can be changed in three ways:



1. To rotate the 3D images manually, click and drag on the image in the direction you want to rotate. The volume rotates about each axis of rotation. You can also **Scale** and **Gate** the images.
2. From the **View** menu, select one of the predefined orientations. The available options are:
  - Anterior
  - Lateral
  - Inferior
  - Septal
  - Apical
  - Basal
  - LAO
  - RAO
  - Echo
3. Click **Spin** to automatically spin the 3D images. Spin rate can be adjusted using the **Rate** arrows. Dual images spin synchronously, but may be oriented independently.

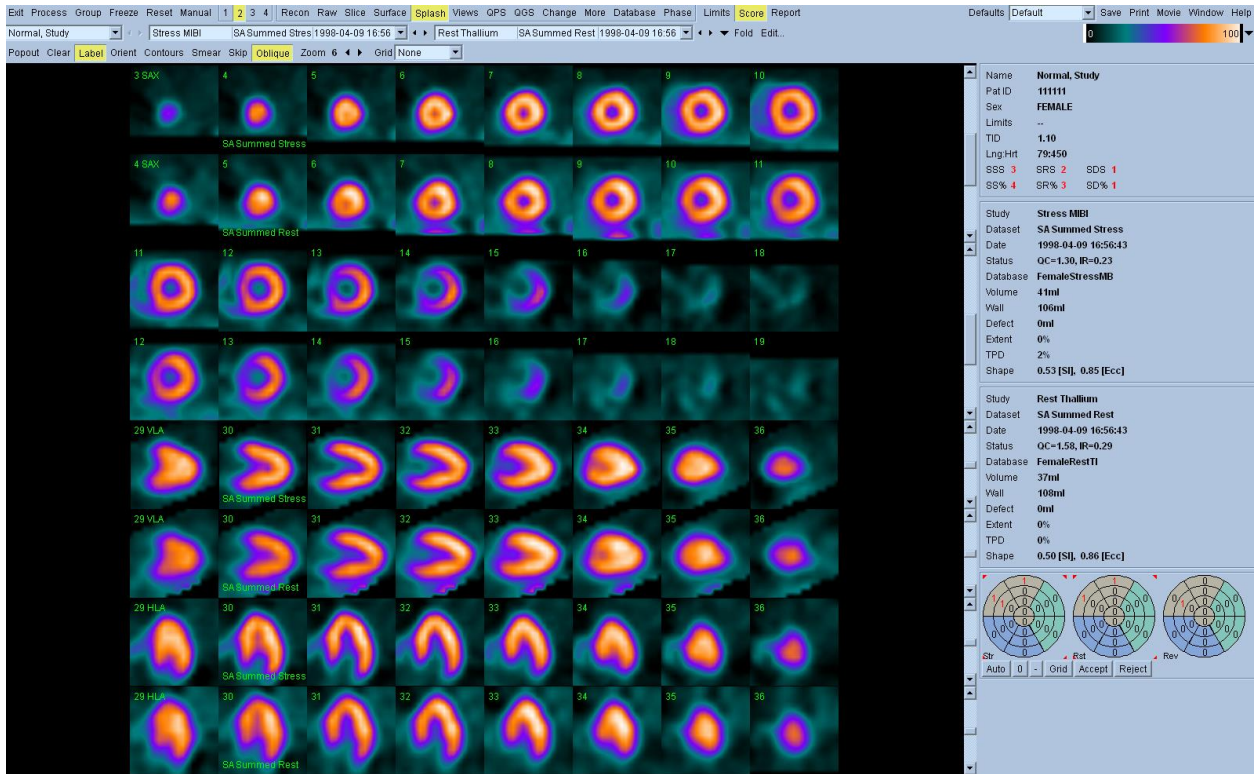
#### Coronary CTA vessel Display



If a segmented and labeled coronary vessel dataset from a CT Angiography (CTA) is loaded along with the SPECT or PET study, the CTA Fusion option allows fusion of the coronary vessels extracted from CTA with the 3D surface images. The coronary artery tree is extracted and saved as a DICOM object by the vendor's CTA software. On the Surface (or Views) page, click **Vessels**

to view the segmented coronary vessels with the 3D surface image. Depending on the specific CTA and PET/SPECT acquisition protocols, the extracted coronary vessels may need further software co-registration.

## 5.5 Splash Page



The splash page displays each dataset as multiple rows of small slices (one or two rows of short axis, one of vertical long axis, one of horizontal long axis), automatically or interactively selected. The corresponding LV surface contours can also be displayed.

The location of each row of slices within its dataset can be changed by scrollbar or by dragging slice reference crosshairs in orthogonal views (these are only visible while the left mouse button is depressed). When more than one dataset is being displayed, the rows of slices are interleaved. For example, with two datasets, rows 1,3,5,7 correspond to the first dataset, 2,4,6,8 to the second.

### Use the Splash page to:

- Visually analyze the slices
- Analyze and review the automatically generated visual scores
- Manually adjust visual scores, if needed
- Review and verify the following summed scores for summed (perfusion) datasets:

- **Summed Stress Score (SSS):** Summation of the stress visual scores indicating the severity of the defect. The higher the score, the more abnormal the defect. (This is the sum of all stress values except where Stress=1 and Rest=1).
- **Summed Rest Score (SRS):** Summation of the Rest visual scores indicating the severity of the defect. The higher the score, the more abnormal the defect. (This is the sum of all Rest values except where Stress=1 and Rest=1).
- **Summed Differential Score (SDS):** Summation of the difference between Stress and Rest scores. The higher the score, the more reversible the defect. For a given segment, this is the sum of all differences between Stress and Rest > 0, except when Stress=4 and Rest=3, or when Stress=3 and Rest=2. In other words, if the Stress is 3 in one segment and the Rest is 2 in the corresponding segment, then the rule does not apply.
- Review and verify the following summed scores for gated (function) datasets:
  - **Summed Motion Score (SMS):** Summation of the Motion visual scores for all segments.
  - **Summed Thickening Score (STS):** Summation of the Thickening visual scores for all segments.

Note that summed scores for both gated and summed datasets are presented in numerical form (SSS, SRS, SDS, SMS, STS) and as a percentage of myocardium involved (SS%, SR%, SD%, SM%, ST%).

The percentage values are derived from the summed stress, summed rest, and summed difference scores by normalizing them to the maximal score for a particular scoring model – i.e., by dividing by the maximum score and multiplying by 100. For example, in a 0-4 score using a 17 segment system, the maximum score is 68. These percentage values express the extent and severity of MPS defects in a more intuitive manner and use a system that could be applied with a segmental scoring system using any number of segments.

#### Perfusion summed scores exception rules

When 'Use classic summed score computation' is selected within the processing tab of the defaults editor, the following rules apply for calculating summed scores for perfusion (summed) datasets:

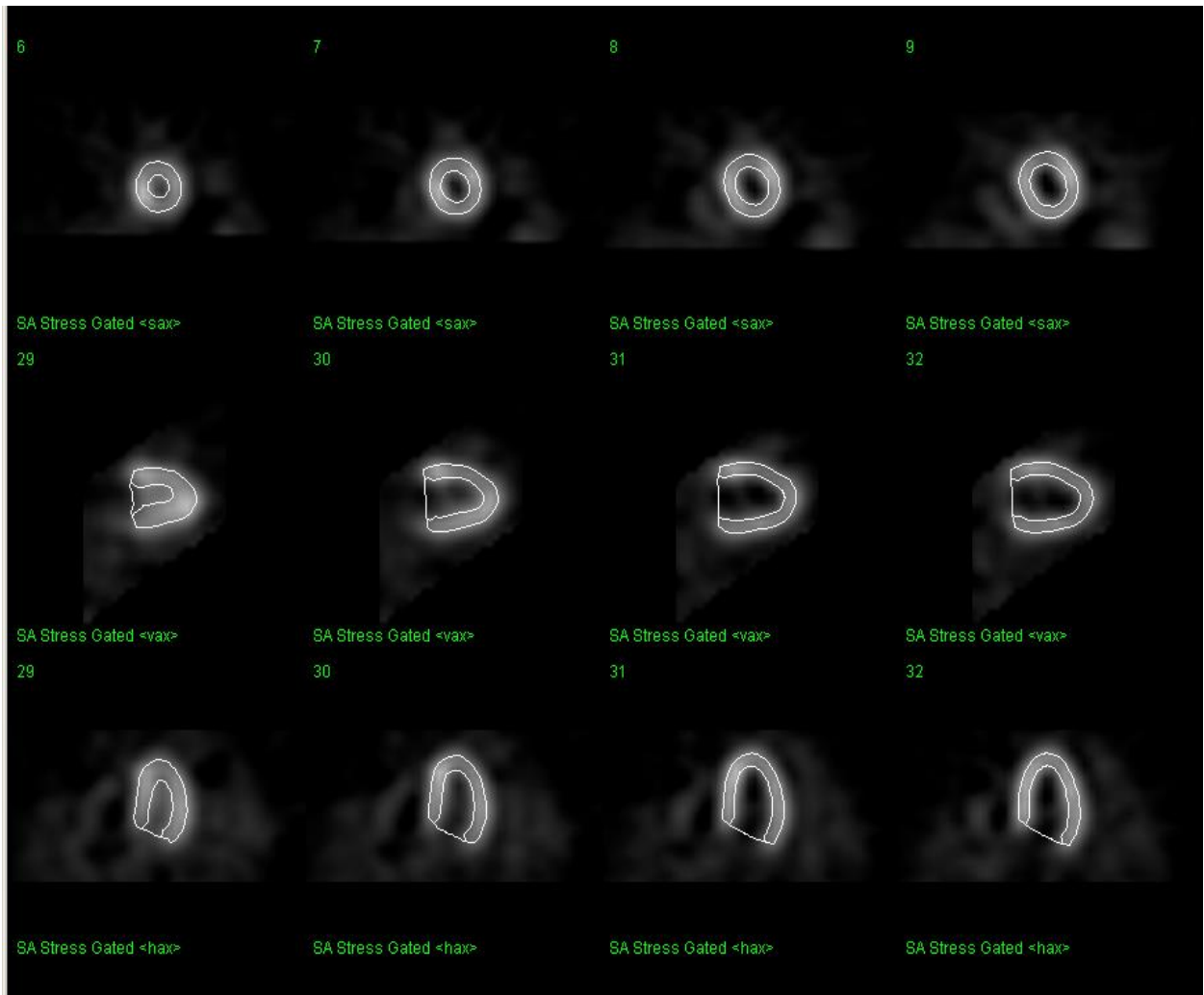
- The first exception rule is when a 4 appears in a segment for stress, and a 3 appears in the same corresponding segment for rest, the difference is a zero, rather than 1.

- The second exception rule is when a 3 appears in a segment for stress, and a 2 appears in the same corresponding segment for rest, the difference is a zero, rather than 1.
- The third exception rule is when a 1 appears in a segment for stress, and a 1 also appears in the same corresponding segment for rest, it is considered as 0 for all three summed scores (SRS, SSS and SDS).

Note: These rules were applied by default on previous versions of the software. For serial comparisons, the same rule should be selected and applied for both studies.

The page-specific controls are:

<b>Popout</b>	Toggles popout mode. When on, only selected slices are visible.
<b>Clear</b>	Deselects all slices selected for popout mode.
<b>Skip</b>	Toggles slice skipping. When on, slice spacing is doubled.



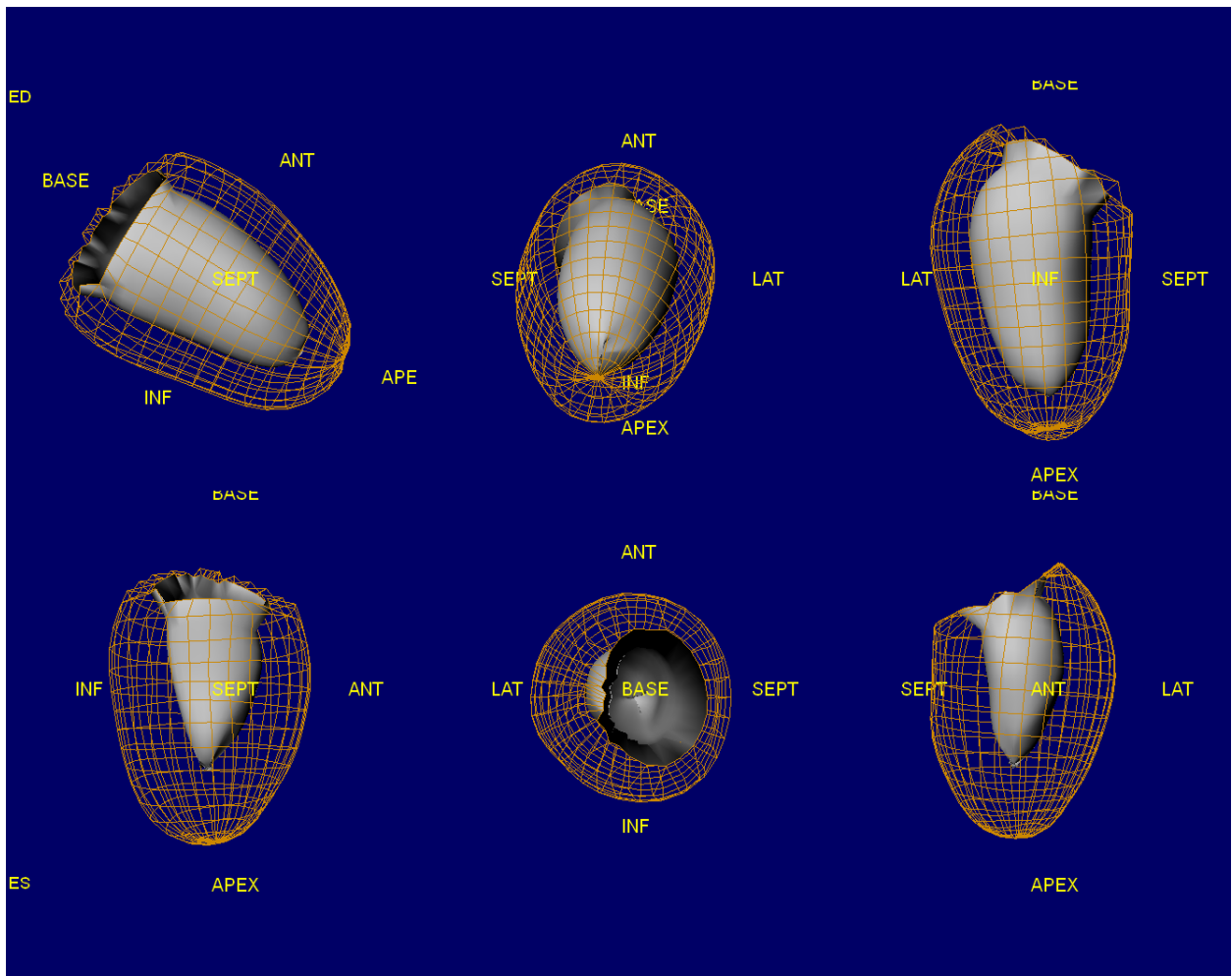
The splash page viewports in popout mode with 12 individual slices. Contours are toggled on.

Popout mode can be used to view only slices of interest.

To use Popout:

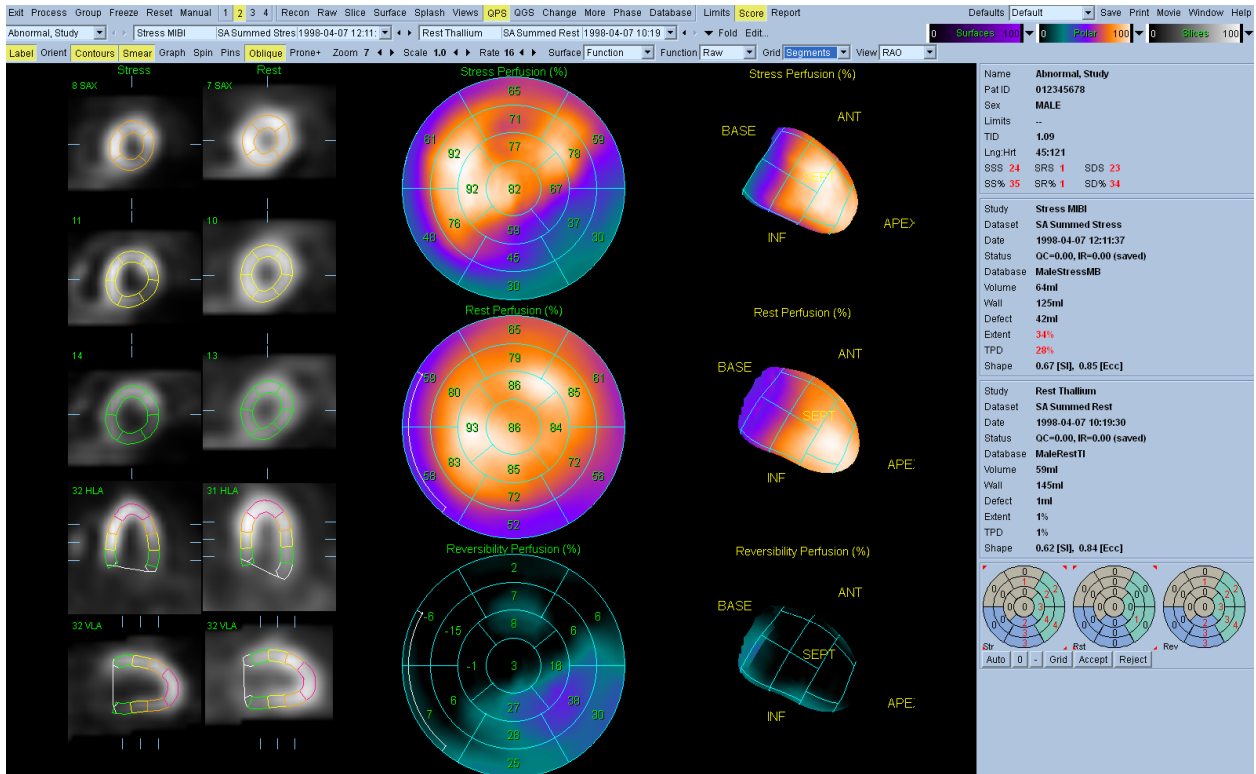
1. Select up to sixteen SAX, VLA and HLA slices by right clicking on the individual slices of interest. To deselect, right-click again or click **Clear** to deselect all.
2. Click Popout.  
The selected slices appear. All of the standard image controls to zoom, smear, grid, label, etc. can still be used. **Skip** cannot be used while in popout mode.
3. Click **Popout** again to return to the standard splash display.

## 5.6 Views Page



The views page displays each processed dataset as one or two rows of small 3D images of the LV surfaces, (for a single gated dataset, one row is at ED and one row is initially at ES), and can be used to interactively visualize features and their spatial relations to each other.

## 5.7 QPS Results Page

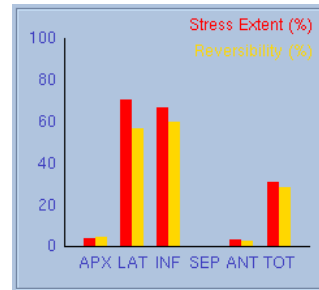


The QPS page displays an overview of processed results and perfusion analysis for one or two datasets, using slices, surfaces, polar maps, graphs, charts, and tables.

- The slices section contains two columns of five slices (one per dataset, each with three short axis, one horizontal long axis, and one vertical long axis).
- The surfaces section contains three LV surface images (one per dataset, plus one for reversibility).
- The polar maps section contains three polar maps (one per dataset, plus one for reversibility), each adjacent to its corresponding surface.

	Stress		Rest		Rev
	Ext	TPD	Ext	TPD	
LAD	8	3.6	0	0.0	8
LCX	78	13.3	3	1.3	61
RCA	44	6.8	0	0.0	45
TOT	34	27.9	1	1.3	31

Extent and TPD by wall.



Extent and reversibility by wall.

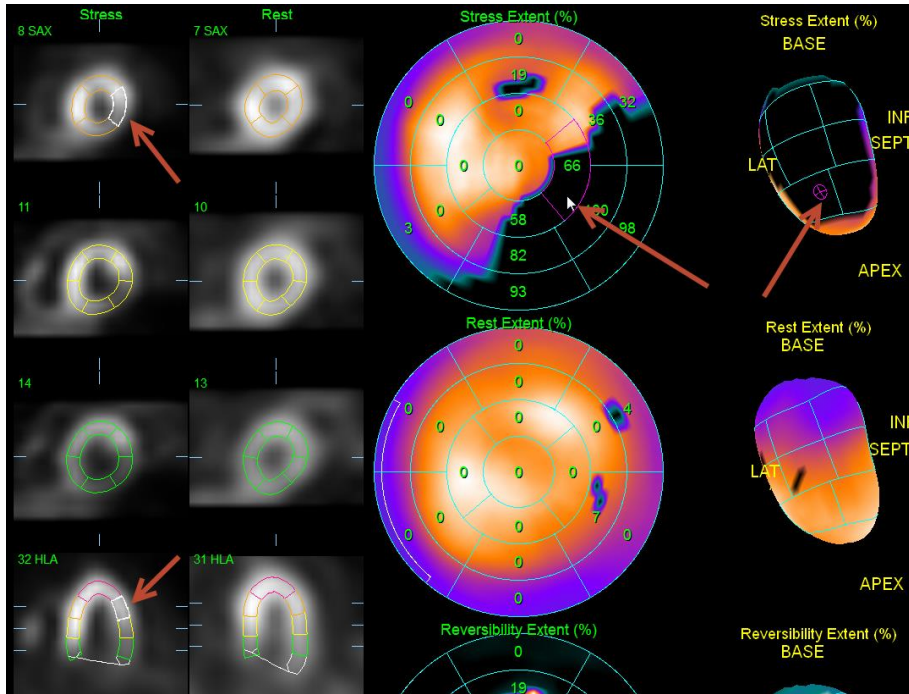
A table of perfusion extent and severity and reversibility extent is displayed for each wall or vessel territory by toggling the **Graph** button. It is possible to alternate between this table and a graph displaying stress defect extent and reversibility by wall or territory. It is further possible to alternate between the graph/table and the segmental function score box by toggling the **Score** button.

#### Use the QPS results page to:

- Display data as 2D and 3D perfusion maps, showing raw perfusion counts and the extent and severity of myocardial perfusion defects.
- Display appropriate values of TPD (total perfusion deficit), defect severity, or defect extent, compared to an applied Normals file or the raw percentage of perfusion.
- Provide comprehensive results, with reports containing quantitative perfusion and reversibility data.
- Display non-gated stress and rest polar maps, compared to a Normals file, and display raw polar maps.
- Provide severity and extent quantification with reversibility, compared to a Normals file.

### Triangulated navigation for the polar maps

If you left-click any region in the 2D polar maps, the selected region is highlighted in the corresponding 2D slice images and additionally a cursor is seen on the corresponding 3D image. In the below example, the mouse cursor is left-clicked in one of Apical segments. A corresponding cursor is seen on the 3D image and also the corresponding segments are highlighted in the appropriate slices.



Similarly, if you right-click a 2D polar map, the cursor's location is indicated at the corresponding grid on the 3D volume (instead of the region), and QGS+QPS rotates the volume to center the point in the window. For example, click the stress perfusion polar map to highlight the corresponding grid location on the stress 3D volume and the stress SAX, HLA, and/or VLA images.



### Combined Prone + Supine quantification

Prone-supine (Prone+) quantification allows quantification of perfusion on prone images as well as combined quantification of prone/supine datasets by applying heuristic rules which allow automatic elimination of image artifacts based on the relative defect locations on prone and supine images.

### Feature requirements

The Prone-Supine (Prone+) quantification feature requires at a minimum one supine perfusion dataset and one prone perfusion dataset from the same patient/study. This feature is available in the QPS Results page and is enabled by toggling on the **Prone+** button of the page control bar.

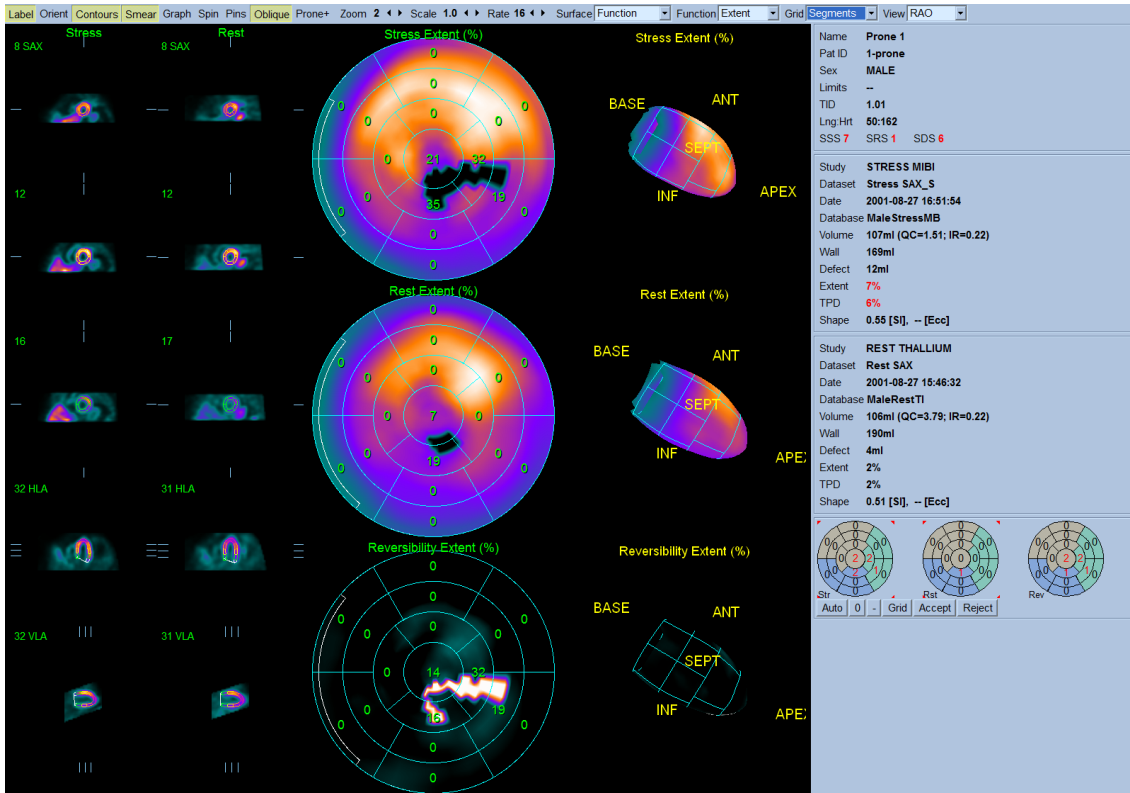
### Implementation

A typical sequence for using the Prone+ feature in the QGS+QPS application is as follows:

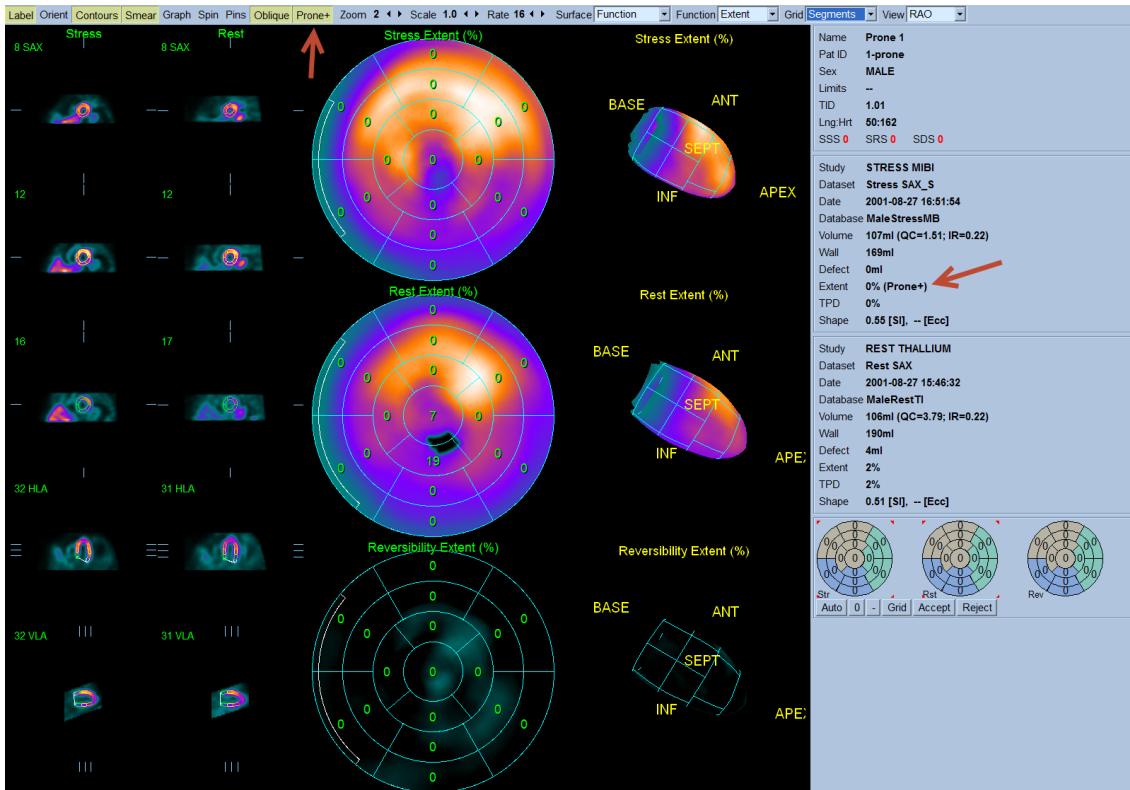
1. User selects necessary myocardial perfusion datasets (and any other desired datasets for a standard QGS+QPS session, raw projections etc.) and then starts the QGS+QPS session.
2. The loaded datasets are processed by QGS+QPS to generate contours.
3. User verifies contours.
4. User displays the QPS Results page and sets the polar maps to display Extent using the function drop down menu.
5. User clicks **Prone+** button to apply Prone-supine quantification algorithm and display results. Results are displayed in the statistics section and also the polar maps.
6. The application of the Prone+ feature is indicated in the statistics section of the QPS Results page and in the change of defect size/location (if any) on the Stress and Reversibility polar maps.

Notes:

1. When the Prone+ feature is been enabled in the QPSResults page it remains in effect for all other pages displaying perfusion results in the statistics section (Surface, Splash, etc.).
2. The Prone+ feature can be automatically enabled by toggling it on in the Application Defaults window, Application Options section and then saving the defaults settings. In this manner, the Prone+ algorithm will be applied during processing of perfusion datasets for all subsequent QGS+QPS sessions.



Sample study with Prone+ toggled off



Same sample study with Prone+ toggled ON (as indicated by the Red arrows)

## Polar maps

### Function menu

Use the **Function** drop down menu to select the parametric perfusion function to display in the polar maps and 3D surfaces. The following options are available:

1. Raw

Displays the raw counts as a percentage before any normal limits processing has been applied. The pixel corresponding to the maximum raw count is set to the maximum color scale brightness and corresponds to a value to 100. Both the raw stress and rest raw maps are normalized for display purposes.

The **raw reversibility** map is built after a pixel by pixel comparison between the stress and rest raw polar maps. It is normalized such that the 90<sup>th</sup> percentile is equal to 100% (so as to minimize the effect of hot spots). The relationship is defined as, Reversibility = normalized rest – normalized stress.

2. Severity

Displays the standard deviations by which each normalized pixel is below normal. If a pixel is above normal, it appears as black (in grayscale mode). If a pixel is below normal by more than 10 standard deviations, it appears as white (in gray scale parlance). In other words, for display purposes, the scale is linear in the 0-10 standard deviation range, and completely saturated outside the range.

The **Severity Reversibility** polar map displays the results of rest-stress severity. It is calculated, pixel by pixel, as stress severity – rest severity. Neither stress severity nor rest severity is constrained to the 0-10 range, and can in fact be negative if pixel counts are above the mean (however, the display for severity reversibility is constrained to 0-10). The overlaid number for a segment is the average of pixel severity reversibility over all pixels in that segment, weighted by the myocardial surface area corresponding to each pixel.

3. Extent

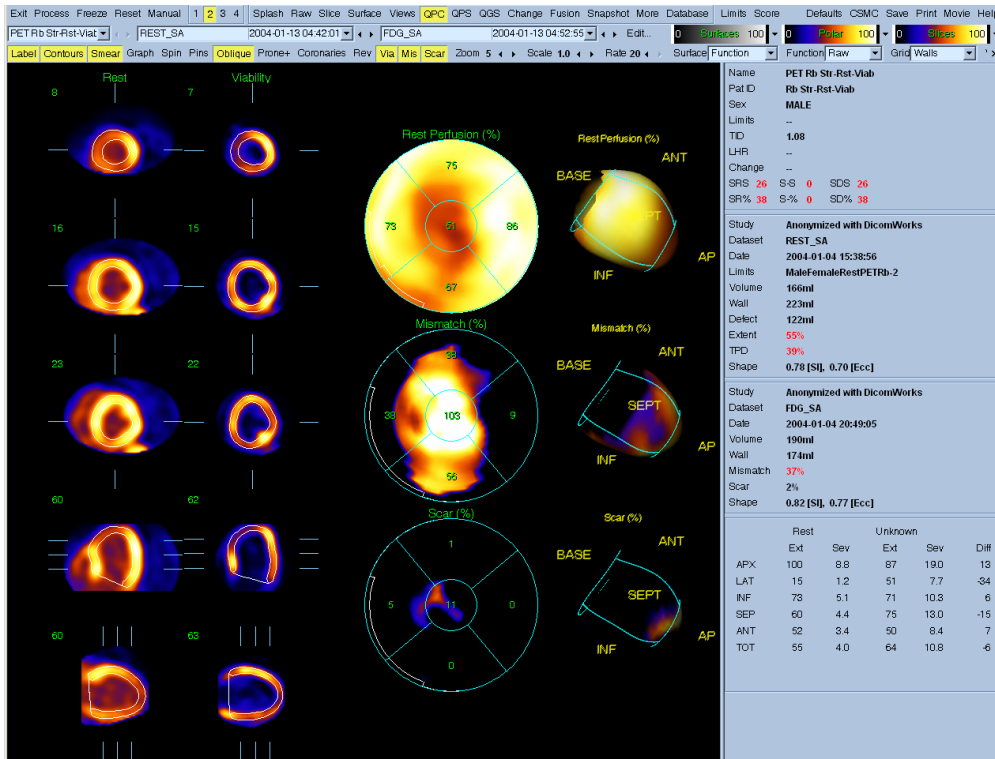
Displays the measure of a defect size. Defect extent is calculated as the percentage of the total surface area of the left ventricle, for which test-data are below 3.0 average (mean absolute) deviations, which is approximately equivalent to 2.5 standard deviations threshold. Average deviation is used instead of standard deviation due to more robust behavior in non-Gaussian distributions. In the extent polar maps, pixels are “blacked out” if they contain counts lower than the threshold. If a pixel is above the threshold and therefore not “blacked out”, it has the same intensity as in the Raw polar map.

#### 4. Quant

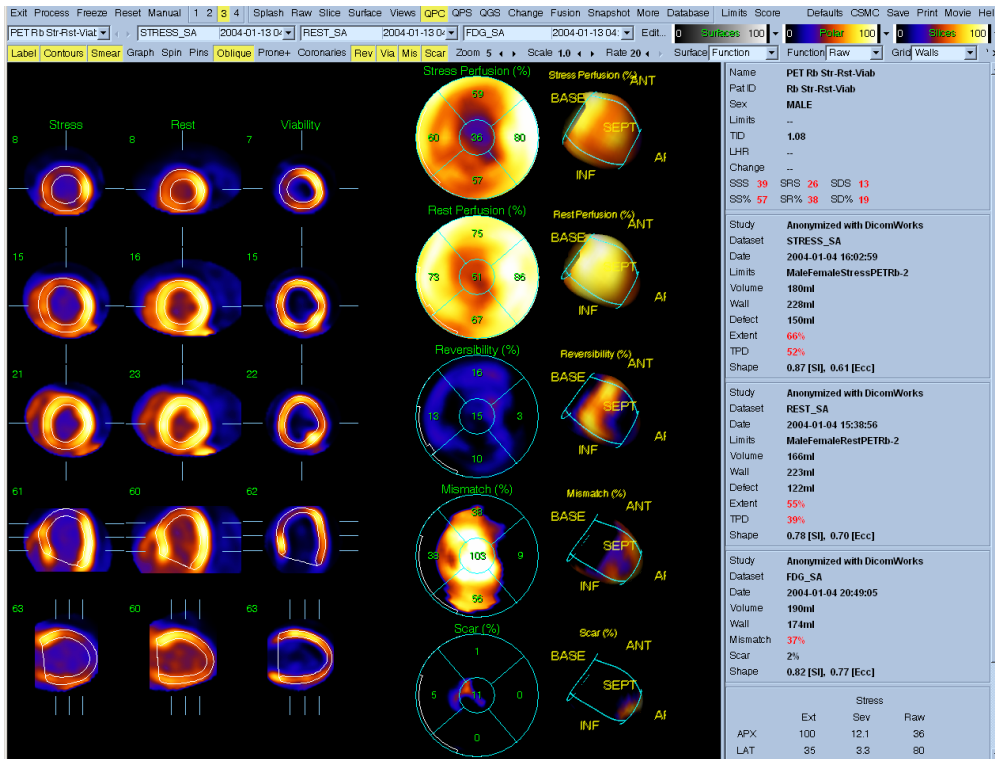
Quant Stress and Rest maps are derived from the Severity Stress and Rest maps by assigning a number (corresponding to a score from 0 to 4) to each pixel, based on automatically and iteratively determined, segment-specific thresholds (see extent stress and rest maps). The myocardial surface area-weighted average of the scores of all pixels in a segment appear in the overlay, and ideally would round off to the automatic segmental scores obtained by pressing the Score button in QPS. The latter are not computed on a pixel by pixel basis, but based on the average segment depth.

The **Quant Reversibility** polar map is derived from the Severity Reversibility map. Segment-specific thresholds are automatically determined in a manner similar to the Extent Stress and Rest maps, and categorize every pixel as 2 (reversible), 0 (non-reversible) or 1 (indeterminate). Segment numbers in the overlay represent the myocardial surface area-weighted average of quant reversibility in the segment. The range of Quant reversibility is 0 to 2. Unlike the Quant stress and rest numbers, the Quant reversibility numbers do not round off to the automatic segmental difference scores obtained when you click the Score button.

## 5.8 QPC Page



QPC page with 2 datasets (Rev, Via, Mis, and Scar toggles enabled)



QPC page with 3 datasets (Rev, Via, Mis, and Scar toggles enabled)

The QPC module performs the quantitative assessment of "hibernating myocardium" in PET or PET/SPECT studies by calculation of relative regional changes between perfusion and viability scans in areas of hypo-perfusion at rest. From the comparison between a rest scan (rest SPECT or rest PET scan) and the viability scan (PET F-18 FDG), scar and mismatch parameters are reported as a percentage of the Left Ventricle. Extent and severity of scar and mismatch can be displayed in polar map coordinates or as a 3D surface display. The program allows automatic scoring of scar or mismatch using 17- or 20-segment model. Simultaneous display of stress, rest and viability quantification results is possible. Stress images are not required for the quantification of scar and mismatch. This method of quantification is based on the following publications:

1. Journal of the American College of Cardiology. 2002;40:1735-1743
2. J Nucl Cardiol.2004;11:369.

### Feature Requirements

The QPC module requires at a minimum one PET or SPECT rest myocardial perfusion dataset and one PET myocardial viability dataset. The datasets can be in short axis or transaxial orientation. Typically, the datasets consist of a PET rest Rb-82 perfusion dataset or a SPECT rest thallium (or sestamibi) dataset and a PET FDG rest viability dataset. The module is accessed in the QGS+QPS application session by clicking the **QPC** button on the main application toolbar. Page specific controls allow for polar map displays of Rest Perfusion, Mismatch, Scar, Reversibility and optionally Stress Perfusion.

