3 NM Viewer

Introduction

About the NM Viewer

The NM Viewer is a tool for reviewing and processing images from Nuclear Medicine, including PET, SPECT, planar NM, and other modalities (CT and MR) operating on Philips IntelliSpace Portal. The NM Viewer provides fused viewing of functional PET images, SPECT and anatomical CT or MR images on the IntelliSpace Portal.

Contraindications

The Philips IntelliSpace Portal and the NM Viewer should not be used if any part of the host equipment or system is known (or suspected) to be operating improperly.

Overview

The NM Viewer provides detailed views of PET, CT, MR, planar NM, and SPECT images. It also provides fusion views of images from different modalities, such as PET and CT images, PET and MR images, or SPECT and CT images.

The NM Viewer does the following:

- supports both single- and dual-monitor configurations
- presents series in factory-defined or custom layouts composed of one or more viewers
- allows users to load and evaluate multiple studies from multiple patients
- enables comparison viewing of up to three series from a single study or six series from two studies
- allows users to reformat cardiac and brain studies
- allows users to annotate and measure ROIs on the images
- supports static, dynamic, and gated planar images, PET/SPECT series, PET/SPECT and CT cardiac and pulmonary gated series, and PET dynamic series
- automatically links follow-up PET-CT studies. Once two PET-CT cases (of the same patient) are loaded, the automatic algorithm registers the two datasets and automatically links them.

The viewer displays the following modalities and data types:

	Static	Gated Cardiac	Gated Pulmonary	Dynamic	Raw Tomo	Recon - Tomo / Slices	Fusion
PET		X	X	X		X	X
NM - Planar	X	X		X			

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	Static	Gated Cardiac	Gated Pulmonary	Dynamic	Raw Tomo	Recon - Tomo / Slices	Fusion
NM - SPECT		X			X	X	X
CT		X	X	X		X	X
MR				X		X	X

Opening the NM Viewer

1. From the IntelliSpace Portal Directory window, select one or more patient studies.

   If you select more than one patient, the viewer opens the patient with the most recent study first.

2. Select the appropriate series from the Series tab, or select the appropriate images from the list on the Images tab.

   The most recent series receives priority if you selected more than one series.

3. Select **Review -> NM Viewer**.

   The NM Viewer opens.

NOTICE

You can run only one copy of the NM Viewer at a time. If you try to open a copy of the viewer while the viewer is running, the system notifies you that a review application is already running and it will be closed if you continue.

Reviewing single studies

1. Select a study from the IntelliSpace Portal Directory window. Load one or more series from a single study into the NM Viewer.
2. If you want to load all series in the study, go to step 3.

   If you want to load some of the series contained in the study, select the series from the Directory window **Series** tab.

3. Click **Review** -> **NM Viewer** to open the application.

   The NM Viewer determines which series to show if you open more than one series.

NOTICE

In some cases, a whole body PET may be loaded with an abdomen CT or a portion of a whole body CT. If the extent of the CT axial is less than the extent of the PET series and you want to review PET slices that are beyond the extent of the CT volume, you can pick a point (triangulate) beyond the CT extent to review the rest of the PET slices.

Your series opens in a layout the Viewer determines is appropriate for the data being loaded.

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4. Select an alternate layout, if desired. You can select a different layout from among the Quick Layouts shown on the Control Panel or from the complete list of available layouts on the Control Panel's **Layout** manager.
5. Adjust the series' appearance as needed, including gray levels and/or colors.
6. Scroll through, zoom, and pan images.
7. Triangulate on areas by clicking on the lesion. When you select an area in a volume viewer, such as a MIP display, any linked Transverse, Sagittal, and Coronal viewers automatically display the selected area.
8. Draw ROIs as needed.
9. Use the **Save** or **Save Batch As** options to save a screenshot or series for review, filming, or reporting.

Working with series

Individual viewers can display images of different modalities from the available series. The NM Viewer designates the series as underlay/overlay or as reference/floating. These sets of terms do not directly correspond to one another.

When you display more than one series, the Viewer designates at least one series as the overlay series and at least one series as the underlay series. Overlay and underlay series can be displayed in separate viewers or together in a fusion-enabled viewer. Where applicable, the NM Viewer provides separate controls for each series. See section "The Series Selection panel" on page 130 for more information on identifying the reference series.

For registration, the viewer designates one series as the reference series and all others as floating series. The reference series is the one to which all others are related. You can move the floating series (which are also overlay series) in relation to the reference series. See section "The Registration panel" on page 114 for more information.

Selecting and reviewing pulmonary gated data

Multiple intervals of pulmonary gated data are represented as individual series. To review a complete pulmonary gated study, select all available series to load into the NM Vewer.

If you are loading data from more than one modality in the same study, ensure the data you select matches between both series. The interval series description appears in the Viewer.

NOTICE

If you do not load matching PET and CT series for gated pulmonary data, the displayed PET intervals and CT intervals may not match.

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Reviewing multiple studies

Review old and new studies from the same patient using the multiple studies workflow. The patient's first name, last name, and ID must match for the viewer to identify studies as coming from the same patient.

1. Select two or more studies from the IntelliSpace Portal Directory window.
2. Select the series to be reviewed from the Directory window Series tab.
3. Click **Review** -> **NM Viewer**.
4. Examine the images as in section “Comparing multiple studies from the same patient” on page 121.
5. Select a different study for review. From the Control panel, open the **Series Selection** panel.
6. Highlight the series you want to view next.
7. Click **Launch** to open the selected study in the Viewer.
8. Examine the images as in section “Comparing multiple studies from the same patient” on page 121.

If you want to add series or studies while the NM Viewer is open:

1. Click **Directory**.
2. Select one or more series or studies.
3. Right-click to open the context menu and select **Add to running application**.
4. Click **Yes.**

   The selected series or studies load in the NM Viewer. To view new patients, use the Patient name drop-down list. To view new series for the current patient, select the series using the **Series Selection** controls.

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NM Viewer Display

1	Control and Information tabs - switch between the Control Panel and the DICOM Information Panel.
2	Control Panel - provides the tools to view and manipulate the patient images.
3	Patient Information Banner - displays information about the patient and the study. Click the Patient Information Banner icon to show or hide the banner.
4 	Patient Information Banner Icon - shows or hides the Patient Information Banner.
5	Image Area - displays the images from one or more series using layouts in one or more types of viewers.

Viewers

The NM Viewer displays images using layouts composed of one or more types of viewers. Linked viewers respond together to certain tools.

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Linked viewers

The NM Viewer automatically links viewers based on a set of rules, such as linking viewers that display the same series. When you select a point in one viewer, the viewer depicts that point in three dimensions (one per viewer) in the other linked viewers. Linked viewers will respond together to certain tools, such as Pan, Zoom, Contrast, and Color Mapping.

- Links typically do not function across grouped series except for triangulation, which can be enabled/disabled manually.
- Colormap linking applies to the same modality for all series displayed in the same viewer type. MIP viewers have independent colormaps. Viewers displaying fused images have independent colormap linking from unfused viewers.
- Reference linking applies to slab viewers.
- Slab thickness linking applies to slab viewers.
- MIP scroll linking applies to MIP viewers.
- NM planar images are linked according to wholebody, static, cardiac gated and dynamic group types.

NOTICE

When sections of data are missing, the viewer interpolates the missing section in order to construct a “well-formed” volume for further processing. The original slices are presented appropriately, as usual. In cases where the missing section is large, the artifacts generated during interpolation may be visible in the viewer. Interpolated volumes with artifacts should not be used for diagnosis.

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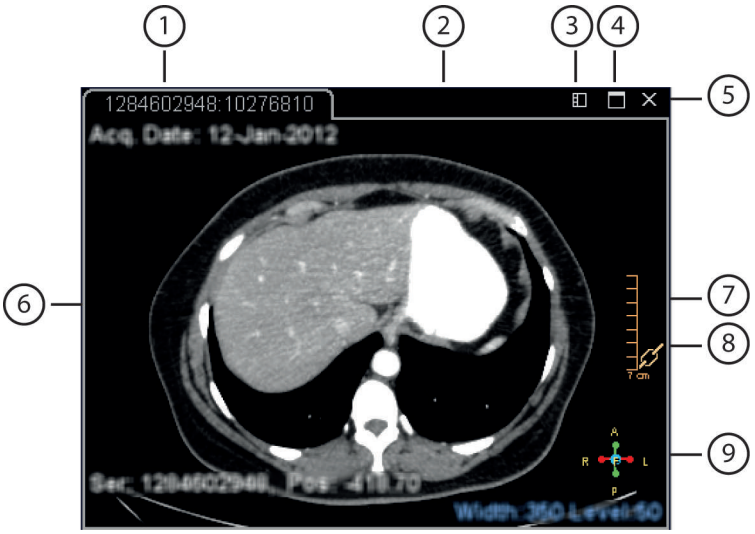
Components of a viewer



1	Tab(s)	Displays series information appropriate to the modality. A tooltip contains additional information. The tab can be used to reposition the viewer or to switch between images if more than one viewer occupies one area of the layout. Refer to section “Moving and resizing viewers” on page 104. When a viewer has multiple tabs, the tab for the active image is highlighted.
2	Title bar	Displays the viewer tab(s), **Image Controls** button, **Minimize/Maximize** button, and **Close** button. You can also maximize and restore the viewer by double-clicking on the title bar.
3	**Image Controls** button 	Displays the **Image Controls** toolbar. The controls on the toolbar are similar to the controls opened by right-clicking on the image, and are determined by viewer type. Refer to section “Image manipulation tools” on page 149 for more details. The toolbar opens on the left hand side of the image, but you can move it to the top, bottom, or right side by clicking on the gray bar at the top of the toolbar and dragging it. Click **Image Controls** to close the toolbar.
4	**Minimize/ Maximize** button 	Enlarges a viewer or returns it to its original size. You can also double-click on the viewer’s title bar to resize it.
5	**Close** button 	Closes the viewer.

		When you close a viewer, all other viewers in the current layout remain open. Closed viewers can only be reopened by resetting the layout. When you reset a layout, all viewers revert to their saved settings. Any changes to the viewers are lost.
6	Image area	Area of the viewer that contains the image, annotation, and Orientation Marker.
7	Image scale	Provides a size reference for features on the image.
8	Smartlink icon	Indicates whether the viewer is linked or not linked. For more information, see section “Smart Links” on page 146.
9	Orientation marker 	3D graphic indicating the current orientation of the image. See table below for list of marker letters. Axial slices are presented with the anterior towards the top of the screen and right towards the left side of the screen. Coronal slices are presented with the head towards the top of the screen and the right towards the left side of the screen. Sagittal slices are presented with the head towards the top of the screen and the anterior towards the left of the screen.

A list of orientation marker letters and what they indicate is listed in the table below.

Letter	Orientation
H	Head
F	Feet
A	Anterior
P	Posterior
R	Right
L	Left

Moving and resizing viewers

To move a viewer, drag and drop the tab onto the menu bar of another image. The dropped tab snaps onto the menu bar of the image underneath it, stacking the viewer. You can switch between stacked viewers using the scroll left and scroll right arrows on the title bar or by clicking the tab of the image you want to view.

Stacked viewers can be moved back to separate spots, if there is an open slot in the layout. Drag the active viewer, using its tab, to an empty slot.

To resize a viewer, move the cursor to the edge of the viewer that you want to resize. The cursor changes to the resize cursor (a straight line with arrows on either side of it). Then click and drag the viewer's edges to make the viewer larger or smaller.

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Viewer types

SlabMPR viewer

Slab Multi-Planar Reconstruction (MPR) viewers display one or more images from one or two series in standard Transverse, Sagittal, and Coronal orientations. SlabMPR viewers do not support reorientation or oblique capabilities.

Any SlabMPR viewer can display fusion views, which blend images from more than one modality. The system designates one fused series as the overlay and one as the underlay.

Fusion views can be manipulated in several ways, including using the Alpha Blending tool to adjust the blending between the overlay and underlay images and using the registration tools to adjust one image's rotation and translation to fine-tune alignment between the fused images. For information about the Alpha Blending tool, see section "Tools description" on page 149. For information about the registration tools, see section "Registration Tools" on page 170.

The Control Panel includes controls that allow you to designate any loaded series as the reference series. For information, see section "The Series Selection panel" on page 130.

NOTICE

If an anatomical series is available, this series becomes the reference series.

Only one series at a time can be the reference series.

Fusion views can contain images from different studies belonging to the same patient.

NOTICE

In order to perform triangulation between Transverse, Sagittal, and Coronal images, the Transverse, Sagittal, and Coronal viewers must be of the same type, either all SlabMPR or all Slab.

Basic2D viewer

The Basic2D Viewer displays planar data. It also displays secondary capture images and data from a single series in its original format (i.e., transverse).

Slab viewer

Slab viewers display one or more images from a single series. Layouts incorporating the slab viewer contain the word "Slab" in their names.

The slab viewer provides additional control of the thickness of the image you are viewing. You can also freely rotate images in a slab viewer to show any plane. If you select a image thickness for a specific layout and then save the layout, the system saves the thickness for that layout. Refer to section "Image manipulation tools" on page 149 for more information.

The triangulation cursor is not available on the slab viewer. Use the reference lines to perform triangulation on the slab viewer.

NOTICE

In order to perform triangulation between Transverse, Sagittal, and Coronal images, the Transverse, Sagittal, and Coronal viewers must be of the same type, either all SlabMPR or all Slab.

Volume viewer

The Volume Viewer displays images individually or in fusion views as rendered 3D images. You can rotate the images freely to show any plane.

The volume can be used for quick location and localization of lesions. Click a point in the Volume Viewer. Linked 2D Viewers will automatically display the area you clicked in the Volume Viewer.

You can display 3D regions of interest in the Volume Viewer.

Cardiac viewer

Cardiac viewers display re-oriented cardiac images in short axis, vertical long axis, and horizontal long axis orientations. When saved, cardiac viewer type, its orientation, cardiac state (stress/Rest), and AC/non AC are saved.

Graph viewer

The Graph Viewer displays a graph presenting calculated values for each ROI over time, for time based datasets (dynamic or gated).

For example, graphs can be used to display X-Y plots of Time Activity curves.

Table viewer

The Table Viewer displays rows and columns of numeric values.

You can save the contents of a Table Viewer and copy and paste the contents into text files.

Context menus

Title bar context menu

Right click on the title bar in any viewer to open a context menu for that viewer. The context menu contains the following choices:

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Maximize/Restore	Resizes the viewer.
Select	Opens a list of viewers stacked in the current viewer. Select a viewer to bring that viewer to the top of the stack.
Toolbar	Shows/hides the toolbar in the current viewer.
New Horizontal Tab Group	Splits tabbed viewers horizontally.
New Vertical Tab Group	Splits tabbed viewers vertically.
Close All	Closes all viewers stacked in the current viewer.
Close	Closes the selected viewer.

