Operating Instructions
The Emory Cardiac Toolbox Application

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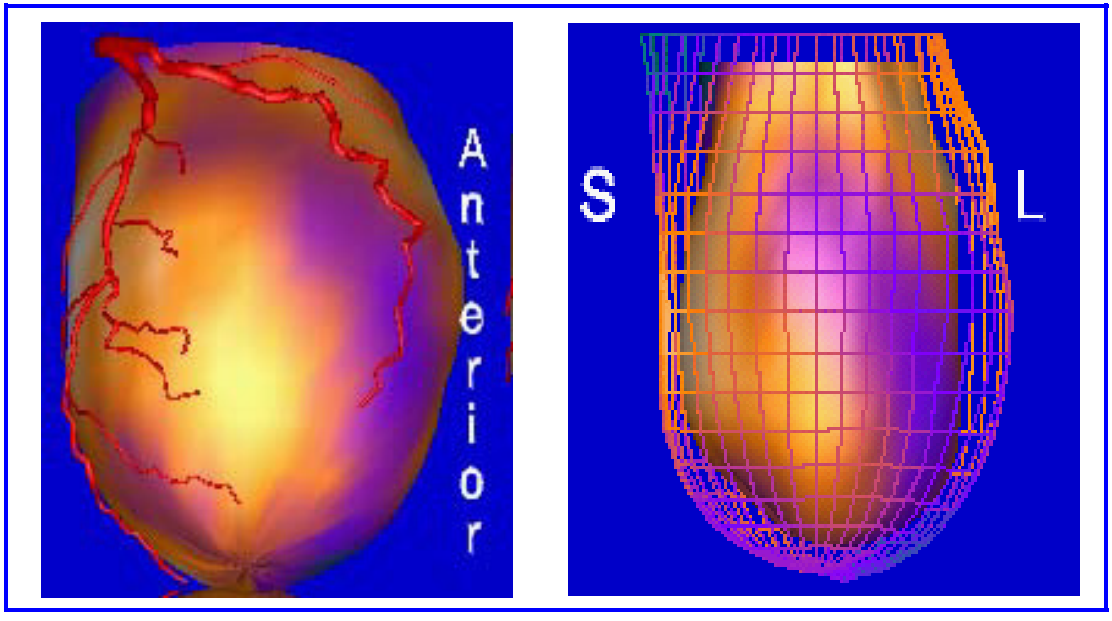
The Emory Cardiac Toolbox™

Version 3.3



Revision 15 (December, 2013)

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Introduction to Emory Cardiac Toolbox

Before You Begin

This chapter contains important information you need to know before using the Emory Cardiac Toolbox™ Application, including warnings, errors, and limitations, as well as information on how to use this manual.

It is assumed that you have a working knowledge of nuclear medicine and are familiar with the operation of your Computer System.

A Minimum of 128MB of RAM is required before installing the Emory Cardiac Toolbox.. Note that this minimum relates only to the ECToolbox application itself.

About the Emory Cardiac Toolbox Application

The Emory Cardiac Toolbox can be used to analyze and display tomographic myocardial images acquired using any of the following SPECT radiotracers: Sestamibi (with or without attenuation correction), Tetrofosmin, Thallium or Dual-Isotope (Tc-99m/Tl-201). In addition, the PET radiotracers Rubidium and Ammonia can also be used, as well as combinations of perfusion and metabolic tracers. See “Selecting Patient, Study and Datasets for Processing” on page 23 of Chapter 2 for a complete list of the protocols supported. Also see Appendix B for details of the recommended acquisition and reconstruction for each protocol.

The Emory Cardiac Toolbox requires both a rest study and a stress study, and provides for the fast and accurate, quantitative analysis of SPECT tomograms of the myocardium.

The Emory Cardiac Toolbox requires minimal operator interaction, and quantifies rest and stress radiopharmaceutical distributions for each of the short-axis myocardial tomograms created with the standard SPECT reconstruction protocol. The program compares the maximum count profiles from each tomogram in both studies to the count distribution values that have been observed in a normal group of patients. The three-dimensional distribution of the radiopharmaceutical (at rest and stress) is then represented as two-dimensional polar maps and three-dimensional PerfSPECTive™ images.

This quantitative methodology offers analysis of: (1) the extent and severity of stress perfusion defects, and also the percent of defect that is reversible; (2) the estimated viability of resting perfusion defects; and (3) myocardial wall motion and estimated wall thickening.

This manual describes the Emory Cardiac Toolbox application, as it has been implemented on your Computer System.

Warnings, Errors, and Limitations of the Emory Cardiac Toolbox Application

Warnings

Warnings display as dialog boxes on the computer monitor screen. If you receive a warning dialog box, you can continue to perform the Emory Cardiac Toolbox application by clicking on the OK button in the dialog box.

If you choose to continue, be aware that your results may be affected. Individual error and alert messages are explained in more detail in the procedural instructions.

Examples of warning dialog boxes that may appear are shown

below:

- The rest and stress studies each have a different patient ID.
- The studies were acquired in a matrix size other than 64 x 64.
- Only one Short Axis (SA) file is selected.
- More than 2 Short Axis (SA) files are selected.

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 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.

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, however, the breast remains a source of artifact, particularly in large-breasted women.

About this Manual

Conventions

Throughout this manual, the following conventions are used to distinguish elements of text:

> **W A R N I N G**
> This is an example of the way warnings will appear in the manual. Warnings are used to alert you to situations that could result in personal injury and/or serious system damage.

Caution: *This is an example of the way cautions will appear in the manual. Cautions are used to alert you to situations that could result in damage to the system hardware or software.*

Note: This is an example of the way notes will appear in the manual. Notes provide additional information about the current process or procedure, as well as parenthetic information regarding operation procedures.

Example: This is an example of how an example appears in the manual. Examples are used to illustrate procedures or concepts.

Underlined text is used to introduce a numbered sequence of steps that the user is to follow.

Bold Text is used for section and sub-section headings. In addition, buttons and menu items that appear in ECToolbox are discussed using their labels--the exact text the user sees--and these are bolded within the text of this manual. For example, several windows have a button to process (or review) a gated study. When it is discussed in the manual, the button is referred to by its name: **Functional Analysis**.

All illustrations in this manual are representative samples only. While your results will be similar in appearance, the data presented will reflect the study you are processing.

Chapter Contents

The chapters in this manual are organized as follows:

- Chapter 1, *Introduction*, provides information about the manual, as well as important information you need to know, before using the Emory

Cardiac Toolbox application.

- Chapter 2, *Opening Studies and Launching the Emory Cardiac Toolbox Application,* provides step-by-step instructions for beginning a processing session.
- Chapter 3, *Using the Emory Cardiac Toolbox Application*, describes all of the processing options and features.
- Chapter 4, *Technical Overview of the Emory Cardiac Toolbox Application*, explains all of the processing options and features.
- Appendix A, *Additional References*
- Appendix B, *Recommended Protocol Parameters*
- Appendix C, *Example Cases*
- Appendix D, *Changing the Default Settings*

About Figures

Throughout this manual, figures are used to illustrate the appearance of review screens and user interface elements such as buttons or lists. The screens that you see in ECToolbox may have blue, gray or tan backgrounds, depending on the Windows settings of the computer on which the software is running. Consequently, the figure background color may not match your particular machine.

Installation Notes for Emory Cardiac Toolbox

When ECToolbox is installed, two example cases are automatically added to the patient database on your nuclear medicine computer system:

- PalRA (ECToolbox Abn Example)
- RamCa (ECToolbox Nml Example)

Selecting Patient Studies and Launching the Emory Cardiac Toolbox Application

About this Chapter

This chapter serves as an introduction to the Emory Cardiac Toolbox application. In this chapter you will learn about:

- Related manuals that accompanied your system.
- Acquisition and processing recommendations.
- Launching the Emory Cardiac Toolbox application.
- Selecting the appropriate patient, studies and datasets.

Before You Begin

Acquisition and Processing Protocols

The Emory Cardiac Toolbox application requires that the acquisition be performed using certain specific parameters. In addition, this application requires reconstructed oblique datasets (Short Axis) for both the rest and stress studies. Appendix B provides recommended acquisition and processing parameters for the various clinical protocols (Dual-Isotope, Tl-201, Tc-99m Sestamibi and Tc-99m Tetrofosmin).

Note: The user must utilize a separate processing application, to reconstruct the transverse and oblique tomographic datasets from the Rest and Stress SPECT projection image datasets.

Caution: *This application is more dependent on technical quality control than a planar imaging protocol. The principal source of false positive studies, is the failure to acquire and process these studies accurately. It is important that the user ensure complete quality control, as described in the manuals that accompanied your nuclear medicine camera system.*

Caution: *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.*

Selecting a Language

Emory Cardiac Toolbox can be used in several different languages. When a language is selected, user interface elements such as button labels and image annotation will appear in the language of choice. Dialogs and error messages will also appear in the selected language.

A language can be selected at any time by using the Preferences button and selecting a different language from a dropdown list (See Appendix D for details). Once a selection has been made, ECToolbox must be re-started for the change to take effect.

Selecting Patient, Study and Datasets for Processing

1. From the Patient Database window, select the patient you will be processing. In order to fully utilize this application, the study should contain 2 Stress Datasets (*Stress SA* and *Stress Projection*), 2 Rest Datasets (*Rest SA* and *Rest Projection*), and up to 2 Gated SA Datasets. However, the only required dataset is: 1 Stress SA or 1 Rest SA dataset.

A perfusion short axis dataset can be selected in combination with an F-18 FDG dataset, for comparison of myocardial perfusion and metabolism. It is strongly recommended that perfusion/metabolism comparisons conform to the following limitations:

1. The FDG data should be acquired using PET.
2. The perfusion data should be reconstructed using iterative methodology and attenuation corrected by a transmission scan-based method.
3. The selected perfusion normal file should have been created from data reconstructed using iterative methodology and attenuation corrected by a transmission scan-based method.

Caution: *Use of non-recommended perfusion-FDG combinations may result in inappropriate comparison of perfusion and metabolism using the Match/Mismatch tool. Perfusion/Metabolism comparison has only been validated for the Rubidium-FDG combination.*

The Study Verification Box

Next, the application displays the *Study Verification* dialog box. This large dialog window is shown in Figure 2-1 through Figure 2-3.

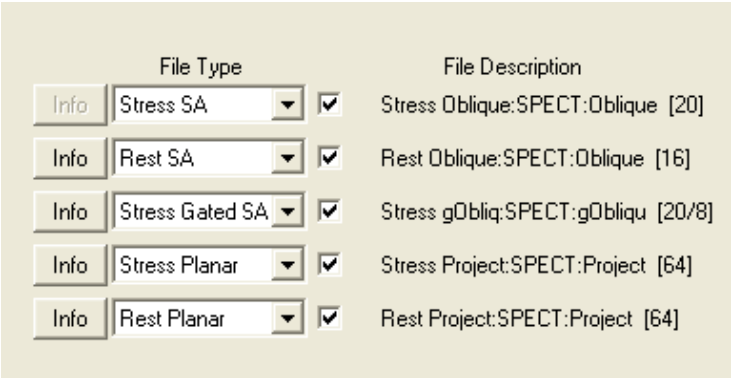


Figure 2-1. The left part of the Study Verification Dialog Box. Note that, under "File Description", the number of images in the file is listed (in this example, the Rest SA has 16 slices). This information can help distinguish one file from another in case the filenames are ambiguous.

The Study Verification dialog shows the list of user-selected files. Those that have a File Type box that is filled in (with "Stress SA" for example) are files which the program was able to identify as valid inputs. The user can examine this list and change the file type by selecting another entry from the drop-down list. Suppose that the software identifies a particular file as Stress SA. If the user is certain that this file is actually the Rest short axis, then "Rest SA" can be selected from the drop-down list, and this will cause the program to use this file as the Rest short axis. Then another file would have to be identified as the Stress short axis. See Figure 2-2.

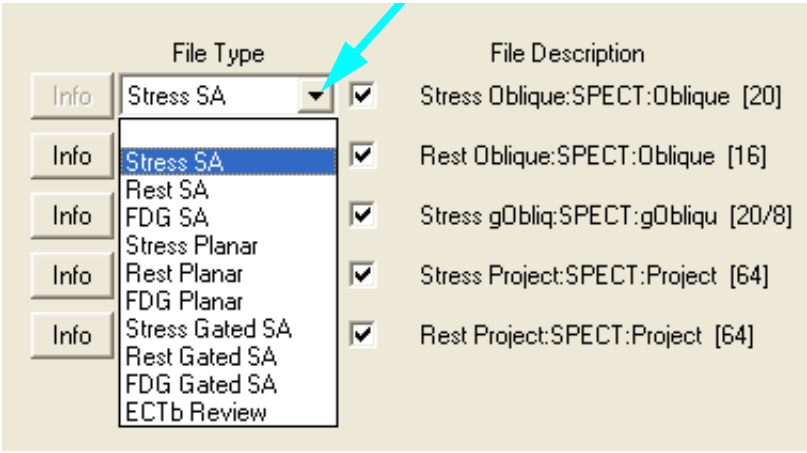


Figure 2-2. A drop-down list of all file types that ECToolbox understands is always available . In this example, the user has clicked the “down arrow” symbol for the Stress SA file (indicated by the blue arrow).

In Figure 2-3, the right-hand portion of the Study Verification dialog is shown. Here, information is given for the currently selected file from the File Type list shown on the left side of the dialog. The selected file is the one whose “Info” button is grayed out (cannot be clicked). To select another file and see its information, click its “Info” button.

The selected images can be 64x64 pixel or 128x128 pixel images. If 128x128 short axis are selected, they will be automatically converted to 64x64 for processing. If 128x128 planars are selected, they willl be displayed on the slice review screen as-is.

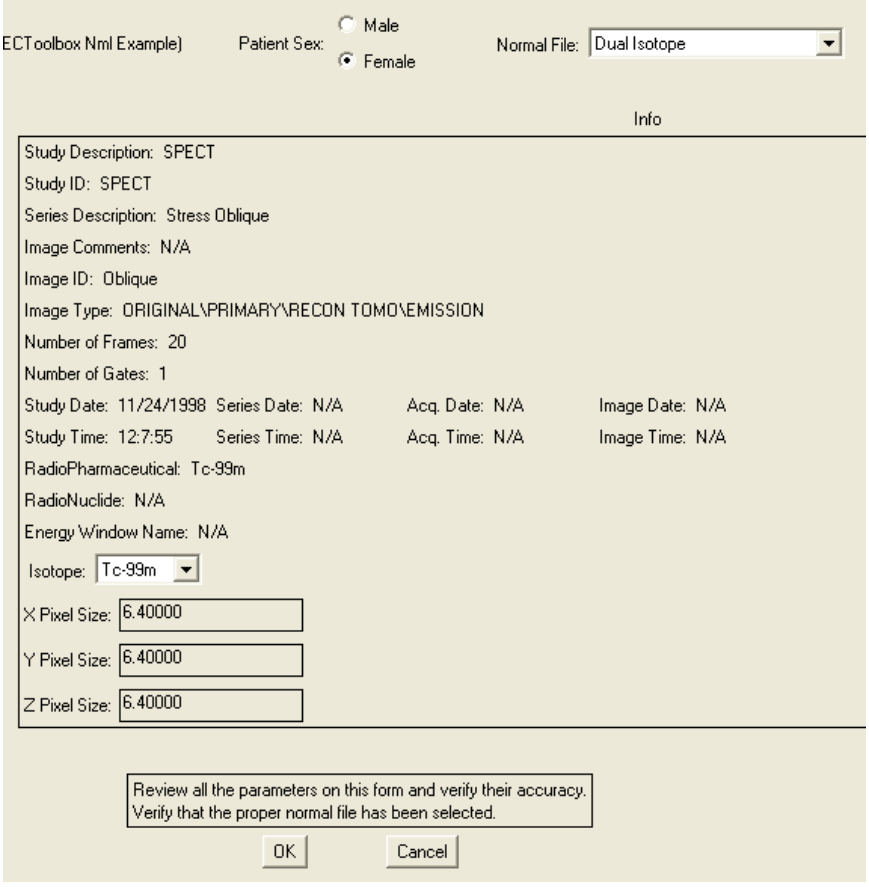


Figure 2-3. The Right-hand portion of the Study Verification dialog.

The appropriate Normal Database files are automatically determined based upon the parameters stored in the selected datasets. The normal file is indicated in the upper right corner of the Study Verification Dialog, as shown in Figure 2-3.

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

The Normal Files listed below are available with the standard installation of ECToolbox. The rest study for each protocol is acquired first unless otherwise noted:

- **Enhanced Thallium** (Applicable to both Stress/Redistribution and Stress/Reinjection protocols.)
- **1 Day Sestamibi**
- **2 Day Sestamibi**
- **Myoview pharm stress (**Tetrofosmin, pharmacologic stress)
- **Optimized Dual-Isotope** (Thallium Rest, Sestamibi Stress)

Depending on your computer system, these normal files may be standard or licensed separately:

- **Standard Dual-Isotope** (Thallium Rest, Sestamibi Stress)
- **Tetrofosmin** (Stress/Rest)

The following additional normal files are available, with the appropriate license:

- **1 Day Sestamibi AC** (with Attenuation Correction)
- **1 Day Sestamibi, adenosine stress**
- **1 Day Sestamibi, adenosine stress, AC** (with Attenuation Correction)
- **Rubidium** (with line source-based Attenuation Correction)
- **Rubidium CTAC** (with CT-based Attenuation Correction)
- **N-13 Ammonia**

In addition, several separately-licensed normal files are available 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. There is no FDG normal database apart from the combination files listed here. Selecting one of these options will activate the Match/Mismatch tool instead of the Polar Maps tool. For details, see the section on “PET FDG/Perfusion Match/ Mismatch Analysis Tools” in Chapter 3.

- **Rest Rubidium/FDG**
- **Rest Ammonia/FDG**
- **Rest Sestamibi** (high dose or low dose)**/FDG**

- **Rest Tetrofosmin** (high dose or low dose)**/FDG**
- **Rest Sestamibi** (low dose, with Attenuation Correction)**/FDG**
- **Rest Enhanced Thallium/FDG**

Note: When selecting resting perfusion and F-18 FDG data that are part of a DISA (Dual Isotope Simultaneous Acquisition) study, for processing in ECToolbox, be sure to use the Study Verification window to select the most appropriate normal file, and to explicitly set the isotope for the FDG study to “F-18”.

User-defined normal files can also be added to the list that is displayed on the Study Verify page. These will appear at the bottom of the list, with “USER:” followed by the name of the file. Up to six such files can appear on the list at one time.

Selecting Series for Review

A review file is saved by ECToolbox when a patient study is processed. This file can be selected at a later time as the sole input for the program. The file contains all data necessary to review the study. It is possible to select more than one review file at a time, and the program will allow all of the patient studies to be reviewed, in sequence.

If more than one patient is selected for review, an additional button will appear on the parameters screen. As shown in Figure 2-4, the button will be labeled with the name of the patient currently being reviewed. When the user clicks this button, a drop-down list appears, showing all the patients whose review files were initially selected (Figure 2-5).

To switch to another patient in review mode:

- highlight one of the names in the list with the mouse cursor
- release the mouse button
- selecting “Quit” from this list will exit ECToolbox

Figure 2-4. When more than one patient is selected for review, the **Quit** button

changes to **Next Pt.** and a new **Review** button appears.

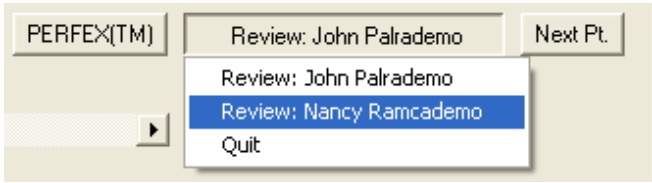


Figure 2-5. User has clicked the **Review** button, producing a list of patients which were selected for sequential review.

The user can also return to a previous patient in the list using this method. Notice that, with multiple patients selected, the **Quit** button has changed to **Next Pt.** To simply advance to the next patient in the list, click this button. When the last patient in the list has been selected, the **Next Pt.** button changes back to **Quit**. Clicking this button now exits the program.

The **Next Pt.** button is available on every ECToolbox screen when multiple review patients are selected. However, the drop-down list of patients is only available on the Parameters Screen.

Using the Emory Cardiac Toolbox Application

About this Chapter

In Chapter 2, you learned how to launch the application and select the appropriate patient studies and datasets. In this chapter, you will learn how to use this application to process rest and stress SPECT studies, specifically:

- Verifying and redefining myocardial boundaries and landmarks.
- Reviewing the various Display and Quantitative tools to evaluate myocardial perfusion and function.

Procedural Overview

The Emory Cardiac Toolbox application runs with little operator input. To process the studies and display the results, the user will perform these steps. Detailed instructions and system responses follow this section.

Quick Steps

1. In the Params Window: Verify the computer-selected LV center for both the rest and stress short-axis (SA) images. If you wish to change either of these: use the mouse cursor to manually select the LV center. Note that the LV Center is defined independently for both the Stress and Rest SA datasets. Correct positioning of the radius and center is necessary, to ensure that only the myocardium is selected and processed.
2. Verify the automatically selected radial search boundaries of the LV epicardium, for both the Stress and Rest Short-axis (SA) datasets. This boundary defines the radius of search used for the formation of myocardial maximum pixel count profiles. If you wish to change either of these: use the slider bars located at the top of the window, to redefine the size of the epicardial boundary. Ensure that the new boundary region encompasses the entire LV myocardium, but excludes non-myocardial activity, i.e. liver and bowel.
3. Verify the LV apex and base as the program defines them. These apical and basal boundaries are shown on both the Stress and Rest Vertical Long-axis and Horizontal Long-axis images. Either boundary

can be changed by using the mouse cursor on the Vertical Long-axis reference images.

Caution: *These boundaries cannot be changed by clicking on the Horizontal Long-axis (HLA) images*.

4. Review the study using the display and analysis tools: **Slices, Polar Maps, PerfSPECTive**, **Functional Analysis** and **Summary Page**.

Processing and Review Sequences

Suggested Processing and Review Sequences for Clinical Protocols

1. **Gated Studies:** For clinical protocols which include either a Gated Stress study (i.e. Gated Stress MIBI) or a Gated Rest Study (i.e. Gated Rest Tetrofosmin), the following processing sequence is suggested for the most efficient use of the ECToolbox:
   a. Params Window
   b. Slices
   c. Polar Maps (Optional: SSS)
   d. Defect Extent / Mass (CEqual™ results)
   e. Functional Analysis: Center & Radius, Apex & Base and Volumes & EF / Cine Slices and Cine 3D.
   f. PerfSPECTive™ / Gated PerfSPECTive
   g. Interactive PerfSPECTive, if a coronary artery tree is available, or a suitable generic tree can be selected.
   h. Return to Polar Maps: Extent / Mass and Estimated Viability
   i. Summary Page

Note: This sequence provides review of the gated data in both Polar Maps and PerfSPECTive, which is only available after the gated processing is performed in Functional Analysis.

2. Non-Gated Studies: For clinical protocols which do not include any Gated Stress studies, the following processing sequence is suggested for efficient use of ECToolbox:
   a. Params Window

b. Slices

c. Polar Maps: Extent / Mass (CEqual™ results), Estimated Viability and SSS (Optional)

d. PerfSPECTive™

e. Summary Page

Note: Functional Analysis is not applicable to non-gated studies.

Using ECToolbox: Permanent Buttons

ECToolbox has a set of buttons that are always displayed on the left side of the screen (Figure 3-6). Since these functions are always available, they will be referred to as the Permanent Button set in the remaining sections of this chapter.

Notice that the buttons are arranged in three columns. The left column's buttons are slightly separated, and their labels are bold. This leftmost sequence of buttons, from top to bottom, reflects the suggested review sequence given in the previous section. The buttons take you to various screens, and you can switch from one screen to another at any time. The function of each button is listed briefly below.

Further details of each screen will be discussed in the remainder of this chapter.

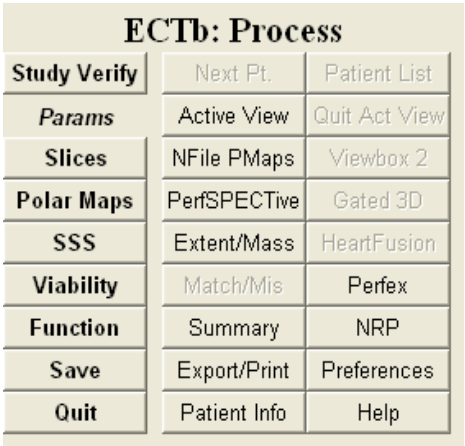


Figure 3-6. Permanent buttons in ECToolbox. In this example, the **Params** button has been selected.

A button has three possible states, indicating whether the option it represents can be selected. This is illustrated in Figure 3-7. The three states are:

- **Available and unselected**. The button label is in black, indicating that it can be selected by clicking with the mouse cursor.
- **Available and selected**. The button loses its border and its label is shown in italics. This is a visual indication that the function has been selected, and that there will be no effect if the button is immediately selected again.
- **Unavailable**. The button label is shown in gray (actually a lighter version of the default color), indicating that the function cannot currently be selected. This state is sometimes referred to as the button being “grayed out”.

Figure 3-7. Part of the Permanent Button set, seen in three different states of the Function button: Available and unselected (A), Selected (B) and Unavailable (C).

Just below the permanent button set is the Patient Info area (Figure 3-8). This block of textual information is filled in as processing proceeds. The user can refer to this area to quickly see calculated values such as left ventricular volumes and perfusion scores, without having to display the image window where these are usually shown.

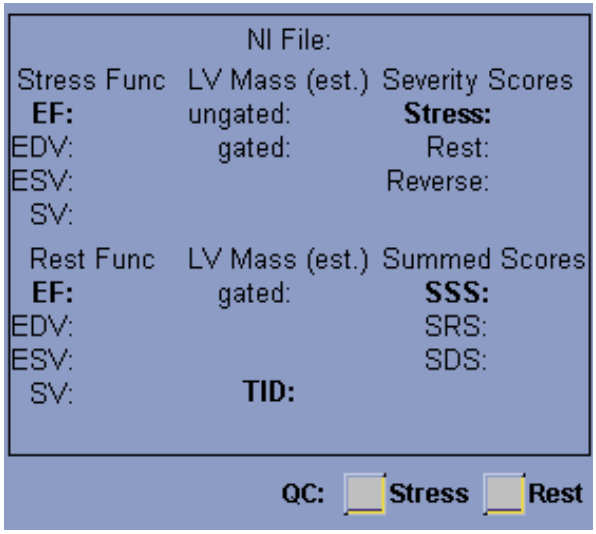


Figure 3-8. The Patient Info area, just below the permanent buttons.

Note: The Patient Info area shows only the *current* values. For example, if a change in parameters occurs, the TID will not be updated until the Slices page has been revisited, because this is where the TID is calculated.

Below this block are two Quality Control (QC) buttons, one for the Stress study and one for the Rest study. Use of these buttons is explained in the section “Gated Quality Control Tool” on page 59.

Buttons to Access the Main Tools

Study Verify: Displays the Study Verification screen.

Params: Displays the parameters screen, for checking ventricular center, radius-of-search, apex and base.

Slices: Displays the slice review screen, which provides the user with various display tools to review the tomographic image slices and rotating Planar projections, in a variety of display formats.

Polar Maps: Displays the polar map screen, with a variety of options for adjusting the various maps.

SSS: Displays stress and rest polar maps with semi-quantitative perfusion scores for 17 or 20 myocardial segments.

Viability: Displays the resting viability screen.

Function: Displays the quantitative functional screen (in review mode) whose information has been derived from the Gated SPECT study (i.e. LVEF, 2D & 3D wall motion cine, estimated wall thickening, etc.). In process mode, this button displays a sequence of screens for setting gated processing parameters.

Save: Saves a review file, after the study has been processed.

Quit: Exits the ECToolbox program.

Buttons to Access Other Tools

PerfSPECTive: Displays a screen of three-dimensional perfusion images, including optional coronary overlays.

Gated 3D: Displays the beating three-dimensional epicardium.

Extent/Mass: Displays a screen showing polar plots with a summary of either defect extent or defect mass in grams. See “Estimated Mass Display” on page 74, and “Extent Display” on page 76.

HeartFusion: Accesses the tool for displaying 3-D myocardial perfusion and patient-specific 3-D coronary artery files (if available), fused into a single display. See “HeartFusion™ Tool” on page 131.

Match/Mismatch Tool: This feature is used in processing perfusion/metabolism studies. See section “PET FDG/Perfusion Match/Mismatch Analysis Tools” on page 120 for details.

PERFEX: This feature provides an Expert System-based automatic interpretation of the perfusion pattern seen on the polar plots. See section “PERFEX™” on page 85 for details.

Summary: Displays a single display window to review key study results, including Rest and Stress Polar Maps, % Thickening Polar Map, ED and ES Volumes, LV Ejection Fraction, Oblique Slice images, Summed Stress Scores and Probability of Survival Data.

NRP: Activates Nuclear Report Professional, an application for structured reporting and databasing of the study. NRP has a separate user manual, which should be consulted for its many features.

Buttons to Aid Study Review

The following options are related to the review of processed studies.

Next Pt.: *not yet implemented*

Patient List: *not yet implemented*

Active View: Displays several ECToolbox screens together in dynamic Viewbox format. The Viewbox concept is discussed more fully in “Using the Viewbox to Review Studies” on page 148.

Quit Act View: Returns from the Active Viewbox to the standard ECToolbox display.

NFile PMaps: Displays polar maps representing the mean normal perfusion distribution for the currently selected normal file, as well as the polar maps of the current patient. When this option is selected, two additional buttons are displayed, as shown in Figure 3-9.

- **Export To Emory Normal Database Generator** - writes a file to disk containing information about the current study which can be used by the Emory Normal Database Generator program (ENDG). This should only be selected if the current study has been

completely processed.

- **Launch Emory Normal Database Generator**, runs the ENDG program itself, which allows the user to build, display and manipulate normal files. A user-created normal database can be added to ECToolbox using the Preferences editor, as explained in Appendix D.

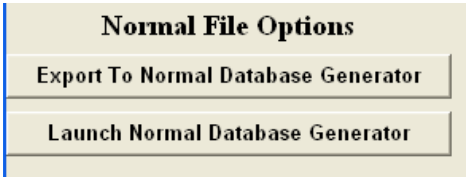


Figure 3-9. Normal file related options, available when **NFile PMaps** is selected.

Viewbox 2: *not yet implemented*

Additional Buttons

Export/Print: Presents several options for saving screens or movies. See “Saving Screens and Movies” on page 154.

Preferences: Displays a screen of options for changing the default behavior of ECToolbox. This option is explained in detail in Appendix D, “Defaults”.

Patient Info: Moves the patient information block onto the Active Viewbox screen.

Help: Displays this User Manual on the screen, in pdf format This function is sensitive to context. For example, if the Slices screen is currently displayed when **Help** is selected, the pdf manual file will automatically open to the section that deals with the Slices screen.

The Parameters Window

The Parameters (“Params”) Window is shown below, in Figure 3-10. This is normally the first window that would be selected when processing a study in ECToolbox. It is also the first window that is displayed when reviewing a saved study, although the user can change this behavior (see Appendix D for information on setting default options).

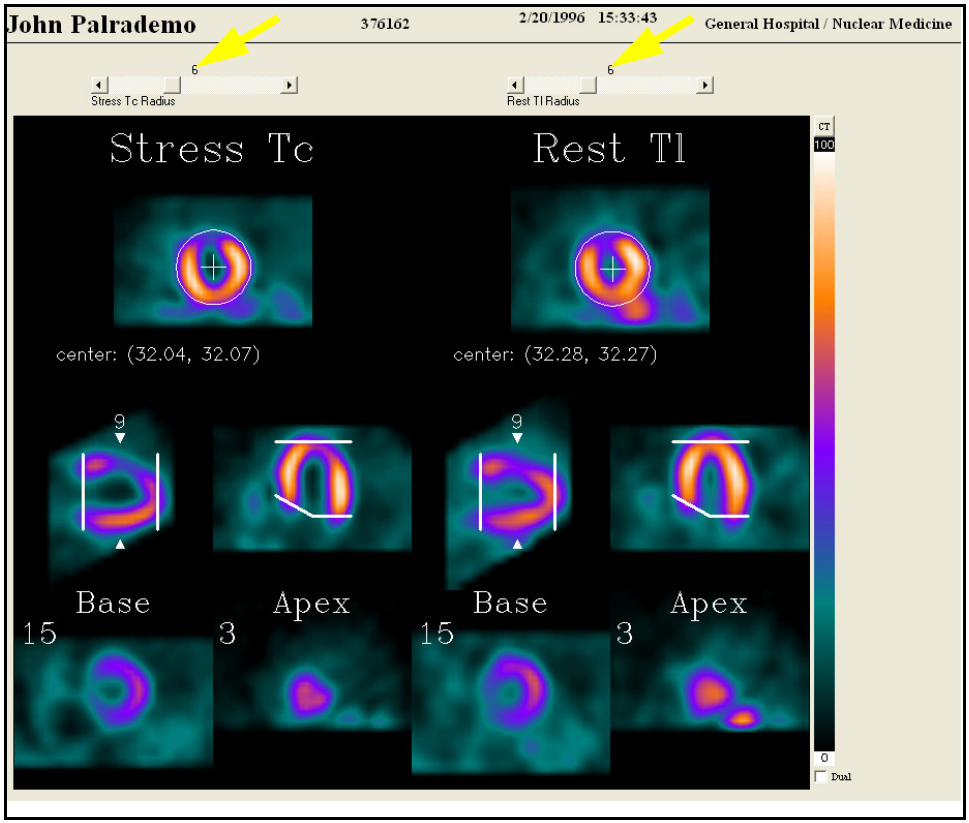


Figure 3-10. The Params Window. Arrows indicate the slider controls used to change the radius of search.

The main purpose of this window is to allow the user to review the program's automatic selection of quantitative parameters, and to allow these parameters to be manually reset if necessary. These parameters are: stress ventricular center, radius, apex and base, and rest ventricular center, radius, apex and base.

Setting Quantitative Parameters

The parameters that are selected are used for quantitative perfusion analysis. We will now discuss how and why this is done. The case illustrated in Figure 3-10 is a typical Dual-Isotope study (Stress Tc / Rest Tl). Note that the left side of the window displays images related to the Stress Study and the right side of the window displays images related to the Rest Study.

The top row shows mid-ventricular short-axis slice images. These are used to illustrate the location of the radial-search boundaries and LV Center. The middle row shows both mid-ventricular vertical and horizontal long-axis slice images. Note that the vertical long-axis slices (VLA) are oriented with the ventricular apex pointed to the right and that the horizontal long-axis slices (HLA) are oriented with the ventricular apex pointed up. The VLA and HLA reference images are used to illustrate the placement of the apical and basal slice selections. The bottom row displays short axis slices which correspond to the apical and basal slice selections identified in the middle row.

Caution: *If the user fails to notice that the program has automatically selected incorrect parameters or if the user manually selects incorrect parameters, then erroneous quantitative results will be generated.*

Changing the LV Center

After close inspection of the automatically defined LV Center for both the Stress and Rest dataset, the user has the option of changing this Center for either one or both reference SA slices. The user may change either of these by using the mouse cursor to manually select the new LV center. Note that the LV Center is defined independently for both the Stress and Rest SA datasets. Also note that the radial search boundary is tied to the LV Center. Changing the LV Center selection causes the radial search boundary to move with the LV Center. As illustrated below, 2 triangular markers on the VLA reference slice identify the location of the displayed SA slice.

Changing the Reference SA Slice

This reference SA slice can be changed by clicking the middle mouse button (or using the CONTROL key with the left mouse button) while the cursor is positioned on the VLA slice. Clicking just to the right of the triangular markers will select a more apical SA slice. Clicking just to the left of the triangular markers will select a more basal SA slice. Examining this LV Center in relation to several different SA slices may be helpful to ensure the most appropriate LV Center selection.

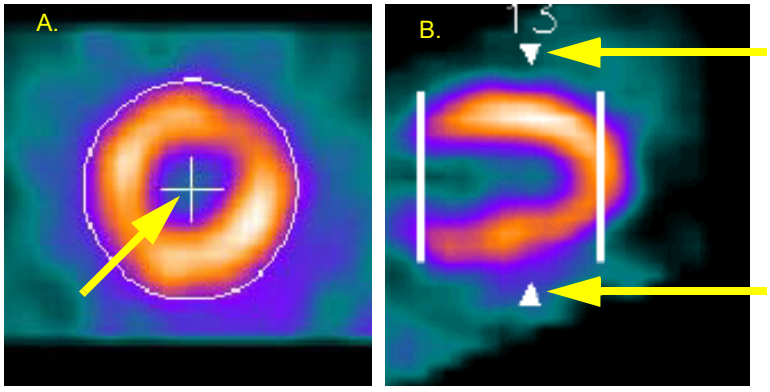


Figure 3-11. In image A., the arrow identifies the LV Center Cursor. Use the mouse pointer to relocate this Center as appropriate. In image B., The 2 arrows each identify small triangular markers on the VLA Reference slice. These 2 markers show the location of the SA Reference slice. Note that the reference lines for the apical and basal boundaries will vary in length, corresponding to the size of the circular Radial Search Boundary.

Changing the Radial Search Boundary

Verify the automatically-defined circular boundaries which define the limits of the LV epicardium, on both the Stress and Rest short-axis (SA) reference slices. This boundary, also called the “radius of search”, is used for the formation of myocardial maximum count profiles. The computer will not search outside this boundary when sampling pixels in the myocardium. The user may change either of these circles by using the slider controls located at the top of the window, to redefine the size of the boundary. The sliders are shown in Figure 3-10. Using the mouse to click on the left side of the slider causes the boundary to decrease in size. Using the mouse to click on the right side of the slider causes the boundary to increase in size. Ensure that the new boundary region encompasses the entire LV

myocardium but excludes non-myocardial activity, i.e. liver and bowel. Note that as this circle is made larger or smaller, the reference lines on both the VLA and HLA reference slices become correspondingly longer or shorter, indicating the extent of pixel sampling.

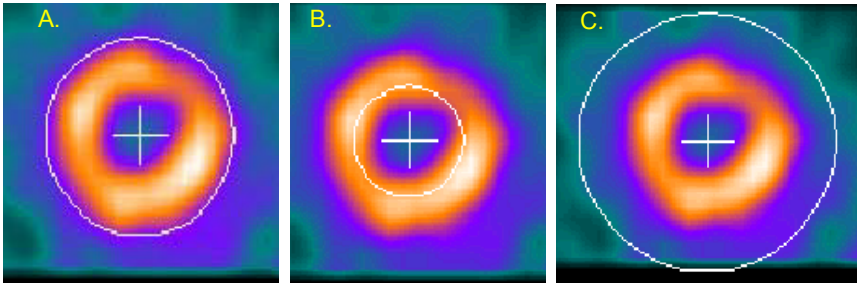


Figure 3-12. Image A shows a correctly defined LV Center and radial search boundary. Image B demonstrates a radial search boundary which is too small, thus missing the maximum count pixels in the myocardium. Image C demonstrates a radial search boundary which is too large.

Changing the Apical and Basal Boundaries

Inspect the LV **apex and base** as automatically defined by the program. These apical and basal boundaries are shown on both the Stress and Rest VLA and HLA reference slices, in the middle row of images on the Main Display Window. To change either or both of these boundaries, the user must click the mouse cursor on the VLA reference image.

Note: These boundaries cannot be changed by clicking on the HLA reference image.

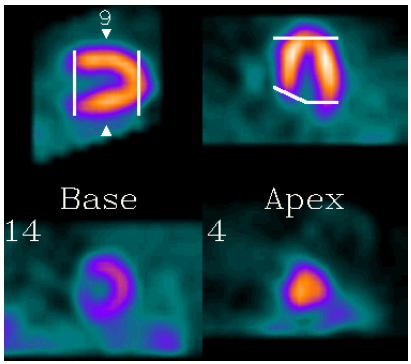


Figure 3-13. This example demonstrates properly defined apical and basal slices. Apex: Note the presence of a clearly defined apical "button". Base: Generally, this is the last slice that clearly shows LV myocardial uptake.

Changing the Apical Slice

To change the apical slice selection for either the Rest or Stress study:

1. Find the Vertical Long Axis (VLA) image for that study, in the middle row on the Main Display Window. Recall that images for the Stress study are displayed on the left hand side of the Window and images for the Rest study are displayed on the right hand side of the Window.
2. Place the mouse pointer near the boundary that you wish to change. For example, to move the apical boundary out, place the cursor to the right of the predefined apical boundary line.
3. Click the mouse button and observe that the boundary closest to the cursor moves in the direction of the cursor, to the point selected by the cursor.

Note: This is not a "drag and drop" operation.

4. Manually adjust the apical slice selections until satisfied.

Changing the Basal Slice

To change the basal slice selection for either the Rest or Stress study:

1. Find the Vertical Long Axis (VLA) image for that study, in the middle row of images on the Main Display Window.

2. Place the mouse pointer (cursor) near the boundary that you wish to change. For example, to move the basal boundary in toward the LV, place the cursor to the right of the predefined basal boundary line.
3. Click the mouse button and observe that the boundary closest to the cursor moves in the direction of the cursor, to the point selected by the cursor.

Note: This is not a “drag and drop” operation.

4. Manually adjust the basal slice selections until satisfied.

Some General Rules

1. A properly defined Apical boundary typically presents a clearly defined apical “button”. This is usually the slice where the apical boundary marker is halfway between the endocardium and epicardium of the apical wall. Please note, however, that this pattern may not be seen when apical perfusion defects are present.
2. A properly defined Basal boundary is the last slice which clearly demonstrates LV myocardial uptake. Note that in typical cases, as the SA slices progress toward the base, tracer uptake in the septal wall tends to disappear before uptake in the lateral wall. Therefore, the typical “donut” shape of the SA slices is usually not observed in the last 1 or 2 basal slices.

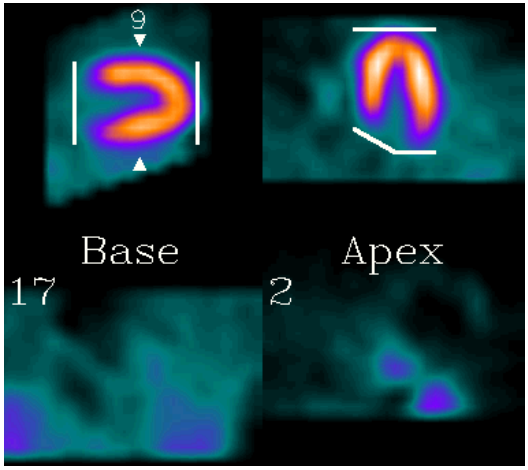


Figure 3-14. This example demonstrates both apical and basal boundaries which are too far from the myocardium. Note that both reference myocardial SA slice images show an absence of any myocardial uptake.

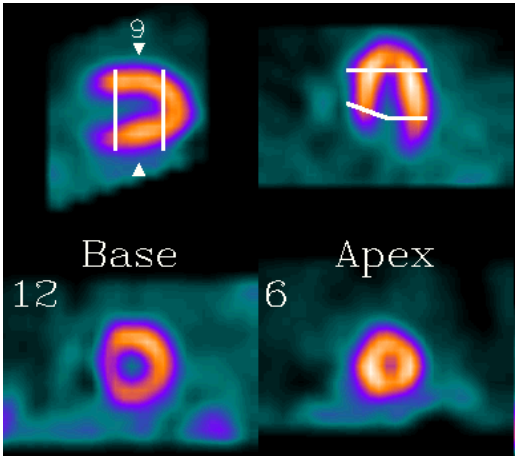


Figure 3-15. This example demonstrates both apical and basal boundaries which are too far *into* the myocardium. Note that the SA slice image for the apex shows the typical “donut” which is normally associated with a mid-ventricular slice.

Params Window Options

When the params window is displayed, an additional set of buttons is displayed in the lower left of the screen, as shown in Figure 3-16.

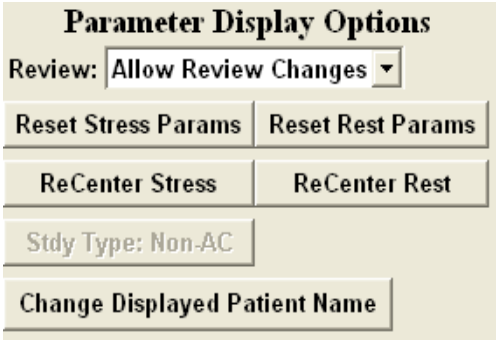


Figure 3-16. Options for the Params Window.

These buttons provide the following options:

- **Allow Review Changes:** Allows the user to select either *Allow Review Changes* or *No Review Changes*. When *Allow Review Changes* is selected, processing may be modified during study review.
- **Reset Stress Parameters:** Restores the Stress parameters to their original values.
- **Reset Rest Parameters:** Restores the Rest parameters to their original values.
- **ReCenter Stress:** This item will cause the stress short axis image to be centered using the current crosshair cursor position, and will re-normalize the imageusing the value of this new center pixel.
- **ReCenter Rest:** This item will cause the rest short axis image to be centered using the current crosshair cursor position, and will re-normalize the image using the value of this new center pixel.
- **Stdy Type: Non-AC**: Allows the user to switch between AC (attenuation-corrected) and non-AC images. Parameters can be adjusted independently for AC and non-AC.
- **Change Displayed Patient Name:** This item will allow the user to modify the Patient Name as displayed in ECToolbox. This does not

change the file names in the patient database.

Color Table Tools

The user has control over the image display to a large extent in the Emory Cardiac Toolbox program. There is a colorbar displayed to the right of all image windows, which indicates the range of colors or shades of gray available in the current color table. By default, images are initially displayed using the entire range of the color table, that is, from zero to 100% of the maximum value. To change the image intensity, use the mouse to click and hold on either the **0** button at the bottom of the colorbar, or the **100** button at the top of the colorbar, and drag it up or down. The image intensity will change as you drag.

Dragging the upper window level down increases image brightness, while dragging the lower window level up increases image contrast.

To change the color table on any screen:

1. Using the mouse, click on the **CM** button, at the top of the colorbar. a list of available color maps will appear. Click the desired color map.

Figure 3-17. An enlarged view of the top of the colorbar which appears to the right of all image windows in ECToolbox. A different Color Map can be selected by clicking the **CM** button.

Normally, all images are displayed so that the maximum pixel value corresonds to 100% of the brightness of the display, hence the label “100” at the top of the window level slider. This can be changed if necessary.

Below the CM button is another button, labeled with an arrow. The arrow is meant to indicate that the maximum window display value can be increased. Clicking this button resets the window maximum so that 50% of the brightness range is above this value. The slider bar will then appear as

in Figure 3-19A. Notice that the button label is now a downward arrow. Once this is done, there are two changes you can make to the window level setting, and each will change the image brightness in a different way.

- Moving the slider up now makes the images less bright. The display maximum value, which starts as 100, will increase as the slider moves up. Depending on the color map that is loaded, text may also change color. Clicking the down arrow button will reset the window to 100%, and the original image brightness setting will be restored.
- Moving the slider down makes the images brighter, which is reflected in the 100 label changing to smaller numbers as the slider moves down. To reset the display to the original brightness level, move the slider to the top (or to exactly 100), and click the arrow button.

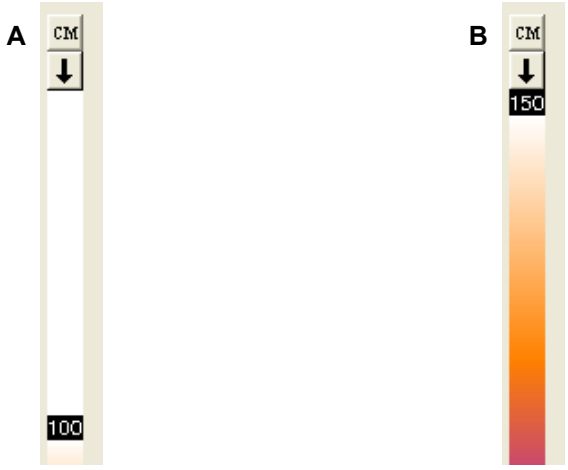


Figure 3-18. Optional controls on the colorbar *after* clicking the up arrow button (below “CM”). In **A** above, the window maximum has just been rescaled. Note that “100” is now below the available maximum. Dragging the 100 upward makes the images less bright. In **B**, the window maximum has been moved to the top of the scale. This reduces image brightness as much as possible.

On certain screens in ECToolbox, it is useful to be able to control the display intensity of two sets of images separately. There is a control for

this, shown in Figure 3-19. The color bar and dual window level controls are explained further in the next section of this chapter.

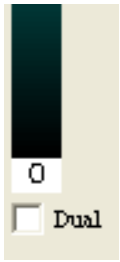


Figure 3-19. An enlarged view of the bottom of the colorbar which appears to the right of certain windows in ECToolbox. Selecting the box next to **Dual** provides a dual colorbar, for separately controlling the intensity of two different sets of images.

The Slices Display Window

This display window shows the oblique slice images for rest or stress or both, depending on the data that was selected when ECToolbox first started up. It also includes the synchronized rotating Stress and Rest planar projection image sets. These images are useful when used as a quality control check for patient motion during the 2 SPECT acquisitions.

This window is shown in Figure 3-20. Note that, since the slices and the planar images are displayed in two different color tables, there are two distinct colorbars shown. Each colorbar has controls which enable the window level (also called the display intensity, or brightness) to be changed. In addition, the color table can be changed for the slices, or for the planar images by clicking the **CT** button at the top of each scale. This will display a list of available color tables.

Clicking the **Dual** box at the bottom of the colorbars causes each colorbar to become a dual bar. In this case, the window will appear as in Figure 3-21. The upper pair of colorbar controls acts on the stress images, while the lower pair of controls acts on the rest images. Stress and rest window levels can be changed independently.

Caution: *ECToolbox attempts to properly normalize stress and rest slices based on counts in the myocardium. So, care should be taken when manually adjusting the window level for slice images.*

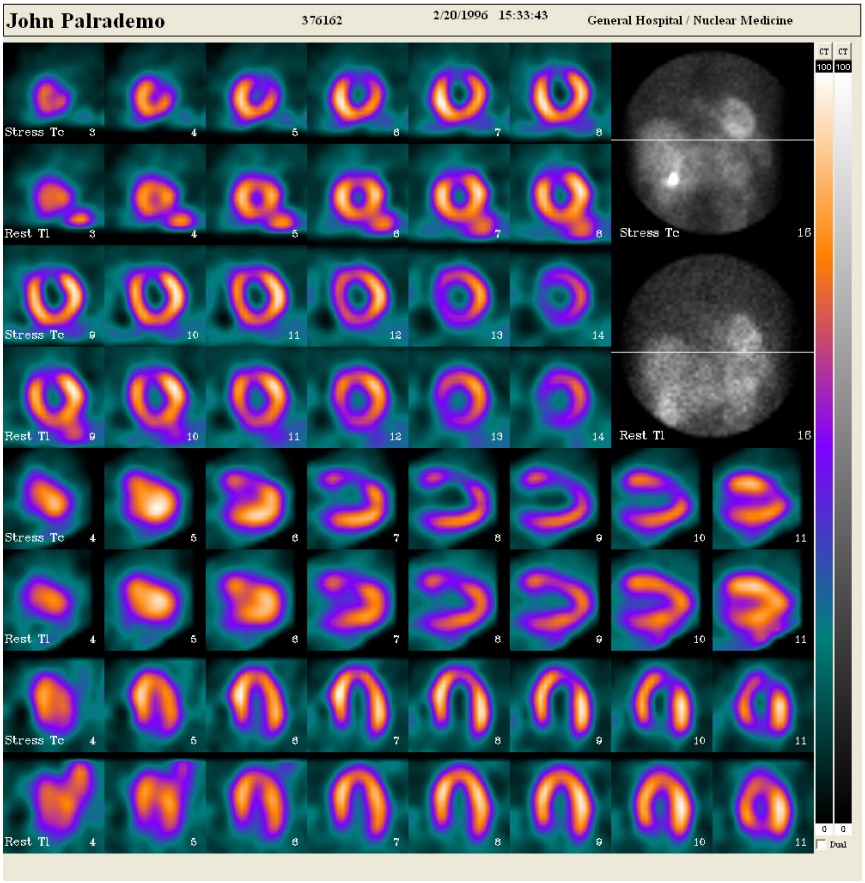


Figure 3-20. The default SLICES display window. The top 4 rows contain Short-axis slices, the next 2 rows contain VLA slices and the bottom 2 rows contain HLA slices. The Planar projection image sets are displayed at the right. in this example, there are two single colorbars for controlling the window level of the slices (in the default color scale) and the planars (in the default black and white scale).

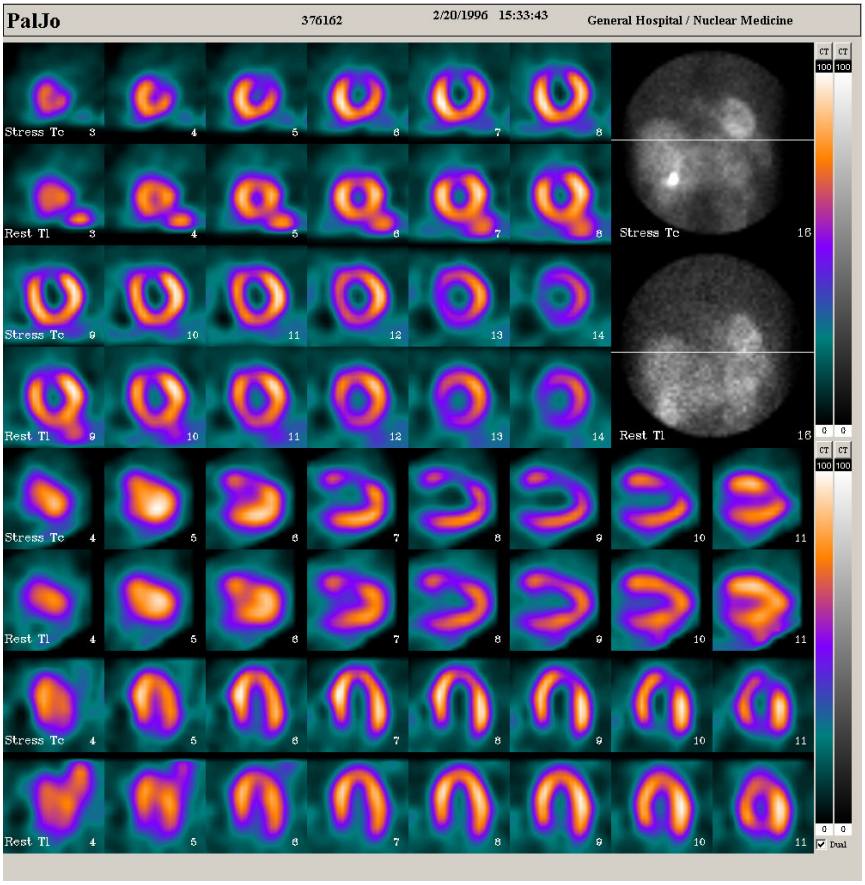


Figure 3-21. The Slices Window, with dual colorbars displayed. Note that the **Dual** box is selected, indicated by a checkmark. Window levels for stress and rest images can be set independently.

Aligning Stress and Rest Images

In the default “Slices” display, the program automatically aligns corresponding slice images for both the Stress and Rest studies. These image alignment selections are based upon the apical and basal boundary slices which were previously defined on the Params Window. For this

display, the user can correct any misalignment of these corresponding images.

To re-align slice images:

1. Visually inspect the SA Stress and Rest images to determine if they are aligned. With correct alignment, the apical and basal slices should be vertically aligned.

1. Move the mouse to the image set you wish to change.

2. Left-click to slide the image set to the left. This will have the effect of showing more images from the end of the set.

or:

3. right-click to slide the image set to the right. This will have the effect of showing more images from the beginning of the set.

Slices Window Opions

Various option buttons for this window are displayed in a block to the lower left. These controls, shown in Figure 3-22, are explained below.

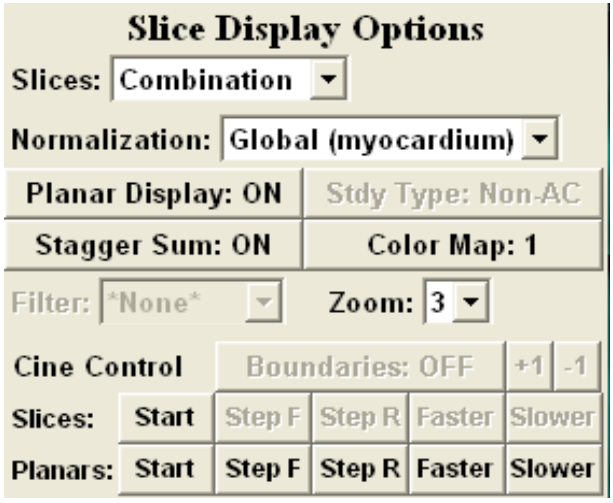


Figure 3-22. These button tools allow the user to set various options for the Slices Window.

