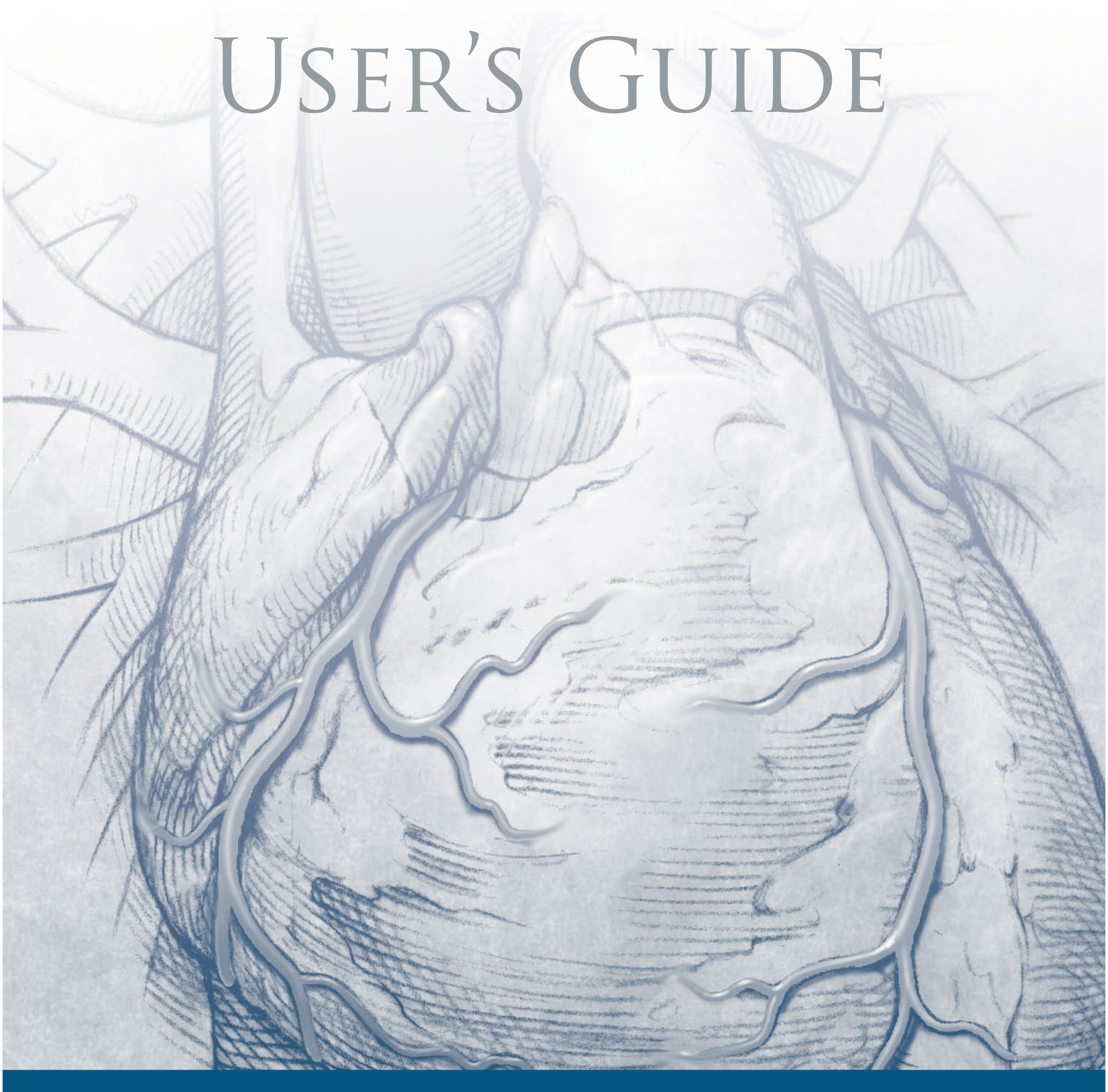
CORRIDOR4DM USER'S GUIDE



INVIA Medical Imaging Solutions

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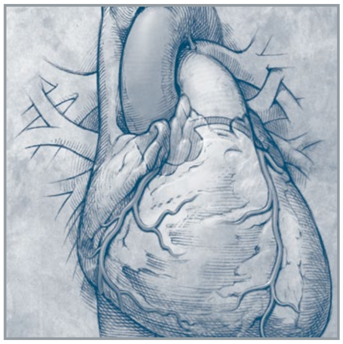
CHAPTER 1 GETTING STARTED



User's Guide Chapters

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 images.

The application supports correlative review and measures of physiologic, functional, and anatomic datasets from multidimensional radiographic images. Corridor4DM provides analytical tools to help the user quantify and document changes in these measures.

Note: The clinician retains the ultimate responsibility for making the pertinent diagnosis based on their standard practices and visual comparison of the separate multimodality datasets. The Corridor4DM application is a complement to these standard procedures.

℞ only

Product 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 the analysis of dynamic sequences.

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, inflammation, and coronary flow and reserve. Corridor4DM provides this regional information in 2D polar maps and 3D surface-rendered images 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 feature integrated into the application. 4DM 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 database, XML, and text formatted reports 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

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.

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 Encapsulated PDF
- DICOM General Waveforms
- DICOM 12 Lead Waveforms
- 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

Common Abbreviations

The User's Guide 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
ECG or EKG	Electrocardiography
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

Abbreviation	Description
MFSC	Multi-Frame Screen Capture
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

CHAPTER 2 CORRIDOR4DM ADMINISTRATION

Overview

Corridor4DM Administration manages Corridor4DM settings specific to licensing, site information, users, global displays, screen captures, and Corridor4DM's Reporting module. Reference the *Corridor4DM Reporting User's Guide* for all reporting-specific information and administrative tools.

This chapter will describe all non-reporting activities within the Corridor4DM Administration module.

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Accessing Corridor4DM Administration

The Corridor4DM Administration module can be accessed from three different locations:

1. Within Corridor4DM
2. Outside Corridor4DM
3. Within Corridor4DM Reporting

Launching Corridor4DM Administration

Accessing from within Corridor4DM

Access Corridor4DM Administration from within the Corridor4DM application via the **Preferences** window.

1. Click **Preferences** from within the Corridor4DM Control Panel *(Figure 2.1)*
2. Click the **Utilities** menu, select **Corridor4DM Administration** *(Figure 2.2)* to open the Corridor4DM Administration Login Window

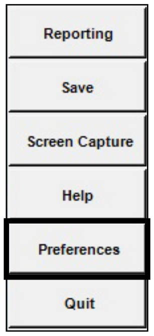


Figure 2.1: *Click Preferences within Corridor4DM*

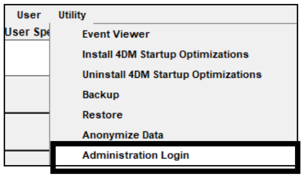


Figure 2.2: *Select Corridor4DM Administration from the Utilities menu in Preferences*

Accessing from outside of Corridor4DM

Corridor4DM Administration is available to launch from the Windows Start menu *(Windows 7 and Windows 10)* or Charm Bar *(Windows 8)*.

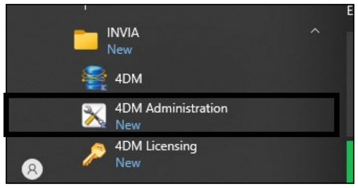


Figure 2.3: *Select Corridor4DM Administration from the Windows Start menu*

Windows 7 and Windows 10 users:

1. Click the **Windows Start** menu icon
2. Locate the **INVIA** folder and select **Corridor4DM Administration** *(Figure 2.3)* to open the Corridor4DM Administration Login Window.
   - You can also use the **Search** box to locate and open **Administration**

Windows 8 users:

1. Select the **Windows Key + C** on the keyboard to display the **Windows Charm Bar**
2. Click **Search** to display the Search Box
3. In the Search Box, type **Administration** and select to open the Corridor4DM Administration Login Window

Accessing from within Corridor4DM Reporting

For users who have Corridor4DM Reporting, access Corridor4DM Administration from within the Reporting interface.

Click the Corridor4DM Administration Login icon in the lower-left corner of the Corridor4DM Reporting application *(Figure 2.4)* to open the Corridor4DM Administration Login Window.

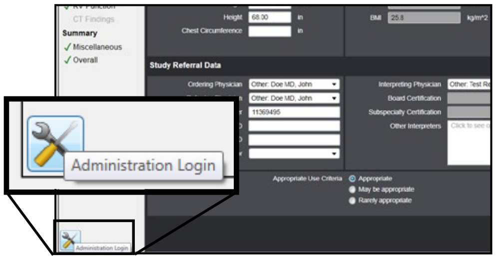
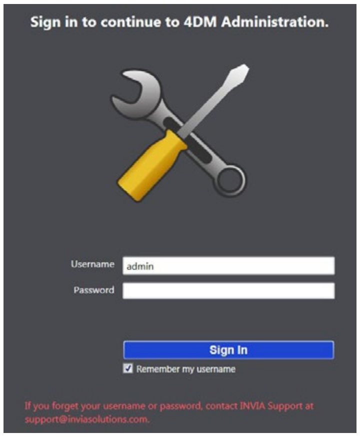


Figure 2.4: *Access Corridor4DM Administration from within Corridor4DM Reporting*

Logging into Corridor4DM Administration

You must have administrative credentials in order to access Corridor4DM Administration. Upon initial launch of Corridor4DM Administration after installation, enter the default Administrator username and password in the login window *(Figure 2.5)*:

- The default username is: **admin**
- *There is no initial password. Leave this field blank.*
- Select **Sign In**



Sign in to continue to 4DM Administration.

Username: admin

Password:

☑ Remember my username

If you forget your username or password, contact INVIA Support at support@inviasolutions.com.

Figure 2.5: *Corridor4DM Administration login*

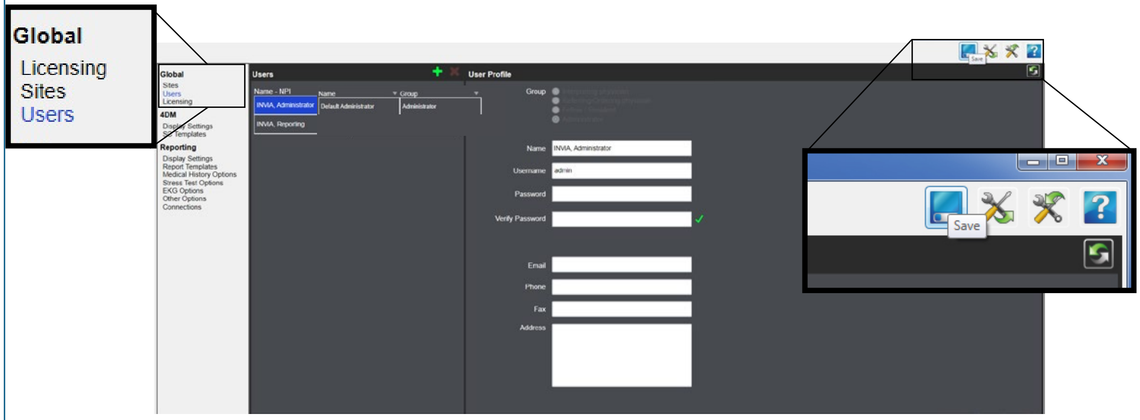
To change the admin password *(Figure 2.6)*:

1. Click **Users** in the left panel.
2. Click on the **INVIA Administrator** name
3. Within the **Password** field, enter the new password
4. Enter the new password again, in the **Verify Password** field
5. Click the **Save** icon in the upper-right corner

Usernames and passwords are case-sensitive.

Usernames and passwords are limited to 16 characters.

There is no restriction on character type used.



Name: INVIA, Administrator

Username: admin

Password:

Verify Password:

Email:

Phone:

Fax:

Address:

Figure 2.6: *Change the Administrator password*

Closing Corridor4DM Administration

To close the Corridor4DM Administration application, click the red “X” in the upper right corner *(Figure 2.7)*.

If changes were made to Corridor4DM Administration during the open session, a window displays and gives you the option to **Save** / **Don’t Save** your edits, or **Cancel**.

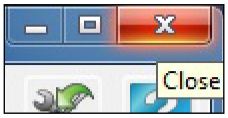
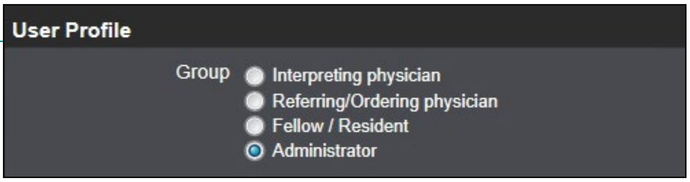


Figure 2.7: *Close application*

Users

Defining Corridor4DM users

User profiles are defined by Groups in the Corridor4DM Administration module. There are four User Groups in Corridor4DM *(Figure 2.8)*:



User Profile

Group
○ Interpreting physician
○ Referring/Ordering physician
○ Fellow / Resident
● Administrator

Figure 2.8: *User Groups*

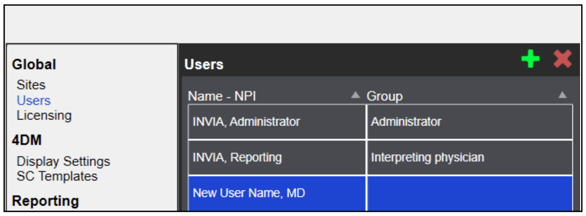
- **Interpreting Physician**: This User Group is applicable to the Corridor4DM Reporting application, and includes credentials allowing signing of final reports from within Corridor4DM. Users in this group are the only Corridor4DM Users that are allowed to be the primary reader on Corridor4DM diagnostic reports. Please see the Corridor4DM Reporting User's Guide for more information.
- **Referring/Ordering Physician**: This User Group is applicable to the Corridor4DM Reporting application, and does not include credentials to sign reports. Please see the Corridor4DM Reporting User's Guide for more information.
- **Fellow / Resident**: This User Group is applicable to the Corridor4DM Reporting application, and does not include credentials to be a primary signing physician on reports. These users are allowed to be a secondary interpreting physician on reports. Please see the Corridor4DM Reporting User's Guide for more information.
- **Administrator:** This group is intended for use by IT/PACS Administrators, and other non-physician Corridor4DM Users who are responsible for executing configuration changes to the Corridor4DM application, as well as INVIA support personnel when required.

> **Important Note:** The Administrator Group is the only Corridor4DM User Group that includes administrative credentials to enable login to Corridor4DM Administration. All other types of users created within Corridor4DM Administration will not be able to access it. A password is created for all super users that are permitted to alter the settings of the application.

Adding additional Corridor4DM user logins

To create **non-Administrator** Corridor4DM Users, please see the Corridor4DM Reporting User's Guide.

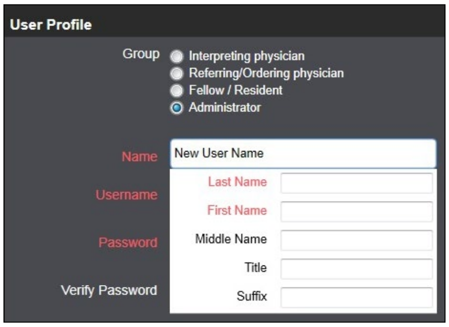
To create a new Corridor4DM **Administrator** *(Figure 2.9)*, follow these steps:



Name - NPI	Group
INVIA, Administrator	Administrator
INVIA, Reporting	Interpreting physician
New User Name, MD	

***Figure 2.9:** Add a new Corridor4DM Administrator user*

1. Click **Users** in the left panel.
2. Click the **Add** tool
3. Select the **Administrator** Group.
4. Click the **Name** field, and in the drop-down window, enter the **Last Name** and **First Name** required fields *(Figure 2.10)*.
5. Create a unique **Username**.
   - If a username is already in use, a warning will appear.
6. Create a **Password** by entering it into the Password field.
7. Enter the new password again, in the **Verify Password** field.



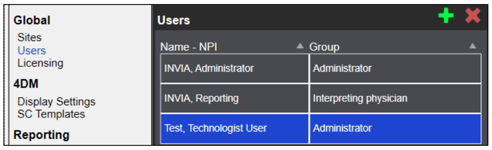
Group: ○ Interpreting physician ○ Referring/Ordering physician ○ Fellow / Resident ● Administrator

Name: New User Name

***Figure 2.10:** Enter required fields*

Deleting Corridor4DM Users

To delete any Corridor4DM user, click to select the user from the user list, and click the **Remove** icon *(Figure 2.11)*.



Name - NPI	Group
INVIA, Administrator	Administrator
INVIA, Reporting	Interpreting physician
Test, Technologist User	Administrator

Figure 2.11: *Select the user & click Remove*

To permanently remove them, click **Save** *(Figure 2.12)* before exiting Corridor4DM Administration.

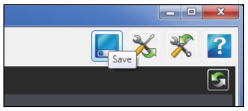
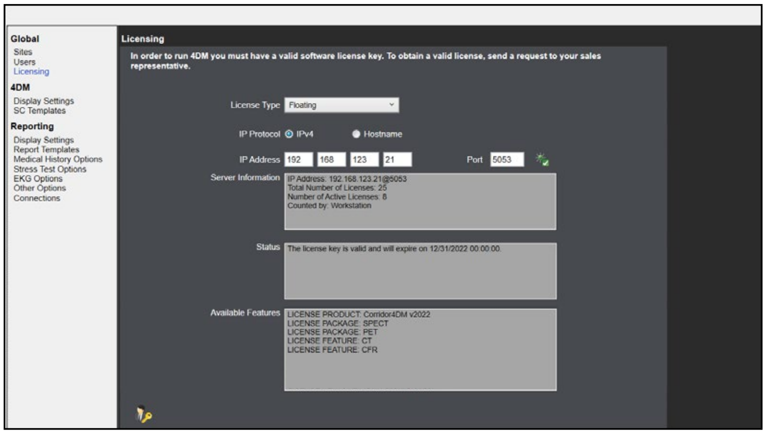


Figure 2.12: *Click Save to permanently remove*

Licensing

Overview

This section provides guidance on the Licensing page *(Figure 2.13)* within Corridor4DM Administration, and basic steps for the most common licensing actions within Corridor4DM Administration.



In order to run 4DM you must have a valid software license key. To obtain a valid license, send a request to your sales representative.

License Type: Floating

IP Protocol: ● IPv4 ○ Hostname

IP Address: 192 168 123 21 Port: 5053

Server Information:
IP Address: 192.168.123.21@5053
Total Number of Licenses: 25
Number of Active Licenses: 8
Counted by: Workstation

Status: The license key is valid and will expire on 12/31/2022 00:00:00.

Available Features:
LICENSE PRODUCT: Corridor4DM v2022
LICENSE PACKAGE: SPECT
LICENSE PACKAGE: PET
LICENSE FEATURE: CT
LICENSE FEATURE: CFR

Figure 2.13: *Licensing Page*

Corridor4DM utilizes a software-based licensing model. A license file is issued based on software features and functionality purchased. Floating licenses, also known as concurrent licenses, enable a user to load Corridor4DM on to a greater number of computers than the number of licenses purchased. Simultaneous users are limited to the number of licenses purchased. Licenses are also available for single systems, called fixed licenses.

Licensing Corridor4DM within Corridor4DM Administration

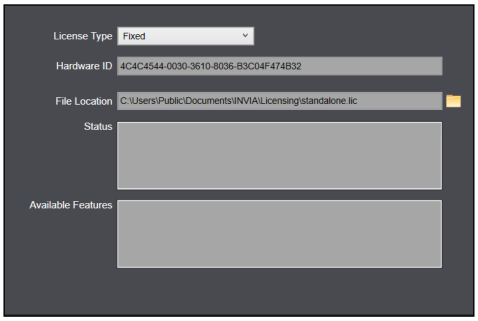
After logging into Corridor4DM Administration, select the Licensing page to license 4DM. Based on the license purchased, steps to license may vary. Follow steps provided in the Installation and Licensing Guide, available on the INVIA website, within the User and Reseller Center logins at www.inviasolutions.com.

Verifying the Corridor4DM license

Corridor4DM Administrators can review and configure the Corridor4DM license from within the Licensing page at any time. The following describes each license model type and the fields displayed with each option.

Selections within the Fixed License Model
(Figure 2.14)

Fixed licenses run Corridor4DM on only the local workstation. Note that fixed licenses will not work on Virtual Machines or Virtual Server environments. Selecting the Fixed option in the License Type dropdown updates the displayed licensing fields to the following:



License Type: Fixed

Hardware ID: 4C4C4544-0030-3610-8036-B3C04F474B32

File Location: C:\Users\Public\Documents\INVIA\Licensing\standalone.lic

Figure 2.14: *Fixed License Model*

- **Hardware ID**: Hardware-specific code that is created when the Hardware ID Reader is run on the system on which Corridor4DM is installed.
- **File Location**: Where the Corridor4DM license file is stored. Click Browse to navigate to where the license file is stored to connect the license to the Corridor4DM software.
- **Check Status**: Initiates Corridor4DM to verify connectivity to the license and whether the license is valid.
- **Status**: The current status of the license is displayed. If there are errors with connectivity to a license, or a license is expired, a warning message will appear here.
- **Available Features**: This window displays all included software features of the Corridor4DM license.

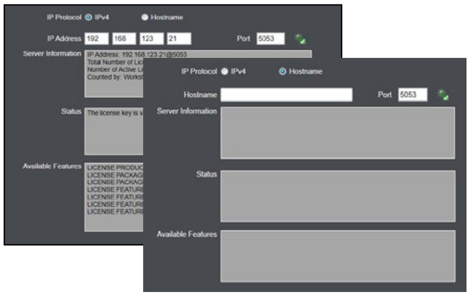
Selections within the Floating License Model *(Figure 2.15)*

The **Floating** model enables Corridor4DM licenses to be shared across a network, provides remote access to Corridor4DM, and enables installation of Corridor4DM on Virtual Server or Virtual Machine. Selecting this option updates the displayed licensing fields to the following:

The Hardware ID Reader is part of the installer, as well as on the INVIA Licensing Website.

For more information on generating a Hardware ID or licensing 4DM, please see the Installation and Licensing Guide.

- **IP Protocol:** Permits the user to choose between entering the IPv4 address or the Hostname of the system hosting the License Manager file.
- **IP Address:** When this option is selected, the IP address of the designated Corridor4DM license manager server can be entered.
- **Hostname:** When this option is selected, the Hostname of the designated Corridor4DM license manager server can be entered.
- **Port:** Port on the network that enables communication of Corridor4DM to the RLM license Manager software. Corridor4DM defaults to 5053, and this should remain unchanged. Ports 5053, 5054 and 5055 need to be open across the network and not blocked by a router or firewall.



IP Protocol ● IPv4 ○ Hostname
IP Address 192 168 123 21 Port 5053
Server Information: IP Address: 192.168.123.21@5053
Status: The license key is v

IP Protocol ○ IPv4 ● Hostname
Hostname Port 5053

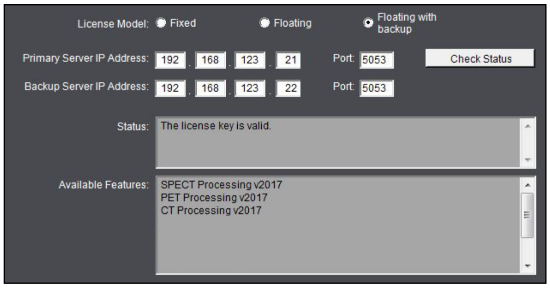
Figure 2.15: *Floating License Model*

- **Server Information:** This window displays the total number of licenses available and the number of active licenses.
- **Status:** Display the status of the license. If there are errors with the connectivity to a license, or a license is expired, a warning message will appear here.
- **Available Features:** This window displays all included software features of the Corridor4DM license, and shows what type of data will be allowed to launch into Corridor4DM.

It is essential that the license manager server has a static IP Address to prevent licensing errors. All 4DM floating client systems should be pointed to the same IP Address after installation.

Selections within the Floating with Backup License Model *(Figure 2.16)*

A backup Corridor4DM floating license on a secondary license server system is configurable in Corridor4DM versions 2016 and higher. In cases where the Primary license server goes down for routine IT maintenance, or is offline, the next time Corridor4DM is accessed, it will



License Model: ○ Fixed ○ Floating ● Floating with backup
Primary Server IP Address: 192 . 168 . 123 . 21 Port: 5053
Backup Server IP Address: 192 . 168 . 123 . 22 Port: 5053
Status: The license key is valid.
Available Features:
SPECT Processing v2017
PET Processing v2017
CT Processing v2017

Figure 2.16: *Floating with Backup License Model*

4DM License Servers are not required to be actual server operating systems.

While it is recommended to utilized servers that are regularly maintained by IT and located in secure areas, any system on the network can be designated as a 4DM license server.

It is recommended to choose systems that do not get shut down or accessed by staff unaware of their purpose.

do a license check and the Backup Server will be called for a Corridor4DM license to run it.

Selecting this option updates the display to show fields to enter the Backup Server IP Address or Hostname and Port number. The Port number can be the same as for the Primary Server. See the Floating License Model section for information on all other displayed fields.

Configuring the Corridor4DM license

Corridor4DM Administrators can at any time update the Corridor4DM license from within the Licensing page. Configurations to the license may include changing the license model from Fixed to Floating, updating the location of the license manager, or viewing an updated Hardware ID. Any edits made to the licensing page from within a Corridor4DM client update the license for only that local client system.

Configuring the license is necessary:

- During the first installation
- When the software is upgraded to a new version
- When new license features or additional licenses are purchased
- When the license manager server is changed, or the license type is changed (e.g., conversion of a license from fixed to floating)

To configure the license:

1. Select a **License Model**
2. Edit the appropriate license fields as described in the above section, **Verifying the Corridor4DM License**.
3. Click the **Check Status** icon to verify the license.
4. Click the **Save License** icon *(Figure 2.17)*
5. It is advised to perform a new Corridor4DM Backup and restore that to all other Corridor4DM client systems to update all systems with the new license information. Please see the section on **Backing up and Restoring** for more information.

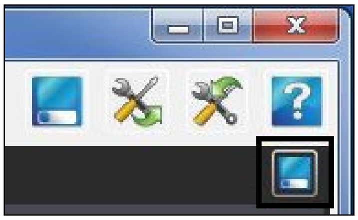
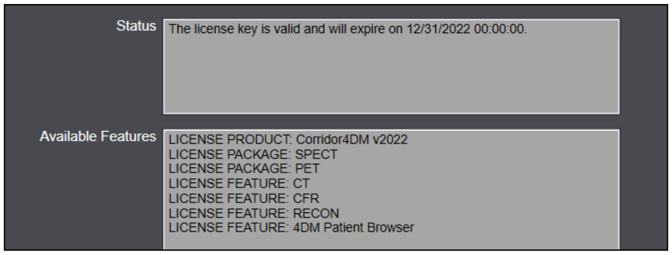


Figure 2.17: *Click Save License icon*

Checking the status of the Corridor4DM license

Corridor4DM Administrators can login to check the status of a Corridor4DM license at any time. Upon login, select the Licensing page to view the status.

Anytime the Licensing page is accessed, it automatically initiates an immediate check for a license and displays the current status in the **Status** field *(Figure 2.18)*.



Status: The license key is valid and will expire on 12/31/2022 00:00:00.

Available Features:
LICENSE PRODUCT: Corridor4DM v2022
LICENSE PACKAGE: SPECT
LICENSE PACKAGE: PET
LICENSE FEATURE: CT
LICENSE FEATURE: CFR
LICENSE FEATURE: RECON
LICENSE FEATURE: 4DM Patient Browser

Figure 2.18: *Check status of license*

When licenses are properly installed and linked to Corridor4DM, the status message states “The license key is valid and will expire on MM/DD/YYYY HH:MM:SS.” Other message displayed here mean the system is not properly licensed, or the license is expired. Corridor4DM licenses do not expire unless a demo, trial, or research type.

It is advised to always click the Check Status icon after any edits are made to the license configuration, to verify that the information was properly input and that the license works as expected.

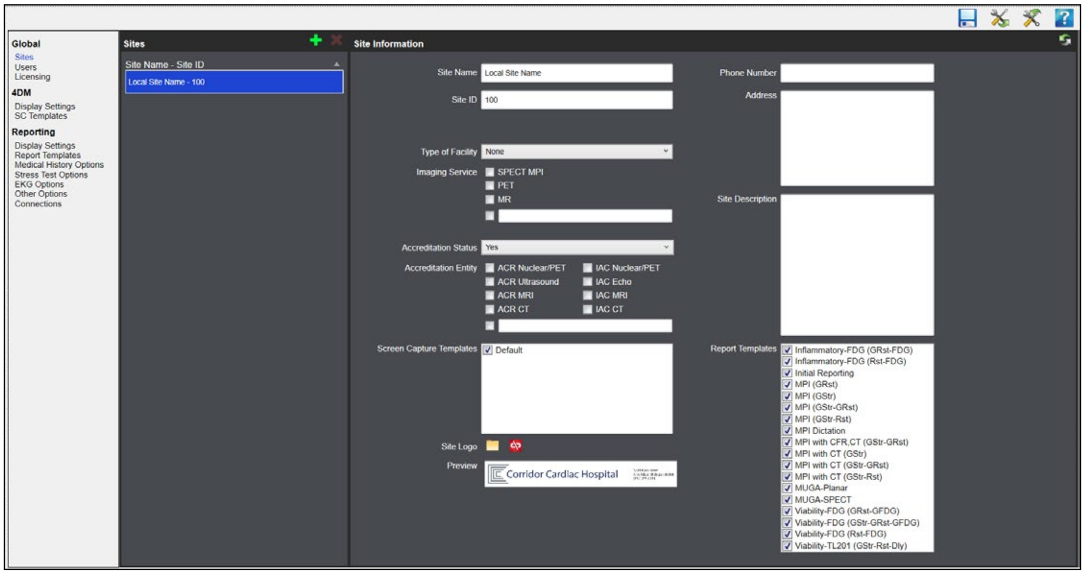
Sites

Overview

Corridor4DM includes the ability to include your site-specific information, for the primary purpose of including facility and accreditation information on Corridor4DM-generated DICOM screen captures. Multiple sites can be added for large Administrators who manage organizations with more than one site/location. Information on the **Sites** page includes:

- Site Name
- Site ID
- Address
- Site Logo
- Type of Facility
- Imaging Service
- Phone Number
- Accreditation Status
- Accreditation Entity
- Site Description
- Associated Report Templates
- Associated Screen Capture Templates

On the **Sites** page *(Figure 2.19)*, a default site labeled "Local Site Name-100" is listed for customization.



Site Name - Site ID
Local Site Name - 100

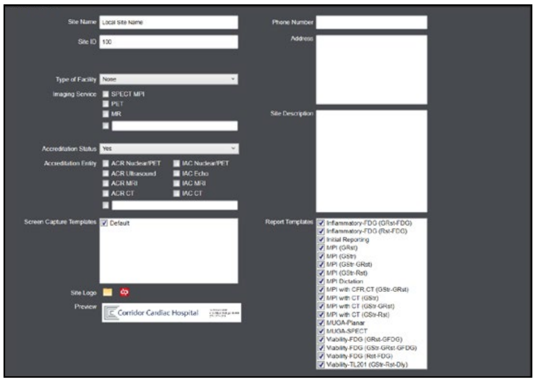
Site Name: Local Site Name
Site ID: 100
Type of Facility: None
Imaging Service: ☐ SPECT MPI ☐ PET ☐ MR ☐
Accreditation Status: Yes
Accreditation Entity: ☐ ACR Nuclear/PET ☐ ACR Ultrasound ☐ ACR MRI ☐ ACR CT ☐ IAC Nuclear/PET ☐ IAC Echo ☐ IAC MRI ☐ IAC CT ☐
Screen Capture Templates: ☑ Default
Site Logo
Preview
Phone Number
Address
Site Description
Report Templates: ☑ Inflammatory-FDG (GRst-FDG) ☑ Inflammatory-FDG (Rst-FDG) ☑ Initial Reporting ☑ MPI (GRst) ☑ MPI (GStr) ☑ MPI (GStr-GRst) ☑ MPI (GStr-Rst) ☑ MPI Dictation ☑ MPI with CFR,CT (GStr-GRst) ☑ MPI with CT (GStr) ☑ MPI with CT (GStr-GRst) ☑ MPI with CT (GStr-Rst) ☑ MUGA-Planar ☑ MUGA-SPECT ☑ Viability-FDG (GRst-GFDG) ☑ Viability-FDG (GStr-GRst-GFDG) ☑ Viability-FDG (Rst-FDG) ☑ Viability-TL201 (GStr-Rst-Dly)

Figure 2.19: *Sites page*

See the 4DM Reporting Users Guide for more information on using the Sites page for generating 4DM Reports.

Creating and editing your site in Corridor4DM

1. Select the default site: "Local Site Name-100"
2. In the **Site Information** section *(Figure 2.20)*, edit the **Site Name** by typing your desired site name in the required field.
3. A **Site ID** field is available for use by accredited sites (e.g., ACR, IAC), but is not required.
4. Other optional fields available include: **Type of Facility**, **Imaging Service**, **Accreditation**



Site Name: Local Site Name
Site ID: 100
Type of Facility: None
Imaging Service: ☐ SPECT MPI ☐ PET ☐ MR ☐
Accreditation Status: Yes
Accreditation Entity: ☐ ACR Nuclear/PET ☐ ACR Ultrasound ☐ ACR MRI ☐ ACR CT ☐ IAC Nuclear/PET ☐ IAC Echo ☐ IAC MRI ☐ IAC CT ☐
Screen Capture Templates: ☑ Default
Site Logo
Preview
Phone Number
Address
Site Description
Report Templates: ☑ Inflammatory-FDG (GRst-FDG) ☑ Inflammatory-FDG (Rst-FDG) ☑ Initial Reporting ☑ MPI (GRst) ☑ MPI (GStr) ☑ MPI (GStr-GRst) ☑ MPI (GStr-Rst) ☑ MPI Dictation ☑ MPI with CFR,CT (GStr-GRst) ☑ MPI with CT (GStr) ☑ MPI with CT (GStr-GRst) ☑ MPI with CT (GStr-Rst) ☑ MUGA-Planar ☑ MUGA-SPECT ☑ Viability-FDG (GRst-GFDG) ☑ Viability-FDG (GStr-GRst-GFDG) ☑ Viability-FDG (Rst-FDG) ☑ Viability-TL201 (GStr-Rst-Dly)

Figure 2.20: *Site Information section*

Status, **Accreditation Entity**, **Phone Number**, **Address**, and **Site Description**.

5. Click **Save** to save your newly entered site information.

Corridor4DM Administrators can edit the site information at any time. Select the site and edit the desired information.

Including a site logo into Corridor4DM screen captures

Attaching a .bmp, .jpg, .jpeg, .gif, .tif, .png, or .ico image of a site logo within the **Sites** page enables your logo to appear on Corridor4DM screen captures and reports.

To include a site logo, locate the **Site Logo** section *(Figure 2.21)* on the **Sites** page:

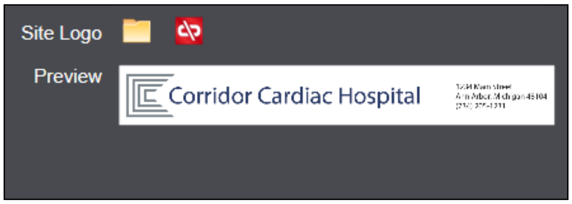


***Figure 2.21:** Add a site logo*

1. On the **Sites** page, click the **Browse** icon to navigate to the location where the logo file is stored to link it to Corridor4DM.
2. Once linked, a preview image of the logo will appear. If the image is not optimal, unlink the image by clicking the **Unlink** icon.
3. Click **Save** *(Figure 2.22)*. Corridor4DM automatically copies the JPEG image to the directory it needs in order to include the logo on screen captures (and Corridor4DM reports, for Corridor4DM Reporting users).

***Figure 2.22:** Click Save*

If there are multiple logos that you would like to include on screen captures or reports, you must first merge the logos into one file before adding it within 4DM Administration.

Adding additional sites

1. On the **Sites** page, click the **Add** tool *(Figure 2.23)* and a new site appears in the list
2. Select the New Site and follow instructions in the [Create your site in Corridor4DM](#) section.

***Figure 2.23:** Click Add tool*

Deleting sites

1. To delete a site, select the site you want to delete, then click the red **Remove** tool *(Figure 2.24)*.
2. Click **Save** to save your changes.

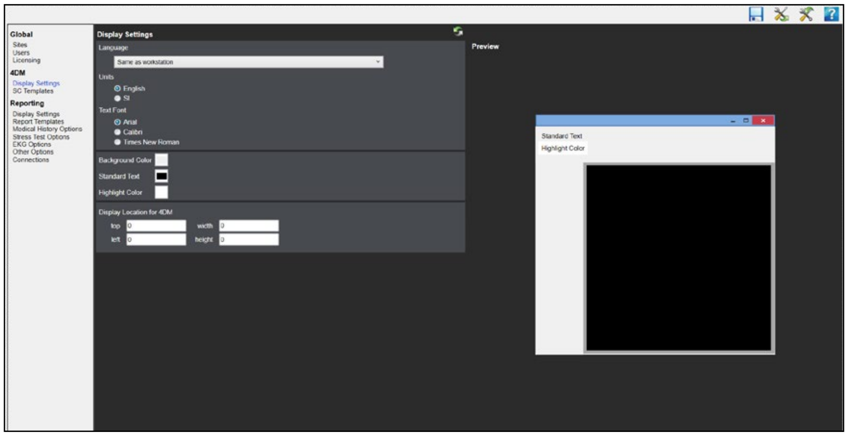
***Figure 2.24:** Click Remove tool*

You can choose to delete the default site, but there must be an additional site created first. Corridor4DM Administration requires at least one site to be present.

Corridor4DM Display Settings

Overview

The **Corridor4DM Display Settings** page *(Figure 2.25)* allows configuration of preferences for the Corridor4DM Administration module and Corridor4DM software application. Corridor4DM Administrators can update the following: displayed language, background, text and button highlight colors, units of measurement, text font style, and Corridor4DM's display location within a large screen or multi-monitor setup.



Display Settings

Language: Same as workstation

Units
- ● English
- ○ SI

Text Font
- ● Arial
- ○ Calibri
- ○ Times New Roman

Background Color
Standard Text
Highlight Color

Display Location for 4DM
top 0
width 0
left 0
height 0

Figure 2.25: Corridor4DM Display Settings page

Set the displayed language

Changing the language will update the Corridor4DM Administration module and Corridor4DM software to display all text in the selected language.

1. On the **Corridor4DM Display Settings** page, click the **Language** drop-down menu *(Figure 2.26)* and select the desired language.
2. To match the system's language setting automatically, select the **Same as workstation** option.
3. Click **Save**
4. **Exit** Corridor4DM Administration and Corridor4DM

The new language displays the next time Corridor4DM Administration and Corridor4DM are launched.

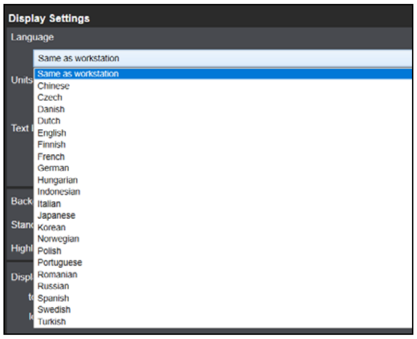


Figure 2.26: Set the displayed language

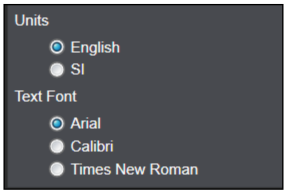
Set units of measurement and font style

Corridor4DM defaults to display in **English** units of measurement for weight (**lb**), height (**in**), and dose (**mCi**). International users can select the **SI** toggle to change to display in the International System of units: weight (**kg**), height (**cm**), and dose (**MBq**). This will update all units of measurement displayed in Corridor4DM, Corridor4DM Administration, and Corridor4DM Reporting.

The default text font in Corridor4DM is Arial, with options to select Calibri or Times New Roman. This font selection will update all text displayed in Corridor4DM, Corridor4DM Administration, and Corridor4DM Reporting.

1. Make selections for units and/or font *(Figure 2.27)*
2. Click **Save**
3. **Exit** Corridor4DM Administration and Corridor4DM.

The next time Corridor4DM is launched, it will display the new settings.



Units
- ● English
- ○ SI

Text Font
- ● Arial
- ○ Calibri
- ○ Times New Roman

Figure 2.27: Set units of measurement & font

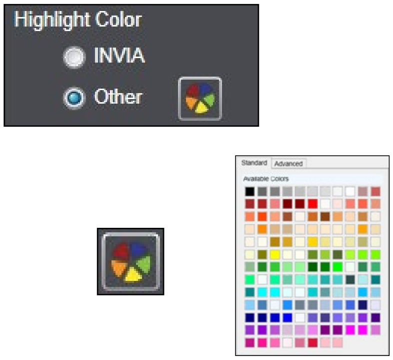
Change Corridor4DM background, text, and highlight colors

Updates to the color of the text and background in Corridor4DM are available. An immediate preview of the selected options appears within the right side of the page. Corridor4DM Administrators can use the INVIA defaults for each or create a custom color using the color panel. Highlight color applies a color change to important areas of the software, like the currently displayed Corridor4DM screen, dataset series ID/name, and the LVEF % quantified value.

To make changes to the background color, text and highlight colors, follow these steps:

1. Select the **Background Color Box** and select from the available standard colors, or click **Advanced** to create your own color *(Figure 2.28)*.
2. Choose the desired color to apply the change
3. An immediate preview of the color changes updates once the selections are complete.
4. Click **Save** to save all changes in Corridor4DM Administration.

Corridor4DM displays will show as updated on the next launch of the Corridor4DM application.



Highlight Color

○ INVIA

● Other

Figure 2.28: *Create your own color*

Configure the size and location of the Corridor4DM application window

Corridor4DM defaults to display on the system's primary monitor, utilizing the size that best fits Corridor4DM's resolution requirements. For multiple monitors, or large screen monitor users, Corridor4DM can be configured to display in a desired location, or on a particular monitor. Additionally, Corridor4DM's default width and height can be defined.

To make edits to the display location of Corridor4DM, command line argument parameters can be entered in the **top**, **width**, **left**, and **height** fields *(Figure 2.29)*. If the user has a dual monitor setup with monitors displaying 1280x1024 resolution, entering **0** in the **top** field, and **1280** in the **left** field opens the Corridor4DM application on the second monitor.

Display Location for 4DM

top ☐ width ☐

left ☐ height ☐

Figure 2.29: *Configure display location for Corridor4DM*

Screen Capture Templates - Create & Edit

Overview

Screen Captures (SC) generated within Corridor4DM are configurable to permit inclusion of: site information, site logos, accreditation entity and status, patient demographics, and radiopharmaceutical and dose information. Corridor4DM provides tools to preview SC templates to ensure information and site logos display as intended.

The **SC Template Toolbar** provides main functions such as opening, saving and previewing templates, and is located in the upper right of the page *(Figure 2.30)*:

Figure 2.30: *SC Template toolbar*

Open Template: Click to open and select from the list of SC Templates available. If templates from another Corridor4DM client have been restored to the system, click the Add tool in the Open Template window, select the template, and click Open.

Preview Template: Click to preview the template as it appears with study images and information.

Preview Template (with drop-down arrow): The drop-down arrow appears on this icon when there are multiple sites defined within Corridor4DM Administration.

Save Template: Click to save edits to the currently displayed template. This will overwrite any settings on the currently displayed template. No menu displays when this icon is clicked.

Save As Template: Click to view the Save As window and create a new template with a unique File Name, based off the currently displayed template edits. This option allows selecting the sites to apply the template

Open/View the default SC template

Upon first installation of Corridor4DM, a default template is included as a general example, including the most commonly used tags and can be used to make custom edits.

To open and review a SC template:

1. Click the **Open Template** icon. This opens up an Open Template window *(Figure 2.31)*.
2. The Default template shows as selected (highlighted in blue). If other templates have been created, click to select the template name to view it.
3. If templates have been restored to the system from different Corridor4DM clients, click the **Add** icon to navigate to it, select, and view it.
4. Click **Open**.

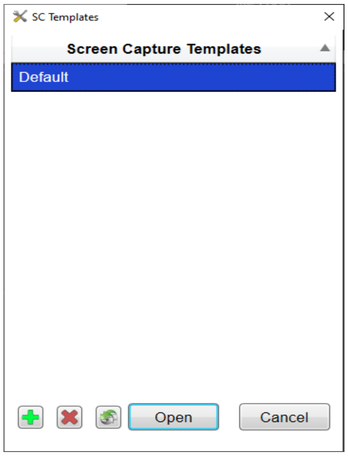


Figure 2.31: *Open Template window*

The selected template will display, showing default tags included on the template. Data elements contained in the patient datasets populate Corridor4DM screen capture templates via tags. Tags are represented by [Bracketed Text] within the template header and footer areas.

Create a new SC template

To create a new SC template, first click **Open** to select an existing template *(Figure 2.32)*. The default template can be used to make custom edits.

1. Make desired edits to the template. See the [Edit the SC Template]() section for more information.
2. Click the **Preview** icon to review the edits as

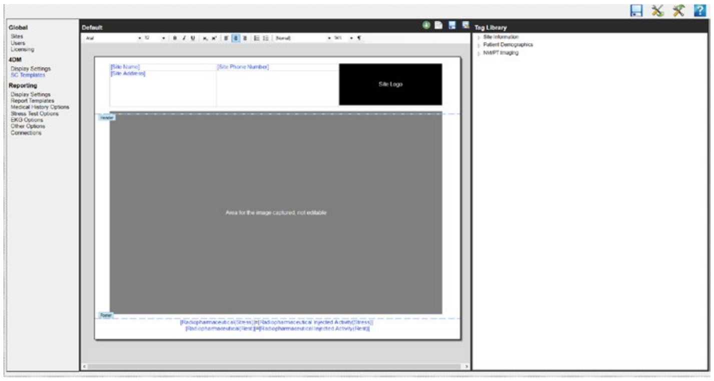


Figure 2.32: *Open an existing template*

It is recommended to save your new 4DM Administration settings and perform a new 4DM Backup so that these new templates can be restored to other 4DM clients. See the [Backup and Restore section]() of this chapter to learn more.

they will appear when Corridor4DM screen captures are generated in the Corridor4DM application *(Figure 2.33)*.

3. Click the **Save As** icon and give the template a unique **File Name**. Select all sites you wish to apply the template to *(Figure 2.34)*.
4. Click **Save as…**

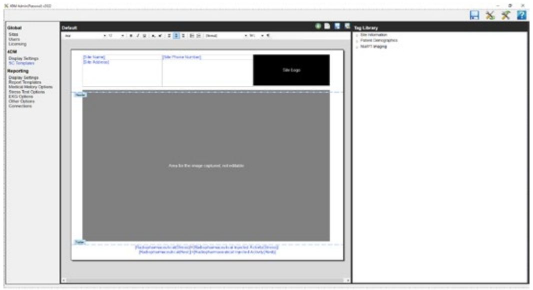


Figure 2.33: *Preview edits within the template*

File Name INVIA

Applied To ☑ Local Site Name - 100

Figure 2.34: *Save As window*

Edit the SC Template

Once a template is opened, basic text editing tools are available in the toolbar.

Corridor4DM includes a Tag Library on the right panel, which can be expanded to show all available tags via a click on the black triangles next to the Site Information, Patient Demographics, and NM/PT Imaging headings.

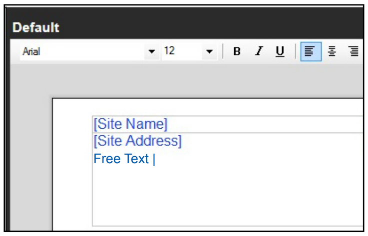
Tags in Corridor4DM are links to the patient and site information, which are automatically imported and displayed in Corridor4DM screen captures and reports. Tags always appear as [Bracketed Text], to differentiate them from typed standard text entered by sites. Open the template by clicking the **Open** icon and selecting the template.

1. Basic Edits

To add standard text *(Figure 2.35)*:

a. Standard text can be typed into the header/footer area. Click to place the cursor in the header/footer area, and use the keyboard to type in free text.

b. Standard text editing tools can be accessed either in the toolbar, or via right-click on selected tags/ text. Click to highlight the text to edit, then select the text editing option.



[Site Name]
[Site Address]
Free Text |

Figure 2.35: *Add standard text*

To edit text/tags:

a. Quick Styles for text and Corridor4DM tags are available in the drop-down menu from the text editing toolbar *(Figure 2.36)*. To apply a quick style, click to select the tag or text, then select the option from the drop-down menu.

   - To add,

Figure 2.36: *Text editing toolbar*

modify, or delete these quick styles, right-click on any free text or Corridor4DM Tags, and select **Styles** *(Figure 2.37)*, which opens a window providing options to change font, paragraph, line spacing, etc.

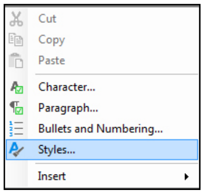


Figure 2.37: *Select Styles*

To edit the Corridor4DM image area or header/footer area:

b. Click to select the area you wish to resize, then click and drag the border of the image *(Figure 2.38)*.

c. Click to select the dotted line noting the header/footer spacing, then click and drag it up or down.

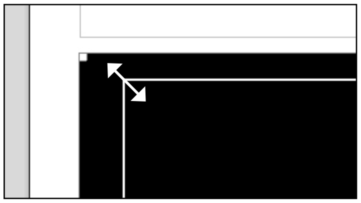


Figure 2.38: *Edit Corridor4DM image area*

2. Editing Tags / Adding Logos

Resizing of the image area is allowed, but other edits are not permitted.

To add a new tag to the template *(Figure 2.39)*:

d. Click to place the cursor in the area of the template where the new tag should appear.

e. Click and drag the tag into the template. In template mode, the tags will appear as [Bracketed Text].