**Note:** The rest perfusion dataset (Rb-82, Tl-201, or Tc-99m) must have a corresponding normal limits database.

How is the Viability Study identified?

The Viability study is identified by any one of several identifiers: (a) If the process ID field contains FDG, F 18 or F-18 (case-insensitive), (b) if the isotope text field contains FDG, F 18 or F-18 (case insensitive), (c) if the isotope enumeration field is FDG.

### Implementation

A typical processing sequence for the QPC module in is as follows:

1. User selects necessary SPECT and PET myocardial perfusion short axis datasets (and any other desired datasets for a standard QGS+QPS session, raw projections etc.) and then starts a QGS+QPS session.
2. The short axis datasets are processed by QGS+QPS to generate contours.
3. User verifies contours.
4. User clicks **QPC** on the QGS+QPS application main toolbar to display the **QPC** page.

5. User confirms correct selection of rest perfusion dataset and viability dataset in the slices section of the **QPC** page. User can manually select appropriate datasets using the dataset drop-down selectors.
6. Using the page controls the user can display polar maps showing mismatch and scar by toggling “on” the **Mis** and/or **Scar** buttons.
7. If a matching stress perfusion dataset has been included in the application session the user can display it in the slices section by clicking 3 display view and selecting the stress dataset from the dataset selector drop-down ( if not already selected). Using the page controls the user can display a reversibility polar map by toggling “on” the **Rev** button. If appropriate stress and rest datasets are not currently selected, a difference polar map will be presented instead.

### Reviewing Results on the QPC page

Clicking on the **QPC** page indicator on the main toolbar will bring up the **QPC** page. One aspect that is quite noticeable to the user is that the **QPC** page is very similar to the QGS+QPS results page. Up to three datasets can be displayed in the slices section of the **QPC** page (the 4 display option is inactive). The datasets most useful for this page are stress perfusion, rest perfusion and a viability dataset although only rest perfusion and viability datasets are required for calculation of **QPC** results.

### Assessing Slices, Polar Maps and Surfaces

**QPC** provides five slice views for each dataset. You can also view up to 5 polar maps and corresponding 3D parametric surfaces representing Stress Perfusion, Rest Perfusion, Reversibility, Mismatch, and Scar.

The **QPC** window control toolbar provides optimal display of slices, polar maps and 3D parametric surfaces.

You can overlay a grid of 20 or 17 segments (**Segments**), 3 vascular territories (**Vessels**) or 4 regions (**Walls**) can be overlaid onto all polar maps and surfaces from the **Grid** pull-down menu. In the polar maps case, the numbers associated with the overlay represent the average value of the parameter measured by each map within the segment, territory or region in which they lie. Both stress and rest perfusion values are normalized to 100.

The following **QPC** window specific controls are available:

- **Rev:** Toggles display Reversibility polar map and corresponding 3D parametric surface (if there are stress and rest datasets).
- **Via:** Toggles display of viability slices in the slices section.
- **Mis:** Toggles display of Mismatch polar map and corresponding 3D parametric surface.

- **Scar:** Toggles display of Scar polar map and corresponding 3D parametric surface.

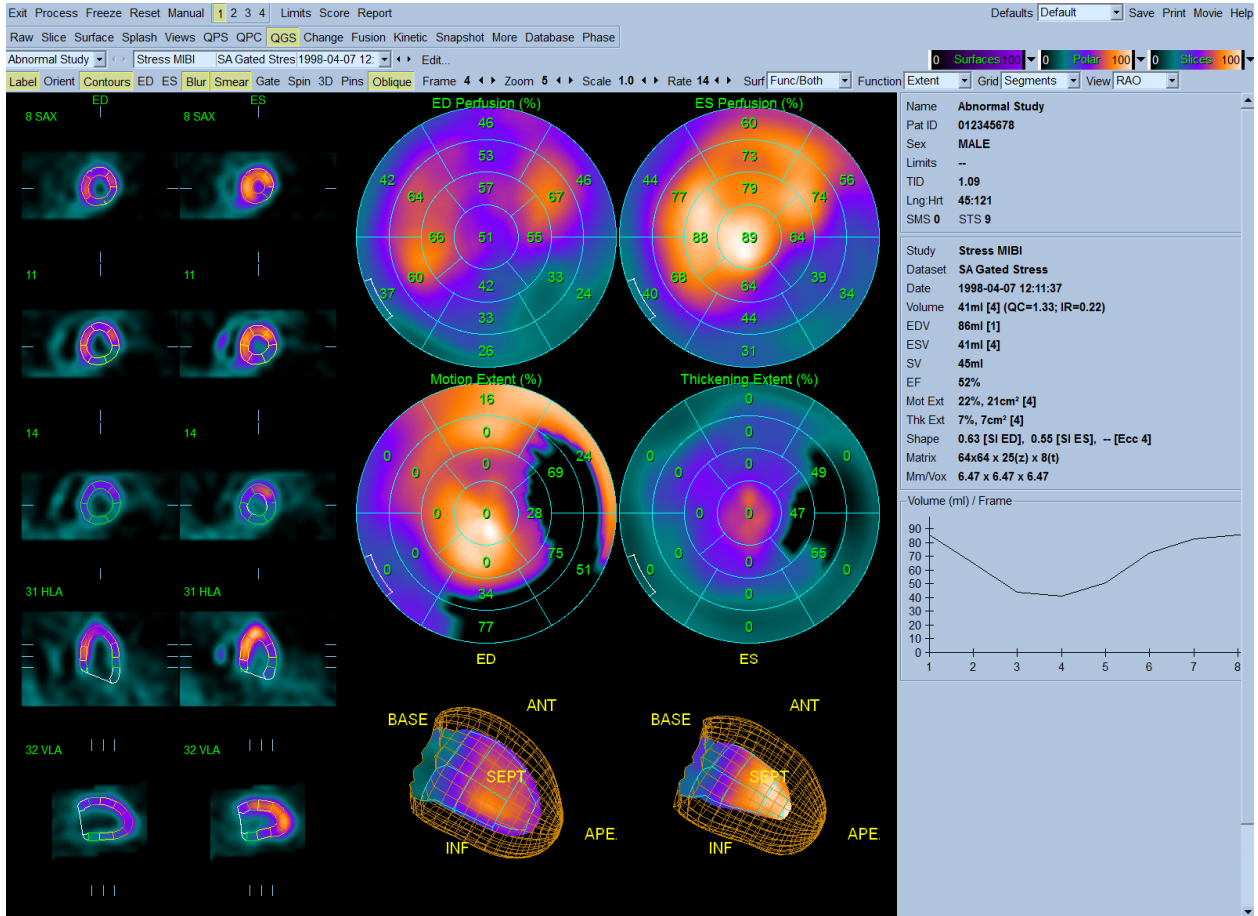
### Page Controls

The following page specific controls are available:

<b>Graph</b>	Toggles graphical display showing regional mismatch and viability
<b>Rev</b>	Toggles display Reversibility polar map and corresponding 3D parametric surface (if there are stress and rest datasets).
<b>Via</b>	Toggles display of viability slices in the slices section.
<b>Mis</b>	Toggles display of Mismatch polar map and corresponding 3D parametric surface.
<b>Scar</b>	Toggles display of Scar polar map and corresponding 3D parametric surface.
<b>Function</b>	<p>Selects the parametric function mode for 3D parametric surfaces when Function, Func/Both or Func/Outer is selected from the Surface drop-down.</p> <p>Selects the parametric function mode for all polar maps (independent from the Surface drop-down setting).</p> <p>Drop-down choices are Raw, Severity and Extent.</p>



## 5.9 QGS Results Page



The QGS page displays an overview of processed results and functional analysis for a single dataset, using slices, surfaces, polar maps, graphs, and statistics.

### Use the QGS page to:

- Display comprehensive results, providing a report encompassing a wide range of quantitative function data
- Show LV function from end diastole through the complete cardiac cycle with the **Volume (ml) and Filling (ml/s) Curve**
- Compare, side-by-side, the ED and ES images that are valuable for visually comparing ED and ES function:
  - SAX/VLA/HLA slice images
  - 2D polar maps
  - 3D surface maps
  - Motion
  - Thickening

### QGS Polar Maps

You can display several different types of polar maps in the QGS window:

- **Perfusion**: one at **ED** and one at **ES**
- **Function**: one for **Motion** and one for **Thickening**

Use the options in the Grid pull-down menu to overlay a grid of 20 segments (or 17 segments), 3 vascular territories, 4 regions, or 5 walls on any polar map. The numbers associated with the grid overlays represent the average value of the parameter measured by each map for the segment, territory or region in which they exist.

You can also switch from polar maps to a 3D view by clicking on the **3D** button.

### *Perfusion (%) Polar Maps*

The **Perfusion** polar maps display the myocardial perfusion at end diastole and end systole as a percentage. The pixel corresponding to the maximum ventricular perfusion equals 100% and is set to the maximum color scale brightness. The polar map brightness decreases as the perfusion decreases.

### *Function Polar Maps*

Use the **Function** pull-down menu to select a function to display in the function polar maps and surfaces. The **Function** pull-down menu contains the following options:

- Raw
- Severity
- Extent
- Quant

1. Raw

The **Motion** polar map displays the change in endocardial wall motion from end diastole to end systole in millimeters. The maximum color scale brightness equals a 10 mm change, and the calculated wall motion appears relative to this value. The polar map brightness increases as the wall motion increases.

The **Thickening** polar map displays the change in myocardial wall thickness from end diastole to end systole as a percentage, calculated in this way:

$$\text{thickening} = \frac{100 \times [\text{thickening(ES)} - \text{thickening(ED)}]}{\text{thickening(ED)}}$$

At ED, an area that is twice the thickness of the ED wall thickness equals 100% and is set to the maximum color scale brightness. Areas displaying no change from the ED thickness are set to the minimum brightness. The brightness increases as the wall thickness increases (dark areas indicate minimum changes in wall thickness).

## 2. Severity

The Severity polar map displays a comparison between the motion and thickening polar maps for the selected Normals file and the normalized polar maps for the displayed dataset. You can determine the relative severity of the defective regions by the color scale brightness. Pixels above normal are set to the minimum color scale brightness regardless of count value. Pixels corresponding to motion and thickening values that are 10 standard deviations below the normal mean in the Normals file are set to maximum color scale brightness. The color brightness decreases with the difference in each region. This is the average of the number of standard deviations below normal for each pixel in the segment, weighted by the myocardial surface area corresponding to each pixel. The averages computation sets all pixels above normal to zero.

## 3. Extent

The Extent polar map displays a measure of defect size. Pixels with counts lower than a certain threshold below the normal mean for that pixel are blacked out. If a pixel is not blacked out, it displays the same intensity as in the corresponding raw map. QGS+QPS calculates the thresholds on a segment-by-segment basis by automatically and iteratively optimizing sensitivity and specificity for that segment, based on correlation to expert visual scores. Select a grid overlay to displays the percent of the myocardial surface area corresponding to that segment that contains pixels having counts below normal for each region.

NOTE: This value is not equivalent to the percent of pixels in the segment, since some pixels represent a greater myocardial surface area corresponding to that segment.

## 4. Quant

Quant Motion and Thickening maps are derived from the Severity Motion and Thickening maps by assigning a number from 0 to 5 to each pixel for Motion, and 0 to 3 to each pixel

for Thickening. This is based on automatically and iteratively determined segment-specific thresholds. Select a Grid overlay to display the average score of all pixels for each region, weighted by the myocardial surface area corresponding to each pixel. These scores reflect the scores displayed when you select the Score button in the QGS window.

**QGS visual scores**

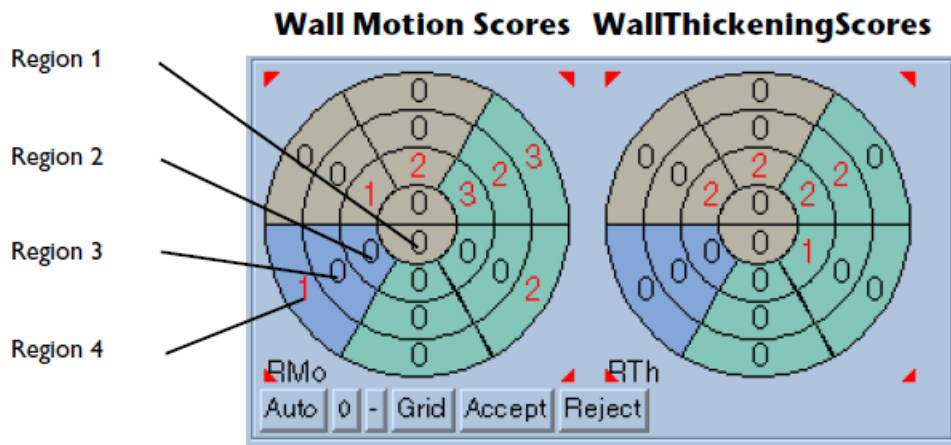
Click **Score** to display the visual scores in 17- or 20-segments. QGS automatically calculates the following values:

- Motion and thickening scores for all segments
- SMS and STS
- Mot Ext and Th Ext

If you think that any of the segmental visual scores are inaccurate, you can increase the visual score by clicking on its numeric value in the visual scores box; QGS+QPS will adjust SMS and STS automatically.

Summed function scores are presented both in numerical form (SMS, STS) and as a percentage of the maximal numerical values obtainable (SM%, ST%). The latter are independent of the number of segments used.

The visual scoring panel (shown below) consists of seventeen or twenty segment polar map for the datasets. Each segment lies in one of four regions formed by concentric circles on the diagram.



Visual scores panel (CS-20 format)

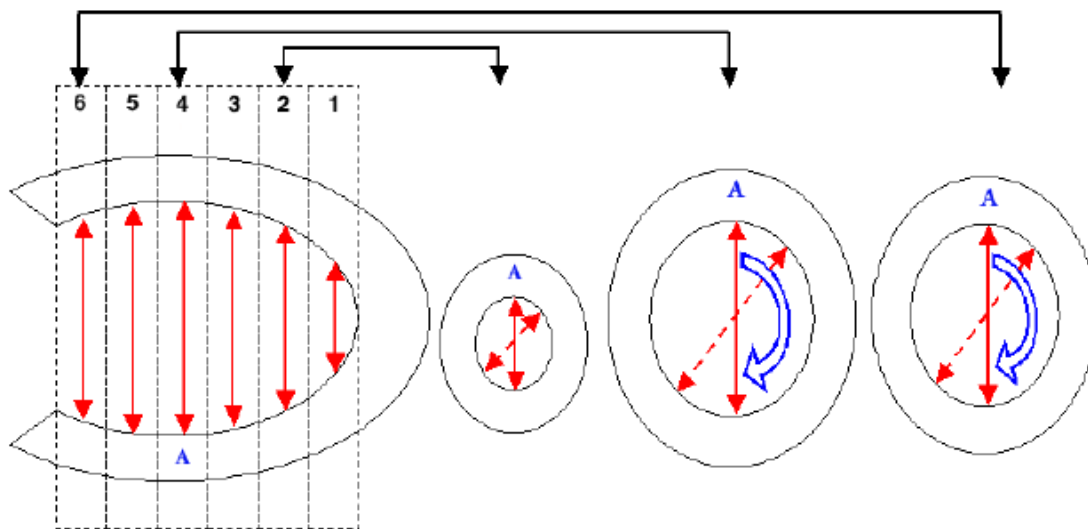
The numerical value for a segment in the visual scoring panel indicates the amount of motion and thickening deviation in this region relative to the Normals file. Values range from a normal of 0 (normal) to a maximum abnormal of 3 for thickening, and from a normal of 0 to a maximum of 5 for motion. If all values in the diagram are zeroes, this indicates that for each segment, there is zero deviation from the Normals file.

### Shape Index

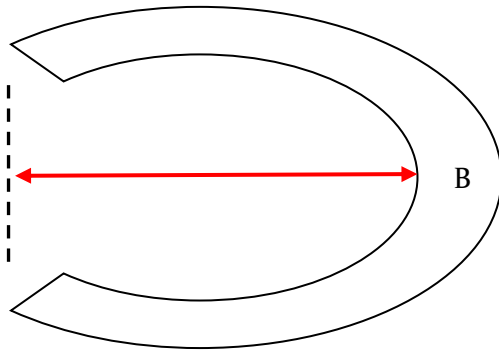
Shape index values are indicated by **SI** in the **Shape** field within the information panel.

This parameter defines 3D left ventricular (LV) geometry derived from LV contours in end systolic and end diastolic phases. Shape index is defined as the ratio between the maximum dimension of the LV in all short-axis planes and the length of the mid-ventricular long axis.

**Reference:** Abidov A, Slomka P, Hayes SW, Aboul-Enein F, Kang X, Yoda S, Nishina H, Yang L, Cohen I, Thomson L, Friedman JD, Germano G, Berman DS. Left Ventricular Shape Index Assessed By Gated Myocardial Perfusion SPECT: A New Scintigraphic Marker Of Congestive Heart Failure. SNM 2004 Abstract, No 500, page 176P



For each short axis plane in the end-diastolic (ED) image series, maximum dimension (A) of the LV is found from the 3D contours derived by the QGS+QPS algorithm, using the endocardial surface as the boundary. Global short-axis end-diastolic dimension (AED) is found as a maximum for all ED short axis slices. The short-axis slice and direction of AED is then used to calculate the maximum short-axis end-systolic dimension (AES) in the end-systolic image series, by measuring the distance between the endocardial points in the identical location (slice and direction) where AED was found.



The long-axis dimension of the myocardium is derived by calculating the distance (B) between the most apical point on the endocardial surface and the center of the valve plane. The ED long-axis dimension (BED) is calculated independently from the ES long-axis dimension (BES).

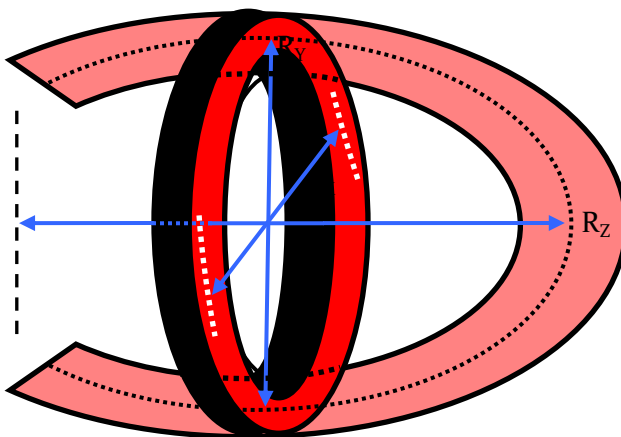
The end-diastolic shape index (SI ED) and the end-systolic shape index (SI ES) are derived by AED/BED and AES/BES, respectively.

### Eccentricity

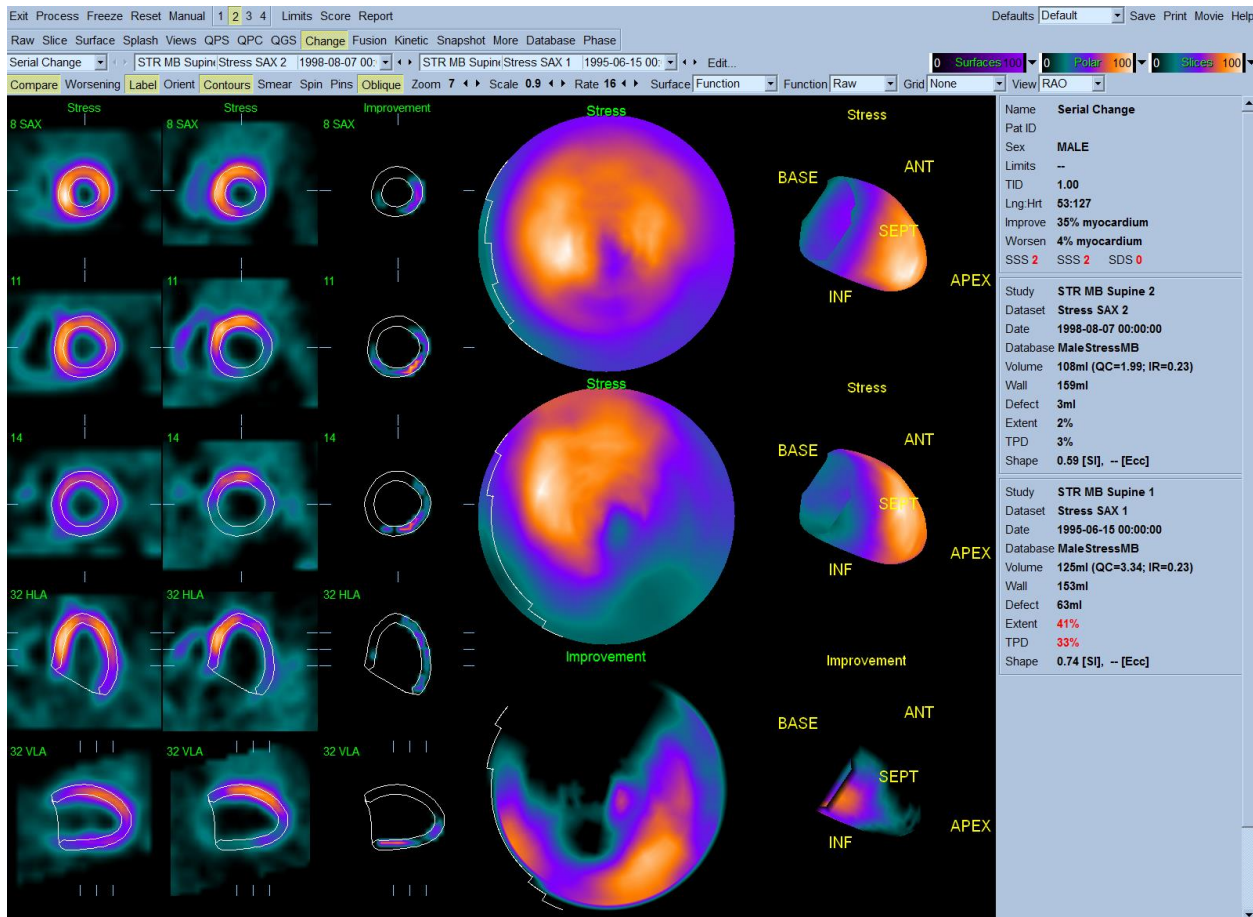
**Eccentricity** is a measure of the elongation of the LV, and varies from 0 (sphere) to 1 (line); it is calculated from the major axis  $R_z$  and the minor axes  $R_x$  and  $R_y$  of the ellipsoid that best fits the mid-myocardial surface, according to the formula:

$$Ecc = \sqrt{1 - \frac{R_x R_y}{R_z^2}}$$

It is calculated for all slices in a gated series.



## 5.10 Change Page



The change feature allows direct quantification of perfusion changes between two datasets by applying 3D elastic registration of two myocardial perfusion studies and direct study-to-study count normalization. Voxel-by-voxel calculation of positive and negative changes between two normalized studies is computed and expressed as the percentage of all the counts in the myocardium. Change is visualized directly on image slices and in polar map coordinates. It is possible to review the quality of image registration by direct overlay of two sets of images using a roving window on the display. No databases are required for the calculation of stress-rest changes (ischemia) or serial (stress/stress) image changes.

The change feature can be used on stress/rest pairs to determine global ischemia measure or on serial stress/stress pairs to evaluate changes over time (both improvement and worsening).

References: J Nucl Med. 2004 Feb;45(2):183-91

JACC Volume 45, Issue 3, Supplement 1, February 1, 2005. 1112-70, 285A.

### Requirements

The change feature requires at a minimum two myocardial perfusion datasets. The pairs can be of any combination but the most useful clinically are a stress/rest pair or a stress/stress pair. Change

feature can be used for a stress/rest pair of datasets to determine global ischemia when normal limits databases are not available, or if standard quantification results are borderline. This feature can also be applied to pairs of data, where the stress or rest studies are performed on different dates, to evaluate perfusion changes over time (serial changes), for example to monitor a therapy.

### Implementation

A typical sequence for using the change feature in QGS+QPS application is as follows:

1. User clicks **Compare** on the page control bar to apply the change algorithm. Since elastic registration is computationally intensive it may take some time for the change results to be reported. Hourglass is displayed to indicate the calculation progress.
2. Change results, polar map and change slice display sections are updated once the change quantitation is performed. Change results are in % myocardium (volume).

If **stress-rest** studies are compared, change slice display is labeled Ischemia and change results are displayed as Ischemia: % myocardium.

If **serial stress** (or serial rest) studies are compared, change results can be displayed as % myocardium Improvement or Worsening. The default display mode is Improvement, in which the results, change slices, and change polar maps for areas where there were positive changes are displayed. If Worsening label is toggled, the results, change slices and change polar maps for areas where there were negative changes are displayed. Note: the order of the serial comparison is determined by the study date. If date is the same, the order is determined by the time of acquisition. Therefore it is essential that the data and time of acquisition in the header are correct for the serial change analysis.

The change feature is available in the QGS+QPS application and can be enabled to automatically apply the change algorithm during QGS+QPS session startup by enabling (toggling on) the **Change** button in the Application Options section of the **Defaults Editor**. Note: This will increase the startup time due to change calculations being performed. If this feature is not routinely used it is best to execute Compare “on-demand” when appropriate 2 studies are selected in the change page.

When **Change** is enabled in the defaults, the **Compare** button on the **Change** page is automatically enabled indicating that the change algorithm has been applied.

### Reviewing Results on the Change page

Clicking on the **Change** page indicator on the main toolbar will bring up the **Change** page. One aspect that is quite noticeable to the user is that the **Change** page is very similar to the QGS+QPS results page. Two datasets will be displayed in the **Change** page (the 1, 3, and 4 display datasets options) are inactive. Change results (Ischemia, Improvement or Worsening) are displayed in the statistic section.



### Assessing Change results

The **Change** page provides three perfusion polar maps and three 3D parametric surfaces (stress, rest and change-labeled as Ischemia, Improvement, or Worsening). The **Function** pull-down menu contains the options “Raw”, “Severity”, and “Extent”, all of which apply to both 2D and 3D displays. A grid of 20 or 17 segments (**Segments**), 3 vascular territories (**Vessels**) or 4 regions (**Walls**) can be overlaid onto all polar maps and surfaces from the Grid pull-down menu: in the polar maps case, the numbers associated with the overlay represent the average value of the parameter measured by each map within the segment, territory or region in which they lie. Both stress and rest perfusion values (and stress pairs) are normalized to 100. In addition, a slice display of change (ischemia, improvement, or worsening) is presented where the change can be visualized in the original slice coordinates. Note: In order to be able to relate the change images and original images it is necessary to display image contours by toggling “Contours”. The contours displayed are that of the first study (or Stress in Stress/ Rest comparison) and are overlaid over the co-registered second study and change images. No separate contours of rest (or second) study are displayed during the comparison.

### Change page controls

The following page specific controls are available:

<b>Compare</b>	Toggling on applies the registration and change algorithm to the currently displayed pair of datasets producing the change slices and change polar map. Toggling off resets the slices and polar map.
<b>Worsening</b>	Applicable for serial stress or serial rest comparisons only. Toggling on shows the results, change slices, and change polar maps for areas where there were negative changes or hypoperfusion.
<b>Contours</b>	Turns contour display on and off. Contours are the intersection of a given slice and the endocardial and epicardial surfaces obtained by QGS+QPS. Note that in the change page only contours from the first study are used and are duplicated for the second study, which is registered to the first.

### Roving Window

The roving window utility allows for quality control of the registration process. The following describes how to use this aspect of the **Change** feature.

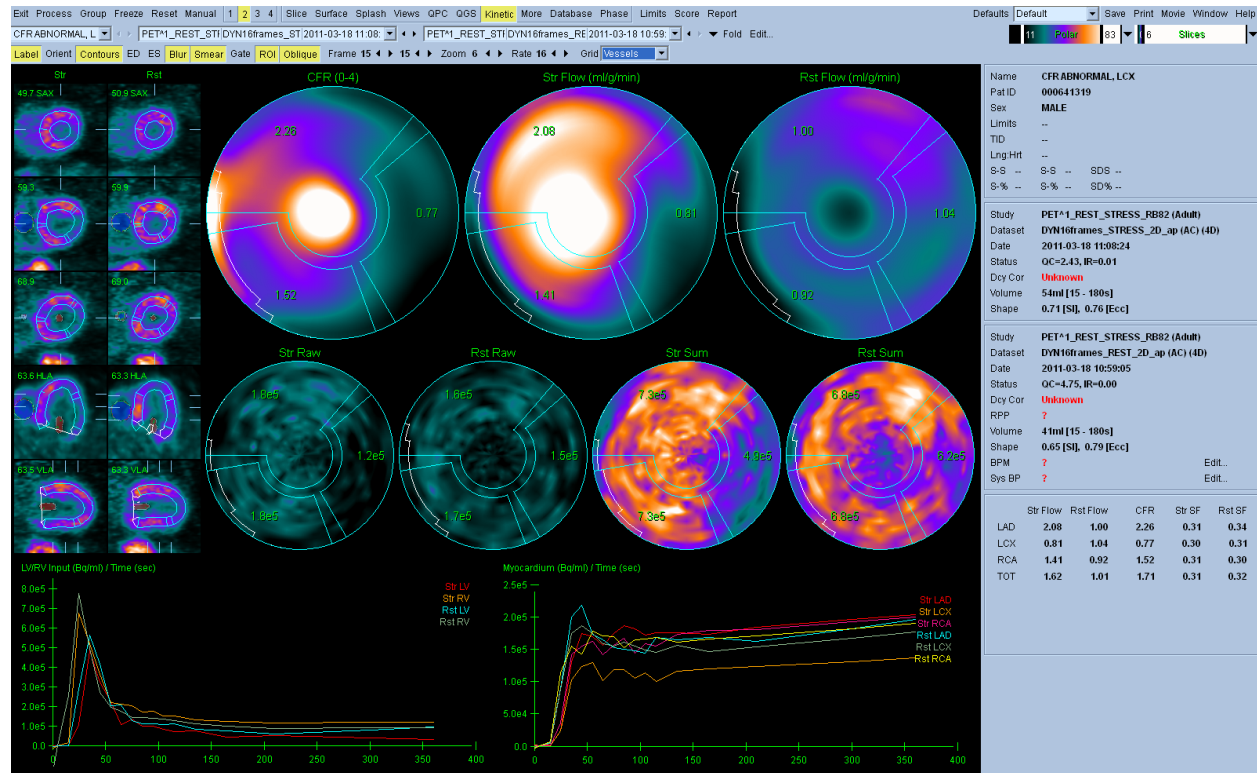
On the Change page:

1. In the slices section, with the mouse pointer on a slice image, click and hold the right mouse button. **Note:** The user may zoom the images prior to performing this step using the **Zoom** page control.
2. A rectangular “window” appears containing slice data as follows.
  - a. If the user performed step 1) on a slice in the left-most column of slices (usually a stress dataset), the window contains slice data from the adjacent slice in the middle column of slices (can be a rest or stress dataset).

- b. If the user performed step 1) on a slice in the middle column of slices (stress or rest dataset), the window contains slice data from the adjacent slice in the left-most column of slices (usually a stress dataset).
    - c. If the user performed step 1) on a slice in the right-most column of slices (the Change slices), the window contains slice data from the corresponding slice in the left-most column of images (usually a stress dataset). An example of this is shown below.
  3. While holding the right mouse button the user can drag the window in that slice area and verify correct registration of the slices by positioning the window over the underlying slice data.



## 5.11 Kinetic Page – Coronary Flow Reserve



The Kinetic analysis feature for dynamic PET studies allows for automated quantification of absolute stress and rest blood flow within the myocardium using algorithms specifically developed for PET  $^{82}\text{Rb}$  and  $^{13}\text{N-NH}_3$  tracers. It also allows for non-invasive determination of absolute coronary flow reserve (CFR). The kinetic modeling method for  $^{82}\text{Rb}$  is the 1-tissue compartment model (Lortie et al., EJNM 34:1765-1774, 2007). Whereas the kinetic modeling method for  $^{13}\text{N-NH}_3$  uses simplified 2-compartment model (Choi et al., JNM 34(3):488-497, 1993).

### References:

1. Slomka PJ, Alexanderson E, Jacome R, Jimenez M, Romero E, Meave A, Meunier LL, Dalhborg M, Berman DS, Germano G, and Schelbert H. Comparison of Clinical Tools for Measurements of Regional Stress and Rest Myocardial Blood Flow Assessed with  $^{13}\text{N}$ -Ammonia PET/CT. *J Nucl Med*, 2012; 53:171-181.
2. DeKemp RA, Declerck J, Klein R, Pan Xiao-Bo, Nakazato R, Tonge C, Arumugam P, Berman DS, Germano G, Beanlands RS, and Slomka PJ. Multisoftware Reproducibility Study of Stress and Rest Myocardial Blood Flow Assessed with 3D Dynamic PET/CT and a 1-Tissue-Compartment Model of  $^{82}\text{Rb}$  Kinetics. *J Nucl Med*, 2013; 54:1-7.

### Kinetic Page Requirements

The Kinetic feature requires at a minimum one processed transverse dynamic cardiac PET dataset however for CFR results, both Rest and Stress dynamic cardiac PET datasets in the transverse

format are required. Kinetic analysis is designed to function with any number of frames but typically 16-26 frames are most commonly used in clinical settings.

### Rate Pressure Product (RPP)

Rate pressure product (RPP) is a measure of stress put on the cardiac muscle based on the number of times it needs to beat per minute (HR) and the arterial blood pressure that it is pumping against (Systolic Blood Pressure). It is the index of myocardial oxygen requirement.

$$\text{RPP} = \text{Heart Rate (beats per minute)} \times \text{Systolic Blood Pressure (mmHg)}$$

Because of the relation of Myocardial blood flow at rest with Rate Pressure Product as an index of cardiac work, the resting flow values should be normalized to the corresponding Rate Pressure Product. Kinetic applies this normalization when  $\text{RPP} \geq 1000$ . The heart rate and systolic blood pressure information may be entered for the resting dataset by clicking **Edit...** next to **BPM** and **Sys BP** as shown in the figure below. A RPP correction factor is applied to the resting flow values if  $\text{RPP} \geq 1000$ .

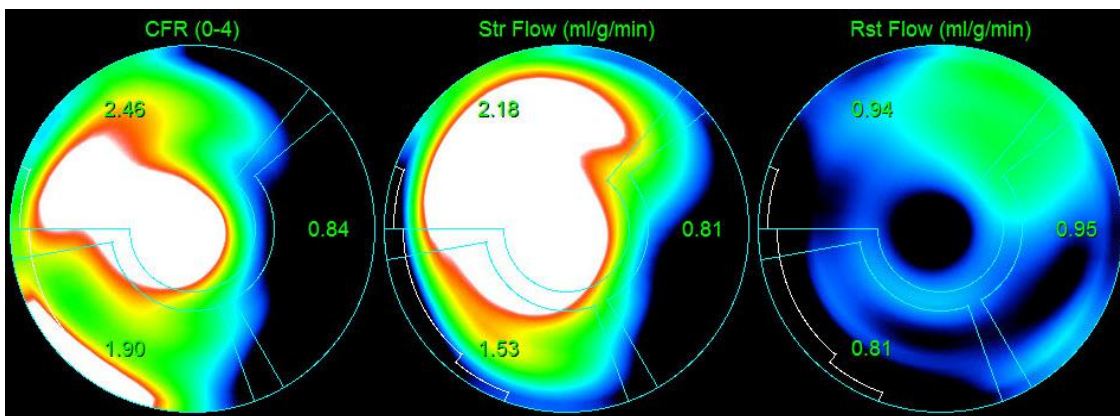
Name	CFRABNORMAL, LCX		
Pat ID	000641319		
Sex	MALE		
Limits	--		
TID	--		
Lng:Hrt	--		
S-S	--	S-S	-- SDS --
S-%	--	S-%	-- SD% --
Study	PET^1_REST_STRESS_RB82 (Adult)		
Dataset	DYN16frames_STRESS_2D_ap (AC) (4D)		
Date	2011-03-18 11:08:24		
Status	QC=2.43, IR=0.01		
Dcy Cor	Unknown		
Volume	54ml [15 - 180s]		
Shape	0.71 [SI], 0.76 [Ecc]		
Study	PET^1_REST_STRESS_RB82 (Adult)		
Dataset	DYN16frames_REST_2D_ap (AC) (4D)		
Date	2011-03-18 10:59:05		
Status	QC=4.75, IR=0.00		
Dcy Cor	Unknown		
RPP	10800		
Volume	41ml [15 - 180s]		
Shape	0.65 [SI], 0.79 [Ecc]		
BPM	90.0		
Sys BP	120		



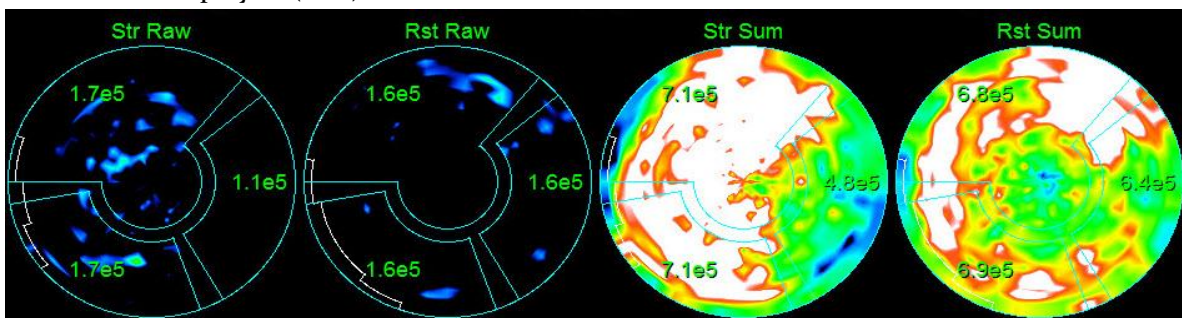
## Kinetic page displays

The Kinetic pages displays quantitative results utilizing polar map, time/activity graphs, and score chart formats.

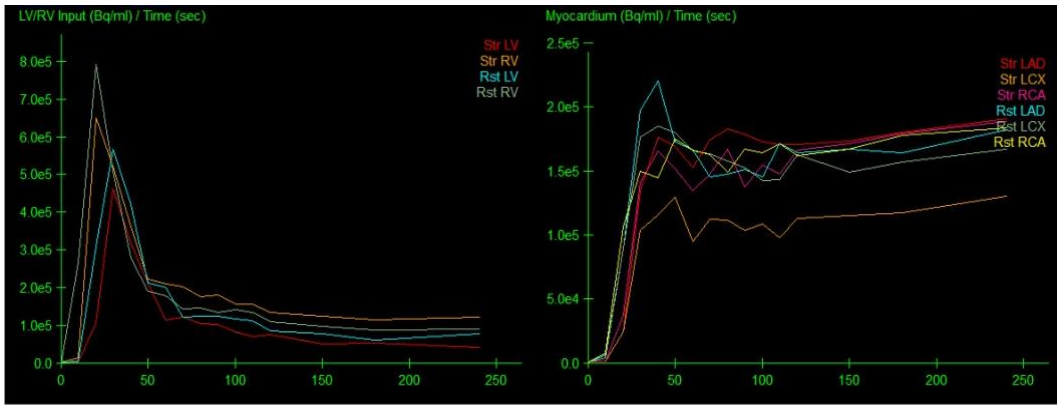
- **Polar Maps**-There are two rows of polar maps displayed on the Kinetic page.
  - The polar maps displayed towards the top of the page show the absolute blood flow in the Myocardium for the loaded datasets in ml/g/min. If both Rest and Stress dynamic flow datasets are loaded, an additional CFR polar map showing the coronary flow reserve is also displayed. The polar maps can be segmented into Vessels, Groups, Walls, and Segments using the grid pull down menu. The values are averaged for the polar map pixels for each user defined segment.



