

**NOTE**

If during bi-weekly detector calibration, the gain has not reached convergence, update the number of iterations to **5** following steps 4 a through c in [Section 8.4.1](#) and restart the Detector Cal process.

**NOTE**

If during detector calibration the following message displays at the end of the map and gain calibration **Cathode settings are outside range, limited thermal adjustment. Calibration required**, prescribe an additional Detector Cal sequence with 3 iterations without review.

This additional calibration step is required to ensure the detectors' cathode settings are set to optimum values. The calibration procedure should automatically terminate the iterative process upon convergence, and the above-mentioned message should not appear. In the unlikely event the message is again displayed, repeat the calibration with 3 iterations.

If this message continues to appear despite prescribing multiple attempts to perform Detector Cal, contact service.

## 8.4.2 Calibration Fails for Detector Cal



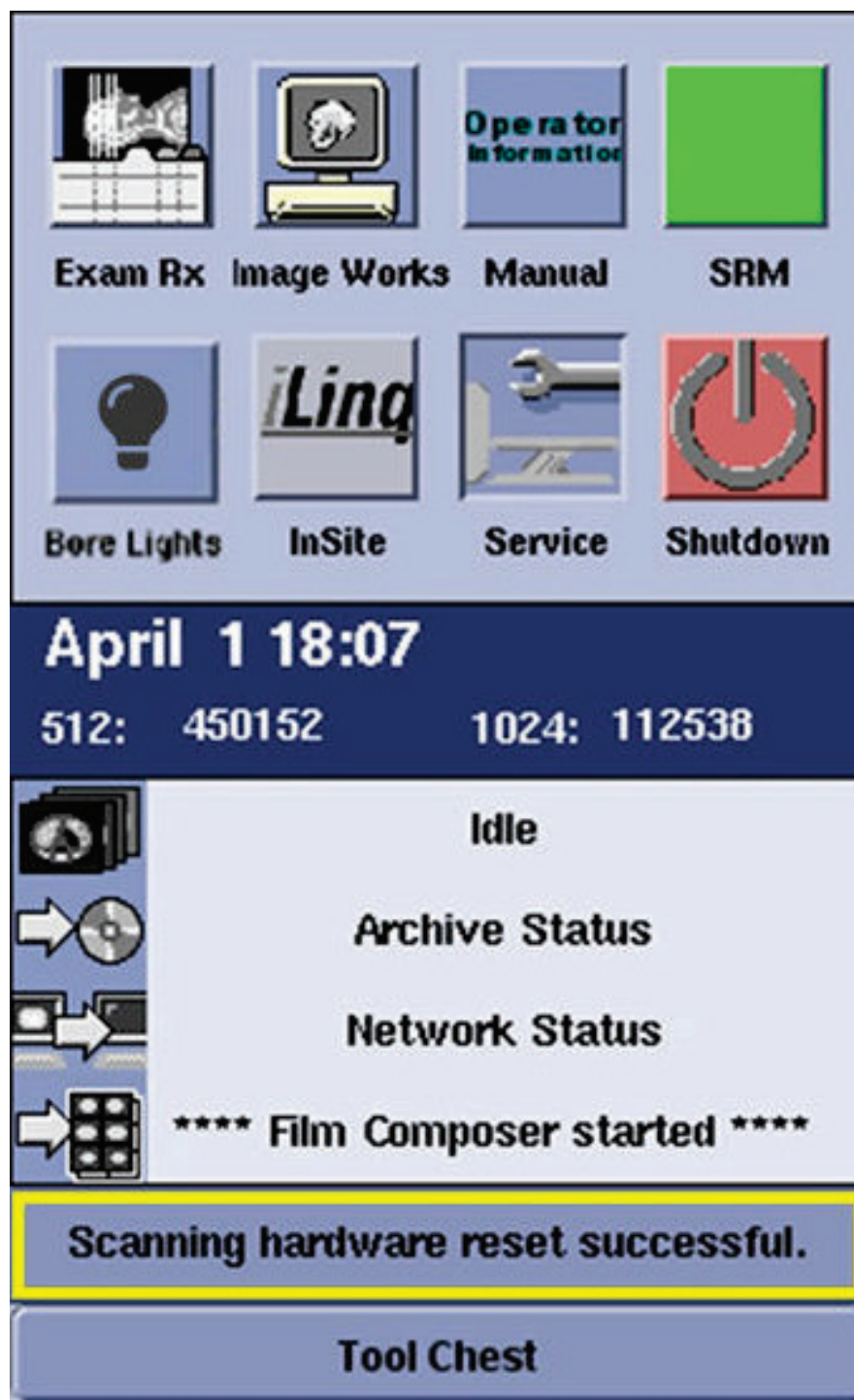
RADIATION EXPOSURE: FOLLOWING THESE STEPS REQUIRE HANDLING THE SEALED GE-68 (DQA) PHANTOM. IF POSSIBLE, AVOID HOLDING THE PHANTOM FROM THE SIDES; ALWAYS USE THE HANDLE AND THE ROUND OPENING ON ITS END-CAP. TO AVOID UNNECESSARY EXPOSURE, MINIMIZE OCCUPANCY OF THE SCANNER ROOM. FOLLOW FACILITY GUIDELINES TO HANDLE RADIOACTIVE MATERIAL.

If the system displays a Detector Cal failure message, follow this procedure to determine the cause of the failure.

1. Click on the **Status Message** area under the Exam Rx Desktop.

The **Current Messages** window opens.

Figure 156 Exam Rx Desktop Feature Status Area



2. Click **View Log** to open the **Message Log Report** window.
3. Click **Last Page** (if active) to display the most recent system messages.

Check for any errors that might contribute to the calibration failure, and document them for service.

4. Click **Close** to exit the **Message Log Report** window.
5. Return to [Detector Calibration](#) and try again.

If the procedure still fails, contact service.

## 8.4.3 Coincidence Timing Correction

### 8.4.3.1 Coincidence Timing Correction (CTC) Overview



RADIATION EXPOSURE: FOLLOWING THESE STEPS REQUIRE HANDLING THE SEALED GE-68 (DQA) PHANTOM. IF POSSIBLE, AVOID HOLDING THE PHANTOM FROM THE SIDES; ALWAYS USE THE HANDLE AND THE ROUND OPENING ON ITS END-CAP. TO AVOID UNNECESSARY EXPOSURE, MINIMIZE OCCUPANCY OF THE SCANNER ROOM. FOLLOW FACILITY GUIDELINES TO HANDLE RADIOACTIVE MATERIAL.

Follow this procedure to correct for timing differences in the detector electronics.

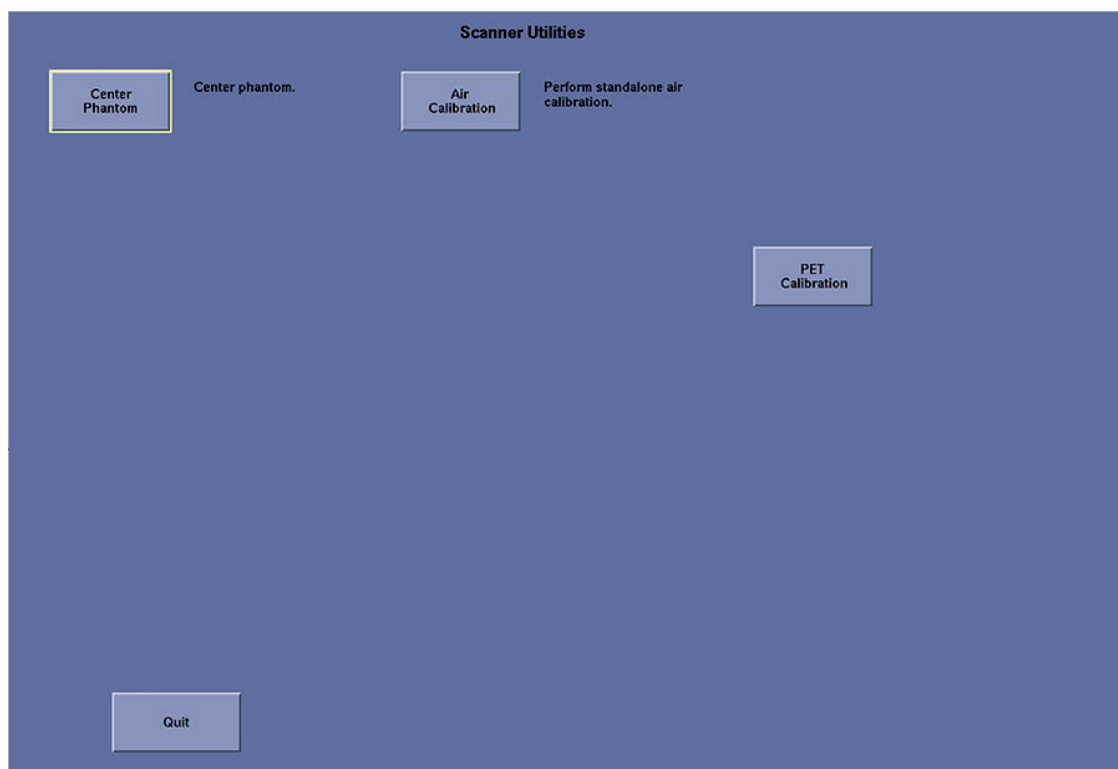
Coincidence Timing Calibration (CTC) is a part of Detector Calibration. CTC is performed after Detector calibration has met the criteria for calibrating the gain. Additionally, the system provides an option to run CTC as a standalone process.

Coincidence Timing Correction has been implemented to automatically iterate multiple times on the same acquired data set, also known as iterative CTC (iCTC). This process greatly reduces the time for calibration, making it increasingly useful as the calibration phantom decays with age.

In addition, the iCTC algorithm must correct for any misalignment of the calibration phantom from the center line of the scanner. The **Source Position** box (see [Figure 158 on page 262](#)) will turn green while the data is acquired and analyzed to produce the position correction.

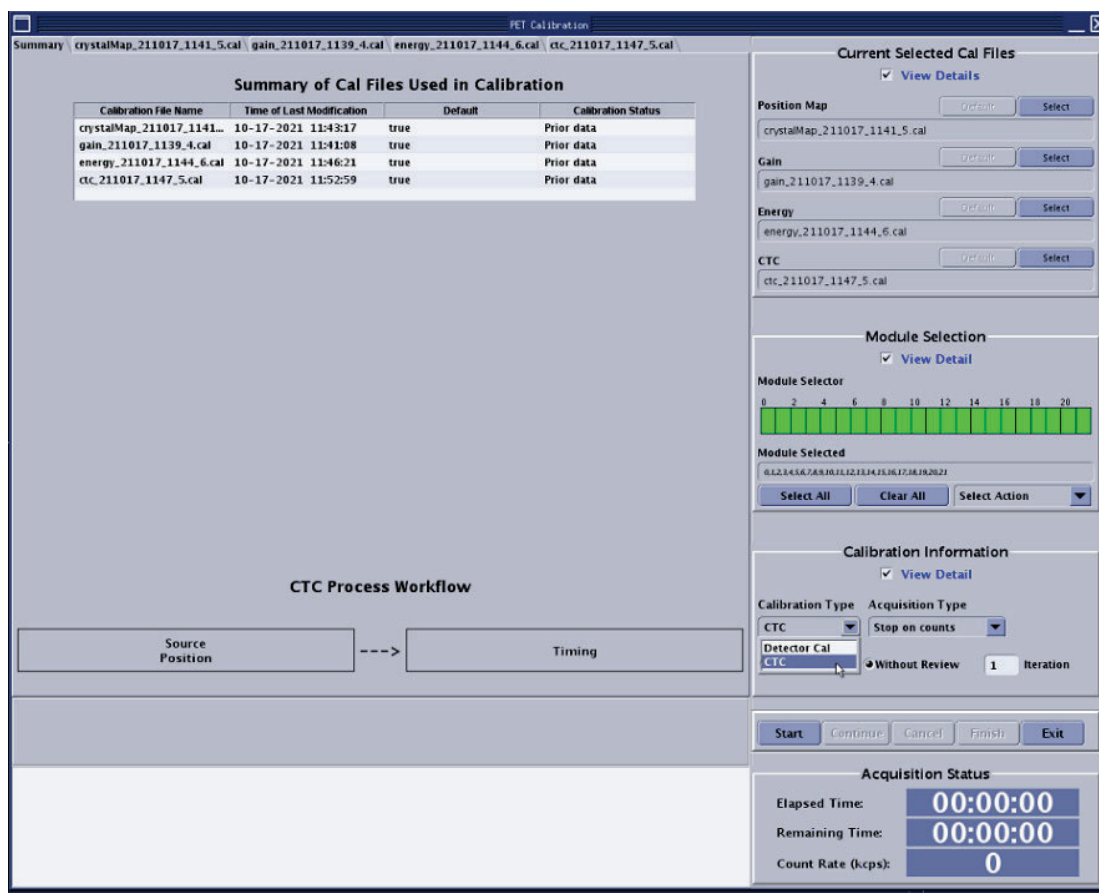
### 8.4.3.2 Coincidence Timing Correction (CTC) Procedure

1. On the scan monitor, click **Scanner Utilities** to open the **Scanner Utilities** window.

**Figure 157 Scanner Utilities Window**

2. Click **PET Calibration** to open the **PET Calibration** window.
3. Click the **View Detail** check box in the **Calibration Information** area to display information similar to that shown in [Figure 158 on page 262](#).



**Figure 158 Calibration Information Area with View Detail and CTC Selected**

- Click the **Calibration Type** down arrow to open the drop-down menu.  
Click or drag to **CTC**. The system defaults to **Stop on counts**.
- Select **Without Review**.  
Alternatively, select **With Review** for an option to save or reject the CTC data.
- Click **Start** to initiate the CTC calibration sequence on all/selected modules. A pop-up window appears prompting you to load the phantom. Refer to [Detector Cal Start Message](#). Follow the on-screen instructions.

For loading the phantom in the scanner room:

- Press/hold the **Home** gantry button. This moves the table to the load position and the height is also adjusted accordingly. Hold the **Home** button until the table stops moving. This indicates the table has reached the predetermined phantom load position.
  - Retrieve and attach the phantom holder to the table.
  - Retrieve and attach the phantom to the phantom holder.
  - Return to the console. Click **OK** on the pop-up menu.
- Make sure all personnel have left the scan room.

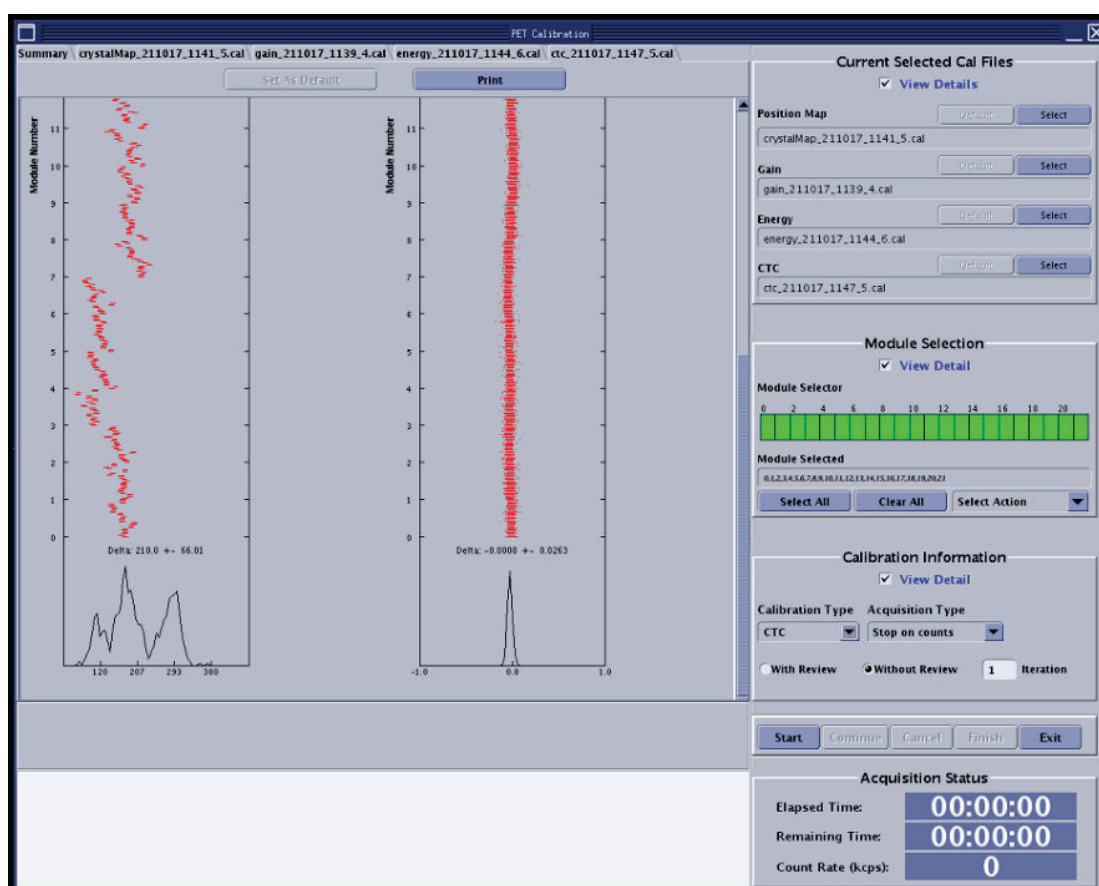
8. Press the flashing **Move to Scan** button to move the phantom to the PET isocenter position.
9. Press the **Start Scan** button to begin the CTC acquisition.

The boxes labeled **Source Position** and **Timing** will turn green while the phantom alignment correction and timing calculations are performed. See [Figure 158 on page 262](#).

The lower left corner of the **PET Calibration** window will display messages reporting progress during the iterations. When CTC calibration is reached, the system will automatically terminate the iterative process and report, “Coincidence Timing Correction has reached convergence”.

[Figure 159 on page 263](#) shows an example of calibrated CTC, which can be viewed by selecting the **ctc\_XXXXXX\_XXXX\_1.cal** tab at the top of the window.

**Figure 159 iCTC - Completed Calibration**



#### NOTE

In order to meet calibration criteria it may require multiple iterations.

10. When CTC finishes and you have selected **With Review**, the system provides the option to **Continue** or **Cancel** the iterative process if more than one iteration was prescribed in the **Iteration** box.

When the calibration is complete, verify the **Status Message** area displays: **Bad Blocks: 0** and **Crystals with low counts: 0**, then click **Save** to save all selected (green) blocks to the new calibration files.

Alternatively, you can click **Reject** to discard the data and try again.

11. Click **Exit** to close the **PET Calibration** window and return to the **Scanner Utilities** window.
12. A confirmation window prompts: “Do you want to delete prior calibration files?”  
Click **Yes** if you want to delete the files or **No** to keep them.

#### NOTE

We recommend that you do not delete the files.

13. Click **Quit** to close the **Scanner Utilities** window.
14. Once the exit is complete, the **Source Out** button starts blinking. Press the **Source Out** button. The table moves to the phantom unloading position.

### 8.4.3.3 Other Considerations for CTC

On a regularly maintained scanner, a single data acquisition followed by a number of automatic iterations are sufficient to reach calibration criteria (convergence) without reaching the maximum number of preset iterations (entered in the calibration window).

In the event that multiple acquisitions are needed to calibrate the scanner, one can prescribe a number larger than 1 in the **Iteration** box. Understand that each acquisition will be followed by a number of automatic iterations until convergence is automatically reached.

The **Reset CTC** option in the drop-down menu in the **Module Selection** area should only be used by the Field Service Engineer. However, if this reset function is executed by mistake, prescribing at least 3 iterations in the **Iteration** box (as explained above) will re-establish the timing calibration on the scanner.

## 8.5 Calibration Updates (Quarterly)

#### NOTE

Run the quarterly maintenance procedures as soon as you complete the tasks below:

1. For quarterly Detector calibration please follow the steps described in [Section 8.4.1](#).
2. Perform a DQA following the steps in [Section 8.3.4](#).
3. Update the DQA baseline following the steps in [Section 8.3.7](#).

## 8.5.1 3D Normalization and Well Counter Correction (WCC)

### 8.5.1.1 Overview

Normalization involves measuring the differences in individual crystal efficiencies to obtain correction factors which are applied to each emission scan. Normalization scans are executed using the Ge-68 DQA phantom landmarked on the scribed line closest to the phantom holder.

The Well Counter Correction (WCC) uses a water-filled phantom and a known quantity of radioisotope to correlate the measured numerical value in each image pixel to a specific activity measured in physical units (activity per volume). Images in physical units are required to calculate SUVs. WCC also maintains a good match of sensitivity between the imaging system and dose calibrator.

3.13.3

7.6

Run the Normalization and WCC procedures quarterly for accurate quantitation.

For best results: Acquire a new Normalization correction, followed by a Well Counter Correction every quarter, immediately after completing the bi-weekly PET Detector calibration and DQA.



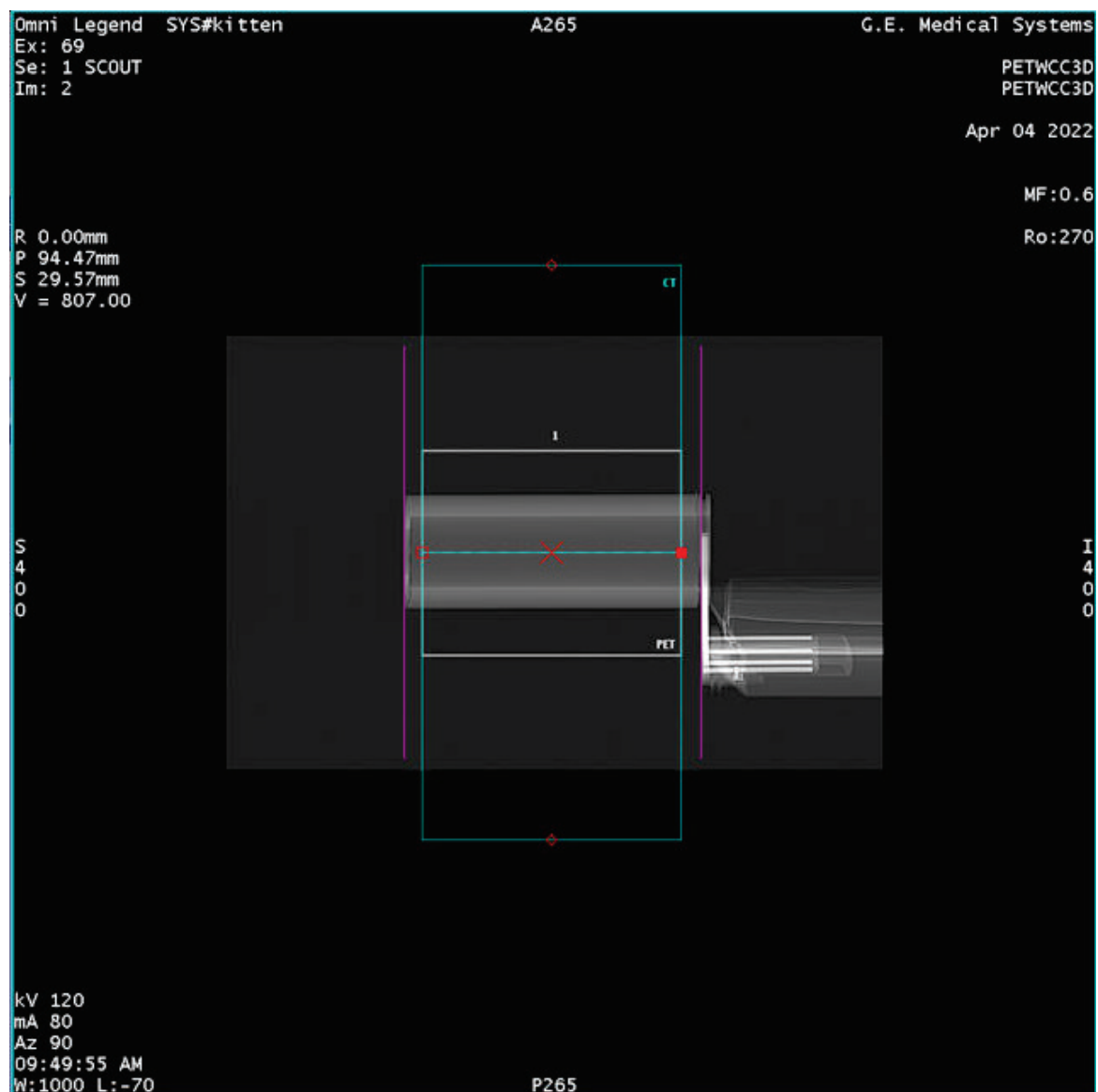
THIS PROCEDURE USES RADIOISOTOPES. FOLLOW FACILITY GUIDELINES TO HANDLE AND DISPOSE OF RADIOACTIVE SUBSTANCES.

### 8.5.1.2 3D Normalization: Position and Scan the DQA Annulus Phantom

Follow this procedure to mount, position and scan the DQA annulus phantom. Follow facility guidelines to transport and handle the radioactive phantom. If possible, avoid holding the phantom from the sides; always use the handle and the round opening on its end-caps.

1. Click the **Exam Rx** icon on the scan monitor.
2. Click **New Patient** on the display monitor.
3. Type **PETWCC3D** into the **Patient Name** and **Patient ID** data fields.
4. Click **Enter PET Tracer Info** and record the information from the phantom label.
  - Type the phantom volume into the **Tracer volume** field. For the exact phantom volume, refer to the label on the annulus phantom.
  - Type the date and total activity into the **Pre-Injection Assay** data field.
  - Do not update the **Injection time** and **Post-Injection Assay** data fields.
5. Click **Accept** to close the tracer window.
6. Click the **GE** tab on the protocol selector.
7. When looking at the Anatomical Adult (under the **GE** tab), place the cursor directly under the toes and click. The **Miscellaneous** protocol selections should display.
8. Click the **Normalization 68Ge Annulus** protocol. Do NOT change the default parameters.

9. Retrieve the phantom holder. Mount the holder to the end of the table. Ensure the phantom holder clips to the cradle securely.
10. Retrieve the DQA annulus phantom. Mount the phantom on the phantom holder. Ensure the phantom is fully seated on the phantom holder.
11. The phantom should always be centered using the lasers and scout scan that assures that all the imaging slices are far from the phantom edges. Align the straight lines scribed along the length of the phantom with the horizontal and vertical lasers, and the mark scribed around the phantom closest to the phantom's holder with the axial laser, then press Landmark. The scout scan will be used to center the phantom in the center of the FOV.
12. Make sure all personnel leave the scan room before you initiate the scan sequence.
13. Click **Confirm** to initiate the scout scan sequence.
14. Press the **Move to Scan** button when it flashes.
15. Press the **Start Scan** button when it flashes. The X-Ray Exposure Indicator on the Acquisition Control illuminates (amber) during the X-ray exposure.
16. Click **Next Series**.
17. Click **Show Localizer** to display 90 degree scout image and ensure that only the active parts of the annulus phantom are located inside the field of view.

**Figure 160 Graphic Rx Localizer**

18. Refer to [Figure 160 on page 267](#). If necessary, use the Graphic Rx Localizer to position the scan field over the center gray area of the phantom, away from the phantom edges.
19. Click **Confirm**.

**NOTE**

The default acquisition time for Normalization is 2 hours and 30 minutes, but the actual acquisition time is shorter calculated on current count rate from the phantom and fix number of counts to acquire ("stop on counts"). Acquisition time will increase as the phantom ages.

20. Press **Move to Scan** when it flashes.

Press **Start Scan** when it flashes.

The system acquires the CTAC required to correct for attenuation in the phantom during the reconstruction of the PET images.

21. Click **PET**.
22. Click **Confirm**.
23. Press **Move to Scan** when it flashes.
24. Press **Start Scan** when it flashes. Wait for scan to complete. Prospective reconstruction begins immediately on scan completion.
25. Click **End Exam**.
26. DO NOT delete or modify the image series created in this test (**Series 12**) until the next Normalization scan.

#### NOTE

If there are other reconstructions pending in the reconstruction queue, wait until these reconstructions are completed before running normalization. Otherwise the new normalization will not be available for the reconstruction of the FDG flood phantom images. Do not delete any pending reconstructions to try to expedite processing of the normalization as this may lead to unpredictable results.

### 8.5.1.3 Well Counter Correction: Prepare and Scan the Water-Filled Flood Phantom

Follow this procedure to load a flood phantom so it has approximately 20 MBq (0.54 mCi) of F-18 at scan time for use in the 3D Well Counter Correction procedure. Remember to record the times and activity values when directed, so you can enter these values into the corresponding **Tracer Information** window fields.

#### 8.5.1.3.1 Preliminary Phantom Preparation

1. WCC requires a flood phantom. Remove all inserts from the PET Image Corrections Phantom. [PET Image Corrections Phantom](#) provides detailed information about this phantom.
2. Fill the phantom with clean water, leaving enough space to hold the injected activity.
3. Tilt and rotate the phantom to dislodge any air bubbles and move them to the fill hole.  
Air bubbles with a diameter of less than 10 mm will not disturb most tests.
4. Verify the time on the dose calibrator clock matches the time on the scanner.
5. If your facility uses a stirring bar and magnetic plate to mix phantoms, follow the manufacturer's instructions and facility guidelines to use them. If the stirring bar will remain in the phantom, make sure it is against one of the end walls of the phantom.

This procedure contains instructions to mix the phantom without using these tools.

### 8.5.1.3.2 Measure Tracer Activity and Inject the Phantom

Follow this procedure to measure the amount of activity you injected into the phantom.

The WCC calibration matches a known amount of activity concentration, calculated in this section, to the display image pixel value. Make sure you set the dose calibrator to the isotope you plan to assay. Make sure the scanner, dose calibrator, and facility clocks are synchronized. A time difference of only two minutes introduces a bias of more than one percent for F-18 FDG.

Please refer to the following formula. This procedure tells you to measure the total activity in the syringe, inject the activity into the phantom, then measure the residual activity in the syringe. Subtract the residual activity from the total activity, then divide this value by the total volume of the flood phantom. The resulting value equals the unit activity per milliliter in the phantom. (1 ml = 1 cc)

$$\frac{\text{Total Activity} - \text{Residual Activity}}{\text{Flood Phantom Volume}} = \text{MBq/ml in Flood Phantom}$$

1. Draw the F-18 tracer into the syringe.
2. Measure and record the time and total activity of the isotope in the syringe.  
Use the patient dose calibrator (set to F-18) to measure total and residual activity.
3. Record the time, then inject the contents of the syringe into the phantom.
4. Rinse the syringe by drawing up some phantom water, and reinjecting it.
5. Return the used syringe to the patient dose calibrator.
6. Measure and record the time and residual activity in the syringe.
7. Fill the remaining air bubble with water and seal the phantom. Do not overfill the hole where the plug connects. If there is no bubble left in the phantom, the plug may create excessive pressure inside the phantom and develop a leak.
8. Thoroughly mix the contents of the phantom to evenly distribute the activity.
  - Use a stir rod.
  - or
  - Before filling the phantom completely, place it on a clean towel and gently roll it back and forth to mix. This method will not be effective with a full tank.
9. Record the total volume of the flood phantom.  
The standard volume of the flood phantom normally equals 5,640 ml. For best results measure the actual volume of the flood phantom and record that value on a label, and place it somewhere on the phantom, for future reference.  
The volume of the water is best measured by subtracting the weight of the empty phantom from the weight of the water-filled phantom. Leave a ~3 cc air bubble to allow expansion of cold water as it reaches room temperature.
10. Subtract the residual activity (measure and record the time and residual activity in the syringe) from the total activity (measure and record the time and total activity of the isotope in the



syringe). Divide this value by the total volume of the phantom (record the total volume of the flood phantom) to obtain the unit activity/ml.

Record the unit activity/ml.

11. Follow facility guidelines to label the phantom as radioactive.

### 8.5.1.3.3 Position and Scan the Flood Phantom

Follow this procedure to mount, position and scan the flood phantom.

Follow facility guidelines to transport and handle the radioactive flood phantom.



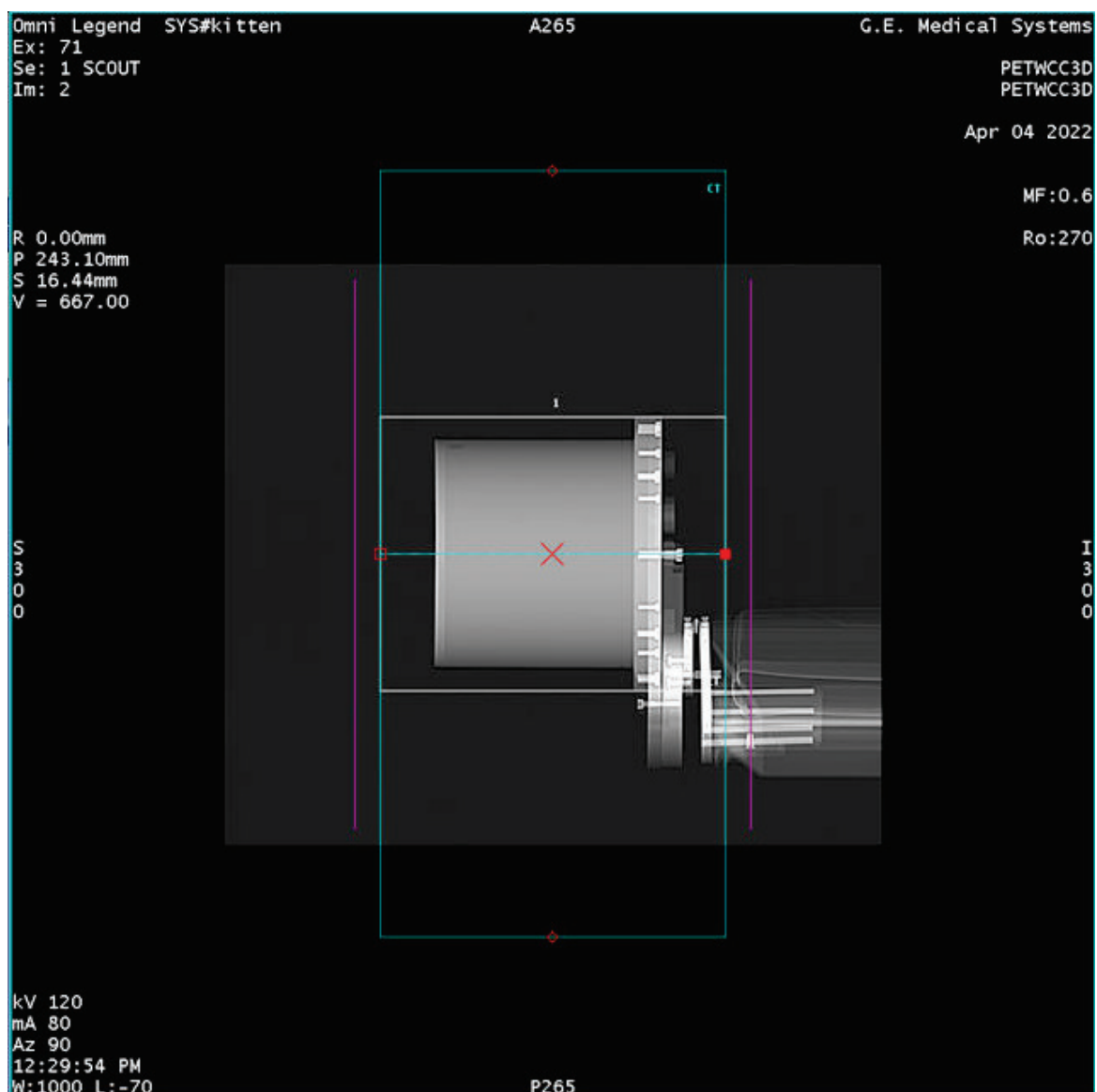
THIS PROCEDURE USES RADIOISOTOPES. FOLLOW FACILITY GUIDELINES TO HANDLE AND DISPOSE OF RADIOACTIVE SUBSTANCES.

1. Mount the phantom on its holder at the end of the patient table as directed in Position the Tank Phantom in the PET Image Corrections Phantom chapter.
2. Click the **Exam Rx** icon on the scan monitor.
3. Click **New Patient** on the display monitor.
4. Enter *PETWCC3D* into the **Patient Name** and **Patient ID** field.
5. Click **Enter PET Tracer Info** and use the information you recorded during the previous section to fill in the data fields.
  - Enter the phantom volume (default 5640 ml) into the **Tracer volume** field. Do not enter the volume of the syringe into this field.
  - Enter the time and total activity into the **Pre-Injection Assay** field.
  - Enter the time and residual activity into the **Post-Injection Assay** field.
6. Click **Accept** to close the **Tracer Information** window.
7. Click the **GE** tab on the protocol selector.
8. When looking at the Anatomical Adult, place the cursor directly under the toes and click. The **Miscellaneous** protocol selections should display.
9. Click the **WCC FDG Flood** protocol. Do not change the default parameters.
10. Align the scribed mark on the phantom to the external lasers and press **Landmark**. The phantom should be centered in the longitudinal direction.
11. Make sure all personnel leave the scan room before you initiate the scan sequence.  
Click **Confirm** to initiate the scout scan sequence.
12. Press the **Move to Scan** button when it flashes.
13. Press the **Start Scan** button when it flashes.

The X-Ray Exposure Indicator on the Acquisition Control illuminates (amber) during the X-ray exposure. Keep all personnel out of the scan room during the X-ray exposure.

14. Click **Next Series**.
15. If necessary, click **Show Localizer** to display the 90 degree scout image.
16. Use the Graphic Rx Localizer to position the scan field over the center gray area of the phantom, with the red cross-hair centered on the phantom.

**Figure 161 Graphic Rx Localizer - Correctly Positioned**



17. Click **Confirm**.
18. Press **Move to Scan** when it flashes.
19. Press **Start Scan** when it flashes.

The system acquires the CTAC required to correct for attenuation in the phantom during the reconstruction of the PET images.

20. Click **PET**.

If you used a isotope other than F-18, click **Nuclide**, select the correct tracer, then click **OK** to continue.

21. Click **Confirm**.
22. Press **Move to Scan** when it flashes.
23. Press **Start Scan** when it flashes.

The selected protocol prescribes the prospective image reconstruction.

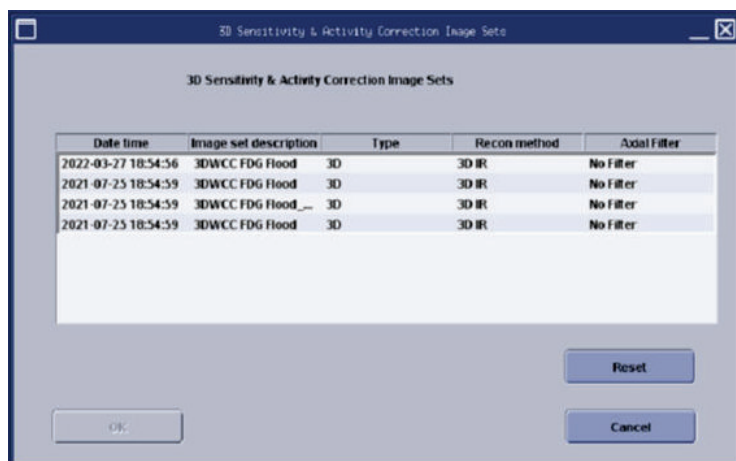
24. When the **System Messages** area displays the message, "Scan Completed," click **End Exam**.

#### 8.5.1.4 Generate the 3D Normalization and Well Counter Corrections

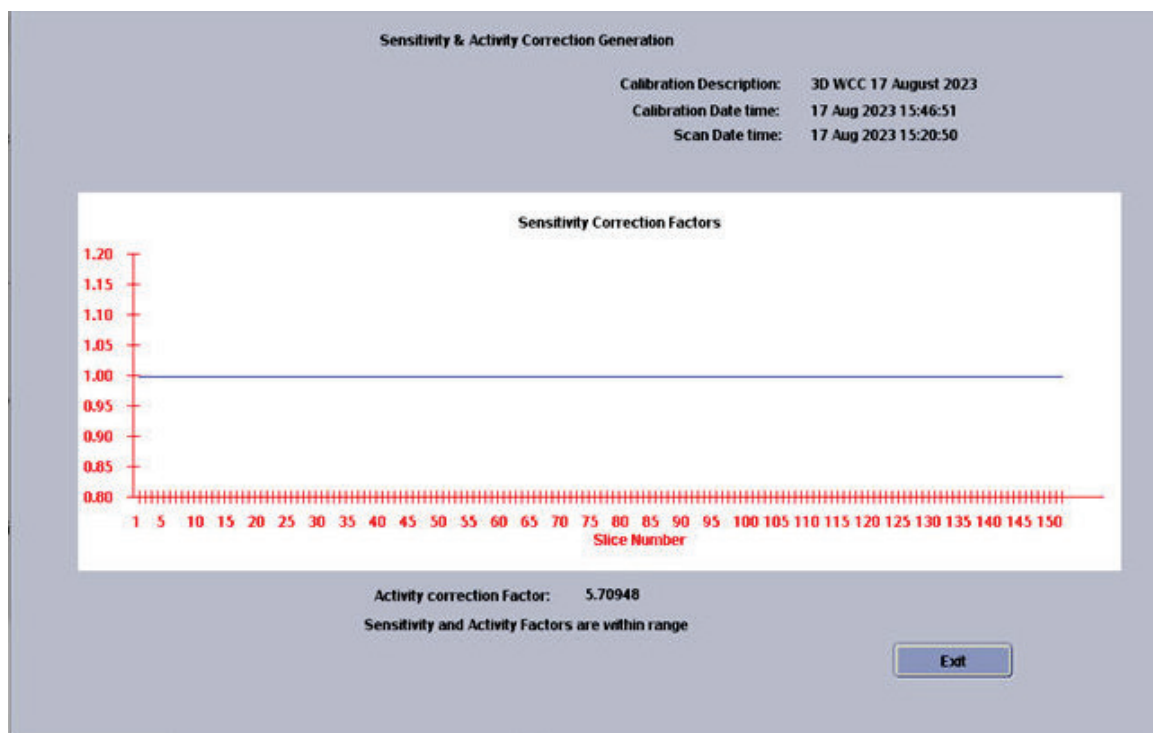
Follow the procedure in this section to generate the 3D Normalization and Well Counter Corrections from the data acquired during the previous section.

1. Click the **Service** icon on the scan monitor to open the service desktop.
2. Click the **PET** radio button to display the PET service desktop.
3. Click the **Image Quality** icon.  
If necessary, click the **Image Quality** folder to display its contents.
4. Click the **3D Normalization** folder to display its contents.
5. Click **3D WCC Calculation** to open the **3D Sensitivity & Activity Correction Image Sets** window.

**Figure 162 3D Sensitivity and Activity Correction Image Sets**

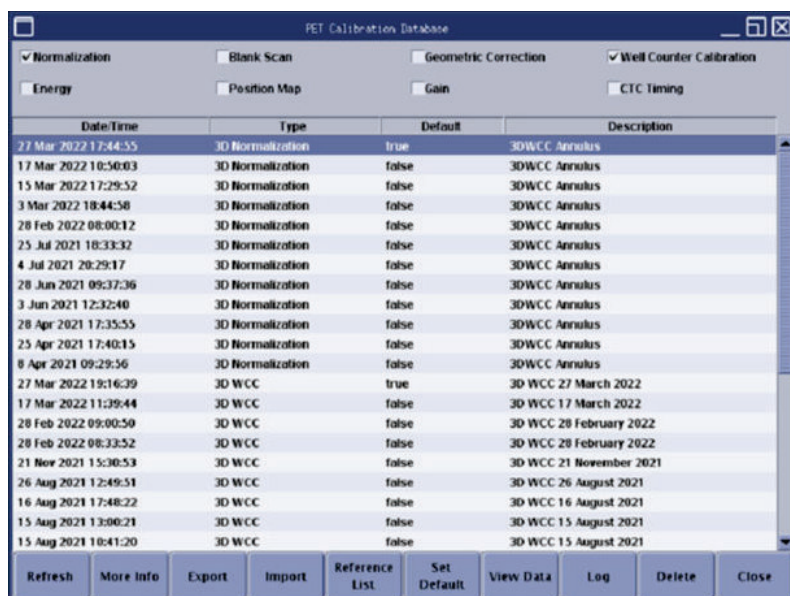


6. Select the image set from the most recent WCC acquisition with description **3DWCC FDG Flood**.
7. Click **OK** to display a **Sensitivity and Activity Correction Generation** output.

**Figure 163 Sensitivity and Activity Correction Generation Graph (for 6-ring system)****NOTE**

The WCC value should remain within 10% of the previous measured value if there were no major changes to the system hardware.

8. Click **Accept** to set the newly generated well counter as the system default, and open a WCC description window with the default description displayed.  
Optional: Enter a descriptive name for the correction into the field.
9. Click **Save** to open an alert window with the message, "WCC results stored in database".
10. Click **OK** to use this as the default correction for all scans.
11. Return to the PET Service Desktop **Image Quality** tab and click **Cal Manager** to open PET Calibration Database Manager, shown in [Figure 164 on page 274](#).
  - Click the **Well Counter Calibration** and **Normalization** check boxes, to display the corresponding database information.
  - Verify the most recently acquired Normalization and 3D WCC appear in the database, with the label, **true**, in the **Default** column.

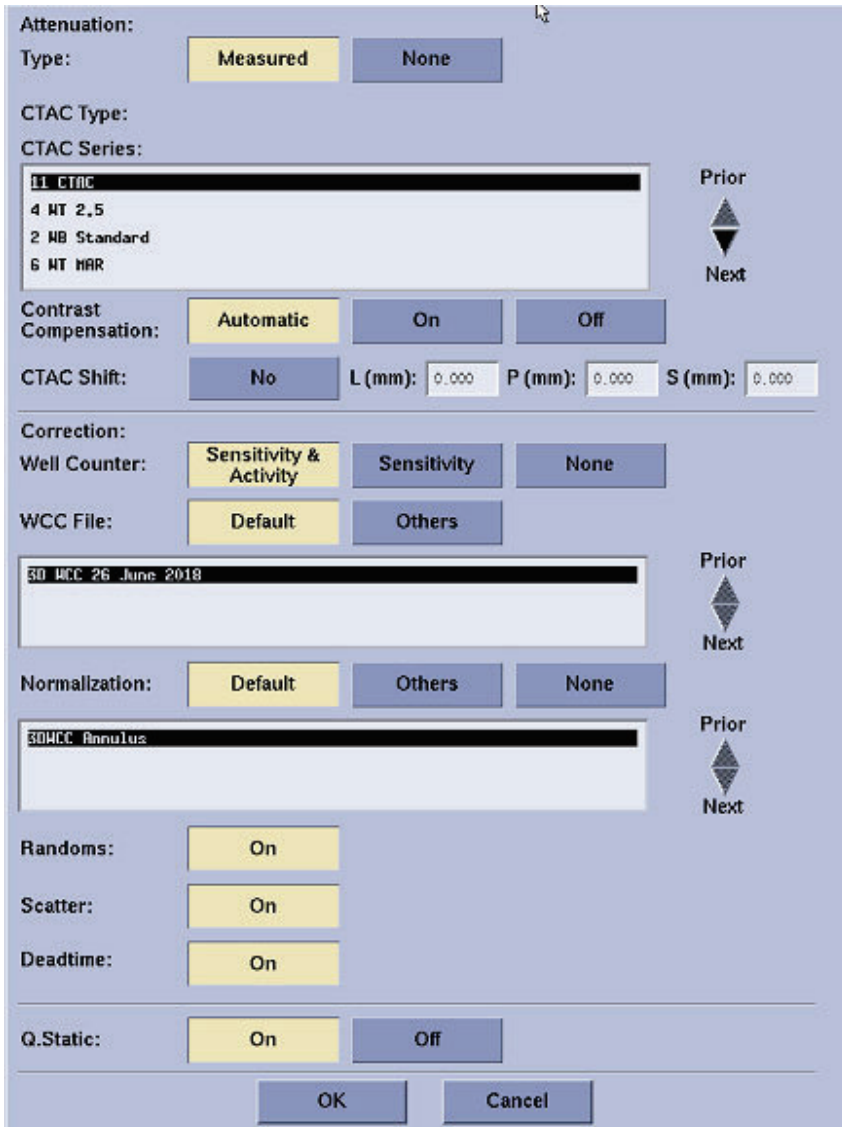
**Figure 164 PET Calibration Database Manager**

12. Optional: To assign a different **Default**, click the corresponding file description, then click **Set Default** to change the corresponding default label to **true**, and move the file to the top of its category.
13. Click **Close** to exit the PET Calibration Database Manager.

## 8.5.2 Measure Quantitative Accuracy of Image Data

Follow these instructions to measure the Well Counter Correction (WCC) factor against the known activity in the flood phantom. Follow this procedure after every WCC acquisition. Follow the procedure in the previous section to acquire the WCC data.

1. Click **PET Recon/Replay** to display the corresponding **PET Retro List Select** window.
2. Click the **PETWCC3D** series from the flood phantom acquisition to select it.
3. Click **Select Series** to display a PET scan window.  
If necessary, click the **Recon** tab to display the reconstruction parameters.
4. Click **Recon Option** to open the **Recon Option** selector.

**Figure 165 Recon Option Selector**


The image shows a software window titled "Recon Option Selector". It contains several sections with buttons and list boxes. The "Attenuation:" section has "Type:" with "Measured" (selected) and "None". The "CTAC Type:" and "CTAC Series:" sections have a list box showing "11 CTAC", "4 NT 2.5", "2 NB Standard", and "6 NT MAR", with "Prior" and "Next" navigation buttons. The "Contrast Compensation:" section has "Automatic" (selected), "On", and "Off". The "CTAC Shift:" section has "No" (selected) and three input fields: "L (mm): 0.000", "P (mm): 0.000", and "S (mm): 0.000". The "Correction:" section has "Well Counter:" with "Sensitivity & Activity" (selected), "Sensitivity", and "None". The "WCC File:" section has "Default" (selected) and "Others". Below this is a list box showing "30 WCC 26 June 2018" with "Prior" and "Next" navigation buttons. The "Normalization:" section has "Default" (selected), "Others", and "None". Below this is a list box showing "30WCC Annulus" with "Prior" and "Next" navigation buttons. The "Randoms:" section has "On" (selected). The "Scatter:" section has "On" (selected). The "Deadtime:" section has "On" (selected). The "Q.Static:" section has "On" (selected) and "Off". At the bottom are "OK" and "Cancel" buttons.

5. For Well Counter Correction: Click **Sensitivity & Activity** to open the WCC file display.
6. Click the WCC file: Click **Others** to display the current list of WCC files.
7. Click the WCC you just created to select it.
8. Click **Normalization**: Click **Others** to display the current list of Normalization files on your system.
9. Click the Normalization you just created to select it.
10. Click **OK**.
11. Enter the **Series Description** into the corresponding field.
12. Click **Confirm**.
13. Reconstruct the data using the same parameters you normally use on patient data.

14. Click **Quit** to close the PET scan window.
15. Enter the radiopharmaceutical activity at the start of the PET acquisition, and the volume of the phantom into the well counter equation. If for some reason the radiopharmaceutical activity and volume was not entered when the 3D WCC phantom was scanned, see below.
  - Remember to consistently use MBq/ml or mCi/ml (milliCi) throughout this procedure.

**Figure 166 Activity Concentration Calculation**

$$\frac{(\text{Sample Activity})}{(\text{Sample Volume})} = \text{Activity per unit of volume}$$

$$\frac{\text{Total Activity} - \text{Residual Activity}}{\text{Flood Phantom Volume}} = \frac{\text{MBq(mCi)}}{\text{mL(cc)}} \text{ in Flood Phantom}$$

- Example: The standard volume of the flood phantom normally equals 5,640 ml. For best results, measure the actual volume of the WCC phantom and record that value on a label, somewhere on the phantom, for future reference.
16. Upon completion of the reconstruction, click **Image Works**.
  17. Select the CT and PET well counter phantom series.
  18. Click **Image QC** and wait for the images to load.
  19. Select a PET series viewport.
 

Make sure you selected the correct units/volume for your system.
  20. Put a 120 mm diameter ROI in the middle of the flood phantom.
 

Click **My Tools > ROI Symbol** to open the **Statistics** window, then enter 120 into the **Vertical Diameter** and **Horizontal Diameter** data fields.
  21. Change the displayed value from MBq to kBq, or change mCi to uCi, by multiplying the average ROI value by 1000.
  22. Compare the ROI information to the known activity in the flood phantom.
    - The ROI readout should equal the known activity  $\pm 10$  percent.
    - Example:  $\frac{20 \text{ MBq}}{5640 \text{ ml}} = 0.0035 \frac{\text{MBq}}{\text{ml}} \times 1000 = 3.5 \text{ kBq/ml}$

This measurement can also be calculated using the QA Calculator tool. Follow the steps described in the section [QA Calculator](#).

### 8.5.3 QA Calculator

This tool intended to help calculate the F-18 Quantitation Accuracy check as per the steps and formula mentioned in the section [Measure Quantitative Accuracy of Image Data](#). Follow the instruction in this section to run the F18 Quantitation tool.

1. Click on the **Tool Chest** and select **QA Calculator**.



2. The default activity unit in QA Calculator is MBq. The user can change input activity to micro Ci as per the site's practice.

A screenshot of a web-based application titled 'F-18 Quantitation Accuracy Check'. At the top, there are two buttons for unit selection: 'MBq' (light blue) and 'µCi' (dark blue). Below this, there are four input fields: 'Net Activity' with a placeholder 'Enter Net Activity in' and a unit selector 'MBq'; 'Tracer Volume (ml)' with the value '5640'; 'Result kBq/ml'; and 'ROI Average' with a placeholder 'kBq/ml'. A horizontal line separates the input fields from the 'Quantitation Accuracy :' section. Below this, there is a 'Note : This tool is intended to be used to compare the image ROI information to the known tracer activity in the WCC F-18 flood phantom.' and a 'Calculate' button at the bottom.



## Calibration

3. Enter the F18 tracer activity at the start of PET acquisition in the **Net Activity** field. Use the same unit selected in step 2. The formula mentioned in above section can be used to calculate net activity.
4. The default value for tracer phantom volume is kept at 5640 ml. If the user wants to insert the actual measured volume of tracer, the value can be edited by double clicking on the input field.

The screenshot shows a web browser window titled "QA Calculator - Mozilla Firefox". The page has a light blue background and is titled "F-18 Quantitation Accuracy Check". At the top, there are two buttons: "MBq" (highlighted in light blue) and "µCi" (dark blue). Below this, there are four input fields with labels to their left: "Net Activity" with a value of "20" and a unit of "MBq" to its right; "Tracer Volume (ml)" with a value of "5640"; "Result kBq/ml" with a value of "3.55"; and "ROI Average" with a unit of "kBq/ml" to its right. Below these fields is a line of text: "Quantitation Accuracy : click calculate to see result". At the bottom, there is a dark blue button labeled "Calculate". A note at the bottom of the form states: "Note : This tool is intended to be used to compare the image ROI information to the known tracer activity in the WCC F-18 flood phantom."

5. Measure the ROI average following the steps in Measure Quantitative Accuracy of Image Data and enter the value in kBq/ml . Click **Calculate** to generate Quantitation Accuracy to

compare the Image Data ROI information to the known activity in the WCC flood phantom.

**F-18 Quantitation Accuracy Check**

MBq **µCi**

---

Net Activity  MBq

Tracer Volume (ml)

Result kBq/ml

ROI Average

---

Quantitation Accuracy : **+2.82%**

---

**Note :** This tool is intended to be used to compare the image ROI information to the known tracer activity in the WCC F-18 flood phantom.

---

**Calculate**

6. Click the **X** on the top right corner to close the QA Calculator tool.

## 8.6 Calibration Quick Steps

### 8.6.1 Warm Up the CT X-Ray Tube

1. Make sure the scan room is empty.
2. Click the **Daily Prep** icon.
3. Click **Tube Warm-up**.
4. Click **Accept & Run Tube Warm-up**.
5. Press **Start Scan** to initiate the warm-up sequence.
6. Click **Quit** to exit.

### 8.6.2 Fast Calibration (Daily Air Calibration)

1. Make sure that no one is in the scan room and the gantry bore is free of any objects.
2. If necessary, complete the CT X-ray Tube Warmup procedure before selecting Fast Calibration.  
For best results: Run Fast Calibration immediately after you warm up the CT X-ray tube.
3. If necessary, click the **Daily Prep** icon to open the menu.
4. Click **Fast Calibration**.
5. If prompted, clean the mylar window and click **Retry** or **Continue**.
6. Click **Quit** to close the **Daily Prep** window.

### 8.6.3 PET DQA (Daily Quality Assurance)

1. Remove all phantoms and extenders from the table and clear the room of radioactive sources.
2. Click **Daily Prep**.
3. Click **PET Daily QA**.
4. Click **Take Current Reading**.
5. From the scanner room, press and hold the gantry **Home** button to move the table to the phantom load position.
6. Retrieve and mount the phantom holder to the cradle.
7. Retrieve and mount the annulus phantom to the phantom holder.
8. Type your initials and click **OK** to proceed with acquisition.
9. Press the flashing **Move to Scan** button to move the phantom to the PET isocenter position.
10. Press the flashing **Start Scan** button to begin acquisition.
11. While DQA is being acquired, check the time synchronization for the scanner, dose calibrator and facility clocks.
12. Upon completion of the DQA, the system displays the **View Summary** window.
13. Click the arrow next to **View Summary**, then click **View Data** to display a more detailed window with graphs, tables and trending tools.
14. Optional: Click **Print** to create a hard copy of the currently displayed window.
15. Press the flashing **Retract** button to move the table to the phantom unload position.
16. Unmount the annulus phantom and store it in a shielded container.
17. Remove the phantom holder.
18. Click **Exit** to return to the **Daily Preparation** window.
19. Click **Quit** to close the **Daily Preparation** window.

### 8.6.4 Establish PET DQA Baseline

1. Click **Daily Prep**.
2. Click **Manage DQA**.
3. Perform steps in [8.3.4 PET Daily Quality Assurance on page 234](#) to complete a PET DQA.  
Alternatively, click **Select Prior** and highlight a previous DQA scan, then click **Select**.
4. Click the arrow next to **View Summary** or **View Data**, then click **View Data**.
5. *Make sure all graphs appear homogeneous.*
6. Click **Establish a Baseline** to open the **Baseline Data Type Selector** panel.
7. Click every *box* to deposit a check mark and select the corresponding data type.
8. Click **Accept** to close the **Baseline Data Type Selector** panel.
9. Optional: Click **Print** to create a hard copy of the currently displayed baseline window.
10. Click **Exit** to return to the **Daily Preparation** window.
11. Click **Quit** to close the **Daily Preparation** window.

### 8.6.5 Save PET Calibrations and DQA Results

1. Insert a new or used USB into the USB port on the console.
2. Click the **Service** icon.
3. If necessary, click the **CT** radio button.
4. Click the **Utilities** icon.
5. Click **System State** or **System State - USB**.
6. Click the **PET Cal Files** and **PET DailyQA** buttons.
7. Click **Save**.
8. When finished, the system displays ““Save/Restore System State: Completed Successfully.””
9. Click **Cancel**.
10. Click **Dismiss**.

### 8.6.6 Restore Calibrations and/or DQA Results

1. Insert the USB with the files you plan to restore into the USB port.
2. Click the **Service** icon.
3. If necessary, click the **CT** radio button.
4. Click the **Utilities** icon on the Service Toolbar.
5. If necessary, click the Utilities folder to display its contents.
6. Click **System State** or **System State - USB**.

7. Click the **PET Cal Files** and/or **PET DailyQA** button.
8. Click **Restore**.
9. Click **Yes** and wait for the “Save/Restore System State: Completed Successfully” message to appear.
10. Click **Cancel**.
11. Click **Dismiss**.

### 8.6.7 Delete DQA Files

1. Click the **Daily Prep** icon.
2. Click **Manage DQA**.
3. Click **Select Prior** to open the window.
4. Click/highlight the prior DQA reading you want to delete.
5. Click **Delete**.
6. Click **Cancel**.
7. Click **Exit**.
8. Click **Quit**.

### 8.6.8 Detector Calibration (Every Two Weeks)

1. Click the **Scanner Utilities** icon.
2. Click **PET Calibration**.
3. Click the radio button next to **Detector Cal** to select it.
4. If the **View Detail** box is checked, select **Detector Cal** from the **Calibration Type** drop-down menu. Select **Stop on counts** from the **Acquisition Type** drop-down menu. Insert **1** in the **Iteration number** window.
5. Optional: Select individual modules for Detector Cal from the **Module Selection** area.
6. Optional: Review results before accepting them (**With Review**).
7. Click **Start** to open a notice window.
8. Make sure all personnel have left the scan room.
9. Follow instructions to mount and position the DQA calibration phantom presented in the pop-up window, then click **OK**.
10. The system displays the message, “All calibration data is saved to the new cal files.” upon completion of the Detector Cal.

**NOTE**

The Detector Calibration will report if the calibration criteria are met. If more than one iteration was prescribed in the **Iteration** box, the calibration process will stop iterating the moment the calibration criteria are met.

Notice: There is always an additional iteration of Detector Calibration above the number of iterations prescribed in the **Iteration** box. This synchronizes the crystal maps and energy calibration with the detector gains used for generating those maps and energies.

11. Click **Exit** to close the PET Calibration panel.

### 8.6.9 Calibration Fails for Detector Cal

1. Click the **Status Message** area under the Exam Rx Desktop.
2. Click **View Log**.
3. Click **Last Page** to display the most recently logged messages.
4. Document any failures for service.
5. Retry the Detector Calibration. Check the **View Detail** box in **Calibration Information**, select **Detector Cal** from the **Calibration Type** drop-down menu. Select **Stop on counts** from the **Acquisition Type** drop-down menu. Insert **5** in the **Iteration number** window.
6. If Detector Calibration continues to fail, follow facility guidelines to log a service call.

### 8.6.10 Coincidence Timing Correction (CTC)

1. Click **Scanner Utilities**.
2. Click **PET Calibration**.
3. Click the **View Detail** check box in the **Calibration Information** area.
4. Click the **Calibration Type** down arrow and select **CTC** from the menu.
5. Use default acquisition mode **Stop on Counts**.
6. Click **Start** to open the warning window.
7. Follow instructions in pop-up window to mount and position the DQA calibration phantom.
8. Make sure all personnel have left the scan room, then click **OK**.
9. When CTC finishes, click **Exit** to close the **PET Calibration** window.

**NOTE**

CTC will report if calibration criteria is met. It will stop iterating if a number larger than one was entered in the **Iteration** box.

Notice: The CTC calibration process automatically iterates up to a fixed number of iterations using the same data acquired at the beginning of each user prescribed iteration.

- Click **Quit** to close the **Scanner Utilities** window.

### 8.6.11 3D Normalization

Mount Ge-68 DQA phantom and landmark on the scribed line closest to the phantom holder.

- Click the **Exam Rx** icon on the scan monitor.
- Click **New Patient** on the display monitor.
- Type **PETWCC3D** into the **Patient Name** and **Patient ID** data fields.
- Enter PET Tracer Info and Volume. For the exact phantom volume, refer to the label on the annulus phantom.
- Click the **GE** tab on the protocol selector.
- Click directly under the toes of the anatomical man.
- Click the **Normalization 68Ge Annulus** protocol.
- Click **Confirm** to initiate the scout scan sequence.
- Press the **Move to Scan** button when it flashes.
- Press the **Start Scan** button when it flashes.
- Click **Next Series**.
- If necessary, adjust position using **Show Localizer**.
- Click **Confirm**.
- Press **Move to Scan** when it flashes.
- Press **Start Scan** when it flashes.
- Click **PET**.
- Click **Confirm**.
- Press **Move to Scan** when it flashes.
- Press **Start Scan** when it flashes.
- Click **End Exam**.

### 8.6.12 Well Counter Correction

Prepare a water-filled flood phantom with approximately 20 MBq (0.54 mCi) of F-18. Record the time and activity of the pre-injection and post-injection activities. Landmark at the center of the phantom.

- Click the **Exam Rx** icon on the scan monitor.
- Click **New Patient** on the display monitor.
- Type **PETWCC3D** into the **Patient Name** and **Patient ID** data fields.
- Click **Enter PET Tracer Info** and use the phantom information. Typical volume is 5640 mL.
- Click the **GE** tab on the protocol selector.

6. Click directly under the toes of the anatomical man.
7. Click the **WCC FDG Flood** protocol.
8. Click **Confirm** to initiate the scout scan sequence.
9. Press the **Move to Scan** button when it flashes.
10. Press the **Start Scan** button when it flashes.
11. Click **Next Series**.
12. Use the Graphic Rx Localizer to position the scan field over the center gray area of the phantom.
13. Click **Confirm**.
14. Press the **Move to Scan** button when it flashes.
15. Press the **Start Scan** button when it flashes.
16. Click **PET**.
17. Click **Confirm**.
18. Press the **Move to Scan** button when it flashes.
19. Press the **Start Scan** button when it flashes.
20. Click **End Exam**.

### 8.6.13 Generate the 3D Normalization and Well Counter Corrections

1. Click the **Service** icon.
2. Click the **PET** radio button.
3. Click the **Image Quality** icon.
4. Click the **3D Normalization** folder.
5. Click **3D WCC Calculation**.
6. Select the image set from the most recent WCC acquisition with description **3DWCC FDG Flood**.
7. Click **OK**.
8. Click **Accept**.  
Optional: Enter a descriptive name for the correction into the field.
9. Click **Save**.
10. Click **OK** to use this as the default correction for all scans.
11. Return to the PET Service Desktop **Image Quality** tab.
12. Click **Cal Manager** to open PET Calibration Database Manager.
13. Click the **Well Counter Calibration** and **Normalization** check boxes.
14. Verify the most recently acquired Normalization and 3D WCC appear in the database, with the label, **true**, in the **Default** column.



15. Click **Close** to exit the PET Calibration Database Manager.

### 8.6.14 Measure Quantitative Accuracy of the Image Data

1. Acquire the well counter data (Calibration Quick Steps).
2. Click **PET Recon/Replay**.
3. Highlight the 3D WCC series and click the **Select Series** button.
4. Click **Recon Option**.
5. Click **Sensitivity & Activity**.
6. Click WCC file: **Others**, then click/highlight the recently created WCC series.
7. Click Normalization: **Others**, then click/highlight the recently created Normalization series.
8. Enter the **Series Description**.
9. Click **Confirm**.
10. Reconstruct the data with regularly used (patient data) parameters.
11. Divide the activity at the start of the PET acquisition by the volume of the flood phantom to get the activity/unit volume.
12. Click **Image Works**.
13. Select the CT and PET well counter phantom series.
14. Click **Image QC** and wait for the images to load.
15. Select a PET series viewport.
16. Deposit an ROI in the middle of the flood phantom.
17. The ROI readout should equal the activity/unit volume  $\pm 10\%$ .
18. This measurement can also be calculated using the QA Calculator tool. Follow the steps described in the section [QA Calculator](#).

## 9 Schedule Patients

### 9.1 Schedule Patients Introduction

This chapter explains the Patient Schedule feature and how to use it to transfer or input patient information into the PET/CT scanner. The chapter includes procedures to manually enter patient information into the schedule, retrieve information from HIS/RIS, retrieve patient information on the day of the scan and manage patient information on the schedule before and after the exam.

Use the Patient Schedule feature to enter patient information, add information to the existing data or edit information, such as patient weight, that may have changed since the original data was entered in the system, add tracer information and select exam protocols in advance, and store them on the system hard drive until you need them. This feature improves efficiency and lets you devote your time to the patient during the procedure.

At scan time, you can browse and select the patient information from the existing Patient Schedule list, enter the patient ID or accession number into the **New Patient** window to populate the data fields, or use the optional bar code reader to call up information from the Patient Schedule list.

You can always manually enter patient information at the time of the appointment, add information to the existing data or edit information, such as patient weight, that can have changed since the original data entered the system.

### 9.2 Display the Patient Schedule

1. Click **Patient Schedule** to open the Patient Schedule list.

**Figure 167 Patient Schedule List**

Schedule						
Status	Accession No.	Patient ID	Patient Name	Date	Time	Exam Description
C*	001-PT-001235487	05092016	SMITH*JOHN	2/8/2016	08:45	PET LYMPHOMA RESTAGING
N	8097-3585	755-66-103	LAMBERT, WYNONA	6/14/1998	09:30	ROUTINE HEAD
N	0426-9964	142-536-608	MORI, JEFF	6/14/1998	09:30	NECK
N	2355-0949	177-820-805	CURRY, BARB	6/14/1998	09:30	CHEST HI RES AT SN
N	3547-0069	865-260-045	REDFERN, MARY	6/14/1998	10:00	TRIPLE PASS LIVER
N	7051-2277	073-44-541	COOPER, ALISE	6/14/1998	10:00	PEDICLE
N	3220-3607	379-864-341	HAILEY, JAVIER	6/14/1998	10:00	SELLA 1X1
N	8420-3959	451-08-477	ISHIHARA, TONY	6/14/1998	10:30	LIMITED SINUSES
N	6223-3485	893-912-233	PEDERSEN, PAMELA	6/14/1998	10:30	NECK
N	2712-9471	727-252-465	HOLLAND, RONALD	6/14/1998	10:30	CHEST/ABDOMEN/PELVIS
N	8137-6218	463-759-157	HONE-KIMURA, LOUIS	6/14/1998	11:00	ABDOMEN / PELVIS
N	9381-2994	366-675-355	MOLERO, BONITA	6/14/1998	11:00	ROUTINE HEAD
N	0439-9878	545-61-751	PHILIP-ADAMS, SAMUEL	6/14/1998	11:00	LIMITED SINUSES
N	9094-6868	124-206-782	SRINIVAS, LOUIE KEVIN	6/14/1998	11:30	LTD SINUS-SUPINE
N	8360-4447	719-652-409	HORNITZ, JIMMY	6/14/1998	11:30	FACIAL / ORBITS
N	7796-6919	915-24-085	SATYANAND, DONALD	6/14/1998	11:30	ABD PELVIS PANCREAS
N	9729-8266	970-383-527	HEIS, MARIA-GRAZIA	6/14/1998	12:00	ROUTINE HEAD

Quit
Select Patient
View More Info
Add Patient
Edit Patient
Delete Selected
Delete All
Preferences
Update
Last Update: 2/8/2016 08:48
Next
Prior

- If the schedule list exceeds one page, click **Next** or **Prior** to navigate through the list.
- Click **Quit** to close the Patient Schedule list.

### Patient Status

The Patient Schedule has a column labeled **Status** with the following meanings:

- N**: New Record, or Not Complete. This patient has not been scanned on this PET/CT.
- N\***: Edited New Record. This patient has not been scanned on this PET/CT, but the schedule information has been edited.
- C**: Complete. The scheduled patient has been scanned.

### NOTE

Recommended: If your system has the Connect Pro option, set **Delete Completed Exams** to 0 days on the **Connect Pro Preferences** panel to prevent inadvertent scanning of patients with the wrong accession number. For best results, keep only New Records on your Patient Schedule list when using the Connect Pro option.

## 9.3 Select a Patient from the Schedule

Follow the steps below to select a patient directly from the Patient Schedule list. You have the option to open the **New Patient** window, and type the **Patient ID** or **Accession Number** into the

corresponding data field to populate the screen with information from the schedule list. If your system has the Connect Pro option with the bar code reader, you may also use it to populate the screen. Refer to [Use the Bar Code Reader](#) for instructions.

1. Click the **New Patient** icon to open the **New Patient** window.
2. Click the **Patient Schedule** icon to display the Patient Schedule.
3. Click on the line of information that corresponds to the patient you plan to scan.  
The information highlights.
4. Click **Select Patient** to populate the **New Patient** window with the information from the Patient Schedule.  
Fill in any missing information.
5. If necessary, select a patient protocol to continue.
  - You had the option to select a protocol when you added the patient to the schedule.
  - You always have the option to select a different protocol or modify the existing protocol information before you proceed to scan.
6. Click **Enter** to proceed to the scan screens.

## 9.4 Manually Add a Patient to the Schedule

1. Click the **Patient Schedule** icon.
2. Click **Add Patient** to open a **New Patient** window.  
The HIS/RIS assigns the **Accession Number**, if your facility uses this option.

**Figure 168 New Patient Window**

3. You must enter a **Patient ID** to activate the remaining data fields, as well as the **Protocol Selection** area of the window.
  - Follow facility guidelines to enter a **Patient ID** of up to 16 characters.
  - If the patient arrives without an ID, enter ?? or *trauma* into the field to activate the window. Use the Edit Patient feature to add the **Patient ID** when you receive it.

**NOTE**

To prevent potential networking issues, do not use the forward slash (/) or backslash (\) characters in typed descriptions and limit the use of all other non-alphanumeric characters, with the exception of the caret (^) character, on the **New Patient** window.

4. Refer to [Table 81 on page 291](#) and follow the guidelines in the Parameter Limits column to fill in the remaining patient information data fields.
  - You can add or modify this information with the Edit Patient feature.
  - When you fill in the patient birth date, the system automatically displays the age. If the patient is less than one year old, the system fills in the Months, Weeks and/or Days field when you enter the birth date.
  - The FE selects the mm/dd/yyyy or yyyy/mm/dd birth date format during installation.

**NOTE**

Japanese systems: Use the yyyy/mm/dd format; then enter the Emperor Era birth year into the yyyy field. The system calculates and displays the western format birth year on the **New Patient** and **Patient Schedule** windows, as well as the in the Image Header.

- The **Patient Information** window contains both metric and imperial data fields for weight and height. If you enter the height/weight value into one field, the system automatically calculates and displays the correct value in the remaining field.
- You can create and store selection lists for the Referring Physician, Radiologist, Operator and Exam Description data fields. [Create Selection Lists for Selected Data Fields](#)

**Table 81 Patient Information Parameter Limits**

Field Name	Parameter Limits
Accession Number	Up to 16 characters assigned by HIS/RIS
Patient ID	Up to 16 characters
Patient Name	Up to 32 characters; DICOM users: Follow the format listed above the Patient Name (lastname^firstname)  <b>NOTE</b> With the <b>Edit Patient</b> utility, you can enter up to 64 characters.
Sex	M (Male) or F (Female)  <b>NOTE</b> With the <b>Edit Patient</b> utility, you can also enter O (Other) for undefined sex. Setting sex to O may limit use of some sex-based quantitation like SUVlbm on the workstation.
Birthdate	Format selectable during software installation: mm/dd/yyyy or yyyy/mm/ddH: Heisei; S: Showa; T: Taisho M: Meiji
Age or Months/Weeks/Days	System fills this value when you enter the birth date
Weight in Pounds and Kilograms	Maximum values: 500 pounds or 227 kilograms
Height in Feet/Inches and Centimeters	Maximum values: 6 ft. 6 in. or 200 cm
Referring Physician	Manual entry: Up to 32 characters HIS/RIS entry: Up to 64 characters
Radiologist	Up to 32 characters
Operator (initials)	Up to 3 characters
History	Up to 60 characters

Patient Information Parameter Limits continued	
Field Name	Parameter Limits
Exam Description	Up to 22 characters  <b>NOTE</b> With the <b>Edit Patient</b> utility, you can enter up to 60 characters.
Protocol Number	Up to 5 characters
Req. Proc. ID	Up to 16 characters

- Press **Enter** or **Tab** to advance to the next available Patient Information field, or move the cursor over a field and click to activate.

Keep the cursor on the scan monitor window while typing. Moving the cursor to the display monitor deactivates the Patient Information data fields.

#### IMPORTANT

To prevent reconciliation problems on a PACS, always verify the Patient ID and Accession Numbers before you scan the patient. Some patients may have multiple procedures scheduled under different Accession Numbers, or New and Completed records on the Patient Schedule under the same ID. Check the Exam Description to make sure you chose the correct Accession Number.

