

**NOTE**

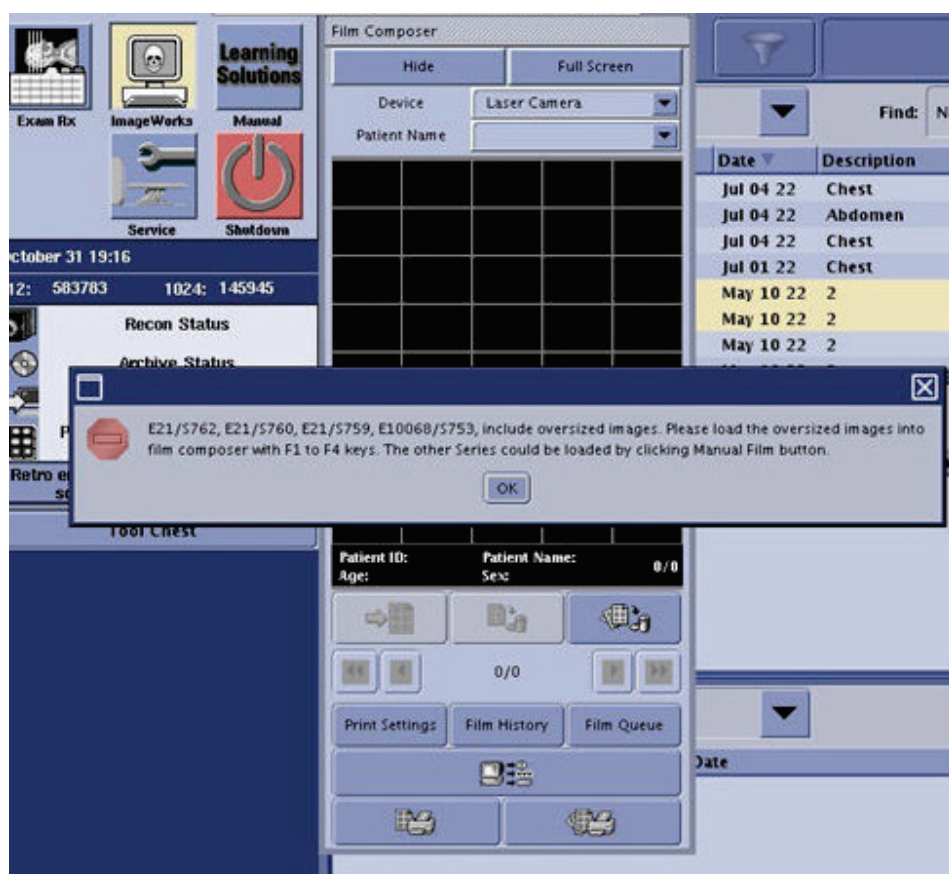
If you hide or minimize the Film Composer work, you can reopen it by clicking the **Film** button from the feature status area or the **Manual**



**Film Composer** button from the ExamRx user interface. When select multiple



series, if any series include oversized images, the message below displays.



Examxx/Seriesxx include oversized images. Please load the oversized images into film composer with F1 to F4 keys. The other Series could be loaded by clicking Manual Film button.

### 21.3.5 Set the Print Series parameters

Any portion of a series may be filmed using the Print Series **F4** key. This is a great timesaving feature if, for example, films are lost, duplicate copies are needed, or if auto filming was not utilized. All images need to be filmed in the same window width and level. If multiple window widths and levels are needed (i.e., soft tissue and bone) the Print Series can be used for each window width and level.

1. On the display monitor, click in one of the lower viewports.
2. Click **List Select**.
3. Select an exam, series, and image.
4. Click the **Manual Film Composer** icon.
5. Place the cursor in the image/series to be used for Print Series.
6. Press **F4**.
7. Set the Print Series parameters.
8. Click **Print Series**.

#### NOTE

To cancel a Print Series request, press **F4** and click **Cancel** from the Current Print Job.

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## 22 Manage Data (Archive and Storage)

### 22.1 Manage Data (Archive and Storage) Introduction

This chapter contains the following instructions:

- Archive patient data (including PET raw data)
- Store and restore data with Scan Data Manager
- Store and restore data with interchange media
- Network data

This chapter does not provide specific instructions to save CT raw data. Please refer to the CT User Manual and CT TRM shipped with your system for detailed instructions to save CT raw data.

#### NOTE

If you intend to save scan files for troubleshooting purposes, remember to anonymize the data to remove the patient identification before saving it, in order to comply with HIPAA regulations.

Refer to [Table 93 on page 561](#). The table contains the list of data types found on the Image Works browser, along with the storage media and software functions that support them.

**Table 93 Storage Compatibility Matrix**

Data Type	Storage Function by Media Type		
	CD/DVD-R	USB External Hard Drive	Network Hard Drive
PET image data	CD/DVD/USB	Scan Data Manager	Scan Data Manager
CT image data	CD/DVD/USB	Scan Data Manager	Scan Data Manager
PET raw data	CD/DVD/USB	Scan Data Manager	Scan Data Manager
PET LIST data	--	Scan Data Manager	Scan Data Manager

#### NOTE

Verify that the selected scan files do not exceed the space available on the media.

Wait until the light on the media drive turns off before you eject the media.

You may confirm that the media is safely ejected by going to **Image Works** -> **Tools** -> **Detach Media**.

#### NOTE

Networking data to a shared server is supported with Scan Data Manager. Please consult your Field Engineer to configure an NFS share.



**NOTE**

Scan Data Manager when used with External Hard Drive, supports up to 2TB drive. The limitations is inherited from formatting utility available on the console. This is not applicable to Scan Data Manager when used with shared NFS.

**NOTE**

For your reference, below is a table summarizing disk space for Local Database Storage on the system.

**Table 94 Local Data Base Disk Space**

Data Type	Store Location	Disk Space
CT RAW	Console Compute	477 GB
PET RAW	PARC	3.0 Tera
PET LIST	PARC	5.9 Tera
DICOM Images (CT and PET)	Console Compute	477 GB*

\*Disk space for DICOM images is separate than disk space for CT RAW. Monitor your database storage through SRM, archive your data when needed and ensure the system has always a space before a new Exam or Acquisition starts.

## 22.2 Archive Patient Data

1. If necessary, click the **Image Works** icon to display the Image Works browser.
2. Select the exams or series you want to archive. Refer to [Figure 357 on page 563](#).

**NOTE**

LIST data series cannot be archived.

Figure 357 Image Works Archive Menu

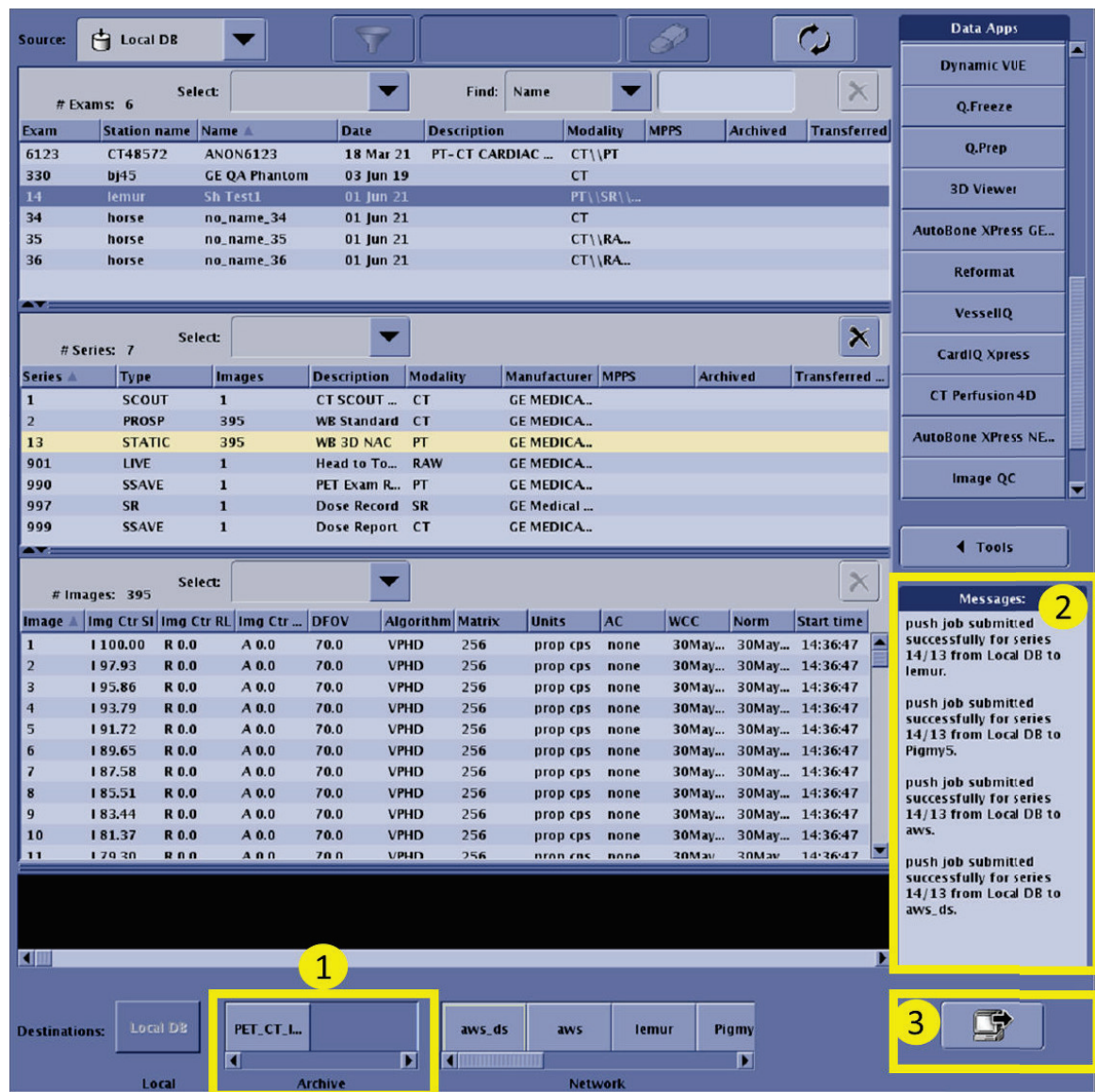


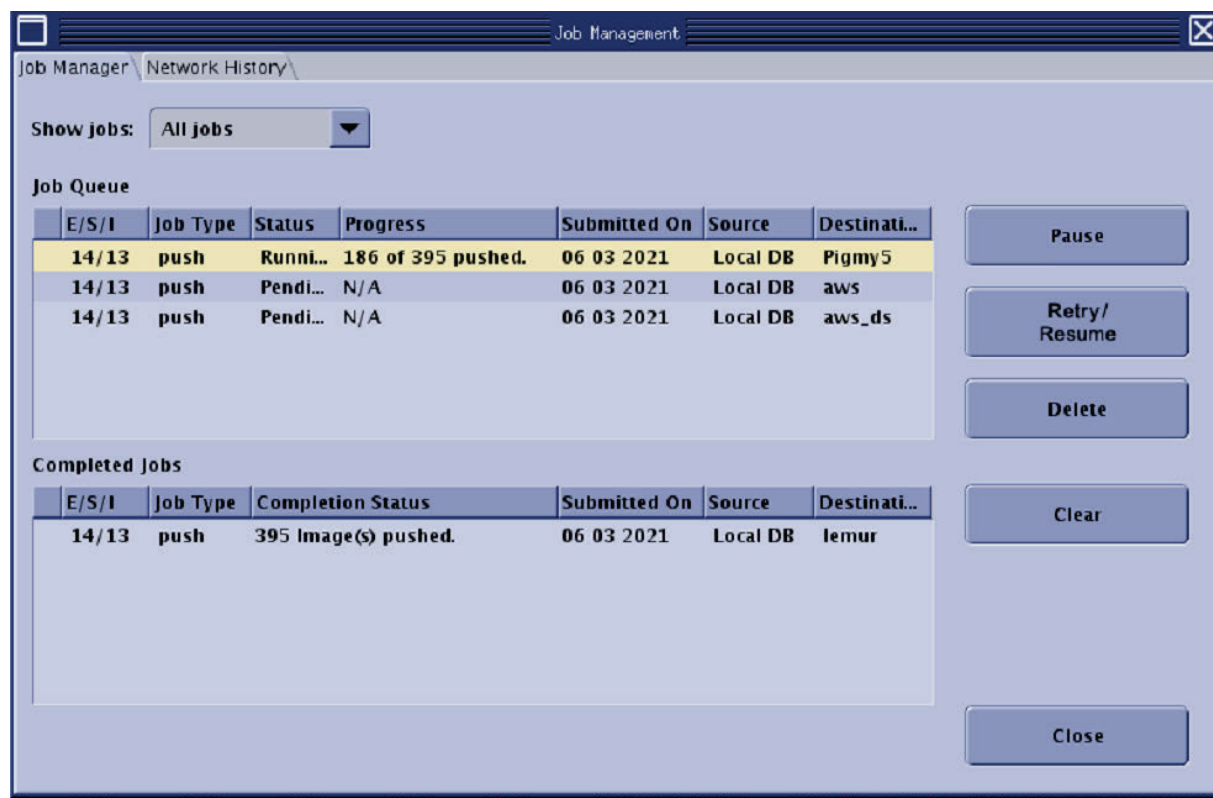
Table 95 Image Works Archive Menu

Number	Description
1	<b>Archive</b> area
2	<b>Messages</b> area
3	<b>Job Management</b> icon

- Click on the desired archive destination in the **Archive** area.

- Click the **Job Management** icon to monitor the progress of the archive task in the **Job Management** window.

**Figure 358 Job Management Window**



#### NOTE

Exams and series that have been archived have an **A** in the archived column on the browser.

#### NOTE

You have the option to direct the field engineer to configure the system to automatically save PET raw data with the exam (default mode), or change the setting to skip **PET RAW** data when you archive the exam. Regardless of the configuration, you can always select the individual Live or Replay raw data series and archive by the series level.

Archive does NOT support LIST data. When you try to save LIST data as a series, the system displays a pop-up message to remind you that Archive does not support LIST data saves. When you save an exam that contains LIST data, Archive automatically skips that series without displaying a message.

#### NOTE

The steps to restore patient data from archive are the same as those to network data from another workstation. Refer to [Network Data](#) for instructions.

## 22.3 Store and Restore Data with Scan Data Manager

Follow the instructions in this section to save ViP LIST data, CT images, PET images and PET raw data to a USB hard drive or network hard drive.

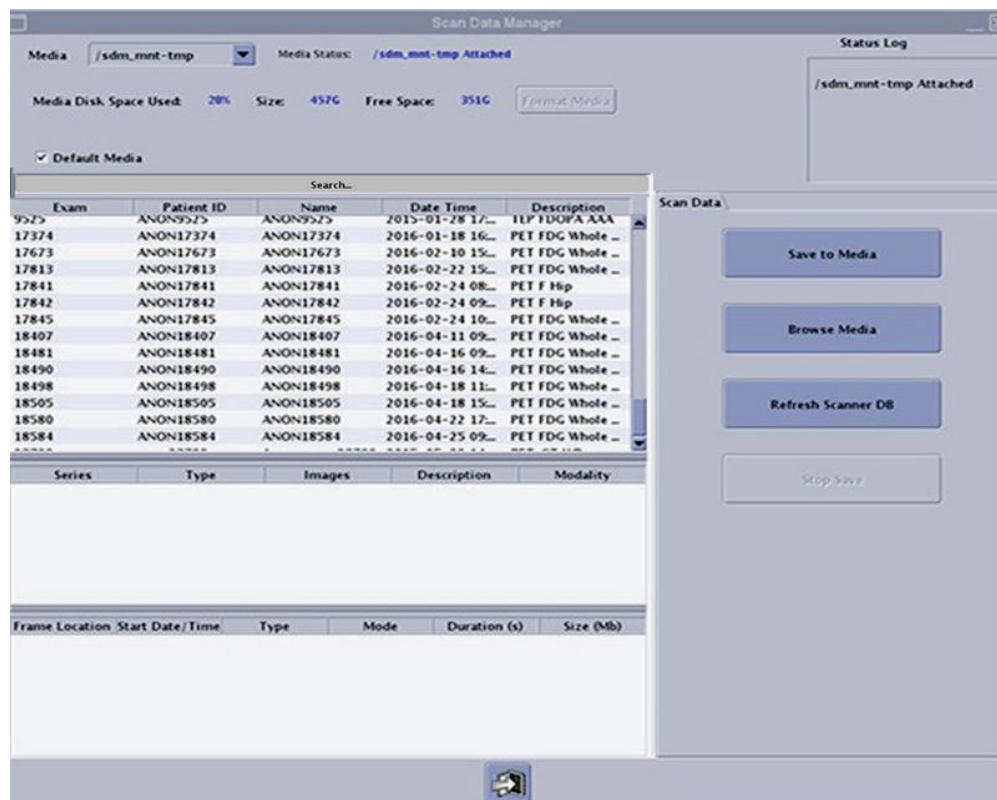
### 22.3.1 Store Data with Scan Data Manager

1. Click **Service** to open the Common Service desktop.
2. If necessary, click the **PET** radio button to select it.
3. Click the **Utilities** icon to open the tab.
4. Click **Scan Data Manager** to open the **Scan Data Manager** window, shown in [Figure 359](#) on page 565.

#### NOTE

The **Scan Data Manager** window displays only the series that qualify, and will not save individual images.

**Figure 359 Scan Data Manager Window**



5. Attach a USB drive to the USB port on the console. If necessary, click the **Media** arrow to display the drop down menu and drag to the desired media type.

If necessary, format the media by clicking **Format Media**.

#### NOTE

Look for a *USB Attached* message to be sure the media is ready for use.

6. If necessary, use the Search to search the data by exam number, patient name, etc..
7. Click/highlight the data series you plan to save.  
You may select multiple data series, as long as they come from the same exam.
8. Click **Save to Media** to copy the selected series to the media.  
Monitor the **Status Log** area in the **Scan Data Manager** window during the data transfer.
9. Click **Close DB Browser** to close the **Scan Data Manager** window.

### 22.3.2 Restore Data with Scan Data Manager

1. Click **Service** to open the Common Service Desktop.  
If necessary, click the **PET** radio button to select it.
2. Click the **Utilities** icon to open the tab.
3. Click **Scan Data Manager** to open the **Scan Data Manager** window, shown in [Figure 359 on page 565](#).
4. Attach a USB drive to the USB port on the console. You can also use a configured network hard drive. If necessary, click the **Media** arrow to display the drop down menu and drag to the desired media type.
5. Click **Browse Media** to open the **Series Restore** window, shown in [Figure 360 on page 567](#).



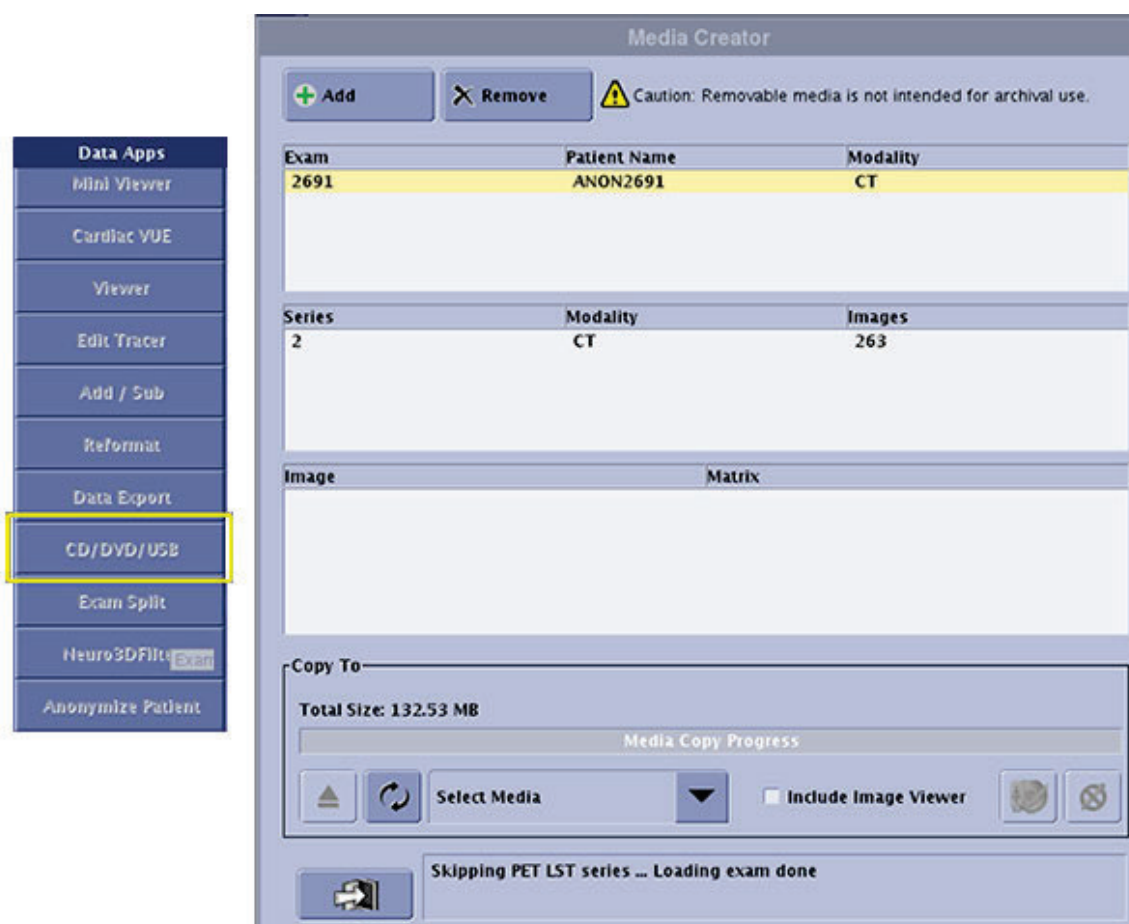


## 22.4.1 Store Data with Interchange Media

Follow these instructions to create a copy of an exam on CD, DVD or USB, to send home with the patient or forward to the patient's physician. Media Creator can automatically load the software that the destination computer needs to display the exam images, along with the files, when it creates the media.

1. Click the **Image Works** icon to display the Image Works browser. Load a new CD-R or DVD-R into the CD/DVD drive in the CD/DVD Drive option, or attach a USB drive to the USB port on the console.
2. Select the desired exams or series to store.
3. Click **CD/DVD/USB** on the Image Works browser to open a **Media Creator** window, similar to the one shown in [Figure 361 on page 568](#).

**Figure 361 Media Creator Example**



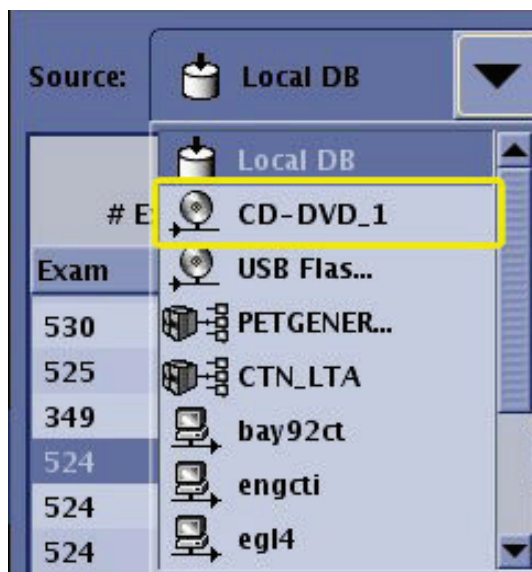
4. Click the **Media** arrow to display the list of available media, then click or drag to the desired media type.

5. Select **Include Image Viewer**, if you want to include the software needed to view the images on the media (recommended).
6. If you want to include additional data, click on the desired exams, series or images in the Image Works browser, and click the **Add** button.
7. If you want to remove some of the data, click the exams, series or images to be removed in the Media Creator list, and click the **Remove** button.
8. To save the data in the Media Creator list to the media, click the **Copy** icon.
9. Click the **Close** icon to close the Media Creator tool.

## 22.4.2 Restore Data with Interchange Media

1. If necessary, click the **Image Works** icon to display the Image Works browser. Load a CD-R or DVD-R into the CD/ DVD drive in the CD/DVD Drive option, or attach a USB drive to the USB port on the console.
2. Select the media from the **Source** menu in the upper left corner of the browser.

**Figure 362 Source Menu**



3. Select the desired exams or series.
4. Click **Local DB** in the **Destinations** area of the browser.

**Figure 363 Destinations Area**

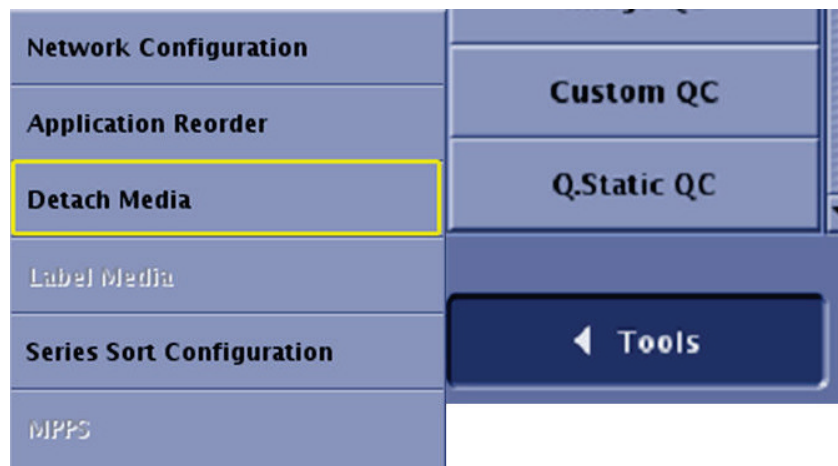


5. Select **Local DB** from the **Source** menu in the upper left corner of the browser.



- Click on **Tools** and select **Detach Media**. Select the media type and click **Detach Media**. Remove the media.

**Figure 364 Detach Media**



**NOTE**

The interchange media can be used to view the data on a personal computer. If the viewer does not automatically launch, go to the media drive on the computer and double-click `CDViewer.exe`.

## 22.5 Network Data

### 22.5.1 Send Data to Remote Hosts on the Network

Follow these instructions to select a remote host and send data.

**NOTE**

Network does not support the transfer of LIST data over the facility network.

- If necessary, click the **Image Works** icon to display the Image Works browser.

Figure 365 Image Works Browser

The screenshot displays the Image Works Browser interface. At the top, the 'Source' is set to 'Local DB'. Below this, there are three main data tables: 'Exams', 'Series', and 'Images'. The 'Exams' table shows 6 exams, including 'ANON6123' and 'GE QA Phantom'. The 'Series' table shows 7 series, with 'STATIC' series 13 highlighted. The 'Images' table shows 395 images, with the first 11 rows visible. At the bottom, the 'Destinations' section is highlighted with a yellow box, showing 'Local DB', 'PET\_CT\_L...', 'aws\_ds', 'aws', 'lemur', and 'Pigmy'. The 'aws\_ds', 'aws', 'lemur', and 'Pigmy' destinations are grouped under the 'Network' category. On the right side, there is a 'Data Apps' panel with various tools like 'Dynamic VUE', 'Q Freeze', '3D Viewer', etc., and a 'Messages' panel showing push job status updates.

Exam	Station name	Name	Date	Description	Modality	MPPS	Archived	Transferred
6123	CT48572	ANON6123	18 Mar 21	PT-CT CARDIAC ...	CT\\PT			
330	bj45	GE QA Phantom	03 Jun 19		CT			
14	lemur	Sh Test1	01 Jun 21		PT\\SR\\...			
34	horse	no_name_34	01 Jun 21		CT			
35	horse	no_name_35	01 Jun 21		CT\\RA...			
36	horse	no_name_36	01 Jun 21		CT\\RA...			

Series	Type	Images	Description	Modality	Manufacturer	MPPS	Archived	Transferred
1	SCOUT	1	CT SCOUT ...	CT	GE MEDICA...			
2	PROSP	395	WB Standard	CT	GE MEDICA...			
13	STATIC	395	WB 3D NAC	PT	GE MEDICA...			
901	LIVE	1	Head to To...	RAW	GE MEDICA...			
990	SSAVE	1	PET Exam R...	PT	GE MEDICA...			
997	SR	1	Dose Record	SR	GE Medical ...			
999	SSAVE	1	Dose Report	CT	GE MEDICA...			

Image	Img Ctr SI	Img Ctr RL	Img Ctr ...	DFOV	Algorithm	Matrix	Units	AC	WCC	Norm	Start time
1	1100.00	R 0.0	A 0.0	70.0	VPHD	256	prop cps	none	30May...	30May...	14:36:47
2	197.93	R 0.0	A 0.0	70.0	VPHD	256	prop cps	none	30May...	30May...	14:36:47
3	195.86	R 0.0	A 0.0	70.0	VPHD	256	prop cps	none	30May...	30May...	14:36:47
4	193.79	R 0.0	A 0.0	70.0	VPHD	256	prop cps	none	30May...	30May...	14:36:47
5	191.72	R 0.0	A 0.0	70.0	VPHD	256	prop cps	none	30May...	30May...	14:36:47
6	189.65	R 0.0	A 0.0	70.0	VPHD	256	prop cps	none	30May...	30May...	14:36:47
7	187.58	R 0.0	A 0.0	70.0	VPHD	256	prop cps	none	30May...	30May...	14:36:47
8	185.51	R 0.0	A 0.0	70.0	VPHD	256	prop cps	none	30May...	30May...	14:36:47
9	183.44	R 0.0	A 0.0	70.0	VPHD	256	prop cps	none	30May...	30May...	14:36:47
10	181.37	R 0.0	A 0.0	70.0	VPHD	256	prop cps	none	30May...	30May...	14:36:47
11	179.30	R 0.0	A 0.0	70.0	VPHD	256	prop cps	none	30May...	30May...	14:36:47

Destinations: Local DB, PET\_CT\_L..., aws\_ds, aws, lemur, Pigmy

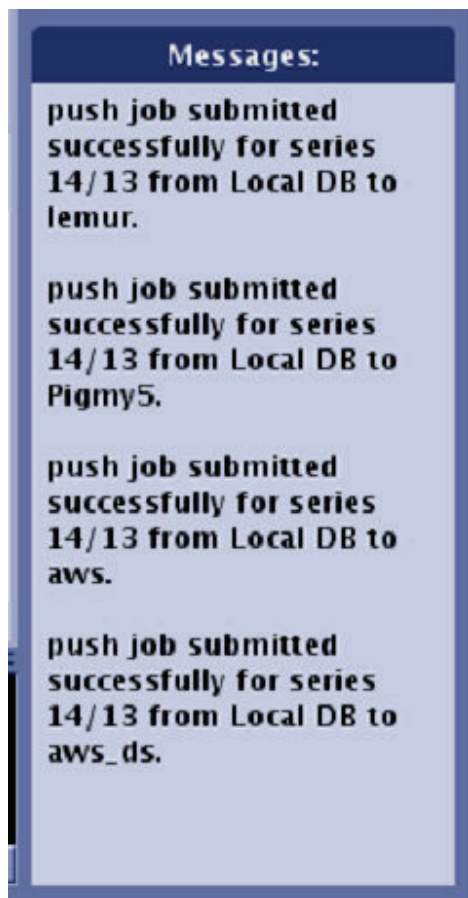
Local, Archive, Network

Messages:

- push job submitted successfully for series 14/13 from Local DB to lemur.
- push job submitted successfully for series 14/13 from Local DB to Pigmy5.
- push job submitted successfully for series 14/13 from Local DB to aws.
- push job submitted successfully for series 14/13 from Local DB to aws\_ds.

2. Select the desired exams, series or images.
3. Click the patient data you plan to network.
4. Select the network location from the **Network** area, as shown in Figure 365 on page 571.  
When the corresponding **Send** window opens, click **OK** to start the process.
5. Monitor the status of the network queue in the **Messages** area on the right side of the screen. Verify that the process has started.

**Figure 366 Messages Area**



6. Optional: Open the **Job Management** window to see the network task process.  
Click **Quit** to close the window.

## 22.5.2 Receive Data from Remote Hosts on the Network or Restore Patient Data from a Remote Device

Follow these instructions to receive data from a remote host on the facility network.

1. If necessary, click **Image Works** to open the browser.
2. Select the network location from the **Source** menu.
3. Enter filter criteria and press **Enter**.
  - a. The system displays the exams that meet the filter criteria on the selected network host.
  - b. Open the **Job Management** window to see task progress.

**NOTE**

To turn on Filtration option to a specific remote host through the network, go to **Display Monitor** -> **Tools** -> **Configure Network Hosts**, select the host of interest and click on **Edit**. On the Services section, check the custom search box, click on **Save** and then **OK**.

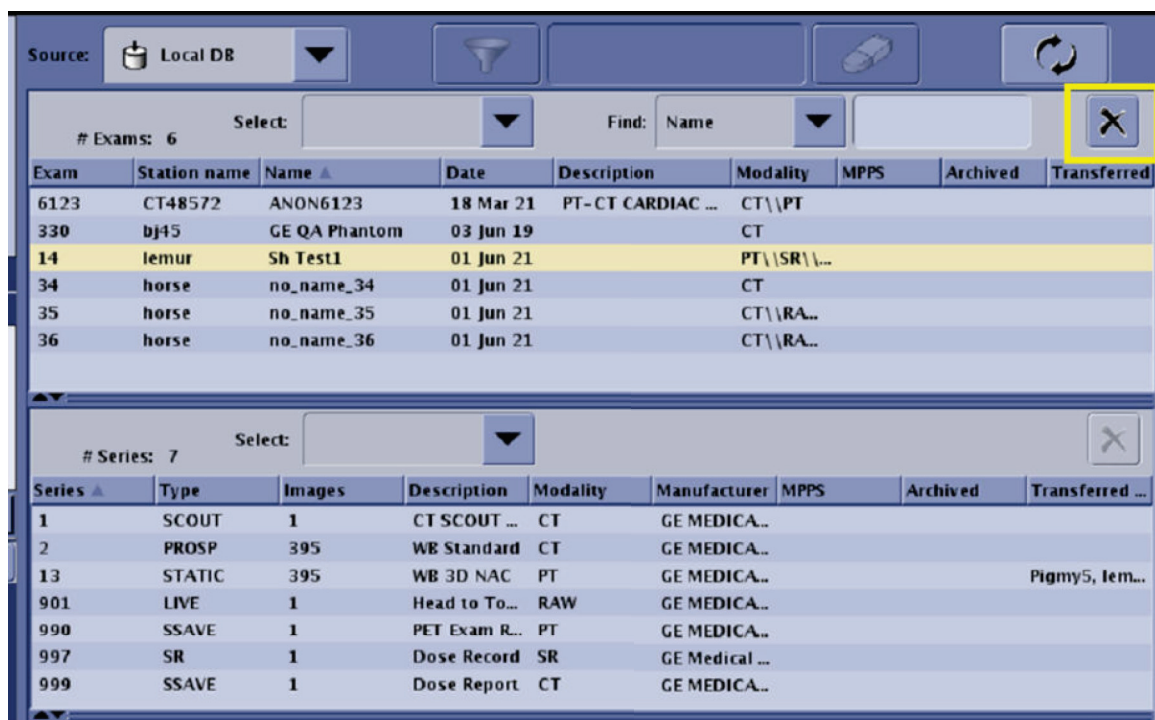
4. Click to highlight the patient data you plan to recall.
5. In the **Destinations** area at the bottom of the screen, click **Local DB**.
6. Verify that the network retrieval process has started in the **Messages** area.
7. To monitor the status of the Network Receive queue:
  - a. Click **Queue**.
  - b. Click or drag to **Network** to display a Dicom window.
  - c. Click **Refresh** to update the Dicom window display.
  - d. Click **Quit** to close the Dicom window.
8. Optional: Click **Network** then click or drag to **Network History** to open a DCS History File Log.
9. Click **Close** to close the **Job Management** window.

### 22.5.3 Delete Patient Data from the Image Works Browser

1. Click the **Image Works** icon to display the Image Works browser.  
Click to highlight the exams, series or images you want to delete from the database.
2. Click **X** to delete the exam, series, or images.

**NOTE**

Before deleting data from console, the user must check and confirm that data has been transferred successfully to archive/network stations.

**Figure 367 Image Works Browser Delete Button**

## 22.6 Manage Data (Archive and Storage) Quick Steps

### 22.6.1 Archive Patient Data

1. Click the **Image Works** icon to open the browser.
2. Click/highlight the patient data you plan to archive.
3. Click on the desired archive **Destination** in the **Archive** area.
4. Click the **Job Management** icon to monitor the status of the archive queue.

### 22.6.2 Store Data with Scan Data Manager

1. Click **Service** to open the PET Common Service Desktop.
2. Click the **Utilities** icon.
3. Click **Scan Data Manager**.
4. Insert or attach the media. Click the **Media** arrow to display the drop down menu and drag to the desired media type.
5. Click/highlight the data series you plan to save.
6. Click **Save to Media**.

- Click **Close DB Browser** to close the **Scan Data Manager** window.

### 22.6.3 Restore Data with Scan Data Manager

- Click **Service** to open the PET Common Service Desktop.
- Click the **Utilities** icon.
- Click **Scan Data Manager**.
- Insert or attach the media. Click the **Media** arrow to display the drop down menu and drag to the desired media type.
- Click **Browse Media**.
- Click/highlight one or more series to select them.
- Click **Restore to Scanner DB** to start the data transfer.
- Click **Close Media Browser** to return to the Scan Data Manager window.
- Click **Close DB Browser** to close the Scan Data Manager window.

### 22.6.4 Store Data with Interchange Media

- Click the **Image Works** icon to open the browser.
- Insert or attach the media.
- Select the desired data.
- Click **CD/DVD/USB** on the browser.
- Select the drive that the media is using.
- Select Include Image Viewer.
- Click the **Copy** icon.
- Click the **Exit** icon.

### 22.6.5 Restore Data with Interchange Media

- Click the **Image Works** icon to open the browser.
- Insert or attach the media.
- On the browser, select the source to be the interchange media.
- Select the desired data.
- Click **Local DB** in the **Destinations** area.
- On the browser, select the source to be the local database.
- Click **Tools** and select **Detach Media**. Select the media type and click **Detach Media**.

## 22.6.6 Send Data to Remote Hosts on the Network

1. If necessary, click the **Image Works** icon to display the Image Works browser.
2. Select the desired data.
3. Click on the desired network destination.
4. Click the **Job Management** icon to monitor the status of the network.
5. Click **Quit** to close the window.

## 22.6.7 Receive Data from Remote Hosts on the Network or Restore Patient Data from a Remote Device

1. If necessary, click the **Image Works** icon to display the Image Works browser.
2. Select the desired remote system as the source.
3. Select the desired data.
4. Click **Local DB** at Destinations.
5. Click the **Job Management** icon to monitor the status of the Network.
6. Optional: Click on the **Network History** tab to see a list of recent transfers.
7. Click **Close** to close the window.



## 23 Build a Protocol

### 23.1 Build a Protocol Introduction

This chapter contains procedures to build and modify PET/CT protocols. It also describes how to manage existing system protocols. For detailed instructions to build and modify diagnostic CT protocols, including use of Related Protocol and Imaging Protocol Manager (IPM) options, please refer to the CT User Manual and CT Technical Reference Manual (CT TRM) shipped with your system.

This is a protocol driven PET/CT system. You must select a protocol to acquire images with this system. A PET/CT protocol normally consists of a scout series, a CT series used for attenuation correction (CTAC), followed by a PET series, but you also have the option to create PET Only or PET First protocols. Once you create and save a protocol, you have the option to add, modify or delete series when you select this protocol during the scan prescription process. In addition to the CTAC series, you have the option to add additional diagnostic CT series and/or CT visualization series to the protocol when you create it, or when you select it during an exam. You also have the option to create a Hybrid PET/CT protocol that uses a diagnostic or visualization CT series to attenuate the PET series.

When you select a protocol during an exam, the system copies the protocol information into the scan window. Any changes you make to this copy will have no effect on the original protocol. However, if you like the results from these changes, you have the option to save this modified protocol as an entirely separate protocol from the original. You can also take a CT protocol and **Add PET** to save a new hybrid protocol.

The system arrives with a few basic protocols stored in the **GE** tab. During applications training, your instructor teaches you how to use the basic protocols to create a unique set of user protocols for your facility. During normal operation, you scan with the protocols stored in the **User** tab. The system provides space to store up to 90 protocols for each adult anatomical region, and 90 protocols for each color area of the pediatric protocols, for a total of 6,840 protocols.

Follow the instructions in this chapter to select a basic PET/CT protocol from the **GE** tab, modify it, then store the newly created protocol in the **User** tab.

#### NOTE

The Pediatric GE tab **ABODOMEN** contains a PET/CT protocol for each color selection, for you to copy into the **User** tab and modify for facility use.

This chapter also contains instructions to manage protocols, and create new protocols from existing protocols in the **User** tab. This chapter also briefly describes the functions of the **Service** and **Most Recent** protocol tabs.

#### NOTE

Build A Protocol functionality is not fully supported for Whole Body Dynamic Acquisition. Use GE protocols and edit their parameters, if needed.

#### NOTE

In order to build and modify PET/CT protocols, and in case that the system is configured with HIPAA, the user should be defined as a standard user in the EA3 configuration.



### 23.1.1 Build Protocols

Use **Protocol Management** to build, edit and manage protocols. The anatomical selector has four tabs: **GE**, **User**, **Service** and **Most Recent**, to store the system protocols. The **User** tab provides access to 10 Adult anatomical regions and 10 Pediatric anatomical regions. Each anatomical region accepts up to 90 protocols. The Pediatric anatomical regions are further divided into color areas and weight classifications, this provides a total of 6,840 available user selected protocols. The **GE** tab contains starter protocols. The **Service** tab contains calibration and alignment protocols for service personnel. The **Most Recent** tab automatically stores a copy of the protocol you used to scan the patient, complete with any additions or modifications. You can copy and paste this protocol into the **User** tab to add it to the list of available protocols. The system stores the protocol of most recently acquired exam in the top line of the **Most Recent** protocol list. Once all the spaces on the **Most Recent** protocol list are filled, the system automatically deletes the oldest protocol from the bottom of the list when it adds the mostly recently scanned protocol to the top of the list.

### 23.1.2 Use Protocols

During the exam prescription process, use the anatomical selector to choose a protocol that most closely matches your scan, then modify it to suit your needs.

### 23.1.3 Edit Protocols

Once you select a protocol and copy its parameters into the acquisition screens, you have the option to add series or modify the existing protocol parameters before proceeding to scan. If you want to permanently change a protocol parameter, click **Protocol Management**, change the parameters, then click **Accept** to save the protocol with the new values. If your system uses the HIPAA Login feature, you must have permission to accept any changes in Protocol Management.

### 23.1.4 View Protocols

Use **Protocol Management** to display the protocol parameters. Click the up and down arrows to page through the protocol list to find a specific anatomical location.

### 23.1.5 Transfer Protocols

There are two ways to transfer Protocols between scanners: using System State or the Protocol Transfer Tool.

#### Follow this procedure to transfer protocols using System State:

1. Save protocols into a USB:
  - a. Insert the USB with the files you plan to restore into the USB port, located in the host console.
  - b. Click the **Service** icon.
  - c. Click the CT radio button to display the CT Service Desktop.
  - d. Click the **Utilities** icon on the Service Toolbar to open the Utilities menu.

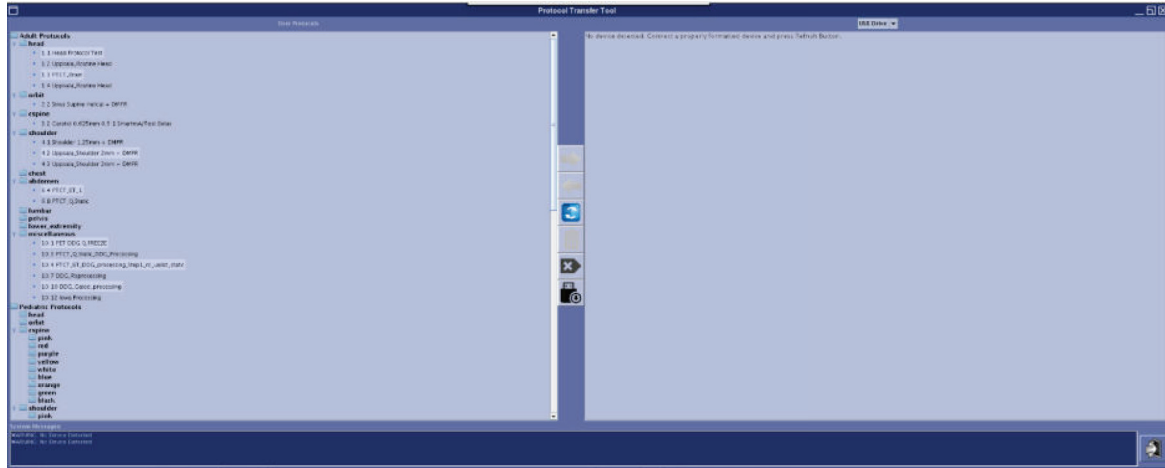
- e. Click the Utilities folder to display its contents.
  - f. Click **System State** or **System State - USB** to open the corresponding selection window.
  - g. If you use a blank USB for the first time, click **Display Preferences** on the **Save State** window, in addition to the **Protocols** button.
  - h. Click **Save** and follow the on-screen instructions.
    - If you inserted a blank USB (recommended) and clicked **Display Preferences**, a format request window opens. Click **Yes** to format the disk before saving the files.
  - i. Click **Save** and follow the on-screen instructions. After successful completion, a window opens to display, "Save/Restore System State: Completed Successfully."
  - j. Click **Cancel** to close the *System State Message* log.
  - k. Click **Dismiss** to close the *System State Save/Restore* window.
2. Transfer protocols to your other system from a USB:
    - a. Insert the USB with the protocols you plan to transfer from the USB port, located in the host console, to your other system.
    - b. Click the **Service** icon.
    - c. Click the CT radio button to display the CT Service Desktop.
    - d. Click the **Utilities** icon on the Service Toolbar to open the *Utilities* menu.
    - e. Click the Utilities folder to display its contents.
    - f. Click **System State** or **System State - USB** to open the corresponding selection window.
    - g. Click the **Protocols** button. The button activates when you click it.
    - h. Click **Restore** to open a query window.
    - i. Click **No** to exit the restore function without retrieving the files.
    - j. Click **Yes** to replace the existing Protocol files with the selected files on the USB.  
Upon successful completion, a window opens to display, "Save/Restore System State: Completed Successfully."
    - k. Click **Cancel** to close the *System State Message* log.
    - l. Click **Dismiss** to close the *System State Save/Restore* window.

**Follow this procedure to transfer protocols using Protocol Transfer Tool:**

1. Save protocols into a USB using the Protocol Transfer Tool:
  - a. Insert your USB
  - b. Click on the **Tool Chest** button on the display monitor (right monitor) and select **Unix Shell – Right (or Left)** to open a command window (or alternatively click **Alt + F3**)
  - c. Type **runProtoTransfer**  
The Protocol Transfer Tool Window opens and displays two screens (left screen: System Protocols; right screen: USB protocols), and a toolbar in the middle. On the top of the right screen, you can select USB.

- d. Select the protocols you want to transfer or click **Ctrl+A** to select all protocols and click on the arrow pointing towards the USB screen.
- e. Safely remove USB.

### Figure 368 Protocol Transfer Tool Window



- Go to your other system and connect your USB
- Click on the **Tool Chest** button on the display monitor (right monitor) and select Unix Shell – Right (or Left) to open a command window (or alternatively click **Alt + F3**)
- Type **runProtoTransfer**
- On the USB screen, select protocols you would like to transfer or click **Ctrl+A** to select all protocols and click on the arrow pointing towards your system

## NOTE

You will get a pop-up that asks you to overwrite what is already on the scanner. Check the box about not asking again. By clicking YES, it is going to overwrite the protocols on the scanner with the same name. New protocols or protocols with different names will be placed into the next available slot under the appropriate anatomy category.

- e. Safely remove USB.

### NOTE

The Protocol Transfer Tool copies all protocol parameters, including prescribed network hosts.

In cases where not all hosts are available (for example, multi-center sites), the system will not send the data to a host and will not provide any error message. Fix should be applied manually for every protocol.



TRANSFER OF PROTOCOLS BETWEEN DIFFERENT SYSTEMS WILL COPY THE EXACT ORIGINAL PARAMETERS OF THE PROTOCOL TO THE DESTINATION. CAREFULLY REVIEW THE PARAMETERS AND ADJUST IF NEEDED PER SYSTEM CONFIGURATION SUCH AS SYSTEM GEOMETRY, SPECIFIC SYSTEM CONFIGURATION AND AVAILABLE INSTALLED OPTIONS.

