Cedars-Sinai Cardiac Suite

User's Manual

CSI, QGS + QPS, QBS, MoCo and AutoRecon

Version 2017 Rev. D

Prescription Device Statement

Caution: Federal law restricts this device to sale by or on the order of a physician (or properly licensed practitioner).

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Neither Cedars-Sinai Medical Center, its parent, nor any of its worldwide affiliates shall be liable or obligated in any manner in respect of bodily injury and/or property damage from the use of the system/software if such is not in strict compliance with instructions and safety precautions contained in the relevant operating manuals and in all supplements thereto, in all product labels, and according to all terms of warranty and sale of the system, or if any change not authorized by Cedars-Sinai Medical Center is made to the software operating the system.

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CE Marking

Cedars-Sinai Cardiac Suite is CE Marked to the Medical Device Directive 93/42/EEC.

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User Assistance Information

For service or support questions, please contact your vendor's customer support line.

WARNING

Do not install software applications not approved directly by your workstation vendor. The system is only warranted and supported as configured and delivered. Refer to the vendor documentation for detailed system requirements.

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

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Introduction

1.1. Indication for Use

The Cedars-Sinai Medical Center (CSMC) Cardiac Suite of applications is intended to enable an automated display, review, and quantification of Nuclear Medicine Cardiology medical images and datasets obtained from patients who have undergone a compatible medical scan. CSMC Cardiac Suite may be used in multiple settings including the hospital, clinic, or office environments. The results provided should be reviewed by qualified healthcare professionals (e.g., radiologists, cardiologists, or general nuclear medicine physicians) trained in the use of medical imaging devices.

1.2. Description of Device

The Cedars-Sinai Cardiac Suite is a stand-alone software solution for Cardiac SPECT and PET imaging processing and review. Cedars-Sinai Cardiac Suite (non-viewer) minimum system requirements include a computer with at least 2GB RAM, 200MB hard disk space for software installation, a display resolution at least 1024x768 with 16-bit color, a network adapter, a mouse (or other pointer device; trackpad, trackball, etc.) and one of the supported operating systems. CSMC Cardiac Suite operates on camera independent reconstructed SPECT and/or PET image files and Cardiac CTA image files.

CSMC Cardiac Suite will be marketed as a comprehensive application suite that includes QGS+QPS (Quantitative Gated SPECT + Quantitative Perfusion SPECT) in a single application (aka AutoQUANT) and CSImport applications. This allows automatic processing and review of quantitative and qualitative information generated by nuclear medicine studies. Purchasable options consist of Quantitative Blood Pool SPECT (QBS), QARG (for reporting purposes), Fusion (SPECT/CT/CTA and/or PET/CT/CTA), AutoRecon, Motion Correction (MOCO) and QPET. QPET also includes viability quantification and two additional databases (rubidium and ammonia) for processing PET studies.

QGS+QPS is an application which combines both Quantitative Perfusion SPECT (QPS) and Quantitative Gate SPECT (QGS) into a common application. Quantitative Perfusion SPECT (QPS) is an application designed for LV (Left Ventricle) and RV (Right Ventricle) extraction and analysis. QPS provides a tool to review and quantify perfusion Cardiac SPECT and PET data sets to determine the location, orientation, and anatomical extent of the left ventricle of the heart, to construct 3D contour maps of the heart, and to calculate the heart volume. Physicians use this information to assess the anatomical and physiological functionality of the heart and analyze the presence of myocardial defects through comprehensive imaging modalities. Stress-Rest Registration is a direct method for detecting changes between stress and rest images. It is a practical and fully automatic algorithm for quantification of stress-induced changed from paired stress and rest scans and does not use protocol-specific databases. Prone-supine 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. The shape index parameter defines 3D left ventricular (LV) geometry derived from LV contours in end systolic and end diastolic phases. QPS includes an algorithm for the quantification of myocardial perfusion, using normal limits created from studies of low-likelihood normal patients only. The algorithm has been validated in a large group of patients demonstrating equivalent diagnostic performance despite the use of simplified normal limits. The following databases are being provided (for male and female): Prone Stress MIBI, Rest MIBI, Rest MIBI AC (Attenuation Corrected), Rest Thallium, Stress MIBI, Stress MIBI AC, Stress Thallium. Optional normal limits databases offered are Rubidium for PET, Ammonia for PET. QPS provides the ability for user generated normal limits files using the simplified method. QPS also includes a variable, Total Perfusion Deficit (TPD), which combines defect extent and severity values. The new quality control (QC) automatically detects quantitative segmentation failures. In the event of a failure a different algorithm is applied. Quantitative Gated SPECT (QGS) is an application designed for LV (Left Ventricle) and RV (Right ventricle) extraction and analysis. QGS provides a tool to review and quantify function Cardiac SPECT and PET data sets to determine the location, orientation, and anatomical extent of the left ventricle of the heart, to construct 3D contour maps of the heart, and to calculate the heart volume (for the left ventricular wall). Physicians use this information to assess the anatomical and physiological functionality of the heart and analyze the presence of myocardial defects through comprehensive imaging modalities. A new Phase page included in QGS page gives access to phase information for gated datasets. A new technique to create cardiac "motion-frozen" perfusion or viability images, by warping ECG-gated images to the end-diastolic position has been added. Such "motion-frozen" perfusion and viability images have improved resolution and contrast by removing blurring effect caused by cardiac motion. The new quality control (QC) automatically detects quantitative segmentation failures. In the event of a failure a different algorithm is applied. QGS+QPS can also generate and display TID (Transient Ischemic Dilation) and LHR (Lung Heart Ratio or Lung Heart Counts). A new group processing algorithm has been added which 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.

Quantitative Blood Pool SPECT (QBS) is an optional application. QBS is an interactive standalone software application for the automatic segmentation and quantification of gated short axis blood pool (red blood cells, RBC) SPECT. The application can be used for automatic generation of left and right ventricular endocardial surfaces and valve planes from three-dimensional (3D) gated short axis blood pool images; automatic calculation of left and right ventricular volumes and ejection fractions; calculation and display of polar maps representing wall motion and parametric values (FFH amplitude and phase); two-dimensional (2D) image display using standard American College of Cardiology (ACC) cardiac SPECT conventions; and 3D image display. It also provides the following functionalities: ability to combine isosurfaces extracted from the data with the calculated endocardial surfaces in various ways (endocardial borders displayed as wireframes, shaded

surfaces, both, or parametric); ability to map parametric values (First Fourier Harmonic (FFH) amplitude and phase) on the surfaces; ability to display parametric images (FFH amplitude and phase) for gated planar, gated raw projections and gated short axis images; ability to display cine loops of the original images; ability to generate count-based quantitative values using the automatically- and semi automatically-computed surfaces as ROIs and user-selectable thresholds; ability to generate and display phase histograms for FFH phase images and to display the mean and standard deviation of the peaks corresponding to atrial and ventricular voxels. After ventricular segmentation, a phase histogram for each ventricle is also computed and displayed; and ability to display normalized images for all gated images (i.e., images that do not exhibit count drop-off caused by arrhythmia). In addition, QBS supports manual identification of the left-ventricular (LV) region, to separate it from the right ventricle (RV) in cases where the automatic algorithm fails or returns unsatisfactory results; ability to generate filling rates from interpolated time-volume curves; and the ability to rotate, zoom, and cine surfaces.

A nuclear image fusion package is available as an option to QGS+QPS for both SPECT/CT and PET/CT hybrid applications. The fusion option includes a page that allows for display of segmented and labeled coronary vessels with PET 3D data. Functionality includes orthogonal planes using alpha blending, roving window and synchronized cursor. It allows users to perform quality control of SPECT/CT/CTA or PET/CT/CTA alignment and has generic multimodality fusion capabilities. This feature provides display of fused images in a visual format. Additionally, included for PET analysis is the Hibernating Myocardium Assessment (mismatch and viability); this module allows quantitative assessment of "hibernating myocardium" by quantification of changes between PET perfusion and viability images in hypo-perfused area. Scar and Mismatch parameters are reported as a percentage of the Left Ventricle and are displayed in polar coordinates or a 3D surface display. A new registration algorithm has been added which automatically registers SPECT/PET with CTA/CT datasets.

Quantitative PET (QPET) is an optional module which adds automatic segmentation, quantification and analysis of static and gated myocardial perfusion PET, with support for both short axis and transverse datasets. The QPET module includes dynamic PET capabilities, such as calculation of absolute blood flow within the myocardium.

CSImport is an application designed to import datasets from a variety of sources, store them in a local image database, and launch any number of applications that use this data for their processing purposes. CSI also provides a variety of data management tools, and includes a DICOM Store Service Class Provider (SCP) service that allows DICOM-compliant systems to push images to your PC for processing and review.

AutoRecon is a one-step application for automatic reconstruction and reorientation of raw tomographic data (raw projections), with an emphasis on cardiac images. The application offers a choice of filtering and reconstruction options (including iterative reconstruction) and automatic

reorientation (>95%). AutoRecon offers several automatic processing modules for single-photon emission computed tomography (SPECT) studies. Although it is mainly designed for cardiac data, many of its functionalities can be applied to other types of SPECT studies. AutoRecon provides automatic reorientation of three-dimensional, transaxial myocardial perfusion SPECT images. AutoRecon is comprised of four modules: reconstruct, reorient, motion and filter. Each module has associated pages that present data and the controls necessary to perform the specific task for which the page has been designed. The program can be used interactively on one or more datasets or in batch mode to process data without further intervention from the user. If matching rest and stress datasets are provided, AutoRecon will automatically operate in dual mode.

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

ARG/QARG (Cedars-Sinai Reporting) is a tool that produces comprehensive nuclear cardiac reports. QARG includes data collection utilities, data consistency checks, report generation, search utilities and several administrative tools. During the data collection process users are automatically prompted to resolve potential inconsistencies. Once the data acquisition is complete, the reports are generated. Reports not only contain derived values, but output clear sentences designed to send to the referring physician. QARG merges data from all3 sources to produce a single comprehensive report.

CSView (Cedars-Sinai Viewer) is an application designed as a generic medical image viewer, with an emphasis on planar Nuclear Medicine (NM) studies. CSView includes customizable display layouts, image manipulation controls; brightness/contrast adjustments, color scales, zooming panning, rotation and flipping. CSView also includes a tool for conducting flood uniformity analysis.

The results provided should be reviewed by qualified healthcare professionals (e.g., radiologists, cardiologists, or general nuclear medicine physicians) trained in the use of medical imaging devices.

1.3. New Features

There are many new features in this version of CSMC Cardiac Suite. These are some of the most important.

2017

- QGS+QPS, QPET, QBS

    o **Coronary Calcium Score** quantification.
    o **SPECT CFR/MBF** quantification.
    o **Motion correction for dynamic PET/SPECT datasets** used for CFR/MBF quantification.
    o **Planar Bloodpool (Muga)** scan quantification.
    o **3D Iterative algorithm** for processing reduced count images.
    o **Raw projections (MIPS)** for PET.
    o **LV count** computed from contoured myocardium.
    o **Updated Splash** page.

- Cedars Report

    o **Simplified Reporting** tool for creating compliant and structured reports.

2015

- QGS+QPS, QPET, QBS

    o **Right Ventricle (RV)** quantification for gated datasets is now available in QGS+QPS.
    o The new **'Quality' page** for QGS+QPS and QBS allows users to easily review raw dataset integrity and easily spot any acquisition errors.
    o The new **Smart Defect Editor** for QGS+QPS gives users the ability to edit defects on perfusion polar maps.
    o The new **Fast Dataset Selector** feature for QGS+QPS allows users to easily toggle between different dataset combinations and layouts.
    o The new **Color Scale Manager** for QGS+QPS, QPET and QBS gives users the ability to import/export color scale palette files.
    o **Phase Analysis** algorithm was modified for QGS+QPS in order to exclude basal count variations that do not correspond to actual myocardial thickening but instead are caused by valve plane motion between diastole and systole.
    o **Group processing / Reproducibility** option for QGS+QPS and QPET, which allows for simultaneously solving left ventricular geometry for all of the available datasets.

- QARG

    o **HL7 support** for structured reports generated using the Automated Report Generator (ARG).
    o **Advanced Distribution Server** provides multiple options for distributing finalized reports.
    o **MIBG** reporting is now supported.

2013

- CSImport has been completely overhauled with improved user interface and performance. Some of the new features include:

  - Support for SQL database backend.
  - User and site centric access control, similar to QARG.
  - User specific options for storing data privately or publically.
  - Enhanced task management system.
  - Deleted items management utility for recovering deleted items.
  - Enhanced logging for operations such as importing, replacing, deleting, etc.
  - Options for reconciling or linking studies.
  - Advanced filtering options that include options such as patient position (prone/supine/…), gating (static/gated/dynamic), patient state (rest/stress/…), etc.

- QARG contains a significant number of enhancements and new features. Some of the new features include:

  - Support for blood pool studies (includes integrated support for QBS), pyrophosphate studies and CTA studies.
  - Advanced appropriate use criteria engine based on ASNC guidelines.
  - Automated options for generating detailed administrative reports.
  - Advanced report distribution engine.
  - Simplified user interface and report templates.
  - Standard, IAC (formerly ICANL) compliant, 1 page report templates.
  - Support for opening multiple studies or reports.

- Multi-monitor (unlimited) display mode for QGS+QPS and QBS.

1.4. Manual Conventions

The following typographical conventions are followed throughout the manual:

- **User interface (UI) elements** (menu items, buttons, etc…) are depicted in **this style** (bold, light-colored serif type).
  The paths to menu items and sub-items are abbreviated as **Menu > Item** or **Menu > Submenu > Item**.
  Similarly, a tab **Tab** on a dialog opened by selecting a menu option **Option** may be referenced as **Menu > Option > Tab**.
- **User input**, including single keys such as shortcuts, is depicted using **this style** (bold, bright-colored sans-serif type).

- **Code or information found in configuration files** is depicted using `this style` (bold, colored fixed-width type).
- **Other items of interest**, such as references to other sections, are depicted using *this style* (bold, italicized, colored sans-serif type).

The following symbols are also used to draw attention to certain information:

Information. The note describes something that may affect the behavior of the application but does not pose an inherent risk.

Caution. Review this information carefully. Misuse of a feature may lead to unwanted consequences and possible data loss.

1.5.   General Warnings and Cautions

Software is designed to manage and analyze data that contains sensitive patient information. Oblige to all HIPAA standards in safeguarding all patient information and allow access to authorized users only. It is recommended to create password protection where offered within the program or device on which the software is installed.

Program is designed to automatically process data and generate quantification results, it is not meant to offer a standalone diagnosis. A qualified physician's assessment of the results is required.

While every effort has been made to ensure the accuracy of the information in this manual, you may occasionally notice slight differences between screen captures and the actual software.

2. Setup Instructions

This section summarizes the installation instructions and assumes you are familiar with various concepts such as installing programs. For more detailed instructions (including screenshots) read the Installation section of the CSI Reference Manual.

You will need:

- A computer running one of the supported Operating Systems (OS) of Microsoft Windows.
- The installation file.

Do the following:

1. Log into the system as a user with "Administrator" privileges.
2. UnZip the download file, then double-click `CSMC_Setup.exe`.
3. Wait for the auto-play application to start.
4. When the setup program starts, go through all steps accepting the default values or check the boxes for the specific software options purchased.
5. The setup program will automatically update the necessary registry keys if you have administrative privileges.
6. When the setup program is finished, reboot the computer if necessary (as suggested by the setup program).
7. Double-click on the "CSImport" icon shortcut on your desktop.
8. Send the system identifier to your CSMC support representative for obtaining a license registration key.
9. Enter the registration key in the licensing dialog.
10. You're done! The data browser CSI will now start and bring you to the main data browser screen.

3. Operating Instructions

3.1. CSImport

Cedars-Sinai Import (CSI) is primarily an image database front-end that is also commonly used for launching external applications. It is designed to allow the user to retrieve datasets from a variety of sources such as the Philips Pegasys, Jet Stream, and EBW workstations, FTP servers, and DICOM Query/Retrieve servers. CSI also provides a variety of data management tools, and includes a DICOM Store Service Class Provider (SCP) service that allows DICOM-compliant systems to push images to your PC for processing and review. Details of the DICOM interaction can be found in the DICOM Conformance Statement.
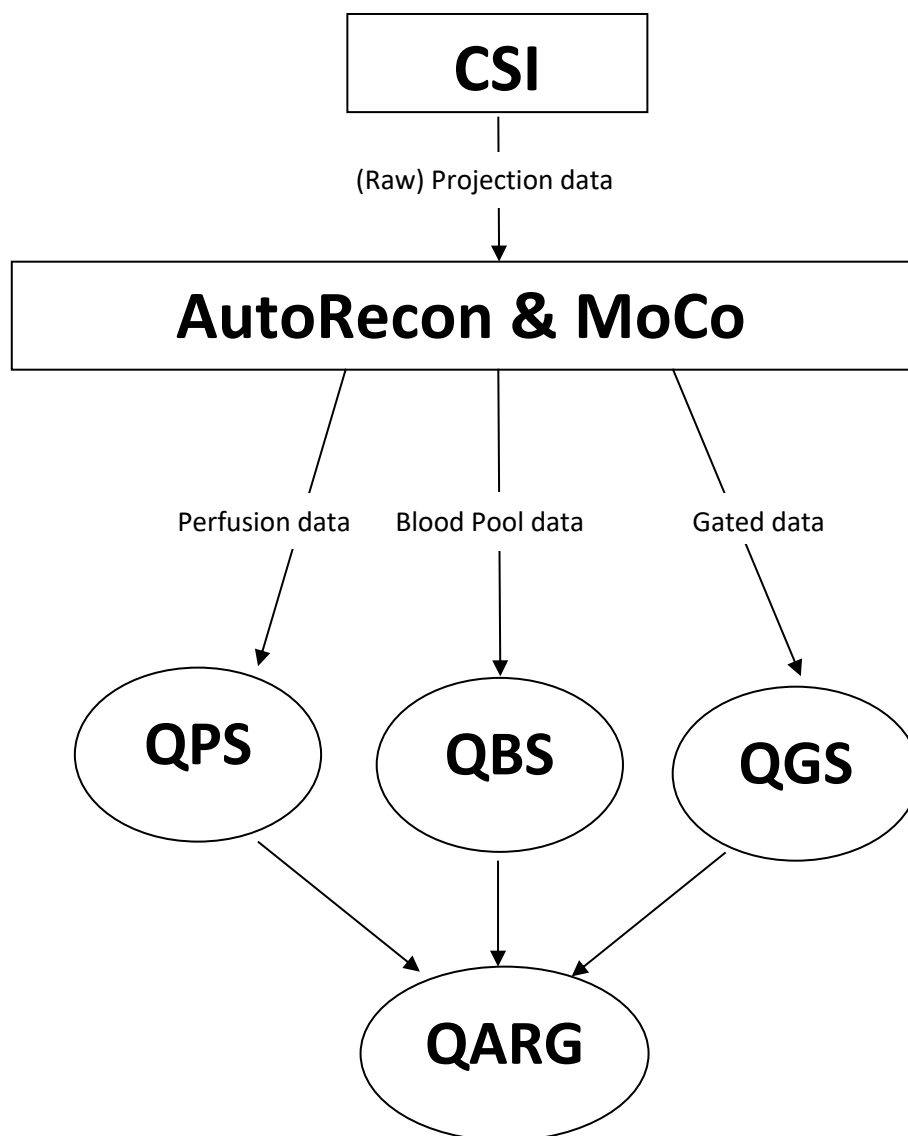
3.1.1. Initial setup

CSImport controls data accessibility via user credentials. The image data base maybe setup as a standalone or Central Server. When CSI is run for the first time, it allows the ability to select the system type that is desired.

STANDALONE is the default selection unless you have multiple computers running the same version of CSImport and you would like to connect to a SQL server based CSImport/ARG database.

Once **STANDALONE** or **CENTRAL SERVER** database selection is made, the next step is setting up the System Administrator user account. The login user name for the Administrator account is *admin*. Enter the password information on this dialog and click **Next**.

The last step is to setup the first user information. Select desired User Type and complete the information on this dialog before clicking **Next**.
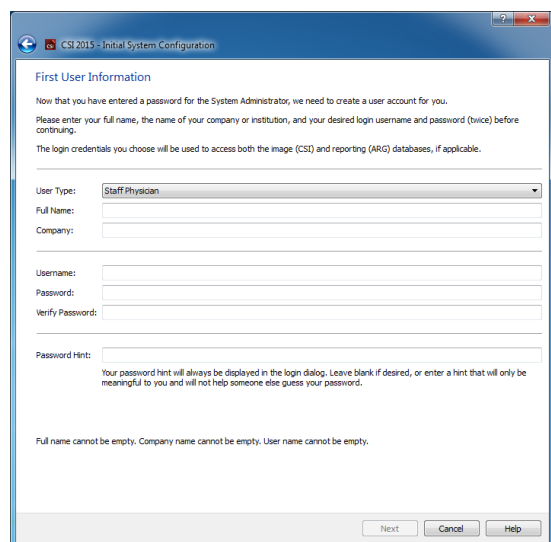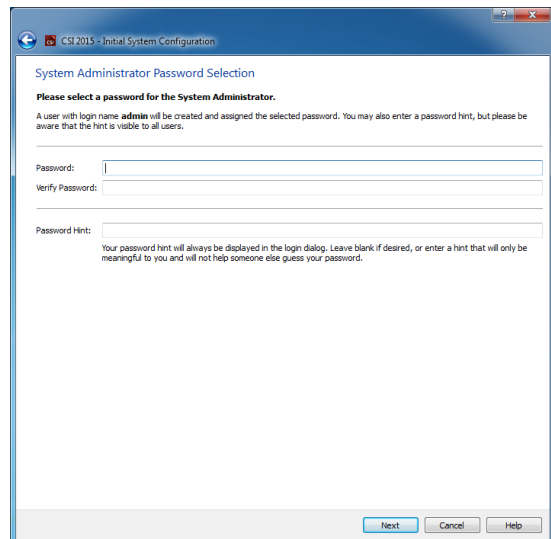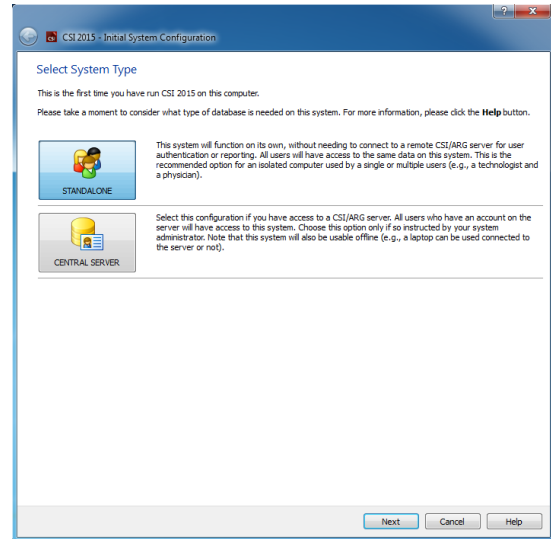
A final confirmation dialog indicates the conclusion of the initial setup process. Verify the information for accuracy and click **Finish**. To make modifications to any of the information, click on the back arrow show in the top left corner of the confirmation dialog.
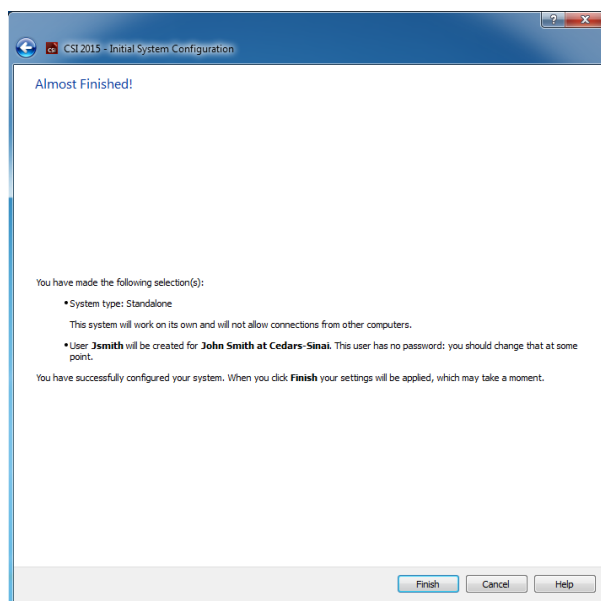
3.1.2. Launching an application

You can select one or more folders that represents DICOM series, studies, or patients, or any other type of data organization (e.g., a folder that contains studies for multiple patients suffering from the same pathology), and launch the application with all datasets contained within the selected folders by clicking the toolbar button for that application (e.g., QGS+QPS, QBS, Arecon, etc).

Note that having launched one application does not prevent you from going back to the data browser and launching another application, either for the same data or for a different selection.

Data selection follows the same conventions as Windows Explorer: clicking an item selects it, clicking another item selects that item instead of the previous selection, and keys such as Shift and Ctrl can be used in conjunction with mouse clicks to extend or modify the selection, respectively.
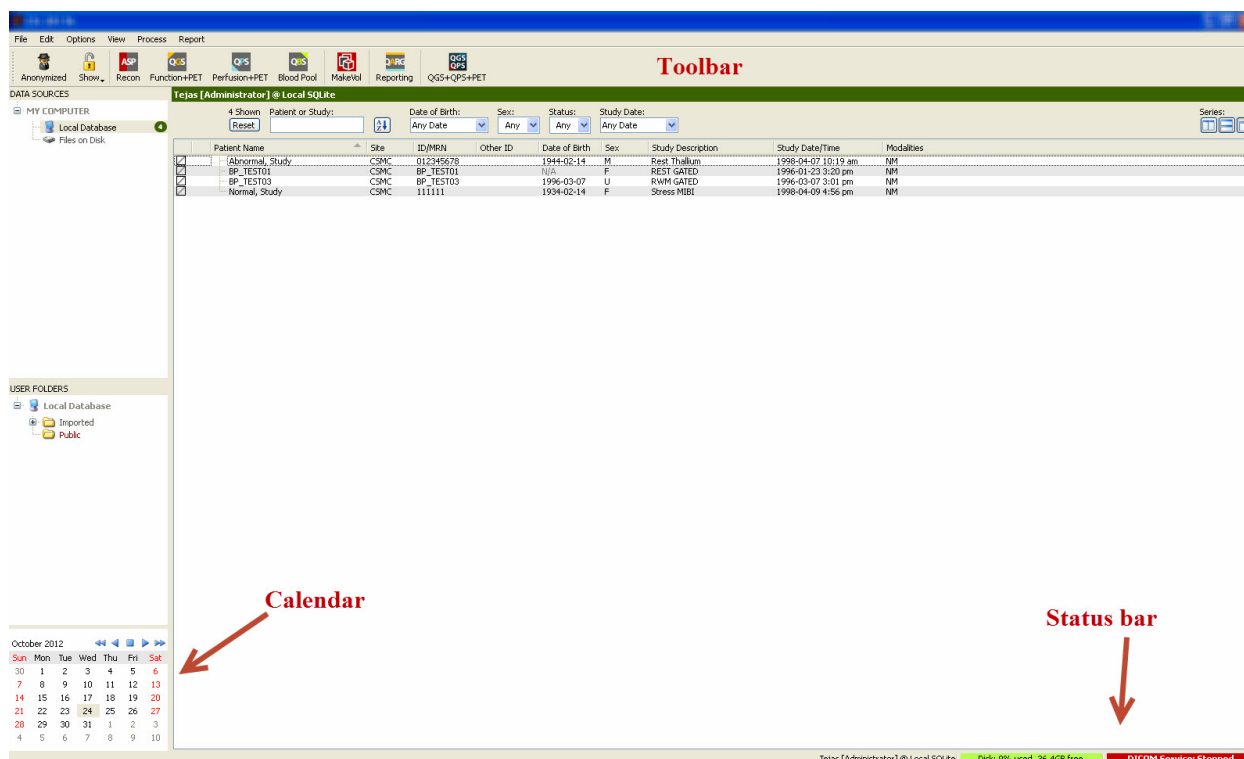
3.1.3. Importing data
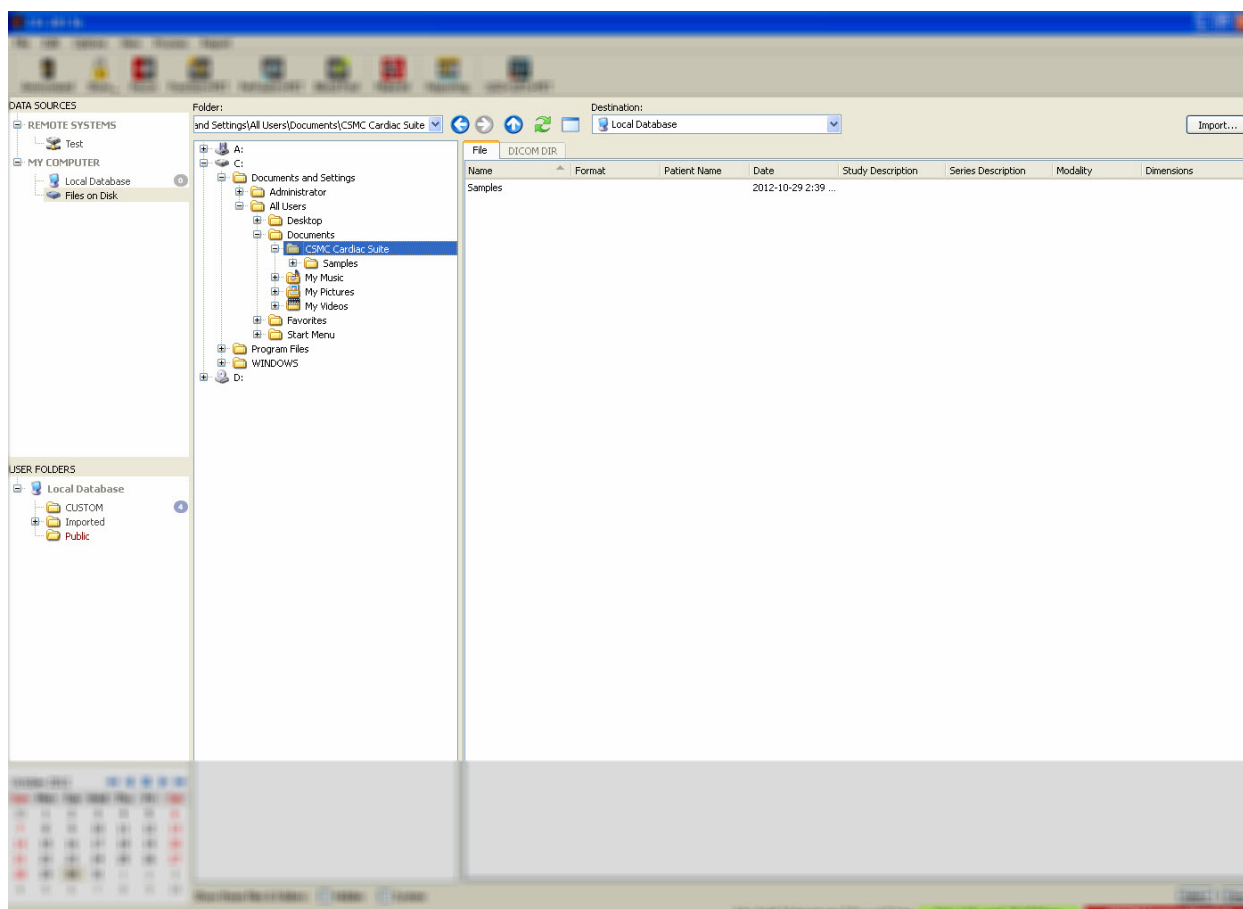
There are multiple options for importing images based on where the data is located. For purposes of this example, let's assume that the data resides on a locally accessible disk (i.e. a local hard disk, mapped drive from another computer, CD or DVD, portable USB drive, etc).

