Corridor4DM

Corridor4DM v2013
User's Guide

Corridor4DM

INVIA | Medical Imaging Solutions

Federal law restricts this device to sale by or on the order of a physician.

Program Intended Use

INVIA's Corridor4DM application is intended to provide processing, quantification, and multidimensional review of the biodistribution of radionuclides in the body using planar and tomographic images. The application performs quantitative measurements of tracer uptake over time to aid in the interpretation of myocardial perfusion emission tomographic images. Cardiac CT interpretation and calcium quantification are optional features that are integrated into Corridor4DM (SPECT-CT and PET-CT). The calcium scoring package is a non-invasive diagnostic tool that can be used to evaluate the calcified plaques in the coronary arteries, a risk factor for coronary artery disease. Co-registration or fusion of volumetric data (ECT and/or CT) is provided as a quality control for the identification of structures where correlative spatial information is necessary for a diagnostic interpretation.

Program Description

Corridor4DM is a comprehensive application designed to process, review, and quantitatively analyze nuclear medicine, PET, and CT patient studies. The application provides tools to process, quantify, and display static, whole body, dynamic, gated planar, standard ungated ECT images, ECG gated ECT images, and dynamic ECT images. ECT data is displayed on both a slice-by-slice basis and as 3D surface-rendered images in many user selectable formats. All of the image formats can be viewed as a single dataset or as a comparison of related datasets (e.g. stress and rest conditions, pre- and post-revascularization). Among several optional display screens are side-by-side displays optimized for the review of uncorrected and attenuation corrected cardiac images.

Corridor4DM algorithmically determines and displays the left ventricular endocardial and epicardial surfaces. These surfaces provide quantitative assessments of cardiac function, e.g. systolic and diastolic function, regional wall thickening, wall motion, transient ischemic dilation (TID), phase analysis, and generalized factor analysis of dynamic sequences (GFADS).

Corridor4DM provides regional assessments of myocardial perfusion, metabolism, wall thickening, wall motion, time to peak contraction, time to peak thickening, perfusion reversibility between stress and resting conditions, viability, and GFADS. Corridor4DM provides this regional information in 2D polar maps and 3D surface-rendered images of the left ventricle and it provides a comparison of the patient-specific regional information in comparison to a similar patient population with a low likelihood of cardiac disease.

The normals database generator is an integrated feature of Corridor4DM that provides the users with a set of tools for generating site, patient population, or protocol specific normal data files. Site specific Normals Databases are integrated seamlessly into the application for research or daily clinical use.

Tomographic dataset reconstruction is an optional feature integrated into Corridor4DM. The reconstruction feature permits the user to generate slice volumes from nuclear medicine tomographic and gated tomographic datasets.

Corridor4DM provides several options for verifying the quality of the input data and processing of that data. Data cines, image co-registration, surfaces, valve plane, and polar map QA displays of all selected studies are provided and available both during processing and subsequently during image interpretation.

Corridor4DM supports the review of nuclear medicine static, dynamic, whole body, gated planar, tomo,

and gated tomo datasets. Additionally, the application permits image manipulation, adding image labels, and the quantification of these nuclear medicine datasets. The application permits the user to review and interpret NM studies in a familiar user interface.

Multi-Gated Acquisition (MUGA) quantification is an optional feature integrated into the application. Corridor4DM can be used to display the left and right ventricular endocardial surface, wall motion, amplitude, phase analysis, stroke volume, ejection fraction, ventricle chamber volumes, and 2D images of first pass and planar MUGA studies. Planar MUGA images can be viewed as a single dataset or as a comparison of related datasets.

Cardiac CT interpretation and cardiac calcium quantification are optional features integrated into Corridor4DM. The CT Viewer provides the user with a clinically tested image layout that supports basic volume and distance quantification in multiple image types, MIP and/or MPR. The program provides tools for the quantification of coronary artery calcification with results tabulated with Agatston score, volume, and number of lesions.

Corridor4DM includes the ability to save and export diagnostic findings in a variety of formats. The application generates DICOM multi-frame (MFSC) and secondary screen captures (SSC) in addition to producing static (JPEG, TIFF) and dynamic (WMV) image files. The user can export results to relational databases, XML and text formatted reports, or delimited text files for data analysis.

Corridor4DM is not intended to provide diagnoses or therapeutic recommendations, but is intended only to be a visual aid for use by trained medical professionals. The Clinician should never rely solely on it in making diagnostic or therapeutic decisions, nor to determine the presence or absence of a condition, but instead interpret all of the patient's clinical and diagnostic information to make a final diagnosis regarding a patient. The Clinician retains the ultimate responsibility for making a diagnosis.

Prior to Use

Training in nuclear cardiology at all levels is essential to conducting safe and clinically accurate molecular imaging cardiac studies. This includes acquisition protocols, image processing, methods of quality control, and image interpretation. INVIA strongly encourages following all procedures and guidelines provided by ASNC (www.asnc.org) and your specific camera manufacturer. Additional resources are available at www.inviasolutions.com.

Data Requirements

Prior to using Corridor4DM, reconstruct cardiac NM Tomo or gated Tomo datasets using the standard reconstruction software for MI images. The following orientations comply with the American College of Cardiology (ACC) standard format and each describes the order in which slices are stored in the reconstructed datasets and the cardiac orientation of the heart within the datasets:

- **Transverse (Trans):** Images in datasets are displayed as viewed from the feet (left ventricle on right side of image) and the stacked images are displayed top to bottom from head to foot.

- **Short Axis (SA):** Images in datasets are displayed from apex to base with the LV lateral wall to the right and anterior wall above.

- **Horizontal Long Axis (HLA):** Images in datasets are displayed from inferior to superior with the apex above and the lateral wall to the right.

- **Vertical Long Axis (VLA):** Images in datasets are displayed from the septum to the lateral wall with the LV apex to the right and the anterior wall above.

Reconstructed MI cardiac images can have a maximum of 16 gating intervals and maximum matrix size of 256x256 (with exception that transverse reconstructed datasets with >256 matrix size are supported). Recommended matrix sizes are 64x64 or 128x128 for SPECT; 128x128 or 192x192 for PET. Recommended temporal resolutions are 8 or 16 frames per cardiac cycle. Cubic voxel dimensions are required with a minimum size of 4.8mm for SPECT and 1.8mm for PET.

Supported Datasets

Corridor4DM will display or analyze the following datasets:

- Nuclear Medicine (NM) Tomographic (Tomo) projection datasets
- NM Gated Planar datasets
- NM Dynamic datasets (NM Viewer screen only)
- NM Static datasets (NM Viewer screen only)
- NM Whole Body datasets (NM Viewer screen only)
- SPECT or gated SPECT reconstructed datasets
    - Trans, SA, HLA, or VLA orientations
- PET, gated PET, or Dynamic PET reconstructed datasets
    - Trans, SA, HLA, or VLA orientations
- Gated Bloodpool SPECT (GBPS) datasets
    - Trans, SA, HLA, or VLA orientations
- Uncorrected (NC) and Attenuation Corrected (AC) reconstructed datasets
    - Trans, SA, HLA, or VLA orientations
- DICOM Secondary Screen Captures (SSC)
- DICOM Multi-Frame Secondary Screen Captures (MFSC)
    - 8- or 24-bit Grayscale, 24-bit RGB
- Static and Gated CT volumetric datasets
- Extracted CT Angiographic (CTA) Coronary Vessels from GE Advance Workstation, Philips Brilliance, or Siemens Circulation programs
- Siemens transformation matrix datasets

User's Guide Conventions

Throughout this guide, INVIA will rely on consistent use of terminology and symbols to best communicate with you, the end user. Below is a summary of these conventions:

- This guide will use the abbreviation **MI** (molecular imaging) when referring to both SPECT and PET modalities.

- Blue, underlined text represents links to help you quickly navigate within this document or launch online content (Internet access required).

- Helpful hints, warnings, and additional information, which appear in the left margin for quick and easy reference, are identified by various symbols:

Note	Warning	Tip	Right Click Option

Of the supported datasets, only Trans **or** SA datasets need to be reconstructed. 4DM will generate the other orthogonal views from these input volumes.

4DM also supports non-cubic datasets.

WARNING
The user must verify that the patient's weight, radiopharmaceutical, dose, and injection time are accurate. Incorrect values can result in an inaccurate estimate of the Standard Uptake Value (SUV).

WARNING
The user must verify that the radiopharmaceutical and injected activity are accurate. Incorrect values can result in an inaccurate estimate of the patient's radiation dose.

Common Abbreviations

The user's manual and user interface will rely on the following abbreviations:

Abbreviation	Description
3D	Three-Dimensional
3SA	Three (3) Short Axis
AC	Attenuation Correction
AC Dly	Attenuation Corrected Delay
AC FDG	Attenuation Corrected Flurodeoxyglucose (FDG)
AC GDly	Attenuation Corrected Gated Delay
AC GFDG	Attenuation Corrected Gated Flurodeoxyglucose (FDG)
AC GRst	Attenuation Corrected Gated Rest
AC GStr	Attenuation Corrected Gated Stress
AC Rst	Attenuation Corrected Rest
AC Str	Attenuation Corrected Stress
bpm	Beats Per Minute
Ca	Calcium
CO	Cardiac Output
CT	Computed Tomography
CTAC	Computed Tomography Attenuation Correction
DB	Database
Dly	Delay
EDV	End Diastolic Volume
EF	Ejection Fraction
ESV	End Systolic Volume
FBP	Filtered Backprojection
FDG	Flurodeoxyglucose (FDG)
fps	Frames Per Second
GDly	Gated Delay
GFDG	Gated Flurodeoxyglucose (FDG)
GRst	Gated Rest
GStr	Gated Stress
HLA	Horizontal Long Axis
HR	Heart Rate
Info	Information
IR	Iterative Reconstruction
LA	Long Axis
LAD	Left Anterior Descending
LAO	Left Anterior Oblique
LCx	Left Circumflex
LM	Left Main
LPO	Left Posterior Oblique
Maps	Polar Maps
MFR3	Mean Filling Rate during the initial one-third of Diastolic or Filling Time
MFSC	Multi-Frame Screen Capture

Abbreviation	Description
MI	Molecular Imaging
MPI	Myocardial Perfusion Imaging
MUGA	Multi-Gated Acquisition
NM	Nuclear Medicine
PER	Peak Ejection Rate
Perf	Perfusion
PFR	Peak Filling Rate
Pmap	Polar Map
Quant	Quantification
RAO	Right Anterior Oblique
RCA	Right Coronary Artery
Rst	Rest
SA	Short Axis
SC	Screen Capture
SDlyS	Summed Delay Score
SDS	Summed Difference Score
SMS	Summed Motion Score
SRS	Summed Rest Score
SS	Summed Scar Score
SSC	Secondary Screen Capture
SSS	Summed Stress Score
Str	Stress
STS	Summed Thickening Score
Surf QA	Surface Quality Assurance
SUV	Standard Uptake Value
TID	Transient Ischemic Dilation
Tomo QA	Tomographic Quality Assurance
TPC	Time to Peak or Maximum Contraction
TPER	Time to Peak Ejection Rate
TPFR	Time to Peak Filling Rate
TPT	Time to Peak Thickening using a four harmonic data fit
TPT-1	Time to Peak Thickening using a single harmonic data fit
Trans	Transverse
UgVol	Ungated Volume
VLA	Vertical Long Axis
VS	Summed Viability Score
WM	Wall Motion
WT	Wall Thickening

Corridor4DM is designed to be user-centered and customizable. Upon launching the application, you'll note several options to define processing limits, screen layouts, image displays, reporting features, and more. This chapter is an introduction to these 4DM user-centered screens and controls.

The 4DM Work Environment

Corridor 4DM is available both as a standalone (4DM Personal) application as well as an integrated plug-in for other medical systems (e.g. PACS review, cardiovascular information system, nuclear workstation). For the integrated systems, the 4DM environment is wrapped within the host medical system. A few examples are shown in *(Figure 2.1)*:

Figure 2.1: *Examples of the 4DM work environment*

The work environment can be broken down into four sections:

1. **Display Windows** — Image Display, Right-click Screen Options
2. **Application Tools** — Workflow Screens, Control Panel, Colorbar, and Toolbar
3. **Information Panels** — Patient and Dataset Information
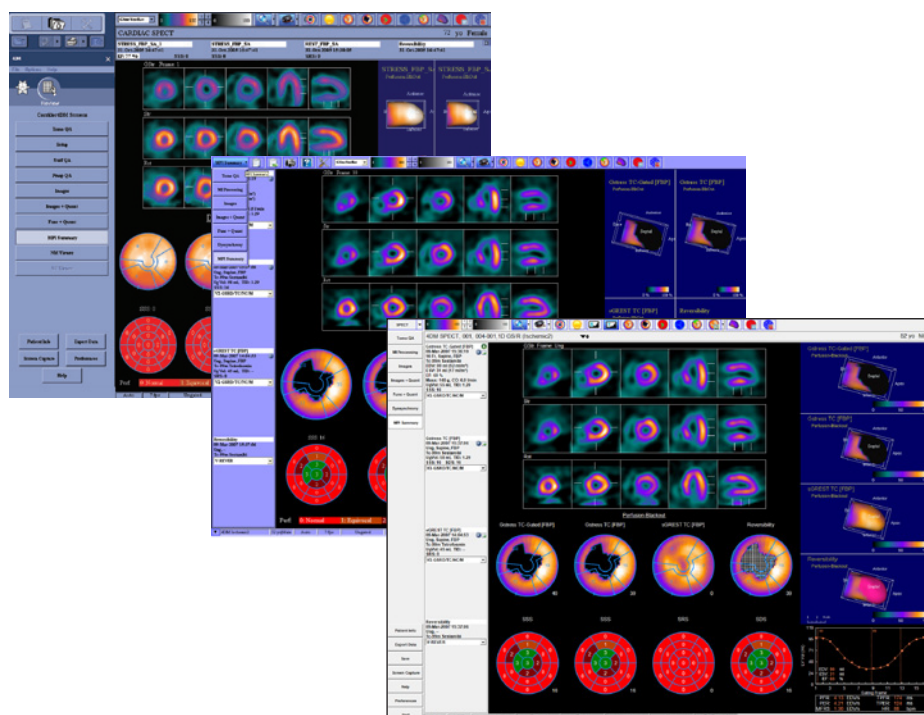4. **Selection Controls** — Patient Selector, Dataset Selector, Normals Database Selector

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Screen Layout refers to the placement or location of **Objects** within the **Image Display Window**. For example, to customize 4DM to fit their needs, users can select desired **Objects** and place or re-size them within the **Image Display Window**.

The **Right-click Screen Options** are applicable to these 4DM **Objects**:
- Tomo
- Splash
- 3SA
- Polar Map
- Scores
- 3D

Display Windows

The most distinguishable component of 4DM is the **Image Display Window** *(Figure 2.2)*. Designed as the largest area for clear, high-contrast image viewing, the contents of this window vary with each screen. The **Right-click Screen Options** *(Figure 2.2 inset)* are accessible by clicking the right mouse button. Its primary function is to provide additional user controls for screen and image customization.
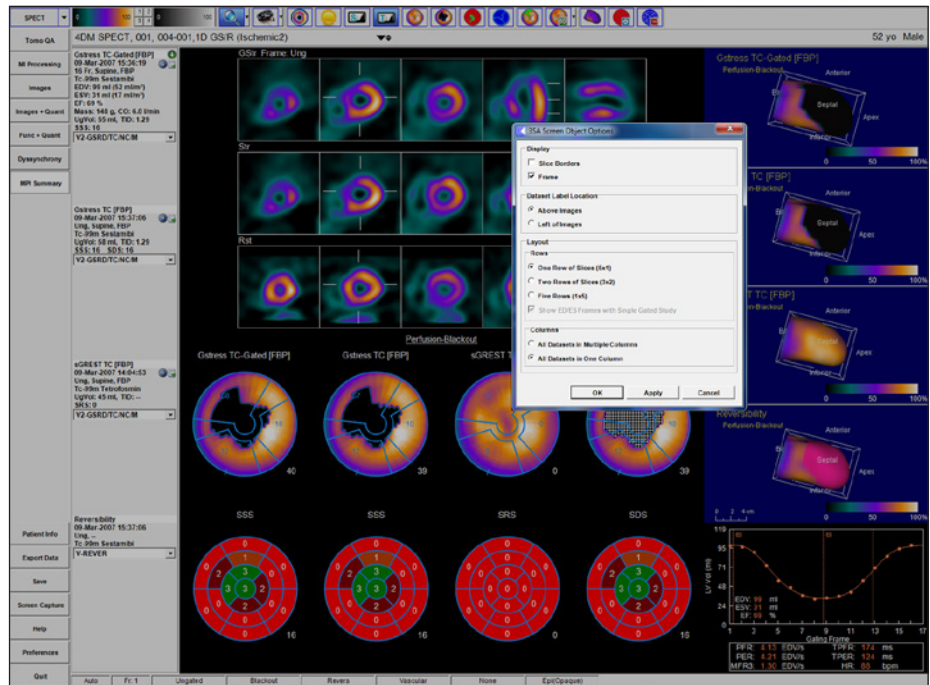
Figure 2.2: Image Display window with the Right-click Splash Object Options window

Application Tools

The **Workflow Screens** *(Figure 2.3)* provide access to the various 4DM processing and review screens. You have the ability to customize these screens to fit your specific workflow. The **Control Panel** *(Figure 2.4)* supports primary functions relevant to saving, reporting, and setting preferences within the application.

Customize the **Workflow Screens** by selecting the **Preferences** button within the **Control Panel**. See User Preferences for detailed instructions.

Figure 2.3: Example of Workflow Screens

Figure 2.4: Examples of Controls within the Control Panel

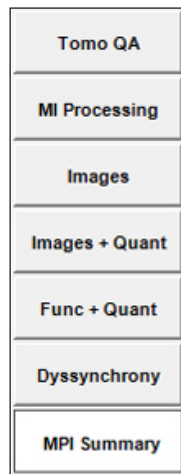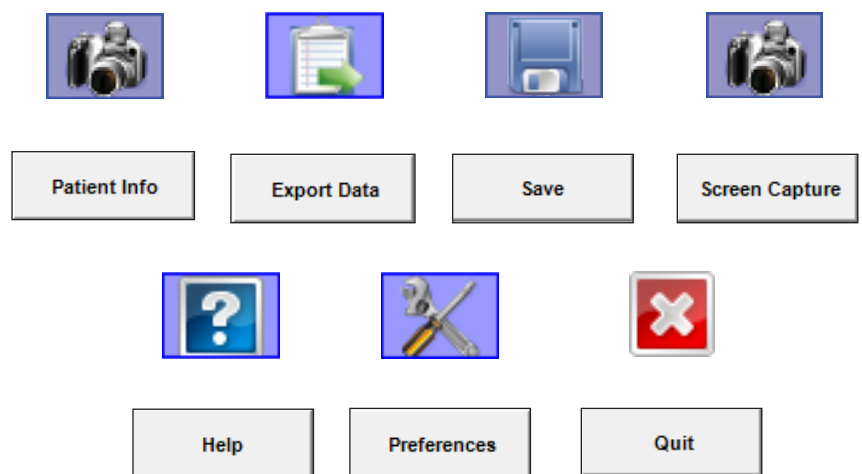The **Colorbar Tool** and **Toolbar** are shown below *(Figure 2.5)*. The color control tool is comprised of the two colorbars separated by a numbered panel. Right-click the colorbar to customize color schemes and adjust intensity mappings. For more information on colorbar management, see the Colorbar Tools section. The tools available within the **Toolbar** (to the right of the **Colorbars**) vary depending on the active screen.

Figure 2.5: Colorbar Tools and Toolbar

Information Panels

The **Patient Information Panel** contains the patient name, identification number, age, and gender. For each dataset, 4DM displays relevant information within the **Dataset Information Panel**, including:

- Dataset Description
- Acquisition Date/Time
- Frames (Fr)
- Imaging Position
- Reconstruction Type
- Radiopharmaceutical Agent
- End Diastolic Volume (EDV)
- End Systolic Volume (ESV)
- Ejection Fraction (EF)
- Cardiac Mass (Mass)
- Cardiac Output (CO)
- Ungated Volume (UgVol)
- Transient Ischemic Dilation (TID)
- Summed Stress/Rest Scores
- Normals Database Selector

Selection Controls

Corridor4DM provides an efficient, streamlined work environment with the ability to load multiple cases and then navigate between patients with the **Patient Selector** *(Figure 2.6)* drop-down menu or double-arrow button. This allows the user to review multiple patients in a single 4DM session.
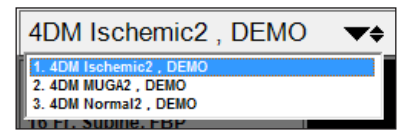
Figure 2.6: Patient Selector Menu

Once the patient is loaded, you can also select which image datasets to review with the **Dataset Selector** *(Figure 2.7)*, by clicking the green arrow in the **Dataset Information Panel** *(Figure 2.8)*. Choose from **Predefined Dataset Layouts** or drag and drop **Available Datasets** into the **Dataset Display Panels** to create your own combination, comparing up to four unique datasets.

Figure 2.7: Dataset Selector

Figure 2.8: Dataset Information Panel with ❶ Dataset Selector and ❷ Normals Database Selector Menu

Within the **Dataset Information Panel**, the user can use the **Normals Database Selector** to select a normals database which applies the corresponding data for polar map quantification and review.

By right-clicking within the **Dataset Information Panel,** the user can edit dataset information that affects normal database matching and database quantificiation. The dataset information that can be viewed and edited depends on the screen and the datasets displayed *(Figure 2.9)*.
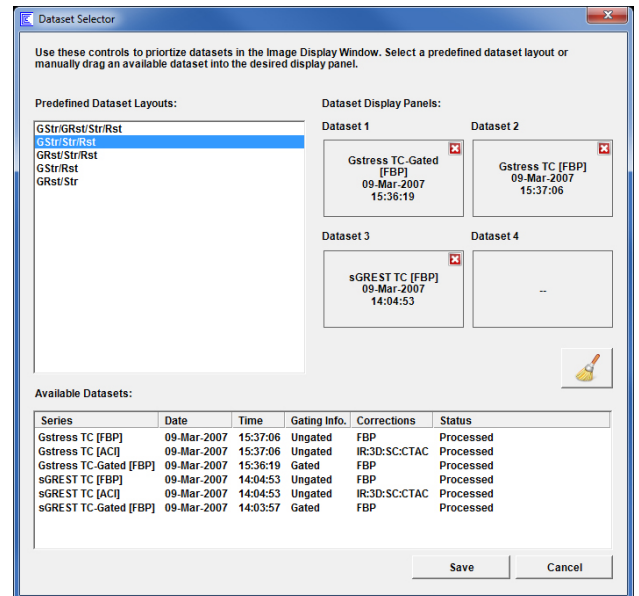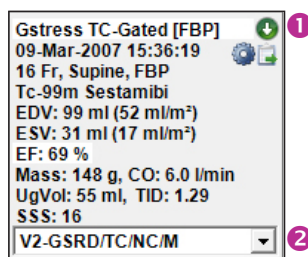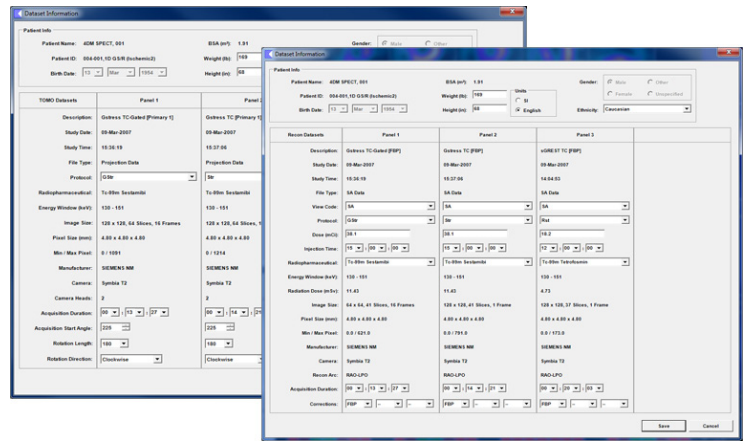

Figure 2.9: *Dataset Information Panels*

Figure 2.10: *Prioritized Dataset*

Figure 2.11: *Not Prioritized Dataset*

A clipboard icon displayed within the Dataset Information Panel informs the user of whether a dataset is prioritized for export (i.e., quantitative data for that dataset is exported to the report). The clipboard with a green arrow *(Figure 2.10)* identifies that a dataset is prioritized for export. A clipboard with a red bar *(Figure 2.11)* indicates that quantitative data for that dataset will not be exported to the report. Left-clicking a non-prioritized dataset changes its state to prioritized.

User Controls

Corridor4DM provides users with significant image display flexibility and application interaction, which are managed with a variety of tools:

- **Mouse Pointer Tools**
- **Dog-ears**
- **Buttons / Icons**
- **Toggles**
- **Sliders**
- **Drop-down Menus**

Mouse Pointer Tools

Throughout 4DM, the mouse pointer will take on a variety of shapes to indicate various user tools. Below is a table identifying the various pointers, their functions, and where to use them.

Pointer		Function	Uses
Arrow		The default mouse pointer	Make selections; Activate buttons, drop-down menus, and check boxes
Double Horizontal Arrow		Use to drag vertical sliders	Adjust VLA basal or apical settings; Modify image brightness in the Color Control Tool; Adjust vertical sliders for magnification and cine; Reposition slice planes
Double Vertical Arrow		Use to drag horizontal sliders	Adjust HLA basal settings; Establish reference lines for Tomo dataset viewports; Reposition slice planes
Crosshairs Tool		Use to reposition center axis	Locate the axial and chamber centers of the left ventricle in processing screens

Rotation Tool		Use to rotate image cross hairs or image co-registration	Reorient slices; Rotate the vascular segmentation overlay; Rotation alignment of images
Image Pan		Use to shift short axis images	Shift SA, HLA, and VLA slices
Hand Tool		Use to align datasets	Reposition images
Drawing Tool		Use to create and manipulate drawing elements	Draw regions of interest and ruler measurements; click-and-drag anchor points
Hourglass		Designates processing	Only non-interactive pointer; signifies application busy time

Dog-ears

When applicable, the Dog-ear tool appears in the top-right corner of an image *(Figure 2.12)*. With this tool, users can navigate through image slices. Left-click the black triangle to advance or the gray triangle to reverse the slice display.
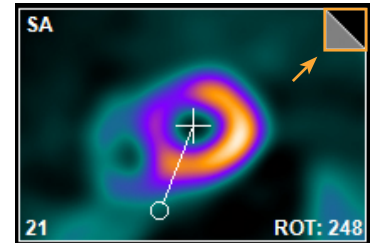
Figure 2.12: The dog-ear tool

Buttons

4DM buttons *(Figure 2.13)* are left-click tools with text that execute commands. Buttons are labeled with identifying text or by an icon (identifiable with tool tips).
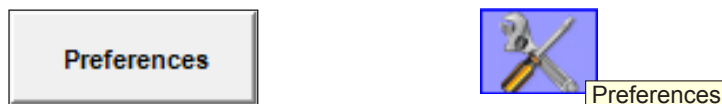
Figure 2.13: The above images are examples of the 4DM button design

Icons

4DM icons are left-click tools represented by an image. Each icon includes a **Tooltip** which appears by hovering the cursor over the icon without clicking it. There are two types of icons:

Figure 2.14: Examples of the two On/Off icon styles – with and without drop-down menus.

▪ **On/Off Tools:** Clicking these icons activates or deactivates a functionality. Three of these icons (Magnification, Cine, and Region of Interest Menu) include a drop-down arrow which expands the icon to provide additional functionality. An icon with a blue background indicates that the icon's functionality is activated *(Figure 2.14)*.

▪ **Menu:** Left-click these tools to open a list of options. Once the menu is activated, users can make their selection *(Figure 2.15)*.

Figure 2.15: Menu Selection icon with menu expanded.

Toggles

Within the application, the user will find two types of toggles: **Check Boxes** and **Radio Buttons** *(Figure 2.16)*. **Check Boxes** are used to select multiple options from a list; **Radio Buttons** are used to select a single option from a list. Toggles are used primarily within the Reporting and Preferences sections.

The key difference between the **Check Box** and **Radio Button** toggles is that the user can activate multiple check boxes at once (x, y, AND z), while radio buttons are limited to one activation per category (x, y, OR, z).
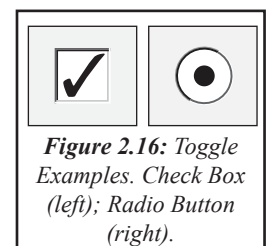
Figure 2.16: Toggle Examples. Check Box (left); Radio Button (right).

Sliders

The slider tool *(Figure 2.17)* is the only 4DM tool to have dual behaviors. The first way to use the tool is to click the "groove" either to the left or right of the indicator. This action adjusts the setting by one increment. The second way to use the tool is to simply click and drag the indicator to your desired location. This tool applies to features with a range of options, such as:

Figure 2.17: Example of the zoom and cine sliders (above) and the image and study offset slider (below).

- **Cine:** Adjust cine speed in gated studies
- **Magnification:** Adjust the display size of objects
- **Slice Shift:** Synchronously shift image slices for all displayed datasets
- **Polar Map Threshold:** Adjust the standard deviation for defect thresholds (**Polar Maps** screen only)
- **Dataset Offset:** Shift the Normals Database datasets when there are too many to view on a single screen (**DB Editor** screen only)
- **Cutoff** and **Order**: Adjust the reconstruction filter setting (**Reconstruction** screen only)

Drop-down Menus

Various drop-down menus are extensively used throughout the **NM Viewer**, **Patient Information,** and **Preferences** screens. Click the down arrow to expand a list of options and make your desired selection or click elsewhere on the screen to collapse the menu.

Colorbar Tool

The **Colorbar Tool** *(Figure 2.18)* is a screen-specific color management tool which applies to **Splash, 3SA, Polar Map**, and **3D Objects**. The tool contains dual colorbars, sliders to adjust contrast, and a right-click menu for managing the color schemes.

Figure 2.18: Colorbar Tools

> **NM Viewer**, **CT**, and **Tomo QA** objects have separate color management options.

Colorbar

4DM applies a color scheme to an acquired image according to the intensity of the tracer uptake *(Figure 2.19)*. The left side of the colorbar correlates to background and the right side correlates to brightness. A variety of color scheme choices are available and can be assigned by user or screen.
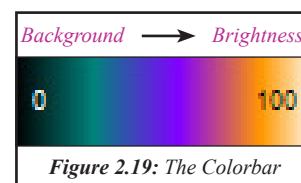
Figure 2.19: The Colorbar

> Certain colorbars with discrete color ranges can accentuate the count differences in an image, giving false impressions of abnormal differences in regional myocardial activity.

Colorbar Menus

Right-click the Colorbar to view the **Colorbar Menu.** This list displays available choices for available color schemes. If the desired color scheme is not listed, check the Colorbars Preferences in the Preferences window. Left-click the desired color scheme; the new scheme applies immediately to the colorbar and displayed data.

Intensity Map

Right-click the Colorbar and left-click the last menu listing to expand the **Intensity Map Menu**. The Intensity Map option adjusts the mapping of the color values to the dynamic intensity range of the colorbars. The default intensity map is **Linear** and evenly distributes the colorbar across the pixel range. To invert the colors, e.g. black to white, choose the **Invert** option. Left-click the desired option; the new intensity map applies immediately to the displayed data.

Brightness Slider Tool

The **Brightness Slider** *(Figure 2.20)* is at the right end of each colorbar and controls the upper color designation threshold. Any pixel value above the threshold is displayed as the color corresponding to the highest value in the colorbar (e.g., white).

To use the **Brightness Slider**, click-and-drag the slider to the left to decrease the threshold; to the right to increase the threshold. Decreasing the brightness threshold displays less detail in high count areas; raising the threshold displays more detail in high count areas.

Figure 2.20: The upper threshold slider for image brightness is illustrated here at 100% (default) and 80%
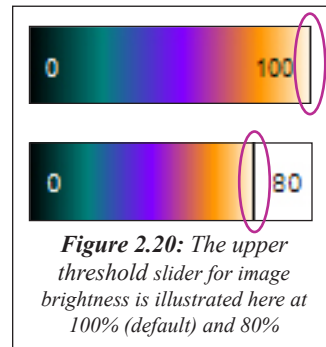
Contrast Slider Tool

The **Contrast Slider** *(Figure 2.21)* is at the left end of each colorbar and controls the lower color designation threshold. Any pixel value below the threshold is displayed as the color corresponding to the lowest value in the colorbar (e.g., black).

To use the **Contrast Slider**, click-and-drag to the right to decrease the contrast level; to the left to increase the contrast level in the display. Raising the contrast threshold makes low count image areas less visible; decreasing the threshold makes the low count image areas more visible.

Figure 2.21: The lower threshold slider for image contrast is illustrated here at 100% (default) and 80%.
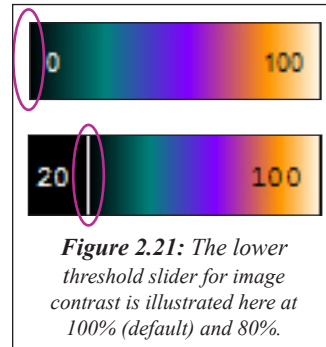
Dual Colorbar Panel Controls

The numbered toggles (1, 2, 3, 4) between the two colorbars determine which displayed datasets are controlled by the left (primary) or right (secondary) colorbars *(Figure 2.22)*. The default setting is for all studies to use the primary colorbar. When a numbered toggle is selected, the control assigns the secondary colorbar to the corresponding dataset.
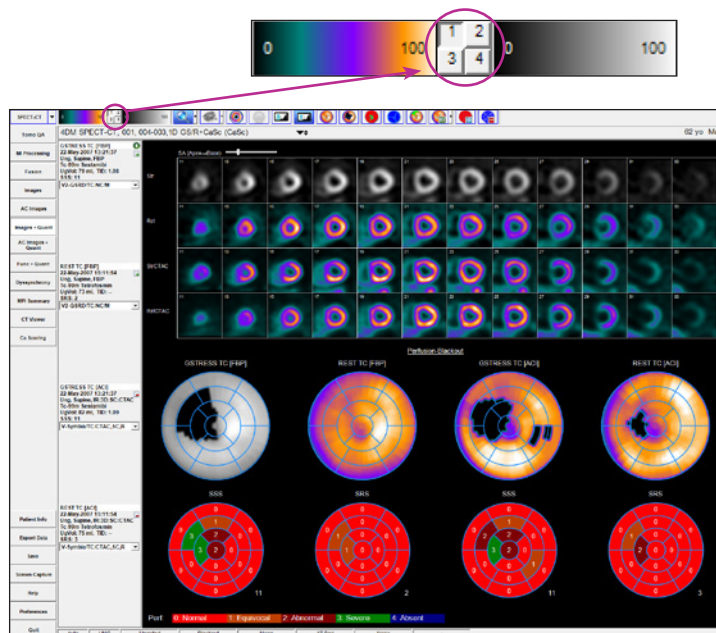
Figure 2.22: This image illustrates the dual colorbar concept — Dataset one displays the right, or secondary, colorbar set to Gray Scale; datasets two and three display the left, or primary, colorbar set to Warm Metal.

The **Tomo Screen
Object** can also be used
within some review
screens; however, only
the **Object Tools** are
activated.

The **Beat Histogram**
is only available on the
Tomo QA screen if the
camera system that the
study was acquired on
saves this data during the
acquisition and stores it
with the images to the
processing workstation.

Click the **Cardiac Beat
Histogram** icon in the
**Tomo QA
Toolbar** to
display.

QA and Processing Screens: Objects and Controls

Corridor4DM includes screens designed specifically for cardiology quality assurance and LV quantification. 4DM users – most often the technologist – will use these screens to review the raw and reconstructed data to confirm the integrity of the study. These screens all use an INVIA-defined template and cannot be redesigned within 4DM Preferences.

Tomo QA

The **Tomo Object** *(Figure 2.23)* displays NM tomographic data for quality assurance.

Object Tools

❶ **Multiple Energy Window Display** (for multiple energy datasets only): The Multiple Energy Window will be active above the image viewport when datasets are launched into 4DM that contain multiple energy (in KeV) windows. The default display will be the primary energy window for the radiopharmaceutical and the drop down arrows will allow the user to select from the energy windows that are listed.
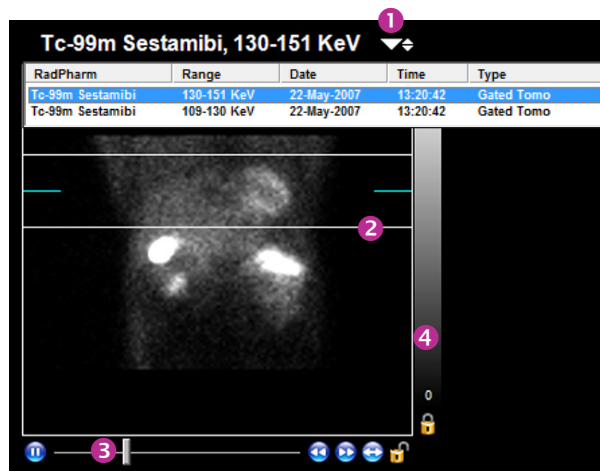
Figure 2.23: The Tomo Object from the Tomo QA screen

❷ **Slice Plane Indicator:** Use the white click-and-drag reference lines on the Tomo object to check for patient motion during acquisition. The blue reference line indicates to which pixel the image is normalized.

❸ **Cine Tools:** Use these tools to manage the cine display: Start/Stop, Frame Slider, Increase/Decrease Cine Rate, Display Next/Previous Frame, Frame Rocking, and Synchronize.

❹ **Tomo Colorbar:** Change the colorbar settings for the **Tomo Object**. Reference the Colorbar Tools section for instructions on how to operate colorbars.

Toolbar

There are five tools *(Figure 2.24)* within the Toolbar with functionality applicable to the Tomo Object:

- ▪ Magnification
- ▪ Spatial Filter
- ▪ Temporal Filter
- ▪ Sum Gating Intervals (includes Frame Slider Tool)
- ▪ Cardiac Beat Histogram

Figure 2.24: Tools from the Toolbar for Tomo Objects

Preferences

Right-click the Tomo Object **Cine Tools** to open the **Cine Options** window *(Figure 2.25)* Changes made within this window apply only to **Tomos** on the active screen.

- **Cine:** Allows users to control the cine speed for the **Tomo Object**.

- **Rocking Increment:** Users can determine the number of frames to rock in a shortened cine loop. For example, if the rocking increment is five frames and the user activates the frame rocking on frame 15, the object will rock the cine between frames 10 and 20.

- **Drop Last Frame:** Allows users to drop the last frame from a cine loop in cases where the heart rate is inconsistent.
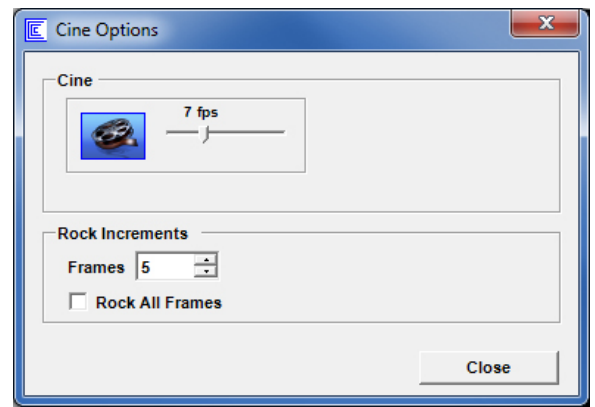
Figure 2.25: Tomo Right-Click Options

MI Processing

There are three screen modes within MI Processing:

Figure 2.26: MI Processing Screen

- **QA** - this screen is used to verify the left ventricular surfaces and the location of the valve plane as estimated by the program. Minor adjustments to the valve plane locations are performed here and the adjustments immediately update perfusion and function quantitative values.

- **Manual Processing** - if the surfaces are in error due to poor orientation or centering of the left ventricle, high intensity extra-cardiac activity, or the dataset requires additional filtering, the study should be reprocessed by clicking the Manual Processing tool *(Figure 2.27)*.

Figure 2.27: Manual Processing tool

- **Reset** - If the dataset needs to be processed from scratch (i.e. no initial estimates from 4DM), click the Reset tool *(Figure 2.28)* from the Manual Processing screen and the set the center, angulation, valve plane location and click the Process button to reprocess.

Figure 2.28: Reset tool

Object Tools

The **QA** screen displays three image objects:

- **Processed Splash Object** *(Figure 2.29)*: Displays reconstructed data on SA, HLA, and VLA formats with and without surface contours.
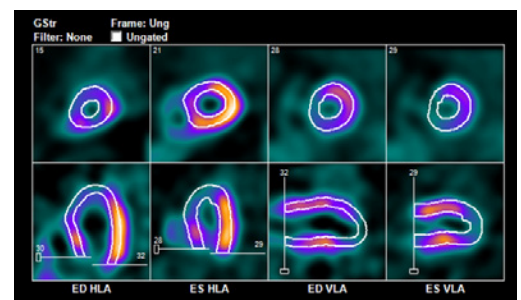
Figure 2.29: Processed Splash Object

WARNING
The user must verify that the Normals Database is compatible with the dataset being reviewed to ensure correct computation of quantitative data.

On the MI Processing Screen, the ability to rotate the VLA and HLA slices will only be available on the **Unprocessed Splash Object** if the user selects the **Manual Processing** tool.

- **Processed Polar Map Object** *(Figure 2.30)*: One or more polar maps associated with each dataset
  - Ungated Studies: Displays the normalized perfusion map
  - Gated Studies: Displays the normalized perfusion, end-diastolic, end-systolic, wall thickening, wall motion, and time to peak contraction polar maps

Figure 2.30: *Processed Map*

- **LV Volume Curve** *(Figure 2.31)*: This object is only available with gated datasets. If a gated study is loaded with two or three other datasets, click the LV Volume Curve tool to display the object.

The **Manual Processing** and **Reset** screens display the Unprocessed Splash Object:

- **Unprocessed Splash Object** *(Figure 2.32)*: When it is necessary to reprocess data or apply constraints, 4DM displays the SA, HLA, and VLA images for reprocessing.

Figure 2.31: *:LV Volume Curve*
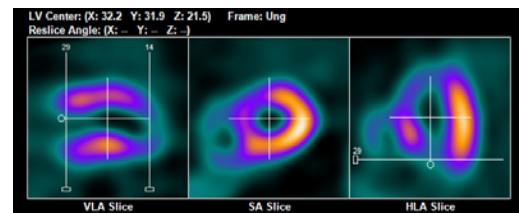
Figure 2.32: *Unprocessed Splash Object*

MI Processing - QA Toolbar

There are eight tools in the **Toolbar** for the MI Processing **QA** screen *(Figure 2.33)*:

Figure 2.33: *MI Processing - QA Toolbar*

❶ **Magnification:** Adjust the image display size

❷ **Cine:** Activate/deactivate cine in gated studies and adjust cine speed

❸ **Manual Processing:** Adjusts LV centering, orientation, and axial limits used by the 4DM surface generator

❹ **Reload:** Reverts to the most recently saved Result File

❺ **Undo:** Reverse a manual adjustment performed by the user one step at a time

❻ **Contours:** Activate and define the maximum-wall radius for LV surfaces

❼ **ED Frame Normalization:** Switch between the ED and ES frames for gated dataset image normalization

❽ **LV Volume Curve:** When active, the LV Volume curve displays in place of the Processing Polar Map Object.

There are nine tools in the **Toolbar** for the MI Processing **Manual Processing** screen *(Figure 2.34)*:
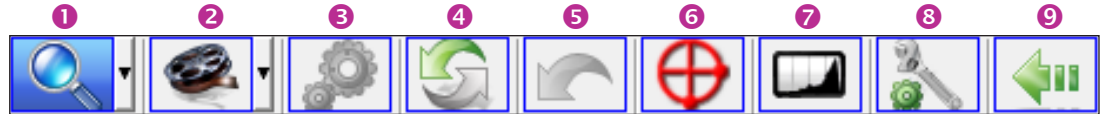
Figure 2.34: *MI Processing - Manual Processing Toolbar*

❶ **Magnification:** Adjust the image display size

❷ **Cine:** Activate/deactivate cine in gated studies and adjust cine speed

❸ **Process:** Calculate dataset(s) LV surface generation

❹ **Reset:** Allows the user to define LV dataset alignments, apical and basal limits, and LV centers on the VLA, SA, and HLA slices;

❺ **Undo:** Reverse a manual adjustment performed by the user one step at a time

❻ **Constraints:** Activate and define the maximum-wall radius for LV surfaces

❼ **Filter:** When active, the **Filtering Tool** provides temporal and spatial filtering options for each dataset.

  – **Temporal Filtering** applies a 1-2-1 temporal filter to the gated dataset
  – **Spatial Filtering** spatially smooths the SA slices (automatically sets the best filter option to use based on the dataset). Filter options include: Filter Types (Butterworth, Hanning, Hamming, Parzen, Shepp, and Gaussian); Filter Cutoff; Filter Order; and an Auto Filter option. The Auto Filter automatically sets the best filter parameters for the dataset.
  – Activate the **Lock** tool to apply filtering options to all active datasets
  – Click the **Reset** tool to revert any changes to the default settings
  – Click the **Apply** tool to save changes to the filtering options

❽ **Processing Options:** Define the centering algorithm (none, centering only, centering and tilt) and the Basal Plane Motion limits.

❾ **Return:** Returns the user to the MI Processing **QA** screen

There are seven tools within the **Toolbar** for the MI Processing **Reset** screen *(Figure 2.35)*:

Figure 2.35: *MI Processing - Reset Toolbar*

❶ **Magnification:** Adjust the image display size

❷ **Cine:** Activate/deactivate cine in gated studies and adjust cine speed

❸ **Process:** Calculate dataset(s) LV surface generation

❹ **Undo:** Reverse a manual adjustment performed by the user one step at a time

❺ **Constraints:** Activate and define the maximum-wall radius for LV surfaces

❻ **Filter:** When active, the **Filtering Tool** provides temporal and spatial filtering options for each dataset.