NOTICE

If you have only one viewer open, the New Horizontal Tab Group and New Vertical Tab Group menu items do not appear in the context menu.

Viewer context menus

Each image has a context menu that is displayed when you right click on the image. For more information, see section “Tools description” on page 149.

Layouts

When you load images into the NM Viewer, the system analyzes the images, selects a layout from the pool of custom and factory-installed layouts, and displays the images in the selected layout. Each layout is made up of one or more viewers and can incorporate multiple viewer types. The factory-installed layouts are defined as clinically appropriate for review.

For information about using layouts, see section “The Layout panel” on page 117.

Control Panel

The Control panel contains the tools you need to manage the NM Viewer layout. It appears on the left side of the left monitor.

The Control panel is divided into the folllowing sections:

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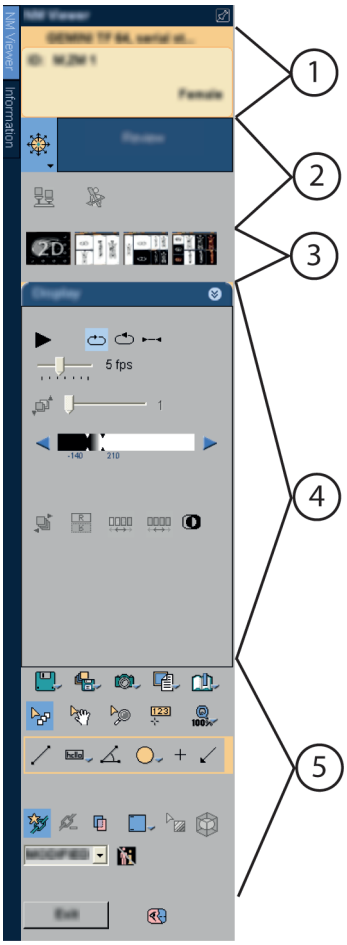

1	Patient Selector - contains patient selection controls and patient demographic information.
2	Workstep Navigator - contains the Application palette and the list of worksteps in the selected application.
3	Quick Layout - allows quick access to five groups of layouts.
4	Tools - contains the data management tools.
5	Utilities - gives quick access to common functions such as Save, Scroll, Zoom, and Pan.

Displaying and hiding the Control Panel

The Auto-Hide icon appears in the top right corner of the Control panel. Click the Auto-Hide icon to hide the Control panel and allow more room for image display. Click the Auto-Hide icon again to re-display the Control panel.

Auto-Hide only affects the current patient. If you have more than one patient open, change each display individually.

When Auto-Hide is enabled, you can move your mouse over the Control or Information tab to temporarily display the Control panel or DICOM Information panel. When you move the cursor out of the toolbar area, the Control panel automatically hides again.

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NOTICE

If the application starts with Auto-Hide enabled, the viewers do not resize when the Control panel is made visible.
If the application starts with Auto-Hide disabled, the viewers resize if the Auto-hide is enabled.
If Auto-Hide is disabled while the application is active, the viewers resize.

Displaying DICOM information

The NM Viewer Information panel contains information for each series that is loaded into the NM Viewer. You can view DICOM tags and their assigned values for each series. You can also drag the DICOM information tab into a viewer slot to keep the DICOM information visible while using the Control panel tools.

DICOM Information Configuration Utility

You can add or delete DICOM tags and their assigned values from the DICOM Information Configuration Utility.

To configure which DICOM Tags are displayed in the DICOM Information Viewer:

1. Click on the Information tab.
2. Right click on the DICOM Information panel.
3. From the context menu select **Configure DICOM tags**.

   The **Configure DICOM tags** window opens.
4. Choose a DICOM group from the **Group** menu to display the associated Available Tags.
5. You can Click, **<Ctrl>** + Click, or **<Shift>** + Click to select **Name** and **Tag** pairs in either list.
   - Click >> to add the selected tags to the **Display Tags** list.
   - Click << to eliminate the selected tags from the **Display Tags** list. If necessary you can search for specific DICOM tags.
     - To search for a DICOM Tag by **Name**, enter the name in the **Search** field for the associated list.
     - Enter an asterisk (*) to perform a wildcard search.
   - Click a column heading to sort a list.
6. Click the tags in the **Display Tags** list to select them for editing. Use the arrow keys to position the cursor and the backspace key to erase existing text then use other keys to insert customized text as desired.
7. Click **OK** when all configuration changes are done or click Cancel to make no changes.

Patients

The Patient Name field displays the name of the current patient. If you loaded images for more than one patient, use the **Previous Patient** and **Next Patient** buttons to navigate to other patients.

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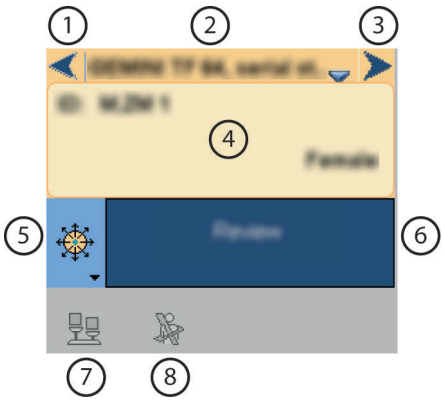

The patient area contains:			
1	Previous Patient button	5	Application Palette
2	Patient Name list	6	Workstep Navigator
3	Next Patient button	7	Patient Compare button
4	Patient information	8	Oblique Reslicing button

Individual tools are active when the correct type of data is loaded in the viewer.

Use the **Application Palette** menu to select another application. If the application you select contains multiple worksteps, **Previous** and **Next** arrows and a drop-down menu appear in the **Workstep Navigator**. Use the arrows or the drop-down menu to switch between steps within the application.

Click **Patient Compare** to launch comparison mode for all open patients.

Use **Oblique Reslicing** when you are loading a saved series of reformatted brain images. The reformatted images, as displayed by default in the NM Viewer, may not reflect the saved orientation assigned in the Brain Oblique application. **Oblique Reslicing** assigns the reference series' saved orientation to all current series.

Sequentially reviewing multiple patients

1. Select studies from multiple patients in the IntelliSpace Portal Directory window.
2. Select the series to be reviewed from the Directory window **Series** tab.
3. Click **Review** > **NM Viewer**.
4. Review the first selected study.

NOTICE

The IntelliSpace Portal determines which patient opens when the viewer initially loads by determining which patient has the most recent series and then loading that patient first.

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5. Using the tools provided in the Patient area of the Control Panel, click the **Next Patient** or the **Previous Patient** arrow buttons to switch between patients.

Skipping studies

1. Load studies for multiple patients as described in steps 1-3 above.
2. Select the patient that you want to review from the Patient Name list.

Comparing multiple patients

Whenever more than one patient is open in the NM Viewer, you can compare any open patients. For example, compare an abnormal PET brain study to a normal PET brain study to illustrate the differences.

1. Open multiple patient tabs as described in section “Sequentially reviewing multiple patients” on page 110.

    Opening more than one patient activates the **Patient Compare** button, under the Patient Name list.
2. Click **Patient Compare**. The current study remains visible, and other patients open in new instances of the viewer.

NOTICE

When the NM Viewer is being run on a dual-monitor system, one instance of the viewer will appear on each monitor when series are loaded for two different patients in comparison mode.

3. View each study as needed.
4. Click **Patient Compare** again in either viewer to close that series and exit comparison mode.

Quick layouts

When loading data in NM Viewer, select the  **Show quick layouts presets** arrow to view the available Quick Layouts.

The layouts area of the Control panel shows five tabs (groups). Each tab may include up to four layouts, which allow you to quickly choose layouts for display in the viewer. You can determine which layouts appear in this area in the **Quick Layouts** section of the **Layout** preferences. See section “Layouts” on page 347.

To choose a layout, select a tab and then choose a layout from the layouts that are displayed.

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You can configure this area to display layouts that you will use often to complete common tasks.

Tools

Select a tool set using the drop-down menu in the tools area of the Control panel:

- Display
- Registration
- Layout
- Application
- Series Selection
- 3D ROI
- ICMT
- Batch

The Display panel

Select **Display** from the drop-down menu in the Tools area of the Control panel to open the Display panel. The Display panel contains controls for viewing images, including movie controls, choices, and auto-SUV settings.

Play starts the movie in the selected viewer.

Stop halts play in the selected viewer. (The Stop button appears after you click the Play button.)

NOTICE

You can play movies in more than one viewer at the same time. Make sure you stop the movie in the same viewer in which you started it. If the viewer where the movie was started is not the active viewer when you click Stop, the movie does not stop.
When you play a movie with viewers linked by an established triangulation point, playing a movie in one viewer causes the triangulation cursor to move in sync in linked viewers.

Rotation Forward and **Rotation Backward** control the sequence in which a movie is played.

Bounce lets you switch on the fly between forward and backward playback.

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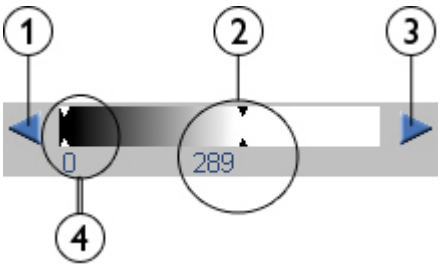
A scrollbar control lets you set the replay speed in frames-per-second (fps). The speed can range from 1-60 fps.

NOTICE

In the NM Viewer, you can use the left and right arrow keys on the keyboard, or drag the mouse left and right, to scroll through images one at a time. Use the up and down arrow keys, or drag the mouse up and down, to move through images one row at a time.

The **Position/Time** control allows you to switch between scrolling through time (bins) and images when viewing gated or dynamic data. Use the associated scroll bar to move to specific bins.

Image Control Bar (ICB): The ICB allows you to control colormaps, intensity maps, pixel values, and upper and lower levels for an image. For fusion studies, there are two ICBs. In this case, the top one is for the overlay image, and the bottom one for the underlay image. Use the following features to control image colors and dynamic range:



1	Previous colormap selector
2	Maximum Slider and value
3	Next colormap selector
4	Minimum Slider and value

Sliders: These adjust the background and brightness (dynamic range) of all images that use the current color palette. The values used in ICB are of the same type as those used in the selected viewer.

The left (lower) slider controls the background, or lower threshold of the colormap, below which pixel values are displayed as one color corresponding to the lowest value in the color table. Lowering this enhances the low-count image areas.

The right (upper) slider controls the brightness, or upper threshold, above which pixel values are displayed as one color corresponding to the highest value in the color table.

You can adjust the background and brightness together by dragging the section of the line between the numbers.

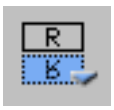
Color Map: Click one of the arrows at either end of the ICB to select a different colormap.

NOTICE

Be sure to use colormaps that are appropriate to the data being viewed. Especially in the case of low-count images, the choice of colormap can make a dramatic difference. For this reason, exercise caution when applying colormaps.

When you right-click on the ICB, the Select overlay/underlay colormap, Overlay/Underlay intensity correction, and CT/SUV preset tools appear in a menu. For information about these tools, see section “Image manipulation tools” on page 149.

Select Phase lets you select the phase to display when you are using multi-phase studies.



Flip/Rotate lets you flip or mirror an image, or rotate the image clockwise or counterclockwise.

Normalize to Frame normalizes each individual frame based on its own minimum and maximum pixel value.

Normalize to Series normalizes all frames based on the minimum and maximum pixel value that is found in all frames of a series (the entire volume for a volume dataset or the entire set of frames for a dynamic dataset).

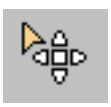
Use the normalization functions carefully because they can have dramatically different effects, depending on the dataset. When the counts are generally low in some frame in a series, if you normalize the frame using Normalize to Frame, it (and every other frame) looks like it has a full range of counts. This means that you may not be able to make a useful comparison between it and other frames. Using Normalize to Series preserves the relationship.

Invert Gray Level lets you invert the colormap or gray scale of the image.

The Registration panel

Select **Registration** from the drop-down menu in the Tools area of the Control panel to open the Registration panel. The Registration panel contains tools for both manual and automatic alignment of the reference and floating images in fusion views.

The **Translate** and **Rotate** buttons allow you to make manual changes to the floating image’s position in relation to the reference image in the selected viewer. After you click the icon you can also use the arrow keys for fine adjustments.



Click **Translate** to drag the floating image up, down, left, or right.

Click **Rotate** to rotate the image clockwise or counterclockwise.

Click **Undo** to remove the previous change to the registration in the selected viewer.

Click **Redo** to reapply changes that have been removed.

Click **Reset** to revert the registration in the selected viewer to its original state or to the state of registration the last time **Apply** was clicked.

Change the x, y, and z values in **Translation Offset (mm)** to move the image by the specified number of millimeters.

Change the x, y, and z values in **Rotation Angle (degrees)** to rotate the image by the specified number of degrees.

Click **Apply** to make the changes that you manually entered in the Translation or Rotation areas.

NOTICE

If you apply your changes at once after changing both the Rotation Angle and Translation Offset, all changes are made from the same (current) registration position.
If you apply your changes after making changes to the Rotation Angle then again after making changes to the Translation Offset, the second set of changes are made from the new Translation Offset

Registering fusion images automatically

The Automatic Registration tool provided in the Registration panel allows you to have the viewer register your fused images for you. You can use the following registration algorithms to complete the automatic registration:

- Local correlation
- Cross correlation
- Normalized mutual information

1. From the Automatic Registration drop-down list, select the registration algorithm you want to use.

2. Click **Automatic Registration** to start the registration.

   If you need to stop the registration while it is in progress, click **Automatic Registration** again.

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3. During the registration process, the viewer shows the progress of the registration as the Score value, which indicates the closeness of the registration between the fused images. The viewer also displays updated x, y, and z values in the Registration panel as the registration progresses.
4. When the automatic registration is complete, the Score value is reset to 0 and the final x, y, and z values are shown in the panel.

NOTICE

You can automatically register images using the optional Automatic Registration application. Refer to section “Automatic Registration Display” on page 167 for more information.

Registering fusion images manually

The controls provided in the Registration panel allow you to manually adjust the fusion views. Use the arrow keys for fine adjustments. You can adjust the floating image’s position in relation to the reference image in the selected viewer.

1. Click **Translate** to drag the floating image up, down, left, or right in the selected viewer.

   For fine adjustments, press the arrow key to move the image 0.5 mm in the direction of the arrow.
2. Click **Rotate** to rotate the image clockwise or counterclockwise in the selected viewer.

   For fine adjustments, press the Up or Right arrow key to rotate the image 0.25 degrees in the clockwise direction. Press the Down or Left arrow key to rotate the image 0.25 degrees in the counterclockwise direction.