- **Slices**: Activates a pulldown list for changing which images are displayed. by default the window includes a combination of short, vertical and horizontal slices. The choices in the drop-down list are:
    - **Combination**: This is the default selection, as illustrated above, displaying all 3 dataset pairs (SA, VLA and HLA). This display only presents the first 6 to 8 slices of each dataset. The user must use the arrow buttons to the right of the slice display in order to advance through and view the rest of the slices for each dataset pair.
    - **Short Axis**: As illustrated below, this selection displays only the SA slices for both studies. Note that this option can display up to 24 slice images for the Stress / Rest pair.
    - **Vertical LA**: This selection displays only the VLA slices for both studies. This option can display up to 24 VLA slice images for this Stress / Rest pair.
    - **Horizontal LA**: This selection displays only the HLA slices for both studies. This option can display up to 24 HLA slice images for this Stress / Rest pair.

- **Zoom**: Activates a pulldown list of zoom factors for the slice images. An image zoom factor of 2 is the default for the initial SLICES display. Other zoom choices are 3, which magnifies the size of the LV myocardium, and 4, which applies the maximum magnification.

Note: Zoom applies only to the slices. The planars are not zoomed.

- **Normalization**: This button controls how the slice images are normalized for display. The choices in the drop-down list are:
    - **Global Normalization (myocardium)**: This is the default normalization method. In this method each study is normalized to the hottest pixel found within the myocardium, as determined in the three dimensional sampling process.
    - **Global Normalization (hottest pixel)**: In this optional normalization method, each dataset is normalized to the hottest pixel found within the entire study volume for that study. This method may be somewhat problematic if there is intense tracer

uptake in non-myocardial structures.

- **normalize rest to stress**: In this optional normalization method, the Rest study is normalized to the Stress study, based upon either an automatically determined or a user defined location, which can be displayed or selected, in the Polar Map display. Refer to “POLAR MAPS, Manual Normalization” (p. 3/23) for further information.

- **Planar Display**: This option allows the user to view the tomographic slice images without the planar projection images. This provides display space for additional slice images.
- **Stdy Type**: This button switches between the primary image set and an optional secondary image set. For example, when ECToolbox is started, the user might select rest and stress short axis files, as well as rest and stress attenuation-corrected short axis files. By default, the uncorrected short axis would be the primary set, and the AC (Attenuation Corrected) files would be the secondary set. Clicking the **Stdy Type** button switches instantly between the two sets, facilitating comparison between them. The user can change a Default Setting to determine which study is considered the primary study. See Appendix D for more information. Note that the button label (“AC” or “Non AC”) indicates which set of images is currently displayed.

- **Stagger Sum**: By default, the oblique slices are displayed with this option on.This option affects the display of slices, but does not change the data stored on disk and does not save additional data files to disk. For display purposes, new short axis and new vertical and horizontal long axis images are created, by summing the original slices as follows: the new slice 1 is composed of the sum of original slice 1 and 2, the new slice 2 is composed of the sum of original slice 2 and 3, and so on. The purpose of this option is to increase the count density of the displayed slices without significantly impacting image resolution within the plane of the slice. The user can choose the un-reframed images by clicking the **Stagger Sum** button. The un-reframed images will appear, and the button label will change to **No Stagger Sum** to reflect which images are being displayed.

- **Color Map**: This button switches between the default color map for slice images, and a secondary color map. The button label will change to **Color 2** to reflect the change in map. The default and secondary maps are user-selectable by using the Defaults editor. See Appendix D for details.

In ECToolbox, you will see references to “cines”. A cine is a sequence of images which, when displayed dynamically, and repeated as a loop, shows a natural progression through the image set. Examples are planar projections and gated slices. The **Cine Control** area under **Slice Display Options** provides buttons for controlling the dynamic display of both planar gated slice cines.

Controlling the Slice Cines

Cine display of the gated slices can be achieved from the slices display window by clicking the **Start** button adjacent to the **Slices:** label. All of the slices will then be replaced by the gated cines. Once the slice cines are in motion, the **Start** button label changes to **Stop**. Note that these cines comprise a different set of images from the perfusion slices, so the **Start**/**Stop** button serves to exchange perfusion slices and gated slices on the display.

The window level controls work for the gated slice cines just as they do for the perfusion slices, even if the Dual checkbox is selected. This means that, if the window level is changed for the perfusion slices, the same window level will be applied to the gated cine slices when they are activated. Similarly, if the window level is changed while the gated cine slices are displayed, the same window level will be applied when the perfusion slices are re-displayed by clicking the **Stop** button.

There are additional cine playback controls for the slice cines just as there are for the planar cines. These buttons are only available if the cine is already running.

- **Step F**: step one frame forward in both images.
- **Step R**: step one frame in reverse in both images.
- **Faster**: increase the rotation speed of both sets of images.
- **Slower**: decrease the rotation speed of both sets of images.

- **Boundaries: OFF**: displays or removes the epicardial and endocardial borders from all gated slice images. This button is only active if the gated slice cines are in motion. The button label indicates whether the boundaries are currently on or off.
- **-1**: removes the last gate from the gated cine loop.
- **+1**: adds the last-removed gate to the gated cine loop.

Like the ungated slices, the gated slices can be shifted using the mouse cursor. For example, if the first displayed stress vertical long axis image is slice 5, left-click this row to “slide” the images to the left. Slice 6 becomes the first VLA image.

The **Filter** dropdown list is only available when the gated slice cines are in motion. The slice filter can be set to None, Spatial, Temporal or Both. For more information, see “Cine Slice Filters” on page 102.

Controlling the Planar Cines

When the slices window is displayed, the rest and stress planar images are also displayed, and will begin rotating automatically. The user can control this cine playback using the buttons in the **Cine Control** area, labelled **Planars:**. See Figure 3-22. The buttons are:

- **Stop/Start**: stop the playback, or re-start the playback if it has been stopped. If the user has moved the reference line, the button label will be: “Re-Load”.
- **Step F**: step one frame forward in both images.
- **Step R**: step one frame in reverse in both images.
- **Faster**: increase the rotation speed of both images.
- **Slower**: decrease the rotation speed of both images.

Adjusting the Planar Reference Line

The user may adjust the position of the Planar Reference line on either the Stress or Rest study. Changing the position of this line will also change the display normalization. In order to be useful in visually assessing patient motion, this reference line should be positioned to just touch the inferior wall of the LV. In cine mode, as the planar images rotate, the LV wall should not be observed to drift or jump, either up or down from the reference line.

If a drift or jump is observed, this is an indication of patient motion. In the event of significant patient motion, the user is advised to either re-acquire the SPECT Study or to utilize a motion correction program to eliminate the motion. Either reacquisition or motion correction must occur prior to processing with the ECToolbox.

Caution: *Significant artifacts will occur, if a study is processed, which demonstrates patient motion. These artifacts tend to mimic significant perfusion defects and may easily be misinterpreted as myocardial disease.*

To adjust the Planar Reference Line:

1. Position the cursor at the point where the Reference Line should be placed (just in contact with the LV inferior wall)
2. Click the left mouse button.
3. Click the **Re-Load** Button on the Cine Control Panel, to apply the change to all of the Rotating Planar Projections.

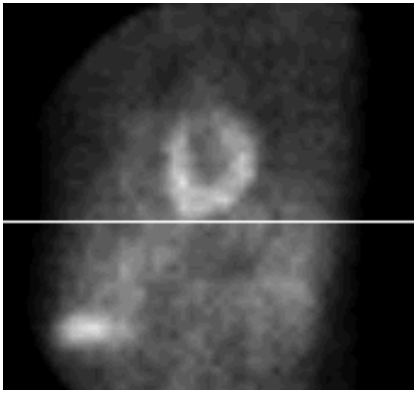


Figure 3-23. A properly positioned Reference Line on a Stress Planar image.

T.I.D. Ratio

When the Slices Window is displayed, the T.I.D. Ratio is provided in the Patient Info area. T.I.D. is used as an index of possible Transient Ischemic Dilatation. Values significantly greater than 1.0 may indicate the presence

of T.I.D. The program calculates the T.I.D. Ratio by dividing the Stress (Ungated) Endocardial Volume by the Rest Endocardial Volume.

Note: The user is advised that the accuracy and clinical value of this ratio has only been validated for the Dual-Isotope protocol. The user is further advised to consult the literature, regarding the potential clinical value of this ratio[1].

Gated Quality Control Tool

If one or more sets of gated projections is available, these will be automatically analyzed by the Gated Quality Control (GQC) tool, at the time the slice window is constructed. GQC operates in the background, independent of user interaction. A few moments after the projections are displayed, QGC indicates its findings by means of the small, colored box adjacent to the **QC:** label below the Patient Info block, as shown in Figure 3-24. If no gated planar datasets are available, the box will be black. If no gating problem is recognized, the box will appear green and captioned with "OK". If GQC finds a problem that it recognizes to be related to ECG-gating, the box is color-coded to indicate the results of Quality Control analysis. For GQC, the possible colors are:

- **red**: a serious gating error was found, one that could potentially affect the functional results
- **yellow**: a minor gating error was found.
- **green**: no gating error was found.
- **black**: no gated planars were loaded for this study (Stress or Rest)
- **gray**: this study type is not present (Stress or Rest)

If the box is some color other than black, the user can click on the box, and GQC will present a window summarizing its findings (Figure 3-25).

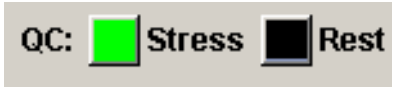


Figure 3-24. Gated control indicator. Each box will be colored to indicate whether gated planars were loaded, and the presence or absence of a gating error in the planar data.

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. In addition, the curves 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.

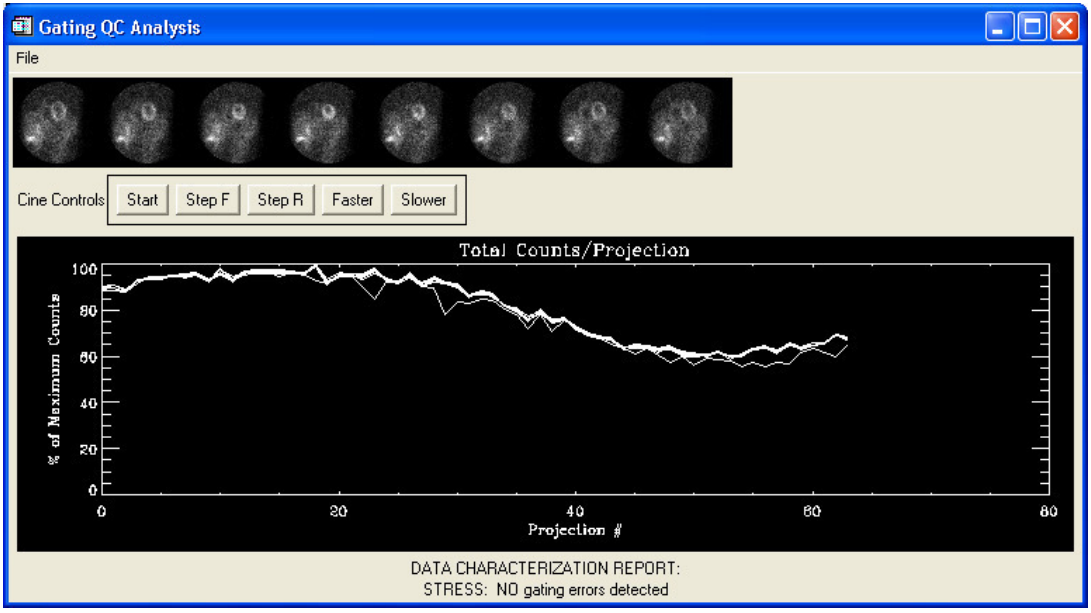


Figure 3-25. The window displayed by GQC, in the case where no gating errors were found. To dismiss the window, click the red close box in the upper right corner.

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 GQC 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, GQC will flag the error as non-critical (yellow box) even if the dropoff appears to be considerable(Figure 3-26). 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 Chapter 4 for a technical discussion of the causes of gating errors, with examples of their different appearance in the GQC window.

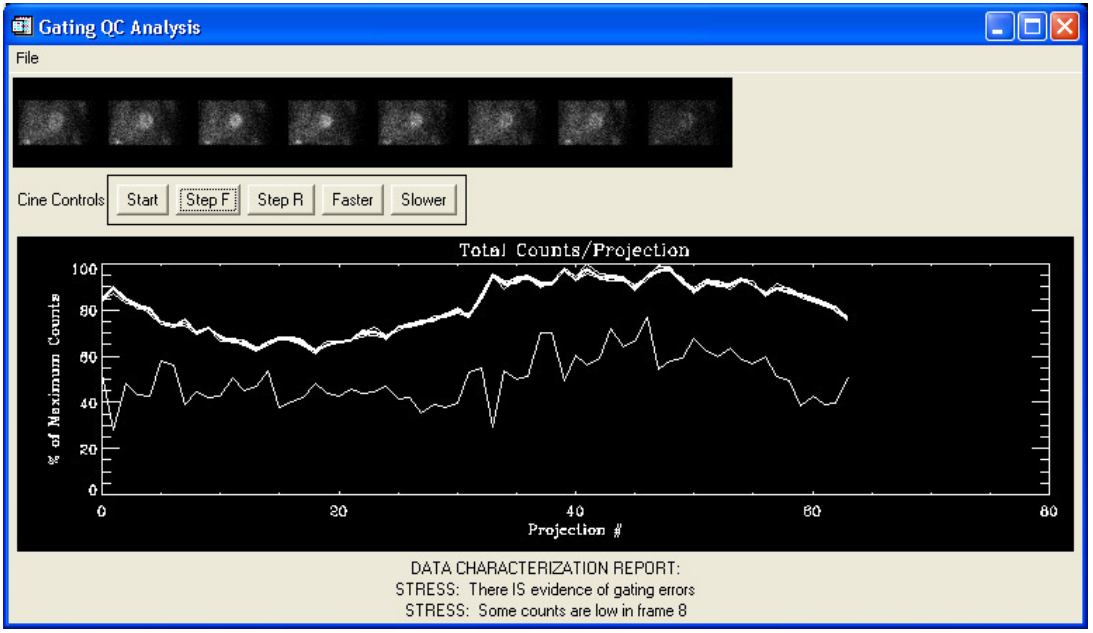


Figure 3-26. Gated projection time-activity curves indicating some count dropoff in gate 8. QGC flags this as a non-critical error.

The Gating QC Analysis window also presents the eight planar files, rotating in synchrony. There are buttons similar to those available on the slice review window, for controlling the rotation speed or stepping through the images. Notice in Figure 3-26 that the projection image for gate 8

appears decreased in counts. This will often cause a flicker in the gated slice cines. For a suggestion on how to remedy this flicker, see the section “The Cine Slice Display” on page 104.

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. An example of a gating error that would warrant a red GQC indicator box is shown in Figure 3-27.

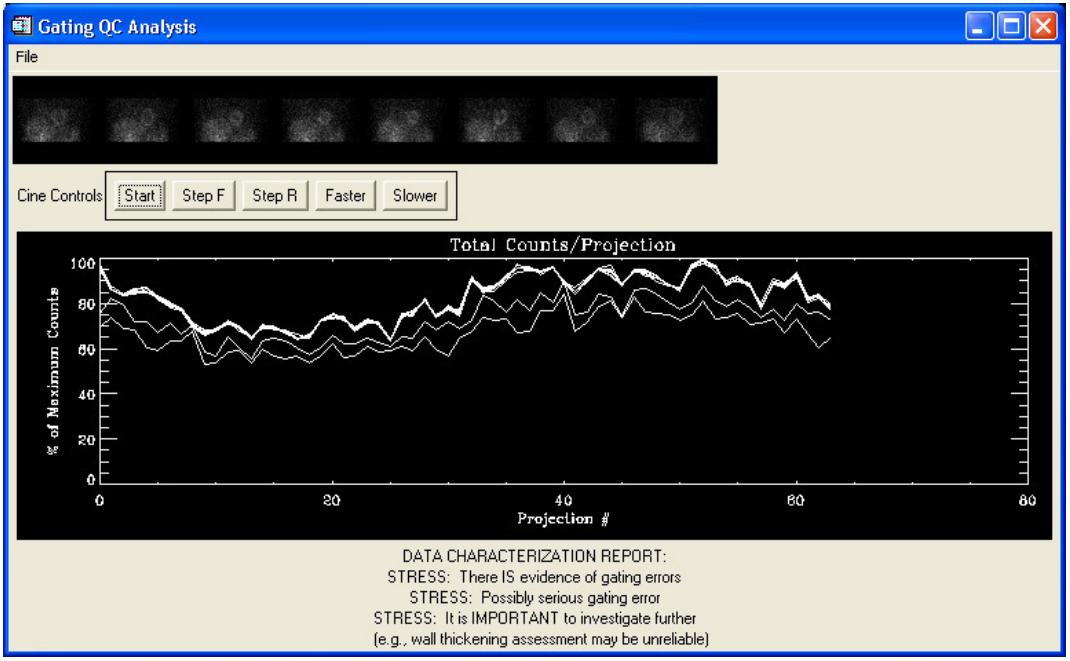


Figure 3-27. A “red” gating error, in which counts from both gates 7 and 8 are “uncoupled” from the time-activity curves of the other gates.

The Polar Maps Window

As illustrated below, the default “Polar Maps” display window contains 9 individual polar map images.

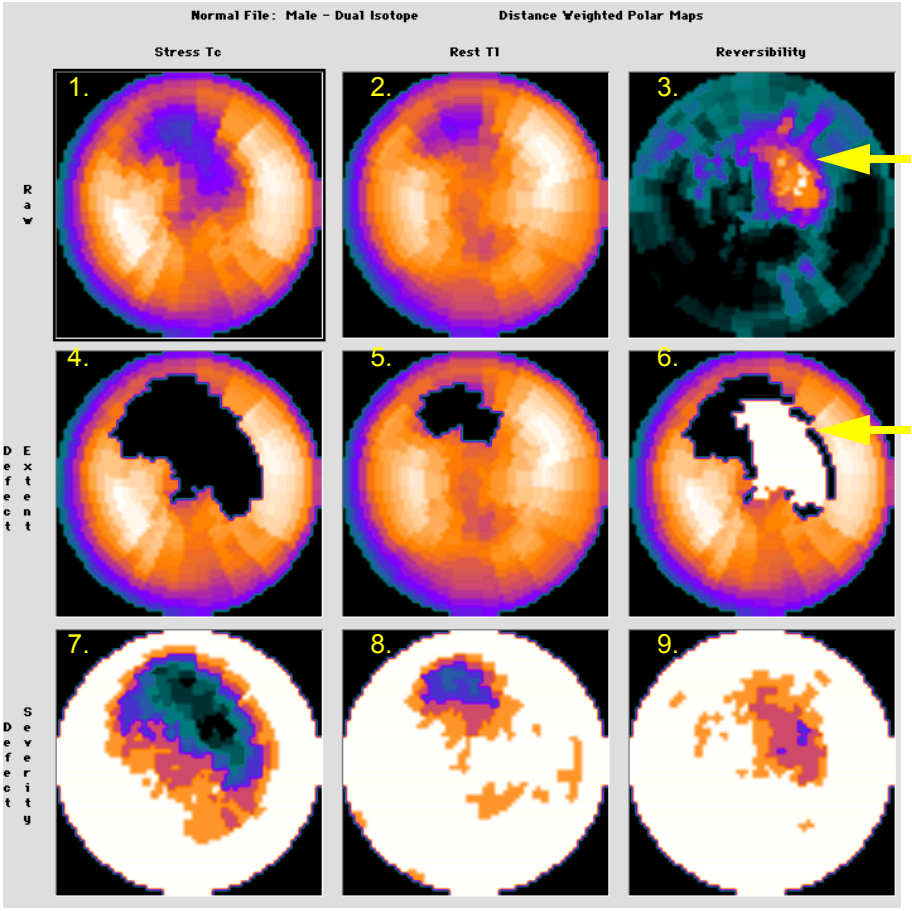


Figure 3-28. An example of abnormal stress myocardial perfusion, with partial resolution at rest. Arrows indicate the difference between stress and rest (position 3) and of statistically significant reversibility (position 6), suggestive of ischemic myocardium. Yellow numbers shown here do not appear on the ECTb screen.

Selecting the Polar Maps Display Window

1. Move the Mouse pointer to the “Polar Maps” button and click.

Top Row: The Raw Polar Maps are shown in the top row. The term “raw” is used to denote that these polar maps have not been compared with the appropriate gender-matched normal database file (Normal File). Position 1 is the Raw Stress Polar Map for the Stress Study. Position 2 is the Raw Rest Polar Map for the Rest Study. Position 3 is the Reversibility Polar Map. This Reversibility Polar Map is a normalized difference map, which is created by subtracting the normalized Stress Polar Map from the normalized Rest Polar Map. Bright clusters of pixels on this polar map indicate areas which may have greater relative tracer uptake on the Rest study than the Stress study.

Middle Row: The “Blackout” Polar Maps, also known as Defect Extent Polar Maps, are shown in the middle row. Position 4 is the Blackout Stress Polar Map. Position 5 is the Blackout Rest Polar Map. These polar maps have been compared to their respective Normal Files. The program blackens those pixels whose count values are significantly lower than the same pixels in the corresponding Normal File. Such blackened pixels identify areas which may correspond to myocardial perfusion defects.

Caution: *The user should note that these apparent 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.*

Position 6 is the Blackout Reversibility Polar Map, this map re-displays the Blackout Stress Polar Map and superimposes any areas of significant reversibility as clusters of “White” pixels. On this Polar Map, the “Black-out” areas show where perfusion is significantly decreased at Stress and the “White-out” areas show where Rest perfusion is significantly better than Stress perfusion. These White-out areas may be useful to identify “reversible” perfusion defects.

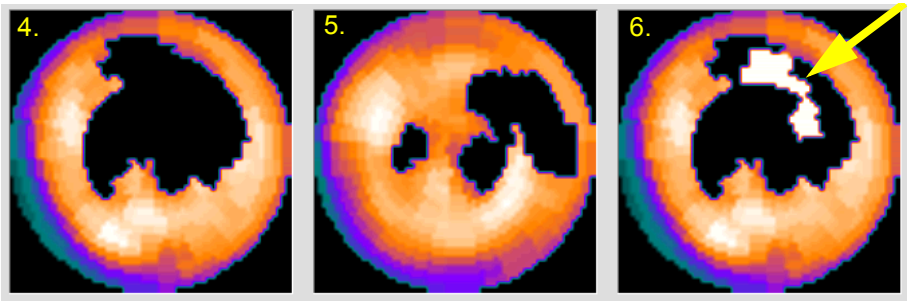


Figure 3-29. In this example, the arrow indicates an area of "White-out" pixels which define that part of the LV myocardium that has undergone perfusion reversibility, i.e. greater relative tracer uptake at Rest than Stress. Such a phenomenon may be consistent with stress-induced ischemia. The numbers 4, 5 and 6 indicate the positions that these plots occupy in the 9-plot window. See also Figure 3-27.

Bottom Row: The Standard Deviation Polar Maps are shown in the bottom row. Position 7 is the Standard Deviation Stress Polar Map. Position 8 is the Standard Deviation Rest Polar Map. These polar maps show relative perfusion variance compared to the corresponding Normal Files. In these polar maps, color is used to designate the relative variance of the tracer uptake when compared to the Normal File. The color codes for both the Stress and Rest Polar Maps demonstrate pixel count values which are below the mean Normal File values. These color codes are defined as follows: Pixels whose count values are between 0 and -1 standard deviations (s.d.) of the corresponding Normal File pixels, are color-coded White; Pixels whose count values are between -1and -2 s.d. of the corresponding Normal File pixels, are color-coded Orange; Pixels whose count values are between -2 and -3 s.d. of the corresponding Normal File pixels, are color-coded Pink; and so on. The s.d. values are displayed to the right of the color bar. Position 9 is the Standard Deviation Reversibility Polar Map. This polar map uses the same color-coding scheme as the Stress and Rest Standard Deviation Polar Maps, except that the colors represent standard deviations (s.d.'s) *above* the mean normal file pixel count values, instead of below the mean. On this polar map, clusters of colored (non-white) pixels indicate areas which may have greater tracer uptake at Rest than during Stress.

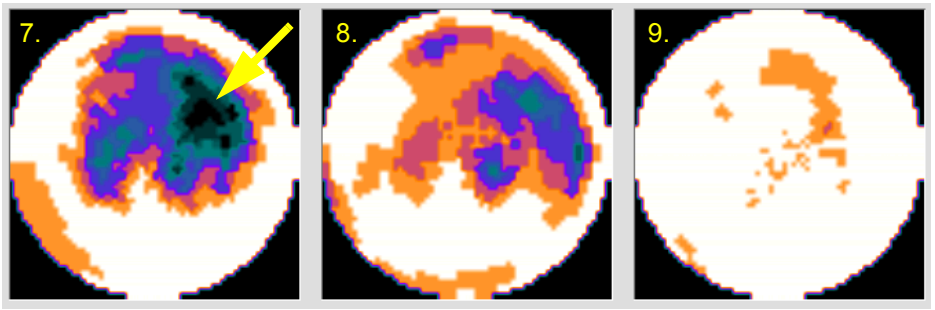


Figure 3-30. In this example, the arrow identifies an area of marked perfusion deficit, note that this cluster of black pixels represents maximum pixel count values which are greater than 7 s.d. below the corresponding mean Normal File pixel values.

When the polar map display is initially shown, a set of option buttons are displayed, as shown in Figure 3-31.

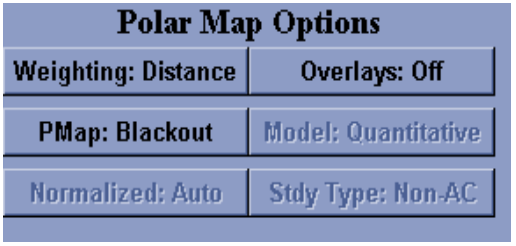


Figure 3-31. Polar Map options buttons.

The available options for changing the polar map display are discussed below.

Volume-Weighted and Distance-Weighted Polar Maps

The default display uses the Distance-Weighted Polar Maps. The user may choose to display the Volume-weighted Polar Maps as follows:

1. Click the **Weighting: Distance** button. The polar maps will change to volume-weighted, and the button label changes to indicate this.

2. If desired, click the **Weighting: Volume** button to reselect the Distance-Weighted Polar Map option.

Volume-Weighting

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 tends to distort defect location but offers an accurate assessment of the defect size.

Distance-Weighting

The Distance-weighted polar map is constructed so that each ring in the polar map is the same width. This map tends to distort defect size but offers an accurate assessment of the defect location.

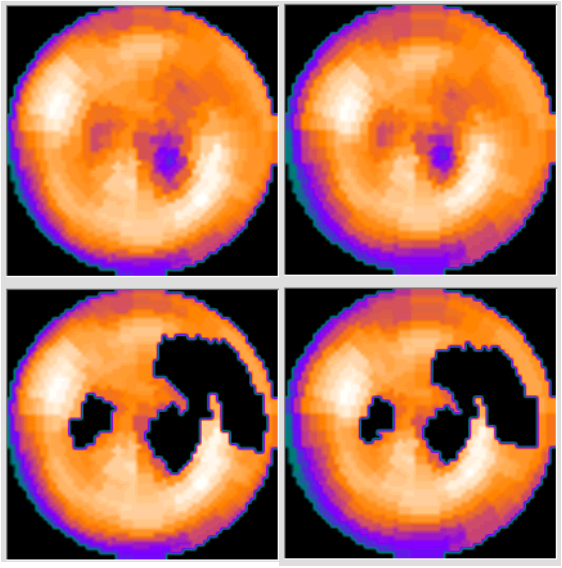


Figure 3-32. This example illustrates the effect of “Volume-weighting” *(left)* and “Distance-weighting” *(Right)* on the same Raw and Blackout Polar Maps.

The Normalization Polar Maps Display

Select this display as follows:

1. In the set of Polar Maps options buttons, find the button: **PMap: Blackout**.
2. Click this button. The blackout maps are replaced by maps which reflect normalization to a specified point. The button label also changes to indicate that Normalization maps are currently displayed.
3. If desired, repeat this same process to reselect the Blackout Polar Map option.

In the display below, positions 1 and 4 both show the Raw Stress Polar Map. Position 2 shows the Raw Rest Polar Map. Position 5 again shows the Raw Rest Polar Map, but now it is normalized to the Stress study. Note that the Stress and Rest Polar Maps are normalized to the pixel location identified in display positions 7 and 8 (see arrows below). Position 3 displays the Reversibility Polar Map (as described above). Position 6 is referred to as a “Quantized Normalization Difference Map”, which is a type of Reversibility Polar Map. This polar map shows the percentage increase in normalized counts, from Stress to Rest. For example, if a normalized pixel had a count value of 750 at Stress and 1000 at Rest, this would be a 33% increase. The program “quantizes” these percentages into eight distinct levels and assigns each level to a specific color. The Color Table displayed in Position 9 shows these levels and their corresponding percentage values.

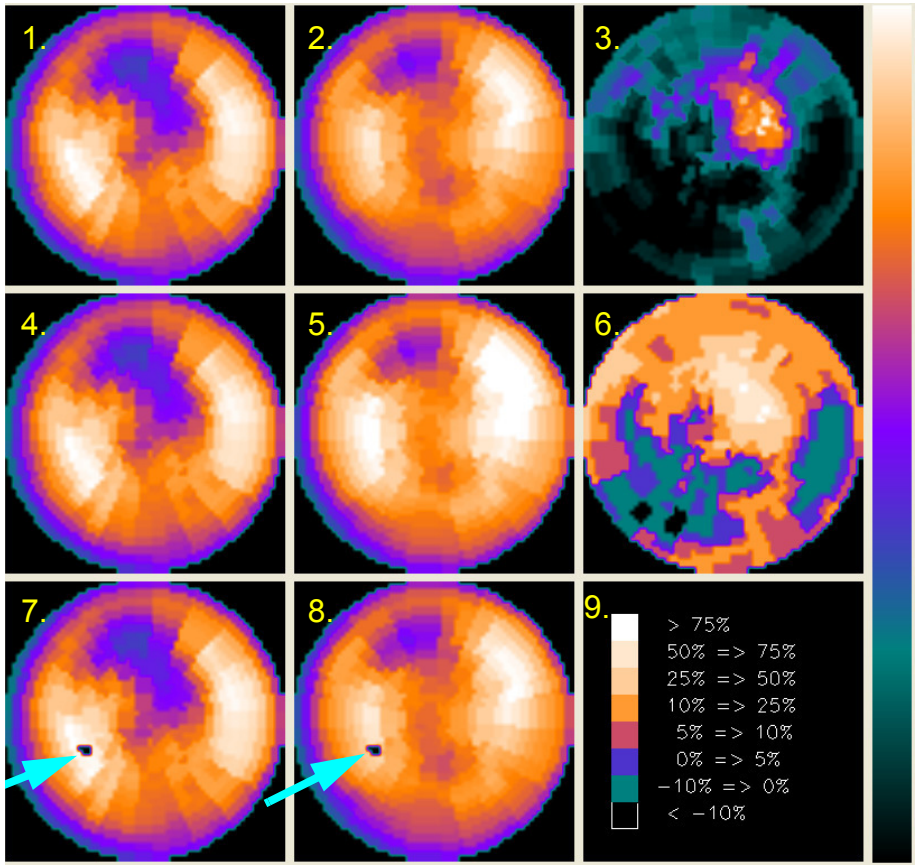


Figure 3-33. In this example, the arrows identify the pixel location which is used to normalize the Rest Polar Map to the Stress Polar Map. Note that this normalization selection also affects the normalization for the Slices Display, described previously.

Manual Normalization

The program automatically specifies the pixel location for normalization, which demonstrates the most normal perfusion at Stress. The user can change this normalization pixel location and thereby cause the program to perform a renormalization.

To change this normalization pixel location, perform the following:

1. Click the **Normalized: Auto** button. The button label changes to indicate that the normalization pixel can be changed.
2. On either display positions 7 or 8, use the mouse pointer to point to a new "normalization pixel" location. Clicking the mouse button will then initiate a renormalization process based upon the relative pixel max-count values for this new location.
3. The user may repeat this pixel relocation process as many times as necessary.
4. To restore the automatically determined Normalization location, click the **Normalized: Manual** button.

When the normalizing pixel is moved (re-selected by the user), the normalization of the slice screen will not change until the option **Normalize Rest...to Stress** is selected. When returning to the plots screen, the normalization will revert to Automatic, causing the normalizing pixel to return to its default location on the plots. This in turn will reset the slice normalization to its default Rest-to-Stress appearance.

Caution: *Changing the location of the normalizing pixel can greatly affect the way the Slices are displayed, if* ***Normalize Rest to Stress*** *is selected on the SLICES display.*

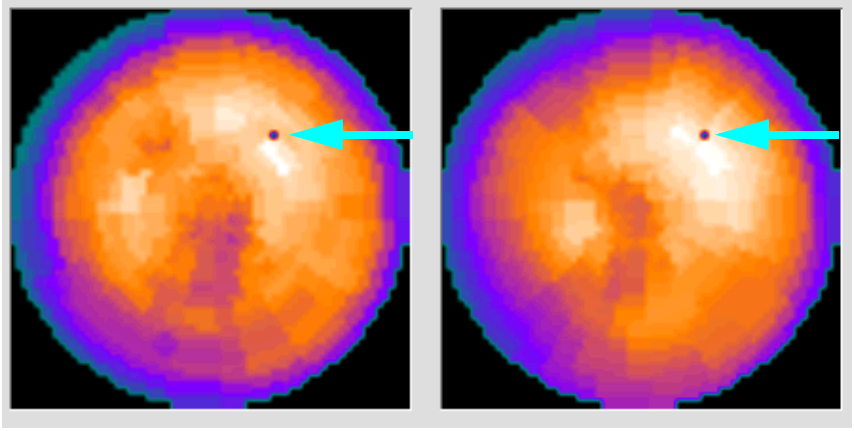


Figure 3-34. This example illustrates the position of the pixel which is used in both Stress and Rest studies to determine normalization.

Quantitative Overlays

The default polar map display does not include any overlay of region or territory boundaries. The user may choose to display the Quantitative Overlays (shown in Figure 3-35) as follows:

1. Click the mouse pointer on the **Overlays: Off** button. The quantitative overlays will be displayed on all polar maps, and the button label will change to “Overlays: On” to reflect the current state of the display.
2. If desired, click the button again to remove the overlays.

The optional Quantitative Overlays are provided to assist the user in visually comparing like regions on Stress and Rest Polar Maps. This option is available for use with either the Blackout Polar Map Display or the Normalized Polar Map Display.

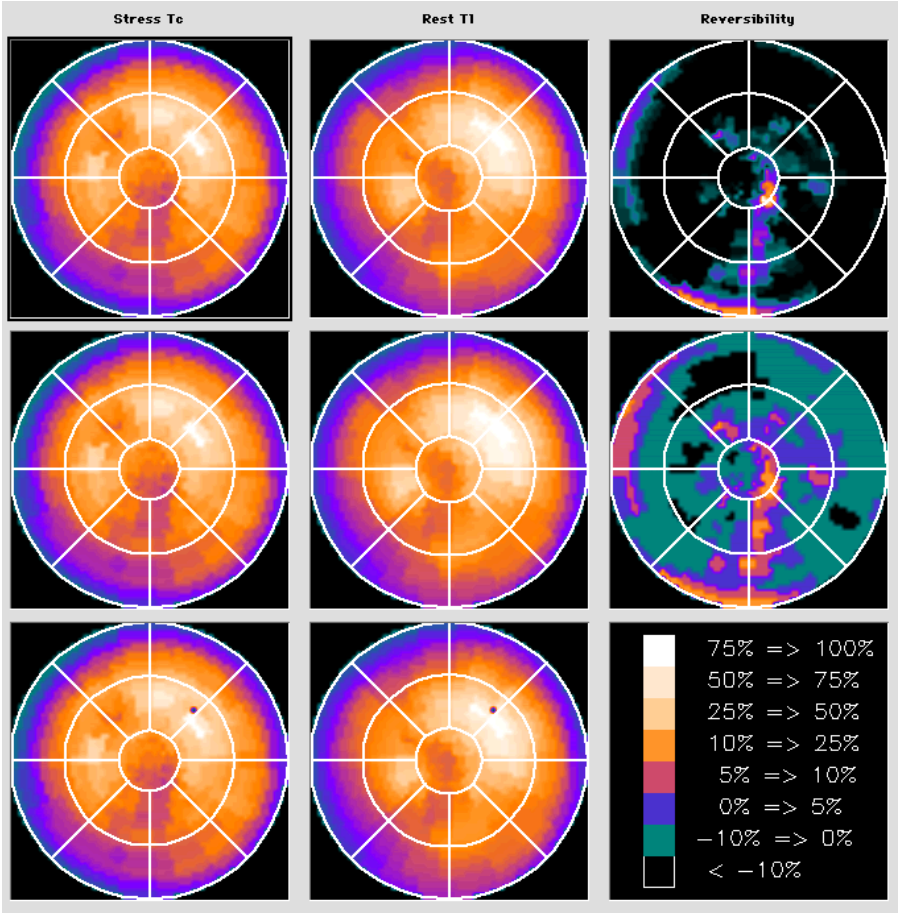


Figure 3-35. This example illustrates a “Normalized Polar Map” display with the “Quantitative Overlays On” option. This option is provided to assist the user in visually comparing like regions.

Clicking the **Extent/Mass** button opens the Estimated Mass window, shown in Figure 3-36 and explained below.

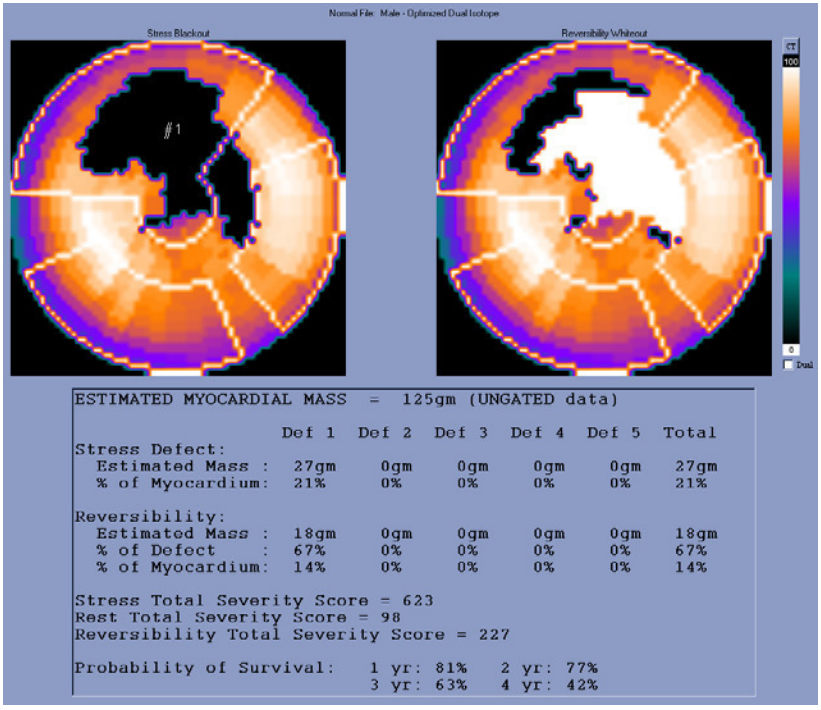


Figure 3-36. The Estimated Myocardial Mass Display Window.

At the same time, Option controls are displayed at the lower left of the screen. See Figure 3-37. The droplist labeled **Extent/Mass** enables the user to switch between the default Mass display and another option. The choices are:

- **Extent** - defect extent, by percent
- **Gated Mass** - defect mass in grams, from the gated study. This is the default if a gated study was done.
- **Ungated Mass** - defect mass in grams, from the ungated study. This is the default if no gated study was done.

The **Study Type** button switches between AC and non-AC studies (if both are available).

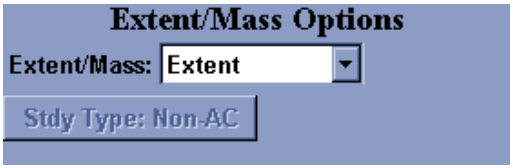


Figure 3-37. Using the dropdown list, the user can switch between the Defect Extent and Defect Mass displays.

The Mass and Extent displays have several aspects in common. Two Polar Maps are included: the Blackout Stress Map and the Blackout Reversibility Map. The Blackout Stress map is used for analysis of the extent of significant stress perfusion defects. The Reversibility map shows the fraction of the defect which normalizes, or “reverses” in the rest study.

Both the Extent and Mass displays will automatically utilize the Stress Gated data, if the functional analysis processing has already been performed. You can always switch to the ungated data.

Note: If more than five defects exist, the program only displays information for the first five defects found, starting at the Apex.

Estimated Mass Display

The Estimated Mass display is shown in Figure 3-36. The following information is displayed:

- Stress defect mass is indicated both in total grams and as a percent of the total LV myocardial mass. Mass determinations based on the gated data are considered to be more accurate than those based on ungated data.
- Reversible mass is indicated in grams.
- Reversible mass is indicated in terms of percent of Stress Defect Mass.
- Reversible mass is indicated in terms of percent of the total LV myocardial mass.
- 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. [35] This value can be removed from the default display by changing a default setting for the program (see Appendix D).

- 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.

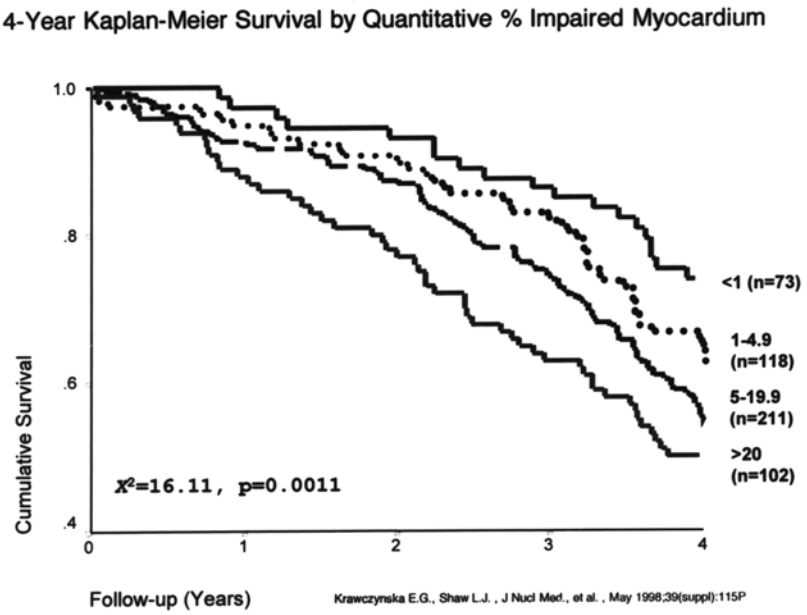


Figure 3-38. Graph of Probability of Survival data

Extent Display

To display the Defect Extent window, click the **Extent** button, which is part of the permanent button group.

The Stress Blackout Map and the Blackout Reversibility Map are included in this display, as they are in the Estimated Mass display. Each defect is broken down into three vascular territories (LAD, LCX, and RCA). In addition, the total of all three areas is displayed, as well as the total of all defects.

If more than five defects exist, the program only displays information for the first five defects, starting at the Apex.

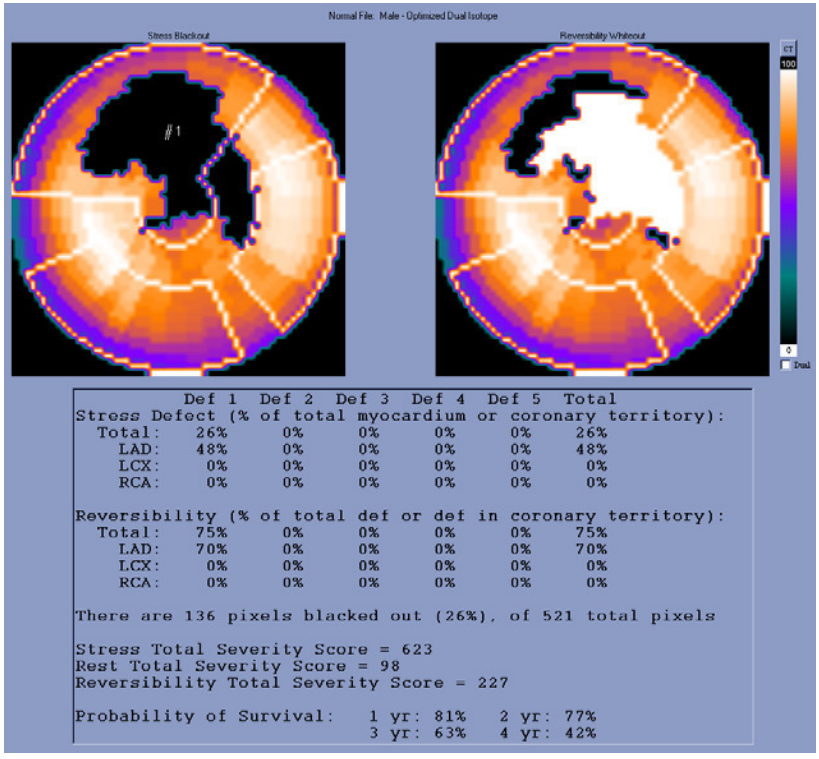


Figure 3-39. The Quantitative Extent Display Window.

Note: 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.

The following information is displayed:

- Stress defect extent is indicated as a percent of the total in the particular area (LAD, LCX, RCA).
- Total reversible extent per territory is indicated as a percent of LV myocardium.
- Stress Total Severity Score.

- Rest Total Severity Score.
- Reversibility Total Severity Score.
- Probability of Survival data.

Estimated Viability Displays

This option allows the raw polar maps to be used to estimate viability by setting a threshold below which pixels in the rest perfusion map are blacked out. There are two parts to the display:

- Estimated Viability - Extent
- Estimated Viability - Estimated Mass

To open the Estimated Viability display screen, click the **Viability** button, which is part of the permanent button group. By default, the Viability Extent display will appear.

Three Polar Maps are included in this display: The Raw Stress Map appears on the left, the Raw Rest Map, appears in the center, and is repeated again on the right (Figure 3-40). These first two maps are provided merely for reference. The viability analysis uses the Rest Map on the right. This map is displayed with a default lower threshold value of 50%. At this threshold, all pixels whose count values are less than 50% of the maximum pixel count in the Rest Study, are set to black, implying a non-viable area.

The program automatically assigns a defect number to each defect, up to a maximum of five. If more than five defects exist, the program only displays Extent information for the first five defects, starting at the Apex.

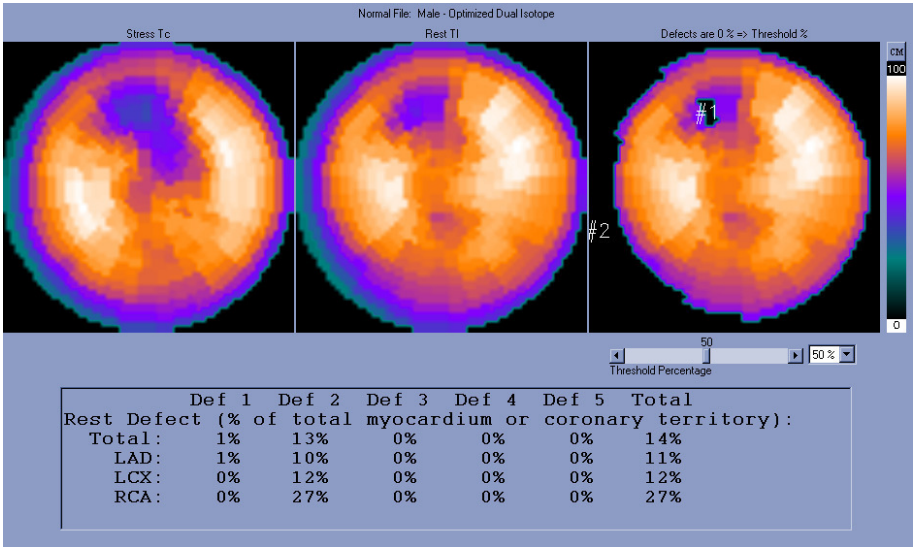


Figure 3-40. The Viability Extent Display

The data table, displayed below the polar map display, provides the following information:

- Defect extent is indicated as both percent of total myocardium and percent of coronary territory, for each identified defect.

To Change the Threshold Value

ECToolbox provides multiple threshold selection options.

To set the threshold:

1. Use the mouse button to click and hold on the **60%** box.
2. This box expands to display 5 options: **60%**, **50%**, **40%**, **30%** and **Other**.
3. Highlight the desired threshold value and release the mouse button. If **Other** is selected, you can then use the mouse button to click on the slider bar to change the threshold value.

As the user changes the “Threshold Value”, the Rest Polar Map display also changes. As seen in Figure 3-41, defects will change in size or may even disappear as a lower threshold percent is selected. The values displayed in the data table may also change for each defect.

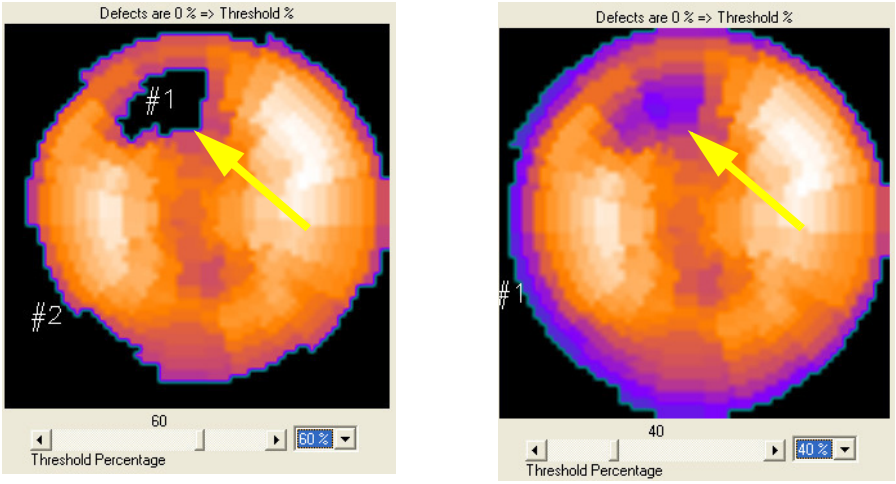


Figure 3-41. This example illustrates the effect of changing the threshold value from 60% (left image) to 40% (right image). In this case, the change in threshold causes a blacked-out non-viable defect to “disappear” (arrow).

Caution: *The user is advised to carefully consider basal defects which are identified by the program. Figure 3-42 illustrates this relatively common artifact, which the program has mis-identified as a defect (#2).*

Viability Mass Display

The Estimated Viability display has a single option control, which is a droplist displayed below the Patient Info area. Using this control, you can change from the default Extent display to a Viability Mass display (Figure 3-42). Either gated or ungated mass calculation can be used. If **Gated Mass** is selected from the droplist, and the gated processing has not been done, a message will be displayed. In this case, ungated mass can be used.

The same three Polar Maps are also included in the Viability Mass display: The Raw Stress Map on the left, the Raw Rest Map in the center, and again on the right (Figure 3-40). This Rest Polar Map is again displayed with a default lower threshold value of 50%. The threshold can be changed using the same procedure as for Viability Extent, described above.

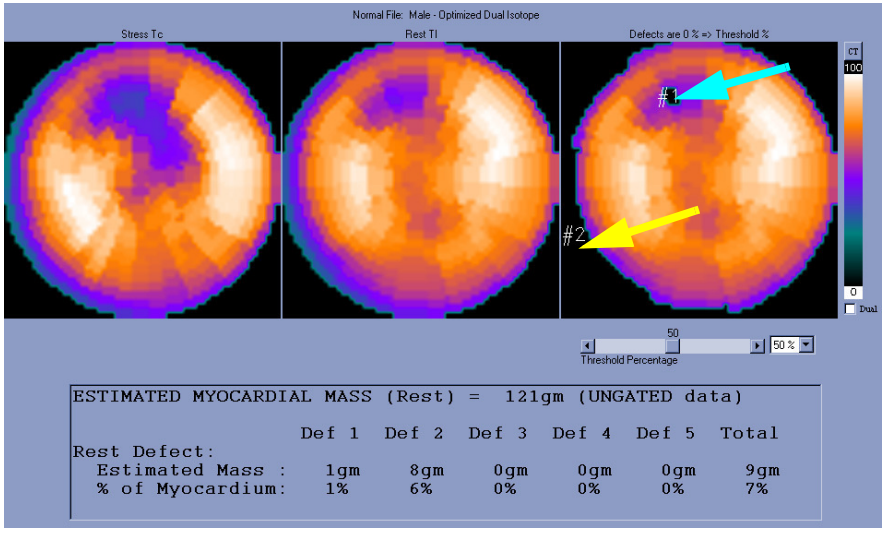


Figure 3-42. Viability Mass Display Window. The arrows identify 2 estimated nonviable defects. Note that the Slider Bar indicates a threshold value of 60. Defect #2 (Yellow Arrow) is a relatively common artifact in this type of analysis.

The following information is displayed in the Data Table below the plots:

- Defect mass is indicated both in total grams and as a percent of the total LV myocardial mass.

Note: The mass values derived in this display are based upon the Rest Study myocardial mass, and may differ from Stress myocardial mass values displayed in the Defect Extent/Mass Display described previously. These differences are attributable to volume changes between Stress and Rest. Please refer to Chapter 4 for further information.

The defects are automatically numbered starting at the apex, up to a maximum of five. If more than five defects exist, the program only displays Mass information for the first five defects.

Using a threshold value to estimate myocardial tissue viability based upon the Rest Tl-201polar map, is supported by research described in the scientific literature. Reference [3] offers the following conclusions:

Table 3-1. Assessing Myocardial Viability.

Threshold %	Pixel Counts	Tissue Viability
> 50%	Individual pixels whose counts are greater than 50% of the max. pixel.	Viable
30% to 50%	Individual pixels whose counts are between 30% and 50% of the max. pixel.	Mixed: Necrotic & Viable
< 30%	Individual pixels whose counts are less than 30% of the max. pixel.	Necrotic, Non-viable

The Summed Stress Score (SSS)

This is a method which has been presented in the literature, as a means to semiquantitatively compare stress and rest perfusion [4]. The polar map is divided into segments and a perfusion value is assigned to each segment, from visual analysis. Following is the scoring scheme:

Table 3-2. Segmental Scoring Options

Segment Score	Perfusion Assessment
0	Normal
1	Equivocal
2	Moderate Reduction
3	Severe Reduction
4	Absent

By default, Emory Cardiac Toolbox uses a 17-segment model for dividing the myocardium.

Note: A 20-segment model is also available by changing a setting in the User Defaults. See Appendix D for details.

The Summed Stress Score (SSS) is the calculated sum for the 17 Stress segments. Similarly, the Summed Rest Score (SRS) is the calculated sum for the 17 Rest segments. The Summed Difference Score (SDS) represents the difference between these 2 scores. A positive SDS represents poorer overall perfusion at Stress compared to Rest (i.e. stress induced ischemia). A negative SDS score, represents poorer overall perfusion at Rest compared to Stress.

The program will automatically determine the segmental scores, and display these scores as shown in Figure 3-43. The user should examine all the scores, and may change them as necessary, using the drop-down boxes displayed in each segment. Using the mouse to click the box will open a list of possible scores. The desired score can be highlighted, and this will become the new score for that segment.

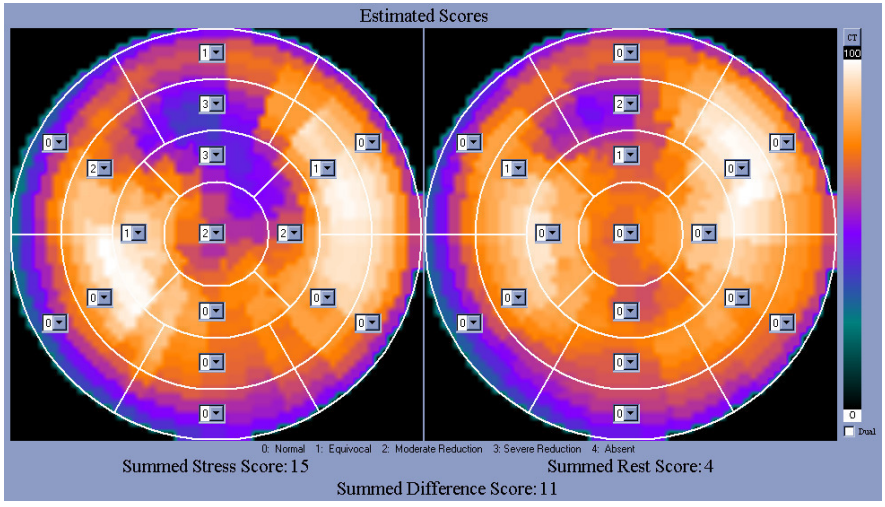


Figure 3-43. The Summed Stress, Summed Rest and Summed Difference Score Display

There is a single option button for the SSS screen. This allows either the attenuation corrected (AC) or non-corrected images to be displayed.

The table below provides guidelines in assessing the significance of the SSS value.