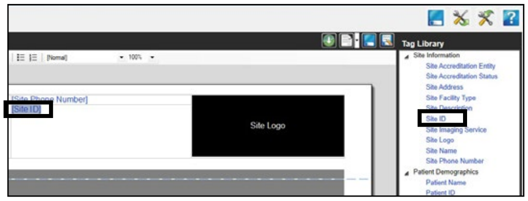


Figure 2.39: *Drag and drop tags into template*

To delete tags from the template:

f. Tags can be deleted by placing the cursor at the end of the tag and hitting the **Backspace** key on the keyboard.

g. You can also right-click on a tag and select **Delete** *(Figure 2.40)*.

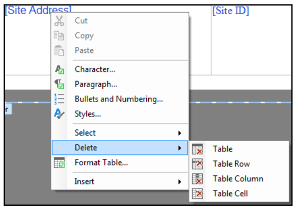


Figure 2.40: *Delete tags*

To insert a site logo into a template *(Figure 2.41)*:

h. Ensure that a [site logo has been added](#) on the **Sites** page within Corridor4DM Administration. Logos that are added on the **Sites** page are automatically linked via the Site Logo tag.

Figure 2.41: *Insert a site logo*

i. Logos can be deleted from templates by clicking on the Site Logo tag and clicking the **Backspace** key on the keyboard.

3. Additional Screen Capture Template Edits

To undo SC Template edits:

j. To undo edits one at a time, click **Ctrl+Z**.

k. Each **Ctrl+Z** click will undo the last change made, in reverse order.

To reset all templates to default settings:

l. Click the **Open** icon.

m. Click the **Reset All** icon *(Figure 2.42)*, which will present a warning message to reset all templates to

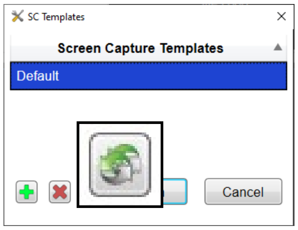
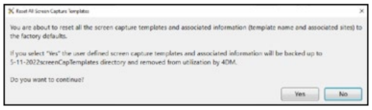


Figure 2.42: *Reset All icon*

factory defaults. Corridor4DM will automatically backup the templates prior to resetting them, with the backup location noted in a warning message that displays *(Figure 2.43)*.


Reset All Screen Capture Templates

You are about to reset all the screen capture templates and associated information (template name and associated sites) to the factory defaults.

If you select "Yes" the user defined screen capture templates and associated information will be backed up to 5-11-2022screenCapTemplates directory and removed from utilization by 4DM.

Do you want to continue?

***Figure 2.43:** Warning message*

- Click **Yes** to proceed with resetting all Corridor4DM screen capture templates. All templates will be available to add back in by clicking the **Add** icon within the SC Templates window.
- Click **No** to proceed without resetting the templates.

To remove/delete a template:

n. Click the **Open Templates** icon.

o. Select the template to remove, then click the **Remove** icon *(Figure 2.44)*. No warning message presents after selecting this, so be sure you want to remove the template. If it was backed up previously it will be available via the **Add** icon.

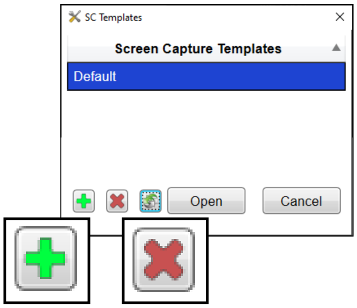


***Figure 2.44:** SC Templates window, select Add or Remove*

Save the SC Template

Once all edits are complete, click the **Save** or **Save As** icons in the SC Toolbar to save all edits made.

It is recommended to save your new 4DM Administration settings and perform a new 4DM Backup so that these new templates can be restored to other 4DM clients. See the Backup and Restore section of this chapter to learn more.

1. Click **Save** *(Figure 2.45)* to overwrite the existing SC template that was originally opened, with intent to keep the template named the same.
2. Click **Save As** *(Figure 2.46)* to permit creation of an additional template with a unique template filename. This also provides the opportunity to apply the new template to additional sites.
   - Edit the File Name, select sites, and click **Save As…**

***Figure 2.45:** Save*

***Figure 2.46:** Save As*

Backup and Restore Configuration Settings

Overview

Performing backups ensures that changes made to Corridor4DM on a local client, such as user-defined colorbars, normals databases, and screen templates, will be saved and can be restored later. Backups are helpful to avoid re-work in such cases as: installations of new or additional Corridor4DM clients, upgrading Corridor4DM versions, hardware crashes, and new Corridor4DM licensing. The backup is then able to be restored to the local Corridor4DM client at a future time. If any workstation has a different configuration than the others, it should be backed-up separately.

Backups from versions older than Corridor4DM v2016 can be restored to Corridor4DM v2016 clients.

Backing up Corridor4DM Settings

This section will cover performing a basic backup from within Corridor4DM Administration. Backups include settings from all Corridor4DM modules (Corridor4DM, Corridor4DM Administration, and Corridor4DM Reporting), and includes the following:

- Corridor4DM users and user-specific settings
- Application configurations
- Corridor4DM and user-defined colorbars
- Corridor4DM licensing
- Corridor4DM and user-defined normals databases
- Corridor4DM report templates and Corridor4DM Reporting module configurations
- Corridor4DM and user-defined screen templates, screen capture templates, and XML templates

Save all 4DM Administration and 4DM application settings. If you do not save prior to selecting the Backup icon, a warning message displays asking to Save or Don't Save current settings. The last-saved 4DM settings will be backed up.

To backup Preferences, perform the following:

1. In Corridor4DM Administration, click the **Backup** tool *(Figure 2.47)*.

Figure 2.47: *Backup tool*

2. In the Backup window *(Figure 2.48)*, first select the **Browse** icon to open the Select Folder window *(Figure 2.49)* and navigate to the desired location.
    - Right-click and choose New > Folder to create and name a folder that is available across the network for users and easy access from other Corridor4DM clients.
    - Click **Select Folder.** The mapped location displays in the File Directory Field.

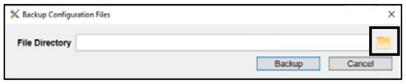
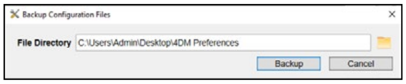


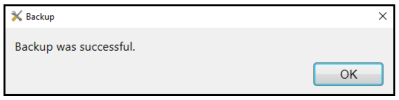
Figure 2.48: *Click Browse*



File Directory C:\Users\Admin\Desktop\4DM Preferences

Figure 2.49: *Browser for Folder window*

3. Once the File Directory has selected, click **Backup**. A *Backup was Successful* message displays when complete *(Figure 2.50)*. Click **OK**.



Backup was successful.

Figure 2.50: *Backup was Successful window*

For more detailed information on 4DM Backups, see the Backup Reference Guide, available on the INVIA website in the User Center. www.inviasolutions.com.

Restoring Corridor4DM Settings

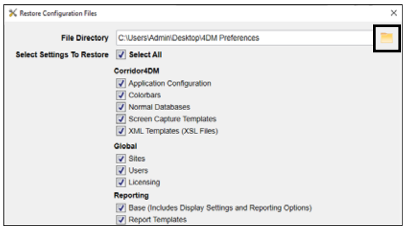
This section will cover performing a basic Restore from within Corridor4DM Administration. The user has the ability to restore individual user-specific workflows, Corridor4DM settings global to a particular workstation, or both. Once a restore is performed, the new user specific workflows are added and existing workflows with the same names are overwritten by the application.

To restore Preferences, perform the following:

1. In Corridor4DM Administration, click the **Restore** tool *(Figure 2.51)*.
2. First, select the **Browse** icon *(Figure 2.52)* to open the Select Folder window *(Figure 2.53)*, and navigate to the location of the stores backup folder.
3. Highlight the folder name, and click the Select Folder button. The mapped location displays in the File Directory field.
4. All backed-up users and settings will appear in the Restore window.
5. The **Select All** button *(Figure 2.54)* selects all users and user-specific settings, and all global settings/directories, and is typically recommended.
6. Click **Restore**.
7. Within the Restore was Successful window *(Figure 2.55)*, click **OK**.

For more detailed information on 4DM Restores, see the Restore Reference Guide, available on the INVIA website in the User Center. www.inviasolutions.com.

Figure 2.51: *Restore tool*



Restore Configuration Files

File Directory: C:\Users\Admin\Desktop\4DM Preferences

Select Settings To Restore ☑ Select All

Corridor4DM
☑ Application Configuration
☑ Colorbars
☑ Normal Databases
☑ Screen Capture Templates
☑ XML Templates (XSL Files)

Global
☑ Sites
☑ Users
☑ Licensing

Reporting
☑ Base (Includes Display Settings and Reporting Options)
☑ Report Templates

Figure 2.52: *Select Browse*

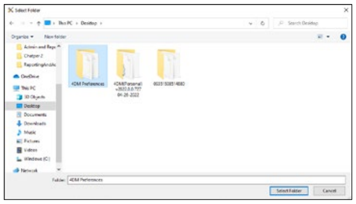
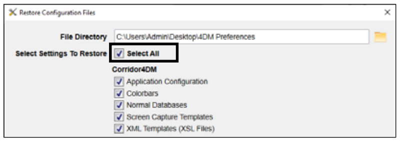


Figure 2.53: *Browse For Folder window*



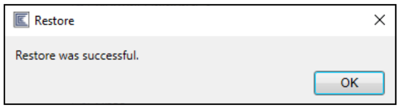
Restore Configuration Files

File Directory: C:\Users\Admin\Desktop\4DM Preferences

Select Settings To Restore ☑ Select All

Corridor4DM
☑ Application Configuration
☑ Colorbars
☑ Normal Databases
☑ Screen Capture Templates
☑ XML Templates (XSL Files)

Figure 2.54: *Click Select All*



Restore

Restore was successful.

Figure 2.55: *Restore was Successful window*

Corridor4DM Help

Accessing Corridor4DM User's Guides

The Corridor4DM User's Guide includes information on the Corridor4DM Administration and Corridor4DM applications. The Corridor4DM Reporting module includes its own User's Guide, accessible from within Corridor4DM Reporting's Help menu. Corridor4DM Personal's Patient Browser also has its own User's Guide, which is found within the patient browser's Help menu.

This Corridor4DM User's Guide is available:

- From within Corridor4DM, by clicking the **Help** button in the Control Panel *(Figure 2.56)*
- From within Corridor4DM Administration, by clicking the **Help** icon *(Figure 2.57)*

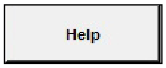
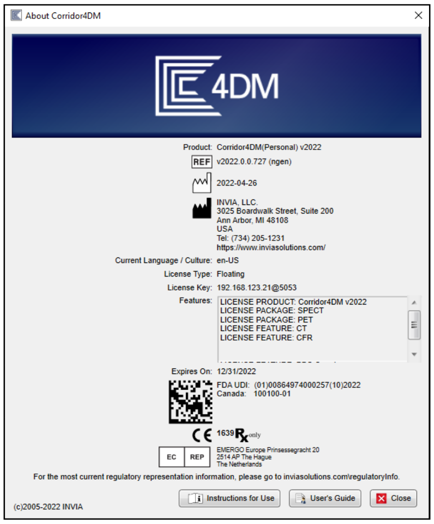


Figure 2.56: *Help button in Corridor4DM Control Panel*

Figure 2.57: *Help icon in Corridor4DM Administration*

Within the Help window *(Figure 2.58)*, click **User's Guide** to display the full User's Guide as a PDF.



Product: Corridor4DM(Personal) v2022
REF v2022.0.0.727 (ngen)
2022-04-26
INVIA, LLC.
3025 Boardwalk Street, Suite 200
Ann Arbor, MI 48108
USA
Tel: (734) 205-1231
https://www.inviasolutions.com/
Current Language / Culture: en-US
License Type: Floating
License Key: 192.168.123.21@5053
Features: LICENSE PRODUCT: Corridor4DM v2022
LICENSE PACKAGE: SPECT
LICENSE PACKAGE: PET
LICENSE FEATURE: CT
LICENSE FEATURE: CFR
Expires On: 12/31/2022
FDA UDI: (01)00864974000257(10)2022
Canada: 100100-01
CE 1639 Rx only
EC REP EMERGO Europe Prinsessegracht 20
2514 AP The Hague
The Netherlands
For the most current regulatory representation information, please go to inviasolutions.com\regulatoryInfo.
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Figure 2.58: *Example Help window*

Instructions for Installation (IFI) and Instructions for Use (IFU) are separate guides, including basic information. From within the Help window, the IFU is also available.

Corridor4DM Help Materials Available

INVIA provides several different user-friendly formats for guidance and help with the Corridor4DM application. Here's a quick list of the types of documents available:

- **Corridor4DM User's Guide** – Manual on all Corridor4DM main features, tools, workflows, and configurations.
- **Corridor4DM Reporting User's Guide** – Manual specific to Corridor4DM's Reporting module. Some Corridor4DM Administration sections specific to Corridor4DM Reporting are covered in this User's Guide.
- **Corridor4DM Personal's Patient Browser User's Guide** – Manual specific to the Corridor4DM Personal's patient browser functionality.
- **Instructions for Installation (IFI)** – Basic steps to install the Corridor4DM application.
- **Instructions for Use (IFU)** – Basic information on how to use Corridor4DM.
- **Reference Guides –** Step-by-step guides specific to common functions in Corridor4DM.
- **Training Videos** – Workflow-oriented videos that give clinically-centered workflow tutorials within Corridor4DM.

All User's Guides, Instructions for Installation, Instructions for Use, Reference Guides, and much more, are available for review and download on the INVIA website in the User Center: www.inviasolutions.com.

CHAPTER 3

CORRIDOR4DM SCREENS AND CONTROLS

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**.

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

The Corridor4DM Work Environment

Corridor4DM is available both as a standalone (Corridor4DM 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 Corridor4DM environment is wrapped within the host medical system. A few examples are shown in *(Figure 3.1)*:

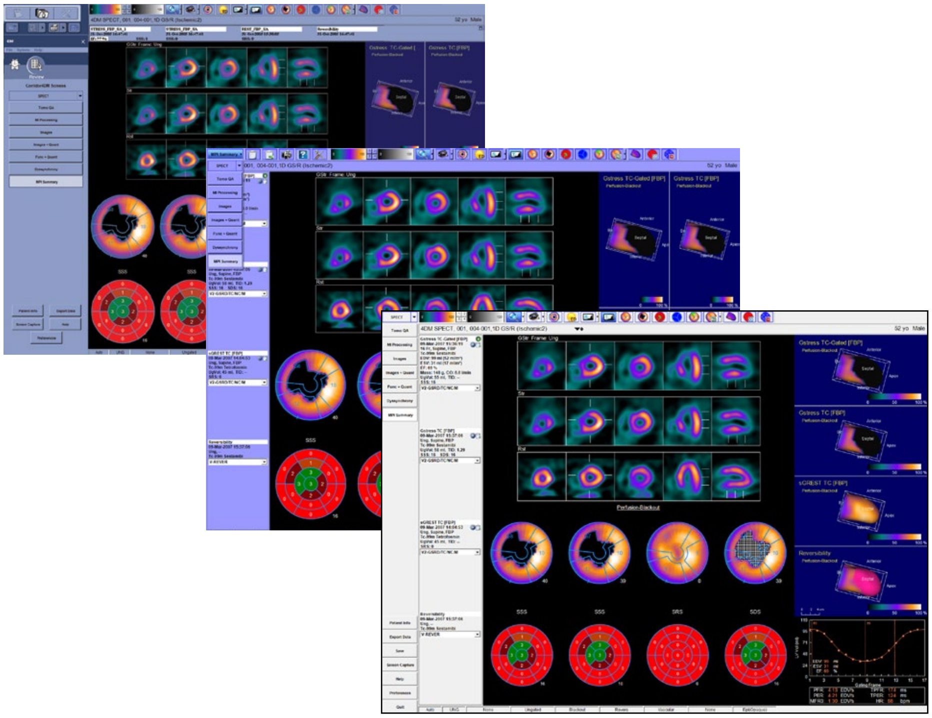


Figure 3.1: *Examples of the Corridor4DM work environment*

The work environment can be broken down into four sections:

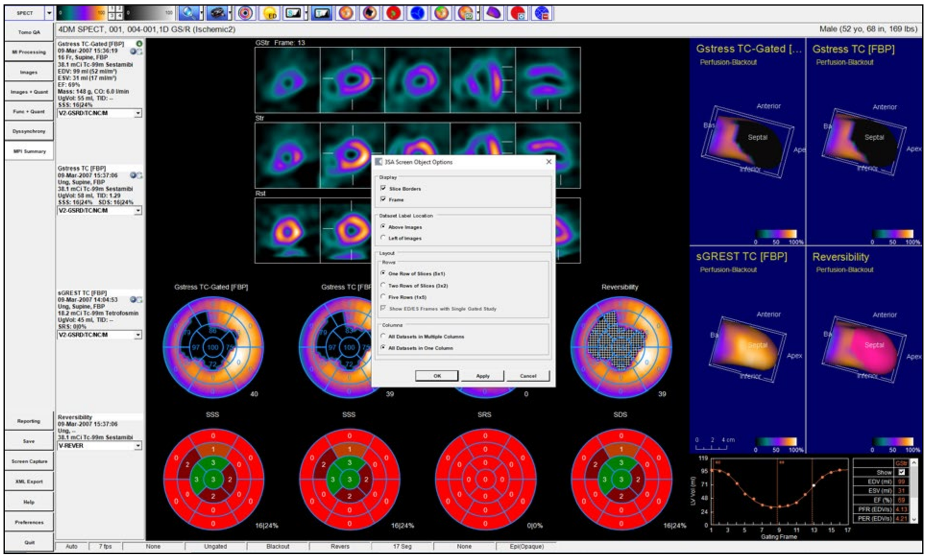
1. **Display Windows** — Image Display, Right-click Screen Options
2. **Application Tools** — Workflow Screens, Control Panel, Colorbar, and Toolbar
3. **Information Panels** — Patient and Dataset Information
4. **Selection Controls** — Patient Selector, Dataset Selector, Normals Database Selector

The **Right-click Screen Options** are applicable to these Corridor4DM **Objects**:

- Tomo
- Splash
- 3SA
- Polar Map
- Scores
- 3D

Display Windows

The most distinguishable component of Corridor4DM is the **Image Display Window** *(Figure 3.2)*. 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 3.2 insert)* are accessible by clicking the right mouse button. Its primary function is to provide additional user controls for screen and image customization.


3SA Screen Object Options

Display

- ☑ Slice Borders
- ☑ Frame

Dataset Label Location

- ● Above Images
- ○ Left of Images

Layout

Rows

- ● One Row of Slices (5x1)
- ○ Two Rows of Slices (3x2)
- ○ Five Rows (1x5)
- ☑ Show ED/ES Frames with Single Gated Study

Columns

- ○ All Datasets in Multiple Columns
- ● All Datasets in One Column

Figure 3.2: *Image Display window with the Right-click Splash Object Options window*

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

Application Tools

The **Workflow Screens** *(Figure 3.3)* provide access to the various Corridor4DM processing and review screens. You have the ability to customize these screens to fit your specific workflow. The **Control Panel** *(Figure 3.4)* supports primary functions relevant to saving, reporting, and setting preferences within the application.

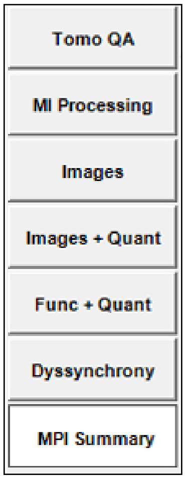


Figure 3.3: *Example of Workflow Screens*

Figure 3.4: *Examples of Controls within the Control Panel*

Some screens and objects have unique colorbar controls. Refer to Colorbar Tools for more information.

The **Colorbar Tool** and **Toolbar** are shown below *(Figure 3.5)*. 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 3.5: *Colorbar Tools and Toolbar*

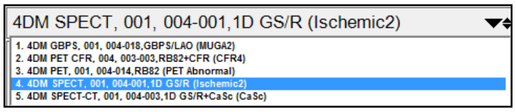
Information Panels

The **Patient Information Panel** contains the patient name, identification number, age, and gender. For each dataset, Corridor4DM displays relevant information within the **Dataset Information Panel**, including:

- Dataset Description
- Acquisition Date/Time
- Frames (Fr)
- Orientation
- 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 patient studies and then navigate between patients with the **Patient Selector** *(Figure 3.6)* drop-down menu or double-arrow button. This allows the user to review multiple patients in a single Corridor4DM session.



4DM SPECT, 001, 004-001,1D GS/R (Ischemic2)

1. 4DM GBPS, 001, 004-018,GBPS/LAO (MUGA2)
2. 4DM PET CFR, 004, 003-003,RB82+CFR (CFR4)
3. 4DM PET, 001, 004-014,RB82 (PET Abnormal)
4. 4DM SPECT, 001, 004-001,1D GS/R (Ischemic2)
5. 4DM SPECT-CT, 001, 004-003,1D GS/R+CaSc (CaSc)

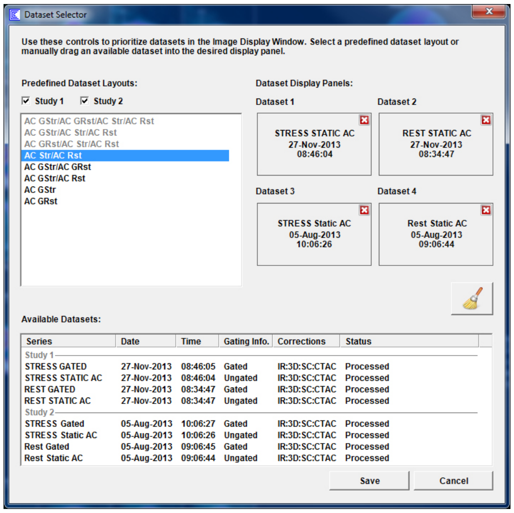
Figure 3.6: *Patient Selector Menu*

The following icons designate a dataset's processing status in the **Dataset Information Panel** *(Figure 3.8)*:

Gear: Identifies datasets loaded from a Corridor4DM results file

If a dataset does not have a **Gear** or **Flag** designation, the user processed the study within the current session or changed a quantification result.

Once the patient is loaded, you can also select which image datasets to review with the **Dataset Selector** *(Figure 3.7)*, by clicking the green arrow in the **Dataset Information Panel** *(Figure 3.8)*. 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 datasets.



Use these controls to prioritize datasets in the Image Display Window. Select a predefined dataset layout or manually drag an available dataset into the desired display panel.

Predefined Dataset Layouts:

☑ Study 1 ☑ Study 2

AC GStr/AC GRst/AC Str/AC Rst
AC GStr/AC Str/AC Rst
AC GRst/AC Str/AC Rst
AC Str/AC Rst
AC GStr/AC GRst
AC GStr/AC Rst
AC GStr
AC GRst

Dataset Display Panels:

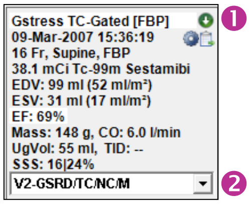
Dataset 1: STRESS STATIC AC 27-Nov-2013 08:46:04
Dataset 2: REST STATIC AC 27-Nov-2013 08:34:47
Dataset 3: STRESS Static AC 05-Aug-2013 10:06:26
Dataset 4: Rest Static AC 05-Aug-2013 09:06:44

Available Datasets:

Series	Date	Time	Gating Info.	Corrections	Status
Study 1					
STRESS GATED	27-Nov-2013	08:46:05	Gated	IR:3D:SC:CTAC	Processed
STRESS STATIC AC	27-Nov-2013	08:46:04	Ungated	IR:3D:SC:CTAC	Processed
REST GATED	27-Nov-2013	08:34:47	Gated	IR:3D:SC:CTAC	Processed
REST STATIC AC	27-Nov-2013	08:34:47	Ungated	IR:3D:SC:CTAC	Processed
Study 2					
STRESS Gated	05-Aug-2013	10:06:27	Gated	IR:3D:SC:CTAC	Processed
STRESS Static AC	05-Aug-2013	10:06:26	Ungated	IR:3D:SC:CTAC	Processed
Rest Gated	05-Aug-2013	09:06:45	Gated	IR:3D:SC:CTAC	Processed
Rest Static AC	05-Aug-2013	09:06:44	Ungated	IR:3D:SC:CTAC	Processed

Figure 3.7: *Dataset Selector*

When a comparison of current to prior studies is desired, the user has the ability to display the corresponding datasets of both studies by selecting the **Study 2** toggle while the **Study 1** toggle is enabled. With the **Study 2** toggle enabled, the user can either select from the **Predefined Dataset Layouts** to automatically load datasets for comparison or manually drag-and-drop the datasets into the **Dataset Display Panels**.

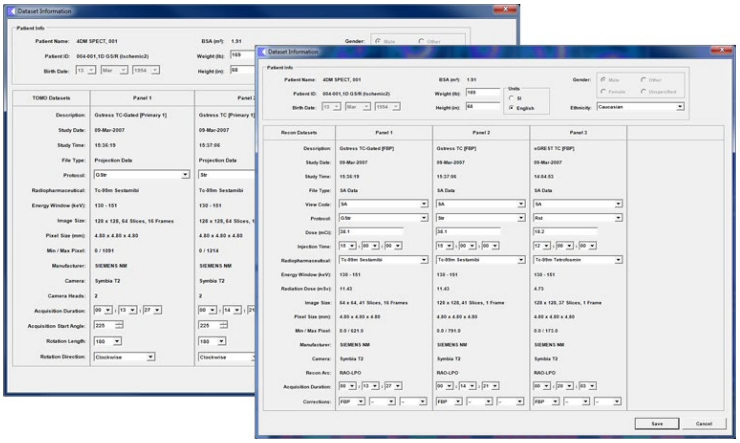


Gstress TC-Gated [FBP]
09-Mar-2007 15:36:19
16 Fr, Supine, FBP
38.1 mCi Tc-99m Sestamibi
EDV: 99 ml (52 ml/m²)
ESV: 31 ml (17 ml/m²)
EF: 69%
Mass: 148 g, CO: 6.0 l/min
UgVol: 55 ml, TID: --
SSS: 16|24%
V2-GSRD/TC/NC/M

Figure 3.8: *Dataset Information Panel with ❶ Dataset Selector and ❷ Normals Database Selector Menu*

Within the **Dataset Information Panel** *(Figure 3.8)*, the user can use the **Normals Database Selector** to select a normals database which applies a comparison of the patients quantification results to the mean statistics of the selected normals databases.

By right-clicking within the **Dataset Information Panel,** the user can edit dataset information that affects normal database matching and database quantification. The dataset information that can be viewed and edited depends on the screen and the datasets displayed *(Figure 3.9)*.



Dataset Information

Patient Info

Patient Name: 4DM SPECT, 001
Patient ID: 004-001,1D GS/R (Ischemic2)
Birth Date: 13 Mar 1954
BSA (m²): 1.91
Weight (lb): 169
Height (in): 68
Gender: ● Male ○ Other

TOMO Datasets	Panel 1	Panel 2
Description:	Gstress TC-Gated [Primary 1]	Gstress TC [Primary 1]
Study Date:	09-Mar-2007	09-Mar-2007
Study Time:	15:36:19	15:37:06
File Type:	Projection Data	Projection Data
Protocol:	GStr	Str
Radiopharmaceutical:	Tc-99m Sestamibi	Tc-99m Sestamibi
Energy Window (keV):	130 - 151	130 - 151
Image Size:	128 x 128, 64 Slices, 16 Frames	128 x 128, 64 Slices, 1
Pixel Size (mm):	4.80 x 4.80 x 4.80	4.80 x 4.80 x 4.80
Min / Max Pixel:	0 / 1091	0 / 1214
Manufacturer:	SIEMENS NM	SIEMENS NM
Camera:	Symbia T2	Symbia T2
Camera Heads:	2	2
Acquisition Duration:	00 : 13 : 27	00 : 14 : 21
Acquisition Start Angle:	225	225
Rotation Length:	180	180
Rotation Direction:	Clockwise	Clockwise

Dataset Information

Patient Info

Patient Name: 4DM SPECT, 001
Patient ID: 004-001,1D GS/R (Ischemic2)
Birth Date: 13 Mar 1954
BSA (m²): 1.91
Weight (lb): 169
Height (in): 68
Units: ○ SI ● English
Gender: ● Male ○ Other ○ Female ○ Unspecified
Ethnicity: Caucasian

Recon Datasets	Panel 1	Panel 2	Panel 3
Description:	Gstress TC-Gated [FBP]	Gstress TC [FBP]	sGREST TC [FBP]
Study Date:	09-Mar-2007	09-Mar-2007	09-Mar-2007
Study Time:	15:36:19	15:37:06	14:04:53
File Type:	SA Data	SA Data	SA Data
View Code:	SA	SA	SA
Protocol:	GStr	Str	Rst
Dose (mCi):	38.1	38.1	10.2
Injection Time:	15 : 00 : 00	15 : 00 : 00	12 : 00 : 00
Radiopharmaceutical:	Tc-99m Sestamibi	Tc-99m Sestamibi	Tc-99m Tetrofosmin
Energy Window (keV):	130 - 151	130 - 151	130 - 151
Radiation Dose (mSv):	11.43	11.43	4.73
Image Size:	64 x 64, 41 Slices, 16 Frames	128 x 128, 41 Slices, 1 Frame	128 x 128, 37 Slices, 1 Frame
Pixel Size (mm):	4.80 x 4.80 x 4.80	4.80 x 4.80 x 4.80	4.80 x 4.80 x 4.80
Min / Max Pixel:	0.0 / 621.0	0.0 / 791.0	0.0 / 173.0
Manufacturer:	SIEMENS NM	SIEMENS NM	SIEMENS NM
Camera:	Symbia T2	Symbia T2	Symbia T2
Recon Arc:	RAO-LPO	RAO-LPO	RAO-LPO
Acquisition Duration:	00 : 13 : 27	00 : 14 : 21	00 : 20 : 03
Corrections:	FBP - -	FBP - -	FBP - -

Figure 3.9: *Tomo and Recon Dataset Information Windows, accessed via right-clicking the Dataset Information Panel*

A Dataset Prioritization Clipboard icon displayed within the Dataset Information Panel informs the user of whether a dataset is prioritized for export (e.g., quantitative data for that dataset is exported to the report). There are four different clipboard icons available:

1. The clipboard with a green arrow *(Figure 3.10)* identifies that a dataset is prioritized for export.
2. A clipboard with a red bar *(Figure 3.11)* indicates that quantitative data for that dataset will not be exported to the report.
3. A clipboard with a caution sign *(Figure 3.12)* indicates that the dataset is prioritized for export, but is a prior study that is outside of the 14 day range from the acquisition date of the most recent study.
4. The caution sign icon will display if the dataset is a prior study, but is not prioritized for export *(Figure 3.13)*.

Figure 3.10: *Prioritized for Export*

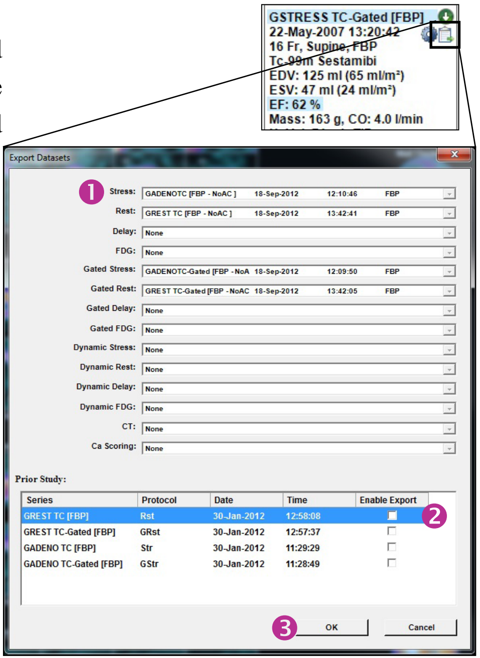
Figure 3.11: *Not Prioritized*

Figure 3.12: *Prior Study Prioritized*

Figure 3.13: *Prior Study*

Left-click on any displayed clipboard icon to verify and configure the desired datasets to prioritize for export. The **Export Datasets** window shows the currently prioritized datasets for export *(Figure 3.14)*.

1. If additional datasets are available to select, (e.g., attenuation corrected stress/rest, or prior study stress/rest) the **Dataset drop-down menu** will be active, allowing the user to select the desired datasets for export.
2. Click the **Enable Export** check-box in the Prior Study list to allow prior study datasets to appear as options to select in the drop-down menus.
3. Click **OK** to proceed with the selections. Next to each dataset in the Dataset Information Panel, new clipboard icons will update with the selections.



GSTRESS TC-Gated [FBP]
22-May-2007 13:20:42
16 Fr, Supine, FBP
Tc-99m Sestamibi
EDV: 125 ml (65 ml/m²)
ESV: 47 ml (24 ml/m²)
EF: 62 %
Mass: 163 g, CO: 4.0 l/min

Export Datasets

① Stress: GADENOTC [FBP - NoAC] 18-Sep-2012 12:10:46 FBP
Rest: GREST TC [FBP - NoAC] 18-Sep-2012 13:42:41 FBP
Delay: None
FDG: None
Gated Stress: GADENOTC-Gated [FBP - NoA 18-Sep-2012 12:09:50 FBP
Gated Rest: GREST TC-Gated [FBP - NoAC 18-Sep-2012 13:42:05 FBP
Gated Delay: None
Gated FDG: None
Dynamic Stress: None
Dynamic Rest: None
Dynamic Delay: None
Dynamic FDG: None
CT: None
Ca Scoring: None

Prior Study:

Series	Protocol	Date	Time	Enable Export
GREST TC [FBP]	Rst	30-Jan-2012	12:58:08	☐ ②
GREST TC-Gated [FBP]	GRst	30-Jan-2012	12:57:37	☐
GADENO TC [FBP]	Str	30-Jan-2012	11:29:29	☐
GADENO TC-Gated [FBP]	GStr	30-Jan-2012	11:28:49	☐

Figure 3.14: *Export Dataset Prioritization window, showing a prior study enabled and available for selection in the Stress drop-down menu.*

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 Corridor4DM, 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, and scroll through PDF and EKG pages	Reposition images; click and drag up and down over PDF and EKG pages
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 3.15)*. 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.

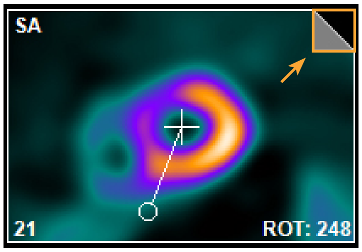


Figure 3.15: *The dog-ear tool*

Buttons

Corridor4DM buttons *(Figure 3.16)* are left-click tools with text that execute commands. Buttons are labeled with identifying text or by an icon (identifiable with tool tips).

Figure 3.16: *The above images are examples of the Corridor4DM button design*

Icons

Corridor4DM 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:

- **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 3.17)*.
- **Menu:** Left-click these tools to open a list of options. Once the menu is activated, users can make their selection *(Figure 3.18)*.

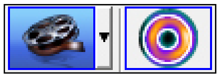


***Figure 3.17:** Examples of the two On/Off icon styles – with and without drop-down menus.*

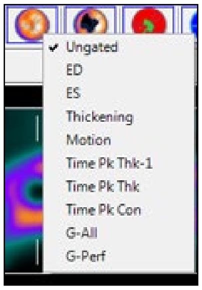


***Figure 3.18:** Menu Selection icon with menu expanded.*

Toggles

Within the application, the user will find two types of toggles: **Check Boxes** and **Radio Buttons** *(Figure 3.19)*. **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 Reporting and Preferences.

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).

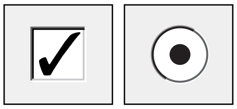


***Figure 3.19:** Toggle Examples. Check Box (left); Radio Button (right).*

Sliders

The slider tool *(Figure 3.20)* is the only Corridor4DM 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:

- **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)

***Figure 3.20:** Example of the zoom and cine sliders (above) and the image and study offset slider (below).*

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

***Figure 3.21:** Colorbar Tools*

The **Colorbar Tool** *(Figure 3.21)* is a screen-specific color management tool which applies to **Splash, 3SA,**

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

Polar Map, and **3D Objects**. The tool contains dual colorbars, sliders to adjust contrast, and a right-click menu for managing the color schemes.

Colorbar

Corridor4DM applies a color scheme to an acquired image according to the intensity of the tracer uptake *(Figure 3.22)*. 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.

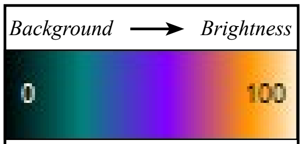


Figure 3.22: *The Colorbar*

Colorbar Menus

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

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 3.23)* 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.

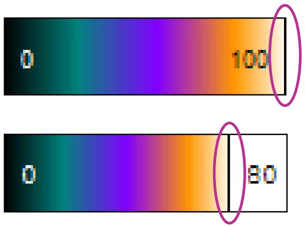


Figure 3.23: *The upper threshold slider for image brightness is illustrated here at 100% (default) and 80%*

Double-click the colorbar to reset the slider after making changes to a colorbar’s brightness or contrast settings.

Contrast Slider Tool

The **Contrast Slider** *(Figure 3.24)* 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.

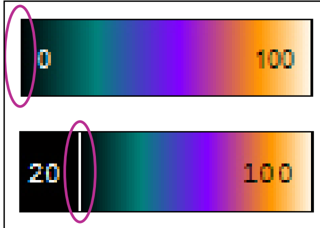


Figure 3.24: *The lower threshold slider for image contrast is illustrated here at 100% (default) and 80%.*

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 3.25)*. 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.

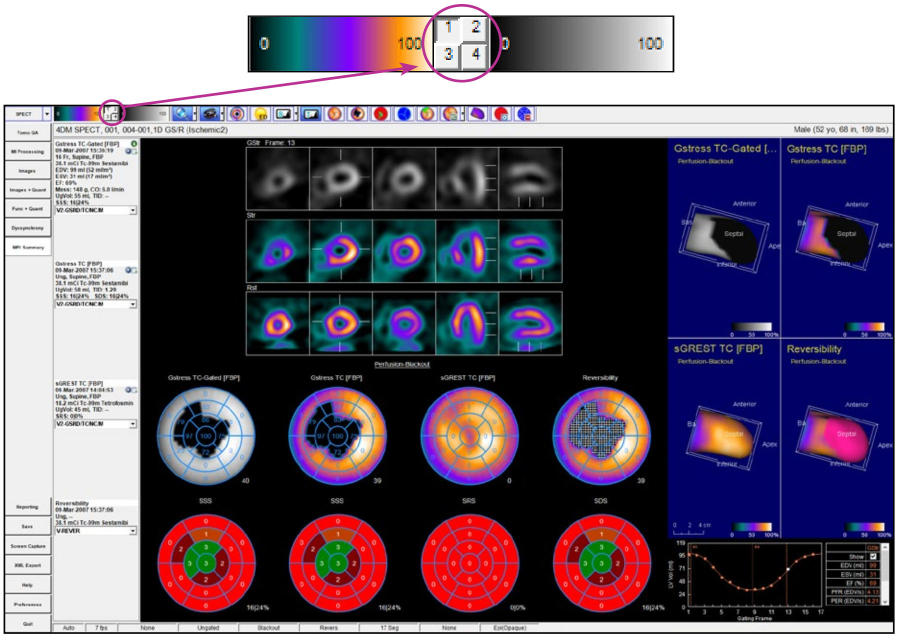


Figure 3.25: This image illustrates the dual colorbar concept — Dataset one displays the right, or secondary, colorbar set to Gray Scale; datasets two and three display the left, or primary, colorbar set to Warm Metal.

QA and Processing Screens: Objects and Controls

Corridor4DM includes screens designed specifically for cardiology quality assurance and LV quantification. Corridor4DM 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 Corridor4DM Preferences.

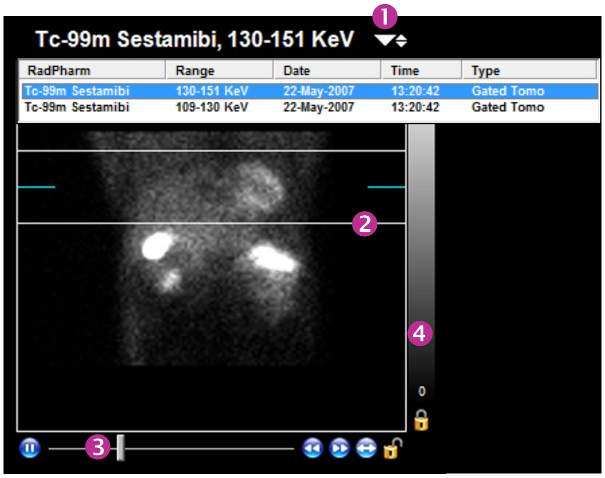
WARNING
Image data to be quantified by 4DM should be evaluated for accurate motion correction, reconstruction, and reorientation. Poorly motion corrected, reconstructed, and/or reorientated data can result in inaccurate quantification and may lead to misdiagnosis.

Tomo QA

The **Tomo Object** *(Figure 3.26)* 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 Corridor4DM 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.



Tc-99m Sestamibi, 130-151 KeV

RadPharm	Range	Date	Time	Type
Tc-99m Sestamibi	130-151 KeV	22-May-2007	13:20:42	Gated Tomo
Tc-99m Sestamibi	109-130 KeV	22-May-2007	13:20:42	Gated Tomo

Figure 3.26: 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.

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

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 3.27)* 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

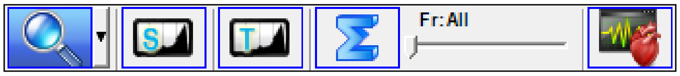


Figure 3.27: *Tools from the Toolbar for Tomo Objects*

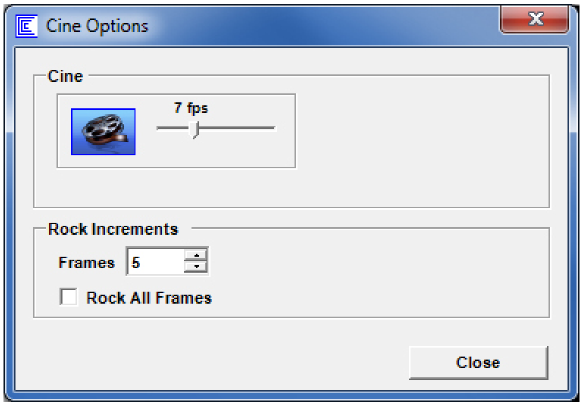
The **Beat Histogram** is only available on the **Tomo QA** screen if the camera system that the study was acquired on saves this data during the acquisition and stores it with the images to the processing workstation.

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

Preferences

Right-click the Tomo Object **Cine Tools** to open the **Cine Options** window *(Figure 3.28)* 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 (Planar MUGA):** Allows users to drop the last frame from a cine loop in cases where the heart rate is inconsistent.



7 fps

Frames 5

☐ Rock All Frames

Figure 3.28: *Tomo Right-Click Options*

MI Processing

The **MI Processing** screen *(Figure 3.29)* provides the user the ability perform quality assurance and validation of the left ventricular estimation within Corridor4DM. The user makes adjustments within the various modes of the **MI Processing** screen to fine tune left ventricular orientation, centering, and extent of calculated volumetric surfaces when necessary.

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

There are three screen modes within MI Processing:

- **QA** *(default display mode)* - 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 can be performed here if needed, and the adjustments immediately update the displayed perfusion and function quantitative values.

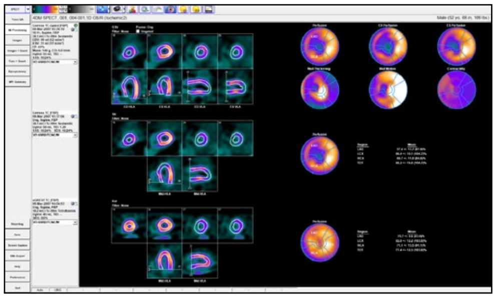


Figure 3.29: *MI Processing Screen*

- **Manual Processing** - If the surfaces are in error due to poor orientation or centering of the left ventricle, high intensity extra-cardiac activity, or if the dataset requires additional filtering, the study should be reprocessed by clicking the **Manual Processing** tool *(Figure 3.30)*.

Figure 3.30: *Manual Processing tool*

- **Reset** - If the dataset needs to be processed without any initial estimates from Corridor4DM, click the **Reset** tool *(Figure 3.31)* from within the Manual Processing mode and set the center, orientation, and valve plane location. Click the Process button to apply your changes and view the new results.

Figure 3.31: *Reset tool*

Object Tools

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

- **Processed Splash Object** *(Figure 3.32)*: Displays reconstructed data on SA, HLA, and VLA formats with and without surface contours.

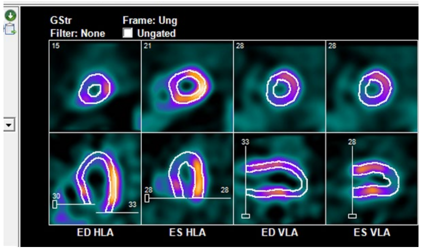


Figure 3.32: *:Processed Splash Object*

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 3.33)*: 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

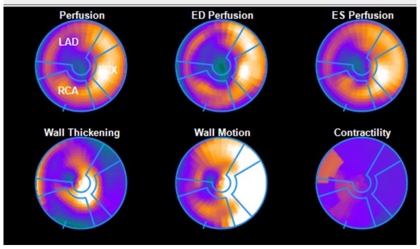
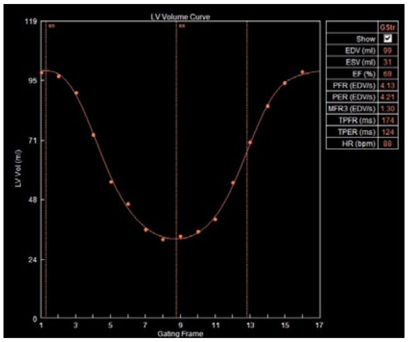


Figure 3.33: *Processed Map*

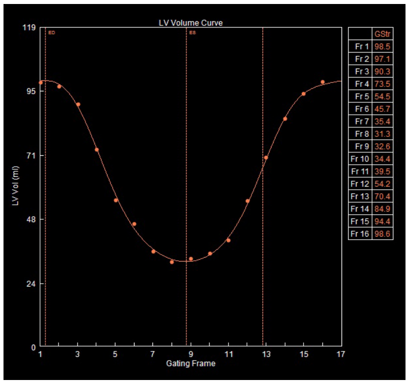
- **Volume Curve** *(Figure 3.34)*: This object is only available with gated datasets. If a gated study is loaded with two or three other datasets, click the Volume Curve tool to display the object.



	GStr
Show	☑
EDV (ml)	99
ESV (ml)	31
EF (%)	69
PFR (EDV/s)	4.13
PER (EDV/s)	4.21
MFR3 (EDV/s)	1.30
TPFR (ms)	174
TPER (ms)	124
HR (bpm)	88

Figure 3.34: *Volume Curve default display*

- Optionally, right-click over the table of statistics for an alternative display showing volumes for each individual frame of the gate *(Figure 3.35)*.



	GStr
Fr 1	98.5
Fr 2	97.1
Fr 3	90.3
Fr 4	73.5
Fr 5	54.5
Fr 6	45.7
Fr 7	35.4
Fr 8	31.3
Fr 9	32.6
Fr 10	34.4
Fr 11	39.5
Fr 12	54.2
Fr 13	70.4
Fr 14	84.9
Fr 15	94.4
Fr 16	98.6

Figure 3.35: *Volume Curve right-click optional display.*

- Left-click and drag over the statistics table to copy using Ctrl+C and paste (using Ctrl+V) values into any format document (e.g., MS Word, Excel, plain text).

For viability studies, manual normalization is only performed on the accompanying perfusion rest dataset, not the delay dataset. The delay dataset normalization corresponds to the hottest pixel selected in the perfusion rest dataset.

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

- **Unprocessed Splash Object** *(Figure 3.36)***:** When it is necessary to reprocess data or apply constraints, Corridor4DM displays left-to-right: VLA, SA, and HLA with interactive tools to aid in reprocessing.

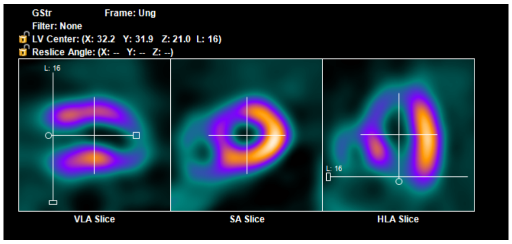

GStr Frame: Ung
Filter: None
LV Center: (X: 32.2 Y: 31.9 Z: 21.0 L: 16)
Reslice Angle: (X: -- Y: -- Z: --)

Figure 3.36: *Unprocessed Splash Object*

MI Processing - QA Toolbar

There are nine tools in the **Toolbar** for the MI Processing **QA** screen *(Figure 3.37)*:

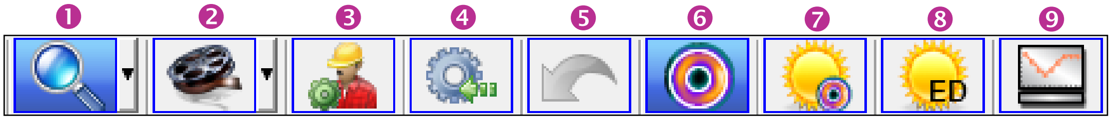


Figure 3.37: *MI Processing - QA Toolbar*

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 Corridor4DM surface generator

❹ **Reload:** Reverts to display 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 **Image Normalization:** Normalize images to the hottest pixel in the heart, the hottest pixel in the entire volume, or manually select the area used for normalization. Manually select a region on the Perfusion polar map to update the normalization

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

❾ **Volume Curve:** When active, the 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 3.38)*:

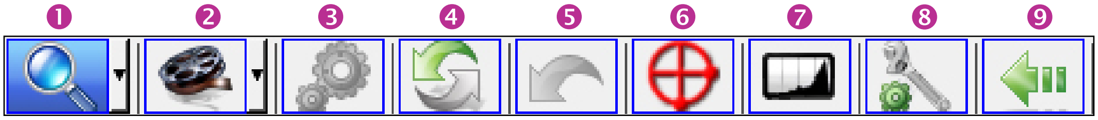


Figure 3.38: *MI Processing - Manual Processing Toolbar*

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 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

❽ **Processing Options:** Define the centering algorithm (Iterative Alignment), the Basal Plane Motion limits, and constrain axial length

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

There are also synchronization tools *(Figure 3.39)* available within the Image Display:

- **Synchronize Edits to LV Center and Limits**: Click the **LV Center** lock icon to activate and apply any left ventricular centering, basal limit, and apical limit adjustments performed on one dataset to all datasets displayed
- **Synchronize Edits to Reslice Angles**: Click the **Reslice Angle** lock icon to activate and apply any left ventricular orientation adjustments performed on one dataset to all datasets displayed

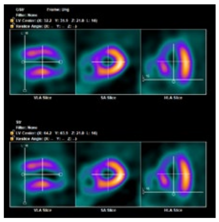


Figure 3.39: *Synchronization tools*

There are seven tools within the **Toolbar** for the MI Processing **Reset**

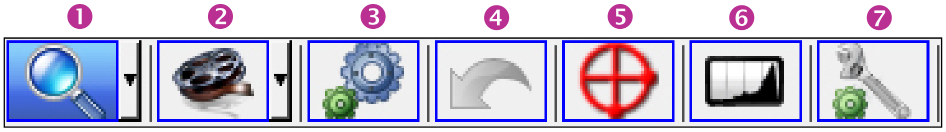


Figure 3.40: *MI Processing - Reset Toolbar*

mode ❶ *(Figure 3.40)*:

❷
- **Magnification:** Adjust the image display size

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

❹
- **Process:** Calculate dataset(s) LV surface generation

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
- **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 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

⑦ – Click the **Reset** tool to revert any changes to the default settings
– Click the **Apply** tool to save changes to the filtering options

- **Processing Options:** Define the centering algorithm (Iterative Alignment), the Basal Plane Motion limits, and constrain axial length

Review Screens: Objects and Controls

Most Corridor4DM review screens are comprised of one or more Corridor4DM Objects. Because Corridor4DM 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 Corridor4DM objects are:

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

Tomo

The **Tomo Object** *(Figure 3.41)* displays NM tomographic data for quality assurance.

