Chapter 4 SPECT Cardiac Imaging

The SPECT cardiac imaging workflow uses these screens:

- Tomo QA
- MI Processing
- Images
- Images + Quant
- Func + Quant
- Dyssynchrony
- MPI Summary

Corridor4DM provides each user with several options to create diagnostic workflows that maximize efficiency while providing accurately quantified data for interpretation. This chapter provides a sample 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

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:

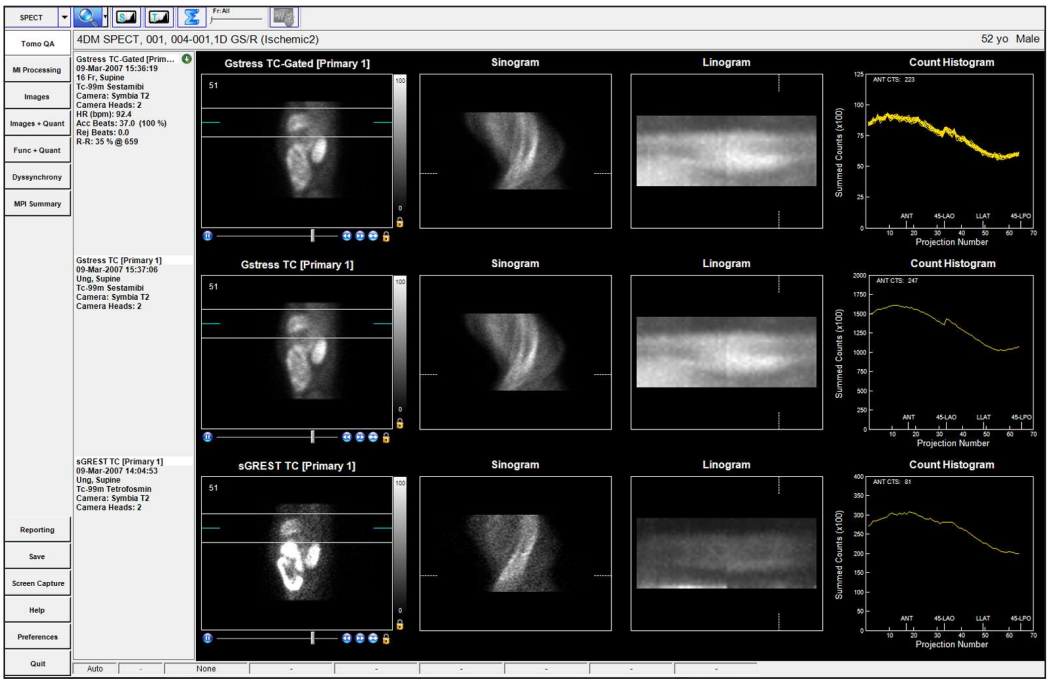

Figure 4.1: *The Tomo QA screen with three datasets displayed. Top: Gated stress (with Gating Information). Middle: Ungated Stress. Bottom: Ungated rest*

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

- **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.

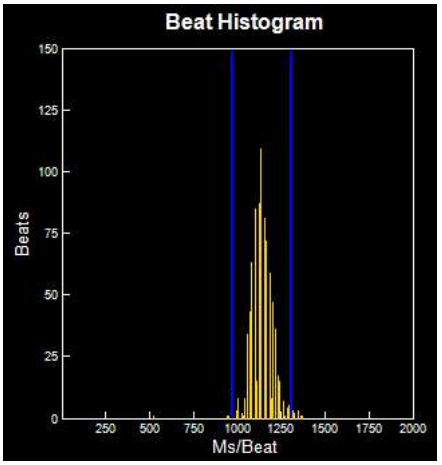

Figure 4.2: *The Beat Histogram on the Tomo QA screen.*

- **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.

- **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).

