ECTb4 User Manual

Emory Toolbox 4.0

1 Title

Emory Cardiac Toolbox 4.0

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Disclaimer: *The interpretation provided by Image Decision Support system (IDS) provided in Emory Cardiac Toolbox 4.0 is intended to assist a trained physician to analyze nuclear cardiology images. It was not meant to replace or eliminate the standard visual analysis of the gated SPECT & PET study. The physician should integrate all of the patients' clinical and diagnostic information, i.e. patients' history, stress and/or rest EKG, quality control images, visual interpretation of the gated tomographic images, and quantitative and decision support interpretative results, prior to making his final interpretation. The final responsibility for interpretation of the study lies with the physician.*

2 Introduction

Basic theory of operation

The Emory Cardiac Toolbox is used to process and review tomographic myocardial studies acquired using one or more of the following radioisotope tracers:

SPECT	PET
Tc-99m sestamibi	Rb-82
Tc-99m tetrofosmin	N-13 ammonia
Tl-201	F-18 FDG
I-123 mIBG	

The input data consists of at least one set of short axis myocardial slices. A set of basic parameters is used to identify the left ventricle, and the tomographic slices are sampled to produce maximum count profiles, one from each slice. The set of profiles, representing the radiotracer distribution in the left ventricle, is presented to the user in the form of 2-dimensional polar maps or 3-dimensional images. Optionally, the distribution can be compared to the mean distribution from a normal group of patients.
This quantitative methodology offers analysis of:

- the extent and severity of stress perfusion defects
- the percent of defect that is reversible
- the estimated viability of resting perfusion defects
- myocardial wall motion and estimated wall thickening, if the study was acquired with ECG-gating

Patient Considerations

For optimal diagnosis of coronary artery disease, it is recommended that patients should be off Propranolol for at least 24 to 48 hours prior to exercise studies to allow the greatest likelihood of achieving an adequate stress. Long-acting nitrates should be discontinued for at least four hours and Nitroglycerine at least one hour before initiation of the study. Adjustment of patient medications, however, must be ordered by the referring physician. For most protocols, separate female normal limits are required in order to account for the breast attenuation which alters the normal distribution of the anterior wall. Even with these normal limits, the breast may still be a source of artifact, particularly in large-breasted women. ECToolbox requires that image acquisition be performed using certain specific parameters. Section 22 of this manual provides recommended acquisition and processing parameters for the various clinical protocols which ECToolbox supports.

Warning Messages

As ECToolbox runs, warning messages may be displayed. If you choose to continue by clicking the OK button, be aware that your results may be affected. Warnings will be displayed if, for example, you have rest and stress studies with different patient IDs, or the selected normal file does not match the expected type. Specific warnings will be discussed in various sections of this user manual.

Caution: ECToolbox is more dependent on technical quality control of images than a planar imaging protocol would be. The principal source of false positive studies is the failure to acquire and process studies accurately. It is important to ensure complete quality control, as described in the manuals that accompany your nuclear medicine camera system. Artifacts of acquisition or reconstruction, including errors in quality control, will affect both the visual images and the quantitative analysis. In the event of conflicting, equivocal or confusing results and/or findings, always verify that proper computer processing has been performed.

2.1 What's New

With Emory Toolbox 4.0 we are bringing a large number of brand new features into the fold.

- Re-written from the ground up.
- Dynamic display architecture allowing for real time screen resizing. Flexible display providing the ability to view multiple studies (prone/supine, AC non-AC, etc.), in a single display simultaneously, or toggle studies.
- Smarter processing, allowing the user to see results as soon as they are available while longer running tasks continue to run in the background. Parallel processing, allowing the system to take advantage of multi-core and multi-processor hardware.
- Enhanced slices page to include perfusion slices, functional gated study, quantitative results, polar maps, and AC transmission images in a single display resulting in increased user efficiency and reducing review time.
- Improved processing functionality allows for gated and non-gated parameters to be reviewed on a single screen with real time updates of perfusion and functional quantitative results resulting in reduced processing and interpretation time.
- New Normal DBs: DNM530c (NonAC, AC and Prone), Astonish (NonAC and AC), Standard SPECT Tc-99m Prone and Spectrum Dynamics.
- Ability to show borders on all Param screens (Gated , Ungated).
- Comprehensive, interactive 3D display including perfusion, extent, reversibility, and coronary overlay.
- Automatic interpretation using a decision support system (IDS) to provide an interpretation (2nd opinion) in SmartReport. System provides over 230 rules used to evaluate perfusion, reversibility, viability, function, & clinical findings.
- Integrated, automated reporting, powered by Syntermed IDS and SmartReport.
- Enhanced quality control providing gated QC, count statistics, patient motion, and imaging artifacts.
- Display of indexed functional values (if height and weight are provided).
- Memory - when navigating around the app, it remembers the state of all your controls (e.g. Color Bar, toolbars, etc...).
- Diastolic function.
- Simultaneous Stress/Rest LV Dyssynchrony display.
- 17 segment % uptake.
- Improved automatic base detection.
- AdreView™ support.
- Simple, post-facto reorientation.

2.2 Missing Features

There are some features included in the previous generation of the Emory Toolbox that have either not been ported into v4.0 yet or are being retired completely.

Export
While the overall export functionality has been simplified and improved, some options are no longer available. Specifically, the export of individual "cines" as well as the ability to export screens to AVI and PPM formats.

Active View / Summary Page
The "Active" view box has been replaced with an updated, comprehensive "Slices" display. This screen contains most of the information users would expect to see on the previous version's Summary page as well. A comprehensive, fully user-configurable "Active/Summary" display will be part of a future release.

3 Layout

The application window has been divided into the components described below to help orient the user to the layout and assist in navigating throughout. Each screen has a control "stripe", a thin vertical section on the left side that contains the Navigation Pane, Study Info, Toolbar and QC controls used to navigate and interact with the application. To the right of the control stripe is the Main Display image window, which takes up most of the screen. Above this is the Patient Info control and at the very top is a standard Main Menu.

Main Display
The primary display area for images and quantitative information. The data displayed within this area is commonly referred to as a "screen" and will change as the user navigates throughout the application.

Main Menu
A standard windows menu of options permanently located at the top of the application window.

Patient Info
An area permanently available at the top of the application window which provides the user with information about the patient and study currently being viewed, such as patient name, gender, patient ID, study date, accession number, normal database used for quantitative comparison, etc...

Navigation Pane[1]
A group of buttons located at the top left of the application window used to navigate through the many different "screens" within the application. The buttons are arranged from top to bottom in the order in which you are likely to use them when processing and/or reviewing a study. Each button takes you to a different screen and you can switch from one screen to another at any time.

Study Info[1]
Located just below the Navigation Pane, this is a block of quantitative data, such as ejection fraction (EF) and volumes, made available on screen in real time as processing occurs.

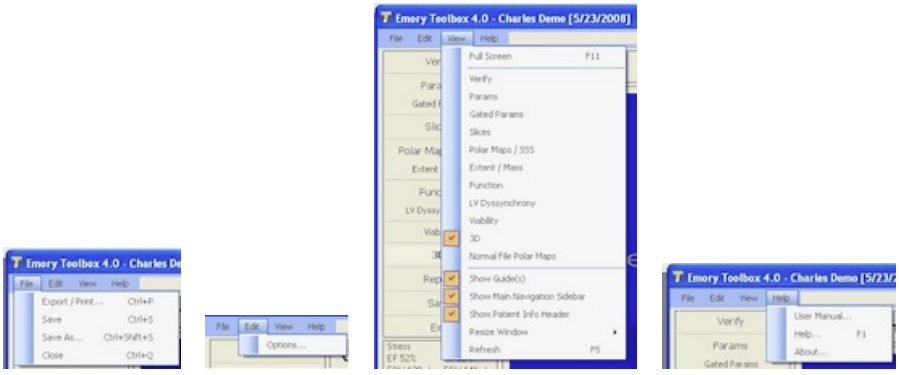
Toolbar[1]
Below the Study Info area is a group of buttons and controls that set various options for the particular screen you are viewing. Each screen has its own set of options.

QC[1]
At the bottom of the left-hand stripe is the Quality Control (QC) button, which is always available.

[1]These items will be hidden from view on the Verify screen if the user has never processed the incoming raw data.

3.1 Main Menu

On the upper left of the application window, there are dropdown menus that are always available in the application, as shown below. The "Edit/Options" menu choice accesses the program configuration options, which are explained in section 3.1.1 of this manual.



3.2 Patient Identification

The figure below shows the stripe of information displayed at the top of every screen in the application.
Note: on the Verify screen, the AC/non-AC buttons are not present.



- The text "(Male) 1Day..." refers to the normal file that was assigned to this study. To change normal files, you can revisit the Verify screen.
- Click the "Ht/Wt" link to enter the patient height and weight. These values will be used on the Function page to calculate ventricular volumes indexed to the patient's Body Surface Area.
- The "non-AC/AC" buttons are used to control whether attenuation corrected or non-attenuation corrected images are shown. This control applies to several screens, including Slices and Polar Maps.

3.3 Navigation Pane

The navigation pane, shown in the figure below, consists of a list of buttons ordered and designed in such a way as to help the user move though the application logically.

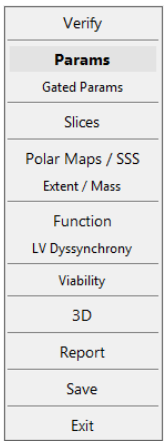


Figure Legend: The Params item appears different because it is the currently selected button.

The functions, which are available at any time, include:

Verify - identify the various images used, as well as normal file and patient gender.

Params - set parameters for quantitative analysis of ungated data: center, radius, apex, base.

Gated Params - set parameters for functional images: center, radius, apex, base for each gate.

Slices - review LV slices in various formats, along with planar images and segmental perfusion scores.

Polar Maps / SSS - review polar map display of perfusion. If you have selected a PET study with rubidium and FDG images, this button will be replaced with a **Match/Mismatch** button.

Extent / Mass - review quantitative perfusion defect extent.

Function - review results of functional analysis: volumes, ejection fraction and wall thickening. Cine of beating slices is also available.

Viability - tool for assessing LV viability using the polar maps.

3D - review 3-dimensional display of perfusion, with optional coronary artery overlays.

LV Dyssynchrony - review phase analysis and LV synchrony, derived from functional analysis using SyncTool™.

Report - launches the SmartReport application.

Save - saves the study.

Exit - quit the application.

3.4 Study Info

This block of textual information, shown in figure below, displayed just below the Navigation Pane, is filled in as processing proceeds. You can refer to this area to quickly see calculated values such as left ventricular ejection fraction (EF), without having to display the image window where these are usually shown.

Note: The Study Info area shows the values most recently calculated. For example, if a change in gated parameters occurs, the EF will not be updated until the user navigates away from the Gated Params screen. *If values are changed that require the study to be reprocessed, the reprocessing will automatically be triggered when the user navigates away from the screen.*



Figure Legend: The Study Info area can be collapsed (left) or expanded (right) to show more or less information. To do this, click the "..." button at the bottom of the control.

TID Ratio

The TID Ratio is provided in the Patient Info area. TID is used as an index of possible Transient Ischemic Dilatation, and is calculated by dividing the stress ungated endocardial volume by the rest endocardial volume. Values significantly greater than 1.0 may indicate the presence of TID.

Note: For the ECToolbox application, the accuracy and clinical value of this ratio has only been validated for the Dual-Isotope protocol. You should consult the literature regarding the potential clinical value of this ratio.

QC Indicator Button

The QC (Quality Control) button is available at the bottom of this and every screen in the application. Click this button to display a screen of QC findings that have been automatically performed. The color of this button indicates the outcome of QC analysis, in particular the assessment of ECG-gating (if a gated study is present).

- **green**: no gating error was found.
- **yellow**: a minor gating error was found (usually a drop off in counts in the last frame of the gate).
- **red**: a serious gating error was found, one that could potentially affect the functional results.

You should review the results of automatic Gated Quality Control for any study for which the indicator button is red, since certain types of gating errors may compromise the diagnostic value of functional results.

4 Verify

Each file that was selected when the application was started is listed here. To the left of the File Description column, checkmarks indicate the files that will be used by the application. If parameters such as Acquisition and Image Type are incorrect, you can change them so the application will use the files appropriately. For example, you may see that a stress file is incorrectly listed as rest.

For file descriptions, note that:

- AC means Attenuation Corrected
- MC means Motion Corrected
- Dyn means a dynamic study

Items in any other column can also be changed if necessary. If you click an item under File Description, that file's DICOM header information appears on the bottom half of this screen.

One of a number of normal databases can be selected, and the patient's study will be compared to the selected database to determine areas of decreased perfusion. In the list of normal databases, an asterisk beside a name indicates a database that has been optimized for use with the Syntermed IDS decision support system.

On the upper right of this page, the patient's height and weight can be entered which will be used to calculate the indexed values for ventricular volumes based on Body Surface Area. Also, there are checkboxes for you to select the filtering to be applied when gated cine images are displayed and functional values are calculated.

When settings on this page are complete, click the Proceed button.

4.1 Display

The top half of the Verify screen is shown in the figure belolw.

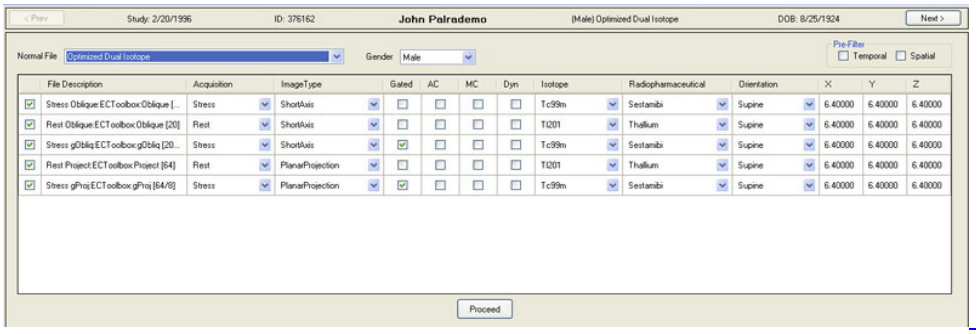


Figure legend: The Verify screen (top half).

As in most screens of the application, a stripe of patient demographic information is displayed on the top row. Just below that are some additional items:

- The normal file automatically selected for this patient. You can change this if necessary.
- The patient gender. If this is "unknown" then you must select either Male or Female.
- The pre-filter, which is filtering that will be applied to gated slice images before they are quantified and displayed.

Caution: It is very important that you verify the accuracy of the parameters such as pixel size and normal file, prior to proceeding with the application.

Clicking any item in the File Description column will display the DICOM image header for that item in the bottom half of this window, as shown in the figure below.

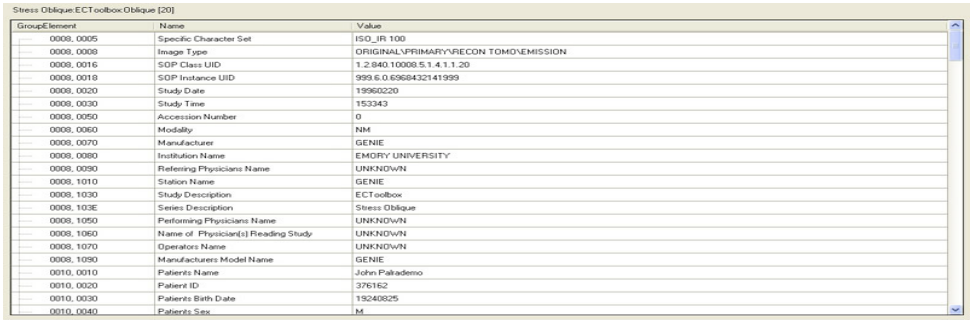


Figure legend: The Verify screen (bottom half).

4.2 Available Normal Databases

There are a number of normal databases currently available for ECToolbox. The SPECT normal files, grouped by radiotracer, are listed below. The thallium database is applicable to both Stress/Redistribution and Stress/Reinjection protocols.
Note: For acquisition and processing details of the protocol corresponding to a particular normal file, refer to section 23 of this manual.

1 Day rest / stress Exercise Std SPECT Tc-99m (sestamibi or tetrofosmin) [1]
1 Day rest / stress Exercise Std SPECT Tc-99m (sestamibi or tetrofosmin) AC (with Attenuation Correction) [1]

1 Day rest/stress Sestamibi [2]
1 Day Sestamibi AC (with Attenuation Correction) [2]
1 Day Sestamibi, adenosine stress
1 Day Sestamibi, adenosine stress, AC
2 Day Sestamibi

Tetrofosmin (stress/rest)
Myoview pharmacological stress

Dual-Isotope (Thallium rest, Sestamibi stress)
Myoview pharmacological stress

Enhanced Thallium

Your system may include databases for use with AdreView in assessing myocardial innervation. Three options exist, for different types of reconstruction. The DSP option assumes an OSEM reconstruction methodology.

AdreView Deconvolution of Septal Penetration (DSP)
AdreView Filtered Back Projection (FBP)
AdreView Ordered Subset Expectation Maximization (OSEM)

There are three databases for the G.E. Healthcare CZT detector cardiac camera, applicable to either sestamibi or tetrofosmin:

1 Day rest / stress Exercise Tc99m DNM 530c [1]
1 Day rest / stress Exercise Tc99m DNM 530c AC (AC from CT) [1]
1 Day rest / stress Exercise Tc99m DNM 530c Prone [1]

There are two databases for use with Philips Astonish, applicable to either sestamibi or tetrofosmin:

1 Day Stress/Rest SPECT Tc-99m Astonish [1]
1 Day Stress/Rest SPECT Tc-99m Astonish AC [1]

There is a group of separately-licensed normal databases for PET. PET perfusion options include:

Rubidium (with line source-based Attenuation Correction)
Rubidium CT AC (with CT-based Attenuation Correction) [2]
Rubidium CT AC 2013 [1]
Ammonia (N-13)

Also part of the PET group are databases for comparing myocardial perfusion and metabolism. These files access the rest portion of the indicated perfusion database, together with metabolism information derived from F-18 FDG PET studies. Selecting one of these options will activate the Match/Mismatch tool instead of the Polar Maps tool in the ECToolbox application.

Rest Rubidium / FDG
Rest Rubidium CTAC / FDG [2]
Rest Ammonia / FDG
Rest Enhanced Thallium / FDG
Low Dose Rest Tetrofosmin / FDG
Low Dose Rest Sestamibi / FDG
Low Dose Rest Sestamibi with AC / FDG
High Dose Rest Tetrofosmin / FDG
High Dose Rest Sestamibi / FDG

Note: There is no separate FDG normal database apart from the combination files listed above. When selecting resting perfusion and F-18 FDG data that are part of a Dual Isotope Simultaneous Acquisition study, be sure to use the Verify screen to select the most appropriate normal file, and make sure the isotope for the FDG study is "F-18".

The list of normal databases also includes the item "None", which allows you to review a study with no normal file comparison, and therefore no blackout or standard deviation polar maps.

[1] This normal database has been optimized for use with IDS.

[2] For legacy data, the use of this normal database will automatically be upgraded to its optimized counterpart.

5 Params

This screen displays the parameters used to define the size and location of the left ventricle. For accurate quantitative analysis of left ventricular perfusion, these parameters must be set appropriately. The application automatically determines these parameters for the stress and rest study (if present):

- center pixel
- radius
- apex slice
- base slice

To re-position any of these, drag its cursor using the mouse. To reset all parameters for stress or rest back to their automatic values, click the adjacent Reset button. In order to compare stress and rest perfusion, parameters for the two studies should be defined in a similar way. For example, the stress and rest apex should be in a similar location relative to the heart, although the actual slice numbers may be different. Note that the lines on the long axis images correspond to the location of the short axis apex and base slices shown.

The application will define borders for the left ventricle based on the parameters chosen and the counts sampled from the images. As an additional check for the appropriateness of the parameters, you can display the borders at any time: click and hold the Show Borders button.

Use the buttons on the upper right to switch between display of attenuation corrected (AC) and non-AC images. Parameters for AC and non-AC are separate and independent.

Post-Facto Reorientation is available via the PF Reorient button on the toolbar, and allows the user to adjust the angle of the short axis images from both the HLA and VLA planes. This feature is designed to allow the user to make changes in the SA angle, within ECTb4, without having to re-visit the acquisition computer and subsequently re-send corrected data back to ECTb4.

Caution: Incorrect parameters, whether selected automatically or manually, will lead to erroneous quantitative results.