3.1.4. Importing data from a local disk

This option should be used to import data that resides on a disk accessible through the computer's file system. This includes data residing on:

- hard disks;
- CDs or DVDs;
- flash drives;
- Remote disks accessed by mapping a drive letter to a remote folder.

The image below depicts a typical display when a folder has been opened and its contents are displayed. Local disk files can be browsed by clicking **Files on Disk** from the Data Sources section and navigating to the location of the files using the windows file explorer like view.

Note the folder selection control to the left (a path can also be typed directly in the text field at the top). To the right, files that are recognized as images are displayed. Enough information is displayed for each file to allow the selection of the appropriate image(s).

There are two ways to import files: by selecting individual files, or by importing entire folders.

To import selected files, click, click-drag, or control-click files. Select the appropriate import options, and then click **import**. After the import process is complete, either navigate to another folder to import more files or click on local database option from Data Sources to go back to the original view.

To import entire folders, select the folder and click import. If **Do not recurse into sub-folders** is checked from the Import Options dialog, only files
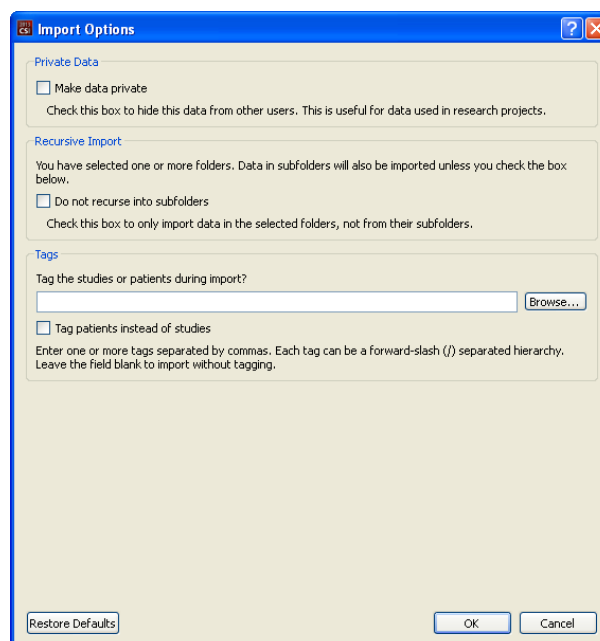
inside the selected folders will be imported. If it is unchecked and if the selected folders contain sub-folders, all datasets within all sub-folders will be imported as well.

The following import options are available:

Make data private – this option can be checked to hide the imported data from other users.

Recursive Import – this option can be checked if only data in the selected folders, not from their subfolders, should be imported.

Tags – Options to add customized tags to the imported data at the patient or study level.

3.1.5. Importing data from a remote system

The four types of supported remote systems are:
- Philips (ADAC) Pegasys
- Philips (Marconi) Odyssey
- FTP server
- DICOM Query/Retrieve server/Store Server

Creating remote system configurations
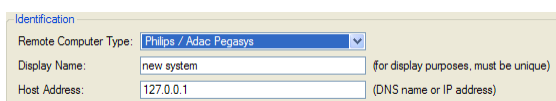
Each remote system must be configured in CSI before it can be contacted to import/export data. DICOM Q/R servers also often require server-side configuration. This will generally need to be performed by the PACS administrator (for Picture Archiving and Communication Systems) or by technical support personnel (for non-PACS imaging workstations such as acquisition systems).

The beginning of the procedure for creating a new configuration for a remote system is the same for all system types:

- Select **Options > Manage Remote Systems…**
- Click **Add…** in the Remote Computer Systems window

The next step is to set basic information for the system in the Remote Computer Systems window:

- Select the "Remote Computer Type"
- Enter a "Display Name" that will be used throughout the program to identify the system
- Enter the IP address of the remote system. It is recommended to use IP addresses instead of names, unless the remote system's address is likely to change due to dynamic address allocation

Once the remote computer type has been set, the lower portion of the dialog will update to reflect the specific settings required by that type of system.

In general:

- For Pegasys systems no changes are required;

- For Odyssey systems, only the data directories need to be updated (usually one or more of the form "/imgX" where "X" is a number);

- For FTP servers, the appropriate account information (username and password) must be entered. "Port" and "Initial Directory" can often be left to default values.

- For DICOM Query/Retrieve/Store servers, the AE titles, port number, and query root level need to be set to values as prescribed by the remote system's administrator. Setting the system's "Vendor" type will in some cases allow CSI to restrict itself to operations that are known to function for those systems (not all DICOM systems offer the same level of functionality).

Field	Value
General	General characteristics of the system
Vendor / Type	Philips / Jetstream
Vendor Comment	Study Root Q/R Only
Local AE Title	STORESCP
Associated Site	CSMC @ Local SQLite: CSMC
Query/Retrieve	☑ Get data from this system
Remote AE Title	FINDSCP
Port	104
Max PDU	16384
Root Level	Study Root
Push	☑ Send data to this system
Remote AE Title	STORESCP
Port	104
Max PDU	16384

Default values can be reset by clicking **Reset**, and basic connectivity tests can be run by clicking **Test**.

Click **OK** to accept the settings when the configuration information of the new remote system is satisfactory. The new system will appear in the remote computer list, where it can be used to retrieve data.

Philips Pegasys

To import data from a Pegasys system, click the name of the system from the remote systems list. This will bring up the Pegasys dialog and start the connection to retrieve the study list.
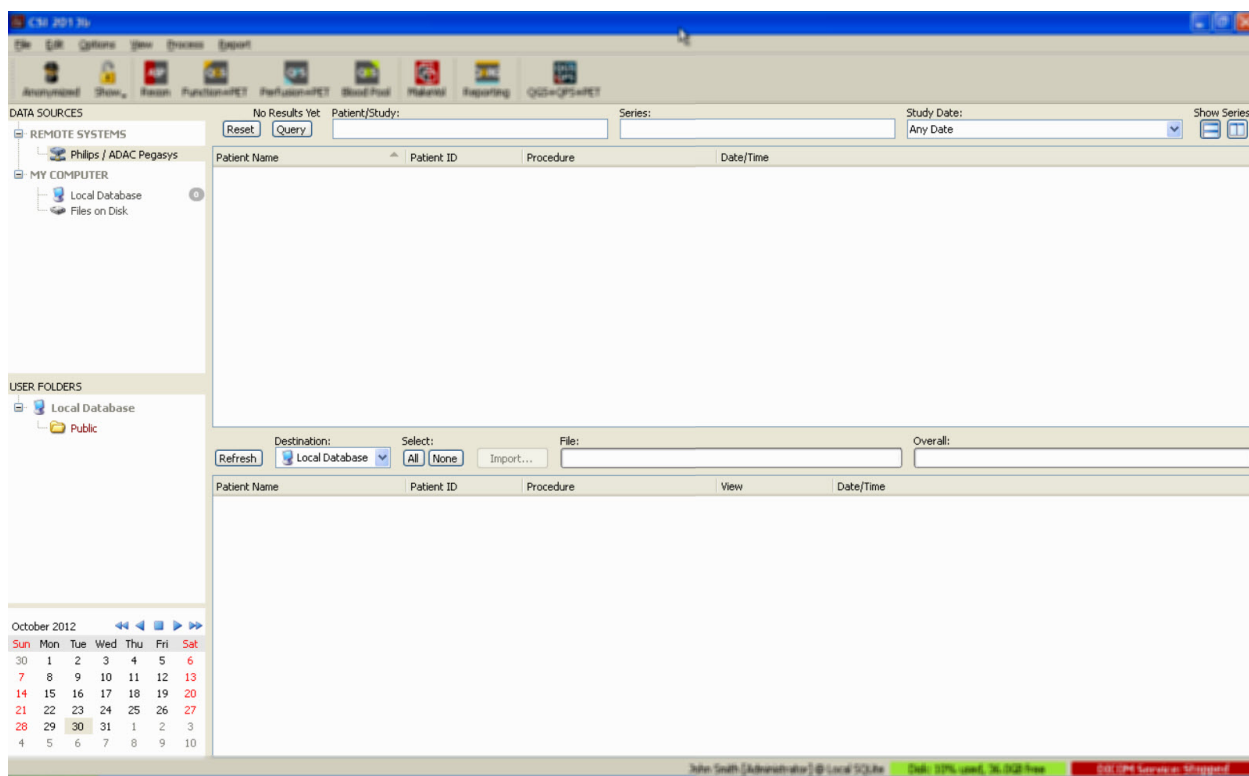
To import entire studies, select one or more desired studies (click, click-drag or control-click in the list), set the import options and click **Import…**.

When done importing, either select more datasets, return to the studies selection page by clicking on Local Database.

Philips Odyssey

Odyssey connectivity is very similar to Pegasys connectivity. Only the information is presented slightly differently, reflecting the naming conventions and fields available on Philips Odyssey systems.

FTP Server

The main downside of using a FTP server to retrieve data is that images can only be selected by file name, without added information such as patient name, study description, etc. A typical file list is shown in the figure below.
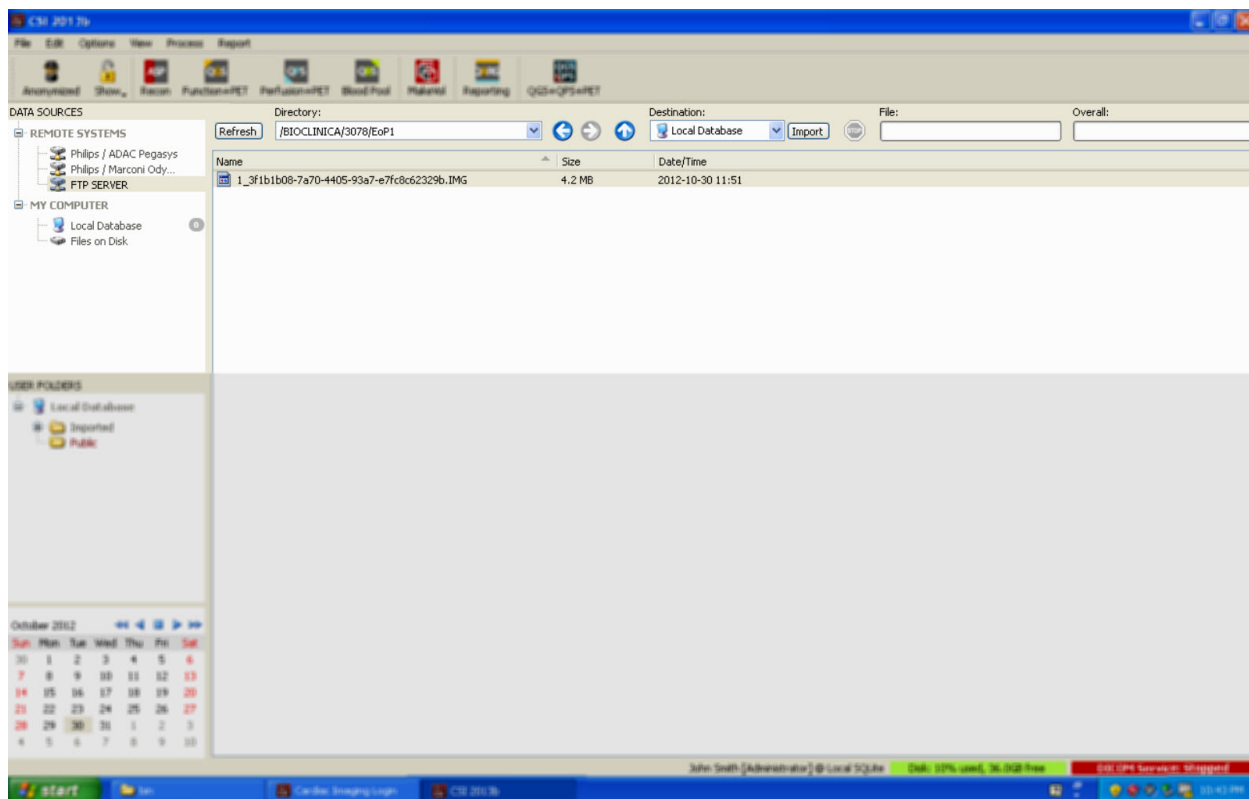
To navigate to another folder, either type the path in the Directory box or double-click folder names in the list (including the special "<UP>" folder to navigate to the parent directory).

By default, all datasets are selected. Use control-click to remove individual items from the selection. When ready, click **Import** to import the selected datasets.

DICOM Query/Retrieve Server

Importing data from a DICOM Q/R/S server requires more configuration than any other type of remote system, but it is the only method to gain access to PACS and other DICOM-based systems. Once the system has been configured and a connection established, the following dialog is presented:
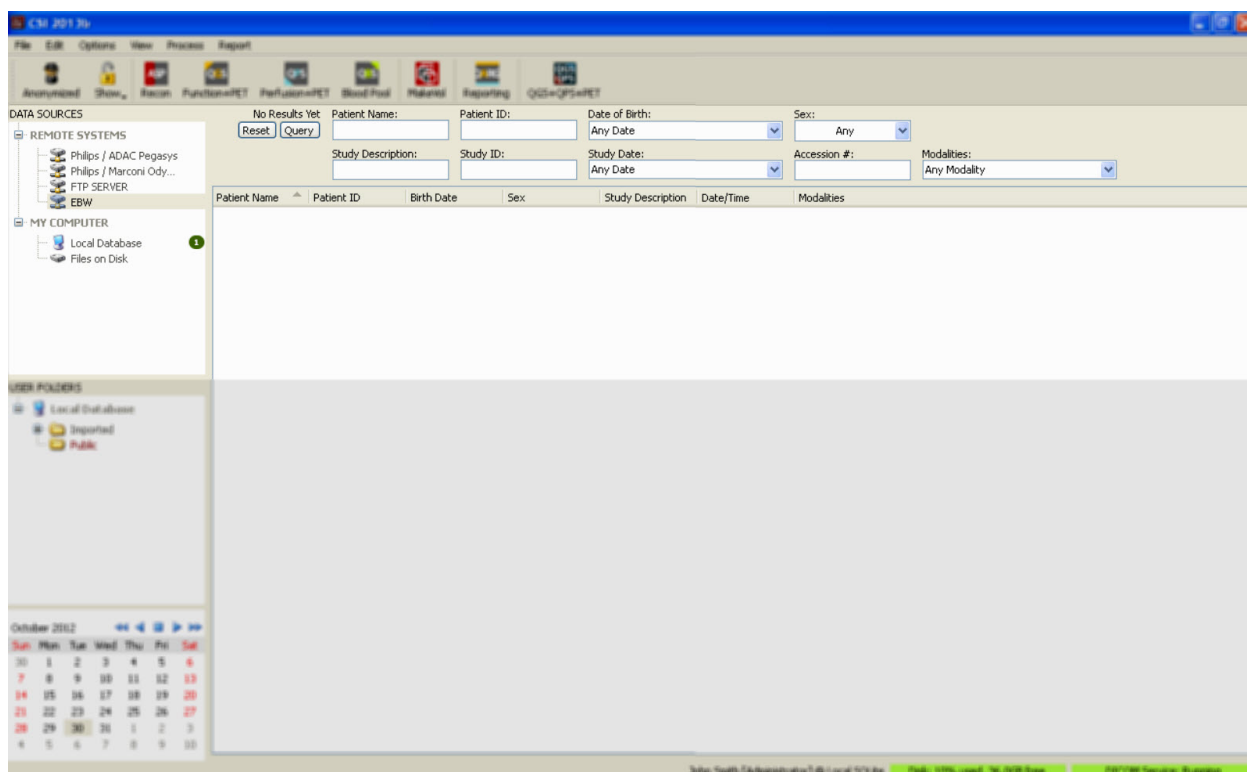
Because PACS systems often store very large amounts of data, no query is sent to the server until **Query** is pressed. This allows for the selection of a study filter to limit the number of results.

For a more detailed explanation of the other capabilities of the DICOM import dialog, please consult the Reference Manual.

Pushing DICOM datasets from a remote system

In addition to the ability to pull data from a variety of sources, it is also possible to push images from other DICOM-compliant systems to the system running CSI. CSI includes a Windows service called "Cedars-Sinai DICOM Store SCP" that listens for incoming connections. Most modern imaging platforms can connect to this service and send images which are then stored locally on your PC and inserted in the local image database.

To use this mechanism, you need to configure the DICOM Store SCP service with the appropriate parameters. The configuration dialog that is shown below can be launched from **Options > DICOM Networking**.
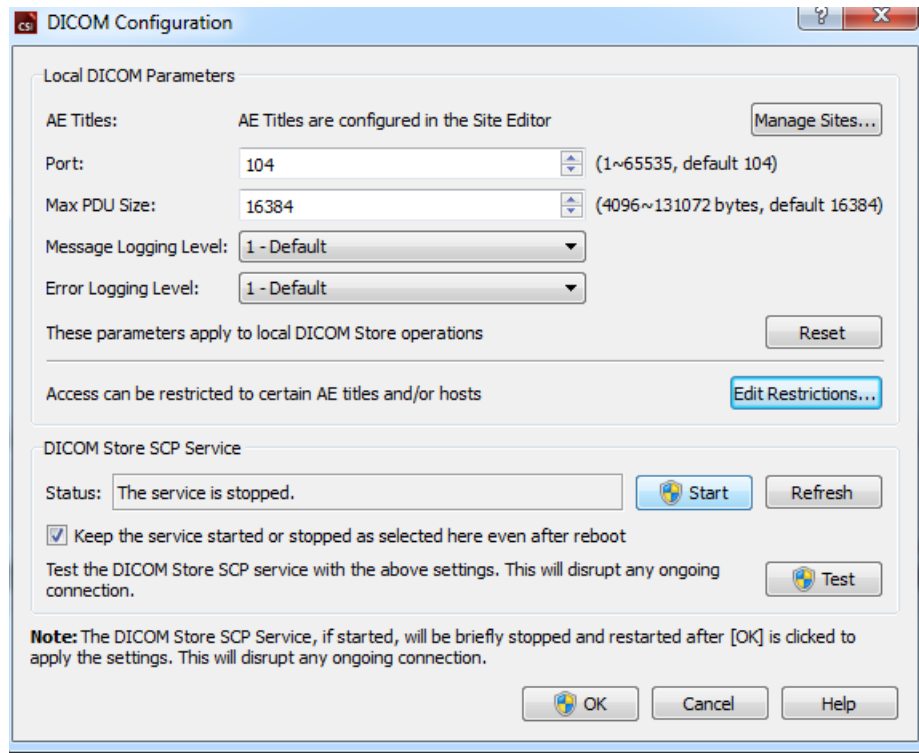
To configure the DICOM Store SCP, follow these steps:

1. Go to **Options > DICOM Networking**
2. Choose an application entity title (AE Title) for your computer. AE Titles are managed by the site manager and can be accessed by clicking **Manage Sites….**
3. Choose a port number on which source systems will contact your computer (default: 104).
4. To limit access to selected remote systems, click **Edit Restrictions…** and enter the acceptable AE title information. By default the system accepts connections from all remote systems.
5. Leave the rest of the options unchanged.
6. Click **Start** to start the DICOM Store SCP service.
7. Click **OK** to apply the changes and restart the service.

You will now need to configure any source system with the appropriate settings to be able to send data. In general, configuration of the source systems will require the following information:

- The IP address of your computer
- The AE Title selected in step 2 above
- The port number selected in step 3 above
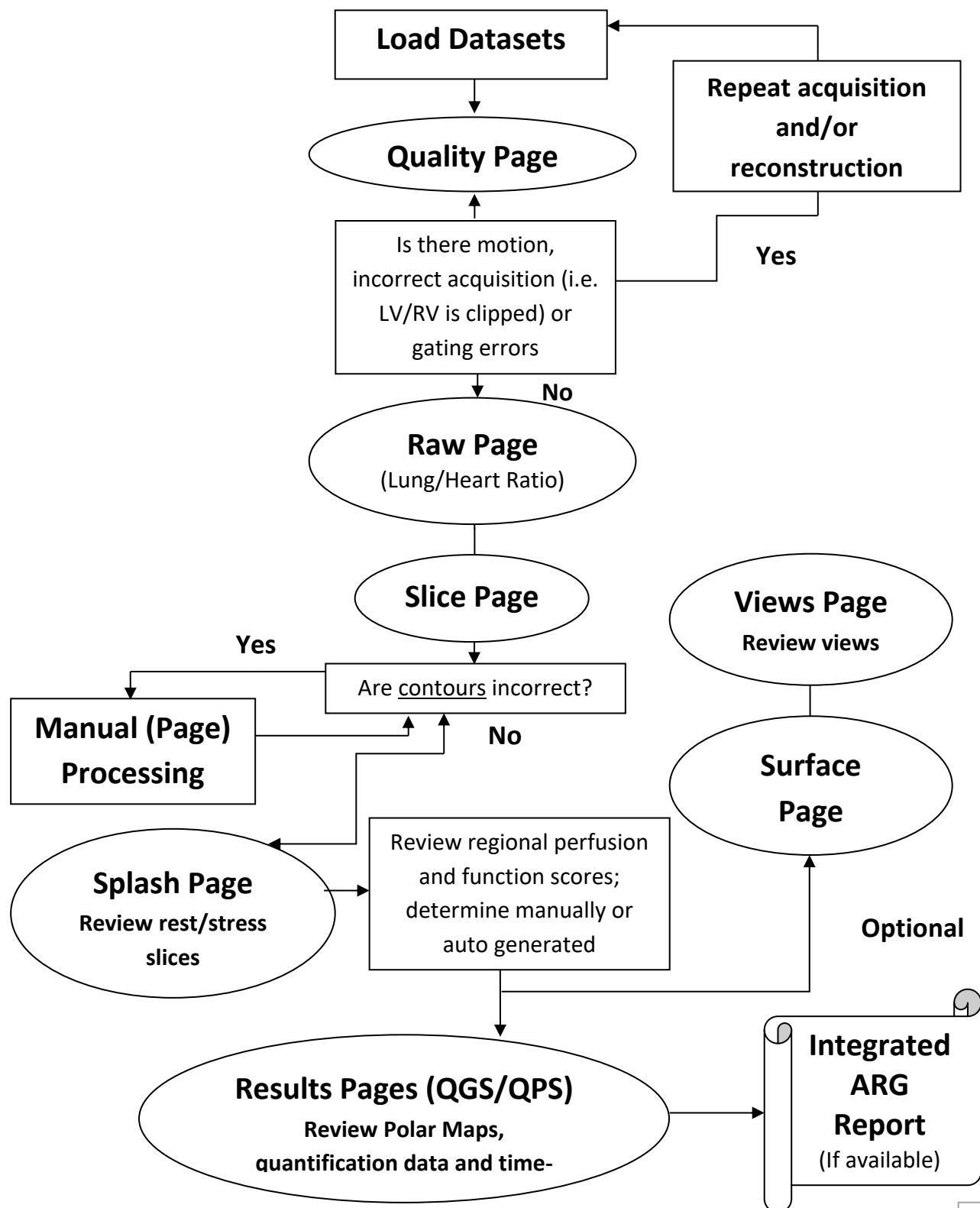
DICOM systems usually have the ability to perform a few connectivity tests (often called "echo" in reference to the DICOM C-ECHO message) to ensure the parameters are correctly configured. These tests should succeed if the DICOM Store SCP service is running on your system.

Users on the remote systems can then select data and send it to your PC. The data should appear in the selected location. It may be necessary to refresh the list and/or modify data filters to see the data. For instance, if you have selected to view only today's studies and the study sent from the source system was acquired yesterday, it won't show up in your list until you remove the date filter.

4. Quantitative SPECT/PET Applications – QGS (Function) + QPS (Perfusion)

The workflow is intentionally modeless. As such, no particular processing sequence is dictated to the user. A typical sequence might proceed as follows:

Load Datasets

Repeat acquisition and/or reconstruction

Quality Page

Is there motion, incorrect acquisition (i.e. LV/RV is clipped) or gating errors

Yes

No

Raw Page (Lung/Heart Ratio)

Slice Page

Views Page Review views

Yes

Are contours incorrect?

No

Manual (Page) Processing

Review regional perfusion and function scores; determine manually or auto generated

Surface Page

Splash Page Review rest/stress slices

Optional

Results Pages (QGS/QPS) Review Polar Maps, quantification data and time-

Integrated ARG Report (If available)

4.1.   Language Selection

CSMC Cardiac Suite supports user interface localization. Some languages may not be available on all platforms. To select a language open **Defaults** dialog, click the **Language** tab and select the desired language from the drop-down menu.

The new language setting will take effect when the program is restarted. Note that this setting affects all CSMC Cardiac Suite applications.

Changing the language setting within CSMC Cardiac Suite will not affect the language settings of the operating system or any other applications not part of the suite.

4.2.   File Selection (using patient example)

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)

4.3.   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.
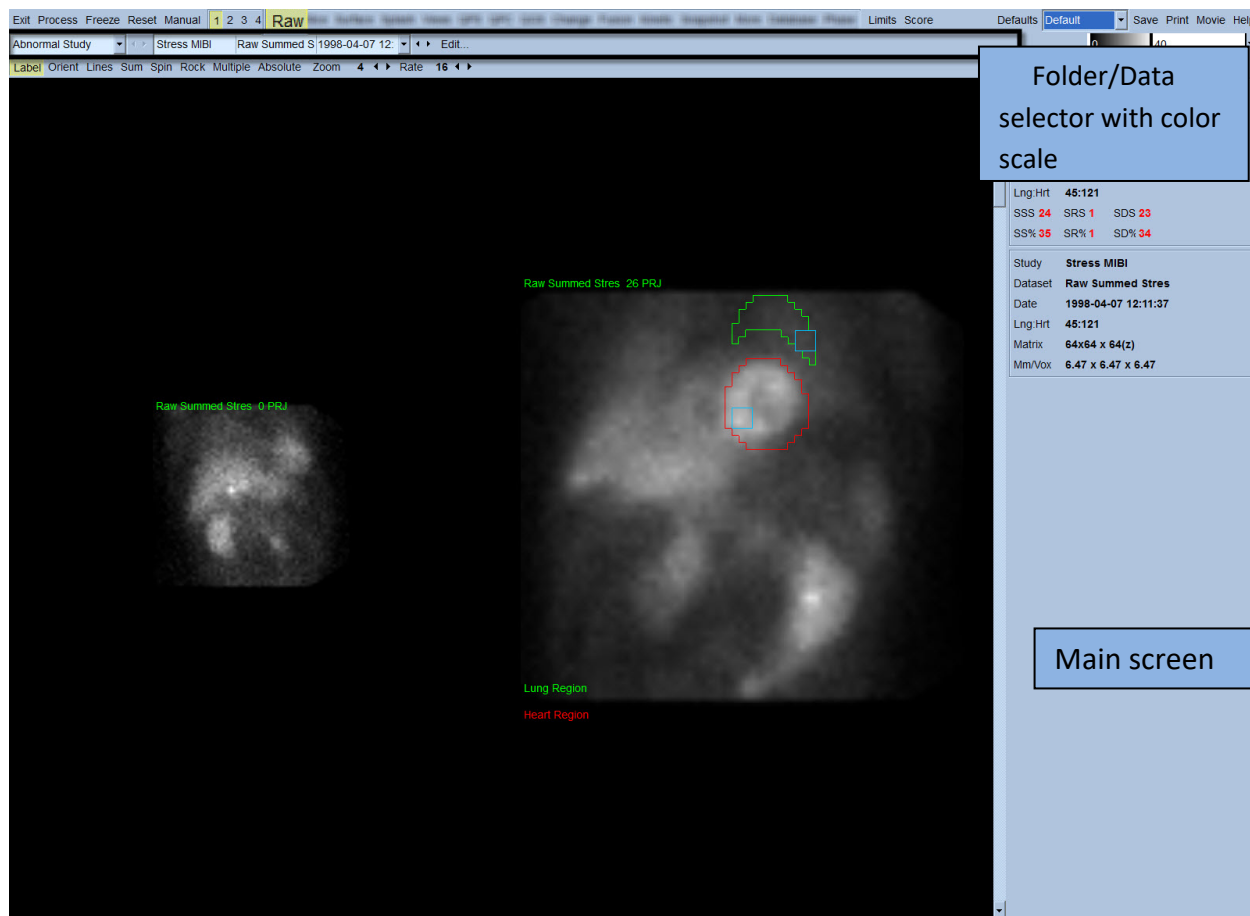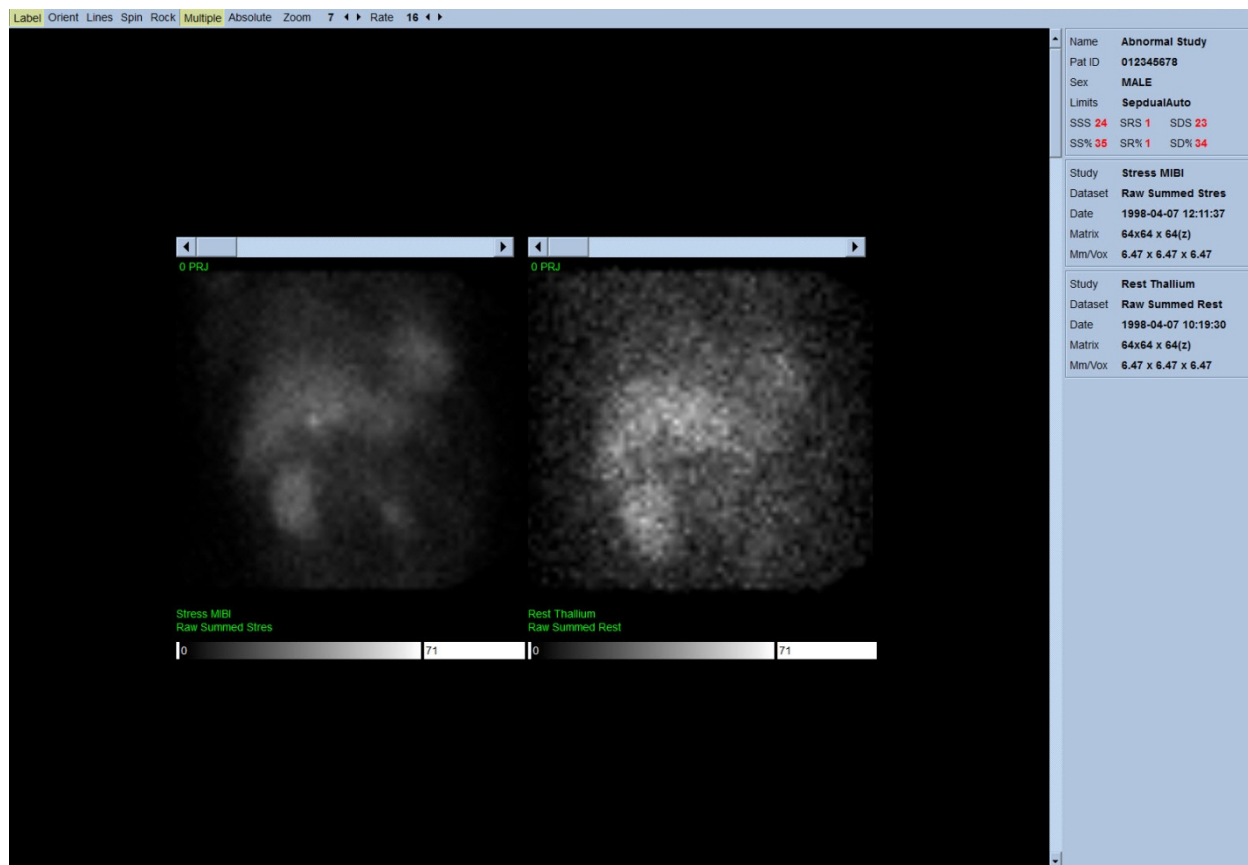
The name of the Folder (generally, a patient name) and that of the projection data set are displayed in the horizontal section that also contains the data set selector, the data set editor and the color scale.