Table 3-3. Significance of the Summed Stress Score

Summed Stress Score	Significance
Less than 4	Normal
4 to 8	Mildly Abnormal
9 - 13	Moderately Abnormal
Greater than 13	Severely Abnormal

These results are also displayed on the Summary Page, which is best viewed at the conclusion of processing. Scores displayed on this window cannot be changed by the user.

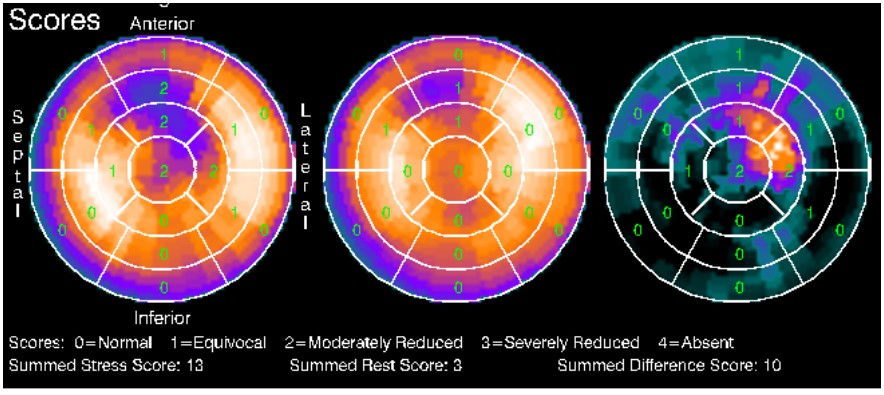


Figure 3-44. Presentation of the Summed Stress Score, Summed Rest Score and Summed Difference Score on the Summary Display Window.

PERFEX™

The PERFEX button is available as part of the permanent set of tools. This option allows the user to view an automatically-generated interpretation of the CEqual perfusion results. PERFEX is an Expert System module that runs in the background when the PERFEX button is selected.

When this option runs, the user is first presented with a dialog, as shown in Figure 3-45. The user must enter the patient age in this window. Patient gender is automatically set, but can be changed if necessary. In addition, the Expert Reading Level is always set initially at “Sens=0.83” and “Spec=0.73”, but the user can select another level, which will cause the Expert System to interpret the study with either greater sensitivity or greater specificity. Select the “Done” button to proceed.

After a few moments, PERFEX will display a text window summarizing its Findings for the current study. PERFEX text windows can be moved or closed, but not re-sized. In the Findings window, there will be several underlined keywords, which serve as hyperlinks to additional windows of text which justify the conclusion reached by that keyword and/or further explain the PERFEX image interpretation. For example, clicking on the word “IMPRESSION” will present a brief summary of the interpretation.

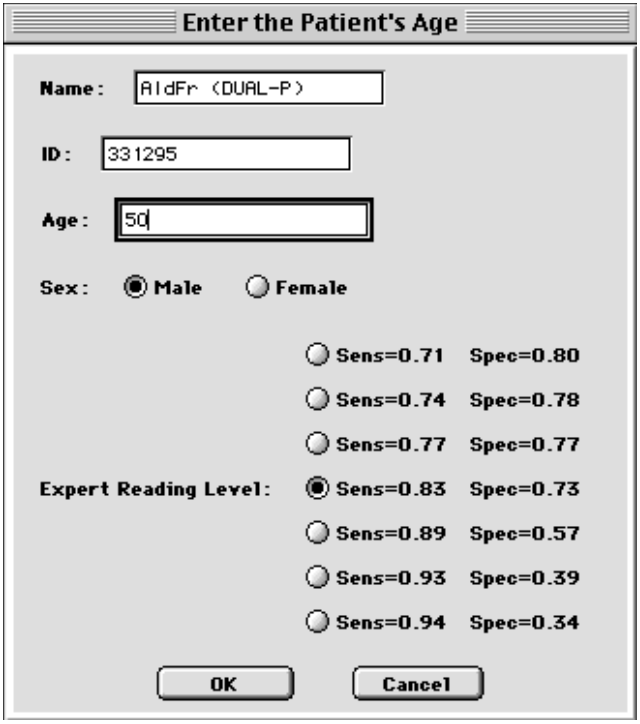


Figure 3-45. User interface dialog for the PERFEX Expert System. If no patient age is entered, a warning message will be displayed, prompting the user to enter an age value.

The IMPRESSION window replaces the original FINDINGS window. At this point, the user can click another underlined word to access further explanation, or use the “BACK” link to return to the previous window. Each window after FINDINGS will have a “BACK” link. An example Findings window is shown in Figure 3-46. Suppose that, in this case, we want to understand the wording “This area, which is diseased...”. Selecting the underlined word “is” presents the text box shown in Figure 3-47. This explains the PERFEX program’s meaning of the word “is”. Any underlined term can be investigated in this way. At any time, you can close the current PERFEX window and select another ECToolbox function.

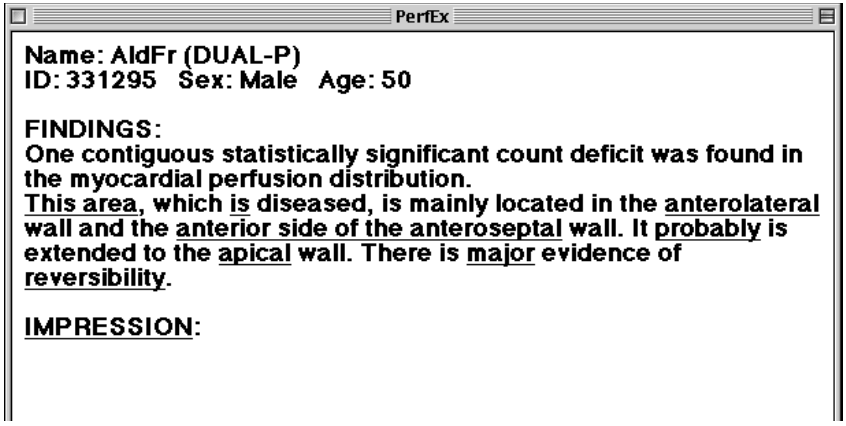


Figure 3-46. PERFEX FINDINGS window. Each underlined word is a hyperlink. Clicking any of these words will cause another window of text to be displayed, which will explain the meaning of the clicked word, explain how some finding was arrived at, or otherwise amplify the interpretation.

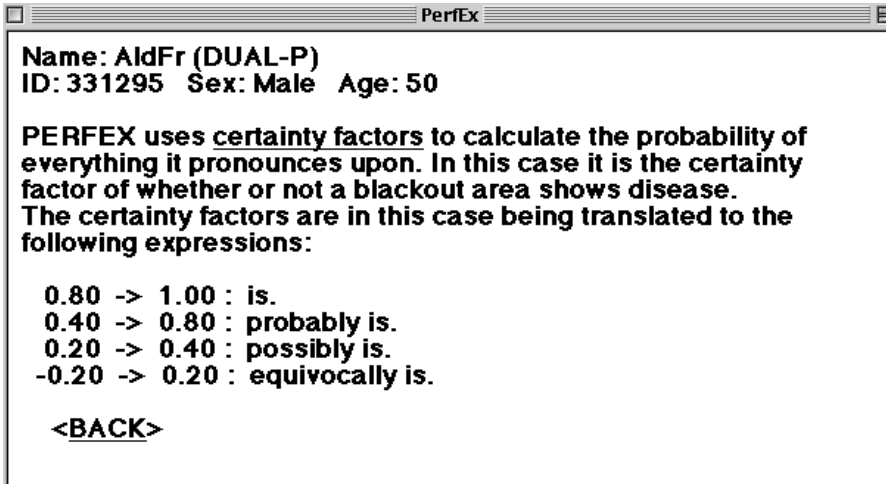


Figure 3-47. This text is displayed when the underlined word “is” in the line “This area, which is diseased...” in Figure 3-46.

The PerfSPECTive™ Three Dimensional Display Window

This display window provides multi-view three dimensional displays for both the Stress and Rest studies. The shape of the three dimensional LV myocardium is intended to present the actual myocardial shape, as determined by the sampling methodology (described in Chapter 4).

PerfSPECTive Display Window

To access the 3-D display window, click the **PerfSPECTive** button, which is part of the permanent button display. A set of 3-D PerfSPECTive maps willl then be displayed (Figure 3-48).

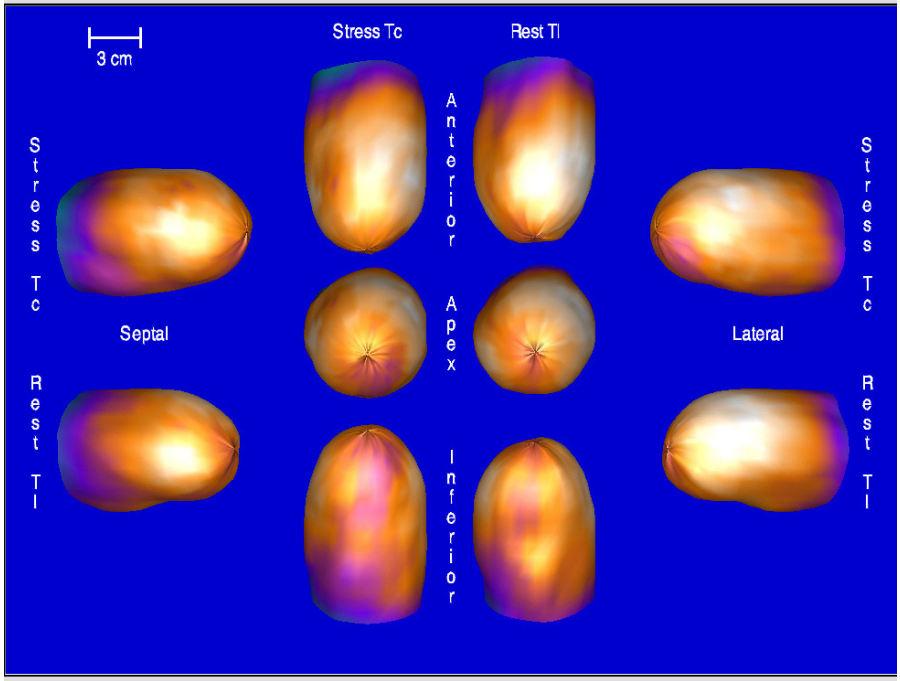


Figure 3-48. The three dimensional paired images provide the ability for direct visual comparison of Stress and Rest LV size and myocardial perfusion.

A size scale is shown in the upper left corner of this window, so that the size of the current patient's myocardium can be judged. The scale is fixed, so that larger hearts will appear larger on the display.

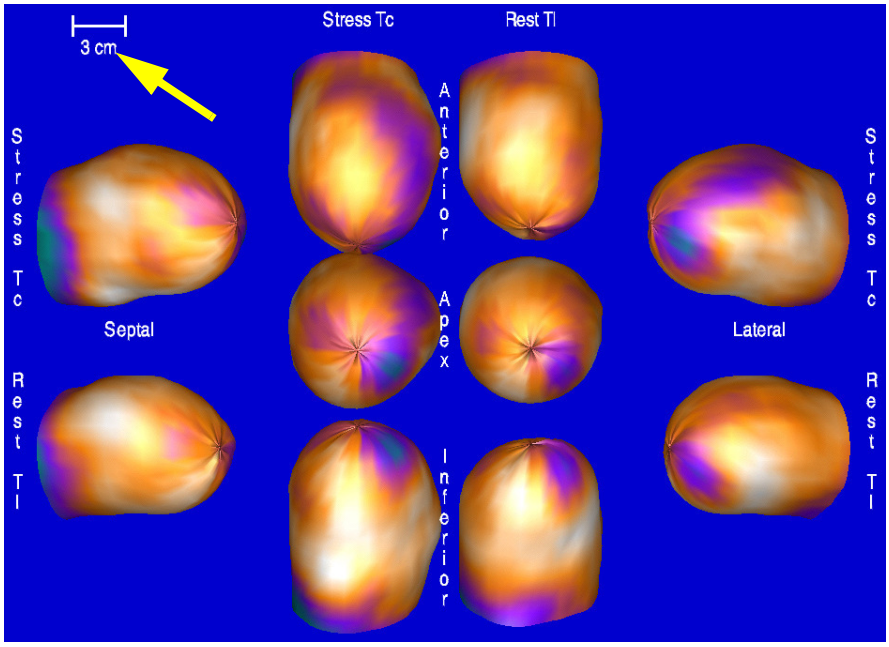


Figure 3-49. This example illustrates the presence of both fixed and reversible perfusion defects. The size scale is indicated by the arrow. Difference in LV size between rest and stress is possibly due to the presence of TID.

Option buttons for the PerfSPECTive display appear below the Patient Info Area, on the left side of the screen. These are shown in Figure 3-50.

The following options are applied by default:

- "Generic Coronaries: Off".
- "Map: Stress / Rest".

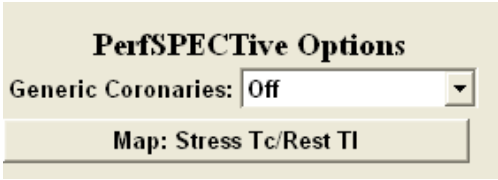


Figure 3-50. Optional controls for the 3-D PerfSPECTive display.

The Generic Coronary Display Option

To select the Generic Coronary Tree Display options, perform the following steps:

1. Using the mouse button, click the arrow button next to the **Generic Coronaries: - Off** listbox.
2. Move the Mouse pointer to select from the 3 available options: **Generic Tree - Right Dominant**, **Generic Tree - Right Dominant 2** or **Generic Tree - Left Dominant**. Release the mouse button to open that option.

The generic tree overlay options may be useful in correlating identified perfusion defects with particular coronary arteries. The user may select the appropriate generic tree, if it is known from prior coronary arteriography in that patient.

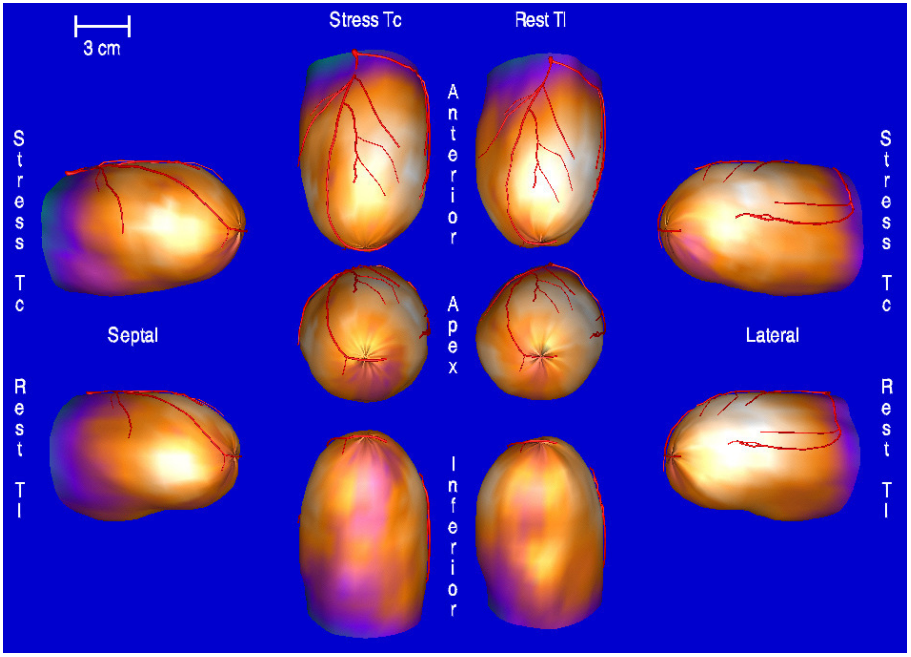


Figure 3-51. The example illustrates an overlaid left dominant coronary tree.

The Map Display Option

By default, perfusion raw maps are displayed in this window, however, the type of map can be changed using the **Map: Stress / Rest** listbox. Note that the label of this button will reflect the type of study. For a dual isotope study, for example, this button may read “Map: Stress Tc / Rest Tl”. Clicking this button changes all of the maps to blackout/reversibility, where perfusion defects are labeled in black and reversibility in white. This is a toggle button, which means that clicking the button switches between two options. So, clicking the **Map: Blackout / Reversibility** button again will return to display of the raw maps.

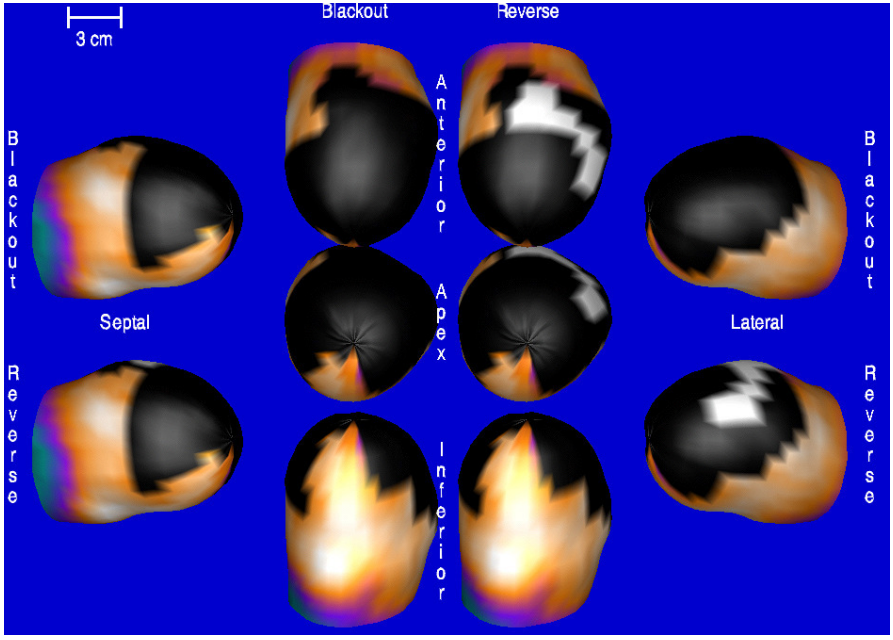


Figure 3-52. An example of the **Blackout / Reversibility** option for the 3-D display. These three dimensional paired images provide the ability for direct visual comparison of Stress and Rest blackout and reversible defects.

The Gated PerfSPECTive Display

To view the Gated PerfSPECTive display, use the mouse button to click the **Gated 3D** button, which is part of the permanent button display.

Note: Gated 3D is available after you have used the **Function** button to review functional analysis results.

The window that appears shows the PerfSPECTive 3D image of the LV myocardium. The image changes shape during the cardiac cycle, as the LV empties and then fills. This gated 3D cine image, can be tumbled and rotated in any orientation, by using the mouse pointer to drag the image. The automatically overlaid coronary arteries provide the user a reference for determining the LV orientation.

A four-view, gated, 3D cine display is also available from the Functional Analysis Window. See “The Cine 3D Display” on page 105.

When the gated 3D images are displayed, a set of option buttons also appear on the lower left of the screen, as shown in . The available options are:

- Drag Quality (explained below)
- Cine Control. This works similarly to other cine control buttons in ECToolbox, for changing the speed of the cine or stepping through individual frames.

Figure 3-53. Options for controlling the Gated 3D display.

The “Drag Quality” Options

There are 3 selectable “Drag Quality” options: Low, Medium and High.

- The Low option displays a “Birdcage” image, while dragging to a new orientation.
- The Medium option displays an intermediate resolution image, while dragging to a new orientation.
- The High option displays an high resolution image, while dragging to a new orientation.

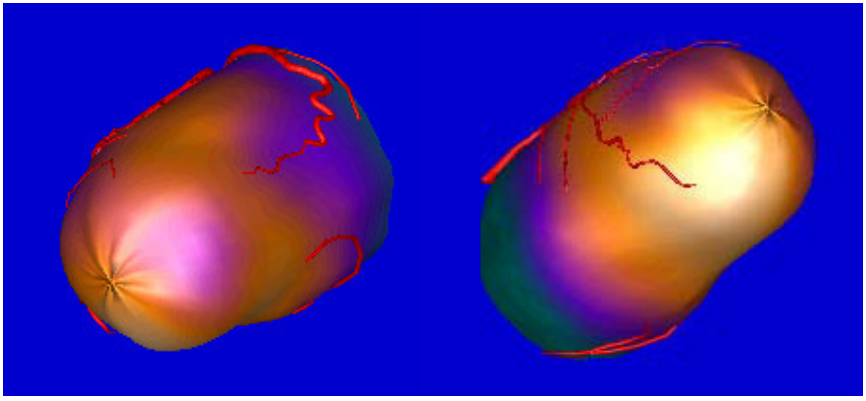


Figure 3-54. The Gated PerfSPECTive Display. Two of the many possible orientations are shown: Antero-lateral (left) and Infero-septal (right).

Note: This display is only available if a Gated SPECT dataset has been selected and processed.

The Functional Analysis Tools

Note: This part of the application requires a Gated SPECT short axis file. The number of gated frames will be interpolated to 8 for functional analysis. Optionally, a second Gated SPECT short axis file can be selected, and the two will be processed together.

The Emory Cardiac Toolbox application provides tools to process and quantitatively analyze myocardial function. These tools include:

- Automated quality control for gated acquisition
- LV Volume Curve
- Calculated LV quantitative parameters: EF, EDV, ESV, SV and Mass.
- Quantitative wall thickening analysis (Estimated)
- Cine display of wall motion and wall thickening
- Three dimensional PerfSPECTive wall motion display

As mentioned in the section covering the “Gated Quality Control Tool” on page 59, it is suggested that the results of automatic Gated Quality Control be reviewed for any study for which the indicator box on the Slice Window is red, since certain types of gating errors may compromise the value of functional results.

A set of **Functional Analysis Options** buttons appears below the Patient Info area. These buttons, shown in Figure 3-55, offer a number of options relating to ECG-gated images. Whether you are in process mode or review mode determines which options are available and which are disabled.

Processing an ECG-Gated Study

To process the ECG-gated part of a study for assessment of left ventricular function, click the **Function** button, which is part of the Permanent Button set. If gated processing has not been done, the Center & Radius screen and the Apex/Base screen will be displayed, for selection of processing parameters. If gated processing has been done, then selecting the **Function** button will display the Functional Review screen.

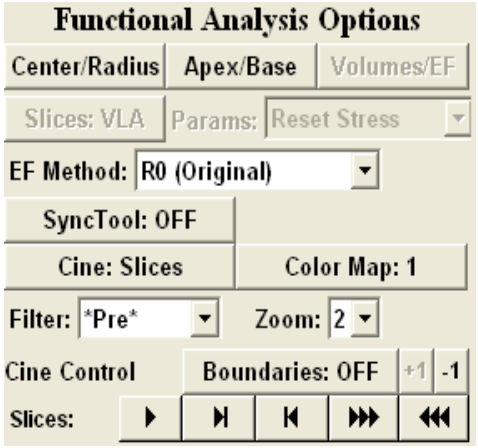


Figure 3-55. Option buttons for functional analysis, as seen in review mode.

In review mode, the **Center/Radius** and **Apex/Base** buttons allow the user to return to the screens that control the functional analysis parameters for each gated image set.

The Center & Radius Display for Gated SPECT

The **Center/Radius** display shows eight SA slice images, one from each of the eight gated SPECT frames. If there is a second gated study, its eight SA slices are displayed in a second row. In this window, the user can both review and modify the automatically selected LV Center and Radial boundaries for each gated frame.

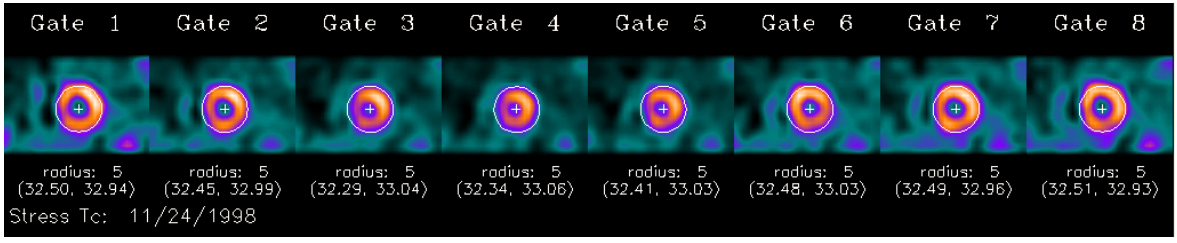


Figure 3-56. The **Center/Radius** display for a single gated study.

Changing the LV Centers

To change one or more LV Centers, perform the following steps for each frame:

1. Using the mouse, place the pointer on the SA slice image whose LV Center is to be changed.
2. Using the mouse button, click on the desired location for the new LV Center.
3. To reset the LV Centers back to their preselected locations, use the droplist labeled **Params** in the **Functional Analysis Options**. Move the mouse pointer to highlight **Reset Stress** (or **Reset Rest**) and release the mouse button.

Note: This action will reset any LV Centers that had been manually changed and causes any apex or base slices which had been changed to be restored to their original locations.

Changing the Radii

To change one or more Radial Boundaries, perform the following steps for each frame:

1. Place the mouse cursor on the SA slice frame whose LV Radius is to be changed.
2. Clicking outside the current Radius using the right mouse button causes that Radius to expand. Clicking inside the current Radius with the right mouse button causes that Radius to contract.
3. To reset all the Radii back to their preselected sizes, use the **Params** droplist. Move the mouse to highlight **Reset Stress** (or **Reset Rest**) and release.

Note: This action will reset any LV Centers that had been manually changed, and causes any apex or base slices which had been changed to be restored to their original locations.

Changing all 8 LV Centers

To simultaneously change all LV Centers for one gated study to the same pixel location, perform the following steps:

1. Using the mouse, place the pointer on one SA slice frame.

2. Use the middle mouse button (or CONTROL key plus left mouse button) to click on the desired location for the new LV Center. Observe that a new, identical LV Center location is assigned for each gate. This step also causes all radial boundaries to be set to the radius of the current gate.
3. To reset the LV Centers back to their preselected locations, use the **Params** droplist, select the list option **Reset Stress** (or **Reset Rest**) and release.

Note: This action will reset any LV Centers that had been manually changed and restores all apex and base slices to their original locations.

Recentering & Renormalizing the Short Axis Volume

In certain cases, it may be useful to recenter and renormalize the gated SA images, if the LV appears either too high or too low in the frame, or in the rare case when the program fails to automatically find a valid LV center.

To re-center and re-normalize the gated Short Axis frames, use the **Params** droplist, select the list option **ReCenter Stress** (or **ReCenter Rest**) and release.

Note: This action will reset any LV Centers that had been manually changed and restores all apex and base slices to their original locations.

When satisfied with the LV Center positions and Radii assignments, click the option button labelled **Apex/Base**.

Apex & Base

The Apex and Base Window displays eight VLA slice images, one from each of the eight gated SPECT frames. Below each VLA slice, are displayed the apical and basal SA slices, which correspond to the selected apex and base. In this window, the user can both review and modify the automatically selected Apex and Base for each of the eight gated frames.

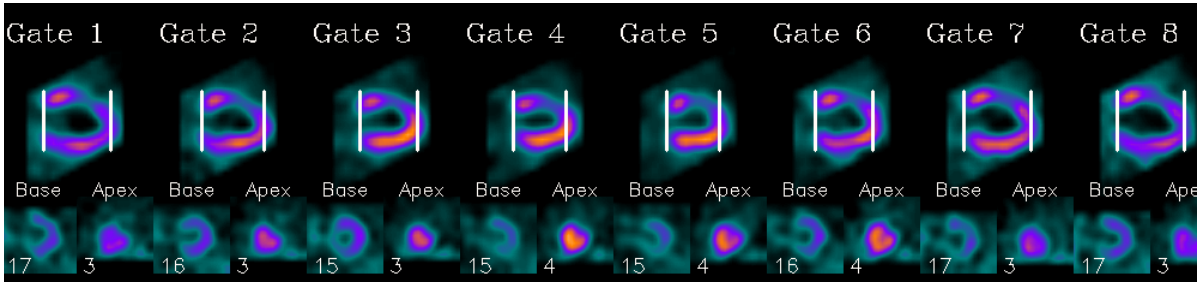


Figure 3-57. The Apex and Base Display, using overlays on the VLA Slices and corresponding apical and basal boundary SA slices.

Changing the Apex and Base

To change either the Apex or Base on one or more VLA frames, perform the following steps for each frame:

1. Using the mouse, place the pointer near the VLA slice image whose Apical or Basal slice selection is to be changed. For example, to move the apical boundary out, place the cursor to the right of the predefined apical boundary line.
2. Click the mouse button and observe that the boundary closest to the cursor, moves to the point selected by the cursor.
3. Manually adjust the apical or basal slice selections as described in Step 2, until satisfied.
4. To reset and restore all the preselected Apex and Base Selections, use the **Params** droplist, select the list option **Reset Stress** (or **Reset Rest**) and then release.

Note: This action will also reset any LV Centers that had been manually changed and causes any apices and bases, which had been changed, to be restored to their original locations.

Changing all 8 Apex and Base Slices

To simultaneously change the Apices and/or Bases on all VLA frames for one gated study, perform the following steps:

1. Using the mouse, place the pointer near one of the VLA images. For example, to move the apical boundary out, place the cursor to the right of the predefined apical boundary line.
2. Click the middle mouse button (or CONTROL key plus left mouse) and observe that the boundary closest to the cursor moves to the point selected by the cursor. Also observe that this boundary changes for each of the 8 VLA frames.
3. Manually adjust the apical or basal slice selections as described in Step 2, until satisfied.
4. To reset and restore all the preselected Apex and Base Selections, use the **Params** button, select the list option **Reset Stress** (or **Reset Rest**) and then release.

Note: This action will also reset any LV Centers that had been manually changed and causes any apices and bases, which had been changed, to be restored to their original locations.

The HLA Slice Display Option

To utilize the horizontal long axis slices for reviewing and changing the Apex and Base, click the **Slices: VLA** option button. This will toggle the display so that HLA slices are displayed. The button label changes to **Slices: HLA**.

Note: The HLA Slices screen is for review only. Apex and Base slices can only be changed on the VLA Display Screen.

The Volumes & EF Display

The “Volumes and EF” Window displays information and images related to LV function, wall motion and estimated wall thickening. The following quantitative data and image displays are included in this window:

- LV Volume Curve
- Calculated LV quantitative parameters: EF, EDV, ESV, SV and Mass.
- Quantitative wall thickening analysis (Estimated)
- Cine display of wall motion and wall thickening

Cine Slice Filters

The user has several options for how the gated cine slice images are to be filtered. These are available in a drop-down list labelled **Filter**, and the choices are shown in Figure 3-58. Changing the filter option using this drop-down list affects only the image display, and not volume calculations. If the global preference setting for filtering is set to pre-filter the data, then the option ***Pre*** will appear instead of ***None***.

It is recommended that gated data be pre-filtered, that is, subjected to spatial and temporal filtering before volumes and ejection fraction are calculated. This might be accomplished on the computer system that reconstructs the gated data but, if it is not, it can be done by ECToolbox, using the Pre-Filter preference setting. If pre-filtering is done before the data is used by ECToolbox, then it should not be pre-filtered again.

Note: Pre-filtering will slightly change the ejection fraction and volumes that are calculated. Choosing **Spatial** or **Temporal** from the dropdown box shown in Figure 3-58 is for display only, and does not affect calculations.

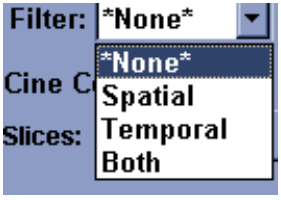


Figure 3-58. Filtering options for gated cine slices. “None” is the default.

Zoom Factor

The **Zoom** drop-down list allows the zoom factor for the images to be set.

The EF Method Option

By default, the ejection fraction shown on the Functional Analysis Screen is computed from the gated SPECT data exactly as described in Chapter 4, using modeled boundary points and geometric calculations. Two additional calculated ejection fractions may also be displayed. The **Options** pull-down menu contains an **EF Method** menu that may be switched between several options.

- **R0 (Original)**
- **R1 (y = .96x-.053)** This option uses the equation y = .96x -.053 to compute an EF that approximates the value that might be expected if the same data was processed using the Cedars' Quantitative Gated SPECT program. The data is assumed to have 8 gates. See the Technical Overview chapter for details on how and why this equation was derived, and when it may be useful.
- **R2 (y=1.22x-.072)**. This option uses the equation y=1.22x -.072, to provide an EF that approximates the value that might be expected if the same patient was studied using multiple gated blood pool analysis. See the technical overview chapter for details on how this equation was obtained.
- **R3 (y=0.855x + .0173)** This option uses the equation y = .855x +.0173 to compute an EF that approximates the value that might be expected if 16-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 EF's.

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.

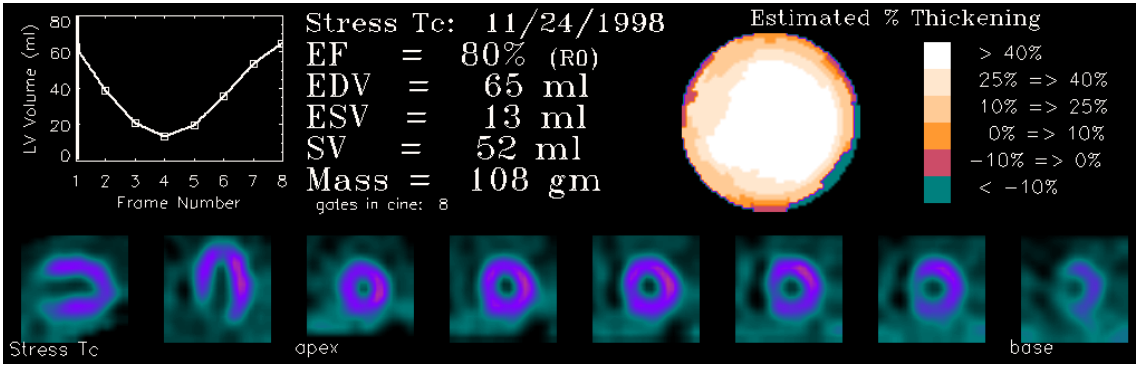


Figure 3-59. The "Volumes & EF" Window provides LV Volume Curve and

associated quantitative parameters, Cine Slice display of wall motion and thickening, and the Estimated % Wall thickening display.

Dynamic display of the gated slices can be used for reviewing both wall motion and wall thickening during the cardiac cycle. The cine is controlled by buttons at the top of the window (Figure 3-60).

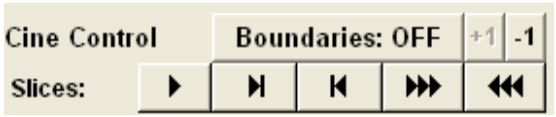


Figure 3-60. Cine display control buttons. The first button is labeled with a black square if the cine is currently running, and the black triangle shown above if it is not. Clicking the triangle starts the cine. Clicking the square stops it.

The Cine Slice Display

The following options are available for controlling the cine display:

1. Using the mouse button, click on the **Start** button. Note that the “Start” button label changes to “Stop” as soon as the cine is initiated.
2. Click on the **Faster** button to increase cine speed and on the **Slower** button to decrease speed.
3. Click on the **Step F** button to step forward through the study, one frame at a time. Similarly, click on the **Step R** button to step backward.
4. Use the **-1** button to subtract one gated frame from the end of the cine. This is useful if a gating error causes the last frame to be count-poor and thus appear much lighter than other frames. The subtracted frame can be restored using the **+1** button. If the number of frames currently included in the cine display is changed to a value less than 8, then the number will be displayed in the window, below the Mass value.

Note: Certain slices are automatically chosen to be representative of the LV myocardium, and cannot be changed by the user.

The Cine Display with Boundaries On

To view the gated slice cine images with overlaid myocardial boundaries, click the **Cine Boundaries: Off** button. To remove the boundaries, click this button again. Note that the button label indicates whether or not boundaries are currently displayed.

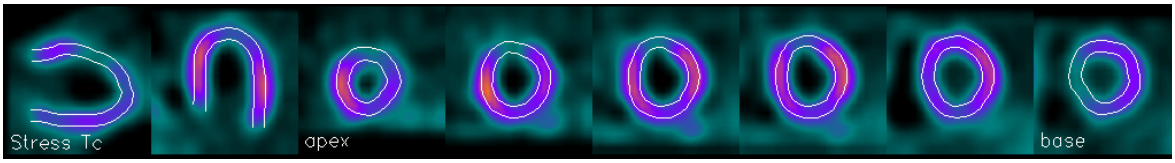


Figure 3-61. Cine Slice Display with overlaid myocardial boundaries.

Cine Image Intensity Controls

Slider bars are available on the Functional Review window, for adjusting image brightness and contrast. The upper slider controls brightness and the lower one controls contrast (lower window level). These controls are analogous to the sliders that appear on the Slices Window. For a detailed explanation of how the sliders operate, see “Color Table Tools” on page 47. Changing the slider position will affect all of the gated cine images. The images cannot be individually adjusted.

The Cine 3D Display

There is a button labeled **Cine: Slices** indicating that the currently-displayed cines are composed of oblique slice images. To view the cine as a set of 3D maps, click the **Cine: Slices** button. The PerfSPECTive 3D cine will replace the cine slices, and the button label will change to **Cine: 3D** to reflect the current state of the display. Clicking the button again will return to display of the cine slices.

When selected, the Cine 3D presents four views of the PerfSPECTive 3D Display. These views change shape during the cardiac cycle, as the LV empties and then fills. The “cage” outline is used to provide an end-diastolic, epicardial surface map reference. The same Cine control tools are used to adjust the cine display.

Note: The **Options** pull-down menu contains a **3D Color Table** menu that may be switched between **Color** and **BW** (black-and-white). The **BW**

option is best used for looking at wall motion, while the **Color** option is best used for looking at wall thickening.

For a single gated 3D cine image, which can be tumbled and rotated in any orientation, please use the Gated PerfSPECTive button on the PerfSPECTive Window. (See “The Gated PerfSPECTive Display” on page 93.)

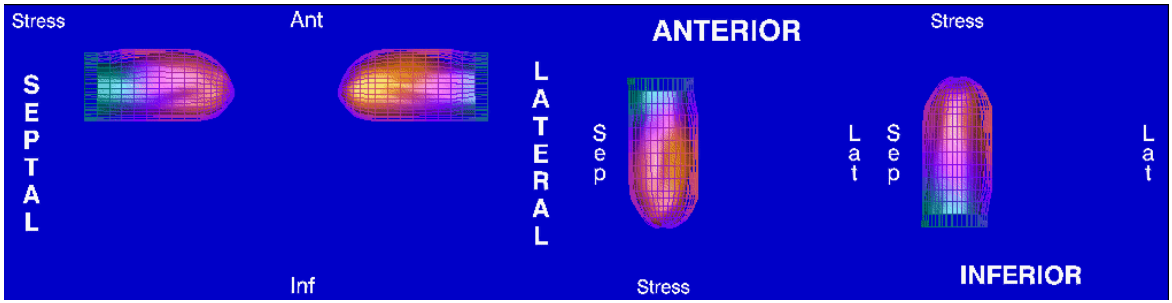


Figure 3-62. The Cine 3D PerfSPECTive Display. Reference labels: “Ant” indicates Anterior Wall, “Inf” indicates Inferior Wall, “Sep” indicates Septal Wall and “Lat” indicates Lateral Wall. “SEPTAL”, “LATERAL”, “ANTERIOR” and “INFERIOR” refer to the view being displayed. For example, the SEPTAL view represents the myocardium as seen from the septal side. Note that space is allocated on the display for images from a second gated study.

The Estimated % Thickening Display

On the Volumes and EF Window, the top right side of the screen is used to display wall thickening. The following images are included in this window:

- Estimated Wall Thickening Polar Map and color reference bar.

Note: 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 Estimated Percent Wall Thickening Polar Map is a useful tool to visually assess relative global thickening over the entire LV.

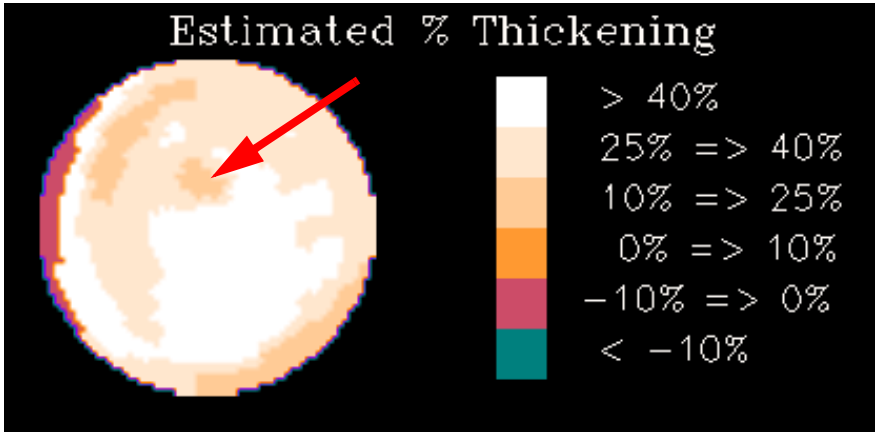


Figure 3-63. The Wall Thickening Display. This case illustrates a thickening defect evident on the End-Systolic SA slice and on the Wall Thickening Polar Map.

SyncTool™ for Phase Analysis

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. Display of this information and the results of analysis of systolic wall thickening are controlled by SyncTool. The tool is invoked by selecting the **SyncTool:** button under **Functional Analysis Options**. The tool's main display screen is shown in Figure 3-64.

This display includes static image elements, a dynamic image, phase histograms, and a summary of numeric parameters of systolic wall thickening.

Note: For phase analysis to work correctly, the gated study must be time-smoothed and properly gated to the R-wave of the ECG.

For discussion of other elements of functional analysis in a gated SPECT study, see "The Functional Analysis Tools" on page 96. To review the filtering of gated images, including the time (temporal) filtering used in ECToolbox, see "Cine Slice Filters" on page 102.

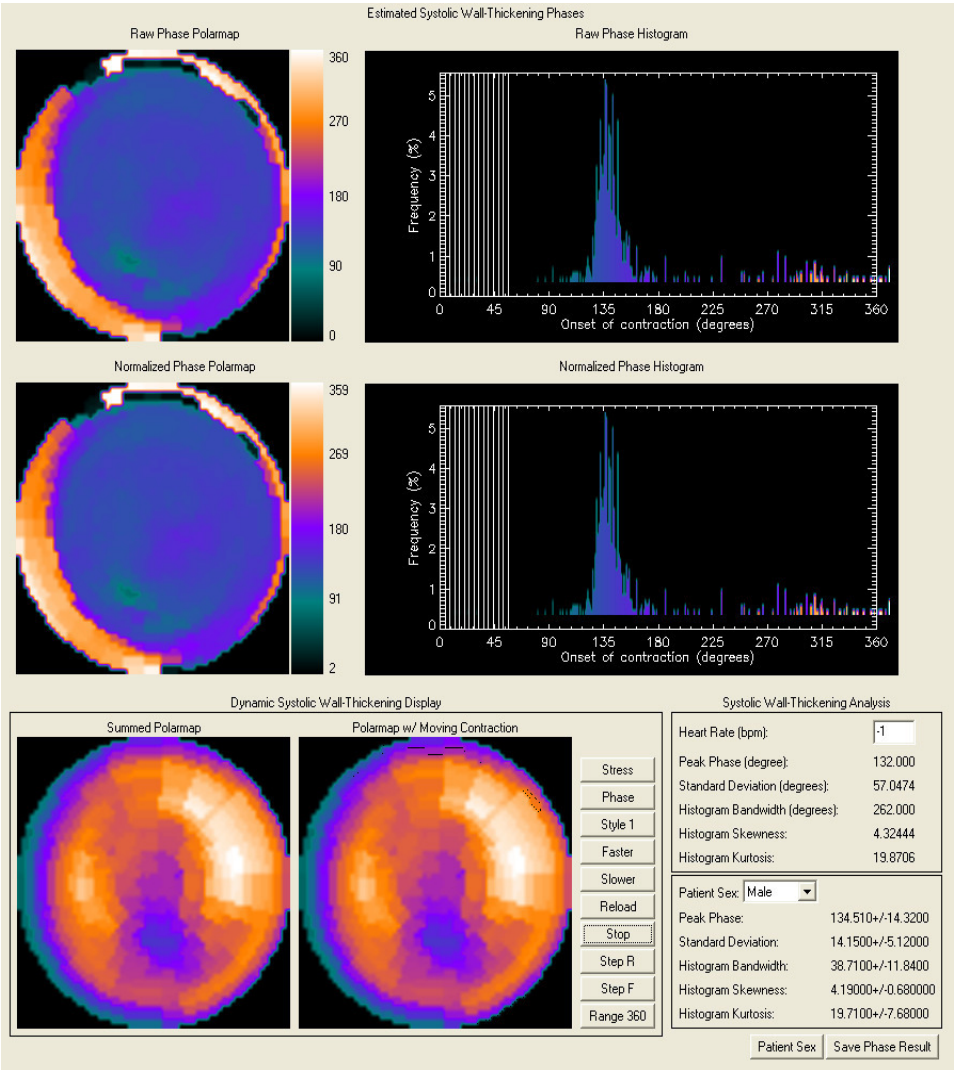


Figure 3-64. The SyncTool phase analysis display.

In the upper left of the display are two polar maps. In each of these is plotted the time at which every pixel begins to contract, expressed as a phase value between zeroand 360. Different values are plotted as colors, with a colorbar displayed for reference. The Raw Phase map plots all possible phases, with zero at the lower (black) end of the colorbar. 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, which is 22 in the example of Figure 3-64. The upper end of the colorbar represents the highest phase value present.

In the lower left of the display screen are two more polar maps, illustrated in Figure 3-65. These maps are identical to each other, and represent the raw perfusion distribution for the study, which is discussed in “The Polar Maps Window” on page 63. The rightmost map is part of a dynamic display of the pattern of contraction across the ventricle.

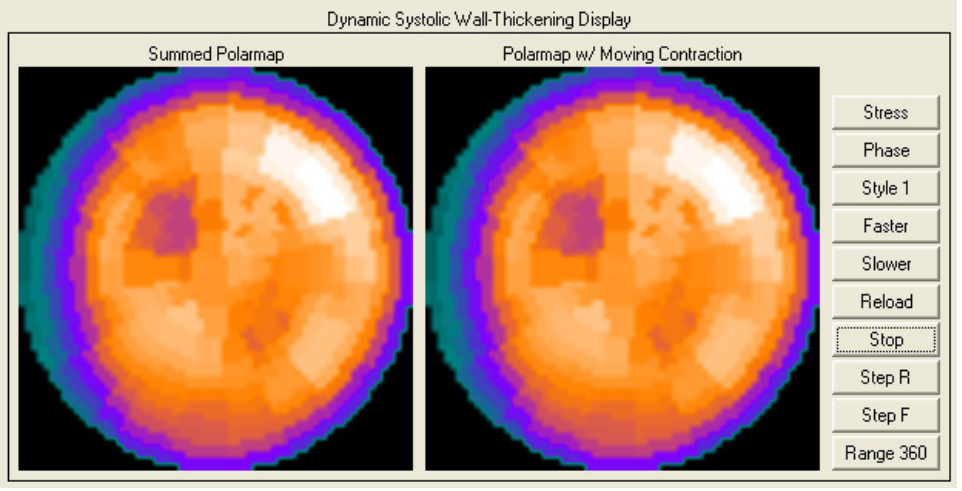


Figure 3-65. The display of systolic wall thickening, part of the SyncTool review screen. Onset of contraction is displayed dynamically on the right-hand polar map, and is controlled by the buttons shown.

Control of Phase Display

When SyncTool is first displayed, this dynamic display will be in motion. Pixels 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.

The dynamic display is controlled by the function buttons, which provide the following options:

- **Rest Only**, indicates what part of the image data is shown. If the button label is **Stress Only**, then only stress gated data is available. If both the stress and rest image acquisitions were ECG-gated, then the stress images and values are shown, and clicking this button will switch to the rest phase analysis results.
- **Phase**, indicates that the x-axis of the histogram displays shows units of degrees (zero to 360) at which various pixels experience onset of contraction. Clicking this button will change the button label to **Time**, indicating that the display's x-axis shows units of time (in milliseconds) at which onset of contraction occurred, relative to the first pixels to contract.
- **Style 1**, switches between style 1 and style 2 for display of the wave of contraction. See the next section for an explanation of styles.
- **Faster**, increases the speed of the dynamic display.
- **Slower**, decreases the speed of the dynamic display.
- **Reload**, re-starts the dynamic display.
- **Stop**, pauses the dynamic display on the current frame.
- **Previous**, moves to the previous frame of the dynamic display. The cursor display changes from a series of lines to a single line drawn on the phase that represents the front of the contraction wave.
- **Next**, moves to the next frame of the dynamic display. The cursor display changes from a series of lines to a single line drawn on the phase that represents the front of the contraction wave.
- **Range 360**, indicates that the current scale of the histogram x-axis is set so as to show a range of 360 degrees. Clicking this button will cycle between the other settings, which show a range of 90, 180 or 270 degrees. Changing this setting has the effect of expanding or contracting the scale of the displayed histogram.

Modes of Phase Display

The histogram of phases, characterizing the patient's LV contraction pattern, is displayed on the screen (Figure 3-68). There are two styles of visually displaying the wave of contraction on the patient's polar map. In Style 1 (Figure 3-66), 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 (Figure 3-67), 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.

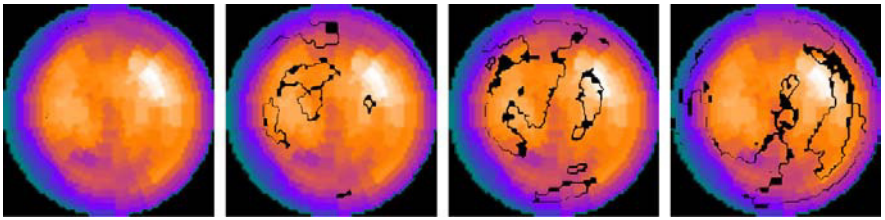


Figure 3-66. Four frames from the dynamic display of ventricular contraction, using the Style 1 setting. Pixels are set to black when the phase changes, then return to their original color.

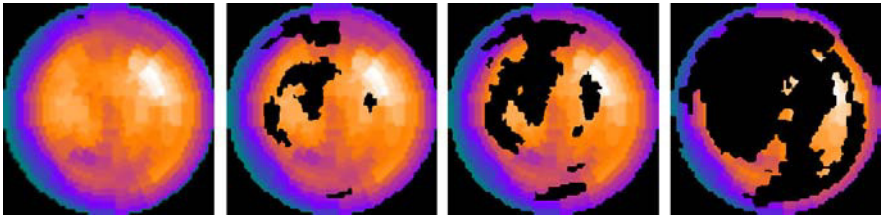


Figure 3-67. Four frames from the dynamic display of ventricular contraction, using the Style 2 setting. Pixels are set to black when the phase changes, and remain black. Eventually, all pixels are black, and then the cycle repeats. These frames closely match those displayed in Figure 3-66.

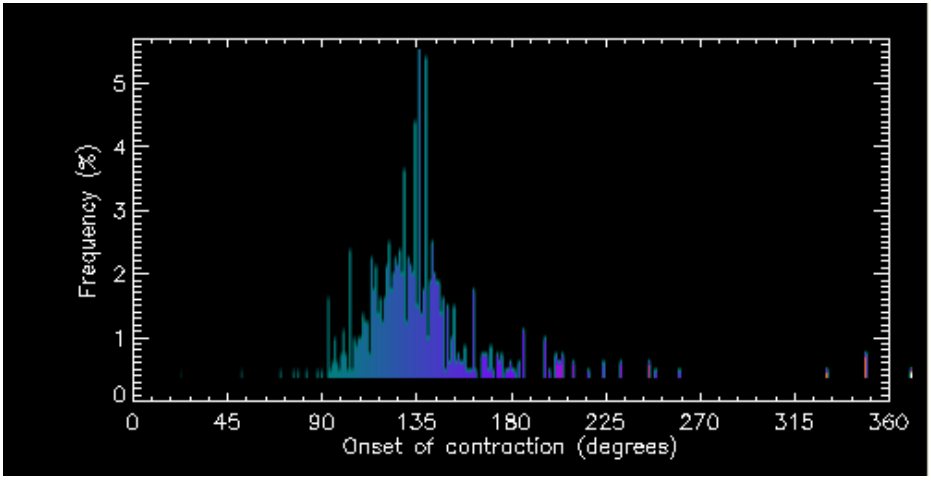


Figure 3-68. The phase histogram display.

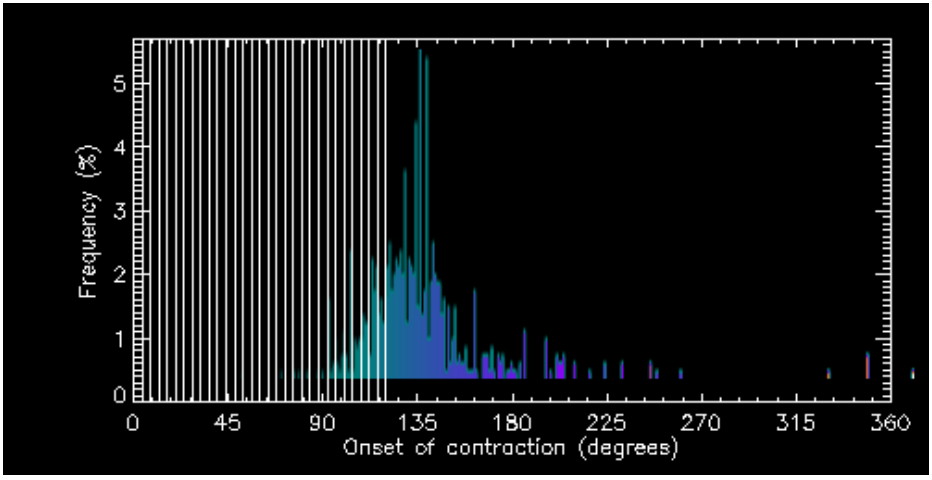


Figure 3-69. The phase histogram, with line markers. During dynamic display of the contraction wave, the vertical lines begin at the left side of the histogram, and progress toward the right side. At any given moment, right rightmost line indicates the current phase at which pixels are blacked out on the polar map.

Systolic Wall Thickening Analysis Results

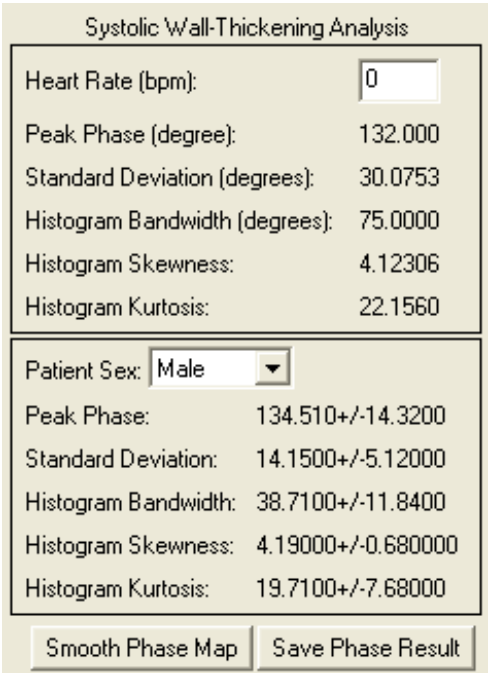


Figure 3-70. The summary of wall thickening and phase analysis.

Quantitative indices calculated from phase, and other values, are displayed in a table on the lower right of the Phase Analysis review screen, as shown in Figure 3-70. The first list contains values relevant to the current patient, and includes the following:

- **Heart Rate**, displays the calculated patient heart rate.
- **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 has the tail longer 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).

The second list of values is similar to the first, but contains normal values, expressed as mean plus-or-minus one standard deviation. The sex of the patient group used to derive the normal ranges is also displayed.

There are two buttons below the value lists, which control aspects of the display and analysis results.

- **Smooth Phase Map**. Selecting this button performs a mild smoothing on the histogram, reducing the visual effect of abrupt changes in adjacent values.
- **Save Phase Result**. Selecting this button saves a textfile to disk, containing all of the values reported in the two lists on the screen.

AdreView™ Tools

ECToolbox contains tools to analyze SPECT images acquired using AdreView (I-123 mIBG), a radiopharmaceutical for imaging myocardial innervation. There are two specific tools:

- determination of uptake of mIBG in the heart relative to uptake of some SPECT perfusion agent such as tetrofosmin, sestamibi or thallium.
- calculation of mIBG heart-to-mediastinum ratio from transaxial images.

Quantifying mIBG uptake

If mIBG and perfusion images are both available, to assess mIBG uptake follow these steps:

1. Display the Match/Mismatch page. Note that the Polar Maps page is not available for this type of study.
2. mIBG and perfusion uptake differences are shown in the top three rows of maps. This display is similar to that for FDG/perfusion. Three additional maps are displayed at the bottom of the page.
3. In the boxes to the left of the maps, enter the actual doses injected for I-123 mIBG and for the perfusion study.
4. The maps will be re-normalized from the dose values entered. Ratios (mIBG/perfusion) are calculated and displayed to the right of the maps.

See Figure 3-71 for an example of how these polar maps appear.