## 23.2 PET Options and Features

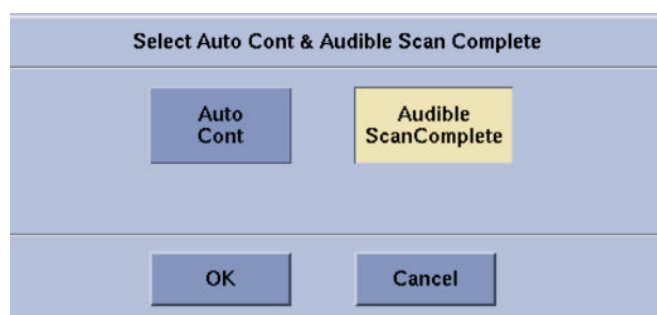
### 23.2.1 Audible Notification

Click the **Audible ScanComplete** button to select the sound that plays through the Acquisition Control speaker during a PET scan. The **Audible ScanComplete** function enables a sound to play when the PET scan successfully completes or a different sound when the PET scan fails to complete properly.

You have the option to turn this function on or off at the series level by clicking the [AutoCnt/Audible Scan] button on the PET series acquisition screen. This function defaults to the off state, but you can turn on the function when you build the protocol, or during the scan.

Regardless of the On/Off state, the system disables **Audible ScanComplete** during ViP Replay.

**Figure 369 Select Auto Cont and Audible Scan Complete Window**



Select the **Reconstruction** tab to enable PET prospective reconstruction, click **Show Recon 1** and set the parameters you plan to use. Repeat for Recon 2 and 3.

### 23.2.2 Auto Continue

Click the **AutoCnt** button to select whether the system continues from one series to another automatically or manually. **AutoCnt** enables the scan to continue automatically from one series to another when On or stop the scan after each series is completed and continue only after the user manually pressed the **Confirm** button on the console, then **Move to Scan** button before continuing to the next series.

You have the option to turn this function On or Off at the scan level by clicking the **AutoCnt/Audible Scan** button on the PET series acquisition screen. This function defaults to the On state, but you can

turn Off the function when you build the protocol. Regardless of the On/Off state, the system disables AutoCnt during ViP Replay.

### 23.2.3 Rad Rx Diagnostic PET/CT Exam (Option)

In addition to the regular CTAC series, a system with the Rad Rx option can use a wide variety of diagnostic or visualization CT series for PET attenuation correction. Follow the same protocol building process, just select the CT series you plan to use from the CT protocol list, and click the [Hybrid] button to enable access to the PET series window. During the exam, the system uses the selected CT series to generate the PET CTAC series in Recon 10. The **Recon 10** tab only activates during hybrid studies that use Rad Rx.

Systems with the Rad Rx option can use any CT series that meets the following criteria:

- The CT scan range encompasses the PET scan range.
- The CT series contains contiguous images, with no gaps between CT image groups or between the edge of the CT scan range. The system can use CT scans with multiple groups for PET attenuation correction as long as the space between groups is less than or equal to one half the slice thickness.
- The CT series was reconstructed with a Standard, Soft or PET AC filter, with a 70 cm FOV.
- The DFOV (Display Field of View) size equals the SFOV (Scan Field of View) and the center of the DFOV aligns to the center of the SFOV.
- The PET/CT acquired the entire image series with a single kV and CT SFOV throughout.

During Retrospective Reconstruction of images acquired with Rad Rx On, a window opens to display a list of CT series that qualify for PET attenuation correction. In addition to the previous criteria, the PET raw data and designated CT series must meet the following criteria in order to qualify.

- Both series reside in the same exam.
- Both series used the same landmark during acquisition.
- Both series have the same patient orientation.

Systems without the Rad Rx option, or series acquired with Rad Rx Off, use a CTAC series that just encompasses the scan range of the prescribed PET series. The Rad Rx feature uncouples the tight relationship between the scan ranges of the two series, permitting the use of CT series with longer than PET scan distances for PET attenuation correction. The operator has the responsibility to acquire at least one CT series that meets the criteria for selection as the PET attenuation correction series, especially when acquiring the PET series before the CT Series (PET First) or loading new PET defaults into the acquisition screen.

You also have the option to prescribe a multiple group CT, where one group meets the criteria for use for PET attenuation correction. The qualifying group becomes the PET CTAC.

### 23.2.4 Add PET to Clinical CT

During Protocol Management, systems with the Rad Rx option can add a PET scan to a diagnostic CT only series. This allows the user to combine an existing diagnostic CT series with a PET scan using the clinical CT series for PET CTAC.

**NOTE**

When adding a PET scan to a reference CT, the PET scan parameters may not match your site's preferences. Check newly added PET scan parameters to ensure they match your site's parameters.

### 23.2.5 ViP Record/Replay (Option)

ViP Record option captures the PET detector coincidence event stream in the form of a time-ordered event list and saves it to disk as ViP files. The system creates ViP files in addition to the sinograms it uses during image reconstruction. The ViP files contain time-stamps with a one-millisecond resolution and physiological triggers, in addition to the coincidence events.

ViP Replay provides the option to re-histogram the ViP Record data into a new set of PET scan data that uses different PET acquisition parameters.

During ViP Replay, you have the option to select:

- A reduced frame time.
- A ViP Replay of a static live ViP Record acquisition into a gated and/or dynamic acquisition.
- Different binning parameters: Number of Bins; Binning Mode (Percentage vs. Time); Trigger Rejection rates
- The acquisition of both cardiac and respiratory physiological triggers during the scan, so you have your choice of physiological triggers during ViP replay.

**NOTE**

The data maintains quantitative accuracy when a ViP Record live scan is ViP Replayed into a dynamic or static acquisition.

**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. 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 the **Recon Options** button 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 this reconstruction.

Clinical applications of ViP include:

- Evaluation of image quality at reduced frame times.
- Creation of cardiac gated scan from a cardiac dynamic scan (to avoid additional injections of the Rb tracer).
- Creation of a multi-FOV respiratory gated scan from a multi-FOV static scan.

ViP Replay acquisitions typically complete in significantly less elapsed time than the prescribed live scan time, with the potential exception of gated scans with many bins.

For best results prescribe all planned ViP scans before you edit or anonymize the corresponding patient data.

### IMPORTANT

ViP Replay cannot change the following features of the recorded acquisition, even though the user interface appears to permit these changes to take place.

- If you selected **Randoms From Singles** mode during ViP Record, do not change it during ViP Replay.
- ViP Replay cannot handle any inter-frame delays prescribed in the live ViP Record scan.
- To prevent potential ViP Replay acquisition failures, always finish all planned ViP Replays before you edit the tracer or anonymize the patient.

### 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.

## 23.2.6 4D Workflow

The 4D Workflow provides greater flexibility and functionality during Gated Radiation Oncology, Diagnostic Imaging and Cardiac PET studies. A Gated PET study produces multiple images that correspond to different physical positions of the designated patient anatomy throughout the gated cycle. This PET/CT provides the means to acquire gated respiratory and/or gated heart studies.

With a gating accuracy of  $\pm 1$  ms and a minimum gating interval of 10 ms, a Live study can use up to 16 bins, while a ViP Replay can use up to 64 bins.

### Binning Options

- **Percent binning:** Provides the option to acquire the entire respiratory or cardiac cycle, then divide the cycle into equal-duration bins for each trigger-trigger interval.
- **Fixed time binning:** Assigns a fixed time interval to each bin between triggers. You have the option to assign a different interval to each bin.
  - **Prevailing trigger interval too long:** Discards events that arrive beyond the last designated time bin.
  - **Prevailing trigger interval too short:** Leaves the trailing bins empty.

### NOTE

Fixed time binning option is available only for cardiac gating.

## 23.2.7 Q.Static Workflow

The Q.Static Workflow provides PET images with reduced motion during Radiation Oncology and Diagnostic Imaging. A Q.Static PET study produces motion reduced images that correspond to the designated patient anatomy at the quiescent period of the respiratory curve.

## 23.3 PET Reconstruction Parameters

The available reconstruction selections vary with the type of acquisition data, the reconstruction method and reconstruction mode you choose.

### 23.3.1 Matrix Size

This PET/CT provides 4 matrix size selections:

- 128 x 128
- 192 x 192
- 256 x 256
- 384 x 384

### 23.3.2 Recon Method

The Reconstruction Method selection determines the availability of the filter/iteration/subset selections. Follow facility guidelines to name the image sets, and select the reconstruction parameters.

The PET/CT provides the following choices:

#### 23.3.2.1 VUE Point HD (3D iterative) Recon

- **VUE Point HD (3D iterative) Recon:** Provides subset, iteration and filter parameter selections during prospective and retrospective reconstruction, with the post-filter value applied after reconstruction. The Light, Standard and Heavy Z-Axis filter selections smooth consecutive axial reconstruction images across frame boundaries. The targeted reconstruction filter produces images with no rim or edge artifact. You have the option to choose a different targeted reconstruction center and Field of View diameter.

#### 23.3.2.2 SharpIR

**SharpIR ON/OFF:** Applies a system response model to VUE Point HD. When you select this function, you may want to choose additional iterations. Follow the advice of the site physician to set these values.

#### NOTE

SharpIR is not a valid reconstruction method for NAC images.

#### 23.3.2.3 Q.Clear

**Q.Clear** (option): A quantification method used during prospective and retrospective reconstructions to iteratively reconstruct PET images to full convergence while maintaining acceptable image quality.





Beta factor can be used to control the smoothness of the image. The larger the Beta factor, the smoother the image. Beta factor has a default value of 350, but allows for a range of 1-10,000.

With Q.Clear, the signal to noise ratio is greatly improved and thus the contrast ratio is 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.

#### NOTE

Q.Clear is not a valid reconstruction method for NAC images.

In cases where the Gibbs artifact is present on PET Q.Clear images, reconstruction with Q.Clear selected as the quantitation method and selection of a larger PET image matrix dimension than the original reconstruction may help to alleviate it.

### 23.3.2.4 Precision DL (Option)

#### 23.3.2.4.1 Intended Use

Precision DL is a deep learning-based image processing method intended for Positron Emission Tomography images.

#### 23.3.2.4.2 Indications for Use

Precision DL is a deep learning-based image processing method intended to enhance image quality of non-ToF PET images for clinical oncology purpose, using F-18 FDG. Precision DL may be used for patients of all ages.

#### 23.3.2.4.3 Precision DL Overview

Precision DL is a deep learning-based image processing method intended for PET oncology 18F-FDG images obtained using non-ToF PET systems. Precision DL enhances the non-ToF images to have image quality (IQ) performance similar to PET images obtained using ToF PET systems, including enhancement in image Contrast Recovery (CR), Contrast to Noise Ratio (CNR), and quantitation accuracy. Precision DL bridges the gap between the absence of hardware based ToF technology and the IQ benefits of ToF reconstruction.

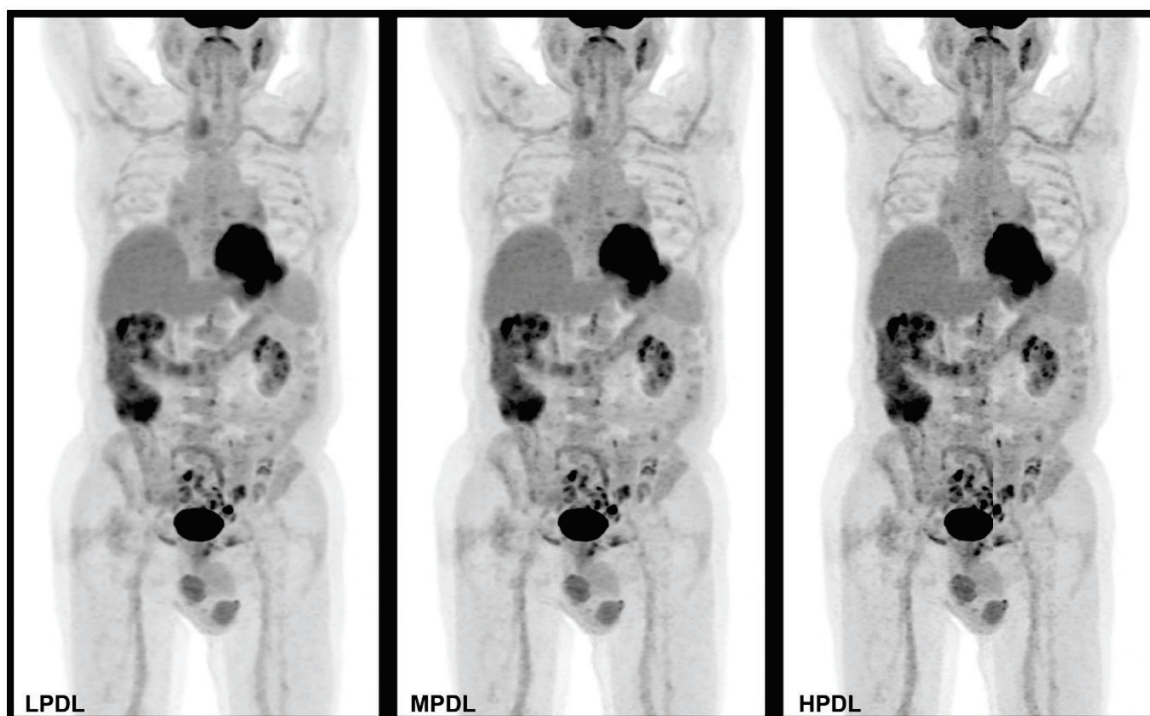
Precision DL brings three deep learning models to provide users the choice between different strengths of contrast enhancement and noise reduction. The three Precision DL models are:

- Low Precision DL (LPDL)
- Medium Precision DL (MPDL)
- High Precision DL (HPDL)

The models are trained such that **High Precision DL** brings the highest contrast enhancement and lowest noise reduction (i.e. sharper images), while **Low Precision DL** brings the lowest contrast

enhancement and highest noise reduction (i.e. smoother images). The **Medium Precision DL** brings contrast-noise tradeoff in between High and Low Precision DL.

**Figure 370 Example DLs Contrast-to-Noise Tradeoffs across Low, Medium and High Strengths.**



The strength selection will vary with individual user's preference and experience with Precision DL for the specific clinical need. Before using Precision DL, the site physicist, in collaboration with the radiologist, should conduct IQ evaluation with varying Precision DL strengths. Medium is recommended as an appropriate starting point for Precision DL strength on your existing protocols.

#### 23.3.2.4.4 Precision DL Theory

Precision DL's models (L-PDL, M-PDL, H-PDL) were trained using a Deep Neural Network designed for PET image processing. The Deep Neural Network can mimic the activity in layers of neurons in the neocortex, the part of the brain where thinking occurs, hence learning and producing highly accurate model parameters that are involved in PET image processing.

The training was performed in supervised learning sessions to transform non-ToF Q.Clear (QCHD) images into images that are similar to a ToF Q.Clear (QCFX) image. The training used data that was acquired on GE Healthcare's ToF capable Discovery MI system. This data was used to generate non-ToF Q.Clear (QCHD) and ToF Q.Clear (QCFX) image reconstructions, which together form pairs of input and target data for Precision DL's deep learning models. The same data was used to train each of the Precision DL models, with the primary difference being the Q.Clear reconstruction regularization value ( $\beta$ ) of the target image. For each PDL model, this value was set to reflect the model's target level of contrast-to-noise.

**Table 96 Range of  $\beta$  Values for Target ToF Q.Clear Images**

Precision DL Strength	Range of $\beta$ Values
HPDL	150-350
MPDL	250-550
LPDL	350-1050

The data used to train PDL's deep learning models included clinical whole-body oncology 18F-FDG patient data and phantom data. The clinical data was obtained from several clinical sites to aid generalizability by accounting for relevant variations in patients and site preferences. The phantom data was obtained using a phantom different than those used in routine IQ tests, with the objective to train Precision DL's models on characteristics present on phantoms but not in clinical data.

Through a supervised training process, the Deep Neural Network analyses the "target" dataset and produces a processing function (i.e. inference engine), which is adjusted and optimized through the process. At the conclusion of the learning process, the performance of the inference engine is tested with an extensive test dataset. If the performance is deemed suboptimal by internal and external experts, both the training parameters and datasets are refined and the process repeats again using transfer learning.

#### **Precision DL Strength Selection - Starting Guide**


The three Precision DL strengths represent different tradeoffs between contrast enhancement and noise reduction, where Medium Precision DL brings a balanced tradeoff between the Low and High Precision DL strengths.

- **Low PDL:** Least contrast enhancement and most noise reduction
- **Medium PDL:** Some contrast enhancement and some noise reduction
- **High PDL:** Most contrast enhancement and least noise reduction

The choice of  $\beta$  in Q.Clear reconstruction has a similar role, with higher  $\beta$  producing images with less contrast and lower noise, and lower  $\beta$  producing more contrast and higher noise. Therefore, the combination of preferred Q.Clear  $\beta$  with subsequent application of Precision DL will require some experimentation to determine a preferred set of parameters based on site preferences. As a starting point, it is recommended to apply the Precision DL strength that corresponds to the  $\beta$  value used for Q.Clear image reconstruction according to [the table](#) above. In many cases this will be Precision DL Medium.

The [table below](#) identifies the recommended Precision DL strength starting point in relation to the Q.Clear  $\beta$  value and scan counts characteristics and describes the expected impact of each strength on the image contrast and noise.

**Table 97 Contrast to noise tradeoffs in relation to Q.Clear PDL's Strengths.**

Q.Clear™ Image Reconstruction Setting	PDL-L Least contrast enhancement Most noise reduction	PDL-M Some contrast enhancement Some noise reduction	PDL-H Most contrast enhancement Least noise reduction
	Contrast and Noise Increase 		
<b>β</b> <b>350-1050</b> low count scans (low dose, short scan time) <i>favors low noise over contrast recovery</i>	<b>Start here:</b> <ul style="list-style-type: none"> <li>Mild contrast boost</li> <li>Least noise</li> </ul>	<ul style="list-style-type: none"> <li>Medium contrast boost</li> <li>Medium noise</li> </ul>	<ul style="list-style-type: none"> <li>Highest contrast boost</li> <li>Most noise</li> </ul> <b>NOTE</b> This may over enhance the contrast and noise
<b>β</b> <b>250-550</b> <i>typical</i> count scans (typical dose and scan time)	<ul style="list-style-type: none"> <li>Mild contrast boost</li> <li>Least noise</li> </ul>	<b>Start here:</b> <ul style="list-style-type: none"> <li>Mild contrast boost</li> <li>Least noise</li> </ul>	<ul style="list-style-type: none"> <li>Highest contrast boost</li> <li>Most noise</li> </ul>
<b>β</b> <b>150-350</b> high count scans (high dose, short scan time) <i>favors contrast recovery over higher noise</i>	<ul style="list-style-type: none"> <li>Minimal contrast boost</li> <li>Minimal noise</li> </ul> <b>NOTE</b> This combination provides very low impact on contrast and noise	<ul style="list-style-type: none"> <li>Mild contrast boost</li> <li>Least noise</li> </ul>	<ul style="list-style-type: none"> <li>Medium contrast boost</li> <li>Medium noise</li> </ul>

After obtaining the original images per the above recommendation you may want to further calibrate the image characteristics that best suit your clinical practice. The impact on image characteristics, as illustrated by the arrow at the top of the table. PDL Strength increase (from Low to Medium and then to High) result in increase to image contrast and noise.

### 23.3.2.4.5 Creating Precision DL Images

Precision DL is implemented as part of the Q.Clear image reconstruction. The reconstructed non-ToF Q.Clear images are used as input to the selected Precision DL models (LPDL, MPDL, HPDL). The Beta value for the Q.Clear reconstruction is set by the user.

**NOTE**

The three Precision DL strengths represents different tradeoff between contrast enhancement and noise reduction, where Medium Precision DL brings a balanced tradeoff between the Low and High Precision DL strengths. The choice of Beta in Q.Clear reconstruction has a similar role, with higher Beta producing images with less contrast and lower noise, and lower Beta producing more contrast and higher noise. Therefore, the combination of preferred Q.Clear Beta with subsequent application of Precision DL will require some experimentation to determine a preferred set of parameters based on site preferences.

Precision DL reconstruction is prescribed under the **AI Method** in the **Recon Type** user interface, with the following options (**None**, **LPDL**, **MPDL**, **HPDL**):

**Figure 371 Recon Type user interface, including Precision DL Prescription**

Select the desired PET Recon Type.

**Recon Method**

VUE Point HD FORE-FBP

**Quantitation Method**

Q.Clear 350 SharpIR

**AI Method**

None LPDL MPDL HPDL

**Filter Type**

Enhanced Hanning Rectangle Shepp-Logan Cardiac 3D Off

Hanning Butterworth Order (1 thru 10)

**Z-Axis Filter**

None Light Standard Heavy

OK Cancel

The user may select one or more of the listed strengths in **AI Method**. The output will be one Precision DL enhanced image series for each of the chosen strengths. The series description for each will identify

of the strength prescribed. The input Q.Clear series may also be saved by leaving the **None** button selected.

The user may select **None** for **AI Method**, if Precision DL reconstruction is not wanted. The output will be a Q.Clear image series with the prescribed Beta.

In Image Works, Precision DL series is identified by the following series description: **< input used> - <strength level>PDL**

For Example: **WB 3D MAC - LPDL**

**Figure 372 Precision DL Series Identification in Image Works**

Series	Type	Images	Description	Modality	Manufacturer	MPPS	Archived	Transferred...
1	SCOUT	2	CT SCOUT ...	CT	GE MEDICA...			
2	PROSP	153	CTAC 3.75 ...	CT	GE MEDICA...			
3	PROSP	153	WB Standard	CT	GE MEDICA...			
12	STATIC	153	test	PT	GE MEDICA...			
13	STATIC	153	test-LPDL	PT	GE MEDICA...			
401	STATIC	153	QClear	PT	GE MEDICA...			
403	STATIC	153	DLT-H-sh...	PT	GE MEDICA...			

The Precision DL reconstruction method can be identified in Image Works through the **Algorithm** field as **<strength level>PDL-<input used>**.

For example: **[LPDL-QCHD]**

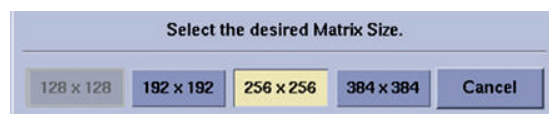
Since only Q.Clear is used as input, input used will always include QCHD. Strength level will change to [L], [M] or [H] if Low, Medium or High strength levels are used, respectively.

**Figure 373 Precision DL Reconstruction Method Identification in Image Works**

Image	Img Ctr SI	Img Ctr RL	Img Ctr ...	DFOV	Algorithm	Matrix	Units	AC	WCC	Norm	Start ti...
1	S 0.00	R 0.0	A 0.0	70.0	LPDL-QCHD	256	Bq/ml	meas...	25N...	25Nov...	15:43:...
2	I 2.07	R 0.0	A 0.0	70.0	LPDL-QCHD	256	Bq/ml	meas...	25N...	25Nov...	15:43:...
3	I 4.14	R 0.0	A 0.0	70.0	LPDL-QCHD	256	Bq/ml	meas...	25N...	25Nov...	15:43:...
4	I 6.21	R 0.0	A 0.0	70.0	LPDL-QCHD	256	Bq/ml	meas...	25N...	25Nov...	15:43:...
5	I 8.28	R 0.0	A 0.0	70.0	LPDL-QCHD	256	Bq/ml	meas...	25N...	25Nov...	15:43:...
6	I 10.35	R 0.0	A 0.0	70.0	LPDL-QCHD	256	Bq/ml	meas...	25N...	25Nov...	15:43:...
7	I 12.42	R 0.0	A 0.0	70.0	LPDL-QCHD	256	Bq/ml	meas...	25N...	25Nov...	15:43:...
8	I 14.49	R 0.0	A 0.0	70.0	LPDL-QCHD	256	Bq/ml	meas...	25N...	25Nov...	15:43:...
9	I 16.56	R 0.0	A 0.0	70.0	LPDL-QCHD	256	Bq/ml	meas...	25N...	25Nov...	15:43:...
10	I 18.63	R 0.0	A 0.0	70.0	LPDL-QCHD	256	Bq/ml	meas...	25N...	25Nov...	15:43:...
11	I 20.70	R 0.0	A 0.0	70.0	LPDL-QCHD	256	Bq/ml	meas...	25N...	25Nov...	15:43:...

Precision DL is compatible with Static and Q.Static scan modes only. It does not support Gated, Dynamic or Whole-body Dynamic scan types.

Precision DL is compatible with matrix size selections: 192x, 256x, 384x, and is disabled for 128x.

**Figure 374 Precision DL Supported Matrix Sizes****NOTE**

The Precision DL reconstruction is enabled only when the Q.Clear reconstruction is prescribed and is currently unavailable for other reconstruction methods.

**NOTE**

Precision DL cannot be used in conjunction with PET DMPR. 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.

**NOTE**

- Precision DL utilizes patient/phantom weight, and tracer information (tracer, nuclide, and injection activity, date, and time) during inferencing. Missing or inaccurate patient/phantom weight or tracer information may consequently lead to inaccurate quantitative values.

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

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



**NOTE**

Precision DL image reconstruction will not start until the reconstruction for the input Q.Clear images has completed. Precision DL image generation includes pre-processing, inferencing via the Deep Learning inference engine and final image installation.

- 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**.

#### 23.3.2.4.6 Precision DL - Edit Patient, Tracer and Nuclide

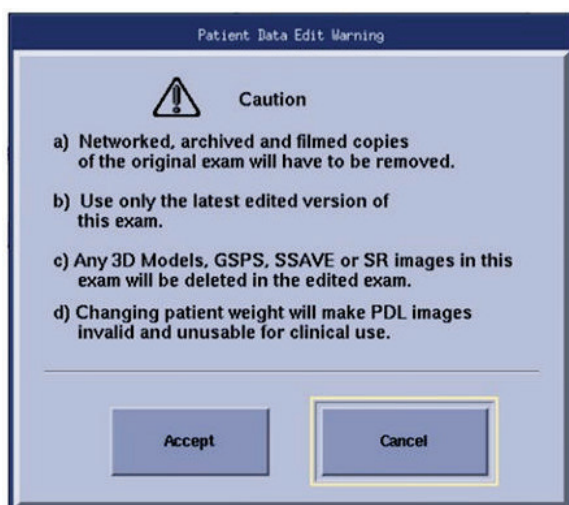
Detailed instructions on editing patient, tracer, and nuclide information is provided in the chapter [Edit Patient, Tracer and Nuclide Information](#). This section of this manual provides user information specifically related to Precision DL and editing patient, tracer, and nuclide information.

- After patient/phantom weight and/or tracer information are changed, Precision DL images are marked as invalid. Manually perform retrospective reconstruction to regenerate accurate Precision DL images with tracer information changes applied.
- When using Precision DL, if a change to patient weight or tracer information is made, perform the changes through **Edit Patient** or **Edit Tracer** applications 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.
- 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.

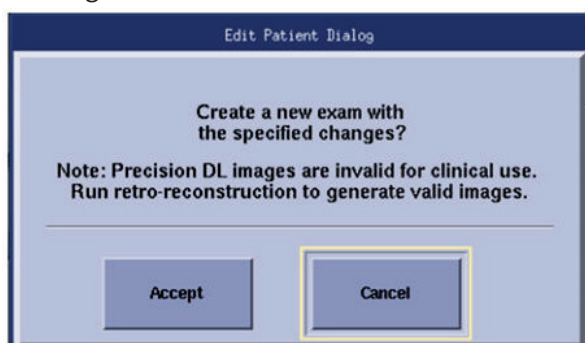


- The following Precision DL related messages are displayed when editing patient information using the **Edit Patient** application.



A) NETWORKED, ARCHIVED AND FILMED COPIES OF THE ORIGINAL EXAM WILL HAVE TO BE REMOVED. B) USE ONLY THE LATEST EDITED VERSION OF THIS EXAM. C) ANY 3D MODELS, GSPS, SSAVE OR SR IMAGES IN THIS EXAM WILL BE DELETED IN THE EDITED EXAM. D) CHANGING PATIENT WEIGHT WILL MAKE PDL IMAGES INVALID AND UNUSABLE FOR CLINICAL USE.

This above message is displayed after clicking on the **Edit Patient Data** from the **Edit Patient Application Selector** window. It warns users that changing the patient weight will make Precision DL images invalid for clinical use.



**Create a new exam with the specified changes?**

**Note: Precision DL images are invalid for clinical use. Run retro-reconstruction to generate valid images.**

This message above is displayed after clicking accept on the Edit Patient Data window. It warns that Precision DL images are invalid for clinical use and instructs to run retro-reconstruction to generate valid images.

- 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.
- 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.



CONTRAST CHANGES WITH PRECISION DL DEPEND ON THE STRENGTH CHOSEN (I.E. LOW, MEDIUM, OR HIGH PRECISION DL). ALWAYS REFER BACK TO THE INPUT Q.CLEAR IMAGE, IF A CONCERN IS OBSERVED IN THE PRECISION DL IMAGE.



PRECISION DL IS TRAINED AND INTENDED ONLY FOR ONCOLOGY 18F-FDG PET IMAGING DATA. DO NOT USE PRECISION DL FOR PROCESSING NON-ONCOLOGY OR NON-18F-FDG IMAGING DATA.



PRECISION DL IS TRAINED ONLY FOR ONCOLOGY 18F-FDG PET IMAGING DATA. IT IS NEITHER TRAINED FOR NOR COMPATIBLE WITH IMAGING DATA OBTAINED FROM PRESCRIBING RADIOTRACERS OTHER THAN 18F-FDG. PRECISION DL WILL BE DISABLED WHEN CHANGING PREDEFINED USER 18F-FDG PROTOCOLS TO A RADIOTRACER OTHER THAN 18F-FDG. THE SYSTEM DISPLAYS A WARNING MESSAGE TO INFORM USERS WHEN PRECISION DL IS DISABLED.



PRECISION DL IS SUPPORTED ONLY WITH STATIC AND Q.STATIC SCAN MODES, AND IS THEREFORE DISABLED FOR THE OTHER UNSUPPORTED SCAN MODES. PRECISION DL WILL BE DISABLED WHEN CHANGING PREDEFINED STATIC OR Q.STATIC USER PROTOCOLS TO USE AN UNSUPPORTED SCAN MODE. THE SYSTEM DISPLAYS A WARNING MESSAGE TO INFORM USERS WHEN PRECISION DL IS DISABLED.



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.



PRECISION DL IS DISABLED FOR 128X MATRIX SIZE.

#### NOTE

Any serious incident that has occurred in relation to the device should be reported to the manufacturer and the competent authority of the Member State in which the user and /or patient is established.



USERS SHOULD BE AWARE THAT, ALTHOUGH PRECISION DL PROCESSED IMAGES ARE ENHANCED, THE IMAGE ACCURACY MAY DIFFER FROM THAT IN TOF PET SYSTEMS.

### 23.3.3 Z-Axis Filters

This PET/CT system has three Z-Axis filter selections that provide the following filtering options:

- No Z-Axis filter
- A three-slice filter with Light, Standard or Heavy Z-Axis smoothing
- A 3D gaussian filter, intended for use during PET Cardiac image reconstruction. You have the option to use this filter on any single-FOV reconstruction.

### 23.3.4 DFOV (Display Field of View)

The Display Field of View, along with DFOV center determines the size, in centimeters, and position of the area of interest on the reconstructed image. In default mode, the DFOV is sized to and centered on the Scan Field of View (SFOV). You have the option to choose a smaller DFOV, and new center point. The size of the DFOV can never exceed the size of the SFOV.

You may change the DFOV by typing a new size and center values into the corresponding data fields, or by positioning a crosshair over the image and clicking and dragging the mouse to resize and/or reposition the DFOV.

The maximum diameter for a dedicated PET reconstruction: 70 cm.

## 23.4 PET Dose Parameters

### PET Tracer Information - Inherit from Exam

During the protocol building session, you can establish three Tracer parameters:

- *Radioisotope*: The scan protocol always defaults to the designated isotope.
- *Radiopharmaceutical*: The scan protocol always defaults to the designated tracer.
- *Propagation of the injection information across designated PET scans*: Determines whether the injection information you enter into the **New Patient PET Tracer Information** panel automatically appears on the **PET Tracer Information** panel associated with each group of PET scans within the series, or within the exam.

During a PET/CT exam, you can enter injection information in the **PET Tracer Information** panel on the **New Patient** window or from the **Patient Schedule** window, or proceed to the **PET Acquisition** window, click the **Dose** tab and click **Dose** to display the **PET Tracer Information** panel for the corresponding group of PET images. At this level, the panel has a **Inherit from Exam** button. Enable this button to establish a relation between the two **PET Tracer Information** panels.

- **Inherit from Exam (enabled)**: The series level panel displays the same information and/or blank data fields as the initial PET Tracer Information panel. If you make a change to the injection information at the series level, the system automatically disables the **Inherit from Exam** button and treats this scan as having unique tracer information.
- **Inherit from Exam (disabled)**: The system treats each scan as having unique tracer information. If you have multiple PET scans or PET series, you must edit the tracer information individually.

Upon completion of the exam, you can select the Image Works **Edit Tracer** button to add or modify tracer information. Please refer to [Edit Patient and Tracer Information](#) for more information.

**NOTE**

Even if you do not intend to enter tracer information before the scan, you must enable or disable the **Inherit from Exam** button when you build the protocol. If, for example, the study consists of two scans, each with a different tracer injection, you must set the protocol to disable the Inherit from Exam function for scans with the second injection. This lets you edit the tracer information for scans using the second injection independently from scans using the tracer information of the first injection.

Take care to select the correct isotope when you build the protocol and/or modify the **View/Edit** window, because you can't change the isotope with Edit Tracer. You can change the name of the radiopharmaceutical after the scan ends. If you accidentally chose two different radiopharmaceuticals but selected the same isotope within the series, the system treats the PET scans as two separate groups, regardless of the state of the **Inherit from Exam** button.

## 23.5 Edit an Existing Protocol

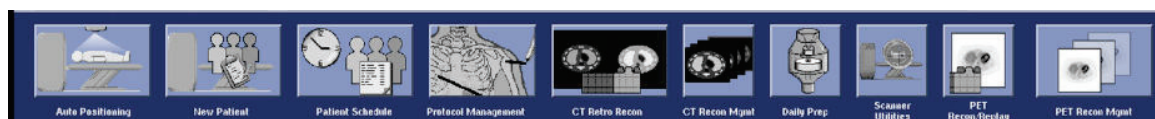
Follow the instructions to select an existing protocol, copy it to a new location, then modify and save the parameters as a new protocol. You can also follow these instructions to edit an existing protocol, and resave it with new parameters.

**NOTE**

[Build a New Hybrid PET/CT Protocol](#) contains a brief, functional description of the standard PET/CT parameters.

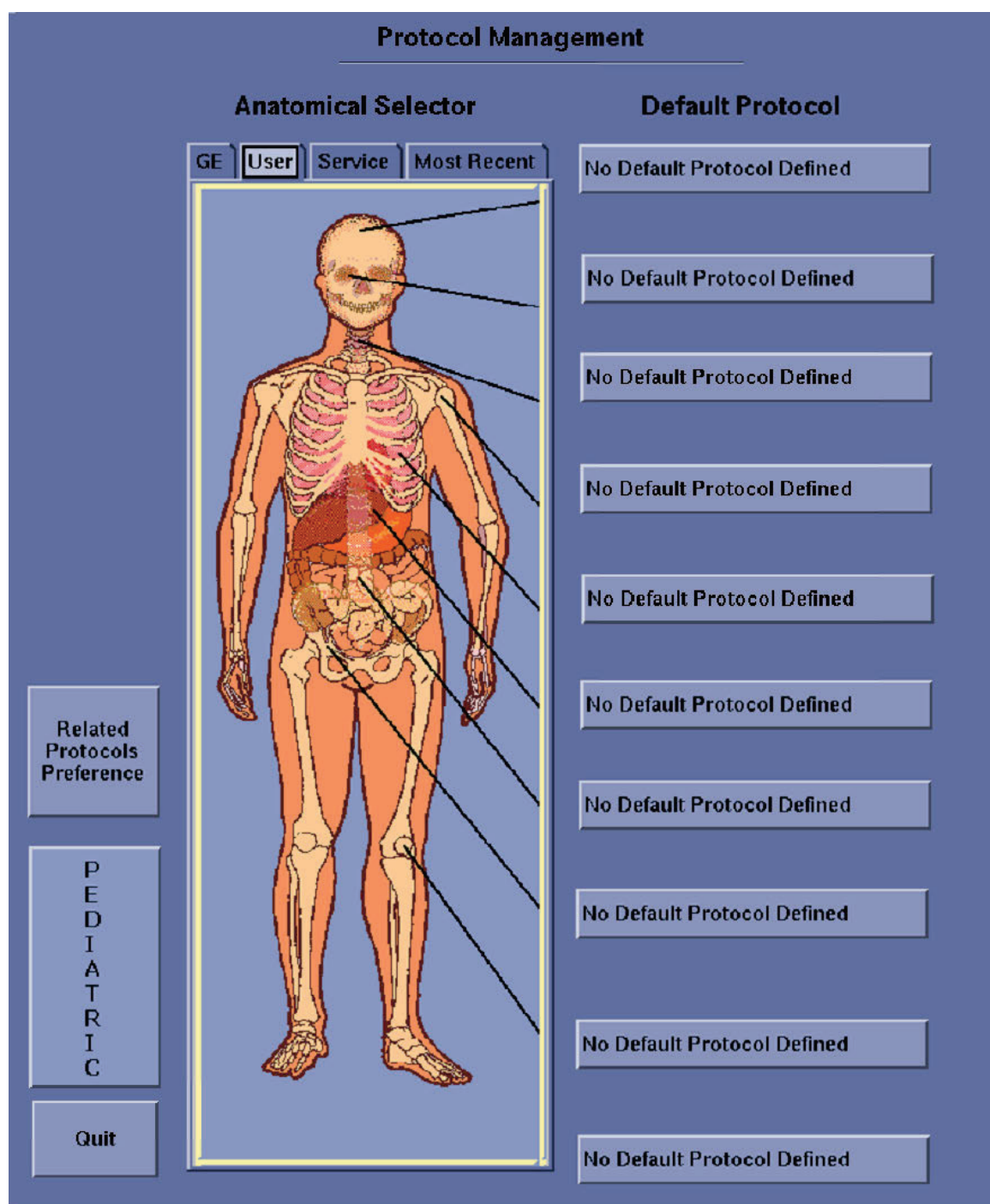
1. Click the **Protocol Management** icon to display the **AutoVoice Record/Protocol Management** window.

**Figure 375 Protocol Management Icon in Scan Monitor Toolbar**



2. Click **Protocol Management** to open the anatomical selector.  
The anatomical selector provides space for up to 6,840 User protocols.

Figure 376 Anatomical Selector



3. Click the **User** tab.

If you plan to copy and modify an existing starter protocol, click **GE** and follow the Quick Steps to copy and paste the protocol into the **User** tab.

4. Click a region of interest on the body, or one of the default protocol buttons to open the corresponding protocol list for that anatomical location.
5. Scroll or click the arrows to display the protocol you plan to modify.
6. Click on the protocol description (or empty space) to highlight the border.
  - If you copied a starter protocol, click **Paste** to deposit the copy in the empty space.
  - If you plan to edit an existing protocol, click the protocol description.
7. Follow facility guidelines to type a new description or modify the existing description.
8. Optional: Click **Set As Default** to permanently highlight the protocol, and display its name in the corresponding default protocol button, to the right of the anatomical selector.

You can designate one default protocol per Adult anatomic region.

#### NOTE

You cannot set a default pediatric protocol.

9. Click **Edit** to open the first available scan window, normally a scout series.  
You can modify or keep the current parameters, add more scouts, create a new series, repeat the series and/or click **Next Series** to open the next available scan window in the selected protocol.
10. Optional: click **Create New Series** to open the **Select New Series Type Selector** window.  
Select the **Scout**, **Axial** or **Hybrid** (PET/CT) button, then click **Create Before** or **Create After** to place this new series into the exam.

#### NOTE

Without the Rad Rx Option, when you click **Axial** you can only access CT series windows (including the scout, if available). Clicking **Hybrid** or using the Add PET feature (requires Rad Rx Option) enables the **CT** and **PET** buttons on the scan windows, so you can toggle between the CT and PET series acquisitions windows. You can always add a PET/CT series to an existing CT protocol by clicking **Create New Series**, followed by **Hybrid**.

11. Click **Next Series** to display the next available series in the selected protocol and/or click the **PET** and **CT** buttons to toggle between windows.
  - You can modify or keep the current parameters, add image groups or PET scans, split CT groups into smaller groups, create a new series, repeat the series and/or click **Next Series**, if available, to open the next available scan window in the selected protocol. Click **Prior Series** to return to the previous series in the exam.
  - You can also delete the currently displayed series from the protocol.
12. Click **Accept** to store the currently selected parameters and series in the designated protocol location. The display returns to the open protocol list.
13. You can change the protocol name, or set it as the default.
14. Click **Done** to save the protocol and close the corresponding list.
15. Click **Quit** to close the anatomical selector.



16. Click **Quit** to close the **AutoVoice Record/Protocol Management** window.

#### NOTE

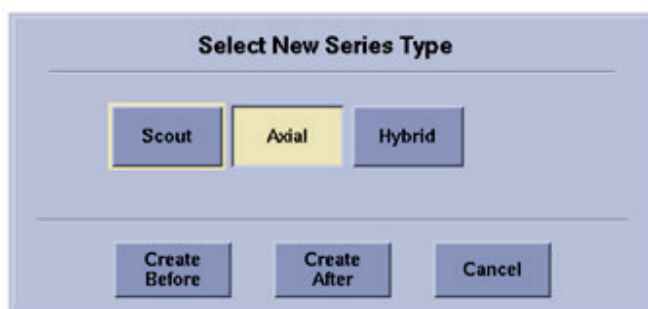
For instruction regarding Related Protocols Preference used for CT protocols, refer to CT user manual shipped with your system.

## 23.6 Build a New Hybrid PET/CT Protocol

Follow this procedure to build a new protocol. The procedure follows a typical PET/CT exam sequence. You can follow this sequence, or create a different scan sequence. A normal PET/CT study starts with a scout. This gives you the option to use the Graphic Rx Localizer to prescribe the PET and CT scan ranges. Typically, the attenuating CT series follows the scout, and the PET series follows the CT series. You can create a protocol without a scout series, or one that acquires the PET series before the CT series. The system warns you if the prescribed CT series fails to qualify for PET attenuation correction. You can create a protocol with multiple scout, PET and CT series, as long as the CT in the Hybrid (PET/CT) series has a scan range that fully encompasses the prescribed PET scan range (number of beds).

1. Click the **Protocol Management** icon to display the **AutoVoice Record/Protocol Management** window.
2. Click **Protocol Management** to open the anatomical selector.
3. Click the **User** tab.
4. Click a region of interest on the body, or one of the **Default Protocol** buttons to open the protocol list for that anatomical location.
5. Scroll to display an empty space in the protocol list.
6. Click on the empty space to select it.
7. Click **New** to move the cursor into the empty field.
8. Follow facility guidelines to type a new description and press **Enter** to open the **Select New Series Type** window.

**Figure 377 Select New Series Type Window**



9. For best results: Click **Scout** to start the exam with a scout series.
  - If you plan to use the Graphic Rx (Localizer) during the subsequent exam, start the protocol with at least one scout scan.

- AutomA and SmartmA require a scout acquisition to generate the mA tables used during subsequent CT acquisitions.
10. Click **OK** to close the **Select New Series Type** window, and open the **Scout Series** window.
  11. Set the patient orientation.
    - Click on the graphic of the patient's head or feet to select the head-first or feet-first orientation.
    - Click above or below the graphic's torso to set the orientation from Supine to Decubitus Left to Prone to Decubitus Right. Each click rotates the patient 90 degrees.
    - Click **Copy Pt.Orient.Pt.Position Anat.Ref.** to display the current orientation on all subsequent PET and/or CT acquisition windows.

#### NOTE

The patient graphic is set at installation to match the orientation of your scan room (gantry to the right or left). If the graphic does not match the PET/CT, contact GE service to reset the graphic.

12. Select the anatomical reference point.
  - a. Click the button beneath the Anatomical Reference label to open the **Anatomical Reference** window.
  - b. Click one of the labeled buttons, or click **Other** and enter the numeral 2 in the landmark reference field.
  - c. Click **OK** to accept the current button selection and close the window.
13. Click **AutoStore**, **AutoTransfer** and/or **Dose Report Auto Transfer**.
  - Click **AutoStore** to copy the prospectively reconstructed images to the designated local storage device, CD-R, DVD-R, or USB media, or send the image to remote storage on PACS when you complete the study and click **End Exam**.
  - Click **AutoTransfer** to send the images to up to four destinations, such as a review workstation or other scanners. You can Auto Transfer by image, by series or by exam.
  - Click **Dose Report Auto Transfer** to transfer the corresponding dose information for the Dose Report and the DICOM Structured Dose Report to up to four destinations. Your Auto Transfer selection (by image, series or exam) determines when the system sends the dose report.
14. Set the Scout Parameters.
  - Scout Parameters include the Scout Number, Start Location and End Location to set the scout scan range, the kV and mA technique factors, Scout Plane (degree location of the X-ray tube during the scout acquisition), AutoVoice and a Window Width/Level value to apply to the Scout image display.
  - Click the parameter label to change the value of every parameter in that column. (In the example figure, below, click **Start Loc.** to open a data entry window. Type a value into the data field and press **Enter** to display that value in Scout 1 and 2.)

- Click an individual parameter in a row to change just that value. (In the example, click the Scout 1 start location to activate the parameter, then type a new value in its place. The Scout 1 value changes and the Scout 2 value remains the same.)

**Figure 378 Set Scout Parameters**

Scout Num	Scan Type	Start Loc.	End Loc.	kV	mA	Scout Plane	Voice Lights Timer	Scout WW / WL
1	Scout	350.00	I250.00	120	10	90	H	500/50
2	Scout	350.00	I250.00	120	10	90	H	500/50

- Click **Add Scout** to display a new row of scout parameters beneath the existing rows. The new row contains the same parameters as the row above it.
- Click a Scout Number and click **Delete Selected Scout** to remove that scan prescription from the **Scout** window.
- The Start Location and End Location determine the scout scan range. **S** stands for Superior (toward the head) and **I** stands for Inferior (toward the feet) regardless of the patient orientation on the table.
- Select the Scout technique. Choose the lowest kV and mA possible. The object is to create an image for use with the Localizer, not for diagnosis.
- The Scout Plane sets the X-ray tube location (in degrees). During a scout, the X-ray tube remains stationary and the table moves to create an image that looks like a flat X-ray.
- You can set an AutoVoice and/or breathing light to prompt the patient when to inhale, hold the breath and exhale. You also can select an alternate language or select a personally prerecorded message. The system returns to the default AutoVoice selection when you end the corresponding exam.
- If Auto Scan is disabled, you must press **Move to Scan** for every bed before Start Scan will become ready.
- Use the Scout WW/WL feature to preset the Scout display window width and level.
- Click the **Series Auto Transfer** button to transfer the image series to up to four remote locations, such as a review workstation or another scanner.

**Figure 379 Scout Acquisition Window**

Name: tst ID: tst Protocol: 26.31 PTCT\_ET Exam: 67 Series: 1

Anatomical Reference  
  
 Patient Orientation: Head First  
 Patient Position: Supine

Series Description: CT SCOUT HEAD IN

Buttons:

Enter the target table location.  
 Elevation-mm: 50 Cradle-mm: 100

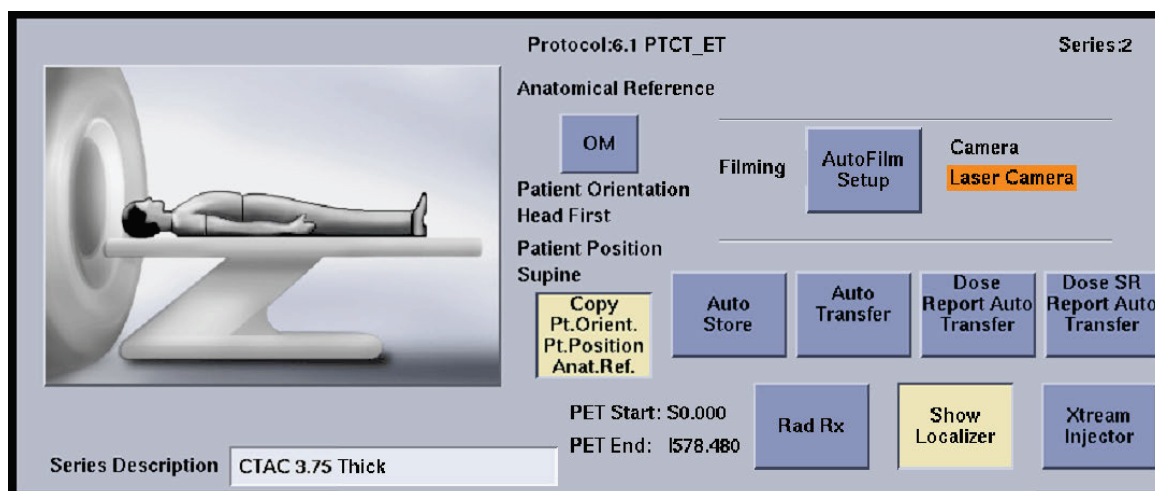
Scout Num	Scan Type	Start Loc.	End Loc.	kV	mA	Scout Plane	Voice Lights Timer	Scout WW / WL
1	Scout	350.00	11100.00	120	10	0	#	1000/-70
2	Scout	350.00	11100.00	120	10	90	#	1000/-70

Buttons:

Bottom Bar:

15. Click **Create New Series** on the **Scout Acquisition** window to display the **Select New Series Type** window, shown in [Figure 377 on page 601](#).
16. Click **Hybrid** to set up the subsequent CT and PET series scans.
17. Click **OK** to close the **Select New Series Type** window and open the CT series window.

