Reconstruction

OVERVIEW

For myocardial perfusion and gated blood pool SPECT studies, the raw tomographic datasets must be reconstructed into volumetric datasets for left ventricular (LV) quantitative processing in 4DM. Tomographic datasets should be evaluated for overall quality, and motion correction should be applied to correct any motion that can detract from the quality of the study and create the potential for misinterpreting LV quantifications.

The 4DM Reconstruction Screen is used to generate gated and non-gated transverse reconstructed datasets, with the option to apply automatic or manual motion correction when necessary. Additionally, 4DM can be used to generate motion corrected tomographic datasets that can be sent to other vendor workstations (e.g., GE Xeleris, Philips EBW, Siemens MMWP) for reconstruction. 4DM utilizes standard filtered back-projection (FBP) to reduce image noise for reconstructed volumes.

4DM Reconstruction is beneficial for those sites using older, non-dicom compliant OEM workstations, or those sites wishing to streamline reconstruction of patient studies from multiple camera vendors to one workstation.

The Reconstruction screen is available within 4DM for users who purchase the Reconstruction option.

Within the 4DM Reconstruction screen, users can select from multiple filter types and make adjustments to order and cutoff settings for up to four datasets simultaneously. Orientation and alignment tools are available to define the reconstruction parameters for individual datasets, and gated datasets are synchronized to the ungated datasets by default for efficiency. The 4DM Reconstruction option allows users to perform image reconstruction and quantification within a single application, and users seamlessly transition into the MI Processing screen for LV quantification quality assurance (QA) and study review.

HOW TO GUIDE

USING 4DM FOR RECONSTRUCTION AND MOTION CORRECTION

To reconstruct and apply motion correction to raw patient image data within 4DM, review each dataset and make changes as required.

*The **Reconstruction** screen is not activated by default. For instructions on how to activate a screen, refer to the **Changing the Workflow** Reference Guide.*

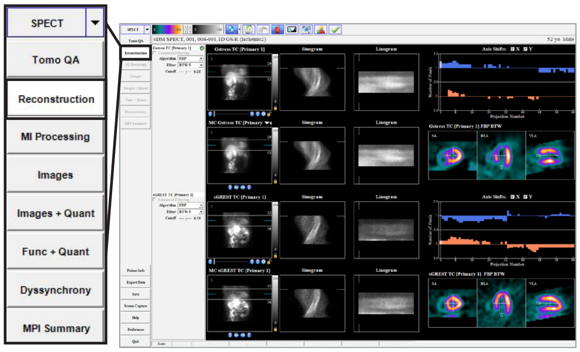


Figure 1. Reconstruction Screen

1. Launch the available raw datasets into 4DM. The number of raw datasets will vary based on the acquisition protocol.
2. Use the **Tomo QA** screen to evaluate patient motion for the raw datasets.
3. Select the **Reconstruction** screen (Figure 1) from within the SPECT workflow. The default layout for the Reconstruction screen displays the Stress and Rest non-gated datasets. Any corrections applied to the non-gated datasets are automatically synchronized to the corresponding gated datasets. When only one dataset is displayed on the Reconstruction screen, a splash object is present with additional image slices for review. The reconstruction settings for each dataset are displayed in the Dataset Information Panel and any changes to reconstruction settings will be reflected in the updated sample slice displays.

   Use the Dataset Layout Selector to display any additional datasets for reconstruction.

4. Review the **Tomo Viewport** (Figure 2) to assess the original tomographic Stress and Rest datasets, prior to motion correction. The original dataset names will be displayed above each Tomo Viewport.

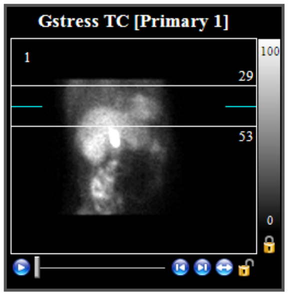


Figure 2. Tomo Viewport

5. Use the **Cine Tools** for each Tomo Viewport to manage the cine display:
    a. **Start/Stop** – Left-click on the Start/Stop button (see ❶ Figure 3) to pause and play the cine.
    b. **Frame Slider** – When the cine is paused, the frame slider (see ❷ Figure 3) will allow the user to manually move through individual projections by left-clicking the slider and dragging to the left or right.
    c. **White Slice Plane Indicators** – Left-click and drag the white slice plane indicators (see ❸ Figure 3) to define the limits of the area around the myocardium used to identify patient motion, the range of slices to include in the reconstructed volume, and to assist the user in visualizing motion artifacts while reviewing the cine. The slice plane indicators within the **Motion Correction Viewport** also define the volume of information displayed in the sample reconstruction **Slice Displays** below the X,Y Axis Shifts Graph. Position the Slice Plane Indicators a few pixels above and below the myocardium to avoid truncation.