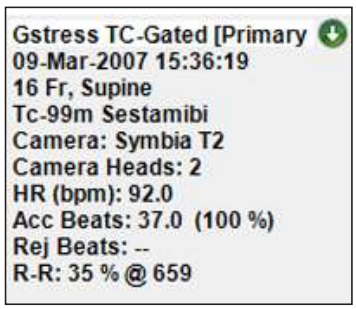

Figure 4.3: *The Gating Information in the Dataset Information Panel*

- **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 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.

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

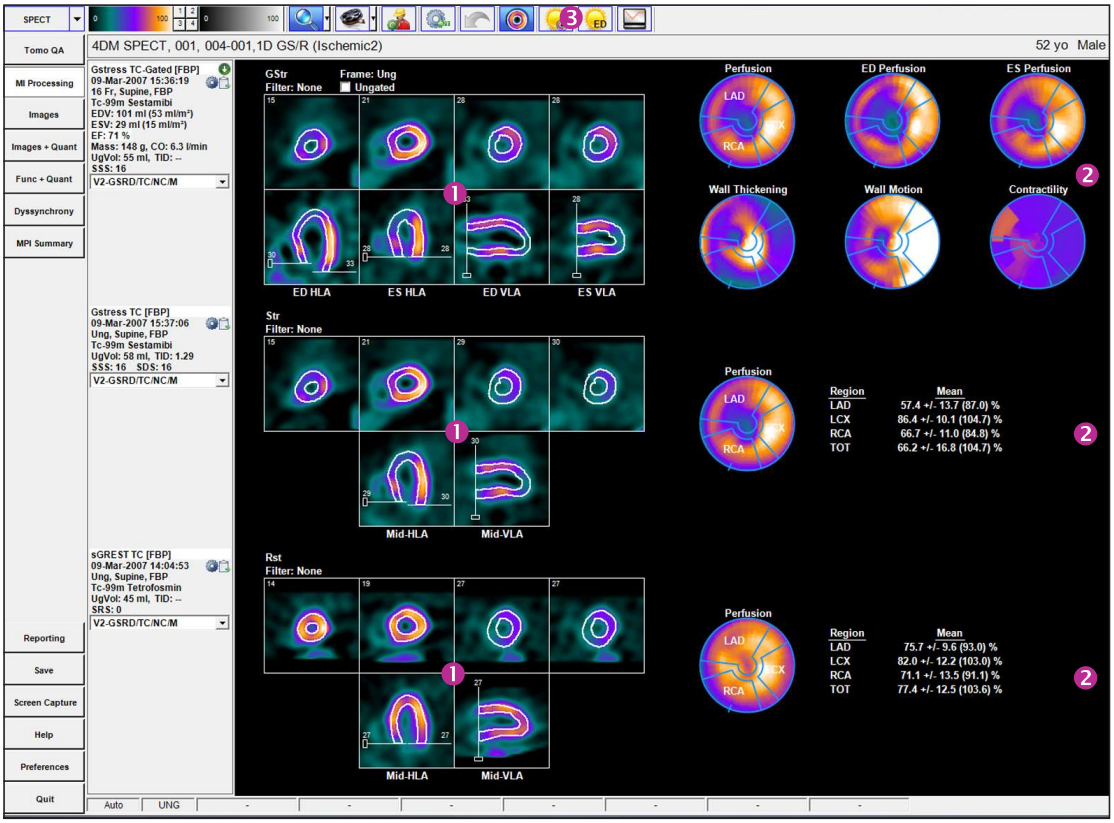

Figure 4.4: *MI Processing Screen with three datasets – gated stress, stress and rest – displays ❶ Processing Splash Objects and ❷ Processing Polar Map Objects for each dataset by default. Click the ❸ LV Volume Curve tool to display the LV Volume Curve for gated studies.*

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

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.

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

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.