You can click **PET** and **CT** to toggle between the two windows and select or modify parameters in tandem. You do not have to finish one window in order to advance to the next window.

**Figure 380 Patient Orientation Area of the CT Series Prescription Window**

## 18. Set the CT scan parameters.

- The scan parameters include: **Patient Position**, **Anatomical Reference** point, **AutoFilm Setup**, **AutoStore**, **AutoTransfer**, **Show Localizer** and **Series Description**, as well as the Technical Parameters and Reconstruction Parameters (next two steps).
- Click the **Copy Pt. Orient. Pt. Position Anat.Ref.** to copy the Anatomical Reference and Patient Orientation on the icon from the scout series to this series. If you want to change any of these values click **Copy Pt. Orient. Pt. Position Anat.Ref.** to disable the button.
- The **AutoFilm Setup** button opens the **AutoFilm Setup** window. Select corresponding parameters to set up the filming format and destination. Please refer to the CT User Manual and CT TRM that shipped with your system for detailed setup information.
- Click **Auto Store** to automatically send the image data to the system storage device. Click **Auto Transfer** and a window displays where you can select the IP address to send the images.
- If you selected **Auto Store**, **Auto Transfer** and/or **Dose Report Auto Transfer** during the Scout setup, the system selects the same parameters for this series. If you select one or both of these functions, the system applies your selections to the scout series. Refer to the scout series steps for additional information about these features. Refer to the CT User Manual and TRM for additional details.
- Click **Show Localizer** to display the scout image with the Graphic Rx Localizer upon completion of the corresponding scout acquisition. The system sizes and positions the Localizer to match the currently selected scan range, start location and prescribed number of scans. During the exam, changing a scan parameter updates the Localizer, and changing the Localizer size or location updates the scan parameter values on the corresponding CT (or PET) scan window.
- Click **ODM** to use Organ Dose Modulation. ODM provides a mode to reduce X-ray tube current (mA) in the anterior direction of the patient where the most radiation sensitive organs are located, while maintaining overall pixel noise standard deviation levels in other areas by

modulating X-ray tube current (mA) according to the X-ray tube angle. For more information, refer to the CT User Manual and TRM for additional details..

- Follow facility guidelines to enter a series description into the data field.

19. Set the Technical Parameters.

- Technical parameters include: **Scan Type**, **Start Location** and **End Location**, **Number of Images**, **Image Thickness** and **Scan Speed**, **Image Interval**, **Scan Field of View (SFOV)**, **kVp**, **mA**, **Total Exposure Time**, **Prep Group**, **Interscan Delay (ISD)**, **Breath Hold**, **Breathe Time**, **AutoVoice Language**, message and breathing light selections. Please refer to the CT User Manual and CT TRM shipped with your system for more detailed information.

**Figure 381 One Group of CT Technical Parameters**

Images	Scan Type	Start Location	End Location	No. of Images	Thick Speed	Interval (mm)	mm	SFOV	kV	mA	Total Exposure Time
1-281	Helical Full 0.5 s	\$0.000	1578.480	281	3.75 39.37 0.984:1	2.066	\$0.0	Large Body	140	180 28.50~	7.93

- Select a **Scan Type** that meets the criteria for PET attenuation correction.
- Select the **Thick Speed** parameters that meet the PET attenuation correction criteria.
- Select a **Start Location** and **End Location** to provide a CT scan range that meets the PET attenuation correction criteria. During the exam, you can adjust these values with the Graphic Rx Localizer. If your system has Rad Rx, you can select a CT scan range that exceeds the PET scan range.
- Erase the Start or End Location contents in CT Recon 1, then enter a *D* or *d* to copy the current CT locations into the corresponding parameter locations in CT Recon 2 and 3.
- With Rad Rx Off, the **No. of Images** parameter updates to reflect the start and end locations of the PET series, as well as the CT start and end locations (whichever has the longer scan range) and CT scan thickness and image interval information. If the system must modify a parameter to meet the criteria, it highlights it orange and displays a message about the scan tool bar.
- With Rad Rx On, you have the responsibility to prescribe a CT scan range that equals or exceeds the PET scan range, if you plan to use the CT series for PET attenuation correction.
- The **Image Interval** selection sets the Helical image interval to match the slice thickness selection, to create contiguous images needed to meet the criteria for PET attenuation correction. Click **Image Interval** to overlap slices or insert spaces between the slices in a CT series that you don't plan to use for PET attenuation correction.
- Select a CT Scan Field of View that completely encompasses the region of interest. With Rad RX On, the system generates a 70 cm CTAC in Recon 10.
- Select the **kV** and **mA** values that provide optimal image quality at the lowest possible dose to the patient. PET/CT studies typically use 120 kV. You can select an mA value in increments of 5 mA, starting with 10 mA. The kV selection determines the maximum available mA selection. Select the **AutomA** or optional **SmartmA** feature to provide consistent image



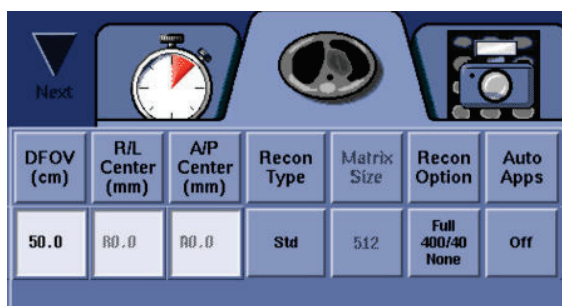
quality. The exam must have a Scout with the same patient orientation to enable AutomA or SmartmA.

- The system calculates and displays a **Total Exposure Time** based upon the prescribed number of images and type of scan. You must reset the number of images and/or type of scan to change this value. Use the total exposure time value to determine breath-hold times and contrast injection timing. The total exposure time equals the actual X-ray exposure time, and does not include interscan delays. The helical scan time always equals the total exposure time.
- If necessary, click the **Stopwatch** tab to display the Prep Group, ISD and breathing instruction parameter selections. Please refer to the CT User Manual and CT TRM that shipped with your system for detailed explanations of these features.
  - The Prep Group feature inserts a delay into the X-ray initiation sequence to delay X-ray On to accommodate a contrast injection. The Scan Type selection determines the delay range you can select, from 0-600 seconds, depending upon the Scan Type selection and number of image groups in the series.
  - The Interscan Delay (ISD) feature activates when you select the Axial Scan Type. The ISD feature inserts a delay between axial image scans, to improve the X-ray tube cooling capacity. Do not select an ISD if you plan to use this series for PET attenuation correction.
  - You can enter a **Breath Hold Time**, a **Breathe Time** and make AutoVoice **Voice/Lights/Timer** selections for each image group.

## 20. Set the Reconstruction Parameters.

- Click the tab with the picture of the Axial image to display the Recon parameters. The Recon parameters include: Display Field of View (DFOV), Right/Left Center, Anterior/Posterior Center, Recon Type (reconstruction algorithm), Matrix Size, Recon Option and Auto Applications (Auto Apps) selections.
- The DFOV size defaults to equal the SFOV. You can select a DFOV from 5 cm, up to the size of the SFOV. During reconstruction the system enlarges the DFOV to fill the viewport, so a smaller DFOV creates a magnified image.
- Use the **R/L Center** and **A/P Center** parameters to shift the designated area of interest to the center of the viewport during image reconstruction. The maximum available offset equals one-half the prescribed SFOV.

**Figure 382 Reconstruction Parameters**





- Click the **Recon Type** button or parameter to open a reconstruction algorithm selector window. Select any of the **PET AC** filters to meet the PET attenuation correction criteria. Reading the buttons from left to right, the algorithms increase spatial resolution and decrease low contrast detectability. Use the Bone Plus algorithm for any study that normally uses the bone algorithm, particularly in studies that used the Edge algorithm. The Bone Plus algorithm has no reconstruction penalty, yet comes close in standard deviation to Edge.

Ultra kernel is a post-processing adaptive enhance filter, which is based on the Bone Plus kernel image. It provides higher spatial resolution than the Bone Plus kernel while suppressing noise and aliasing artifact increase compared to the Bone Plus kernel.

The Chest algorithm provides soft tissue resolution and contrast when viewing the images in a soft tissue/mediastinal window (W/L), and high resolution of the lung tissue when viewing the image in a lung window (W/L).

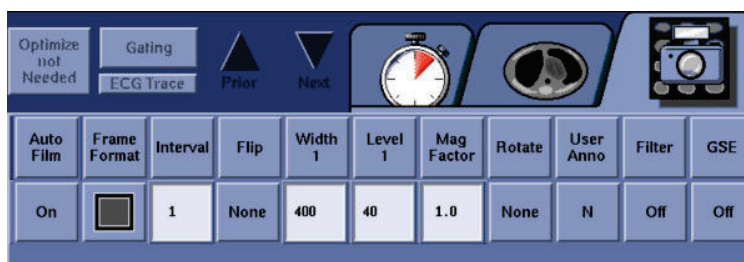
#### NOTE

You can program up to three reconstructions of data and Cardiac phases from one exposure. Click **Show Recon 2** and/or **Show Recon 3** to display the corresponding sets of reconstruction parameters. If the system has the Rad Rx option, and you select it, the **Show Recon 10** button activates. Recon 10 creates a CTAC series for PET attenuation correction when you select Rad Rx.

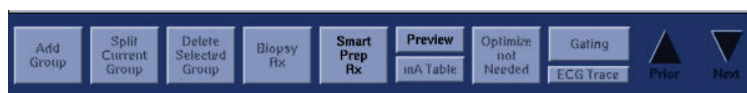
- Select the **Series Auto Transfer** feature to transfer Recon 2 and Recon 3 series to remote hosts. You can select up to four different destinations for each Recon series. You can choose unique destinations for each of the series that differ from the destinations you set at the exam level.
- The **CT Matrix Size** always equals 512 x 512.
- The **Recon Options** button opens a window that contains reconstruction options for CT images. The CT Scan Type selection and system software options determine the Recon Mode functions. The **Recon Options** window also contains Window Width and Window Level data fields, for setting the initial Window W/L of the recon display images. Please refer to the CT User Manual and CT TRM that shipped with your system for detailed information.
- Use the **Auto Apps** feature to create additional, specialized images from the scan data. The software options determine function availability. Please refer to the CT User Manual and CT TRM that shipped with your system for detailed information.

#### 21. Set the Film Parameters.

- Click the **Camera** tab to display the filming parameter selections. Please refer to the CT User Manual and CT TRM that shipped with your system for detailed filming instructions.

**Figure 383 Film Parameters**

- The Filming parameters include **Auto Film** (On/Off), **Frame Format**, **Interval**, **Flip**, Window **Width**, Window **Level**, **Mag Factor**, **Rotate**, **User Annotation**, **Filter** and Gray Scale Enhancement (**GSE**).
  - The system uses these **Window Width** and **Window Level** settings to initially display the images in the AutoFilm viewport. You can adjust the Window W/L in the filming viewport, prior to filming.
  - Use the **Mag Factor** to establish a preset magnification for each image in the filming viewport. Select a magnification factor from 0.5 to 2, by increments of 0.1 (Ex: 1.6).
  - Use the **Rotate** function to establish consistent image orientation of the filmed images, especially if the patient orientation is decubitus. You can rotate (a row or column of) images 90 degrees to the right, 90 degrees to the left or 180 degrees.
  - The **User Annotation** feature provides the means to display information in the middle of each cell, above the image. Use this feature to label delayed studies or other unusual film sequences. Use this feature during spinal studies to label vertebral levels. Click **User Anno** to open a window. Type the label or comment and click **Accept**.
  - Use the **Filter** to sharpen (Edge) or soften (Smooth) the images for filming.
  - The **Gray Scale Enhancement** changes the gray scale curve to enhance areas of low contrast for filming.
22. Select Additional Features. The system options determine the number and types of available features. Some buttons can only be available during scan.

**Figure 384 Additional Feature Buttons**

- **Add Group** displays another group of images with the same parameters as the group above it, except for the Start and End Locations. The system sets the Start Location to immediately follow the End Location of the previous group, to create contiguous images. You can change any parameter in the new group.
- **Split Current Group** divides the currently selected group of images into two groups. You can split the group according to scan location or image number. Use this feature to accommodate tube cooling and breath-holds.

- Use **Delete Selected Group** to remove images from the series prescription. Select the image group and click **Delete Selected Group** to remove the images. If necessary, the system rennumbers the remaining images to fill any gaps in the numbers.
  - Use **Smart Prep Rx** to monitor the peak the enhancement levels of IV contrast injections. Please refer to the CT User Manual and CT TRM that shipped with your system for details and instructions.
23. Click the **PET** button on the CT series acquisition window to display the PET series acquisition window.
- You can toggle between the CT and PET scan windows and modify parameters throughout the protocol building process.
  - The orientation area of the PET window displays the selections you made during the Scout or CT series prescription process. When you select **Hybrid**, any changes you make to the patient orientation on one hybrid window updates on the other hybrid window, however, the orientation on the Scout series or a separate Axial series window do not update.
  - The PET orientation area displays the CT Start and End scan locations. If your system has the Rad Rx function, the CT scan range equals the PET scan range with Rad Rx Off. The CT scan range may exceed the PET scan range with Rad Rx On.
24. Follow facility guidelines to enter a **PET Scan Description** and **Series Description** into the corresponding fields.

**Figure 385 PET Series Acquisition Window**

Protocol: 6.1 PTCT\_ET Series: 2

Anatomical Reference: OM

Patient Orientation: Head First

Patient Position: Supine

Copy Pt.Orient, Pt.Position, Anat.Ref.

Auto Store, Auto Transfer, Dose Report Auto Transfer, Dose SR Report Auto Transfer

Scan Description: Eyes to Thighs Emission CT Start: S0.000 CT End: 1578.480 Rad Rx Show Localizer

Series Description: WB 3D MAC

PET Scan Status

Scan Time Remaining: 00:00:00

System Count Rate (kcps)

True Rate: 3.505 kcps  
Random Rate: 1.593 kcps  
Total Prompts: 211,217,012 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
1-281	Static VIP Off	S0.000	1578.480	Toward Feet	2	25	00:00:00	00:04:00	0	0	N / N

Dose: 0.00 MDq Nuclide/Tracer: 18F FDG - fluorodeoxyglucose

Cancel Prior Series Next Series Create New Series Repeat Series Delete Series CT PET Auto Scan Accept

25. Click **Scan Type** to open a **PET Scan Type** window. The system options determine the feature selection availability.

**Figure 386 Select the Desired PET Scan Type Window**

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	
<div>OK Cancel</div>				

- The standard PET/CT has four Scan Types:
  - **Static:** Select Static to acquire images with a stationary distribution of tracer over the scan time. You can scan multiple (contiguous) bed positions in Static mode.
  - **Gated:** Select Gated to trigger the acquisition and binning of live scan data with physiological triggers such as respiration or heart beats. If your system has the ViP option, you can also enable the acquisition of static images with ViP Record, then ViP Replay the data as gated images.
  - **Dynamic:** Select Dynamic to acquire a series of images at the same physical location, to show the evolution of the tracer distribution over time. If your system has the ViP option, you can also enable the acquisition of static images with ViP Record, then ViP Replay the data as Dynamic images.
  - **Q.Static (option):** Select Q.Static to trigger the acquisition and segmentation of live scan data with respiratory triggers. If your system has the ViP option, you can also enable the acquisition of static images with ViP Record, then ViP Replay the data as Q.Static images.
- PET/CT has two Gating Mode selections:

- **Cardiac Gating Mode** uses the patient heart rate to trigger acquisitions. When you select this function, the Scan Type button label changes to **Gated-C**.
- **Respiratory Gating Mode** uses the patient respiratory cycle to trigger acquisitions. When you select this function, the button label changes to **Gated-R**.
- PET/CT has two Trigger Mode selections:
  - External: respiratory waveform and triggers are measured using an external device. When you select this option, the button label includes the letter **E**.
  - Derived: respiratory waveform and triggers are derived from coincidence events representing physiological motion (activity movement due to respiratory motion) without a need for a device. This option is not available during Live Gated acquisition. When you select this option, the button label includes the letter **D**.
- PET/CT has three Cardiac State selections:
  - **Stress**: The patient receives a pharmacological stressor before scanning.
  - **Rest**: The patient is scanned with the heart at rest (no stress medication).
  - **Off**: Not a Rest or Stress Cardiac Study.
- PET/CT has three ViP Modes for acquisition:
  - **Off**: No ViP selected.
  - **Record**: The system generates list mode data for the acquisition, which lets you reprocess the data as though you were acquiring a live study. For example, if you acquire a Static PET series with ViP mode, you can ViP Replay as a dynamic or gated series with the same quantitative accuracy as a live study.

**NOTE**

This mode is mandatory when using Derived Trigger Mode.

- **Replay**: The system generates a new raw data set with different parameters from the ViP Record list mode data.
26. Click the Start and End Locations and enter the PET scan range.
    - The system updates the End Location to the nearest PET bed.
    - **Rad Rx Off**: The CT series scan range must equal the PET scan range.
    - **Rad Rx On**: The CT scan range may equal or exceed the PET scan range.
  27. Click **Scan Direction** to toggle between **Toward Feet** and **Toward Head**.
    - The Start and End Locations update to reflect the Scan Direction selection. The patient orientation icon does not change.
    - **Toward Feet** directs the PET system to start at the head and scan toward the legs.
    - The Start and End Locations update to reflect the Scan Direction selection. The patient orientation icon does not change.

28. Click **No. Bed Positions** to change the PET Bed prescription.
  - The Images and End Location update to reflect the prescribed number of beds. If Rad Rx is Off, the CT scan range and number of images also update.
  - The scan range and overlap selections determine the maximum number of beds you can prescribe.
29. Click in the **Overlap** field to choose the amount of overlap between PET beds.
  - You can choose an odd or even number of images to overlap. The maximum number of available overlap slices cannot exceed one-half the number of single frame slices for the system.
  - If you select **Show Localizer** the number of beds and overlap display on the Localizer. The bed number followed by Q are displayed in the Localizer for Q.Static beds, if Q.Static scan type is selected.
30. Click **Pre Scan Delay** and enter a value in the **hh:mm:ss** format to insert a delay between pressing the **Start Scan** button and the actual start of scan.
31. Click the **Scan Time** parameter to enter the total PET series scan time.
  - If you select a **Static** PET scan, you can enter a unique scan time for each PET bed. Click **All Beds** to evenly divide the scan time among beds, and assign the same scan time to every bed. Click **Variable** to assign a unique time to each prescribed bed. In both cases, the total scan time in the **Scan Time** field updates to reflect any changes you made to the **Enter the Desired Scan Time per Bed Position** window. If you select ViP Record, you can click a box to record list mode data for the corresponding bed. Yellow box=ViP Record On; gray box=ViP Record Off.
  - If you select a **Dynamic** PET scan, you can select the number of phases, the number of frames per phase and the time per frame, as well as a pre-frame delay. The **Enter the Desired Scan Phase Information** window displays the time per frame and the time per phase, as well as the total scan time. The **Scan Time** field displays the total scan time for the PET scan, including any pre-frame delay time.
  - If you select a **Gated** PET scan, you can choose the time per bed position and the number of bins and the system updates the binning value.
  - If you select a **Q.Static** PET scan (option), you can click a box to acquire Q.Static data for the corresponding bed. Yellow box=Q.Static On; gray box=Q.Static Off. You can enter a unique scan time for each PET bed.
    - Click **All Beds** and enter time per bed to specify the scan time for each non-Q.Static PET bed and Q.Static bed time for each Q.Static bed.
    - Click **Variable** to assign a unique time for each prescribed bed.

In both cases, the total scan time in the **Scan Time** field updates to reflect any changes you made to the **Enter the Desired Scan Time per Bed Position** window.
  - Under **Q.Static Phase**, click the field on the right side of **Offset (%)** to enter the Q.Static phase offset, and **Width (%)** to enter the Q.Static phase width.

Q.Static uses data between phase offset (%) and (phase offset + phase width) (%) in each respiratory cycle with valid trigger for reconstruction. The phase parameters should be set so the data for reconstruction is distributed in the quiescent period of the respiratory curve. These two parameters can be adjusted per facility requirement. For example, reducing phase width can provide more motion reduction with a trade off on extended scan time, if equivalent photon counts need to be maintained.

- Under **Trigger Rejection**, you can enable or disable the trigger rejection for Q.Static beds. Yellow button=Enabled; gray button=Disabled.

When **Trigger Rejection** is enabled, you can specify the average breath rate and the deviation to reject the trigger.

Click the field on the right side of **Avg/min** to enter the average triggers per minute for trigger rejection.

Click the field on the right side of **% Dev** to enter the tolerance for trigger rejection. The system calculates the deviation based on %Dev \* Avg/min and adds and subtracts that value from the number in the **Avg/min** data field. For example: 60 triggers/min with a 30% deviation=an acceptable range of 42 to 78 triggers/min. Anything above 78 triggers, or below 42 triggers qualifies as a bad cycle.

#### NOTE

Trigger Rejection is not supported by the MotionFree option. Refer to [Chapter 13 Respiratory Gating](#) for more information about respiratory gating options.



**Figure 387 Q.Static (with external device) Scan Time**

Enter the Desired Scan Time per Bed Position

Time per Bed: 
 Q.Static Bed Time: 
 Total Scan Time:

Q.Static	Bed	Scan Time	Scan Range
<input type="checkbox"/>	1	<input type="text" value="00:02:00"/>	\$0.00 - 1246.40
<input type="checkbox"/>	2	<input type="text" value="00:04:00"/>	1179.20 - 1425.60
<input type="checkbox"/>	3	<input type="text" value="00:02:00"/>	1358.40 - 1604.80
<input type="checkbox"/>	4	<input type="text" value="00:02:00"/>	1537.60 - 1784.00
<input type="checkbox"/>	5	<input type="text" value="00:02:00"/>	1716.80 - 1963.20

Q.Static Phase

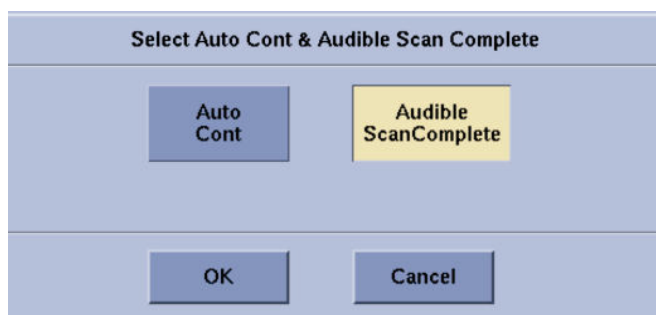
Offset (%): 
 Width (%):

Trigger Rejection

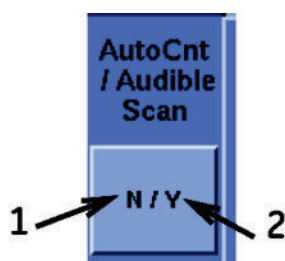
Avg/min: 
 Deviation (%):

32. Click the **Start on Count Rate** field to initiate the PET acquisition when the system detects the designated number of count-rate. (Ex: 100 in the field=100,000 counts per second)  
 During acquisition, press **Start Scan** to prompt the system to begin monitoring the activity level. When the activity level reaches the prescribed count rate, the system begins the PET data acquisition.
33. Click the **Stop on kcounts** field to terminate the PET acquisition when the system exceeds the designated number of total kilo-counts. (Ex: 1000 in the field=1,000,000 counts)
34. Click **AutoCnt/Audible Scan** to open the selector window.
  - Click **Audible ScanComplete** to play an audible notification through the Acquisition Control speaker during a live PET scan. The Audible ScanComplete function enables a sound when the PET scan successfully completes and a scan failure sound that plays when the PET scan fails to complete as prescribed.

- You can turn this function on or off at the series level by clicking the **AutoCnt/Audible Scan** button on the PET series acquisition window. Regardless of the on/off state, the system disables Audible ScanComplete during ViP Replay.

**Figure 388 Select Auto Cont & Audible Scan Complete Window**

35. Click the **Auto Cont** field to toggle between **Y** and **N**.
  - Auto Continue Y: Upon completion of the current PET scan, the system moves to the next PET series in the prescription.
  - Auto Continue N: The system pauses until you click **Confirm**.
36. Click **OK** to accept the currently displayed state of the buttons and close the **Select Auto Cont & Audible Scan Complete** window.  
Click **Cancel** to close the window and revert to the original button status.
37. The buttons in the AutoCnt/Audible Scan column display the status of the auto continue and audible scan completion buttons for the corresponding scan.
  - 1: Auto Continue status (Y = enabled; N = disabled)
  - 2: Audible Scan Completion status (Y = enabled; N = disabled)

**Figure 389 AutoCnt/Audible Scan Button Label**

38. Click the radioactive syringe to display the **Dose Parameters** tab.
  - Click **Dose** or a button in a row beneath it to open the **PET Tracer Information** window.
    - Click **Dose** to update the corresponding information in all prescribed PET scans, or a row button to change the information for the corresponding PET scan.

- Click **Inherit from Exam** to populate the data fields with information entered into the **PET Tracer Information** data fields from the **Patient Information** window during the actual exam.
  - Click the **MBq** button to change the tracer activity data fields to **MBq** and toggle the button label to **mCi**. Click the **mCi** button to change the tracer activity data fields to **mCi** and toggle the button label to **MBq**.
  - Click **Nuclide/Tracer** or a button in a row beneath it to open the Select the desired Radionuclide and Tracer window.
    - Click **Nuclide/Tracer** to update the corresponding information in all prescribed PET scans, or a row button to change the information for the corresponding scan.
    - Click/highlight a radionuclide in the left column to display the list of available tracers in the right column. Click the up/down arrows to scroll through the lists. The up/down arrows activate (turn black) when the corresponding list exceeds the visible space.
    - Click/highlight a tracer in the right column to select it.
    - Click **OK** to close the window and change the button label(s) to the selected radionuclide and display the selected tracer next to the button.
39. If Gated Study scan type is selected, click the picture of the heart and lungs to open the **Gating** tab.
- Click a **Binning Mode** button to open the **Select the Desired Binning Mode** window. Follow facility guideline to select the **Binning Type**. For respiratory, only [Percent] binning is available. For cardiac, the recommended: binning type is **Time**.
  - Click the field beneath **Avg Trig/min** to enter the average triggers per minute value, for use during data rejection.
 

During the acquisition the fields on the right side of the **Gating** tab display the cardiac and/or respiratory triggers, along with the current and average trigger rate. Wait for the patient to relax and the triggers to stabilize, then type the average value into the **Avg Trig/min** data field. The system averages ten triggers and updates the display every ten counts.
  - Click the field beneath **% Dev. Allowed** to enter the tolerance level for cycle rejection, or the allowed amount of deviation before rejection occurs.
 

The system calculates the percentage of deviation and adds and subtracts that value from the number in the **Avg Trig/min** data field. Example: 60 triggers/min with a 30 percent deviation=an acceptable range of 42 to 78 triggers/min. Anything above 78 triggers, or below 42 triggers qualifies as a bad cycle.
40. Click the stack of images to open **Prospective Reconstruction** tab.
- Click the field beneath **DFOV** to enter a new Display Field of View between 6.4 cm and 70 cm. The DFOV defaults to the SFOV of 70 cm.
  - Click the field beneath **R/L Center (mm)** and type a positive value to shift the DFOV to the right, or a negative value to shift the DFOV to the left.

- Click the field beneath **A/P Center (mm)** and type a positive value to shift the DFOV in the Anterior direction (up), or a negative value to shift the DFOV in the Posterior direction (down).
- Click a **Recon Type** button to open the **Select the Desired PET Recon Type** window. Refer to [Post-Processing](#) for more detailed descriptions of the reconstruction parameters.

**Figure 390 Select the Desired PET Recon Type Window**

**Select the desired PET Recon Type.**

**Recon Method**

VUE Point HD FORE-FBP

**Quantitation Method**

Q.Clear 350 SharpIR

**AI Method**

None LPDL MPDL HPDL

**Filter Type**

Enhanced Hanning Rectangle Shepp-Logan Cardiac 3D Off

Hanning Butterworth Order 4 {1 thru 10}

**Z-Axis Filter**

None Light Standard Heavy

**Filter Cutoff (mm)**

5.0

**Subsets**

1 2 4 8 12 22 Prior Next

**Iterations**

3

OK Cancel

- Select a **Reconstruction Method**. Select **VUE Point HD** for 3D reconstructions. Select **VUE Point FX** for 3D TOF reconstructions. Select **FORE-FBP** for Filter Back Projections reconstructions.
- Select a **Filter Type**. The **Reconstruction Method** selection determines the available **Filter Type** selections.
- Select a **Z-Axis Filter**. Select **VUE Point HD** or **VUE Point FX** to enable the **Z-Axis Filter** buttons. The Z-Axis Filters smooth between transaxial slices.
- The **Filter Cutoff (mm)** function changes with the chosen **Reconstruction Method**. When you choose **VUE Point HD** or **VUE Point FX** this field operates as a post filter or Gaussian filter.
- The **VUE Point HD** or **VUE Point FX** buttons activate the **Subsets** and **Iterations** fields. Follow the advice of the site physician to set these values.

- Select **SharpIR** to apply detector response modeling to VUE Point HD or VUE Point FX. When you select this function, you may want to choose additional iterations. Follow the advice of the site physician to set these values.
- Select the Matrix Size that provides the best resolution for the number of available counts. The larger the Matrix Size the longer it takes to reconstruct the image.

Choose a Matrix Size: 128 x 128, 192 x 192, 256 x 256, 384 x 384.

- Click a button below the **Recon Option** to open the **Select the Desired Attenuation Correction Method** window.

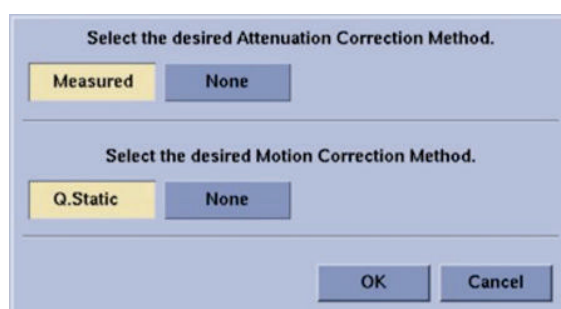
To select the desired Attenuation Correction Method:

- Click **Measured** to apply a measured attenuation correction and change the button label to **MAC**.
- Click **None** to select no attenuation and change the button label to **NAC**.

To select the desired Motion Correction Method:

- Click **Q.Static** (option) to enable Q.Static reconstruction (reconstruct with data from motion reduced period).
- Click **None** to disable Q.Static reconstruction (reconstruct with all data).

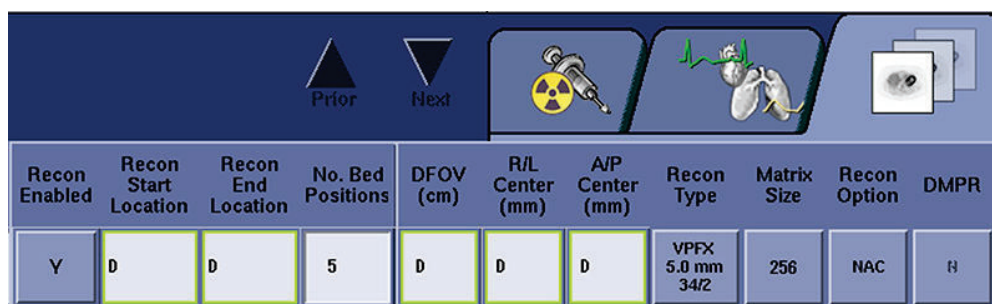
**Figure 391 Select the Desired Attenuation Correction Method Window**



- Click the buttons below the **DMPR** label to toggle the function on and off.  
Click **Y** to reconstruct and display the sagittal/coronal/transaxial images in the four viewports on the display monitor.

41. Click the **Show Recon 2** and **Show Recon 3** buttons to prescribe additional Prospective Reconstructions.

To automatically duplicate parameters from Recon 1, enter *D* or *d* in the desired field. When enabled, the field displays **D** and is outlined in green.

**Figure 392 Duplicate Recon 1 Parameters**


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
Y	D	D	5	D	D	D	VPFX 5.0 mm 34/2	256	NAC	R

This feature is supported for: **Recon Start Location**, **Recon End Location**, **DFOV (cm)**, **R/L Center (cm)** and **A/P Center (cm)** for Recons 2 and Recon 3.


To disable this feature, enter a valid parameter value.

- The **Reconstruction** tab expands to include additional selections to prospectively prescribe different Reconstruction Start and End Locations and Bed Numbers.
  - If the PET series contains multiple scans, you can select individual PET scans for prospective reconstruction in Recon 2 and Recon 3.
42. Select Additional Features. The system options determine the number and types of available features. Some buttons may only be available during scan.

**Figure 393 Additional PET Feature Buttons**

- The **Add Scan** button displays another PET scan with the same parameters as the group above it. You can change any parameter in the new group. **Add Scan** always adds the new PET scan to the bottom of the list.
- The **Insert Scan** button activates when the PET series contains two or more scans. Click/highlight a PET scan then click **Insert Scan** to duplicate the selected scan and display the new scan's parameters directly beneath it. **Insert Scan** always adds the new PET scan beneath the selected scan.
- The **Delete Selected Scan** button activates when the PET series contains two or more scans. Click/highlight a PET scan, then click **Delete Selected Scan** to remove the highlighted PET scan from the series.
- If more than one PET scan is present, a **Lock** icon is displayed. If the **Lock** icon is selected, essential scan parameters are automatically copied from the previous scan.

**Figure 394 Lock Icon**

Images	Scan Type	Start Location	End Location
1-345	Static Record	\$0.000	I956.320
 1-345	Static Replay	\$0.000	I956.320

43. Optional: Click **Repeat Series** at the bottom of the PET or CT window to duplicate the currently displayed window and create a new series with it.
44. Optional: Click the **Delete Series** button at the bottom of the PET or CT window to delete the displayed series from the exam.
45. Click **Accept** to close the protocol build windows and store the newly built protocol in the designated **User** tab location.  
You still can change the newly built protocol name.
46. Optional: Click **Set As Default** to permanently highlight the protocol, and display its name in the corresponding Default Protocol button, to the right of the anatomical selector.
47. Click **Done** to close the corresponding protocol list.
48. Click **Quit** to close the anatomical selector.
49. Click **Quit** to close the **AutoVoice Record/Protocol Management** window.

## 23.7 Build a Hybrid PET/CT Protocol from a CT Protocol

Follow this procedure to add a PET scan to an existing diagnostic CT protocol. This converts the existing Axial series into a Hybrid series.

1. Follow the steps in [Edit an Existing Protocol](#) to copy the starting protocol and rename it to a Hybrid protocol.
2. Click **Next Series** until the desired Axial series is displayed.
3. Click **Add PET**.
4. Click **PET** to switch to the PET window.



5. Adjust the PET scan parameters as desired.

Refer to [Build a New Hybrid PET/CT Protocol](#) for a brief functional description of standard PET/CT parameters.

6. Click **CT** to return to the CT window.

7. If the CT scan range does not fully cover the PET scan range, click **Add Group**.

Change the new group scan type and other parameters as desired. Adjust the Start and End Locations to extend the existing CT scan range to match or exceed the PET scan range in one direction. The new group or groups added to cover the PET scan range can be either diagnostic CT scan parameters or the site preferred CTAC scan parameters.

8. Repeat the previous step, if needed, to ensure that the diagnostic CT or CTAC scan range meets the PET scan range for CT attenuation correction for the other end of the scan range.
9. Click **Accept** to save the new protocol.

#### NOTE

When adding a PET scan to a reference CT, the PET scan parameters may not match your site's preferences. Check newly added PET scan parameters to ensure they match your site's parameters.

## 23.8 Build a Protocol Quick Steps

### 23.8.1 Edit an Existing Protocol

1. Click the **Protocol Management** icon.
2. Click the **Protocol Management** button to open the anatomical selector.
3. Click the **User** tab.
4. Click a region of interest on the body, or one of the Default Protocol buttons.
5. Click on the protocol description to highlight the border.
6. Follow facility guidelines to type a new description.
7. Click **Edit** to open the first available scan window in the protocol.
8. Modify the parameters, then click **Next Series** or **Create New Series**.
9. Once again, you have the option to modify or keep the displayed parameters.
10. Click the **PET** and **CT** buttons to toggle between windows.

or

Click **Next Series**, if available; click **Prior Series** to return to the previous series in the exam.

11. Click **Accept** to keep the changes and return to the protocol list.
12. You still have the option to change the protocol name, or set it as the default.
13. Click **Done** to save the protocol.

14. Click **Quit** to close the anatomical selector.
15. Click **Quit** to close the **AutoVoice Record/Protocol Management** window.

## 23.8.2 Build a Hybrid PET/CT Protocol

1. Click the **Protocol Management** icon.
2. Click the **Protocol Management** button.
3. If necessary, click the **User** tab.
4. Click a region of interest on the body, or one of the Default Protocol buttons.
5. Scroll or click the arrows to display a empty space in the protocol list.
6. Click on the empty space to highlight the border.
7. Click **New** to deposit a cursor into the data field.
8. Follow facility guidelines to name the protocol.
9. Press **Enter** to open the **Select New Series Type** window.
10. For best results: Click **Scout** to start the exam with a scout series.
11. Click **OK** to proceed to the scout series screen.
12. Set the Patient Orientation icon.
13. Click **Copy Pt.Orient.Pt.Position Anat.Ref** to display the current orientation on all subsequent PET and/or CT acquisition screens.
14. Select the anatomical reference point.
15. Type a **Series Description** into the data field.
16. Optional: Click **AutoStore** and/or **AutoTransfer**.
17. Set the Scout Parameters.
18. Click **Create New Series**.
19. Click **Hybrid**, then click **Create After**.
20. Set the CT scan, technical, reconstruction and filming parameters.
21. Click [Show Localizer] to display the scout image with the Graphic Rx.
22. Type a **Series Description** into the data field.
23. Click **PET** (and **CT**) to toggle between the two windows.
24. Type a **PET Scan Description** and **Series Description** into the data fields.
25. Select the PET Scan Type.
26. Set the PET Scan Parameters.
27. Set the PET Dose Parameters.
28. Gating Studies: Click the heart/lung tab and set the Gating parameters.
29. Click the stack of images tab and set the PET Prospective Recon Parameters.

30. Optional: Click the **Show Recon 2** and **Show Recon 3** buttons to prescribe additional Prospective Reconstructions.
31. Click **Accept** to close the protocol build screens.
32. Optional: Click **Set As Default**.
33. Click **Done** to close the protocol list.
34. Click **Quit** to close the anatomical selector.
35. Click **Quit** to close the **AutoVoice Record/Protocol Management** window.

### 23.8.3 Build a Hybrid PET/CT Protocol from a CT Protocol

1. Follow the steps in [Edit an Existing Protocol on page 622](#) to copy the starting protocol and rename it to a Hybrid protocol.
2. Click **Next Series** until the desired Axial series is displayed.
3. Click **Add PET**.
4. Click **PET** to switch to the PET window.
5. Adjust the PET scan parameters as desired.
6. Click **CT** to return to the CT window.
7. If the CT scan range does not fully cover the PET scan range, click **Add Group**.
8. Repeat the previous step, if needed, to ensure that the diagnostic CT or CTAC scan range meets the PET scan range for CT attenuation correction for the other end of the scan range.
9. Click **Accept** to save the new protocol.

### 23.8.4 Copy and Paste Protocols

1. Click the **Protocol Management** icon on the scan monitor to open an **AutoVoice Record/Protocol Management** window.
2. Click **Protocol Management** to access the anatomical selector.
3. If necessary, click the **User** (or **GE** or **Most Recent**) tab to access the protocol.
4. Click the anatomy of interest to display the corresponding list of protocols.
5. Click/highlight a protocol to select it.
6. Click **Copy** to select the protocol and close the protocol list.
7. Click the anatomy of interest to open the destination protocol list.
8. Click a line in the list to select the protocol destination.
9. Click **Paste** to deposit the information and display the Protocol Name.
10. Click/highlight the Protocol to change or modify the name.
11. Type the new name.
12. Click **Edit** to open the corresponding scan screens and display the protocol parameters.

13. Modify the parameters, as needed, then click **Accept** to return to the open destination protocol list.
14. Click **Done** to close the protocol list.
15. Click **Quit** to close the anatomical selector.
16. Click **Quit** to close the **AutoVoice Record/Protocol Management** window.

### 23.8.5 Delete a User Protocol

1. Click the **Protocol Management** icon on the scan monitor to open an **AutoVoice Record/Protocol Management** window.
2. Click **Protocol Management** to access the anatomical selector.
3. If necessary, click the **User** tab to access the corresponding protocols.
4. Click the anatomy of interest to display the corresponding list of protocols.
5. Click/highlight a protocol to select it.
6. Click **Delete** to open the **Delete Protocol Confirmation** window.
7. Click **OK** to delete the selected protocol.
8. Click **Done** to close the selected protocol list.
9. Click **Quit** to close the anatomical selector.
10. Click **Quit** to close the **AutoVoice Record/Protocol Management** window.

### 23.8.6 Select the Default Language for AutoVoice 1, 2 & 3

1. Click the **Protocol Management** icon on the scan monitor to open an **AutoVoice Record/Protocol Management** window.
2. Click **Auto Voice Record** to display the **AutoVoice Record** window.
3. Click the **Pre-recorded Message Language Selection** button (default: [English-Male]) to open the **AutoVoice Language Selection** window.
4. Click on a new primary language button to highlight/select it and close the window.
5. Click **Done** to close the **AutoVoice Record** window.
6. Click **Quit** to close the **AutoVoice Record/Protocol Management** window.

### 23.8.7 Record a Personalized AutoVoice

1. Click the **Protocol Management** icon on the scan monitor to open an **AutoVoice Record/Protocol Management** window.
2. Click **AutoVoice Record** to display the **AutoVoice Record** window.
3. Click a blank area and type a unique name for the message.
4. Click **Record** and start speaking.

5. Click **Stop** as soon as you stop speaking.
6. Optional: Click **Play** to listen to the recorded message.
7. Click **Pre-Message** to activate the **Record** and **Save Message** buttons.
8. Click **Record** and speak your message. (Optional: Click **Play** to hear the message.
9. Click **Save Message** to keep the recorded pre-scan message.
10. Click **Post- Message** to activate the **Record** and **Save Message** buttons.
11. Click **Record** and speak your message. Optional: Click **Play** to hear the message.
12. Click **Save Message** to save the original personalized recording, along with the pre-scan and post-scan messages.
13. Click **Done**.

If you failed to record a pre-scan or post-scan message, the system displays a pop-up that gives you the option to **Return to AutoVoice Record** or **Quit**. If you recorded all three messages, the system returns directly to the **AutoVoice Record/Protocol Management** window.

14. Click **Quit** to close the **AutoVoice Record/Protocol Management** window.

### 23.8.8 Delete a Personalized AutoVoice Message

1. Click the **Protocol Management** icon on the scan monitor to open an **AutoVoice Record/Protocol Management** window.
2. Click **Auto Voice Record** to display the **AutoVoice Record** window.
3. Click/highlight the title of the message you plan to delete.
4. Click **Delete Set**.
5. Click **Done** to close the **AutoVoice Record** window.
6. Click **Quit** to close the **AutoVoice Record/Protocol Management** window.

## 24 CT Use for PET Attenuation Correction

### 24.1 CT Use for PET Attenuation Correction Introduction

This chapter describes how the PET/CT system uses the CT series X-ray images to correct the attenuation of the 511 keV gamma rays imaged during the PET series.

This chapter contains the following content:

- X-Ray CT Measurements
- Attenuation Correction of PET Emission Scans
- CTAC Scan Series
- CT kVp Selection
- CT Contrast
- Overlapping CT Slices
- Q.AC (Option)

### 24.2 X-Ray CT Measurements

X-Ray Computed Tomography uses transmission measurements taken around the patient to reconstruct cross-sectional images in which each pixel represents the attenuation of the corresponding object. CT uses an expanded attenuation scale, referenced to the linear attenuation coefficients of water and air, to compute the value of a particular material represented in the following formula as :

$$CT[material] = 1000 * \frac{\{\mu[material] - \mu[water]\}}{\mu[water] - \mu[air]}$$

The density and atomic number of the material, as well as the effective energy of the X-ray beam, determine the linear attenuation value for the imaged material, .

According to this definition of CT numbers, water has a CT number of 0; and air has a CT number of -1000. This expanded scale gives sufficient range of CT numbers to differentiate body tissues such as muscle, fat, and organ tissues with similar attenuation coefficients.

### 24.3 Attenuation Correction of PET Emission Scans

During PET reconstruction, the software uses the selected CT series to calculate the attenuation of the PET emission data.<sup>1</sup>

In order to use the CT values for attenuation correction (AC), an attenuation map is constructed by converting the CT values into attenuation coefficients at the required energy of 511 keV for coincidence

imaging. Different conversions are used for soft tissue and denser material containing bone mineral. The soft tissue conversion is assumed to be independent of the kVp, but the bone conversion takes into account the variation of CT number of the bone with the CT scan kVp. The appropriate conversion is applied to each pixel using the following formulae.

Materials with a CT value less than 0 are assumed to have an energy dependence similar to water, and the attenuation values at the required energy keV are obtained as follows:

$$\mu[\text{mat}, \text{keV}] - \mu[\text{air}, \text{keV}] = \frac{\{\mu[\text{water}, \text{keV}] - \mu[\text{air}, \text{keV}]\} * \{\text{CTmat} + 1000\}}{1000}$$

Materials with CT numbers above 0 are treated as though they are a mixture of bone and water, and the attenuation values are converted from measurements at the X-ray effective energy, kVeff, to attenuation values at the required energy keV as follows:

$$\mu[\text{material}, \text{keV}] = \mu[\text{water}, \text{keV}] + \frac{\text{CT}[\text{kVp}] * \mu[\text{water}, \text{kV}_{\text{eff}}] * \{\mu[\text{bone}, \text{keV}] - \mu[\text{water}, \text{keV}]\}}{1000 * \{\mu[\text{bone}, \text{kV}_{\text{eff}}] - \mu[\text{water}, \text{kV}_{\text{eff}}]\}}$$

equals the CT number (Hounsfield Units) of the material measured at the tube high voltage setting kVp.

## 24.4 CTAC Scan Series

CT images are used in PET attenuation correction processing.<sup>2</sup> This manual uses the term, CTAC, to describe any CT image series used to correct PET attenuation. The scanner can use a low-dose low-resolution CT series acquired solely for CTAC attenuation correction, or it can generate the CTAC series from a user-defined CT scan for localization or diagnostic use when the Q.AC option is installed, as described in [Scan the Patient](#) and [Build a Protocol](#).

The remaining sections provide notes on changing CT technique factors in the CTAC scan and a description of the Q.AC option.

## 24.5 CT kVp Selection

The GEHC-defined CTAC protocol uses 140 kVp for adult whole body scans. The higher kVp provides a more penetrating radiation which produces lower noise image data at low mA through thick body sections such as adult shoulders and hips. For diagnostic purposes, lower kVp will provide more image contrast between bone and soft tissue, but higher mAs may be required to compensate for the image noise produced by the higher attenuation of the low kVp. The PET attenuation map created from the lower kVp scan is compensated for the change in HU of the bones.

## 24.6 CT Contrast

The normal CTAC scan does not specify contrast. Low concentrations of contrast media have a minor effect on the attenuation map.

High concentrations of high density radiographic contrast which elevate the CT numbers into dense bone regions could cause an increase of the apparent PET activity.<sup>3</sup> To prevent this effect, you can



select the contrast conversion scale when specifying the PET reconstruction parameters. This scale is automatically selected when the IV contrast button is set for the CT scans.

## 24.7 Overlapping CT Slices

The default CTAC series has one CT image corresponding to each PET slice location. If the CT scan has been optimized for diagnostic purposes, the CT slice spacing may not match the PET spacing. Such a CT series may be used as a CTAC scan as long as the axial range of the CT series covers the PET scan range.

If the selected CT series contains multiple scan groups or combinations of cine and axial scan series, the overlapping scans will be averaged to produce the average attenuation map.

## 24.8 Q.AC (Option)

The Q.AC option provides CTAC processing modifications designed to improve CTAC accuracy in regions of low CT signal. Q.AC may provide improvements in quantitation in very large patients and also offers the ability to utilize very low CT techniques when CT scans are used only for the CTAC (PET only), and not for CT diagnostic or localization purposes.