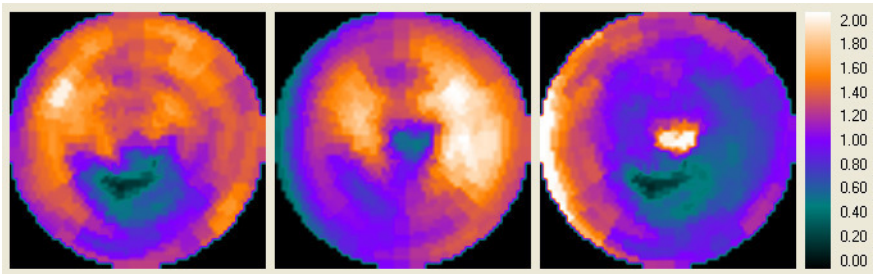


Figure 3-71. I-123 mIBG polar map (left), myocardial perfusion (center) and ratio map (right). Numbers adjacent to the color bar give mIBG/perfusion ratios that correspond to different colors in the ratio map.

Heart to Mediastinum Ratio

ECToolbox allows calculation of the heart-to-mediastinum ratio for SPECT images of I-123 mIBG. To access this tool, there is a button at the bottom of the options buttons on the Parameters page of ECToolbox. Clicking this **AdreView Parameters** button sends the mIBG planar projection dataset, and the perfusion planar projections if present, to the H/M Ratio tool. To operate the tool, 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:
   a. position the cursor in the center of the heart.

b. click and hold the left mouse button, and move toward the ventricular apex. A line will be drawn. Release the mouse button.

c. click and hold the right mouse button. As you move the mosue, 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 ratio of heart to mediastinum, are displayed in boxes to the far right of the screen.

Figure 3-72 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.

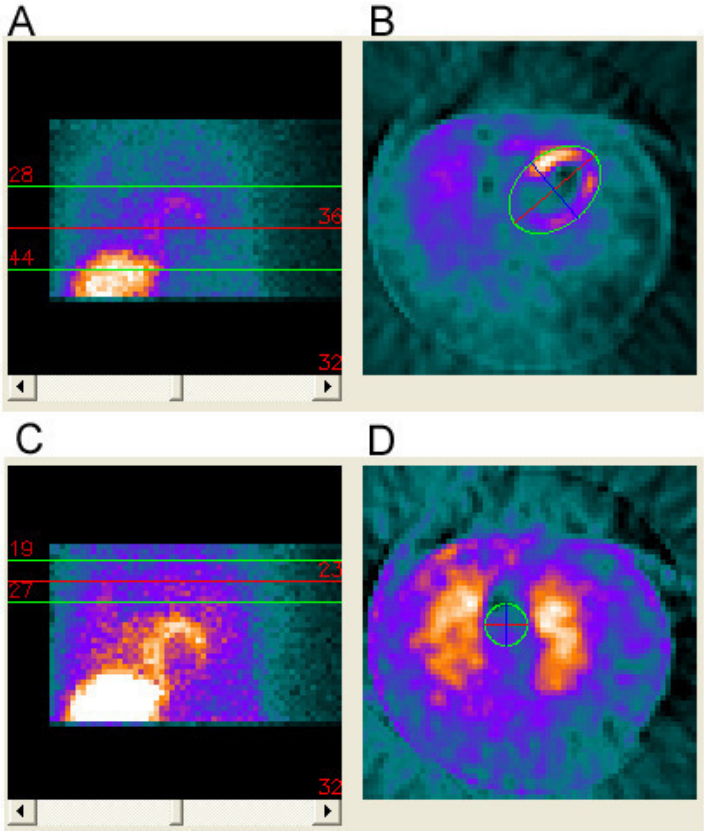


Figure 3-72. Images used for determining heart-mediastinum ratios. Heart limits are set on the mIBG projections (A), and the heart volume more precisely identified on a mid-transaxial slice (B). Mediastinum volume is set using projections (C) and a transaxial slice (D).

For More Information

For more information on the operation of tools within ECToolbox that relate to I-123 mIBG, please refer to the ECToolbox user manual webpage:

someURL

PET FDG/Perfusion Match/Mismatch Analysis Tools

Myocardial tracer uptake seen on F-18 FDG studies is an indicator of myocardial glucose metabolism. The pattern of myocardial perfusion can be seen by using tracers such as Rb-82. ECToolbox contains special tools for analyzing the relationship between metabolism and function, and for showing matches and mismatches between the two. These tools are automatically made accessible when one chooses an FDG image as one of the studies to be analyzed. In this case, the button **Match/Mis**, in the permanent button group, will become active. Selecting this button starts the analysis.

There are three screens that are part of the match/mismatch analysis, and these are discussed in the following pages. In addition, other standard screens have been modified to handle these types of combined perfusion-metabolic studies. Once the Match/Mismatch tool has started, the permanent button set will change to reflect the fact that certain options are unavailable, since they are not appropriate for combined perfusion and metabolism data. This is illustrated in Figure 3-73.

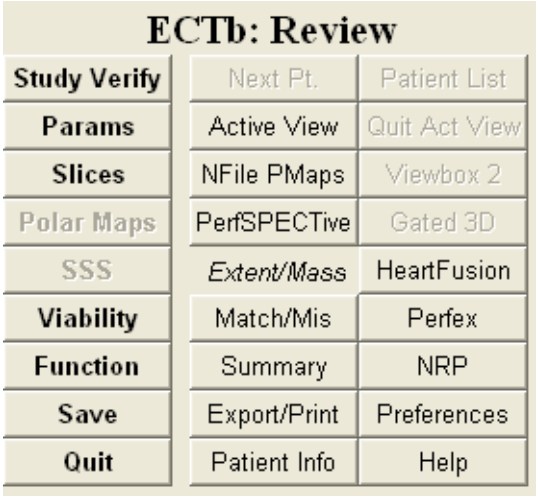


Figure 3-73. The permanent buttons, after starting ECToolbox with a perfusion dataset and an FDG metabolism dataset.

The Match/Mismatch tool has several option buttons, which appear below the Patient Info area. These are shown in Figure 3-74.

Figure 3-74. Option controls for the Match/Mismatch tool.

The options are:

- **Overlays: Off** - by default, there are no segment overlays on the polar plots. Clicking this button displays a 17-segment overlay on the plot, useful for localizing areas of perfusion or metabolic abnormality.

  Note: This is not the same 17-segment model as used for perfusion scores.

- **Model: Quantitative** - When overlays are displayed, this button becomes active. Presently, the only option is “Quantitative”.
- **Normalized: Auto** - Switches between automatic (default) and manual methods of normalizing the FDG polar map display to the perfusion map.

The % Difference Match/Mismatch Page

This page, shown in Figure 3-75, has a similar layout and look as the standard polar maps screen. It allows the user to normalize the FDG and perfusion polar maps, to look at the difference between the two distributions, and set a threshold according to percent difference as a baseline value for mismatch.

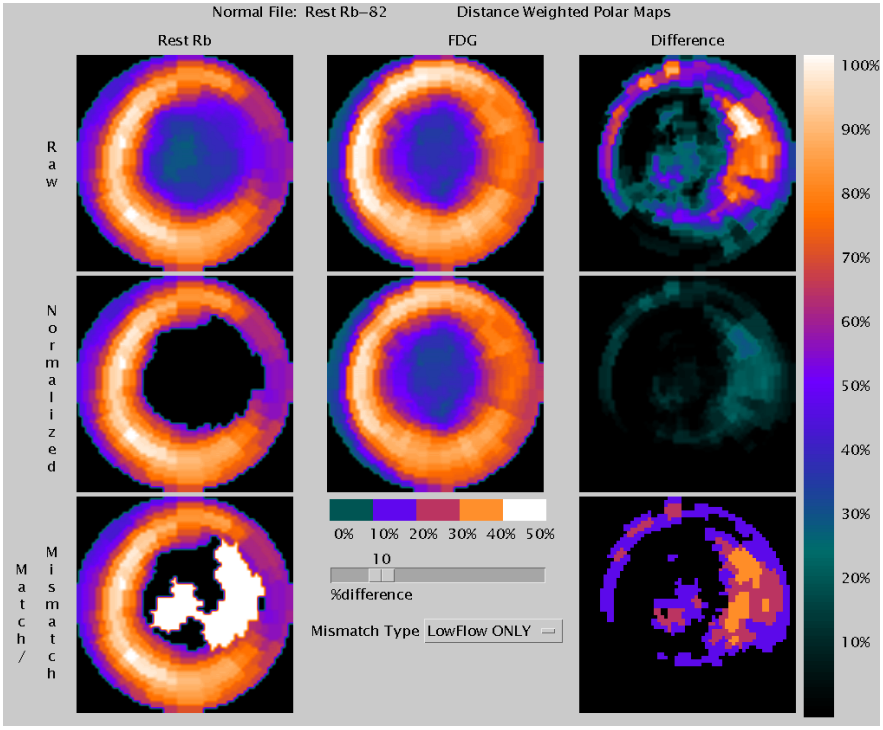


Figure 3-75. The % Difference Match/Mismatch page.

The top row of the match/mismatch page shows distance-weighted raw polar maps of the perfusion study (left), the FDG study (middle) and the difference between the two (right). All of these polar maps are normalized so that their individual maximums are displayed as white. The middle row of this page shows the perfusion study (left) after it has been compared to the appropriate normal database; thus, it is dispalyed as a blackout map. Areas blacked out in this polar map are those areas which have abnormal resting perfusion. The middle window in the middle row shows the FDG study normalized to the perfusion study. The types of normalization are discussed below. The rightmost polar map is the %difference between the normalized FDG and perfusion study. The color bar on the right of this page is labeled to indicate which colors correspond to which percentages

on this polar map. On the rightmost side of the bottom row is a quantized map of %difference between FDG and perfusion. The colors on this map correspond to percent differences in increments of 10%. The color bar in the middle of the bottom row shows these colors and their corresponding percent difference values. A user-set threshold value of %difference is the baseline for mismatch. That is, 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 the threshold percentage set by the user are defined as a mismatch.

To Change the %Difference Threshold Value.

1. Use the mouse button to click and hold on the slider bar.
2. While holding the mouse button down, move the slider to the desired threshold (Figure 3-76).
3. Release the mouse button when the desired threshold is obtained.

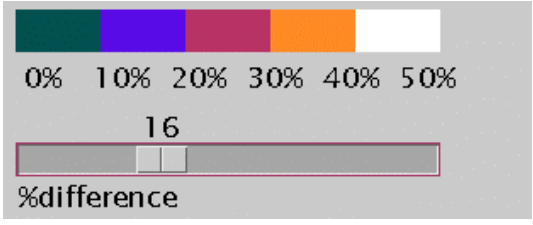


Figure 3-76. Enlarged view of the slider bar shown in Figure 3-75, for setting the % Difference Threshold.

The %difference map on the right in Figure 3-76 is adjusted as the user modifies the slider bar, so that regions below the threshold are displayed as black. On the left side of the bottom row, the resting perfusion blackout map is shown with any areas of mismatch displayed as white. Note that this map also changes as the threshold percentage difference slider bar is changed.

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.

This causes all regions that survive the %difference threshold, as displayed in the lower right hand polar map, to be displayed as white in the lower left hand polar map. This is shown in Figure 3-77; contrast this screen with the example shown in Figure 3-75.

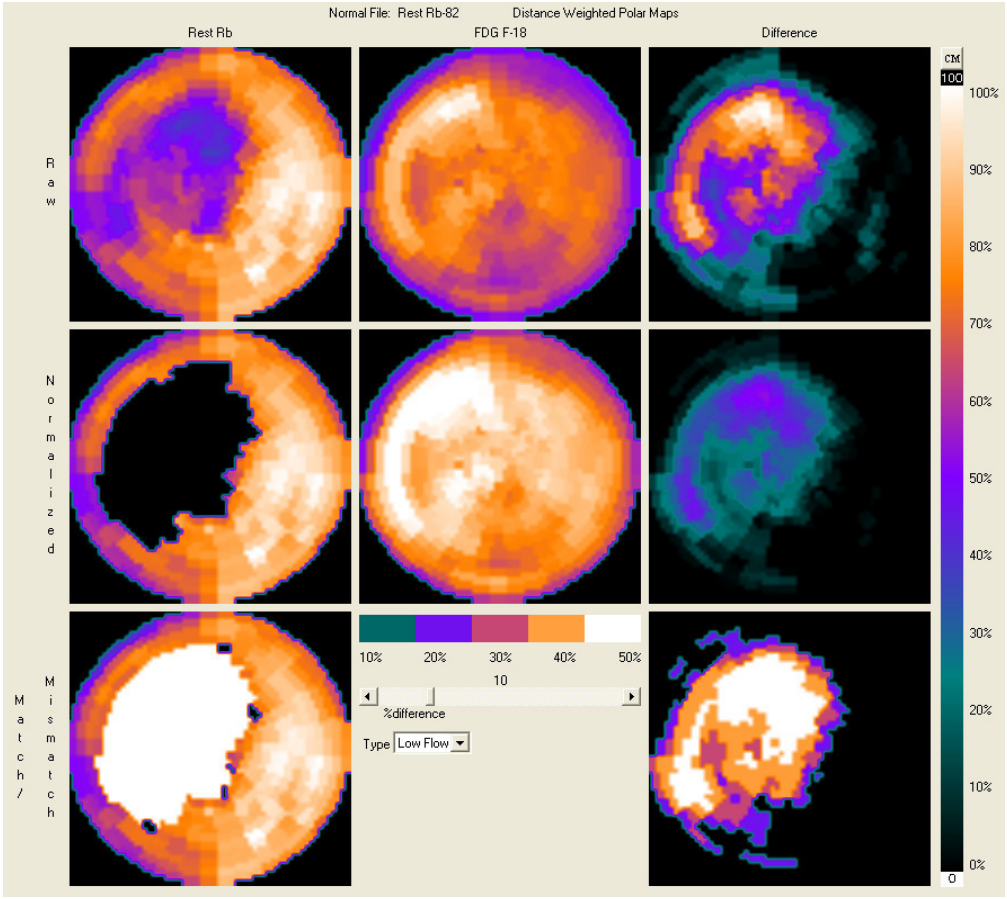


Figure 3-77. The lower right polar map shows all pixels that are above the user-set 10% threshold. The same pixels are shown in white on the lower left map.

To Change the Type of Mismatch:

1. Use the mouse button to click on the **Type** pull-down menu underneath the %difference threshold slider bar. This control is shown enlarged, in Figure 3-78. Choose **ALL regions** to indicate that all differences above the threshold should be considered mismatches.
2. Choose **Low Flow Only** to indicate that only differences above the threshold and in the region of a perfusion abnormality should be considered mismatches.

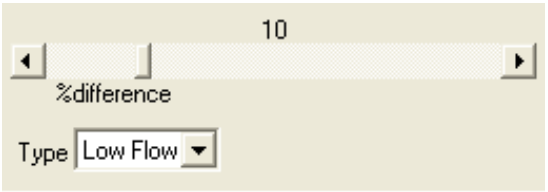


Figure 3-78. Enlarged view of a portion of Figure 3-77, showing the pulldown menu used to indicate how mismatch areas should be displayed.

Normalization Options

One of the option buttons for the match/mismatch tool is the **Normalized: Auto** button. This allows switching between automatic (default) and manual normalization of the polar maps.

Automatic normalization is performed by finding the average value of perfusion in the normal areas of the perfusion study and scaling the FDG study such that it has the same average value as the perfusion study in the same areas. Manual normalization in this context is similar to that used for the Normalization Plots in a standard perfusion study. See “Manual Normalization” on page 69. If manual normalization is selected, the pixel currently being used for normalization is highlighted as a black point on the perfusion (upper left) and metabolism (upper middle) maps. The user can choose any part of either map to use as the normalization point. The FDG scan will then be scaled such that it has the same value as the perfusion map at the chosen point. Difference images and match/mismatch maps are adjusted accordingly. The pixel chosen for normalization is again displayed in black, as seen in Figure 3-79.

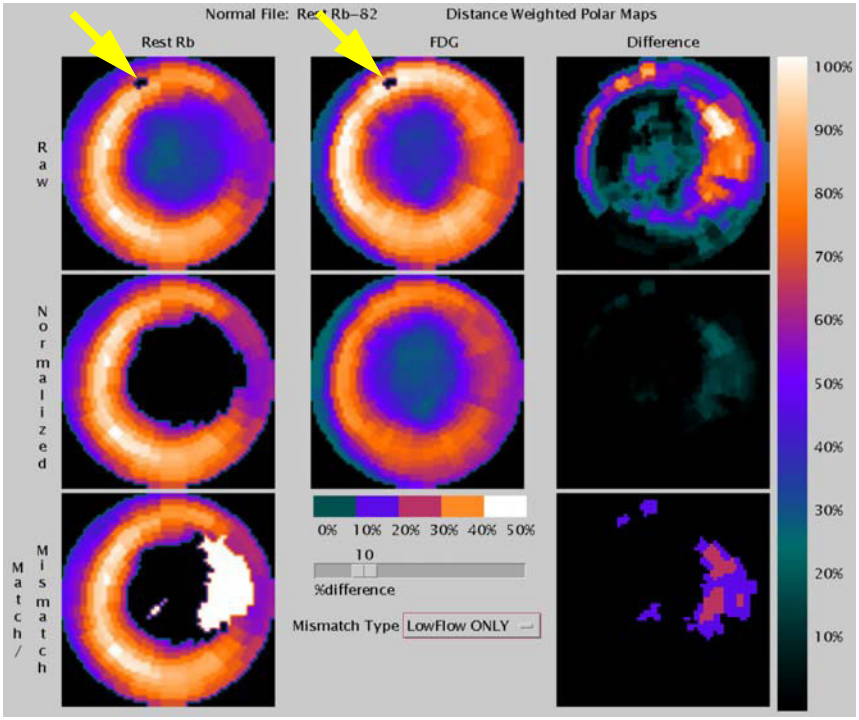


Figure 3-79. The pixel that is used for normalizing the FDG study relative to the perfusion study is set to black on this display, as indicated by the yellow arrows.

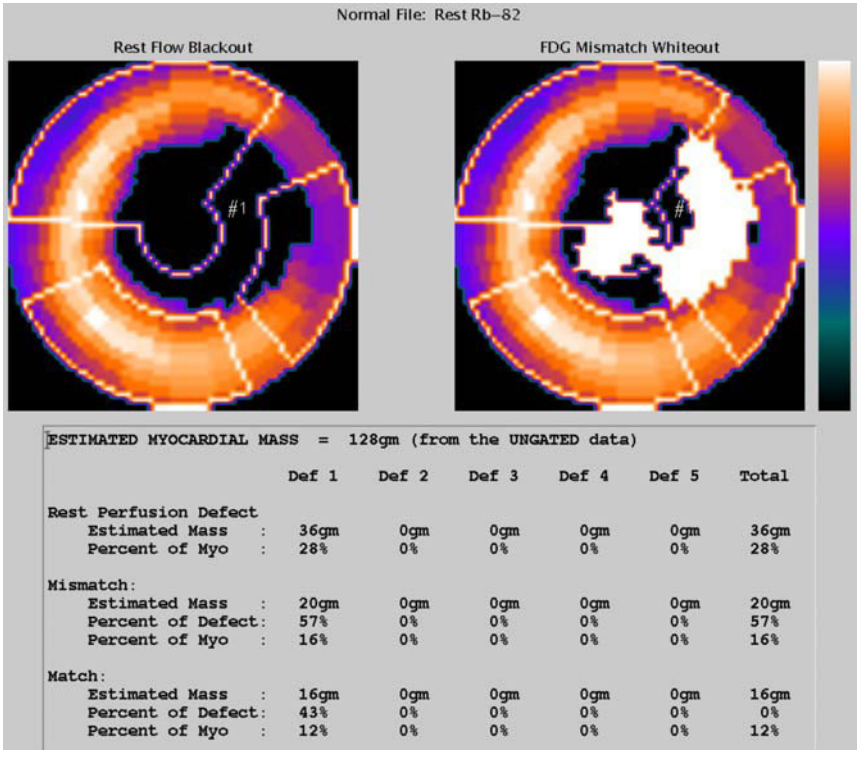
To Choose a Region for Manual Normalization.

1. Use the mouse to move the cursor to the desired place on the top left or top middle polar map.
2. Click the mouse button.

Extent/Mass Screen

Extent and mass of myocardial areas of match and mismatch are displayed on this screen; this screen is similar to the Extent/Mass screen used for perfusion quantification. In this case, however, the extent and mass values listed in the table are based on the most recent processing

(including normalization, threshold, and mismatch type) performed on the match/mismatch screen. Therefore, if the mismatch type is Low Flow Only, only regions above the user-set threshold in the abnormally perfused region of the myocardium will be used to calculate the mass of mismatches. This is shown in Figure 3-80.



ESTIMATED MYOCARDIAL MASS = 128gm (from the UNGATED data)

	Def 1	Def 2	Def 3	Def 4	Def 5	Total
Rest Perfusion Defect						
Estimated Mass :	36gm	0gm	0gm	0gm	0gm	36gm
Percent of Myo :	28%	0%	0%	0%	0%	28%
Mismatch:						
Estimated Mass :	20gm	0gm	0gm	0gm	0gm	20gm
Percent of Defect:	57%	0%	0%	0%	0%	57%
Percent of Myo :	16%	0%	0%	0%	0%	16%
Match:						
Estimated Mass :	16gm	0gm	0gm	0gm	0gm	16gm
Percent of Defect:	43%	0%	0%	0%	0%	0%
Percent of Myo :	12%	0%	0%	0%	0%	12%

Figure 3-80. Estimated extent and myocardial mass for match/mismatch.

If the mismatch type is set to "All Regions", i..e., all areas of the myocardium that survive the 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. This is shown in Figure 3-81.

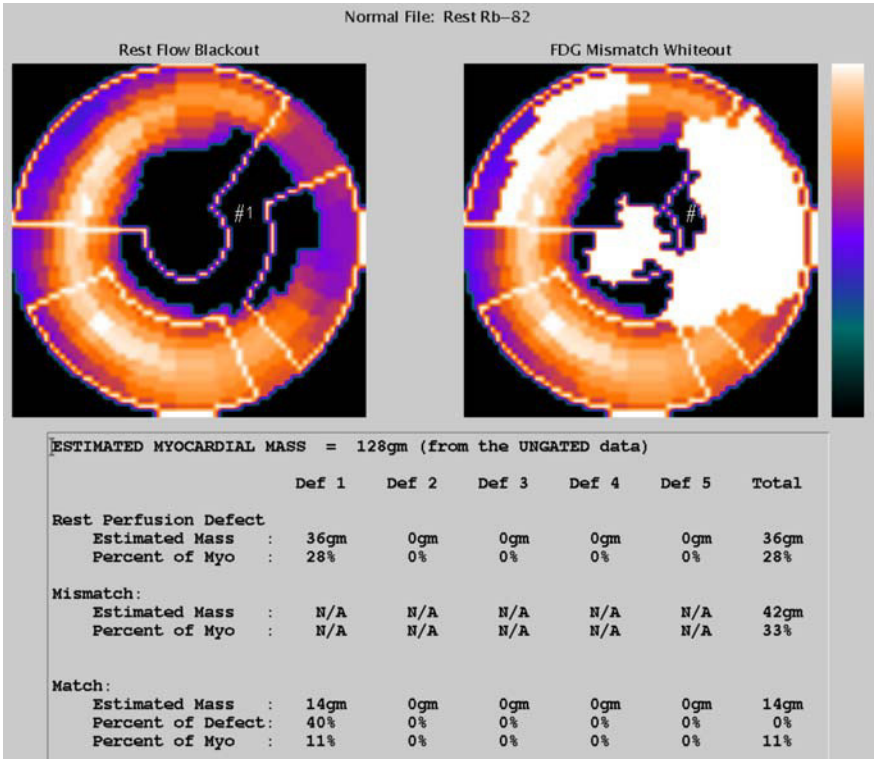


Figure 3-81. Extent and mass, in an example where the mismatch area extends outside the single blacked-out defect.

The Estimated Match/Mismatch Window

This window allows the user to define matches and mismatches between a rest perfusion distribution and FDG metabolism distribution using an automatically quantitated perfusion study and a thresholded raw FDG study.

The quantitated rest perfusion polar map is shown on the left; abnormal regions of perfusion are displayed as blacked out areas. The FDG metabolism polar map is shown in the middle. This metabolism

distribution can be thresholded so that regions below the threshold are displayed as black. Areas that are black in both perfusion and metabolism maps (matches) are displayed as black in the right hand map. Areas that are black in the perfusion map but not in the metabolism map (mismatches) are displayed as white in the right hand map. As in the Extent/Mass Screen, statistics about each area of match and mismatch are detailed in the table. This is shown in Figure 3-82.

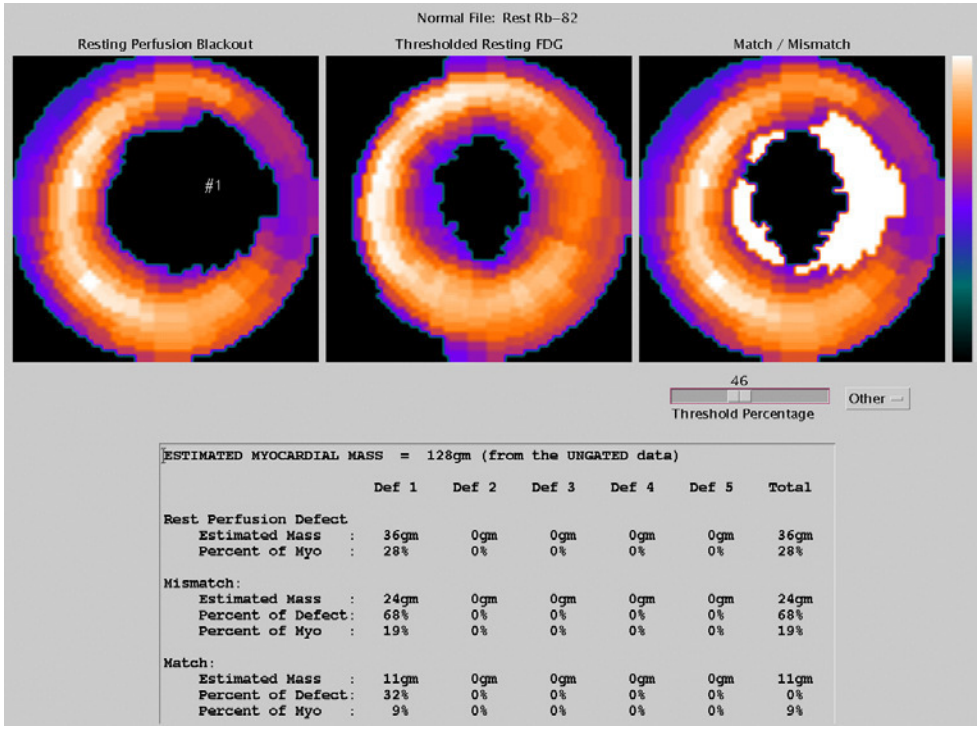


Figure 3-82. Estimated match/mismatch between raw FDG and rest perfusion..

The threshold is expressed as a percentage of the maximum metabolism count value. It can be modified by the user as desired.

To Change the %Maximum Metabolism Threshold Value, perform either of the following sequences of steps. (See Figure 3-83)

1. Use the mouse button to click and hold on the slider bar.
2. While holding the mouse button down, move the slider to the desired threshold.
3. Release the mouse button when the desired threshold is obtained.

OR:

1. Use the mouse button to click on the Drop List next to the slider bar.
2. While holding the mouse button down, move the cursor to the desired preset threshold selection.
3. Release the mouse button when the desired threshold is obtained.

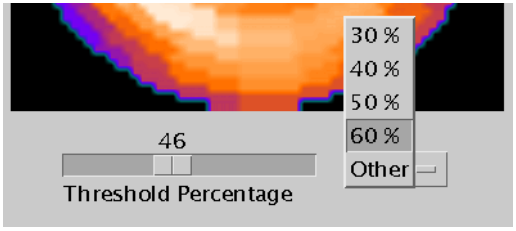


Figure 3-83. Several preset thresholds are available from the popup window, or the threshold can be set to any value using the slider bar.

HeartFusion™ Tool

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 PET short axis datasets and one or two coronary model files. At least one of the selected PET 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.

After data is selected the usual ECToolbox data validation window is displayed. The perfusion part of the study is processed in a similar way to a standard perfusion SPECT or PET study. On the Parameters page, ventricular center, radius of search and apex and base slice limits can be set, in preparation for quantitative analysis. See “Setting Quantitative Parameters” on page 40 for an explanation of these steps.

Once parameters have been set correctly, all of the standard ECToolbox options and screens relating to perfusion are available, including slices, polar maps and defect extent/mass.

If a gated dataset was selected as input when starting ECToolbox, you can select **Functional Analysis** to process these images. Parameters for functional analysis are set just as they would be for standard gated processing. There are two steps in this process:

1. Click the **Center & Radius** button to review center and radius of search for each gate. These settings should be changed only if they are incorrect.
2. Click the **Apex & Base** button to review slice limits for each gate. These should be changed only if they are incorrect.

See the sections beginning with “Changing the Radii” on page 98 for the details of these steps. Once all gated parameters have been set correctly, the functional review screen is available by clicking the **Functional Analysis** button.

The Interactive PerfSPECTive Display

The controls and options used by HeartFusion can be accessed by clicking the **HeartFusion** button, which is in the Permanent Button group. If the coronary models do not include the posterior descending artery, the program will present a message stating that warping may not work. If this happens, click the **OK** button on this message window to proceed.

The next image window that appears is an interactive PerfSPECTive display. It shows stress and rest 3-D maps, coronary arteries, and short axis and vertical long axis slices. When first displayed, the window appears as in Figure 3-84, with each 3-D map contained within a white box. The 3-D maps can be interactively dragged to various orientations using the mouse by clicking on one of the models with the left mouse button and holding the button while moving the mouse. Both 3-D maps move together. As the heart is rotated into various angles, the box, which is labelled with text, serves to orient the user to which myocardial wall is in front.

By using the mouse to drag the slider bar adjacent to each slice, any slice number can be viewed, to relate the slice images to the 3-D map.

Note: To reset the maps to their default Anterior orientation, you can either:

- drag the model manually, or
- click any other button in the Permanent Button set, and then click **HeartFusion** again.

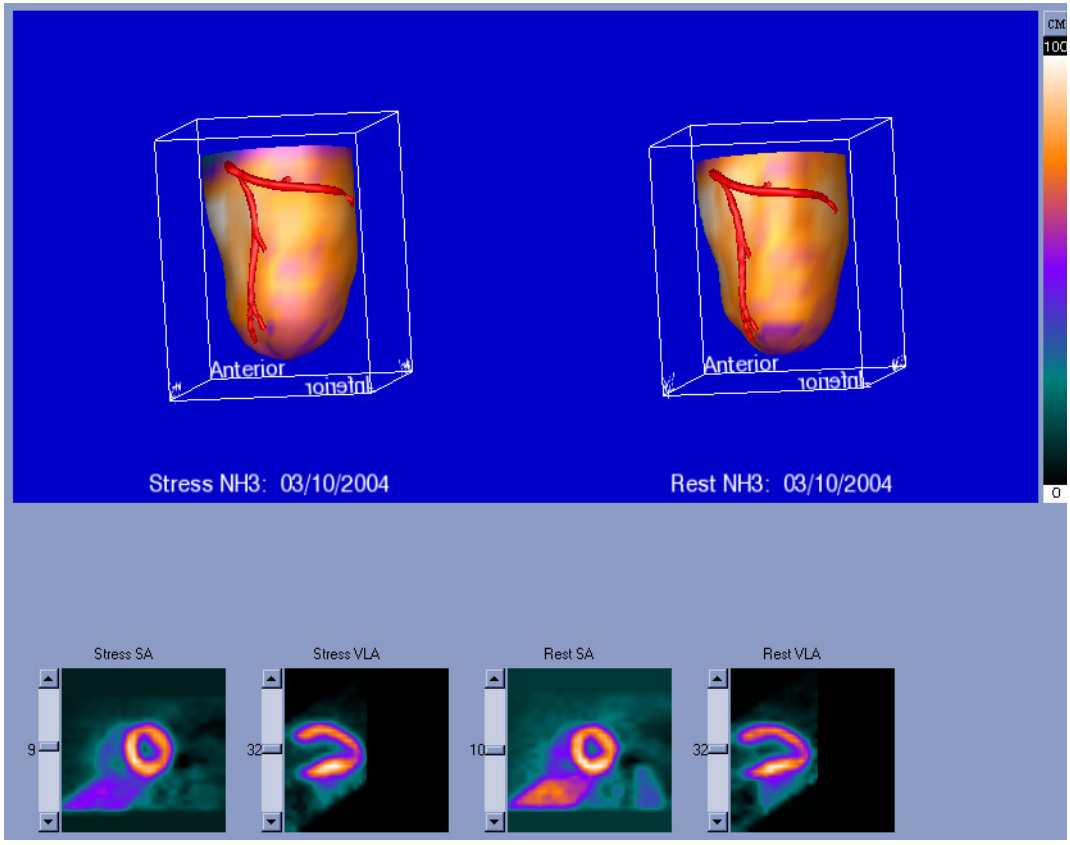


Figure 3-84. The Interactive PerfSPECTive window. The white box containing the 3-D map shows a label indicating which myocardial wall is in front. Each side has a label, which can be seen when the box is rotated into various angles.

Controlling Fusion Options

Tools for controlling the 3-D maps and coronary trees are activated by the buttons shown in Figure 3-85.

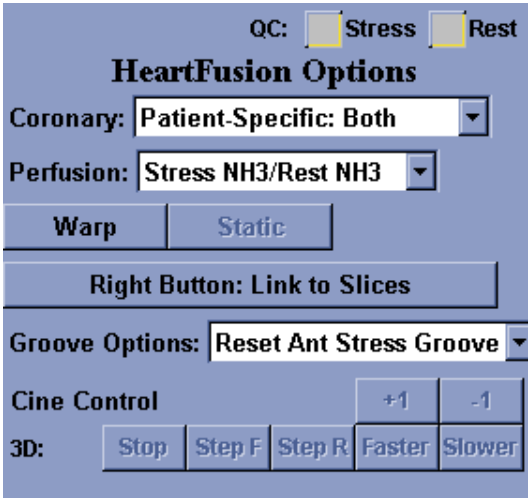


Figure 3-85. Options available for HeartFusion.

All of the options will be discussed in detail below, but briefly, they are:

- **Coronary**: controls which type of coronary trees are displayed.
- **Perfusion**: controls which type of 3-D perfuion maps are displayed.
- **Warp**: warps or un-warps the coronary model to the 3-D perfusion map.
- **Right Button**: controls the function of the right mouse button.
- **Groove Options**: allows interactive re-positioning of the inter-ventricular groove point, which affects the warping operation.
- **Cine Control**: controls the 3-D gated display, if gated data is available.

Selecting 3-D Maps

The **Perfusion** droplist controls which 3-D map is displayed. This list is similar to the one that is available on the standard PerfSPECTive display. The choices are:

- **Stress/Rest** - displays stress and rest raw maps.
- **Blackout/Reversibility**. This is a standard ECToolbox map indicating a significant defect in black, and significant reversibility in white.
- **Mass-at-Risk** - Illustrated in Figure 3-92, this is for viewing the extent of myocardium predicted to be at risk due to a coronary vessel stenosis. See the next section for details.
- **No Left Ventricle** - The 3-D maps are removed, for viewing the coronary trees alone.

Selecting Coronary Trees

The **Coronary** dropdown list controls which coronary tree is displayed. The choices are:

- **Generic Tree: Right Dominant**
- **Generic Tree: Right Dominant 2**
- **Generic Tree: Left Dominant**
- **Patient-Specific: Left**
- **Patient-Specific: Right**
- **Patient-Specific: Both**
- **Tree: Off**

Controlling Display of Coronary Trees

You can choose to overlay a generic coronary tree on the 3-D perfusion map, with a left dominant or right dominant structure. The ability to display the patient's own coronary trees is unique to the HeartFusion module of ECToolbox. In order to display patient-specific trees, the left and/or right coronary artery files must have been selected when entering the program. An example of a patient-specific left coronary tree model, fused to a 3-D perfusion map, is shown in Figure 3-86.

Once the coronary artery model is displayed, there are several tools and other considerations for manipulating the model and how it appears in relation to the 3-D map.

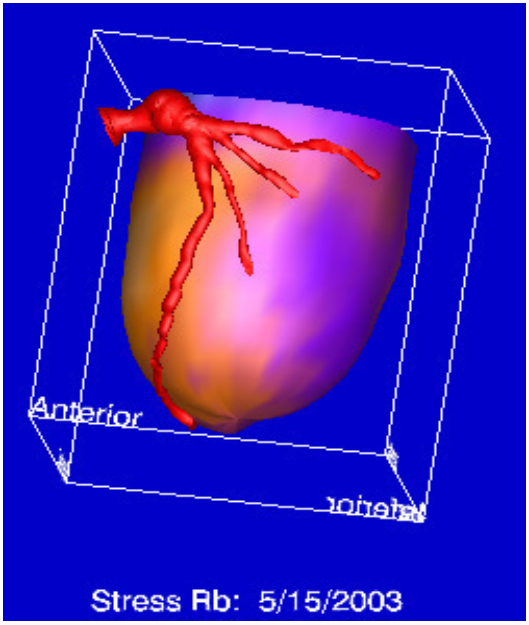


Figure 3-86. Left coronary artery tree, specific to this particular patient, has been superimposed on the 3-D map. The tree and 3-D map rotate together when they are dragged using the mouse. Recall that the drag operation is a left mouse click that is held while moving the mouse around the screen.

Right Mouse Button Control

Clicking the **Right Button** control allows the user to change the function of the right mouse button in controlling the image display. This button toggles between two functions, **Right Button: Link to Slices** and **Right Button: Artery Data**.

Linking 3-D Maps and Slices

- **Right Button: Link to Slices**. This option enables the user to identify a particular point on the 3-D map and see the corresponding location on the slices, or to identify a point on the slices and see the corresponding location on the 3-D map. Examples are illustrated below
    - To mark a point on the 3-D map, right-click the desired area. The slice images that contain the marked point will automatically be shown, and a small white crosshair will mark the point on each slice. (Figure 3-87)
    - To mark a point on the slice image, right-click the desired area of either the short axis or the long axis image. The corresponding point will be highlighted on the 3-D map by a blue spot. (Figure 3-88)

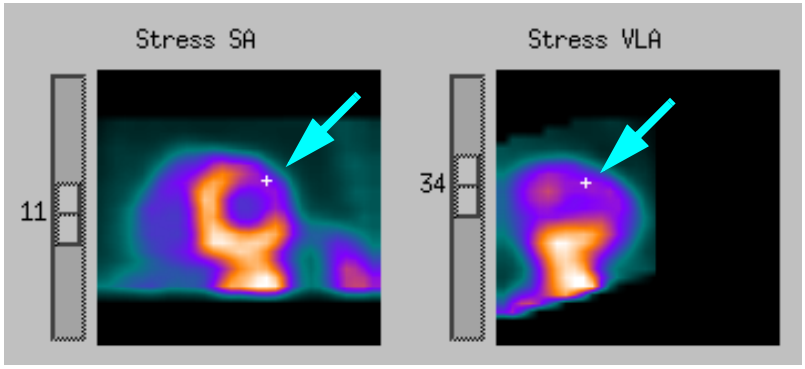


Figure 3-87. A marked point is shown on the slices as a small white crosshair (blue arrows).

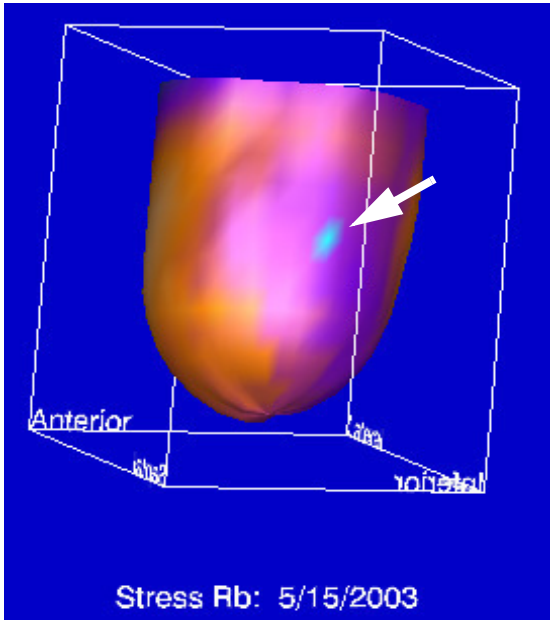


Figure 3-88. A marked point is shown on the 3-D map as a blue spot (arrow).

Note: to remove the blue spot from the 3-D maps without changing anything else, remove and re-display the 3-D maps using the **Perfusion** droplist control. Select **No Left Ventricle** from the list, followed immediately by **Stress/Rest**, or whichever map was originally displayed.

Marking a Stenosis

- **Right Button: Artery Data**. This option enables the definition of a coronary vessel stenosis. To mark a stenosis, right-click on the patient-specific coronary tree at a point where a stenosis is present, and any vessels distal to this point will be turned green. As soon as a stenosis is marked, the cross-sectional area of the vessel at the selected point will be displayed. To entirely remove the green color from the vessel, use the mouse to right-click outside the white 3-D box. When the stenosis has been removed in this way, the cross-sectional value that was displayed is replaced with “N/A”

for “Not Available”.

Note: a stenosis cannot be marked on one of the generic coronary trees.

An example of a stenosis is shown in Figure 3-89.

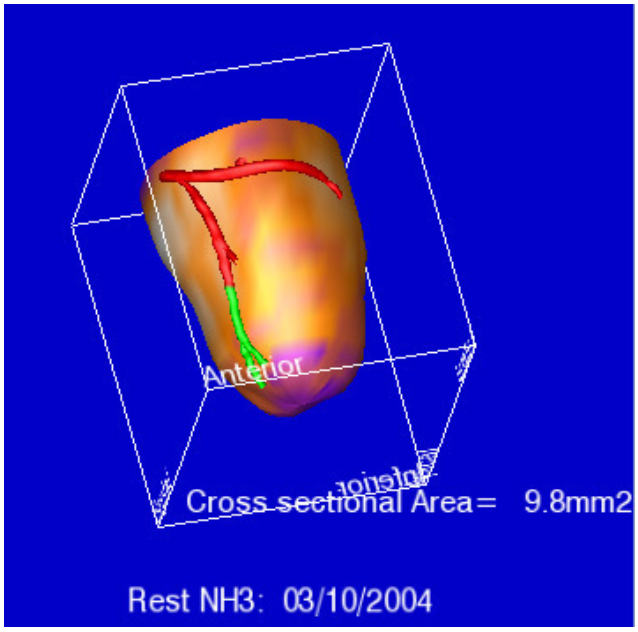


Figure 3-89. A stenosis has been marked, causing the vessel distal to the marked point to turn green. The cross-sectional area at the stenosis point is displayed.

Warping

Because a coronary tree model has its own shape, it may need to be rotated, translated or otherwise deformed in order to join it to the 3-D map in such a way that the coronary tree lies on the surface of the LV. This process is known as “warping” the model, and is handled automatically by the program. The **Warp** button, at the top of the screen, toggles between "warping" and "not warping" the coronary tree. By default, warping is turned on because this allows the best fit of the tree to the shape of the myocardium. If the warping has failed for any reason, the tree will not

appear to be oriented correctly in relation to the 3-D map. In this case, the tree can be displayed with warping turned off. To do this, click the **Warp** button. The button label changes to **Un-Warp** and the coronary tree shifts position.

The **Warp** option is only available when the Patient-Specific coronary trees are displayed. When generic trees are being displayed, warping is handled automatically.

Note that there is only one set of patient-specific coronary vessels, so the same coronary tree will be displayed on both the stress and rest 3-D maps. Because the myocardium may be a different size or shape at stress than at rest, warping may result in a slightly different appearance of the vessels on each map.

In order for the warping process to be successful, there must be some landmark features which the program can identify on the myocardium. The chief anatomic landmarks are the anterior and inferior grooves which, because they occur at the juncture between left and right ventricles, are called inter-ventricular grooves. As part of the process of joining the coronary tree to the 3-D map, the program automatically identifies these landmark points.

Groove Options

If warping is suboptimal, the user can re-position these groove points, using the options available under the **Groove Options** button. There are four choices:

- Reset Anterior Stress Groove. This will display the anterior groove point on one stress short axis slice image. The point is labeled “agr”.
- Reset Inferior Stress Groove. Displays the inferior groove point, labeled “igr”.
- Reset Anterior Rest Groove. This point will be marked on a rest short axis slice, and is labeled “agr”.
- Reset Inferior Rest Groove. Displays the inferior groove point for rest, labeled “igr”.

Figure 3-90 shows a correctly positioned model, and its groove points on the stress slices. Figure 3-91 shows the same model shifted to an incorrect position due to incorrect manual placement of groove points. In nearly all

cases, the automatic definition of groove points by the program will be sufficient to accurately join the coronary tree model to the 3-D myocardium. No changes will need to be made.

There are several points to keep in mind about **Groove Options**, which apply to all of the **Reset...** options listed above:

- The groove point is displayed only on the short axis image, usually on a slice near the base, since this is where the anatomic groove begins.
- Selecting one of the **Reset...** options displays the default (automatic) groove points. Once they are displayed, the groove points can be moved by clicking on a different spot on the short axis image. The default groove point can be retrieved by selecting the same “Reset” option again.
- The groove point should be at the outer edge of the LV myocardium, and near the insertion of the right ventricle.
- If a new groove point causes the warping to change, the change will be immediately seen on the 3-D model.

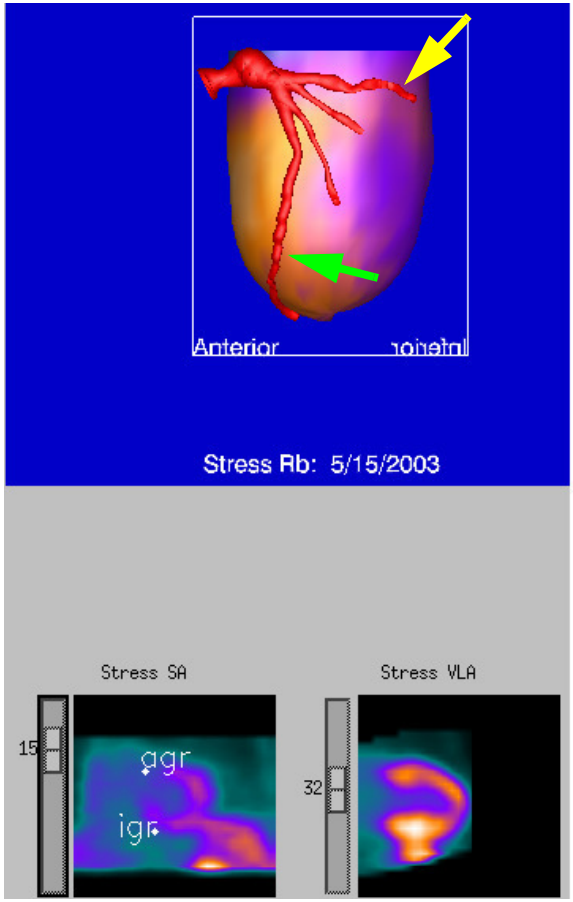


Figure 3-90. Correctly-placed anterior (agr) and inferior (igr) groove points. The 3-D coronary tree is well-aligned with the 3-D perfusion map in this case: the Left Anterior Descending coronary artery (green arrow) runs down the anterior surface and the Left Circumflex artery (yellow arrow) rides across the base.

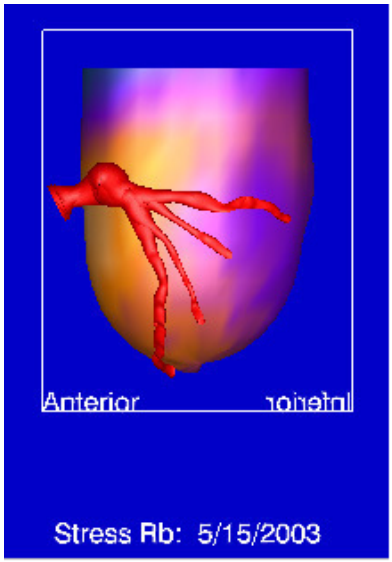


Figure 3-91. Incorrect joining of the 3-D coronary tree to the 3-D perfusion map. This situation may be correctable by changing the anterior or inferior groove point, or both.

One of the optional 3-D maps is Mass-at-Risk. Based on the location of a marked vessel stenosis, the area of myocardium supplied by this vessel is calculated and highlighted in purple when "Options/Perfusion/Mass-at-Risk" is selected. This purple area is the area predicted to be at risk due to the stenosis. The remainder of the myocardium is white in this map. See Figure 3-92 for an example. The Mass-at-Risk option can be selected without marking a stenosis, but in this case no purple at-risk area will be shown.

It can be useful to compare the mass-at-risk area to the area of blackout on the defect extent map.

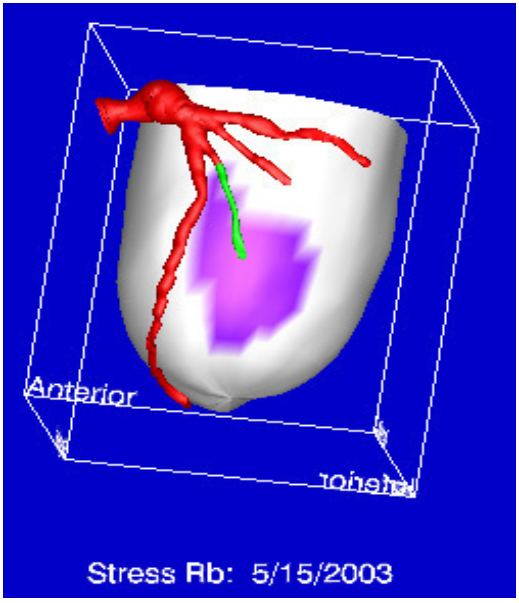


Figure 3-92. 3-D display type has been set to "Mask-at-Risk". A stenosis has been marked, causing the affected vessel to be shown in green, and the myocardial area at risk is shown in purple.

Cine Control for HeartFusion

The **Cine Control** section of **HeartFusion Options** allows control over the dynamic cine loop display of gated 3-D maps. These buttons work exactly as they do on the standard Slices and Functional review screens:

- **Stop**: stops the cine loop.
- **Step F**: steps forward one frame (one gate) in the cine loop.
- **Step R**: steps back one frame in the cine loop.
- **Faster**: Increases the speed of the cine playback.
- **Slower**: Decreases the speed of the cine playback.
- **+1**: Adds one gate back to the end of the cine loop.
- **-1**: Removes one gate from the end of the cine loop.

The Summary Page

This Display Screen provides the user with a single display window to review key study results, including Rest and Stress Polar Maps, Percent Thickening Polar Map, ED and ES Volumes, LV Ejection Fraction, Oblique Slice images, Summed Stress Scores and Probability of Survival Data.

Note: The data and images displayed on this screen must have been previously generated earlier in the application. For example, Summed Stress Score (SSS) results must have been generated in the “Polar Maps / SSS” section. Similarly, Thickening Polar Maps, LVEF and ED/ES Volumes must have been generated in the “Functional Analysis” Section.

There is one option button for this screen, **Export XML Report**. This button saves a new folder of patient-specific information to the NRPData folder, which is within the ECToolbox directory. The folder will be named to match the current patient’s coded name, and contains a textfile with demographic information and a summary of perfusion scores. In the same folder are TIFF format image files of the stress and rest raw polar maps, the stress and rest polar maps with 17-segment overlays (or 20-segment overlays, if that preference is set), and the summary page itself.

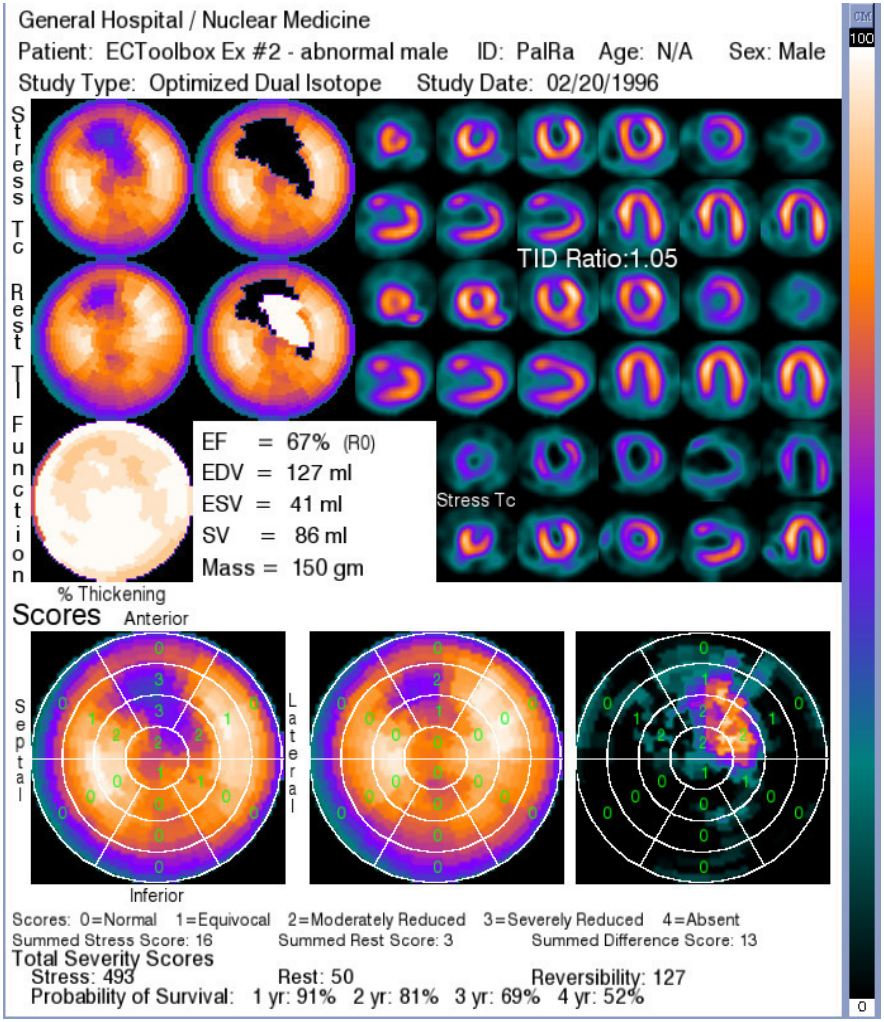


Figure 3-93. The Summary Page provides a summary of key results processed earlier in the ECToolbox program.

Review Mode

To review a study that has been previously processed and saved using the ECToolbox, the user must first select one or more ECToolbox review files. The necessary steps are described in Chapter 2.

After selecting the appropriate Review File, the ECToolbox Params Window will be displayed, using the previously processed parameters. The user can change this default behavior by setting the program to open a review file in a different screen. For example, to have ECToolbox always start a review file with the Slices Display, perform the following steps:

- In the Params Window (Parameters Page), select the “Options” button.
- On the dialog window that appears, select “Advanced Options”.
- A second dialog window appears. In the middle of this window is a drop-down list labeled “Default Window for Starting Review”. Select “Slices” from this list.

At this point any of the previously described options and displays may be used.

Note: In Review Mode, none of the processing parameters can be changed (Apex, Base, Center and Radius of Search). This applies to both the Params Window and Functional Analysis Window. The user can choose to enable review changes however. To do this, use the “Options” button on the Parameters page. The first option on the drop-down menu shows the current status of review changes. Using the mouse, slide across to activate the submenu, and select “Allow Review Changes”.

Note: In Review Mode, the button “Quit” appears on all screens. Clicking this button causes ECToolbox to exit immediately, without saving any additional files. In Process Mode, the button in this location would read “Save & Exit”.

Using the Viewbox to Review Studies

Emory Cardiac Toolbox includes a tool called the Viewbox, which has been referred to in earlier sections of this manual. Viewbox is designed to provide a way to summarize the results of a study in a flexible way, and to facilitate the comparison of one study to another. Figure 3-94 shows the permanent button display, which has been discussed previously, in “Buttons to Access the Main Tools” on page 36. The following permanent buttons relate to Viewbox functions:

- **Active View**. Displays the currently active Viewbox screen. This button can be selected at any time during the review process.
- **Quit Act View**. Exits the active Viewbox display and returns to standard review mode.
- **Viewbox 1**. *Not yet implemented.*
- **Viewbox 2**. *Not yet implemented*.

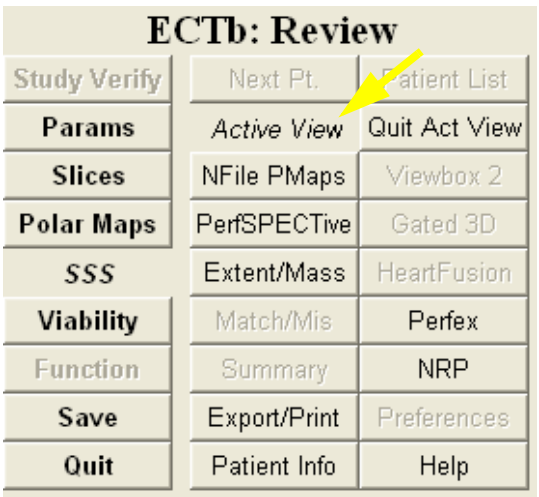


Figure 3-94. The permanent button display, with **Active Viewbox** selected (arrow).