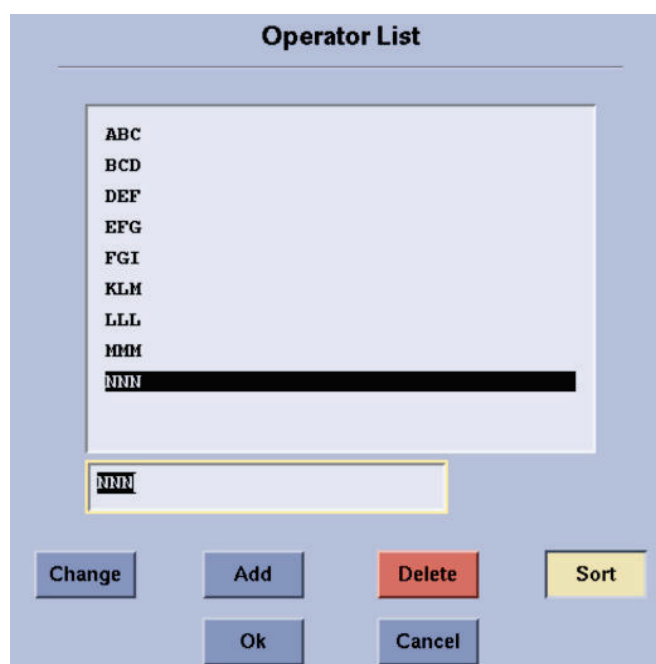
- Enter the patient information into the corresponding fields.
  - Optional: Select the protocol by typing the corresponding protocol number into the **Protocol Number** field or selecting the protocol from the anatomic selector.
  - Optional: Enter the exam date and time into the corresponding fields.
- Click **Accept** to add the currently displayed information to the patient list.  
-or-
- Click **Cancel** to discard the information and return to the Patient Schedule List window.
- Click **Quit** to exit the Patient Schedule List window.

## 9.5 Create Selection Lists for Selected Data Fields

You can create lists of doctors, operator initials and frequently used exam descriptions to expedite the data entry process. The corresponding Patient Information labels appear as buttons. Follow the same procedure to create and manage all available lists.

### 9.5.1 Add a Name or Description to the List

- Click **Referring Physician**, **Radiologist**, **Operator** or **Exam Description** to open the **Operator List**.

**Figure 169 Selection List with Sort Selected**

2. Enter a name, description or set of initials into the field.
3. Click **Add** to update the list.  
Click **Sort** to display the list entries in alphabetical order.

**NOTE**

If you click **OK** before you click **Add**, the system displays what you typed in the corresponding **Patient Information** field without saving it to the list.

4. Click **OK** to display the name in the corresponding **New Patient** field.  
If the list contains more than 10 entries, the **Next** and **Prior** arrows appear.
5. Click **Cancel** to close the list without updating the **New Patient** field.

## 9.5.2 Display the Name or Description in the Corresponding Field

1. Click **Referring Physician**, **Radiologist**, **Operator** or **Exam Description** to open the **Selection List**.
2. Click the **Next** and **Prior** arrows to navigate through the list.  
Each list holds up to 100 entries.
3. Click the name or description to display it in the field below the list.
4. Click **OK** to close the list and display the name or description in the corresponding Patient Information field.



**NOTE**

**Save State** saves a copy of the list contents

### 9.5.3 Modify or Delete an Existing Name or Description from the List

1. Click **Referring Physician, Radiologist, Operator**, or **Exam Description** to open the **Selection List**.

**NOTE**

**Save State** saves a copy of the list contents.

2. Click the **Next** and **Prior** buttons to navigate through the list.
3. Click the name or description to display it in the field.
4. To modify the existing name or description:
  - Change the information in the field below the list.
  - To replace the existing information with the new entry, click **Change**.
  - To add the new entry to the list and keep the existing entry, click **Add**.
  - To remove the existing entry from the list, click **Delete**.
5. Click **Sort** to list the entries alphabetically.
6. Click **OK** to update the list, or click **Cancel** to close the list without updating it.

## 9.6 Delete Patients from the Schedule

You have the option to select and delete individual patients, or delete all patients from the list.

1. Click **Patient Schedule** to display the Schedule List.
2. Use one of the following methods to select patients to delete from the list:
  - Click on a single line to select the corresponding patient.
  - Click and drag to select a contiguous group of names from the list.
  - Press and hold the **Ctrl** key and click on the individual lines to select multiple patients. This option lets you select a group of non-contiguous patients from the list.
3. Click **Delete Selected** to remove each highlighted patient from the list.  
-or-
4. Click **Delete All** to remove every patient from the list.
5. Click **Quit** to close the Patient Schedule List window.

## 9.7 Edit Patient Information Listed on the Schedule

You can modify patient information on the Patient Schedule List, or wait until you download the information into the **New Patient** window to modify it.

1. Click **Patient Schedule** to display the current Patient Schedule List.
2. Click on a line to highlight it for selection.
3. Click **Edit Patient** to open the information window. Edit fields, as needed.

### NOTE

During an acquisition, you can edit other patient records except for the patient record currently in use in Edit Patient.

### NOTE

You can not edit the patient record information if it came from the HIS/RIS and the Edit Modality Worklist is set to **No**.

4. Click **Accept** to save changes to the Patient Schedule List or click **Cancel** to abandon the changes and keep the original information.
5. Click **Edit Tracer Info** to add or modify tracer information fields and data fields, such as blood glucose and diabetic status.
6. Click **Accept** to save changes to the Patient Schedule List or click **Cancel** to abandon the changes and keep the original information.
7. Click **Quit** to close the Patient Schedule List.

## 9.8 Set up Patient Schedule Preferences

All Systems: Use this feature to set up the sort order of the Patient Schedule List, along with the delete times for the Patient Schedule entries. Systems with the Connect Pro Option: Use this feature to select the system response to information from the HIS/RIS.

### NOTE

A software update or *load from cold* restores all preferences to their default value. Review and update the preferences after every software update or load from cold.

1. Click the **Patient Schedule** icon.
2. Click **Preference** to open the **Preferences** window.

**Figure 170 Preferences Window**

The Preferences window is divided into two main sections: **Preferences** and **Default Update Parameters**.

**Preferences Section:**

- Update Schedule Automatically?** Buttons: Yes (blue), No (yellow).
- Sort By:** Buttons: Date/Time (yellow), Name (blue), ID (blue).
- Show Update Parameters?** Buttons: Yes (yellow), No (blue).
- Delete Completed Exams After:** A text input field containing '3' followed by 'Days'.
- Use Study UID?** Buttons: Yes (blue), No (yellow).
- Edit Modality Worklist?** Buttons: Yes (yellow), No (blue).

**Default Update Parameters Section:**

- Get Patient List For:** A row of buttons: This System (blue), All CT Systems (yellow), All Systems (blue), This PET System (blue), All PET System (blue), All NM System (blue).
- With a Date Range:**
  - Today (blue button)
  - Days Before Today (blue button) with an adjacent text input field.
  - Days After Today (blue button) with an adjacent text input field.
  - All Dates (yellow button)

At the bottom of the window are **OK** and **Cancel** buttons.

3. To sort exams, select one of the following **Sort By:** buttons, then click **OK**:
  - **Date/Time:** Sorts the Patients by appointment Day and Time. Patients without Date/Time information appear in alphabetical order at the top of the list.
  - **Name:** Lists the Patients in alphabetical order, by Last Name.
  - **ID:** Sorts the Patients by their facility assigned Patient ID number.
4. Set the number of days to delete completed exams from the list. (Default = 3 days)
  - Enter a number between 0 and 30.
  - Recommended: Select 0 days when the system receives its information from a HIS/RIS. When you select 0 days, the system automatically deletes the corresponding patient information from the list when you click **End Exam**.
5. Systems with Connect Pro Option, click **Yes** or **No** to **Update Schedule Automatically**.  
Click **Yes** to automatically update the schedule, using the Update Parameter selections, every time you click **Patient Schedule**.
6. Systems with Connect Pro Option, click **Yes** or **No** to **Show Update Parameters**.  
Click **Yes** to display the Update Parameters window every time the system starts to automatically update. You can change the update parameters at this time.
7. Systems with Connect Pro Option, click **Yes** or **No** to **Use Study UID**.
  - Click **Yes:** The HIS/RIS assigns the Unique Identifier (UID) to the exam.
  - Click **No:** The PET/CT assigns the UID to the exam.

**NOTE**

Select to **Use Study UID** only when a single exam is acquired in the study. Otherwise (e.g. both cardiac stress and rest exams) unexpected system behavior may occur.

8. Systems with Connect Pro Option, click **Yes** or **No** to **Edit Modality Worklist**.
  - Click **Yes** to allow editing of patient information from the HIS/RIS.
  - Click **No** to prevent the editing of any patient information from the HIS/RIS. You can add information to empty data fields, but you can not add to, or edit the existing patient information.
9. Click **OK** to accept the currently displayed selections and parameters or, click **Cancel** to discard the current selections and close the window.

## 9.9 Update the Patient Schedule List from HIS/RIS

Follow the steps in this section to update the Patient Schedule List from the HIS/RIS.

1. Click the **Patient Schedule** icon.
2. Click **Update** to open the **Update Parameters** window.

**Figure 171 Update Parameters**

3. Select one or more systems on the HIS/RIS to query:
  - **This System** pulls the patient schedule for the PET/CT you are using.
  - **All CT Systems** pulls the patient schedule for all of the CT systems on the HIS/RIS.
  - **All Systems** pulls the patient schedule for ALL systems on the HIS/RIS.
  - **This PET System** pulls the patient schedule for the PET/CT you are using.
  - **All PET Systems** pulls the patient schedule for all of the PET systems on the HIS/RIS.

- **All NM Systems** pulls the patient schedule for all of the Nuclear Medicine systems on the HIS/RIS.
4. Select a **From/To Date Range**.  
Follow the displayed Month/Day/Year format when you type your selection.
  5. Optional: You can pull a single patient from the HIS/RIS by typing the **Requested Proc. ID**, **Accession Number**, **Patient Name** or **Patient ID** into the corresponding data field.
  6. Click **Continue Update** to search for the designated information, or click **Cancel** to close the panel without updating the Patient Schedule List.

## 9.10 View More Patient Information on the HIS/RIS

If the system has the Connect Pro option, you can display additional information about the patient that resides on the HIS/RIS.

1. Click the **Patient Schedule** icon to open the Patient Schedule list. See [9.2 Display the Patient Schedule on page 287](#).
2. Click a line of information to select it.
3. Click **View More Info** to open the **Detailed Patient Information** window.

**Figure 172 Detailed Patient Information Window**

**Detailed Patient Information**

CT Patient Information	Additional Patient Information
Patient ID : 124-378-846	Pregnancy Status : NOT PREGNANT
Accession Number :	Medical Alerts : LATEX ALLERGY
Name :	Contrast Allergies : IODINE
Sex : Male	Requested Contrast Agent : IOMIC
Birthdate : 1/7/1945	Special Needs : SPEAKS HANGARIN, NO ENGLISH
Height In Kgs : 109	Telephone :
Height In Lbs : 240	Patient History : KIDNEY STONES
Height In Cms :	Study Instance UID :
Height In Ft :	Requesting Physician : OB/GYN
Height In Ins :	Requesting Service :
Referring Physician :	Patient Ethnic Group :
Radiologist :	Other Patient IDs :
Operator :	Patient Comments :
Patient History : KIDNEY STONES	Recipients Of Results :
Exam Description : KIDNEY STONE	Performing Physician :
Protocol ID : 10.6	Requested Proc. ID :
	Scheduled Proc. ID :
	Imaging Service Req. Comments :
	Scheduled Action Item Value :

This is patient sensitive information, please adhere to patient confidentiality rules. The information about the patient has been manually entered. Please verify the information either with the patient's medical records or directly with the patient to guarantee its accuracy.

Cancel

Next Prior

4. Click **Cancel** to close the window.

## 9.11 Use the Bar Code Reader to Access Patient Information

Systems with Connect Pro: If your system has the optional Bar Code Reader, you can use it to access information in the Patient Schedule List.

1. Click the **New Patient** icon.
2. Aim the Bar Code Reader at the bar code for either the **Accession Number** or the **Patient ID** on the patient requisition.

The system loads the patient information from the Patient Schedule List and populates the Patient Information window.

### NOTE

The system truncates the **Exam Description** to 22 characters when it imports it from the HIS/RIS. The **Study Description** field in the DICOM header maps to the **Exam Description** field on Patient Schedule List and **New Patient** windows.

3. Select a patient protocol to continue.

### NOTE

The system displays a dialog box when it finds more than one record with the same **Patient ID** in the Patient Schedule List. Make sure you select the correct information for the intended exam. To avoid this situation, set the **Delete Completed Exams** preference to 0 so the Patient Schedule List only contains new records.

## 9.12 Schedule Patients Quick Steps

### 9.12.1 Display the Patient Schedule

1. Click the **Patient Schedule** icon to display the browser.
2. Click **Next** and **Prior** to view the entire list.
3. Click **Quit** to exit.

### 9.12.2 Select a Patient from the Schedule List

1. Click the **New Patient** icon.
2. Click the **Patient Schedule** icon.
3. Click on the patient information to highlight it.
4. Click **Select Patient**.
5. If necessary, select a patient protocol to continue.

6. Click **Enter**.

### 9.12.3 Delete One or More Patients from the Schedule

1. Click **Patient Schedule**.
2. Select one or more patients from the list.
3. Click **Delete Selected** to remove every highlighted patient from the list.
4. OR- Click **Delete All** to remove every patient from the Schedule List.
5. Click **Quit** to close the Patient Schedule List.

### 9.12.4 Edit Patient Information Listed on the Schedule

1. Click the **Patient Schedule** icon.
2. Click on a line of information.
3. Click **Edit Patient** and modify the information.
4. Click **Edit Tracer Info** and add tracer information. Click **Accept**.
5. Click **Quit** to close the Patient Schedule List.

### 9.12.5 Set up Patient Schedule Preferences

1. Click the **Patient Schedule** icon.
2. Click **Preference**.
3. Select a sort method of **Date/Time**, **Name** or **ID**.
4. Select the number of days to retain a completed “C” status exam (0-30 days; default = 3 days).
5. Connect Pro option: **Update Schedule Automatically?** - **Yes** or **No**.
6. Connect Pro option: **Show Update Parameters?** - **Yes** or **No**.
7. Connect Pro option: **Use Study UID?** - **Yes** or **No**.
8. Connect Pro option: **Edit Modality Worklist?** - **Yes** or **No**.
9. Click **OK** to retain selections and close panel, or click **Cancel** to discard new selections and close the panel.

### 9.12.6 Update the Patient Schedule List from HIS/RIS

1. Click the **Patient Schedule** icon.
2. Click **Update**.
3. Select one or more systems on the HIS/RIS to query.
4. Enter a **From/To** range of dates.

5. Optional: Type information into one of the remaining data fields to pull a single patient from the HIS/RIS.
6. Click **Continue Update** to transfer the designated information to the Patient Schedule List and close the panel, or click **Cancel** to close the panel without updating the Patient Schedule List.

### 9.12.7 View More Patient Information on the HIS/RIS

1. Click the **Patient Schedule** icon.
2. Click/highlight a line of information to select it.
3. Click **View More Info**.
4. Click **Cancel** to close the panel.

### 9.12.8 Use the Bar Code Reader to Call up Patient Information

1. Click the **New Patient** icon.
2. Aim the Bar Code Reader at the bar code on the patient requisition.
3. If necessary, select a patient protocol to continue.



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# 10 Scan the Patient

## 10.1 Scan the Patient Introduction

This chapter contains procedures to prepare the patient and system for a typical oncology study. It also describes how to open an exam, retrieve information from the patient schedule, position the patient, select a scan protocol, acquire the data and end the exam.

Please refer to Respiratory Gating and [PET Cardiac Imaging](#) for additional setup information for these specialized studies.

### NOTE

You can acquire the PET series before or after the CT series. The system notifies you if you acquire the PET series first; click **End Exam** before you acquire the CTAC series.

## 10.2 Prepare the System for Daily Operation

Perform the following at the start of each day:

- Restart the system.
- Warm up the X-ray tube.
- Run the Fast Calibration.
- Run the PET Daily QA. Perform scanner, dose calibrator, and facility clock synchronization check.
- Follow facility guidelines to check CT image quality.
- Inspect the patient accessories for cleanliness and signs of damage. Do not use any accessory that appears broken or torn.
- Gather and organize supplies and any specialized equipment, such as an injector or cardiac monitor and leads.
- Inspect the table area, cradle pads and gantry opening for dried contrast.
- Update or review the Patient Schedule.

## 10.3 Prepare Two-Meter Table Top (Optional)

Follow these instructions to attach the optional two-meter table top to the permanently installed cleat on the PET/CT cradle.

1. Peel back the cradle pad to expose the cleat (1).

Scan the Patient



TO PREVENT INJURY, BE OBSERVANT WHEN LATCHING THE TWO-METER EXTENDER TO THE CLEAT TO AVOID PINCHING YOUR FINGERS.

2. Carefully lay the two-meter table top on the cradle, with the padded end facing the gantry.

**NOTE**

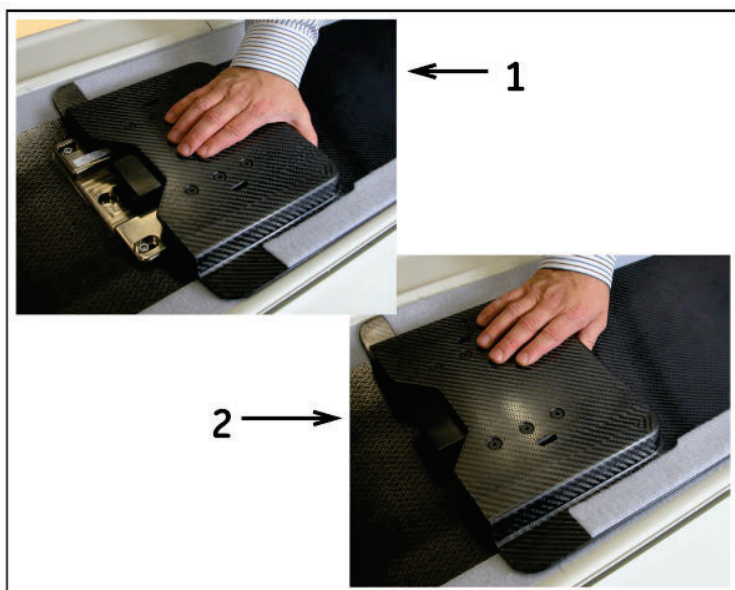
All two-meter scans are feet first.

**Figure 173 Permanently Installed Cleat (1) and Two-Meter Table Top Accessory Latch (2)**



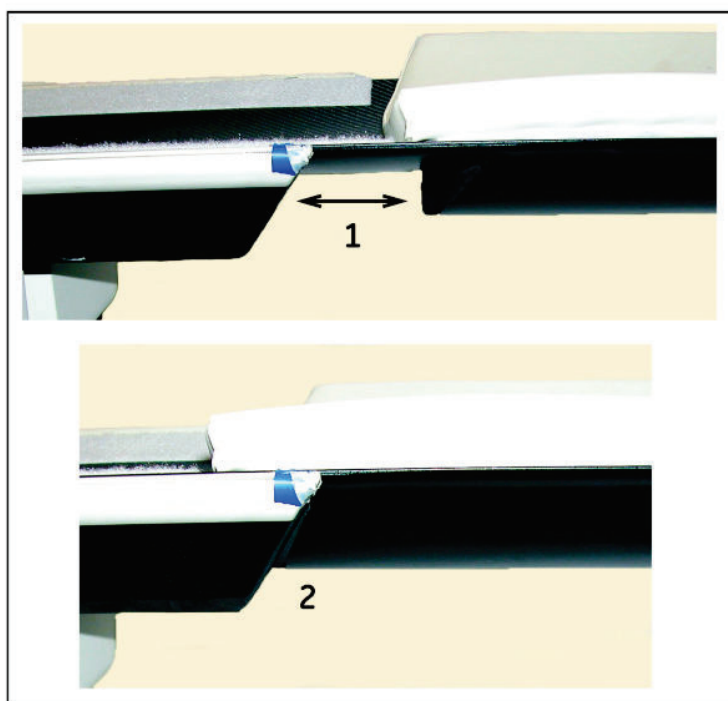
3. Slide the two-meter table top latch onto the cleat until it clicks into place.

**Figure 174 Latch Two-Meter Table Top to Cleat**



4. When successfully latched, the bottom edge of padded foot extension rests against the front of the cradle.

**Figure 175 Two-Meter Table Top Correctly Attached**

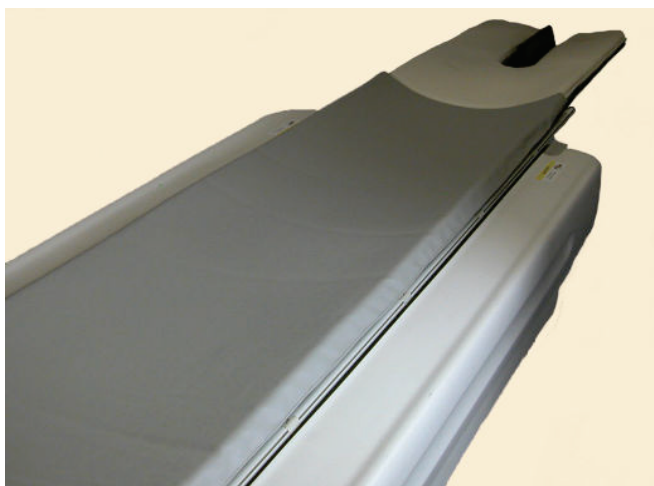


5. Roll the cradle pad over the two-meter table top accessory and fasten to the Velcro loops on the sides of the accessory.

### IMPORTANT

To prevent damage to the Two-Meter Table Top Accessory and the Gantry Front cover, do not lower the table past 284 mm below isocenter. Follow facility guidelines to transfer non-ambulatory patients to the PET/CT Table.

**Figure 176 Fasten the Cradle Pad back into Place**



### NOTE

***2 meter total scan range Rx adjustment on Scout scan.***

When attempting to adjust Scan Rx for the CT acquisition of the 2-meter protocol, the axial and helical groups can move independently of each other and cause undesired spacing between axial and helical groups. Click on each helical group in Scan Rx to link them together. Then when grabbing the red **x** in the center of the helical acquisition, all three CT groups should move together.

## 10.4 Prepare for a Follow-up PET/CT Scan

An important part of PET quantitation for restaging (follow-up) procedures is understanding how the prior study was done. This helps minimize differences between studies and allows for more precise comparisons during review.

QPrep allows you to review important quantitation parameters from the prior patient study, including:

- Review a patient's prior study details from the scanner.
- Compare the current exam with the prior exam details.

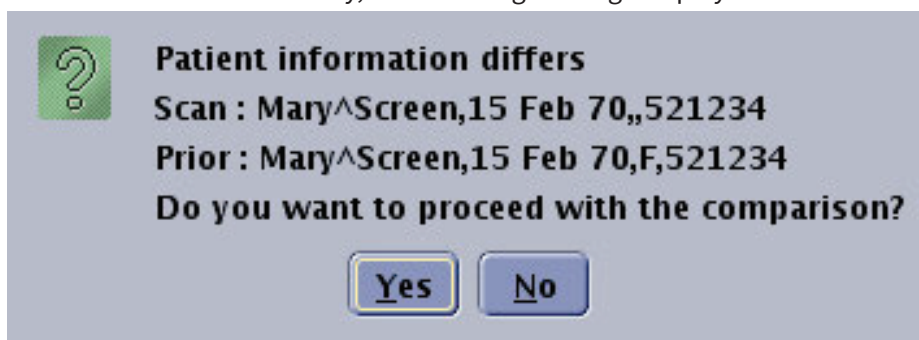
To review the prior study of a patient and compare it to the current exam, follow the steps below:

1. Click **Image Works**.
2. Restore the patient's prior PET/CT exam on the scanner from your archive, such as PACS, or from a CD/DVD.
3. Select the prior exam and the attenuation-corrected PET image series.

**NOTE**

Make sure to select an attenuation-corrected PET series. If an attenuation-corrected PET series is not selected, the first attenuation-corrected PET series from the exam displays.

4. Click **QPrep**. QPrep displays the quantitation parameters.
5. To proceed with compare, click **Exam Rx**, otherwise, click **Close** to close QPrep.
6. Follow the procedure in [Open the Exam](#) to select the patient, followed by protocol selection.
7. Follow the procedure in [Prescribe and Acquire the Scout Series](#) to acquire and display the scout image.
8. Click **Next Series** to display the next available series in the protocol, typically the CTAC.  
Hybrid Protocol: Click **PET** and **CT** to toggle between the CT series and PET series scan screens.
9. To compare the current scan prescription with the prior study of the same patient, click on **Image Works**. In the QPrep window, check **Compare**.
  - If the patient demographic information from the prior study differs from that of the current study, the following message displays:



- Click **Yes** to continue, **No** to exit the application.
10. QPrep displays the prior exam and the current exam in a table, highlighting differences.
    - Review the values for the prior exam in QPrep and make updates to the current prescription, if appropriate.
    - Click **Refresh** to update the QPrep table to the latest prescription values.

Scan the Patient

**Figure 177 QPrep display showing previous and current exams**

☒ Compare Report

Parameters	Study Date: 09 Sep 21	Current
<b>Patient</b>		
Name	WHOLEBODY^WALTER	WHOLEBODY^WALTER
ID	53549	53549
Date Of Birth	15 Mar 80	15 Mar 80
Sex	M	M
Weight (kg)	86.4	84
Height (cm)	198	198
Glucose Lvl (mmol/L)	10.5449	10.5449
Diabetic	Unknown	Unknown
Last Treatment		
Institution	G.E. Medical Systems	G.E. Medical Systems
Model	Discovery AI	Discovery AI
Manufacturer	GE MEDICAL SYSTEMS	GE MEDICAL SYSTEMS
Software Ver	pet_omni.5	pet_omni.5
<b>Patient Preparation</b>		
Admin Time	09 Sep 21 10:15:00	09 Sep 21 10:39:00
Uptake time (min)	124	62
Tracer	FDG -- fluorodeoxyglucose	FDG -- fluorodeoxyglucose
Radionuclide	18F	18F
Inj dose (MBq)	364.2325	432.9000
<b>Study</b>		
Study Description	WB ONCOLOGY	WB ONCOLOGY
Series Description	WB 3D MAC	WB 3D MAC
Slice thickness (mm)	2.070	2.070
Recon Diameter (mm)	700	700
Recon Method	VPHD	VPHD
Recon Iter/Subs	3/22	3/22
Protocol	26.31 PTCT_ET	26.31 PTCT_ET
Acq Method	3D	3D
Scan duration	00:01:00	00:01:30
Scan Type	STATIC	STATIC
Matrix size	256x256	256x256
Image Units	BQML	BQML
Patient position	HFS	HFS
Scan Direction	HEAD_TO_FEET	

11. Click **Close** to close QPrep.

## 10.5 Prepare the Patient for the Study

For best results, open the exam and fill in the patient information before you escort the patient into the scan room and prepare them for the study. You have the option to populate the **New Patient** window by selecting the patient from the Patient Schedule, or manually entering the information into the **New Patient** window.

- Follow the procedures in this chapter to open the schedule, select a patient and load the information into the **New Patient** window.

- Follow the instructions in [Schedule Patients](#) to manually enter the information into the **New Patient** window. You have the option to enter the tracer information prior to opening the exam through this method.

Escort patients into the scan room and help them onto the table.

- Use foam blocks, pads and positioning straps to help the patient feel as secure and comfortable as possible.
- Use positioning straps to restrain the patient to the cradle and prevent patient movement during scan and secure patient limbs, body and head as necessary.
- Securely fasten the IV poles, arm holders and catheter bags in place. If patient positioning is performed manually, monitor the devices while you manually drive the cradle and table into and out of the gantry to check for possible interference with the system covers. Check IV lines and monitor leads lengths.
- Tuck in the patient clothes, sheets and blankets, and make sure they do not catch or drag along the table during cradle motion. If necessary, use positioning straps to keep excess material off the table surface.
- Explain the procedure to your patients, so they know what to expect. If they can anticipate table motion and gantry noises, they are more likely to remain calm and motionless during the study.
- Practice breathing and breath-holds with patients, to make sure they respond correctly to commands during the study, and to make sure they are physically capable of holding their breath for the required duration.
- Describe the alignment process and direct your patients to close their eyes while you position and landmark them to the alignment lights.

#### NOTE

If Auto-In or Auto-Positioning features are used to position the patient, refer to chapter [10.7.2](#) and [10.7.3](#) for more instructions on use of these features.

#### NOTE

If you plan to use the Xstream Injector for CT contrast injection during a Hybrid PET/CT exam, and you plan to acquire the PET series before the CT series, you must complete the Xstream Injector air check step before you click **Confirm** to initiate the PET acquisition. Please refer to the CT User Manual and CT TRM shipped with your system for detailed instructions.

## 10.6 Open the Exam

Follow these instructions to select a patient from the Patient Schedule, and start the exam.

- Click **New Patient** in the scan monitor tool bar.

The **New Patient** window opens, and displays the next available **Exam Number** (1 - 49,999) in the corresponding field.



**NOTE**

If you plan to manually enter the patient information, please follow the instructions to [Manually Add a Patient to the Schedule](#). If an emergency patient arrives without an ID, enter ?? or *trauma* into the field to activate the window. Use the Edit Patient feature to add the Patient ID when you receive it.

Yellow data fields must be filled in prior to selecting a protocol. When a protocol is selected prior to entering these fields, an alert message will prompt you to fill in the required fields. In emergency situations, you can select the **Proceed** button on the alert message to proceed to protocol selection without filling in the required fields.

**Figure 178 New Patient Window**

**Patient Information**

Exam Number: 210

Accession Number: [Field]

Patient ID: [Field]

Format: LastName\*FirstName\*Middle\*Prefix\*Suffix

Patient Name: [Field]

Sex: [Field] Birthdate: [Field]

Age: [Field]

Weight: [Field] Height: [Field]

Referring Physician: [Field]

Radiologist: [Field]

Operator: [Field]

History: [Field]

Exam Description: [Field]

Protocol Number: [Field]

Req. Proc. ID: [Field]

**Protocol Selection**

Anatomical Selector: GE, User, Service, Most Recent

Default Protocol:

- 21.10 PTCT\_Brain
- 22.1 Sinus Supine Helical + DMPP
- 23.1 C-Spine C5-C7 Axial
- 24.1 Shoulder 2.5mm + DMPP
- 25.35 PTCT\_Rb\_Rest-Stress
- 26.24 PTCT\_ET
- 27.1 L-Spine 3 Level Axial
- 28.1 Pelvis for Fracture + DMPP/Sin
- 29.1 Lower Extremity Survey 2.5mm
- 30.1 Quality Assurance

**P E D I A T R I C**

Buttons: End Exam, Enter PET Tracer Info, View More Information

Tool Bar: Auto Positioning, New Patient, Patient Schedule, Patient Management, CT Reac Recon, CT Recon Mipol, Daily Prep, Shared 4D Mipol, PET Recon Replay, PET Recon Mipol

- Click the **Patient Schedule** icon in the scan monitor tool bar.
- Click the patient information, taking care to choose the correct **Patient ID** and **Accession Number**, if the patient information comes from a HIS/RIS.  
The HIS/RIS assigns the **Accession Number**, if your facility uses this option.
- Click **Select Patient** to load the corresponding information into the **Patient Information** area of the **New Patient** window.

5. Add or edit information at the Patient Information area before you select the protocol.
6. Press **Enter** or **Tab** to advance to the next available **Patient Information** data field, or move the cursor over a field and click to activate.
  - Keep the cursor on the scan monitor window while typing. Moving the mouse to the display monitor deactivates the **Patient Information** data fields.
  - Yellow data fields must be filled in prior to selecting a protocol. Required fields can be configured. Refer to [Edit Patient and Tracer Information](#). If a protocol is selected prior to entering these fields, an alert message will prompt you to fill in the required fields.



PRECISION DL UTILIZES PATIENT WEIGHT AND TRACER INFORMATION (TRACER, NUCLIDE, AND INJECTION ACTIVITY, DATE AND TIME) DURING INFERENCING. ANY RETROSPECTIVE CHANGE TO A RELATED FIELD WILL REQUIRE RETROSPECTIVE RECONSTRUCTION OF THE PRECISION DL IMAGE(S). THE PRECISION DL IMAGE(S) WILL BE MARKED AS INVALID WHEN RETROSPECTIVELY CHANING PATIENT WEIGHT OR TRACER RELATED INFORMATION

#### NOTE

Unlike other reconstruction techniques, patient/phantom weight, and tracer information (tracer, nuclide, activity dose, date and time) are a prerequisite for Precision DL. Missing or inaccurate patient information may lead to inaccurate quantitative values.

Where Patient information and /or tracer information is missing or inaccurate, use **Edit Patient** and **Edit Tracer** apps available on the console to correct errors before performing retrospective reconstruction with Precision DL to re-generate images.

Warning messages are displayed as part of Q.Check to remind you if patient or tracer information are missing. Ensure you populate this information if you plan to prescribe Precision DL in your prospective reconstruction.

#### NOTE

Precision DL is trained mostly on clinical data of 18F-FDG only. It is never trained on Phantom scans such as NEMA, EARL or other, and it is not verified or validated for that use. Performance of Precision DL is not tested for acceptance testing of the system. Follow guidance of acceptance testing and use conventional reconstructions as instructed.

#### IMPORTANT

To prevent reconciliation problems on a PACS, always verify the Patient ID and Accession Numbers before you scan the patient. Some patients can have multiple procedures scheduled under different Accession Numbers, or new and completed records on the Patient Schedule under the same Patient ID. Check the Exam Description to make sure you chose the correct Accession Number.

7. Click **Enter PET Tracer Info** to open the **PET Quantification Information** window and enter the injection information into the corresponding data fields.
  - Fill the corresponding data fields with the available information.
  - Yellow data fields are required to be filled in prior to confirming the PET scan. Required fields can be configured. Refer to the Edit Patient and Tracer Information chapter. If PET scan is confirmed prior to entering these fields, an attention message will prompt the user to fill in the required fields.
  - The system propagates the injection and patient information to each PET scan in the exam, for which the Quantification **Inherit From Exam** button is enabled.
8. Click **Accept** to keep the current information and close the **PET Quantification Information** window.  
Click **Cancel** to discard any entered information and close the window.

#### NOTE

You can add or modify Quantification Information in the **View/Edit** window (scan window) before acquiring the data, (see [Acquire the PET Series](#) and [End the Exam](#)) and again after the exam ends. Click **Edit Tracer** on the patient browser to open the **Update Tracer Activity** window. See [Edit Patient and Tracer Information](#).

9. Optional: Click **View More Information** to open the **Detailed Patient Information** window.
  - The window displays any additional information that was manually entered on HIS/RIS.
  - Click **Cancel** to close the window and return to the **New Patient** window.
10. Verify all the information on the **New Patient** window before you select the protocol.  
You can click **Select New Protocol** from the first scan window before you start scanning, but once you select the patient protocol, you cannot return to the **New Patient** window, unless you click **End Exam** and start over.

#### NOTE

You must use the two meter table top protocol, **PTCT\_2m\_WB**, from the **GE** tab for 2M scan. Do not modify the Scout, CT or PET scan ranges from the protocol defaults.  
You can modify the reconstruction parameters, filming options, and CT kV and mA.

11. Select a patient protocol or manually enter the **Protocol Number** to proceed to positioning the patient for the scan.
  - Click a region of interest on the **Anatomical Selector** to display the corresponding protocol list, then click a protocol to open the first scan window, or click the labeled default button to open the first available scan window in the default protocol.
  - Place cursor in the **Protocol Number** section and enter the protocol number that you want to use for this imaging procedure.

## 10.7 Position the Patient for a Standard PET/CT

## 10.7.1 Manual positioning

Prepare the scan room before you escort the patient into the room.

1. Attach the head holder or foot extender to the cradle, if applicable.

Do not use the Two-Meter Table Top Accessory during pediatric studies.

### IMPORTANT

To prevent damage to the Two-Meter Table Top Accessory and the Gantry Front cover, do not lower the table past 284 mm below isocenter with the accessory in place. Follow facility guidelines to transfer non ambulatory patients to the table.

2. Help the patient onto the table.
  - Head studies: Take time to properly position and secure the patient's head to the head holder with the Velcro straps. An improperly positioned head in the head holder can produce alternating light and dark images.
  - Check the body straps for a secure connection to the table before fastening them.
  - Use positioning straps to restrain the patient to the cradle and prevent patient movement during scan to secure patient limbs, body and head as necessary.



THE PATIENT POSITIONING STRAPS SHOULD BE USED TO RESTRAIN THE PATIENT TO THE CRADLE AND LIMIT THE PATIENT MOVEMENT DURING SCAN.



THE PATIENT POSITIONING STRAPS WILL NOT SUPPORT THE FULL WEIGHT OF THE PATIENT AND SHOULD NEVER BE USED TO RESTRAIN A COMBATIVE PATIENT.

3. Use the control buttons on the gantry to raise the table and drive the cradle into position.

Check for potential interference between the table, gantry and monitoring equipment or patient garments, IV lines, etc.



TO PREVENT EYE DAMAGE, ALWAYS WARN PATIENTS TO CLOSE THEIR EYES BEFORE YOU TURN ON THE ALIGNMENT LASERS. TELL THEM TO KEEP THEIR EYES CLOSED UNTIL YOU FINISH THE ALIGNMENT PROCESS, TURN OFF THE LASERS AND TELL THEM THEY CAN OPEN THEIR EYES.

4. Press the **Alignment Light** button to turn on the lasers.
5. Use the table and cradle positioning buttons to align the patient area of interest to the lasers. Choose a standard anatomic landmark.

If necessary, reposition the patient on the cradle to center the area of interest to the center of the scan field.

6. Align the patient anatomy to the laser, then press the **Landmark** button to enable the **Confirm** button on the first scan series acquisition screen.

A heavy patient may cause a deflection when the cradle extends. If you use the external lasers to align a large patient, drive the cradle to the internal alignment lights, verify the alignment, and if necessary, adjust the table height to compensate for any deflection of the cradle in the extended position.

7. Press the **Alignment Light** button to toggle the lasers off.

A timer automatically turns off the lasers when it reaches the preset limit.

## 10.7.2 Remote positioning with Table Auto In (Optional)

### Auto In Overview

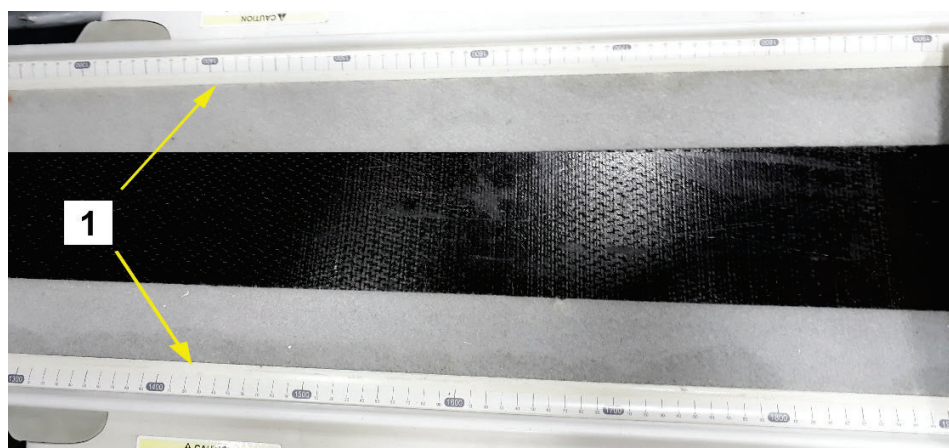
Auto In is a feature which allows the user to move the table to the desired position from the console. The feature has a mini UI on the scan monitor and a measurement scale on the table which enables user to move the table from the console. This is an optional feature which can be enabled through service desktop. Contact service to install this option.

### Auto In Table Positioning

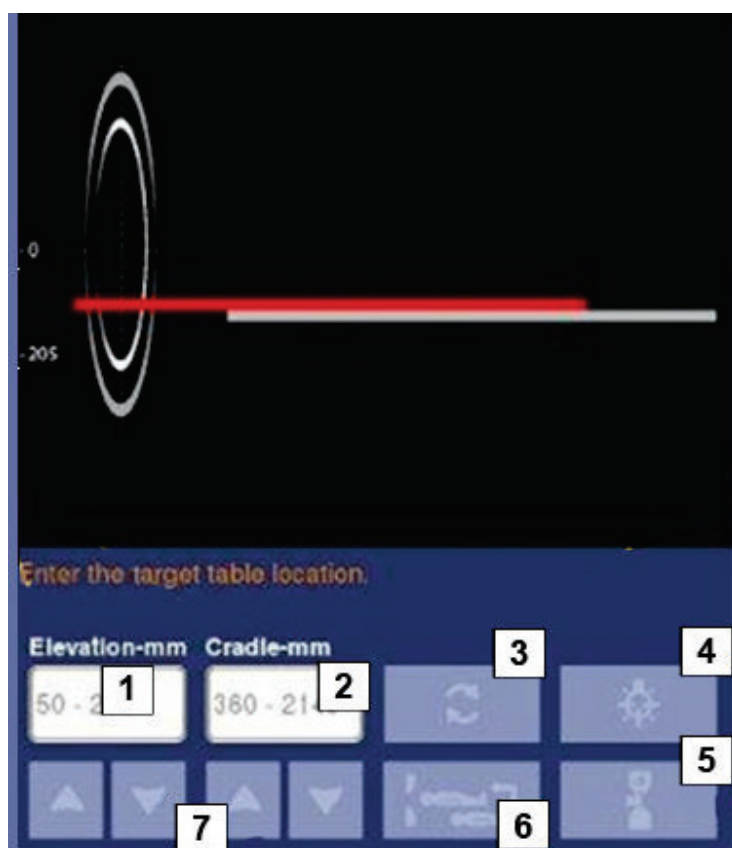
1. Position the patient on the cradle in the scan room and note the number on the cradle scale corresponding to the desired table/landmark position.



THE PATIENT POSITIONING STRAPS SHOULD BE USED TO RESTRAIN THE PATIENT TO THE CRADLE AND LIMIT THE PATIENT MOVEMENT DURING SCAN.

**Figure 179 Auto In scale on both sides of cradle**

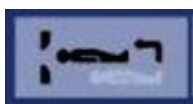
2. Select any hybrid protocol and the Auto In UI is displayed at the scout page. Enter the desired target cradle (cradle -mm) and elevation (Elevation-mm) position in the Auto In UI.

**Figure 180 Auto In UI**

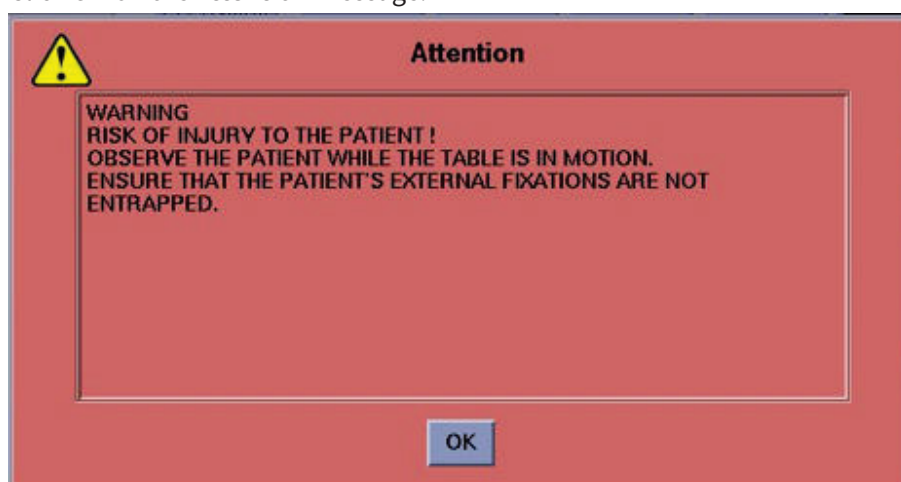
## Scan the Patient

1	Elevation (50-205 mm) - UI displays the valid range, and validates the input
2	Cradle location (360 – [2015-2200 ]) - UI displays the valid range, and validates the input
3	Reset the cradle and elevation values
4	Laser light button for turning the light ON for 3 secs
5	Internal CT landmark
6	Auto In Enable/Confirmation button for confirming the values and starting the Auto In
7	Refine target position – up/down arrows (+/- 1mm)

- Click the **Auto In Confirmation** button.

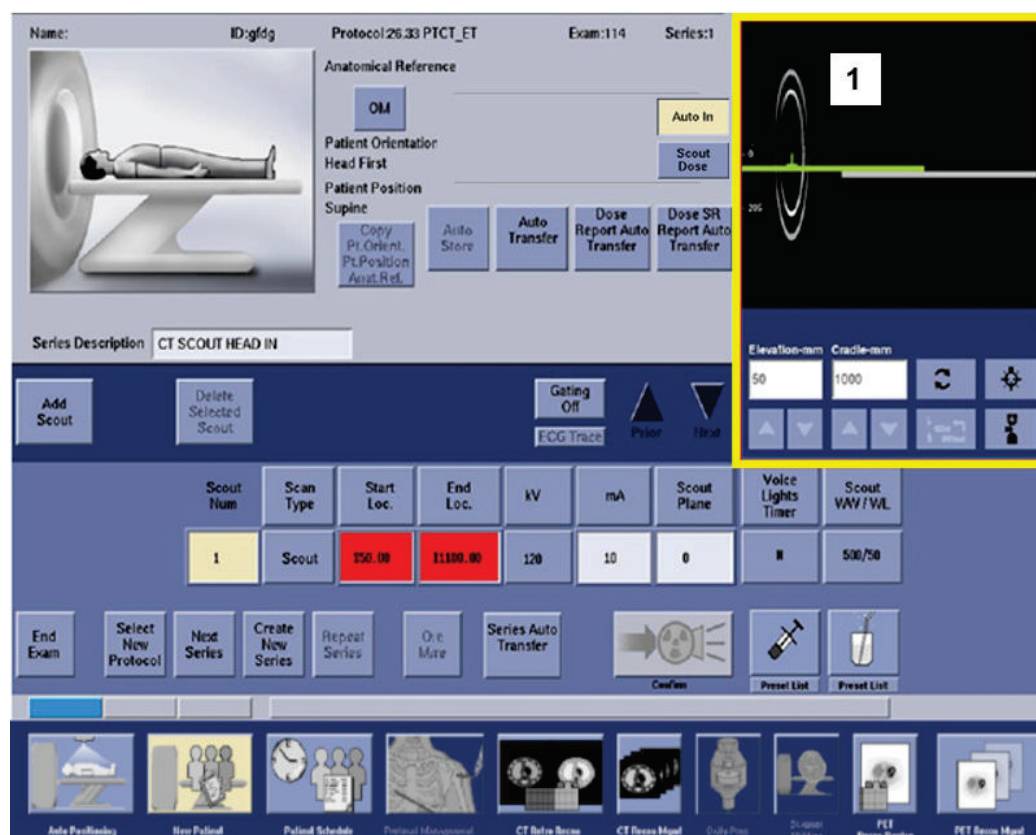


- Click **OK** on the **Attention** message.



- Press and hold the **Auto In/Retract** button on Scan Control Interface continuously until table reaches the target location and Auto In UI displays cradle in “green” color.



**Figure 181 Auto In region on the Scan Monitor: Cradle displayed in green**

6. 

1	Cradle displayed in green
---	---------------------------
7. Use the laser button to switch ON the laser to verify patient positioning (if applicable). The laser turns OFF automatically after 3 seconds. Make sure laser is not falling in patient's eye.
8. If the table position needs to be modified, repeat the above steps by using the **Reset** button.
9. Once patient is positioned at desired location, click the **Landmark** button on Auto In UI.

**NOTE**

- Ensure that the patient is iso-centered before clicking the **Landmark** button.
- If the gantry controls are used, the Auto In workflow resets to default launch state.

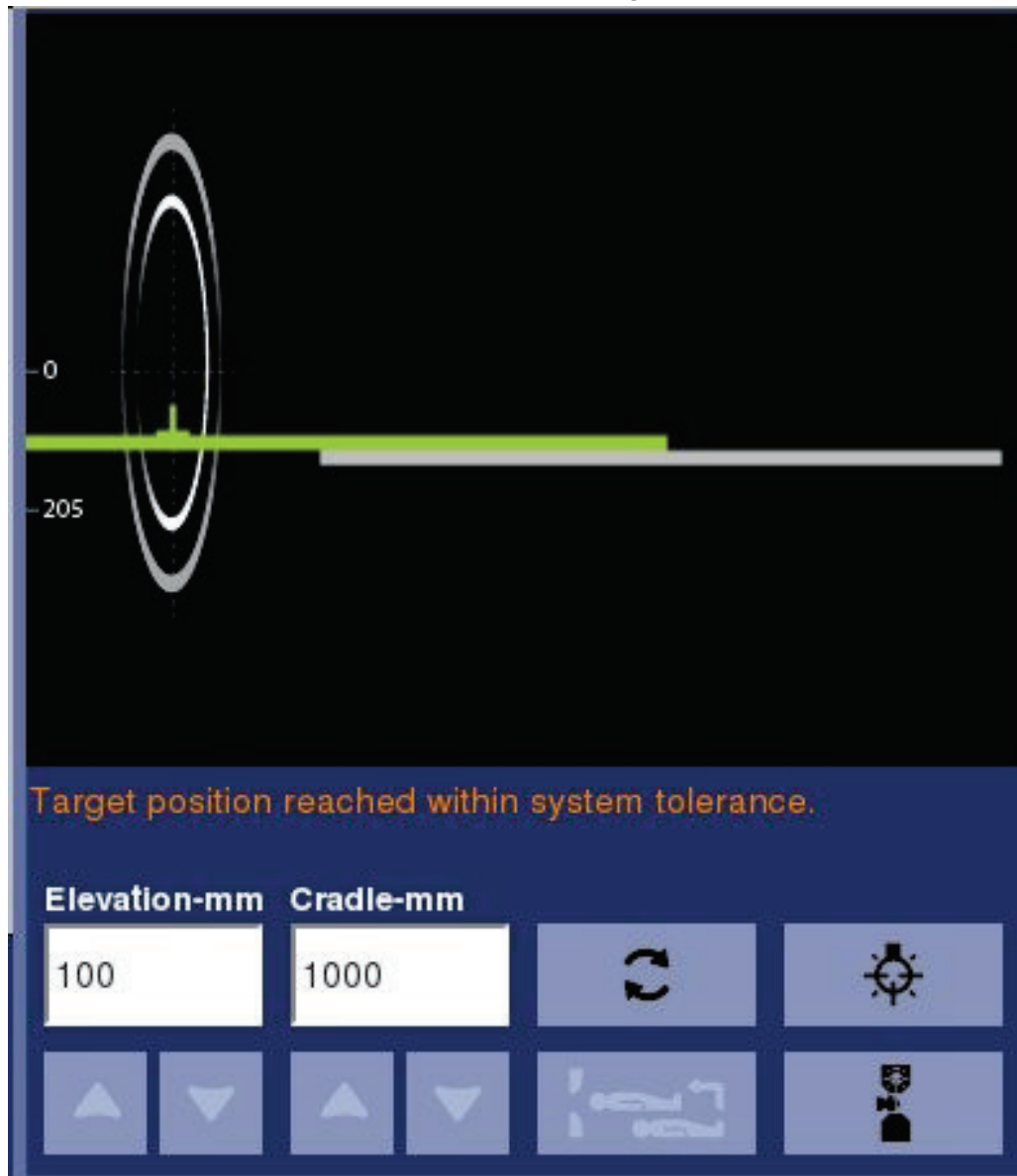
**Interpretation of Auto In messages**



Scan the Patient

**Message:** Target position reached within system tolerance

**Interpretation:** Table has reached the prescribed target location within +/- 2 mm of prescribed value.



**Message:** E-stop button is pressed! Aborting the Auto-In workflow! /Gantry button is pressed! Exiting Auto-In workflow! Re-initiate the workflow.

**Interpretation:** One of the following events has occurred. Please restart the Auto In workflow, if required.

- Gantry button press
- E-Stop button press
- Unintended table motion

**NOTE**

Once patient positioning is completed with Auto-In, make sure to review “Scout Dose Report” prior to Scout confirmation and scan start.

### 10.7.3 Automatic and remote patient positioning with Auto Positioning (Optional)

#### 10.7.3.1 Automatic and Remote Patient Positioning Workflow

The Auto Positioning option uses a depth Xstream camera image to detect patient position, calculate the Scout Scan Range and center of the anatomy, to achieve an automated workflow for patient positioning and scout scanning. After patient preparation, the user does not need to manually move the table or turn on laser light.

The Remote Auto Positioning allows you to position the patient using the Auto Position remotely, from the Operator Console, by duplicating the Gantry display on to the console. It is available from the console until scout scan is approved, and scout scan position is reached.

**NOTE**

The Remote Auto Positioning is optional and can be used only if the Remote Control Kit is also installed. See Remote Control kit for more information on how to operate the Remote Control Kit.

Follow the instructions below to use Auto Positioning or Remote Auto Positioning:

View the patient video on the gantry display to ensure there is no obstruction from people or objects. If necessary, use the **Cradle In/Cradle Out, Table Up/Table Down** buttons on the gantry, or on the Remote Control Panel if installed, to move the cradle so that patient is in the video range.



THE PATIENT POSITIONING STRAPS SHOULD BE USED TO RESTRAIN THE PATIENT TO THE CRADLE AND LIMIT THE PATIENT MOVEMENT DURING SCAN.



AUTO POSITION OPTION IS NOT APPLICABLE FOR USE WITH FLAT-TABLE TOP. THIS MAY CAUSE TABLE COLLISION WITH GANTRY AND RESULT IN PATIENT INJURY AND PROPERTY DAMAGE

**NOTE**

Table base must be in CT scan position in order to start Auto Positioning or Remote Auto Positioning. If table base is not in CT position, hold and continuously press the **CT Scan Position** button on the Gantry panel until it reaches CT scan position and the CT scan position lights up on the gantry display.

## Scan the Patient

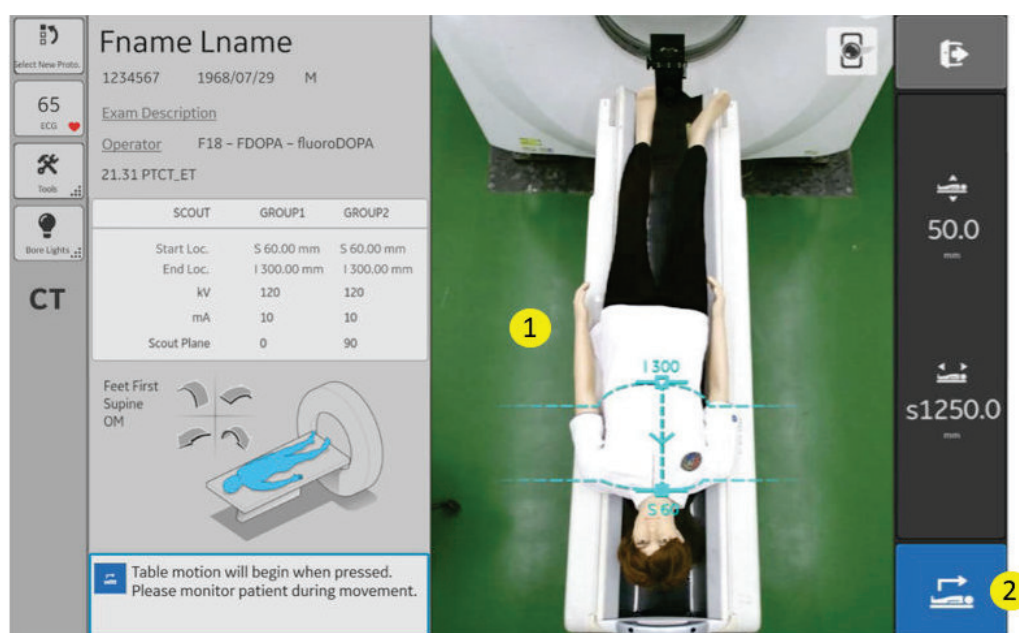
1. Observe whether the Scout Range Indicator displayed on the video is appropriate. The user can fine-tune the Scout scan Range on the Xstream tablet, or Remote Auto Positioning screen, if needed.

### NOTE



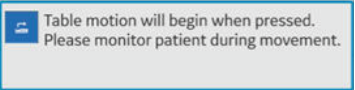
When you update the scan range, the **Camera** icon  will turn Off, to indicate

the scan range is no longer set by the auto detection algorithm. To revert to using the scan range defined by the auto detection algorithm, press the **Camera** icon, and turn it On.

**Figure 182 Scout Image Range Confirmation**



**Table 82 Scout Image Range Confirmation**

Number	Icon	Description
1		Scout Range Indicator. Scout Range is inherited from the protocol. Drag and drop the small cyan edges to change the scan range as desired.
2		Confirm and table move in, as instructed in the message area: 

**NOTE**

Auto Positioning sets the scan range based on the Anatomical Reference set in the scan protocol. Anatomical References supported by Auto Positioning include:

- OM – Orbital Meatal line
- SN – Sternal Notch
- XY – Xyphoid
- IC – Iliac Crest
- SP – Symphysis pubis
- KN – Knee
- AJ – Ankle Joint

If the anatomical reference set in the scan protocol is not in the above list, the Scout Image Range Indicator will not show up automatically. If this occurs, use Internal Landmark or External CT Landmark button to position patient manually.

**NOTE**

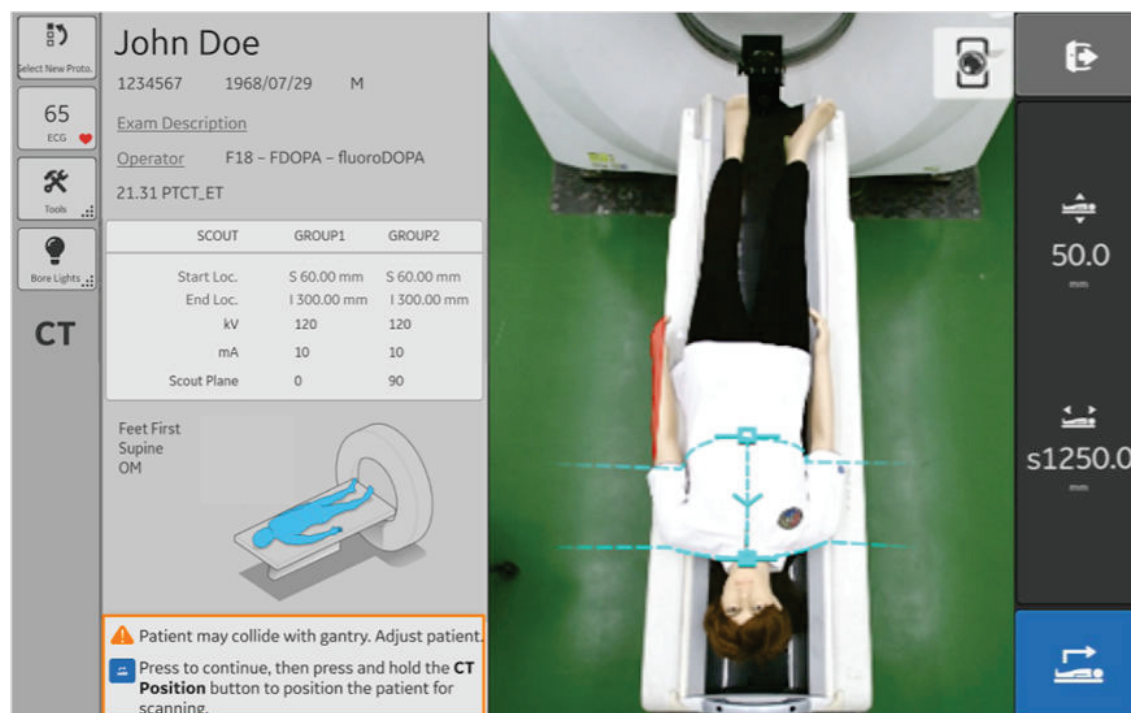
The accuracy of scan range can be affected by lighting conditions, and patient positioning to the Xstream camera. Make sure the scan range is appropriate and perform the next steps.

**NOTE**

If Auto Positioning detects possible collision (automatic motion will cause patient's body, clothing or accessories come into contact with gantry), a warning message displays and the expected collision area will be highlighted in red in the video area. Adjust patient, clothing or accessories to clear the collision.

If the prediction for collision persists, you may still proceed with the positioning process, but you will control table movement. See next step.

**Figure 183 Possible Collision detected during Auto / Remote Auto Positioning**



2. Press the **Confirm** icon. The table automatically rises to the optimal height and the cradle moves forward to the beginning of the scout image. During this movement, please pay attention to patient. If the auto move needs to be stopped, select **Pause** on the gantry display or the **Emergency Stop** button on the front cover of the gantry.

**NOTE**

If Auto Positioning detects a possible collision, the motion will not start automatically.

Try again to adjust the patient to clear the collision. If you are unable to do so and want to proceed with the positioning, hold and continuously press the **CT Scan Position** button on the Gantry Control Panel, or the **Load** button on the Remote Control Panel, if installed, to move table to the target position. Motion of the table will stop once target is reached.



DURING TABLE MOTION TO THE START POSITION, MAKE SURE TO KEEP OBSERVING THE PATIENT FOR POTENTIAL COLLISION OF THE PATIENT BODY WITH THE PET-CT GANTRY DUE TO PATIENT MOTION OR DAMAGE TO DEVICES CONNECTED TO THE PATIENT LIKE INTRAVENOUS INJECTORS, ANASTHESIA MACHINES OR ECG GATING DEVICES.

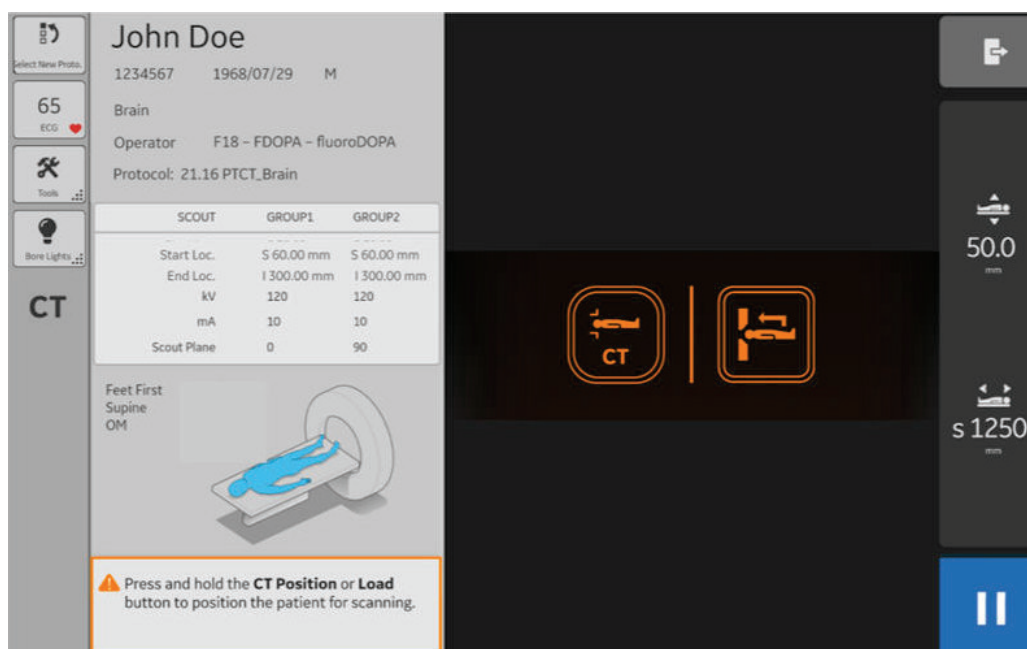


KEEP OBSERVING THE PATIENT DURING AUTO TABLE MOVEMENT USING THE CAMERA MONITORING SYSTEM TO AVOID POTENTIAL COLLISION OF THE PATIENT BODY WITH THE CT GANTRY OR DAMAGES TO DEVICES CONNECTED TO THE PATIENT.

## NOTE

Manual patient positioning is optional also if positioning started with Auto / Remote Auto positioning. To stop Auto positioning and switch to manual positioning, press one of table / cradle motion buttons on the Gantry Control Panel, or on the Remote Control Panel if installed, then press the **Internal/External CT Landmark**. To return to Auto Positioning, Exit the exam and start it from the beginning.

**Figure 184 Confirming Auto / Remote Auto Positioning under possible collision condition**



- Once the table has arrived at the position and stopped, please return to the control room, if not already there. When this happens, the **Start Scan** button on the **Scan Control Interface** will flash.

Scan the Patient

Please continue to complete scout image acquisition according to the procedures Prescribe and Acquire the Scout Series in section 10.9

**NOTE**

The Auto Positioning option is not applicable to 2-meter protocols.

### **10.7.3.2 Auto Table Elevation Configuration (Auto Centering)**

By clicking **Auto Table Elevation Configuration** button in Protocol Management, the user can configure whether they would like to disable auto table elevation during auto positioning.

**Figure 185 Auto Table Elevation Configuration**

If the user selects **OFF** from the **Auto Table Elevation Configuration**, there will be only cradle in/out motion during auto positioning and table will not move up/down.

If set to **ON** (Default selection) from Auto Table Elevation Configuration, the table will move up/down to the target centering position at first to position patient into the isocenter and then cradle moves in/out to target scout scan start position.

In order to get accurate centering for head scans, the user should select **Axial** or **Coronal** from **Head Holder Type**. The user should also configure the head holder pad thickness if using it.



## 10.8 Prescribe and Acquire the Scout Series

A typical PET/CT study begins with a scout series. The scout provides visual confirmation of proper patient position on the table, and the means to graphically prescribe the subsequent CT and PET scan location, scan range(s), and DFOV. Please refer to the CT User Manual and CT Technical Reference Manual shipped with your system for more detailed information.

1. Follow the procedure in [Open the Exam](#) to load the information into the **Patient Information** area, select the protocol and open the scout scan window.

Start the exam with a scout if you plan to use the Graphic Rx Localizer to prescribe the CT and PET scan range, location and display field of view (DFOV).

2. Make sure the scan room is free of all persons except the patient.
3. Make sure the patient orientation on the table matches the patient orientation icon on the scout acquisition window.

Review the remaining scout parameters, and modify if necessary, before proceeding.

### NOTE

The two-meter whole body scout scan range will not fully image the patient. Move the table to 205 mm below isocenter. Make sure the patient's head does not extend beyond the two-meter mark your service representative placed on the table during installation. As you raise the table toward isocenter, the scan range moves away from the gantry and closer to the end of the table. (125 mm = landmark at the end of the table). Monitor the relationship between the internal laser landmark and the tips of the patient's toes, to make sure the toes remain inside the scannable range. The PET/CT system cannot image anatomy extending beyond the two-meter mark.

4. Click **Confirm** to initiate the scan process.

If the **Confirm** button appears gray or fails to respond, make sure you pressed the **Patient Landmark** button on the Gantry Control Panel.

5. Press the flashing **Move to Scan** button to drive the cradle to the start scan position.

If necessary, press **Stop Move** to stop the scan sequence.

6. Press **Start Scan** when it flashes to initiate the X-ray sequence.

- Press **Stop Scan** to stop the scan sequence, or **Pause Scan** to complete the scan in progress, then pause the sequence.
- If you paused the sequence, click **Resume** to continue.

7. If the protocol contains multiple scouts, press the flashing **Move to Scan** and **Start Scan** buttons to acquire the remaining scans.

**NOTE**

Check the Scout image display to make sure you scanned the entire area of interest before proceeding to the next series. If necessary, click **Add Scout** and adjust the Start and End Locations (scan range) to completely encompass the area of interest, then rescan the patient before proceeding to the next section.

## 10.9 Prescribe the CT and PET Series

Follow these instructions to use the Graphic Rx Localizer to prescribe the CT and PET scan range, scan location and DFOV. The system uses the currently prescribed PET and CT scan parameters to display the green PET scan range and blue-gray CT scan range over the scout image.

- Rad Rx OFF: The PET scan range exactly matches the CT scan range, and changing series one automatically updates the other series.
- Rad Rx ON: You can independently change the PET and CT scan ranges, as long as the designated PET scan range fits within the CTAC series.

**NOTE**

Different combinations of CT and PET scans may be prescribed. The following procedure describes a CT/PET scan. PET/CT, PET-only, and Diagnostic CT-only scans may also be prescribed.

1. Follow the procedure on [Prescribe and Acquire the Scout Series](#) to acquire and display the scout image.

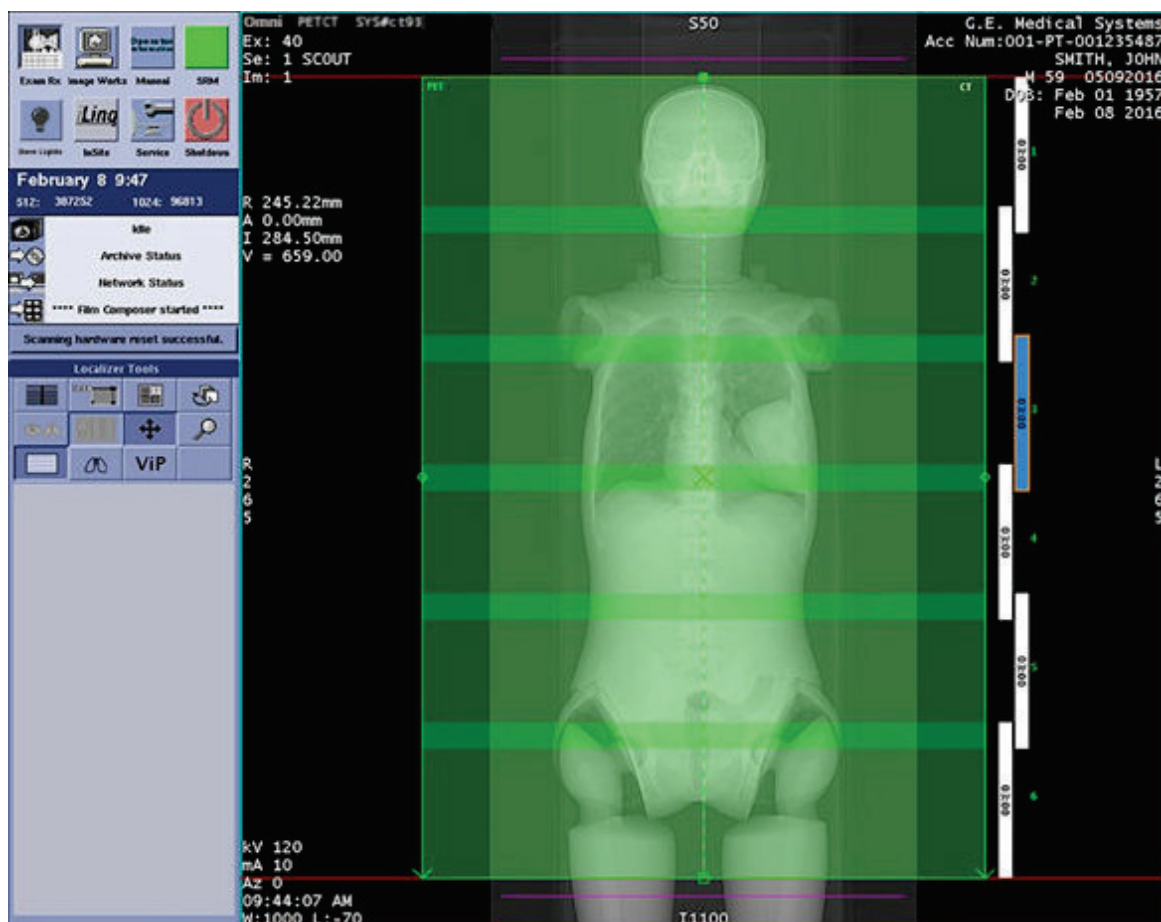
Make sure the scout displays the entire area of interest before proceeding.

2. Click **Next Series** to display the next available series in the protocol, typically the CTAC.
  - Hybrid Protocol: You can click **PET** and **CT** to toggle between the CT series and PET series scan screens.
  - Diagnostic CT Protocol: Please refer to the CT User Manual and CT TRM shipped with your system for additional information and instructions for Smart Score Pro and Prospective Gating Studies, as well as detailed description of all the CT scan parameters.
3. Press **Show Localizer** to display the scout and activate the Graphic Rx Localizer.

**NOTE**

If the Graphic Rx Localizer fails to appear, click **Restart Show Loc.** in the tool bar. If the Localizer still fails to appear, use the mouse and position the cross-hair cursor over the Start and End Locations on the scout image.

**Figure 186 Scout Image with the Graphic Rx Localizer Displayed**



4. Press and hold the **Shift** key while you click and drag the center red X to position the entire scan range over the anatomy of interest.
  - The corresponding parameters on the scan monitor update to reflect the Start Location, End Location.
  - The RAS (Right, Anterior and Superior) coordinates update on the display monitor.
5. Click and drag the solid box to change the Start Location.
6. Click and drag the empty box to change the End Location.
7. Press and hold the **Shift** key while you click and drag either the solid box or the empty box to adjust the Start and End Locations and expand and collapse the scan range.
8. Click and drag a diamond to resize both sides of the Display Field of View (DFOV).  
Press and hold **Shift** while you click and drag a diamond to change the corresponding edge of the DFOV.
9. Change the Graphic Rx Localizer to show or hide the individual image slices. The **Hide/Show Slices** button label always updates to show the alternate setting.

- Click **Hide Slices** to display the scan range as a solid graphic, and change the label to **Show Slices**.
- Click **Show Slices** to display each prescribed slice in the scan range, and change the label to **Hide Slices**.
- Click **Hide PET Overlay** to display the scan range without the green PET overlay, and change label to **Show PET Overlay**.
- Click **Show PET Overlay** to display the scan range with the green PET overlay, and change label to **Hide PET Overlay**.

10. Review the updated parameters on the scan screen before proceeding to scan.

#### NOTE

Do not change the table height or patient landmark once you start the exam. The system displays the notification, **“The table landmark has been changed. This changes the location of all scans you have prescribed. Double check all scan locations before you start scanning,”** when the table landmark changes during the exam.

The system displays the notification, **“The table must be adjusted to original elevation to scan this prescription,”** if you change the table height during the exam.

## 10.10 Acquire the CT Series

Follow these instructions to acquire the Hybrid protocol CT attenuation series. This section assumes you acquired a scout series and used the Graphic Rx Localizer to optimize the series scan range and DFOV. You can acquire the PET series before the CT series, but this section assumes the CT series comes first.

1. Follow the instructions in the previous sections to acquire the scout, then use the Graphic Rx Localizer to adjust the scan range Start Location and End Locations and/or DFOV.
2. Make sure the scan room is free of all persons except the patient.

Prepare the patient for the next phase of scanning.



IF YOU CHANGE THE PATIENT ORIENTATION BETWEEN THE SCOUT AND CT SERIES, THE SYSTEM TURNS AUTOMA OFF, AND REVERTS TO THE MANUAL MA VALUE IN THE PROTOCOL. TO PREVENT EXCESS RADIATION EXPOSURE TO THE PATIENT, ALWAYS CHECK THE MA SETTINGS BEFORE PROCEEDING TO SCAN.

3. Make sure the patient orientation on the table matches the patient orientation icon on the CT acquisition window.

Review the remaining CT parameters, and modify if necessary, before proceeding. Please refer to the CT User Manual and CT TRM shipped with your system for detailed explanations of all the CT scan parameters and CT scan options.

#### NOTE

If the current heat load on the X-ray tube prevents the system from completing the entire scan prescription with the current scan parameters, a red box appears around the **Optimize** button.