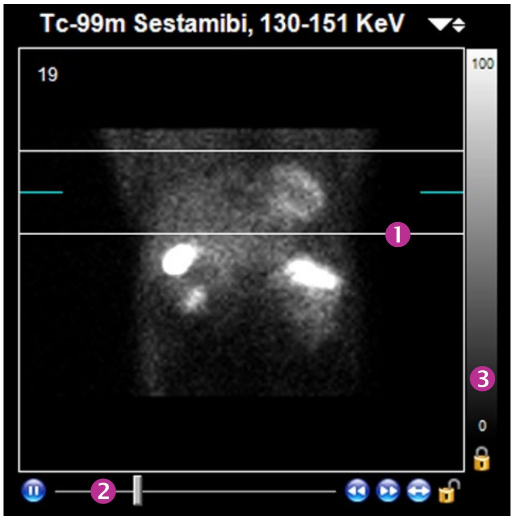


***Figure 3.41:** The Tomo Object from the Tomo QA screen*

Object Tools

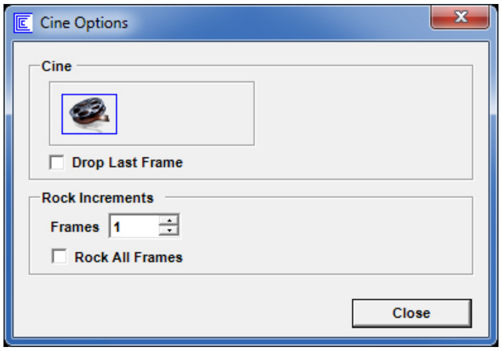
① **Slice Plane Indicator:** Use the white click-and-drag reference lines on the Tomo object to check for patient motion during acquisition. The blue reference line indicates to which pixel the image is normalized.

② **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.

③ **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 3.42)*. Changes made within this window apply only to **Tomos** on the active screen.


Cine Options

Cine

☐ Drop Last Frame

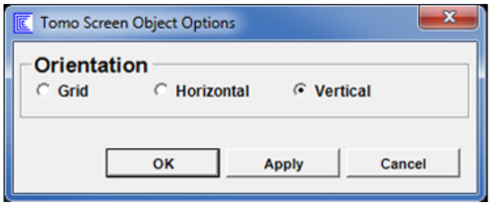
Rock Increments

Frames: 1

☐ Rock All Frames

***Figure 3.42:** Tomo Object Cine Controls right-click options*

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



Tomo Screen Object Options

Orientation

○ Grid ○ Horizontal ● Vertical

Figure 3.43: *Tomo Object right-click options*

- **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 3.43)*.
- **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

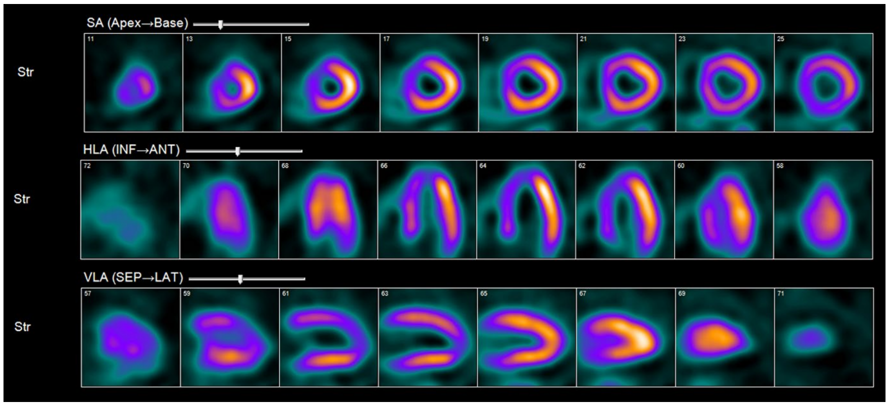


Figure 3.44: *From Top-to-Bottom-SA, HLA, and VLA Splash Objects*

Splash

A **Splash Object** *(Figure 3.44)* displays slice orientations as SA, HLA, and VLA. These images are used to observe tracer uptake within the myocardium.

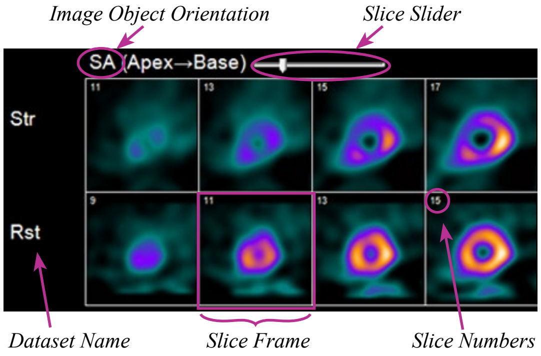


Figure 3.45: *SA Splash Object slices*

Object Tools

For the **Splash Object**, *(Figure 3.45)* 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.
- **Individually**: Click-and-drag any slice frame to the right or left to change the starting slice in the splash display for that dataset.

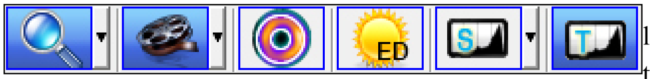


Figure 3.46: *Toolbar for Splash Object*

Toolbar

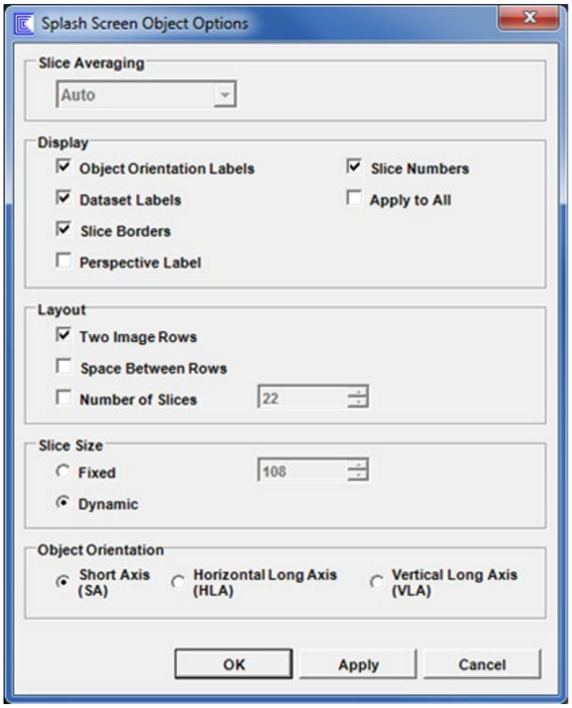
There are six tools *(Figure 3.46)* in the Toolbar with functionality applicable to the Splash Object:

- Magnification
- Cine
- Contours
- ED Frame Normalization
- Spatial Averaging (Reference the Spatial Averaging section in Preferences for filter options)
- Temporal Filter

Preferences

Right-click any **Splash Object** to open the **Splash Object Options** window *(Figure 3.47)*. 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).


Splash Screen Object Options

Slice Averaging
Auto

Display
☑ Object Orientation Labels
☑ Slice Numbers
☑ Dataset Labels
☐ Apply to All
☑ Slice Borders
☐ Perspective Label

Layout
☑ Two Image Rows
☐ Space Between Rows
☐ Number of Slices 22

Slice Size
○ Fixed 108
● Dynamic

Object Orientation
● Short Axis (SA)
○ Horizontal Long Axis (HLA)
○ Vertical Long Axis (VLA)

Figure 3.47: *Splash Object right-click options*

- **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.
- **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 3.48)* 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.

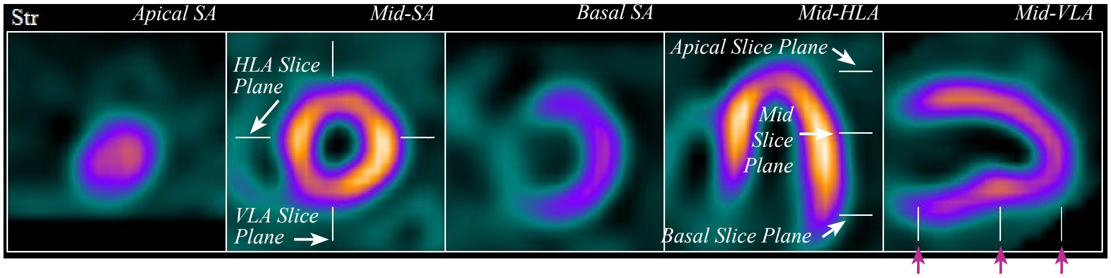


Figure 3.48: *A diagrammed example of the 3SA Object*

Object Tools

Adjust the SA, VLA, and HLA slices by clicking-and-dragging the slice planes (white lines) to the desired location. The image display

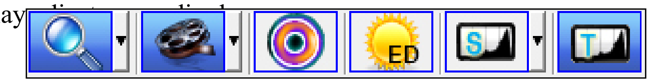


Figure 3.49: *Toolbar for 3SA Object*

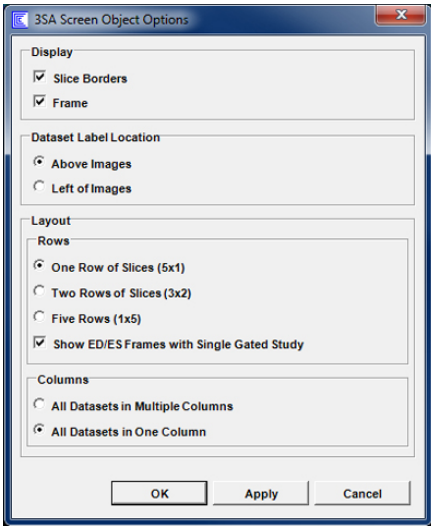
Toolbar

There are six tools *(Figure 3.49)* in the Toolbar with functionality applicable to the 3SA Object:

- Magnification
- Cine
- Contours
- ED Frame Normalization
- Spatial Averaging (Reference the Spatial Averaging section in Preferences for filter options)
- Temporal Filter

Preferences

Right-click the 3SA Object to open the **3SA Object Options** window *(Figure 3.50)*. 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
☑ Slice Borders
☑ Frame

Dataset Label Location
● Above Images
○ Left of Images

Layout
Rows
● One Row of Slices (5x1)
○ Two Rows of Slices (3x2)
○ Five Rows (1x5)
☑ Show ED/ES Frames with Single Gated Study

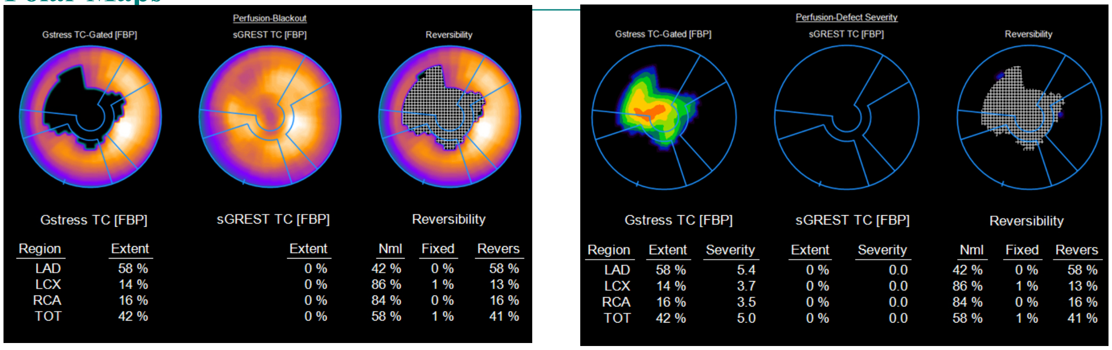
Columns
○ All Datasets in Multiple Columns
● All Datasets in One Column

Figure 3.50: *3SA Object right-click options*

- **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.

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.

Polar Maps



	Gstress TC [FBP]	sGREST TC [FBP]	Reversibility		
Region	Extent	Extent	Nml	Fixed	Revers
LAD	58 %	0 %	42 %	0 %	58 %
LCX	14 %	0 %	86 %	1 %	13 %
RCA	16 %	0 %	84 %	0 %	16 %
TOT	42 %	0 %	58 %	1 %	41 %

	Gstress TC [FBP]		sGREST TC [FBP]		Reversibility		
Region	Extent	Severity	Extent	Severity	Nml	Fixed	Revers
LAD	58 %	5.4	0 %	0.0	42 %	0 %	58 %
LCX	14 %	3.7	0 %	0.0	86 %	1 %	13 %
RCA	16 %	3.5	0 %	0.0	84 %	0 %	16 %
TOT	42 %	5.0	0 %	0.0	58 %	1 %	41 %

Figure 3.51: *(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.*

The **Polar Map Object** *(Figure 3.51)* 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**:

- **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
  - **Flow:** Displays RAW myocardial blood flow in the unit of ml/min/g.
  - **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.

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.

- **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.
  - **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.
  - **Reserve:** The comparison of stress flow to rest flow.

- **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 (Corridor4DM 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:** Corridor4DM 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 (Corridor4DM default)
  - **Extracted CTA**: Fuses extracted coronary vessels from CTA studies. CTA overlays appear red *(Figure 3.52)*.

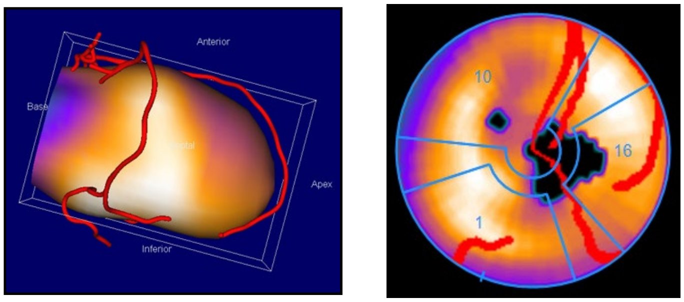


Figure 3.52: *CTA Coronary Vessel Fusion on 3D and 2D polar maps.*

  - **Calcium**: Fuses Corridor4DM-quantified calcium deposit overlays. Calcium overlays appear neon green *(Figure 3.53)*.

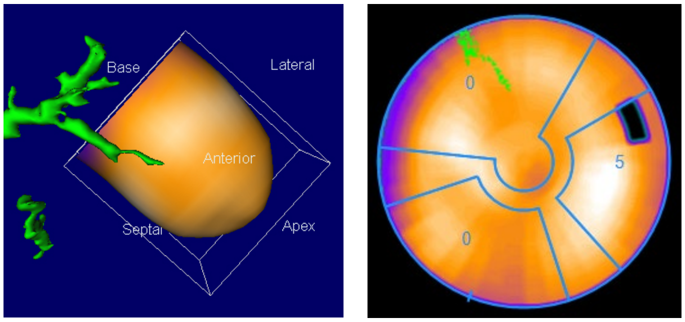


Figure 3.53: *Calcium overlay on 3D and 2D polar maps*

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.

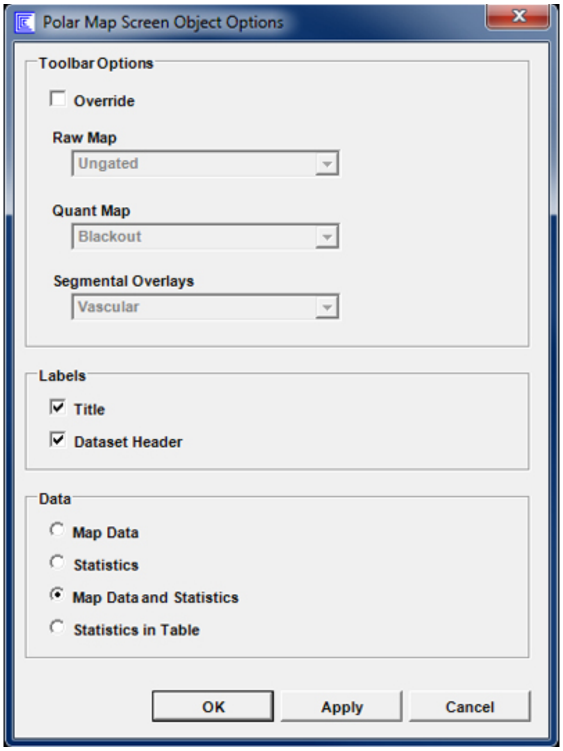
To activate the **CTA Overlay** option, 4DM has integrated a QA measure which requires users to check the co-registration of the NM dataset(s) to the CTA on the **Fusion** screen.

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 Corridor4DM-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 3.54)*. Changes made using this right-click method apply only to **Polar Map Objects** on the active screen.



Polar Map Screen Object Options

Toolbar Options

☐ Override

Raw Map: Ungated

Quant Map: Blackout

Segmental Overlays: Vascular

Labels

☑ Title

☑ Dataset Header

Data

○ Map Data

○ Statistics

● Map Data and Statistics

○ Statistics in Table

Figure 3.54: *Polar Map Object Options*

- **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 3.55)*.

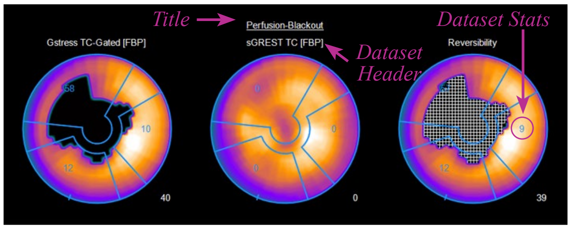
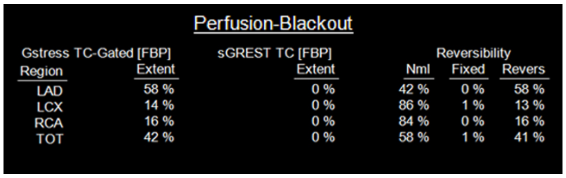


Figure 3.55: *Polar Map Object*

  - – **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.



Perfusion-Blackout

Gstress TC-Gated [FBP]		sGREST TC [FBP]	Reversibility		
Region	Extent	Extent	Nml	Fixed	Revers
LAD	58 %	0 %	42 %	0 %	58 %
LCX	14 %	0 %	86 %	1 %	13 %
RCA	16 %	0 %	84 %	0 %	16 %
TOT	42 %	0 %	58 %	1 %	41 %

Figure 3.56: *Polar Map Statistics in Table Format*

- **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

SSS=Summed Stress Score

SRS=Summed Rest Score

SDS=Summed Difference Score

the polar map overlay.

- **Statistics in Table:** Displays the quantitative data numerically in a table *(Figure 3.56)*.

Scores

The **Scores Object** *(Figure 3.57)* 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**.

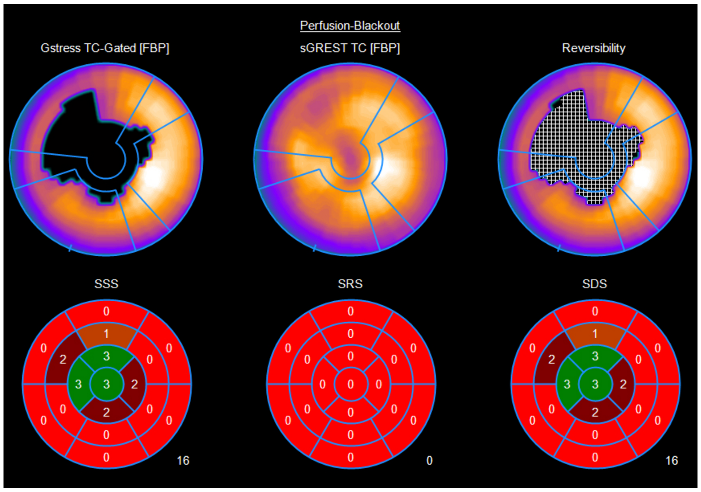


Figure 3.57: *Polar Map Objects (top) and Scores Objects (bottom)*

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

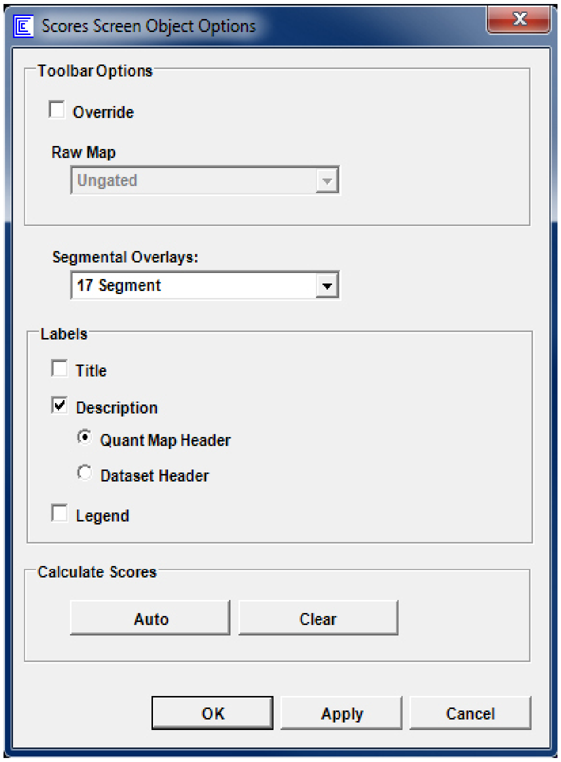
Figure 3.58: *Scores Object Defect Ratings*

Object Tools

The Corridor4DM **Scores Object** automatically displays quantified score results. The scores generated are on a numbered 0-4 scale with Corridor4DM defect ratings *(Figure 3.58)*. To manually change the scores,

- **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 Corridor4DM 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.


Scores Screen Object Options

Toolbar Options

☐ Override

Raw Map: Ungated

Segmental Overlays: 17 Segment

Labels

☐ Title

☑ Description

● Quant Map Header

○ Dataset Header

☐ Legend

Calculate Scores

Figure 3.59: *Scores Object Options*

Toolbar

- **Auto**: Click the **Auto** tool located in the **Toolbar** to display the Corridor4DM-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 3.59)*. Changes made to Auto, Clear, or the Segmental Overlay apply to all Scores objects across *all* screens.

- **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 3.60)*. The 3D object appears on a dark blue background.

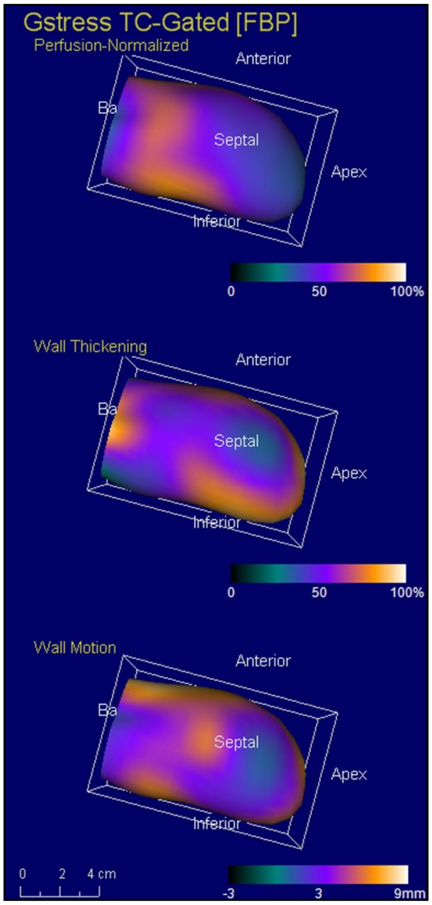


Figure 3.60: *An example of the 3D Object with the Raw Map menu set to G-All*

When viewing ungated datasets in the **3D Object**, the only available option within the **Raw Map** Menu is **Ungated.**

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.
  - **Flow:** Displays RAW myocardial blood flow in the unit of ml/min/g.
  - **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

- **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.

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.

- **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.
  - **Reserve:** Derived from stress and rest flow maps, also known as ratio maps.

- **Fusion Overlay**: If extracted coronary vessels from a CTA study or Calcium Scoring CT are launched in Corridor4DM, this option is used to overlay the reconstructed, extracted vessels or the Corridor4DM-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.

Preferences

Right-click a 3D Object to open the **3D Object Options** window *(Figure 3.61)*. Changes made using this right-click method apply only to 3D Objects on the active screen.

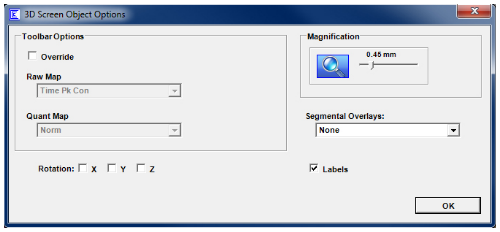

3D Screen Object Options
Toolbar Options
☐ Override
Raw Map: Time Pk Con
Quant Map: Norm
Magnification: 0.45 mm
Segmental Overlays: None
Rotation: ☐ X ☐ Y ☐ Z
☑ Labels

Figure 3.61: *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.

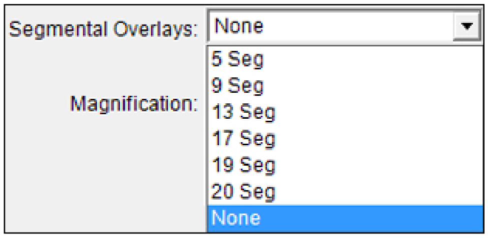

Segmental Overlays: None

Figure 3.62: *3D Segmental Overlay Menu*

- **Segmental Overlays:** This drop-down menu *(Figure 3.62)* 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**

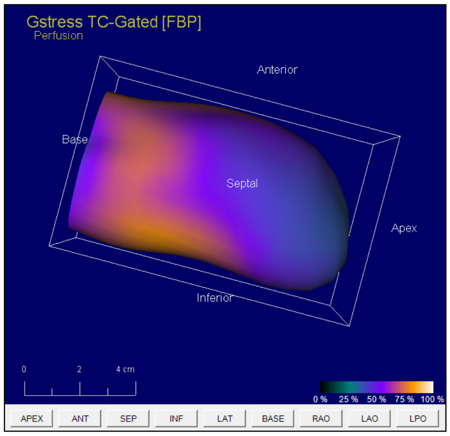
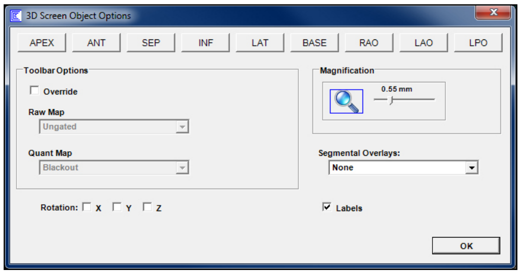


Figure 3.63: *3D Object including Perspective buttons along the bottom of the 3D image*

- **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 Screen Object Options

Toolbar Options
☐ Override
Raw Map: Ungated
Quant Map: Blackout
Magnification: 0.55 mm
Segmental Overlays: None
Rotation: ☐ X ☐ Y ☐ Z
☑ Labels

Figure 3.64: *Right-click 3D Object Options with Perspective buttons*

- **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 3.63)*. However, the perspective buttons on the **MPI Summary** screen and **User Defined** screens are available in the **3D Object Options** right-click window *(Figure 3.64)*.

To display the diastolic functional parameters in the **Volume Curve**, select the **Compute Diastolic Function Parameters** check box located within the **Preferences** menu on the **Algorithms** Page.

Volume Curve

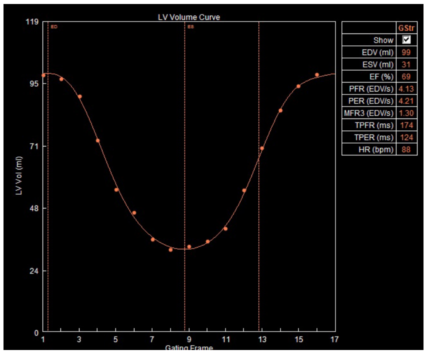


Figure 3.65: *The Volume Curve default display*

The **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 3.65)*. The information displayed within the object is summarized below:

- **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 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.

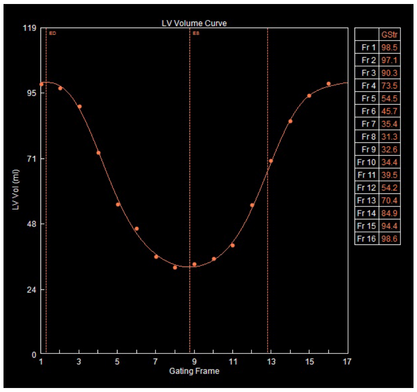


Figure 3.66: *Volume Curve right-click optional display*

Object Tools

Right-click over the LV statistics table to display the LV volume for each gated frame *(Figure 3.66)*. Right-click again to return to the default display.

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 3.67)* in the Toolbar with functionality applicable to the Volume Curve Object is **Cine**.

Figure 3.67: *The Cine tool for Volume Objects*

PDF Viewer Screen

For purposes of reviewing EKG Summary reports, patient history forms, and technologist acquisition protocol information from the camera systems, Corridor4DM provides a PDF Viewer screen. This screen displays DICOM format encapsulated PDF files. Please check with your camera and EKG vendors for compatibility with Corridor4DM's PDF Viewer *(Figure 3.68)*.

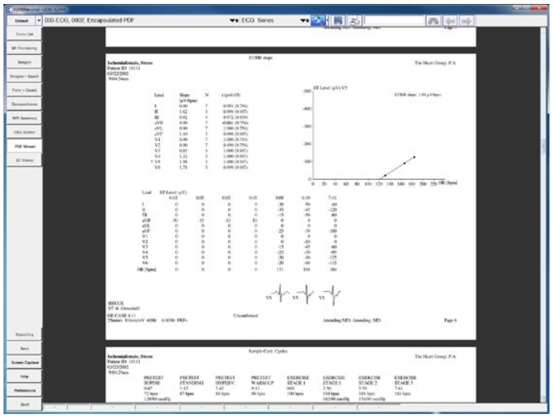


Figure 3.68: *PDF Viewer, showing a DICOM-encapsulated PDF Lead Summary from an EKG machine*

By default, the PDF Viewer screen is not in the active workflow list.

To activate the PDF Viewer screen, perform the following:

1. Click **Preferences**.
2. Within Screen Layout, locate **Inactive Screens**.
3. Scroll through the list of Inactive Screens, and click **PDF Viewer**.
4. Click **Activate**.
5. Click **Save**.

For more information on how to Move Up/Move Down screens refer to Chapter 12 Preferences: Screen Setup.

There are six tools available in the PDF Viewer screen *(Figure 3.69)*:

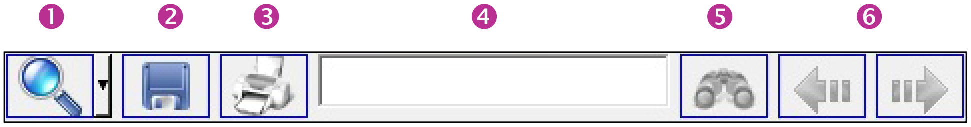


Figure 3.69: *PDF Viewer Toolbar*

Standard non-DICOM format PDF files are not supported for display within 4DM.

❶ **Magnification Tool**: Adjusts the PDF size. Click the arrow next to the icon to use the slider for custom zooms.

❷ **Save Tool**: Saves the document in standard .pdf format and permits saving it to a local or networked user-defined directory. The default save location is C:\Users\Public\Documents\INVIA\4DMExport\snapshots\Patient Name-Corridor4DM-PDFViewer.pdf.

❸ **Print Tool**: Define print settings and print the PDF to a networked or local printer.

❹ **Find/Search Text Box**: Type in key words to define a specific search, up to 32 characters, then click the Search Tool. Found results will be highlighted in yellow within the PDF.

❺ **Search Tool**: Once text is entered in the Find/Search Text Box, this button becomes active. Select it to initiate a search based on the text entered. When a match is found, the text is highlighted in yellow in the PDF.

❻ **Find Previous/Find Next Tools**: The left and right arrow keys become active when a search and a matched result is found. Use these to go forward (right arrow) or backward (left arrow) to the matched words in the PDF document.

SC Viewer Screen

The **SC Viewer** *(Figure 3.70)* 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 Corridor4DM-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 Corridor4DM, see Capturing Corridor4DM Results.

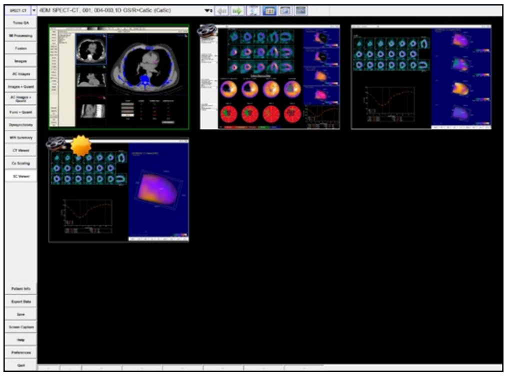


Figure 3.70: *SC Viewer Toolbar*

Second, the SC Viewer can supplement the clinical workflow by enabling review of DICOM static and multi-frame screen captures generated outside of Corridor4DM. 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 3.71)* on the SC Viewer screen:

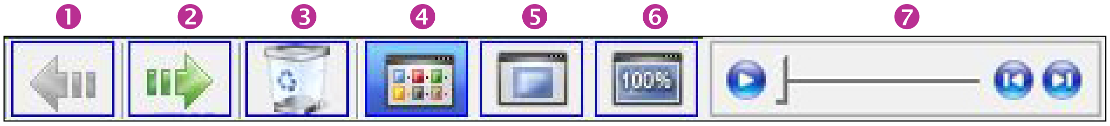


Figure 3.71: *SC Viewer screen*

❶ **Return:** When a screen capture is selected this will move the selection to the previous screen capture in the list.

❷ **Next:** When a screen capture is selected this will move the selection to the next screen capture in the list.

❸ **Delete Tool:** Allows deletion of any Corridor4DM screen captures generated within the current session. Screen captures sent from other workstations, or from previous sessions, cannot be deleted using this button.

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

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

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

❼ **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

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.

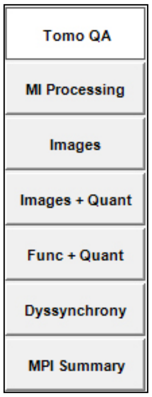
These seven objects are used within standard Corridor4DM screens and templates; or can be mix-and-matched to create custom, user-defined screens. The Corridor4DM standard screens are consistent with common clinical workflows — specifically perfusion review; perfusion and quantification review; and function review. For each of these clinical workflows, a screen template exists which users can import when building custom screens. Refer to the table on the next page to review Corridor4DM-provided templates and the objects utilized within them:

Corridor4DM Template	**Corridor4DM Object**						
	Tomo	**Splash**	**3SA**	**Polar Map**	**Scores**	**3Ds**	**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

CHAPTER 4 SPECT CARDIAC IMAGING

The SPECT cardiac imaging workflow uses these screens:



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 Corridor4DM Clinical Workflow Tutorial for the image review, quantification, and interpretation of SPECT Myocardial Perfusion Imaging (MPI).

Quality Assurance

Users should always ascertain the integrity of the study that has been provided for review prior to the interpretation process. Corridor4DM 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

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

Tomo QA

The **Tomo QA** screen *(Figure 4.1)* 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:

4DM SPECT, 001, 004-001,1D GS/R (Ischemic2)

Male (52 yo, 68 in, 169 lbs)

Gstress TC-Gated [Prim...
09-Mar-2007 15:36:19
16 Fr, Supine
Tc-99m Sestamibi
Camera: Symbia T2
Camera Heads: 2
HR (bpm): 92.4
Acc Beats: 37.0 (100%)
Rej Beats: 0.0
R-R: 35% @ 659

Gstress TC [Primary 1]
09-Mar-2007 15:37:06
Ung, Supine
Tc-99m Sestamibi
Camera: Symbia T2
Camera Heads: 2

sGREST TC [Primary 1]
09-Mar-2007 14:04:53
Ung, Supine
Tc-99m Tetrofosmin
Camera: Symbia T2
Camera Heads: 2

Figure 4.1: *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 plane slicer that allows you to normalize the image to the counts in the heart by aligning it with the hottest pixel in the heart. The plane slicer also defines the plane for constructing the **Sinogram**. The white click-and-drag reference lines above and below the blue plane slicer 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 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.

- **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.

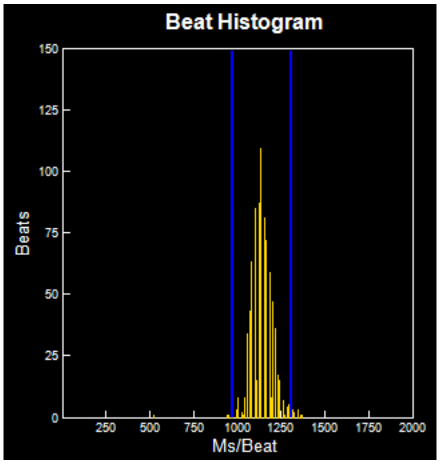
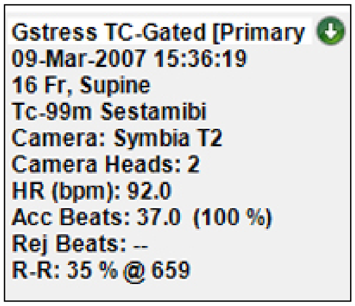


Figure 4.2: *The Beat Histogram on the Tomo QA screen.*

- **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 [Primary
09-Mar-2007 15:36:19
16 Fr, Supine
Tc-99m Sestamibi
Camera: Symbia T2
Camera Heads: 2
HR (bpm): 92.0
Acc Beats: 37.0 (100 %)
Rej Beats: --
R-R: 35 % @ 659

Figure 4.3: *The Gating Information in the Dataset Information Panel*

- **Gating Information** (for gated datasets only)
  - The **Gating Information** *(Figure 4.3)* 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).

- **Multiple Energy Windows (for multiple energy radiopharmaceuticals only)**
  - The Multiple Energy Window is active above the image viewport when datasets are launched into Corridor4DM 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.

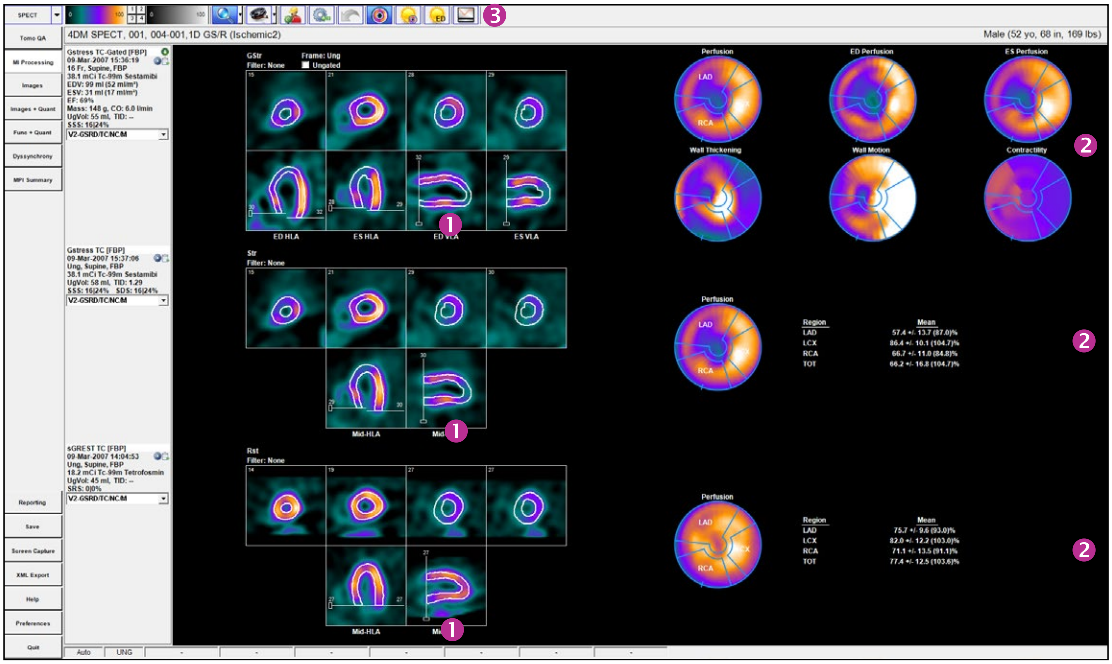
Once you have reviewed and noted any anomalies on the **Tomo QA** screen, proceed to the next QA step in our sample workflow, the **MI Processing** screen.

MI Processing

Upon launching a patient in Corridor4DM for the first time, the program automatically quantifies the study using Corridor4DM default algorithm settings. The **MI Processing** screen *(Figure 4.4)* 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.

The user should confirm that the basal limits are consistent between datasets and that the Corridor4DM LV surface generation algorithm has accurately identified the endo- and epicardial surfaces of the LV. These contours are used to calculate the following parameters:

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



4DM SPECT, 001, 004-001,1D GS/R (Ischemic2)

Male (52 yo, 68 in, 169 lbs)

Gstress TC-Gated [FBP]
09-Mar-2007 15:36:19
16 Fr, Supine, FBP
38.1 mCi Tc-99m Sestamibi
EDV: 99 ml (52 ml/m²)
ESV: 31 ml (17 ml/m²)
EF: 69%
Mass: 148 g, CO: 6.0 l/min
UgVol: 55 ml, TID: --
SSS: 16|24%
V2-GSRD/TC/NC/M

Gstress TC [FBP]
09-Mar-2007 15:37:06
Ung, Supine, FBP
38.1 mCi Tc-99m Sestamibi
UgVol: 58 ml, TID: 1.29
SSS: 16|24% SDS: 16|24%
V2-GSRD/TC/NC/M

Region	Mean
LAD	57.4 +/- 13.7 (87.0)%
LCX	86.4 +/- 10.1 (104.7)%
RCA	66.7 +/- 11.0 (84.8)%
TOT	66.2 +/- 16.8 (104.7)%

sGREST TC [FBP]
09-Mar-2007 14:04:53
Ung, Supine, FBP
18.2 mCi Tc-99m Tetrofosmin
UgVol: 45 ml, TID: --
SRS: 0|0%
V2-GSRD/TC/NC/M

Region	Mean
LAD	75.7 +/- 9.6 (93.0)%
LCX	82.0 +/- 12.2 (103.0)%
RCA	71.1 +/- 13.5 (91.1)%
TOT	77.4 +/- 12.5 (103.6)%

Figure 4.4: *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.*

WARNING
The user should visually verify the processing limits-

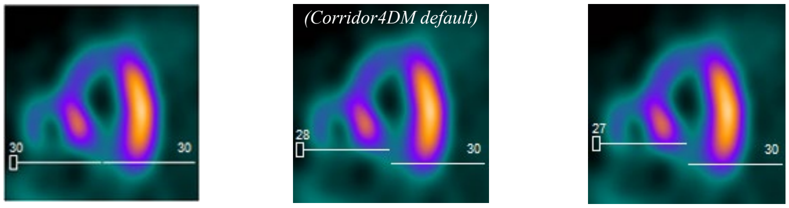
- Heart Centering
- Basal and Apical Limits
- Volume Orientations

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

Note that Corridor4DM 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)*.

If the cardiac 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.



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

Figure 4.5: *The three Corridor4DM basal limit Preference settings for determining the basal limit for perfusion maps.*

The default algorithm is the Septal Wall Mid-Membranous Septum.

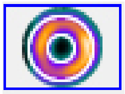


Figure 4.6: *The Contours tool*

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.

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.

Figure 4.7: *Manual Processing 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)*.

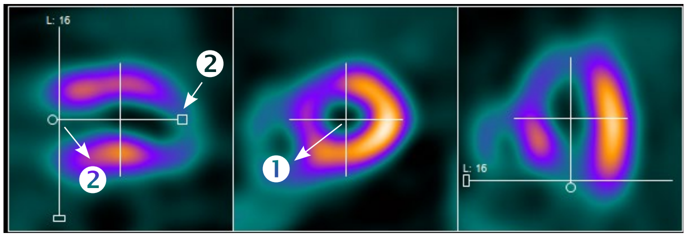
❶	Proper positioning of the LV center aligns the crosshairs in the center of the ventricle.	
❷	Proper positioning of the apical and basal limits are at the center of the apical myocardium and the mitral valve plane.	

Figure 4.8: *Examples of proper positioning on the MI Processing - Manual Processing screen*

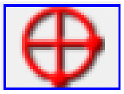


Figure 4.9: *Constraints tool*

If the dataset has significant 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 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.

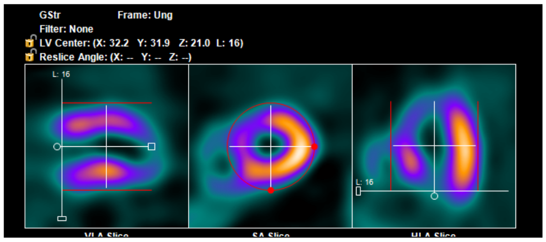

GStr Frame: Ung
Filter: None
LV Center: (X: 32.2 Y: 31.9 Z: 21.0 L: 16)
Reslice Angle: (X: -- Y: -- Z: --)

Figure 4.10: *Constraints activated and properly positioned*

If the dataset needs to be processed from scratch (i.e. no initial estimates from Corridor4DM), click the Reset tool *(Figure 4.12)* and then set the center,

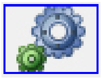


Figure 4.11: *Process tool*

Figure 4.12: *Reset tool*

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 complete.

LV Surface Editor

Corridor4DM includes the **LV Surface Editor Tool**, for use in rare cases where standard automated and manual processing does not output optimal LV surfaces. Clinical cases this can occur on are: large fixed defects where an entire wall has little to no uptake; or extreme extra-cardiac activity that isn't corrected with use of the Constraints Tool. Follow the steps below to estimate and display location of the left wall when faced with such patient studies.

Access the **LV Surface Editor Tool** on the **MI Processing** screen while in **QA Mode** where the white LV surface contours are shown.

1. Right-click directly on the slices of the dataset to correct. Select the **LV: Edit Surfaces** option from the menu *(Figure 4.13)*.
2. A new **Edit Surfaces** window appears, which provides eight slice viewports: Four short axis (SA) in the top row; and four horizontal long axis (HLA) in the bottom row *(Figure 4.14)*.
3. Corrections can be applied in both the short and long axis plane views, except for the upper-leftmost SA slice, which is designated as the control, or starting point, for the algorithm.

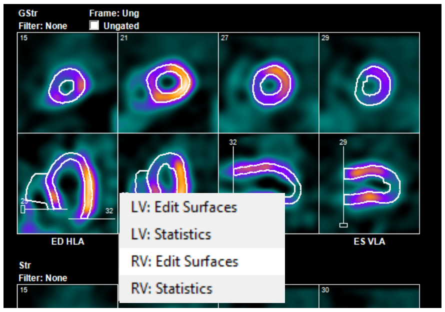


Figure 4.13: *MI Processing in QA Mode, showing a study with bad contours in an area of almost no myocardial uptake.*

4. Left click inside a viewport. Based on the proximity of the mouse cursor to the red midline points, the cursor will show as a small, medium or large-sized blue circular nudge tool. When the cursor is close to the red midline, the circular nudge tool is small. When further away, the circular nudge tool is larger *(Figure 4.15)*.

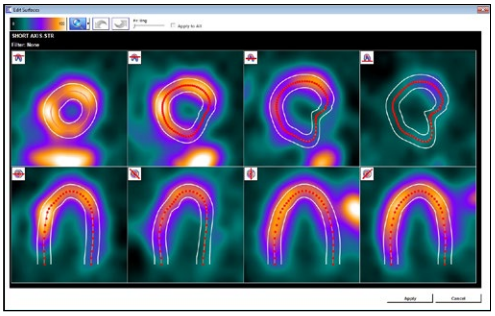


Figure 4.14: *Edit Surface window showing a study before corrections*

5. Left-click and drag with the nudge tool near the red midline will adjust it based on how the mouse is moved. Once the mouse is released, the new white epi- and endocardial contours will appear for evaluation.
6. Plane slicers can be overlaid to help guide corrections by clicking on the small icons in the upper-left corner of each viewport *(Figure 4.16)*.
    - Click the SA plane slicer toggle to show the line of reference on the long axis views.