***There are specific GE PET/CT protocols which use ultra-low dose CT techniques (ULDAC) provided on the GE protocol tab. The CT parameters in these protocols have been optimized for use with the Q.AC filter option and should not be modified except for the scan range. These ULDAC protocols should not be used with other CT reconstruction filters.***

- When the Q.AC option is enabled, the Q.AC CT reconstruction filter will replace the PETAC CT reconstruction filter for PET attenuation correction. The Q.AC filter may improve PET accuracy and uniformity particularly in heavy attenuating regions of very large patients.
- The Q.AC option provides a whole body protocol (PT\_ET\_ULDAC) and Q.Static protocol (PT\_Q.Static\_ULDAC). The protocols are based off the default whole body protocol (PTCT\_ET); however it utilizes a very low technique helical CT scan which is meant for CTAC only. The CT helical scan has been designed for use with the Q.AC filter only and should not be used with other CT reconstruction filters. The CT helical scan is designed to supply an optimal tradeoff between AutomA settings, CT pitch, and detector configuration and should not be modified except for scan range.
- The Q.AC option provides a two-meter protocol (PT\_2m\_WB\_ULDAC). The protocol is based off the default two-meter protocol (PTCT\_2m\_WB); however, all CT groups utilize very low CT technique. The CT scans have been designed for use with the Q.AC filter only and should not be used with other CT reconstruction filters. The axial and helical CT scans are designed to supply an optimal tradeoff between AutomA settings, CT pitch, and detector configuration and should not be modified.
- The Q.AC option provides two Q Freeze protocols (PT\_Q.Freeze\_ULDAC) and (PT INTEG\_Q.Freeze). Both protocols utilize a very low technique CT cine scan which is meant for CTAC only. The CT cine scan has been designed for use with the Q.AC filter only and should not be used with other CT reconstruction filters. The CT cine scan is designed to supply an optimal tradeoff between AutomA settings, CT pitch, and detector configuration and should not be modified except for scan range. The helical scan is unchanged from the original Motion Match protocol.



THE CT AUTOMA NOISE INDEX UPPER LIMIT IS INCREASED TO 250 TO FACILITATE LOWER TECHNIQUE CTAC SCANS USED WITH THE NEW CTAC ONLY Q.AC PROTOCOLS. FOR CT DIAGNOSTIC SCANS NOISE INDEX VALUES SHOULD CONTINUE TO BE USED AS PER THE CT USER MANUAL AND CT TRM.

## 24.9 CT Use for PET Attenuation Correction

### References

- <sup>1</sup> C. Burger, G. Goerres, S. Schoenes et al; PET Attenuation Coefficients from CT Images: Experimental Evaluation of the Transformation of CT numbers into PET 511 keV Attenuation Coefficients Eur J Nuc Med 2002 Vol. 29 No. 7 pp. 922-927
- <sup>2</sup> T. Z. Wong, E.K. Paulson, R.C. Nelson, et al. Practical Approach to Diagnostic CT Combined with PET AJR 2007; 188:622–629
- <sup>3</sup> O. Mawlawi, J. Erasmus, R. Munden, T, Pan, et al. Quantifying the Effect of IV contrast Media on Integrated PET/CT: Clinical Evaluation AJR 2006 186: pp308-319

## 25 Troubleshooting

### 25.1 Troubleshooting Introduction

This chapter contains three procedures, FAQ, Quick Snap and IQ Snap, that capture system information for use by the field engineer or facility service personnel during system troubleshooting. If the PET/CT system experiences intermittent problems or image quality issues, your service representative may ask you to use the Quick Snap or IQ Snap tools to capture information to help them determine what problems may exist. The **Tool Chest** toolbar on the right monitor contains the **Quick Snap** and **IQ Snap** buttons.

**Figure 395 Tool Chest Toolbar**



## 25.2 Quick Snap

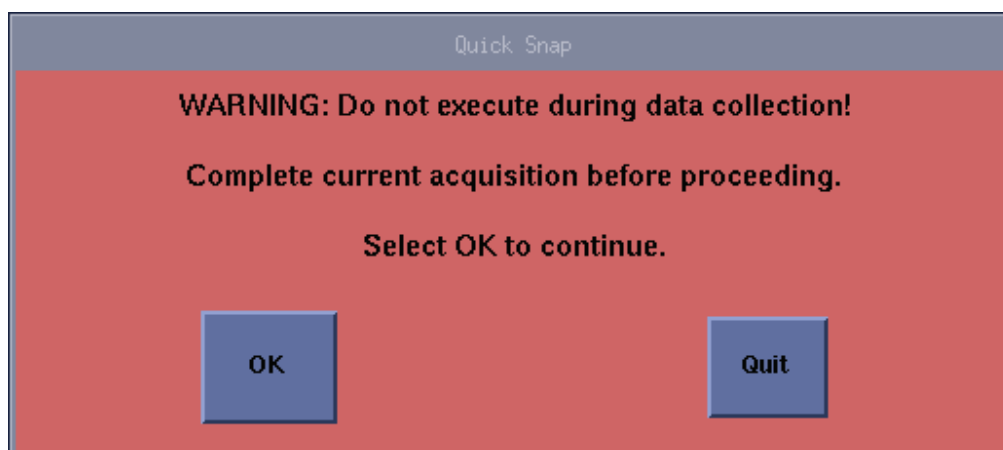
Quick Snap provides the ability to collect data for system troubleshooting. Both monitor toolbars contain the **Quick Snap** button. Follow your service representative's instructions to use this function.

1. From the monitor toolbar, click **Quick Snap** and an alert window opens.



To prevent loss of data, do not initiate a Quick Snap during a PET/CT acquisition. Wait until the current acquisition finishes before you click **OK**.

**Figure 396 Quick Snap Warning**



2. Click **OK**.

The message window closes when Quick Snap completes.

3. Record the time and date of the Quick Snap for the service representative.

## 25.3 IQ Snap

IQ Snap lets you collect data for system troubleshooting. The **Tool Chest** toolbar on the right monitor contains the **IQ Snap** button. IQ Snap can reserve up to 500 images in a single series. IQ Snap also reserves the corresponding CT scan data in the anonymous exam. Follow the instructions in the Anonymize the Patient Data chapter to create an anonymous series for IQ Snap.

1. When you discover images with artifacts during an acquisition, wait until the exam ends and all the images have reconstructed before attempting to use the IQ Snap function.
2. Create an anonymous series or a set of anonymous images from the series with the Image Quality (IQ) issues.

If you forget to anonymize the images, a pop up opens to remind you.

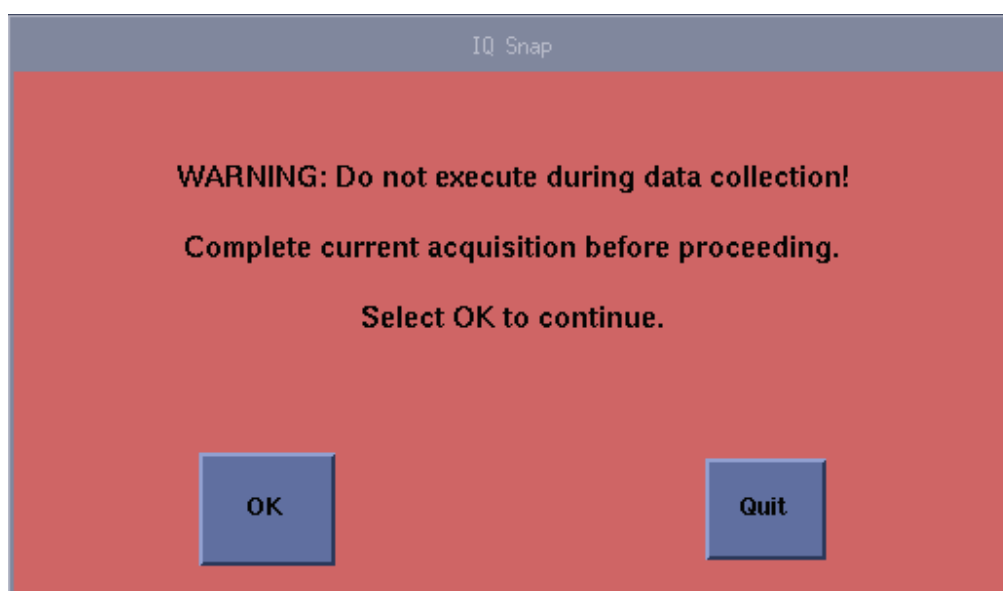
3. Select the anonymous exam from the browser.

If you select by exam or by series, IQ Snap only saves the first image in the list. Remember to highlight all the images in the anonymous exam or series to reserve them for later investigation by the service representative.

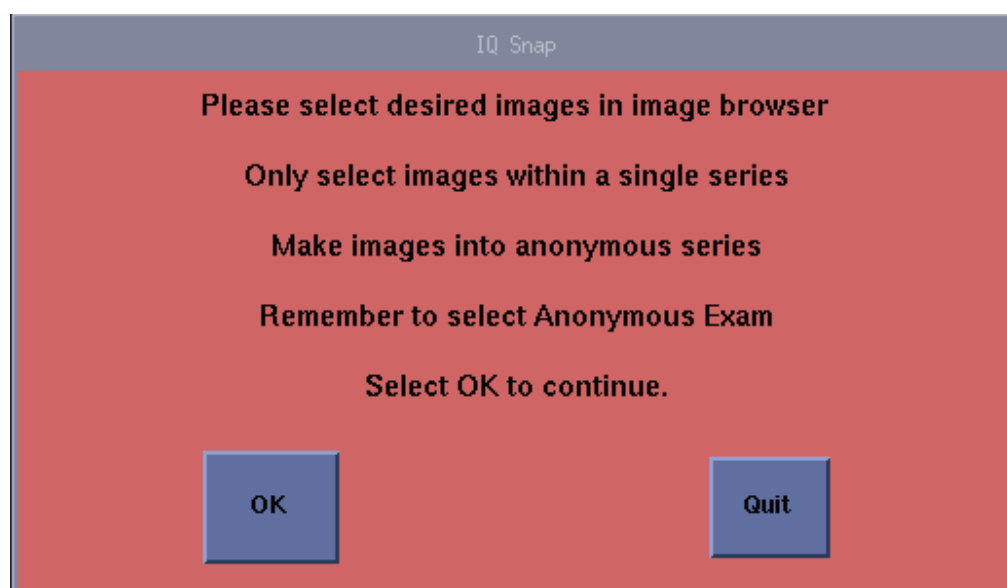
4. Select the anonymous images with quality issues from the Image Works Browser.

- Helical scans: Reserve the entire group, or scan group with the questionable image or images.
  - Axial scans: Reserve each axial rotation that contains the questionable image or images. For best results, reserve a few rotations on either side of the questionable image, to make sure the service representative has enough scan data.
  - PET scans: Reserve each PET image that contains the questionable image or images. For best results, reserve a few images on either side of the questionable image to make sure the service representative has enough data.
5. Click ***IQ Snap*** in the ***Tool Chest*** toolbar. The system displays a warning not to use IQ Snap during image acquisition or reconstruction.

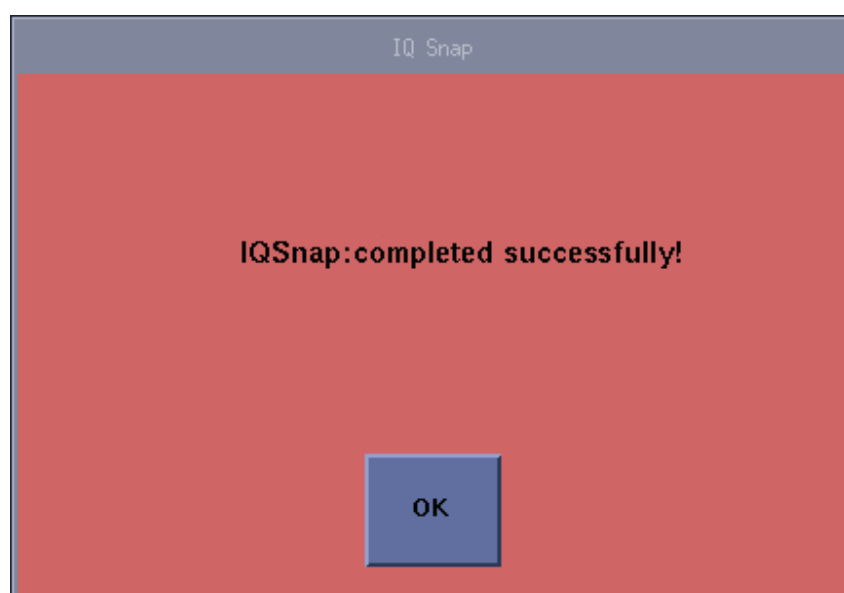
**Figure 397 IQ Snap Usage Warning**



6. Click ***OK***. A message window displays the IQ Snap instructions.

**Figure 398 IQ Snap Instructions**

7. Click **OK** to reserve the designated images.

**Figure 399 IQ Snap Success**

8. If the images selected included CT images, verify that IQ Snap reserved the correct images. Open the **CT Recon Management** window and click **Release Scan Data** to display the list of reserved CT scans. Make sure the IQ Snap images appear on the list.



## 25.4 Troubleshooting Quick Steps

### 25.4.1 Quick Snap

1. Wait until the acquisition ends.
2. Click **QuickSnap**.
3. Click **OK**.
4. Record the time and date for the service representative.

### 25.4.2 IQ Snap

1. Wait until the exam ends and the reconstruction queues empty.
2. Follow the procedure in the Anonymize the Patient Data chapter to anonymize the selected images.
3. Click **IQ Snap** to open the warning message.
4. Click **OK** to proceed to the next message.
5. Click **OK** to reserve the designated images.
6. If CT images are selected, open the **CT Recon Management** window and click **Release Scan Data**. Make sure the IQ Snap images appear on the list.

## 26 PET Image Corrections Phantom 3.13.1

7.6

### 26.1 PET Image Corrections Phantom Introduction

This chapter explains assembly, mounting alignment, care, cleaning and maintenance of your PET Image Corrections Phantom. You should complete the phantom alignment procedure described in [Align the Table Fixture](#) before proceeding to fill the phantom.

The PET Image Corrections Phantom, also known as a flood phantom, is used to perform the Well Counter Correction (WCC) discussed in [Calibration](#). Follow the instructions for WCC in [Calibration](#) for best results. This phantom is also used to test for image uniformity and activity concentration.

#### Kit Components:

When you receive your Image Corrections Phantom kit, inspect it to make sure the following parts arrived in good condition:

#### NOTE

To help ensure both accuracy and simplicity, your phantom kit includes a special phantom bracket that uses the same table mounting surface as the head holder for precise, repeatable positioning. Mount the phantom tank in this bracket.

1. Image Corrections Phantom tank
2. Drop-in bracket and table attachment
3. Delrin mounting posts
4. Various containers, attachment screws required for using and storing the kit

**Figure 400 Image Corrections Phantom**

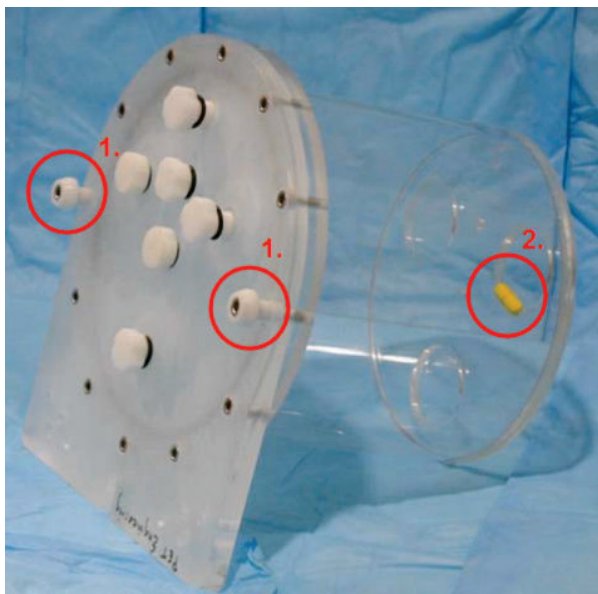


Table 98 Phantom Components

Number	Component
1	Delrin mounting posts
2	Magnetic stir rod

NOTE

Your phantom kit includes a special phantom bracket that uses the same table mounting surface as the head holder for precise, repeatable positioning. Mount the phantom tank in this bracket.

Figure 401 Phantom on drop-in bracket, mounted at the end of table

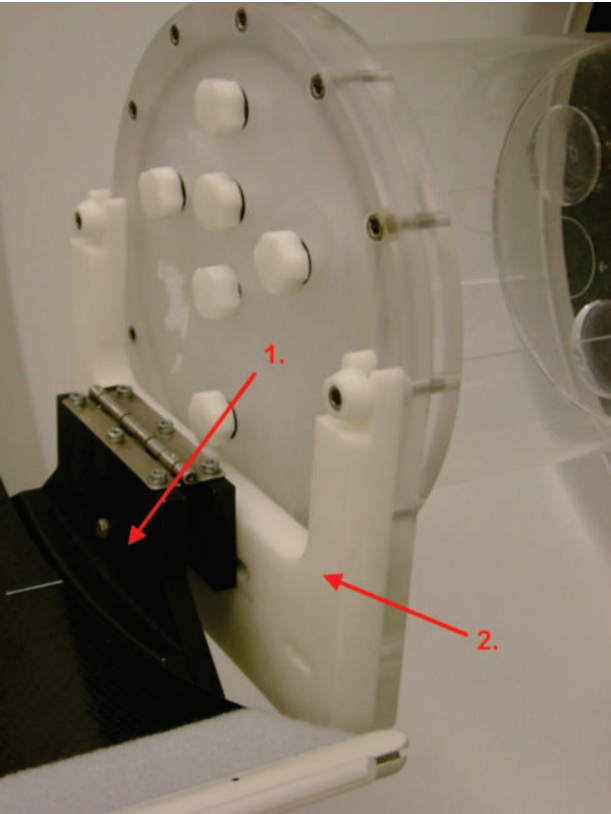


Table 99 Phantom Mounted Components

Number	Component
1	Table attachment
2	Drop-in bracket

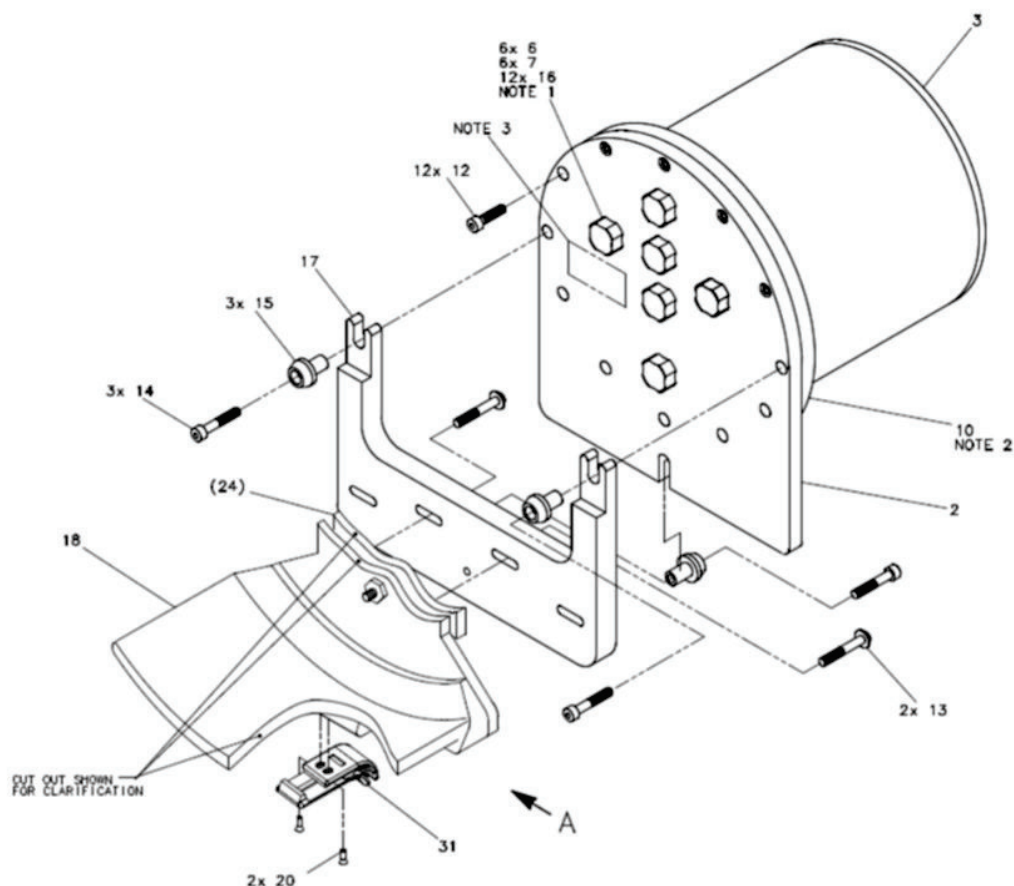
## 26.2 Seal the Phantom

Your phantom ships disassembled. You will have to assemble the configuration you need from the component pieces. Keep the shipping container on hand for safely storing the components.

The Image Corrections Phantom was designed for leak-free ease of use. The rubberized O-rings on the cover plate and filler plugs seal easily and more effectively than bare Lucite-to-Lucite joints. The O-rings require minimal pressure to create a leak-proof seal.

If the kit includes inserts for the phantom (large cylinders), do not place the inserts inside the phantom. Procedures described in this chapter do not require these inserts, and the phantom should be assembled free of any objects inside, except for a magnetic stir rod (optional). Refer to the [Image Corrections Phantom](#).

**Figure 402 Image Corrections Phantom - Assembly Drawing**



1. Inspect the O-rings for damage. Replace any O-rings that have nicks or splits.
2. Seat the large O-ring in its recessed groove of the flange.
3. Attach the two mounting posts at the 3 o'clock and 9 o'clock positions (#15).  
Insert the M6 x 35 screw (#14) through the Delrin mounting posts.

4. Fasten the flood phantom tank (#3) to the end plate (#2) with ten M6 x 16 screws (#12).
5. If available, place the magnetic stir rod in the tank.
6. Seal the fill ports with the thumb screws (#6 and #7) and O-rings.
7. Gently hand tighten the cover plate until you see the O-ring blacken as it presses against the cover plate.
  - If the O-ring appears uniformly black and of uniform thickness — about the width of the uncompressed O-ring, you have created a water tight seal.
  - Periodically apply a light coating of petroleum jelly or stopcock grease to the cover plate O-ring and filler plug O-rings.
  - Tighten the filler plugs by hand. Do not use pliers.

## 26.3 Position the Tank Phantom

Follow this procedure to position the flood phantom.

1. Use the three mushroom-shaped mounting posts to attach the phantom to the drop-in table bracket.  
 Two of these posts are attached to the tank portion of the phantom, at the 3 o'clock and 9 o'clock bolt-ring positions. Refer to [Phantom on Bracket](#). The third post is fastened to the bottom center of the table bracket.
2. To ensure a good fit, loosen the bolts and adjust their position before injecting activity into the phantom.
3. Center the phantom axially in the field of view.
  - The phantom mounting posts engage two slots on the table bracket and the table bracket mounting post engages a slot on the tank phantom.
  - Align the scribe mark on the phantom to the external alignment lasers.
4. Follow the instructions in the individual procedures to vertically position the phantom.
5. Use the center reference position location you attained during fixture alignment.

## 26.4 Align the Table Fixture

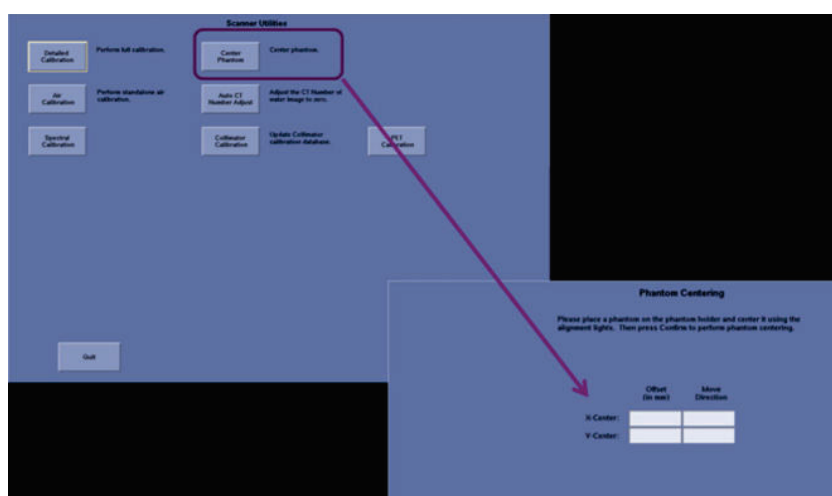
Use the drop-in table mounting bracket to consistently position the phantom. Make this adjustment at the time of installation, and any time you disassemble the bracket or change tables.

Although the table provides motor control in the Z (in and out) and Y (up and down) directions, it does not provide control in the X (side to side) direction or correct for vertical tilting (pitch) of the phantom. The drop-in table mounting bracket provides about 1 cm adjustment in the  $\pm X$  direction. It also features a mechanism to provide for phantom adjustment to correct for tilt in the  $\pm Y$  direction, to provide precise perpendicular adjustment with a non-tilting gantry, so you can align the phantom to the gantry isocenter.

Follow this procedure to center and align the phantom in the scan field of view.

1. Loosen the X-direction locking screws to allow X-direction adjustment, as well as the tilting screw locking nut.
2. Mount the phantom on the table bracket with drop-in plate on the end of the table and center the phantom using the laser lights and lines marked on the phantom. Refer to [Image Corrections Phantom](#).
3. Adjust the phantom tilt screw to raise or lower the far end of the phantom. Rotate the adjusting screw clockwise to raise the phantom.
4. On the **Scanner Utilities** window, click **Center Phantom** to open the **Phantom Centering** window.

**Figure 403 Phantom Centering Window**



5. Adjust the table height and slide the phantom in the X-direction by the offset values calculated by the center phantom utility tool.
6. Tighten the locking nut on the adjusting screw.

## 26.5 Fill the Flood Phantom

This section contains general instructions to fill the phantom.

For best results: Follow the instructions in the individual calibration procedure to prepare the phantom and align the table fixture. It is recommended to practice the following steps without radioactivity, in particular to avoid mistakes or having to repeat a step under the time pressure of decaying radioactive source (FDG).

1. Assemble the phantom and fill it with water. Regular tap water is generally clean enough for this purpose.
2. Tilt and rotate the phantom until the air bubbles move to the fill hole and leave the phantom. Leave enough air in the phantom to hold the activity injection.
3. Position the phantom on a magnetic stir plate so the air bubble moves over the fill hole.
4. Load the activity syringe.

5. Inject the activity into the phantom fill hole. If you use a funnel, make sure air has a path out of the phantom. One option is to remove a second filler plug.
6.
  - Fill the remaining air bubble with water.
  - Air bubbles smaller than 10 ml in volume will not disturb most tests.
7. Insert filler plugs. There should be room for the plugs. If there is no room, the water will not compress and you can break a seal or a seam in the phantom and create a leak.
8. Label the phantom as radioactive.
9. Follow facility guidelines when using the magnetic stir rod with the flood phantom. The bar will be contaminated and should be treated as radioactive material.

## 26.6 Clean and Care for the Phantom

Wait until the radioactivity decays away, then drain and clean the phantom to prevent residue build-up from the water supply and/or contamination by biological growths. Follow this procedure after each use:

1. Open any two fill ports to remove the water.
2. Collect the water in a separate container until it decays to zero. Follow facility guidelines to dispose the water.
3. Disassemble the phantom and clean the pieces with antibacterial detergent and lukewarm water. Gently scrub the pieces with a soft cloth or brush.
4. Place the components in a low humidity environment to dry.
5. Keep the large cover plate O-ring pliable by periodically rubbing it with a thin coat of petroleum jelly or stopcock grease. Periodically lubricate the table bracket mounting posts and fill port O-rings.
6. Store the clean, dry phantom components in the shipping container.

## 26.7 Additional Suggestions for the Phantom Kits

The calibration procedures require additional supplies not included in the phantom kit. You can usually find these items in the facility hot lab. Before you start acceptance testing during installation, make sure you have the following supplies:

- Optional: Magnetic stir plate and assorted stir bars
- Proper lab attire (coat, gloves, eye protection and dosimeter)
- Assorted sizes of syringes and needles
- Sharps disposal kit
- Absorbent materials for spills and clean ups
- Patient dose calibrator (to measure syringe activity)
- M5 hex wrench (Allen wrench) to disassemble the tank



- 1/4 inch flat blade screwdriver and 6 inch crescent wrench (adjustable spanner) to adjust the tank bracket.

The phantom kit components are made from durable materials, but it is still possible to damage them. Follow these suggestions to reduce wear and tear on the phantom components.

- Do not over tighten the screws.
- Use the correct sized (5 mm) hex wrench to fasten and loosen the bolts.
- Replace damaged or missing screws with metric hardware only.
- Never use hand tools to tighten the fill plugs, hand tighten only. If the fill plugs leak, check the O-rings for damage. Replace damaged O-rings and lubricate undamaged O-rings.

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## 27 Standalone PET/CT Console

### 27.1 Standalone PET/CT Console Introduction

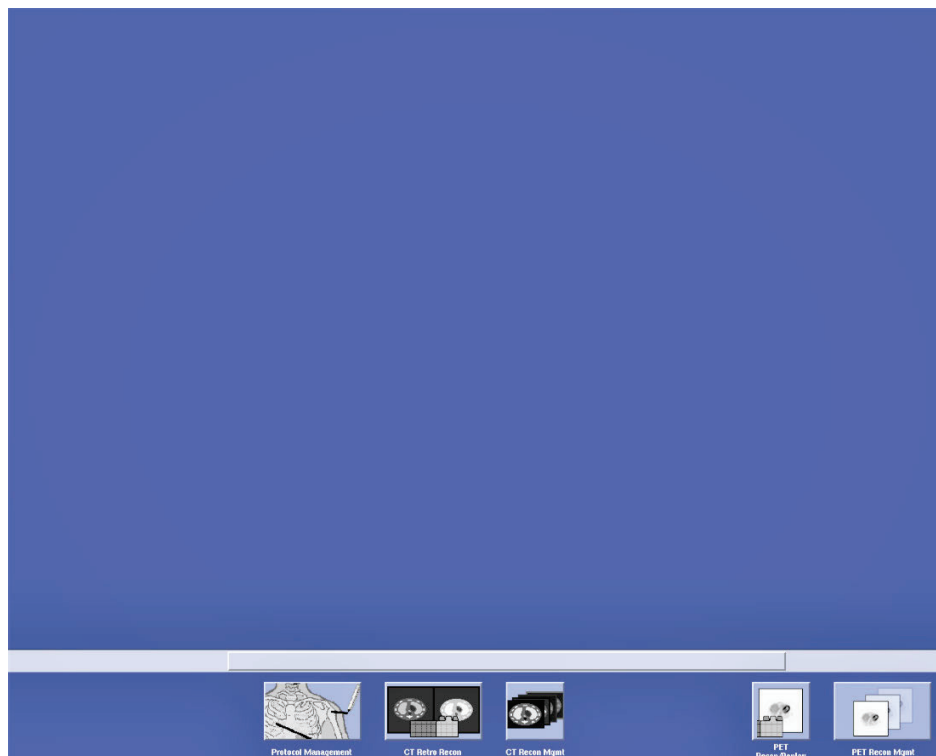
The Standalone Console **can** be used to:

- Review and post process images, using the same functions as the PET-CT scanner.
- Retrospectively replay acquired scans and reconstruct images.
- Export, archive, network Image data; create DVD/USB or hardcopies.
- Access the full suite of Data Management capabilities within the ImageWorks Browser.
- Manage Site Protocols: Use the Protocol Manager to create or modify protocols.
- Support research activities without disrupting the patient schedule.

The Standalone Console **cannot** be used to control a PET-CT scanner. Although the Standalone Console has the look and feel of a PET-CT Scanner Console, the scan-related functions are disabled or missing. You **cannot** use the Standalone Console to:

- Perform any activities that require a PET-CT scanner Scan Prescription such as PET or CT Scanning, Daily QA, etc.
- Manage scanner-related data, such as the Patient Schedule, System Calibrations or Daily Prep files.
- **NOTE**  
Edit Patient/Tracer Information can be applied only on data that is anonymized.

The following illustration shows the defeatured toolbar on the left hand of the Standalone Console:



This chapter contains the following sections:

- Applicable User Manual Topics for Standalone PET/CT Console
- Power Up, Reboot and Shutdown the Standalone Console
- Transfer information to the Standalone Console
- Protocol Management and Transfer

## 27.2 Applicable User Manual Topics for Standalone PET/CT Console

For operation instructions, refer to the previous chapters in this document. The following table contains the list of chapters and topics that relate directly to the Standalone Console, including all of the compatible options.

### NOTE

Your Standalone Console may not have every option.

Chapter 1	<a href="#">Safety Notice Conventions</a>
	<a href="#">Manual Conventions</a>
Chapter 2	<a href="#">Accuracy of Measurements</a>
	<a href="#">Operator Console Ergonomics</a>

Chapter 4	System Hardware: Operator Console
	PET/CT Application Scan Windows
	PET/CT Application Display Windows
	Tool Chest
	Image Works Browser
	Image Works Display Tools
	Data Apps List
	PET 3D Viewer Tools
	PET ACQC Tools
	PET Cardiac VUE Tools
	PET Dynamic VUE Tools
	PET Motion Match Tools
Chapter 5	Quantitation: Section 4 – Managing the Impact of Patient Respiratory Motion
	Quantitation: Section 5 - Image Reconstruction
	Quantitation: Section 6 - Post-Processing Applications
Chapter 11	Edit Patient and Tracer Information PET  <b>NOTE</b> Edit Patient/Tracer Information is supported only on anonymized data
Chapter 12	Anonymize the Patient Data (entire chapter)
Chapter 13	Use Advantage 4D to Segment a Cine CTAC
	Use Motion VUE to Display Binned CTAC Images
	Use Motion VUE Q.Freeze to Generate Motion Reduced Registered Images
	Use Motion Correct to Average the Cine CTAC
	Motion Match
Chapter 14	PET Cardiac ACQC
	Manually Initiate PET Cardiac ACQC Retro Recon
Chapter 15	PET Cardiac VUE
	Set User Preferences
	Remaining Option Menu

	<a href="#">View Menu</a>
	<a href="#">Help Menu</a>
	<a href="#">Display Images with Cardiac VUE</a>
Chapter 16	<a href="#">Dynamic VUE</a> (Entire Chapter)
Chapter 17	<a href="#">PET Volume Viewer</a> (Entire Chapter)
Chapter 18	<a href="#">Post-Processing</a> (Entire Chapter)
Chapter 19	<a href="#">Film</a> (Entire Chapter)
Chapter 20	<a href="#">Manage Data</a> (Entire Chapter)
Chapter 21	<a href="#">Build a Protocol</a> (Entire Chapter)
Chapter 22	<a href="#">CT Use for PET Attenuation Correction</a>
Chapter 23	<a href="#">Troubleshooting</a>

## 27.3 Power Up, Reboot and Shutdown the Standalone Console

- Power ON/OFF button is located on the front of the computer.
- Modified System Readiness Monitor (SRM) only monitors the PET Recon and Database, and the Replay portion of the Acquisition. The SRM still displays the inactive PET Calibrations and PET Gantry readiness indicators

Follow facility guidelines to determine when to shut down the Standalone Console. For best results, periodically reboot the Standalone Console. Chapter 6 of the user manual contains a detailed description of the PET-CT scanner power start and shutdown procedure, including information about the System Readiness Monitor (SRM).

### Power Up the Standalone Console

1. If an external USB device is connected to the operator console, disconnect the device.
2. Turn the operator console power ON.
3. HIPAA Configuration:
  - a. Follow facility guidelines to enter your Logon Name and Password.
  - b. Click **Logon**.
4. Wait for the SRM desktop icon to turn green.

### Reboot the Standalone Console

1. If an external USB device is connected to the operator console, disconnect the device.
2. Click **Shutdown**.
3. Select **Restart** and click **OK**.

4. HIPAA Configuration:
  - a. Follow facility guidelines to enter your Logon Name and Password.
  - b. Click **Logon**.

5. Wait for the SRM icon to turn green.

#### **Shutdown the Standalone Console**

1. Click **Shutdown**.
2. Select **Shutdown** and click **OK**.
3. Wait for the **System Halted** message to display.
4. Turn OFF console power.

## **27.4 Transfer information to the Standalone Console**

Follow the instructions in Chapter 20 of the user manual to transfer the Image and Scan data between the PET-CT scanner and the Standalone Console. Follow facility guidelines to set up a remote host on the network, so the Standalone console can receive data over the network from the PET-CT Scanner. Use the Scan Data Manager to transfer ViP LIST data, CT images, PET images and PET RAW data to a USB hard drive or network hard drive. You can also store and restore data with Interchange Media.

## **27.5 Protocol Management and Transfer to/from the Standalone Console**

Chapter 21 contains instructions to build, edit, view and transfer protocols. You may build protocols on the Standalone Console for use during Retrospective Replay and Image Reconstruction and transfer them to other scanners on your facility that have a supported software version.



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# Appendix A Glossary

## A.1 Glossary

**Table 100 Glossary**

Term	Definition
Activity Curve	Plot over time: The plot of the image statistics over time, from the same location of a dynamic scan. Plot over location: The plot of the image statistics over location, from a single time.
ANT	Anterior
AW	Advanced Workstation
Bin	The name for a frame in a gated scan or series.
CoH	Center of Heart
CTAC	CT Attenuation Correction
Decay Correction	The decay correction compensates for isotope decay over the course of the study. The system displays the actual activity detected at each time slice, but adjusts the image intensity to create a consistent look to all the images in the series. The decay corrected images all appear to be the same intensity, instead of gradually fading as the activity reached its half-life.
DICOM	Digital Imaging and Communications in Medicine: the preferred standard for the vendor-independent exchange of medical images and related information. The DICOM format defines data structures for medical imaging modalities and network services for clinical applications, such as image transmission, archive access, printing, and workflow support.
Dynamic	A series of images acquired over a period of time, from a single bed position. Use Dynamic mode to show tracer uptake.
ED	End Diastolic
EF	Ejection Fraction
ES	End Systolic
Frame	In a PET scan, a single frame contains all the slices acquired from a single bed position, during a single time or time phase.
Gated	A type of PET Scan that uses patient physiology to bin the acquisition data, to produce a series of PET images that, when viewed in cine mode represent different phases of the patient's cardiac or respiratory cycle.
HLA	Horizontal Long Axis - provides a 4 chamber view of the heart

Glossary continued	
Term	Definition
Image	An image represents a tomograph or projection from a specific location at a specific time, or time phase. An image may also consist of a screen capture or a projection view.
INF	Inferior
Info-Tip	A cursor function that interactively displays statistics for a point or region on an image, without the need to first deposit an ROI.
LAT	Lateral
LMB	Left Mouse Button
LVSD	Left Ventricle Surface Detection
Maximum phase error	This number represents images from all table locations within the target data set that fall farthest from the target phase. For example, if the target phase is 0% and the Maximum phase error is 4%, then the images farthest from the 0% target phase are at 96% and 4% of the respiratory cycle.
Minimum phase error	This number represents images from all table locations within the target data set that fall closest to the target phase. For example, if the target phase equals 0% and the Minimum phase error equals 1%, then the images closest to the 0% target phase are at 99% or 1% of the respiratory cycle.
MIP	Maximum Intensity Projection
MMB	Middle Mouse Button
NECR	Noise Equivalent Count Rate
Passes	Multiple scans over the same area of interest. Passes cover multiple beds (more than 1).
Phase	<p>When viewing the respiratory cycle as a waveform, a Phase equals the percentage or portion of the total respiratory cycle, where: 0% and 100% represent peak of inspiration; 50% denotes the center of expiration; 0% to 50% represents the patient exhaling, and 50% to 100% represents the patient inhaling.</p> <p>In reality, all images acquired within the CT acquisition are not going to fall into discreet categories of the patient's breathing cycle at every table location. In order to create an automatic data set, the system selects images at each table location that fall closest to the target phase and within the designated acceptable ranges.</p>
Phase Gating	A PET function that divides each scan of a heartbeat or breath cycle into different bins, with each bin corresponding to one phase in the motion of a heart or chest.
Phase Range	The phase range consists of the phases included into the data set, centered on either side of the target phase. For example, a Target phase of 0%, and a Phase Range of 95% - 5% means that images acquired between 95% - 5% of the respiratory cycle have been included in the 0% phase target image data set.

Glossary continued	
Term	Definition
Rebin	The process of combining bins in a gated study to cover a larger phase of the physiological cycle.
Reframe	The process of combining (adding) frames in a dynamic scan to make longer duration frames.
Rest	The physiological state where the blood flow represents the patient in a resting condition during acquisition. (opposite state to stress condition).
RMB	Right Mouse Button
ROI	Region Of Interest: A two-dimensional boundary or map encompassing the pixels of interest in an image.
SA	Short Axis
SEP	Septal
Slice	The unique location an image represents for a specific time or time phase. One PET frame contains 47 slices.
Series	A collection of related images, usually from the same scan, or as an output from some image analysis application. A series contains all the views for the same volume, such as SA, VLA, HLA views for a stress study.
Session	The period of time from the start of an Application with a single data set, until you Quit the application, or the load a new data set.
SST	Sum Start Time: The beginning of Dynamic summing
Static	A type of PET scan that does not consider the time phase during scan acquisition. A static PET series may consist of a single frame (47 images) or multiple frames.
Stress	The physiological state of stress that increases the patient blood flow, during an acquisition, compared to the patient's resting state.
Target Phase	Motion Match divides the breathing cycle from one peak inspiration to the next peak inspiration into segments from 0% to 100%. A target phase consists of a phase ("segment") selected for evaluation made up of a set of images that were acquired at the corresponding respiratory phase of the breathing cycle. For example, a 10% Target phase consists of a set of images that were acquired slightly after peak inspiration.
Tolerance	Sets the criteria for adding images to the target phase data set. For example, if the Tolerance is $\pm 5\%$ and the Target phase is 0%, then images that qualify for addition to the 0% target phase fall within 95% to 5% of the breathing cycle.
Viewport	A predefined image display area
VLA	Vertical Long Axis - provides a two-chamber view of the heart

## Glossary

Glossary continued	
Term	Definition
VOI	Volume Of Interest: A three-dimensional boundary or map depicting the voxels of interest from a set of contiguous trans-axial images.
WBDA	Whole-Body Dynamic Acquisition





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GE Medical Systems Israel, Functional Imaging  
Alexandra Lifshits  
Sr. Program Manager, Regulatory Affairs  
(GE Healthcare)  
4 Hayozma Street  
Tirat HaCarmel, WI 30200  
Israel

August 8<sup>th</sup>, 2024

Re: K241665

Trade/Device Name: Omni Legend  
Regulation Number: 21 CFR 892.1200  
Regulation Name: Emission Computed Tomography System  
Regulatory Class: Class II  
Product Code: KPS, JAK  
Dated: June 10, 2024  
Received: June 10, 2024

Dear Alexandra Lifshits:

We have reviewed your section 510(k) premarket notification of intent to market the device referenced above and have determined the device is substantially equivalent (for the indications for use stated in the enclosure) to legally marketed predicate devices marketed in interstate commerce prior to May 28, 1976, the enactment date of the Medical Device Amendments, or to devices that have been reclassified in accordance with the provisions of the Federal Food, Drug, and Cosmetic Act (the Act) that do not require approval of a premarket approval application (PMA). You may, therefore, market the device, subject to the general controls provisions of the Act. Although this letter refers to your product as a device, please be aware that some cleared products may instead be combination products. The 510(k) Premarket Notification Database available at <https://www.accessdata.fda.gov/scripts/cdrh/cfdocs/cfpmn/pmn.cfm> identifies combination product submissions. The general controls provisions of the Act include requirements for annual registration, listing of devices, good manufacturing practice, labeling, and prohibitions against misbranding and adulteration. Please note: CDRH does not evaluate information related to contract liability warranties. We remind you, however, that device labeling must be truthful and not misleading.

If your device is classified (see above) into either class II (Special Controls) or class III (PMA), it may be subject to additional controls. Existing major regulations affecting your device can be found in the Code of Federal Regulations, Title 21, Parts 800 to 898. In addition, FDA may publish further announcements concerning your device in the Federal Register.

Additional information about changes that may require a new premarket notification are provided in the FDA guidance documents entitled "Deciding When to Submit a 510(k) for a Change to an Existing Device" (<https://www.fda.gov/media/99812/download>) and "Deciding When to Submit a 510(k) for a Software Change to an Existing Device" (<https://www.fda.gov/media/99785/download>).



Your device is also subject to, among other requirements, the Quality System (QS) regulation (21 CFR Part 820), which includes, but is not limited to, 21 CFR 820.30, Design controls; 21 CFR 820.90, Nonconforming product; and 21 CFR 820.100, Corrective and preventive action. Please note that regardless of whether a change requires premarket review, the QS regulation requires device manufacturers to review and approve changes to device design and production (21 CFR 820.30 and 21 CFR 820.70) and document changes and approvals in the device master record (21 CFR 820.181).

Please be advised that FDA's issuance of a substantial equivalence determination does not mean that FDA has made a determination that your device complies with other requirements of the Act or any Federal statutes and regulations administered by other Federal agencies. You must comply with all the Act's requirements, including, but not limited to: registration and listing (21 CFR Part 807); labeling (21 CFR Part 801); medical device reporting (reporting of medical device-related adverse events) (21 CFR Part 803) for devices or postmarketing safety reporting (21 CFR Part 4, Subpart B) for combination products (see <https://www.fda.gov/combination-products/guidance-regulatory-information/postmarketing-safety-reporting-combination-products>); good manufacturing practice requirements as set forth in the quality systems (QS) regulation (21 CFR Part 820) for devices or current good manufacturing practices (21 CFR Part 4, Subpart A) for combination products; and, if applicable, the electronic product radiation control provisions (Sections 531-542 of the Act); 21 CFR Parts 1000-1050.

Also, please note the regulation entitled, "Misbranding by reference to premarket notification" (21 CFR 807.97). For questions regarding the reporting of adverse events under the MDR regulation (21 CFR Part 803), please go to <https://www.fda.gov/medical-devices/medical-device-safety/medical-device-reporting-mdr-how-report-medical-device-problems>.

For comprehensive regulatory information about medical devices and radiation-emitting products, including information about labeling regulations, please see Device Advice (<https://www.fda.gov/medical-devices/device-advice-comprehensive-regulatory-assistance>) and CDRH Learn (<https://www.fda.gov/training-and-continuing-education/cdrh-learn>). Additionally, you may contact the Division of Industry and Consumer Education (DICE) to ask a question about a specific regulatory topic. See the DICE website (<https://www.fda.gov/medical-devices/device-advice-comprehensive-regulatory-assistance/contact-us-division-industry-and-consumer-education-dice>) for more information or contact DICE by email ([DICE@fda.hhs.gov](mailto:DICE@fda.hhs.gov)) or phone (1-800-638-2041 or 301-796-7100).

Sincerely,

Ningzhi Li-S

for

Daniel Krainak, Ph.D.

Assistant Director

DHT8C: Division of Radiological

Imaging and Radiation Therapy Devices

OHT8: Office of Radiological Health

Office of Product Evaluation and Quality

Center for Devices and Radiological Health

Enclosure

## Indications for Use

Submission Number (if known)

k241665

Device Name

Omni Legend

Indications for Use (Describe)

The GE Omni Legend is a PET/CT system for producing attenuation corrected PET images. It is intended to be used by qualified health care professionals for imaging the distribution and localization of any positron-emitting radiopharmaceutical in a patient, for the assessment of metabolic (molecular) and physiologic function in patients, with a wide range of sizes and extent of disease, of all ages.

Omni Legend is intended to image the whole body, head, heart, brain, lung, breast, bone, the gastrointestinal and lymphatic systems, and other organs. The images produced by the system may be used by physicians to aid in radiotherapy treatment planning, therapy guidance and monitoring, and in interventional radiology procedures. The images may also be used for precise functional and anatomical mapping (localization, registration, and fusion).

When used with radiopharmaceuticals approved by the regulatory authority in the country of use, the raw and image data is an aid in; detection, localization, evaluation, diagnosis, staging, restaging, monitoring, and/or follow up, of abnormalities, lesions, tumors, inflammation, infection, organ function, disorders, and/or disease, such as, but not limited to, those in oncology, cardiology, and neurology.

Examples of which are:

Cardiology:

- Cardiovascular disease
- Myocardial perfusion
- Myocardial viability
- Cardiac inflammation
- Coronary artery disease

Neurology:

- Epilepsy
- Dementia, such as Alzheimer's disease, Lewy body dementia, Parkinson's disease with dementia, and frontotemporal dementia
- Movement disorders, such as Parkinson's and Huntington's disease
- Tumors
- Inflammation
- Cerebrovascular disease such as acute stroke, chronic and acute ischemia
- Traumatic Brain Injury (TBI)

Oncology/Cancer:

- Non-Small Cell Lung Cancer
- Small Cell Lung Cancer
- Breast Cancer
- Prostate Cancer
- Hodgkin disease
- Non-Hodgkin lymphoma
- Colorectal Cancer
- Melanoma

Omni Legend is also intended for stand-alone, diagnostic CT imaging in accordance with the stand-

alone CT system's cleared indications for use.