5.1 Changing Parameters

The Params screen is shown in the figure below. The left half of the screen relates to the stress study, and the right half to the rest study. The application will automatically choose the ventricular center, radius, apex and base. You should review all these parameters and change them if they are clearly wrong. An "exploded" view of the stress half of the screen is shown below, with explanations of the various parts.

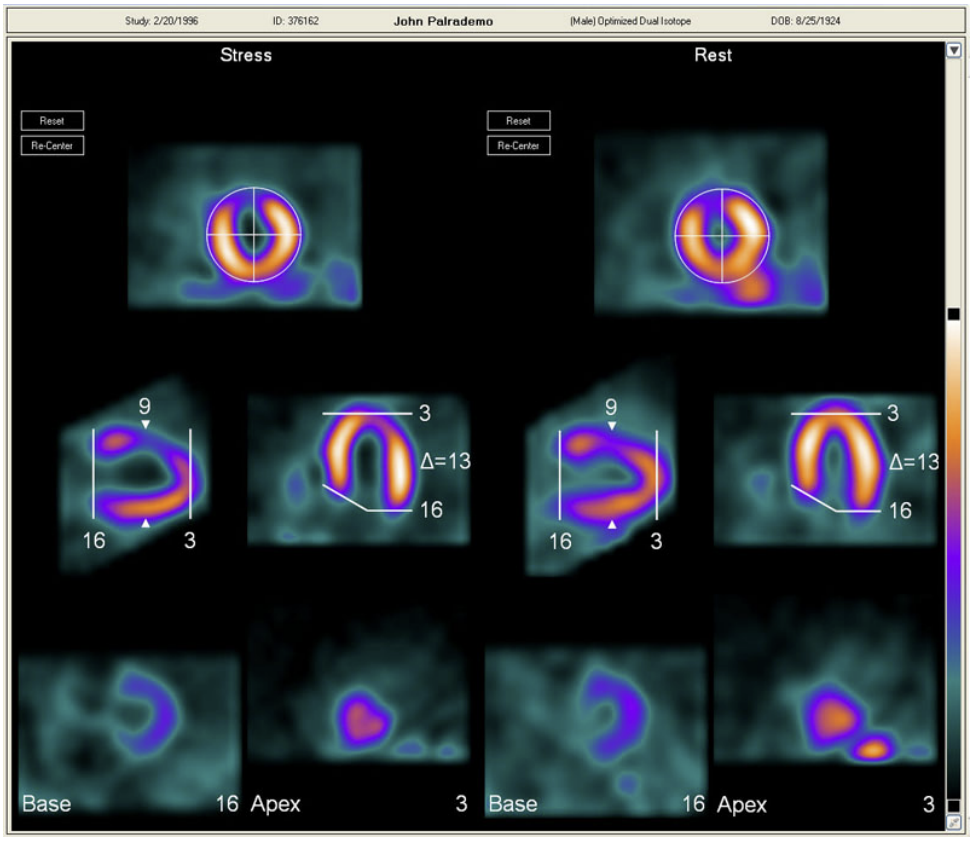
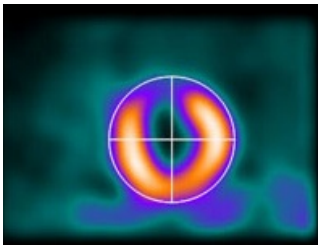
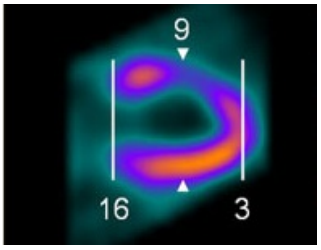


Figure legend: Images and user controls for setting quantitative parameters.

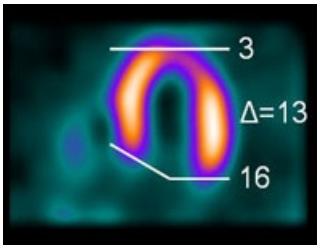
These are the parts of the params screen: the images you can interact with to ensure the parameters for quantitative analysis are optimized.



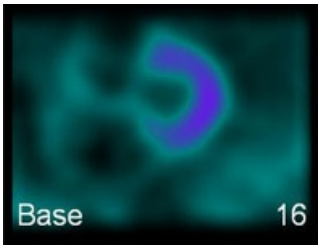
The reference short axis for center and circular radius. To change the center, drag the large crosshair by its center. The circle will also move. To change just the radius, drag the circle by its perimeter.



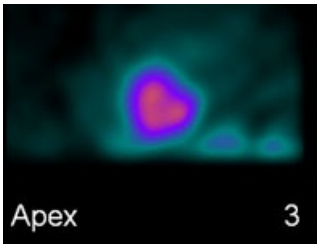
Drag the vertical limit lines to change apex or base. Drag the arrowhead to select a new reference short axis on which to display center and radius.



Apex and base can also be set on the horizontal long axis image. The delta value (13 in this example) is the difference between base and apex.



The base slice corresponding to the line labeled "16" in the vertical long axis image. This image should have activity from 12 to 6 o'clock or a backwards C.



The apex should have a "button" appearance (not a ring).

On the long axis images, the length of the indicator lines corresponds to the diameter of the circle seen on the short axis.

Tip : You may have to make the circle smaller to exclude bowel and liver activity. It may not be possible to completely exclude this activity in some cases.

Tip : You may have to enlarge the circle if the LV is much wider at the base than in the mid ventricular region. Examining the center and radius in relation to several short axis slices may be helpful to ensure the best parameter selection.

Tip : The appropriate short axis base slice should have a backwards "C" shape, and should include the inferior wall of the ventricle. Because of perfusion defects, not all studies will fit this pattern.

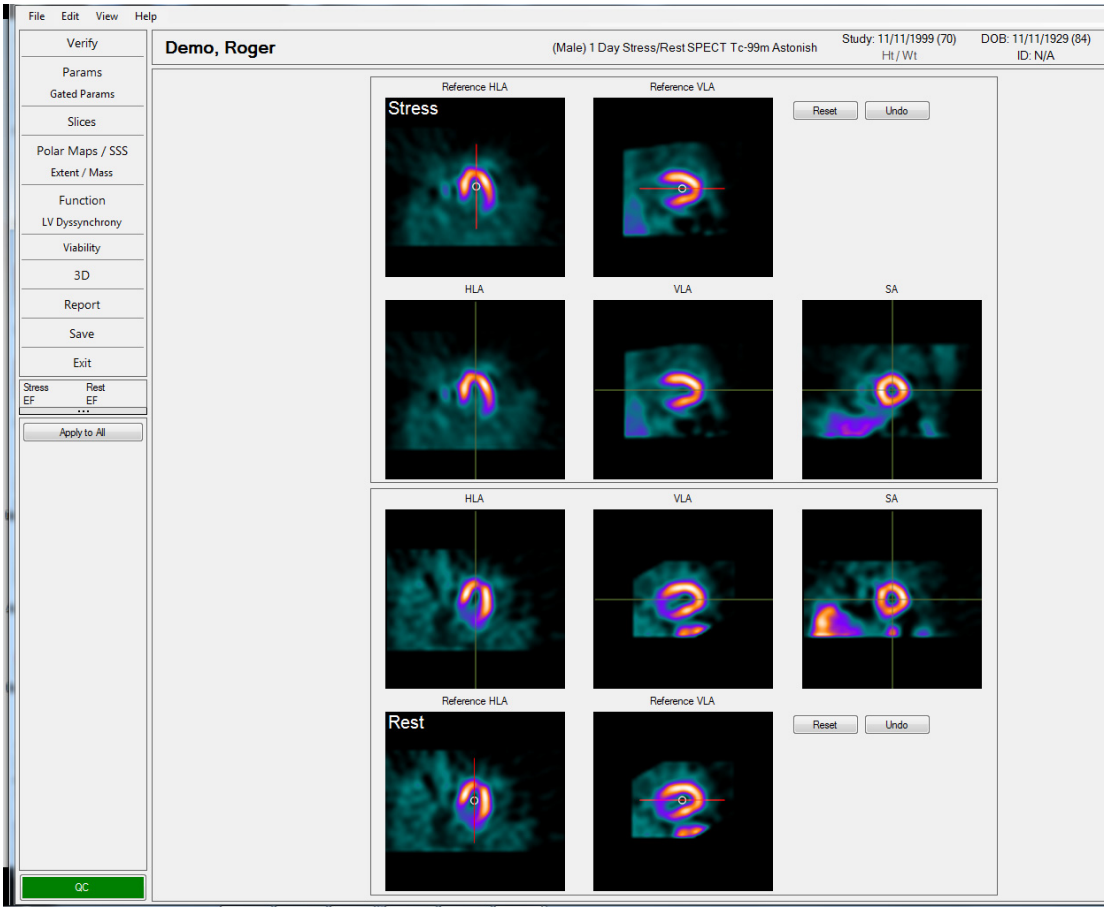
Tip : The appropriate short axis apex slice should have a "button" appearance (not a ring). Because of perfusion defects, not all studies will fit this pattern.

Tip : If an apical perfusion defect is present, you may have to increase image intensity to determine how far "out" to move the apical line cursor. In this case, you should set the apical line where you think the apex would have been if there was no defect.

5.2 Post-Facto Reorientation

The Post-Facto Reorientation screen allows the user to adjust the angle of the short axis images from both the HLA and VLA planes. This feature is designed to allow the user to make changes in the SA angle, within ECTb4, without having to re-visit the acquisition computer and subsequently re-send corrected data back to ECTb4.

The Reorientation screen can be accessed on any screen (Params, Slices, etc.) that shows the Reorient button and the following screen will be displayed.



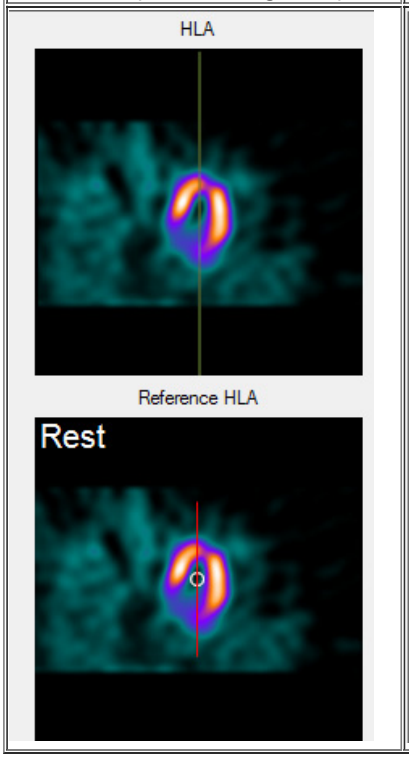
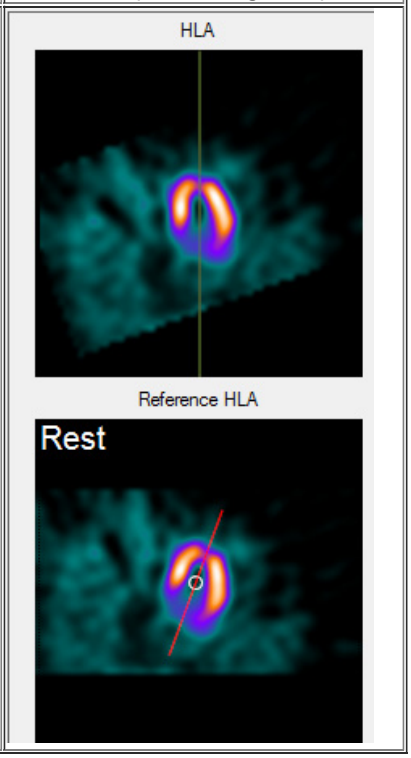
In any A/B type view (Stress/Rest, Match/Mismatch, etc) the acquisitions have their own section top and bottom.

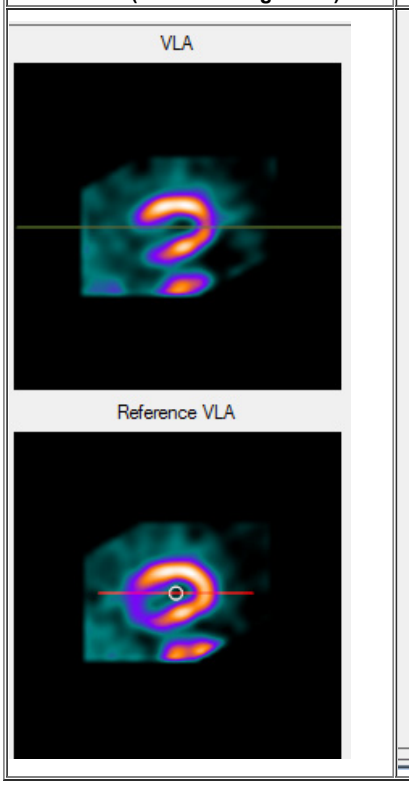
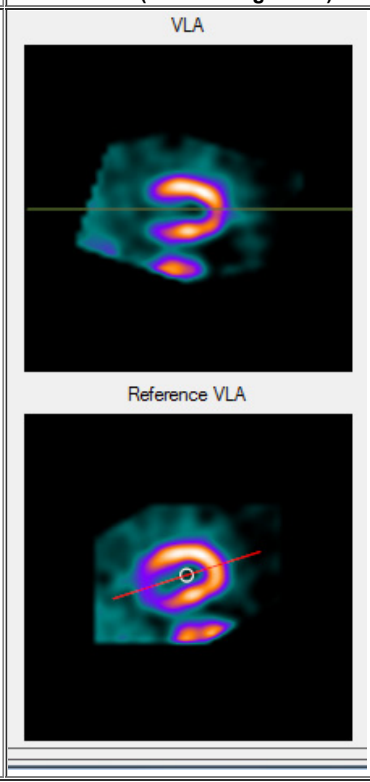
The first acquisition is displayed at top, and the top row of images represent a reference HLA and reference VLA from the incoming (original, unreoriented) data. On these, the user positions a center marker and sets a reorientation angle.

The bottom row of images are resultant HLA, VLA, and SA images. These are a preview of the reorientation represented by the markers on the reference slices. Overlay lines to verify orientation exist on each preview slice and do not persist beyond the reorientation page.

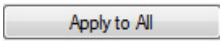
The second acquisition is displayed at the bottom and has the top/bottom rows flipped such that the resultant HLA, VLA, and SA slices from each acquisition can be compared more easily.

On the screen above the resting set of images need to be realigned. This is accomplished by clicking in the middle of the cavity for the Reference HLA image to set the center and then grabbing the line and moving it left or right so that the line is parallel to the long axis walls of the myocardium. The before and after images of alignment are shown below for the HLA and VLA images.

Before (Incorrect Alignment)	After (Correct Alignment)
	

Before (Incorrect Alignment)	After (Correct Alignment)
	

Correct alignment would have the apex of the heart for the HLA image pointing at 12 o'clock and the apex of the VLA image pointing to 3 o'clock.

Corrections made on this screen are only effective if they are applied by clicking the Apply All button 

Views (AC/non-AC or Prone/Supine) can be swapped on this screen, where available.

5.3 Options

Options for the Params page are shown in the figure below.



Available options are:

PF Reorient - allows the user to adjust the angle of the short axis images from both the HLA and VLA planes.

Show Borders - click and hold this button to display epicardial and endocardial borders, as determined from the myocardial sampling process. If the borders do not follow the ventricular edges, you may need to change one or more of the parameters (see section 5.1, Changing Parameters). Also, see section 21, Technical Overview, for details of how sampling is done.

Reset Stress - restores the automatic center, radius, apex and base for the stress study. A reset button also appears onscreen with the stress images.

Re-Center Stress - moves the currently defined Stress center to the center of the Stress viewport.

Reset Rest - restores the automatic center, radius, apex and base for the rest study. A reset button also appears onscreen with the rest images.

Re-Center Rest - moves the currently defined Rest center to the center of the Rest viewport.

6 Gated Params

This screen displays the parameters that will be used to define the size and location of the left ventricle as it progresses from diastole through systole. For accurate calculation of function, wall thickening and phase, these parameters must be set appropriately for each gate. In case of a low count study, the images on this page can be filtered using the "Filter" dropdown menu. This filter is for display only, and does not affect functional calculations.

The parameters are initially defined automatically by the application. Exactly as on the main Params screen, you can change any parameter as necessary by dragging its cursor. The apex and base slices are very important, as incorrect choices will affect ejection fraction and possibly introduce image artifacts. It is recommended that the apex or base should change by no more than one slice from gate to gate. There are two choices for setting parameters for all gates at once:

- Holding the CTRL key and dragging will first set all the centers to match the image under the cursor, and then move the center on each gate.
- Holding the ALT key and dragging will move all centers relative to their previous position.
- Holding the CTRL key and dragging any apex selector line will first set all apex selector lines to match the image under the cursor, and then move the line on each gate. The base can be set similarly.
- Holding the ALT key and dragging the apex selector line will move all apex selector lines relative to their previous position. The base can be set similarly.

To display left ventricular borders at any time, click and hold the Show Borders button.

6.1 Changing Gated Parameters

Similar to setting ungated parameters, you can view the automatic parameters for each gate, and change them as necessary. The window is shown in the figure below. To reset all changes, use the Stress Reset or Rest Reset button.

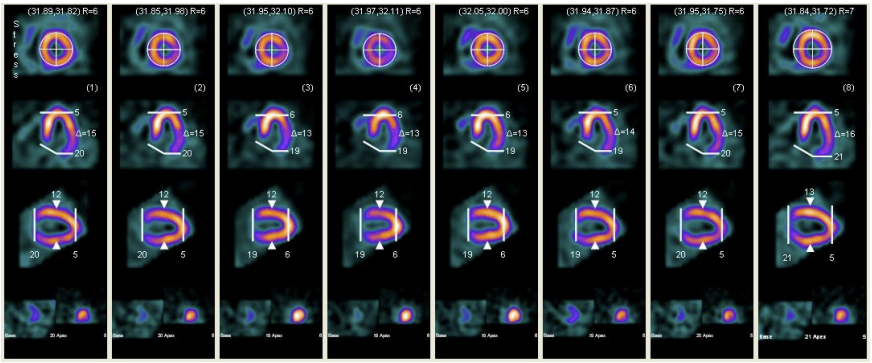


Figure legend: Display window for reviewing and changing gated parameters.

To change the center for any gate, drag the crosshair on the short axis image. To change the circle size, drag the circle by its perimeter.

You can change the center or set the circle size for all gates at once by holding down the CTRL key while dragging with the mouse. You can also move all the centers relative to their current position by holding down the ALT key while dragging with the mouse.

To change the apex or base slice for any gate, drag the corresponding limit line on the reference long axis (either vertical or horizontal). By default, the displayed apex or base on the bottom row will be zoomed to a larger size so that you can compare slices for all gates. There is an Option to change this behavior (see section 6.2).

To change the apex or base for all slices, hold the CTRL key while dragging one of the slice marker lines. You can also change all apex or base slices and also maintain the relative difference between gates by holding the ALT key while dragging a slice marker line.

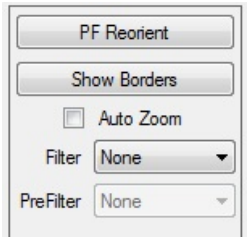
TIP : The appropriate base slice will often be different for different gates. For example, the base slice for gates around end systole may be closer to the center of the ventricle, and will be further "out" at the beginning and end of the cycle. The apex may also change during the cycle, but usually not as much as the base.

TIP : In a case where there is poor function, heart motion is reduced, so the apex and base slice numbers will change less from gate to gate.

TIP : It is recommended that the apex and base slice numbers not change by more than 1 from one gate number to the immediately following gate number.

6.2 Options

Options for the Gated Params page are shown in the figure below.



Available options are:

PF Reorient - allows the user to adjust the angle of the short axis images from both the HLA and VLA planes.

Show Borders - click and hold this button to display epicardial and endocardial borders on the slices, as determined from the myocardial sampling process. See manual section 21, Technical Overview, for details of how sampling is done.

AutoZoom - when selected, as it is by default, this option enlarges the apex or base short axis slice when the location line is being adjusted. With this option off, you can drag the location line and both base and apex slices remain on the display.

Filter - this dropdown list controls how the images are filtered for display. This filter is only applied to the display during parameter selection. Volumes and other calculations are not affected. The default is "None".

PreFilter - indicates whether the gated short axis were prefiltered before analysis. The prefilter is selected on the Verify screen, and may affect calculated volumes.