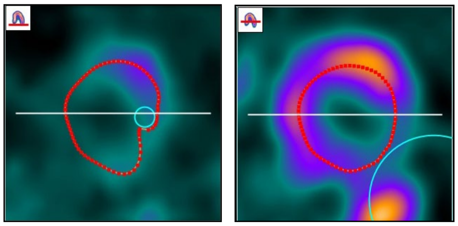


Figure 4.15: *(Left image) Click close to the red midline points to use the small nudge tool. (Right image) Click further away from the red midline to use the large nudge tool.*

  - Click the LA plane slicer toggle to show the line of reference on the short axis views.
  - Oblique plane slicer toggles are also available.

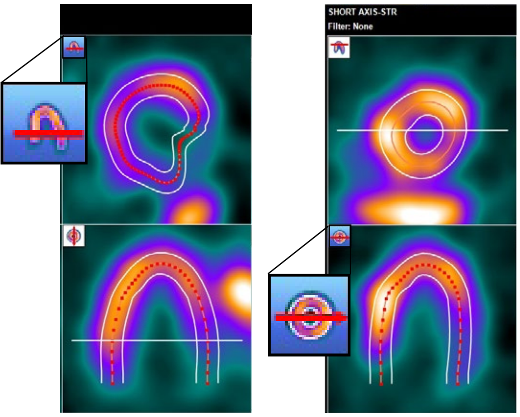


Figure 4.16: *(Left image) – Click the SA plane slicer to show the SA line of reference on the LA view below it. (Right image) – Click the LA plane slicer to show the LA line of reference on the SA image above it.*

The toolbar provides five tools to assist the user while making surface corrections *(Figure 4.17)*:

- **Colorbar**: Click and drag the sliders at 0 and 100 to adjust the brightness and contrast. Right-click on the colorbar to view and select from the color schemes available.
- **Magnification Tool**: Click the arrow next to the icon to use the slider to adjust the slice size.
- **Undo/Redo Tools**: Click the left-arrow to undo the last moves. Click the right-arrow to redo the last move.
- **Gated Frame Slider Tool**: **Only available for gated datasets.** When the slider is all the way to the left, all gated frames are summed and the summed image is shown as "Ung." Click and drag the slider to review individual frames of the gate.
- **Apply to All**: **Only available for gated datasets.** When selected, applies the corrections made across all gated frames.

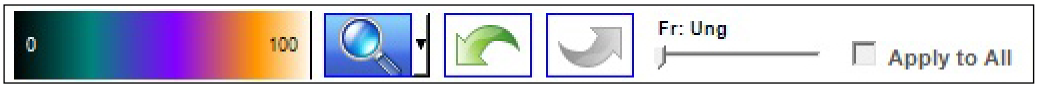


Figure 4.17: *LV Surface Editor Toolbar*

When all corrections are complete, click the **Apply** button in the Edit Surfaces window to apply the changes and review the corrected contours on the MI Processing screen in QA Mode. Or, click the **Cancel** button to discard any changes made and revert to the original surfaces *(Figure 4.18)*.

If corrections are made, be sure to click **Save** within the Corridor4DM Control Panel so that all new surfaces are saved for subsequent reviews of the patient study.

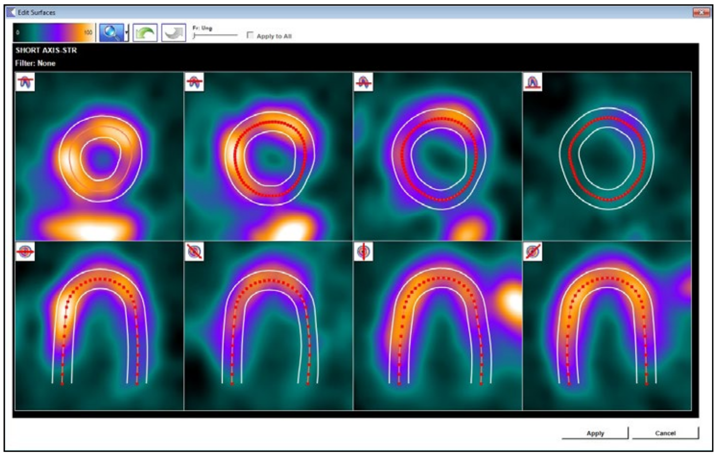


Figure 4.18: *Contours after corrections are made. Click the Apply button to apply the new surfaces to the dataset.*

Qualitative Perfusion Review

Qualitative Perfusion Review

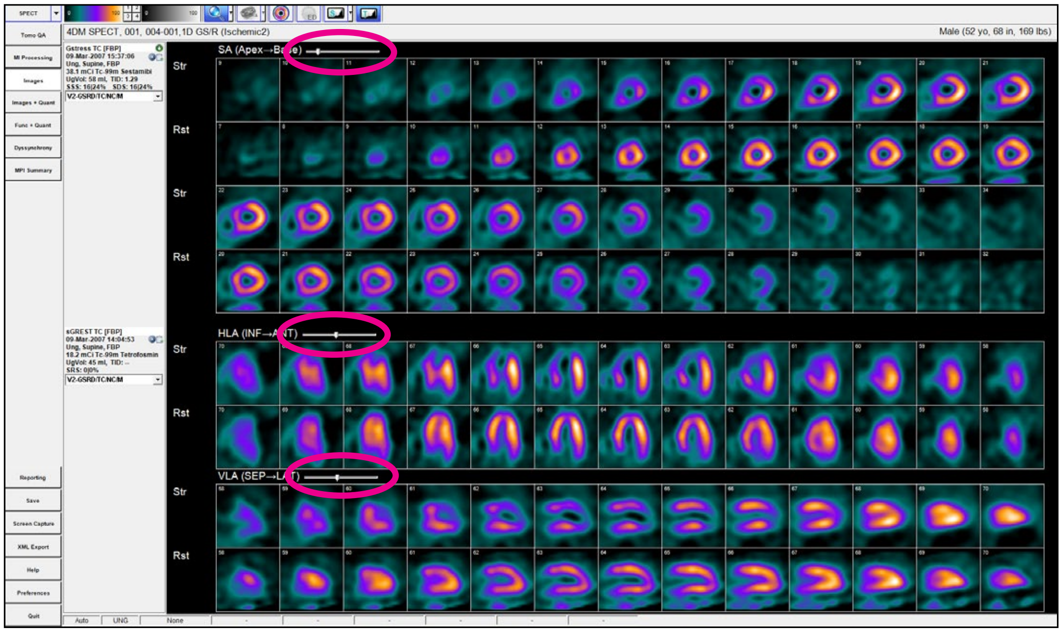
The next step in our SPECT MPI workflow is to begin the image interpretation process. Perfusion abnormalities can be visually assessed by a review of the perfusion images for areas of pronounced decreased tracer uptake. Identification of differences in the myocardial tracer intensity between the stress 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, The **Splash Objects** consist of viewing the reconstructed datasets in a slice-by-slice format in the following order: SA (Apex->Base), HLA (Inf->Ant), and VLA (Sep->Lat). This layout is also commonly referred to as a **Splash** display.

aligned one over the other, in the three cardiac planes: SA, HLA and VLA. In Corridor4DM this layout is referred to as a **Splash** display. The Corridor4DM **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 4.19)*. 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 Corridor4DM 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**.


4DM SPECT, 001, 004-001,1D GS/R (Ischemic2)

Male (52 yo, 68 in, 169 lbs)

Gstress TC [FBP]
09-Mar-2007 15:37:06
Ung, Supine, FBP
38.1 mCi Tc-99m Sestamibi
UgVol: 58 ml, TID: 1.29
SSS: 16|24% SDS: 16|24%
V2-GSRD/TC/NC/M

sGREST TC [FBP]
09-Mar-2007 14:04:53
Ung, Supine, FBP
18.2 mCi Tc-99m Tetrofosmin
UgVol: 45 ml, TID: --
SRS: 0|0%
V2-GSRD/TC/NC/M

Figure 4.19: *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.*

Quantitative Perfusion Review

Quantitative Perfusion Review

In addition to the qualitative perfusion assessment, Corridor4DM recommends utilizing the quantification data available to supplement visual perfusion findings. To quantify the perfusion information, Corridor4DM 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 Corridor4DM 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 Corridor4DM displays both the perfusion **3SA Object** and the supporting quantification information. Corridor4DM recommends using this screen during quantitative perfusion review of SPECT MPI cases.

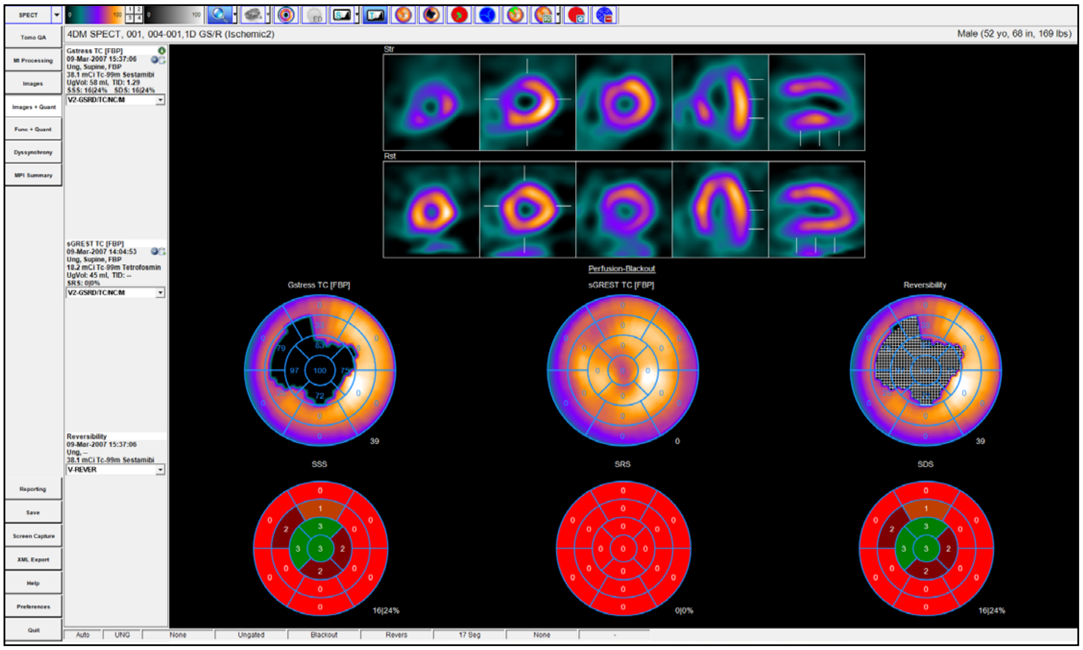
WARNING
The user must verify that the Normals Database is compatible with the dataset being reviewed to ensure correct computation of quantitative data.

Most 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.

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 4.20)*. Corridor4DM 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.

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.



4DM SPECT, 001, 004-001,1D GS/R (Ischemic2)

Male (52 yo, 68 in, 169 lbs)

Gstress TC [FBP]
09-Mar-2007 15:37:06
Ung, Supine, FBP
38.1 mCi Tc-99m Sestamibi
UgVol: 58 ml, TID: 1.29
SSS: 16|24% SDS: 16|24%
V2-GSRD/TC/NC/M

sGREST TC [FBP]
09-Mar-2007 14:04:53
Ung, Supine, FBP
18.2 mCi Tc-99m Tetrofosmin
UgVol: 45 ml, TID: --
SRS: 0|0%
V2-GSRD/TC/NC/M

Reversibility
09-Mar-2007 15:37:06
Ung, --
38.1 mCi Tc-99m Sestamibi
V-REVER

Figure 4.20: *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 4.21)*.

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

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.

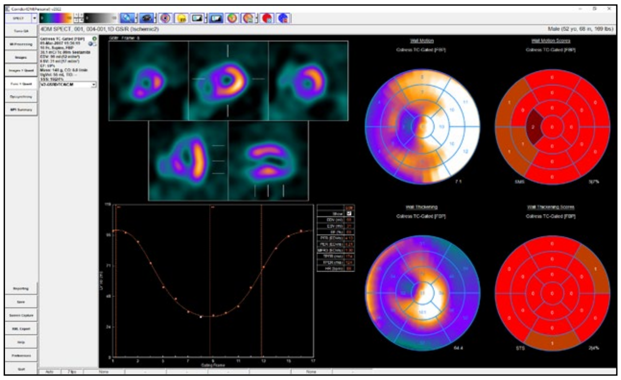


Figure 4.21: *The Func+Quant screen with one gated dataset displayed.*

Dyssynchrony

The **Dyssynchrony** screen was created for assessing the phases of contraction for the left ventricle *(Figure 4.22)*. 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:

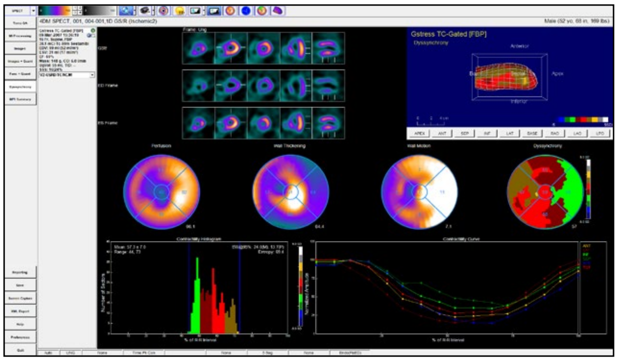


Figure 4.22: *The Dyssynchrony screen was created for assessing the phases of contraction for the left ventricle.*

- **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 4.23)***:** 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.

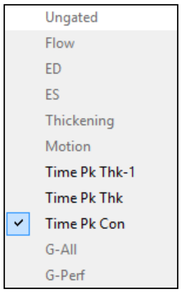


Figure 4.23: *Raw Map Menu*

SPECT MPI
Study
Interpretation

Interpretation of the SPECT MPI Study

MPI Summary

The **MPI Summary** screen is considered the Corridor4DM 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 4.24)* supports all NM datasets and includes:

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

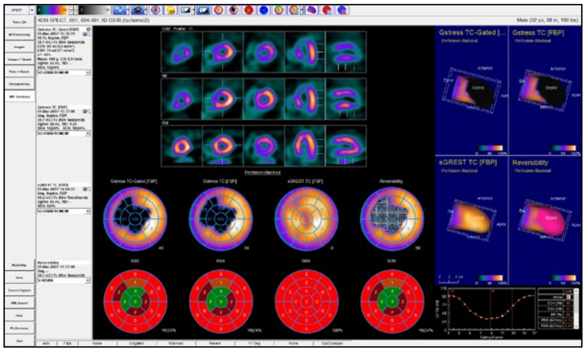


Figure 4.24: *The MPI Summary screen displaying gated stress, ungated stress and rest datasets and all perfusion and function information on one screen for quick review*

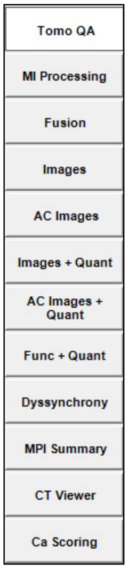
Corridor4DM recommends displaying the **MPI Summary** screen when performing the final interpretation and exporting information to your report.

Conclusion

This concludes your SPECT MPI Clinical Workflow Tutorial. Prior to exiting the program, users should save the Corridor4DM result files. Technologists can transfer the saved results and study data to the interpreting physician for review. Corridor4DM recognizes the most current saved result files, so if physicians make any changes to the saved study they should save the updated results.

CHAPTER 5 HYBRID SPECT/CT CARDIAC IMAGING

The SPECT/CT Cardiac Imaging Workflow uses these screen:



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 Corridor4DM Clinical Workflow Tutorial for the image review, quantification, and interpretation of SPECT/CT MPI studies. The following SPECT/CT datasets can be launched into Corridor4DM:

- 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

Users should always ascertain the integrity of the study that has been provided for review prior to beginning any processing or interpretation. Corridor4DM 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

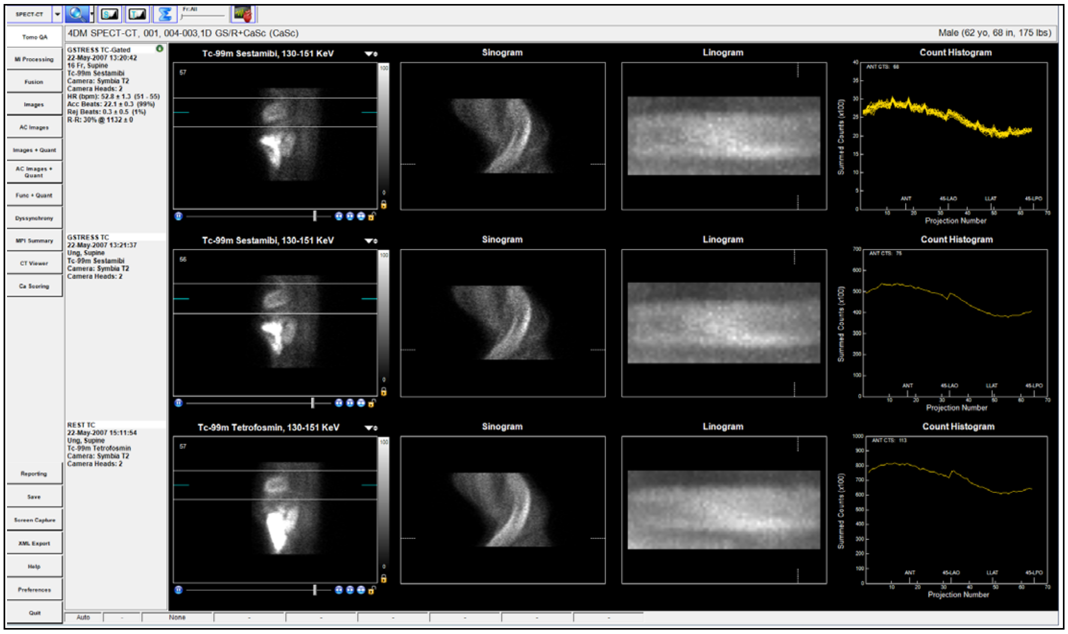
Similar to the SPECT MPI workflow, users should begin the QA portion by reviewing the raw NM Tomo datasets on the **Tomo QA** screen.

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.

Tomo QA

The **Tomo QA** screen *(Figure 5.1)* 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 SPECT-CT, 001, 004-003,1D GS/R+CaSc (CaSc)

Male (62 yo, 68 in, 175 lbs)

GSTRESS TC-Gated
22-May-2007 13:20:42
16 Fr, Supine
Tc-99m Sestamibi
Camera: Symbia T2
Camera Heads: 2
HR (bpm): 52.8 ± 1.3 (51 - 55)
Acc Beats: 22.1 ± 0.3 (99%)
Rej Beats: 0.3 ± 0.5 (1%)
R-R: 30% @ 1132 ± 0

GSTRESS TC
22-May-2007 13:21:37
Ung, Supine
Tc-99m Sestamibi
Camera: Symbia T2
Camera Heads: 2

REST TC
22-May-2007 15:11:54
Ung, Supine
Tc-99m Tetrofosmin
Camera: Symbia T2
Camera Heads: 2

Figure 5.1: *The Tomo QA screen with three datasets displayed. From top-to-bottom: Gated stress (with Gating Information), ungated stress, and ungated rest*

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

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 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.

- **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** *(Figure 5.2)* shows the length of

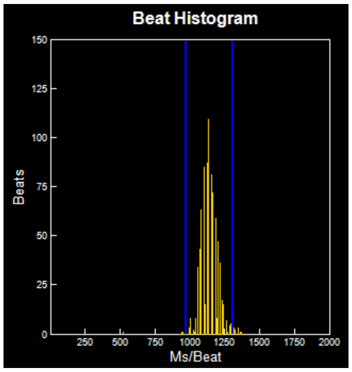
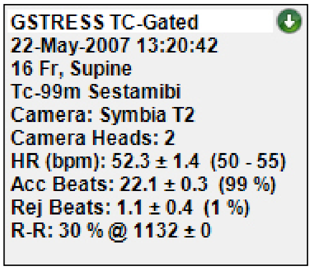


Figure 5.2: *The Beat Histogram on the Tomo QA screen*

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 each applicable NM dataset).
  - The **Gating Information** *(Figure 5.3)* 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).



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 5.3: *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 Corridor4DM 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 Corridor4DM 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 5.4)*.

!

WARNING

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

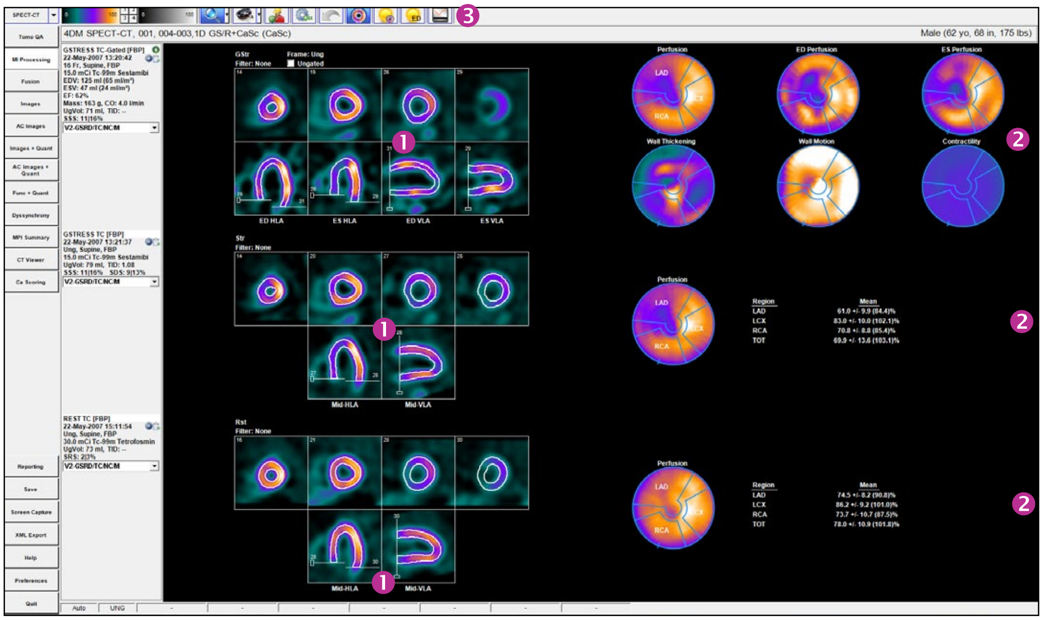


Figure 5.4: *The MI Processing screen with three datasets – gated stress, stress, and rest – displays* ❶ *Processing Splash Objects and* ❷ *Processing Polar Map Objects for each dataset by default. Click the* ❸ *LV Volume Curve tool to display the LV Volume Curve for gated studies.*

!

WARNING

The user should visually verify the processing limits-

- Heart Centering
- Basal and Apical Limits
- Volume Orientations

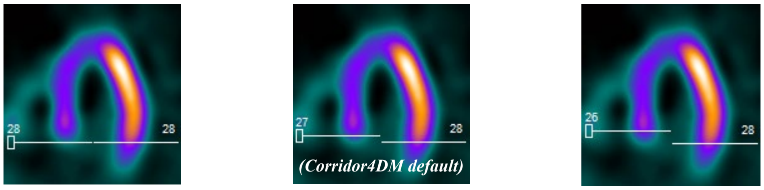
If the cardiac surface generated includes extra-cardiac activity, it is recommended that the user processes the images utilizing the Constraints Tool. Inclusion of extra-cardiac activity can lead to false impressions and image normalization.

The user should confirm that the basal limits are consistent between datasets and that the Corridor4DM 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 Corridor4DM 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 5.5)*. The default algorithm is the Septal Wall Mid-Membranous Septum.

4DM-provided normals databases were generated using the Septal Wall Mid-Membranous Septum basal extent placement. To provide consistency, the Corridor4DM default basal extent setting is the same.



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

Figure 5.5:*The three Corridor4DM basal extent Preference settings for Pmap QA*

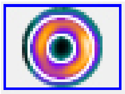


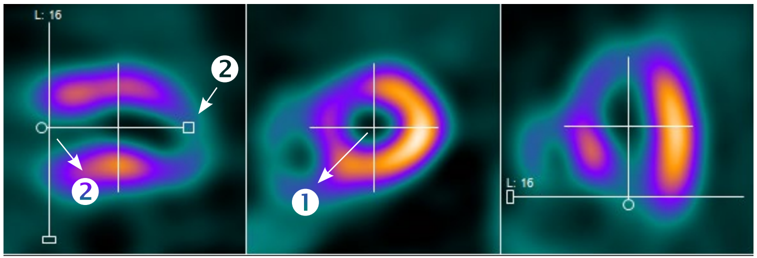
Figure 5.6:*Contours tool*

Activating the **Contours** tool *(Figure 5.6)* 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.

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.]()

Figure 5.7:*Manual Processing 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 5.7)*. Centering, orientation and axial limits are adjusted using the sliders as shown in *(Figure 5.8)*.

❶	Proper positioning of the LV center aligns the crosshairs in the center of the ventricle.	 ***Figure 5.8:*** *Examples of proper LV center, apical and basal limits positioning*
❷	Proper positioning of the apical and basal limits are at the center of the apical myocardium and the mitral valve plane.	

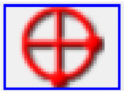


Figure 5.9: *Constraints tool*

If the dataset has significant extra-cardiac activity, click the **Constraints** tool *(Figure 5.9)* 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 5.10)*. Once adjustments to the LV center, orientation, and basal limit are complete, the user must click the **Process** tool *(Figure 5.11)* to generate the endo- and epicardial surfaces.

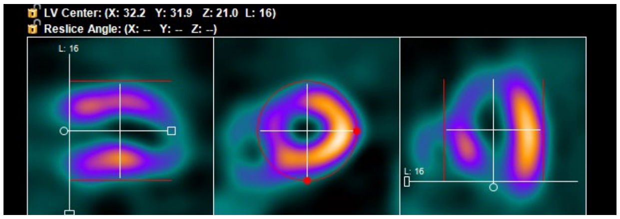


Figure 5.10: *Constraints activated and properly positioned*

If the dataset needs to be processed from scratch (i.e. no initial estimates from Corridor4DM), click the **Reset** tool *(Figure 5.12)* and then set the center, angulation, valve plane location and click the Process tool to reprocess.

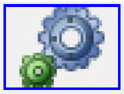
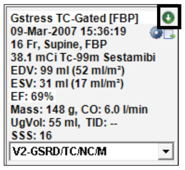


Figure 5.11:
Process tool

Figure 5.12:
Reset tool

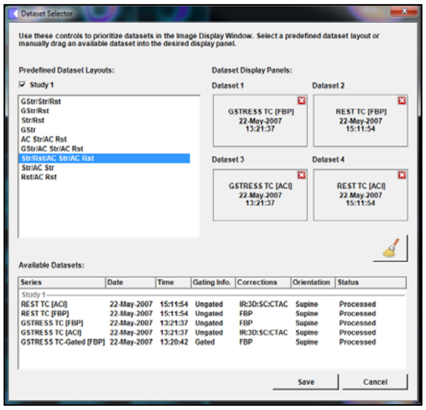
Repeat these MI Processing screen QA steps for any additional reconstructions passed to Corridor4DM (e.g., AC Stress and AC Rest). To check additional datasets on the MI Processing screen, click the **Dataset Selector** tool *(Figure 5.13)*, located in the Dataset Information Panel of the first displayed dataset only.



Gstress TC-Gated [FBP]
09-Mar-2007 15:36:19
16 Fr, Supine, FBP
38.1 mCi Tc-99m Sestamibi
EDV: 99 ml (52 ml/m²)
ESV: 31 ml (17 ml/m²)
EF: 69%
Mass: 148 g, CO: 6.0 l/min
UgVol: 55 ml, TID: --
SSS: 16
V2-GSRD/TC/NC/M

Figure 5.13:
Dataset Selector tool

In the **Dataset Selector window**, either click to display the predefined layouts *(Figure 5.14)*, or click and drag each dataset into the Dataset Display Panels from the list of Available Datasets. Click **Save** to display the selected datasets. Define custom predefined layouts, and edit available dataset layout options from with Corridor4DM Preferences on the Screen Layout page, in the Dataset Builder section.



Use these controls to prioritize datasets in the Image Display Window. Select a predefined dataset layout or manually drag an available dataset into the desired display panel.

Predefined Dataset Layouts:

☑ Study 1

- GStr/Str/Rst
- GStr/Rst
- Str/Rst
- GStr
- AC Str/AC Rst
- GStr/AC Str/AC Rst
- Str/Rst/AC Str/AC Rst
- Str/AC Str
- Rst/AC Rst

Dataset Display Panels:

Dataset 1: GSTRESS TC [FBP] 22-May-2007 13:21:37
Dataset 2: REST TC [FBP] 22-May-2007 15:11:54
Dataset 3: GSTRESS TC [ACI] 22-May-2007 13:21:37
Dataset 4: REST TC [ACI] 22-May-2007 15:11:54

Available Datasets:

Series	Date	Time	Gating Info.	Corrections	Orientation	Status
Study 1						
REST TC [ACI]	22-May-2007	15:11:54	Ungated	IR:3D:SC:CTAC	Supine	Processed
REST TC [FBP]	22-May-2007	15:11:54	Ungated	FBP	Supine	Processed
GSTRESS TC [FBP]	22-May-2007	13:21:37	Ungated	FBP	Supine	Processed
GSTRESS TC [ACI]	22-May-2007	13:21:37	Ungated	IR:3D:SC:CTAC	Supine	Processed
GSTRESS TC-Gated [FBP]	22-May-2007	13:20:42	Gated	FBP	Supine	Processed

Figure 5.14: *Dataset Selector window*

LV Surface Editor

Corridor4DM includes the **LV Surface Editor** tool, for use in rare cases where standard automated and manual processing does not output optimal LV surfaces. Clinical cases this can occur on are: large fixed defects where an entire wall has little to no uptake; or extreme extra-cardiac activity that isn't corrected with use of the Constraints Tool. See the LV Surface Editor section for steps to estimate and display location of the left wall when faced with such patient studies.

Fusion

Corridor4DM has integrated the **Fusion** screen *(Figure 5.15)* 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.

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).

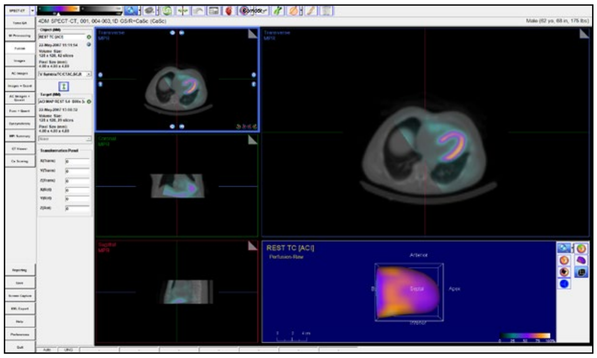
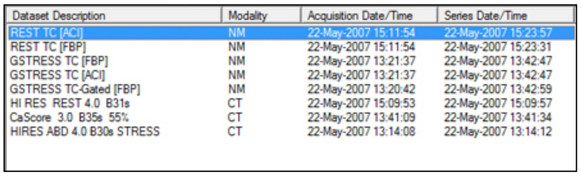


Figure 5.15: *The NM AC-Rst data as the Object Volume and the CT as the Target Volume. The three image panels are set to view the three orthogonal planes in Transverse space orientation.*

On the **Fusion** screen, the **Object Volume** is the overlay, or top image. The **Target Volume** is the base, or bottom image. The Object

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.

Volume can be repositioned, while the Target Volume is stationary. Use the Object Volume and Target Volume menus provided to select different datasets, if desired *(Figure 5.16)*. To switch the Object and Target Volume datasets, click the **Swap Datasets** tool *(Figure 5.17)*. Change the Orientation of the images by clicking the **Orientation** tool *(Figure 5.18)*.



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 B35s 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 5.16: *The Object/Target menu in the Fusion screen*

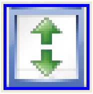


Figure 5.17: *Swap Datasets tool*

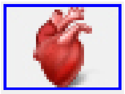


Figure 5.18: *Orientation tool*

The default layout for 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 5.19)* provides different layout options of the Fusion screen:

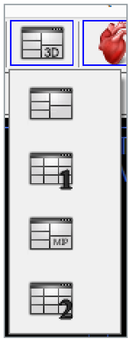


Figure 5.19: *Dataset Layout tool*

- **Four Panel with 3D Object:**
  The Four Panel with 3D object is used to view the co-registration of extracted CTA coronary vessels or Corridor4DM-quantified coronary calcium deposits.
- **Four Panel with Slice Display:**
  The Four Panel with Slice Display is used to view the Transverse Target and Object slices.
- **Nine Panel display:**
  The Nine Panel layout displays the Object, Target, and fused Object/Target volumes – each in a three orthogonal view.
- **Four Panel with 3D Rotating MIP:**
  The Four Panel with 3D Rotating MIP is used to view the rotating MIP display of the object and target data separately.
- **Nine Panel display with two datasets for comparison:**
  The Nine Panel display with two datasets for comparison is used to view two rows of fused Object/Target volumes for the datasets in comparison (e.g., PET-FDG vs. PET-MPI), followed by a third row of fused Object/Object volumes from the datasets -each in a three orthogonal view.

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**.

Figure 5.20: *Dual Colorbar with Alpha Blending 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 5.20)* is located below the left object colorbar. Slide the alpha-blending tool to adjust the transparency of the Object volume.

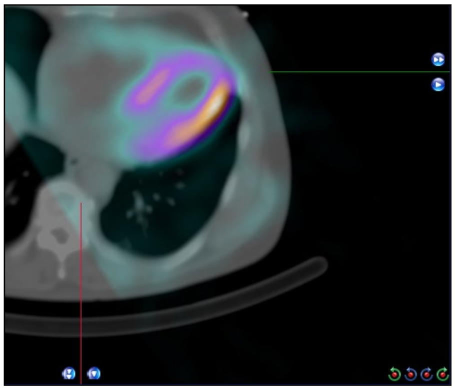


Figure 5.21: *A zoomed in view of the Coarse and Fine adjustment tools available on the Fusion screen*

If the target and object datasets need to be manually co-registered, Corridor4DM provides several tools within the Fusion screen to aide users during the manual alignment process:

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.

- **Coarse and Fine adjustment alignment tools** for image panning and rotation are provided when the mouse cursor is hovered over each image panel *(Figure 5.21)*.
- 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.
  - 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 5.22)* in the top left corner of an image panel to change settings for MPR/MIP thickness.

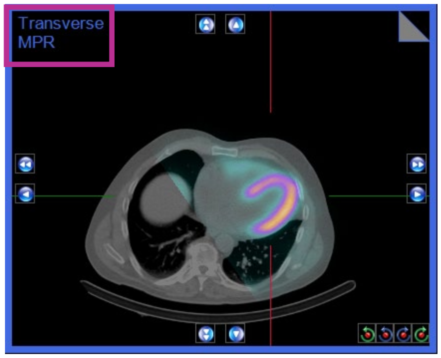


Figure 5.22:*Example of MPR label location*

- The **Center Datasets** tool *(Figure 5.23)* provides the following functionality:
  - **Center Datasets** allows the user to align the Object and Target datasets in the center of the image panel to aid in manual registration.
  - **Center LV** allows the user to co-register Object and Target SPECT and/or PET datasets by automatically aligning the Object and Target based upon the center of the left ventricle. This option is only active when the Object and Target datasets are both SPECT and/or PET datasets.

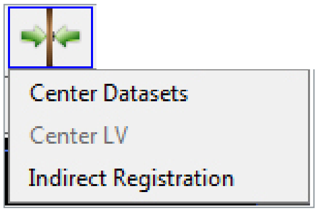


Figure 5.23:*Center Datasets tool*

  - **Indirect Registration** allows the user to co-register two SPECT and/or PET emission datasets (e.g. FDG metabolism and Rest Tc99m Sestamibi perfusion for viability evaluation). This tool is useful in cases where one of the emission datasets (e.g. FDG) may not have enough uptake to perform the co-registration to the perfusion data with certainty. On screen instructions walk the user through first verifying the co-registration of the two emission datasets with their corresponding higher resolution CT datasets. The third step applies registration of the SPECT and/or PET emission datasets to each other.

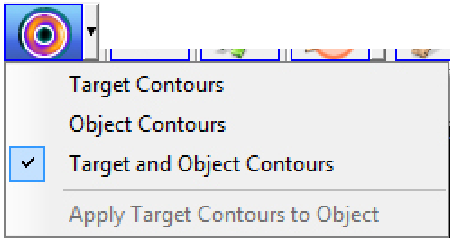


Figure 5.24:*Contours tool*

- Click the **Contours** tool *(Figure 5.24)* to display the endo- and epicardial LV surfaces by selecting Target Contours (red), Object Contours (white), or Target and Object Contours (both red and white contours display) for processed NM cardiac datasets.
  - **Apply Target Contours to Object** allows the user to take the contour generated for the Target NM cardiac dataset and applies this contour to the Object NM cardiac dataset after using the **Indirect Registration** tool or manual co-registration. This action can be undone by clicking Reset.

- Draw elliptical, freehand, rectangular, or polygon ROI's by selecting one from the **ROI Menu** tool *(Figure 5.25)*.

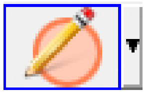


Figure 5.25: *ROI Menu tool*

- Draw straight-line measurements and automatically display the length for each (in mm) when the **Ruler** tool *(Figure 5.26)* is turned on.

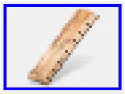


Figure 5.26: *Ruler tool*

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

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

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 Corridor4DM this layout is referred to as **Splash Object** display. The Corridor4DM **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.

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

Images

The **Images** and **AC Images** screens present the datasets as SA, HLA, and VLA **Splash Objects** *(Figure 5.27)*. Review and compare the tracer perfusion of all ungated NC and AC Stress and 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 Corridor4DM quantitative perfusion analysis.

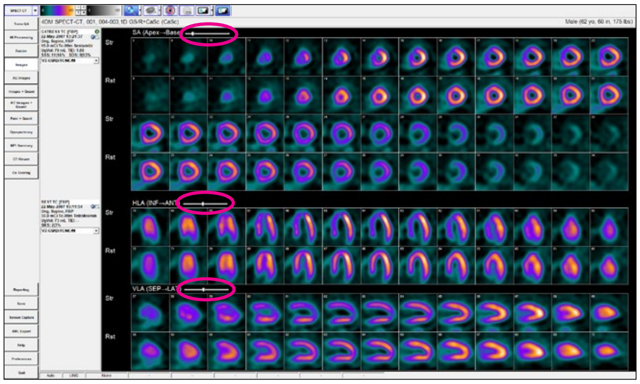


Figure 5.27:*Ungated datasets can be viewed together on the Images screens to check for differences between the NC and AC datasets. The Dataset Slice slider is circled in pink above each Splash Object.*

Quantitative
Perfusion
Review

Quantitative Perfusion Review

In addition to the qualitative perfusion assessment, Corridor4DM recommends utilizing the quantification data available to supplement visual perfusion findings. To quantify the perfusion information

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

Corridor4DM 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 Corridor4DM 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 Corridor4DM display both the perfusion **Splash Objects** and the supporting quantification information. Corridor4DM recommends using these screens during quantitative perfusion review of SPECT/CT MPI cases.

Images+Quant

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.

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. Corridor4DM 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.

It is recommended to view the **Images+Quant** screens with two datasets in order to view the reversibility polar map comparison. Corridor4DM 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 5.28)* and **AC Images+Quant** *(Figure 5.29)* 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.

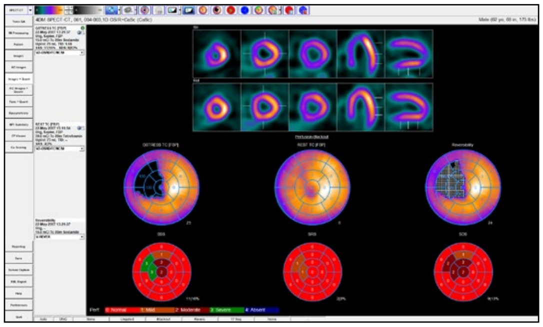


Figure 5.28: *Corridor4DM recommends viewing the Images+Quant screen with two datasets*

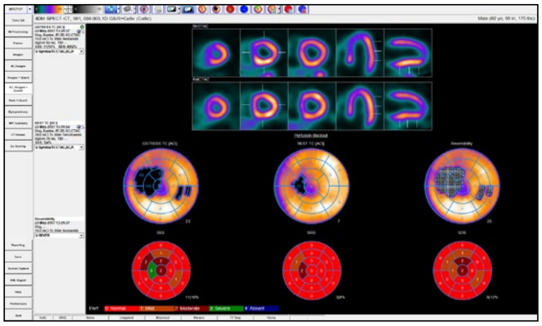


Figure 5.29: *The AC Images+Quant screen displaying AC Str/AC Rst datasets*

Quantitative
Functional
Review

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 5.30)*.

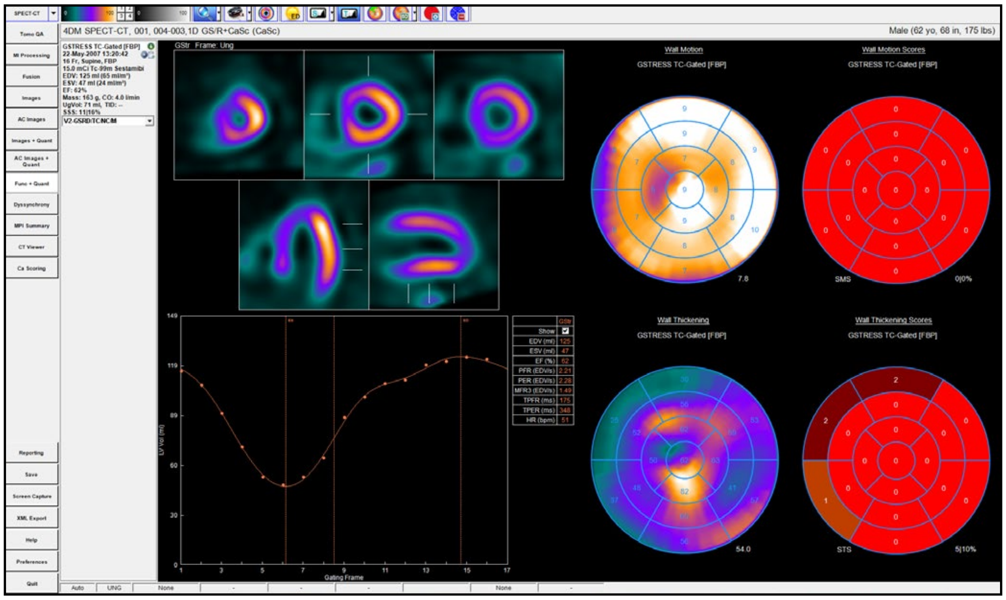


Figure 5.30: The Func+Quant screen with one gated dataset displayed

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.

Dyssynchrony

The **Dyssynchrony** screen was created for assessing the phases of contraction for the left ventricle *(Figure 5.31)*. 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:

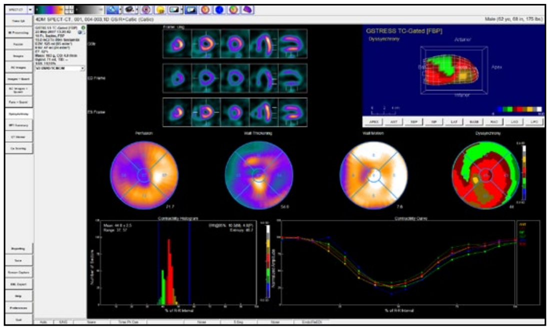


Figure 5.31: *The Dyssynchrony screen was created for assessing the phases of contraction for the left ventricle.*

- **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 5.32)***:** 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.

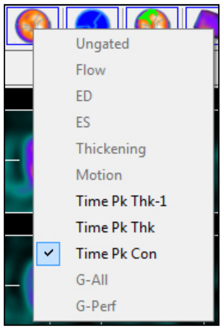


Figure 5.32:*The Raw Map menu*

Interpretation of the SPECT/CT MPI Study

MPI Summary

The **MPI Summary** screen *(Figure 5.33)* is the Corridor4DM 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

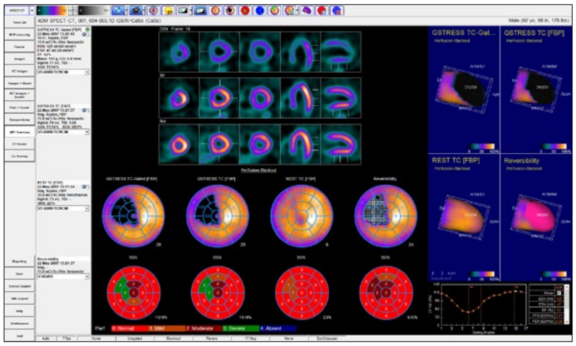


***Figure 5.33:** The MPI Summary Screen*

Corridor4DM recommends displaying the **MPI Summary** screen when performing the final interpretation and exporting information to your report.

CT Viewer

Reporting incidental CT findings for SPECT/CT studies is recommended. Corridor4DM includes the **CT Viewer** screen so that users can easily accomplish this task within the program *(Figure 5.34)*. Use this screen to review both contrast and non-contrast CT studies. Corridor4DM 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:

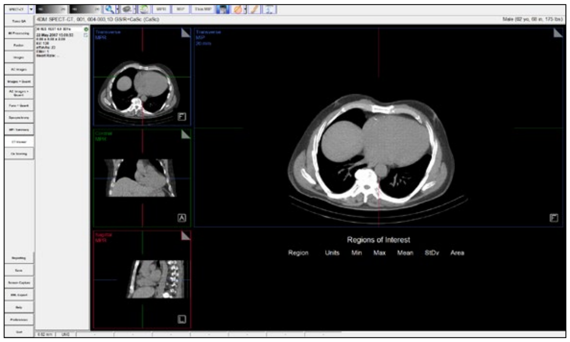


***Figure 5.34:** The CT Viewer screen with the Thin MIP button selected. The large image display panel is highlighted in blue to note it is the selected panel.*

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 1-100 mm).

- **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 5.35)*. 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 Corridor4DM 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

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.

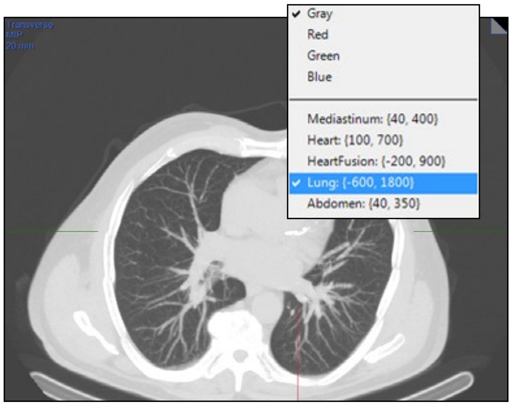


***Figure 5.35:** The CT Viewer with the MIP colorbar HU window changed to the Lung option to assess the lung structures for any incidental findings.*

the image panel and then clicking on the **MPR**, **MIP**, or **Thin MIP** button.

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

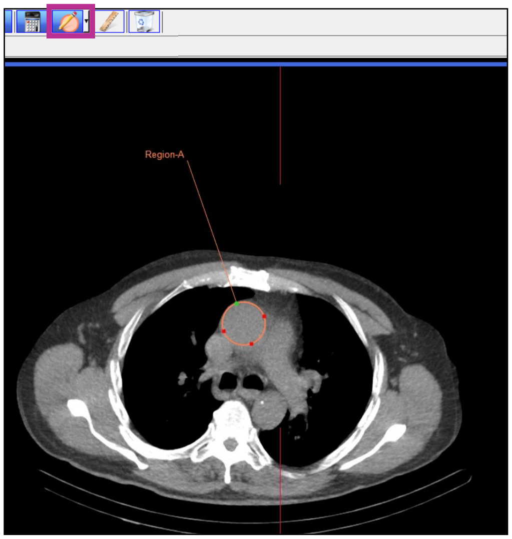


Figure 5.36: *The CT Viewer with the Table and ROI tools selected. The ROI information immediately updates to the Regions of Interest Table below the large image panel.*

Users can edit the **HU Range** names and numerical values from within the **Preferences** menu.

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 5.36)*.
- **Display** the information for any ROI's that have been drawn by clicking on the **Table** tool.

Once an **ROI** has been drawn, a **right-click ROI** menu will become available for quick ROI edits or deletions.

- **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. Corridor4DM 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 Corridor4DM **Ca Scoring** and **Conclusion** sections.

Ca Scoring

Corridor4DM provides quantification and review of coronary artery calcium deposits from within the **Ca Scoring** screen. Corridor4DM 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 5.37)* and the **ROI** tool *(Figure 5.38)*. Images displayed are based on slice thickness. Additionally, the **Highlight Calcium** tool *(Figure 5.39)* and **Delete Calcium** tool *(Figure 5.40)* are tools specific to the **Ca Scoring** screen. The status 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 5.41)*.

Figure 5.37: *Results Table tool*

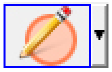


Figure 5.38: *ROI tool*

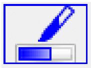


Figure 5.39: *Highlight Calcium tool*

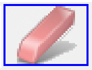


Figure 5.40:*Delete Calcium tool*

Figure 5.41: *Processing Options tool*

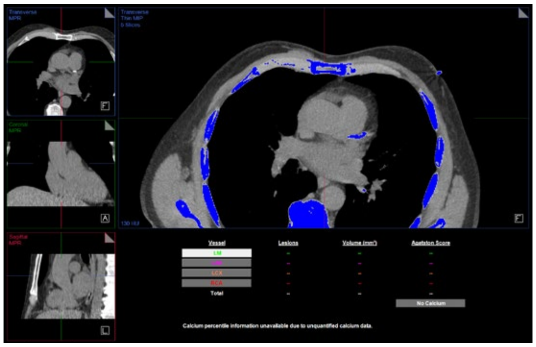
WARNING
Users must ensure that a non-contrast Calcium Scoring CT dataset is input to the **Ca Scoring** screen prior to assigning scores.

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.

Corridor4DM provides color-coded calcium scoring buttons for the following coronary vessels: **LM** – Left Main (green), **LAD** – Left Anterior Descending (pink), **LCX** – Left Circumflex (Coral), and **RCA** – Right Coronary Artery (red).