- The Polar maps displayed in the middle of the page show radiotracer activity within the myocardium in [(Bq/ml)/Time (Sec)]. There are up to 4 polar maps displayed in this region if both the rest and stress flow datasets are loaded. Two of the polar maps show summed data that sums the information from all frames (Right); the remaining two polar maps show data for the specific frame being displayed (Left).



- **Time/Activity graphs**-The time/activity curves display radiotracer activity both within the blood pool of the right and left ventricles (left) and for the Myocardium (right). When the **Grid** setting is set to **Vessels**, the Myocardium graph will also display the curves for each of the 3 main coronary blood vessels (LAD, LCX, and RCA). The values in the time/activity graphs represent absolute radiotracer activity [Bq/ml]/Time [sec].



- Results (Scores)**-The bottom right side of the screen shows results for absolute flow, CFR, and the spill-over fraction (SF) for each area of the Myocardium. SF is the amount of radiotracer that has “spilled-over” into the Myocardium (as defined by the segmentation or contours) from the blood pool region for stress and rest. The SF value helps the clinician QC the technical quality of the dataset. A SF value of  $\geq 60\%$  or 0.60 is considered to be of poor quality.

	Str Flow	Rst Flow	CFR	Str SF	Rst SF
LAD	2.18	0.94	2.46	0.32	0.33
LCX	0.81	0.95	0.84	0.30	0.30
RCA	1.53	0.81	1.90	0.32	0.30
TOT	1.70	0.93	1.91	0.32	0.32

## Manual processing mode for dynamic PET datasets

Manual mode may be used to supply hints to the segmentation algorithm in cases where the fully automatic LV segmentation fails or returns unsatisfactory results. For best reproducibility, the weakest possible hint or combination of hints that returns satisfactory results should be preferred. These hints are provided using essentially the same interface as the slice page, with masking graphics (volumetric ROIs) superimposed upon the slices. The shape and position of the masking graphics, which are initially configured to resemble an idealized LV, can be changed by dragging its handles (the small blue boxes).

To apply manual corrections, the mask should first be shaped and positioned so that it encompasses the LV while excluding all extra-cardiac activity (before doing so, it may be advisable to toggle the incorrect contours off by clicking the **Contours** button). It may be easier to visualize the LV on the Manual page by using longer frames (typically the last 3-6 frames of the acquisition protocols are commonly acquired for longer durations). Time information for the displayed frame is shown in the right side of the page next to the volume information. Then try processing with a suitable combination of hints enabled (when the **Process** button is pressed all enabled hints are applied).

The available hints, in order of increasing strength (i.e. decreasing preference) are:

<b>Localize</b>	Restricts the initial LV search to the volume defined by the masking graphics. Use if the algorithm completely missed the LV.
<b>Mask</b>	Restricts the entire LV segmentation algorithm to only use data within the volume defined by the masking graphics. Use to exclude extra-cardiac activity (e.g. spleen) that caused contours to be distorted.
<b>Constrain</b>	Constrains the long axis used by the LV segmentation algorithm to lie on the end-points (apex and base) specified by the masking graphics. Use to force valve-plane to be at a specific basal position.

As transverse data sets are often generated for PET studies, manual mode can also be used for automatically determining reorientation angles, and then displaying the results in either transverse/sagittal/coronal format or short axis/horizontal long axis/vertical long axis format.

In cases where the automatic LV segmentation or reorientation is unsatisfactory, transverse manual mode can be used to apply corrections to both. Transverse manual mode is the same as short axis manual mode with the exception that reorientation may be interactively specified by dragging the handles (small blue boxes) attached to the reorientation circles (yellow dashed circles) so that both yellow arrows point towards the apex.

The following page specific controls are available for transverse manual mode.

<b>Align</b>	Forces the reorientation angles to be those specified using the reorientation circles. Otherwise, they will be automatically generated.
--------------	---

#### **Manual processing detailed steps:**

1. Load the flow datasets (both Stress and Rest). Click **Process** (1) to auto process the datasets as this is the step where the software will automatically try to identify the LV and generate the contours.
2. If necessary, click **Manual** (2) to go to the manual processing page. On the Manual Page it is recommended to have **Blur** (3) and **Smear** (3) toggled ON as they will better help visualize the LV. These filters are only visual filters (temporal and spatial) and no modifications are made to the actual datasets. Using the **Frame** (4) control arrows, select one of the later frames that are longer in duration and where the LV tissue is better visualized. These are typically the frames that are towards the end of the dataset.

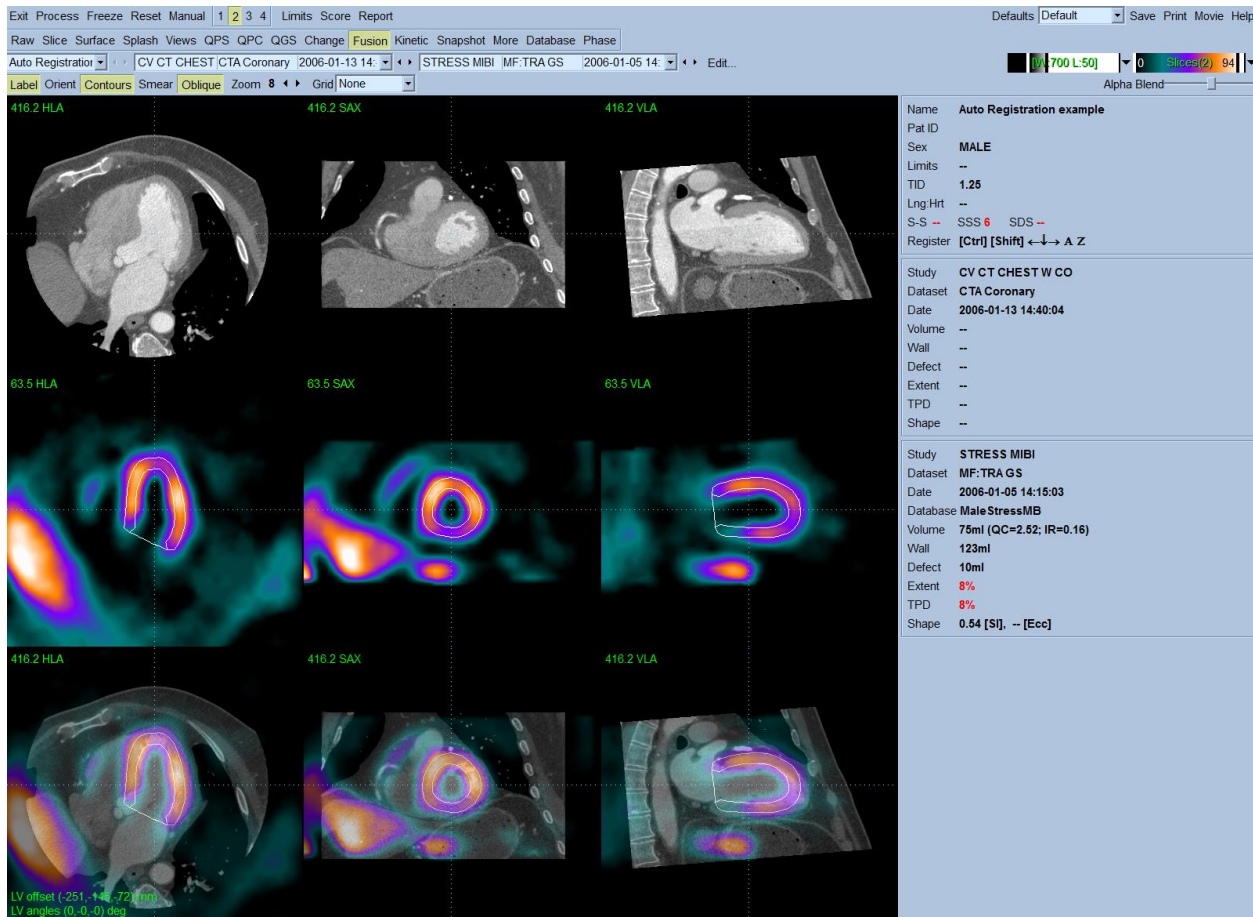


- Using the masking graphics, reorient the datasets using the reorientation handles (5). When datasets have significant extra cardiac activity (6), toggle ON the **Mask** (7) option from the tool bar. If you do have to use this option, you only need to position the short axis masking graphics to avoid the extra cardiac activity, it is not necessary to tighten the masking graphics really close to the LV.
- Click **Process** (1) to process the dataset using the manual changes.

The screenshot displays the QGS+QPS 2012 software interface. The main window shows a grid of PET scan slices in various orientations (SAX, HLA, VLA). Red arrows indicate key UI elements: 1 points to the 'Process' button in the top toolbar; 2 points to the 'Manual' button; 3 points to the 'Mask' checkbox; 4 points to the 'Zoom' control; 5 points to the reorientation handles on the slices; 6 points to extra cardiac activity on a slice; 7 points to the 'Mask' checkbox. A right-hand panel shows patient and study information, including 'Name: CFR ABNORMAL LCX', 'Pat ID: 000641319', 'Sex: MALE', and 'Volume: 54ml [14 - 150s] (QC=4.81)'. A legend at the bottom left provides instructions for the manual process steps.

- Position short axis crosshairs over LV center.
- Position long axis line end-points over LV apex and base.
- Position mask outside of LV.
- Select Localize (limits initial LV search to mask) and then process.
- If necessary, reprocess with Mask (disregards all counts outside of mask) and/or Constrain (locks LV apex and base) and/or Align (locks reorientation angles).

## 5.12 Fusion Page



This feature allows fused review of original SPECT/PET, CT, and CTA transverse slices in three orthogonal planes. Interactive 3D alignment correction of SPECT/PET, CT and CTA is possible. All standard image fusion features are provided such as interactive alpha blending, roving-window, and synchronized orthogonal reformatting. CT window/level presets are read from the DICOM header or can be predefined. The feature allows users to perform quality control of SPECT/PET/CT or SPECT/PET/CTA alignment (for verification of attenuation correction). LV contours can also be displayed in the fusion mode.

In addition, the feature allows display of segmented and labeled coronary vessels from CT Angiography (CTA) fused with 3D surface perfusion SPECT/PET data or viability PET data. The coronary artery tree is extracted and saved as DICOM by the vendor's CTA software.

This feature is accessed by clicking the Fusion button on the application main toolbar.

### Requirements

The **Fusion** feature requires at a minimum one CT dataset and one SPECT/PET perfusion or PET viability dataset. For coronary artery fusion and display, the segmented coronary tree dataset must be available in addition to the SPECT/PET perfusion/viability dataset.

## Implementation

A typical sequence for using the **Fusion** feature is as follows:

1. User selects necessary CT/CTA and SPECT/PET datasets.
2. User starts application session. Session will create contours for the SPECT/PET dataset(s).
3. Optionally, user verifies contours.
4. User clicks **Fusion** on the main toolbar to display the **Fusion** page.
5. Note: If the data comes from a Hybrid scanner and is aligned by the vendor, the Fusion page shows “hardware fusion” on the image display in the bottom.
6. Misalignment of CT and SPECT/PET images can be visually ascertained.

## Reviewing Images on the Fusion page

Clicking on the **Fusion** page indicator on the main toolbar will bring up the **Fusion** page. Two datasets will be displayed in the **Fusion** page (the 1, 3, and 4 display datasets options) are inactive.

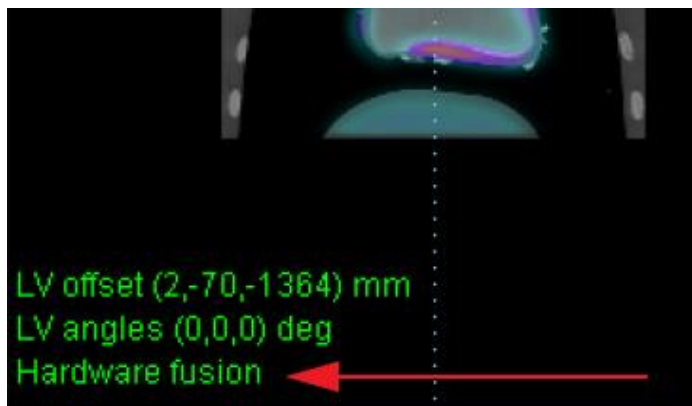
The **Fusion** page provides an image display area comprised of three rows and three columns. The three rows (starting from the top) consist of NM, CT and fused images, respectively. The three columns (starting from the left) comprise the orthogonal views, Coronal, Transverse and Sagittal, respectively.

Visual inspection of the fused images provides an indication of the alignment between the CT acquisition and the NM acquisition. Accurate alignment between the two acquisitions is necessary when applying attenuation correction of PET data using CT data. The degree of misalignment noted on visual inspection will determine if repeat imaging/processing is necessary.

Slice reference lines are provided to allow the user to change the displayed slices interactively using a mouse. Mouse controls are described in the section below.

In addition, keyboard controls (described in the section below) allow manual alignment of mis-registered SPECT/PET and CT data.

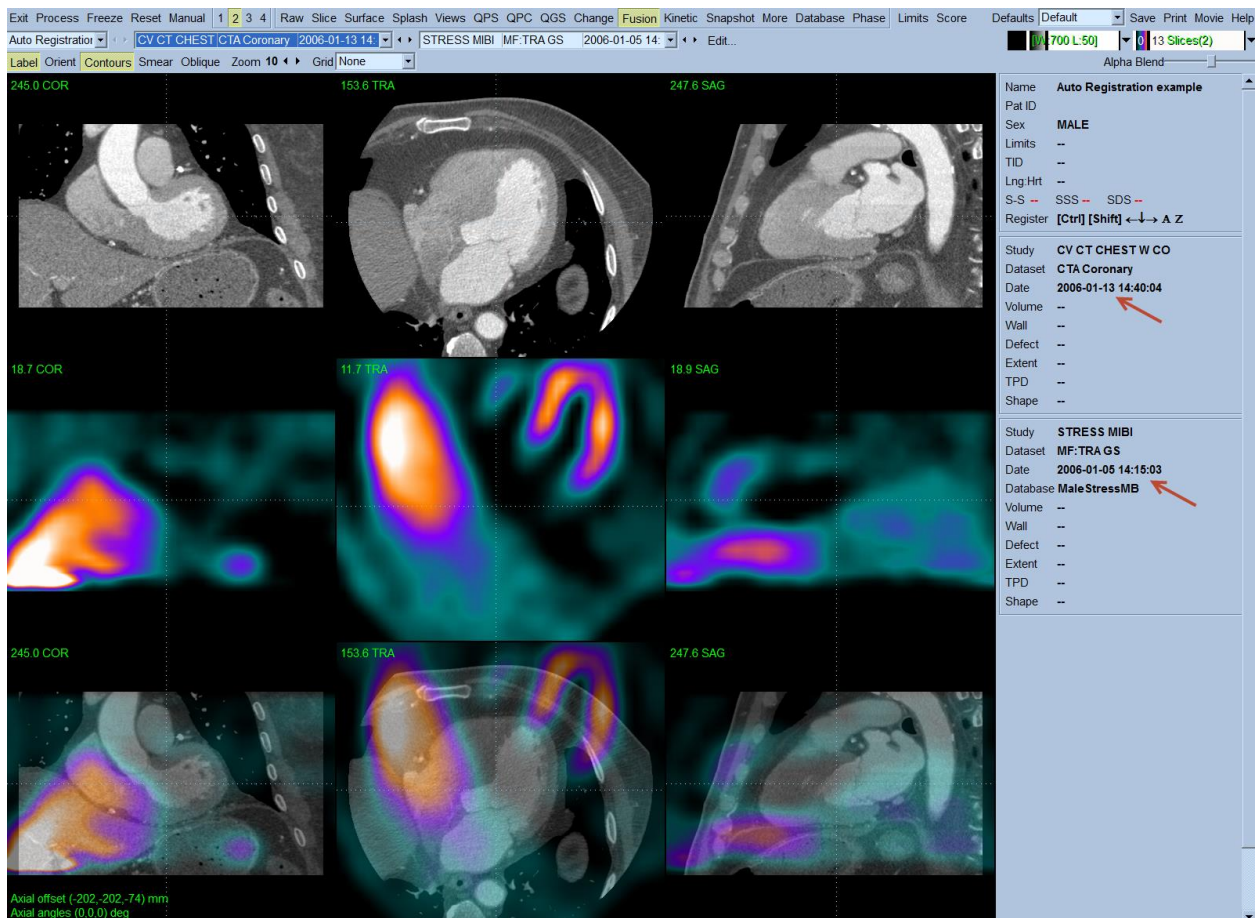
**Note:** The text “Hardware fusion” appears if the data being displayed has already been fused prior to being used in QGS+QPS.



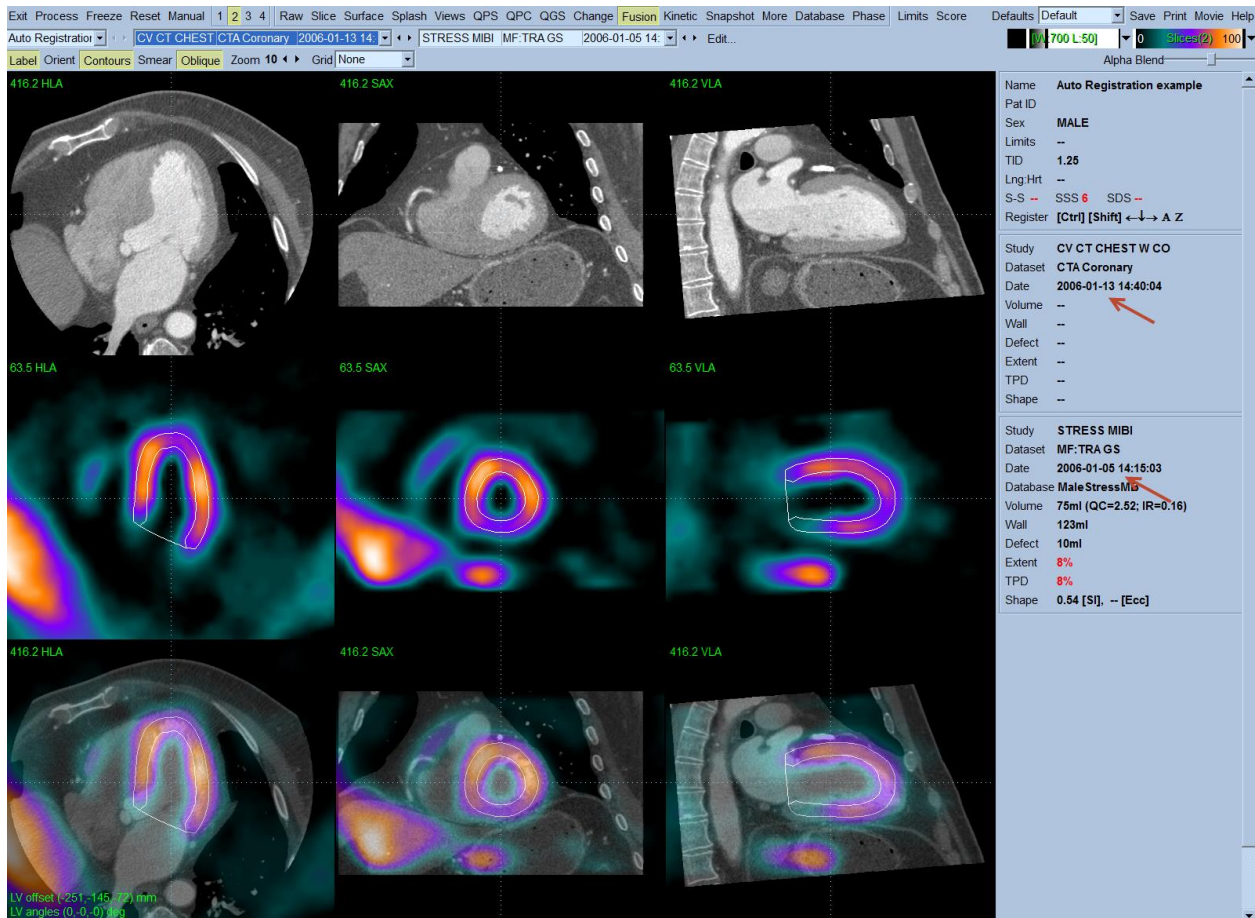
## Automatic Registration

Software co-registration of coronary CTA and MPS images obtained on separate scanners can be acquired rapidly and automatically. Sequential testing by coronary CT angiography (CTA) and myocardial perfusion SPECT (MPS) obtained on stand-alone scanners may be needed to diagnose cardiac disease in equivocal cases. The automatic registration algorithm allows for improved MPS quantification by guiding the co-registered physiologic (MPS) with anatomic (CTA) information. The images below show 1) Fused but unregistered MPS and CTA images and 2) Same images after automated volume registration. As indicated by the red arrows, the CTA and MPS images were acquired serially, about 8 days apart, and on separate scanners.

**Reference:** Slomka P, Cheng V, Dey D, Woo J, Ramesh A, Kriekinge SV, Suzuki Y, Elad Y, Karlsberg R, Berman DS, and Germano G. Quantitative Analysis of Myocardial Perfusion SPECT Anatomically Guided by Coregistered 64-Slice Coronary CT Angiography. *J Nucl Med*, 2009; 50:1621-1630.



1) Fused unregistered MPS and CTA images



## 2) Same images after automated volume registration

The main difficulty in accurate registration of MPS with coronary CTA is that different anatomic features appear on these images. In this technique, the automatic registration algorithm registers pre-segmented MPS volumes using the QGS LV segmentation algorithm and the additional segmentation of the blood-pool region, derived from the MPS LV definition. In addition, to match cardiac phases between the two images, the program aligns the coronary CTA-reconstructed slices in diastolic phases with segmented motion-frozen slices of SPECT created from the gated images. Therefore the success of the auto registration algorithm depends on successful MPS contour determination.

### Controls

The following page specific controls are available:

<b>Contours</b>	Turns contour display on and off. Contours are the intersection of a given slice and the endocardial and epicardial surfaces obtained by QGS+QPS. Note that in the change page only contours from the first study are used and are duplicated for the second study, which is registered to the first.
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<b>Alpha Blend</b>	Sets the opacity level of SPECT/PET images on CT images in the fused image section
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### Mouse Controls

The following page specific mouse controls are available for interactive slice display.

<b>Left-click, hold+drag</b>	Left-click, hold sets the slice reference lines to the current mouse pointer position. Dragging the mouse repositions the slice reference lines on the displayed images and updates the displayed slices.
<b>Middle-click, hold+drag</b>	Allows movement of any of the nine display images within its individual display area. Releasing the middle button resets all other displayed images within their respective display areas.
<b>Right-click, hold+drag</b>	Enables the “Roving window” utility
<b>Double left click</b>	Enlarges the viewport containing the volume (CT, SPECT/PET, or Fused), so that it takes up majority of the screen

### Keyboard Controls

The following page specific keyboard controls are allowed for manual alignment of mis-registered NM and CT data. **Note:** User must click once in image display area to activate the keyboard controls

<b>A</b>	Moves the NM data upwards by one pixel.
<b>Shift+A</b>	Moves the NM data upwards by ten pixels.
<b>Z</b>	Moves the NM data downwards by one pixel.
<b>Shift+Z</b>	Moves the NM data downwards by ten pixels.
<b>Left Arrow</b>	1 pixel left shift
<b>Shift+Left Arrow</b>	10 pixels left shift
<b>Right Arrow</b>	1 pixel right shift
<b>Shift+Right Arrow</b>	10 pixels right shift

Using the Control (Ctrl) key in addition to the above keys performs a rotation of the NM dataset instead of a translation. Rotations are performed in increments of 2 or 20 degrees, depending on whether the Shift key is also pressed.

### Changing the Display of Fused Images

#### Alpha-Blending

Use the **Alpha-Blend** slider to adjust the relative contribution of each dataset to the 2D fusion images. If you position the slider in the middle of the bar, each dataset is equally represented. If you position the slider at the left end of the bar, only images from the primary dataset are

displayed; if you position the slider at the right end of the bar, only images from the secondary dataset are displayed.

### **W/L Image Control Bar (ICB)**

The **W/L ICB** controls the display of CT and CTA images. This ICB only appears in the Fusion page.

The following basic bar configuration options are available in the **W/L ICB colormap** pull-down menu:

- Reset
- Invert
- Step
- Gamma
- Window/Level
- Normalize

The following additional bar configuration options are available only for this ICB:

- **W/L Presets:** These are preset combinations of window and level settings for various types of images. Options include:
  - Lung
  - Fat
  - Water
  - Muscle
  - Liver
  - Bone
  - CTA
  - Edit

Clicking **Edit** opens a Window/Level editor dialog in which you can change and delete presets, and create your own new presets.

The parameters available in the **Defaults** window reflect the Fusion functionality. Additional parameters for which you can select default settings include:

- Application Options
  - W/L preset
- Page options

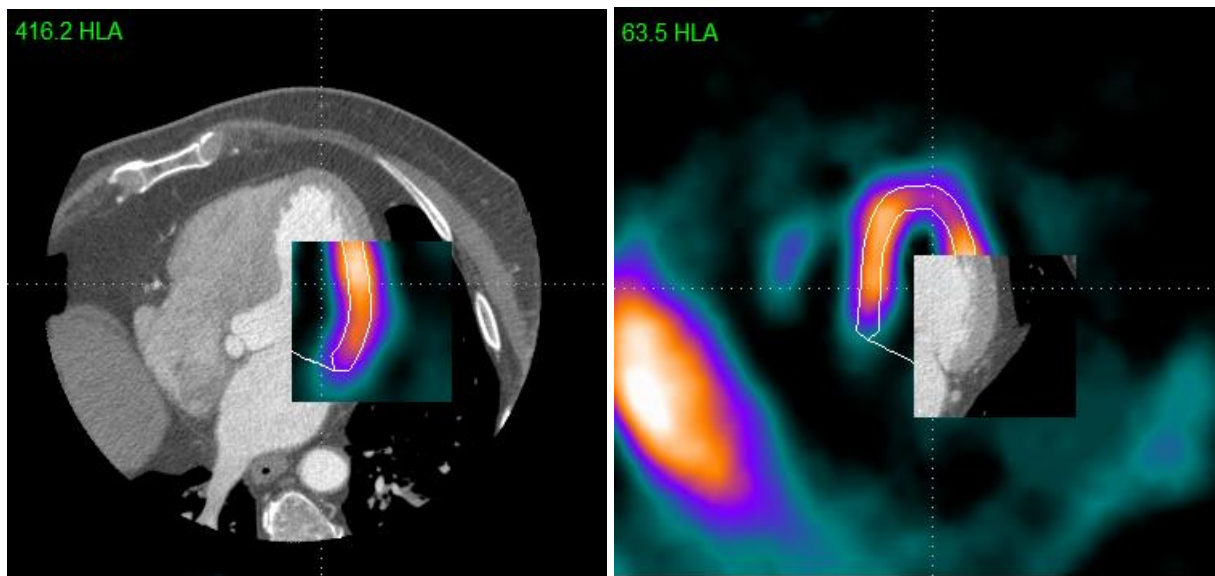
- Fusion window
- Oblique

### Roving Window

The roving window feature allows for quality control of the registration process. The following describes how to use this feature on the **Fusion** page.

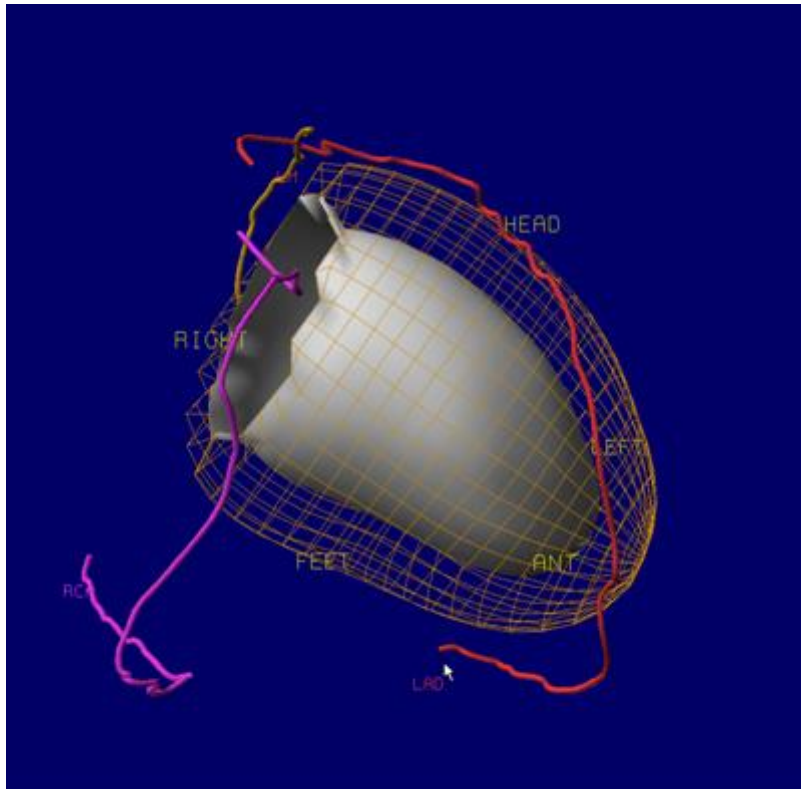
**Note:** The user may wish to enlarge the images prior to performing this step using the **Zoom** page control.

- 1) In the display area, with the mouse pointer on a slice image, click and hold the right mouse button. A rectangular “window” appears containing slice data as follows.
  - a. If the user performed step 1) on a slice in the upper row of slices (CT image), the window contains slice data from the corresponding middle row slice (SPECT/PET image). An example is shown in the below image where the roving window displays the perfusion image overlaid on top of the CT image.
  - b. If the user performed step 1) on a slice in the middle row of slices (SPECT/PET image), the window contains slice data from the corresponding upper row slice (CT image). An example is shown in the below image where the roving window displays the CT image overlaid on top of the perfusion image.
  - c. If the user performed step 1) on a slice in the lower row of slices (Fused SPECT/PET/CT image), the window contains slice data from the corresponding upper row slice (CT image).
- 2) While holding the right mouse button the user can drag the window in that slice area and verify correct registration of the slices by positioning the window over the underlying slice data.





## Coronary CTA Vessels Display



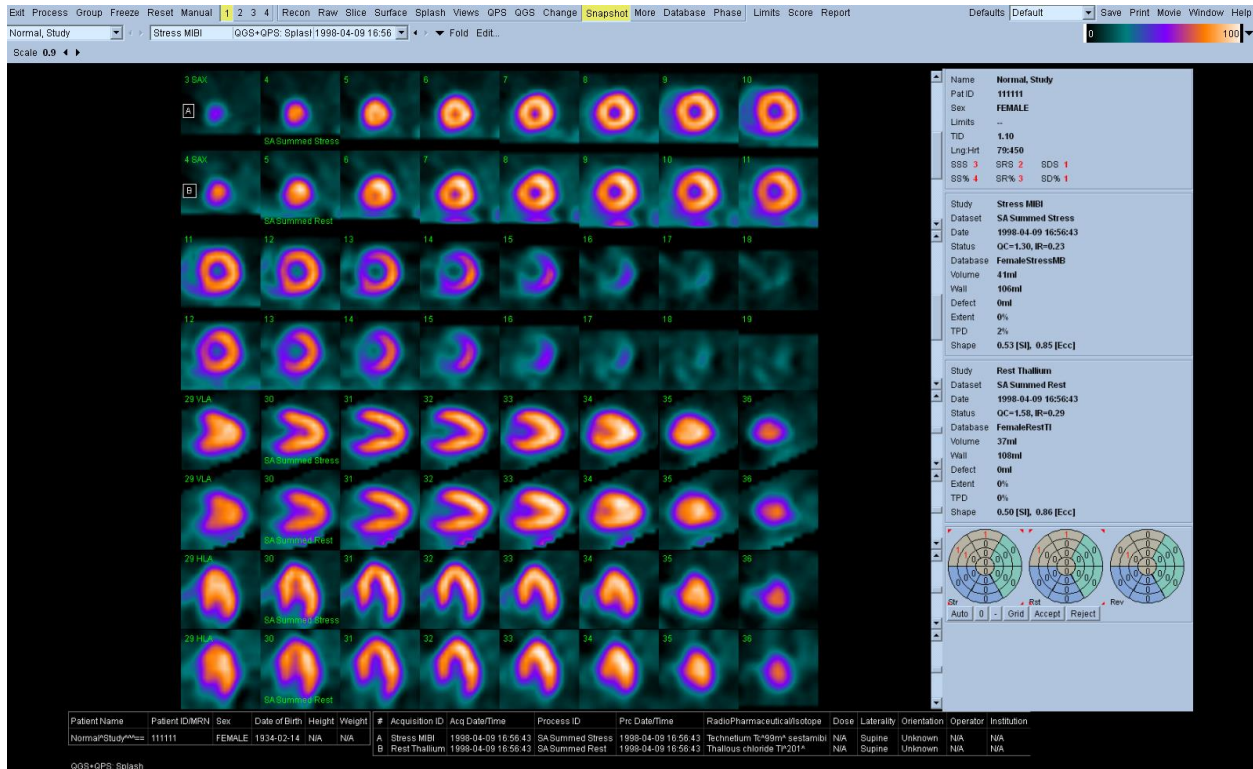
If a segmented and labeled coronary vessel dataset from CT Angiography (CTA) is loaded with SPECT/PET perfusion or PET viability data, the Vessels and Fuse option allows fusion of the coronary vessels extracted from CTA with the 3D surface. The coronary artery tree is extracted and saved as a DICOM object by the vendor's CTA software.

In Surface/Views page the user can click on Vessels label to visualize the loaded segmented coronary vessel with the 3D surface data. Depending on the CTA and SPECT/PET acquisition, the extracted coronary vessels may need further software co-registration. This can be done by pressing Fuse, which co-registers the CTA -extracted vessels to the surface and updates the fusion display.

Note: If the patient name or patient ID is different from that of the perfusion/viability scan, it is necessary to Edit the dataset using the "Edit..." option and use "Attach..." to attach the object to the perfusion/viability study.

### 5.13 Snapshot page

Use the **Snapshot** page to review secondary screen capture files. If you only load snapshot files, QGS+QPS automatically presents the **Snapshot** page. Conversely, if you select the **Snapshot** page, QGS+QPS displays the first, if any, snapshot image files in the pull-down menu.



If the selected image is too large to fit in the image window, you can change the image display in the following ways:

- Drag the image up and down to view the area of the image beyond the window's frame.
- Adjust the Scale factor so that the entire image fits within the image window.

If a Multi-Frame Secondary Capture (MFSC) is loaded, the **Cine** toggle will also be available.

## 5.14 More Page

Attribute	Dataset 1	Dataset 2
<b>PATIENT</b>		
Name	ABNORMAL	ABNORMAL
Patient ID	123456789	123456789
Date of birth	00/00/0000 00:00:00	00/00/0000 00:00:00
Sex	MALE	MALE
Weight	0.00	0.00
Height	0.00	0.00
<b>STUDY</b>		
Acquisition ID	STRESS MIBI	REST THALLIUM
Acquisition time	04/07/1998 12:11:37	04/07/1998 10:19:30
Process ID	SA Stress	SA Rest
Process time	04/07/1998 12:11:37	04/07/1998 10:19:30
Process history		
Organ		
View		
Camera		
Comment		
Miscellaneous		
Isotope 1	Tc-99m	Tl-201
Isotope 2		
Tags		
<b>FILE</b>		
Filename	D:\Hometwsl\db\local\417.gsi	D:\Hometwsl\db\local\416.gsi
Format	GSI	GSI
Format version	1.00	1.00
Source format	ADAC	ADAC
Source version		
Source key		
<b>IMAGE</b>		
Image type	SHORT AXIS	SHORT AXIS
Modality	NUCLEAR	NUCLEAR
Dimensions	64 x 64 x 25	64 x 64 x 24
Voxel size	6.466 x 6.466 x 6.466	6.466 x 6.466 x 6.466
Time per frame	834.000	908.000
Number of heads	0	0
Acquisition zoom	1.460 x 1.460	1.460 x 1.460
Acquisition dimensi...	64 x 64 x 25	64 x 64 x 24
Acquisition voxel size	6.466 x 6.466 x 834.000(t)	6.466 x 6.466 x 908.000(t)
Start angle	315.000	315.000
Angle range	180.000	180.000
Angle direction	CW	CW
Angle step	7.200	7.500
Patient direction	HEAD IN	HEAD IN

The more page displays demographic data from each image dataset header, and can be used to confirm that all relevant fields are filled appropriately.

## 5.15 Database Page

### Overview

QGS+QPS uses normals databases during quantification of perfusion defects by QPS. A normal database is a collection of polar maps derived from a group of normal (typically low-likelihood) datasets. These normal databases are automatically applied to images based on the object attributes. Although the application allows you great freedom in manipulating databases, you must take great care when doing so. Only the proper personnel should attempt this; if you are unsure whether you know enough, find someone who does. Using databases that contain conflicting or incompatible patient data may lead to misdiagnosis.

The screenshot displays the QGS+QPS software interface. The top menu bar includes options like 'Edit', 'Process', 'Group', 'Freeze', 'Reset', 'Manual', 'Recon', 'Raw', 'Slice', 'Surface', 'Splash', 'Views', 'QPS', 'QGS', 'Change', 'Snapshot', 'More', 'Database', 'Phase', 'Limits', 'Score', and 'Report'. The 'Database' menu is currently selected. Below the menu bar, there are several tabs: 'Label', 'Contours', 'Grid', and 'None'. The 'Database' tab is active, showing a list of patient entries on the left. The central area displays four polar maps: 'PATIENT\_01', 'Normal\_Study', 'Database Average', and 'Database Variation'. The right sidebar contains patient and study details, including Name, Pat ID, Sex, Limits, TID, Lung-Hrt, SSS, SRS, SS%, SR%, and SD%. The patient details for 'Normal\_Study' are: Pat ID 111111, Sex FEMALE, Limits --, TID 1.10, Lung-Hrt 79:450, SSS 3, SRS 2, SS% 4, SR% 3, SD% 1. The study details for 'Stress MIBI' are: Dataset SA Summed Stress, Date 1998-04-09 16:56:43, Status OC=1.30, R=-0.23, Database FemaleStressMB, Modality Nuclear, Isotope Tc-99m, Protocol Stress, Orientation Supine, Att Cor Off, Volume 41ml, Wall 106ml, Defect 0ml, Edent 0%, TPD 2%, Shape 0.53 [SI], 0.85 [Ecc], Matrix 64x64 x 19z, and MinVox 6.58 x 6.58 x 6.58.