Type of Use (Select one or both, as applicable)



Prescription Use (Part 21 CFR 801 Subpart D)



Over-The-Counter Use (21 CFR 801 Subpart C)

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**CONTINUE ON A SEPARATE PAGE IF NEEDED.**

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**510(k) SUMMARY OF SAFETY AND EFFECTIVENESS**

This 510(k) summary of Safety and Effectiveness information is submitted in accordance with the requirement of 21 CFR Part 807.87(h):

**Date:** June 10, 2024

**Submitter:** GE Medical Systems Israel, Functional Imaging (GE Healthcare)  
4 Hayozma Street  
Tirat Hacarmel, 30200, Israel

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**Device Trade Name:** Omni Legend

**Device Classification** Class II

**Regulation number:** 21CFR 892.1200 and 21CFR 892.1750

**Product Code** KPS and JAK

Predicate Device Information	
Device Name	Omni Legend
Manufacturer	GE Medical Systems Israel, Functional Imaging
510(k) number	K221932
Regulation number	21CFR 892.1200 and 21CFR 892.1750
Product Code	KPS and JAK



Reference Device Information	
Device Name	Precision DL
Manufacturer	GE Medical Systems Israel, Functional Imaging
510(k) number	K223212
Regulation Number	21CFR 892.1200
Product Code	KPS

Reference Device Information	
Device Name	Discovery MI
Manufacturer	GE Medical System, L.L.C.
510(k) number	K161574
Regulation number	21CFR 892.1200 and 21CFR 892.1750
Product Code	KPS and JAK

### Marketed Devices

GE Healthcare's (GEHC) proposed **Omni Legend** device is a modification of the predicate Omni Legend device (K221932). The modification adds a new intermediate "4 Ring" 21 cm Axial Field of View (AFOV) system configuration to the predicate's "3 Ring" 16 cm and "6 Ring" 32 cm AFOV system configurations, as well as adds the "Enhanced AC" software option for the correction of image attenuation artifacts resulting from natural respiratory motion. The PET portion of the proposed **Omni Legend** uses the same design elements that are used in its predicate device. The software of the proposed **Omni Legend** is also developed from that of the predicate.

### Device Description

GE Healthcare's subject **Omni Legend** device, same as the unmodified predicate device, is a hybrid digital PET/CT diagnostic imaging system combining a GEHC Positron Emission Tomography (PET) System and a current production diagnostic GEHC Computed Tomography (CT) System. The proposed **Omni Legend** is a conventional, general-purpose PET/CT system using existing technological characteristics with identical Intended Use and Indications for Use as its predicate.

**Omni Legend** is made available with a "6 Ring", "4 Ring", and a "3 Ring" configuration of its PET detector that correspondently provide an AFOV of 32 cm, 21cm, 16 cm. **Omni Legend's** major components include PET gantry / detector, GEHC commercially available Revolution Maxima CT system (K192686), patient table, operator console / workspace, computing hardware, power distribution unit, system software, and image reconstruction software. The operator console and system software control

image acquisition and reconstruction, image display and post processing analysis, protocol and patient management, CT dose display, networking, filming, etc.

**Intended Use**

*The Omni Legend PET/CT system is intended for CT attenuation corrected, anatomically localized PET imaging of the distribution of positron-emitting radiopharmaceuticals. It is intended to image the whole body, head, heart, brain, lung, breast, bone, the gastrointestinal and lymphatic systems, and other organs. The system is also intended for stand-alone, diagnostic CT imaging.*

**Indications for Use**

*The GE Omni Legend is a PET/CT system for producing attenuation corrected PET images. It is intended to be used by qualified health care professionals for imaging the distribution and localization of any positron-emitting radiopharmaceutical in a patient, for the assessment of metabolic (molecular) and physiologic function in patients, with a wide range of sizes and extent of disease, of all ages.*

*Omni Legend is intended to image the whole body, head, heart, brain, lung, breast, bone, the gastrointestinal and lymphatic systems, and other organs. The images produced by the system may be used by physicians to aid in radiotherapy treatment planning, therapy guidance and monitoring, and in interventional radiology procedures. The images may also be used for precise functional and anatomical mapping (localization, registration, and fusion).*

*When used with radiopharmaceuticals approved by the regulatory authority in the country of use, the raw and image data is an aid in; detection, localization, evaluation, diagnosis, staging, restaging, monitoring, and/or follow up, of abnormalities, lesions, tumors, inflammation, infection, organ function, disorders, and/or disease, such as, but not limited to, those in oncology, cardiology, and neurology. Examples of which are:*

**Cardiology:**

- Cardiovascular disease
- Myocardial perfusion
- Myocardial viability
- Cardiac inflammation
- Coronary artery disease

**Neurology:**

- Epilepsy
- Dementia, such as Alzheimer's disease, Lewy body dementia, Parkinson's disease with dementia, and frontotemporal dementia
- Movement disorders, such as Parkinson's and Huntington's disease
- Tumors
- Inflammation
- Cerebrovascular disease such as acute stroke, chronic and acute ischemia
- Traumatic Brain Injury (TBI)

Oncology/Cancer:

- Non-Small Cell Lung Cancer
- Small Cell Lung Cancer
- Breast Cancer
- Prostate Cancer
- Hodgkin's disease
- Non-Hodgkin's lymphoma
- Colorectal Cancer
- Melanoma

*Omni Legend is also intended for stand-alone, diagnostic CT imaging in accordance with the stand-alone CT system's cleared indications for use.*

### Technological Characteristics

The proposed **Omni Legend** employs the same basic operating principles and fundamental technologies as the predicate Omni Legend device. The table below summarizes the substantive feature / technological differences between the predicate and proposed devices.

Specification / Attribute	<u>Predicate Device:</u> Omni Legend (K221932)	<u>Proposed Device:</u> Omni Legend	
PET Gantry	Multiple detector ring configurations (16, 32 cm axial FOV).70 cm bore.	Multiple detector ring configurations (16, <b>21</b> , 32 cm axial FOV).70 cm bore	4.5
Detector Unit	SiPM-based light sensor with ASIC	SiPM-based light sensor with ASIC	3.3
	BGO scintillator crystals	BGO scintillator crystals	
CT System	Revolution Maxima (K192686)	Revolution Maxima (K192686)	
Image Reconstruction / Processing	Iterative Image Reconstruction, including Precision DL (K223212)	Iterative Image Reconstruction, including Precision DL (K223212). <b>PET Digital Gating (DDG) also known as MotionFree (K180318)</b> <b>Enhanced AC option</b>	
Standards Conformance	IEC 60601-1 and applicable Collateral and Particular Standards.	IEC 60601-1 and applicable Collateral and Particular Standards.	

**Omni Legend's** technological characteristics do not create new questions of safety or effectiveness, and did not introduce any new risks/hazards, warnings, or limitations.

## Determination of Substantial Equivalence

### Summary of Non-Clinical, Design Control Testing

**Omni Legend** has successfully completed the design control testing per our quality system. No additional hazards were identified, and no unexpected test results were observed. **Omni Legend** was designed and is manufactured under the Quality System Regulations of 21CFR 820 and ISO 13485. GE believes that the extensive bench testing and the physician evaluations performed are sufficient for FDA's substantial equivalence determination.

**Omni Legend** has been independently tested and conforms with IEC 60601-1 and its applicable Collateral and Particular Standards including IEC 60601-1-2, 60601-1-3, 60601-2-44, as well as performance testing per NEMA NU 2-2018.

The following quality assurance measures were applied to the development of the system:

- Risk Analysis
- Required Reviews
- Design Reviews
- Testing on unit level (Module verification)
- Integration testing (System verification)
- Performance testing (Verification)
- Safety testing (Verification)
- Simulated use testing (Validation)

### Additional Non-Clinical Testing

Additional engineering bench testing was performed to support substantial equivalence, demonstrate performance, and substantiate the product claims. Where applicable the testing was conducted according to NEMA NU-2-2018. This included testing for:

- System Sensitivity
- Noise Equivalent Count Rate (NECR)
- Contrast Recovery and Contrast to Noise Ratio
- Spatial Resolution
- Quantitation
- Dose / Time Reduction (Acquisition and Image Quality)
- Design for Scalability

Testing of PET Digital Gating (K180318) verified use with **Omni Legend** and included substantiation of PET Digital Gating cleared performance claims. Testing of Enhanced AC included qualitative and quantitative evaluation of PET images corrected with Enhanced AC, including demonstration of improvement in lesion quantitation.

All testing and results did not raise new or different questions of safety and effectiveness than associated with predicate device. GE believes the proposed **Omni Legend** is of comparable type and substantially equivalent to our currently marketed system **Omni Legend** (K221932).



**Clinical Testing**

A clinical reader study using PET/CT exams acquired on Omni Legend was conducted. The exams constituted a clinically representative sample for evaluating the performance of **Omni Legend**'s Enhanced AC option. The results of the study support the determination of substantial equivalence. Each image was read by NM physicians who provided an assessment of overall diagnostic image quality using a Likert Scale as well as the ability of Enhanced AC to correct artifacts. All of the physicians attested that their assessments demonstrated acceptable diagnostic results.

**Substantial Equivalence Conclusion:**

The modifications associated with proposed **Omni Legend** do not create a new Intended Use or Indications for Use and represent equivalent technological characteristics, with no changes to the control mechanisms, operating principle, and energy type. GEHC's quality system's design verification, and risk management processes did not identify any new questions of safety or effectiveness, hazards, unexpected results, or adverse effects stemming from the changes to the predicate.

Based on development under GEHC's quality system, the successful system and software verification and validation testing, conformance to standards, the additional engineering bench testing, and the clinical reader study demonstrates that the proposed **Omni Legend** is substantially equivalent to, and hence as safe and as effective for its Intended Use, as the legally marketed predicate device.

# Parts List - Omni Legend PET/CT

Last Revised:	February 21, 2024
---------------	-------------------

Lists of available Field Replaceable Units (FRUs) / Spare Parts for the system are provided for the following categories:

- Console
- [Global Scan Control Box \(GSCB\)](#)
- [Gantry \(PET/CT\)](#)
- [Table 5](#)
- [PARC](#)
- [PDU](#)
- [Power Distribution Box](#)
- [Table](#)
- [Chiller](#)
- [Options](#)
- [Software](#)

## 1 Console

Table 1. Open Console

	<i>Last Revised:</i>
	Description
	Ethernet Cable for PROP Subnet, CAT5E, 3.4m
	Ethernet Cable for PROP PDD, CAT5E, 3.8m
	Ethernet Cable for ECB, CAT5E, 3.0m
	Ethernet Cable for Accessory Panel, CAT5E, 2.5m
	Ethernet Cable for Accessory Panel "RESP"
	Ethernet Cable for Accessory Panel "CARDIAC"
	LABEL, Read Docs, Edition 3, English
	Product Locator Card Form for Rating Plates, Printed by Duplitech
	WEEE Label with Bin Only
	Large Flat Washer, ISO7093, M8, Steel 140HV, Zinc Plated, RoHS Fastener
	Dongle Mini DP Male to DP Female DP1.2a
	Velcro Tape, Length, 830

2 - Wide, White, ADH Back, Velcro Loop, 25 YD
3.5m USB Extension Cable for Keyboard
Power Cable, Scan Monitor to Open Console J1, IEC C14 to C13 Connectors
C13 to C14 Interconnect Cord Straight, 3.05M
Host Grounding Wire, 8AWG, 500mm
Key Cap on TIO Front Cover
Loctite 222, 10CC Bottle, 12 Month Shelf Life From Date of Shipment from the Manufacturer
Outlet AC Box Assembly
Circuit Breaker-ABB-S201-C20
Hubbell Flanged Inlet HBL2315
Cable Harness from Power Supply to GSCB
Curved Spring Lock Washer, DIN 128A, M3, Class 430HV Steel, Zinc Plated RoHS Fastner
Cables for Power Switch for Small AC Box
Omron Power Switch
Label, Protective Earth Ground IEC Standard Graphics Symbol
Open Console Wheel
MIL-S8TB Switch HUB
Data Acquisition System Interface Processor Board, 2x2.5Gb, PCIe PWA
Fiber Optic Transceiver SFP 4Gb Multimode, RoHS-Compliant
Female Jackscrew, #4-40 Thread, 12.7mm Overall Length, RoHS Compliant Plating, 7.92mm Bottom, Single Jackscrew Only, RoHS Compliant
Host Computer, HP Z8G4 for CT TaiX
Power Cable, Display Monitor to Open Console J2, IEC C14 to C13 Connectors
C13 to C14 Interconnect Cord Straight, 3.05M
3.5m USB Extension Cable for Mouse
2 - Wide X, 25 YD, White Velcro Hooks
Power Cable, Hub, Open Chassis
Flat Washer, ISO7089, M6, Steel 200HV, Zinc Plated, RoHS Fastener
DP to DVI Cable with CORE, 3 Meter
Power Cable, Host, Open Chassis
USB 2 Button Scroll Mouse
Ethernet Cable, CAT6 24AWG Solid Conductor Foil Braid CM 1m, ETH3 to Hub-2
Ethernet Cable, CAT6 24AWG Solid Conductor Foil Braid CM 1m
GE Logo, Domed Polycarbonate
19 Inch Data and Image Frozen Display, EIZO FlexScan S1934-Black

5.4

5.3



# Volume Viewer

GE Healthcare's premium 3D Advanced Visualization and Image Processing platform brings you powerful capabilities to help you visualize and interpret your multimodality imaging data with confidence and ease.



Imaging modalities provide a wealth of diagnostic information, but also present a challenge to your Radiology workflow as image volumes continue to increase while your time for reading and reporting decreases.

**Volume Viewer** provides you with a rich 3D image processing toolset aimed at creating and displaying the views you need with little user input and streamlining interpretation and reporting by providing the visualization tools you need with minimum clicks.

With an intuitive, modern user interface, Volume Viewer helps a wide diversity of users to learn and master the expanding portfolio of sophisticated tools and applications that it provides. This customizable user interface maximizes the real estate allocated for displaying images and provides access to the users' favorite tools directly from the image viewport. In addition, a customizable toolbar provides one click access to commonly used tools to facilitate a productive review.

## Overview

**Volume Viewer** provides excellent 3D visualization and processing capabilities for reading and comparing CT, MR, 3D X-ray, PET, PET/MR and PET/CT datasets. Volume Viewer also features a broad portfolio of high-performance analysis tools, automating routine tasks and helping to make 3D image processing a stress-free component of your routine workflow.

**Volume Viewer** is available on VolumeShare 7, a multi-modality advanced visualization workflow solution that helps to enhance diagnostic precision and productivity.

## Volume Viewer options\*

- Volume Illumination
- Q.Freeze 2
- Autolaunch / Pre-processing

## Compatible Products\*\*

- 3D Suite
- Integrated Registration
- Bone VCAR
- GSI Viewer

\* Volume Viewer option requiring license key

\*\* Separate medical device requiring specific license key – refer to dedicated product datasheet



Visit us:

<https://www.gehealthcare.com/products/advanced-visualization/all-applications/volume-viewer>



## General Features

- Unified **user interface**, with one click access to your favorite tools and more space for displaying images.
- **Customizable protocol-driven workflows** designed to help enhance your clinical review productivity for a wide range of care areas, with 3D and 4D real time interaction.
- **“Smart layout”** protocol, which adapts the screen layout to the type of loaded exams.
- **High resolution, real-time rendering modes:** MIP/Min IP/Average; standard volume rendering and enhanced volume rendering with **Volume Illumination\*** on the fly; Navigator view for endoluminal fly-through; lumen and curved views.
- **Compare mode** for reviewing multiple exams and modalities, simplified with **Dynamic Load**, to load and register new series into the current review session, with **Integrated Registration\*\***
- Rich set of **2D/3D ROI** tools, including **AutoContour** for 3D semi-automatic contouring of structures of interest (CT, MR, PET), and **ROI color coded** for tissue classification based on voxel values.
- **Advanced tools**, to take advantage of full 3D capabilities: **AutoSelect**, for easy point-and-click segmentation; One or two clicks **Quick Vessel Trace** to analyze all vessels, in curved reformat, lumen, or MPR view; Advanced 3D processing tools.
- **Summary Table** extends reporting capabilities, while collecting measurements as they are deposited on the images.

## Additional modality solutions

- **Bone VCAR\*\*** combines spine labelling on the fly for all CT review and a dedicated layout to improve spine review.
- **Dual energy images** supported within dedicated review protocols.
- **GSI Viewer\*\*** provides dedicated capabilities for Gemstone Spectral Imaging (GSI) visualization.
- **MR review** support: Recognition of PSD name, and specific MR parameters at image loading, which simplifies protocol customization.
- Dedicated review workflows for **PET/CT** and **PET/MR** images, including **PET SUV measurements**.
- **Q.Freeze 2\*** combines the quantitative benefits of **4D PET gated** imaging into an image that provides both frozen patient motion and reduced image noise.
- **Reformat XA** provides a dedicated review with MPR 3D and endoluminal navigation for 3D X-ray angiography (also known as Cone-Beam CT).

## Platform features

- “Smart Compression” technology for fast and responsive client performance on AW Server.
- Fast automated **Pre-processing\***

## System Requirements

- Refer to AW Applications platform compatibility document
- Recommended monitor resolution is up to dual 2MP (1600 x 1200) or a single 3MP (1536 x 2048)

## Intended use / Indications for use

Volume Viewer is a medical diagnostic software that allows the processing, review, analysis and communication of 3D reconstructed images and their relationship to originally acquired images from CT, MR, X-Ray Angiography and PET Scanning devices. The combination of acquired images, reconstructed images, annotations, and measurements performed by the clinician are intended to provide to the referring physician clinically relevant information for diagnosis, and surgery and treatment planning.

## Regulatory Compliance

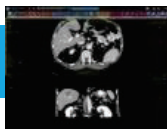
This product complies with the Regulation (EU) 2017/45 of the European Parliament and the Council of medical device (MDR)

**Rx Only**

This product, its features, options, and compatible products may not be available in some other countries or regions. Please contact your sales associate.



## Volume Viewer



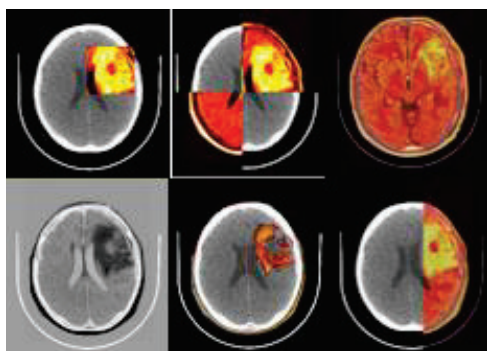
### General Features

#### Unified User Interface

- The user interface provides one click access to favorite tools and more space for clinical images.
- The page layout is organized to facilitate navigation through the review steps. Guided protocols walk the unfamiliar user through a clear workflow of creating and manipulating volumetric data, helping to reduce the learning curve by providing a consistent workflow.
- The customizable toolbar can be docked at the top, bottom, left, or right, by a simple drag & drop. This preferred location is saved for future use for each user.
- An extensive set of advanced tools are grouped into categories on the toolbar to facilitate quick retrieval when needed.
- Each category and tool are easily configurable by a simple drag & drop in the Toolbar so that they are only one click away for your future reviews
- To reduce long mouse trips, up to 6 favorite tools can be accessible from each image via a right mouse menu.
- Customization of the toolbar and tool behaviors with a user's preferences is provided in a single intuitive Preferences menu.
- Keyboard shortcuts and quick access tools for on-viewport controls

The following mouse modes are available to help you manipulate the images:

- Interactive VR adjustment lets you adjust VR opacity interactively with the mouse as Window Level/Window Width
- Direct Paging (continuous or contiguous)
- Free hand rotation on 3D and oblique views
- Percentage fusion, to easily change the transparency of objects on fused images. There are several fusion modes available for your use.
- Mag glass displays zoomed-up imagery around the cursor.



### Protocol management and loading

- Customizable protocol-driven workflows for a wide range of clinical applications, including support for multiple review steps. You are guided through the review steps by a Navigation bar at the top of the User Interface.
- Review protocols created by user with Volume Viewer can be saved as favorite protocols and accessed easily in routine.
- Progressive Load enhances image loading performance. This feature has two modes:  
Images are loaded in sequential mode (e.g., Reformat)  
Images are loaded in interlaced mode (e.g., 3D/VR)
- In either case, image review can begin as soon as the first image is displayed.
- Navigation through series and exams can be performed without exiting the patient list.



### Smart layout

- Volume Viewer General Review protocol presents an adaptive layout for single and multi-modality PACS-like reading of data. This protocol distributes and displays all loaded series of a single exam in an intelligent layout to maximize use of available monitor space. With multiple exams, the protocol automatically detects and distributes "like" series for optimal comparison.

### Advanced visualization capabilities

Volume Viewer offers various capabilities to display advanced rendering modes:

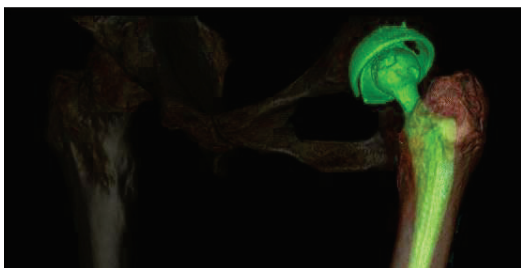
- 3D Volume Rendering / Volume Illumination\* images
- MPR views with different slice thickness. The following rendering modes are available for all Thick Slab: MIP, Min IP, Volume Rendering, Average.
- Navigator views which display interactive endoluminal views exportable as movies.
- Curvilinear reformatting allowing display of curved, lumen and cross section views for various structures (vessels, spine, etc.).



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- Merge multiple volume rendered models into a single view.



## Multiple Volume Rendering and Volume Illumination\* objects

- Volume Viewer allows you to merge up to 8 Volume Rendered models from the same series into a single 3D view.
- You can adjust independently the threshold, colors, and transparency of each Volume Rendering or **Volume Illumination\***



Volume Rendering

Volume Illumination

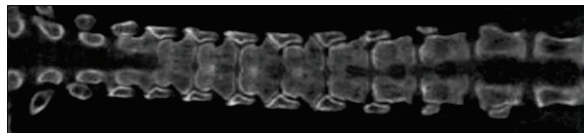
## Predefined cut planes

- Volume Viewer lets the user define cut planes to isolate specific structures in the VR model, in 16 configurations, including Left / Right / Inferior / Superior / Anterior / Posterior / Front.
- You can then display the voxels values on each plane.



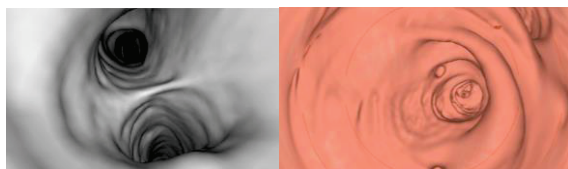
## Lumen view

- Lumen View provides an unfolded 3D view around a user defined centerline. The lumen view can be interactively adjusted (rotation around the centerline, width, field of view).



## Auto-center fly through with smart cursor

- In fly-through studies (airways, colon, angiography) navigation along the centerline of the structure of interest can be recorded step by step and can be exported as a movie.
- In addition to the regular 180° or less Navigator view, Volume Viewer enables a Fish-Eye View with any wide camera angle value from 180° to 360°. This provides a view of structures both in front of and behind the users' virtual location on the same image.



## 3D and 4D capabilities

- Volume Viewer allows 3D cursor synchronization in any orientation on the fly.
- Real time reformat in oblique planes is available for your exams, as well as simple and double oblique interactive modes.
- Quick access to cross reference display gives you the ability to display the current slice location or all slices, or other planes.
- Real time interaction in 4D mode, by using Cine tool on all planes and 3D views for CT, MR, and PET multiphase data.

## Compare mode

- With Volume Viewer several volumes can be loaded either from the same exam or from different exams. This is useful for exam comparison (Compare Mode) or for Multiphase examinations (of the liver for example). The Compare Mode is also available for PET/CT examinations and takes advantage of a dual screen configuration.
- Multi-phase CT and MR data are listed as separate phases in the Series Selection screen, allowing selection of all phases or a subset of phase data for review. The Series Selection Panel displays the multi-phase data split into arterial and portal phases, for example.
- Dynamic Load, compatible with both Volume Viewer and Fusion protocols, lets you drag & drop 3D volumes from CT,



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MR, PET, and 3D XA modalities into a desired viewport. With **Integrated Registration\*\***, Dynamic Load allows new volumes to be registered and loaded on the fly. Save State series can be restored as a separate session. For dual monitor configurations, a Save State series can be displayed on the right monitor together with a current session on the left monitor. For single monitor configurations, a user may simply switch between the two sessions.

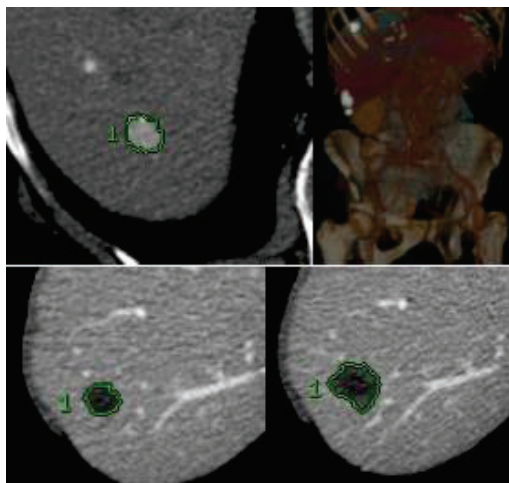
- The zoom and pan functions are propagated to all images displayed in the same orientation.

## 2D/3D ROI for quantitative measurements

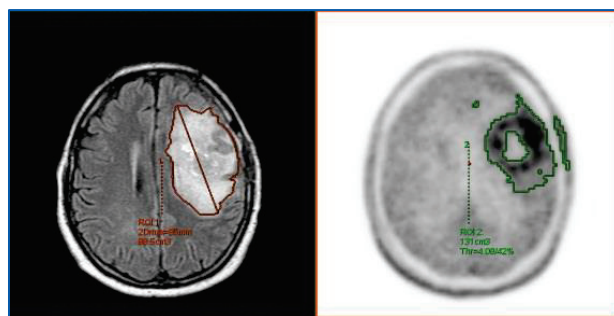
- Volume Viewer contains a set of basic 2D/3D tools: distance, angle, report cursor, arrow tool, annotation, free hand ROI tool, that can be placed on fused images as well.
- Easy deposition and labelling of measurements.
- All 3D ROIs can be customized, and color coded to display statistics computed on different intensity range and help assessing tissue classification based on voxel values.
- All measurements are considered bookmarks and can be accessed by navigating through the list of measurements.

## AutoContour tool

- AutoContour provides consistent tools for 3D contouring ROI, with the same workflow used for CT, MR, and PET images.
- For CT and MR images, the contouring tool will suggest contour boundaries after defining 1 point or a diameter on a structure of interest, which can be edited prior to validation.



- For PET images, the contouring tool has been adapted for standard SUV calculations.



## Advanced 3D tools

### Segmentation tools

- AutoSelect segmentation tool helps adding or removing any continuous structures of interest by simple point and click.
- You can also access advanced segmentation tools such as Scalpel, Threshold, Dilate, Erode, Subtraction, Intersection, Addition, Filter Floaters.

### Quick Vessel Trace (CT and MR images)

- You can perform vessel analysis with one or two points clicks from any CT or MR Angiography images.
- Quick Vessel Trace automatically extracts the vessel after user clicks and launches vessel tracking for fast review in curved reformat, cross-sectional, best L-section, lumen, and MRP view.
- Tracking can be extended proximally or distally for a full view of the vessel.

## Summary table

- The Summary Table collects measurements and organizes them according to finding and exam date.
- The Summary Table allows interactive navigation through findings in the image viewports and can be docked or expanded.
- The Summary Table can be copied into the client clipboard and then pasted in email, reports, office software etc. (on AW Server only)

Summary Table			
Demo_OncoQuant_CTCTCT3TPS			
	Sep 11 2007	Oct 17 2007	Dec 27 2007
1 - Finding 1	CT 3 ROI 1 2Dmax : 9 mm Short Axis : 9 mm Vol : 608 mm3	CT 2 ROI 2 2Dmax : 15 mm (+67%) Short Axis : 12 mm (+33%) Vol : 1.58 cm3 (+160%)	CT 1 ROI 3 2Dmax : 17 mm (+89%) Short Axis : 12 mm (+33%) Vol : 1.91 cm3 (+214%)
2 - Finding 2	CT 3 ROI 4 2Dmax : 13 mm Short Axis : 11 mm Vol : 848 mm3	CT 5 ROI 5 2Dmax : 21 mm (+62%) Short Axis : 19 mm (+73%) Vol : 4.98 cm3 (+487%)	CT 1 ROI 6 2Dmax : 23 mm (+77%) Short Axis : 17 mm (+55%) Vol : 4.25 cm3 (+401%)
Comments			



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## Export capabilities

- Volume Viewer contains multiple standard options for exporting the results of a review session:
- Save images to the database, as new DICOM series.
- Save the significant images as Key Image Note objects in the database. Key Image Notes and End Review allow you to flag images of interest as Key Image Notes (IHE profile) and push them to the archiving system when you exit the application.
- Save State object are used to save the work in a new series containing all the post processing data (3D Model, displays, measurements, annotations, etc), for future review.
- Save STL, OBJ, VRML or 3MF file from 3D Volume Rendering / **Volume Illumination\*** viewport for 3D printing purposes through **3D Suite\*\***.

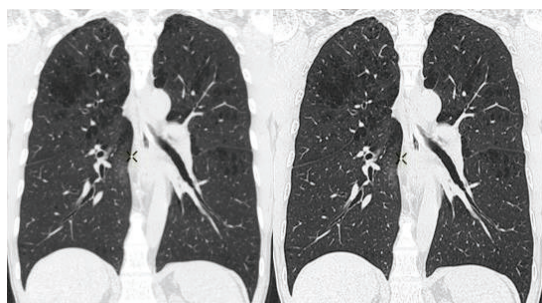
Additional export tools are available to create specific sequences of images to be exported:

- The Batch tool allows creating a sequence of reformatted images or a sequence of rotating 3D views.
- The Movie tool creates a comprehensive movie including different rotations, zooms, and pan of the image, which can be exported as DICOM series or mpeg file.
- Quick Export: Exports in a single click a full batch of contiguous images at the displayed thickness for 2D images, or a batch of rotations of a 3D View.
- Cardiac Review and Export: Processing and reviewing cardiac exams for CT, MR and PET with manual oblique reformatted protocols can be exported into a multi-phase Cine movie that allows the referring physician to review the exam in a dynamic mode.
- Capture and send images from the viewport to your computer clipboard on the fly (Copy/Paste on AW Server only).

## Additional modality solutions

### CT image quality

- CT filters to enhance or smooth CT images to help improve image quality on the fly.
- The lung filter helps enhance contours of images reconstructed in standard mode for excellent visualization of lung structures



Standard recon w/o filter

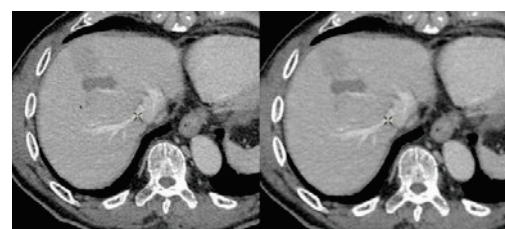
Standard recon with Lung filter

- A smoothing filter reduces noise while maintaining high image contrast



No filter

Smooth 3D+ filter



No filter

Smooth filter

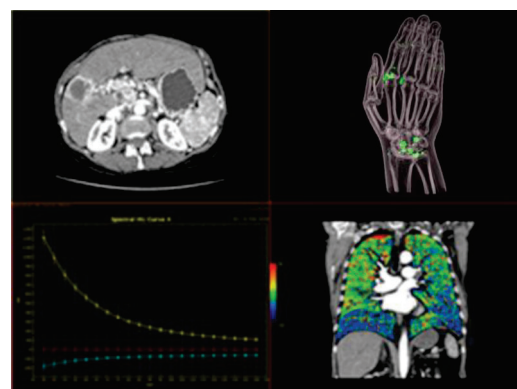
### CT Dual energy protocols

- Three protocols are available to enable review of dual energy images acquired on compatible GE Healthcare scanners and enhancing pixels with specific ratio: DE Calcium ( $HU_{80}/HU_{140} \geq 1.25$ ), DE Uric Acid ( $HU_{80}/HU_{140} \leq 1.25$ ) and DE Custom (custom threshold on HULow/HUHigh)

### GSI Viewer\*\*

GSI Viewer is the primary method of viewing and manipulating spectral images. It allows for:

- Review of monochromatic energy images at user selectable energy levels.
- Detailed analysis using material decomposed images (such as water-iodine, water calcium, liver fat, etc.) and complementary information using the Effective-Z images.
- Creation of virtual unenhanced (VUE) images.
- Gout protocol with automated workflow.



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## Bone VCAR\*\*

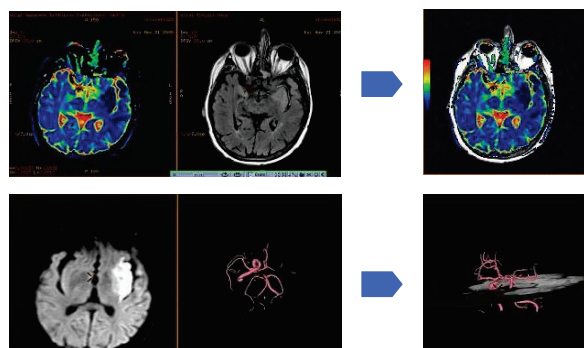
- Bone VCAR is available in Volume Viewer toolbar and can be launched on the fly
- Vertebrae are automatically recognized and labelled (deep learning algorithm)
- A dedicated tool provides a specific layout of the spine including curved views



## Review of MR studies

Volume Viewer offers support for review of MR studies, through dedicated protocols.

- The MR-specific parameters (PSD name, image weighting, scan plane, etc.) are recognized at loading and are used to customize the layout display.
- Anatomy-based protocols for standard review (e.g. spine, brain stroke...), with dedicated and guided review steps, to help review standard MR exams.
- Dedicated MR Cardiac Viewer for single and multiple Cine Review. Enables comparison between cardiac series such as Time Course and Myocardial Delayed Enhancement (MDE) images.
- Support of MR Multi Echo, Multiphase, Diffusion series.
- Support of parametric series (e.g., ADC, MTT, and other parametric maps) created in READY View, allowing direct functional measurements.



- 2D and 3D ROI propagation to other phases / series / exams allowing you to easily correlate information from multiple sources.
- In combination with **Integrated Registration\*\***, enables direct access to MR image registration (inter/intra exam), image fusion and Whole Body MR Review protocols
- Ability to automatically bind several MR axial series corresponding to sequential axial locations into a single series. This is useful for consolidating multi-stage acquisitions for displaying Whole Body MR scanning.

## SUV measurements on PET images

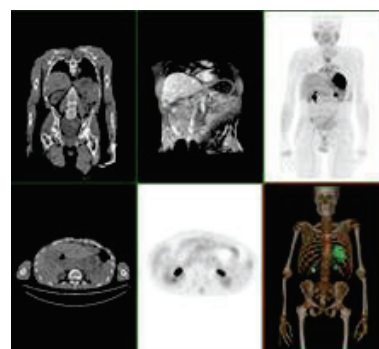
- Volume Viewer supports Standardized Uptake Values (SUV) for image display and measurements. Several SUV scales are available like SUVbw, SUV lbm, SUVbsa, as well as SUV Peak.
- Window/level presets may be user-defined for PET images based on SUV values.
- The SUV values are available in all the basic 2D/3D ROI tools of Volume Viewer and in the AutoContour tool.

## PET IQ improvements

- Enhanced 3D visualization algorithm to fully support Q.Clear PET images.
- **Q.Freeze 2\*** provides a respiratory motion-corrected Gated PET volume, statistically similar to conventional static PET with significantly reduced or eliminated blurring effects due to patient respiration. It provides also a corrected Gated PET series where counts are summed back to each respiratory phase.

## PET/CT and PET/MR dedicated protocols

- Volume Viewer contains a list of predefined protocols allowing the review of PET/CT and PET/MR data. The screen layouts contain fused views between the morphological and functional images, as well as 3DMIP rendering of PET images.
- Factory protocols are customizable for your own review.
- PET 4D protocol allows users to load and display gated and dynamic PET series, as well as summing or reframing these series.



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## Platform features

### Smart compression

- The Smart Compression technology automatically displays images with full fidelity when the image is still, then uses the selected compression level for increased interaction speed during user interaction. This allows for diagnostic reads on full fidelity static images with responsive dynamic display even at low bandwidth. On-image visual indicators notify the user when compression is in effect.

### Pre-processing\* features

- **Preprocessing\*** is a Volume Viewer option that automatically performs routine processing tasks and saves the results, so they are ready for you.
- When new exams are transferred to the database, Volume Viewer recognizes user-defined keywords in the Series Description and launches the appropriate pre-processing. The results are stored in a Save State object with the original study so you can load it when you are ready for review.
- **Preprocessing\*** is compatible with the following purchasable medical devices as separate products: AutoBone™ Xpress, CardIQ Xpress Reveal, CardIQ Xpress Function, CardIQ Xpress Process, Advanced CTC Pro 3D EC, Colon VCAR (*not available for sales in the US*), and CT Perfusion 4D and FastStroke

### AutoLaunch\* features on AW workstation

- **AutoLaunch\*** is a Volume Viewer feature that automatically preloads exams, so they are ready for your review.
- When you are processing a study and a new exam is transferred to the AW Workstation, this feature automatically launches the new exam with an appropriate Volume Viewer protocol in the background. When you are ready, one click in the **AutoLaunch\*** window instantly brings up the exam in the Volume Viewer application, eliminating waiting time and extra steps to load the exam into computer memory for processing.
- **AutoLaunch\*** is compatible with CT, MR and PET single volume protocols of Volume Viewer.
- When combined with optional applications (see “Pre-processing” section), this feature gives access to data already preprocessed, that you can review by just clicking on **AutoLaunch\*** window.

## Summary of Operation

Volumetric models are loaded by selecting the exam or series. The user can select a protocol category from an anatomical selector or go directly to a Review Layout. In either case, images are loaded progressively in the background; this gives control to the user in just a few seconds after selecting the images. Selecting a Review Layout launches a volumetric display protocol with predefined layout preferences. Review Layouts may be customized and combined to suit the user's workflow. Selecting a protocol category unlocks a variety of visual protocols that include the layout, threshold, rendering mode and filming formats. Some of these protocols direct the user through the process providing capabilities to interactively view and manipulate the model, increasing productivity and consistency for all modalities.



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MOLECULAR IMAGING AND NUCLEAR MEDICINE

# Diagnostic Solutions



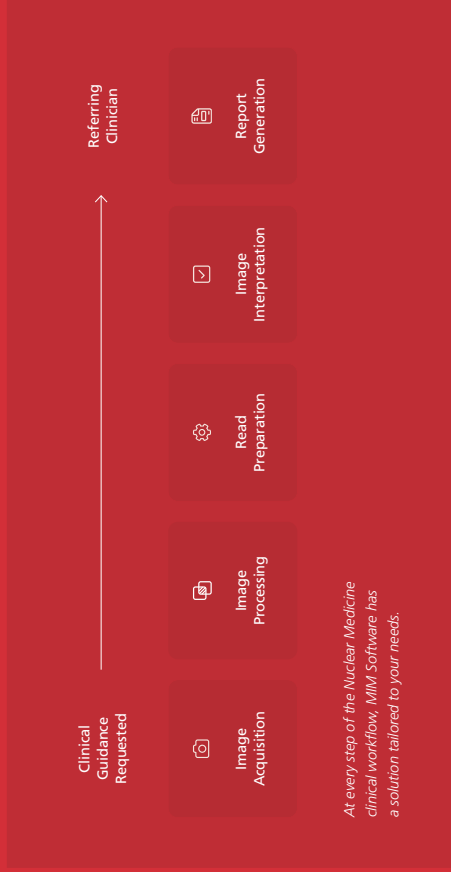


# Define Efficiency and Improve Patient Care

## Why MIM™?

MIM Software, a GE Healthcare Company, provides indispensable solutions that organize and improve department workflows for centers with diverse software and equipment. Through constant innovation, MIM Software continues to develop technologies that exceed the expectations of clinicians and hospital administration.

### THE NUCLEAR MEDICINE DIAGNOSTIC WORKFLOW



## Standardize the Nuclear Medicine Workflow

### A Central Solution

MIM Software offers a comprehensive suite of applications that support Radiology and Nuclear Medicine's important role in the patient care pathway. MIM Software products emphasize the importance of clinical efficiency, quantitation, and collaboration, helping to drive data empowered decisions that provide physicians with the necessary information needed to generate confident clinical guidance and inform effective treatments.



#### Image Acquisition

Standardize the imaging department from the start with a single, vendor-neutral reconstruction solution—**SPECTRA Recon™**, available in **MIM Encore™**—and help physicians gain new insights and capture new reimbursement opportunities with **SPECTRA Quant™**.



#### Image Interpretation

New radiotracer technology requires specialized viewing techniques that PACS systems won't provide. Comprehensive and efficient, MIM Encore provides physicians with an intuitive interface to tackle the busiest workloads with ease. Flexible **MIM Workflows™** keep you prepared for the next generation of radiotracer technology.



#### Image Processing

Give technologists a modern software solution that can handle the full imaging workload and take on new imaging protocols without paying for an expensive hardware or software upgrade.



#### Report Generation

Overcome the shortcomings of SUVmax with new diagnostic tools to provide referrers with better insights. Capture the latest, relevant therapy response information in data-rich reports, and send it to PACS for better communication with referrers.



#### Read Preparation

Fetch prior imaging, prepare cases to be read, and suspend work in a presentation state automatically with **MIM Assistant™**.



#### Remote Solutions

Read at home or on the road. Whether you're catching up on a busy caseload, conducting research, or maintaining productivity when unforeseen events occur, MIM's **flexible deployment options** allow for unprecedented image access—anytime, anywhere.



IMAGE ACQUISITION

## SPECT/CT Reconstruction and Quantitation

Reconstruct Virtually Any Image from Any Manufacturer

**SPECTRA Recon**, featured in **MIM Encore**, offers a vendor-neutral SPECT reconstruction method, including iterative reconstruction, attenuation correction, energy window-based scatter correction and resolution recovery for **virtually any camera manufacturer**.

Go Quantitative to Capture Therapy Response

**SPECTRA Quant** enables the conversion of counts to activity (Bq/ml and SUV) through a vendor-neutral SPECT reconstruction method, including iterative reconstruction, attenuation correction, energy window-based scatter correction, and resolution recovery.

Preserve Department Resources for the Most Impactful Clinical Tasks

Increase image throughput and reduce patient dose with **half-time, half-dose imaging**, available in SPECTRA Recon, featured in MIM Encore.

## Intelligent Image Automated Processing

Reduce Errors and Improve Consistency

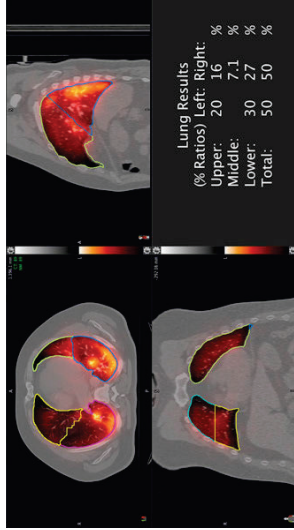
**MIM Workflows**, available in MIM Encore, are engineered to provide clinicians with consistent and reproducible results for all clinical Nuclear Medicine and Molecular Imaging studies.

Support for the Imaging Protocols of Today and Tomorrow

MIM Encore includes a **comprehensive catalog** of processing workflows for every type of Nuclear Medicine exam, and easy access to **software upgrades** mean you'll never fall behind due to an expensive software or hardware upgrade.

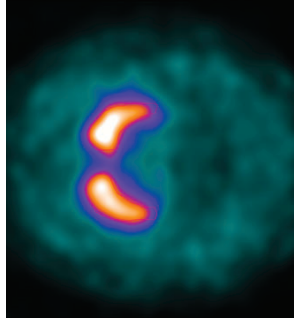
Support for image post-processing available in MIM Encore includes, but is not limited to:

- Renal MAG3
- Lung Shunt
- Gallbladder
- Lung V/Q
- MUGA
- Gastric Emptying
- HIDA
- Thyroid
- Parathyroid
- Bone Scans



3D SPECT/CT Lung Quant

MIM Encore includes helpful tools for segmentation and quantification that support lung SPECT perfusion imaging.



DaTscan™

View any SPECT image in MIM Encore. Quantification for DaTscan imaging is available in MIMneuro™.



WHAT MIM USERS ARE SAYING

“Transitioning to a new system is never easy, especially within an extensive hospital network like ours. Before implementing MIM, we used various OEM hardware and software at our different facilities.

Over the past year, we have phased out those systems and replaced them with MIM. Their dedicated support team has optimized our workflows to standardize image processing and provide consistent output from every location, regardless of the camera manufacturer or technologist.

MIM's flexibility and automation of Nuclear Medicine processing has made the change more manageable and has led to the successful adoption at all of our facilities.”

**Breece Perry**

Internal Process Coordinator—Molecular Imaging  
INTERMOUNTAIN HEALTHCARE





WORKFLOW AUTOMATION

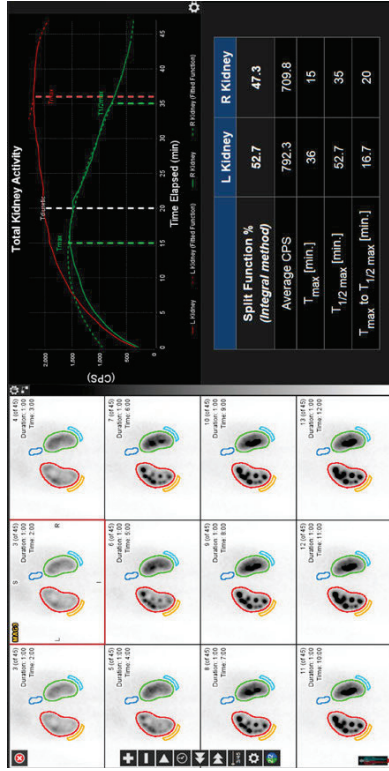
## Workflow Automation

### Refocus Staff Attention on Patient Care

Increase efficiency for technologists and physicians by using MIM Assistant to complete ordinary tasks. **Automatically fetch** prior imaging, send, archive, and delete data to spend more time on patient care.

### Automate Routine Clinical Tasks

MIM Encore works in concert with MIM Assistant to **automate image post-processing**, a time-consuming responsibility previously held by the technologists. MIM Encore can automatically reconstruct SPECT image data, generate regions of interest on most Nuclear Medicine study types, and prepare image displays for screen captures, all before a user opens the images.



#### Renal MAG-3 Analysis

MIM Encore helps with easy analysis of everyday exams, including automatic kidney delineation for MAG-3 scans.

## Centralized User and Data Management

### Effortless IT Implementation

MIM Encore is built to run on virtually **any hardware set up**. Servers can be virtual or real, making it easy for your IT team to set up and manage MIM Encore. Run MIM Encore as a stand-alone or as a PACS plug-in. Deploy MIM Encore as a thin client with Citrix® or VMware®.

### Imaging Data is Secure and Accessible

Configure a central data store for image data that helps you avoid having PHI on client disk space. MIM Assistant runs on a **centralized server location** to host and manage image data.

### Anticipate Changes to Clinical Data Storage Needs

**Add storage** as necessary without having to migrate to a larger disk. MIM Encore automatically rolls data over, saving your IT department the headache of migrating data.

### Optimize the Interface to Fit Your Role

Integrated with your existing LDAP or AD profiles, MIM Software provides a **tailored user experience** that's geared to your role in the department.





IMAGE INTERPRETATION

## Empower Clinical Decisions

### Experience Speed and Consistency

**Custom reading workflows** for PET/CT, PET/MR, SPECT/CT, and Nuclear Medicine in MIM Encore provide a tailored reading experience that helps expedite the clinical oncology image interpretation process.

Switch between fuse images, multiple layouts, link studies automatically, and create screen captures—all without having to click a mouse.

### Adopt Emerging Radiotracers Without Delay

Image volumes are expected to rise thanks to emerging radiotracers. These new tracers have unique viewing and processing requirements that conventional viewing tools won't support. MIM Encore's **flexible design** is adaptable to these specialized PET reading needs and allows Nuclear Medicine departments to adopt new radiotracer techniques without any hassle.



**PET Edge+ for Individual Lesion Segmentation**  
For low burden cases, MIM Encore includes PET Edge+, a proprietary, gradient-based segmentation method.

MIM Software

Molecular Imaging and Nuclear Medicine

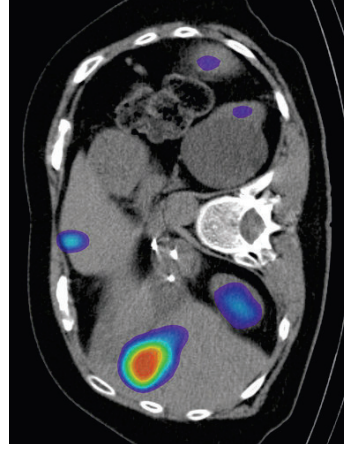
### Provide Referrers with Latest Therapy Response Information

MIM Encore provides physicians with a full suite of segmentation tools that make it possible to capture and report the latest therapy response statistics. Proprietary tools like **LesionID™** and **PET Edge+™** are designed to help physicians capture MTV, SUV Peak, and TLG for high and low burden cases. **6.1.3**

### Capture the Dosimetry Opportunity

Patient-specific dosimetry is a valuable tool for demonstrating value and enhancing patient care. **MIM SurePlan™ MRT** and **MIM SurePlan LiverY90** make capturing dosimetry information clinically feasible by standardizing the process in a single, vendor-neutral solution. **Contour ProtégéAI+™\*** is included and offers deep-learning algorithms that expedite the segmentation process.