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.

Finally, the 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.

4.4. Assessing image quality

The quality page displays projection images and contains several quality-control tools to help users identify potential problems (e.g., motion artifacts, poor count density, gating errors, etc...) to assess the overall quality of the loaded study. The QC information will only be available on the **Quality** page if it is included in the dataset headers by the vendor.

In addition to the raw projection images, sinograms and linograms, the quality page can also display:

1. Gated counts per projection
2. Summed counts per gating interval
3. Accepted/rejected beats
4. Nominal heart rate per projection
5. Additional information – average heart rate, camera, collimator, zoom, accepted/rejected beats percentage and R-R window.
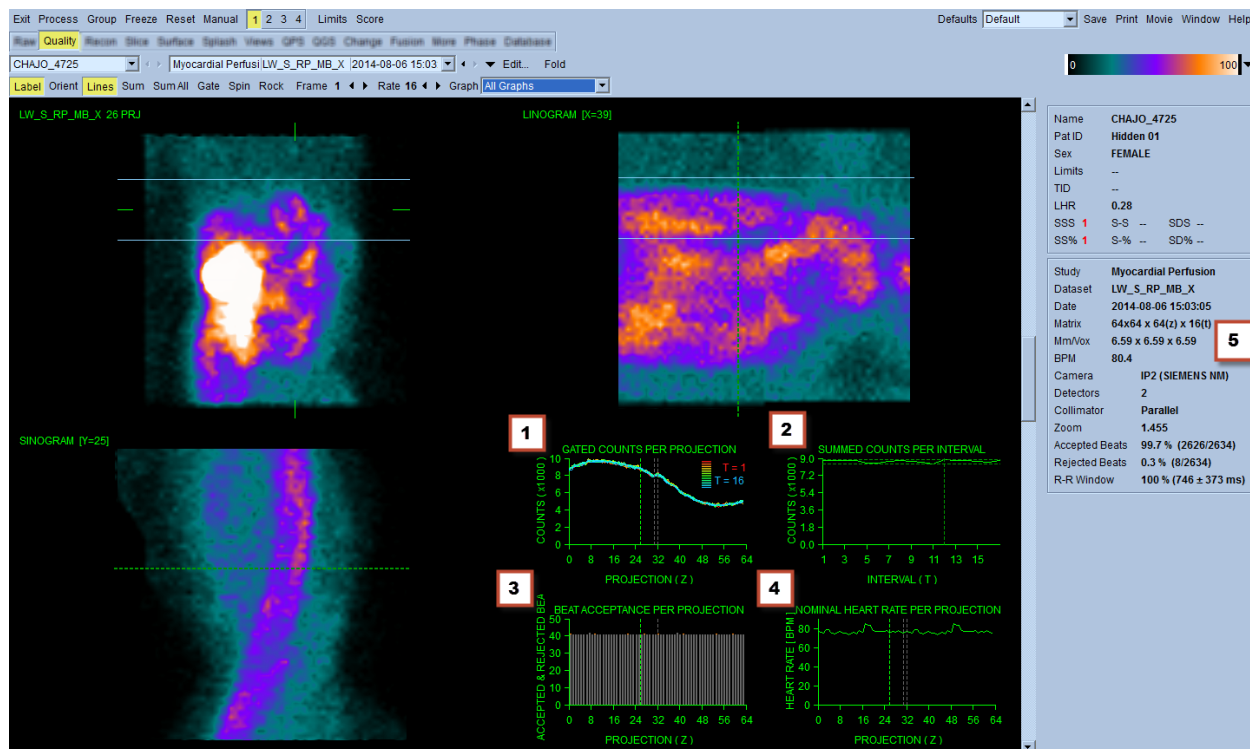
4.5.   Reviewing the Rotating Projection Images

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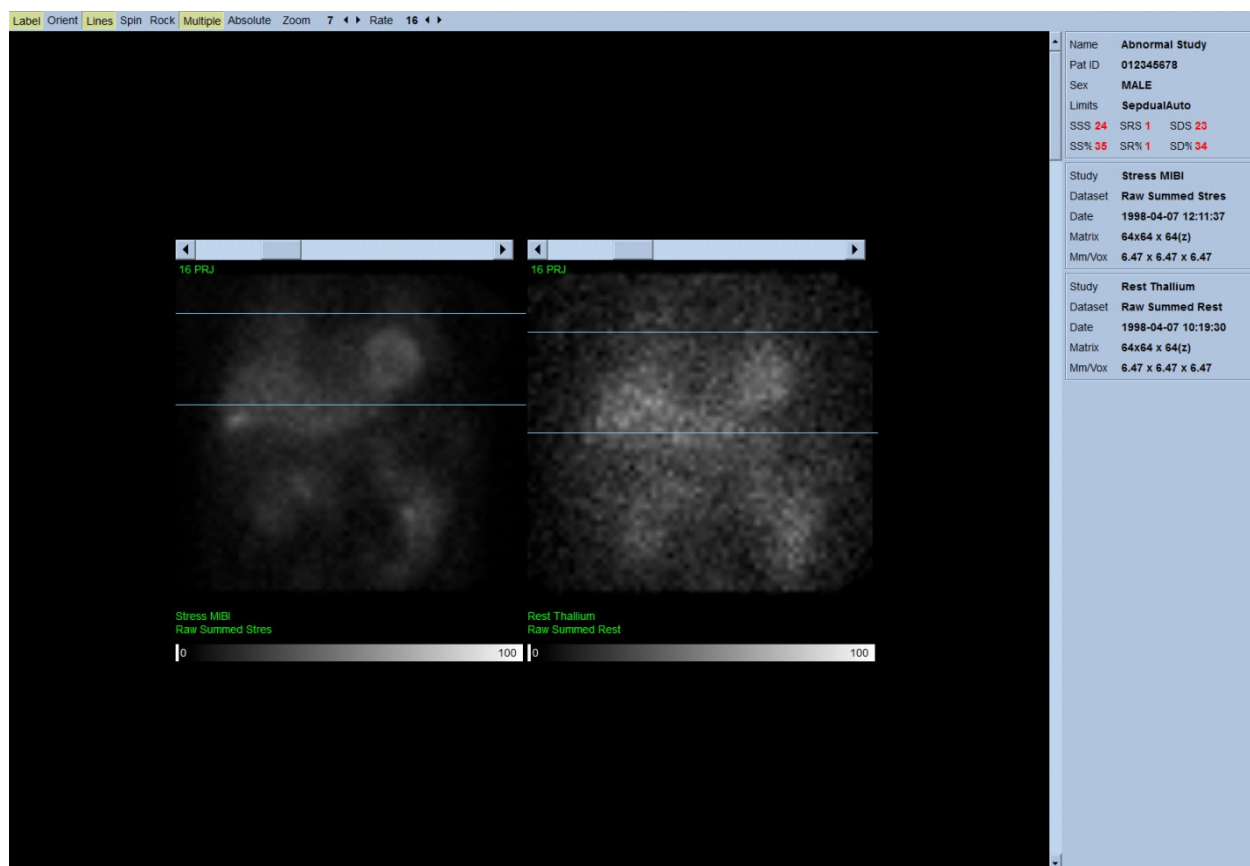
In addition to patient or organ motion, flickering (sudden variations in brightness between adjacent projections) can be assessed by reviewing the projections cine. Flickering is often an indication of gating errors, which are reflected in the ungated projection images when the latter are built through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

4.6.   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.
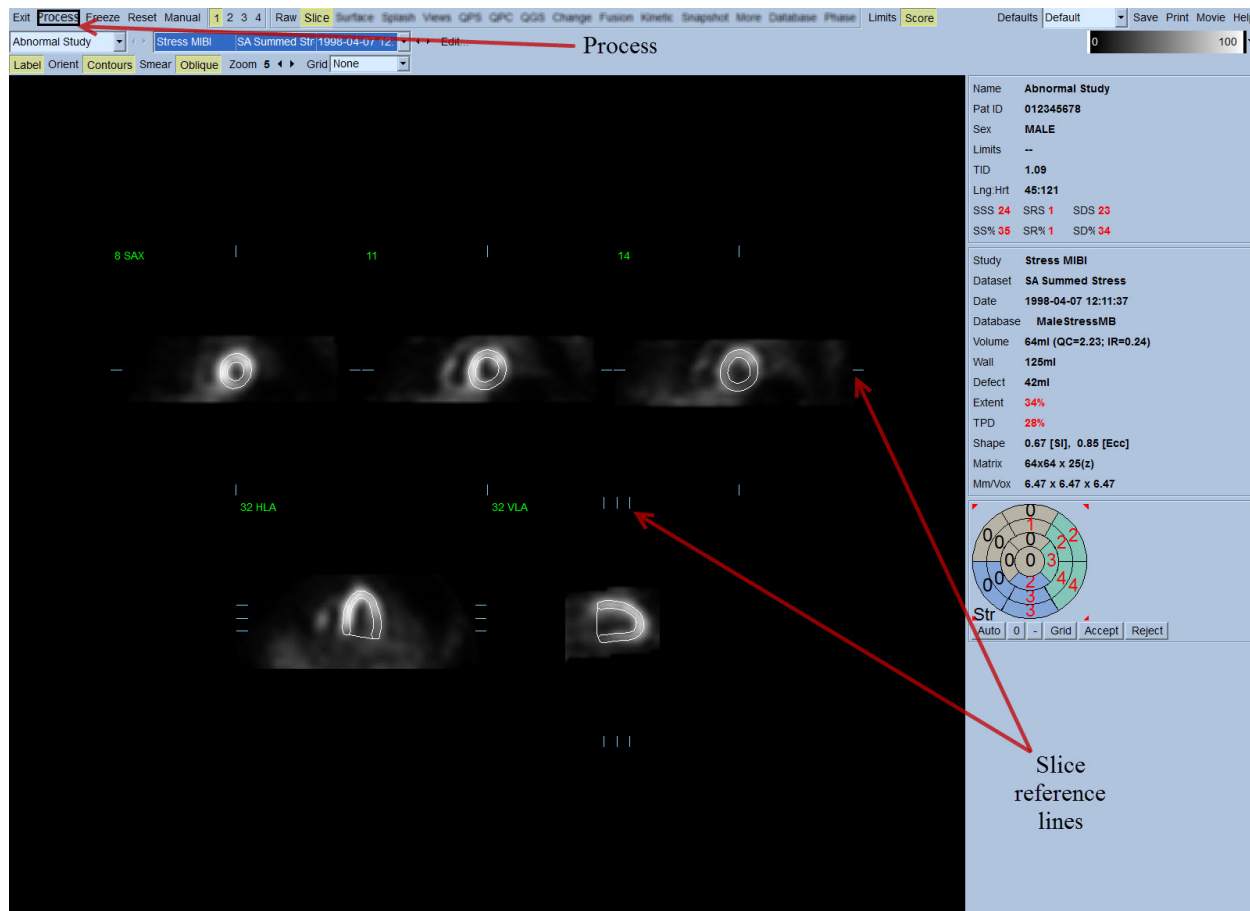
Moreover, all quantitative parameter fields in the right portion of the screen should now be filled with numeric values, in addition to the creation of time-volume and filling curves (for gated short axis datasets). We'll examine and discuss the quantitative measurements in more detail later.
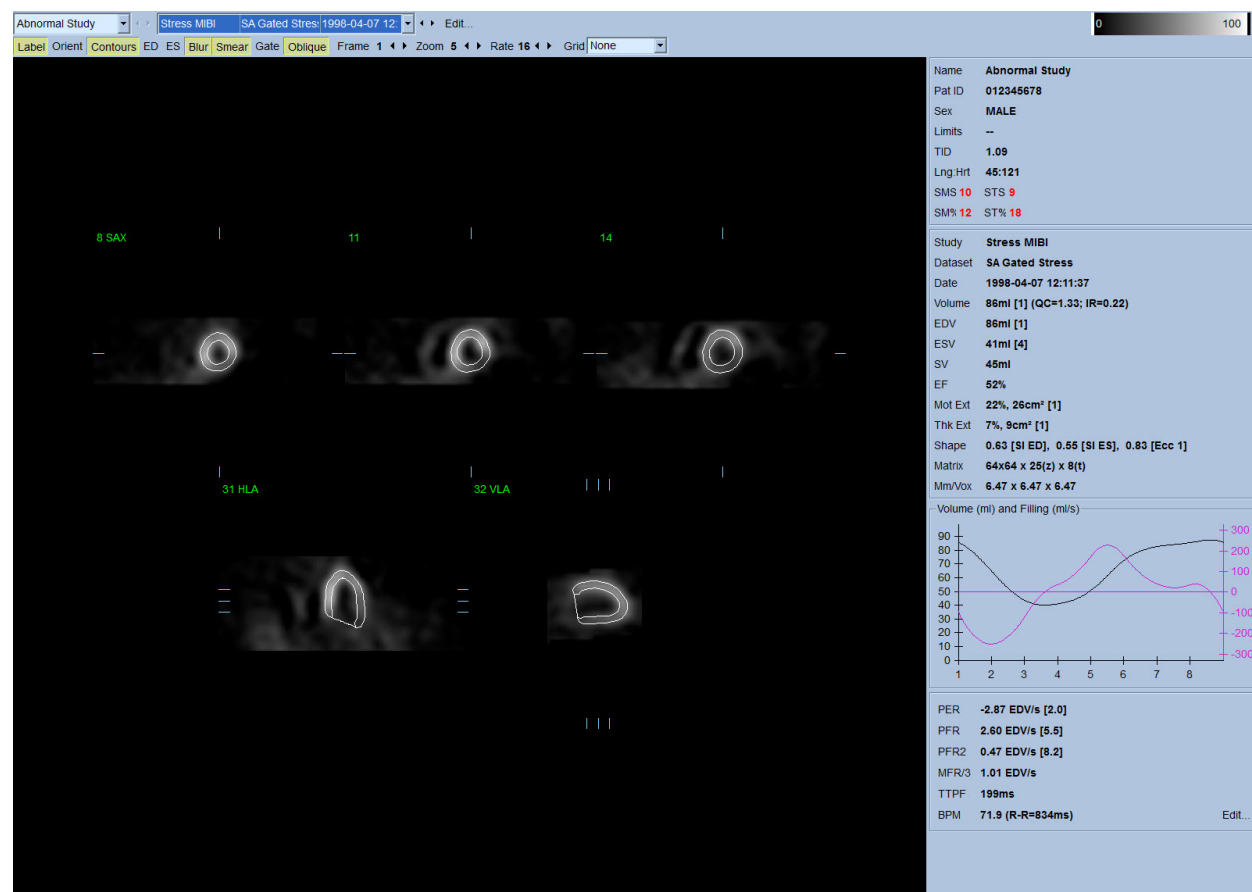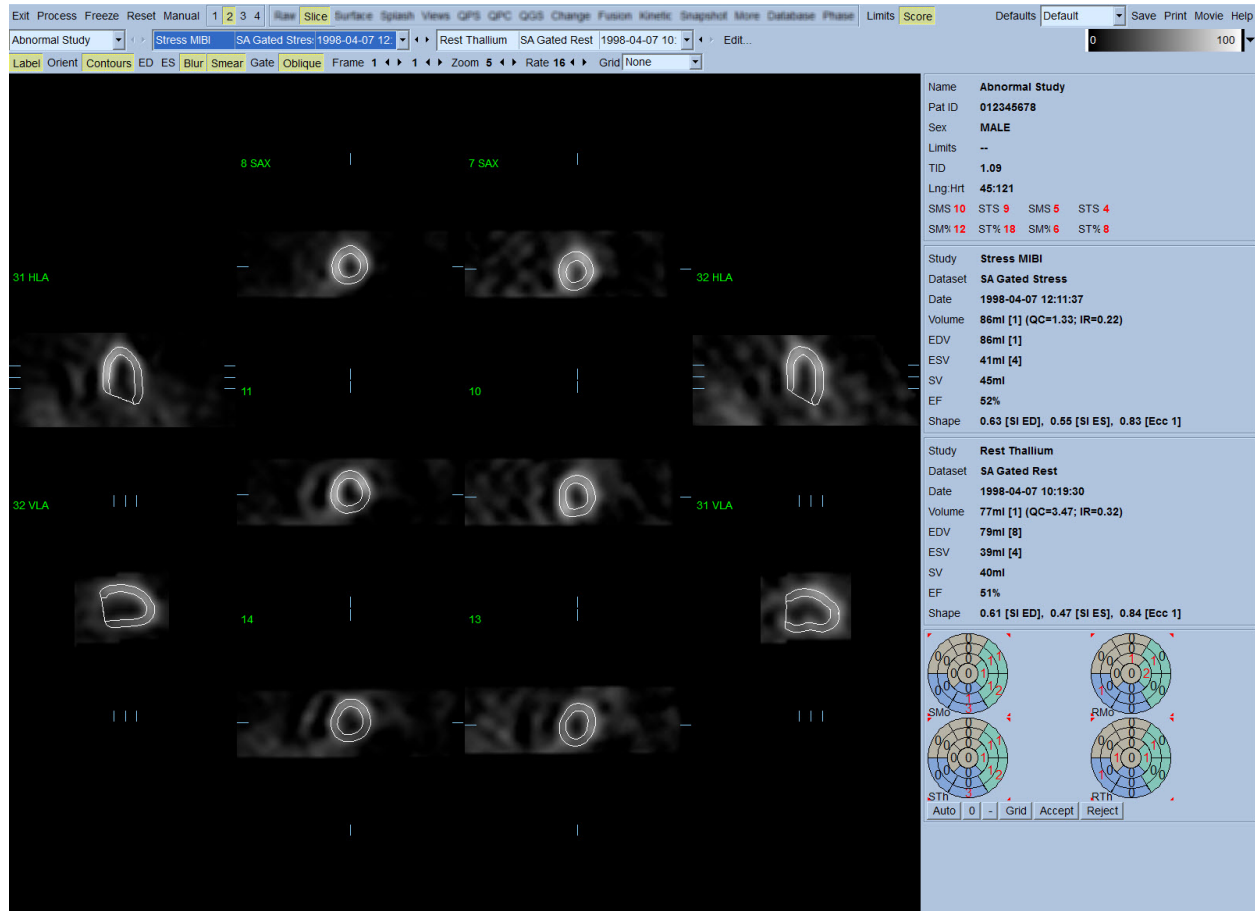
4.6.1. Group Processing

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").

4.6.2. Checking the contours

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
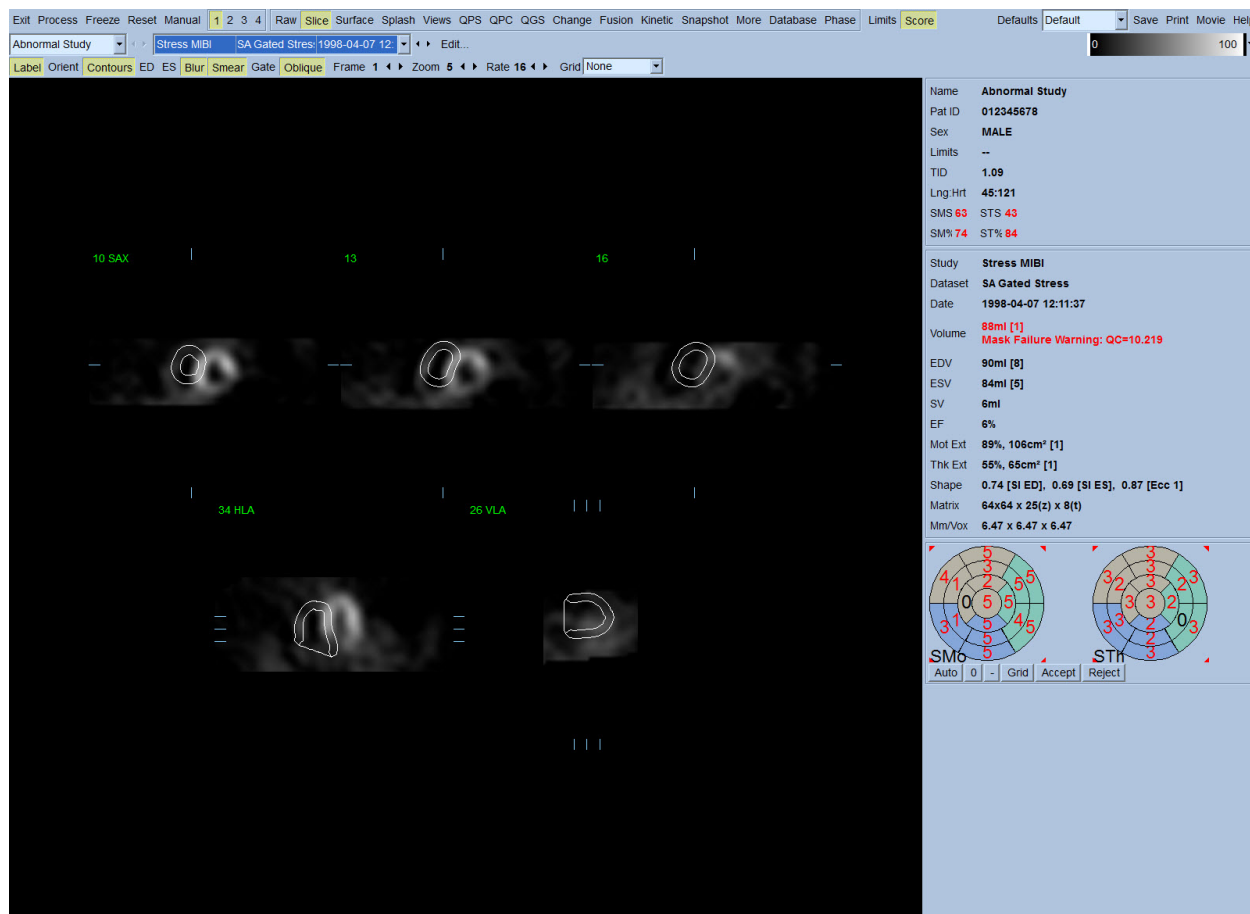
4.7. Modifying the Contours (Manual Page)

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.
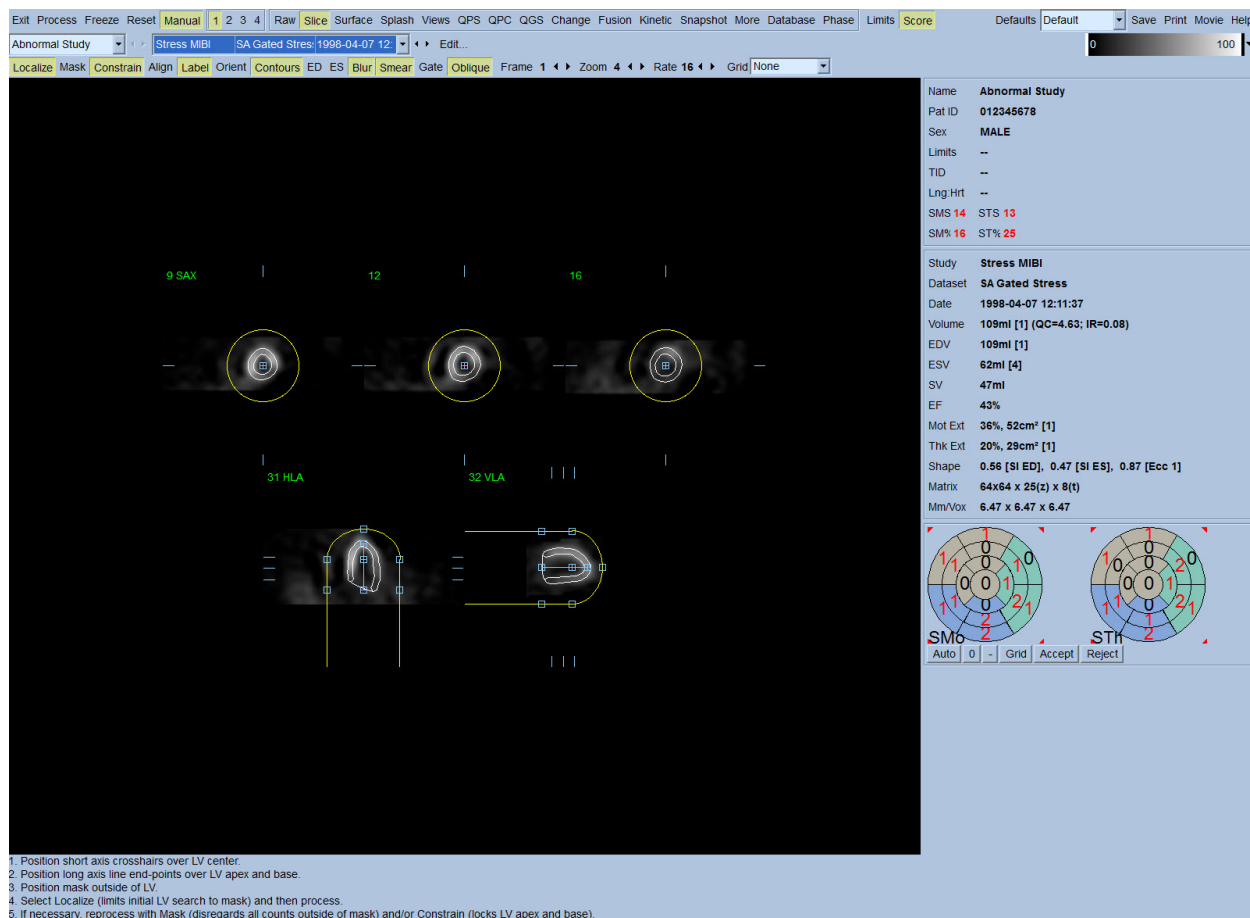
Note that the segment positioned on the LV's long axis serves only as a reference. In cases where simple masking has not produced satisfactory contours as show below, one has the option of setting two exact locations through which the apical and basal portion of the contours must pass; this is done by 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.
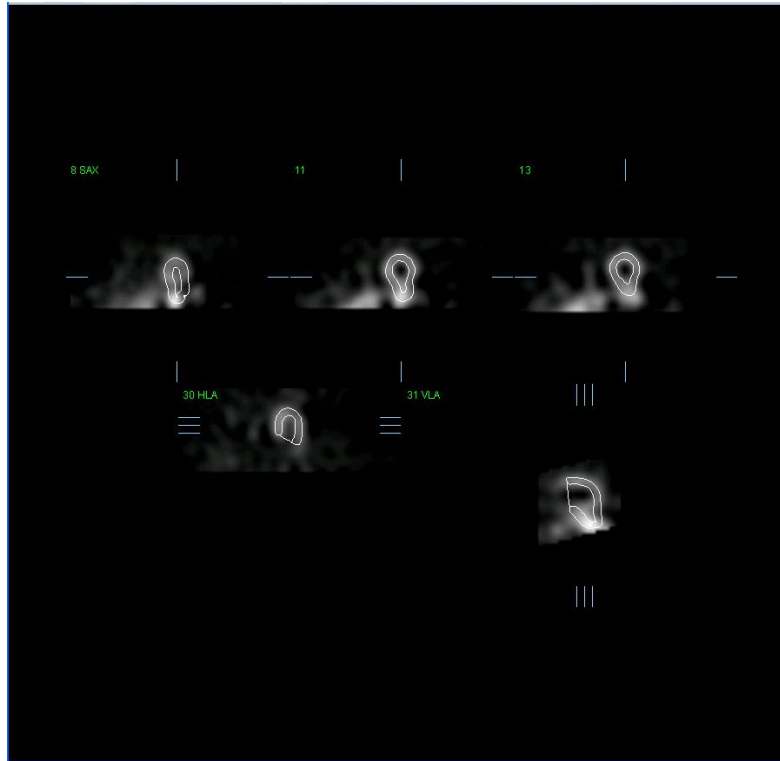
4.8.   Reviewing Gated SPECT images on the Slice page

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.
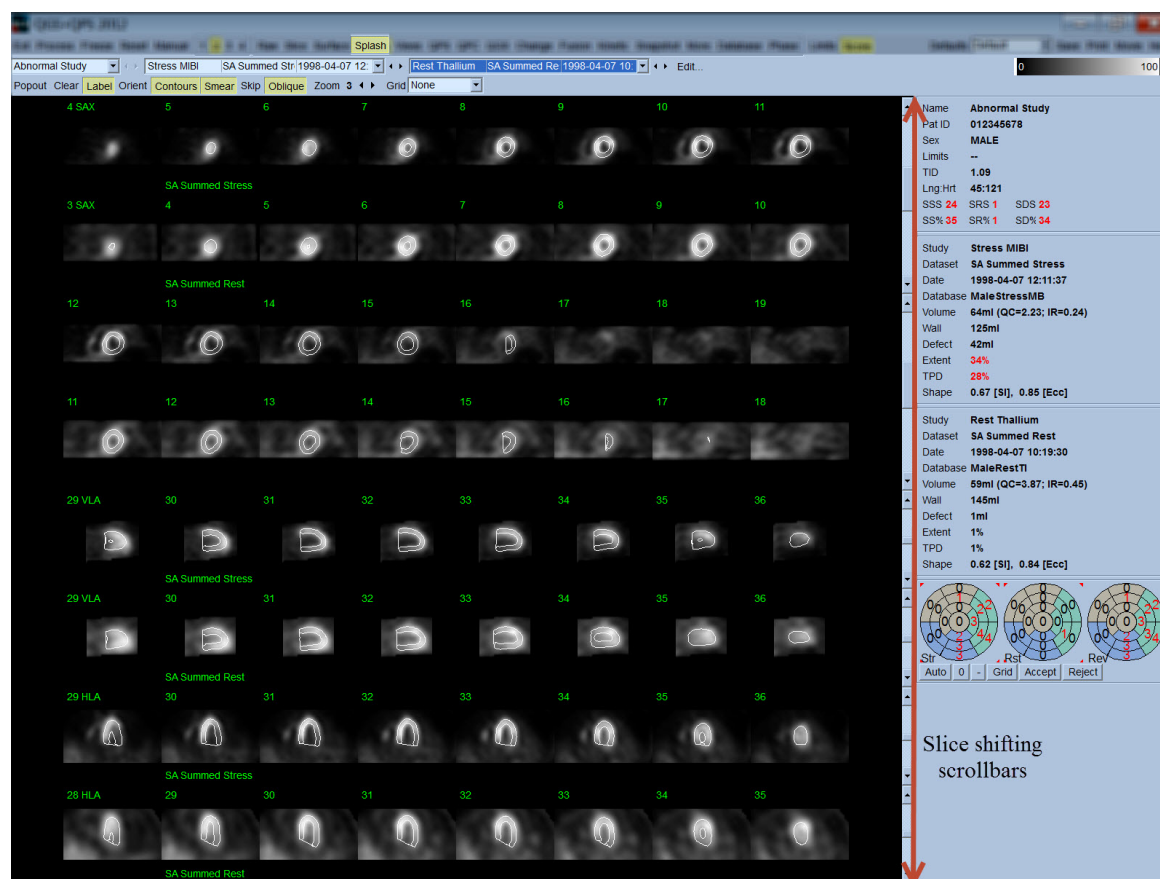
INFORMATION: At Cedars-Sinai Medical Center (CSMC), a gray or thermal scale is typically used to assess motion, and a 10-point scale (Step10) is used to assess thickening. A comprehensive description of the CSMC segmental scoring method can be found in "*Berman D, Germano G. An approach to the interpretation 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).