Click **Optimize** to display a window that calculates and displays (up to three) suggestions to delay the start of scan, increase the delay between scan groups or change the mA setting to acquire the series without damaging the X-ray tube. If the CT series contains multiple groups, the system displays a separate window for each image group. For best results, delay the start of scan until the tube cools. If you choose to modify the mA, make sure your mA selection provides optimum image quality. Please refer to the CT User Manual and CT TRM shipped with your system for additional information and instructions.

4. Click **Confirm** to initiate the CT scan sequence.
5. If necessary, press **Move to Scan** when it flashes.
6. Press **Start Scan** when it flashes to initiate the scan sequence.
  - Upon completion of the prescribed CT series, you can add an additional group to the current series, or add a new CT series to the prescription.
  - The system follows the protocol (or prescribed parameters) to reconstruct, transfer, film and/or display the resulting images.
7. Click **PET** to proceed to the PET series acquisition window.

If the table height or landmark changes after you acquire either the CT or PET series, the system displays a notification message that requires a user response.

## 10.11 Acquire the PET Series

Follow this procedure to acquire the PET series. This section assumes you followed the instructions in the previous section to acquire the CTAC series. You have the option to acquire the PET series before or after the CT series.

The system warns you if you acquire the PET series first, then click **End Exam** before you acquire the CTAC series.

1. If necessary, click **PET** to display the **(Hybrid) PET Acquisition** window.

Prepare the patient for the PET phase of the scan prescription.

2. Make sure the patient orientation on the table matches the patient orientation icon on the **(Hybrid) PET Acquisition** window.

Review the remaining PET parameters, and modify if necessary, before proceeding. Please refer to [Build a Protocol](#) for detailed explanations of the PET parameter selections.

**NOTE**

Changing patient positions between PET and CT acquisitions is not recommended, and may cause attenuation artifacts and incorrect registration of images.

**NOTE**

Click the **Radiation** tab and review the quantification information, isotope and radiopharmaceutical selections before proceeding to scan. This is your last chance to select **Inherit from Exam** before starting the scan.

**NOTE**

Yellow data fields in the **Dose** tab are required to be filled in prior to confirming the PET scan. Required fields can be configured. Refer to [Edit Patient and Tracer Information](#). If the PET scan is confirmed prior to entering these fields, an attention message will prompt the user to fill in the required fields.

**NOTE**

**Copy PMR** allows the scan range, DFOV and isocenter for Recon 2 and Recon 3 to be locked with the same values as Recon 1. These fields are displayed with a green border around the value field. To release the lock and set to different values, click in the field and type a new value. You may use Graphic Rx afterward to adjust the value.

3. Click **Confirm** to initiate the PET scan sequence.
4. If necessary, press **Move to Scan** when it flashes.
5. Press **Start Scan** when it flashes to either start the PET scan or initiate the sequence to start the PET scan when the Pre-set Delay or Count Rate reaches the prescribed levels.
  - Upon completion of the prescribed PET series, you have the option to add an additional PET scan to the current series, or add a new CT series to the prescription.
  - The system follows the protocol (or prescribed parameters) to reconstruct, transfer, film and/or display the resulting images.
6. Review the patient images before you drive the table to the home position and escort the patient from the scan room.

## 10.12 End the Exam

1. Click **End Exam** to close the current study.
2. For systems with the Performed Procedure Step (PPS) option:
  - Click **Complete** to tell the HIS/RIS that you completed the exam, or click **Discontinue** to stop the exam without finishing it, and plan to rescan and reuse the information on the Patient Schedule.
  - Click **Defer** to delay the decision until you enter Image Works browser and click **PPS** in the tool bar. Click **Complete** or **Discontinue**.

3. If the Patient Auto Retract feature is enabled, the **Move to Scan/Retract** button will light up. This feature can be enabled/disabled; reference [System Introduction](#) for instructions.

Press and hold the **Move to Scan/Retract** button to drive the cradle and table to the home position. While holding the **Move to Scan/Retract** button, the table will move out of the bore and automatically begin to lower. Once the table reaches approximately 284 mm below isocenter, the table will stop movement. To continue lowering the table to its lowest position, release the **Move to Scan/Retract** button, then press and hold again. The table will lower to its minimal height. While retracting the patient, monitor for potential interference between the table, gantry and equipment or patient garments, IV lines, etc.

Removing pressure from the **Move to Scan/Retract** button will stop the cradle and table motion.

#### NOTE

If the 2-meter table top is attached, do not try to move the table lower than the first stopping point, approximately 284 mm below isocenter.

4. Press **Home** on the Gantry Control Panel to drive the cradle and table to the patient load position. Help patients off the table and escort them from the room.

## 10.13 Two meter scan and RadRx

### 10.13.1 Position the Patient for a Two-Meter Whole Body Scan

Two-meter whole-body scans require the use of the Two-Meter Table Top accessory. ALL two-meter whole body scans must be acquired with the patient in the feet first orientation. Never acquire a head first study with the Two-Meter Table Top accessory in place.

Prepare the scan room before you escort the patient into the room.

1. Follow the instructions in the [Prepare Two-Meter Table Top \(Optional\)](#) section, to fasten the Two-Meter Table Top accessory to the cleat on the cradle.

#### IMPORTANT

To prevent damage to the Two-Meter Table Top Accessory and the gantry front cover, do not lower the table past 284 mm below isocenter with the accessory in place. Follow facility guidelines to transfer non ambulatory patients to the table.

2. Help the patient onto the table.
  - Position the patient feet first with the heels aligned to the edge of the padded area of the Two-Meter Table Top accessory, to ensure optimal whole body scan coverage.

#### NOTE

Feet first enables covering whole body scan range without losing space due to head holder.

**NOTE**

Feet first is required to position the body center of mass closer to the table base, for safety.

- Check the body straps for a secure connection to the table before fastening them.



THE PATIENT POSITIONING STRAPS SHOULD BE USED TO RESTRAIN THE PATIENT TO THE CRADLE AND LIMIT THE PATIENT MOVEMENT DURING SCAN.



THE PATIENT POSITIONING STRAPS WILL NOT SUPPORT THE FULL WEIGHT OF THE PATIENT AND SHOULD NEVER BE USED TO RESTRAIN A COMBATIVE PATIENT.

3. Use the control buttons on the gantry to raise the table and drive the patient into the bore of the CT gantry.

Check for potential interference between the table, gantry and monitoring equipment or patient garments, IV lines, etc.



TO PREVENT EYE DAMAGE, ALWAYS WARN PATIENT TO CLOSE THEIR EYES BEFORE YOU TURN ON THE ALIGNMENT LASERS. TELL THEM TO KEEP THEIR EYES CLOSED UNTIL YOU FINISH THE ALIGNMENT PROCESS, TURN OFF THE LASERS AND TELL THEM THEY CAN OPEN THEIR EYES.

4. Press the **Alignment Light** button to turn on the lasers.

**NOTE**

During a two-meter whole-body scan, you set internal landmark just past the soles of the patient's feet, resulting in a complete, head-to-toe scan of the patient.

5. Adjust the table height to align the patient to isocenter.

The patient isocenter must fall between 125 mm and 205 mm on the Gantry Display.

6. Use the center table motion buttons to drive the cradle out of the CT Gantry.

Do not use the **Home** button to drive the cradle out of the gantry bore.

7. Retract the cradle to the home position, with the table at the CT position.

- If the table height equals 205 mm, the laser light will fall approximately 50 mm beyond the accessory.



- If the table height equals 125 mm, the laser light will fall at the edge of the accessory.
8. Select **PTCT\_2m\_WB** or **PTCT\_2m\_WB\_ULDAC** protocols for 2 meter scan.
  9. Set **Internal** Landmark.
  10. Press the **Alignment Light** button to toggle the lasers off.

#### NOTE

The Auto Positioning option is not applicable to 2-meter protocols.

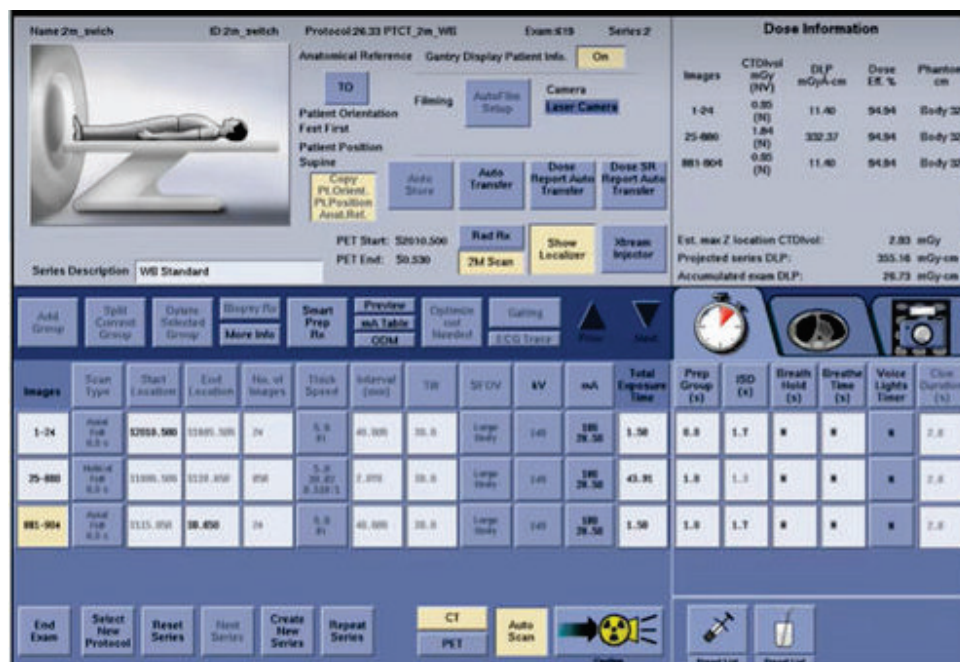
11. Follow the procedure in Open the Exam to load the information into the Patient Information area, and open the scout scan window.

Review the remaining scout parameters, and modify, if necessary, before proceeding. If the protocol contains multiple scouts, press the flashing **Move to Scan** and **Start Scan** buttons to acquire the remaining scans.

#### NOTE

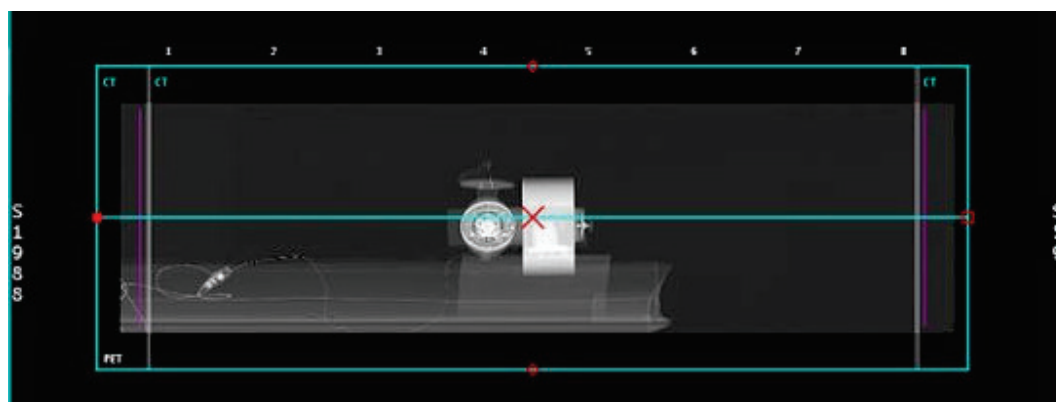
The two-meter whole body scout scan range will not fully image the patient. Make sure the patient's head does not extend beyond the two-meter mark your service representative placed on the table during installation. As you raise the table toward isocenter, the scan range moves away from the gantry and closer to the end of the table. (125 mm = landmark at the end of the table). Monitor the relationship between the internal laser landmark and the tips of the patient's toes, to make sure the toes remain inside the scannable range. The PET/CT system cannot image anatomy extending beyond the two-meter mark.

12. Click **Next Series** to display the next available series in the protocol, typically the CTAC. 13. 14.  
In Hybrid Protocol: You can click **PET** and **CT** to toggle between the CT series and PET series scan screens.
13. Make sure the **2m Scan** button is on and press **Show Localizer** to display the scout and activate the Graphic Rx Localizer.
14. CT scan – the two meter protocol is composed of three different CT scans: Axial, Helical and Axial. In 2M scan, the CT scans are linked together and are connected to the PET scan.  
Use the Graphic Rx Localizer to prescribe the CT and PET scan range, scan location and DFOV. The system uses the currently prescribed PET and CT scan parameters to display the green PET scan range and blue-gray CT scan range over the scout image.
  - Rad Rx OFF: The PET scan range exactly matches the CT scan range, and changing series one automatically updates the other series.
  - Rad Rx ON: You can independently change the PET and CT scan ranges, as long as the designated PET scan range fits within the CTAC series.



For 2M scan, RadRx is off and only the start and end range of the entire CT scan can be changed. Once the range has been changed, the number of the different CT scans might be changed as well.

**Figure 187 Graphic Rx for RadRx – off scan. The three CT scans are connected to each other and to the PET scan.**

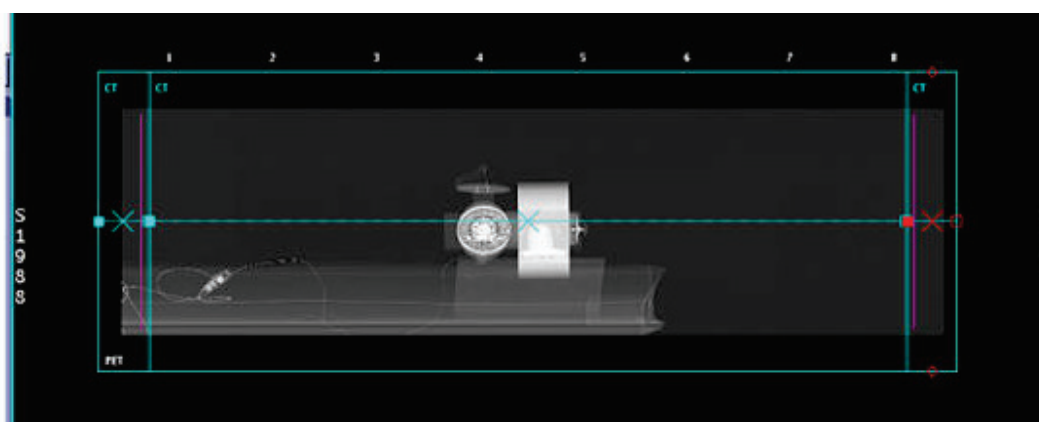


15. Press and hold the **Shift** key while you click and drag the center red X to position the entire scan range over the anatomy of interest.
  - The corresponding parameters on the scan monitor update to reflect the Start Location, End Location.
  - The RAS (Right, Anterior and Superior) coordinates update on the display monitor.
16. Click and drag the Red box to change the Start Location.
17. Click and drag the empty box to change the End Location.

18. Press and hold the **Shift** key while you click and drag either the solid box or the empty box to adjust the Start and End Locations and expand and collapse the scan range.
19. Click and drag a diamond to resize both sides of the Display Field of View (DFOV). Press and hold **Shift** while you click and drag a diamond to change the corresponding edge of the DFOV.
20. Change the Graphic Rx Localizer to show or hide the individual image slices. The **Hide/Show Slices** button label always updates to show the alternate setting.
21. Review the updated parameters on the scan screen before proceeding to scan.

If RadRx is ON, the range of each CT scan type can be changed separately by dragging the red dot on the CT borders. Make sure the PET scan range fits inside the prescribed CT scan range if you plan to use this series to attenuate the PET series images.

**Figure 188 Graphic RX with RadRx on**



Do not change the table height or patient landmark once you start the exam. The system displays the notification, **The table landmark has been changed. This changes the location of all scans you have prescribed. Double check all scan locations before you start scanning,** when the table landmark changes during the exam.

The system displays the notification, **The table must be adjusted to original elevation to scan this prescription,** if you change the table height during the exam.

22. Click Confirm to initiate the CT scan sequence.
23. If necessary, press **Move to Scan** when it flashes.
24. Press **Start Scan** when it flashes to initiate the scan sequence.
25. Click **PET** to proceed to the PET series acquisition window.
26. Click **Confirm** to initiate the PET scan sequence.
27. Press **Move to Scan** when it flashes.
28. Press **Start Scan** when it flashes to either start the PET scan or initiate the sequence to start the PET scan when the Pre-set Delay or Count Rate reaches the prescribed levels.

29. Review the patient images before you drive the table to the home position and escort the patient from the scan room.

## 10.14 Scan the Patient Quick Steps

### 10.14.1 Open the Exam

1. Click the **New Patient** icon in the scan monitor tool bar.
2. Click the **Patient Schedule** icon.
3. Click/highlight the patient information.
4. Click **Select Patient** to load the corresponding information into the **Patient Information** area of the **New Patient** window.
5. If necessary, add information or modify existing information.
6. Click **Enter PET Tracer Info**, fill the corresponding data fields with the available information, then click **Accept**.
7. Verify all the information on the **New Patient** window.
8. Select a patient protocol to proceed directly to the first scan window.

### 10.14.2 Position the Patient

1. Attach the head holder or foot extender to the cradle, if applicable.
2. Help the patient onto the table and ensure she is centered and comfortable.
3. Raise the table and drive the cradle into position with the gantry buttons.
4. If manual or with Auto-In positioning is used:
  - a. Tell the patient to close his/her eyes during alignment process.
  - b. Press the alignment light button to turn ON the lasers.
  - c. Adjust the table and cradle to isocenter and align the area of interest to the laser lights.
  - d. Press the alignment light button to turn OFF the lasers.
  - e. Press the internal or external landmark button to landmark the region of interest beneath the corresponding internal or external laser, and enable the **Confirm** button on the first acquisition window.
5. If Auto Positioning feature is used
  - a. View the patient video on the gantry display to ensure there is no obstruction from people or objects.
  - b. Observe whether the **Scout Range Indicator** displayed on the video is appropriate. Modify if necessary.

- c. If the message area on the gantry touch display instructs to confirm and move table, press the blue button to confirm, otherwise follow instructions in message area to fine tune positioning.
- d. Pay attention to patient during table movement. Use **Pause** or **Emergency Stop** buttons during emergency.
- e. Once the table has arrived at the position and stopped, push the **Start Scan** on the **Scan Control Interface** in the scan room to start the scout scan.
- f. Continue according to instructions in [Prescribe and Acquire the Scout Series](#) section.

### 10.14.3 Prescribe and Acquire the Scout Series

1. Follow the Quick Steps to Open the Exam, if not already open.
2. Make sure the scan room is free of all persons except the patient.
3. Make sure the patient orientation on the table matches the patient orientation icon on the scout acquisition window.
4. Review the remaining scout parameters, and modify if necessary.
5. Click **Confirm** to initiate the scan process.
6. Press the flashing **Move to Scan** button.
7. Press **Start Scan** when it flashes to initiate the X-ray sequence.
8. If the protocol contains multiple scouts, press the flashing **Move to Scan** and **Start Scan** buttons to acquire the remaining scans.
9. Check the scout image display to make sure you scanned the entire area of interest before proceeding to the next series.

### 10.14.4 Use the Scout (Graphic Rx Localizer) to Prescribe the CT and PET Series

1. Follow the Quick Steps to acquire a scout series that captures the entire area of interest.
2. Click **Next Series** to display the CTAC acquisition window.
3. If necessary, click **Show Localizer** to display the Graphic Rx Localizer.
4. Press and hold the **Shift** key while you click and drag the center red **X** to position the entire scan range over the anatomy of interest.  
or  
Click and drag the solid box to change the Start Location.  
or  
Click and drag the empty box to change the End Location.  
or

Press and hold **Shift** while you click and drag either the solid box or the empty box to adjust the Start and End Locations at the same time.

5. Click and drag a diamond to resize both sides of the Display Field of View (DFOV).  
or  
Press and hold **Shift** while you click and drag a diamond to change the corresponding edge of the DFOV.
6. Click the **Show/Hide Slices** button to toggle the Graphic Rx Localizer to show or hide the individual image slices.
7. Click the **Show/Hide PET Overlay** button to show or hide the green PET overlay on the Graphic Rx Localizer.
8. If Rad Rx ON: Make sure the PET scan range fits inside the prescribed CT scan range if you plan to use this series to attenuate the PET series images.
9. Review the updated scan parameters before proceeding to scan.

### 10.14.5 Acquire the CT Series

1. Follow the Quick Steps to acquire the scout.
2. Follow the Quick Steps to use the Graphic Rx Localizer to adjust the scan range Start location and End location and/or DFOV.
3. Make sure the scan room is free of all persons except the patient.
4. Make sure the patient orientation on the table matches the patient orientation icon on the CT acquisition window.
5. Review the remaining CT parameters, and modify if necessary.
6. If prompted, follow the instructions to **Optimize** the parameters.
7. Click **Confirm** to initiate the CT scan sequence.
8. If necessary, press **Move to Scan** when it flashes.
9. Press **Start Scan** when it flashes to initiate the scan sequence.

### 10.14.6 Acquire the PET Series and End the Exam

1. If necessary, click **PET** to display the **(Hybrid) PET Acquisition** window.
2. Make sure the patient orientation on the table matches the patient orientation icon on the PET acquisition window.
3. Review the remaining PET parameters, and modify if necessary.
4. Click **Confirm** to initiate the PET scan sequence.
5. If necessary, press **Move to Scan** when it flashes.
6. Press **Start Scan** when it flashes to either start the PET scan or initiate the sequence to start the PET scan when the count rate reaches the prescribed levels.
7. Click **End Exam** to close the current study.

#### Scan the Patient

8. The system warns you if you acquire the PET series first, then try to click **End Exam** before you acquire the CTAC series. Click **CT** to display the CT acquisition window, then follow the Quick Steps to acquire the CT series, then click **End Exam**.

# 11 Edit Patient, Tracer and Nuclide Information

## 11.1 Edit Patient,Edit Tracer and Edit Nuclide Information Introduction

This chapter describes how to access and modify selected patient information after completion of the corresponding exam. The chapter also contains the procedure to access and modify PET tracer and Nuclide information for selected series within an exam.

### NOTE

Edit Patient and Edit Tracer should not be used during an active exam, acquisition or during PET Recon/Replay. This can cause damage to the data and leave it in an unusable state.

### NOTE

If you plan to edit the patient data, edit the tracer or anonymize the patient, wait until all PET Cardiac ACQC reconstructions finish! If you change the patient or tracer information first, PET Cardiac ACQC will not work.

### NOTE

If you plan to edit the patient radionuclide, all PET images sharing the same UID will be labeled as invalid. A retrospective reconstruction is necessary to generate images with the nuclide change applied.

### NOTE

When Edit Patient or Anonymize tools have been used to modify the exam, the link to the CT used as the attenuation map for a PET raw series is no longer available. This is a concern for retro-reconstruction of a PET raw series or VIP Replay with prospective reconstruction of a PET raw or PET list series. Select the appropriate CT for use as the attenuation map for the PET reconstruction. To do this, select the **PET Reconstruction** tab and click the **Recon Options** button to open a window that contains all the reconstruction options available. Under the CTAC Series, select the CT series to be used for this reconstruction.

## 11.2 Edit Patient,Edit Tracer and Edit Nuclide Information

You can edit only the Patient and Tracer information on exams that were acquired on this PET/CT. You cannot edit non-anonymized exams that you imported onto your system. You cannot edit CT contrast.



You may edit the same exam multiple times. You cannot edit an active exam. An active exam means one or more of the following functions are using the information you plan to edit:

- New Patient (Click **End Exam** to release the information.)
- Network Send
- Archive Save
- 3D Rendering (If you edit an exam with a saved 3D model, the system deletes the model when you save the newly edited exam.)
- Reformat
- Denta Scan
- Navigator
- Viewer or Mini Viewer active
- Autofilm or free viewport in the Exam Rx desktop
- ViP Replays
- All reconstructions in the queue

If you try to edit an active exam, the system displays a warning message. You have the option to end the active process, or check the queues, and wait until the active process completes.

## 11.3 Introduction to Edit Tracer and Nuclide Information

Once you click **End Exam**, you still can change or modify tracer and nuclide information you entered for each PET scan at the time of the exam. The Edit Tracer function automatically updates all scans in the study that share the same tracer information. The status of the **Inherit from Exam** button at the time of each PET scan determines whether all scans receive the updated information during an Edit Tracer session.

- Scans acquired with **Inherit from Exam** enabled: Edit Tracer sees all such scans as sharing the same tracer information, and changes the information for all these scans (refer to [Figure 189 on page 343](#)).
- Scans acquired with **Inherit from Exam** disabled: Edit Tracer sees these scans as having unique tracer information, and changes the information for data from this scan only.
- If only Tracer information is changed, all data originating from a common scan automatically receives the updated tracer information, with the exception of reformatted PET images, as well as images generated from Precision DL. (refer to [11.5 Edit the Tracer and Nuclide Information on page 348](#)).

### NOTE

After tracer information is changed, Precision DL images are marked as invalid. Manually perform retrospective reconstruction to regenerate accurate Precision DL images with tracer information changes applied. Refer to [Precision DL – Edit Patient, Tracer, and Nuclide information](#).

- Follow instructions in [11.5 Edit the Tracer and Nuclide Information on page 348](#) for nuclide change.

**Figure 189 PET Tracer Information with Inherit from Exam (Acquisition mode)**

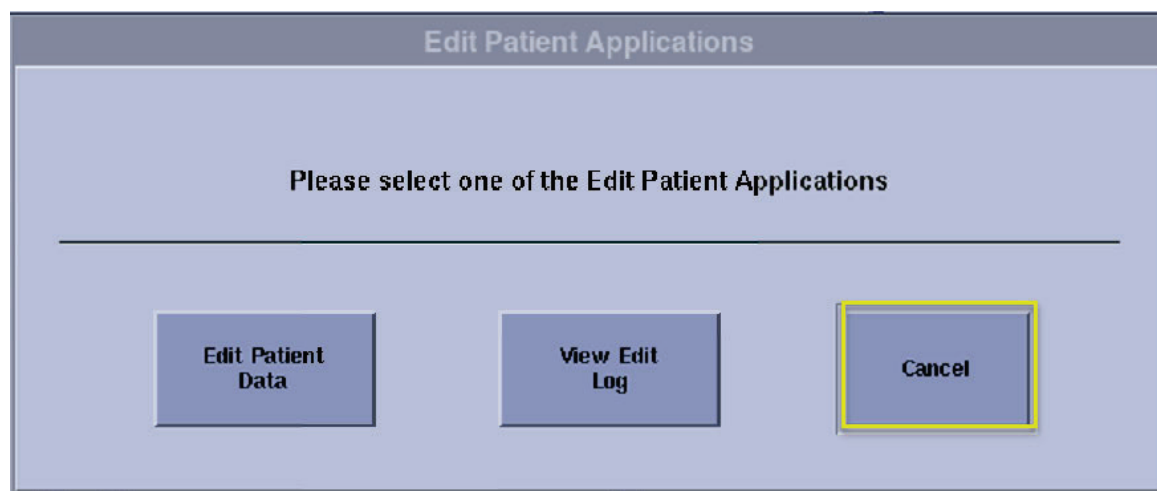
PET Quantification Information					
			<input type="button" value="Inherit from Exam"/>		<input type="button" value="mg/dL"/> <input type="button" value="mCi"/>
— PET Tracer Information					
Batch Description	<input type="text"/>				
Tracer Volume (mL)	<input type="text"/>				
Pre-Injection Assay					
Tracer Activity	<input type="text" value="0.0000"/>	MBq	<input type="text" value="21/1/2021"/>	Date	<input type="text" value="22:03:44"/>
				Time	
Injection Time					
			<input type="text" value="21/1/2021"/>	Date	<input type="text" value="22:03:44"/>
				Time	
Post-Injection Assay					
Tracer Activity	<input type="text" value="0.0000"/>	MBq	<input type="text" value="21/1/2021"/>	Date	<input type="text" value="22:03:44"/>
				Time	
— PET Patient Information					
Blood Glucose Level	<input type="text" value="0.0000"/>	mmol/L	Diabetic	<input type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown	
Last Treatment	<input type="text"/>	Date			
<input type="button" value="OK"/>		<input type="button" value="Cancel"/>			

## 11.4 Edit Patient Information

Follow the instructions in this section to edit patient information after the exam ends, all the exam information has finished reconstruction and none of the system functions is actively using the data.

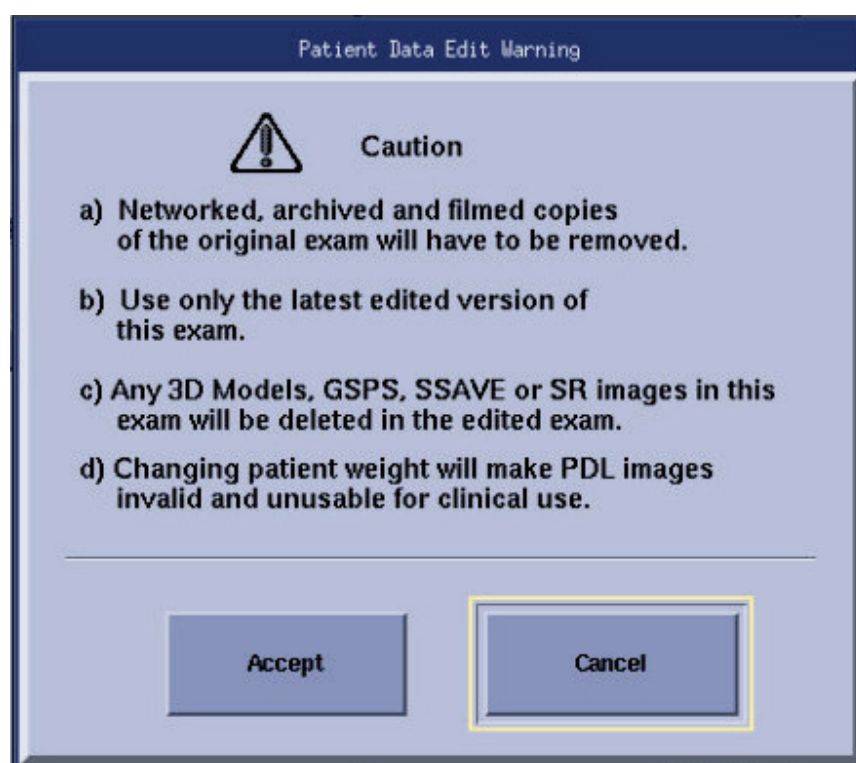
- Click **Image Works** on the display monitor to open the browser.
- Click the exam information in the browser to select it.
- Click **Edit Patient** on the right side of the browser to open the Edit Patient Applications selector window.

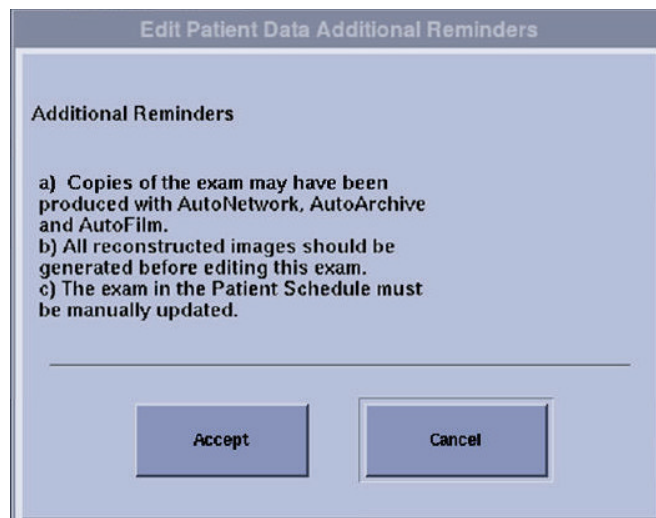
**Figure 190 Edit Patient Application Selector**



4. Click **Edit Patient Data** to open the first of two warning alerts.

**Figure 191 Patient Data Edit Warning**



**Figure 192 Edit Patient Data Additional Reminders**

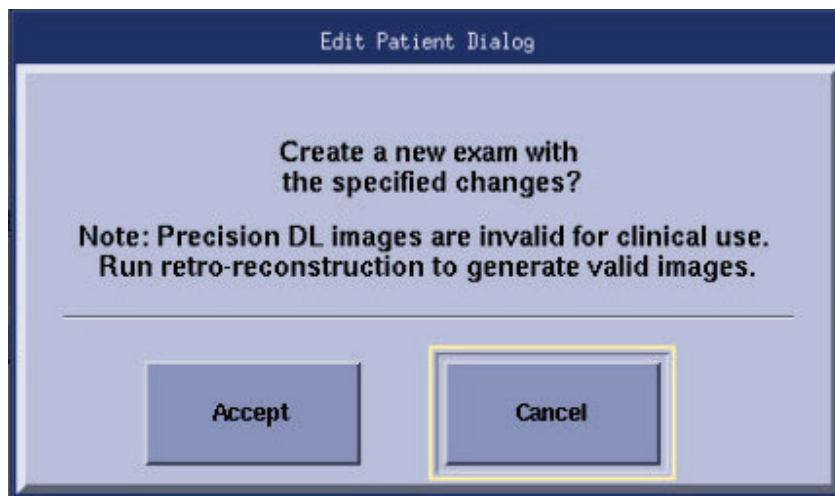
5. Read the warning messages.
  - If necessary, **Cancel** out of the function, resolve any issues, then return to try again.
  - Click **Accept** to open the patient information window with the currently entered information displayed in the corresponding data fields.
6. You must enter at least three characters into the **Edited By** data field to continue. Modify the parameter or fill in the blank data fields as needed.
  - If you change a field, and decide to change it back to its original value, move the cursor into the data field to activate it, then click **Reset Selected Value**.
  - If you edit multiple fields, and decide to change them all back to the original data, click **Reset All Original Values**.
  - Click **Cancel** to discard any changes, and exit the Edit Patient function with the original Patient Information intact.

**Figure 193 Edit Patient Data Window**

The screenshot shows the 'Edit Patient Data' window with the following fields and values:

- Patient Information**
  - Exam Number: 216
  - Accession Number: (empty)
  - Patient ID: OMNI-002
  - Patient Name: S-M
  - Sex: F
  - Birthdate: (empty)
  - Weight: 189.1 Pounds, 86.0 Kilograms
  - Height: 5 Feet, 3 Inch, 160 Centimeters
  - Age: 23 Years, (empty) Months, (empty) Weeks, (empty) Days
  - Referring Physician: (empty)
  - Radiologist: (empty)
  - Operator: (empty)
  - History: (empty)
  - Exam Description: PET
  - Edited by: (empty)
- Buttons**
  - Reset Selected Value
  - Reset All Values
  - Accept
  - Cancel

7. Click **Accept** to retain all the currently displayed data, and open the **Edit Patient Dialog** window.

**Figure 194 Edit Patient Dialog Window**

8. If necessary, click **Cancel** to return to the **Edit Patient Data** window. Click **Accept** to remove the current exam and replace it with the edited exam.

The system displays a percentage countdown as it removes the old exam and replaces it with the edited exam. It displays the message “Closing Application” countdown as it closes out the Edit Patient function and updates the Patient Information Edit Log.

**NOTE**

Upon completion of the exam update, the system displays the newly edited exam on the browser, with an **e+** indicator, followed by the editing iteration. If this is the first time you edited this patient’s information, the system displays **e+1** with the exam description. The browser shifts the exam description to the right to make room for the additional editing information.

To view the history of patient data edits, click **Edit Patient**, then click **View Edit Log**.

**NOTE**

Any time an edit is made to patient data, double check the accuracy of the edit result.

**NOTE**

Precision DL pre-processing requires SUVbw conversion which leverages Patient Weight. Prospective patient weight changes using **Edit Patient** will result in the Precision DL images being marked as invalid. Manually perform retrospective reconstruction to regenerate Precision DL images after any patient weight change.

Changes of Patient Weight through reading and post processing stations (even if save state or screen captures are used) will not reflect the changes correctly and may affect image quantitation. Users are advised to fix the information on the console and re-generate the Precision DL images using retrospective reconstruction.

## 11.5 Edit the Tracer and Nuclide Information

Follow the instructions in this section to update the tracer and nuclide information after the exam ends. Upon completion of the exam, you can select Image Works **Edit Tracer** to open the **Update Tracer Activity** window which lists all the series that will change when you modify the data for the select PET images or PET series.

### NOTE

The state of the **Inherit from Exam** button during acquisition determines the Edit Tracer workflow once the exam ends.

1. Click **Image Works** on the display monitor to open the browser.
2. Click the exam information in the browser to select it.  
Select one PET series.
3. Click **Edit Tracer** to open an intermediate window that lists the series that will change when you update the tracer data.
  - If you pick a series containing PET RAW, LIST, or IMAGES, the software looks for PET RAW, LIST, and IMAGE series created from the same scan as the selected series.
  - The software also updates series from other scans in the study that share the same nuclide/tracer information (referred to as Tracer Injection IUD); the software will update all PET scan series in the study for which **Inherit from Exam** was enabled at the time of acquisition, including PET RAW, LIST, and IMAGES from each of those scans.
  - Edit Tracer will not update "Save State" files created during post-processing.

**Figure 195 Update Tracer Message**

4. Click **OK** to close the message window and open an **Update Tracer Activity** window.



**Figure 196 Example of an Update Tracer Activity**

Update Tracer Activity		
PreInjection	<input type="text" value="1"/>	(dd/mm/yyyy)
<input type="text" value="0"/> MBq	<input type="text"/>	(hh:mm:ss)
Administration	<input type="text"/>	(dd/mm/yyyy)
(date/time only)	<input type="text"/>	(hh:mm:ss)
PostInjection	<input type="text"/>	(dd/mm/yyyy)
<input type="text" value="0"/> MBq	<input type="text"/>	(hh:mm:ss)
Batch Description	<input type="text"/>	
Volume	<input type="text" value="0"/> ml	
Nuclide/Tracer	<div> <div> 18F 13N 11C 15O </div> <div> FDG – fluorodeoxyglucose FDOPA – fluoroDOPA F – Fluorine [18F]Fluciclatide </div> </div>	
Patient Name	<input type="text" value="TimoTom2"/>	
Exam Number	<input type="text" value="36"/>	
Series Number	<input type="text" value="901"/>	
Blood Glucose Level	<input type="text" value="0"/> mmol/L	
Patient Diabetic	<input checked="" type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown	
Last Treatment Date	<input type="text"/>	(dd/mm/yyyy)
<input type="button" value="Apply"/> <input type="button" value="Recall"/> <input type="button" value="Close"/>		

5. The **Update Tracer Activity** window displays the currently selected **Patient Name** and **Exam Number**, as well as the **Series Number** area that lists all the series the system will update with the new nuclide/tracer information.
  - If you do not see a series on the list, you must access and update that series separately.
  - If you make a change to existing nuclide/tracer information, or fill in a blank data field, the information changes for every PET RAW, IMAGE or LIST series on the **Series Number** list.
6. You can change the tracer (radiopharmaceutical) and/or the nuclide set at the time of acquisition with Edit Tracer.

**NOTE**

If you chose two different tracers (by mistake) but selected the same nuclide or vice versa, within the series, the system treats the PET scans as two separate groups, regardless of the state of the **Inherit from Exam** button.

7. Optional: Click **Recall** to reload the existing tracer/nuclide information into the data fields. Click **Close** to discard any changes and close the window without any updates.
8. Modify the parameters or fill in the blank data fields, as needed, then click **Apply** to update the tracer/nuclide information on all the series on the **Series Number** list. Then click **Close** to exit the tool.
  - The software creates a newer series that contains your changes, then deletes the original series.
  - The new series description contains the **e+** and an index of the number of times the tracer information has been edited.

**NOTE**

If you edit the nuclide information, all reconstructed images generated with the original nuclide will be marked as invalid. Manually perform retrospective reconstruction or replay to regenerate the images with the new updates (refer to [11.8 Edit Patient and Edit Tracer Information Quick Steps on page 359](#)).

**NOTE**

If you want to edit the tracer information of PET scans that did NOT appear on the **Series Number** list, remember to select and edit that information separately.

**NOTE**

When using Edit Tracer, a pop-up will inform you that the following series are being edited with the new tracer information. The maximum number of series displayed in the pop-up is 10. When there are more than 10 series, including the PET list (951+), PET raw (901+), and PET images, only 10 of the total number will be listed.

**NOTE**

If you plan to edit patient data, edit the tracer or anonymize the patient, wait until all PET Cardiac ACQC reconstructions finish! If you change the patient or tracer information first, PET Cardiac ACQC will not work.

**NOTE**

Any time an edit is made to tracer information, double check the accuracy of the edit result.

## 11.6 Nuclide-Tracer Manager

Nuclide-Tracer Manager is an advanced utility that provides advanced users with the following abilities:

- Define, modify and delete user-defined nuclides
- Define, modify and delete user-defined tracers to both pre-defined and user-defined nuclides

Nuclide-Tracer Manager is accessed through the PET Service Desktop Utilities menu.

1. Click the **Service** button.
2. On the PET/CT Service Desktop, select the **PET** radio button in the upper left corner of the window.
3. Click on the **Utilities** tab.

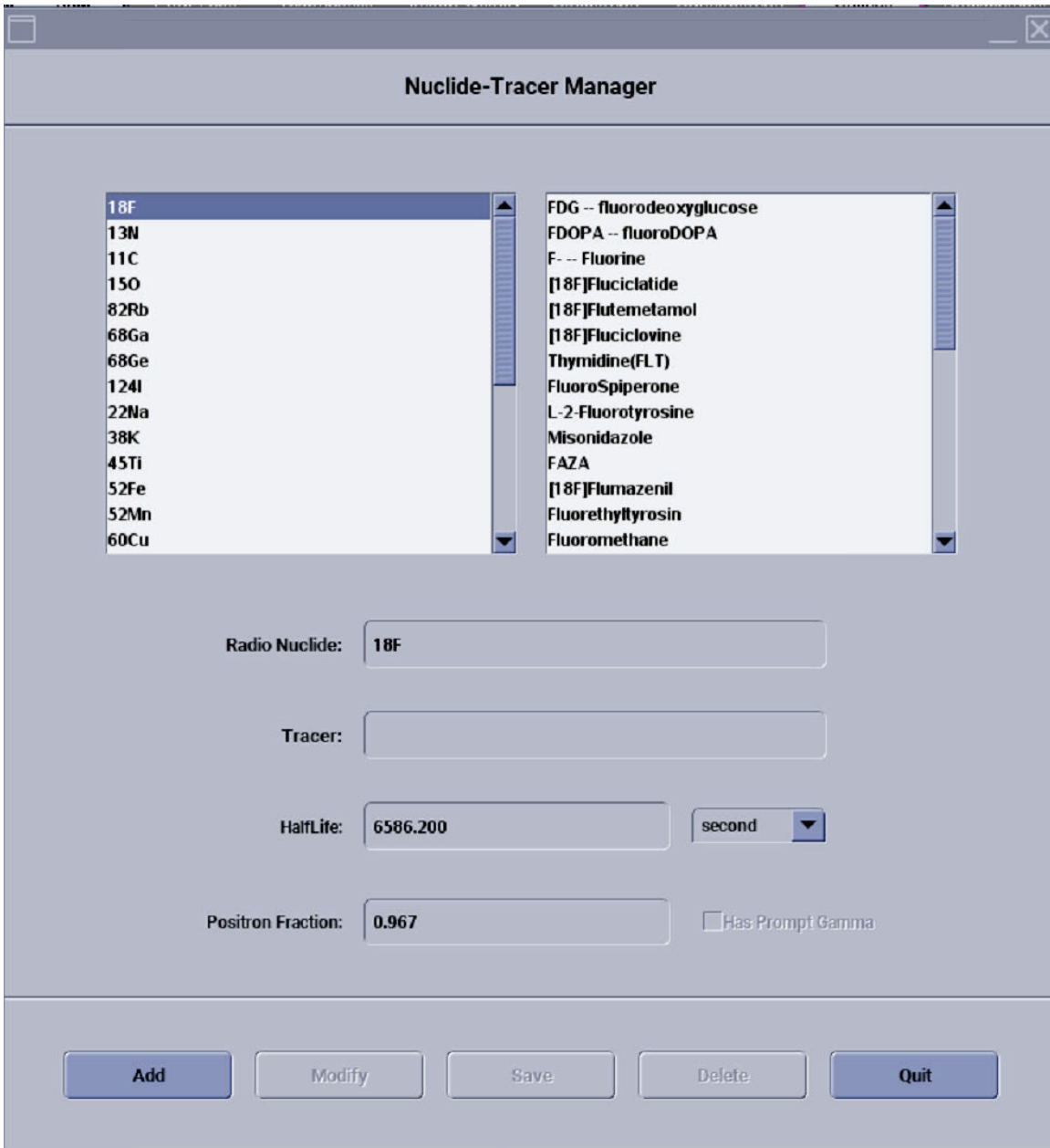
Figure 197 PET Service Desktop Utilities Menu



**NOTE**

Service Desktop menus are not translated.

4. Select the **User Tracer Input** link and the **Nuclide-Tracer Manager** window will display.

**Figure 198 Nuclide-Tracer Manager Window**

The Nuclide-Tracer Manager window is a software interface for managing nuclear medicine data. It features two list boxes at the top: the left one contains a list of radioisotopes (18F, 13N, 11C, 15O, 82Rb, 68Ga, 68Ge, 124I, 22Na, 38K, 45Ti, 52Fe, 52Mn, 60Cu), and the right one contains a list of tracers (FDG -- fluorodeoxyglucose, FDOPA -- fluoroDOPA, F- -- Fluorine, [18F]Fluciclatide, [18F]Flutemetamol, [18F]Fluciclovine, Thymidine(FLT), FluoroSiperone, L-2-Fluorotyrosine, Misonidazole, FAZA, [18F]Flumazenil, Fluorethyltyrosin, Fluoromethane). Below these lists are input fields for 'Radio Nuclide' (set to 18F), 'Tracer' (empty), 'HalfLife' (6586.200) with a unit dropdown (set to second), and 'Positron Fraction' (0.967) with a 'Has Prompt Gamma' checkbox. At the bottom are five buttons: Add, Modify, Save, Delete, and Quit.

Radio Nuclide	Tracer	HalfLife	Unit	Positron Fraction	Has Prompt Gamma
18F		6586.200	second	0.967	<input type="checkbox"/>

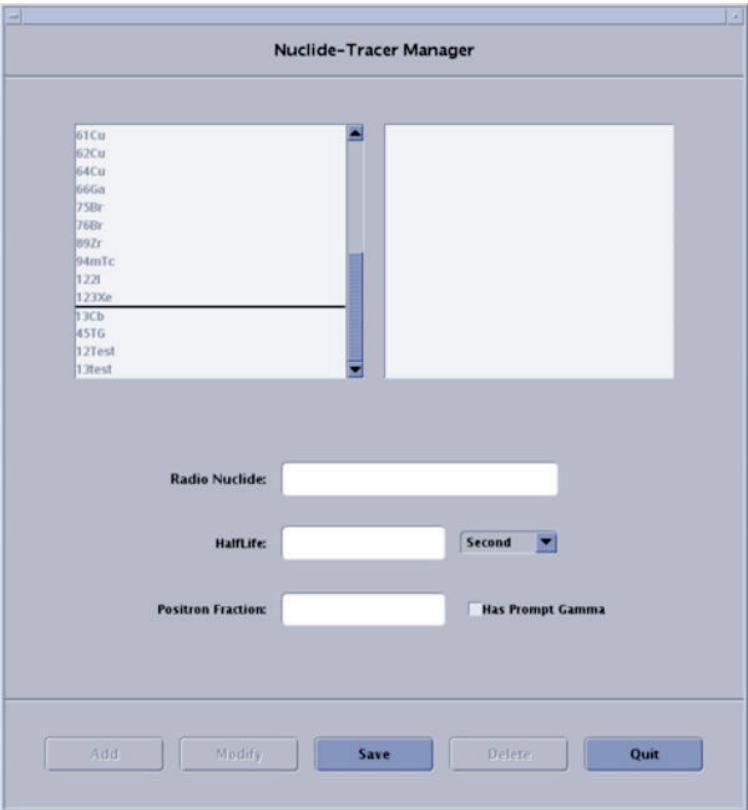
**Add** **Modify** **Save** **Delete** **Quit**

5. Click **Add** to add a user-defined nuclide or tracer.

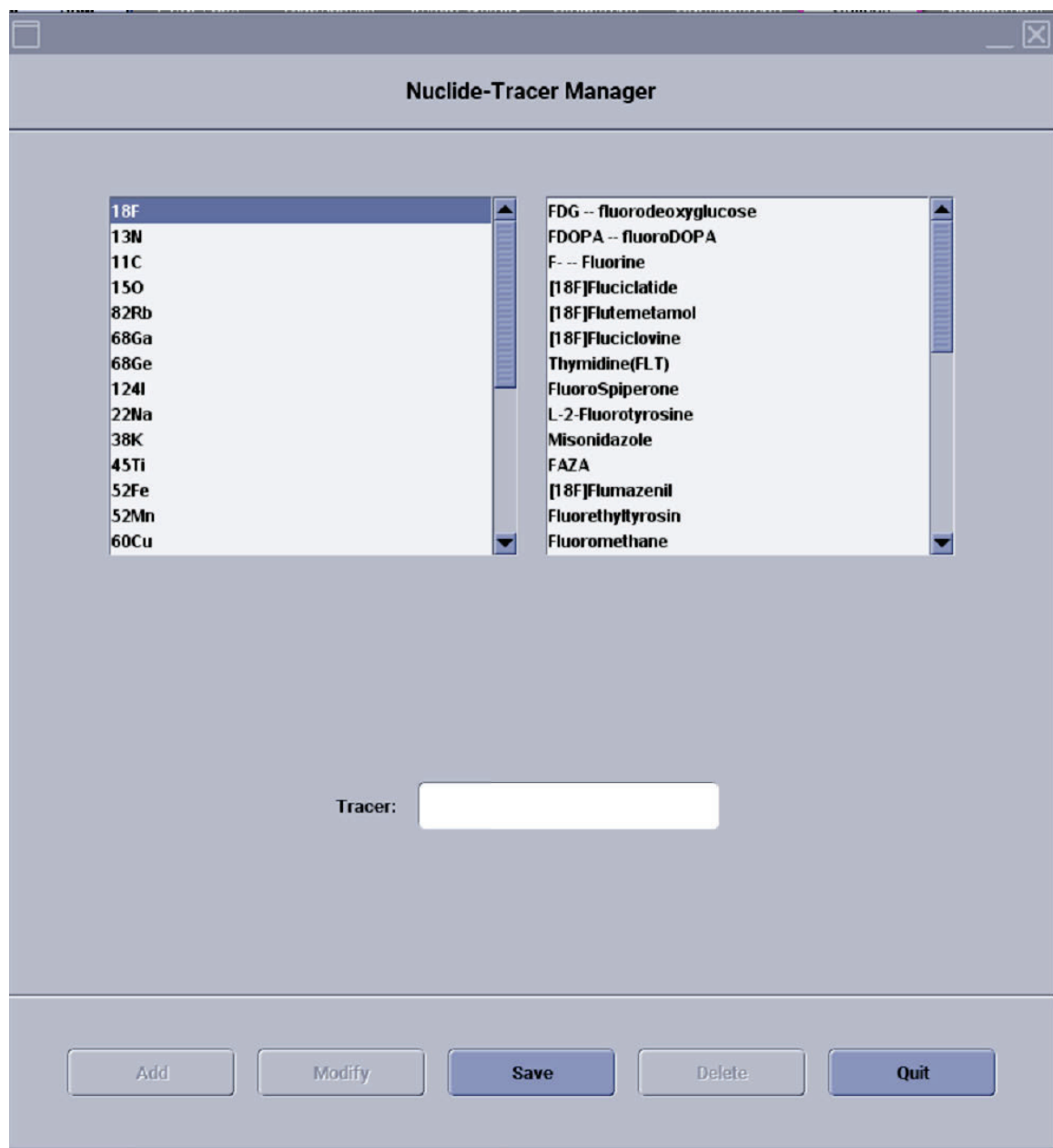
Figure 199 Choice Window



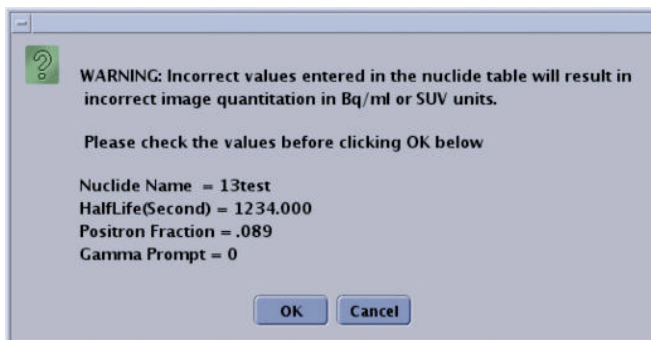
Figure 200 Nuclide-Tracer Manager



**Figure 201 Nuclide-Tracer Manager**



6. Select the type of data to add and click **Save**. A pop-up prompts you to confirm the values.

**Figure 202 Nuclide Confirmation**

Enter the user-defined tracer information and click **Save**. A pop-up prompts you to confirm the values.

**Figure 203 Tracer Confirmation**

7. Verify values and click **OK**.
8. To modify a user-defined nuclide or tracer, select the desired nuclide or tracer and click **Modify**. After the information has been updated, click **Save**, then **OK** on the confirmation pop-up.
9. To delete a user-defined nuclide or tracer, select the desired nuclide or tracer and click **Delete**. Then click **OK** on the confirmation pop-up.
10. Click **Quit** to exit.

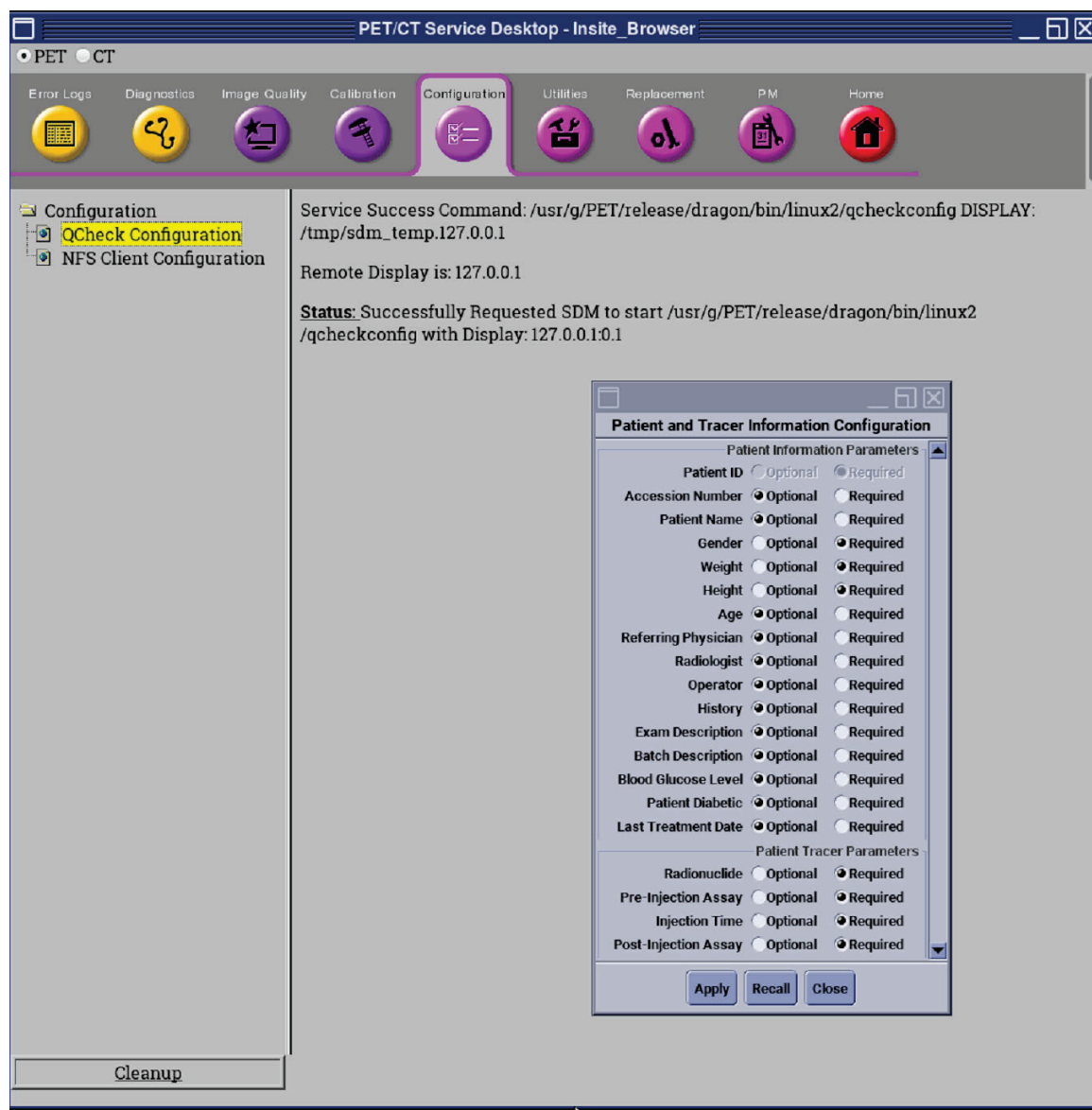
## 11.7 Q.Check Configuration

Q.Check is a quality control link between the scanner and workstation. This connection ensures that all the patient and tracer information required for quantitative imaging is saved in the patient exam before the acquisition begins. If the required fields are left empty, the system will prompt the user to fill in the fields. Fields are configured as Optional or Required with the Q.Check Configuration tool.

1. Q.Check Configuration is accessed through the PET Service Desktop Configuration menu.



**Figure 204 PET Service Desktop Configuration**



2. Patient and Tracer information can be selected as **Required** or **Optional**.

Select **Optional** or **Required** for each parameter.

- **Optional** — If fields are empty, the system will not prompt you to fill in the field prior to proceeding.
- **Required** — If fields are empty, the system will prompt you with the option to fill in the field or proceed.

**NOTE**

Patient Information field prompts are displayed when a protocol is selected from the **New Patient** window.

Tracer Information field prompts are displayed when confirming the PET scan prescription.

3. Click **Apply** to save selections.
4. Click **Close** to exit.

## 11.8 Edit Patient and Edit Tracer Information Quick Steps

### 11.8.1 Edit Patient Information

1. Click **Image Works**.
2. Click/highlight the exam to select it.
3. Click **Edit Patient**.
4. Click **Edit Patient Data**.
5. Click **Accept**.
6. Enter at least 3 characters into the **Edited By** field.
7. Modify the patient information.
8. Click **Accept**.
9. Click **Accept**. The new exam description contains the e+ and an index of the number of times the exam information has been edited.

### 11.8.2 Edit Tracer Information

1. Click **Image Works**.
2. Click/highlight the exam and select one PET series.
3. Click **Edit Tracer** to open an intermediate panel that lists the series that will change when you update the tracer data.
4. Click **OK**.  
Click **OK**. The system displays a pop-up message indicating which series are about to be affected by this activity.



5. Click **OK**.
6. Modify existing data or fill in blank fields.
7. Click **Apply** to update the tracer information on all the series on the **Series Number** list. The new series description contains the e+ and an index of the number of times the tracer information has been edited.

### 11.8.3 Edit Nuclide Information

1. Click **Image Works**.
2. Click/highlight the exam and select one PET series.
3. Click **Edit Tracer** to open an intermediate panel that lists the series that will change when you update the nuclide data.
4. Click **OK**. The system displays a pop-up message indicating which series are about to be affected by this activity.



5. Click **OK**.
6. Modify Nuclide data and other existing information if desired, or fill in blank fields.
7. Click **Apply**. The system begins updating all the relevant series. Click **Close** when finished.

**NOTE**

All PET reconstructed DICOM images sharing the same tracer Injection UID originated from the previous Nuclide will be marked as **e+1 <INVALID-Previous tracer name>**. RAW and List files with the same Tracer Injection UID will be updated with the new nuclide and tracer information and will be marked with e+1 to reflect the update. Manually perform retrospective reconstruction or replay to regenerate the desired images based on the corrected Nuclide. Remember to send the correct PET images to remote storage , PACS or reading station.

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## 12 Anonymize the Patient Data

### 12.1 Anonymize the Patient Data Introduction

This chapter describes the anonymization feature which creates a de-identified copy of selected exams, series and/or images. You can replace identifying information on the image display with the words “Anonymous”, “Anon” or a blank space, helping protect the patient’s privacy. The anonymization feature provides two levels of privacy, and changes the **Patient Name**, **Patient ID**, **Exam Number**, **Exam Description** and **Series Description**. You may apply this option to a single image, a series or the entire exam. Use the anonymization feature whenever:

- You scan a test patient or volunteer, and do not want to display the name.
- You plan to display the images to the public.
- You reserve images for troubleshooting purposes with IQ Snap, or plan to send the images to GE Healthcare for analysis or display.

#### NOTE

This feature automatically excludes Screen Save images, Series Text pages and the Dose Report text page from the copy of the anonymized exam.

If you plan to edit the patient data, edit the tracer or anonymize the patient, wait until all PET Cardiac ACQC reconstructions finish! If you change the patient or tracer information first, PET Cardiac ACQC will not work.

### 12.2 Anonymize the Patient Data

Follow the instructions in this section to change the patient name to Anonymous by exam, series, or image after you complete the exam. You still have to enter information into the **Patient Name** and **Patient ID** fields to acquire the exam.

1. Click **Image Works** to open the desktop.
2. Click/highlight the exam, series or individual images you plan to anonymize.
3. Click **Anonymize Patient** on the **Data Apps** toolbar to anonymize the selected data. Refer to [Figure 205 on page 364](#).

**Figure 205 Data Apps Toolbar**



**NOTE**

The **Anonymize Patient** button anonymizes the selected data only. For example, if two series are selected, **Anonymize Patient** will anonymize only these two series, and not the entire patient exam.

**NOTE**

When Edit Patient or Anonymize tools have been used to modify the exam, the link to the CT used as the attenuation map for a PET raw series is no longer available. This is a concern for retro-reconstruction of a PET raw series or VIP Replay with prospective reconstruction of a PET raw or PET list series. Select the appropriate CT for use as the attenuation map for the PET reconstruction. To do this, select the **PET Reconstruction** tab and click the **Recon Options** button to open a window that contains all the reconstruction options available. Under the CTAC Series, select the CT series to be used for this reconstruction.

## 12.3 Set Anonymous Patient Privacy Level

The **Anon Pat. Level** selection toggles between the two levels of privacy available to the Anonymous Patient by Exam, Series or Image function, described in the previous section [Anonymize the Patient Data](#). [Table 83 on page 365](#) lists the Patient ID data normally visible on display image fields, and their appearance in the Full Anonymous and Partial Anonymous modes. The Full privacy mode is the most HIPAA compliant mode.

### NOTE

This feature does not anonymize Screen Save images, Series Text pages or the Dose Report text page.

**Table 83 Full and Partial Mode Field Descriptions**

Field	Full Mode	Partial Mode
Exam Number	ANON OR ANONYMIZED	ANON OR ANONYMIZED
Patient ID	ANON OR ANONYMIZED	ANON OR ANONYMIZED
Patient Name	ANON OR ANONYMIZED	ANON OR ANONYMIZED
Exam Description	ANON OR ANONYMIZED	Shown
Series Description	ANON OR ANONYMIZED	Shown
Birthdate	Removed	Removed
Age	Removed	Removed
Weight	Removed	Removed
Operator Name	Removed	Removed
Site Name	Removed	Shown
Sex	Blank	Blank
Referring Physician	Blank	Blank
Accession Number	Blank	Blank

1. Click **Tool Chest**, then **Anon Pat. Level** to display the current Full or Partial status and the option to toggle between the modes.

### Figure 206 Tool Chest

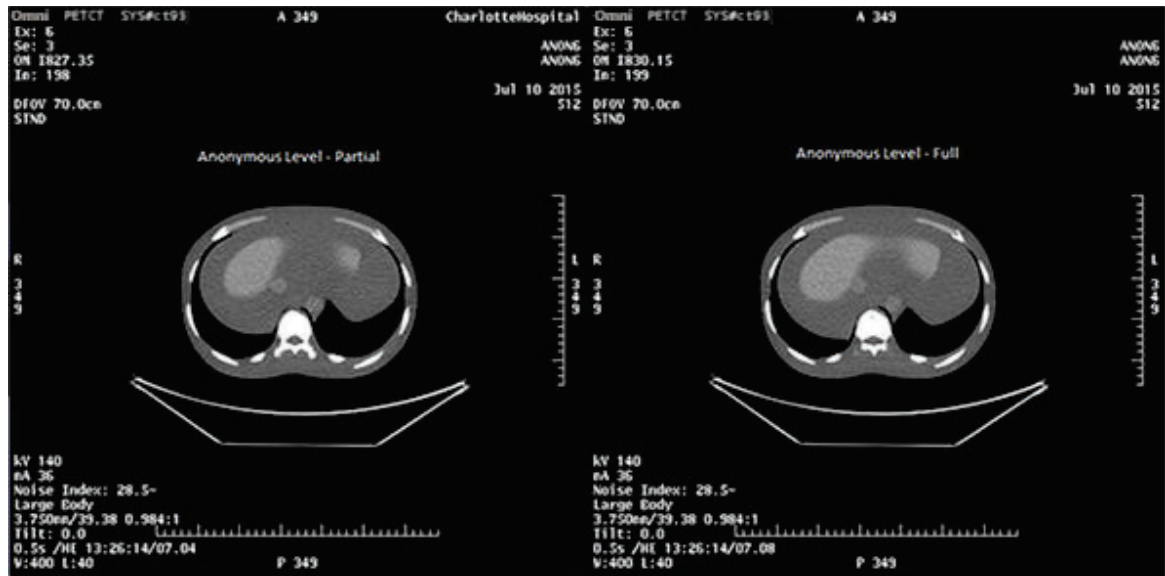
2. Refer to [Figure 207 on page 366](#), [Figure 208 on page 366](#) and [Figure 209 on page 367](#). The system displays the currently selected Full Anonymous or Partial Anonymous window.
  - Click **OK** to change to the other level of privacy.



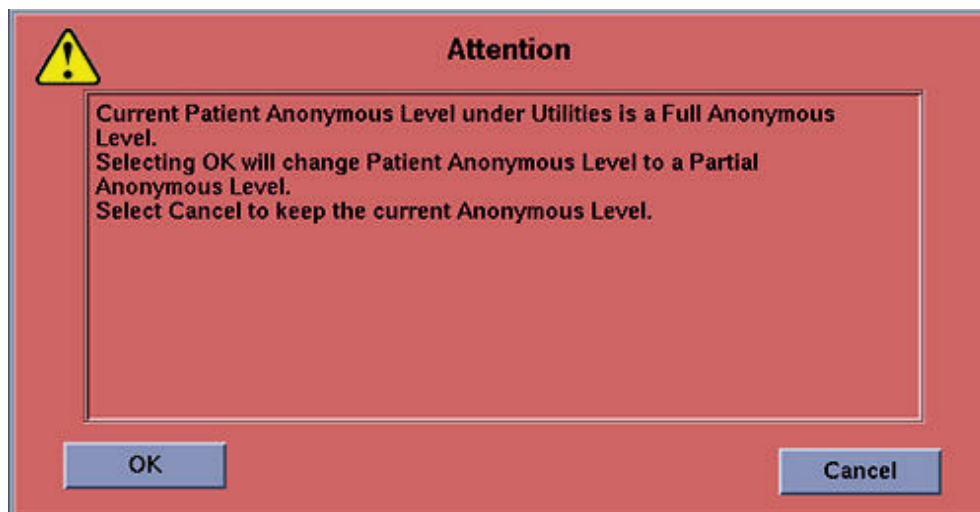
Anonymize the Patient Data

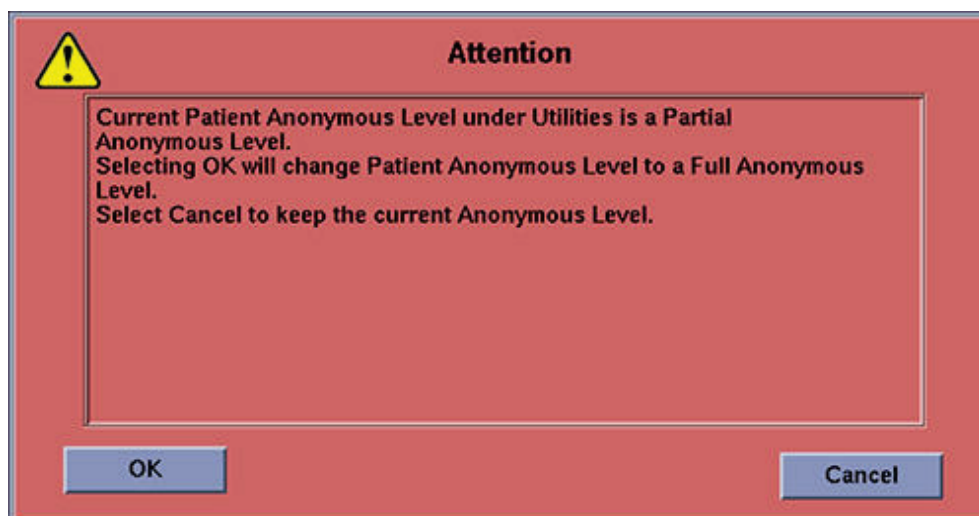
- Click **Cancel** to retain the currently displayed level of privacy.

**Figure 207 Full Anonymous and Partial Anonymous Annotated Images**



**Figure 208 System Set to Full Anonymous Privacy Level**



**Figure 209 System Set to Partial Anonymous Privacy Level**

## 12.4 Anonymize and Save CT Scan Data

### NOTE

Use this procedure to anonymize and save CT scan data from a PET/CT study or a stand-alone CT study. If you want to save a PET/CT study (including image data and all PET scan data) you made anonymous by following the instructions in the first section of this chapter, refer to the Manage Data (Archive and Storage) chapter for detailed instructions.

You can save the anonymous CT scan data, then restore and reconstruct this data with the patient identity removed. The anonymous save function addresses HIPAA concerns regarding patient privacy. Raw data, saved anonymously also reconstructs with the Patient Name and ID anonymized.

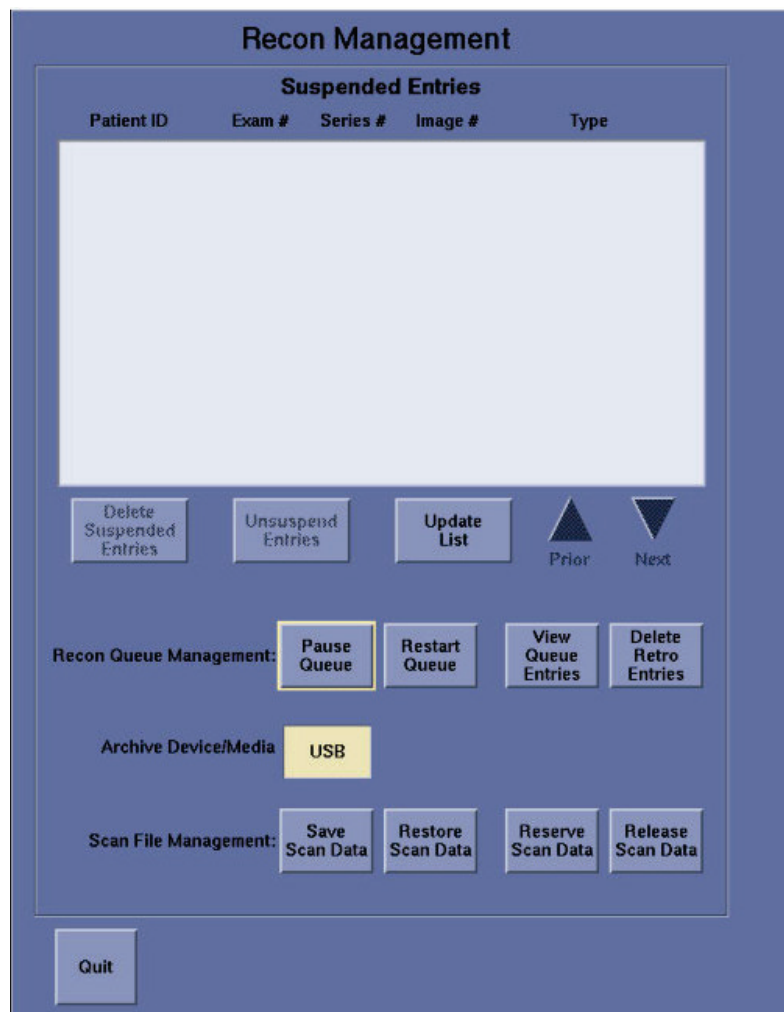
### NOTE

This procedure of anonymizing CT Scan Data does not guarantee that data will be rendered anonymous in compliance with applicable data privacy laws. Review the scan data before sharing it with third parties to ensure compliance with applicable privacy laws or regulations.

CT Scan must be idle when you start this procedure. This procedure can take 5 seconds (helical scan) to 10 minutes (a single Cardiac file) to save to USB drive.

1. Attach the USB drive.
2. Click the **CT Recon Mgmt** button in the scan monitor toolbar to open **Recon Management** window shown in [Figure 210 on page 368](#).

**Figure 210 Recon Management Window**



3. Click the **Archive Device/Media** button that matches the media you plan to use.
4. Click the **Scan File Management Save Scan Data** button to open the **Recon Management Save Scan Files** window.
5. Click the Exam, Series or Scans you plan to save.
6. Click **Save Selected Annon. Data**.

**NOTE**

If using USB media, a pop-up may display to reformat the media. Click **Yes** to proceed with formatting.

7. Click **OK** to acknowledge the scan files saved message.
8. Click **Quit** to close the **Recon Management** window.

## 12.5 Anonymize the Patient Data Quick Steps

### 12.5.1 Anonymize the Patient Data

1. Open the **Image Works** desktop.
2. Select the exam, series and/or images from the browser.
3. Click **Anonymize Patient**.

### 12.5.2 Set Anonymous Patient Privacy Level

1. Click **Tool Chest**, then **Anon Pat. Level** on the Image Works toolbar.
2. Read the displayed message:
  - Click **OK** to change to the other level of privacy.
  - Click **Cancel** to retain the currently displayed level of privacy.

### 12.5.3 Anonymize and Save CT Scan Data

1. Attach the USB drive.
2. Click **CT Recon Management** and select the media type.
3. Click **Save Scan Data**.
4. Select the anonymous exam/series/scans you want to save.
5. Click **Save Selected Annon. Data**.
6. Click **Quit** to exit.

Anonymize the Patient Data

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# 13 Respiratory Gating

## 13.1 Introduction

Respiratory motion can lead to reduced image quality in PET and CT imaging. Images that are motion-corrected are intended to aid physicians in: detection; localization; evaluation; diagnosis; staging; restaging; monitoring; and/or follow up of disease, abnormality, and/or function, and for therapy planning and guidance; radiotherapy treatment planning; and for Nuclear Medicine interventional procedures. Areas of the body most impacted by respiratory motion are the chest (including the heart), abdomen and pelvis. Disease types in which respiratory motion may have a significant impact, if uncorrected, include, but are not limited to:

- Lung Cancer (e.g. Small Cell and Non-Small Cell);
- Liver Cancer;
- Colorectal Cancer;
- Lymphoma used to detect and characterize respiration (e.g. Hodgkin's and Non-Hodgkin's);
- Cancers that have metastasized to the liver;
- Cancers in the Thorax; and
- Heart disease.

This chapter contains information for 4D respiratory gated PET studies performed with an external device or with software-only gating feature (MotionFree, also known as PET Digital Gating or Data Driven Gating - DDG). It also contains the Motion Match workflow and post acquisition processing.

MotionFree is a software-only feature by which gating triggers are computed from a spatio-temporal analysis of the acquired PET data. Using MotionFree, no external gating device or hardware is necessary. MotionFree may be used with PET radiopharmaceuticals approved by the regulatory authority in the country of use, in patients of all ages, with a wide range of sizes, body habitus, and extent/type of disease.