The PerFusion Quant (PFQ) database page is used to create, modify, and manage normal limits (normal databases), which are used during quantification of perfusion defects by QGS+QPS. A normal database is defined as a collection of polar maps derived from a group of normal (typically low likelihood) exams, where each exam is defined as a SPECT/PET myocardial perfusion dataset and its processed results. Typically, 30-40 normal exams are used in the creation of a given database. Multiple databases can be created and stored on one system. For example, separate databases can be created for stress and rest datasets, or for datasets of male or female patients. Databases can have arbitrary names as specified by the user. In order to match automatically a

given database to a particular dataset during QGS+QPS quantification of perfusion, the user can define database attributes. This will allow assignment of a given database to a given dataset. In a typical quantification of a standard stress/rest myocardial perfusion study, 2 separate databases will be used: one for stress dataset and the second for the rest dataset. Using the limits menu, the user can define a set of limits containing various normal databases. The user limits can then be set as a default in the application defaults editor.

The database page consists of the database control panel and database display panel. The database control panel includes the following items: **Page Specific Controls**, **Database Menu**, **Exam Menu**, **Limits Menu**, **Current Database Attributes**, and **Current Database Exam List**. In the **Database Display Panel** the following 4 polar maps are shown: **Top-left polar map**-exam highlighted in the **Current Database Exam List**, **Top-right polar map**- current exam from the QPSResults page, **Bottom-left polar map**-database Average (Normalized Mean of all exams in the Current Database), **Bottom-right polar map**-database Variation (Normalized Variation of all exams in the Current Database). Exam selection in the **Current Database Exam List** can be interactively changed and polar maps for all cases included in a given database can be quickly previewed in this manner as a quality control measure.

#### **Difference between a database file and a limits file**

A Limits file is a collection of normal databases. The goal of a limits file is to allow the user to quickly select a subset of databases based on a unique protocol or camera. It's recommended for a site to configure the selection of their most popular protocol as the default matching criteria and create a limits file for quickly applying a new set of databases.

When using batch processing (processing of multiple studies within a single application session), manually selecting a normals limit applies that limit to all the studies that are loaded in the session.

Using the **Database** page, you can review and modify user-defined Normals databases, Limits, and associated files. You can also generate your own Normals databases according to your patient population and the specific protocols and isotopes used at your facility.

#### **Page Specific Controls**

The following Database page specific controls are available:

Label	Turns labeling on and off for the polar map of the current QGS+QPS exam. Labeling consists of segments, vessels, or walls (if enabled) for the polar maps.
Contours	Turns contour display on and off for the polar maps for the current QGS+QPS exam. This will toggle display of the valve plane position display on the polar map.
Grid	Selects the grid mapping mode (None, Segments, Vessels, and Walls) for the current QGS+QPS exam

### Database Menu

New	Create a new database.
Open...	Open a dialogue, which allows selection of a previously created database.
Save	Save a modified database under current name.
Save As...	Save a database using modified name.
Backup...	Open a dialogue, which allows backup of all defined databases to a separate directory.
Restore...	Open a dialogue, which allows selective restoration of databases from a directory containing one or more database files. Existing databases with the same name will be renamed.
List...	Open a view window, which lists all defined databases and their attributes.
Import...	Open a dialogue, which allows importing a single database from a user specified location.
Export...	Open a dialogue, which allows exporting a single database to a user specified location.
Anonymize	Remove patient names and other identification from the current database.
Delete...	Open a dialogue, which allows deletion of a previously created database.
Close	Close the currently open database.

### Exam Menu

Add Current	Add the current QGS+QPS exam, if processed and of valid type, to the Current database.
-------------	--

Add All	Add all loaded QGS+QPS exams, if processed and of valid type to the Current database.
Delete Selected	Delete the exams selected in the Current Database Exam List from the Current Database.
Mismatch Check	When selected – a check is performed during adding of new exams to the current database to verify if the added exams match the attributes (such as Sex, Protocol) of Current Database.
Duplicate Check	When selected – a check for existing duplicates in the Current Database is performed during the process of adding new exams to the current database.

### Limits Menu

Create	Create a new user normal limits file.
Edit	Edit an existing normal limits file
View	View the contents of an existing normal limits file.
Delete	Delete an existing normal limits file.

### Current Database Attributes

Current Database Attributes define the type of studies which are included in the database and which will be matched during processing. These attributes are listed below.

File	Name of <b>Current Database</b> .
Modified	This checkbox notifies the user that some attributes or exam selection have been changed in the <b>Current Database</b> . This field is read-only.

Description	Optional text description for the <b>Current Database</b> .
Allow automatic selection during processing	When checked, it enables the automatic matching of a given database to the type of the processed exam. By selecting this option, the <b>Current Database</b> becomes default for the exam with matching combination of attributes (such as Sex, Protocol, Orientation etc.). Note, it is possible to have more than one matching database for a given exam. The first (alphabetically) matching will be applied in such case. By default, this option is disabled. If the user wishes that the database be matched automatically, this option should be enabled. If there is no appropriate database matched during processing, the database can be selected manually using the Dataset Editor Database field ( <b>Edit ...</b> button) on the QPSResults page
Sex*	Defines the Sex attribute (Any, Female, Male) for the exams in the <b>Current Database</b>
Protocol*	Defines the acquisition protocol (Any, Stress, Rest) for the exams in the <b>Current Database</b>
Orientation*	Defines patient orientation (Supine, Prone, Any) for the exams in the <b>Current Database</b>
Isotope*	Defines the Isotope for the exams in the <b>Current Database</b> .
Modality*	Defines the Modality of the exams in the <b>Current Database</b> .
Att Cor*	Defines the Attenuation correction attribute (AC, NAC, Any) for the exams in the <b>Current Database</b> . Currently not used.
Study Filter**	Text string to be matched in the Study header field of the exams included in the <b>Current Database</b> .
Dataset Filter**	Text string to be matched in the Dataset header field of the exams included in the <b>Current Database</b> .
Isotope Filter**	Text string to be matched in the Isotope header field of the exams included in the <b>Current Database</b> . This is an alternative method for matching the databases by isotope during QGS+QPS processing.
Camera Filter**	Text string to be matched in the Camera header field of the exams included in the <b>Current Database</b> .

\* It is highly recommended to not leave 'Any' selected in the drop down, as this can lead to <Multiple Matches><Multiple Matches> errors.



\*\*It is recommended to leave these empty.

### Creating a New Database

These are steps to follow when creating normal databases:

1. Select all exams, which should be included in the new database and load all these patients in the QGS+QPS program. These should be normal short-axis myocardial perfusion datasets of low-likelihood patients.
2. Make sure that all datasets are processed by QGS+QPS, that all the contours\* are defined correctly, and that there are no obvious perfusion defects in the images.
3. Go to the database page and from the Database Menu, select New, which will clear all the attribute fields in the Current Database Attributes panel.
4. From the Exam Menu select Add All. This will populate the Current Database Exam List.
5. Specify all required database attributes. Note that if "Any" is selected for a particular attribute, the program will not consider this parameter during auto-matching when running QGS+QPS.
6. If you like the created database to become default for perfusion quantification of exams with a given combination of attributes, enable Allow automatic selection during processing option. Note that if multiple matching databases are available the program will produce message "Multiple matches" during the quantification. In such a case user must select the desired database manually.
7. To anonymize the database and remove all patient information from the created database, select Anonymize from the Database Menu. Generic patient names will appear in the Current Database Exam list.
8. From the Database Menu select Save As... This will bring up a dialogue in which existing database names are shown. Type in a new name in the text-box below the list of Database names and Click OK.

\* The user must verify correct contour creation. If contours appear too long, too short or do not encompass the myocardium, they should be manually adjusted and saved. Incorrect contours generated for the normal limits population will degrade the quantification results when applied to clinical studies.

### Adding Patients to a Database

1. Start QGS+QPS with the studies to be added.
2. Make sure that all patients are processed and contours for all studies are defined correctly.
3. From the Database Menu, select Open... and select the database to modify.
4. From the Exam Menu, select either Add Current to add the current patient, or Add All to add all currently open patients.
5. From the Database Menu, select Save. This will overwrite the selected database with the modified database, which includes additional patients.

### Removing Patients from a Database

1. From the Database Menu, select Open..., and select the database to modify.
2. Select the patient(s) to delete from the database exam list.
3. From the Exam Menu select Delete Selected. This will update the database exam list.
4. From the Database Menu, select Save. This will overwrite the selected database with the modified database which does not include deleted patients.

### Creating a New Normal Limits File

1. From the Limits Menu, select Create...
2. From the Create Limits window, select Add to open the Limits Database selection window.
3. From the Limits Database window, select a database to add.
4. Repeat step 3 until all database files required have been added.
5. From the Create Limits window, select Save to open the Save Limits window
6. From the Save Limits window, enter an appropriate name for this limits file and click OK.

### Editing a Normal Limits File

1. From the Limits Menu, select Edit...
2. From the Edit Limits window, select limits file to edit and click OK.
3. From the Edit Limits-limits file window, Add, Remove or Clear database name as necessary.
4. Click Save to save with the current limits name. Click Save As to save limits with a new file name preserving the original limits name and entries. Click Cancel to abort the editing process preserving the original limits file and entries.

### Viewing a Normal Limits File

1. From the Limits Menu, select View...
2. From the View Limits window, select a limits file.
3. The View Limits-limits file window displays the current database entries for the selected limits file.

Click Dismiss to close the View Limits-limits file window

### Deleting a Normal Limits File

1. From the Limits Menu, select Delete...
2. From the Delete Limits window, select a limits file to delete.
3. Click OK to delete the limits file.

### Backing up Database Files

After modifying or creating a limits database it is recommended to backup all databases.

1. From the Database Menu, select Backup...
2. From the Backup Databases to Directory window, select a location (directory) to backup to.

3. Click OK to backup files. All database files will be copied to the directory selected in step 2.

### Restoring Database Files

1. From the Database Menu, select Restore...
2. From the Restore Databases from Directory window, select a directory where previously backed up databases are located.
3. From the database list window, select database(s) to restore. Existing databases with the same names will be renamed.
4. Click OK to restore files. All database(s) selected will be restored to their original location.

### View List of Existing Database Files

1. From the Database Menu, select List...
2. A Database List window shows the existing databases files on the system.
3. Click Dismiss to close the window.

### How databases are automatically matched

When the application loads each perfusion dataset it attempts to match it with a perfusion database. Only databases with the ' Allow automatic selection during processing' flag will be considered during automatic processing. Databases with this flag should be the 'default' databases to consider.

The application matches based on the information in the Current Database Attributes.

The most important matches are the non-string matches: Sex, Protocol, Orientation, Modality, Isotope, and Attenuation Correction. These are most important since identification of these parameters are explicitly defined in the DICOM file, which leads to reliable identification. String matching (Study, Dataset, Isotope and Camera Filters) is considered less reliable, since different camera manufactures often use different nomenclature for these fields. In nearly all cases, the explicit Isotope dropdown should be used in place of the isotope filter.

For string matching, the database must contain the code in order to be matched. Multiple codes may be used as a comma separated list. Each entry in the list may appear anywhere in the field. For example, if the database had a Study filter of 'STRESS' defined, it would match:

```
"PERFUSION STRESS"  
"STRESS PERFUSION "  
"REST-STRESS PERFUSION "
```

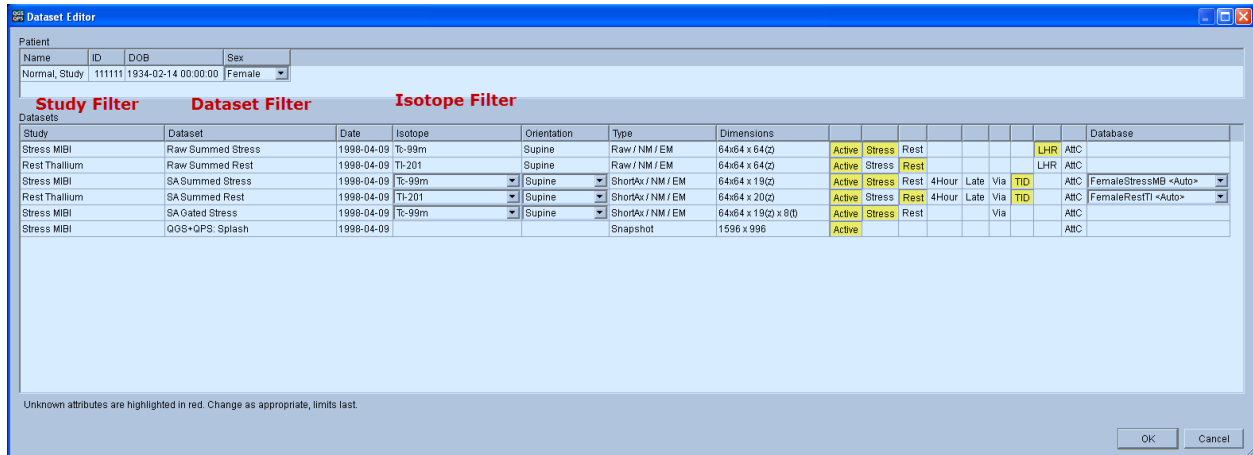
but would not match

```
" PERFUSION STR"  
"R_S_F"
```

However a study filter of '\_S\_,STR', would match all the above datasets, but would also match:

```
"REST STRESS"  
and  "STRICT PROTOCOL"
```

## Advanced Database Matching



Starting with v2012, there is 'String Matches Best' policy. This means that if multiple matches occur and one of the databases is more specific (due to a string filter), then that database will be selected over the 'generic database'. For example:

If you have two databases defined as:

Sex: Male Protocol: Stress Orientation: Supine Isotope: Tc99m Att-Cor: Off Modality: SPECT Camera Filter: **<blank>**

Sex: Male Protocol: Stress Orientation: Supine Isotope: Tc99m Att-Cor: Off Modality: SPECT Camera Filter: **cardioMD**

In previous versions, of the software you would receive <Multiple Matches> if a CardioMD dataset was encountered. The new version of the software allows the user to specify more specific string criteria and have both databases available during automatic selection, and in those cases the more specific database will be automatically selected.

### User Limits

When a database is included in a limits file the same matching criteria above is applied with one key difference: The ' Allow automatic selection during processing' is only true for databases in the list. This means that only the databases listed in the limits file are available for selection.

For example, the SepDualAuto Limits file includes the following databases:

- FemaleRestTL
- FemaleStressMB
- MaleRestTL
- MaleStressMB

If you wanted to setup the default database selection to use MibiMibi databases, you should make sure that the correct normal limits databases get applied to your datasets. For example, if you were to load a MibiMibi study, applying the SepDualAuto Limits would remove any matching normals databases for the rest datasets. Since normal limit databases are automatically applied to the images, it is usually not necessary to apply a limits file. However, the use of limits can be particularly useful if you have multiple matches.

#### <Multiple Matches>

The multiple matches error occurs when more than one database is matched. This is typically caused by one of the databases containing an 'Any' option in the explicit fields. Note that only databases with the 'Allow automatic selection during processing' flag set would cause this error, unless a limits file is selected. This is best diagnosed from the 'List' option in the database page. See

How **databases are automatically** matched for more information.

#### <No Matches>

This error occurs if no suitable databases can be found for the specified datasets. This is best diagnosed by identifying the database you think should have been automatically selected and comparing the database attributes (Database Page) to the attributes in the dataset. Likely causes are:

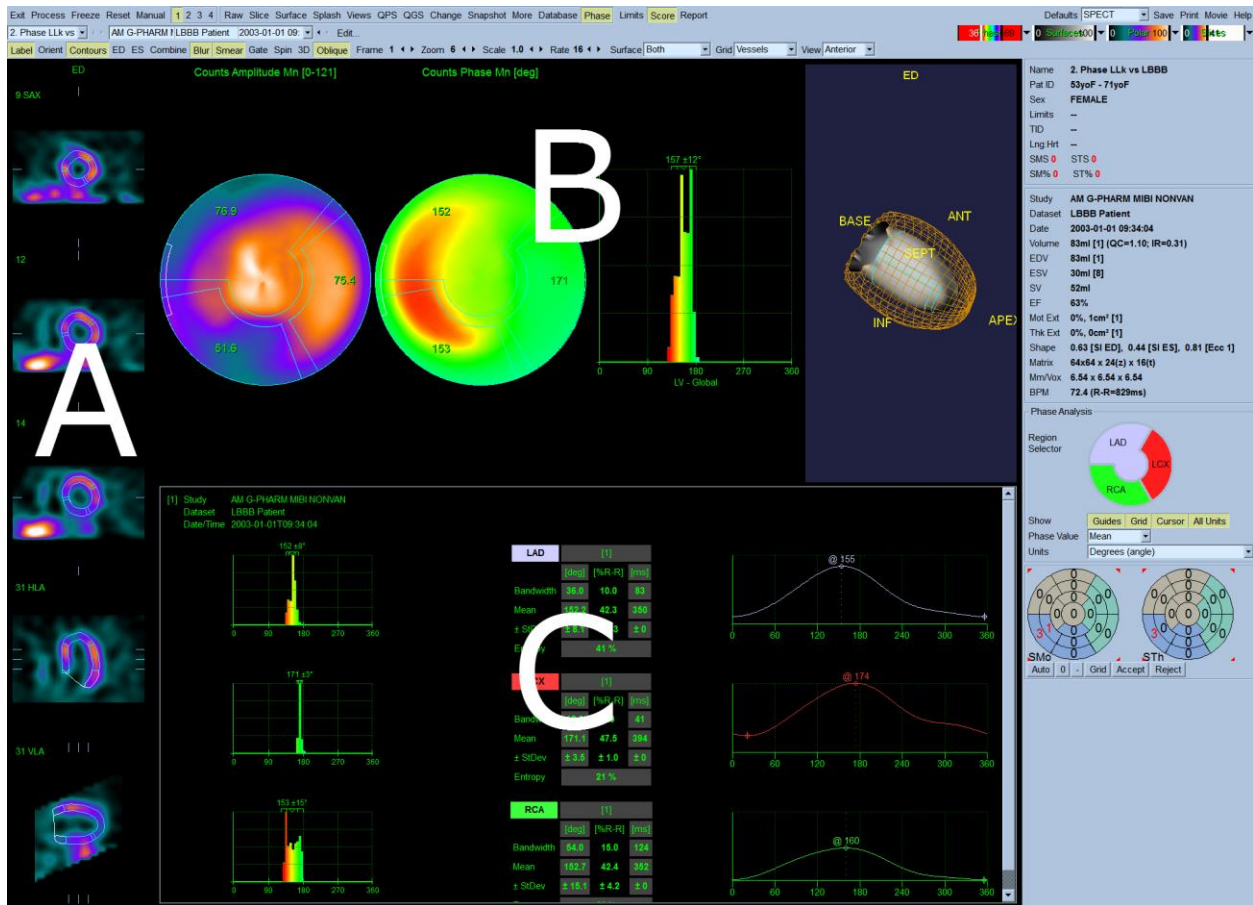
- The database uses string matching (filters) and they are not matching
- The database isn't selected as 'Allow automatic selection during processing'
- The selected limits file doesn't contain database

## 5.16 Phase Page

Phase Analysis is used to assess left ventricular dyssynchrony based on thickening information derived from count variations throughout the cardiac cycle. To view global and regional phase information for gated studies, click the **Phase** page button.

The Phase page is divided in 3 main sections:

- The left side (A) displays slices (3 short axis, 1 horizontal long axis and 1 vertical long axis) for up to 4 datasets.
- The top portion of the right side (B) displays global phase information for each dataset: parametric phase polar maps (switchable to 3D views), the global phase histogram, and a surface view that can be gated. Global information is displayed for up to 4 datasets
- The bottom portion of the right side (C) displays regional phase information. In single dataset mode, this includes regional phase histograms as well as regional time/activity curves. In dual dataset mode, only regional phase histograms are displayed. Regional information is not available in 3- and 4-dataset mode.



If the **Grid** toolbar setting is set to **None**, global statistics will be shown in the regional area. If a grid such as **Vessels** (shown above) is selected, statistics are shown for each region. Use the **Combine** toolbar toggle to switch between separate and combined phase and amplitude polar maps or parametric surfaces. The additional controls made available in the info box (right side of the application) control display options such as a real-time graph cursor or display units, and the polar map toggle allows the regional display to be restricted to certain regions only.

## Requirements

The phase analysis feature requires at a minimum one processed gated dataset. The gated acquisition can be eight or sixteen frames per cardiac cycle, however, sixteen-frame gating is recommended for increased accuracy of ejection fraction and diastolic function calculations. Other gating options (such as 12 or 32 gates) should be admissible but have not been validated.

## Reviewing Results

### Phase calculations

Gated short-axis images are segmented using a modified version of the QGS algorithm that provides new global and regional quantitative parameters for the assessment of intra-ventricular dyssynchrony. The QGS algorithm operates by first computing a mid-myocardial LV surface. It then computes endocardial and epicardial surfaces using count-profile and thickening

information derived from myocardial mass conservation combined with count increases caused by partial-volume effects. For the phase analysis algorithm, a unidimensional array is created for each spatial sampling point that contains the local maximum myocardial counts at each interval, obtained by searching between the epicardium and endocardium along a direction normal to the mid-myocardial surface. This array represents a time-varying, periodic function from which the first Fourier harmonic (FFH) is determined, the phase angle of which forms the basis of all of the synchrony measurements. Amplitude information is used by the algorithm to eliminate phase measurements for which the corresponding amplitude was deemed too low to yield accurate measurements: 5% of the samples corresponding to the lowest amplitudes across the whole myocardium are automatically removed from the analysis because phase measurements are essentially ill-defined for signals that exhibit low temporal variations.

Phase values can be expressed in degrees [deg] (0-359), in milliseconds [ms] with heartbeat length information that is available in the dataset header (assuming a default heart rate of 60bpm if the actual beat length is not available), or as a percentage of the cardiac cycle duration [%cy] (0-99). Amplitude is expressed in counts, and quantitative values should only be used in relative terms as scaling of the dataset's voxel values may have occurred.

### **Regional values**

Once timing parameters have been calculated for all sampling points, multiple global and regional LV synchrony measures are computed on the basis of whole-ventricle, wall-based, vessel-based, and segment-based (17 or 20 segments) statistics. Within any region the following values are calculated and can be displayed on the polar map: mean (average over the region), standard deviation, mode (location of the peak of the distribution of values), and entropy. The entropy  $E$  is calculated for the distribution of values as follows:

$$\frac{-\sum_{i=1}^n f_i \times \log_e f_i}{\log_e n}$$

The formula used to compute  $E$  is shown above, in which  $n$  represents the number of histogram bins,  $f_i$  is the frequency of the histogram bin  $i$  (i.e., the number of measured phase angles that fall within bin  $i$  divided by the total number of phase-angle measurements in the histogram; range, 0. . .1), and  $\log_e x$  is the natural logarithm of number  $x$ .

Mean and mode are indicators of regional value and can be used to evaluate interregional variations, while standard deviation and entropy measure intraregional variability.

### *Global values*

To provide an assessment of global ventricular synchrony, the phase panel includes the global LV entropy. This value is calculated as indicated in the previous section, with the calculation extended to all LV samples.

**Note:** the type of value provided in this space may change in future releases as the clinical value of this information is assessed.

### *Global vs. Regional values*

Generally for global dyssynchrony assessment variability measures such as standard deviation, bandwidth, and entropy are most useful. For regional dyssynchrony assessment the comparison of the regional means or modes may be most useful. In particular, small regions (such as those in 17-segment mode) may not contain enough data samples to provide useful variability measures.

### *Phase-related graphs and histograms*

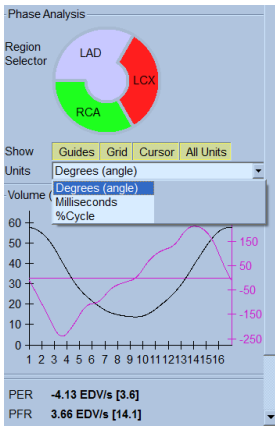
The following options are available to control the display of phase graphs and histograms:

- **Regional Selector:** These controls are used for showing thickening and regional counts curves, as well as phase histograms. The following controls are available:

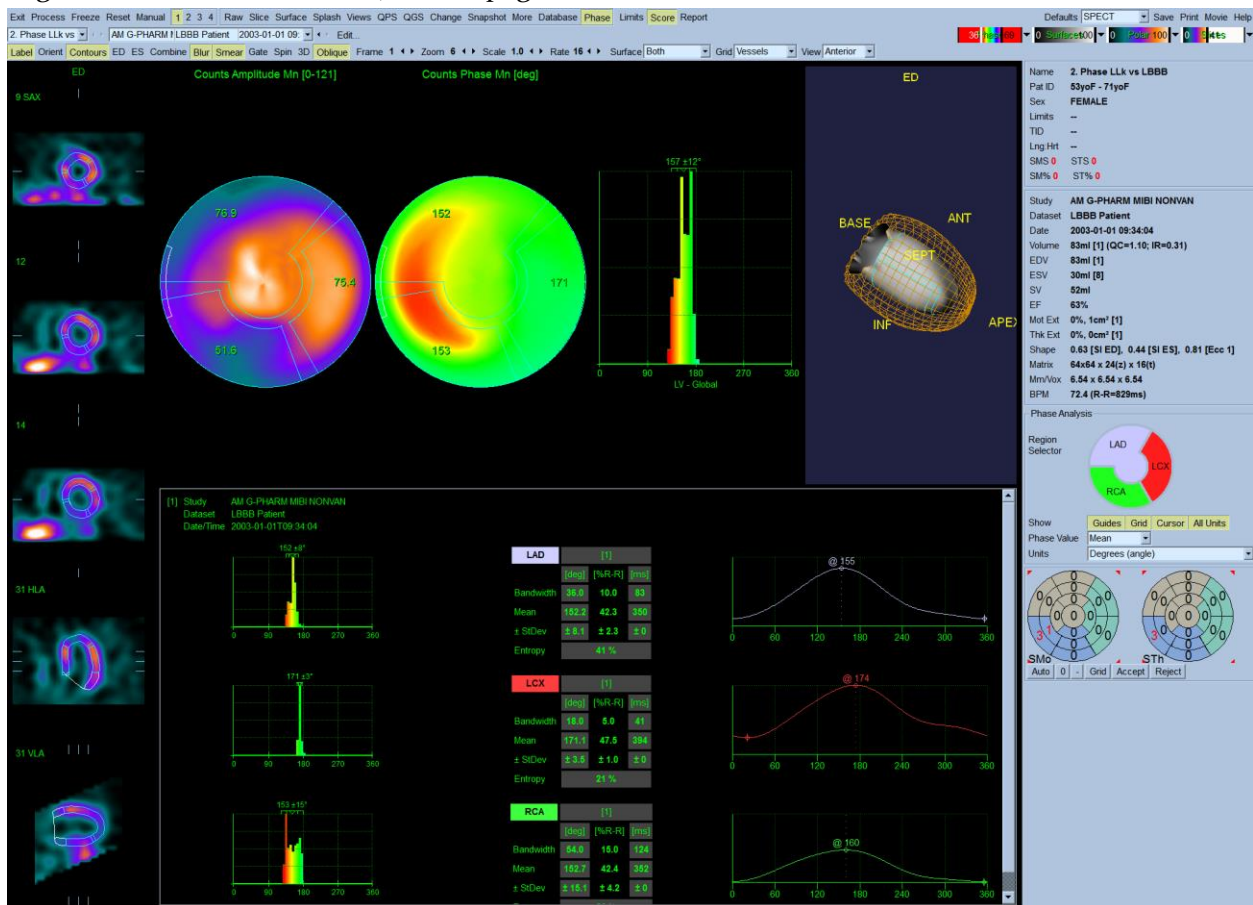
Guides	Toggle shows or hides guidelines that indicate the location of the minimum and maximum displacement and maximum (positive and negative) velocities.
Grids	Toggle shows or hides gridlines for time values.
Cursor	Toggle turns the interactive value readout cursor on or off.
All Units	Toggles “on” display of all dyssynchrony values in degrees, % cycle, and milliseconds.

- **Units** drop-down: this control determines how timing values are displayed in the polar maps. Options are: **Degrees**, **Milliseconds**, and **%Cycle**. If the dataset header does not contain heartbeat length information, a 60bpm heart rate is assumed for all timing calculations, as is done elsewhere in QGS+QPS (e.g., for diastolic function calculations).





The phase info box section is also affected by settings of the Phase page: the regions and the units selectors determine respectively which regions are displayed and whether timing information is shown in degrees, milliseconds, or % R-R. Regions are determined by the **Grid** settings (None, Segments, Vessels, and Walls) on the page control bar.



The Region map allows the user to interactively select which curves or histograms are displayed. Clicking the mouse in a region will toggle “on” or “off” the corresponding displacement and velocity graphs allowing selective viewing of graphs.

## Comments

Normal limits or expected values for these measurements have not yet been derived by the AIM Program at Cedars-Sinai for myocardial perfusion gated SPECT/PET.

## 6 Manual Mode

7 SAX | 10 | 13

32 HLA | 32 VLA

1. Position short axis crosshairs over LV center.  
2. Position long axis line end-points over LV apex and base.  
3. Position mask outside of LV.  
4. Select Localize (limits initial LV search to mask) and then process.  
5. If necessary: reprocess with Mask (disregards all counts outside of mask) and/or Constrain (locks LV apex and base).

Name	Normal_Study
Pat ID	111111
Sex	FEMALE
Limits	--
TID	1.10
Lng Hrt	79:450
SSS	3
SRS	2
SDS	1
SS%	4
SR%	3
SD%	1

Study	Stress MBI
Dataset	SA Summed Stress
Date	1998-04-09 16:56:43
Status	OC=L30, IR=0.23
Database	FemaleStressMB
Volume	41ml
Vwall	106ml
Defect	0ml
Extent	0%
TPD	2%
Shape	0.53 [SI], 0.85 [Ecc]
Matrix	64x64 x 19(z)
Mm/Vox	6.58 x 6.58 x 6.58

Manual mode is used to supply hints (constraints) to the LV segmentation algorithm in cases where the fully automatic LV segmentation fails or returns unsatisfactory results. For best reproducibility, the weakest possible hint or combination of hints that returns satisfactory results should be preferred. These hints are provided using essentially the same interface as the slice page, with masking graphics (volumetric ROIs) superimposed upon the slices. The shape and position of the masking graphics, which are initially configured to resemble an idealized LV, can be changed by dragging its handles (the small blue boxes).

To apply manual corrections, the mask should first be shaped and positioned so that it encompasses the LV while excluding all extra-cardiac activity (before doing so, it may be advisable to toggle the incorrect contours off by clicking the **Contours** button). Then try

processing with a suitable combination of hints enabled (when the **Process** button is pressed all enabled hints are applied).

The available hints, in order of increasing strength (i.e. decreasing preference) are:

<b>Localize</b>	Restricts the initial LV search to the volume defined by the masking graphics. Use if the algorithm completely missed the LV.
<b>Mask</b>	Restricts the entire LV segmentation algorithm to only use data within the volume defined by the masking graphics. Use to exclude extra-cardiac activity (e.g. spleen) that caused contours to be distorted.
<b>Constrain</b>	Constrains the long axis used by the LV segmentation algorithm to lie on the end-points (apex and base) specified by the masking graphics. Use to force valve-plane to be at a specific basal position.

## 6.1 Quality Score

Two major types of segmentation failures are observed in clinical practice, incorrect LV shape determination and incorrect valve plane positioning. The new quality score (QS) feature aims to provide the user with a reliable contour quality feedback that issues a warning if the LV contours are incorrect and need manual adjustments. There are two components to quality score, which are QC and IR. QC refers to the shape quality control (SQC) and IR (Intensity Ratio) refers to the valve plane quality control (VQC). Quality Score currently only warns users of incorrect contours based on shape quality control (SQC) parameters. IR (Intensity Ratio) or VQC (valve plane quality control) is not currently being used to generate the warning flags.

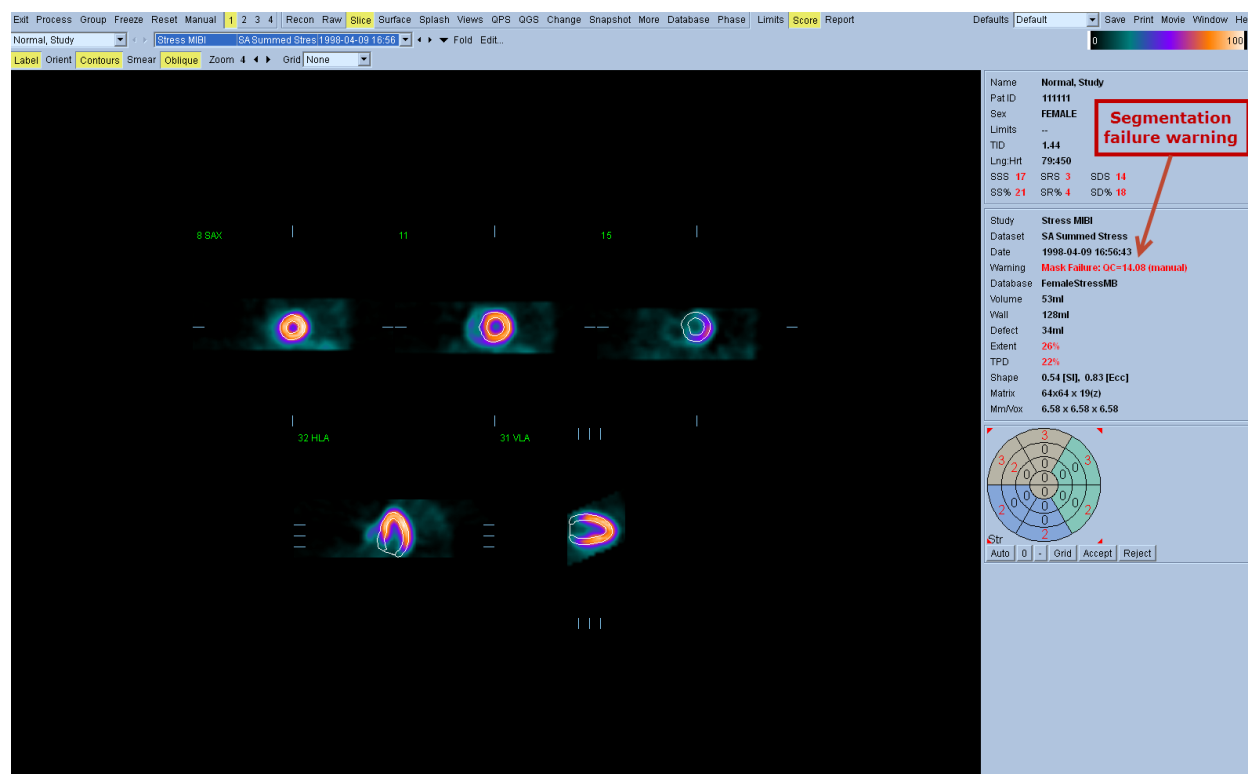
### Shape Quality Control

The shape QC parameter of Quality Score uses the following 8 unique shape parameter (7 for non-gated datasets) to generate its numerical value. This shape qc value is assigned to each volumetric short axis dataset loaded into QGS+QPS. A red warning message flag is displayed only if the shape qc value is above the normal threshold ( 7.0 for gated datasets and 4.11 for ungated or summed datasets).

- LV orientation – Long-axis angle
- Area – Normalized VP area
- Volume
  - Normalized volume difference
  - LV volume (nongated)/end-diastolic LV volume
  - Stroke volume (gated images only)
- Eccentricity
  - Long-axis eccentricity
  - Short-axis eccentricity
- Intensity – Normalized count deviation

## Valve Plane Quality Control

The valve plane quality control (VQC) parameter qualifies valve plane overshooting (VPO) as well as undershooting (VPU), usually caused by low myocardial photon counting statistics, especially in the basal region. VQC is calculated based on the intensity ratio (IR) around the valve plane to detect VPO or VPU failures. The Quality Score feature currently does not consider the intensity ratio when displaying a failure warning.



Quality Score validation shows excellent sensitivity and high specificity for incorrect LV shape determination (SQC) and high sensitivity and reasonable specificity for the detection of incorrect position of the valve plane (VQC). However SQC currently only includes specific parameters for evaluation mask-failure cases. These may not be able to capture all of the LV shape details. It is recommended that the Quality Score feature be used as a quality control aid. As shown in the above screen capture, the contours should be visually verified any time a segmentation failure warning is displayed.

Reference: Xu Y, Kavanagh P, Fish M, Gerlach J, Ramesh A, Lemley M, Hayes S, Berman DS, Germano G, Slomka P. Automated Quality Control for Segmentation of Myocardial Perfusion SPECT. J Nucl Med 2009; 50:1418-1426.

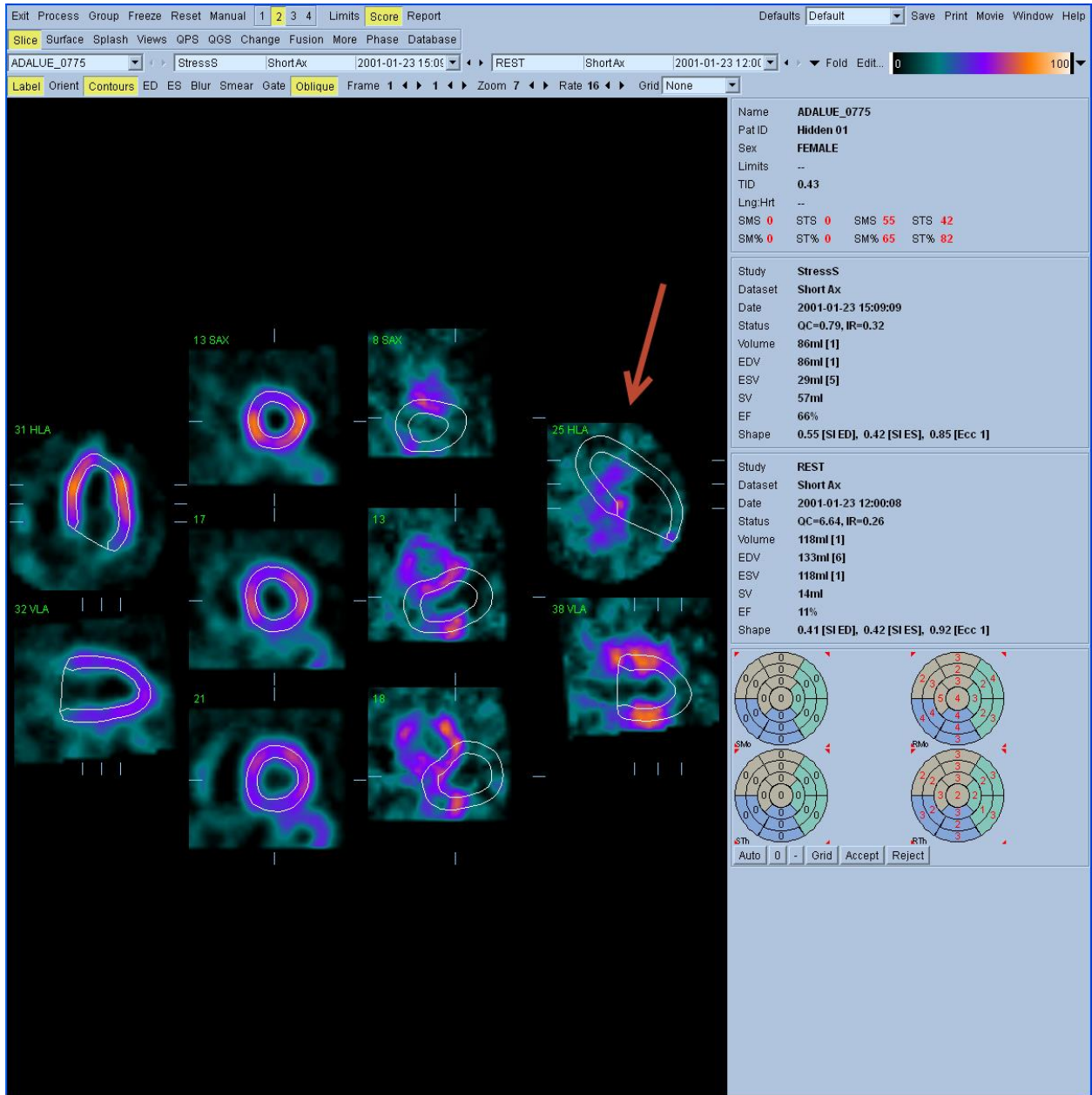
## 6.2 Group Processing

We consider the reproducibility of measurements of cardiac perfusion and function from gated SPECT and gated PET images to express the agreement between values obtained by applying a computer algorithm twice to the same image dataset. Therefore, reproducibility is proportional to the degree to which the algorithm is automated. Measurements from automated, “push-button” algorithms that operate in a deterministic manner are, by definition, perfectly reproducible, regardless of when or by whom the button is pushed. On the other hand, algorithms that require some degree of operator interaction will have less than perfect intra- and inter-operator reproducibility. High reproducibility means small differences ( $\Delta$ ), so we can describe it in terms of a quantity  $\Delta_{\text{repro}}$  that should be minimized.