The Viewbox Concept

The Viewbox divides the image display conceptually into three regions, as shown by the diagram in Figure 3-95.

- Section A is fixed and “live”. It always contains the Slices display, since this is a fundamental starting point for interpretation of either myocardial perfusion or metabolism.
- Section B is user-selectable, and sometimes “live”, depending on what is displayed there.
- Section C is fixed, and, summarizes the remainder of the study by showing polar maps, functional results and 3-D PerfSPECTive maps.

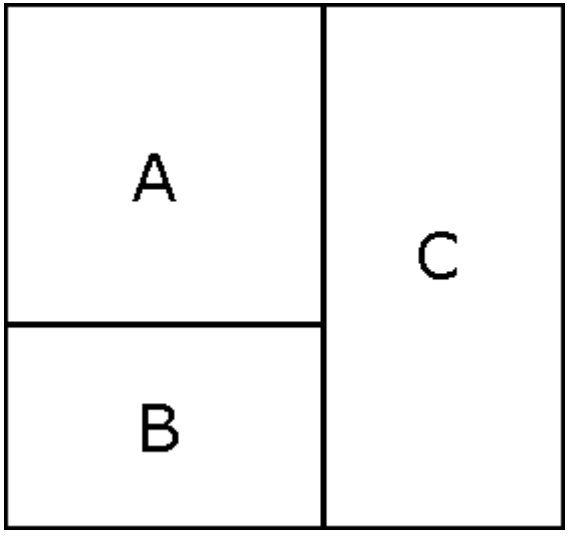


Figure 3-95. The concept of the Viewbox image display. Section A always shows the Slices display, and is “live”. Section B is user-selectable. Section C is fixed.

Section A is always used to reproduce the Slices display. This is exactly the same display as shown on the Slices screen in standard review mode. Section A is “live”, meaning that all of the same control options for changing slices, controlling planar cines, etc. are available in the Viewbox version of the Slices display. The various Slice Display options are

explained in detail in “Aligning Stress and Rest Images” on page 52 and “Slices Window Opions” on page 53. Because Section A is interactive, the option buttons for the Slices display appear on the lower left of the screen, just as they do for the Slices display in standard review mode.

In Figure 3-94, we can see that various Permanent Buttons are available, and others are not available. (Recall that available buttons have black text, while inactive ones are grayed-out.) By default, the Summed Score display appears in section B (Figure 3-96). This is indicated on the permanent button display by the fact that the **SSS** button is has a “selected” appearance (the button appears to be depressed, and the text label is in italics). By selecting any of the other available buttons while in Viewbox mode, the display indicated by the button label will replace the SSS display in section B of the Viewbox window.

Thus, in Viewbox mode, clicking an available button has a different effect than clicking the same button in standard review mode.

While Section A of the Viewbox is entirely live and interactive, section B is partially interactive. The window level can be adjusted, or the color table can be changed, for any image display that appears in Section B. Most displays that can appear here will be static and require no further user interaction, such as Defect Extent scores and 3D PerfSPECTive. However, the SSS display is interactive: stress and rest scores can be adjusted when the SSS display is in Section B of the Viewbox display. The Resting Viability display is also interactive, so the threshold level can be changed when this display appears in Section B.

Section C images are fixed, except that the window level and color table can be changed for the polar plot display in the upper right.

Regardless of what images are displayed on the Viewbox, the way to return to standard review mode is to select the **Quit Act View** button, which exits the active Viewbox and returns to the Slices display.

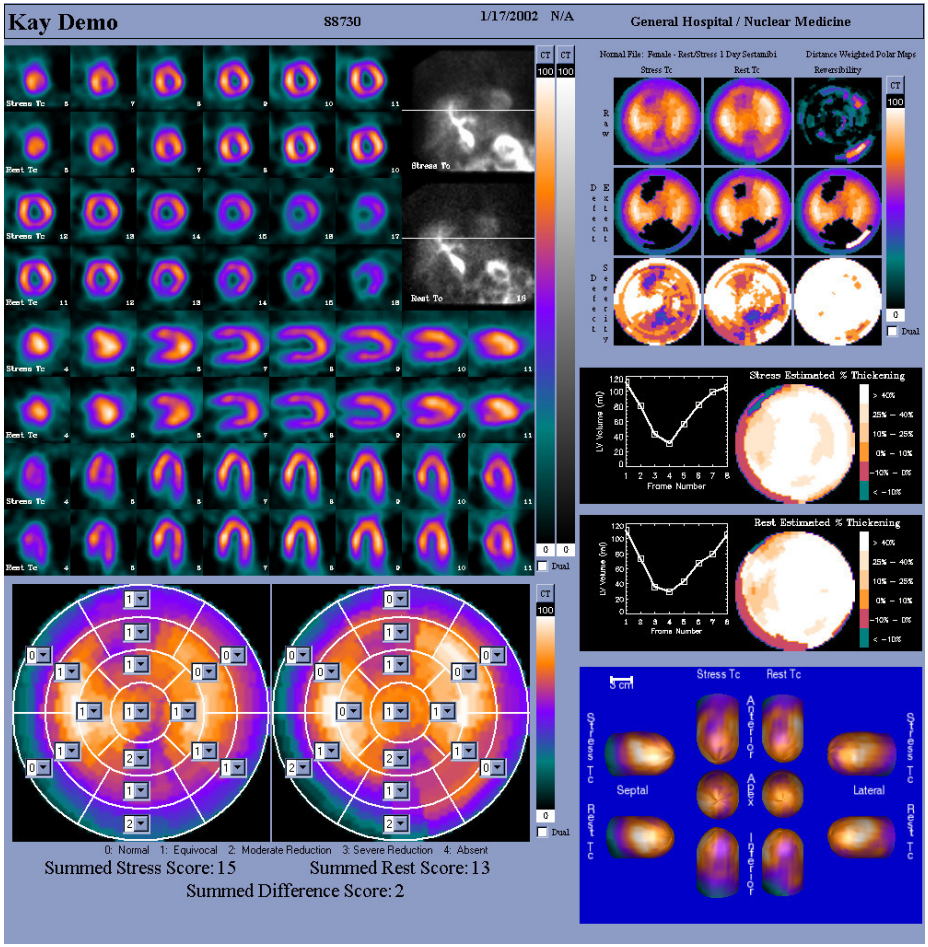


Figure 3-96. The default Viewbox display. This study includes rest gated as well as stress gated data, so both are displayed.

In Figure 3-96, the example is a dual-gated study. If this had been a study with one gated and one ungated part, the functional report area of the Viewbox would have changed to reflect the study content. This area would appear as in Figure 3-97.

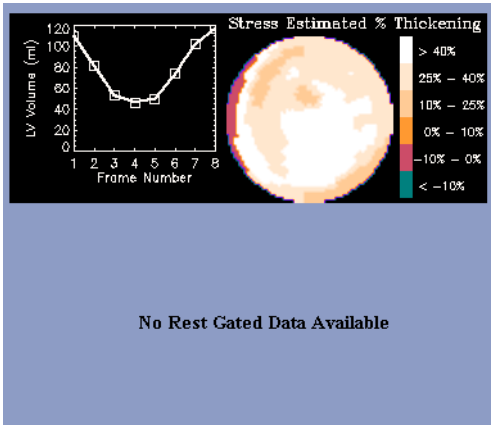


Figure 3-97. Part of the Viewbox display, as it would appear in a study with only one gated part.

As discussed above, various image displays can be moved into Section B of the Viewbox using the Permanent Buttons. Using the **Patient Info** button, the block of information and calculated values in the middle of the button display can be added to section B, replacing whatever image was there.

Most all of the image displays that are available through the Permanent Button list can be placed into section B of the Viewbox. The only exceptions are Gated 3D and the Summary display.

Viewbox for FDG

If the current study is a perfusion-only study (thallium, technetium, rubidium or ammonia), the standard 9 polar plots are displayed in area C. If the current study is a perfusion-metabolism study (that is, it includes a rest FDG part) then the Match/Mismatch plots are displayed in area C.

Figure 3-98 shows the default Viewbox display for a perfusion-metabolism study. The other difference between this display and the standard perfusion Viewbox is that a table of scores appears in Section B. Summed Scores are not applicable to a metabolism (FDG) study.

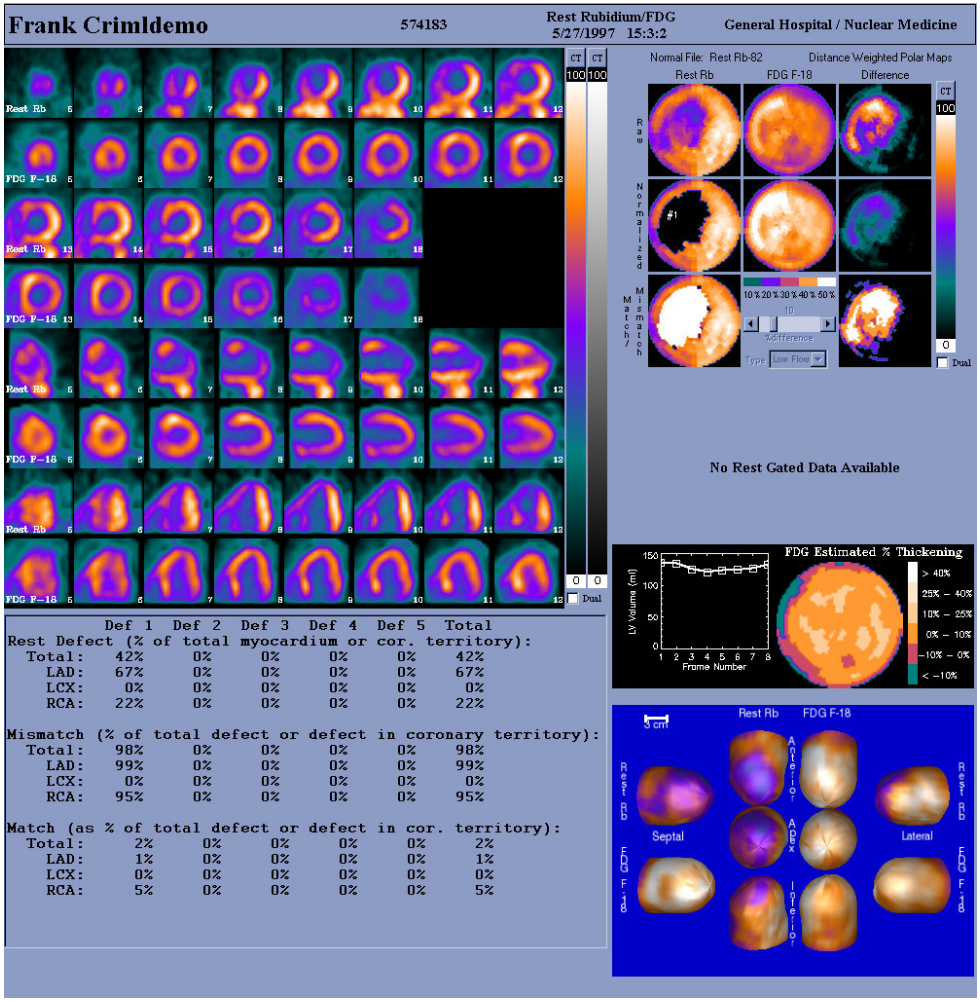


Figure 3-98. The default Viewbox display in a perfusion-metabolism study.

Saving Screens and Movies

Export/Print Options

The **Export/Print** button, in the permanent button set, provides several options for printing or saving the current screen, or part of it, as a file on disk. When this button is selected, several additional buttons are displayed in the Optional Area, as shown in Figure 3-99.

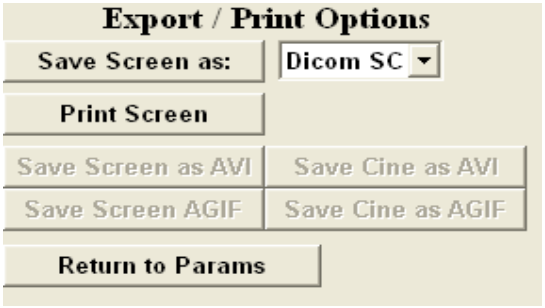


Figure 3-99. Options for the **Export/Print** button.

The options are:

- **Save Screen as:** allows the currently displayed screen to be saved to disk for later review. The type of file to be saved can be selected from the droplist to the right of the button. Types include DICOM Secondary Capture, and standard graphics filetypes such as BMP (Windows bitmap) and TIFF.
- **Print Screen:** allows the currently displayed image screen to be printed on the default printer. It is recommended that a high quality color printer be used to produce color hardcopy images from the ECToolbox application.
- **Save Screen as AVI:** allows the entire image area of the current screen to be saved as a movie file in AVI format. If this option is selected, the user will be presented with a dialog that allows a choice of compression methods to be used. Note that if the “no compression” option is selected, the resulting file will be much larger. In addition, it may take several seconds for the save operation to complete. This option is available from the Slices window and the Functional Review window.

- **Save Cine as AVI:** Allows the current cine display to be saved as a movie file in AVI format. If this option is selected, the user will be presented with a dialog that allows a choice of compression methods to be used. Note that if the “no compression” option is selected, the resulting file will be much larger. This option is available from the Slices window, the Functional Review window and the Gated PerfSPECTive
- **Save Screen AGIF:** Allows the entire current screen to be saved as a movie in Animated GIF format. AGIF files are highly compatible for inclusion in files created by other applications.
- **Save Cine as AGIF:** Allows the current cine display to be saved as a movie in Animated GIF format.
- **Return to...:** You must click this button to exit from **Export/Print** and return to the screen that was previously displayed. The button label will reflect the previous screen, such as “Polar Maps”.

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99m Sestamibi Myocardial Perfusion Single-Photon Emission Computed Tomography. JACC 26: 639-647, 1995.

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Technical Overview of the Emory Cardiac Toolbox Application

Automatic Selection of Center, Radius, Apex, and Base

When the application begins, four parameters are identified automatically. These are 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. This 2-piece valve plane is shown in Figure 4-100. These parameters 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.

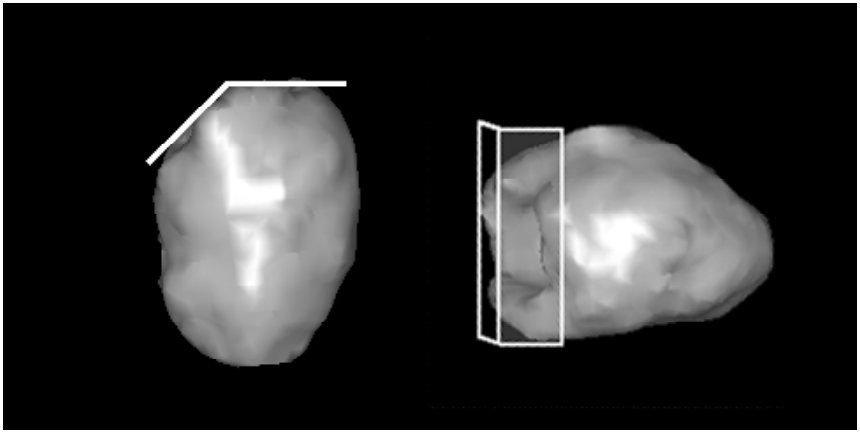


Figure 4-100. Detection of the valve plane as two connected planes.

Sampling of Images And Creation of the Raw Polar Map

Sampling

Only the 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[1].

Apical slices are sampled spherically; while the mid and basal slices are sampled using a cylindrical search. See Figure 4-101 and Figure 4-102.

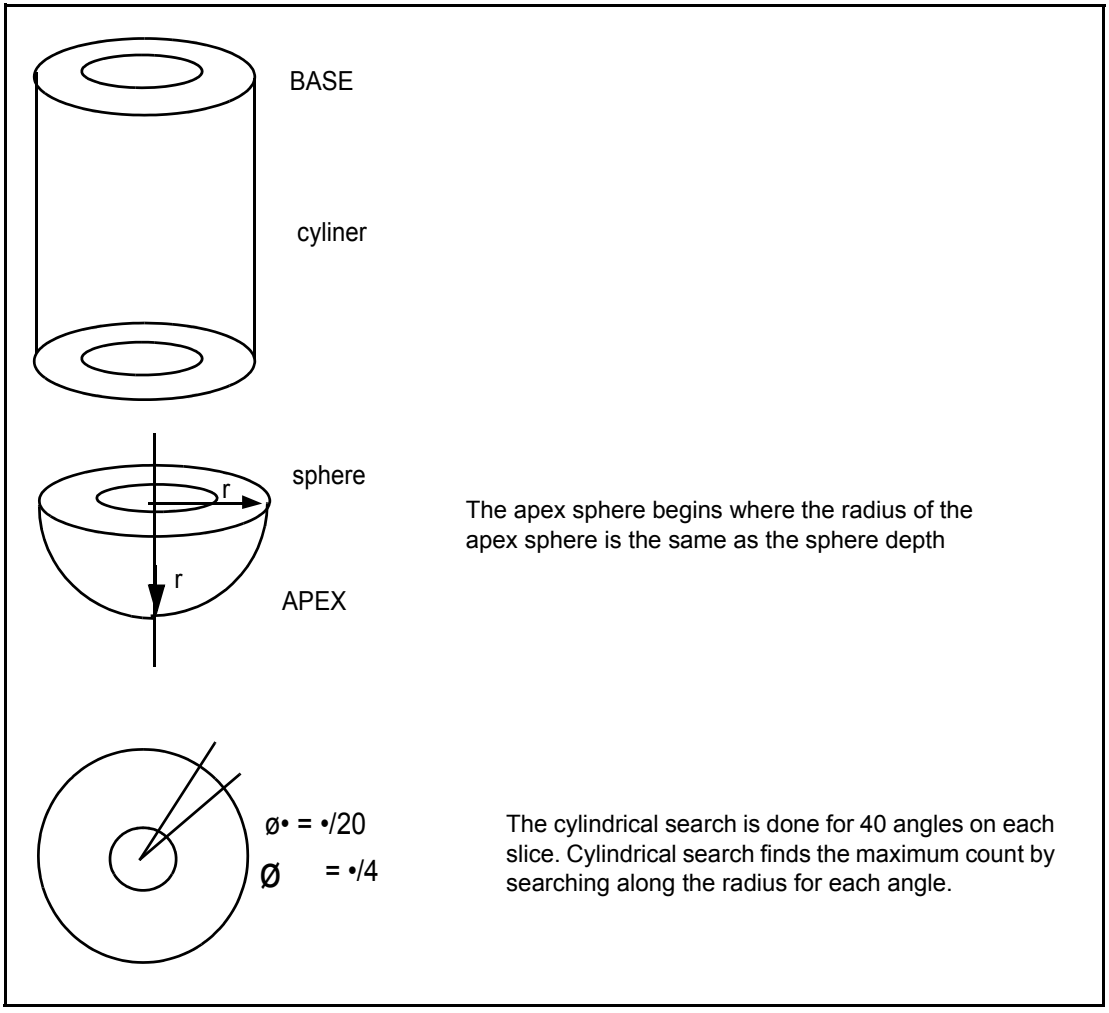
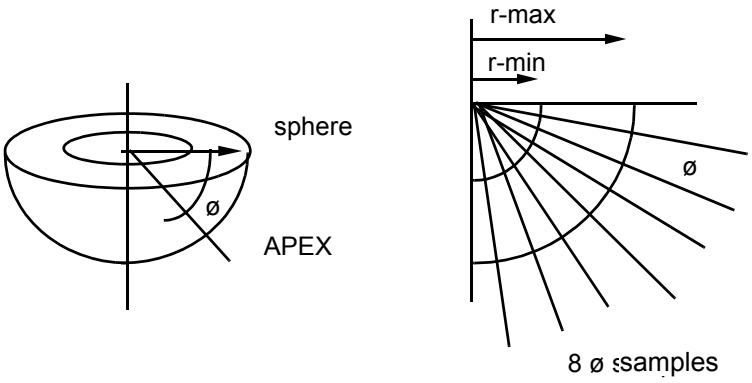


Figure 4-101. Cylindrical Search.



Instead of sampling slices as in the cylindrical search, the spherical search samples sectors.

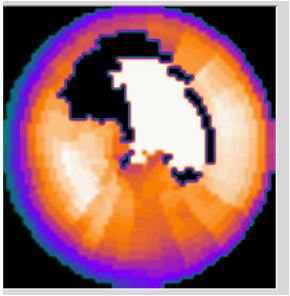
Figure 4-102. Spherical Search.

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.

Polar Maps

After the calculations are performed, the computer creates the “raw” polar maps (representative sample shown on the following page).



Typical Polar Map

These maps represent the actual counts in rest and stress profiles, and the scaled counts in the reversibility profiles. The rest and stress data are also 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.

Profiles, Blackout, and Standard Deviation Maps

Normal values consist of twelve profiles, comprised of forty points each, representing the mean and standard deviation for each of the three measurements under consideration:

- stress;
- rest; and,
- reversibility.

Profiles

The first step in this program 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 profile is assigned to one normal limit.

The next step is to determine if each of the patient's points are normal or abnormal. The criteria developed assigns a different threshold to each point. The threshold is in standard deviation units which differ depending on the myocardial location and the Normal File. Please refer to Appendix B of this Manual, for the criteria for each of the Normal Files.

After each point is analyzed, a clustering algorithm is employed to eliminate isolated abnormal points. This routine looks at each abnormal point and its neighboring points. If the neighboring points are all normal, then the point 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) in 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" to accurately evaluate 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.*

Feature Extraction and Table of Results

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.

Polar Maps

For describing defect/reversibility location, the following can be used:

- three coronary territories, the LAD, LCX and RCA, as well as total myocardial territory (Figure 4-103, bottom).

Extracted Information Tables

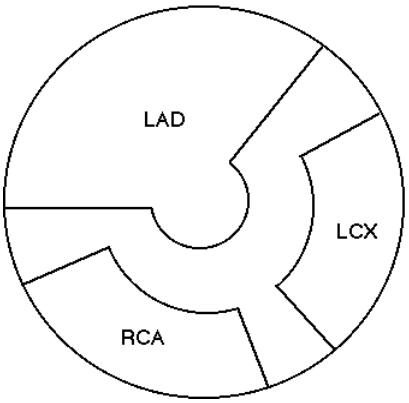
The extracted information is stored in a descriptor array and used to generate a table which contains the severity (number of standard deviations below mean normal) and extent (in either mass or percent) of each defect/reversibility.

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.

Note: The descriptor array can only store information for five defects; therefore, if a patient has more than five defects, only the first five defects are displayed, starting at the Apex.

Typical
Polar Map



Three coronary territories: LAD, LCX, and RCA

Figure 4-103. Polar Maps.

Automatic Summed Stress and Rest Scores

After automatically quantifying perfusion, the ECToolbox uses standard deviation maps to assign scores to the 20 regions. A sample in the middle of the LV chamber is taken; this value is translated into the number of standard deviations below the mean for each CEqual sample. And region having a CEqual sample with standard deviation below this is scored as 0, since perfusion is “missing”. Likewise, the lower limit of normal in standard deviations below the mean is obtained for each CEqual sample. Any region having a CEqual sample with standard deviation below mean above this value is scored as 4, since it is “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.

Display of Quality Control Information

After automatically determining the original parameters (Apex, Base, Center, Radius of search), the Main ECToolbox Window is presented to ensure that automatic selection of parameters was performed adequately. Please refer to Chapter 3 of this Manual (Using the Emory Cardiac Toolbox Application), for information on changing parameters, which are determined to be incorrect.

On the Slice Review Window, the slices are displayed by default with “staggered summation” on. The intrinsic resolution of many SPECT scanners is on the order of 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. There is an option to turn off this staggered summation.

If gated planar datasets are available for stress, or rest, or both, they are automatically analyzed for gating errors at the time the slice review window is created. Adjacent to each planar image on this window, there is a box which indicates the result of automatic analysis of the gated planar datasets.

Gated Quality Control (GQC)

ECT gating errors can adversely affect perfusion assessment[10,11]. 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[12], 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 cases in which the curves may not overlap.

1. 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[11], and counts of curve #8 will be slightly lower than those of curves #1-7.
2. If heartbeats vary widely all of the time, so that the heart rate is consistently variable, then during the time required for each projection, some counts are lost in frames 6-8 consistently throughout the entire tomographic acquisition (Figure 4-104).
3. During a period of transient tachycardia, or for ectopic beats (Figure 4-105), 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.
4. During atrial fibrillation, sudden shortening of the R-R interval occurs randomly and chaotically, resulting in a drastic departure from the ideal (Figure 4-106).

It should be recognized that gating errors are often not of any one “pure” type, but are admixtures of the types described above.

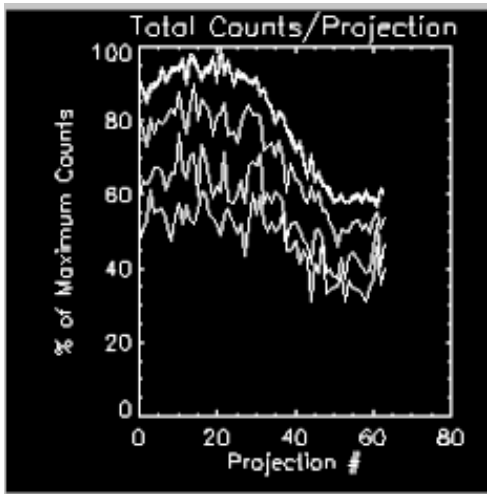


Figure 4-104. “Consistently variable” heart rate, as seen when all 8 gated planar datasets are plotted as counts vs. projection angle.

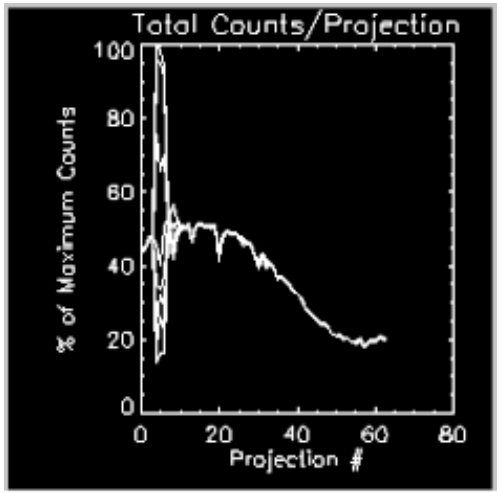


Figure 4-105. Transient tachycardia.

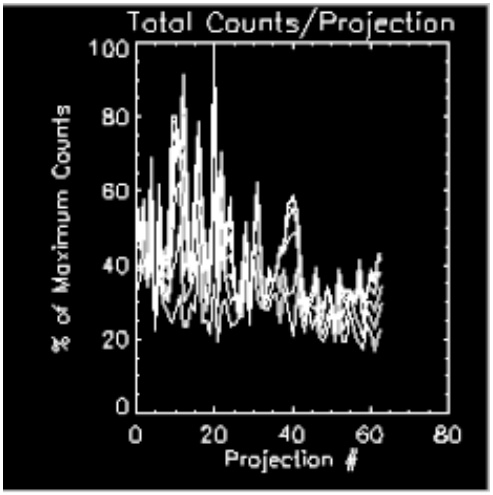


Figure 4-106. Atrial fibrillation, probably superimposed on varying heart rate.

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[10,12]. 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 “Estimating boundaries for additional gates” on page 170). 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[11], 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[10]. 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.

Calculating Left Ventricular 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[2, 3, 4].

Wall Thickening

Wall thickening throughout the cardiac cycle is computed using a Fourier analysis of the size-intensity relationship[5]. 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 can be seen in Figure 4-107.

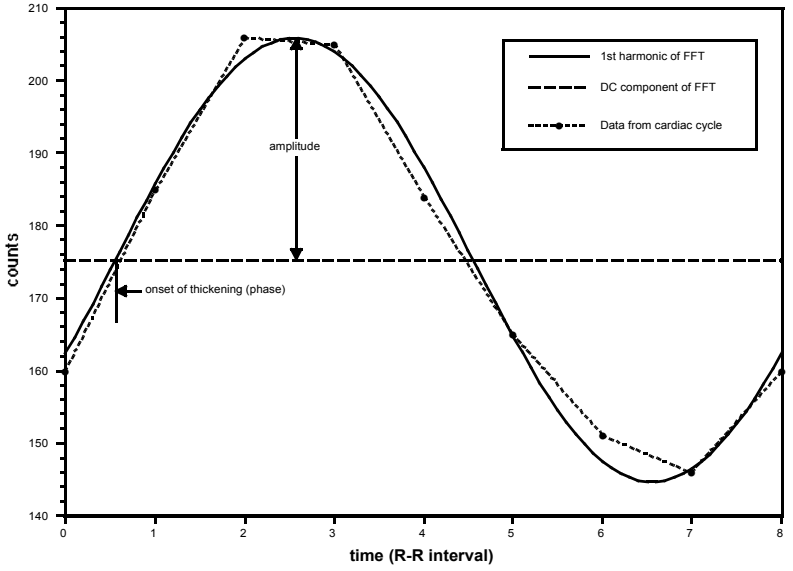
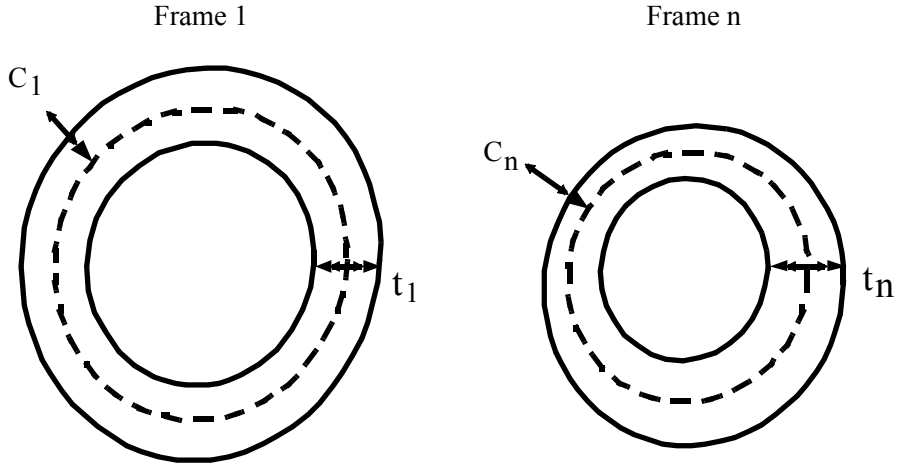


Figure 4-107. Phase and amplitude of the first harmonic of the Fourier transform is used to compute Wall Thickening throughout the cardiac cycle.

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 Figure 4-108.



c_n = myocardial center points at frame n
t_n = myocardial thickness at frame n
$t_n = t_1 * \%\text{thickening}_n + t_1$
$\text{Endo}_n = c_n - t_n$
$\text{Epi}_n = c_n + t_n$

Figure 4-108. 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 approximate 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.

Computing Function

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 6.

EF Method

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[6, 7] computed using the Emory Cardiac Toolbox (ECTb) with those calculated with the Cedars Sinai Quantitative Gated SPECT program (QGS) for 8-gate data[8]. 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 $y = 1.05x + 0.055$, $r=0.95$, SEE = 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 (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[9]. 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: y = 1.22x -.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-gated QGS yielded r = .91 and r-squared = .83. The equation to convert 16-gated QGS EFs into ECTb EFs is 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 the three possible (R0,R1,R2) 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 volume/rest volume) is reported as a TID ratio.

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9) Bartlett ML, Srinivasan G, Barker WC, et al. Left Ventricular Ejection Fraction: Comparison of Results from Planar and SPECT Gated Blood-Pool Studies. J Nucl Med 1996; 37:1795-1799.

10) DePuey EG. Artifacts in SPECT myocardial perfusion imaging. In: DePuey EG, Garcia EV, and Berman DS, eds. Cardiac SPECT Imaging. New York: Lippincott Williams & Wilkins, 2001:231-262.

11) Cullom SJ, Case JA, Bateman TM. Electrocardiographically gated myocardial perfusion SPECT: technical principles and quality control considerations. J Nucl Cardiol 1998;5: 418-25.

12) Nichols K, Dorbala S, DePuey E, Yao SS, Sharma A, Rozanski A. Influence of arrhythmias on gated SPECT myocardial perfusion and function quantification. J Nucl Med 1999;40:924-34.

The Emory Normal Database Generator

Introduction

Emory Normal Database Generator (ENDG) is a software application which enables you to create your own normal database for use with the Emory Cardiac Toolbox. Creation of a normal file requires certain data to be specifically extracted from each patient study that is to be part of the file. This step is accomplished in ECToolbox, therefore each patient who is to be part of the normal group must first be processed in ECToolbox.

Briefly, the major steps to create a new normal file are as follows:

- Create a new database, or open an existing one.
- Add normal patients to the database.
- Calculate and display the normal distribution of all patients.
- Decide on the threshold for abnormality, to be used when a patient is compared to the normal file.
- Export the file for use with Emory Cardiac Toolbox.

Saving Data for ENDG

To save a file which ENDG can use for building a normal file, follow these steps in ECToolbox:

- Select the button **NFile PMaps**, which is one of the permanent buttons on the left side of the screen. This will display the current patient's raw polar maps, and the composite polar maps for the currently-selected normal file.
- On the lower left of the screen, under Normal File Options, there are two buttons. One, **Export To Normal Database**, will export the file the ENDG needs. The other button, **Launch Normal Database Generator**, will start the ENDG application. The appearance of the buttons is shown in Figure 2-109.

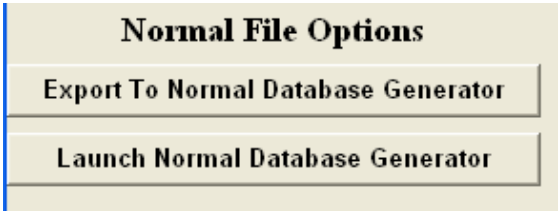

Figure 2-109. Normal File Option buttons in ECToolbox.

Selecting the **Export**... button saves a file to the computer's hard disk, to a location inside the ECToolbox (a folder named ENDGData). As the file is about to be saved, a dialog is displayed showing the filename that will be used. The name can be edited if necessary.

Buttons and Controls in ENDG

There are several parts to the ENDG window, which are always displayed. These basic elements are shown in Figure 2-110, and include menu items, buttons, an area for display of images and curve plots, and a status bar.

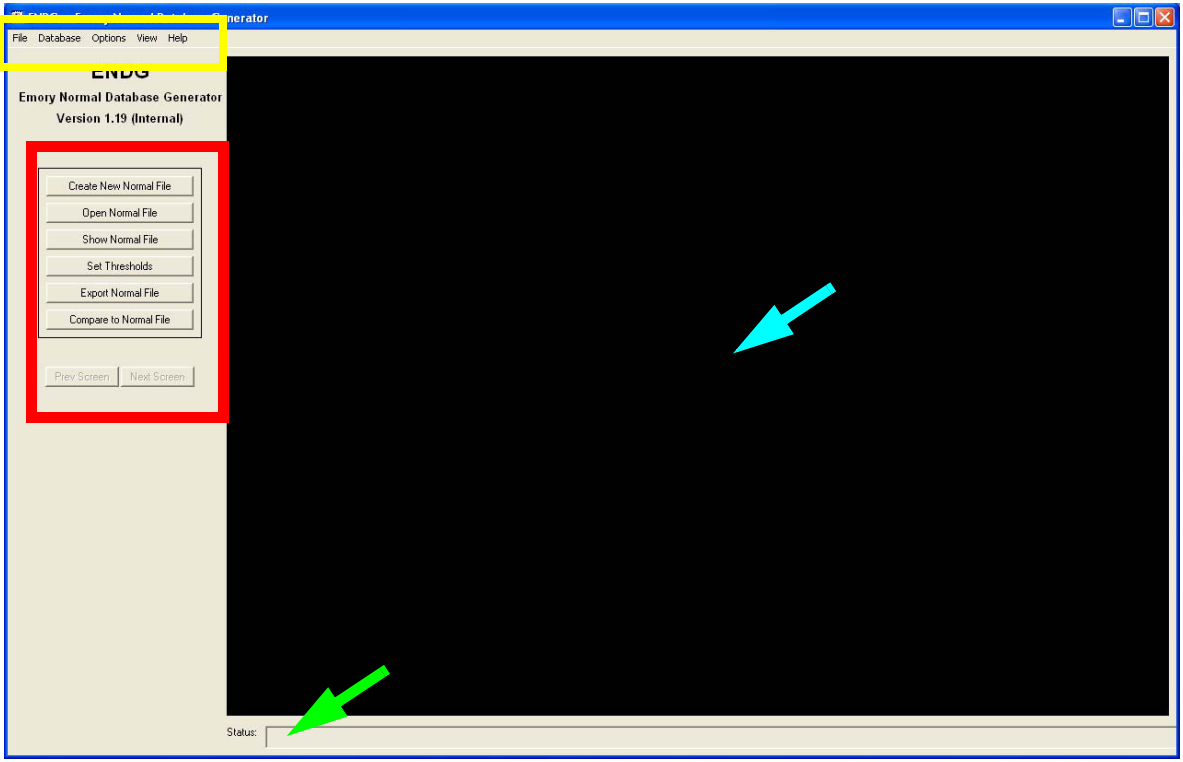

Figure 2-110. The parts of the ENDG window are highlighted. There is a main menu (yellow box), a set of buttons to access the main functions (red box), an image display area (blue arrow) and a status bar for text messages (green arrow).

Most of the user interaction that is necessary in ENDG takes place via the main buttons, which activate functions that represent the major steps that would be followed in creating and using a normal file.

main buttons

The menu and main buttons are shown in Figure 2-111. The buttons are shown from top to bottom in the approximate sequence in which the steps would be performed--opening a normal file, showing its contents, etc. The choices in the menu are additional functions, some of which are related to the button functions, but providing more details, or giving finer control over what the program is doing.

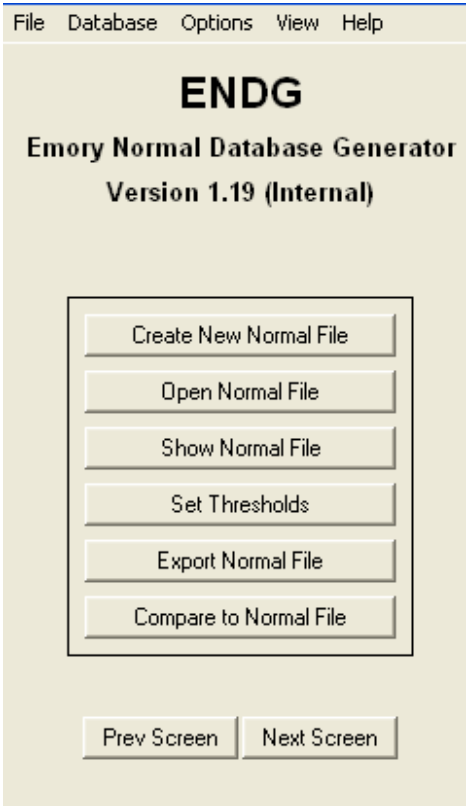

Figure 2-111. The main menu and main buttons for interacting with ENDG.

The buttons have tooltips, meaning that if the mouse cursor hovers over the button, a small text box appears, giving a brief hint of the button's function (Figure 2-112).

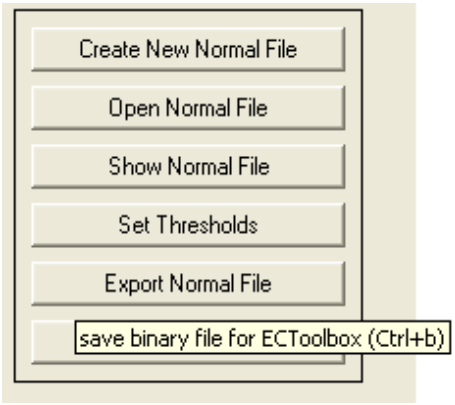

Figure 2-112. The tooltip hint for button **Export Normal File**.

The status bar is an area at the bottom of the window where a single line of text is occasionally displayed by the program. This is a message to the user, usually reporting the results of some action, as when a file has been saved to disk. See Figure 2-113 for an example.

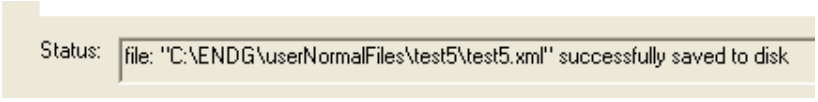

Figure 2-113. The status bar. In this example, the program is reporting that a file was saved as intended. If the File Save operation had failed, the message would be different.

Managing Normal Files

Selecting a File to Work With

The first step after ENDG starts is to select a normal file to work with. If the file already exists and you want to modify it in some way, then the file just has to be selected from a list. If you are just starting to work with the file, then it will have to be created.

To create a new normal file in ENDG, select the New Normal File button. The form shown in Figure 2-114 will be displayed. The form is in three sections, and asks the user to make several choices.

- The name of the new normal file. This can be any name desired, but typically would be descriptive of the type of scan data involved, such as thallium or sestamibi, and perhaps the acquisition protocol or some other element that distinguishes this file from any other. The name entered is the name the file will have when it is selected later for use inside ECToolbox.
- How to handle genders. There are two buttons here: Separate will indicate that you intend to create a normal file for females and another file for males. Combined indicates the intention to combine males and females into a single file. A combined file would be created, for example, if there was accurate attenuation correction or some other factor that would cause gender-related image differences to be minimal.
- Which gender group to work with initially. You must select to work with male data or female data. If the normal file is of the gender-combined type, it doesn't matter which group you select to work with.

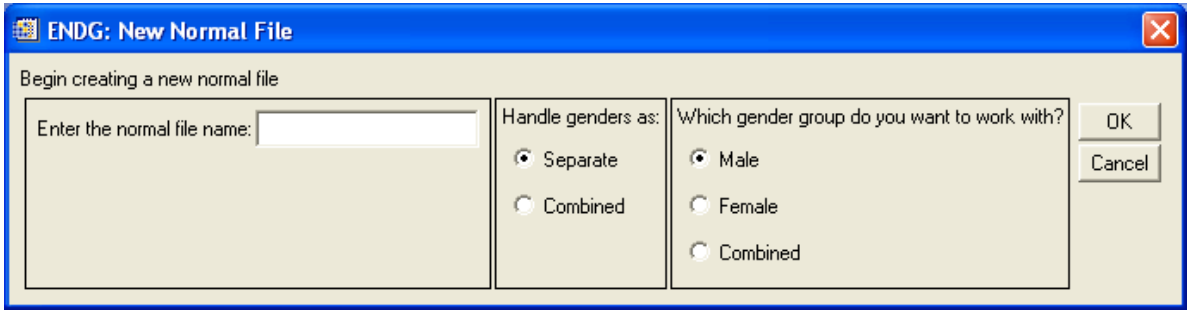

Figure 2-114. The form for describing the new normal file that is about to be created.

To select an existing file, use the **Open Normal File** button. The dialog shown in Figure 2-116 will be displayed. All of the existing normal files that you have previously created will be in the folder “userNormalFiles”. Each subfolder has a name corresponding to the normal file name, which was entered when the file was initially created--using the form shown in Figure 2-114. Highlight the folder corresponding to the file you want and select **OK**.

Note: The Make New Folder button appears on this dialog form, as it always does when Windows is waiting for a user’s file selection. Although this function can be used, it serves no particular purpose at this point in ENDG.

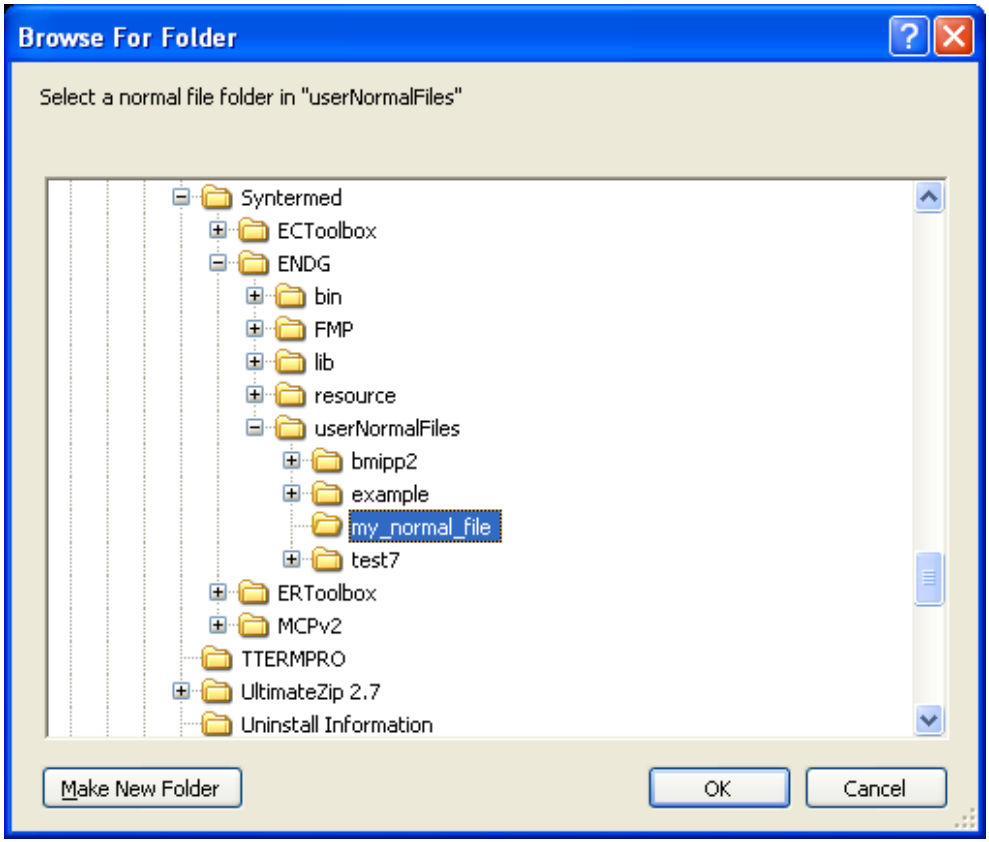

Figure 2-115. Selecting a normal file to work with. All user-created files are in the folder “userNormalFiles”.

Once the desired folder has been selected, you will be asked which gender group is to be used first, via the dialog form shown in Figure 2-116. The default choice is male. Once this choice is made, the previously-saved data for the selected normal file is loaded by ENDG, and the normal file is available for examination. If a normal mean was saved, the results will be immediately displayed in curve and polar plot formats.

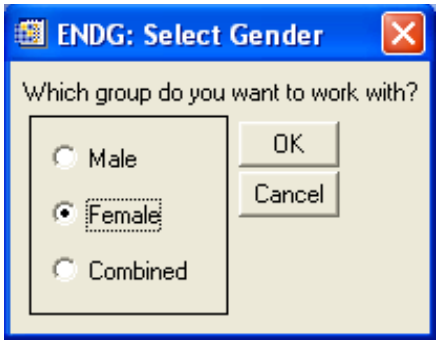

Figure 2-116. The form for selecting which gender group of data to look at. This setting can be changed at any time while working in ENDG.

If you have a separate-gender normal file, and you select to work initially with male data, for example, you can switch to female data at any time by using the menu choice **Options/Select Working Group**, which is explained below.

The next section discusses all of the menu options in ENDG. Most of these have keyboard shortcuts.

The File Menu

The File menu (Figure 2-117) has five options.

- **Open XML in Internet Explorer**. Use this option to open any XML-format file for viewing.
- **Save Normal File**. This option saves the current “state” of the normal file that is open. This includes the number of patients, the ENDG version in use, the creation date and the mean arrays
- **Save Screen**. Saves a snapshot of the current screen as a graphic file on disk.
- **Save and Exit**. Saves the current “state” of the normal file and then exits the program.

- **Quit--Don't Save**. Exits the program without saving anything.

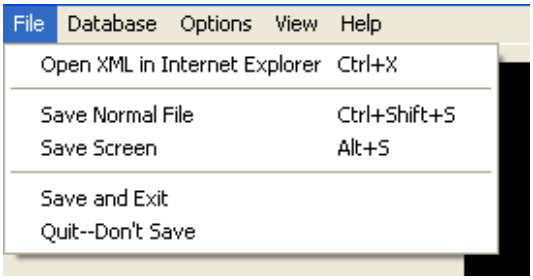

Figure 2-117. The File menu.

The Database Menu

The Database menu (Figure 2-118) has four options. All of these relate in some way to the list of patients that comprise the database for the current normal file.

- **Add Patient(s)**. Allows a user to add one or more patients to the current normal file.
- **Delete One Patient**. Allows one patient to be deleted from the current normal file. See also the later section of this manual: "Comparison Screen Options" on page 200.
- **Undelete One Patient**. Allows one patient that was previously deleted to be restored to the current normal file.
- **View Patient List**. Allows the current patient database to be displayed.

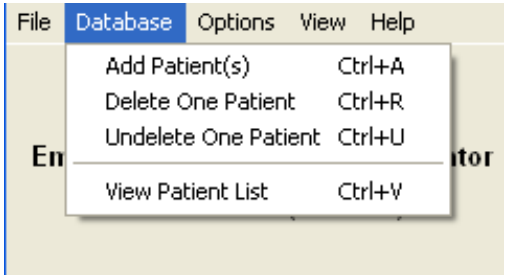

Figure 2-118. The Database menu.

The Options Menu

The Options menu (Figure 2-119) has two options.

- **Select Working Group**. Allows a user to select which gender group to work with. This can be different from the group selected when the normal file was first opened or created.
- **Save Means as Textfile**. Saves a textfile to disk, which summarizes the mean values for each sampled pixel in the normal file. For details, see “Comparison Screen Options” on page 200.

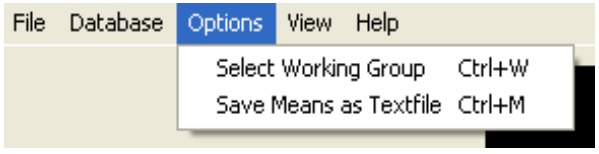

Figure 2-119. The Options menu.

The View Menu

The View menu (Figure 2-120) has three options.

- **Mean Profiles...**. Displays mean profile curves for stress, rest or reversibility. The three choices are accessed through a submenu that appears when **Mean Profiles...** is selected.
- **Mean Polar Maps**. displays a new window showing the mean and standard deviation maps for the current normal file.
- **Patient Polar Maps**. shows polar maps for all patients in the current working group, and their defect extent as compared to the normal mean and thresholds.

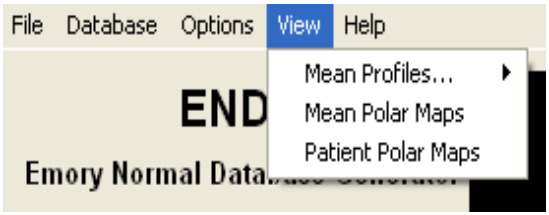

Figure 2-120. The View menu.

The Help Menu

The Help menu (Figure 2-121) has two options.

- **Quick Help**. This options displays a web page that gives brief instructions on using ENDG, including the steps for creating a normal file. This web page is found on the local computer, so you don’t have to have an active internet connection to view it.
- **About ENDG**. displays the full name and version of the program.

Figure 2-121. The Help menu.

Managing the Patient Database

Normal files are used to highlight perfusion deficits in a patient study by providing a normal range to compare against. The terms normal file and normal database are often used interchangeably. When we are developing a normal file, we have the concept of a *patient database*, which is the collection of patients whose data is used to generate the file. The patient database is one component of normal file development, but not the only one. We also have to set the thresholds for the normal file, and be aware of the mean and standard deviation for different segments of the left ventricle. This section of the manual deals with the various aspects of the database--the collection of patients--how to add to it, delete from it and review the contents of it.

Adding Patients

Patient studies can be added to the database by selecting **Add Patient(s)** from the **Database** menu, as shown in Figure 2-118. This menu selection causes the program to access a folder where patient data has been saved from ECToolbox, for the express purpose of being used in ENDG. See “Saving Data for ENDG” on page 177 to review how this works.

Selecting **Add Patient(s)** causes the patients available from ECToolbox to be displayed in a dialog. The dialog is shown in Figure 2-122.

When the dialog is displayed, use the mouse to highlight one or more files, and click the **Open** button. The selected files are immediately moved out of the displayed directory and into the **Patients** directory for the current normal file. Once this is completed, a message will be displayed in ENDG’s status bar at the bottom of the screen, indicating how many patients were imported to the database.

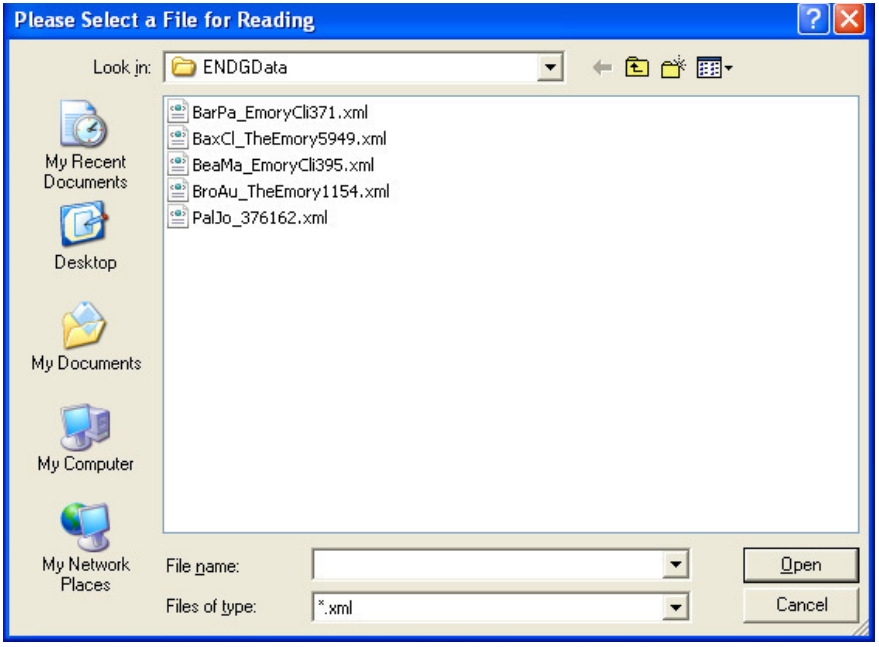

Figure 2-122. The dialog that is displayed when **Add Patients** was selected. The files listed, ending in ".xml" are available for import to the current database. Once imported, the files will disappear from this directory, and appear in the **Patients** folder of the current normal file.

Deleting Patients

There are two ways to delete a patient from the current normal file. In method one, you will identify a patient you want to delete, perhaps from a list of the patients in the file. Make a note of the ID of the patient to be deleted, and then select **Delete One Patient** from the **Database** menu. The dialog window shown in Figure 2-123 will then be displayed.

Enter the patient ID in the first textbox, and click the **Accept** button. This tells ENDG to find a patient with that ID.

Figure 2-123. The dialog displayed in response to the menu choice **Database/ Delete One Patient**. You can only type into the **Patient ID** textbox.

If ENDG finds a patient with the indicated ID value, you will see the dialog window shown in . If the patient was not found, a message will be displayed.

Figure 2-124. The dialog displayed after ENDG has located the patient with selected for deletion. In this example, the patient has an ID of “120214”, the name is “Rb-F20” and the study date is “6/3/2004”. Note that the **Delete** button is now active.

To actually delete the patient, click the **Delete** button, which is now active.

You can also delete patients from the polar plot comparison page. See “Comparison Screen Options” on page 200.

Displaying the Database

To view the list of patients in the database of the current normal file, select **View Patient List** from the **Database** menu. In a few moments, a new window will open. This is an external application that displays the patient database, as shown in Figure 2-125.