7 Slices

This screen allows perfusion to all regions of the left ventricle to be assessed, and compared between stress and rest, or between attenuation-corrected and non-corrected images. The screen is divided into three areas:

1. sets of slices through the left ventricle
2. planar projections, if available
3. AC attenuation (transmission) maps, if available
4. polar maps

To shift any row left or right, click the left or right mouse button, respectively, over that row.

Use the Cine Control at the bottom left of the page to convert these to a beating gated cine display

The planar, transmission and polar map sections can be collapsed and/or expanded by clicking the 3-dot widget above each section.

Right-click on the polar map to see the blackout (defect extent) map. Left-click to return to the raw map.

Various combinations of slice images can be shown; by default the arrangement is:

- short axis on the upper rows (starting with the selected apex)
- vertical long axis on the middle rows
- horizontal long axis on the lower rows

Caution: When the user modifies the combination of slice images, those images will not change in accordance with the View selector radio buttons until the display has been reset using the Reset button. To help prevent confusion, the user will be prompted when attempting to change the default image set in this manner and the Reset button will change color until the display has been reset back to the default.

7.1 Display

The Slices display has evolved into a minimalist version of the ActiveView from the previous version of the ECToolbox application. This is shown in the figure below.

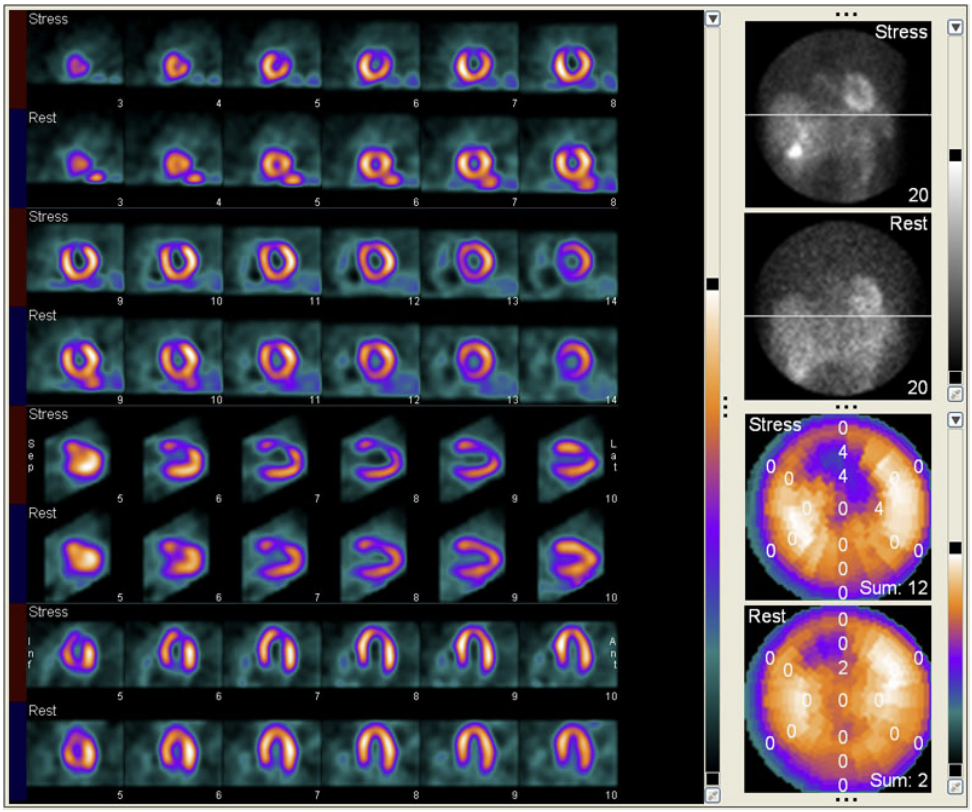


Figure legend: Standard display of left ventricular slices, planar projections (upper right) and polar maps with superimposed segmental perfusion scores.

Each display area has its own independent color bar for changing image brightness, with a button at the bottom for changing the color table. For the rotating projection data, the brightness may also change if you move the reference line to a different position.

Caution: for the slices, be aware that the ECToolbox application attempts to properly normalize stress and rest slices based on counts in the myocardium, that is, pixels inside the circular radius which is set on the Params page (see section 5.1). Take care when manually adjusting the window level for slice images. Such adjustment may be necessary when bowel or liver activity has been unavoidably included within the circle.

The horizontal line on the planar projections can be used as a fixed reference for assessing patient motion.

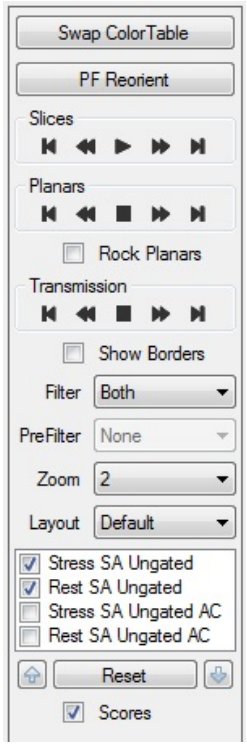
Caution: in the event of significant patient motion, it is recommended to either re-acquire the SPECT Study or to utilize a motion correction program to eliminate the motion.

The application automatically aligns corresponding slice images for both the Stress and Rest studies. The alignment is based upon the apical and basal boundary slices which were previously defined on the Params Window. You can correct any misalignment by clicking that row with the mouse, as follows:

- left-click to slide the row to the left, so that more of the later slices are seen.
- right-click to slide the row the the right, so that more of the earlier slices are seen.

7.2 Options

Options for the Slices page are shown in the figure below.



Available options are:

Swap Color Table - switches between two color tables, as defined in Configuration settings. See manual section 18 for instructions on changing the default color tables.

PF Reorient - allows the user to adjust the angle of the short axis images from both the HLA and VLA planes.

Animation controls for **Slices, Planars** and **Transmission** - these buttons control the dynamic cine display for the indicated images. The same type of controls appear on each screen which has dynamic content, such as Function review (see section 10.2), Dyssynchrony (11.3), and 3D review (15.2). From left to right, the buttons are:

- single-step forward through the sequence.
- slow down the dynamic display.
- start or stop the dynamic display.
- speed up the dynamic display.
- single-step backward through the sequence.

Rock Planars - when selected, the planar projections will rock back and forth instead of a continual cine.

Show Borders - when selected, this option displays epicardial and endocardial borders on the slice images, as determined from the sampling process. See section 21.2 in the Technical Overview.

Filter - controls what type of filtering is applied to the gated slice images. This filter is for display only, and does not affect functional calculations. Filters can be changed at any time. The choices are:

- spatial filter
- temporal filter
- both spatial and temporal
- none

PreFilter - Only applicable if the gated data is being displayed. Depending on the pre-filter setting on the Verify page (see section 4.1), the gated data may have been pre-filtered before being displayed and quantified (the pre-filter option does effect both the images displayed and the functional calculations). The options are:

- spatial filter
- temporal filter
- both spatial and temporal
- none

Zoom - controls the magnification of the slice images.

Layout - controls which slices are displayed. The options are:

- Combined - one row each of short, vertical and horizontal
- Combined SAx2 (the default)
- SA only - all short axis for stress and rest
- VLA only - all vertical long axis for stress and rest
- HLA only - all horizontal long axis for stress and rest

Custom image selection - these checkboxes control which categories of images are included in the display. This is useful when there are more than two sets of images.

Caution: When the user modifies the default image set for display, the images will not change in accordance with the View selector radio buttons until the display has been reset using the Reset button, described below. To help prevent confusion, the user will be prompted when attempting to change the default image set in this manner and the Reset button will change color until the display has been reset back to the default.

Reset - restores the screen layout to its default status. This is an "undo" button for changes you have made in the image selection options.

Up/Down Arrows - These arrows, on either side of the Reset button, control the ordering of datasets within the image selection window and likewise control the ordering of displayed datasets on the screen.

Scores - displays perfusion scores on each segment of the polar maps. These are automatically determined by comparison to the normal database, or manually set by a user.

8 Polar Maps / SSS

This screen shows polar map representations of left ventricular perfusion.

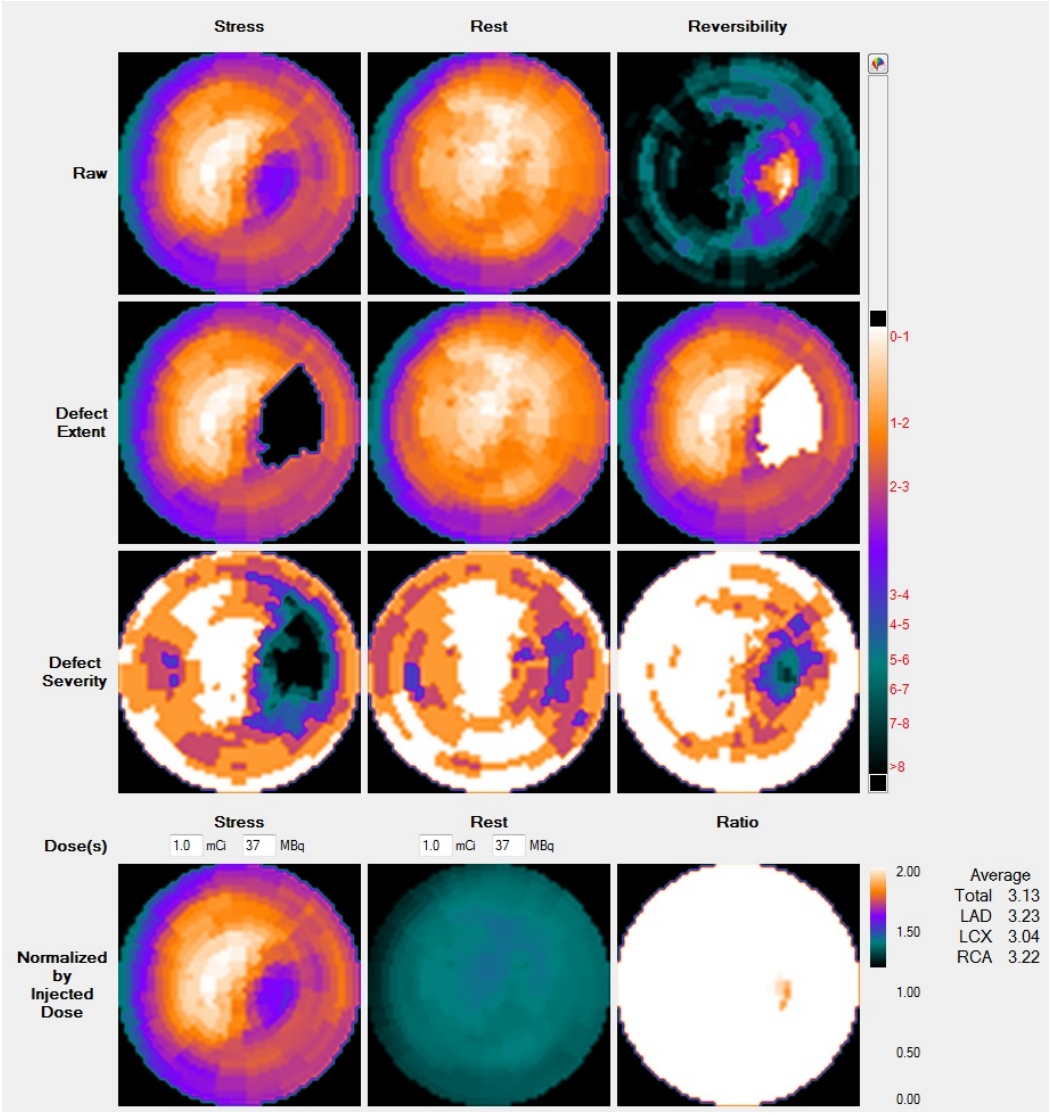
- The top row shows raw, unprocessed plots depicting perfusion to the entire left ventricle. The Reversibility map is produced by subtracting stress from rest after a count normalization step, and thus highlights areas that are more normal at rest.
- Maps on the second and third rows relate the current study to the selected normal file. In the second row significant perfusion defects are shown in black. On the rightmost map of this row, defect pixels which reverse at rest (are significantly more normal) are set to white. For defects and reversible areas, a threshold is used with the normal file.
- In the third row, non-white pixels represent any difference from the normal file, without using a threshold. Colors used in this row correspond to different numbers of standard deviations below normal, which are labeled on the color bar with red numerals.
- There is an optional fourth row showing polar maps that reflect the ratio between stress and rest counts. To display these maps, use the "Show Ratio" checkbox on the left of this page. The ratio maps will be meaningful only if the stress and rest doses have been entered by the user.

The 17 segment perfusion scores can also be assigned on this screen. Use the Scores checkbox on the left side of the display to show the scores. To change a score, click the number and make a selection from the dropdown. Scores range from zero (normal) to 4 (absent perfusion).

8.1 Display

An example of the Polar Maps display is shown in the figure below. If you have a study for which it is not appropriate to calculate perfusion map ratios, the bottom row of maps will not be present.

Each map represents the pixels of the left ventricle, plotted in polar coordinates, that is, as a series of rings, each corresponding to one short axis slice. The center-most ring is the apex, and the outer-most ring is the base. The anterior wall is at the top, septal wall on the left, inferior on the bottom and lateral wall on the right.



When referring to the raw polar maps (top row), “raw” denotes that these polar maps have not been compared with the appropriate gender-matched normal database. The right-most map on the first row shows normalized rest minus stress. Non-black areas on this map represent myocardium that is more normal at rest than stress. In this case, a stress defect is said to have "reversed" in the resting state.

The “blackout” polar maps (second row) are also known as defect extent maps. After comparing the study to a normal database, the application blackens those pixels whose count values are significantly lower than the same pixels in the database. Significance is determined by regional thresholds present in the database. Such blackened pixels identify areas which may correspond to myocardial perfusion defects. The far right polar map on the second row is the reversibility polar map or "whiteout" polar map. After comparing the study to a normal database, the application turns pixels white whose count values are significantly above the same pixels in the database, when they fall within a blacked-out defect.

Caution: Apparent perfusion defects might also be caused by artifacts due to non-uniform tissue attenuation or other technical problems. It is strongly recommended that the user visually correlate defects observed on the polar maps with defects observed on the tomographic slice images.

On the standard deviation maps (third row), color is used to designate the relative variance of tracer uptake when compared to normal. The color codes for different numbers of standard deviations below normal are shown on the color bar, and are defined as follows:

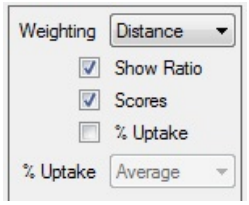
- Pixels whose count values are between 0 and 1 standard deviations (s.d.) below the corresponding Normal File pixels, are color-coded White
- Pixels whose count values are between 1 and 2 s.d. below the corresponding Normal File pixels, are color-coded Orange
- Pixels whose count values are between 2 and 3 s.d. below the corresponding Normal File pixels, are color-coded Pink; and so on down the color scale to black, which means greater than 8 standard deviations.

The rightmost map on row 3 is the standard deviation reversibility map, which uses the same color-coding scheme as the other maps on this row in that colors correspond to the number of standard deviation. The different is that, in this map, the colors represent s.d.’s *above* the mean normal pixel counts. On this polar map, clusters of colored (non-white) pixels indicate areas which may have greater tracer uptake at Rest than during Stress. In other words, they are "reversible".

The bottom row shows stress and rest perfusion, normalized to the dose injected (if available), and a polar map of the stress / rest ratio. The injected doses are retrieved from the DICOM files, if available, if not, they can be entered directly above the corresponding polar map.

8.2 Options

Options for the Polar Maps / SSS page are shown in the figure below.



Available options are:

Weighting -

- The default Distance-weighted polar map is constructed so that each ring in the polar map is the same width. This map offers an accurate assessment of the defect location, but may distort defect size.
- The volume-weighted polar map is constructed so that the volume of the apex and the remainder of the myocardium that is represented on the polar map is proportional to the volume of the corresponding slice. This makes the relative two-dimensional area of a defect equal to the relative three dimensional volume of that defect. This map offers an accurate assessment of the defect size, but may distort defect location.

Show Ratio - When selected, as it is by default, this option displays the ratio of counts in the stress and rest raw polar maps.

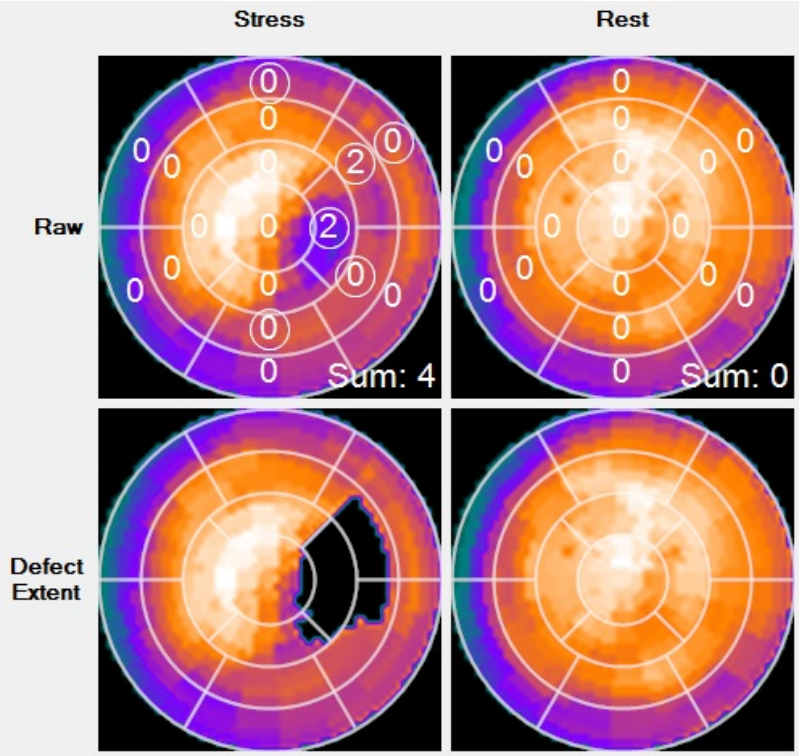
Isotope Doses - In these textboxes, you can enter the stress and rest doses injected, for calculation of the polar map ratios.

Scores - When selected, this option displays the segmental perfusion scores over the polar maps.

% Uptake - When selected, this option displays segmental radiotracer uptake values on the perfusion map. To obtain these values, the global maximum count value is found, and then for each segment, the mean of all pixels in that segment is compared to the maximum and expressed as a percentage.

8.3 Segmental Scores

The Polar Maps / SSS screen optionally displays perfusion scoring for 17 segments of the myocardium, as shown in the figure below. Click the Scores checkbox to display scores. If you want scores to always appear on this screen, there is a setting in ECToolbox Options for this. From the Edit menu, select Options, find the tab labeled "Polar Maps / Viability / Extent" and click the "Show Scores" box.



Numerical scores representing regional perfusion are shown within segmental boundaries on the Stress, Rest and Reversibility polar maps. Segmental boundaries only are displayed on the other polar maps. The scoring system is a five-point scale:

0 = Normal
1 = Equivocal
2 = Moderate Reduction in perfusion
3 = Severe Reduction in perfusion
4 = Absent perfusion

By default, the scores that are displayed are generated automatically by the application, based on two types of analysis. First, the patient is compared to the selected normal file on a regional basis. The image counts are then analyzed by IDS (Intelligent Decision Support), a clinical decision support system, which may modify one or more of the initial scores.

Types of score display

Scores that have been modified by IDS are displayed with circles around the numbers. Un-modified scores have no circles. By using the mouse to hover over a score, you will briefly see a display which gives the original score, as well as the IDS score. A physician interpreter can manually modify any of the scores by left-clicking the segment and selecting a score from the dropdown list that appears. If this score is different from the default score, it will appear in a square box. To dismiss the droplist without making a selection, move the pointer out of the list and right-click.

Using this scheme, you can always see which scores derive from normal file comparison, from IDS analysis or from manual modification.

If you select the SmartReport reporting software by clicking the Report button, the scores will be included in the report. See section 20 of this manual for details of SmartReport.

Tip: Segmental scores can also be displayed on the Slices screen, and can be modified there. Changes made to scores on either the Slices or Polar Maps screen will immediately be seen on the other screen.

9 Extent / Mass

This screen shows the stress polar map with abnormal pixels in black. The right-hand map also whitens pixels within the defect that are significantly more normal at rest, that is, show reversibility. Coronary artery territories are outlined in white:

- LAD, the left anterior descending artery, is the largest territory
- LCX, the left circumflex artery, is rightmost on the maps
- RCA, the right coronary artery, is the one toward the bottom of the maps
- A significant area of the ventricle is not assigned to any one territory because coronary artery anatomy differs from patient to patient. The application displays the average territories.