The MotionFree feature incorporates a real-time principal component analysis (PCA) of PET coincidence list data, computing the principal components of spatio-temporal variation due to respiration. For each PC, a unitless index, referred to as "R-Value" in this document, is calculated, representing the strength of respiratory motion. The principal component with the largest R-Value is selected for generation of 1D waveform and for further processing. Similar to the case with existing device-based techniques, the respiratory waveform is used to find per-cycle triggers. These triggers are then used with the existing motion compensation techniques, e.g. Q.Static. MotionFree allows an automated motion detection and correction of PET images with respiratory motion by making the decision on which bed to correct for respiratory motion. This automatic decision is based on the measured R-Value per bed and the user-selected motion threshold, prescribed under Motion Screen, in Scan Time window.

**NOTE**

When using Q.Static, the user has the option to extend scan time per bed for beds selected for motion correction. In this case, MotionFree automatically decides for which bed to extend the acquisition time beyond Static bed time. Hence, no scan time extension if respiratory motion is not detected.

**NOTE**

MotionFree cannot be combined on top of the Whole-Body Dynamic Acquisition.

The system provides the following respiratory gated workflows:

- Q.Static Workflow with Varian (external device)
- Q.Static workflow with MotionFree (deviceless gating)
- Integrated Q.Freeze Workflow
- Whole Body + Q.Freeze Workflow

The PET protocols associated with these are typically called:

- PTCT\_Q.Static
- PT\_Q.Static\_ULDAC
- PTCT\_Derived\_Q.Static (MotionFree)
- PTCT\_INTEG\_Q.Freeze
- PTCT\_Q.Freeze

**NOTE**

The protocol name may vary if your facility customized the GE supplied protocol.

## 13.2 Respiratory Gating Workflows

### 13.2.1 Q.Static Workflow

1. Pre-enter tracer information into the patient schedule (optional).  
Refer to [Chapter 10, Prepare the Patient for the Study](#) for additional details.
2. [Chapter 10, Open the Exam.](#)
3. [Chapter 10, Position the Patient for a Standard PET/CT.](#)
4. Position the patient for a gated study.  
Follow the instructions in the Varian Medical User Manual for using the Varian Respiratory gating system to position the tracking block over the patient anatomy with the greatest respiratory motion.
5. Setup the Varian Respiratory Gating Monitor.
6. [Chapter 10, Prescribe and Acquire the Scout Series.](#)

7. [Prescribe the CT and PET Series \(Q.Static\).](#)
8. [Chapter 10, Acquire the CT Series.](#)
9. In case Cine CT is acquired stop recording, save waveform and send to the system.
10. In case CT acquired is not Cine, [Acquire the PET Series \(Q.Static\).](#)
11. [End the Exam \(Q.Static\)](#)
12. Check image quality using the Q.Static application.
13. Remove the tracking block and release the patient.

### 13.2.2 Derived Q.Static (MotionFree) Workflow

1. Pre-enter tracer information into the patient schedule (optional). Refer to [Chapter 10, Prepare the Patient for the Study](#) for additional details.
2. [Chapter 10, Open the Exam](#)
3. [Chapter 10, Position the Patient for a Standard PET/CT.](#)
4. [Chapter 10, Prescribe and Acquire the Scout Series.](#)
5. [Prescribe the CT and PET Series \(Derived Q.Static\).](#)
6. [Chapter 10, Acquire the CT Series](#)
7. [Acquire the PET Series \(Derived Q.Static\).](#)
8. Check image quality using the Q.Static application (ImageQC or CustomQC) prior to releasing patient.

### 13.2.3 Integrated Q.Freeze Workflow

1. Pre-enter tracer information into the patient schedule (optional). Refer to [Chapter 10, Prepare the Patient for the Study](#) for additional details.
2. [Chapter 10, Open the Exam.](#)
3. [Chapter 10, Position the Patient for a Standard PET/CT.](#)
4. Position the Patient for a gated study.  
Follow the instructions in the Varian Medical User Manual for using the Varian Respiratory gating system to position the tracking block over the patient anatomy with the greatest respiratory motion.
5. Setup the Varian Respiratory Gating Monitor.
6. [Chapter 10, Prescribe and Acquire the Scout Series.](#)
7. Acquire the Cine (CTAC or Diagnostic) Series with site specified number of bins.
8. [Chapter 10, Acquire the CT Series.](#)
9. [Acquire the Whole Body PET ViP Record Series.](#)
10. [Disable Gating and End the Exam \(Integrated Q.Freeze / Whole Body + Q.Freeze\).](#)



11. Check the Whole Body image quality (Integrated Q.Freeze).
12. Remove the tracking block and release the patient.
13. Check that the Varian trigger file exists by loading the Cine CT images into Motion VUE and selecting Advantage 4D.
14. Create a CTAC series that matches the PET acquisition (if Cine CT has different number of bins) and ViP Replay PET using this new CTAC. Refer to [Use Advantage 4D to Segment a Cine CTAC](#).
15. Use Motion VUE for QC display of Cine CT and Phased Matched PET. Refer to [Use Motion VUE to Display Binned CTAC Images](#).
16. Perform Q.Freeze post-processing. Refer to [Use Motion VUE Q.Freeze to Generate Motion Reduced Registered Images](#).

#### NOTE

Refer to [Use Motion Correct to Average the Cine CTAC](#), if needed.

### 13.2.4 Whole Body + Q.Freeze Workflow

1. Pre-enter tracer information into the patient schedule (optional). Refer to [Chapter 10, Prepare the Patient for the Study](#) for additional details.
2. [Chapter 10, Open the Exam](#).
3. [Chapter 10, Position the Patient for a Standard PET/CT](#).
4. Setup the Varian Respiratory Gating Monitor.
5. [Chapter 10, Prescribe and Acquire the Scout Series](#).
6. [Chapter 10, Prescribe the CT and PET Series](#).
7. [Chapter 10, Acquire the CT Series](#).
8. [Chapter 10, Acquire the PET Series](#).
9. Position the patient for a gated study.  
Follow the instructions in the Varian Medical User Manual for using the Varian Respiratory gating system to position the tracking block over the patient anatomy with the greatest respiratory motion.
10. [Acquire the Cine \(CTAC or Diagnostic\) Series](#) with site specified number of bins.
11. [Acquire the Whole Body PET ViP Record Series](#).
12. [Disable Gating and End the Exam \(Integrated Q.Freeze / Whole Body + Q.Freeze\)](#).
13. Check the image quality (Whole Body + Q.Freeze).
14. Remove the tracking block and release the patient.
15. Check that the Varian trigger file exists by loading the Cine CT images into Motion VUE and selecting Advantage 4D.
16. Create a CTAC series that matches the PET acquisition (if Cine CT has different number of bins) and ViP Replay PET using this new CTAC. Refer to [Use Advantage 4D to Segment a Cine CTAC](#).

17. Use Motion VUE for QC display of Cine CT and Phased Matched PET. Refer to [Use Motion VUE to Display Binned CTAC Images](#).
18. Perform Q.Freeze post-processing. Refer to [Use Motion VUE Q.Freeze to Generate Motion Reduced Registered Images](#).

**NOTE**

Refer to [Use Motion Correct to Average the Cine CTAC](#), if needed.

**NOTE**

For respiratory gating, *Trigger Source* option was added to *Scan Type* window, allowing the user to choose “External” for a device-based respiratory gating option, or “Derived” for the MotionFree option. Cine CT can be gated only with an external gating device.

On the PET prescription window, the Scan Type button will display an annotation of the user’s scan type selection. ViP stands for Record, the letter “C” stands for Cardiac, the letter “E” stands for External (device based respiratory gating option) and the letter “D” stands for Derived (MotionFree gating option)

## 13.3 Setup the Varian Respiratory Gating Monitor

This section assumes the external respiratory gating mode is selected and the Varian monitor is plugged in and correctly cabled to the accessory panel.

**NOTE**

This section provides “quick steps” to set up the respiratory gating monitor. Please refer to the Varian Medical Systems Instructions for Use manual that shipped with the Varian monitor for detailed instructions and information.

1. Turn on the gating device and log in the application
2. Select an existing patient, or enter data for a new one

**NOTE**

Patient ID Number must match the Patient ID Number on the scanner for the Motion Match application to automatically choose the correct .vxp file. If the ID match fails, you must choose the correct .vxp file from a list of available choices when you launch Motion Match.

3. Position the tracking block over the patient anatomy and start a gating session
4. Once the confidence level has stabilized, start to record and enable gating
5. Note the breathing period and add one second. Input the time as the Cine Duration Time on the **CT View/Edit** window.

## 13.4 Prescribe the CT and PET Series

### 13.4.1 Prescribe the CT and PET Series (Q.Static)

Use the scout to graphically prescribe the Start and End Locations of the subsequent CT and PET scans, as well as the Display Field of View. The CT provides the PET scan attenuation map. You can reconstruct the CT images with a Standard or Soft filter.

1. Click **Next Series** from the protocol.  
If necessary, click **Show Localizer** to display the Graphic Rx Localizer over the scout.
2. Position the PET and CT scans to cover eyes to thighs.
3. Position the PET Q.Static beds to cover the area with motion.
4. Click **PET** and select **Scan Time** to edit the Q.Static bed position.

#### NOTE

On Graphic Rx, Q.Static bed shows scan bed time on a blue background.

5. Check and update the non-Q.Static bed time and Q.Static bed time, if needed.

#### NOTE

Only authorized personnel can revise Q.Static trigger rejection and Q.Static phase parameter settings when necessary. Please refer to Chapter 21, Build a New (Hybrid) PET/CT Protocol for details on parameter adjustment.

If your facility uses a custom protocol, make sure the **Inherit from Exam** button is selected on the **Tracer Information** window.

#### NOTE

The user can choose to record beds for a retrospective analysis: go to **Scan Type** and click the **Record** Button. Then, go to **Scan Time** and check (yellow) /uncheck the beds you would like to record.

6. Click the **CT** button to review the CTAC protocol parameters and modify as needed.
7. Click the **Auto Apps** option to select MotionFreeApps (optional).

#### NOTE

Check the CT reconstruction Start and End Locations and other parameters prior to starting CT. Moving the Graphic Rx Localizer will change the Start, End, Diameter and Center parameters.

Figure 211 Q.Static (with external device) Scan Time window

**Enter the Desired Scan Time per Bed Position**

---

All Beds

Variable

**Base  
Bed Time**

**Q.Static  
Bed Time**

**Total Scan Time**

Prior

Next

---

Q.Static	Bed	Scan Time	Scan Range
	1	<input type="text" value="00:02:00"/>	S0.00 - I246.40
	2	<input type="text" value="00:04:00"/>	I179.20 - I425.60
	3	<input type="text" value="00:02:00"/>	I358.40 - I604.80
	4	<input type="text" value="00:02:00"/>	I537.60 - I784.00
	5	<input type="text" value="00:02:00"/>	I716.80 - I963.20

---

**Q.Static Phase**

Offset (%)

Width (%)

---

**Trigger Rejection**

Avg/min

Deviation (%)

---

OK

Cancel

8. Review the recon parameters, and select Q.Static as the desired Motion Correction Method.

### 13.4.2 Prescribe the CT and PET Series (Derived Q.Static - MotionFree)

Use the scout to graphically prescribe the Start and End Locations of the subsequent CT and PET scans, as well as the Display Field of View. The CT provides the PET scan attenuation map. You can reconstruct the CT images with a Standard or Soft filter.

1. Click **Next Series** from the protocol.  
If necessary, click **Show Localizer** to display the Graphic Rx Localizer over the scout.
2. Position the PET and CT scans to cover eyes to thighs.
3. Choose the bed positions to screen for respiratory motion. Click **PET** and select **Scan Time** to edit the Motion Screen parameters.

#### NOTE

On Graphic Rx, Motion Screen beds show scan time in a blue background.

4. Click the **CT** button to review the CTAC protocol parameters and modify as needed.
5. Check and update the static bed time and Q.Static bed time, if needed.

#### NOTE

Click on the **Variable** option to set different Q.Static scan times for the different bed positions.

#### NOTE

Only authorized personnel can revise Q.Static phase parameters and derived Q.Static Motion Screen Threshold parameter settings when necessary. Please refer to Chapter 21, Build a New (Hybrid) PET/CT Protocol for details on parameter adjustment.

If your facility uses a custom protocol, make sure the **Inherit from Exam** button is selected on the **Tracer Information** window.

6. Click the **CT** button to review the CTAC protocol parameters and modify as needed.
7. Click the **Auto Apps** option to select MotionFreeApps (optional).

#### NOTE

Derived Q.Static requires that the Record option is on when bed is selected for respiratory gating.

#### NOTE

Coincidence events detected during pre-scan delay period will not be included in the calculation of triggers, waveforms and R-Values.

**NOTE**

Check the CT reconstruction Start and End Locations and other parameters prior to starting CT. Moving the Graphic Rx Localizer will change the Start, End, Diameter and Center parameters.

- Review the recon parameters, and select Q.Static as the desired Motion Correction Method.

**Figure 212 Derived Q.Static Scan Time window**

Enter the Desired Scan Time per Bed Position

Base Bed Time  
00:02:00

Q.Static Bed Time  
00:04:00

Total Scan Time  
00:10:00 - 00:16:00

Record	Motion Screen	Bed	Base Scan Time		Q.Static Scan Time	Scan Range
<input type="checkbox"/>	<input checked="" type="checkbox"/>	1	00:02:00			S0.00 - I246.40
<input type="checkbox"/>	<input type="checkbox"/>	2	00:02:00	-	00:04:00	I179.20 - I425.60
<input type="checkbox"/>	<input type="checkbox"/>	3	00:02:00	-	00:04:00	I358.40 - I604.80
<input type="checkbox"/>	<input type="checkbox"/>	4	00:02:00	-	00:04:00	I537.60 - I784.00
<input type="checkbox"/>	<input checked="" type="checkbox"/>	5	00:02:00			I716.80 - I963.20

Q.Static Phase

Offset (%)  Width (%)

Motion Screen

Threshold

### 13.4.3 Prescribe the CT MotionFreeApps (Optional)

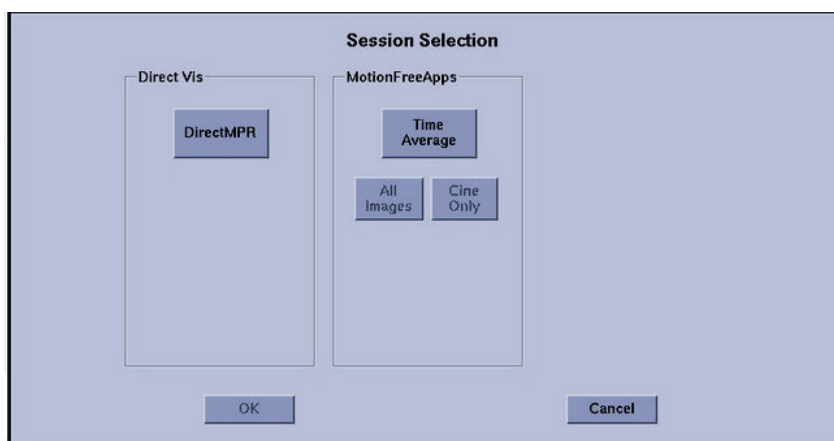
During CT acquisition you may select the option to generate a time average of Cine CT using the MotionFreeApps and save it in the image database as reformatted series.

- Click the **Recon Parameters**  icon tab.

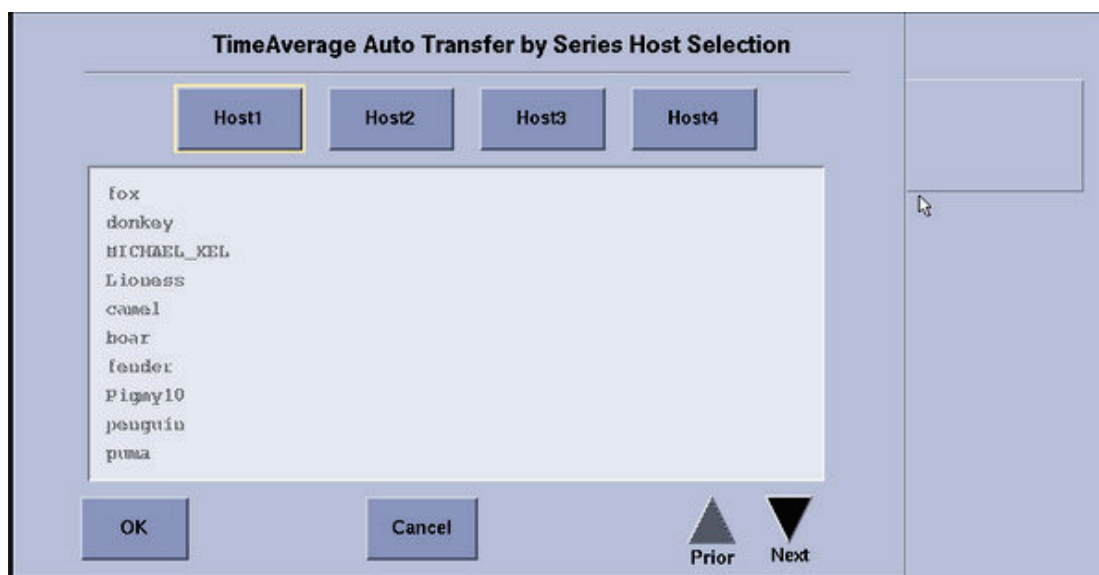
- Click Auto Apps option. Under the MotionFree Apps section, select the preferred option:

- Click **Time Average** to generate an average CT from the acquired Cine CT. The result will be displayed as reformatted series (numbered 80X). Click again to turn off the **Time Average** option.
- The default option for Time Average is **All Images** option, which creates an average all the CT series.
- Click **Cine Only** option to create an average of the Cine CT series only.

Press **OK** to accept the changes or **Cancel**.



- If **OK** was selected the system opens a pop-up window to select the host to which the images will be transferred automatically.
- Click the required Host and select the desired location to which to transfer the images.
- Press **OK** to accept the changes or **Cancel**.



**NOTE**

In case you would like to accept the changes without selecting any Host for series transfer, click the OK button in [Figure](#) without selecting any Host. Pressing **Cancel** in this step will cancel all the AutoApps changes selected.

## 13.5 Acquire the Cine (CTAC or Diagnostic) Series

Follow these instructions to acquire the respiratory gated Cine CTAC series you will use during attenuation correction of the PET respiratory gated series.

1. Click **Next Series** from the protocol.  
If necessary, click **Show Localizer** to display the Graphic Rx Localizer over the scout.
2. Position the PET and CT scans to cover the region with motion.
3. Review the selected protocol values, and modify as needed.
4. Make sure no one is in the scan room other than the patient.
5. Check the facility respiratory gating method and start as indicated for the CT cine series.
6. Click **Record** and enable **External Gating**, if not already done, and continue to watch for X-ray indication on the Varian respiratory gating device, once the Cine CTAC is initiated. Click **Confirm** to initiate the Cine CTAC scan sequence.

The system displays a message to warn you that the system will scan a single tomographic plane. Click **Continue** to initialize the start scan sequence.

7. Press the flashing **Move to Scan** button to move the cradle to the CT start location.
8. Press the flashing **Start Scan** button to enable X-ray and scan the patient.

## 13.6 Acquire the PET Series

1. Click the **PET** button to display the PET scan protocol in the **PET View/Edit** window.
2. Review the PET protocol parameters and modify them as needed following the facility guidelines.
3. Click **Confirm** to initiate the PET scan sequence.

**NOTE**

Check the PET reconstruction Start and End Locations and other parameters prior to starting PET. Moving the Graphic Rx Localizer will change the start, end, diameter, and center parameters. Motion beds are filled with blue color, while non-motion beds are filled with white color. Recorded beds are bounded by red borders.



**Figure 213 GraphicRx Screen**



4. Press the flashing **Move to Scan** button to move the table to the PET start location.
5. Press the flashing **Start Scan** button.

## Notes

### If using Q.Static:

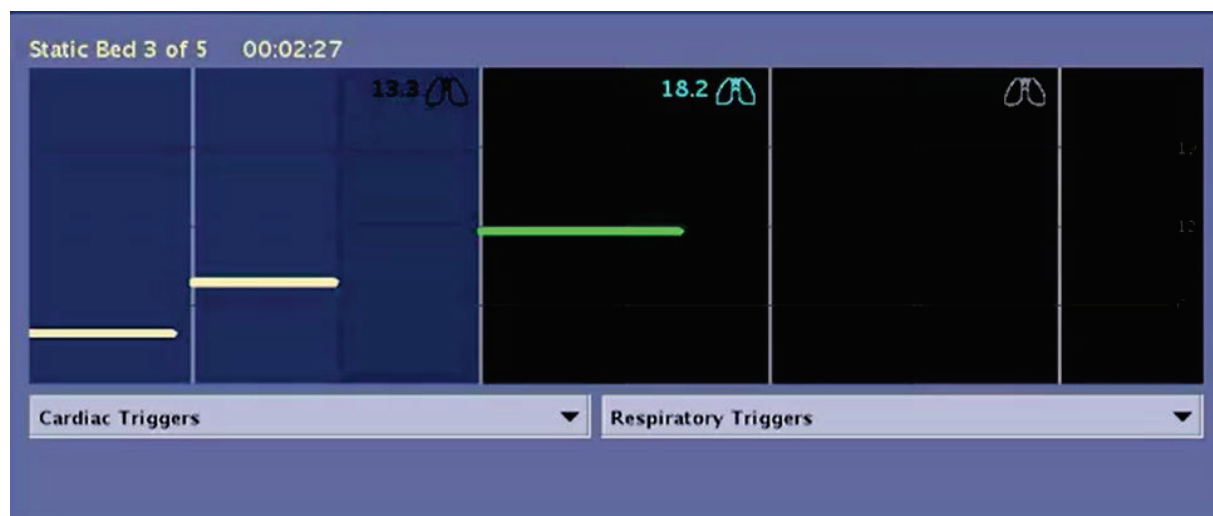
- Monitor the System Messages and **Dynaplan** windows for respiratory trigger and scan status throughout the acquisition.
- Monitor the accepted and rejected triggers during each respiratory gated bed position for QC. An alternative method to check the QC is to load the PET images into Motion Match to view the accepted, rejected and total trigger information.
- Upon completion of each Q.Static bed, the effective Q.Static bed time (mm:ss) that will be reconstructed is displayed in the **Dynaplan** window. Make sure the scan time meets facility guidelines.
- The alternative method to check the effective Q.Static bed time (mm:ss) is to select the 951 or 901 series in the exam and check the time per bed of the Q.Static bed positions.

### If using Derived Q.Static:

- During acquisition of Motion Screen bed positions, the system will extract the waveforms and triggers out of which it derives the R-Value, that indicates the strength of respiratory motion in a given bed position. The reference motion threshold is set to 15. This threshold can be adjusted by the user, either prospectively or retrospectively. Please note that this threshold is also unitless and not equivalent to breath per minute value.
- A higher threshold means that a stronger respiratory motion, i.e. a larger R-Value, must be detected in order for the system to act. A lower threshold means that a less strong respiratory motion, i.e. lower R-Value, must be detected in order for the system to act.
- Under Scan Time window, the user prescribes Base Bed (represents static time) and Q.Static time. Since MotionFree automatically decides to extend the time and correct for motion based on R-Value, a minimum and maximum scan time will be displayed to show how the scan time may vary depending on the settings defined by the user and the decisions taken by MotionFree during acquisition.
- If the threshold is exceeded during a prospective acquisition, the scan will automatically extend to the user defined "Q.Static Bed Time". If the threshold is not exceeded, the scan will complete at the "Base Bed Time", then continue to the next bed position.
- R-Value representing the strength of motion during base bed time will be displayed on the DynaPlan window prior to completion of the base bed time for all bed positions selected for motion screening.
- This R-Value will notify the user if the assessed motion exceeds the prescribed threshold and automatically extend that bed position as prescribed by Q.Static Bed Time. If no significant motion is seen, the acquisition will complete that bed position at end of Static Bed Time and move on to the next bed position.

Once scan is completed for each bed, a final R-Value will be calculated for whole data detected for the scanned bed and will be saved into the list file.

- If no time extension is prescribed by the user, i.e. "Base Bed Time" is equal to "Q.Static Bed Time", then, MotionFree will only decide on motion correction based on R-Value. This R-Value will be calculated only at the end of bed acquisition, to represent all data detected for that bed. It will not be displayed on Dynaplan, but only on System Messages window.

**Figure 214 DynaPlan window during acquisition**

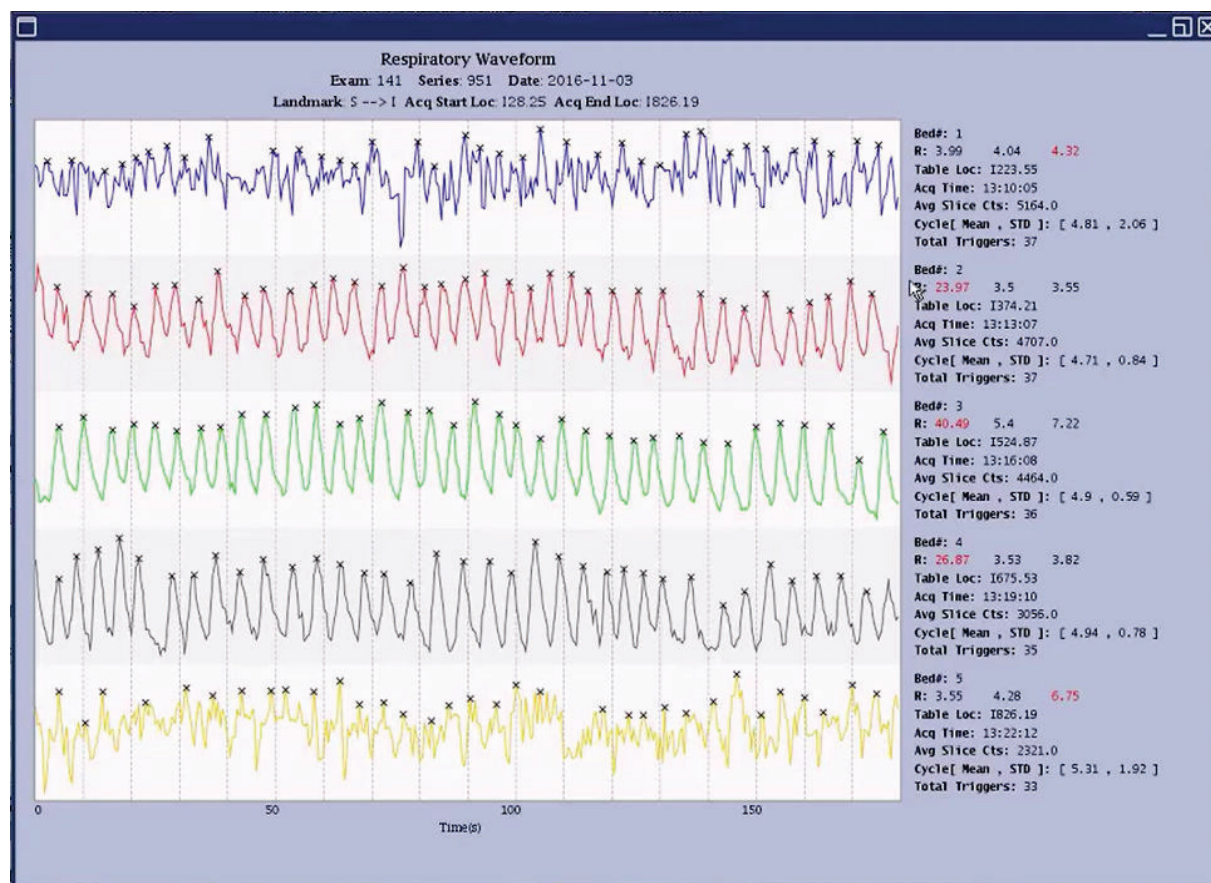
This is an example of a 5-beds scan. Motion threshold was set to 15. Only beds 2-4 were selected for motion screening. R-Value for bed 2 did not exceed threshold, and did not extend scan to Q.Static Scan Time accordingly. For bed 3, Threshold was exceeded and scan time per bed was extended.

### Motion Screen Threshold

- Motion Threshold default value, set to 15, is selected as the default value based on a study, composed mainly of 18-FDG scans. Some tracers may require a finetuning of the threshold.
- Motion threshold value may be tuned to perform clinical or research tasks. Retrospective processing allows the user to change the threshold value and see the effects on image quality and motion correction. This can be performed with multiple motion thresholds to assess the appropriate setting for the application of interest. The motion threshold can be customized on a per-protocol basis under the **Scan Time** window -> **Motion** screen.
- An example use case of adjusting the motion threshold would be for shallow breathing patients. The strength of motion may be reduced and therefore a lower threshold may be indicated to automatically correct for respiratory motion. Retrospective correction on static bed time is always available in the instances in which the threshold was not exceeded, but you still want to see the effects of respiratory motion correction. Refer to [Chapter 18 Post Processing](#) for retrospective replay workflow.
- Images can always be reconstructed without MotionFree applied, by simply reconstructing the PET acquisition with the gating technique (i.e. Q.Static) turned off, i.e. using only static mode.
- Also, static images acquired with list data (Record is on) can always be reconstructed with MotionFree, by simply reconstructing the PET acquisition with Derived Q.Static turned on. Derived Q.Static time can be up to base bed time as was acquired with the prospective scan. Refer to [Chapter 18 Post Processing](#) for more details on MotionFree Replay options.
- The user may view the respiratory triggers/waveforms post acquisition using the Investigator tool. The Investigator tool can be found under **Service -> PET -> Image Quality**. Open the investigator tool, select the patient and click on list data (LST) series that was acquired with Derived Q.Static. For the selected LST data, a waveform icon will display. Click on the icon to view the waveforms

per bed. By selecting one/some of the beds under the LST series, only waveforms of the selected beds will be displayed. For each bed, final R-Value per bed is displayed in red.

**Figure 215 Investigator Tool**



## 13.7 Acquire the Whole Body PET ViP Record Series

### If using Q.Static with external device (Varian):

1. Click the **PET** button to display the **PET View/Edit** window.
2. Review the PET protocol parameters and modify as needed.
3. Return to the respiratory monitor (Varian) and verify that the system is still tracking.
4. Open the **Cardiac/Respiratory Trigger** tab, monitor the current and average triggers per minute, (Varian) and enter the new average respiratory rate at the time of scan into the **Avg Trig/min** field.

### NOTE

The system records the respiratory triggers and uses them during ViP Record for Gated. Update the gating parameters average rate prior to scanning.

5. (Varian) Click **Confirm** to initiate the PET scan sequence.

6. If flashing, press **Move to Scan** to move the cradle to the PET start location.
7. Press the **Start Scan** button when it flashes.
8. Remember to open the **Respiratory Trigger** window (Varian) and continue to monitor the respiratory rate and status throughout the acquisition.
9. Upon completion of the PET ViP Record phase, the system automatically starts the ViP List Replay using the facility preferences determined when the protocol was built.

**If using Derived Q.Static:**

ViP Record is always on. No actions are required.

**NOTE**

Real time triggers are not displayed in real time with MotionFree. Respiratory triggers will be available offline post exam completion under the Investigator Tool.

Refer to [Chapter 18, Post Processing, Reconstruction and Replay](#), for information about Replay options for MotionFree feature.

## 13.8 Disable Gating and End the Exam (Q.Static)

**If using Q.Static with external device (Varian):**

1. After completing the scan, return to the respiratory monitor to end the gating session.  
Click **Stop** then discard the waveform file export to the Scanner.
2. Click **End Exam**.

**If using Derived Q.Static:**

1. Click **End Exam**.

**NOTE**

Triggers can now be displayed (offline) using the Investigator Tool when selecting LST data.

## 13.9 Disable Gating and End the Exam (Integrated Q.Freeze / Whole Body + Q.Freeze)

Return to the respiratory monitor to export the waveform file to the PET/CT console.

1. Click **Stop** to stop the gating window on the Varian device.
2. Enter the **Exam Number** displayed at the top of the **PET/CT View/Edit** window into the **Exam Number** field.
3. Enter the **Series Number** displayed with the Cine CTAC information on the Image Works browser into the **Series Number** field.

4. Click **OK** to display a confirmation window that lists the Patient ID Number and corresponding File name.

## 13.10 Use Advantage 4D to Segment a Cine CTAC

1. Select one cine CT series with an associated .vxp file.
2. Click **Motion Match**.
3. If necessary, click **Advantage 4D** then click **OK** to launch the application.
4. If necessary, select the correct .vxp file from the **File Selection** panel.
5. The **Advantage 4D** window opens and follows the User Preferences to format and display the images, **Waveform** panel and **Phase Bins** panel.
6. Click the **Motion VUE** tab to display the resulting CT segments in the Coronal, Sagittal and Axial orthogonal formats.
7. Scroll through the images to check image quality.
8. Click the **Series Save** icon to display the **Series Save** panel, which lists the bins and assigns series numbers.
9. Click **Save Series** to save the file to the Image Works database.
10. Click **Continue** to return to the **Motion VUE** window.
11. Click **Exit**.
12. Click the **PET Recon/Replay** icon.
13. Click/highlight the gated raw PET series (903 Series) and click **Select Series**.
14. Click the **Recon** tab and review the recon parameters.
15. Click **Recon Option** and click/highlight the binned CTAC Series.
16. Click **OK**.
17. Enter a unique **Series Description** into the data field on the **View/Edit** window.
18. Click **Confirm** to submit the request.
19. Load the binned CTAC and phase matched PET series into Motion Match and check the image quality with the Motion VUE application.

## 13.11 Use Motion VUE to Display Binned CTAC Images

1. Select the binned Cine CTAC series from the Image Works browser.
2. If necessary, click **Motion VUE** and **OK** to launch the application.
3. Move the cursor to the bottom of the viewport to display the Cine controls, and click **Play** to view the images.
4. Optional: Click **Options** to film the image or screen.
5. Click the **Exit Door** icon to quit Motion Match.



## 13.12 Use Motion VUE Q.Freeze to Generate Motion Reduced Registered Images

1. From the **Q.Freeze** area, select the reference gate from the **Select Reference Gate** menu.
2. Click **Q.Freeze** to initiate the Non-Rigid Registration.
3. Once registration has completed, click **File > Save as Series** from the **Motion VUE** menu bar.
4. From the Save as Series window, select the desired selection boxes. Both may be selected.
5. Click **OK** to generate a new series in the Patient List. Click **Save as Default** to save the selected option boxes as the default.

## 13.13 Use Motion Correct to Average the Cine CTAC

1. Select the Cine CTAC series from the Image Works browser.
2. Click **Motion Match**.
3. Click **Motion Correct** and **OK** to launch the application.
4. Click the **Save as Series** icon.
5. Type a unique **Series Name** into the corresponding data field.
6. Click **OK** to save the averaged Cine CTAC file.
7. Click **Exit**.

## 13.14 Motion Match

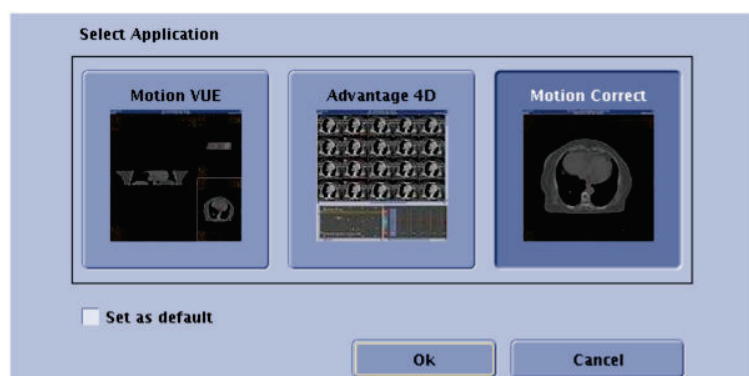
### 13.14.1 Post-Processing with Motion Match

Motion Match includes three applications:

- Motion VUE: Displays the binned PET and CT image sets for assessment of alignment and motion between the images. The Q.Freeze premium option provides the registrations of all gates of a gated PET to a single reference gate, please refer to [Image Registration](#) for more details.
- Advantage 4D: Segments and rebins the Cine CTAC to match the PET respiratory phases.
- Motion Correct: Averages the Cine CT images for use in PET attenuation correction.

Your User Preference choices determine the Motion Match application selection and display format, as does the type of series you select.

You also can set up the Motion Match workflow to automatically process and display the phase matched images with minimal user intervention.

**Figure 216 Select Application**

### 13.14.2 Set Motion Match User Preferences

Click **File** and click or drag to **Preferences...** to open a **Motion Match User Preferences** window, similar to the one shown in [Figure 218 on page 389](#).

**Figure 217 Motion Match File Menu**

**Preferences...** opens the **User Preference** tabs.

You must choose the Advantage 4D application to activate the **Advantage 4D** tab.

**Figure 218 Motion Match User Preferences — Color Maps Tab**

**Tracer Info** lets you edit tracer information. Note that changes are not saved upon exiting the application.



### 13.14.2.1 Color Maps Tab

1. Click the arrow to display the list of available color maps.
2. Click or drag to select a new image display color map, and update the corresponding field on the **Color Map** tab.

The color map display returns to the current default setting when you end the session, unless you click **Save Settings**.

3. Save, discard or temporarily use the current color map selections:
  - Click **Save Settings** to make the current selections the new defaults.
  - Click **Load Defaults** to return to the most recently saved default settings.
  - Click **Cancel** to close the window and return to the original settings.

### 13.14.2.2 F Keys Tab

**Figure 219 Motion Match User Preferences — F Keys Tab**



1. Click the arrow to select the default **CT Window Leveling** display parameters from the list.
  - The CT Window Leveling value sets the default W/L value for the Vertebrae when you press **F11**.
  - Move the cursor over the W/L annotation in the lower left corner of the viewport, right-click to display the menu shown in the following illustration, then click or drag to the new selection. You also can press an **F** key at any time to change to the corresponding default W/L selection.

**Figure 220 F Keys Menu**

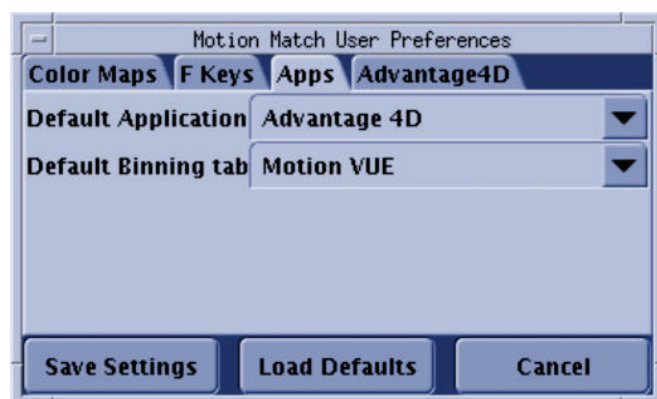
- Click the arrow to set the default PET/CT Blend Ratio that appears as annotation in the lower right corner of the PET/CT fused images.

You can click-middle on the % CT annotation, then drag right and left to change the blend, or left-click and right-click on the % CT annotation to decrease and increase the blend ratio.

- Save, discard or temporarily use the Motion Match User Preference selections:
  - Click **Save Settings** to make the current selections the new defaults.
  - Click **Load Defaults** to return to the most recently saved default settings.
  - Click **Cancel** to close the window and return to the original settings.

### 13.14.2.3 Apps Tab

This tab sets the application launch preference when you click **Motion Match**.

**Figure 221 Motion Match User Preferences — Apps Tab**

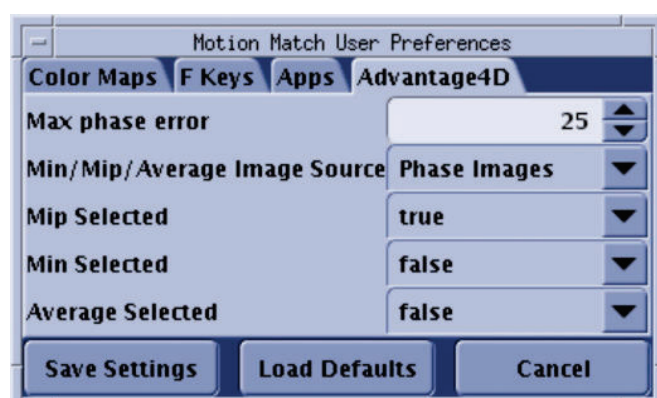
- Click the **Default Application** arrow to select your binning (Advantage 4D) or averaging (Motion Correct) preference when you open Motion Match with a Cine CT selected.
  - If you select Advantage 4D, the software automatically bins the Cine CTAC. Your **Default Binning** tab selection determines what the software does next.

- You also can select **None** which always opens the application selection window every time you launch the Motion Match software.
2. Click the **Default Binning** tab arrow to determine the path Motion Match takes when you select the Advantage 4D application as the default.  
The system automatically bins the Cine CTAC, regardless of your choice. This selection determines whether the software shows you the results in Motion VUE or remains in Advantage 4D to display the original images, the waveform and phase bins.
  3. Save, discard or temporarily use the Motion Match User Preference selections:
    - Click **Save Settings** to make the current selections the new defaults.
    - Click **Load Defaults** to return to the most recently saved default settings.
    - Click **Cancel** to close the window and return to the original settings.

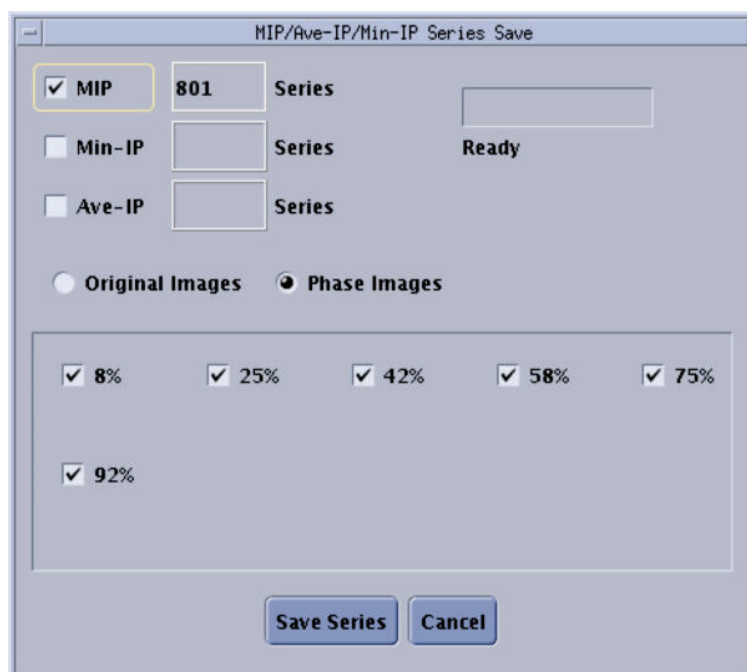
### 13.14.2.4 Advantage4D Tab

Select the **Advantage4D** application to enable the **Advantage4D** tab in User Preferences.

**Figure 222 Motion Match User Preferences — Advantage4D Tab**

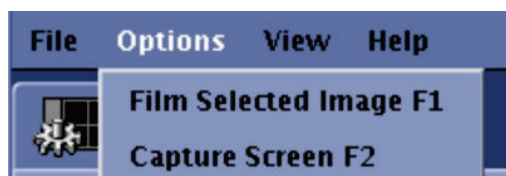


1. Click the **Max phase error** field and enter a new value, or click the up/down arrows to increase and decrease the allowable maximum value between the image with the greatest phase deviation (in the selected phase) and the selected target phase.
2. Click the **Min/Mip/Average Image Source** field arrow and select the type of data you want the system to use to create the intensity projection images when you save it.  
The software automatically selects the corresponding **Original Images** or **Phase Images** radio button on the **Series Save** window when it opens.

**Figure 223 MIP Series Save Window**

3. Click the **MIP Selected** field arrow and select **True** to automatically check the **MIP** check box on the **MIP/Ave-IP/Min-IP Series Save** window when it opens.
4. Click the **Min Selected** field arrow and select **True** to automatically check the **Min-IP** check box on the **MIP/Ave-IP/Min-IP Series Save** window when it opens.
5. Click the **Average Selected** field arrow and select **True** to automatically check the **Ave-IP** check box on the **MIP/Ave-IP/Min-IP Series Save** window when it opens.
6. Save, discard or temporarily use the Motion Match User Preference selections:
  - Click **Save Settings** to make the current selections the new defaults.
  - Click **Load Defaults** to return to the most recently saved default settings.
  - Click **Cancel** to close the window and return to the original settings.

### 13.14.2.5 Options Menu Description

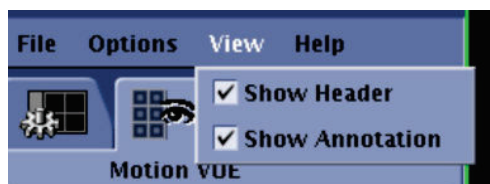
**Figure 224 Motion Match Options Menu**

1. Click **Options** to display the drop-down menu.

2. Click or drag to **Film Selected Image**, or press **F1** to film the active viewport.
3. Click or drag to **Capture Screen**, or press **F2** to send all the images in the image display area to the filmer as a single image.

### 13.14.2.6 View Menu Description

**Figure 225 Motion Match View Menu**

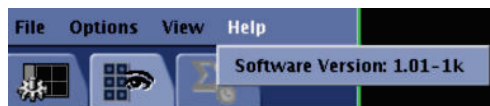


1. Click **View** to display the drop-down menu.
2. Click/check the corresponding box to show the Header and/or Annotation information.
3. Click the box to toggle the check mark OFF and hide the corresponding information.

### 13.14.2.7 Help Menu Description

Click **Help** to display the current software revision information.

**Figure 226 Motion Match Help Menu**



### 13.14.3 Motion VUE Concept

Respiratory motion presents significant challenges for PET/CT acquisitions that last several minutes and, in which, breath holding is not an option. The induced motion artifacts may introduce significant image distortion, potentially leading to clinical misinterpretation involving apparent increase of lesion size, apparent reduction of measured SUV, and in many cases, potential miss of small lesions. Furthermore, motion artifacts may also directly impact radiotherapy planning, treatment, and eventually, interpretation of treatment response over time. These considerations clearly indicate the need for robust motion management tools to ensure reliable and confident clinical assessment, diagnosis, and therapy planning.

Motion VUE is a post-processing application used to visualize and assess respiratory motion. Phase gated PET and CT images are utilized to provide a simultaneous visualization of gated PET and gated CT in a color overlay representation and the ability to play a cine movie loop through all available gates. This application can be used for the following:

- To check the quality assessment of the motion differences between PET and CT respiratory-gated data sets.
- To understand range of motion.

- To quantify activity in lesions.

Although Motion VUE does not support a specific diagnosis, phase gated PET/CT scans are commonly used to visualize:

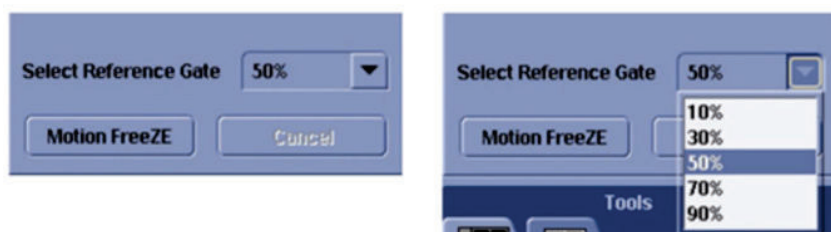
- lung nodules
- colon polyps
- pancreas lesions
- esophageal lesions
- gastric lesions

### 13.14.4 Q.Freeze

Q.Freeze is a premium option within Motion Vue that provides registration for all gates of a gated PET to a single reference gate. This volume is referred to as PET Registered Gated (PET Reg Gated). It then combines the results of the registration process to generate a new motion-corrected 3D PET image volume. This volume is referred to as PET Registered Median volume (PET Reg Med). This new volume looks statistically similar to the ungated PET image volume but has the blurring effect of respiration reduced or removed. In effect, the signal-to-noise of any moving feature should increase as compared to the same feature as measured in the ungated PET data set.

The Q.Freeze area displays on the **Motion VUE** tab.

**Figure 227 Motion FreeZE Selections**



#### **Select Reference Gate**

The menu displays available reference gated options. In this example, the items in the menu refer to the five available phases that can be selected as the Reference Gate. The Reference Gate is the phase that best represents the optimum location of the anatomy/pathology relative to the breathing cycle. This phase is used as the reference gate/phase when the non-rigid registration process generates the new volume of data. The default reference gate is configurable. Refer to [Define Default Reference Gate Value](#).

#### **Motion FreeZE**

This button activates the Non-Rigid Registration processing to generate a new volume of data. The progress bar indicates processing time. Refer to [Generate Registered Images](#) and [Save Registered Gated and Registered Median PET Series](#) for steps to perform and save registered results.

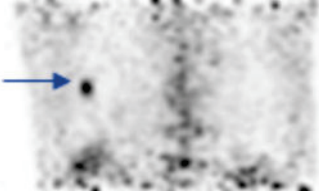
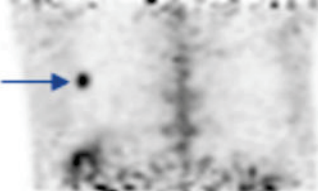
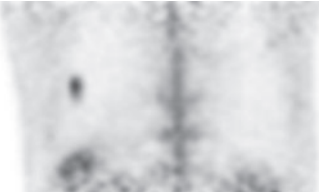
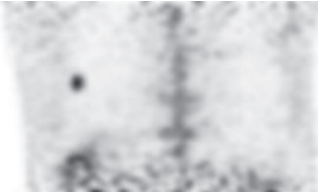
#### **Cancel**

Stops the progress of the registration.

13.14.5 Image Registration

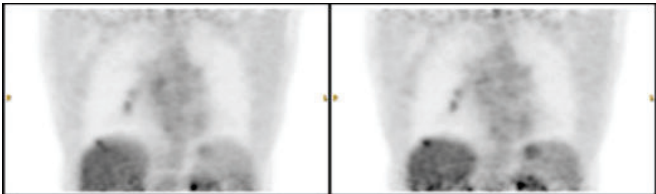
Integration of a motion correction, Non-Rigid Registration (NRR) allows generation of a new volume of data that has the same dimensionality as the whole-body ungated dataset, but has had the blurring effects of motion (with respect to a Reference Gate) reduced via the registration process. The intent is improved lesion conspicuity, quantification accuracy and lesion volume determination.

Table 84 Pre-Registration and Post-Registration Comparison

	Pre-Registration	Post-Registration
Gated		
Average		

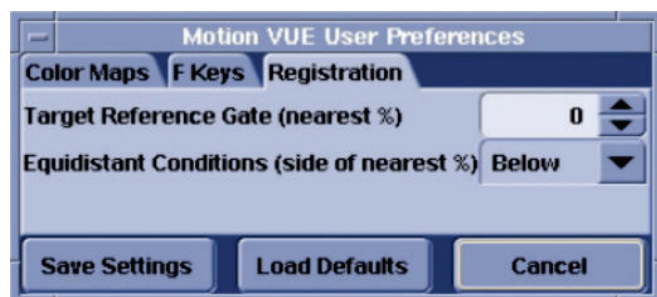
Registered images demonstrate the same or better clinical results in comparison to an ungated image.

Figure 228 Ungated Image (left) and Registered Image (right)



13.14.6 Define Default Reference Gate Value

Use these steps to define a unique Reference Gate value that is used as the default value for registration.

**Figure 229 Preference Registration Window**

1. From the **Motion VUE** menu bar, click **File > Preferences**.
2. From the **Motion VUE User Preferences**, click the **Registration** tab.
3. Modify the **Target Reference Gate** field.
  - a. Highlight and enter a new value.
  - b. Use the slider to select a new value.
4. When there are two gates that are equal distant from the **Target Reference Gate**, you must select the value that is above or below the target value.
5. Click **Save Settings** to save the new value as the new default.
6. Optional: Click **Load Defaults** to reset the **Target Reference Gate** value to the manufacturer's default value.
7. Optional: Click **Cancel** to exit the **User Preferences** window without making any change.

### 13.14.7 Generate Registered Images

Use these steps to create a motion correction, Non-Rigid Registration (NRR) that allows generation of a new volume of data that has the same dimensionality as the whole-body ungated dataset, but has had the blurring effects of motion (with respect to a reference gate) reduced via the registration process. Refer to [Q.FreeZE Selections](#) [Motion FreeZE Selections](#) .

1. From the **Q.FreeZE** area, select the Reference Gate from the **Select Reference Gate** menu. Typically, navigate to the slice that best demonstrates the pathology of interest and then view each phase to identify the desired phase to enter as the **Select Reference Gate**.

#### NOTE

You can select a new default Reference Gate value other than the manufacturer's default. For details, see [Define Default Reference Gate Value](#).

2. Click **Q.FreeZE** to initiate the Non-Rigid Registration.  
View the progress bar, which indicates the process time.
3. Optional: Click **Cancel** to stop the Q.FreeZE registration.



### 13.14.8 Save Registered Gated and Registered Median PET Series

Use these steps to save **Registered Gated** and **Registered Median** PET series so that you can use the data set in another AW application such as PET VCAR.

**Figure 230 Save as Series Window**



**Figure 231 File Menu**



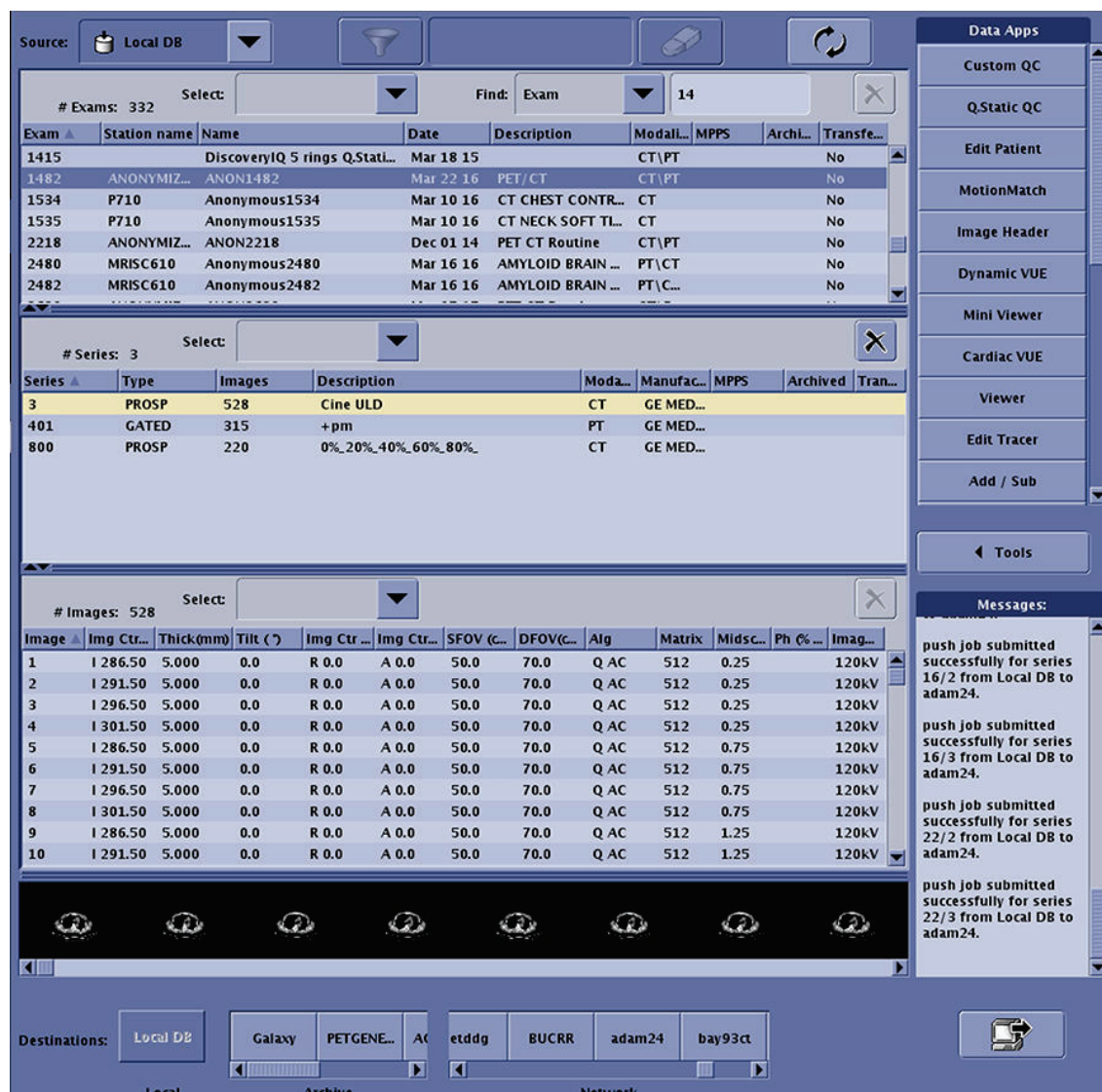
1. You must have executed Motion FreeZE and thus have a selectable Registered Results in the presentation area.
2. From the **Motion VUE** menu bar, click **File > Save as Series**.
3. From the **Save as Series** window, select the desired selection boxes. Both may be selected.
4. Click **OK** to generate a new series in the Patient List. Click **Save as Default** to save the selected option boxes as the default.

### 13.14.9 Use Advantage 4D to Segment a Cine CTAC

Follow these instructions to segment a Cine CTAC for use during attenuation correction of a respiratory gated PET scan. Use the segmented Cine CTAC to display fused PET/CT images with Motion VUE.

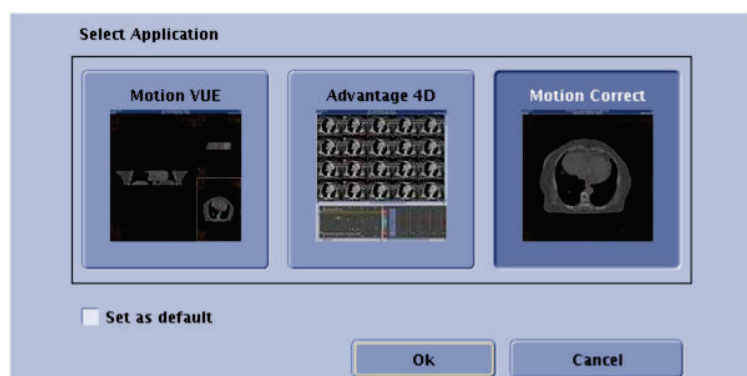
1. Select a study from the examinations database on the Patient List.
2. Click a qualifying series.  
Select one Cine CT series with an associated .vxp file.

Figure 232 Image Works Browser



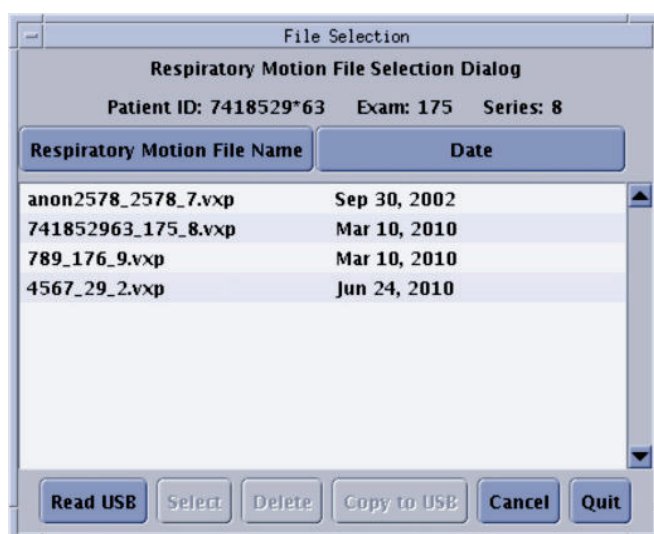
3. Click **Motion Match** from the **Data Apps** list on the right side of the browser.
4. If the **Select Application** window opens, click **Advantage 4D**, then click **OK** to proceed to the initial display window.

You can click the **Set as default** box, then one of the Motion Match function buttons to skip this window and proceed directly to the selected application. You can restore this interim window from User Preferences.

**Figure 233 Select Application Window**

5. If the Motion Match software fails to find a perfect match between the .vxp file and the scan data, for example, due to the entry of a different Patient ID into the Respiratory Gating Monitor, it displays a **File Selection** window that lists all the possible choices on the system.

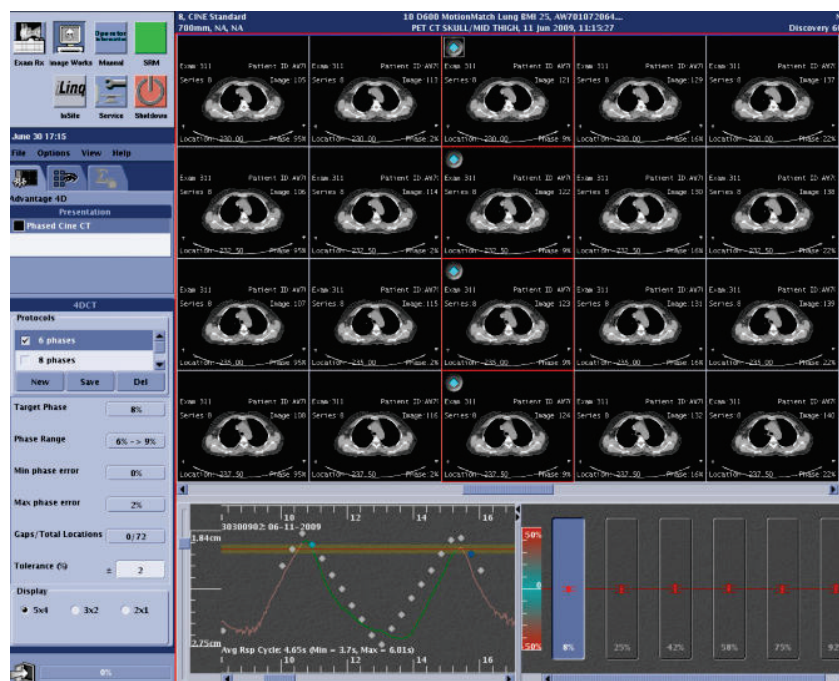
Click on the name of the file you plan to use, then click **Select** to continue.

**Figure 234 File Selection Window**

6. The Motion Match software follows the User Preferences to set up the initial Advantage 4D display. The following illustration shows an example of the initial display with Advantage 4D selected. The User Preferences chosen for your system determines the appearance of the initial display image layout.

Follow facility guidelines to establish and use a standardized display format.

Figure 235 Initial Advantage 4D Display



- If you use the default 6 Phase protocol, the application presorts the data and selects the best image, relative to the timing of the waveform file.

See [Respiratory Waveform Annotation Descriptions](#).

- Click the **Motion VUE** tab to display the resulting CT segments in the Coronal, Sagittal and Axial orthogonal formats.

Optional: Scroll through the images or bins and check image quality.

- Click the **Series Save** icon to display the **Series Save** window, which lists the bins and assigns series numbers.

Recommended: Click the radio button to save as a **Single Series**, to preserve the automatic phase matching ability.

Figure 236 Series Save Window

Series	Target Phase	Selected
803	T=8%,PR=3% -> 11%,AR0=1 -> 7	✓
803	T=25%,PR=22% -> 29%,AR0=32 -> 65	✓
803	T=42%,PR=38% -> 46%,AR0=91 -> 100	✓
803	T=58%,PR=54% -> 61%,AR0=78 -> 99	✓
803	T=75%,PR=72% -> 79%,AR0=21 -> 42	✓
803	T=92%,PR=89% -> 96%,AR0=0 -> 5	✓

10. Click **Save Series** to save the file to the Image Works database.  
A ready status bar updates while the software saves the data.
11. Upon successful completion, the software opens an **Attention Message** window.  
Click **Continue** to return to the **Motion VUE** window.
12. Click the **Exit** icon at the bottom of Motion Match tool display area to exit Motion Match.
13. Click the **PET Recon/Replay** icon in the display window toolbar to open the **Pet Retro List Select** window.  
Highlight the **Patient**, then the correlating **List Data** series and click **Select Series** to close the **Pet Retro List Select** window and open a PET retrospective reconstruction **View/Edit** window.
14. Click the **Recon** tab and review the recon parameters.  
Follow facility guidelines to modify the parameters, as needed.
15. Click **Recon Option** to open the **Reconstruction** window.  
Click the binned CTAC Series.
16. Click **OK** to close the **Reconstruction** window.
17. Enter a unique **Series Description** into the field on the **View/Edit** window.
18. Click **Confirm** to submit the request to the reconstruction queue.  
Load the binned CTAC and phase matched PET series into Motion Match to verify image quality with the Motion VUE application.

### 13.14.10 Create a New Binning Protocol

Follow these instructions to create and store a custom binning protocol. Select the number and center of target phases that best matches your PET scan prescription.

1. Select a qualifying Cine CTAC series to launch the Motion Match application.
2. Click **Motion Match**.  
If necessary, click **Advantage 4D** and **OK** to launch the application.
3. Click **New** in the **Protocols** area to display the **Create a New Protocol** window.

**Figure 237 Create A New Protocol Window**

**: Create A New Protocol**

You can create up to 20 target phases with a minimum phase difference of 5%.

Name of the new protocol:

Number of target phases:

☒ **Evenly distributed**

☐ **Enter manually**

1.	<input type="text" value="0"/>	%
2.	<input type="text" value="10"/>	%
3.	<input type="text" value="20"/>	%
4.	<input type="text" value="30"/>	%
5.	<input type="text" value="40"/>	%
6.	<input type="text" value="50"/>	%
7.	<input type="text" value="60"/>	%
8.	<input type="text" value="70"/>	%
9.	<input type="text" value="80"/>	%
10.	<input type="text" value="90"/>	%

4. Enter a unique name for the protocol into the **Name of the new protocol** field.
5. Select a value for the **Number of target phases** field.
  - Enter a value between 1 and 20 into the field, or click the up/down arrows to increase or decrease the value from 1 to 20.
  - The **% Target Phase** bins at the bottom of the window update to reflect your selection.
6. You can evenly or manually distribute the center of the CT target phase within the PET bin. The system defaults to the **Evenly distributed** mode.
  - Click the **Enter manually** radio button to activate the **% Target Phase** fields.
  - Click or erase each value and enter a new value to replace it.
7. Click **OK** to save the binning protocol to the **Protocols** drop-down menu list.  
You may have to scroll to the bottom of the list to see your selection.
8. To delete a custom protocol, click it then click **Delete** to remove it from the list.



You can not delete the two permanent (6 Phase and 8 Phase) protocols from the list.

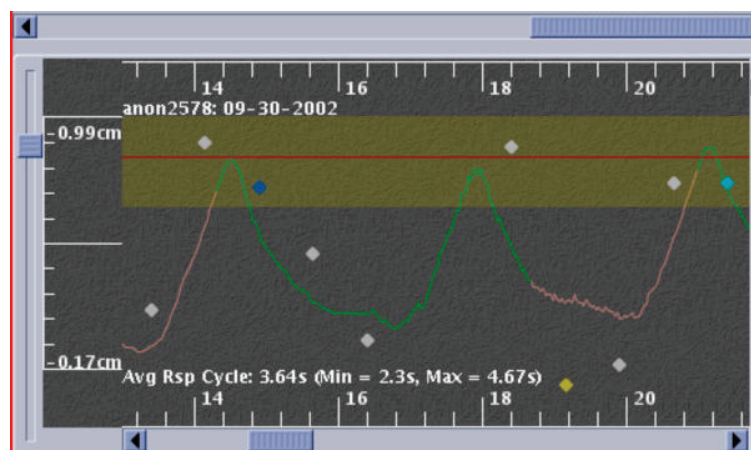
#### NOTE

You can move the cursor over the bin window at the bottom of the Advantage 4D screen, then right-click to display an adjustment menu. You can add, remove and/or adjust the tolerance of the phase bins on display. When you finish, you can click **Save** to store the new protocol on the list. The system prompts for a protocol name. Enter a unique name into the field, then click **OK**.

### 13.14.11 Respiratory Waveform Annotation Descriptions

Motion Match uses the .vxp file from the Varian Respiratory Gating Monitor to generate and display the patient respiratory waveform in the panel in the lower left corner of the **Advantage 4D** window. The vertical scale represents both amplitude (in units provided by the gating monitor) and respiratory phase, where 0% represents the peak inspiration and 50% represents peak expiration. The **Respiratory Waveform** window uses the following color conventions:

**Figure 238 Waveform Example**



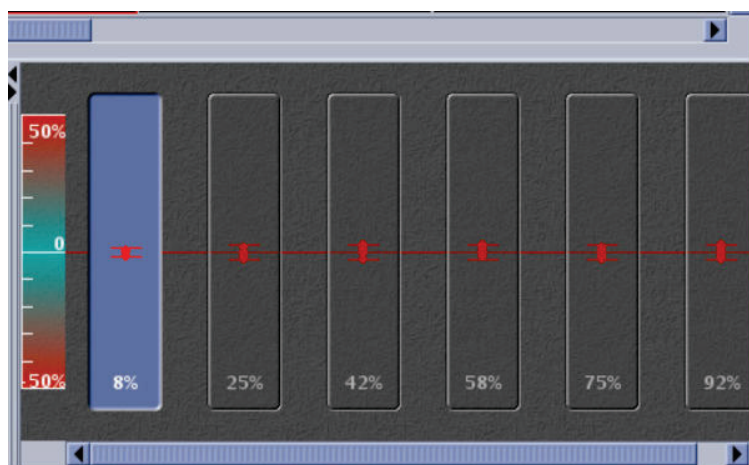
- **Green/pink trace:** continuous respiratory signal trace represented by images displayed on either side of the selected target phase
- **Red horizontal line:** currently selected target phase
- **Cyan diamonds:** currently selected images
- **Red diamonds:** default selection overwritten by manual page selection
- **Yellow diamonds:** images that cannot be attached to a phase, labeled phase-less images
- **Dark blue diamonds:** images within tolerance; double-click to manually select
- **White diamonds:** images displayed in the image display area were acquired at the same table location during the scan but are not in the currently selected target phase tolerance.
- **Gray diamonds:** images outside the display area; single-click to view these images
- **|--<--|:** image duration

- **Vertical slider:** adjusts the time domain; move it up to compress the time domain and down to stretch the time domain
- **Vertical ruler:** represents the signal amplitude, in mm.
- **Horizontal ruler:** represents time, in one-second increments
- **Tolerance area:** shaded light brown, it represents the tolerance range within which you may manually select target phase images

### 13.14.12 Phase Panel Annotation Descriptions

The **Phase List** window displays all the target phases from the currently selected respiratory protocol. The CT4D Protocol selection determines the number of phase bins on display. Use this window to sort the images in the viewer. Click a phase bin to display all the images acquired during the corresponding phase % in a vertical column in the center of the window.

**Figure 239 Phase List Window**



- **Phase tolerance:** The vertical scale on the **Phase List** window.
- **Phase bins:** Click a bin to view the images that fall within the phase tolerance % displayed at the bottom of the bin. The system displays the corresponding images in a vertical column in the center of the viewer. The phase values on the bins refer to a segment (or phase) of the respiratory cycle, where 0 or 100% represents peak inspiration and 50% represents peak expiration.
- **Phase horizontal scroll bar:** Click and drag to display all available phase bins.
- Move the cursor over a phase bin and right-click to display a menu of editing options. You can manually edit the bins from this menu, then save the results on the Protocols list.



**Figure 240 Phase List Right-Click Menu**

### 13.14.13 Use Motion Correct to Average the Cine CTAC

1. Select the Cine CTAC series from the Image Works browser.
2. Click **Motion Match** to open the application.
3. Click **Motion Correct** then click **OK** to launch the Motion Correct application.
4. Click the **Save as Series** icon (bottom of **Presentation** area of **Motion Correct** tab) to open a **Save as Series** window.

**Figure 241 Save as Series Window**

- The system displays the default **Series Number** but you can change it.
  - Enter a unique **Series Name** into the corresponding field.
5. Click **OK** to save the averaged Cine CTAC file.  
The status bar in the display tool area updates to 100 percent to indicate a successful save.
  6. Click **Exit** to quit the Motion Match application.  
Use this averaged Cine CTAC during PET ACQC or during Volume Viewer display.

**Figure 242 Motion Correct Window**

### 13.14.14 Viewport Menu Descriptions for Motion VUE and Motion Correct

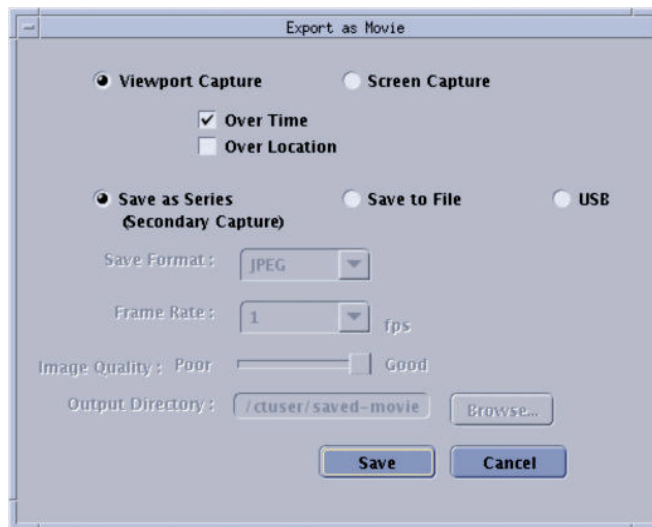
Move the cursor over a viewport, then right-click to open the viewport menu. Click or drag to the menu item to select it and close the viewport menu

**Figure 243 Viewport Menu**

<b>Enlarge</b>
<b>Reset Pan Zoom</b>
<b>Reset W/L</b>
<b>Hide Annotations</b>
<b>Show All Annotations</b>
<b>Show/Hide Cube Trackball</b>
<b>Toggles 3D Cursor</b>
<b>Save Selected Viewport</b>
<b>Screen Capture</b>
<b>Export as Movie</b>

**Table 85 Viewport Menu Elements**

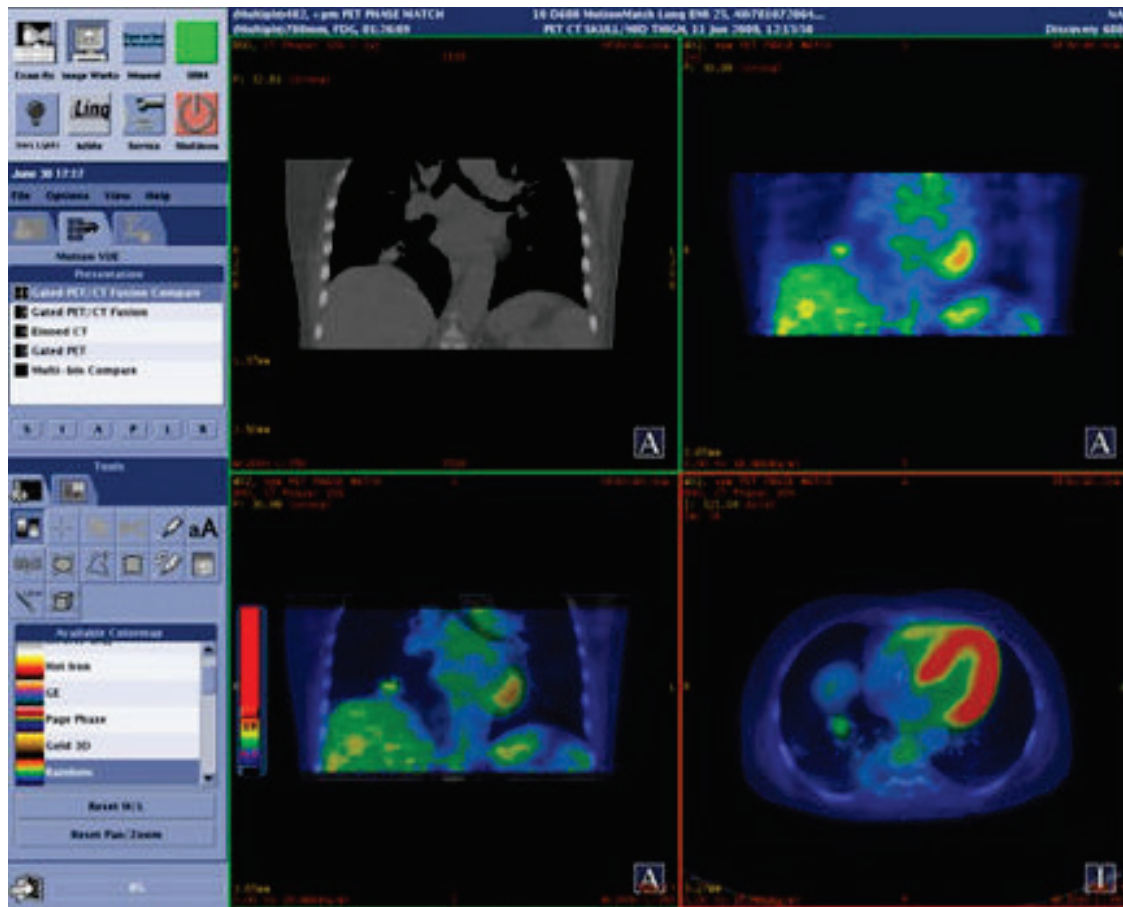
Name	Description
<b>Enlarge</b>	Move the cursor over a viewport and select <b>Enlarge</b> to display the active viewport as the only viewport.
<b>Reset Pan/Zoom</b>	Restores the image to the default magnification and original center coordinates.
<b>Reset W/L</b>	Restores the image to the default Window Width and Level.
<b>Hide Annotation</b>	Removes all annotation from all the viewports.
<b>Show All Annotations</b>	Displays all available annotation.
<b>Show Less Annotation</b>	Active only when you select <b>Show All Annotation</b> . Select <b>Show Less Annotation</b> to remove most of the annotation from the viewport display.
<b>Show/Hide Cube Trackball</b>	Toggles the cube trackball On and Off.
<b>Toggles 3D Cursor</b>	Toggles the 3D cursor On and Off.
<b>Save Selected Viewport</b>	Saves the selected viewport as a screen save in Image Works.
<b>Screen Capture</b>	Saves the screen with all visible viewports as a screen save in the Image Works browser.
<b>Export as Movie</b> (see <a href="#">Figure 244 on page 409</a> ).	Saves as a series of screen captures or viewport captures and sends them to the system or to the USB for use during presentations. Remember to hide all annotation before saving the series, to protect patient privacy.