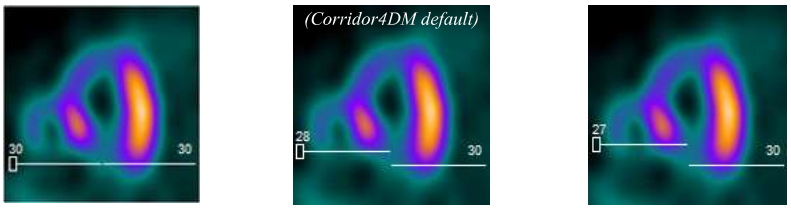

Figure 4.5: *The three Corridor4DM basal limit Preference settings for determining the basal limit for perfusion maps.*

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.

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

Figure 4.6: *The Contours tool*

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

Figure 4.7: *Manual Processing tool*

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.

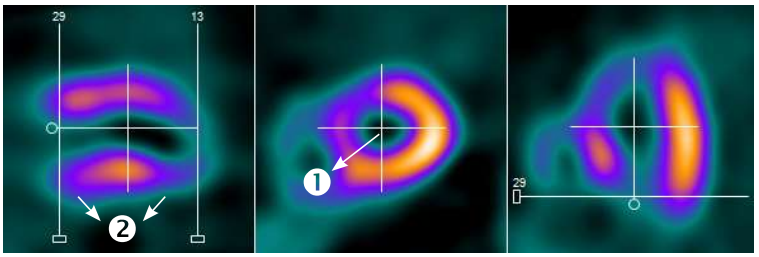

Figure 4.8: *Examples of proper positioning on the MI Processing - Manual Processing screen*

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.

Figure 4.9: *Constraints tool*

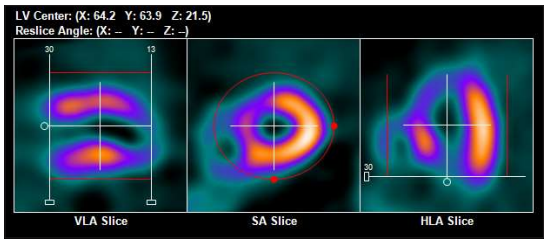

Figure 4.10: *Constrains activated and properly positioned*

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, angulation, valve plane location and click the Process tool to reprocess.

Figure 4.11: *Process tool*

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

Figure 4.12: *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. 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.
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)*.
5. Left-click and drag with the nudge tool near the red midline will adjust it based on how mouse is moved. Once the mouse is released, the white epi- and endocardial contours will appear evaluation.
6. Plane slicers can be overlaid to help 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.

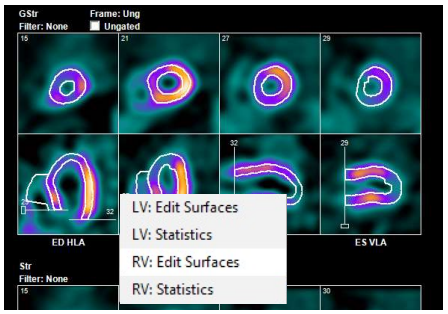

Figure 4.13: *MI Processing in QA Mode, showing a study with bad contours in an area of almost no myocardial uptake.*

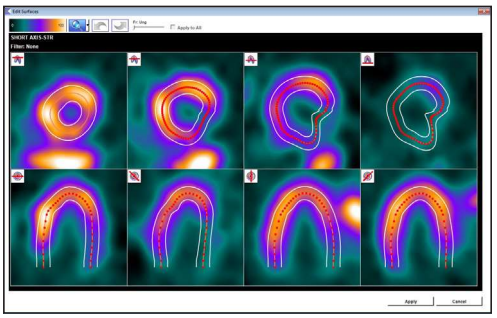

Figure 4.14: *Edit Surface window showing a study before corrections*

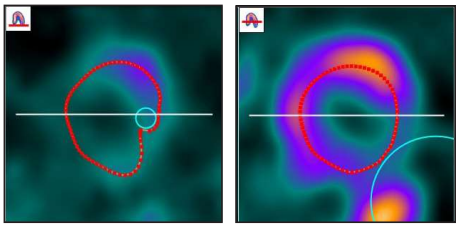

Figure 4.15: *(Left image) Click close to the red midline points to use the small nudge tool. (Right image) Click further away from the red midline to use the large nudge tool.*