Below the polar maps is a table which summarizes the size of each perfusion defect in terms of area (Extent) or mass. Extent values are expressed as percent of coronary territory, and mass is given as percent of territory and also in grams. Mass can be calculated from the gated or ungated images.

9.1 Display

On this screen, shown in the figure below, perfusion defects are identified and quantified in several different ways. By default, defect extent, or area, is shown.

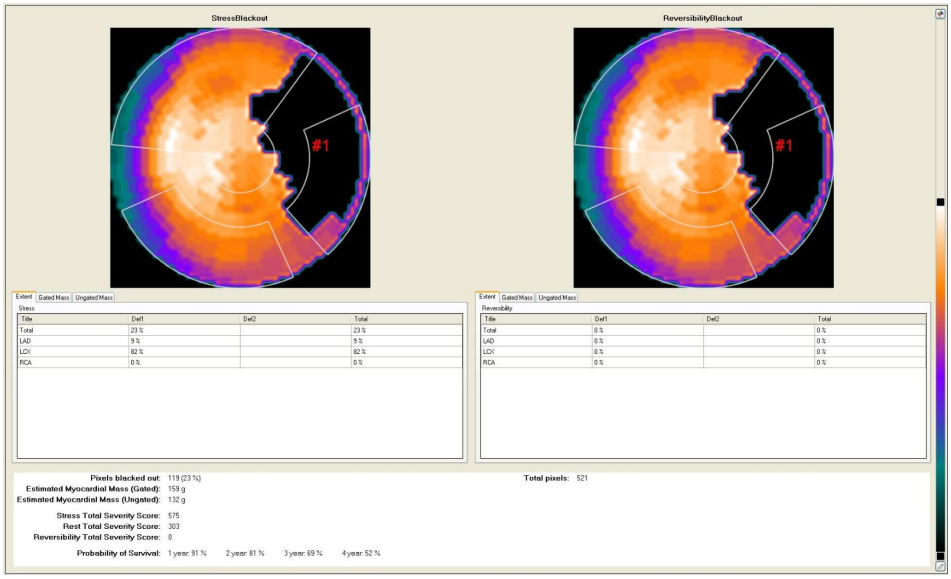


Figure Legend: The polar maps are stress blackout (left) and reversibility blackout (right).

Defects are numbered on the map and on the grid of values displayed below the maps. If more than five defects exist, the applicaton only displays information for the first five. Defects are identified and numbered starting at the apex and moving outward, so that a very basal defect may not be numbered or included in the grid if it is the sixth (or higher) defect found.

Besides defect extent, the other tabs summarize the detected defects in terms of mass from the gated study, or mass from the ungated study. The total defect mass in grams is also displayed in the lower portion of the extent tab. Mass determinations based on the gated data are considered to be more accurate than those based on ungated data.

Defining and Characterizing Perfusion Defects

You will notice that the area below the polar maps consists of tabs, for defect extent (or area), defect mass derived from the gated data, and defect mass derived from ungated data. Each tab displays the blackout and reversibility polar maps, below which there is a grid of values characterizing defects in terms of how they relate to the total myocardium as well as to a given coronary territory. Territories are areas of myocardium that correspond to the three main coronary arteries: LAD (Left Anterior Descending), LCX (Left Circumflex) and RCA (Right Coronary Artery).

In the left-most column of each grid, the "Total" defect refers to the combination of all myocardial areas that are significantly abnormal. The percent value for this Total refers to the percent of myocardium that is abnormal. The right-most column, also labeled "Total", refers only to the sum of all values in that row.

The Defect Extent percentages determined in the Extent display, are based on the number of pixels in each defect. These percentages may differ somewhat from the Defect Extent percentages determined in the Estimated Mass Display.

Other Displayed Values

Stress Total Severity Score - This value is the sum of standard deviations below the mean, for all blacked-out pixels in the Stress Blackout Polar Map. It has been shown that patients with a Stress Total Severity Score of <114.5 (<8% LV impairment), had a statistically significant, improved chance of long term survival, at the five year follow-up point. This value can be removed from the display if desired.

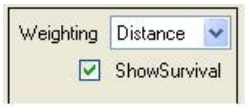
Rest Total Severity Score - This value is the sum of standard deviations below the mean, for all blacked-out pixels in the Rest Blackout Polar Map.

Reversibility Total Severity Score - This value is the sum of standard deviations in all pixels that are significantly more normal at rest than at stress. "Significantly" means a difference of at least one standard deviation.

Probability of Survival data - This data is derived from the study referenced above. It represents statistical survival probability from 1 to 4 years, at 1 year increments, based on the patient's Stress Total Severity Score. These values are based on data reported by Krawczynska, et. al. (J Nucl Med 1998;39(suppl):115P).

9.2 Options

Options for the Extent/Mass screen are shown in the figure below.



Available options are:

Weighting - This option determines how the polar maps are constructed. Distance weighting ensures that defect location is most accurate, while volume weighting ensures that defect size is most accurate. For more information, see manual section 8.2 (Polar Maps / SSS Options).

Show Survival - When selected, this option displays the calculated probability of long-term patient survival. These values are derived from population studies.

10 Function

This screen summarizes the results of functional processing. For each study, several dynamic cine slices are shown, and are controlled by the "Animation" widgets left of the image display. To display image borders calculated from the gated parameters and image counts, click the "Show Borders" checkbox.

The ejection fraction (EF) and volumes can be subjected to several different regressions using the EF dropdown to the left of the image display. The following regressions can be selected:

- R0, the default
- R1, allows the values to be compared to Cedars QGS results when there are 8 gates
- R2, allows the values to be compared to multigated blood pool results
- R3, allows the values to be compared to Cedars QGS results when there are 16 gates

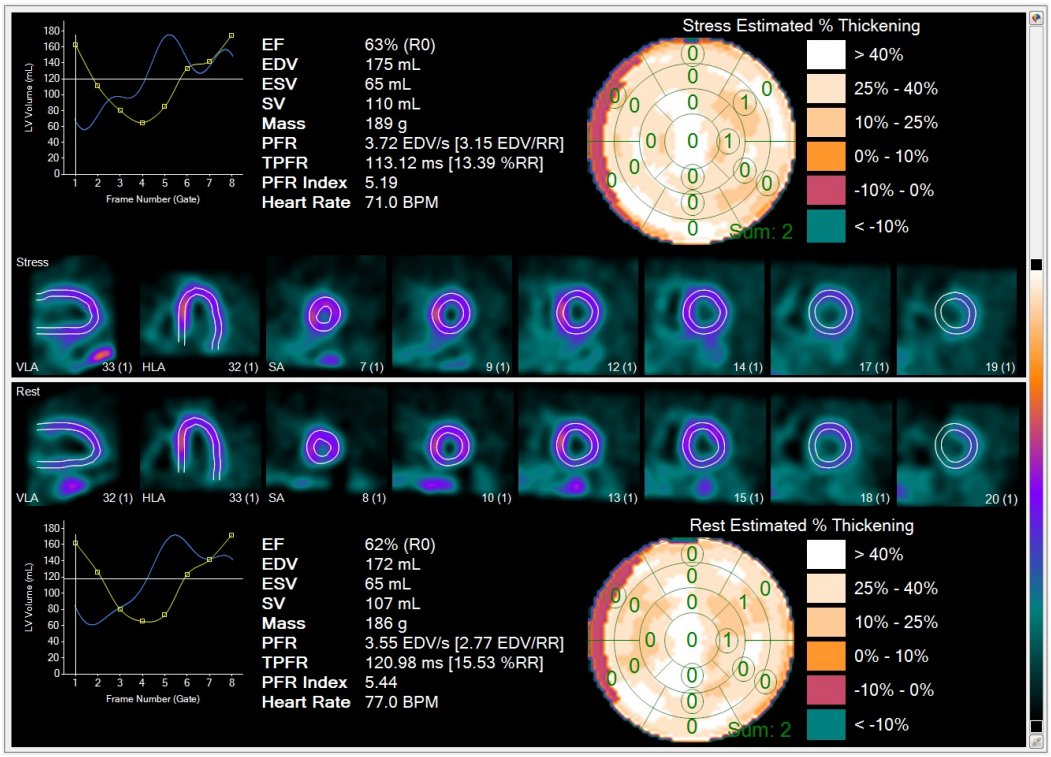
If you entered the patient's height and weight, there will be a column labeled "Indexed", for LV volumes normalized to body surface area. To enter height and weight, click the blue "Ht/Wt" link at the top right of the screen.

Several parameters of diastolic function are also displayed (peak filling rate, time to peak filling rate, peak filling rate index and heart rate), as well as the derivative of the LV Volume curve (overlayed in blue on the LV Volume curve).

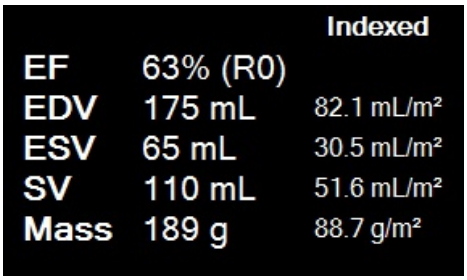
Left ventricular Wall thickening is shown in polar map form. Negative thickening implies that the myocardial wall becomes thinner during systole.

10.1 Display

The first figure below shows an example of the Function screen, summarizing the analysis of LV function, calculated volumes and estimated wall thickening.



The elements of this review screen include the LV volume curve, which plots ventricular volumes for each gate, from end diastole (the first point), through systole and back to end diastole (last point). Optionally, overlayed on the LV volume curve is the derivative of the LV volume curve, from which the diastolic function parameters are derived. LV ejection fraction, volumes, mass, and optionally, diastolic function parameters (peak filling rate, time to peak filling rate, peak filling rate index and heart rate) are also displayed. If the patient height and weight have been entered, then an additional set of "index" values are displayed, showing the volumes normalized for body surface area. An example is shown here:



The slice images are a set of gated cines, depicting the short axis and mid-ventricular long axis images. When viewed in motion, these can be used for assessing wall motion.

Wall Thickening

In general, normal myocardial tissue should uniformly thicken at end-systole. This should result in a relatively homogenous brightening of the myocardial pixels. This "brightening" phenomenon is caused by the partial volume effect. Myocardium which demonstrates thickening at end-systole, is considered to be viable. Conversely, myocardium which demonstrates no thickening at end-systole, is considered to be non-viable. The Wall Thickening polar map is a useful tool to visually assess relative global thickening over the entire LV.

10.2 Options

Options for the Function page are shown in the figure below. This block of controls also displays the calculated LV ejection fraction, volumes and summed segmental perfusion score for stress and rest, as well as the calculated TID (transient ischemic dilatation) index. TID is the ratio of stress LV cavity size to rest cavity size.



Available options are:

Swap Color Table - there are two color tables which can be chosen for standard use in the application. This button switches between tables.

Animation - these controls start, stop and adjust the speed of display for sequential frames of for the oblique slice cines. For details, see section 7.2.

Show Borders - when selected, displays epicardial and endocardial borders on the slice images, as determined from myocardial sampling. For details of the sampling process, see section 21.2.

Zoom - sets the magnification factor used for the slice images.

EF - sets the regression used for LV ejection fraction values. See section 10.3

Scores - displays wall thickening scores over 17 segments of the polar map. Scores are derived from comparison to normal limits for wall thickening.

Filling - when selected, adds information related to LV filling rate to the display. A second plot, the derivative of the LV volume curve, appears in blue overlayed on the LV volume curve display.

Filter - controls what type of filtering is applied to the gated slice images. This filter is for display only, and does not affect functional calculations. Filters can be changed at any time. The choices are:

- spatial filter
- temporal filter
- both spatial and temporal
- none

If the global preference setting for filtering is set to pre-filter the data, then the option "Pre" will appear instead of "None".

PreFilter - controls what type of filtering is applied to the gated short axis images after they are accepted for processing on the Verify screen. This filter may affect functional calculations, and cannot be removed. The choices are:

- spatial filter
- temporal filter
- both spatial and temporal
- none

Note: pre-filtering will slightly change the calculated ejection fraction and volumes.

10.3 EF Regressions

By default, the ejection fraction shown on the Functional Analysis Screen is computed from the gated SPECT data exactly as described in the Technical Overview, using modeled boundary points and geometric calculations. Three additional calculated ejection fractions may also be displayed. The EF pull-down menu allows you to switch between several variations of the ejection fraction calculation. These are regression equations, meaning that the EF is calculated and then modified using a mathematical equation. Details on these equations, how they were derived and when they may be useful can be found in the Technical Overview (section 21.8).

R0 - (Original) This is the default method.

R1 - This option uses an equation to compute an EF that approximates the value that might be expected if 8-frame gated data was processed using the Cedars Quantitative Gated SPECT program.

R2 - This option uses an equation to provide an EF that approximates the value that might be expected if the same patient was studied using the multi-gated planar blood pool technique.

R3 - This option uses an equation to compute an EF that approximates the value that might be expected if 16-frame gated data was processed using the Cedars Quantitative Gated SPECT program.

After choosing a regression option, end systolic volumes are recomputed using the original end-diastolic volume and the regressed EFs.

The decision as to which regression, if any, to use for calculating EF is totally at the discretion of the physicians in charge of each laboratory. We suggest that each laboratory choose one of the approaches (R0, R1, R2, R3) and not switch between them.

11 LV Dyssynchrony

*Also know as **SyncTool™**.*

This screen displays the results of phase analysis of the gated stress and rest studies. For each study the following items are shown:

- A phase polar map.
- A histogram plotting the frequency of occurrence of each possible phase (0-360) within the polar map.
- The raw polar map shown twice. The rightmost one will contain an animation of the wave of contraction when the Animation control's Play button is left-clicked.
- A list of calculated values that characterize the phase histogram.

Eccentricity values are also calculated as a way to characterize the ventricular shape. Values are usually between zero and one. Lower values suggest a more normal, elliptical shape. As values approach one, the ventricle is becoming more spherical in shape, which is abnormal.

11.1 Display

Theory

If gated SPECT has been performed, phase information can be extracted from the image data. This is information related to the time point at which any given part of the myocardium begins to contract. The contraction time point for each pixel in the ventricle can be plotted on a standard polar map, producing a dynamic visual representation of the contraction pattern across the entire left ventricle.

The three types of results summarized on this screen, 1) the dynamic contraction cine, 2) the histogram and 3) the numerical values, characterize the degree of synchrony (or dyssynchrony) of ventricular contraction.

Note: For phase analysis to work correctly, the imaging study must be properly gated to the R-wave on the patient's ECG.

Screen Layout

The following figure shows an example of the LV Dyssynchrony results display.

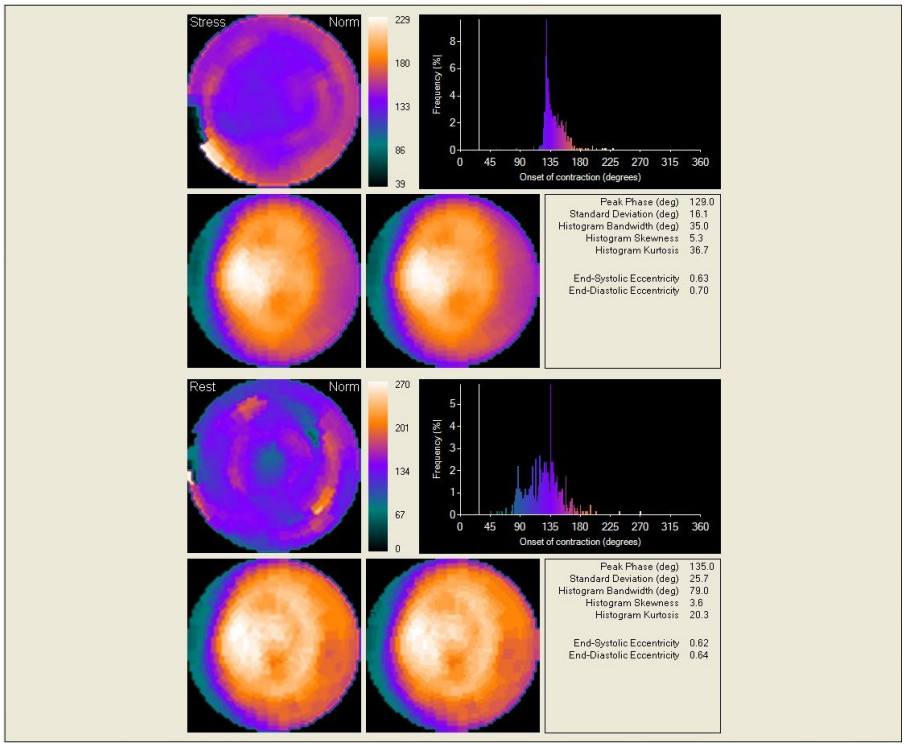


Figure Legend: Review screen summarizing results of analysis of the contraction phase of the LV. In this example, the top half of the display pertains to stress and the bottom half pertains to rest.

Taking the stress data as an example, the upper left polar map is the phase map, plotting the time at which every pixel begins to contract, expressed as a value between zero and 360 degrees. Different values are plotted as colors, with a colorbar displayed for reference. This "Raw Phase" map plots all possible phases, with zero at the lower (black) end of the colorbar.

The two lower maps show raw (unprocessed) perfusion, the right right-hand map is used for dynamic display of the propagation (sometimes called the "wave") of ventricular contraction. See section 11.2 for further details, and 11.3 for options related to this dynamic display. There is a histogram on which the phase values present for this study are plotted, and below this is a list of calculated values derived from the histogram.

In general, the narrower the histogram, the more normal the synchronization of contraction. To further characterize the histogram, several calculated values are shown:

Peak Phase, in degrees. This is the most frequent phase (the phase corresponding to the peak of the phase histogram).

Standard Deviation, in degrees. This is the standard deviation of the phase distribution;

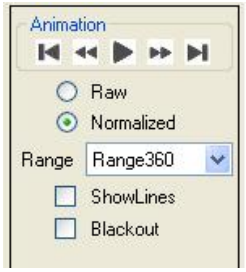
Histogram Bandwidth, in degrees. This is the width of that band which includes 95% of the elements in the phase distribution

Histogram Skewness, which indicates the symmetry of the histogram. Positive skewness is when the tail of the histogram is longer to the right of the peak. Negative skewness shows a longer tail to the left.

Histogram Kurtosis, which indicates the degree to which the histogram is peaked (a histogram with a higher peak within a narrower band has higher kurtosis).

11.2 Options

Options for the LV Dyssynchrony page are shown below.



Available options are:

Animation - These controls start, stop and adjust the speed of display for sequential frames of the phase "cine".

Raw / Normalized - The Raw phase map plots all possible phase values from zero, at the bottom of the color scale, to 360 at the top. The Normalized phase map plots all phase values that are actually present in the image. The lower end of the colorbar represents the lowest phase present. The upper end of the colorbar represents the highest phase present.

Range - sets the range of phases included in the histogram. Selecting a lower value from the droplist "stretches" the same histogram to occupy more of the width of the display.

Show Lines - when selected, causes all lines, corresponding to all phases, to be displayed in sequence on the histogram, as the wave of contraction plays dynamically on the polar map. When not selected, only the current phase line is displayed, which means you will see a single line progressing across the histogram.

Blackout - controls the "style" in which the animation of contraction is shown on the polar map. When this box is selected, the "blackout" style is used. See section 11.3 for an example.

11.3 Modes of Phase Display

When the Dyssynchrony screen is first displayed, the dynamic display will be in motion. As the sequence plays, pixels on the polar map will be blacked out in the order in which they change phase during the cardiac cycle. In sync with this display, a series of vertical line cursors will progress across the phase histogram, displayed above the polar maps.

There are two styles of visually displaying the wave of contraction on the patient's polar map. In Style 1, pixels are blacked out when the cursor reaches that point on the histogram at which the phase changes for that pixel, and then the pixel returns to its original color. In Style 2, the pixel blacks out when its phase changes, and stays black for the remainder of the dynamic display, until the cursor returns to phase zero. The figure below shows the visual difference between these styles.

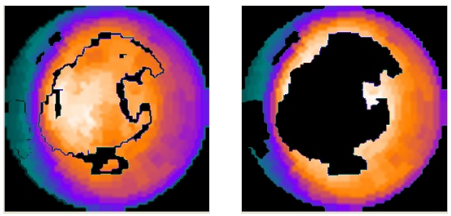


Figure Legend: Style 1 (left) for showing the contraction pattern, and style 2 (right).