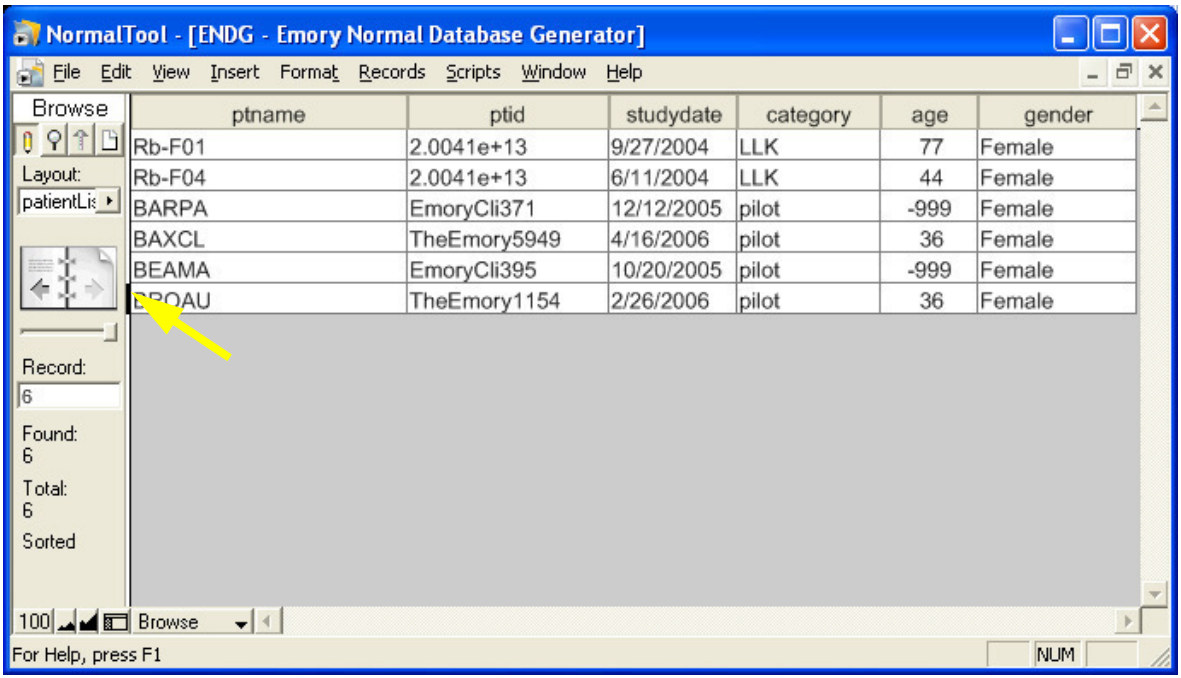

Figure 2-125. Displaying the patient list. The yellow arrow points to a small vertical line that is the current record indicator.

There are a number of tools included in this window. Briefly, some of the main options are:

- A column on the left side showing the number of patients in the database (“Total”), the number of patients shown in the window (“Found”) and the record number that is current (“Record”). The current record is indicated by the small vertical line next to the patient name. See the figure above.

- small buttons for zooming the display, as shown in Figure 2-126.
- The patient information, displayed in columns. To sort the entire list by a particular descriptor such as name or gender, click the column header.

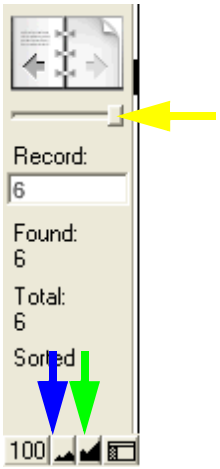

Figure 2-126. The database list window has controls for stepping from one patient to the next (yellow arrow), and zooming in (green arrow), or out blue arrow).

ptname	ptid	studydate
Rb-F01	2.0041e+13	9/27/2004
Rb-F04	2.0041e+13	6/11/2004
BARPA	EmoryCli371	12/12/2005
BAXCL	TheEmory5949	4/16/2006
BEAMA	EmoryCli395	10/20/2005
BROAU	TheEmory1154	2/26/2006

Figure 2-127. A portion of the database list window. Data can be sorted by any column. To sort by patient name, for example, click the column header labeled “ptname”.

Note: Any time the database list window closes, whether automatically ENDG exits or because the user manually closed it, an informational window will display for about two seconds (Figure 2-128), and then disappear.

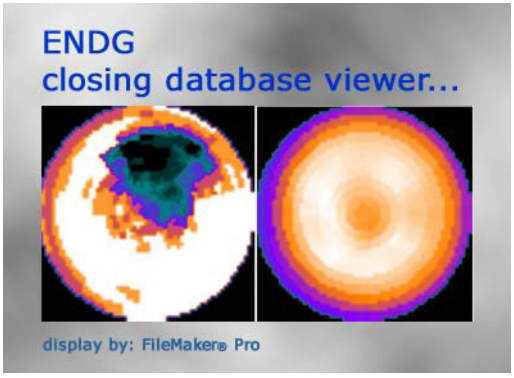

Figure 2-128. The information box displayed when ENDG's database list window closes.

Defining the Normal Mean

Calculating Means

At any time when there are two or more patients in the database, the mean and standard deviation can be calculated by clicking the **Show Normal File** button. The mean +/- 1 standard deviation for each of the 12 profiles in the normal file will be displayed. Each profile represents 40 sampled pixels from one short axis slice from apex (profile 0) to base (profile 11). An example is shown in Figure 2-129.

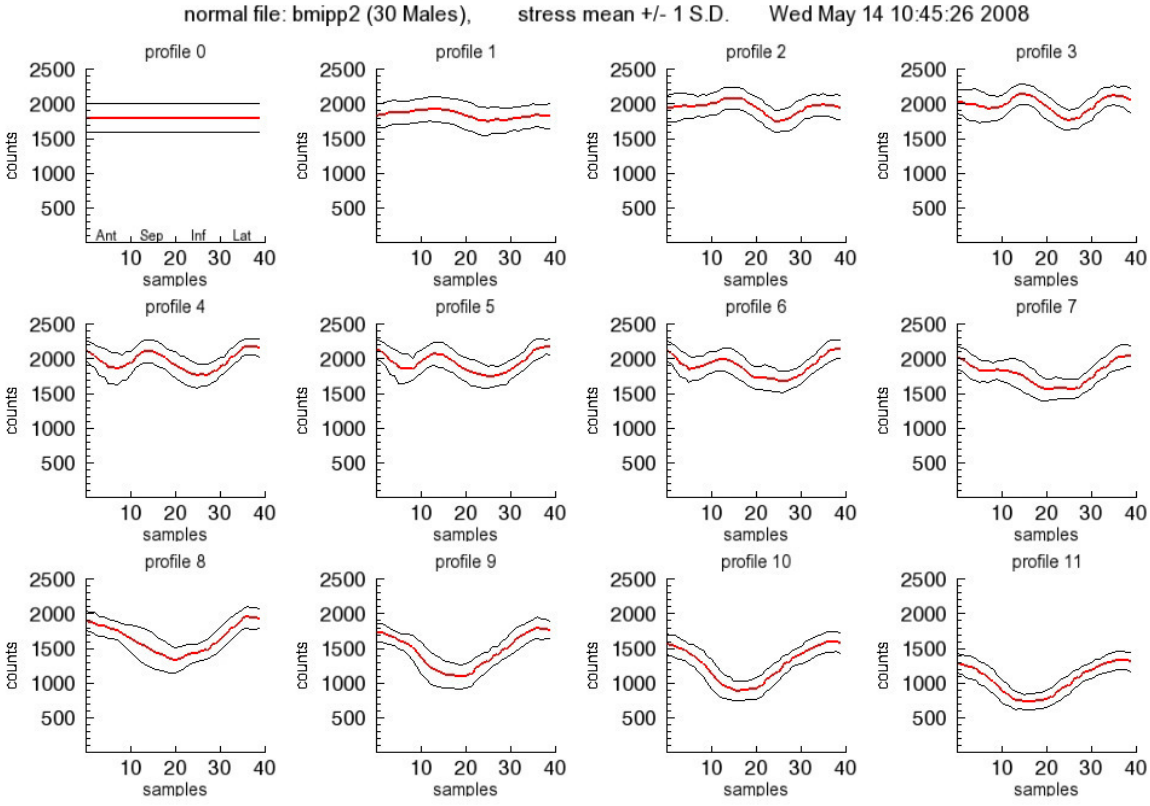

Figure 2-129. Red curves are mean values, black curves represent one standard deviation above and below the mean. Apex is profile 0.

The mean curve display characterizes the entire normal file. Sampled pixels are on the horizontal axis, and counts on the vertical axis. Sampling begins at 45 degrees in the antero-lateral direction when viewing the heart from the apex, so the myocardial sections are represented on the curves as shown in Figure 2-130, with the anterior quadrant being the first section of the curve, followed by septum, inferior wall and lateral wall.

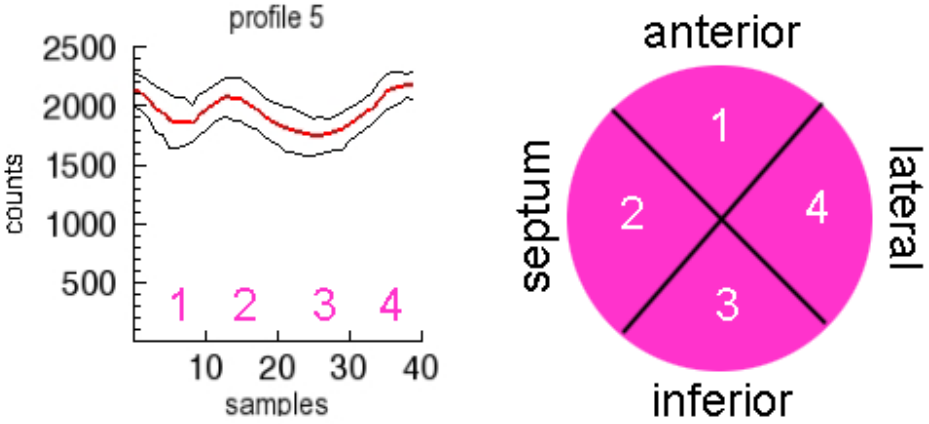

Figure 2-130. Myocardial walls as seen on each profile curve (left): 1=anterior, 2=septum, 3=inferior, 4=lateral. These correspond to the simple polar map style diagram on the right, which is the left ventricle in short axis as seen from the apex..

Be default, the stress mean curves are displayed first. To see the rest plots, either click the **Next Screen** button at the left, or use the **View** menu and select **Mean Profiles.../Rest**. To return to the stress curves from viewing rest or reversibility, use the **Prev Screen** button (“Previous Screen”), or use the View menu. The **View** menu can be used to recall the mean plots of your choice--stress, rest or reverse--at any time while ENDG has a valid normal file open. Once the curves are displayed, **Next Screen** and **Prev Screen** can be used to move between the three sets.

At the same time as the mean curves are displayed, ENDG will display a new window showing polar plots representing the mean for the current normal file. This display is shown in Figure 2-131. Stress, rest and

reversibility mean are shown across the top row, and stress, rest and reversibility standard deviation are across the bottom row.

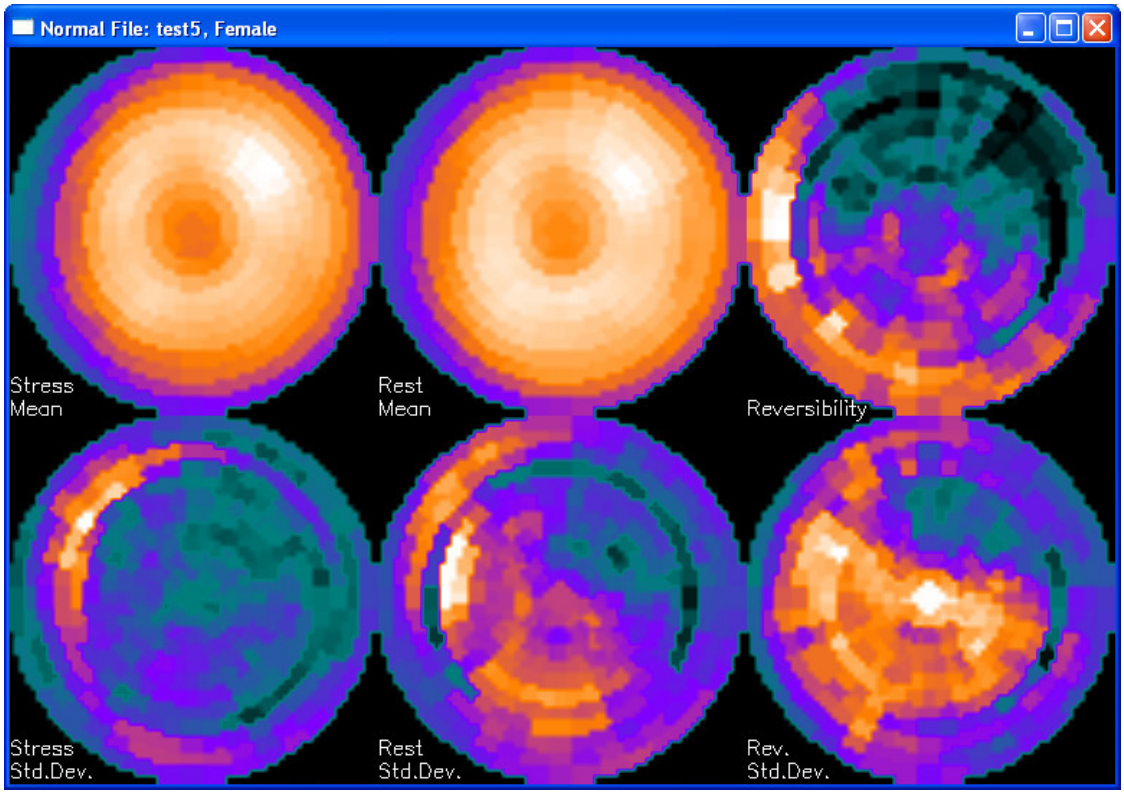

Figure 2-131. Mean and standard deviation polar maps representing the entire database of normal patients in the normal file.

The stress and rest maps represent the distribution against which a patient map is compared when the normal file is used in Emory Cardiac Toolbox.

Setting Thresholds

Normal files are used to determine the presence and size of perfusion defects in a patient study. Accurate definition of abnormal perfusion depends not only on the normal mean values that are present in the file, but on the thresholds for abnormality that have been set. Pixels in the patient myocardium that fall below the defined threshold are said to be abnormal. With a different threshold, that same pixel value may or may not be abnormal.

In ENDG, all thresholds are set to zero when a normal file is defined. To set thresholds for all regions of the myocardium, select the Set Thresholds button. The dialog shown in will be displayed.

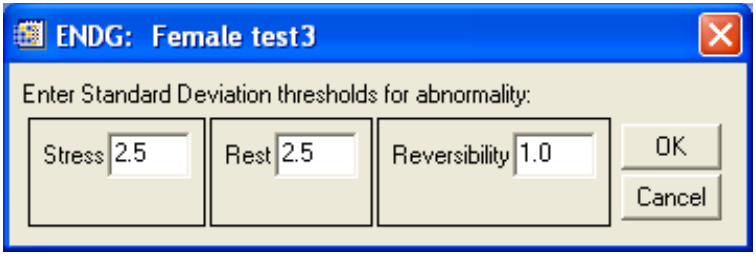

Figure 2-132. Dialog for setting abnormal thresholds

By default, thresholds are set to 2.5 standard deviations for the stress and rest polar maps, and reversibility is set to 1.0 std. dev. Any of these values can be changed. To save thresholds, click the OK button. The thresholds will be saved to a file on disk. To indicate that this operation was successful, ENDG displays a message in the status bar at the bottom of the screen.

An example of the contents of the threshold file is shown in Figure 2-133.

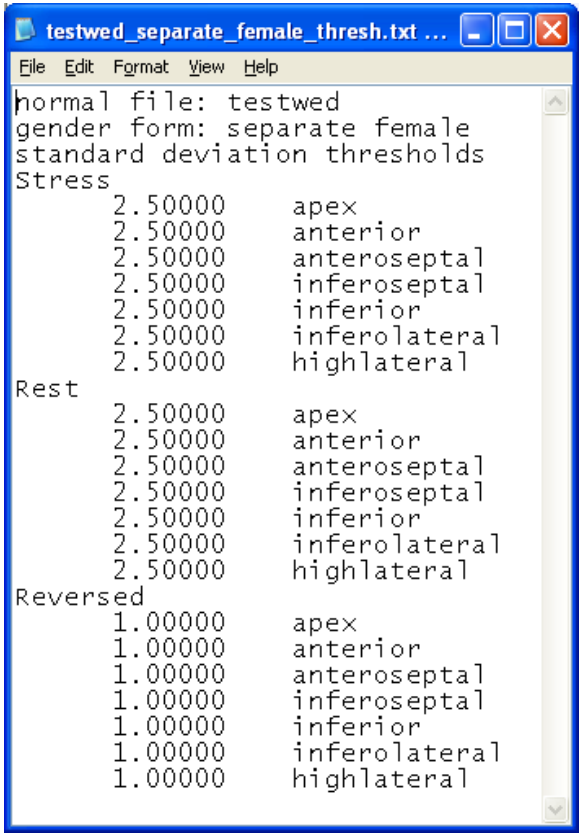

Figure 2-133. Contents of the threshold file.

Comparing Patients to Normal

Displaying Patient Polar Maps

The current set of patients can be compared to the normal file you are developing, just as if they were clinical patients in ECToolbox. To do this, select the **Compare to Normal File** button. This produces a screen similar to the one shown in Figure 2-134, with each patient represented by a polar map. Areas of the map are blacked out if they differ significantly from the mean of all normal patients. Under each map is the ID and Name of that patient.

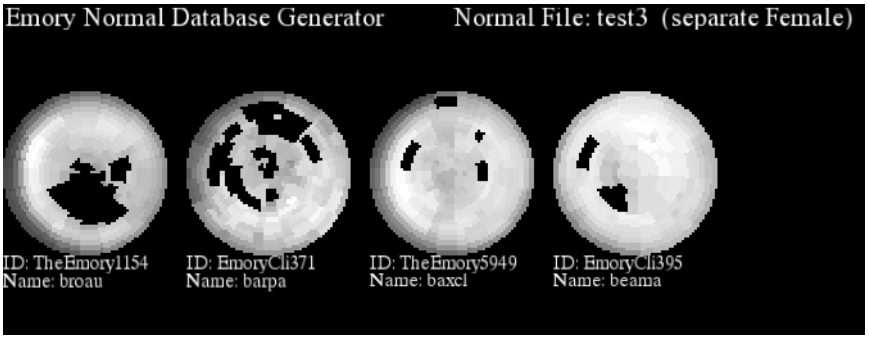

Figure 2-134. Four patients displayed with comparison to the current normal file.

Comparison Screen Options

There are several options that can be exercised on the normal comparison display.

A maximum of 3 rows of 7 polar maps are displayed at once. If there are more patients than this, you can see the next group by using the **Next Screen** button. Return to earlier patients using the **Prev Screen** button.

For any displayed polar map, a quantitative summary of the defects that are shown in black can be obtained by left-clicking the map. A small window will appear (Figure 2-135). Defect extent refers to the size of the abnormal black area within the polar map. Note that defect severity and reversibility values can *only* be seen by using the left-click method. To

dismiss the defect summary window, click either the **OK** or **Cancel** button, or the red “X” close widget in the corner.

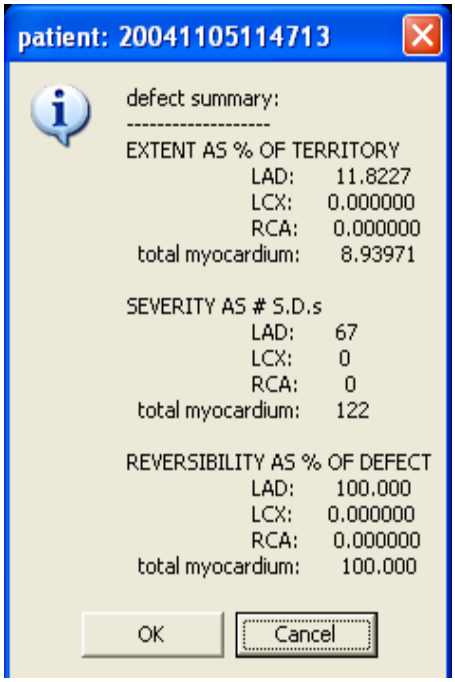

Figure 2-135. The defect summary window, which appears when a patient polar map is clicked with the left mouse button. Defect severity refers to the total number of standard deviations below the mean for every pixel within the blackout area.

As discussed in the section “Deleting Patients” on page 190, you can delete a patient from the database while on the Compare screen. You might want to do this if, for example, you see a patient with an unusually large defect. To delete the patient, click the polar map with the *right* mouse button. You will get a small question dialog. Selecting Yes will delete the patient, and draw an “X” through the map. This is a visual indicator that the patient was removed from the database, but still allows you to see the map, in case you decide to restore the patient. These displays are shown in Figure 2-136 and Figure 2-137.

Figure 2-136. This dialog is displayed when you right-click a polar map while on the **Compare to Normal File** screen. Selecting **Yes** removes the patient from the database.

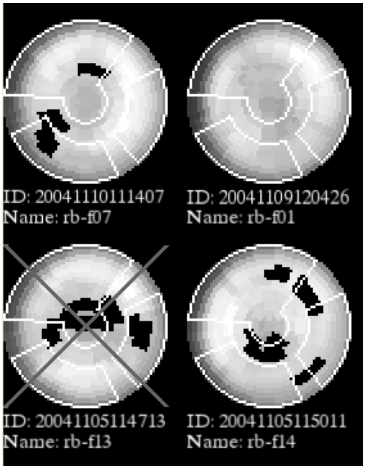

Figure 2-137. The patient comparison screen after one patient was deleted from the database, as indicated by the “X” on that polar map.

Deleting a patient has several effects: the polar map is marked on the display, the patient’s record is removed from the current database, and the file saved by ECToolbox (from which the patient data was loaded) is removed from the normal file’s **Patients** folder. However, the patient data has not disappeared entirely. It is still available to be restored to the

database in the future, at your discretion. This operation, which ENDG calls “Undelete”, can be used immediately or at a later time when ENDG has been opened again. To restore a deleted patient, select Undelete from the Database menu. A window will be displayed, listing the patients in the Deleted Patients folder. Highlight one and select Open. The Compare screen will be re-drawn to include the restored patient’s polar map, which no longer has an “X” on it. Note however that the restored polar map may not appear in the same place on the display, since the database is resorted when a patient is deleted.

Saving Normal File Results

Saving the Database

When a normal file has just been created and named, several objects are saved into the userNormalFiles folder on disk. There is a **Patients** folder, which holds data for every patient added to the normal file, and a **Deleted Patients** folder, which holds patients that have been removed from the file. Two XML format files are also created, one which has the name of the normal file, such as “testfile.xml”, which holds administrative details such as the number of patients in the file and the date it was created, and a database file with a similar name, such as “testfile_db.xml”, which holds the actual patient data, including the pixel arrays used to construct the mean.

If you add patients to the normal file using the **Database/Add Patient(s)** menu option, the database file is immediately updated with the data from those patients. However, the administrative file is *not* updated unless you select the **Show Normal File** button. This option calculates the means and standard deviations for the normal file and updates the administrative XML file. **Show Normal File** will also display the means, both as curves and as polar maps.

Saving the Means

Once the means have been calculated and displayed, the complete set of values can be saved to disk as a file. Use **Save Means as Textfile** from the Options menu. Afterward, the file can be opened in any text editor, and can also be opened using other applications such as a spreadsheet. See Figure 2-138 for an example.

	A	B	C	D	E
1	Patient	LAD % defect extent	LCX % defect extent	RCA % defect extent	total % defect extent
2	broau	17.5115	16.6667	18.1818	24.952
3	barpa	22.1675	7.93651	0	12.474
4	baxcl	23.5023	8.33333	0	14.0115
5	beama	0	3.7037	0	1.36054
6					
7					

Figure 2-138. A portion of the saved means file, as it appears when opened using a spreadsheet program such as (in this example) Microsoft Excel.

Saving the Thresholds

Thresholds for abnormality (explained in “Setting Thresholds” on page 198), are automatically saved to the administrative XML file as soon as they are set. The textfile listing the thresholds is also created automatically.

Saving the Current Screen

Any display screen in ENDG can be saved as a JPEG format image to disk. Use the **Save Screen** function under the **File** menu. The image is saved to the directory folder under userNormalFiles that has the same name as the current normal file.

Saving the Normal File for ECToolbox

Once your normal file is completed, it must be converted into a binary file in order to be used with Emory Cardiac Toolbox. There is only one step: select the button **Export Normal File**. The file will have the same base name as the normal file itself, with the extension “.nlg”, and will be written to the appropriate directory inside the ECToolbox folder heirarachy.

User-Defined Normal Files in Emory Cardiac Toolbox

Once you have created a normal file and exported it for use in ECToolbox, the last step to make the file usable is to set the preference in ECToolbox so that the file is recognized.

Using the dialog shown in , perform the following steps:

- Click the Edit button.
- The dialog shown in Figure 2-140 will appear.
- Use the Browse button, and choose the normal file you want to add from the list that is displayed. If there are male and female sections to the file, you must add them both.

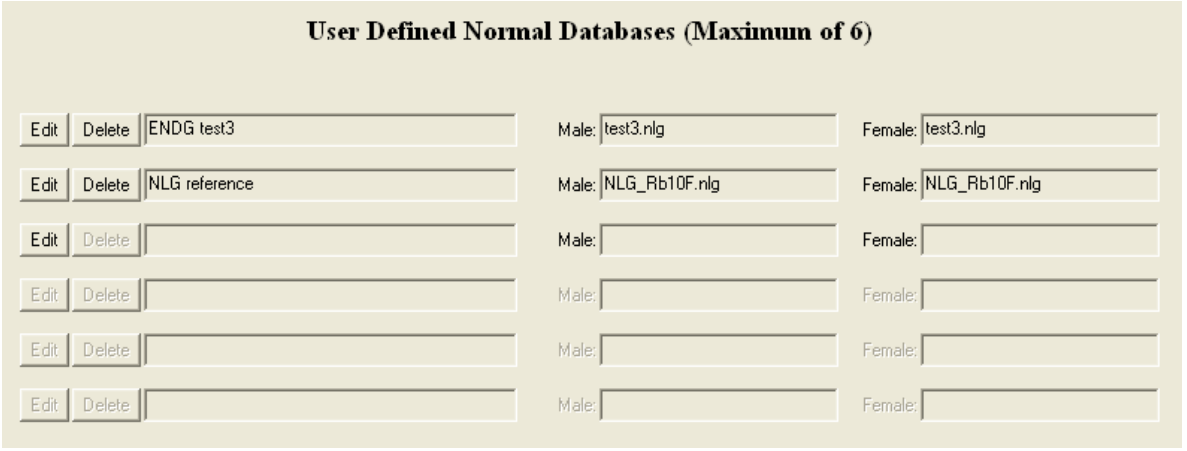

Figure 2-139. Setting up a user-defined normal database in ECToolbox.

A maximum of 6 user normal files can be handled by the current version of ECToolbox. If you have more than that, you will have to delete one in order to add a new one.

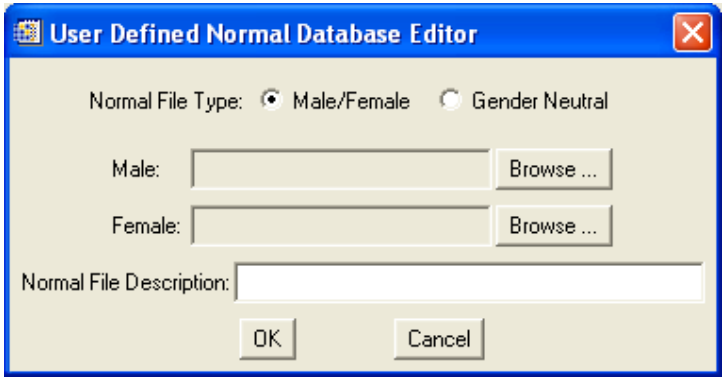

Figure 2-140. The dialog used for locating a user-defined normal file to be added to the ECToolbox list of available files.

Your normal file should now appear in the list of available files in ECToolbox's Study Verify window.

Appendix A: Additional References

Primary References

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Appendix B: Recommended Protocol Parameters

The protocols and related parameters listed in this Appendix are provided as a reference to the user. These are the recommended protocols to be followed in order to produce clinical images that can be accurately compared to the normal files included with the ECToolbox application. They are based in part upon the “Imaging Guidelines for Nuclear Cardiology Procedures”, published in the Journal of Nuclear Cardiology [1,2].

Note: Unless specifically stated otherwise, all SPECT protocols were developed using treadmill exercise stress.

For each of the protocols in this appendix, a parameter table and a criteria diagram are provided.

- **Parameter table**. This table provides recommended acquisition and processing parameters.
    - For SPECT collimator choices, “LEHR” refers to a Low Energy, High Resolution collimator.
    - SPECT protocols use Butterworth filters, and critical frequencies are given in units of cycles per centimeter. Most SPECT protocols use the same filter strength for acquisitions where similar count density is expected. Conversions can be made to other units according to the table below.

cycles/cm	fraction of Nyquist
0.4	0.5
0.52	0.66

    - Butterworth filters are also characterized by Power factor, which can also be expressed as the filter Order. In this appendix, the Power is given. Generally, the value for filter order is half that for the power. However, you should check the definition of filter order that is used by your manufacturer to see if this relationship between power and order is true for your particular system.

- **Criteria diagram**. This diagram, in polar map format, gives the normal file's criteria for abnormality in different regions of the left ventricle. The values listed represent standard deviations below the mean, for stress and rest; and standard deviations above the mean for Reversibility.

Protocol recommendations are provided for the following normal files:

- Dual Isotope (Rest Tl-201, Stress Tc-99m)
- Optimized Dual Isotope (Rest Tl-201, Stress Tc-99m)
- Enhanced Thallium
- One-Day Sestamibi
- Two-Day Sestamibi
- Tetrofosmin
- Tetrofosmin with pharmaceutical stress
- Rubidium-82
- Rubidium-82/F-18 FDG
- N-13 Ammonia

Dual Isotope Protocol:

	Rest Tl201	Stress Tc99m MIBI
Dose Range	3.0 mCi	25.0 mCi
Dose Adjustment (>70 kg)	0.04 mCi / kg	0.31 mCi / kg
Inject-to-Image Time	15 minutes	15 min. for Treadmill ex. 45 min. for pharmacologic stress.
Patient Position	Supine	Supine
Collimator	LEHR	LEHR
Energy Windows	70 kEv, 30% 167 kEv, 20%	140 kEv, 15%
Matrix	64 x 64	64 x 64
Pixel Size	6.0 +/- 0.4 mm	6.0 +/- 0.4 mm
# Projections	64	64
Orbit	180	180
	Circular, Step & Shoot	Circular, Step & Shoot
Start Angle	RAO 45	RAO 45
End Angle	LPO 45	LPO 45
Time / View	30 sec	20 sec

	Rest Tl201	Stress Tc99m MIBI
Gated Bins	n/a	8
Pre-Filter	Butterworth	Butterworth
Filter Critical Frequency	0.40	0.52
Filter Power	10.0	5.0
Reconstruction Filter	Ramp	Ramp

Normal File Criteria for Dual Isotope

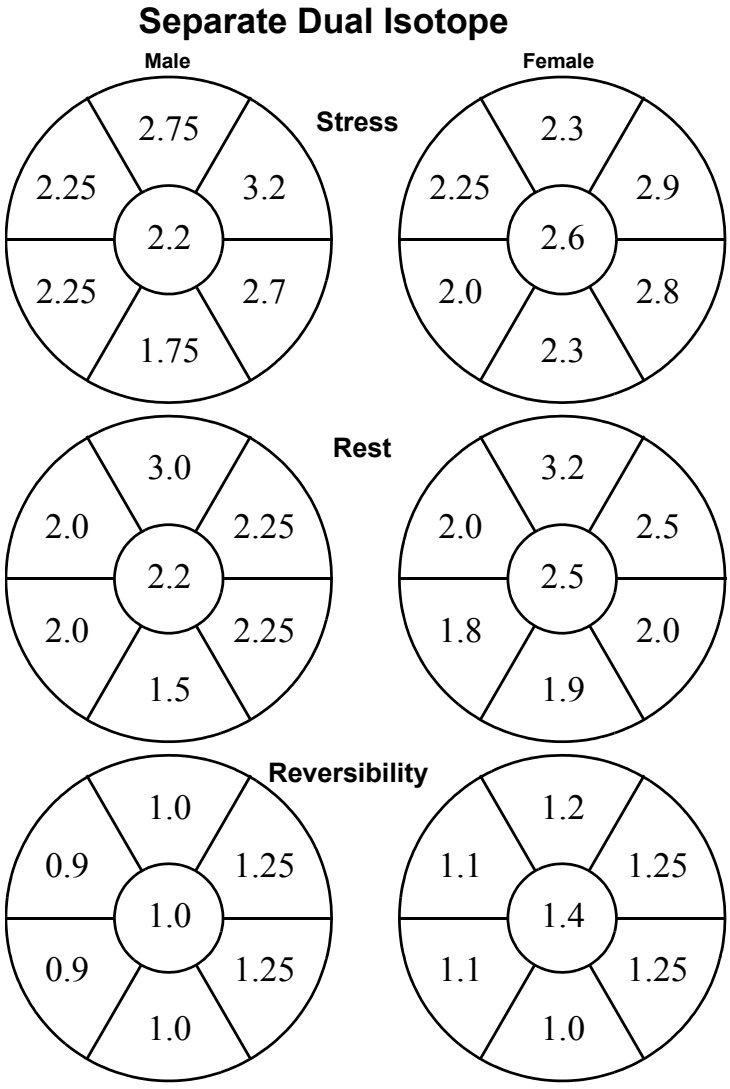


Figure B-141. Normal File Criteria for the Dual-Isotope Protocol.

Optimized Dual Isotope Protocol:

	Rest Tl201	Stress Tc99m MIBI
Dose Range	3.0 mCi	25.0 mCi
Dose Adjustment (>70 kg)	0.04 mCi / kg	0.31 mCi / kg
Inject to Image Time	15 minutes	15 min. for Treadmill ex. 45 min. for pharmacologic stress.
Patient Position	Supine	Supine
Collimator	LEHR	LEHR
Energy Windows	70 kEv, 30% 167 kEv, 20%	140 kEv, 15%
Matrix	64 x 64	64 x 64
Pixel Size	6.0 +/- 0.4 mm	6.0 +/- 0.4 mm
# Projections	64	64
Orbit	180	180
	Circular, Step & Shoot	Circular, Step & Shoot
Start Angle	RAO 45	RAO 45
End Angle	LPO 45	LPO 45
Time / View	30 sec	20 sec

	Rest Tl201	Stress Tc99m MIBI
Gated Bins	n/a	8
Pre-Filter	Butterworth	Butterworth
Filter Critical Frequency	0.40	0.52
Filter Power	10.0	5.0
Reconstruction Filter	Ramp	Ramp

Normal File Criteria for Optimized Dual-Isotope

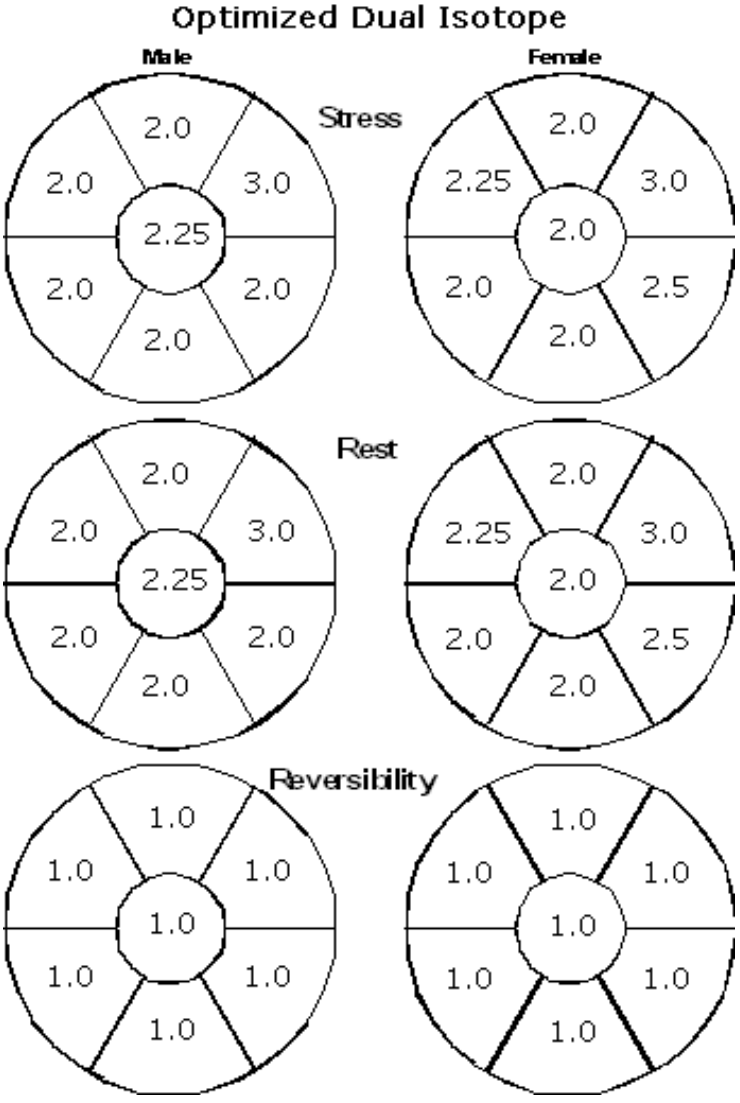


Figure B-142. Normal File Criteria for the Dual-Isotope Protocol.

Enhanced Thallium-201 Protocols

The Thallium Normal Files were generated from normal, gender matched patient studies, acquired using the Stress / Redistribution Protocol. Application of these same Normal Files to the Thallium Stress / Reinjection Protocol, is justified based upon the following rationale:

- The Stress acquisition is the same for both protocols;
- Since Reinjection tends to provide a more marked difference than simple Redistribution, when compared to Stress perfusion; the program is actually better able to identify Reversibility defects.

If a resting study from this protocol is to be used in conjunction with an F-18 FDG study for perfusion/metabolism comparison, iterative methodology should be used for reconstruction, and transmission scan-based attenuation correction should be applied.

	Tl201 Stress:	**Redistribution / Reinjection**
Dose Range	3.0 mCi	Redistribution: n/a Reinjection: 1.5 mCi
Dose Adjustment (>70 kg)	0.04 mCi / kg (not to exceed 5.0 mCi)	0.02 mCi / kg
Minimum time interval between acquisitions	N/A	3 hours
Inject to Image Time	10 - 15 minutes	Redistribution: n/a Reinjection: 15 minutes
Patient Position	Supine	Supine

	Tl201 Stress:	**Redistribution / Reinjection**
Collimator	LEHR	LEHR
Energy Windows	70 kEv, 30% 167 kEv, 20%	70 kEv, 30% 167 kEv, 20%
Matrix	64 x 64	64 x 64
Pixel Size	6.0 +/- 0.4 mm	6.0 +/- 0.4 mm
# Projections	64	64
Orbit	180	180
	Circular, Step & Shoot	Circular, Step & Shoot
Start Angle	RAO 45	RAO 45
End Angle	LPO 45	LPO 45
Time / View	20 sec	25/20 sec
Gated Bins	n/a	n/a
Pre-Filter	Butterworth	Butterworth
Filter Critical Frequency	0.50	0.40
Filter Power	5.0	10.0
Reconstruction Filter	Ramp	Ramp

Normal File Criteria for Enhanced Tl-201

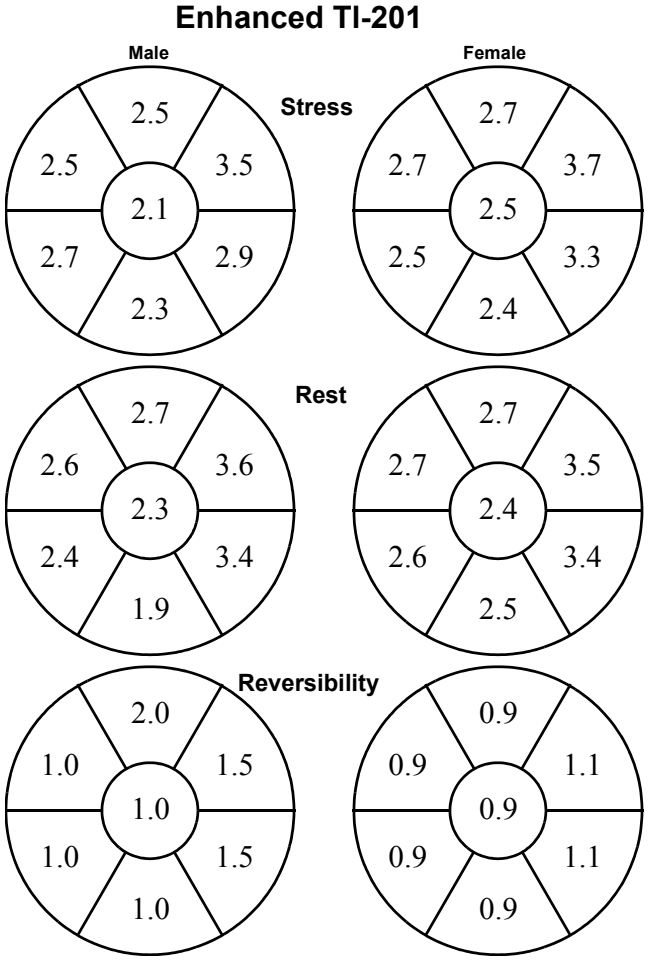


Figure B-143. Normal File Criteria for the Enhanced Thallium Protocol.

Sestamibi Protocols:

Following are recommended acquisition and processing parameters for both the One and Two Day Tc-99m Sestamibi SPECT protocols. If a resting study from this protocol is to be used in conjunction with an F-18 FDG study for perfusion/metabolism comparison, iterative methodology should be used for reconstruction, and transmission scan-based attenuation correction should be applied.

	Rest Tc99m MIBI	Stress Tc99m MIBI
Dose Range	8.0 - 9.0 mCi (1Day) 22.0 - 25.0 mCi (2Day)	22.0 - 25.0 mCi
Dose Adjustment (>70 kg)	0.11 mCi / kg(1Day) 0.31 mCi / kg(2Day)	0.31 mCi / kg
Minimum time interval between acquisitions	N/A	3 hours
Inject to Image Time	45 minutes	15 min. for Treadmill ex. 45 min. for pharmacologic stress.
Patient Position	Supine	Supine
Collimator	LEHR	LEHR
Energy Windows	140 kEv, 15%	140 kEv, 15%
Matrix	64 x 64	64 x 64
Pixel Size	6.0 +/- 0.4 mm	6.0 +/- 0.4 mm

	Rest Tc99m MIBI	Stress Tc99m MIBI
# Projections	64	64
Orbit	180	180
	Circular, Step & Shoot	Circular, Step & Shoot
Start Angle	RAO 45	RAO 45
End Angle	LPO 45	LPO 45
Time / View	25 sec (1 Day) 20 sec (2 Day)	20 sec
Gated Bins	n/a	8
Pre-Filter	Butterworth	Butterworth
Filter Critical Frequency	0.40 (1 Day) 0.52 (2 Day)	0.52
Filter Power	10.0 (1 Day) 5.0 (2 Day)	5.0
Reconstruction Filter	Ramp	Ramp

Normal Files for Sestamibi

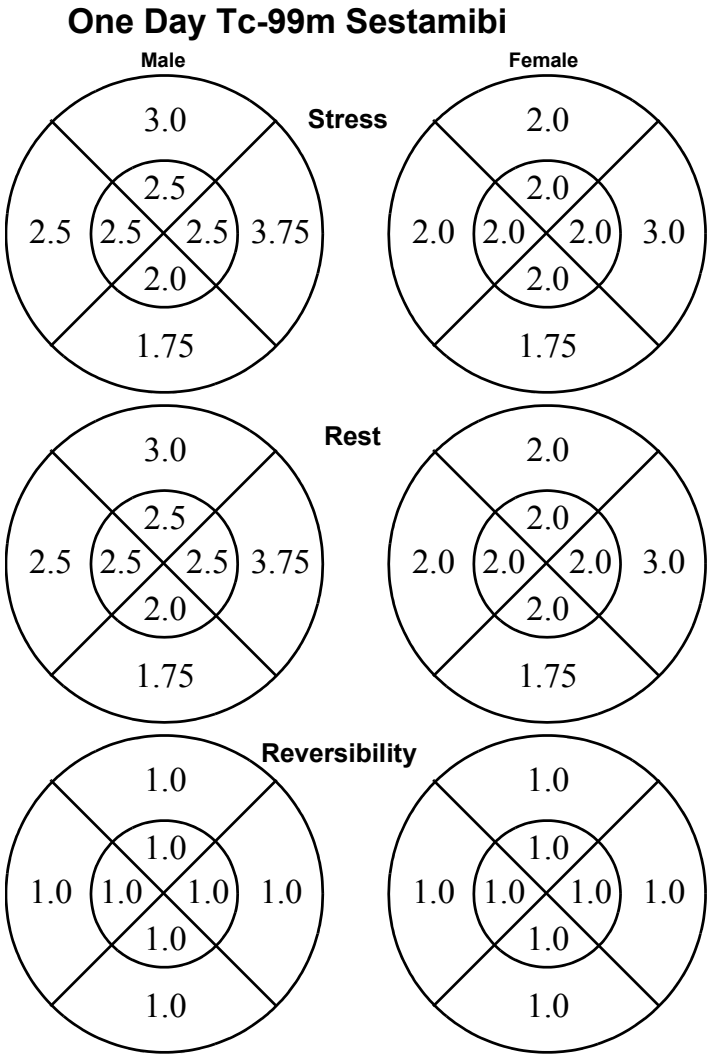


Figure B-144. Normal File Criteria for the One-Day Sestamibi Protocol.

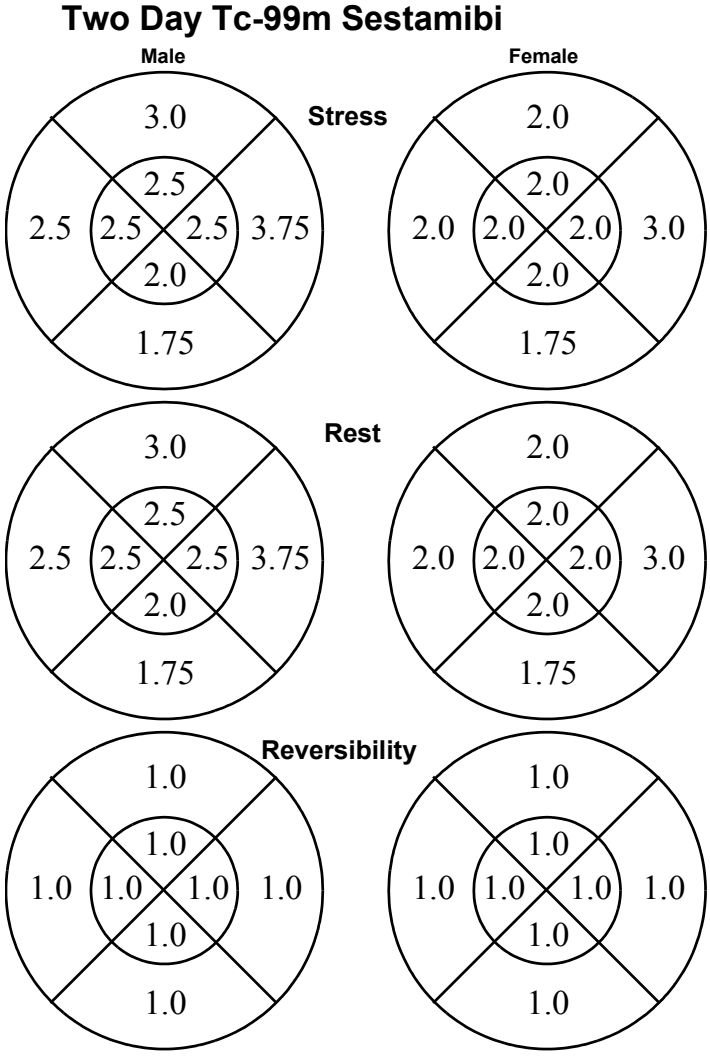


Figure B-145. Normal File Criteria for the Two-Day Sestamibi Protocol.

Tetrofosmin Protocol:

This Tetrofosmin SPECT protocol uses exercise stress. If a resting study from this protocol is to be used in conjunction with an F-18 FDG study for perfusion/metabolism comparison, iterative methodology should be used for reconstruction, and transmission scan-based attenuation correction should be applied.

Note: This protocol assumes a low-dose stress study in conjunction with exercise stress, and a high-dose rest study. For cases in which a high-dose stress study and low-dose rest study are done, it is recommended to use the 1-Day Sestamibi normal file for comparison.

	Stress Tc99m Tetrofosmin	Rest Tc99m Tetrofosmin
Dose Range	5.0 - 8.0 mCi	15.0 - 24.0 mCi
Dose Adjustment (>70 kg)	0.11 mCi / kg	0.31 mCi / kg
Minimum time interval between acquisitions	N/A	4 hours
Inject to Image Time Interval	15 minutes	45 minutes
Patient Position	Supine	Supine
Collimator	LEHR	LEHR
Energy Windows	140 kEv, 15%	140 kEv, 15%
Matrix	64 x 64	64 x 64
Pixel Size	6.0 +/- 0.4 mm	6.0 +/- 0.4 mm

	Stress Tc99m Tetrofosmin	Rest Tc99m Tetrofosmin
# Projections	64	64
Orbit	180	180
	Circular, Step & Shoot	Circular, Step & Shoot
Start Angle	RAO 45	RAO 45
End Angle	LPO 45	LPO 45
Time / View	25 sec	20 sec
Gated Bins	n/a	8
Pre-Filter	Butterworth	Butterworth
Filter Critical Frequency	0.40	0.52
Filter Power	10.0	5.0
Reconstruction Filter	Ramp	Ramp

Normal Files for Tetrofosmin

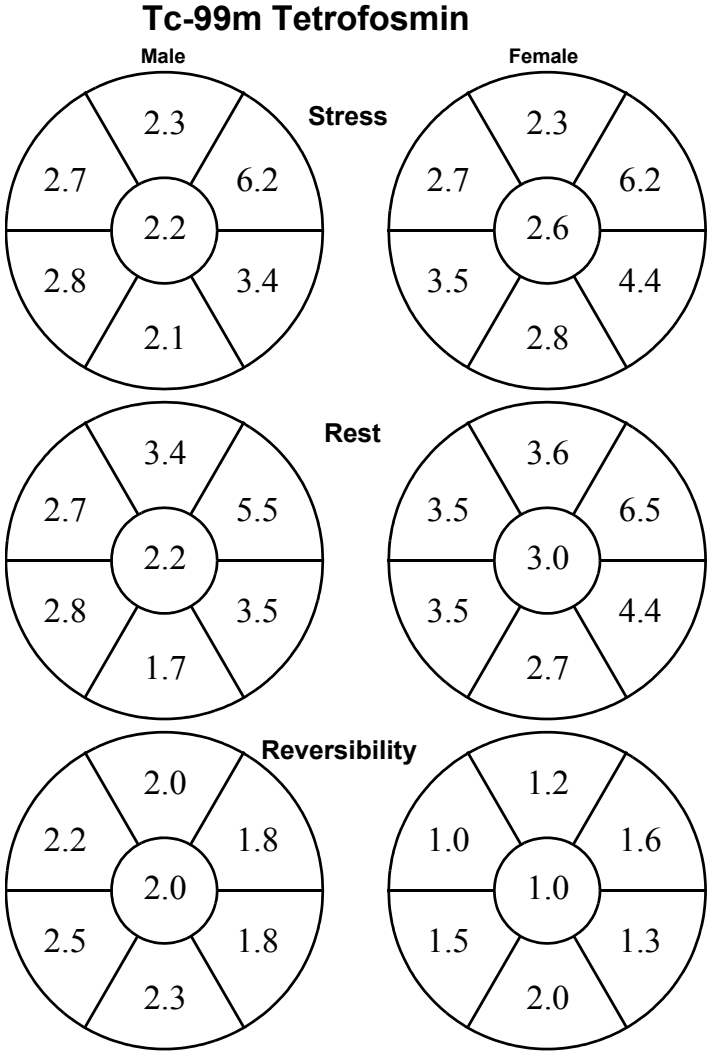


Figure B-146. Normal File Criteria for the Tetrofosmin Protocol.

Tetrofosmin Protocol, Pharmaceutical Stress:

If a resting study from this protocol is to be used in conjunction with an F-18 FDG study for perfusion/metabolism comparison, iterative methodology should be used for reconstruction, and transmission scan-based attenuation correction should be applied.

Note: This protocol assumes a low-dose stress study in conjunction with pharmaceutical stress, and a high-dose rest study. For cases in which a high-dose stress study and low-dose rest study are done, it is recommended to use the 1-Day Sestamibi normal file for comparison.

	Stress Tc99m Tetrofosmin	Rest Tc99m Tetrofosmin
Dose Range	5.0 - 8.0 mCi	15.0 - 24.0 mCi
Dose Adjustment (>70 kg)	0.11 mCi / kg	0.31 mCi / kg
Minimum time interval between acquisitions	N/A	4 hours
Inject to Image Time Interval	45 minutes	45 minutes
Patient Position	Supine	Supine
Collimator	LEHR	LEHR
Energy Windows	140 kEv, 15%	140 kEv, 15%
Matrix	64 x 64	64 x 64
Pixel Size	6.0 +/- 0.4 mm	6.0 +/- 0.4 mm

	Stress Tc99m Tetrofosmin	Rest Tc99m Tetrofosmin
# Projections	64	64
Orbit	180	180
	Circular, Step & Shoot	Circular, Step & Shoot
Start Angle	RAO 45	RAO 45
End Angle	LPO 45	LPO 45
Time / View	25 sec	20 sec
Gated Bins	n/a	8
Pre-Filter	Butterworth	Butterworth
Filter Critical Frequency	0.40	0.52
Filter Power	10.0	5.0
Reconstruction Filter	Ramp	Ramp

Normal Files for Pharmaceutical Stress Tetrofosmin

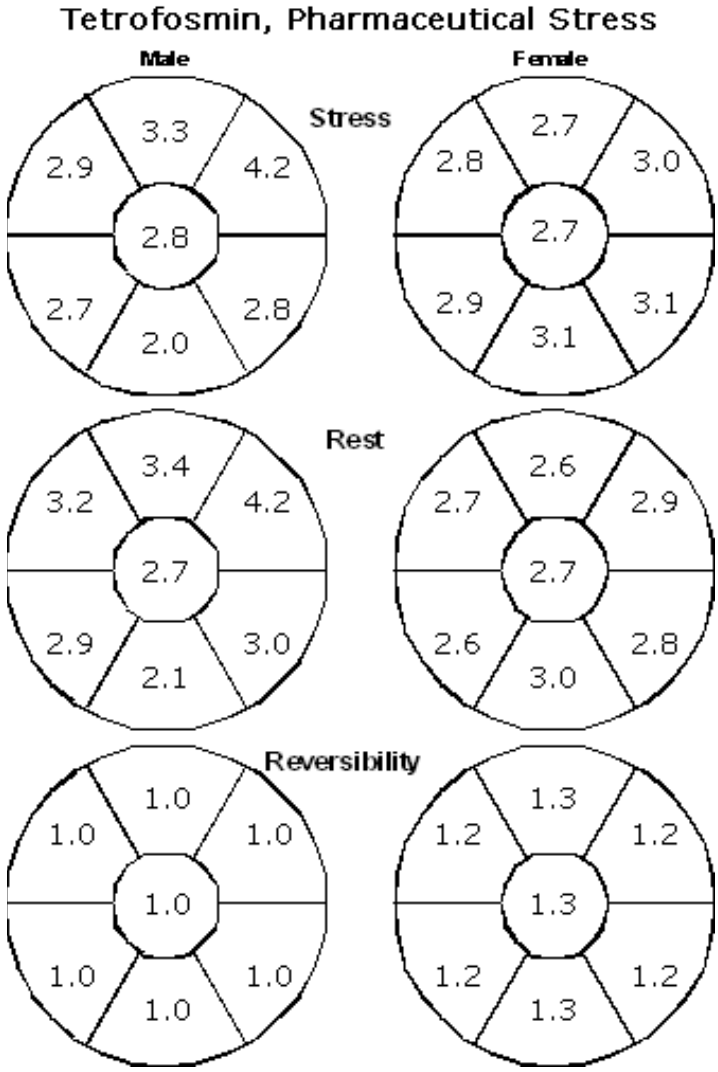


Figure B-147. Normal File Criteria for the Tetrofosmin pharmaceutical stress protocol.

Rubidium-82 Protocol:

The following table provides recommended acquisition and processing parameters for the Rest/Stress Rb-82 protocol. There is a 5 minute transmission scan after each Rb-82 acquisition. For this study, stress is always pharmacological.

	Rest Rb-82	Stress Rb-82
Dose Range	35-55 mCi	35-60 mCi
Dose Adjustment	depends on age of generator	depends on age of generator
Minimum time interval between acquisitions	N/A	15 minutes
Inject to Image Time Interval	N/A	N/A
Patient Position	Feet First/Supine	Feet First/Supine
Matrix	128 x 128	128 x 128
Pixel Size	3.375 mm	3.375 mm
Orbit	360	360
Time / Scan	7 min	7 min
Uniformity & COR Correction	COR N/A	COR N/A
Filter	Hanning	Hanning
Filter Cutoff (cycles/ pixel)	0.30	0.30

Rest Rb-82 / Rest Gated FDG Protocol:

The following table provides recommended acquisition and processing parameters for the Resting Rb-82/Gated FDG protocol.

There is a 5 minute transmission scan after the resting Rb-82 acquisition, and again after the FDG acquisition. Prior to FDG administration, 50g of glucose is given orally and the patient's plasma glucose level is monitored by venous sampling. In diabetic or glucose intolerant patients, insulin is also given. Thus, the time between Rb-82 and FDG scanning is somewhat variable.