4.9.   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 **2** 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.
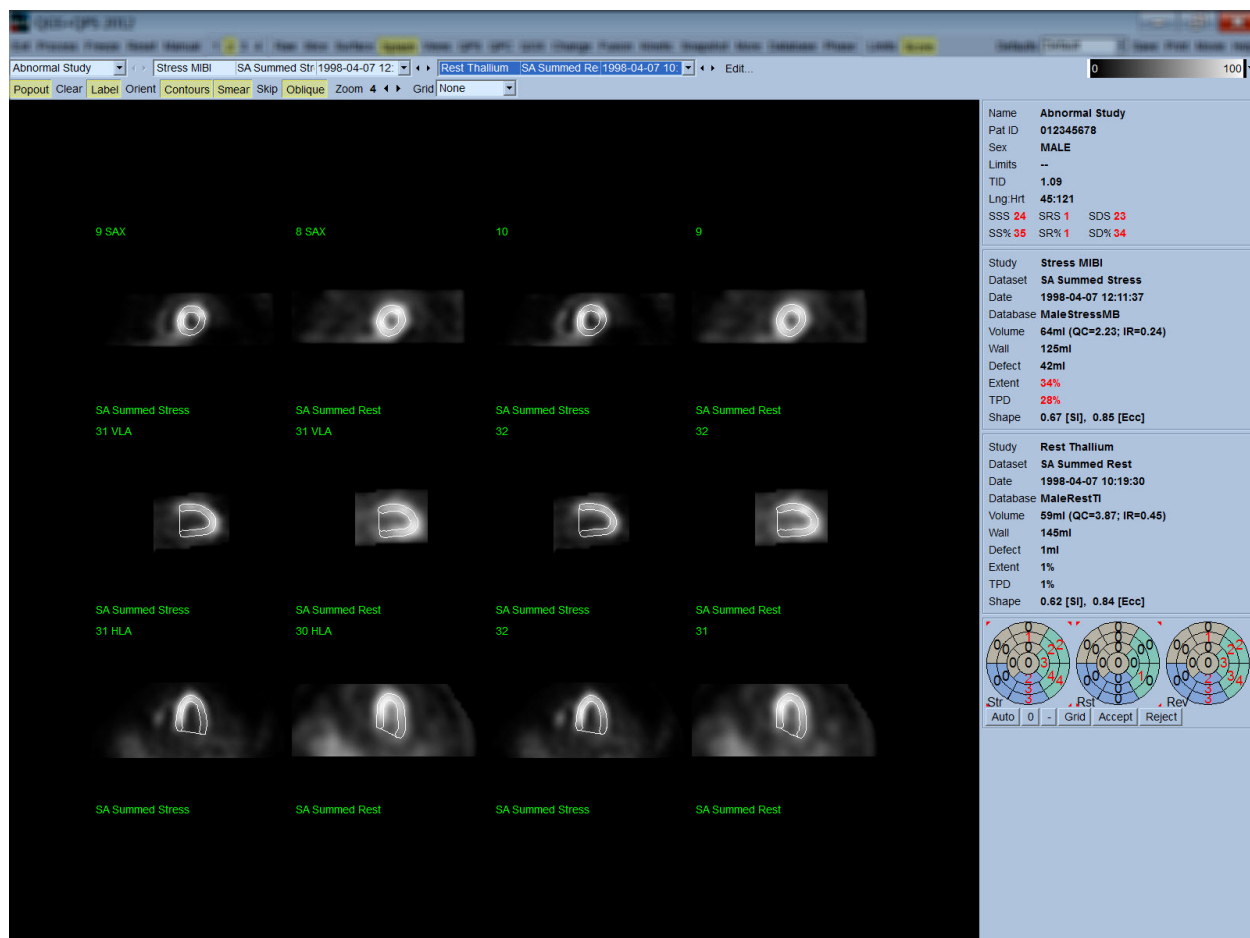
ⓘINFORMATION: At Cedars-Sinai Medical Center (CSMC), a gray or thermal scale is typically used to assess perfusion. A comprehensive description of the CSMC segmental scoring method can be found in "*Berman D, Germano G. An approach to the interpretation and reporting of gated myocardial perfusion SPECT. 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).

4.9.1. 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.
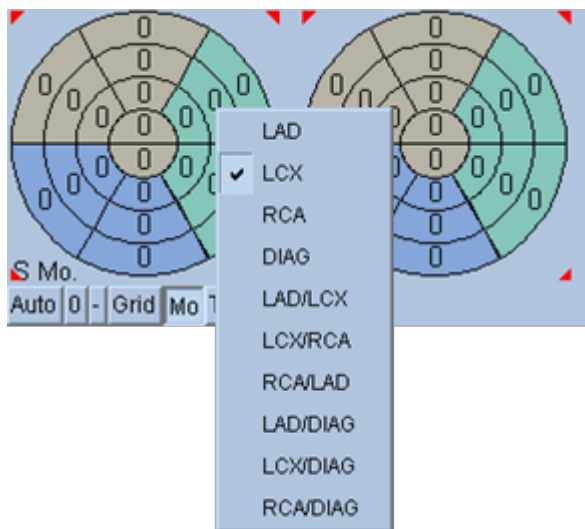
A universal set of normal limits is applied to all gated short axis datasets to automatically calculate motion and thickening scores for all segments, as well as the summed motion and thickening scores (SMS and STS), the percent summed motion and thickening scores (SM% and ST%) and the extent of motion and thickening abnormality (Mot Ext and Th Ext) expressed both as area in cm^2, 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.
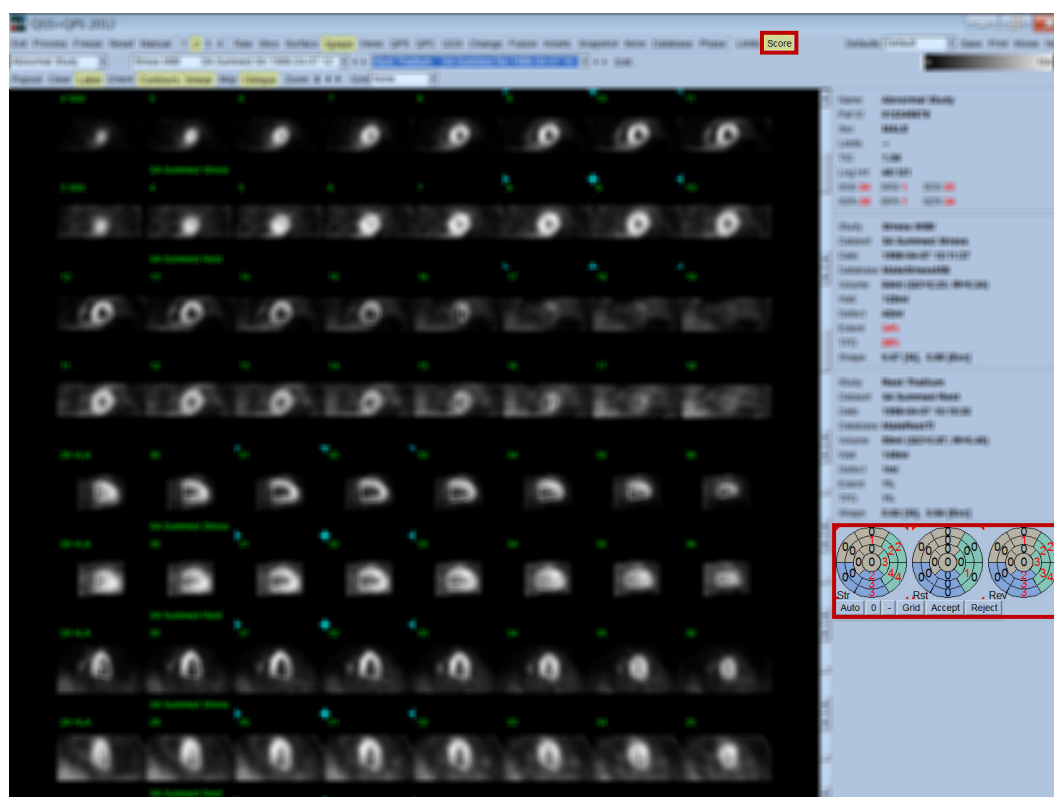
If the appropriate normal limits are preset for this patient, the program will automatically calculate perfusion scores for all segments, as well as the summed stress, rest and difference scores (SSS, SRS and SDS) and the corresponding summed percent scores (SS%, SR% and SD%) and the extent of perfusion 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.

4.10. 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.
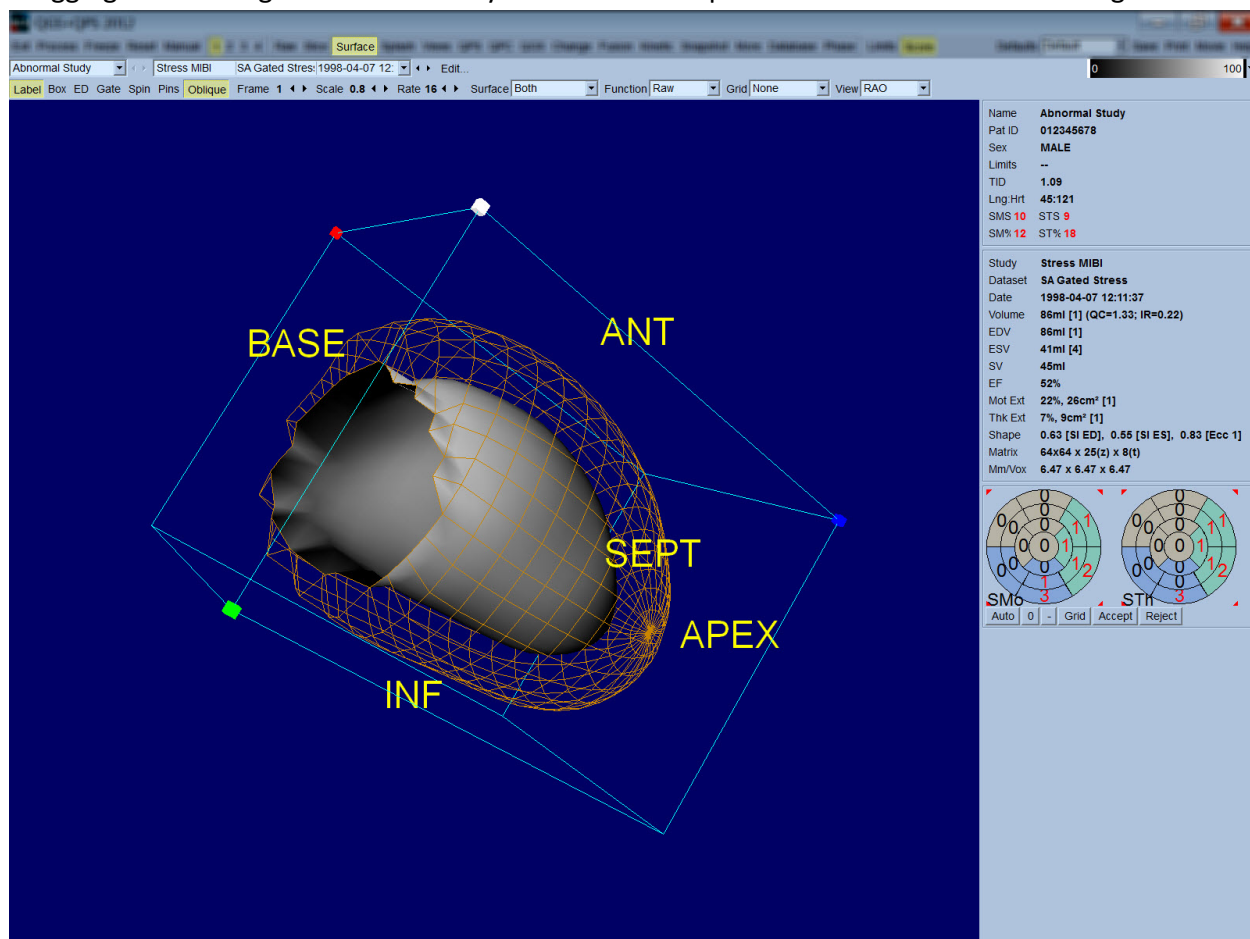
While myocardial thickening can be conceivably assessed from the epi-/endocardial display, it is easier to assess motion from a display containing the endocardium as well as its position at end-diastole. This is achieved by selecting the **Inner** option from the Surface pull-down menu, and clicking **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. It is a good idea to display all three surfaces by selecting **Both** in the Surface pull-down menu.

ANT

BASE

SEPT

APEX

INF

Name **Abnormal Study**
Pat ID **012345678**
Sex **MALE**
Limits **--**
TID **1.09**
Lng:Hrt **45:121**
SMS **10** STS **9**
SM% **12** ST% **18**

Study **Stress MIBI**
Dataset **SA Gated Stress**
Date **1998-04-07 12:11:37**
Volume **65ml [2] (QC=1.33; IR=0.22)**
EDV **86ml [1]**
ESV **41ml [4]**
SV **45ml**
EF **52%**
Mot Ext **22%, 24cm² [2]**
Thk Ext **7%, 8cm² [2]**
Shape **0.63 [SI ED], 0.55 [SI ES], 0.83 [Ecc 2]**
Matrix **64x64 x 25(z) x 8(t)**
Mm/Vox **6.47 x 6.47 x 6.47**
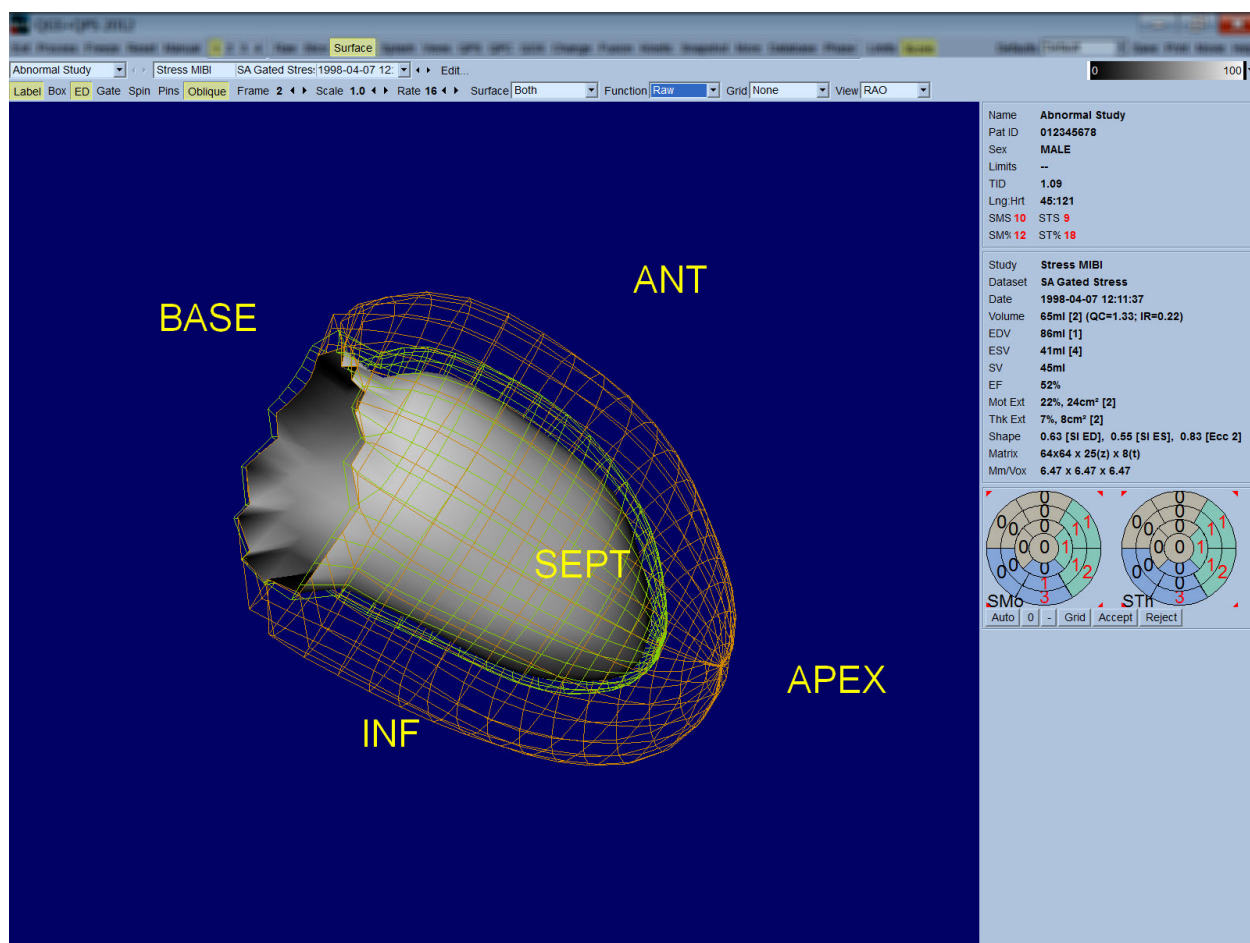
For function evaluation, the endocardial surface does not have counts mapped onto it, because it would make it harder to evaluate regional function in patients with large perfusion defects. If one wants to visualize the evolution of perfusion during the cardiac cycle, selecting the **Counts** option from the Surface pull-down menu will display the mid-myocardial surface with maximal counts mapped onto it.

Similarly, for perfusion evaluation, the endocardial surface does not have counts mapped onto it, because it would make it harder to evaluate LV size and shape in patients with large perfusion defects. If one wants to visualize 3D perfusion, selecting the Function option from the Surface pull-down menu will display the mid-myocardial surface with maximal counts mapped onto it.

4.11. 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.
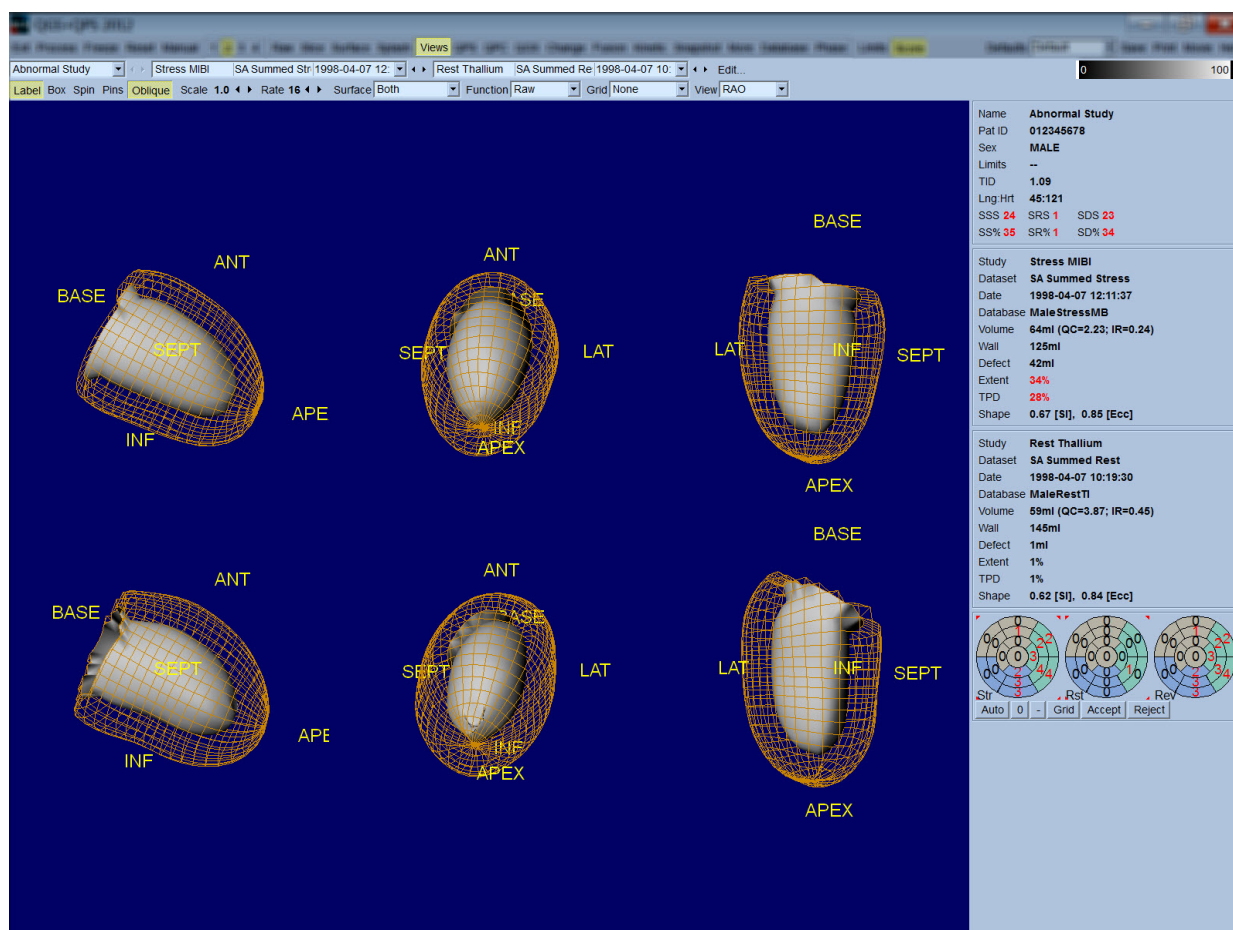
4.12. Putting it All Together: the QPS Results Page

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.
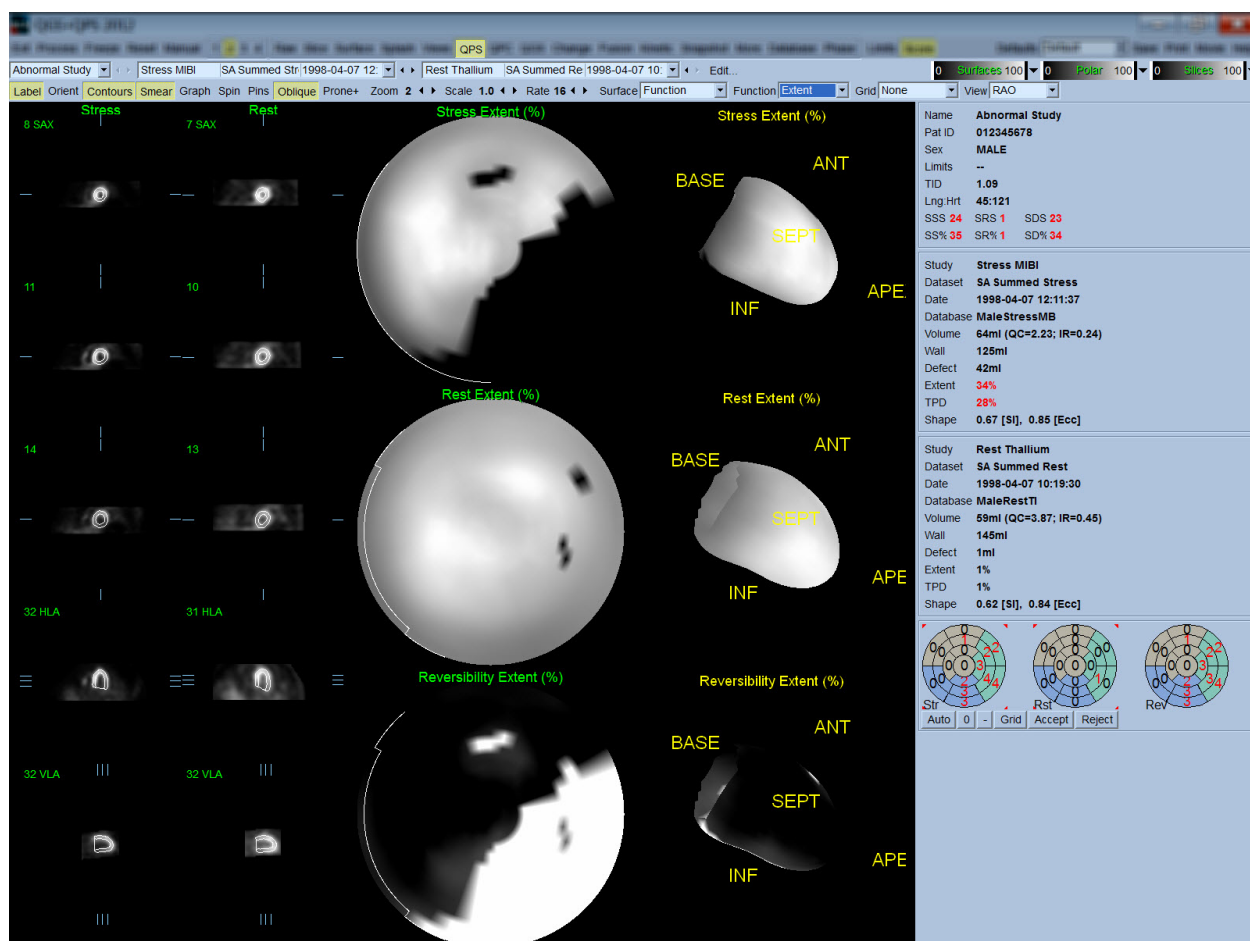
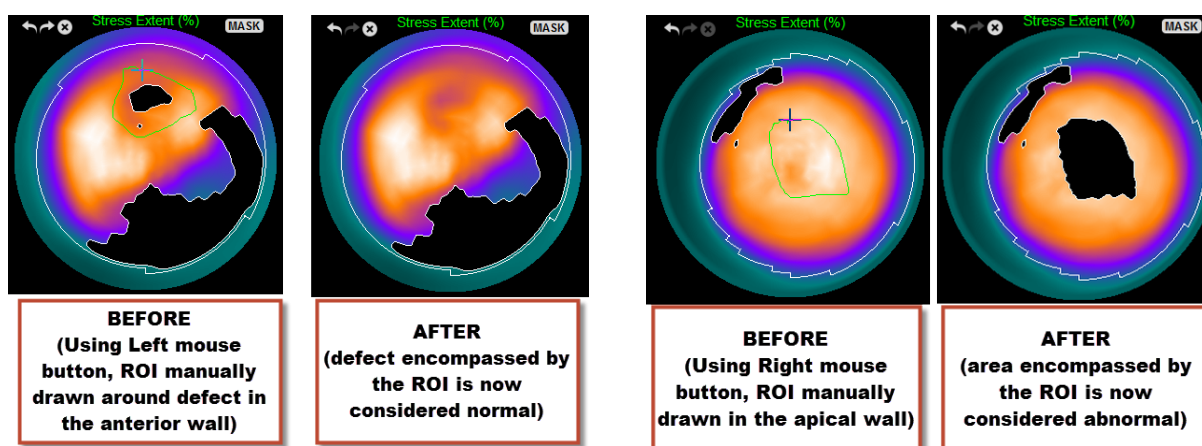### 4.12.1.   Assessing the Polar Maps

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.
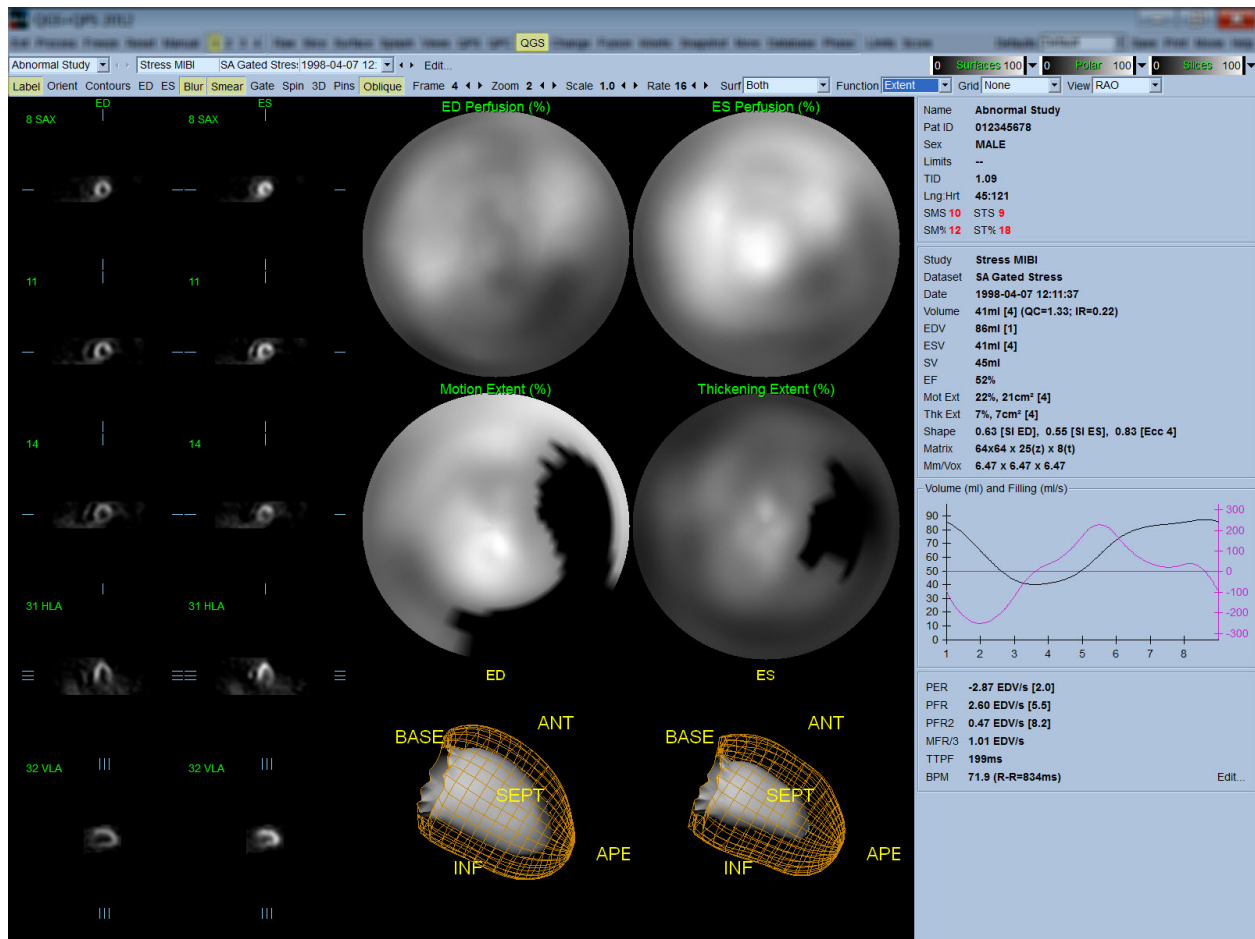
4.12.2.   Smart defect editor

Smart defect editor can be used to manually edit the extent polar maps. The tool allows users to add, remove or modify defects. Manual edits will also affect the quantitative results such as defect, extent, TPD, segmental visual scores and summed scores. To use the defect editor, click on the **Mask** toggle on the **QPS** page. Abnormal areas can be made normal by holding down the left mouse button and drawing a region around the abnormal pixels. Similarly, normal areas can be made abnormal by holding down the right mouse button and drawing a region.