  – **Temporal Filtering** applies a 1-2-1 temporal filter to the gated dataset

– **Spatial Filtering** will spatially smooth the SA slices according to these options: Filter Type (Butterworth, Hanning, Hamming, Parzen, Shepp, and Gaussian); Filter Cutoff; and Filter Order

– Activate the **Lock** tool to apply filtering options to all active datasets

– Click the **Reset** tool to revert any changes to the default settings

– Click the **Apply** tool to save changes to the filtering options

❼ **Processing Options:** Define the centering algorithm (none, centering only, centering and tilt) and the Basal Plane Motion limits.

Review Screens: Objects and Controls

Most 4DM review screens are comprised of one or more 4DM Objects. Because 4DM provides users with the option of designing custom review screens using the objects listed below, it is important to understand each object's clinical value. Refer to the Predefined Screen Templates Table or User Preferences for more information. The 4DM objects are:

- **Tomo**
- **Splash**
- **3SA**
- **Polar Map**
- **Scores**
- **3D**
- **LV Volume Curve**

Tomo

The **Tomo Object** *(Figure 2.36)* displays NM tomographic data for quality assurance.

Object Tools

❶ **Slice Plane Indicator:** Use the white click-and-drag reference lines on the Tomo object to check for patient motion during acquisition. The blue reference line indicates to which pixel the image is normalized.

❷ **Cine Tools:** Use these tools to manage the cine display: Start/Stop, Frame Slider, Increase/Decrease Cine Rate, Display Next/Previous Frame, Frame Rocking, and Synchronize.
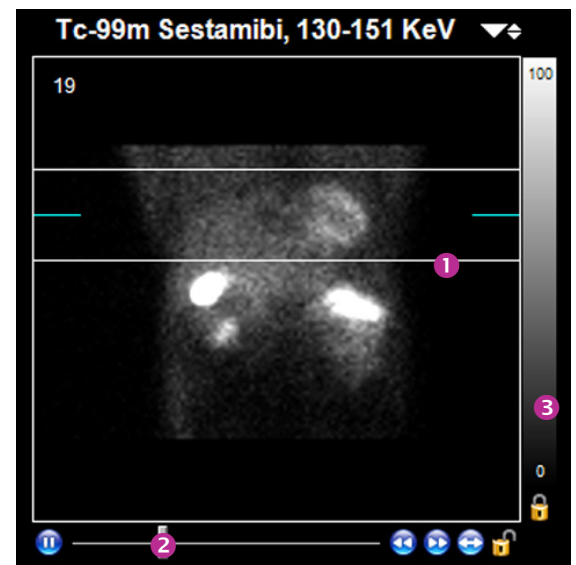
Figure 2.36: The Tomo Object from the Tomo QA Screen

❸ **Tomo Colorbar:** Change the colorbar settings for the **Tomo Object**. Reference the Colorbar Tools section for instructions on how to operate colorbars.

Preferences

Right-click the Tomo Object **Cine Tools** to open the **Cine Options** window *(Figure 2.37)*. Changes made within this window apply only to **Tomos** on the active screen.

- **Cine:** Allows users to control the cine speed for the **Tomo Object**.

- **Rocking Increment:** Users can determine the number of frames to rock in a shortened cine loop. For example, if the rocking increment is five frames and the user activates the frame rocking on frame 15, the object will rock the cine between frames 10 and 20.

- **Drop Last Frame:** Allows users to drop the last frame from a cine loop in cases where the heart rate is inconsistent. This option is only available if the dataset is a Gated Planar Bloodpool study. Right-click the **Tomo Object** to open the Tomo Object Options window *(Figure 2.38)*.

- **Grid:** Displays Tomo Objects for active datasets in rows and columns

- **Horizontal:** Displays Tomo Objects for active datasets horizontally

- **Vertical:** Displays Tomo Objects for active datasets vertically
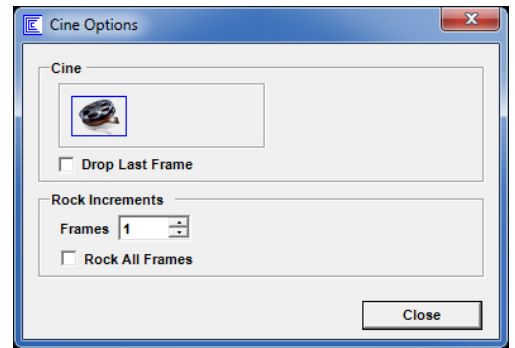
Figure 2.37: Tomo Object Cine Controls right-click options
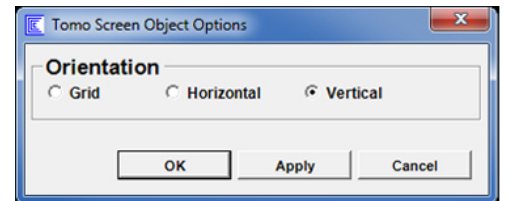
Figure 2.38: Tomo Object right-click options

Splash

A **Splash Object** *(Figure 2.39)* displays slice orientations as SA, HLA, and VLA. These images are used to observe tracer uptake within the myocardium.
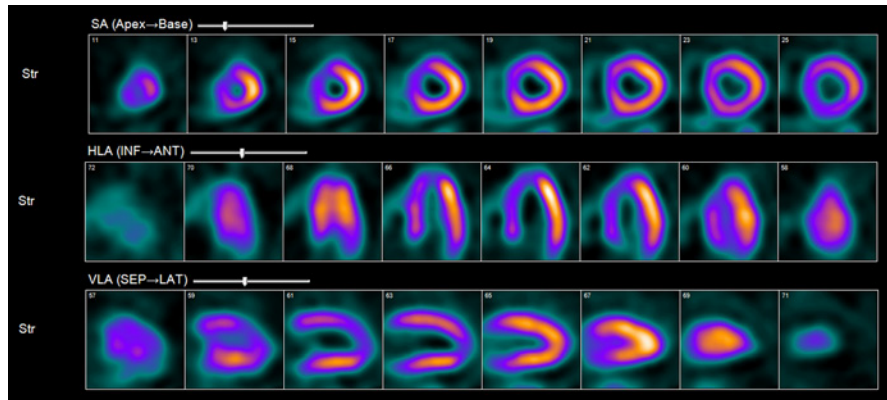
Figure 2.39: From Top-to-Bottom-SA, HLA, and VLA Splash Objects

Object Tools

For the **Splash Object**, *(Figure 2.40)* there are two ways to shift slices: all datasets simultaneously or individually.

- **Simultaneously:** Click-and-drag the **Slice Slider** to shift all displayed datasets together. Drag the slider to the right to display slices closer to the base; to the left to display slices closer to the apex.
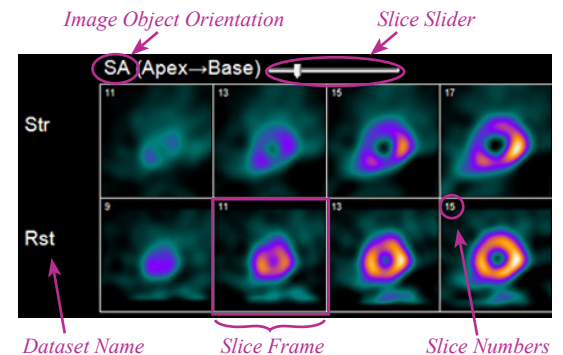
Figure 2.40: SA Splash Object slices

- **Individually**: Click-and-drag any slice frame to the right or left to change the starting slice in the splash display for that dataset.

Toolbar

There are six tools *(Figure 2.41)* in the Toolbar with functionality applicable to the Splash Object:

- Magnification
- Cine
- Contours
- ED Frame Normalization
- Spatial Filter
- Temporal Filter
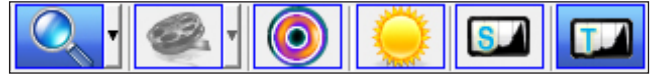
Figure 2.41: Toolbar for Splash Object

Preferences

Right-click any **Splash Object** to open the **Splash Object Options** window *(Figure 2.42)*. Changes made apply only to **Splash Objects** on the active screen.

- **Slice Averaging:** Only available when the global preference is turned off. Choose to automatically average the slice array (Auto) to fill the total number of slice frames or specify the number of slices to average (between one to six slices).

- **Display:** Turned on/off by a check box, these options control the labels, borders, slice numbers and perspective label. Check **Apply to All** to apply display changes to all **Splash Objects**.

- **Layout:** Users can modify the image layout (display images in one or two rows; add space between rows; change the number of images displayed) using check boxes.

Figure 2.42: Splash Object right-click options

- **Slice Size:** Users can choose **Dynamic** to size images to fit the available screen space, or specify a **Fixed** image size between 20 and 300 pixels.

- **Object Orientation:** Each Splash Object can be assigned either an SA, HLA, or VLA orientation.

3SA

The **3SA Object** *(Figure 2.43)* provides a display with three short axis (SA) images (apical, mid, and basal), an HLA image slice, and a VLA image slice. The mid-SA, mid-HLA, and mid-VLA slices include adjustable slice planes which determine the displayed slices.

Object Tools

Adjust the SA, VLA, and HLA slices by clicking-and-draging the slice planes (white lines) to the desired location. The image display adjusts accordingly.
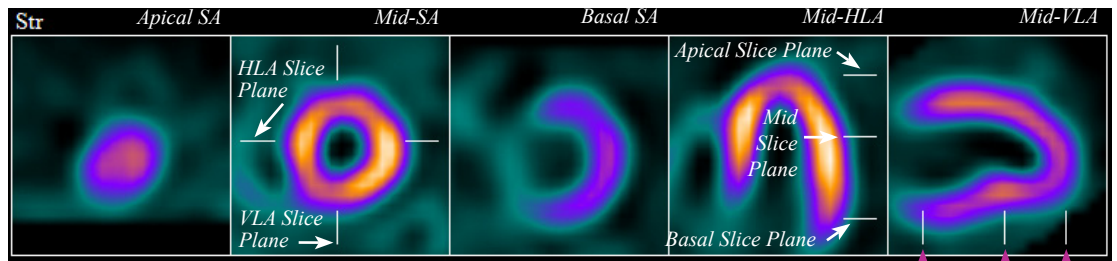
Figure 2.43: *A diagrammed example of the 3SA Object*

Toolbar

There are six tools *(Figure 2.44)* in the Toolbar with functionality applicable to the 3SA Object:

- Magnification
- Cine
- Contours
- ED Frame Normalization
- Spatial Filter
- Temporal Filter
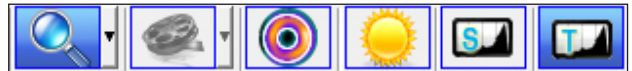
Figure 2.44: *Toolbar for 3SA Object*

Preferences

Right-click the 3SA Object to open the **3SA Object Options** window *(Figure 2.45)*. Changes made using this right-click method apply only to objects on the active screen for this session. To make changes to default settings, refer to User Preferences.

- **Display:** When checked, these check boxes apply **Slice Borders** and display the gating **Frame** information (gated studies only) within the 3SA Object.

- **Dataset Label Location:** Choose between displaying the dataset label (GStr, Str, Rst, etc.) above or to the left of the object.

- **Layout:** Define how the object displays slices.
  - **Row:** Arranges slices in one, two, or five rows.
   - **Show ED/ES Frames with Single Gated Study**: When viewing a single gated dataset, selecting this check box displays the End Diastolic and End Systolic Frames
  - **Column:** Arranges datasets within one or multiple columns.
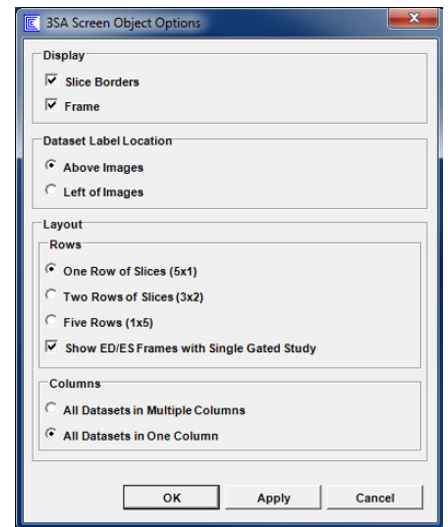
Figure 2.45: *3SA Object right-click options*

Polar Maps

The **Polar Map Object** *(Figure 2.46)* displays LV perfusion and/or function as compared to Normals database files in easily interpretable images. The two-dimensional graphic, sometimes called a bull's eye, represents the reconstructed volume from apex (the polar map center) to base (the polar map outer edge).

Toolbar

The **Polar Map Object** has six menu selection tools in the **Polar Map Toolbar**:

The **Polar Maps** screen in 4DM displays quantified polar maps but does not have a right-click **Polar Map Object Options** window because it is an INVIA-defined screen.
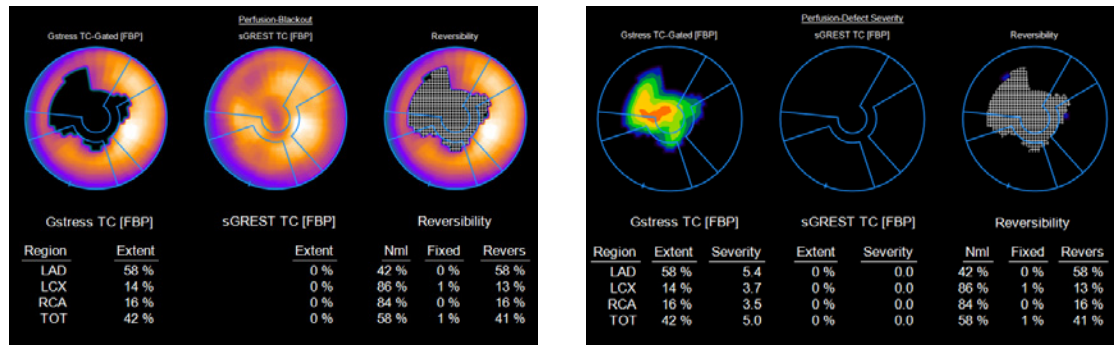
Figure 2.46: *(Left) An example of the Defect Blackout Quant Map option with the Reversibility Comparison Map. (Right) An example of the same patient datasets displayed using the Defect Severity option from Quant Map drop-down menu.*

- **Raw Map Menu:** Controls the raw information that is mapped or displayed on the polar map. The available options are:
  - **Ungated**: Displays raw perfusion mapping
  - **ED**: Displays ED perfusion (gated studies only).
  - **ES**: Displays ES perfusion (gated studies only).
  - **Thickening**: Displays wall thickening (WT) (gated studies only).
  - **Motion**: Displays wall motion (WM) (gated studies only).
  - **Time Pk Thk**: Displays the time to peak thickening (gated studies only).
  - **Time Pk Con**: Displays the time to peak contractility (gated studies only).
  - **G-All**: Displays Ungated, Thickening, and Motion polar maps together (gated studies only).
  - **G-Perf**: Displays Ungated, ED, and ES polar maps together (gated studies only).

- **Quant Map Menu:** Controls the type of quantification (Quant) performed on the raw data. The available options are:
  - **Raw**: Displays the values reconstructed from image voxel values.
  - **Norm**: For Perfusion maps, displays values normalized such that regional maximum is 100.
  - **Severity**: Displays pixels in units of StDv from the normal mean.
  - **Def-Sev**: Displays all defect pixels that fall below the defect threshold in units of StDv below the normal mean.
  - **Blackout**: Displays all defect pixels that fall below the defect threshold with a zero value.
  - **DB Mean**: Displays normal database mean map for applied Normals database.
  - **DB StDv**: Displays normal database StDv map for applied Normals database.
  - **Thresholds**: Displays the number of standard deviations used to define the defect threshold.
  - **PDS Quant:** Quantifies the extent and severity of the perfusion defect size (requires PDS license key).
  - **SUV:** Displays the Standard Uptake Value Scale of 0-10. Primary functionality is to review FDG uptake in patients (PET datasets only) with inflammatory disease.

- **Comparison Map Menu:** Controls the information displayed in a comparison map, representing data generated from a comparison of two datasets [an ungated dataset takes precedence over a gated dataset if the three studies (GStr/Str/Rst) are selected.] The available options are:
  - **None**: No comparison is made; a map is not displayed.
  - **Revers**: The crosshatch pattern indicates 10% or greater improvement between stress and rest perfusion signifying areas of tissue reversibility
  - **Viability**: Perfusion + FDG viability combination.
  - **DIFF12**: A normalized subtraction of Map 2 (e.g. Rest) from Map 1 (e.g. Stress) is presented.

The **Comparison Map** displays information derived from a comparison of two datasets. It is not displayed if four datasets are viewed together on one screen due to space availability in the image display panel.

- **DIFF21**: A normalized subtraction of Map 1 (e.g. Stress) from Map 2 (e.g. Rest) is presented.
- **Washout**: Time normalized change (e.g. washout) of tracer from Map 1 to Map 2.
- **T ½**: Estimated change of intensity from Map 1 to Map 2 in units of half-life of radionuclide.

▪ **Segmental Overlay Menu:** Changes the overlay used to calculate regional statistics for the Quant or Comparison map The available options are:
- **Vascular**: LAD, LCx, and RCA vascular territories (4DM default).
- **Vasc(NG1)**: **Vascular** overlay with no gaps between territories.
- **Vasc(NG2)**: A second variation of the **Vascular** overlay with no gaps between territories.
- **5 Seg**: Overlay of the four Myocardial Walls (ANT, LAT, INF, SEP) and the apical segment.
- **9 Seg**
- **13 Seg**
- **17 Seg**
- **19 Seg**
- **20 Seg**
- **Bar Plot:** Available on the **Polar Maps** screen only
- **Circ Plot:** Available on the **Polar Maps** screen only
- **None**: No overlay or statistics are displayed
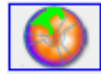
▪ **Fusion Overlay:** 4DM has integrated the **Calcium** and **CTA Coronary Vessel Fusion Overlay** options for all **2D** and **3D Polar Map Objects**. With these new options, users can view the location of calcium deposits and coronary vessels in relation to perfusion defects that are present on the 2D and/or 3D polar maps. Available options are:
- **None**: No Fusion overlay is applied (4DM default)
- **Extracted CTA**: Fuses extracted coronary vessels from CTA studies. CTA overlays appear red *(Figure 2.47)*.

Figure 2.47: CTA Coronary Vessel Fusion on 3D and 2D polar maps.

- **Calcium**: Fuses 4DM-quantified calcium deposit overlays. Calcium overlays appear neon green *(Figure 2.48)*.
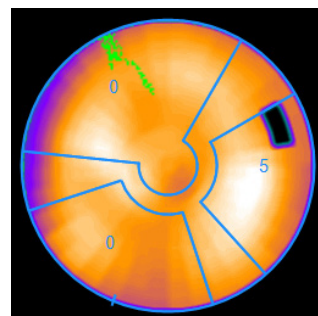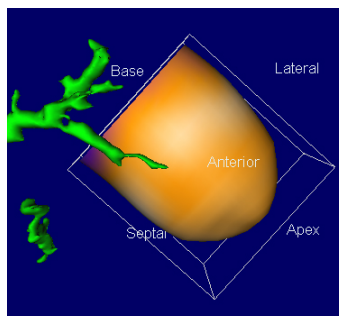
Figure 2.48: Calcium overlay on 3D and 2D polar maps

The **Fusion Overlay** drop-down menu defaults to **None**. The **Extracted CTA** and **Calcium** options are only enabled for use if the Calcium Scoring CT or the reconstructed CTA dataset on the same patient has been launched **and** QA has been completed on the **Fusion** and/or **Ca Scoring** screens.

To activate the **CTA Overlay** option, 4DM has integrated a QA measure which requires users to check the co-registration of the NM dataset(s) to the CTA on the **Fusion** screen.

To activate the **Calcium Overlay** option users are required to check the co-registration of the NM dataset(s) to the Calcium Score CT on the **Fusion** screen and also QA the 4DM-generated calcium scores on the **Ca Scoring** screen.

▪ **Defect Threshold Slider**: Adjusts the defect threshold in standard deviations (StDv) below the normal mean distribution of the matched Normals database. This slider is applicable to perfusion polar maps only if a uniform defect threshold has been selected on the Polar Map Defects Thresholds section of the Normals Databases page available from the Preferences window.

Preferences

Right-click a **Polar Map Object** to open the **Polar Map Object Options** window *(Figure 2.49)*. Changes made using this right-click method apply only to **Polar Map Objects** on the active screen.

- ▪ **Toolbar Options:**
  - – **Override Check Box:** Select the check box to independently control multiple **Polar Map Objects** via the right-click **Polar Map Objects** window.
  - – **Raw Map:** Same as the Polar Map Toolbar.
  - – **Quant Map:** Same as the Polar Map Toolbar.
  - – **Segmental Overlays**: Same as the Polar Map Toolbar.
- ▪ **Labels:** Check boxes determine the content displayed within the **Polar Map Object** *(Figure 2.50)*.

  - – **Title:** When the check box is selected, the title of the Quant Map displays above the Polar Map Object.

  - – **Dataset Header:** When the check box is selected, the dataset name displays above each individual polar map within the Polar Map Object.

- ▪ **Data:** Radio buttons determine the content displayed within the **Polar Map Object**.

  - – **Map Data:** Displays the quantitative polar map image using colorbar settings.

  - – **Statistics:** Displays the quantitative data numerically within a polar map overlay without displaying the image.

  - – **Map Data and Statistics:** Displays the quantitative polar map and the numerical information the polar map overlay.

  - – **Statistics in Table:** Displays the quantitative data numerically in a table *(Figure 2.51)*.
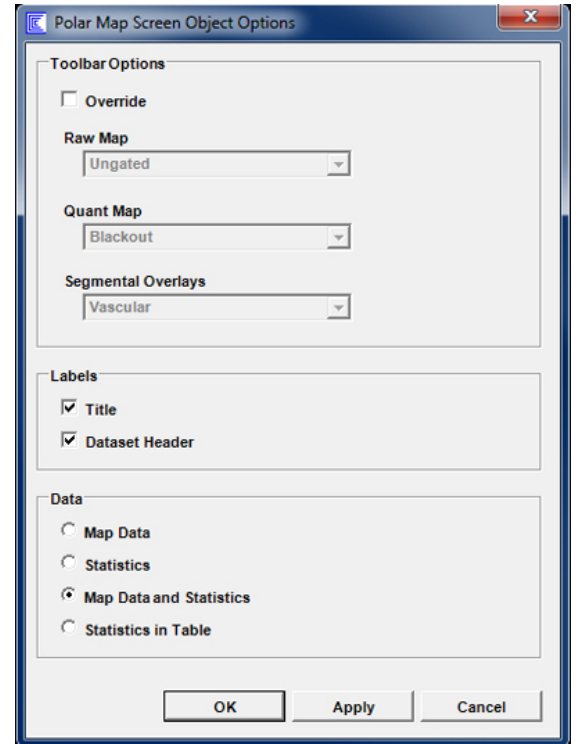
Figure 2.49: Polar Map Object Options
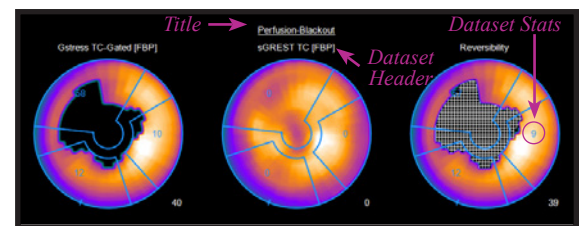
Figure 2.50: Polar Map Object

Figure 2.51: Polar Map Statistics in Table Format

Scores

The **Scores Object** *(Figure 2.52)* displays automatically generated semi-quantitative segmented scores in the same circular format as polar maps. The **Scores Object** is typically displayed directly below a polar map object to provide users with the ability to perform quick visual comparisons between the two. Scores that are generated are relative to the perfusion, wall thickening, or wall motion of the LV depending upon which **Raw Polar Map** option is selected from the drop-down menu in the **Toolbar**.
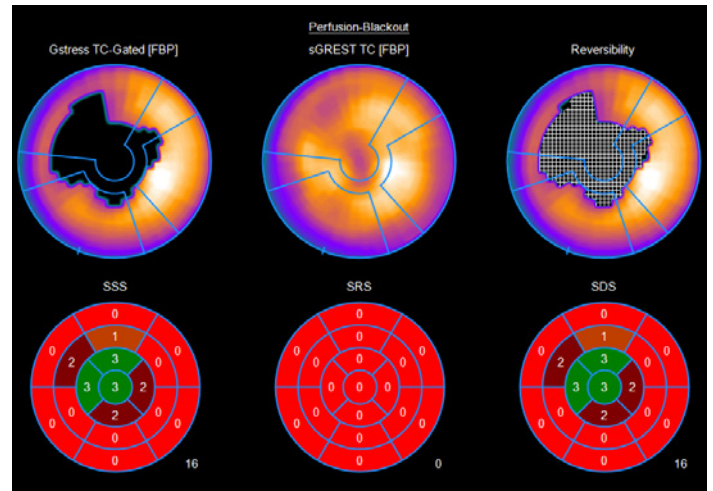
Figure 2.52: Polar Map Objects (top) and Scores Objects (bottom)

Object Tools

The 4DM **Scores Object** automatically displays quantified score results. The scores generated are on a numbered 0-4 scale with 4DM defect ratings *(Figure 2.53)*. To manually change the scores,

Score	Perfusion	Thickening	Motion
0	Normal	Normal	Normal
1	Equivocal defect	Equivocal	Equivocal
2	Abnormal	Abnormal	Hypokinetic
3	Severe defect	None	Akinetic
4	Absent Uptake		Dyskinetic

Figure 2.53: Scores Object Defect Ratings

- **Increase:** Left-click inside a segment to increase the score by one with each click
- **Decrease:** Right-click inside a segment to decrease the score by one with each click.

Automated scoring within 4DM uses threshold settings defined in either StDv or absolute units of the measured variable. The user may customize the threshold and color settings designated for each score. Both functions are accessed from within Preferences Segmental Scoring Thresholds.

Toolbar

- **Auto**: Click the **Auto** tool located in the **Toolbar** to display the 4DM-quantified segmented scoring results.

- **Clear**: Click the **Clear** tool located in the **Toolbar** to clear all displayed scores.

Preferences

Right-click the **Scores Object** to open the **Scores Object Options** window *(Figure 2.54)*. Changes made to Auto, Clear, or the Segmental Overlay apply to all Scores objects across *all* screens.

Figure 2.54: Scores Object Options

- **Toolbar Options:**

  - **Override Check Box:** Selecting this check box allows the user to define Raw Map settings

  - **Raw Map:** Same as the [Polar Map Toolbar](#).

- **Segmental Overlays**: Choose from three segmented overlays — 17, 19, or 20 segments.

- **Labels:** Check boxes and radio toggles determine the content displayed within the **Scores Objects**

  - **Title:** When selected, the title of the Scores Object displays above the Score Object.

  - **Description:** When selected, the user can view either the **Quant Map Header** or **Dataset Header** above the Scores Objects.

  - **Legend:** This check box enables viewing the scoring legend below the **Scores Objects** when selected.

- **Calculate Scores**: Click the **Auto** button to automatically compute the scores. Click the **Clear** button to erase the scores.

3Ds

Users can evaluate myocardial perfusion and function by observing 3D-rendered images of the left ventricle *(Figure 2.55)*. The 3D object appears on a dark blue background.

Object Tools

Left-click and drag any of the 3Ds to manually adjust the orientation of the object.

Toolbar

These tools are in the **Toolbar** on screens with 3D Objects.

- **Raw Map:** Controls the raw information that is mapped to the 3D object. The available options are:
  - **Ungated:** Displays raw perfusion mapping.
  - **ED:** Displays ED Perfusion (gated studies only).
  - **ES:** Displays ES Perfusion (gated studies only).
  - **Thickening:** Displays Wall Thickening (WT) (gated studies only).
  - **Motion:** Displays Wall Motion (WM) (gated studies only).
  - **Time Pk Thk:** Displays the time to peak thickening (gated studies only).
  - **Time Pk Con:** Displays the time to peak contractility (gated studies only).
  - **G-All:** Includes Ungated Perfusion, Wall Thickening, and Wall Motion
  - **G-Perf:** Includes Ungated Perfusion, ED Perfusion, and ES Perfusion

When viewing ungated datasets in the **3D Object**, the only available option within the **Raw Map** Menu is **Ungated.**
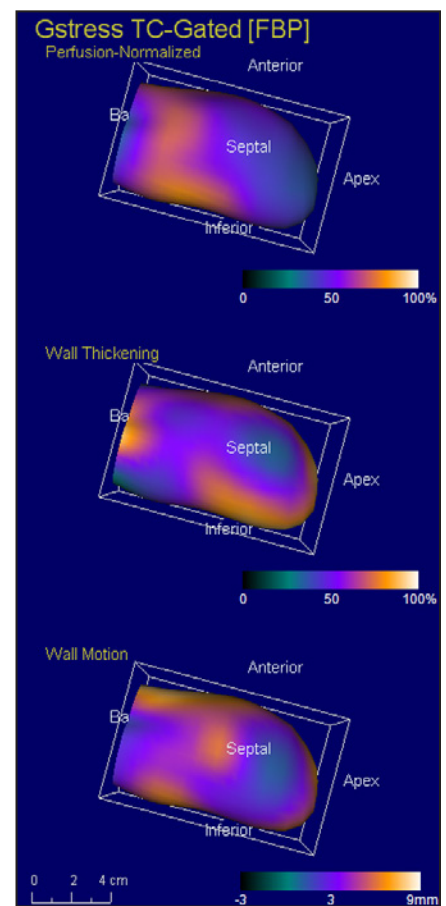
Figure 2.55: An example of the 3D Object with the Raw Map menu set to G-All

- **Quant Map:** Displays quantification (Quant) information for a comparison to a normals database. The available options are:
  – **Raw:** Displays the values reconstructed from image voxel values.
  – **Norm:** For perfusion maps, displays values normalized such that regional maximum is 100.
  – **Severity:** Displays pixels in units of standard deviation (StDv) from the normal mean.
  – **Def-Sev:** Displays all defect pixels that fall below the defect threshold in units of StDv below the normal mean.
  – **Blackout:** Displays all pixels that fall below the defect threshold with a zero value.
  – **DB Mean:** Displays the normals database mean map.
  – **DB StDv:** Displays normals database standard deviation map.
  – **Thresholds:** Displays the number of standard deviations used to define the defect threshold.
  – **SUV:** Displays the Standard Uptake Value Scale of 0-10. Primary functionality is to review FDG uptake in patients (PET datasets only) with inflammatory disease.

- **Comparison Map:** Controls the information displayed in a Comparison 3D Object. It represents data generated from a comparison of two maps. [An ungated dataset takes precedence over a gated dataset if three datasets (GStr/Str/Rst) are selected.] The available options are:
  – **None:** No comparison is made; 3D object is not displayed.
  – **Revers**: The crosshatch pattern indicates 10% or greater improvement between stress and rest perfusion signifying areas of tissue reversibility
  – **DIFF12:** Displays a normalized subtraction of Map 2 (e.g. Rest) from Map 1 (e.g. Stress).
  – **DIFF21:** Displays a normalized subtraction of Map 1 (e.g. Stress) from Map 2 (e.g. Rest).
  – **Washout:** Time normalized change (e.g. washout) of tracer from Map 1 to Map 2.
  – **T ½:** Estimated change of intensity from Map 1 to Map 2 in units of half-life of the radionuclide.

- **Fusion Overlay**: If extracted coronary vessels from a CTA study or Calcium Scoring CT are launched in 4DM, this option is used to overlay the reconstructed, extracted vessels or the 4DM-quantified coronary calcium deposits onto the displayed 3D LV surfaces.

- **Defect Threshold Slider**: Adjusts the defect threshold in standard deviations (StDv) below the normal mean distribution of the matched Normals database. This slider is applicable to perfusion maps only if a uniform defect threshold has been selected on the Polar Map Defects Thresholds section of the Normals Databases page available from the Preferences window.

- **3D Surface:** Controls the geometric appearance and combinations of the 3D myocardial surfaces:
  – **Endocardial:** Displays an opaque endocardial surface only.
  – **Epi(Opaque):** Displays an opaque epicardial surface surrounding an opaque endocardial surface.
  – **Epi(Trans):** Displays a transparent epicardial surface surrounding an opaque endocardial surface.
  – **Epi(Wire):** Displays a wire frame epicardial surface around an opaque endocardial surface.
  – **Endo(FixED):** Displays an opaque endocardial surface with a fixed ED endocardial wire frame overlay.
  – **EndoEpi(FixED):** Displays an opaque endocardial surface with fixed ED endocardial and epicardial wire frame overlays.

The **Fusion Overlay** drop-down menu defaults to **None**. The **Extracted CTA** and **Calcium** options are only enabled for use if the Calcium Scoring CT or the reconstructed CTA dataset on the same patient has been launched in 4DM **and** QA has been completed on the **Fusion** and/or **Ca Scoring** screens.

Right-click a 3D Object to open the **3D Object Options** window *(Figure 2.56)*. Changes made using this right-click method apply only to 3D Objects on the active screen.

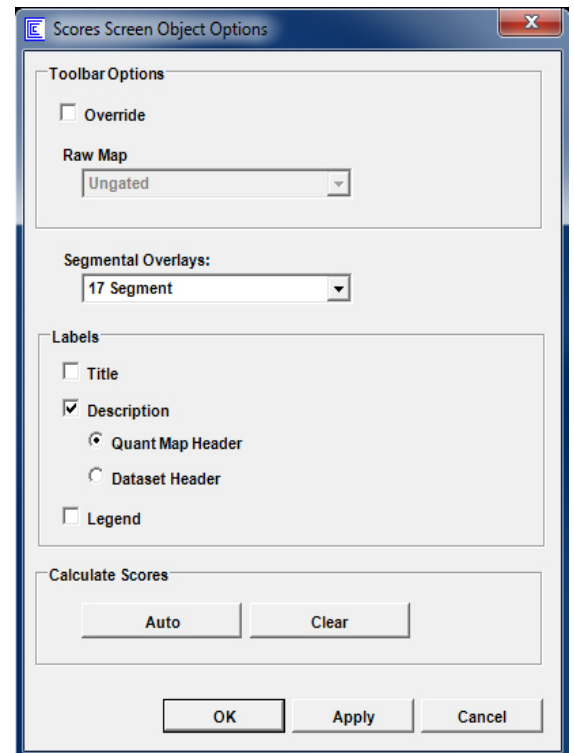*Figure 2.56: 3D Object Options*

- **Toolbar Options:**
  – **Override Check Box:** Selecting this check box allows the user to define Raw Map and Quant Map settings
  – **Raw Map:** Same as the Polar Map Toolbar.
  – **Quant Map:** Same as the Polar Map Toolbar.
- **Segmental Overlays:** This drop-down menu *(Figure 2.57)* applies a segmental overlay to the 3D image:
  – **5 Seg** Overlay of the four Myocardial Walls (ANT, LAT, INF, SEP) and the apical segment.
  – **9 Seg**
  – **13 Seg**
  – **17 Seg**
  – **19 Seg**
  – **20 Seg**
  – **None**

Figure 2.57: 3D Segmental Overlay Menu

- **Rotation:** Auto-rotate the 3D volume(s) around any one of three axes:
  – X: Rotate the 3D volume around a horizontal axis through the image center.
  – Y: Rotate the 3D volume around a vertical axis through the image center.
  – Z: Rotate the 3D image around the LV long axis at the image center.
- **Labels:** When checked, the orientation labels and a bounding box are displayed.
- **Orthogonal Lock:** When checked, 3D orientation remains aligned for displayed images (Available on **3D Splash** screen only.)
- **3D Perspectives:** These buttons change the angle of the user's view of the 3D LV surfaces and are usually included directly within the 3D Object *(Figure 2.58)*. However, the perspective buttons on the **MPI Summary** screen and **User Defined** screens are available in the **3D Object Options** right-click window *(Figure 2.59)*.

Figure 2.58: 3D Object including Perspective buttons along the bottom of the 3D image
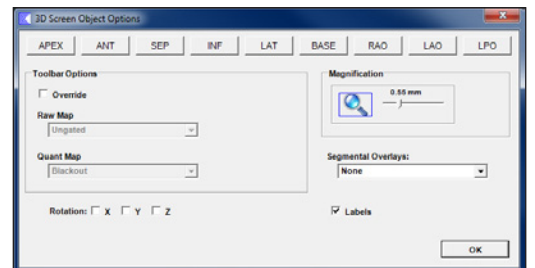
Figure 2.59: Right-click 3D Object Options with Perspective buttons

LV Volume Curve

The **LV Volume Curve** graphically displays the LV volume for gated studies in milliliters (ml) on the y-axis with respect to the gated frame number along the x-axis *(Figure 2.60)*. The information displayed within the object is summarized below:

Figure 2.60: The LV Volume Curve Object

- **EDV** – End diastolic volume
- **ESV** – End systolic volume
- **EF** – LV Ejection Fraction

For users who acquire 16-frame gated studies, the following diastolic function parameters are also displayed within the LV Volume Curve:

- **PFR** – LV peak filling rate
- **PER** – LV peak emptying rate
- **TPFR** – Time to peak filling rate measured from time of ES. This position is marked with a vertical dashed line.
- **TPEF** – Time to peak emptying rate measured from time of ED.
- **MFR3** – Mean filling rate in first third of filling cycle.
- **HR** – Heart rate measured during the gated acquisition.

Object Tools

To select a specific gating frame for display, turn off the cine in the **Toolbar** and left-click either the frame number (on the x-axis) or the plotted data point within the curve.

Toolbar

The only tool *(Figure 2.61)* in the Toolbar with functionality applicable to the LV Volume Curve Object is **Cine**.

Figure 2.61: The Cine tool for LV Volume Objects

SC Viewer Screen

The **SC Viewer** *(Figure 2.62)* screen displays DICOM static (SSC) and multi-frame (MFSC) screen captures. Within a clinical workflow, SC Viewer may be used two ways. First, to review 4DM-generated screen captures that are created by the technologist during QA and image preparation. A common use is to send these to PACS for storage and easy reference of quantitative findings, and for serial study comparisons. For more information on taking screen captures within 4DM, see Capturing 4DM Results.
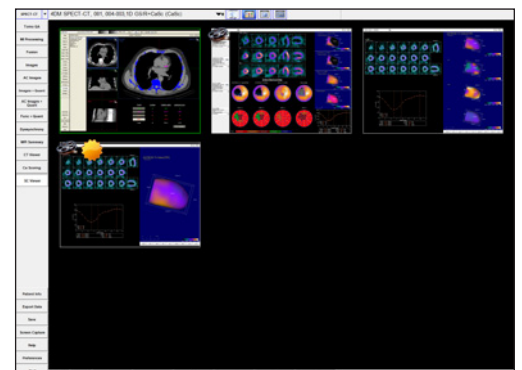
Figure 2.62: SC Viewer screen

Second, the SC Viewer can supplement the clinical workflow by enabling review of DICOM static and multi-frame screen captures generated outside of 4DM. For example, DICOM screen captures generated during hybrid image co-registration to display parameters utilized by the technologist.

There are five tools available in the **Toolbar** *(Figure 2.63)* on the SC Viewer screen:
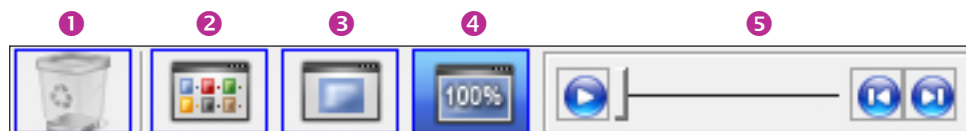
Figure 2.63: SC Viewer Toolbar

❶ **Delete Tool:** Allows deletion of any 4DM screen captures generated within the current session. Screen captures sent from other workstations, or from previous sessions, cannot be deleted using this button.

❷ **Thumbnail Display:** All screen captures displayed at a reduced size

❸ **Full Screen Display:** Fills the screen with a single screen capture

❹ **Original Resolution Display:** Displays the screen capture at its original resolution

❺ **MFSC Player Controls:** When a multi-frame screen capture is enlarged for display, an additional set of cine controls display. Play, pause, cine speed increase (right arrow), and cine speed decrease (left arrow) tools are available. If the MFSC is paused, the user can also click-and -drag the frame slider to display a particular frame of interest.

Predefined Screen Templates

These seven objects are used within standard 4DM screens and templates; or can be mix-and-matched to create custom, user-defined screens. The 4DM standard screens are consistent with common clinical workflows — specifically perfusion review; perfusion and quantification review; and function review. For each of these clinical workflows, a screen template exists which users can import when building custom screens. Refer to the table below to review 4DM-provided templates and the objects utilized within them:

Prior to building your own custom screen, review this table to see if we have already built a screen template that fits your needs and includes all of your desired objects.

4DM Template	4DM Object						
	Tomo	Splash	3SA	Polar Map	Scores	3Ds	LV Volume Curve
Images Only		●					
3SA Only			●				
Images+Tomos	●	●					
3SA+Tomos	●		●				
Images+Maps		●		●			
3SA+Maps			●	●			
Images+Scores		●		●	●		
3SA+Scores			●	●	●		
3D+Images*		●				●	●
3D+3SA*			●			●	●
3D Only*						●	
3D Splash*						●	
3SA Func			●	●	●		●
Splash Func*		●		●	●		●
MPI Summary		●		●	●	●	●
3SA MPI Summary			●	●	●	●	●

*Templates are INVIA-defined and non-editable

The SPECT cardiac imaging workflow uses these screens:

Tomo QA

MI Processing

Images

Images + Quant

Func + Quant

Dyssynchrony

MPI Summary

Corridor4DM provides each user with several options to create diagnostic workflows that maximize efficiency while providing accurately quantified data for interpretation. This chapter provides a sample 4DM Clinical Workflow Tutorial for the image review, quantification, and interpretation of SPECT Myocardial Perfusion Imaging (MPI).

| Quality Assurance | Qualitative Perfusion Review | Quantitative Perfusion Review | Quantitative Functional Review | SPECT MPI Study Interpretation |

Quality Assurance

Users should always ascertain the integrity of the study that has been provided for review prior to the interpretation process. 4DM has integrated Quality Assurance (QA) screens which enable users to assess study quality from within the software to save time and maximize efficiency.

The key QA screens utilized for SPECT MPI review are:

- Tomo QA
- MI Processing

Quality Assurance

Tomo QA

The **Tomo QA** screen *(Figure 3.1)* allows users to view the tomographic datasets to assess motion, counts, and gating information to assess overall study quality. Specific information consists of the following:

Users can right-click over the viewport cine controls on **Tomo QA** to set: **Cine Speed** and **Rocking Increments.**

Figure 3.1: *The Tomo QA screen with three datasets displayed. Top: Gated stress (with Gating Information). Middle: Ungated Stress. Bottom: Ungated rest*

- **NM Tomo Datasets**
  - Each Tomo dataset panel has a click-and-drag blue slice plane indicator that allows you to normalize the image to the counts in the heart by aligning it with the hottest pixel in the heart. This plane indicator also defines the plane for constructing the **Sinogram**. The white click-and-drag reference lines above and below the blue slice plane indicator can be used to check for patient motion during cine review of the tomogram and they also define the parameters for the Linogram.

- **Sinogram**
  - The **Sinogram** is a two-dimensional mapped representation of each one-dimensional frame acquired during a SPECT tomogram. It is useful as another option to visually assess each dataset for patient motion or shifting of the detectors between multi-detector systems. Reference lines identify the corresponding projection image and the location in the Linogram.

- **Linogram**
  - The Linogram is a summed representation of each frame that is acquired during a SPECT tomogram. It can be used to visually assess each dataset for vertical patient motion or shifting of the detectors between multi-detector systems. The Linogram image is zoomed to fill the display window. Reference lines identify the corresponding projection image and the location in the Sinogram.

- **Count Histogram**
  - The **Count Histogram** plots the summed counts per projection number so users can assess whether there were any significant count drop-offs during the acquisition which would indicate a poorly-gated dataset. The Count Histogram also provides the peak pixel activity (in cts) for the anterior projection. This data should be noted during the QA process because it can signify whether an acquisition is count-poor.

Figure 3.2: The Beat Histogram on the Tomo QA screen.

- **Beat Histogram**
  - The **Beat Histogram** *(Figure 3.2)* shows the length of time (in milliseconds) for each acquired heartbeat's R-R interval (yellow). The accepted R-R range is noted in blue. This is useful as a quick way to see if there was an unacceptable amount of rejected beats during a gated acquisition. The Beat Histogram is currently available only for Siemens-acquired gated datasets.

- **Gating Information** (for gated datasets only)
  - The **Gating Information** *(Figure 3.3)* provides further details such as the number of Accepted (Acc Beats) vs. Rejected Beats (Rej Beats), Average Heart Rate (HR) and HR Range (in bpm), and R-R Interval settings (in ms).

Figure 3.3: The Gating Information in the Dataset Information Panel

Count Histogram
Frames can be viewed three different ways: **All**, **Sum**, or **Individually**. Click on the **Frame slider** tool in the **Toolbar** to show **Frames: All** which plots all frames together on one graph. **Frames: Sum** adds all frame counts together. Click and drag the **Frame slider** while the selection is **Frames: All** to view the selected frame's counts.

- **Multiple Energy Windows (for multiple energy radiopharmaceuticals only)**
  - The Multiple Energy Window is active above the image viewport when datasets are launched into 4DM that contain multiple energy (in KeV) windows. The default display will be the primary energy window for the radiopharmaceutical and the drop down arrows will allow the user to select from the energy windows that are listed.

Once you have reviewed and noted any anomalies on the **Tomo QA** screen, proceed to the next QA step in our sample workflow, the **MI Processing** screen.

MI Processing

Upon launching a patient in Corridor4DM for the first time, the program automatically quantifies the study using 4DM default algorithm settings. The **MI Processing** screen *(Figure 3.4)* allows users to define LV dataset alignments, apical and basal limits, and LV centers on the VLA, SA, and HLA slices. Users should review all reconstructed datasets on the **MI Processing** screen.