When you know the values to move the images, you can:

1. Change the x, y, and z values in the **Translation Offset (mm)** field to move the image up, down, left, or right by the specified number of millimeters.
2. Change the x, y, and z values in the **Rotation Angle (degrees)** field to rotate the image clockwise or counterclockwise by the specified number of degrees.
3. Click **Apply** to make the specified changes in the selected viewer.

NOTICE

If you apply your changes at once after changing both the Rotation Angle and Translation Offset, all changes are made from the same (current) registration position.
If you apply your changes after making changes to the Rotation Angle then again after making changes to the Translation Offset, the second set of changes are made from the new Translation Offset.

To save registered images created within the Registration panel, select the **Save image(s)** icon and choose the **Save resampled series** option from the menu.

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The Layout panel

Select **Layout** from the drop-down menu in the Tools area of the Control panel to open the Layout panel. The Layout panel contains thumbnail images of the default layouts available in the NM Viewer. The current layout is indicated by a blue outline. Click a thumbnail to use that layout.

Refer to section “Layouts” on page 347 for instructions on how to limit the layouts displayed to only those that are used at your site.

Use the drop-down list at the top of the Layout panel to select which layouts to show in the panel.

- **All layouts** shows all available layouts.
- **Applicable layouts** shows those layouts that apply to the data selected.
- **Custom layouts** show the layouts created by your facility.
- **Comparison layouts** shows those layouts available when you have more than one study open.

The following tools are available in the Layout panel.

Save layout as: lets you save new layouts or the changes that you make to existing layouts. For detailed information, see section “Creating custom layouts from existing layouts” on page 118, section “Using the Layout Editor” on page 118, and section “Deleting custom layouts” on page 120.

Edit layout: Click **Layout Editor** to access the layout creation tool. See section “Using the Layout Editor” on page 118.

Reset layout: Factory-installed layouts continue to show your changes after you save a modified layout as a custom layout. Click **Reset** to restore the original settings. Altered viewers will reset to the original configuration when a new session begins.

Delete layout: Click **Delete** to remove a custom layout from the list of available layouts. You cannot delete the factory-installed layouts. If you attempt to delete a factory-installed layout, the system displays a message that the layout is read-only.

When you are working in a layout, viewers can be closed and added using the Layout Editor. Viewers you add will be synchronized with existing viewers based on linking policies. Closing a viewer does not delete that image from the study. The NM Viewer keeps your changes to a layout until that layout is reset or until the viewer session ends.

NOTICE

When the viewer interprets the selected series, it generates image numbers that are specific to the NM Viewer. This is the case for all layouts except the 2D layout.

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Creating and editing layouts

The NM Viewer comes with factory-installed layouts, but you can also create custom layouts that best fit your specific tasks. You can also edit existing layouts and save them as custom layouts or use the Layout Editor to create new custom layouts.

Creating custom layouts from existing layouts

1. Open a default layout that has at least as many viewers as you need for your custom layout.

   If you need a specific type of viewer in your custom layout, base your custom layout on a default layout that contains that type of viewer.
2. Close any viewers you do not need for your custom layout.
3. Move viewers to new locations as necessary.
4. Adjust each viewer using the tools from the Control Panel or the menu that appears when you right-click on the image.

Using the Layout Editor

The Layout Editor consists of a tools area and a viewer area. Use the tools to select a layout template and to assign characteristics to the component viewers. Use the viewer area to position customized viewers in your layout template.

1. Click the **Layout Editor** icon in the Layout panel.
2. Select **Keep viewers** to incorporate the viewer types contained in the current layout into your new layout. Deselect **Keep viewers** if you want to create an empty grid to add all viewers.
3. Specify the basic grids you want for a one- or two-monitor configuration.

   The grid displays in the viewer area.
4. Resize, move, and close the viewer slots within the grid to get the exact layout you want.

   You can resize and close slots within the grid throughout the process of creating a layout.
5. Make a selection from the **Viewer Type** drop-down list. For more information, see section “Viewer types” on page 105.

   If your layout contains Slab viewers, the first viewer you add in each orientation does not display reference lines. Reference lines appear in the viewers as you add subsequent viewers.

   Add any Basic2D Viewers last. When you add a Basic2D Viewer, create the viewer using the modality you want to display in the viewer when you launch the NM Viewer.
6. Use the controls to select the characteristics of each viewer.

   Some controls do not apply to every viewer type. The options available correspond to the data types you currently have loaded in the viewer. When using a saved custom layout, the viewer matches data types similar to the data used to create the layout.

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7. After you choose your viewer, drag the viewer graphic and drop it into a slot within the layout.
8. Repeat until you have completed the layout.

   You can resize, move or close viewers as needed.

Create a page

You can use the Layout Editor to create a page in which to place viewers.

1. In the Layout Editor, select the grid that you want to use for your page from the **Page** drop-down list. The grid you select is shown on the right side of the Layout Editor.
2. Drag the page from the Layout Editor to the image area.
3. Add viewers to the page as you would normally add them to a layout by dragging the viewer graphic to a slot on the page.

You can repeat this procedure to create multiple tabs in your viewing area.

Saving custom layouts

After you edit an existing layout or create a new layout, save your changes for future use.

1. Click the **Save** icon on the Layout panel. The **Save Layout** dialog opens.
2. Type a name and description for your new layout.

   The name and description are shown as a tooltip for your layout in the Control Panel.

   When editing a planar layout, mark the **Use image ID for layout matching** check box to save the image ID for layout matching.

NOTICE

When you save a new layout, that layout can only be accessed by the login you used when you created the layout. If you want the newly saved layout to be accessible by all user logins for the system, include ".shared" at the end of the name. For example, a layout named "TSC Fusion.shared" will be accessible by all users of the system.

The shared layout can only be seen after users log off and then log back into the IntelliSpace Portal client application.

3. Click **OK**. The information saved for the layout consists of:
   - Layout geometries
   - Layout name, description and thumbnail image
   - Screen index (the monitor number)
   - Image ID (optional) for planar layouts
   - Viewer types

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- Fusion states
- Cine on/off mode
- Movie control bar show/hide states
- Toolbar show/hide states
- Zoom factor
- Modality

The new custom layout appears in the Layout panel. You can add your saved custom layouts to the Quick Layouts in the NM Viewer Preferences. For information, see section “Layouts” on page 347.

Deleting custom layouts

1. On the Layout panel, select the custom layout you want to delete.
2. 
Click the **Delete** icon.
3. Click **OK** to delete the layout, or click **Cancel** to keep the custom layout.

NOTICE

Layouts provided by the factory cannot be deleted.

Using the 2D layout

The 2D layout is a special layout in which images are presented without modification. In other layouts, images are interpolated for presentation, while the 2D layout presents the images as they have been stored.

Reviewing DICOM secondary captures

1. Load one or more secondary capture series from the IntelliSpace Portal Directory window.
2. If necessary, after the NM Viewer loads, select the secondary capture series you want to review in the Series Selection panel. For information, see section “The Series Selection panel” on page 130.
3. 
Click **Launch** to display the new series. The series opens in the 2D layout or the Overview layout.
4. View the secondary capture series as needed.
5. To open a different secondary capture series loaded in the NM Viewer, launch the series from **Series Selection** panel on the Control Panel as in steps 2 and 3.

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Using comparison layouts

The NM Viewer allows comparison viewing of two studies or groups showing the same patient.

When entering a comparison view of two studies from the same patient, the viewer automatically selects a comparison layout. You may choose a different comparison layout from the Layout panel on the Control Panel.

NOTICE

You can also compare studies from different patients. When two studies from different patients are loaded in comparison mode, they each open in separate instances of the NM Viewer. Refer to section “Comparing multiple patients” on page 111.

You can set the viewer to automatically start in comparison mode if appropriate data is selected at launch. See section “Layouts” on page 347.

Comparing multiple studies from the same patient

You can compare up to three studies from the same patient at once.

1. Load up to three studies from the same patient into the NM Viewer.

   The Viewer opens in single-study mode, and the latest study appears in the layout.

2. From the Control Panel drop-down menu, select **Series Selection**.

3. Click **Expand** to view the tree for all currently loaded series, if necessary.
4. Click to select a series or use **<Ctrl>** + click to select more than one series in the **Series Selection** screen. The current studies are marked with + or > symbols.

   To view multiple series from the same study, you may first need to manually group and launch the series, such as CT and SPECT series. Then select additional sets of CT and SPECT series for comparison.

5. Click **Compare Studies**.

   The study you selected in the **Series Selection** screen appears along with any study that was already loaded in the Viewer.

   The Viewer searches for a comparison layout that matches the selected series. If it does not find a match, no images display. You may select a layout or another series combination.
6. View each study as needed, selecting a different comparison layout if necessary.

7. If the Viewer is in comparison mode, switch back to single-study mode by selecting one or more series from the same study in the Control Panel Series Selection screen and clicking Launch.

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Linking studies or groups

You can only link viewers containing studies from the same patient. After the studies are selected for comparison, you can manually link viewers in each study for synchronized scrolling and triangulation.

1. Use the available viewers to identify an anatomical landmark in each series. You may want to use a fusion view or CT image to do so, if one is available.
2. Click on the chosen anatomical landmark in each study.

NOTICE

You can link viewers whether the triangulation cursor is visible, hidden, or set as the 3D value cursor.

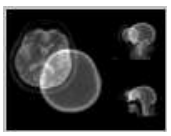
3. Click **Link Viewers** from the Control panel.

   This links the viewers, which will now scroll together. Other viewers from each study will also scroll together.

NOTICE

If you change layouts after linking studies, the links are not preserved in the new layout. Link the studies again as described above.

Register other modalities layout



Typically the NM Viewer designates the PET or SPECT image, when available, as the overlay image in fusion views. To designate an image from a different modality, such as CT or MR as the overlay, use the Register other modalities layout. This layout allows you to register series combinations that cannot be registered using other layouts.

NOTICE

The Register other modalities layout is not enabled by default. To access this layout, make sure it is designated as “In Use” in the layout preferences. Refer to section “Layouts” on page 347.

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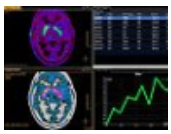
Axial PET-CT + Table + Graph layout



Select the Axial PET-CT + Table + Graph layout and the Generate Statistics tool to evaluate dynamic data or cardiac gated data.

You can use the 3D ROI tools to draw ROIs in the Axial PET-CT + Table + Graph layout or in other layouts prior to selecting the Axial PET-CT + Table + Graph layout.

NOTICE

Use the Generate Statistics tool only for gated and dynamic acquisitions that are reconstructed as the same data type. You cannot use dynamic data that is generated from a gated acquisition to generate statistics.

1. From the **Layout** panel, select the Axial PET-CT + Table + Graph layout.
2. Use the tools available on the **ROI** screen to draw one or more regions of interest.
3. Right-click on the image and select **Generate Statistics**.

The application populates the table and graph viewers based on the calculated values.

You can add more regions using the 3D ROI tools and display statistics for these new regions using steps 2 - 3.

2 Series TSC + 2 Fused Volumes layout

Select the 2 Series TSC + 2 Fused Volumes layout to access the 3D Volume Viewer. You can also create custom layouts containing the 3D Volume Viewer.

Overview layout

Presents all the selected images in all modalities for the current patient. Body images display in the correct aspect ratio.

PLANAR_TABLE_GRAPH layout

Select the PLANAR_TABLE_GRAPH layout and use the Generate Statistics tool to evaluate dynamic planar data or cardiac gated planar data. You can use the Graphic element measurement tools to draw ROIs in the PLANAR_TABLE_GRAPH layout or in other layouts prior to selecting the PLANAR_TABLE_GRAPH layout.

1. From the Layout panel, select the PLANAR_TABLE_GRAPH layout.
2. Use the Graphic element measurement tools available in the Control panel to draw one or more regions of interest.
3. Right-click on the image and select **Generate Statistics**.

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The application populates the table and graph viewers based on the calculated values. You can add more regions using the Graphic element measurement tools and display statistics for these new regions using steps 2 - 3.

The Application panel

Select **Application** from the drop-down menu in the Tools area of the Control panel to open the Application panel. The Application panel contains the Brain Oblique and Cardiac Oblique applications. When an application is selected, the oblique layout for that application is displayed along with the panel containing the tools for setting the orientation of the image in the active viewer.

The Brain Oblique application lets you set the transverse, coronal, and sagittal rotation. For more information, see Brain Oblique application. The Cardiac Oblique application lets you align from Base to Apex on transverse or sagittal rotation. For more information, see Cardiac Oblique application.

Both the Brain Oblique and Cardiac Oblique applications use the Reset icon and the Voxel Size field.

Click **Reset** to restore the original image orientation to the whole viewing area.

Type a value into the **Voxel Size** field or increase/decrease the default value of 2.000 using the up and down arrows. Increasing the voxel / pixel size has the same effect as zooming in on an image. Decreasing the voxel / pixel size has the same effect as zooming out on an image.

Brain Oblique application

When you select **Brain Oblique** in the Application panel, the layout changes to the Brain Oblique layout, and orientation and rotation information is shown in the Application panel.

The layout that is displayed for the Brain Oblique application contains six viewers. Each viewer includes a label that describes the image it displays. Use the transverse, coronal, and sagittal viewers on the top row for reorienting brain images. Use the three viewers on the bottom row to view the reoriented images.

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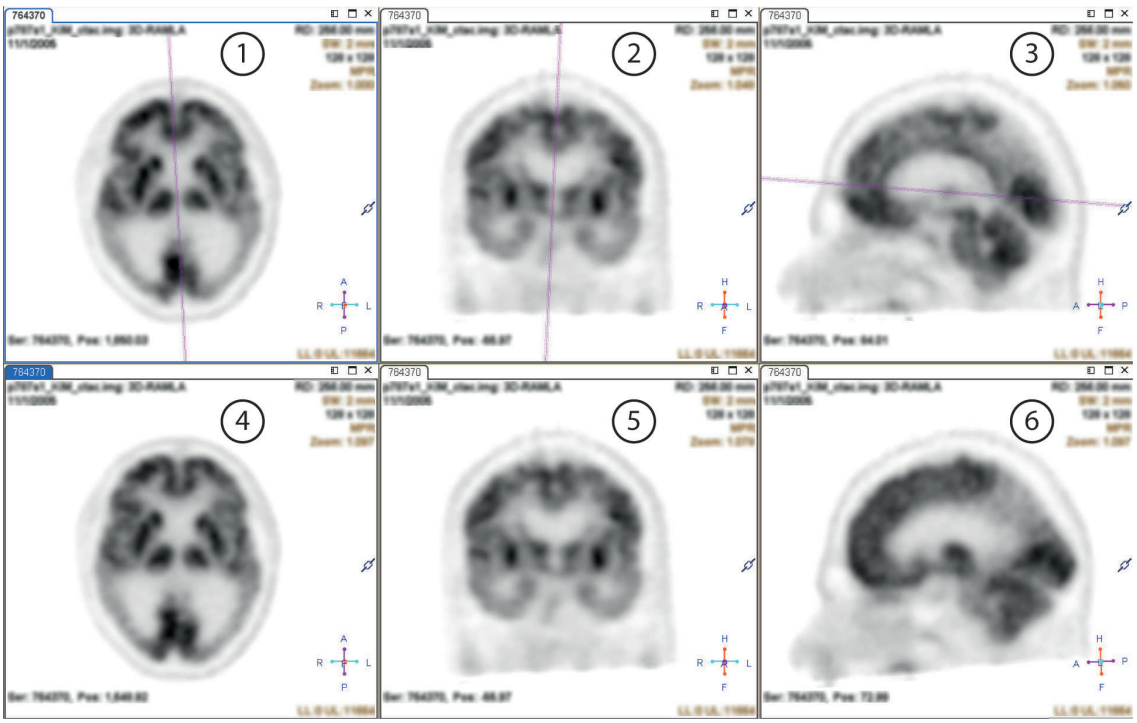

1	Transverse	4	Oblique Axial
2	Coronal	5	Transformed coronal
3	Sagittal	6	Transformed Sagittal

The orientation of the images is indicated by the orientation marker that appears in the lower right corner of each viewer. Adjust the orientation by moving and rotating the lines that appear in the transverse and coronal images, and a plane tool on the sagittal image. Specify the center of the reformatted volume in using the transverse and sagittal orientation tools.