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

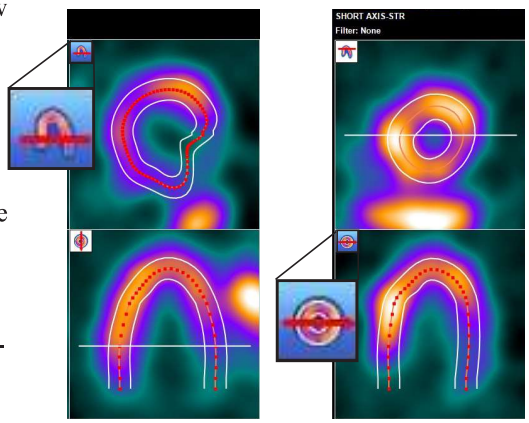

Figure 4.16: *(Left image) – Click the SA plane slicer to show the SA line of reference on the LA view below it. (Right image) – Click the LA plane slicer to show the LA line of reference on the SA image above it.*

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)*.

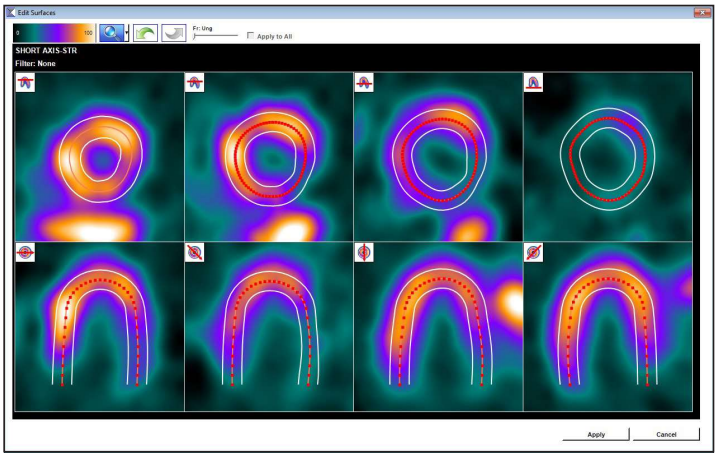

Figure 4.18: *Contours after corrections are made. Click the Apply button to apply the new surfaces to the dataset.*

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.

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 (Post->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**.