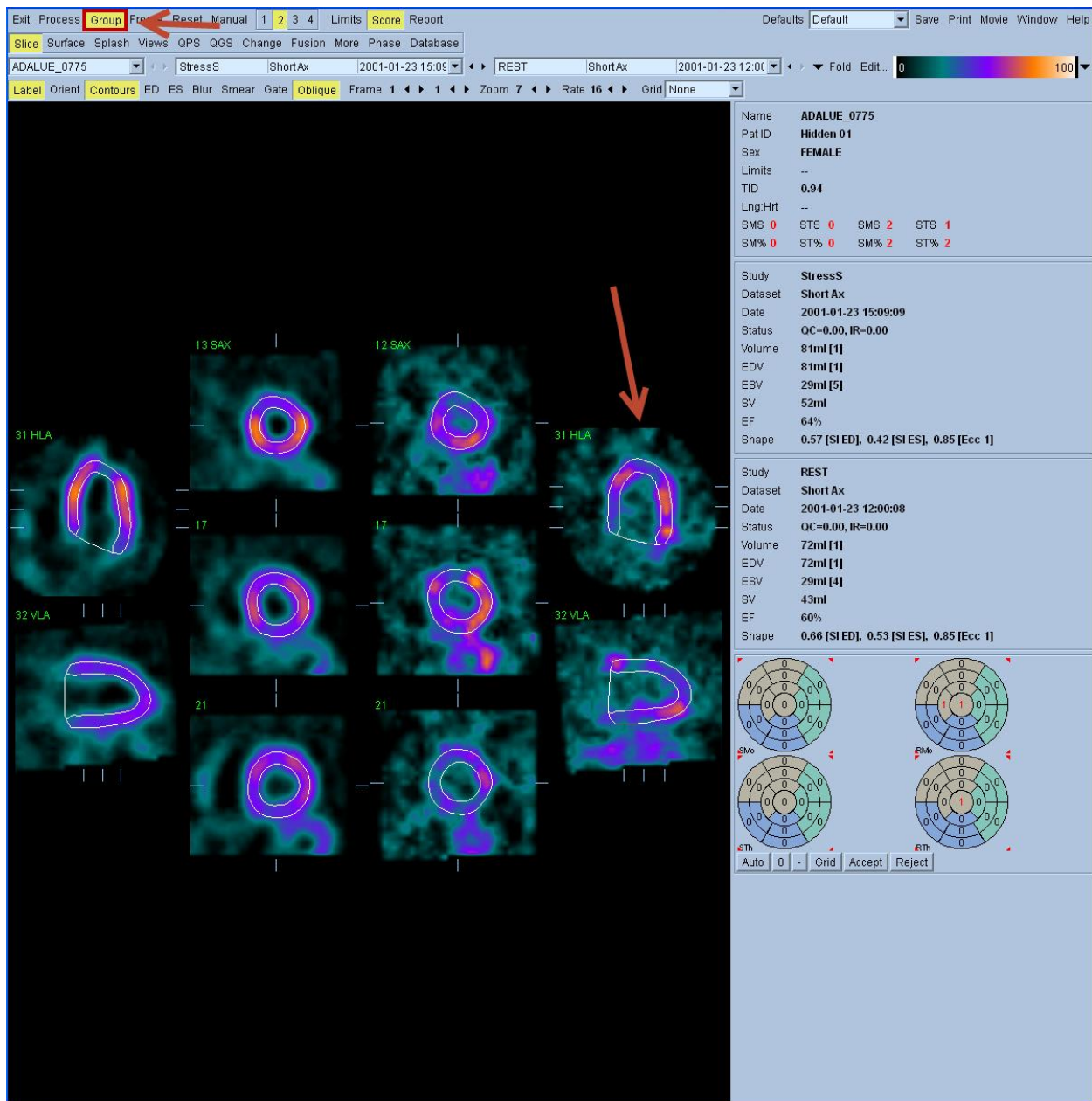
Conversely, repeatability of measurements is related to applying a computer algorithm to two separately acquired image sets belonging to the same patient (images ideally acquired without changes in the acquisition protocol or patient condition), and measuring the difference between the quantitative results. Low repeatability can be due to (a) changes in the acquisition setup (the patient moved, the radiopharmaceutical uptake pattern changed, gating abnormalities occurred), (b) changes in the reconstruction and reorientation parameters used to generate the tomographic images input to the algorithm, (c) changes in the way the quantitative algorithm operated, or was applied to the data, and/or (d) true physiologic variation in the patient’s state at imaging. In other words, repeatability is a measure of the combined “stability” of the quantitative algorithm, the acquisition protocol itself, and the patient conditions. As with reproducibility, high repeatability is equivalent to low  $\Delta_{\text{repeat}}$ .

While serial measurements fall obviously under the repeatability category, examining the potential limitations of reproducibility offers us a way to determine, in a more controlled environment, the effect of operator interaction on quantitative measurements. Specifically, we can ascribe imperfect reproducibility to variabilities in processing (by which tomographic images are produced from the acquired “raw” projection images) as well as variabilities in quantification:  $\Delta_{\text{repro}} = \Delta_{\text{proc}} + \Delta_{\text{quant}}$ .

Group processing allows for simultaneously solving left ventricular geometry for all of the available datasets. It allows the algorithms, in regions where structure cannot be definitively determined for one or more of the datasets, to make decisions that exploit all the available information and that do not introduce arbitrary inter-study inconsistencies. When **Group** is ON, datasets belonging to the same patient are processed as a “pair” (or, if more than two studies are involved, as a “group”). Group processing can be used to improve  $\Delta_{\text{repro}}$  and  $\Delta_{\text{repeat}}$ . Of note, group processing should also greatly reduce the number of studies requiring manual adjustment of the automatically derived contours.



Sample SPECT study auto-processed with contour failure



Same study auto-processed using Group processing

### 6.3 Lung/Heart Regions Manual Mode

After processing datasets, if the heart or lung bounding boxes contain structures, irregularities, or high count areas outside of the ROIs, use manual mode to redefine the ROIs. Manual mode in the RAW window is for redefining the heart and lung ROIs. Manual mode in the Slide window is for redefining the ventricular contours.

The following table outlines some of the parameters you must consider when evaluating the bounding boxes to determine if you need to reposition or resize the ROIs.

Contour	Acceptable	Unacceptable
Heart bounding box	Completely contains LV without clipping.	Contains other structures such as gall bladder or a loop of bowel
Heart ROI	Fully inside of the LV myocardium	Not inside the LV
Lung bounding box	Excludes high count areas inside the lung field	Fully or partially outside of the lung fields
Lung ROI	Fully within the lung field	Contains a high count structure within the lung field

To modify the lung and heart ROIs in the Raw window:

1. Click **Manual**.

The **Raw** window displays unprocessed heart and lung bounding boxes. The unprocessed bounding boxes have four resizing handles and a center handle.

2. Reposition the heart and lung bounding boxes:

- Drag the center handle of the red unprocessed heart bounding box to the center of the left ventricle.
- Drag the center handle of the green unprocessed lung bounding box to the center of the lung ROI.

Resize the heart and lung bounding boxes. Drag the handle(s) to the new positions.

Make sure that the lung bounding box is large enough to contain the ROI within the lung, but still excludes high count areas outside of the lung. If you define the search box too close to the outer boundary of the lung wall, you may clip the lung, which produces inaccurate lung/heart ratios. Make sure that the heart bounding box completely contains the left ventricle but excludes high count areas outside of the left ventricle. Areas outside of the boxes are excluded from the surface detection procedure.

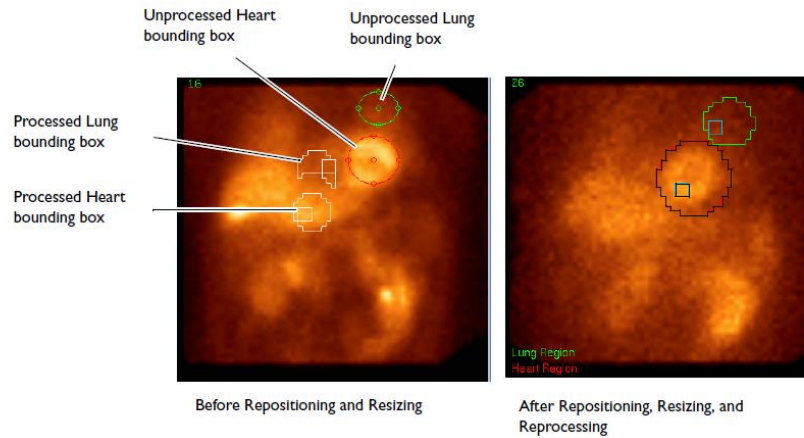
3. Click **Process**.

QGS+QPS should redraw the bounding boxes and ROIs.

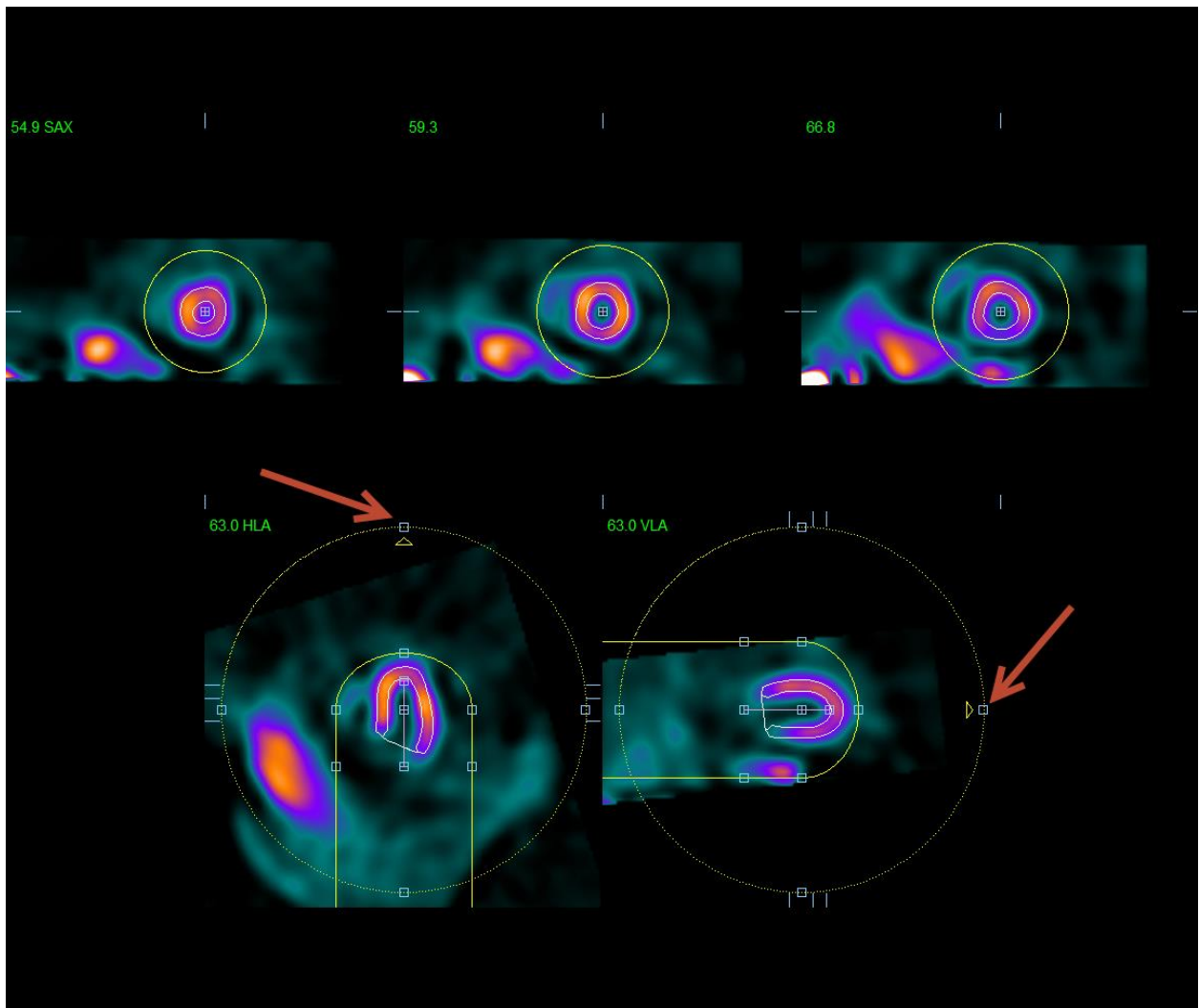


If you select **Process** when you are working in Manual mode, only the raw dataset that were displayed when in Manual mode are reprocessed.

**Note:** Make sure that placement of the heart and lung ROIs is accurate, and verify that these ROIs are over the proper organs. Inaccurate heart and lung ROIs can result in incorrect computation of quantitative data, which can lead to misdiagnosis.



## 6.4 Transverse Manual Mode



Transverse datasets may be reoriented from the HLA/VLA viewports using the handles marked by the arrows

In addition to processing short axis datasets QGS+QPS can also process transverse datasets (which often arise in PET studies), automatically determining LV surfaces and reorientation angles, and then displaying the results in either transverse/sagittal/coronal format or short axis/horizontal long axis/vertical long axis form.

In cases where the automatic LV segmentation or reorientation is unsatisfactory, transverse manual mode can be used to apply corrections to both. Transverse manual mode is the same as short axis manual mode with the exception that reorientation may be interactively specified by dragging the handles (small blue boxes) attached to the reorientation circles (yellow dashed circles) so that both yellow arrows point towards the apex.

The following page specific controls are available for transverse manual mode.

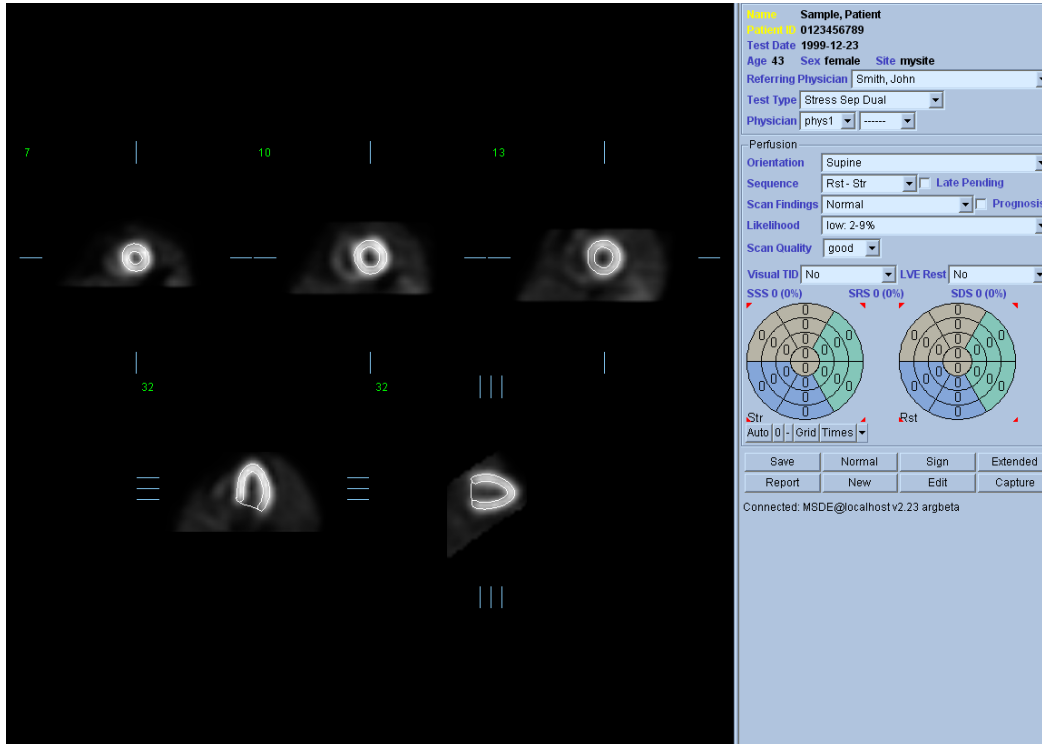
---

**Align** Forces the reorientation angles to be those specified using the reorientation circles. Otherwise, they will be automatically generated.

---

## 7 ARG (Automated Report Generator)

Integration of ARG (Automatic Report Generator) provides the ability within QGS+QPS to create, edit, sign, review, archive, and share customizable, consistency-checked, reports. A reporting pane and a few extra dialogs have been added to QGS+QPS for this purpose. ARG is enabled by the **Report** button on the right hand side of the top row of buttons. When ON, the info panel is replaced by the ARG panel.

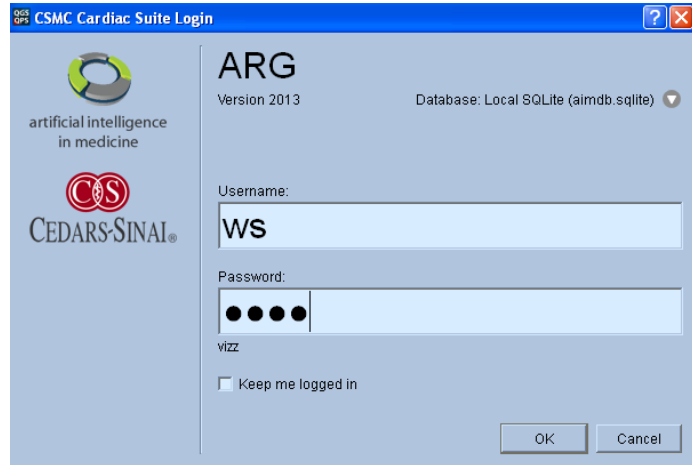


### 7.1 Starting QGS+QPS with ARG

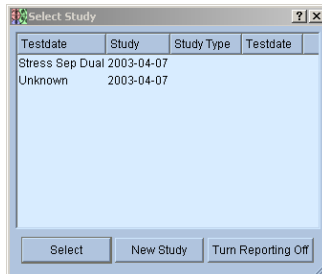
ARG will automatically match the identifying information contained in the image headers with existing (previously saved) studies. If an existing study is found, then it is possible to modify the data or view the report associated with that study. If no study is matched, then ARG will automatically create a new study. This new study will not get permanently saved to the database until the Save button is clicked.

## User Login

When QGS+QPS is launched with ARG integration, users must login with their username and password credentials. The program will remember the Username and Password for up to 2 hours of inactivity if “Keep me logged in” is selected. Refer to the ARG reference manual for more details.

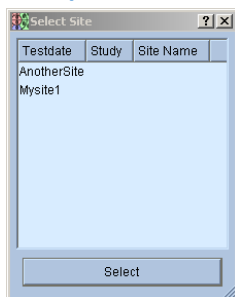


## Multiple Studies



If a patient has more than one study within two days of one another, then a dialog is displayed prompting the user to choose the relevant study. Multiple studies are a unique occurrence, and should only be used when the user wishes to bill for multiple studies. To create multiple studies, click the **New** button located in the Reporting Panel of QGS+QPS, or the **New** button on the multiple study dialog.

## Multiple Sites



Many physician groups read studies for more than one hospital or location (site). ARG is designed to support multiple sites. When more than one site has been configured, a dialog will be displayed each time a new study is created. The user must choose the site to which the patient belongs. If the intended use of ARG is to support only one site, then this dialog will not be displayed.

## 7.2 Reporting Panel

The ARG fields are displayed on the right hand portion of the screen. These fields can be toggled on or off at any time by using the **Report** button located on the toolbar.

## Patient Information

<b>Name</b>	Sample, Patient
<b>Patient ID</b>	0123456789
<b>Test Date</b>	1999-12-23
<b>Age</b> 43	<b>Sex</b> female <b>Site</b> mysite
<b>Referring Physician</b>	Smith, John
<b>Test Type</b>	Stress Sep Dual
<b>Physician</b>	phys1

The items listed in the patient information portion contain the values as contained in the database. These values can be easily edited by double clicking on any of the fields or by using the **Edit** button in the reporting panel. Three fields that must be filled in by the user are the Referring Physician, Test Type and (Reading) Physician fields.

## Perfusion Fields

Perfusion	
Orientation	Supine
Cam	SPECT 1
Sequence	Rst- Str
Late Pending	<input type="checkbox"/>
Scan Findings	Definitely Abnormal
Prognosis	<input type="checkbox"/>
Likelihood	intermediate: 30-69%
Scan Quality	good
Reversible	<input checked="" type="checkbox"/>
Nonreversible	<input type="checkbox"/>
Rev. Redist	<input type="checkbox"/>
Visual TID	No
LVE Rest	No
CT/CCS Details	
SSS 18 (26%)	SRS 0 (0%)
SDS 18 (26%)	
Str	Rst
Auto	0
-	Reload
Grid	Times

Perfusion fields are filled in by the reporting physician and allow a natural language sentence construction by ARG depending on the field entries. Descriptions of the field entries are listed in the table below.

<b>Orientation</b>	Patient orientation during test.
<b>Cam</b>	The imaging camera used to acquire the images.
<b>Sequence</b>	The sequence of tests performed.
<b>Late Pending</b>	If the sequence currently does not contain a 'late' test, but one will be performed later, this box is checked.
<b>Late Dist.</b>	If the sequence contains a 'late' study, then this allows entering the number of hours after the original test that it was performed.
<b>Scan Findings</b>	The overall perfusion scan findings.
<b>Likelihood</b>	Pretest likelihood.
<b>Scan Quality</b>	The technical quality of the scan.
<b>Reversible</b>	If the study contains reversible defects, this box should be checked.
<b>Nonreversible</b>	If the study contains nonreversible defects, this box should be checked.
<b>Revers-redist</b>	If the study contains reverse-redistribution, this box should be checked.
<b>Prognosis</b>	To include a prognosis statement in the final report, this box should be checked.
<b>Visual TID</b>	Does the patient have visually assessable transient ischemic dilation. It may

be one of the following values: *Yes, No, Equivocal*

**LVE Rest** Does the patient exhibit left ventricular enlargement at rest. It may be one of the following values: *Yes, No, Equivocal*

**Function Fields**

Function fields are filled in by the reporting physician and allow a natural language sentence construction by ARG depending on the field entries.

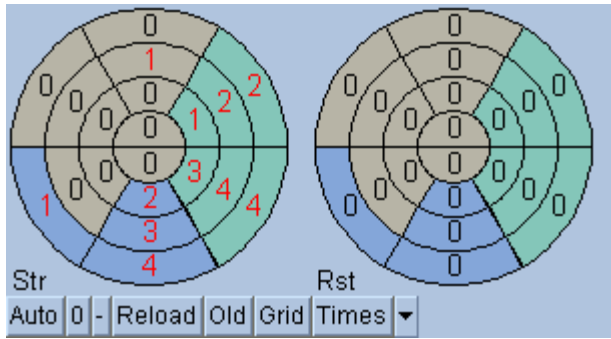
Descriptions of the field entries are listed in the table below.

The quantitative results for stress and rest are displayed in this figure. The TID and LHR fields are entered in manually by the clinician (they are not calculated by QGS+QPS). Stress and Rest WMWT (Wall Motion and Wall Thickening) check boxes should be checked if the study exhibits wall motion/wall thickening at stress and rest, respectively.

The GSSS (Gated Summed Stress motion Score) and GSRS (Gated Summed Rest motion Score) are automatically calculated and display if the data has been processed. Manually adjusting the polar map scores, automatically re-calculates and updates these values.

<b>Gated Sequence</b>	Selects which gated sequences were acquired.
<b>Stress EF</b>	Stress Ejection Fraction.
<b>Stress EDV</b>	Stress end diastolic volume.
<b>Stress ESV</b>	Stress end systolic volume.
<b>Rest EF</b>	Rest Ejection Fraction.
<b>Rest EDV</b>	Rest end diastolic volume.
<b>Rest ESV</b>	Rest end systolic volume.
<b>TID</b>	Allows user entry of TID (Transient Ischemic Dilation).
<b>LHR</b>	Allows user entry of LHR (Lung Heart Ratio).
<b>Scan Findings</b>	Overall findings of the function test.
<b>Scan Defects</b>	If Scan findings is not normal, this describes the type of defect.
<b>Stress WMWT</b>	If the study exhibits wall motion/wall thickening defects at stress, this box should be checked.
<b>Rest WMWT</b>	If the study exhibits wall motion/wall thickening defects at rest, this box should be checked.

## Visual Scores



ARG extends scoring by assigning a coronary vessel to each segment. By default ARG will attempt to choose the vessel based on the visual scores. This can be overwritten by right clicking on a segment and selecting the appropriate vessel. In some cases it is unclear to which vessel the defect belongs. When this occurs, select the abnormal segment in question and choose a combination of vessels. The **Reload** button will load the previously saved scores.

## Edit Panel

The Edit Panel allows editing of patient demographic data for reporting purposes only. This will not change the data in the image header.

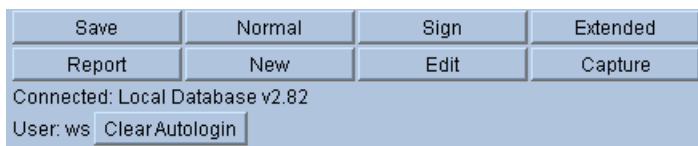
Note that either DOB (date of birth) or Age can be filled in at any given time. DOB will always take precedence over age, if age was originally entered.

## Reporting Panel

Up to two physician signatures can be placed on the report. The physician drop down displays all Signing Physicians as defined in the QARG database (See ARG Reference Manual).

The primary physician is displayed topmost.

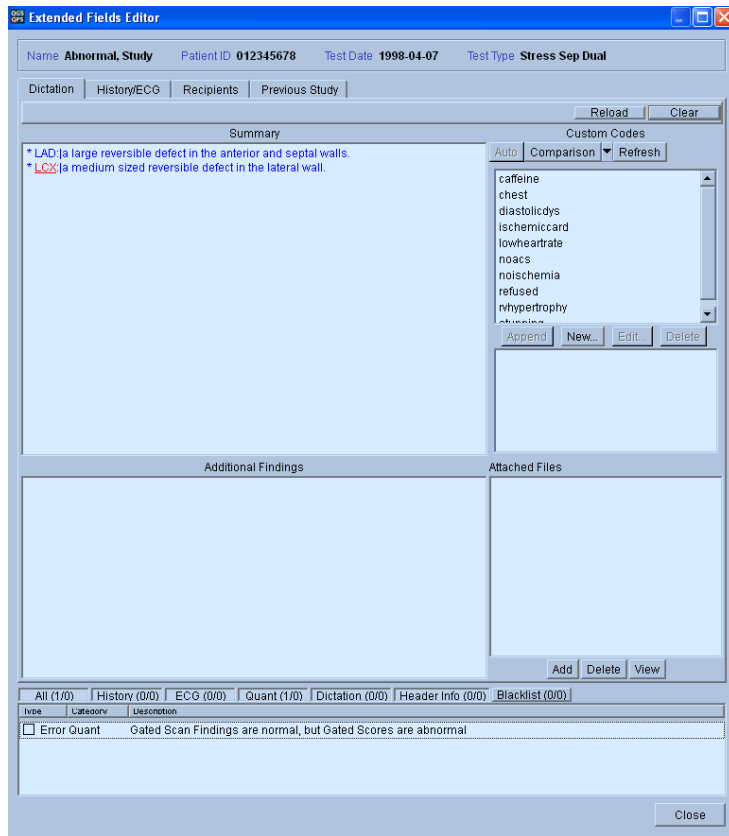




The ARG action buttons shown on the left are described in the table below.

<b>Save</b>	Saves all ARG information to the database.
<b>Normal</b>	Sets all blank fields to values consistent with a normal study.
<b>Sign / Unsign</b>	Reports must be signed (by the physician entering their password) prior to the signature appearing. Once the study has been signed, it is locked from future modifications. If it is necessary to modify the study, physicians may un-sign the study by entering their password, thus releasing the study lock. However, once the data is un-signed and re-saved, the old data (and corresponding report) will be overwritten.
<b>Extended</b>	Opens the extended editor, which permits editing of the dictation, history and ECG sections.
<b>Report</b>	Displays the PDF report.
<b>New</b>	Creates a New (multiple) study for this patient.
<b>Edit</b>	Displays the study editor dialog.
<b>Capture</b>	Captures the current screen to save in report. (Ctrl+Shift+P will also capture the current screen. The key combination is useful if the ARG Panel is not desired in the screen capture).
<b>Clear Autologin</b>	If “Keep me logged in” was checked when QGS+QPS was launched, this option clears it out so that the user is required to login when QGS+QPS is re-launched.

## Extended Editor



The Extended editor contains areas for dictation, History/ECG, Recipients and Previous Studies. Each study may have a main dictation associated with it, in addition to a history dictation. The dictation is free text that is included on the report cover letter. The dictation editor is designed to make this process as efficient as possible. ARG includes powerful built-in macros and a very flexible custom code editor.

For more details, reference the ARG manual.

### Dictation

Two powerful macros are included on the dictation editor. The buttons for these macros are located directly underneath the Custom Codes title in the Dictation Editor window beside the Refresh button.

---

#### Auto

An automatic dictation is used by default. This dictation updates real-time as fields are modified. The automatic dictation is shown in blue. Note that text can be added before or after the automatic dictation without affecting the behavior of the auto dictation. You may alter or remove the automatic dictation at any time simply by editing it.

Note that once the automatic sentence(s) have been modified then the dictation will no longer be updated automatically. To re-enable the automatic dictation, click the Auto button.

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**Comparison**

If the patient is returning for a follow-up visit, the Comparison button is enabled. If this is the case then the signing physician should mention any changes (or no change) since the patient's last visit. ARG will provide a warning if no mention is made. Clicking the comparison button will initialize the comparison sentence.

ARG matches the previous study based on patient ID. If the patient ID was mistyped in the original study, it must be changed before ARG can auto match. Of course you may also manually enter the old study date and ARG will be able to auto-match any future studies.

For more information on editing the comparison sentence or viewing raw changes, refer to the dictation section in the QARG manual.

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**Refresh**

Refreshes the list of codes in the database.

---

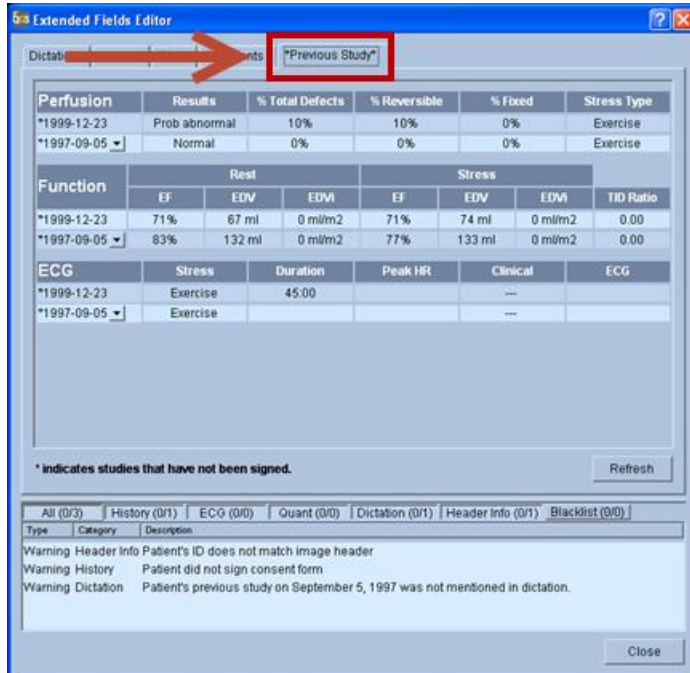
**Custom Codes**

Custom codes are simple macros that provide a mechanism to store frequently typed sentences. Codes are made up of a code-key (small word describing the code) and code-value (text which is appended to the dictation). Codes are accessed by highlighting the code-key and clicking the Append/Add button, double clicking a code-key or typing @code-key in the dictation editor. Please see the Custom Code Manager section in the QARG User Manager for details regarding customization of these codes.

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### Previous Study

The previous study pane gives a very informative comparison of the patient's previous studies. From this pane you can view how the patient was reported in previous visits.

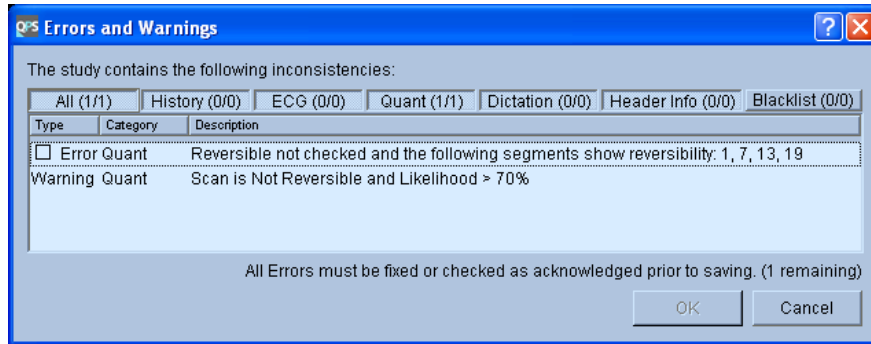


### Consistency Checks

ARG contains a collection of checks resulting in various notifications of errors and warnings. These checks ensure that the report data is consistent.

For Example: If 'Normal' was entered for overall perfusion scan findings and a large defect exists in the visual scores, then an error will occur. Most checks can be viewed directly from the ARG interface by looking at the color of the field name (field inconsistencies resulting in errors are labeled in red, warnings in yellow). Descriptions of errors and warning are displayed in the Errors and Warnings window (shown below) after clicking the **Save** button.

### Critical Errors and Warnings



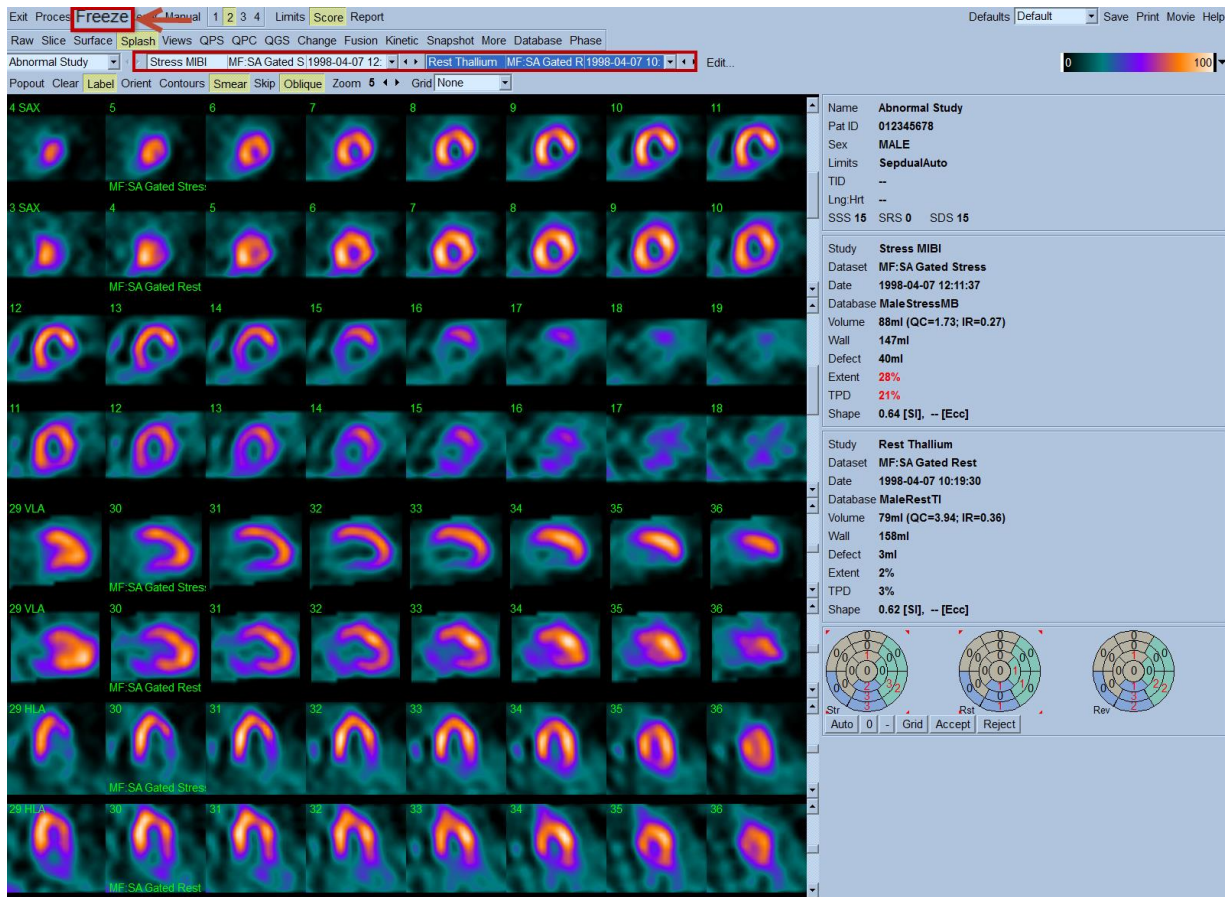
Critical errors prevent the report from being saved. These fields show up red in the ARG panel and are listed next to a check box in the errors and warning dialog. Most critical errors deal with the absence of required data; however some are due to major inconsistencies with the data. If errors exist in the report it is possible to continue, however the errors must be acknowledged by clicking the checkbox next to the error. Clicking the checkbox will accept the error for the current study only. To permanently disable (hide) an error right click the error and select 'Add consistency check to blacklist'.

Warnings do not prevent the report from being saved. However the physician must review them and explicitly choose to ignore them prior to saving. Theoretically, warnings should not be allowed. However, in some circumstances the inconsistency should be allowed (i.e.: the patient had a bypass surgery). Ignoring warnings should be done scarcely and only after careful consideration.

### Hiding unwanted consistency checks

Users may disable errors and warnings that are irrelevant to their site by right clicking the consistency check once the dialog is opened. This moves the consistency check to a "hidden" group. The consistency check can be re-enabled by right clicking on the error inside the black listed group.

## 8 Motion Frozen



This feature employs a novel technique to create cardiac "motion-frozen" perfusion or viability images, by warping all frames of ECG-gated images to the end-diastolic position. Such "motion-frozen" perfusion and viability images improve resolution and contrast since the blurring effect of cardiac motion is removed.

Reference J Nucl Med 2004; 45:1128-1134.

### 8.1 Feature Requirements

The motion frozen feature requires at a minimum one processed gated short axis dataset.