**Figure 244 Export as Movie Window**

### 13.14.15 Use Motion VUE to Display Binned CTAC Images

1. Select the binned Cine CTAC series from the Image Works browser.  
The **Series Description** usually contains the phase percentage(s).
2. Click **Motion VUE**, then click **OK** to launch the application.  
Optional: Click a presentation description to update the display.
3. Move the cursor to the bottom of the viewport to display the Cine controls.  
Click **Play** to start the cine display. Click and drag the slider to increase or decrease the speed of the cine display
4. To stop the cine, move the cursor back to the bottom of the window to display the cine controls, then click the square **Stop** key.
5. Optional: Click **Options** to film the image or the screen.  
You can press **F1** to save the selected image, or press **F2** to save the entire display area as a single image.
6. Click the **Exit** icon to quit Motion Match and return to the Image Works browser.  
You also can click **File** in the toolbar, and click or drag to **Quit**.

**Figure 245 Initial Motion VUE Window**



# 14 PET Cardiac Imaging

## 14.1 PET Cardiac Imaging Introduction

This chapter contains procedures to set up a cardiac specific scan and optimize alignment between anatomy in the PET and CTAC series with PET Cardiac ACQC.

- Prepare the Patient for a Cardiac Study
- Acquire the Scout and CTAC Scans
- Optimize the alignment between the CT and PET series with PET Cardiac ACQC
- Reconstruct the PET images

### NOTE

If you plan to edit patient information, edit tracer information or anonymize the patient, wait until all PET Cardiac ACQC reconstructions have finished. If you change the patient or tracer information first, PET Cardiac ACQC will not work.

### NOTE

Cardiac VUE is called CardIQ Physio on the Advantage Workstation (AW).

### NOTE

This chapter contains information to perform cardiac perfusion imaging using Rb-82/ N-13 ammonia/O-15 bolus water studies where ViP Record is used to ViP Replay Gated and Dynamic imaging.

### NOTE

Review cardiac or respiratory gating trigger information for accepted, rejected, and total triggers for PET gated acquisitions using ACQC, Dynamic VUE, and/or Cardiac VUE.

## 14.2 Typical Cardiac R/S Workflow with Rb-82

This section describes a typical cardiac workflow.

Please refer to SNM or ASNC guidelines for detailed instructions, suggestions and explanations.

1. Prepare the patient before entering the scan room.
2. Position the patient on the table, open the exam and enter the information.  
Enter the tracer type into the **Tracer Information** window.
3. Acquire the CT Scout series.
4. Acquire the Rest CTAC series.
5. Inject the Rb-82.
6. Acquire the seven-minute Rest Static ViP Record mode series.

7. Administer the pharmacologic stress agent under direction of the physician.
8. Inject Rb-82 at appropriate time for the pharmacologic agent used.
9. Acquire the seven-minute Stress Static ViP Record mode series.
10. Acquire the Stress CTAC series (if you cannot align stress series to rest CTAC).
11. Optional: Return to CT.  
Repeat the series and select new CT protocol to proceed with CTCS and CTA.
12. At any time after the Static ViP Record acquisition:
  - a. ViP Replay — Gated and Dynamic
  - b. Retro Recon Gated and Dynamic
  - c. See [PET Cardiac VUE](#) to Reformat, Filter and Sum (AW) or [PET Dynamic VUE](#) to Sum (AW).
  - d. Review the cardiac or respiratory gating trigger information for accepted, rejected, and total triggers for PET gated acquisitions using ACQC, Dynamic VUE, and/or Cardiac VUE.
  - e. Optional: Dynamic TAC
  - f. Network data to designated destination(s).
  - g. Archive data.

## 14.3 Prepare the Patient for a Cardiac Study

Prepare the system and make sure everything is ready before escorting the patient into the scan room. Prepare the patient and apply the leads in the patient prep room.

1. Set out a supply of fresh, unexpired ECG electrodes.

### NOTE

Use electrodes made with silver/silver chloride (Ag/AgCl) gel on the pad. Do not use any additional gels.

2. Ask the patient if she consumed any caffeine containing substances, such as coffee, soda and over the counter analgesics in the previous 12 hours. If yes, alert the physician, as caffeinated substances could raise the heart rate.
3. Ask the patient if she engaged in any cardiovascular exercise before the exam. If yes, alert the physician.
4. Explain the exam to the patient.
5. Start an IV line.
6. Prepare the patient for lead placement.
  - a. Position the patient's arms above her head, preferably in the 10 o'clock to 2 o'clock position.
  - b. Do not position the electrodes over muscle, scar tissue or hair.  
If necessary, shave a four-square-inch area for each electrode.
  - c. Gently scrub the location with cotton gauze to remove the layers of dead skin.

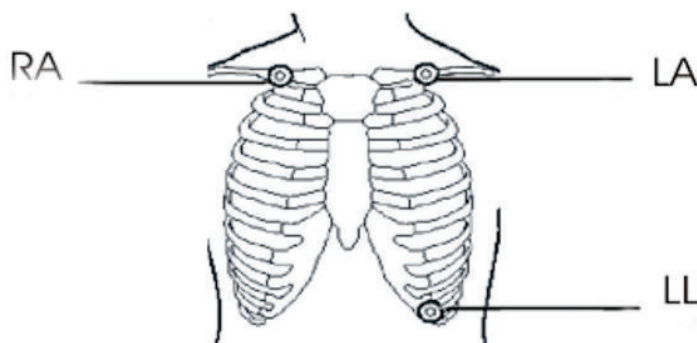
Do not use alcohol.

d. Dry the area well before attaching the ECG electrodes.

7. Apply the ECG electrodes and leads to the patient.

- For best results, position the electrodes over the clavicle, medial to the center of the clavicle, to avoid the muscle tissue. The electrical activity of muscle tissue can interfere with the ECG trigger.
- If the patient has scar tissue in a recommended area, refer to [Figure 247 on page 413](#) for alternate areas for electrode placement.

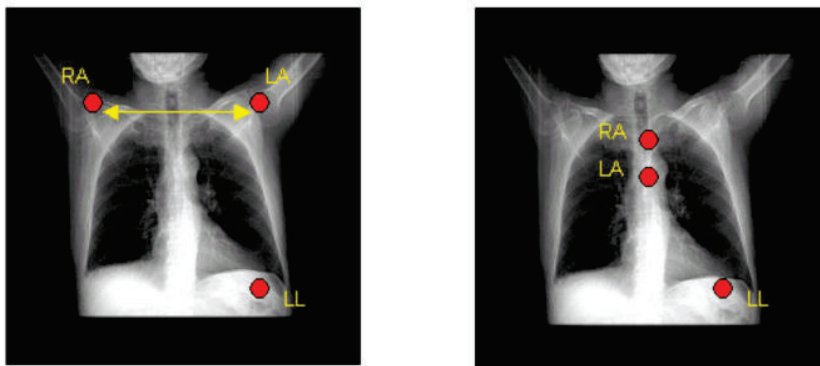
**Figure 246 Recommended Lead Placement Locations**



**Table 86 Recommended Lead Placement Locations**

Lead	US Lead Color	EU Lead Color	Physical Location
RA	White	Red	Right chest, mid clavicle
LA	Black	Yellow	Left chest, mid clavicle
LL	Red	Green	Left abdomen, below angle of ribs

**Figure 247 Alternate Electrode Locations for Signal Clarity**





**NOTE**

Monitor the ECG waveform for any irregular heart beat patterns before you start the exam acquisition. Alert the physician if you find irregularities.

## 14.4 Prepare the Scan Room and Position the Patient

1. Check the ECG monitor connections before escorting the patient into the scan room.
  - Is it plugged into the power outlet?
  - Is the cable connected between the ECG monitor and the PET/CT accessory panel?
2. Make sure the system has a cardiac protocol in the **User** tab ready for use.
3. Escort the patient into the scan room.
  - Position the patient supine, head first on the cradle.
  - Position the patient's arms above her head.
  - Use arm rest and leg rest sponges for patient's comfort.
4. Press the **Alignment Light** button to enable the alignment lasers.  
Center the patient in the Scan Field of View (CT bore isocenter) to optimize the exposure under AutomA or SmartmA control.
5. Follow the facility guidelines to align the patient's Sternal Notch or Xyphoid Process to the laser, and press the **Landmark** button.

## 14.5 Scan the Patient

Follow these instructions to scan a patient with a previously built cardiac protocol. To build a cardiac protocol, follow the instructions in [Build a Protocol](#).

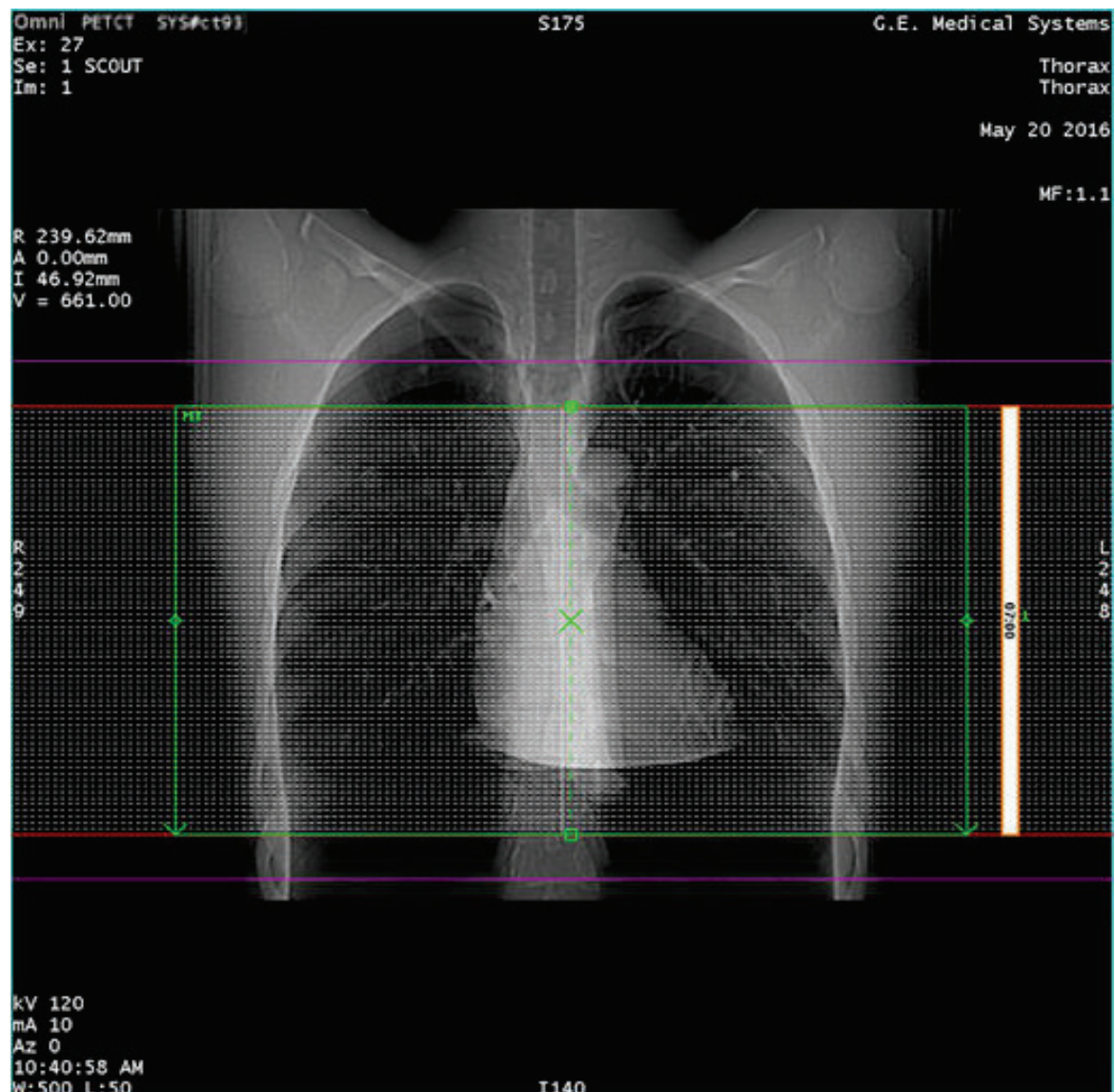
### 14.5.1 Acquire the Scout and CTAC Scans

Use the Scout to graphically prescribe the Start and End locations of the subsequent CTAC and PET scans, as well as the Display Field of View. The CTAC provides the PET scan attenuation map. You can reconstruct the CT images with a Standard or Soft filter.

1. Click **New Patient** and import the patient information from the Patient Schedule, or manually enter the patient information into the corresponding fields.
  - If you need detailed instructions, please refer to [Scan the Patient](#).
  - If your facility uses a custom protocol, make sure the **Inherit from Exam** button is not selected on the **Tracer Information** window.
2. Select the **PET/CT Cardiac** protocol you plan to use:
  - a. Click on the **Chest** in the **Anatomical Selector** (or click the default button).

- b. Select the **PTCT\_Rb\_REST-STRESS** protocol (your site can have a customized name).
  - c. Click **Accept** to proceed to the **Scout Acquisition** window.
3. Review the Scout Parameters, and modify as needed.
4. Make sure that no one other than the patient is in the scan room.
5. Make sure the patient orientation on the table matches the patient orientation icon on the **Scout Acquisition** window.
6. Click **Confirm** to initiate the scout scan sequence.
7. Press the flashing **Move to Scan** button to move the cradle to the start location.
8. Press the flashing **Start Scan** button to enable X-ray and scan the patient.  
Repeat the scan sequence, if the protocol calls for an AP and LAT scout.
9. Click **Next Series** from the protocol.  
If necessary, click **Show Localizer** to display the Graphic Rx Localizer over the scout image.

**Figure 248 Use the Graphic Rx Localizer to Prescribe the Start and End Locations**



10. Position the PET and CT scans to cover the area of the heart you plan to image.
11. Prepare to acquire the CTAC scan.
  - a. Review the CTAC protocol parameters, and modify as needed.
  - b. Review the **Recon 1** parameters, and verify the **DFOV** equals 70cm.
  - c. Review the selected protocol values, and modify as needed.
12. Review the **Recon 2** values, used for QC, and modify the parameters, as needed.

**NOTE**

You can select **Expert Mode** and use a calcium scoring protocol for the CTAC acquisition. The **Expert Mode** selection automatically selects a 70 cm FOV, a Soft algorithm, and creates a CTAC for attenuation correction.

13. Click **Confirm** to initiate the CTAC scan sequence.
14. Press the flashing **Move to Scan** button to move the cradle to the CT start location.
15. Press the flashing **Start Scan** button to enable X-ray and scan the patient.

## 14.5.2 Acquire the PET Rest Series

1. Click **PET** to display the PET scan protocol, typically called **PTCT\_Rb\_REST-STRESS**, but the name may vary if your facility customized the GE supplied protocol.
2. Review the PET protocol parameters and modify as needed.

**NOTE**

The system records the cardiac triggers and uses them during ViP Record for Gated. Update the gating parameters average rate prior to scanning.

3. Open the **Cardiac/Respiratory Trigger** tab, monitor the average triggers per minute, and enter the average heart rate at the time of scan.

Open the **Cardiac Trigger** window and continue to monitor the status throughout the acquisition. The message area turns red to alert you to sudden changes in status, such as the heart rate dropping out of range or a lead becoming dislodged.

4. Click **Confirm** to initiate the PET scan sequence.
5. Press the flashing **Move to Scan** button to move the table to the PET start location.
6. Simultaneously press the flashing **Start Scan** button and start the tracer.

**NOTE**

If your facility starts the scan on the patient heart rate, or some other determination, change the acquisition start time accordingly.

7. Open the **Cardiac Trigger** window and continue to monitor (and record) the heart rate and status throughout the acquisition.
8. Upon completion of the Rest phase of the scan, wait for the reconstruction to finish, then refer to [PET Cardiac ACQC](#) to check the alignment between the CT and PET images.\*

Save and record the ACQC shift vectors for later use.

\*For information on the AutoACQC application, refer to [Chapter 19 AutoACQC \(Optional\)](#).

## 14.5.3 Acquire the PET Stress Series

1. Click on PET Stress ViP Record group to display the PET scan protocol.
2. Review the PET protocol parameters and modify as needed.

#### NOTE

The system records the cardiac triggers and uses them during ViP Record for Gated. Update the gating parameters average rate prior to scanning.

3. Administer the pharmacologic stress agent under direction of the physician.
4. Open the **Cardiac/Respiratory Trigger** tab, monitor the average triggers per minute, and enter the new average heart rate at the time of scan.
5. Click **Confirm** to initiate the PET scan sequence.
6. If flashing, press **Move to Scan** to move the cradle to the PET start location.
7. Simultaneously press the flashing **Start Scan** button and start the tracer.

#### NOTE

If your facility starts the scan on the patient heart rate, or some other determination, change the acquisition start time accordingly.

8. Open the **Cardiac Trigger** window and continue to monitor the heart rate and status throughout the acquisition.
9. Upon completion of the Stress phase of the scan, wait for the reconstruction to finish, then refer to [PET Cardiac ACQC](#) to check the alignment between the CT and PET images.\*

Save and record the ACQC shift vectors for later use.

#### NOTE

If you can align the heart in the PET Stress images to the original CTAC series, and produce good images, you can release the patient. If you cannot generate good fused images with ACQC, proceed to [14.5 Scan the Patient on page 414](#), and acquire a separate CTAC for the PET Stress series.

\*For information on the AutoACQC application, refer to [Chapter 19 AutoACQC \(Optional\)](#).

### 14.5.4 PET Rest and Stress Series Post Processing Workflow

1. Click **PET Recon/Replay** and select the Rest Series with ViP Data.
2. Click **Select New Protocol** and select the cardiac acquisition protocol.
3. Select the Dynamic Rest Replay protocol from the list.  
Verify the scan parameters match your site preferences.
4. Click **Recon Options**.
  - Review and verify the previously saved Rest ACQC Shift Vectors. If they do not match your recorded values, change them.
  - Review and verify the Recon parameters, then close the **Recon Options** window.
5. Click **Confirm**.
6. After the ViP Replay completes, go back to the Scan Setup view and select the Dynamic Stress Replay Scan.

Verify the scan parameters match your site preferences for a Dynamic Stress Scan.

7. Click **Confirm**.

- Review and verify the previously saved Stress ACQC Shift Vectors. If they do not match your recorded values, change them.
- Review and verify the Recon parameters, then close the **Recon Options** window.

8. Click **Confirm**.

**NOTE**

Now that the Recon Queue contains several jobs, reconstruction will take a while to complete.

9. When the Rest Dynamic image reconstructions finish, load the Rest Dynamic images into Dynamic Vue and create a Time Activity Curve (TAC) to determine the Rest Gated Pre-Scan Delay.

10. Click **PET Recon/Replay**, and select the Rest Series with ViP Data.

Verify the Gated Rest Scan parameters match your site preferences.

11. Enter the **Rest Gated Pre-Scan Delay** from a previous step.

12. Click **Recon Options**.

- Review and verify the previously saved Rest ACQC Shift Vectors. If they do not match your recorded values, change them.\*
- Review and verify the Recon parameters, then close the **Recon Options** window.

13. Click **Confirm**.

14. When the Stress Dynamic image reconstructions finish, load the Stress Dynamic images into Dynamic Vue and create a TAC to determine the Stress Gated Pre-Scan Delay.

Record this value for use later in the procedure.

15. Click **PET Recon/Replay**, and select the Stress Series with ViP Data.

Verify the Gated Stress Scan parameters match your site preferences.

16. Enter the **Stress Gated Pre-Scan Delay** from a previous step.

17. Click [Recon Options].

- Review and verify the previously saved Stress ACQC Shift Vectors. If they do not match your recorded values, change them.\*
- Review and verify the Recon parameters, then close the **Recon Options** window.

18. Click **Confirm**.

19. Review the Rest and Stress Gated image sets for image quality.

Follow facility guidelines to continue post-processing in PET Cardiac VUE and/or other Cardiac processing packages.

**NOTE**

If you apply the 3D Cardiac filter to the reconstructed images, please check with the Cardiac post processing software to verify it does not apply 3D cardiac filter, as well.

**NOTE**

The amount of space used during ViP record depends upon the number of counts in the study, with higher count studies occupying more disk space. Check the SRM monitor **List file database used** area daily for the current ViP disk space occupancy.

**NOTE**

Review the cardiac or respiratory gating trigger information for accepted, rejected, and total triggers for PET gated acquisitions.

For information on the AutoACQC application, refer to [Chapter 19 AutoACQC \(Optional\)](#).

## 14.6 PET Cardiac ACQC

### 14.6.1 Introduction

ACQC stands for Attenuation Correction Quality Control.

This section explains how to use PET ACQC to:

- Display fused PET and CT cardiac images to determine alignment between the exams.
- Adjust the alignment between the PET and CT cardiac images.
- Request automated reconstruction of aligned PET Cardiac AC images.
- Manually initiate a PET Cardiac ACQC retrospective reconstruction.
- Review the cardiac or respiratory gating trigger information for accepted, rejected, and total triggers for PET gated acquisitions.

Figure 249 PET ACQC Tool Window



## 14.6.2 Set the PET Cardiac ACQC User Preferences

Follow this procedure to select the default color map and create a standard ACQC series description. You can change the series description during ACQC.

1. Select any qualifying series from the Image Works browser.
2. Click **ACQC** from the **Data Apps** list.
3. If the intermediate browser opens, then select a qualifying CTAC series.



**Figure 250 Options Menu**



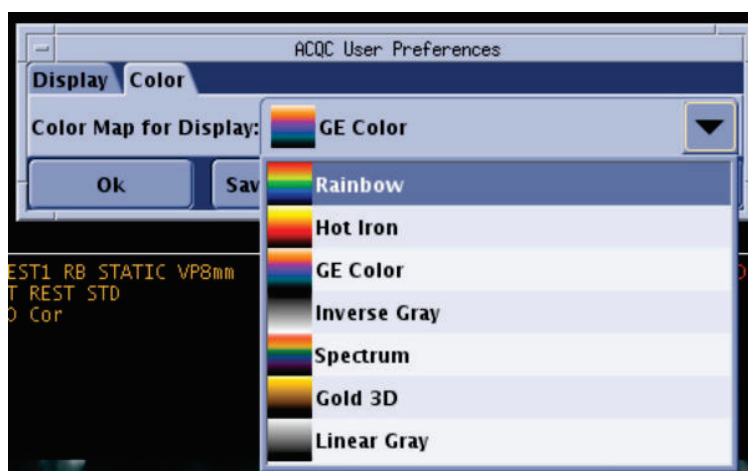
4. From the **ACQC Tool** window, select **Options > User Preferences** to open the **ACQC User Preferences** window.

**Figure 251 ACQC User Preferences Window**



5. Click the **Colors** tab.
  - Click the down arrow button to display the color map list.
  - Click or drag to a color map to select it as the default.

**Figure 252 Color Map List**



6. Click the **Display** tab to access the **Series Description** field.

**Figure 253 Series Description Field**

7. Type a default series description into the field.

**NOTE**

The series description appears in the browser, so choose an easy to identify name.

8. Click **Save Settings** to save the current color map selection and series description.
9. Click **OK** to close the **ACQC User Preferences** window.

The **ACQC Tool** window updates to show the new color map selection the next time you start an ACQC session.

10. Optional: Click the **Exit** icon to close ACQC and select another exam.

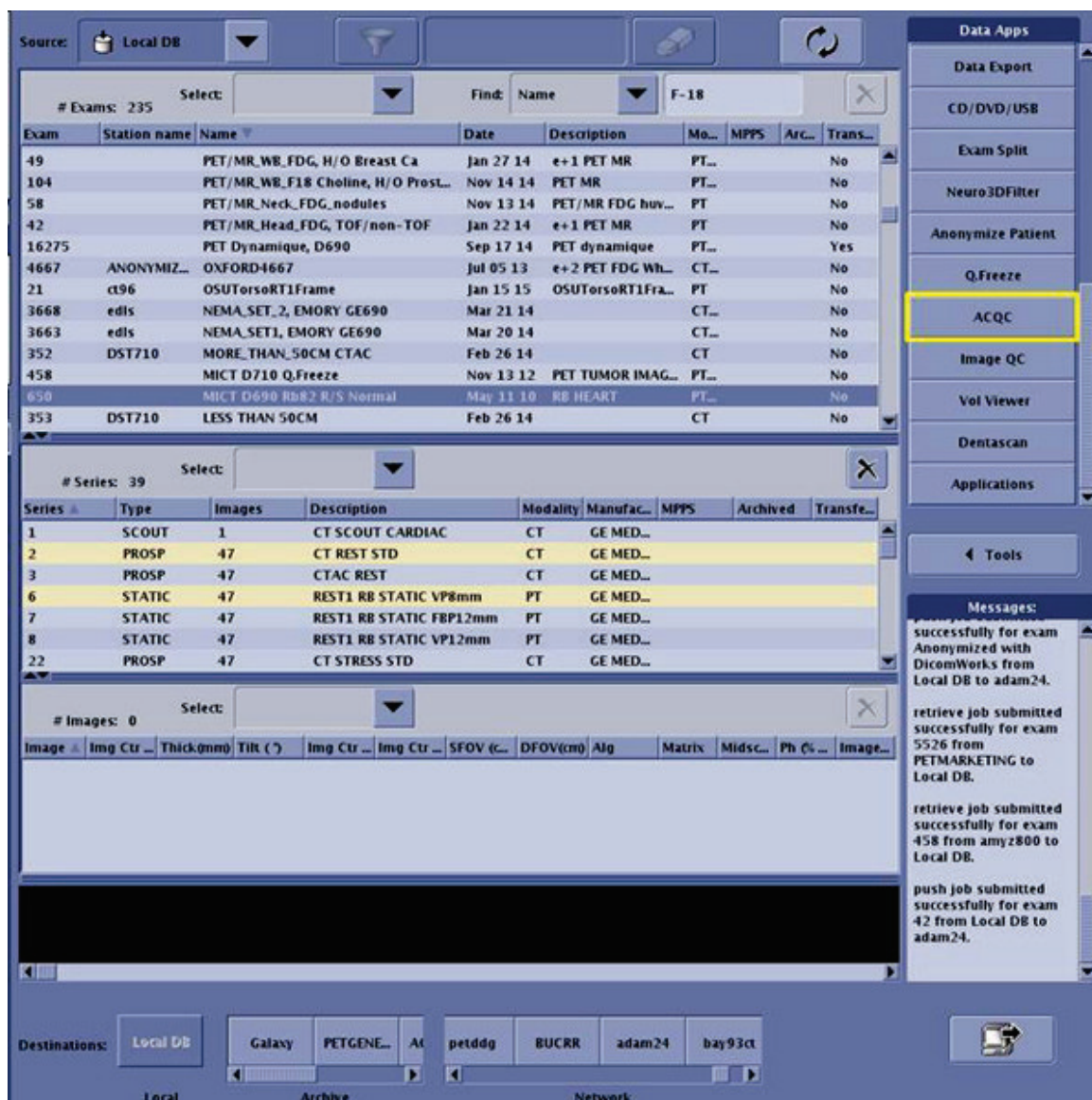
### 14.6.3 Start the PET Cardiac ACQC Application

Use the PET ACQC application to correct small differences in cardiac alignment between the CT and PET portions of the exam. Follow this procedure to select and align the PET and CT cardiac images, save the shift vectors and submit the images for retrospective reconstruction.

For information on the AutoACQC application, refer to [Chapter 19 AutoACQC \(Optional\)](#).

1. Select a study from the **Examinations** database on the Patient List. See [Figure 254 on page 424](#).
2. Click to highlight a PET series and one or two CT series from the list. You can select either a PET AC or PET NAC series.

Figure 254 Select PET and CT Series from the Image Works Patient Browser



3. Click **ACQC** from the **Data Apps** list on the right side of the browser. Your PET and CT series selections determine the next step.
  - If you select one CT series and one PET series, the **Edit Alignment** tab opens in the **ACQC Tool** window, and the software loads the images into the ACQC viewports. Proceed to **Step 6**.
  - If you select one PET series and two CT series, the **CT Selection** tab opens in the **ACQC Tool** window, and the software loads examples of the PET images fused with both CTAC series into the ACQC viewport. Select the CTAC you plan to use and the system updates the viewports and opens the **Edit Alignment** tab. Proceed to **Step 6**.

- If you select more than one PET series or more than two CT series, a Selection Table opens. Proceed to the next step.

**Figure 255 ACQC Selection Table**

**Selection Table**

Directions: Please select one PET series and up to two CT series from the lists below with which to perform alignment.

Patient ID: ANON650 Study ID: 650 Study Desc: RB HEART

**PET Datasets**

Series #	Series Desc	Series Date	Isotope	# Images
6	REST1 RB STATIC VP...	11 May 2010	Rubidium chloride	47
7	REST1 RB STATIC FB...	11 May 2010	Rubidium chloride	47
8	REST1 RB STATIC VP...	11 May 2010	Rubidium chloride	47

**CT Datasets**

Series #	Series Desc	Series Date	# Images
2	CT REST STD	11 May 2010	47
3	CTAC REST	11 May 2010	47

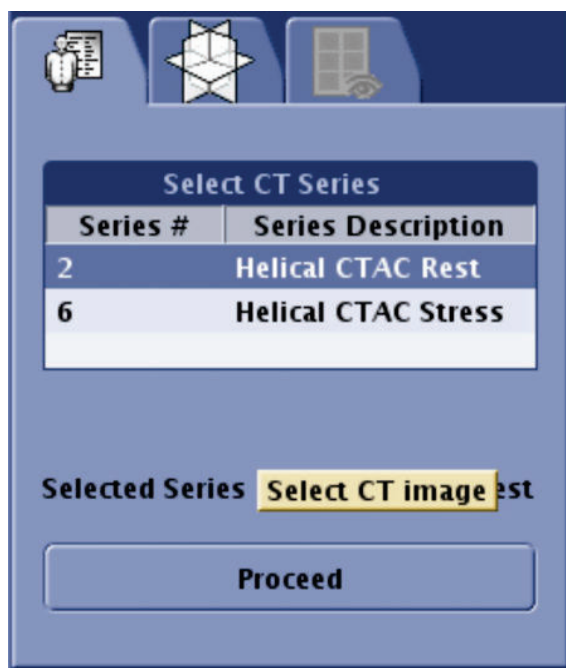
Accept Cancel

- Click to highlight the PET and CT series you plan to use. Click **Accept** to load the images into the application.

Proceed to **Step 6**.

- If you acquired separate Rest and Stress CTAC series, and select both series, the **CT Selection** tab opens in the **ACQC Tool** window. Click the CTAC series you plan to use, then click **Proceed** to display a single set of PET images fused with the CTAC you chose.

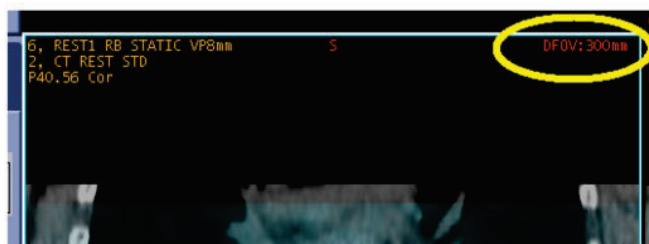
Proceed to the next step.

**Figure 256 CT Selection Tab**

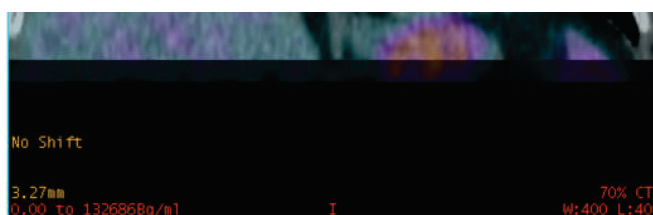
6. Click on the MIP Viewport, move the mouse to the bottom of the viewport, and click the play arrow to start Cine.
  - Rotate the MIP and examine the PET study.
  - Optional: Click and drag the slider to change the Cine speed.

**Figure 257 MIP Viewport Cine Buttons**

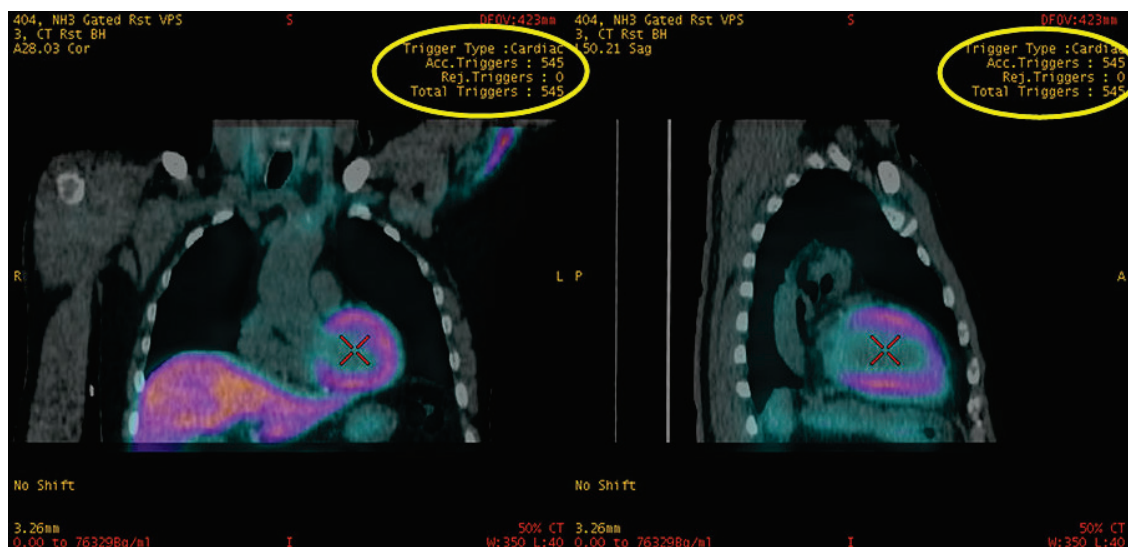
7. Optional: Adjust the image magnification with the Zoom function.
  - Move the cursor over the DFOV control in the upper right corner of the viewport.
  - Click-middle and drag the mouse left to right.
  - Click-right on the DFOV annotation to zoom in; click-left to zoom out.
  - Manually change the zoom value: Move the cursor over the red annotation in the (non MIP) viewport, type a new value and press **Enter**.

**Figure 258 DFOV Control in the Upper Right Corner**

8. Optional: Change the CT Window Width and Level and/or PET scaling value.
  - Position the cursor over a viewport, click-middle and drag the cursor from the top to the bottom of the viewport to change the PET scaling value.
  - Position the cursor over the PET scaling value in the lower left corner of the corresponding viewport, then click-middle and drag the cursor to the left and right.
  - Position the cursor over the CT W/L control in the lower right corner of the corresponding viewport, then click-middle and drag the cursor toward the top and bottom of the viewport to change the CT Window.
  - Click the **Reset W/L** button to return to the original Window Width and Level values.

**Figure 259 CT (right corner) and PET (left corner) Window Width and Level Values**

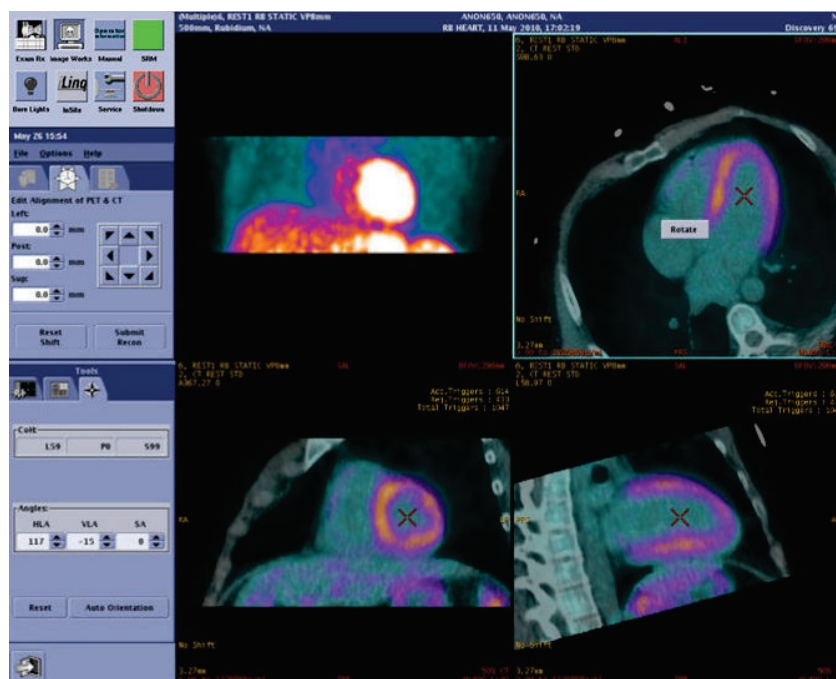
9. Optional: Move the area of greatest interest to the center of the viewport (Pan function).
  - Move the cursor over the area of interest, then click and drag this area to the center of the viewport, or move the cursor over the red orientation annotation (**S** in [Figure 258 on page 427](#), or **I** in [Figure 259 on page 427](#)), middle-click and drag to reposition the image in the viewport.
  - Click the **Reset Pan Zoom** button to recenter the image and return it to its original size.
10. Optional: Review the cardiac or respiratory gating for accepted, rejected, and total triggers for PET gated acquisitions. You can find this information in both the lower left and lower right viewports, in the top right corner of each. Take note of the trigger information for future reference.

**Figure 260 Trigger Information**

11. Scroll to select the best fused image.
  - Right-click and drag the 3D cursor (red crosshair) to page through the fused views.
  - Check the alignment of the fused PET and CT images to verify good agreement in the position of the two scans.
12. To better understand the alignment between the PET and CT images, adjust the balance of blending between the PET and CT images.
 

Move the cursor over the % blend annotation, then middle-click and drag to the left and right to change the visible CT percentage of each non MIP image, or position the cursor over the % blend annotation and click the right and left mouse buttons to incrementally increase and decrease the amount of CT in the images.
13. Adjust the oblique reorientation of the views to better visualize the alignment between the PET and CT images. You can adjust the reorientation of the cardiac volume two ways:
  - **Option 1: Auto Orientation**
    - a. Click the **Orientation** tab to display the corresponding window.
    - b. Click **Auto Orientation** to automatically reorient the standard transaxial views (axial, sagittal, coronal) to the standard cardiac views (SA, VLA, HLA).
  - **Option 2: Manual Orientation**
    - a. Right-click on a non MIP viewport to display the **Rotate** button over the viewport.

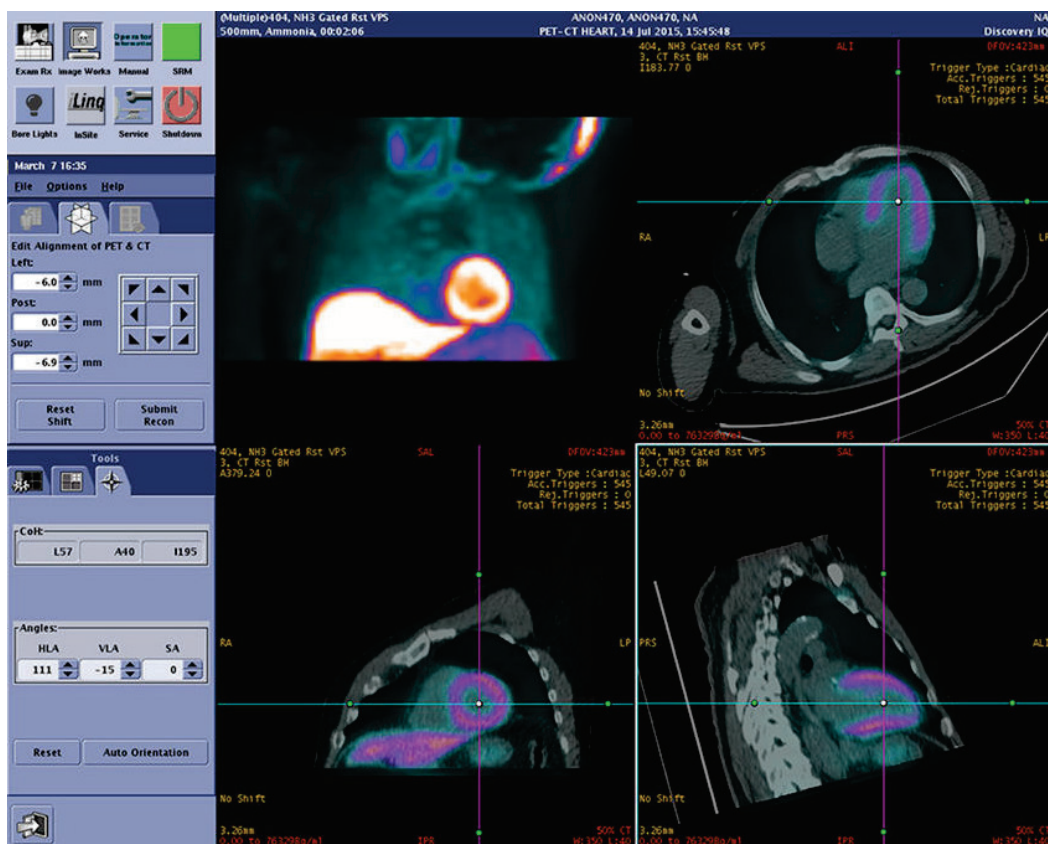


**Figure 261 Right-Click to Display the Rotate Button**

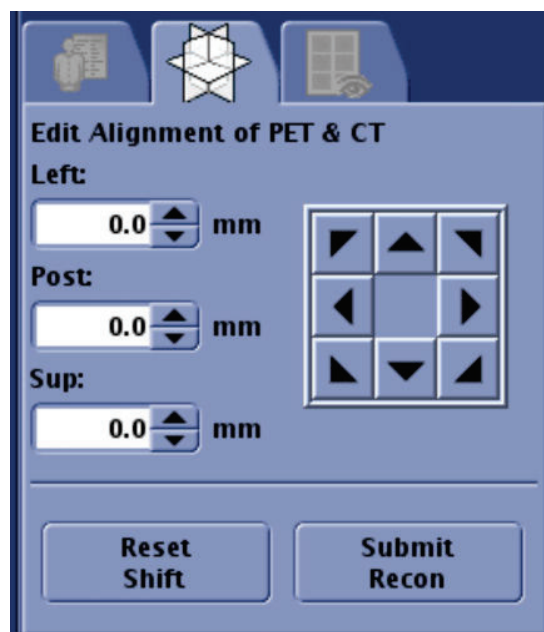
- Left-click on the **Rotate** button to display crosshairs over the Axial, Sagittal and Coronal viewports, as shown in [Figure 262 on page 430](#).
- Left-click on the white dot in the center of the crosshairs and move the crosshairs to the center of the heart chamber.
- Left-click on the green dots to rotate the crosshairs, which in turn rotate the chamber.



Figure 262 Manually Change Image Orientation

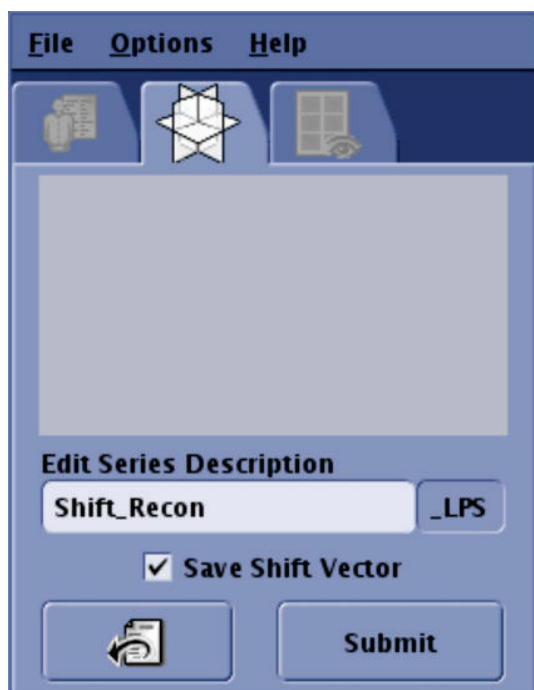


14. Use one of the following methods to shift the PET data to align it to the CT data:
  - **Option 1:** Press and hold the **SHIFT** key with one hand; middle-click and drag to move the PET data, relative to the CT image.
  - **Option 2:** Click on a viewport to select it, then click the eight arrows in the **Alignment** tab, shown in [Figure 263 on page 431](#), to move the PET image relative to the CT image.
  - **Option 3:** Click on the Left, Posterior and Superior fields to activate them, then enter values into the corresponding text boxes.
    - Positive values move the PET image in the Left, Posterior and Superior directions.
    - Negative values move the PET image in the Right, Anterior and Inferior directions.
15. Optional: Click **Reset Shift** to return to the original alignment, and start over.

**Figure 263 ACQC Tools Alignment Tab**

16. When you like the alignment, click **Submit Recon**.
17. The **Alignment** tab updates to display a **Recon Submission** window, with the current default series description on display.

You can edit the Series Description at this time.

**Figure 264 ACQC Tools Alignment Tab — Recon Submission window**

18. Optional: Select the **Save Shift Vector** check box to save the shift vectors to the database for use during subsequent retrospective reconstructions.

- **Option 1:** Click **File** and click or drag to **Save State** to save an **ACQC Save State** to the image browser without submitting a reconstruction request.

Click the  button to return to the **Alignment** tab (Figure 263 on page 431).

#### NOTE

The system stores all **ACQC Save States** for the selected exam in Series 99 with the series description, **ACQC SS**.

- **Option 2:** Select the **Save Shift Vector** check box before you click **Submit** in the **Protocol Selection** window. This sequence saves an **ACQC Save State** to image browser series 99, in addition to submitting the reconstruction request.
19. Click **Submit** to initiate an AC PET reconstruction with the currently prescribed alignment between the PET and CT images.
- If you chose Option 2, this action also saves an **ACQC Save State** to the image browser in addition to submitting the reconstruction request.
20. When the “**Submitting to recon...**” message appears, click **OK**.
21. Click **Exit** in the lower left corner of the **ACQC Tools** window to close the application.
- If you are checking alignment during a study, and you need to acquire a second CTAC, click **Exam Rx** to return to the study.

## 14.7 Manually Initiate PET Cardiac ACQC Retro Recon

Use this method to start a retrospective reconstruction when you clicked **File > Save State** without submitting a reconstruction request during the PET Cardiac ACQC session.

1. Select **PET Retro Recon/Replay**.
2. Select the exam and series you plan to reconstruct.
3. Click **Select Series** to display the corresponding **Scan Reconstruction** window.
4. Select the **Recon Options** tab (Axial image tab).
5. Click **Recon Option** button to open the **Reconstruction Parameter** window.
  - The Left, Posterior and Superior values that you saved in the **ACQC Save State** correlate to the values that appear on the retrospective reconstruction window.
  - The CTAC selection list displays the CT series you used to align the PET image set.
  - Review the reconstruction parameters, and modify if necessary.
6. Click **OK** to accept the current reconstruction parameters and close the window.
7. Click **Confirm** to reconstruct the images with the designated series and shift vectors.

## 14.8 PET Cardiac Imaging Quick Steps

### 14.8.1 Set up the Patient for a Cardiac Study

1. Plug in the ECG and connect it to the PET/CT accessory panel.
2. Ask the patient about caffeine consumption and cardiovascular exercise.
3. Explain the exam to the patient.
4. Position the patient on the cradle in the Supine, Head First orientation.
5. Prepare the patient for lead placement.
6. Apply the electrodes and attach the leads.
7. Monitor the ECG waveform for irregularities prior to scanning.

### 14.8.2 Acquire the Scout and CTAC Series

1. Click **New Patient** and fill in the data fields.
2. Select the PET Cardiac REST Gated protocol you plan to use.
3. Align the patient to gantry isocenter and landmark on the **SN** or **XY**.
4. Review and modify the scout scan parameters, as needed.
5. Make sure the scan room is free of all persons except the patient.

6. Make sure the patient orientation on the table matches the patient orientation icon on the Scout Scan window.
7. Click **Confirm**.
8. Press the flashing **Move to Scan** button.
9. Press the flashing **Start Scan** button.
10. Repeat the scan sequence, if the protocol calls for an AP and LAT scout.
11. Click **Next Series** to display the **CT Acquisition** window.
12. If necessary, click **Show Localizer** to display the Graphic Rx Localizer.
13. Position the CT and PET scans to cover the area of the heart you want to image.
14. Review the CTAC protocol parameters, and modify as needed.
15. Review the Recon 2 parameters, used for QC, and modify as needed.
16. Click **Confirm** to initiate the CTAC scan sequence.
17. Press the flashing **Move to Scan** button.
18. Press the flashing **Start Scan** button.

### 14.8.3 Acquire the PET Rest Series

1. Click **PET** to display the PET acquisition window.
2. Review the PET protocol parameters, and modify as needed.
3. Open the **Cardiac/Respiratory Trigger** tab, monitor the average triggers per minute, and enter the average heart rate at the time of scan.
4. Click **Confirm** to initiate the PET scan sequence.
5. Press the flashing **Move to Scan** button to move the table to the PET start location.
6. Simultaneously press the flashing **Start Scan** button and start the tracer.
7. Open the **Cardiac Trigger** window and continue to monitor the heart rate and status throughout the acquisition.
8. Upon completion of the Rest phase of the scan, wait for the reconstruction to finish, then use ACQC to align the PET and CTAC images.
9. Save and record the ACQC shift vectors for later use.

For information on the AutoACQC application, refer to [Chapter 19 AutoACQC \(Optional\)](#).

### 14.8.4 Acquire PET Stress Series

1. Click **Next Series**.
2. Review the PET protocol parameters, and modify as needed.
3. Administer the pharmacologic stress agent.

4. Open the **Cardiac/Respiratory Trigger** tab, monitor the average triggers per minute, and enter the average stressed heart rate at the time of scan.
5. Click **Confirm**.
6. If flashing, press **Move to Scan**.
7. Simultaneously press the flashing **Start Scan** button and start the tracer.
8. Open the **Cardiac Trigger** window and continue to monitor the heart rate and status throughout the acquisition.
9. Upon completion of the Stress phase of the scan, wait for the reconstruction to finish, then use PET ACQC to check the alignment between the CT and PET images.
10. Save and record the ACQC shift vectors for later use.
11. If you cannot align both sets of PET images to original CTAC series with ACQC, acquire an additional CTAC series to use with the PET Stress images.

For information on the AutoACQC application, refer to [Chapter 19 AutoACQC \(Optional\)](#).

### 14.8.5 PET Rest and Stress Series Post Processing Workflow

1. Click **PET Recon/Replay** and select the Rest Series with ViP Data.
2. Click **Select New Protocol** and select the cardiac acquisition protocol.
3. Select the Dynamic Rest Replay scan from the list.
4. Click **Recon Options** and review/verify the parameters.
5. Click **Confirm**.
6. Select the Dynamic Stress Replay scan from the list.
7. Click **Recon Options** and review/verify the parameters.
8. Click **Confirm** and wait for the Reconstruction Queue to empty.
9. Load the Rest Dynamic images into Dynamic Vue and create a Time Activity Curve (TAC) to determine the Rest Gated Pre-Scan Delay.
10. Click **PET Recon/Replay**, and select the Gated Rest Replay scan.
11. Enter the Rest Gated Pre-Scan Delay.
12. Click **Recon Options** and review/verify the parameters.
13. Click **Confirm** and wait for the Reconstruction Queue to empty.
14. Load the Stress Dynamic images into Dynamic Vue and create a TAC to determine the Stress Gated Pre-Scan Delay.
15. Click **PET Recon/Replay**, and select the Gated Stress Replay scan.
16. Enter the Stress Gated Pre-Scan Delay.
17. Click **Recon Options** and review/verify the parameters.
18. Click **Confirm**.
19. Review the Rest and Stress Gated image sets for image quality.

20. Follow facility guidelines to continue post-processing in PET Cardiac VUE and/or other Cardiac processing packages.

### 14.8.6 Manually Initiate PET Cardiac ACQC Retro Recon

1. Click **PET Recon/Replay**.
2. Select the exam and series you plan to reconstruct.
3. Click **Select Series**.
4. Select the **Recon Options** tab.
5. Click **Recon Option** and review/modify the reconstruction parameters, including the corresponding CTAC and shift vectors.
6. Click **OK**.
7. Click **Confirm** to reconstruct the images.

For information on the AutoACQC application, refer to [Chapter 19 AutoACQC \(Optional\)](#).

### 14.8.7 Set the PET Cardiac ACQC Preferences

1. Select a series from the Image Works browser.
2. Click **ACQC**.
3. If the intermediate browser opens, then select the corresponding CTAC series.
4. Select **Options > User Preferences**.
5. Click the **Colors** tab.
6. Select a colormap from the drop down menu.
7. Click the **Display** tab.
8. Type a default series description into the **Series Description** data field.
9. Click **Save Settings**.
10. Click **OK**.

Optional: Click **Exit** to quit ACQC and select another exam.

### 14.8.8 Start the PET Cardiac ACQC Application

1. Select a series from the Image Works browser.
2. Click **ACQC**.
3. If the intermediate browser opens, select the CT series that most closely matches the PET series you plan to use and click **Accept**.
4. Rotate the PET MIP and examine the PET study.
5. Optional: Use the Zoom feature to adjust image magnification.
6. Optional: Change the Window Width and Level.

7. Optional: Click and drag the area of interest to the center of the viewport (Pan).
8. Optional: Review the cardiac or respiratory gating for accepted, rejected, and total triggers for PET gated acquisitions.
9. Use the 3D cursor to scroll through the images.
10. Adjust the blending balance.
11. Adjust the oblique reorientation of the views.
12. Shift the PET data to align it to the CT data.
13. Click **Submit Recon** to open the **Recon Submission** window.
14. Click the **Save Shift Vector** check box to save the shift vectors to the database.
15. Click **Submit** to save the ACQC Save State then click **OK** to retrospectively reconstruct the images.

or

Click **File > Save State** to save an ACQC Save State to the image browser without submitting a reconstruction request.

16. Click **Exit** to close the PET Cardiac ACQC application.

For information on the AutoACQC application, refer to [Chapter 19 AutoACQC \(Optional\)](#).

### 14.8.9 Start the PET Cardiac VUE Application

1. Select 1-3 PET series from the Image Works browser.
2. Click **Cardiac VUE**.
3. If the intermediate browser opens, select up to three PET series you plan to use and click **Accept**.
4. If the intermediate browser prompts for the series study type, select one from the dropdown menu.
5. Optional: Recenter the ROI over the heart on all the displayed image sets.
6. Optional: Review the cardiac or respiratory gating for accepted, rejected, and total triggers for PET gated acquisitions.
7. Check the angles and slices and optimize as needed, while monitoring the corresponding VLA, HLA, and SA images on all the displayed image sets.
8. Select the Review screen to process and display the cardiac data.
9. Review the Splash screen images.
10. Display the Five Slice screen and review the images.
11. If you selected a Gated image set, display the ED/ES screen and review the images.
12. Click **File** then click or drag to **Save**.
13. Click **File** then click or drag to **Save As** and follow facility guidelines to Save State, Save a DICOM series and/or capture the screen.
14. Click **Exit** to close the PET Cardiac VUE Application. Refer to [PET Cardiac VUE](#) for more information.



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# 15 FDG Viability Cardiac

## 15.1 FDG Viability Cardiac Introduction

This chapter contains procedures to set up an FDG Viability Static Cardiac scan and Cardiac VUE post-processing instructions.

- Prepare the patient for a cardiac study
- Acquire the scout and CTAC scans
- Optimize the alignment between the CT and PET series with PET Cardiac ACQC
- Reconstruct the PET images
- Use Cardiac VUE for image post-processing
  - Set user preferences
  - Display images with Cardiac VUE

For information on the AutoACQC application, refer to [Chapter 19 AutoACQC \(Optional\)](#).

### NOTE

If you plan to edit patient information, edit tracer information or anonymize the patient, wait until all PET Cardiac ACQC reconstructions have finished. If you change the patient or tracer information first, PET Cardiac ACQC will not work.

### NOTE

Cardiac VUE is called CardIQ Physio on the Advantage Workstation (AW).

## 15.2 Typical Cardiac FDG Viability Workflow

This section describes a typical FDG viability static scan workflow.

Please refer to the SNM or ASNC guidelines for detailed instructions, suggestions and explanations.

1. Prepare the patient for the F-18 FDG injection using site preference guidelines (SNM and ASNC have recommendations on their prospective websites).
2. Inject the F-18 FDG dose and record the appropriate information (syringe pre-dose activity and time, syringe post-dose activity and time, and injection time).
3. Keep patient quiet and still for the site preferred uptake time, open the exam on the console, enter the patient and dose information, escort the patient to the scan room and position him on the scanner and landmark on the **SN** or **XY** landmark (site preference).
4. Acquire the CT scout series.
5. Acquire the CTAC series.
6. Acquire the FDG viability 10-minute static scan.

7. Check the FDG viability measured attenuation (MAC) and the CTAC in the Image Quality layout to assure that the PET and CT are aligned.
8. Perform cardiac reformat using Cardiac VUE.
9. Network and archive using site preferences.

## 15.3 PET Cardiac VUE

Cardiac VUE is a single application for display and analysis of Cardiac PET images. You can use Cardiac VUE to evaluate patients with suspected or known coronary artery disease. Cardiac VUE aids in assessing myocardium viability, myocardial perfusion, and wall motion of gated PET Cardiac slices.

### NOTE

Cardiac VUE is called CardIQ Physio on the Advantage Workstation (AW)

Use Cardiac VUE to:

- Reformat the data in the standard cardiac orientations.
- Analyze the myocardial perfusion by the VLA, HLA and SA obliques generated from the selected input data.
- Compare myocardial perfusion in rest, stress, and viability studies.
- Generate synchronized, gated-beating slices to view wall motions.
- Compare myocardial perfusion of corrected and uncorrected data sets.

You can customize Cardiac VUE to:

- Mask out activity of neighboring organs with high uptake characteristics, such as the liver and the spleen, with the volume and slice masking function.
- Generate short axis images with a specified pixel size with reconstruction zoom. Reconstruction zoom controls the reconstruction limit locators to avoid image truncation.
- Process three sets of data with different sets of recon/reformat parameters.
- Customize and apply 3D filtering.
- Review the cardiac or respiratory gating trigger information for accepted, rejected, and total triggers for PET gated acquisitions.

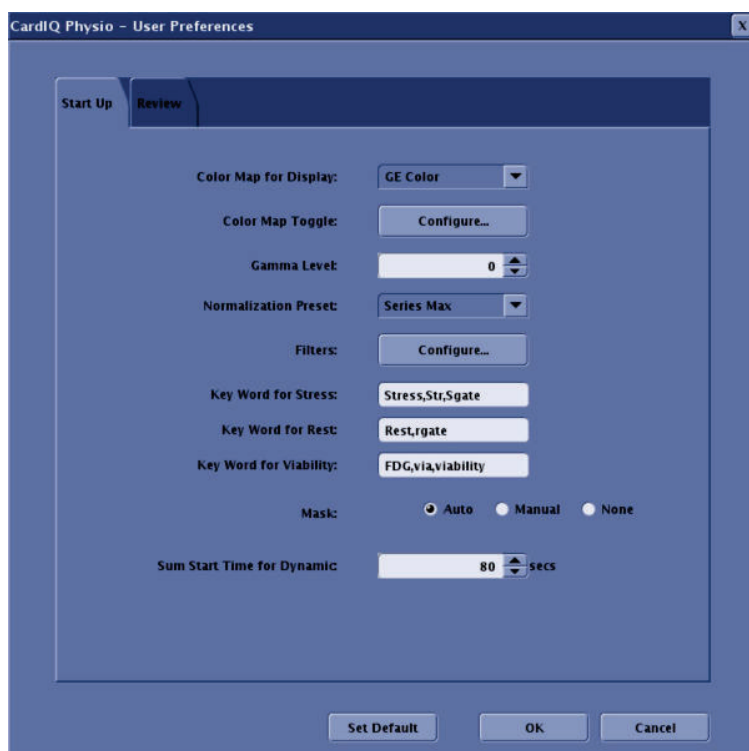
## 15.4 Set User Preferences

Follow these instructions to set default parameters and designate the response Cardiac VUE makes to certain key-clicks and display buttons. While you can return to this window at any time, most facilities establish and use a single set of standards.

Click **Options > Preferences** to open the Cardiac VUE (CardIQ Physio) Options Menu.

**Figure 265 Cardiac VUE (CardIQ Physio) Options Menu**

Refer to the following illustrations, descriptions and related instructions to understand user preferences.

**Figure 266 Cardiac VUE (CardIQ Physio) User Preferences**

1. **Color Map for Display:** Sets the color map the software uses when it displays the initial set of Cardiac VUE images. You can select different color maps from the list on the **Window Level** tab in the display tool area throughout the Cardiac VUE session.

Click on the arrow and drag to the color map on the drop down menu.

**NOTE**

Each new color map and/or image scaling selected for a certain series is applied across all the corresponding SA, VLA, and HLA images.

2. **Color Map Toggle:** Click **Configure...** to select the three most popular color maps. During Cardiac VUE operation, press **F5**, to sequence through the designated color maps.
  - a. Click **Options > Preferences**.
  - b. Click **Configure...** to open the **Color Map Toggle** window.

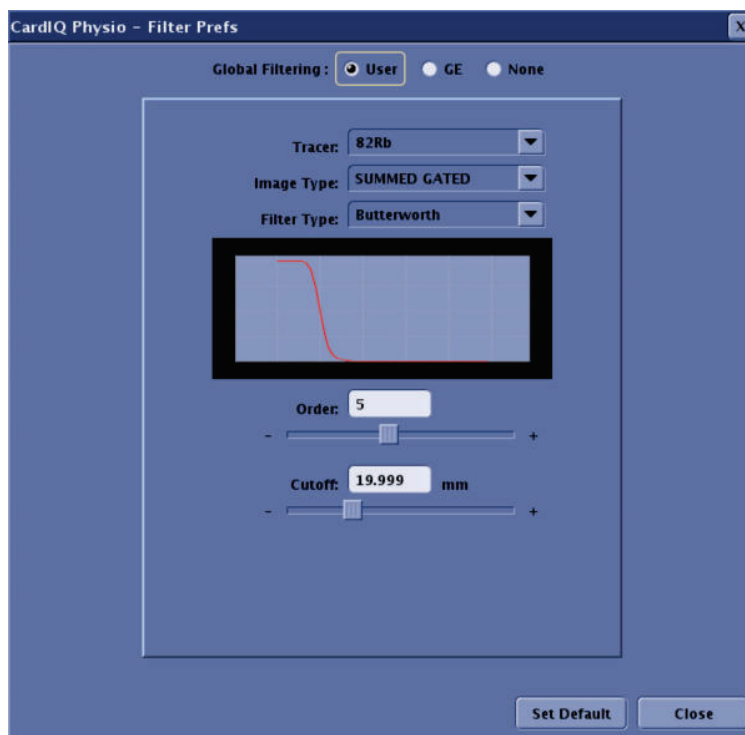
**Figure 267 Cardiac VUE (CardIQ Physio) — Color Map Toggle Window**



- c. Click each arrow and drag to a color map to select it.
  - d. Click **OK** to accept the currently displayed color maps for use during this session, and close the window. The color maps reset to the original defaults when you close the current session.
  - e. Click **Set Default** button to set the current selections as the new default. Click **OK**.
  - f. Click **Cancel** to discard the current selections and close the window without change.
3. **Gamma Level:** Determines the initial starting position and gamma value of the Gamma slider bar on the **Window Level** tab.  
Click the up/down arrows to increase or decrease the displayed value, or enter a new value into the field.
4. **Normalization Preset:** Determines the default color map scaling selection the system uses when you stop clicking the forward or backward Cine buttons.
  - Click the arrow and select **Global Max** or **Series Max** as the default.
  - The **Global Max** selection scales all the images against the highest threshold value in the entire exam.  
The **Series Max** selection scales each series against the highest threshold value in the corresponding series.
5. **Filters:** Click **Configure...** to select the applied filter for a specified image type, radiopharmaceutical, and summing status of the selected series.
  - a. Click the **Global Filtering** radio button, and follow facility guidelines to set up the global filtering parameters. Or, click the **GE** radio button to display GE's recommended filter matrix. These recommendations are the factory default.
  - b. Click the **None** radio button to display the filter matrix with no filters selected.

- c. Click **Set Default** to save the current selection(s) as the new default. The system displays a status message. Click **OK** to close the message.
- d. Click **Close** to return to the **User Preferences** window.

**Figure 268 Cardiac VUE (CardIQ Physio) - Filter Preferences Window**

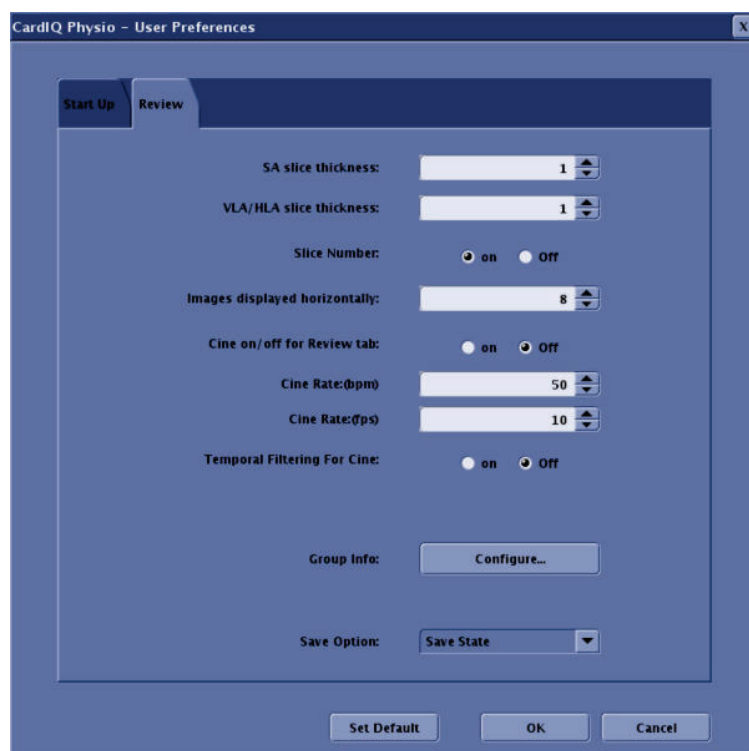


6. **Key Word for Stress:** Determines the search parameters to identify the series type.  
Enter the words or abbreviations into the field, separated by commas, that you commonly use to describe the current scan when you enter the series description.
7. **Key Word for Rest:** Determines the search parameters to identify the series type.  
Enter the words or abbreviations into the field, separated by commas, that you commonly use to describe the current scan when you enter the series description.
8. **Key Word for Viability:** Determines the search parameters to identify the series type.  
Enter the words or abbreviations into the field, separated by commas, that you commonly use to describe the scan type when you type the series description.
9. **Mask:** Determines the initial state of the Masking selection on the **Reformat** tab when Cardiac View displays the first set of images.
  - Click the **Auto** radio button to set Masking to Auto.
  - Click the **Manual** radio button to set Masking to Manual.
  - Click the **None** radio button to set Masking to None.

10. **Sum Start Time for Dynamic:** Determines the start time for summation of a dynamic series. The system removes the number of frames specified by the time entry, then sums the subsequent frames of data.

Click the up/down arrows to increase or decrease the displayed sum start time, or enter a value into the field.

**Figure 269 Cardiac VUE (CardIQ Physio) - User Preferences - Review Tab**



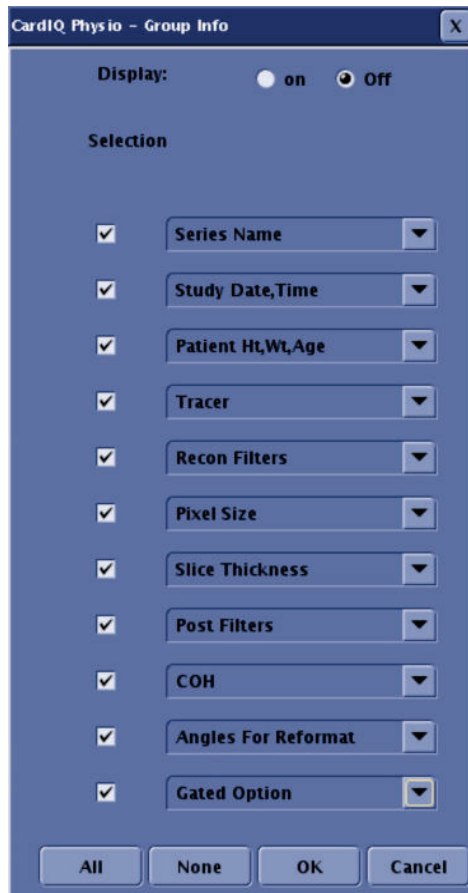
11. **SA Slice Thickness:** Determines the thickness of the SA slices in mm by 1 = thickness of 1 PET image slice and 2 = thickness of 2 PET image slices, etc.
- Click the up/down arrows to increase or decrease displayed slice thickness, or enter a value into the field.
12. **VLA/HLA Slice Thickness:** Determines the thickness of the VLA and HLA slices in mm by 1 = thickness of 1 PET image slice and 2 = thickness of 2 PET image slices, etc.
- Click the up/down arrows to increase or decrease displayed gamma value, or enter a new value into the field.
13. **Slice Number:** Hides or displays the slice number on each image viewport.
- Click the **On** radio button to display the slice numbers in the viewports, or enter a new value into the field.
  - Click the **Off** radio button to turn the slice number annotation OFF.

14. **Images displayed horizontally:** Determines the maximum number of display viewports in each row of the Splash and ED/ES windows. The number of series chosen determines the maximum number of rows on the window.  
  
Click the up/down arrows to select **6, 8, 10** or **12** images per row. Or, enter the number into the field.
15. **Cine on/off for Review tab:** Determines the state of the cine player when you click **Review**.
  - Click the **On** radio button to automatically play the cine images whenever you click to display the Review tab.
  - Click the **Off** radio button to pause the cine until you manually start it.
16. **Cine Rate: (bpm)** Determines the default beats per minute displayed in the **Cine Speed** field when you click the bpm radio button.  
  
Click the up/down arrows to increase or decrease the displayed speed, or enter a new value into the field.
17. **Cine Rate: (fps)** Determines the default frames per second displayed the **Cine Speed** field when you click the **fps** radio button.  
  
Click the up/down arrows to increase or decrease the displayed speed, or enter a new value into the field.
18. **Temporal Filtering for Cine:** Determines the availability of the **Temporal Filtering** check box on the **Cine** tab.
  - Click the on radio button to activate the **Temporal Filtering** check box. You then can check the box to apply temporal filtering to the Cardiac VUE images.
  - Click the **Off** radio button to disable the **Temporal Filtering** check box.
19. **Group Info:** Click **Configure...** to open the selector window to select the parameters, and they are displayed when you click the **Group Information** check box on the **Review** tab.
  - a. **Display:** Click the on radio button to automatically check the box and display the group information when you open a Cardiac VUE window. Click the Off radio button to leave the check box empty. In both cases, you can check or remove the check box to display or hide the Group Information.
  - b. Check the box to the left of each field to display the corresponding information when you check the Group Information check box on the **Review** tab.
  - c. Click the down arrow to open the menu. See the illustration below. You can change the display order by changing the location of menu item on the list.
  - d. Click **All** to check all the boxes and display the corresponding information.
  - e. Click **None** to remove the checks from all the boxes.
  - f. Click on individual boxes toggle the check mark on or off.
  - g. Click **OK** to accept the current configuration as the new default and close the window.
  - h. Click **Cancel** to close the window with the current selections in place. The next time you enter Cardiac VUE, the parameters revert to most recent default.



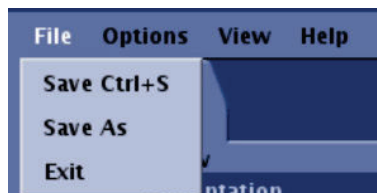
- i. The changes will not take effect until you click **Set Default** and close User Preferences.

**Figure 270 Select the Group Information parameters to display**

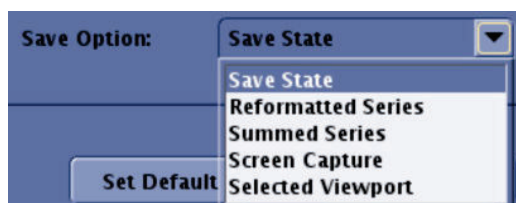


20. **Save Option** : Determines the behavior of the File > Save function, shown in the illustration below.
  - a. Click the **Save Option** arrow to open the **File Save** menu.

**Figure 271 File Save Menu**



- b. Click or drag to program the Cardiac VUE **File > Save** function format.

**Figure 272 Save Option Menu**

21. Accept or reject the current User Preference selections:

- Click **OK** to accept the currently selected parameters for the current session. The parameters return to the default setting when you close the session.
- Click **Set Default** to make the currently displayed parameters the new User Preference defaults. The software uses the User Preferences parameters to display the initial set of Cardiac VUE images and program the **Reformat** and **Review** tabs.
- Click **Cancel** to discard the current selections and close the window.

## 15.5 Remaining Option Menu

This section provides a brief description of the remaining Options Menu items. The previous section described the first item on the **Cardiac VUE (CardIQ Physio) Options** Menu.