BEFORE
(Using Left mouse button, ROI manually drawn around defect in the anterior wall)

AFTER
(defect encompassed by the ROI is now considered normal)

BEFORE
(Using Right mouse button, ROI manually drawn in the apical wall)

AFTER
(area encompassed by the ROI is now considered abnormal)

4.13. 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.

4.13.1. 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.
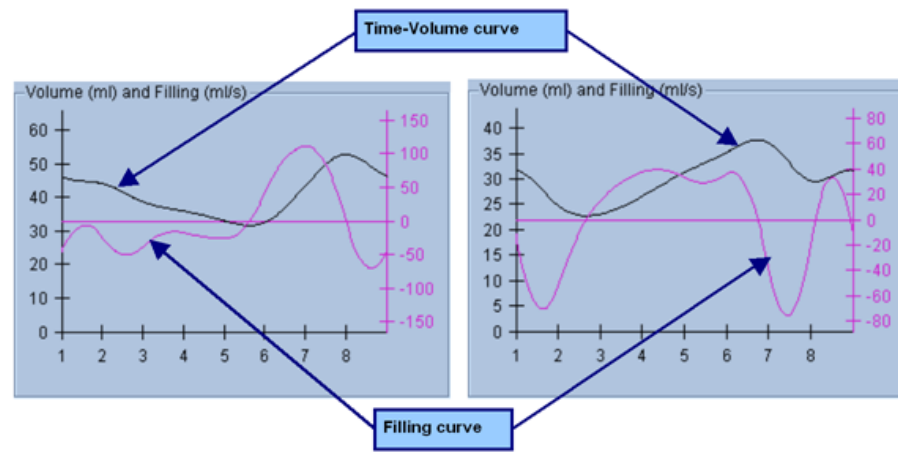
4.13.2. Assessing the Polar Maps

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.

4.13.3. 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.

4.14. 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 ***Reference Manual*** for additional information.

NOTE: Phase analysis algorithm in version 2015 and newer was modified in order to exclude basal count variations that do not correspond to actual myocardial thickening but instead are caused by valve plane motion between diastole and systole.
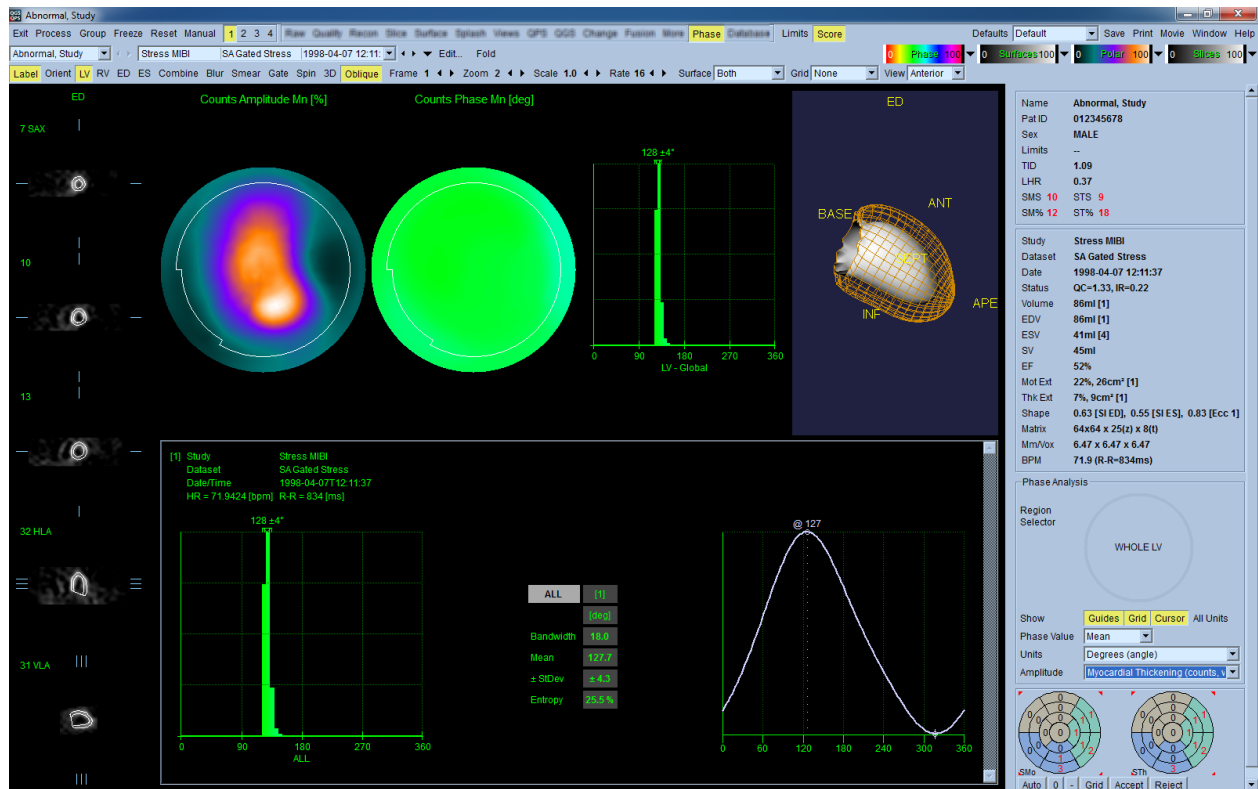
4.15. Kinetic Analysis - Coronary Flow Reserve

The Kinetic analysis feature for dynamic PET and SPECT studies allows for automated quantification of absolute stress and rest blood flow within the myocardium using algorithms specifically developed for PET Rb and NH3 and SPECT Tc99m based tracers. It also allows for non-invasive determination of absolute coronary flow reserve (CFR). The kinetic modeling method for Rb-82 is the 1-tissue compartment model (Lortie et al., EJNM 34:1765-1774, 2007). Whereas the kinetic modeling method for Nitrogen-13 ammonia uses simplified 2-compartment model (Choi et al., JNM 34(3):488-497, 1993). The kinetic modeling method for Tc-99m SPECT images uses the 1-compartment model (Leppo et al., Circ Res. 1989;65:632-639).
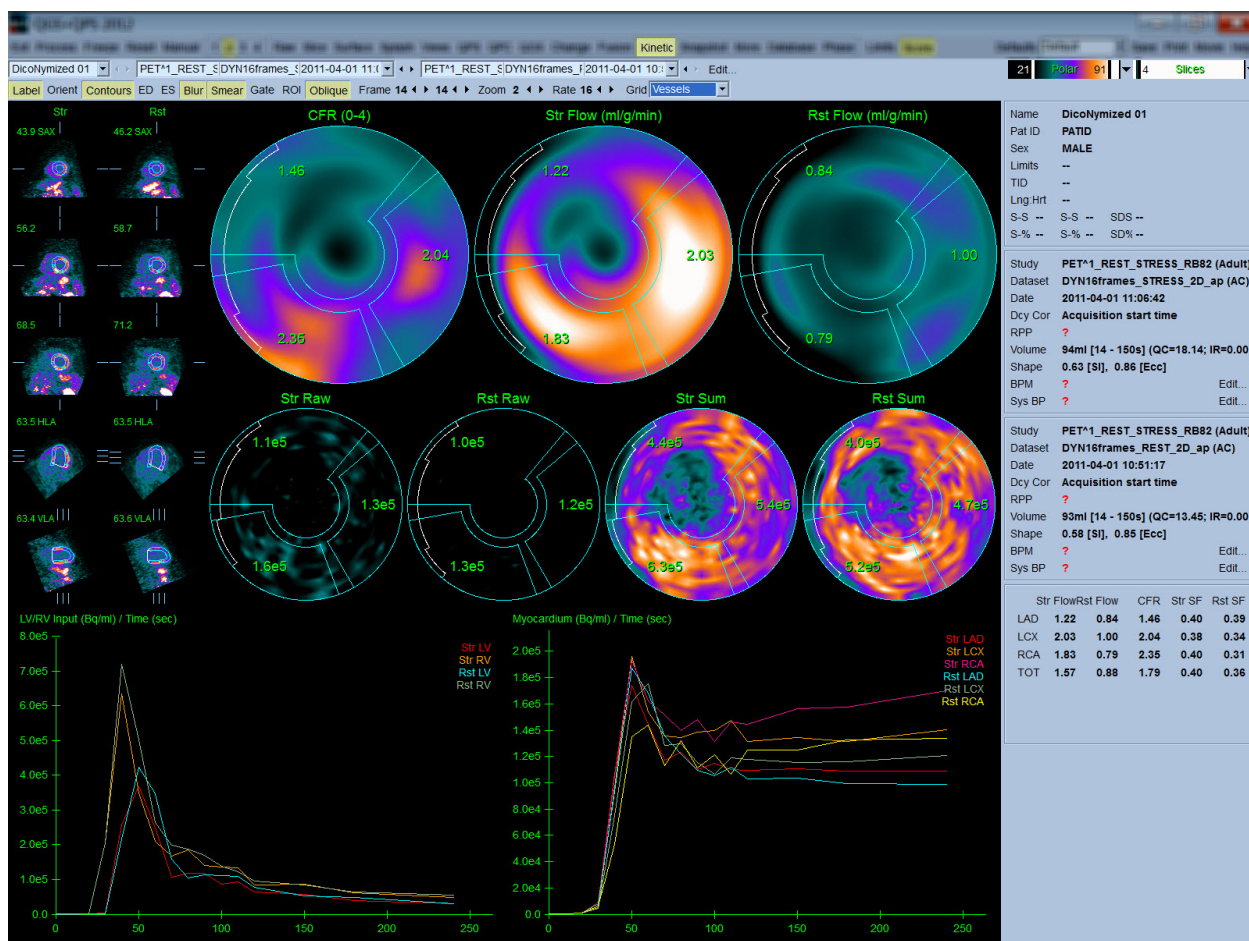
4.15.1.   Kinetic page requirements

The Kinetic feature requires at a minimum one processed transverse dynamic cardiac PET or SPECT dataset. 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.

4.15.2.   Kinetic page displays

The Kinetic page displays quantitative results utilizing polar map, time/activity graph, 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 stress and rest 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.
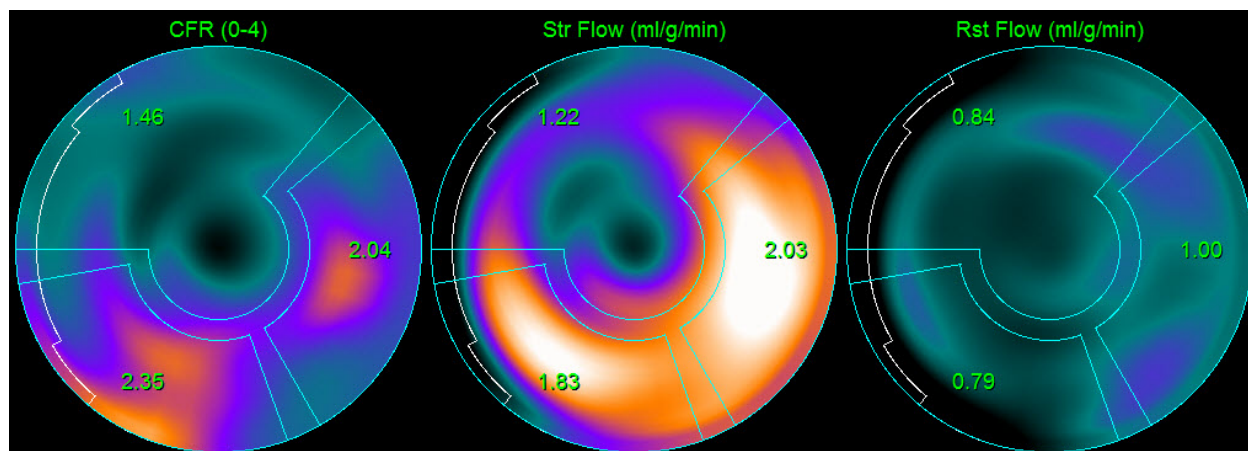
- o The Polar maps displayed in the middle of the page show radiotracer activity within the myocardium in [(Bq/ml)/Time(Sec)]. There are up to 4 polar maps displayed in this region if both the rest and stress flow datasets are loaded. Two of the polar maps show summed data that sums the information from all frames; the remaining two polar maps show data for the specific frame being displayed.
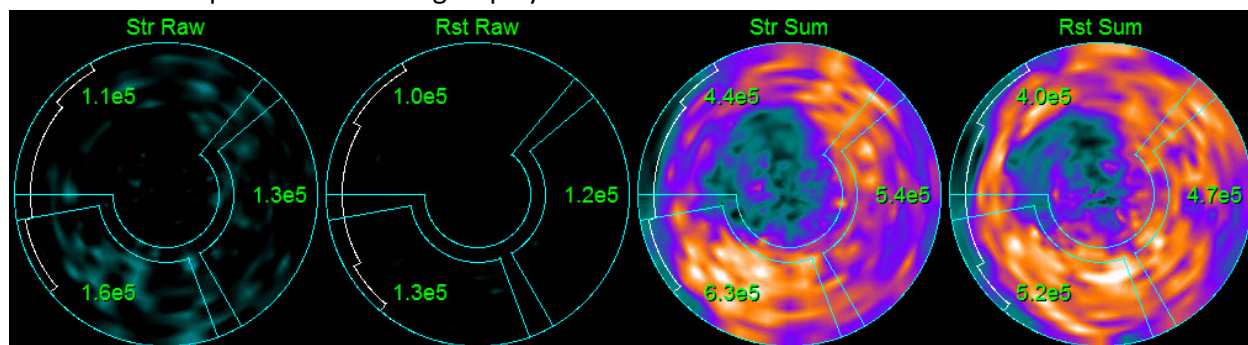
- **Time/Activity graphs-**The time/activity curves display radiotracer activity both within the blood pool of the right and left ventricles (left) and for the Myocardium (right). When the **Grid** setting is set to **Vessels**, the Myocardium graph will also display the curves for each of the 3 main coronary blood vessels (LAD, LCX, and RCA). The values in the time/activity graphs represent absolute radiotracer activity [Bq/ml]/Time[sec].
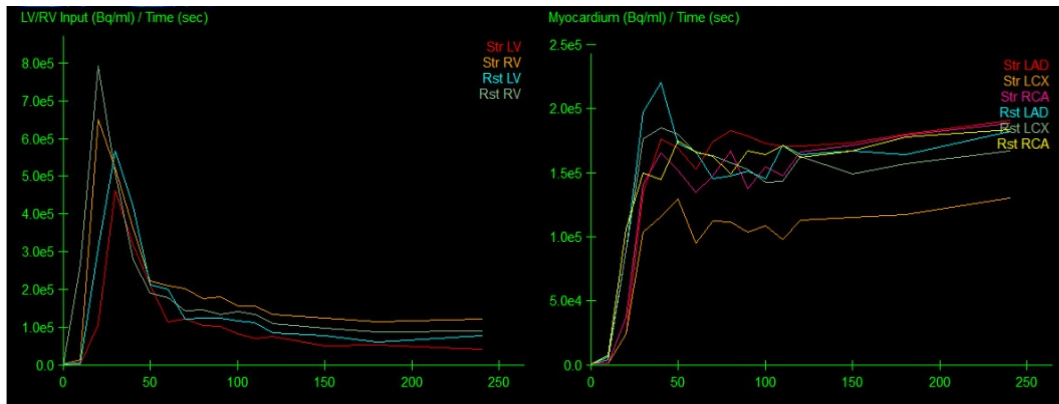
- **Results** (Scores)**-**The bottom right side of the screen shows results for absolute flow, CFR, and the spill-over fraction (SF) for each area of the Myocardium. SF is the amount of radiotracer that has "spilled-over" into the Myocardium (as defined by the segmentation or contours) from the blood 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	1.11	1.07	1.08	0.30	0.30
LCX	1.28	1.02	1.30	0.30	0.29
RCA	1.20	0.72	1.70	0.30	0.29
TOT	1.18	1.00	1.25	0.30	0.30

4.16. Right ventricle (RV) quantification
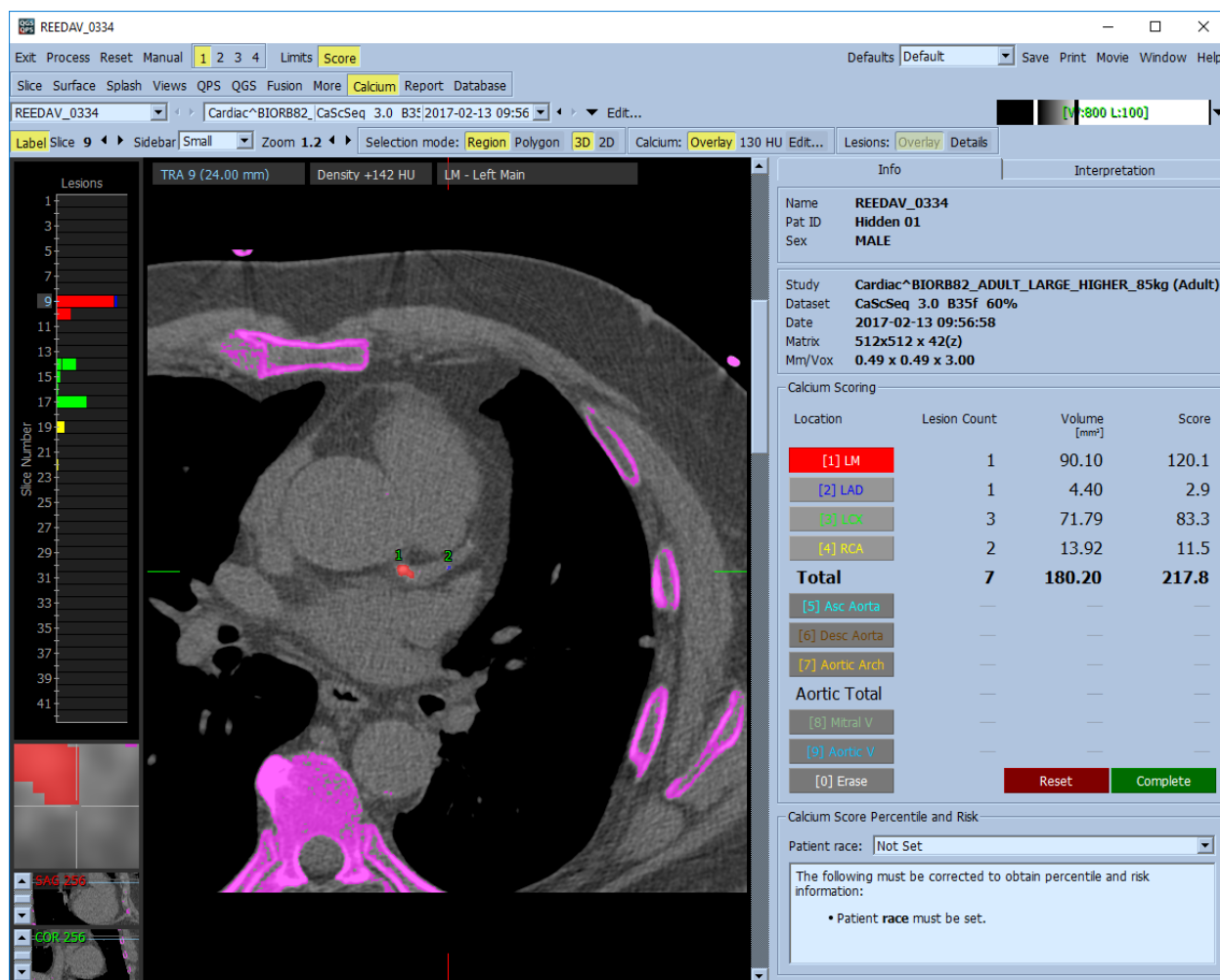
Automated right ventricular quantification and analysis is now available for supported gated datasets. Toggle on **RV** and then click **Process** to generate RV contours and quantitative results.
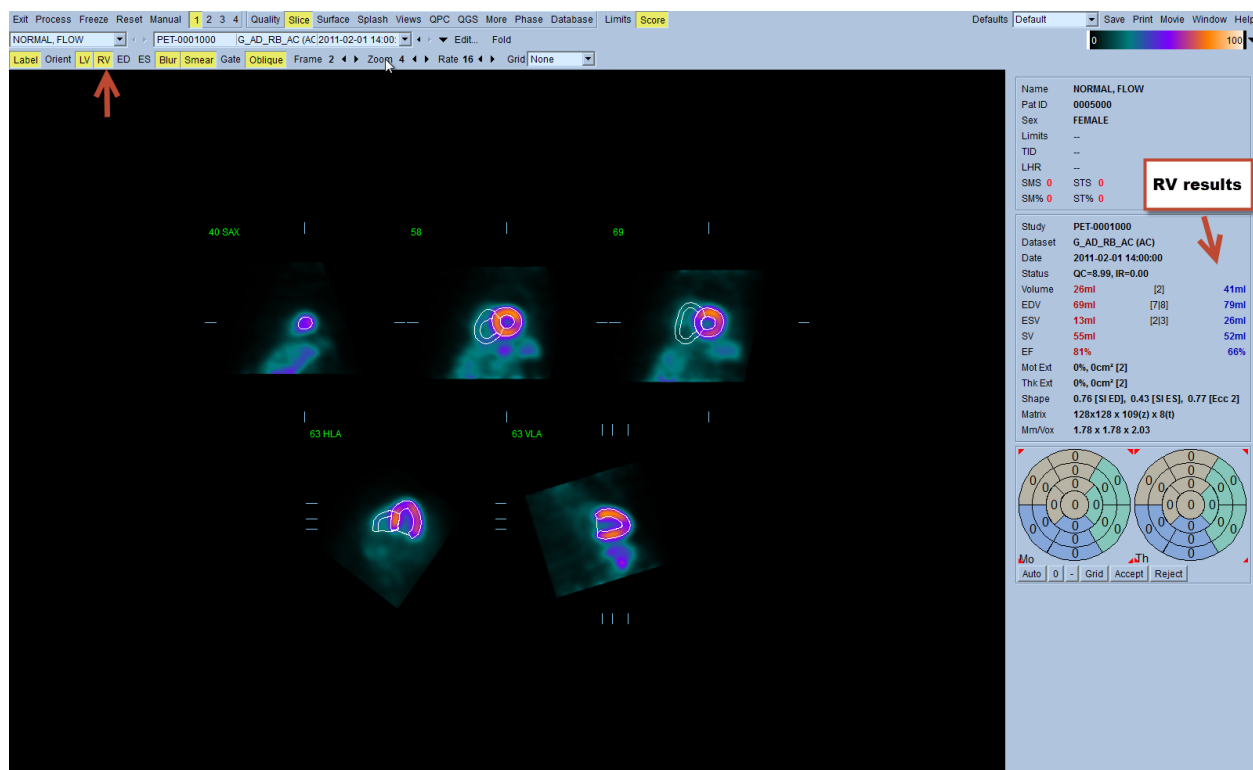
4.17. Calcium Scoring

The Calcium page is used for quantification and review of coronary artery calcium deposits. A diagnostic quality non-contrast CT dataset is required for the calcium page. The page provides tools for identifying calcium lesions throughout the scan. Only lesions assigned to one of the coronary arteries (LM, LAD, LCX or RCA) are used for computing the total coronary calcium Agatston score. Additional details for the Calcium page are described in the QGS+QPS reference guide.

4.18. Saving your Results

With completion of the processing and reviewing steps outlined above, the user has the option of saving the results to a composite results file. From the main tool bar click **Save** to display the **Save Results** dialog window.
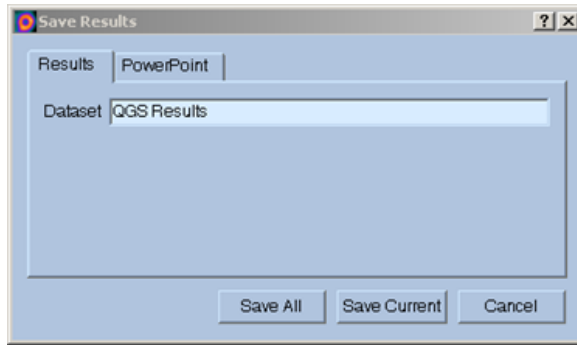
There are two main choices available for saving results files, **Results** and **PowerPoint**. Selecting the **Results** tab (default) allows saving of processed results as a single file within the patient study.

Selecting the **PowerPoint** tab allows saving of results and application configuration information in a format that allows for fast and easy launching of case studies directly from a PowerPoint presentation. The PowerPoint saving feature is described in the reference guide.

The following actions are supported:

Save All	Saves results for all selected studies
Save Current	Saves results for the currently display study.
Cancel	Exits the dialog without saving results. The user may also exit the dialog by clicking the "X" in the upper right-hand corner of the dialog window.

4.19. Exiting

To exit from any of the programs, click the **Exit** button.

5. QBS Application (Quantitative Blood Pool)

The QBS workflow is intentionally modeless. As such, no particular processing sequence is dictated to the user. A typical sequence might proceed as follows:

```
                          ┌─────────────────┐◄──────────────────┐
                          │  Load Datasets  │                   │
                          └─────────────────┘          ┌─────────────────────┐
                                  │                     │ Repeat acquisition  │
                                  ▼                     │      and/or         │
                          ╭─────────────────╮           │   reconstruction    │
                          │  Quality Page   │           └─────────────────────┘
                          │ Review quality of│                    │
                          │ raw projection  │──────────────── Yes
                          │    images       │
                          ╰─────────────────╯
                                  │
                                  ▼
                          ┌─────────────────┐           ╭─────────────────╮
                          │ Is there motion,│           │   Views Page    │
                          │ incorrect acqui-│           │  Review views   │
                          │ sition (i.e.    │           ╰─────────────────╯
                          │ LV/RV is clipped)│                  │
                          │ or gating errors │                  ▼
                          └─────────────────┘           ╭─────────────────╮
                                  │                     │    Surface      │
                                  ▼                     │     Page        │
                          ╭─────────────────╮           ╰─────────────────╯
                          │   Slice Page    │                   │
                          ╰─────────────────╯                   ▼
         Yes                      │                     ╭─────────────────╮
   ┌────────────────┐    ┌─────────────────┐            │  Planar Page    │
   │ Manual (Page)  │    │ Are contours    │            ╰─────────────────╯
   │  Processing    │────│  incorrect?     │                   ▲
   └────────────────┘    └─────────────────┘   No
                  │      ┌─────────────────┐
          ╭───────────╮  │ Review regional │            Optional
          │ Splash Page│  │ perfusion and   │
          │ Review 2D  │→ │ function scores;│         ┌─────────────┐
          │  slices    │  │ determine       │         │ Integrated  │
          ╰───────────╯  │ manually or auto│         │    ARG      │
                          │  generated      │         │   Report    │
                          └─────────────────┘         │(If available)│
                                  │                    └─────────────┘
                                  ▼
                    ╭─────────────────────────╮
                    │      Results Page       │
                    │   Review Polar Maps,    │
                    │ quantification data and time-│
                    ╰─────────────────────────╯
```
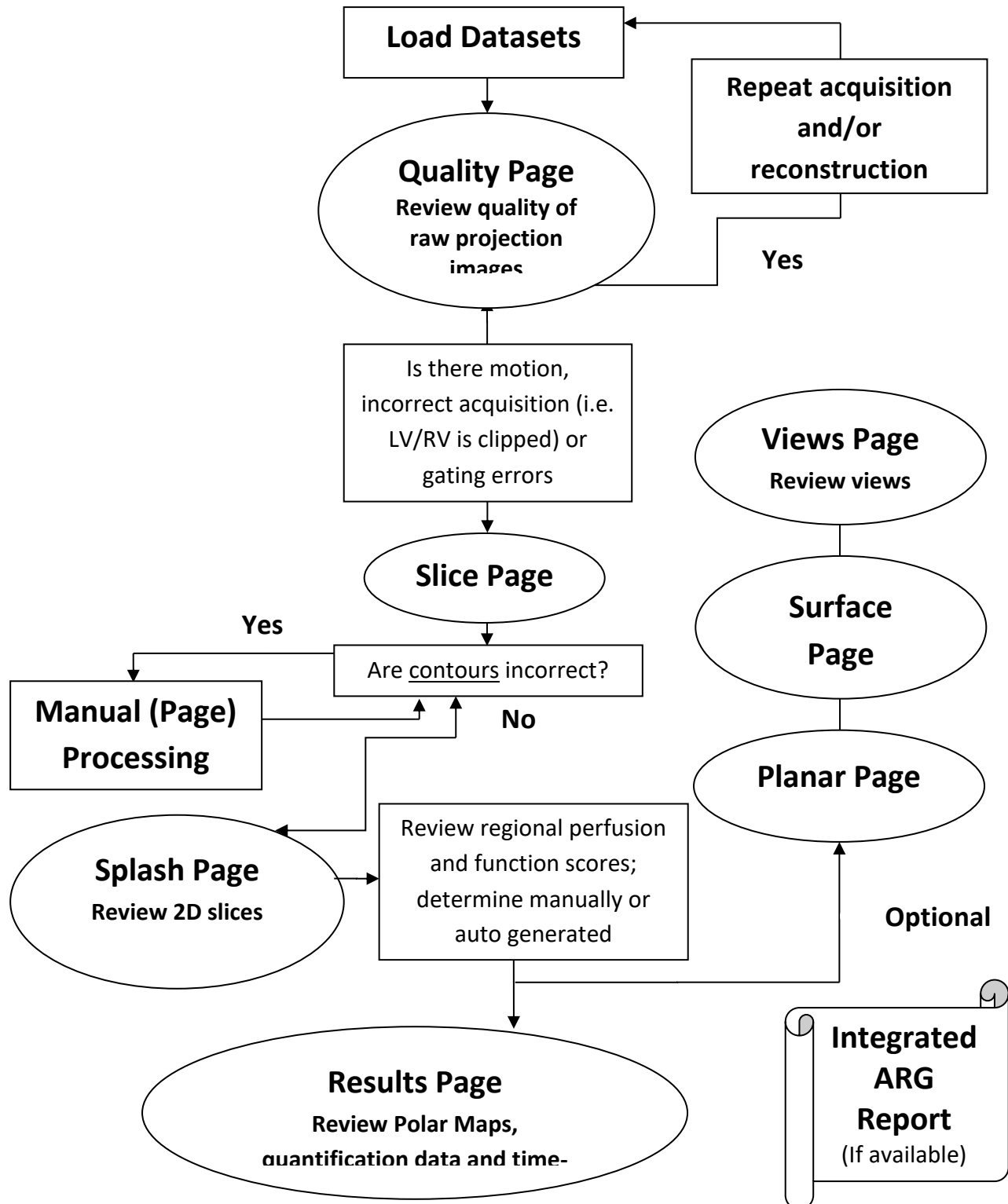
Note: QBS is able to quantify parameters of global and regional LV and RV function using only a short axis gated blood pool dataset.