The Corridor4DM default calcium threshold value is 130 HUs. Users can adjust this setting within the **Ca Scoring** screen from within **Preferences**.



Vessel	Lesions	Volume (mm³)	Agatston Score
LM	-	-	-
LAD	-	-	-
LCX	-	-	-
RCA	-	-	-
Total	-	-	-

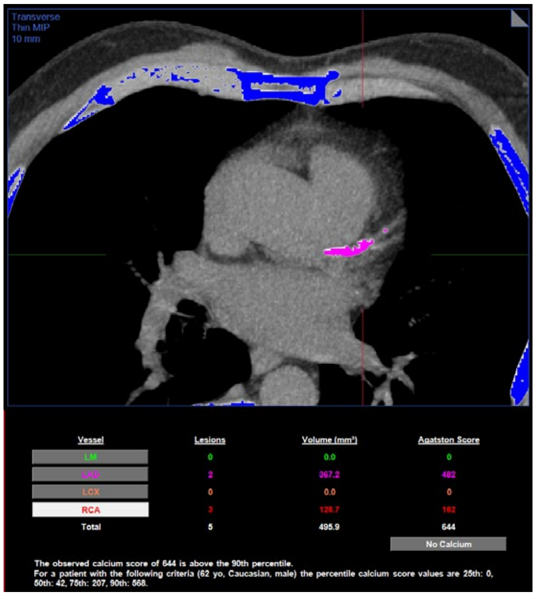
Calcium percentile information unavailable due to unquantified calcium data.

Figure 5.42: *The Ca Scoring screen launches with areas of calcium noted in blue.*

In the **Ca Scoring** screen, click on the **Highlight Calcium** tool to indicate areas of calcification with the color blue *(Figure 5.42)*. In order to remove calcifications 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. Corridor4DM 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 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 5.43)*.

Use the **ROI Tool** to assign calcium scores to areas where calcium deposits are present at vessel junctions or where the calcium may overlap from one vessel into another. Use the **Region-Growing Technique** to assign calcium scores to areas where calcium deposits are isolated or do not overlap into more than one vessel.



Vessel	Lesions	Volume (mm³)	Agatston Score
LM	0	0.0	0
LAD	2	367.2	482
LCX	0	0.0	0
RCA	3	128.7	162
Total	5	495.9	644

The observed calcium score of 644 is above the 90th percentile.
For a patient with the following criteria (62 yo, Caucasian, male) the percentile calcium score values are 25th: 0, 50th: 42, 75th: 207, 90th: 568.

Figure 5.43: *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.*

- **Region-Growing Technique**:
  - – Click on the **Vessel** button name

Click the **No Calcium** button to quickly erase all calcium scores.

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.

Right-click on Dataset Info to verify and enter patient age/ ethnicity and gender to permit percentile risk calculations as compared to MESA.

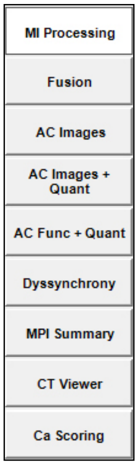
Once the review (and scoring, if necessary) is complete on the **Ca Scoring screen**, save the results so that they can be recalled at any time.

Conclusion

This concludes your SPECT/CT MPI Clinical Workflow Tutorial. Prior to exiting the program, users should save the Corridor4DM results files. Technologists can transfer the saved results and image dataset(s) to the interpreting physician for review. Corridor4DM recognizes the most current saved result files, so if physicians make any changes to the saved study they should save the updated results.

CHAPTER 6 PET CARDIAC IMAGING

The PET/CT cardiac imaging workflow uses these screens:



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 Corridor4DM 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 Corridor4DM:

- 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

Users should always ascertain the integrity of the study that has been provided for review prior to beginning any processing or interpretation. Corridor4DM 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.

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

MI Processing

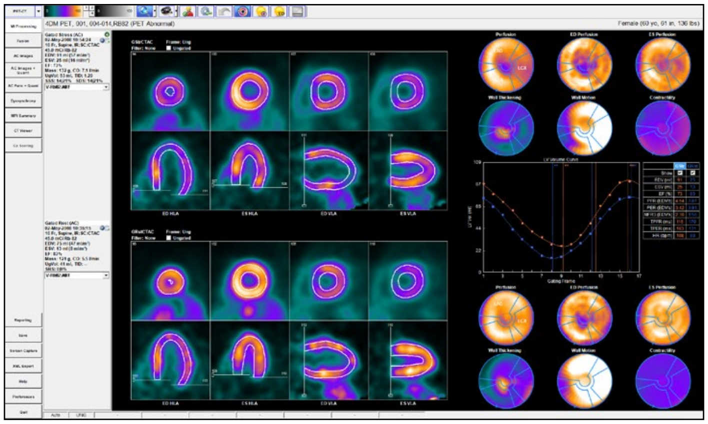


Figure 6.1: *The MI Processing screen with three datasets – gated stress, stress, and rest – displays ❶ Processing Splash Objects and ❷ Processing Polar Map Objects for each dataset by default. Click the ❸ LV Volume Curve tool to display the LV Volume Curve for gated studies.*

Upon launching a patient in Corridor4DM for the first time, the program automatically quantifies the study using Corridor4DM 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 6.1)*.

The user should confirm that the

WARNING
The user should visually verify the processing limits-

- Heart Centering
- Basal and Apical Limits
- Volume Orientations

basal limits are consistent between datasets and that the Corridor4DM 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

If the cardiac 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 Corridor4DM 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 6.2)*. The default algorithm is the Septal Wall Mid-Membranous Septum.

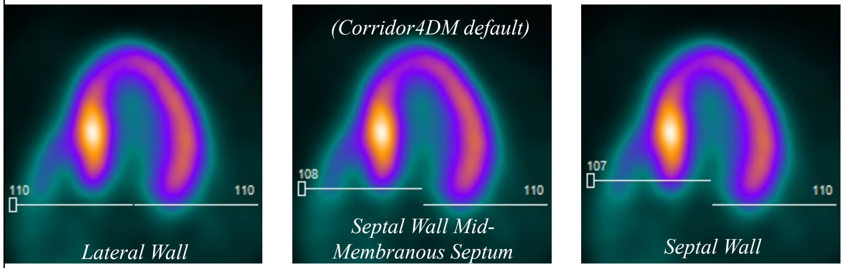


Figure 6.2: *The three Corridor4DM basal limit Preference settings for Pmap QA*

4DM-provided normals databases were generated using the Septal Wall Mid-Membranous Septum basal extent placement. To provide consistency, the Corridor4DM default basal extent setting is the same.

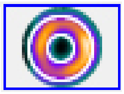


Figure 6.3: *Contours tool*

Activating the **Contours** tool *(Figure 6.3)* 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 6.4: *Manual Processing 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 6.4)*. Centering, orientation and axial limits are adjusted using the sliders as shown in *(Figure 6.5)*.

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 center of the apical myocardium and the mitral valve plane.

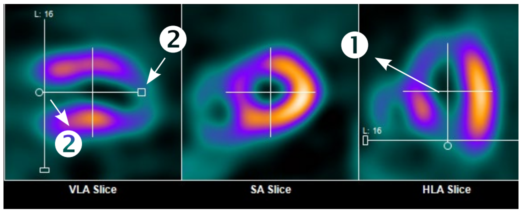


Figure 6.5: *Examples of proper positioning on the Setup screen*

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.]()

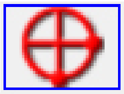


Figure 6.6: *Constraints tool*

If the dataset has significant extra-cardiac activity, click the **Constraints** tool *(Figure 6.6)* 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 at three and six o'clock and centering the crosshairs *(Figure 6.7)*. Once adjustments to the LV center, orientation, and basal limit are complete, the user must click the **Process** tool *(Figure 6.8)* to generate the endo- and epicardial surfaces.

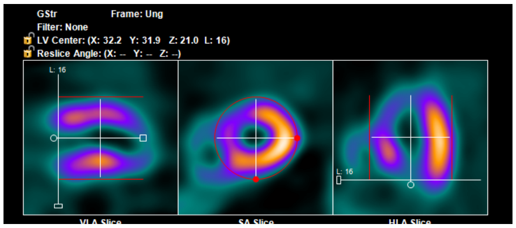


Figure 6.7: *The Constraints tool is selected which overlays adjustable constraints onto all four PET datasets. These constraints are properly positioned to include the entire LV, while excluding extra-cardiac activity such as liver or a loop of bowel.*

If the dataset needs to be processed from scratch (i.e. no initial estimates from Corridor4DM), click the **Reset** tool *(Figure 6.9)* and then set the center, angulation, valve plane location and click the Process tool to reprocess.

LV Surface Editor

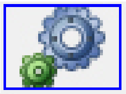


Figure 6.8: *Process tool*

Figure 6.9: *Reset tool*

Corridor4DM includes the LV Surface Editor tool, for use in rare cases where standard automated and manual processing does not output optimal LV surfaces. Clinical cases this can occur on are: large fixed defects where an entire wall has little to no uptake; or extreme extra-cardiac activity that isn't corrected with use of the Constraints Tool. See the LV Surface Editor section in Ch 4 for steps to estimate and display location of the left wall when faced with such patient studies.

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.

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).

Fusion

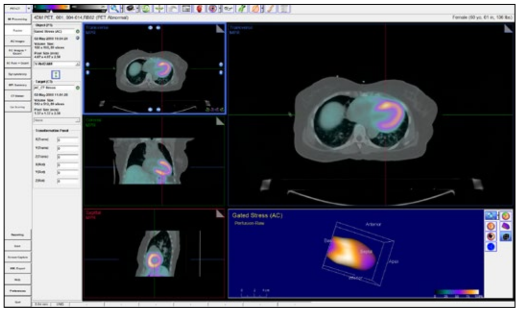
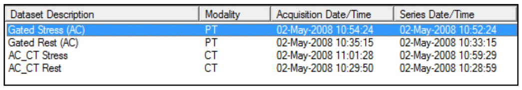


Figure 6.10: *Shows proper co-registration of the Stress PET dataset to the corresponding Stress CT dataset.*

Corridor4DM has integrated the **Fusion** screen *(Figure 6.10)* 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.

On the **Fusion** screen, 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. Use the Object Volume and Target Volume menus provided to select different datasets, if desired *(Figure 6.11)*. Additionally, gated CT datasets are supported within the **Fusion** screen. To switch the Object and Target Volume datasets, click the **Swap Datasets** tool *(Figure 6.12)*. Change the Orientation of the images by clicking the **Orientation** tool *(Figure 6.13)*.

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.



Dataset Description	Modality	Acquisition Date/Time	Series Date/Time
Gated Stress (AC)	PT	02-May-2008 10:54:24	02-May-2008 10:52:24
Gated Rest (AC)	PT	02-May-2008 10:35:15	02-May-2008 10:33:15
AC_CT Stress	CT	02-May-2008 11:01:28	02-May-2008 10:59:29
AC_CT Rest	CT	02-May-2008 10:29:50	02-May-2008 10:28:59

Figure 6.11: *The Object/Target menu in the Fusion screen*

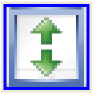


Figure 6.12: *Swap Datasets tool*

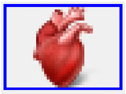


Figure 6.13: *Orientation tool*

The default layout for 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

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**.

the large panel, double-click one of the three orthogonal images on the left.

The **Dataset Layout** tool *(Figure 6.14)* provides different layout options of the Fusion screen:

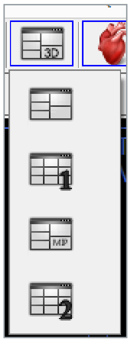


Figure 6.14: *Dataset Layout tool*

- **Four Panel with 3D Object:**
  The Four Panel with 3D object is used to view the co-registration of extracted CTA coronary vessels or Corridor4DM-quantified coronary calcium deposits.
- **Four Panel with Slice Display:**
  The Four Panel with Slice Display is used to view the Transverse Target and Object slices.
- **Nine Panel display:**
  The Nine Panel layout displays the Object, Target, and fused Object/Target volumes – each in a three orthogonal view.
- **Four Panel with 3D Rotating MIP:**
  The Four Panel with 3D Rotating MIP is used to view the rotating MIP display of the object and target data separately.
- **Nine Panel display with two datasets for comparison:**
  The Nine Panel display with two datasets for comparison is used to view two rows of fused Object/Target volumes for the datasets in comparison (e.g., PET-FDG vs. PET-MPI), followed by a third row of fused Object/Object volumes from the datasets -each in a three orthogonal view.

When **Cardiac Orientation** is selected the three **Fusion** screen image panel names change from: Transverse to SA, Coronal to HLA, and Sagittal to VLA.

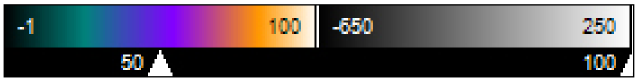


Figure 6.15: *Dual Colorbar with Alpha Blending*

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 6.15)* is located below the left object colorbar. Slide the alpha-blending tool to adjust the transparency of the Object volume.

If the target and object datasets need to be manually co-registered, Corridor4DM provides several tools within the Fusion screen to aide users during the manual alignment 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 6.16)*.
- 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.

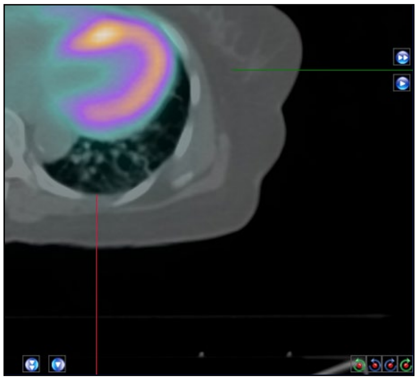


Figure 6.16: *A zoomed in view of the Coarse and Fine adjustment tools available on the Fusion screen*

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 6.17)* in the top left corner of an image panel to change settings for MPR/MIP thickness.

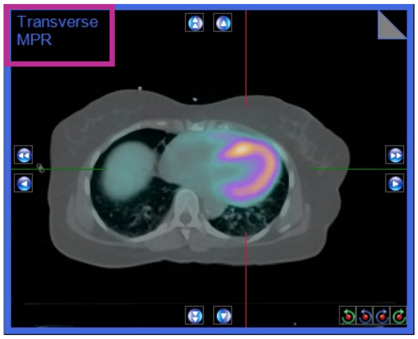


Figure 6.17: *Example of MPR label location*

- The **Center Datasets** tool *(Figure 6.18)* provides the following functionality:
  - **Center Datasets** allows the user to align the Object and Target datasets in the center of the image panel to aid in manual registration.
  - **Center LV** allows the user to co-register Object and Target SPECT and/or PET datasets by automatically aligning the Object and Target based upon the center of the left ventricle. This option is only active when the Object and Target datasets are both SPECT and/or PET datasets.

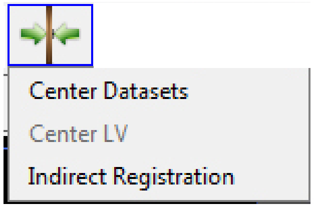


Figure 6.18: *Center Datasets tool*

  - **Indirect Registration** allows the user to co-register two SPECT and/or PET emission datasets (e.g. FDG metabolism and Rest Tc99m Sestamibi perfusion for viability evaluation). This tool is useful in cases where one of the emission datasets (e.g. FDG) may not have enough uptake to perform the co-registration to the perfusion data with certainty. On screen instructions walk the user through first verifying the co-registration of the two emission datasets with their corresponding higher resolution CT datasets. The third step applies registration of the SPECT and/or PET emission datasets to each other.

- Click the **Contours** tool *(Figure 6.19)* to display the endo- and epicardial LV surfaces by selecting Target Contours (red), Object Contours (white), or Target and Object Contours (both red and white contours display) for processed NM cardiac datasets.
  - **Apply Target Contours to Object** allows the user to take the contour generated for the Target NM cardiac dataset and applies this contour to the Object NM cardiac dataset after using the **Indirect Registration** tool or manual co-registration. This action can be undone by clicking Reset.

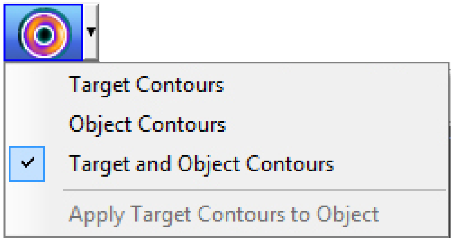


Figure 6.19: *Contours tool*

- Draw elliptical, freehand, rectangular, or polygon ROI's by selecting one from the **ROI Menu** tool *(Figure 6.20)*.
  - **SUV** measurements will be calculated if the patient's weight and injected dose are included in the dataset information.

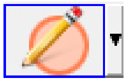


Figure 6.20: *ROI Menu tool*

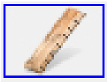


Figure 6.21: *Ruler tool*

- Draw straight-line measurements and automatically display the length for each (in mm) when the **Ruler** tool *(Figure 6.21)* is turned on.
- Delete any ROI or ruler measurements by selecting the element and clicking on the Delete tool in the Toolbar.

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

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 Corridor4DM this layout is referred to as **Splash Object** display. The Corridor4DM **AC Images** screen was created specifically to accomplish this step in the clinical workflow.

AC Images

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

The **AC Images** screen presents the datasets as SA, HLA, and VLA **Splash Objects** *(Figure 6.22)*. 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 Corridor4DM quantitative perfusion analysis.

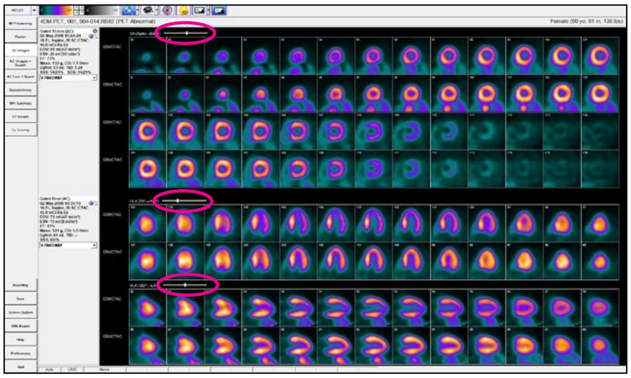


Figure 6.22: *The AC Images screen with the AC Str/Rst Rb-82 datasets selected to view ECT slices in all three orthogonal planes*

Quantitative Perfusion Review

Quantitative Perfusion Review

WARNING

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

In addition to the qualitative perfusion assessment, Corridor4DM recommends utilizing the quantification data available to supplement visual perfusion defects. To quantify the PT perfusion information Corridor4DM 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-

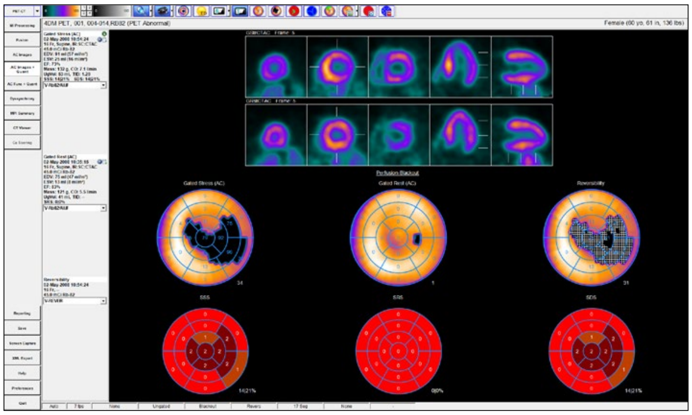


Figure 6.23: *The AC Images+Quant screen with the Str/Rst Rb-82 datasets launched to enable viewing the Reversibility polar map which is selected from the Comparison polar map menu.*

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.

quantitative scoring. The accuracy of the Corridor4DM 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 Corridor4DM displays both the perfusion **3SA Objects** and the supporting quantification information. Corridor4DM recommends using this screen during quantitative perfusion review of PET/CT MPI cases.

AC Images+Quant

The **AC Images+Quant** screen *(Figure 6.23)* 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. Corridor4DM 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.

It is recommended to view the **AC Images+Quant** screen with two datasets in order to view the reversibility polar map comparison. Corridor4DM 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.

Quantitative
Functional
Review

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

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

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 6.24)* 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.

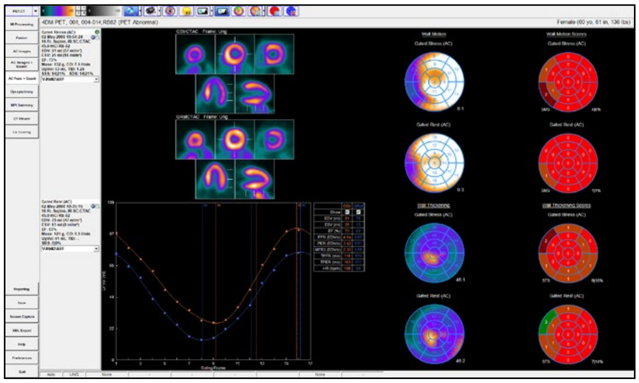


Figure 6.24: *The AC Func+Quant screen with one gated dataset displayed.*

Dyssynchrony

The **Dyssynchrony** screen was created for assessing the phases of contraction for the left ventricle *(Figure 6.25)*. 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:

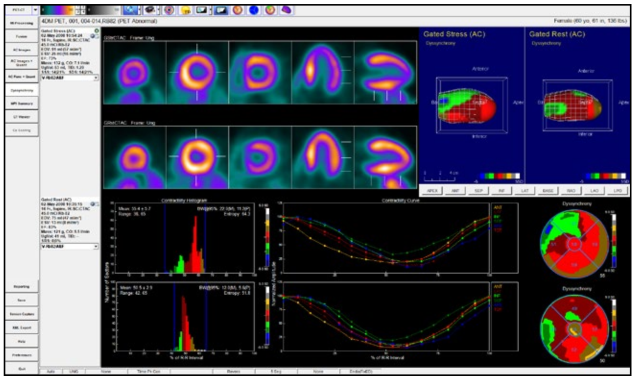


Figure 6.25: *The Dyssynchrony screen was created for assessing the phases of contraction for the left ventricle.*

- **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 6.26)***:** 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.

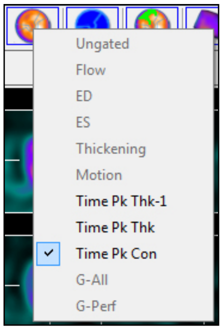


Figure 6.26:
Raw Map Menu

Interpretation of the PET/CT Study

MPI Summary

The **MPI Summary** screen is the Corridor4DM 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 6.27)*. It supports all PET datasets and includes:

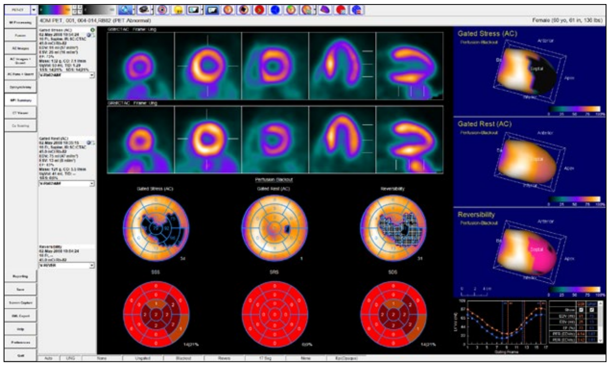


Figure 6.27: *The MPI Summary screen displays both perfusion and functional quantification information.*

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

CT topograms, commonly referred to as scout images, are not Corridor4DM-supported datasets. Only volumetric or reconstructed CT datasets can be viewed in Corridor4DM.

Corridor4DM recommends displaying the **MPI Summary** screen when performing the final interpretation and exporting information to your report.

CT Viewer

Reporting incidental CT findings for PET/CT studies is recommended. Corridor4DM includes the **CT Viewer** screen so that users can easily accomplish this task within the program *(Figure 6.28)*. Use this screen to review both contrast and non-contrast CT studies. Corridor4DM 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:

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 1-100 mm).

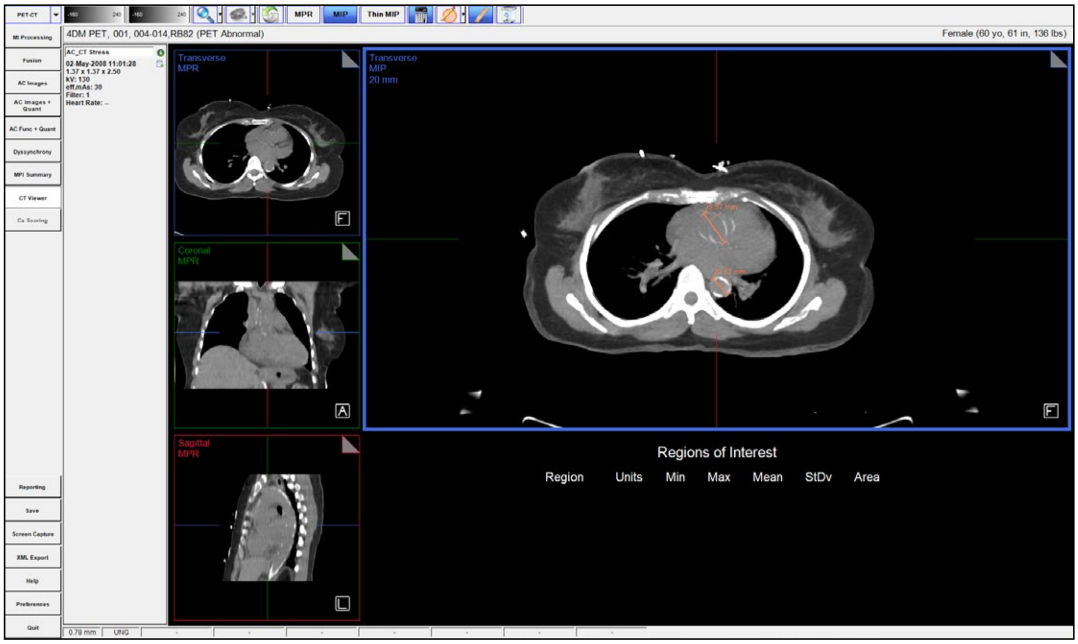


Figure 6.28: *Shows the CT Viewer screen with two ruler measurements drawn: one on the ascending aorta (upper) and one on the descending aorta (lower).*

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.

- **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 Corridor4DM 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 dataset(s).

- **Draw** elliptical, rectangular, or freehand ROI's by selecting the ROI type from the **ROI** menu *(Figure 6.29)*.
- **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

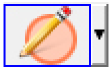


Figure 6.29: *The ROI menu*

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**.

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

***Figure 6.30:** The Result Table tool*

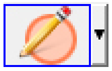


***Figure 6.31:** The ROI tool*

Corridor4DM provides quantification and review of coronary artery calcium deposits from within the **Ca Scoring** screen. Corridor4DM 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 6.30)* and the **ROI** tool *(Figure 6.31)*. Additionally, the **Highlight Calcium** tool *(Figure 6.32)* and **Delete Calcium** tool *(Figure 6.33)* are tools specific to the **Ca Scoring** screen. The status 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 6.34)*.

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

***Figure 6.32:** The Highlight Calcium tool*

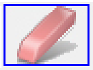


***Figure 6.33:** The Delete Calcium tool*

***Figure 6.34:** The Processing Options tool*

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

Corridor4DM provides color-coded calcium scoring buttons for the following coronary vessels: **LM** – Left Main (green), **LAD** – Left Anterior Descending (pink), **LCX** – Left Circumflex (Coral), and **RCA** – Right Coronary Artery (red).

- **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.

The Corridor4DM default calcium threshold value is 130 HUs. Users can adjust this setting within the **Ca Scoring** screen toolbar and from within **Preferences**.

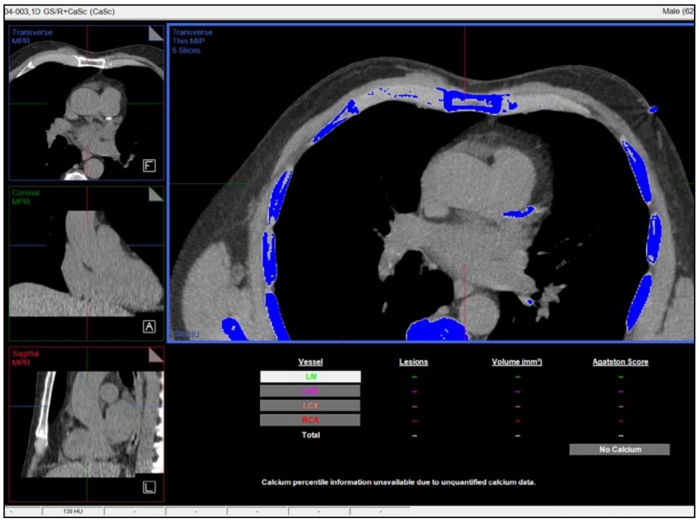
Right-click on Dataset Info to verify and enter patient age/ ethnicity and gender to permit percentile risk calculations as compared to MESA.

In the **Ca Scoring** screen, click on the **Highlight Calcium** tool to indicate areas of calcification with

Use the **ROI Tool** to assign calcium scores to areas where calcium deposits are present at vessel junctions or where the calcium may overlap from one vessel into another. Use the **Region-Growing Technique** to assign calcium scores to areas where calcium deposits are isolated or do not overlap into more than one vessel.

Click the **No Calcium** button to quickly erase all calcium scores.

the color blue *(Figure 6.35)*. In order to remove calcifications 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. Corridor4DM provides two different methods that can be used to manually assign coronary calcium:

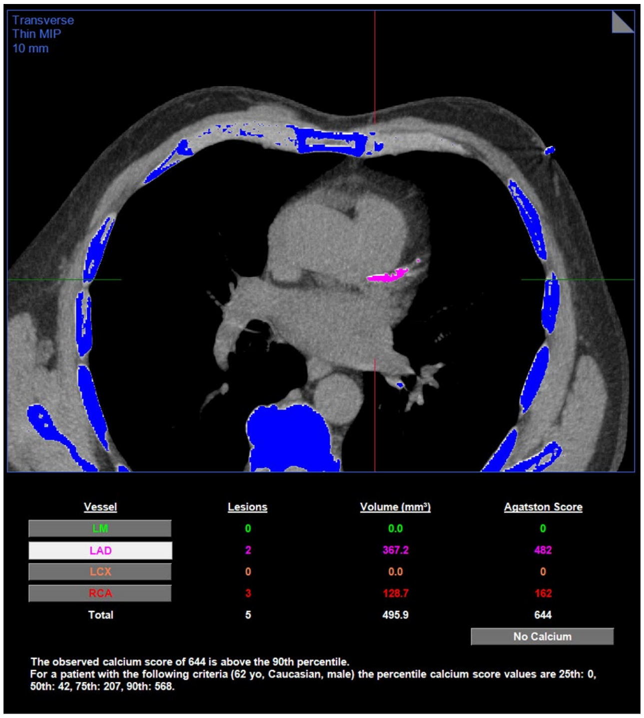


Vessel	Lesions	Volume (mm³)	Agatston Score
LM	–	–	–
LAD	–	–	–
LCX	–	–	–
RCA	–	–	–
Total	–	–	–

Calcium percentile information unavailable due to unquantified calcium data.

Figure 6.35: *The Ca Scoring screen launches with areas of calcium noted in blue*

- **ROI Tool:**
  - – Click on the **Vessel** button name that you wish to 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 6.36)*.
- **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.**
  - – The region growing limits can be set to **Full Volume**, the default, or **MPR/MIP Thickness.** This setting can be edited within **Preferences** under Screen Layout for the **Ca Scoring** screen.



Vessel	Lesions	Volume (mm³)	Agatston Score
LM	0	0.0	0
LAD	2	367.2	482
LCX	0	0.0	0
RCA	3	128.7	162
Total	5	495.9	644

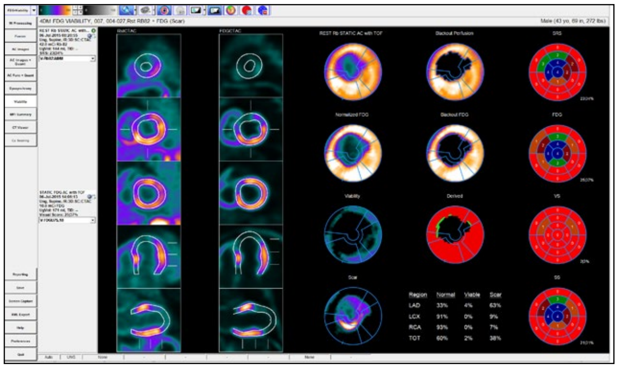
The observed calcium score of 644 is above the 90th percentile.
For a patient with the following criteria (62 yo, Caucasian, male) the percentile calcium score values are 25th: 0, 50th: 42, 75th: 207, 90th: 568.

Figure 6.36: *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.*

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 Viability Review



Region	Normal	Viable	Scar
LAD	33%	4%	63%
LCX	91%	0%	9%
RCA	93%	0%	7%
TOT	60%	2%	38%

Figure 6.37: *The Viability screen displaying a gated Rb-82 rest dataset and an ungated F-18 FDG viability dataset.*

The Corridor4DM **Viability** screen was created specifically for reviewing SPECT and/or PET viability studies *(Figure 6.37)*.

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.

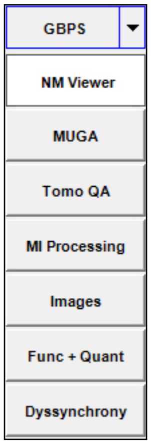
The **Derived Polar Map** is specific to the Viability screen. It displays the regional quantitative estimates for normal (red), viable (green), ischemic (blue), and scar (black) tissue.

Conclusion

This concludes your PET/CT Clinical Workflow Tutorial. Prior to exiting the program, users should save the Corridor4DM results files. Technologists can transfer the saved results and image dataset(s) to the interpreting physician for review. Corridor4DM recognizes the most current saved result files, so if physicians make any changes to the saved study they should save the updated results.

CHAPTER 7 GATED BLOOD POOL IMAGING

This Corridor4DM Tutorial uses the following Workflow Screen Preferences:



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

Gated Planar Quantitative Functional Review

As with any imaging protocol, assessment of the integrity of the study that has been submitted for interpretation is a critical first step. Corridor4DM 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.

Gated Planar Quantitative Function Review

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 **tool bar** to display calculations.

The **NM Viewer** screen *(Figure 7.1)* 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.

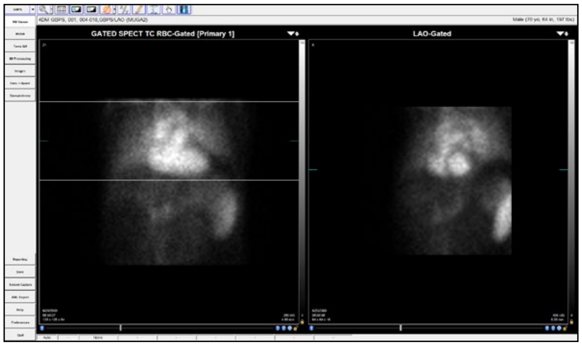


Figure 7.1: *The NM Viewer screen displaying a Planar Gated study*

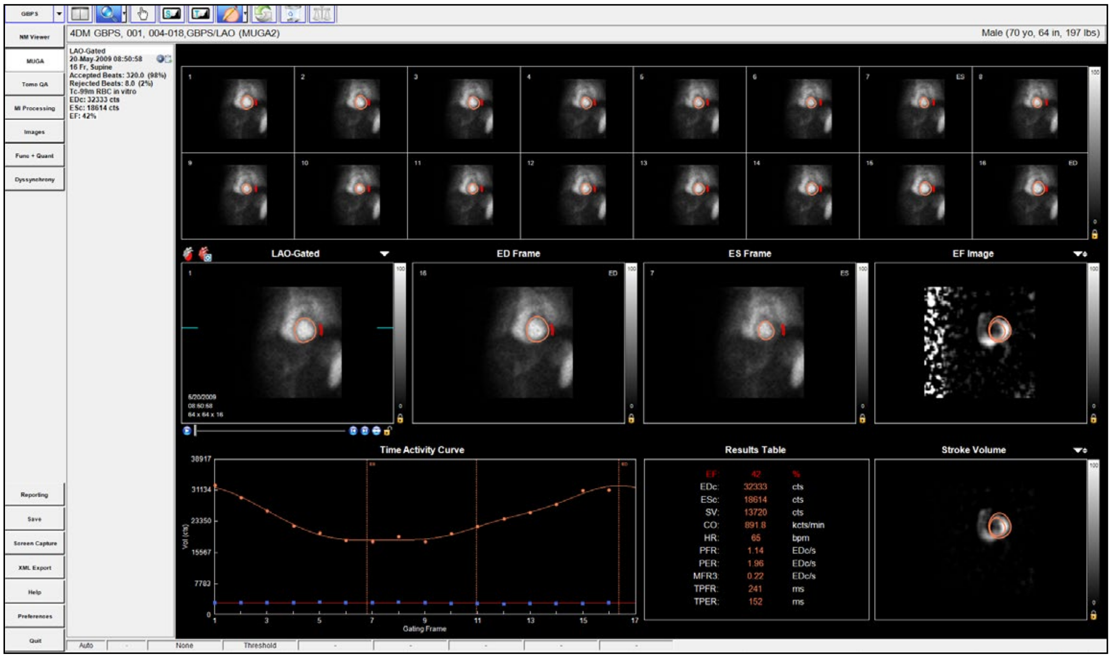
If the MUGA screen does not match the preferred dataset, check the Special File Strings by clicking on the Dataset Matching Strings button within the Preferences menu. To learn more about editing matching strings, go to [User Preferences.](#)

Apply **Spatial** and/ or **Temporal** filters as needed to enhance image quality.

Additionally if gate or count quality is poor for the last frame, right-click on the cine playback tools to open Cine Options and select Drop Last Frame to enhance image quality.

MUGA

The MUGA screen *(Figure 7.2)* quantifies 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.



4DM GBPS, 001, 004-018,GBPS/LAO (MUGA2)

Male (70 yo, 64 in, 197 lbs)

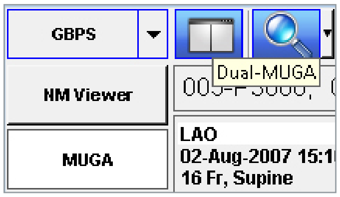
LAO-Gated
20-May-2009 08:50:58
16 Fr, Supine
Accepted Beats: 320.0 (98%)
Rejected Beats: 8.0 (2%)
Tc-99m RBC in vitro
EDc: 32333 cts
ESc: 18614 cts
EF: 42%

Results Table

EF:	42	%
EDc:	32333	cts
ESc:	18614	cts
SV:	13720	cts
CO:	891.8	kcts/min
HR:	65	bpm
PFR:	1.14	EDc/s
PER:	1.96	EDc/s
MFR3:	0.22	EDc/s
TPFR:	241	ms
TPER:	152	ms

Figure 7.2: *The MUGA screen displaying results for one gated planar dataset*

When a single study is loaded, Corridor4DM displays as shown in Figure 7.2. When there is more than one MUGA study loaded, Corridor4DM automatically displays two studies side-by-side, called Dual-MUGA mode. To manually activate this, click the Dual-MUGA tool in the Toolbar *(Figure 7.3)*. Click the tool again to turn Dual-MUGA mode off. Change the displayed datasets by clicking the white triangle drop-down arrow next to the dataset name.



LAO
02-Aug-2007 15:1
16 Fr, Supine

Figure 7.3: *Dual-MUGA tool*

Dual-MUGA Mode is useful for:

1. **Display and quantify left ventricle (LV) and right ventricle (RV) at the same time.** Corridor4DM automatically selects the RV or LV tool for quantification of each dataset, based on the camera acquisition angle (e.g., LAO vs. RAO). Click on the Ventricle tool above the Quantification Viewport to manually select LV (red) or RV (blue) *(Figure 7.4)*.

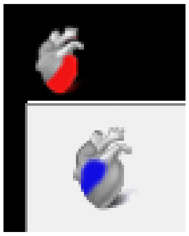
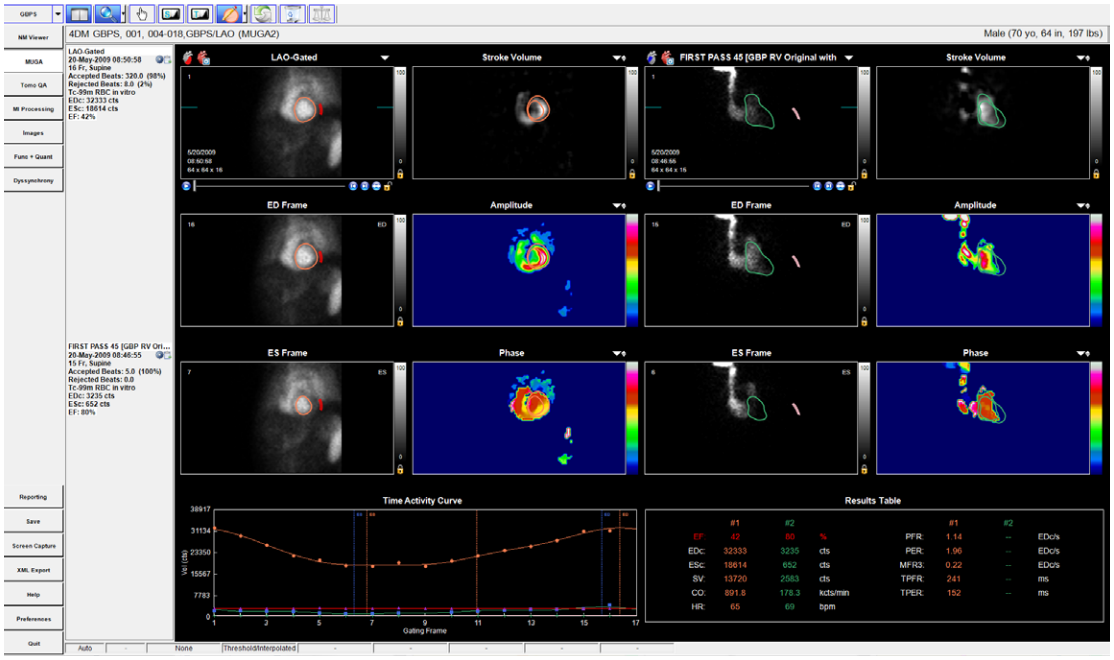


Figure 7.4: *Ventricle tool to select LV or RV*

2. **Serial study processing** - Corridor4DM detects when serial studies are loaded, and displays in Dual Mode automatically. When two serial studies are both quantified for LV, (e.g., current and prior LAO datasets are loaded), Corridor4DM will automatically quantify the change between datasets analyzing the same chamber, noted as the Δ column shown in purple on the Results Table *(Figure 7.5)* on the next page.



LAO-Gated
20-May-2009 08:50:58
16 Fr, Supine
Accepted Beats: 320.0 (98%)
Rejected Beats: 8.0 (2%)
Tc-99m RBC in vitro
EDc: 32333 cts
ESc: 18614 cts
EF: 42%

FIRST PASS 45 [GBP RV Ori...
20-May-2009 08:46:55
15 Fr, Supine
Accepted Beats: 5.0 (100%)
Rejected Beats: 0.0
Tc-99m RBC in vitro
EDc: 3235 cts
ESc: 652 cts
EF: 80%

Results Table

	#1	#2			#1	#2	
EF:	42	80	%	PFR:	1.14	--	EDc/s
EDc:	32333	3235	cts	PER:	1.96	--	EDc/s
ESc:	18614	652	cts	MFR3:	0.22	--	EDc/s
SV:	13720	2583	cts	TPFR:	241	--	ms
CO:	891.8	178.3	kcts/min	TPER:	152	--	ms
HR:	65	69	bpm				

Figure 7.5: *Dual Mode with results table shown in lower right corner*

Click the **Quantification Menu** tool *(Figure 7.6)*) above the **Quantification Viewport** to choose from the following four types of MUGA quantification:

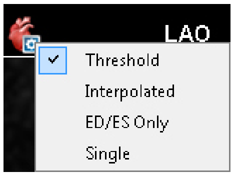


Figure 7.6: *Quantification Menu tool*

- **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. If the ED or ES ROI's are edited, Corridor4DM automatically interpolates new ROI's between the ED and ES frames.
- **Interpolated**
  - Semi-automatic method where the user selects the ED and 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. If the ED or ES ROI's are edited, Corridor4DM automatically interpolates new ROI's between the ED and ES frames.
- **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.

All ROIs allow resizing and panning to ensure proper placement in the viewports.

Corridor4DM provides on-screen instructions in the **Dataset Information Panel** for the user to follow. When in Dual Mode, they appear below each dataset. The quantification steps vary depending upon the quantification method selected. Corridor4DM 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 (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.

Once the calculations are completed, additional results windows display further information in the remaining viewports. The **Ejection Fraction (EF) Image** and **Stroke Volume (SV)** display by default, but users can select other options such as **Regional EF**, **Amplitude** and **Phase** by clicking the dataset selector arrow *(Figure 7.7)*. The Regional EF option (shown in Figure 7.7) is available for LV quantified results and divides the ED and ES ventricle ROI's into 6 pie-shaped segments extending from a central point of the ROIs. The EF calculations are shown on the ED ROI and frame in the display viewport.

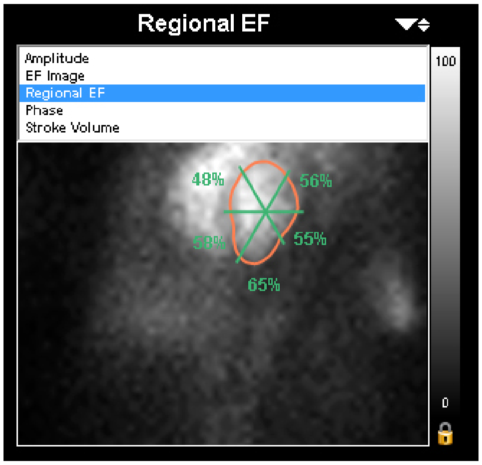


Figure 7.7: *The Tomo QA screen displaying a raw GBPS dataset.*

The **Time Activity Curve** (TAC) *(Figure 7.8)* 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.

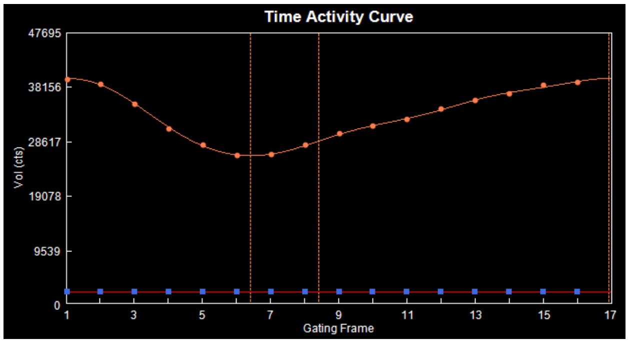
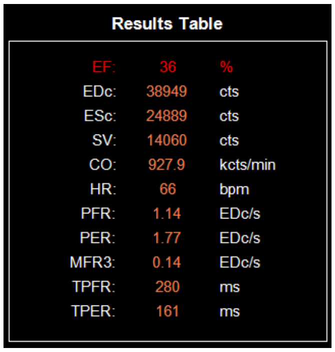


Figure 7.8: *Time Activity Curve on the MUGA screen for Gated Planar studies.*

The **Result Table** *(Figure 7.9)* 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 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



Results Table

EF:	36	%
EDc:	38949	cts
ESc:	24889	cts
SV:	14060	cts
CO:	927.9	kcts/min
HR:	66	bpm
PFR:	1.14	EDc/s
PER:	1.77	EDc/s
MFR3:	0.14	EDc/s
TPFR:	280	ms
TPER:	161	ms

Figure 7.9: *Quantitative results table on the MUGA screen for Gated Planar studies.*

- 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. Corridor4DM 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.

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

Tomo QA

The **Tomo QA** screen *(Figure 7.10)* 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.

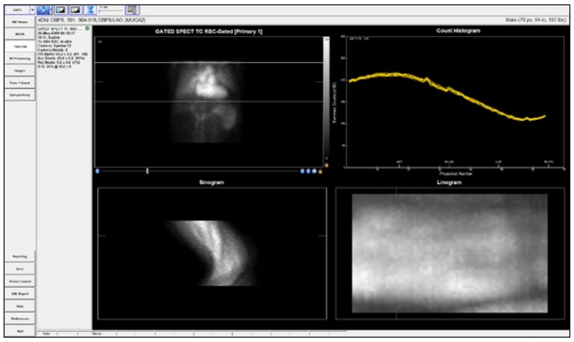


Figure 7.10: *The Tomo QA screen displaying a raw GBPS dataset.*

- **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 Frames can be viewed three different ways: **All**, **Sum**, or **Individually**. Click on the **Frame slider** tool in the **Screen Option Panel** 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.

- **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 7.11)* 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).

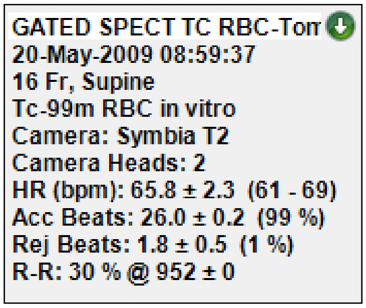

GATED SPECT TC RBC-Tom
20-May-2009 08:59:37
16 Fr, Supine
Tc-99m RBC in vitro
Camera: Symbia T2
Camera Heads: 2
HR (bpm): 65.8 ± 2.3 (61 - 69)
Acc Beats: 26.0 ± 0.2 (99 %)
Rej Beats: 1.8 ± 0.5 (1 %)
R-R: 30 % @ 952 ± 0

Figure 7.11: *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 Corridor4DM 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 Corridor4DM processing results.