<table>
<tr>
<td>

WARNING

The user should verify that the estimated LV contours are correct and track the myocardial walls. Inaccurate contours can result in incorrect computation of quantitative data, which can lead to misdiagnosis.

</td>
</tr>
</table>

<table>
<tr>
<td>

WARNING

The user should visually verify the processing limits-

- Heart Centering
- Basal and Apical Limits
- Volume Orientations

</td>
</tr>
</table>

Figure 3.4: MI Processing Screen with three datasets – gated stress, stress and rest – displays ❶ *Processing Splash Objects and* ❷ *Processing Polar Map Objects for each dataset by default. Click the* ❸ *LV Volume Curve tool to display the LV Volume Curve for gated studies.*

The user should confirm that the basal limits are consistent between datasets and that the 4DM LV surface generation algorithm has accurately identified the endo- and epicardial surfaces of the LV. These contours are used to calculate the following parameters:

▪ LVEF	▪ LV Volume Curve	▪ Perfusion Maps
▪ ED/ES Volumes	▪ Cardiac Mass	▪ Wall Motion and Thickening Maps
▪ Cardiac Output	▪ TID	▪ Contractility Maps

If the LV surface generated includes extra-cardiac activity, it is recommended that the user processes the images utilizing the Constraints Tool. Inclusion of extra-cardiac activity can lead to false impressions and image normalization.

Note that 4DM allows the valve plane definition to differ for volumetric estimates and the generation of polar maps. Adjustments to the basal sliders on the VLA images affect volumetric estimates (systolic, diastolic, TID). For volume estimates, the basal limit is typically placed at the end of the LV as seen on the anterior, lateral and inferior walls. For polar maps, the basal sliders on the HLA images are used to define the axial extent of the myocardium that is mapped to the polar maps where the axial location is typically chosen to be near the mid-membranous septum to minimize the inclusion of slices involving the outflow tract and the aortic valve. For the polar maps, there are three algorithm options that are available to automatically identify the location of the valve plane for perfusion studies *(Figure 3.5)*. The default algorithm is the Septal Wall Mid-Membranous Septum.

(4DM default)
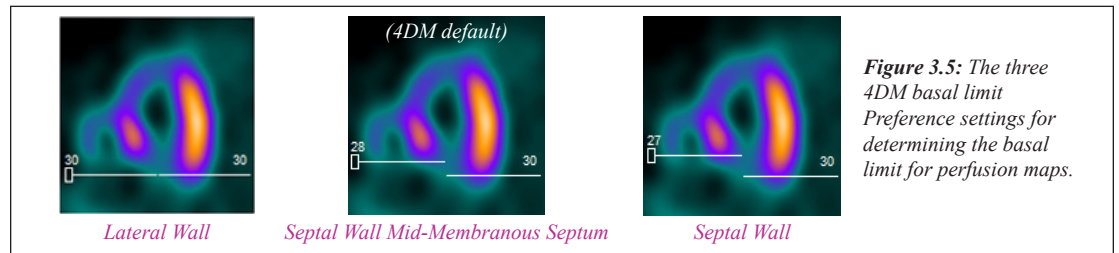
Figure 3.5: *The three 4DM basal limit Preference settings for determining the basal limit for perfusion maps.*
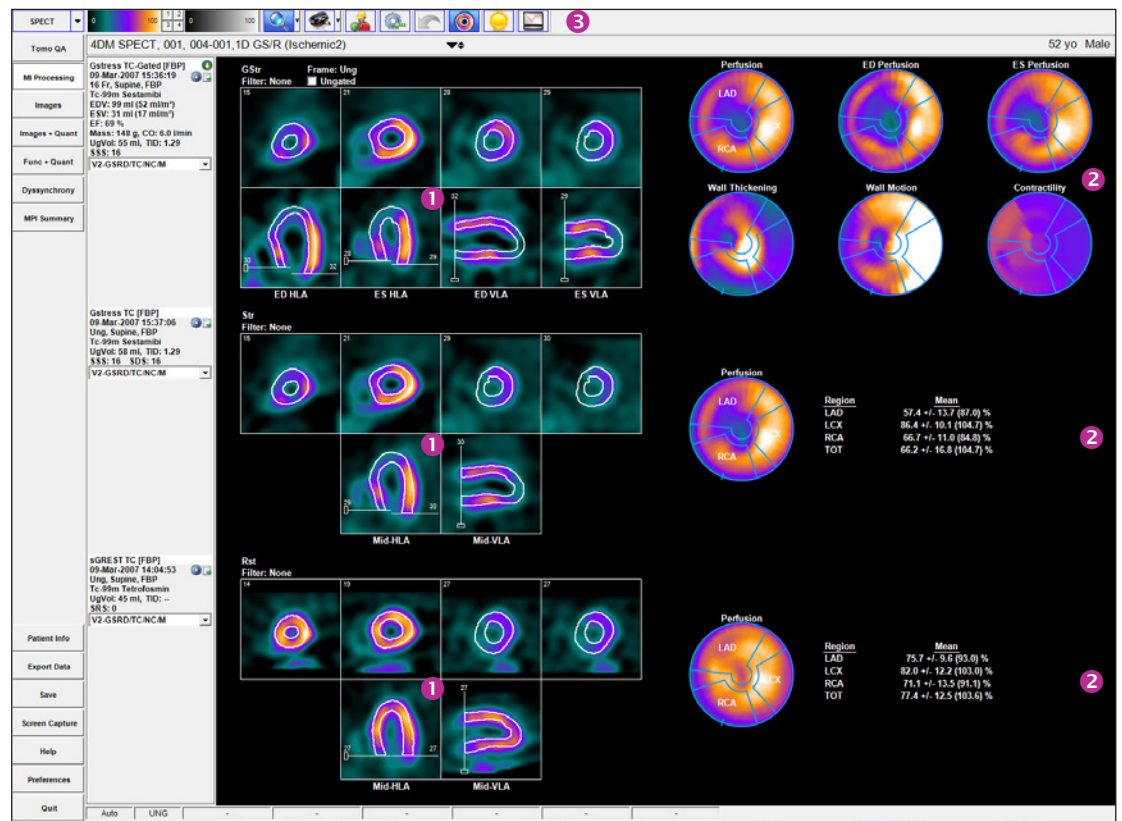
Lateral Wall   *Septal Wall Mid-Membranous Septum*   *Septal Wall*

Activating the **Contours** tool *(Figure 3.6)* applies white contour overlays on the endo- and epicardial surfaces of the LV myocardium for all datasets. If the contours properly track the myocardium and if no changes are necessary to the limits/positions, users can proceed to the Images screen to begin the perfusion review portion of the workflow.

Figure 3.6: *The Contours tool*

If contours do not track the myocardium due to poor orientation or centering of the left ventricle, high intensity extra-cardiac activity, or the dataset requires additional filtering, the study should be reprocessed by clicking the **Manual Processing** tool *(Figure 3.7)*. Centering, orientation and axial limits are adjusted using the sliders as shown in *(Figure 3.8)*.

Figure 3.7: *Manual Processing tool*

1	Proper positioning of the LV center aligns the crosshairs in the center of the ventricle.
2	Proper positioning of the apical and basal limits are at the center of the apical myocardium and the mitral valve plane.
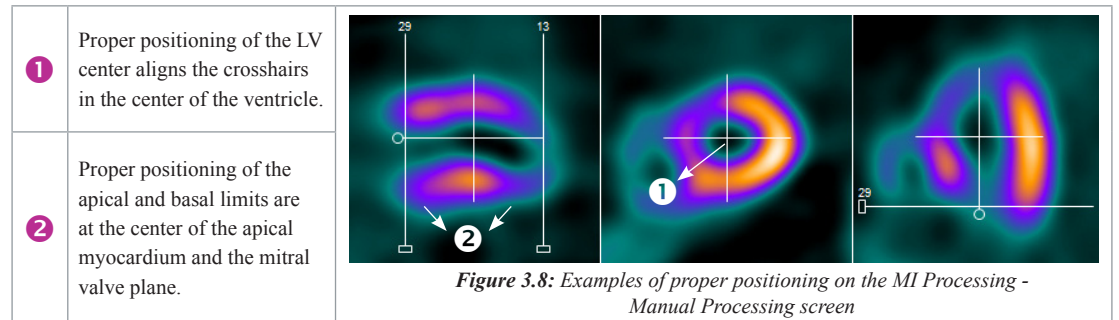
Figure 3.8: *Examples of proper positioning on the MI Processing - Manual Processing screen*

If the dataset has signficant extra-cardiac activity, click the **Constraints** tool *(Figure 3.9)* to define a constraint to prevent the contour from tracking the extra-cardiac activity rather than the ventricle. Once selected, modify the size and shape of the constraint limits on the SA slice by adjusting the red constraint handles located at three and six o'clock and centering the crosshairs *(Figure 3.10)*. Once adjustments to the LV center, orientation, and basal limit are complete, the user must click the **Process** tool *(Figure 3.11)* to generate the endo- and epicardial surfaces.

Figure 3.9: *Constraints tool*

VLA Slice   SA Slice   HLA Slice

Figure 3.10: *Constrains activated and properly positioned*

If the dataset needs to be processed from scratch (i.e. no initial estimates from 4DM), click the Reset tool *(Figure 3.12)* and then set the center, angulation, valve plane location and click the Process tool to reprocess.

It is important to visually confirm the contours and the basal limits used to quantify functional and perfusion estimates. Also verify that the basal positions are consistent between datasets and make adjustments if necessary. Once users are finished reviewing the MI Processing screen, the QA portion of the workflow is now complete.

***Figure 3.11:** Process tool*

***Figure 3.12:** Reset tool*

Qualitative Perfusion Review

The next step in our SPECT MPI workflow is to begin the image interpretation process. Perfusion abnormalities can be visually assessed by a review of the perfusion images for areas of pronounced decreased tracer uptake. Identification of differences in the myocardial tracer intensity between the stress and rest datasets is important for the assessment of tracer reversibility, a marker for myocardial ischemia. This task is most accurately accomplished by reviewing the ungated stress and rest images as slices, aligned one over the other, in the three cardiac planes: SA, HLA and VLA. In 4DM this layout is referred to as a **Splash** display. The 4DM **Images** screen was created specifically to accomplish this step in the clinical workflow.

Images

The **Images** screen represents the datasets as SA, HLA, and VLA **Splash Objects** *(Figure 3.13)*. Review and compare the tracer perfusion of all ungated datasets on this screen and note any areas of abnormal decreased tracer uptake. If dataset slices are not properly aligned to one another, left-click and drag on one slice in the dataset until it matches the desired slice directly above and/or below it. Once the qualitative perfusion review is complete, the next step in our SPECT MPI workflow is to assess the 4DM quantitative perfusion analysis.

The **Splash Objects** consist of viewing the reconstructed datasets in a slice-by-slice format in the following order: SA (Apex->Base), HLA (Post->Ant), and VLA (Sep->Lat). This layout is also commonly referred to as a **Splash** display.

To move all displayed datasets slices together at the same time, left-click and drag the **Dataset Slice** slider located above each **Splash Object**.
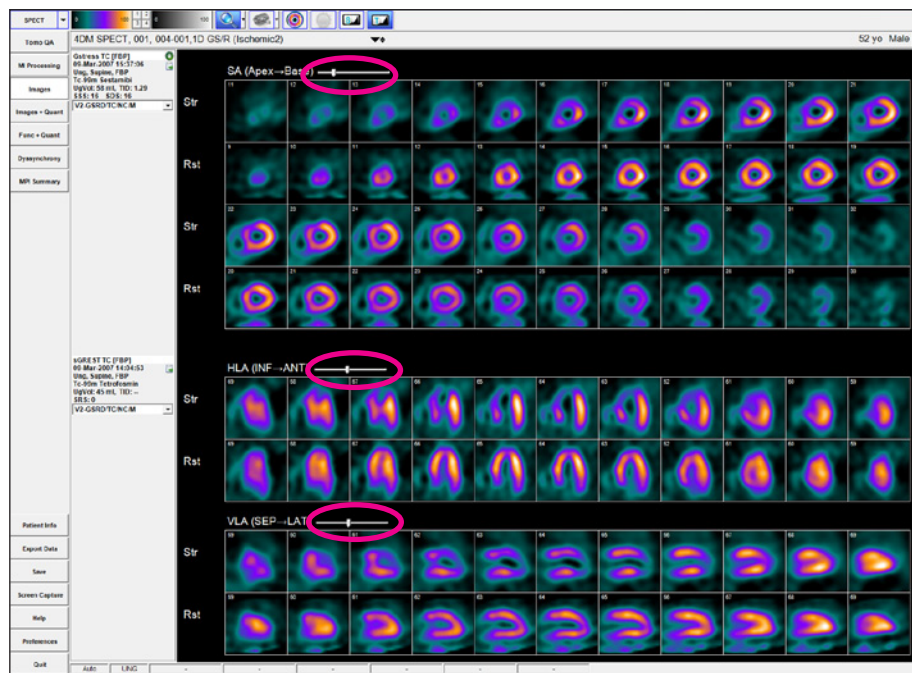
***Figure 3.13:** The Images screen with ungated stress and rest SA, HLA, and VLA Splash Objects displayed. The Dataset Slice Slider is circled in pink above each Splash Object.*

All 4DM screens support viewing up to four datasets. When the **Images+Quant** screen is loaded with four datasets, 4DM must compensate the viewing space by excluding the Comparison Polar map so that all four datasets fit.

4DM automatically calculates the semi-quantitative scores for the displayed datasets. Users can clear the scores and manually score the segments if desired by clicking the **Clear** tool in the **Toolbar**. Conversely, to reload the automatic scores, click the **Auto** tool.

Once your assessment is complete, right-click the **Patient Info** button to document your findings.

Quantitative Perfusion Review

In addition to the qualitative perfusion assessment, 4DM recommends utilizing the quantification data available to supplement visual perfusion findings. To quantify the perfusion information, 4DM automatically compares the currently displayed dataset(s) to a normal database that contains patients of the same gender who had normal studies utilizing a similar protocol and tracer. Two of the most clinically validated methods to quantitatively assess perfusion defect extent and severity are polar map comparisons and semi-quantitative scoring. The accuracy of the 4DM algorithms used for quantification provides users with important supplemental information that aids the clinician in the interpretation process by assigning extent and severity ratings to the perfusion defects in question. The **Images+Quant** screen provided within 4DM displays both the perfusion **3SA Object** and the supporting quantification information. 4DM recommends using this screen during quantitative perfusion review of SPECT MPI cases.

Images+Quant

The **Images+Quant** screen presents the SA, HLA, and VLA **3SA Objects** and displays perfusion polar maps with the supporting automatic semi-quantitative scores all on one screen *(Figure 3.14)*. 4DM displays the **Scores Objects** already calculated and users have the option to manually adjust them if desired. Within the **Images+Quant** screen users have access to several polar map menus in the **Toolbar**. This enables on-the-fly changes if different assessments are desired. After review of these screens is complete, the next step in our workflow is to review the functional data.
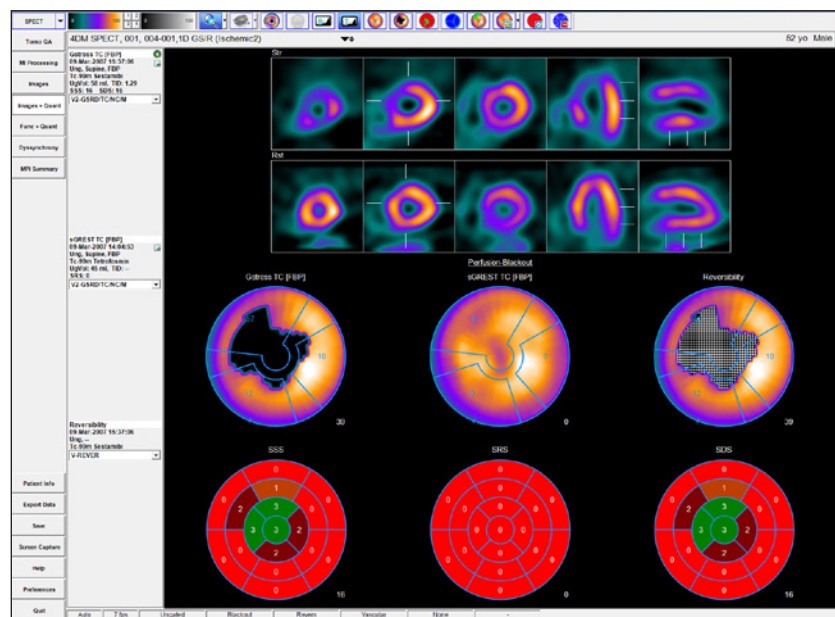
Figure 3.14: The Images+Quant screen utilizing the Defect Blackout reversibility Polar maps and correlating semi-quantitative scores.

Quantitative Functional Review

Functional quantitation refers to correlating the clinician's visual estimates of LV function with the following calculated parameters:

- LVEF
- ED/ES Volumes
- LV Volume Curve
- Cardiac Output

- TID
- Cardiac Mass
- Wall Motion
- Wall Thickening

To appropriately assess and report on these values, we recommend viewing the gated **Splash Object**, and **LV Volume Curve** in cine mode on the **Func+Quant** screen *(Figure 3.15)*.

Func+Quant

> Facilities that acquire 16-bin gated studies should assess the **LV Volume Curve** because it provides detailed systolic and diastolic functional information.

The Func+Quant Screen displays a gated 3SA Func layout for reviewing the Function of the gated datasets. When only one gated dataset is present, the LV Volume Curve is included to display LV Volume (in ml). The Temporal Filter tool allows the user to apply a filter for enhancing the image quality of the gated slices. The Polar Maps allow the user to view Wall Motion and Wall Thickening while visually comparing to the relative score calculations visible in the Scores Objects.

> Once your assessment is complete, right-click the **Patient Info** button to document your findings.
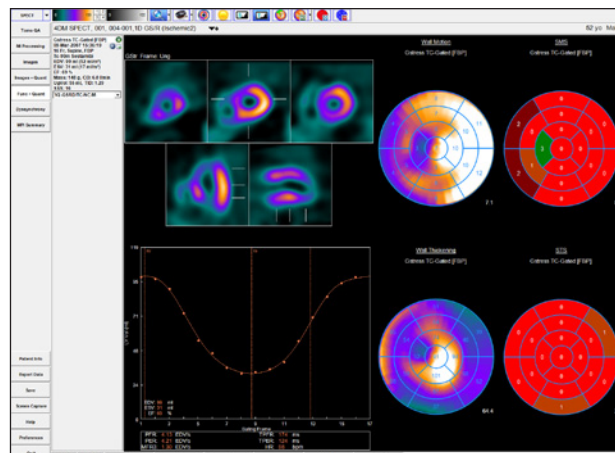
Figure 3.15: The Func+Quant screen with one gated dataset displayed.

Dyssynchrony

The **Dyssynchrony** screen was created for assessing the phases of contraction for the left ventricle *(Figure 3.16)*. Dyssynchrony is defined as delayed ventricular activation and contraction. Analysis of regional and global contraction patterns in the left ventricle can help identify those patients who may benefit from Cardiac Resynchronization Therapy (CRT). To accurately assess patients for dyssynchrony, physicians can use the following image displays to identify abnormalities in contractile function:
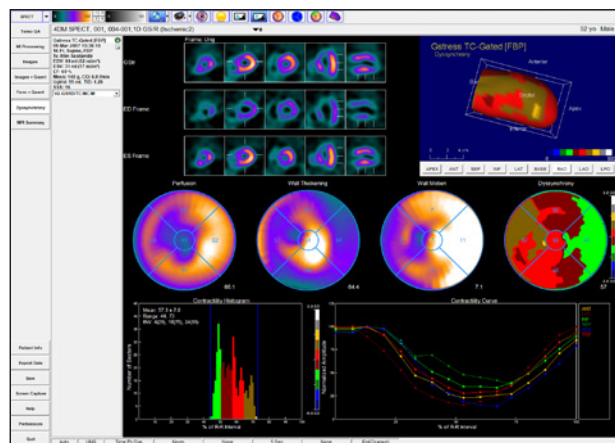
Figure 3.16: The Dyssynchrony screen was created for assessing the phases of contraction for the left ventricle.

- **Contractility Histogram:** Plots the time to peak contraction expressed as the percent of the R-R frame within the left ventricle. Vertical blue indicators signify the start and end points of contractility.

- **Contractility 2D and 3D Polar Maps** *(Figure 3.17)*: Choose between Time to Peak Thickening using First Harmonic Fit, Time to Peak Thickening, and Time to Peak Contractility.
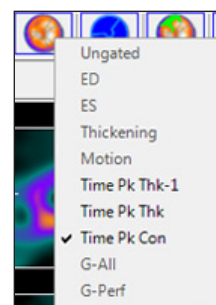
Figure 3.17:
Raw Map Menu

The **Dyssynchrony** screen also provides a 3SA Object with optional contours; Perfusion, Wall Thickening, and Wall Motion Polar Maps; and 3D Objects. The screen layout varies between one or two gated datasets. If two gated datasets are displayed, the Perfusion, Wall Thickening, and Wall Motion Polar Maps are omitted from the screen.

Interpretation of the SPECT MPI Study

MPI Summary

The **MPI Summary** screen is considered the 4DM standard review screen because it accomplishes the task of fitting all perfusion and functional data necessary for interpretation of the study onto one screen. The **MPI Summary** screen *(Figure 3.18)* supports all NM datasets and includes:

- **3SA Object**
- **Polar Map Object**
- **Scores Object**
- **3D Object**
- **LV Volume Curve**

4DM recommends displaying the **MPI Summary** screen when performing the final interpretation and exporting information to your report.
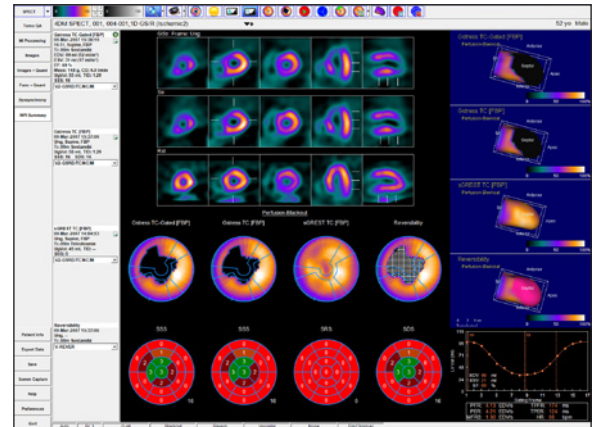
Figure 3.18: *The MPI Summary screen displaying gated stress, ungated stress and rest datasets and all perfusion and function information on one screen for quick review*

Conclusion

To quickly view a summary of the entire report, right-click **Patient Info** and select **Miscellaneous/ Summaries**.

This concludes your SPECT MPI Clinical Workflow Tutorial. Prior to exiting the program, users should save the 4DM result files. Technologists can transfer the saved results and study data to the interpreting physician for review. 4DM recognizes the most current saved result files, so if physicians make any changes to the saved study they should save the updated results.

The SPECT/CT Cardiac Imaging Workflow uses these screen:

Tomo QA
MI Processing
Fusion
Images
AC Images
Images + Quant
AC Images + Quant
Func + Quant
Dyssynchrony
MPI Summary
CT Viewer
Ca Scoring

Corridor4DM provides each user with a multitude of options to create diagnostic workflows that maximize efficiency while providing accurately quantified data for interpretation. This chapter provides a sample 4DM Clinical Workflow Tutorial for the image review, quantification, and interpretation of SPECT/CT MPI studies. The following SPECT/CT datasets can be launched into 4DM:

- Nuclear Medicine (NM) Tomo datasets:
  – Ungated Stress/Rest SPECT datasets
  – Gated-Stress/Rest SPECT datasets

- NM reconstructed Short-Axis (SA) datasets:
  – Uncorrected (NC) Stress/Rest
  – Attenuation-corrected (AC) Stress/Rest

- Sealed Source (SS) or Computed Tomography (CT) Attenuation Correction maps (μ-maps)

- CT Volumetric datasets

- Optional: Non-contrast low-dose CT for Calcium Scoring

- Optional: Cardiac CT Angiogram (CTA) with Extracted Coronary Vessels

Quality Assurance → Qualitative Perfusion Review → Quantitative Perfusion Review → Quantitative Functional Review → SPECT / CT MPI Study Interpretation

Quality Assurance

Quality Assurance

Users should always ascertain the integrity of the study that has been provided for review prior to beginning any processing or interpretation. 4DM has integrated Quality Assurance (QA) screens which enable users to assess study quality from within the software to save time and maximize efficiency. The key QA screens utilized for SPECT/CT MPI review are:

- Tomo QA
- MI Processing
- Fusion

Similar to the SPECT MPI workflow, users should begin the QA portion by reviewing the raw NM Tomo datasets on the **Tomo QA** screen.

Tomo QA

The **Tomo QA** screen *(Figure 4.1)* allows users to view the projection datasets to assess motion, counts, and gating information to assess overall study quality. Specific information consists of the following:

- **NM Tomo Datasets**
  – Each Tomo dataset panel has a click-and-drag blue slice plane indicator that allows you to normalize the image to the counts in the heart by aligning it with the hottest pixels in the

4DM users who utilize a sealed-source for attenuation correction (instead of CT) can follow this workflow tutorial but skip the **CT Viewer**, **Ca Scoring**, **CT Interp** and **Vessel Fusion** sections.
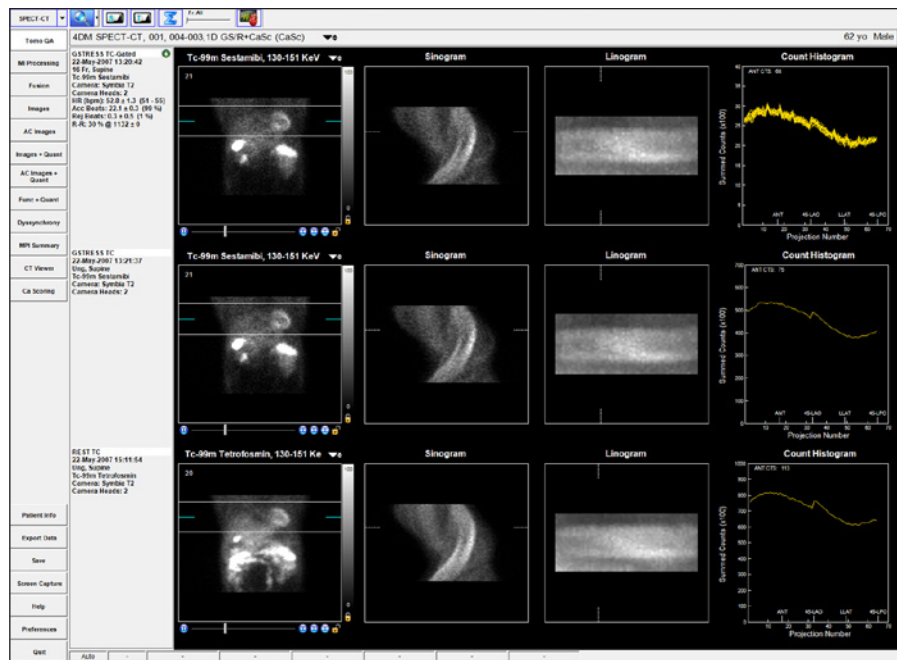
Figure 4.1: The Tomo QA screen with three datasets displayed. From top-to-bottom: Gated stress (with Gating Information), ungated stress, and ungated rest

heart. This plane indicator also defines the plane for constructing the **Sinogram**. The white click-and-drag reference lines above and below the blue slice plane indicator can be used to check for patient motion during cine review of the tomogram and they also define the parameters for the Linogram.

▪ **Sinogram**
– The **Sinogram** is a two-dimensional mapped representation of each one-dimensional frame acquired during a SPECT tomogram. It is useful as another quick way to visually assess each dataset for patient motion or shifting of the detectors for multi-detector systems. Reference lines identify the corresponding projection image and the location in the Linogram.

▪ **Linogram**
– The Linogram is a summed representation of each frame that is acquired during a SPECT tomogram. It can be used to visually assess each dataset for vertical patient motion or shifting of the detectors between multi-detector systems. The Linogram image is zoomed to fill the display window. Reference lines identify the corresponding projection image and the location in the Sinogram.

▪ **Count Histogram**
– The **Count Histogram** plots the summed counts per projection number so users can assess whether there were any significant count drop-offs during the acquisition which would indicate a poorly-gated dataset. The Count Histogram also provides the peak pixel activity (in cts) for the anterior projection. This data should be noted during the QA process because it can signify whether an acquisition is count-poor.

Figure 4.2: The Beat Histogram on the Tomo QA screen

▪ **Beat Histogram**
– The **Beat Histogram** *(Figure 4.2)* shows the length of

time (in milliseconds) for each acquired heartbeat's R-R interval (yellow). The accepted R-R range is noted in blue. This is useful as a quick way to see if there was an unacceptable amount of rejected beats during a gated acquisition. The Beat Histogram is currently available only for Siemens-acquired gated datasets.


```
GSTRESS TC-Gated              ⊙
22-May-2007 13:20:42
16 Fr, Supine
Tc-99m Sestamibi
Camera: Symbia T2
Camera Heads: 2
HR (bpm): 52.3 ± 1.4 (50 - 55)
Acc Beats: 22.1 ± 0.3 (99 %)
Rej Beats: 1.1 ± 0.4 (1 %)
R-R: 30 % @ 1132 ± 0
```

Figure 4.3: The Gating Information in the Dataset Information Panel

▪ **Gating Information** (for each applicable NM dataset).
  – The **Gating Information** *(Figure 4.3)* gives further details such as the number of Accepted (Acc Beats) vs. Rejected Beats (Rej Beats), Average Heart Rate (HR) and HR Range (in bpm), and R-R frame settings (in ms).

▪ **Multiple Energy Windows** (for multiple energy radiopharmaceuticals only)
  – The Multiple Energy Window is active above the image viewport when datasets are launched into 4DM that contain multiple energy (in KeV) windows. The default display will be the primary energy window for the radiopharmaceutical and the drop down arrows will allow the user to select from the energy windows that are listed.

Once you have reviewed the NM Tomo datasets on the **Tomo QA** screen, proceed to the next QA step in our sample workflow, the **MI Processing** screen.

MI Processing

Upon launching a patient in Corridor4DM for the first time, the program automatically quantifies the study using 4DM default algorithm settings. The **MI Processing screen** allows users to define LV dataset alignments, apical and basal limits, and LV centers on the VLA, SA, and HLA slices. Users should review all reconstructed datasets on the **MI Processing** screen *(Figure 4.4)*.

Figure 4.4: The MI Processing screen with three datasets – gated stress, stress, and rest – displays ❶ Processing Splash Objects and ❷ Processing Polar Map Objects for each dataset by default. Click the ❸ LV Volume Curve tool to display the LV Volume Curve for gated studies.

The user should confirm that the basal limits are consistent between datasets and that the 4DM LV surface generation algorithm has accurately identified the endo- and epicardial surfaces of the LV. These contours are used to calculate the following parameters:

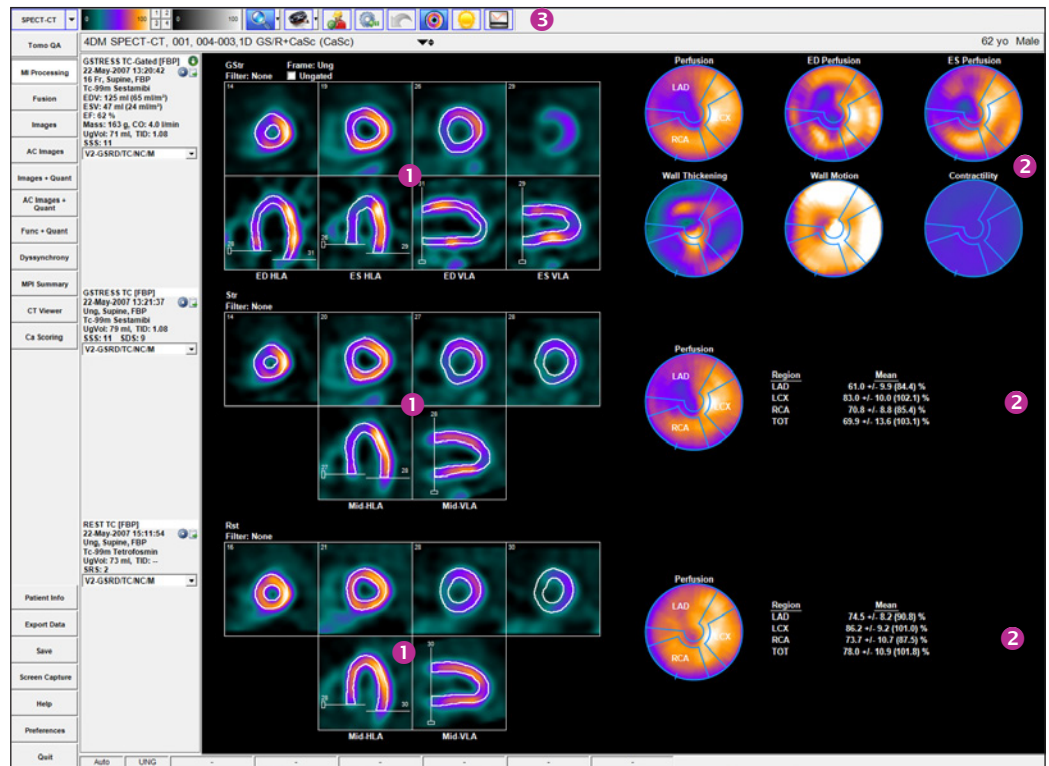|		
▪ LVEF	▪ LV Volume Curve	▪ Perfusion Maps
▪ ED/ES Volumes	▪ Cardiac Mass	▪ Wall Motion and Thickening Maps
▪ Cardiac Output	▪ TID	▪ Contractility Maps

Note that 4DM allows the valve plane definition to differ for volumetric estimates and the generation of polar maps. Adjustments to the basal sliders on the VLA images affect volumetric estimates (systolic, diastolic, TID). For volume estimates, the basal limit is typically placed at the end of the LV as seen on the anterior, lateral and inferior walls. For polar maps, the basal sliders on the HLA images are used to define the axial extent of the myocardium that is mapped to the polar maps where the axial location is typically chosen to be near the mid-membranous septum to minimize the inclusion of slices involving the outflow tract and the aortic valve. For the polar maps, there are three algorithm options that are available to automatically identify the location of the valve plane for perfusion studies *(Figure 4.5)*. The default algorithm is the Septal Wall Mid-Membranous Septum.
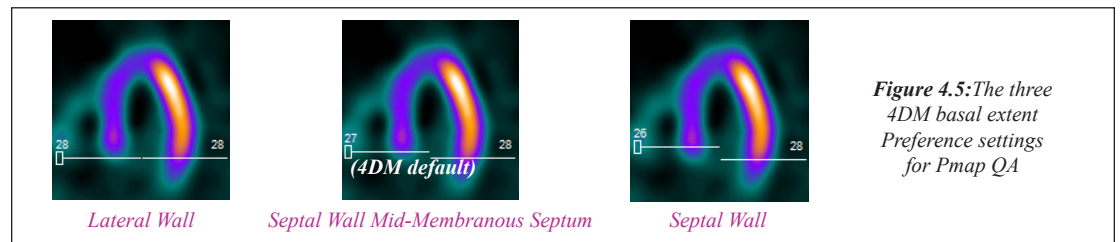
Figure 4.5: The three 4DM basal extent Preference settings for Pmap QA

Lateral Wall   *Septal Wall Mid-Membranous Septum*   *Septal Wall*

Activating the **Contours** tool *(Figure 4.6)* applies white contour overlays on the endo- and epicardial surfaces of the LV myocardium for all datasets. If the contours properly track the myocardium and if no changes are necessary to the limits/positions, users can proceed to the Images screen to begin the perfusion review portion of the workflow.

Figure 4.6: Contours tool

If contours do not track the myocardium due to poor orientation or centering of the left ventricle, high intensity extra-cardiac activity, or the dataset requires additional filtering, the study should be reprocessed by clicking the **Manual Processing** tool *(Figure 4.7)*. Centering, orientation and axial limits are adjusted using the sliders as shown in *(Figure 4.8)*.

Figure 4.7: Manual Processing tool

1	Proper positioning of the LV center aligns the crosshairs in the center of the ventricle.	
2	Proper positioning of the apical and basal limits are at the center of the apical myocardium and the mitral valve plane.	
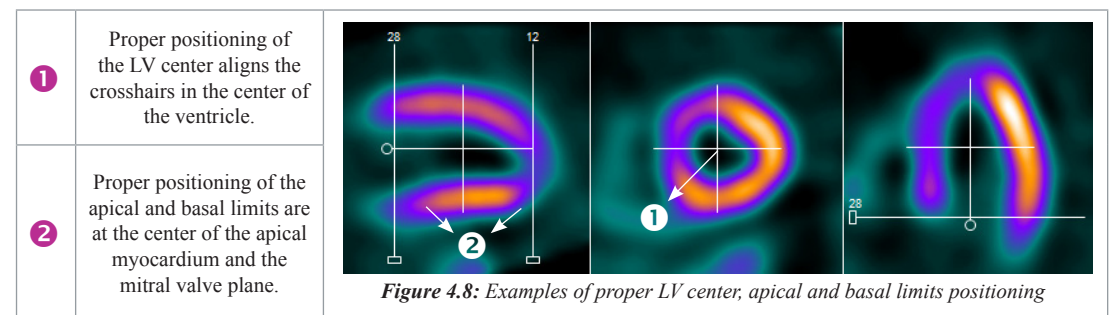
Figure 4.8: Examples of proper LV center, apical and basal limits positioning

If the dataset has signficant extra-cardiac activity, click the **Constraints** tool *(Figure 4.9)* to define a constraint to prevent the contour from tracking the extra-cardiac activity rather than the ventricle. Once selected, modify the size and shape of the constraint limits on the SA slice by adjusting the red constraint handles located

Figure 4.9: Constraints tool

Sidebar notes:

If the LV surface generated includes extra-cardiac activity, it is recommended that the user processes the images utilizing the Constraints Tool. Inclusion of extra-cardiac activity can lead to false impressions and image normalization.

4DM-provided normals databases were generated using the Septal Wall Mid-Membranous Septum basal extent placement. To provide consistency, the 4DM default basal extent setting is the same.

If only endocardial surfaces are generated, the incorrect radiopharmaceutical was assigned to the dataset. Check the Special File Strings by clicking on the Dataset Matching Strings button within the Preferences menu. To learn more about editing matching strings, go to User Preferences.

at three and six o'clock and centering the crosshairs *(Figure 4.10)*. Once adjustments to the LV center, orientation, and basal limit are complete, the user must click the **Process** tool *(Figure 4.11)* to generate the endo- and epicardial surfaces.
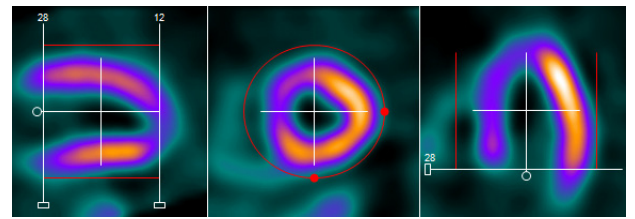
Figure 4.10: Constraints activated and properly positioned

If the dataset needs to be processed from scratch (i.e. no initial estimates from 4DM), click the Reset tool *(Figure 4.12)* and then set the center, angulation, valve plane location and click the Process tool to reprocess.

Figure 4.11:
Process tool

Figure 4.12:
Reset tool

It is important to visually confirm the contours and the basal limits used to quantify functional and perfusion estimates. Also verify that the basal positions are consistent between datasets and make adjustments if necessary. Once users are finished reviewing the MI Processing screen, the QA portion of the workflow is now complete.

Fusion

4DM has integrated the **Fusion** screen *(Figure 4.13)* as part of the QA process to accommodate the evolution of hybrid imaging. In addition to performing the standard NM processing for MPI datasets, technologists and physicians are now tasked with verifying that the reconstructed NM dataset and the attenuation map are properly co-registered.
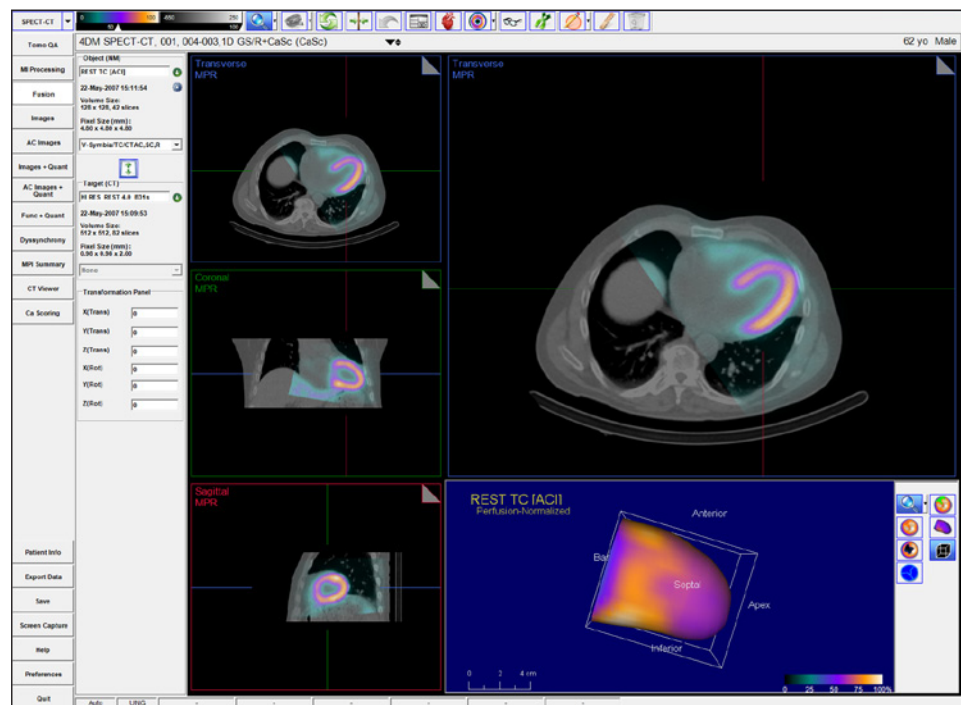
Figure 4.13: *The NM AC-Rst data as the Object Volume and the CT as the Target Volume.*
The three image panels are set to view the three orthogonal planes in Transverse space orientation.

> **WARNING**
> When viewing NM data fused to CT data on the Fusion screen, verify they represent the same portion of the protocol (e.g., Stress NM to Stress CT).

> The **Object Volume** is the overlay, or top image. The **Target Volume** is the base, or bottom image. The **Object Volume** can be repositioned, while the **Target Volume** is stationary.

4DM can be configured to auto-match the AC-NM dataset as the **Object Volume** and the attenuation map as the **Target Volume**. Use the Object Volume and Target Volume menus provided to select different datasets, if desired *(Figure 4.14)*. To switch the Object and Target Volume datasets, click the **Swap**

Datasets tool *(Figure 4.15)*. Change the Orientation of the images by clicking the **Orientation** tool *(Figure 4.16)*.

Dataset Description	Modality	Acquisition Date/Time	Series Date/Time
REST TC [ACI]	NM	22-May-2007 15:11:54	22-May-2007 15:23:57
REST TC [FBP]	NM	22-May-2007 15:11:54	22-May-2007 15:23:31
GSTRESS TC [FBP]	NM	22-May-2007 13:21:37	22-May-2007 13:42:47
GSTRESS TC [ACI]	NM	22-May-2007 13:21:37	22-May-2007 13:42:47
GSTRESS TC-Gated [FBP]	NM	22-May-2007 13:20:42	22-May-2007 13:42:59
HI RES REST 4.0 B31s	CT	22-May-2007 15:09:53	22-May-2007 15:09:57
CaScore 3.0 B35e 55%	CT	22-May-2007 13:41:09	22-May-2007 13:41:34
HIRES ABD 4.0 B30s STRESS	CT	22-May-2007 13:14:08	22-May-2007 13:14:12

Figure 4.14: The Object/Target menu in the Fusion screen

Figure 4.15:
Swap Datasets tool

Figure 4.16:
Orientation tool

The Fusion screen displays the fused Object and Target volumes in three orthogonal views (Transverse, Coronal, and Sagittal) along the left side of the image window. On the right, a large panel displays a fused transverse image with a configurable display object below. To change the view in the large panel, double-click one of the three orthogonal images on the left.

The **Dataset Layout** tool *(Figure 4.17)* provides options for different layouts of the Fusion screen: four panel with 3D Object, four panel with Slices, and a nine panel display. The four panel with 3D object is used to view the co-registration of extracted CTA coronary vessels or 4DM-quantified coronary calcium deposits. The four panel with Slice object displays transverse Target and Object slices. The nine panel layout displays the Object, Target, and fused Object/Target volumes – each in a three orthogonal view.

Figure 4.17:
Dataset Layout Selector tool

To help verify the co-registration of two datasets, the Fusion screen provides enhanced interactive mouse controls. A **Dual Colorbar** with an **Alpha-Blending tool** *(Figure 4.18)* is located below the left object colorbar. Slide the alpha-blending tool to adjust the transparency of the Object volume.
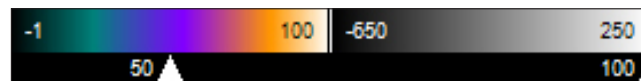
Figure 4.18: Dual Colorbar with Alpha Blending tool

If the datasets are misaligned, 4DM provides several correction tools within the Fusion screen to aide users during the QA process:

- **Coarse and Fine adjustment alignment tools** for image panning and rotation are provided when the mouse cursor is hovered over each image panel *(Figure 4.19)*.

- The **Transformation Panel** provides the user options for further adjustment tools on the Fusion screen for rotation and translation in the X, Y, and Z planes for each image panel.