Your cursor will change based on where on the line it is located.

-  Your cursor appears with rotating arrows when it is positioned to rotate the line.
-  Your cursor appears with directional arrows when it is positioned to reposition the center.

As you adjust the orientation of an image, the orientation information listed in the Application panel is updated. In addition, the oblique axial, transformed coronal, and transformed sagittal viewers on the lower row automatically adjust with your changes.

The viewer retains the user-defined angles set in the Brain Oblique application when multiple series from the same patient are loaded into the NM Viewer.

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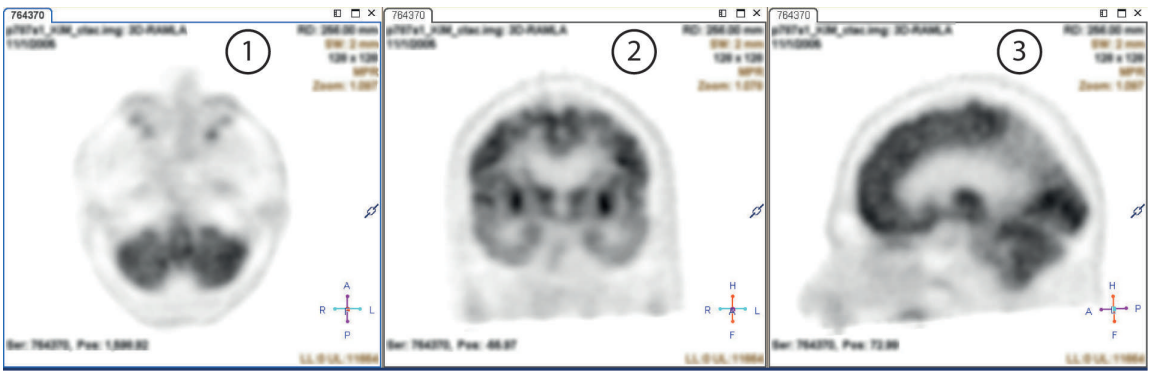
NOTICE

You cannot load series reformatted in the NM Viewer Brain Oblique application into NeuroQ for review. You can load the original transverse data into NeuroQ.

To reformat brain images:

1. Load one or more brain series into the NM Viewer from the IntelliSpace Portal Directory window.
2. Select **Application** from the drop-down menu in the Tools area of the Control panel to open the Application panel.
3. Select the Brain Oblique application from the Application panel.
4. Use the orientation tools in the transverse, coronal, and sagittal viewers to reorient the image as needed.
5. Review your changes in the oblique axial, transformed coronal, and transformed sagittal viewers to ensure that all relevant anatomy is included in the reformatted volume.
6. To save your changes, select the oblique axial viewer and then select **Save images**. You can select **Save images** from either the Utilities section of the Control panel or the toolbar in the oblique axial viewer.
7. After you save your changes, you can load the reformatted images into the NM Viewer for viewing and analysis.



1	Oblique Axial	2	Transformed Coronal	3	Transformed Sagittal

Viewing reoriented images

1. Load one or more brain series into the NM Viewer from the IntelliSpace Portal Directory window.

   The NM Viewer processes the data, creating Transverse/Sagittal/Coronal images that may not reflect the saved orientation assigned in the Brain Oblique application. If the viewer does not display the saved orientation, you must restore the saved orientation as described in the following steps.

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2. Make sure the reformatted series is the reference series. In cases where you load more than one series together, the reformatted series may not be designated by default as the reference series. If you load only one series, that is the reference series.

   To reassign the reformatted series as the reference series, open the **Series Selection** panel from the Control Panel, right-click on the series you want to designate as the reference series, and then select **Set as Reference** from the menu.

3. Click **Oblique Reslicing** to assign the reference series saved orientation to all current series.

NOTICE

If you click Oblique Reslicing while a series other than the reformatted series is set as reference, perform steps 2 and 3 again to correct the orientation. No saved data is lost or changed.

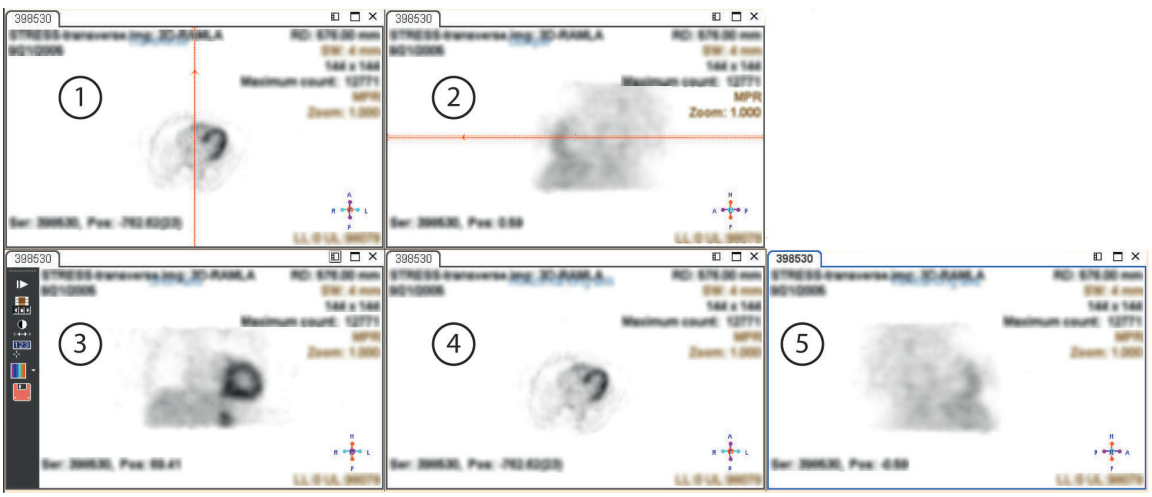
4. Review the reformatted images.

   Any adjustments made using the **Oblique Reslicing** tool continue to display after you switch layouts.

Cardiac Oblique application

When you select **Cardiac Oblique** in the Application panel, the layout changes to the Cardiac Oblique layout, and orientation and rotation information is shown in the Application panel.

The layout that is displayed for the Cardiac Oblique application contains a transverse viewer (1) and a oblique viewer (2) used to specify the rotation angles and image center. The application also contains short axis (3) , horizontal long axis (4) , and vertical long axis (5) viewers for evaluating the resulting oblique images. Each viewer includes a label that describes the image it displays.



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You identify the axial cardiac rotation then the cranial/caudal rotation. The system displays the short axis images. The orientation of the images is indicated by the orientation marker that appears in the lower right corner of each viewer. Adjust the orientation by moving and rotating the lines that appear in the transverse and oblique viewers.

Your cursor will change based on where on the line it is located.

-  Your cursor appears with rotating arrows when it is positioned to rotate the line.
-  Your cursor appears with directional arrows when it is positioned to reposition the center.

When you move the line in the axial or oblique viewer, the short axis, horizontal long axis, and vertical long axis viewers automatically adjust to reflect the movement.

 Click **Reset** to undo your changes to the rotation or position in the transverse or oblique viewers.

The viewer retains the user-defined angles set in the Cardiac Oblique application when multiple series from the same patient are loaded into the NM Viewer. When you switch between series, including between gated and non-gated series, the viewer displays any user-defined angles.

NOTICE

When gated series are viewed in movie mode and set to scroll through time (bins) in a viewer, that viewer will continue to adjust in time when linked viewers are scrolled in space (images). The bin and image numbers in each individual viewer update as you scroll to display the correct information.

You can save reformatted cardiac studies and submit them to a cardiac quantification application for analysis. You can also view them in the 2D layout of the NM Viewer.

NOTICE

After a cardiac study has been reformatted and saved, it can be loaded into the viewer for verification. However, the viewer may load in TSC mode. This does not indicate a problem with the short axis save. Select **Cardiac Oblique** from the Application panel to view the saved images.

To reformat cardiac images:

1. Load one or more cardiac studies into the NM Viewer from the IntelliSpace Portal Directory window.
2. Select **Application** from the drop-down menu in the Tools area of the Control panel to open the Application panel.

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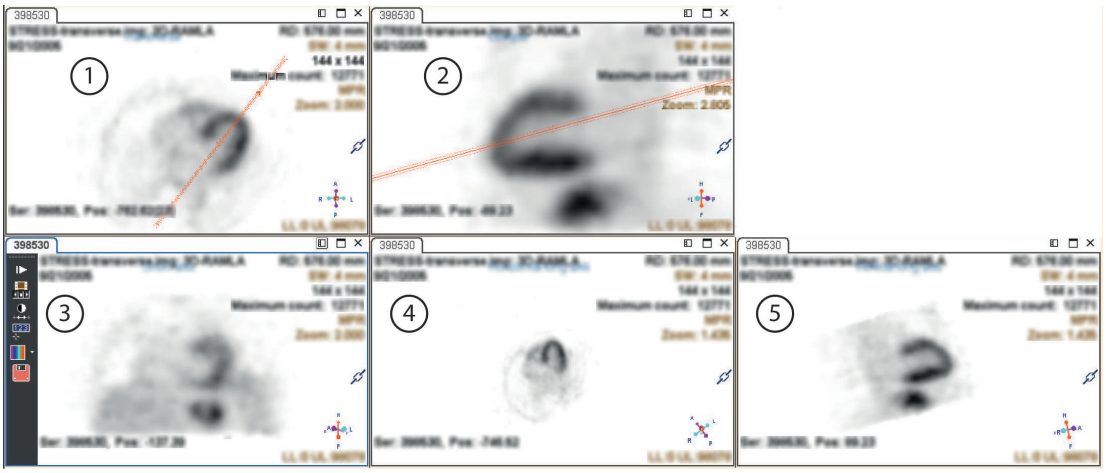
3. Select the Cardiac Oblique application from the Application panel.
4. Scroll, pan, and zoom the images as needed to identify the image you want to use to set the short axis.

   The transverse viewer contains an arrow tool used to set the angle and center of the short axis.
5. Rotate the arrow to set the angle of the short axis.

   When you move the arrow, the other viewers display images based on the transverse viewer's (1) arrow position . The oblique viewer (2) now contains an arrow for further reformatting of the series.

   The images in the oblique, short axis (3), horizontal long axis (4), and vertical long axis (5) viewers update each time you move the arrow to reflect the new positioning.



6. Drag the center of the arrow to adjust the center point of the cardiac image.
7. Adjust the angle and center of the image in the oblique viewer.

   The short axis, horizontal long axis, and vertical long axis viewers update each time you move the arrow to reflect the new positioning.
8. Review the reformatted images in the short axis, horizontal long axis, and vertical long axis viewers.
9. To save your changes, select the short axis viewer and then select **Save images**. You can select **Save images** from either the Utilities section of the Control panel or the toolbar in the short axis viewer.
10. You can load reformatted short axis views into a cardiac viewer or the 2D layout in the NM Viewer for viewing.

NOTICE

You can apply the angles set for one cardiac series to other series loaded at the same time. Format one series, then launch another series from the Series Selection panel and apply the angles from the Application panel to the new series.

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The Series Selection panel

Select **Series selection** from the drop-down menu in the Tools area of the Control panel to open the Series Selection panel. The Series Selection panel contains a tree view of all series loaded into the viewer for the currently active patient. Expand the tree view to show all loaded series or collapse the tree to show only the root studies. For planar data, select and display data at the image level. The tree view displays each individual planar image name.

Use the Series Selection tree to manually select series, to show groupings of series, and to indicate the currently selected series. Numerical indicators indicate the group to which the series belong. The first group is the collection of series launched automatically or by the user. The second group consists of series being used for comparison.

A greater than sign (>) by the series name indicates the reference series for that group, while a plus sign (+) by the series name indicates a selected series that is not the reference series.

Colormap indicators reflect the colormaps in use in the selected viewer.

Right-click on a series or study and select from the available options:

- **Launch**: Opens the selected study in the viewer.
- **Replace Group**: Lets you replace the last study in compared studies and lets you replace a series within a study with a series from another study.

  To replace the last study in a comparison of studies, select the new study or series in a study that you want to use, right-click, and select **Replace Group** from the menu. For example, if your existing comparison is comparing PET1,CT1 with PET2,CT2, and you want to compare PET1,CT1 with PET3,CT3, select PET3 and CT3 in the Series Selection panel, right-click, and select **Replace Group**. Use <Ctrl> + click to select more than one study or series.

  To replace series in a comparison, select the new series you want to use in the comparison, then right-click and select **Replace Group** from the menu. For example, if your existing comparison is comparing PET1,CT1 with PET2,CT2, and you want to compare PET1,CT1 with PET2,MR2, select PET2 and MR2 in the Series Selection panel, right-click, and select **Replace Group**. Use <Ctrl> + click to select more than one series.
- **Maximum IP/Minimum IP/Average IP**: Condenses the available gated series into a single static series. Based on your selection, the created series displays the maximum, minimum, or average value of all selected intervals for each voxel. These options are only available when a respiratory gated dataset is loaded.
- **Set as Reference**: The selected series replaces the current reference series. If the series selected for reference is already one of the three series selected then the series exchange their designations.
- **Add To Compare**: Adds selected data for comparison within the viewer.
- **DICOM Information**: Shows the DICOM information for the selected study.

Click **Expand All** at the bottom of the **Series Selection** panel to view the tree for all currently loaded series. If the tree is expanded, the button changes to **Collapse All** and it closes all the expanded series. You can also click the **plus** sign (+) to expand and the **minus** sign (-) to collapse views.