	Rest Rb-82	Rest F-18 FDG
Dose Range	35-55 mCi	10 mCi
Dose Adjustment	depends on age of generator	
Minimum time interval between acquisitions	N/A	45 minutes
Inject to Image Time Interval	N/A	30 minutes
Patient Position	Feet First/Supine	Feet First/Supine
Matrix	128 x 128	128 x 128
Pixel Size	3.375 mm	3.375 mm
Orbit	360	360
Time / Scan	7 min	25 min
Gated Bins	N/A	8

	Rest Rb-82	Rest F-18 FDG
Uniformity & COR Correction	COR N/A	COR N/A
Filter	Hanning	Hanning
Filter Cutoff (cycles/ pixel)	0.30	0.30

Rest/Stress N-13 Ammonia Protocol:

Note: A 5 minute transmission scan is performed after each acquisition. The wait between tracer injection and imaging is to allow clearance of tracer from the blood pool. Pharmacological stress is used for this protocol.

	Rest Ammonia	Stress Ammonia
Dose Range	20 mCi	20 mCi
Dose Adjustment	--	--
Minimum time interval between acquisitions	N/A	30 minutes
Inject to Image Time Interval	2 minutes	2 minutes
Patient Position	Feet First/Supine	Feet First/Supine
Matrix	128 x 128	128 x 128
Pixel Size	3.375 mm	3.375 mm
Orbit	360	360
Time / Scan	15 min	15 min
Gated Bins	8 (optional)	8 (optional)
Uniformity & COR Correction	COR N/A	COR N/A
Filter	Hanning	Hanning
Filter Cutoff (cycles/ pixel)	0.30	0.30

References

1. Garcia EV(Ed.): Imaging Guidelines for Nuclear Cardiology Studies. J Nuclear Cardiol, May/June 1996;3:G34-G44.(suppl.)

2.)DePuey EG, Garcia EV (Ed.): Updated Imaging Guidelines for Nuclear Cardiology Procedures (Part I). J Nucl Cardiol 2001;8:G1-G58.

Appendix C: Example Cases

The two case examples in this Appendix are provided as a reference to the user. Both cases were acquired using the Dual-Isotope Protocol (Tl-201 Rest and Tc-99m MIBI Gated Stress). The first example illustrates normal myocardial perfusion at both Rest and Stress. The second example illustrates abnormal myocardial perfusion, consistent with myocardial ischemia. These cases are available to the user, for review using the Emory Cardiac Toolbox application. Correct use of the application should yield processed display screens and quantitative results which are similar to those presented in this appendix.

Normal Case:

The following Case Example is provided to illustrate a normal finding consistent with intact LV myocardial perfusion.

To select this case for on-line review:

1. Start the Emory Cardiac Toolbox.
2. Select the patient name, studies and datasets associated with patient: RamNa (ECToolbox Nml Example).
3. Confirm that this is a Dual Isotope (Tl, MIBI) study.
4. Proceed to the ECToolbox Main Window

Study Verification

In the ECToolbox Study Verification Window, the User should note that the program has correctly identified the Patient, Sex and Study (Dual Isotope).

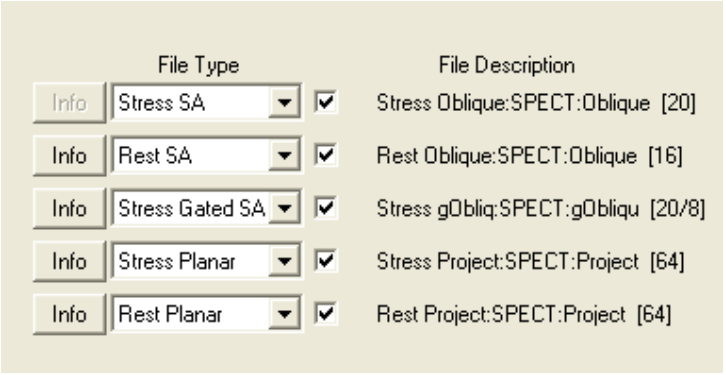


Figure C-110. Normal Case (RamNa): Study Verification Window. Only the left side of the window is shown here. See Chapter 2 for details of this window.

Main Window

In the ECToolbox Main Window, the User should note that the program has correctly identified LV Center and radius for both sets of Short-axis datasets. Also note that the program has correctly identified the apical and basal boundaries for both studies. User intervention to modify these selections, is not required in this case.

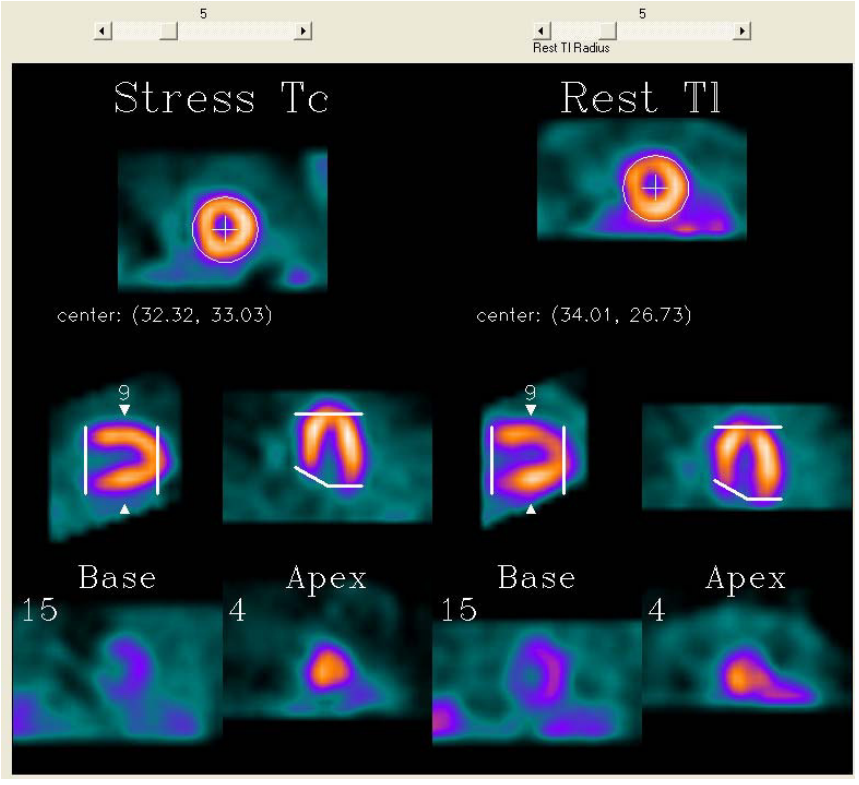


Figure C-111. Normal Case (RamNa): Main Window Display.

Slices Window

In the Slices Display Window, the User should note the absence of any significant perfusion defects on the tomographic slice images. In the Rest Study, tracer uptake in the Anterior Wall appears to be somewhat diminished, but appears normal in the Stress Study. This is considered to be a normal variant, and likely attributable to breast attenuation, which is evident on the Tl-201 Rest Study, but not evident on the Tc-99m MIBI Stress Study. Also, note that the T.I.D. Ratio is calculated to be 0.86, as displayed in the Patient Info area.

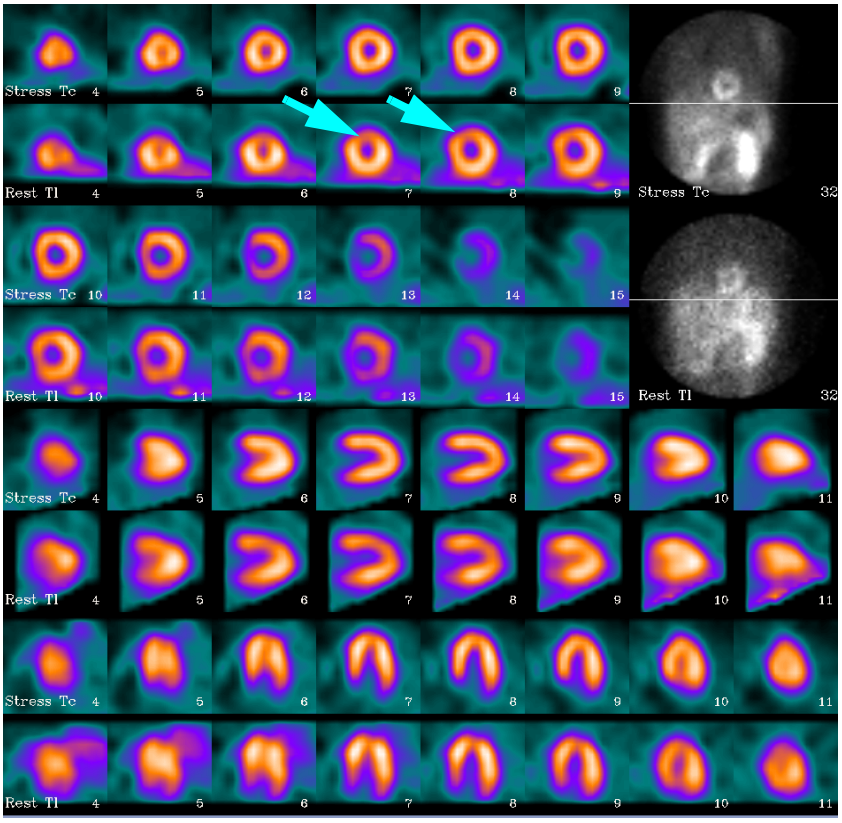


Figure C-112. Normal Case (RamNa): Slices Window. Tomographic slices demonstrate homogeneous tracer uptake with no appreciable perfusion defects. In the Rest Study, note that tracer uptake in the Anterior Wall appears to be somewhat diminished (Arrows).

Polar Maps Window

In the Polar Maps Display Window, the User should compare the Stress and Rest Polar Maps and note the absence of any significant differences between them. Note the presence of the small anterior wall defect on both the Defect Extent and Severity Polar Maps for the Rest Study, which is consistent with the visual findings seen on the myocardial slice images (noted above). Also note that on the Reversibility Polar Maps (Third column), the program has not identified any areas of significant Reversibility:

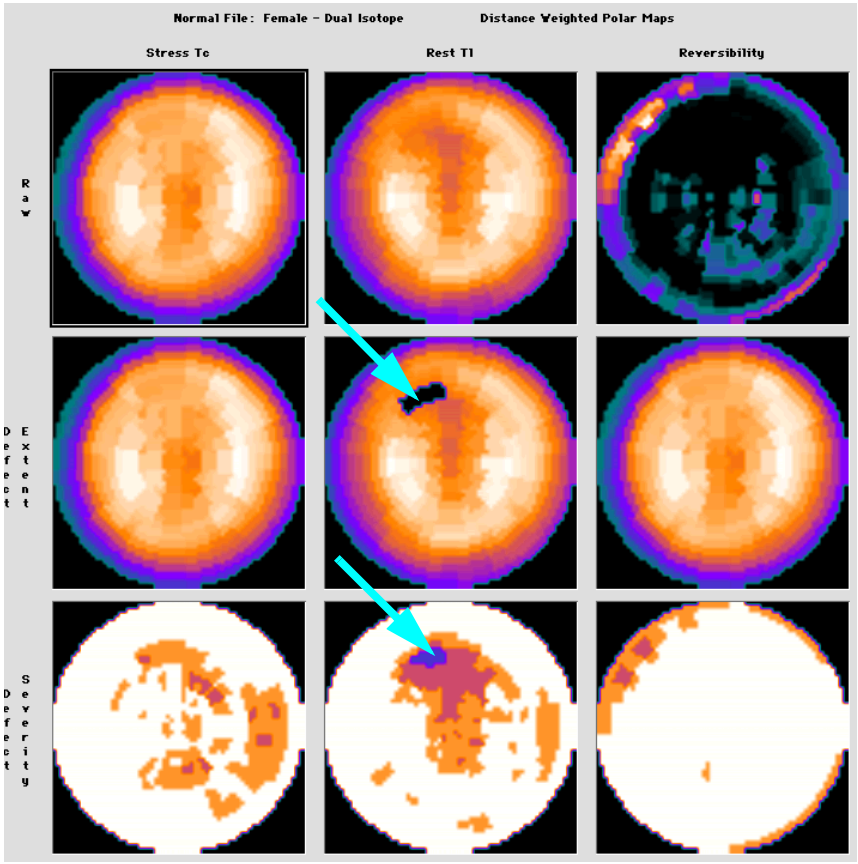


Figure C-113. Normal Case (RamNa): Polar Maps Display Window. The arrows indicate area of decreased tracer uptake on Rest Study.

Summed Scores

In the Summed Scores Display Window, the User qualitatively assigns a perfusion value to each segment of the Stress and Rest Polar Maps. The analysis illustrated below provides a Summed Difference Score of -3, indicating that the Stress Study demonstrates more normal perfusion than the Rest Study:

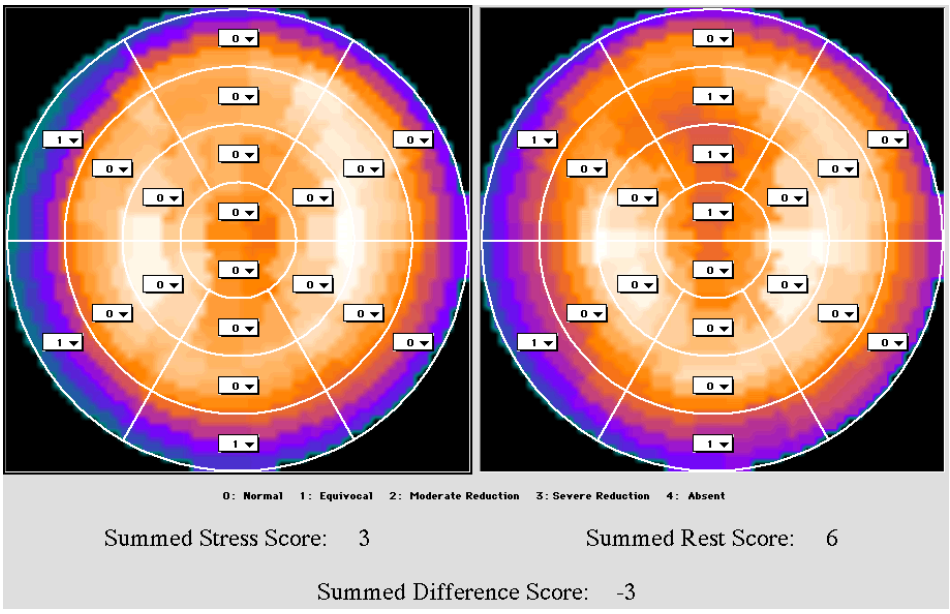


Figure C-114. Normal Case (RamNa): Summed Scores (SSS) Display Window.

Functional Analysis

In the Functional Analysis Display Window, the User verifies the LV Center and radial boundary locations for each of the 8 gated frames. The apical and basal boundaries are likewise verified. Note that no changes are indicated for this Case. Also note that this analysis demonstrates normal resting values for ventricular contraction, volume measurements and wall thickening:

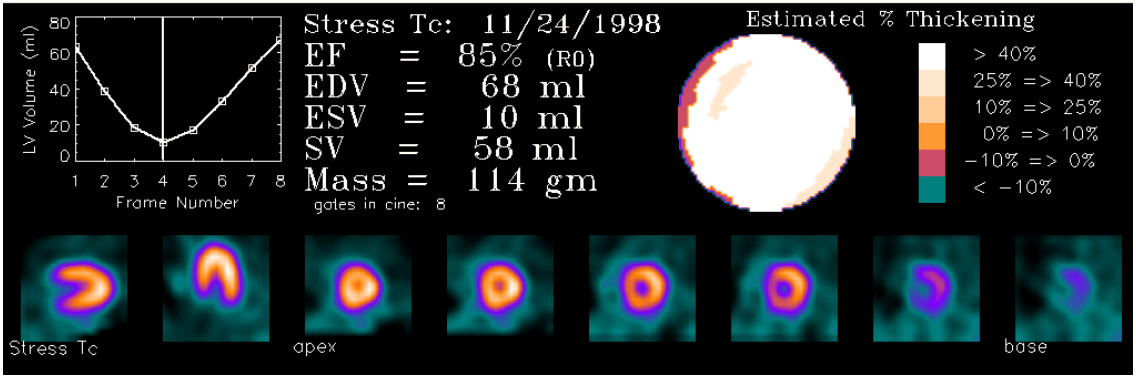


Figure C-115. Normal Case (RamNa): Functional Analysis Display Window.

Estimated Mass

In the Estimated Myocardial Mass Display Window, note that the program provides a display and analysis of the polar maps, using mass values determined from the gated study. This is now available because processing of the gated images has already been completed in the previous Functional Analysis section. Since no Stress defects were identified, note that the estimated mass and percentage of all five "defects", is displayed as 0gm and 0%. The "Stress Total Severity Score" is calculated to be 0, yielding a "Probability of Survival at 4 years" of 99%.

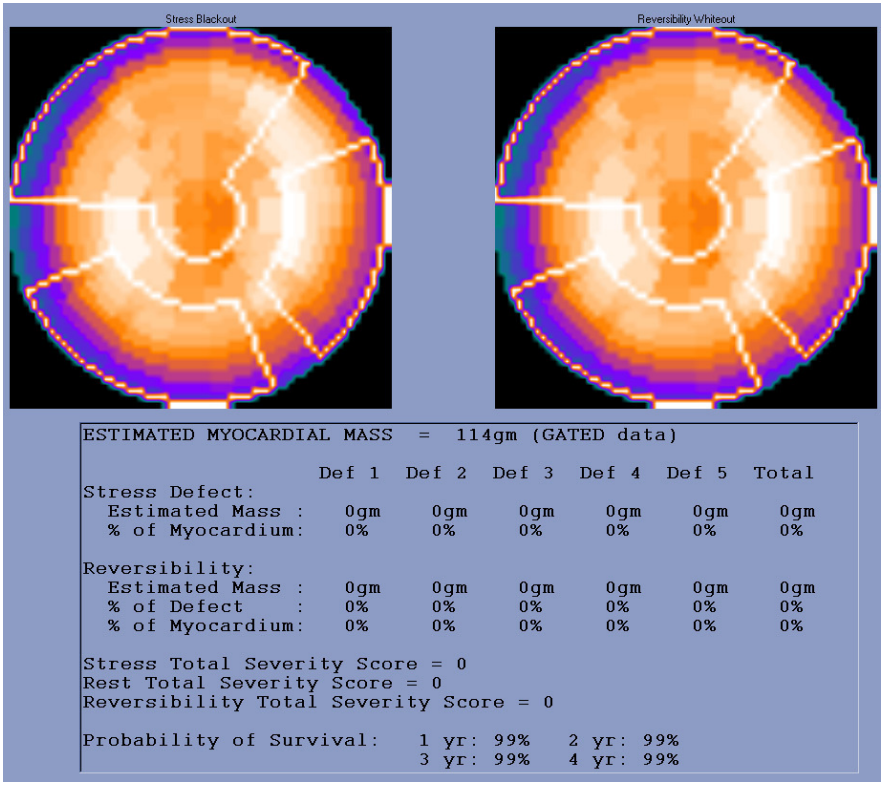


Figure C-116. Normal Case (RamNa): Myocardial Mass Display Window.

Estimated Extent

In the Estimated Extent Display Window, again note that the program provides a display and analysis of the gated polar maps. Note that because no defects are identified, the estimated extent of all five “defects”, is displayed as 0%. The same “Stress Total Severity Score” and “Probability of Survival” data is redisplayed in this window.

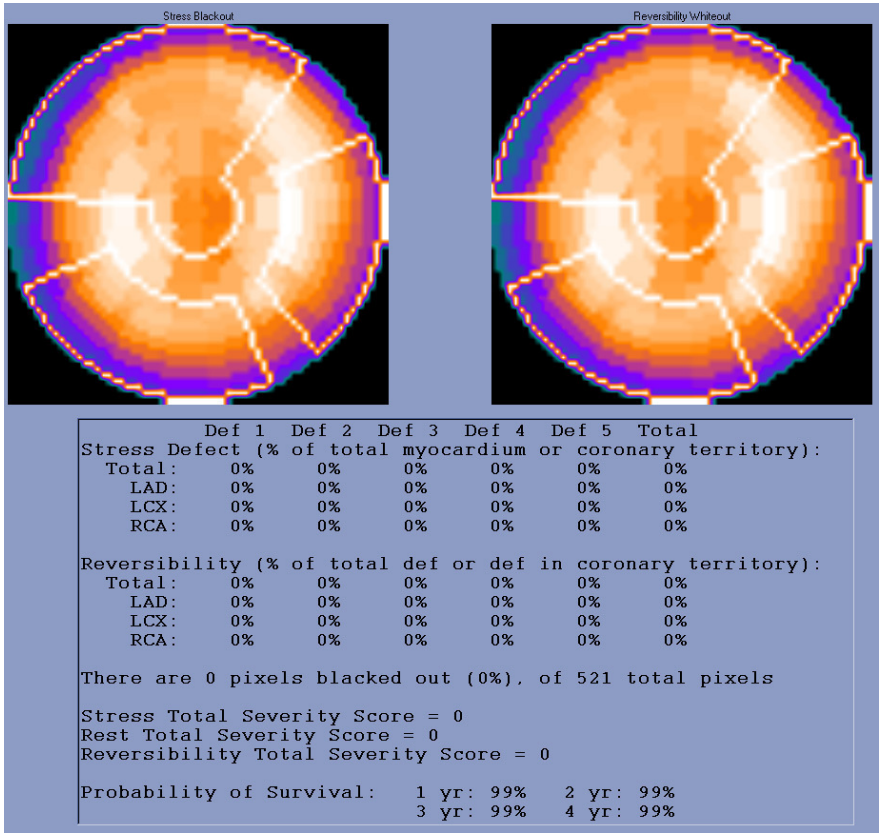


Figure C-117. Normal Case (RamNa): Extent Display Window.

Estimated Viability

For the Estimated Viability Display Window, recall that the program performs an analysis of the Rest Tl-201 Study. Note that one Rest defect is identified in this Case; however, this defect is located at the base of the septal wall. Whenever such a basal defect occurs in conjunction with an otherwise normal study, it is generally regarded as artifactual and should be discounted as such.

In this case, the Threshold has not been manually adjusted from the default value of 50%.

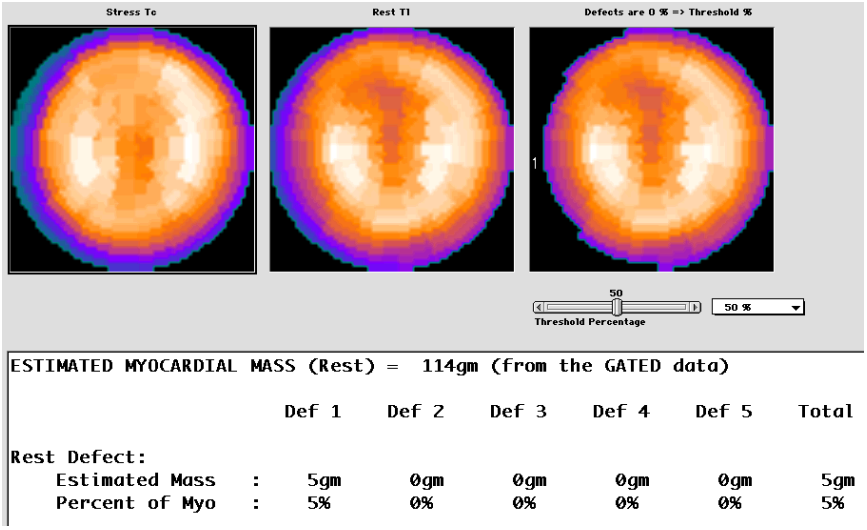
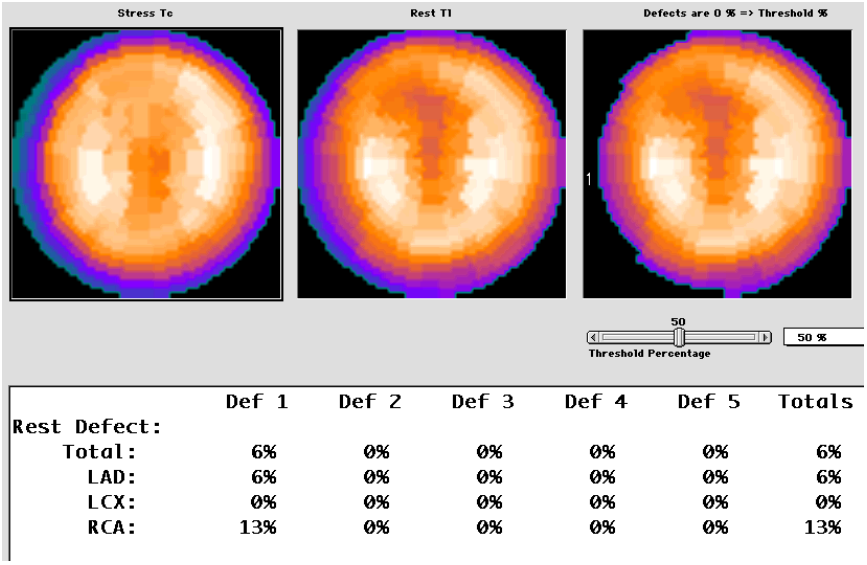


Figure C-118. Normal Case (RamNa): Estimated Viability (Mass) Window. The arrow identifies the location of an artifactual defect at the base of septum.

Viability Extent

Note that the Estimated Viability Extent display provides an assessment of the Rest defect, by coronary territories.



	Def 1	Def 2	Def 3	Def 4	Def 5	Totals
Rest Defect:						
Total:	6%	0%	0%	0%	0%	6%
LAD:	6%	0%	0%	0%	0%	6%
LCX:	0%	0%	0%	0%	0%	0%
RCA:	13%	0%	0%	0%	0%	13%

Figure C-119. Normal Case (RamNa): Estimated Viability (Extent) Window.

PerfSPECTive

In the PerfSPECTive Display Window, the 3D images provide a truer representation of the size and location of both the Stress and Rest defects.

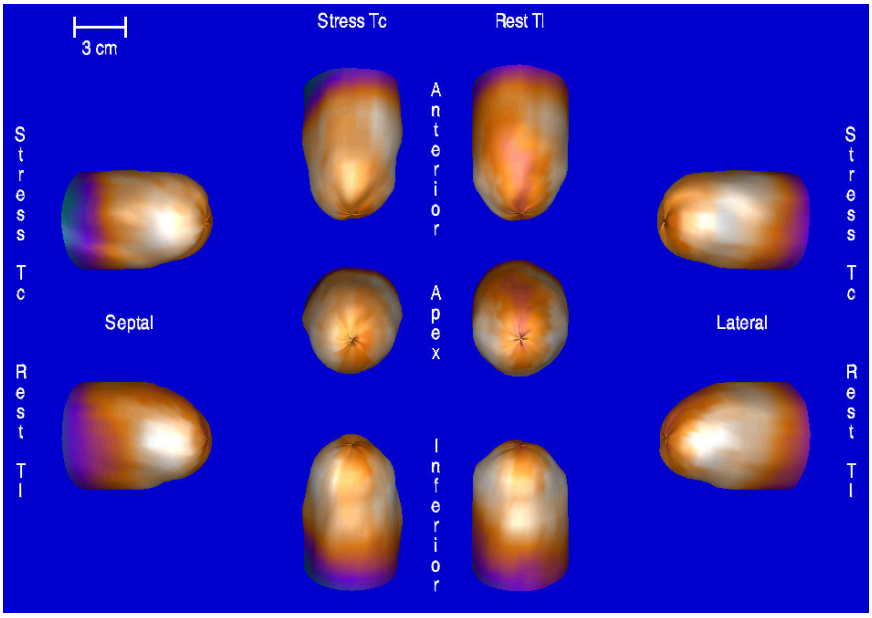


Figure C-120. Normal Case (RamNa): PerfSPECTive Window.

Gated PerfSPECTive

In the Gated PerfSPECTive Display Window, the 3D image can be “spun and tumbled” to allow visual assessment of perfusion and wall motion, from any angle. This Gated PerfSPECTive display is only available because processing of the gated images has already been completed in the previous Functional Analysis section.

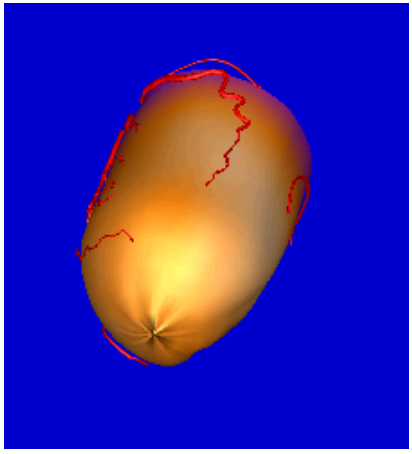


Figure C-121. Normal Case (RamNa): Gated PerfSPECTive Window.

Summary Window

On the Summary Display Window, the user is provided the ability to review the slice images, polar maps and Summed Score analysis, all on one display. Also included are key perfusion and function values (EF, Volumes, Summed Scores, Stress Total Severity Score and Survival Probability).

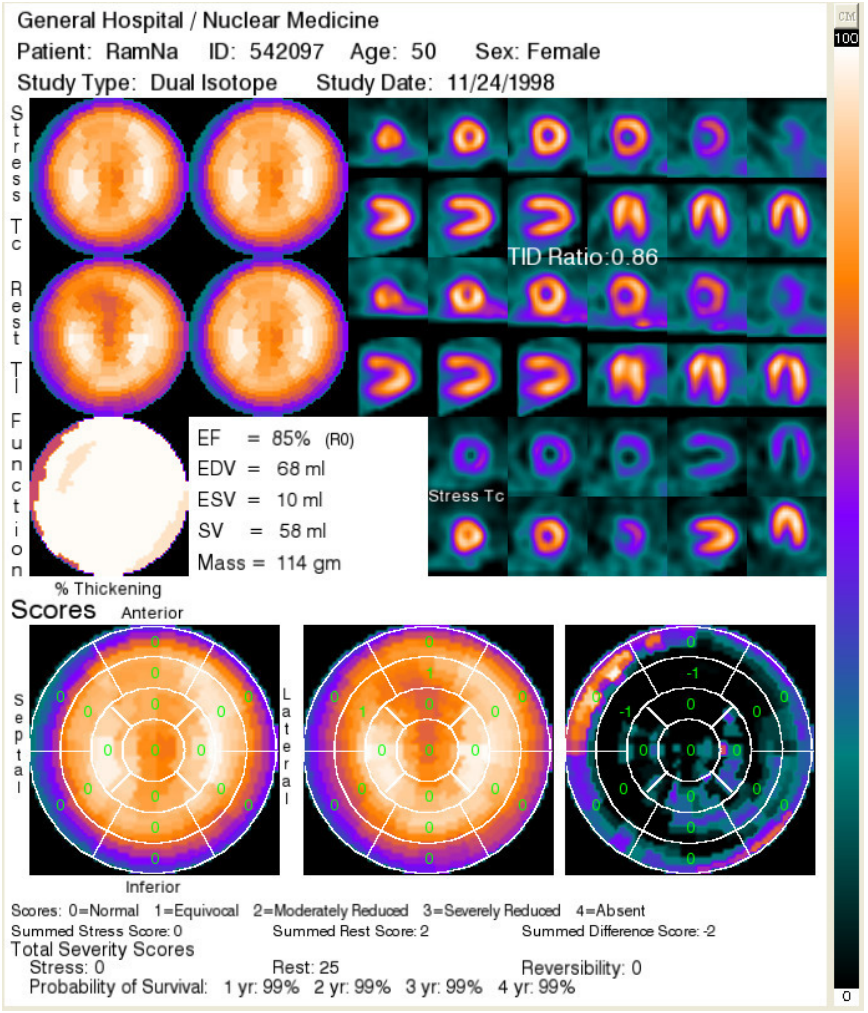


Figure C-122. Normal Case (RamNa): Summary Window.

Impression

The following text is provided as an example of the “Impression” section of a diagnostic report for this Case:

This patient’s myocardial perfusion gated SPECT study demonstrates normal patterns of tracer distribution in the LV myocardium at both Rest and Stress. No myocardial perfusion defects were identified. The Trans-Ischemic Dilatation (TID) Ratio is measured to be 0.87. The resting LV ejection fraction is also normal (85%).

Abnormal Case:

The following Case Example is provided to illustrate an abnormal finding, which is consistent with an ischemic myocardial perfusion defect.

To select this case for on-line review:

1. Start the Emory Cardiac Toolbox.
2. Select the patient name, studies and datasets associated with patient: PalRa (ECToolbox Abn Example).
3. Confirm that this is a Dual Isotope (Tl, MIBI) study.
4. Proceed to the ECToolbox Main Window

Main Window

In the ECToolbox Main Window, the User should note that the program has correctly identified the LV Center and radius for both sets of Short-axis datasets. Also note that the program has correctly identified the apical and basal boundaries for both studies. User intervention to modify these selections, is not required in this case.

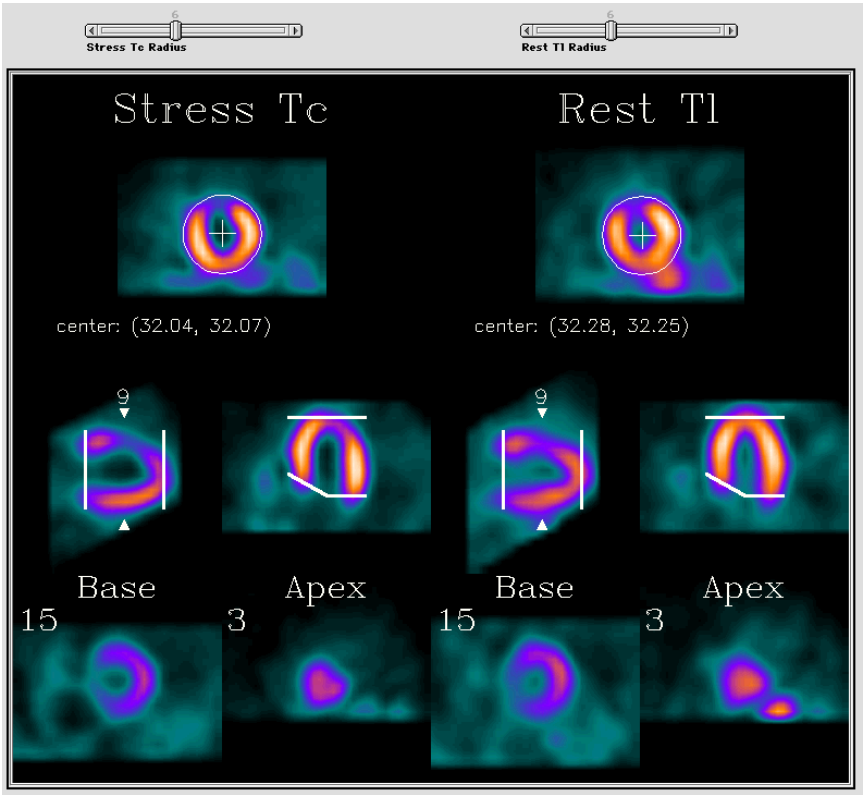


Figure C-123. Abnormal Case (PalRa): Main Window Display.

Slices Window

In the Slices Display Window, the User should visually note the presence and location of the perfusion defects on the slice tomographic images. Also note that the stress defects appear to be more severe than the Rest defects. The T.I.D. ratio, 1.08, appears in the Patient Info area.

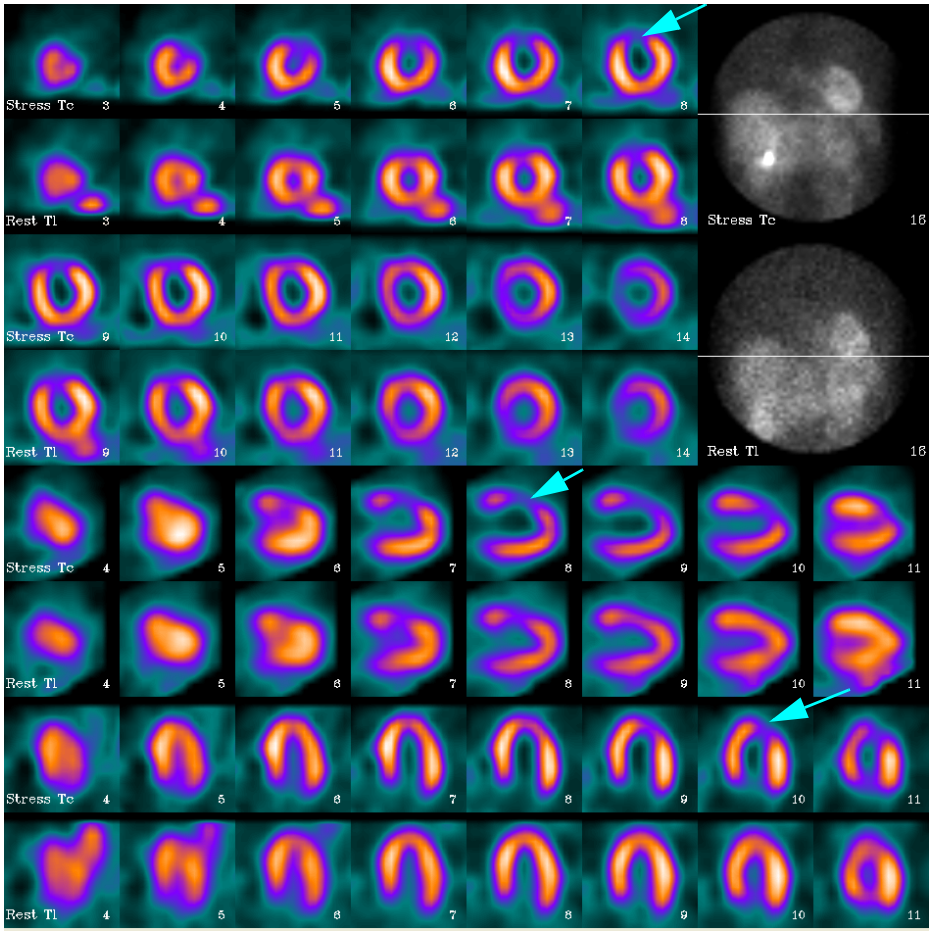


Figure C-124. Abnormal Case (PalRa): Slices Display Window. The arrows indicate stress perfusion defects.

Polar Maps Window

In the Polar Maps Display Window, the User should compare the Stress and Rest Polar Maps and appreciate the significant difference between them. Note that this difference mirrors the defects seen on the myocardial slice images. On the Reversibility Polar Maps (Third column), note that the program has identified an area of significant Reversibility:

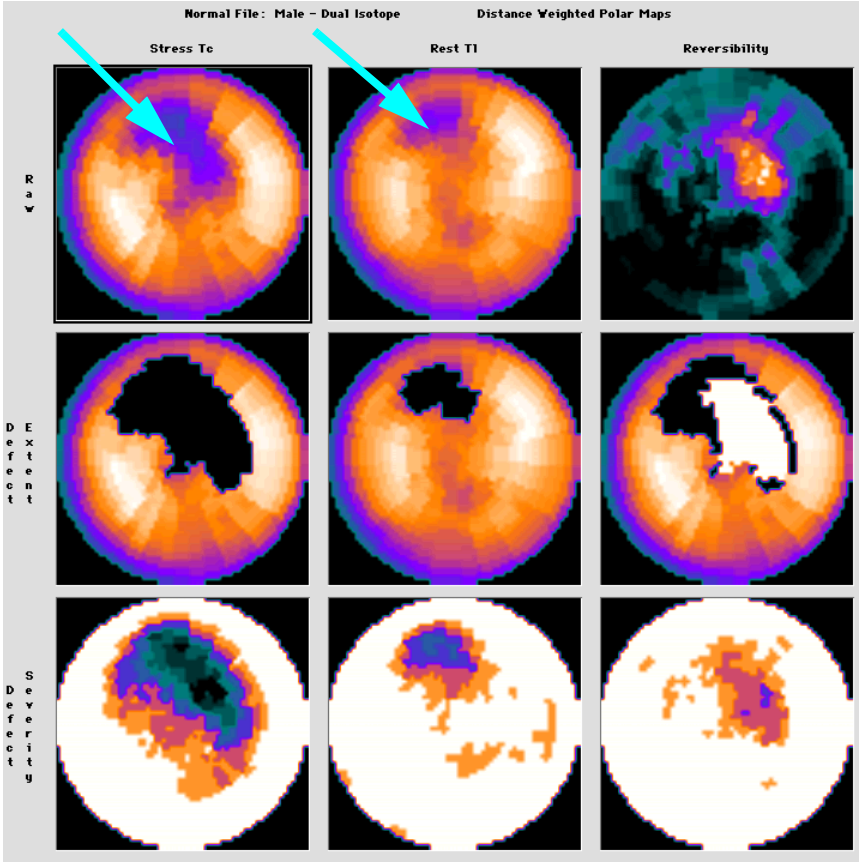


Figure C-125. Abnormal Case (PalRa): Polar Maps Display Window. Note perfusion defects and area of Reversibility.

Summed Scores

In the Summed Scores Display Window, the User qualitatively assigns a perfusion value to each segment of the Stress and Rest Polar Maps. The analysis illustrated below provides a Summed Difference Score of 9.:

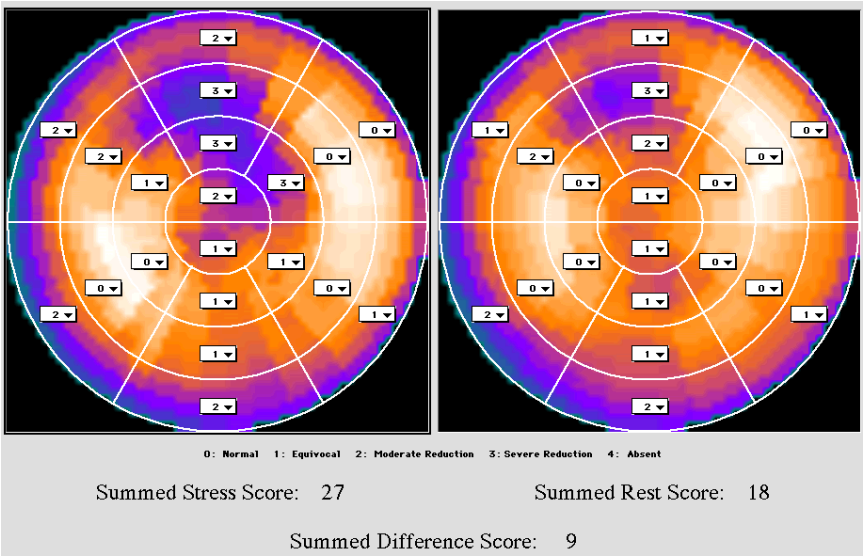


Figure C-126. Abnormal Case (PalRa): Summed Scores (SSS) Display Window.

Functional Analysis

In the Functional Analysis Display Window, the User verifies the LV Center and radial boundary locations for each of the 8 gated frames. The apical and basal boundaries are likewise verified. Note that no changes are indicated for this Case. Also note that this analysis demonstrates normal resting values for ventricular contraction, volume measurements and wall thickening:

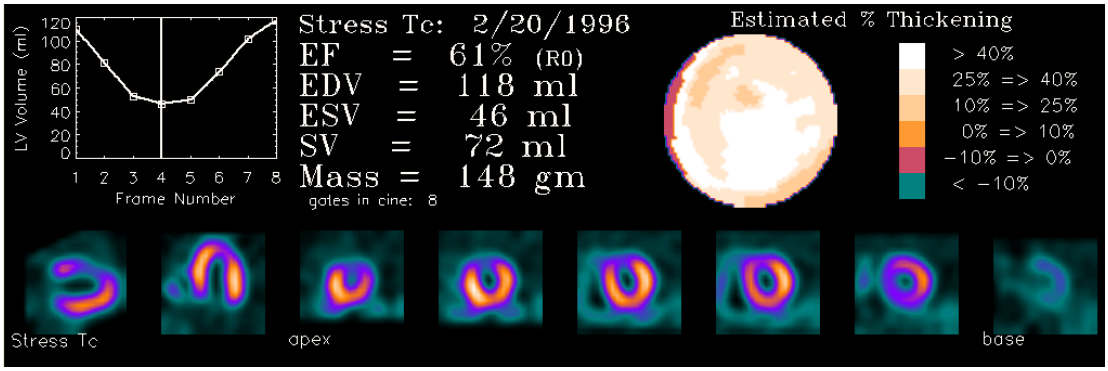


Figure C-127. Abnormal Case (PalRa): Functional Analysis Display Window.

Estimated Mass

In the Estimated Myocardial Mass Display Window, note that the program provides a display and analysis of the polar maps, using mass values determined from the gated study. This is now available because processing of the gated images has already been completed in the previous Functional Analysis section. Note that the estimated mass of this single Stress perfusion defect, is estimated at 25% of the LV myocardial mass and that 53% of this defect demonstrates reversibility. The “Stress Total Severity Score” is calculated to be 772, yielding a “Probability of Survival at 4 years” of 42%.

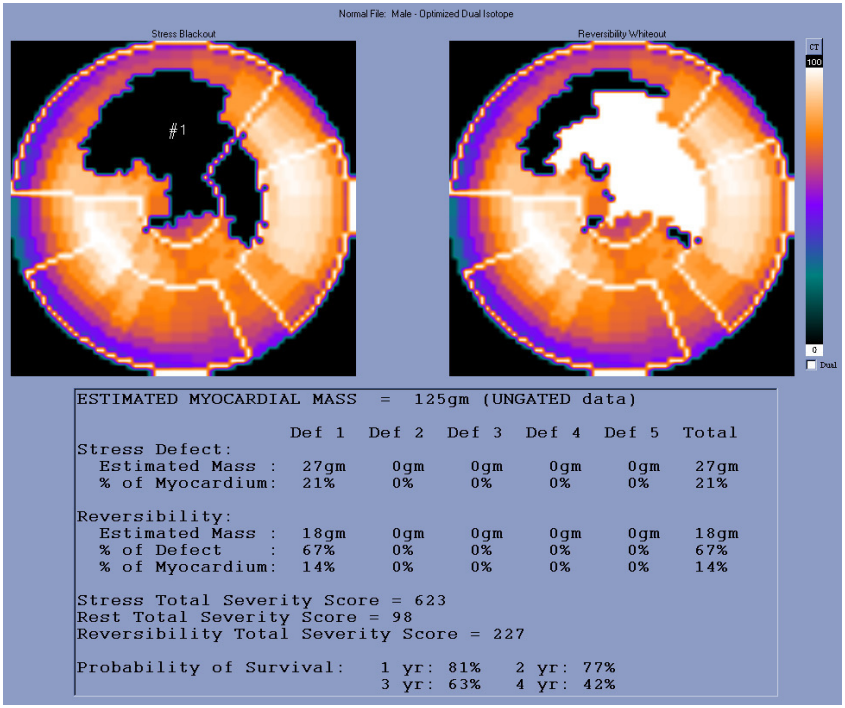


Figure C-128. Abnormal Case (PalRa): Myocardial Mass Display Window.

Estimated Extent

In the Estimated Extent Display Window, again note that the program provides a display and analysis of the gated polar maps. Note that the estimated extent of this single Stress perfusion defect, based on “blacked-out” pixels, is estimated at 29% of the LV myocardium and that 57% of this defect demonstrates reversibility. The same “Stress Total Severity Score” and “Probability of Survival” data is redisplayed in this window.

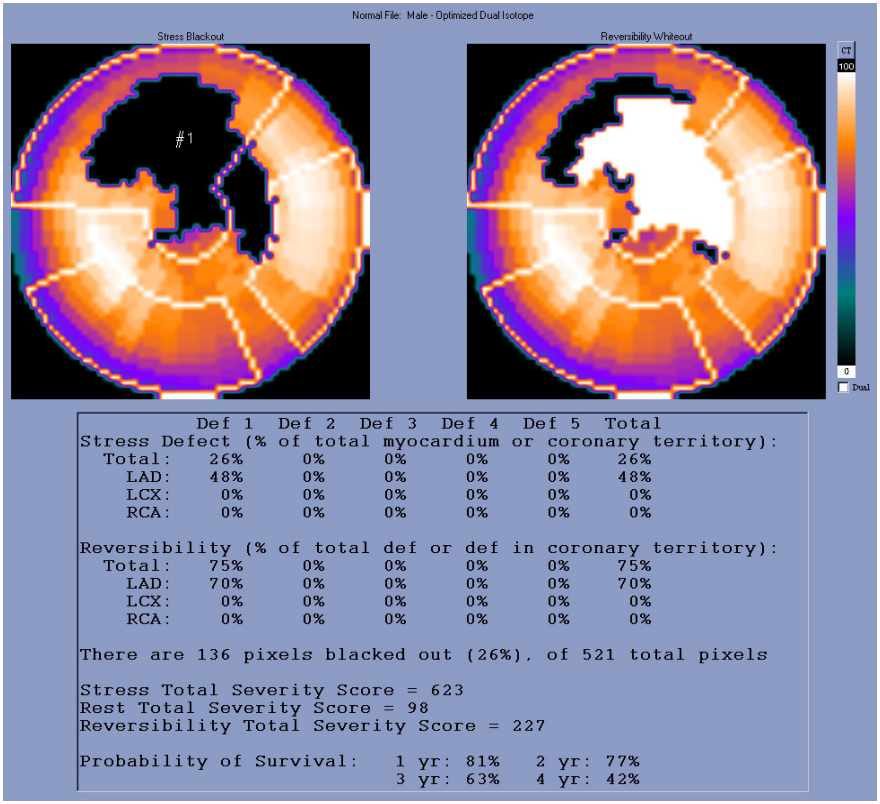


Figure C-129. Abnormal Case (PalRa): Extent Display Window.

Estimated Viability

For the Estimated Viability Display Window, recall that the program performs an analysis of the Rest Tl-201 Study. Note that two Rest defects are identified in this Case; however, the second defect is located at the myocardial base. Whenever this occurs, it is generally regarded as artifactual and should be discounted as such.

In this case, the Threshold has been manually adjusted to 60%. Using this threshold, the Myocardial Mass Estimated Viability display demonstrates a percent non-viable myocardium value for Defect #1, of 4% of the LV myocardium (6 gm.).

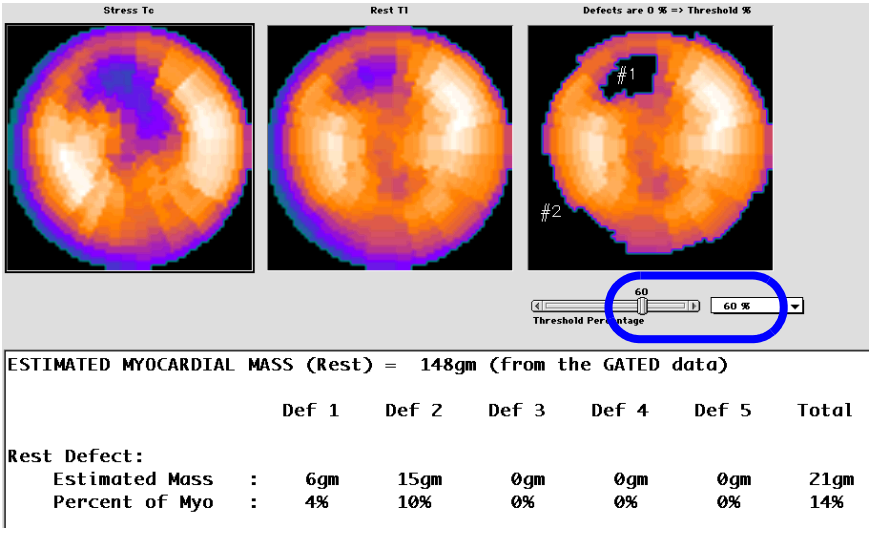
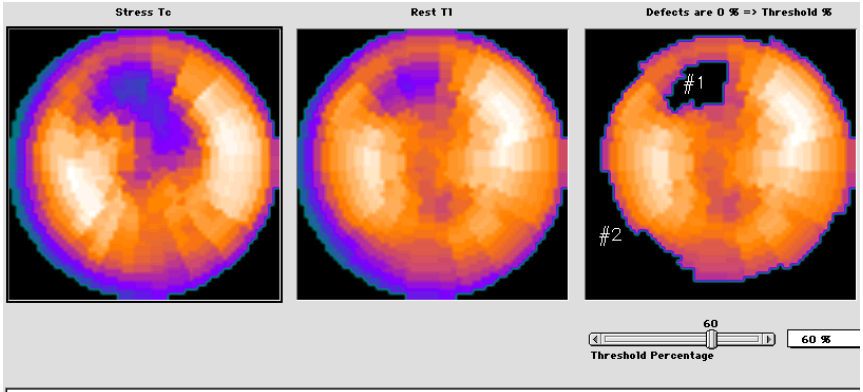


Figure C-130. Abnormal Case (PalRa): Estimated Viability (Mass) Window. Note that the Threshold value has been manually adjusted to 60% (blue oval).

Viability Extent

Note that the Estimated Viability Extent display provides an assessment of the Rest defect, by coronary territories.



	Def 1	Def 2	Def 3	Def 4	Def 5	Totals
Rest Defect:						
Total:	4%	12%	0%	0%	0%	16%
LAD:	9%	8%	0%	0%	0%	17%
LCX:	0%	4%	0%	0%	0%	4%
RCA:	0%	35%	0%	0%	0%	35%

There are 80 pixels blacked out (16%), of 521.000 total pixels

Figure C-131. Abnormal Case (PalRa): Estimated Viability (Extent) Window.

PerfSPECTive

In the PerfSPECTive Display Window, the 3D images provide a truer representation of the size and location of both the Stress and Rest defects.

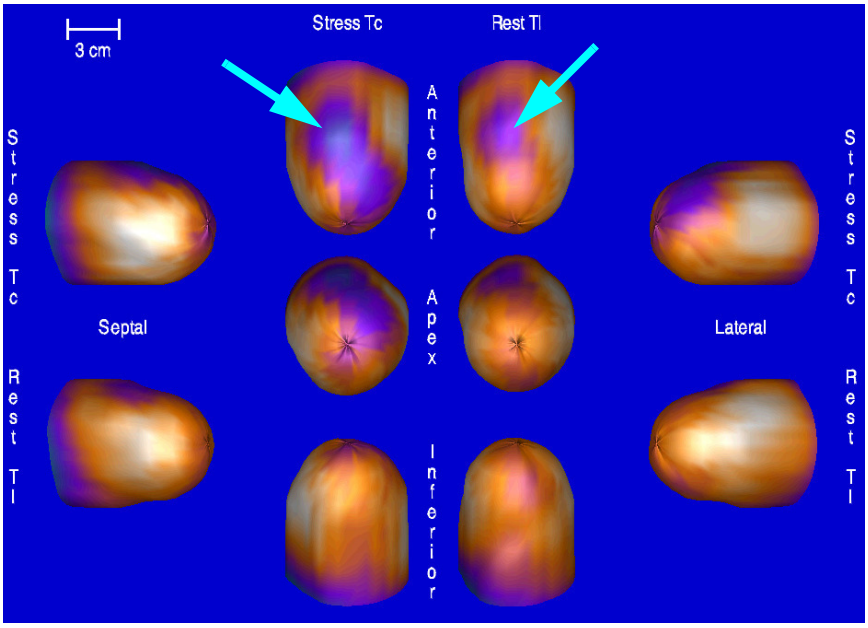


Figure C-132. Abnormal Case (PalRa): PerfSPECTive Window. Note defect size and location on 3D images (arrows).

Gated PerfSPECTive

In the Gated PerfSPECTive Display Window, the 3D image can be “spun and tumbled” to allow visual assessment of perfusion and wall motion, from any angle. This Gated PerfSPECTive display is only available because processing of the gated images has already been completed in the previous Functional Analysis section.

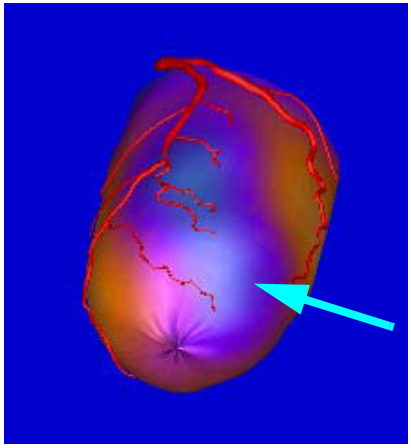


Figure C-133. Abnormal Case (PalRa): Gated PerfSPECTive Window. The arrow indicates a perfusion deficit.

Summary Window

On the Summary Display Window, the user is provided the ability to review the slice images, polar maps and Summed Score analysis, all on one display. Also included are key perfusion and function values (EF, Volumes, Summed Scores, Stress Total Severity Score and Survival Probability).