The following interactive display tools are available within the Fusion screen:

- Each image panel has colored **Slice Plane Indicators** which have two main purposes:
  – Position them to triangulate over an area of interest. The slice plane colors provided in each image panel signify which plane they correspond to.
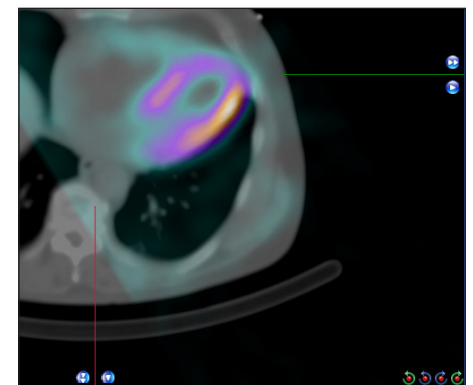
Figure 4.19: A zoomed in view of the Coarse and Fine adjustment tools available on the Fusion screen

To make manual **Pan** adjustments, place the mouse cursor in the inner one-third of the image panel. The cursor will change to a hand icon, which allows you to Pan the image by clicking-and-dragging the **Object Volume**.

To make manual **Rotation** adjustments, place the cursor on the outer two-thirds of the image panel. The mouse cursor will change to a circle with double arrows which allows you to left-click and rotate the **Object Volume**.

When **Cardiac Orientation** is selected the three **Fusion** screen viewport names change from Transverse to SA; Coronal to HLA; and Sagittal to VLA.

– Click-and-drag the Slice Plane Indicators to quickly scroll through datasets.

- To scroll slowly through individual image slices, click on the **Dog-ear** tool in the top right corner of each image panel.

- Right-click on the MPR or MIP label *(Figure 4.20)* in the top left corner of an image panel to change settings for MPR/MIP thickness.

Figure 4.20: *Exmaple of MPR Label location*

- Click the **Contours** tool *(Figure 4.21)* to display the endo- and epicardial LV surfaces by selecting Target Contours, Object Contours, or Target and Object Contours for processed NM cardiac datasets.

- Draw elliptical, freehand, rectangular, or polygon ROI's by selecting one from the **ROI Menu** tool *(Figure 4.22)*.

- Draw straight-line measurements and automatically display the length for each (in mm) when the **Ruler** tool *(Figure 4.23)* is turned on.

- Delete any ROI or ruler measurements by selecting the element and clicking on the Delete tool in the Toolbar.

Figure 4.21: *Contours tool*

Figure 4.22: *ROI menu*

Figure 4.23: *Ruler tool*

Users should verify the co-registration for both the Stress-AC and Rest-AC datasets with the corresponding Stress and Rest attenuation maps on the Fusion screen before continuing to the review portions of this SPECT/CT MPI workflow.
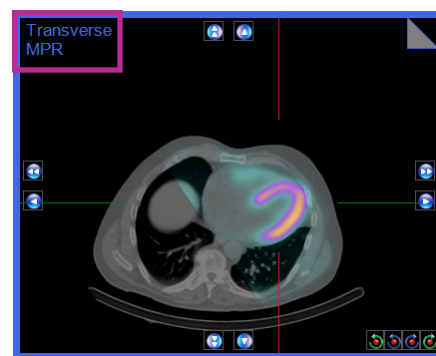
Qualitative Perfusion Review

The next step in our SPECT/CT MPI workflow is to begin the image interpretation process. Perfusion abnormalities can be visually assessed by a review of the perfusion images for areas of pronounced decreased tracer uptake. Identification of differences in the myocardial tracer intensity between the stress and rest datasets is important for the assessment of tracer reversibility, a marker for myocardial ischemia.This task is most accurately accomplished by reviewing the ungated NC Str/Rst and AC Str/Rst as slices, aligned one over the other, in the three cardiac planes: SA, HLA and VLA. In 4DM this layout is referred to as **Splash Object** display. The 4DM **Images** screen was created specifically to accomplish this step in the clinical workflow and allows for all four datasets to be reviewed on one screen.

Images

The **Images** and **AC Images** screens present the datasets as SA, HLA, and VLA **Splash Objects** *(Figure 4.24)*. Review and compare the tracer perfusion of all ungated NC and AC Stress and
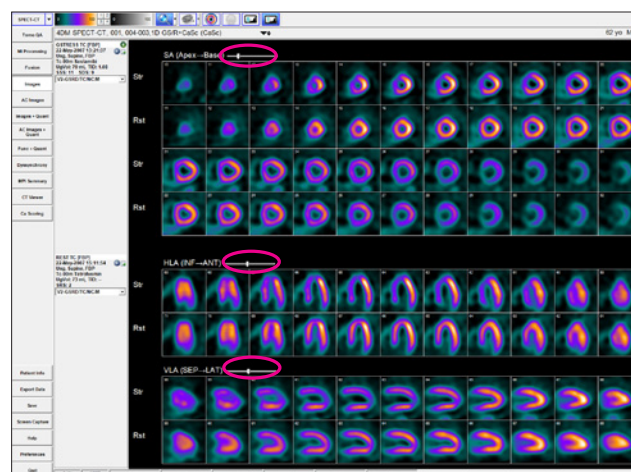

Figure 4.24: *Ungated datasets can be viewed together on the Images screens to check for differences between the NC and AC datasets. The Dataset Slice slider is circled in pink above each Splash Object.*

To move all displayed datasets slices together at the same time, left-click and drag the **Dataset Slice** slider located above each **Splash Object**.

Rest datasets on these screens to note any areas of abnormal decreased tracer uptake. If dataset slices are not properly aligned to one another, left-click and drag on one slice in the dataset until it matches the desired slice directly above and/or below it. Once the qualitative perfusion review is complete, the next step in our SPECT/CT MPI workflow is to assess the 4DM quantitative perfusion analysis.

Quantitative Perfusion Review

In addition to the qualitative perfusion assessment, 4DM recommends utilizing the quantification data available to supplement visual perfusion findings. To quantify the perfusion information 4DM automatically compares the currently displayed datasets to a normal database that contains patients of the same gender who had normal studies utilizing a similar protocol and tracer. Two of the most clinically validated methods to quantitatively assess perfusion defect extent and severity are polar map comparisons and semi-quantitative scoring. The accuracy of the 4DM algorithms used for quantification provide users with important supplemental information that aids the clinician in the interpretation process by assigning extent and severity ratings to the perfusion defects in question. The **Images+Quant** screens provided within 4DM display both the perfusion **Splash Objects** and the supporting quantification information. 4DM recommends using these screens during quantitative perfusion review of SPECT/CT MPI cases.

WARNING
The user must verify that the Normals Database is compatible with the dataset being reviewed to ensure correct computation of quantitative data.

Images+Quant

The **Images+Quant** and **AC Images+Quant** screens present the SA, HLA, and VLA **Splash Objects** in addition to providing perfusion polar maps with the supporting automatic semi-quantitative scores all on one screen. 4DM displays the **Scores Objects** already calculated and users have the option to manually adjust them if desired. Within the **Images+Quant** screen users have access to several polar map menus in the **Toolbar.** This enables on-the-fly changes if different assessments are desired.

4DM automatically calculates the semi-quantitative scores for the displayed datasets. Users can clear the scores and manually score the segments if desired by clicking the **Clear** tool in the **Toolbar**. Conversely, to reload the automatic scores, click the **Auto** tool.

It is recommended to view the **Images+Quant** screens with two datasets in order to view the reversibility polar map comparison. 4DM automatically selects the ungated NC Str/Rst option from the **Dataset Selector** menu in the **Toolbar**. Next, select the **AC Images+Quant** screen from the **Workflow Screens**. View both the **Images+Quant** *(Figure 4.25)* and **AC Images+Quant** *(Figure 4.26)* screens to help identify artifacts due to soft tissue photon attenuation (e.g., diaphragm and breast). After review of these screens is complete, the next step in our workflow is to review the functional data.

Once your assessment is complete, right-click the **Patient Info** button to document your findings.
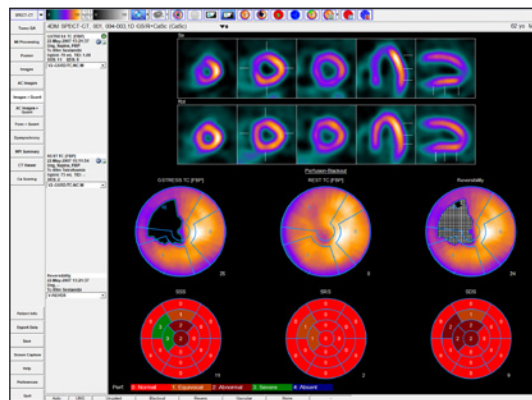

Figure 4.25: 4DM recommends viewing the Images+Quant screen with two datasets
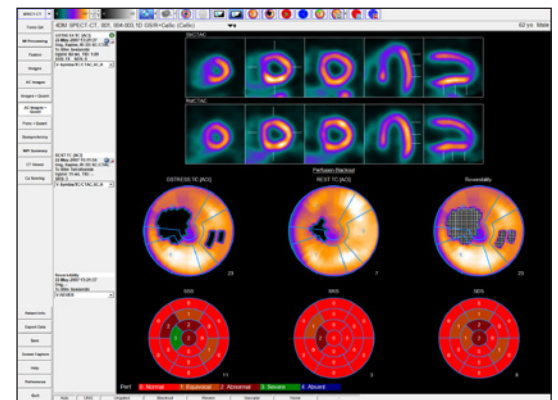

Figure 4.26: The AC Images+Quant screen displaying AC Str/AC Rst datasets

Quantitative Functional Review

Functional quantitation refers to correlating the clinician's visual estimates of LV function with the following calculated parameters:

- LVEF
- ED/ES Volumes
- LV Volume Curve

- Cardiac Output
- TID
- Cardiac Mass

- Wall Motion
- Wall Thickening

To appropriately assess and report on these values, we recommend viewing the **Splash Object** and the **LV Volume Curve** in cine mode on the **Func+Quant** screen *(Figure 4.27)*.

Func+Quant

The Func+Quant Screen displays a gated 3SA Func layout for reviewing the Function of the gated datasets. When only one gated dataset is present, the LV Volume Curve is included to display LV Volume (in ml). The Temporal Filter tool allows the user to apply a filter for enhancing the image quality of the gated slices. The Polar Maps allow the user to view Wall Motion and Wall Thickening while visually comparing to the relative score calculations visible in the Scores Objects.
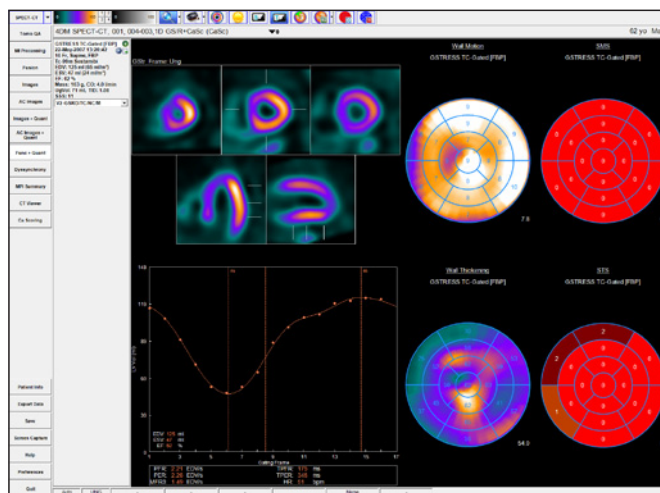

Figure 4.27: The Func+Quant screen with one gated dataset displayed

Dyssynchrony

The **Dyssynchrony** screen was created for assessing the phases of contraction for the left ventricle *(Figure 4.28)*. Dyssynchrony is defined as delayed ventricular activation and contraction. Analysis of regional and global contraction patterns in the left ventricle can help identify those patients who may benefit from Cardiac Resynchronization Therapy (CRT). To accurately assess patients for dyssynchrony, physicians can use the following image displays to identify abnormalities in contractile function:
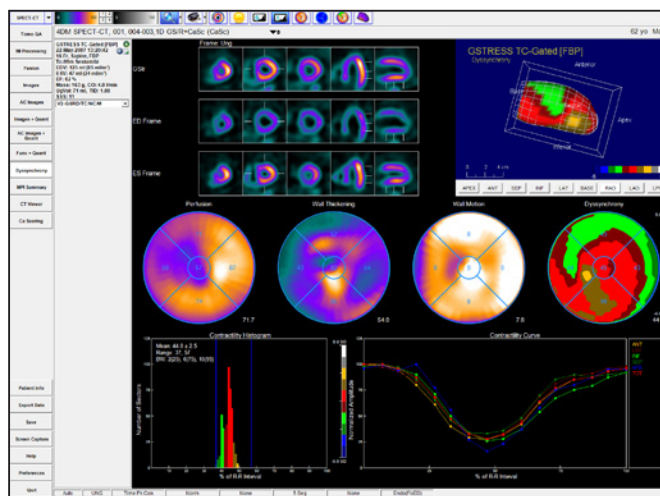
Figure 4.28: The Dyssynchrony screen was created for assessing the phases of contraction for the left ventricle.

- **Contractility Histogram:**
  Plots the time to peak contraction expressed as the percent of the R-R frame within the left ventricle. Vertical blue indicators signify the start and end points of contractility.

- **Contractility 2D and 3D Polar Maps** *(Figure 4.29)***:** Choose between Time to Peak Thickening using First Harmonic Fit, Time to Peak Thickening, and Time to Peak Contractility.

The **Dyssynchrony** screen also provides a 3SA Object with optional contours; Perfusion, Wall Thickening, and Wall Motion Polar Maps; and 3D Objects. The

Figure 4.29: The Raw Map menu

Once your assessment is complete, right-click the **Patient Info** button to document your findings.

screen layout varies between one or two gated datasets. If two gated datasets are displayed, the Perfusion, Wall Thickening, and Wall Motion Polar Maps are omitted from the screen.

Interpretation of the SPECT/CT MPI Study
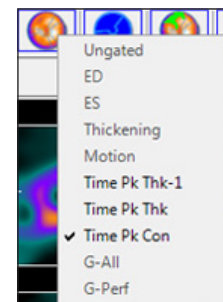
MPI Summary

The **MPI Summary** screen *(Figure 4.30)* is the 4DM standard NM review screen because it accomplishes the task of fitting all perfusion and functional data necessary for interpretation of the study onto one screen. It supports all NM datasets and includes:

- 3SA Object
- Polar Map Object
- Scores Object
- 3D Object
- LV Volume Curve

4DM recommends displaying the **MPI Summary** screen when performing the final interpretation and exporting information to your report.
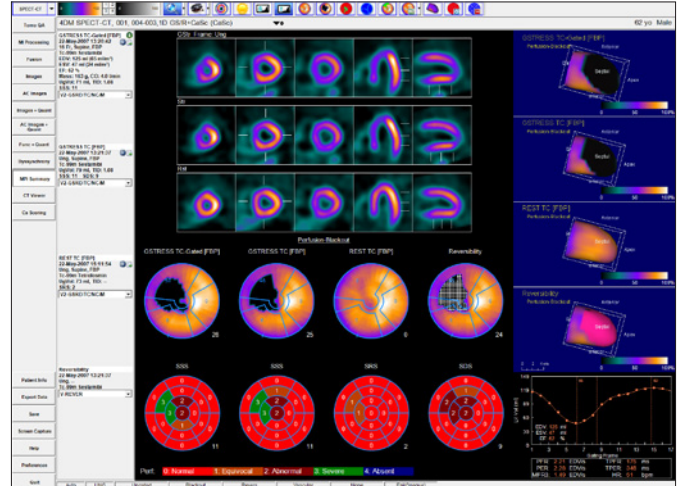

Figure 4.30: *The MPI Summary screen*

CT Viewer

Reporting incidental CT findings for SPECT/CT studies is recommended. 4DM includes the **CT Viewer** screen so that users can easily accomplish this task within the program *(Figure 4.31)*. Use this screen to review both contrast and non-contrast CT studies. 4DM supports Gated CT datasets which can be reviewed from this screen by using the cine tool. The following customization tools have been implemented within the **CT Viewer** screen to assist users during the CT review and interpretation process:

Figure 4.31: *The CT Viewer screen with the Thin MIP button selected. The large image display panel is highlighted in blue to note it is the selected panel.*

- **Select** the correct CT dataset (if multiple CT's were acquired) from the **Dataset Selector** menu.

- **Change** the HU windowing by right-clicking on the **CT Colorbar** that is provided in the **Toolbar** *(Figure 4.32)*. The left colorbar controls the MPR image panels and the right colorbar controls the MIP/Thin MIP image panels.

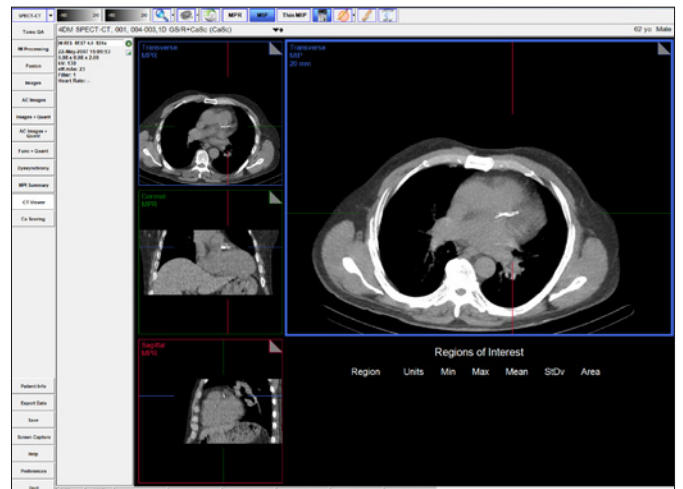- **Magnify** the image by using the **Magnification** slider.

- **Reset** the images back to the 4DM default by selecting the **Reset** tool.

- **Switch** any one or all of the four image panel types to MPR, MIP, or Thin MIP by selecting the image panel and then clicking on the **MPR**, **MIP**, or **Thin MIP** button.

- **Cine** the Gated CT dataset by selecting the **Cine** tool.

The following **CT Viewer** tools are located in the **Toolbar** to aide users in the assessment of incidental findings on the CT scan:

- **Draw** elliptical, rectangular, or freehand ROI's by selecting the ROI type from the ROI menu *(Figure 4.33)*.

- **Display** the information for any ROI's that have been drawn by clicking on the **Table** tool.

- **Draw** straight-line measurements and automatically display the length (in mm) for each with the **Ruler** tool.

- **Delete** any ROI's or ruler measurements by selecting the element and clicking on the **Delete** tool in the **Toolbar**.

Once the analysis of the CT images from within the **CT Viewer** screen is complete and incidental findings have been recorded, the basic SPECT/CT workflow is finished. 4DM users that incorporate additional CT scans into their SPECT/CT MPI protocol (e.g., Calcium Scoring CT's and/or CTA's) should continue this workflow tutorial to include the 4DM **Ca Scoring** and **Conclusion** sections.

Figure 4.32: The CT Viewer with the MIP colorbar HU window changed to the Lung option to assess the lung structures for any incidental findings.
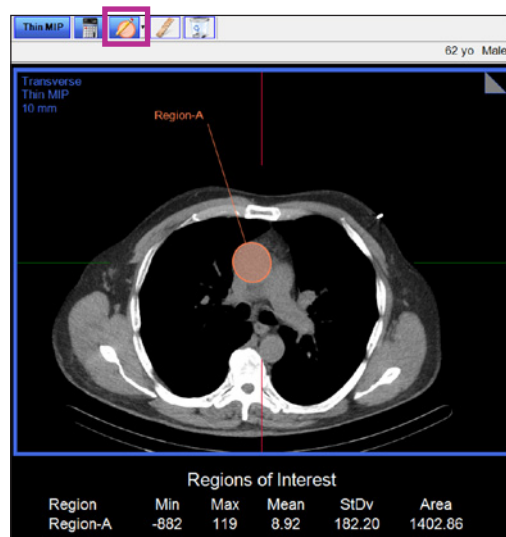
Figure 4.33: The CT Viewer with the Table and ROI tools selected. The ROI information immediately updates to the Regions of Interest Table below the large image panel.

Ca Scoring

4DM provides quantification and review of coronary artery calcium deposits from within the **Ca Scoring** screen. 4DM strongly recommends that physicians review the calcium scores calculated within this screen. Upon display of the **Ca Scoring** screen, users will note that the image panels and layout are similar to the **CT Viewer** screen. All screen controls function the same with the exception of the **Result Table** tool *(Figure 4.34)* and the **ROI** tool *(Figure 4.35)*. Images displayed are based on slice thickness. Additionally, the **Highlight Calcium** tool *(Figure 4.36)* and **Delete Calcium** tool *(Figure 4.37)* are tools specific to the **Ca Scoring** screen. The status
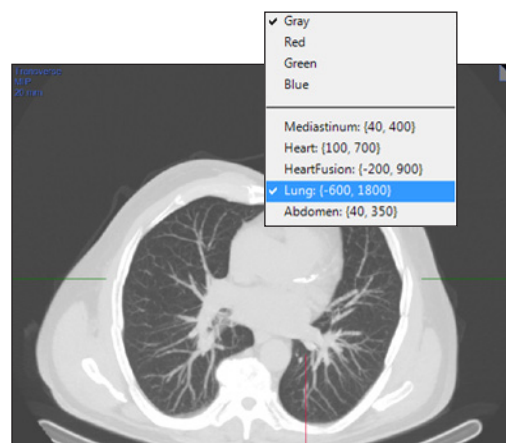

Figure 4.34: The Result Table tool

Figure 4.35: The ROI tool

Figure 4.36: The Highlight Calcium tool

bar located at the bottom of the screen displays the **HU threshold** preference setting used to identify calcifications. The HU threshold utilized during quantification is displayed within the lower left corner of the image display. The **Processing Options** tool on the **Ca Scoring** screen allows the user to adjust HU thresholds and the Region Growing Limit *(Figure 4.38)*.

Figure 4.37: The Delete Calcium tool

Figure 4.38: The Processing Options tool

Activating the **Result Table** tool within the **Ca Scoring** screen provides users with the following information:

- **Vessel** name buttons
  - Lists the four main coronary vessels, each as its own color-coded button
  - Click on the **Vessel Name** to activate the corresponding color to be manually assigned to areas of coronary calcium deposits.

- **Lesions**
  - Automatically calculated as the number of calcified lesions within the corresponding coronary vessel after a volume has been manually assigned.

- **(mm3)**
  - The total volume of all calcified lesions within the corresponding coronary vessel.
  - Automatically calculated after a volume has been manually assigned.

- **Agatston Score**
  - Automatically calculated once an area of calcium for the corresponding coronary vessel has been manually assigned.

- **Calcium Percentile Findings**
  - Automatically calculated based on total Agatston score and patient demographic information.

In the **Ca Scoring** screen, click on the **Highlight Calcium** tool to indicate areas of calcification with the color blue *(Figure 4.39)*. In order to remove calicifications from calculation within the CT display, click on the **Delete Calcium** tool to activate the delete tool. All contiguous pixels will be erased from calculation when the user clicks the cursor over calcifications within the image panel. 4DM provides two different methods that can be used to manually assign coronary calcium:

- **ROI Tool:**
  - Click on the **Vessel** button name that you wish to begin assigning calcium scores to. Click the **ROI** tool with

Figure 4.39: The Ca Scoring screen launches with areas of calcium noted in blue.

the desired shape selected, and then draw the ROI around any coronary vessel calcifications you wish to designate as the color-coded vessel lesion. All contiguous pixels within the ROI

that you draw that are calcified deposits will change to your newly-specified vessel color and scores will automatically populate in the **Result Table** below *(Figure 4.40)*.

▪ **Region-Growing Technique**:
  – Click on the **Vessel** button name that you wish to begin assigning calcium scores to. Left-click inside the blue calcified region that corresponds to the activated Vessel button and the entire calcified region and all pixels connected to it will be assigned to the new vessel color; scores will automatically populate in the **Result Table** below.

Once the review (and scoring, if necessary) is complete on the **Ca Scoring screen**, save the results so that they can be recalled at any time.

Figure 4.40: *The Ca Scoring screen after the calcified vessels have been assigned appropriate calcium scores which auto-populate to the table below the large image panel.*

Conclusion

This concludes your SPECT/CT MPI Clinical Workflow Tutorial. Prior to exiting the program, users should save the 4DM results files. Technologists can transfer the saved results and image dataset(s) to the interpreting physician for review. 4DM recognizes the most current saved result files, so if physicians make any changes to the saved study they should save the updated results.
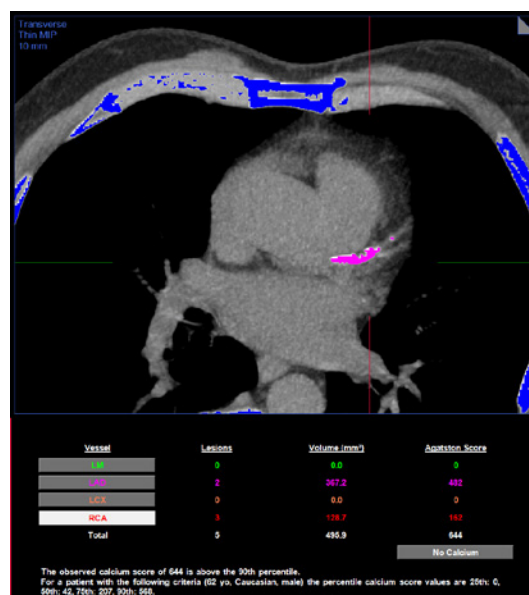
The PET/CT cardiac imaging workflow uses these screens:

- MI Processing
- Fusion
- AC Images
- AC Images + Quant
- AC Func + Quant
- Dyssynchrony
- MPI Summary
- CT Viewer
- Ca Scoring

Corridor4DM provides each user with numerous options to create diagnostic workflows that maximize efficiency while providing accurately quantified data for interpretation. This chapter provides a 4DM Clinical Workflow Tutorial for the image review, quantification, and interpretation of PET/CT MPI and PET/CT FDG Viability studies. The following PET/CT datasets can be launched into 4DM:

- PET (PT) Transverse datasets:
  - Ungated Attenuation-corrected (AC) Stress/Rest datasets
  - Gated AC -Stress/Rest datasets
  - Dynamic AC -Stress/Rest datasets
- Computed Tomography (CT) Volumetric datasets
- Optional: Non-contrast low-dose CT for Calcium Scoring
- Optional: Cardiac CT Angiogram (CTA) with Extracted Coronary Vessels

Quality Assurance → Qualitative Perfusion Review → Quantitative Perfusion Review → Quantitative Functional Review → PET / CT Study Interpretation → Special Protocols

Quality Assurance

Quality Assurance

Users should always ascertain the integrity of the study that has been provided for review prior to beginning any processing or interpretation. 4DM has integrated Quality Assurance (QA) screens which enable users to assess study quality from within the software to save time and maximize efficiency. The key QA screens utilized for PET/CT MPI review are:

- MI Processing
- Fusion

As the first QA step in the PET/CT workflow, visit the MI Processing screen.

MI Processing

Upon launching a patient in Corridor4DM for the first time, the program automatically quantifies the study using 4DM default algorithm settings. The **MI Processing screen** allows users to define LV dataset alignments, apical and basal limits, and LV centers on the VLA, SA, and HLA slices. Users should review all reconstructed datasets on the **MI Processing** screen *(Figure 5.1)*.

WARNING

The user should verify that the estimated LV contours are correct and track the myocardial walls. Inaccurate contours can result in incorrect computation of quantitative data, which can lead to misdiagnosis.

WARNING

The user should visually verify the processing limits-

- Heart Centering
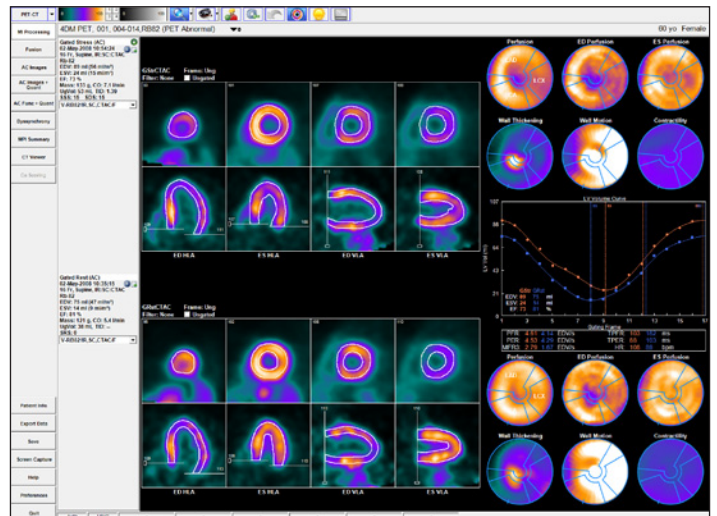- Basal and Apical Limits
- Volume Orientations

Figure 5.1: *The MI Processing screen with three datasets – gated stress, stress, and rest – displays ❶ Processing Splash Objects and ❷ Processing Polar Map Objects for each dataset by default. Click the ❸ LV Volume Curve tool to display the LV Volume Curve for gated studies.*

The user should confirm that the basal limits are consistent between datasets and that the 4DM LV surface generation algorithm has accurately identified the endo- and epicardial surfaces of the LV. These contours are used to calculate the following parameters:

- LVEF
- ED/ES Volumes
- Cardiac Output

- LV Volume Curve
- Cardiac Mass
- TID

- Perfusion Maps
- Wall Motion and Thickening Maps
- Contractility Maps

Note that 4DM allows the valve plane definition to differ for volumetric estimates and the generation of polar maps. Adjustments to the basal sliders on the VLA images affect volumetric estimates (systolic, diastolic, TID). For volume estimates, the basal limit is typically placed at the end of the LV as seen on the anterior, lateral and inferior walls. For polar maps, the basal sliders on the HLA images are used to define the axial extent of the myocardium that is mapped to the polar maps where the axial location is typically chosen to be near the mid-membranous septum to minimize the inclusion of slices involving the outflow tract and the aortic valve. For the polar maps, there are three algorithm options that are available to automatically identify the location of the valve plane for perfusion studies *(Figure 5.2)*. The default algorithm is the Septal Wall Mid-Membranous Septum.

(4DM default)

Lateral Wall

Septal Wall Mid-Membranous Septum

Septal Wall

Figure 5.2: *The three 4DM basal limit Preference settings for Pmap QA*

Activating the **Contours** tool *(Figure 5.3)* applies white contour overlays on the endo- and epicardial surfaces of the LV myocardium for all datasets. If no changes are necessary to the limits/positions, users can proceed to the Images screen to begin the perfusion review portion of the workflow.

Figure 5.3: *Contours tool*

If contours do not track the myocardium due to poor orientation or centering of the left ventricle, high intensity extra-cardiac activity, or the dataset requires additional filtering, the study should be reprocessed by clicking the **Manual Processing** tool *(Figure 5.4)*. Centering, orientation and axial limits are adjusted using the sliders as shown in *(Figure 5.5)*.

Figure 5.4: *Manual Processing tool*

1	Proper positioning of the LV center aligns the crosshairs in the center of the lumen.	
2	Proper positioning of the apical and basal limits are at the center of the apical myocardium and the mitral valve plane.	

Figure 5.5: *Examples of proper positioning on the Setup screen*

If the dataset has signficant extra-cardiac activity, click the **Constraints** tool *(Figure 5.6)* to define a constraint to prevent the contour from tracking the extra-cardiac activity rather than the ventricle. Once selected, modify the size and shape of the constraint limits on the SA slice by adjusting the red constraint handles located

Figure 5.6: *Constraints tool*

If the LV surface generated includes extra-cardiac activity, it is recommended that the user processes the images utilizing the Constraints Tool. Inclusion of extra-cardiac activity can lead to false impressions and image normalization.
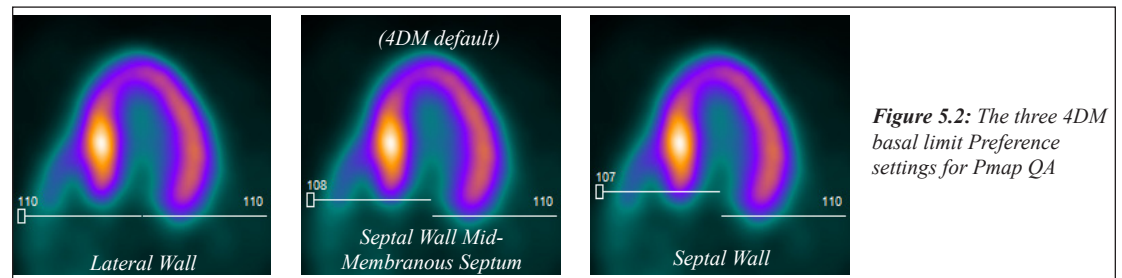
4DM-provided normals databases were generated using the Septal Wall Mid-Membranous Septum basal extent placement. To provide consistency, the 4DM default basal extent setting is the same.

If only endocardial surfaces are generated, the incorrect radiopharmaceutical was assigned to the dataset. Check the Special File Strings by clicking on the Dataset Matching Strings button within the Preferences menu. To learn more about editing matching strings, go to User Preferences.

at three and six o'clock and centering the crosshairs *(Figure 5.7)*. Once adjustments to the LV center, orientation, and basal limit are complete, the user must click the **Process** tool *(Figure 5.8)* to generate the endo- and epicardial surfaces.

If the dataset needs to be processed from scratch (i.e. no initial estimates from 4DM), click the **Reset** tool *(Figure 5.9)* and then set the center, angulation, valve plane location and click the Process tool to reprocess.

It is important to visually confirm the contours and the basal limits used to quantify functional and perfusion estimates. Also verify that the basal positions are consistent between datasets and make adjustments if necessary. Once finished reviewing the MI Processing screen, users should proceed to the Fusion screen to assess the co-registration of the NM datasets to the attenuation maps.
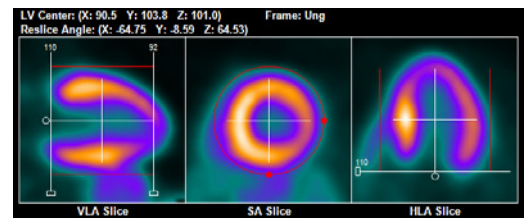

Figure 5.7: The Constraints tool is selected which overlays adjustable constraints onto all four PET datasets. These constraints are properly positioned to include the entire LV, while excluding extra-cardiac activity such as liver or a loop of bowel.

Figure 5.8: Process tool

Figure 5.9: Reset tool

Fusion

4DM has integrated the **Fusion** screen *(Figure 5.10)* as part of the QA process to accommodate the evolution of hybrid imaging. In addition to performing the standard NM processing for MPI datasets, technologists and physicians are now tasked with verifying that the reconstructed NM dataset and the attenuation map are properly co-registered.

4DM can be configured to auto-match the AC-NM dataset as the **Object Volume** and the attenuation map as the **Target Volume**. Use the Object Volume and Target Volume menus provided to select different datasets, if desired *(Figure 5.11)*. Additionally, gated CT datasets are supported within the **Fusion** screen. To switch the Object and Target Volume datasets, click the **Swap Datasets** tool *(Figure 5.12)*. Change the Orientation of the images by clicking the **Orientation** tool *(Figure 5.13)*.

The Fusion screen displays the fused Object and Target volumes in three orthogonal views (Transverse, Coronal, and Sagittal) along the left side of the image window. On the right, a large panel displays a fused transverse image
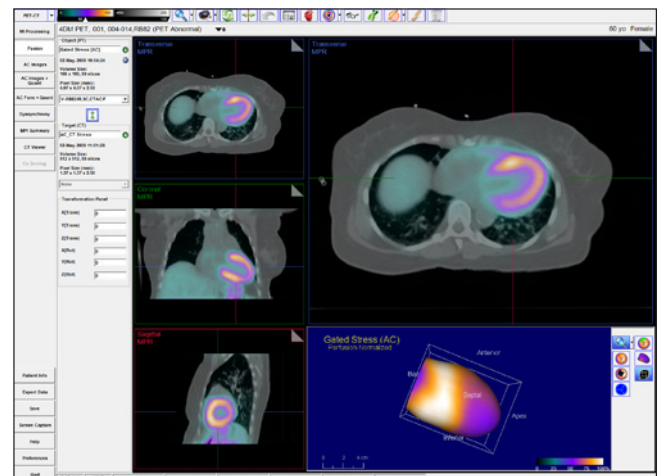

Figure 5.10: Shows proper co-registration of the Stress PET dataset to the corresponding Stress CT dataset.

Figure 5.11: The Object/Target menu in the Fusion screen

Figure 5.12: Swap Datasets tool

Figure 5.13: Orientation tool

WARNING
When viewing NM data fused to CT data on the Fusion screen, verify they represent the same portion of the protocol (e.g., Stress NM to Stress CT).

The **Object Volume** is the overlay, or top image. The **Target Volume** is the base, or bottom image. The **Object Volume** can be repositioned, while the **Target Volume** is stationary.

To make manual **Pan** adjustments, place the mouse cursor in the inner one-third of the image panel. The cursor will change to a hand icon, which allows you to Pan the image by clicking-and-dragging the **Object Volume**.

with a configurable display object below. To change the view in the large panel, double-click one of the three orthogonal images on the left.

The Layout Selector tool *(Figure 5.14)* provides options for different layouts of the Fusion screen: four panel with 3D Object, four panel with Slices, and a nine panel display. The four panel with 3D object is used to view the co-registration of extracted CTA coronary vessels or 4DM-quantified coronary calcium deposits. The four panel with Slice object displays transverse Target and Object slices. The nine panel layout displays the Object, Target, and fused Object/Target volumes – each in a three orthogonal view.

Figure 5.14: *Dataset Layout tool*

To help verify the co-registration of two datasets, the Fusion screen provides enhanced interactive mouse controls. A **Dual Colorbar** with an **Alpha-Blending tool** *(Figure 5.15)* is located below the left object colorbar. Slide the alpha-blending tool to adjust the transparency of the Object volume.
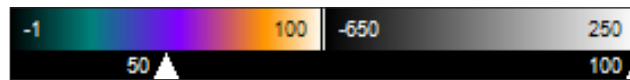

Figure 5.15: *Dual Colorbar with Alpha Blending*

If the datasets are misaligned, 4DM provides several correction tools within the Fusion screen to aide users during the QA process:

- **Coarse and Fine adjustment alignment tools** for image panning and rotation are provided when the mouse cursor is hovered over each image panel *(Figure 5.16)*.

- The **Transformation Panel** provides the user options for further adjustment tools on the Fusion screen for rotation and translation in the X, Y, and Z planes for each image panel.
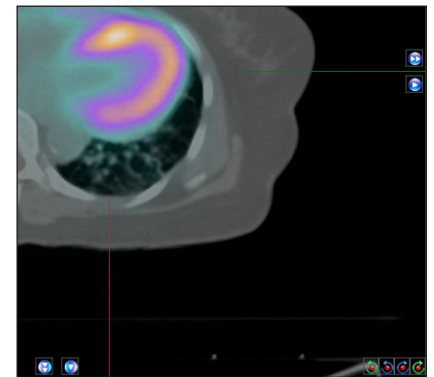
Figure 5.16: *A zoomed in view of the Coarse and Fine adjustment tools available on the Fusion screen*

The following interactive display tools are available within the Fusion screen:

- Each image panel has colored **Slice Plane Indicators** which have two main purposes:
  - Position them to triangulate over an area of interest. The slice plane colors provided in each image panel signify which plane they correspond to.
  - Click-and-drag the Slice Plane Indicators to quickly scroll through datasets.

- To scroll slowly through individual image slices, click on the **Dog-ear** tool in the top right corner of each image panel.

- Right-click on the MPR or MIP label *(Figure 5.17)* in the top left corner of an image panel to change settings for MPR/MIP thickness.

- Click the **Contours** tool *(Figure 5.18)* to display the endo-

Figure 5.17: *Example of MPR label location*

Figure 5.18: *Contours tool*

and epicardial LV surfaces by selecting Target Contours, Object Contours, or Target and Object Contours for processed NM cardiac datasets.

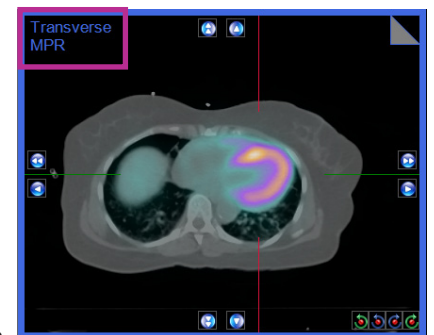- Draw elliptical, freehand, rectangular, or polygon ROI's by selecting one from the **ROI Menu** tool *(Figure 5.19)*.

  – **SUV** measurements will be calculated if the patient's weight and injected dose are inlcuded in the dataset information.

- Draw straight-line measurements and automatically display the length for each (in mm) when the **Ruler** tool *(Figure 5.20)* is turned on.

- Delete any ROI or ruler measurements by selecting the element and clicking on the Delete tool in the Toolbar.

Figure 5.19:
ROI Menu tool

Figure 5.20:
Ruler tool

Users should verify the co-registration for both the Stress-AC and Rest-AC datasets with their corresponding Stress and Rest attenuation maps on the Fusion screen before continuing to the review portions of this SPECT/CT MPI workflow.

Qualitative Perfusion Review

The next step in our PET/CT MPI workflow is to begin the image interpretation process. Perfusion abnormalities can be visually assessed by a review of the perfusion images for areas of pronounced decreased tracer uptake. Identification of differences in the myocardial tracer intensity between the stress and rest datasets is important for the assessment of tracer reversibility, a marker for myocardial ischemia. This task is most accurately accomplished by reviewing the ungated AC Str/Rst as slices, aligned one over the other, in the three cardiac planes: SA, HLA and VLA. In 4DM this layout is referred to as **Splash Object** display. The 4DM **AC Images** screen was created specifically to accomplish this step in the clinical workflow.

AC Images

The **AC Images** screen presents the datasets as SA, HLA, and VLA **Splash Objects** *(Figure 5.21)*. Review and compare the tracer perfusion of the ungated AC Str/Rst datasets on this screen and note any areas of abnormal decreased tracer uptake for assessment of reversibility. If the dataset slices are not properly aligned to one another, left-click and drag on one slice in the dataset until it matches the desired slice directly above and/or below it. Once the qualitative perfusion review is complete, the next step in our PET/CT MPI workflow is to assess the 4DM quantitative perfusion analysis.

To move all displayed datasets slices together at the same time, left-click and drag the **Dataset Slice** slider located above each **Splash Object**.
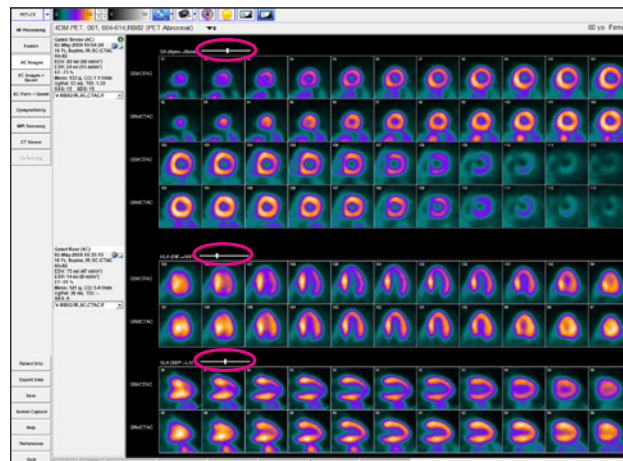
Figure 5.21: *The AC Images screen with the AC Str/Rst Rb-82 datasets selected to view ECT slices in all three orthogonal planes.*

Quantitative Perfusion Review

In addition to the qualitative perfusion assessment, 4DM recommends utilizing the quantification data available to supplement visual perfusion defects. To quantify the PT perfusion information 4DM automatically compares the currently displayed datasets to a normal database that contains patients of the same gender who had normal studies utilizing a similar protocol and tracer. Two of the most clinically validated methods to quantitatively assess perfusion defect severity and extent are polar map comparisons and semi-quantitative scoring. The accuracy of the 4DM algorithms used for quantification provide users with important supplemental information that aids the clinician in the interpretation process by assigning extent and severity ratings to the perfusion defects in question. The **AC Images+Quant** screen provided within 4DM displays both the perfusion **3SA Objects** and the supporting quantification information. 4DM recommends using this screen during quantitative perfusion review of PET/CT MPI cases.

AC Images+Quant

The **AC Images+Quant** screen *(Figure 5.22)* presents the SA, HLA, and VLA **3SA Objects** in addition to providing perfusion polar maps with the supporting automatic semi-quantitative scores all on one screen. 4DM displays the **Scores Objects** already calculated and users have the option to manually adjust them if desired. Within the **AC Images+Quant** screen users have access to numerous polar map menus in the **Toolbar.** This enables on-the-fly changes if different assessments are desired.
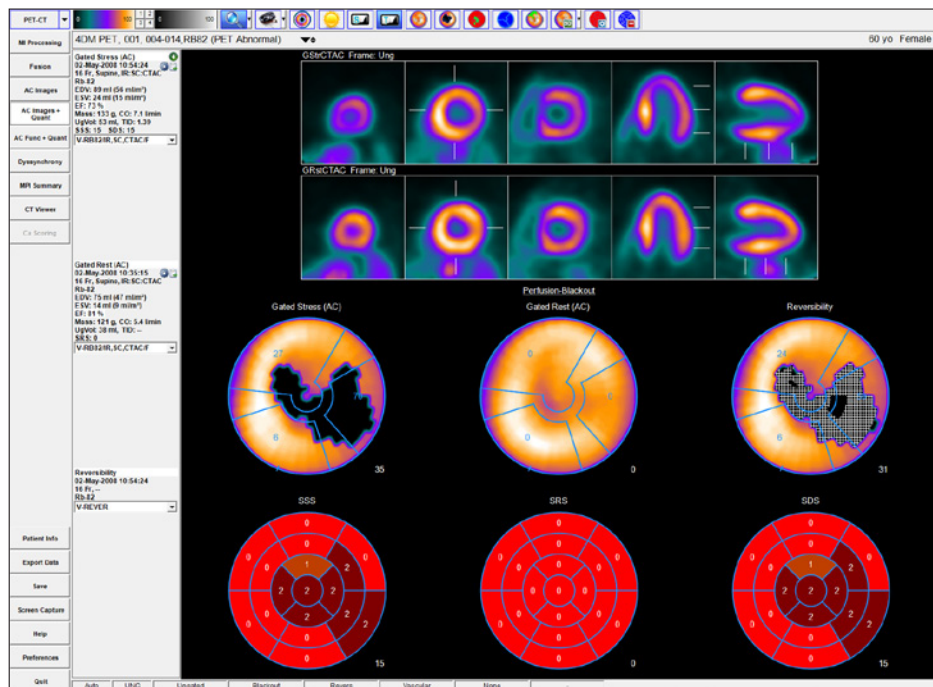

Figure 5.22: The AC Images+Quant screen with the Str/Rst Rb-82 datasets launched to enable viewing the Reversibility polar map which is selected from the Comparison polar map menu.