5.1. Launching QBS

Launching QBS in its standard configuration will bring up the Main screen with the **Slice** page indicator and the **Label, LV** and **RV** toggles highlighted shown below. Representative slices are shown, with the number to the top-left of each slice showing its order in the short axis dataset. Left-clicking on Label toggles that number and the slice reference lines on and off.
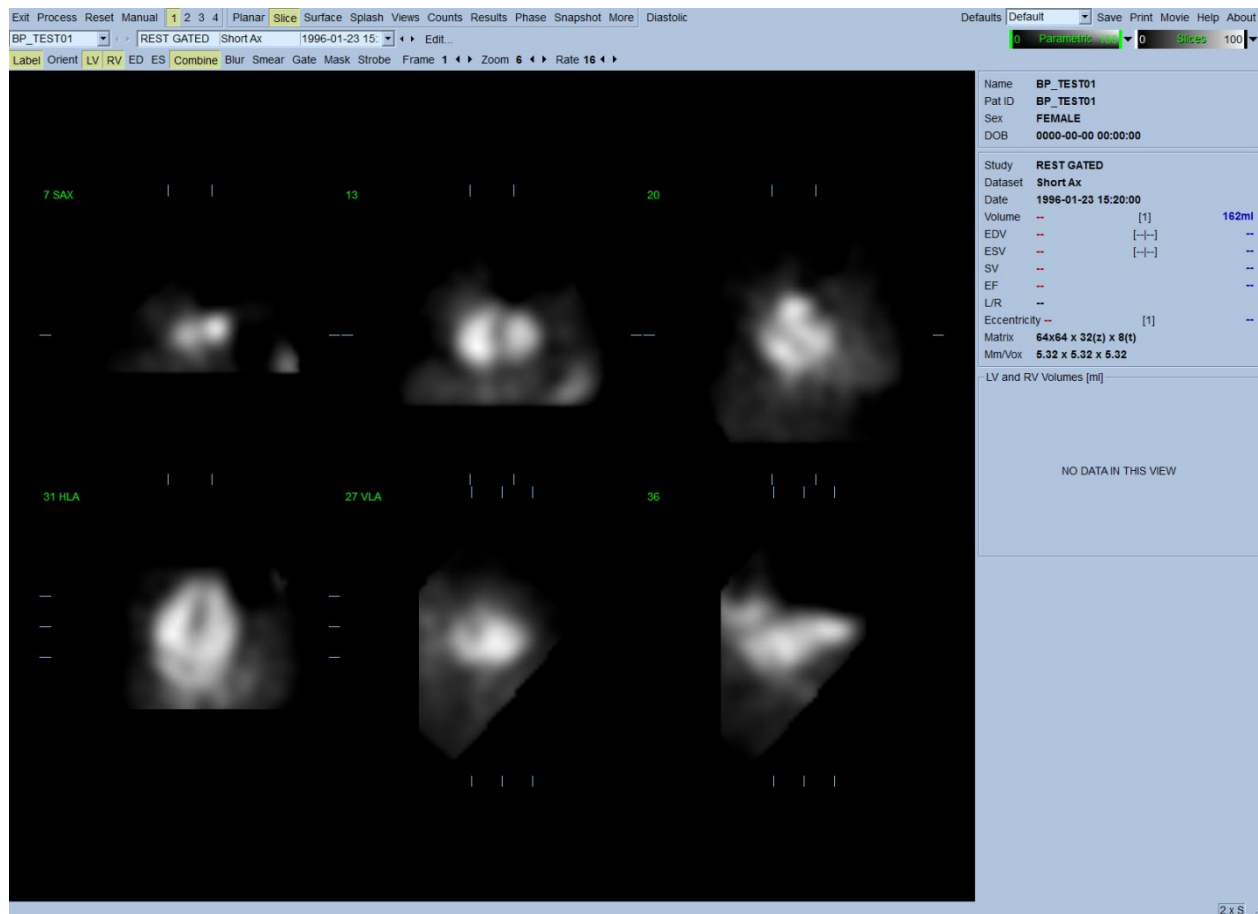

The name of the folder (generally, a patient name) and a description of the dataset are displayed in the horizontal section that also contains the color scales shown below. Left-clicking and dragging (in the **Slices** color scale) the vertical black stripe to the rightmost will "saturate" the scale and make the heart visible in cases where strong extra-cardiac activity exists. The *Parametric* color scale is available only if FFH Phase images are displayed on the **Slice** page.

5.2. Reviewing the Rotation Projection Images

Clicking the **Planar** page indicator will bring up the Planar page shown below. The Planar page consists of four display areas; the raw Counts projection area, the FFH Amplitude area, the FFH Phase area, and the Phase Histogram area (FFH = First Fourier Harmonic).

Prior to processing the data, it is always a good idea to view the raw projection data in cine fashion to assess patient motion. Clicking the **Lines** toggle brings up two horizontal lines, that should be manually positioned so that they tightly straddle the heart. Clicking the **Controls** toggle will bring up individual color scale and projection slider adjustment controls for the *Counts*, *FFH Amplitude* and *FFH Phase* display areas. A continuous loop cine display of the projection dataset(s) can then be started by clicking the **Spin** toggle (continuous rotation). Clicking the **Rock** toggle (in addition to the **Spin** toggle) will display an alternating, back-and-forth cine. The cine speed can be adjusted by clicking the ◄ ► symbols on the right side of the **Rate** label. Any sudden movement of the heart's perceived boundaries towards, or away from the lines should be noted. Major motion may affect the quantitative parameters measured by QBS; if such motion is detected, it would be prudent to repeat the gated acquisition.
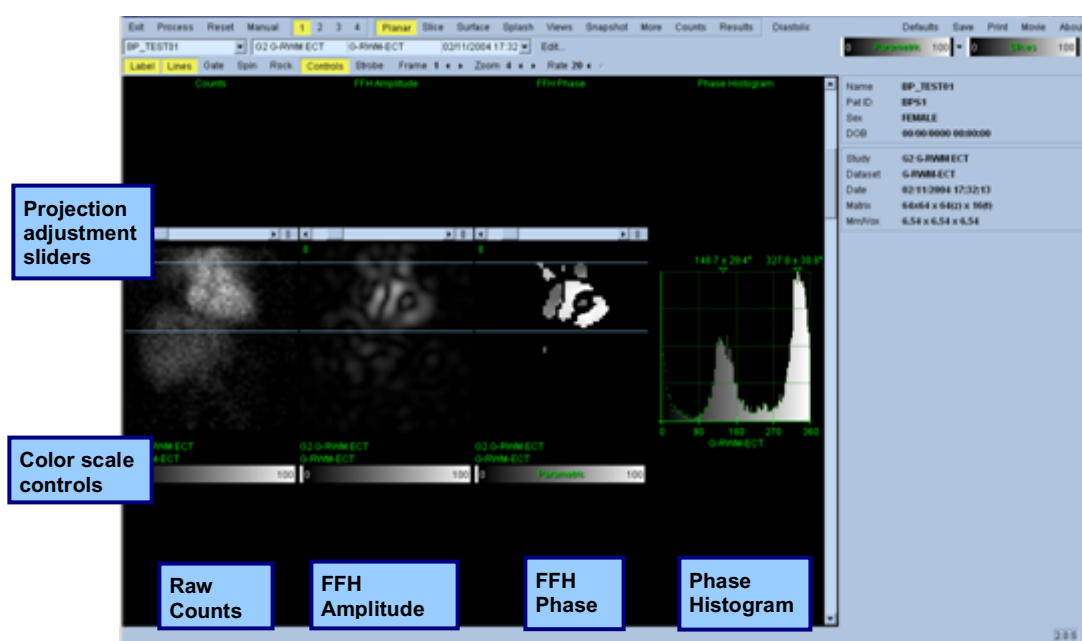

In addition to patient or organ motion, flickering (sudden variations in brightness between adjacent projections) can be assessed by reviewing the projections cine. Flickering is often an indication of gating errors, and can be accompanied by alterations of the time-volume curves shown in the Results page.

5.3.   Processing the Images

Clicking on the **Slice** page indicator will highlight it and advance QBS to the **Slice** page. Clicking **Process** will automatically apply the QBS algorithms to the data, segmenting the LV and RV, calculating the endocardial 3D surfaces, and determining all the global and regional quantitative cardiac parameters. The intersection of the 3D surfaces with the 2D slices planes are displayed as "contours" overlaid onto the six slices (yellow = RV, white = LV), which are now representative of equally spaced (short axis images) or mid-ventricular (long axis images) portions of the *LV* and *RV*. Moreover, all quantitative parameter fields in the right portion of the screen should now be filled

with numeric values shown below. We'll examine and discuss the quantitative measurements in more detail later.
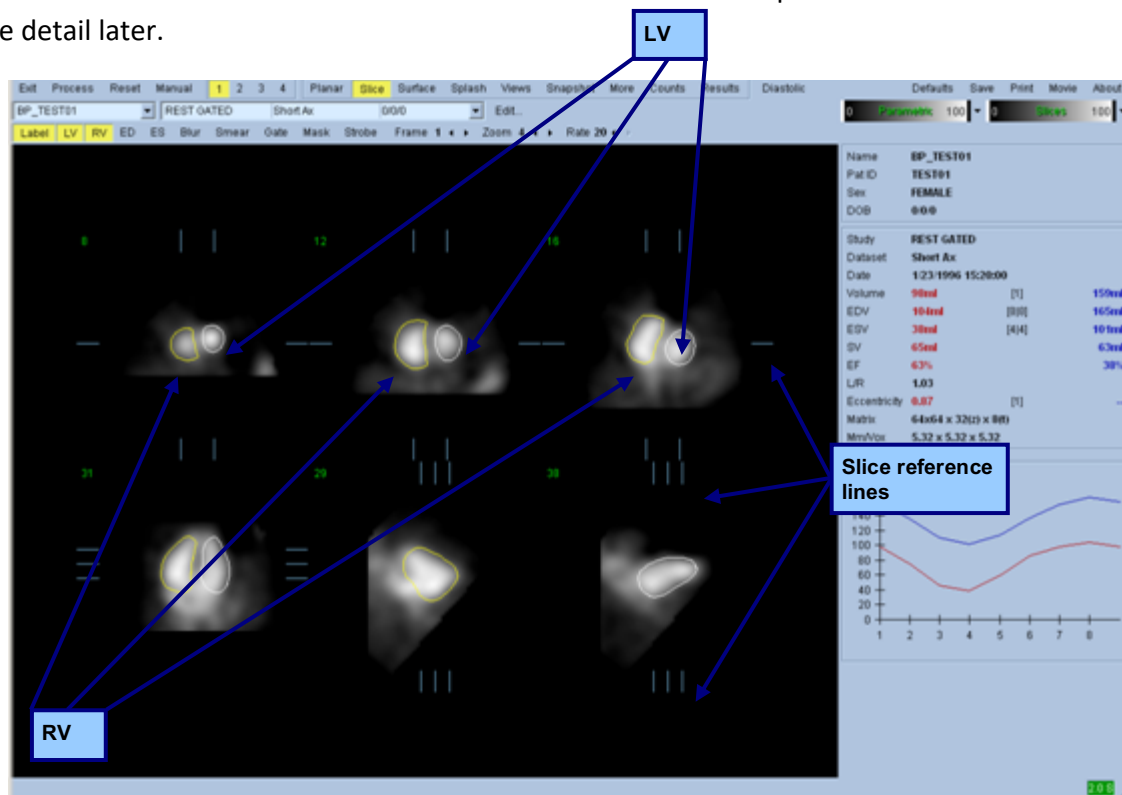
5.4. Checking the QBS Contours

The location of the six slices displayed can be interactively adjusted by moving their corresponding slice reference lines in orthogonal views shown above; however, in most patient studies this will not be necessary.

At this point, a visual check for obvious inaccuracies in the way the contours follow the LV and RV must be performed. This will likely involve toggling the **LV** and **RV** contour toggles on and off, and setting the images in motion (cine) by left-clicking the **Gate** toggle. Most major inaccuracies are due to the presence of extra-cardiac activity. In particular, one would expect to a) see the contours centered on a structure other than the heart, or b) see the contours "pulled away" from the ventricles to follow closely adjacent activity. These occurrences are infrequent, and should be dealt with using the Manual option discussed in the next section.

Another potential source of error is excessive blurring of the short axis data. If the dataset was over filtered during reconstruction, it is possible that the algorithm will fail to differentiate between the left and right ventricles correctly. The ventricular contours may interpenetrate, or be completely erroneous.

Note: Since the algorithm requires a phase difference between the ventricles and atria to correctly identify these structures, at this time it is not possible to obtain measurements from a static phantom, even if a gated acquisition was performed.

5.5.   Modifying the Contours (Manual Page)

Clicking the **Manual** toggle will bring up a modified version of the **Slice** page, with 4 slices for the *ED* interval and 4 slices for the *ES* interval, as well as 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 and circles placed at various points on the masking graphics.
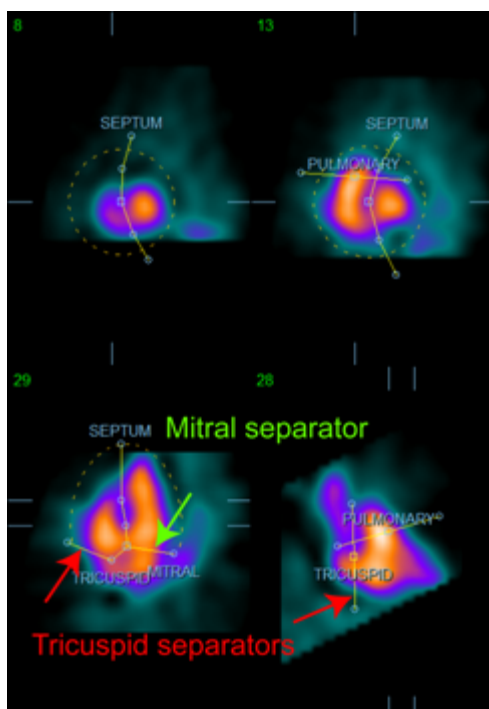
For each interval, two short-axis slices (mid-ventricular and apical), one mid-ventricular long axis and one mid-RV vertical long axis slice. Because of constraints imposed between the various points that constitute the mask, selection of the slices may be limited (as compared to slice selection in other pages). The masking graphics are designed to achieve:
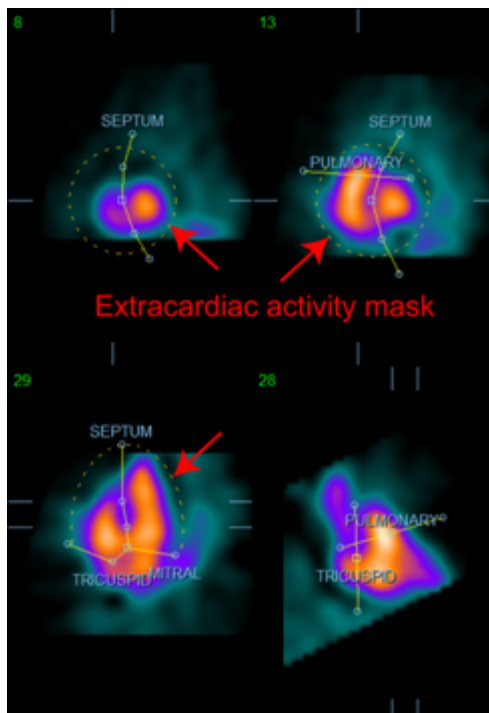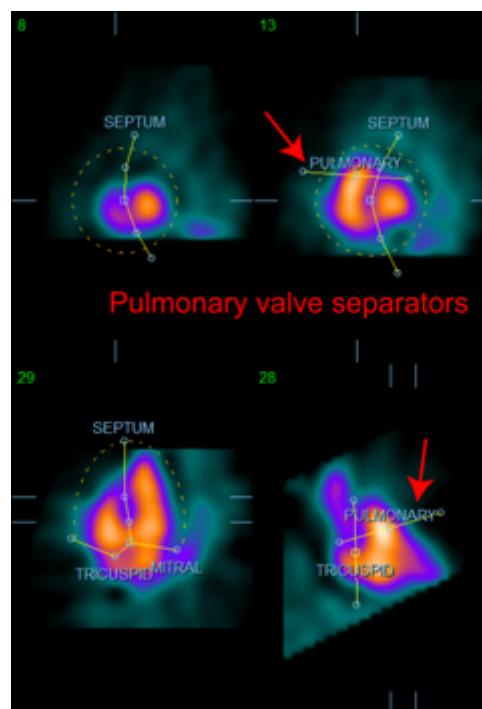

Masking of extra-cardiac activity
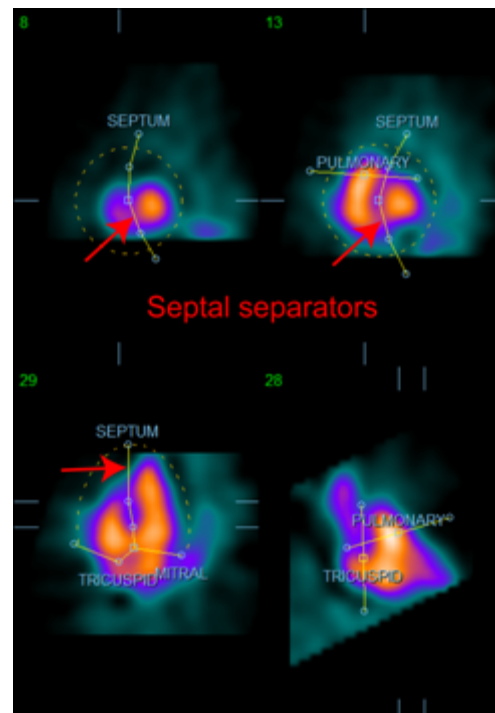
Separating between the LV and RV

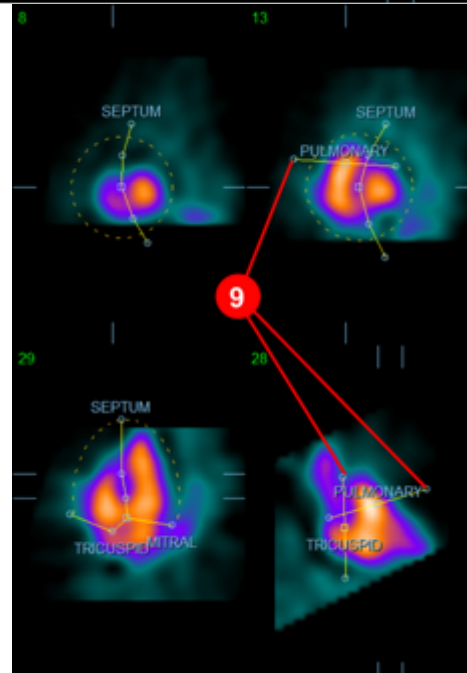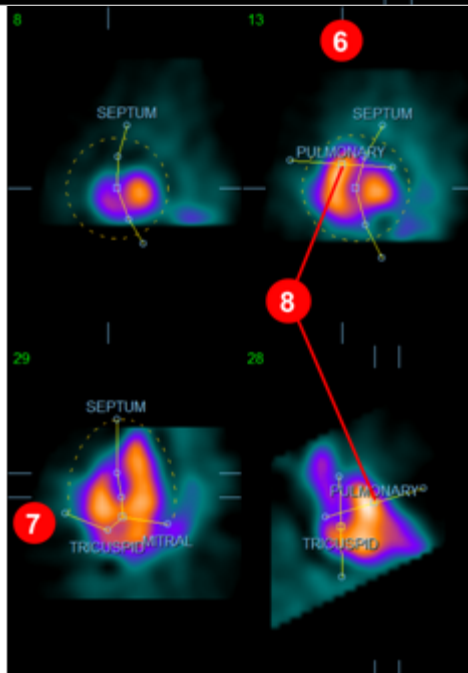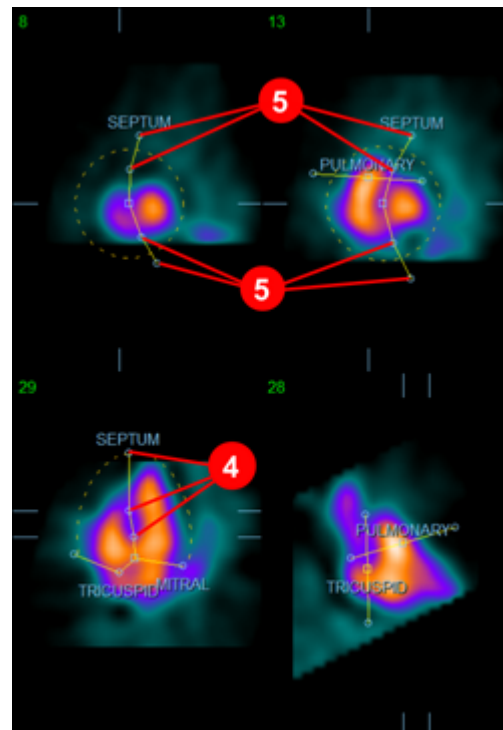**Separation of the ventricles from the atria (Tricuspid and mitral separators)**
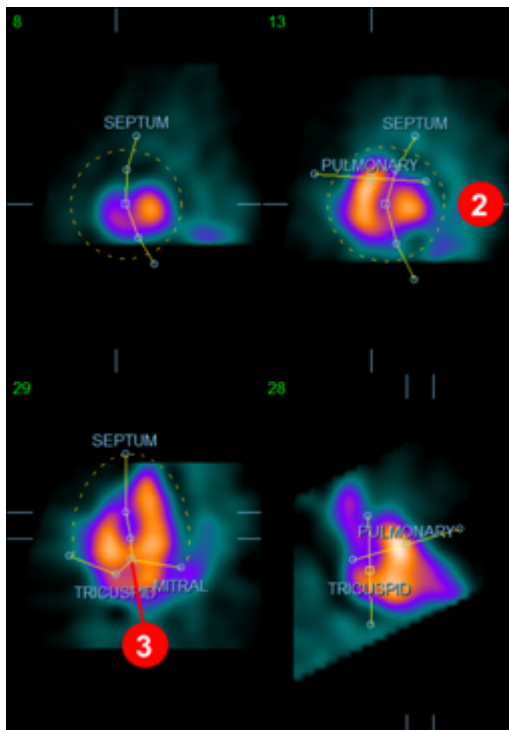

Separation of the RV from the pulmonary trunk (Pulmonary valve separator)

In general, the following sequence should be followed for optimal placement of the mask:

1. Start with the *ED* interval (left half of the page);
2. adjust the HLA guide in the basal SAX slice to select a mid-ventricular HLA slice;
3. move the whole mask in the HLA slice by dragging the square handle;
4. adjust the circular handles for the septal and mitral separators in the HLA slice (this process may cause the selection of different SAX slices, just place the handles and slices in a way that allows for a good delineation of the septum in SAX and HLA views);
5. adjust the circular handles for the septal separators in the SAX slices
6. adjust the VLA guide in the basal SAX slice to select a mid-RV VLA slice, this will automatically adjust the first tricuspid handle in the HLA view;
7. adjust the second tricuspid handle in the HLA view to correctly separate the RV from the RA;
8. if **RV Truncation** is on, move the square pulmonary valve handle to the appropriate location;
9. Adjust the orientation of the pulmonary and tricuspid valves in the SAX and VLA slices using the circular handles.

Using a non-linear color lookup table may help in determining the best location for the various mask separators (in the example images, the "Cool" colormap is used). The following gives a graphical depiction of the mask placement steps.

Having correctly positioned the ED mask, use the **Copy to ES >>** button to copy the mask's position to the ES interval. The correct ES interval should be selected manually by examining the image and visually determining in which frame the ventricles seem fully contracted. The program will automatically attempt to select the appropriate interval, but manual adjustment may be required. Is so desired, the mask can also be adjusted in the ES interval and copied back to the ED interval using the **<< Copy to ED** button (note that the ES mask will completely replace the ED mask).

When the mask has been copied and the interval adjusted, repeat the above procedure for the ES interval.

Shown below are the viewports from the manual page after positioning the ED and ES masks.
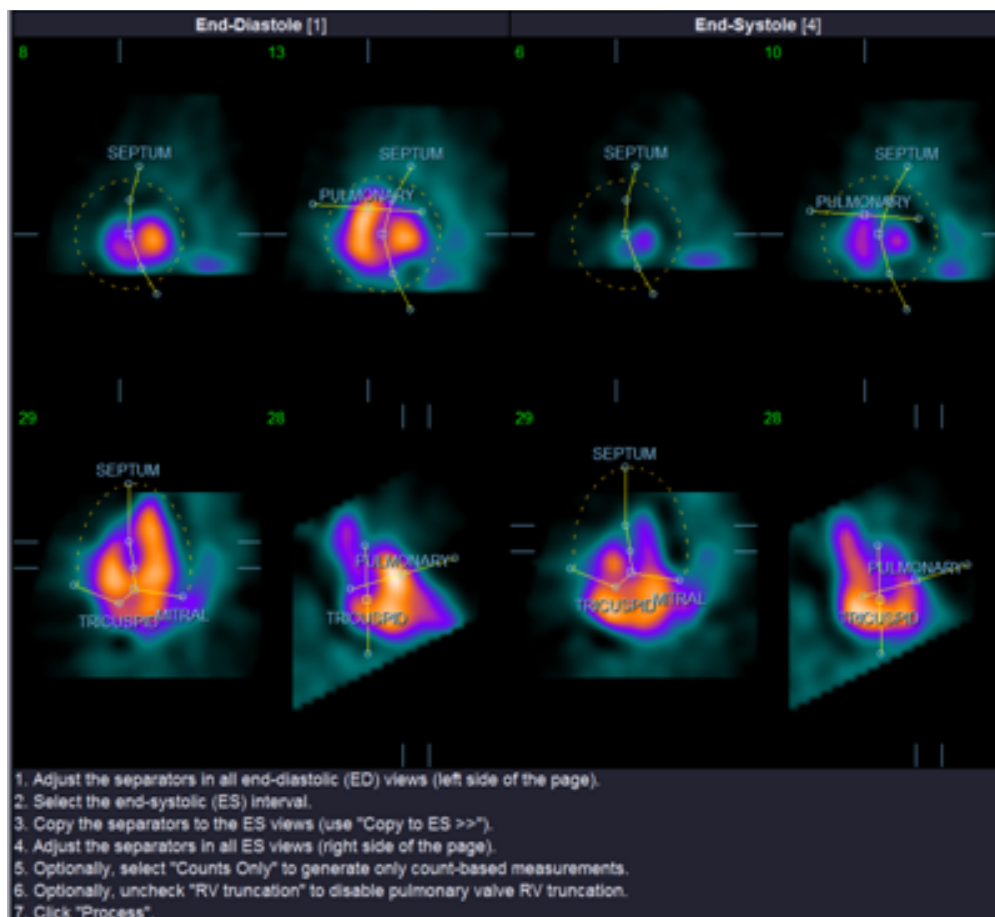
Once the mask has been correctly positioned, click **Process** to process the data using the mask, or select **Counts Only** then click **Process** to perform count-based calculations only. Note that if **Counts Only** is selected, no surfaces will be generated and limited information only will be available in the **Counts** page.

If the **RV Truncation** is off, no RV truncation will be performed. At any time, use the **Reset** button to reset the mask to its original (non dataset-specific) configuration. This will void all user changes.

The remaining page controls (**LV, RV, ED, ES, Blur, Smear, Gate, Mask, Frame, Zoom***,* and **Rate**) perform the same function as they do in the **Slice** page.

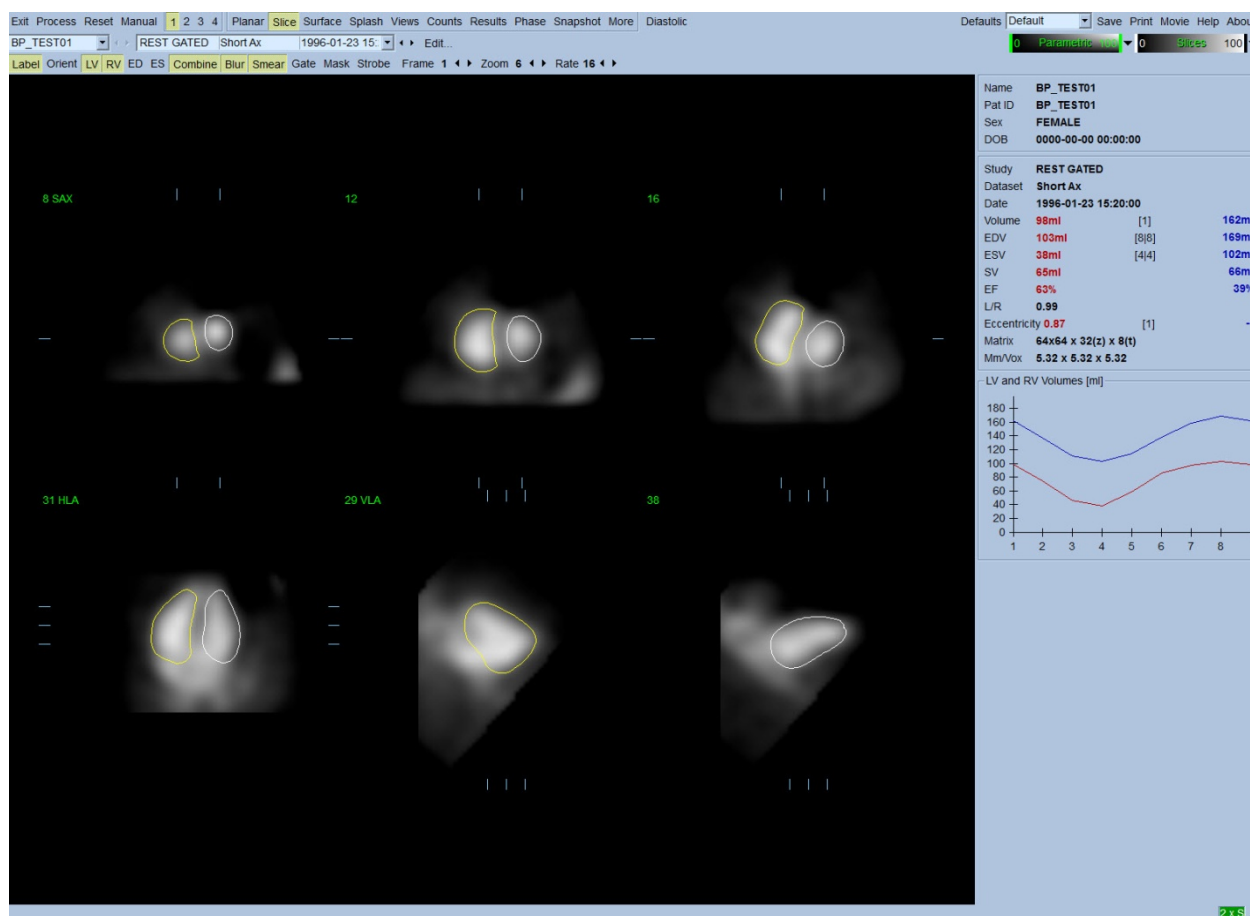## 5.6.   Reviewing Gated SPECT Blood Pool Images in the Slice Page

A first visual assessment of LV and RV function can be performed by left-clicking the **Gate** toggle to display a cine of the six slices while clicking the **LV** and **RV** toggles on and off. The cine speed can be adjusted by clicking the ◄► symbols on the right side of the **Rate** label. Moreover, a temporal and

spatial smoothing filter can be applied to the images by 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. Shown below is the **Slice** page set for review of gated images.