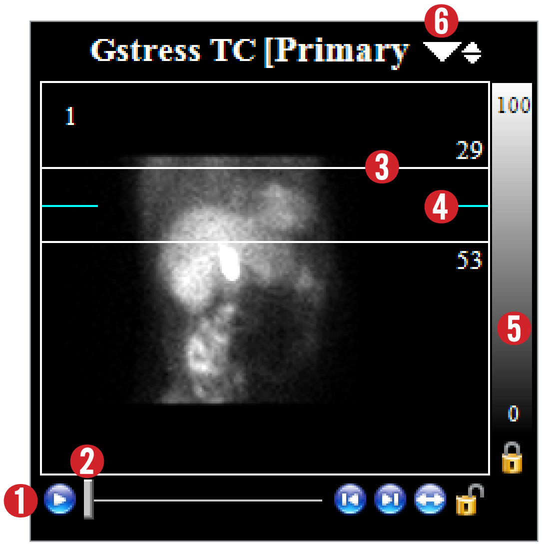


Figure 3. Tomo Viewport tools

    d. **Blue Slice Plane Indicator** – Left-click and drag the blue slice plane indicator (see ❹ Figure 3) to define the maximum intensity pixel for image normalization and the slice used for Sinogram composition and display.
    e. **Tomo Colorbar** – Left-click and drag the ends of the colorbar spectrum (see ❺ Figure 3) to make adjustments to the **Background** and **Brightness**.
    f. When a gated dataset is present, left-click the drop-down arrow to the right of the dataset name (see ❻ Figure 3) to display and verify corrections applied to the gated dataset.

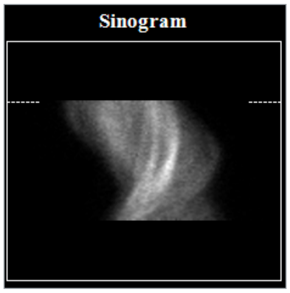


Figure 4. Sinogram

6. Review the **Sinogram** (Figure 4) for identification of side-to-side patient motion or shifting of the detectors between multi-detector systems. Sinogram reference lines identify the corresponding projection in the tomographic data.
7. Review the **Linogram** (Figure 5) for identification of axial patient motion and heart motion (e.g. cardiac creep). Linogram reference lines identify the corresponding projection in the tomographic data.

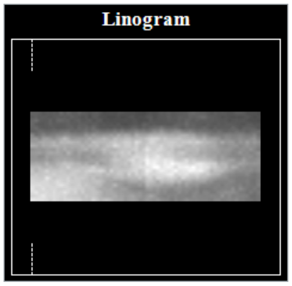


Figure 5. Linogram

8. Review the **<u>Motion Correction</u> Tomo Viewport** (Figure 6) using the Cine Tools to assess the motion corrected tomographic Stress and Rest datasets and slices. An **MC** will be added to the dataset name to signify the study has been motion corrected.
9. The corresponding motion corrected **Sinogram** and **Linogram** screen objects are available to review any updates post-motion correction.

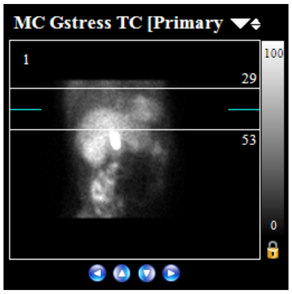


Figure 6. Motion Correction Tomo Viewport

10. **Automatic Motion Correction**

    a. Use the **X,Y Axis Shifts Graphs** (Figure 7) to review the number of pixel corrections applied to the Stress and Rest datasets through automatic motion correction. The graphs plot 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.

    b. Users can select to correct in one or both axes by selecting the **X** (see ❶ Figure 7) and/or **Y** (see ❷ Figure 7) **checkboxes** above the axis shifts graph.