It is recommended to view the **AC Images+Quant** screen with two datasets in order to view the reversibility polar map comparison. 4DM automatically selects the ungated AC Str/Rst option from the **Dataset Selector** menu in the **Toolbar**. After review of these screens is complete, the next step in our workflow is to review the functional data.

WARNING

The user must verify that the Normals Database is compatible with the dataset being reviewed to ensure correct computation of quantitative data.

4DM automatically calculates the semi-quantitative scores for the displayed datasets. Users can clear the scores and manually score the segments if desired by clicking the **Clear** tool in the **Toolbar**. Conversely, to reload the automatic scores, click the **Auto** tool.

Once your assessment is complete, right-click the **Patient Info** button to document your findings.

Quantitative Functional Review

Functional quantitation refers to correlating the clinician's visual estimates of LV function with the following calculated parameters:

- LVEF
- ED/ES volumes
- LV Volume Curve
- Cardiac Output

- TID
- Cardiac Mass
- Wall Motion
- Wall Thickening

To appropriately assess and report on these values, we recommend selecting only the gated AC PET dataset(s) so that users can view the AC PET **Splash Object** and **LV Volume Curve** in cine mode together on the **AC Func+Quant** screen.

AC Func+Quant

The AC Func+Quant Screen *(Figure 5.23)* displays a gated 3SA Func layout for reviewing the Function of the gated datasets. When only one gated dataset is present, the LV Volume Curve is included to display LV Volume (in ml). The Temporal Filter tool allows the user to apply a filter for enhancing the image quality of the gated slices. The Polar Maps allow the user to view Wall Motion and Wall Thickening while visually comparing to the relative score calculations visible in the Scores Objects.
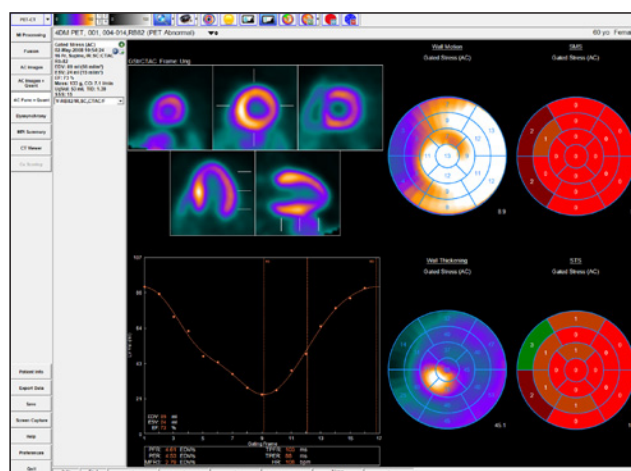

Figure 5.23: *The AC Func+Quant screen with one gated dataset displayed.*

Dyssynchrony

The **Dyssynchrony** screen was created for assessing the phases of contraction for the left ventricle *(Figure 5.24)*. Dyssynchrony is defined as delayed ventricular activation and contraction. Analysis of regional and global contraction patterns in the left ventricle can help identify those patients who may benefit from Cardiac Resynchronization Therapy (CRT). To accurately assess patients for dyssynchrony, physicians can use the following image displays to identify abnormalities in contractile function:
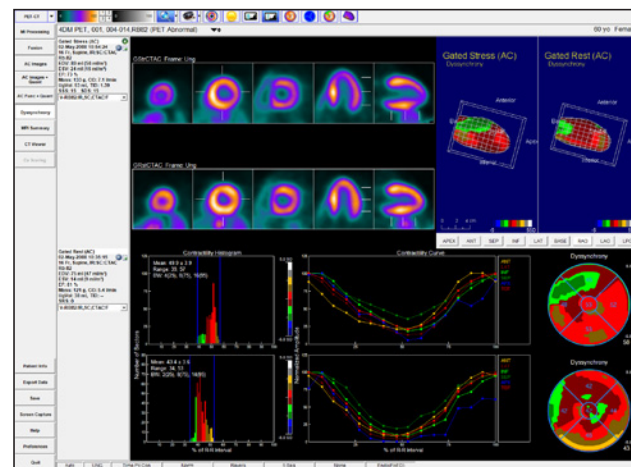
Figure 5.24: *The Dyssynchrony screen was created for assessing the phases of contraction for the left ventricle.*

- **Contractility Histogram:** Plots the time to peak contraction expressed as the percent of the R-R frame within the left ventricle. Vertical blue indicators signify the start and end points of contractility.

Sidebar notes:

Facilities that acquire 16-bin gated datasets should utilize the **LV Volume Curve** because it provides detailed systolic and diastolic functional information.

Users can easily switch the order of the datasets loaded for each of the four image panels by selecting the **User Defined** option from the **Dataset Selector** menu in the **Toolbar**.

Once your assessment is complete, right-click the **Patient Info** button to document your findings.

- **Contractility 2D and 3D Polar Maps** *(Figure 5.25)***:** Choose between Time to Peak Thickening using First Harmonic Fit, Time to Peak Thickening, and Time to Peak Contractility.

The **Dyssynchrony** screen also provides a 3SA Object with optional contours; Perfusion, Wall Thickening, and Wall Motion Polar Maps; and 3D Objects. The screen layout varies between one or two gated datasets. If two gated datasets are displayed, the Perfusion, Wall Thickening, and Wall Motion Polar Maps are omitted from the screen.
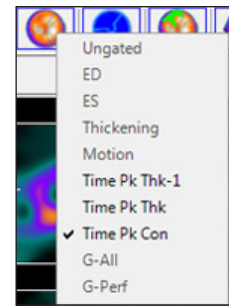

Figure 5.25:
Raw Map Menu

Interpretation of the PET/CT Study

MPI Summary

The **MPI Summary** screen is the 4DM standard PT review screen because it accomplishes the task of fitting all perfusion and functional data necessary for interpretation of the study onto one screen *(Figure 5.26)*. It supports all PET datasets and includes:

- **3SA Object**
- **Polar Map Object**
- **Scores Object**
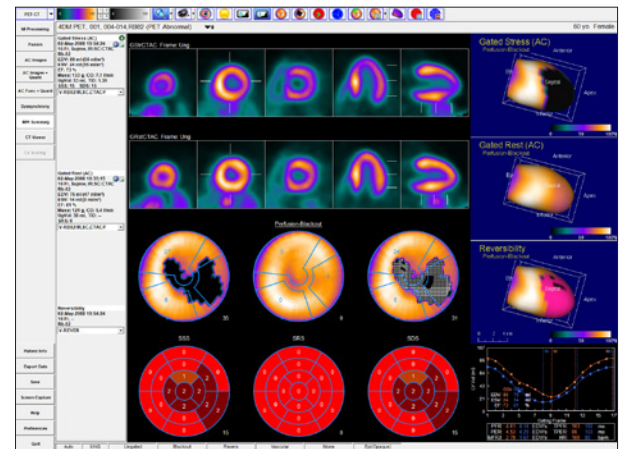- **3D Object**
- **LV Volume Curve**

4DM recommends displaying the **MPI Summary** screen when performing the final interpretation and exporting information to your report.

Figure 5.26: The MPI Summary screen displays both perfusion and functional quantification information.

CT Viewer

Reporting incidental CT findings for PET/CT studies is recommended. 4DM includes the **CT Viewer** screen so that users can easily accomplish this task within the program *(Figure 5.27)*. Use this screen to review both contrast and non-contrast CT studies. 4DM supports Gated CT datasets which can be reviewed from this screen by using the cine tool. The following customization tools have been implemented within the **CT Viewer** screen to assist users during the CT review and interpretation process:

- **Select** the correct CT dataset (if multiple CT's were acquired) from the **Dataset Selector** menu.

- **Change** the HU windowing by right-clicking on the **CT Colorbar** that is provided in the **Toolbar**. The left colorbar controls the MPR image panels and the right colorbar controls the MIP/Thin MIP image panels.

- **Magnify** the image by using the **Magnification** slider.

- **Reset** the images back to the 4DM default by selecting the **Reset** tool.

CT topograms, commonly referred to as scout images, are not 4DM-supported datasets. Only volumetric or reconstructed CT datasets can be viewed in 4DM.
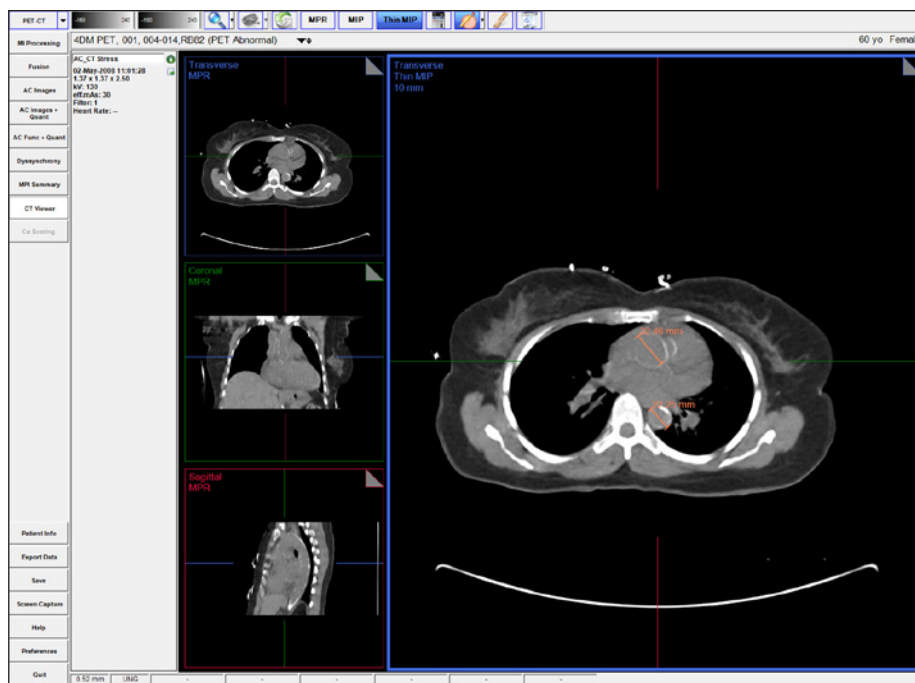
Figure 5.27: Shows the CT Viewer screen with two ruler measurements drawn: one on the ascending aorta (upper) and one on the descending aorta (lower).

Users can right-click over the **MPR**, **MIP**, and **Thin MIP** buttons in the **Toolbar** to type in a specific slice thickness (within the range of 1-50 mm).

- **Switch** any one or all of the four image panel types to MPR, MIP, or Thin MIP by selecting the image panel and then clicking on the **MPR**, **MIP**, or **Thin MIP** button.

- **Cine** the Gated CT dataset by selecting the **Cine** tool.

The following **CT Viewer** tools are located in the **Toolbar** to aide users in the assessment of incidental findings on the CT dataset(s).

Right-click on either of the **CT Colorbars** to change the **HU Range** you wish to display. For example, during assessment of the lung fields, select the **Lung** window.

- **Draw** elliptical, rectangular, or freehand ROI's by selecting the ROI type from the **ROI** menu *(Figure 5.28)*.
- **Display** the information for any ROI's that has been drawn by clicking on the **Table** tool.
- **Draw** straight-line measurements and automatically display the length for each (in mm) with the **Ruler** tool.
- **Delete** any ROI's or ruler measurements by selecting the element and clicking on the **Delete** tool in the **Toolbar**.

Figure 5.28: The ROI menu

Once your assessment is complete, right-click the **Patient Info** button to document your findings.

Once the analysis of the CT images from within the **CT Viewer** screen is complete and incidental findings have been recorded, the basic PET/CT workflow is finished.

Ca Scoring

WARNING

Users must ensure that a non-contrast Calcium Scoring CT dataset is input to the Ca Scoring screen prior to assigning scores.

4DM provides quantification and review of coronary artery calcium deposits from within the **Ca Scoring** screen. 4DM strongly recommends that physicians review the calcium scores calculated within this screen. Upon display of the **Ca Scoring** screen, users will note that the image panels and layout are similar to the **CT Viewer** screen. All tools function the same with the exception of the **Result Table** tool *(Figure 5.29)* and the **ROI** tool *(Figure 5.30)*. Additionally, the **Highlight Calcium** tool *(Figure 5.31)* and **Delete Calcium** tool *(Figure 5.32)* are tools specific to the **Ca Scoring**

Figure 5.29: The Result Table tool

Figure 5.30: The ROI tool

The status bar located at the bottom of the screen displays the **HU thresholdpreference setting used to identify calcifications. The HU threshold utilized during quantification is displayed within the lower left corner of the image display. The Processing Options** tool on the **Ca Scoring** screen allows the user to adjust HU thresholds and the Region Growing Limit *(Figure 5.33)*.

***Figure 5.31:** The Highlight Calcium tool*

***Figure 5.32:** The Delete Calcium tool*

***Figure 5.33:** The Processing Options tool*

Activating the **Result Table** tool within the **Ca Scoring** screen provides users with the following information:

- **Vessel** name buttons
  - Lists the four main coronary vessels, each as its own color-coded button
  - Click on the **Vessel Name** to activate the corresponding color to be manually assigned to areas of coronary calcium deposits.

- **Lesions**
  - Automatically calculated as the number of calcified lesions within the corresponding coronary vessel after a volume has been manually assigned.

- **(mm3)**
  - The total volume of all calcified lesions within the corresponding coronary vessel.
  - Automatically calculated after a volume has been manually assigned.

- **Agatston Score**
  - Automatically calculated once an area of calcium for the corresponding coronary vessel has been manually assigned.

- **Calcium Percentile Findings**
  - Automatically calculated based upon total Agatston score and patient demographic information.

In the **Ca Scoring** screen, click on the **Highlight Calcium** tool to indicate areas of calcification with the color blue *(Figure 5.34)*. In order to remove calicifications from calculation within the CT display, click on the **Delete Calcium** tool to activate the delete tool. All contiguous pixels will be erased from calculation when the user clicks the cursor over calcifications within the image panel. 4DM provides two different methods that can be used to manually assign coronary calcium:

- **ROI Tool:**
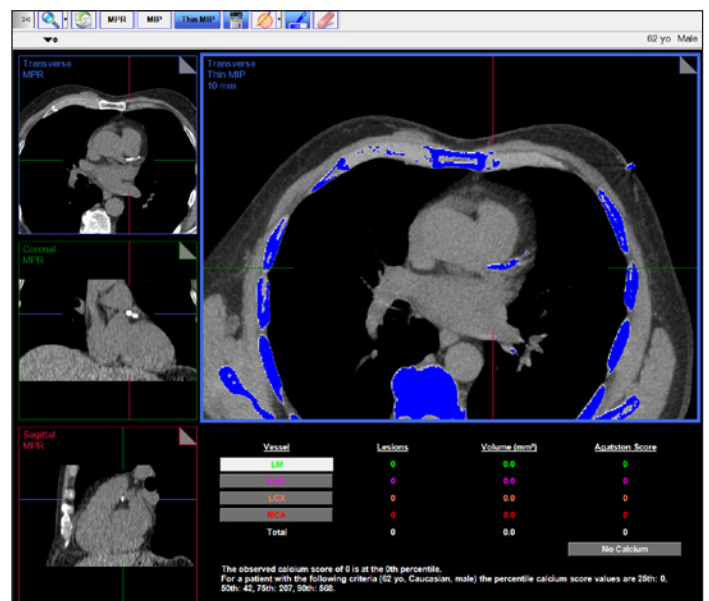 - Click on the **Vessel** button name that you wish to

***Figure 5.34:** The Ca Scoring screen launches with areas of calcium noted in blue*

begin assigning calcium scores to. Click the **ROI** tool with the desired shape selected, and then draw the ROI around any coronary vessel calcifications you wish to designate as the color-coded vessel lesion. All contiguous pixels within the ROI that you draw that are calcified deposits will change to your newly-specified vessel color and scores will automatically populate in the **Result Table** below *(Figure 5.35)*.

- **Region-Growing Technique**:
  – Click on the **Vessel** button name that you wish to begin assigning calcium scores to. Left-click inside the blue calcified region that corresponds to the activated Vessel button and the entire calcified region and all pixels connected to it will be assigned to the new vessel color and scores will automatically populate in the **Result Table below.**
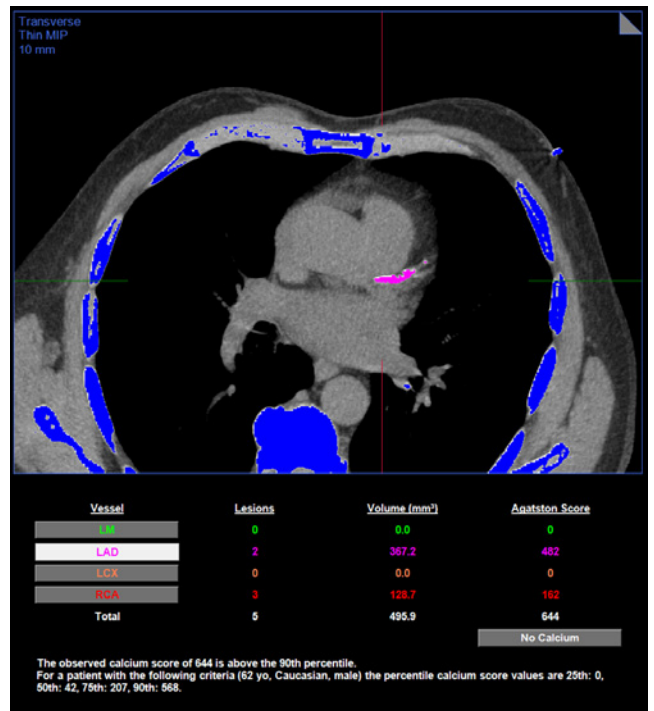

Figure 5.35: The Ca Scoring screen after the calcified vessels have been assigned appropriate calcium scores which auto-populate to the table below the large image panel.

  – The region growing limits can be set to **Full Volume**, the default, or **MPR/MIP Thickness.** This setting can be editied within **Preferences** under Screen Layout for the **Ca Scoring** screen.

Once the review (and scoring, if necessary) is complete on the **Ca Scoring screen**, save the results so that they can be recalled at any time.

Special Protocols

Quantitative Flow Reserve

The **Reserve** screen *(Figure 5.36)* provides the capability to process and review dynamic cardiac PET datasets. Dynamic datasets can be used to estimate absolute myocardial blood flow and coronary flow reserve (CFR). Such measures often provide a more reliable assessment of perfusion abnormalities than conventional quantification of myocardial perfusion.

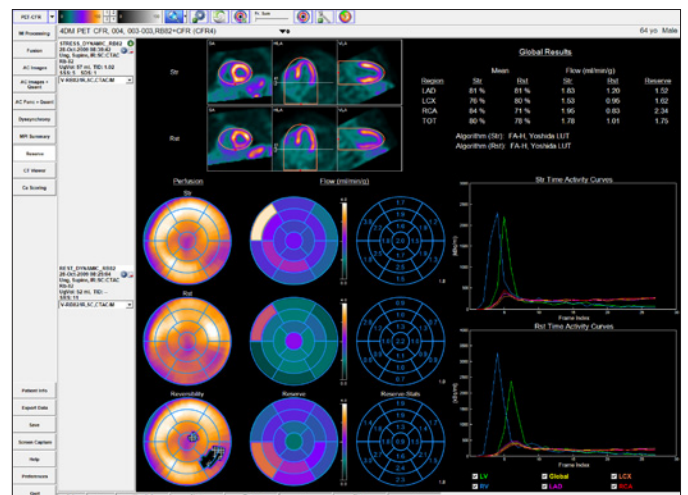CFR processing should be preceded by the PET/CT QA workflow.

Figure 5.36: The 4DM Reserve Screen

Input Data

A dynamic PET dataset consists of a series of 3D image volumes acquired at different time points (called frames) during the first pass and uptake of the radiotracer in the heart. When a dynamic PET dataset is loaded into 4DM, static images are automatically generated by summing the frames from a portion of the dynamic series. The portion of the dynamic series to be summed is configurable in **Preferences**, on the **Image Display** page *(Figure 5.37)*.
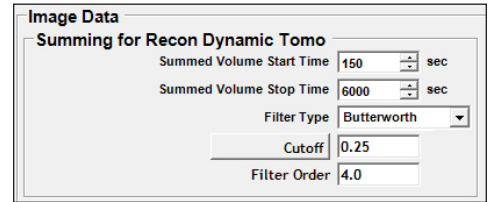

Figure 5.37: *Image Data section of the Image Display Page within Preferences*

Generally, the Summed Volume Start Time should be set to a time after the tracer has cleared from the RV and LV blood pool, and the Summed Volume Stop Time should be set to the end of the last frame. In addition, options are available to adjust smoothing filters that can be applied to summed datasets. These summed static datasets are displayed on all PET/CT image review and processing screens, as well as the **Reserve** screen.

CFR Processing

Stress and rest datasets are displayed and processed together on the **Reserve** screen. Summed static images are displayed in the image viewports. Users can perform the following actions using the tools in the **Toolbar**:

Figure 5.38: *Contours tool*

- **Contours** *(Figure 5.38)***:** Overlay surface contours on the images

- **Dynamic Frames** *(Figure 5.39)***:** Drag the slider to review the input dynamic frames in the image viewports

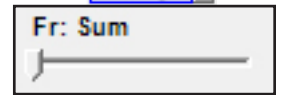As the image viewports are displayed in cardiac orientation, a basal slider is provided on the HLA and VLA images allowing the user to change the LV basal limit.

Figure 5.39: *Dynamic Frame slider*

Changes using the basal slider automatically trigger re-sampling of the tissue curves used for quantification.

By clicking the **Processing Options** tool *(Figure 5.40)* in the **Toolbar**, the available flow models defined to fit the dynamic data for estimating myocardial blood flow and reserve are presented *(Figure 5.41)*. Click the **Details** icon next to the Flow Model Name to view the characteristics of each flow model.

Figure 5.40: *Processing Options tool*

- For the **Factor Analysis (FA)** model, the LV and RV blood time activity curves (TAC) are estimated using the factor analysis algorithm. The flow and CFR values are then calculated from the blood and tissue TACs using the compartment model.

Figure 5.41: *CFR Processing Options*

- The **Factor Analysis-Hybrid (FAH)** model uses a subset of the pixels from Factor Analysis for the RV and LV blood TACS. This derivative algorithm has shown improvements for studies where there is significant overlap between the blood and tissue factors.

- For the **ROI Compartment** model, only the LV blood TAC is sampled from a ROI. The flow and CFR values are then calculated from the blood and tissue TACs using the compartment model.
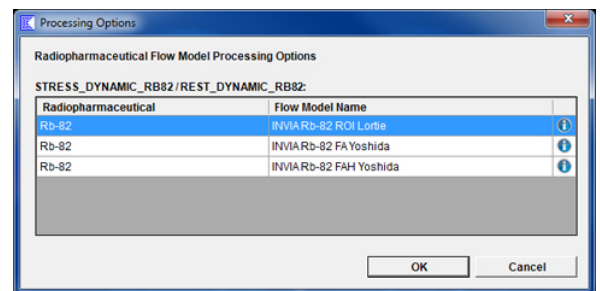
When the **Factor Analysis** algorithm is applied, the ellipsoid-cylindrical bounding volume can be dragged to change the height or width of the factor analysis bounds in each viewport *(Figure 5.42)*. The user should adjust the size of the bounds to ensure inclusion of the blood pool regions and to exclude non-cardiac regions.
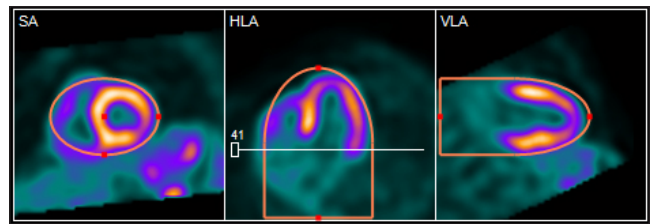

Figure 5.42: *Factor Analysis Bounds*

When the **ROI** algorithm is applied, the rectangular ROI can be dragged to change the height or width of the LV blood pool sampling region in the HLA and VLA viewports *(Figure 5.43)*. The user may increase the size of the ROI to improve statistics in the LV blood TAC.
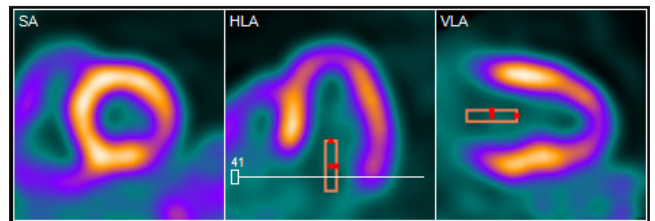

Figure 5.43: *ROI Compartment Sampling Region*

To initiate CFR processing, click the **Process** *(Figure 5.44)* tool in the Toolbar. Both stress and rest datasets are processed at the same time. The processing is fully automated and typically takes 1-2 minutes to complete for Factor Analysis, and a few seconds to complete for ROI analysis.

Figure 5.44: *Processing tool*

QA

After processing with the **Factor Analysis** algorithm, the Reserve screen provides two components to assess the quality of the CFR processing results.

First, the user should review the blood and tissue **Time Activity Curves** (TACs) *(Figure 5.45)*. The RV curve peak (blue) should be somewhat higher than the LV curve peak (green), and should occur earlier than (to the left of) the LV curve peak. Both RV and LV curves should gradually approach zero toward the end of the dynamic series. The myocardial tissue TACs should have peak magnitudes that are lower than RV and LV TACs, and should be relatively flat.

Second, the user should examine the factor analysis by clicking the **QA Images** tool *(Figure 5.46)*. The image viewports display the output of the factor analysis for stress and rest. The user should confirm the factor analysis in the RV *(Figure 5.47)*, LV *(Figure 5.48)*, and tissue factor images *(Figure 5.49)*.

If this is not the case, the flow results will be incorrect. The user can reassign the factor analysis labels (RV, LV, and Tissue) in the image viewports by clicking the drop-down button and selecting the correct label. The flow and CFR values are then recalculated automatically.
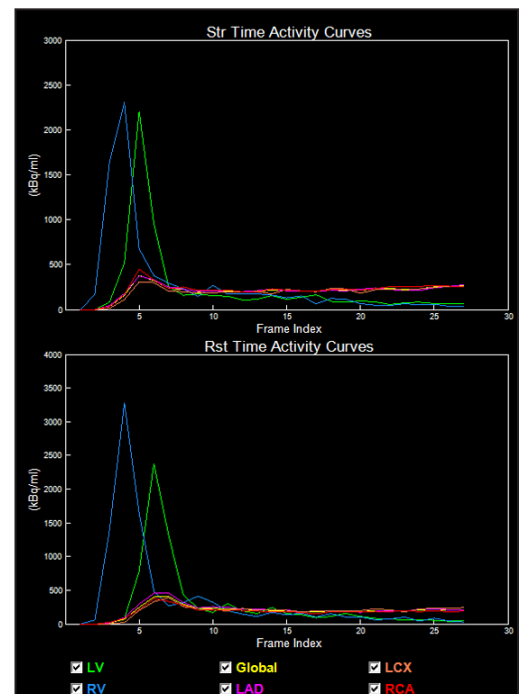
Unchecking LV and RV under the TAC plots will cause the TACs to rescale, allowing better visualization of the myocardial TACs.

After the user has processed the study, any HLA slider adjustments automatically recalculates the processing results.
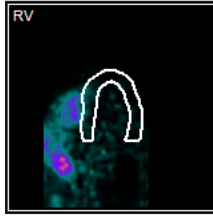

Figure 5.45: *Factor Analysis Time Activity Curve*

Figure 5.46: QA Images tool

Figure 5.47: *Correspondance of the RV factor to the RV blood pool.*
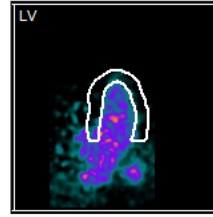

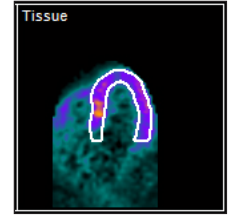**Figure 5.48:** *Correspondance of the LV factor to the LV blood pool.*

Figure 5.49: *Correspondance of the tissue factor to the myocardium.*

When using the **ROI** algorithm, the user can assess the quality of the CFR processing results by also reviewing the blood and tissue TACs *(Figure 5.50)*. The RV curve (blue) is flat with a value of zero. The LV curve (green) should peak and then gradually approach zero toward the end of the dynamic series. The QA Images toggle is not available for the ROI algorithm.

Several tools are provided to modify the appearance of the TAC graphs:

- **LV, RV, Global, LAD, LCX, RCA check boxes:**
  - Allow the user to selectively display the color-coded TACs on the graph (unchecking the RV or LV curves automatically rescales the y-axis, and allow more detail to be seen in the relatively low myocardial tissue TACs).
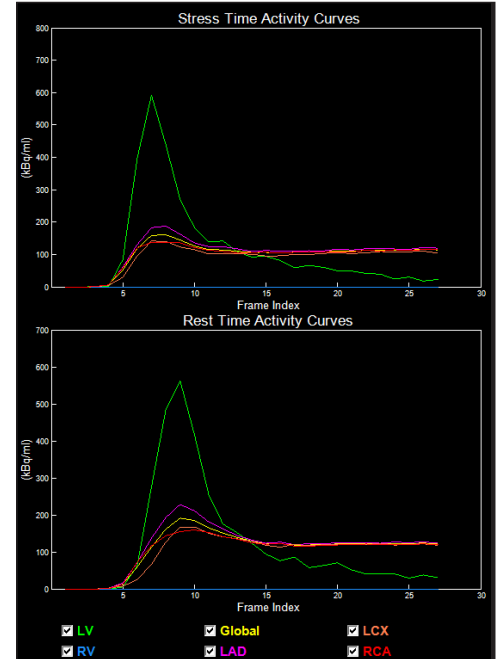

Figure 5.50: *ROI Compartment Time Activity Curve*

> Right-click the TAC Object to display the Curves Options dialog.

Right-click the Time Activity Curves to display the **Curves Options** window *(Figure 5.51)* and further customize the display by selecting any of the following:

- **Kinetic Model:**
  - When checked, the kinetic model fitted tissue TACs (solid line), the measured tissue TACs (circular markers), and kinetic model parameters (rate constants K1, K2, K3, spillover values FV and RV, and model fit error ChiSq) are displayed. When unchecked, only the measured tissue TACs are displayed (solid line).

- **Use Linear Scale:**
  - When unchecked, the vertical axes are converted to a log-scale.

- **Time Normalize Graphs:**
  - When checked, scales the activity concentration in each frame by the frame duration. When unchecked, no scaling is applied.

Figure 5.51: *Curves Options window*

- **Use Frame Index:**
  - When checked, graphs the activity concentration versus frame index. When unchecked, graphs the activity concentration versus time.
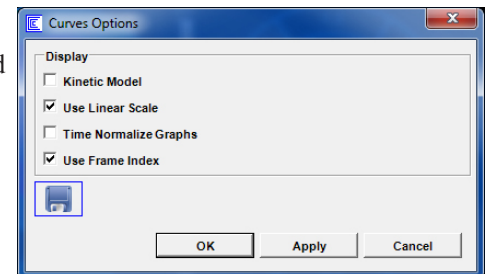
Processing Results

The processing results are displayed in several different components on the **Reserve** screen. The **Global Results** table *(Figure 5.52)* shows regional results for perfusion (Stress Mean, Rest Mean) and absolute blood flow (Stress Flow, Rest Flow) for each of the vascular territories (LAD, LCX, and RCA), as well as globally (TOT). Also shown is the regional CFR (Reserve), which is the ratio of Stress to Rest blood flows.

Global Results

	Mean		Flow (ml/min/g)		
Region	Str	Rst	Str	Rst	Reserve
LAD	81 %	81 %	1.83	1.20	1.52
LCX	76 %	80 %	1.53	0.95	1.62
RCA	84 %	71 %	1.95	0.83	2.34
TOT	80 %	78 %	1.78	1.01	1.75

Algorithm (Str): FA-H, Yoshida LUT
Algorithm (Rst): FA-H, Yoshida LUT

***Figure 5.52:** Global Results Table*

The algorithms used for both Stress and Rest are displayed beneath the table for reference.

The **Polar Map** table *(Figure 5.53)* displays the corresponding visual results on a per-segment basis. Left-click on a polar map segment to display the TAC for that segment as a white curve on the graph.
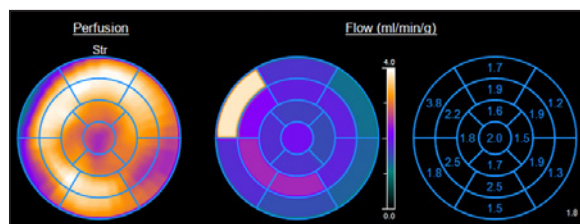

***Figure 5.53:** CFR Polar Maps*

Quantitative Viability Review

The 4DM **Viability** screen was created specifically for reviewing SPECT and/or PET viability studies *(Figure 5.54)*.

The **Viability** screen displays **3SA Objects**; **Perfusion, Viability, Scar** and **Derived Polar Maps**; automatically calculated semi-quantitative **Scores**; and a table displaying the percent of normal, viable, and scar tissue present for each vascular territory. For Stress/Rest Perfusion + FDG Viability studies, this screen displays quantitative polar maps and results for normal, ischemic, viable, and scar areas both globally and for each of the vascular territories.
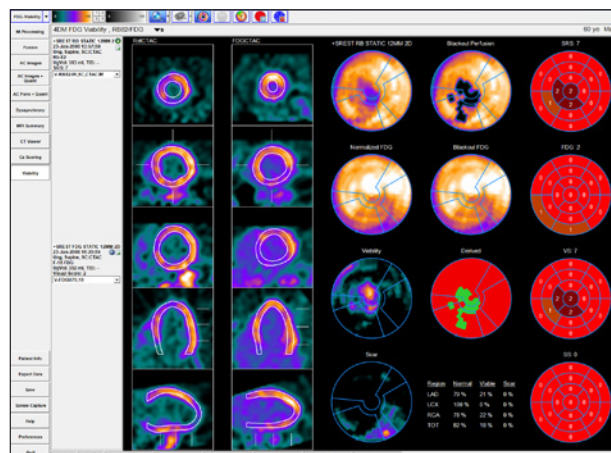

***Figure 5.54:** The Viability screen displaying a gated Rb-82 rest dataset and an ungated F-18 FDG viability dataset.*

The **Derived Polar Map** is specific to the Viability screen. It displays the regional quantitative estimates for normal (red), viable (green), ischemic (blue), and scar (black) tissue.

Conclusion

This concludes your PET/CT Clinical Workflow Tutorial. Prior to exiting the program, users should save the 4DM results files. Technologists can transfer the saved results and image dataset(s) to the interpreting physician for review. 4DM recognizes the most current saved result files, so if physicians make any changes to the saved study they should save the updated results.

The **Viability** screen is accessible only when a study includes the following dataset combinations:

- Perfusion/FDG
- Gated Perfusion
- Rest Tl/Delay Tl
- Stress/Rest/FDG

To quickly view a summary of the entire report, right-click **Patient Info** and select **Miscellaneous/ Summaries**.

This 4DM Tutorial uses the following Workflow Screen Preferences:

| GBPS ▼ |
| NM Viewer |
| MUGA |
| Tomo QA |
| MI Processing |
| Images |
| Func + Quant |
| Dyssynchrony |

Corridor4DM provides the ability to quantify and review both Gated Planar and SPECT Gated Blood Pool (GBPS) acquisitions. This chapter provides two 4DM Clinical Workflow Tutorials for the image review, quantification, and interpretation of both Gated Planar and SPECT Blood Pool studies.

Gated Planar Quantitative Function Review ⟩ GBPS Quality Assurance ⟩ GBPS Qualitative Functional Review ⟩ GBPS Quantitative Functional / Final Review

Gated Planar Quantitative Functional Review

Gated Planar Quantitative Function Review

As with any imaging protocol, assessment of the integrity of the study that has been submitted for interpretation is a critical first step. 4DM has integrated Quality Assurance (QA) screens which enable users to ascertain study quality from within the software to save time and maximize efficiency. The NM Viewer screen is used to QA the gated planar data prior to review of MUGA quantification results on the MUGA screen. See Chapter 7: Non-Workflow Screens for more information on the NM Viewer screen.

NM Viewer

The **NM Viewer** screen is a generic image review screen that displays up to 16 NM datasets at a time. The **NM Viewer** screen is multi-purpose and supports the following NM datasets:

- Tomo
- Gated Tomo
- Dynamic
- Gated Planar
- Static
- Whole Body

To generate a ratio on the **NM Viewer** screen, draw the background ROI first (e.g., lung) and the target ROI (e.g., heart) second. Once regions are drawn, click the **x/y tool** in the **Toolbar** to display calculations.

The **NM Viewer** screen *(Figure 6.1)* automatically displays all applicable NM datasets most recent to oldest and auto-scales the image to fit the display area. Each image panel has a dataset selection drop-down menu to change the order of the displayed images, if desired. Users can cine each individual image panel or cine all panels together. To cine multiple panels together, click on the **Play** button on one of the selected panels to begin the cine and select the Lock tool. Each image panel has a vertical **Colorbar** located to the right of the image display to provide image windowing and customization. The **Cine Tool Options** are accessed by right-clicking over the **Cine Tool** area of each image panel.
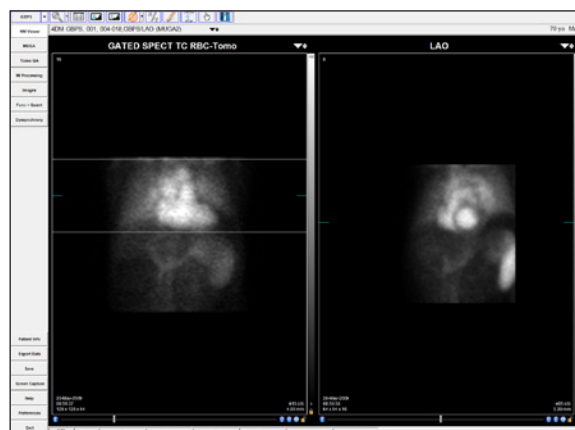

Figure 6.1: The NM Viewer screen displaying a Planar Gated study

MUGA

The MUGA screen *(Figure 6.2)* was created to quantify systolic and diastolic ventricular function from gated planar datasets that contain 8 to 32 frames. The MUGA screen serves as the processing interface, as well as the physician's interpretation and review screen.
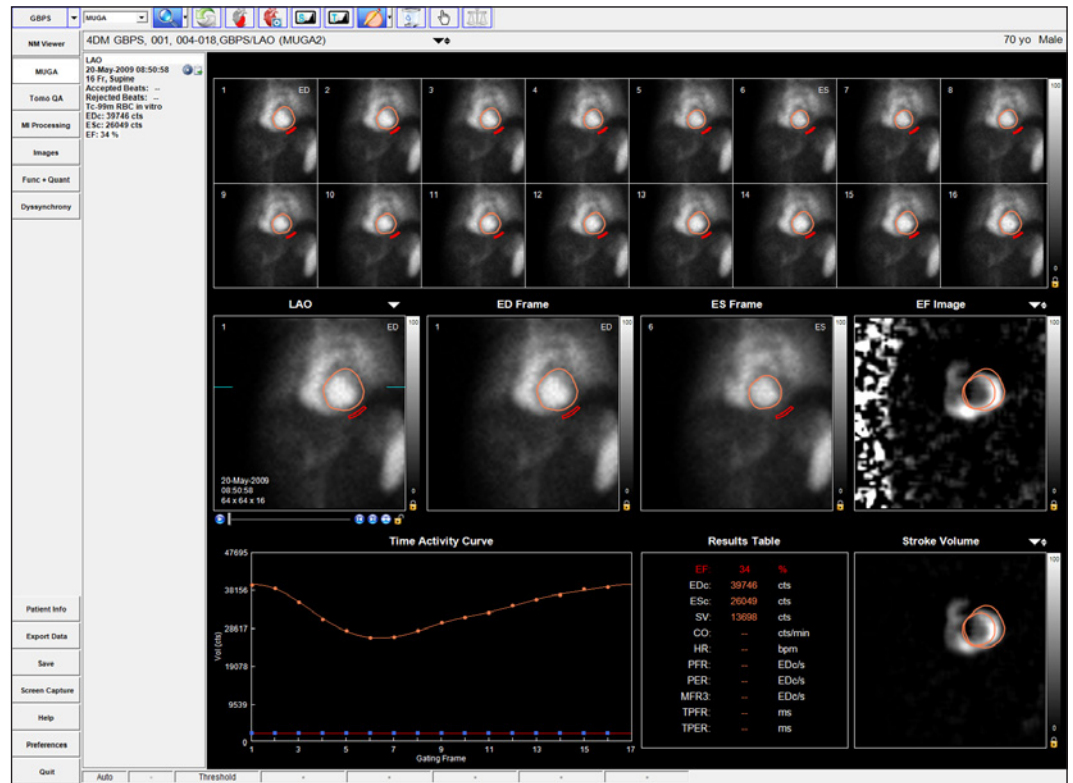

Figure 6.2: The MUGA screen displaying results for one gated planar dataset

For efficient serial study processing, 4DM provides the option to display and process two MUGA studies at one time. Select either the MUGA (one study) or Dual MUGA (two studies) option from the **Study Selector** drop-down menu in the Toolbar.

4DM provides options to process both the right ventricle (RV) and left ventricle (LV). Click on the **Ventricle** tool to select LV or RV *(Figure 6.3)*. Options are available to process studies automatically or manually. Click the **Quantification Menu** tool *(Figure 6.4)* in the Toolbar to choose from the following four types of MUGA quantification:
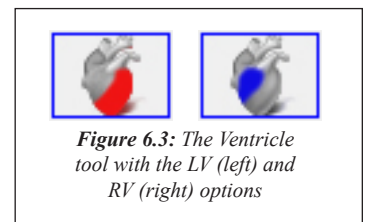

Figure 6.3: The Ventricle tool with the LV (left) and RV (right) options

- **Threshold**
  - Automated method by which the user draws a single Region of Interest (ROI) around the ventricle on any frame in the Quantification Window. The program uses this ROI to localize the ventricle and then applies a threshold technique to draw ROI's on all frames and identify the End Diastole (ED) and End Systole (ES) images. The background ROI is automatically drawn for the user.

- **Interpolated**
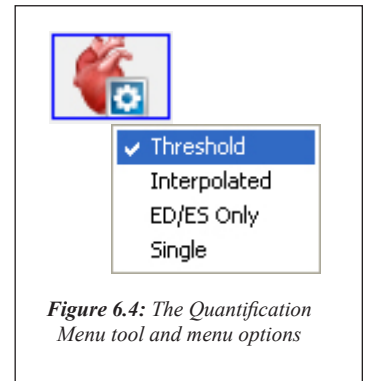 - Semi-automatic method where the user selects the ED and

Figure 6.4: The Quantification Menu tool and menu options

ES frames and draws a specific ROI for ED and ES in the Quantification Window. For the remaining frames, the program generates ROI's by interpolation and automatically draws the background ROI. During interpolation, the program may identify a different frame for ED or ES based on the counts in the study, and will prompt the user to apply the suggested changes. The Interpolated method provides information on filling and emptying rates and displays a complete Time Activity Curve.

- **ED/ES Only**
  - Manual method where the user selects the ED and ES frames and draws a specific ROI for ED and ES in the Quantification Window. The program automatically draws the background ROI and calculates the EF. Both the ED and ES points are used to generate an estimated Time Activity Curve based on single harmonic. For this mode, filling and emptying rates are not calculated.

- **Single**
  - Manual method by which the user selects the ED frame and draws only the ED ROI in the Quantification Window. The program then draws a background ROI automatically and displays the ED ROI on all frames.

4DM provides on-screen instructions in the **Dataset Information Panel** for the user to follow. The quantification steps vary depending upon the quantification method selected. 4DM displays calculations after the required ROI(s) is drawn by the user in the **Quantification Window**. Once the ED and ES frames are identified by the program

Figure 6.5: Dataset selection menu for each viewport

(or defined by the user), each is displayed in their own viewports called the **ED/ES Frame Windows**. These windows display the ED/ES and background ROI's to enable resizing, if necessary. The Ejection Fraction (EF) Image and Stroke Volume (SV) display by default in the remaining viewports, but users can select other options such as **Amplitude** and **Phase** by clicking the dataset selector arrow *(Figure 6.5)*.

The **Time Activity Curve** (TAC) *(Figure 6.6)* plots the ventricular counts for each gating frame. Additionally, the TAC plots the background counts for all frames to assess dropped counts in any of the frames. For Dual MUGA processing, the TACs for both studies are displayed together on the same plot and in different colors.

The **Result Table** *(Figure 6.7)* provides the following quantitative information: EF %, ED counts (EDc), ES counts (ESc), SV, Cardiac Output (CO) in counts/minute, Heart Rate (HR) in beats/minute, and Diastolic Function Parameters which display only for gated datasets that contain 16 or more frames, and
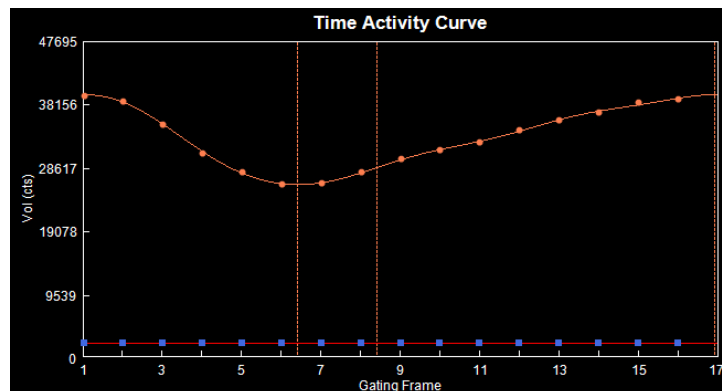
All ROIs allow resizing and panning to ensure proper placement in the viewports.