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

At Cedars-Sinai Medical Center, a gray or thermal scale is typically used to visually assess wall motion.
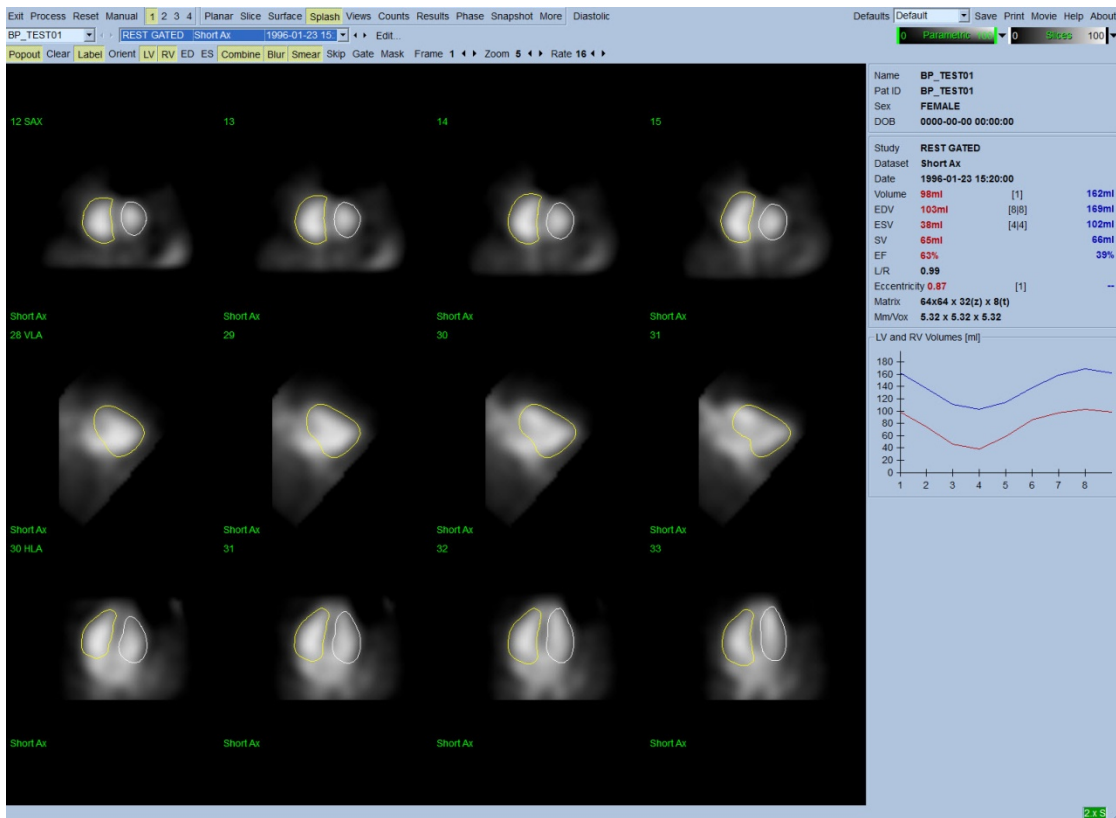

5.7.   Reviewing Gated SPECT Blood Pool Images in the Splash Page

Clicking on the **Splash** page indicator will bring up the **Splash** page shown below, with all the available short images, which can be then gated simultaneously by left-clicking the **Gate** toggle. At times, a user may want to select images for closer inspection. This is accomplished by using the "popout" feature. This is performed 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 shown on the bottom.
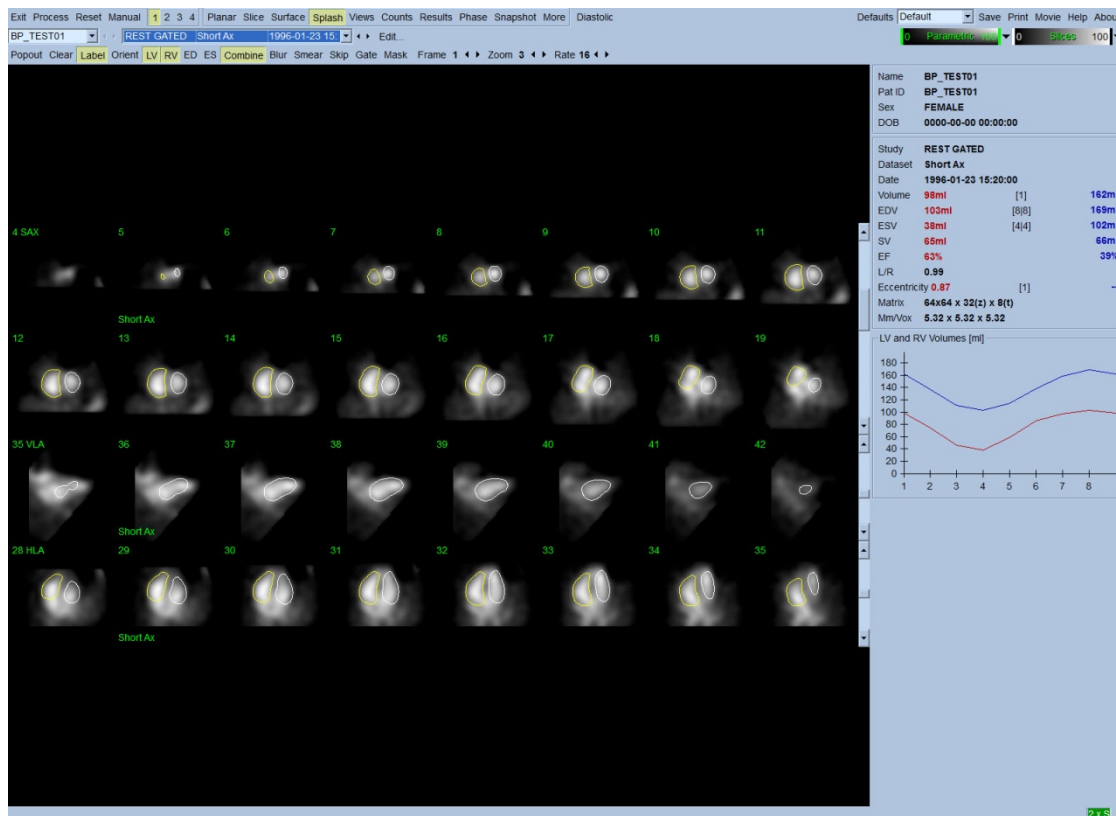
Splash page after Popout enabled

## 5.8.   Reviewing Gated SPECT Blood Pool Images in the Surface Page

Clicking on the **Surface** page indicator will bring up the **Surface** page shown below; a parametric representation of the ventricles, consisting of green wireframe surfaces (ventricular ED endocardium) and shaded surfaces (ventricular endocardium). The **Gate** toggle allows the user to follow the 3D wall motion throughout the cardiac cycle, while clicking and dragging on the image will interactively and in real time position it to the observer's liking.
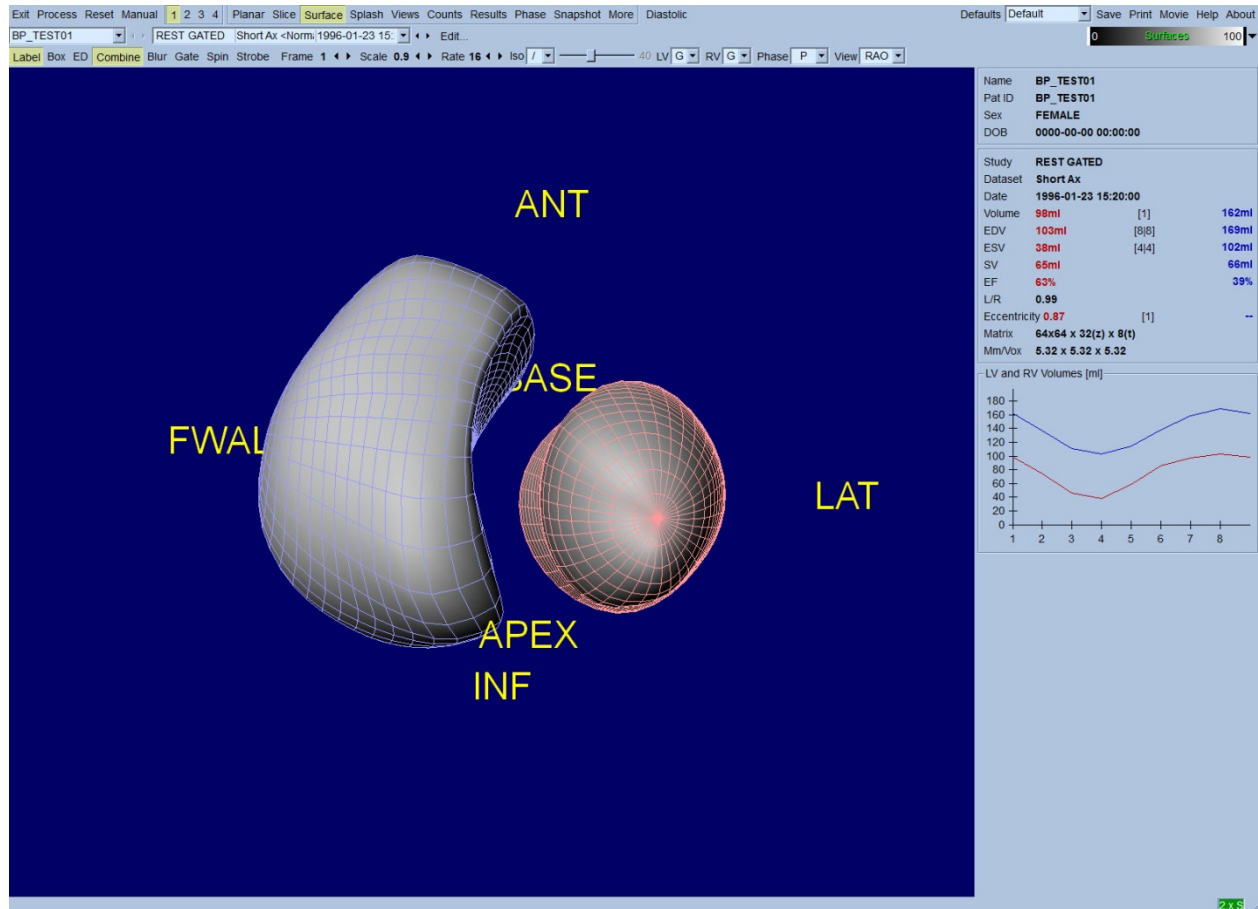
It is also possible to display an isosurface extracted from the counts data. This surface can potentially be used to visually assess wall motion as well, though no isosurface (at any level) gives the location of the endocardium. The user can then superimpose the calculated surfaces onto the isosurface display. The best way to do this is to display the LV and RV surfaces as wireframes (red and blue, respectively) along with the shaded isosurface. To minimize noise effects in the isosurface extraction, it is recommended to toggle on temporal smoothing by clicking the **Blur** toggle. Display characteristics can be set separately for the LV and RV using the appropriate option menus.
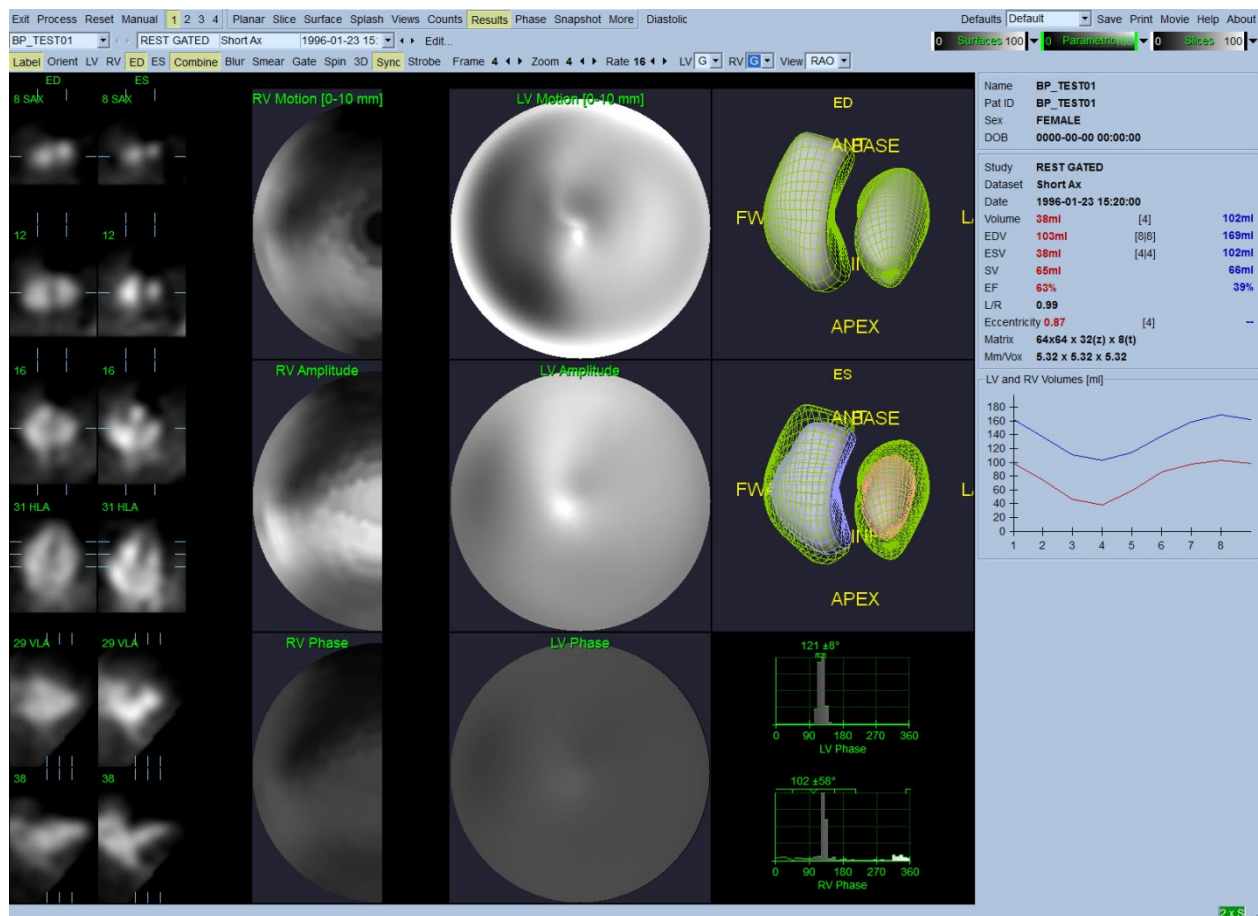
5.9. Reviewing Gated SPECT Blood Pool Images in the Views Page

Clicking on the **Views** page indicator will bring up the **Views** page with six 3D viewports shown below, very similar to that in the **Surface** page. In fact, the main purpose of this page is to allow full coverage of the LV and RV, albeit with smaller images compared to the one in the **Surface** page.
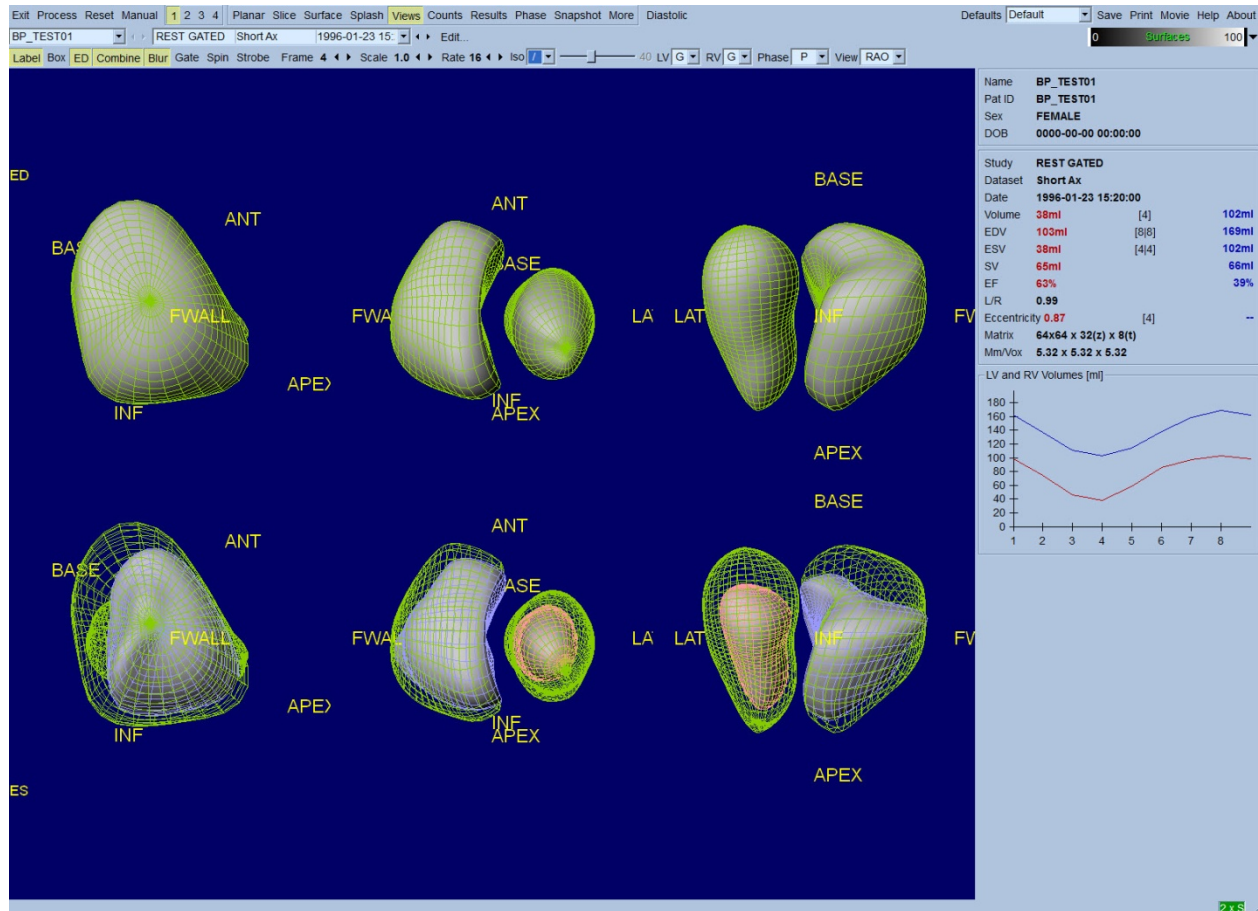
5.10. Putting it All Together: The Results Page

Clicking on the **Results** page indicator will bring up the **Results** page shown below, which aims at presenting, in synthetic format, all information related to the gated SPECT blood pool study in this patient. If a screen capture is taken of this page with the LV and RV contour toggles off, it would represent a good image to send the referring physician.

Results page

5.10.1.　　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, 7 or 8 of an 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 gating or processing was unsuccessful and the study needs to be repeated. An example of a correct curve is shown above.

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.

5.10.2.　　Assessing the Polar Maps

QBS provides two wall motion polar maps, one each for the LV and RV.

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. The parametric surfaces displayed on the Results page are not normalized to this 10 mm limit but to the maximum wall motion value

instead. The FFH Amplitude polar maps and surfaces are not normalized in any way. The FFH Phase polar maps and surfaces are displayed in such a manner than angles between 0 and 360° span the color stripe (negative angles wrap around to the 0-360 range, i.e., -20° is displayed as 340°). Note that paradoxical motion would appear to have a non-zero amplitude and a phase value opposed to normal areas (i.e., the color of the phase will correspond to a different portion of the parametric color stripe).

Note: 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).

5.10.3. Diastolic Function

Clicking the **Diastolic** toggle replaces the LV and RV volumes curves with LV and RV volume and filling curves as well as computed diastolic parameters. The user may have to scroll down the Info box or maximize the QBS window to see all the computed parameters.
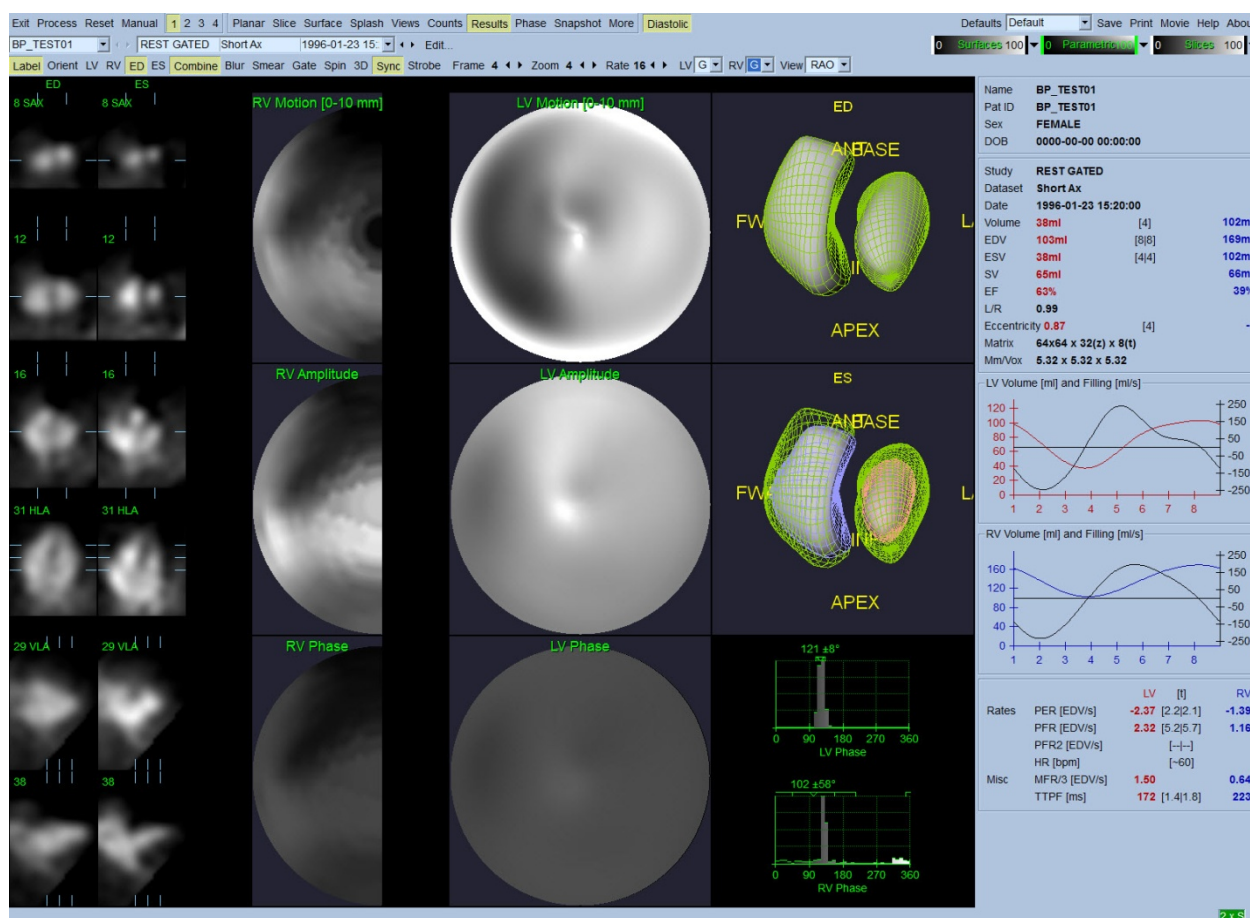

Diastolic results

5.11. Phase Analysis

With the optional "PlusPack" component, QBS offers a phase analysis page with global and regional histograms and parametrically-mapped surfaces. Clicking the **Phase** page button brings up the
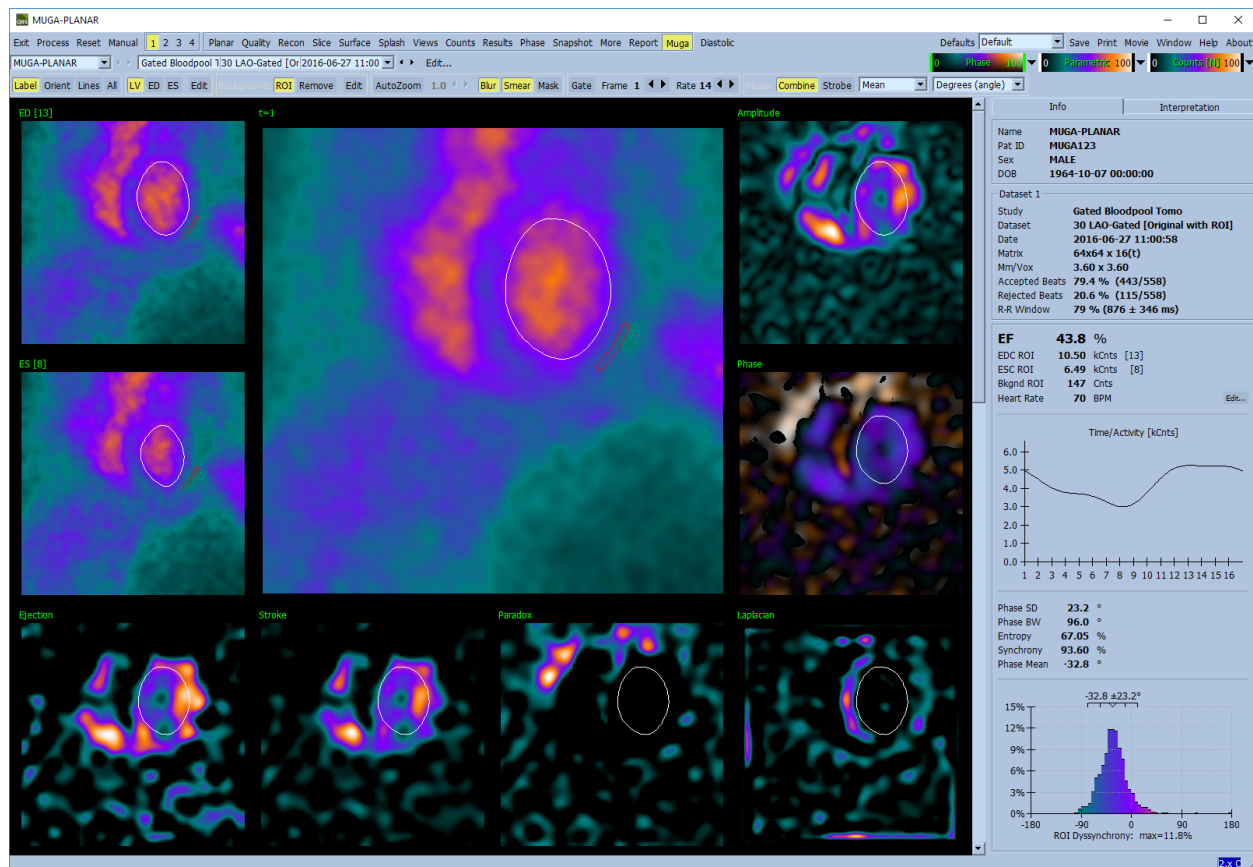
phase analysis page. Detailed statistics and timing differences between regions can be found in the info box (right side of the application). The user may have to scroll down the Info box or maximize the QBS window to see all the computed parameters.
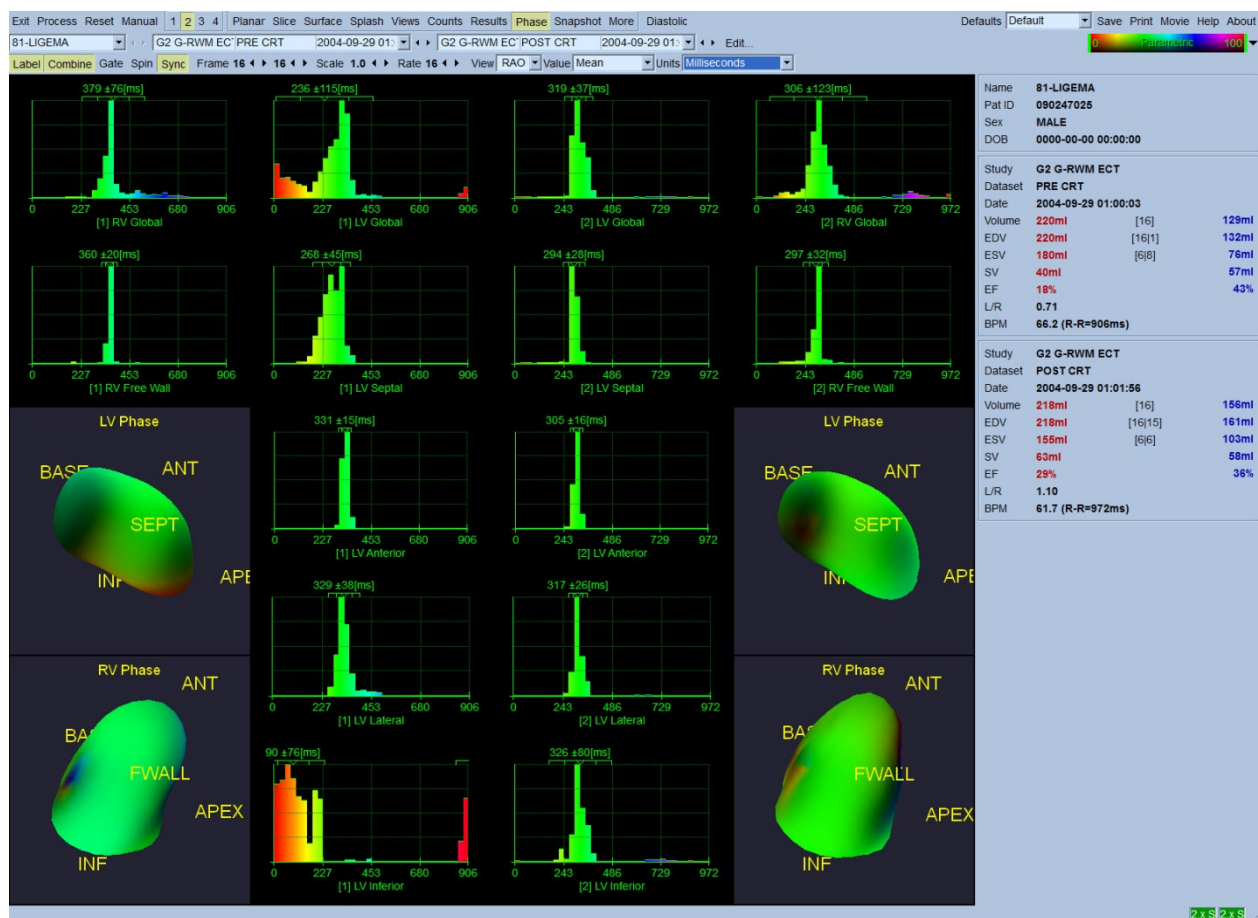
5.12. Muga page

The muga (multi-gated acquisition) page is used for planar gated bloodpool datasets that contain 8 or 16 frames. It is used for both processing and reviewing quantitative results from muga scans. Additional details for the Muga page are described in the QBS reference guide.