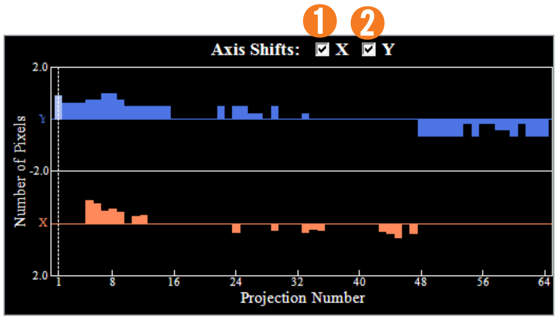


Figure 7. X,Y Axis Shifts Graphs

*Deselect the X and Y checkboxes above to turn automatic motion correction off for the study. The Motion Correction Viewport will update the dataset name to **No Corrections** to reflect that motion correction has been turned off for the dataset.*

11. **Manual Motion Correction**

    a. There are two methods for manual motion correction:

    - Left-click and drag anywhere outside of the white slice plane indicators within the motion corrected viewport (see ❶ Figure 8) to pan the image in the either the x or y planes to update the pixel corrections applied to the x and y axis.
    - Use the four manual pan controls located below the motion corrected viewport (see ❷ Figure 8). The up and down arrows will pan the image up or down within the motion corrected viewport and the axis shifts graph will display updated pixel corrections applied to the y-axis. The left and right arrows will pan the image left or right within the motion corrected viewport and the axis shifts graph will display updated pixel corrections applied to the x-axis. Each click moves the dataset in the selected direction ¼ of a pixel.

      Datasets that require more than 2 pixels of correction in any frame should be re-acquired if possible.

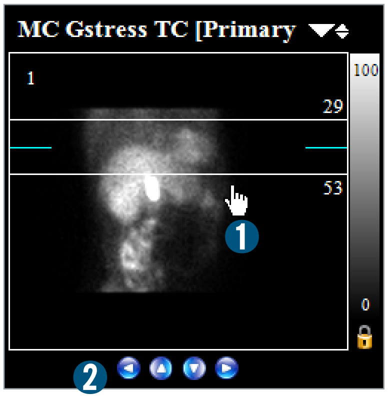


Figure 8. Motion Correction Viewport

12. Left-click and drag the **cross-hair** to the center of the LV within the sample **SA Slice Display** (see ❶ Figure 9).

13. Left-click and drag the **orientation tool** at the base of the **HLA** and **VLA Slice Displays** (see ❷ Figure 9) to correctly orient the sample slices for reconstruction. For correct orientation, the apex should point towards 12 o'clock for the HLA sample slice and 3 o'clock for the VLA sample slice.

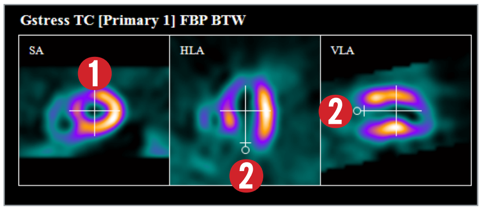


Figure 9. SA, HLA, and VLA Slice Displays

14. After all adjustments have been made, left-click on the dataset name (see ① Figure 10) above the SA slice display to rename the reconstructed dataset to be generated.

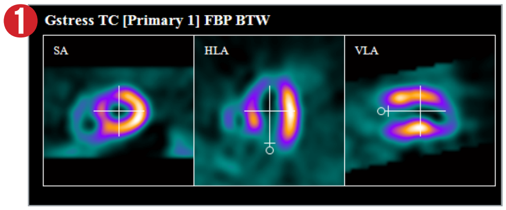


Figure 10. SA Slice Display

15. Click the **Apply Tool** (Figure 11) to accept and apply automatic adjustments.
    - If the Apply Tool is not selected, and another workflow screen is clicked for display, a window will present that provides an option to proceed and apply the corrections and reconstructions (click OK), or to proceed without applying (click Cancel).

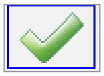


Figure 11. Apply tool

16. 4DM will automatically display the MI Processing screen for users to verify and process the newly created reconstructed datasets (for post-reconstruction processing assistance, refer to the MI Processing Reference Guide).