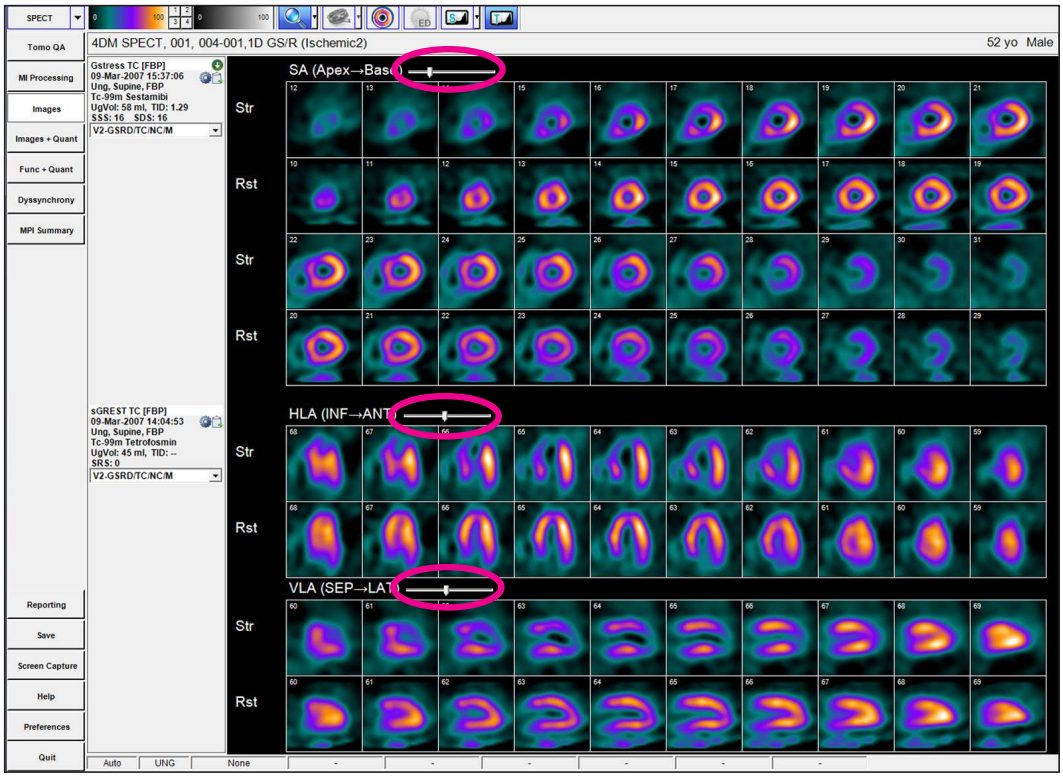

Figure 4.19: *The Images screen with ungated stress and rest SA, HLA, and VLA Splash Objects displayed. The Dataset Slice Slider is circled in pink above each Splash Object.*

Quantitative Perfusion Review

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 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.

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

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

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.

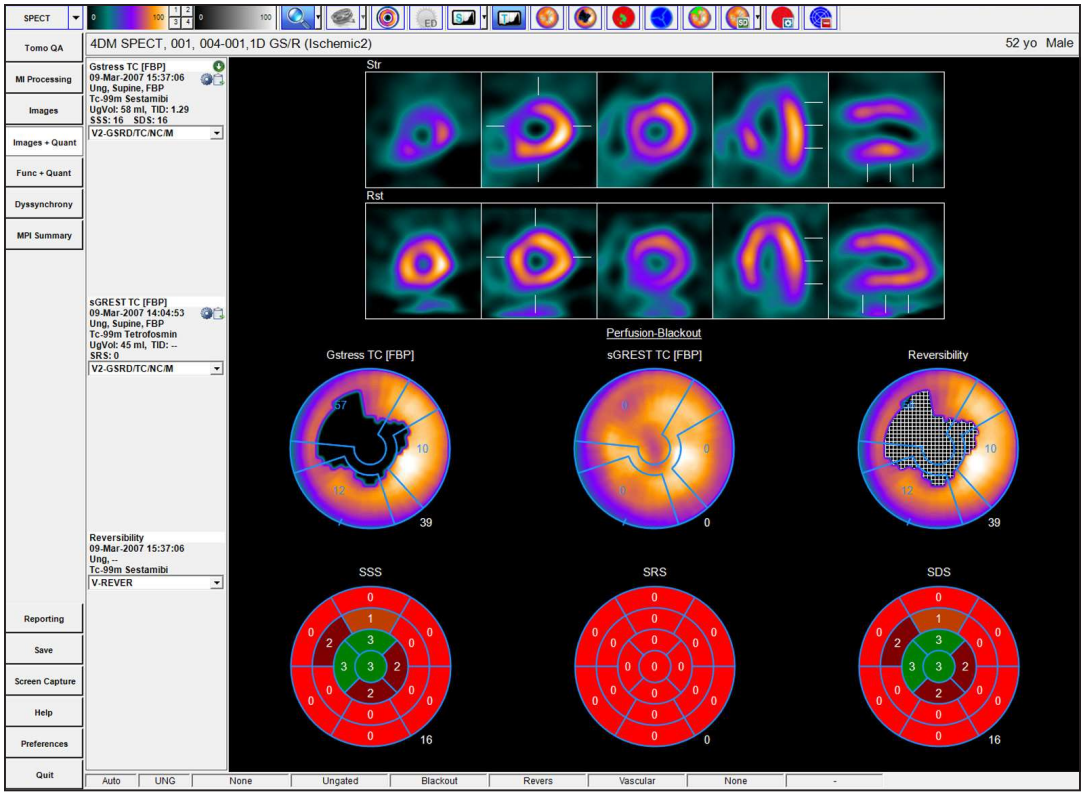

Figure 4.20: *The Images+Quant screen utilizing the Defect Blackout reversibility Polar maps and correlating semi-quantitative scores.*

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 studies should assess the **LV Volume Curve** because it provides detailed systolic and diastolic functional information.