12 AdreView

Emory Toolbox contains tools to analyze SPECT images acquired using ^{123}I AdreView, a radiopharmaceutical for imaging myocardial innervation. There are several tools for assessing AdreView uptake:

- Quantifying AdreView uptake relative to normal.
- Determination of uptake of AdreView in the heart relative to uptake of a perfusion agent such as tetrofosmin or sestamibi.
- Calculation of heart-to-mediastinum ratio from transaxial AdreView images.

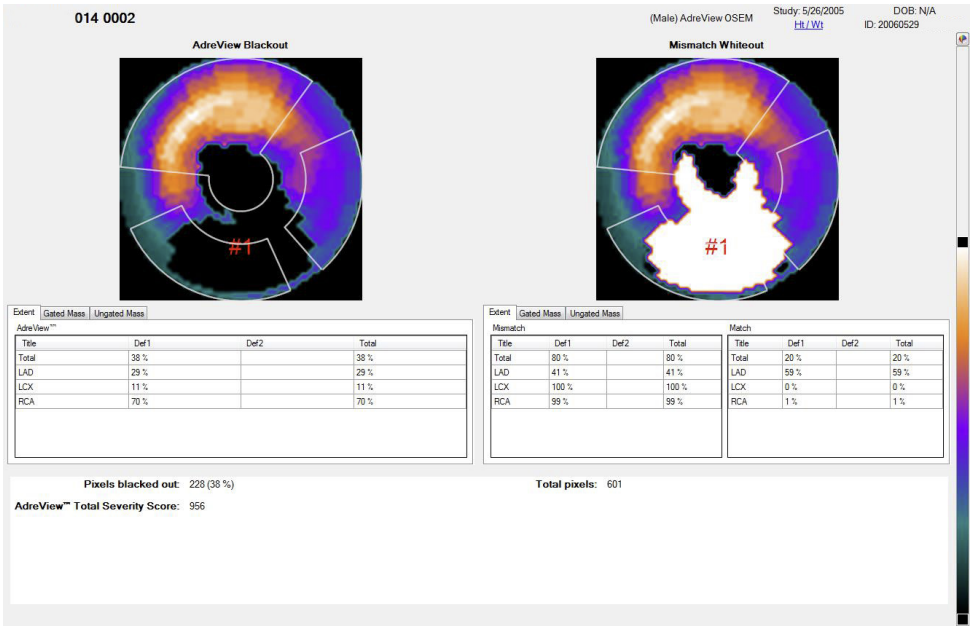
If mIBG and perfusion images are both available, to assess mIBG uptake click the AdreView™ button.

Note: If your version of the application does not appear to have this functionality that could be due to the fact that this feature is not included with a standard license. Please contact the manufacturer to enable this functionality.

12.1 Display

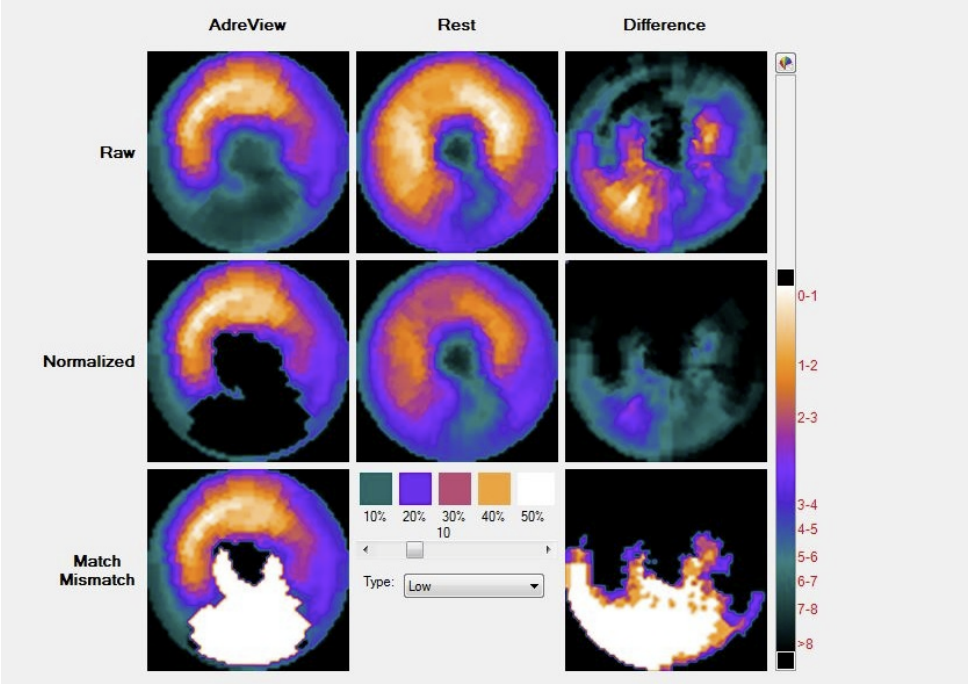
Quantification of Innervation Defects

The left ventricular uptake of AdreView can be quantified by comparing the patient to a normal database. This is similar to the comparison of myocardial perfusion to a normal database, and the results are presented in a similar way, as shown in the figure below.

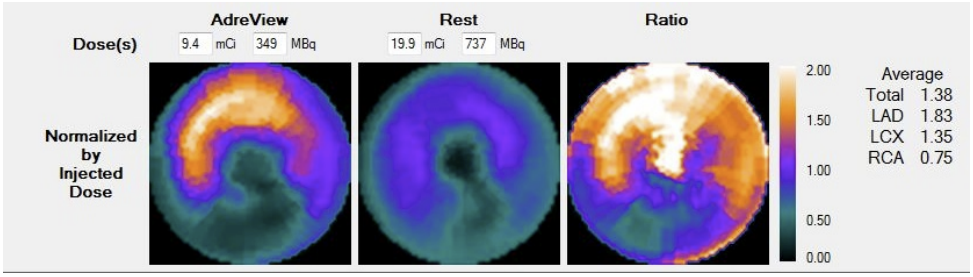


Comparing Innervation to Perfusion

If both AdreView and perfusion images are available, the relative uptake of the two radiotracers can be compared by selecting "Match / Mismatch" from the main Navigation Pane (buttons at upper left of the screen). Note that the Polar Maps page is not available for this type of study. A set of polar maps are displayed, as shown in the next figure, below. AdreView and perfusion uptake differences are shown in the top three rows of maps. If you are familiar with PET scan protocols, this display is similar to that used for comparing perfusion to FDG metabolism.



Three additional maps are displayed at the bottom of the page. In the boxes to the left of the maps, you can enter the actual doses injected for AdreView and for the perfusion tracer. The maps will be re-normalized from the dose values entered, and ratios (AdreView/perfusion) are calculated and displayed to the right of the maps. An example is shown here:



12.2 Heart to Mediastinum Ratio

ECToolbox allows calculation of the heart-to-mediastinum ratio for SPECT images of AdreView. To access this tool, there is a button at the bottom of the options buttons on the Parameters page of ECToolbox. Clicking this button sends the AdreView and perfusion planar projection datasets to the H/M Ratio tool. Operating this tool is a matter of defining two locations, the heart and the center of the mediastinum. Follow these steps, working first with the upper row of images:

1. Use the slider control under each projection image to locate the heart. If the heart is difficult to find on the mIBG image, use the perfusion image as a guide.

2. On the top set of projections, position the green lines to encompass the left ventricle, and the red line to pass through the slice mid way between the green lines. For example, if the upper limit line is at row 28 and the lower at row 44, the red line should be at row 36. Transaxial slices will be

reconstructed for all rows between the green lines. The position of the red line determines the transaxial slice that is displayed to the right.

3. On the transaxial slice, position the ellipse to include the heart, without including extracardiac activity. To draw the ellipse:

- Position the cursor in the center of the heart.
- Click and hold the left mouse button, and move toward the ventricular apex. A line will be drawn as the mouse moves. Release the mouse button.
- To change the width of the ellipse, click and hold the right mouse button. As you move the mouse, the minor axis of the ellipse (its width) will change. Release the button when the ellipse includes the entire heart except for the right ventricle. The right ventricle may not always be visible.

Working next with the second row of images to define the mediastinum:

4. Use the left mouse button to position the limit lines for the mediastinum so that the lower green line is no lower than the upper limit for the heart. For example, if the heart extends up to row 28, the mediastinum might extend down to row 27. Note that for the mediastinum, all of the lines move together as you drag with the mouse.

5. On the transaxial image to the right, position the circle so that it is between the lungs and just anterior of the middle of the chest. If the lungs are not well visualized, position the circle just above the center of the body. Lungs should be excluded from the circle as much as possible. The circle's size cannot be changed.

6. Mean count values for the heart and mediastinum, and the value for the ratio of heart to mediastinum, are displayed in boxes to the far right of the screen.

The figure below shows example images with proper placement of limits and ellipses. Keep in mind that these settings detemine a volume for the heart and for the mediastinum, not simply a region of interest on a single image. Thus both the limits and the ellipses are important for obtaining the most meaningful ratio.

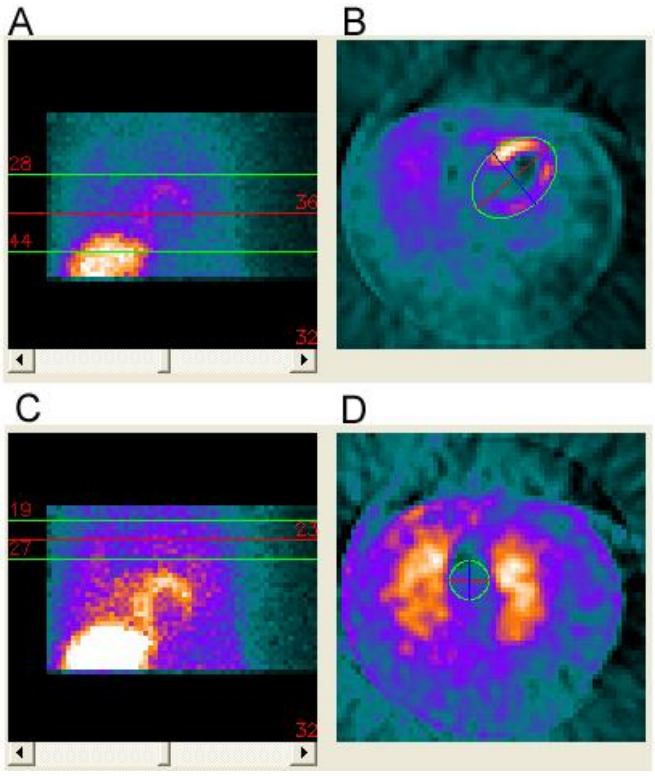


Figure Legend: AdreView projection data (A), and the heart volume more precisely identified on a mid-transaxial slice (B). Mediastinum volume is defined using projections from the perfusion study (C) and a transaxial slice (D).

13 Match / Mismatch

F-18 FDG studies provide a way to assess myocardial glucose metabolism. ECToolbox contains tools for analyzing the relationship between metabolism and perfusion, and for showing matches and mismatches between the two. The primary tool is the Percent Difference Match/Mismatch Page, which shows defect extent on the FDG polar map, and significant mismatch as a white area within the defect. The mismatch area can optionally be defined to include areas outside the defect.

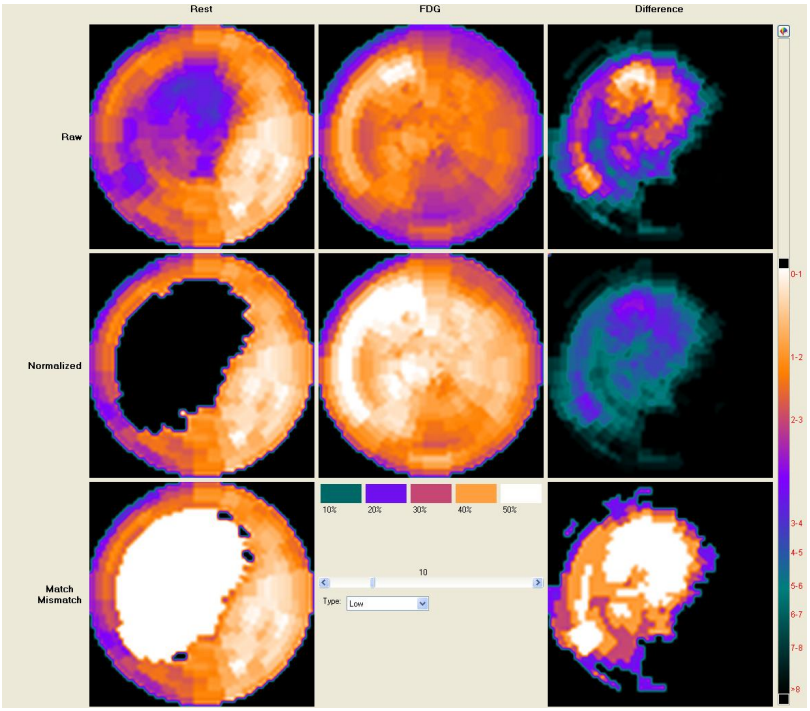
The threshold for what constitutes a defect is also user-selectable.

Segmental scores can be displayed on these polar maps, and are derived from comparing the patient study to a combined perfusion-metabolism normal database. You should select a normal database with the same perfusion component as the patient study (rubidium, 1-day sestamibi, etc.).

13.1 Display

If an FDG image is chosen as one of the studies to be analyzed, you will see among the permanent button set (upper left) a button for the "Match / Mismatch" tool, and there will be no button for "Polar Maps / SSS".

Layout of Polar Maps



The display of match / mismatch polar maps is shown in the figure above. Perfusion is shown in the left column of maps, FDG metabolism in the center column, and the difference between the two is mapped in the right-most column. The maps are as follows:

Top row: shows distance-weighted raw polar maps. All of these polar maps are normalized so that their individual maximums are displayed as white.

Middle row: shows the perfusion study (left) after it has been compared to the appropriate normal database; thus, areas blacked out are those which have abnormal resting perfusion. The middle image is the FDG study, normalized to the perfusion study. The types of normalization are discussed below. The right-most polar map is the percent difference between the normalized FDG and perfusion study.

Bottom row: shows at left the perfusion blackout map again, with areas of significant mismatch flagged in white.

On the rightmost side of the bottom row is a quantized map of percent difference between FDG and perfusion. The colors on this map correspond to percent differences in increments of 10%, as indicated on the color bar in the middle of this row.

How Mismatch is Determined

There is a threshold for determining what degree of difference between perfusion and metabolism constitutes a "mismatch". Abnormal areas of perfusion that are also decreased in metabolism, and therefore show little difference between perfusion and FDG scans, are defined as a match. Areas in the FDG map that are increased as compared to abnormal areas of perfusion, and therefore show a difference above a specific threshold percentage are defined as a mismatch. By default, the application uses 10% as the threshold.

To change the Percent Difference Threshold:

1. Find the horizontal slider control on the bottom of the screen, between polar maps.
2. Using the left mouse button, move the slider to the desired threshold.

The percent difference map on the bottom right is adjusted as the slider moved, so that regions below the threshold are displayed as black. On the left side of the bottom row, the resting perfusion blackout map also changes as the threshold percent difference slider bar moves.

The Type of Mismatch

By default, the application defines a "mismatch" area only within a blacked-out defect on the perfusion map. It is possible to define as "mismatch" all areas that survive the user-set threshold, instead of just those areas that have abnormal resting perfusion. The effect is that all regions that survive the %difference threshold, (namely, all pixels displayed in the lower right hand polar map), to be displayed as white in the lower left hand polar map. See the figure below for an example. The type of mismatch is controlled by the "Type" drop-down list, which has two possible values:

Low - Indicates that only differences which are both 1) above the threshold and 2) in the region of a perfusion abnormality, should be considered mismatches.

ALL - Indicates that all differences above the threshold should be considered mismatches.

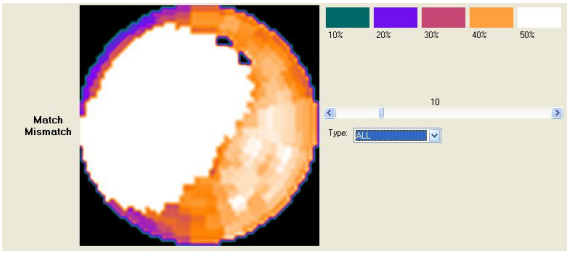


Figure Legend: Mismatch type set to "ALL". Note especially how, in this example, the white mismatch area extends into the infero-septal area, which is outside the blacked-out defect. Compare this to the left lower plot in the figure at the top of this page.

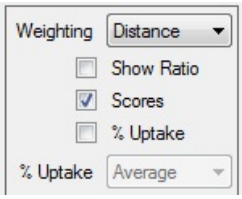
Extent / Mass Display

Selecting the Extent / Mass button displays a screen which shows the size and mass of myocardial areas of match and mismatch between perfusion and metabolism. This screen is similar to the Extent / Mass screen used for standard perfusion quantification. If the mismatch type was set to "Low", only regions above the user-set threshold in the abnormally perfused region of the myocardium will be used to calculate the mass of mismatches.

If the mismatch type is set to "ALL", (meaning all areas of the myocardium above a threshold are being used to define areas of mismatch), then it is no longer meaningful to describe mismatches as % of a given defect. A mismatch may, for example, extend over more than one defect. Thus, these rows in the extent/mass table are marked as N/A, for "not applicable".

13.2 Options

The Match / Mismatch tool has several options.



Weighting - This option determines how the polar maps are constructed. Distance weighting ensures that defect location is most accurate, while volume weighting ensures that defect size is most accurate. For more information, see manual section 8.2 (Polar Maps / SSS Options).

Scores - When selected, this option displays segmental scores over the perfusion, FDG metabolism and difference polar maps. These are derived from comparison of the patient to a combined perfusion-metabolism normal database.

Caution: You should make sure that the selected normal database includes a perfusion component that matches the radiotracer and protocol used in the patient study. For example, rubidium, 1-day sestamibi, tetrofosmin, etc.

% Uptake - When selected, this option displays segmental radiotracer uptake values on the perfusion map. To obtain these values, the global maximum count value is found, and then for each segment, the mean of all pixels in that segment is compared to the maximum and expressed as a percentage.

14 Viability

This screen provides an objective estimate of viability within the left ventricle, by applying a single threshold to the entire LV. The rightmost polar map shows the rest distribution with a particular threshold applied, set by the slider control or dropdown menu below the image. Perfusion defects are numbered on the map. These defect numbers may not correspond to those shown on the Extent/Mass screen. The table characterizes each defect in terms of percent of the total myocardium, or mass in grams.

14.1 Display

This screen (shown below) represents left ventricular viability as estimated from analysis of the rest polar map.

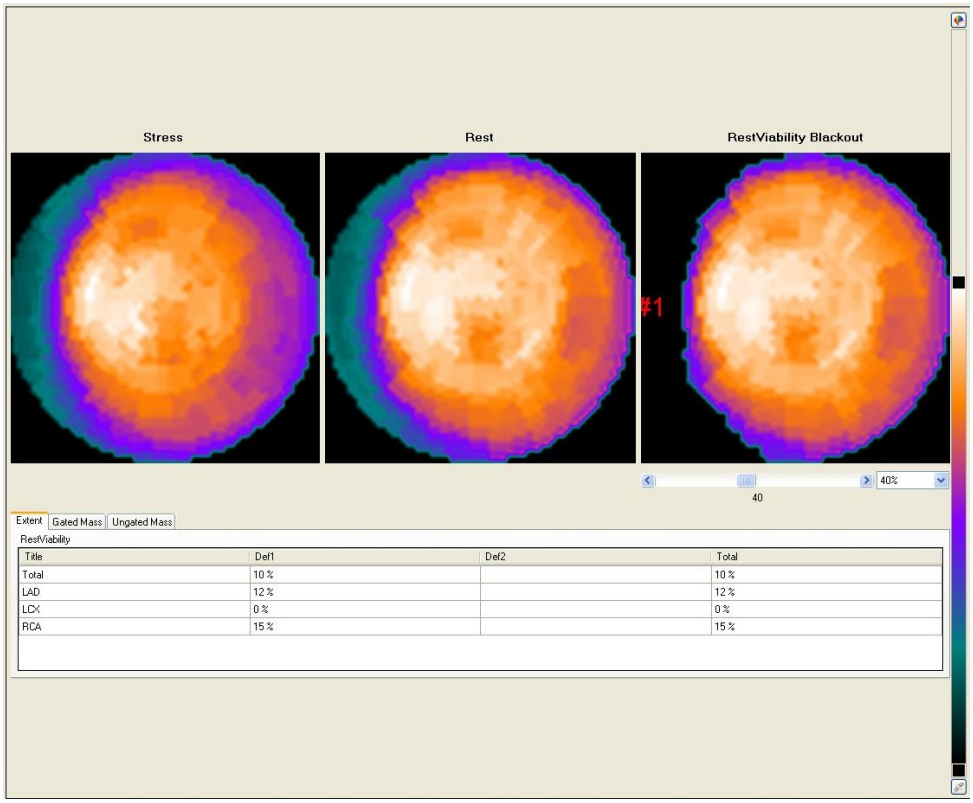


Figure Legend: Non-viable areas are shown as blacked out areas on the rest polar map, which in this example is only the base of the septum. The stress polar map is shown for comparison.