WARNING
The user should verify that the estimated cardiac 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

MI Processing

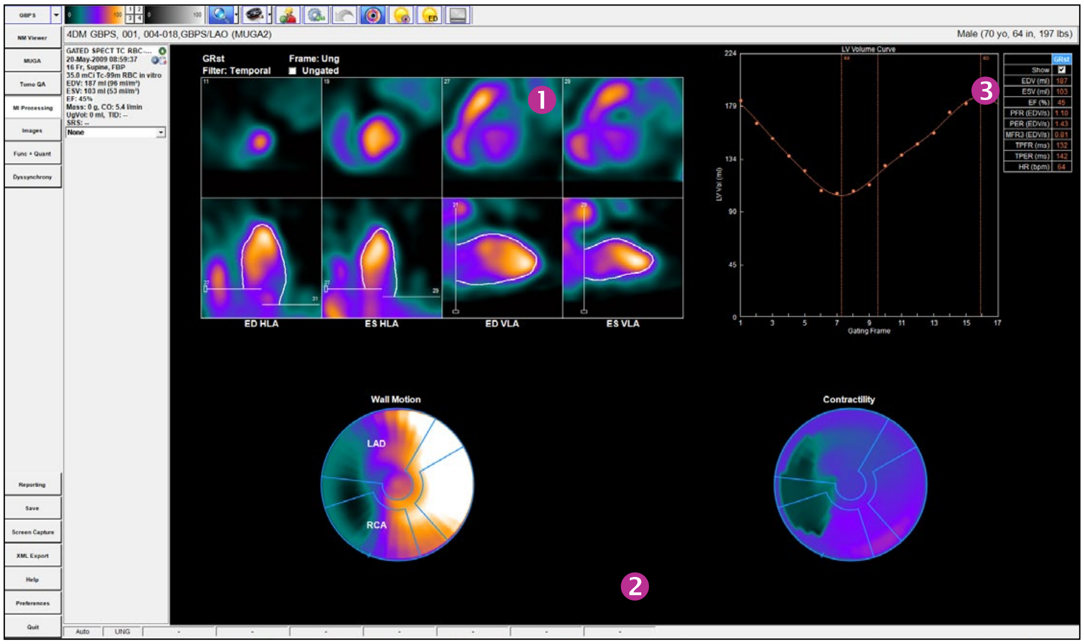
Upon launching a patient in Corridor4DM for the first time, the program automatically quantifies the study using Corridor4DM default algorithm settings. The **MI Processing screen** allows users to define LV dataset alignments, apical and basal limits, and LV centers on the VLA, SA, and HLA slices. Users should review all reconstructed datasets on the **MI Processing** screen *(Figure 7.12)*.

The user should confirm that the basal limits are consistent between datasets and that the Corridor4DM 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 Corridor4DM 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). For volume estimates, the basal limit is typically placed at the end of the LV as seen

If only endo- and epicardial 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 GBPS, 001, 004-018,GBPS/LAO (MUGA2)

Male (70 yo, 64 in, 197 lbs)

GATED SPECT TC RBC....
20-May-2009 08:59:37
16 Fr, Supine, FBP
35.0 mCi Tc-99m RBC in vitro
EDV: 187 ml (96 ml/m²)
ESV: 103 ml (53 ml/m²)
EF: 45%
Mass: 0 g, CO: 5.4 l/min
UgVol: 0 ml, TID: --
SRS: --
None

	GRst
Show	☑
EDV (ml)	187
ESV (ml)	103
EF (%)	45
PFR (EDV/s)	1.10
PER (EDV/s)	1.43
MFR3 (EDV/s)	0.81
TPFR (ms)	132
TPER (ms)	142
HR (bpm)	64

Figure 7.12: The MI Processing screen with a single gated blood pool rest dataset displays the following objects: ❶ Processing Splash, ❷ Processing Polar Map, and ❸ LV Volume Curve.

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.

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.

Activating the **Contours** tool *(Figure 7.13)* applies white contour overlays on the endocardial 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 functional review portion of the workflow.

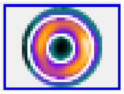
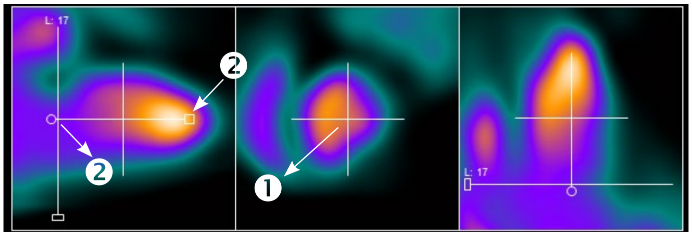


Figure 7.13: *Contours tool*

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 7.14)*. Centering, orientation and axial limits are adjusted using the sliders as shown in *(Figure 7.15)*.

Figure 7.14: *Manual Processing tool*

If the cardiac 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.

❶	Proper positioning of the LV center aligns the crosshairs in the center of the lumen.	 ***Figure 7.15:*** *Examples of proper LV center, apical and basal limits positioning*
❷	Proper positioning of the apical and basal limits are at the tip of the apical endocardium and at the mitral valve plane.	

If the dataset has significant extra-cardiac activity, click the **Constraints** tool *(Figure 7.16)* 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 7.17)*. Once adjustments to the LV center, orientation, and basal limit are complete, the user must click the **Process** tool *(Figure 7.18)* to generate the new surfaces.

If both epi- and endocardial surfaces are generated by 4DM, the incorrect radiopharmaceutical was assigned to the dataset. Check the Special File Strings for Blood pool studies by clicking on the Dataset Matching Strings button within the Preferences menu. To learn more about editing matching strings, go to User Preferences.

If the dataset needs to be processed from scratch (i.e. no initial estimates from Corridor4DM), click the **Reset** tool *(Figure 7.19)* and then set the center, angulation, valve plane location and click the Process tool to reprocess.

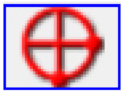
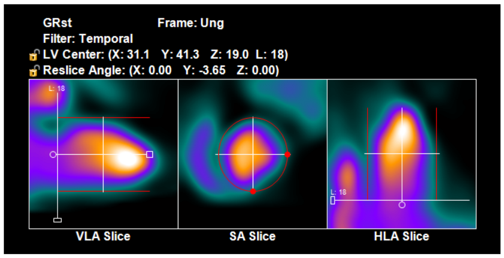


Figure 7.16: *Constraints tool*



GRst
Frame: Ung
Filter: Temporal
LV Center: (X: 31.1 Y: 41.3 Z: 19.0 L: 18)
Reslice Angle: (X: 0.00 Y: -3.65 Z: 0.00)

Figure 7.17: *Constraints activated and properly positioned*

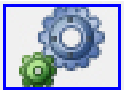


Figure 7.18: *Process tool*

Figure 7.19: *Reset tool*

LV Surface Editor

Corridor4DM includes the LV Surface Editor tool, for use in rare cases where standard automated and manual processing does not output optimal LV surfaces. Clinical cases this can occur on are: large fixed defects where an entire wall has little to no uptake; or extreme extra-cardiac activity that isn't corrected with use of the Constraints Tool. See the LV Surface Editor section for steps to estimate and display location of the left wall when faced with such patient studies.

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 7.20)* represents the GBPS dataset as SA, HLA, and VLA **Splash Objects**. Corridor4DM 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.

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

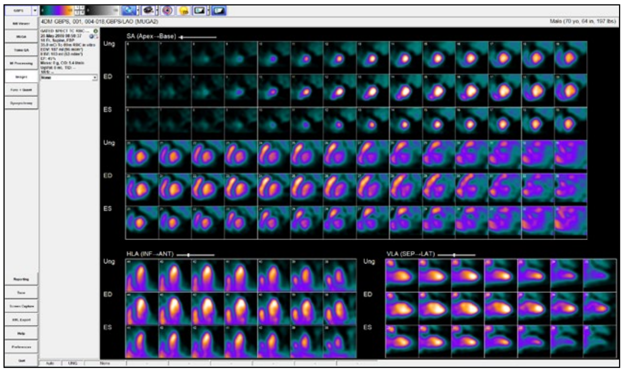


Figure 7.20: *The Images screen with a GBPS dataset displayed. This screen is used primarily to perform qualitative review of the Splash Objects in all three orthogonal planes.*

GBPS Quantitative Functional Review and Final Interpretation

GBPS Quantitative Functional / Final Review

Functional quantitation for GBPS refers to correlating the clinician’s visual estimates with the following Corridor4DM-calculated parameters:

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

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

Func+Quant

Corridor4DM recommends utilizing the **Func+Quant** screen *(Figure 7.21)* 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 gated slices. The Polar Maps allow the user to view Wall Motion while visually comparing to the relative score calculations visible in the Scores Objects.

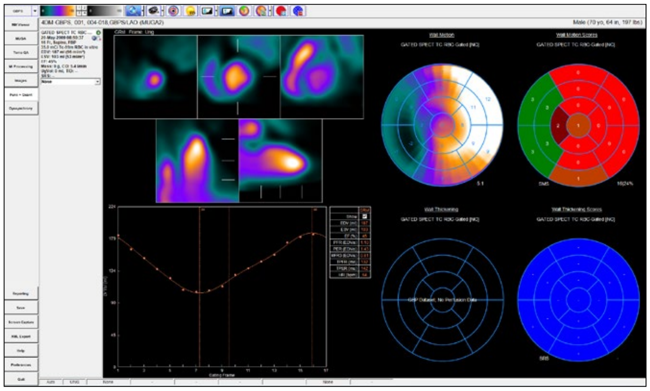


Figure 7.21: *The Func+Quant screen displays the LVEF, Splash Objects, Polar Maps and Scores Objects, and the LV Volume Curve together all on one screen*

Dyssynchrony

The **Dyssynchrony** screen was created for assessing the phases of contraction for the left ventricle *(Figure 7.22)*. 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:

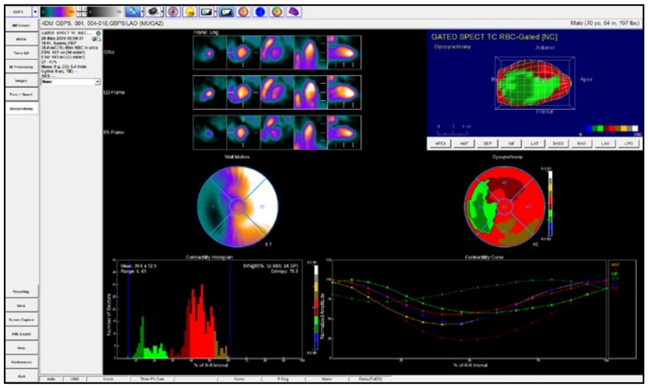


Figure 7.22: *The Dyssynchrony screen was created for assessing the phases of contraction for the left ventricle*

- **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 7.23)***:** Choose between Time to Peak Thickening using First Harmonic Fit, Time to Peak Thickening, and Time to Peak Contractility.

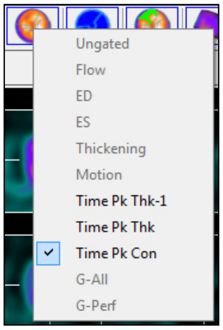


***Figure** 7.23:*
Raw Map Menu

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.

Conclusion

This concludes your GBPS Clinical Workflow Tutorial. Prior to exiting the program, users should ensure to save the Corridor4DM result files. Technologists can transfer the saved results and image datasets to the interpreting physician for review. Corridor4DM recognizes the most current saved result files, so if physicians make any changes to the saved study they should save the updated results.

CHAPTER 8

MYOCARDIAL BLOOD FLOW AND RESERVE

Quantitative Coronary Flow Reserve (CFR)

The **Reserve** screen *(Figure 8.1)* provides the capability to process and review dynamic cardiac PET and SPECT datasets from validated camera systems. 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.

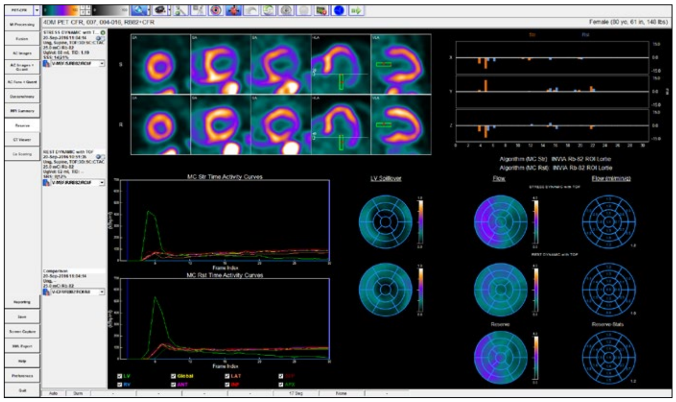


***Figure 8.1:** The Corridor4DM Reserve Screen*

CFR processing should be preceded by the QA workflow on the MI Processing screen to verify accurate automated LV contour generation on all datasets. These LV contours are used for ROI/bounds placement within the Reserve screen and also to help do quality checks for patient motion and flow model processing.

Input Data

A dynamic 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 dataset is loaded into Corridor4DM, 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 8.2)*. 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 image review and processing screens, as well as the **Reserve** screen.

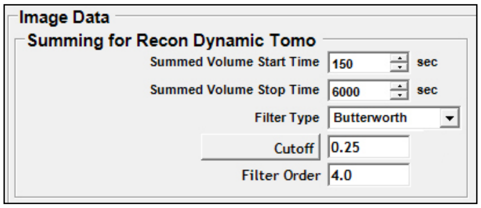


Image Data

Summing for Recon Dynamic Tomo

Summed Volume Start Time: 150 sec

Summed Volume Stop Time: 6000 sec

Filter Type: Butterworth

Cutoff: 0.25

Filter Order: 4.0

***Figure 8.2:** Image Data section of the Image Display Page within Preferences*

CFR QA, Processing, and Results Review

Stress and rest datasets are displayed and processed together on the Reserve screen which has two modes: **QA** and **Results Mode**. The Reserve screen defaults to the **QA Mode** when unprocessed stress and/or rest dynamic data is displayed. The Reserve screen defaults to **QA Mode** to ensure the results have been properly QA'd.

QA Mode Workflow

1. **Evaluate data for motion and correct frames if:** Respiratory motion prevalent in dynamic data and is known to affect flow and reserve results so it is important to evaluate every patient's

dynamic dataset(s) for the presence of motion. To check this, click the Cine tool in the toolbar and view the dynamic frame sequences for motion of the blood pool uptake spilling over into the Corridor4DM-generated LV contours *(Figure 8.3)*, or for the LV tissue frames to show tissue uptake outside of the LV contours.

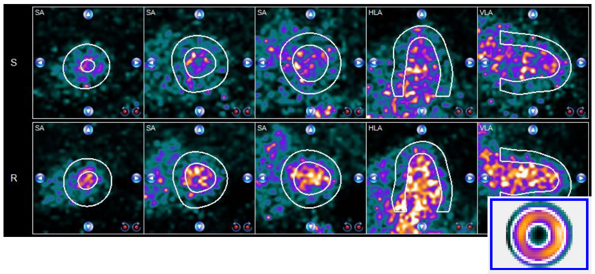


Figure 8.3: *Dynamic frame sequences with contours enabled*

- To evaluate for motion frame-by-frame, pause the Cine, and click the **Cine** tool drop-down arrow *(Figure 8.4)* to access the frame slider. Scroll the slider through all frames in the sequence and review the stress and/or rest slice viewports below.

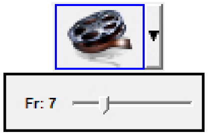


Figure 8.4: *Cine tool with frame slider*

- If motion is present, manually correct for motion in each frame where the dynamic tracer activity does not align properly to the displayed LV contours, by clicking directly on the image and dragging it to the desired location. Alternatively, apply adjustments in the X (left/right) and/or Y (up/down) directions *(Figure 8.5)* using the Fine Pan arrow tools where each click represents 1 mm of movement.

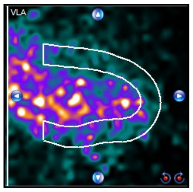


Figure 8.5: *Fine Pan arrow tools and Fine Rotate tools*

- All preliminary motion correction changes to the data appear on the motion correction graph to the right of the viewports, showing X, Y, and Z updates made throughout the frame sequence, in mm of motion. To view preliminary flow results and apply the corrections, click the **Apply** tool *(Figure 8.6)* after corrections are made.

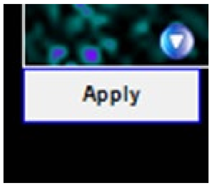


Figure 8.6: *Apply tool*

2. **Verify the bounds/ROI are properly positioned, depending on default method selected**: Turn the Cine tool off to view the bounds/ROI placement. Corridor4DM defaults to the ROI method, with others available.

- When either the Factor Analysis or the Factor Analysis-Hybrid algorithms are applied, the ellipsoid-cylindrical bounding volume can be dragged to change the height or width of the factor analysis bounds in each viewport *(Figure 8.7)*. The user should adjust the size of the bounds to ensure inclusion of the blood pool regions and to exclude non-cardiac regions.

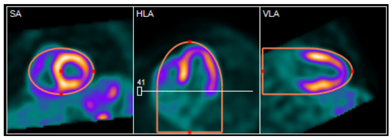


Figure 8.7: *Factor Analysis algorithm*

- 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 8.8)*. The user may increase the size of the ROI to improve statistics in the LV blood Time Activity Curve (TAC).

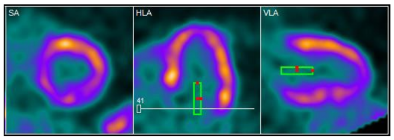


Figure 8.8: *ROI algorithm*

Prior to proceeding to the Results Mode, check to verify the perfusion and flow normals databases are selected for stress, rest and CFR. Selection of these ensures CFR quantification of perfusion defect regions on the Reserve Results page, as well as other derived comparison results to relative perfusion polar maps.

3. **Corridor4DM automatically processes flow results when: any motion correction is applied; changes are made to the ROI/Bounds; or a different flow model is selected for processing.** 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.

4. **Review Preliminary Results**: Once processing completes, additional QA results display on the QA Mode of the Reserve screen to permit detailed analysis of the acquisition, motion correction, and kinetic flow model results. **It is important to click Save in the Control Panel once completed with Reserve processing and QA.** Once reviewed, to enter the Results Mode, click the **Next** button *(Figure 8.9)* in the Toolbar.

Figure 8.9: *Next tool*

Preliminary Results Review in QA Mode

It is important to click Save in the Control Panel once completed with Reserve processing and QA. Review the following information prior to continuing to the Results Mode.

Time Activity Curves (TACs)

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 8.10)*. 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.

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 TACs *(Figure 8.11)*. 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.

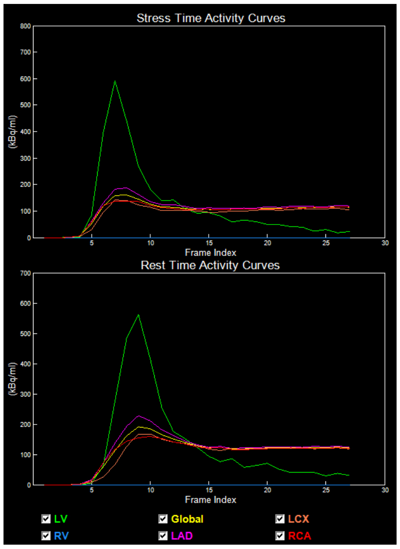


Figure 8.10: *Time Activity Curves*

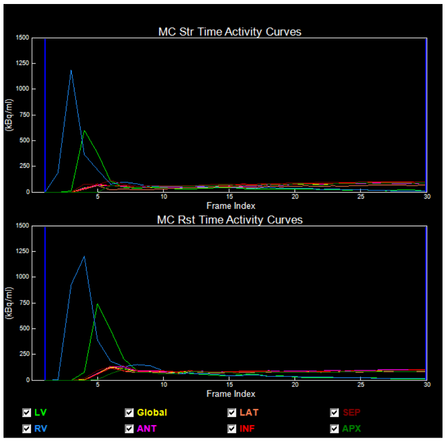


Figure 8.11: *TACs after Factor Analysis algorithm is processed*

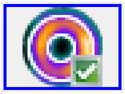


Figure 8.12: *QA Images tool*

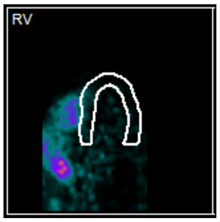


Figure 8.13: *Correspondence of the RV factor to the RV blood pool.*

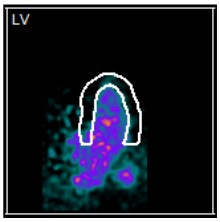


Figure 8.14: *Correspondence of the LV factor to the LV blood pool.*

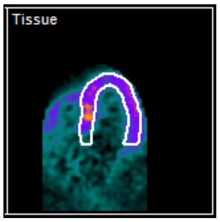


Figure 8.15: *Correspondence of the tissue factor to the myocardium.*

- Second, the user should examine the factor analysis by clicking the QA Images tool *(Figure 8.12)*. 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 8.13)*, LV *(Figure 8.14)*, and tissue factor images *(Figure 8.15)*.
- 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.

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

☑ LV ☑ Global ☑ LAT ☑ SEP

☑ RV ☑ ANT ☑ INF ☑ APX

Figure 8.16: *Time Activity Curve check boxes*

- **LV, RV, Global, ANT, LAT, INF, SEP, APX check boxes** *(Figure 8.16)***:** 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).
- **Start/Stop blue reference lines** *(Figure 8.17)***:** Allows manual updates to the start and end point of CFR analysis. Click and drag to the desired point on the TAC.

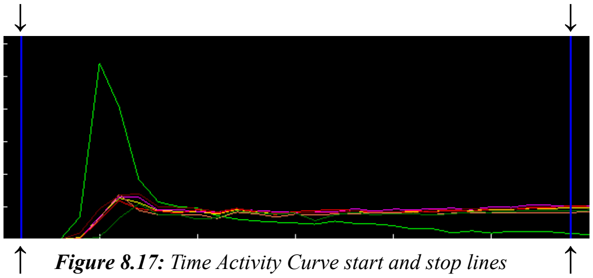
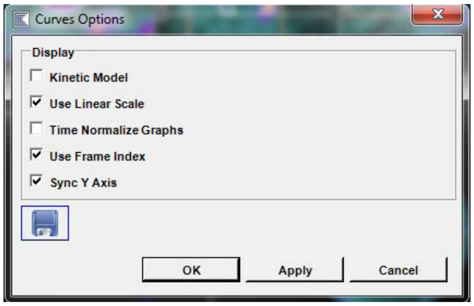


Figure 8.17: *Time Activity Curve start and stop lines*

- Right-click the Time Activity Curves to display the Curves Options window *(Figure 8.18)* 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).



Curves Options

Display

☐ Kinetic Model

☑ Use Linear Scale

☐ Time Normalize Graphs

☑ Use Frame Index

☑ Sync Y Axis

Figure 8.18: *Curve Options window*

- **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.
- **Use Frame Index:** When checked, graphs the activity concentration versus frame index. When unchecked, graphs the activity concentration versus time.
- **Sync Y Axis:** Synchronizes the y-axis scales for stress and rest to compare curve peaks more accurately.

LV Spillover

Corridor4DM displays stress and rest Spillover maps *(Figure 8.19)* next to the TACs to help aide in the detection of patient motion after results have been processed. The polar maps represent a summed image of the dynamic sequence. These should show little to no activity with homogenous appearance, signifying that blood pool activity is not spilling over into the LV contours displayed above in the slice viewports. If the polar maps show mottled, heterogeneous activity, this signifies a need to make additional motion correction changes in the viewports above.

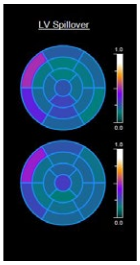


Figure 8.19: *Spillover maps*

Flow Polar Maps

Preliminary stress, rest, and reserve flow calculations *(Figure 8.20)* display in two columns:

- The middle column displays, top-down: the absolute stress, rest, and reserve flow values in units of ml/min/g, sampled over 460 sectors to provide a pixel-level flow polar map for review.
- The right-most column displays the flow values without pixel data included, called Stats maps. These show the absolute flow and reserve value results based on the overlay map selected. The global LV flow value is displayed at the 5 o'clock position just outside of each of these polar maps, for stress, rest, and reserve.

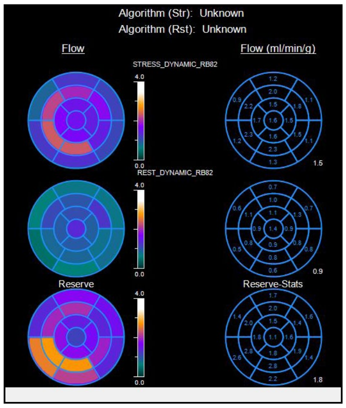


Figure 8.20: *Flow Polar Maps*

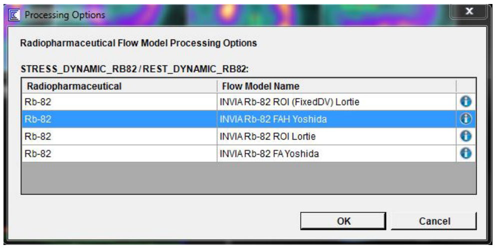
Figure 8.21: *QA Mode Toolbar Options*

QA Mode Toolbar Options *(Figure 8.21)*:

1. **Dual Colorbar Tool:** 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.
2. **Magnification Tool:** Adjust the image display size.
3. **Cine Tool:** Activate/Deactivate cine of dynamic sequences. When active, motion correction tools display on all viewports. When deactivated, using the frame slider from the drop-down also activates the motion correction tools. Cine must be deactivated to view the flow ROI or Bounds.

Prior to processing the flow results, check to verify the perfusion and flow normals databases are selected for stress, rest and CFR. Selection of these ensures CFR quantification of perfusion defect regions on the Reserve Results page, as well as other derived comparison results to relative perfusion polar maps.

4. **Processing Options Tool:** Click to view and select the available flow models defined to fit the dynamic data for estimating myocardial blood flow and reserve. Click the Details icon next to the Flow Model Name to view the characteristics of each flow model *(Figure 8.22)*. Corridor4DM can be defaulted within Preferences to the preferred model for each tracer, to permit skipping this step each time the data is launched.



Radiopharmaceutical Flow Model Processing Options

STRESS_DYNAMIC_RB82 / REST_DYNAMIC_RB82:

Radiopharmaceutical	Flow Model Name	
Rb-82	INVIA Rb-82 ROI (FixedDV) Lortie	ⓘ
Rb-82	INVIA Rb-82 FAH Yoshida	ⓘ
Rb-82	INVIA Rb-82 ROI Lortie	ⓘ
Rb-82	INVIA Rb-82 FA Yoshida	ⓘ

***Figure 8.22:** Processing Options Tool*

- 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.
- The **FlowQuant (FQ) ROI Lortie** processing option samples the LV and blood TAC from a ROI, but uniquely utilizes a constant distribution volume and frame time weighting in the kinetic modeling.
- 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.
  NOTE: With v2018 and later, this model must be manually created.
- 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.
  NOTE: With v2018 and later, this model must be manually created.

5. **Residual Subtraction Toggle Tool:** This tool is necessary in current SPECT dynamic protocols using Tc99m-based tracers, where due to the longer half-life of approximately 6 hours, there is residual activity remaining in the heart from the first to the second acquisition. This tool is enabled/available in cases where the time between the first and second acquisitions is less than the time difference threshold, where the tracer level of the second dataset hasn't decayed to 5% or less from the first dataset acquisition time. Corridor4DM will use the frame prior to the start of the input curve on the TAC of the second acquisition as the baseline activity and subtract this from all subsequent frames in the dynamic sequence.

- To apply this tool, click to turn on Residual Subtraction in the Toolbar. Once the Residual Subtraction tool is clicked, Corridor4DM automatically computes the second acquisition with residual subtraction applied. To permanently save the CFR processing, click the Save button in the Control Panel.
- Corridor4DM will disable this tool when the dataset acquisition times between the first and second datasets meet or exceed the time difference threshold. The time difference threshold is calculated taking into account the radiotracer's half-life, decay ratio, and the timestamp of the first and second acquisitions.

6. **Contours Toggle Tool:** Overlay Corridor4DM-generated LV surface contours on the images.

7. **Auto Motion Correction Tool:** This tool turns on and off the ability to automatically correct the image data for motion that may occur during the dynamic acquisition.

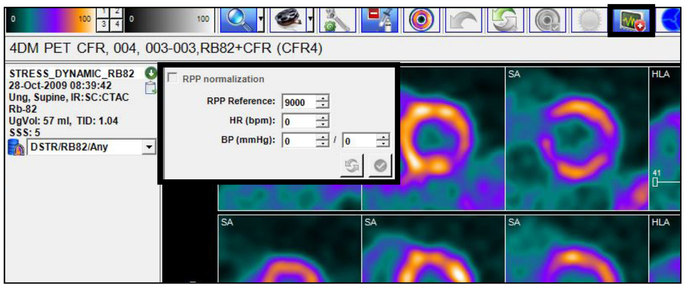
8. **Undo Tool:** Once changes are made to correct for motion or ROI placement, this tool becomes active to undo the last move with each click of the tool.

9. **Reset Tool:** Resets the screen to an unprocessed state.

10. **QA Images Tool:** Available for FA and FAH methods only. The image viewports display the output of the factor analysis for stress and rest. The user should visually confirm the factor analysis accurately identified the RV, LV, and tissue factor time points by showing RV blood pool uptake, LV blood pool uptake and Tissue uptake in these viewports. Click the RV, LV or Tissue viewport labels to change assignments if necessary.

11. **Frame Normalization Tool:** Available only when Cine mode is on, this normalizes each frame in the dynamic sequence to the peak intensity in the volume.

12. **Rate Pressure Product (RPP)** *(Figure 8.23)*: RPP is defined as the heart rate (HR) in beats-per-minute (bpm) multiplied by the systolic blood pressure (SBP, in mmHg). RPP provides a measure of a patient's cardiac workload and hemodynamic response. Due to patient-to-patient variation in HR and SBP during stress and rest imaging, this can affect the absolute coronary flow and coronary flow reserve values. The RPP tool is available to provide RPP-normalized flow values on a case-by-case need.



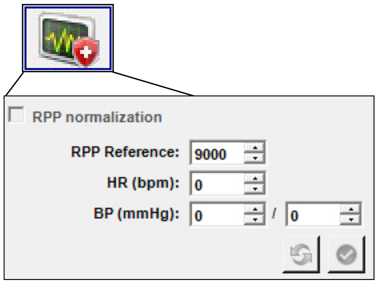
4DM PET CFR, 004, 003-003,RB82+CFR (CFR4)

STRESS_DYNAMIC_RB82
28-Oct-2009 08:39:42
Ung, Supine, IR:SC:CTAC
Rb-82
UgVol: 57 ml, TID: 1.04
SSS: 5
DSTR/RB82/Any

☐ RPP normalization
RPP Reference: 9000
HR (bpm): 0
BP (mmHg): 0 / 0

Figure 8.23: *Rate Pressure Product tool*

- Click the RPP toggle to access the RPP options window *(Figure 8.24)*, where stress and/or rest HR and blood pressure are manually input. For the BP, enter the systolic BP in the left field, and the diastolic BP in the right field.
- The RPP Reference value is defined at 9000, the mid-point of the normal range (6000 – 12000) in the normal patient population. The RPP Reference is definable, but likely rarely changed unless a particular RPP reference value is preferred.



☐ RPP normalization
RPP Reference: 9000
HR (bpm): 0
BP (mmHg): 0 / 0

Figure 8.24: *RPP options window*

- Once the HR and BP are entered, click the RPP corrected checkbox, and then click Apply, to calculate new flow and reserve calculations for the patient.
- To see the dataset's updated flow calculations, without calculating new reserve calculations, after entering HR and BP, click Apply, but do not click the RPP normalization checkbox.
- Click the Reset button to reset the values.
- Click Save in the Corridor4DM Control Panel to save the reserve results and all other Corridor4DM calculations before exiting the program. Once a dataset has been RPP-normalized, the global flow value and tabular flow values for that dataset will display an asterisk (*) next to them. Additionally, a footnote with an asterisk (*) appears below the Flow Table Results.

13. **Segmental Overlay Tool:** Displays blue overlays on the Spillover, Flow, and Reserve polar maps. Options range from the default vascular option to 20 segments.

14. **Next Tool:** Clicking this moves the user from **QA Mode** to **Results Mode**.

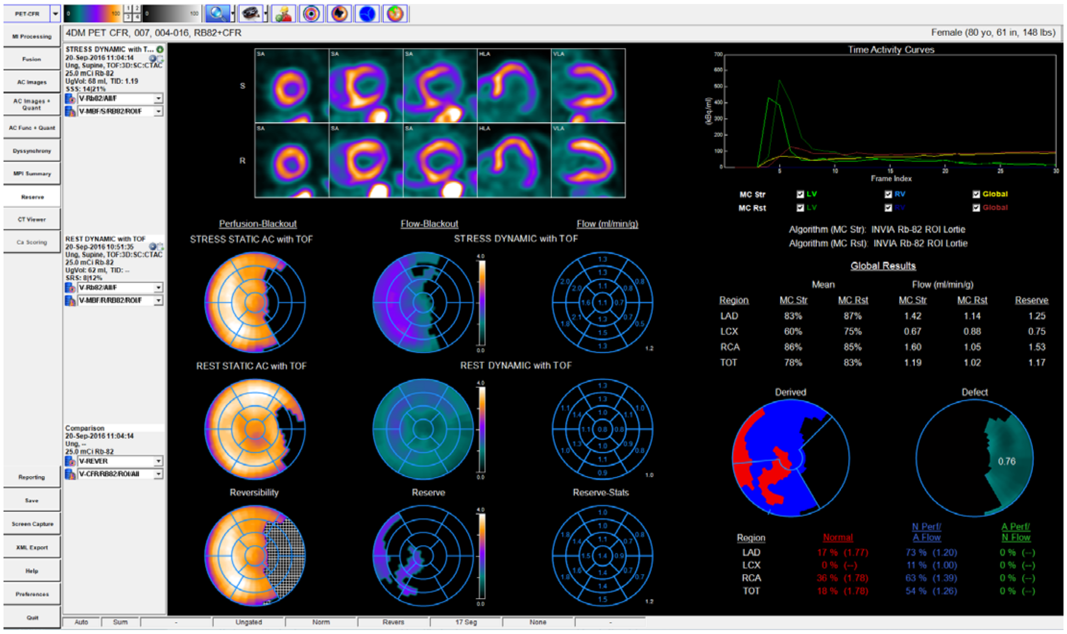
Once all data is confirmed in QA Mode, click the Next button in the Toolbar to enter the Results Mode.

Results Mode Workflow:

1. Once the **Next** button is clicked, the **Results Mode** displays primary information needed to interpret flow and reserve findings. From this screen, if changes to the results are desired, click the **Manual Processing** tool *(Figure 8.25)* in the Toolbar to return to QA Mode.

***Figure 8.25:** Manual Processing tool*

2. In **Results Mode**, the dynamic input data is available to cine and review LV contours while viewing statistical results of the processing *(Figure 8.26)*.



4DM PET CFR, 007, 004-016, RB82+CFR

Female (80 yo, 61 in, 148 lbs)

STRESS DYNAMIC with T...
20-Sep-2016 11:04:14
Ung, Supine, TOF:3D:SC:CTAC
25.0 mCi Rb-82
UgVol: 68 ml, TID: 1.19
SSS: 14|21%
V-Rb82/All/F
V-MBF/S/RB82/ROI/F

REST DYNAMIC with TOF
20-Sep-2016 10:51:35
Ung, Supine, TOF:3D:SC:CTAC
25.0 mCi Rb-82
UgVol: 62 ml, TID: --
SRS: 8|12%
V-Rb82/All/F
V-MBF/R/RB82/ROI/F

Comparison
20-Sep-2016 11:04:14
Ung, --
25.0 mCi Rb-82
V-REVER
V-CFR/RB82/ROI/All

MC Str ☑ LV ☑ RV ☑ Global
MC Rst ☑ LV ☑ RV ☑ Global

Algorithm (MC Str): INVIA Rb-82 ROI Lortie
Algorithm (MC Rst): INVIA Rb-82 ROI Lortie

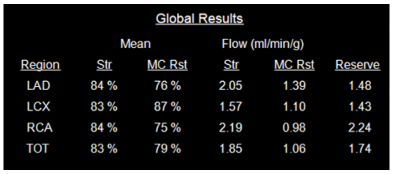
Global Results

	Mean		Flow (ml/min/g)		
Region	MC Str	MC Rst	MC Str	MC Rst	Reserve
LAD	83%	87%	1.42	1.14	1.25
LCX	60%	75%	0.67	0.88	0.75
RCA	86%	85%	1.60	1.05	1.53
TOT	78%	83%	1.19	1.02	1.17

Region	Normal	N Perf/ A Flow	A Perf/ N Flow
LAD	17 % (1.77)	73 % (1.20)	0 % (--)
LCX	0 % (--)	11 % (1.00)	0 % (--)
RCA	36 % (1.78)	63 % (1.39)	0 % (--)
TOT	18 % (1.78)	54 % (1.26)	0 % (--)

***Figure 8.26:** Results Mode*

3. The **Global Results Table** *(Figure 8.27)* 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. The algorithms used for both Stress and Rest are displayed beneath the table for reference.



Global Results

	Mean		Flow (ml/min/g)		
Region	Str	MC Rst	Str	MC Rst	Reserve
LAD	84 %	76 %	2.05	1.39	1.48
LCX	83 %	87 %	1.57	1.10	1.43
RCA	84 %	75 %	2.19	0.98	2.24
TOT	83 %	79 %	1.85	1.06	1.74

***Figure 8.27:** Global Results table*

4. Review the **Polar Maps** and **Tables** *(Figure 8.28)*, left-to-right, to compare relative perfusion findings to absolute flow findings.

   - The left-most column displays, top-down: the stress, rest, and comparison of the two, in standard relative distribution format.

     - The default quant map display is Blackout, where any sector with uptake below the normal threshold is 'blacked-out' to distinguish it from normal uptake sectors. Options for the quant map are available for selection from the Quant Map Tool in the toolbar (e.g., Norm option shows normalized maps to peak intensity within the myocardium).

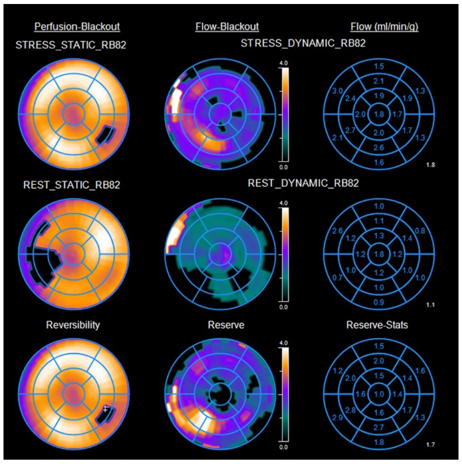


***Figure 8.28:** Result Mode Polar Maps and Tables*

- The left-middle column displays, top-down: the absolute stress, rest, and reserve flow values in units of ml/min/g, sampled over 460 sectors to provide a pixel-level flow polar map for review.
- The right-middle column displays the flow values without pixel data included, called Stats maps. These show the absolute flow and reserve value results based on the overlay map selected. The global LV flow value is displayed at the 5 o'clock position just outside of each of these polar maps, for stress, rest, and reserve.
  - The vascular overlay displays on the polar maps by default. Click the **Segmental Overlay Options** tool in the toolbar *(Figure 8.29)* to select a different overlay (e.g., select 5 Seg option to review the walls).

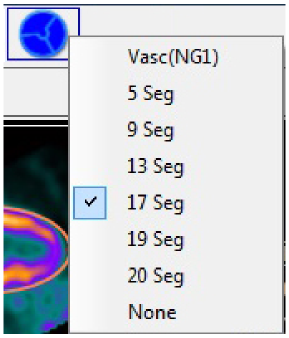
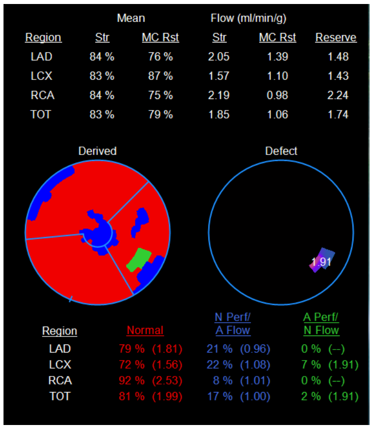


Figure 8.29: *Segmental Overlay Options dropdown*

- The right-most column displays a **CFR Defect Polar Map** above a **CFR Derived Polar Map** *(Figure 8.30)***.**
  - **The CFR Defect Polar Map** shows areas of perfusion defect on the Reversibility map in the selected color scheme. All other sectors are blacked out. Segmental overlays are not allowed on this polar map. Defects are labeled with reserve mean value, with a maximum of 5 non-contiguous defect regions allowed.
  - **The CFR Derived Polar Map** incorporates the CFR Defect Polar Map results and the Reversibility Polar Map results and compares them in vascular territories and globally, to provide the map and the percentage information below in the Derived Results Table. Region color in the polar map corresponds with the text colors in the table, with exception of the black areas which use white text due to the black background of the application.



	Mean		Flow (ml/min/g)		
Region	Str	MC Rst	Str	MC Rst	Reserve
LAD	84 %	76 %	2.05	1.39	1.48
LCX	83 %	87 %	1.57	1.10	1.43
RCA	84 %	75 %	2.19	0.98	2.24
TOT	83 %	79 %	1.85	1.06	1.74

Region	Normal	N Perf/ A Flow	A Perf/ N Flow
LAD	79 % (1.81)	21 % (0.96)	0 % (--)
LCX	72 % (1.56)	22 % (1.08)	7 % (1.91)
RCA	92 % (2.53)	8 % (1.01)	0 % (--)
TOT	81 % (1.99)	17 % (1.00)	2 % (1.91)

Figure 8.30: *CFR Defect and Derived Polar Maps*

    - **Red:** Areas quantified as normal perfusion and normal reserve. Table heading shows as "Normal."
    - **Blue:** Areas quantified as normal perfusion with abnormal reserve. Table heading shows as "N Perf/ A Flow."
    - **Green:** Areas quantified as abnormal perfusion with normal reserve. Table heading shows as "A Perf/N Flow."

Results Mode Toolbar Options *(Figure 8.31)*:

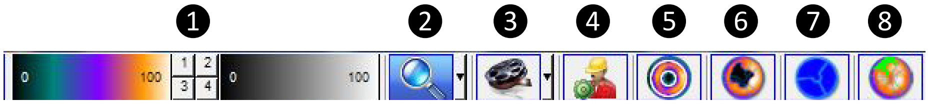


Figure 8.31: *Results Mode Toolbar*

1. **Dual Colorbar Tool:** 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.

2. **Magnification Tool:** Adjust the image display size.

3. **Cine Tool:** Activate/Deactivate cine of dynamic sequences. When active, motion correction tools display on all viewports. When deactivated, using the frame slider from the drop-down also activates the motion correction tools. Cine must be deactivated to view the flow ROI or Bounds.

4. **Manual Processing Tool:** Click to return to the QA Mode within the Reserve Screen.

5. **Contours Toggle Tool:** Overlay Corridor4DM-generated LV surface contours on the images.

6. **Quant Map Menu:** Controls the type of quantification (Quant) performed on the raw data. See Chapter 3: Corridor4DM Screens and Controls for more information.

7. **Segmental Overlays Menu:** Changes the overlay used to calculate regional statistics for the Quant or Comparison map. Note that the CFR Defect Polar Map is locked to not allow overlays. The Derived Polar Map is locked to showing a vascular overlay to correspond with results calculated in the Derived Results Table. See Chapter 3: Corridor4DM Screens and Controls for more information.

8. **Comparison Map Menu:** Controls the information displayed in a comparison map, representing data generated from a comparison of two datasets. See Chapter 3: Corridor4DM Screens and Controls for more information.

    - Prior to exiting Corridor4DM, ensure to click Save in the Control Panel to save all perfusion and flow results information *(Figure 8.32)*.

Figure 8.32: *Save control*

CHAPTER 9 INFLAMMATORY PROTOCOL REVIEW

Inflammatory Screen

Sarcoidosis patients with cardiac involvement account for most deaths associated with the disease. Identifying presence and extent of cardiac sarcoidosis before, during, and after immunosuppressive therapy aides in determining a sarcoid patient's prognosis, and guides whether treatments are working to improve cardiac function.

Specific cardiac inflammatory preparation, dosing, and imaging protocols have been developed to compare rest perfusion images to rest F-18 FDG PET/CT metabolic images. Active cardiac inflammation is identified in areas where LV perfusion uptake is normal, and FDG LV uptake is abnormally high. In order to identify cardiac inflammatory involvement, LV contours generated in Corridor4DM on the rest perfusion dataset are indirectly registered and applied to the FDG study to identify if any FDG activity is within the LV myocardial borders. Further, if there are focal areas of FDG activity within the LV myocardium, quantitative SUV thresholding tools in combination with rest perfusion comparison to normals databases provide regional and global results to identify normal, infarct, and mixed tissue versus inflamed myocardium. Utilize the **Inflammatory** screen's Indirect Registration Mode within Corridor4DM to perform quality assurance and registration to processed inflammatory results and review them in Results Mode.

Input Data

The **Inflammatory** workflow and screen include some data requirements the user should be aware of prior to use.

Corridor4DM license requirements:

The Corridor4DM license must include the PET package (to launch the rest perfusion PET and F-18 FDG PET datasets) **and** Hybrid CT option if the CT datasets are to be passed to Corridor4DM for purposes of indirect registration.

Note: If using rest SPECT data for the rest perfusion, the combined SPECT + PET license is required. NM and PT attenuation maps can be used in place of the CT datasets or CT-attenuation maps.

Indirect registration processing requirements:

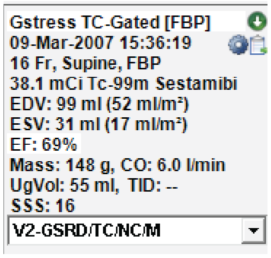
ALL of the following four (4) datasets must be launched in Corridor4DM in order for the Inflammatory screen to be enabled/active:

1. Static/summed rest perfusion dataset (can be PET or SPECT but must be attenuation-corrected) **and**
2. Corresponding CT (or attenuation map) used for attenuation correction of rest perfusion dataset
3. Static/summed PET F-18 FDG Inflammatory dataset (hereafter referred to as the inflammatory dataset) **and**
4. Corresponding CT (or attenuation map) used for attenuation correction of PET F-18 FDG dataset

Inflammatory workflow and screen requirements:

Because of current multiple uses of F-18 FDG (e.g., for viability and inflammatory protocols), it is necessary to ensure that the F-18 FDG inflammatory dataset name includes a unique identifier, such as "Sarcoid," to ensure the Inflammatory workflow and screen will automatically be available for use.

Gated rest perfusion and Gated FDG-18 datasets are also typically reviewed in 4DM but are not requirements for the Inflammatory screen. They are usually reviewed within other pages such as the MI Processing, AC Func + Quant, and AC MPI Summary screens to evaluate functional results such as the LVEF %, ED/ES Volumes, and wall motion. If static and gated datasets are present, the static datasets take precedence to display on the Inflammatory screen.



Gstress TC-Gated [FBP]
09-Mar-2007 15:36:19
16 Fr, Supine, FBP
38.1 mCi Tc-99m Sestamibi
EDV: 99 ml (52 ml/m²)
ESV: 31 ml (17 ml/m²)
EF: 69%
Mass: 148 g, CO: 6.0 l/min
UgVol: 55 ml, TID: --
SSS: 16
V2-GSRD/TC/NC/M

***Figure 9.1:** Right-click in the Dataset Information Panel*

- Corridor4DM includes the ability to add site-specific series descriptions, called dataset matching strings. This is accomplished in Corridor4DM Preferences on the Dataset Matching Strings Page in the FDG Inflammatory field. Please see Chapter 12: User Preferences for more information.
- As a fallback in cases where the FDG dataset does not include a unique identifier, Corridor4DM includes the capability to assign the datasets as Inflammatory protocols.
    - While on the MI Processing screen, right-click in the Dataset Information Panel *(Figure 9.1)* and select the F-18 FDG Inflammatory option in the Radiopharmaceutical drop-down menu for the F-18 FDG Dataset *(Figure 9.2)*.
- **SUV calculations requirements:**
    - The rest perfusion and F-18 FDG datasets must include the injected radiopharmaceutical and dose, injection time, and patient weight. This information can be input in the Dataset Information window, accessed via right-click on the Dataset Information Panel.

Panel 2
STATIC FDG AC
28-May-2014
15:21:24
Transverse Data
Transverse
AC FDG
9.0
14 : 01 : 41
F-18 FDG

***Figure 9.2:** Dataset Information window with F-18 FDG Inflammatory drop-down selected*

If all four datasets are not loaded, and the F-18 FDG dataset is not properly named, the Inflammatory screen will not be available for use. If the patient weight, radiopharmaceutical, injected dose, and injection time are not entered, SUV will not calculate.

Inflammatory QA, Processing, and Results Review

The MI Processing and Inflammatory screens are utilized for this workflow. All other screens in the workflow are available for purposes of reviewing the standard gated and static/summed datasets for perfusion and functional review as covered earlier in this chapter.

MI Processing Screen

As with all Corridor4DM workflows, the user should begin the quality assurance of the automated processing on the **MI Processing** screen *(Figure 9.3)* to verify the contours generated on the **rest perfusion dataset(s)** properly track the endo- and epicardial surfaces of the left ventricle. These will be used to indirectly register and apply onto the FDG datasets. For more information

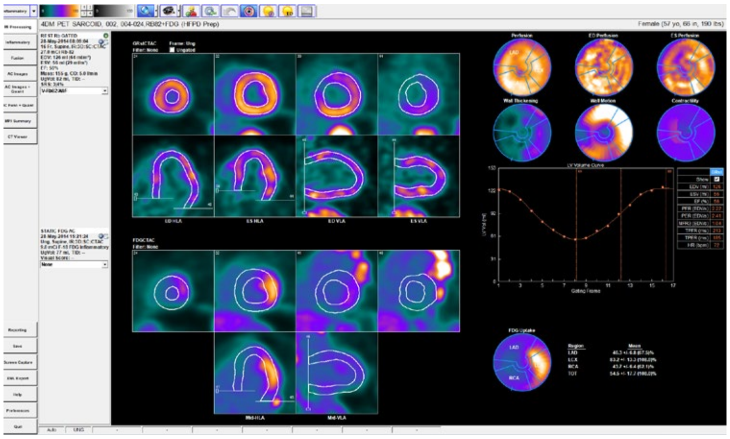


***Figure 9.3:** MI Processing screen*

on QA and processing on the MI Processing screen, please see that section of this chapter.