USING ADVANCED RECONSTRUCTION MODE

To apply separate reconstruction parameters to gated and ungated raw patient image data, perform the following:

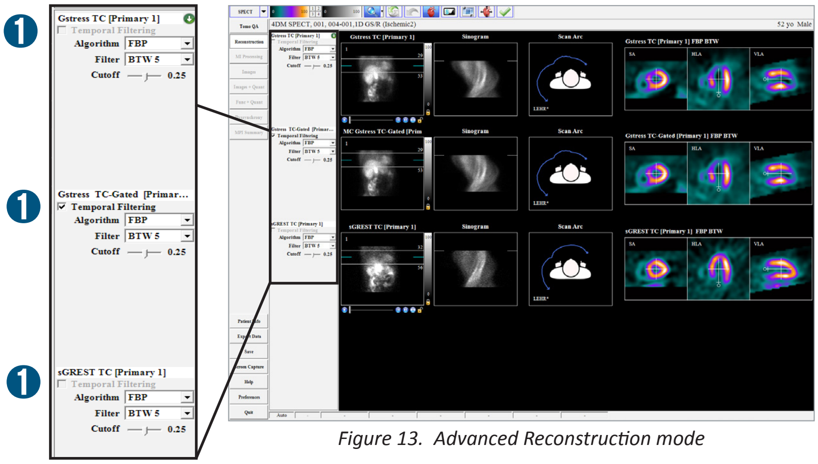
1. Select the **Advanced Reconstruction** button (Figure 12) from the 4DM toolbar and a combination of up to four datasets will display simultaneously (Figure 13). When only one dataset is displayed on the Reconstruction screen, a splash object is present with additional image slices for review.

Figure 12. Advanced Reconstruction mode

NOTE: When motion correction is turned off as a default setting, the Advanced Reconstruction Mode displays when initially launching the Reconstruction screen.

Datasets cannot be motion corrected within Advanced Reconstruction mode. Users who wish to apply or make changes to motion correction for datasets must select the Motion Correction button (Figure 14) from the 4DM toolbar to return to Motion Correction Mode.

2. Individual reconstruction settings are available in the Dataset Information Panel for the gated and ungated datasets within Advanced Reconstruction Mode (see ① Figure 13).



Gstress TC [Primary 1]
☐ Temporal Filtering
Algorithm FBP
Filter BTW 5
Cutoff 0.25

Gstress TC-Gated [Primar…
☑ Temporal Filtering
Algorithm FBP
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Algorithm FBP
Filter BTW 5
Cutoff 0.25

Figure 13. Advanced Reconstruction mode

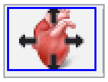


Figure 14. Motion Correction mode

3. Review the **Tomo Viewport** and adjust as required.
   - Left-click and drag the white slice plane indicators (see ❶ Figure 15) to define the range of slices to include in the reconstructed volume.
   - Left-click and drag the blue slice plane indicator (see ❷ Figure 15) to define the maximum intensity pixel for image normalization and the slice used for Sinogram composition and display.
4. The **Scan Arc** (Figure 16) replaces the Linogram for a visual assessment of the camera rotation and patient scan orientation for the dataset. The blue reference line indicates the rotation, and the circle and arrow indicate the camera's starting position and direction of rotation. Collimator type (e.g., LEHR) is displayed within the lower-left corner of the Scan Arc viewport.

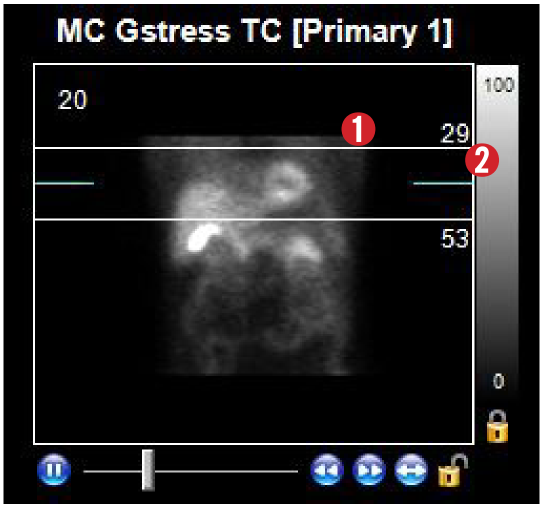


Figure 15. Motion Correction Tomo Viewport

5. Left-click and drag the **cross-hair** to the center of the LV within the sample **SA Slice Display** (see ❶ Figure 17).
6. Left-click and drag the **orientation tool** at the base of the **HLA** and **VLA Slice Displays** (see ❷ Figure 17) to correctly orient the sample slices for reconstruction. For correct orientation, the apex should point towards 12 o'clock for the HLA sample slice and 3 o'clock for the VLA sample slice.
7. After all adjustments have been made, left-click on the dataset name above the SA slice display (see ❶ Figure 18) to rename the reconstructed dataset to be generated.