*\*Contour ProtégéAI+ may not be available in all countries. Please speak with your MIM Software representative to see if Contour ProtégéAI+ is available in your region.*



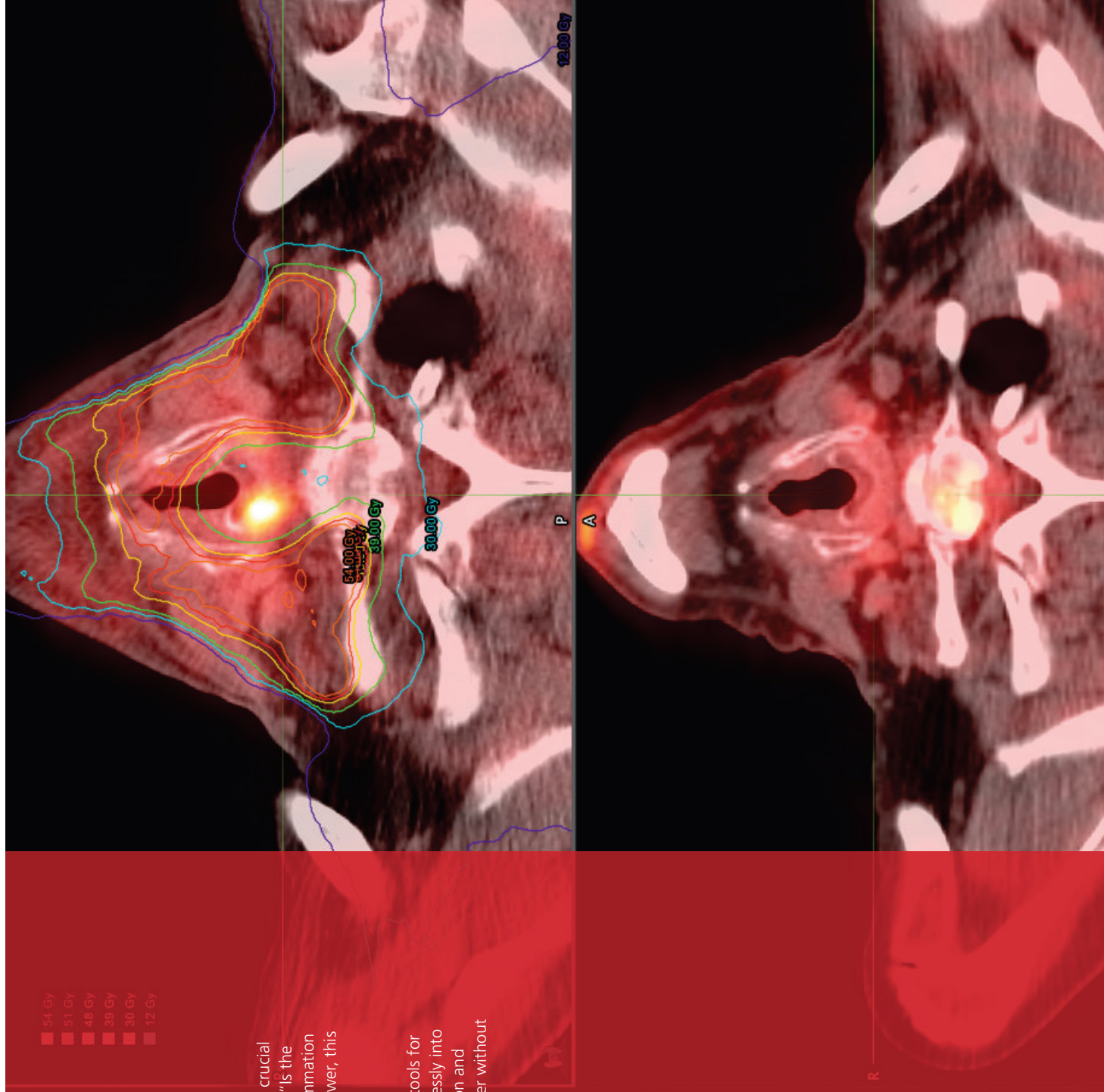
**Patient-Specific, Voxel-Based Dosimetry**  
Voxel-based dosimetry for Radiopharmaceutical Molecular Radiotherapy is included with MIM SurePlan MRT.



#### IMPROVED ACCURACY.<sup>1</sup> IMPROVED CONFIDENCE.

Reporting for post-radiation treatment patients is difficult without crucial information related to the treatment plan and treatment delivery. “Is the new area of uptake on the post-treatment PET/CT related to inflammation from the radiation, or is it recurrent disease?” Without a clear answer, this can leave you in an ambiguous reporting situation, or worse, a misinterpretation.

MIM Encore provides industry-leading viewing and segmentation tools for PET/CT and allows radiologists to integrate treatment plans seamlessly into their viewing protocols. MIM Assistant, MIM Software’s automation and data management software, brings this critical data to the end-user without disrupting the clinical workflow.





SOLUTIONS FOR NEURO, CARDIAC, AND REMOTE VIEWING

## Specialized Neuro and Cardiac Quantitative Solutions

### Comprehensive Neuroimaging Quantitation

**MIMneuro™** provides a single platform, vendor-neutral solution for image processing, reading, and reporting. Increase reader confidence with quantification by comparing to a normals database (**FDG**, **Vizamyli™**, **Neuroceq™**, **Amyvid®**, **DaTscan**, **HMPAO**, and more). Image subtraction and dynamic neuroimaging quantification are also available.

### Increase Confidence with Cardiac Imaging Quantitation

**MIMcardiac™** includes reading workflows for viability, sarcoidosis, and stress/rest exams. The normals database available for quantitative comparison includes SPECT sestamibi. MIM Software also supports integrations with both Cedars® and INVIA® 4DM, allowing users to process, view, quantify, and report any Nuclear Cardiology study from within a single application.



#### Centiloid Scaling\*

An automated workflow in MIMneuro simplifies quantitative analysis of amyloid plaque levels with the Centiloid scale.

\*May not be available in your region. Contact your MIM Software representative for more information.

## Remote Solutions and Integrations

### Full Image Access Anywhere

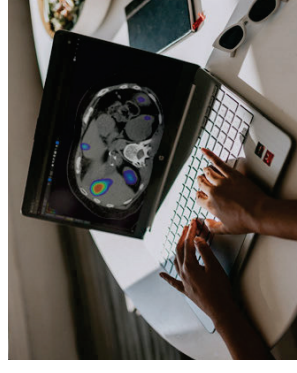
**MIM Zero Footprint™** allows you to **securely access** all MIM Software products with the same licensed features you use in the clinic anywhere you have internet access. Unlike other products that often fail risk reviews, MIM Software takes a **zero-knowledge approach** to customer data.

### Store, Share, and View

With more than a decade of use and innovation, MIMcloud™ is a **secure**, internet-based medical image service that provides an **easily accessible** resource for storing, sharing, and viewing your data. Enhance teleradiology and multi-institution reading operations and utilize MIMcloud as a secure, long-term off-site storage backup.

### Integrations

MIM Software supports a variety of **plug-in integrations** with many different PACS vendors. MIM Software also provides integration with PowerScribe® 360 to help improve reading efficiency and capture additional diagnostic information beyond conventional reporting templates.



#### Read from Anywhere

Flexible deployment options are available to support your image access needs with MIM Zero Footprint.



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MIM Software, a GE HealthCare Company, is also represented globally by a network of well-established distributors and agents. Please contact your local MIM Software representative to obtain more information for your region.

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**TD-972**  
23 July 2025



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MIM Encore® for Radiology and Nuclear Medicine  
User Guide

Version 7.1 - 7.4

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**Important:** Contact support for the most up-to-date versions of documentation. Downloaded or printed content may be supplanted or superseded by updated versions.

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## Symbols Used in Documentation



**Caution:** Indicates potential hazards or restrictions on use that are critical for safe use of the product or for compliance with legal or regulatory standards.



**Important:** Indicates information that must be read and understood to successfully complete a task. Failure to review and act on important information may result in unexpected system behavior.



**Tip:** A helpful hint related to system behavior or usability. Tips are not required for task completion.



**Related:** Introduces a link to additional optional information that may be relevant or helpful when learning about a topic or completing a task.



# Regulatory Information

MIMTD-759 • 24 Apr 2025



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



**Important:** This product may not yet be commercially available in some countries. Please contact your local MIM Software representative for further details.



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**Caution:** The following intended uses and indications apply to MIM in its entirety. Depending on your specific licenses and functionality, and the region where you use the software, some indications may not apply to your use of MIM.

## Intended Use

MIM software is intended for trained medical professionals including, but not limited to, radiologists, oncologists, physicians, medical technologists, dosimetrists, and physicists.

MIM is a medical image and information management system that is intended to receive, transmit, store, retrieve, display, print, and process digital medical images, as well as create, display, and print reports from those images. The medical modalities of these medical imaging systems include, but are not limited to, CT, MR, CR, DX, MG, US, SPECT, PET, and XA as supported by ACR/NEMA DICOM 3.0.

MIM provides the user with the means to display, register, and fuse medical images from multiple modalities. Additionally, it evaluates cardiac left ventricular function and perfusion, including left ventricular end-diastolic volume, end-systolic volume, and ejection fraction. The Region of Interest (ROI) feature reduces the time necessary for the user to define objects in medical image volumes by providing an initial definition of object contours. The objects include, but are not limited to, tumors and normal tissues.

MIM provides tools to quickly create, transform, and modify contours for applications including, but not limited to, quantitative analysis, aiding adaptive therapy, transferring contours to radiation therapy treatment planning systems, and archiving contours for patient follow-up and management.

MIM aids in the assessment of PET/SPECT brain scans. It provides automated quantitative and statistical analysis by automatically registering PET/SPECT brain scans to a standard template and comparing intensity values to a reference database or to other PET/SPECT scans on a voxel by voxel basis, within stereotactic surface projections or standardized regions of interest.

MIM allows the dose distribution of an implant to be individually shaped for each patient and is a general purpose brachytherapy planning system used for prospective and confirmation dose calculations for patients undergoing a course of brachytherapy using permanent implants of various radioisotopes (not including radioactive microspheres).

MIM allows voxel-based dose calculations for patients who have been administered radioisotopes or radioactive microspheres.

MIM assists with the planning and evaluation of ablation procedures by allowing the energy zone that comprises the ablation zone to be visualized on medical imaging through the placement of virtual ablation devices for the purpose of confirming ablation zone placement.



## Indications for Use

MIM software is used by trained medical professionals as a tool to aid in evaluation and information management of digital medical images. The medical image modalities include, but are not limited to, CT, MR, CR, DX, MG, US, SPECT, PET, and XA as supported by ACR/NEMA DICOM 3.0. MIM assists in the following indications:

- Receive, transmit, store, retrieve, display, print, and process medical images and DICOM objects.
- Create, display, and print reports from medical images.
- Registration, fusion display, and review of medical images for diagnosis, treatment evaluation, and treatment planning. **6.1.5**
- Evaluation of cardiac left ventricular function and perfusion, including left ventricular end-diastolic volume, end-systolic volume, and ejection fraction.
- Localization and definition of objects such as tumors and normal tissues in medical images. **6.1.3**
- Creation, transformation, and modification of contours for applications including, but not limited to, quantitative analysis, aiding adaptive therapy, transferring contours to radiation therapy treatment planning systems, and archiving contours for patient follow-up and management.
- Quantitative and statistical analysis of PET/SPECT brain scans by comparing to other registered PET/SPECT brain scans.
- Planning and evaluation of permanent implant brachytherapy procedures (not including radioactive microspheres).
- Calculating absorbed radiation dose as a result of administering a radionuclide.
- Assist with the planning and evaluation of ablation procedures by providing visualization and analysis, including energy zone visualization through the placement of virtual ablation devices validated for inclusion in MIM-Ablation. The software is not intended to predict specific ablation zone volumes or predict ablation success.

When using the device clinically within the United States, the user should only use FDA-approved radiopharmaceuticals. If used with unapproved ones, this device should only be used for research purposes.

Lossy compressed mammographic images and digitized film screen images must not be reviewed for primary image interpretations. Images that are printed to film must be printed using a FDA-approved printer for the diagnosis of digital mammography images. Mammographic images must be viewed on a display system that has been cleared by the FDA for the diagnosis of digital mammography images. The software is not to be used for mammography CAD.

When used for diagnostic purposes, the mobile thin client is not intended to replace a full workstation and should only be used when there is no access to a workstation.

# Use of MIM on Mobile Devices

MIM Software Inc. has previously worked with board certified radiologists to evaluate mobile devices for diagnostic reading. Devices tested included Apple iPad, Kindle Fire HDX, Samsung Galaxy Note Pro, and Microsoft Surface. In these cases, testers affirmed that the devices they evaluated were capable of displaying images at diagnostic quality.

Due to the number of available mobile devices, and the frequency with which new mobile devices are released, MIM cannot evaluate all available mobile devices for diagnostic reading. However, displays have dramatically increased in quality (e.g., resolution, contrast) since these earlier devices were tested. It is at the discretion of the user and their employer to determine which mobile devices are acceptable for diagnostic reading, and to ensure that these devices are properly calibrated.



**Caution:** All treatment plan reports shall be approved by a qualified person before the information in them is used for radiotherapy treatment purposes. The responsible organization shall ensure that individuals authorized to perform treatment planning functions are appropriately trained for the functions they perform, and the operator shall always be aware that the quality of the output depends critically on the quality of the input data. Any irregularities or uncertainties about input data units, identification, or quality of any other nature shall be thoroughly investigated before the data are used.



**Caution:** Any health professional having a complaint or grounds for dissatisfaction relating to the identity, quality, durability, reliability, safety, effectiveness, or performance of a device should notify MIM Software. Moreover, if a device has malfunctioned, MIM Software or its representative must be informed immediately. If a MIM Software product could have caused or contributed to the death or serious injury of a patient, MIM Software or its representative must be informed immediately. These serious incidents must also be reported to the Competent Authority of the European Member State or, when applicable, the equivalent regulatory authority, where the user and/or patient is established.



**Caution:** Users must perform validation when developing their own extensions or workflows and when modifying any default extensions or workflows that MIM Software provides. For extensions and workflows developed or modified by the user or provided by a third-party, MIM Software (i) does not endorse, control, monitor, or verify the contents, (ii) does not provide any warranty; and (iii) is not liable for any loss, damage, or injury sustained resulting from downloading, installing, accessing, integrating, supporting, or using the extension or workflow.



**Caution:** Due to the inherent nature of medical images, with their variable characteristics (e.g., level of noise and artifacts), the degree of accuracy may be variable as well. These limitations must be considered before making any decision based on images and quantitative values. It is recommended that acceptance testing be performed prior to use. This testing should include, at a minimum, all representative data sets (images) intended for transfer, all types of transfers desired for a type of data set, and clinical evaluation of each representative data set on the receiving end after each desired type of transfer.

For more information on accuracy details, see appendix or white paper information.

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# Notable Changes in MIM<sup>®</sup> 7.4 Documentation

MIMTD-1646 • 18 Jan 2024

## Overview

Based on user feedback, the Knowledge Center has new documents available with this release, as well as updates to existing documents.

## Contents

- [New Documentation](#)
  - [General](#)
  - [MIM Encore<sup>®</sup>](#)
  - [Reconstruction](#)
- [Updated Documentation](#)
  - [Viewing](#)
  - [Contouring](#)
  - [Patient Data](#)

## New Documentation

### General

Description	Document
How to navigate the MIM interface.	<a href="#">Work with Onscreen Information and Tools in MIM<sup>®</sup> Viewports</a>
How to optimize fusions automatically.	<a href="#">Optimize Fusions Automatically</a>
How to combine two anatomic series with differing fields of view.	<a href="#">Combine Anatomical Images Using the Stitcher Workflow</a>
How to view quantitative data about registrations in MIM.	<a href="#">Evaluate Fusions Quantitatively</a>
Adjust settings for the alignment of images, including blend amount and hiding the fusion tools.	<a href="#">Configure Fusion Settings</a>
An overview for creating contours.	<a href="#">Create Contours Overview</a>
Helpful options to speed up contouring and do more with contours in MIM.	<a href="#">Tips for Efficient Contouring</a>

Description	Document
How to crop contours and use hard edges in areas where contours may overlap.	<a href="#">Work with Overlapping and Adjacent Contours</a>
How to move contours.	<a href="#">Move Contours</a>
How to contour using the Pen tool.	<a href="#">Create Contours with the Pen Tool</a>
How to create contours and dose surface views.	<a href="#">Create Contour and Dose Surface Views</a>
How to annotate images.	<a href="#">Annotate Images</a>
How to sign workflows you have reviewed.	<a href="#">Sign Workflows You Have Reviewed</a>

## MIM Encore®

Description	Document
How to visualize and report on PSMA studies by automatically contouring regions of high uptake with the LesionID® Pro workflow.	<a href="#">Quantify PSMA with LesionID® Pro</a> <a href="#">Set Up LesionID® Pro</a> <a href="#">LesionID® Scenarios</a>
How to create your own Sector Assist model to more quickly segment surfaces.	<a href="#">Use Your Own Segmentation Model</a>
Information describing how MIM autonormalizes PET contrast.	<a href="#">Autonormalize PET Series in MIM®</a>
How the PET Edge+ tool can save time and clicks compared to the legacy PET Edge tool.	<a href="#">The Advantages of PET Edge®+</a>
How to use the Create Projection Images tool to generate projection images from a SPECT with optional attenuation.	<a href="#">Create Projection Images</a>
Definition of how various fit types are calculated.	<a href="#">Fit Type Calculations: Technical Details</a>

## Reconstruction

Description	Document
How users can reconstruct images in MIM.	<a href="#">SPECTRA Recon® Overview</a>
How to use the updated SPECTRA Reconstruction workflow.	<a href="#">Manually Run a Reconstruction Workflow</a>
Information about which pages are created after reconstructing an image in MIM.	<a href="#">Review the Reconstruction Output</a>

# Updated Documentation

## Viewing

Description	Document
<ul style="list-style-type: none"><li>How to use the mouse wheel to adjust image contrast.</li><li>How to create custom contrast presets.</li><li>How to adjust upper and lower contrast bounds.</li></ul>	<a href="#">Adjust Image Contrast</a>
Information about accessing tools via the toolbar and radial menu has been combined into a single document.	<a href="#">Access Tools: The Toolbar and the Radial Menu</a>
<ul style="list-style-type: none"><li>How to adjust slices by resampling.</li><li>How to view composite slices by slabbing.</li><li>How to view slices on a grid.</li></ul>	<a href="#">View and Adjust Slice Thickness</a>
Additional information for saving secondary captures.	<a href="#">Save Patient Data</a>
Recommended scenarios for different capture options.	<a href="#">Create and Save Secondary Captures</a>
One-time settings you can adjust to enable faster and more efficient captures.	<a href="#">Configure Default Settings for Faster Captures</a>

## Contouring

Description	Document
How to use the 2D Brush companion tools.	<a href="#">Create Contours with the 2D Brush</a>
How to use PET Edge+ to create long and short measurements for a tumor assessment, such as RECIST.	<a href="#">Define Lesions with PET Edge®+</a>
The Sector Assist tool can now remove key planes and re-segment a previously segmented contour.	<a href="#">Segment ROIs with Sector Assist</a>
Information about alternative saving options for contours and auto-save contour backups.	<a href="#">Save Contours</a>

## Patient Data

Description	Document
How to send updated patient data along with non-updated patient data simultaneously.	<a href="#">Merge Patients</a>

Description	Document
<ul style="list-style-type: none"> <li>• How to search for export destinations.</li> <li>• How to search for information for the file structure applied to DICOM data when it is exported.</li> </ul>	<a href="#">Export Data from MIM®</a>
How to encapsulate documents as DICOM.	<a href="#">Manage Patient Data</a>
Details about increased functionality to compare DICOM series in the DICOM Viewer.	<a href="#">View and Edit DICOM Information</a>
How to revoke workflow signatures.	<a href="#">Manage Workflow Signatures</a>


Personalize MIM®

# Use Default Preferences with Radiology and Nuclear Medicine User Profiles

MIMTD-688 • 09 Aug 2023

## Overview



**Important:** The following feature applies if your organization uses user logins. If you are not sure whether user logins are enabled, look for the  icon in the upper-right corner of MIM. If you do not see it, you are not using user logins and this topic does not apply to you.

User profiles group together default settings that are particularly helpful for a given role. They are a customized starting point for a new user.

Selecting a user profile does not override previously configured individual preferences or prevent future changes to preferences. Site defaults also continue to be respected, regardless of the profile.

MIM Encore® users can select between the following profiles:

6.1.1

- **Radiologist** — Loads patient data with 3D viewing tools for PET/CT and SPECT/CT, as well as relevant workflows and saved searches.
- **Technologist** — Loads patient data with tools particular to 2D NM processing, as well as relevant workflows and saved searches.
- **None (Keep Current Settings)** — Loads patient data with default MIM tools.

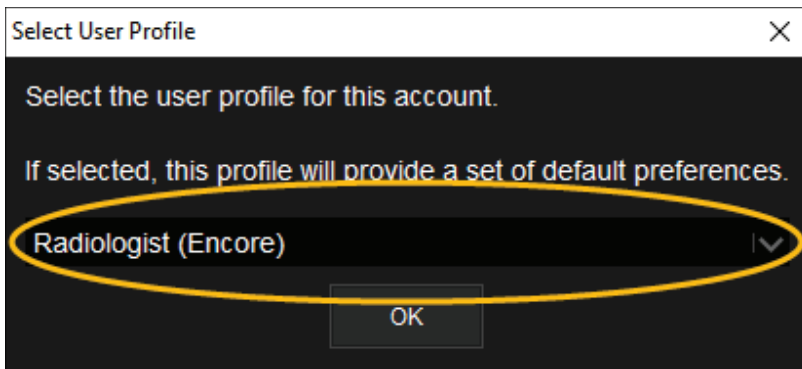


**Tip:** Users who use multiple MIM products or serve in different roles can choose **Prompt at Startup** if they want to select the applicable profile every time they log in.


## Select a Profile

The first time that a user logs in to MIM, they are prompted to select a profile.





If a user selects **None (Keep Current Settings)** or later wants to change their selection, complete the following steps:

1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**user profile**". Select **Application** on the left side.
3. Use the **Apply Settings from User Profile** option to select the desired profile.
4. Click **OK**.
5. Close and relaunch MIM to apply the changes.

# Set Keyboard Shortcuts

MIMTD-616 • 30 Aug 2023

## Overview

MIM® has hundreds of commands that you can assign to keyboard shortcuts. Keyboard shortcuts give you quick access to CT contrast presets, zooming functionality, localizing functionality, and more.




**Related:** By default, many commands are already assigned to keyboard shortcuts. For a list of default keyboard shortcuts, see [Default Keyboard Shortcuts](#).

## Contents

- [Assign or Reassign Keyboard Shortcuts](#)
- [Export a PDF of Keyboard Shortcuts for Reference](#)

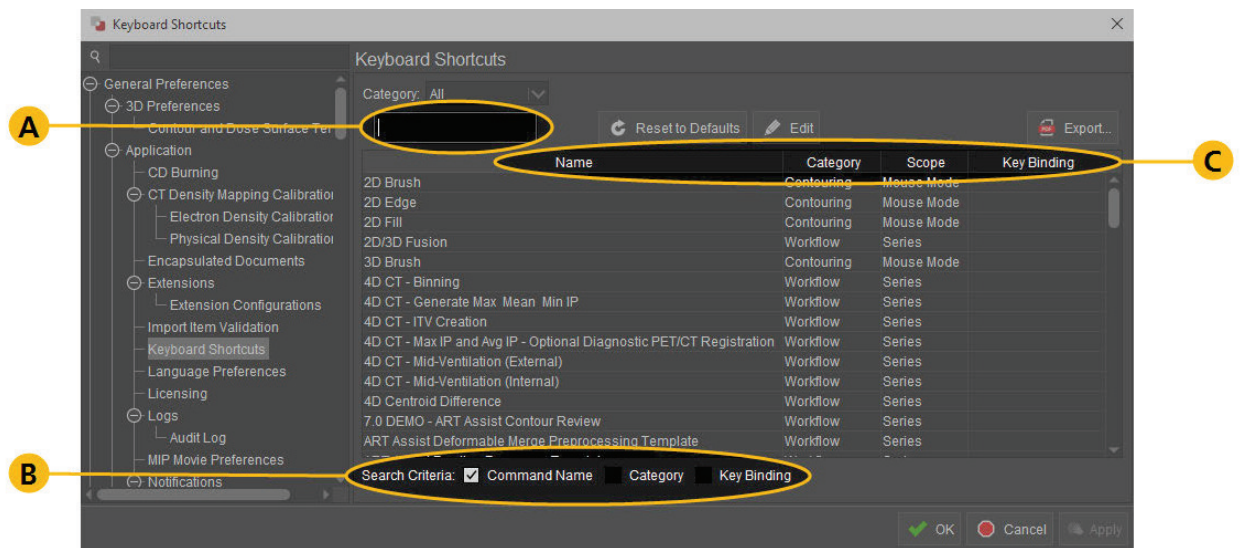
## Assign or Reassign Keyboard Shortcuts

1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **Keyboard Shortcuts...**
3. In the Keyboard Shortcuts window, find the command that you want to assign or reassign a keyboard shortcut to:
  - A. Enter search terms in the empty field below the Category dropdown.
  - B. To change the search criteria, select or deselect **Command Name**, **Category**, or **Key Binding** at the bottom of the Keyboard Shortcuts window.



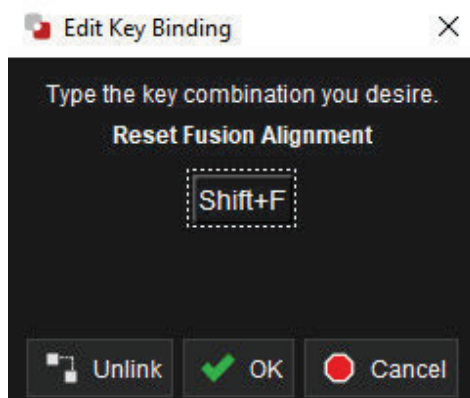
# MIM Encore® User Guide

C. To sort the columns, click the **Name**, **Category**, **Scope**, or **Key Binding** column headers.



**Important:** The **Scope** column indicates where the cursor needs to be in order for the keyboard shortcut to work. If the scope is **Series**, the cursor needs to be hovering over a specific viewport. If the scope is **Mouse Mode** or **Session**, the keyboard shortcut functions as long as the cursor is active within MIM.

- Double-click the command that you want to change. The Edit Key Binding window opens.
- Type the key binding that you want to assign to the command. The Edit Key Binding window updates with the key binding that you typed.






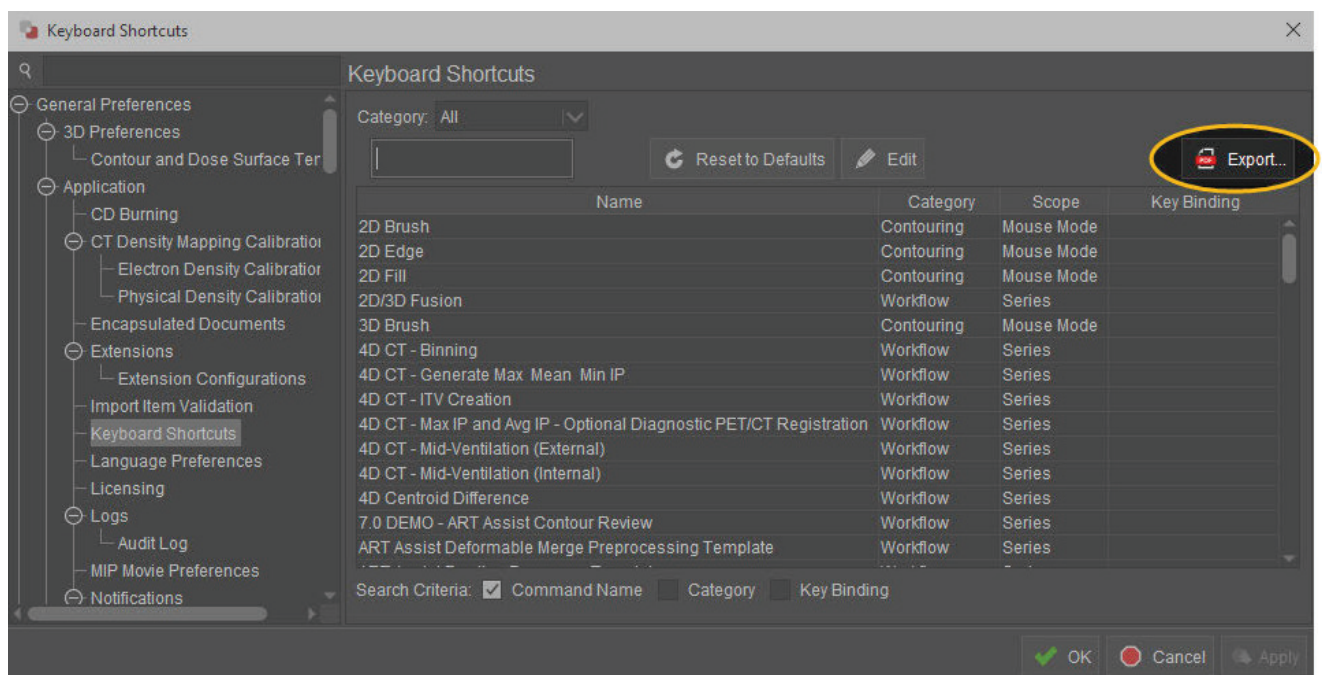
**Important:** If the key binding is already in use, MIM warns you and shows the command that the key binding is assigned to. Type a different key binding, or click **OK** to use the key binding that you entered and unassign the key binding from the other command.

6. Click **OK**. The Key Binding column updates to show the assigned key binding.
7. Click **OK** at the bottom of the Keyboard Shortcuts window to save your changes and close the window.

## Export a PDF of Keyboard Shortcuts for Reference

To export a list of keyboard shortcuts for reference, follow these steps:

1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **Keyboard Shortcuts...**
3. Click the **Export...** button in the upper-right corner of the Keyboard Shortcuts window.



4. To include or exclude keyboard shortcuts from the list, select or deselect the desired shortcuts.
5. Click **Save PDF...**
6. Browse to the file location where you want to save the PDF.
7. Enter a filename.
8. Click **Save**. The PDF of keyboard shortcuts is now available in your save location.

# Configure Mouse Behaviors

MIMTD-1282 • 07 Aug 2023

## Overview

The click and drag behaviors for your mouse buttons can help you complete several actions in MIM® more quickly. *MIM 7.3 and later:* You have the ability to configure which mouse buttons control which actions based on what is most intuitive and useful for you. *MIM 7.2 and earlier:* The [Default Mouse Behaviors](#) are always used and are not configurable.

For example, you may want to scroll quickly through a series with a left-click drag instead of the default right-click drag (see [Examples](#) below for instructions). You can also add key modifiers to each mouse button. You may want to match your mouse button behaviors to your PACS system to allow for easy transitions between MIM and PACS.

## Contents

- [Default Mouse Behaviors](#)
- [Adjust Mouse Behaviors](#)
- [Examples](#)

## Default Mouse Behaviors

MIM includes the following default mouse behaviors:

Action	Mouse Behavior	More Information
Localize	Left-click and left-click drag	<a href="#">Localize and Scroll</a>
Adjust Contrast*	Middle-click drag	<a href="#">Adjust Image Contrast</a>
Radial Menu	Right-click	<a href="#">Access Tools: The Toolbar and the Radial Menu</a>
Scroll Slices	Right-click drag	<a href="#">Localize and Scroll</a>


\*The adjust contrast default is new in MIM 7.3 and later. In MIM 7.2 and earlier, there is no mouse behavior for this action.

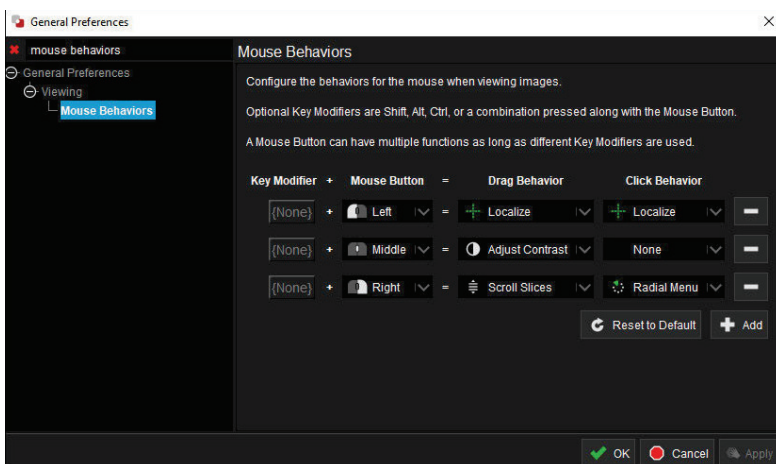
## Adjust Mouse Behaviors



**Tip:** To share and standardize these settings across your organization, a MIM administrative user should make the additions or updates while logged in to the **Edit Site Defaults** login mode. See [Update Default Settings for Users](#) for prerequisites and instructions.

To adjust the mouse behaviors, follow these steps:

1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**mouse behaviors**". Select **Mouse Behaviors** on the left side.
3. Adjust the existing behaviors or click **Add** to set a new behavior.
  - Use the dropdowns to choose the **Mouse Button**, **Drag Behavior**, and **Click Behavior**.
  - Click the **Key Modifier** field and then press a key to set the modifier.



The following options can be combined:

Key Modifiers*	Mouse Button	Behaviors
----------------	--------------	-----------

<ul style="list-style-type: none"> <li>Windows® <ul style="list-style-type: none"> <li>Shift</li> <li>Alt</li> <li>Ctrl</li> </ul> </li> <li>Mac® <ul style="list-style-type: none"> <li>shift</li> <li>option</li> <li>control</li> </ul> </li> </ul>	<ul style="list-style-type: none"> <li>Left</li> <li>Middle**</li> <li>Right</li> </ul>	<ul style="list-style-type: none"> <li>Scroll Slices</li> <li>Adjust Contrast</li> <li>Localize</li> <li>Rotate View</li> <li>Pan</li> <li>Zoom</li> <li>Quick MIP</li> </ul>
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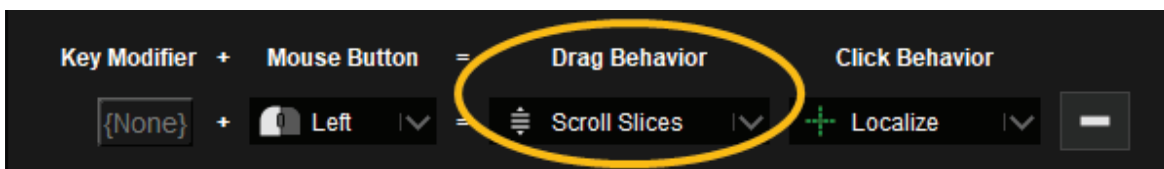
\*Neither the Command key (for Macs) nor the Windows key are allowed with mouse behaviors.

\*\*Clicking or click-dragging the middle button (usually the scroll wheel) can be configured with the behaviors listed above. Configuring the behavior for scrolling the wheel, however, is not available at this time.

## Examples

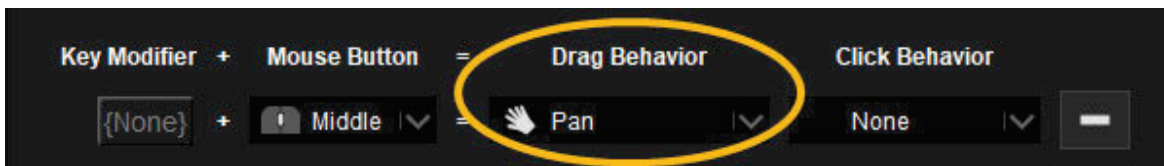
If you want to scroll quickly through a series by left-click dragging:

1. Find the Left Mouse Button preference.
2. Change the Drag Behavior dropdown to **Scroll Slices**.



If you want to pan a series by dragging the middle button:

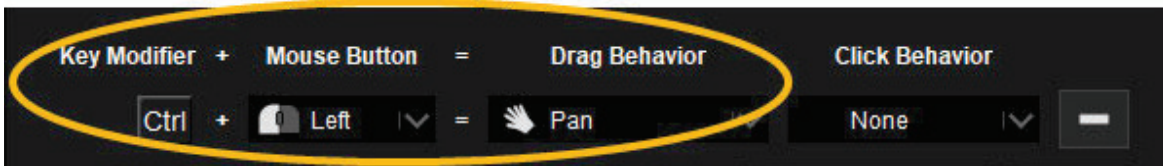
1. Find the Middle Mouse Button preference.
2. Change the Drag Behavior dropdown to **Pan**.



If you want to pan a series using the Ctrl key and left-click dragging:

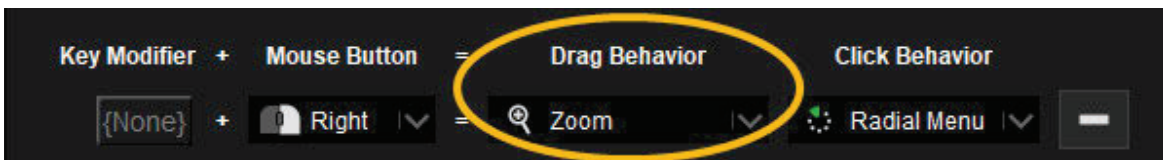


1. **Add** a new behavior.
2. Set the Key Modifier to **Ctrl**
3. Set the Mouse Button to **Left**.
4. Set the Drag Behavior to **Pan**.



If you want to zoom a series by right-click dragging:

1. Find the Right Mouse button preference.
2. Change the Drag Behavior dropdown to **Zoom**.



## Find, Save, and Move Data

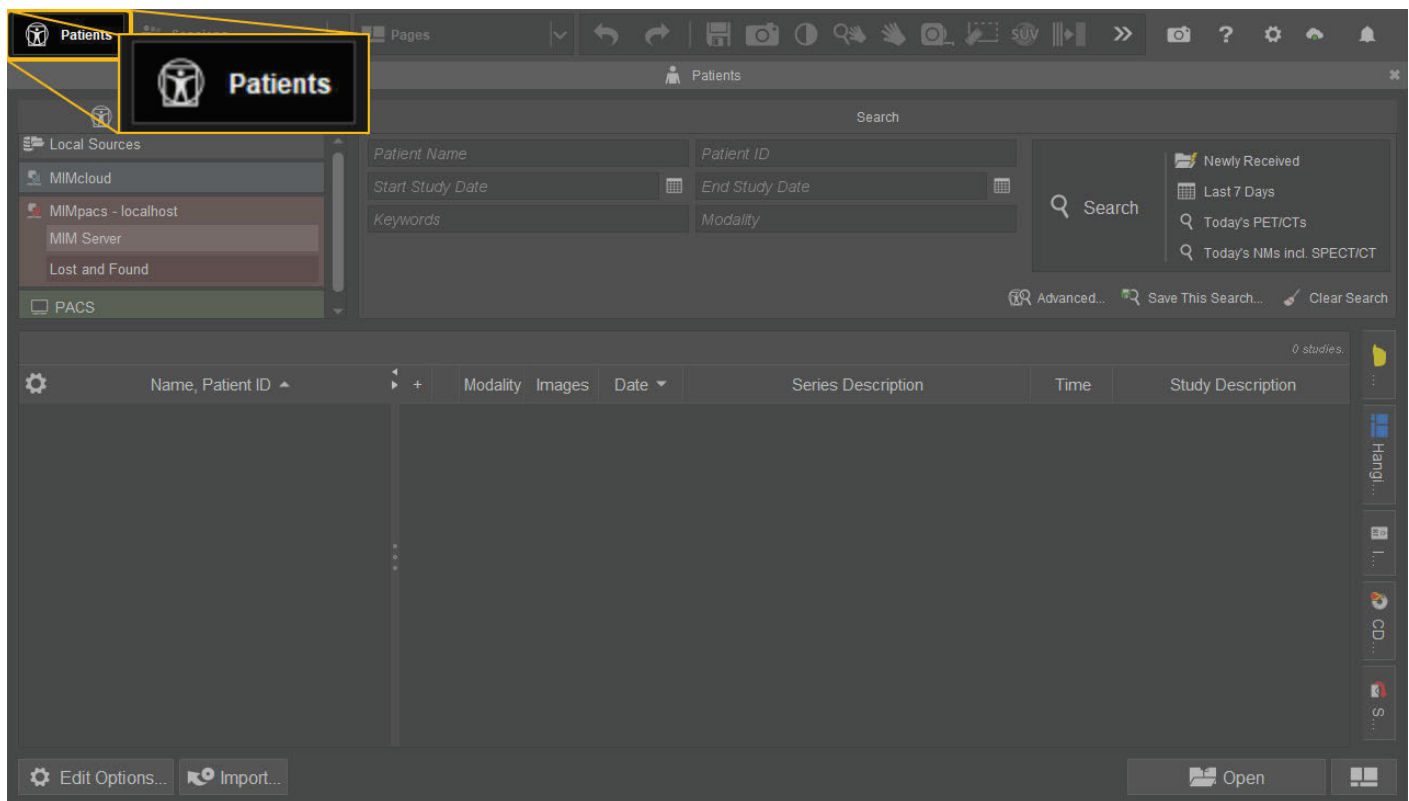
# Find and Open Patient Data

MIMTD-1642 • 07 Sep 2023

## Overview

Use the patient list to find and open patient data. When you launch MIM®, the patient list appears by default.

To return to the patient list anytime, click the **Patients** button in the upper-left corner.



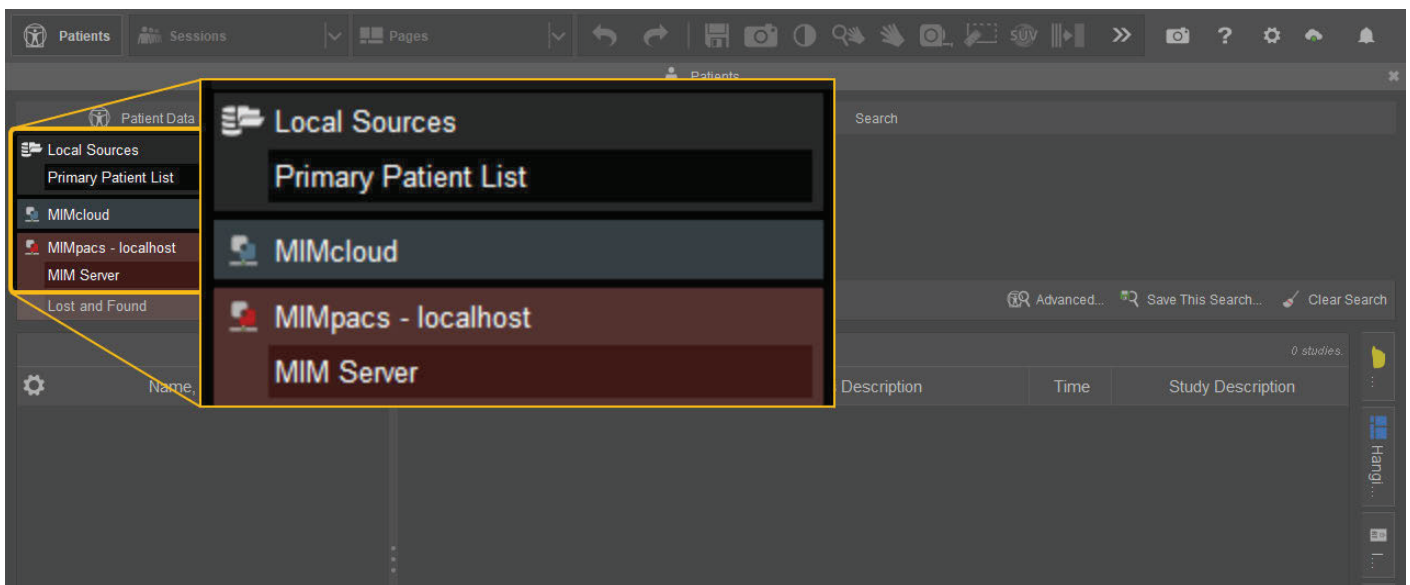
## Contents

- [Find and Open Data](#)
- [Tips for Searching](#)
- [Do Advanced Searches](#)
- [Query and Retrieve from PACS](#)
- [Import Data from a Local File, Folder, or CD](#)

## Find and Open Data

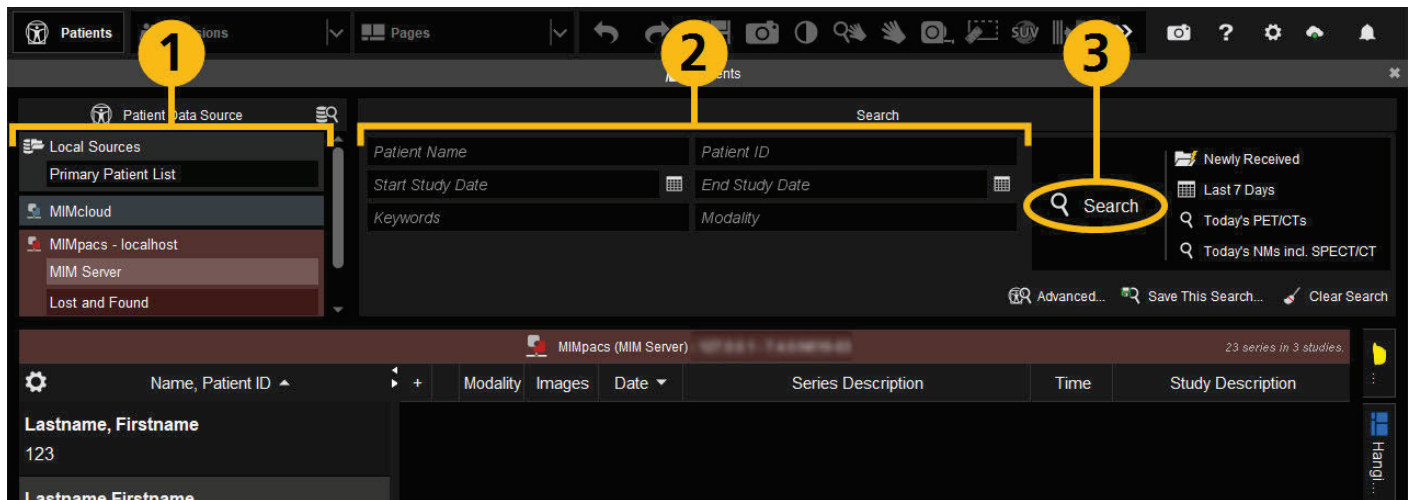
Patient data sources are in the upper-left corner. Search for patient data and open it directly from any of the following patient data sources:

- **Local Sources** (Gray) — Data in these sources is stored on your computer.
- **MIMcloud® Sources** (Blue) — Data in these sources is stored in MIMcloud. For more information about MIMcloud, go to [mimcloud.com](https://mimcloud.com).
- **MIMpacs™ Sources** (Red) — Data in these sources is stored on your organization's MIM server.