The viability calculation works by setting a threshold below which pixels in the rest map are blacked out. Blackened pixels are assumed to represent non-viable areas. Because there is not universal agreement on the best threshold to use, it is user-selectable, with a default starting threshold of 40%. The threshold can be changed by means of the slider control under the rightmost polar map, or the droplist which allows selection of pre-defined values taken from the nuclear cardiology literature.

TIP: Blacked-out areas that are only at the most basal portion of the polar map may represent normal basal thinning, rather than true non-viability.

The grid of values below the polar maps is similar to that shown on the Extent / Mass display (see manual section 9.1), and expresses viability in terms of extent (percent of area), or mass in grams, derived from either the gated or ungated short axis slices. The application automatically assigns a defect number to each discreet blackout area, up to a maximum of five. If more than five defects exist, the program only displays extent information for the first five. Defects are identified starting at the apex, and moving outward.

Note: The mass values derived in this display are based upon the rest study, and may differ from stress myocardial mass values displayed in the Defect Extent/Mass Display. These differences are attributable to volume changes between stress and rest. Please refer to the Technical Overview Chapter of this manual for further information.

14.2 Options

Options for the Viability page are shown below.



The single option for resting viability is a droplist which allows you to switch between distance-weighting and volume-weighting for the polar map style. Just as for the main Polar Maps display, this option determines how the maps are constructed. Distance weighting ensures that defect location is most accurate, while volume weighting ensures that defect size is most accurate. For more information, see manual section 8.2 (Polar Maps / SSS Options).

15 3D

*Also known as **3DTool**.*

This screen shows 3-dimensional representations of the left ventricular perfusion distribution which can be dragged to new orientations using the left mouse button. The images can be zoomed to larger or smaller size by dragging with the right mouse button. Characteristics of each 3D map include:

- A wire "mesh" that remains stationary in the end diastolic shape when the Animation control's Play button is left-clicked. Animation consists of a cine loop of the gated frames through the cardiac cycle
- A translucent epicardial shell that moves with the cine loop
- A generic coronary artery tree superimposed on the epicardial shell

15.1 Display

Shown below is an example of the 3D display. The shape of the three dimensional LV myocardium is intended to present the actual myocardial shape, as determined by the sampling methodology (described in the section 21.2 of the Technical Overview in this manual.

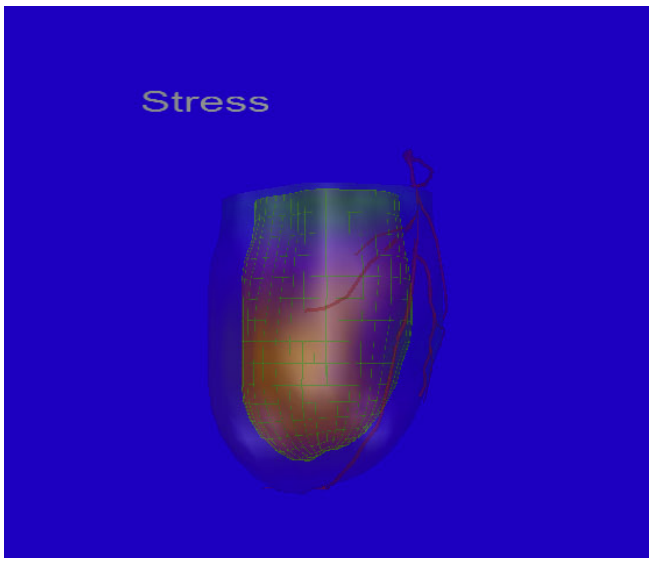


Figure Legend: Interactive 3D display of left ventricular perfusion. The image can be dragged to a different orientation using the mouse.

15.2 Options

Options for the 3D page are shown in the figure below.



Available options are:

Animation - These controls start, stop and adjust the speed of display for sequential frames of the 3D cine images.

Show Frame - when selected, this control displays a labeled box around the LV, which rotates with the 3D model.

Epicardium Opacity - moving this slider makes the epicardial shell more opaque or less opaque. At full opaqueness, you cannot see the inner endocardial model.

Camera Distance - this slider controls the size of the 3D models. For very large hearts, you can increase this value to shrink the models on the screen.

Stress and Rest Surface options - by default, raw perfusion maps are overlaid on the 3D model, however, the type of map can be changed using this slider control. For each epicardial and endocardial shell, the following overlays are available. Not all of these are applicable to all radiotracers:

- Stress
- Rest
- Reversibility

- Blackout
- SD (standard deviation map)
- Colorized
- Defect

- FDG
- FDG Normalized
- FDG Percent Difference

Demo - demonstrates the various options for 3D display, using animations.

In reviewing the 3D display, you may find that different options are needed for optimal perfusion assessment and for the best viewing of wall motion. For example, changing the Epi Opacity significantly changes the appearance of the 3D ventricle, as shown here.

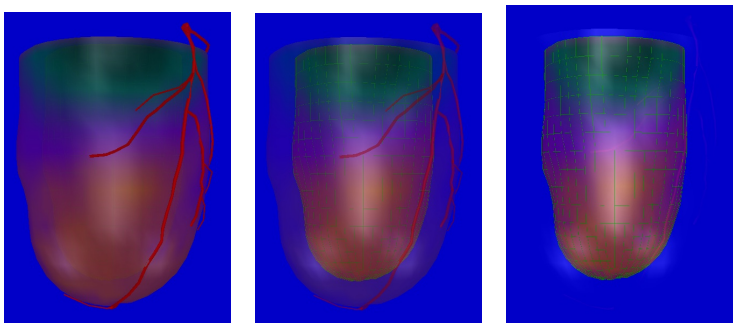


Figure Legend: Epi (epicardial) Opacity set to maximum (left), midrange (center) and minimum (right).

TIP: if you set Epi Opacity to minimum, you may want to enable the LV framework, so that you keep a frame of reference for identifying the myocardial walls.

16 HeartFusion

This tool provides provides a method for fusing a 3-dimensional myocardial map, derived from a PET study, with a 3-dimensional image of a coronary artery tree. Data files expected for HeartFusion include one or two short axis datasets and one or two coronary model files. At least one of the selected short axis datasets must be ungated, but a gated dataset can optionally be selected. For example, if a stress acquisition was done, and a separate stress gated acquisition was done, both can be selected. Model files can be selected for the left coronary arterial tree, the right coronary arterial tree, or both.

Caution: If there are more than one left and right coronary artery model files, be sure to select the ones that correspond to the selected perfusion study.

This tool is integrated into the 3D screen. Use the Arteries drop down menu to select which data should be displayed on the model. The alignment of the arteries will be auto detected. If the alignment needs to be modified, use the Adjust Groove button in the toolbar.

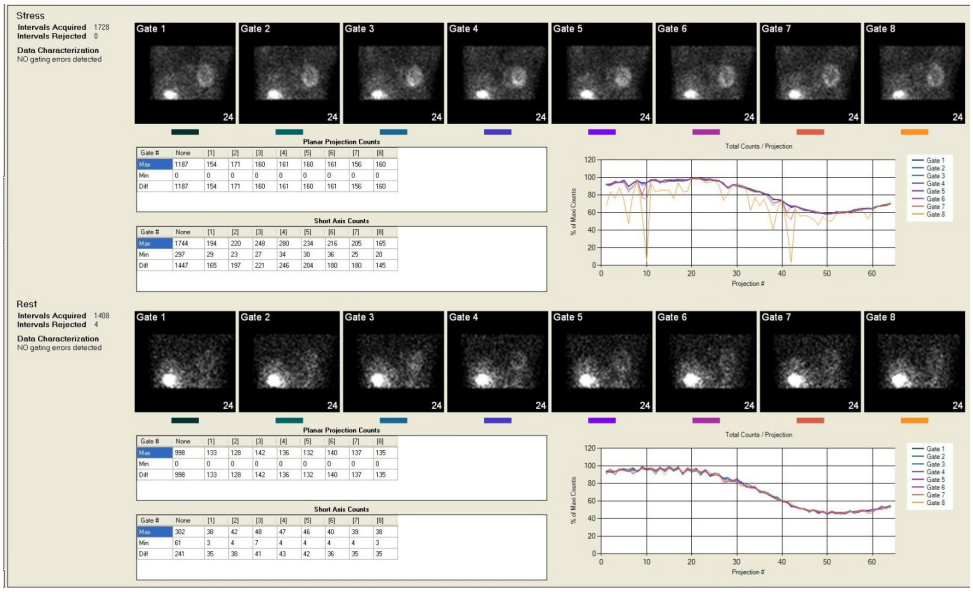
Note: If your version of the application does not appear to have this functionality that could be due to the fact that this feature is not included with a standard license. Please contact the manufacturer to enable this functionality.

17 QC

The ECToolbox application includes a screen which summarizes quality control of the current studies. This includes assessment of image count density and ECG gating. Gated planar data is subjected to gate-by-gate analysis for count consistency. Curve plots of counts per planar projection, color-coded for each gate, are shown. All curves will nearly overlie each other if there are no gating errors. With different kinds of gating problems, such as patient arrhythmia or variable heart rate, one or more of the curves will separate from the others.

17.1 Display

The figure below shows the Quality Control display screen.



Findings for two quality control aspects of each study are summarized on this screen: 1) integrity of ECG-gating, and 2) count density.

Gated QC

The screen displays "Intervals Acquired", referring to the number of heartbeats for which counts were acquired by the camera. Assessment of gated quality control (GQC) is automatic, and the results are displayed on this screen.

GQC works by constructing a time-activity curve for each of the 8 sets of gated projections. The curves are plotted and displayed together, with counts on the y-axis and projection angle on the x-axis. In the normal case, the eight curves should nearly overlie each other, and will have a characteristic sine shape. If there has been a gating problem, one or more of the curves will diverge from the others. The extent of the divergence (along the x-axis) indicates the duration of the problem during camera acquisition, while the magnitude of the divergence (along the y-axis) indicates the severity of the problem.

GQC attempts to differentiate between critical and non-critical gating errors. Consider a set of 8 time-activity curves in which the counts in gate 8 are somewhat decreased. This is not an unusual occurrence in gated SPECT, and it would cause the application to flag the study as having a non-critical gating error. The indicator box would be yellow in this case, because calculation of systolic function and wall thickening should not be affected. As long as the count dropoff is only in gate 8, the application will flag the error as non-critical (yellow box) even if the dropoff appears to be considerable. If counts in gate 8 are extremely low, or if counts from more than one gate are decreased, the box will be red, indicating a more serious error. See the Technical Overview for a discussion of the causes of gating errors, with examples of their different appearance on this screen.

For more serious gating errors, GQC will include suggestions on its report window as to what the source of the error might be, and a statement to indicate the severity of the error.

Count Density QC

For each study, two tables of count values are shown: 1) counts in each gated projection, and in the ungated projection set, and 2) counts in the short axis for each gate, and in the ungated short axis.

TIP: comparing counts in the stress and rest studies is a good way to determine adequate dose delivery, and to assess whether counts in the acquired images reflect the doses administered.

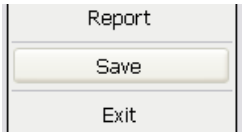
18 Save / Export

Emory Toolbox 4.0 provides the user with convenient methods to both save and export data. The save functionality will store data in its current state for retrieval at a later time. The export functionality allows the user to create screen-captures in a wide variety of formats for use in presentations, sharing with colleagues and/or storage in a 3rd party imaging system such as PACS.

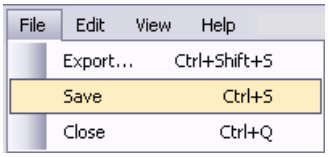
18.1 Options

Save

A study can be saved multiple ways in Emory Toolbox 4.0. The simplest way is to use the **Save** button located in the navigational bar on the left side of the screen as shown in the figure below.

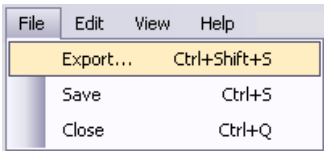


Alternatively, there is a **Save** item available within the **File** menu located at the top of the screen as shown below. This functionality is also available via a keyboard shortcut, CTRL + S.

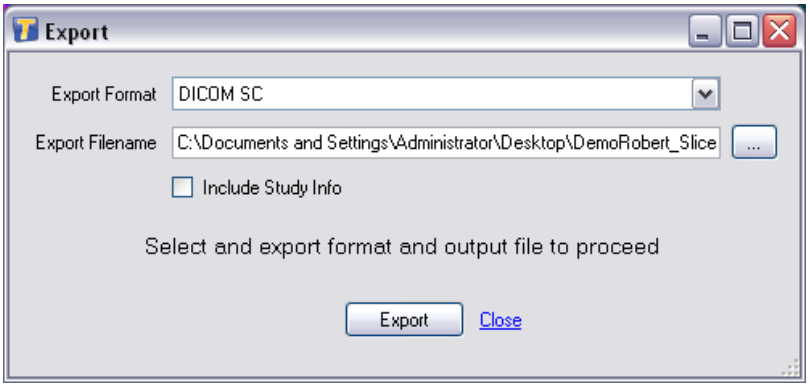


Export

Data from the currently viewed study can be exported in a wide variety of formats by selecting the **Export...** item from the **File** menu located at the top of the screen as shown below. This functionality is also available via a keyboard shortcut, CTRL + SHIFT + S.



By selecting **Export...**, the user will be presented with the dialog shown in the next figure.



The user may choose how to perform the export by setting the following values:

Export Format
The **Export Format** drop down list allows the user to choose on of the following methods for exporting data. By default, the "DICOM SC" format will be selected.

DICOM SC
A single frame DICOM Secondary Capture of the current screen.

BMP
A single frame BMP formatted image of the current screen.

PNG

A single frame PNG formatted image of the current screen.

TIF
A single frame TIF formatted image of the current screen.

JPG
A single frame JPG formatted image of the current screen.

Multi-frame DICOM SC
A multi-frame DICOM Secondary Capture of the current screen. The capture will take place over a single cycle of the longest running animation on the screen.

Animated GIF
An animated GIF image of the current screen. The capture will take place over a single cycle of the longest running animation on the screen.

Legacy XML
The legacy (Emory Cardiac Toolbox 3.x) formatted XML file.

Export Filename
The **Export Filename** text field represents the exact path where the exported file will be saved. The user is free to type a full path manually, or use the **...** button to navigate to a path via a save dialog. By default, the exported file will be saved to the currently logged in user's Desktop.

Include Study Info
The **Include Study Info** checkbox allows the user to decide if patient/study information should be included in the exported image(s).

When all options have been set to the user's satisfaction, pressing the **Export** button will start the process of creating the exported data. *Please note that multi-frame export formats may take a few minutes to complete. When the process is complete, the user will be updated via the status label within the Export dialog.*

Export Default Options
The user can easily modify the default export options within the Options dialog of Emory Toolbox 4.0 as shown:



19 Configuration

From the ECToolbox application's Edit menu, selecting "Options" allows you to change various configuration settings that affect all aspects of ECToolbox operation. There are several tabs in the Configuration window, including:

- **Global** - General options such as which ECToolbox screen is displayed when the application starts.
- **Params / Function / PET** - Change default settings related to the Params and Functional review windows, and for comparing PET and perfusion datasets, such as the color table used.
- **Slices** - Change default settings that apply to the Slices window, such as the image zoom factor.
- **Polar Maps / Viability / Extent** - Change default settings that apply to the Polar Maps screens, such as whether perfusion scores are displayed over the maps.
- **Normal DBs** - Change the default list of normal databases that are available in a list when starting to process a study.
- **Color Table(s)** - Change the list of color tables that are available in a list by clicking the top of the color bar on any application window.
- **Advanced** - Miscellaneous options.

20 IDS

Syntermed's Image Decision Support (IDS) program is a plugin for the 2nd generation application architecture that works directly with Emory Toolbox 4.0. IDS extracts regional quantitative parameters of myocardial perfusion, reversibility, viability and function during the processing of the SPECT and PET studies within the Emory Toolbox 4.0. These regional parameters are converted to probability of abnormality (certainty factors) and submitted to a decision support algorithm that is updated with the latest scientific/clinical knowledge to reach an impression of the patient's heart status. The IDS expert system is comprised of the knowledge base, the inference engine and the justification engine. The knowledge base consists of heuristic rules derived from domain experts. The conclusions reached by the IDS and justifications for each conclusion are used to automatically generate a structured report (SmartReport) for the diagnostician to review, learn from the justifications, and either modify and/or approve.

Types of score display

Scores that have been modified by IDS are displayed with circles around the numbers. Un-modified scores have no circles. By using the mouse to hover over a score, you will briefly see a display which gives the original score, as well as the IDS score. A physician interpreter can manually modify any of the scores by left-clicking the segment and selecting a score from the dropdown list that appears. If this score is different from the default score, it will appear in a square box. To dismiss the droplist without making a selection, move the pointer out of the list and right-click.

Using this scheme, you can always see which scores derive from normal file comparison, from IDS analysis or from manual modification.

Sensitivity Threshold
The sensitivity of the IDS algorithm in registering defects can be set to **Low**, **Medium** or **High** in the "IDS Options" dialog.. By setting this option, IDS will use this sensitivity threshold for every study that is processed. We recognize that the user may want to adjust this value on a per study basis. This will be an option within the SmartReport user interface in the near future.

Disclaimer: *The interpretation provided by IDS is intended to assist a trained physician to analyze nuclear cardiology images. It was not meant to replace or eliminate the standard visual analysis of the gated SPECT & PET study. The physician should integrate all of the patients' clinical and diagnostic information, i.e. patients' history, stress and/or rest EKG, quality control images, visual interpretation of the gated tomographic images, and quantitative and decision support interpretative results, prior to making his final interpretation. The final responsibility for interpretation of the study lies with the physician.*

21 Report

SmartReport is a comprehensive nuclear cardiology reporting program that is powered by a decision support system (Syntermed IDS) as part of the Emory Toolbox v4.0 application. The SmartReport system initially generates an automatic structured report based on the interpretation determined by Syntermed IDS for the patients perfusion, function, and viability. The physician can then either accept or modify the interpretation if necessary. The program is then able to quickly and efficiently generate a nuclear cardiology report of the patient's study.

Options are available to generate a normal or abnormal report either with a few clicks or by using the comprehensive tools provided in SmartReport. User interaction involves selecting and entering comments and phrases from drop down boxes and entering text in edit boxes located within the various SmartReport menu screens. This information is ultimately assimilated to generate the final patient's report. The final report offers flexibility to be modified to an output specified by the user.

For more information, please refer to the SmartReport User Manual.

22 Technical Overview

This section explains the theory of operation for the Emory Cardiac Toolbox application. There are technical details for each step in the preparation of images and the quantitative analysis of myocardial perfusion and function. The steps are:

Automatic Parameter Selection: how center, radius, apex and base are determined

Sampling and Polar Map Creation: extracting counts from the left ventricle

Profiles, Blackout and Standard Deviation: preparing extracted counts for display

Feature Extraction: comparison of a patient study to a reference standard

Automatic Summed Scores: quantitating regional myocardial perfusion

Staggered Summation of Slices: improving image statistics for display

Gated Quality Control (GQC): identifying and characterizing gating errors

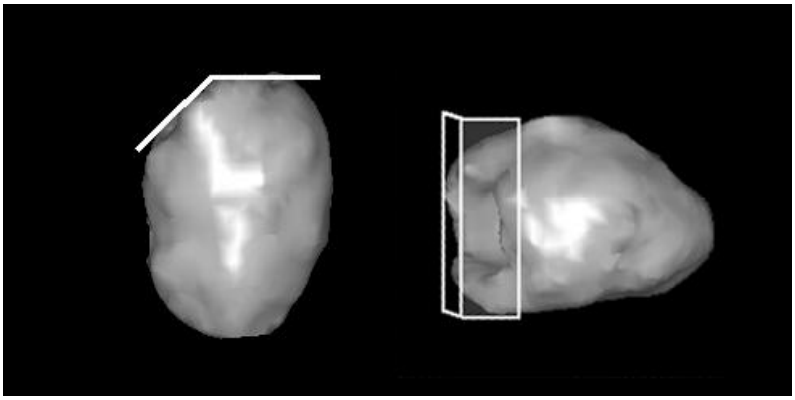
Calculating LV Function: left ventricular function, volume and thickening determination

22.1 Automatic Parameter Selection

There are a few parameters that must be set before quantitation of perfusion, and these are used to specify the location and size of the left ventricle.