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)*.

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.

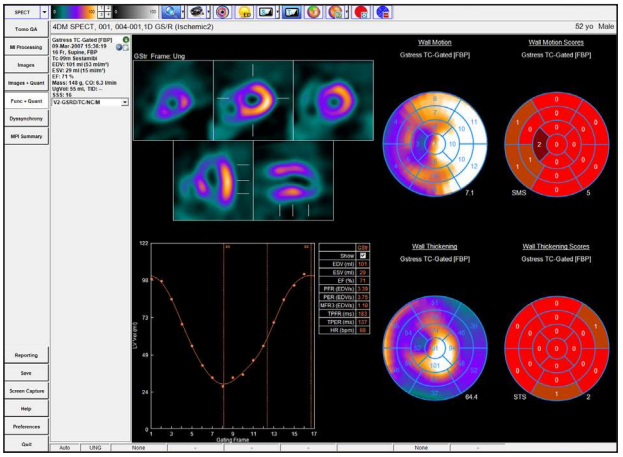

Figure 4.21: *The Func+Quant screen with one gated dataset displayed.*

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:

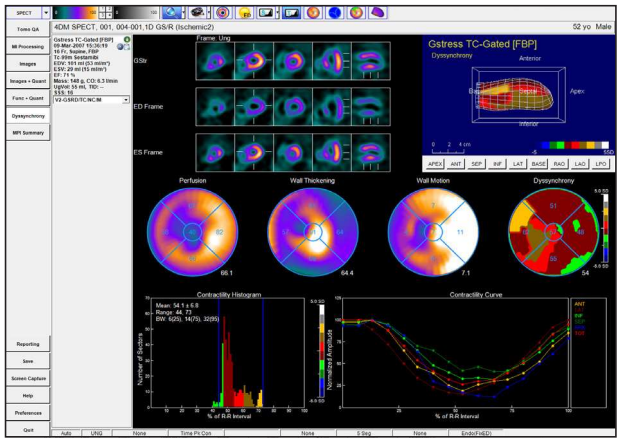

Figure 4.22: *The Dyssynchrony screen was created for assessing the phases of contraction for the left ventricle.*

- **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.

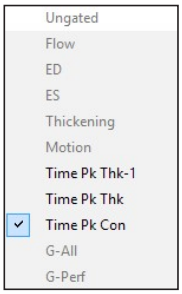

Figure 4.23: *Raw Map Menu*

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.

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**

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

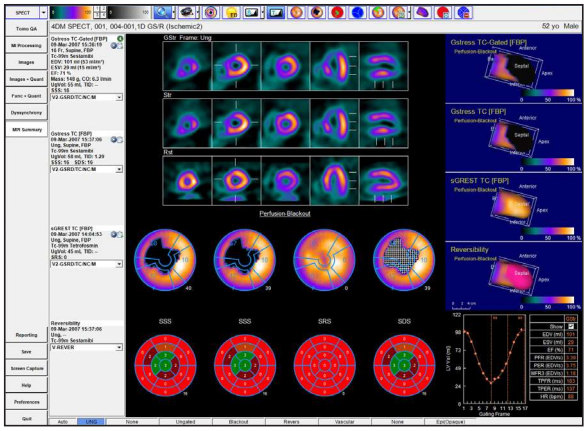

Figure 4.24: *The MPI Summary screen displaying gated stress, ungated stress and rest datasets and all perfusion and function information on one screen for quick review*

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.