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Click **Launch** to open the selected study or series in the viewer.

Click **Compare Studies** after the second study is selected in the series in order to compare the studies.

The 3D ROI panel

Select **3D ROI** from the drop-down menu in the Tools area of the Control panel to open the 3D ROI panel. The 3D ROI panel contains controls for creating and managing new and existing ROIs. The NM Viewer provides tools for manual or semi-automated creation of ROI contours. ROIs are always applied to the overlay image when fusion is activated.

After you create an ROI, you can modify the way in which the ROI and image are displayed using tools described in:

- section “Image manipulation tools” on page 149
- section “Slab and volume viewer tools” on page 155
- section “Visualization” on page 145

The **Name** field displays the names of all ROI contours on the current series. You can click on the name of an ROI to rename it.

The color control shows the color of each ROI contour on the current series. Click the color control to select a new color for the selected ROI.

The **Show** check box allows you to turn on or turn off the display for each ROI.

Create 3D ROIs

You can create 3D ROIs by manually drawing them on the images, or you can create SUV-based ROIs.

Create ROIs manually

The following ROI tools are available in the 3D ROI panel.

Click **Create ROI**, and then select one of the following tools to create the ROI.

Paintbrush: Create or edit contours. Specify the width of the paintbrush tool in millimeters. Click-and-drag the mouse to create the contour.

Freehand: Draw contours by hand. Click-and-drag the mouse to create the contour.

Point to Point: Draw contours using straight lines to connect between points you place.

Spline: Draw contours using curved lines to connect between points you place.

Interpolate Contours: Click to connect contours for a particular ROI.

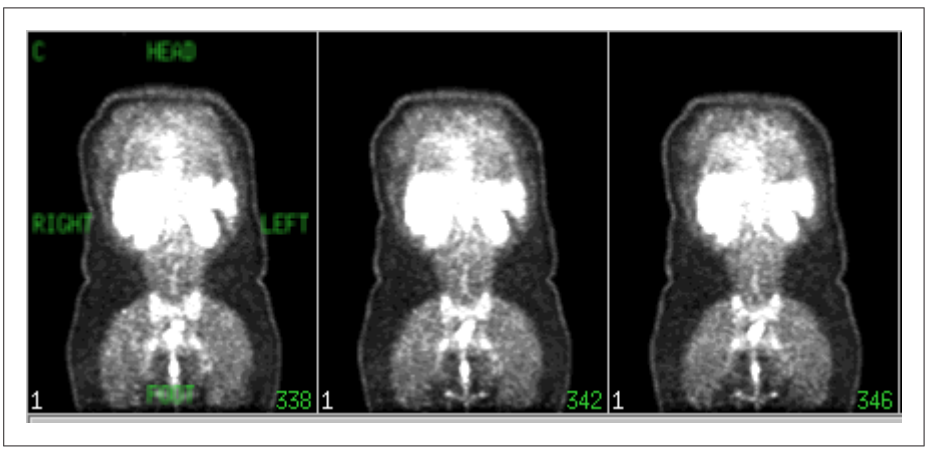
The procedure below describes using the spline and interpolate contours tools to create an ROI, but you can use any of the other tools, as necessary.

1. Identify an image containing a region of interest in a transverse, sagittal, or coronal viewer.
2. From the 3D ROI panel, click **Create ROI**.
3. Click **Spline**, and draw contours on non-sequential images of a larger structure.
4. Use the arrow keys to move between images.
5. Click **Interpolate Contours** to generate a complete ROI of the structure.
6. Scroll through the images to view the complete ROI.

Create ROIs based on SUV values

NOTICE

Full body PET images acquired using the GEMINI TF can show the patient's skin, as shown below. If a lesion is located near the visible skin in the image, take extra care when evaluating the body surface.



You can mark regions of interest for PET data that contain SUV scaling information. Control the defaults for your ROI tools from the ROI preferences. Refer to section “ROI” on page 347. Adjust the settings for the ROIs as you go by using the controls in the **3D ROI** panel.

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NOTICE

For seed based threshold ROIs, when placing the seed on the volume image verify its location on the reference images.

SUV threshold value (Fixed)

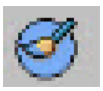
Follow this procedure to create an ROI based on an SUV threshold value.

1. Move the **SUV threshold** slider to create the ROI by setting a specific SUV threshold value. You can set a value from 0.1 to the maximum SUV value.

2. Click in the area of interest in a viewer to create a 3D ROI.
3. Scroll through the images to view the complete ROI.
4. To modify an ROI after it has been created, move the slider that appears below the image to adjust the SUV threshold value. The ROI changes as you move the slider.

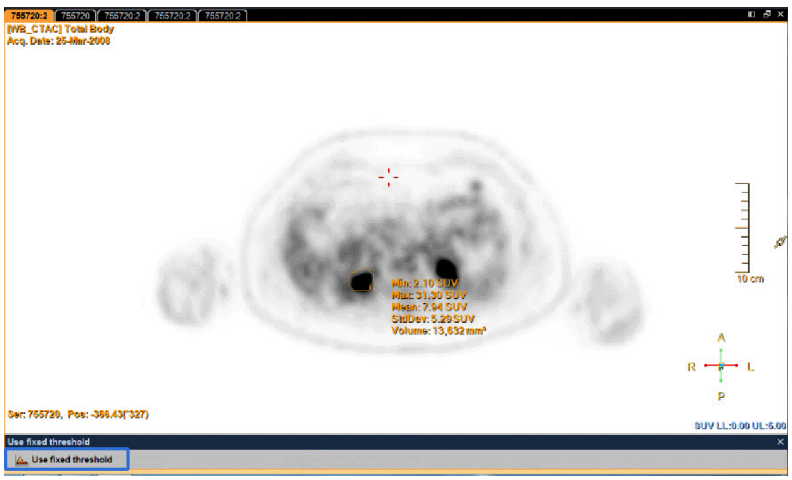
Adaptive Threshold

An adaptive threshold segmentation algorithm is available for accurate and reliable segmentation.

1. Click on the  Seed or the  Sphere icon and click on the lesion to create a ROI.

   The sphere icon can be used to define a boundary around the lesion. The size of the sphere can be adjusted by using **Ctrl** + **mouse scroll**.

   Once the lesion is segmented, the message “Use fixed threshold” with the graph icon appears below the viewer.



2. Click on the **Use fixed threshold** icon to change from the adaptive to fixed threshold algorithm and to adjust the SUV threshold using the slider bar.

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NOTICE

The adaptive threshold algorithm is not active once **Use fixed threshold** is selected. Any adjustments to the slider bar will work as fixed threshold for the selected lesion.

3. Multiple lesions can be segmented using the Sphere or Seed options.

Percent of maximum threshold value

Follow this procedure to create an ROI based on a percent of maximum SUV threshold value.

1. Move the **Percent Max** slider to create the ROI as a percentage of the maximum counts. The percentage ranges from 0-99%. Use the field to the right of the slider to specify the number of points to average when calculating the percent of maximum for the ROI. A percentage of the average maximum will be used to choose which points are included in the 3D ROI.

2. Click in the area of interest in a viewer to create a 3D ROI.
3. Scroll through the images to view the complete ROI.
4. To modify an ROI after it has been created, move the slider that appears below the image to adjust the percent of maximum value. The ROI changes as you move the slider.

Save ROIs

You can save your 3D ROIs as RTSTRUCT objects using one of the following methods. The RTSTRUCT objects, along with the original data, can be reloaded into NM Viewer for review.

-  To save the ROIs, click the Save drop-down arrow in the Utilities section of the Control panel, and select **Save ROI(s)**.
-  To include a description with the saved ROIs, click the Save As drop-down arrow in the Utilities section of the Control panel, and select **Save ROI(s) As**.

Remove ROIs

Click **Remove ROI** to delete one or more selected ROIs. To select the ROI you want to delete, click the name of the ROI in the 3D ROI panel and then click **Remove ROI**.

ROI menu options

Right-click on an existing ROI to open a menu with the following options:

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Delete Selected Contour: Click to delete the selected contour from the selected image.

Delete All Contours: Click to delete all existing contours in the selected ROI.

VOI Measurements: Click to display measurements associated with the selected contour.

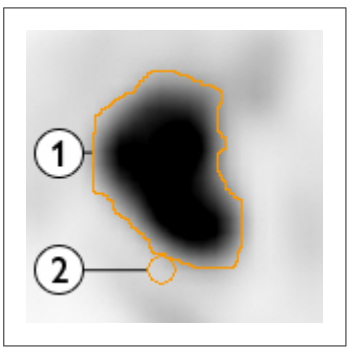
PET Units: Click to display PET units in **SUV**, **Counts**, or **Activity per Volume** when the VOI Measurements option is selected.

Statistics: Click to display **Minimum**, **Maximum**, **Mean**, **StdDev**, **Number of Voxels**, **Volume** or **Peak SUV** when the VOI Measurements option is selected.

Editing ROIs

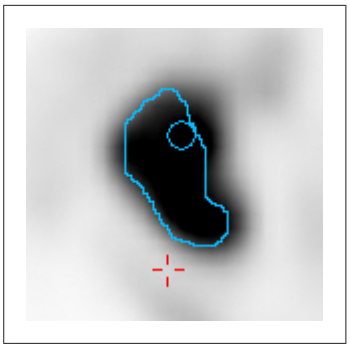
You can use the paintbrush tool to edit existing ROIs. If you use the paintbrush to edit a multi-image ROI, your edits only apply to the current image.

1. Find an image with an existing ROI.
2. Adjust the width of the paintbrush tool, if necessary.
3. Select the paintbrush tool. The circle cursor appears.
4. Move the cursor in proximity to the ROI and click. You can reduce or enlarge the current contour. If the cursor appears outside the contour, you can use the tool to reduce the ROI by pushing the contour in.



1	Contour
2	Circle cursor

If the cursor appears inside the contour, you can use the tool to enlarge the ROI by pushing the contour out.



Changing the name and/or color of an ROI

Use the 3D ROI controls tools to control the appearance and names of contours.

1. From the 3D ROI controls click the name field and type in a custom name.
2. Click the color control to choose a new color for the selected ROI.

Generating statistics from ROIs

Right-click on the ROI to open the ROI context menu. This menu gives you several choices including:

- delete the selected contour
- delete all existing contours
- display measurements associated with the selected contour
- display PET units in SUV, Counts, or Activity per Volume
- display Minimum, Maximum, Mean, StdDev, Sum of Voxel Values, Number of Voxels, Volume, or Peak SUV

The ICMT panel

Select **ICMT** from the drop-down menu in the Tools area of the Control panel to open the ICMT panel. The ICMT panel contains tools that let you perform processing operations on images and generated curves. For detailed information about the ICMT tools, see section “Image and Curve Manipulation” on page 41.

The Batch panel

Select **Batch** from the drop-down menu in the Tools area of the Control panel to open the Batch panel. The Batch panel contains controls for creating image batches that you can save as new image series from a scan series.

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NOTICE

If you close the viewer, change the layout, or change the **Generate batch to enable tiling** settings after defining your batch settings, all of your batch settings will be changed.

If you change slab thickness after defining your batch settings, the images will be saved with the new slab thickness.

1. Click in the viewer you want to use to generate your batch. The selected viewer type determines which options in the Batch panel are available to you.
2. Right-click in the viewer and use the tools in the menu to set the slice thickness and slice angle.

NOTICE

Slice thickness and slice angle are not available for Basic2D layouts. Slice angle is not available for SlabMPR viewers.

3. Select the area to use for the batch.
   - **Viewer** uses the viewer you currently have selected. Select this option if you want to save data, such as the coronal views, to a new series.
   - **Display** uses the entire viewing area. Select this option for secondary captures.
4. Select the batch type. The batch type determines the format of the batch you want to save.
   - **Data** - saves the images as a new series that you can use for further display or analysis.
   - **Secondary Capture (SF)** - secondary capture (single frame)
   - **Secondary Capture (MF)** - secondary capture (multi frame)
   - **Monochrome Secondary Capture (SF)** - secondary capture (single frame) in grayscale
   - **Monochrome Secondary Capture (MF)** - secondary capture (multi frame) in grayscale
   - **AVI**
   - **JPEG**

NOTICE

The Data option is only available for Slab, SlabMPR, Basic2D, and Cardiac viewers. Volume viewers can only be saved as secondary captures. Also, if you select the Data option, you will not be able to specify time bins. If you select the Display option, the Data option is disabled.

5. If you selected the Data batch type, select a batch option.
   - **Activity** - stores the data as activity concentration. (This option is only available if the data can be converted to activity concentration.)

- **Share** - adds the saved batch to the Series list.
- **Square** - creates the batch as square images for viewing on those systems that require the X,Y pixel spacing to be the same.

6. Click the **Select Batch Viewer** icon.

7. Set the range of images you want to use in the batch.

   Scroll in the selected batch viewer (or alternately triangulate using any other related viewer) until the first image you want to use appears in the selected batch viewer. Then click the **First Slice in Batch** icon. The position of the selected image is shown next to the icon.

NOTICE

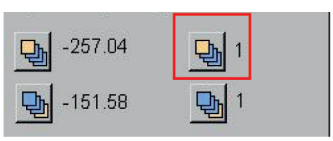
For volume viewers, the image range is labeled "Oblique" and you do not need to define the range of images. For other oblique viewers, you must define the range of images.

8. Scroll in the selected batch viewer (or alternately triangulate using any other related viewer) until the last image you want to use appears in the selected batch viewer. Then click the **Last Slice in Batch** icon. The position of the selected image is shown next to the icon.

9. If you are using gated or dynamic data, set the range of time bins you want to use in the batch. The time bin is defined by the viewer movie control. The first time bin is displayed by default.

   If you are not using gated or dynamic data, continue to step 13.

10. To change the displayed time bin, select the movie control from the viewer context menu.
11. Move the slider to the time bin you want to use as the first bin in the batch, and click the first time bin icon in the Batch panel. The number of the bin you selected is shown next to the icon in the panel.