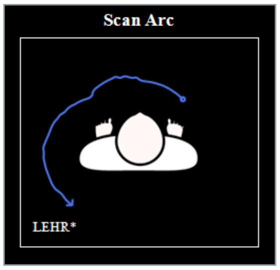


Figure 16. Scan Arc

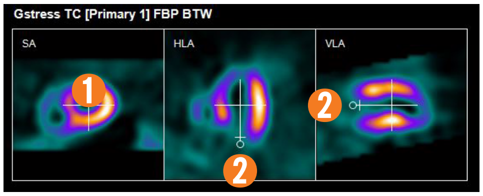


Figure 17. SA, HLA, and VLA Slice Displays

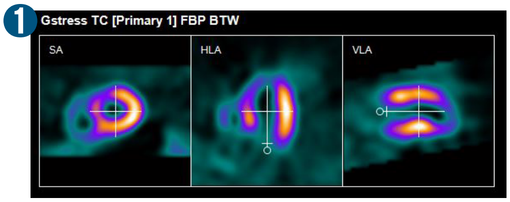


Figure 18. SA Slice DIsplay

8. Click the **Apply** tool (Figure 19) to apply the selected reconstruction parameters to the stress and rest images within the Advance Reconstruction Mode.
   - If the Apply Tool is not selected, and another workflow screen is clicked for display, a window will present that provides an option to proceed and apply the corrections and reconstructions (click OK), or to proceed without applying (click Cancel).

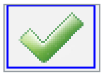
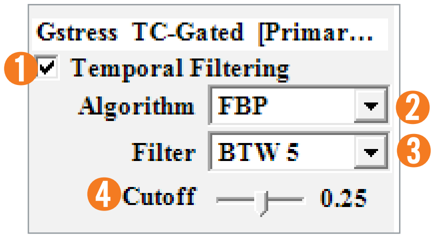


Figure 19. Apply tool

After reconstruction of the raw datasets, continue on with QA of the auto processed 4DM results and physician review.

ADJUSTING RECONSTRUCTION SETTINGS

Users can make adjustments to filter settings to achieve optimal image quality and apply masking if extra-cardiac activity is affecting the visual analysis of cardiac motion. To make adjustments to filtering and apply masking, perform the following:



Gstress TC-Gated [Primar...

☑ Temporal Filtering

Algorithm FBP

Filter BTW 5

Cutoff 0.25

Figure 20. Dataset Information Panel

1. For gated datatsets that are displayed on the Reconstruction screen, select the **Temporal Filtering** toggle (see ❶ Figure 20) within the Dataset Information Panel to apply a Temporal Filter to the gated study. Temporal filtering is useful for smoothing the transitions between adjacent frames on the cardiac cycle. Temporal filtering can be turned on as a default setting by making the preference change within 4DM.

2. The only available reconstruction algorithm option is filtered back-projection and is displayed in the **Algorithm** dropdown (see ❷ Figure 20) within the Dataset Information Panel.

3. The reconstruction **Filter** dropdown (see ❸ Figure 20) is located below the Algorithm Options within the Dataset Information Panel and allows the user to select from the following filter types:

   a. BTW 2 (Butterworth Order 2)

   b. BTW 5 (Butterworth Order 5)

   c. BTW 10 (Butterworth Order 10)

   d. Hanning

   e. Hamming

   f. Parzen

   g. Shepp

   h. Guassian

   The 4DM default reconstruction filter type is BTW 5.

4. Left-click and drag the slider tool to make adjustments to the Filter **Cutoff** frequency (see ❹ Figure 20). Moving the slider to the right will sharpen the sample images in the slice display, and moving the slider to the left will smooth the sample images in the slice display. The 4DM default frequency cutoff is 0.25.

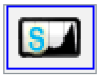


Figure 21. Spatial Filter tool

5. In the toolbar, left-click the **Spatial Filter** tool (Figure 21) to smooth the appearance of the Tomo, Motion Corrected Tomo, Sinogram, and Linogram displays for all datasets currently displayed on the Reconstruction screen.

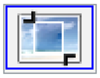


Figure 22. Image Mask tool

6. Left-click the **Image Mask** tool (Figure 22) to black out all image data outside the white slice plane indicators on the Tomo and Motion Corrected Tomo Viewports. This tool can be helpful in assessing cardiac motion in the presence of extensive extra-cardiac activity.