Once your assessment is complete, right-click the **Patient Info** button to document your findings.

Figure 6.6: Time Activity Curve on the MUGA screen for Gated Planar studies.

Figure 6.7: Quantitative results table on the MUGA screen for Gated Planar studies.

Compute **Diastolic Function Parameters** is activated in User Preference settings. Harmonic Fitting can be applied to the TAC and results by activating the Apply Harmonic Fit to Volume Curve in Preferences. Diastolic Function Parameters displayed in the Result Table consist of:

- Peak Filling Rate (PFR) in ED counts/second (EDc/s)
- Peak Emptying Rate (PER) in EDc/s
- Mean Filling Rate during the initial one-third of Diastolic or Filling Time (MFR3) in EDc/s
- Time to Peak Filling Rate (TPFR) in milliseconds (ms)
- Time to Peak Emptying Rate (TPER) in ms

Once the processing and/or review of the MUGA screen is finished, the Gated Planar Blood Pool Workflow is complete. Those users who acquire Gated SPECT Blood Pool studies should continue to the SPECT Blood Pool workflow.

GBPS Quality Assurance

GBPS Quality Assurance

As with any imaging protocol, assessment of the integrity of the study that has been submitted for interpretation is a critical first step. 4DM has integrated four Quality Assurance (QA) screens which enable users to ascertain study quality from within the software to save time and maximize efficiency. The key QA screens utilized for GBPS review are:

- Tomo QA
- MI Processing

For the first QA step in our GBPS workflow, review the tomographic dataset(s) on the **Tomo QA** screen.

Tomo QA

Users can right-click over the viewport cine controls on **Tomo QA** to set: **Cine Speed** and **Rocking Increments.**

The **Tomo QA** screen *(Figure 6.8)* allows users to view:

- **NM Tomo Datasets**
  - Each Tomo dataset panel has a click-and-drag blue slice plane indicator that allows you to normalize the image to the counts in the heart by aligning it with the hottest pixel in the heart. This plane indicator also defines the plane for constructing the **Sinogram**. The white click-and-drag reference lines above and below the blue slice plane indicator can be used to check for patient motion during cine review of the tomogram and they also define the parameters for the Linogram.

Figure 6.8: The Tomo QA screen displaying a raw GBPS dataset.

- **Sinogram**
  - The **Sinogram** is a two dimensional mapped representation of each one-dimensional frame acquired during a SPECT tomogram. It is useful as another option to visually assess each dataset for patient motion or shifting of the detectors for multi-detector systems. Reference lines identify the corresponding projection image and the location in the Linogram.

- **Linogram**
  - The Linogram is a summed representation of each frame that is acquired during a SPECT
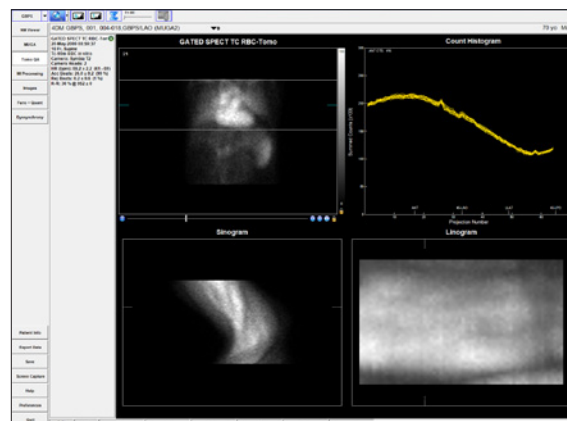
tomogram. It can be used to visually assess each dataset for vertical patient motion or shifting of the detectors between multi-detector systems. The Linogram image is zoomed to fill the display window. Reference lines identify the corresponding projection image and the location in the Sinogram.

- **Count Histogram**
    - The **Count Histogram** plots the summed counts per projection number so users can assess whether there were any significant count drop-offs during the acquisition which would indicate a poorly-gated dataset. The Count Histogram also provides the peak pixel activity (in cts) for the anterior projection. This data should be noted during the QA process because it can signify whether an acquisition is count-poor.

- **Beat Histogram**
    - The **Beat Histogram**, if available, shows the length of time (in milliseconds) for each acquired heartbeat's R-R interval (yellow). The accepted R-R range is noted in blue. This is useful as a quick way to see if there was an unacceptable amount of rejected beats during a gated acquisition. The Beat Histogram is currently available only for Siemens-acquired gated datasets.

- **Gating Information**
    - The **Gating Information** *(Figure 6.9)* gives further details such as the number of Accepted (Acc Beats) vs. Rejected Beats (Rej Beats), Average Heart Rate (HR) and HR Range (in bpm), and R-R Interval settings (in ms).

```
GATED SPECT TC RBC-Tom ⬇
20-May-2009 08:59:37
16 Fr, Supine
Tc-99m RBC in vitro
Camera: Symbia T2
Camera Heads: 2
HR (bpm): 65.8 ± 2.3  (61 - 69)
Acc Beats: 26.0 ± 0.2  (99 %)
Rej Beats: 1.8 ± 0.5  (1 %)
R-R: 30 % @ 952 ± 0
```

Figure 6.9: *The Gating Information in the Dataset Information Panel*

- **Multiple Energy Windows** (for multiple energy radiopharmaceuticals only)
    - The Multiple Energy Window is active above the image viewport when datasets are launched into 4DM that contain multiple energy (in KeV) windows. The default display will be the primary energy window for the radiopharmaceutical and the drop down arrows will allow the user to select from the energy windows that are listed.
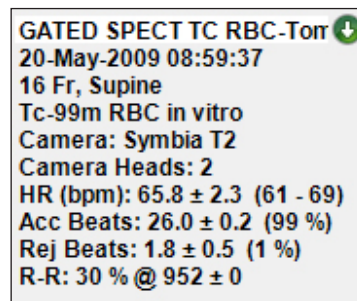
Once you have reviewed the NM data and noted any anomalies on the **Tomo QA** screen, proceed to the **MI Processing** screen to begin your assessment of the automatic 4DM processing results.

MI Processing

Upon launching a patient in Corridor4DM for the first time, the program automatically quantifies the study using 4DM default algorithm settings. The **MI Processing screen** allows users to define LV dataset alignments, apical and basal limits, and LV centers on the VLA, SA, and HLA slices. Users should review all reconstructed datasets on the **MI Processing** screen *(Figure 6.10)*.

The user should confirm that the basal limits are consistent between datasets and that the 4DM LV surface generation algorithm has accurately identified the endocardial surfaces of the LV. These contours are used to calculate the following parameters:

- LVEF
- ED/ES Volumes
- LV Volume Curve
- Cardiac Mass
- Cardiac Output
- Wall Motion Maps
- Contractility Maps

Note that 4DM allows the valve plane definition to differ for volumetric estimates and the generation of polar maps. Adjustments to the basal sliders on the VLA images affect volumetric estimates (systolic,

If only endocardial surfaces are generated, the incorrect radiopharmaceutical was assigned to the dataset. Check the Special File Strings by clicking on the Dataset Matching Strings button with the Preferences menu. To learn more about editing matching strings, go to User Preferences.

4DM recommends selecting **Centering Only** from the **Advanced Algorithm Options** window for GBPS processing.

GBPS studies are present on the **MI Processing** screen in the same VLA, SA, and HLA orientation as SPECT MPI studies. However, users will note that the GBPS dataset displays the blood pool volume of the LV rather than the actual myocardial tissue uptake.

If the LV surface generated includes extra-cardiac activity, it is recommended that the user processes the images utilizing the Constraints Tool. Inclusion of extra-cardiac activity can lead to false impressions and image normalization.
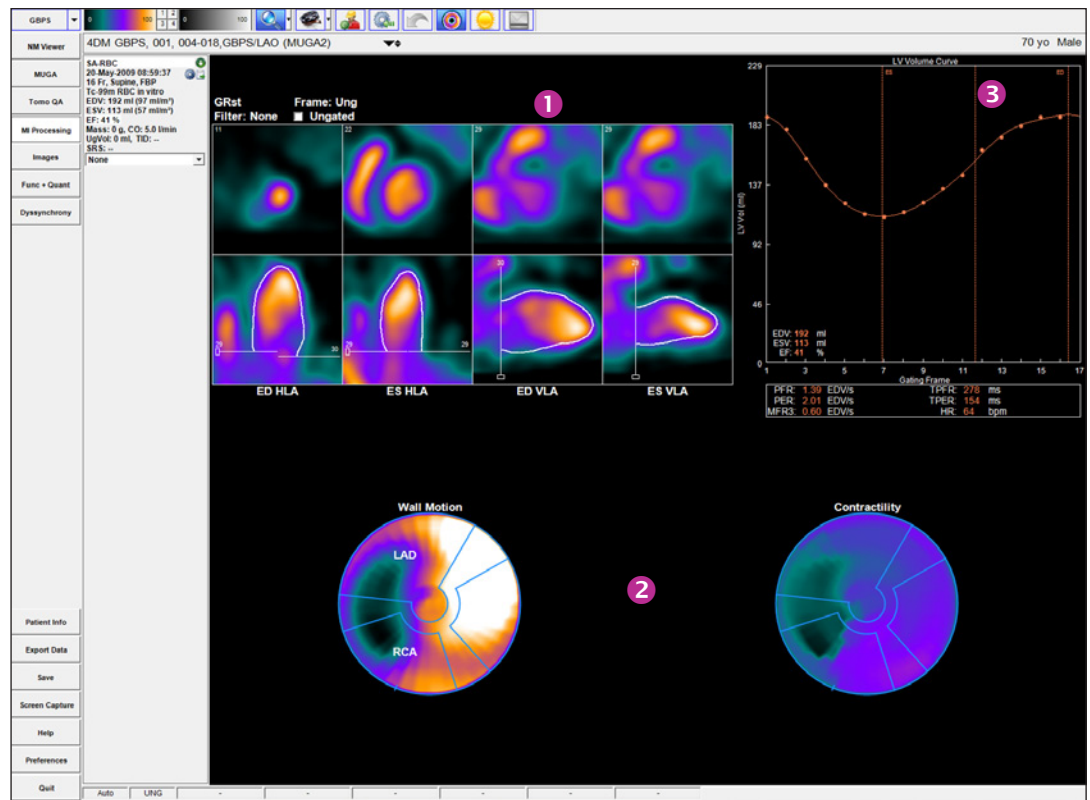

Figure 6.10: The MI Processing screen with a single gated stress dataset displays the following objects: ❶ Processing Splash, ❷ Processing Polar Map, and ❸ LV Volume Curve.

diastolic). For volume estimates, the basal limit is typically placed at the end of the LV as seen on the anterior, lateral and inferior walls. For polar maps, the basal sliders on the HLA images are used to define the axial extent of the myocardium that is mapped to the polar maps. For GBPS it is recommended to use the lateral wall as a guide for setting the limit.

Activating the **Contours** tool *(Figure 6.11)* applies white contour overlays on the endo- and epicardial surfaces of the LV myocardium for all datasets. If the contours properly track the myocardium and if no changes are necessary to the limits/positions, users can proceed to the Images screen to begin the perfusion review portion of the workflow.

Figure 6.11: Contours tool

If contours do not track the myocardium due to poor orientation or centering of the left ventricle, high intensity extra-cardiac activity, or the dataset requires additional filtering, the study should be reprocessed by clicking the **Manual Processing** tool *(Figure 6.12)*. Centering, orientation and axial limits are adjusted using the sliders as shown in *(Figure 6.13)*.

Figure 6.12: Manual Processing tool

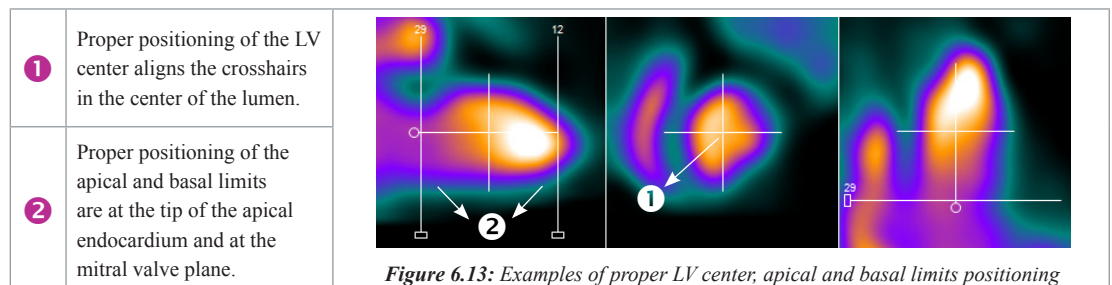|		
❶	Proper positioning of the LV center aligns the crosshairs in the center of the lumen.	
❷	Proper positioning of the apical and basal limits are at the tip of the apical endocardium and at the mitral valve plane.	

Figure 6.13: Examples of proper LV center, apical and basal limits positioning

If the dataset has signficant extra-cardiac activity, click the **Constraints** tool *(Figure 6.14)* to define

a constraint to prevent the contour from tracking the extra-cardiac activity rather than the ventricle. Once selected, modify the size and shape of the constraint limits on the SA slice by adjusting the red constraint handles located at three and six o'clock and centering the crosshairs *(Figure 6.15)*. Once adjustments to the LV center, orientation, and basal limit are complete, the user must click the **Process** tool *(Figure 6.16)* to generate the endo- and epicardial surfaces.
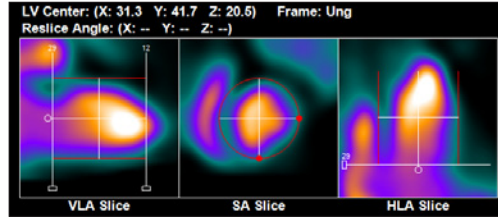

Figure 6.14: Constraints tool

Figure 6.15: Constraints activated and properly positioned

Figure 6.16: Process tool

If the dataset needs to be processed from scratch (i.e. no initial estimates from 4DM), click the **Reset** tool *(Figure 6.17)* and then set the center, angulation, valve plane location and click the Process tool to reprocess.

Figure 6.17: Reset tool

It is important to visually confirm the contours and the basal limits used to quantify functional estimates. Also verify that the basal positions are consistent between datasets and make adjustments if necessary. Once users are finished reviewing the MI Processing screen, the QA portion of the workflow is now complete.

GBPS Qualitative Functional Review

GBPS Qualitative Functional Review

The next step in our GBPS workflow is to begin the image interpretation process. Visual comparison of the gated, ED, and ES **Splash Objects** in the three orthogonal planes is recommended and can be accomplished by visiting the **Images** screen.

Images

The **Images** screen *(Figure 6.18)* represents the GBPS dataset as SA, HLA, and VLA **Splash Objects**. 4DM automatically displays the top row as the gated slices, the middle row as the ED slices, and the bottom row as the ES slices. This screen is useful for thorough visual assessment of individual ED/ES slices in all three orthogonal planes.
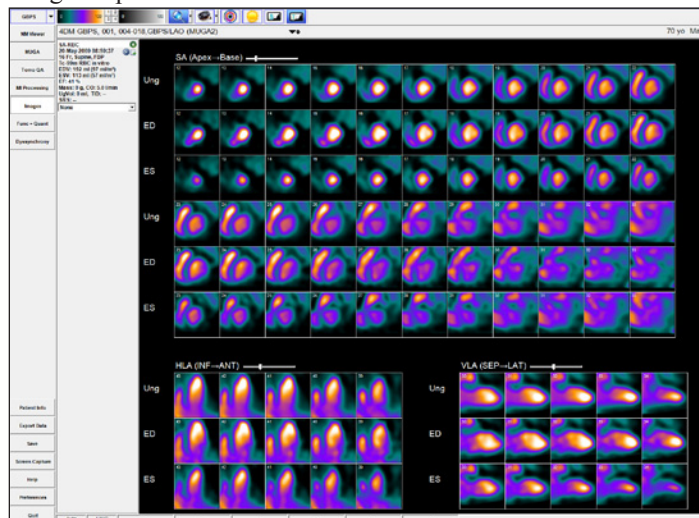
Figure 6.18: The Images screen with a GBPS dataset displayed. This screen is used primarily to perform qualitative review of the Splash Objects in all three orthogonal planes.

GBPS Quantitative Functional Review and Final Interpretation

Functional quantitation for GBPS refers to correlating the clinician's visual estimates with the following 4DM-calculated parameters:

- LVEF
- ED/ES Volumes
- LV Volume Curve
- LV Regional Wall Motion (WM)
- Time to Peak Contractility (TPC)

Func+Quant

4DM recommends utilizing the **Func+Quant** screen *(Figure 6.19)* because it displays the following objects necessary to accurately interpret GBPS studies: **Splash Objects** and the **LV Volume Curve**, and also displays the LVEF calculation.

The Func+Quant Screen displays a gated 3SA Func layout for reviewing the Function of the gated datasets. When only one gated dataset is present, the LV Volume Curve is included to display LV Volume (in ml). The Temporal Filter tool allows the user to apply a filter for enhancing the image quality of the

Figure 6.19: *The Func+Quant screen displays the LVEF, Splash Objects, Polar Maps and Scores Objects, and the LV Volume Curve together all on one screen*

gated slices. The Polar Maps allow the user to view Wall Motion and Wall Thickening while visually comparing to the relative score calculations visible in the Scores Objects.
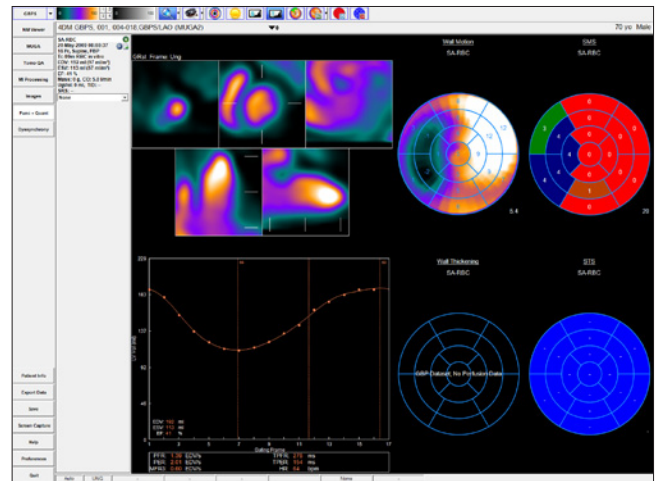
Dyssynchrony

The **Dyssynchrony** screen was created for assessing the phases of contraction for the left ventricle *(Figure 6.20)*. Dyssynchrony is defined as delayed ventricular activation and contraction. Analysis of regional and global contraction patterns in the left ventricle can help identify those patients who may benefit from Cardiac Resynchronization Therapy (CRT). To accurately assess patients for dyssynchrony, physicians can use the following image displays to identify abnormalities in contractile function:

- **Contractility Histogram:** Plots the time to peak contraction expressed as the percent of the R-R frame within the left ventricle. Vertical
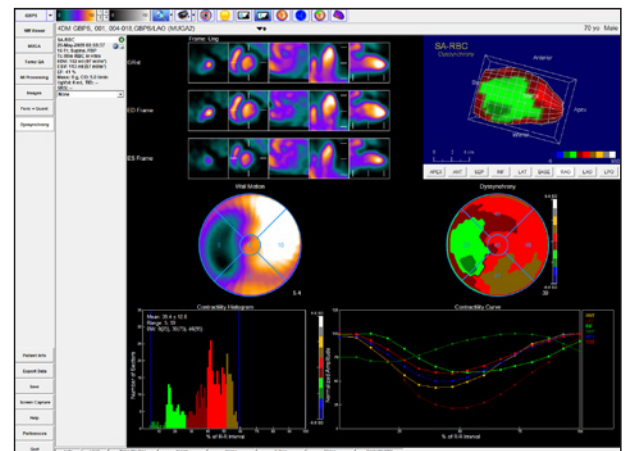

Figure 6.20: *The Dyssynchrony screen was created for assessing the phases of contraction for the left ventricle*

blue indicators signify the start and end points of contractility.

- **Contractility 2D and 3D Polar Maps** *(Figure 6.21)*: Choose between Time to Peak Thickening using First Harmonic Fit, Time to Peak Thickening, and Time to Peak Contractility.

The **Dyssynchrony** screen also provides a 3SA Object with optional contours; Perfusion, Wall Thickening, and Wall Motion Polar Maps; and 3D Objects. The screen layout varies between one or two gated datasets. If two gated datasets are displayed, the Perfusion, Wall Thickening, and Wall Motion Polar Maps are omitted from the screen.
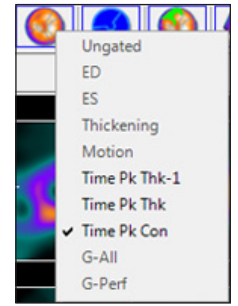

Figure 6.21:
Raw Map Menu

Conclusion

This concludes your GBPS Clinical Workflow Tutorial. Prior to exiting the program, users should ensure to save the 4DM result files. Technologists can transfer the saved results and image datasets to the interpreting physician for review. 4DM recognizes the most current saved result files, so if physicians make any changes to the saved study they should save the updated results.

Reconstruction Screen

The **Reconstruction** screen *(Figure 7.1)* is used to motion correct and reconstruct volumetric images from single photon emission computed tomographic (SPECT) imaging. The motion correction tools from within the Reconstruction screen can be used to generate motion corrected tomographic datasets, which can minimize the need for reacquiring the study. Examples of motion that can be corrected are: patient axial motion, slight shifts between detectors, and cardiac creep. By default, tomographic data is automatically corrected for motion, and images are reconstructed with filtered back projection (FBP) and filtered to reduce the noise in the image data. For cardiac studies, the volumetric images can be formatted in transverse or short axis space for LV quantitative processing.
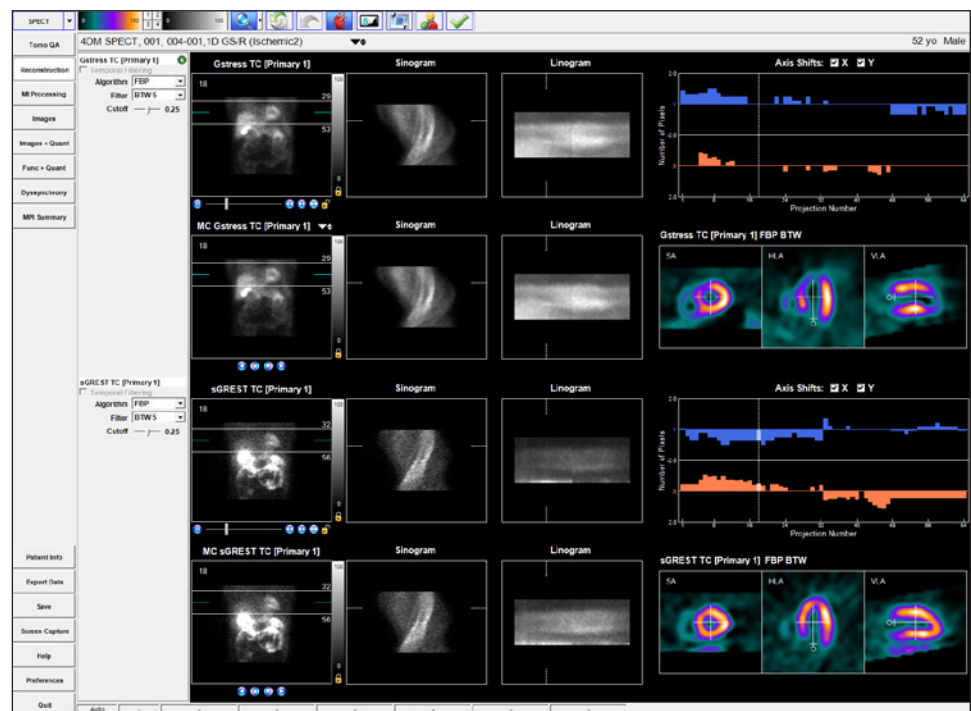

Figure 7.1: The 4DM Reconstruction Screen

The Reconstruction screen includes two modes: **Motion Correction** and **Advanced Reconstruction**:

- **Motion Correction Mode:** This mode provides the capability of correcting the tomographic data for motion prior to image reconstruction. This mode is displayed when motion correction is turned on within preferences for the Reconstruction screen. While only the ungated datasets (e.g., Stress and Rest) are displayed, any corrections applied to them are automatically applied to the corresponding gated dataset(s). The datasets are automatically motion corrected and reconstructed, using pre-defined settings. Options to turn motion correction off for x and/or y axis shift are available above the Motion Correction histogram. Users can also manually motion correct, and/or update reconstruction settings from this mode, for displayed datasets.

- **Advanced Reconstruction Mode**: When motion correction is turned "off" by default, this mode displays on the Reconstruction screen. This mode allows adjusting filter and reconstruction parameters for up to four datasets at a time (e.g., gated and ungated studies are displayed

independently). This mode is also accessed by clicking the "Advanced Reconstruction" Tool in the Toolbar, when in "Motion Correction" Mode. The datasets are automatically reconstructed, using the default settings. Options to adjust the settings are available in the dataset information panel for each displayed dataset.

The primary purpose of this mode is to provide separate controls for reconstruction and filtering of the gated and ungated datasets with the ability to view both simultaneously. In Motion Correction mode, reconstruction controls are available but the ungated and gated datasets cannot be viewed together; the user must toggle between the two datasets.

Motion Correction Displays and Tools

4DM's motion correction includes several display options and tools to assess for motion, apply correction, and make adjustments when necessary.

The tomographic (e.g., "raw") datasets display in cine mode in two formats: the top Tomo Viewport is the original uncorrected tomograph; and the second motion-corrected tomograph is located just below it, in the Motion Correction Tomo Viewport, for comparison purposes.

By default, the ungated datasets (e.g., Stress and Rest) are displayed, and any corrections applied to them are automatically applied to the corresponding gated dataset(s). Gated datasets can be viewed by selection from the drop-down menu, located next to the dataset name in the **Motion Correction Tomo Viewport**.

Displays available in Motion Correction Mode:

- **Tomo Viewport:** Displays the original tomographic dataset, to evaluate in cine mode for motion throughout the acquisition. Standard Tomo cine tools are located below it, and to the right, colorbar tools. The click-and-drag blue slice plane indicates the maximum intensity pixel for image normalization. This indicator also defines the slice used for Sinogram composition and display. The white click-and-drag reference lines define the limits of the area used to identify motion, the range of slices to include in the reconstructed volume, and assist the user in visualizing motion artifacts while reviewing the cine. These limits also define the volume of information displayed in the sample reconstruction (SA/HLA/VLA) and the Linogram.

- **Motion Correction Tomo Viewport** *(Figure 7.2)***:**
  Review of the corrected tomogram in cine mode is accomplished in the Motion Correction Tomo Viewport, located just below the Tomo Viewport. This new dataset is named with "MC" preceding the original dataset name. The movement of the white reference lines on the corrected or uncorrected Tomo viewport are locked to one another. When a gated dataset is present, the ungated dataset corrections are applied to it automatically. To display the corresponding corrected gated study for review and verification of proper correction, a drop-down arrow to the right of the dataset name is present. If no gated study is present, no drop-down arrow is available. In cases where there is an additional acquisition (e.g., prone or viability delays), the user can switch to these by using the dataset layout selector.
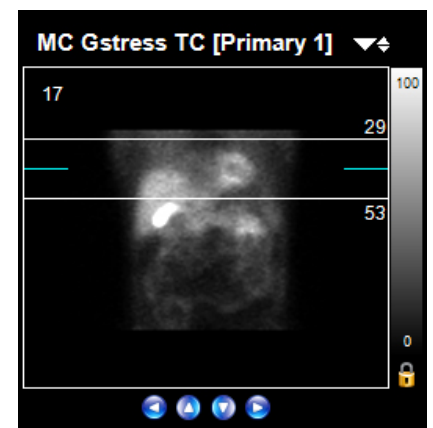

Figure 7.2: Motion Correction Tomo Viewport

- **Sinogram:** The sinogram is a two-dimensional mapped representation of a single image slice acquired during a SPECT tomogram. If the dataset is gated, all frames are summed for this display. Reference lines identify the corresponding projection image and the location in the Linogram. The sinogram is most helpful in identifying in-plane (side-to-side) patient motion or shifting of the detectors between multi-detector systems.

- **Linogram** *(Figure 7.3)*: The linogram is a compression of each projection image to a single vertical line profile and then stacking each projection profile from left-to-right, incorporating counts per frame. If the dataset is gated, all frames are summed for this display. Reference lines identify the corresponding projection image and the location in the Sinogram. The linogram is most helpful in identifying axial patient motion and/or heart motion (e.g. cardiac creep).
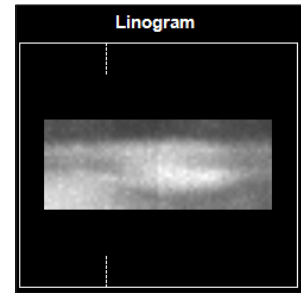

Figure 7.3: *4DM Linogram*

- **X, Y Axis Shifts Graph** *(Figure 7.4)*: Plots the pixel shifts (Number of Pixels) vs. Projection Number for both X (coral color) and Y (blue color) motion that is detected and corrected. Colored bars note frames that required correction, where the longer the bar is, the more motion that was corrected. Datasets that require more than 2 pixels of correction in any frame should be re-acquired if possible. Users can select to correct in one or both axes by selecting the X and/or Y checkboxes above the graph in the Motion Correction Mode of the Reconstruction screen. Defaults can be set for one or both axes to be selected from within Preferences.
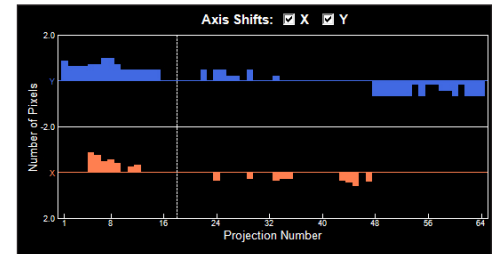

Figure 7.4: *X, Y Axis Shifts Graph on the Motion Correction Screen*

- **Manual Processing Options:** Two methods are provided for manual corrections. Either left click-and-drag (anywhere outside of the white reference lines) on the corrected viewport, to pan the image either in the x or y planes, or use the four manual pan/move controls located below the viewport: Move Left, Move Up, Move Down, and Move Right buttons, which with each click moves the dataset in the selected direction ¼ of a pixel.

- **Slice Displays:** The Reconstruction screen displays a sample SA, HLA and VLA slice that includes orientation and centering tools. These are provided to check for motion artifacts on sample reconstruction that may persist after a first attempt of correction. When one dataset is displayed, two additional rows of slices showing SA, HLA, and VLA orthogonal views will display, to check for motion artifact across more slices.

Tools Available in the Reconstruction Screen Toolbar:

- **Reset Tool** *(Figure 7.5)*: Resets the study to apply and display the original 4DM automatic motion correction.

Figure 7.5: *Reset tool*

- **Undo Tool** *(Figure 7.6)*: Each click of this tool acts to undo each last manual movement. Tool activates when any manual pan or move up/down buttons are used.

Figure 7.6: *Undo tool*

- **Orientation Tool** *(Figure 7.7)***:** Toggle that when selected, displays the sample reconstruction slice viewports in cardiac SA/HLA/VLA orientation, which is the default. When unselected, display is in patient orientation (i.e., Transverse, Coronal, and Sagittal).

Figure 7.7: Orientation tool

- **Spatial Filtering** *(Figure 7.8)***:** Can be applied to smooth the appearance of the Tomo, Motion Corrected Tomo, Sinogram, and Linogram displays..

Figure 7.8: Spatial Filtering

- **Image Mask Tool** *(Figure 7.9)***:** Toggle that when selected, blacks out all image data outside of the upper and lower white reference lines on the Tomo and Motion Correction Tomo Viewports. Useful if extra-cardiac activity is affecting visual analysis of cardiac motion.

Figure 7.9: Image Mask tool

- **Apply Tool** *(Figure 7.10)***: Must be clicked to accept and apply the automatic and/or manual adjustments.** If the Apply tool is not selected, and another screen is clicked for display, a window will present that provides an option to proceed and apply the corrections and reconstructions (click OK), or proceed without applying (click Cancel). When the Apply tool is selected, 4DM will automatically display the MI Processing screen to quantify the newly created reconstructions.

Figure 7.10: Apply tool

- **Advanced Reconstruction Tool** *(Figure 7.11)*: **This tool displays the screen in Advanced Reconstruction Mode.**

Figure 7.11: Advanced Reconstruction tool

Advanced Reconstruction Processing and Tools

The Advanced Reconstruction Mode allows users to perform standard SPECT reconstruction processing for one-to-four datasets at the same time on a single screen and includes the following displays and tools (which can be set as defaults from within Preferences):

- **Slice Selection:** White slice plane indicators on the Tomo viewport determine which slices to include in the reconstructed volume. They should be positioned a few pixels above and below the heart in the field of view to ensure the heart does not get truncated.

- **Reconstructed Algorithm Options:** Located in the Dataset Information Panel to the left of the Tomo Viewport, Filtered Back Projection (FBP) is the only available reconstruction method.

- **Reconstruction Filter Adjustments:** Located below the Algorithm Options, select the filter from the drop-down - Butterworth (BTW) with orders of 2, 5 or 10; Hanning, Hamming, Parzen, Shepp, or Gaussian. Adjust the cutoff and order (BTW only) settings. BTW 5 with a cutoff of 0.25 is the 4DM default filter setting.

- **Reorientation Controls:** To display the reconstructed volume in patient or cardiac space, use the **Reorientation** tool *(Figure 7.12)*. To adjust reconstructed cardiac volumes along the long axis of the heart, click and drag the circular control on the SA, HLA, and VLA slices. After making desired alignment changes, click **Apply** tool to generate the volume.
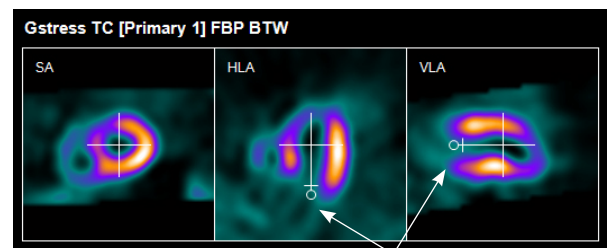

Figure 7.12: Reorientation Controls

- **Scan Arc** *(Figure 7.13)*: Provides a visual of the camera rotation and patient positioning (only available on the Advanced Reconstruction Mode screen).

- **Multiple Image Displays:** A Splash object displays for visualization of the reconstructed volume when one dataset is displayed on the Reconstruction screen. When two or more datasets are displayed together, the Splash object is not displayed.

- **Apply Tool** *(Figure 7.14)*: **Must be clicked to accept and apply the automatic and/or manual adjustments.** If the **Apply** tool is not selected, and another screen is clicked for display, a window will present that provides an option to proceed and apply the corrections and reconstructions (click OK), or proceed without applying (click Cancel). When the **Apply** tool is selected, 4DM will automatically display the MI Processing screen to quantify the newly created reconstructions.

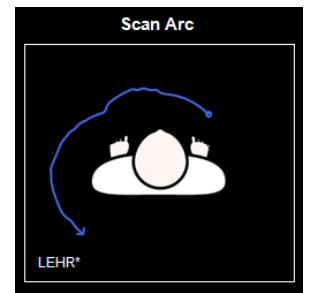- **Motion Correction Tool** *(Figure 7.15)*: **This tool displays the screen in Motion Correction Mode.**

Figure 7.13: *Scan Arc*

Figure 7.14: *Apply tool*

Figure 7.15: *Motion Correction tool*

CHAPTER 8 | CAPTURING 4DM RESULTS

Corridor4DM allows the user to capture and save results for consistent and accurate reference when interpreting patient studies. This chapter will expand upon these two options to capture 4DM results:

- Generate screen captures
- Save individual or composite results

Screen Captures

4DM includes functionality for capturing Static (SSC) and Multi-Frame Screen Captures (MFSC) of any 4DM default or custom screen. To initiate a screen capture, left-click the **Screen Capture** control from the **Control Panel** to open the **Screen Capture Options** window *(Figure 8.1)*. Here you can select from the following options:
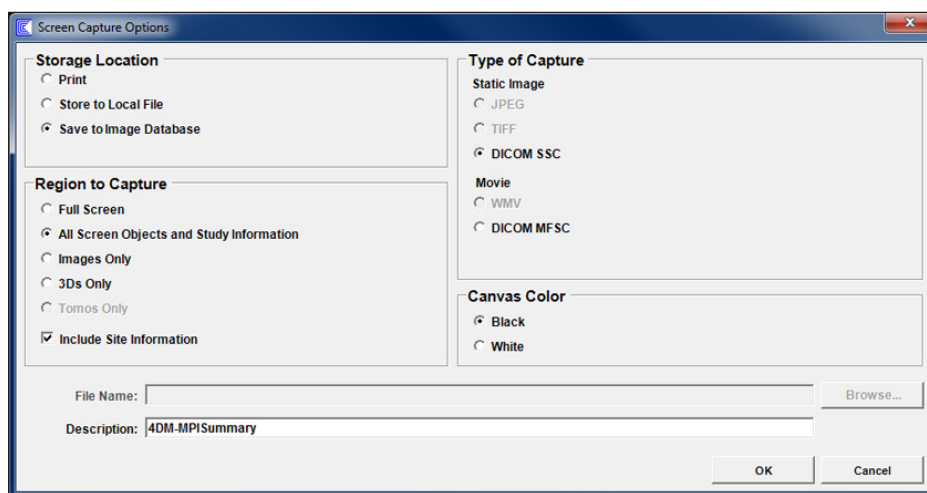

Figure 8.1: *Screen Capture Options window*

- **Storage Location:** Identify where you want to store the screen capture
  – Print
  – Store to Local File
  – Save to Image Database
    • On the GE Xeleris system, **Save to Image Database** is not available. Xeleris users should utilize the Xeleris print tool.
  – Film (only available on the Philips EBW workstation)
    • Transfers 4DM screen capture to filming interface.
  – Report (only available on the Philips EBW workstation)
    • Transfers 4DM screen capture to reporting interface.
  – Direct to Film (only available on the Philips EBW workstation)
    • Transfers 4DM screen capture to DICOM Printer

- **Region to Capture:** Identify the portion of the displayed screen for capture
  – Full Screen
  – All Objects and Study Information
  – Images Only
  – 3Ds Only
  – Tomo Only

Within **Preferences/ Data Export**, users can configure default **Screen Capture** options. In addition, users can choose the **Hide Dialog** option, which prevents the window from appearing each time the **Screen Capture** control is pressed.

If the **Hide Dialog** option is selected and you wish to change **Screen Capture** options, right-click on the **Screen Capture** control to view the window and update your selections.

WARNING
The user should ensure that any screen capture output (print, static pictures, movies) that is intended to be used for interpretation is of diagnostic quality. Interpretation using nondiagnostic output may lead to a misdiagnosis

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– Site Information: Users can define site-specific information to include on all generated screen captures, such as: site logo, site ID, site of service, site name, address, phone number, accreditation status - including accrediting entity, type of imaging service provided, and a free text box to enter miscellaneous information. Site Information is defined from within Preferences, on the Site Information page within Global Settings.

▪ **Type of Capture:** Identify the output format for the screen you wish to capture
   – Static Image
      • JPEG
      • TIFF
      • DICOM SSC
   – Movie
      • WMV
      • DICOM MFSC

▪ **Canvas Color:** When generating a screen capture, users can choose either a Black or White background.

▪ **Filename:** When saving to a **Local File**, users can edit the **Filename** and/or the location. To navigate to a different folder, left-click **Browse**.

▪ **Description:** When saving a DICOM SSC or MFSC, users can edit the Description which will be stored or printed with the image.

Saving 4DM Processed Data

Corridor4DM saves processed data to the database for easy access and review for subsequent uses. If multiple processed files are saved for a single patient and selected for a future review session, Corridor4DM searches through the list and loads the most-recent saved results into the application.

To initiate saving processed data, left-click the **Save** control in the **Control Panel** which displays the **Save Data** window *(Figure 8.2)*. Select from the following options:

▪ **Result Format:** Use this menu to select the result file format.

   – **Individual Pre v7.0:** Stores individual result files for each dataset launched into the application that are compatible with 4DM versions earlier than v7.0 (e.g., 4DM v5.2).
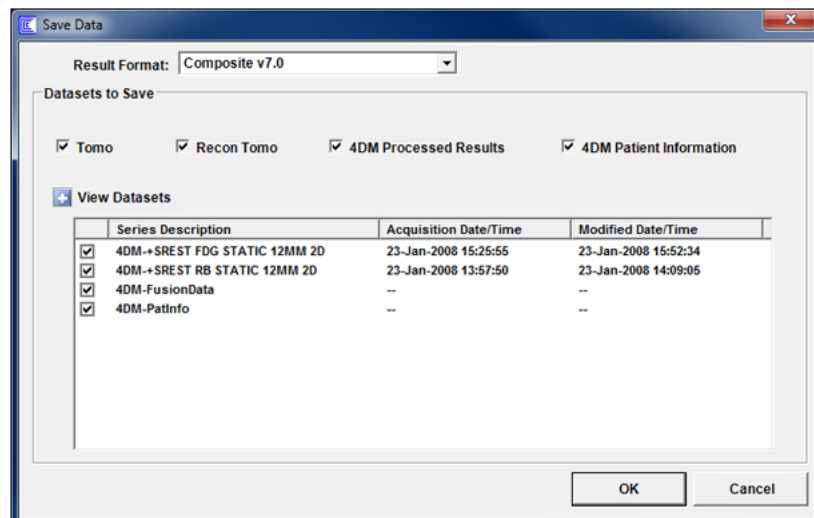

Figure 8.2: Save Data window

– **Individual v7.0:** Stores individual result files for each dataset launched into the application that are compatible with 4DM v7.0 and later (e.g., 4DM v2010).

– **Composite Pre v7.0:** Stores the results for all datasets, including raw data, into a single file that is compatible with 4DM versions earlier than v7.0 (e.g., 4DM v5.2).

– **Composite v7.0:** Stores the results for all datasets, including raw data, into a single file that is compatible with 4DM v7.0 and later (e.g., 4DM v2010).

▪ **Datasets to Save:** Use these toggles to select which results to save.

– **4DM Result Types**

• **Tomo: This option is only applicable for 4DM Reconstruction Option users.** Selecting this option saves any 4DM generated motion-corrected (MC) tomographic (e.g., "raw") datasets in DICOM format. These files are supported by systems that can read and display DICOM format NM tomographic datasets (e.g., PACS).

• **Recon Tomo: This option is only applicable for 4DM Reconstruction Option users.** Selecting this option saves any 4DM generated MC or non-MC reconstructed datasets in DICOM format. These files are supported by systems that can read and display DICOM format NM reconstructed datasets (e.g., PACS).

• **4DM Processed Results:** Saves patient data processed with the 4DM processing screens (automatically or manually), ROIs, and manually entered scores are saved when the toggle is selected. **It is not recommended to deselect this option. Saving these results eliminates the need to QA/Process the study each time 4DM is launched.**

• **4DM Patient Information:** Text data as entered in the Patient Information window (for English versions of 4DM only).

– **View Datasets**

• Click the **Plus Sign** toggle to view all 4DM datasets that are queued to be saved as part of the results. The Series Description, Acquisition Date/Time, and Modified Date/Time are displayed when the toggle is selected. By default, View Datasets is turned off. This toggle, and all Save Data defaults, can be set from within Preferences on the Data Export page. See Chapter 9: Preferences to learn more.

• **Checkbox toggles** next to each Series Description allow the user to deselect any duplicative or unnecessary datasets to save (e.g., user creates multiple reconstructed datasets on the Reconstruction screen, but only wants to save the most current). By default, all datasets are selected.

▪ **Window Controls:** These controls allow you to save information or cancel the save feature.

– **OK:** Saves information as specified with selections made in the **Save Data** window.
– **Cancel:** Closes the window without saving any data.

USER PREFERENCES

The **Corridor4DM Preferences** window *(Figure 9.1)* allows users to configure the application so different users can personalize their workflow environment. Users can quickly select their custom settings by right-clicking on the **Preferences** button within the **Control Panel**. To customize different screens, define layout options, or customize individual users left-click the **Preferences** control within the **Control Panel** to open the window.