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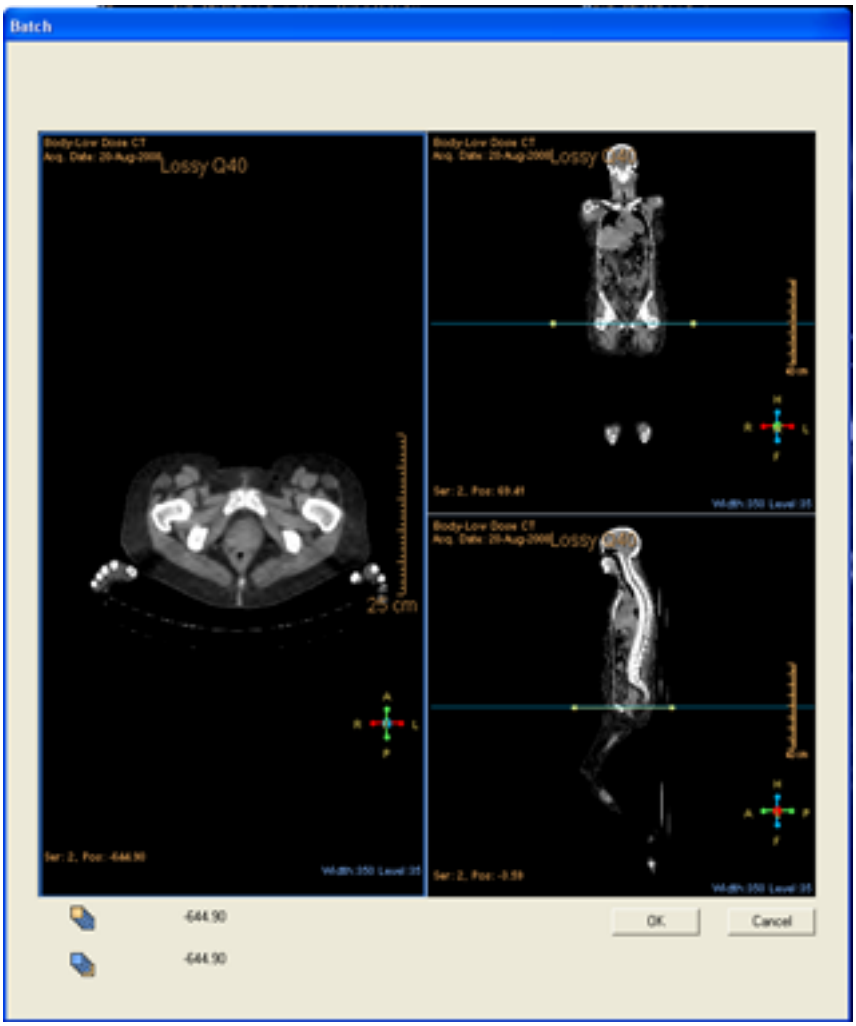
12. Move the slider to the time bin you want to use as the last bin in the batch, and click the last time bin icon in the Batch panel. The number of the bin you selected is shown next to the icon in the panel.

13. From the Save As drop-down menu, select **Save Batch As**. The Saving dialog opens.
14. Choose the saving options, as necessary, and click **OK** to save the batch. Image parameters, such as slab thickness, are applied when you save the batch. Pan and zoom settings are saved when you save secondary capture images or reoriented images such as short axis, vertical long axis , and horizontal long axis.

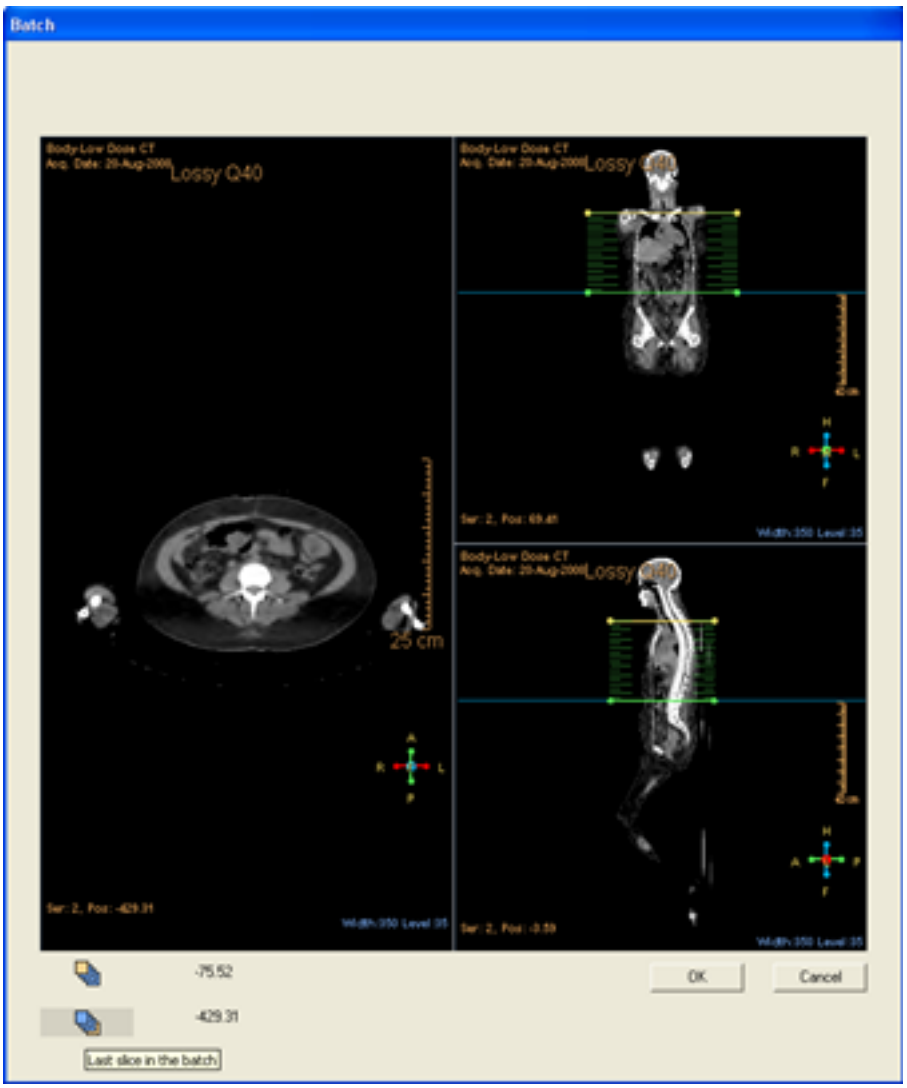
Within the Batch tool, a feature was provided to enable selecting the range of slices for inclusion within the resultant file. After accessing the Batch tool and setting up the batch area, the resultant file format, the additional batch options and the batch viewer, the **Set image range** icon becomes active.

1. Click the **Set image range** icon to open a panel similar to the following:



2. Use the blue line displayed on the sagittal and coronal images to identify the starting and ending slice for the image file to generate.
   - First, move the line to the slice you wish to start at and click the **First Slice in Batch** icon.
   - Then, move the line to the slice you wish to end at and click the **Last Slice in Batch** icon.

     After you have set the position of the First and Last slices, the Batch window appears similar to the following:



3. If no further adjustments are required, click **OK**, to close the Batch window.

   The slice range in the Batch tool panel is updated with the values from the Set image range window.

4. Select Save Batch as to save the newly defined file.

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Utilities

The Utilities section of the Control panel contains the controls for saving images (see the section that follows), viewing tools (see section “Viewing tools” on page 144), and measurement tools (see section “Measurement tools” on page 144).

Saving images

To save one or more images or films, click the drop-down arrow next to **Save**, **Save As**, **Film**, or **Report** and choose the appropriate option from the dropdown list.

NOTICE

Save controls are not available when the viewer is in comparison mode.

When you save images from a 3D viewer, use the Save Batch As option. Control the saving options from the Batch panel to select a file format other than Data. See section “The Batch panel” on page 136 for more information.

In fused displays, saving saves the visible series. If both the overlay and underlay series are visible, saving saves the overlay series.

Save

Click the Save drop-down arrow to choose **Save image(s)**, **Save display**, **Save secondary captures**, **Save ROI(s)**, or **Save resampled series** from the drop-down menu.

Save image(s) saves all images in the series in the selected viewer as a new series in the same study as the selected series. Images are saved with square pixel spacing based on the current slab thickness.

Save display takes a screenshot of the current display. The saved display becomes a new series in the same study as the selected series.

Save secondary captures saves all images as a DICOM secondary capture based on the current slab thickness. Saves one view for the referring physician.

Save All saves all open viewers. The viewer saves single PET, SPECT and CT series in the format specified in the **Save All Format** preference, while fusion views are saved as secondary captures. Refer to section “PET” on page 344 for information about the Save All Format preference.

NOTICE

The **Save All** option is only available on the IX and LX workstation configurations.

Save ROI(s) saves ROIs as RT Struct objects.

Save resampled series saves the resampled series.

Save As

Click the **Save As** drop-down arrow to choose **Save Batch As** or **Save ROI(s) As**.

Save Batch As saves the defined batch as a new series. For information about creating a batch, see section “The Batch panel” on page 136.

1. Click **Save Batch As**.
2. Type a description for the new series. The default description is prepended with the orientation of the defined batch.
3. Select a location for the saved files.
4. Click **OK**.

Save ROI(s) As saves the ROIs as DICOM RT Struct objects.

1. Click **Save ROI(s) As**.
2. Type a description for the new series.
3. Click **OK**.

Film

Click the **Film** drop-down arrow to choose what you want to film.

Film image sends the image in the current viewer to FilmView.

Film display in gray scale sends the current display to FilmView in gray scale.

Film display sends the current display to FilmView.

Direct film display sends the current display to the default printer. This command does not send images to the **FilmView** function.

Film Batch sends the defined batch to film. For information about creating a batch, see section “The Batch panel” on page 136.

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Report

Click the **Report** drop-down arrow to choose the desired report.

Report image sends the image in the current viewer as a secondary capture to the Reporting application.

Report display sends the current display as a secondary capture to the Reporting application.

Report Batch As sends the defined batch to the Reporting application. For information about creating a batch, see section “The Batch panel” on page 136.

NOTICE

Images are sent to the Film viewer and the Report viewer as secondary capture images. These images do not retain pixel size or value information. ROIs and size measurements are not available for these images within the print and report applications. View measurements from within the NM Viewer.

Click the **Bookmark** drop-down arrow to choose the desired option.

Save Bookmark saves the current state of the viewer for future use. The bookmark contains:

- Series selection
- Registration matrices between series in the series selection
- Picked points
- Window/level
- Colormaps
- Zoom/Pan
- Cine states
- Toolbars
- Movie control bars
- Layout geometries (viewer sizes, positions, tiles etc)
- Fusion states
- Alpha blending values
- Link states

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NOTICE

2D ROIs are not saved as part of bookmarks. 3D ROIs can be saved as part of bookmarks if they are saved as RT Struct objects first.

The **Open Bookmark** control opens the bookmark selection dialog when one or more bookmarks are available. Select and load any available bookmark from the dialog.

Setting the quality level

The **Quality Level** tool lets you change the compression of images to improve the performance of the system when it is downloading images using a connection other than your main connection to your server. The default quality level is 100%. Using a quality level of less than 100% will impact the image quality because image compression leads to a loss of image quality, but compressed images will download faster when you are downloading images using a connection other than the one to your server.

When you click the Quality Level drop-down menu, you have several options to choose from:

- Quality Level 100%: recommended for image download to your local server.
- Quality Level 80%: recommended for image download over a Wide Area Network (WAN).
- Quality Level 60%: recommended for image download through a cable modem or DSL modem.
- Quality Level 40%: recommended for image download through ISDN or a modem.

Viewing tools

The Utilities section of the Control panel contains viewing tools, such as Scroll, Pan, and Zoom. Actions you perform using this set of tools affects linked viewers. For information about the individual viewing tools, see section “Image manipulation tools” on page 149.

Measurement tools

The Utilities section of the Control panel contains measurement tools that you can use to mark locations and measure 2D distances or angles on images, such as a line tool, an angle tool, and a tool for drawing shapes.

You can use the measurement tools only in the active viewer, or you can set the tools to be persistent and available for use in all viewers. To make the tools persistent, click the box that surrounds the measurement tools. When the box appears orange, the tools are not persistent. When the box appears blue, the tools are persistent.

For information about the measurement tools, refer to section “Graphic elements” on page 157.

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NOTICE

You cannot export shapes drawn using the measurement tools from the NM Viewer as RT Struct objects.

NOTICE

Shapes drawn using the measurement tools incorporate resampled data and display slightly different values than those presented when you use the 3D value cursor. For comparison, view the original images in the 2D layout in the NM Viewer.

Visualization

The global visualization section of the control area contains window preset and annotation controls.

Contrast controls

Click the drop-down list and select one of the available options.

- The **Modified** preset describes any value that doesn't match one of the other CT presets.
- The **SUV-10** preset sets the UL SUV value to 10 and the LL SUV value to 0. When used with the SUV colorstripes, the SUV-10 preset displays highlights in color regions with an SUV value greater than 2.5.
- Factory defaults (shown in the table that follows) are based on typical CT preset window/level values.

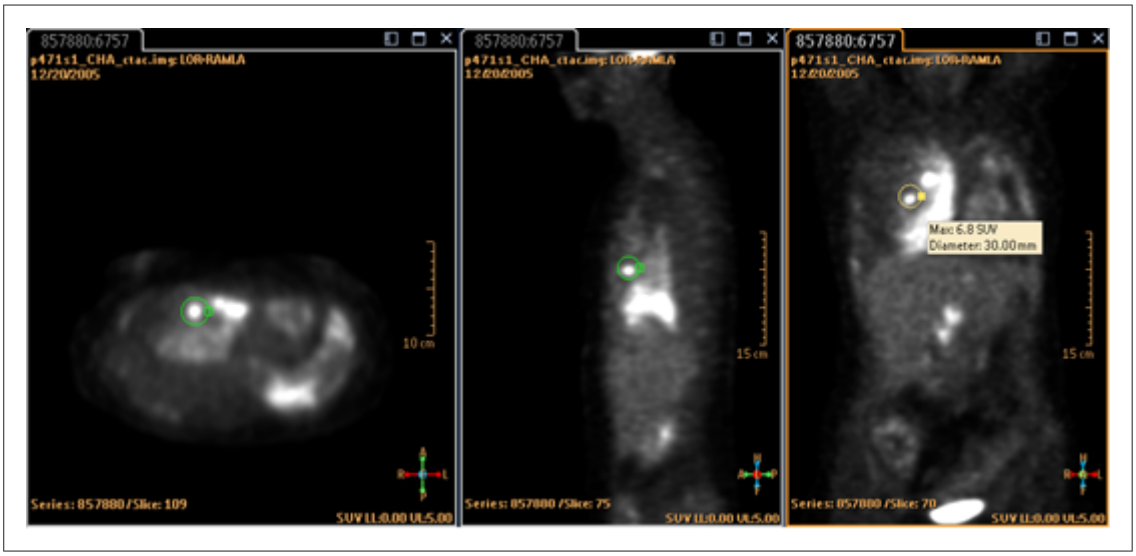
	Center	Width
Abdomen	60	360
Bone	800	2000
Brain	35	70
Cardiac	90	750
Colon	0	2000
IAC	600	4095
Liver	100	200
Lung	600	1600
PF	35	150
Spine	60	300

You may modify the CT presets using the CT Viewer preferences.