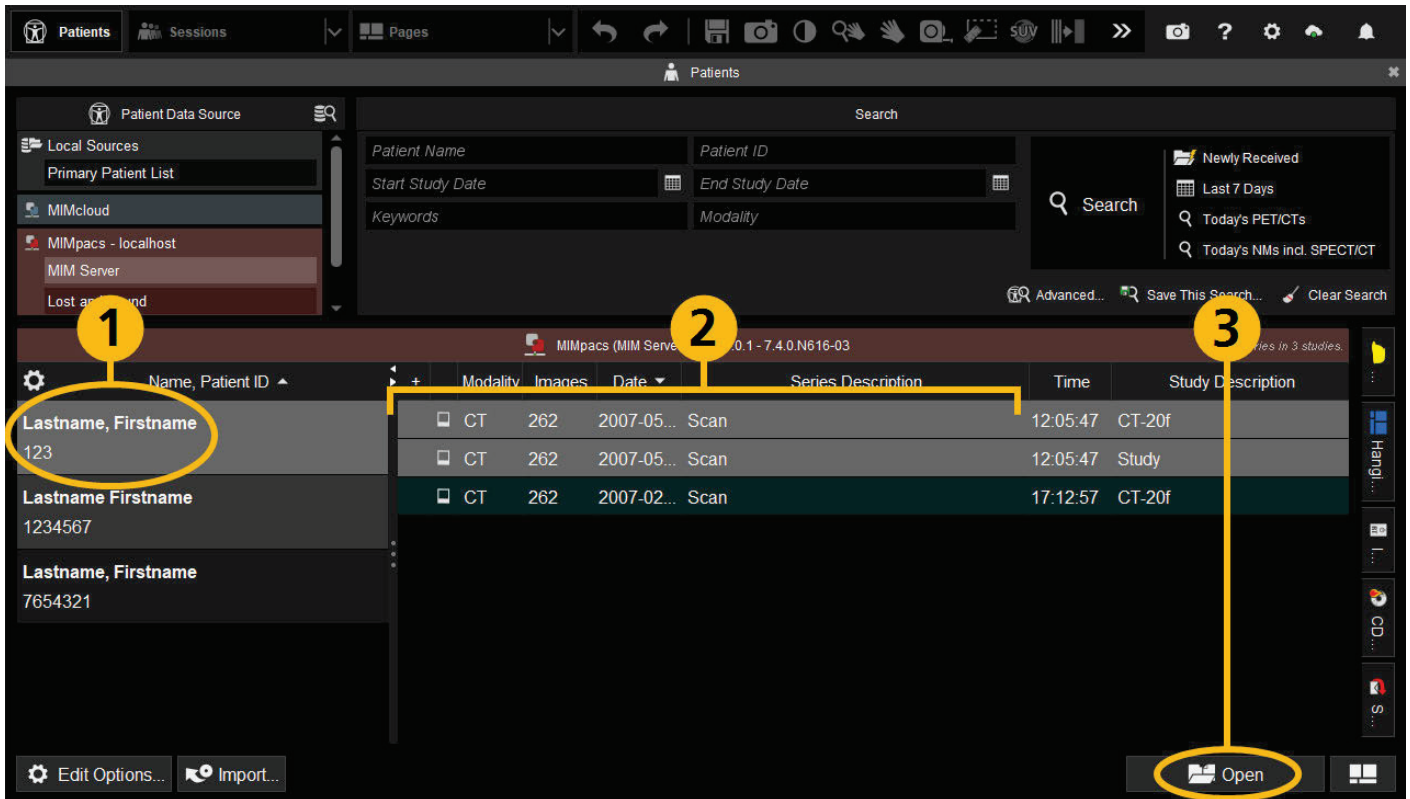
**Important:** If the data that you want to open is not in local sources, MIMcloud sources, or MIMpacs sources, you must first retrieve or import the data. Refer to [Query and Retrieve from PACS](#) or [Import Data from a Local File, Folder, or CD](#) below.

## Find Data



1. Select the desired patient data source.
2. Enter search criteria as necessary. All search fields are optional.
3. Click the **Search** button. Search results appear below the data sources, in the column on the left side.

## Open Data



The screenshot shows the MIM Encore interface with the following components:

- Left Sidebar (Patient Data Source):** Contains a list of patient sources. A yellow circle labeled '1' highlights the 'Lastname, Firstname' entry.
- Central Table:** Displays patient data with columns: Name, Patient ID, Modality, Images, Date, Series Description, Time, and Study Description. A yellow circle labeled '2' highlights the 'CT' series in the first row.
- Right Sidebar:** Contains search and filter options. A yellow circle labeled '3' highlights the 'Open' button at the bottom right.

1. Select the desired patient from the column on the left side. Individual series appear in the center of the screen.
2. If you want to open only certain series, select one or more individual series. If you do not select individual series, all series for the patient will open.



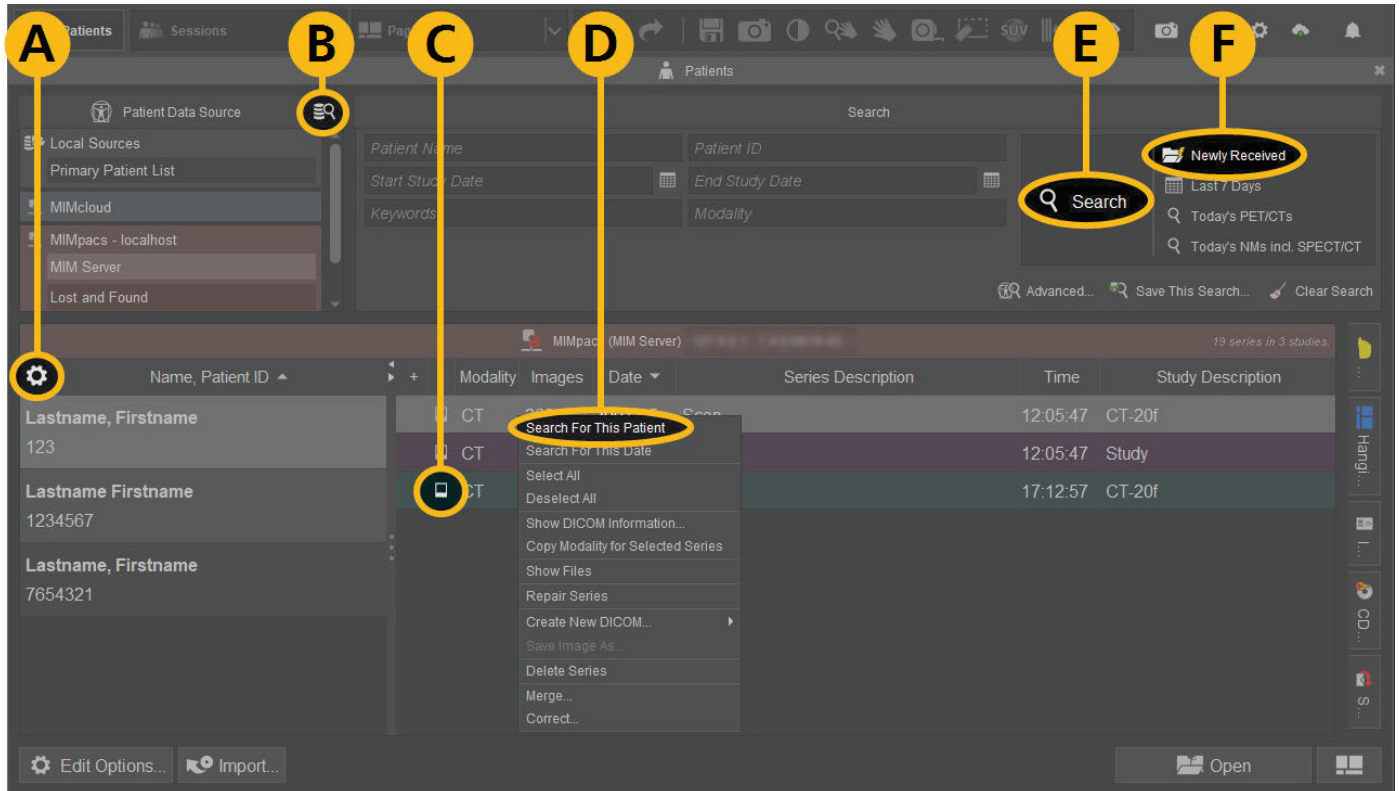
**Tip:** To select multiple patients or series at a time, hold the Ctrl key while clicking, or left-click drag over multiple items.




3. To open the data into a MIM session, click the **Open** button. Or, to automate processing, launch a MIM Workflow™.



**Related:** For more information about workflows, refer to [Launch MIM Workflows™](#).

## Tips for Searching



- To change how the search results are sorted, click the settings  button above the search results on the left side.
- MIM 7.2 and later:* To search for a specific patient data source, click the  button and start typing the name of the source. This is useful if one of your data sources has many individual patient lists.  
*MIM 7.1 and earlier:* This functionality is not available.
- To preview an image before you open it, hover over the thumbnail  symbol on the left side of the series information.
- To see all series for a patient, instead of only those returned by the search criteria, right-click a search result and select **Search for This Patient**.



**Related:** For instructions on using the other options in this right-click menu, refer to [Manage Patient Data](#).


- To clear all search criteria, right-click the **Search** button.
- To show only newly received data, click **Newly Received** next to the **Search** button.





**Related:** To set up other one-click search buttons that bundle a set of search criteria, refer to [Search Quickly with Saved Searches](#).

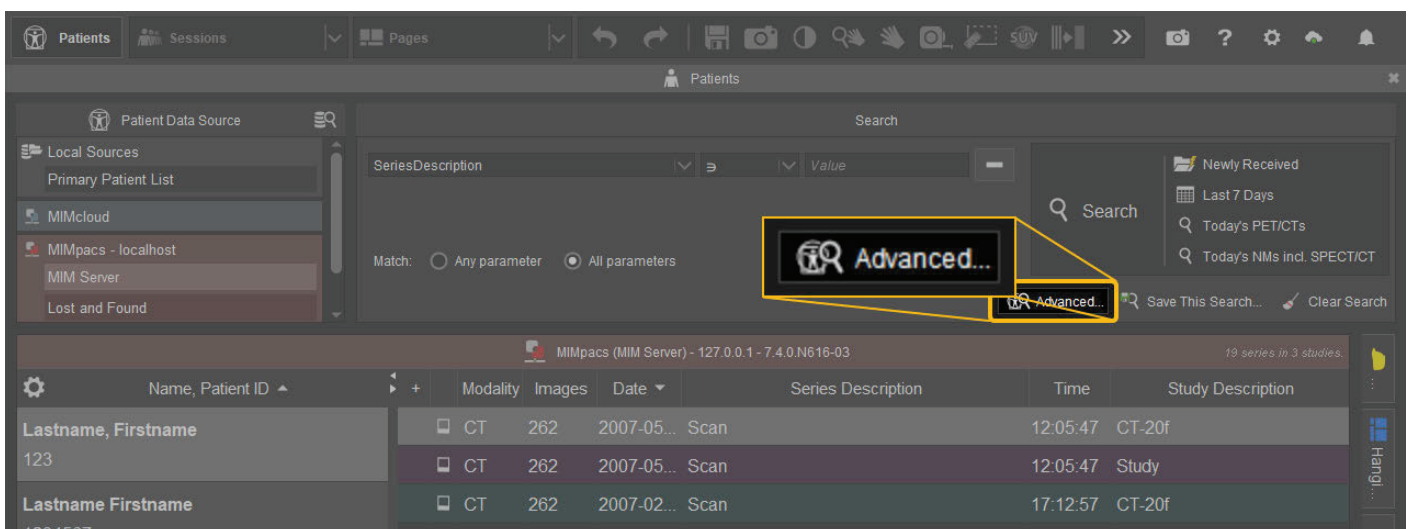
## Adjust Patient List Options

To personalize a variety of patient list functions, go to Settings  in the upper-right corner of MIM and choose **Patient List Options**. Adjustments that you can make include the following:

- Choose which series columns (e.g., Modality, Series Description, Time) are shown and in which order.
- Set the patient list view to show newly received series by default.
- Change the default sorting method for search results.

## Do Advanced Searches

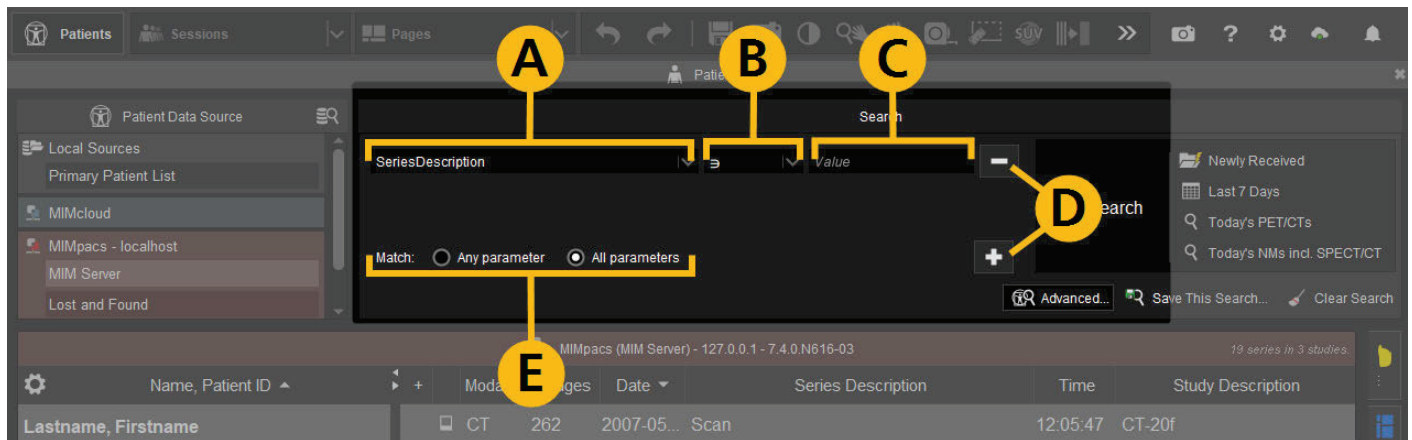
If desired, click the **Advanced...** button in the middle of the search panel to find data using DICOM tag-based search filters.



The screenshot shows the MIM Encore interface. The top navigation bar includes 'Patients', 'Sessions', and 'Pages'. The left sidebar shows 'Patient Data Source' with options like 'Local Sources', 'MIMcloud', 'MIMPacs - localhost', and 'Lost and Found'. The main search panel has a 'Search' section with a 'SeriesDescription' dropdown and a 'Value' input field. Below this is a 'Match' section with radio buttons for 'Any parameter' and 'All parameters'. The 'Advanced...' button is highlighted with a yellow box. To the right of the search panel is a 'Newly Received' section with a list of search filters: 'Last 7 Days', 'Today's PET/CTs', and 'Today's NMs incl. SPECT/CT'. Below the search panel is a table of patient data. The table has columns for 'Name, Patient ID', 'Modality', 'Images', 'Date', 'Series Description', 'Time', and 'Study Description'. The table shows three rows of data for a patient named 'Lastname, Firstname 123'.

Name, Patient ID	Modality	Images	Date	Series Description	Time	Study Description
Lastname, Firstname 123	CT	262	2007-05...	Scan	12:05:47	CT-20f
Lastname, Firstname 123	CT	262	2007-05...	Scan	12:05:47	Study
Lastname, Firstname 123	CT	262	2007-02...	Scan	17:12:57	CT-20f

Follow these tips to use the advanced search options:



- A. Select a DICOM tag (e.g., SeriesDescription). Scroll through the menu to see common tags, or start typing to find other tags.
- B. Select an operator (e.g., =). To see an explanation of what the operator does, select the operator and hover over the field.
- C. Enter a value (e.g., WB AC).
- D. To add a search filter, click the **+** button. To remove a search filter, click the **-** button.
- E. Select whether the search should return results that match any or all of the filters that you configure.

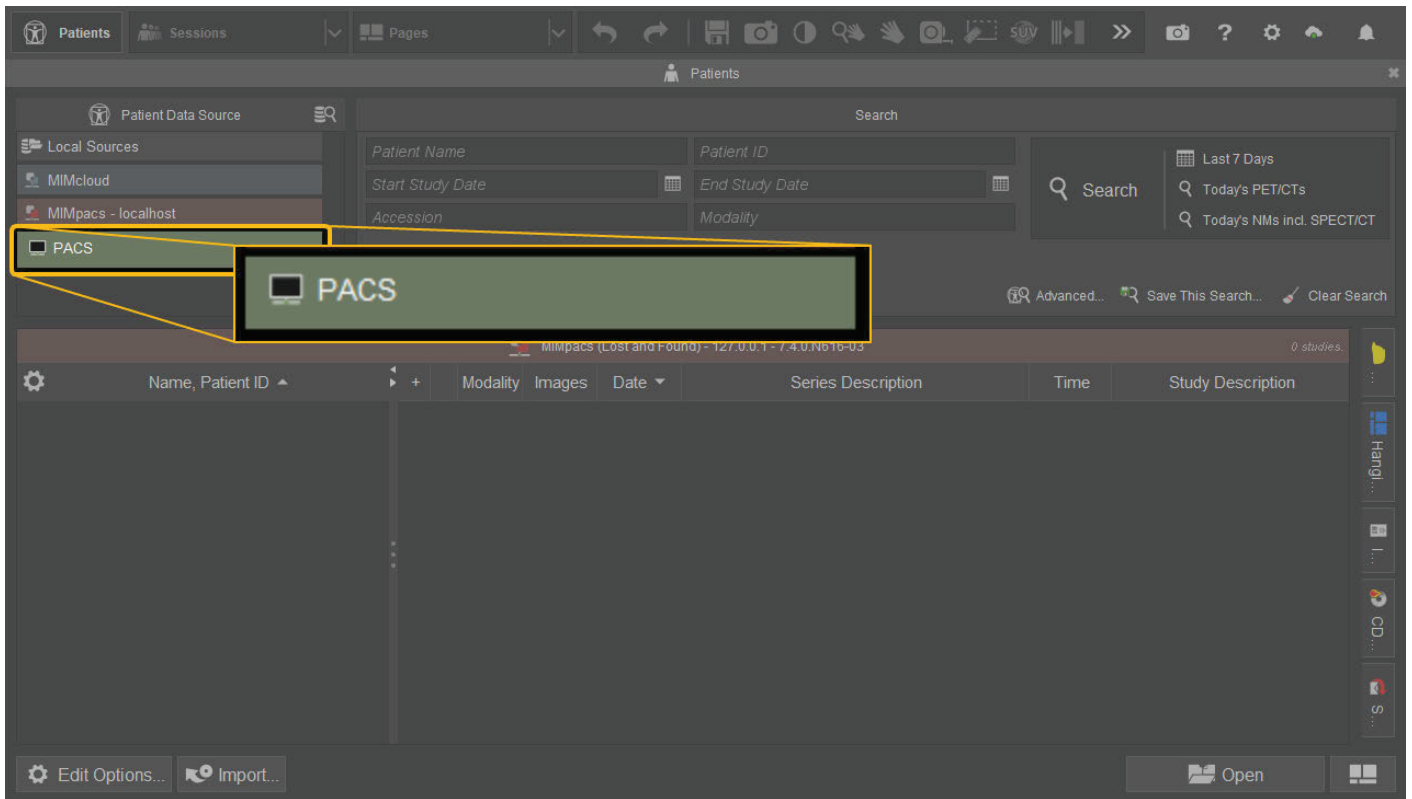


**Related:** To save advanced searches as one-click search buttons, refer to [Search Quickly with Saved Searches](#).

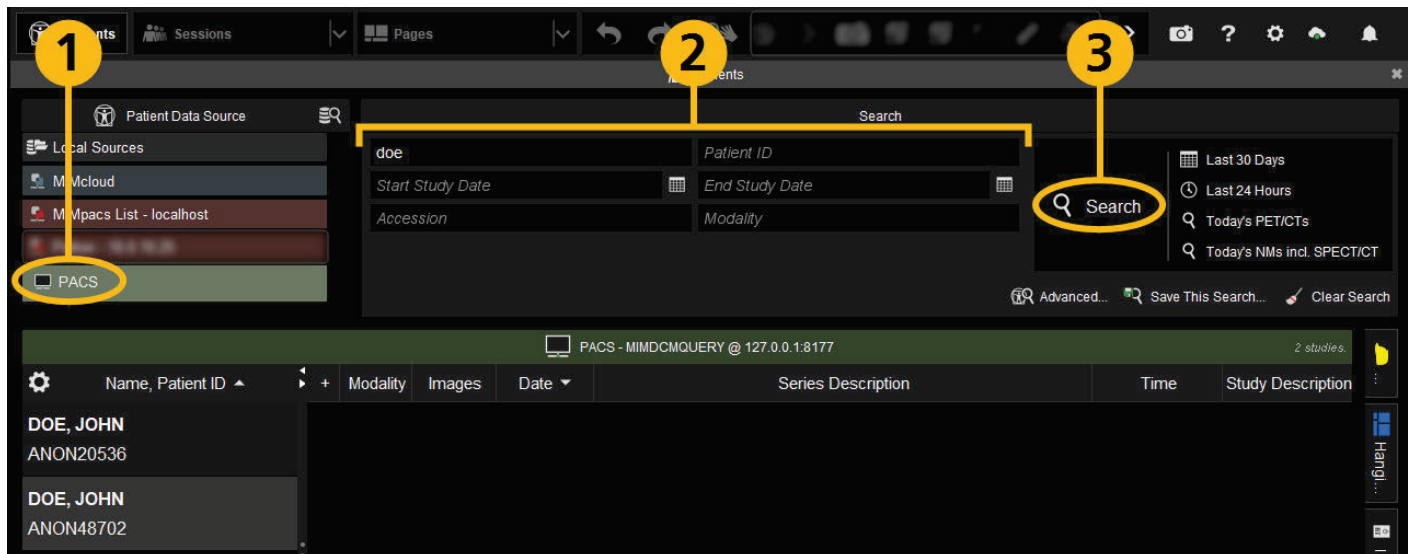
## Query and Retrieve from PACS

PACS lists, or third-party DICOM locations, are highlighted in green and located under MIM patient lists. You can search for patient data in these data sources. To open the data, you must send it to a MIM patient

list.



## Search a PACS List



1. Select the desired PACS list.
2. Enter search criteria as necessary. All fields are optional.



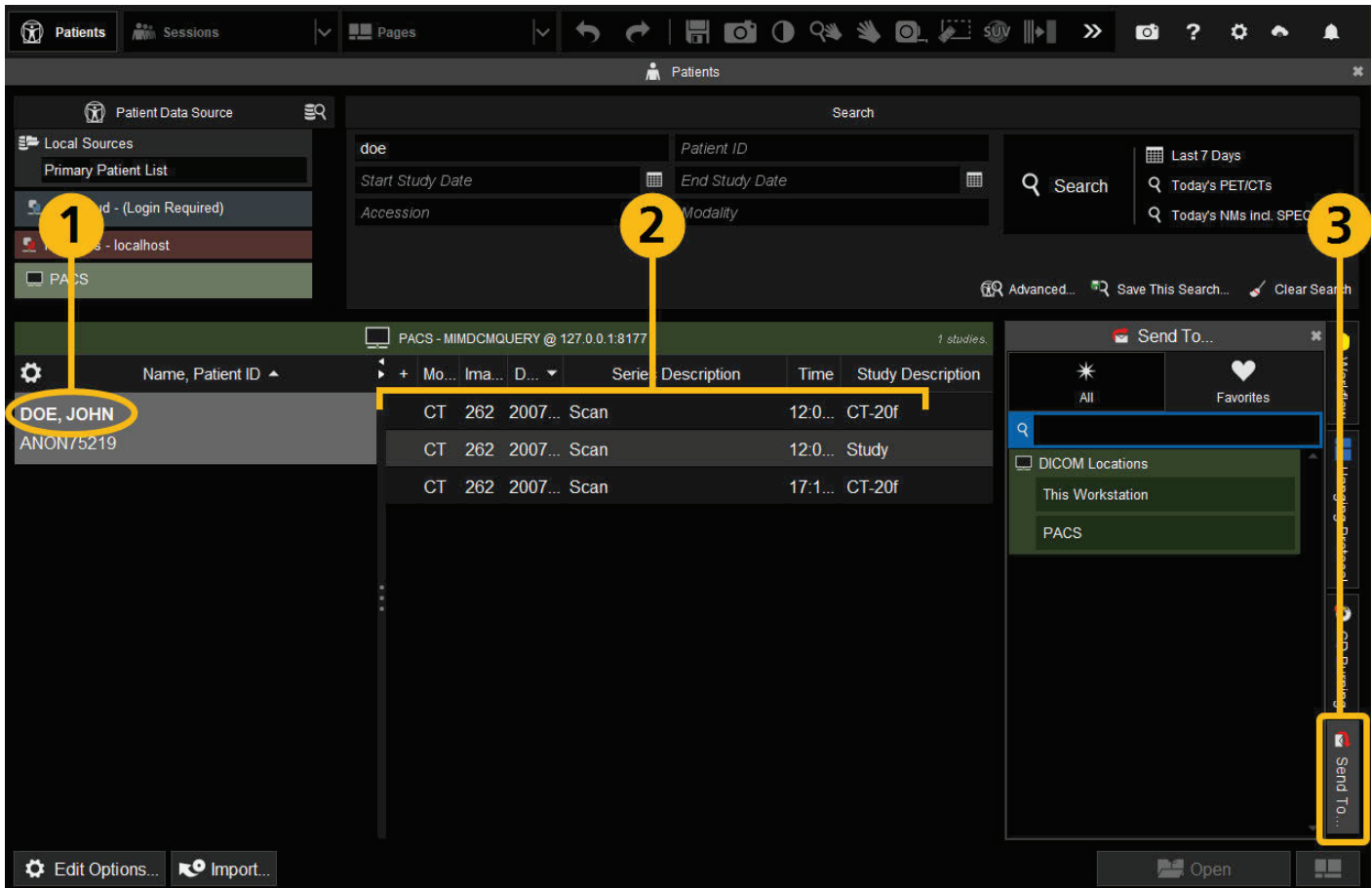
**Important:** Each PACS supports different search criteria when queried by another system such as MIM. Some search criteria may not return results.

3. Click the **Search** button. Search results appear below the data sources, in the column on the left side.



**Tip:** For more details about search options, refer to [Tips for Searching](#) and [Do Advanced Searches](#) above.

## Send Data from PACS to a MIM Patient List



The screenshot shows the MIM Encore interface with the following elements:

- Left Panel:** A list of patient data sources. Item 1 points to the selected patient, **DOE, JOHN** (ANON/5219).
- Main Table:** A table of study series. Item 2 points to the selected series, **CT 262 2007... Scan**.
- Bottom Right:** A **Send To...** dialog box. Item 3 points to the **Send To...** button in the bottom right corner of the main interface.


1. Select the desired patient from the column on the left side.
2. If you want to send only certain series, select one or more individual series. If you do not select individual series, all series for the patient are sent.



**Tip:** To select multiple patients or series at a time, hold the Ctrl key while clicking, or left-click drag over multiple items.

3. Click the **Send To...** tab in the lower-right corner, then click the desired destination. The data is sent to the selected location.



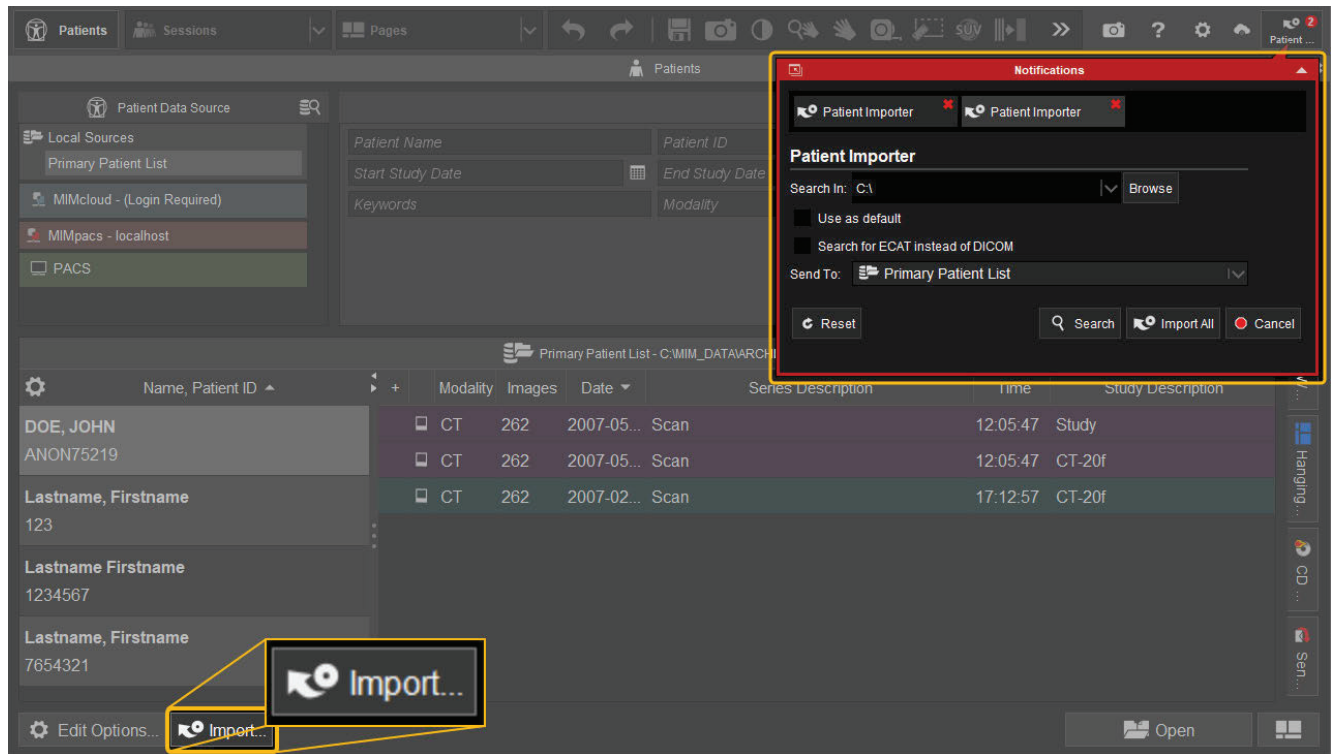
**Tip:** The **This Workstation** destination sends data to the MIMpacs patient list set up in Settings  >> **Network Services** >> **DICOM Store**.

To open the data, go to the patient list that you sent the data to. Follow the steps in [Find and Open Data](#) above.

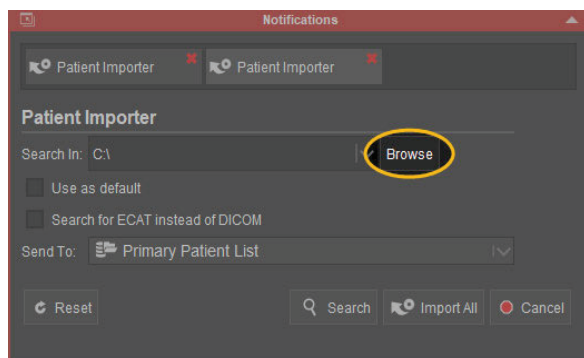
## Import Data from a Local File, Folder, or CD

To import data from a local file, folder, or CD into a MIM patient list, follow these steps:

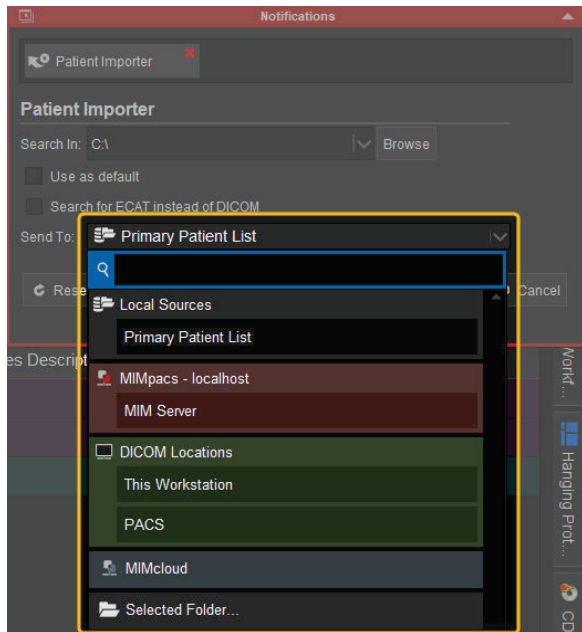
1. Click the **Import...** button in the lower-left corner. A Notifications window appears.



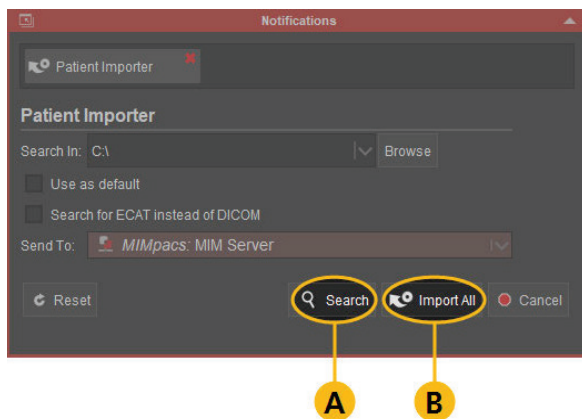
2. Click the **Browse** button in the Notifications window to find the filepath or drive where data is stored.



3. Choose a **Send To** location in the Notifications window dropdown.



4. Click **Search** or **Import All**:



- To select only some of the data to import, click the **Search** button.
  - In the **Patient Search** window that appears, check the individual series that you want to send to a MIM patient list.
  - Click the **Import** button in the lower-right corner of the window.
- To import all of the data from the filepath or drive that you browsed to, click the **Import All...** button.

To open the data, go to the patient list that you imported the data into. Follow the steps in [Find and Open Data](#) above.

# Search Quickly with Saved Searches

MIMTD-619 • 12 Sep 2023

## Overview

Saved searches let you find patient data in one click. Use MIM®'s default saved searches, or add your own.

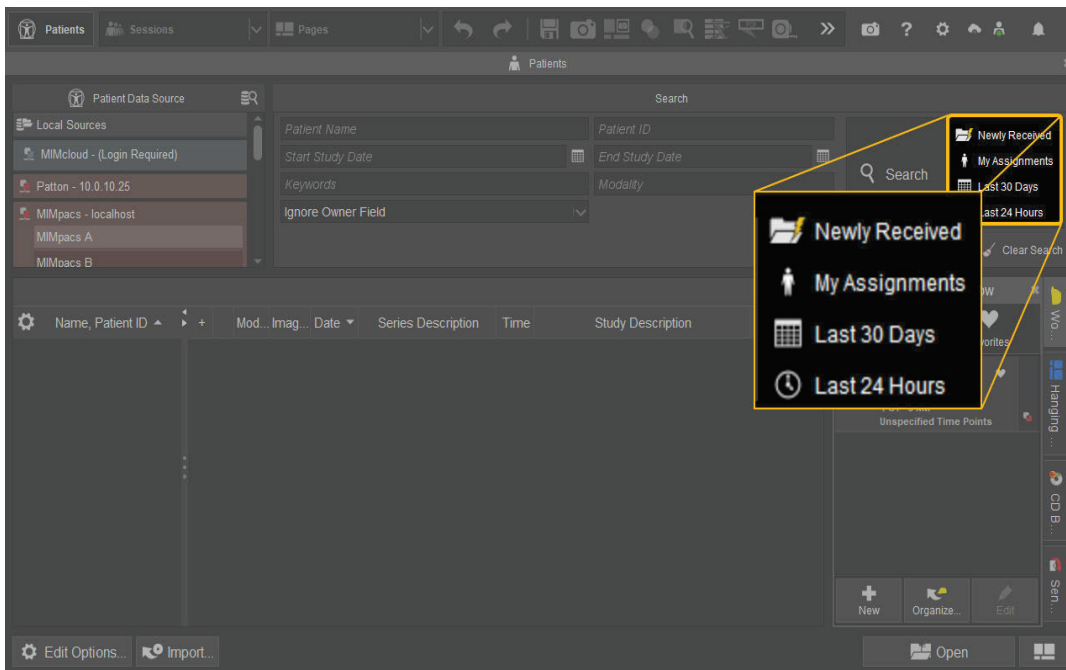
## Contents

- [Use MIM's Default Saved Searches](#)
  - [Default Saved Searches](#)
  - [Default Radiology and Nuclear Medicine Saved Searches](#)
  - [Enable or Restore Default Searches](#)
- [Save Your Frequently Used Searches](#)
  - [Indicate Exact Matches](#)
  - [Search with Relative Date Ranges](#)
  - [Search for Today's Series](#)

## Use MIM's Default Saved Searches

Click one of the default saved search buttons to find data that match pre-set parameters.





## Default Saved Searches

- **Newly Received** — Find the most recent 100 series based on the MIMDateAdded tag.
- **My Assignments** — Find series that are owned by the logged-in user. This button only appears if user logins are enabled and you are searching a MIMpacs™ patient list.
- **Last 30 Days** — Find series that have a StudyDate DICOM tag within the last 30 days.
- **Last 24 Hours** — Find series that have a StudyDate DICOM tag of today or yesterday. For more information, see [Search for Today's Series](#).

## Default Radiology and Nuclear Medicine Saved Searches

- **Today's PET/CTs** — Find PET/CTs with today's date, and associated priors.
- **Today's NMs (SPECT/CT)** — Find NMs with today's date, and any SPECT/CTs with today's date that are also available.
- **Today's NMs** — Find only NMs with today's date.
- **Today's NM Sessions** — Find NM sessions that were created today.


## Enable or Restore Default Searches



**Important:** Changing the default radiology and nuclear medicine saved searches is not recommended because clicking the **Restore Radiology and Nuclear Medicine Searches** or **Restore Default Searches** button undoes any changes that you made. Please add new saved searches instead. For instructions, see [Save Your Frequently Used Searches](#).



**Tip:** If you want to share and standardize these settings across your institution, a MIM administrative user should make these additions or updates while logged into the **Edit Site Defaults** login mode. See [Update Default Settings for Users](#) for prerequisites and instructions.

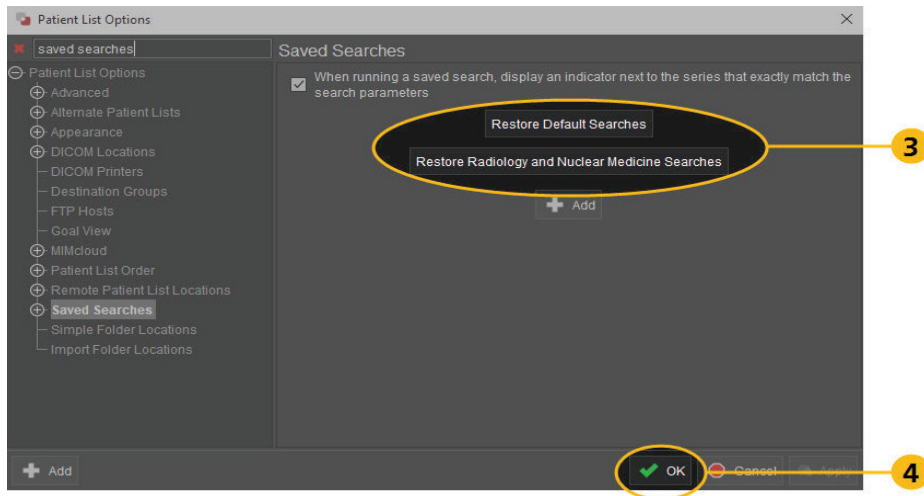
1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **Patient List Options** and search for "**saved searches**". Select **Saved Searches** on the left side.
3. Enable or restore default searches.
  - *If you need to enable Radiology and Nuclear Medicine Searches, click **Restore Radiology and Nuclear Medicine Searches**.*



**Important:** If the Radiology and Nuclear Medicine Searches are already enabled, clicking this button undoes all previous edits to these search parameters.

- *If you need to restore Radiology and Nuclear Medicine Searches, click **Restore Radiology and Nuclear Medicine Searches**.*
- *If you need to restore Default Searches, click **Restore Default Searches**.*

- Click **OK** in the lower-right corner. Radiology and nuclear medicine saved search buttons now appear in the upper-right corner of the patient list.



## Save Your Frequently Used Searches



**Tip:** If you want to share and standardize these settings across your institution, a MIM administrative user should make these additions or updates while logged into the **Edit Site Defaults** login mode. See [Update Default Settings for Users](#) for prerequisites and instructions.

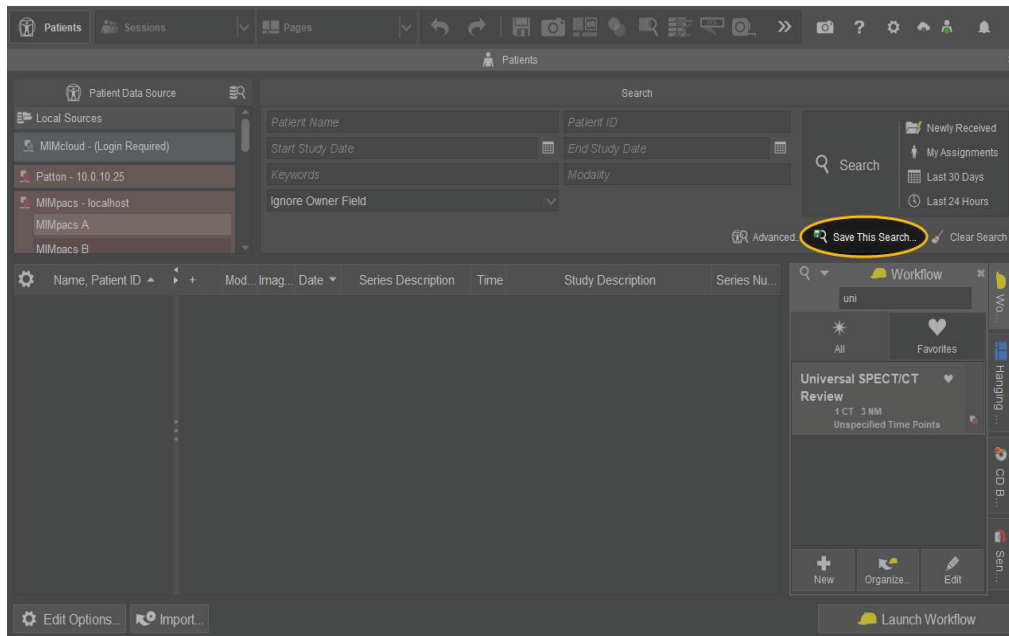
To save frequently used searches:

- In the patient list, enter the search parameters that you want to save.



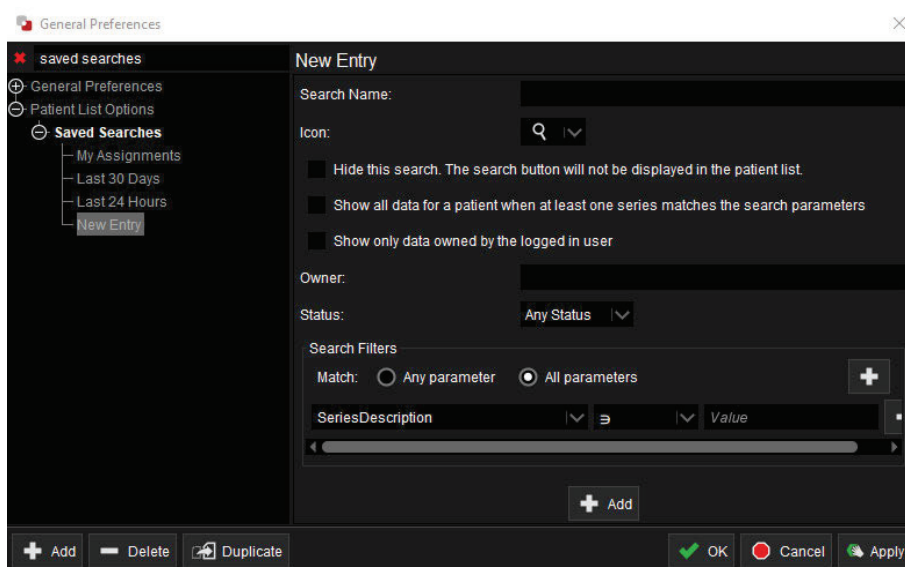
**Related:** For detailed instructions on searching for patient data, see [Find and Open Patient Data](#).

- Click the **Save This Search...** button below the **Search** button.



A settings window appears.

- Review and adjust the settings for the saved search as necessary.



- **Search Name** — Enter the name that will appear on the button for this saved search.
- **Icon** — Select the icon that will appear on the button for this saved search.
- **Hide this search. The search button will not be displayed in the patient list.** — Select this option to prevent the saved search from appearing in the patient list. This is useful if you are working on a search that is not yet ready for other users.

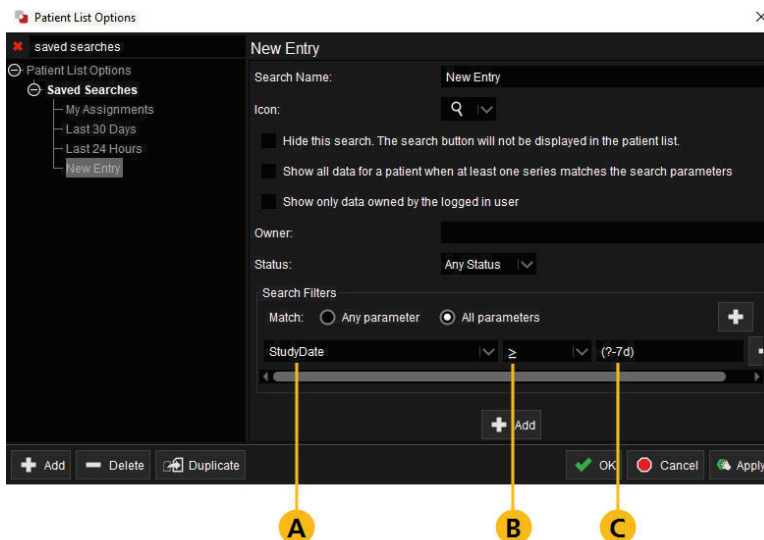
- **Show all data for a patient when at least one series matches the search parameters** — Select this option to show all of the patient's series in the results, even if some of the series do not match the search parameters.

- This setting automates the right-click **Search for This Patient** option that you may be familiar with.



**Related:** For more information, see [Find and Open Patient Data](#).

- For instructions on enabling an indicator next to the results that are exact matches, see [Indicate Exact Matches](#).
- **Show only data owned by the logged in user** — Select this option to only show results that are owned by the logged in user.
  - When this option is selected, the **Owner** field below it is disabled.
  - If user logins are not enabled in MIM, saved searches that have this option selected are disabled and do not appear in the search field.
- **Owner** — Enter a username to search by an owner that is not the logged in user. User logins must be enabled to use this feature.
- **Status** — Select an option to find series that have a specific status.
- **Search Filters** — Add DICOM-tag based filters using the **+** button. Choose whether to match **Any parameter** or **All parameters**. This selection only affects whether the search matches any or all of the DICOM tag search filters; any search parameters configured above this section are always applied.




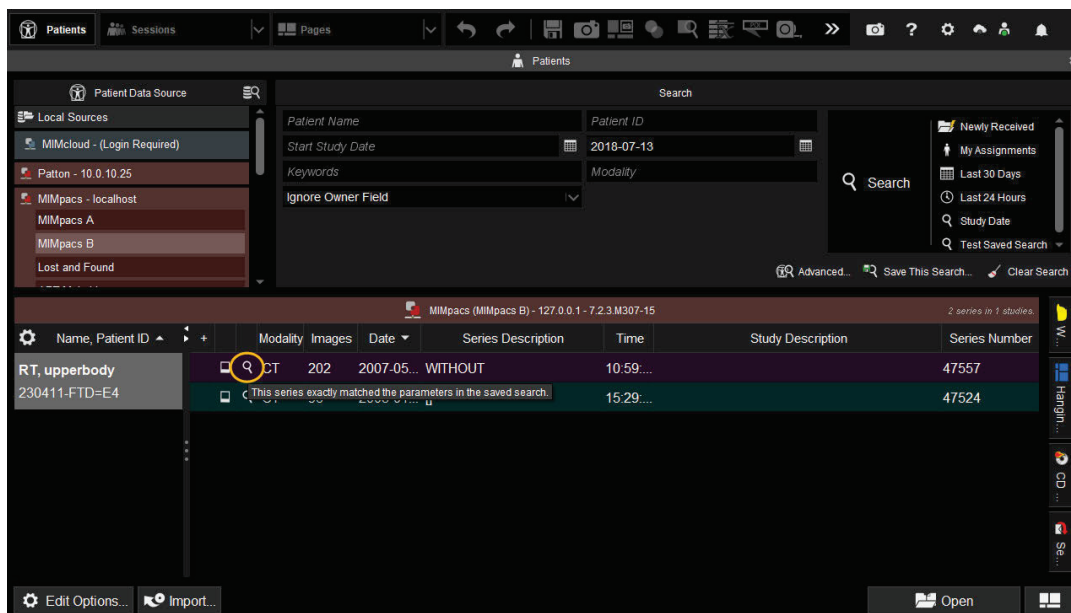
- Select a DICOM tag (e.g., StudyDate) for the filter that you added. Scroll through the dropdown menu to see common tags, or start typing to find other tags.
- Select an operator (e.g.,  $\geq$ ). To see an explanation of what the operator does, select the operator and hover your cursor over the field.
- Enter a value (e.g., (?-7d)). For more information on the date format used in this example, see [Search with Relative Date Ranges](#).

## Indicate Exact Matches

When saved searches are set up to show all data for a patient, you may still want to see which results match the search parameters exactly.

To display an indicator next to exact matches:

- Click the Settings  button in the upper-right corner of MIM.
- Go to **Patient List Options** and search for "**saved searches**". Select **Saved Searches** on the left side.
- Select **When running a saved search, display an indicator next to the series that exactly match the search parameters**.
- Click **OK** in the lower-right corner. An indicator now appears next to exact matches.



For more information on setting up saved searches to show all data for a patient, see [Save Your Frequently Used Searches](#).

## Search with Relative Date Ranges

Relative date ranges let you set up saved searches that do not need to be updated in the future. For example, your search can find studies that are older than the current date instead of studies that are older than the absolute date of 1 January 2021.

To configure relative date ranges in search filter fields:

1. Enter a question mark (?) as the variable that stands for "today."
2. Enter a plus (+) or minus (-) sign to offset the time from today.
  - Plus (+) — After today.
  - Minus (-) — Before today.
3. Enter an integer followed by a single character ("d" for days, "m" for months, or "y" for years) to indicate the amount of offset.
4. Place parentheses around the entire text.

### Examples:

- |        |   |
|--------|---|
| (?-5d) | Five days before today.                               |
| (?-6m) | Six months before today.                              |
| ?-2d   | This example is invalid because it lacks parentheses. |

## Search for Today's Series

MIM's default **Last 24 Hours** saved search finds series with a StudyDate of today or yesterday. It uses two search filters: StudyDate  $\geq$  (?-1d) and StudyDate  $\geq$  (?-0d)

If you would like to find only series with a StudyDate of today, set up a saved search that uses one filter: StudyDate  $\geq$  (?-0d).