When the ECToolbox application begins, these four parameters are identified automatically: the LV long axis center, apex, base, and the radius of a circular region centered about the long axis that encloses the LV in every short axis slice. The apex and base limit the short axis extent of myocardial sampling. The long axis center and radius limit the ranges of perfusion sampling so that the application does not include extraneous "hot" structures in the maximum count profiles.

In addition, the LV valve plane is detected as two connected planes: one perpendicular to the LV long axis in the lateral half of the LV, and one angled plane in the septal half of the LV. The 2-piece valve plane is shown in the figure below.



The four parameters listed above are identified separately for the ungated study and for every frame of a gated study; however, the parameters of each frame of the gated study are constrained to be similar between adjacent frames. All of the automatically selected parameters can be manually overridden by the user if so desired.

After this step, the following parameters are saved:

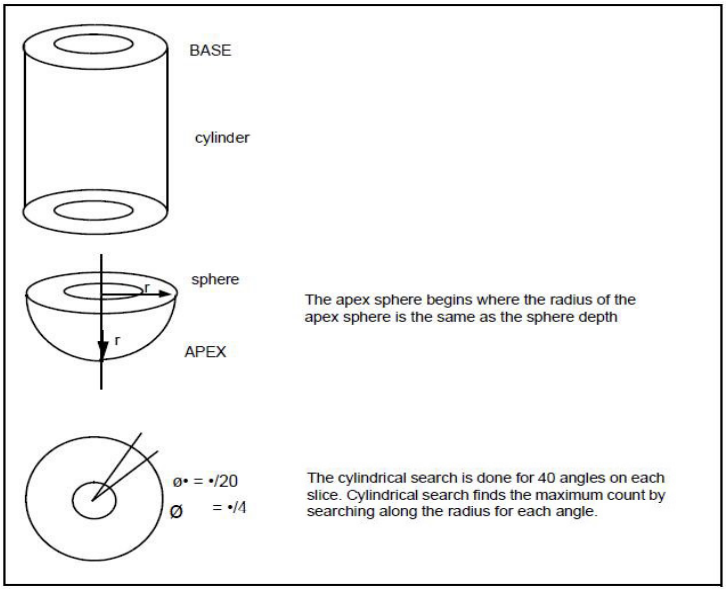
- The apical slice number
- The basal slice number, which is identical to the location of the flat portion of the valve plane
- The angle of the septal valve plane
- The x,y coordinates of the long axis center
- The limiting radius of search for the maximum count circumferential profiles.

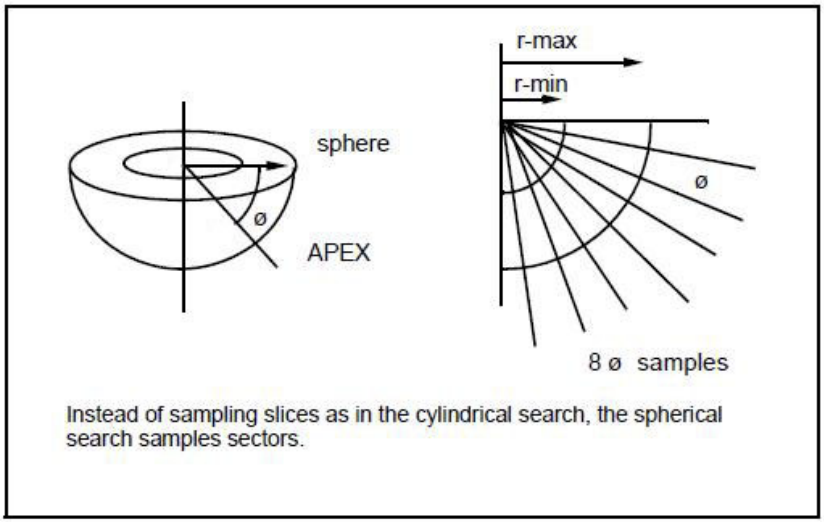
22.2 Sampling and Polar Map Creation

The Sampling Process

Only the short axis oblique images are used to create the maximum count circumferential profiles. The computer uses a hybrid search mechanism to give a true three-dimensional representation of myocardial activity[18].

Apical slices are sampled spherically; while the mid and basal slices are sampled using a cylindrical search, as shown in the two figures below.





In addition to sampling the rest and stress images, this step also creates the reversibility profile.

The computer calculates reversibility by scaling the rest and stress images to a common value and subtracting the stress from the rest. Thus, areas with a defect at stress and no defect at rest will contain a high positive number.

The complete set of sampled pixels comprises a set of profiles, one for each short axis slice. Each profile contains 40 sampled values. If we think of this set of profiles as a "stack", with the apical profile at the top and the most basal profile at the bottom, then we have a rectangular array of values.

Polar Maps

After the calculations are performed, the computer creates the "raw" polar maps by converting the x-y coordinates of every pixel in the rectangular array into polar coordinates, and interpolating the necessary values to display the polar map as a 64x64 image.

These maps represent the actual counts in rest and stress profiles, and the scaled counts in the reversibility profiles. The rest and stress data can also be presented as volume-weighted polar maps.

The volume weighted polar maps compensate for the distortion inherent in a two-dimensional polar plot. The amount of myocardium represented by a pixel sampled near the apex and one sampled near the base is the same. When shown in the standard and distance weighted polar maps, a pixel at the base appears as a much larger space than one at the apex. In other words, a one-pixel area from apex to base presents a pie-shaped object. The volume weighted plot compensates by varying the thickness from apex to base so that the apical slices are thicker, and the basal slices are thinner.

22.3 Profiles, Blackout, Standard Deviation

Comparison to mean normal profiles

Normal values consist of twelve profiles, comprised of 40 points each, representing the mean and standard deviation for each of the three measurements under consideration: stress rest and reversibility.

The first step in this part of the analysis is to convert the values in each of the patient's raw profiles into the number of standard deviations from the mean normal value. Each patient profile is assigned to one normal limit profile for purposes of comparison.

The next step is to determine if each of the patient's sampled pixels are normal or abnormal. At the time the normal file was created, threshold criteria for abnormality were developed for various regions of the myocardium. The thresholds are in standard deviation units, thus each patient pixel can be compared to a specific threshold. If below the threshold, that pixel can be set to black on the polar map.

After each pixel is analyzed, a clustering algorithm is employed to eliminate isolated abnormal pixels. This routine looks at each abnormal pixel and its immediate neighbors. If the neighboring pixels are all normal, then the pixel itself is also called normal.

Blackout and Standard Deviation

Each measurement (stress, rest, reversibility) has a blackout and a standard deviation map created. The blackout indicates the extent and the standard deviation indicates the severity.

The blackout maps for rest and stress contain raw values in pixels determined to be normal, and zeros (represented as Black) for pixels determined to be abnormal. Each pixel in the rest and stress standard deviation polar maps, represents the number of standard deviations below the corresponding pixel in the selected Normal File.

The reversibility maps use the appropriate stress blackout map with points within the blacked-out regions which significantly reverse highlighted in white (the maximum count value in the image).

Caution: The reversibility polar map offers the potential for identifying the presence of filing or reversible defects in the patient's study. However, a word of caution must be made if the map is to be used for this purpose. The ability for the reversibility polar map to detect reversible vs. non-reversible myocardial tissue is difficult to validate since there is currently no acceptable "gold standard" for this phenomenon. The reversibility maps have been optimized based on visual readings of patient studies. Visual analysis comparing the corresponding stress and rest myocardial tomographic territories is still the technique of choice for differentiating reversible vs. non-reversible myocardial tissue. The quantitative reversibility polar maps should only be used to confirm the visual findings of stress and rest perfusion defects or the presence of filling defects from the patient's tomographic images.

22.4 Feature Extraction

Feature extraction is the process of identifying the number of blacked-out defects in a stress study and describing each defect in terms of the total number of standard deviations below the gender-matched mean normal file and the extent of the defect in either myocardial mass or percent of myocardium. The degree of reversibility can also be extracted for each defect and described in terms of the total number of standard deviations above the gender-matched mean normal file and the extent of reversibility in terms of mass or percent of defect that reversed.

Extracted Information Tables

For describing defect/reversibility location, three coronary territories, the LAD, LCX and RCA, as well as total myocardial territory (figure below) can be used.

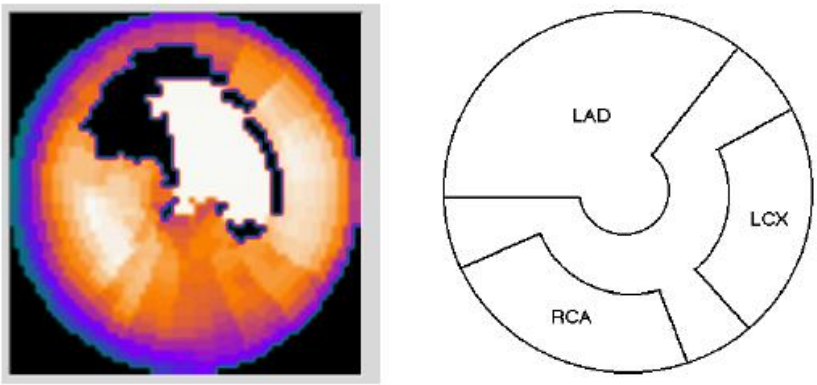


Figure Legend: Polar plot of perfusion with comparison to normal file (left). Coronary territories used in ECToolbox (LAD=left anterior descending artery, LCX = left circumflex artery, RCA=right coronary artery).

The extracted information is stored internally in an array of descriptors, and used to generate a table which contains the extent (in either mass or percent) of each defect, and the reversibility of each defect.

For each defect in the stress and reversibility profiles, the extent is calculated as the percent of the myocardium. For each defect in the stress and reversibility profiles, the severity is calculated as the number of standard deviations above or below the mean.

This information can be displayed in terms of myocardial mass. Please see the following section on computing LV function for details of how volumes and mass are computed. The myocardial volume underneath each blacked out defect is computed, and multiplied by myocardial density. This number is reported in grams and in percent of total myocardial mass for each defect. This calculation can be performed using ungated data when gated images are not available. The same operations are performed for reversed regions. Myocardial volume within a white-out area is computed and multiplied by myocardial density. The mass of each reversed region can be reported as grams, or as percent of the blacked out region associated with the reversibility. Once again, these values can be relative to either gated or ungated volumes and mass.

22.5 Automatic Summed Scores

After automatically quantifying perfusion, the ECToolbox application uses the standard deviation maps to assign perfusion scores to the 17 or 20 segments of the myocardium, using a 5-point scale. The process has several steps.

- A pixel sample is chosen in the middle of the LV chamber.
- This pixel value is translated into the number of standard deviations below the mean for each sampled pixel.

so that…

- Any segment having a sampled pixel with standard deviation below this is scored as 4, since perfusion is considered to be "absent".
- Likewise, the lower limit of normal in standard deviations below the mean is obtained for each sampled pixel in the myocardium.
- Any segment having a sampled pixel whose standard deviation is less than the mean *above* this value is scored as 0, and is considered "normal".
- The remaining standard deviation values used to define scores of 1,2, and 3 are obtained by linear interpolation of the standard deviations assigned to 0 and 4.

22.6 Staggered Summation of Slices

On the Slices screen, the oblique slices are displayed by default with "staggered summation" on. The intrinsic resolution of many SPECT scanners is on the order of 10-12mm, and the pixel resolution of most SPECT studies with a 64x64 acquisition matrix is on the order of 6mm. Executing the staggered summation (output 1 = input 1 + input 2, output 2 = input 2 + input 3, etc.) produces slices of approximately 12mm, close to the intrinsic resolution of the scanner.

This option also improves statistics in individual slices, without changing resolution within the slice. In may cases where there is adequate count density, the visual effect of staggered summation will be subtle.

There is an option to turn off staggered summation.

22.7 Gated Quality Control (GQC)

ECT gating errors can adversely affect perfusion assessment[9,12]. Analysis of curves from raw gated data, performed in a large group of patients chosen at random, has shown gating errors in over 40% of cases[31], so it is not rare to detect some form of arrhythmic influences among myocardial perfusion SPECT data. When optionally displayed, the GQC window shows the following:

- The curves of total counts versus projection, for each gate.

- The results of algorithmic analyses of curves, along with advice as to how to interpret abnormal findings.

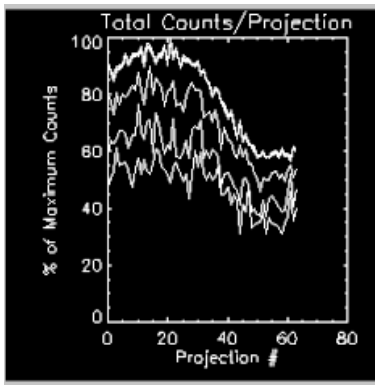
- Cine display of all eight gated tomograms.

For a patient in sinus rhythm, total frame counts for raw data should be identical regardless of the phase of the cardiac cycle, so that ideally all 8 curves of total counts versus projection angles should overlap perfectly. There are several settings in which, because of the patient's heart rhythm, all of the the curves may not overlap. These are listed below, some with example curves.

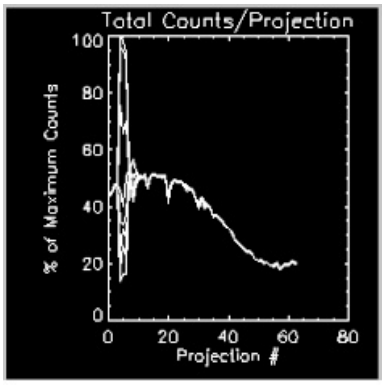
Note: gating errors are often not of any one "pure" type, but are admixtures of the types described here.

- If the heart rate accelerates sufficiently mid-way through the acquisition, counts of a few heart beats are "lost" because they occurred sooner than the preset heartbeat acceptance window[9], and counts of curve #8 will be slightly lower than those of curves #1-7.

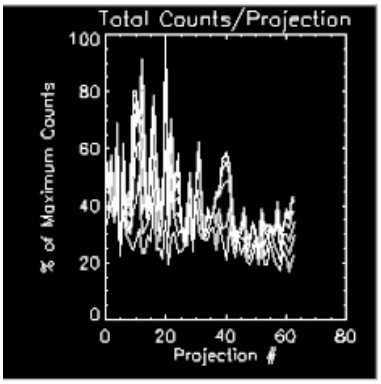
- If heartbeats vary widely all of the time, then during the time required for each projection, some counts are lost in frames 6-8 consistently throughout the entire tomographic acquisition. An example of this condition, referred to in GQC as "consistently variable" heart rate, is shown here:



- During a period of transient tachycardia, or for ectopic beats, total counts are incorrectly shifted into frames 1-3 at the expense of depleting counts in frames 6-8, since the patient's R-R shortens during that time period but not so much that beats are shorter than the preset window. Here is an example of transient tachycardia:



- During atrial fibrillation, sudden shortening of the R-R interval occurs randomly and chaotically, resulting in a drastic departure from the ideal:



Impact of Gating Errors

The primary effect of gating errors is to disrupt the usual linear relationship between myocardial wall thickness and observed counts, which is associated with partial volume effects[12,31]. In ECTb, end diastolic (ED) volumes are estimated primarily from LV shape information, that is, from the location of sampled counts together with assumptions of LV thickness (see manual section 21.8). For gated segments subsequent to ED, calculated volumes depend largely on systolic count change. Thus end systolic volumes are more affected by gating errors than ED volumes. Moreover, ED counts can be incorrectly too high and ES counts incorrectly too low for some arrhythmias, and in atrial fibrillation, it can be impossible to accurately define ED or ES.

Different camera vendors have various mechanisms for dealing with gating errors[9], so that it is conceivable that acquiring data from the same patient with an arrhythmia can produce somewhat different errors, depending on which manufacturer's equipment has been used to acquire the data. Nonetheless, data for any patient should be interpreted with caution if a severe arrhythmic such as chaotic atrial fibrillation is detected.

Patients exhibiting atrial fibrillation should not be acquired gated, but rather as ungated for the accurate analysis of the perfusion information alone. If it is discovered through the use of the Gating Quality Control software that AF has produced erratic, chaotically varying tomographic curves, sufficiently severe as to produce obvious flickering of the cinematic display of summed gated tomograms, then ungated data should be acquired for that patient. Otherwise, it is possible that a false impression of wall thickening would lessen the benefits of incorporating visual assessments of thickening and motion into perfusion observations so as to recognize imaging artifacts[12]. Therefore, gated SPECT data always should be tested for the presence of gating errors, so as to temper the interpretation of visual impressions and of quantified parameters.

22.8 Calculating LV Function

Estimating end diastolic and ungated boundaries

The endocardial and epicardial boundaries of the LV are estimated based on the detected count values and the locations of where each was found. The short axis slice corresponding to the flat base plane is used for the basal limit of perfusion quantification.

To create the anatomically based model of the LV boundaries, the radial lengths describing the location of the quantitated perfusion values are considered to be a 2-D function of the radial sampling angles and the vertical samples (along the long axis). The quantitated intensity values are the points of maximum intensity within the myocardium. These points should occur at the center of the imaged myocardium because of the SPECT point spread function (PSF). For this reason, the myocardial center points are used as a basis to estimate and model endocardial and epicardial boundaries. By making an assumption that the myocardium is approximately 10mm thick at end-diastole, the end diastolic endocardial and epicardial boundary points can be estimated by subtracting and adding 5mm to all radii in the first frame, in order to move the endocardial surface in from the myocardial center and to move the epicardial surface out from the myocardial center. This assumption of a 10mm-thick end diastolic myocardial thickness is well supported in the literature[5,23,34].

Wall Thickening

Wall thickening throughout the cardiac cycle is computed using a Fourier analysis of the size-intensity relationship[7]. Late-frame drop-off is corrected by scaling all samples in the final frame so that their sum is equal to the sum of all sampled counts in the first frame. For each quantitated perfusion sample, a time-intensity curve is created, and its Fourier transform is computed. The phase and amplitude of the first harmonic of the transform is used to calculate percent thickening (with respect to the first, end-diastolic frame) for all frames in the cardiac cycle. This is plotted in the following graph:

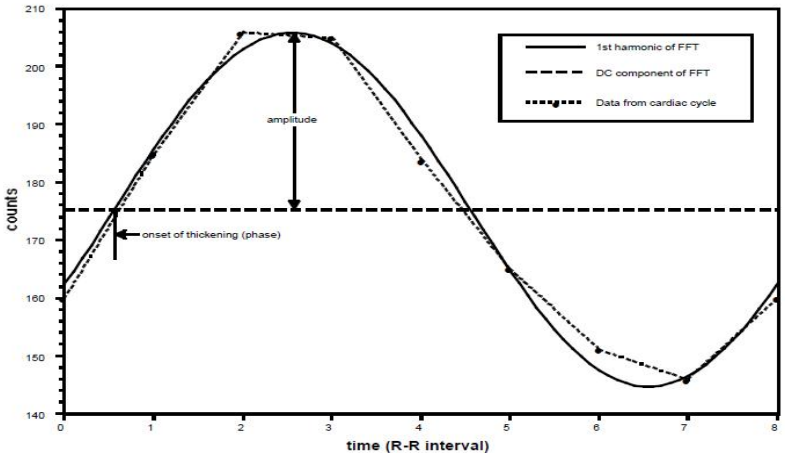


Figure Legend: Phase and amplitude of the first harmonic of the Fourier transform is used to compute Wall Thickening throughout the cardiac cycle.

Estimating boundaries for additional gates

Since the myocardial thickness at end diastole is presumed to be uniformly 10mm, the percent thickening information can be used to approximate "absolute" myocardial thickness at each sampled point in the LV, at every gated frame. Once again, endocardial and epicardial boundary points can be determined by subtracting and adding one-half of the myocardial thickness to the myocardial center, respectively. These operations result in a set of endocardial and epicardial surface points, corresponding to each quantitated perfusion sample, for all frames in the cardiac cycle. The modeling procedure is shown in the following figure.