The Preferences window is divided into four areas:

1. Window Menus
2. User Specific Settings
3. Global Settings
4. Window Control Buttons
5. Preference Settings Screen

User Specific Settings and **Global Settings** are customized using the **Preference Settings** window.
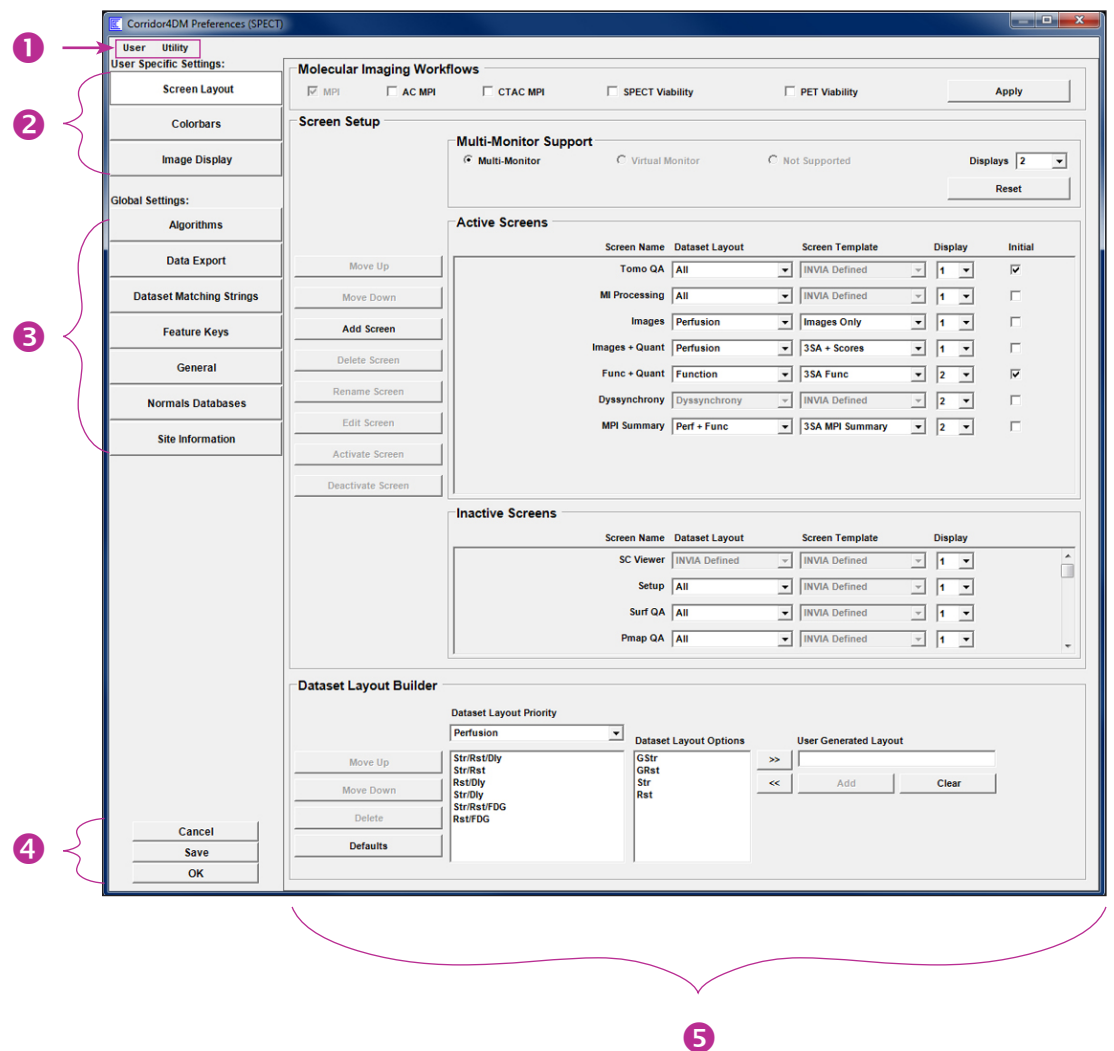

Figure 9.1: *The default page within the Corridor4DM Preferences window.*

Window Menus

The two menus at the top of the screen (**User** and **Utility**) provide tools for custom-defined users and file management.

User Menu *(Figure 9.2)*

- **Create New User:** Opens **Create New User** window; use to create new custom user settings.

- **Select User:** Select which user to activate for preferences editing. If editing, make selections and left-click on **Save** at bottom of screen to apply changes.

- **Delete User:** Select which user settings to delete. If deleted, all preferences files for that user are permanently deleted from the system and 4DM activates the preferences for the Default configuration.

Figure 9.2: Preferences User Menu

- **Initialize Current User:** Left-click this option to reset the current user created preference settings to the original, Corridor4DM default preferences.

- **Reload Current User:** Left-click this option to reload the last saved preferences for the current user, overwriting any changes that may have been made in the preferences window.

- **Reinitialize Workflow:** Left-click this option to reset the selected workflow to the original Corridor4DM default preferences.

- **Automatic Workflow Selection:** Left-click this option to enable automatic matching of Corridor4DM workflows to study type
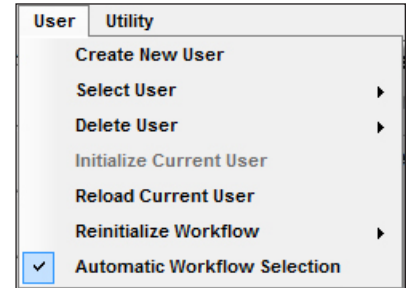
Utility Menu *(Figure 9.3)*

- **Event Viewer:** Displays the local system Event Viewer log, which is useful when troubleshooting 4DM program errors.

- **Backup:** Utility to save 4DM user configurations, screen and report templates, and database files. Users have the option to save in formats compatible with previous versions of 4DM:

Figure 9.3: Preferences Utility Menu

  – Use v4.1 format to backup configurations to be used in 4DM v4.1 or lower.
  – Use v4.2 format to backup configurations to be used in 4DM v4.2 only.
  – Use v5.0 format to backup configurations to be used in 4DM v5.0 and higher.

- **Restore:** Restores 4DM user configuration files that were saved using the Backup utility.

- **Clean Up Files On Exit:** Initiates a clean up of the Corridor4DM temporary files on the local drive when the 4DM application closes.

- **Anonymize Data:** Turn on/off anonymization of the patient name and identifcation number. Anonymization will only be temporary for the current session of 4DM.
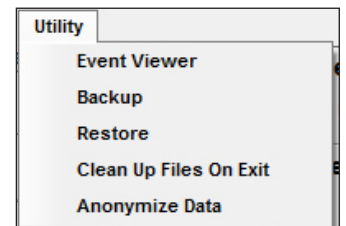
Window Control Buttons

These buttons control the **Preferences** window and appear at the bottom-left of the screen *(Figure 9.4)*.

Cancel

Left-click the **Cancel** button to close the **Preferences** window without saving any changes.

Save

Left-click the **Save** button to apply any and all changes made within the **Preferences** window and close the screen.

OK

Left-click **OK** to apply the current preference settings and close the **Preferences** window.
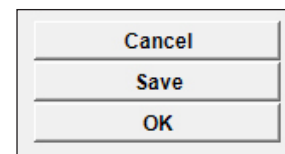

Figure 9.4: Preferences window control buttons

User Specific Settings

The **Preferences** window is comprised of two sections: **User** and **Global Settings** *(Figure 9.5)*. Each page displays in the Preferences Setting Screen. Each button is discussed in detail below.

Screen Layout

The **Screen Layout** page contains three sections to help customize information when configuring the application for specific dataset types. These sections consist of the following:

Molecular Imaging Workflows *(Figure 9.6)*

This section is designed to help the user choose one of five pre-configured workflows. This quickly configures the system to display a series of active screens based on a specific workflow. In addition, users can further customize each screen for display. Molecular Imaging Workflows support the following study protocols: Myocardial Perfusion Imaging (MPI), Attenuation Correction (AC) MPI, CT AC MPI, SPECT Viability, or PET Viability. Check the desired workflow(s) and then left-click **Apply**.
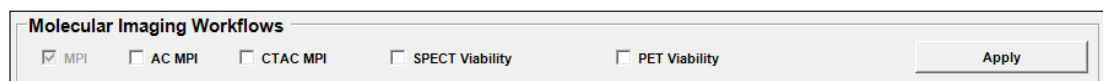

Figure 9.6: 4DM Molecular Imaging Workflows

Screen Setup

The **Screen Setup** section consists of **Multi-Monitor Support** settings, **Active Screens,** and **Inactive Screens** lists *(Figure 9.7)*. Corridor4DM automatically detects the number of hardware displays on the system and auto-selects the corresponding multi-monitor configuration toggle: **Multi-Monitor**, **Virtual Monitor**, or **Not Supported**. The user is only presented with the toggle(s) that fits their monitor configuration, with the remaining toggle(s) grayed-out.

The **Multi-Monitor** toggle is auto-selected when two or more hardware displays are detected. The **Virtual Monitor** toggle is auto-selected when a minimum display of 2560 x 1024 or 1280 x 2048 is detected. This selection divides a single, oversized monitor into multiple displays (up to four). If changes are made to display settings or the number of hardware displays change, the user can click the **Reset** button to revert to the last saved monitor settings. In a single monitor setup, the **Not Supported** toggle is auto-selected.

Active Screens appear in the 4DM **Workflow Screens**. To activate a screen from the **Inactive Screens** list, select the desired screen and then left-click the **Activate Screen** button. The **Deactivate Screen** button moves an active screen to the **Inactive Screens** list.

- Users can configure screens by performing the following tasks:
  - Assign each 4DM screen a specific hardware or virtual display by selecting the **Display** number from the drop down menu.

Figure 9.5: Page Selection Buttons within the Preferences Window

For additional information on 4DM review screens, refer to Customizing the List of Active Screens on the INVIA website.

Figure 9.7: 4DM Screen Setup Section

- Customize the screen order by left-clicking the Screen Name and then left-clicking the **Move Up** or **Move Down** buttons.

- Assign **Dataset Layout** options from a menu for active screens. The dataset layout determines which datasets display on the screen, and with what priority. Users can define Dataset Layouts in the **Dataset Layout Builder**.

- Select 4DM **Screen Templates** from a menu. Templates define which objects display on the page. See the 4DM Objects and Templates Matrix for more information.

- Choose which screen from your workflow displays first when the application is launched. Select the check box in the **Initial** column next to your desired Active Screen(s).

▪ Screens can be added, deleted, renamed, and edited for specific customization. For customization step-by-step instructions, refer to How to Create a Custom Summary Screen on the INVIA website.

Dataset Layout Builder

4DM includes a variety of **Dataset Layout Priorities** which can be configured to user specifications within the Dataset Layout Builder *(Figure 9.8)*.

If the datasets available do not match the dataset layout defined for the screen, or any of the other defined dataset layouts, 4DM displays the first four reconstructed datasets for the patient.

Figure 9.8: Dataset Layout Builder section

- The **Dataset Layout Priority** menu lists available dataset layouts (e.g., Perfusion, Function, Perf + Func, etc.). Users assign a **Dataset Layout** to screens in the [Screen Setup](#) area.

- For each **Dataset Layout Priority**, datasets are grouped and displayed in the window below the menu (e.g., Str/Rst/Dly, Str/Rst, Rst/Dly, etc.). Each dataset group defines for 4DM the sequence in which to display data within objects.

  - 4DM first determines which dataset grouping matches the loaded datasets for the patient, starting at the top and going down the list *(Figure 9.9)*.

  - Once 4DM determines with dataset grouping to use, the application displays the datasets according to the left-to-right order within the group. *(Figure 9.10)*.

- Users can configure dataset layouts by performing the following tasks:

  - Prioritize dataset groups by selecting the group from the list and then left-clicking the **Move Up** or **Move Down** button.

  - Delete a dataset group by selecting the group from the list and then left-clicking the **Delete** button.

  - Add a dataset group by building it within the **User Generated Layout** field. Left-click the desired dataset from the **Dataset Options** window and click the double-right arrow to add it to the field. Build the group and then click **Add**.

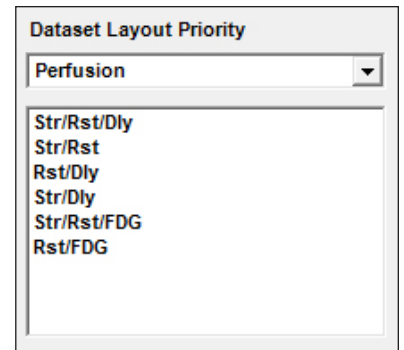- Reload 4DM defaults by clicking the **Defaults** button.

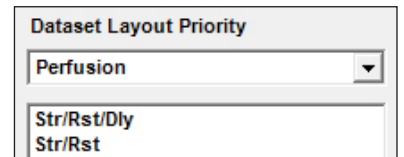*Figure 9.9: Matching a dataset group to a priority first by list order.*

Figure 9.10: After 4DM matches the dataset group, the application displays datasets in left-to-right order.

Colorbars

The user can activate or deactivate color schemes available in 4DM from this page *(Figure 9.11)*. Sync colorbars for all screens, create or modify HU Ranges for CT Imaging, and set default color schemes for CT and Tomo displays.

A check box designates the status of an active color scheme; click the check box next to the corresponding color scheme to make it available. The three buttons located beneath the color scheme list execute the following tasks:

- **Reload System Color Schemes:** Select this button to query a list of all available color schemes currently on the system. Use this button to update new system color schemes.

- **Select All: S**elect this button to activate all listed color schemes.

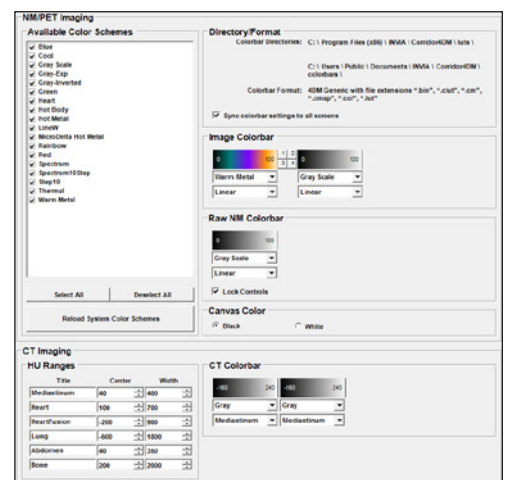- **Deselect All:** Select this button to deactivate all listed color schemes.

Figure 9.11: Colorbars page

The **Deselect All** button does not apply to color schemes assigned to the Image, Severity, and Tomo display screens.

The **Directory/Format** shows where colorbar file directories are located and the acceptable colorbar file formats. In order for users to add colorbars to 4DM and save within the 4DM **Backup**, the files need to be added to the directory folder labeled **colorbars** (e.g., C:\Users\Public\Documents\INVIA\ Corridor4DM\colorbars)**.**

Within this preference page, the user can also set the default color schemes for the following type of images:

- **Image Colorbar:** Select the default color settings for 2D and 3D image and polar map displays. (Does not apply to the Defect Severity polar maps.)
- **Raw NM Colorbar :** Select the default color settings for Tomo object.
- **CT Imaging Colorbar:** Edit upper and lower HU limits for six preset CT HU Ranges. Set dual color schemes specific to each HU Range specified.

Image Display

The Image Display page *(Figure 9.12)* allows users to define common preferences for image data, polar map, and scoring data throughout the entire application.

- **Image Data**
  - **Summing for Recon Dynamic Tomo:** Allows user to define the time range used to sum dynamic recon tomo datasets for analysis in 4DM. Filter type, cutoff, and order can also be defined.
  - **Image Interpolation:** Cubic creates a smoother, magnified image by averaging multiple nearby pixels. Linear creates a faster, magnified image by averaging a few nearby pixels.

Figure 9.12: Image Display page

  - **Image Normalization:** Normalize images to hottest pixel in the heart or the entire volume.
  - **Frame Normalization:** Normalize gated images to end-diastolic or end-systolic frame.
  - **Auto Magnification:** Turn on/off the auto-magnification on the **Splash** and **3SA Objects**. When activated the image fills 70% of the object using the largest volume in the dataset.
  - **Slice Averaging:** Turn on/off the automatic slice averaging for **Splash Objects**. When activated, the program averages the slices to fill the total number of slices allowed for display.
- **Polar Map Data**
  - **Polar Map Smoothing:** Turn on/off the polar map smoothing option.
  - **Vascular Overlay Results:** Set default vascular overlay type: Vascular, Vasc(NG1), or Vasc(NG2) for exporting results.
  - **Comparison Map:** Set default comparison map type for the **Polar Map Object**: None, Revers, Viability, Diff12, Diff21, or T1/2.
  - **Severity Map Stats:** Define the units for severity map statistics as Extent(%) or Severity (StDv).
- **Scoring Data**
  - **Scoring Overlay:** Define the segmental model (17, 19, or 20) for the **Scores Object**.

Global Settings

The Global Settings are not specific to any one user, but instead apply to all users of the 4DM application.

Algorithms

The Algorithms preferences page *(Figure 9.13)* is used to modify parameters used to track the surfaces of the left ventricle. The parameters can be modified based on users preferences of how the software generates contours.

Figure 9.13: Algorithms preferences page

WARNING

Changing the algorithm settings can have a significant impact on the accuracy of the surface generator. Only users familiar with the surface generator algorithm should adjust the values from the default settings.

Iterative Alignment

- **None:** Turns off the Iterative Alignment Algorithm for the surface generator.

- **Centering Only:** When the endo- and epicardial surfaces are detected, 4DM estimates the true center and apical plane from the surface data. If these values have changed significantly from the last positions used, the surface estimator is restarted with these new "improved" positions. This process significantly reduces the variability with the initial LV center and apical plane positions. The default is five iterations which provides improved inter-study variability with minimal impact on computation time.

Extensive validation has been performed with the default, **Centering Only**, and its use is recommended.

- **Centering and Tilt:** Identical conditions apply from **Centering Only** with the addition of tilt. In perfusion studies with angular variation between reconstructed datasets, processing with the tilt option will assist in making all processed datasets orthogonal to the long axis, improving image alignment. Due to differences in surface detection algorithms, the tilt option may not be optimal when applied to SPECT blood pool images.

In rare occurrences where there is high hepatic activity in conjunction with large inferior defects, the surface algorithm may iteratively put the surface into the liver. For these rare cases, the user could turn the iterative centering option OFF.

- **Constrain Axial Length:** When checked, the initial LV axial length found prior to surface estimation is constrained based on the length averaged from all of the datasets associated with the patient.

Basal Plane Motion

For serial LVEF comparisons to QGS, constraining the basal motion (0 to 6mm) is acceptable. It is strongly advised to use the default values (5mm to 20mm).

- **Min/Max:** Based on MRI and echocardiography data, 4DM assumes that the base of the left ventricle will move between 5mm to 20mm. Other software packages may limit the motion of the valve plane to a range of 0 to 6 mm. While this has appeal if serial EF assessments are being performed, the accuracy of the estimates is reduced by using the basal range of (0,6)mm rather than (5,20)mm.

- **Valve Plane Algorithm:** Users can choose where 4DM sets the valve plane for polar map generation:
  - **Lateral Wall:** Places valve plane near the base of the lateral wall.
  - **Septal Wall—Mid Membranous Septum (4DM default):** Centers the valve plane between lateral and septal walls.
  - **Septal Wall:** Places valve plane at base of the septal wall.

Functional Estimates

- **Apply Harmonic Fit to Volume Curve:** If active, 4DM smooths the volume curve displayed for gated data using a fourth order harmonic.

- **Compute Diastolic Function Parameters:** (For 16-frame studies only) If active, 4DM computes diastolic function parameters which display on the volume curve. 4DM applies harmonic curve fitting by default if this option is active.

Polar Map Algorithms

- **Volume Normalization:** When this option is selected, polar map normalization is determined by the volume

- **Slice Normalization:** When this option is selected, polar map normalization is determined per image slice for each non-apical slice in the polar map. The apex is normalized to the most distal image slice.

Data Export

The Data Export page *(Figure 9.14)* allows users to configure settings for the default Save and Screen Capture options. Each time the **Save** or **Screen Capture** buttons are pressed within the application, the program automatically recognizes the options entered on this page within Preferences.

The user can select the **Hide Dialog** toggle, to eliminate viewing/verifying the **Save Data** or **Screen Capture Option** windows each time these buttons are pressed in the application. When the Hide Dialog option is selected, users can right-click on the **Save** or **Screen Capture** buttons to view or edit these window options on an as-needed basis.

Figure 9.14: The Preferences Data Export page

In the Save Data window, users can view and choose which datasets to save by selecting the **View Datasets** button.

The **DICOM Settings** box allows the user to define the character encoding scheme for DICOM files from 4DM:

- The option **ISO_IR 192**, the default, supports all characters for international languages

- The option **ISO_IR 100** supports basic Latin1 characters (English, Romance languages)

Dataset Matching Strings

4DM relies on the default text strings to automatically recognize certain files and protocols. In addition to the 4DM standard strings, users can add strings so 4DM can recognize site-specific naming conventions. These added strings are matched to the site-specific dataset description (e.g., Instance or Series Description) entered at acquisition. If the file type is properly defined in the image file, these strings are not used.

Protocol Strings

4DM identifies the protocol type (e.g., Stress, Rest, and Delay) by matching the dataset description with the character strings *(Figure 9.15)*. Users can reset all dataset matching strings fields to 4DM defaults by selecting the **Reset** button.

Figure 9.15: Protocol Strings

File Type Strings

The image files of some vendors do not specify the type of data in the file (e.g. Tomo, Transverse, Short Axis). In order for 4DM to recognize these files, identification strings can be defined *(Figure 9.16)*.

Figure 9.16: File Type Identification Strings

Special File Strings

4DM uses these strings to identify and differentiate gated blood pool from perfusion datasets, attenuation maps from emission datasets, and non-contrast from contrast CT datasets. *(Figure 9.17)*.

Figure 9.17: Special File Identification Strings

Reconstruction Strings

4DM uses these strings *(Figure 9.18)* to identify the corrections used during image reconstruction to accurately compare the dataset to the appropriate normals database. 4DM initially tries to determine the reconstruction method by searching the DICOM header fields. 4DM will consider all files that don't match a minimum of one of these fields as generated utilizing FBP.

Figure 9.18: Reconstruction Type Identification Strings

Feature Keys

This page displays information for the user to identify which features Corridor4DM contains and when the license key expires. Depending on which License Model radio button is selected, the licensing information below will change. *(Figure 9.19)*

Fixed License:

- The **File Location** must be identified, and the **Check Status** button must be clicked to verify that the **Status** displays that the license key is valid.

Floating License:

- **License Model:** Displays the type of license identified (e.g., Fixed, Floating, Floating with backup, Other)
- **IP Address: Displays the IP Addess of the License Manager and subsequently the Port**.
- **Server Information:** Displays the Total Number of Licenses, Number of Active Licenses, and Counted by fields.
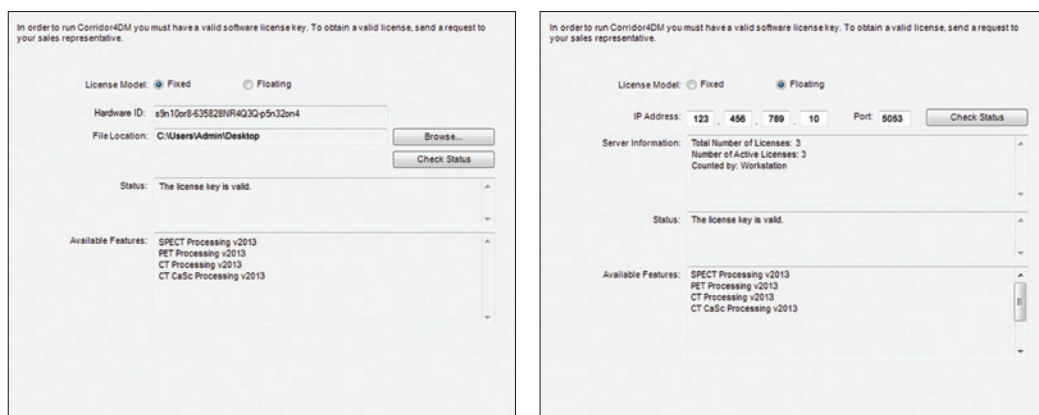

Figure 9.19: *Feature Key Licensing Options*

General

The General page within Preferences *(Figure 9.20)* provides the capability to change settings for Audit Logging, Clean Up Schedule, and Display Performance.

Audit Log

The Corridor4DM **Audit Log** option enables the ability to track access and changes to patient files by turning the option on or off, and the user has the ability to specify the **Audit Log Location** to retrieve the log files.

- **Maximum Log File Size:** Defines the amount of disk space each audit log will occupy prior to creating a new log.
- **Backup:** The user can back up audit logs to a different directory from the **Audit Log Location**.
- **Validate:** Provides validation report for the Master Log file and subsequent log.

Clean Up Schedule

Corridor4DM writes processed data to temporary files for retrieval when the user changes display layouts. 4DM offers the convenience of keeping these files available to the network so that processing can occur at one computer and a physician can review the results on a different computer without having
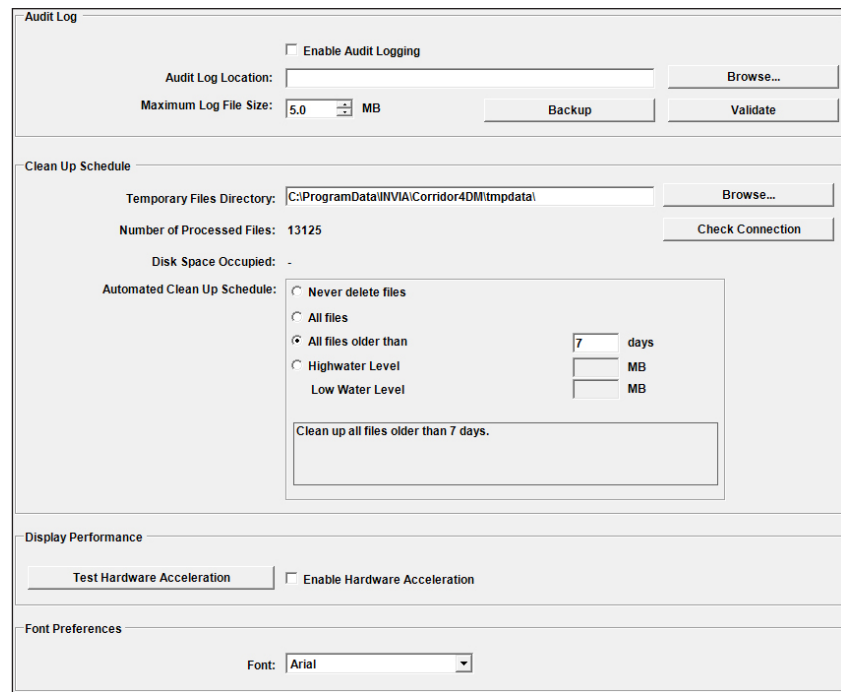
Figure 9.20: *The Preferences General page*

to reprocess the studies. These files are small (500k for a 16 frame gated SA dataset), so several days can be kept online without filling up the disk.

To manage this process, users can define a variety of parameters:

▪ **Temporary Files Directory:** This is the directory where 4DM stores processed files. Local and network directories are allowed; however, if a network directory is defined, the user is not permitted to automatically delete files from this directory. A manual or automatic clean up can only be performed on a local directory.
 – **Browse:** This button allows the user to define an alternate location for the processed files directory, if desired.
 – **Check Connection:** This button verifies the ability to write to the selected directory. If the defined directory is not accessible, 4DM will use the directory defined during installation.

▪ **Number of Processed Files:** Displays the actual number of processed files currently found in the directory.

▪ **Disk Space Occupied:** Displays the amount of disk space occupied by those processed files.

▪ **Automated Clean Up Schedule:** Users may access this option only if the processed file directory is local. To change the clean up schedule, modify the following options:
 – **Never delete files:** Saves all processed files. Use this with caution as eventually these files will use all of the available disk space and the system will become unstable.
 – **All files:** Deletes all processed files at the end of each 4DM session. Use this option if you save the processed and patient information to the image database. If this is done, there is no need to store a temporary copy of the processed files.
 – **All files older than:** Deletes all files older than the specified number of days.
 – **High and Low Water Levels:** When the total size of processed files exceeds the High Water Level, the oldest files are deleted until total size is less than the Low Water Level.

Display Performance

The Display Performance section provides an option to test the system hardware acceleration (e.g., graphics card) and driver, which determines the optimal settings for handling displays of the following types of objects:

- 3D surface renderings
- CT MPR displays
- CT MIP displays

Once the **Test Hardware Acceleration** button is selected, a window displays which begins the automated testing of the system. The Enable Hardware Acceleration toggle is not selected upon default. Upon test completion, a window displays providing the option to select yes or no to enable the hardware acceleration.

Font Preferences

The user can change the system font style used within 4DM to a different selection from the drop down menu. The application must be restarted before this setting will take effect.

Normals Databases

The case-sensitive password to unlock and edit this page is **MSPECT4D**.

The Normals Databases page within Preferences *(Figure 9.21)* is a password protected page that allows the user to control which Normals Databases are active in 4DM, and make any changes to the Segmental Scoring Thresholds and Defect Threshold Settings for **Perfusion**, **Wall Thickening**, and **Wall Motion**.

The Normals Databases preferences page is used to resolve conflicts with database matching. To ensure that a specific database is given the highest priority, the user should deactivate other databases that are in conflict. Check Database Last Modified date to verify that the database has not been modified.

To select a database from the list, left-click anywhere within the row for that database.

To select multiple databases at once, hold the shift key while selecting the first and last in a consecutive list; hold the control key [Ctrl] while selecting multiple non-consecutive items.

Figure 9.21: Normals Databases page in Preferences

Normals Databases

The directories for the Normals Databases within 4DM are displayed above the list of currently activated Normals databases. The Normals Databases are listed by Database Filename and Status to let the user know which databases are currently active. Selecting a database from the selection window will display the Name, Protocol, Radiopharmaceutical, Gender, Gating, Corrections, Recon Arc, Manufacturer, Model, and Filename for that specific database. The five buttons in this display function as follows:

- **Init DB List:** Activates all 4DM Normals Databases on the system. If no databases appear in the list, clicking on this button will reload all Normals Databases and make them active.
- **Activate:** Makes the highlighted Normals Database active in the list.
- **Deactivate:** Makes the highlighted Normals Database inactive in the list.
- **Reset:** Resets the highlighted Normals Database polar map defect and segmental scoring thresholds back to the default database settings.
- **Reset All:** Resets all Normals Database polar map defect and segmental scoring thresholds back to the default database settings.

Normals Database Thresholds

The user can set the Polar Map Defect and Segmental Scoring Thresholds presented in units of standard deviations (StDv) below the normal mean. The **Perfusion**, **Wall Thickening**, and **Wall Motion** tabs allow parameters to be defined for the polar map defect and segmental scoring thresholds. The three tab controls are only present when the Normals Database that is highlighted in the selection window contains the associated parameters.

<table>
<tr><td width="50%">

- **Polar Map Defect Thresholds:** These settings are used in computing Blackout and Severity maps on the display screens. The default values are uniform 2.5σ for all defect threshold maps. When Use Global Threshold Slider is selected, the threshold settings are applied uniformly throughout the polar maps in 4DM. When Use Database-specific Regional Thresholds is chosen, the user can apply different regional thresholds by segmenting each polar map using one of four segmental overlays provided in the Thresholds drop-down menu *(Figure 9.22)*. The segmental overlays are:

</td><td width="50%">

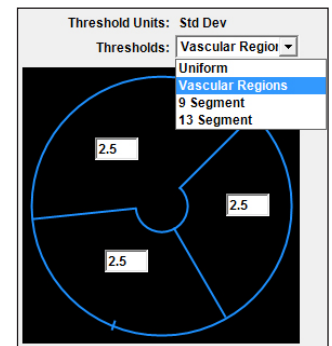*Figure 9.22: Polar Map Regional Segmentation Menu*

</td></tr>
</table>

- Uniform
- Vascular
- 9 Segment
- 13 Segment

4DM does not support user-specific, multiple regional polar map defect thresholds for a single database. Only one set of regional threshold values can be stored per database.

- **Segmental Scoring Thresholds** *(Figure 9.23)***:** These settings allow the user to change the automatic, semi-quantitative scoring thresholds in 4DM. Users can define the numerical value (in StDv) for **Units for Comparison**, and can set the color scheme that is associated with each threshold.
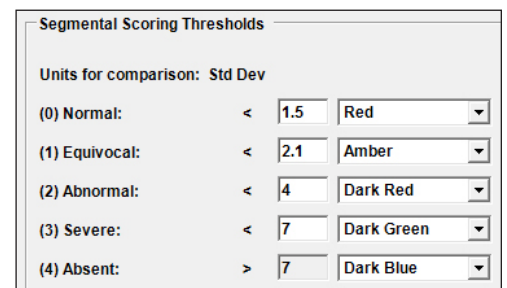

Figure 9.23: Segmental Scoring Thresholds page

Site Information

The **Site Information** page *(Figure 9.24)* allows the user to define site-specific labeling, contact, and accreditation information to be displayed on 4DM screen captures and formatted reports. Define a standard label for your site by entering any of the following information:

Figure 9.24: Site Information page

- **Site Logo: Browse** to select the desired image file (e.g. jpg, gif, tiff, png, or bitmap). The **Delete** Button will delete any previously selected file used for a Site Logo.

- **Site ID:** Enter the facility's unique site identification number

- **Site of Service:** Select this drop-down menu to define the type of facility. Classifications for the site are as follows:

  - Hospital-inpatient (Default option)
  - Hospital-outpatient
  - Nonhospital-inpatient
  - Nonhospital-outpatient
  - Mobile-based-inpatient
  - Mobile-based-outpatient

- **Name**, **Address**, and **Phone Number:** Enter site-specific contact information as you would like it to appear on screen captures and formatted reports.

- **Accreditation Status:** This drop-down menu allows the user to select the accreditation status for the facility. Indicate that the site is accredited, non-accredited, or pending approval for accreditation.

  - Under Accreditation Status, the user also has the ability to select the **Accreditation Entity**(s) that the site is affiliated with. The user can also select the type of **Imaging Service**(s) for which they are accredited.

- **Free Text:** The text box permits the user to enter any additional site information to be included on screen captures and formatted reports.

Chapter 10 | Creating Normals Databases

Corridor4DM provides users with a variety of Normals databases developed for 4DM. 4DM also includes an efficient and user-friendly tool to create and manage Normals databases. A Normals database is used to assess a patient's radiotracer distribution (e.g., perfusion) as compared to a normal distribution. It is customary to generate specific Normal databases based on radiopharmaceutical, gender, acquisition, and processing protocols. Modifying or creating a Normals database file must be done with great care.

To ensure accurate quantitative analysis, it is recommended that a Normals database appropriate for the patient's datasets be used. Likewise, when creating or modifying a Normals database, it is important that all the individual normal volunteers' or low likelihood normal patients' data be matched for imaging variables.

To access the **Database Generator** *(Figure 10.1)*, left-click the **DB Generator** button from the **Workflow Screens**.

DB Generator Screen

This screen is designed to review and generate new databases. The following parameters can be selected when customizing Normals databases:

❶ Stats Tool – Activates or deactivates segmental myocardial or functional statistics displayed superimposed on Normalized polar maps.

❷ Raw Map Menu – Provides a list of tomo data types (Ungated, ED, ES, Wall Thickening (WT) and Wall Motion (WM)) that can be displayed for the patient's dataset.

❸ Comparison Map Menu – Provides a list of maps that can be generated from a comparison of two datasets (only available when two or three datasets are displayed).

❹ Create Database Tool – Left-click to display the **Create New Database** window.

❺ Add Patient to Database Tool – Left-click to add a patient's data to the selected Normals database. Once added, the tool becomes inactive.

> It is customary to generate specific normal databases based on gender, radiopharmaceutical, acquisition, and processing protocols.

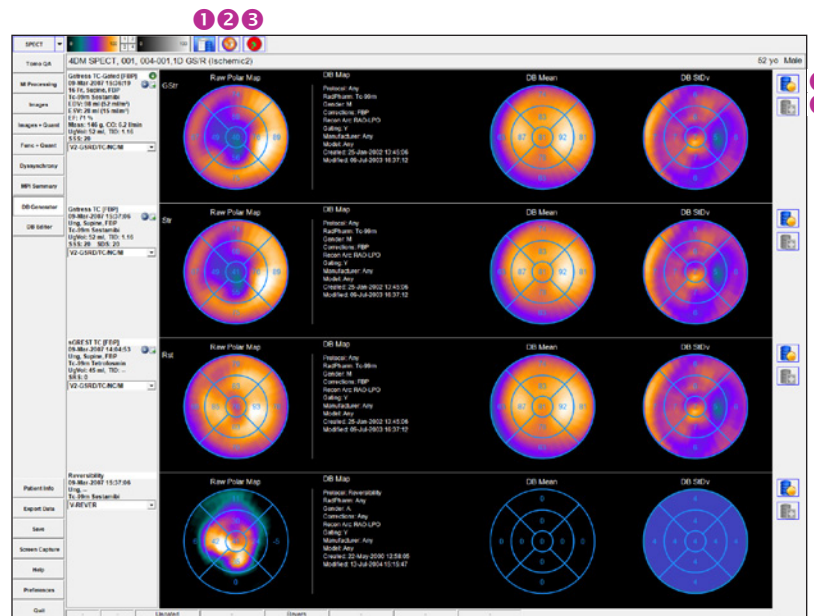> You cannot edit a 4DM-supplied Normals database.

Figure 10.1:
Left-click DB Generator button in the Workflow Screens to display the DB Generator Screen

- If the selected patient's image data does not match the selected Normals Database with respect to gender, radiopharmaceutical, acquisition, and/or processing parameters, the **Add Patient to Database** tool will be inactive.

Create New Database Window

The **Create New Database** window provides a series of fields designed to streamline the creation of a new database. The window is divided into three sections: Acquisition/Processing Options *(Figure 10.2)*, Database Filename and Description *(Figure 10.3)*, and List of Database Files on System *(Figure 10.4)*.

Figure 10.2: Acquisition / Processing Options

- **Acquisition/Processing Options**
  – These selections define the acquisition and processing parameters for the database.
  – **Radiopharmaceutical:** Choose from a menu of nuclear cardiology-specific radiopharmaceuticals.
  – **Protocol:** Choose the protocol used from a menu (e.g., Stress, Rest, etc.)
  – **Database Gender**: Choose the gender from a menu (Male, Female, Composite, Any).
  – **ECG Gated:** e.g., Yes or No
  – **Corrections:** Select the type of applied reconstruction corrections from a series of drop-down menus
    • Choose reconstruction method: **FBP**, **IR**, or **Any**
    • If **IR** or **Any** is selected, the second drop-down provides dimensional display options: **2D**, **3D**, or **Any**
    • The third drop-down allows for the selection of Scatter Correction (**SC**) or **Any**
    • And the final drop-down menu displays selections for Attenuation Correction (**AC**), **CTAC**, **Composite**, or **Any**
  – **Recon Arc:** Reconstruction Arc (e.g., Unknown, 180 degrees, or 360 degrees)
  – **Imaging Orientation:** Choose from a menu (e.g., Supine, Prone, Incline, Upright, or Any)
  – **Manufacturer:** Choose from a menu of supported manufacturers.
  – **Model:** Choose from a menu of supported camera models.

Figure 10.3: Database Filename and Description

- **Database Filename and Description**
  – **Database Filename:** Name must be unique. The names should be compared against the List of Database files on system in the bottom section of the window to ensure uniqueness.
  – **Description:** Alphanumeric description of no more than 20 characters. The Description is what is listed in the Normals Database menus within 4DM screens.

Figure 10.4: Databases on System and window control buttons

- **List of Database Files on System** – This contains a complete list of available Normals database on the system including the database filename, description, and status as active or inactive.

- **Save Button:** Saves the new database and exits the window.

- **Cancel Button:** Exits the window without saving.

DB Editor Screen

The **DB Editor** screen displays all polar map data used for creating the selected Normals Database in 4DM. The user can customize the selected Normals Database by excluding one or more of the datasets in the Database. To access the DB Editor, the screen must be activated within Preferences. Once the screen is listed in the Active Screens, the user can select the **DB Editor** button from the **Workflow Screens**.

The **DB Editor** screen *(Figure 10.5)* includes the following components:
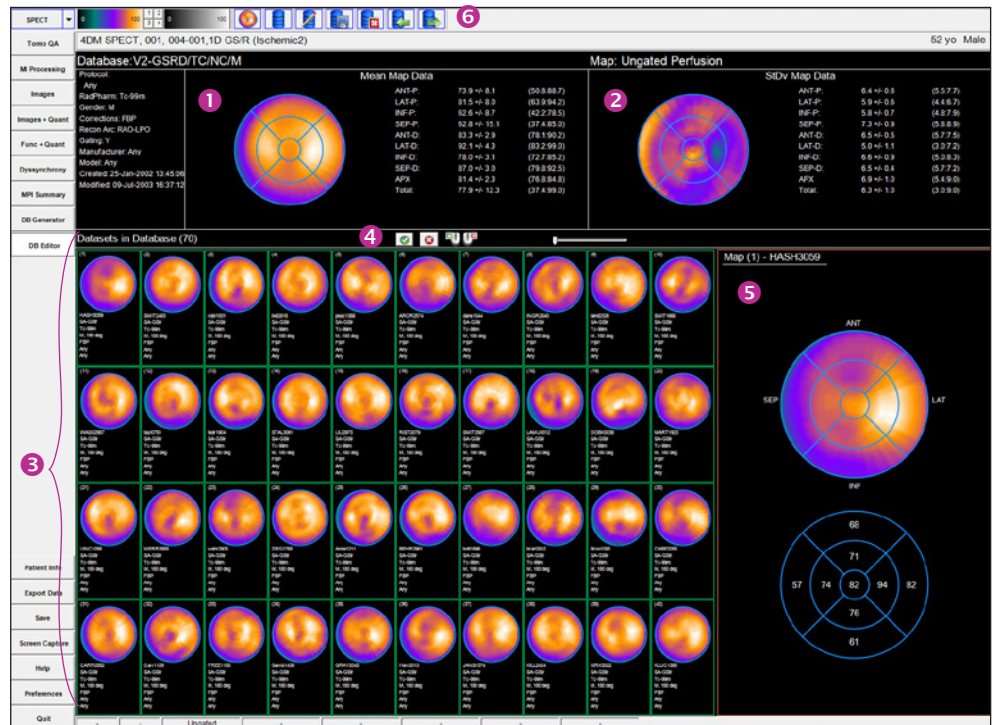
Figure 10.5: 4DM's DB Editor Screen

❶ **Mean Map Data** – Displays the mean distribution for the current Normals file with a 9 segment overlay and tabulated segmental statistics, which include the mean and standard deviation (StDv) for each segment, followed by the minimum and maximum ranges for each segment in parentheses.

❷ **Standard Deviation (StDv) Map Data** – Displays the variance distribution with a 9-segment overlay derived from to the standard deviation analysis of the normal distribution. The tabulated segmental statistics are shown to the right of StDv Polar Map. The mean StDv for each segment and their StDv's are shown, followed by the minimum and maximum ranges for each segment in parentheses.

❸ **Datasets in Database** – Displays individual datasets in the selected Normals Database file. General control options within this area include:
  – **Right-Click Option:** Right-click on an individual Normal Polar Map to exclude it from the database. The border around the polar map changes from green to red with a red line through it to signify its exclusion.

You cannot edit a 4DM-supplied Normals database.

– **Left-Click Option:** Left-click to include any previously excluded polar maps and the border around polar map returns to green to signify its inclusion.
– **Click-and-Drag Option:** Click-and-drag any individual dataset to the **Statistics Panel** to display the polar map and segmental mean values.

④ Editing Controls – User controls to manage the database datasets, including:
– **Datasets in Database (#):** Displays the number of datasets included in the Normals Database file.
– **Activate All Datasets:** Left-click the green check mark to include all datasets in computations related to the current Normals Database file. Selecting this option will include any previously excluded datasets.
– **Deactivate All Datasets:** Left-click the red X to exclude all datasets from computations.
– **Dataset Slider:** Use the slider control to navigate forward or backward through datasets in the Normals Database file.

⑤ Statistics Panel – Displays the polar and mean segmental maps with a 9 segment overlay for the selected dataset from the Normals Database.

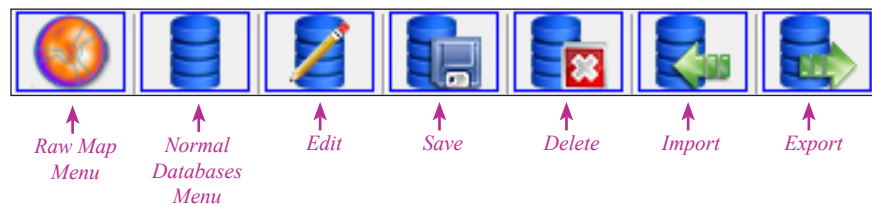**⑥ Toolbar –** The DB Editor Toolbar consists of the following tools *(Figure 10.6)*:

| Raw Map Menu | Normal Databases Menu | Edit | Save | Delete | Import | Export |

Figure 10.6: *DB Editor Toolbar*

– **Raw Polar Map Menu:** Lists available raw polar map types. The potential raw map types are:
  • **Ungated**: Ungated perfusion data
  • **ED**: End-diastolic perfusion data
  • **ES**: End-systolic perfusion data
  • **Thickening**: Quantified wall thickening data
  • **Motion**: Quantified wall motion data
– **Normal Database Menu:** Lists all the available Corridor4DM Normals Databases.
– **Edit Database Tool**: Left-click to edit the attributes for the selected database.
– **Save Database Tool**: Left-click to save the current changes to the selected database. When selected, a window appears with two options:
  • **Yes, Save**: Saves the current database as edited under the original filename. Excluded datasets will be deleted from the file and will not appear if the file is reopened for editing.
  • **Yes, Save As**: Saves the current database as edited under a new filename by opening the Create Database information/control panel. Excluded datasets will be deleted from the file and will not appear if the file is reopened for editing.
– **Delete Database Tool:** Left-click to delete the selected database from the system.
– **Import Database Tool:** Left-click to import a database into Corridor4DM.
– **Export Database Tool:** Left-click to export the database to a new filename or directory.

4DM-supplied databases may be deleted from the menu but not the system disk.

Corridor4DM integrates recording patient information within the diagnostic workflow. This streamlined process can help you improve the efficiency and effectiveness of your daily routine. While performing your perfusion, function, and quantitative review of a patient study, you can enter your findings directly into 4DM. These same findings can be used to generate a report or the results can be stored in a database for further analysis. For more information on 4DM Results, see Exporting 4DM Results.

There are two ways to enter your findings within the application — right-click on the **Patient Info** control while you're on a review screen, or left-click on **Patient Info** and click on the desired page to enter your patient information and findings.