After confirmation of the rest perfusion contours is completed, continue to the Inflammatory screen . The F-18 FDG Gated and Static datasets in most cases will not have enough LV myocardial activity available to permit automatic generation of accurate LV contours.

Inflammatory Screen

The **Inflammatory** screen includes two modes: **Indirect Registration Mode** and **Results Mode**. The Indirect Registration Mode is initially displayed and utilized to verify the co-registration of the perfusion and inflammatory datasets to their respective CT datasets.

Indirect Registration Mode

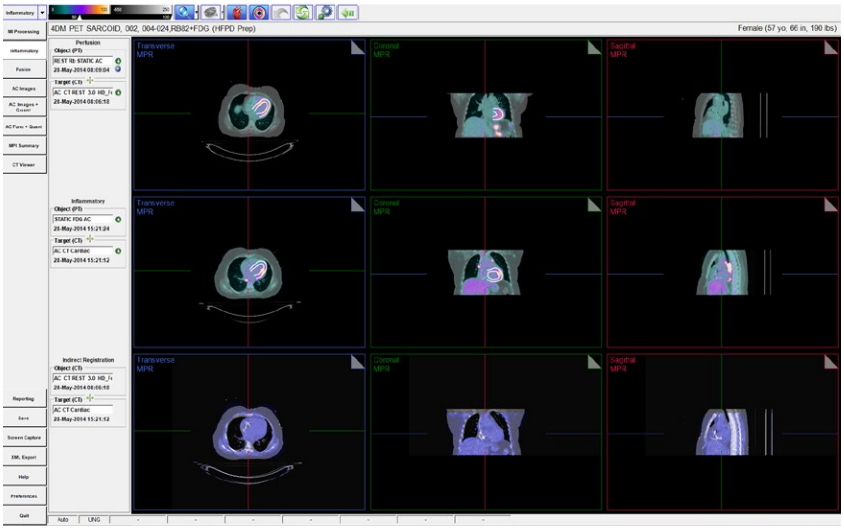
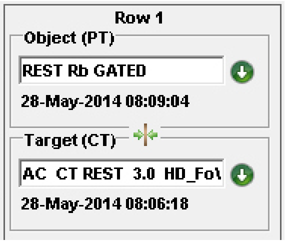


Figure 9.4: *Inflammatory Screen*

1. Click in the workflow screens list to display the **Inflammatory screen** *(Figure 9.4)*. If the screen is not available, verify that the datasets loaded meet the requirements noted above.
2. The **Indirect Registration Mode** of the screen is utilized to:

    a. **Row 1** (Figure 9.5): Check the co-registration of the perfusion dataset to its respective CT or attenuation map. Corridor4DM automatically places the static SPECT or PET as the Object (moveable overlay) and corresponding CT or attenuation map dataset as the Target.



Row 1
Object (PT)
REST Rb GATED
28-May-2014 08:09:04
Target (CT)
AC CT REST 3.0 HD_FoV
28-May-2014 08:06:18

Figure 9.5: *Row 1 on the Inflammatory screen*

        i. Use the plane slicers to triangulate to the heart in all three viewports and scroll through slices using the slicers or dog ears to verify alignment in all three planes (Transverse, Coronal, and Sagittal in default patient orientation).

        ii. Click the **Orientation** Tool to switch to cardiac orientation (SA, HLA, VLA) (Figure 9.6).

Figure 9.6: *Orientation tool*

        iii. If re-alignment is needed, click in a viewport to use the panning or fine/coarse pan/rotate tools embedded on the selected viewports to ensure alignment of the datasets in all viewports (Figure 9.7).

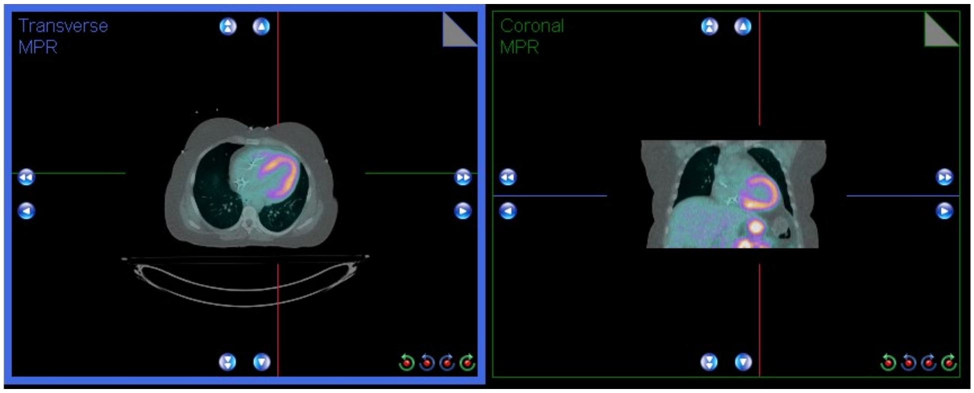
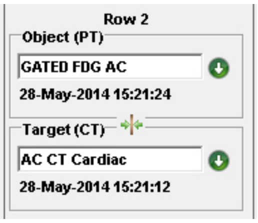


Figure 9.7: *The panning or fine/course pan/rotate tools in the Transverse viewport*

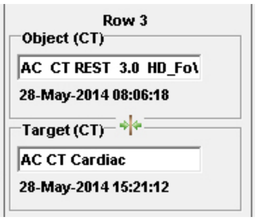
b. **Row 2** *(Figure 9.8)*: Check the co-registration of the inflammatory dataset to its respective CT or attenuation map. Repeat above steps to ensure alignment.

c. **Row 3** *(Figure 9.9)*: Displays the Row 1 CT or attenuation map as the Object in blue, and the Row 2 CT or attenuation map as the Target, in gray. On the Inflammatory screen, the right colorbar defines the Target color scheme for Rows 1, 2, and 3. The Object color scheme in Row 3 can be changed within the Preferences/Colorbars page, in the CT Colorbars section. For more information on colorbar management, see the Colorbar Tools section.



Row 2
Object (PT)
GATED FDG AC
28-May-2014 15:21:24
Target (CT)
AC CT Cardiac
28-May-2014 15:21:12

Figure 9.8: *Row 2 on the Inflammatory screen*

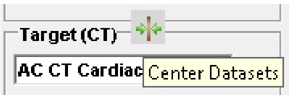


Row 3
Object (CT)
AC CT REST 3.0 HD_Fo\
28-May-2014 08:06:18
Target (CT)
AC CT Cardiac
28-May-2014 15:21:12

Figure 9.9: *Row 3 on the Inflammatory screen*

i. It is likely that these will be mis-aligned since they are different imaging sessions and potentially acquired on different scanner systems, requiring manual alignment. Care should be exercised to ensure these are aligned as best as possible, as this is the indirect registration step that enables placing the perfusion dataset LV contours onto the inflammatory dataset.

ii. If the datasets are grossly off-center, click the **Center Datasets** Tool *(Figure 9.10)* to center them in the viewport before making manual alignment changes.



Target (CT)
AC CT Cardiac
Center Datasets

Figure 9.10: *Center Datasets Tool*

iii. Once the alignment checks are completed in Indirect Registration Mode, click the **Process Tool** *(Figure 9.11)* in the Toolbar to proceed to the Results Mode of the Inflammatory screen.

Figure 9.11: *Process Tool*

Indirect Registration Mode Toolbar Options *(Figure 9.12)*:

1. **Dual Colorbar Tool**: 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. On the Inflammatory screen, the left colorbar defines the perfusion and inflammatory Object dataset

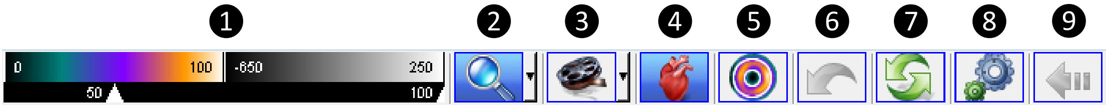


Figure 9.12: *Indirect registration mode toolbar*

color schemes for rows 1 and 2. The right colorbar defines the Target color scheme for Rows 1, 2, and 3. The Object color scheme in Row 3 can be changed within the Preferences/Colorbars page, in the CT Colorbars section. For more information on colorbar management, see the Colorbar Tools section.

2. **Magnification Tool**: Adjust the image display size.
3. **Cine Tool**: Activate/Deactivate cine of dynamic sequences. When active, motion correction tools display on all viewports. When deactivated, using the frame slider from the drop-down also activates the motion correction tools. Cine must be deactivated to view the flow ROI or Bounds.
4. **Cardiac Orientation Toggle Tool**: Displays the datasets in SA, HLA, and VLA orientation.
5. **Contours Toggle Tool**: Overlay Corridor4DM-generated LV surface contours on the images.
6. **Undo Tool**: Once changes are made to alignment, this tool becomes active to undo the last move with each click of the tool.
7. **Reset Tool**: Resets the screen to an unprocessed state. Or, select Reload to display the last saved Corridor4DM results file if one is present.
8. **Process Tool**: Applies manual corrections to the transformation matrices within each row; Fuses the perfusion and inflammatory datasets with the co-registration applied in Row 3 and applies the perfusion contours to the inflammatory dataset(s). Exits the user from the Indirect Registration Mode and displays the Inflammatory Results Mode.
9. **Return Tool**: Tool is disabled until the Process Tool has been selected at least one time on the Inflammatory screen. When available, the tool permits the user to return to the Inflammatory Results Mode without applying any changes made within the current Indirect Registration Mode screen session.

Inflammatory Results Mode

Results display once indirect registration processing completes. Interactive fused image results, perfusion and SUV polar maps, regional and global results, and derived comparisons are available to provide detailed quantitative analysis of the perfusion and inflammatory datasets.

1. **Review and Verify Fused Image Displays**: In the top row of images, the perfusion and inflammatory datasets display in patient orientation as fused with the perfusion as the Object and the inflammatory dataset as the Target, centered to the heart. Click the **Orientation** tool to update the viewport displays to cardiac orientation. A maximum of two datasets can display on this mode of the screen at one time.
    a. Use the plane slicers or dog ears *(Figure 9.13)* to scroll through the fused dataset viewports in all three planes to verify the datasets appear properly co-registered and the red contours accurately track the LV for both datasets.

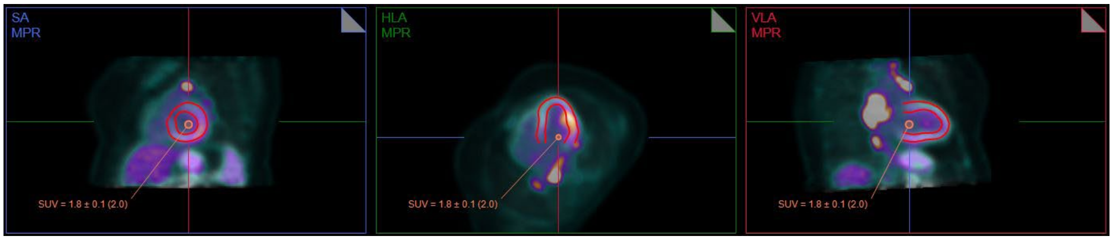


Figure 9.13: *Plane slicers and dog ears in viewports*

   i. If there is any minor mis-registration noted, click in a viewport and pan the Object using the left mouse, or use the fine/coarse pan/rotate tools that display. If any changes are made, results immediately reprocess and display.

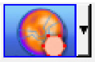
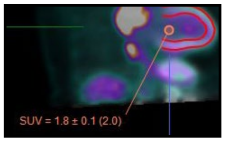


Figure 9.14: *Relative SUV Threshold*

b. When the default Relative SUV Threshold option is selected *(Figure 9.14)*, a Volume of Interest (VOI) is automatically drawn and placed within the blood pool cavity near the base of the LV, to be used as a background reference for SUV on the inflammatory dataset *(Figure 9.15)*.



SUV = 1.8 ± 0.1 (2.0)

Figure 9.15: *Volume of Interest (VOI)*

c. The VOI displays the SUV mean value, and the maximum SUV value (in parentheses).

d. When the Relative SUV Threshold option is selected, the mean VOI SUV value is multiplied by the factor noted in the drop-down menu. Click the drop-down to view and update the multiplier value, which is 1.5 on default and can be set to a desired value within the Inflammatory screen Preferences.

e. Click and drag a selected VOI to pan/move it. The Text can be moved by clicking and dragging it to a desired location in the viewport.

f. When the Absolute SUV Threshold option is selected *(Figure 9.16)* the default absolute threshold is set to 2.7 on default. Click the drop-down to view the SUV slider or make adjustments. When this option is in use, the VOI is not drawn or displayed on the fused images.

Figure 9.16: *Absolute SUV Threshold*

2. **Review Polar Map Results** *(Figure 9.17)*: Corridor4DM displays four polar maps in a row, all with a 5-wall segmental overlay to match the tabular results presented below:

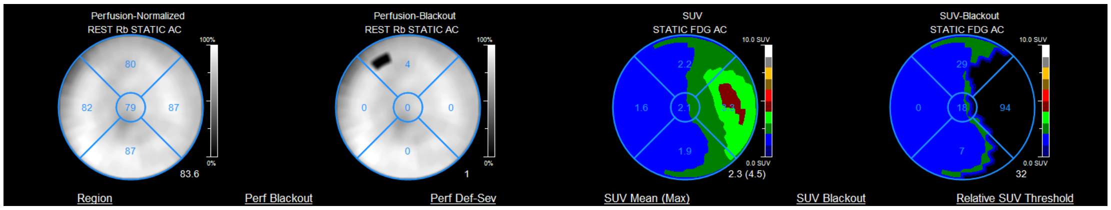


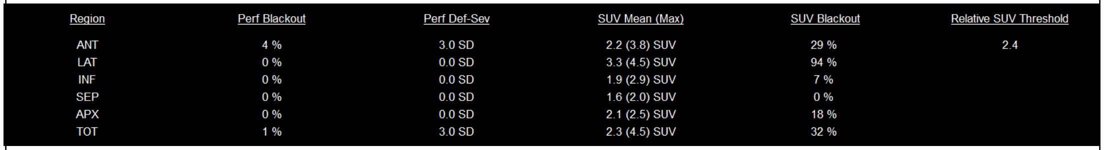
Figure 9.17: *Polar Maps*

a. Left-most: The Perfusion Normalized polar map shows the perfusion dataset normalized to peak intensity within the myocardium. The default is to display it as grayscale. This can be updated to a different color scheme by right-clicking the right colorbar and selecting a different color scheme. The global mean intensity value displays in the lower right-hand corner outside of the polar map.

b. Left-middle: The Perfusion Blackout polar map shows the perfusion dataset with the Blackout quant map applied, where any sectors that are abnormal as compared to the normals database will be blacked out within the polar map. The percent of defect for each of the 5-wall segments displays within each segment. The global percentage of LV defect displays in the lower right-hand corner outside of the polar map.

c. Right-middle: The SUV inflammatory polar map shows the SUV value calculated for each of the 5-wall segments and is displayed within the polar map. The colorbar default used for SUV maps is Step 10 and cannot be changed. The global mean SUV and max SUV in parentheses display in the lower right-hand corner outside of the polar map.

d. Right-most: The SUV Blackout polar map compares the inflammatory dataset to the SUV threshold which is noted in parentheses next to the dataset title. Any area calculated as higher than the SUV threshold value displays as blacked out. Percentage of abnormal SUV uptake is displayed within each of the 5-wall segments. The global percentage of LV with abnormal SUV as compared to the threshold is displayed in the lower right-hand corner outside of the polar map.



Region	Perf Blackout	Perf Def-Sev	SUV Mean (Max)	SUV Blackout	Relative SUV Threshold
ANT	4 %	3.0 SD	2.2 (3.8) SUV	29 %	2.4
LAT	0 %	0.0 SD	3.3 (4.5) SUV	94 %	
INF	0 %	0.0 SD	1.9 (2.9) SUV	7 %	
SEP	0 %	0.0 SD	1.6 (2.0) SUV	0 %	
APX	0 %	0.0 SD	2.1 (2.5) SUV	18 %	
TOT	1 %	3.0 SD	2.3 (4.5) SUV	32 %	

Figure 9.18: *Table of Regional and Global Results*

3. **Review the Table of Regional and Global Results:** *(Figure 9.18)* The 5-wall and global results for each of the following are provided in table format for visual comparison to polar map and image displays:

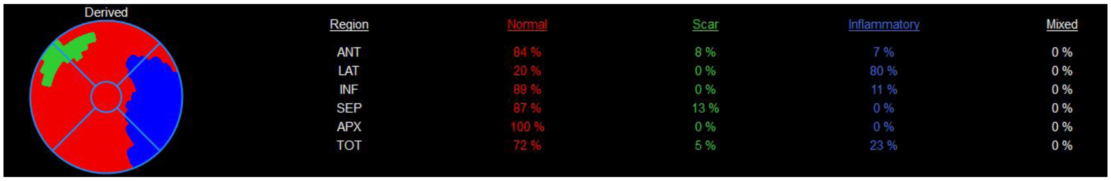
    a. **Perf Blackout:** Provides regional abnormal (defect) extent for each wall and globally.

    b. **Perf Def-Sev:** Gives the number of standard deviations below the normal database mean uptake for each wall and globally.

    c. **SUV Mean (Max):** Gives the mean and maximum SUV value for each wall and globally.

    d. **SUV Blackout:** Provides the regional SUV abnormal (defect) extent for each wall and globally. The abnormal threshold is defined by the SUV threshold tool.

    e. **Relative SUV Threshold:** The abnormal threshold value is displayed here. SUV larger than this threshold are considered abnormal and indicative of cardiac inflammation.



Region	Normal	Scar	Inflammatory	Mixed
ANT	84 %	8 %	7 %	0 %
LAT	20 %	0 %	80 %	0 %
INF	89 %	0 %	11 %	0 %
SEP	87 %	13 %	0 %	0 %
APX	100 %	0 %	0 %	0 %
TOT	72 %	5 %	23 %	0 %

Figure 9.19: *Derived Map and Results Table*

4. **Review the Derived Map and Results Table** *(Figure 9.19)***:** Corridor4DM quantifies results comparing the perfusion and inflammatory results, displaying this in a single Derived polar map. The map is color-coded with 5-wall segmental and global results displayed in a table next to it.

    a. **Red:** Normal perfusion and normal SUV, noted as the “Normal” column with results in red text.

    b. **Green:** Abnormal perfusion and normal SUV, noted as the “Scar” column with results in green text.

    c. **Blue:** Normal perfusion and abnormal SUV, noted as the “Inflammatory” column with results in blue text.

    d. **Black:** Areas in the derived map that display abnormal perfusion and abnormal SUV display as black in the Derived polar map, but in white text in the “Mixed” column.

Inflammatory Results Toolbar Options *(Figure 9.20)*:

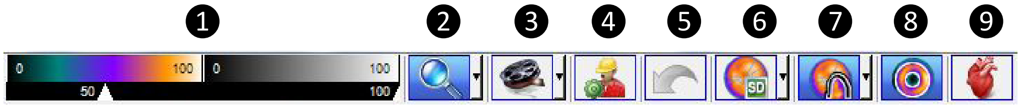


***Figure 9.20:** Inflammatory Results toolbar*

1. **Dual Colorbar Tool:** 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. On the Inflammatory screen, the left colorbar defines the inflammatory Object dataset color scheme. The right colorbar defines the perfusion Target color scheme and polar map displays. The SUV polar map color scheme is Step 10 and not definable. For more information on colorbar management, see the Colorbar Tools section.

2. **Magnification Tool:** Adjust the image display size.

3. **Cine Tool:** Activate/Deactivate cine of dynamic sequences. When active, motion correction tools display on all viewports. When deactivated, using the frame slider from the drop-down also activates the motion correction tools. Cine must be deactivated to view the flow ROI or Bounds.

4. **Manual Processing Tool:** Returns the user to the Indirect Registration mode of the Inflammatory screen.

5. **Undo Tool:** Once changes are made to alignment, this tool becomes active to undo the last move with each click of the tool.

6. **Standard Deviation Threshold Slider Tool:** Displays the perfusion defect threshold set and allows adjustments for perfusion dataset defect quantification. Units are in Standard Deviations.

7. **SUV Threshold Slider Tool:** Provides two options for setting the SUV Abnormal Threshold: Absolute and Relative.

    - Relative SUV Threshold option (default): Uses an automatically drawn Volume of Interest (VOI) within the blood pool region. The default value is set to 1.5 and this is multiplied by the mean SUV within the VOI to define the SUV abnormal threshold.

    - Absolute SUV Threshold option: A particular absolute value is defined as the SUV abnormal threshold via a slider. The default is set to 2.7.

8. **Contours Toggle Tool:** Overlay Corridor4DM-generated LV surface contours on the images.

9. **Cardiac Orientation Toggle Tool:** Displays the datasets in SA, HLA, and VLA orientation.

Prior to exiting Corridor4DM, ensure to click Save in the Control Panel to save all perfusion and Inflammatory results information *(Figure 9.21)*.

***Figure 9.21:** Save control*

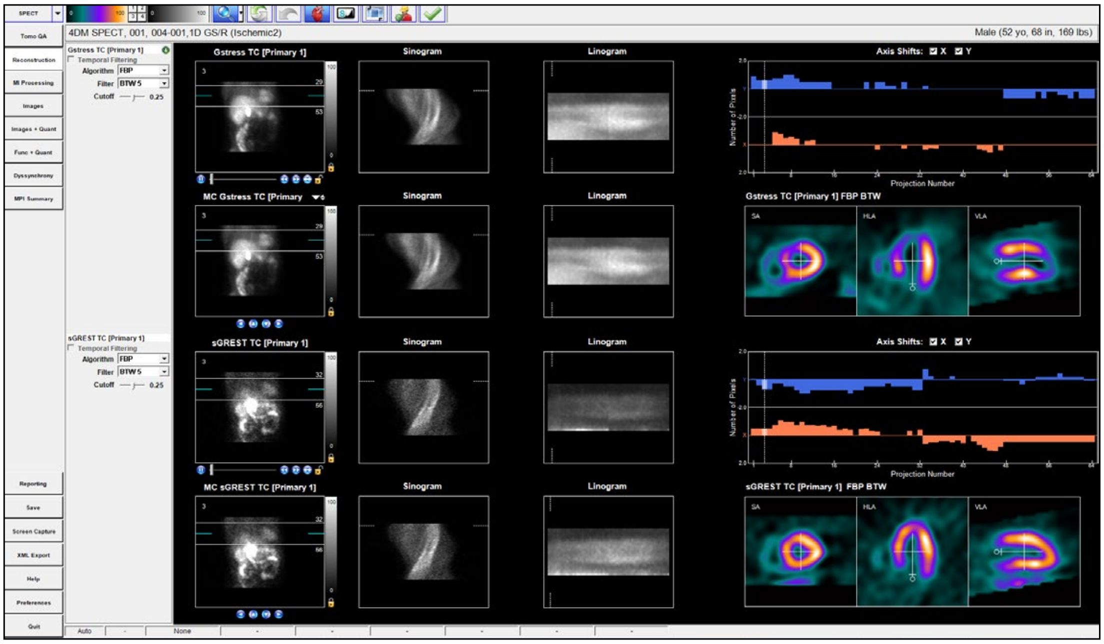
CHAPTER 10 SPECT IMAGE RECONSTRUCTION

Reconstruction Screen

WARNING
Tomographic data should be evaluated prior to reconstruction and corrections should be applied to minimize artifacts (e.g. motion), when possible. Failure to perform such corrections may result in misleading data, which may lead to misdiagnosis.

The **Reconstruction** screen *(Figure 10.1)* 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.

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



Gstress TC [Primary 1]
☐ Temporal Filtering
Algorithm FBP
Filter BTW 5
Cutoff 0.25

sGREST TC [Primary 1]
☐ Temporal Filtering
Algorithm FBP
Filter BTW 5
Cutoff 0.25

Figure 10.1: *The Corridor4DM Reconstruction Screen*

- **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

WARNING
Tomographic data should be evaluated prior to reconstruction and corrections should be applied to minimize artifacts (e.g. motion), when possible. Failure to perform such corrections may result in misleading data, which may lead to misdiagnosis.

Corridor4DM’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 10.2)***:** 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.

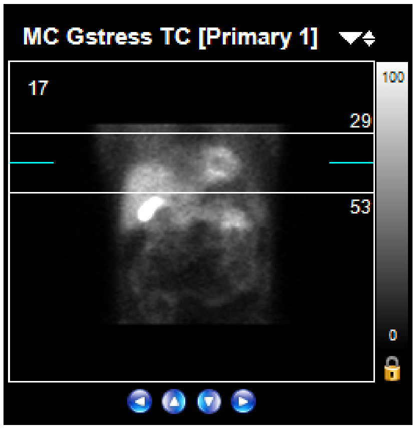


Figure 10.2: *Motion Correction Tomo Viewport*

- **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 10.3)***:** 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).

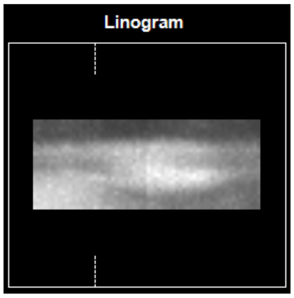


Figure 10.3: *Corridor4DM Linogram*

- **X, Y Axis Shifts Graph** *(Figure 10.4)***:** 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.

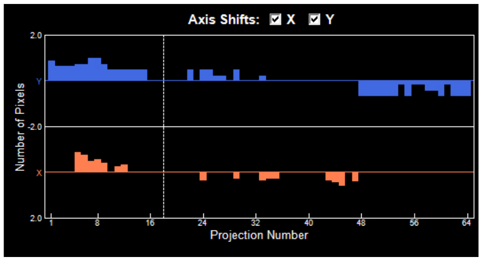


Figure 10.4: *X, Y Axis Shifts Graph on the Motion Correction Screen*

- **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 10.5)***:** Resets the study to apply and display the original Corridor4DM automatic motion correction.

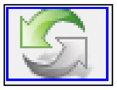


Figure 10.5: *Reset tool*

- **Undo Tool** *(Figure 10.6)***:** 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.

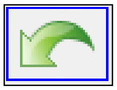


Figure 10.6: *Undo tool*

- **Orientation Tool** *(Figure 10.7)***:** 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).

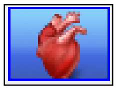


Figure 10.7: *Orientation tool*

- **Spatial Filtering** *(Figure 10.8)***:** Can be applied to smooth the appearance of the Tomo, Motion Corrected Tomo, Sinogram, and Linogram displays..

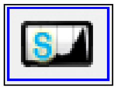


Figure 10.8: *Spatial Filtering*

- **Image Mask Tool** *(Figure 10.9)***:** 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.

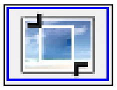


Figure 10.9: *Image Mask tool*

- **Apply Tool** *(Figure 10.10)***: 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, Corridor4DM will automatically display the MI Processing screen to quantify the newly created reconstructions.

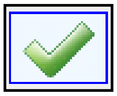


Figure 10.10: *Apply tool*

- **Advanced Reconstruction Tool** *(Figure 10.11)*: **This tool displays the screen in Advanced Reconstruction Mode.**

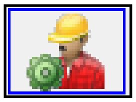


Figure 10.11: *Advanced Reconstruction tool*

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 Corridor4DM default filter setting.
- **Reorientation Controls:** To display the reconstructed volume in patient or cardiac space, use the **Reorientation** tool *(Figure 10.12)*. 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.

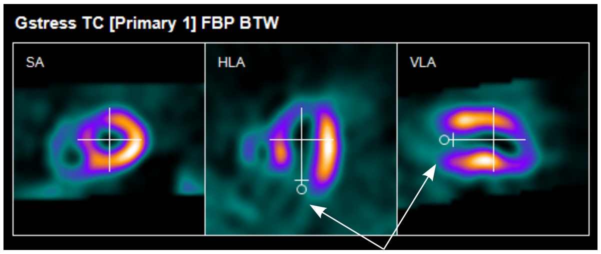


Figure 10.12: *Reorientation Controls*

- **Scan Arc** *(Figure 10.13)*: 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 10.14)*: **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, Corridor4DM will automatically display the MI Processing screen to quantify the newly created reconstructions.
- **Motion Correction Tool** *(Figure 10.15)*: **This tool displays the screen in Motion Correction Mode.**

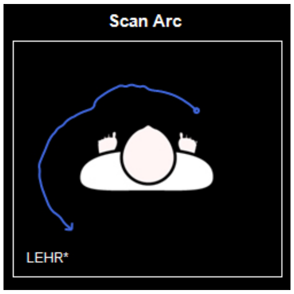


Figure 10.13: *Scan Arc*

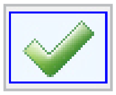


Figure 10.14: *Apply tool*

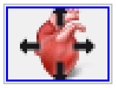


Figure 10.15: *Motion Correction tool*

CHAPTER 11 CAPTURING CORRIDOR4DM 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 three options to capture Corridor4DM results:

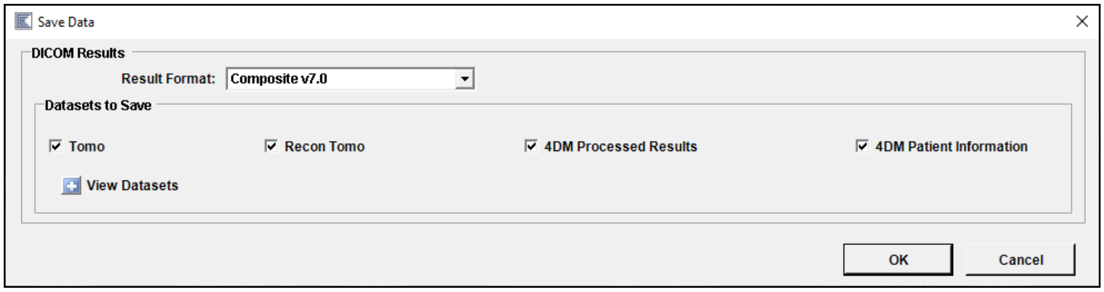
- Save processed data files in individual or composite DICOM format
- Save and export data in XML
- Generate and save site-specific screen captures in DICOM, TIFF, JPEG, or WMV format

Composite result files, when associated with 4DM in Windows, can be used to automatically launch 4DM with the saved images and results (e.g., from within a PowerPoint presentation).

Saving Processed Data Files

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, click the **Save** control in the **Control Panel** which displays the **Save Data** window *(Figure 11.1)*. Select from the following options:



Result Format: Composite v7.0

☑ Tomo ☑ Recon Tomo ☑ 4DM Processed Results ☑ 4DM Patient Information

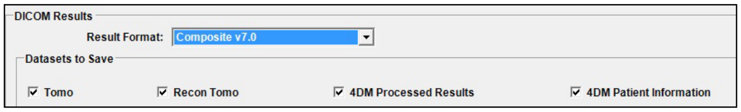
Figure 11.1: *Save Data window, highlighting the DICOM Result Format section*

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

- **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 Corridor4DM versions earlier than v7.0 (e.g., Corridor4DM v5.2).
  - **Individual v7.0:** Stores individual result files for each dataset launched into the application that are compatible with Corridor4DM v7.0 and later (e.g., Corridor4DM v2010 and higher).
  - **Composite Pre v7.0:** Stores the results for all datasets, including raw data, into a single file that is compatible with Corridor4DM versions earlier than v7.0 (e.g., Corridor4DM v5.2).
  - **Composite v7.0:** Stores the results for all datasets, including raw data, into a single file that is compatible with Corridor4DM v7.0 and later (e.g., Corridor4DM v2010 and higher).
- **Datasets to Save:** Use these toggles to select which results to save.

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

Corridor4DM Result Types (Figure 11.2)


DICOM Results

Result Format: Composite v7.0

Datasets to Save

☑ Tomo ☑ Recon Tomo ☑ 4DM Processed Results ☑ 4DM Patient Information

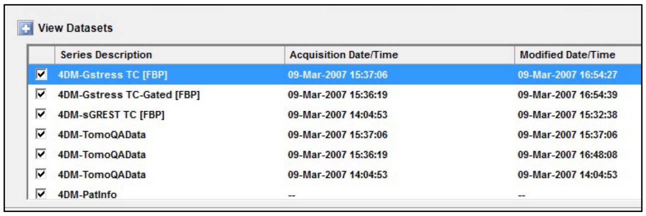
Figure 11.2: *Save Data window, noting the Datasets to Save section*

To learn more about configuring **Save** and **Screen Capture** defaults within Preferences, go to User Preferences.

- **Tomo: This option is only applicable for Corridor4DM Reconstruction Option users.** Selecting this option saves any Corridor4DM 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 Corridor4DM Reconstruction Option users.** Selecting this option saves any Corridor4DM 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).
- **Corridor4DM Processed Results:** Saves patient data processed with the Corridor4DM 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 Corridor4DM is launched.**
- **Corridor4DM Patient Information:** Saves all data entered and selected in Reporting, and the datasets prioritized for export (for English, French, and German versions of Corridor4DM only).

View Datasets

- Click the **Plus Sign** toggle to view all Corridor4DM datasets that are queued to be saved as part of the results (Figure 11.3). 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 12: Preferences to learn more.


View Datasets

	Series Description	Acquisition Date/Time	Modified Date/Time
☑	4DM-Gstress TC [FBP]	09-Mar-2007 15:37:06	09-Mar-2007 16:54:27
☑	4DM-Gstress TC-Gated [FBP]	09-Mar-2007 15:36:19	09-Mar-2007 16:54:39
☑	4DM-sGREST TC [FBP]	09-Mar-2007 14:04:53	09-Mar-2007 15:32:38
☑	4DM-TomoQAData	09-Mar-2007 15:37:06	09-Mar-2007 15:37:06
☑	4DM-TomoQAData	09-Mar-2007 15:36:19	09-Mar-2007 16:48:08
☑	4DM-TomoQAData	09-Mar-2007 14:04:53	09-Mar-2007 14:04:53
☑	4DM-PatInfo	--	--

Figure 11.3: *Save Data window, noting the View Datasets section*

- **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.

To add a new option to the **Format menu**, place an XSL style sheet in the **xmlTemplate** folder located at C:\Users\Public\Documents\INVIA\Corridor4DM\xmlTemplates.

Save and export data in XML or Delimited Text

Configuring an XML Export

Within Corridor4DM Preferences, click to display the **Data Export** page. In the **XML Formatted Results** box, configure the following fields (Figure 11.4):

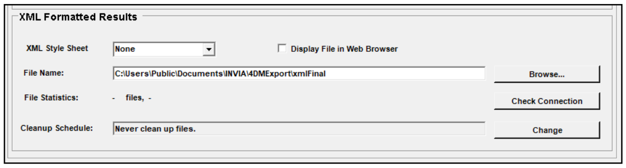

XML Formatted Results
XML Style Sheet: None
☐ Display File in Web Browser
File Name: C:\Users\Public\Documents\INVIA\4DMExport\xmlFinal
File Statistics: - files, -
Cleanup Schedule: Never clean up files.

Figure 11.4: *XML Formatted Results within Corridor4DM Preferences*

- **Format**: Select from the drop-down to use choose the default XSL style sheet option.
  - – Corridor4DM includes all patient and study information; patient demographics, patient history, study indications, procedure data, EKG and stress test data, perfusion, function, and site information.
  - – ExampleConversion includes only study perfusion information.
- **Display with Web Browser**: If activated, the output XML file displays in a Web browser.
- **File Name**: Enter the name for the output XML file. To navigate to a different location, click **Browse**.
- For more information on **Check Connection** and **Cleanup Schedule**, see the 4DM Preferences chapter.

Exporting XML Formatted Results

To export Corridor4DM data to an XML Formatted file, click the **XML Export** button in the Corridor4DM application Control Panel (Figure 11.5).

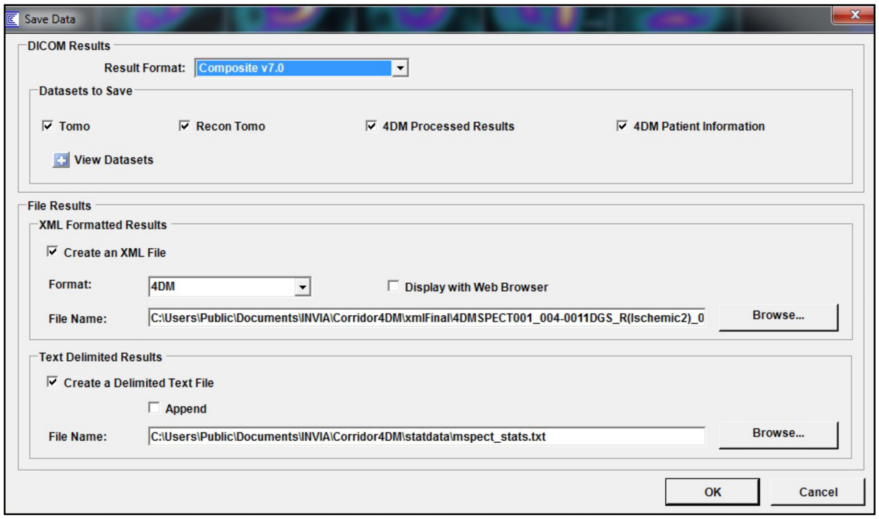
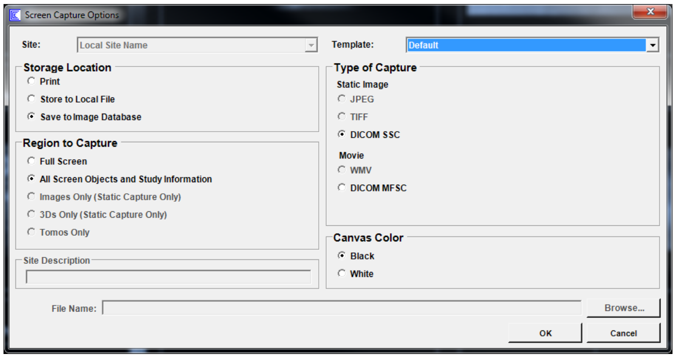

Save Data
DICOM Results
Result Format: Composite v7.0
Datasets to Save
☑ Tomo
☑ Recon Tomo
☑ 4DM Processed Results
☑ 4DM Patient Information
File Results
XML Formatted Results
☑ Create an XML File
Format: 4DM
☐ Display with Web Browser
File Name: C:\Users\Public\Documents\INVIA\Corridor4DM\xmlFinal\4DMSPECT001_004-0011DGS_R(Ischemic2)_0
Text Delimited Results
☑ Create a Delimited Text File
☐ Append
File Name: C:\Users\Public\Documents\INVIA\Corridor4DM\statdata\mspect_stats.txt

Figure 11.5: *XML Results options within the Save Data window*

Screen Captures

Corridor4DM includes functionality for capturing Static (SSC) and Multi-Frame Screen Captures (MFSC) of any Corridor4DM default or custom screen. To initiate a screen capture, click the **Screen Capture** control from the **Control Panel** to open the **Screen Capture Options** window *(Figure 11.8)*. Here you can select from the following options:



Site: Local Site Name
Template: Default

Storage Location
○ Print
○ Store to Local File
● Save to Image Database

Region to Capture
○ Full Screen
● All Screen Objects and Study Information
○ Images Only (Static Capture Only)
○ 3Ds Only (Static Capture Only)
○ Tomos Only

Site Description:

Type of Capture
Static Image
○ JPEG
○ TIFF
● DICOM SSC
Movie
○ WMV
○ DICOM MFSC

Canvas Color
● Black
○ White

File Name:

Figure 11.6: *Screen Capture Options window*

- **Site:** Select the site from the drop-down menu. This will include the selected site's entered information, based on what information is input within Corridor4DM Administration for the site. This will be dithered, or grayed-out if only one site is configured within the Corridor4DM Administration module. For information on adding sites, see the **4DM Administration** chapter. Within Administration module 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 Administration, on the Sites page within Global Settings.
- **Template:** The template selected defines what site, patient, and dosing information is included on the screen capture. If **None** is selected, no site information will be included on the screen capture. Select the template from the drop-down to apply for the screen capture. A **Default** template is included in the software with basic site and dosing information included. Configure the **Default** template, and new templates within the Corridor4DM Administration module. An **Administrator** login is required to access Corridor4DM Administration. Multiple templates can be created and used across all defined sites. For more information on creating and editing templates, see the **4DM Administration** chapter.
- **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 Corridor4DM screen capture to filming interface.
  - – Report (only available on the Philips EBW workstation)
    - Transfers Corridor4DM screen capture to reporting interface.
  - – Direct to Film (only available on the Philips EBW workstation)
    - Transfers Corridor4DM 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

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

DICOM MFSC and WMV screen captures are limited to 16 frames or less. To capture Tomo cines choose **Tomos Only** in the **Region to Capture** section of the **Screen Capture Options** window.

It is recommended that you use standard alphanumeric characters when naming files to ensure cross-platform compatibility. Do not use non-standard characters such as *, @, #, \, or /.

  - 3Ds Only
  - Tomo Only

- **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.

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

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

Window Controls

These controls allow you to save information or cancel the save feature.

- **OK:** Saves information as specified with selections made in the **Screen Capture** window.
- **Cancel:** Closes the window without saving any data.

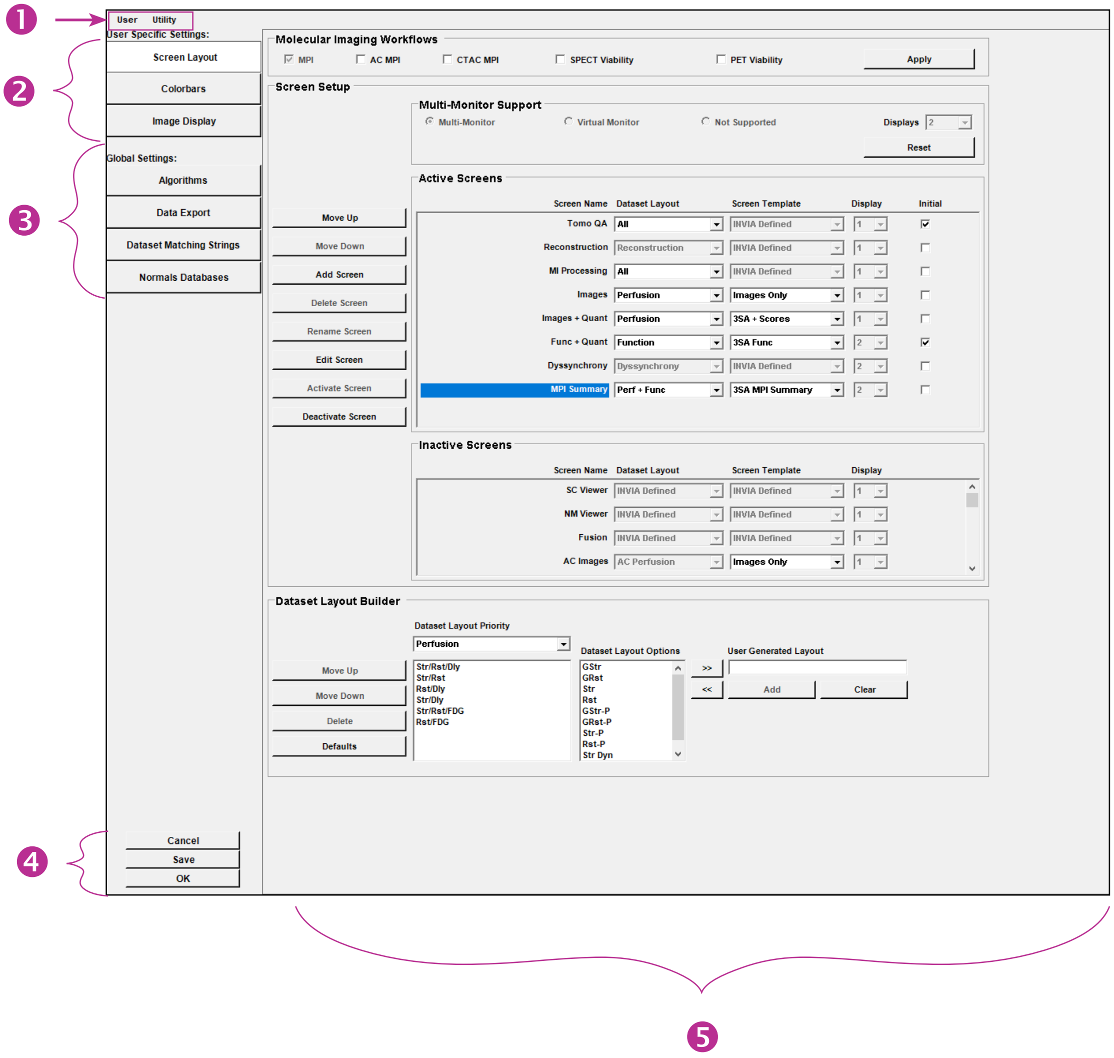
CHAPTER 12 USER PREFERENCES

The **Corridor4DM Preferences** window *(Figure 12.1)* 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 five 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.



Molecular Imaging Workflows

☑ MPI ☐ AC MPI ☐ CTAC MPI ☐ SPECT Viability ☐ PET Viability

Multi-Monitor Support

● Multi-Monitor ○ Virtual Monitor ○ Not Supported Displays 2

Active Screens

Screen Name	Dataset Layout	Screen Template	Display	Initial
Tomo QA	All	INVIA Defined	1	☑
Reconstruction	Reconstruction	INVIA Defined	1	☐
MI Processing	All	INVIA Defined	1	☐
Images	Perfusion	Images Only	1	☐
Images + Quant	Perfusion	3SA + Scores	1	☐
Func + Quant	Function	3SA Func	2	☑
Dyssynchrony	Dyssynchrony	INVIA Defined	2	☐
MPI Summary	Perf + Func	3SA MPI Summary	2	☐

Inactive Screens

Screen Name	Dataset Layout	Screen Template	Display
SC Viewer	INVIA Defined	INVIA Defined	1
NM Viewer	INVIA Defined	INVIA Defined	1
Fusion	INVIA Defined	INVIA Defined	1
AC Images	AC Perfusion	Images Only	1

Dataset Layout Priority: Perfusion

Str/Rst/Dly
Str/Rst
Rst/Dly
Str/Dly
Str/Rst/FDG
Rst/FDG

Dataset Layout Options

GStr
GRst
Str
Rst
GStr-P
GRst-P
Str-P
Rst-P
Str Dyn

User Generated Layout

Figure 12.1: 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.

The menu selections — **Initialize Current User** and **Reload Current User** — will apply only to the current user. The preferences settings defined for the other users on the system will not be affected.

User Menu *(Figure 12.2)*

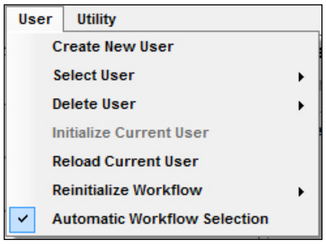


Figure 12.2: *Preferences User Menu*

- **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 Corridor4DM activates the preferences for the Default configuration.
- **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 12.3)*

For version-specific step-by-step instructions on how to Backup and Restore configuration files, refer to the User Center at www.inviasolutions.com.

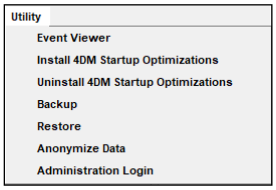


Figure 12.3: *Preferences Utility Menu*

- **Event Viewer:** Displays the local system Event Viewer log, which is useful when troubleshooting Corridor4DM program errors.
- **Install 4DM Startup Optimizations:** Runs a batch file that improves the speed of 4DM startup on future launches by generating a cache of the 4DM architecture.
- **Uninstall 4DM Startup Optimizations:** Uninstalls the batch file.
- **Backup:** Utility to save Corridor4DM user configurations, screen and report templates, and database files.
- **Restore:** Restores Corridor4DM user configuration files that were saved using the Backup utility.
- **Anonymize Data:** Turn on/off anonymization of the patient name and identification number. Anonymization will only be temporary for the current session of Corridor4DM.
- **Administration Login**: Access Corridor4DM Administration module to configure licensing, site information, screen capture templates, and reporting preferences.

Window Control Buttons

These buttons control the **Preferences** window and appear at the bottom-left of the screen *(Figure 12.4)*.

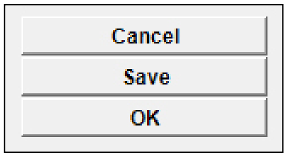


Figure 12.4: *Preferences window control buttons*

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.

User Specific Settings

The **Preferences** window is comprised of two sections: **User** and **Global Settings** *(Figure 12.5)*. Each page displays in the Preferences Setting Screen. Each button is discussed in detail below.

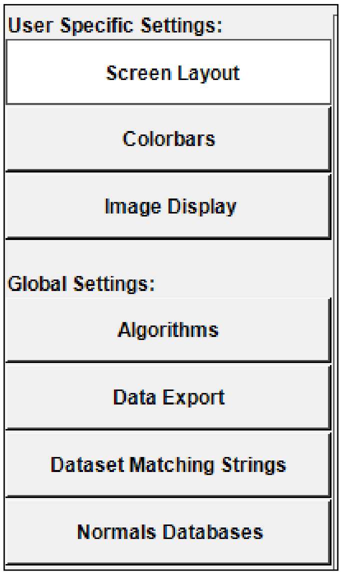


Figure 12.5: *Page Selection Buttons within the Preferences Window*

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 12.6)*

The Molecular Imaging Workflows selection configures the system to display a series of active screens and activates dataset layouts available, based on the site's specific protocols in use. 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**.