### 8.2 Implementation

A typical sequence for using the motion frozen feature in the QGS+QPS application is as follows:

1. User selects necessary myocardial gated short axis datasets (and any other desired datasets for a standard QGS+QPS session, raw projections etc.) and then starts a QGS+QPS session.
2. The gated (and ungated) short axis datasets are processed as usual by QGS+QPS to generate contours.

3. User verifies automatically-derived contours.
4. User selects the necessary gated short axis dataset(s) from the Dataset Selector pull-down menu (from 1 to 4 gated datasets) depending on the display mode (single, dual, triple or quadruple). The user can select gated datasets on any display page (Splash, Slice, Views etc.) with *Splash* and *Slice* pages being more useful to view the created perfusion images.
5. On the *Splash* page, select the necessary gated short axis dataset(s) from the dataset selector(s). Clicks **Freeze** on the QGS+QPS application main toolbar to initiate the motion frozen algorithm.
6. The currently displayed gated dataset(s) in the Dataset Selector pull-down are replaced with the newly created motion frozen datasets as identified by “**MF:**” in front of the original dataset name.
7. The display window is updated with the newly created motion frozen perfusion images. **Note:** Contours are automatically generated for the newly created images. Toggle the **Contours** button on the page control bar to view contours.

Note: There are no user configurable settings in the **Defaults Editor** for this feature.

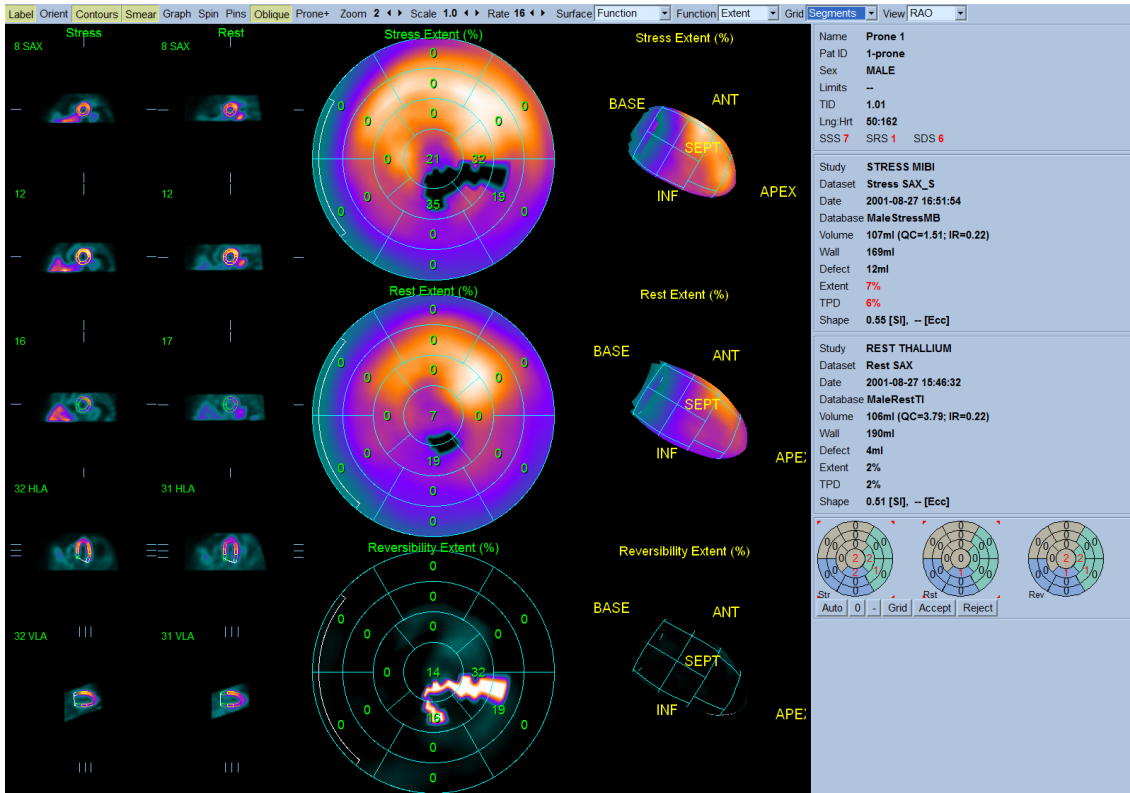
### 8.3 Reviewing Motion Frozen perfusion images

Typically, motion frozen perfusion images are reviewed on the *Splash* page as are the usual perfusion short axis datasets. The figure shows the **Splash** page with a stress summed short axis dataset and a motion frozen perfusion dataset created from the same stress gated short axis dataset as the stress summed short axis dataset.

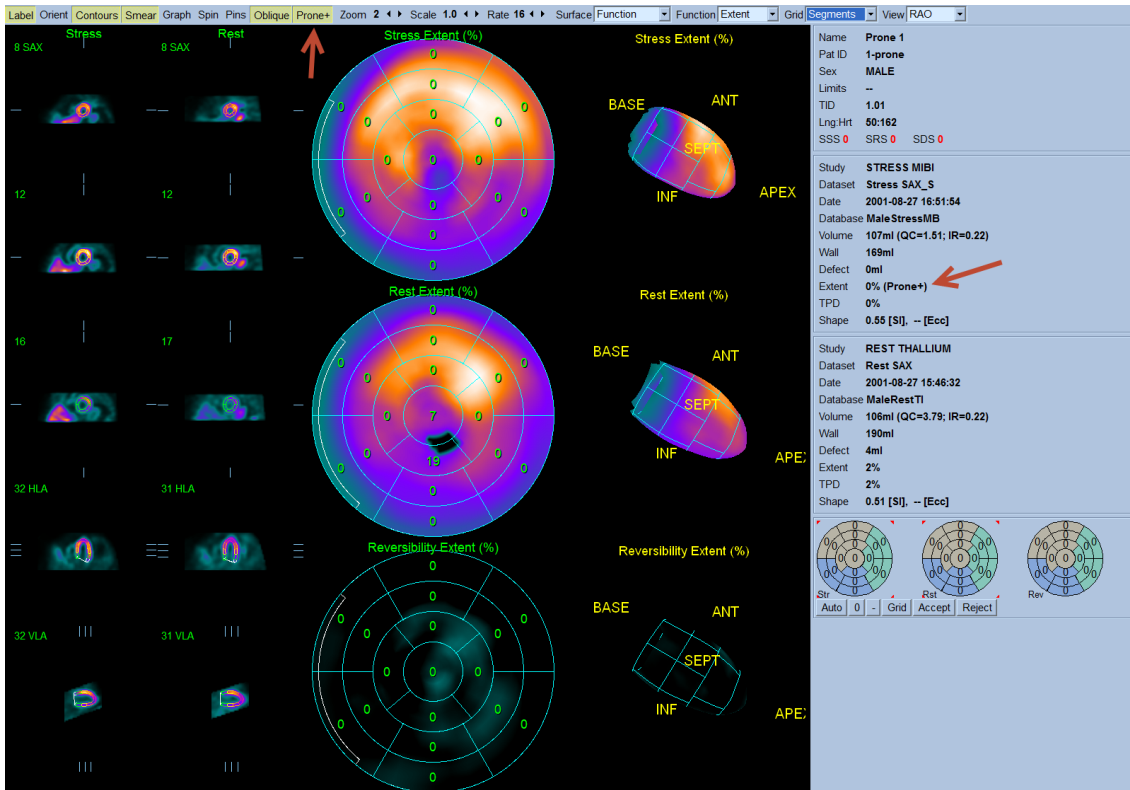
## 9 Prone-Supine (Prone+) Quantification

Prone-supine (Prone+) quantification allows quantification of perfusion on prone images as well as combined quantification of prone/supine datasets by applying heuristic rules which allow automatic elimination of image artifacts based on the relative defect locations on prone and supine images.

Reference: Nishina H, Slomka, PJ, Abidov AA, Yoda S, Akincioglu, C, Kang, X, Cohen, I, Hayes, SW, Friedman, JD, Germano, G, Berman, DS. Combined Supine and Prone Quantitative Myocardial Perfusion SPECT: Method Development and Clinical Validation in Patients with no Known Coronary Artery Disease. (In Press J Nucl Med).



Sample study with Prone+ toggled off using QPS Results Page



Same sample study with Prone+ toggled ON (as indicated by the Red arrows)

## 9.1 Feature Requirements

The Prone-Supine (Prone+) quantification feature requires at a minimum one supine perfusion dataset and one prone perfusion dataset from the same patient/study. This feature is available in the **QPS Results** page and is enabled by toggling on the **Prone+** button of the page control bar.

## 9.2 Implementation

A typical sequence for using the Prone+ feature in the QGS+QPS application is as follows:

7. User selects necessary myocardial perfusion short axis datasets (and any other desired datasets for a standard QGS+QPS session, raw projections etc.) and then starts the QGS+QPS session.
8. The short axis datasets are processed by QGS+QPS to generate contours.
9. User verifies contours.
10. User displays the **QPS Results** page.
11. User clicks **Prone+** button to apply Prone-supine quantification algorithm and display results. Results are displayed in the statistics section.
12. The application of the Prone+ feature is indicated in the statistics section of the **QPS Results** page and in the change of defect size/location (if any) on the Stress and Reversibility polar maps.

Notes:

1. When the Prone+ feature is been enabled in the QPS Results page it remains in effect for all other pages displaying perfusion results in the statistics section (Surface, Splash, etc.).
2. The Prone+ feature can be automatically enabled by toggling it on in the Application Defaults window, Application Options section and then saving the defaults settings. In this manner, the Prone+ algorithm will be applied during processing of perfusion datasets for all subsequent QGS+QPS sessions.
3. It is advisable to use **Extent** (via the Function drop-down menu) to display the blackout regions on the polar maps.

## 10 Saving Results

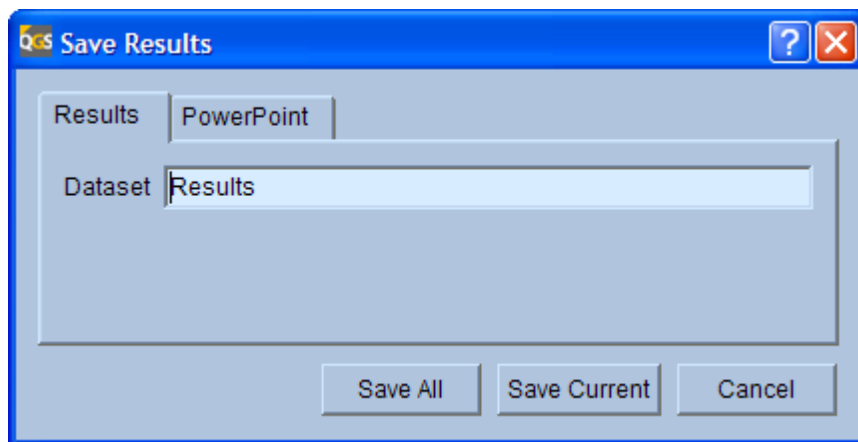
Processing results can be saved from within the QGS+QPS application for later recall. This feature allows manually-adjusted contours and visual scores to be saved in order to avoid repeating this operator-dependent step. When results are saved, all datasets pertaining to the study being saved are associated with the results file, which becomes a self-contained entity. Transferring the results file without any other datasets to another system (e.g., using a DICOM transfer mechanism on platforms supported by QGS+QPS) is sufficient to retain all necessary information. At this time only transfers to a system that uses the same vendor platform is fully supported, though interoperability between vendors may be possible if CSMC application versions match.

To save results for one or more studies, follow these steps:



1. Select your study(ies) and start your application.
2. Review the results of the study(ies) and adjust contours and/or scores if necessary.
3. Click the **Save** button to open the **Save Results** dialog.
4. Click the **Results** tab to display save options. See figure below.
5. If so desired, enter a description in the **Dataset** field (this field may have a different name on some platforms).
6. Click **Save Current** to save the currently displayed study or click **Save All** to save all the selected studies currently loaded. As multi-study or multi-patient processing may not be available on all platforms, on some systems **Save Current** and **Save All** will perform the same task.

Note: To save results with embedded CT dataset, check the **Embed CT** checkbox. This will include CT data into the Results File. Note that embedding CT datasets will significantly increase the size of the results file.



Save Results with Results tab selected

Note: the PowerPoint tab may not be present in all software configurations.

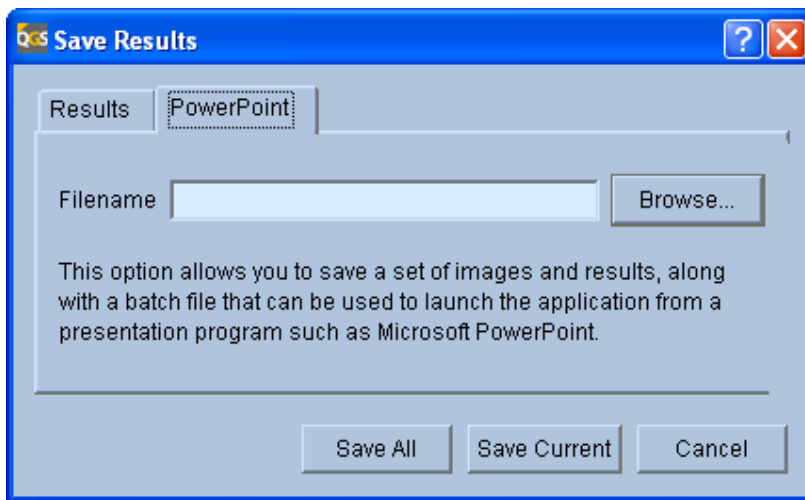
## 11 PowerPoint Integration

The PowerPoint save feature is a useful tool that allows saving a set of images and results along with a batch file. The batch file launches the QGS+QPS application and loads the images and results. This is useful for showing case studies within a Microsoft PowerPoint presentation. PowerPoint integration is supported in Office 2000 SR1a and above.

To save a study for showing in a PowerPoint presentation, follow these steps:

1. Select your study(ies) and start your application.

2. Review the results of the study(ies) on the display page you wish to save (eg. **Slice page**) and make changes as necessary (intensity/color scale, zoom, frame rate settings etc.). The changes applied will be automatically saved as the default setting for the study(ies).
3. Click the **Save** button to open the **Save Results** dialog.
4. Click the **PowerPoint** tab to display save options. See figure below.
5. Click **Browse** to select a directory to store the images and batch file.
6. Type a name in the **Filename** text area
7. Click **Save Current** to save the currently displayed study or click **Save All** to save all the selected studies for the current application session.



Save Results with PowerPoint tab selected

### 11.1 Description of Saved Files

Three files per study will be saved and have extensions of "vbs", "gsi" and "xml". The "vbs" file is a Visual Basic script file that will launch the QGS+QPS application and load the corresponding "gsi" data file along with the "xml" file containing the saved default settings for the study(ies).

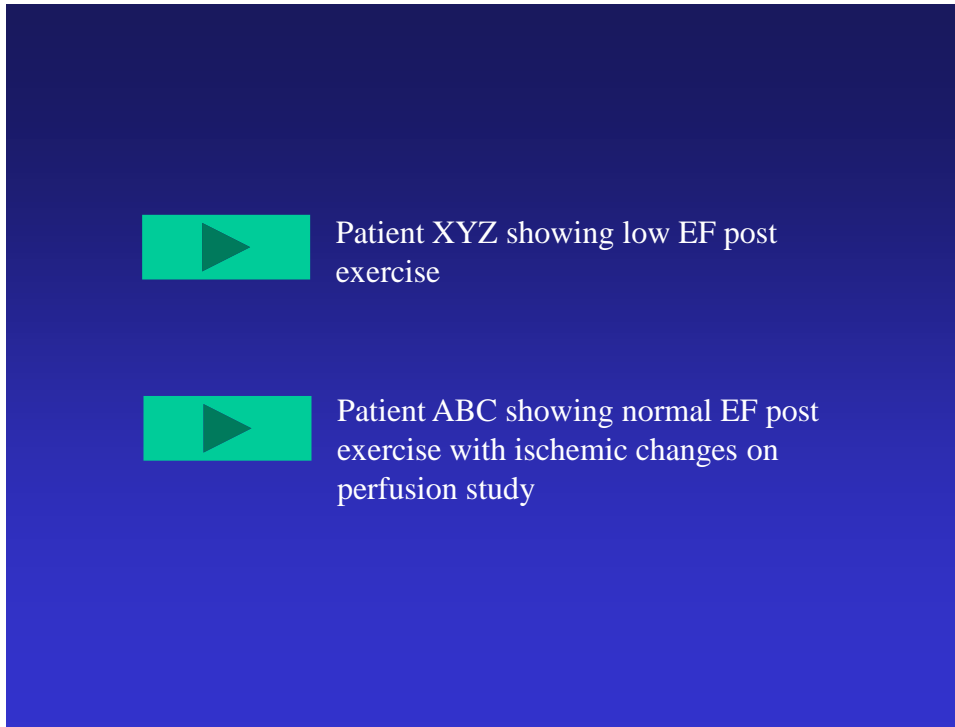
### 11.2 Launching application studies from PowerPoint

Studies must be saved using the procedure in the preceding section in order to use this PowerPoint feature.

To create a slide that will launch an application (QGS+QPS) study session follow these steps.

1. Open PowerPoint and insert a new slide.
2. Under the Slide Show menu drop-down, select Action Buttons and choose an action button graphic from the list.
3. Draw the action button on the slide. An Action Settings dialog window should be displayed when finished drawing. Optionally, right-click on the action button and select Properties to bring up the Action Settings dialog.

4. In the Action Settings dialog click the **Run program** toggle.
5. Using the **Browse** command, locate the “vbs” file and select it. The **Files of type** selection in the browse window may have to be changed from Programs (\*.exe) to All Files (\*.\*) .
6. Click OK.
7. Launch the slide show for the current slide and click the action button to verify correct launching of the study.
8. Adding a text description beside the Action button will aid in reminding what the study was about during a presentation.



PowerPoint slide with Action button

## 12 Saving Screen Captures and Printing

Snapshots of the application’s screens can be saved by clicking the **Print** button. These screen captures include the information box to the right of the main viewport, but not the application controls at the top of the application’s main window. Screen captures can be saved either to the host system’s image database (if supported by the host system), to a file (always available), or printed to a Windows printer (if available). On DICOM-based systems, snapshots are saved as true-color DICOM secondary captures (SC). Proprietary formats may be used for other platforms, but exporting screen captures as DICOM SCs is always an option when saving a file to the file system as opposed to saving to the image database.

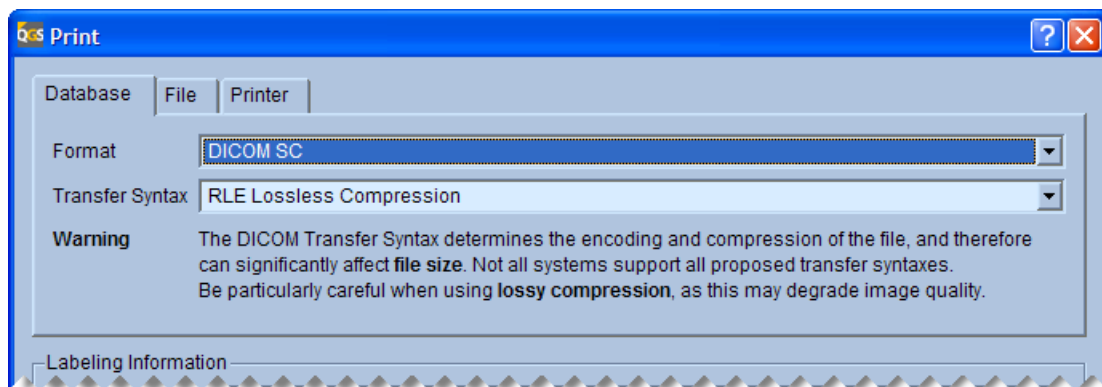
To save a screen capture, follow these steps:

1. Select your study(ies) and start your application.

2. Configure the screen as desired (e.g., process the data, change the selected dataset, adjust the zoom factor, select a different color scale, etc...).
3. Click the **Print** button to open the **Print** dialog.
4. Click the **Database**, **File**, or **Printer** tab as appropriate. See settings sections below. Fill out or select the appropriate information.
5. Select labeling options. See “Labeling” section below.
6. If so desired, enter a description in the **Series Description** or **Dataset** field (this field may have a different name depending on the platform).
7. Click **OK** to save or print the screen capture or click **Cancel** to cancel the task.

## 12.1 Database Settings

If saving screen captures to the image database is possible, a **Database** tab will be part of the **Print** dialog.

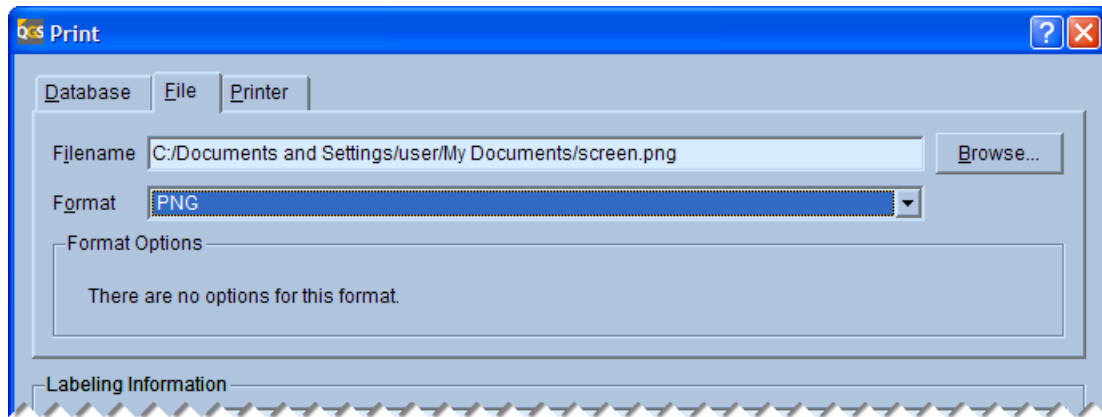


Database tab of Print dialog

On most systems only one format will be available (**DICOM SC**). When **DICOM SC** is selected as the output format, a **Transfer Syntax** setting drop-down will be available, allowing the **SC** to be saved in a compressed mode (**RLE Lossless Compression**). On some systems known to not support compression, only **Uncompressed (largest file size)** will be available. Additional transfer syntaxes may be added in future versions. Note that selecting a compressed transfer syntax will result in decreased storage requirements, but may cause problems if the file is later to be sent to another system that does not support this transfer syntax correctly. Despite the warning displayed in the **Database** tab, lossy compression is currently not available.

## 12.2 File Settings

A **File** tab will always be available on the **Print** dialog. Multiple formats are always available. These include **TIFF**, **JPEG**, **PNG**, **BMP**, and **DICOM SC**. **TIFF**, **PNG**, and **BMP** offer lossless compression. **JPEG** is always lossy-compressed (even with the quality setting set at the maximum value), and **DICOM SC** is compressed only if the **RLE** transfer syntax is selected.

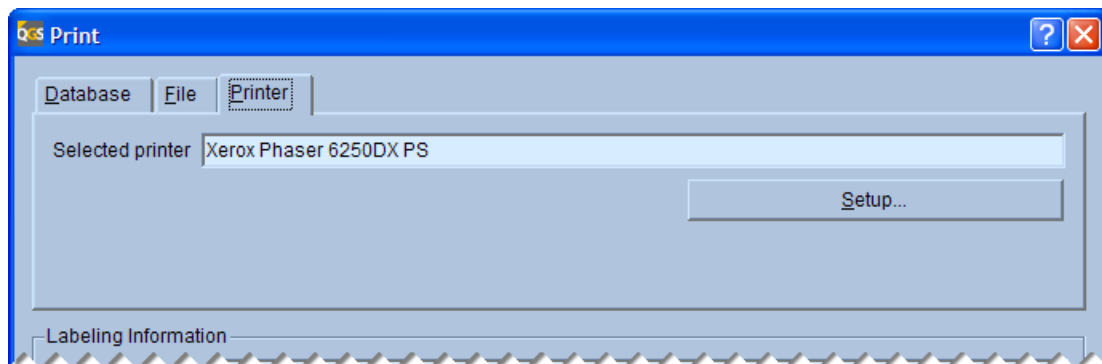


File tab of Print dialog

Note that the **Format Options** panel will only display controls if the format has optional settings. These settings are a **Quality** slider for JPEG (quality can be set from 40 to 100, with 40 providing the lowest image quality and 100 the highest image quality) and a **Transfer Syntax** setting for DICOM SC (see previous section for restrictions on transfer syntaxes). All output file formats except for DICOM SC shall be water marked to indicate that they are not for diagnostic purposes.

### 12.3 Printer Settings

A **Printer** tab will always be available on the **Print** dialog. The currently selected printer is listed under **Selected printer**. To change to a different printer, or to edit the properties of the printer click the **Setup...** button. This will open the operating system's **Print** dialog that will allow the selection of a different printer and a number of other options (on Microsoft Windows, these options include the number of copies). On Windows, clicking **Print** in this dialog will cause printing to happen immediately. Alternatively, one may click **OK** in the QGS+QPS **Print** dialog to print, or **Cancel** to abort the operation.



Printer tab of Print dialog

### 12.4 Labeling

The bottom portion of the **Print** dialog remains the same no matter what tab is selected. This portion of the dialog is dedicated to image labeling. On DICOM-based systems a **Series Description** and **Comment** can be entered. On other systems these fields may have a different name or be absent altogether, depending on what fields the proprietary host platform supports.

These fields are meant to allow for the identification of the screen capture when listed in a typical medical image database browser.

The **Datasets** section lists all datasets present on the current page. For each dataset acquisition and processing information are listed, along with image generation time. This allows for the identification of the datasets. The **Operator** and **Institution** fields are filled in automatically from the dataset headers if available, otherwise they can be edited before printing. If the Include a dataset legend checkbox is checked, each dataset on the printed screen will be identified by its designation letter (A, B, or C in the example below), and a legend that includes the information in the table will be added at the bottom of the printed or saved output. The legend table will also include patient information (name, patient ID, date of birth) unless anonymization is enabled, and dataset orientation and laterality (as provided by the dataset headers).

	Acquisition ID	Process ID	Date/Time	Operator	Institution
A	Myocardial Perfusion	Cardiac Stre	2007-01-23 09:36:49	Tech 1	Hospital
B	Myocardial Perfusion	Cardiac Stre	2007-01-23 09:36:44	Tech 1	Hospital
C	Myocardial Perfusion	Resting Stat	2007-01-23 09:40:28	Tech 2	Imaging center

Labeling section of Print dialog

Note that the **Format Options** panel will only display controls if the format has optional settings. These settings are a **Quality** slider for JPEG (quality can be set from 40 to 100, with 40 providing the lowest image quality and 100 the highest image quality) and a **Transfer Syntax** setting for DICOM SC (see previous section for restrictions on transfer syntaxes).

### 13 Saving Movies

Movies of the application's screens can be saved by clicking the **Movie** button. These movies only include the relevant portion of the viewport as decided by each application for each page, and does not include the information box to the right of the main viewport or the application controls at the top of the application's main window. Movies can be saved either to the host system's image database (if supported by the host system), or to a file (always available). On DICOM-based systems, movies are saved as true-color DICOM multi-frame secondary captures (MFSC).

Proprietary formats may be used for other platforms, but exporting screen captures as DICOM MFSCs can be an option when saving a file to the file system as opposed to saving to the image database, unless the platform is known to not support MFSCs, in which case the option is disabled to avoid creating files that the host system cannot handle.

When generating a movie, note that the final frame rate of the movie will vary with the application's **Rate** setting in the top application controls and attempt to match this rate. For example, to create a faster movie of a beating heart, increase the **Rate** setting.

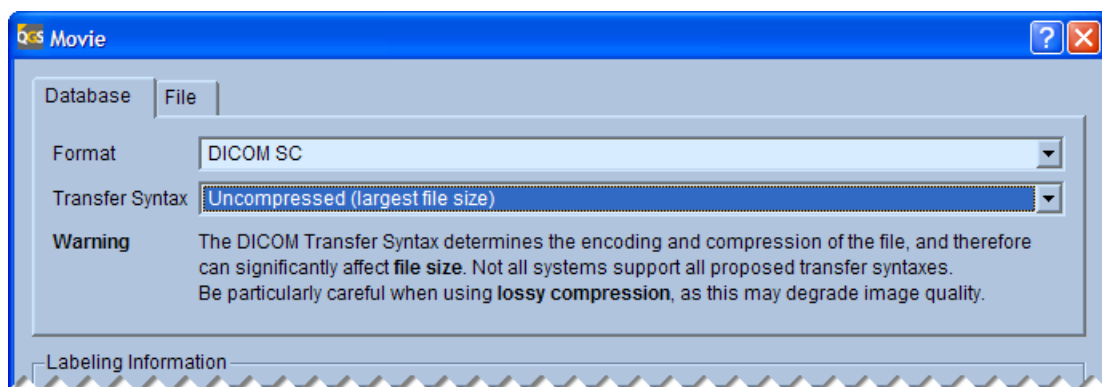
The application will pick automatically how the movie will be generated, i.e., by gating the image or displaying a rotating image, based on the current page selection.

To save a screen capture, follow these steps:

1. Select your study(ies) and start your application.
2. Configure the screen as desired (e.g., process the data, change the selected dataset, adjust the zoom factor, select a different color scale, etc...).
3. Click the **Movie** button to open the **Movie** dialog.
4. Click the **Database** or **File** tab as appropriate. See settings sections below. Fill out or select the appropriate information.
5. Select labeling options. See “Labeling” section below.
6. If so desired, enter a description in the **Series Description** or **Dataset** field (this field may have a different name depending on the platform).
7. Click **OK** to save the movie or click **Cancel** to cancel the task.

### 13.1 Database Settings

If saving screen captures to the image database is possible, a **Database** tab will be part of the **Print** dialog.



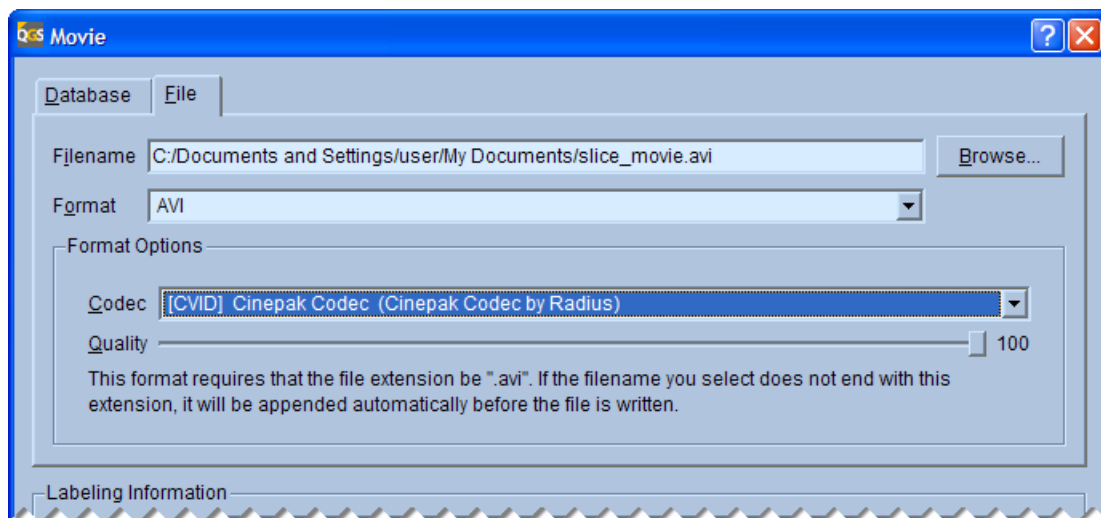
Database tab of Print dialog

On most systems only one format will be available (**DICOM SC**). When **DICOM SC** is selected as the output format, a **Transfer Syntax** setting drop-down will be available, allowing the **SC** to be saved in a compressed mode (**RLE Lossless Compression**). On some systems known to not support compression, only **Uncompressed (largest file size)** will be available. Additional

transfer syntaxes may be added in future versions. Note that selecting a compressed transfer syntax will result in decreased storage requirements, but may cause problems if the file is later to be sent to another system that does not support this transfer syntax correctly. Despite the warning displayed in the **Database** tab, lossy compression is currently not available.

## 13.2 File Settings

A **File** tab will always be available on the **Movie** dialog. Multiple formats are usually available. These include AVI and DICOM SC. AVI offers lossless or lossy compression, depending on the codec (coder/decoder) used. DICOM SC is compressed only if the RLE transfer syntax is selected.



File tab of Print dialog

Note that the **Format Options** panel will only display controls if the format has optional settings. These settings are a **Codec** selector and **Quality** slider for AVI (quality can be set from 0 to 100, with 0 providing the lowest image quality and 100 the highest image quality) and a **Transfer Syntax** setting for DICOM SC (see previous section for restrictions on transfer syntaxes).

For certain AVI codecs the **Quality** slider may be disabled if the codec does not offer an adjustable quality setting.

Note that using uncompressed output may lead to extremely large files that may not play well in the format's display program. For example, a large screen movie of a beating epicardial surface saved as an uncompressed AVI may display poorly when played in Windows Media Player if the system's resources are insufficient. Generally, it is recommended to use a compressed codec when generating AVI movies.

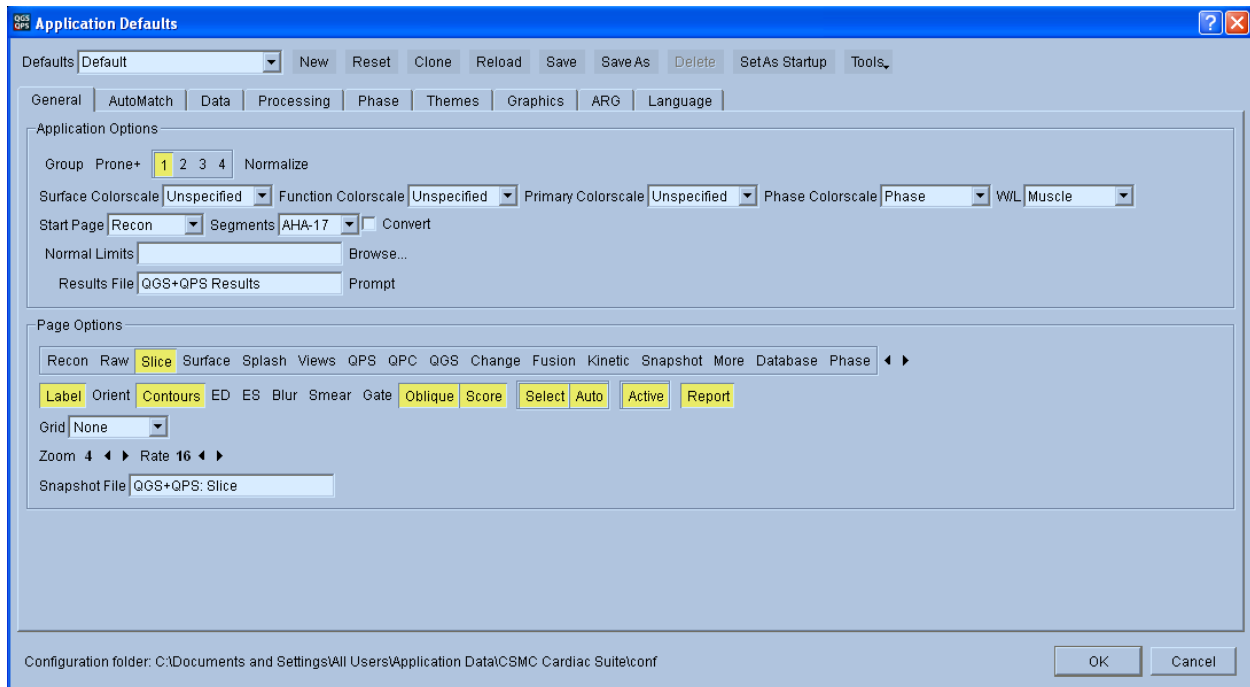
Also note that the list of codecs available on a system varies depending on what software has been installed. It is possible to install codecs individually and thereby obtain improved display performance, but doing so may reduce the portability of the file (e.g., when sending a movie to a colleague, the other person will also need that codec in order to view the file).



### 13.3 Labeling

The bottom portion of the **Movie** dialog remains the same no matter what tab is selected. This portion of the dialog is dedicated to image labeling. For details on labeling, please consult the corresponding section for labeling screen captures in the **Print** dialog (section 12.4).

## 14 Application Defaults Editor



The **Application Defaults** window allows you to load, modify, reset, and save the most frequently used QGS+QPS parameters. When you have set up the defaults according to your preferences and the established clinical protocols for your facility, QGS+QPS provides the following advantages:

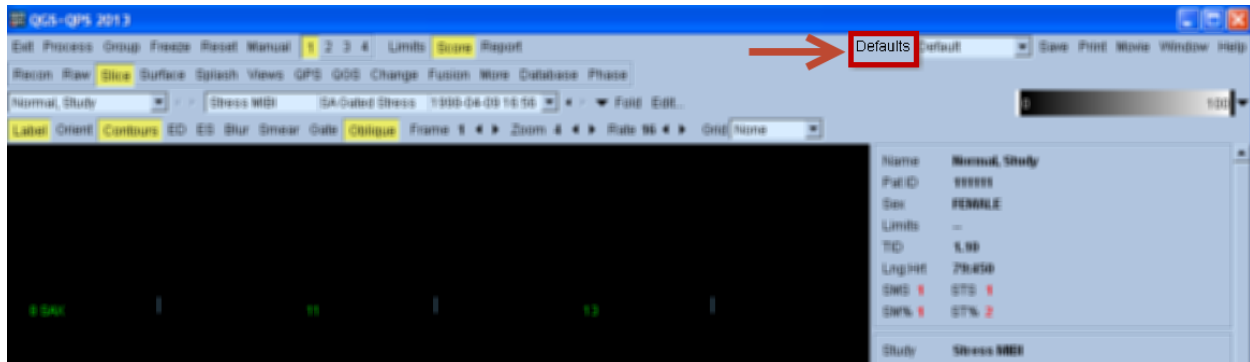
- You can customize the appearance and functionality of each QGS+QPS window.

For example, you can designate the Slices window to open with two datasets displayed (Cardiac Dataset Display button 2 selected), with the Contours and Labels off. Or, you can designate the Surfaces window to initially display only one dataset, with the septal surface in front of the 3D volume.

- Different users can personalize their own default settings (e.g., Doctor 1, Doctor 2, Technologist 1, etc...).
- You can use automated file selection features.

## 14.1 Launching

To open the **Application Defaults** editor window, click on **Defaults**. This will launch the **Application Defaults** editor window.



## 14.2 Universal controls for Defaults Editor

The top row of the **Application Defaults** dialog allows multiple sets of application defaults to be defined and stored. The bottom **OK** and **Cancel** buttons are also described here. The following controls are available:

Control	Purpose
<b>Defaults</b>	Select the current defaults.
<b>New</b>	Creates a new set of defaults based on factory settings.
<b>Reset</b>	Resets the current set of defaults to factory settings.
<b>Clone</b>	Captures the current settings of all of the controls within the application.
<b>Reload</b>	Reloads the current set of defaults from its last saved state.
<b>Save</b>	Saves the current set of defaults.
<b>Save As</b>	Saves the current set of defaults under a new name.
<b>Delete</b>	Deletes the current set of defaults. Not available for <b>None</b> , <b>Default</b> , or <b>Factory</b> defaults.
<b>Set As Startup</b>	Sets the current set of defaults to be loaded automatically upon application startup.
<b>Tools</b>	<b>Contains the following 3 options:</b>
<b>Import</b>	Import a set of defaults that previously been exported.
<b>Export</b>	Exports the current set of defaults to the file system.
<b>Reinitialize</b>	Resets the “Default” defaults to its factory settings and makes this the startup set of defaults.