To enter findings while on a review screen, simply right-click the **Patient Info** *(Figure 11.1)* button from the Control Panel and choose from the available **Findings** windows:

- ▪ LV Perfusion Findings
- ▪ RV Perfusion Findings
- ▪ Myocardial Stress LV Function Findings
- ▪ Myocardial Rest LV Function Findings
- ▪ Myocardial RV Function Findings
- ▪ Blood Pool Stress LV Function Findings
- ▪ Blood Pool Rest LV Function Findings
- ▪ Blood Pool Stress RV Function Findings
- ▪ Blood Pool Rest RV Function Findings
- ▪ CT Findings
- ▪ Ca Scoring Findings
- ▪ Miscellaneous/Summaries

Patient Info right-click options will be determined by the datasets loaded with each study.
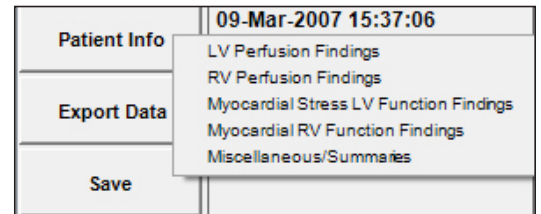
Figure 11.1: Right-click on the Patient Info control to access the Findings windows. Pictured here are the right-click options for a MPI study.

The primary method to enter diagnostic information is to access the dedicated **Patient Information** *(Figure 11.2)* screen by left-clicking on the **Patient Info** control.

4DM now supports both stress and rest function for MPI and GPBS studies. Results from 4DM version 7.0 and earlier will map LV function to a resting state.

Figure 11.2: The Corridor4DM Patient Information window (default is the History/Demographics page).

There are eight pages within the **Patient Information** screen that are accessible by clicking the corresponding button on the top-left area of the window. These buttons are:

- **History/Demographics:** Patient Demographics, Patient History, and Hospital information.
- **Rest/Stress EKG Data:** Rest EKG Data, Stress EKG Data, and Stress Protocol information.
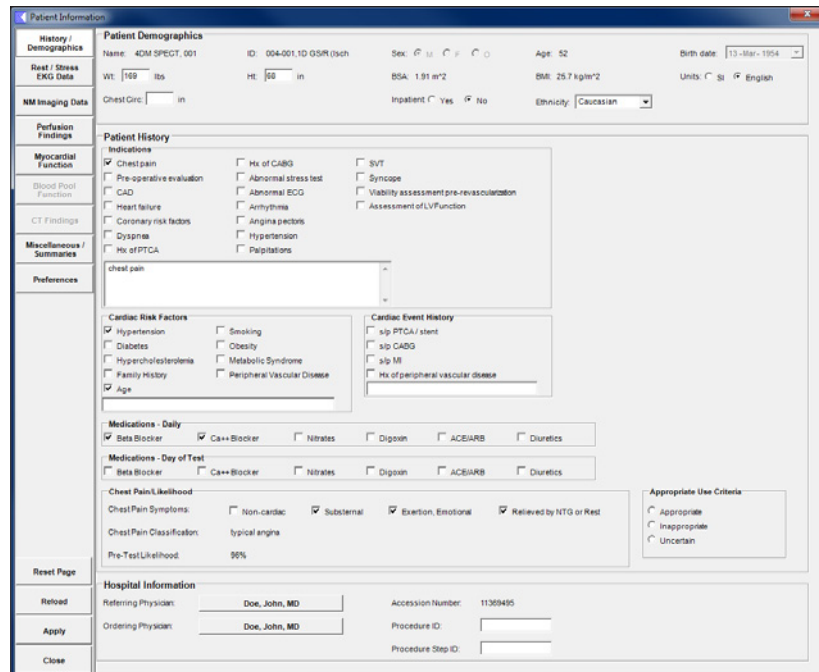- **NM Imaging Data:** Acquisition Parameters, Radiopharmaceutical, Dose, and Injection Time information.
- **Perfusion Findings:** Global LV Perfusion, Scan Significance, Stress LV Dilation, and Global RV Perfusion.
- **Myocardial Function Findings:** Stress LV Function, Rest LV Function, and RV Function
- **Blood Pool Function Findings:** Stress LV Function, Rest LV Function, Stress RV Function, and Rest RV Function
- **RV Findings/Impressions:** RV Perfusion, RV Volume, and RV Regional Wall Motion.
- **CT Findings/Impressions:** Dataset Name, Imaging Position, Contrast, Incidental Findings, and Regional Calcium Scoring Findings and Summary.
- **Miscellaneous/Summaries:** Overall Study Quality, Extra Cardiac Activity, Study Quality/Artifacts, and Summary information in the areas of Stress Test, LV Findings, RV Findings, Event Risk, Comparison Study, and CT Findings.
- **Preferences:** Set defaults and customize preferences for the **Patient Information** pages.

The **Patient Information Control** buttons are located on the bottom-left area of the window. The buttons are as follows:

- **Reset Page:** This button clears and resets the current patient information to default values.
- **Reload:** This button reloads the current patient information last-saved to disk file.
- **OK:** This button saves the current patient information to disk file.
- **Cancel:** This button exits the **Patient Information** window without making any updates to the current patient information data either in memory or in the disk file.

Patient History and Demographics

The **Patient History and Demographics** page is divided into three areas: Patient Demographics, Patient History, and Hospital Information. These are the fields available in each area:

Patient Demographics *(Figure 11.3)*

Figure 11.3: The Patient Demographics window of the History/Demographics page on the Patient Information window

- **Name:** Patient name. This field is taken from the DICOM image file and is not modifiable by the user.

- **ID:** Patient ID. This field is taken from the DICOM image file and is not modifiable by the user.

- **Sex:** Patient gender. This field is taken from the DICOM image file. Supported values are male (M) and female (F). If the value is defined in the image file, it will display in 4DM and can not be changed. In the event that the sex is not defined in the image file, the user can select the proper gender for the patient.

- **Age:** Patient age in years. This field is always calculated from the birth date and the study date.

- **Birth date:** Patient birth date. If available, this value is read from the DICOM image file. If the birth date is known, this field can not be edited. If this value is not defined, the user can input the date and 4DM will automatically calculate the age.

- **Weight:** Patient weight in pounds (lbs) or kilograms (kgs). The user can enter the value in the text box.

- **Height:** Patient height in inches (in) or centimeters (cm). The user can enter the value in the text box.

- **BSA:** Body surface area using the Dubois (Dubois and Dubois, Arch Int Med 1916;17:863-71) formula:
  - BSA (m^2) = 0.007184 x Height(cm)$^{0.725}$ x Weight(kg)$^{0.425}$. Units are always in m^2.

- **BMI:** Body mass index using the relation Wt(kg) / [Ht(m)]^2. Units are kg/m^2.

- **Units for Height and Weight:** Toggle to switch between Standard International (SI) units for weight (kg) and height (cm) and English units for weight (lbs) and height (in).

- **Chest Circ:** Chest circumference in dimension units (cm or in).

- **Bra Cup Size:** For female gender only. The size of her bra cup.

- **Inpatient Status:** Status as to whether the patient is an inpatient or an outpatient.

- **Ethnicity:** The ethnic origin of the patient.

Patient History *(Figure 11.4)*

Figure 11.4: *The Patient History window of the History/Demographics page on the Patient Information window*

- **Indication:** Indications for the study. The reasons the patient was referred for the cardiac study. User defined indications can be added using the **Patient Information Preferences** page.

- **Cardiac Risk Factors:** Cardiac-related risk factors for the patient.

- **Cardiac Event History:** Previous cardiac events experienced by the patient.

- **Medications — Daily:** Daily use of cardiac-related medications.

- **Medications — Day of Test:** Use of cardiac-related medication on the day of the imaging test.

- **Chest Pain Symptoms:** Identify the patient's onset of chest pain.

- **Chest Pain Classification:** This classification is based on the selected **Chest Pain Symptoms** toggles.

- **Pre-Test Likelihood:** The pre-test likelihood for coronary artery disease is automatically calculated using the Diamond and Foster table (Diamond, G. and Foster, J., New England Journal of Medicine, 300, 1979, p 1350) which is based on gender, age, chest pain classification, and ST segment changes.

- **Appropriate Use Criteria:** Indicates the appropriateness of the nuclear radionuclide for the patient based on ACC Appropriate Use Criteria.

Hospital Information *(Figure 11.5)*

Figure 11.5: *The Hospital Information section of the History/Demographics page on the Patient Information window*

- **Referring Physician:** Menu for specifying the name of the physician referring the patient for the cardiac imaging study.

- **Ordering Physician:** Menu for specifying the name of the physician ordering the patient for the cardiac imaging study.

- **Accession Number:** A RIS-generated number which identifies the order for the study. This number will be generated for systems utilizing DICOM work lists. If this number is not defined, the user can assign one.

- **Procedure ID:** Identifies the Requested Procedure in the Imaging Service Request. This number will be generated for systems utilizing DICOM work lists. If this number is not defined, the user can assign one.

- **Procedure Step ID:** Identifies the Scheduled Procedure Step. This number will be generated for systems utilizing DICOM work lists. If this number is not defined, the user can assign one.

Rest/Stress EKG Data

The **Rest/Stress EKG Data** page is divided into three areas: Rest EKG Data, Stress EKG Data, and Stress Test Protocol. These are the page's available fields:

Rest EKG Data *(Figure 11.6)*

This area is provided for information related to the patient's baseline or resting EKG test.

- **Status:** The user indicates status of the study from predefined toggles such as: Not done, Normal, or Abnormal. Upon selection, additional fields are expanded to add details for the rest EKG report.

- The user selects from predefined menu lists in the areas of:

Figure 11.6: *The Resting EKG Data section of the Rest/Stress EKG Data page on the Patient Information window*

– Rhythms
– AV Blocks
– IV Conductions
– Arrythmias
– Repolarization
– Resting EKG is able to be interpreted for ischemia
– Hemodynamic Data: HR (bpm) and BP (mm Hg)

Stress EKG Data *(Figure 11.7)*

This area is provided for data related to the EKG portion of the stress test. In addition to the Rest EKG fields, fields specific to Stress EKG findings are:

- **ST Response:** User selects from a drop-down menu of predefined ST response descriptions occuring at stress. **ST Response Leads:** By default, the **Leads** button is grayed out. When the user selects an ST response that utilizes Lead information, a popup window appears for defining location, timing, configuration, and amplitude *(Figure 11.8)*.

- **BP Response:** Blood pressure response during stress.

Stress Protocol *(Figure 11.9)*

This area is provided for information related to the stress portion of the study. The stress protocol selected and a description of symptoms experienced during the stress test are provided.

- **Stress Protocol:** The protocol used during the test.
- **Chest Pain Symptoms:** Chest pain that was experience during the protocol.

Figure 11.7: The Stress EKG Data section of the Rest/Stress EKG Data page on the Patient Information window

Figure 11.8: The ST Response Leads Modifiers window that presents when the Leads button is selected.

Figure 11.9: The Stress Test section of the Rest/Stress EKG Data page on the Patient Information window with the Pharmaceutical/Exercise Protocol selected.

4DM supports the following ASNC-approved **Stress Protocols**:

Rest Only
- No Stress

Exercise
- Bicycle
- Bruce
- Modified Bruce
- Cornell
- Naughton
- Balke

Pharmaceutical
- Adenosine
- Dipyridamole
- Dobutamine
- Regadenoson

Pharmaceutical/ Exercise
- Adenosine
- Dipyridamole
- Regadenoson

- **Other Symptoms:** Other symptoms experienced during the protocol.

- **Adequacy of Stress:** Patient responsiveness to the stress protocol selected.

- **Reason for Termination:** Reason which best describes why the protocol was terminated.

- **Post Stress Pharmaceutical Parameters:** Defines pharmaceuticals and the dosages administered post pharmacologic stress.

If the user selects an exercise protocol, these additional exercise parameters are available:

- **Exercise Parameters:** Allows user to select protocol, exercise duration, and functional capacity.

If a pharmacologic protocol is selected, these additional pharmacologic parameters are available:

- **Pharmaceutical:** Select the type of pharmaceutical used during stress test.

- **Infusion Rate:** Infusion rate for pharmacologic stress protocol.

- **Duration:** Duration time in minutes (precision to tenths of a minute) for pharmacologic stress protocol.

- **Indication for Pharma Protocol:** Reason pharmacologic stress was prescribed over exercise.

If the user selects a pharmacologic/exercise protocol, these additional pharmacologic stress parameters are available:

- **Pharmaceutical Parameters:** See pharmaceutical protocol above.

- **Exercise Parameters:** Allows user to select protocol and functional capacity.

- **Exercise Stages:** Ability to add exercise stages along with duration per stage.

NM Imaging Data

The **NM Imaging Data** page *(Figure 11.10)* allows users to enter data related to the nuclear imaging test for each dataset. These are the fields available:

- **Imaging Position:** The orientation of the patient during imaging (e.g. supine, prone, upright). This value is reported from the image file and can not be changed.

- **Attenuation Correction:** Conveys if the imaging data was corrected for photon attenuation. This value is reported from the image file and can not be changed.

- **Radiopharmaceutical:** The name of the injected radiopharmaceutical. This value is read from the image file, but it can be modified by the user.

- **Dose:** The activity of the injected radiopharmaceutical measured in mCi.

Figure 11.10: The NM Imaging page on the Patient Information window

- **Injection Time:** The time that the radiopharmaceutical was injected.

- **Injection Site:** The location where the radiopharmaceutical was injected.

- **Radiation Dose:** Displays the calculated radiation exposure to the patient in millisieverts (mSv) based on the quantity (in mCi) of the administered radiopharmaceutical.

- **Fasting State:** The type of fasting performed. Options include: Gluclose-loaded, Fasting, Fasting and heparin, High fat preparatory diet, and High fat preparatory diet and heparin.

Perfusion Findings

The user enters diagnostic perfusion findings for the LV and RV on this form using either free text or drop-down menus *(Figure 11.11)*.

Figure 11.11: The Perfusion Findings page on the Patient Information window

LV Perfusion Findings
- **Global LV Perfusion:** This consists of Normal and Abnormal toggles for selection.
  - If normal is selected, default text is displayed which can be edited.
  - If abnormal is selected, additional menus are presented to define perfusion abnormalities for further editing and identifying impressions.

- **Stress LV Dilation:** Findings based on the transient ischemic dilation (TID) value.

RV Perfusion Findings
- **RV Perfusion Status:** This consists of Normal and Abnormal toggles with a Free Text box to further describe perfusion defects.

Myocardial Function Findings

The user enters diagnostic myocardial functional findings on this form using either free text or drop-down menus *(Figure 11.12)*. These are the fields available in each area:

Figure 11.12: The LV Perfusion Findings section of the LV Findings/ Impressions page on the Patient Information window

Functional Findings can be defined both globally and regionally within 4DM. To report function regionally, select the **Segmental overlay** from the drop-down menu. Next, click on the **Regional WM button** to select the statement that best describes the regional WM abnormality. 4DM also provides a **Free Text** box that displays the regional WM defects you described so that you can edit them, if desired.

Stress LV, Rest LV, and RV Function Findings

- **Global Function:** Findings for systolic function include Normal, Abnormal, Mildly Reduced, Moderately Reduced, and Severely Reduced toggles.

- **Timing of Function Assessment:** The timing of the stress study acquisition (available for LV Stress Function Findings only)

- **Ejection Fraction:** User has the option to change the Corridor4DM estimated ejection fraction (EF) value (available for LV stress and rest findings only).

- **Ejection Fraction State:** If the user manually enters the EF value, 4DM displays EF State as **Visual**. If 4DM calculates the EF value, this field displays **Quant**.

- **ED Volume:** Left ventricular volumes at end-diastole (available for LV stress and rest findings only).

- **ES Volume:** Left ventricular volumes at end-systole (available for LV stress and rest findings only).

- **Subjective Volume:** User's interpretation of the left ventricular volume.

- **Regional Wall Motion:** Findings for regional ventricular wall motion.

- **Regional Wall Thickening:** Findings for regional ventricular wall thickening.

Blood Pool Function Findings

The user enters diagnostic blood pool functional findings on this form using either free text or drop-down menus *(Figure 11.13)*. These are the fields available in each area:

Figure 11.13: The RV Perfusion Findings section of the RV Findings/ Impressions page on the Patient Information window

Functional Findings can be defined both globally and regionally within 4DM. To report function regionally, select the **Segmental overlay** from the drop-down menu. Next, click on the **Regional WM button** to select the statement that best describes the regional WM abnormality. 4DM also provides a **Free Text** box that displays the regional WM defects you described so that you can edit them, if desired.

Stress LV, Rest LV, Stress RV, and Rest RV Function Findings

- **Global Function:** Findings for systolic function include Normal, Abnormal, Mildly Reduced, Moderately Reduced, and Severely Reduced toggles.

- **Timing of Function Assessment:** The timing of the stress study acquisition (available for LV and RV Stress Function Findings only)

- **Ejection Fraction:** User has the option to change the Corridor4DM estimated ejection fraction (EF) value.

- **Ejection Fraction State:** If the user manually enters the EF value, 4DM displays EF State as **Visual**. If 4DM calculates the EF value, this field displays **Quant**.

- **Peak Filling Rate:** Displays the peak filling rate in milliliters per second.

- **Peak Emptying Rate:** Displays the peak emptying rate in milliliters per second.

- **ED Volume:** Ventricular volumes at end-diastole.

- **ES Volume:** Ventricular volumes at end-systole.

- **Subjective Volume:** User's interpretation of the ventricular volume.

- **Change in LV size from exercise to rest:** Displays the LV size change in milliliters

- **Regional Wall Motion:** Findings for regional ventricular wall motion.

CT Findings and Impressions

The **CT Findings and Impressions** page is divided into two sections: CT Incidental Findings and CT Calcium Scoring. These are the fields available in each section:

CT Incidental Findings *(Figure 11.14)*

This form provides the dataset information and allows editing of the following fields:

- **Imaging Position:** Enter text identifying the patient's imaging position.

- **Contrast:** This consists of a **Yes** and **No** toggle. If contrast was injected, the user has the ability to include contrast volume, infusion rate, and infusion start time to the report.

- **Incidental Findings:** This consists of **Not defined**, **Normal**, and **Abnormal** toggles and the user has the ability to enter text to define the findings.

CT Calcium Scoring *(Figure 11.15)*

- **Regional CaSc Findings:** This provides the ability to review which vessels have calcium quantified.

- **CaSc Findings Summary:** This generates a findings statement related to the calcium score report.

Figure 11.14: The CT Incidental Findings section of the CT Findings/ Impressions page on the Patient Information window

Figure 11.15: The CT Calcium Scoring Incidental Findings section of the CT Findings/ Impressions page

> The **Update Field** button will be inactive unless you have visited the **Ca Scoring** screen and altered the Calcium Scores so they differ from the values in the last saved result file.

Miscellaneous and Summary Data

The **Miscellaneous/Summaries** page *(Figure 11.16)* allows the user to edit miscellaneous and summary data related to the image interpretation.

Figure 11.16: Miscellaneous, Scan Significance, LV Quantification Values, and Results Communication sections

Miscellaneous

The Miscellaneous fields provide information to assess the quality of the overall patient study prior to quantification. The following fields are available:

- **Overall Study Quality:** Describe the overall quality of the study.
- **Extra Cardiac Activity:** Describe the presence and degree of extra-cardiac activity.
- **Study Quality/Artifacts:** Describe the quality of the study related to the presence of artifacts.
- **Blood Pool Activity:** Define the level of blood pool activity as normal or increased

Scan Significance

This section allows the user to select the scan significance as it relates to the risk for hard cardiac events.

LV Quantification Values

The **LV Quantification Values** section displays the following values for the Stress and Rest datasets:

- **End Diastolic Volume (EDV):** The volume of blood in the LV at end-diastole (in ml).
- **End Systolic Volume (ESV):** The volume of blood in the LV at end-systole (in ml).
- **Transient Ischemic Dilation (TID):** The ratio of the diameter of the LV at stress, compared to rest.
- **Ejection Fraction (EF):** The fraction of blood pumped from the LV with each cardiac cycle.
- **Score:** The summed scores which provide a global risk assessment at stress and rest.

Results Communication

This section allows the user to select the date and time the results are communicated to the designated referring/ordering physician.

Summaries

The **Summaries** fields *(Figure 11.17)* provide information that was identified and captured within the information on previous tabs. These summaries include details applicable to the Stress Test, LV Findings, RV Findings, Event Risk, Comparison Study, and CT Findings.

Figure 11.17: Summaries section within Preferences

- **Stress Test Summary:** Automatically generated from information entered in the EKG and Stress Protocol forms.

- **LV Findings Summary:** Automatically generated from information entered on the LV Findings and Impressions page.

- **RV Findings Summary:** Automatically generated from information entered on the RV Findings and Impressions page.

- **Event Risk Summary:** Automatically generated from information entered for Scan Significance and Stress LV Dilation on the LV Findings and Impressions page.

- **Comparison Study Summary:** Allows choosing either **Yes** or **No** toggles and provides a text box to enter in comparison results to prior studies, if applicable. If there is not a previous study available and the **No** toggle is selected, 4DM automatically generates an editable sentence in the text box stating "No previous study available for comparison."

- **CT Findings Summary:** Automatically generated from information entered from the Regional CaSC findings and CaSc Findings Summary within the CT Calcium scoring section in combination with the Incidental Findings on the CT Findings and Impressions page.

Preference Settings

This **Preferences** page *(Figure 11.18)* is used to set consistent options for entering patient-specific information. Those configurable options consist of:

Defaults

The default units for the height and weight fields are defined with the toggle control

- **English:** For entering height and weight in inches and pounds.

- **SI:** For entering height and weight in centimeters and kilograms.

- **Functional Overlays Synchronization:** Allows the user to synchronize the segmental overlays used to report functional information for both LV and RV.

Figure 11.18: The Preferences page within the Patient Information window

Indications

The current list of **Indications** provides default text to be selected within your report.
- **Add:** New indications can be added by the user by left-clicking the **Add** button and entering the new indication in the following window.

- **Remove:** Indications can be removed from the list. To remove an indication from the list, select the indication and left-click the **Remove** button.

- **Add Defaults:** To reload the system defaults for indications, left-click the **Add Defaults** button.

Referring and Ordering Physician

Users may Add, Edit or Remove specific physicians from a list of Referring and/or Ordering Physicians to select from when modifying your report.

- **Add:** To include new Physicians, the user can left-click the **Add** button and fill out specific criteria in the **Add Referring Physician** window *(Figure 11.19)*.

- **Edit:** To edit the information, highlight the name and left-click the **Edit** button.

- **Remove:** To remove the name of a Referring Physician from the list, highlight the name and left-click the **Remove** button.

Reporting Physician

Users may add, edit or remove physicians from the list of Reporting Physicians to select from when finalizing your report.

- **Add User:** To add a new Reporting Physician, left-click the **Add User** button and enter the necessary information in the window *(Figure 11.20)*. In addition, each Reporting Physician will have to provide a password for security purposes.

- **Edit User:** To edit the information, highlight the name and left-click on the **Edit User** button. The password will need to be entered to edit the Reporting Physician from this list or to change the password.

- **Delete User:** To remove the name of a Reporting Physician, highlight the name and left-click the **Delete User** button. The password will need to be entered to remove the Reporting Physician from this list.

Figure 11.19: Add Referring Physician window

Figure 11.20: Add User (Reporting Physician) window

- **Changing Password:** To change the password for a specific physician, highlight the name and left-click the **Change Password** button. Using the window, enter in the old password and then enter the new password twice for verification. Left-click **OK** to store this new password.

- **Signature Image:** To add a Signature Image for a specific physician, highlight the physician name and left-click the **Edit User** button to modify existing information. From the **Edit User** window, the **User Password** is required for any modifications. Click the **Browse** button to select the correct directory location of the electronic signature image (in jpeg or bitmap). Once the directory location has been added, select **OK** to store the signature for that physician. Left-click the **Apply** button before closing the Preferences window to apply these changes.

The password assigned for a Reporting Physician will need to be entered before 4DM generates a Text, MS Word, PDF or HTML final report. See Exporting 4DM Results for more information.

Corridor4DM allows the user to export results for consistent and accurate reference when interpreting patient studies. This chapter will expand upon how to export Corridor4DM data into formatted diagnostic reports, XML result files, or SQL databases.

Exporting Results

4DM allows the user to export results by left-clicking the **Export Data** control *(Figure 12.1)* in the **Control Panel**. The user can select from a variety of formats to export data which include:

- **ODBC Database:** Creates a Microsoft Access database
- **XML Formatted Results:** Creates an XML formatted file
- **Text Formatted Reports:** Creates a report in HTML, MS Word, Text, PDF, HL7 V2 (Embedded PDF) and HL7 V2 (Referenced PDF), or HL7 V3 (CDA) formats
- **Text Delimited Results:** Creates a delimited text file

Within the **Export Data** window, users can select desired options and define additional properties for each type of export. Custom parameters can be easily reconfigured to meet site-specific parameters. This configuration is managed within the **Export Parameters** section.
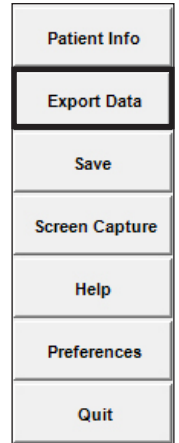
Figure 12.1: The Export Data control in the Control Panel

Export Parameters

Within the **Export Data** window is **Export Parameters** *(Figure 12.2)*. This section contains controls designed to streamline export selections with user-defined drop-downs thus minimizing user interactions and ensuring consistency. The following parameters can be configured based on site-specific needs:
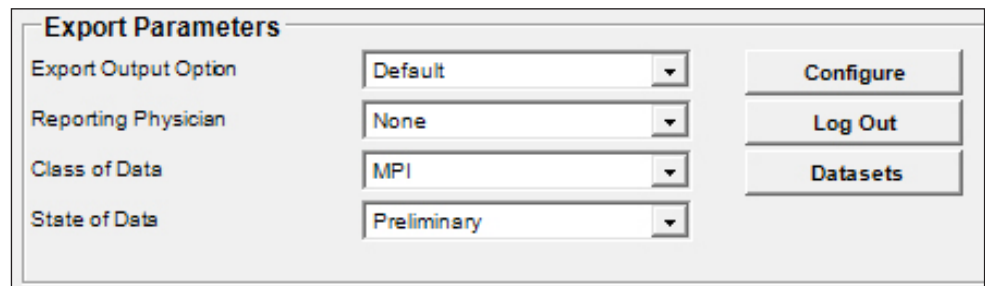
Figure 12.2: Export Parameters

- **Export Output Option:** Use this drop-down menu to select which configured option to utilize. This allows the user to customize and hide other methods of exporting capabilities. Use of the **Default** setting will allow the user to select and customize any of the available export options.

- **Reporting Physician**: Select from a list of pre-configured reporting physicians. This list is configured on the **Preferences** page within the **Patient Information** screen.

- **Class of Data:** Select the study protocol - MPI or Blood Pool for the datasets to be exported. For example, if both MPI and blood pool datasets are present, by default the

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Sidebar notes:

A 4DM best practice is to configure the **Export Data from Corridor4DM** window to streamline the user's workflow.

WARNING
The user must verify that the Normals Database is compatible with the dataset being reviewed to ensure correct computation of quantitative data.

WARNING
The user should ensure that uncorrected and attenuation corrected data are not mixed when generating a clinical report.

To complete the export, the user will have to enter the password created when the reporting physician was added.

Once a Reporting Physician is selected and the export function has successfully executed, *all* reports will be associated with this Reporting Physician unless the user quits 4DM or the user logs out from this name.

quantitative values from the MPI datasets are exported. By selecting the menu option Blood Pool, the quantitative values from the blood pool datasets are exported rather than the values from the MPI datasets.

- **State of Data:** Identify the state of the data to be exported as Preliminary (default), Final, or Corrected.

- **Configure** button**:** This option allows the user to create, modify, and remove customized export options.

- **Log Out** button**:** This option allows the physician to log out of all subsequent exports.

- **Datasets** button**:** Specify the selected datasets to be exported. This is used when there are multiple datasets (e.g. repeat studies, NC and AC) for Stress, Rest or Delay. Clicking this button provides dataset selection menus where specific datasets can be assigned priority for their data values to be exported.

Export Configuration

The **Export Output Configuration** window *(Figure 12.3)* allows the user to create and define custom configurations for easy, consistent selections. To customize the selections click on the **Configure** button within the **Export Parameters** window.

Managing Default and Custom Configurations:

Within the Export Parameters area the user can customize with the following parameters:

- **Create New:** Left-click on the button to create a new configuration and entering a title to be selected in the drop-down. Assign specific formats to this configuration and left-click **Save**.
- **Delete:** To remove a configuration from the list, select it and left-click **Delete**.

To modify a current configuration, select it, make changes to the preferences, and left-click **Save**.

Figure 12.3: Export Output Configuration window

Users can also assign a configuration as the default by selecting it from the list and activating the **Use for default** toggle. There can be only one default configuration.

Format Configuration Preferences:

The available export types for customized configuration are the same as the available export types as seen on the **Export Data from** window. Specific formats to export data include:

- **ODBC Database:** Use this option to export results to a Microsoft Access database.

- **XML Format:** Use this option to export results in XML format for use in PACS or other information systems.

- **Text Formatted:** Use this option to create and export diagnostic reports in HTML, MS

Word, Text, PDF, HL7 v2 (Embedded PDF) and HL7 v2 (Referenced PDF), or HL7 V3 (CDA) formats

- **Text Delimited Results:** Use this option to export data to spreadsheets, e.g. Microsoft Excel.

To activate specific export options for a custom configuration, activate the toggle next to the export name and set the preferences. For example, to export a **Text Formatted Report** in HTML format, left-click the toggle next to **Create a Report** and choose the **HTML** option from the **Output Format** drop-down menu *(Figure 12.4)*.
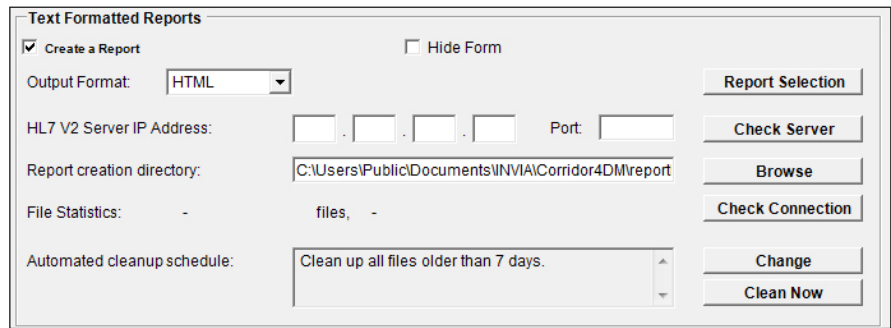
Figure 12.4: *Custom Export Configuration for an HTML Text Formatted Report*

For export options that will not be utilized, select the **Hide Form** toggle within the specific area. For example, if Text Delimited reports are not desired, activate the **Hide Form** toggle in the **Text Delimited Results** area *(Figure 12.5)*. Left-click the **Save** button to activate user preferences.
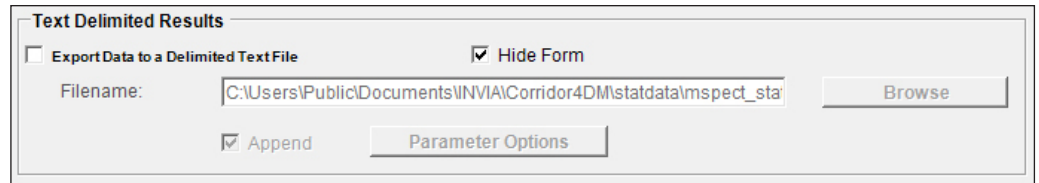

Figure 12.5: *The Text Delimited Results section with the Hide Form toggle activated*

ODBC Databases

The ODBC Database *(Figure 12.6)* area within the **Export Data** includes a list of database tables recognized by 4DM. To search your system for an ODBC database registered within Windows, click the **Refresh List** button.
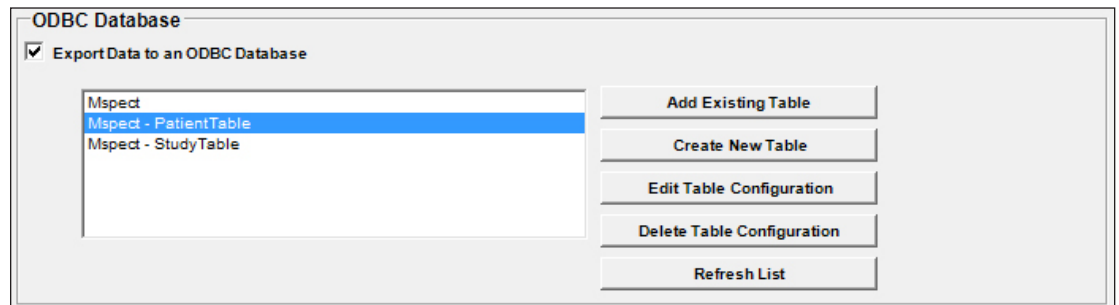

Figure 12.6: *Use this section within the **Export Data** window to define the tables within the ODBC Database*

As default, 4DM creates and defines the **Patient** table and the **Study** table. For a **Patient Table**, the following fields identify a unique record:

- Patient Name
- Patient ID
- Study Instance UID

With these fields identified, stress and rest specific fields and all interpretation fields are written to a common record for that patient. Multiple exports for the same patient study will overwrite the record. A patient study that is not in the database will create a new record. If these fields are not identified, every export request will create a new record and the database will expand in size quickly.

For a **Study Table**, the following fields identify a unique record. With data provided for these fields, each acquired study (dataset) will be written as a unique record in the database.

- Patient Name
- Patient ID
- Study Data (in DICOM terms – the series date)
- Study Time (in DICOM terms – the series time)
- Study Description (in DICOM terms – the series description)
- Study ID – this is a 4DM attribute constructed from the protocol type – stress or rest, corrections applied; uncorrected or attenuation corrected; and gating properties

Table Management

Within the ODBC Database form, there are buttons to create, manage, and delete database tables. The window for **Add Existing Table**, **Create New Table**, and **Edit Table Configuration** *(Figure 12.7)* are very similar – all contain the following fields:

- Database Name
- Table Name (either a drop-down menu, editable text field, or non-editable text field)
- Table Row Content (Patient data or Study data)
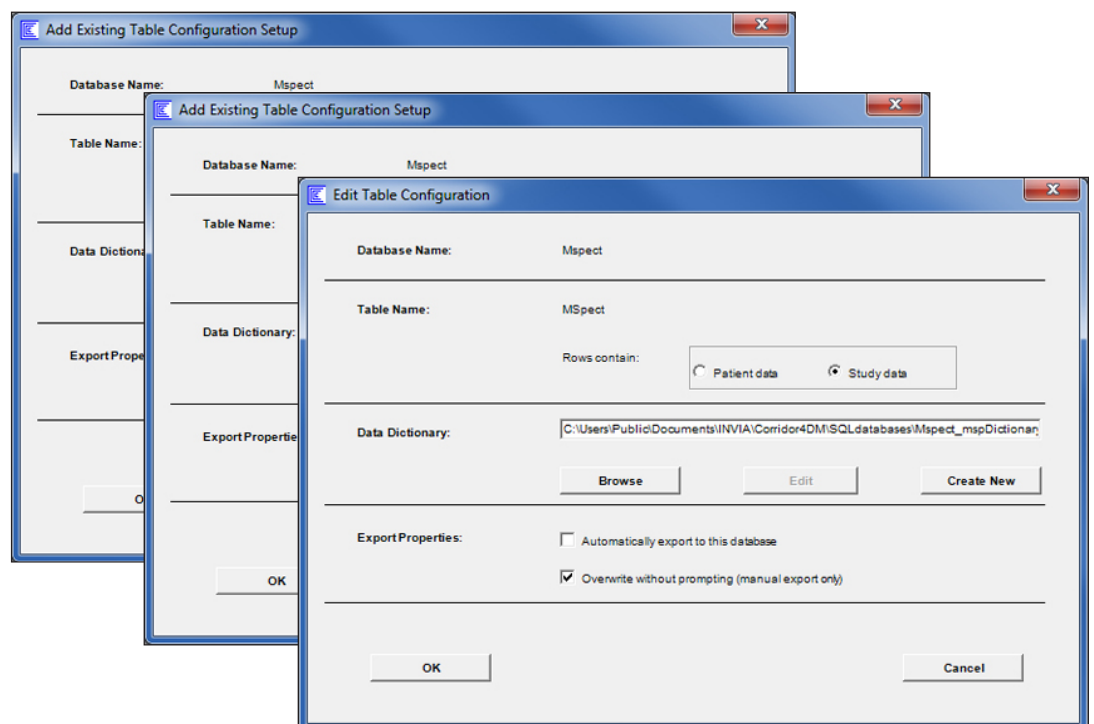- Data Dictionary (Browse, Edit, or Create New buttons)
- Export Properties

Figure 12.7: The Table Configuration Setup for ODBC Database Exports

To delete a configuration for a database table, select the database table from the list and left-click on the **Delete Table Configuration** *(Figure 12.8)* button.

Figure 12.8: The Delete Table Configuration button.

XML Export

Configuring an XML export

Within the **Export Configuration** window, users can configure an XML export using the following components available within the **XML Formatted Results** form *(Figure 12.9)*:

Figure 12.9: The XML Formatted Results Configuration Form

- **Format menu:** Use this to select a default XSL style sheet to convert the 4DM XML file to a different XML document type definition.

- **Allow user to change filename:** Use this option to have the ability to edit the output filename for the XML export. When this is deactivated, 4DM generates a unique filename that can not be changed.

- **Display with browser:** If activated, the output XML file displays in a Web browser.

- **Report creation directory:** The path within the text field identifies where XML result files are stored. To navigate to a different location, left-click **Browse**.

- **Check Connection button:** Once a new location is selected for the Report creation directory, left-click this button to verify writing privileges.

- **Automated Clean Up Schedule:** Deletes XML result files that are older than seven days. To alter the schedule, left-click **Change** to open the **4DM Clean Up Schedule** *(Figure 12.10)* window and make the desired changes. Left-click **OK** to save.
  - **Never delete files:** Saves all XML result files. Use this with caution as eventually these files will use all of the available disk space and the system will become unstable.
  - **All files:** Deletes all XML result files at the end of each 4DM session.
  - **All files older than "x" days:** Deletes all files older than the specified number of days.

Figure 12.10: 4DM Clean Up Schedule window

> To add a new option to the **Format menu**, place an XSL style sheet in the **xmlTemplate** folder located at C:\Program Files\INVIA\Corridor4DM.

– **High Water and Low Water Levels:** When the total size of all XML result files exceeds the High Water Level, the oldest files are deleted until total size is less than the Low Water Level.

Initiating an XML Export

To export 4DM data to an XML file, activate the **Create an XML Report** toggle *(Figure 12.11)*. Select parameters and click **Proceed** at the bottom of the **Export Data** window. This form consists of the following components:

Figure 12.11: XML Export options in the Export Data from Corridor4DM window

- **Format Menu:** See XML Configuration

- **Display with Browser** toggle**:** See XML Configuration

- **Output file:** Enter the name for the output XML file. Only available if **Allow user to change filename** is activated in the configuration menu. To navigate to a different location, left-click **Browse**.

Text Formatted Reports

Configuring a Text Report Export

Within the Export Output Configuration window, users can configure a text report using the following components available within the Text Formatted Reports form *(Figure 12.12)*:

Figure 12.12: The Text Formatted Results Configuration Form

- **Report Selection:** Displays the **Automatic Report Configuration** window and allows the user to specify the parameters for the report templates

- **Output Format:** Select the default file format desired (HTML, MS Word, Text, PDF, HL7 V2 (Embedded PDF) and HL7 V2 (Referenced Format), or HL7 V3 (CDA))

- **HL7 V2 Server IP Address:** Input the server IP address destination for HL7 V2 (Referenced PDF) export format

Users need to ensure that the correct datasets are prioritized for export. For example, stress and rest datasets should be selected from the same study protocol and have the same processing corrections (e.g., do not mix NC and AC datasets).

The Microsoft Word option for Text Formatted Reports is only available if the workstation has Microsoft Word installed.

- **Port:** Input the Port number for the Server

    – **Check Server:** Verify network connectivity to the HL7 V2 (Referenced PDF) export destination

- **Report creation directory:** This identifies where the text reports are stored. To navigate to a different location, left-click **Browse**.

- **Check Connection:** If a directory is created from the **Report creation directory** field, left-click to verify write privileges to that directory.

- **Automated cleanup schedule:** See XML Configuration. This has the same functionality as described for the XML results.

Initiating a Text Report Export

To export 4DM data into a formatted text report file, activate the **Create a Report** toggle *(Figure 12.13)*. Define your preferences and click **Proceed** on **Export Data from Corridor4DM** window. This form consists of the following preferences:
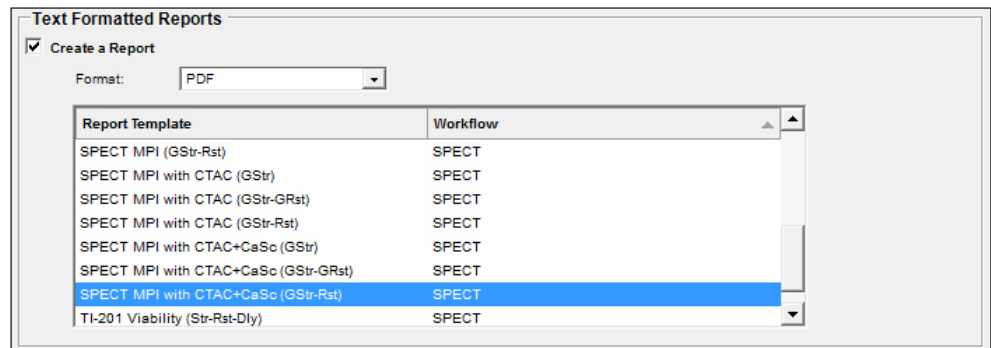

Figure 12.13: Text Formatted Reports options in the Export Data from Corridor4DM window

- **Template Selection List:** This area displays available templates stored in the report template directory for the desired **Output Formats**. 4DM includes several default templates but users can create and save custom reporting templates.

- **Option Format:** Select a text formatted file type to export your data to (HTML, MS Word, Text, PDF, HL7 V2 (Embedded), HL7 V2 (Referenced), or HL7 V3 (CDA))

Customizing a Report Template

Corridor4DM uses formatted templates when generating a report. Users can edit existing templates or create new ones. Customize your template with logos, specific data, formatting or even an electronic signature. These templates are stored within a specific folder on the workstation.

To specify report parameters, click the **Report Selection** button in the Text Formatted Reports section within the **Export Output Configuration** window. This will open the **Automatic Report Configuration** window.

Begin configuring the **Report Selection Rules** by selecting one of the report format toggles within the **Rules For** section. Then select the Report Template from the list of available templates, and make changes to the **Workflow** by using the drop-down menu. The check boxes indicate which datasets are **Required Datasets** for the selected report template.

The following buttons are available for making changes within the **Automatic Report Configuration** window:

It is recommended to save templates for both HTML and MS Word in HTML format (.htm extension). The templates for ASCII reports are text files (.txt) and have no formatting.

It is the responsibility of the user to delete any locally stored report files from the system. If disk space is low, check the directory where the report files are stored and delete those that are not needed.

▪ **Move Up:** Allows the user to move the selected report template up one position in the list.

▪ **Move Down:** Allows the user to move the selected report template down one position in the list.

▪ **Delete:** Allows the user to remove the selected report template from the list.

▪ **Initializ**e: Allows the user to reset to the default 4DM settings for report templates and their associated matching rules. Initializing will move all user-defined templates to a new directory defined by date: **mm-dd-yyyyreportTemplates**.

▪ **Save:** Checks to verify that no conflicting matching rules exist and saves the changes made by the user.

▪ **Cancel:** Discard all user changes made during the current session and closes the **Automatic Report Configuration** window.

Template Folders

▪ Users can locate templates on the workstations hard drive (e.g., C:\Documents and Settings\All Users\Application Data\4DM Backup)

▪ If users desire to add any non-text elements (logos, signatures, graphics, clip art, etc.) in a custom template they must add elements to the **reportFinal** folder located in the Corridor4DM root folder (e.g., C:\Documents and Settings\All Users\Application Data\4DM Backup)

Template Components

There are three components to a report template.

1. Fixed, unchanged text and graphics that are built into the template and remain the same regardless of which patient data the user exports *(Figure 12.14)*.

2. Placeholders (tags) for 4DM data which will change depending on which patient data the user exports *(Figure 12.15)*. Denoted by brackets [ ] on either side of the tag.

3. Optional customizations to the report templates such as company logos, graphics, or electronic signatures.

Figure 12.14: *A sample template with only fixed text showing*

Figure 12.15: *A sample template with only the tags showing*

Delimited Text File Export

Configuring a Delimited Text File for Export

To access the **Export Output Configuration** window, left-click **Configure** within the **Export Data from Corridor4DM** window. In the **Text Delimited Results** box, select the **Export Data to a Delimited Text File** check box and configure the following fields *(Figure 12.16)*:

Figure 12.16: The Text Delimited Results Configuration Form

- **Filename:** The current target location for the text appears within the field. To navigate to a different location, left-click **Browse**.

- **Parameter Options:** Left-click to select which data to export within the delimited text file. Click **Save** to export the selected parameters or click **Reset** to only include the default parameter options.

- **Append:** If activated, this will append the current stats to the end of a file. If deactivated, the new stats file will overwrite previous data .

Exporting a Delimited Text File

To export 4DM data to a Delimited Text file, activate the **Export Data to a Delimited Text File** toggle *(Figure 12.17)*. Define options and click **Proceed** on **Export Data from Corridor4DM** window. This form consists of the following options:

Figure 12.17: Text Formatted Reports options in the Export Data from Corridor4DM window

- **Filename:** The current target location for the text appears within the field. To navigate to a different location, left-click **Browse**.

- **Append:** If activated, this will append the current stats to the end of a file. If deactivated, the new stats file will overwrite previous data.

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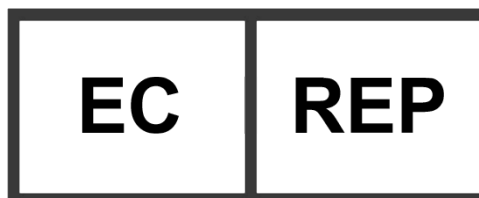
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