Triangulation cursor

The triangulation cursor is shown when you click in a viewer. Use the **F9** key to cycle through the triangulation cursor's three states:

- Triangulation cursor cross-hairs
- Triangulation cursor off
- Triangulation cursor sphere



The sphere cursor places a sphere in the selected viewer and all linked viewers. An associated tooltip displays statistics about the selected area. Refer to section "Viewing" on page 344 for information about setting the preferences for the cursor.

Smart Links

The **Smart Links** control links or unlinks viewers. When Smart Links are turned on, changes to colormap, window/level, triangulation/picked point links, zoom, pan, and scroll affect the linked viewers. When Smart Links are turned off, changes only affect the current viewer. Click the Smart Links icon to toggle linking on or off. By default Smart Links are turned on.

You can also click on the Smart Links icon in an individual viewer to change the link setting of that viewer.

-  Indicates that Smart Links are turned on for this viewer. Changes made for this image will also occur in other linked viewers.
-  Indicates that Smart Links are turned off for this viewer. Changes made for this image only impact this viewer. Clicking this icon again will add the viewer back to the link group.

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The **Link Viewers** control links or unlinks the scrolling for two groups in a study comparison layout. You can link viewers from different series so that scrolling in a plane in the first series results in a change in the slice presentation of the same plane in the linked series. For example, when comparing two studies from different time points, find the same anatomical location in both studies and click the Link Viewers icon to link that point. Then as you scroll in one study, the other study will scroll simultaneously. Refer to section “Linking studies or groups” on page 122.

Indicates that **Automatic linking of compared studies** was performed. This control automatically links follow-up PET-CT studies. Once two PET-CT cases (of the same patient) are loaded, the automatic algorithm registers the two datasets and automatically links them. To un-link the studies, click the **Automatic linking of compared studies** icon.

Smart Link behavior

The following sections explain the behavior of the software when you use the Smart Link control to link viewers.

Colormaps are linked between viewers displaying images from the same modality. For example, data views from PET series will have linked colormaps when they are presented in different views. There are some instances, however, where colormaps are not linked:

- Colormaps are not linked between volumetric or planar datasets or rendered images.
- Colormaps are not linked between overlay and underlay images in the same viewer. For example, changing the overlay colormap has no affect on the underlay colormap for any fused viewer.
- Colormaps are not linked across compared groups.

Window/Level settings are linked between viewers displaying the same series. The following restrictions apply to window/level settings for volumetric datasets.

- Window/Level settings are not linked between overlay and underlay images in the same viewer. For example, changing the overlay window/level has no affect on the underlay window/ level for any fused viewer.
- Window/Level settings are not linked across compared groups or in MIP viewers

The following restrictions apply to window/level settings for planar datasets.

- Window/Level settings are not linked for different image types. For example, window/level settings for a whole body image are not linked to window/level settings for planar bone spot views.
- Window/Level settings are not linked for different scan phases of the same acquisition. For example, the flow and function phases of a renal exam each have their own window/level setting.
- Window/Level settings are not linked for computer-generated images such as phase and amplitude images in an MUGA study.
- Window/Level settings are not linked across compared groups.

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Triangulation Cursor/Picked Point Sphere is linked between viewers displaying volumetric data from the same group. For example, Triangulation is linked in the MIP viewer as well as the Transverse, Sagittal, and Coronal viewers of a layout displaying a PET, CT, or a fused PET/CT study.

Zoom, Pan, and Scroll functions are linked for viewers displaying the same orientation of volumetric data from the same group.

Zoom and Pan are linked for viewers displaying the same orientation of the same type of NM planar data from the same group. Zoom and Pan are not linked for images of different types, but Zoom and Pan are linked for images of the same type displaying the same view from opposite angles.

Fusion and Alpha Blend are linked for all Transverse, Sagittal, and Coronal viewers if the viewers display the same series pair (overlay or underlay). The following restrictions apply for fusion links.

- Fusion and Alpha Blend are linked for viewers that have the same initial fusion state. For example, if you have a row of Transverse, Sagittal, and Coronal viewers that are displaying PET/CT fusion with only PET displayed initially, and you have a second row that is also displaying PET/CT fusion with only CT being displayed initially when Fusion is enabled for any one of the PET viewers, Fusion is enabled for all of the PET Transverse, Sagittal, and Coronal viewers. When Fusion is enabled for any one of the CT viewers, then it is enabled for all of the CT Transverse, Sagittal, and Coronal viewers. When Alpha Blend is adjusted in these cases, it will apply to the entire fused Transverse, Sagittal, and Coronal group.
- Fusion and Alpha Blend are not linked across compared groups.

Statistical Data is linked between viewers displaying gated or dynamic data, Table viewers, and Graph viewers. For example, analysis performed on an image viewer will propagate statistical results to the Table and Graph viewers in the same layout.

3D ROI links let you propagate an ROI drawn on a CT image to a PET image in another viewer as long as both the CT and PET images have the same orientation and are in the same group.

Slab Markers are linked for one set of Transverse, Sagittal, and Coronal viewers in a layout. When you rotate the Slab Markers, the software maintains the three orthogonal views in a Transverse, Sagittal, and Coronal layout.

Slab thickness is linked between slab viewers of the same type (SlabMPR or Slab).

Annotation controls

To change the annotation you want displayed in the viewers, select from the following options on the control panel.

All Annotation Off: Turns off annotation in the selected viewer.

NOTICE

If the preferences specify that no annotation is shown, only the base annotation appears.

Minimal Annotation On: Shows minimal annotation in the selected viewer. The fields shown vary depending on image modality/type.

Normal Annotation On: Shows normal annotation in the selected viewer. The fields shown vary depending on image modality/type.

Extended Annotation On: Shows all available annotation in the selected viewer. The fields shown vary depending on image modality/type.

Fusion controls

Toggle Fusion: Click the fusion button to create a fusion view in a non-fusion viewer.

Activating the fusion display in a viewer activates the fusion display for all viewers showing the same series, as long as Smart Links are turned on.

Alpha Blending: Controls the ratio of the overlay image to the underlay image.

Lesion mask display

Activate the lesion mask display from the visualization tools to limit the PET or SPECT data displayed in volume viewers to the areas enclosed in an ROI. In fusion views, the PET or SPECT ROI is shown along with full CT data.

Closing the application

Close the NM Viewer using the Exit button.

Tools description

Access tools in the NM Viewer in any of these ways:

- From the Control Panel
- From the Image Controls toolbar
- By right-clicking on an image

Image manipulation tools

Right-click on an image to view a menu of tools available for that image.

Generate Statistics: Displays data from dynamic ROIs or cardiac gated ROIs created using the ROI tools. This option appears in the menu when at least one ROI is created on gated or dynamic data. The option is also available for multi-frame NM planar data.

To generate statistics:

1. Draw an ROI using the graphic element measurement tools.
2. Right-click on the viewer and select **Generate Statistics**.

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Alpha Blending: Controls the ratio of the floating image in the floating/overlay image. The **Alpha Blending** tool is active only when fusion is turned on.

To adjust the alpha blending:

1. Click the **Alpha Blending** icon and then click in a fusion image.
2. Drag the mouse up or right to view a greater proportion of the overlay image.
3. Drag the mouse down or left to view a greater proportion of the underlay image.

   As you adjust the alpha blending, the viewer displays the percentage of the contribution of the overlay to the display.

   The **Alpha Blending** tool is active only when fusion is turned on.

Scroll: Use any of the following options to scroll through the series:

- Hold down the left mouse button and drag it vertically. Dragging the scroll tool up advances the images, and dragging it down goes back through the images.
- Use the up and down arrow keys to go to the next or previous images in single image steps in the vertical (Y-) dimension.
- Use **<Page Up>**/**<Page Down>** keys to advance or go back through the images.
- Use the **<Home>** or **<End>** keys to go to the first or last image in the horizontal (X-) dimension.
- Use the scroll wheel on your mouse, if available, to advance or go back through in single image steps.

Zoom: To magnify or reduce the size of the image, select the Zoom tool, and drag up to zoom in or drag down to zoom out.

Pan: Move the image to center the feature of interest in the image frame.

Gray Level: Use this tool to increase or decrease the gray level in the image. Drag vertically to adjust the gray level in the selected viewer.

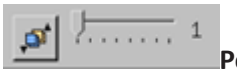
Contrast Stretch: Automatically adjust contrast to emphasize areas of low intensity or density.

CT/SUV Preset: The NM Viewer uses the preset scale values defined for the CT viewer as in the Contrast controls. The SUV preset is for 2D only. Adjust the image contrast based on the SUV threshold value.

Play/Stop Movie: Starts or ends the movie.

Movie: Shows or hides the movie controls.

- **Play**: Starts the movie.

- **Stop**. Ends the movie. (The Stop button appears after you click the Play button).
- **Frames Per Second**: Slider bar controls the speed at which the movie plays. The movie can be played at between 0 and 60 frames per second.
- 

Position/Time Control: Allows user to switch between scrolling through time (bins) and images when viewing gated or dynamic data.
- The movie can be played forward or backward. Refer to section “The Display panel” on page 112 for a list of movie controls.
- Image and position numbers increase when forward is selected.
- 3D images rotate around the central body axis.
- Forward rotation of a 3D image is clockwise when viewed from the top of the volume.

Generate batch to enable tiling: Allows you to show a sequence of tiled images in increments of one. After selecting the tool, right-click in the image to bring up the context menu again. Directly under **Generate batch to enable tiling**, select a tile setting to control how many images from each series will be visible in a single viewer. The context menu displays the most recent tiling choice, such as “1x1”.

You can tile an individual viewer into the following numbers of rows and columns.

1x1	1x2	1x3	1x4
2x1	2x2	2x3	2x4
3x1	3x2	3x3	3x4
4x1	4x2	4x3	4x4
5x5	8x8		

Additionally, <**Ctrl**> + the keyboard arrow keys can be used to add or remove rows and columns from viewers. <**Alt**> + click maximizes a single tile without changing the current viewer tiling. <**Alt**> + click again restores the original tiled view. Refer to section “Keyboard shortcuts” on page 162.

Fusion: Turns fusion display on or off in the selected viewer. You can also press the F12 key to turn the fusion display on or off.

Reset layout: Restores the original settings in the current layout.

Fit Width: Fit the current image to the width of the viewer.

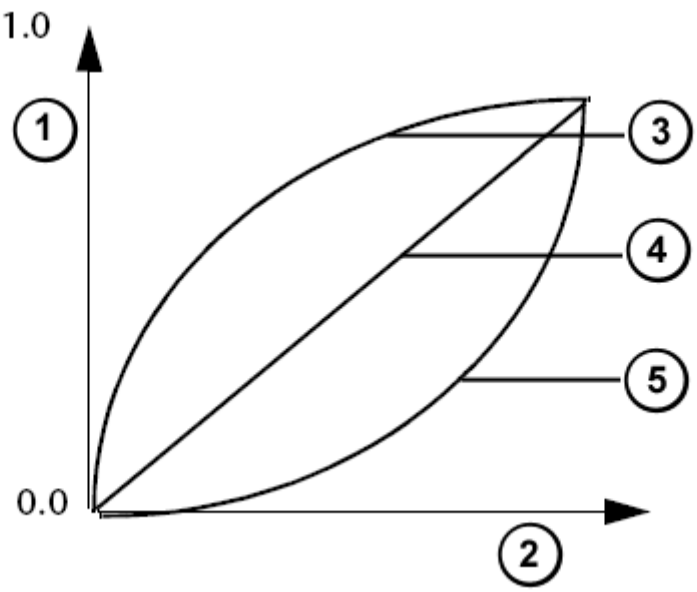
Fit Height: Fit the current image to the height of the viewer.

Colormap Tools. Expands to display the Colormap selection controls and the Color Scale control.

-  **Select Overlay Colormap**: Choose a colormap scheme. You can also adjust the intensity of the overlay.
-  **Select Underlay Colormap**: Choose a colormap scheme. You can also adjust the intensity of the underlay when fusion is active for the chosen viewer.
- **Overlay Intensity Correction/Underlay Intensity Correction**: Select an intensity map to change the intensity of the displayed image. It is available in the drop-down menu at the right end of the color bar.

Weight	Function
Log3	y = e1/2.3
Log2	y = e1/2.0
Log1	y = e1/1.5
Linear	y = x
Exp1	y = e1.5
Exp2	y = e2.0

Use Log1, Log2, or Log3 when you want to enhance the lower count portions of an image. Use Exp1 or Exp2 when you want to enhance the higher count portions of an image.



1	Intensity Factor	4	Linear
2	Counts	5	Exp
3	Log		

-  **Color Scale**: Turns the color scale display on or off in the selected viewer.

 **SUV or CT Value**: Calculates and displays the pixel value as you move the cursor over the image.

The value is an average calculated from the Cursor Area set in the Value Cursor preferences. Refer to section “Viewing” on page 344.

 **Measurements**: Expands to show the measurement options for the active image. Refer to section “Graphic elements” on page 157 for a full list of options.

 **Show/Hide Contour Set**: Displays or hides any existing contours or regions of interest.

 **Show/Hide Colorwash**: Displays or hides the colorwash in the selected viewer.

 **Select Image Orientation**: Expands to show image orientation options:

-  **Axial Feet**: Changes the orientation in the selected viewer to an axial view.
-  **Sagittal Left**: Changes the orientation in the selected viewer to a sagittal view.
-  **Coronal Front**: Changes the orientation in the selected viewer to a coronal view.

 **Capturing**: Expands to show save options for the selected viewer.

-  **Save image(s)**: Saves all images in the series in the selected viewer. The saved images become a new series in the same study as the selected series.
-  **Save display**: Saves a screenshot of the current display. The saved display becomes a new series in the same study as the selected series.
-  **Save secondary captures**: Saves the current display as a secondary capture image.

 **Toggle smart links**: Turns the Smart Links on or off.

 **Text**: Expands to allow you to place an alphanumeric annotation on the image.

-  **Text**: Creates a text box in which you can place alphanumeric annotation on the image.
-  **Arrow + Text**: The Arrow + Text tool allows you to add text and set its properties. The Arrow + Text tool adds text at the cell level, and is cropped if it extends beyond a cell.

CAUTION

When you add annotations, be careful not to accidentally cover some patient information. If you do, you could misidentify a patient, potentially causing misdiagnosis.

NOTICE

The text you type is not saved; to preserve it you must create a secondary capture.

To add text using the **Text** or **Arrow + Text** tool:

1. Shift-click where the text (or arrowhead in the case of Arrow + Text) should be.
2. For Arrow + Text, click to define the other end of the arrow and the text.
3. When the text dialog appears, type some text in the top of the box or select some text in the bottom of the box.
4. Set the color using the color pull-down menu.
5. Set the font size using the middle pull-down menu.
6. Use the eraser to delete a text entry.
7. Dismiss the box by clicking the X or by clicking anywhere outside the box.
8. Drag to move the text (and arrow).