**Figure 273 Cardiac VUE (CardIQ Physio) Options Menu**

**Table 87 Cardiac VUE (CardIQ Physio) Options**

Number	Name	Description
1	<b>Series Info</b> or <b>Ctrl+M</b>	<p>Display a list of information and attributes for each series. See <a href="#">Figure 274 on page 449</a>.</p> <ul style="list-style-type: none"> <li>Click and drag the slider to display all the information.</li> <li>Click the labeled tab to display the corresponding series information.</li> <li>Click <b>Save to File</b> to open a directory browser. Select a directory and click <b>Save</b> to store the series attributes.</li> </ul>
2	<b>Tracer Information</b> or <b>Ctrl+T</b>	<p>Edit the tracer information, as long as the Cardiac VUE <b>Window Level</b> tab displays the <b>kBq/ml</b> or <b>uCi/ml</b> Units selection. See <a href="#">Figure 275 on page 449</a>.</p> <ul style="list-style-type: none"> <li>The system displays the current header values in the <b>Tracer Info</b> window</li> <li>Follow facility guidelines to set the date/time formats.</li> <li>The system refuses to activate the <b>OK</b> button until the required inputs are present and valid.</li> <li>You can <b>Cancel</b> out at any time.</li> </ul>
3	<b>Film Selected Image</b> or <b>F1</b>	Send the currently selected viewport to the filmer.
4	<b>Capture Screen</b> or <b>F2</b>	Send all of the viewports in the image display area to the filmer as a single image.
5	<b>Capture Region</b> or <b>F3</b>	Not used in this software version.

Figure 274 PET Cardiac Review – Series Info Window

CardIQ Physio – Series Info

Series 1 Series 2

Series Attributes

Field Name	Value
Patient Name	10 D600S Rb82 R/S Normal
Patient ID	AW281276890.378.12749016...
Study Identifier	650
Study Description	RB HEART
Study Date Time	11 May 2010 17:14:53
Patient Height	1.83 Meters
Patient Weight	98 kgs
Patient Sex	
Patient Age	Not Available
Patient DOB	Not Available
Referring Physician	
Reading Physician	Not Available
Accession Number	
Scanner Manufacturer	GE MEDICAL SYSTEMS
Scanner Model	Discovery 690

Save to File OK

Figure 275 PET Cardiac Review – Tracer Info Window

PET Cardiac Review – Tracer Info

Units

☒ Metric Units  
☐ English Units

Patient Information:

☐ Male Patient Height: 170.00 cms  
☒ Female Patient Weight: 82 kgs

Tracer Information:

☒ MBq  
☐ mCi

Measured Tracer Activity: 0.0 at : : on : : :  
Administered: at : : on : : :  
Patient Scanned With: at 09 : 31 : 54 on 2004 : 04 : 10  
Post Injection Measured: 0.0 at : : on : : :  
Isotope: 13N 9.97m Half-life

OK Cancel

## 15.6 View Menu

Click **View** to toggle the Header and/or Colorbar On and Off.

**Figure 276 Cardiac VUE (CardIQ Physio) View Menu**



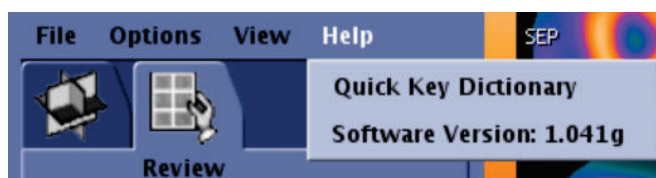
**Table 88 Cardiac VUE (CardIQ Physio) View Menu**

Menu Item	Description
<b>Show/Hide Header</b> or <b>Ctrl + H</b>	Select this function to toggle the display screen header information On and Off.
<b>Show/Hide Colorbar</b>	Select this function to toggle the Colorbar and slider to the left of the display area On and Off.

## 15.7 Help Menu

1. Click **Help** to display the menu. This information may change after a system software update.

**Figure 277 Help Menu**



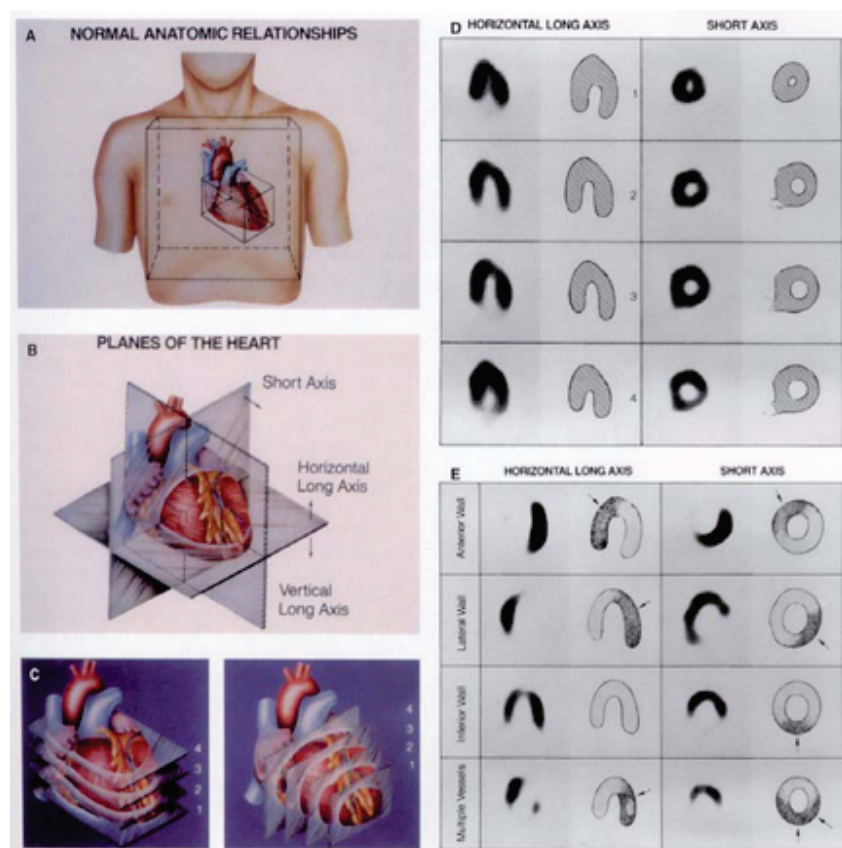
2. Click **Quick Key Dictionary** to open a list of keyboard shortcuts. Click and drag on the slider to viewer all the shortcuts.

**Figure 278 Cardiac VUE (CardIQ Physio) — Quick Key Dictionary**

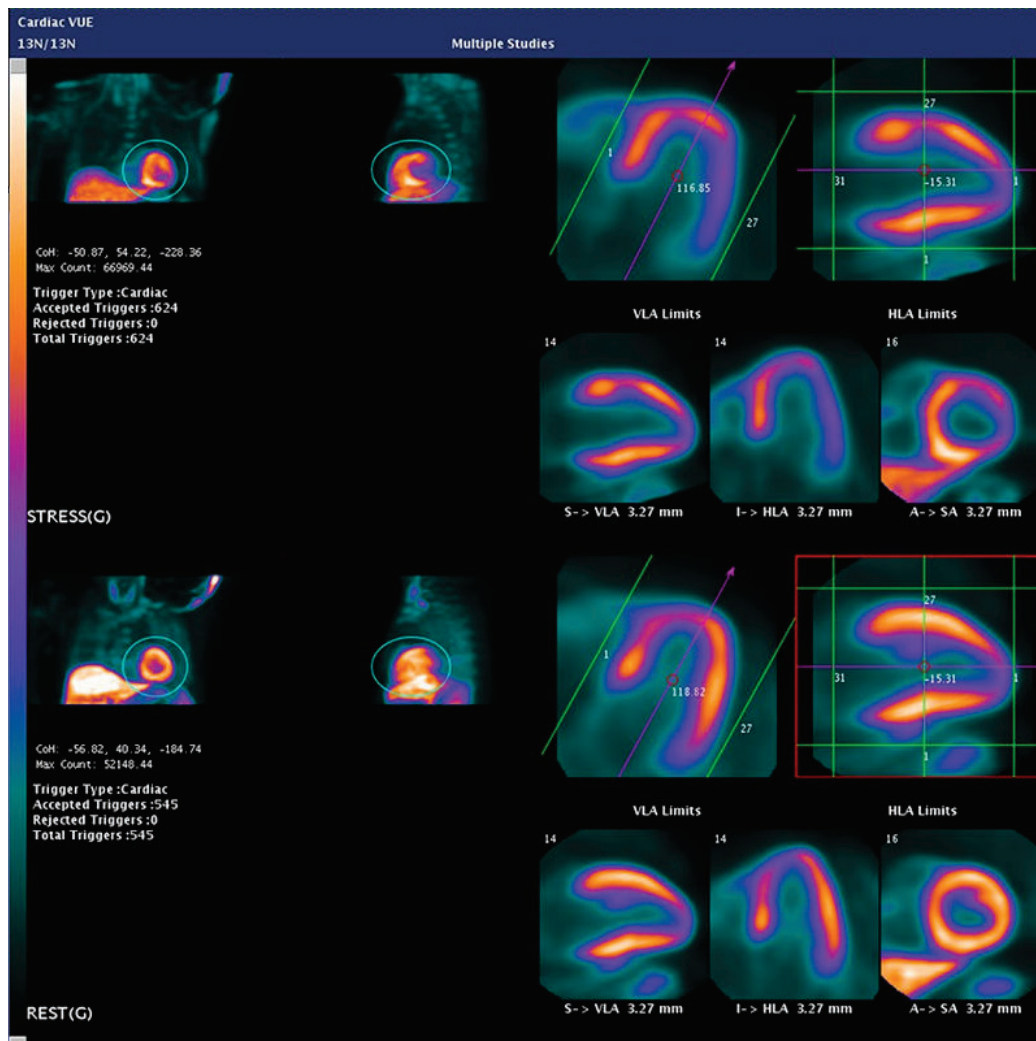
CardIQ Physio – Quick Key Dictionary	
F1	Film Selected Image
F2	Capture Screen
F5	PET color maps
CTRL+S	Save
CTRL+M	Series Info
CTRL+H	Show/Hide Header
CTRL+T	Tracer Information
Up/Right arrow	Moves one image forward all series
Down/Left arrow	Moves one image backward all series
CTRL+Up/Right arrow	Moves one image forward one series
CTRL+Down/Left arrow	Moves one image backward one series
Page Up	Full step forward in location all series
Page Down	Full step backward in location all series
CTRL+Page Up	Full step forward in location one series

## 15.8 Display Images with Cardiac VUE

Follow these instructions to select series that qualify for display with Cardiac VUE. The illustrations below are for education and reference purposes. See the SNM cardiac guidelines for additional information.

**Figure 279 Display Anatomy**

## FDG Viability Cardiac



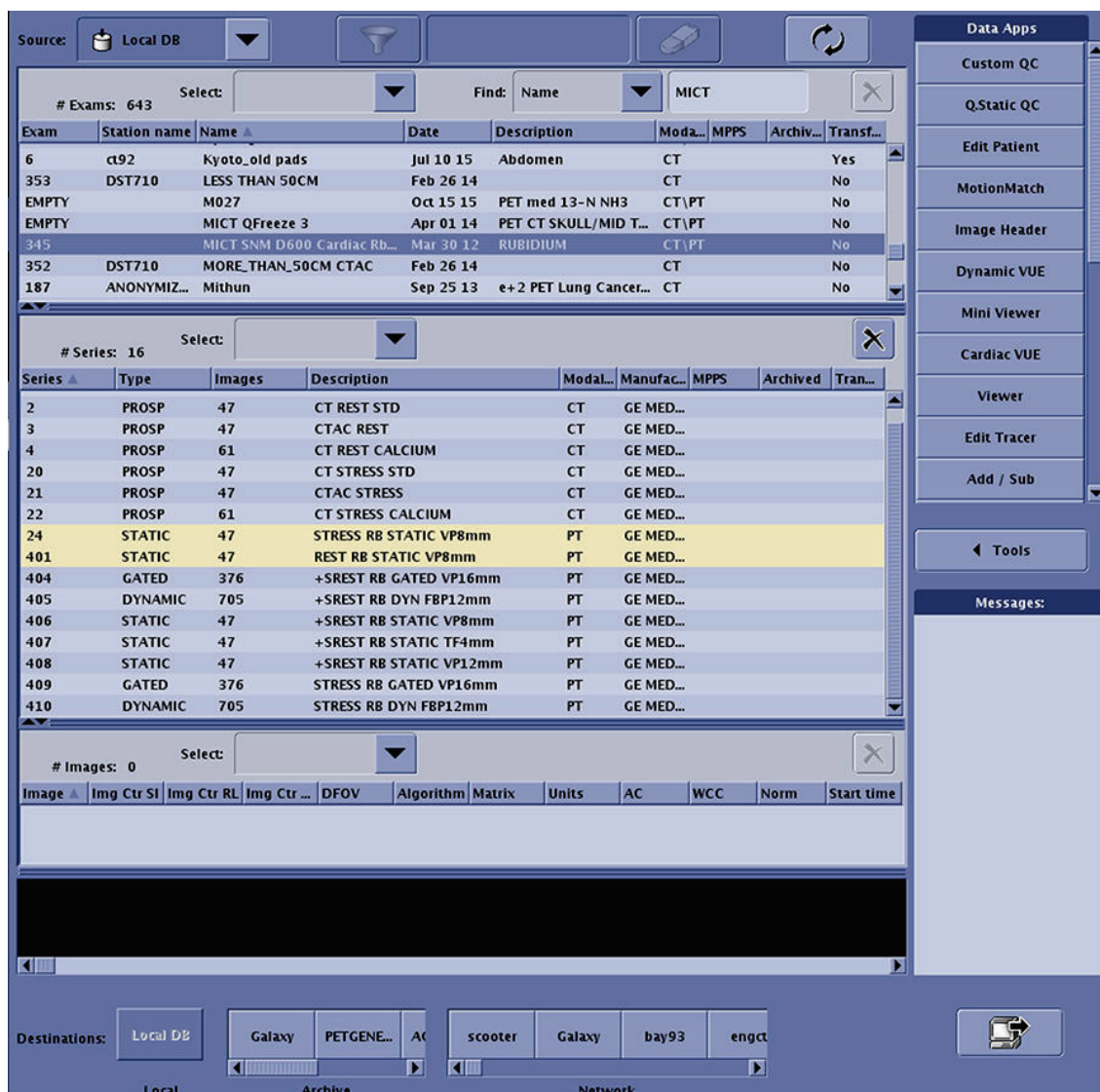
## NOTE

Cardiac triggers are now displayed in Cardiac VUE.







**Figure 280 Image Works Browser with Two Series Selected**

3. Click **Cardiac VUE** from the **Data Apps** list on the right side of the browser.
  - If you select one, two or three PET series, the software loads the images into the viewports and opens the **Cardiac VUE Tool** window on the **Reformat** tab.  
Proceed to Step 8.
  - If you select more than three PET series, an intermediate selection window opens.  
Proceed to Step 5.
  - If you select an ambiguously labeled series, the intermediate selection window prompts you to identify the PET study type.  
Proceed to Step 7.

- If you select series from more than one exam, the system displays a different intermediate selection window.

Proceed to Step 4.

**Figure 281 Intermediate Selection Window for Multiple Exam Selections**

**Selection**  
Patient Name: ANON470

Selected	Series Date	Series Desc	# Images	Modality	Matrix
<input type="checkbox"/>	14 Jul 2015	NH3 Rest 15m	79	PT	192x192
<input type="checkbox"/>	14 Jul 2015	NH3 Static Rst VPS	79	PT	192x192
<input type="checkbox"/>	14 Jul 2015	NH3 Dynamic Rst VPS	1501	PT	192x192
<input type="checkbox"/>	14 Jul 2015	NH3 Gated Rst VPS	1264	PT	192x192
<input type="checkbox"/>	14 Jul 2015	NH3 Static Rst VPS2	54	PT	192x192
<input type="checkbox"/>	14 Jul 2015	Static Rst QC200	54	PT	192x192

Patient Name: ANON471

Selected	Series Date	Series Desc	# Images	Modality	Matrix
<input type="checkbox"/>	14 Jul 2015	NH3 Str 15m	79	PT	192x192
<input type="checkbox"/>	14 Jul 2015	NH3 Static Str VPS	54	PT	192x192
<input type="checkbox"/>	14 Jul 2015	NH3 Dynamic Str VPS	1501	PT	192x192
<input type="checkbox"/>	14 Jul 2015	NH3 Gated Str VPS	1264	PT	192x192
<input type="checkbox"/>	14 Jul 2015	NH3 Static Str VPS	79	PT	192x192
<input type="checkbox"/>	14 Jul 2015	Static Str QC200	54	PT	192x192

**Selected Series**

Accept Cancel

- Select the series you plan to use from each exam.

Follow the next steps to select and identify the series you plan to use. When you click **Accept** the system displays the following message: **“Selected data sets belong to different patients!”** Check to make sure you selected different exams for the same patient, then click **OK** to proceed.

Proceed to the next step.

- If you select more than three PET series, the system opens an intermediate selection window. Check up to three boxes to select the corresponding series.

**Figure 282 Intermediate Selection Window**

Selection  
Patient Name: MICT SNM D600 Cardiac Rb 5ACC

Selected	Series Date	Series Desc	# Images	Modality	Matrix
<input type="checkbox"/>	23 Apr 2012	STRESS RB STATIC VP8mm	47	PT	128x128
<input type="checkbox"/>	23 Apr 2012	STRESS RB STATIC TF4mm	47	PT	128x128
<input type="checkbox"/>	23 Apr 2012	STRESS RB STATIC VP12mm	47	PT	128x128
<input type="checkbox"/>	23 Apr 2012	+SREST RB GATED VP16mm	376	PT	128x128
<input type="checkbox"/>	23 Apr 2012	+SREST RB DYN FBP12mm	705	PT	128x128
<input type="checkbox"/>	23 Apr 2012	+SREST RB STATIC VP8mm	47	PT	128x128

Selected Series

Accept Cancel

6. As you check each box, the system displays the corresponding series information and the tentative study type in the data field.

If the system correctly identified the study types, click **Accept**.

Proceed to Step 8.

**Figure 283 Intermediate Selection Window with Correct Study Type Query**

Selection  
Patient Name: MICT SNM D600 Cardiac Rb 5ACC

Selected	Series Date	Series Desc	# Images	Modality	Matrix
<input checked="" type="checkbox"/>	23 Apr 2012	STRESS RB STATIC VP8mm	47	PT	128x128
<input type="checkbox"/>	23 Apr 2012	STRESS RB STATIC TF4mm	47	PT	128x128
<input type="checkbox"/>	23 Apr 2012	STRESS RB STATIC VP12mm	47	PT	128x128
<input checked="" type="checkbox"/>	23 Apr 2012	+SREST RB GATED VP16mm	376	PT	128x128
<input type="checkbox"/>	23 Apr 2012	+SREST RB DYN FBP12mm	705	PT	128x128
<input type="checkbox"/>	23 Apr 2012	+SREST RB STATIC VP8mm	47	PT	128x128

Selected Series

Series Date: 23 Apr 2012 Series Desc: STRESS RB STATIC VP8mm # Images: 47 Modality: PT Matrix: 128x128 Stress 82Rb

Series Date: 23 Apr 2012 Series Desc: +SREST RB GATED VP16mm # Images: 376 Modality: PT Matrix: 128x128 Rest 82Rb

Accept Cancel

7. The system looks for the key words you entered into the **User Preference** data fields to identify the selected study type as: Stress, Rest or Viability. If the system incorrectly identifies the selected series, or displays **Unknown** in the data field, click on the corresponding arrow to display the Study Type selection list.

Click or drag to the correct Study Type, then click **Accept**.

Proceed to the next step.

**Figure 284 Intermediate Browser with Unknown Study Types**

**Selection**  
Patient Name: 10 D600 MotionMatch Lung BMI 25

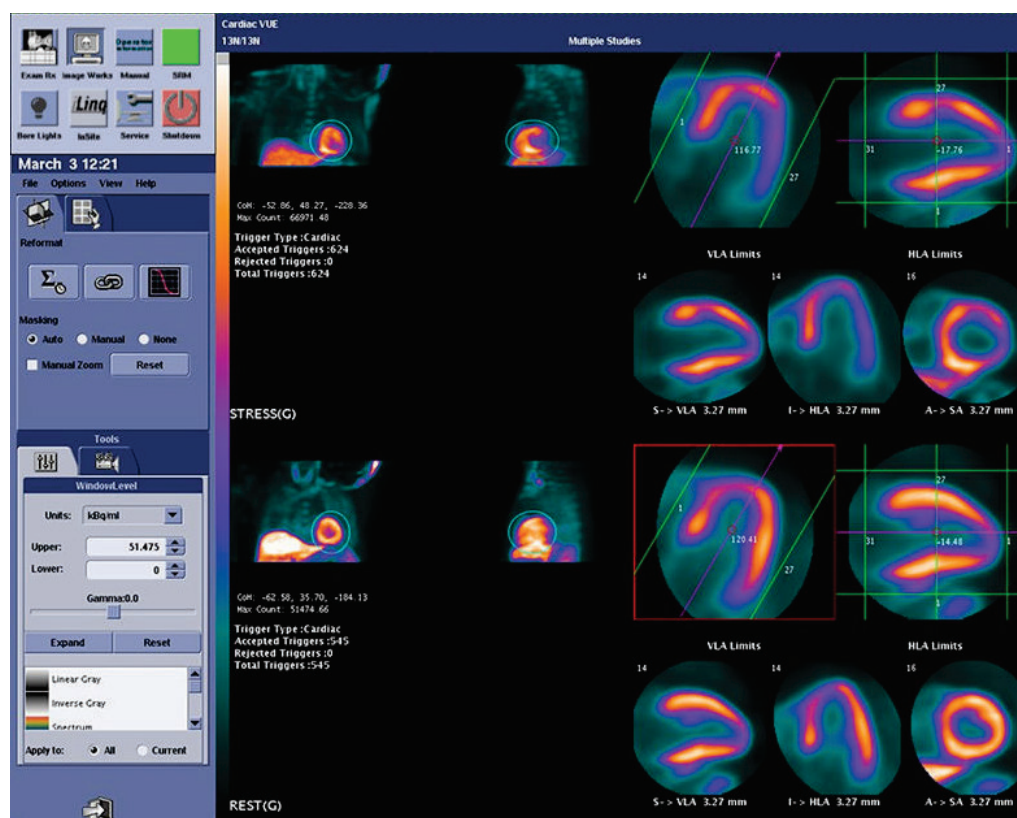
Selected	Series Date	Series Desc	# Images	Modality	Matrix
<input type="checkbox"/>	11 Jun 2009	WB 3D MAC	299	PT	192x192
<input type="checkbox"/>	11 Jun 2009	WB 3D NAC	299	PT	192x192
<input type="checkbox"/>	11 Jun 2009	Resp Static MAC	47	PT	192x192
<input checked="" type="checkbox"/>	11 Jun 2009	Resp Gated MAC	235	PT	192x192
<input checked="" type="checkbox"/>	11 Jun 2009	+pm PET PHASE MATCH	235	PT	192x192
<input type="checkbox"/>	11 Jun 2009	+pm PET PHASE MATCH	235	PT	192x192

**Selected Series**  
 Series Date: 11 Jun 2009 Series Desc: Resp Gated MAC # Images: 235 Modality: PT Matrix: 192x192  
 Series Date: 11 Jun 2009 Series Desc: +pm PET PHASE MATCH # Images: 235 Modality: PT Matrix: ...

Unknown 18F  
 Unknown 18F  
 Stress  
 Rest  
 Viability  
 Unknown

Accept Cancel

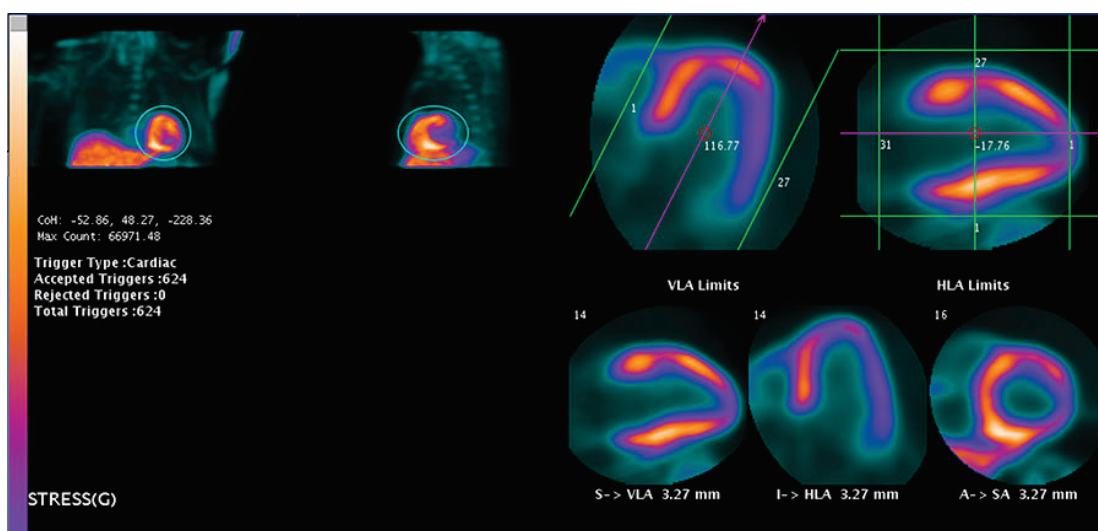
8. Cardiac VUE follows the User Preferences to set up the initial display. Your User Preferences will determine how your initial display looks. Follow facility guidelines to establish and use a standardized display format.

**Figure 285 Cardiac VUE****NOTE**

Cardiac triggers are now displayed in Cardiac VUE.

9. Center the ROI over the heart.
  - a. Click over an image to activate its viewport, as indicated by the red box.
  - b. Click on the ROI ellipse over one of the volumes on the left side of the screen. Click and drag the edges to resize the ROI and/or left-click and drag the center crosshair to reposition the ROI over the image.
  - c. The other images in the series update when you release the mouse button.
  - d. Left-click and drag the green lines in the VLA or HLA Limits image viewports to enlarge or decrease the area delineated by the green lines.
  - e. Left-click and drag the circle on the pink lines to reposition and center the lines.
  - f. Left-click and drag on either end of the pink line, to change the angle of intersection.
  - g. The other images in the series update when you release the mouse button.


**Figure 286 Optimize the Image Display**



10. Click and drag the mouse up and down over the image to optimize the Window Width and Level. If visible, the color bar along the left side of the display area updates to show the current W/L scaling.

#### NOTE

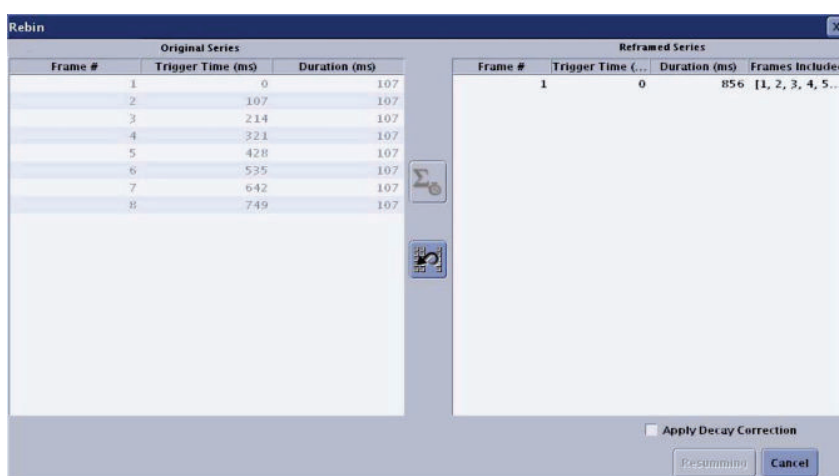
If you forget the name of a button, hover the cursor over it. After a second or two, a label identifies the button or provides a brief description of its function.


11. Optional: Click the **Summing**  button on the **Reformat** tab to Rebin and Reframe the series. Use this function to remove the blood pool from the image.
  - a. The **Rebin** window opens with a list of all frames in the **Original Series** on the left, and the **Reframed Series** on the right.
  - b. Rebin opens with the **Reframed Series** containing all the frames.
  - c. Click the **Undo** button to clear the **Reframed Series** area and enable **Summing**.



- d. Click to highlight the frames you plan to sum. You have the option to press and hold **Ctrl** while you click on individual frames to highlight them for selection, or press and hold **Shift** while you click or drag to select contiguous frames.
- e. Click the **Summing** button to display your selections in the **Reframed Series** area.
- f. The software grays out the frame information in the **Original Series** to show you what you selected.
- g. If you selected a Dynamic Study, you have the option to check the box to **Apply Decay Correction** (adjust the image brightness to compensate for activity decay over time).
- h. Click **Resumming** to add the selected frame data together and display the results.

**Figure 287 Rebin/Reframe the Series**



12. Optional: Click **Angles**  on the **Reformat** tab to apply the CoH and Angles you optimized on one series to another series.
  - a. Click **Angles** to display a **Reformat Angles** window with the current CoH and Angles for the series you selected.  
 If you select two or three series, the system displays the CoH and angle information for each series, along with a radio button for each series on display. It automatically matches the radio button selection to the series number.
  - b. In the example, shown in [Figure 288 on page 460](#), clicking the **2** radio button in Series 1 applies the Series 2 CoH and Angles to Series 1 when you click **Apply** or **OK**.
  - c. You have the option to enter values into the fields.  
 If you select a single series, the system displays a modified **Reformat Angles** window without the radio buttons. You have the option to enter values into the fields, and click **Apply** or **OK** to change the series orientation.
  - d. Click **Apply** to apply the new data field values and/or series radio button selections to the images without closing the **Reformat Angles** window.

- e. Click **OK** to apply the new values and series radio button selections to the images and close the **Reformat Angles** window.
- f. Click **Cancel** to discard the changes and close the window.

**Figure 288 Reformat Angles with Two Series Selected.**

The figure consists of two screenshots of the 'PET Cardiac Review - Reformat Angles' dialog box. Both screenshots show two series with their respective CoH and Angles values. In the top screenshot, Series 1 is selected (radio button 1 is active). In the bottom screenshot, Series 2 is selected (radio button 2 is active). In both screenshots, the radio button for Series 2 is highlighted with a yellow box.

Series	CoH	Angles	Use CoH/Angles from Series
Series 1	-79.41, 2.5, -128.92	128.72, -27.67	1 (selected in top, unselected in bottom)
Series 2	-80.15, 2.94, -125.37	129.54, -27.14	2 (unselected in top, selected in bottom)

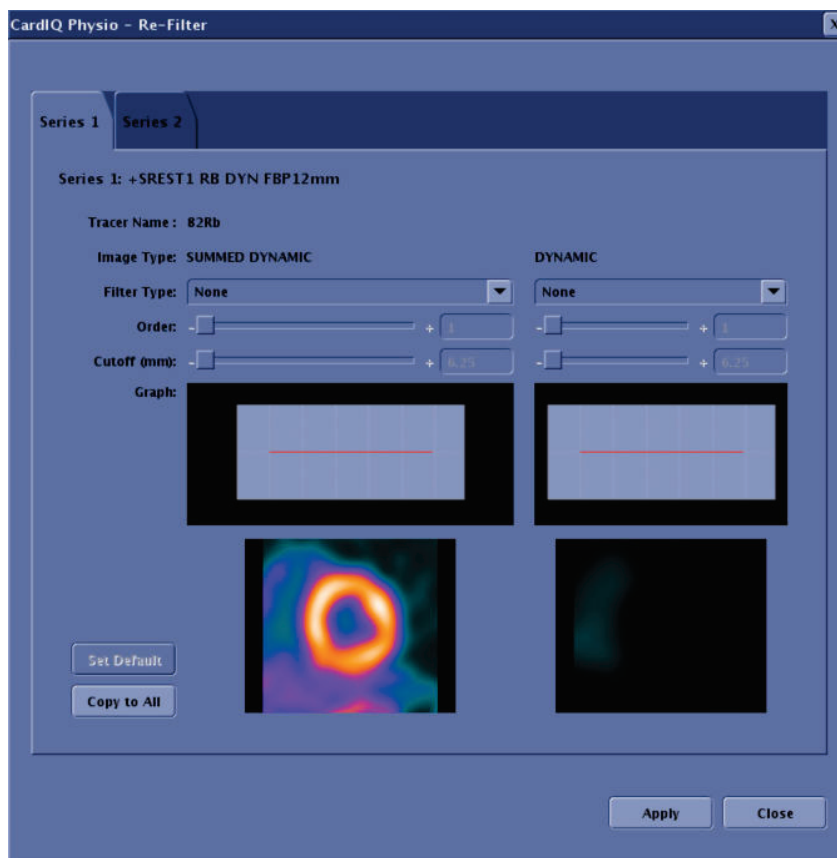
13. Optional: Click **Filter**  on the **Reformat** tab apply a filter or modify the existing filter

information.

- Most facilities apply a filter during reconstructions, and set the **User Preferences Filters Type** selection to **None** to reduce the risk of applying multiple filters. Follow facility guidelines to establish a filtering standard.
- The **Re-Filter** window displays the Tracer Name, Image Type, Filter Type, a graph that shows in real-time how the filter parameters change the filter calculations, as well as a preview window.
- Click and drag the slider to change the **Order** and/or **Cut Off (mm)** frequency values, or enter new values into the corresponding fields.
- Click **Copy to All** to apply the new parameters to all the series.
- Click **Set Default** to make the current settings the new default for series with this tracer and image type.

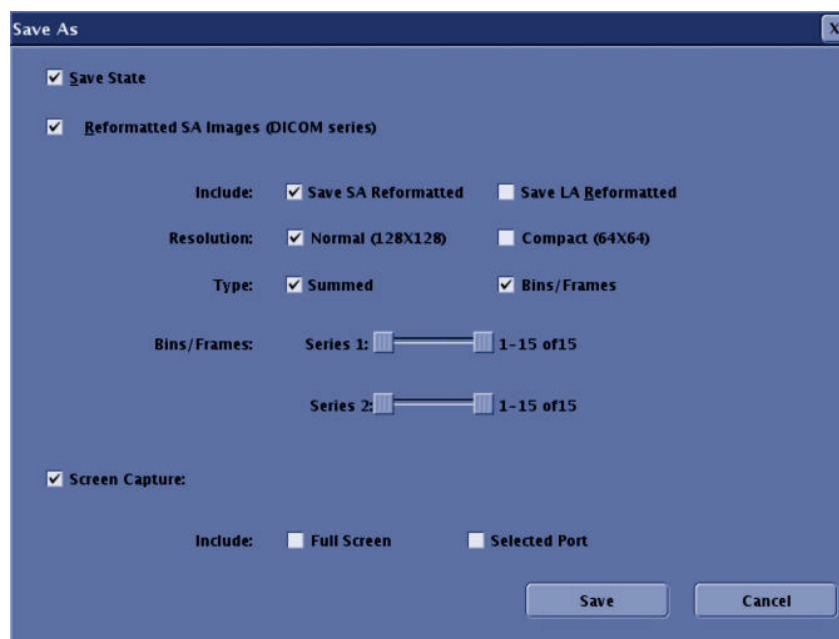
- Click **Apply** to apply the current filter selections to the corresponding series for the duration of the current session, and close the window.
- Click **Close** to quit the Re-Filter function and close the window.

**Figure 289 Cardiac VUE (CardIQ Physio) — Re-Filter Window**



- Click the **Review** tab to change the display format to Splash, Five Slice or ED/ES if you selected Gated PET images.  
Use the Page Up, Page Down and arrow keys to scroll through the images.
- Optional: Save the Cardiac VUE images.
  - Click **File** and click or drag to **Save** to follow the User Preferences setting to save the image, series or state.
  - Click **File** and click or drag to **Save As** to open a selector window similar to the one shown in [Figure 290 on page 462](#).
    - Check the boxes to save the corresponding information and formats. You can check a single format, or multiple formats.
    - Click **Save** to save the selected information and close the window, or click **Cancel** to close the window without saving the changes.



**Figure 290 Save As Selector Window**

# 16 Dynamic VUE

## 16.1 Dynamic VUE Introduction

The Dynamic VUE application provides the tools to display and analyze PET images acquired on the PET/CT system.

Use Dynamic VUE for the following functions:

- Display PET dynamic, static or gated images, sorted by time and location.
- View and measure tracer activity in a slice or user-determined region of interest over location or over time.
- Reframe or rebin images.
- Sum images over time or over location.
- Create ROIs (Region of Interest).
- Create plot over time or over location for mean, minimum, maximum and standard deviation from selected slices or user defined ROIs.
- Export statistics to a text file.

### NOTE

Each function button or icon has a tool tip associated with it that describes its function. Simply hover the mouse cursor over the button to display a description.

This chapter also contains the Dynamic VUE workflow for post acquisition processing, display and curve analysis of dynamic, static and gated imaging studies.

- Set Dynamic VUE user preferences.
- Display images with Dynamic VUE
- Review and/or document the cardiac or respiratory gating trigger information for accepted, rejected and total triggers for PET acquisitions.

## 16.2 Set Dynamic VUE User Preferences

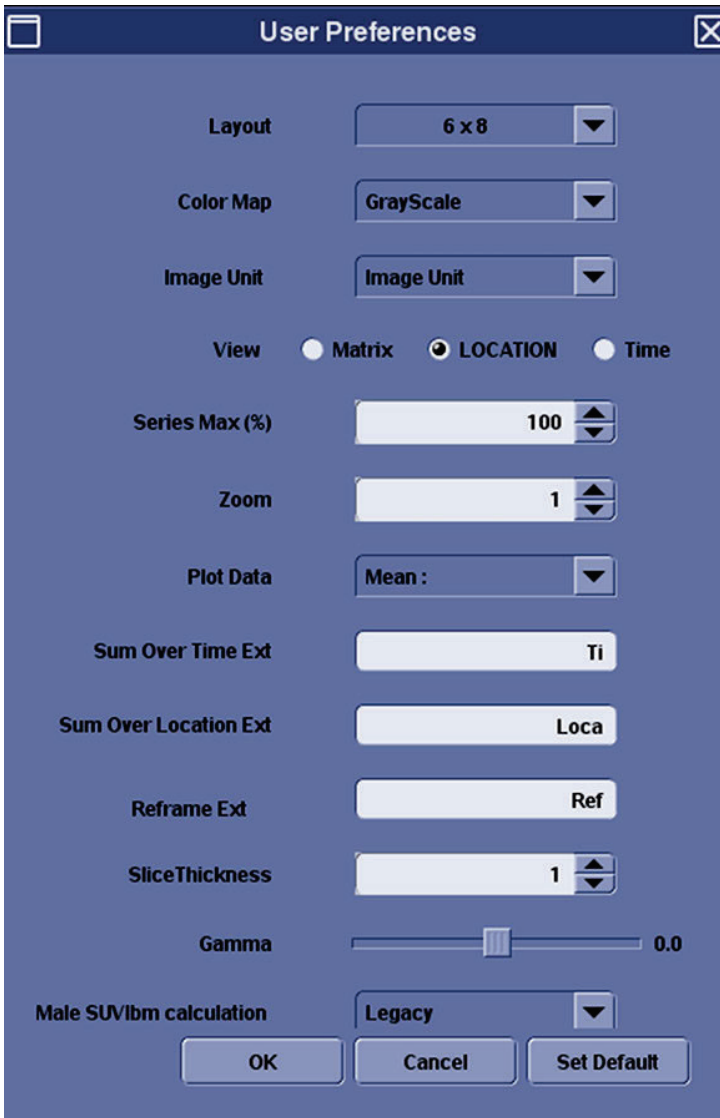
Follow these instructions to set the default Dynamic VUE user preference parameters. You can return to this window, but most facilities establish a single set of standards.

1. Click **Options** and select **Customize...** to open the **User Preferences** window.

**Figure 291 Dynamic VUE Options Menu**



2. Select the desired User Preferences.

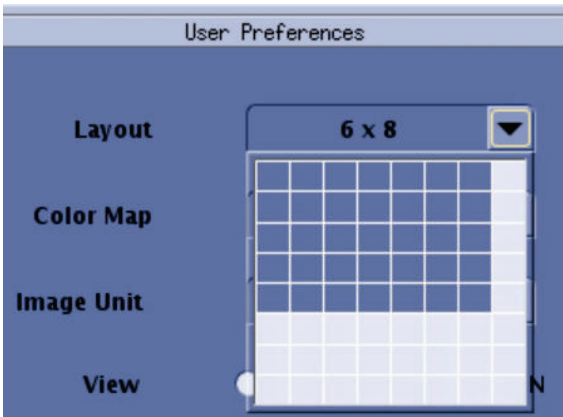
**Figure 292 Dynamic VUE User Preferences Window**

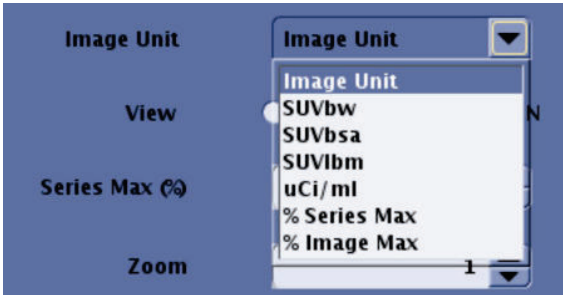
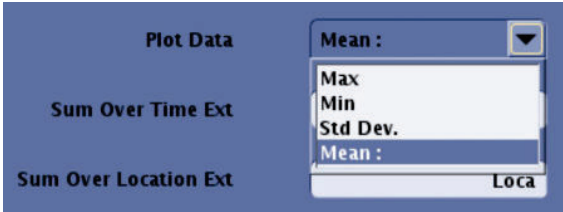
The image shows a 'User Preferences' window with a dark blue header and a light blue body. The window contains several settings: 'Layout' is a dropdown set to '6 x 8'; 'Color Map' is a dropdown set to 'GrayScale'; 'Image Unit' is a dropdown set to 'Image Unit'; 'View' has three radio buttons: 'Matrix' (unselected), 'LOCATION' (selected), and 'Time' (unselected); 'Series Max (%)' is a spinner set to '100'; 'Zoom' is a spinner set to '1'; 'Plot Data' is a dropdown set to 'Mean :'; 'Sum Over Time Ext' is a text field with 'Ti'; 'Sum Over Location Ext' is a text field with 'Loca'; 'Reframe Ext' is a text field with 'Ref'; 'SliceThickness' is a spinner set to '1'; 'Gamma' is a slider with a vertical bar in the middle and '0.0' on the right; 'Male SUVlbm calculation' is a dropdown set to 'Legacy'. At the bottom are three buttons: 'OK', 'Cancel', and 'Set Default'.

Setting	Value
Layout	6 x 8
Color Map	GrayScale
Image Unit	Image Unit
View	<input type="radio"/> Matrix <input checked="" type="radio"/> LOCATION <input type="radio"/> Time
Series Max (%)	100
Zoom	1
Plot Data	Mean :
Sum Over Time Ext	Ti
Sum Over Location Ext	Loca
Reframe Ext	Ref
SliceThickness	1
Gamma	0.0
Male SUVlbm calculation	Legacy

OK Cancel Set Default

**Table 89 Dynamic VUE User Preferences Window**

Function	Description
<b>Layout</b>	<p>Determines the initial display format of the matrix window.</p> <p><b>Figure 293 Layout Selection Grid</b></p>  <ul style="list-style-type: none"> <li>Click the down arrow to display a grid representing the maximum number of image viewports available to the <b>Matrix Review</b> window.</li> <li>Click and drag down to select the initial number of rows, and drag right to select the number of images in a row.</li> <li>The field shows the most recently selected default format until you release the mouse button and the drop-down grid disappears.</li> </ul>
<b>Color Map</b>	<p>Sets the color map the software uses when it displays the initial set of Dynamic VUE images. You can select different color maps from the list on the <b>Window Level</b> tab in the display tool area throughout the Dynamic VUE session.</p>

Dynamic VUE User Preferences Window continued	
Function	Description
<b>Image Unit</b>	<p>Determines the initial selection of the unit used to describe the range of the colorbar scale.</p> <p><b>Figure 294 Image Unit Menu</b></p>  <ul style="list-style-type: none"> <li>Click the arrow and click or drag to the unit you plan to use.</li> <li>Default to the image units used during image acquisition.</li> <li>The Window Level tool displays the default selection in the <b>Image Unit</b> field.</li> </ul>
<b>View</b>	Set the Dynamic VUE default. Click the radio button to select <b>Matrix</b> , <b>Location</b> or <b>Time</b> .
<b>Series Max (%)</b>	Set the default upper scaling value, relative to the maximum value of the corresponding series. Click the up/down arrows to increase or decrease the displayed value, or enter a value into the field.
<b>Zoom</b>	Set the initial magnification factor of the matrix and location screen images, normally <b>1</b> . Click the up/down arrows to increase or decrease the displayed value, or enter a value into the field.
<b>Plot Data</b>	<p>Set the default value of the <b>Curve Type</b> field on the <b>Analyze</b> tab. Click on the arrow and click or drag to the parameter you want to plot.</p> <p><b>Figure 295 Plot Data Menu</b></p> 
<b>Sum Over Time Ext</b>	Set the extension of <b>Sum Over Time</b> files you can save.
<b>Sum Over Location Ext</b>	Set the extension of <b>Sum Over Location</b> files you can save.
<b>Reframe Ext</b>	Set the extension of <b>Reframed</b> files you can save.

Dynamic VUE User Preferences Window continued	
Function	Description
<b>Slice Thickness</b>	Set the thickness of the initial Dynamic VUE slice display. Click the up/down arrows to increase or decrease displayed slice thickness, or enter a value into the field.
<b>Gamma Level</b>	Set the initial starting position and gamma value of the <b>Gamma</b> slider bar on the <b>Window Level</b> tab. Click the up/down arrows to increase or decrease displayed gamma value, or enter a value into the field.
<b>Male SUVlbm Calculation</b>	<p>Indicates the calculation used to determine Male SUVlbm, either <b>Legacy</b> or <b>Consensus</b>. The default value is <b>Legacy</b>.</p> <p><b>Legacy</b></p> <ul style="list-style-type: none"> <li>• <math display="block">lbm \left( \frac{g}{ml} * \right) = 1.10 WT - 120x \left( \frac{WT}{HT} \right)^2</math>for males.</li> <li>• Based on reprint by Morgan et al. [1994] as <math>1.10 x WT - 120 x \left( \frac{WT}{H} \right)^2</math>, and consequently adopted (Legacy) by the PET community [Sugawara et al. 1999].</li> <li>• Earlier versions of PET applications use this formula for males.</li> </ul> <p><b>Consensus</b></p> <ul style="list-style-type: none"> <li>• <math display="block">lbm \left( \frac{g}{ml} * \right) = 1.10 WT - 128x \left( \frac{WT}{HT} \right)^2</math>for males.</li> <li>• The original (Consensus) formula for computing for males was <math>1.10 x WT - 128 x \left( \frac{WT}{H} \right)^2</math> [James 1976].</li> <li>• Newer versions of PET applications use this calculation for males when the preference is selected.</li> </ul>

3. Apply the User Preferences.

- Click **OK** to accept the currently selected parameters for the current session only. The parameters return to the default setting when you close the session.
- Click **Set Default** to save the new user preference as default parameters. The software uses the User Preferences parameters to display the initial set of Dynamic VUE images and program the **Analyze** and **Review** tabs.
- Click **Cancel** to discard the current selections and close the window.

## 16.3 Remaining Option Menu Items

The previous section described the last item on the **Dynamic VUE Options** menu. This section provides a brief description of the remaining **Options** menu items.

**Figure 296 Dynamic VUE Options Menu**



**Table 90 Dynamic VUE Options Menu**

No.	Name	Description
1	<b>Series Info...</b> or <b>Ctrl + M</b>	Displays a list of information and attributes for each series. Refer to <a href="#">Figure 297 on page 470</a> . <ul style="list-style-type: none"> <li>Click and drag the slider to display all the information.</li> <li>Click <b>OK</b> to close the <b>Series Attributes</b> window.</li> </ul>
2	<b>Show/Hide Header</b> or <b>Ctrl + H</b>	Toggle the display header information On and Off.
3	<b>Info Tip On/Off</b> or <b>Ctrl + I</b>	Toggle the Info Tip feature On or Off. Box Checked=On: Move the cursor over the image, wait a few seconds to display the temporary ROI information.

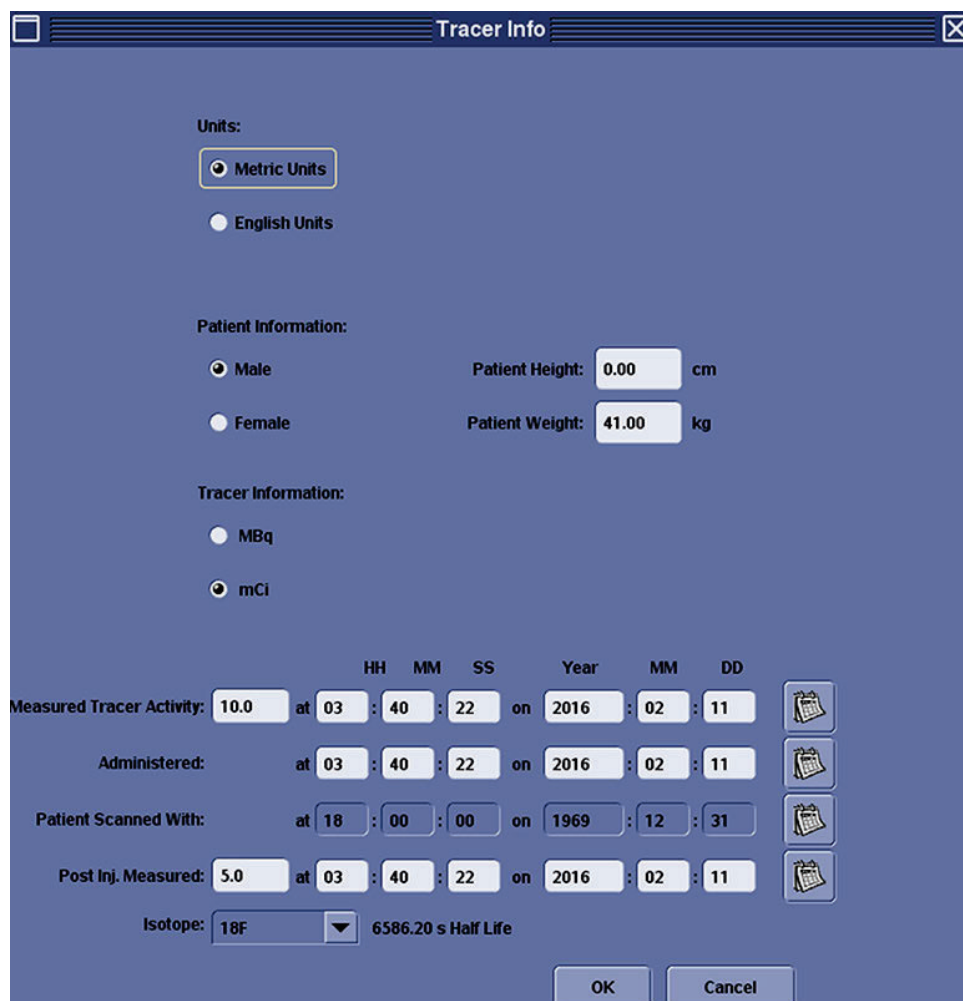


Dynamic VUE Options Menu continued		
No.	Name	Description
4	<b>Film Screen</b> or <b>F2</b>	Send all the images in the image display area to the filmer as a single image.
5	<b>Tracer Info...</b> or <b>Ctrl + T</b>	<p>Edit the tracer information. Refer to <a href="#">Figure 298 on page 471</a>.</p> <ul style="list-style-type: none"> <li>The system displays the current header values in the <b>Tracer Info</b> window.</li> <li>Follow facility guidelines to set the date/time formats.</li> <li>The system refuses to activate the <b>OK</b> button until the required inputs are present and valid.</li> <li>You can cancel out at any time.</li> </ul>

**Figure 297 Dynamic VUE — Series Attributes Window**

Field Name	Value
Patient Name	10 D600S Rb82 R/S Normal
Patient ID	AW281276890.378.1274901637
Study Identifier	650
Study Description	RB HEART
Study Date Time	11 May 2010 17:06:09
Patient Height	1.83 m
Patient Weight	98
Patient Sex	
Patient Age	Not Available
Patient Birth date	Not Available
Referring Physician	
Reading Physician	null
Accession Number	
Scanner Manufacturer	GE MEDICAL SYSTEMS
Scanner Model	Discovery 690
Institution Name	
Suite Name	null
Scanned ID Number	null

Figure 298 Dynamic VUE — Tracer Info Window



The Tracer Info window is a dialog box with a title bar containing a minimize button, the text 'Tracer Info', and a close button. The window has a blue background and contains the following sections:

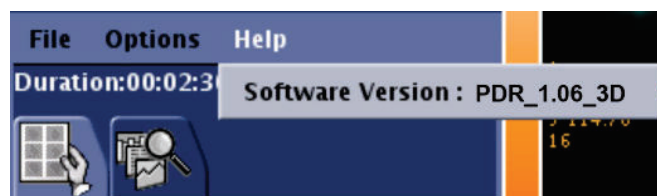
- Units:**
  - ☒ Metric Units
  - ☐ English Units
- Patient Information:**
  - ☒ Male      Patient Height: 0.00 cm
  - ☐ Female      Patient Weight: 41.00 kg
- Tracer Information:**
  - ☐ MBq
  - ☒ mCi
- Measured Tracer Activity:** 10.0 at 03 : 40 : 22 on 2016 : 02 : 11 [Calendar Icon]
- Administered:** at 03 : 40 : 22 on 2016 : 02 : 11 [Calendar Icon]
- Patient Scanned With:** at 18 : 00 : 00 on 1969 : 12 : 31 [Calendar Icon]
- Post Inj. Measured:** 5.0 at 03 : 40 : 22 on 2016 : 02 : 11 [Calendar Icon]
- Isotope:** 18F ▼ 6586.20 s Half Life

At the bottom are 'OK' and 'Cancel' buttons.

## 16.4 Help Menu

Click **Help** to display the current software revision.

Figure 299 Help Menu



## 16.5 Display Images with Dynamic VUE

Follow these instructions to select series that qualify for display with Dynamic VUE.

### NOTE

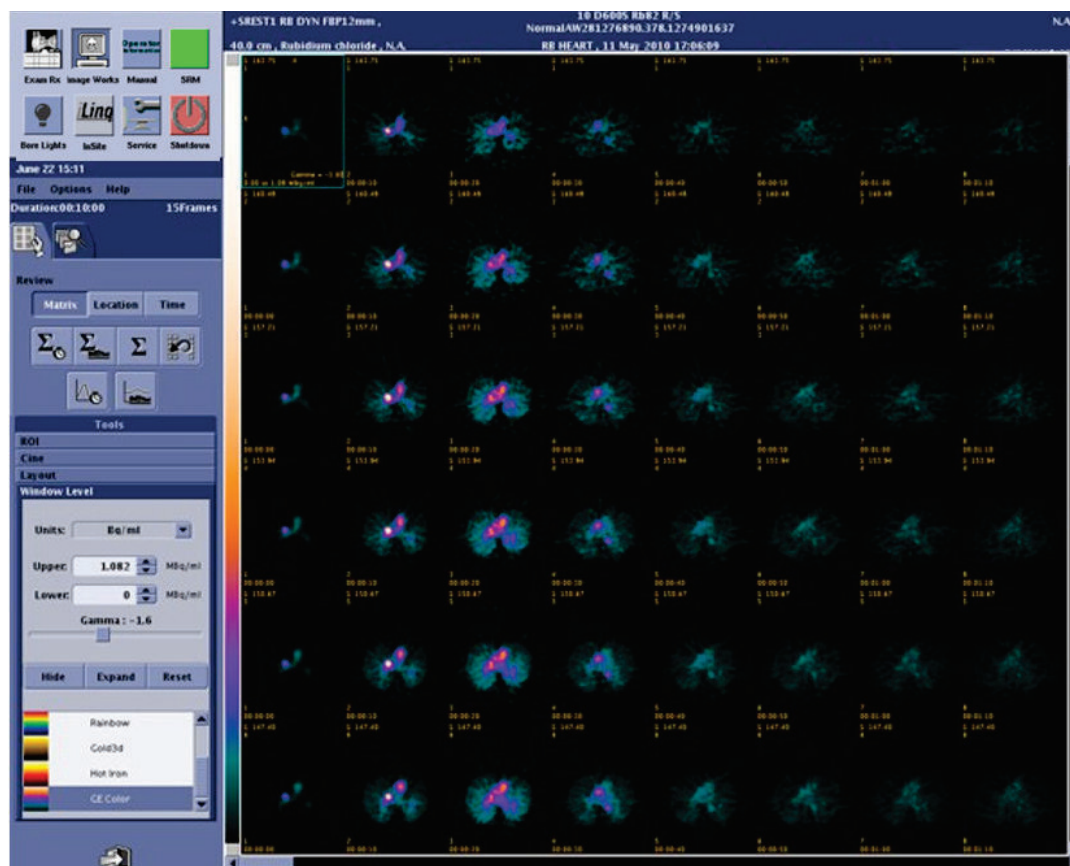
These instructions assume that you are sitting at the console, are using Dynamic VUE, and have ready access to the Dynamic VUE tools displayed along the left side of the display monitor. [PET Dynamic VUE Tools](#) contains illustrations and descriptions of the tools for reference.

1. Select a study from the examinations database in the Patient List.
2. Click a qualifying series: ***Dynamic***, ***Static*** or ***Gated PET***.

Figure 300 Image Works Patient Browser

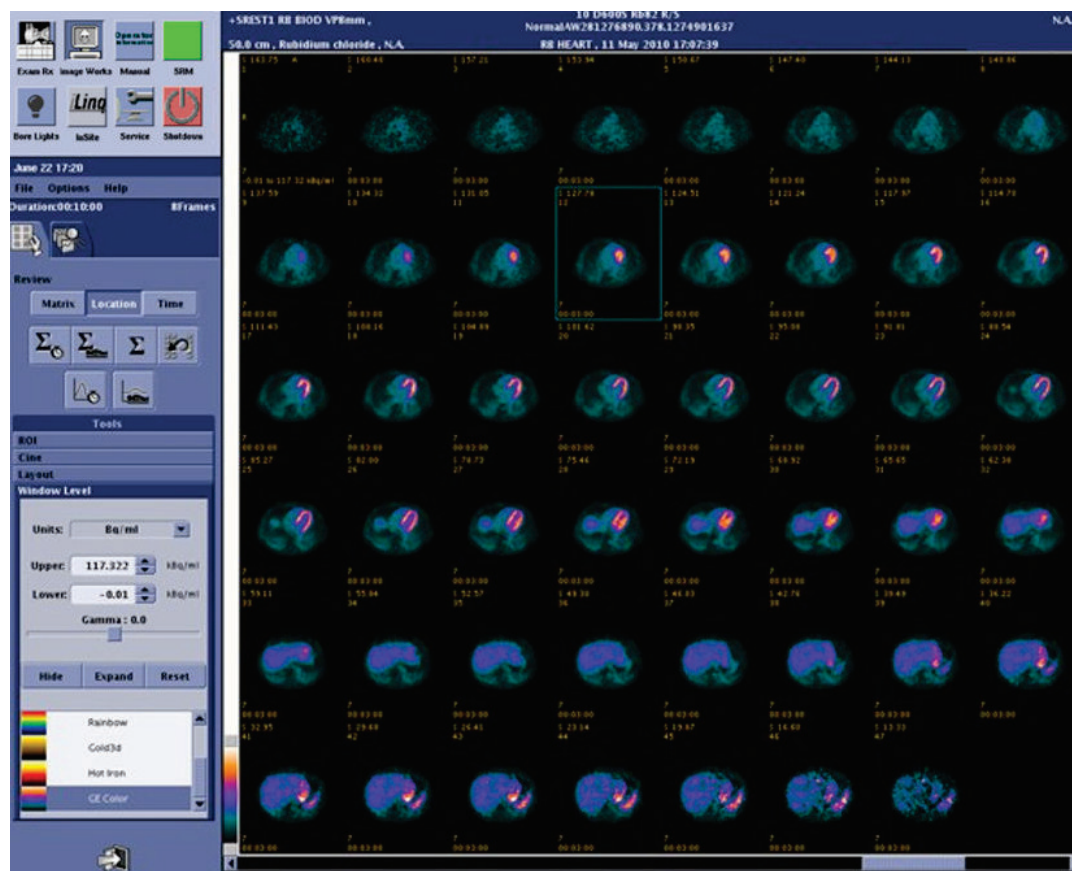


3. Click **Dynamic VUE** from the **Data Apps** list on the right side of the Patient Browser.
4. The software utilizes User Preferences to set up the initial display. The User Preferences chosen for your system will determine how the initial display images look.  
Follow facility guidelines to establish and use a standardized display format.
5. Click **Matrix** to open a **Dynamic VUE Matrix Review** window.

**Figure 301 Dynamic VUE Matrix Review Window**

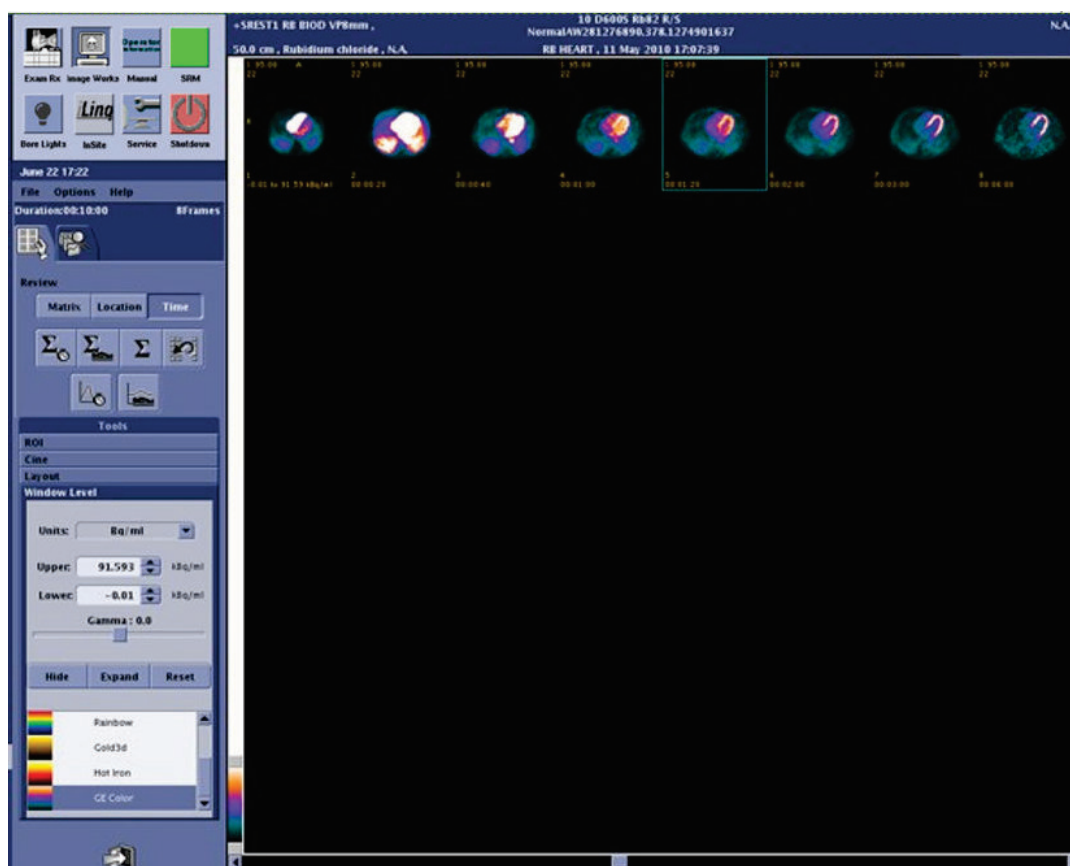
- In the Matrix view, paging in time is independent of paging in location.
  - Click and drag the horizontal scroll bar to page through the time intervals. Scroll right to move forward in time, scroll left to move backward through time.
  - Click and drag the vertical scroll bar to page through the locations. Scroll down to move in the inferior direction; scroll up to display locations in the superior direction.
  - You can press the left and right arrows to shift the window to the left and right by one column.
  - Press **Page Up** or **Page Down** to scroll through the images.
6. Click **Location** to open a **Dynamic VUE Location Review** window.
- Click and drag the horizontal scroll bar to observe tracer activity in all locations during sequential time periods. Dynamic VUE displays the images in rows from the most superior location to the most inferior location.
  - Drag and scroll right to display later times; drag and scroll left to display earlier times.
  - Press the right and left arrow keys to shift the window by the FOV (47 images).

Figure 302 Dynamic VUE Location Review Window



7. Click **Time** to open the **Dynamic VUE Time Review** window.
  - Use the **Time** function to observe tracer activity in all times at a specific location.
  - Click and drag the horizontal scroll bar to the right to display more inferior locations; click and drag left to display more superior locations.
  - Press the left/right arrow keys to display all of the time frames per slice, for each slice in order from superior to inferior.
  - Press the up/down arrow keys to increase or decrease the number of frames on display for that slice.






**Figure 303 Dynamic VUE Time Review Window****NOTE**

If you forget the name of a button, move the cursor over the button without clicking. After a second or two, a display identifies the button or a brief description of its function.

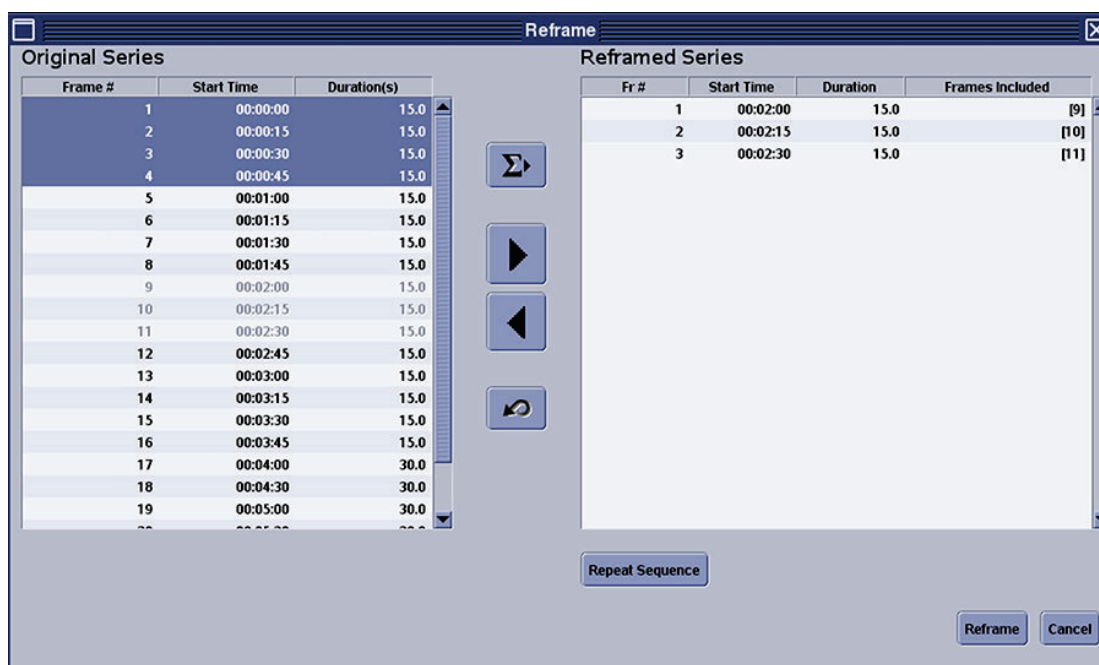
8. Click **Sum over Time** or **Sum over Location**.

The system sums the images and updates the display.

9. Optional: Click the **Reframe or Rebin**  button on the **Review** tab to open a Reframe window similar to the one shown in [Figure 304 on page 477](#).
  - a. The **Original Series** area contains a list of all the frames in the original series.
  - b. Click **Undo** to clear the **Reframed Series** area.
  - c. Click to highlight the frames you plan to sum. You can press and hold **Ctrl** while you click on individual frames to highlight them for selection, or press and hold **Shift** while you click or drag to select contiguous frames.
  - d. Click **Sum** to add the selected frames and display the resulting frame in the **Reframed Series** area.

- e. If you summed two or more frames, you can click **Repeat Sequence** to apply the same summing formula to the remaining frames.
- f. Click one or more frames and click the  arrow to shift the frames to the **Reframed Series** area without adding the frame data together.
- g. Click one or more frames in the **Reframe Series** area and click the  arrow to transfer the data back to the **Original Series** area as individual (original) frames.
- h. The software grays out the frame information in the original series to show what was selected. You may only select each frame one time.
- i. Click **Reframe** to add the selected frame data together and display the results.

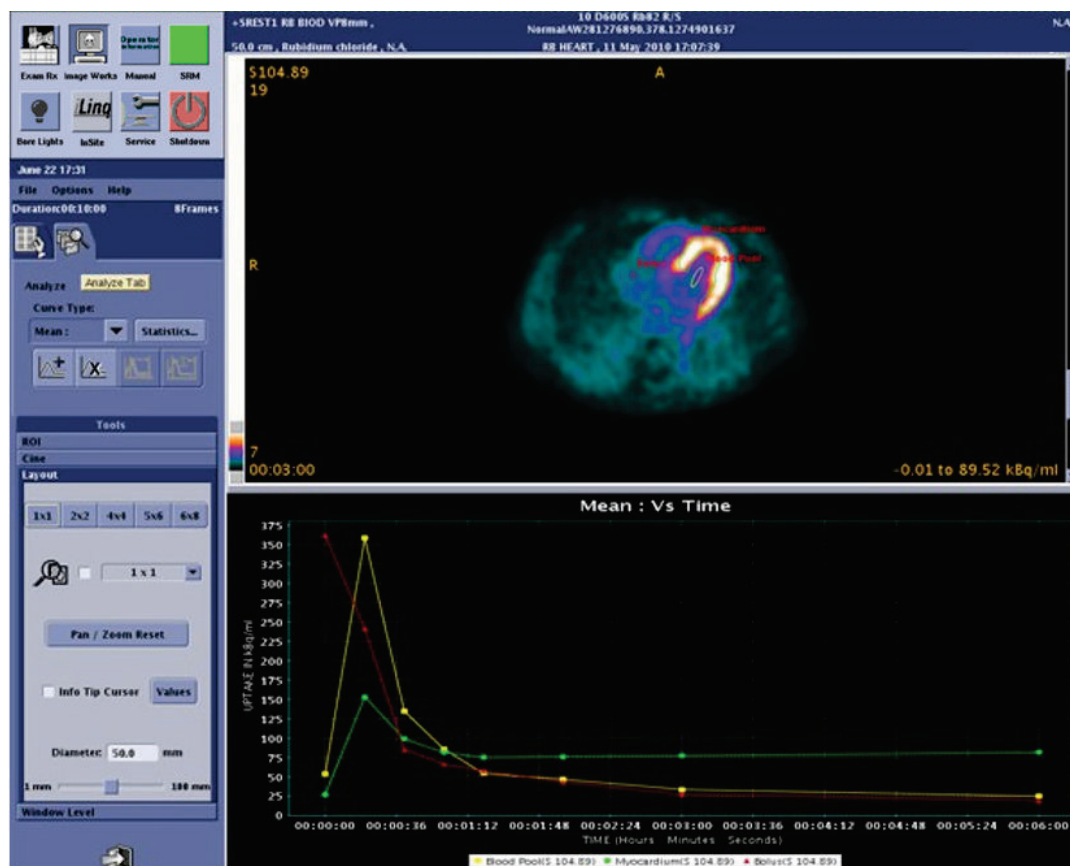
**Figure 304 Rebin/Reframe the Series**



10. Click **Plot Over Time** or **Plot Over Location** to open the **Analyze** tab and display the activity of the image statistics and/or ROIs over time or over location.
  - Use the vertical scroll bar to scroll through the images in the top display area.
  - The **Analyze** tab parameters determine the activity curve in the graph in the bottom of the display area. You can change the curve type during the session.



Figure 305 Plot Over Location Window



11. Click **Statistics...** on the **Analyze** tab to open the **Dynamic VUE Statistics** window.
  - a. Optional: Click **Save** to open a browser of save destinations, similar to [Figure 307](#) on page 479

Figure 306 Dynamic VUE Statistics Window

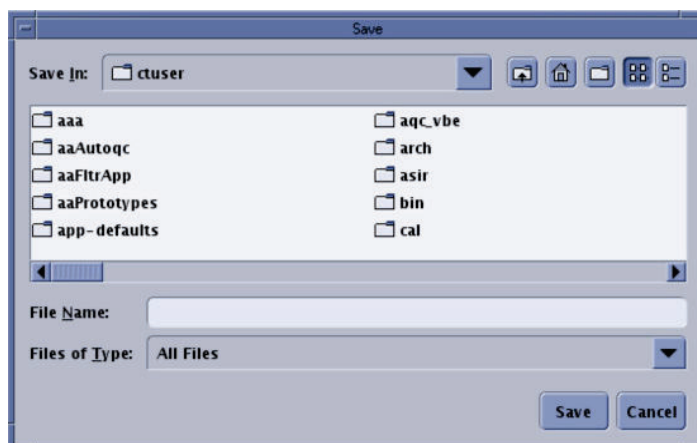
Dynamic VUE					
Patient Name: 10 D6005 Rb82 R/S Normal		Patient ID: AW281276890.378.1274901637		Normal AW281276890.378.1274901637	
Study Date: 11 May 2010		Series Name: Frame Time		RS HEART, 11 May 2010 17:07:39	
Date: 17 Jun 2010				00:03:00	
ROI	Location	Mean	Max	Min	Std Dev.
No ROI	S 163.75	3.778	41.261	-14.942	7.143
No ROI	S 160.48	5.101	50.431	-14.181	8.518
No ROI	S 157.21	5.783	51.313	-12.320	8.869
No ROI	S 153.94	5.936	49.605	-9.203	8.682
No ROI	S 150.67	5.932	49.917	-8.738	8.487
No ROI	S 147.40	6.023	49.783	-7.873	8.542
No ROI	S 144.13	6.218	51.863	-8.450	8.826
No ROI	S 140.86	6.496	49.614	-8.566	9.317
No ROI	S 137.59	6.832	58.453	-7.858	10.031
No ROI	S 134.32	7.202	77.403	-6.699	10.959

Units for Mean, Max, Min &amp; Std Dev.: kBq/ml

- b. Browse to the destination folder.
- c. Follow facility guidelines to name the statistics file.
- d. Click **Save** to save the file and close the file browser.

- e. Click **Cancel** to close the window.


**Figure 307 Save Browser**



12. Optional: Save the Dynamic VUE images.
- Click **File** and click or drag to **Save** to save the designated window with the extension shown on the **User Preferences** window.
  - Click **File** and click or drag to **Save As** to open a selector window similar to the one shown in [Figure 308 on page 479](#).
    - The file name defaults to the extension shown on the **User Preferences** window, but you can change the file name and extension before saving.
    - Click **Save** to save the file and close the window, or click **Cancel** to close the window without saving any data.

**Figure 308 Save As Selector Window**



13. Click  at the bottom of the Dynamic VUE tool area to exit the application.

You can click **File** then click or drag to **Exit**.

## 16.6 Dynamic VUE Quick Steps

### **Calculate the Activity Curve over the Entire Volume**

1. Select a patient exam and series from the Image Works browser.

#### Dynamic VUE

2. Click **Dynamic VUE** and wait for the initial display.
3. Click on an image to activate it.
4. Click **Sum Over Time** or **Sum Over Location** from the Sum Series.
5. Select an image and use the display tools to create a region of interest (ROI).
6. Click the **Plot Over Time** or **Plot Over Location** button.
7. Optional: Click **File** and drag to **Save** or **Save As** to save the resulting series to the series database.