For more information on relative date ranges, see [Search with Relative Date Ranges](#).

# Save Patient Data

MIMTD-1261 • 19 Dec 2023



## Overview

MIM® has several options for saving images and associated data. To keep your work organized, the default save destination is the same location the data was opened from. This can be adjusted when saving the data.

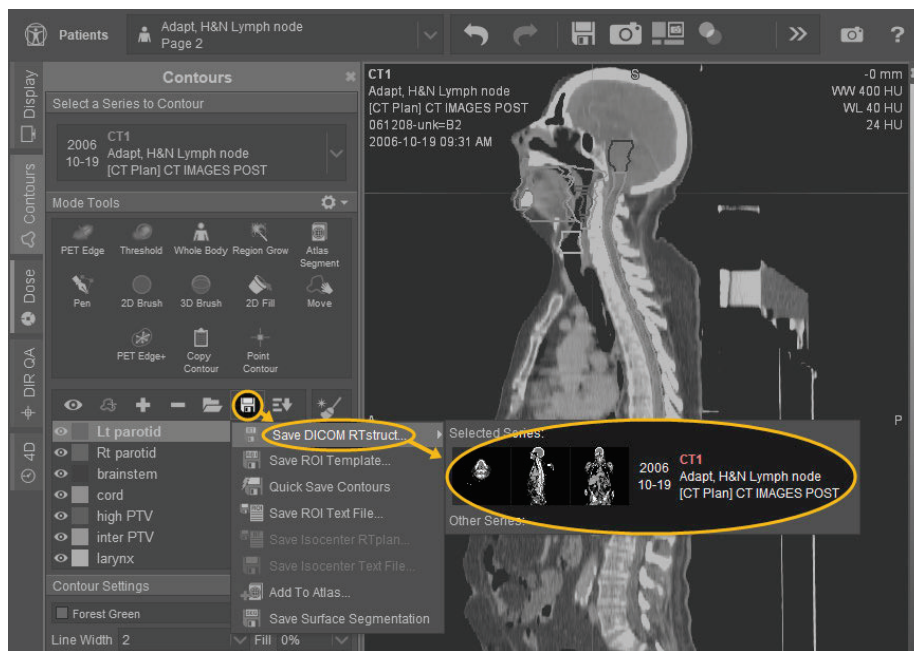
## Contents

Type	Compatibility
<a href="#">Contours</a>	All
<a href="#">Findings</a>	MIM only
<a href="#">Fusions</a>	See below
<a href="#">Images</a>	All
<a href="#">Secondary Captures</a>	All
<a href="#">Sessions</a>	MIM only

## Save Contours

1. Click the save  button above the list of contour names in the Contours sidebar. Or, you can click the save  button in the top toolbar.
2. Select the **Save DICOM RTstruct...** and select the series that you want the contours to be associated with. This saves contours as an RTstruct file that you can access from the patient list or send to third-party DICOM systems, such as PACS.






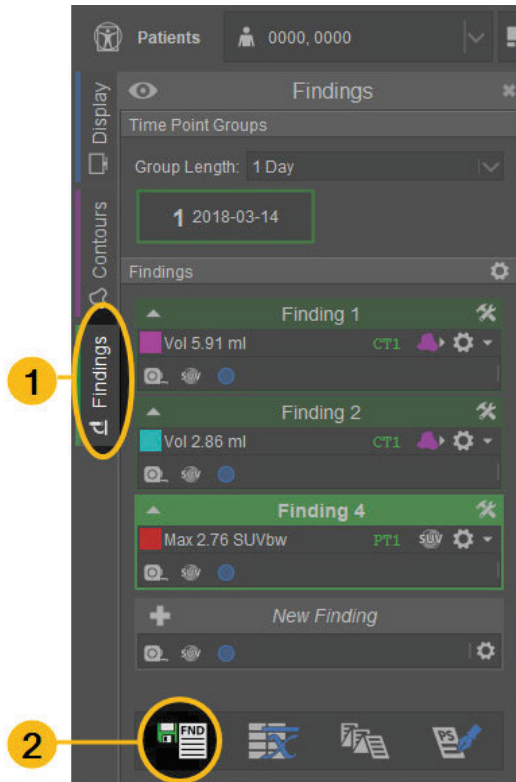
3. In the Notifications window, specify the desired destination and options.
4. Click **OK**.



**Related:** Refer to [Save Contours](#) for more information about saving contours and alternative saving methods.



## Save Findings

1. Select the Findings sidebar.
2. Click the save findings  button at the bottom of the Findings sidebar.



3. In the Notifications window, specify the desired destination and options.
4. Click **OK**.


## Save Fusions

1. Click the save  button in the main toolbar.
2. Select **Save DICOM Image Data** .
3. Select the fused series you wish to save.
4. Select how to want to save the fusion:
  - **Secondary Capture** — A secondary capture is an image derived from a series. It is DICOM type OT and does not include voxel data and typically cannot be processed. It is like a screenshot of each slice.
  - **Registration** — This option saves the registration file between the two images. The images themselves are not saved.



- **Aligned Secondary** — An aligned secondary image is the secondary image as it was altered to align to the primary image. Send an aligned secondary to your treatment planning system to fuse it to the primary and recreate the fusion as it is shown in MIM.

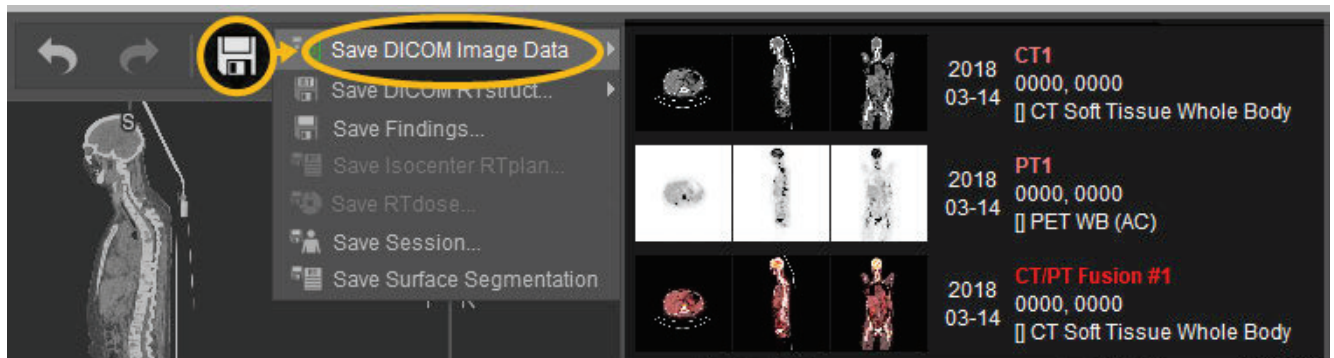
5. In the Notifications window, specify the desired destination and options.
6. Click **OK**.



**Tip:** You can set which series in the fusion the capture is associated with. By default, the capture is associated with the primary series. Go to Settings  >> **General Preferences** >> **Viewing** >> **Capture** >> **DICOM Captures** and adjust the **Default Save Capture Association (for Fusion Captures)** setting if needed.

## Save Images

1. Click the save  button in the main toolbar.
2. Select **Save DICOM Image Data** .
3. Select the series you wish to save. If the series you wish to save is a fusion, see [Save Fusions](#).



4. Specify the desired destination and options.
5. Click **OK**.

## Save Sessions

When you load any patient data, it opens into a MIM session. When you save a session, MIM retains exactly where you are and what you've done. This includes images, fusions, contours, doses, findings, annotations, and more.

When you or another user re-opens the session, everything is exactly as you left it. Think of it as a bookmark or a pause button in your work.





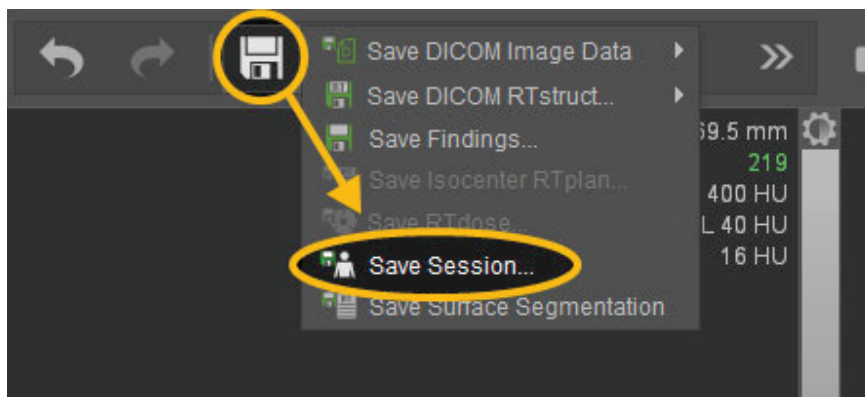
**Related:** Refer to [View and Process Data in MIM® Sessions](#) for more information about working with sessions.

Take note of the following:

- Sessions cannot be opened by third-party systems.
- Sessions are not backwards compatible (e.g., a session saved in MIM 7.2 may not open in MIM 7.1). It is recommended that all workstations use the same version of MIM.
- If a session contains patient data that is subsequently deleted from MIM, that session will no longer open since the referenced data no longer exists.
- Sessions do not overwrite one another. It is recommended that you save each session with a unique name.

To save a session:

1. Click the save  button in the toolbar at the top of MIM.
2. Select  **Save Session...**
3. In the Notifications window, specify the desired destination and options.



4. Click **OK**.


## Save Secondary Captures

You can save secondary captures from the Capture Gallery.



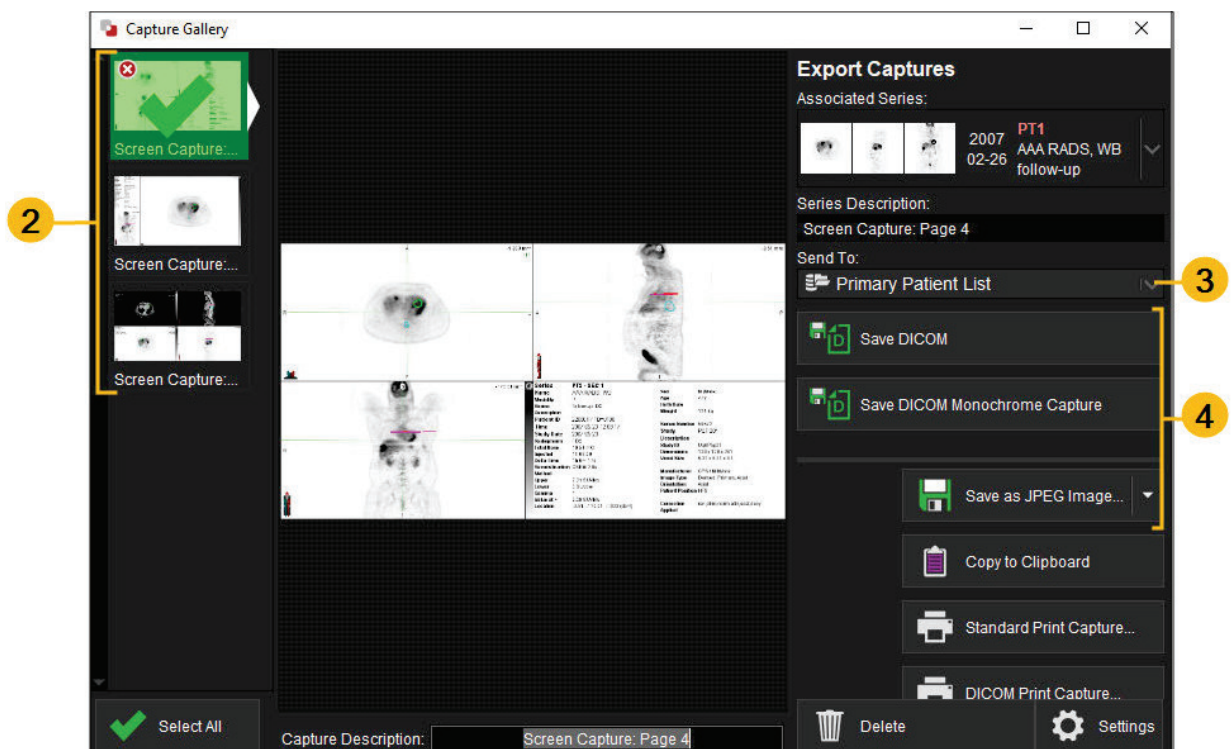
**Related:** Refer to [Create and Save Secondary Captures](#) for more information about working with secondary captures.

To save a secondary capture:

1. Open the **Capture Gallery**  from the upper-right corner of MIM.
2. On the left side of the Capture Gallery, select the captures that you want to save or click **Select All**.
3. On the right side of the Capture Gallery, select the Send To destination where you want to save the capture. You can select a MIM patient list, third-party DICOM location, CD, or folder.
4. Select the file type based on where you are saving:
  - **Save DICOM** — Save to MIM or to a third-party system that accepts DICOM.
  - **Save DICOM Monochrome Capture** — Save to a third-party system that accepts DICOM and allow the window/level to be adjusted after being sent to the other system.
  - **Save as JPEG Image** — Save an image file to a folder or a location that does not support DICOM. Use the dropdown arrow to choose between file formats.



**Tip:** If you need to copy the image to your clipboard or print the image instead of saving, select the applicable option.



5. If desired, update the **Capture Description**, which becomes the series description of the OT file when saving DICOM.



**Tip:** Click **Settings** in the lower-right corner to update save options. Refer to [Configure Default Settings for Faster Captures](#) for more information about configuring default save settings.

## Export Data from MIM®

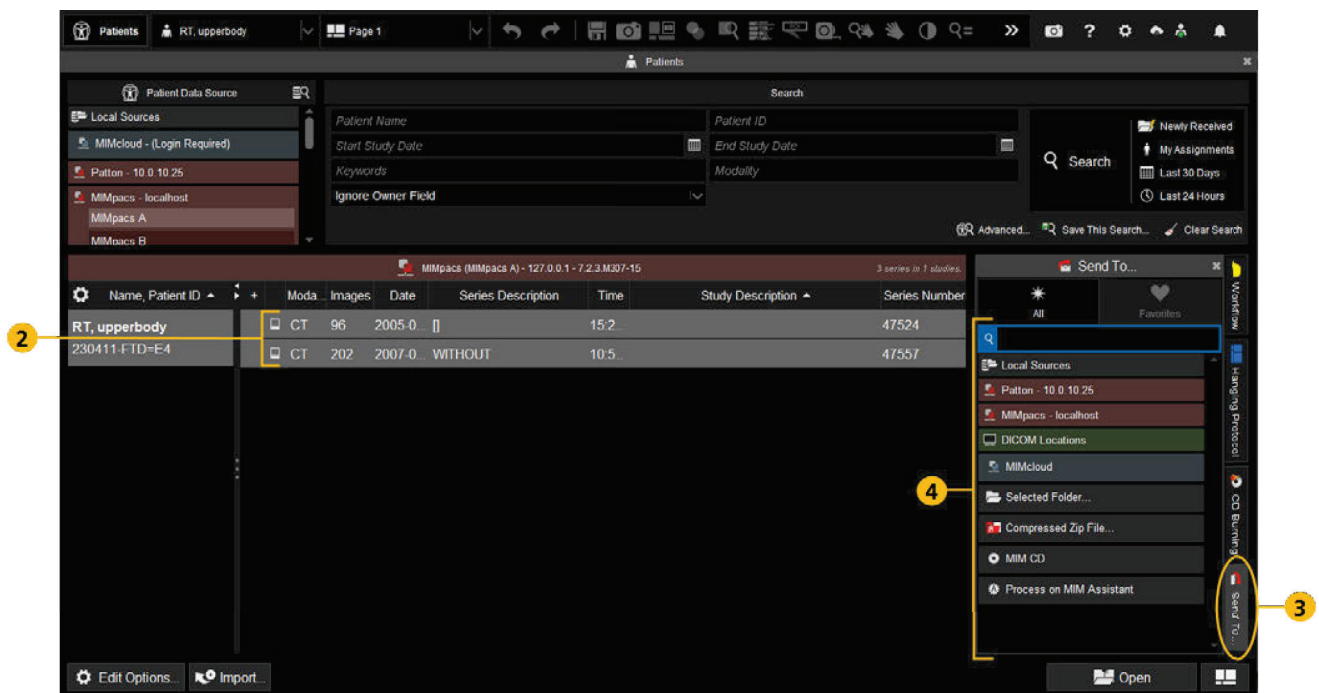
MIMTD-613 • 19 Jul 2023

### Overview

You can export data to a third-party location, burn data to a disc, send data to a folder, or create a zipped file.

### Export Data

1. Search for the patient data you want to export
2. Select the patient on the left and then select individual series from the center of the screen.
3. Open the **Send To...** tab on the right side of the screen.
4. Click on the desired destination. *In MIM 7.4 and later*, you can search for a specific export destination using the search bar at the top of the Destinations section. *In MIM 7.3 and earlier*, this functionality is not available.



- If you're sending to a local patient list, MIMpacs list, or PACS, click the destination to send the data.



# MIM Encore® User Guide

- If you're sending data to a **MIMcloud®** location, follow the prompts in the Notifications window.
- If you're sending data to a **MIM CD**, the **CD Burning** tab opens. Choose the desired options in the CD Burning tab and then click **Burn CD...** Additionally, you can use the MIM CD option to send to a folder instead of a CD, similar to using the Selected Folder... option. The MIM CD option also lets you include a DICOM viewer with the exported data.




**Related:** See [Burn Discs from MIM®](#) for more information.

- If you're sending data to a **Selected Folder...**, browse to the desired file location.
- If you're sending data to a **Compressed Zip File...**, browse to the desired file location.

When DICOM data is exported from MIM to a folder, an initial folder is created and named with the month and year of the study (i.e., 2022-12\_Studies). When the initial folder is opened, there are sub-folders with names that contain the patient name, patient ID number, modality, date of scan, time of scan, study description, series description, and number of slices in the scan. The individual DCM files are contained within these sub-folders. It is not possible to configure the file structure for DICOM exported from MIM.



**Tip:** You can favorite a destination so that it moves to the top of the list by clicking the  next to each destination name.



# Burn Discs from MIM®

MIMTD-1121 • 09 Aug 2023


## Overview

You can export series from MIM to a CD/DVD, file location, or folder location. When burning to a disc, you can choose to include a copy of MIM CD along with the data. Use this option if you are giving the disc to a patient or to another party that does not have a DICOM viewer.



**Related:** Refer to [Troubleshoot Burning Data to Discs](#) if you encounter an error or are unable to complete the steps below to successfully burn a disc.

## Prerequisites

- Data that exists on a local or MIMpacs™ patient list. If you want to burn data from MIMcloud® or a third-party PACS, first send the data to a local or MIMpacs patient list.
- A CD-R, DVD-R, or DVD+R disc. (CD-RW, DVD-RW, and DVD+RW disc types are not supported.)
- The correct drive letter entered in your MIM preferences. Go to Settings  >> **General Preferences** and search for "**CD burning**". Check the configured **Drive Letter**.

## Burn a Disc from MIM

To burn a CD/DVD from MIM, follow these steps:

1. Search for and select the data you would like to burn from a local or MIMpacs patient list. See [Find and Open Patient Data](#) for more information.

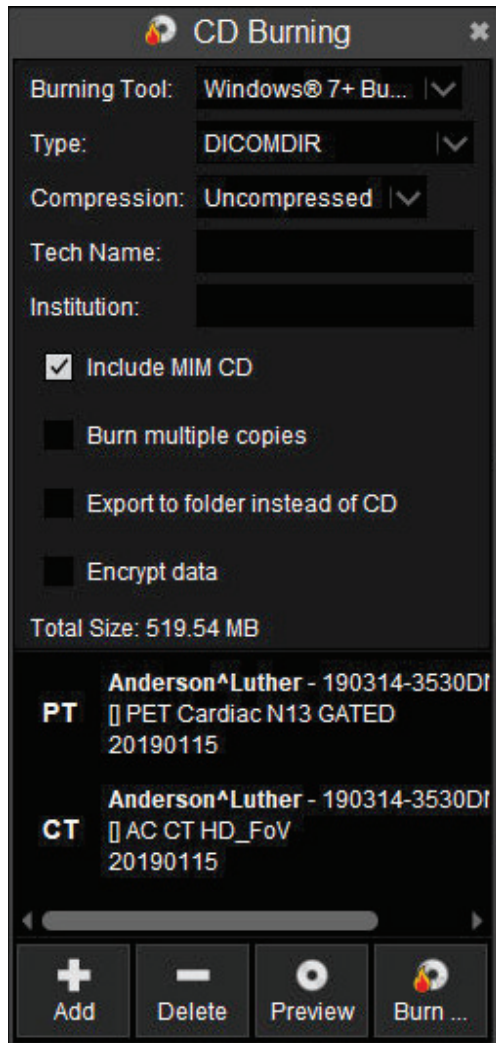


**Tip:** If you want to burn data from multiple patients or studies, or different searches, you can add data at a later step below.

2. Go to the **CD Burning** tab on the right side of the screen.



3. Click **Add** to add the data that you selected to list of data to be burned.



4. In most cases, keep the default **Burning Tool**, **Type**, and **Compression** settings. You may need to update these settings if burning initially fails or if the receiving system has specific needs. See [Troubleshoot Burning Data to Discs](#) for more information.
5. Enter a **Tech Name** and **Institution**.
6. Select **Include MIM CD** to include a DICOM viewer on the burned disc. If the receiving institution already has a way to view the DICOM, do not select **Include MIM CD**.
7. If you want to burn multiple discs that contain the same data, select **Burn multiple copies**. After the first disc is burned, MIM will prompt you to burn another copy.
8. Select **Encrypt data** if you want to encrypt the data. With this option, MIM will prompt you to configure a password when you burn the disc. You need to provide that password to the recipient so that they can access the data.




9. If there are additional series that you want to include, select them and then click the **Add** button. You can also **Delete** series from the list of series to be burned.
10. *If you want to burn a disc:*
  - i. Insert a CD-R, DVD-R, or DVD+R into the disc drive.
  - ii. Click **Burn...**

*If you want to send the data to a folder or file location:*

- i. Check **Export to folder instead of CD**.
- ii. Click **Export...** and browse to the desired destination.



**Tip:** If you frequently burn discs, you can favorite **MIM CD** as a destination by clicking the  next to it. This moves it to the top of the list alongside other favorite destinations.

View Data

# View and Process Data in MIM® Sessions

MIMTD-605 • 09 Nov 2023

## Overview

MIM opens patient data into a workspace called a **session**.

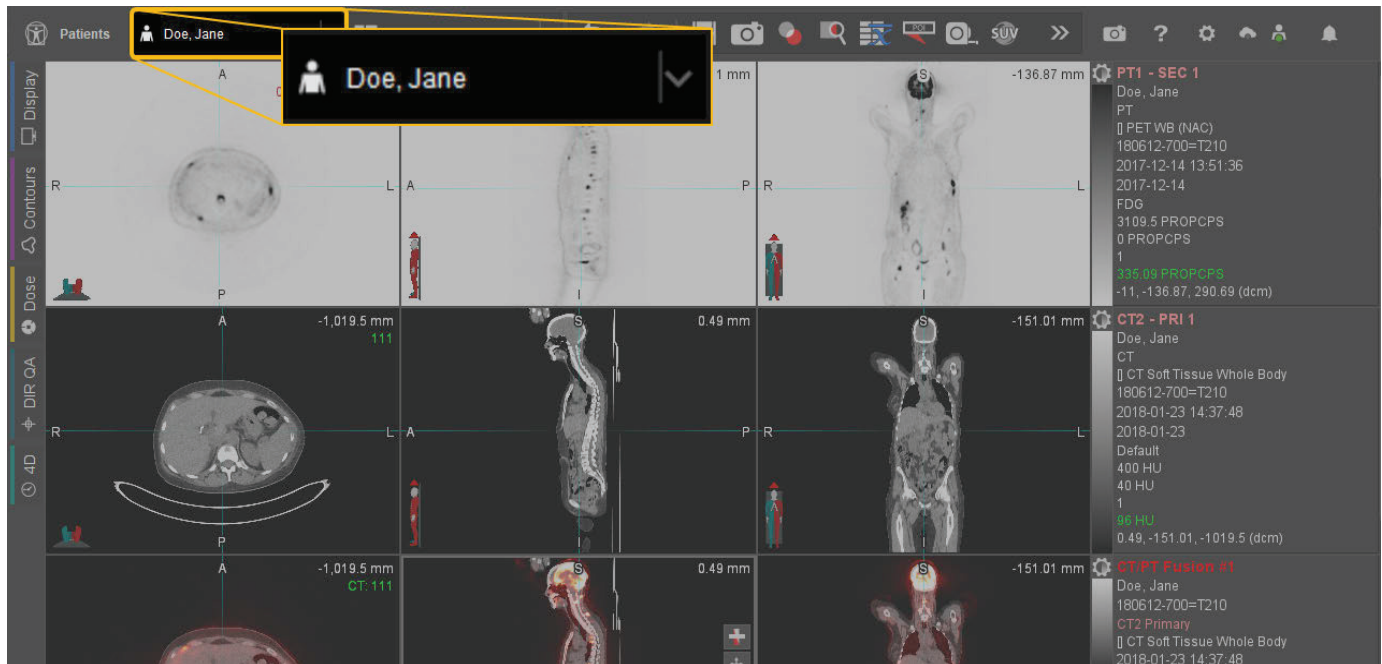
- You can open multiple sessions at once to keep your work separated and organized.
- You can save sessions. Saving a session preserves your work, including all images, displays, and registrations. When you save a session, it can be reopened at any time.

## Contents

- [Session Basics](#)
- [Pages](#)
  - [Rename a Page](#)
  - [Close a Page](#)
- [Session Tools](#)
- [Rename a Series in a Session](#)

## Session Basics

When patient data is open in a session, the patient name is displayed in the session dropdown menu. This menu is located in the upper-left corner of MIM.

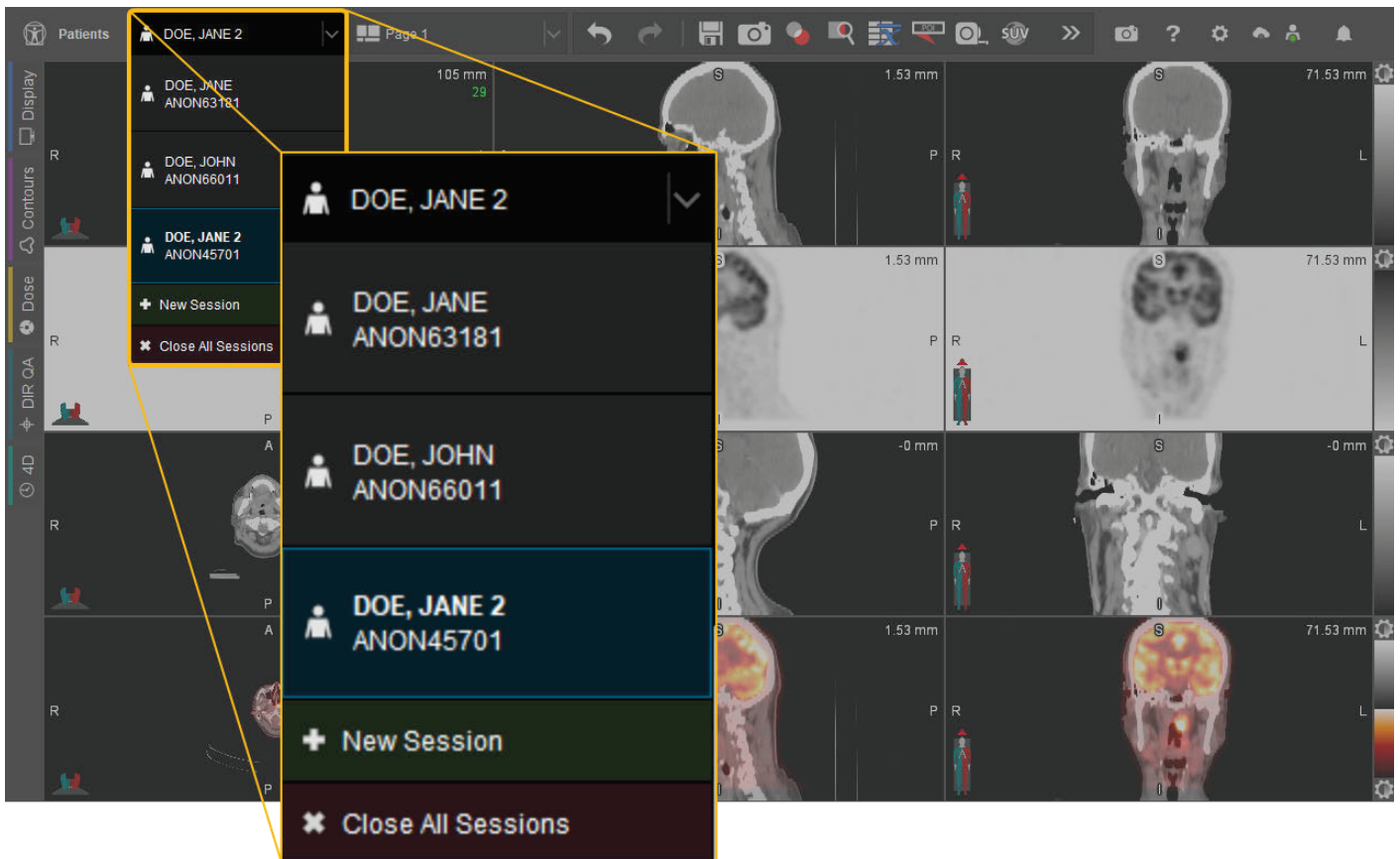


**Important:** *MIM 7.3 and later:* There is a separate pages dropdown menu to the right of the session dropdown menu. *MIM 7.2 and earlier:* The session dropdown menu also contains information about the pages in the session.

For more information, see [Pages](#) below.

Use the dropdown menu to:

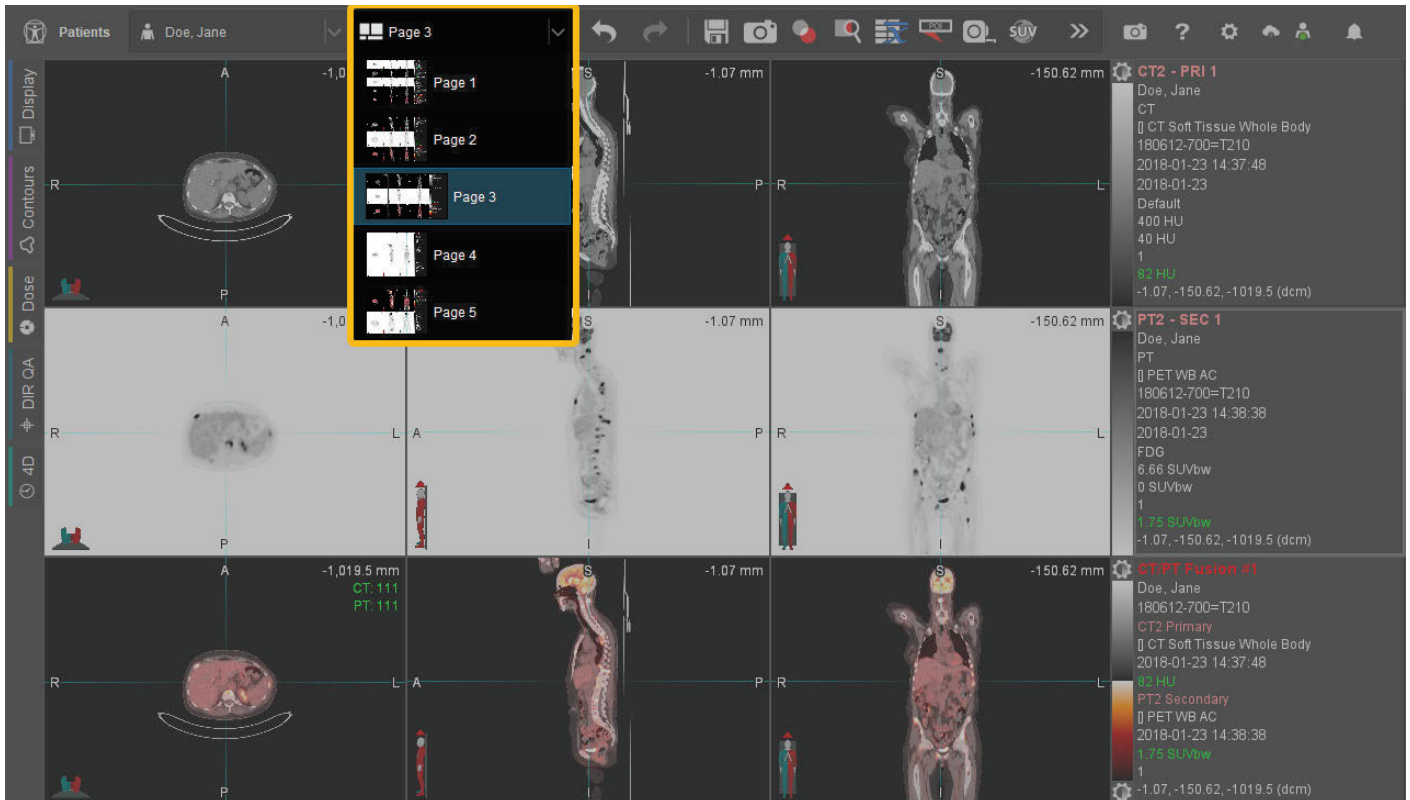
- Switch from one session to another — Select the session you would like to switch to.
- Start a new session — Click **New Session**. You are returned to the patient list. Select and open data to start a new session.
- Close a session — Hover the mouse over the session name and click the **✕** button. Or, click **Close All Sessions** to close all sessions.




## Pages

Each session can have multiple pages. Pages display images, and sometimes tables or graphs of additional information. Move from page to page using the left and right arrow keys.


To see a list of all pages and switch to any page, click the dropdown menu in the upper-left corner of MIM.



## Rename a Page

1. Open the dropdown in the upper-left corner of MIM and hover over the page you want to rename.
2. Click the  button to rename the page. The Notifications window opens.
3. Enter a name for the page in the **Page name** field.
4. Click the **OK** button.

## Close a Page

1. Open the dropdown menu in the upper-left corner of MIM and hover over the page you want to close.
2. Click the  button for the page.

## Session Tools

After patient data is open in a session, use the following options to adjust the view, process the data, and more:



- **MIM toolbar** — The toolbar is found near the top of MIM. It can be configured to include the tools you use most. See [Access Tools: The Toolbar and the Radial Menu](#).
- **Radial menu** — Right-click to access the radial menu. Configure the tools found in your radial menu by going to Settings ⚙ >> **General Preferences** and searching for "radial menu". See [Access Tools: The Toolbar and the Radial Menu](#) for more information.
- **Sidebars** — The sidebars you see on the left side of MIM depend on your license. Each sidebar contains various processing options.
- **Keyboard shortcuts** — Keyboard shortcuts can be mapped to many of MIM's tools and let you navigate sessions more quickly. See [Set Keyboard Shortcuts](#) for more information.
- **Workflows** — You can launch a workflow after patient data is already open in a session, just like you would from the patient list. Use the ▶▶ button in the upper-right corner of MIM and search for the **Launch Workflow** tool.

## Rename a Series in a Session

When you rename a series in a session, the name is displayed in the upper-left corner of each viewport the series appears in. Assigning names is often easier than trying to differentiate series based on their default names (CT1, CT2, PT1, etc.). Applying a name in this way does not change the series description or any other metadata. The name only serves as a label in the session.





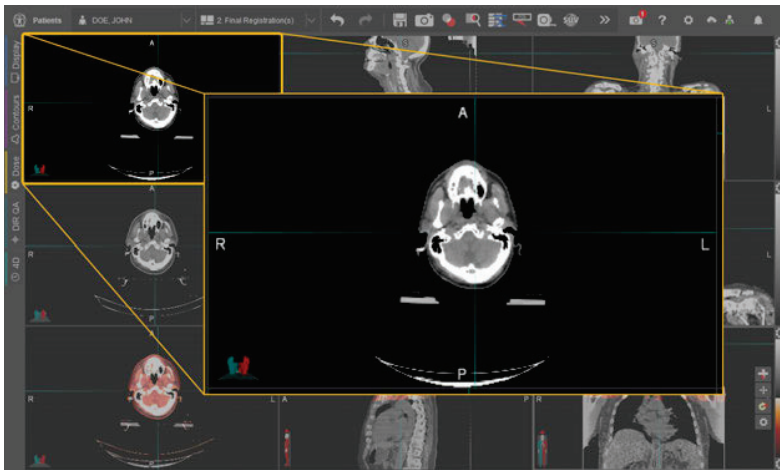
1. With images open in a session, click the **Display** tab to expand the Display sidebar.
2. In the lower half of the Display sidebar, click the arrow button next to the series you want to rename.
3. Select **Set Series Name**. The Notifications window opens.
4. Enter a name for the series, then click **OK**.

# Work with Onscreen Information and Tools in MIM® Viewports

MIMTD-1592 • 06 Nov 2023

## Overview

Each rectangular section of the MIM display is called a viewport. In addition to displaying images, viewports display patient and study information, provide options for adjusting viewing conditions, and display additional functionality for some MIM tools.



A viewport is considered active when your cursor is hovering in it or when the cursor was in it most recently. The active viewport has a slightly thicker border than other viewports.



**Tip:** Move your cursor back and forth between viewports to see how the border of the active viewport changes.

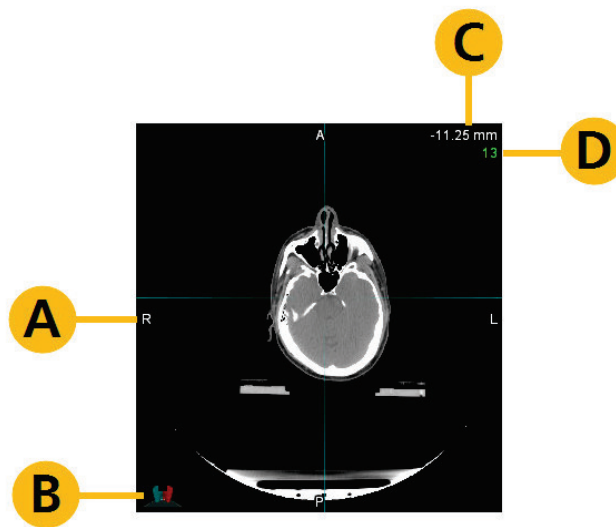
## Contents

- [Default Viewport Information](#)
- [Information Displayed When the Info Panel Is Not in Use](#)
- [Hide Viewport Info](#)
- [Choose What Information Is Shown in Viewports](#)
- [Adjust Contrast and Color Tables in the Viewport](#)

- [Tool Menus in Viewports](#)
- [Dynamic Series Controls in Viewports](#)

## Default Viewport Information

The information in the viewport varies based on your configured preferences, the type of image you are viewing, and whether or not a separate information panel is part of your display. At a minimum, you typically see the following:



- A. **Orientation Label** — Orientation labels indicate the patient's anterior, posterior, superior, inferior, left, and right.



**Related:** You may occasionally receive series that are labeled incorrectly. MIM provides tools that you can use to correct the orientation and labeling of a series. See [Correct Patient Orientation](#) for more information.

- B. **Orientation Man** — The orientation man is an illustration that assists with determining patient position.

- The figure has an **A** on its anterior and a **P** on its posterior.
- The table in the illustration shows whether the patient was prone or supine.
- An arrow at the figure's head or feet shows the direction the patient entered the scanner.



- C. **DICOM Position** — This is the DICOM position of the slice, as indicated in the Image Position (Patient) DICOM tag.



- D. **Slice Number** (In acquisition plane only) — MIM displays the slice number in the acquisition plane. This number comes from the Instance Number (0020, 0013) DICOM tag.
- When the slice number is shown in green, it means you are looking at an actual slice of the image as it was acquired.
  - When the slice number is shown in red, it means you are not localized directly in the "center" of a slice and some interpolation is occurring.
    - It is common to get into this state by localizing to a point in a reconstructed plane.
    - When you resume scrolling in the acquisition plane, MIM once again displays the actually acquired slices.
  - If an image is the secondary in a fusion, the slice number is replaced by its current rotation metrics.



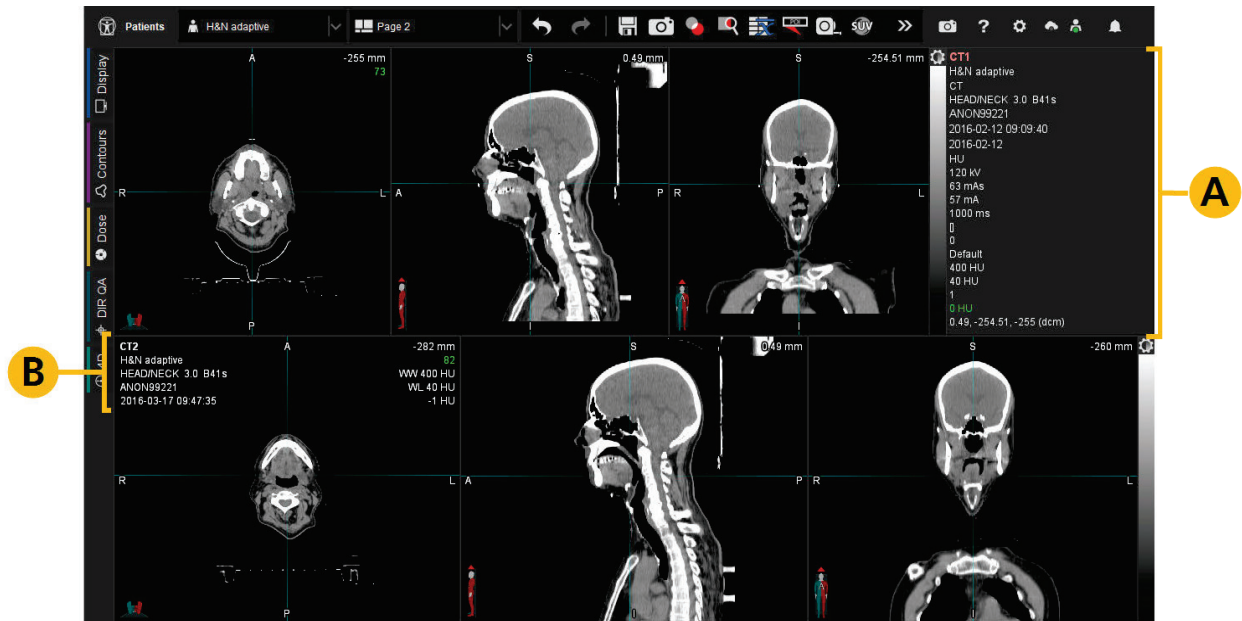
**Tip:** To see expanded series information in any viewport, press the space bar. The series information will be displayed over the image. Press the space bar again to hide this information.

The information shown in this view is adjustable via a JSON file. If you would like to change the information shown in this view, please contact MIM Software Support at [support.mimsoftware.com](https://support.mimsoftware.com).

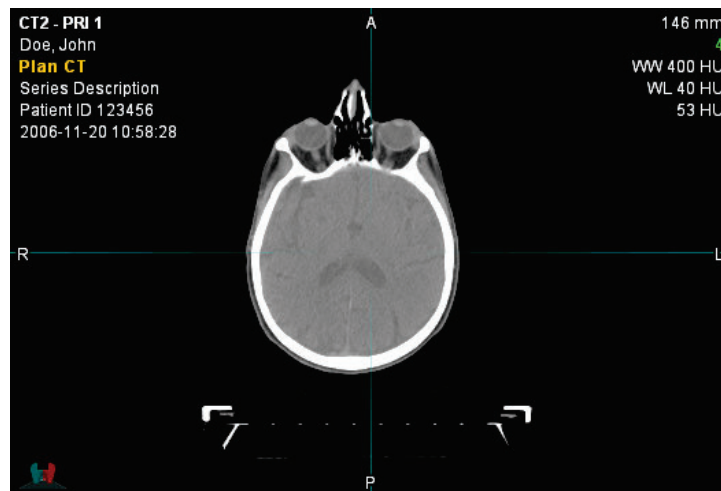
## Information Displayed When the Info Panel Is Not in Use

The info panel is a special viewport that appears on the right side of the screen when you open a series in MIM. The info panel displays detailed information from the series DICOM.

You can manually close the info panel. It may also be excluded when you create a new display page or run a workflow. When the info panel is not on the screen, some additional series information appears in the viewport.



In this two row display, the top row shows the info panel (A), which opens by default when you open a series in MIM. In the bottom row, the info panel has been closed. Note the additional information that is added to the top of the axial viewport when the info panel is not on screen (B).



When the info panel is not shown, the following information appears in the leftmost viewport for any series:



## Upper Left

- Identifying information about the series
- Patient name
- Name assigned to the series by the user or workflow (if applicable)
- Patient ID
- Study date & study time (In a fusion the study date and study time are shown for each series.)

## Upper Right

- DICOM location
- Slice number (The slice number appears on the acquisition plane. The acquisition plane is often, but not always, the leftmost viewport of a series.)
- Window width
- Window level
- Voxel value at the localization point (In a fusion the units are shown for the secondary image, which is indicated by the (S) annotation.)

## Hide Viewport Info

- To hide most viewport information, press i on your keyboard.
- The DICOM location and slice number are always visible. If a name has been assigned to a series by a user or workflow, this name is also always visible.



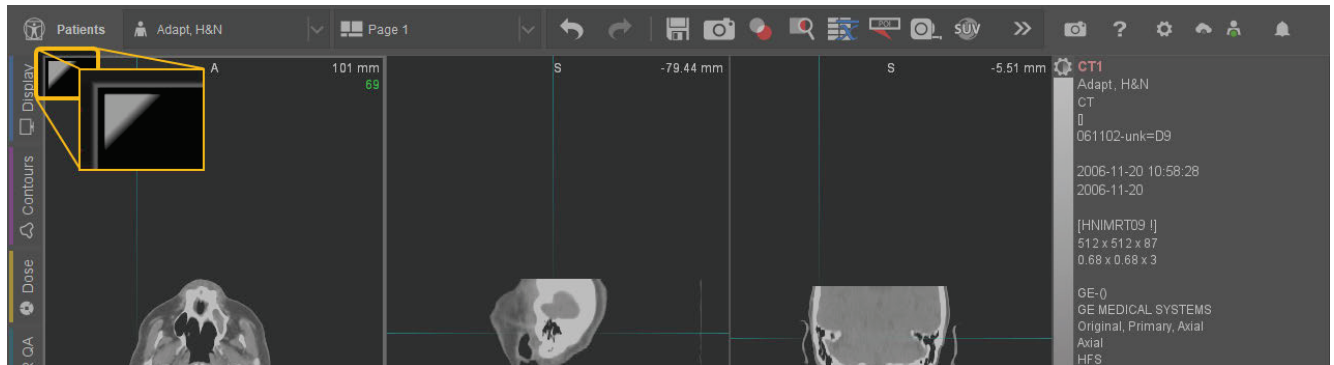
**Related:** See [View and Process Data in MIM® Sessions](#) to learn how to set a series name.

## Choose What Information Is Shown in Viewports

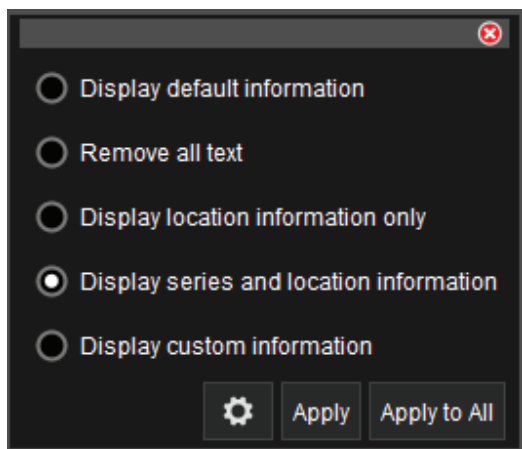
Viewports can be personalized to show any information you would like. Several standard information layouts are available from a menu, and additional information layouts can be created using JSON files. To choose an alternative information layout, follow these steps:

1. *MIM 7.3 and later:* Hover your cursor in the upper-left corner of a viewport until the corner turns gray.

*MIM 7.2 and earlier:* Hover your cursor in the upper-right corner of a viewport until the corner turns gray.




- Click the gray corner of the viewport to open a menu of information layout options.



- Select the information you would like to display.



**Important:** The **Display custom information** option requires a JSON file to define the information layout. If you are interested in this option, please contact MIM Software Support at [support@mimsoftware.com](mailto:support@mimsoftware.com).

- Optional: Click the gear  to adjust colors for the information display.
- If you would like to apply the information layout to only one viewport, click the **Apply** button.

If you would like to apply the information layout to all viewports on the current page, click the **Apply to All** button.

## Adjust Contrast and Color Tables in the Viewport

MIM provides onscreen tools for adjusting color tables and contrast. By default, these tools appear in the rightmost viewport for most image types. For detailed information, please see [Adjust Image Color Tables](#)