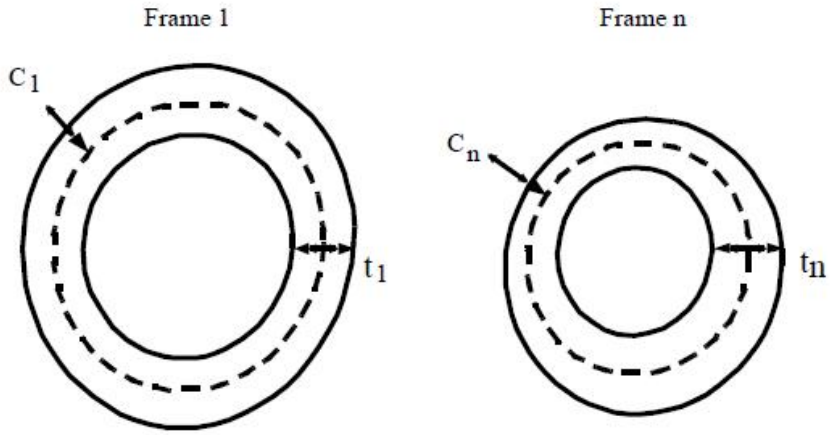


Figure Legend: The modeling procedure provides a set of endocardial and epicardial surface points which correspond to each quantitated perfusion sample, for all frames in the cardiac cycle.

Post processing of the surface points

For each frame, the 2-D function of radii is post-processed using a two-dimensional 7x7 median filter to remove any extreme, incorrect values. Then a 3x3 smoothing filter is applied to create a surface that better approximates the smoothness of the LV surface. Finally, these radii are converted back into the Cartesian coordinate locations of the endocardial and epicardial surface points, which are then connected together into triangles.

The volumes of the resulting polygons associated with endocardial and epicardial surface triangles can be easily computed. Edge points beyond (i.e., more basal than) the angled septal valve plane and their corresponding polygons are excluded from all further LV volume and mass calculations. Following this adjustment, the volume enclosed by the endocardial surface points is the endocardial chamber volume. The difference between epicardial and endocardial volumes is the myocardial volume; myocardial mass was obtained by multiplying the volume by a density of 1.05g/ml. Finally, ejection fraction is calculated using end diastolic and end systolic volumes. Validation of the accuracy of these calculations can be found in reference 14.

The original EF, as calculated by ECTb, is referred to as R0 by the program. This value can be transformed using one of three regression equations, in order to relate it to EF values calculated by other techniques.

One regression equation (R1) is based on a comparison of EF values[14,47] computed using the Emory Cardiac Toolbox (ECTb) with those calculated

with the Cedars Sinai Quantitative Gated SPECT program (QGS) for 8-frame gated data[19]. Thirty subjects underwent both 8-frame gated dual-isotope SPECT imaging and 12-16 frame gated MRI. Endocardial boundaries on short axis MRI were hand-traced by experts blinded to any SPECT results to compute LV volumes, and then EF. QGS and ECTb were used to compute EFs from the gated SPECT images automatically, with no user interaction. Bland-Altman plots demonstrated that the average difference between ECTb and MRI EFs was -0.008; this was not significantly different from 0. The average difference between QGS and MRI EFs was significant, with QGS underestimating MRI values by an average of 0.084. Thus, EFs obtained from ECTb were greater on average, by .076, than those obtained from QGS. ECTb EFs correlated to QGS EFs as: y = 1.05x + 0.055, with r=0.95, SEE (Standard Error of Estimate) = 0.039. In order to provide EFs approximating those from QGS, the Emory Cardiac Toolbox includes a regression equation (R1) to transform the EFs as computed by ECTb into values similar to those that might be computed from QGS, using the inversion of the above equation:

R1: y = 0.96x - 0.053

A similar process was used to obtain the second regression available with the Emory Cardiac Toolbox. In this case, R2 is a regression based on the comparison of ECTb values with multiple gated blood pool (MUGA) EFs. It is well-understood that MUGA ejection fractions may underestimate the actual ejection fraction because of atrial overlap in the planar studies[1]. Twenty-nine subjects underwent both 8-frame gated dual-isotope SPECT imaging and MUGA studies. The EFs computed from ECTb correlated with those determined using MUGA as: y = 0.82x + 0.059, r = .80, SEE = .095. In order to provide an EF comparable to what might be obtained using MUGA methods on the same patient, the inverse of the above regression equation is included to transform ECTb EF values into approximate MUGA EFs:

R2: y = 1.22x - 0.072.

A third regression is available, called "R3" in the program. This is based on a comparison of ECTb values (with 8 gates) with values obtained from QGS performed with 16 gates. To obtain the regression, 99 studies from 50 patients were processed automatically by both programs. For ECTb processing, pre-filtering was enabled. The correlation of EFs from ECTb with those of 16-frame QGS yielded r = .91 and r-squared = .83. The equation to convert 16-frame gated QGS EFs into ECTb EFs is:

R3: y=0.855x + 1.73

The rationale for providing these regressions is to maintain flexibility in the available tools and allow the user to decide how best to apply them clinically in studying their patients. In developing a method for quantifying left ventricular ejection fraction there remains controversy as to what is accepted as the best gold standard for comparison. In ECToolbox validations, high resolution 12-16 frame (in systole) gated MR imaging was used. Although the toolbox approach compares quite favorably with this gold standard, we and others have shown that these results are considerably higher than those obtained from other techniques such as planar blood pool gated acquisition, first pass, and QGS. In order to facilitate comparison to these other techniques we have compared our technique to theirs and the resulting regression equations have been implemented. As we and others perform more correlative studies we will continue to implement the new regressions in a similar manner as we have offered perfusion data bases for differences in protocol.

The decision as to which approach to use is totally at the discretion of the physicians in charge of each laboratory. We suggest that each lab choose one method from among those listed here, and not switch between them.

Ungated LV boundaries and Mass

The boundaries for the ungated study are modeled by using an estimated myocardial wall thickness of 1cm, as described previously. Therefore, each endocardial boundary point is 5mm internal to the sampled perfusion point; each epicardial boundary point is 5mm external to the sampled perfusion point. Because it is truly impossible to find exact ungated edges because of the motion blur, ungated mass based on these edges will not be as accurate as that based on gated studies. Therefore, a conversion factor was determined experimentally to transform an ungated mass into an estimate that better approximated gated mass. Thus, the ungated mass is determined by finding the myocardial volume within a LV wall of thickness = 1cm; this mass is then multiplied by a correction factor.

Transient Ischemic Dilatation Index

The ratio between ungated stress and rest chamber volumes (stress Dilatation Index volume/rest volume) is reported as a TID ratio.

23 Suppported Protocols

In the table below, the normal databases available in the ECToolbox application are listed by "Title", in the same order as they appear in the dropdown list on the Verify window. The Description column gives details of the suggested acquisition and processing parameters for use when handling patient data that is to be compared to each normal database. The column "IDS Optimized" will contain "yes" if the database has been converted for use with the IDS artificial intelligence system. See section 19 of this manual for more on IDS.

Title	SPECT/PET	IDS Optimized	Description
AdreView Deconvolution of Septal Penetration (DSP)	SPECT		tbd
AdreView Filtered Back Projection (FBP)	SPECT		tbd
AdreView Ordered Subset Expectation Maximization (OSEM)	SPECT		tbd
Ammonia	PET		Supine Rest/Stress Ammonia with Rotating Ge-83 Rod Source Attenuation Correction Rest Dose: 20.0 mCi Ammonia Stress Dose: 20.0 mCi Ammonia Acquisition: 128x128 matrix, 3.375 mm pixel size Rest Acquisition: 15 minutes Stress Acquisition: 15 minutes Rest Reconstruction: .3 cycles/pixel Hanning

			Stress Reconstruction: .3 cycles/pixel Hanning
Dual Isotope	SPECT		Same as Optimized Dual Isotope. Different criteria for abnormality
Enhanced Thallium	SPECT		Supine Enhanced Tl-201 Stress Dose: 3.0 mCi Tl-201 Rest Reinjection Dose: 1.5 mCi Rest Tl-201 Redistribution Dose: 0.0 mCi Acquisition: 64x64 matrix, 5.5mm - 6.5mm pixel size Acquisition: LEHR Colimator, 64 projections over 180 degrees, Circular Orbit Stress Acquisition: 20 seconds/projection Rest Reinjection Acquisition: 20 seconds/projection Redistribution Acquisition: 25 seconds/projection Stress Reconstruction: Butterworth filter 0.52 cycles/cm, power factor 5.0 Rest Reinjection Reconstruction: Butterworth filter 0.4 cycles/cm, power factor 10.0 Redistribution Reconstruction: Butterworth filter 0.4 cycles/cm, power factor 10.0
High Dose Rest Sestamibi/FDG	PET		Supine High Dose Rest Tc-99m Sestamibi/FDG Rest Dose: 22.0 - 25.0 mCi Tc-99m Sestamibi FDG Dose: 10.0 mCi FDG Rest Acquisition: 64x64 matrix, 5.5mm - 6.5mm pixel size, LEHR Colimator, 64 projections over 180 degrees, Circular Orbit Rest Acquisition: 20 seconds/projection FDG Acquisition: 128x128 matrix, 3.375 mm pixel size FDG Acquisition: 25 minutes Rest Reconstruction: Butterworth filter 0.52 cycles/cm, power factor 5.0 FDG Reconstruction: .3 cycles/pixel Hanning
High Dose Rest Tetrofosmin/FDG	PET		Supine High Dose Rest Tc-99m Tetrofosmin/FDG Rest Dose: 15.0 - 24.0 mCi Tc-99m Tetrofosmin FDG Dose: 10.0 mCi FDG Rest Acquisition: 64x64 matrix, 5.5mm - 6.5mm pixel size, LEHR Colimator, 64 projections over 180 degrees, Circular Orbit Rest Acquisition: 20 seconds/projection FDG Acquisition: 128x128 matrix, 3.375 mm pixel size FDG Acquisition: 25 minutes Rest Reconstruction: Butterworth filter 0.52 cycles/cm, power factor 5.0 FDG Reconstruction: .3 cycles/pixel Hanning
Low Dose Rest Sestamibi/FDG	PET		Supine Low Dose Rest Tc-99m Sestamibi/FDG Rest Dose: 8.0 - 9.0 mCi Tc-99m Sestamibi FDG Dose: 10.0 mCi FDG Rest Acquisition: 64x64 matrix, 5.5mm - 6.5mm pixel size, LEHR Colimator, 64 projections over 180 degrees, Circular Orbit Rest Acquisition: 25 seconds/projection FDG Acquisition: 128x128 matrix, 3.375 mm pixel size FDG Acquisition: 25 minutes Rest Reconstruction: Butterworth filter 0.4 cycles/cm, power factor 10.0 FDG Reconstruction: .3 cycles/pixel Hanning
Low Dose Rest Sestamibi AC/FDG	PET		Supine Low Dose Rest Tc-99m Sestamibi/FDG Rest Dose: 8.0 - 9.0 mCi Tc-99m Sestamibi FDG Dose: 10.0 mCi FDG Rest Acquisition: 64x64 matrix, 5.5mm - 6.5mm pixel size, LEHR Colimator, 64 projections over 180 degrees, Circular Orbit Rest Acquisition: 25 seconds/projection FDG Acquisition: 128x128 matrix, 3.375 mm pixel size FDG Acquisition: 25 minutes Rest Reconstruction: Butterworth filter 0.4 cycles/cm, power factor 10.0 FDG Reconstruction: .3 cycles/pixel Hanning
Low Dose Rest Tetrofosmin/FDG	PET		Myoview Pharm Stress Protocol? But the manual states the Myoview Pharm Stress is a low-dose stress/high-dose rest?
Myoview Pharmacological Stress	SPECT		Supine 1 Day Tc-99m Myoview Pharmacologic Stress/Rest Stress Dose: 5.0 - 8.0 mCi Tc-99m Myoview Rest Dose: 15.0 - 24.0 mCi Tc-99m Myoview Acquisition: 64x64 matrix, 5.5mm - 6.5mm pixel size Acquisition: LEHR Colimator, 64 projections over 180 degrees, Circular Orbit Stress Acquisition: 25 seconds/projection Rest Acquisition: 20 seconds/projection Stress Reconstruction: Butterworth filter 0.4 cycles/cm, power factor 10.0 Rest Reconstruction: Butterworth filter 0.52 cycles/cm, power factor 5.0
1 Day Rest/Stress Ex Tc99m DNM 530c	SPECT	yes	CZT (G.E. DNM530c) 1 day Non AC Low Dose Rest/Stress 5 mCi rest/20 mCi stress

1 Day Rest/Stress Ex Tc99m DNM 530c AC	SPECT	yes	CZT(G.E. DNM530c) 1 day AC Low Dose Rest/Stress 5 mCi rest/20 mCi stress
1 Day Rest/Stress Ex Tc99m DNM 530c Prone	SPECT	yes	CZT(G.E. DNM530c) Prone 1 day Low Dose Rest/Stress 5 mCi rest/20 mCi stress
1 Day Rest/Stress Exercise Std SPECT Tc-99m	SPECT	yes	Same protocol as 1 Day Mibi. Different patients in normal file
1 Day Rest/Stress Exercise Std SPECT Tc-99m AC	SPECT		Same protocol as 1 Day Mibi. Different patients in normal file
1 Day Rest/Stress Sestamibi	SPECT		Supine 1 Day Tc-99m Sestamibi Rest/Stress Rest Dose: 8.0 - 9.0 mCi Tc-99m Sestamibi Stress Dose: 22.0 - 25.0 mCi Tc-99m Sestamibi Acquisition: 64x64 matrix, 5.5mm - 6.5mm pixel size Acquisition: LEHR Colimator, 64 projections over 180 degrees, Circular Orbit Rest Acquisition: 25 seconds/projection Stress Acquisition: 20 seconds/projection Rest Reconstruction: Butterworth filter 0.4 cycles/cm, power factor 10.0 Stress Reconstruction: Butterworth filter 0.52 cycles/cm, power factor 5.0
1 Day Rest/Stress Sestamibi AC	SPECT		Same protocol as 1 Day Mibi
1 Day Stress/Rest Tetrofosmin	SPECT		Supine 1 Day Tc-99m Tetrofosmin Stress/Rest Stress Dose: 5.0 - 8.0 mCi Tc-99m Tetrofosmin Rest Dose: 15.0 - 24.0 mCi Tc-99m Tetrofosmin Acquisition: 64x64 matrix, 5.5mm - 6.5mm pixel size Acquisition: LEHR Colimator, 64 projections over 180 degrees, Circular Orbit Stress Acquisition: 25 seconds/projection Rest Acquisition: 20 seconds/projection Stress Reconstruction: Butterworth filter 0.4 cycles/cm, power factor 10.0 Rest Reconstruction: Butterworth filter 0.52 cycles/cm, power factor 5.0
1 Day Stress/Rest SPECT Tc-99m Astonish	SPECT	yes	Supine 1 Day Tc-99m Stress-First/Rest <u>Acquisition</u> stress dose: 12.0 - 15.0 mCi Tc-99m rest dose: 30.0 - 33.0 mCi Tc-99m time from injection to imaging: Stress: 30 min, Rest: 30 min or more patient position: supine collimator: LEHR energy window: 140kev, 20% matrix size: 64 pixel size: 6.39mm projections: 64 orbit: 180 time per view: 7 min for small patient 10 min for large gated bins: 8 <u>Reconstruction</u> method: Iterative recon with corrections ("Astonish") filter: Hanning filter units: stress and rest 1 number of subsets: stress and rest: 8 number of iterations: Stress: 4 and rest: 8
1 Day Stress/Rest SPECT Tc-99m Astonish AC	SPECT	yes	Same protocol as 1 Day Stress/Rest SPECT Tc-99m Astonish
Optimized Dual Isotope	SPECT		Supine Optimized Dual Isotope (optimized criteria for abnormality) Rest Dose: 3.0 mCi TI-201 Stress Dose: 25 mCi Tc-99m Sestamibi Acquisition: 64x64 matrix, 5.5mm - 6.5mm pixel size Acquisition: LEHR Colimator, 64 projections over 180 degrees, Circular Orbit Rest Acquisition: 30 seconds/projection Stress Acquisition: 20 seconds/projection Rest Reconstruction: Butterworth filter 0.4 cycles/cm, power factor 10.0 Stress Reconstruction: Butterworth filter 0.52 cycles/cm, power factor 5.0
Rest Ammonia/FDG	PET		Supine Rest Ammonia / F-18 FDG Rest Dose: 20.0 mCi Ammonia FDG Dose: 10.0 mCi FDG Acquisition: 128x128 matrix, 3.375 mm pixel size Rest Acquisition: 15 minute FDG Acquisition: 25 minute Rest Reconstruction: .3 cycles/pixel Hanning FDG Reconstruction: .3 cycles/pixel Hanning
			Supine Rest TI-201/FDG

Rest Enhanced Thallium/FDG	PET		Rest Dose: 1.5 mCi Tl-201 FDG Dose: 10.0 mCi FDG Rest Acquisition: 64x64 matrix, 5.5mm - 6.5mm pixel size, LEHR Colimator, 64 projections over 180 degrees, Circular Orbit Rest Acquisition: 20 seconds/projection FDG Acquisition: 128x128 matrix, 3.375 mm pixel size FDG Acquisition: 25 minutes Rest Reconstruction: Butterworth filter 0.4 cycles/cm, power factor 10.0 FDG Reconstruction: .3 cycles/pixel Hanning
Rest Rubidium CTAC/FDG	PET		Supine Rest Rb-82 with CTAC/ F-18 FDG Rest Dose: 35.0 - 55.0 mCi Rb-82 FDG Dose: 10.0 mCi FDG Acquisition: 128x128 matrix, 3.375 mm pixel size Rest Acquisition: 5.5 minute FDG Acquisition: 25 minute Rest Reconstruction: Gaussian Spatial Filter @ 7 mm FWHM FDG Reconstruction: .3 cycles/pixel Hanning ???
Rest Rubidium/FDG	PET		Supine Rest Rb-82 with Rotating Rod source AC/ F-18 FDG Rest Dose: 35.0 - 55.0 mCi Rb-82 FDG Dose: 10.0 mCi FDG Acquisition: 128x128 matrix, 3.375 mm pixel size Rest Acquisition: 7 minute FDG Acquisition: 25 minute Rest Reconstruction: .3 cycles/pixel Hanning FDG Reconstruction: .3 cycles/pixel Hanning
Rubidium	PET		Supine Rest/Stress Rb-82 with Rotating Ge-83 Rod Source Attenuation Correction Rest Dose: 35.0 - 55.0 mCi Rb-82 Stress Dose: 35.0 - 55.0 mCi Rb-82 Acquisition: 128x128 matrix, 3.375 mm pixel size Rest Acquisition: 7 minute Stress Acquisition: 7 minute Rest Reconstruction: .3 cycles/pixel Hanning Stress Reconstruction: .3 cycles/pixel Hanning
Rubidium CT AC	PET		Supine Rest/Stress Rb-82 with CT Attenuation Correction Rest Dose: 35.0 - 55.0 mCi Rb-82 Stress Dose: 35.0 - 55.0 mCi Rb-82 Acquisition: 128x128 matrix, 3.375 mm pixel size Rest Acquisition: 5.5 minute Stress Acquisition: 5.5 minute Rest Reconstruction: Gaussian Spatial Filter @ 7 mm FWHM Stress Reconstruction: Gaussian Spatial Filter @ 7 mm FWHM
Rubidium CT AC 2013	PET	yes	2013 Rubidium CT AC (1/2 DiCarli, 1/2 Prompt Gamma) Same protocol as original RB-82 CTAC but with different patients in the normal file and newly optimized criteria
2 Day Sestamibi	SPECT		Supine 2 Day Tc-99m Sestamibi Stress/Rest Stress Dose: 22.0 - 25.0 mCi Tc-99m Sestamibi Rest Dose: 22.0 - 25.0 mCi Tc-99m Sestamibi Acquisition: 64x64 matrix, 5.5mm - 6.5mm pixel size Acquisition: LEHR Colimator, 64 projections over 180 degrees, Circular Orbit Stress Acquisition: 20 seconds/projection Rest Acquisition: 20 seconds/projection Stress Reconstruction: Butterworth filter 0.52 cycles/cm, power factor 5.0 Rest Reconstruction: Butterworth filter 0.52 cycles/cm, power factor 5.0
None	None	None	n/a

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