# 17 PET 3D Viewer

## 17.1 PET 3D Viewer Introduction

3D viewer, also known as Volume Viewer, is a 3D post-processing software package that includes PET and CT features. The following section covers PET related features. For CT features, including the options AutoBone Xpress, VessellQ Xpress, CT Perfusion 4D and CardIQ Xpress, refer to user manual of each feature provided with option installation.

This chapter contains instructions to reformat image data into a new series of images with a different slice orientation than the acquisition data, as well as instructions to access, fuse and/or display CT and PET images using Custom QC, Image QC and 3D Viewer. 3D Viewer provides a comprehensive application on the scanner console to display volumetric CT, PET and Hybrid PET/CT studies for review and analysis. Image QC provides a set of PET specific 3D Viewer protocols. Custom QC provides the means to further customize the 3D Viewer protocol set to match the facility workflow.

The Image Works desktop provides the following four buttons as methods of launching 3D Viewer:

- **Custom QC:** Launches a Facility-specific PET/CT 3D Viewer that initially matches the Image QC format
- **Image QC:** Launches the GE recommended PET/CT specific 3D Viewer
- **3D Viewer:** Launches general CT and PET 3D Viewer
- **Reformat:** Launches a CT specific 3D Viewer described in the CT Learning and Reference Guide (User Manual).

The different 3D Viewer selections generally use the same tools, although some application selections may determine the availability of certain tools. Once you learn the core interface, the general concepts apply to the Custom QC, Image QC, 3D Viewer and Reformat 3D Viewer applications. The [System Introduction](#) chapter contains the PET 3D Viewer Tool Panel Descriptions for your reference

### NOTE

With Q.Clear, the signal to noise ratio is greatly improved and thus the contrast ratio is now much higher. This provides excellent image quality with enhanced lesion border detection. When images with significant transitions between high activity and low activity are viewed on a system with tri-cubic interpolation of the native PET voxels, the enhanced border detection may cause a small visual anomaly called a Gibbs artifact. While the visual anomaly is present, the underlying quantitative information is unaffected and is accurate. To minimize this visual anomaly reconstruct images with Q.Clear selected as the quantitation method and choose a larger PET image matrix dimension.

This applies to all reconstruction options utilizing Q.Clear, such as Precision DL reconstruction option.

**NOTE**

When using Precision DL, if a change to patient weight or tracer information is made, perform the changes through **Edit Patient** or **Edit Tracer** Apps on the console. Once the change is made, manually retrospectively reconstruct Precision DL images to reflect the changes as the Precision DL model uses this information in the reconstruction process. Applying weight or tracer changes directly from the viewers may provide incorrect quantitative accuracies during reading. Additionally, saving state or screen capture after changing this information from the viewer will not reflect the actual changes Precision DL reconstruction generates. Hence, rely only on the images retrospectively reconstructed after the change made on the console with the dedicated applications.

**NOTE**

3D Viewer allows for changes to PET patient and tracer information within the application (edit information). This feature can be used to correct errors or missing information for more accurate PET quantitation. When used in conjunction with save state, the changes can be networked to other stations utilizing 3D Viewer Applications. This feature of 3D Viewer should not be utilized with Precision DL images, rather the images should be retrospectively fixed on the Console and the Precision DL images re-generated.

**NOTE**

When 3D Viewer is used to load images with overlapping CT groups, the following message may be displayed on load: **"The slices \_ and \_ are \_ mm apart. Missing data will be interpolated. Any quantitative data in these regions must not be used for diagnosis. Do you want to continue?"**

This has been seen in series where the slice spacing is not uniform, which may occur in overlapped regions of CT groups. The intent of the 3D Viewer message is to report varying spacing which may indicate a data gap in the input series. This message reports the first location of the largest space it finds. The operator should review the message and acknowledge and proceed if:

- The series was produced from a CT scan with overlapping scan groups. and
- The reported spacing in the message is the largest slice spacing of a group in the input series and the location of the spacing is between images in that group.

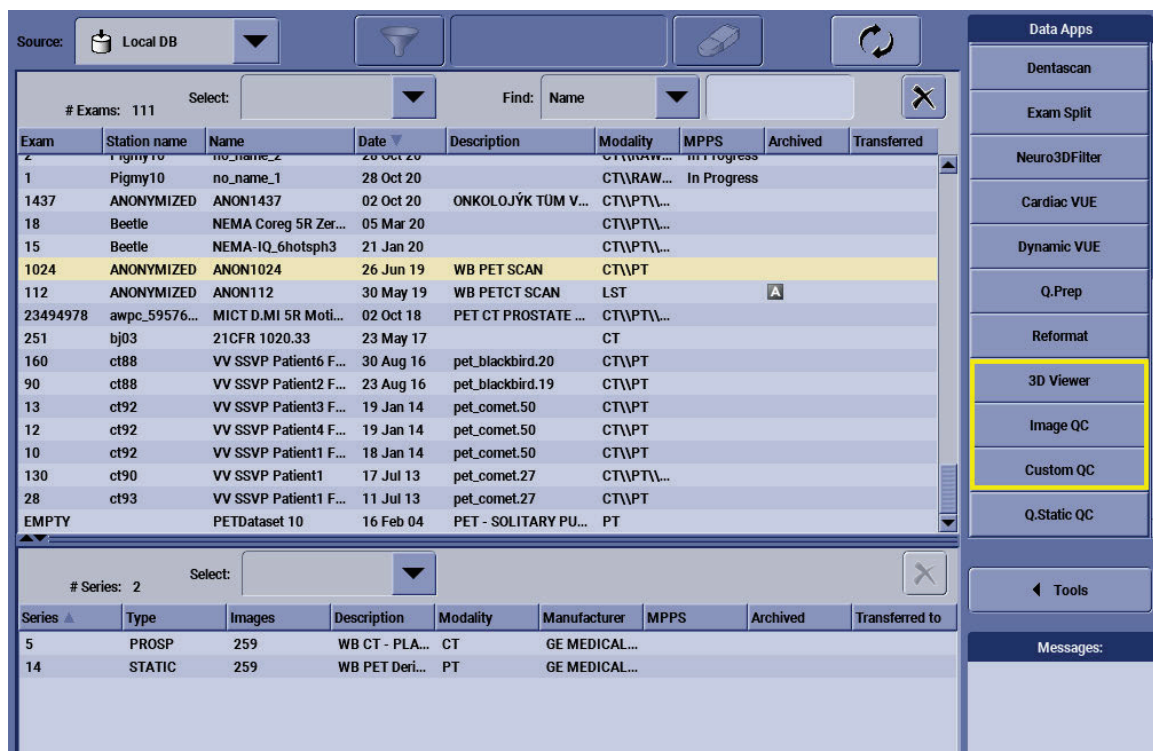
If the above conditions are met, the data does not actually contain gaps. Select OK to continue. The message will not be displayed if the images in the series have uniform slice spacing.

## 17.2 Image QC

Image QC launches 3D Viewer with a predefined fused PET/CT layout, designed specifically to maximize screen space and provide a place to check the registration and image quality of the hybrid exam.

1. In the Image Works browser, click an Exam.

**Figure 309 Custom QC, Image QC and 3D Viewer buttons on the Image Works Browser**



2. Click at least one CT and one PET series, excluding scout series.
  - You can select multiple PET and/or volumetric CT series. Press and hold the **Ctrl** key to make multiple selections. Do not select a scout series.
  - 3D Viewer selects the most recently added CT and PET series on the list for fusion and display.
3. Click **Image QC** or **Custom QC** to launch the corresponding 3D Viewer application.
4. An interim selection window opens that shows all the compatible series in the selected exam. The application always excludes scout series. Click the check box(es) to select the corresponding series, then click **OK**.

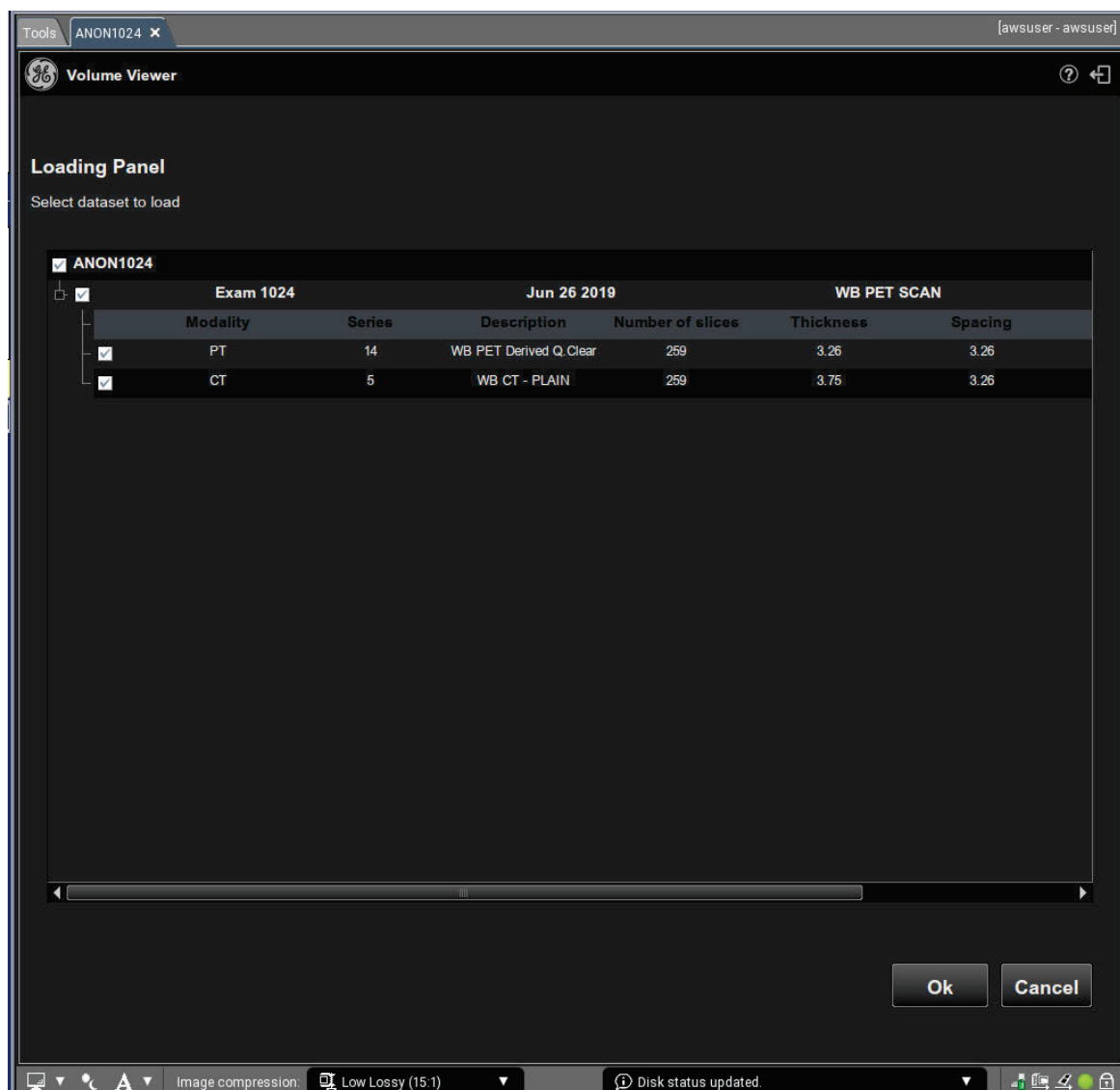
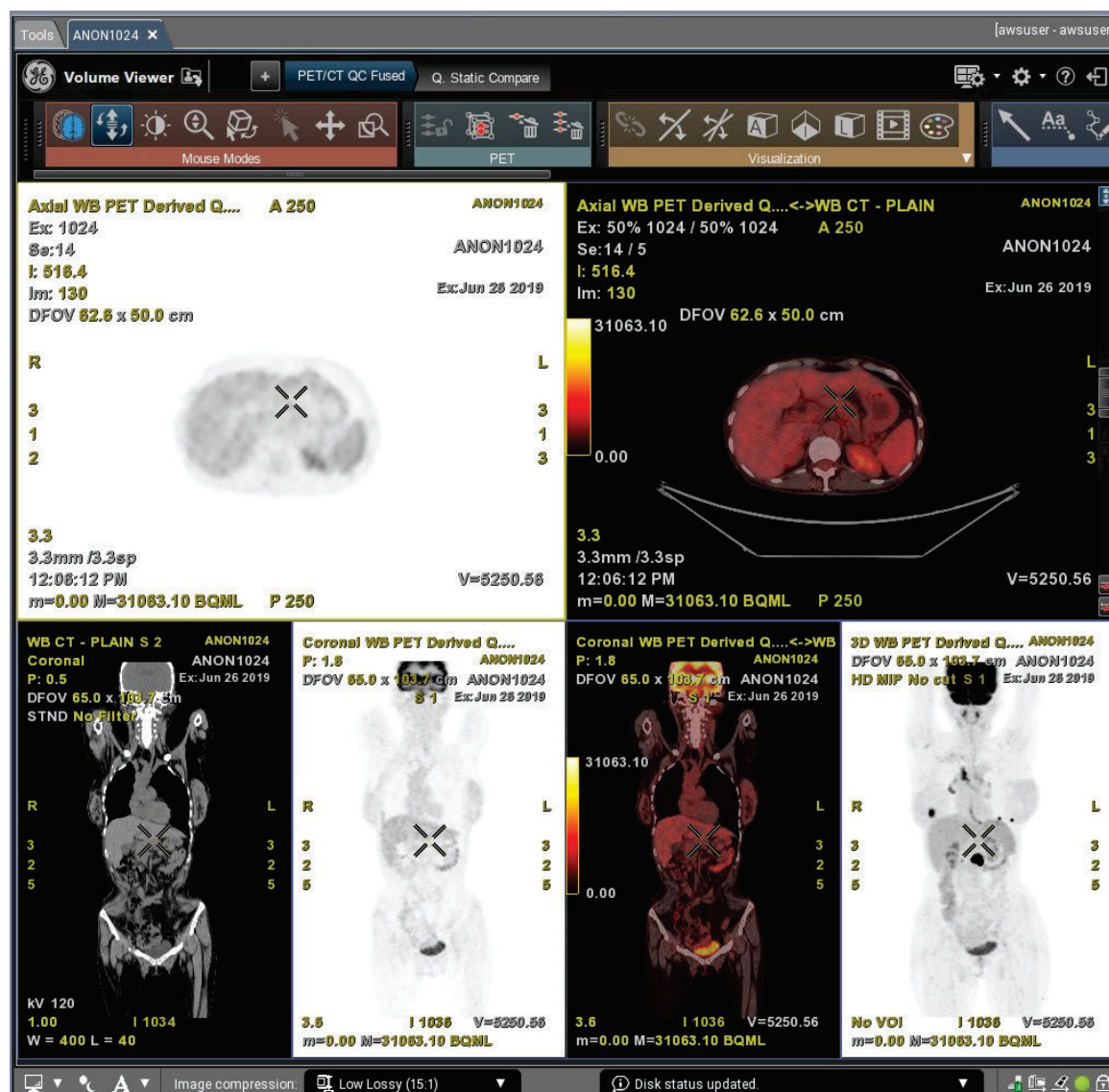
**Figure 310 3D Viewer Loading Window**



Figure 311 Hybrid PET/CT Exam Loaded with Image QC

**NOTE**


When using Edit Patient (weight, height, dose, etc.) in the Image QC or other 3D Viewer applications, the changes made are not saved when the application is closed.

## 17.3 Custom QC

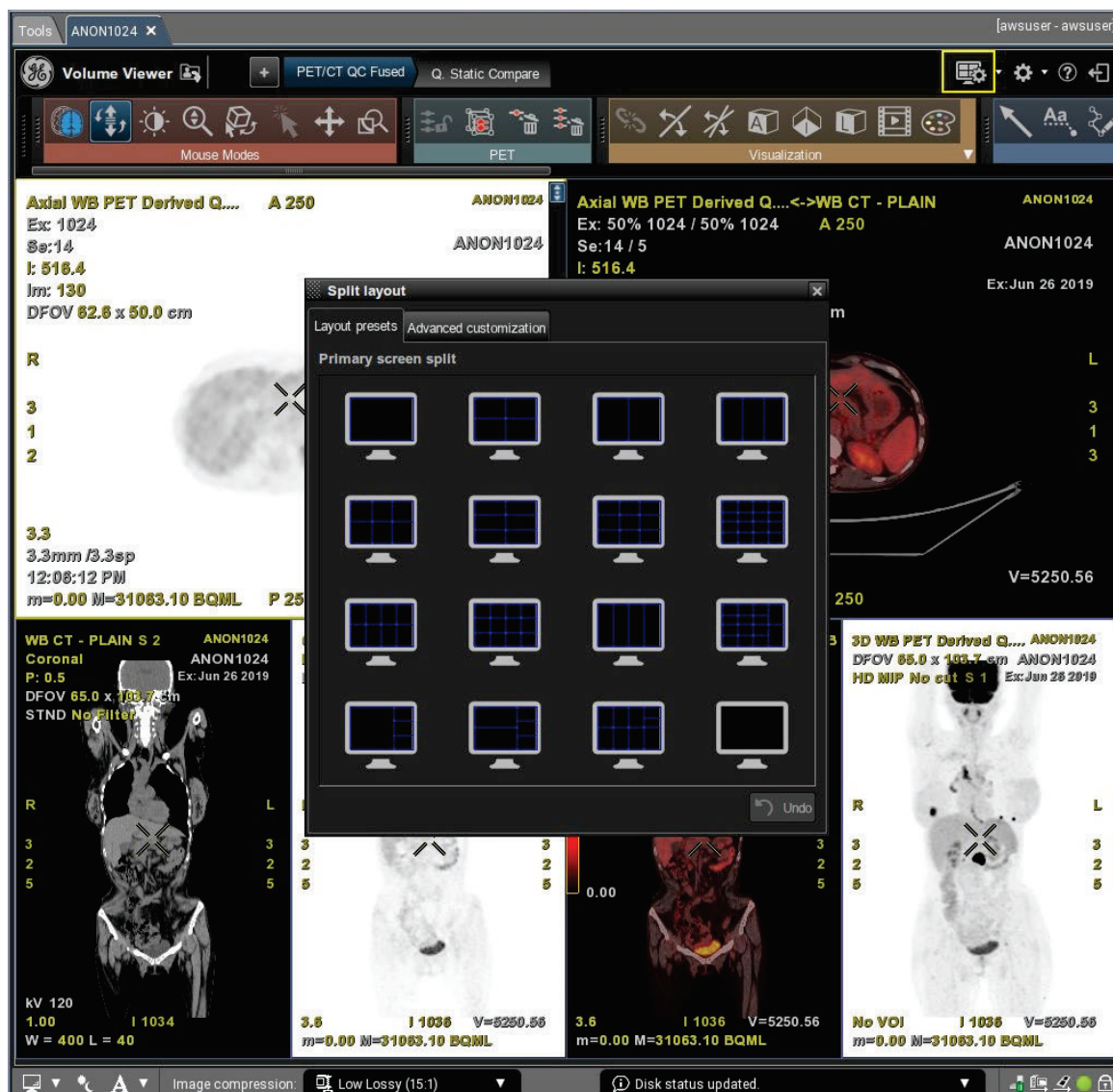
Follow the instructions in this section to save a site-specific custom PET/CT image layout.

1. Click the exam in the Image Works browser. Refer to [4.7 Image Works Browser on page 147](#).
2. Click at least one CT and one PET series, excluding scout series.



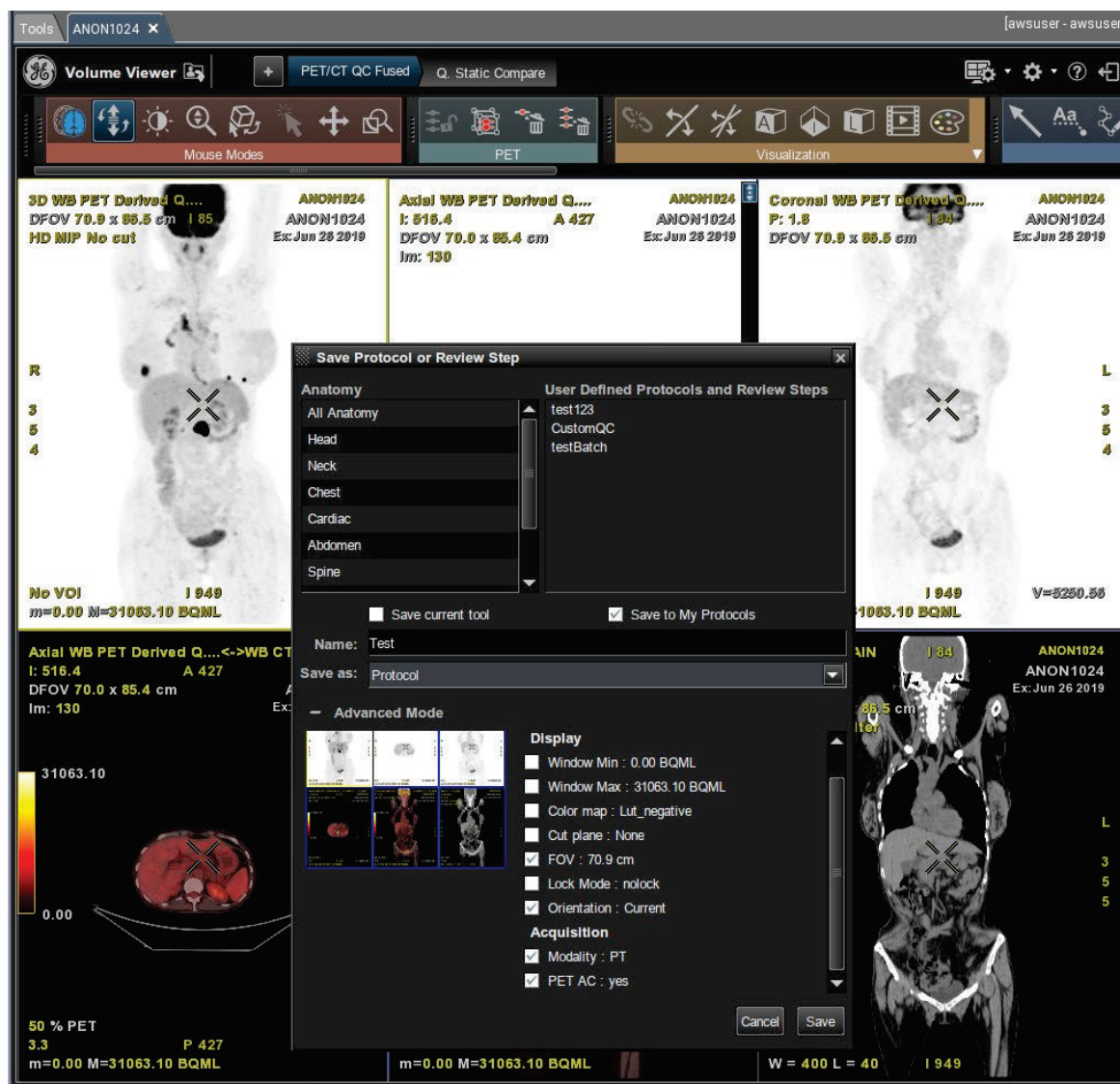
3. Click **Custom QC** to launch the application.
4. Click the **Layout and Preference** icon  to display the split window.

**Figure 312 Modify Screen Split**



5. Click on the Monitor icon with the viewport format you want to use.
6. Optional: Click **Customize** to modify and link the viewports.  
Refer to the 3D Viewer user guides shipped with your system for detailed instructions.
7. When you finish modifying the viewport layout, click on **Save Layout** to open the Save new layout preset window.

Figure 313 Save New Layout Preset Window



8. Enter CustomQC into the **Name:** field.
9. Click **Save** to replace the existing Custom QC protocol.

When the message window opens, click **Overwrite** to accept the new protocol.

## 17.4 3D Viewer

The 3D Viewer button on the Image Works desktop provides a simple interface to Volume Viewer and all of the available protocols. Click **3D Viewer** to choose a layout from a comprehensive suite of protocols, tailored to specific anatomies, that support the needs of different aspects of clinical scanning.

1. Click one or more Exams on the Image Works browser. Refer to [4.7 Image Works Browser on page 147](#).
  2. Click at least one CT and one PET series.
    - You may select multiple PET and/or CT series. Press and hold the **Ctrl** key to make multiple selections.
    - 3D Viewer automatically selects the most recently added CT and PET series on the list for fusion and display.
  3. Click **3D Viewer** to open the Volume Viewer Protocol Selection window.
- Click a protocol to select it.

**Figure 314 3D Viewer Protocol Selection Window**



4. An interim selection window opens that shows all the compatible series in the selected exam. (The application always excludes Scouts series.) Click the check boxes to select the corresponding series, then click **OK**.

## 17.5 3D Viewer Learning References

The Advantage Workstation (AW) based PET/CT Volume Viewer uses a single monitor to access a host of applications to display, analyze and reformat PET/CT images. It is not within the scope of this manual to define and discuss all the possible 3D Viewer tools. The System Introduction chapter includes [PET 3D Viewer Tools](#) which provides a brief description of the tools you are likely to use with PET/CT images.

The system ships with AW Volume Viewer operator manual on USB and on the console. To open 3D Viewer manual on the console, open the Image QC application and click on **Tools (top left corner) > Utilities > Launch**.

### NOTE

The manual window display might not correctly fit to the size of the monitor. It can be resized once by dragging the edges and the manual opens with modified window size from subsequent launches.

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# 18 Whole-Body Dynamic Acquisition (Optional)

## 18.1 Introduction to Parametric Imaging

Whole-Body Dynamic is an acquisition mode of scanning, enabling you to scan the patient's whole body, or part of it, repeatedly.

Acquiring a time sequence of PET images is the foundation to quantify tracer kinetics in vivo, by applying kinetic models that enable temporal analysis. The kinetic modeling is based on mathematical modeling, also known as compartment modeling. Kinetic modeling can be reversible or irreversible, depending on the injected tracer. Irreversible kinetic models assume that the injected tracer moves around between the different compartments, but there is at least one compartment where it remains trapped. These models are highly dependent on the input function (input conditions), hence, the more accurately the input function is estimated, the more accurate the derived quantitation. The input function can be estimated either by:

- Imaging a relatively large blood pool (usually capturing the heart including aorta and ventricles, but it can also be heart ventricles, descending or ascending aorta, aortic arch, etc.) dynamically, immediately post injection.
- Analyzing data collected previously by the user of arterial blood scans samples. A population average normalized and scaled to the particular patient.

The process of accepting the Parametric Imaging technique as part of the imaging protocol for diagnosis process still requires more research to better identify clinical use cases, to define a recommended workflow, and establish a knowledge building process among MI society on how-to use, read and interpret this temporal information to improve diagnostic value and reporting. Omni Legend PET/CT systems allow you to acquire WB dynamic data sets smoothly and easily, helping you engage into this research activity if desired and take part in investigating the potential of WBDI.

## 18.2 Whole-Body Dynamic Acquisition – General Workflow

Whole Body Dynamic Acquisition (WBDA) allows you to scan the patient's whole body or part of it, multiple times using one of the two clinical workflows described in [Whole-body dynamic clinical protocols](#).

This chapter contains information about the option to use Whole-Body Dynamic Acquisition (WBDA) functionality in PETCT studies performed with software only WBDA feature.

Whole-Body dynamic Acquisition may be used with PET radiopharmaceuticals approved by the regulatory authority in the country of use, in patients of all ages, with a wide range of sizes, body habitus, and extent/type of disease.

The Whole-Body Dynamic Acquisition allows the user to scan the body in multiple beds (at least 2 beds). The PET protocols associated with this feature are called:



- PTCT\_WBDyn\_w\_BP
- PTCT\_WBDyn

## NOTE

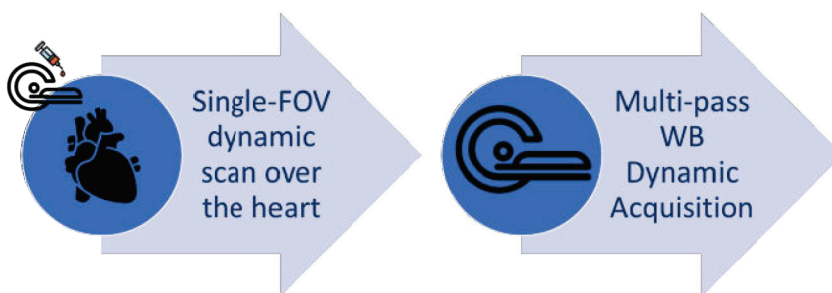
Both of the Whole-Body Dynamic Acquisition protocols are available in the GE Factory protocols under Abdominal body area.

The user can perform the scan using ready-to-use protocols, with the ability to generate the input function based on injection uptake time or on Blood Pool acquisition (a dynamic acquisition covering a blood pool, e.g. cardiac dynamic exam, or other field of view (FOV) that covers the aorta or any other large blood vessel), followed by multiple whole-body scans, termed passes, with different time rates prescription for the different passes and the different fields of view.

**Figure 315 Whole-body dynamic clinical protocols: in Protocol 1 (top) the patient is injected while on the table for a single bed dynamic blood pool (over the cardiac area / aorta, etc.) scan followed by multi-pass WB dynamic acquisition. For protocol 2 (bottom) the patient is injected while in the uptake room, waits for uptake time and then is scanned for multi-pass WB dynamic acquisition.**

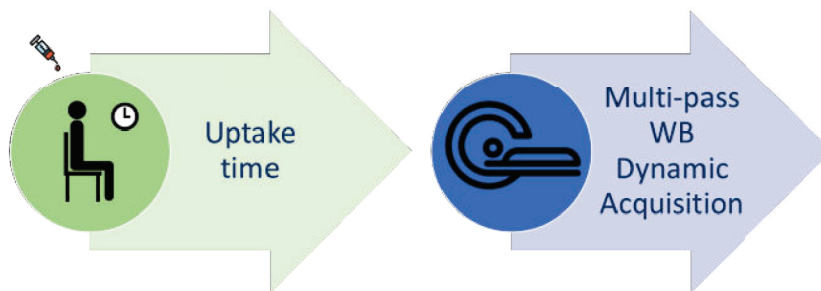
### Protocol 1:

- Inject patient on the table
- Acquire Dynamic Cardiac scan
- Acquire Multi-Pass WB Dynamic scan



### Protocol 2:

- Inject patient in uptake room
- Wait for uptake time
- Acquire Multi-Pass WB Dynamic scan



WBDA provides two clinical GE protocols, through which you can perform one of the following scan options, depending on the desired clinical protocol as described above in [Whole-body dynamic clinical protocols](#):

1. Protocol 1 – Whole Body Dynamic Acquisition with blood pool (two-step scans):
  - Single FOV Dynamic blood pool scan for offline input function calculation. Acquisition starting right before or simultaneously with the injection
  - Followed by a scan of multiple WB passes
  - Protocol 1 is available on GE factory protocols called ***PTCT\_WBDyn\_w\_BP***
2. Protocol 2 – Whole Body Dynamic Acquisition (without blood pool); one step scan
  - Multiple WB passes
  - Protocol 2 is available on GE factory protocols called ***PTCT\_WBDyn***

You can switch between clinical protocol 1 and 2 by selecting a different protocol.

#### NOTE

Whole-Body Dynamic Acquisition mode is available for scanning the patient in one direction only. Scanning the patient back and forth is not available.

The outcome of WBDA are list data file (in case VIP Mode Record option was selected), raw data and DICOM images for each exam. The system enables data transfer for offline analysis outside the scanner console. For more information, refer to [Manage Data \(Archive and Storage\)](#).

## 18.3 WBDA Clinical Workflow

### 18.3.1 WBDA General Workflow

1. Prepare the patient for the Study. Refer to user manual section 10.5

#### NOTE

Whole-Body Dynamic Acquisition scan may take a long time, depending on your prescription parameters. Explain to the patient the need to lay very still for optimal image quality. Gaining patient cooperation in advance reduces the need for repeat studies and additional dose if the patient moved during the study.

Remember that your attitude and demeanor affect your patient. Try to remain calm and cheerful throughout the procedure.

2. Open the Exam. Refer to user manual section 10.6
3. Select the relevant WBDA protocol from the Abdominal body area (***PTCT\_WBDyn\_w\_BP*** for a WBDA with Blood Pool protocol, or ***PTCT\_WBDyn*** for a WBDA protocol). Alternatively, you can prescribe a new scan and select the desired scan type.



**NOTE**

Two Dynamic Mode options are available for prescription of a Dynamic scan:

- **Single** FOV is used for Blood Pool Scans, as well as other Dynamic scans with a single FOV.
- **Whole-Body** is used for scans of the whole-body or part of it (e.g. in a scan with more than a single FOV).

**Figure 316 Select the desired PET scan Popup**

Select the desired PET Scan Type.				
VIP Mode	Off	Record	Replay	
Scan Type	Static	Gated	Dynamic	QStatic
Gating Mode	Cardiac	Respiratory		
Trigger Mode	External	Derived		
Cardiac State	Stress	Rest	Off	
Dynamic Mode	Single FOV	Whole-Body		
<div>OK</div> <div>Cancel</div>				

4. Position the patient and set landmark. Refer to user manual section 10.7



FOR PATIENTS SCANNED FOR WHOLE-BODY DYNAMIC ACQUISITION WITH BLOOD POOL, ENSURE TO SECURE THE IV LINE, TO PREVENT IT FROM GETTING CAUGHT DURING TABLE MOVEMENT.

**NOTE**

Whole-Body Dynamic Acquisition scans may take a long time depending on your prescription and requires patient to stay still. Consider positioning the patient's arms in a way to allow the user to stay still for a long time, as well as to have clear access to the IV line if needed.

**NOTE**

Whole-Body Acquisition landmark and positioning can be done either via gantry landmark (see section 10.7 in user manual) or by using Auto In option for remote positioning (see section 10.7.1 in the user manual).

5. Prescribe and acquire the Scout series. Refer to section 10.9 in the user manual.
6. Prescribe CT series and adjust parameters if needed.

If necessary, click Show Localizer to display the Graphic Rx Localizer over the scout.

Use the scout to graphically cover the relevant anatomical structures and prescribe the Start and End Locations of the subsequent CT and PET scans, as well as the display Field/s of View.

Make sure the CT scan range covers the entire PET scan range. You may prescribe a larger CT scan range than the PET range, as long as it covers the entire PET scan.

**NOTE**

For WBDA PET scans, when RadRx is set to OFF, the CT scan range will align with the largest prescribed PET scan range, for optimal coverage of the scanned area. User may adjust CT prescription by turning ON RadRx.

7. Prescribe PET scans. See Prescribe Blood Pool PET scan followed by Whole-Body Dynamic Acquisition Scan section 18.3.2, or Prescribe Whole-Body Dynamic Acquisition (WBDA) PET Scan section 18.3.3

**NOTE**

Reconstruction method and parameters selected affect the reconstruction time. consider the selection of parameters to be used in the live Whole-Body Dynamic Scan. If necessary, replay the data later to have different reconstruction parameters.

8. Acquire CT Scan

**NOTE**

CT scan may be done either before or after PET scans, as needed.

9. Acquire PET Scans. See Acquire Whole-Body Dynamic Acquisition (WBDA) with Blood Pool section 18.3.4, or Acquire Whole-Body Dynamic Acquisition (WBDA) section 18.3.5.
10. If available, review DMPR images
11. Add scans if needed.
12. Once all prescribed scans are completed press End Exam
13. Unload the patient

**NOTE**

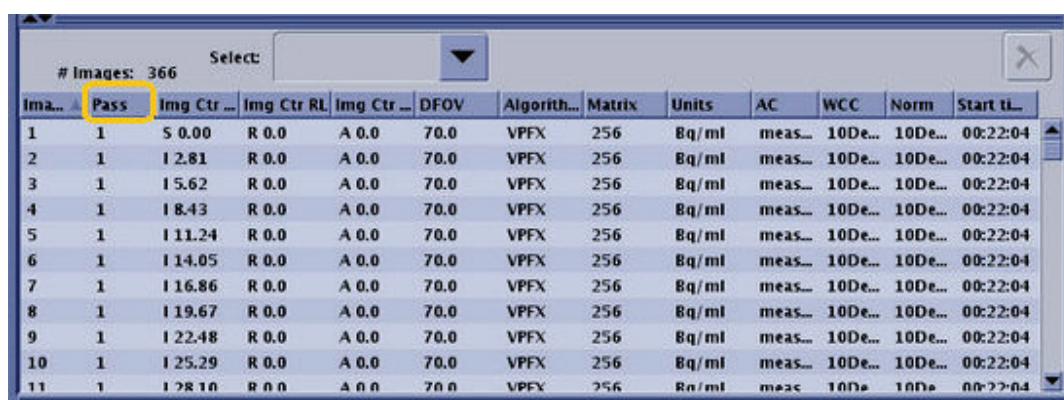
As WBDA scans may be relatively long (~1 hour), for patient safety at the end of the exam, please instruct the patient to get up slowly from the bed.

- Update tracer information using Edit Tracer App if needed. See user manual Chapter 11.

**NOTE**

The display of the Whole-Body Dynamic Acquisition scans in the Image Works Browser. The display of the Whole-Body Dynamic Acquisition will contain a new column displaying the whole-body pass number.

**Figure 317 Image Works display of the images. Note the for Whole-Body Dynamic Acquisition new column of the WBD Pass highlighted with orange rectangle**



Ima...	Pass	Img Ctr ...	Img Ctr RL	Img Ctr ...	DFOV	Algorith...	Matrix	Units	AC	WCC	Norm	Start ti...
1	1	5 0.00	R 0.0	A 0.0	70.0	VPPX	256	Bq/ml	meas...	10De...	10De...	00:22:04
2	1	1 2.81	R 0.0	A 0.0	70.0	VPPX	256	Bq/ml	meas...	10De...	10De...	00:22:04
3	1	1 5.62	R 0.0	A 0.0	70.0	VPPX	256	Bq/ml	meas...	10De...	10De...	00:22:04
4	1	1 8.43	R 0.0	A 0.0	70.0	VPPX	256	Bq/ml	meas...	10De...	10De...	00:22:04
5	1	1 11.24	R 0.0	A 0.0	70.0	VPPX	256	Bq/ml	meas...	10De...	10De...	00:22:04
6	1	1 14.05	R 0.0	A 0.0	70.0	VPPX	256	Bq/ml	meas...	10De...	10De...	00:22:04
7	1	1 16.86	R 0.0	A 0.0	70.0	VPPX	256	Bq/ml	meas...	10De...	10De...	00:22:04
8	1	1 19.67	R 0.0	A 0.0	70.0	VPPX	256	Bq/ml	meas...	10De...	10De...	00:22:04
9	1	1 22.48	R 0.0	A 0.0	70.0	VPPX	256	Bq/ml	meas...	10De...	10De...	00:22:04
10	1	1 25.29	R 0.0	A 0.0	70.0	VPPX	256	Bq/ml	meas...	10De...	10De...	00:22:04
11	1	1 28.10	R 0.0	A 0.0	70.0	VPPX	256	Bq/ml	meas...	10De...	10De...	00:22:04

### 18.3.2 Prescribe Blood Pool PET Scan Followed by Whole-Body Dynamic Acquisition Scan

- Click PET to review the PET scans prescriptions.
- You may prescribe Whole-Body Dynamic Acquisition with Blood Pool by selecting the relevant protocol from the GE factory protocols list under Abdominal body area, or by manually prescribing a single FOV dynamic scan followed by a WBDA scan.

**NOTE**

System is optimized to support WBDA with or without Blood Pool GE factory protocols. Any other manual prescription option (for example, selecting a different protocol and changing it to fit WBDA scan) may not have all supported options of the WBDA feature.

- Review the scan parameters and adjust if necessary. Prescribe the WBDA scan to be the second PET scan (and the Blood pool scan to be the first PET scan).

**NOTE**

Blood Pool Scan is a Single FOV Dynamic scan. Changing it to Static Scan and Replaying it later on as Dynamic Scan is not recommended, as this scan may not have all system capabilities supporting the proper connection to the Whole-Body Dynamic Scan.

**NOTE**

If you manually prescribed a WBDA with Blood Pool scans, ensure that the Blood Pool is a Single FOV Dynamic scan and that the WBDA is prescribed to take place right after Blood Pool scan, for optimal scan results. Other prescription options may not be fully supported and may provide sub optimal results.

**NOTE**

The Blood Pool and the WBDA scans Scan Directions need to be aligned; Thus, Blood Pool scan direction cannot be changed in this prescription. Changing the Scan Direction of the WBD, shall also change the Blood Pool scan direction.

4. Adjust the Blood Pool Dynamic single FOV scan location to fit the relevant anatomical location (usually over the aorta or the left ventricle) over the scout scan results, as shown on the Graphic Rx.

**NOTE**

Blood Pool scan range prescription is restricted to be within the Whole-Body scan range.

If necessary, click Show Localizer to display the Graphic Rx Localizer over the scout to assure the Blood Pool bed location is set within the Whole-Body scan range. Adjust it if needed.

**NOTE**

System may slightly adjust Blood Pool scan Start and End prescribed location, to align with the WBDA scan Start and End prescribed location - to fit images alignment between the two, for optimal data analysis.

**NOTE**

It is recommended that the Blood Pool scan parameters will be aligned with the Whole-Body Scan parameters, for example recon parameters, Matrix Size etc.

5. Prescribe WBDA PET scan parameters. See section 18.3.3.

**NOTE**

Blood Pool scan Single FOV dynamic scan can be viewed and analyzed using Dynamic VUE application.

**Figure 318 Example for scan parameters of WBDA with Blood Pool PET protocol. On a WBDA scan without Blood Pool, only the second WBDA scan appears.**

**PET Scan Status**  
Scan Time Remaining: **00:37:48**  
System Countrate (kcps): **0**  
True Rate: 0 kcps  
Random Rate: 0 kcps  
Total Prompts: 0 c

Images	Scan Type	Start Location	End Location	Scan Direction	No. Bed Positions	Overlap	Pre-Scan Delay	Scan Time	Start on Count Rate	Stop on Counts	AutoCnt / Audible Scan	Dose	Nuclide/Tracer
1-4455	Record	50.000	11022.580	Toward Feet	4	39	00:00:00	00:37:40	0	0	N / N	0.00 MBq	18F
1-495	Static Record	50.000	11022.580	Toward Feet	4	39	00:00:00	00:56:00	0	0	N / N	0.00 MBq	18F

FDG – fluorodeoxyglucose

### 18.3.3 Prescribe Whole Body Dynamic Acquisition (WBDA) PET Scan

1. Review the WBDA PET scan parameters (such as recon parameters, matrix size, etc.). Adjust if necessary.

If you selected a WBDA with Blood Pool protocol, prescribe the Blood pool scan to be the first PET scan, and the WBDA scan to be the second PET scan.



2. Set DMPR display per your needs. Click the Passes for which you would like to apply the DMPR prescription. Unclick the passes to un-select them. Click the **Apply for** option to select **All Passes** or click it again to un-select all passes. Use the up  and down  buttons to scroll between the passes DMP selection.
3. You may press the **Off** button, to turn off the DMPR display for WBDA.

Figure 319 DMPR of WBDA including Pass selection option

**Session Setup**

**Session Selection**

**Start New** **Combine Current** **Off**

Batch Protocol	Filming	Auto Batch	Auto Store	Auto Transfer
PETCoronal	Setup	Off	On	Off
Unused	Setup	Off	Off	Off
Unused	Setup	Off	Off	Off
Unused	Setup	Off	Off	Off
Unused	Setup	Off	Off	Off

**Apply for**

☒ Pass 1 ▲

☐ Pass 2

☐ Pass 3

☐ Pass 4

☐ Pass 5

☐ Pass 6

☐ Pass 7

☐ Pass 8 ▼

**OK** **Cancel**

**NOTE**

In case that the WBDA DMPR is selected as **Y**, at least one pass should be selected for DMPR display. Press the **Off** button if you want to turn it off for all passes.

- 4. Update the tracer information, if not done already.
- 5. Review and adjust the scan range if needed.

Make sure the relevant anatomical parts are covered within the scan range, and the CT scan range covers the entire WBDA scan range. If necessary, click Show Localizer to display the Graphic Rx Localizer over the scout to verify this, or to update the CT scan range.

**NOTE**

In WBDA scan type, the CT scan range is aligned with the largest PET scan range prescribed.

**NOTE**

The Graphic Rx display of the Whole-Body Dynamic Acquisition presents the beds scan time of the first pass of the scan.

- 6. Prescribe WBDA Scan Time. See section 18.3.3.1

**NOTE**

You may add more scans after the prescription of the WBDA scan per patient clinical need.

**18.3.3.1 Prescribed WBDA Scan Time**

- 1. Review the prescribed Scan Time and number of passes and adjust them if needed.







**Figure 320 Whole Body Dynamic Acquisition Scan popup**

The screenshot shows the 'Whole Body Dynamic Acquisition Scan' popup window. It contains the following elements:


- 1**: 'No. of Passes' field set to 9.
- 2**: 'Pre-Pass Delay' field set to 00:00:00.
- 3**: 'Passes' tab area with buttons 1 through 8, where button 1 is selected.
- 4**: 'Time Per Bed' field set to 00:01:03, with 'All Beds' and 'Variable' buttons.
- 5**: A table with columns 'Record', 'Beds (5)', 'Scan Time', and 'Scan Range'.
- 6**: The 'Record' column in the table, showing checkboxes for each bed.
- 7**: 'Pass Scan Time' field set to 00:05:15 and an 'Apply to All Passes' button.
- 8**: 'Add Time to Next Passes by:' buttons: 'None', 'Decay', and 'Increasing Time'.
- 9**: A numeric field set to 0, followed by 'Sec'.
- 10**: 'Total Scan Time' field set to 00:47:15.
- 11**: 'OK' and 'Cancel' buttons at the bottom.

Record	Beds (5)	Scan Time	Scan Range
<input type="checkbox"/>	1	00:01:03	S0.00 - I297.86
<input type="checkbox"/>	2	00:01:03	I213.56 - I511.42
<input type="checkbox"/>	3	00:01:03	I427.12 - I724.98
<input type="checkbox"/>	4	00:01:03	I640.68 - I938.54
<input type="checkbox"/>	5	00:01:03	I854.24 - I1152.10

Number	Description
1	Set the number of passes you would like to scan by typing a number to the <b>No. of Passes</b> area. Click <b>Enter</b> . The number of passes will update the <b>Passes Tab Area</b> display.
2	<p>Set <b>Pre-Pass Delay</b> to delay the system from scanning prior to every pass. Update the value of the delay accordingly HH:MM:SS, so that H-Hours, M-Minutes and S-Seconds. <b>Pre-Pass Delay</b> value will be added to the <b>Pass Scan Time</b> of the selected pass, as well as to the <b>Total Scan Time</b> of the entire WBDA.</p> <p><b>NOTE</b></p> <p>You cannot set <b>Pre-Pass Delay</b> for selected passes. Setting <b>Pre-Pass Delay</b> is applied automatically to all passes.</p>

(continued)	
Number	Description
3	<p><b>Passes Tabs Area</b> will set a dedicated tab per pass. The number on the top of the tab display the number of the pass. Click the desired pass to review and adjust the pass parameters. Use the right  and left  scrollers to scroll between the passes display.</p> <p>If scrollers are grayed out, then no further passes display is available.</p>
4	<p>Toggle between <b>All Beds</b> to <b>Variable</b> options to change the scan time prescription of the selected pass. Click <b>All Beds</b> option to set the same <b>Time per Bed</b> to all the beds in the selected pass. Click <b>Variable</b> option to allow you to prescribe variable scan time per bed for a selected pass.</p>
5	<p>Use the up  and down  scrollers to scroll between the beds.</p> <p>If scrollers are grayed out, then no further beds display is available.</p>
6	<p>Click the check box next to <b>Record</b> to record all beds in the selected Pass. Click the check box next to <b>Record</b> again to turn <b>OFF</b> the record option of the bed.</p> <p><b>NOTE</b></p> <p>In the Whole-Body Dynamic Acquisition option, the <b>Record</b> option per pass is available only for a continuous selection of passes.</p> <p>The top <b>Record</b> check box controls the record <b>ON/OFF</b> of all the beds in the selected pass. The option to control the <b>Record</b> option per bed is disabled for the Whole-Body Dynamic scan type option. Pressing the <b>Record</b> buttons of specific beds will be ignored.</p>
7	<p>Click <b>Apply to All Passes</b> to apply the selected pass parameters (scan time prescription and record mode) to all the passes in the WBDA scan.</p>
8	<p>Pass Scan Time display the scan time of the selected pass, which is the sum of the scan time of all beds in this pass, including pre-pass delay, if applicable.</p>



(continued)	
Number	Description
9	<p><b>Add Time to Next Passes by:</b></p> <p><b>None</b> – No additional time is added to the next passes automatically by the system. This option is set as the default.</p> <p><b>Decay</b> – Press <b>Decay</b> option to add additional time to the next passes to compensate for the decay of the tracer during the scan acquisition.</p> <p><b>Increasing Time [Sec]</b> – Press Increasing Time option and enter a value in seconds in the box: . The system automatically increases the following passes time with the increment value that was set.</p> <p><b>NOTE</b></p> <p>Carefully review the passes time set by the system by clicking the <b>Passes Tab Area</b>. Adjust if needed.</p> <p><b>NOTE</b></p> <p>The option to add time to the next passes by the above options is available only for prescription only in the first pass. This option will be disabled for the rest of the passes.</p>
10	Total Scan Time displays the total Whole-Body scan time, which is the sum of the scan time in all beds in all passes, including the pre-passes delays, if applicable.
11	Press <b>OK</b> to accept the prescribed Whole Body Dynamic Acquisition Scan Parameters or press <b>Cancel</b> to exit without change.

2. Click **No. of Passes** and enter the desired number of passes in the WBDA scan.
3. Prescribe the desired scan time on the first pass. Select one of the following options:
  - Press **Apply to All Passes** to set the identical same prescription to all the passes.
  - Alternatively, press the **Decay** option to increase the time for the rest of the passes in such way that the time is increasing per pass to compensate for the tracer decay.
  - Press the **Increasing Time [Sec]** option and add the incremental time to be added to each of the following passes.
  - Manually prescribe each pass scan time by scrolling between the passes and set scan time per pass manually.
4. If needed, set **Pre-Pass Delay** (prior to each pass) to add a delay time before each of the passes.

#### NOTE

If you prescribed a **Pre-Pass Delay** as well as Pre-Scan delay (in the main scan parameters window), both delays will take place – first the Pre-Scan delay prior to the whole scan, and then the Pre-Pass delay prior to each on the WBDA scan passes. It means, that prior to the first pass, you will have both delays.

5. Click the pass you would like to view or edit from the **Passes Tab Area**. To see details of the other passes, click on the **Passes Tab Area**, or use the arrows to scroll right and left.
6. View **Pass Scan Time** and **Total Scan Time** values to ensure prescription fits your patient needs.
7. Scroll between the passes in the **Passes Tab Area** and adjust scan time parameters, if necessary.
8. Switch record On/OFF for different beds or passes per need. Recording will allow you to potentially Replay the data later.

**NOTE**

WBDA may have a longer scan time than conventional scans. Make sure to empty the database prior to starting a Whole-Body Dynamic Acquisition with Record mode on, to allow the system to save all the data.

**NOTE**

When the WBDA scan is defined with **VIP Mode** as **Record**, at least one bed from WBDA prescription must remain selected for recording.

9. Click **OK** to approve to the WBDA scan times and recording of the beds' definitions. Click **Cancel** to revert all changes.

### 18.3.4 Acquire Blood Pool PET Scan

1. Prepare patient for tracer injection.
2. Review the prescription and press Confirm to start Scan
3. Start the tracer injection.
4. Carefully review the patient and press **Move to Scan** button when it flashes.
5. Press **Start Scan** when it flashes to either start the PET scan or initiate the sequence to start the PET scan when the count rate reaches the prescribed levels.
6. Review acquisition progress using the DynaPlan.

**NOTE**

Ensure to remove any unnecessary IV line that can be caught during the scan from the patient prior to proceeding with the Whole-Body Dynamic Acquisition scan.

**NOTE**

Instruct the patient to stay still and not to move while the IV line is removed, for optimal scan results.

7. Proceed to Acquire Whole Body Dynamic Acquisition (WBDA) PET scan (section 18.3.5)

### 18.3.5 Acquire Whole Body Dynamic Acquisition (WBDA) PET Scan

1. Review the prescription and press **Confirm** to start Scan.

**NOTE**

If you are scanning WBDA that was prescribed following a Blood Pool scan, it is important not to change landmark or scan parameters such as Scan Direction, to ensure the Blood Pool and the Whole-Body dynamic scans are aligned.

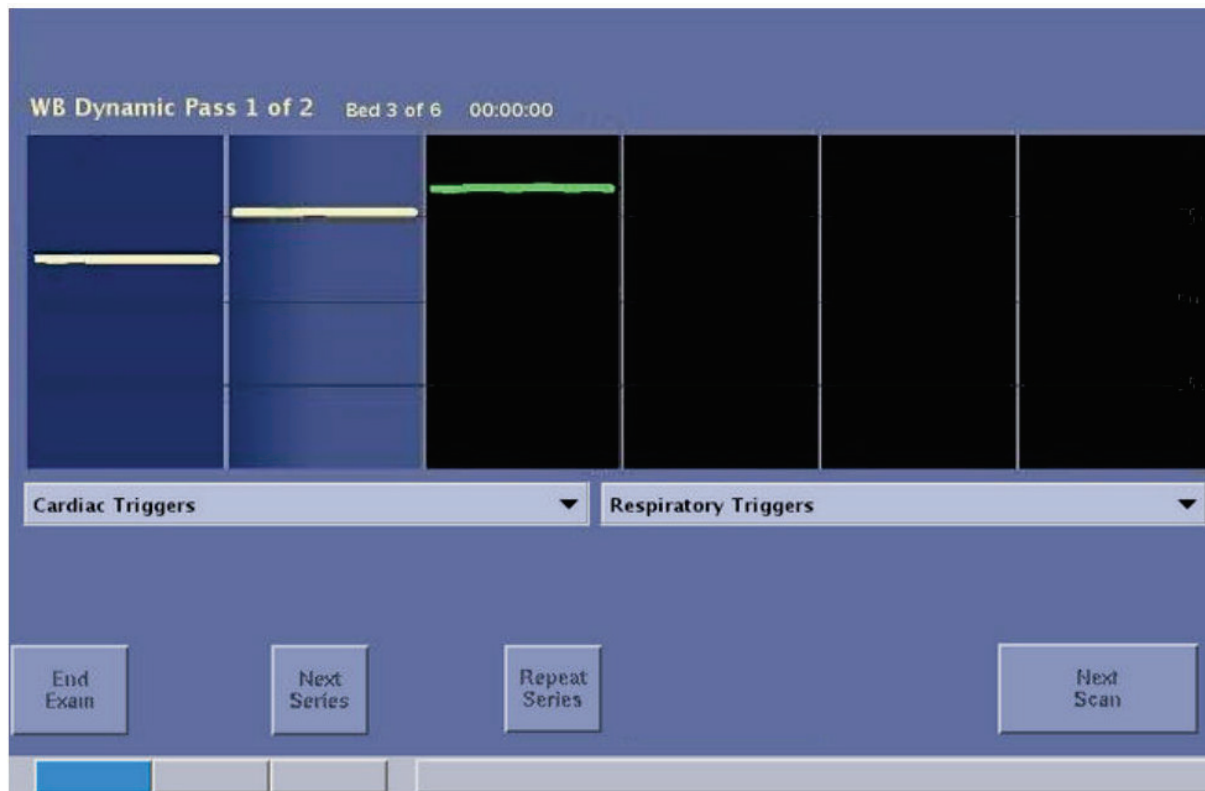
2. If necessary, press **Move to Scan** when it flashes.
3. Press **Start Scan** when it flashes to either start the PET scan or initiate the sequence to start the PET scan when the count rate reaches the prescribed levels.
4. Review acquisition progress using the DynaPlan display. See Figure below. The Passes progress is displayed per pass per bed. The progress of each pass is displayed same as any other scan.

**NOTE**

The remaining time displayed reflects the **total prescribed scan time** for the WBDA. During table and cradle movements the **Remaining Scan Time** will freeze with the latest Remaining Scan Time and will continue to count down as the next scan section will start.

5. Review DMPR images. Check image quality and look for potential patient movement. Consider adding another scan, if needed.
6. End exam.

**Figure 321 Whole-Body Dynamic Acquisition DynaPlan example of scan with 2 passes with 6 beds per pass**



## 18.4 Retrospective Recon/Replay

1. Click the **PET Recon/Replay** icon in the scan monitor toolbar to open the **PET Retro List Select** window.
2. Select the range of passes you want to replay and press **Select Series** option.

**Figure 322 Example of a PET Retro List Select Window**

The screenshot shows the 'Pet Retro List Select' window. It contains two main tables: 'Exams' and 'Series'. The 'Exams' table has columns for Patient ID, Patient Name, Exam #, Date, Time, and Suite. The 'Series' table has columns for Series #, Series Description, Landmark, and List Data. Below the tables are controls for sorting, passing, and selecting series.

Exams					
Patient ID	Patient Name	Exam #	Date	Time	Suite
stat2qst	stat2qst	835	21/1/2021	16:48	jaguar
NBD_REPLAy	NBDREP	834	21/1/2021	15:01	jaguar
sadfsadf	asdfsadf	833	21/1/2021	14:37	jaguar
36541		3471	20/1/2021	13:08	jaguar
qstatic_req_test_req-QStatic		831	17/1/2021	20:21	jaguar
qst_mul_h_ts testqstaticmultibed		830	17/1/2021	19:02	jaguar
ANONH830	ANONH830	830	17/1/2021	19:02	ANONYMI?
sod		830	17/1/2021	13:06	jaguar
vhjv.		830	17/1/2021	12:51	jaguar
vhjvm		830	17/1/2021	12:10	jaguar
bjj.		830	17/1/2021	12:05	jaguar
bjds		830	17/1/2021	12:01	jaguar
ghj		829	17/1/2021	10:39	jaguar
asdf	sadf	828	14/1/2021	17:45	jaguar
sdfasf	asdfsadf	827	14/1/2021	17:41	jaguar

Series			
Series #	Series Description	Landmark	List Data
901	blood_pool_bed_start	SP	N
902	whole_body_passes	SP	N
951	blood_pool_bed_start	SP	Y
952	whole_body_passes	SP	Y

Sort By: Date / Time Patient Name Patient Id Exam # Prior Next

Passes: 1 to 3 Beds: 1 to 6 Prior Next

Quit Select Series Update

### NOTE

Selection of passes range should be continuing. For example, in the [Example of a PET Retro List Select Window above](#), there are 3 passes. User can select to replay passes 1-3, 1-2, or 2-3, or 1-1, 2-2, 3-3, but not 1 and 3.

### NOTE

In Replay of WBDA scans, using a Beds range different from the one originally prescribed is disabled.

3. Click to highlight an exam and a series.
4. Click Select Series to open the corresponding Retro Recon View/Edit screen.

**Figure 323 Retro Recon View/Edit Window**

Name: TestChiller ID: TestChiller Protocol: Exam: 83 Series: 851

Anatomical Reference

OM

Patient Orientation Head First

Patient Position Supine

Scan Description: WBDyn Passes

Series Description:

Default Protocol: 26.42 PTCT\_WB\_Dyn

Protocol Number:

Show Localizer

PET Scan Status

Scan Time Remaining

00:00:00

System Countrate (kcps)

0

Trues Rate: 0 kcps

Randoms Rate: 0 kcps

Total Prompts: 0 c

Images	Scan Type	Start Location	End Location	Scan Direction	No. Bed Positions	Overlap	Pre-Scan Delay	Scan Time	Start on Count Rate	Stop on kcounts	AutoCnt / Audible Scan	Dose	Nuclide/Tracer	
1-4455	Record	10.000	11022.580	Toward Feet	4	39	00:00:00	00:35:36	0	0	Y / N	0.00 MBq	18F	FDG -- fluorodeoxyglucose
1-4455	Replay	10.000	11022.580	Toward Feet	4	39	00:00:00	00:35:36	0	0	Y / N	0.00 MBq	18F	FDG -- fluorodeoxyglucose

Buttons: Add Scan, Insert Scan, Delete Selected Scan, Prior, Next, Quit, Select New Protocol, List Exams

- Press **Show Localizer** to display the scout and activate the Retro Graphic Rx Localizer. See section 19.6.
- Set the parameters of the Replay/Recon.
- Press **Confirm**.
- Press **Quit**.

**NOTE**

WBDA may take longer than conventional scans. After completing the acquisition and reconstructions, Save the data using Scan Data Manager and consider deleting the scan from the Database to ensure there is enough database space for future scans.

## 18.5 Whole-Body Dynamic Acquisition Quick Steps

### 18.5.1 Typical Steps for Scanning Whole-Body Dynamic Acquisition with Blood Pool

- Start a new scan and select WBDA protocol with Blood Pool from the Abdominal body area.

2. Position the patient and set landmark.
3. Enter tracer information and dose.
4. Prescribe the scan range
5. Prescribe the blood pool scan
6. Prescribe the Whole-Body Dynamic Acquisition scan. Set the time of the first pass and apply to all passes.
7. Acquire CT localizer.
8. Acquire the CT scan.
9. Acquire the blood pool PET scans.
10. Remove the I.V. line from the patient after PET Blood Pool scan .
11. Acquire the WBDA PET scan.
12. Review the DynaPlan and DMPR images.
13. Retract the table and remove the patient.

### **18.5.2 Typical Steps for Scanning Whole-Body Dynamic Acquisition (without Blood Pool)**

1. Start a new scan and select WBDA protocol from the Abdominal body area.
2. Position the patient and set landmark.
3. Enter tracer information and dose.
4. Prescribe the scan range
5. Prescribe the Whole-Body Dynamic Acquisition scan. Set the time of the first pass and apply to all passes.
6. Acquire CT localizer.
7. Acquire the CT scan.
8. Acquire the WBDA PET scan.
9. Review the DynaPlan and DMPR images.
10. Retract the table and take out the patient.

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## 19 AutoACQC (Optional)

### 19.1 Introduction

The AutoACQC feature, which stands for Automatic Attenuation Correction Quality Control, is intended to automatically align PET and CT images to ensure proper cardiac registration. The AutoACQC output, which is displayed by the ACQC application, presents an optimal registration of cardiac PET and CT images.

AutoACQC enables two new registration correction options which are automatically calculated:

- **Automatic (Rigid):** In the automatic option, the registration metric is calculated on the identified sub-volume of the heart, but the transformation is applied on the whole scanned body. The transformation includes translations in X, Y, Z axes of the image volume. As a result, the PET series is automatically shifted in 3 axes (L,P,S) to be aligned with the CT series.
- **Advanced (Non-rigid):** In the advanced option, the CTAC is deformed by a combination of affine registration and rigid registration. The affine registration is applied on an identified sub-volume of the heart, and it smoothly merged with a global rigid transformation of the scanned body. Affine transformation includes shifts, rotations, scales, and shears, generating a better aligned CTAC deformed series. Based on this new deformed CTAC, a new PET series is reconstructed.

In addition to these options, a **Manual** registration option is available, in which the user can manually shift the PET image to align with the CT image. A **None** option is also available for the user to review the original alignment between the PET and CT data.



Figure 324 PET AutoACQC Tools

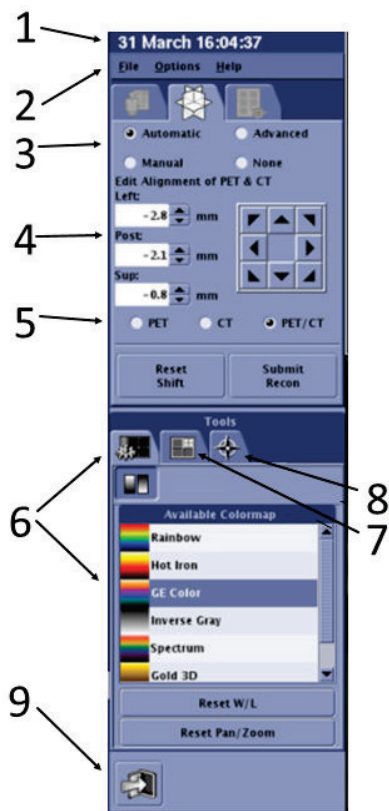


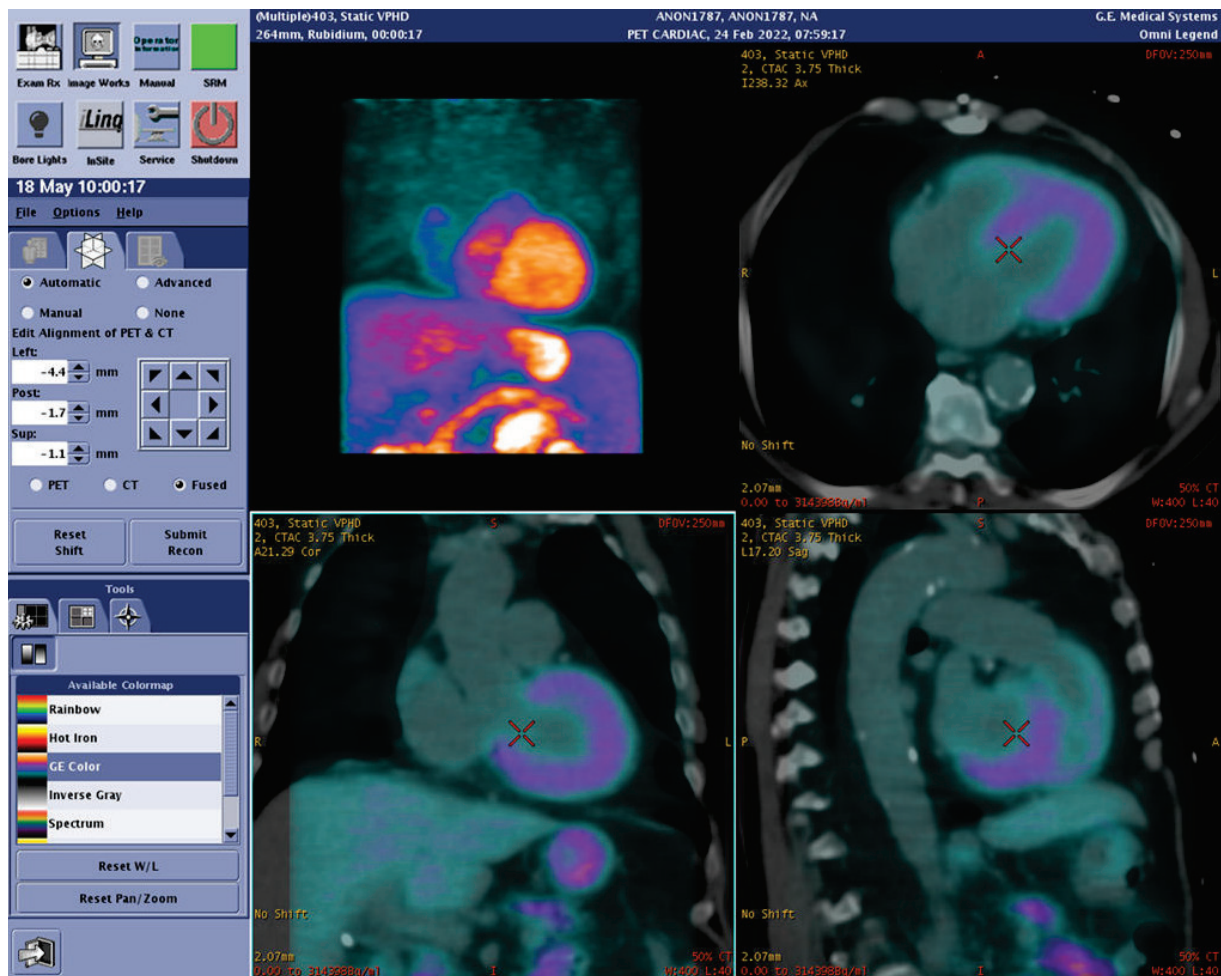
Table 91 PET AutoACQC Tools

Number	Name	Description
1	Date/Time	The current date and time.
2	Menu	Click on menu name to display its drop-down menu.
3	Registration type options	Click on the registration option to display: <ul style="list-style-type: none"><li>Automatic</li><li>Advanced</li><li>Manual</li><li>None</li></ul>

PET AutoACQC Tools continued		
Number	Name	Description
4	<b>PET/CT Alignment</b> tab	Type a value in the field, click the up/down arrows next to a field, or click the directional arrows to shift the PET image in the corresponding direction, relative to the CT image.  This tab also contains a button to reset the alignment back to the starting point and a button to submit the images for reconstruction with the currently displayed alignment.  If registration option is on <b>Automatic</b> , using this tab will switch the registration option from <b>Automatic</b> to <b>Manual</b>  If registration option is on <b>Advanced</b> , no manual shifts can be applied, and this tab will be disabled.
5	<b>Display</b> mode	Select the image display mode/type: PET, CT and fused (PET/CT) Registration type options are enabled on PET/CT display only
6	<b>Display Tool</b> tab	Select this tab to change the appearance of the images on display. Refer to <a href="#">Figure 81 on page 151</a>
7	<b>Display View Format</b> tab	Select this tab to change the number of image viewports on display and configure the contents of the viewports.
8	<b>Display Orientation</b> tab	Select this tab to change the orientation of the display images from the standard trans-axial views (axial, sagittal, coronal) to the standard cardiac views (SA, VLA, HLA).  The <b>Orientation</b> window displays the Center of the Heart (CoH) co-ordinates and the angles associated with the reorientation process.  This tab also contains a <b>Reset</b> button to restore the cardiac views to the original trans-axial orientation.
9	<b>Exit Door</b>	Click to close PET ACQC.

AutoACQC is launched by the ACQC application with the **Automatic** registration output, by default. After the application is launched, all other registration options will be available as well (**Advanced/Manual/None**), and the user can review, approve, or readjust the re-aligned data before submitting it to reconstruction.

Figure 325 AutoACQC user interface



After registration option is set, user can submit to reconstruction:

1. **Automatic (Rigid registration):** PET and CT data alignment displays automatically. The PET series is automatically shifted in 3 axes (L, P, S) to be aligned with the CT series. The Left, Posterior and Superior fields are updated automatically with the corresponding shift values. The user can submit the registration to recon if satisfied with the alignment by clicking on **Submit Recon**. The default series description of the new reconstructed PET series is **+SAu- Original PET Series Description**. The user can edit the series description in the **Recon Submission** window.

Optional: Click the **Save Shift Vector** check box to save the shift vectors to the database for use during subsequent retrospective reconstructions.

#### NOTE

User can adjust the alignment by shifting the values in the Left, Posterior and Superior fields in the PET/CT Alignment tab. In this case the registration option will be presented as **Manual** and not **Automatic**.

2. **Advanced (Non-rigid registration):** PET and CT data alignment is displayed automatically. The CTAC series is transformed by a 12 degrees of freedom transformation generating a better aligned CTAC deformed series. The new deformed CTAC series is added to the exam under the following default description: **Non-Diagnostic CTAC-PT Series Description-CT Series Description** Refer to [Figure 326 on page 513](#). Based on the new deformed CTAC, a new PET series is reconstructed.

#### NOTE

The series description of the new deformed CTAC series is limited to 64 characters.

**Figure 326 ACQC Advanced registration option: series description of the new deformed CTAC**

Series ▲	Type	Images	Description	M...	Manu...	MPPS	Arch...	Tr...
404	STATIC	153	+SAu-Static	PT	GE M...			
404	PROSP	153	Non diagnostic CTAC-Static VPHD-CTAC 3.75 T...	CT	GE M...			
405	STATIC	153	+S-Static	PT	GE M...			
407	STATIC	153	+SAd-Static	PT	GE M...			
408	STATIC	153	+S-Static VPHD	PT	GE M...			
409	STATIC	153	+S-Stress Static Emission	PT	GE M...			
410	STATIC	153	+S-Stress Static VPHD	PT	GE M...			
411	STATIC	153	+S-Stress Static VPHD	PT	GE M...			
903	REPLAY	4	Rest Static Emission	R...	GE M...			



THE NEW DEFORMED CT IS A NON-DIAGNOSTIC CTAC SERIES. THIS SERIES IS TO BE USED ONLY FOR RECON REVIEW AND NOT TO BE USED FOR DIAGNOSTIC PURPOSES.

The user can submit the registration to recon if satisfied with the alignment by clicking on **Submit Recon**. The default series description of the new reconstructed PET series is **+SAd- Original PET Series Description**. The user can edit the series description in the **Recon Submission** window.

#### NOTE

Manual shifts are disabled for this option and the **PET/CT Alignment** tab is disabled.

3. **Manual:** an option for the user to manually shift the PET data to align it to the CT data using one of the following methods:
- **Option 1:** Press and hold the **Shift** key with one hand; middle-click and drag to move the PET data relative to the CT image.
  - **Option 2:** Click on a viewport to select it, then click the eight arrows in the **Alignment** tab, shown in [Figure 263 on page 431](#), to move the PET image relative to the CT image.
  - **Option 3:** Click on the Left, Posterior and Superior fields to activate them, then enter values into the corresponding text boxes.
    - Positive values move the PET image in the Left, Posterior and Superior directions.
    - Negative values move the PET image in the Right, Anterior and Inferior directions.

Optional: Click **Reset + Shift** to return to the original alignment, and start over.

The user can submit the registration to recon if satisfied with the alignment by clicking on **Submit Recon**. The default series description of the new reconstructed PET series is **+S- Original PET Series Description**. The user can edit the series description in the **Recon Submission** window.

4. **None**: an option to display the original alignment between the PET data and CT data.

**Figure 327 ACQC New PET series description by reg. type option**

410	STATIC	153	+SAd-Static	PT	GE ME...	aws...
411	STATIC	153	+SAu-Static	PT	GE ME...	aws...

For the prospective scan workflow, the CT and PET series used for the AutoACQC feature are under recons **R1** and **Recon 1** respectively:

- CT **R1** values: Recon Type = Q.AC Wide View
- PET **Recon 1** values: Recon Type = VUE Point HD (default)/FORE-FBP; Recon option = MAC

The AutoACQC output should be reviewed in the **Fused Display** mode only. Choosing the PET or **CT** display modes disables all registration options. To go back to the PET and CT data alignment, choose **back the Fused Display** mode.

To set user preferences, refer to [Set the Cardiac ACQC User preferences](#).

## 19.2 Application Prescription

The ACQC application can be launched automatically during prospective (live) scan workflow or by retrospective recon/replay of cardiac scans. The application will launch with the **Automatic** registration output (by default) and will display all registration options: **Automatic**, **Advanced**, **Manual**, **None**. The **Advanced** option will be available when option loading is completed.

### 19.2.1 Prospective scan (Live mode)

In the **PET Acquisition** window, under the **PET Reconstruction** tab, click the **ACQC** button (displayed with the **Recon Option** button) and select **On**, refer to [Figure 328 on page 515](#). The user can turn this feature **On/Off**. In cardiac protocols, AutoACQC is **On** by default. AutoACQC prescription can be changed to **On/Off** when building user protocol in protocol management.

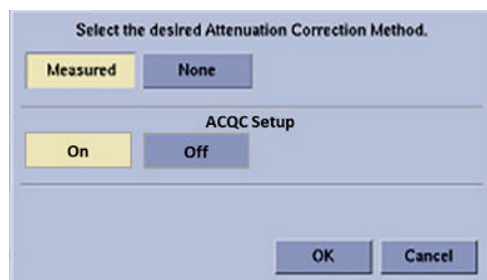


**Figure 328 PET AutoACQC Application prescription for live scan (PET acquisition window + ACQC setup window)**



The screenshot displays the PET Scan Status and Acquisition Window. The top section shows patient information (Name: ID:ddd, Protocol: 25.38 PETCT\_Rb\_Rest-Stress, Exam: 236, Series: 1) and a patient diagram. The middle section contains various setup buttons (XY, Filming, AutoFilm Setup, Camera, Laser Camera) and scan parameters (Scan Description: Rest Static Emission, CT Start: 5100.000, CT End: 5214.640). The bottom section features a table of scan parameters and a series of buttons for scan management.