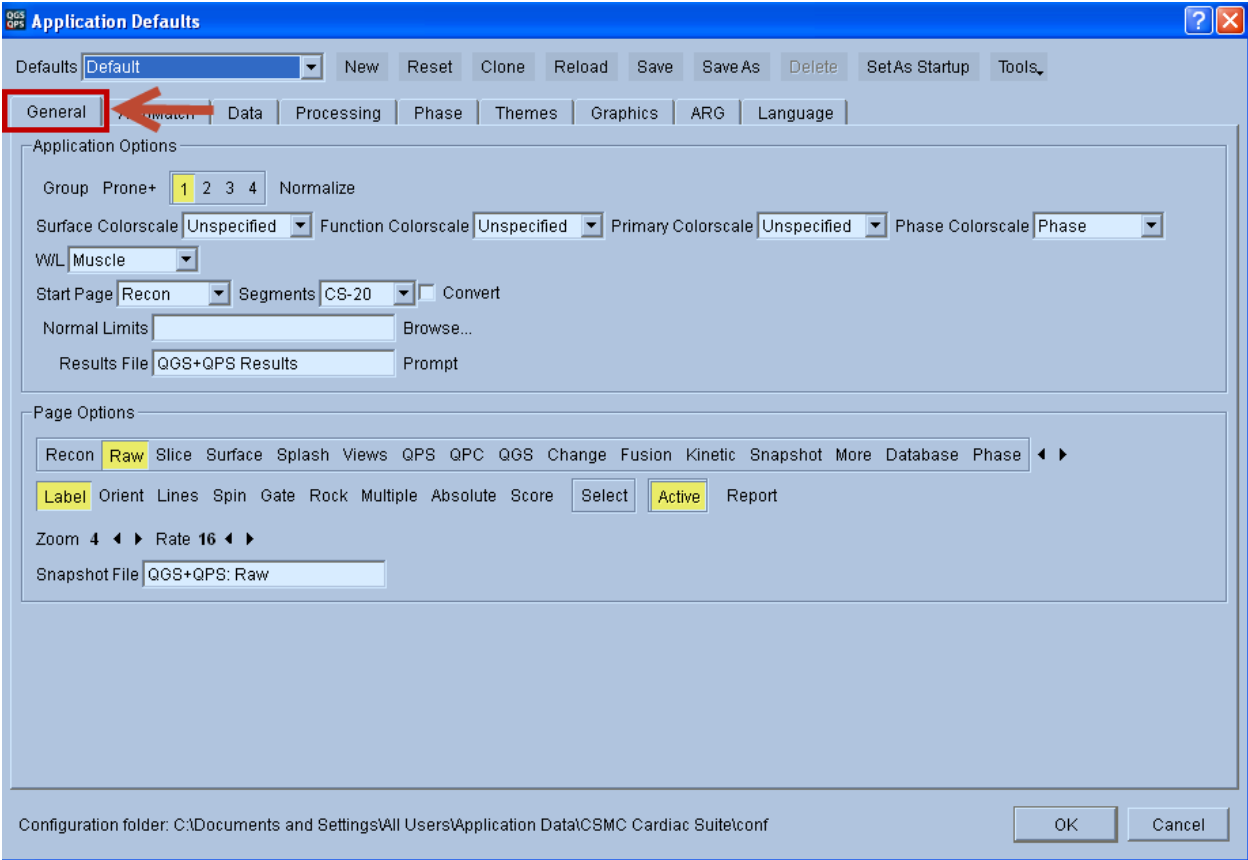
<b>OK</b>	Applies current defaults to the application (one-time). Click <b>Save</b> before <b>OK</b> to make the changes permanent.
<b>Cancel</b>	Exits default dialog without making any changes.

Defaults can be selected on the fly from the main application window by selecting a set from the **Defaults** drop-down list.



### 14.3 General Tab

The general panel is divided into two sections: The top section labeled **Application Options** is for application wide settings and bottom section labeled **Page Option** is for page specific settings.

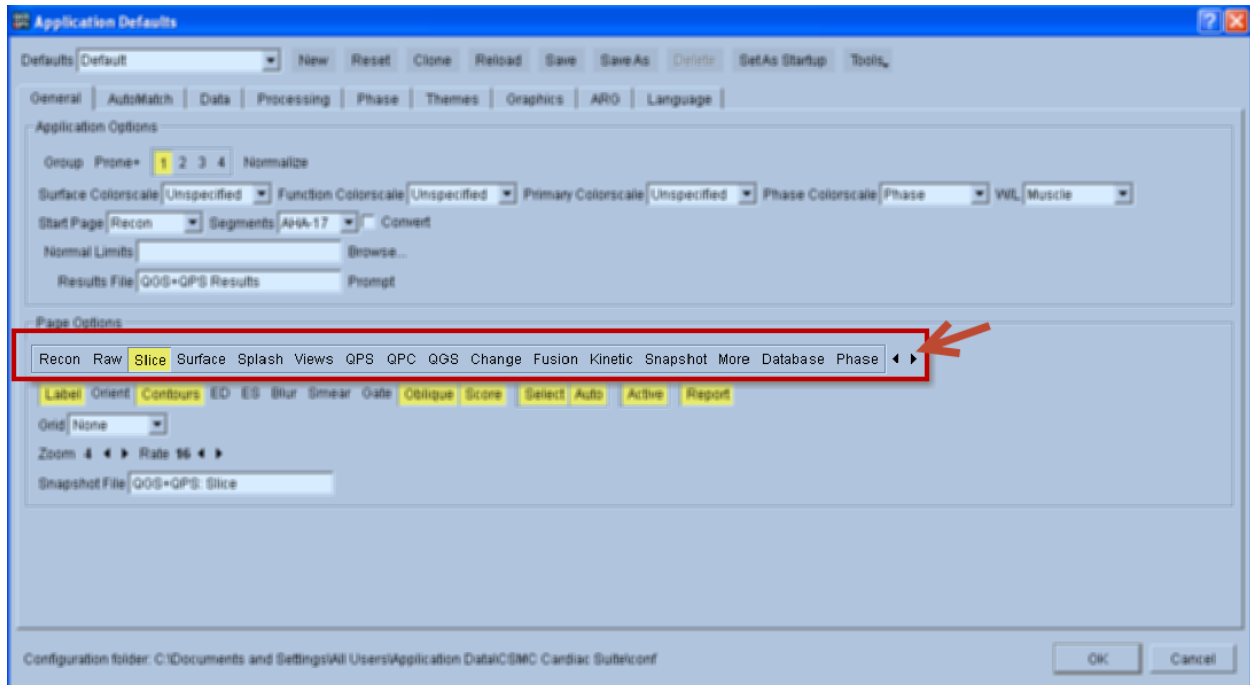


The application wide settings are:

<b>Group</b>	Toggles group processing of studies
<b>Prone+</b>	Toggles automatic application of Prone+ algorithm whenever applicable.
<b>1 2 3 4</b>	Sets default display mode (one, two, three or four datasets).
<b>Normalize</b>	Sets the brightness on all images to a normalized level. Before processing, this control finds the brightest pixel in the dataset volume, sets that pixel to 100%, and scales all pixels in the dataset from there. After processing, this control finds the brightest pixel in the dataset within the myocardium contours, sets that pixel to 100%, and scales all pixels in the dataset from there.
<b>Surface Color scale</b>	Sets the default surface color scale for all 3D surface images.
<b>Function Color scale</b>	Sets the default polar map / parametric surface color scale.
<b>Primary Color scale</b>	Sets the default color scale for all 2D images.
<b>Phase Color scale</b>	Sets the default color scale for all phase images.
<b>W/L</b>	Sets the default value for display of CT and CTA images.
<b>Start Page</b>	Used to select the page in which QGS+QPS opens upon initial launch. If the loaded data cannot be displayed in this window, QGS+QPS opens instead on the first applicable window in the sequence.
<b>Segments</b>	
<b>Convert</b>	Converts old ARG studies from 20 segments to 17 segments (if applicable). If unchecked, old ARG studies will load in the number of segments they were saved with.
<b>Normal Limits</b>	Sets default perfusion normal limits.
<b>Browse</b>	Allows selection of default normal limits.
<b>Results File</b>	Sets results file dataset ID.
<b>Prompt</b>	Toggles prompting for a file name when saving results.

The following settings are available on the bottom section of the **General** tab page in the **Page Options** section: Availability of any setting is specific to the page selected in this section. Each QGS+QPS window can be customized with its own window-specific parameters.

<b>Page Sequence arrows (◀▶)</b>	Allows the ability to reorder the page sequence as desired. To change the default sequence of QGS+QPS pages listed at the top of the application's main window, click on a window name and use the arrows to move it (left or right) to the desired location in the sequence.
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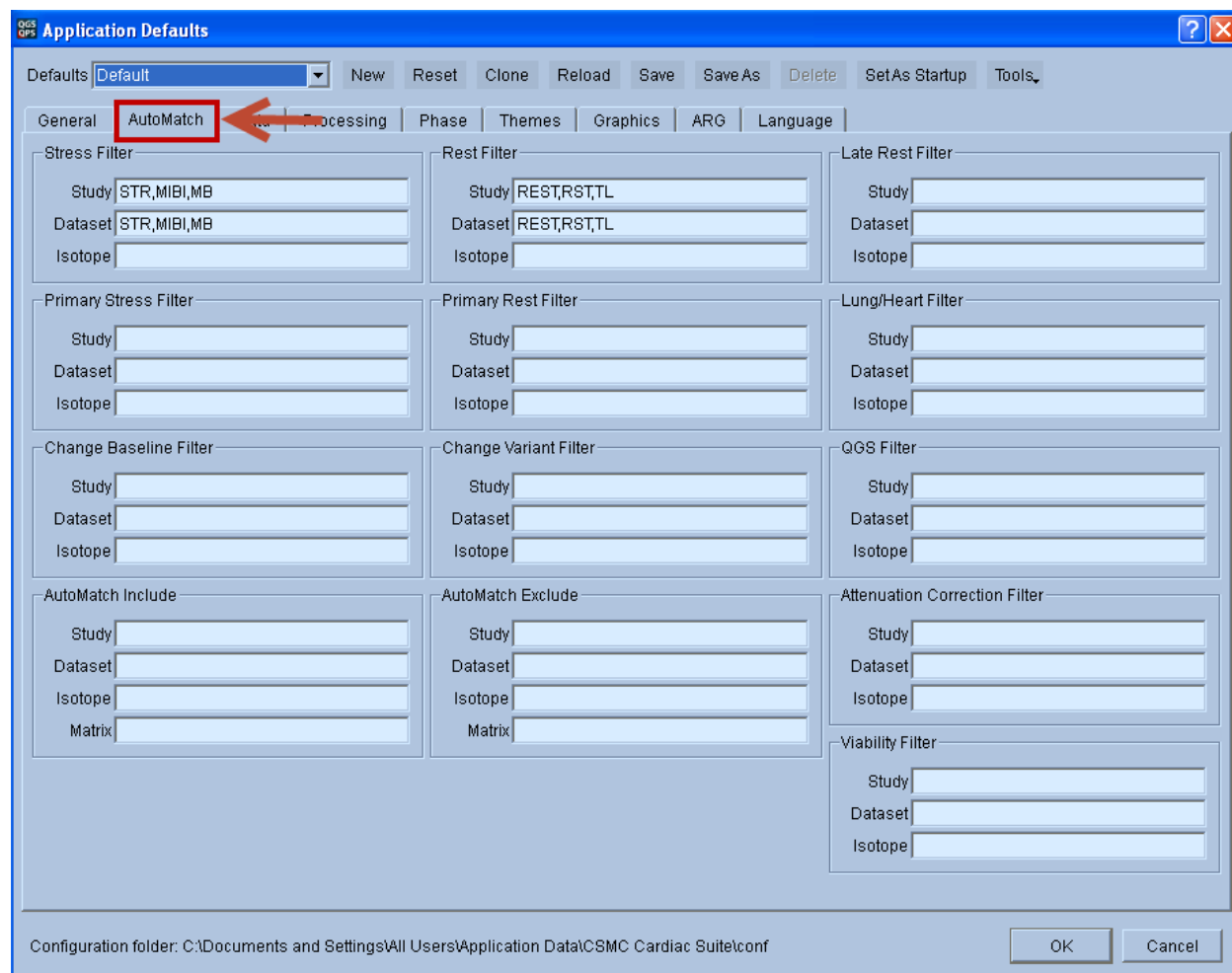
<b>Label</b>	Toggles image labeling.
<b>Orient</b>	Toggles orientation labels adjacent to each image.
<b>Lines</b>	Toggles motion reference lines.
<b>Spin</b>	Toggles continuous spatial cine.
<b>Gate</b>	Toggles temporal cine.
<b>Oblique</b>	Toggles the display of transverse datasets within to short axis orientations.
<b>Score</b>	Toggles the display of visual scores polar maps.
<b>Rock</b>	Toggles bi-directional angular projection cine for sub-360° acquisitions.
<b>Multiple</b>	Toggles multiple mode.
<b>Box</b>	Toggles LV surface orientation box.
<b>Contours</b>	Toggles LV surface contour display.
<b>ED</b>	Toggles end-diastole contour/surface reference overlay.
<b>ES</b>	Toggles end-systole contour/surface reference overlay.
<b>Blur</b>	Toggles 1-2-1 temporal smooth of displayed slices.
<b>Smear</b>	Toggles 1-2-1 spatial smooth of displayed slices.
<b>Skip</b>	Toggles display of every second slice.
<b>Surface</b>	Selects surface render mode (Inner, Outer, Both, Middle, Function).
<b>Function</b>	Selects parametric function mode (when Surface is set to Function).
<b>Grid</b>	Selects grid mapping mode.
<b>View</b>	Selects surface orientation.
<b>Zoom</b>	Selects planar zoom.
<b>Scale</b>	Selects surface zoom.
<b>Value</b>	Selects the value to be displayed in phase information labels.
<b>Units</b>	Selects the units to be used for phase information labels.

<b>Snapshot File</b>	Sets snapshot file dataset ID.
<b>Select</b>	Selects preferred page display mode (Auto, 1, 2, 3, 4, QGS or QPS). QGS is for gated data and QPS is for non-gated data. It is possible to select both QPS and QGS; in this case, QPS will override the QGS selection and only non-gated data appears.
<b>Active</b>	Activates/Deactivates page selection on the toolbar.
<b>Report</b>	Toggles ARG reporting panel.

## 14.4 AutoMatch Tab

The **AutoMatch** tab in the defaults settings can be used to set the default automatic file and object attribute selection parameters. The use of the filters is necessary when object attributes are not correctly being recognized by the application due to missing DICOM information.

The automatic file selection parameters determine the Procedure ID, View ID, or Isotope that QGS+QPS searches for when it selects one or more datasets for each category.



The following settings are available on the **AutoMatch** tab page of the Application Defaults editor:

<b>Stress Filter</b>	Tags a dataset as stress based on text strings in study, dataset or isotope fields.
<b>Rest Filter</b>	Tags a dataset as rest based on text strings in study, dataset or isotope fields.
<b>Late Rest Filter</b>	Tags a dataset as Late (delayed) rest based on text strings in study, dataset or isotope fields.
<b>Primary Stress Filter</b>	Tags a dataset as primary stress based on text strings in study, dataset or isotope fields. This is useful when multiple stress datasets may be present (i.e., Stress immediate, Stress 30 minutes, Stress 1 hr.).
<b>Primary Rest Filter</b>	Tags a dataset as primary rest based on text strings in study, dataset or isotope fields. This is useful when multiple rest datasets may be present.
<b>Lung/Heart Filter</b>	Tags a dataset to be used for Lung/Heart calculations
<b>Change Baseline Filter</b>	Tags dataset to be used as baseline dataset for the Change Analysis feature.
<b>Change Variant Filter</b>	Tags dataset to be used as the variant dataset (one that is compared against the baseline dataset) for the Change Analysis feature.
<b>QGS Filter</b>	Tags dataset to be used for QGS Results calculations.
<b>AutoMatch Include</b>	Tags a dataset as active based on text strings in study, dataset, isotope or matrix fields. In the Dataset Editor, active datasets are highlighted in yellow.
<b>AutoMatch Exclude</b>	Tags a dataset as inactive based on text strings in study, dataset, isotope or matrix fields. In the Dataset Editor, inactive datasets are not highlighted.
<b>Attenuation Correction Filter</b>	Tags a dataset as one that has been Attenuation Corrected.
<b>Viability Filter</b>	Tags a dataset as Viability.

The following actions are supported:

<b>OK</b>	Applies AutoMatch settings for the current QGS+QPS processing session and closes the Application Defaults screen. Settings are <b>not</b> saved for future processing sessions.
<b>Cancel</b>	Closes the Application Defaults screen <b>without</b> applying or saving changes.
<b>Save</b>	Saves all AutoMatch settings to a file and are effective for every QGS+QPS session until changed and re-saved.
<b>Reset</b>	Restores the AutoMatch defaults to the factory shipped settings.

### Using Filters to Automatically Determine Dataset Category

Filters are used to automatically identify datasets as stress, rest, raw, short axis etc. A dataset is identified by a **Study** name and a **Dataset** name. Carefully selecting filters to identify datasets

allows the QGS+QPS application to run automatically and in a continuous manner without user intervention. For example, if the QGS+QPS application is capable of determining which of all the datasets selected are the stress and rest short axis datasets, then selection of normal limits and generation of results is automatic. If QGS+QPS is unable to determine the stress and rest short axis datasets, then results may not be calculated and the user must manually set the datasets using the **Dataset Selector** pull-down menu.

Definitions used in this section:

**Study:** refers to the name of a dataset and typically identifies the dataset in general terms. For example, a dataset with a study name of Rest Thallium suggests that the data is from either a rest thallium acquisition or the data was generated from a processing procedure (raw data or processed data, respectively).

**Dataset:** refers to the name of a dataset and typically identifies the dataset in more specific terms. For example, a dataset name containing Raw or Short Axis suggests the dataset is raw data or processed data, respectively.

When the two terms are used together, a dataset can be uniquely identified. A dataset with a **Study** name of Rest Thallium and **Dataset** name of Short Axis identifies the dataset as a set of rest thallium short axis tomographic slices.

The QGS+QPS application uses internal criteria to distinguish raw datasets from processed datasets and then uses the **AutoMatch** filter settings to determine which processed datasets are to be used for automatic processing. In particular, QGS+QPS needs to be able to identify a **Primary** stress and/or rest short axis dataset. Typically, a study will contain a processed stress dataset and a processed rest dataset but QGS+QPS will work if only one processed dataset is selected and used as input. If a study contains more than two processed datasets (for example, processed stress, processed rest, processed 24 hour delayed etc.), QGS+QPS will need a way to identify which two datasets are the **Primary** stress/rest datasets.

The user has two methods to set the correct Primary stress/rest datasets.

1. Use the **Dataset Editor** and click the required Stress (or Rest) and Primary labels for the datasets to highlight them (yellow Stress, yellow Primary).
2. Adjust the filter settings on the **AutoMatch** page of the **Defaults Editor** and let QGS+QPS select (highlight) the correct datasets.

Using method 1), the user cannot select a Primary dataset unless the Stress and/or Rest label for the dataset has also been selected. A further constraint is imposed (using either method) in that QGS+QPS will not allow two Primary Stress datasets or two Primary Rest datasets, only one of each.

Note: Using the first method, the user cannot select a Primary dataset unless the Stress and/or Rest label for the dataset has also been selected. A further constraint is imposed (using either



method) in that QGS+QPS will not allow two Primary Stress datasets or two Primary Rest datasets, only one of each.

QGS+QPS, along with the **AutoMatch** filter criteria, uses a process of “pattern-matching” to match user string entries in the Study and Dataset fields with the Study name and Dataset name to identify stress datasets, rest datasets, a primary stress dataset and a primary rest dataset. Optionally, isotope criteria may be entered in the Isotope field to further narrow down the identity of the correct datasets.

The string entries may consist of complete names (e.g. Stress) or partial names (e.g. Str), numbers (e.g. 24) and can include the wildcard characters question mark (?) and asterisk (\*) for single and multiple characters, respectively. A carat (^) can be used to match the beginning or the end of a line. Multiple entries for the same field are permitted but must be separated by commas and not have any spaces.

Note: Use longer filter strings rather than shorter. Shorter strings can have unwanted matches. For example, if **res** is used for a rest filter and STRESS for stress, an image called sax-**stress** would have a two conflicting matches. A better filter would be -RES. For example, for patient studies that include emission files with View IDs of Raw -EM, enter -EM in the **AutoMatch Exclude View ID** field to exclude only the Raw -EM files but not all other Raw projection files.

Automatch text fields are not case sensitive.

Multiple text strings may be entered, separated by commas.

## Examples using AutoMatch with filters

### General examples

#### 1. Stress Filters.

If you are using a dual isotope protocol, the stress filter may already work. If not, remove any text that appears in the **Isotope** field, take a common string from the View ID and enter that value as the stress filter in the **Dataset** field.

For example, if you currently label your stress datasets as:

- Raw proj -str
- SAX -str
- Proc GSPECT -str

It is not necessary to enter each View ID in the **Dataset** field of the Stress Filter. Simply enter **-str** (the common text string), and QGS+QPS tags these datasets as stress.

#### 2. Rest Filters.

For example, if you currently label your rest datasets as:

- Raw proj -rst
- SAX -rst
- SAX -del
- Proc GSPECT delay

It is not necessary to enter each View ID in the **Dataset** field of the Rest Filter. Enter **-rst**, **del** (the common text strings), and QGS+QPS tags these datasets as rest.

### 3. Late Rest Filter.

Use this filter when you want to redistribute an ungated SAX delayed rest dataset. This filter also provides a third dataset type which you can create a report for. If you associate datasets with **Late**, you can then select a sequence that includes **Late**, automate the scores, and create a report.

### 4. Primary Stress/Rest Filters.

Determine if the program finds more than one non-gated stress or nongated rest SAX dataset by checking the following:

- If QGS+QPS auto matches on two datasets, and they are properly labeled stress and rest, then the program automatically calculates the TID ratio from these files when it performs processing and you need to take no action.
- If QGS+QPS auto matches on multiple stress or rest datasets, as sometimes can be the case for corrected and uncorrected files, then select the common text string of the stress and the rest SAX datasets that should be considered as primary and enter it in the View ID for the TID calculation.

In these cases, the exact stress and rest datasets must be specified.

### 5. Lung/Heart Filter.

QGS+QPS calculates the Lung/Heart ratio (LHR) based on the projection dataset of your choice. It is not necessary to enter the entire View ID of your preferred dataset. For example, if you use a dual isotope protocol and you want QGS+QPS to calculate the LHR on the rest dataset, enter **TI** in the **Isotope** field. If you do not use a dual isotope protocol and want QGS+QPS to calculate the LHR on the rest dataset, enter a text string that is common to the Procedure ID or View ID.

For example, you may label your rest datasets as:

- Raw proj -rst
- Proj -rst

You only need to enter **-rst** in the Dataset field.

### 6. AutoMatch Include and AutoMatch Exclude Filters.

If you select all datasets before launching QGS+QPS, the datasets are filtered based on the factory default **AutoMatch Include** and **AutoMatch Exclude** parameters. To see which datasets are active initially, click on **Edit** in an active window and view the list. Define the active datasets for the **AutoMatch Include** filter, and the inactive datasets for the **AutoMatch Exclude** filter. On the **Edit** list, the active datasets (**AutoMatch Include** filter) are highlighted (yellow), and the inactive datasets (**AutoMatch Exclude** filter) are not highlighted. By default, QGS+QPS accepts a wide range of dataset types. To exclude other dataset types, enter criteria in the **AutoMatch Exclude Dataset** field for:

- VLA files
- HLA files
- Emission and transmission files

- Any other datasets, such as reference or test files, that you do not want loaded into QGS+QPS.

For example, you may label some of the above-mentioned datasets as:

- Stress VLA
- Delay HLA
- Raw -EM
- Raw -TR
- Stress -TRA

For these examples, use these common text strings to enter in the **AutoMatch Exclude Dataset** field:

VLA, HLA, EM^, -TR, TRA

Note: It is not necessary to use both **AutoMatch Include** and **AutoMatch Exclude**. In most cases, **AutoMatch Exclude** is used to filter out unwanted datasets.

### 7. QGS Filter

This pertains to the gated short axis dataset to be used by default when reporting EF, motion, etc. You can specify datasets to be associated with QGS, which you can then configure to appear by default in specific windows by selecting the QGS button in the window-specific parameters in the General tab of the Defaults window.

### 8. Attenuation Correction Filter.

Define criteria for recognizing attenuation-corrected datasets for easier selection and comparison on display windows.

For example, if you use -AC as the **Attenuation Correction** filter, it means that for any dataset containing the text string -AC in its name are considered Attenuation Corrected.

### 9. Base Line Filter.

Define criteria for recognizing baseline datasets for easier selection and comparison on display windows. For example, you can set AXIS as the Baseline filter. This means that for any dataset containing the text string AXIS in its name, images are tagged as Base images in both the exam object list and the object selector.

#### *Specific Case example 1*

In this first example, a demo patient will be used. All of the datasets for this patient will be selected as input to the QGS+QPS application.

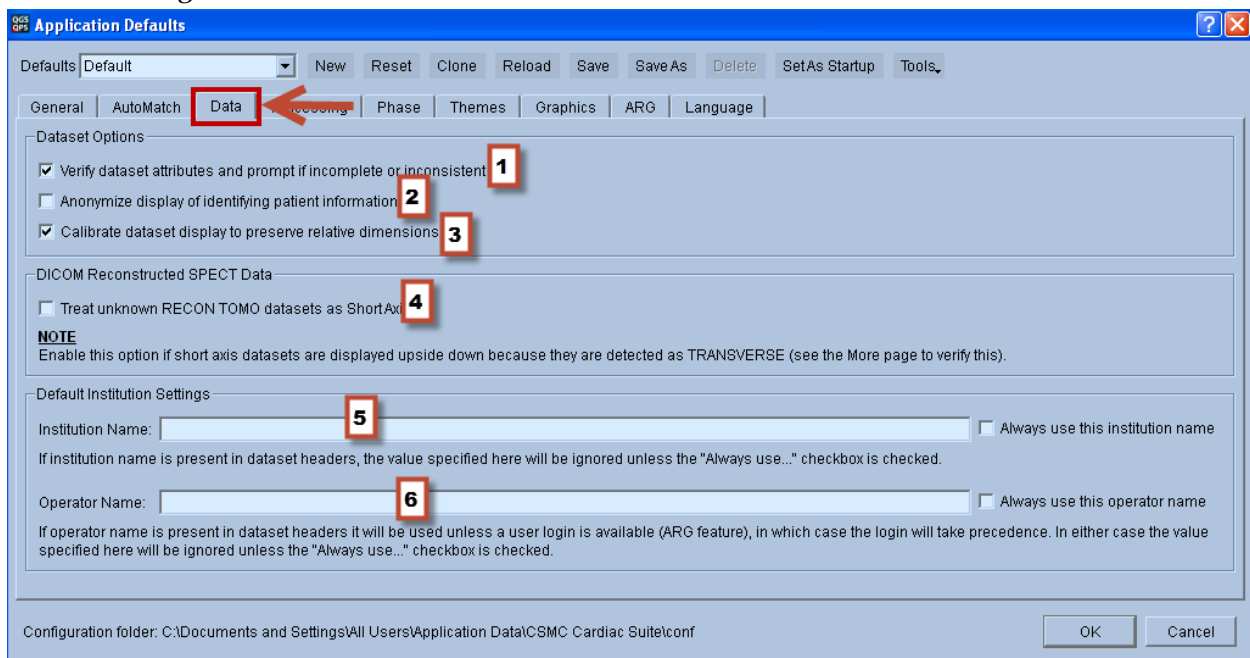
Selecting all the datasets for this demo patient and then clicking the QGS+QPS button will run the QGS+QPS application with factory default settings for **AutoMatch**. Opening the **Dataset Editor** reveals the default rest and stress datasets including primary datasets highlighted in yellow based on the current **AutoMatch** settings. Using the factory shipped filter settings, the STR MIBI Prone short axis dataset (Stress SAX) is automatically selected as the Primary stress dataset by QGS+QPS. Normally, the STR MIBI Supine short axis dataset (Stress SAX) would be used as the Primary stress dataset.

As mentioned previously, the user can use the **Dataset Editor** to manually select the correct Stress/Rest Primary datasets. However, careful setting of filter parameters on the **AutoMatch** page requires no manual intervention by the user. In this example, the user could type Supine (or Sup, or sup etc.) in the Study field of the Primary Stress Filter, click OK or Save to automatically set the Primary Stress dataset.

Setting **AutoMatch** filters for the first time is probably done best by clearing the existing factory shipped settings and then trying the most common combinations of Study name and Dataset name for the user's site naming conventions.

## 14.5 Data Tab

The **Data** tab in the defaults settings can be used to set general default settings dealing with dataset settings.



The following settings are available on the **Data** tab:

### Dataset Options

1. When this option is checked, QGS+QPS automatically opens the **Dataset Editor** window when it first launches anytime the automatch criteria cannot determine which normal limits database(s) to apply.
2. Check this option to toggle off display of patient identifiers.
3. When this option is checked, all displayed slices from short axis and transverse datasets (gated and ungated) for the patient are scaled so that they share the same number of millimeters per screen pixel, assuming that they share equal screen zooms (as is the case for all side by side displays). You typically use this feature when you display PET and SPECT images in the same window. For example, if you display PET and SPECT data side by side in the Splash window, you may see an apparent visual discrepancy in the LV sizes

between PET and SPECT for the same patient, because PET image data typically have smaller pixel sizes than SPECT image data. This option compensates for this visual discrepancy.

#### DICOM Reconstruction SPECT Data

4. When this option is checked, the application will assume that DICOM datasets that are of RECON TOMO or GATED RECON TOMO image type but contain no view type are short axis datasets.

#### Default Institution Settings

5. Use this field to enter a default institution name. This will be used for the institution field for the dataset legend within secondary screen captures.

Note: If institution name is present in dataset headers, the value specified here will be ignored unless the “Always Use this institution name” checkbox is also selected.

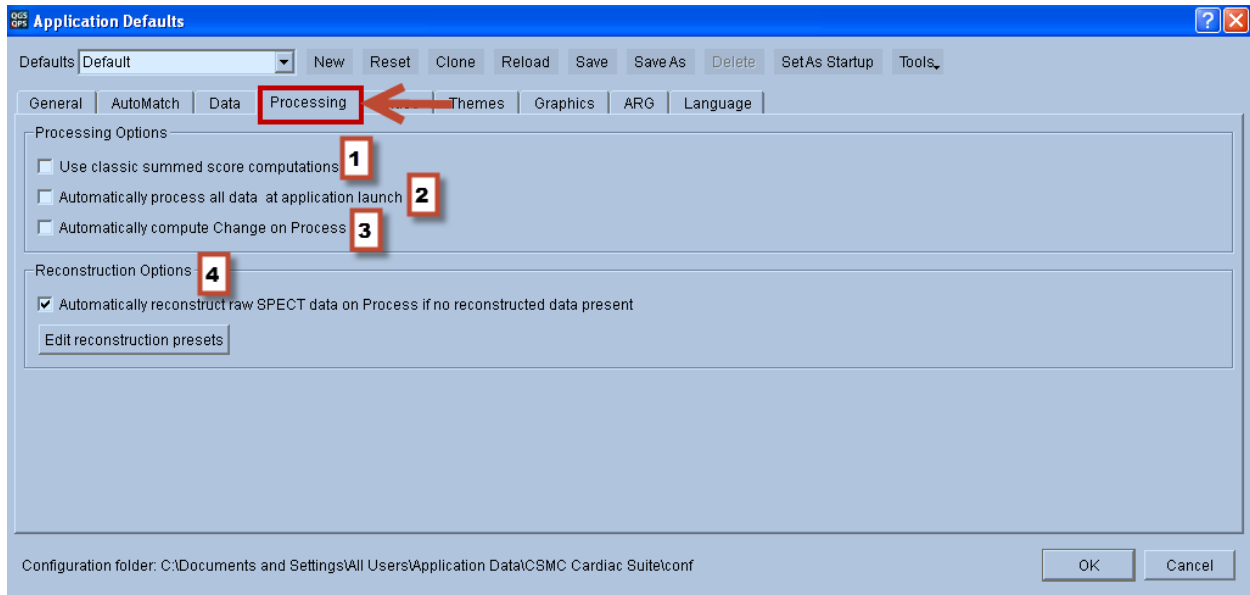
6. Use this field to enter a default operator name. This will be used for the operator name field for the dataset legend within secondary screen captures.

Note: If operator name is present in dataset headers it will be used unless a user login is available (ARG feature), in which case the login will take precedence. In either case the value specified here will be ignored unless the “Always Use this institution name” checkbox is also selected.

Note: Operator name is specific to a user at the Windows Operating System level (one logged into Windows) and not at the application level. If all QGS+QPS defaults are created using the same Windows user, the operator name cannot be different as this field is user specific to the Windows Operating System user.

## 14.6 Processing Tab

The **processing** tab can be used to specify dataset processing related settings.



The following settings are available on the **Processing** tab:

1. When this option is checked, QGS+QPS using the classic summed score computation rules. These are outlined below.

When this option is checked, the following rules are applied for calculating summed scores (SRS, SSS, SDS) for perfusion datasets:

- The first exception rule is when a 4 appears in a segment for stress, and a 3 appears in the same corresponding segment for rest, the difference is a zero, rather than 1.
- The second exception rule is when a 3 appears in a segment for stress, and a 2 appears in the same corresponding segment for rest, the difference is a zero, rather than 1.
- The third exception rule is when a 1 appears in a segment for stress, and a 1 also appears in the same corresponding segment for rest, it is considered as 0 for all three summed scores (SRS, SSS and SDS).

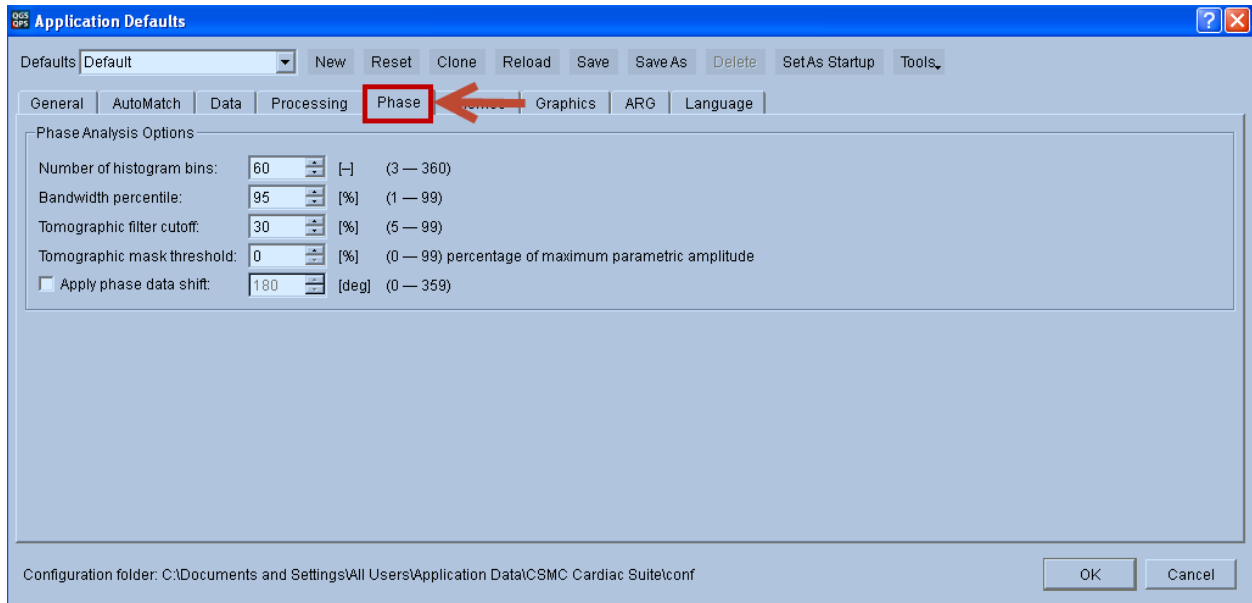
Note: For serial comparisons, the same scoring rules should be used for both studies.

2. When this option is checked, QGS+QPS automatically processes all loaded studies when it is launched.
3. When this option is checked, QGS+QPS automatically compares loaded and processed datasets when the **Change** page is displayed.

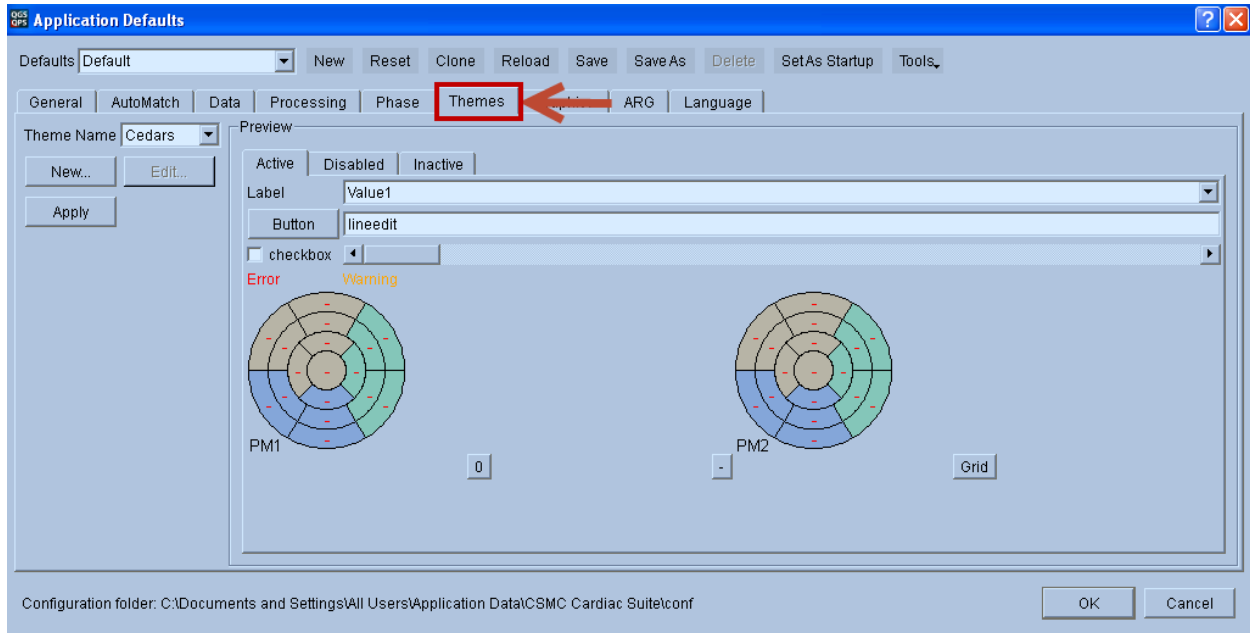
- This option specifically controls settings for the reconstruction and motion correction programs (AutoRECON and MoCo). These options may not be available on all platforms. Please refer to the AutoRECON reference manual for more details.

## 14.7 Phase Tab

The **Phase** tab of the defaults editor controls phase related parameters. The default factory settings are recommended for Phase Analysis. These settings should only be modified by advanced users dealing in research applications.