The text choices in the bottom of the box are set in the IntelliSpace Portal Preferences. See section “PET” on page 344 for details.

Copy: captures a copy of the selected image for use in word processing or another application.

Apply ROIs to Underlay: Places an ROI element on the underlay view. This tool is only available in the ROI context menus in a fused viewer when a 2D ROI has been applied to that viewer.

Apply ROIs to Overlay: Places an ROI element on the overlay view. This tool is only available in the ROI context menus in a fused viewer when a 2D ROI has been applied to that viewer.

2D layout image manipulation tools

The 2D layout contains modified tools to control the image tiling. These tools are available in addition to the regular tiling option:

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Histogram Windowing: Resets viewer contrast level to a reasonable value for data that does not have SUV values calculated. Use this tool to make a quick contrast adjustment when the values are far from normal.

Add Row: Adds one new row to the selected image.

Add Column: Adds one new column to the selected image.

Remove Row: Removes one row from the selected image.

Remove Column: Removes one column from the selected image.

Rows x Columns: Sets the tiling, for example 1 x 1.

Set Auto Pan/Zoom: Positions the image within the viewer to allow maximum sizing within the viewer's parameters. Centers the image in linked viewers of the same orientation.

Orientation Labels: Select the applicable orientation labels.

- Left - right
- Right - left
- Anterior - posterior
- Posterior - anterior

Slab and volume viewer tools

Slab and volume viewers use many of the general image manipulation tools, along with tools specific to these viewer types. The viewer-specific tools appear when you right-click a viewer or are in the image controls for the viewer.

Slab Thickness: Controls the thickness of the volume displayed in the slab viewer. Select **Enter the size** and select a value in mm from the drop-down menu. Then click **Generate Batch** to implement the change.

Select Volume Preset for Overlay/Underlay: Controls the display mask for the overlay or underlay image in a volume viewer.

Position: Selects the portion of the volume to display in the slab.

Roll/Rotate: Adjust the orientation of the volume.

Rotate: Rotate the image in the current viewer.

Reset Layout: Restore the original settings for the current layout.

Fit Width: Fit the current image to the width of the viewer.

Fit Height: Fit the current image to the height of the viewer.

Contrast Stretch: Automatically adjust contrast to emphasize areas of low intensity or density.

Show/Hide Mesh: Show or hide the mesh display of an ROI for a volume viewer.

Show/Hide Mask: In a volume viewer, show or hide the portions of the image not contained within the ROI. Please note that you can also use the Lesion Mask Display control. Refer to Lesion Mask Display in section “Visualization” on page 145. You can use the Show/Hide Mesh, Show/Hide Mask, and Show/Hide Contour Set tools in any combination.

Couch Removal: Toggles on/off couch removal from a 3D rendering.

Table viewer tools

Copy: Copy a selected graphic element for pasting onto new slices.

Table Background Color: Select the applicable background color for the table viewer.

Graph viewer tools

Rulers: Select a ruler display.

Statistics Item to Display: Select a statistic display.

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Graphic elements

Use the NM Viewer's graphic element tools during image analysis to mark and measure 2D locations on the image. These graphic elements apply to individual images in a series.

Graphic elements can be copied from one image and pasted into another in a position relative to that of the graphic elements in the source image. They may also be selected, dragged, resized, and annotated within a viewer.

By default, in fusion views the graphic element is applied to the overlay image. Any graphic element will only be associated with one image at any time. If fusion is turned off in a viewer, the graphic element will appear on the currently active series.

In cases where the graphic element was drawn on the overlay image and the viewer displays the former underlay image when fusion is turned off, the graphic element will be associated with the visible series, but not with the former overlay image.

In cases where an image with an associated graphic element is brought into a fusion viewer, the graphic element will remain associated with the original series.

NOTICE

Graphic elements can be drawn on 3D Slab MPR viewers. However, they cannot be drawn on 3D full volume rendered images.

NOTICE

Measurements for 2D ROI's applied to SlabMPR and Slab viewers are reported for the rendered image and not the original data. To obtain measurements for original data use 3D ROI tools.

Graphic element measurement tools

Auto SUV ROI: Create an ROI based on the values set in the Control Panel's Auto SUV feature. This option only appears in the menu if you are using PET SUV data. Refer to section "Tools" on page 112 for information on setting the Auto SUV level.

NOTICE

The Auto SUV ROI tool is only available in 2D layouts.

Point: Show the location of the point at the center of the cursor. Select the **Point** tool and click on the spot you want to measure.

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Line: Draw a line between any two points on the image.

Left-click on the starting point and drag in the desired direction. Click to set the end point. The system calculates and marks the distance between the endpoints of the line in millimeters.

Angle: Draw two joined lines, which can be placed along two image features to measure the angle between them.

Click where you want to start the first line. Click where you want to end the line, which becomes the vertex of the angle. Click where you want to end the line to complete the angle.

Open Angle: Draw two separate lines, which can be placed along two image features to measure the angle between them.

Click where you want to start the first line. Click at the end point of the first line to end the line. Click where you want the end of the line. Click where you want to start the second line. Click where you want the end of the line.

NOTICE

The Open Angle tool is only available in 2D layouts.

Polyline: Draw a line with corners at set points.

Click where you want to start the line. Drag the mouse to the point where you want to change the line's direction. Click to set a corner. Draw other line segments in the same way. Double-click at the end of the line.

NOTICE

The Polyline tool is only available in 2D layouts.

Open Contour: Draw a curved contour line along the edge of a feature of an image.

Click where you want to start the contour. Move the mouse along the perimeter of the area you want to mark. A line appears along the mouse's path. Click to end the line.

You can edit open contours by selecting the contour and drawing a path that starts and ends on the contour. The new path replaces the contour segment between those points.

Circle: Draw a circle on the selected image.

Click where you want to start the circle. Drag the mouse until the circle is the correct size. Click to complete the circle.

Ellipse: Draw an ellipse on the selected image.

Click and drag the cursor in the direction of the major axis of the ellipse. When the line drawn reaches the desired length, release the mouse. Move the cursor at right angles to the first line until the ellipse is the desired size.

Smoothed Polyline: Draw a line with curves at set points.

Click where you want to start the line. Drag the mouse to the point where you want to change the line's direction. Click to set a curve. Draw other line segments in the same way. Double-click at the end of the line.

Box: Draw a box on the selected image.

To use, click to set a starting point for the box. Drag the mouse until the box is the correct size and shape. Click to complete the box.

Rectangle: Draw a rectangle on the selected image.

Click where you want to start the rectangle. Draw one side of your rectangle. Drag the mouse until the line reaches the desired length, and click to complete the line. Move the mouse at a right angle to the line to expand the rectangle. Click to complete the rectangle.

You can rotate or resize the rectangle by selecting it, clicking on a handle on the rectangle's corner, and dragging that corner to a new location. The entire rectangle will rotate and/or change size.

NOTICE

The Rectangle tool is only available in 2D layouts.

Polygon: Draw a multi-point polygon.

Click where you want to start the polygon. Drag the mouse to expand the shape and click to set corners. Double-click to set the final corner and complete the polygon.

NOTICE

The Polygon tool is only available in 2D layouts.

Smoothed Polygon: Draw a multi-point polygon with curved corners.

Click where you want to start the polygon. Drag the mouse to expand the shape and click to set corners. Double-click to set the final corner and complete the polygon.

Freehand Contour: Draw a curved contour shape around a feature of an image.

Click where you want to start the curve. Move the mouse along the perimeter of the area you want to mark. A line appears along the mouse's path. Click to complete the shape.

Edit freehand contours by selecting the contour and drawing a path that starts and ends on the contour. The new path replaces the contour segment between those points.

Rulers: Click to show or hide a ruler on the image.

Grid: Click to show or hide a grid on the image.

Selecting and changing graphic elements

Use this procedure to change the shape or position of an existing graphic element or to select an existing graphic element for annotation.

1. Hover your mouse over the graphic element you want to change.
   - A selected line appears bold.
   - A selected handle changes from an outline of a box to a solid colored shape.
2. To modify the element, click and drag one of the handles, or right-click on the selected element to view a list of tools available.

Graphic element notation tools

The NM Viewer contains notation tools for labeling and manipulating any graphic elements that have been added to an image. Some of the notation tools are available for all graphic elements while others are only available for certain graphic elements.

To use the notation tools, select the graphic element by clicking on it (the graphic element will become yellow). Then right-click on the graphic element to display the notation tools that are available for that graphic element.

NOTICE

Each notation you place on the image has a tooltip by default. Hover your mouse over a notation to view the tooltip.

Properties: Change the line width, line style, color, or font size of the graphic element.

Cut: Remove the selected graphic element from the viewer while retaining the element for use in another viewer.

1. Right-click on the graphic element you want to cut. The menu of notation tools opens.
2. Click **Cut**. The graphic element is removed from the viewer.
3. Right-click in the viewer to which you want to add the graphic element. A menu of tools opens.

   Click **Paste**. The graphic element you cut appears in the viewer.

Copy: Copy a selected graphic element for pasting onto new slices.

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1. Right-click on the graphic element you want to copy. The menu of notation tools opens.
2. Click **Copy**.
3. Right-click in the viewer to which you want to add the graphic element. A menu of tools opens.

   Click **Paste**. The graphic element you copied appears in the viewer.

Delete: Delete a graphic element.

1. Right-click on the graphic element you want to delete. The menu of notation tools opens.
2. Click **Delete**.

NOTICE

In some cases, such as when a label is being deleted, you can delete only part of a graphic element.

Histogram: Place a histogram chart in the image.

NOTICE

The Histogram tool is only available in 2D layouts.

Length: Display the length of the selected line.

Profile: Place a profile chart on the image.

NOTICE

The Profile tool is only available in 2D layouts.

Text Label: Click where you want to place the label in the image. Type the label text.

Statistics: Click to display **Minimum**, **Maximum**, **Mean**, **StdDev**, **Perimeter**, **Area**, **Sum of Pixel Values**, **Diameter**, or **Number of Pixels**. Statistics are only available in the ROI context menus.

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Mask In: The masking process sets the pixels inside of the shape to 0 and adjusts the brightness and background in the rest of the image accordingly. Mask In is only available in 2D viewers. It is available for all NM data except for tomo and gated tomo image types.

Mask Out: The masking process sets the pixels outside of the shape to 0 and adjusts the brightness and background in the rest of the image accordingly. Mask Out is only available in 2D viewers. It is available for all NM data except for tomo and gated tomo image types.

Keyboard shortcuts

The NM Viewer responds to the integer (1-8) keys on the keyboard as defined by the IntelliSpace Portal CT Viewer preferences for CT presets.

The 0 key sets the PET windowing in accordance with the PET Scaling preference. The 9 key sets the window range from 0 to 10 SUV for use with the SUV colorstripes.

Keystroke	Function
F4	Move to the next intensity map.
<Shift> + F4	Move to the previous intensity map.
F5	Move to the next colormap.
<Shift> + F5	Move to the previous colormap.
F9	Switch between triangulation cursor cross-hairs, triangulation cursor sphere, and triangulation cursor off.
F10	Saves a screenshot of the current display. The saved display becomes a new series in the same study as the selected series. A dialog appears with save options (Parameters, Local Devices, and Remote Devices). Select the desired options and click OK to save.
<Ctrl> + F10	Saves all images in the currently selected viewer as a new series. A dialog appears with save options (Parameters, Local Devices, and Remote Devices). Select the desired options and click OK to save.
F12	Fusion on/off
<Alt> + Left Mouse Button	Change Single Image/Tiled images in a viewer.
<Ctrl> + Middle Mouse Button	Change Gray Level for underlay image.
<Down Arrow>	Scroll to the next image in the vertical (Y-) dimension. (Next Row).
<Ctrl> + <Down Arrow>	Add row to the bottom in a tiled layout.
<Left Arrow>	Scroll to the previous image in the horizontal (X-) dimension.
<Ctrl> + <Left Arrow>	Remove column from the right in a tiled layout.
<Right Arrow>	Scroll to the next image in the horizontal (X-) dimension.
<Ctrl> + <Right Arrow>	Add column to the right in a tiled layout.
<Up Arrow>	Scroll to the previous image in the vertical (Y-) dimension (Previous Row).

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Keystroke	Function
<Ctrl> + <Up Arrow>	Remove row from the bottom in a tiled layout.
<End>	Go to the last image in the horizontal (X-) dimension.
<Home>	Go to the first image in the horizontal (X-) dimension.
<Page Down>	Scroll to the next page of images, if there is only one image dimension. Scroll to the next page of images in the vertical dimension, if there is more than one image dimension.
<Ctrl> + <Page Down>	Scroll to the next page of images in the horizontal dimension, if there is more than one image dimension.
<Page Up>	Scroll to the previous page of images, if there is only one image dimension. Scroll to the previous page of images in the vertical dimension, if there is more than one image dimension.
<Ctrl> + <Page Up>	Scroll to the previous page of images in the horizontal dimension, if there is more than one image dimension.
<Ctrl> + <Tab>	Cycle forward through pages in a tabbed viewer.
<Ctrl> + <Shift> + <Tab>	Cycle backward through pages in a tabbed viewer.
- (numeric keypad)	Zoom out
+ (numeric keypad)	Zoom in
<Ctrl> + C	Copy selected annotations/graphics
<Ctrl> + X	Cut selected annotations/graphics
<Ctrl> + V	Paste
<Ctrl> + I	Show/Hide Image Annotation
Pause	Start/Stop Cine display of images

Additional Information

- In NM Viewer, displays of volume data, the option to compress the SPECT images or change the slice thickness is represented by the Slab Thickness option in the context menu.
- The default colormap set in Global NM Preferences is not reflected when displaying planar data, such as Whole Body Bone images in NM Viewer. The default colormap used for planar data displayed in NM Viewer is determined by the default colormap set for **Reference** in the Global NM Preferences.
- Image filter changes, such as applying Astonish, are not applied to linked viewers. This is intentional behavior.

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- If a planar application is launched using the application palette from within NM Viewer, the initial workstep displayed is the Review workstep within the selected application. Because the initial workstep displayed is Review and no analysis has been performed, the application returns to the Setup workstep when clicking the back arrow so that you can proceed through the entire set of worksteps to analyze the images.
- When scrolling through orthogonal slices, the mouse scroll wheel scrolls through the images row by row; the left and right arrow keys or a left-to-right mouse motion moves the images cell by cell.
- Secondary capture images created within an NM application are not immediately available or shared when using the intra-application launch into a third party application (AutoQUANT, Corridor 4DM, ECTb, NeuroQ). Return to the Patient Directory, select the patient and the secondary captures that you want to use, and then launch the third-party application from the Patient Directory.

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