Images	Scan Type	Start Location	End Location	Scan Direction	No. Bed Positions	Overlap	Recon Enabled	Recon Start Location	Recon End Location	No. Bed Positions	DFOV (cm)	R/L Center (mm)	AP Center (mm)	Recon Type	Matrix Size	Recon Method	DMPR
1-153	Static Rest Record	5100.000	5214.640	Toward Feet	1	0	Y	5100.000	5214.640	1	26.4	14.0	82.0	VN10 5.0 mm 3302	128	MAG20n	H
1-153	Static Stress Record	5100.000	5214.640	Toward Feet	1	0	Y	5100.000	5214.640	1	26.4	14.0	82.0	VN10 5.0 mm 3302	128	MAG20n	H



Select the desired Attenuation Correction Method.

Measured ☐ None ☐

ACQC Setup

On ☐ Off ☐

OK Cancel

#### NOTE

For cardiac scans, ACQC setup default is **On**. This means the application launches automatically when the PET series reconstruction (Recon 1) is completed.

## 19.2.2 Retrospective scan (Replay mode)

In the **PET Acquisition** window, under the **PET Reconstruction** tab, click the **ACQC** button (displays with the **Recon Option** button) and select **On**, refer to [Figure 329 on page 516](#). You have the option to turn this function **On/Off**.

**Figure 329 ACQC setup window in retrospective workflow**

The screenshot shows the ACQC setup window with the following settings:

- Attenuation:** Type: **Measured** (selected), **None**
- Open ACQC:** **On** (selected), **Off**
- CTAC Type:** CTAC Series: **CTAC 3.75 Thick** (text box). Navigation: **Prior** (up arrow), **Next** (down arrow).
- Contrast Compensation:** **Automatic** (selected), **On**, **Off**
- CTAC Shift:** **No** (selected), L (mm): **0.000**, P (mm): **0.000**, S (mm): **0.000**
- Correction:** Well Counter: **Sensitivity & Activity** (selected), **Sensitivity**, **None**
- WCC File:** **Default** (selected), **Others**
- Normalization:** **Default** (selected), **Others**, **None**. Text box: **50 MCC 01 November 2021**. Navigation: **Prior** (up arrow), **Next** (down arrow).
- Randoms:** **On** (selected), **Deadtime:** **On** (selected)
- Scatter:** **On** (selected)
- Buttons:** **OK**, **Cancel**

### NOTE

For retrospective recon/replay, the ACQC setup is **Off** by default. This means the application will not launch automatically when the PET series reconstruction is completed. The user must select **On** to have the application launch automatically.

### NOTE

For offline processing, the user needs to launch the AutoACQC application from the [Data Apps List](#).

## 19.3 AutoACQC - Prospective Scan Workflow

1. Open the Exam.
2. Select the relevant cardiac protocol.
3. Prescribe and acquire the scout scan.
4. Prescribe and acquire the CT scan.
5. Prescribe the PET scan.
6. (Optional) To launch the AutoACQC application during the exam, go to the PET Reconstruction tab, click on the ACQC button and make sure the ACQC setup is On.
7. Acquire the PET scan.
8. When PET recon is ready, ACQC application will launch automatically with the AutoACQC output.
  - Application will launch when in ImageWorks display. If not, a system message displays that the application cannot be launched. Press **Ok** to transfer the display from Exam Rx to ImageWorks in order for application to launch. The user can remain in Exam Rx display and dismiss application launch by pressing **Cancel**.
  - If the ACQC application was open already, a system message displays that ACQC application is ready to launch with the new exam/series. Press **Ok** to confirm closing the current display of ACQC and to launch the application with the new referred exam/series. The user can dismiss application launch by pressing **Cancel**.
9. Proceed with registration steps of AutoACQC, refer [section 19.1](#).

## 19.4 AutoACQC - Retrospective Scan Workflow

1. Click the **PET Recon/Replay** icon in the scan monitor toolbar to open the **PET Retro List Select** window.
2. Select the series you want to replay and click **Select Series**.
3. Click to highlight an exam and a series.
4. Click **Select Series** to open the corresponding **Retro Recon View/Edit** screen.
5. (Optional) To launch the AutoACQC application, go to the **PET Reconstruction** tab, click the **ACQC** button and select **On** for the ACQC setup.

### NOTE

For retrospective recon/replay, the ACQC setup is **Off** by default. This means the application will not launch automatically when the PET series reconstruction is completed. Select **On** to have the application launch automatically.



6. Press **Confirm**.
7. When PET recon is ready, ACQC application will launch automatically with the AutoACQC output.
8. Proceed with registration steps of AutoACQC [section 19.1](#).

**PET Recon/Replay** with AutoACQC **Automatic/Manual** registration output shifts:

If you previously submitted the reconstruction shifts by checking the **Save Shift Vector** box, the vector shifts will appear in the **Recon Option/ACQC** set-up window:

Attenuation:	
Type:	<input checked="" type="button" value="Measured"/> <input type="button" value="None"/>
Open ACQC: <input type="button" value="On"/> <input checked="" type="button" value="Off"/>	
CTAC Type:	
CTAC Series:	<div> <input type="button" value="0 Non diagnostic CTAC-Stress Static HAC-CTAC 3.75 Thick"/> <input checked="" type="button" value="2 CTAC 3.75 Thick"/> <input type="button" value="0 Non diagnostic CTAC-Rest Static HAC-CTAC 3.75 Thick"/> </div> <div> <input type="button" value="Prior"/> <input type="button" value="Next"/> </div>
Contrast Compensation:	<input checked="" type="button" value="Automatic"/> <input type="button" value="On"/> <input type="button" value="Off"/>
CTAC Shift:	<input checked="" type="button" value="Yes"/> L (mm): <input type="text" value="-3.80"/> P (mm): <input type="text" value="-1.60"/> S (mm): <input type="text" value="-0.80"/>
Correction:	
Well Counter:	<input checked="" type="button" value="Sensitivity &amp; Activity"/> <input type="button" value="Sensitivity"/> <input type="button" value="None"/>
WCC File:	<input checked="" type="button" value="Default"/> <input type="button" value="Others"/>
<input type="text" value="50 WCC 01 November 2021"/> <div> <input type="button" value="Prior"/> <input type="button" value="Next"/> </div>	
Normalization:	<input checked="" type="button" value="Default"/> <input type="button" value="Others"/> <input type="button" value="None"/>
<input type="text" value="SOURCE Annulus"/> <div> <input type="button" value="Prior"/> <input type="button" value="Next"/> </div>	
Randoms:	<input checked="" type="button" value="On"/>
Deadtime:	<input checked="" type="button" value="On"/>
Scatter:	<input checked="" type="button" value="On"/>
<input type="button" value="OK"/> <input type="button" value="Cancel"/>	

The CTAC shift will be set to **Yes**. The L, P, S shift values you have submitted will be presented.

**PET Recon/Replay** with AutoACQC **Advanced** registration output:

The Non-Diagnostic CTAC series will be chosen. Note the CTAC shift is set to **No** before proceeding to **Confirm**.

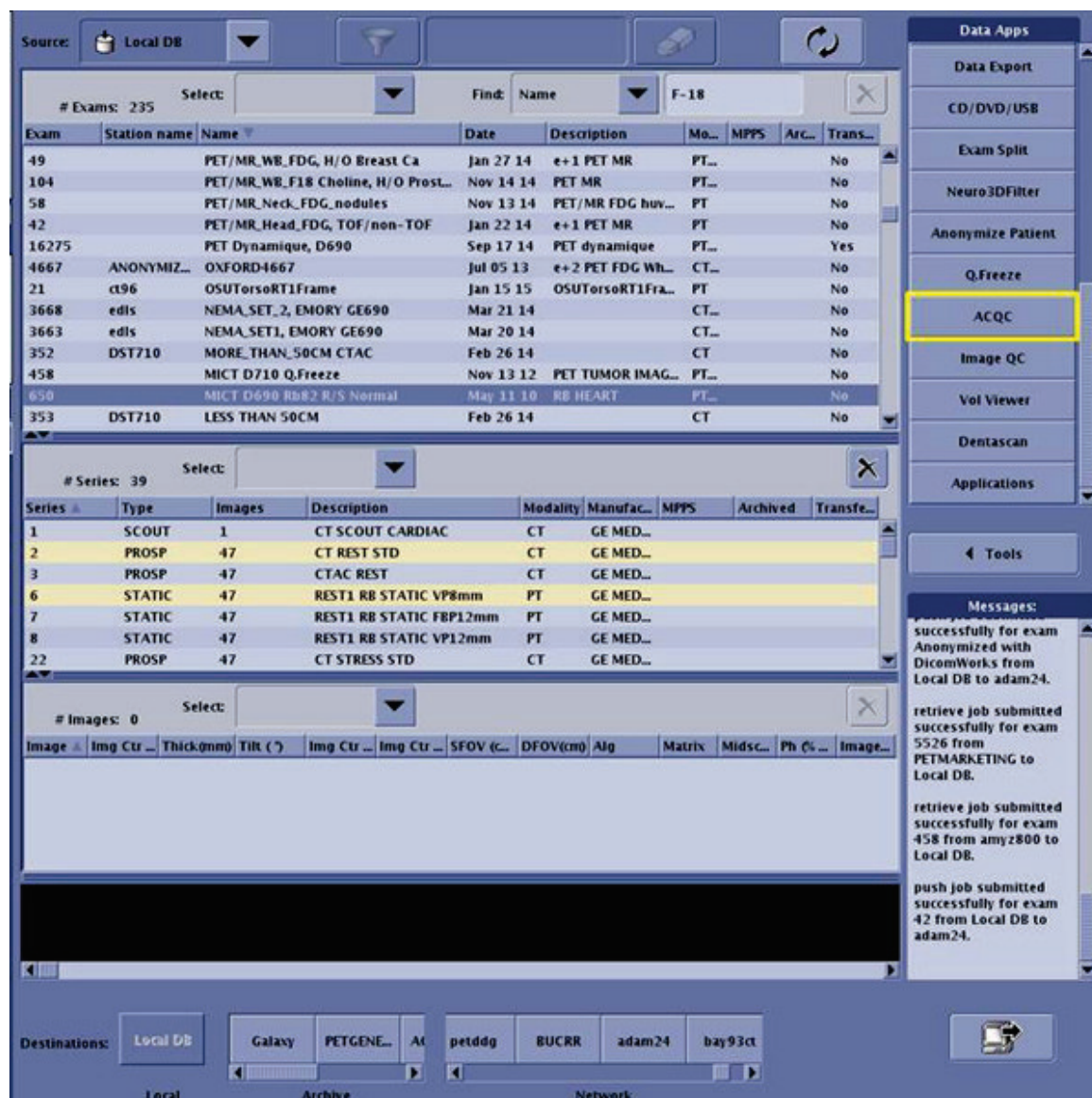
Attenuation:	
Type:	<input checked="" type="button" value="Measured"/> <input type="button" value="None"/>
Open ACQC: <input type="button" value="On"/> <input checked="" type="button" value="Off"/>	
CTAC Type:	
CTAC Series:	<div> <div> <div>0 Non diagnostic CTAC-Stress Static MHC-CTAC 3.75 Thick</div> <div>2 CTAC 3.75 Thick</div> </div> <div> <div>Prior</div> <div>Next</div> </div> </div>
Contrast Compensation: <input checked="" type="button" value="Automatic"/> <input type="button" value="On"/> <input type="button" value="Off"/>	
CTAC Shift:	<input type="button" value="No"/> L (mm): <input type="text" value="0,000"/> P (mm): <input type="text" value="0,000"/> S (mm): <input type="text" value="0,000"/>
Correction:	
Well Counter:	<input checked="" type="button" value="Sensitivity &amp; Activity"/> <input type="button" value="Sensitivity"/> <input type="button" value="None"/>
WCC File:	<input checked="" type="button" value="Default"/> <input type="button" value="Others"/>
<div> <div>SD MHC 01 November 2021</div> <div>Prior</div> <div>Next</div> </div>	
Normalization: <input checked="" type="button" value="Default"/> <input type="button" value="Others"/> <input type="button" value="None"/>	
<div> <div>SDMCC Annulus</div> <div>Prior</div> <div>Next</div> </div>	
Randoms:	<input checked="" type="button" value="On"/> <input type="button" value="Off"/>
Scatter:	<input checked="" type="button" value="On"/> <input type="button" value="Off"/>
Deadtime: <input checked="" type="button" value="On"/> <input type="button" value="Off"/>	
<input type="button" value="OK"/> <input type="button" value="Cancel"/>	

## 19.5 Start the PET Cardiac ACQC Application

The user can launch AutoACQC by selecting the ACQC application from the [Data Apps list](#).

1. Select a study from the **Exams** database on the Patient List. See [Figure 330 on page 521](#).
2. Click to highlight the PET and CT series you plan to use from the series list.
3. Click **ACQC** from the **Data Apps list** on the right side of the browser.

Figure 330 Select PET and CT Series from the Image Works Patient Browser



- AutoACQC is launched with **Automatic** registration output. After application is launched, all other registration options will be available (**Advanced/Manual/None**), and you can review, approve, or readjust the re-aligned data before submitting it to reconstruction.

AutoACQC (Optional)

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## 20 Post-Processing

### 20.1 Post-Processing Introduction

This chapter describes how to replay the ViP Record list data with new acquisition parameters, then reconstruct images with the new acquisition parameters set, or use a different filter and display parameters to retrospectively reconstruct the PET raw data. This chapter also contains instructions to manage the PET Reconstruction Queue.

- Typical PET Series Retrospective Reconstruction
- Typical ViP Replay and Prospective Reconstruction
- PET Reconstruction Management

#### NOTE

If you make a **Save State** screen capture file during post-processing, and then use the Edit Tracer function. Edit Tracer will not update the “Save State” file.

#### NOTE

If you make a Save State screen capture file of Precision DL images during post-processing, then change Patient weight or Tracer information from a viewer screen, the quantitation of the image after the change will not reflect the necessary update of Precision DL image generation with the new information as it will need regeneration with the updated weight and/or tracer information. Use **Edit Tracer** and **Edit Patient Information** on the console to apply the changes, then manually perform retrospective reconstruction to generate new Precision DL images with the change, then perform Save State recapturing.

In general, it is not recommended to apply weight or tracer information changes through save state or screen capture to any image type.

#### NOTE

When Edit Patient or Anonymize Patient tools have been used to modify the exam, the link to the CT used as the attenuation map for a PET raw series is no longer available. This is a concern for retro-reconstruction of a PET raw series or ViP Replay with prospective reconstruction of a PET raw or PET list series. The user must select the appropriate CT for use as the attenuation map for the PET reconstruction.

To do this, the user must select the **PET Reconstruction** tab and click **Recon Options** to open a window that contains all the reconstruction options available. Under the CTAC Series, the user needs to select the CT series to be used for the reconstruction.

### 20.2 PET Reconstruction and Replay



## 20.2.1 Typical PET Series Retrospective Reconstruction

1. Click the **PET Recon/Replay** icon in the **Scan Monitor** toolbar to open the **Pet Retro List Select** window.

**Figure 331 Pet Retro List Select Window**



2. Click on an exam or a **901 - 950** series.
  3. Click **Select Series** to open the **Retro Recon View/Edit** window.
- The window opens with the **Recon** tab open and Recon enabled.

Figure 332 Retro Recon View/Edit Window

Name: Single FOV Respiratory ID: Single FOV Re Protocol: Exam: 31 Series: 901

Anatomical Reference

OM

Patient Orientation  
Head First

Patient Position  
Supine

Scan Description: VIP Record+ Static Default Protocol: 26.31 PTCT\_ET

Series Description: Retro Static VPHD Protocol Number:

PET Scan Status

Scan Time Remaining

00:00:00

System Countrate (kcps)

Trues Rate: 0 kcps  
Randoms Rate: 0 kcps  
Total Prompts: 0 c

Add Scan Insert Scan Delete Selected Scan

Prior Next

Images

Images	Scan Type	Start Location	End Location	Scan Direction	No. Bed Positions	Overlap	Recon Enabled	Recon Start Location	Recon End Location	No. Bed Positions	DFOV (cm)	R/L Center (mm)	A/P Center (mm)	Recon Type	Matrix Size	Recon Option	DMPR
1-89	Static VIP Off	1118.650	1127.750	Toward Head	1	0	Y	1118.650	1127.750	1	70.0	80.0	80.0	VPHD 6.4 mm 17/4	256	NAC	N

Quit Select New Protocol List Exams

Confirm

Series Auto Transfer Show Recon 1 Show Recon 2 Show Recon 3

- Click **Recon Type** to open the **Select Desired PET Recon Type** window.  
Review and modify the parameters as needed, then click **OK** to close the window.
- If there are multiple CTAC series available, click **Recon Option** and select the appropriate CTAC series for the Retrospective Reconstruction.



**Figure 333 Recon Options**

Attenuation:  
Type:

CTAC Type:  
CTAC Series:

Contrast Compensation:

CTAC Shift:  L (mm):  P (mm):  S (mm):

Correction:  
Well Counter:

WCC File:

Normalization:

Randoms:

Scatter:

Deadtime:

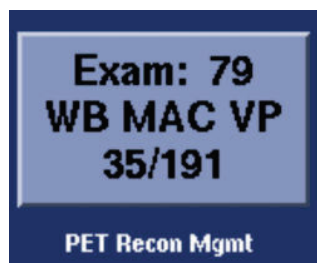
Q.Static:

6. Enter a **Series Description** in the provided field.
7. Click **Confirm** to send the data to the PET Recon Management Queue.

**NOTE**

The **PET Recon Mgmt** icon displays the exam in progress information, instead of the icon picture, while data remains in the queue.

**Figure 334 PET Reconstruction Management Icon Label**



8. If **Confirm** is clicked without entering the series description, the system adds the series description based on the scan type and recon type selected. The figure below shows an example of series description automatically added by the system for a static scan type with recon type VPHD, 6.4mm filter, 12 subsets and 4 iterations.

**Figure 335 System-added Series Description**

# Series: 8		Select:							
Series ▲	Type	Images	Description	M...	Manuf...	MPPS	Archiv...	T...	
12	STATIC	83	WB 3D NAC	PT	GE M...				
401	STATIC	35	QStatic-D VPHD6.4S12/4	PT	GE M...				
402	STATIC	83	Static VPHD6.4S12/4	PT	GE M...				
403	STATIC	83	Static VPHD6.4S12/4	PT	GE M...				
901	LIVE	5	Eyes to Thighs Emission	R...	GE M...				
902	REPLAY	5	Eyes to Thighs Emission	R...	GE M...				
951	LIST	5	Eyes to Thighs Emission	L...	GE M...				

## 20.2.2 Typical ViP Replay and Prospective Reconstruction

Follow these instructions to use ViP Record list data to ViP Replay with prospective reconstruction parameters.

1. Click the **PET Recon/Replay** icon in the **Scan Monitor** toolbar to open the **PET Retro List Select** window.
2. Click to highlight an exam or a **951 - 990** series.
3. Click **Select Series** to open the corresponding **Retro Recon View/Edit** window.
  - The **Retro Recon View/Edit** window displays the original acquisition and reconstruction parameters for your information, but deactivates them so you cannot select them.
  - The **Retro Recon View/Edit** window also displays a set of Replay parameters that match the original acquisition and reconstruction parameters.
  - Review and modify the Replay parameters.

4. Enter a scan description and series description in the corresponding fields.
5. Click **Confirm** to send the data to the PET Recon Management Queue.

An acquisition window opens to provide feedback.

**Figure 336 ViP Record Acquisition Window**

Name: Single FOV Respiratory ID: Single FOV Re Protocol: Exam: 31 Series: 951

**PET Scan Status**  
Scan Time Remaining: **00:02:23**  
System Countrate (kcps): **353**  
Trues Rate: 298 kcps  
Randoms Rate: 54 kcps  
Total Prompts: 34,369,192 c

Anatomical Reference: OM  
Patient Orientation: Head First  
Patient Position: Supine

Scan Description: VIP Record+ Static  
Series Description: Retro Static VPHD

Static Bed 1 of 1 00:02:23

Cardiac Triggers: [Dropdown]  
Respiratory Triggers: [Dropdown]

Quit

**System Messages**

Scan Number	Scan Type	Start Location	End Location	Bed Positions	Scan Time
1	Static List	1118.65	5127.75	1	240
2	Static Unlist	1118.65	5127.75	1	240
3	Static Unlist	1118.65	5127.75	1	240

## NOTE

MotionFree option offers two Replay modes:

1. Standard mode (default):
  - a. If derived triggers are not available in the list series file for least one of the beds selected for replay, this mode calculates and writes to list series file, triggers, waveforms and R-Value (respiratory motion measure) for the entire bed scan time.
    - The SW will not overwrite waveforms and triggers for those beds with previously extracted waveforms and triggers.
  - b. If derived triggers are available in list series file for all beds selected for replay, then triggers, waveforms and R-Value will be inherited from list series file and used for image reconstruction.
    - User can change scan time per bed, yet R-Value will not be recalculated, instead, it will be inherited from list series file and used for motion correction automatic decision. For the scan time selected by the user, the corresponding waveforms and triggers will be

inherited from the list series file as well. Notice, that R-Value in list series files represents full scan time per bed, as scanned in the original acquisition.

c. **NOTE**

When replaying data originally acquired with MotionFree, some beds that were corrected for motion based on R-Value calculated at Base Bed Time, may not be corrected for motion in replay, in case the final R-Value is below the threshold. You may decrease the threshold during replay to be able to correct those beds for respiratory motion.

2. Advanced mode:

- a. This mode calculates triggers, waveforms and R-Value for beds selected for motion, mimicking actual acquisition, as it allows the user to set base bed time and Q.Static bed time and experience MotionFree automatic decision to extend scan time based on different base bed time and Q.Static bed time.
- b. This mode does not write triggers, waveforms and R-Value to list series file.
- c. This mode allows the user to change pre-scan delay value.

**NOTE**

When using fast tracers, R-Value may be significantly affected by the intrinsic period.

**NOTE**

Pre-scan delay does not contribute to calculation of triggers, waveforms and R-Values during replay as well.

**NOTE**

MotionFree could be used for Replay of static acquisition into single or multi FOV 4D gated. 4D gated images could be used to show the movement of hot spots or findings due to respiration, and to correct for motion using post processing analysis by applying Q.Freeze technique.

## 20.3 PET Reconstruction Management

Follow these instructions to manage the data in the Reconstruction Queue.

1. Click **PET Recon Mgmt** in the **Scan Monitor** toolbar to open the **PET Recon Management** window.

**Figure 337 PET Recon Management Window**

2. You have the following options:

- Use the active **Prior/Next** arrows to scroll through the list.
- Click **Update List** to update the list and refresh the display.
- Click on a job, then click **Delete Selected** to remove it from the list. An alert window opens and prompts for a confirmation. Click **OK** to delete the job.
- Click on a job, then click **Priority Recon** to move that job to the top of the list. The **Status** column lists the new jobs, as well as the job in progress. The system reconstructs the priority job as soon as it finishes the job in progress.
- If a reconstruction fails, click **Delete Failure** when it displays to clear the failed reconstruction out of the queue.
- Click **Quit** to close the **PET Recon Management** window.

**NOTE**

Precision DL image reconstruction will not start until the reconstruction for the input images (Q.Clear) has completed. Precision DL reconstruction includes pre-processing, inferencing via the Deep Learning inference engine and final image installation.

Note that Precision DL images will not be installed on a frame by frame bases into Image Works like other reconstruction methods. It will show all slices for all beds, only once images are ready and inferencing is complete.

When Precision DL(s) is prioritized using the priority recon feature, It`s input reconstruction will be prioritized as well, and vice versa.

If the Q.Clear reconstruction required as input to Precision DL(s) is deleted, the Precision DL reconstruction(s) will also be deleted.

If a Precision DL reconstruction is deleted, the associated Q.Clear reconstruction will remain.

In the case where more than one Precision DL strength is chosen for a single reconstruction option (i.e. L, M and H), only the first of the Precision DL jobs will update Recon status as follows: **New**, **Pending CTAC**, **Progress** per the QClear state, and then **Inferencing**, and **Completed**.

## 20.4 PET PMR (Prospective Multiple Reconstructions)

When prescribing multiple reconstructions for a PET series, always use **Recon 1** for the image series used to review the patient's scan prior to releasing the patient. In the event of a reconstruction backlog, **Recon 1** for a patient is prioritized ahead of other pending recons. If a second patient is scanned before all the reconstructions of the first patient scan are completed, the **Recon 1** for the new patient will go to the front of the queue. This will give you the ability to visualize PET images prior to releasing the patient.

**NOTE**

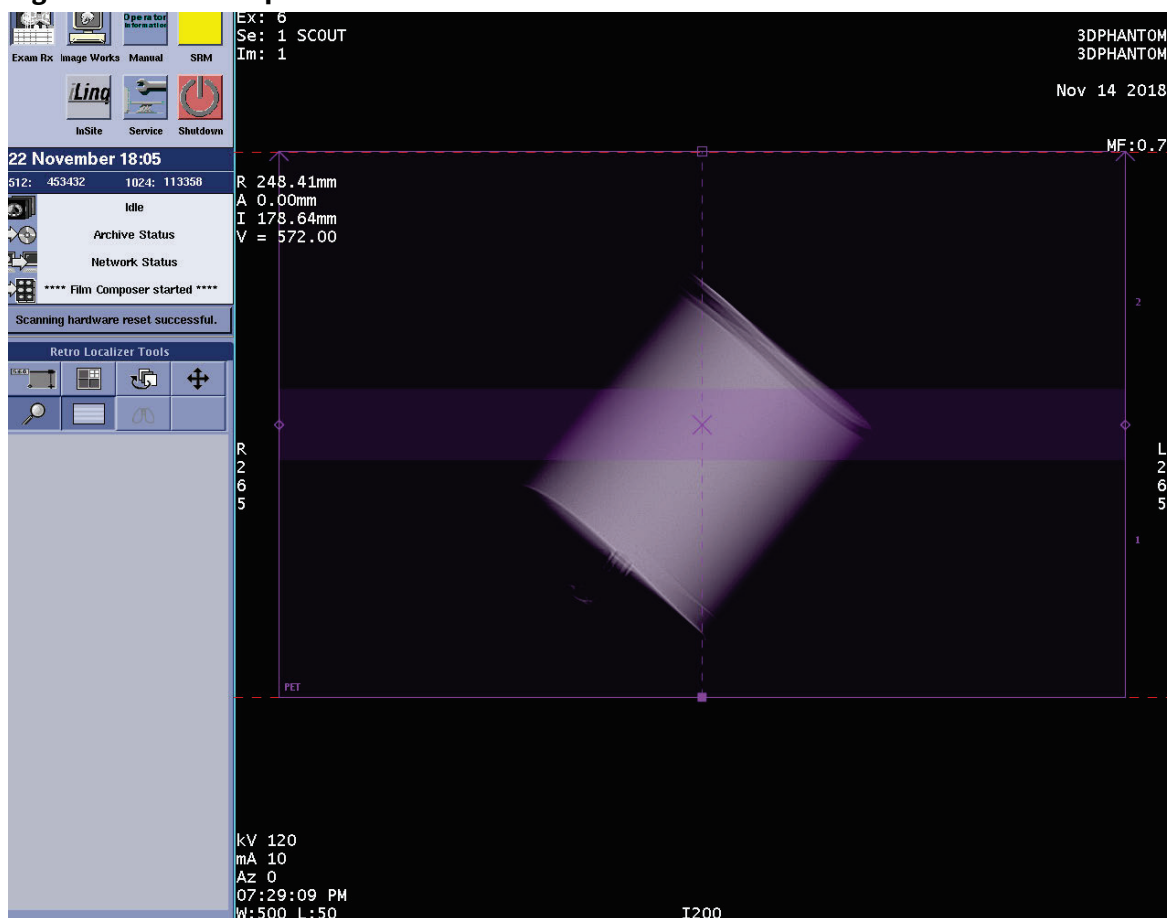
DMPR is disallowed with Precision DL reconstructions. However, DMPR is allowed for a PET reconstruction prescribed with the Precision DL image enhancement if the user has chosen to save the input Q.Clear images. This can be accomplished by selecting the **None** option under the **AI Method** in the **PET Recon Type** panel.

## 20.5 Retro Graphic Rx Localizer

1. Press **Show Localizer** to display the scout and activate the Retro Graphic Rx Localizer.
2. Click the **Show Recon 2** button and enable the Recon.

**NOTE**

Retro Graphic Rx will not launch if there is no Scout in the Selected Exam.

**Figure 338 Retro Graphic Rx Localizer****NOTE**

Retro Graphic Rx will not allow the user to change the start and end location of Recon 1. Recon 2 and Recon 3 can be modified.

3. Click and drag the solid box to change the Start Location.
4. Click and drag the empty box to change the End Location.
5. Press and hold the **Shift** key while you click and drag either the solid box or the empty box to adjust the Start and End Locations and expand and collapse the scan range.
6. Click and drag a diamond to resize both sides of the Display Field of View (DFOV). Press and hold while you click and drag a diamond to change the corresponding edge of the DFOV.
7. Review the updated parameters on the scan screen before clicking **Confirm**.






## 20.6 Data Application PET Exam Split


Use these steps to split a PETCT exam into separate exams. In this procedure, a PETCT Whole Body exam was performed with the desired result to split the PETCT series from all the PET series with the original exam. Considerations:


- The original exam and series are not modified with PET Exam Split.
  - Exam split does not support PET RAW and LIST data.
  - An exam cannot be split if it is in use by another application.
1. Navigate to the **Image Management** work area.
  2. Select the exam you want to split and then select the series for the new exam.

**Figure 339 PETCT exam, series selection**


Source:  Local DB 









# Exams: 62


Select: 


Find: Name 




Exam	Station n...	Name	Date	Description	Modality	MPPS	Archived	Transferred
69	armadillo	no_name_69	14 Jan 21	Abdomen	RAW\LS...			
69	armadillo	no_name_69	14 Jan 21	Abdomen	RAW\LS...			
69	armadillo	no_name_69	14 Jan 21	Abdomen	RAW\LS...			
69	armadillo	no_name_69	14 Jan 21	Abdomen	RAW\LS...			
65001	armadillo	DIAGNOSTIC ACQ...	28 Dec 20	Diagnostic Acqui...	RAW\LST			
65002	armadillo	DIAGNOSTIC ACQ...	28 Dec 20	Diagnostic Acqui...	RAW\LST			
2	ladybird	no_name_2	22 Dec 20	Abdomen	CT\PT\R...			

# Series: 6

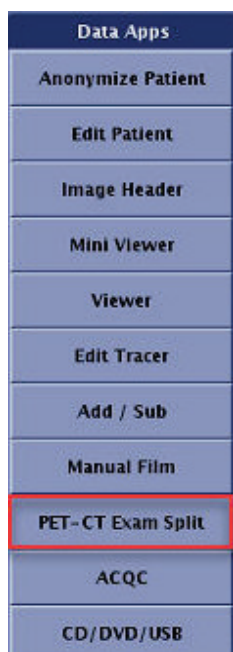
Select: 



Series	Type	Images	Description	Modality	Manufacturer	MPPS	Archived	Transferred ...
1	SCOUT	2	CT SCOUT ...	CT	GE MEDICA...			
2	PROSP	317	CTAC 3.75 ...	CT	GE MEDICA...			
3	PROSP	317	WB Standard	CT	GE MEDICA...			
23	STATIC	89	WB 3D NAC	PT	GE MEDICA...			
901	LIVE	4	Eyes to Thi...	RAW	GE MEDICA...			
951	LIST	4	Eyes to Thi...	LST	GE MEDICA...			

3. From the Data Apps list, click **PET-CT Exam Split**.



**Figure 340 Data Apps list screen**

4. From the PET Exam Split screen, complete the following steps:

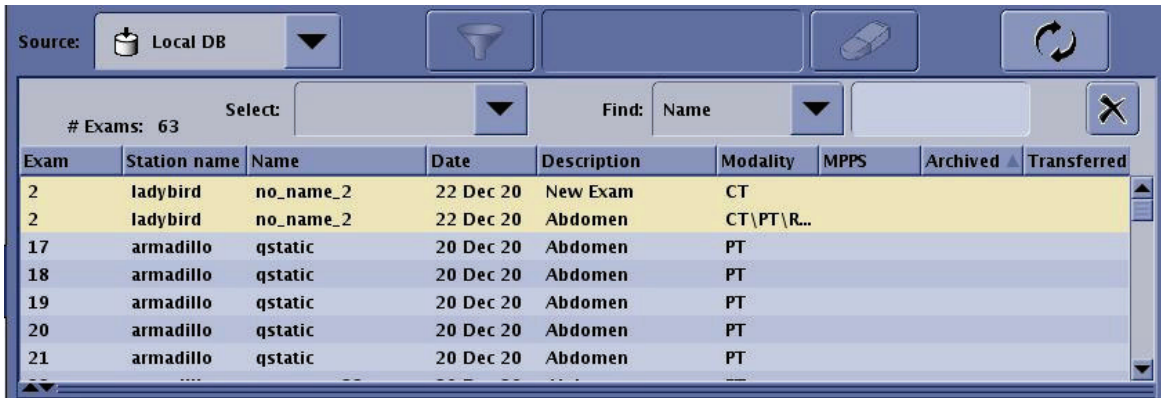
- Enter an Accession Number.
- Enter an Exam Description.
- Click **Proceed** when you are satisfied with the changes.

**Figure 341 Exam Split screen**

5. The Patient list now display two exams:

- The original unmodified exam.
- The new Exam with the selected series, the entered Accession Number and the Exam Description.

Figure 342 Patient list with two exams after split



Exam	Station name	Name	Date	Description	Modality	MPPS	Archived	Transferred
2	ladybird	no_name_2	22 Dec 20	New Exam	CT			
2	ladybird	no_name_2	22 Dec 20	Abdomen	CT\PT\R...			
17	armadillo	qstatic	20 Dec 20	Abdomen	PT			
18	armadillo	qstatic	20 Dec 20	Abdomen	PT			
19	armadillo	qstatic	20 Dec 20	Abdomen	PT			
20	armadillo	qstatic	20 Dec 20	Abdomen	PT			
21	armadillo	qstatic	20 Dec 20	Abdomen	PT			

## 20.7 Post-Processing Quick Steps

### 20.7.1 Typical PET Series Retrospective Reconstruction

1. Click **PET Recon/Replay**.
2. Click/highlight an exam or a **901 - 950** series and click **Select Series**.
3. Click **Recon Type**, review and modify the parameters as needed, then click **OK**.
4. Enter a series description into the corresponding field.
5. Click **Confirm**.

### 20.7.2 Typical ViP Replay and Prospective Reconstruction

1. Click **PET Recon/Replay**.
2. Click/highlight an exam or a **951 - 990** series and click **Select Series**.
3. Follow facility guidelines to review and modify the replay parameters.
4. Follow facility guidelines to type/enter a scan description and series description.
5. Click **Confirm**. An acquisition window opens to provide feedback.

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# 21 Film

## 21.1 Film Introduction

The Film Composer connects with your camera so you can automatically or manually film images. Available film formats depend on your camera. This section includes procedures to film images.

## 21.2 Automatic Filming

Autofilm is designed to maximize filming efficiency.

### 21.2.1 Autostart

Autostart can be used to start filming as soon as the images are acquired and reconstructed. At the **Autofilm Setup** screen, select **Autostart**. From the **ViewEdit** screen, select **Autofilm** and verify that **Autostart** is turned on. Autostart maximizes efficiency.

### 21.2.2 Image filters

There are several display enhancement filters available on the system.

- **Edge Enhancement filters** — useful for filming bone windows, as they sharpen the image.
  - There are six levels — E1, E21, E2, E22, E23, and E3. E1 applies the least amount of enhancement and E3 applies the most.
  - The image is annotated with E1, E2, E21, E22, E23, or E3.
- **Lung Enhancement filter** — useful when filming lung windows. When the Lung enhancement filter is applied, the image is annotated with the word, “Lung”.
- **Smoothing filters** — useful for filming soft tissue windows to decrease the appearance of noise in an image or enhance low contrast areas.
  - There are five levels - S1, S11, S2, S22, and S3. S1 applies the least amount of smoothing and S3 applies the most.
  - The image is annotated with S1, S11, S2, S22, or S3.

### 21.2.3 Gray Scale Enhancement

The Gray Scale Enhancement (GSE) feature changes the slope and gamma curve of an image. It can be used in head studies to improve the bone/brain interface which helps with gray/white matter differentiation.

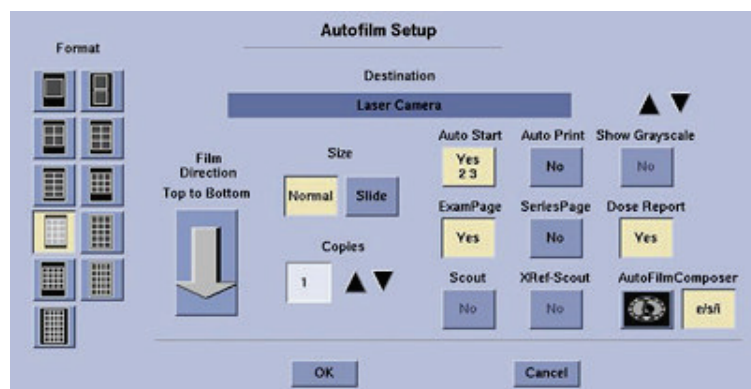
There are three levels of GSE, G1, G2, and G3. G1 applies the least amount of enhancement and G3 applies the most.

When a filter is applied, the image is annotated with G1, G2, or G3 above the vertical tick mark scale on the right side of the image.

## 21.2.4 Autofilm Setup screen

From the **Film Parameters** tab in **ViewEdit**, click **Autofilm** to display the **Autofilm Setup** screen.

**Figure 343 Autofilm Setup screen**



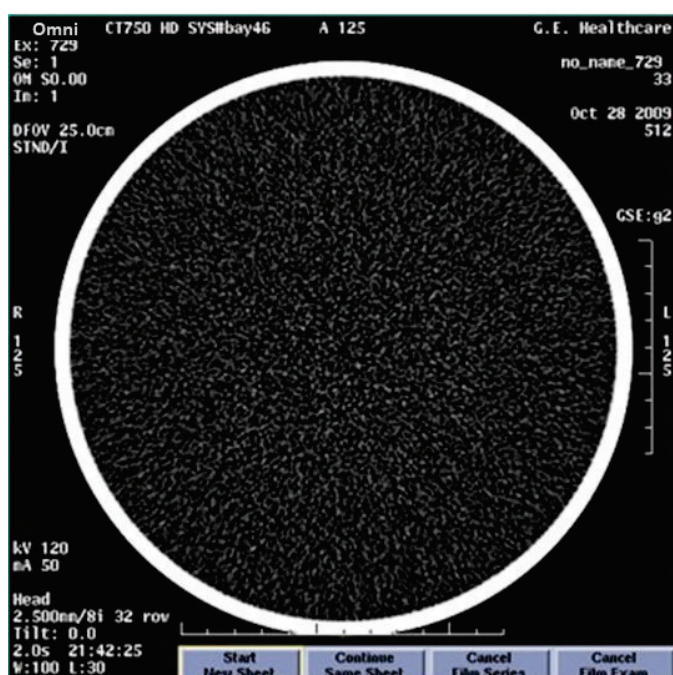
Element	Description
<b>Format</b>	Click a format icon to select the arrangement of images on a sheet of film. Available format selections depend on your camera settings.
<b>Destination</b>	Displays the name of the current camera.
<b>Film Direction</b>	<ul style="list-style-type: none"> <li>Arrow down: Film the images top to bottom.</li> <li>Arrow up: film the images bottom to top.</li> </ul>
<b>Size</b>	If your camera is set up for slides, click <b>Slide</b> to set the print size of the slides.
<b>Copies</b>	The number of copies print.
<b>Auto Start</b>	<b>Yes</b> turns Auto Start on. <b>No</b> turns Auto Start off. If Autofilm is on and Auto Start is off, start Autofilm from the Autofilm viewport.
<b>Auto Print</b>	<b>Yes</b> turns Auto Print on, and sends the film to the printer when all frames of the film are filled. <b>No</b> turns Auto Print off. To print, click <b>Print</b> to manually print the film.
<b>Show Grayscale</b>	Displays a vertical bar on the left side of the image with a grayscale gradient.
<b>Exam Page</b>	Prints an Exam Page with patient demographic information.
<b>Series Page</b>	Prints a Series Page with scan parameter information for the series.
<b>Dose Report</b>	Prints a Dose Report.
<b>Scout</b>	Prints a Scout image.

<b><i>XRef-Scout</i></b>	Prints a cross-reference of the prescription lines on the Scout image.
<b><i>Autofilm Composer</i></b>	Select the way the images are displayed in the frames of the Autofilm Composer. <ul style="list-style-type: none"> <li>E/S/I displays the exam number, series number, and image number in the frame.</li> <li>The image icon displays a small picture of the image being printed in that frame.</li> </ul>

## 21.2.5 Autofilm screen

During a series scan with **Autofilm** turned on, the Autofilm viewport displays.

**Figure 344 Autofilm screen**



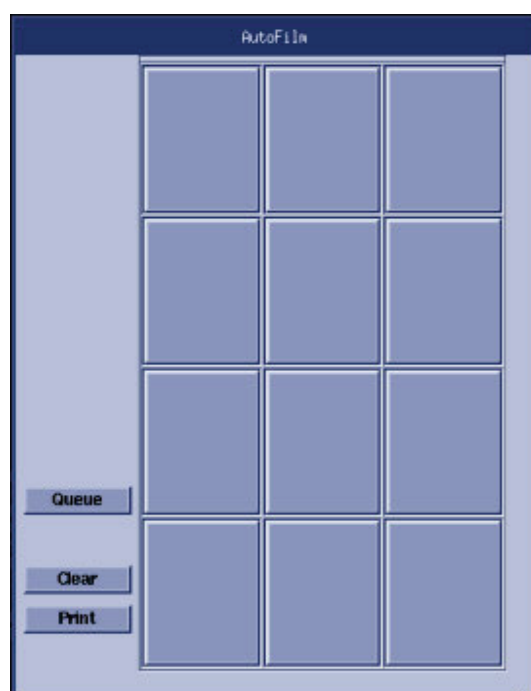
Element	Description
<b><i>Start New Sheet</i></b>	Starts auto filming when Autofilm is selected for the series and No Autostart is selected from Autofilm Setup screen. A new sheet of film is started and the settings prescribed in Autofilm Setup are applied. The film process uses the format which was selected from Autofilm Setup.
<b><i>Continue Same Sheet</i></b>	Continues filming where you left off, on the same sheet of film, keeping the settings used in the previous auto filming exam. Alternatively, use to start Autofilm rather than <b><i>Start New Sheet</i></b> so that you continue filming on the same sheet of film that is currently active in the film composer.
<b><i>Cancel Film Series</i></b>	Cancel a series so it is not filmed.

<b>Cancel Film Exam</b>	Cancels the entire exam from Autofilm.
<b>Pause Filming</b>	Temporarily pauses auto filming to allow WW/WL adjustment or to perform any display features such as ROI and measure distance.

## 21.2.6 Autofilm Composer screen

If **Autofilm** is turned on, the **Autofilm Composer** screen opens.

**Figure 345 Autofilm Composer screen**



Element	Description
<b>Clear</b>	Erases the current images displayed in the Film Composer.
<b>Print</b>	Prints the images displayed in the Film Composer.
<b>Queue</b>	Displays jobs waiting to be printed on any dedicated or networked cameras on the Queue screen.

## 21.2.7 Set the Autofilm parameters

Use the following procedures to set **Autofilm** parameters.

### 21.2.7.1 Film parameters

Use this procedure to set the parameters on the film output for Autofilm. For Autofilm details, see *Automatically film images*.

1. From the **ViewEdit** screen **Series Level Function** area, click **Autofilm Setup**.
2. Make selections for the following parameters:
  - camera or printer
  - film format
    - The format built into the protocol may be changed due to an invalid condition.
    - Verify that you selected the proper format.
  - image exposure direction
  - image frame size
  - number of film copies
  - Automatically film images
  - Auto Print parameters
  - film composer display
  - scoutview image
  - scoutview image with reference lines
  - exam and/or series information
  - grayscale
  - film Dose report
3. Click **OK**.

### 21.2.7.2 Image parameters

To set the parameters on the viewing screen for Autofilm, follow these steps:

1. From the **ViewEdit** screen, click the **Autofilm** tab.
2. Set Autofilming to **On**.
3. Select the following parameters:
  - frame format for each film space
  - image interval
  - image flip
  - window width and level
  - magnification
  - image rotation
  - add image annotation
  - image filters
  - grayscale enhancement



4. Click **OK**.

## 21.2.8 Automatically film images

### 21.2.8.1 Considerations

Keep the Autofilm backlog to a minimum. Start Autofilm as soon as possible to keep current on filming.

### 21.2.8.2 Start Autofilm

- At the **Filming** tab on the **ViewEdit** screen, set **Autofilm** to **On** to launch Autofilm.
- If AutoStart is not selected from Autofilm Setup screen, click **Start New Sheet** to apply the parameters defined in Autofilm Setup.
- Alternatively, click **Continue Same Sheet**, which does not use the parameters defined in Autofilm setup, but instead uses the film parameters from the last time Start New Sheet was used. This could be from a previous patient.
- Autofilm may stop if the Autofilm viewport selection shows active and the Autofilm status shows paused. Toggle **Pause** in the Autofilm viewport and click **Start New Sheet** or **Continue Same Sheet** to restart filming.

### 21.2.8.3 Pause Autofilm

- From the **Autofilm** screen, click **Pause Filming**.
- From the **Autofilm** screen, click **Continue Same Sheet** to restart filming.

### 21.2.8.4 Delete a series or exam from Autofilm

To delete a series, from the **Autofilm** screen, click **Cancel Film Series**.

To delete an exam, from the **Autofilm** screen, click **Cancel Film Exam**.

### 21.2.8.5 Add an image to the Autofilm composer

Follow these steps to add an image to the Autofilm composer:

1. When Autofilm is paused or finished, place the cursor on the image or MID to be filmed.
2. Press **F12** to place a single image into the Autofilm composer.
3. Press **Shift-F3** to place an MID into the Autofilm composer.

## 21.2.9 Autofilm recon troubleshooting tips

Autofilm may fail to display images in the following situations:

- There is a recon problem.

- Images failed to install in the database.
- A large exam has not reconstructed all images and scanning is started on a new exam.

The following dialog is posted if Autofilm cannot display images:

- Exam XXX
- Series X
- Cannot find XX images
- Skip Missing images, Continue, Cancel Film Series

When this situation occurs, complete one of the following steps:

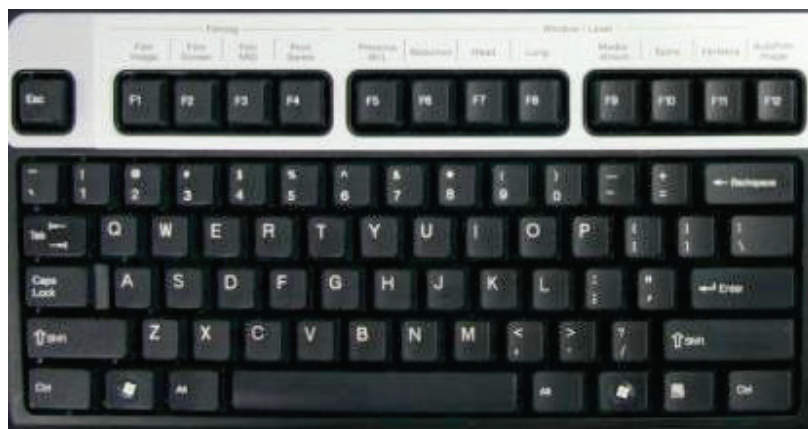
1. Click **Skip Missing images** to skip the images that Autofilm cannot find. For example, if Autofilm filmed images 1 to 10 and you then got the message that 10 images were missing and selected Skip Missing Images, Autofilm would then start filming again with image 21.
2. Click **Continue** to look for the images again. If they are not found, the dialog is posted again. Before selecting **Continue** verify:
  - recon is active
  - the images have been reconstructed
  - the images are able to be displayed
  - the missing images are not suspended or paused in the Recon Queue
  - If the images are suspended or paused in the recon queue, then restart recon before selecting **Continue**.
3. Select **Cancel Film Series** to cancel Autofilm for the series currently being automatically filmed. Manually film the images. If you get this dialog because you have begun an exam while the previous exam still has images to reconstruct, then select **Continue**, Pause Autofilm, resume Autofilm after the exam, series, images from the previous exam have reconstructed.

## 21.3 Manual Filming

To manually film images, you must first place the images on the Film Composer so they can be printed. The Film Composer connects to your camera and lets you to film images. You can open the Film Composer from the browser, the Viewer, the Mini Viewer, Exam Rx, and Reformat.

### 21.3.1 Function keys

The **F1-F14** function keys are used for Manual Film Composer procedures.

**Figure 346 Film Function Keys****Table 92 Film Function Keys**

Key	Description
F1	Film image
F2	Film screen
F3	Film MID
F4	Print series

### 21.3.2 Window width and level presets

The F5-F11 function keys can be programmed for different window width and window level settings. This gives the system a wide variety of appearances for specific image types. The system comes with settings for each key already set. However, these may be easily adjusted and programmed into the system according to your facility's preferences. This allows you to use a single key to adjust window widths and levels. The widths and levels may be programmed to follow a template on the keyboard or set to any image type you choose.

1. On the display monitor, double click one of the lower viewports.
2. From the display monitor, click **List Select**.
3. From the pop up window select an exam and an image.
4. Enter the window width setting in the **Accelerator Command Bar** (gray bar in the lower left corner of display screen, i.e. WW 400).
5. Enter the window level setting in the **Accelerator Command Bar** (i.e. WL 35).
6. Hold down **Shift** and press any F5-F11 key.

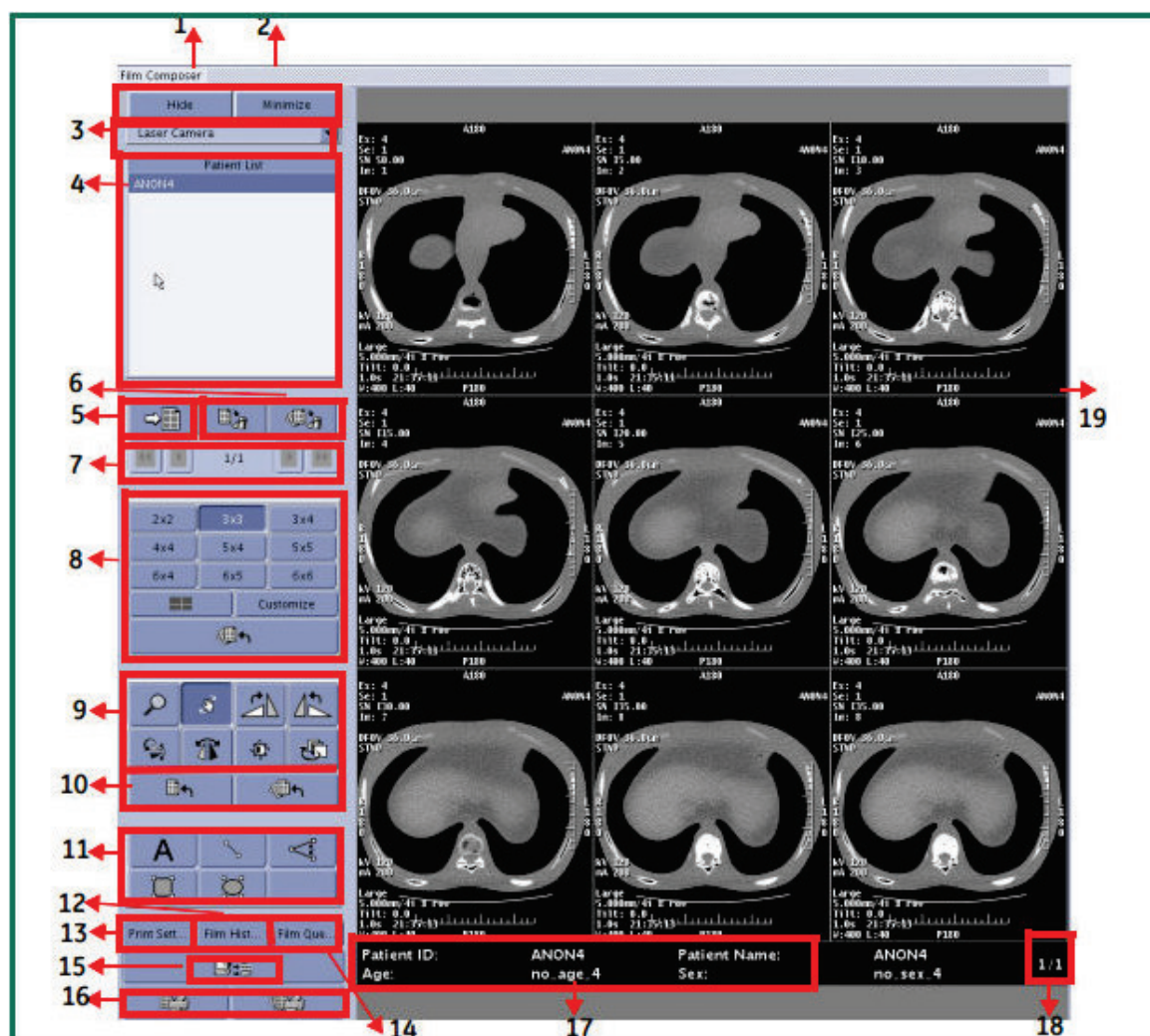
Repeat Steps 4, 5 and 6 to set any of the F5-F11 key settings.

### 21.3.3 Film Composer Layout and Parameters Setting

The film composer can be displayed by Full Screen or Minimum. When placed images on the film composer, you can see what the images are, and edit or measure on the images.

1. The routine layout of the manual film composer is displayed as following figure. When you click **Minimum**, there will show the minimum layout.

**Figure 347 Manual Film composer layout (full)**

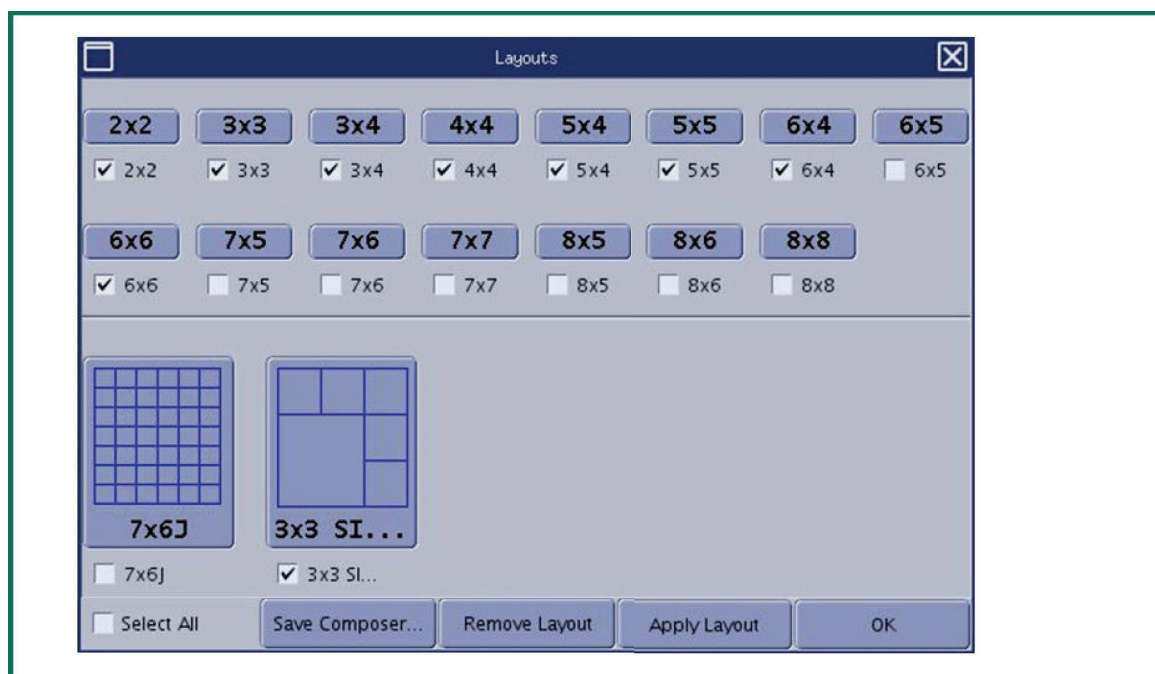


Number	Selection	Description
1	Hide	Hide the Manual Film Composer
2	Minimize	Minimize the Manual Film Composer
3	Select camera	Select the camera for film print.

(continued)		
Number	Selection	Description
4	Patient list	Display the Patient information that has been loaded to film.
5	Add page	Add a blank page to add images for filming.
6	Delete page	Delete the current page or all pages.
7	Page number, page up and down	Current page number / total page number in the middle and view first page, previous page, next page and the last page.
8	Layout preset	<p>Select one of the fixed layout configurations: 1x1, 1x2, 2x2, 2x3, 2x4, 3x3, 3x4, 3x5, 4x4, 4x5, 4x6, 5x5, 5x6, 5x7, 5x8.</p> <p>Customer can set up Special layout configuration by clicking the <b>Customize</b> button. Refer to <a href="#">Figure 348 on page 547</a> for details.</p> <p>Customer can apply the layout to all pages by click <b>Apply layout to all pages</b> button.</p>
9	Adjust	Zoom In/Out ROIs, Flip, WW/WL, Display normal.
10	Apply to page/all page	Apply the edit to page or all pages.
11	Routine operation	Including distance, angle, area Measurement and put label/text on the images.
12	Film history	Allow user to save the print jobs to a persistent storage space with the ability to Remove, Print, Film Display, Image Display and Close the recorder from persistent storage space.
13	Print setting	Set the print parameters.
14	Film queue	Allow to pause/resume/delete printing jobs.
15	Export	Export the JPEG film to USB.

(continued)		
Number	Selection	Description
16	Print	Print the film, page by page or all the pages.
17	Patient information	Display the patient information at the bottom of film(s).
18	Page number	Show the current page number of the total printing pages.
19	Show print page layout.	Show print page layout.

**Figure 348 Customize layout**



Click [Customize], there show all the layouts that can be selected by the customer. The upper area shows the preset layouts. These layouts cannot be added, updated or removed. The lower area is for the customer to save personalized layouts.

There is one check box in front of the name of every layout. The user can select the default layouts by click ✓ in the check box.

**Save Composer Layout:** to save personalized layout in the below area with unique name.

**Remove Layout:** to remove the customized layouts.

**Apply Layout:** to apply the selected layout to current film task.

**OK:** to set the default layouts on the film composer interface.



**NOTE**

When you want to remove or apply layout, you must select the layout button rather than selecting the layout name.

**Figure 349 The minimum layout**



Number	Selection	Description
1	Hide	Hide the Manual Film Composer
2	Full Screen	Switch to full screen
3	Select Camera	Select the camera for film print.
3	Patient Name	Display the Patient Name that has been loaded to film composer
4	Layout preset	Select one of the fixed layout configurations: 1x1, 1x2, 2x2, 2x3, 2x4, 3x3, 3x4, 3x5, 4x4, 4x5, 4x6, 5x5, 5x6, 5x7, 5x8. Customer can set up Special layout configuration by click [Customize] button. Refer to <a href="#">Figure 348 on page 547</a> for details. Customer can apply the layout to all pages by clicking the <b>Apply layout to all pages</b> button.
5	Image layout	Show print page layout.
6	Add/Delete page(s)	Add a page, delete the current page or all pages.
7	Page # , Page up/down	Current page # / total page # in the middle and view first page, previous page, next page and the last page.
8	Print Setting	Set print parameters.
8	Film history	Allow user to save the print jobs to a persistent storage space with the ability to Remove, Print, Film Display, Image Display and Close the recorder from persistent storage space.
8	Film Queue	Allows to pause/resume/delete printing jobs.
9	Export	Export the JPEG film to USB.
10	Print	Print the film, page by page or all the pages.

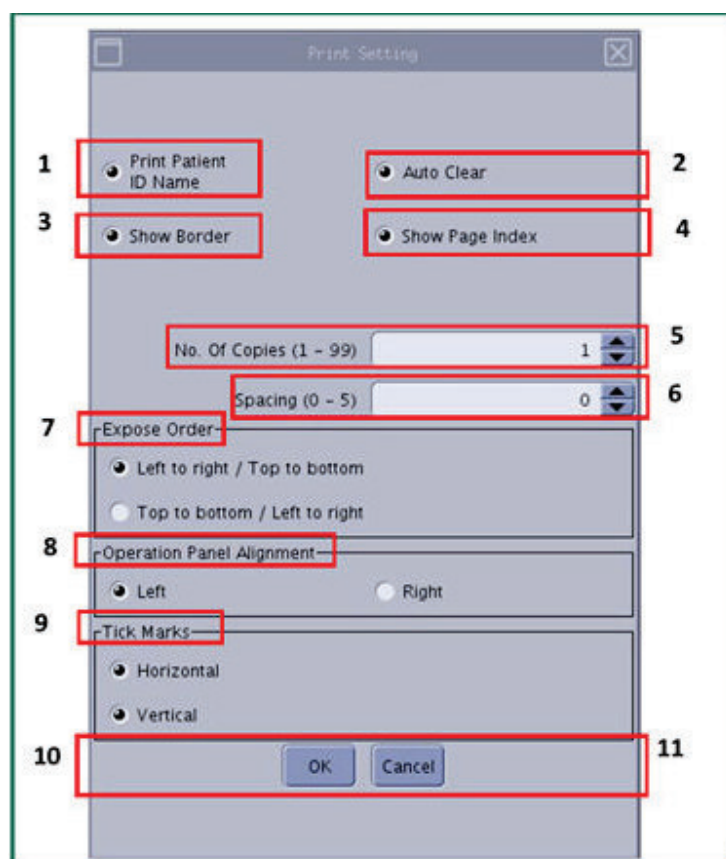
## 2. Set print parameters:



Several settings are available on the Manual Film Composer. The system retains the changes until next change is made. Settings may be changed prior to actual printing of the images in the composer.

Click **Print Settings** button, A dialog window opens allowing you to set up the parameters of print. Please refer to the next chapter to review the print settings parameters.

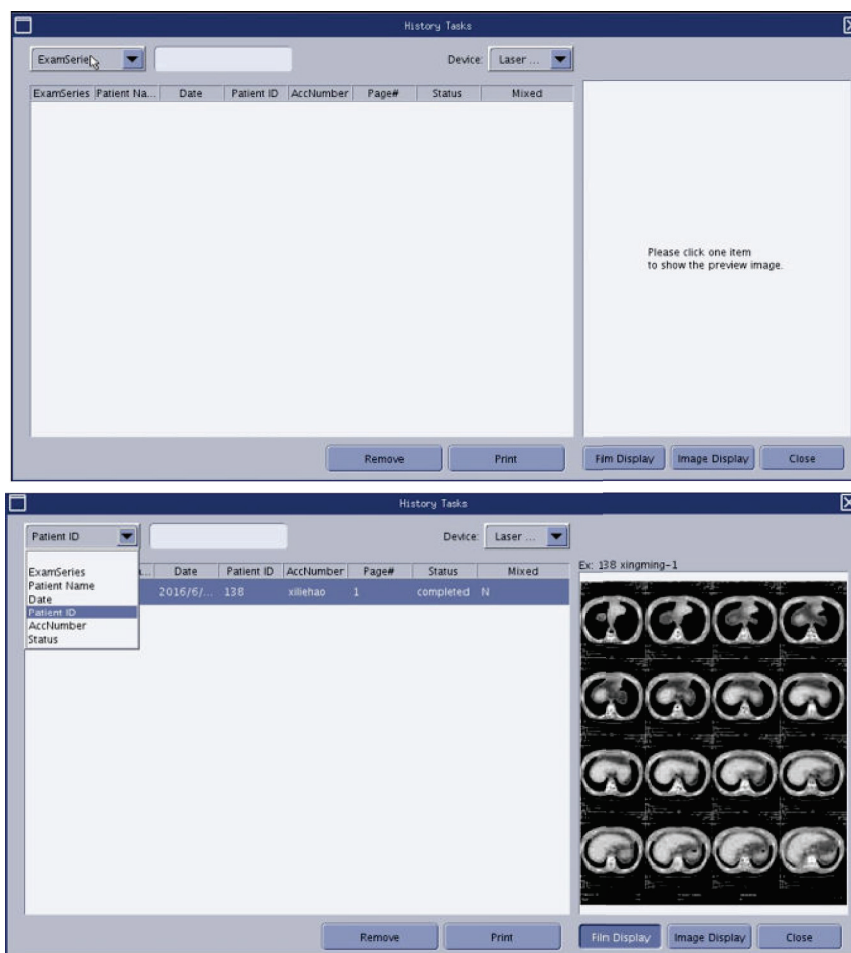
**Figure 350 Set printing parameters**



Number	Item	Description
1	Print Patient ID Name	Prints the patient name and ID on each film sheet.
2	Auto Clear	Automatically clears the films sheet when printed.
3	Show Border	Show a border outline on each image frame on the film sheet.
4	Show page Index	Show the page index and number , for example 1/10.
5	No. of Copies	Determines the number of copies to be printed.

(continued)		
Number	Item	Description
6	Spacing	Adjusts the vertical and horizontal blank space between images frames.
7	Expose Order	<p><b>Expose Order:</b> Set images filling order:</p> <p><b>Left to right/Top to bottom:</b> Fill images in the film sheet from left to right, row by row and top to bottom.</p> <p><b>Top to bottom / Left to right:</b> Fill images in the film sheet from up to down, column by column and left to right.</p>
8	Operation Panel Alignment	Set the panel location on the left or the right of the filming User Interface.
9	Tick Marks	Displays horizontal or vertical or both tick marks (rulers ) along the border of the image
10	OK	Accepts the selections made and closes the menu
11	Cancel	Closes the menu without executing the selections on the menu

3. Print History: Provide fuzzy search, sort printed recorders by column tile, re-print recorder and view/display printed recorder in full film format or in image format.
  - **Search area:** Search printed recorders by Exam/Series, Patient Name, Date, Patient ID, AccNumber and Status. The user also can perform fuzzy search.
  - **Device:** Select printer.
  - **Printed recorder area:** Displays all the printed recorder and also displays detail information in column including ExamSeries, Patient Name, Date, Patient ID, AccNumber, Status and Mixed.
  - **Film/Image display area:** Displays the printed recorder in full film format or in image format.
  - **Film Display:** When the user selects one printed recorder, then clicks the **Film Display** button, the full film format will be showed in **Film/Image display area**.
  - **Image Display:** When the user selects one printed recorder, then clicks the **Image Display** button, one magnified image of the film will be showed.

**Figure 351 History task**

4. **Print Queue:** Displays detail print information such as exam/series/patient name /film number / printer type/ print status and so on; and it can auto load print information when opening.
  - Click the **Film Queue** button, the printing queue window opens.
  - Click **Pause** to pause the selected printing jobs.
  - Click **Resume** to resume the jobs which is paused
  - Click **Refresh** to refresh the printing job list.
  - Click **Clear** to delete the selected printing jobs.\
  - Click **Close** to close.

Figure 352 Print Queue



5. **Export:** To export the JPEG images by USB device, click the **Export** button. A dialog window opens, allowing the export of patient images. If the system cannot recognize your save media, please click **Refresh**.

Figure 353 Export patient images



6. **Right-click button function on the mouse:** Right-click on the mouse to access the cut, copy/paste, remove or insert functions. The user can change the Image Filter or the Gray Scale Enhancement level, and can edit the image annotation, and apply the function by **Apply To Page** or **Apply To All Pages**. After the user cuts or removes the image, the following images will automatically fill the blank viewport.

**Cut:** Cut the image you select.

**Copy:** Copies one image

**Paste:** Paste one image to the desired location, covering any image already there.

**Insert Empty:** Inserts an empty image allowing the desired image to be pasted.

**Insert Patient Info:** Inserts one blank image containing only patient information.

**Gray Scale Enhancement:** Select g1, g2, g3 scale levels or a scale level of none to adjust the gray scale within the image. \[Filter]: Adjust the images by selecting a smooth filter (S1, S2, S3) and edge enhancement level (e1, e2, e3).

**Cross Reference:** Displays the localizer for different series.

**Figure 354 Right click on the scout image**

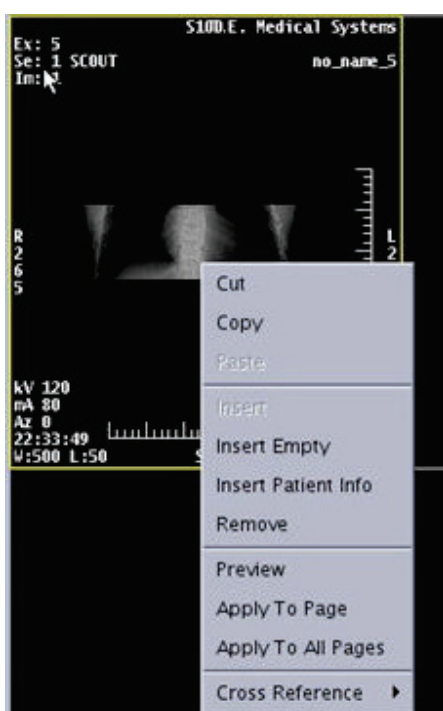


Figure 355 Right click, then Preview on the axial image

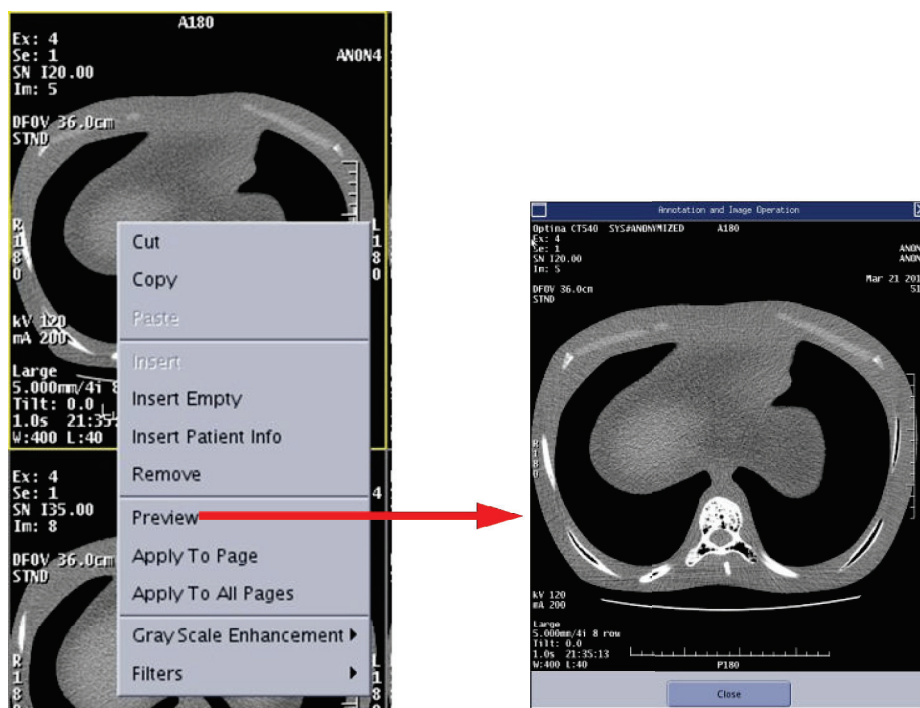
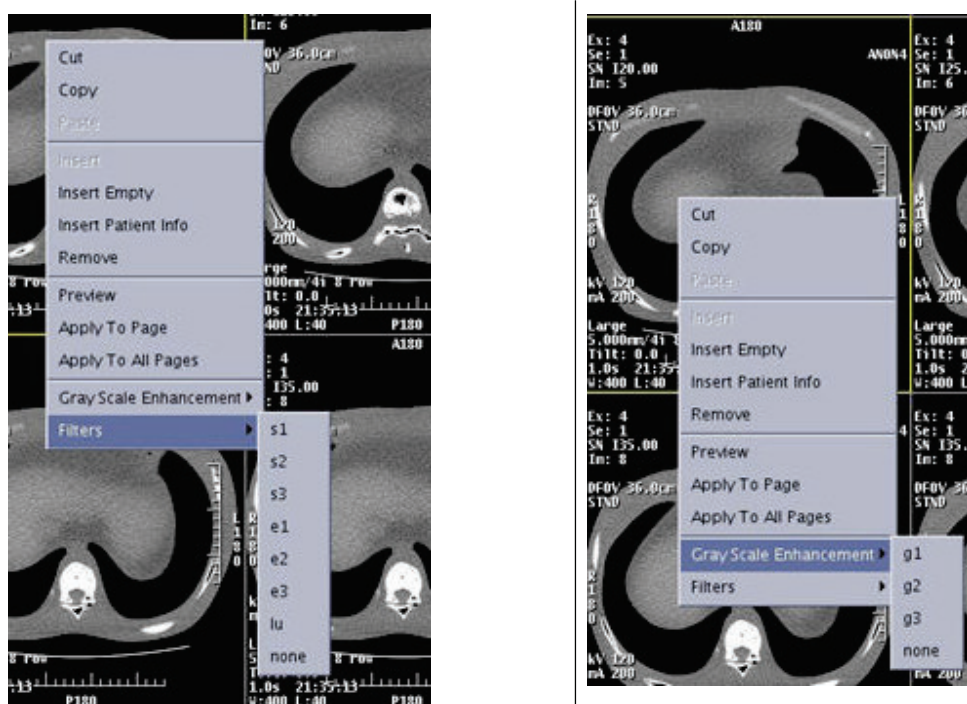


Figure 356 Right click on the axial image



- Right-click on one selected image, then select the **Preview** from the pop-up menu. The system displays one magnified image, on which the user can perform some operations, such as measurement, ROI, annotation and so on.

### 21.3.4 Place images in the Manual Film Composer

All images to be filmed must be placed in a composer for transfer to the camera. This may be done automatically or manually. This section deals with the Manual Film Composer. Images may be placed in the composer individually or in series. There are three ways to place the images in the film composer, one using Exam Rx and two using Image Works.

#### 21.3.4.1 Exam Rx

- From **Exam Rx**, double-click in one of the lower viewports.
- From the display monitor, click **List Select**.



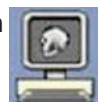
- Select an exam, series and image.
- Click **View**.
- Click **Manual Film Composer**.



- Place images by F Keys.
- When the Film Composer screen is ready for printing, click **Print**.

#### 21.3.4.2 Image Works

- From the display monitor, click to display the **ImageWorks** icon.



- From the browser **Patient List**, select the images. From this point, two methods are available to place images into the Film Composer.

##### Method 1:

- From the list of applications, click **Viewer** or **Mini Viewer**.
- Click a viewport to make it primary.
- From the **Viewer** or **Mini Viewer** control panel, click **Film Composer**.
- Place images using the F Keys.



- e. When the Film Composer screen is ready for printing, click **Print**.

**Method 2:**

- a. Click **Manual Film** from the list of applications. The Film Composer opens and the selected images are loaded into the Film Composer.
- b. To edit the images in the film composer. <writer question: are there supposed to be steps here?>
- c. When the Film Composer screen is ready for printing, click **Print**.

**NOTE**

When you only click the exam, the selected images by default are all the images in first series. When you click the series, the default selected images are all the images in the first series. When you click the series, the selected images by default are all the images in the specified series.

**NOTE**

To select multiple series or exams, use the **Shift** or **Control** buttons.