5.12.1.   Pixel Size

QBS volume measurements can be hampered by incorrect listing of the pixel size in the image header (this is usually not a problem with the ejection fractions, which are derived from a ratio of volumes). 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.

5.13. Saving your Results

With completion of the processing and reviewing steps outlined above, the user has the option of saving the results to a results file. From the main tool bar click **Save** to display the *Save Results* dialog window as shown below.
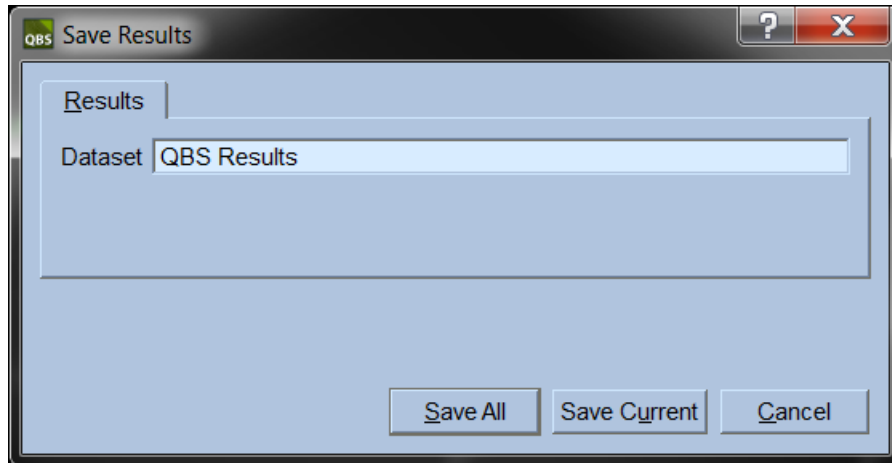
There are two tab choices for saving, **Results** and **PowerPoint**. Selecting the **Results** tab (default) allows saving of processed results as a dataset within the patient study. The user gives the results dataset a name that will appear in the patient study dataset list upon exiting QBS. In some cases, there may be an additional option to select the format of the results file. This is to ensure some compatibility with older versions of the software. Note that all calculation results from the most recent version may not be available in older versions of the software.

Selecting the **PowerPoint** tab allows saving of results and application configuration information in a format that allows for fast and easy launching of case studies directly from a PowerPoint presentation.

The following actions are supported:

Action	Purpose
Save All	Saves results for all selected studies
Save Current	Saves results for the currently displayed study.
Cancel	Exits the dialog without saving results. The user may also exit the dialog by clicking the "X" in the upper right-hand corner of the dialog window.

6. AutoRecon Application (Automated Reconstruction)

AutoRecon is an optional application for the automatic and manual reconstruction, reorientation and motion correction of Cardiac, Brain, other (liver, bone, etc) SPECT and gated SPECT datasets. The amount of automation and processing options provided by AutoRecon depends upon the type of dataset selected. AutoRecon applies validated rules to reconstructing and reorienting projection images, and reduces the number of decisions required when processing studies.

6.1. Launching AutoRecon

Launching AutoRecon in its standard configuration will bring up the Reconstruct page with the selected dataset(s) loaded as shown in the figure below.
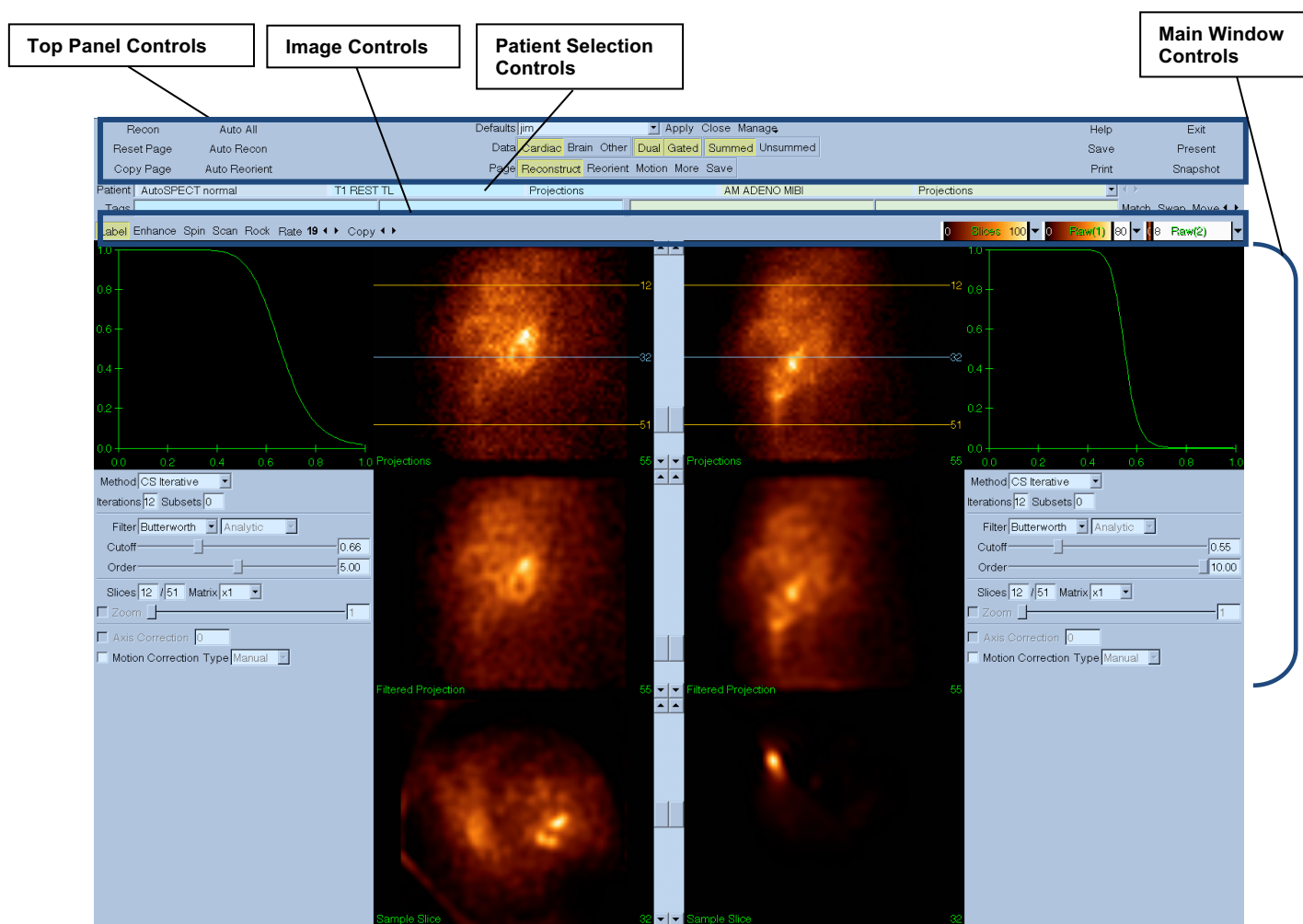
6.1.1. Top Panel Controls

The AutoRecon top panel controls allow you to perform application functions such as selecting defaults files, saving files, or formatting images. You can access most of these controls regardless of

the currently displayed AutoRecon window. A brief description of some of the buttons contained in this panel is shown below.

- **Recon** - Clicking it will manually reconstruct the currently displayed dataset(s). To manually process a dataset, define the reconstruction limits, verify and adjust the main window controls as desired and then click the **Recon** button. AutoRecon does not automatically advance to the Reorient window when using the **Recon** button. If Motion Correction type is set to **Auto**, the Motion window will be displayed after reconstruction of the dataset(s) has commenced.
- **Reset Page** - Clicking it will restore the processed dataset(s) and viewport settings to their initial values. It also removes any processed dataset(s) that have not been saved.
- **Copy Page** - Clicking it will copy the processing settings from one set of viewports to all other objects loaded in memory.
- **Auto All** - **Auto All** is only available for cardiac dataset(s). Using this option will automatically determine the reconstruction limits, reconstruct and reorient cardiac dataset(s). **Auto All** generates the transverse slices, proceeds automatically to the Reconstruct window, and automatically reorients the ventricular volume. If Motion Correction type is set to **Auto**, the Motion window will be displayed after reconstruction has commenced using the motion corrected dataset(s).
- **Auto Recon** - This option automatically determines the reconstruction limits and reconstructs the cardiac dataset(s). **Auto Recon** automatically generates the transverse slices, but does not proceed to the Reorient window. If Motion Correction type is set to **Auto**, the Motion window will be displayed after reconstruction has commenced using the motion corrected dataset(s).
- **Auto Reorient** - Clicking it will automatically reorient cardiac dataset(s). If you have not reconstructed the dataset(s), **Auto Reorient** will reconstruct and then reorient the datasets. If Motion Correction type is set to **Auto**, the Motion window will be displayed after reconstruction has commenced using the motion corrected dataset(s).
- **Defaults** - The Defaults field displays the name of the currently selected default settings.

6.2. Workflow

Typical processing sequence for Cardiac datasets in AutoRecon might be as follows:

1) Load desired dataset(s) from the patient browser and click **AutoRecon** button.
2) From the Reconstruct Page, click **Auto All** to automatically reconstruct and reorient the unprocessed SPECT or gated SPECT cardiac datasets, **Auto Recon** to automatically generate the cardiac SPECT or gated SPECT transverse dataset, **Auto Reorient** to automatically reorient the cardiac SPECT or gated SPECT transverse datasets.
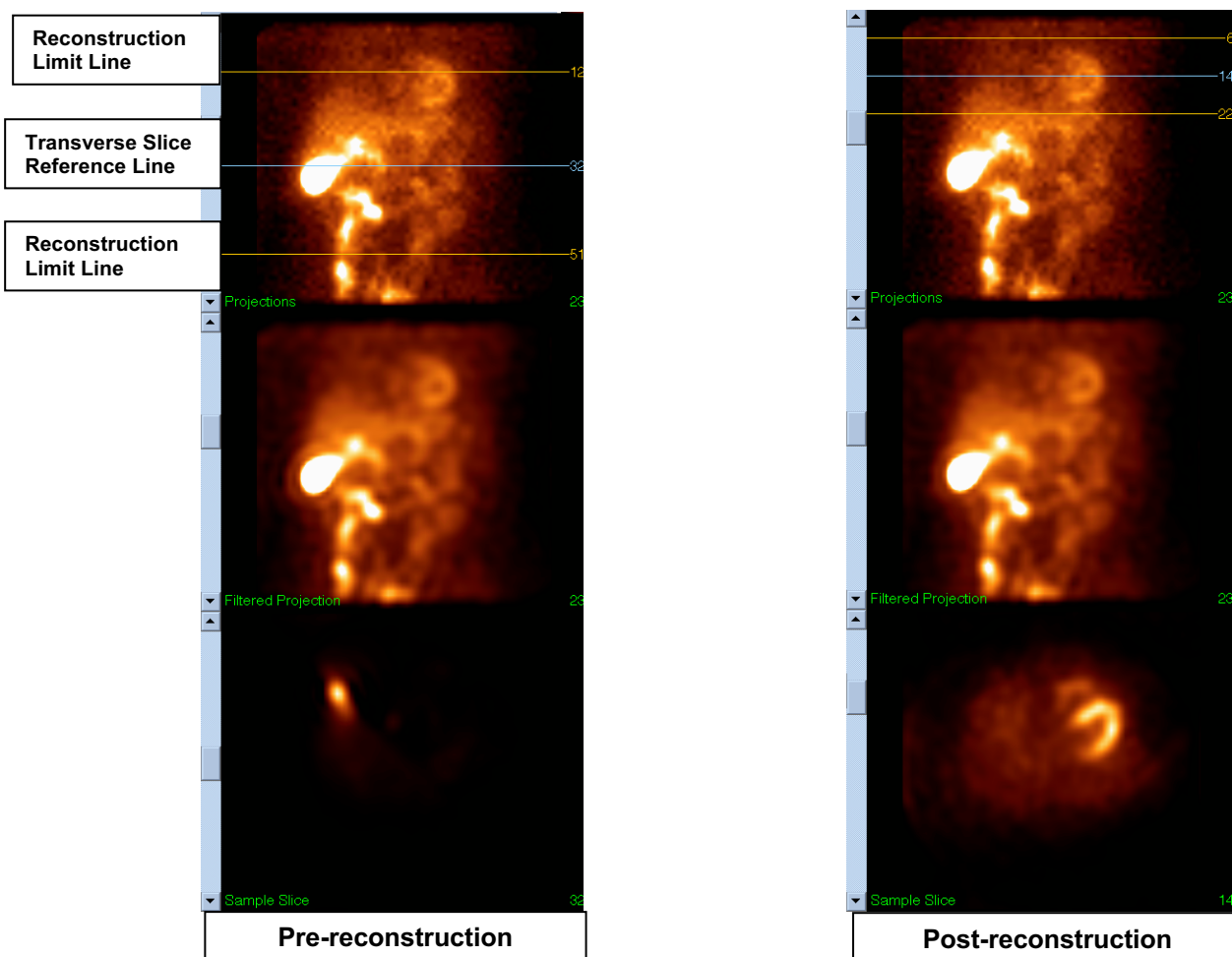
Note: If you have not reconstructed the transverse dataset, **Auto Reorient** will automatically reconstruct the dataset prior to reorienting the dataset. AutoRecon will automatically proceed to the Reorient window if **Auto All** or **Auto Reorient** options were selected.

3) Evaluate the images to ensure no further manipulation is necessary by checking the following pages:

(1)Reconstruct page
a. The reconstruction limits should completely enclose the left ventricle and be symmetrically placed above and below the left ventricle less than 5 pixels from the ventricle.
b. The reconstruction limits should not clip the left ventricle.
Note: If the reconstruction limits are not properly determined, you can manually process the cardiac dataset(s). Press the left mouse button and drag the reconstruction limit lines close to the ventricle, and then left click the **Recon** button. If motion correction type is set to **Auto,** the Motion window is displayed after reconstruction.

Pre-reconstruction

Post-reconstruction

a. The reoriented left ventricle should be visible in the Short Axis, Vertical Long Axis, and Horizontal Long Axis viewports.

b. Verify placement and orientation of the Azimuth line in the Transverse viewport.

c. Verify placement and orientation of the Elevation line in the Sagittal viewport.

Note: If necessary, manually reorient the ventricle. Left click and drag the circle on the Azimuth or Elevation reference line to the center of the ventricle. Left click and drag the ends of the Azimuth or Elevation reference line in the direction that you want to orient the ventricle. Left click and drag the dataset reference lines so that they are close to the ventricle but not clipping the ventricle.


| Pre-reorientation | Post-reorientation |
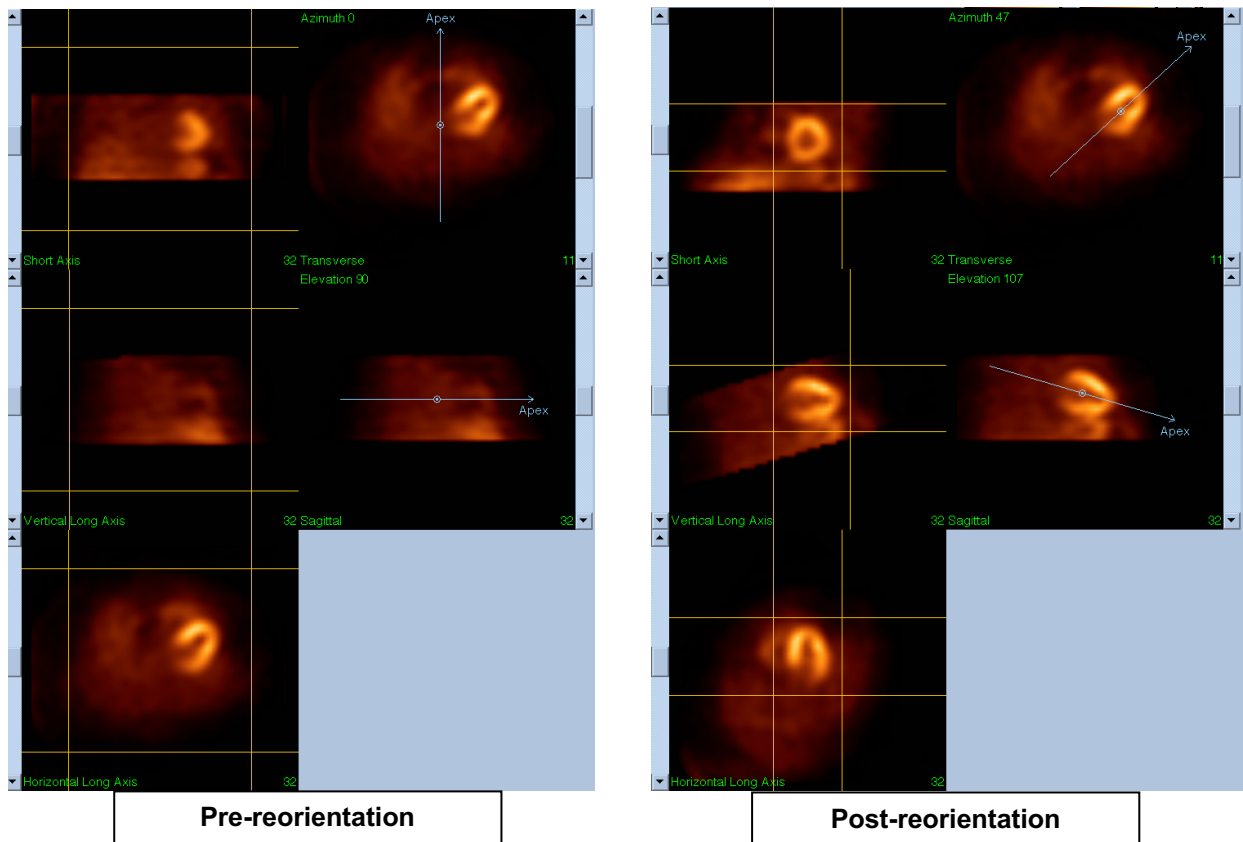
(2) Motion page

The Motion page houses the MoCo (Cedars-Sinai Motion Correction) application, which is used for automatic and manual correction of SPECT acquisition motion artifacts. Datasets will be automatically corrected for motion artifacts if the motion correction type is set to Auto on the Reconstruction page.

a. Verify that any motion artifact has been accurately corrected for.

Note: To manually correct for motion, step through each slice in the reference viewport, move the image in each slice as needed to align the images using the motion correction clickers. Change the motion correction type to **Manual** on the Reconstruct page to reconstruct the study with the manually motion corrected dataset(s).
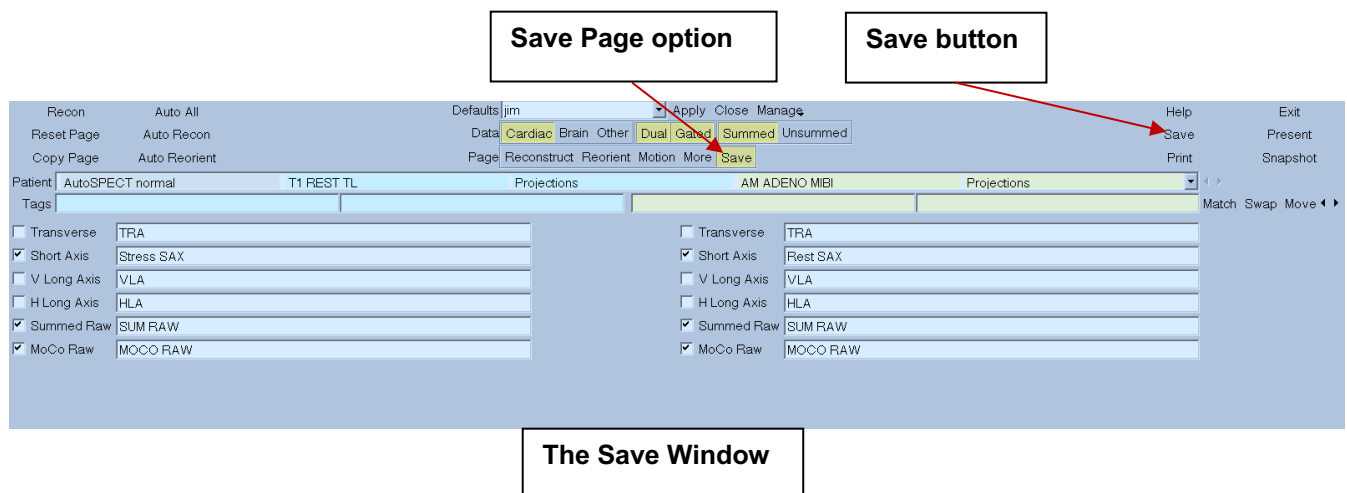

Motion Correction Clickers

Reset

Horizontal Reference Lines

Motion Correction Viewports
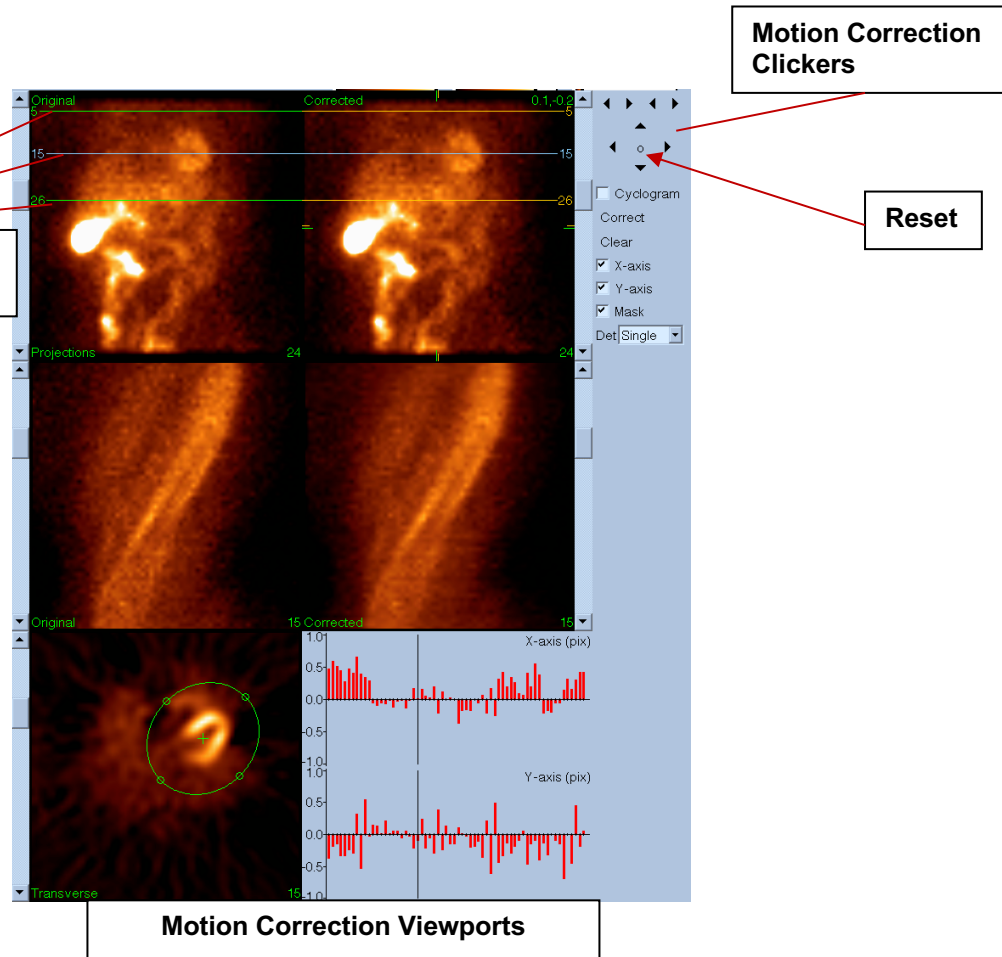
4) **Save Page**

   a. Enable the toggle boxes for each dataset that you want to save and verify that the View IDs are correct.

   b. Left click on the **Save** button to save the datasets.

⚠ CAUTION: Do not confuse the Save Page option with the Save button in the far right side of the Top Panel Controls. The Save button saves all of the datasets without allowing you to change the save parameters.

**Save Page option**

Save button

The Save Window

5)   Left click on the **Exit** button to exit AutoRecon.

7.   MoCo Application (Motion Correction)

MoCo is constructed from the following components:

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

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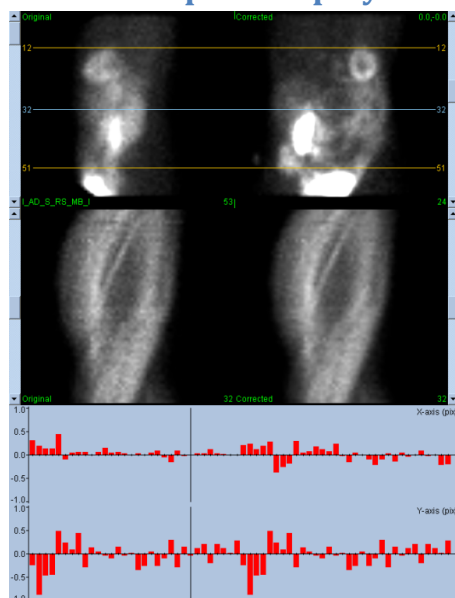
The interface, which does not include externally accessible exit or save functionality as it is intended primarily to be embedded in a containing application, is constructed from the following components:

Original Projection Viewport	Displays a single projection from the uncorrected dataset. The current projection is selected by its corresponding scrollbar; horizontal motion reference lines are moved by dragging.
Corrected Projection Viewport	Displays a single projection from the corrected dataset. The current projection is selected by its corresponding scrollbar; horizontal motion reference lines are moved by dragging. The motion correction x and y axis offsets are also displayed.
Original Sinogram Viewport	Displays a single sinogram from the uncorrected dataset. The current sinogram is selected by dragging the sinogram reference line in the corresponding projection viewport.
Corrected Sinogram Viewport	Displays a single sinogram from the corrected dataset. The current sinogram is selected by dragging the sinogram reference line in the corresponding projection viewport.
X-axis Motion Graph	Displays the current x-axis motion correction offsets.
Y-axis Motion Graph	Displays the current y-axis motion correction offsets.
Motion Cursor	Manually selects the x and y axis motion correction offsets. Also selects the current projections for the Original and Corrected Projection Viewports.

7.2. Color Control

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

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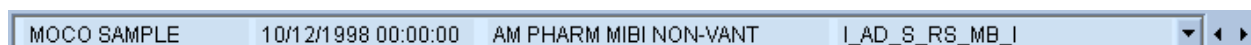
The lower and upper levels of the intensity mapping, represented with the lower and upper level bars, can be set through the color scale viewport, which supports the following interactions:

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

The following features are also provided through the option menu:
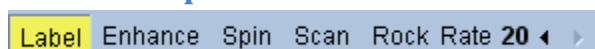
Reset	Resets lower and upper levels.
Invert	Toggles the sense of the lower and upper levels.
Step	Toggles color scale discretization.
Gamma	Toggles display of color scale gamma control.
Expand	Toggles dynamic range expansion of lower and upper levels.
Normalize	Toggles automatic dataset normalization based on segmentation results.

7.3. Dataset Selector

| MOCO SAMPLE | 10/12/1998 00:00:00 | AM PHARM MIBI NON-VANT | I_AD_S_RS_MB_I | ▼ ◄ ► |

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

7.4. Viewport Control

| Label | Enhance | Spin | Scan | Rock | Rate **20** ◄ ► |

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

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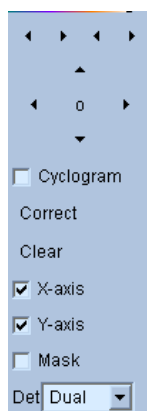
The MoCo Control is used to control automatic and manual motion correction processing and validation. The following controls are available:

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

8.   Troubleshooting

Symptom: I receive a "database connection failed" error message when launching QPS or QGS
Resolution:
1. Verify that ARG Server has been correctly installed.
2. Verify that the ARG Server is reachable over the network (try "ping [argserver]" from the command prompt, where argserver is the IP address of the arg server)

Symptom: I can't push images to CSImport from my camera.
Resolution:
1. Verify that both systems have been configured correctly; consult the connectivity section of CSImport configuration, and the camera vendor's user manual.
2. Verify that the windows firewall has an exception for the Cedars-Sinai DICOM Store
3. Verify that the "pushing" workstation is able to reach the CSImport station (try "ping [csimport_ip]" from the command prompt on the camera's workstation, where csimport_ip is the IP address of the CSImport machine)

Symptom: In QPS I receive "multiple matches" when opening a dataset
Resolution:
1. Verify that the necessary matching fields (e.g. patient sex) are getting populated. If they are not, they will show up in yellow in the dataset editor window. If fields are not correctly populated this could indicate an error with the DICOM data. Contact the camera manufacturer for more information.
2. Note the sex, isotope, and acquisition state for the dataset.
3. Open the Database page, select "List..." verify that there is only 1 active database for sex/isotope/acquisition state combination. If more than one active databases are present, open the database which should not be selected, turn off "allow automatic selection" and save.

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