## 14.8 Themes Tab



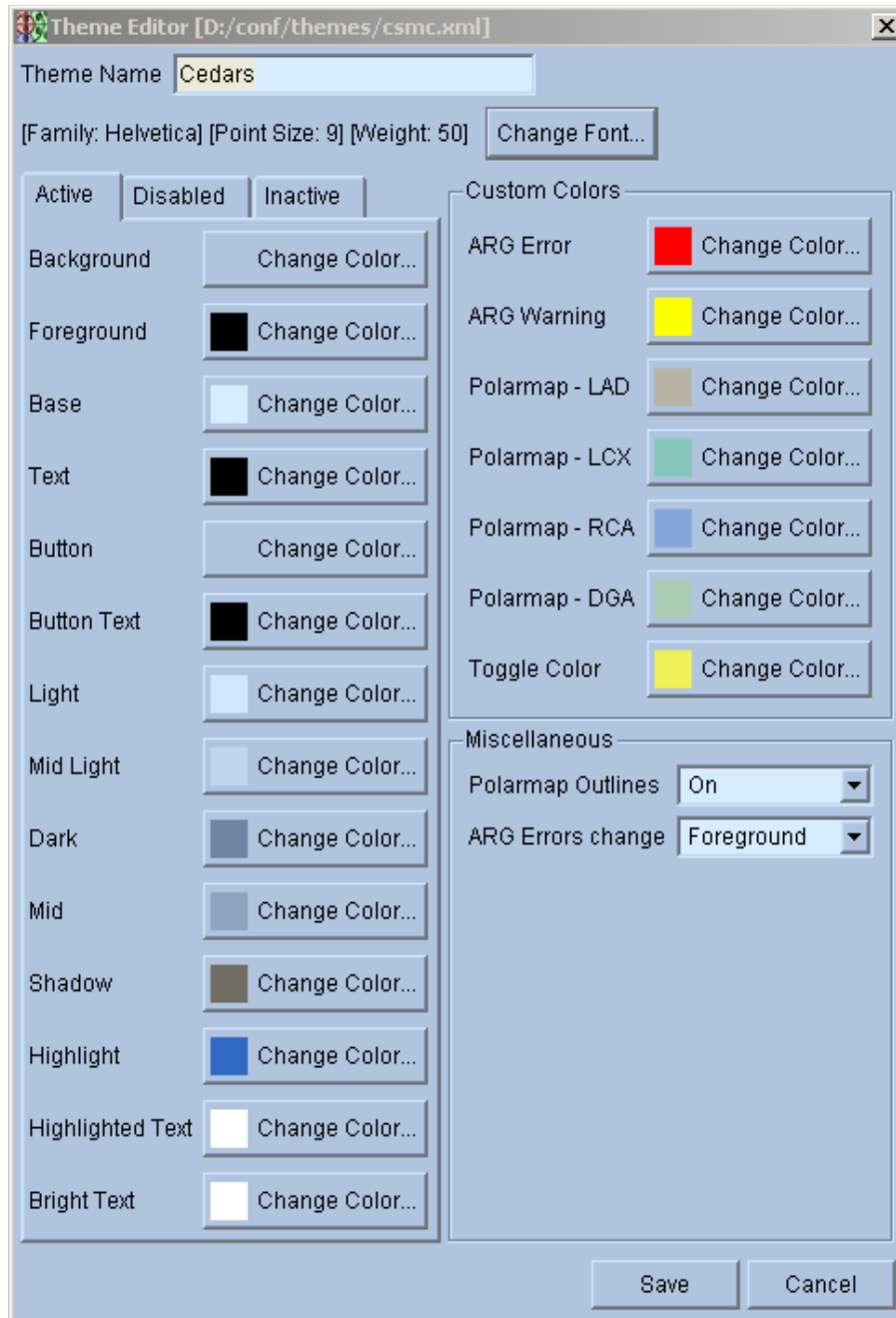
The Themes tab page allows the user to set default colors and fonts for QGS+QPS's user interface (buttons, labels, background etc.). The user can view changes in the Preview area prior to saving them permanently. The user creates a new theme by clicking the **New...** button or the edit the currently displayed theme (in the Theme Name box) by clicking the **Edit...** button.

To change colors and fonts for the currently selected theme click the **Edit** button to display the Theme Editor window.

To change the font, click the **Change Font...** button to display the Select Font win. The Select Font window is similar to the regular Windows 2000 and Windows XP dialog for font selection. Select font, font style and font size from this window and then click **OK** to accept the choices or **Cancel** to abort.

There are also other choices for the user interface such as Foreground/Background color etc. for the Active, Disabled, and Inactive regions of the display. The user is allowed great range in tailoring the user interface to his/her liking.





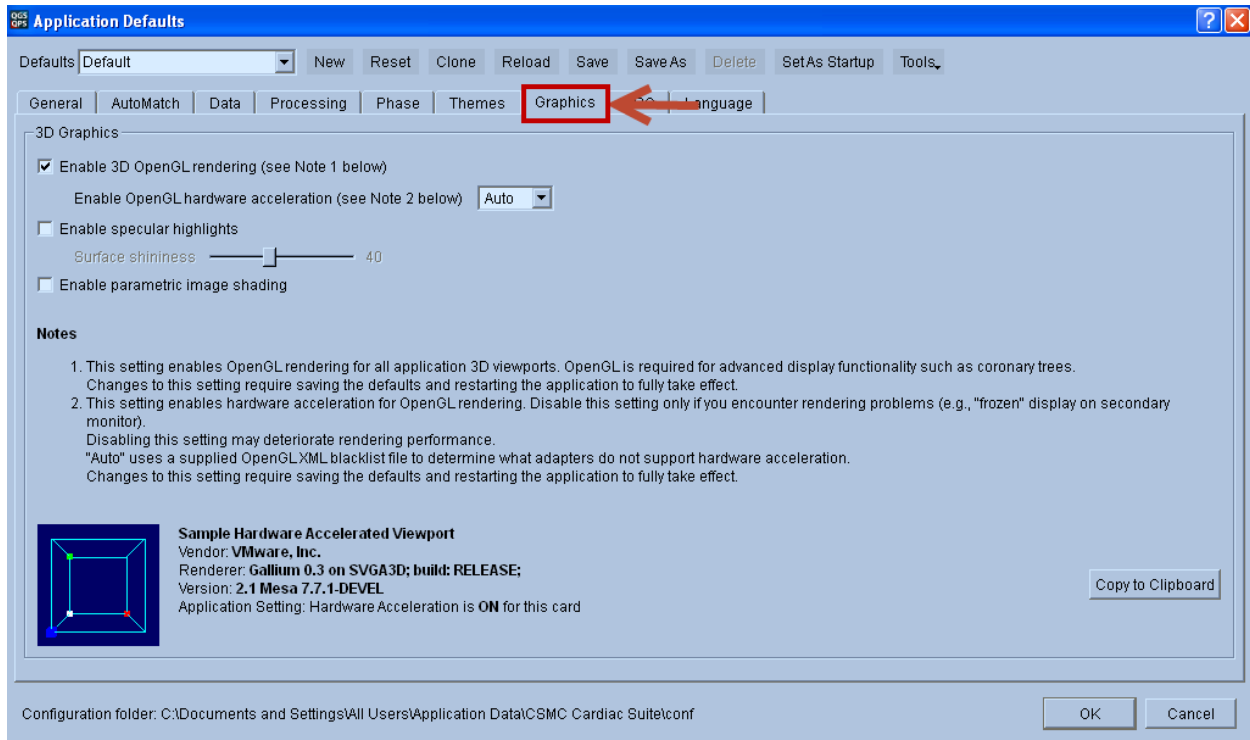
Theme Editor window

## 14.9 Graphics Tab

The **Graphics** tab page allows the user to set certain parameters that affect the rendering of 3D surfaces. In general, using hardware acceleration is beneficial as the program is more responsive when surfaces are interactively rotated. In some instance, however, there may be degradation in image quality that may justify disabling hardware acceleration. QGS+QPS uses OpenGL hardware

acceleration, which is available on most systems. The following options are available in the graphics tab:

<b>Enable 3D OpenGL hardware rendering</b>	<p>If hardware rendering causes problems, it may be necessary to disable OpenGL by unchecking this checkbox. Turning off this option may adversely affect performance for some advanced visualization tasks such as viewing coronary trees. In case of issues with rendering, try turning off hardware <i>acceleration</i> first (see below).</p> <p>Note: changing this setting will only affect viewports that have not been created yet, i.e., to pages that have not been visited. To apply this setting fully, save the defaults and restart the application.</p>
<b>Enable OpenGL hardware acceleration</b>	<p>If hardware acceleration causes problems, it is recommended to disable OpenGL hardware acceleration by setting this option to <b>No</b>.</p> <p>A typical issue involves dual monitor setups where on the secondary display the 3D viewports appear “frozen.” If this is the case, set acceleration to <b>No</b>, save the defaults and restart the application.</p> <p>Note: changing this setting will only affect viewports that have not been created yet, i.e., to pages that have not been visited. To apply this setting fully, save the defaults and restart the application.</p>
<b>Enable specular highlights</b>	<p>If OpenGL is enabled, surfaces can be rendered with added specular reflections. This adds a “shiny” appearance to the surfaces, potentially making it easier to visually assess the shape of the surface. This can be useful for isosurfaces, but may also be distracting. If checked, the amount of specular reflection can be controlled using the Surface shininess slider.</p>
<b>Surface shininess</b>	<p>Controls the amount of specular reflection (or “shine”), from 0 (none) to 100 (maximum reflection).</p>
<b>Enable parametric image shading</b>	<p>If enabled, parametrically-mapped surfaces (such as perfusion-, Fourier phase- and amplitude-mapped surfaces) are also shaded. In some cases, the shading may interfere with the interpretation of the parametric mapping, hence the ability to disable this option.</p>



Graphics tab

### Hardware rendering and acceleration

The **Notes** in the graphics tab help describe the OpenGL hardware rendering options. The viewport with the cube at the bottom left of the tab is active and can be used to determine what functionality is available on multiple monitors by dragging the **Defaults** dialog to another screen, then attempting to rotate the cube by left-dragging with the mouse. If the rotation succeeds, hardware acceleration is supported on that monitor. If the viewport appears frozen, hardware acceleration is not supported and should be disabled for this system, which will allow OpenGL viewport to function correctly on all monitors, trading rendering performance for compatibility.

It is also possible to use a configuration file to let the system decide whether to enable hardware acceleration or not “automatically.” Acceleration will be enabled by default if the setting is set to **Auto**, unless the identifier of the graphics card is found in a “blacklist” file named **opengl.xml** and located in the system’s configuration folder for CSMC software (listed at the bottom of the **Defaults** dialog after **Configuration folder**). The contents of this XML file look as follows:

```
<!DOCTYPE OpenGLRendererBlackList>
<OpenGLRendererBlackList>
  <Renderer Id="Implementation_String_1" />
  <Renderer Id="Implementation_String_2" />
</OpenGLRendererBlackList>
```

...

```
<Renderer Id="Implementation_String_n" />
```

```
</OpenGLRendererBlackList>
```

Where the line containing “Implementation\_String\_x” may be repeated for a variety of graphics adapters. A complete line can be obtained by clicking **Copy to Clipboard** in the **Graphics** tab. For the adapter in the graphics tab example above, the line with the implementation string should read

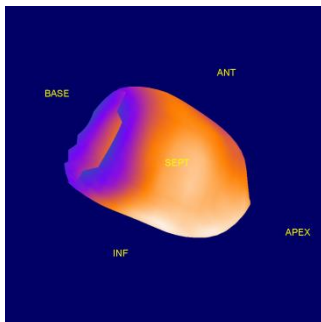
```
<Renderer Id="NVIDIA Corporation: GeForce 8800 GTS/PCI/SSE2" />
```

If the setting is **Yes**, hardware acceleration will be enabled whether the adapter’s identification string is found in the blacklist file or not. This can be used for testing without requiring changes to the blacklist file.

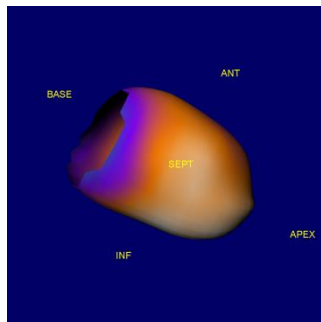
### Highlights and shading

The following figures show examples of parametrically-mapped perfusion surfaces with various settings for the graphics options.

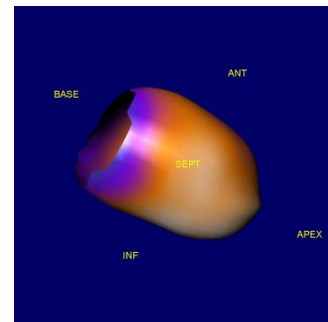
**NOTE:** specular reflection and shading should be taken into account if parametric surfaces are evaluated. If such surfaces are used to assess the patient’s condition, it is recommended to turn off parametric shading and specular reflections.



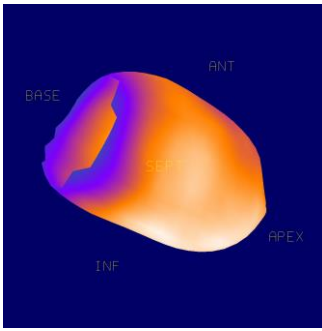
**Hardware acceleration, no parametric shading or specular reflections**



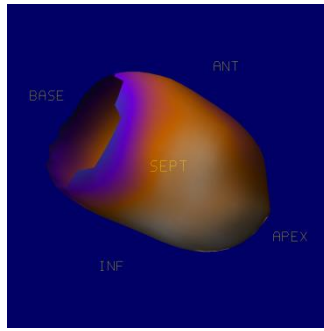
**Hardware acceleration, parametric shading enabled**



**Hardware acceleration, parametric shading and specular reflections enabled**



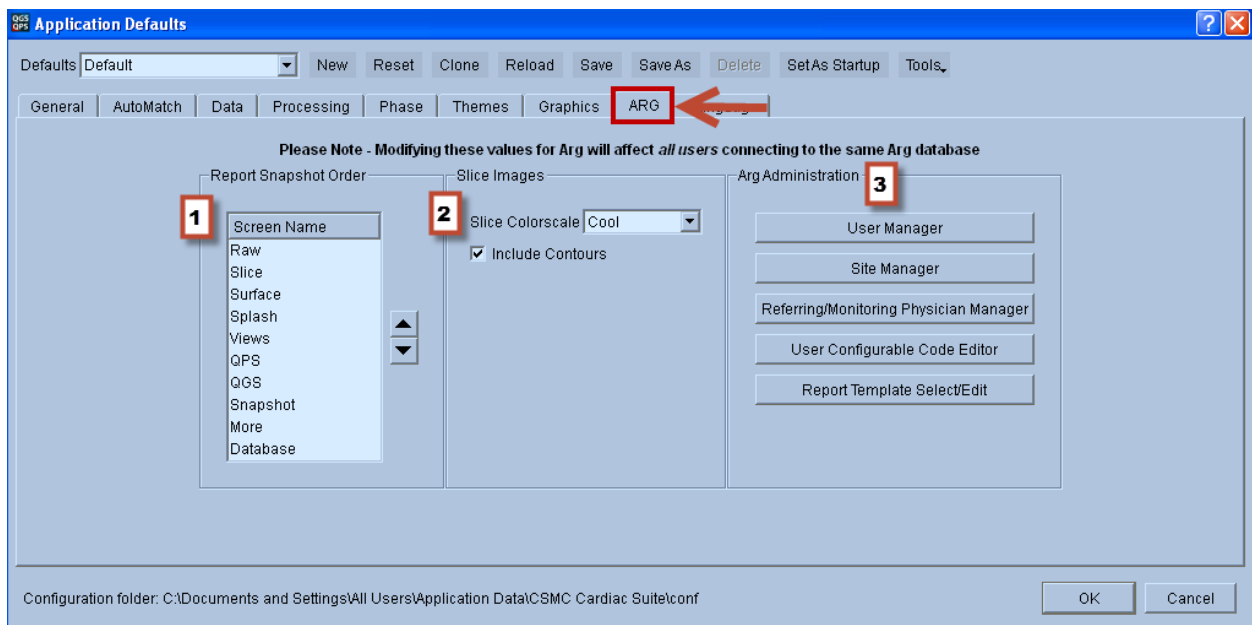
No hardware acceleration, parametric shading, or specular reflections



No hardware acceleration, parametric shading enabled, no specular reflections

## 14.10 ARG Tab

The **ARG** tab within the defaults editor contains options specifically pertaining to Cedars-Sinai's Automated Report Generator (ARG). This option may not be available on all platforms.

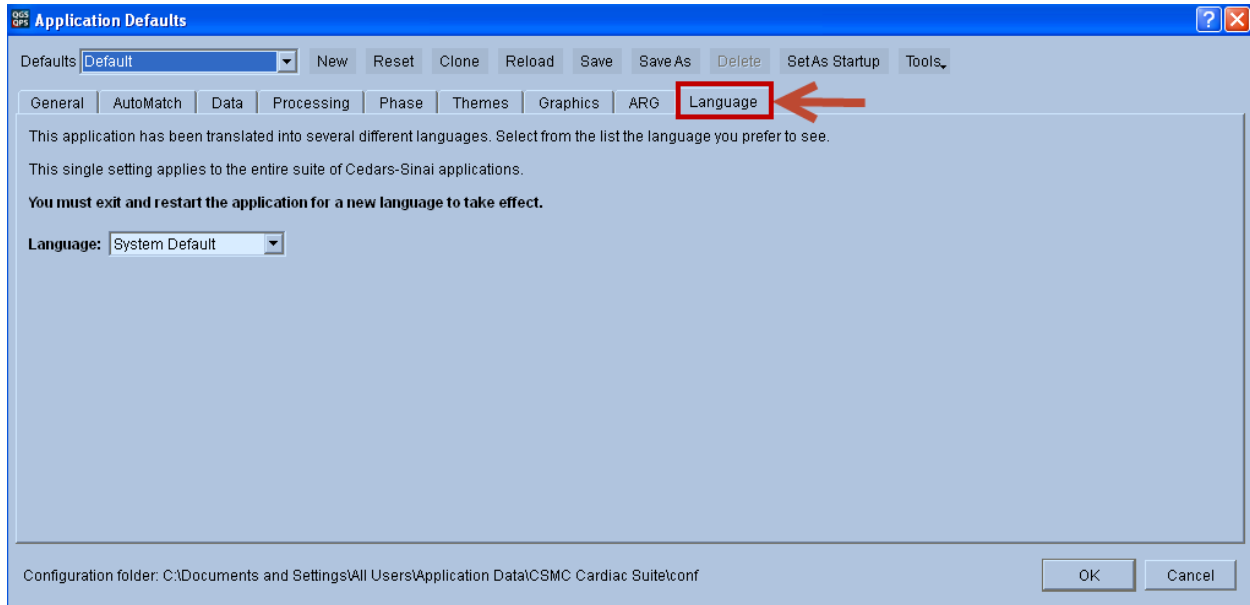


1. Report Snapshot order is the order in which captured snapshots should appear in the report. If multiple snapshots of the same page are included, they will be appended in the order they were created.
2. Slice images are automatically captured for all studies at the time of saving. These are included in the report by default, but can be removed, by creating a manual report and removing the slices from the perfusion page.
3. The ARG Administration section provides a method within QGS+QPS to access the QARG administrative features. For descriptions on the dialogs here, please refer to the administration section of the ARG reference manual.

## 14.11 Language Tab

The **Language** tab within the defaults editor can be used to localize the user interface to a non-english language. QGS+QPS supports a wide range of languages, including but not limited to: Chinese (Simplified), Czech, Danish, Dutch, English, Finnish, French, German, Hungarian, Italian, Japanese, Korean, Norwegian, Polish, Portuguese, Russian, Spanish, Swedish, Turkish.

**Note: Application must be restarted for the new language to take effect.**



## 15 Algorithms

This is a brief overview of the LV processing algorithms used in QGS+QPS. These algorithms include volumetric LV segmentation, endocardium and epicardium definition, and segmental normal limits generation and application. A variety of global and regional metrics can be derived from the application of these algorithms to datasets. This overview does not describe in any detail the theory behind, or the design and validation of the CSMC (Cedars-Sinai Medical Center) quantification and analysis algorithms that are at the core of QGS+QPS. For a more detailed overview, see the Bibliography section in this document.

### 15.1 Volumetric LV Segmentation

Volumetric LV segmentation is a two-step process. The first step is an approximate segmentation, used to locate the region in which the LV lies. This step uses a variety of clustering techniques and heuristics to eliminate many extraneous structures (e.g. the bowel) from consideration, and provides a starting LV location and shape for the second, more exact, segmentation step. This second segmentation uses sub-voxel sampling within an iteratively refined ellipsoidal coordinate system to generate a set of points with high likelihood of belonging to the mid-myocardial

surface. This set of points is then used, in conjunction with a set of spatial continuity constraints, to generate a mid-myocardial surface. This mid-myocardial surface, in conjunction with the underlying data and various physically based constraints, is then used to generate the inner and outer walls and valve plane.

## 15.2 Normal Limits Generation and Perfusion Quantification

The QGS+QPS normal limits use a simplified approach as presented at the 2004 ASNC (*J Nucl Cardiol* 2004;11(4):S12). Briefly, ellipsoidal model and contours derived by QGS+QPS algorithm are used to extract polar maps samples from the patient data. Patient polar maps are compared to the set of polar maps (obtained from normal low-likelihood patients) stored in a given normal database.

**Selection of normal patients for the database.** The standard or normal population consists of patients with a low probability of coronary artery disease that also have a normal test. The low probability is determined by sequential Bayesian analysis of patient history and diagnostic tests other than myocardial perfusion resulting in a value of less than 5%. In addition, an expert interpreter using visual inspection should determine that the images are normal and that contours are derived correctly. Typically, 30-50 patient studies will make up the standard population. Databases are created from the short-axis images.

**Perfusion Quantification.** The normalization factor by which the counts in the test-study are multiplied is found by an iterative technique minimizing the cost function between the study and the normal polar maps included in the database. Subsequently the test-study is compared to the normal limits. The perfusion defect extent (**Defect Extent**) is calculated as the percentage of the total surface area of the left ventricle, for which test-data are below 3.0 mean absolute deviations (approximately equivalent to 2.5 standard deviations) threshold. Average deviation is used instead of standard deviation due to more robust behavior in non-Gaussian distributions. A method for assignment of a defect to a particular vascular territory is based on the assignment of segments to a given territory, based on segmental scores. Estimated percentages of abnormal polar-map pixels in each vessel territory are then reported. Defect extent is marked on the polar map display in the form of “blackout” maps.

**Calculation of Total Perfusion Deficit (TPD).** This measure combines defect severity and extent. A continuous score is assigned to each abnormal polar-map pixel by linear mapping based on the degree the perfusion value fell below the normal limit. A score of 4.0 was assigned to all pixels more than 70% below the normal limit (as derived from subjective criteria used for a score of 4 in visual reading). A score of 0.0 is set for pixels below the minimum abnormal score. Subsequently, TPD is defined as follows:

$$TPD = 100\% * \sum_{a=0}^{a<A} \sum_{p=0}^{p<P} score(a, p) / (4 * A * P) \quad (1)$$

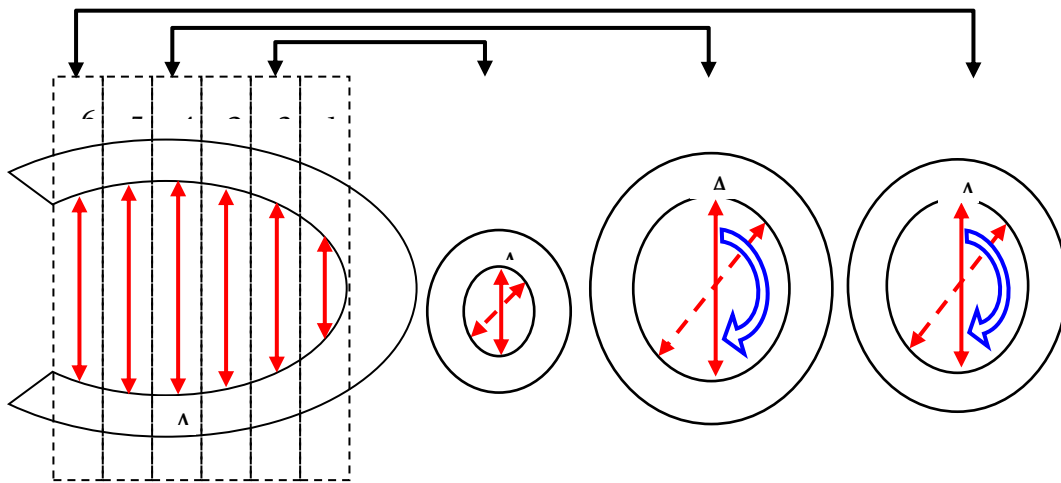
where  $a, p$  are the radial coordinates of the polar map,  $A, P$  is the maximum number of samples in each dimension, and  $score(a, p)$  is the pixel score at the polar map location  $(a, p)$ . The theoretical maximum value for TPD is 100% for a case with no visible uptake (less than 70% below normal) in the entire LV myocardium.

**Segmental Scoring.** Average continuous pixel severity scores are computed within each segment. Segmental scores are rounded to the nearest integer values for each segment. The segmental scores are calculated for stress and rest images independently. Summed scores are derived for stress (**SSS**) and rest (**SRS**) images.

### 15.3 Shape Index

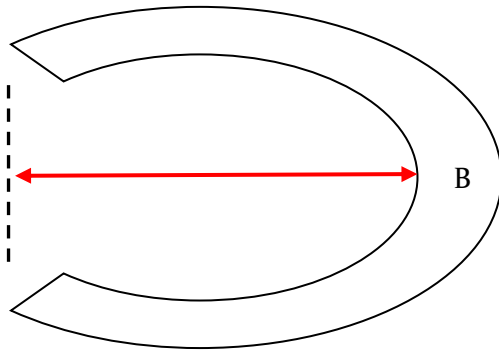
This parameter defines 3D left ventricular (LV) geometry derived from LV contours in end systolic and end diastolic phases. Shape index is defined as the ratio between the maximum dimension of the LV in all short-axis planes and the length of the mid-ventricular long axis.

Abidov A, **Slomka P**, Hayes SW, Aboul-Enein F, Kang X, Yoda S, Nishina H, Yang L, Cohen I, Thomson L, Friedman JD, Germano G, Berman DS. Left Ventricular Shape Index Assessed By Gated Myocardial Perfusion SPECT: A New Scintigraphic Marker Of Congestive Heart Failure. SNM 2004 Abstract, No 500, page 176P



For each short axis plane in the end-diastolic (ED) image series, maximum dimension (A) of the LV is found from the 3D contours derived by the QGS+QPS algorithm, using the endocardial surface as the boundary. Global short-axis end-diastolic dimension (AED) is found as a maximum for all ED short axis slices. The short-axis slice and direction of AED is then used to calculate the maximum short-axis end-systolic dimension (AES) in the end-systolic image series, by measuring the distance between the endocardial points in the identical location (slice and direction) where AED was found.





The long-axis dimension of the myocardium is derived by calculating the distance (B) between the most apical point on the endocardial surface and the center of the valve plane. The ED long-axis dimension (BED) is calculated independently from the ES long-axis dimension (BES).

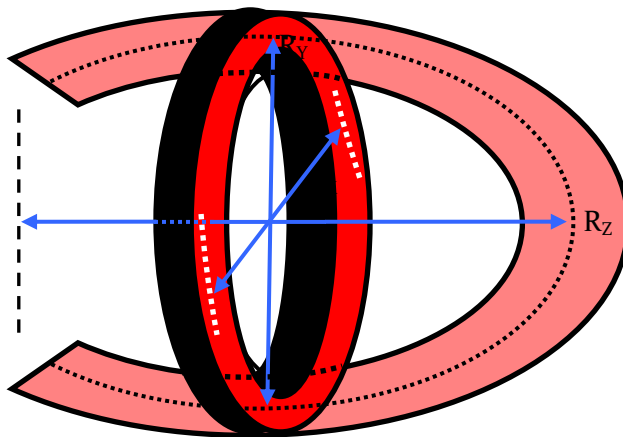
The end-diastolic shape index (SI ED) and the end-systolic shape index (SI ES) are derived by AED/BED and AES/BES, respectively.

#### 15.4 Eccentricity

**Eccentricity** is a measure of the elongation of the LV, and varies from 0 (sphere) to 1 (line); it is calculated from the major axis  $R_z$  and the minor axes  $R_x$  and  $R_y$  of the ellipsoid that best fits the mid-myocardial surface, according to the formula:

$$Ecc = \sqrt{1 - \frac{R_x R_y}{R_z^2}}$$

It is calculated for all slices in a gated series.



#### 15.5 Global Functions

The following standard global functions are computed:

Volume	The LV chamber volume in ml.
Area	The mid-myocardial surface area in $\text{cm}^2$ .

## 15.6 Regional Function

The regional functions are computed by generating parametric surfaces within the canonical LV coordinate system.

The perfusion parametric surface is generated by assigning to each point on the mid-myocardial surface the maximum end-diastolic counts along the count profile normal to that point and lying between the inner and outer myocardial surfaces.

## 16 References

Please visit [www.csaim.com](http://www.csaim.com) for additional references.

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## 17 FAQs

### 1. What should I do if I keep getting "multiple matches" message when loading a study into QGS or QPS?

- i. Ensure that dataset headers contain the sex, isotope, and acquisition state for the study. Normally this information is entered on the acquisition workstation.
- ii. Verify that the necessary matching fields (e.g. patient sex) are getting populated properly. They will show up in yellow in the dataset editor window if they are not being properly populated, which could indicate an error with the DICOM data. Contact the camera manufacturer for more information.
- iii. Verify that there is only 1 active database for sex/isotope/acquisition state combination by going to the Database page and selecting List.... If more than one active database is present, open the database which should not be selected and uncheck the box that says, "Allow automatic selection during processing" and save.

### 2. What is Localize?

The localize feature (manual processing) restricts the initial LV search to the volume defined by the masking graphics.

### 3. What is Mask?

The Mask feature (manual processing) restricts the entire LV segmentation algorithm to only use data within the volume defined by the masking graphics. The feature is most useful when overlying extra-cardiac activity causes the contours to be distorted in certain frames.

### 4. What is Constrain?

The Constrain feature (manual processing) constrains or forces the long axis used by the LV segmentation algorithm to lie on the end-point (Apex and Base) specified by the masking graphics. It is used to force the valve-plane to be at a specific basal position.

## 5. Why are all of my scores missing?

Data must be processed first. Defaults can be set to use Auto-Process and automatic selection of limits file can also be set in defaults.

## 6. What is TPD and how is it different from summed scores?

TPD (Total Perfusion Deficit) is a measure that combines defect severity and extent, which is similar to visual segmental scores. A continuous score is assigned to each abnormal polar-map pixel by linear mapping based on the degree the perfusion value falls below the normal limit. A score of 4.0 is assigned to all pixels more than 70% below the normal limit. A score of 0.0 is set for pixels below the minimum abnormal score. TPD is similar to summed scores, however, TPD assigns finer scores and assigns a value per pixel instead of per segment (instead of 0,1,2,3 or 4, it assigns any value between 0-4 [i.e., 0.1, 0.2, 0.3, 0.4...]). Segmental scores are rounded off to integer values and use coarse segment boundaries, unlike continuous variables such as TPD, defect extent or perfusion deficit. Therefore they may be inaccurate for small defects that are located between two segments. TPD is completely automated and the scores cannot be changed by the user.

Reference: *Slomka P, Nishina H, Berman D, Akincioglu C, Abidov A, Friedman J, Hayes S, Germano G. Automated quantification of myocardial perfusion SPECT using simplified normal limits. J Nucl Cardiol 2005; 12:66-77.*

## 7. What is stroke volume and L/R ratio?

Stroke volume (SV) is end diastolic volume (EDV) minus end systolic volume (ESV) represented in ml. It is the amount of blood pumped by the heart in a single heartbeat. In QBS, L/R ratio is LV stroke volume divided by RV stroke volume ( $L/R = \{LV-SV/RV-SV\}$ ).

## 8. Why are there no visual scores, extent or severity polar maps displayed for certain studies?

In order for the software to display visual polar map scores, the loaded datasets for the study must be first processed (segmented). Additionally, corresponding normal limits databases must also be selected. User defaults may be set to auto-process and automatically select corresponding limits files. For more details, refer to the defaults editor section of the user's manual.



**9. Why does the software score certain rest score segments as 0 even though there is a visual defect on the slices?**

Whenever a Stress/Rest dataset pair exists and the stress data for the study is scored as normal or 0, the same segment for the rest data is automatically scored as normal or 0, even if a defect is suggested by visual review of the slices.

**10. Why do my Summed Stress Scores (SSS) and Summed Rest Scores (SRS) not add up properly in the Summed Differential Scores (SDS) for some patients?**

The Summed Differential Scores get generated by subtracting the SRS from the SSS (SDS=SSS-SRS). However, the following rules are also applied when generating the SDS values:

- i. Segmental SRS scores with values higher than the corresponding segmental SRS scores are automatically assigned the SSS score.
- ii. Scores with a value of 1 for both the Stress and Rest corresponding segments are automatically adjusted to 0 throughout (SRS, SSS, and SDS).
- iii. Segmental stress score of 4 with corresponding segmental rest score of 3 is considered as 0 for the differential score.
- iv. Segmental stress score of 3 with corresponding segmental rest score of 2 is considered as 0 for the differential score.

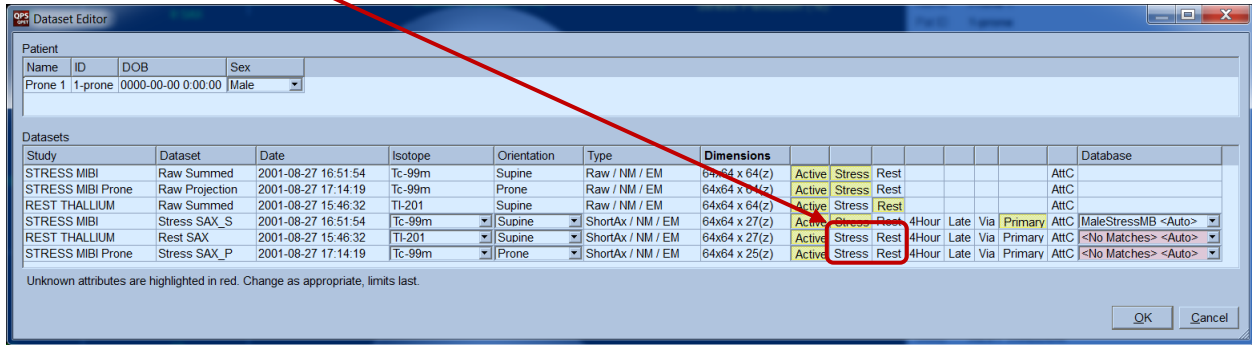
Refer to the [Perfusion summed scores exception rules](#) section of the manual for more detailed information about these rules.

**11. How can I see the entire image on the Snapshot page in case the image is clipped?**

The images on the Snapshot page can be panned in the event the image is greater than the display. In order to do this, click with the mouse pointer on the image and drag to the desired position.

## 12. Why does QPS sometimes display S-S instead of SSS/SRS?

Due to various reasons, QPS is not able to automatically identify short axis datasets as Stress or Rest. For this reason, it is not able to determine which datasets are to be used to generate the SRS/SSS values. Use the dataset editor dialog to select the appropriate short axis datasets as stress or rest.



Furthermore, consult the user's manual or contact your support representative to diagnose the specific reason for this behavior.

## 13. What is Prone +?

Prone-supine (Prone+) allows combined quantification of prone/supine or prone/upright datasets by applying heuristic rules that allow automatic elimination of image artifacts based on the relative defect locations on prone and supine images.

Reference: *Nishina H, Slomka PJ, Abidov A, Yoda S, Akincioglu C, Kang X, Cohen I, Hayes S, Friedman JD, Germano G, Berman DS.* Combined Supine and Prone Quantitative Myocardial Perfusion SPECT: Method Development and Clinical Validation in Patients with No Known Coronary Artery Disease. *J Nucl Med* 2006; 47:51-58.

## 14. What is Motion Frozen or "Freeze"?

The motion frozen feature generates an ungated or summed image from the gated dataset by "warping" all of the individual images from the gating intervals (typically 8 or 16) to the ED position. This tool helps improve resolution and contrast since the blurring effect created from Cardiac motion is eliminated.

Reference: *Slomka PJ, Nishina H, Berman DS, Kang X, Akincioglu C, Friedman JD, Hayes SW, Aladl UE, Germano G.* "Motion-Frozen" Display and Quantification of Myocardial Perfusion. *J Nucl Med* 2004; 47:1128-1134.

**15. What is Serial Change or "Change"?**

Serial Change is most useful in measuring temporal perfusion changes. It can also be used to measure global ischemia between Stress/Rest datasets when normal limits are not available. Change allows direct quantification of perfusion changes between two datasets by performing 3D elastic registration of the two myocardial perfusion studies, giving direct study to study count normalization.

References: *Slomka PJ, Nishina H, Berman D, Kang X, Friedman JD, Hayes SW, Aladl UE, Germano G. Automatic Quantification of Myocardial Perfusion Stress-Rest Change: A New Measure of Ischemia. J Nucl Med 2004; 45:183-191.*

**16. Why is the data displayed on raw page extremely hot in intensity?**

On the image control panel, turn off normalize, and then scale the images individually as needed. Normalize can also be turned off in the Defaults page either as a permanent change or just as needed. You may also need to adjust the placement of the ROIs themselves.

**17. How can I scale the stress and rest images individually since they are displaying in different intensities?**

On the image control panel, highlight dual (or split), then scale the images as needed. Reprocessing or using an image extract or mask program may help in these instances.

**18. Why are there no motion and thickening maps on the QGS page of AutoQUANT?**

A processed gated SPECT image must be loaded into the program and the Score option selected in order to see motion and thickening maps on the QGS page.

**19. Why are the stress images on the splash page lighter in intensity when compared to the rest images?**

This is most likely because the gated short axis slices are being displayed. When a gated image is displayed, only one interval of the gated cycle is displayed (1/8 or 1/16 of the entire dataset). The default can be set to load the summed short axis data instead of the gated short axis data. In the defaults window, in the Page Options section, verify that **Select**, **2** and **QPS** are highlighted.

**20. What are the fewest number of files needed to present results on all the pages in AutoQUANT Plus?**

The fewest number of files needed to have results presented for all the pages is 5; stress and rest projection datasets, stress and rest short axis datasets and a gated short axis dataset. Of course, additional objects may be loaded including motion corrected projection images, gated projection images, additional gated short axis files, attenuation corrected short axis data, and snapshots.

**21. What strings should be in the automatch exclude field on the defaults page?**

The automatch exclude field should contain identifying strings for any datasets not needed for the AutoQUANT Plus processing. This includes any non-short axis data (horizontal long axis and vertical long axis data) and polar maps. You may also wish to exclude some projection data such as -EM or -EMSCR data, or gated projection data. Make sure that when modifying the exclude auto matching, the string entered in does not inadvertently exclude something other than what is desired. Example: To exclude the transverse slices, do not use **tr** because that could also exclude “short axis-str”. Use **-tr** instead.

**22. What criterion is used to sort the raw data displayed on the raw Page?**

The sort criteria for projection data is (in order of decreasing precedence), is as follows:

1. Non-Gated > Gated
2. Lung Heart Ratio > Non-Lung Heart Ratio
3. Stress > Rest > Neither

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