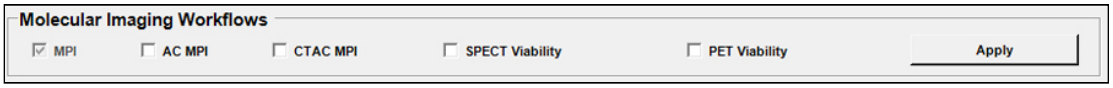


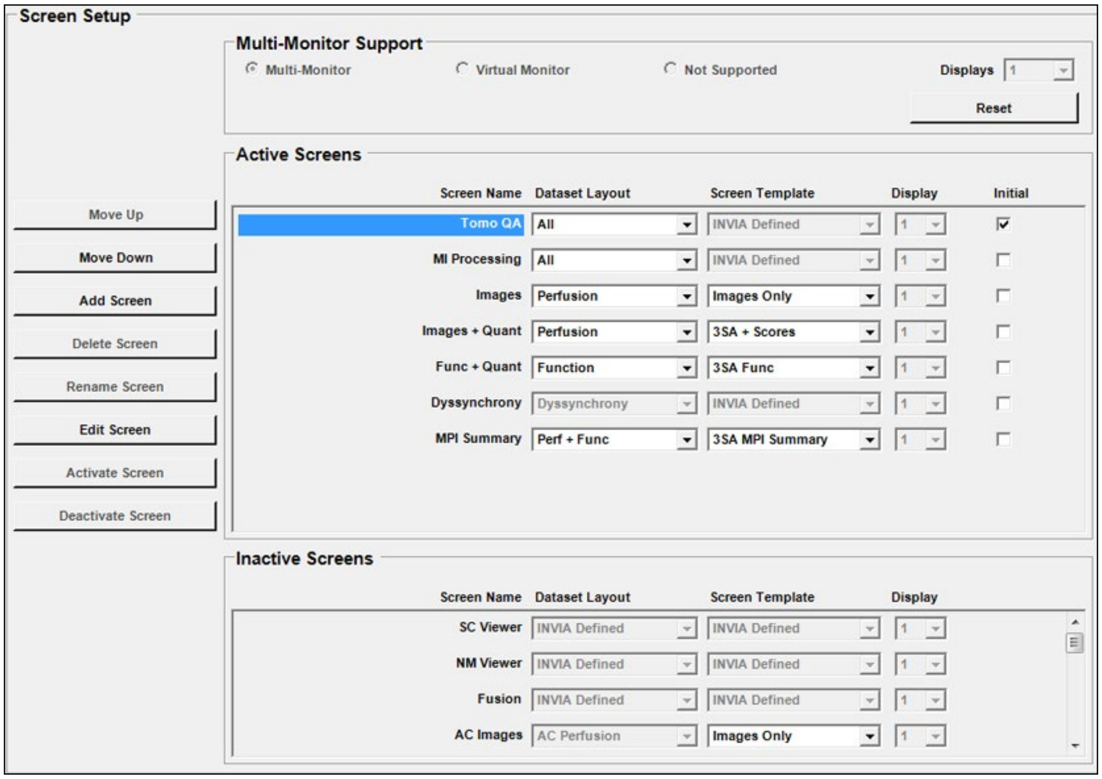
Figure 12.6: *Corridor4DM Molecular Imaging Workflows*

Screen Setup

The **Screen Setup** section consists of **Multi-Monitor Support** settings, **Active Screens,** and **Inactive Screens** lists *(Figure 12.7)*. 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 Corridor4DM **Workflow Screens**. To activate a screen from the **Inactive**



Screen Setup

Multi-Monitor Support

● Multi-Monitor ○ Virtual Monitor ○ Not Supported

Displays 1

Active Screens

Screen Name	Dataset Layout	Screen Template	Display	Initial
Tomo QA	All	INVIA Defined	1	☑
MI Processing	All	INVIA Defined	1	☐
Images	Perfusion	Images Only	1	☐
Images + Quant	Perfusion	3SA + Scores	1	☐
Func + Quant	Function	3SA Func	1	☐
Dyssynchrony	Dyssynchrony	INVIA Defined	1	☐
MPI Summary	Perf + Func	3SA MPI Summary	1	☐

Inactive Screens

Screen Name	Dataset Layout	Screen Template	Display
SC Viewer	INVIA Defined	INVIA Defined	1
NM Viewer	INVIA Defined	INVIA Defined	1
Fusion	INVIA Defined	INVIA Defined	1
AC Images	AC Perfusion	Images Only	1

Figure 12.7: *Corridor4DM Screen Setup Section*

For additional information on 4DM review screens, refer to **Customizing the List of Active Screens** within the User Center on www.inviasolutions.com.

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 Corridor4DM screen a specific hardware or virtual display by selecting the **Display** number from the drop down menu.
  - – 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 the drop-down 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 Corridor4DM **Screen Templates** from the drop down menu. Templates define which objects display on the page. See the Corridor4DM 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** within the User Center on the INVIA website: www.inviasolutions.com.

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.

Dataset Layout Builder

Corridor4DM includes a variety of **Dataset Layout Priorities** which can be configured to user specifications within the Dataset Layout Builder *(Figure 12.8)*.

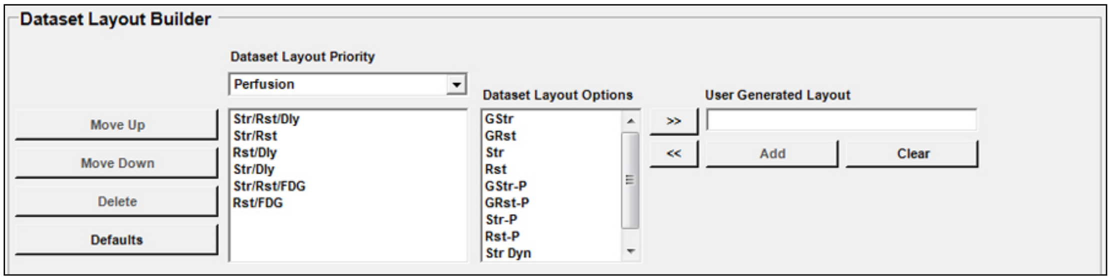


Figure 12.8: *Dataset Layout Builder within Corridor4DM Preferences*

- 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 Corridor4DM the sequence in which to display datasets.
  - Corridor4DM first determines which dataset grouping matches the loaded datasets for the patient, starting at the top and going down the list *(Figure 12.9)*.
  - Once Corridor4DM determines with dataset grouping to use, the application displays the datasets according to the left-to-right order within the group. *(Figure 12.10)*.

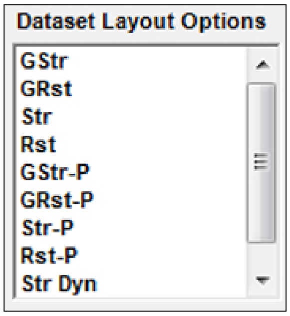


Figure 12.9: *Matching a dataset group to a priority first by list order.*

- 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 Corridor4DM defaults by clicking the **Defaults** button.

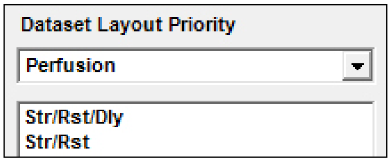
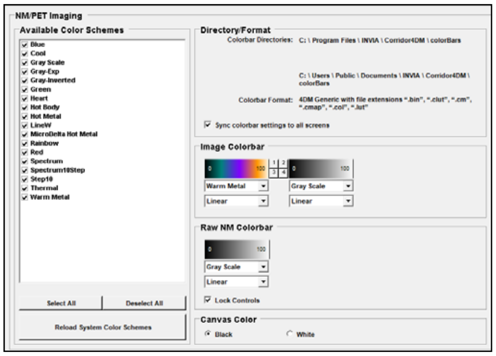


Figure 12.10: *After Corridor4DM matches the dataset group, the application displays datasets in left-to-right order.*

Colorbars

The user can activate or deactivate color schemes available in Corridor4DM from this page *(Figure 12.11)*. 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:


NM/PET Imaging

Available Color Schemes
☑ Blue
☑ Cool
☑ Gray Scale
☑ Gray-Exp
☑ Gray-Inverted
☑ Green
☑ Heart
☑ Hot Body
☑ Hot Metal
☑ LineW
☑ MicroDelta Hot Metal
☑ Rainbow
☑ Red
☑ Spectrum
☑ Spectrum10Step
☑ Step10
☑ Thermal
☑ Warm Metal

Directory/Format
Colorbar Directories: C: \ Program Files \ INVIA \ Corridor4DM \ colorBars
C: \ Users \ Public \ Documents \ INVIA \ Corridor4DM \ colorBars
Colorbar Format: 4DM Generic with file extensions "*.bin", "*.clut", "*.cm", "*.cmap", "*.col", "*.lut"
☑ Sync colorbar settings to all screens

Image Colorbar: Warm Metal, Linear; Gray Scale, Linear

Raw NM Colorbar: Gray Scale, Linear
☑ Lock Controls

Canvas Color: ● Black ○ White

Figure 12.11: *Colorbars page*

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

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

The **Directory/Format** shows where colorbar file directories are located and the acceptable colorbar file formats. In order for users to add colorbars to Corridor4DM and save within the Corridor4DM **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 12.12)* allows users to define common preferences for image data, polar map, and scoring data throughout the entire application.

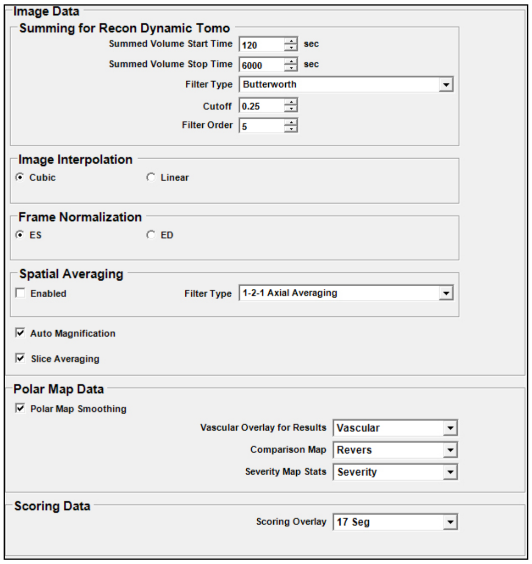


Image Data

Summing for Recon Dynamic Tomo
Summed Volume Start Time: 120 sec
Summed Volume Stop Time: 6000 sec
Filter Type: Butterworth
Cutoff: 0.25
Filter Order: 5

Image Interpolation: ● Cubic ○ Linear

Frame Normalization: ● ES ○ ED

Spatial Averaging
☐ Enabled
Filter Type: 1-2-1 Axial Averaging

☑ Auto Magnification
☑ Slice Averaging

Polar Map Data
☑ Polar Map Smoothing
Vascular Overlay for Results: Vascular
Comparison Map: Revers
Severity Map Stats: Severity

Scoring Data
Scoring Overlay: 17 Seg

Figure 12.12: *Image Display page*

- **Image Data**
  - **Summing for Recon Dynamic Tomo:** Allows user to define the time range used to sum dynamic recon tomo datasets for analysis in Corridor4DM. 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

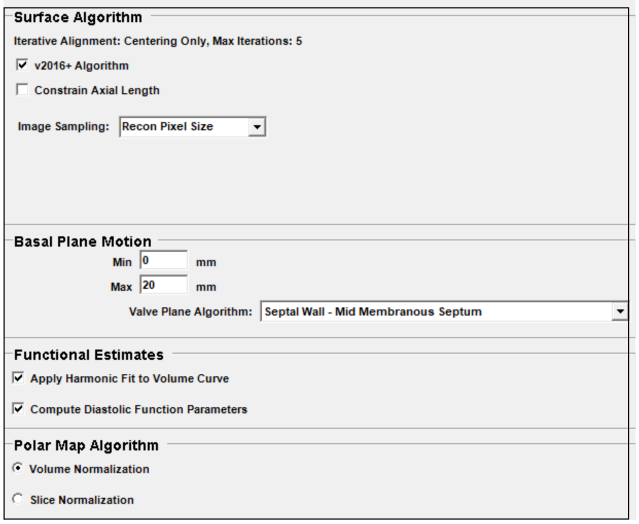
  few nearby pixels.

  - **Frame Normalization:** Normalize gated images to end-diastolic or end-systolic frame.
  - **Spatial Averaging:** When Enabled, the Filter Type selection is applied to all screens in the workflow. Filter Types include:
    - **1-2-1 Axial Averaging** *(default when enabled)*: Filtering is applied in the axial direction regardless of viewport orientation, resulting in a smooth appearance.
    - **1-2-1 Slice Averaging**: Filtering is applied perpendicular to the viewport, so the impact of the smoothing varies based on viewport orientation.
    - **1-1 Axial Averaging** and **1-1 Slice Averaging**: These filters are similar to the 1-2-1 versions, but use two slices instead of three.
  - **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 Corridor4DM application.

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.


Surface Algorithm
Iterative Alignment: Centering Only, Max Iterations: 5
☑ v2016+ Algorithm
☐ Constrain Axial Length
Image Sampling: Recon Pixel Size

Basal Plane Motion
Min 0 mm
Max 20 mm
Valve Plane Algorithm: Septal Wall - Mid Membranous Septum

Functional Estimates
☑ Apply Harmonic Fit to Volume Curve
☑ Compute Diastolic Function Parameters

Polar Map Algorithm
● Volume Normalization
○ Slice Normalization

Figure 12.13: *Algorithms page within Corridor4DM preferences*

Algorithms

The Algorithms preferences page *(Figure 12.13)* is used to modify parameters used to track the surfaces of the left ventricle. The parameters can be modified based on user's preferences of how the software generates contours.

Extensive validation has been performed with the default, **Iterative Alignment algorithm**, and its use is recommended.

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).

Surface Algorithms

- **Iterative Alignment (Default):** When the endo- and epicardial surfaces are detected, Corridor4DM 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.

- **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. When active, any user adjustments to processing override this tool.

- **Image Sampling:** This menu defines the image pixel size that is used to estimate the endo- and epicardial surfaces. The standard default method is to use the input reconstructed pixel size. New to v2018 and later are options to use a fixed pixel size of 4.8mm or 2.4mm. These options can allow for finer sampling of axial shortening and more consistency for clinics where images are reconstructed with varying pixel sizes.
  NOTE: If the reconstructed pixel size (e.g. 3.6mm) is smaller than the option selected (e.g. 4.8mm), the smaller of the two (i.e. reconstructed pixel size of 3.6mm) is used.

Basal Plane Motion

- **Min/Max:** Based on MRI and echocardiography data, Corridor4DM 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 Corridor4DM 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 (Corridor4DM 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, Corridor4DM smooths the volume curve displayed for gated data using a fourth order harmonic.

- **Compute Diastolic Function Parameters:** (For 16-frame studies only) If active, Corridor4DM computes diastolic function parameters which display on the volume curve. Corridor4DM 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.

To learn more about the Save and Screen Capture options 4DM provides, please go to Capturing 4DM Results.

Data Export

The **Data Export** page *(Figure 12.14)* allows users to configure settings for the default Save, Reporting export, 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.

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

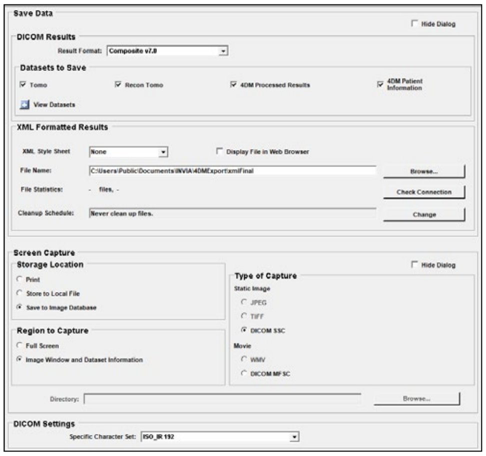

Save Data
☐ Hide Dialog
DICOM Results
Result Format: Composite v7.0
Datasets to Save
☑ Tomo
☑ Recon Tomo
☑ 4DM Processed Results
☑ 4DM Patient Information
XML Formatted Results
XML Style Sheet: None
☐ Display File in Web Browser
File Name: C:\Users\Public\Documents\INVIA\4DMExport\xmlFinal
File Statistics: - files, -
Cleanup Schedule: Never clean up files.
Screen Capture
☐ Hide Dialog
Storage Location
○ Print
○ Store to Local File
● Save to Image Database
Region to Capture
○ Full Screen
● Image Window and Dataset Information
Type of Capture
Static Image
○ JPEG
○ TIFF
● DICOM SSC
Movie
○ WMV
○ DICOM MF SC
Directory:
DICOM Settings
Specific Character Set: ISO_IR 192

Figure 12.14: *Data Export page within Corridor4DM Preferences. Set defaults for Saving DICOM Results and File Results.*

The **DICOM Settings** box allows the user to define the character encoding scheme for DICOM files from Corridor4DM:

- 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)

XML Export

Configuring an XML Export

Within the **Data Export** page in Corridor4DM Preferences, users can configure an XML export using the following components available within the **XML Formatted Results** form *(Figure 12.15)*. For purposes of research data collection, define exports within the **XML Formatted Results** section of Data Export within Preferences. **This functionality is separate from exporting diagnostic Corridor4DM Reports. See the *Corridor4DM Reporting Users Guide* for more information on configuring and exporting Corridor4DM Reports.**

To add a new option to the **Format** menu, place an XSL style sheet in the **xmlTemplate** folder located at C:\Users\Public\Documents\INVIA\Corridor4DM\xmlTemplates.

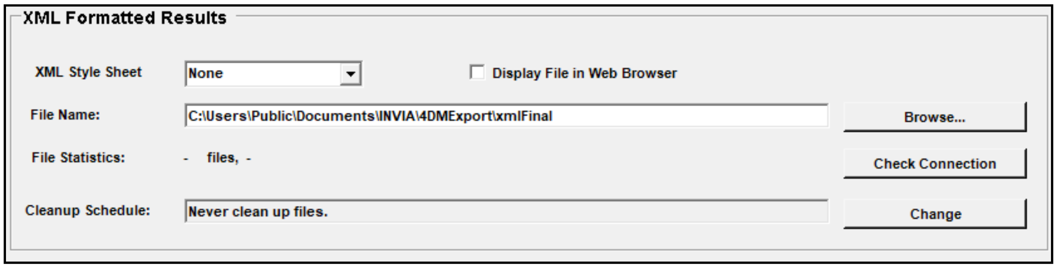
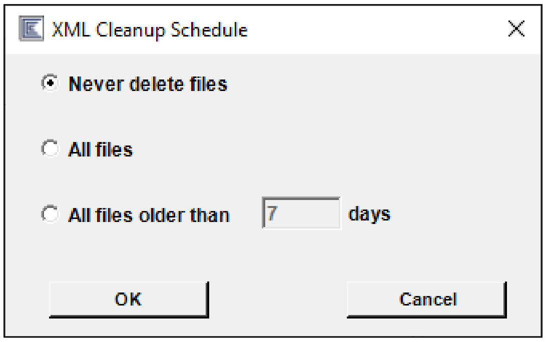

XML Formatted Results
XML Style Sheet: None
☐ Display File in Web Browser
File Name: C:\Users\Public\Documents\INVIA\4DMExport\xmlFinal
File Statistics: - files, -
Cleanup Schedule: Never clean up files.

Figure 12.15: *XML Formatted Results within Corridor4DM Preferences*

Within Corridor4DM **Preferences**, click to display the **Data Export** page. In the **XML Formatted Results** box, select and configure the following fields:

- **Format**: Select from the drop-down to use choose the default XSL style sheet option.
- **Display with Web Browser**: If activated, the output XML file displays in a Web browser.
- **File Name**: Enter the name for the output XML file. To navigate to a different location, click **Browse**
- **Check Connection**: Once a new location is selected for the Report creation directory, left-click this button to verify writing privileges..

- **Clean Up Schedule**: Deletes XML result files as specified by the conditions configured in the cleanup schedule. To alter the schedule, left-click Change to open the Corridor4DM Clean Up Schedule *(Figure 12.16)* 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 Corridor4DM session.
  - **All files older than "x" days**: Deletes all files older than the specified number of days.


XML Cleanup Schedule

● Never delete files

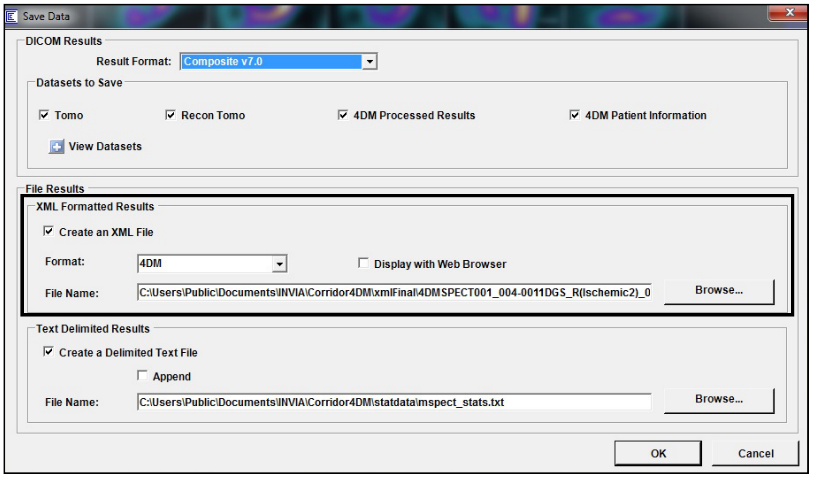
○ All files

○ All files older than 7 days

Figure 12.16: XML Cleanup Schedule window

Exporting XML Formatted Results

To export Corridor4DM data to an XML Formatted file, click the **XML Export** button in the Corridor4DM application Control Panel *(Figure 12.17)*.


Save Data

DICOM Results

Result Format: Composite v7.0

Datasets to Save

☑ Tomo ☑ Recon Tomo ☑ 4DM Processed Results ☑ 4DM Patient Information

File Results

XML Formatted Results

☑ Create an XML File

Format: 4DM ☐ Display with Web Browser

File Name: C:\Users\Public\Documents\INVIA\Corridor4DM\xmlFinal\4DMSPECT001_004-0011DGS_R(Ischemic2)_0

Text Delimited Results

☑ Create a Delimited Text File

☐ Append

File Name: C:\Users\Public\Documents\INVIA\Corridor4DM\statdata\mspect_stats.txt

Figure 12.17: *XML Results options within the Save Data window*

Dataset Matching Strings

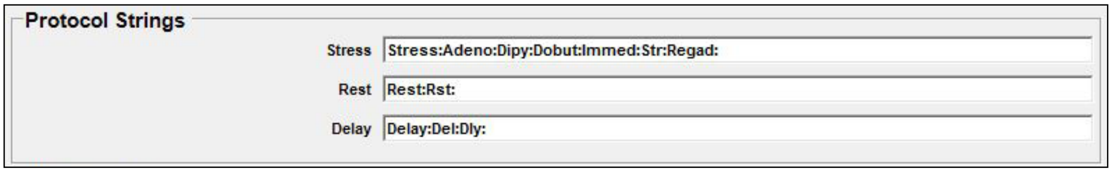
Corridor4DM relies on the default text strings to automatically recognize certain files and protocols. In addition to the Corridor4DM standard strings, users can add strings so Corridor4DM can recognize site-specific naming conventions. These added strings are matched to the site-specific dataset description (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.

To add a string to any of the protocol fields, type the new string in the appropriate field followed by a colon.

Protocol Strings

Corridor4DM identifies the protocol type (e.g., Stress, Rest, and Delay) by matching the dataset description with the character strings *(Figure 12.18)*. Users can reset all dataset matching strings fields to Corridor4DM defaults by selecting the **Reset** button.

WARNING
Matching a dataset to the wrong protocol type could lead to the misinterpretation of a study. The user must verify that the string is entered in the proper protocol category and that a dataset can't be matched to multiple protocol types.



Protocol Strings

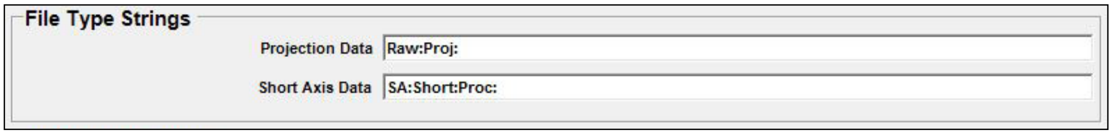
Stress	Stress:Adeno:Dipy:Dobut:Immed:Str:Regad:
Rest	Rest:Rst:
Delay	Delay:Del:Dly:

Figure 12.18: *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 Corridor4DM to recognize these files, identification strings can be defined *(Figure 12.19)*.

WARNING
Matching a dataset to the wrong **file type** could cause the program to load the wrong dataset into a display screen.



File Type Strings

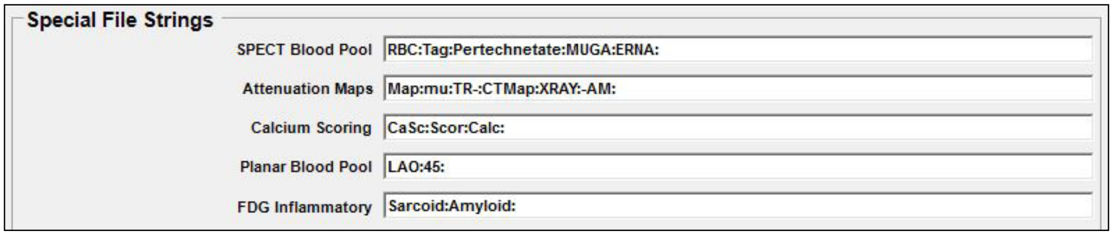
Projection Data	Raw:Proj:
Short Axis Data	SA:Short:Proc:

Figure 12.19: *File Type Strings*

Special File Strings

Corridor4DM 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 12.20)*.

The user must review the volume loaded to ensure that the image was acquired without the utilization of a contrast medium. In the case that the dataset is not excluded automatically, the user should edit the **Ca Scoring** strings (within the **Special File Strings**) to eliminate the dataset from the **Ca Scoring** Screen.



Special File Strings

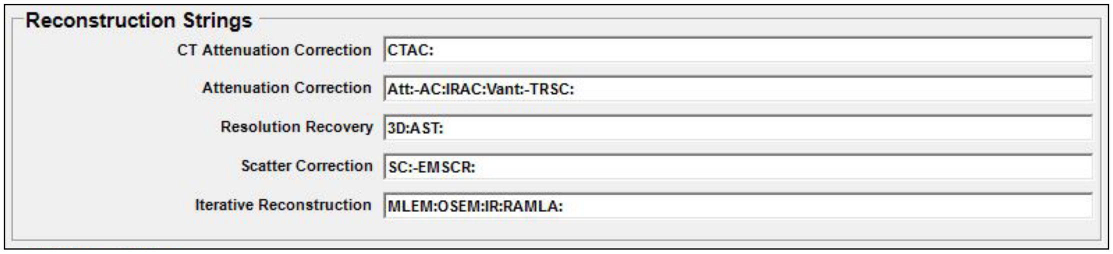
SPECT Blood Pool	RBC:Tag:Pertechnetate:MUGA:ERNA:
Attenuation Maps	Map:mu:TR-:CTMap:XRAY:-AM:
Calcium Scoring	CaSc:Scor:Calc:
Planar Blood Pool	LAO:45:
FDG Inflammatory	Sarcoid:Amyloid:

Figure 12.20: *Special File Strings*

Reconstruction Strings

Corridor4DM uses these strings *(Figure 12.21)* to identify the corrections used during image reconstruction to accurately compare the dataset to the appropriate normals database. Corridor4DM

If datasets available on the MUGA screen does not include the dataset of choice, check the Special File Strings by clicking on the Dataset Matching Strings button in the Preferences menu. To learn more about editing matching strings, go to [User Preferences.]()



Reconstruction Strings

CT Attenuation Correction	CTAC:
Attenuation Correction	Att:-AC:IRAC:Vant:-TRSC:
Resolution Recovery	3D:AST:
Scatter Correction	SC:-EMSCR:
Iterative Reconstruction	MLEM:OSEM:IR:RAMLA:

Figure 12.21: *Reconstruction Strings*

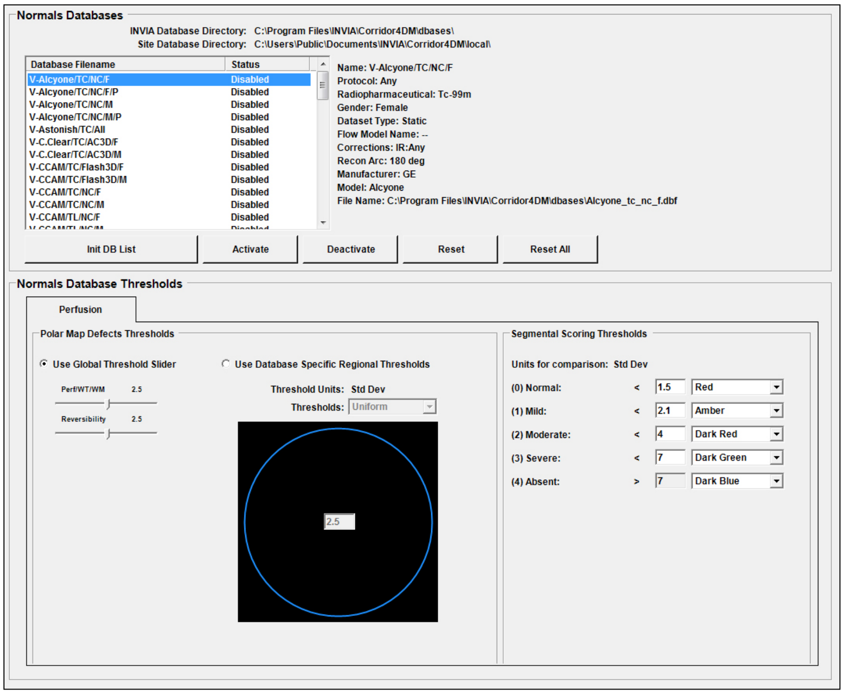
initially tries to determine the reconstruction method by searching the DICOM header fields. Corridor4DM will consider all files that don't match a minimum of one of these fields as generated utilizing FBP.

Normals Databases

The Normals Databases page within Preferences *(Figure 12.22)* is a password protected page that allows the user to control which Normals Databases are active in Corridor4DM, and make any changes to the Segmental Scoring Thresholds and Defect Threshold Settings for **Perfusion**, **Wall Thickening**, and **Wall Motion**.

The password to unlock and edit this page is **MSPECT4D**.

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.



Normals Databases

INVIA Database Directory: C:\Program Files\INVIA\Corridor4DM\dbases\
Site Database Directory: C:\Users\Public\Documents\INVIA\Corridor4DM\local\

Database Filename	Status
V-Alcyone/TC/NC/F	Disabled
V-Alcyone/TC/NC/F/P	Disabled
V-Alcyone/TC/NC/M	Disabled
V-Alcyone/TC/NC/M/P	Disabled
V-Astonish/TC/All	Disabled
V-C.Clear/TC/AC3D/F	Disabled
V-C.Clear/TC/AC3D/M	Disabled
V-CCAM/TC/Flash3D/F	Disabled
V-CCAM/TC/Flash3D/M	Disabled
V-CCAM/TC/NC/F	Disabled
V-CCAM/TC/NC/M	Disabled
V-CCAM/TL/NC/F	Disabled

Name: V-Alcyone/TC/NC/F
Protocol: Any
Radiopharmaceutical: Tc-99m
Gender: Female
Dataset Type: Static
Flow Model Name: --
Corrections: IR:Any
Recon Arc: 180 deg
Manufacturer: GE
Model: Alcyone
File Name: C:\Program Files\INVIA\Corridor4DM\dbases\Alcyone_tc_nc_f.dbf

Normals Database Thresholds

Perfusion

Polar Map Defects Thresholds

● Use Global Threshold Slider
○ Use Database Specific Regional Thresholds

Perf/WT/WM 2.5
Reversibility 2.5

Threshold Units: Std Dev
Thresholds: Uniform

Segmental Scoring Thresholds

Units for comparison: Std Dev

(0) Normal: < 1.5 Red
(1) Mild: < 2.1 Amber
(2) Moderate: < 4 Dark Red
(3) Severe: < 7 Dark Green
(4) Absent: > 7 Dark Blue

Figure 12.22: *Normals Databases page in Preferences*

Normals Databases

The directories for the Normals Databases within Corridor4DM 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, Database Type, Flow Model Name, 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 Corridor4DM 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

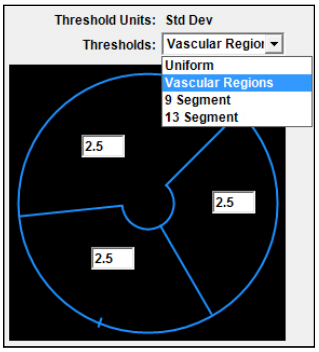
The user can set the Polar Map Defect and Segmental Scoring Thresholds presented in units of standard deviations (StDv) below the normal mean. The **Perfusion**, **Wall Thickening**, and **Wall Motion** tabs allow parameters to be defined for the polar map defect and segmental scoring thresholds. The three tab controls are only present when the Normals Database that is highlighted in the selection window contains the associated parameters.

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.

- **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 Corridor4DM. 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 12.23)*. The segmental overlays are:
  - Uniform
  - Vascular
  - 9 Segment
  - 13 Segment

  Corridor4DM 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.


Threshold Units: Std Dev

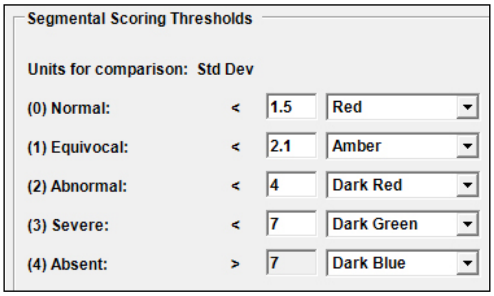
Thresholds: Vascular Regions

Figure 12.24: *Polar Map Regional Segmentation Menu*

WARNING
Changing thresholds used to classify defects can **significantly** impact the accuracy of myocardial perfusion data.

Only users familiar with Receiver Operating Characteristic (ROC) curves and the impact that changing defect thresholds can have on test sensitivity and specificity should adjust the values from the default settings.

- **Segmental Scoring Thresholds** *(Figure 12.24)***:** These settings allow the user to change the automatic, semi-quantitative scoring thresholds in Corridor4DM. Users can define the numerical value (in StDv) for **Units for Comparison**, and can set the color scheme that is associated with each threshold.


Segmental Scoring Thresholds

Units for comparison: Std Dev

(0) Normal:	<	1.5	Red
(1) Equivocal:	<	2.1	Amber
(2) Abnormal:	<	4	Dark Red
(3) Severe:	<	7	Dark Green
(4) Absent:	>	7	Dark Blue

Figure 12.23: *Segmental Scoring Thresholds page*

WARNING
Changing thresholds used to classify defect severity can **significantly** impact the prognostic value of the summed score index.

Only users familiar with Receiver Operating Characteristic (ROC) curves and the impact that changing defect thresholds can have on test sensitivity and specificity should adjust the values from the default settings.

CHAPTER 13 CREATING NORMALS DATABASES

Corridor4DM provides users with a variety of Normals databases developed for Corridor4DM. Corridor4DM 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 13.1)*, 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:

It is customary to generate specific normal databases based on gender, radiopharmaceutical, acquisition, and processing protocols.

➊ **Stats Tool –** Activates or deactivates segmental myocardial or functional statistics displayed superimposed on Normalized polar maps.

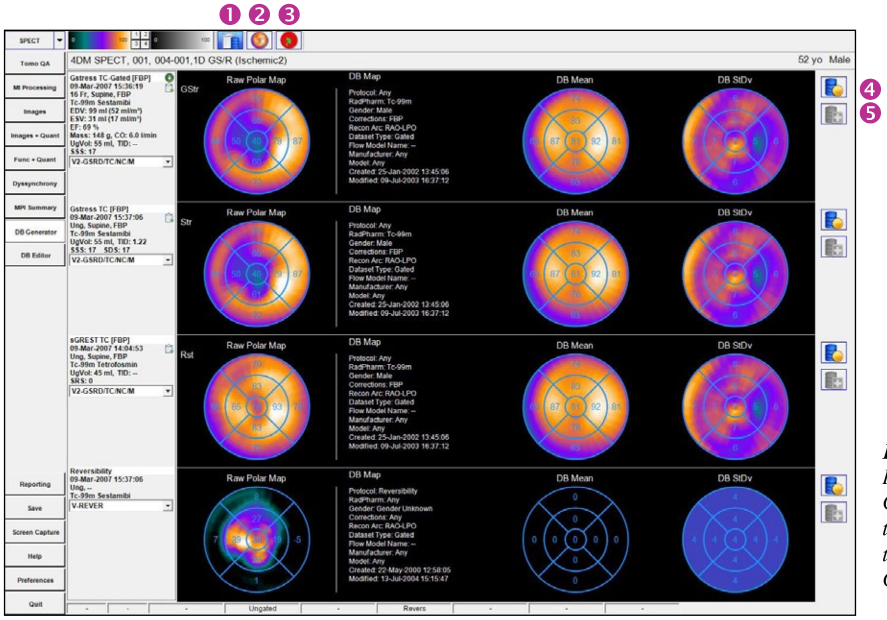
➋ **Raw Map Menu –** Provides a list of tomo data types (Ungated, ED, ES, Wall Thickening (WT) and Wall Motion (WM)) that can be displayed for the patient's dataset.

➌ **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).

➍ **Create Database Tool –** Left-click to display the **Create New Database** window.

➎ **Add Patient to Database Tool –** Left-click to add a patient's data to the selected Normals database. Once added, the tool becomes inactive.

You cannot edit a 4DM-supplied Normals database.



4DM SPECT, 001, 004-001,1D GS/R (Ischemic2)

52 yo Male

Gstress TC-Gated [FBP]
09-Mar-2007 15:36:19
16 Fr, Supine, FBP
Tc-99m Sestamibi
EDV: 99 ml (52 ml/m²)
ESV: 31 ml (17 ml/m²)
EF: 69 %
Mass: 148 g, CO: 6.0 l/min
UgVol: 55 ml, TID: --
SSS: 17
V2-GSRD/TC/NC/M

Gstress TC [FBP]
09-Mar-2007 15:37:06
Ung, Supine, FBP
Tc-99m Sestamibi
UgVol: 55 ml, TID: 1.22
SSS: 17 SDS: 17
V2-GSRD/TC/NC/M

sGREST TC [FBP]
09-Mar-2007 14:04:53
Ung, Supine, FBP
Tc-99m Tetrofosmin
UgVol: 45 ml, TID: --
SRS: 0
V2-GSRD/TC/NC/M

Reversibility
09-Mar-2007 15:37:06
Ung, --
Tc-99m Sestamibi
V-REVER

Protocol: Any
RadPharm: Tc-99m
Gender: Male
Corrections: FBP
Recon Arc: RAO-LPO
Dataset Type: Gated
Flow Model Name: --
Manufacturer: Any
Model: Any
Created: 25-Jan-2002 13:45:06
Modified: 09-Jul-2003 16:37:12

Protocol: Any
RadPharm: Tc-99m
Gender: Male
Corrections: FBP
Recon Arc: RAO-LPO
Dataset Type: Gated
Flow Model Name: --
Manufacturer: Any
Model: Any
Created: 25-Jan-2002 13:45:06
Modified: 09-Jul-2003 16:37:12

Protocol: Any
RadPharm: Tc-99m
Gender: Male
Corrections: FBP
Recon Arc: RAO-LPO
Dataset Type: Gated
Flow Model Name: --
Manufacturer: Any
Model: Any
Created: 25-Jan-2002 13:45:06
Modified: 09-Jul-2003 16:37:12

Protocol: Reversibility
RadPharm: Any
Gender: Gender Unknown
Corrections: Any
Recon Arc: RAO-LPO
Dataset Type: Gated
Flow Model Name: --
Manufacturer: Any
Model: Any
Created: 22-May-2000 12:58:05
Modified: 13-Jul-2004 15:15:47

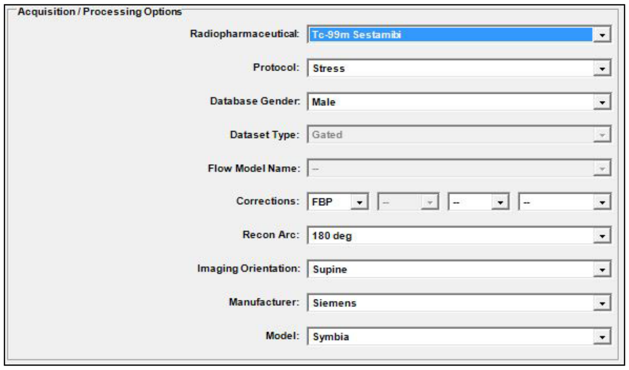
Figure 13.1: *Left-click DB Generator button in the Workflow Screens to display the DB Generator Screen*

- 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 13.2)*, Database Filename and Description *(Figure 13.3)*, and List of Database Files on System *(Figure 13.4)*.

WARNING
Creating or modifying a Normals Database must be done with extreme caution. Users should match **Acquisition and Processing Options** when generating or modifying Normals Databases. Using databases that contain conflicting or incompatible patient data can result in inaccurate quantification and the potential for a misdiagnosis.



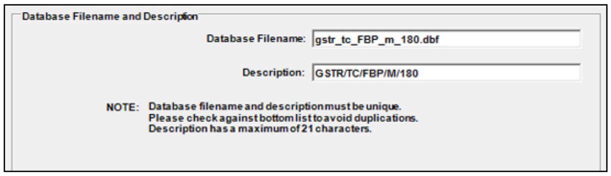
Acquisition / Processing Options

Radiopharmaceutical: Tc-99m Sestamibi
Protocol: Stress
Database Gender: Male
Dataset Type: Gated
Flow Model Name: --
Corrections: FBP | -- | -- | --
Recon Arc: 180 deg
Imaging Orientation: Supine
Manufacturer: Siemens
Model: Symbia

Figure 13.2: *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).
  - **Dataset Type:** Selected automatically based on the type of data (e.g., Gated, Static, Dynamic).
  - **Flow Model Name:** Select from a menu of available flow models (only available when the Dataset Type is Dynamic).
  - **Corrections:** Select the type of applied reconstruction corrections from a series of drop-down menus
    - Choose reconstruction method: **FBP**, **TOF**, **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.

It is strongly recommended to backup all normal database files and any patient datasets used to generate the database. To learn more, go to [User Preferences.](#) Visit the Utilities menu section for specific information on 4DM Backup features.



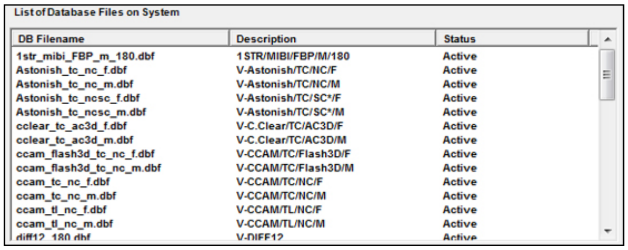
Database Filename and Description

Database Filename: gstr_tc_FBP_m_180.dbf
Description: GSTR/TC/FBP/M/180

NOTE: Database filename and description must be unique.
Please check against bottom list to avoid duplications.
Description has a maximum of 21 characters.

Figure 13.3: *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



List of Database Files on System

DB Filename	Description	Status
1str_mibi_FBP_m_180.dbf	1STR/MIBI/FBP/M/180	Active
Astonish_tc_nc_f.dbf	V-Astonish/TC/NC/F	Active
Astonish_tc_nc_m.dbf	V-Astonish/TC/NC/M	Active
Astonish_tc_ncsc_f.dbf	V-Astonish/TC/SC*/F	Active
Astonish_tc_ncsc_m.dbf	V-Astonish/TC/SC*/M	Active
cclear_tc_ac3d_f.dbf	V-C.Clear/TC/AC3D/F	Active
cclear_tc_ac3d_m.dbf	V-C.Clear/TC/AC3D/M	Active
ccam_flash3d_tc_nc_f.dbf	V-CCAM/TC/Flash3D/F	Active
ccam_flash3d_tc_nc_m.dbf	V-CCAM/TC/Flash3D/M	Active
ccam_tc_nc_f.dbf	V-CCAM/TC/NC/F	Active
ccam_tc_nc_m.dbf	V-CCAM/TC/NC/M	Active
ccam_tl_nc_f.dbf	V-CCAM/TL/NC/F	Active
ccam_tl_nc_m.dbf	V-CCAM/TL/NC/M	Active
diff12_180.dbf	V-DIFF12	Active

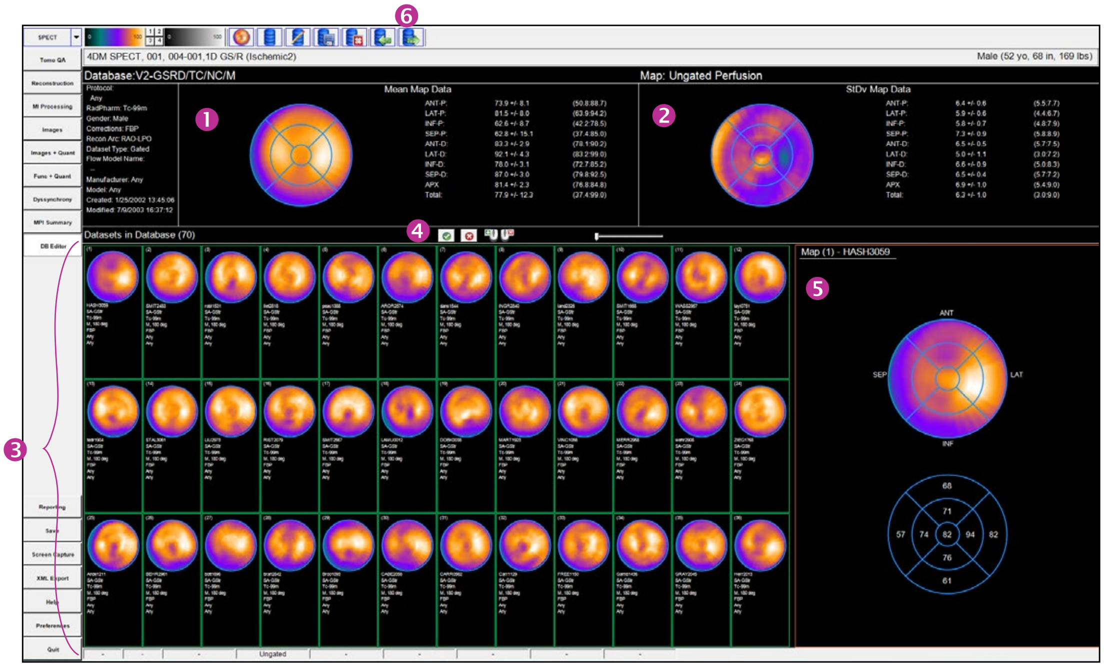
Figure 13.4: *Databases on System and window control buttons*

description of no more than 20 characters. The Description is what is listed in the Normals Database menus within Corridor4DM screens.

- **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 Corridor4DM. 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**.



4DM SPECT, 001, 004-001,1D GS/R (Ischemic2)

Male (52 yo, 68 in, 169 lbs)

Database:V2-GSRD/TC/NC/M

Map: Ungated Perfusion

Protocol:
Any
RadPharm: Tc-99m
Gender: Male
Corrections: FBP
Recon Arc: RAO-LPO
Dataset Type: Gated
Flow Model Name:
--
Manufacturer: Any
Model: Any
Created: 1/25/2002 13:45:06
Modified: 7/9/2003 16:37:12

Mean Map Data

ANT-P:	73.9 +/- 8.1	(50.8:88.7)
LAT-P:	81.5 +/- 8.0	(63.9:94.2)
INF-P:	62.6 +/- 8.7	(42.2:78.5)
SEP-P:	62.8 +/- 15.1	(37.4:85.0)
ANT-D:	83.3 +/- 2.9	(78.1:90.2)
LAT-D:	92.1 +/- 4.3	(83.2:99.0)
INF-D:	78.0 +/- 3.1	(72.7:85.2)
SEP-D:	87.0 +/- 3.0	(79.8:92.5)
APX	81.4 +/- 2.3	(76.8:84.8)
Total:	77.9 +/- 12.3	(37.4:99.0)

StDv Map Data

ANT-P:	6.4 +/- 0.6	(5.5:7.7)
LAT-P:	5.9 +/- 0.6	(4.4:6.7)
INF-P:	5.8 +/- 0.7	(4.8:7.9)
SEP-P:	7.3 +/- 0.9	(5.8:8.9)
ANT-D:	6.5 +/- 0.5	(5.7:7.5)
LAT-D:	5.0 +/- 1.1	(3.0:7.2)
INF-D:	6.6 +/- 0.9	(5.0:8.3)
SEP-D:	6.5 +/- 0.4	(5.7:7.2)
APX	6.9 +/- 1.0	(5.4:9.0)
Total:	6.3 +/- 1.0	(3.0:9.0)

Datasets in Database (70)

Map (1) - HASH3059

Figure 13.5: Corridor4DM's DB Editor Screen

You cannot edit a 4DM-supplied Normals database.

The **DB Editor** screen *(Figure 13.5)* includes the following components:

① **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.

② **Standard Deviation (StDv) Map Data –** Displays the variance distribution with a 9-segment overlay derived from 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 StDvs are shown, followed by the minimum and maximum ranges for each segment in parentheses.

③ **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.
- **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 13.6)*:

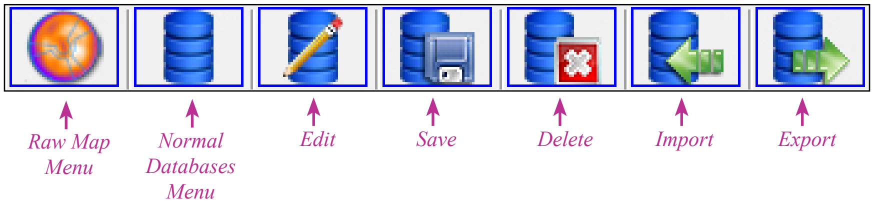


Figure 13.6: *DB Editor Toolbar*

- **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

4DM-supplied databases may be deleted from the menu but not the system disk.

- **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.

Symbols

	**MANUFACTURER**
	**DATE OF MANUFACTURE**
REF	**CATALOGUE NUMBER**
	**CONSULT INSTRUCTIONS FOR USE**
	UNIQUE DEVICE IDENTIFIER (UDI)
Rx only	**PRESCRIPTION DEVICE**

Rx only

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