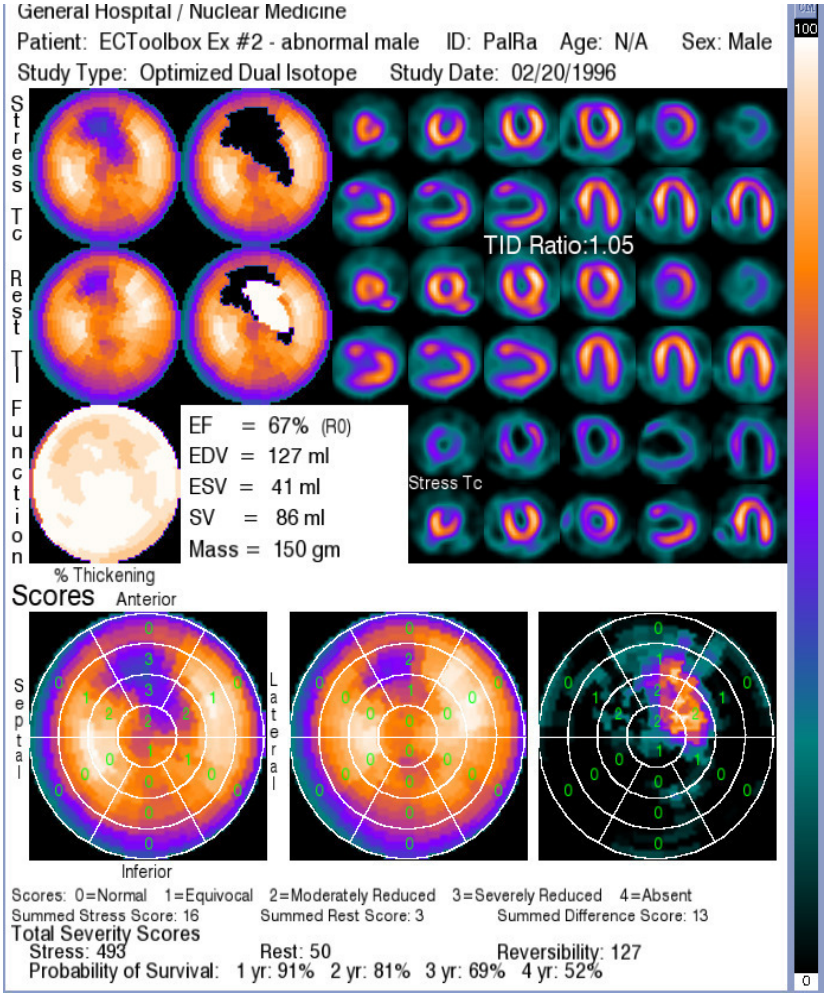


Figure C-134. Abnormal Case (PalRa): Summary Window.

Impression

The following text is provided as an example of the “Impression” section of a diagnostic report for this Case:

This patient’s myocardial perfusion gated SPECT study shows a large stress perfusion defect in the anterior and lateral walls, which normalizes (reverses) in the resting study. The Trans-Ischemic Dilatation (TID) Ratio is measured to be 1.09. The extent of the stress defect is determined to be 24% of the LV myocardial mass, when compared to a normal database. Approximately half (48%) of this stress defect significantly improves at rest (reverses). The resting LV ejection fraction is normal (61%).

Appendix D: Changing the Default Settings

There are a number of default settings for the Emory Cardiac Toolbox that can be set by the user to determine how the program identifies the files it is given for processing, and how images are displayed in its various windows. The default settings are changed by selecting the **Preferences** button, which is part of the permanent button group on the left side of the screen. A small set of option buttons are displayed to the left, below the permanent buttons. These are illustrated in Figure D-135 below. These buttons access further forms for controlling other aspects of ECToolbox operation.

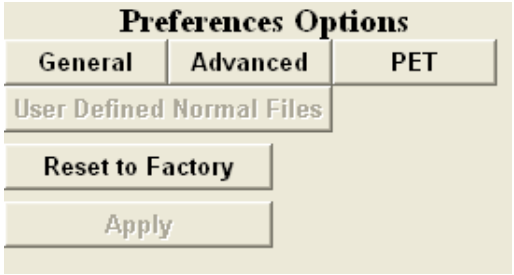


Figure D-135. Option buttons for setting Preferences.

- **General**: displays a screen with options that can be changed.
- **Advanced**: displays a second screen with more program options.
- **PET**: displays a screen with options related to PET data.
- **User Defined Normal Files**: displays additional controls related to user-created normal databases which will be used in ECToolbox.
- **Reset to Factory**: sets all preferences to their default values.
- **Apply**: This button is active when any change is made to the General, Advanced or PET forms. Clicking this button saves your changes.

To exit Preference selection without saving changes, click any of the permanent buttons, such as Slices or Polar Maps.

When the **Preferences** button is first selected, the General form is displayed so that your site may customize the basic operation of ECToolbox to your own specifications. The form is illustrated in Figure D-

136. Making changes on this form causes changes to be made in a file that controls the program's behavior.

W A R N I N G

It is possible to modify the defaults file in such a way as to prevent the Emory Cardiac Toolbox from running. For example, entering a non-existent path for normal files will disable the program from finding the normal files. Care should be taken to edit the defaults file properly.

At the top of this form is displayed the exact version number of the ECToolbox application that is running.

The following paragraphs explain how to set the various options.

Hospital Name

To change the Hospital name text that is displayed on the Summary window:

Move the mouse cursor into the text window to the right of the text "Hospital/Practice Name", and click the mouse button. The text can be edited.

Full Screen Windows

Each window generated during processing with the Emory Cardiac Toolbox can be displayed so that it takes up the entire screen. Some users find this to be simpler and less cluttered; others prefer to see windows overlap each other. Decide which appearance you would prefer the Toolbox to have.

To change the default of displaying each window as a full screen:

Use the mouse to position the cursor in either the on or off circular button. Click the left mouse button to turn on (yes) or off (no) the ability to display each window as a full screen.

Figure D-136. The General Defaults Editor window, for changing basic settings. Additional settings can be changes using the **Advanced** and **PET** buttons.

Multiple Windows

Each window generated during processing with the Emory Cardiac Toolbox can be displayed such that it is the only window open (other than the initial parameter window), or such that it overlays all of the currently open windows. Some users prefer to have only one window overlay the initial parameter window, to facilitate getting to the desktop to perform other tasks. Other users prefer to have windows stay open, such that they can

jump between windows very rapidly. Displaying each window as a separate window is the default behavior of ECToolbox.

To select between the two window behaviors:

Use the mouse to position the cursor in either the “on” or “off” circular button. Click the left mouse button to turn on (yes) or off (no) the ability to display each window by placing it over all of the previous windows.

Rotating Planar Projection Images

This default controls whether or not the rotating planar projection images are automatically shown in the slice window. As a quality control check, it is strongly recommended that this option be set to on, which will automatically show the rotating planar projection images. This is the ECToolbox default.

To change the default of showing rotating planar projection images on the slice screen:

Use the mouse to position the cursor in either the “on” or “off” circular button. Click the left mouse button to turn on (yes) or off (no) automatic displays of the projection images on the slice screen.

Use Staggered Summing

To change the default of using staggered summation on the Slices Window:

Use the mouse button to turn on (yes) or off (no) the option. Staggered summation is the 2-by-1 reframing of oblique slices. The option is on by default.

Display STSS

This default controls whether or not the Stress Total Severity Score (STSS) is displayed on both the Polar Map Defect Mass Window and the Summary Display. This calculated value is displayed by default.

To change the default of showing Stress Total Severity Score:

Use the mouse to position the cursor in either the “on” or “off” circular button. Click the left mouse button to turn on (yes) or off (no) automatic display of the STSS.

Default Slice Zoom

This default controls the zoom factor used for oblique slices on the Slice Review Window. This factor does not affect the rotating raw images. A zoom of 2.0 is the default.

To change the default zoom factor applied to Oblique Slice Review:

Use the mouse to select one of the zoom factors listed.

Default Gated Slice Zoom

This default controls the zoom factor used for gated oblique slices on the Slice Review Window. This factor does not affect the rotating raw images. A zoom of 2.0 is the default.

To change the default zoom factor applied to Gated Oblique Slice Review:

Use the mouse to select one of the zoom factors listed.

Display the TID

This default controls whether the Transient Ischemic Dilatation (TID) Index value is displayed on the slices window and summary page.

To change the default zoom factor applied to Gated Cine Slice Review:

Use the mouse to select one of the option buttons shown.

Default Number of Segments for SSS

The default model for Summed Stress Score (SSS), the visual scoring of perfusion, is to use 17 segments. This is the model currently recommended by the American Heart Association.

To change the default number of segments for SSS:

Use the mouse to click the drop-down menu next to “17”. Choose 17 or 20 segments for visual scoring.

Default setting for PERFEX Sensitivity

This default controls the sensitivity/specificity level at which the PERFEX expert system interprets perfusion patterns. The sensitivity and specificity cannot be independently adjusted.

To change the default PERFEX sensitivity and specificity:

Use the mouse to select one of the sensitivity/specificity settings listed.

Default Tc-99m Study

If both the stress and rest studies used Tc-99m as the isotope, there are 3 possible normal files that could be used. In the current version of ECToolbox, the type of Tc-99m study is not automatically determined, but is set to a default study type. You can set the default to the type of Tc-99m study most commonly done in your lab.

To change the default Tc-99m study:

Move the mouse cursor into the pull-down menu item to the right of the text “Default TC Study Type:” Using the left mouse button, click on this menu. While continuing to hold down the left mouse button, move the cursor onto the type of study you wish to be the default. The study highlighted when you release the mouse button will be the one selected as the default.

Default EF Regression

The EF can be displayed as computed, or transformed using one of two regression equations. The default is to display the value as computed. (See Chapter 3, ‘Volumes and EF Display’ for a description of these equations.)

To choose which EF is displayed:

Move the mouse cursor into the pull-down menu item to the left of the text “Default EF Regression” Using the left mouse button, click on this menu. While continuing to hold down the left mouse button, move the cursor onto the type of regression you wish to be the default. The regression equation highlighted when you release the mouse button will be the one selected as the default.

Options for Prefiltering Gated Data

The user has three options for filtering gated slice data before processing. Filtering can always be applied, it can never by applied, or the program can determine whether to prefilter based on the source of the data.

To change the pre-filtering option:

Use the mouse to select the radio button next to the desired option. If the “Prefilter According to Machine” option is selected, the DICOM image header must contain a value that indicates which vendor’s camera acquired the data. In this case, one or more vendor checkboxes can be selected, and data that is determined to have come from the selected vendor(s) will have prefiltering applied.

W A R N I N G
Changing the prefilter option will affect the calculated volumes and ejection fraction for the study.

Viability Threshold

To change the default threshold for the viability window:

Move the mouse cursor to the slider bar indicator, in the window to the right of the text that reads “Viability Threshold Percentage”. Click with the left mouse button, and while holding the button down, move the indicator to the right or left until the desired percentage is displayed above the indicator.

(see Chapter 3, 'Estimated Viability Displays' for a description of this threshold).

Date Format

Set this default to change how the study date is displayed on all ECToolbox windows.

To choose the format for the displayed date:

Use the mouse to choose the U.S. (MM/DD/YYYY) format, for example 5/23/2001 for May 23, 2001, or the European (DD/MM/YYYY) format, for example 23/5/2001 for 23 May, 2001. A change to the date format will not be seen immediately, but will take effect the next time ECToolbox is started.

Language

Use this option to select a new language for ECToolbox to display image labels, buttons and messages to the user.

To change languages:

Open the dropdown list labeled **Default Language** and select a language from the list. To see the change, you must click **Apply**, then quit the ECToolbox program and re-start it.

Setting Advanced Defaults

There is another page of preference settings for ECToolbox, accessed by clicking the **Advanced** option button. This will display the window shown in Figure D-137.

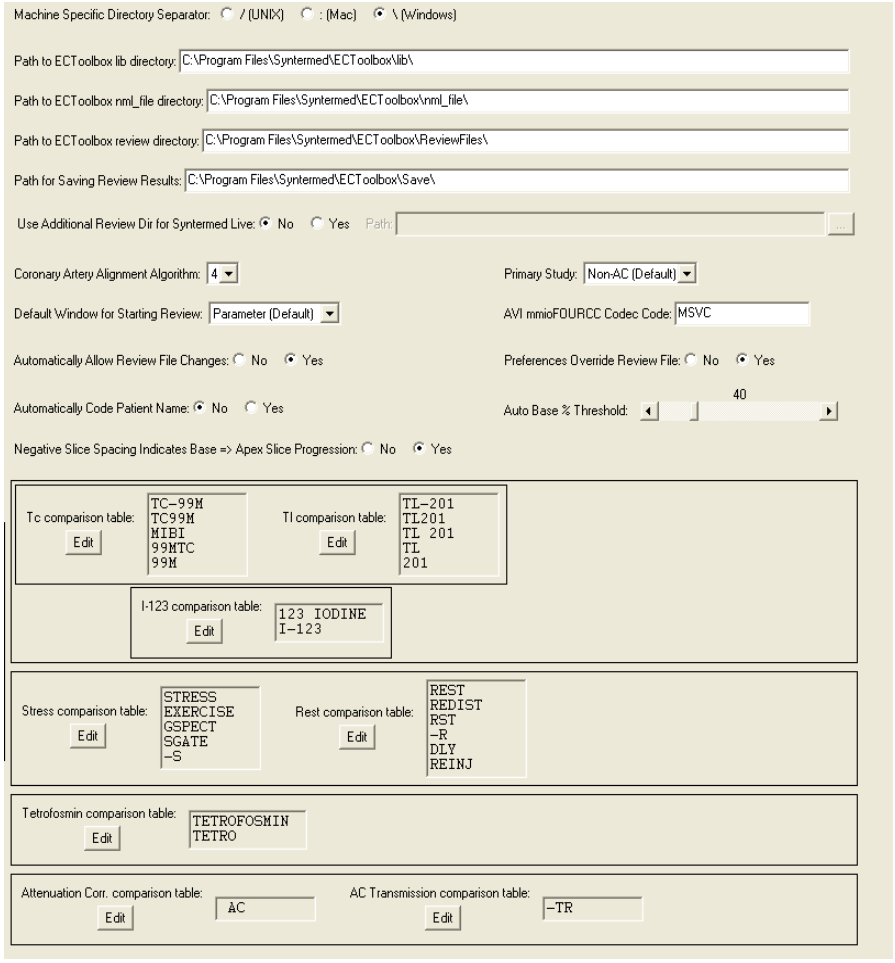


Figure D-137. Advanced Options window, accessed via the **Advanced** button.

Advanced options include the following:

Machine-Specific Directory Separator

Note: TThis default should be preset at installation time. Contact your technical representative if you are unsure of whether to change this, or what to change it to.

To change the character that denotes directory paths on a specific machine:

Use the mouse to position the cursor in one of the circular buttons reading a) / (UNIX) b) (Mac) or c)\ (Windows), depending on the operating system being used on your computer.Click the left mouse button within the button indicating the desired operating system.

Path to ECToolbox lib Directory

Note: This default should be preset at installation time. Contact your technical representative if you are unsure of whether to change this, or what to change it to.

To change the location in which the Emory Cardiac Toolbox will search for additional programs and other information:

Move the mouse cursor into the text window to the right of the text “Path to ECToolbox lib directory”. Click the mouse button in this text window, and the text can be edited.

Path to ECToolbox nml_file Directory

Note: This default should be preset at installation time. Contact your technical representative if you are unsure of whether to change this, or what to change it to.

To change the location in which the Emory Cardiac Toolbox will search for the normal files used in perfusion quantification:

Move the mouse cursor into the text window to the right of the text “Path to ECToolbox nml_file directory”. Click the mouse button in this text window, and the text can be edited.

Path to ECToolbox review Directory

To change the location to which Emory Cardiac Toolbox will write patient review files:

Use the mouse to click in the textbox to the right of “Path to ECToolbox review directory” and type in a valid directory path.

Default Window for Starting Review

Be default, ECToolbox displays the Parameters Window as its Main Window, whether starting in process mode or review mode. The user can change this behavior.

To change the window that is displayed first when ECToolbox starts:

Use the mouse to open the drop-down menu. Select the desired window from the list that is displayed.

Setting the Primary Study

The primary study is that one whose slices are displayed on the Main Window, which is where quantitative parameters are set and displayed. The primary study also determines which normal file will be used for comparison. The secondary study will always be labeled “AC” on the Slices Window. “AC” in this context means “Attenuation Corrected”. The default behavior is for the Non-Attenuation-Corrected study to be used as the primary study.

To change the primary study:

Use the mouse to open the drop-down list next to “Primary Study”. Choose from “AC Study” or “Non-AC Study”.

Coding the Patient Name

The patient name is normally displayed at the bottom of all ECToolbox windows, and is embedded into the Summary Page display. This name can be coded when it is necessary to shield patient identity. This will not change the patient name in the original data files.

To code the patient name displayed in ECToolbox:

Select the “Yes” option next to “Automatically Code Patient Name”. All patients subsequently processed or reviewed will be shown with the name coded as: first 3 letters of last name + first 2 letters of first name.

Setting the AVI Codec

Normally, when the Save “Cine as AVI” or “Save Screen as AVI” options are selected, the user is shown a dialog in which a Codec can be chosen. This is the compressor/decompressor (“codec”) software used to store and interpret the AVI file. In order to bypass this dialog, a codec name can be set as the default. ECToolbox uses the MSVC for this purpose.

To set the codec used by ECToolbox when saving AVI files:

Enter the 4-letter codec name in the text box provided. If the entered name is not recognized, the program will fail to save the AVI file, and will present an error message to the user at the time the save is attempted.

Allowing Review Changes

Normally, when reviewing a study from a stored ECToolbox review file, processing parameters cannot be changed without first selecting “Allow Review Changes” from the pulldown list that is part of the Option Button Set of the Parameters Display. This behavior can be changed so that you can always immediately change parameters when reviewing.

To always allow parameters to be changed while in review mode:

Select the “Yes” option button.

Overriding Review File Preferences

The preferences that are in effect at the time an ECToolbox review file is saved determine how that study appears when the file is opened later for review. You can change this behavior so that, when the review file opens, it will use the currently-active set of preferences instead of those saved with the Review File. This is userful, for example, for changing the screen that is first displayed when a review file opens.

To override Review File preferences:

Select the “Yes” option button.

Auto Base % Threshold

ECToolbox uses a count threshold (and other, more complex optimizations) for automatically determining the base slice of gated and ungated short axis perfusion studies. The default threshold is 40% for SPECT, meaning that once the maximum count in the LV is found, the first slice toward the base that has a maximum count below 40% of this value is identified as the base. This threshold may be too generous and the base may be

consistently found too far out in some circumstances, such as with radioisotopes having more background activity, and certain PET or SPECT cameras. The user can adjust this threshold upward, which should result in the automatic base being found closer to the apex.

Note: Use caution when adjusting this parameter, as changing the base slice will have an impact on quantification.

Slice Progression

When set, this option specifies that negative slice spacing in the image set corresponds to slices that begin at the base and proceed toward the apex. This is for the purpose of matching datasets from certain systems to the ECToolbox display convention.

Isotope Comparison Tables

There are three tables used in automatically determining which isotope was used to acquire the selected dataset: the Tc comparison table, the Tl comparison table and the I-123 comparison table. For a chosen dataset, the isotope is read from the database, converted to uppercase, and compared first to the Tl, then the Tc and I-123 tables in turn. If any of the strings in each table match any part of the string describing the isotope, then the isotope is set appropriately. If no match is found, the isotope is set to 'unknown'. Several aspects of this matching process are important to note: 1) the first match determines which isotope type is set, 2) the sequence of comparison tables searched for a match is Tl, then Tc, then I-123, and 3) the strings are searched in the order they appear in the table (for example, “Tc-99m”, then “Tc99m” and so on). By default, these tables are set to the following:

Tl comparison table = [TL-201, TL201, TL 201, TL, 201]

Tc comparison table = [TC-99M, TC99M, MIBI, 99MTC, 99M]

I-123 comparison table = [123 Iodine, I-123]

User may change any of these strings, add strings of their own, or delete any of the default strings, so that isotopes are correctly identified in their lab. Since the database elements are converted to uppercase before any comparisons are done, all changes/additions should be in upper case.

Note the list of text strings in the boxes to the right of the text reading “Tc comparison table”, and to the right of the text reading “Tl comparison

table". These strings are listed in the order they will be used to search study headers to determine what type of study the file holds. The two lists are modified using the same procedures.

To change or delete a string in the comparison list:

move the mouse cursor to the button labeled **Edit**, to the left of the list of strings, and click the mouse button to open the editing window.

In the editing window, the list of test strings is repeated in a box on the left.

1. To delete a text string, highlight the string using the mouse and click the **Delete** button.
2. To add a text string, click the button labeled **Add**, on the right hand side of the Editing window. In the window that next opens, type the string you wish to add. Clicking the left mouse button with the cursor over the **OK** button on this window will insert the new text string into the list of strings to be considered when study headers are searched for isotope types. Clicking the left mouse button with the cursor over the **Cancel** button on this window will exit the "Add" procedure without creating a new string.
3. When you are finished editing strings in the comparison table, use the mouse button to click **OK** in the Edit window. This will save your changes in the list of strings in the comparison table. Clicking the **Cancel** button in this window ends the editing session without saving any of your latest changes.

Study Type Comparison Tables

There are two tables used in automatically determining the study type (rest or stress) associated with a chosen dataset. The study type is read from the database for each selected dataset, converted to uppercase, and compared first to the Stress Comparison table and then to the Rest Comparison table. If any of the strings in each table match any part of the study type, then the study type is set appropriately for database comparison within the Emory Cardiac Toolbox. If no match is found, the study type is set to 'unknown'. It is important to note that 1) the first match determines which study type is set, 2) the stress comparison table is the first table searched for a match, and 3) the strings are searched in the order they appear in the table ('STRESS', then 'EXERCISE', ...). As shipped, these two tables are set to the following:

stress comparison table = [STRESS, EXERCISE, GSPECT, SGATE, -S]

rest comparison table = [REST, REDIST, RST, -R, DLY, REINJ]

The user may change any of these strings, add strings of their own, or delete any of the default strings, so that the study type is set correctly in their lab. Since the database elements are converted to uppercase before any comparisons are done, all changes/additions should be in upper case.

Note the lists of text strings in the boxes to the right of the text reading “Stress comparison table”, and to the right of the text reading “Rest comparison table”. These strings are listed in the order they will be used to search study headers to determine what type of study the file holds. The two lists are modified using the same procedure.

To change or delete a string in the comparison list:

move the mouse cursor to the button labeled as **Edit**, to the left of the list of strings, and click the left mouse button to open the editing window.

In the editing window, the list of test strings is repeated in a box on the left.

1. To delete a text string, highlight the string using the mouse and click the **Delete** button.
2. To add a text string, click the button labeled **Add**, on the right hand side of the Editing window. In the window that next opens, type the string you wish to add. Clicking the mouse button with the cursor over the **OK** button on this window will insert the new text string into the list of strings to be considered when study headers are searched for study types. Clicking the mouse button with the cursor over the **Cancel** button on this window will exit the “Add” procedure without creating a new string.
3. When you are finished editing strings in the comparison table, use the mouse button to click **OK** in the Edit window. This will save your changes in the list of strings in the comparison table. Clicking the **Cancel** button in this window ends the editing session without saving any of your latest changes.

Tetrofosmin comparison table

By default, the program recognizes “TETROFOSMIN” or “TETRO” in the study name. To add to this list of key words that distinguish a tetrofosmin study at your institution, use the mouse to click the **Edit** button. This will display another window. The user can edit the list shown in this small window using a similar sequence of steps to that given above for changing the Isotope and Study Type comparison tables.

To change or delete a string in the comparison list:

In the editing window, the list of text strings is repeated in a box on the left.

1. To delete a text string, highlight the string using the mouse and click the **Delete** button.
2. To add a text string, click the button labeled **Add**, on the right hand side of the Editing window. In the window that next opens, type the string you wish to add. Clicking the left mouse button with the cursor over the **OK** button on this window will insert the new text string into the list of strings to be considered when determining whether the current study is tetrofosmin. Clicking the **Cancel** button on this window will exit the “Add” procedure without creating a new string.
3. When you are finished editing strings in the comparison table, use the mouse button to click **OK** in the Edit window. This will save your changes in the list of strings in the comparison table. Clicking the **Cancel** button in this window ends the editing session without saving any of your latest changes.

Attenuation Corr. comparison table

The program uses “ AC” to distinguish attenuation-corrected files. Note that this key includes a space before the “AC”, so that names such as “cardiac” will not be misinterpreted as being attenuation-corrected.

To change or delete a string in the comparison list:

Use the mouse to click the **Edit** button. This will display another window. The user can edit the list shown in this small window using a similar sequence of steps to that given above for changing the Isotope and Study Type comparison tables:.

1. To delete a text string, highlight the string using the mouse and click the **Delete** button.

2. To add a text string, click the button labeled **Add**, on the right hand side of the Editing window. In the window that next opens, type the string you wish to add. Clicking the mouse button with the cursor over the **OK** button on this window will insert the new text string into the list of strings to be considered when determining whether the current study is attenuation-corrected. Clicking the **Cancel** button on this window will exit the “Add” procedure without creating a new string.
3. When you are finished editing strings in the comparison table, use the mouse button to click **OK** in the Edit window. This will save your changes in the list of strings in the Comparison table. Clicking the **Cancel** button in this window ends the editing session without saving any of your latest changes.

AC Transmission comparison table

ECToolbox uses the keyword “-TR” to identify the transmission scan acquired along with an attenuation-corrected SPECT study.

To change the comparison table that determines how ECToolbox recognizes a transmission study:

Use the mouse to click the **Edit** button. This will display another window. The user can edit the list shown in this small window using a similar sequence of steps to that given above for changing the Isotope and Study Type comparison tables.

In the editing window, the list of test strings is repeated in a box on the left.

1. To delete a text string, highlight the string using the mouse and click the **Delete** button.
2. To add a text string, click the button labeled **Add**, on the right hand side of the Editing window. In the window that next opens, type the string you wish to add. Clicking the mouse button with the cursor over the **OK** button on this window will insert the new text string into the list of strings to be considered when determining whether the current study is tetrofosmin. Clicking the **Cancel** button on this window will exit the “Add” procedure without creating a new string.
3. When you are finished editing strings in the comparison table, use the mouse button to click **OK** in the Edit window. This will save your changes in the list of strings in the comparison table. Clicking the

Cancel button in this window ends the editing session without saving any of your latest changes.

Setting PET Defaults

Options that apply to PET studies have been grouped on their own window, which is accessible by clicking the **PET** button in the Preferences Options button set. This will produce another window, as shown in Figure D-138.

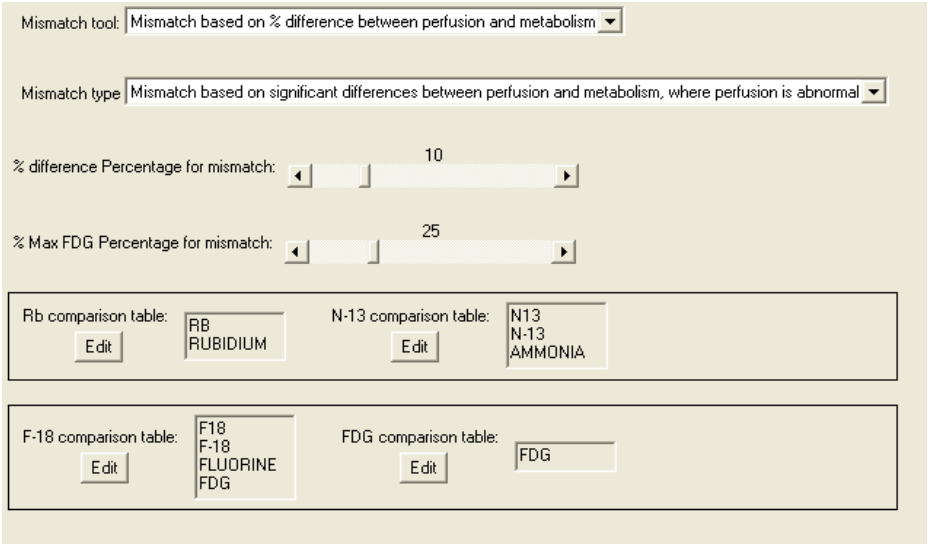


Figure D-138. The PET Options window.

Options that can be set from within this window are:

Mismatch tool

By default, the program calculates the quantitative extent of perfusion-metabolism mismatch based on the % difference between the two findings. Alternatively, mismatch can be based on % maximum metabolism.

To switch between these two options:

Use the mouse to open the drop-down list next to “Mismatch tool”, and select one of the two options.

Mismatch type

By default, ECToolbox determines whether a mismatch between perfusion and metabolism exists by using two criteria:

- finding significantly abnormal perfusion.

AND

- finding significant differences between perfusion and metabolism.

Alternatively, the program can be instructed to determine mismatch based on ALL significant differences between perfusion and metabolism, whether or not perfusion is significantly abnormal.

To switch between these two options:

Use the mouse to open the drop-down list next to “Mismatch type”, and select one of the two options.

% Difference percentage for Mismatch

By default, ECToolbox uses 10% as the initial threshold for determining that there is a difference between perfusion and metabolism. This percentage can be set by the user.

To set the % Difference percentage:

Use the mouse to drag the slider bar control left or right. The % value will change accordingly.

% Max FDG Percentage for Mismatch

By default, the program uses 25% of maximum FDG counts as the initial value for thresholding the FDG polar plot. In other words, pixels containing less than 25% of the maximum FDG counts will be blacked out on the FDG plot. This value will determine the size of the perfusion-metabolism mismatch area that is displayed.

To set the default % Max FDG percentage:

Use the mouse to drag the slider bar control left or right. The % value will change accordingly.

Rb comparison table

To change the comparison table that determines how ECToolbox recognizes a rubidium study:

Use the mouse to click the **Edit** button. This will display another window. The user can edit the list shown in this small window using a similar sequence of steps to that given above for changing the Isotope and Study Type comparison tables.

In the editing window, the list of test strings is repeated in a box on the left.

1. To delete a text string, highlight the string using the mouse and click the **Delete** button.
2. To add a text string, click the button labeled **Add**, on the right hand side of the Editing window. In the window that next opens, type the string you wish to add. Clicking the left mouse button with the cursor over the **OK** button on this window will insert the new text string into the list of strings to be considered when determining whether the current study is rubidium. Clicking the **Cancel** button on this window will exit the “Add” procedure without creating a new string.
3. When you are finished editing strings in the comparison table, use the mouse to click the **OK** button in the Edit window. This will save your changes in the list of strings in the comparison table. Clicking the **Cancel** button in this window ends the editing session without saving any of your latest changes.

N-13 comparison table

To change the comparison table that determines how ECToolbox recognizes a Nitrogen-13 ammonia study:

Use the mouse to click the **Edit** button. This will display another window. The user can edit the list shown in this small window using a similar sequence of steps to that given above for changing the Isotope and Study Type comparison tables.

In the editing window, the list of test strings is repeated in a box on the left.

1. To delete a text string, highlight the string using the mouse and click the **Delete** button.
2. To add a text string, click the button labeled **Add**, on the right hand side of the Editing window. In the window that next opens, type the string you wish to add. Clicking the mouse button with the cursor over the **OK** button on this window will insert the new text string into the list of strings to be considered when determining whether the current

study is N-13. Clicking the **Cancel** button on this window will exit the "Add" procedure without creating a new string.

3. When you are finished editing strings in the comparison table, use the mouse to click the **OK** button in the Edit window. This will save your changes in the list of strings in the comparison table. Clicking the **Cancel** button in this window ends the editing session without saving any of your latest changes.

F-18 comparison table

To change the comparison table that determines how ECToolbox recognizes a Fluorine-18 study:

Use the mouse to click the **Edit** button. This will display another window. The user can edit the list shown in this small window using a similar sequence of steps to that given above for changing the Isotope and Study Type comparison tables.

In the editing window, the list of test strings is repeated in a box on the left.

1. To delete a text string, highlight the string using the mouse and click the **Delete** button.
2. To add a text string, click the button labeled **Add**, on the right hand side of the Editing window. In the window that next opens, type the string you wish to add. Clicking the mouse button with the cursor over the **OK** button on this window will insert the new text string into the list of strings to be considered when determining whether the current study is F-18. Clicking the **Cancel** button on this window will exit the "Add" procedure without creating a new string.
3. When you are finished editing strings in the comparison table, use the mouse to click the **OK** button in the Edit window. This will save your changes in the list of strings in the comparison table. Clicking the **Cancel** button in this window ends the editing session without saving any of your latest changes.

FDG comparison table

To change the comparison table that determines how ECToolbox recognizes a rubidium study:

Use the mouse to click the **Edit** button. This will display another window. The user can edit the list shown in this small window using a similar sequence of steps to that given above for changing the Isotope and Study Type comparison tables.

In the editing window, the list of test strings is repeated in a box on the left.

1. To delete a text string, highlight the string using the mouse and click the **Delete** button.
2. To add a text string, click the button labeled **Add**, on the right hand side of the Editing window. In the window that next opens, type the string you wish to add. Clicking the mouse button with the cursor over the **OK** button on this window will insert the new text string into the list of strings to be considered when determining whether the current study is FDG. Clicking the **Cancel** button on this window will exit the "Add" procedure without creating a new string.
3. When you are finished editing strings in the comparison table, use the mouse to click the **OK** button in the Edit window. This will save your changes in the list of strings in the comparison table. Clicking the **Cancel** button in this window ends the editing session without saving any of your latest changes.

IMPORTANT

After you have made the appropriate changes to basic default settings, advanced options or PET options, save the defaults by clicking the **Apply** button.

If you decide that you do not want to save the changes you have made to the various defaults, you may instead simply select any other button in the permanent group, such as **Slices** or **Params**. Selecting any button other than **Apply** exits the Default Editor without making any changes to the defaults.

The new defaults will take effect immediately, unless otherwise noted.

ECTB Version 3.3 Addendum

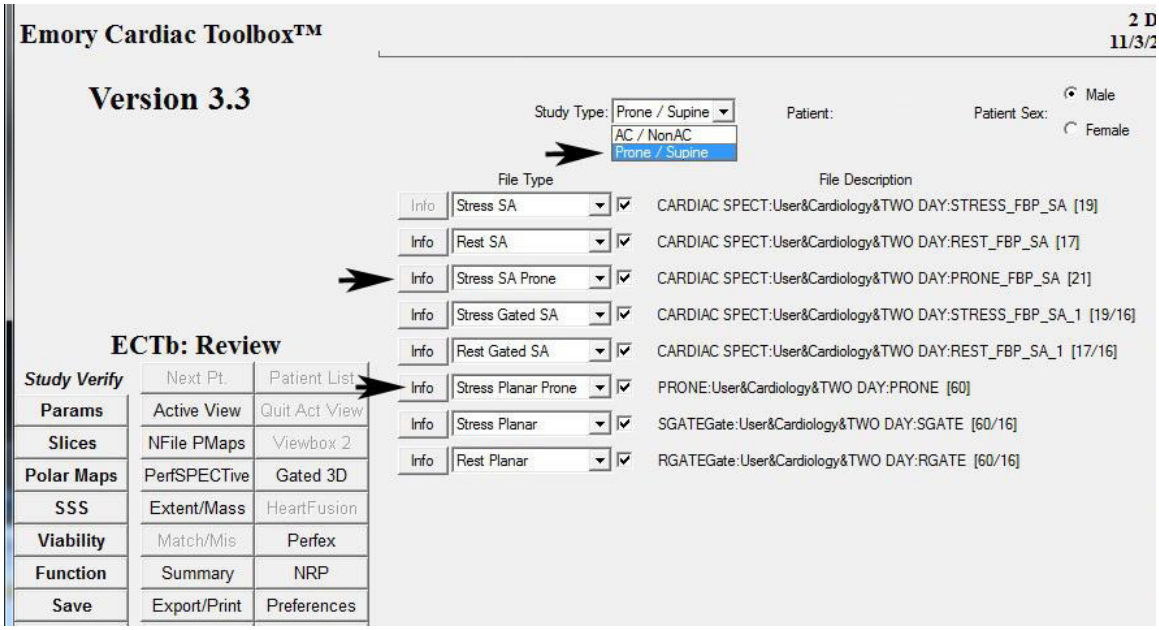
User's Manual Addendum

Prone/Supine, Label Editing, Display Orientation Labels and Ratio Polar Maps

Prone/Supine

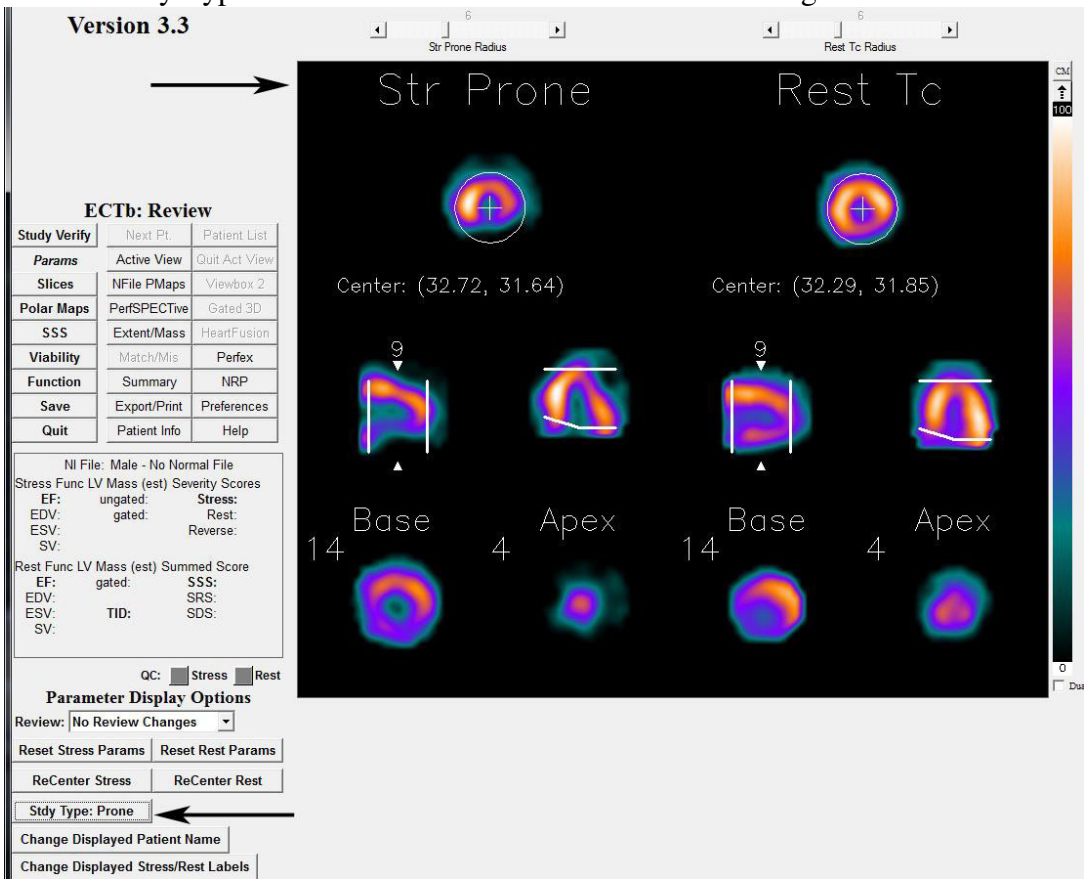
This version of the Emory Toolbox allows for designation of Prone/Supine studies similar to how Attenuation Correction studies were previously handled.

1. From the Study Verification Page the user should select the prone/supine entry from the Study Type drop down box as shown in the figure below. Also, the user needs to associate the correct prone files from the File Type list. In this case the Stress SA Prone and Stress Planar Prone are selected for the corresponding files.

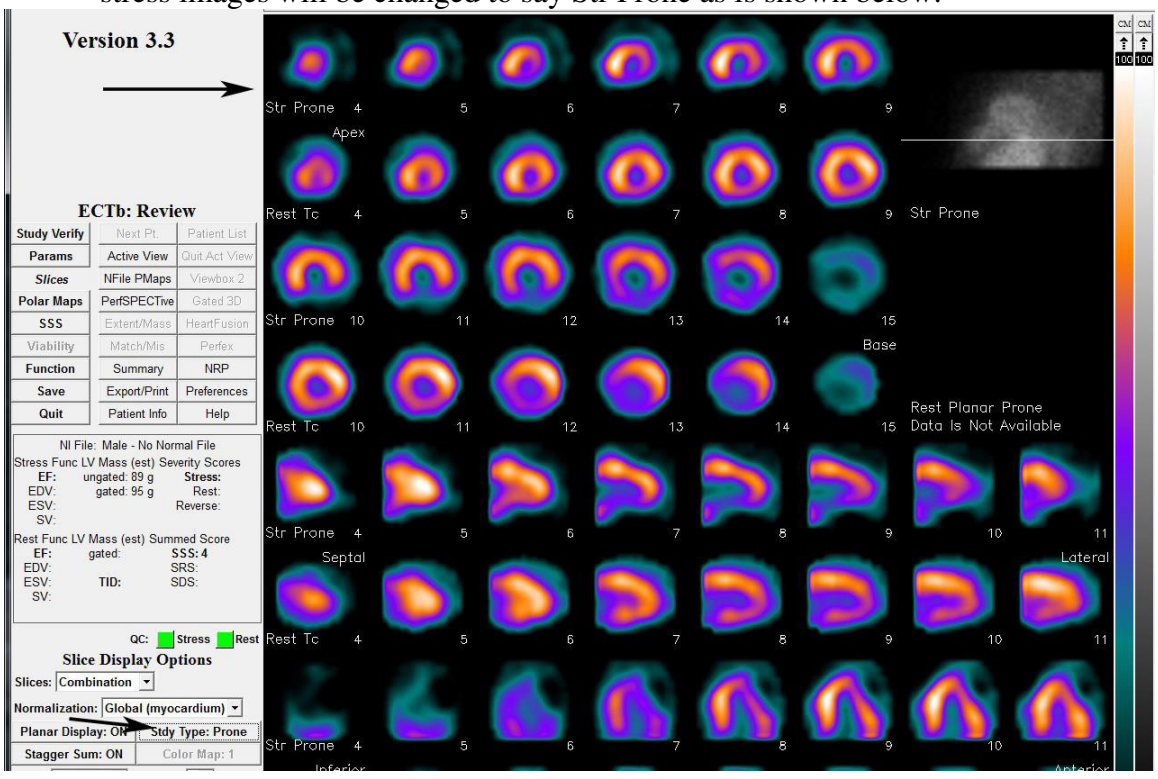


Note: there is a preference that can be set for AC/non AC or Prone/Supine by clicking on the Preferences button shown above. This is used to set the default to the type of study that the site does most often.

2. The Params screen will initially show the stress and rest images but when the Study Type button is selected the stress label will change to the Str Prone label.



3. When the Slices screen is displayed the stress and rest supine images will initially be displayed but when the user selects the Study Type Prone then the label for the stress images will be changed to say Str Prone as is shown below.

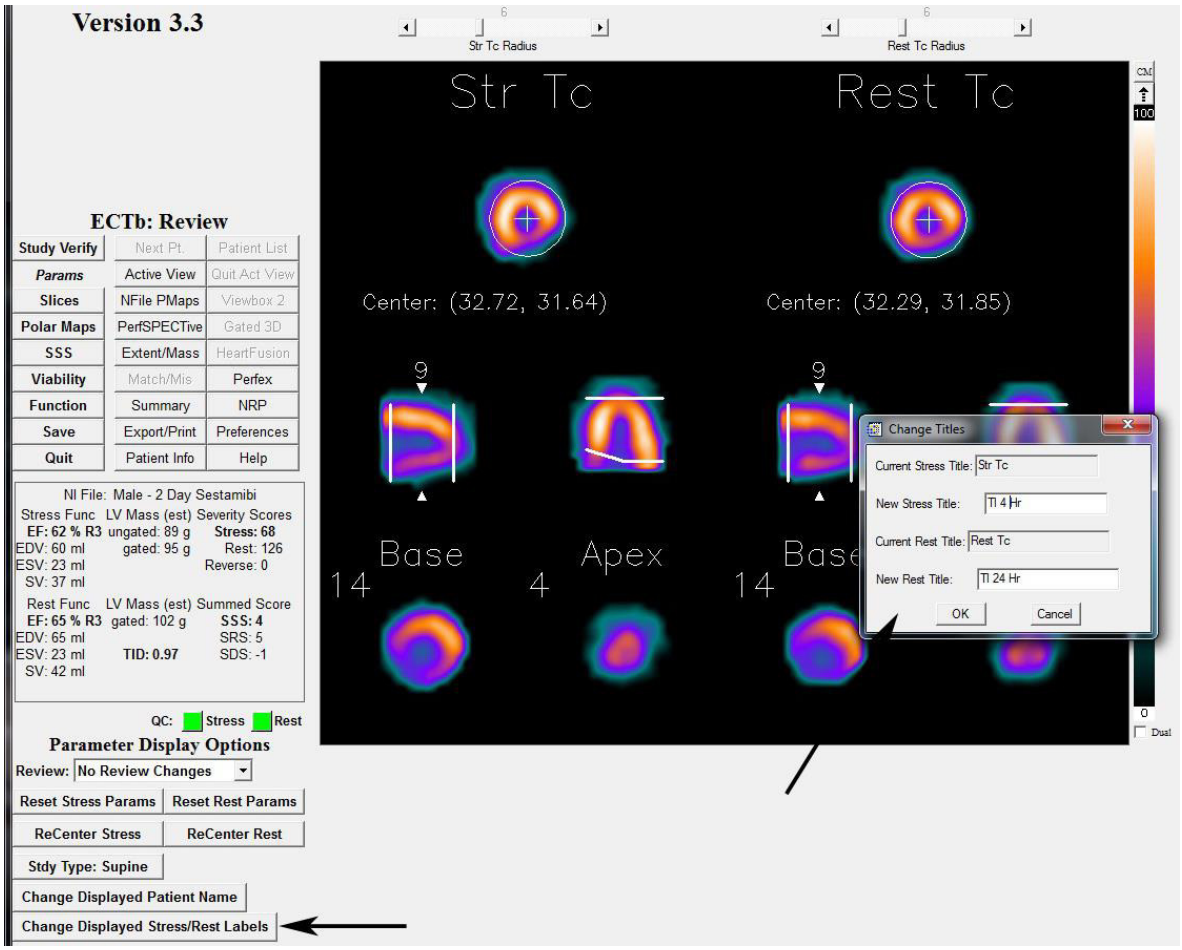


Label Editing

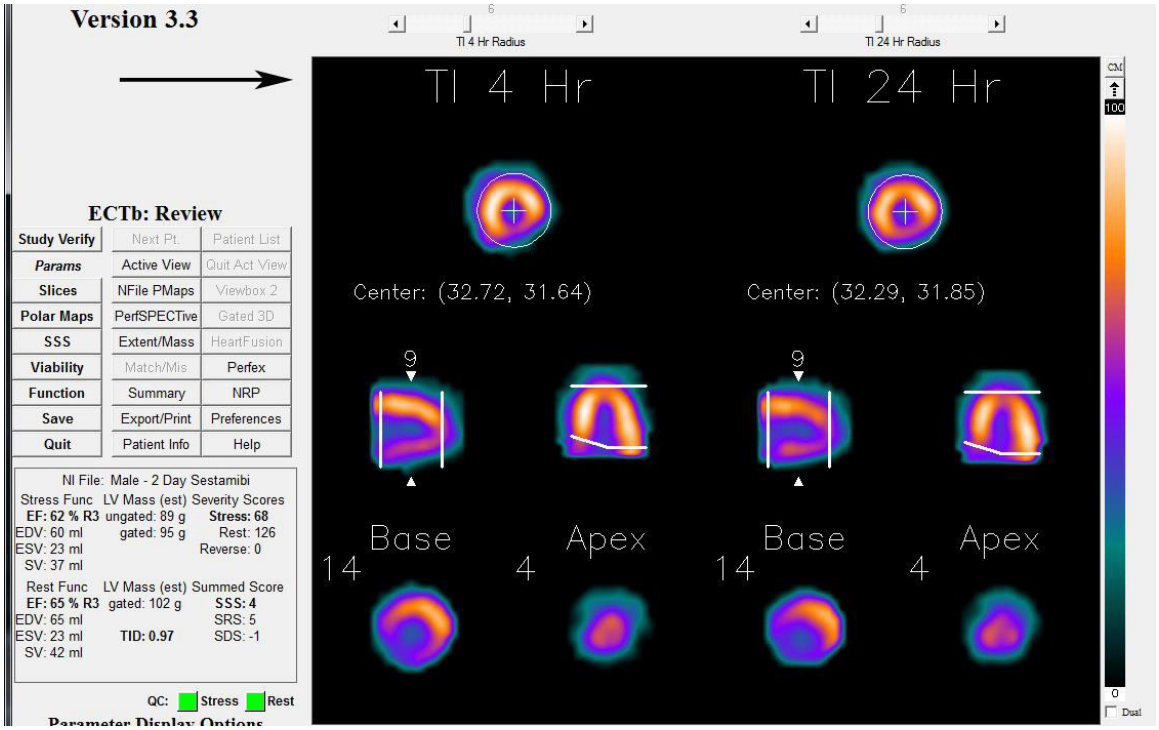
This version of ECTb also allows the user to change the labels if required.

1. For example if the study is a 4hr and 24 hr Thallium study the labels can be manually changed. Changing the labels happens on the Params screen. Click on the Change Displayed Stress/Rest Labels button at the bottom of the page. Once this is done a window will be displayed allowing the user to change the names for stress and rest as is shown in the figure below.

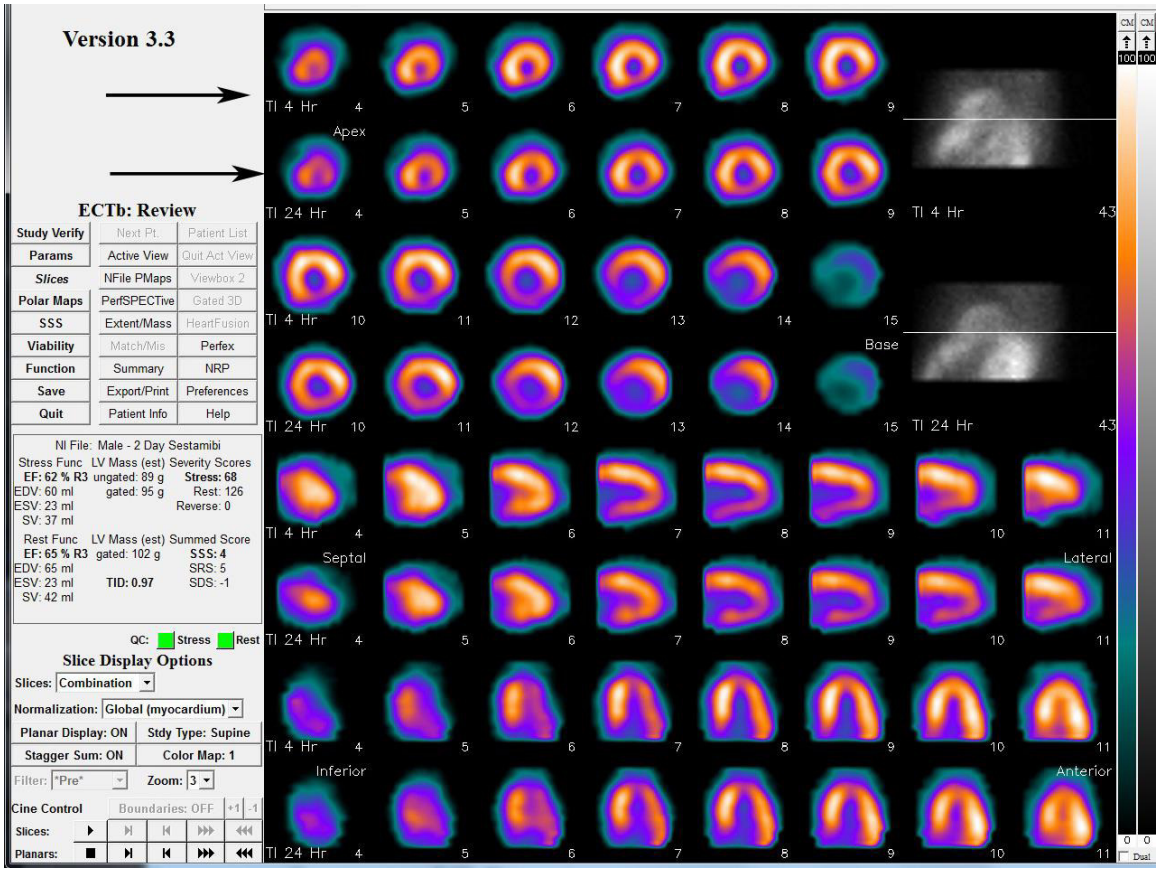
   Note: on the initial study verification page the studies need to be assigned as "Stress" and "Rest" then on the Params page the displayed labels for stress and rest can be changed to correspond to the appropriate study. Also, the labels for Prone (or AC) can also be changed by selecting the study type button to display the Prone (or AC) and then click on the Change Displayed Stress/Rest Labels button and the labels can then be changed.



2. Once the text is entered in the boxes then click the OK button and the labels will be changed as is shown below.

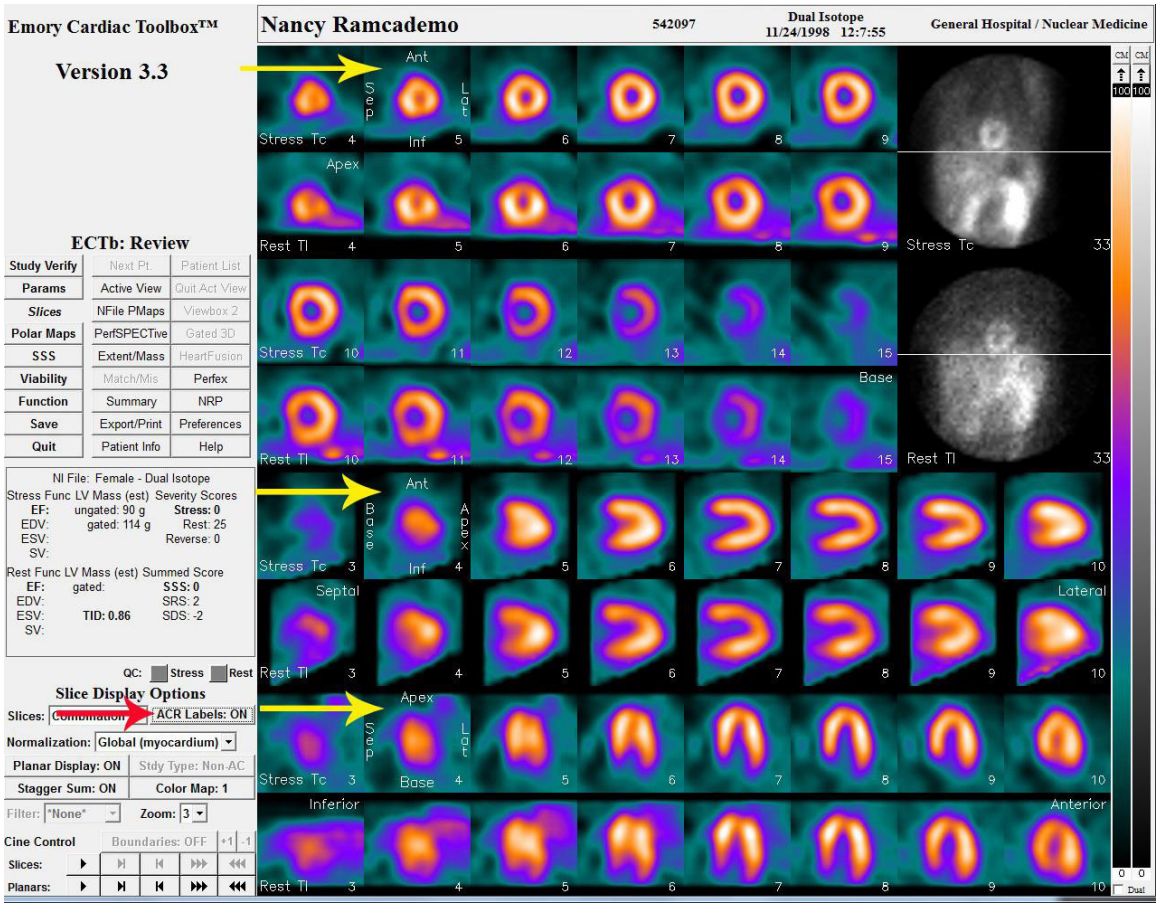


3. All of the labels on the rest of the screens, i.e. slices, polar maps, functional screen, summary screen, etc. will be displayed with the labels that were entered. The slices screen is displayed below.



ACR Orientation Labels

The American College of Radiology (ACR) has specified that orientation labels need to be displayed on the SPECT perfusion images. These labels can be overlaid on the images by clicking on the ACR Label button (red arrow). Once this is done the labels are displayed on the short, vertical, and long axis stress tomograms (yellow arrows) in the second column. To remove the labels click on the ACR Labels button again.



Ratio Polar Maps

If the same isotope is used for both the stress and rest studies, then three additional polar maps will be displayed at the bottom of the polar maps page. These three polar maps (from left to right) represent the stress raw sampled counts normalized to injected dose, the rest raw sampled counts normalized to injected dose and the stress/rest ratio. In the boxes to the left of the polar maps, you can enter the actual doses injected for stress and for rest. The maps will be re-normalized from the dose values entered, and ratios (Stress/Rest) are calculated and displayed to the right of the maps. An example is shown here: