3 Multimodality Review

Introduction

For Intended Use, Safety and Security information, please refer to the System Instructions for Use provided with your version of the IntelliSpace Portal system

NOTICE

The screen shots in the Instructions for Use can differ from the user interface screens on details. The screens captured in these Instructions for Use may not reflect the latest User Interface coloring of the product, however the Instructions For Use remain applicable in all other aspects.

Multimodality Viewer Application Preferences

NOTICE

Multimodality application preferences can only be changed by an Administrator or a Clinical Administrator.

You can manage preferences for loading data using the **Preferences** dialog box in the **Directory**.

1. Click **Preferences** in the **Directory** screen to open the **Preferences** dialog box.
2. Click the **MR** expander in the list of preferences on the left side of the **Preferences** dialog box, and then click **DataLoading**.
3. In the Data Loading preferences, select or clear the check box for study level selection as desired.

⇨ By default, the scope of selection includes all series in a study, irrespective of whether a subset of series is selected when the viewing package or analysis package is started. However, depending on the configuration of your system, a large study might not load properly (a system message is displayed to inform you). In this case, clear the study level selection check box. You can then make a selection of specific series in the study and load only those series.

NOTICE

If you choose to select individual series from a study, ensure that you select all series that are required for analysis.

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4. In the MR Display Protocol preferences, select whether to launch MultiModality Viewer with the default display protocol or a user-defined display protocol.
5. You can then select which default display protocols are available in the application.

⇨ When reviewing series, you can switch to these additional display protocols using the **Display Protocol** list in the **Tools** area of the application.

6. Select or clear the **Study Matching Criteria** options.

⇨ These options define which types of studies are matched to user-defined display protocols.

7. Select or clear the **Series Matching Criteria** options.

⇨ These options define which types of series are matched to user-defined display protocols.

Indications for Use

The Multimodality Viewer (MMV) is an image visualization and post-processing software application designed to visualize and analyze multi-modality images in order to assist clinician's diagnostic process. This software application supports study review, side-by-side comparison, image fusion, 2D and 3D manipulation, series arrangement, and measurements of MR, CT, PET, NM, US, DX, CR, RF and XA images. This software application also supports exporting the processed image series in a dedicated format for assisting neurosurgical procedures.

Starting and stopping Multimodality Viewer

Loading studies in MultiModality Viewer

▷ You select studies for viewing in MultiModality Viewer using the IntelliSpace Portal client. For full details of using the IntelliSpace Portal client, please refer to the “Instructions for Use” supplied with the client package.

▷ Imaging series acquired at Philips, GE, or Siemens MRI systems are valid for postprocessing with MultiModality Viewer.

1. In the Directory, select the data that you want to load in MultiModality Viewer. You can select:
   - A single study - all series in the study are loaded.
   - Multiple studies - all series in all selected studies are loaded.
   - Selected series within a single study - only the selected series are loaded.
   - Selected series within multiple studies - only the selected series are loaded.

NOTICE

If you select individual series in an MR study, the entire study is loaded. To be able to load individual MR series, you should deselect this option in the MR Data preferences.

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NOTICE

If you choose to select individual series from one or more studies, ensure that the series selection that you make is appropriate for the viewing and analysis tasks that you want to perform. Otherwise you will not be able to analyze the data in an analysis application. For example, a spectroscopy series also requires an anatomical series for reference.

⇨ It is useful to open multiple studies if you want to view series that are from the same patient, but that appear in different studies. This situation might arise if, for example, the patient's name has been spelled differently in each study, or if a study is received from another hospital with a different ID, and is not recognized as the same patient.

2. Use the viewer tool in the **Review** panel of the Portal client to start MultiModality Viewer.

⇨ The viewer tool may contain options for different viewers.

⇨ If the viewer tool button displays a different viewer, click the arrow next to the button, and then click **Multimodality Viewer**.

⇨ MultiModality Viewer displays your selected series in a presentation state that is optimal for the type of modality and the type of images in the series. At any time you can switch to a different presentation state according to your workflow preferences.

⇨ If you selected one or more studies containing MR series in the Directory, the viewing area is divided into viewports and studies are loaded according to the type of data you are viewing. You can also select the series that you want to view and compare as desired from the Series panel.

⇨ If you made an explicit selection of series within a study in the Directory (including MR series), these series are automatically displayed in the viewing area when MultiModality Viewer starts. If there are more series than available viewports, the remaining series from the selection are available in the **Series** panel.

3. If you decide that you want to include other series in the review that were not part of the original selection, switch to the Directory screen, right-click the series or study and click **Add to running application**.

⇨ Series that you add in this way are not automatically opened, but they are available in the **Series** panel.

NOTICE

When MMV is loaded with a study that is in the process of being imported from a remote device, the study is loaded into MMV. The part of the study that is being imported is updated in the pictorial index of MMV. If a partially imported series is loading for viewing, the following message appears:

The study under review was updated with new images. Viewing an incomplete set of images could lead to an incorrect diagnosis!

The series that were imported via the MMV Pictorial index are updated automatically and can be viewed.

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For multi-vendor data, if a series is split by the application on launch, this can be cancelled by the user.

To disable this split, select **Cancel Automatic Split** from the pictorial index context menu (or from image context menu).

The application automatically adds this series to the **Split Series Matching Criteria** table as a preference in the **MR** > **Data Loading** Preference page for all users.

A message notifies the user that the change will be applied after relaunch of the application.

To delete this preference, select the series on the **Data Loading** Preference page and select **Remove**.

NOTICE

If the study that you want to open contains an MR series, you can double-click it to open MultiModality Viewer automatically.

Closing MultiModality Viewer

1. To close MultiModality Viewer and return to the Directory, click **Exit** below the Common tools panel in the side panel.

Viewing environment

Overview of the viewing environment

The MultiModality Viewer is divided into two areas:

- A side panel on the left containing tools and panels for viewing and manipulating the displayed series.
- A viewing area on the right for displaying and comparing selected series.

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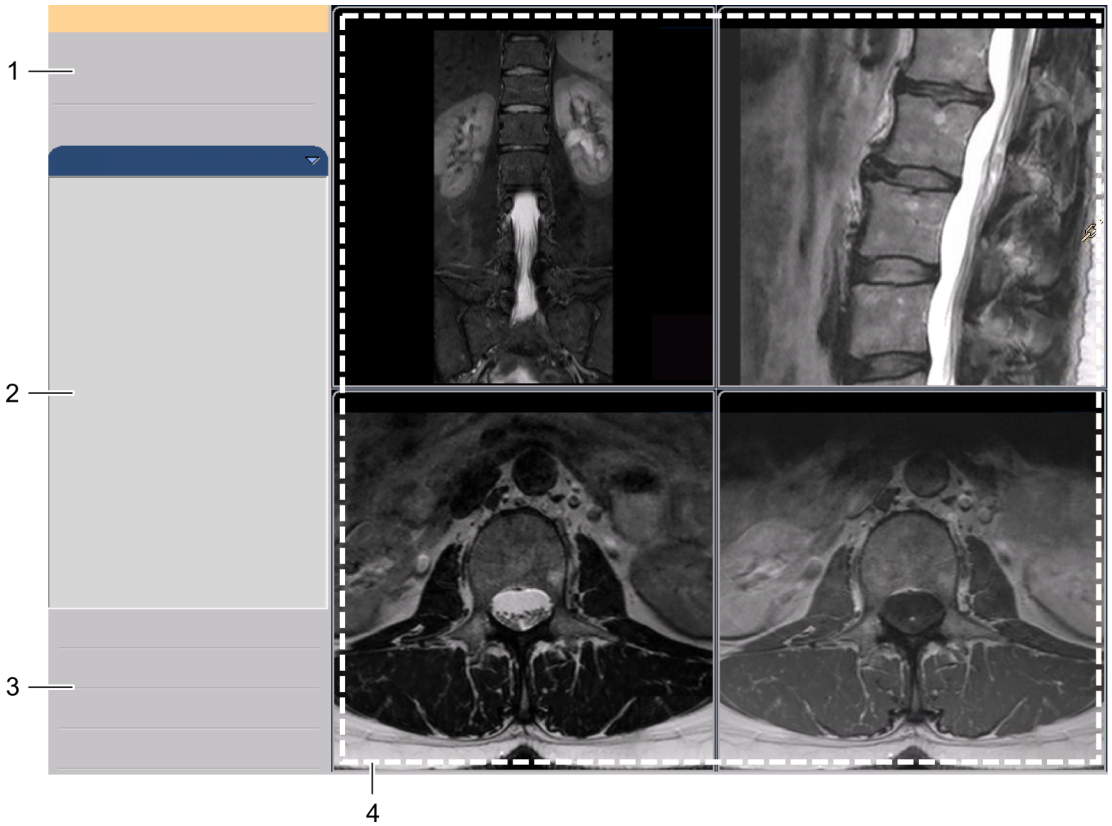

Fig. 6: MultiModality Viewer

1	Review mode panel	3	Common tools panel
2	Task panel	4	Viewing area (contains views and viewports)

Tab. 1: Legend

Hiding the side panel

You can hide the side panel to provide more space for the viewing area.

To hide the side panel, click **Auto Hide** in the upper left corner of the side panel.

After hiding the side panel, you can display it temporarily by moving the pointer over the **Tools** tab at the edge of the screen on the left. The side panel is displayed and remains visible while you keep the pointer positioned over it.

To dock the side panel again, display the side panel and click **Dock** in the upper left corner.

Review mode panel

The Review mode panel contains tools for setting the following viewing options:

- Orientation
- Arrangement of views
- Linking between views

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- Intersections of orthogonal planes

The viewing tools that are available depend on the review mode of the selected view, and they differ between 2D views and 3D views. The Review mode panel displays only the tools that are applicable for the selected view.

Task panel

The Task panel provides tools for performing specific tasks with series. Several tasks are available, but only one task can be active at any time. Where appropriate, guidance is provided in the Task panel to help you complete the selected task. The following tasks are available:

Series

The **Series** panel allows you to select series for display in the viewing area. The **Series** panel is displayed when MultiModality Viewer starts, to allow you to display one or more series for investigation in the viewing area.

Bookmarks

The **Bookmarks** panel allows you to view and manage stored bookmarks for the current study.

Key Images

The **Key Images** panel allows you to view and manage stored key images for the current study.

Display Protocol Manager

The **Display Protocol Manager** panel allows you to activate or delete display protocols, and add public protocols from other users. You can also make your display protocols public for other users.

Batch (Slab and Volume viewing only)

The **Batch** panel allows you to create a “batch” of images from a view: a batch is a new set of images derived from the original images. When you create a batch, it is saved as a new series in the study.

Clip (Slab and Volume viewing only)

The **Clip** panel allows you to remove parts of a slab or volume. You can use the clip tool to get an unobstructed view of a region of interest.

Fusion Registration

The **Fusion Registration** panel allows you to adjust the registration of two volumes or images in a fused view. You can use a combination of manual and automatic registration. The **Fusion Registration** panel is only available when a fused view is selected.

Volume Measurement

The **Volume Measurement** panel allows you to define and measure a volume in a PET or NM series.

MR Segmentation

The **MR Segmentation** panel allows you to segment a region of interest in an MR image and create a VOI.

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Object Manager

The **Object Manager** panel allows you to view and manage ROIs and VOIs that you have created in the current study.

XA Vascular Tools

The **XA Vascular Tools** panel allows you to perform processing on XA images in MultiModality Viewer. You can perform subtraction on XA series and apply pixel shift adjustment and landmarking.

Switching Between Tasks

To switch between tasks in the Task panel, select the view that you want to investigate, click the arrow in the top right corner of the Task panel, and then select a task.

Common tools panel

The common tools panel contains tools for performing the following functions:

- Saving images and views
- Sending images and views to the Film application
- Sending images and views to the Report application
- Creating bookmarks
- Interacting with views (for example; pan, zoom, and rotate)
- Making measurements and creating annotations
- Viewing additional image information
- Setting the gray level

Below the common tools panel is the **Exit** button, which closes MultiModality Viewer and displays the Directory.

Viewing area

The viewing area displays images from displayed series. You can view a single series in the viewing area, or you can divide the viewing area into several view containers, each displaying a view of a series.

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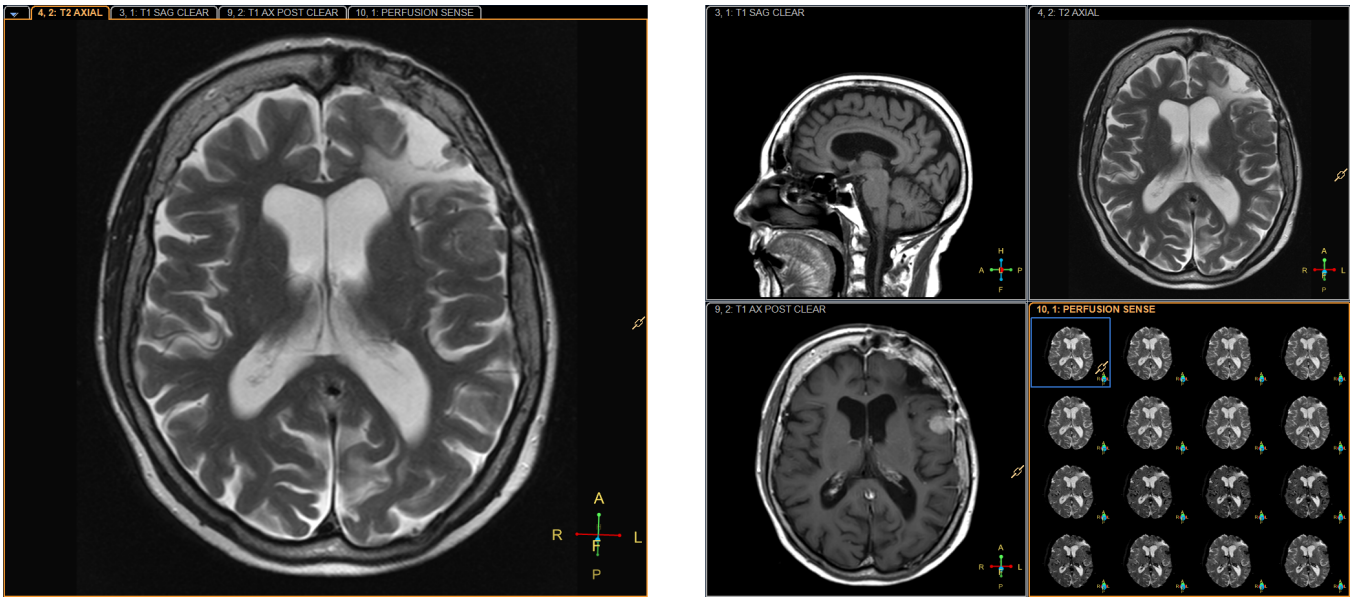

Fig. 7: Viewing area: maximized (left) and view containers (right)

When you open series in the viewing area, the series is displayed in a dedicated view, which in turn is displayed in a view container. A view can only contain one series, but a view container can contain multiple views of the same series, or of several series, as tabbed views. When a view container contains multiple views, the images from only one view are visible at any time, and the other views are stacked behind.

Each view in the stack has a tab in the title bar of the view container, allowing you to display a view by clicking on its tab. Tabbed views allow you to alternate between views of different series. The name of the series is displayed in the title bar of the view container if only one series is open in the view, or in the corresponding tab if series are tabbed.

The following series information is displayed:

- Series identification (for CT the series number is displayed, and for MR the scan number and reconstruction number are displayed).
- Series description or protocol name.
- For 3D views, the selected render mode is displayed.
- For fused views (NM/PET fused with CT) both series are identified.

Tab titles may be condensed if there are many tabs are open.

Click the arrow in the tab at the left of the open tabs to view a list of all open views. You can display a view by selecting it in the list.

If there are many tabs open, and the tab selector is not visible, click the left arrow in the title bar to display it.

You can modify the arrangement of views and view containers in the viewing area. For details, see section “Arranging the viewing area” on page 78.

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Using multiple monitors

If two monitors are connected to the IntelliSpace Portal system, the viewing environment can be extended to the additional screen.

▷ To be able to span the viewing environment across two monitors, both monitors must have the same screen resolution.

1. To extend the viewing environment to an additional monitor, click **Dual screen** in the Review mode panel.

⇨ When you start dual screen viewing, the viewing area is spread over both screens, and a viewing arrangement is automatically selected that tries to distribute the currently displayed views evenly across the screens. For example, if views are arranged in a 4 x 4 layout on a single screen, starting dual view distributes the views in a 2 x 4 layout on each screen:

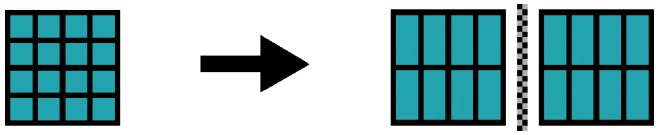

Fig. 8: Switching from single screen viewing to dual screen viewing

⇨ To accommodate all the views that are currently open, there may be some empty tiles in the new arrangement. In this case, the views on the left screen are filled first, and then the views on the right screen are filled.

2. To change the tiling arrangement, click the tiling arrangement tool in the Review mode panel and select a tiling arrangement.

⇨ The tiling arrangement tool provides preset arrangements for both screens (it is not possible to set the tiling arrangement for each screen individually).

⇨ An image or a standard view cannot span both screens. A view containing a layout protocol with multiple viewports can span both screens, although such a view cannot be stacked with a standard view in a tabbed container while dual screen viewing is enabled.

⇨ Opening series in dual screen viewing is the same as for a single monitor situation. You can open series in views in either screen using the procedure described in the next section.

3. To stop dual screen viewing, click **Dual screen** again.

Opening series

You use the **Series** panel to open series for viewing in the viewing area. The **Series** panel contains all the series from the study that you selected in the Directory. If multiple studies were selected, the series are grouped by study in the **Series** panel.

Each series is represented by a pictorial. The series pictorial displays information to help you identify series:

- Series number and series name

- Modality and number of images

For MR series, the series number is represented by two numbers separated by a comma. The first number is the scan number and the second is the image set number.

A series that contains only one image does not display a series type icon in its pictorial.

The series pictorials provide visual feedback about the series.

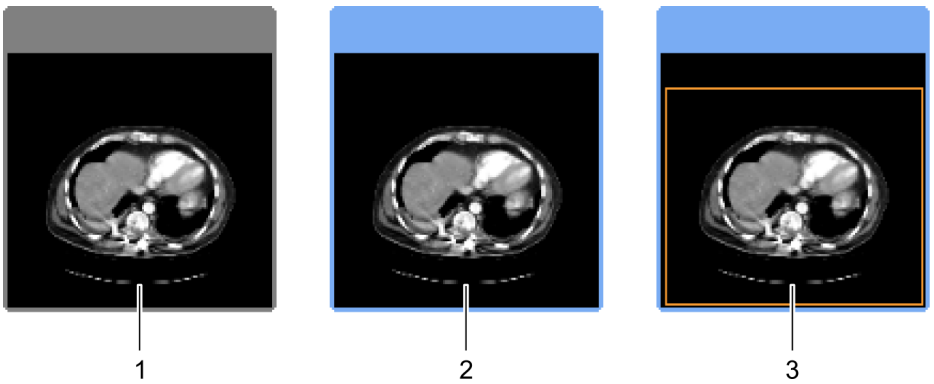

Fig. 9: Series status in the Series panel

1	Series is not displayed in the viewing area	2	Series is displayed in the viewing area	3	Series is displayed in the viewing area and is currently selected

Tab. 2: Legend

▷ The following series types can be opened in MultiModality Viewer:

- Series with multiple images
- Snapshot, or collection of snapshots

1. If the **Series** panel is not displayed, click the arrow in the top right corner of the Task panel, and then select **Series**.
2. To open a series in the viewing area, click the series in the **Series** panel.

⇨ If there are empty view containers in the viewing area, the series is opened in the first empty container (top to bottom, left to right). You can continue to select series from the **Series** panel until all containers are filled.

⇨ If all view containers are filled, the view that is selected when you click another series in the **Series** panel is replaced. If the selected view is a tabbed view, only the tab is replaced.

3. To open a series in a specific view, drag the series from the **Series** panel to the desired view.

⇨ If the view container is empty, the series is opened in the view.

⇨ If the view container already contains one or more views, drop the series on the view to display a shortcut menu of available actions. For example, you can choose to replace the existing view, or add the series in a new tab. Fusion actions are also available, if applicable.

4. Right-click the **Series** panel to open a shortcut menu for displaying series in the viewing area.

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⇨ The shortcut menu in the **Series** panel allows you to override the default review modes when opening series. For details, see section “Series panel shortcut menu” on page 162. You can also drag a series to a view with the right mouse button and access the shortcut menu.

5. To close a view, click the **Close** button in the view's title bar. If the view is stacked, clicking **Close** closes the active tab only. Click the view's tab to bring it to the front of the view before closing it.

Review modes

The review mode is the combination of geometry and render mode. MultiModality Viewer provides the following review modes:

- **2D Slice View** (original images). Displays the series as original images. For MR series, Slice review mode provides a display for viewing and comparing multiple series, supporting multi-dimensional sorting and navigation.
- **Thin Slab / MPR View**. Displays the series as a 3D slab (Average intensity projection), with the option to display reference views of orthogonal slices.
- **Volume / MIP View**. Displays the series as a 3D volume (Maximum intensity projection).

When you open a series, it is displayed in the viewing area as a 2D slice (default review mode). For PET and SPECT data, the default review is defined by the default display protocol associated with the series. A display protocol view can contain sub-views, and the views can be any combination of slice, slab, or volume.

Selecting a review mode

▷ To view a series with an alternate review mode (geometry and render mode setting), you can open a new view and select the desired render mode in a single action.

▷ When you change the review mode, the current view remains open in a tabbed view, and a new tabbed view is opened displaying the newly selected review mode. If the newly selected review mode is already displayed for the series, the view is selected.

1. To open a new view as a slice, right-click the view and select **Add 2D Slice View**.

2. To open a new view as a slab (MPR), right-click the view and select **Add Thin Slab / MPR View**.

3. To open a new view as a volume (MIP), right-click the view and select **Add Volume / MIP View**.

⇨ The new view is opened as a tabbed view in the same view container as the selected view. you can switch between the views using the view tabs.

Changing the review mode

1. To add a new view of the displayed series with a different review mode, right-click the view and select a review mode.

-  **Add 2D Slice View**
-  **Add Thin Slab / MPR View**
-  **Add Volume / MIP View**

⇨ A view is added as a new tab in the view container, using the selected review mode.

2. To change the render mode of an existing view without affecting the current geometry, click the render mode viewport control in the view and select an available option.

⇨ The render mode of the current view is updated without changing the geometry (slab position, orientation, and thickness). You can use viewport controls to change the render mode of sub-views or reference views individually.

⇨ For details of viewport controls, see section “Viewport controls” on page 82.

Arranging the viewing area

You can configure the viewing area to display various tiling arrangements to suit your preferred workflow. An arrangement describes the configuration of views in the viewing area.You can configure the viewing area to display up to 16 views simultaneously, or you can display a single view filling the whole viewing area.

To change the arrangement of the viewing area, click the tiling arrangement tool in the Review mode panel, and select a tiling arrangement.

The tiling arrangement tool applies the selected tiling option to the whole viewing area. To set the tiling layout of an individual view in Slice viewing mode, right-click the view and select a tiling option from the shortcut menu. Tiling arrangements and tiling layouts can be applied independently.

To maximize a view to fill the whole viewing area, click **Maximize** in the view's title bar.

NOTICE

You can also maximize a view by double-clicking on its title bar.

When you maximize a view, it is enlarged to fit the whole viewing area. All other views are stacked behind this view and can be displayed by selecting the corresponding tab.

Click **Restore** or double-click the title bar (including tabs) to return the viewing area to the previously configured tiling layout.

To change the size of views in an arrangement, position the mouse pointer over the boundary between two view containers and drag to resize them as desired.

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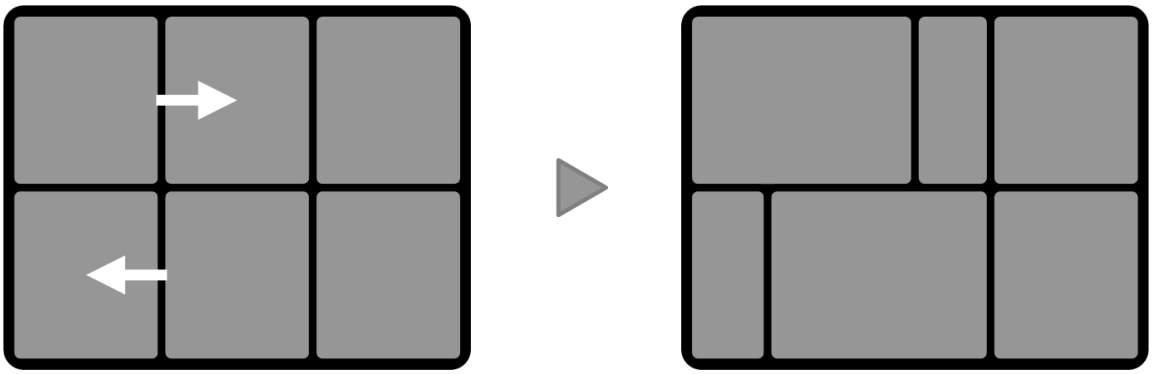

Fig. 10: Changing the size of two views by dragging a boundary

When the boundaries of two or more views are aligned, you can change the size of all adjacent views by pressing SHIFT while dragging the boundary.

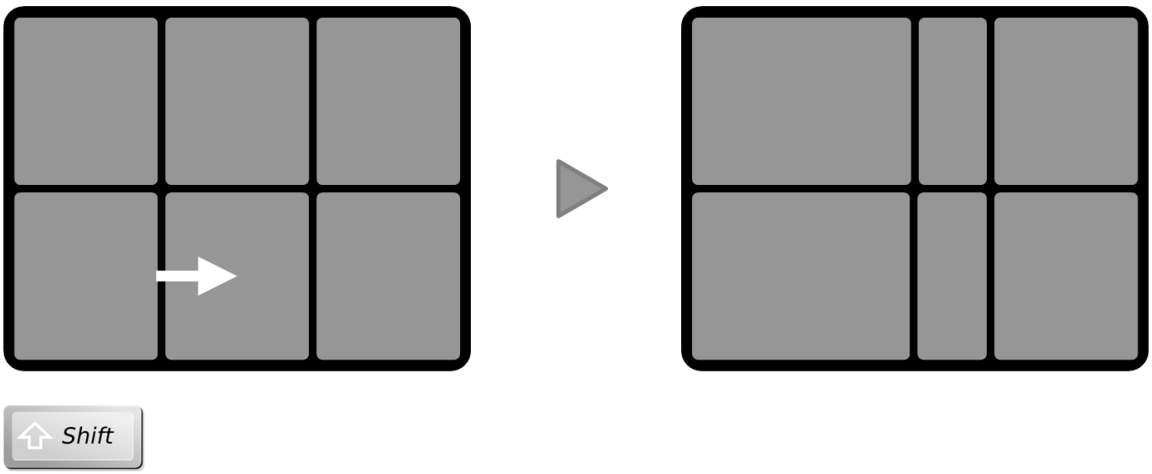

Fig. 11: Changing the size of all views adjacent to a boundary

NOTICE

If dual screen viewing is enabled, you cannot drag a boundary from one screen to the other.

To move a view to another position in the viewing area arrangement, drag the view using its title bar.

In a tabbed view, click a tab to display the series.

To move a single tab from a tabbed view to another position, drag the tab.

If the view container to which you drag a view already contains other views, the view is added as a tabbed view.

You can drag single views, or drag tabs from a tabbed container to another location.

If you drag over an empty location, you can drop the view to reposition it.

If dropped on another view, the dragged view is added as tabbed view to the tab container of the target view, and it becomes the selected tab.

By dragging views, you can create the desired layout for your workflow. However, custom arrangements cannot be saved.

Using and creating display protocols

1. To select an existing display protocol, click the **Display Protocol** list in the **Tools** area and select a display protocol.

⇨ The **Display Protocol** list contains default protocols and user-defined protocols that match the loaded study. Display protocols that do not match are not listed. You can select the available default display protocols in the application preferences of the **Directory**. See section “Multimodality Viewer Application Preferences” on page 67.

2. To create a user-defined display protocol, do the following:
   - Arrange the series of a study according to your preference. For example, you can configure views to display MPR or MIP, and switch reference lines or point links on or off.
   - Click **Save Display Protocol** in the **Tools** area.
   - In the **Save Display Protocol** dialog box, modify the name of the display protocol, if desired, and then click **Save**.

⇨ The new user-defined display protocol is added to the **Display Protocol** list and is available for selection.

⇨ By creating a new display protocol, you train the system to recognize essential information about the study, so that the system knows to use this display protocol as the best matching protocol for this type of study.

Managing display protocols

1. To manage display protocols on the system, click the Task selector in the Task panel, and then click **Display Protocol Manager**.

⇨ The **Display Protocol Manager** displays the following items:

- **My Protocols**: These protocols are display protocols that are currently available to you in the application.
- **Public Protocols**: These protocols are public display protocols that you can add to your own list for use in the application.

2. To activate a display protocol, select a protocol and click **Activate**.

3. To delete a display protocol, select a protocol and click **Delete**.

4. To add a public display protocol to your own list, select the protocol in the **Public Protocols** list and click **Add**.
5. To make one of your own display protocols available to other users in the **Public Protocols** list, select the **Pub.** check box.

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PET/SPECT display protocols

PET, SPECT, or NM series are displayed in a dedicated layout known as a display protocol. A display protocol is optimized to display multiple subviews displaying different views of the selected data, including a fused view of the PET, SPECT, or NM data with CT data, if applicable, or different review modes. The display protocol defines the layout of sub-views inside the view container, keeping all the views and sub-views organized as a group. You can view display protocols alongside view containers of data from other modalities for comparison.

When you open a PET, SPECT, or NM series, it is displayed using the default display protocol. The default display protocol provides the optimal view and sub-view layout for the selected series. Several preset display protocols are available, and you can select a different display protocol at any time. Display protocols cannot be modified.

Sub-views that display the same image data in a display protocol are linked across shared attributes, such as geometry, render mode, gray level setting, color map, zoom, pan, and alpha blending.

Changing the display protocol

▷ When you open a PET, SPECT, or NM series with associated CT data, it is displayed using the default display protocol. MultiModality Viewer provides, several different display protocols that provide a variety of sub-view arrangements. Different display protocols can be used for different purposes. For example, you can use a display protocol that optimized for Fusion viewing while you are performing registration of the fused series, and then switch to another display protocol for the clinical procedure without losing the registration data.

1. To change the display protocol, select the view in the viewing area and click **Protocol Selection**, in the Review mode panel.

⇨ The Protocol Selection panel is displayed along the edge of the viewing area. This panel contains all available display protocols for the selected view.

⇨ Each display protocol is shown as a thumbnail, indicating the layout contained in the protocol. Commonly used protocols are displayed at the top of the panel. Pause the pointer on a thumbnail to see the name of the protocol.

⇨ The contents and the display order of the Protocol Selection panel cannot be changed.

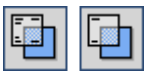
⇨ When you select a new display protocol, all views are displayed with their default viewing settings.

2. In the **Protocol Selection** panel, click the display protocol that you want to use.

⇨ The view is displayed in a new tab in the view container, using the selected display protocol. The Protocol Selection panel stays open, so that you can prepare another tabbed view with an alternative display protocol for a different part of your workflow.

3. To close the Protocol Selection panel, click **Close** in the upper-right corner of the panel.

Viewport controls



When you enable **Full Image Info** or **Limited Image Info** in the Common tools panel, viewport controls are displayed in blue text in a view, and they can be adjusted directly by clicking them with the pointer. You can use viewport controls to change the following items:

- Window level
- Window width
- Slab position
- Slab thickness
- Render mode

General viewing tools

Setting the image orientation

1. In the viewing area, select the view that you want to modify.
2. For 2D views, use the Orientation tools in the Review mode panel to mirror, rotate, or flip the view.

   If the desired transformation is not displayed in the Review mode panel, click the arrow next to the Orientation tool.

   - **Mirror**: Mirrors the image around a vertical axis.
   - **Rotate clockwise**: Rotates the view 90 degrees clockwise.
   - **Rotate counter-clockwise**: Rotates the view 90 degrees counterclockwise.
   - **Flip**: Flips the image around a horizontal axis.
3. For 3D views, use the Preset Orientation tools in the Review mode panel to set the orientation of a slab or volume:

   - **Axial Feet**
   - **Coronal Front**
   - **Sagittal Left**

⇨ The applied image orientation is propagated to all images in the series.

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Panning a view

1. Click **Pan** in the Common tools panel.
2. Move the mouse pointer over the view you want to pan and then drag the image in the desired direction.

⇨ The applied panning offset is propagated to all images in the series.

NOTICE

You can activate the Pan tool temporarily by dragging while pressing the left mouse button and the middle mouse button.

Zooming a view

▷ The Zoom tool is selected by default when a single image is selected. When you apply a zoom factor to an image, it is propagated to all images in the series.

1. Click **Zoom** in the Common tools panel.
2. Move the mouse pointer over the view you want to zoom and then do one of the following:
   - Drag up to zoom in.
   - Drag down to zoom out.

NOTICE

You can activate the Zoom tool temporarily by dragging while pressing the right mouse button and the middle mouse button.

Adjusting the gray levels

1. Click **Gray Level** in the Common tools panel.
2. Move the mouse pointer over the view you want to adjust and then do one of the following:
   - Drag right to increase the contrast.
   - Drag left to decrease the contrast.
   - Drag up to increase the brightness.
   - Drag down to decrease the brightness.
3. To reset the gray levels to the original settings (as defined by the acquisition system), click the **Window** arrow in the Common tools panel, and then select **Default**.

   To apply a preset window setting, select the view, click the **Window** arrow in the Common tools panel, and then select a preset.

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Window presets can only be applied to CT images.

When you change the gray levels of a view (not including selecting a preset), the Window preset selector in the Common tools panel indicates that the window settings are “modified”.

4. If viewport controls are visible, you can apply a specific value to the window level or window width. Click the “L” or “W” viewport control, and then do one of the following:
   - Type a new value, and then press ENTER or click outside the field. • Click the up or down arrows in the image information interactor to change the value.
   - Press the UP ARROW or DOWN ARROW key.
   - Rotate the wheel button.

5. To invert the gray level values in all images of the selected series, click **Invert Gray Level** in the Common tools panel.

NOTICE

You can activate the Gray level tool temporarily by dragging while pressing the middle mouse button.

NOTICE

Image Information must be enabled in the Common tools panel to use the viewport controls.

Propagation of gray levels

Gray level settings are propagated to other images in the series according to the following rules:

- For CT series, gray level settings are propagated to all images in the series.
- For MR series, gray level settings are only propagated over the applicable dimensions, that is, all dynamics and all dimensions for which the gray level settings should not be independent per instance in that dimension. Gray level settings are generally not propagated to different image types, diffusion values, and with some exceptions, also not to echoes.
- For Fusion views, the window is propagated to all images that correspond to the underlay and independently over those that correspond to the overlay, whether fused or not, if they have the same render mode.

You can control the gray level propagation settings across dimensions in MR series using the shortcut menu. Right-click an MR view and then point to **Apply Window** To in the shortcut menu. Available dimensions are displayed in a submenu, and a check mark is displayed next to the dimensions that receive the propagated settings. To stop propagation to a dimension, clear the check mark, or to include the dimension in the propagation, select it in the submenu.

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These settings are not saved when a series is closed. Default gray level settings are reapplied whenever a series is opened.

Selecting a color map

- ▷ When viewing MR, PET, or NM series, you can select from a variety of color map settings, according to your needs.
- ▷ Color mapping can be used instead of gray scales to optimize visualization of a range of pixel values, and to highlight different aspects when combined with a gray scale anatomical background image (CT series) a in a fused view.
- ▷ When viewing MR series, you can select a color map for 2D, MPR, and MIP views.

1. Right-click the view, point to **Select Color Map**, and then select a color map.

   The choice of available color maps depends on the type of series being viewed.

⇨ The selected color map is propagated to all views and sub-views within the display protocol that display the same image data.

⇨ In Fusion views, the selected color map is propagated to all sub-views with the same fusion state (that display the reference series, the floating series, or the fused images) and the same render mode.

2. The color scale is displayed by default. If it is not already displayed, right-click the view and click **Color scale**.

   The color scale shows the units used in the color map. If the view contains reference views, you can display the color scale independently for each reference view and the main view.

3. Click **Color scale** in the shutter menu again to hide the color scale.
4. If you save images as secondary capture images (including filming or reporting), the images are saved in color along with the color scale. If you save original image, they are saved as original grayscale images.

Presentation state

- ▷ When viewing images, you can make changes to their presentation state, using the pan and zoom settings, the window setting, and graphical overlays such as annotations and measurements. The current presentation state of a view when it is closed is not saved.

1. To save the presentation state of a view, right-click in a view, and then select **Save Image Viewing Settings** from the shortcut menu.

2. To reset the presentation state of a view to the last saved presentation state, right-click in a view, and then select **Reset All** from the shortcut menu.
3. You can reset the window setting to default values, if desired: click **Window** in the Common tools panel and then click **Default**.

Cine viewing

- ▷ You can start cine viewing using the keyboard or using the **Movie** panel.

1. To start cine viewing automatically from the current position without opening the **Movie** panel, press PAUSE on the keyboard.

   Press PAUSE again to pause cine viewing at the current position. You can now scroll to another image, or continue cine viewing from the current image.

2. To control cine viewing using the **Movie** panel, select a view, and then click **Movie** panel in the Common tools panel.

⇨ The **Movie** panel is displayed in the selected view, and cine viewing is automatically started.

3. If the series has multiple dimensions, click the arrow to select a dimension to use for cine viewing.

4. While cine viewing is playing, click **Pause** to pause cine viewing at the current position.

5. Click **Play** to start cine viewing from the current position.
6. To set the cine viewing mode, click the viewing mode arrow and select a viewing mode:
   -  Cyclical forward: when cine viewing reaches the last image, it loops back to the beginning of the series, and then continues from the first image.
   -  Bounce: when cine viewing reaches the last image, the series is replayed in reverse direction until the first image is reached, and then continues from the first image.
7. To adjust the speed of cine viewing, do one of the following:
   - Type a value in the **Speed** field.
   - Click the up or down arrow in the **Speed** field.
   - Drag the slider to the right to increase the speed, or to the left to decrease the speed.
   -  Click **Reset** to reset the speed to the default value.
8. To hide the **Movie** panel, click **Movie** in the Tools panel again, or click the **Close** button in the panel.

   Hiding the **Movie** panel while cine viewing is playing does not stop playback.

NOTICE

Cine viewing is automatically paused if you start scrolling the view during playback, either using the Scroll tool or using the mouse wheel button.

Using the keyboard

Several items in the viewing area can be modified using the keyboard, such the standard Windows keyboard shortcuts and the ARROW keys. When using the keyboard, please ensure the item that you want to modify is selected or has focus.

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The **Movie** panel and the **Display Sorting / Scrolling Directions** panel (Dimension navigation) do not take focus away from a view. When these panels are open, the ARROW keys on the keyboard do not change the controls in the panel, they affect the view as normal (image navigation).

Showing additional information

▷ You can use tools in the Common tools panel to show or hide additional information on images.

1. To show image information, click **Image Information** in the Common tools panel.

   You can select from the following levels of information:

   -  Full image information
   -  Limited image information
   -  No image information

⇨ When enabled, image information is displayed in all views in the main display area.

2. To show the image grid in the selected view, click **Grid** in the Common tools panel.

   Click the tool again to hide the grid.

3. To show the **DICOM Information** panel in the selected view, click **DICOM Information** in the Common tools panel.

   To hide the **DICOM Information** panel, click **DICOM Information** again, or click the **Close** button in the panel.

Setting the image quality

1. Select the view for which you want to set the image quality.

2. Click **Image Quality** in the Common tools panel and select an image quality level.

Comparing series

MultiModality Viewer provides tools to display, link, and reference multiple views for comparing series.

You can use linking to synchronize viewing for views that have the same frame of reference and a similar orientation as the currently selected view. The following linking tools are available:

- Smart linking synchronizes image interactions in linked views (of the same orientation).
- Point linking displays the position of a link point in linked views (orthogonal).
- Reference linking indicates the position of a source image in linked views as reference lines.

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As well as the linking methods described above, which you can turn on or off according to your needs, CT views with the same absolute window settings are automatically linked for gray level settings. Linking for gray level settings is always absolute. Views that are linked for gray scale settings can be different from the views that are linked using the linking tools described here.

Smart linking

You can use smart linking to link image interactions while comparing series. Smart linking is turned on by default.

For 2D views with the same orientation, the geometric properties are combined in one link group consisting of the following:

- Zoom link
- Pan link
- Image display orientation link
- Scroll link

3D views are also linked with a 2D view if the slab or volume has the same original scan orientation as the 2D view. In case of a slab view, the slab position is aligned with the slice position (slab thickness is ignored). If you roll the 3D view, the link with the 2D view is broken. The position link and pan link between 2D views and 3D views are absolute if they have the same frame of reference, otherwise they are relative.

3D views with the same initial orientation can have a geometry link, consisting of the following:

- Zoom link
- Pan link
- Image display orientation link
- Slab position link (not applicable for volume views)
- Center of rotation
- Roll/Rotate link, including linking a slab and a volume.

The pan link and the slab position link between 3D views are absolute if they have the same frame of reference, otherwise they are relative. The roll/ rotate link is always relative.

1. Display all the series that you want to compare, and then use the tiling arrangement tool to configure the viewing area so that all series are displayed.

   You can compare up to 16 series in a 4 x 4 grid.

2. If smart linking is not already turned on, click **Smart Link** in the Review mode panel to turn it on.
3. Select a view in the viewing area.

⇨  All views that have a similar orientation as the selected view are linked.

⇨ Window settings are also linked when views are linked, but only if they have the same absolute window scale (CT series).

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⇨ All series that are subsequently opened while smart link is turned on are automatically checked for links with open series. Views that have the same frame of reference have an absolute link. However, views that do not have the same frame of reference, but do have a similar orientation are also linked. In this case, you might need to adjust the link offset of a view to get a better alignment with the other linked views.

4. To adjust the link offset of a view do the following:

   -  Click the link icon in the view to unlink it temporarily. The view is unlinked for all linking relationships (geometry and gray level settings). It is not possible to unlink a view for geometry and maintain the link for gray level.
   - Adjust the scroll, pan, or zoom factor to align it more closely with the other views.
   -  Click the unlinked icon in the view to relink it. The offset is preserved when making interactions on the linked views (the link is now relative).

5. To turn smart link off, click **Smart Link**.

⇨ When you turn smart link off using **Smart Link** in the Review mode panel, manual link adjustments are not saved.

Point linking

▷ You can use point linking to assist with navigation in 3D space. Point linking displays a link point that represents the same physical point in all views. Point linking can be used in 3D views and in MPR reference views, but it can only be used with series with the same frame of reference.

1. Click **Point Link** in the Review mode panel to turn point link on.
2. Click anywhere in a view to set the link point.

⇨ Any view with the same frame of reference displays the same position in the stack of slices and the link point. Point linking is especially useful if the views are orthogonal. If the link point is outside the geometry of an image set the image set scrolls to its first or last slice, whichever is closest.

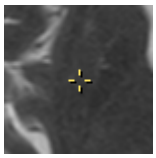
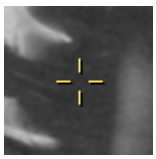
⇨ While point linking is active, the link point also defines the rotation point for 3D views.

3. To set a different link point, click anywhere in the view while **Point Link** is enabled, or move an existing link point by dragging it.

⇨ Visualization of the link point changes according to its position in the geometry:

⇨ Link points are only visible in the views that have the same frame of reference as the current view. If you select a view with a different frame of reference, the link point in the first view is hidden until you select that view again.

-  Link point is in the plane of the currently displayed slice

-  Link point is in front of the currently displayed slice
-  Link point is behind the currently displayed slice

4. To turn point link off, click **Point Link** again.

Reference linking

▷ Reference lines display the intersection of the currently selected view in other views in the same frame of reference.

1. Select the “source” view in the viewing area.
2. Click **Show reference lines** in the Review mode panel.

⇨ Intersections with all visible slices of the source view are displayed on all “reference” views that have a different orientation to the source view. A reference view is any view from a series acquired during the same examination as the source view, without patient repositioning.

⇨  The source view displays an icon to identify it as the source for reference lines.

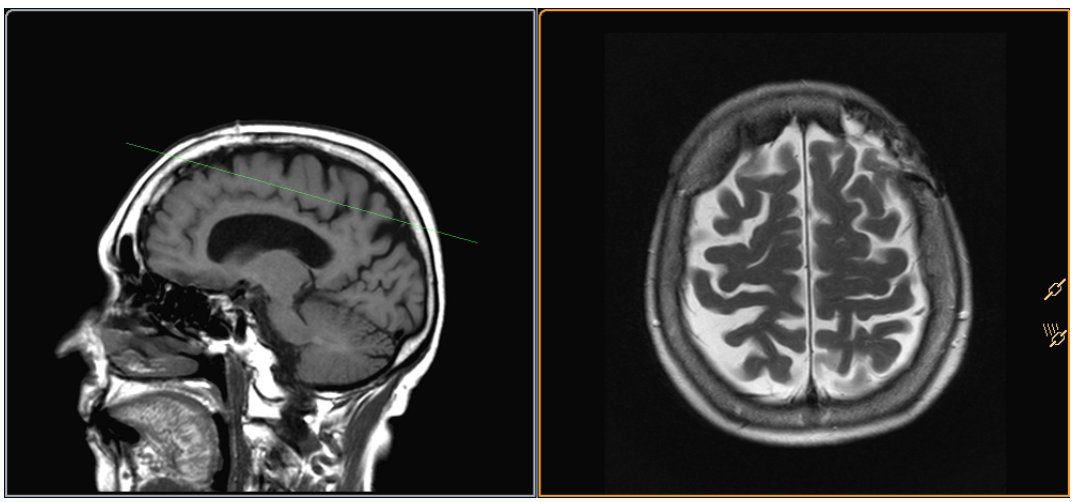


Fig. 12: Displaying reference lines from a source view with a single slice

⇨ If the slice distance in the source view is very small, only the outer portions of the reference lines are shown to avoid obscuring the reference view.

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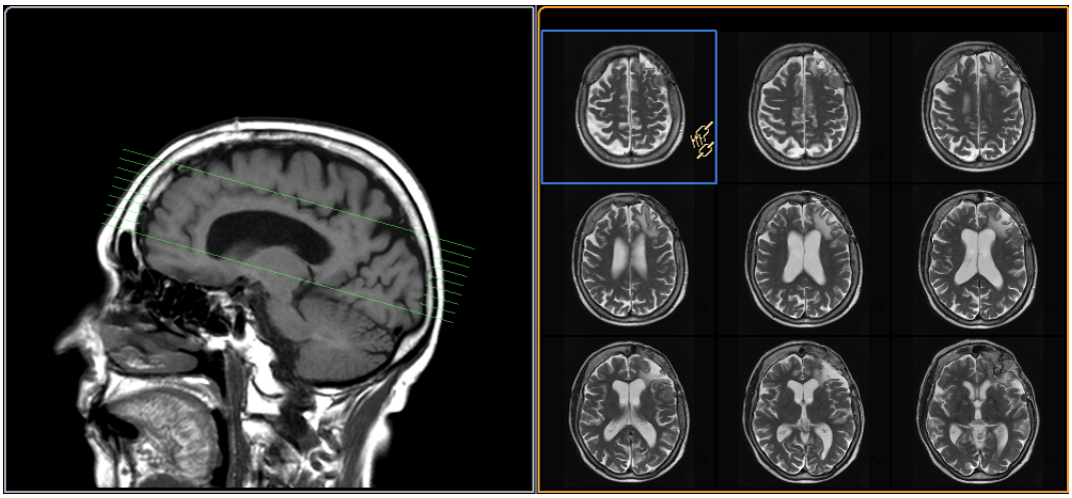

Fig. 13: Displaying reference lines from a source view with multiple slices

3. As you scroll the source view, the reference lines are updated in the reference views.

   If you click another view, it becomes the source view.

4. If you tile the source view, each displayed slice of the source view generates a reference line in the reference views (all intersections of the tiled viewports are displayed on the reference views).

⇨ If a reference view is tiled, the reference lines are displayed in the selected slice only.

5. To turn reference lines off, click **Show reference lines** again.

Aligning and linking views manually

▷ As well as the linking methods described above, you can align and link views from the shortcut menu.

1. Select the view to which you want to align other open views.

⇨ The view that you select is the “source view”.

2. Right-click the source view and click **Align Other Views**.

⇨ Other open views are aligned with the source view, and a geometry link is created between these views (this link replaces an existing geometry link).

- If the source view is a 3D view, the orientation and rotation center of other 3D views are matched with the source view (including slab position if the source view is a slab view).
- If the source view is a 2D view, the orientation of 3D views is matched with the source view, and any slab views are moved to the same position. The center of the source view becomes the center of rotation for 3D views.

Slice viewing

Slice viewing is suitable for viewing several images from one series side by side, or for comparing several series side by side. MR series are automatically displayed as a slice.

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Slice viewing display settings

▷ When the review mode is set to Slice, you can configure the layout of an individual view to display one or several consecutive images from the series.

1. To set the layout of a view, right-click in the view, point to the tiling options, and then select a tiling option.

⇨ When you tile a view, the view is divided into viewports. Each viewport displays an image from the series.

2. To set the layout of a view using the keyboard, select the view in the viewing area and then use the following keyboard shortcuts:
   - To add a row, press CTRL+DOWN
   - To remove a row, press CTRL+UP
   - To add a column, press CTRL+RIGHT
   - To remove a column, press CTRL+LEFT

3. To set the layout automatically to an optimal layout, right-click in the view, point to the tiling options, and then click **Auto**.

⇨ The **Auto** layout option displays as many images as possible in the view, but at a size that is still comfortable to view. If a series contains multiple dimensions, the layout is optimized for the number of images in the displayed dimensions. For example, if a series contains only two echoes and many slices, the **Auto** layout option displays the two echoes side-by-side for simultaneous scrolling through the slices of both echoes.

4. When the layout of a view is tiled, you can double-click one of the images to display it full size in the view. Double-click the image again to return to the tiled layout.

Scrolling

▷ The **Scroll** tool is selected by default in Slice viewing. For the purposes of scrolling direction, images are sorted in anatomically correct order, regardless of slice numbering.

1. Click **Scroll** in the Common tools panel.
2. Move the mouse pointer over the view you want to scroll and then do one of the following:

   Scrolling stops at the first or last image of the series.
   - Drag up to scroll to the image behind the currently displayed image in the slice order.
   - Drag down to scroll to the image before the currently displayed image in the slice order.
3. To scroll while another interaction tool is selected, rotate the mouse wheel button:

   Scrolling stops at the first or last image of the series.
   - Rotate the wheel button forward to scroll to the previous image in the slice order.
   - Rotate the wheel button backward to scroll to the next image in the slice order.

4. To change the sorting direction, click **Select and Sort** in the Review mode panel, and then click **Sorting Direction** in the **Display Sorting / Scrolling Directions** panel:

   By default, the scrolling direction is set to anatomical order.

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-  Standard sorting direction
-  Reversed sorting direction

For details of scrolling through multiple dimensions in a series, see section “Dimension navigation” on page 93.

Dimension navigation

If a series has multiple dimensions (sorting attributes), for example, slices, echoes, and dynamics, you can use MultiModality Viewer to display and navigate series in these dimensions. Dimension navigation is typically used with MR series, but MultiModality Viewer provides dimension navigation for dynamic and gated NM and PET scans, and for CT scans that have cardiac phases stored in an additional dimension.

MultiModality Viewer supports the following sorting attributes.

- Slices
- Stacks
- Echoes
- Cardiac phases
- Frames and Frame phases (NM/PET)
- Dynamics
- Image types
- Chemical shifts
- Diffusion values
- Diffusion directions
- Inversion delay time (IDT)
- MR Elastography phases

 If a series has multiple dimensions, the multiple dimension scroll cursor is displayed when the Scroll tool is active.

 If a series has only one dimension, the single dimension scroll cursor is displayed when the Scroll tool is active. In this case, images are displayed left to right, top to bottom in a linear mode, and the series cannot be sorted by dimension. You can scroll through the images using the standard scrolling procedure described earlier.

When a series has multiple dimensions, the images are sorted by default according to a number of rules to assist with viewing. In most cases, you do not need to change the sorting order.

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 However, if desired, you can define the sorting mode for dimension navigation using the **Display Sorting / Scrolling Directions** panel. To open the Display Sorting / Scrolling Directions panel, select a view and then click **Select and Sort** in the Review mode panel. The **Display Sorting / Scrolling Directions** panel is opened in the selected view.

NOTICE

On some monitors, the Display Sorting / Scrolling Directions panel cannot be displayed properly if views are tiled.

If your monitor uses a resolution lower than 1280 x 1024, maximize the view before opening the Display Sorting / Scrolling Directions panel.

Depending on the dimensions available in the selected series, the following sort modes are supported:

1D All

This sorting mode allows you to display and navigate all dimensions of a series in one linear sequence. In this mode, you scroll through, for example, all the phases of the first slice, then all the phases of the second slice, and so on. You can define the sort order of the dimensions using the **Select and Sort** tool.

When cine viewing with 1D All dimension sorting active, the display switches to single image view. If you navigate images during cine playback, the playback is paused and navigation returns to manual scrolling.

1D Stacked

This sorting method allows you to display one dimension in the view, and scroll through a second dimension. This is useful when viewing dual-echo scans or multi-slice / multi-phase scans.

The “running” dimension is displayed in the view, and each image in the layout is considered a stack in the second dimension. If there is a third dimension you can choose which dimensions should be assigned to the scrolling directions, using the **Display Sorting / Scrolling Directions** panel. For details, see section “Sorting in 1D Stacked mode” on page 96.

If the running dimension is assigned to the vertical navigation direction, navigation is row by row. If the running dimension is assigned to the horizontal direction, navigation is image by image.

When cine viewing with 1D Stacked dimension sorting active, you can choose the playback dimension in the **Movie** panel.

- If the playback dimension is the same as the running dimension, the view is switched to single image view.
- If the playback dimension is the stacked dimension, the playback runs simultaneously for all displayed images.

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During cine viewing, you can navigate in dimensions other than the playback dimension, as desired. If you navigate in the playback dimension, the playback is paused and navigation returns to manual scrolling.

Matrix

This sorting method allows you to compare images over multiple dimensions. Two dimensions are displayed in the view: one dimension is sorted across columns (left to right) and the other dimension is sorted across rows (top to bottom). The navigation direction matches the sorting mode. If a third dimension is available, it is stacked, and you can select a custom navigation direction in the **Display Sorting / Scrolling Directions** panel.

Viewing calculated maps

If a series contains calculated maps (such as T2, T2*, R2, R2*, and T1), these maps are appended to the end of the second dimension. For example, if the second dimension contains all echoes of a series, you can scroll horizontally through this dimension to view the echoes followed by the T2* map that was created from these echoes.

Sorting in 1D All mode

1.  Select the view that you want to sort and then click **Select and Sort** in the Review mode panel.

   The **Display Sorting / Scrolling Directions** panel is displayed in the selected view.

2.  In the **Display Sorting / Scrolling Directions** panel, ensure that the Display Sorting mode is set to **1D All**.
3. Select the desired dimension sorting order using the sorting order arrows.
   - The first dimension is the slowest running dimension and the last one is the fastest. In the figure shown above, for example, the sequence starts with the slices for the first dynamic of the first stack, then all slices of the second dynamic, and so on until the last dynamic, and then again for the second stack.
4. To change the sorting direction for the displayed order of slices, click **Sorting Direction**:
   -  Standard sorting direction
   -  Reverse sorting direction
5.  Click **Stacks as Separate Dimensions** to split the dimensions into separate stacks, if desired.
6. Scroll vertically to move through the images in the dimension:
   - Drag up or down.
   - Rotate the mouse wheel button forward or backward.

– Press the UP ARROW key or the DOWN ARROW key.

7. Scroll horizontally to move through the images image by image:
   – Drag left or right.
   – Press the LEFT ARROW key or the RIGHT ARROW key.
8. To scroll one page up or down, Press the PAGE UP or PAGE DOWN key.

Sorting in 1D Stacked mode

1. Select the view that you want to sort and then click **Select and Sort** in the Review mode panel.

⇨ The **Display Sorting / Scrolling Directions** panel is displayed in the selected view.

2. In the **Display Sorting / Scrolling Directions** panel, ensure that the Display Sorting mode is set to **1D Stacked**.
3. Select the running dimension.
4. Assign available dimensions to the vertical, the horizontal, and the third navigation directions using the scroll direction arrows.

5. To change the sorting direction for the displayed order of slices, click **Sorting Direction**:

   Changing the sorting direction is useful if the slice numbering order, as created during acquisition, is opposite to the most convenient display order.

   -  Standard sorting direction
   -  Reverse sorting direction

6. Click **Stacks as Separate Dimensions** to split the dimensions into separate stacks, if desired.

   This function allows you to view stacks in separate viewports and scroll through the slices synchronously.

7. To scroll through the vertical dimension, do one of the following:
   - Drag up or down.
   - Rotate the mouse wheel button forward or backward.
   - Press the UP ARROW key or the DOWN ARROW key.

⇨ If the vertical dimension is the same as the displayed dimension (the running dimension), the view scrolls to the previous or next row of images in that dimension. If the vertical dimension is a different dimension the whole set of displayed images steps forward or backward in the vertical dimension.

8. To scroll through the horizontal dimension, do one of the following:
   - Drag left or right.
   - Press the LEFT ARROW key or the RIGHT ARROW key.

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⇨ If the horizontal dimension is the same as the displayed dimension (the running dimension), all images in the view scroll to the next or previous image in that dimension. If the horizontal dimension is not assigned to the running dimension, the previous or next images in the horizontal dimension are displayed, for all of the displayed images of the running dimension.

9. To scroll through the third dimension, use the following keyboard shortcuts:
   - SHIFT+CTRL+UP ARROW
   - SHIFT+CTRL+DOWN ARROW
10. To scroll one page up or down, Press the PAGE UP or PAGE DOWN key.

Sorting in Matrix mode

1. Select the view that you want to sort and then click **Select and Sort** in the Review mode panel.

⇨ The **Display Sorting / Scrolling Directions** panel is displayed in the selected view.

2. In the **Display Sorting / Scrolling Directions** panel, ensure that the Display Sorting mode is set to **Matrix**.

3. Select the dimension to display across columns (vertical sorting order).

4. Select the dimension to display across rows (horizontal sorting order).
5. If desired, use the scroll direction arrows to change the mapping of navigation directions (vertical, horizontal, and diagonal) to available dimensions.

   By default, navigation directions match the selected sorting dimensions.

6. To change the sorting direction for the displayed order of slices, click **Sorting Direction**:
   -  Standard sorting direction
   -  Reverse sorting direction

     Changing the sorting direction is useful if the slice numbering order, as created during acquisition, is opposite to the most convenient display order.

7. Click **Stacks as Separate Dimensions** to split the dimensions into separate stacks, if desired.

   This function allows you to view stacks in separate viewports and scroll through the slices synchronously.

8. To scroll through the vertical dimension, do one of the following:
   - Drag up or down.
   - Rotate the mouse wheel button forward or backward.
   - Press the UP ARROW key or the DOWN ARROW key.

⇨ If the vertical dimension is assigned to a dimension that is displayed in the view, the view scrolls up or down one image. If the vertical dimension is not displayed in the view, all displayed images simultaneously scroll in the direction of the assigned dimension.

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9. To scroll through the horizontal dimension, do one of the following:
   - Drag left or right.
   - Press the LEFT ARROW key or the RIGHT ARROW key.

⇨ If the horizontal dimension is assigned to a dimension that is displayed in the view, the view scrolls left or right one image. If the horizontal dimension is not displayed in the view, all displayed images simultaneously scroll in the direction of the assigned dimension.

10. To scroll through the third dimension, use the following keyboard shortcuts:
    - SHIFT+CTRL+UP ARROW
    - SHIFT+CTRL+DOWN ARROW
11. To scroll one page up or down, Press the PAGE UP or PAGE DOWN key.
12. To move the contents of the view one page to the left or right (not including 1D dimensions), use the following keyboard shortcuts:
    - CTRL+PAGE DOWN (one page to the left)
    - CTRL+PAGE UP (one page to the right)

Slab and Volume viewing

Slab and Volume viewing allows you to view a series as a slab or as a volume. You can use tools in the Common tools panel to change the slab position, or roll and rotate the slab or volume. You can also display reference views of orthogonal slices.

Viewing a slab

▷ A slab view is displayed using Average Intensity Projection rendering. The **Scroll** tool is the default interaction tool when viewing a slab.

1. To change the position or thickness of the slab, ensure that the **Scroll** tool is selected, move the mouse pointer over the view, and then do one of the following:
   -  Drag up to move the slab backward through the volume.
   -  Drag down to move the slab forward through the volume.
   -  Drag left to increase the slab thickness.
   -  Drag right to decrease the slab thickness.

⇨ If a series has multiple dimensions, slab position and thickness is propagated across the dimensions, so that if you switch to another dimension, the dimension is displayed with the corresponding slab position and thickness.

2. If viewport controls are visible, you can also change the position of the slab using the position viewport control: click the position viewport control and then do one of the following:

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- Type a new value.
- Click the up or down arrows in the position viewport control box to change the value.
- Press the UP ARROW or DOWN ARROW key.
- Rotate the wheel button.

3. If viewport controls are visible, you can also change the thickness of the slab using the thickness viewport control: click the thickness viewport control and then do one of the following:
   - Type a new value.
   - Click the up or down arrows in the thickness viewport control box to change the value.

4. To roll or rotate the slab, click **Roll/Rotate** in the Common tools panel, and then do one of the following:
   - To rotate the slab, move the mouse pointer to the edge of the view, and then drag.
   - To roll the slab, move the mouse pointer over the middle of the view, and then drag.

   Propagation of 3D orientation is applicable in case of multiple dimensions in a series, for example, if you switch to another echo or cardiac phase, the 3D orientation is the same.
5. To display the center of rotation in the view, select **Rotation Center** in the Review mode panel.

⇨ The center of rotation is indicated by crosshair in the view.

6. To change the center of rotation, drag the crosshair to a new position

⇨ When you change the center of rotation, the intersections of the lines in the reference images are updated. You can also change the center of rotation by dragging an intersection in a reference view.

7. To move the rotation point (with the image) to the center of the display, right-click the rotation point and then click **Center Rotation Point**.
8. To center the image and move the rotation point to the center of the display, right-click the rotation point and then click **Reset Rotation Point**.

NOTICE

Image Information must be enabled in the Common tools panel to use the image information interactors.

NOTICE

You can activate the Roll/Rotate tool temporarily by dragging while pressing the left mouse button and the right mouse button.

Reference views

Reference views display orthogonal views of the anatomy in the main viewport.

Lines that are color-coded to the orientation model are displayed in each reference view, and represent the position of the slices displayed in the other reference views. A line representing the viewing plane of the main viewport is also displayed. This gives information about the viewing angle by means of its intersection with the reference images.

1. To change the layout of the main viewport and reference views, right-click the main viewport, point to the references layout command and then select a layout option.

⇨ By default, reference views always display the standard orthogonal views: axial, coronal, and sagittal.

2. To display reference views orthogonal to the orientation of the current view in the main viewport, click **Planar Mode** in the Review mode panel.

⇨ In planar mode, planes are always maintained in a perpendicular orientation.

⇨ To return to standard orthogonal views, click **Planar Mode** again to turn it off.

3. To display the intersections of orthogonal planes in the reference views, select **Crosshair** in the Review mode panel.

⇨ Reference lines indicate orthogonal slices, and are displayed by default.

4. To change the slab using a reference view, move the mouse pointer over the slab reference line so that the line is highlighted, and then do one of the following:

-  Position the mouse pointer over the slab reference line and drag to change the position of the slab.
-  Position the mouse pointer over the end of the slab reference line (indicated with a cross) and drag to rotate the slab.
-  Position the mouse pointer at the edge of the slab reference line and drag to change the slab thickness.

⇨ Dragging the reference line that corresponds to the other reference image also changes the rotation point.

Viewing a volume

▷ When viewing a series as a volume, you can select between **Volume (MIP)** render mode and **MinIp** render mode. The **Roll/Rotate** tool is the default interactor when viewing a volume.

1. To roll or rotate the volume, click **Roll/Rotate** in the Common tools panel, and then do one of the following:
   - To rotate the volume, move the mouse pointer to the edge of the view, and then drag.
   - To roll the volume, move the mouse pointer over the middle of the view, and then drag.

⇨ Propagation of 3D orientation is applicable in case of multiple dimensions in a series, for example, if you switch to another echo or cardiac phase, the 3D orientation is the same.

2. To change the center of rotation, select **Rotation Center** in the Review mode panel, and do the following:
   - Click a point in one of the reference views. The center of rotation (yellow point) moves to that location.
   - Clear the **Rotation Center** check box in the Review mode panel to set the new rotation point.

⇨ When you change the center of rotation, the reference images and their cross hair positions move to that location.

3. To reset the center of rotation to the center of the display, right-click the rotation point and click **Center rotation point**.
4. To change the geometry of the volume to a slab, do one of the following:
   - Click the **Thickness** image information interactor and type a value for the thickness of the slab.
   - Use the **Scroll** tool to change the slab thickness by dragging horizontally. You can then change the position of the slab by dragging vertically with the **Scroll** tool.

NOTICE

You can activate the Roll/Rotate tool temporarily by dragging while pressing the left mouse button and the right mouse button.

Reference views

Reference views display orthogonal views of the anatomy in the main viewport.

Lines that are color-coded to the orientation model are displayed in each reference view, and represent the position of the slices displayed in the other reference views. A line representing the viewing plane of the main viewport is also displayed. This gives information about the viewing angle by means of its intersection with the reference images.

1. To change the layout of the main viewport and reference views, right-click the main viewport, point to the references layout command and then select a layout option.

⇨ By default, reference views always display the standard orthogonal views: axial, coronal, and sagittal.

2. To display reference views orthogonal to the orientation of the current view in the main viewport, click **Planar Mode** in the Review mode panel.

⇨ In planar mode, planes are always maintained in a perpendicular orientation.

⇨ To return to standard orthogonal views, click **Planar Mode** again to turn it off.

3. To display the intersections of orthogonal planes in the reference views, select **Crosshair** in the Review mode panel.

⇨ When viewing a volume, reference views indicate the center of the volume and a plane through that center, parallel to the viewing screen. This gives information about the viewing angle by means of its intersection with the reference images.

⇨ Dragging the reference line that corresponds to the other reference image also changes the rotation point.

Viewing a 3D ortho volume

A 3D ortho volume view is a view composed of the three main orthogonal planes: transversal, sagittal, and coronal.

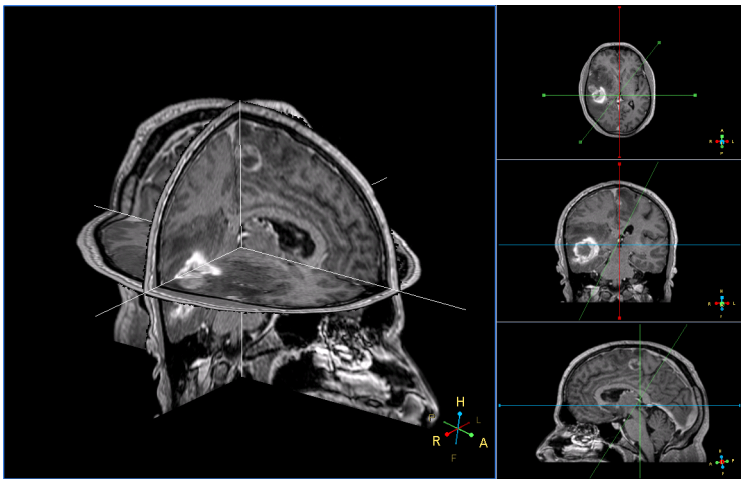

Fig. 14: 3D ortho volume view

▷ 3D ortho viewing is available for MR volumes only.

1. To roll or rotate the volume, click **Roll/Rotate** in the Common tools panel, and then do one of the following:
   - To rotate the volume, move the mouse pointer to the edge of the view, and then drag.
     - You can also rotate the volume by dragging with the right mouse button from any pointer position.
   - To roll the volume, move the mouse pointer over the middle of the view, and then drag.

⇨ Propagation of 3D orientation is applicable in case of multiple dimensions in a series, for example, if you switch to another echo or cardiac phase, the 3D orientation is the same.

2. To change the position of a plane, click **Scroll** in the Common tools panel, position the pointer over a plane in the main viewport, and then drag.
3. To hide one of the orthogonal planes in the volume view, click the arrow next to the orthogonal plane selector in the Review mode panel and deselect a plane.

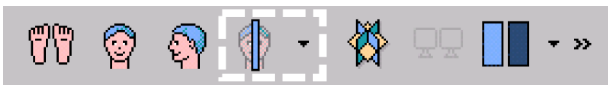

Fig. 15: Orthogonal plane selector in the Review mode panel

⇨ Orthogonal planes:

-  Transversal
-  Coronal

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-  Sagittal

4. To change the center of rotation, select **Rotation Center** in the Review mode panel, and do the following:
   - Drag the rotation center point (yellow) in the main viewport, or click a point in one of the reference views.
   - Clear the **Rotation Center** check box in the Review mode panel to set the new rotation point.

⇨ When you change the center of rotation, the reference images and their cross hair positions move to that location.

5. To reset the center of rotation to the center of the display, right-click the rotation point and click **Center rotation point**.

Reference views

Reference views display orthogonal views of the anatomy in the main viewport.

Lines that are color-coded to the orientation model are displayed in each reference view, and represent the position of the slices displayed in the other reference views. A line representing the viewing plane of the main viewport is also displayed. This gives information about the viewing angle by means of its intersection with the reference images.

1. To change the layout of the main viewport and reference views, right-click the main viewport, point to the references layout command and then select a layout option.

⇨ By default, reference views always display standard orthogonal views: axial, coronal, and sagittal.

2. To display reference views orthogonal to the orientation of the current view in the main viewport, click **Planar Mode** in the Review mode panel.

⇨ In planar mode, planes are always maintained in a perpendicular orientation.

⇨ To return to standard orthogonal views, click **Planar Mode** again to turn it off.

3. You can manipulate the volume using the reference views:
   - Drag either end of the viewing plane line to rotate the volume.
   - Drag up or down in the reference view to change the position of the displayed slice.
4. To show or hide the lines representing orthogonal slices, select or clear the **Crosshair** check box in the Review mode panel.

Clipping views

▷ The **Clip** panel provides the following functions:

- You can use the clipping box to restrict the visibility of the volume to the area that you want to focus on, temporarily rendering the rest of the volume invisible.
- You can define an area in the volume and cut the volume data from either inside or outside the area.

1. Select a slab or volume in the viewing area, click the task selector in the Task panel, and then click **Clip**.

⇨ The **Clip** panel is displayed.

2. To use the bounding box, click **Show/Hide Clipping Box**.

⇨ The clipping box is a frame around the volume that is initially displayed with the same size and orientation of the original volume (the total stack of slices).

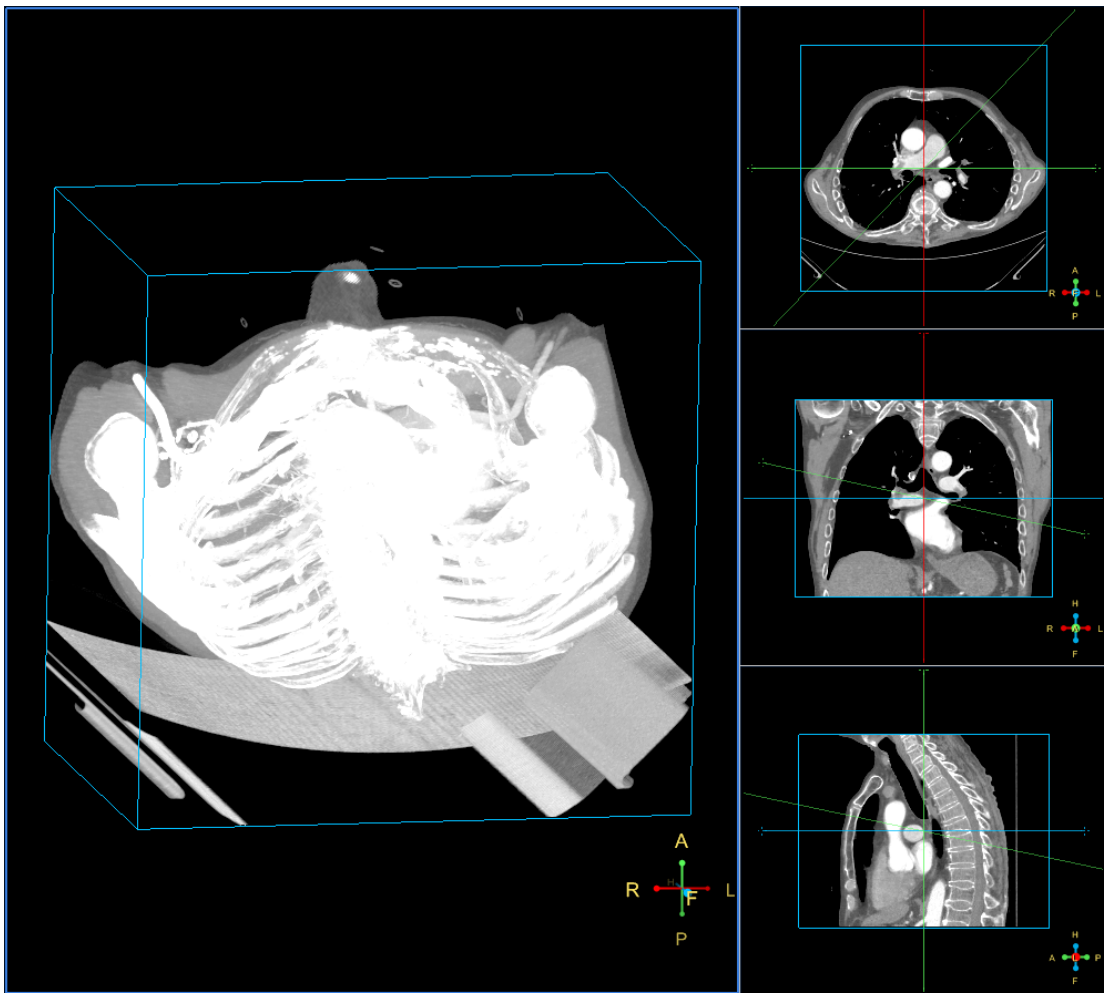

Fig. 16: Clipping box

3. To modify the size of the clipping box, do the following:
   - Display the reference views. Reference views are displayed automatically when the view is maximized, or you can right click a view and select a layout option. The clipping box is displayed as a blue box in the reference views.
   -  Move the mouse pointer over an edge of the clipping box in a reference view. When the “move” cursor is displayed, drag the edge of the box over the volume.
   - To view the clipped volume without the clipping box, click **Show/Hide Clipping Box**.
4. To define an area in the volume to be cut, do one of the following:

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You define the area in a 2D plane, but it extends through the whole 3D volume.

-  Draw a selection around the part to be kept and click **Include Freehand Contour**.
-  Draw a selection around the part to be cut and click **Exclude Freehand Contour**.

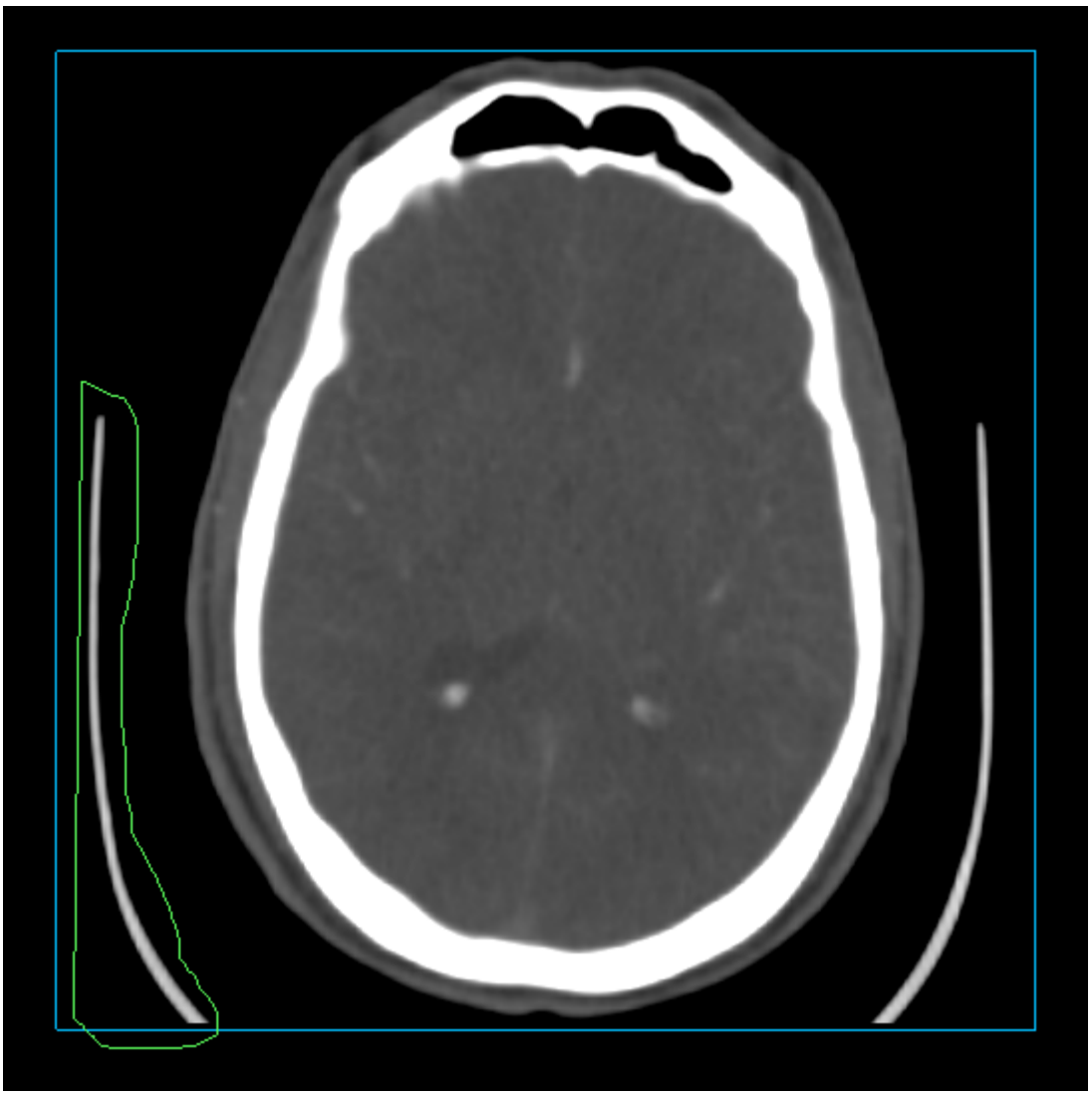

Fig. 17: Drawing a selection

5. To correct errors when cutting volume data, do one of the following:
   -  To undo the last cut, click **Undo**. You can use this tool to undo successive cuts.
   -  To remove all cuts, click **Reset**.

Fusion viewing

Using Fusion viewing, you can compare images that have been acquired at different times or with different modalities, but that display the same anatomy from one patient.

Fusion viewing is available for comparing the following types of series:

An MR series overlaid on a corresponding MR series.

A CT series overlaid on a corresponding CT series.

A PET or SPECT series overlaid on a corresponding CT series.

It is not possible to fuse an MR series with a CT series.

The series that is used as the overlay is called the “floating series”. The corresponding series is called the “reference series”.

Fusion viewing with display protocols

When you create a fused view of a PET or SPECT series with a CT series, the view opens in a display protocol. Depending on the selected display protocol, other views or sub-views might be available in the display protocol. These views simultaneously display alternate views of the fused series, or views of the original images in the floating series or reference series.

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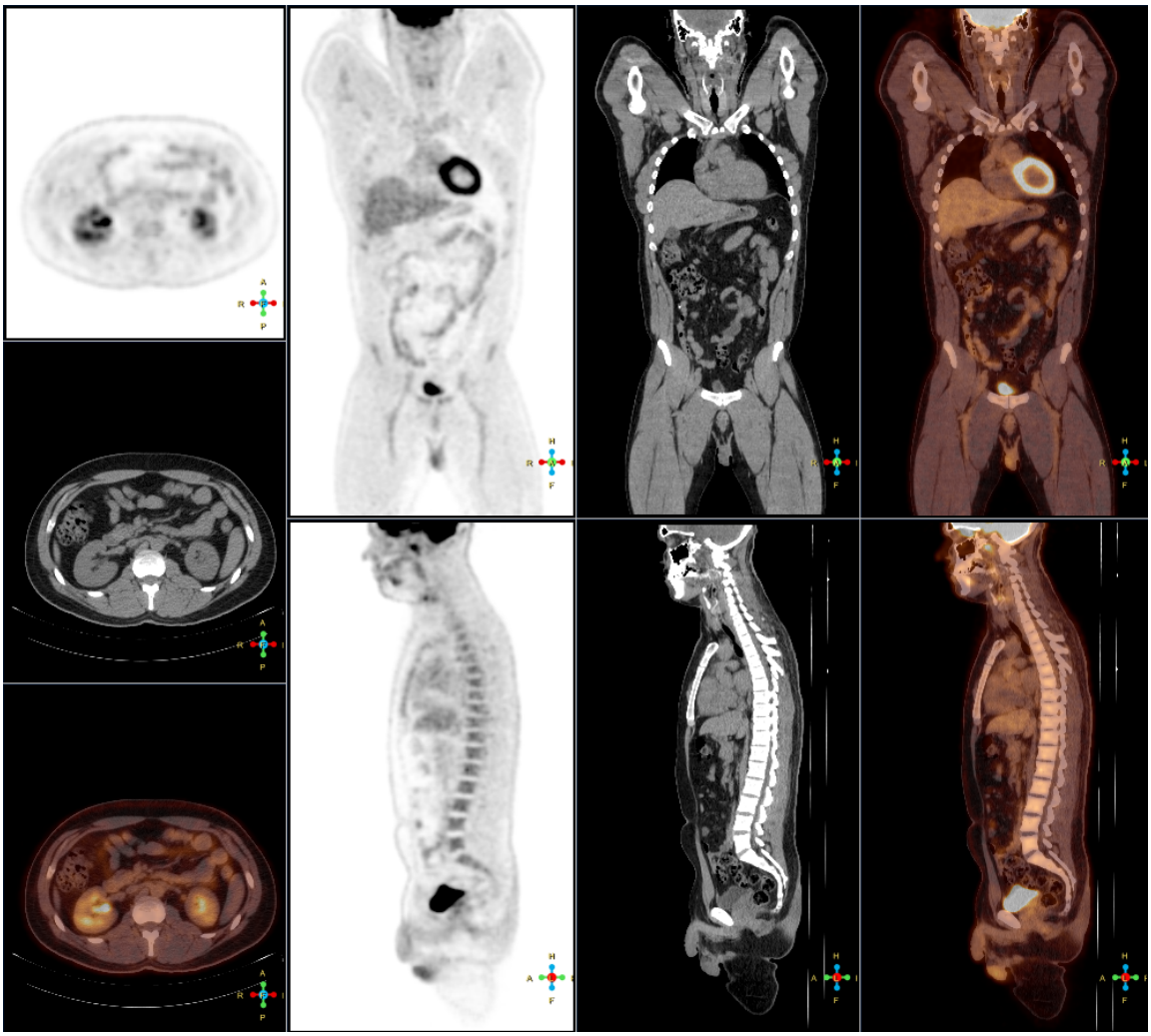

Fig. 18: A display protocol showing fused views with views of the source data

Fusing series

▷ When fusing MR with MR, or CT with CT, the reference series must be a 3D view.

▷ When fusing PET or SPECT, the reference series must be a CT series.

1. Open one of the series that you want to fuse, or select the series in the viewing area if it is already open.

2. Right-click the series in the **Series** panel that you want to fuse with the selected view and then click **Layout protocols**.

⇨ If the fusion configuration cannot be determined automatically, the Layout protocols function is not available. Use one of the following functions to create the fused view:

⇨ The images are combined to create a fusion view. Both series are automatically displayed in slab review mode, if possible.

⇨ If the series have been registered previously, the registration data is loaded and applied to the fused view.

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⇨ If there is no registration data available, both series are displayed centered in the screen and with their axes aligned. You should register the series before continuing with this procedure to ensure that the series display a correctly fused view. Registration allows you to adjust the geometrical link between the series. For details, please see section “Registration” on page 109.

⇨ For MR series, if the series are co-registered, you do not need to perform the registration procedure.

- Click **Add As Reference Series (underlay)** to add the selected series as the reference series.
- Click **Add As Floating Series (overlay)** to add the selected series as the floating series.

3. To select an alternative display protocol to match your workflow, click **Protocol Selection** in the Review mode panel and then select a new display protocol.

Fusion viewing interactions

▷ After creating a fused view, the following interactions are available.

1. To adjust the opacity of the floating series, right-click the view, click **Alpha Blend** in the shortcut menu, and then do the following:
   - Drag up to increase the opacity of the floating series.
   - Drag down to decrease the opacity of the floating series.

⇨ The amount of blending is displayed as a percentage in the view.

2. Position dimensions (stack, slices) are linked between the series in the fused view, but other dimensions are not. To navigate to another dimension in the floating series (if available), right-click the fused view and click Fusion to turn fusion off: you can then navigate to the desired dimension and turn fusion on again.

   For PET or SPECT fusion views with CT, you can navigate to the other dimension in a sub-view containing image data from the floating series, if available in the display protocol, without turning fusion off. Your changes in the sub-view are linked to the floating series in the fused view.

3. You can use geometry interactors to obtain the desired view of the fused series.

⇨ The floating series and the reference series are linked for panning, zooming, rotating and rolling, slab position, slab thickness, and render mode.

⇨ For PET/NM fusion views with CT, any sub-views that contain the same image data as either the floating series or the reference series are also linked to geometry and render mode interactions that you make in the fused view.

4. Gray level settings are not linked between the floating series and the reference series in the fused view. If you make adjustments to the gray level settings, only the floating series is modified.

   To adjust the gray level settings of the reference series, do the following:

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For PET/NM fusion views with CT, you can adjust the gray levels in a subview containing image data from the reference series, if available in the display protocol, without turning fusion off. Your changes in the sub-view are linked to the reference series in the fused view.

- Right-click the fused view and click **Select Underlay**.
- Make adjustments to the gray level settings of the reference series.

5. If desired, you can make measurements and place annotations on the floating series in the fused view.

 To make measurements or place annotations on the reference series, you must first select the reference series: right-click the fused view and click **Select Underlay.** After selecting this option, the reference series remains selected until you turn it off, and the option remains highlighted in the shortcut menu. Click **Select Underlay** again to turn the selection off.

Registration

The registration procedure matches the position and orientation of the two series in a fused view. You can use this procedure to align series from different modalities, or to compensate for patient movements between scans.

There are two methods of registration:

- Manual registration is an interactive process, in which you make a combination of translation and rotation adjustments on the floating series to match it with the reference series.
- Automatic registration matches the floating series with the reference series using a computer algorithm. Automatic registration works best when there is only a small mismatch between the series.

You can combine both methods to achieve the best registration result. For example, you can use manual registration to visually match the series as closely as possible, and then use automatic registration to fine-tune the result.

You can change display protocols without losing registration data, so that you can use one layout that is appropriate for registration, and then switch to another layout that is appropriate for clinical purposes.

The registration data is not saved with the images if you close the series, but after performing registration, you can save the image data of the floating series, with the registration adjustments applied to it, as a new series.

MR inter-series registration (co-registration)

If you are registering two MR series, you also have the option to save the results of the registration as a co-registered series.

Registering series

- ▷ The Fusion Registration task panel is only available if the active view is a fusion view of two different series.
- ▷ The best method for registering the floating series with the reference series is to make manual registration adjustments until the series are matched as closely as possible, and then to complete the procedure using automatic registration.
- ▷ Registration adjustments using tools in the Fusion Registration task panel are made on the floating image in all displayed orientations.

1. In the task panel (in the side panel), click the task selector and then click **Fusion Registration** to display the **Fusion Registration** panel.
2. If the fused view is a slab or a slice, check that the floating series and reference series are displayed in the same position.

   If you need to adjust the position of one of the series to match the other series, right-click the fused view and select Fusion to temporarily unlink the series. You can then change the position of one of the series in relation to the other. When you have matched the slab position, turn fusion on again from the shortcut menu.

3. Click **Registration Pan** and drag the floating series to match it with the reference series.
4. To fine-tune the position of the floating series, click one of the translation fine tuning arrows.

   The translation fine tuning buttons move the floating series 0.5 mm in the direction of the arrow on the button.

   Fine tuning using the arrow keys on the keyboard is not available.

5. Click **Registration Rotate** and drag the floating series to match it with the reference series.

   Rotations are made in the currently viewed plane.
6. To fine-tune the rotation of the floating series, click one of the rotation fine tuning arrows.

   The rotation fine tuning buttons rotate the floating series 0.25 degrees in the direction of the arrow on the button.

7. If you make a mistake with the matching process, click **Undo** to undo the last adjustment that you made with the translate, rotate, or fine tuning tools in the task panel.

   You can undo consecutive adjustments by clicking **Undo** repeatedly.

8. If you undo an adjustment, but then decide that you want to reinstate it, click **Redo**.

   The **Redo** function is only available after you click Undo, and before you make another adjustment.

9. If you want to start over, click **Reset** to reset the position and orientation of the floating series to the state is was in when you opened the **Fusion Registration** task panel.

   Registration adjustments that are made prior to starting the current registration task (in a different session) cannot be reset with the **Reset** button.
10. You can use tools from the Common tools panel at any time (for example, zoom, pan, roll, rotate, and scroll).

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⇨ Adjustments that you make using the Common tools are applied to the whole fused image (both series). Selecting a tool from the Common tools panel cancels the selection of the **Registration Pan** tool or the **Registration Rotate** tool. However, you can use direct mouse manipulation shortcuts without canceling selection of these tools. For details, see section “Direct Mouse Manipulation” on page 161.

11. To complete the registration process, select a registration algorithm, and then click **Automatic Registration**.

    The following registration algorithms are available:

⇨ **Normalized Mutual Information**

- Best used to perform multi-modality registration in cases where there is limited anatomical data or large misalignments.
- Uses a histogram-based method.
- Calculates the probability distribution of gray values in each data set and uses this in the mutual information equation.
- Does not rely on a functional relationship between the gray values in the data sets.

⇨ **Cross Correlation**

- Best used for single modality registration.
- Assumes a linear relationship between distributions of the two data sets.
- Based on simple squared difference equation between gray values.

⇨ **Local Correlation**

- Best used for multi-modality registration in cases where there is significant anatomical detail and only small misalignment.
- Similar to Cross Correlation, but applies a similarity equation in many small neighborhoods of the data sets.

⇨ The **Automatic Registration** function matches the volumes as closely as possible, assisted by the manual registration adjustments that you have made.

⇨ The images in the viewing area are updated periodically during the Automatic Registration process. You can stop the process at any time by clicking **Automatic Registration** to cancel the function.

NOTICE

Inspect the registration thoroughly before continuing. If necessary, use the manual registration tools to refine the registration. You can also reapply automatic registration after making adjustments.

The accuracy of the registration could affect image interpretation.

⇨ After performing registration, you can close the **Fusion Registration** task panel without losing the registration data. However, the registration data is lost if you close the series.

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12. To save the results of the registration adjustments, as applied to the floating series, click **Save Registered Results As** in the Common tools panel.

⇨ The image data of the floating series, with the registration adjustments applied to it, is saved as a new series. The new series has the same number of slices and the same slice thickness as the original floating series. The new series is available in the Series panel when you reload the original series from the Directory.

13. To save the results of the registration as an MR inter-series registration (MR series only), click **Save MR inter-series Registration As** in the Common tools panel.

⇨ The inter-series registration is saved as a new series on the study.

WARNING

When using the "Export to Surgical Nav. Format for MR Data'" option, there is a remote possibility that even with all registration steps being performed on the fused images (fMRI maps or Fiber Tracks aligned to anatomical images), there is still a residual misalignment which may be introduced due to small patient motion during the acquisition of the images. This may result in inaccurate information for surgical planning and it is recommended for the surgery planning review board to inspect the results.

MR Review

The following options are available to extend the MR viewing capabilities of MultiModality Viewer. The availability of these options depends on the configuration of your system. Some or all of these options might not be available.

MR Segmentation

Segmentation of MR series is available in MultiModality Viewer using the **MR Segmentation** tool.

1. To open the MR Segmentation tool, click the task selector in the Task panel and then click **MR Segmentation**.

⇨ The **MR Segmentation** panel is displayed.

2. To start MR segmentation, click **MR Segmentation** in the task panel.

⇨ The series is automatically opened in an MPR view. The resulting segmentation is also visible in the reference views.

⇨ The pointer becomes a circle, which you can use to identify a region in the anatomy.

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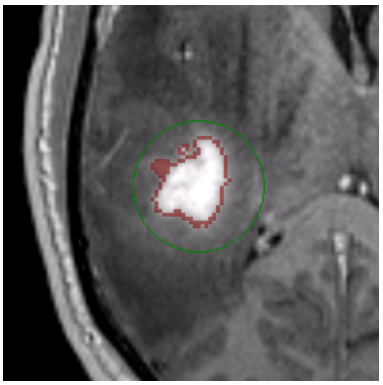

Fig. 19: MR segmentation tool - selection circle

3. To change the size of the circle, press CTRL and rotate the scroll wheel on the mouse.

⇨ By default **Bright** is the selected **Target Volume**. If **Bright** does not suit your workflow, select **Dark** from the drop down list.

4. Locate the area of interest in the series, resize the selection circle appropriately, and double-click the anatomy that you want to segment.

⇨ A VOI is created and displayed in the series.

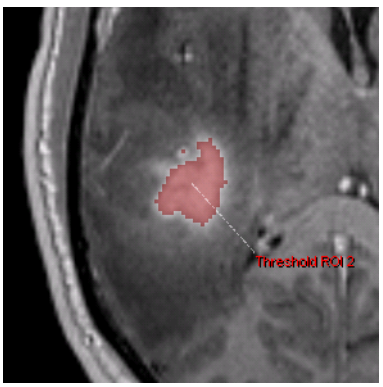

Fig. 20: MR Segmentation - VOI

5. If desired, drag the **Adapt Proposed Threshold** slider to adjust the threshold of the VOI boundary.

6. To view the dimensions of the VOI, right-click the VOI and click **Longest Diameter**.

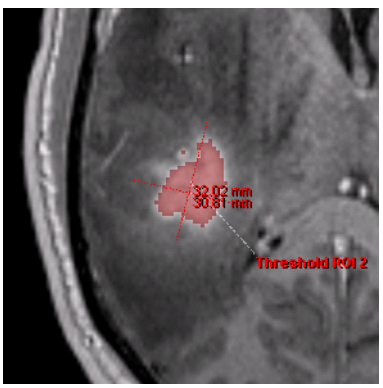

Fig. 21: Viewing the longest diameters of the VOI

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7. To remove part of the VOI, click **Eraser** in the task panel, resize the selection circle appropriately, and click the area that you want to remove.

NOTICE

When you switch to a different function, the segmentation is finalized and can no longer be edited.

MobiView

Indications for Use

The MobiView option automatically combines images from multiple acquisitions from the same examination to create one overall volume.

MobiView

WARNING

After applying the fusion operation, double-check whether the result of the fusion operation is correct. Always keep the original images. Horizontal lines on the image indicate where the operation took place. Check for any artifacts that could indicate a fusion error, like cut-off objects or anatomy. The fused images must be of the same acquired plane. Be aware that the resolution at the edges of a station can be lower than in the center.

It is not recommended to perform measurements inside the fused area indicated by horizontal lines.

▷ MultiModality Viewer displays the MobiView volume as a regular 3D view, either as a volume (MIP), or as a slab (MPR).

▷ You can create a MobiView volume from a series in the Series panel, or from a series that is already open in the viewing area.

1. Right-click the selected series and do one of the following:

   -  Click **MobiView MPR** to create a MobiView slab (MPR).
   -  Click **MobiView MIP** to create a MobiView volume (MIP).

⇨ If you created the MobiView volume from a series in the **Series** panel, it is opened as a new view in the viewing area. If you created the MobiView volume from a series that is already open, it is added as new tab in the view.

⇨ The standard 3D viewing tools in MultiModality Viewer are available for investigation of the MobiView volume, but it is not possible to adjust the stitching of the volume.

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⇨ For full details of MobiView, please refer to the documentation provided with the MobiView system.

NOTICE

A MobiView volume or slab can only be created from an MR series that contains MR multistation data.

NOTICE

If the scans that have to be fused do not have GeoLinks (for example, because the scan is aborted), select multiple scans to overcome this problem: in this case, fusing will be done for these multiple scans.

Indications for Use

The MobiView option automatically combines images from multiple acquisitions from the same examination to create one overall volume.

FiberTrak

If fiber bundles are available in a series, MultiModality Viewer can display them in 2D and 3D views of the series.

You can access fiber bundles in the Object Manager.

1. To open the Object Manager, click the task selector in the Task panel and then click **Object Manager**. section “Using the Object Manager” on page 140.

⇨ The Object Manager indicates the state of each object for each view.

2. To display the fiber bundle in the main viewport, right-click the fiber bundle in the Object Manager and click **Show**.

⇨ In 2D views, the intersection of the fiber bundle with the plane is displayed.

⇨ In a 3D ortho view, the fiber bundle is shown as a 3D model.

3. To change the color of a fiber bundle, right-click the bundle in the Object Manager, point to **Color**, and then select one of the following options:
   - **Use Directional Color**
   - Select a color from the submenu.

NOTICE

If you change the color of a fiber bundle, the new color is not saved when you close MultiModality Viewer.

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WARNING

When fibertract settings are changed to low values (meaning no signal threshold, very low FA, and very high curvature acceptance) the white matter tracts may include erroneous results.

This may consequently lead to misdiagnoses. It is advised to use default settings whenever possible.

WARNING

With FiberTrak the resulting fibers depend strongly on the parameter settings in the package.

NOTICE

Low SNR in the DTI dataset can influence the results, leading to limited or no tracts.

Spectroscopy

NOTICE

If you choose to select individual series from one or more studies, ensure that *all* series that are required for analysis are selected. For example, a spectroscopy series also requires an anatomical series for reference. If you do not select all the required series, the application cannot be launched.

In MultiModality Viewer, you can view the processed frequency domain analysis results of the Spectroscopy data, but the actual time signal (raw data) cannot be viewed.

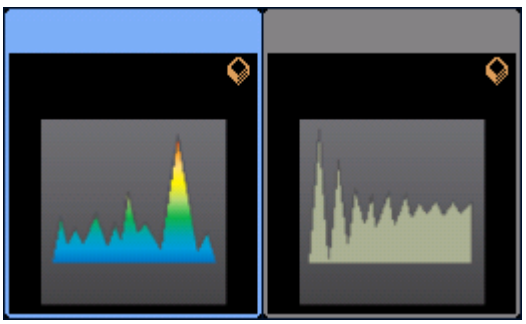

Fig. 22: Spectroscopy data as viewed in the Series panel: left - processed analysis results, right - raw data

1. To view Spectroscopy analysis, do the following:
   - Select the analysis results series in the **Series** panel.
   - Drag the analysis results series on to a viewport that already displays the anatomy.

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⇨ The view displays the spectrum graph in one viewport, with a view of the anatomy underlay with the voxel grid in a second viewport. The quality indicator and mini spectra are displayed. (The mini spectra is automatically displayed if one of the spectro voxels side planes is parallel to the underlay image plane, and intersects with this plane.)

NOTICE

You can load multiple Spectroscopy analysis results series in a viewport by dragging them on to the anatomy image. This allows you to compare multiple single-voxel data sets acquired at different locations.

⇨ When you maximize the view, the analysis graph is displayed in the main viewport with one anatomical reference view to the right. You can change the layout using the right mouse menu. To maximize the view, double-click the title bar of the view.

2. To swap the analysis graph with the upper reference view, right click the main viewport and click **Swap Main and Chart**.

⇨ Repeat this step to swap the graph back again.

3. To show or hide the grid, right click in a reference view (outside the grid, if displayed) and enable or disable **Show Grid**.
4. To show or hide the quality indicator, right click the grid and enable or disable **Show Quality Indicator**.
5. To show or hide the mini spectra, right click the grid and enable or disable **Show Mini Spectra**.
6. To align the view to the Spectroscopy grid, right-click the grid and click **Align View to Grid**.

fMRI

In MultiModality Viewer, you can view series statistical parameter maps as an overlay.

When viewing fMRI series you can adjust the following settings:

1. To change the threshold of the colormap, right-click the image and click **ColorMap Threshold** in the right mouse menu.

   Changing the threshold allows you to increase or decrease the range of pixels included in the color overlay.

   - Drag up or down to adjust the threshold. The range is indicated in the colormap legend on the right side of the viewport.

⇨ The colormap scale is displayed on the right side of the viewport. By default, only positive values are displayed.

2. To view negative values, right-click the viewport and click **Show Negative T-Scores**.

3. To change the blending (transparency) of the SPMs, right-click the image and click **Alpha Blending** in the right mouse menu.

- Drag up or down to adjust the blending. The level of blending is displayed as a percentage at the top of the viewport.

4. To change the cluster size, click the **ClusterSize** viewport control and enter a value.

⇨ Changing the cluster size allows you to filter out smaller activation areas or "false positives".

WARNING

Alignment between functional and anatomical series should be inspected and corrected using the registration inspection step in IViewBOLD and FiberTrack.

Ultrasound Review

Single-frame and multi-frame Ultrasound images can be viewed in MultiModality Viewer. 3D Ultrasound images can be analyzed by launching the QLAB analysis application from within MultiModality Viewer. Multi-vendor data is supported.

Multiple series can be viewed side-by-side for comparison, or alongside images of the patient from different modalities. You can send Ultrasound images to the Film and Report applications using tools in the Common Tools panel. Measurements can also be performed on Ultrasound images in MultiModality Viewer.

MultiModality Viewer supports the following Ultrasound modes:

- **B-mode**: In B-mode (brightness mode) ultrasound, a linear array of transducers simultaneously scans a plane through the body. The image can be viewed as a single frame or multi-frame object.
- **M-mode:** In M-mode (motion mode) ultrasound - a transmit and receive m-line is position in the 2D image, the data from the m-line is presented as grayscale image presented on a timeline.
- **Doppler mode**: This mode makes use of the Doppler effect in measuring and visualizing blood flow.
  - **Color Doppler**: Velocity information is presented as a color-coded overlay on top of a B-mode image.
  - **Continuous Doppler**: Blood flow information is sampled along a line through the body, and all velocities detected at each time point are presented on a timeline.
  - **Pulsed wave (PW) Doppler**: Blood flow information is sampled from only a small sample volume (defined in 2D image), and is presented on a timeline.
  - **Duplex**: This is a common name for the simultaneous presentation of 2D and (usually) PW Doppler information. (Using modern ultrasound machines color Doppler is almost always also used, hence the alternative name Triplex.)

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Ultrasound Display Settings

If you selected images in the **Patient Directory**, these images are automatically displayed in viewports when you launch **MultiModality Viewer**. If you did not select images, the first 4 images are displayed in viewports in a 2x2 layout.

To enlarge a view to a single-viewport layout, double-click the view. Double-click the single view to return to the 2x2 layout.

Images in the viewing area and pictorials in the **Series** panel are ordered by acquisition time. In the **Series** panel, the header of each pictorial displays the view name, instance number, and number of frames for that image.

Display Modes

You can select a display mode in the **Review Mode** panel. The following display modes are available:

- **Display by Sequence**: Displays the images in order of acquisition. This is the default display mode if none of the images in a series has a view number (this is the case if the acquisition was not protocol-based).
- **Display by Views**: Displays the images by view number to support Ultrasound protocols. This is the default display mode if images in the series have a view number (this mode is available only if the study was acquired with a protocol). When this display mode is selected, images that do not have view number are displayed at the end of the sequence of images.
- **Manual Selection**: Using this mode you can manually select images to display in viewports in the layout. When this mode is selected, the layout automatically changes to single view (1x1 layout).

NOTICE

Dual monitor display is currently only supported when using the **Manual Selection** display mode.

Navigating Images

To navigate the images in a study (according to the selected display mode), do the following:

-  Click **Next** in the Review Mode panel, or press PAGE DOWN, to display the next image.
-  Click **Previous** in the Review Mode panel, or press PAGE UP, to display the previous image.

When viewing a layout with multiple viewports, image navigation is synchronized across viewports: the next or previous images in all viewports are displayed.

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Image Interactions

You can use image interaction tools available from the Common tools panel on Ultrasound images in MultiModality Viewer:

-  **Scroll**
-  **Pan**
-  **Zoom**
-  **Window Level**

NOTICE

The Window Level tool does not currently work on a multi-frame image in cine mode. Pause the image to use this tool.

Cine Viewing for Multi-frame Images

When you open a multi-frame image for viewing, the image is replayed in cine mode by default. Pictorials in the Series panel indicate if the series is a multi-frame image using a cine annotation on the pictorial.

You can pause or play cine mode using the **Pause/Play** tool in the Common tools panel, or by pressing Break/Pause on the keyboard.

NOTICE

The **Play/Pause** tool is not available if the image in the upper-left viewport is a single frame image. Select a multi-frame image to enable the control.

Alternatively, select a multi-frame image and click **Movie** in the Common tools panel to display the **Movie** panel.

To synchronize movie interactions across all visible multi-frame images, select the check box on the left side of the **Movie** panel.

The default frame rate is the acquisition frame rate. You can change the frame rate to a percentage value of the acquisition frame rate using the up and down arrows next to the frame rate indicator, or by dragging the slider. The current frame rate is also indicated as an image overlay on the image.

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NOTICE

The first time that a multi-frame image is replayed, the frame rate might be slightly slower while the image is transferred to your workstation.

Measurements

You can use the line, angle, ROI, and point measurement tools, as well as the annotation tools, when viewing Ultrasound images. For full details of the standard tools, please refer to the *Measurements and graphics* section in the *Instructions for Use* for MultiModality Review.

Multi-region Line Measurements

Ultrasound images may have several different regions, for example, a tomographic region and a PW Doppler region. You can use the line tools in the Common tools panel in multiple regions, but a single line measurement cannot cross a region boundary (the measurement valid becomes invalid). The type of measurement obtained with this tool depends on the region in which it is used.

2D Regions

On 2D regions, a line measurement provides distance.

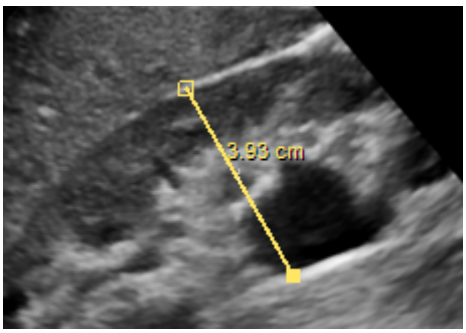

Fig. 23: Line measurement on a 2D region

MMode Regions

On MMode regions, a line measurement provides the difference in depth and time between the end points.

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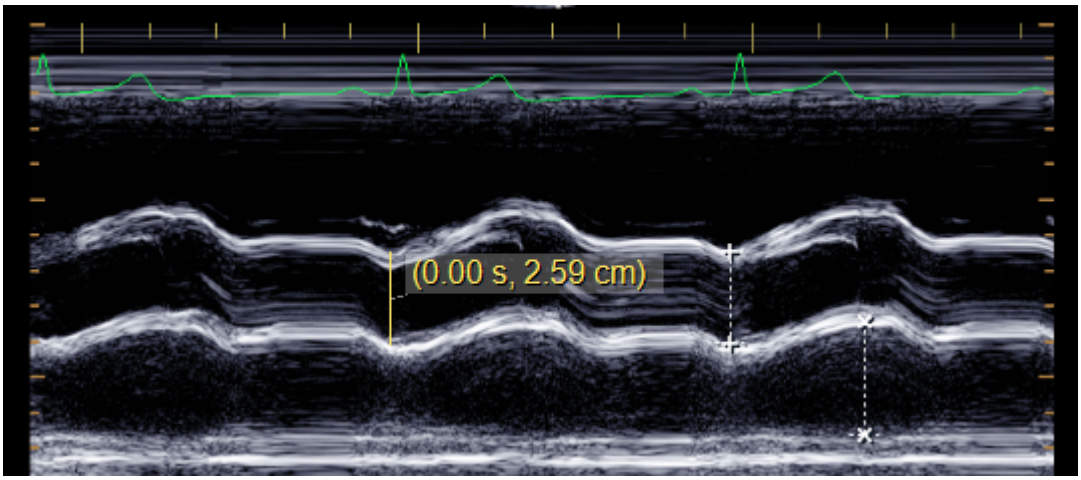

Fig. 24: Line measurement on an MMode region

Doppler Regions

On Doppler regions, a line measurement provides the difference in velocity and time between the end points.

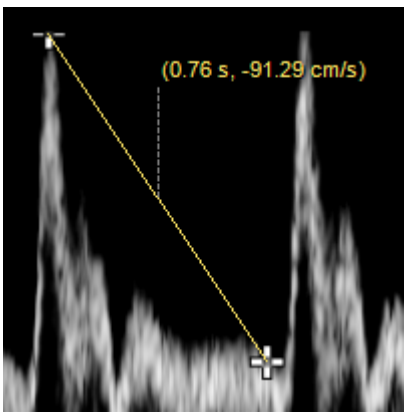

Fig. 25: Line measurement on a Doppler region

To measure the absolute velocity of a specific point, draw a vertical line from the baseline to the point of interest.

QLAB

NOTICE

QLAB applications support only Philips data.

NOTICE

A separate license is required to use the QLAB applications. Please contact your Philips representative for details.

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You can launch the following **QLAB** applications from **MultiModality Viewer** while viewing 3D Ultrasound images:

- ROI
- GI3DQ
- Elastography
  - EA
  - EQ (this option may not be available on some systems)
- Vascular
  - IMT
  - VPQ
- Contrast
  - MVI

Images that support QLAB analysis are indicated with a **Q** annotation on the image.

The QLAB annotation is also indicated on the pictorial in the Series panel.

To launch a QLAB application, right-click the image, point to **QLAB Apps**, and then click a QLAB application in the submenu.

X-Ray Angiography Review

MultiModality Viewer is the default viewer for X-ray Angiography images (XA). You can load processed and unprocessed series from the X-ray equipment or from a workstation. MultiModality Viewer provides tools for basic viewing and image manipulation of XA images (for example: zoom, pan, rotate, and replay movie).

MultiModality Viewer supports processing of raw DSA XA studies to produce subtraction images from vascular contrast studies.

You can also load reconstructed volumes (CT-like data) and snapshots from the following Interventional Tools: 3D-RA, 3D-CA, and XperCT.

NOTICE

When you open an iXR (XA) study in MultiModality Viewer, all series under the study are imported to your client system. Depending on the size of the study, there may be a small delay before images are displayed.

NOTICE

XA images can be viewed, sent to reports, and exported. Printing is also available, but images are sent to the print application in Secondary Capture (SC) format only.

Multi-Vendor Support

Multi-vendor support is included for basic viewing functions with XA images, but only for specific releases of third-party scanners. For details, please contact your Philips representative.

Multi-vendor support not available with XA vascular processing functions. Only data acquired on Philips systems can be used with these functions.

Viewing XA Images

When you load an XA series in MultiModality Viewer, the complete study is loaded and all series in the study are available in the **Series** panel pictorial index. The first run is loaded in the viewing area in a 1x1 layout. The series is displayed in run replay mode, replaying at the acquisition frame rate. If the acquisition frame rate cannot be used, the percentage of the rate is displayed.

You can open XA series from the Series panel for side-by-side review with other multimodality studies.

You can use standard tools such as **Scroll**, **Zoom**, **Pan**, and **Contrast/Brightness** in the common tools panel when viewing XA images. When you use these tools on an XA image, the changes are automatically propagated to all frames in the run.

You can use the **Movie** panel to replay the run with standard cine viewing functions, including variable frame rate.

You can also apply measurements and annotations to XA images using tools in the common tools panel. Measurements and annotations are only visible on the image that they are applied to.

3D Volumes

When viewing volumes that have been created on the Interventional Tools, the following rendering options are available:

- MIP (Maximum Intensity Projection)
- VR (Volume Rendering)
- ISR (Iso Surface Rendering)

The freestyle batch tool can also be used with these volumes.

Exporting Images

It is possible to send/export processed XA images directly from the Patient Directory.

By default, this option is enabled when you select an XA study. If you deselect this option, the original unprocessed data is exported.

To enable the automatic processing of raw XA images:

1. Select an XA study.
2. Select **Copy To** from either the Control Panel or the context menu.
3. Place a check mark in the **Process raw XA images** check box .
4. Click **Ok**.

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NOTICE

Once the **Process raw XA images** option is enabled, bookmarks linked to unprocessed data will not be copied to destination devices and a warning message appears.

The saved non-DICOM images will also be skipped if this option is checked.

This option appears *only* if the selection contains at least one XA study.

Saving of View Settings

All of the changes made as part of XA Vascular Processing are automatically saved when:

- exiting from MMV
- moving to next or previous runs
- selecting a new run from Pictorial Index

The following settings are saved:

- Pan position
- Windowing
- Measurements and annotations
- Electronic shutter positions
- Vascular processing:
  - Mask image or mask run (including displacement)
  - Landmarking percentage
  - Pixel shift adjustment
  - Displacement in case of Run

Manual Saving of View Settings

To manually save your view settings, right click in the image area and click **Save Image Viewing Settings**.

These view settings are also stored when you create a bookmark of an XA series.

Saving Images

Standard functions are available in the common tools panel to save XA images. You can save any of the following:

- Save selected images
- Save the display
- Save a series as processed

Biplane Viewing

When you select a series that is part of a biplane acquisition, the series from the frontal and lateral channel are selected.

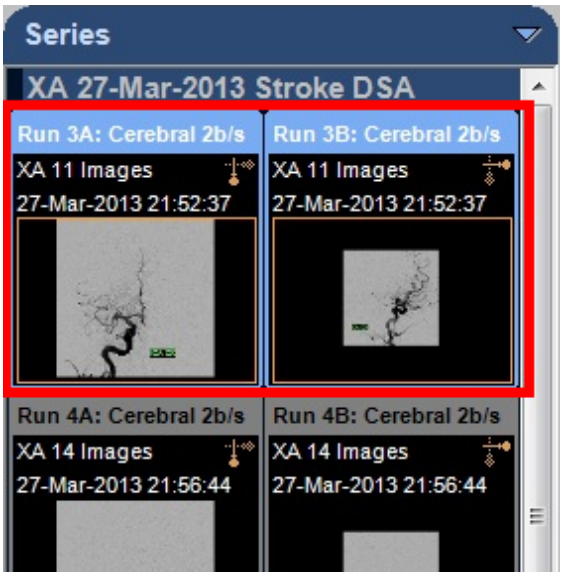

Fig. 26: Biplane series in the Series panel

When you open a biplane series, both series are automatically displayed side-by-side. The frame number and the replay rate are synchronized when reviewing the series.

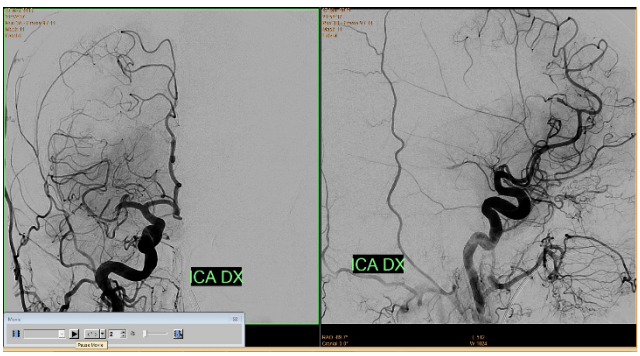

Fig. 27: Viewing biplane series

You can maximize one of the views of linked biplane series by double clicking the image. Double-click the image again to return to side-by-side linked view.

Dual-Monitor Mode

When viewing biplane series in dual-monitor mode, the frontal image is displayed on the primary monitor and the lateral image is displayed on the secondary monitor.

Pixel Size Calibration

You can apply manual calibration to images to display calibrated values for measurement annotations.

1. Right-click an image, point to **Pixel Size Calibration**, then do one of the following:
   - To create a calibration line and apply the calibration value manually, click **User-defined**.
   - To create a calibration line with a specific value, click one of the available options. You can select a value based on French or millimeters.

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2. Draw a calibration line along a known length in the image.
   ⇨ For example, you can draw a line along a ruler that may be included in the image.
   ⇨ If you selected a calibration line with a specific value, ensure that the line represents that value in the image.

WARNING

If you use a small distance on the screen for the calibration line, the calibration may be inaccurate.

3. Enter a value for the length of the calibration line.
   ⇨ The calibration factor is calculated and applied to all images in the series.
   ⇨ While the calibration line is displayed, all measurement annotations, including existing measurements, display a calibrated value.
   ⇨ While the calibration line is displayed, a message is also displayed in the image as a reminder that manual calibration is in effect.

NOTICE

When you are working with biplane series, you need to perform calibration separately in each plane.

4. You can adjust the calibration by modifying the length of the calibration line and changing the calibration value of the line.
5. To delete the calibration line, right-click the line and click **Delete**.
   ⇨ When you delete the calibration line, existing measurements no longer display calibrated values.

Electronic Shutters

You can overlay electronic shutters on XA images to hide parts of the image.

To apply a shutter, right click the image and choose a shutter option:

- **Circular Shutter**
- **Polygonal Shutter**
- **Rectangular Shutter**

Rectangular shutters (horizontal and vertical) can be synchronized.

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Using XA Vascular Tools

To process XA images in MultiModality Viewer, select **XA Vascular Tools** using the task selector arrow in the Task panel. The task guidance panel provides the following processing tools:

- **Standard Subtraction**
- **Run Subtraction**

NOTICE

The vascular processing options on the task guidance panel are enabled once the cine has stopped.

Standard Subtraction

Standard subtraction uses a single image from the series as the subtraction mask for all other images in the same series. The image used as the subtraction mask is selected by default. You can change the mask image if desired using tools in the task guidance panel.

Remasking

If the default mask image is not the optimal image to be used as a mask for subtraction, you can select another image as the subtraction mask using the **Remasking** tools in the task guidance panel.

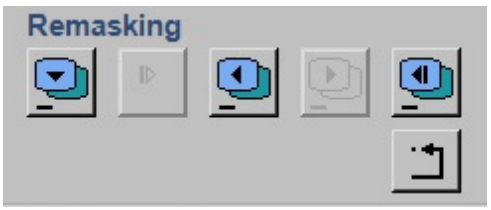

Fig. 28: Remasking panel

NOTICE

Processing tools in the task guidance panel are not available while cine viewing is active. Stop cine viewing to access the tools.

You can select one of the following images for the mask image:

- The currently viewed image
- The next or previous image relative to the current mask image
- The first or last image in the series

For biplane studies, the selected mask image is applied automatically for each plane.

If you change your mind, click **Reset** to go back to the default mask image.

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Run Subtraction

Run subtraction uses two separate series to generate a subtracted series. To perform run subtraction, at least two series must be available: the first series should have been acquired with contrast and the corresponding mask series, which should have been acquired without contrast.

NOTICE

If you perform the run subtraction at the cathlab suite, the system automatically chooses the corresponding mask run and displays the subtracted series in MultiModality Viewer.

Remasking

If the selected mask series is not suitable and another corresponding contrast series is available, you can change the mask series using the **Mask Run** tools in the task guidance panel.

Fig. 29: Mask Run tools

Click **Reselect Mask** to select the alternative mask series.

If the mask series is not exactly aligned with the contrast series, you can shift the run backward or forward relative to the contrast run using the arrows in the **Mask Run** tools in the task guidance panel.

Pixel Shift

You can use the **Pixel Shift** tools in the task guidance panel to correct for patient movements during contrast injection.

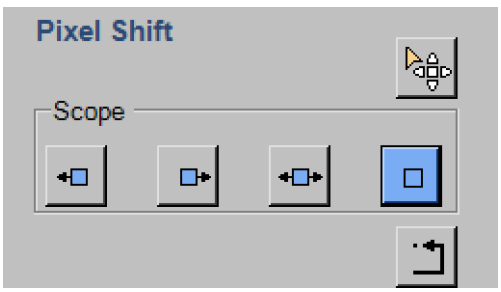

Fig. 30: Pixel Shift tools

These tools allow you to manually shift the image a small amount in any direction by dragging in the view with the **Pixel Shift** tool enabled.

The movement is applied to the whole image and you can propagate the adjustment to other images in the series:

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- Previous images including the current image
- Following images including the current image
- All images
- The current image only

For biplane studies, the adjustment is applied separately for each plane.

To remove any pixel shift adjustment that you have applied to the series, click **Reset**.

Landmarking

You can use the **Landmarking** tools in the task guidance panel to blend the vascular structure of the subtracted image with the surrounding anatomy.

Select **Show Landmarking** in the trask guidance panel and use the **Landmarking** tool to set a partial subtraction factor. Depending on how much landmarking you set with the tool, the details of the complete image will show through the subtracted image.

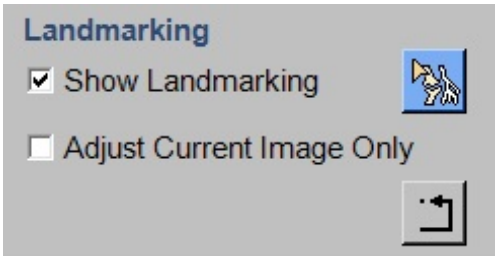

Fig. 31: Landmarking tools

For biplane studies, landmarking is applied separately for each plane.

To remove landmarking from the series, click **Reset**.

Spatial Downscaling

When you open a high resolution XA study that has a matrix size greater than 512x512, it is automatically downscaled to 512x512 (or an equivalent scale for non-square data). This allows the study to be loaded faster and provides better performance when cine viewing. When a study has been automatically downscaled, an annotation is displayed in the viewport to inform you.

You can turn off automatic downscaling by clicking **Spatial Downscaling** in the common tools panel to deselect the function.

NOTICE

If you save or print a high resolution study, high resolution images are sent even if **Spatial Downscaling** is turned on.

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ISP – iXR Integration (sharing MRN Context) Functionality

The IntelliSpace Portal (ISP) - iXR Integration feature enables integration between ISP and Philips iXR Cathlab System (Allura) systems. This is based on sharing MRN/PatientID between Allura Cathlab and ISP.

This integration tool brings ISP a step closer to the intervention room and leverages the advanced clinical tools available within ISP before performing the procedure (or during the procedure). This integration utilizes the bookmark concept in ISP to enable the activation of the required clinical applications within the examination/control room. ISP client can be configured to be viewed on the FlexVision screen in the examination room so that it is visible during the procedure.

The IntelliSpace Portal - iXR Plugin needs to be installed and configured on the ISP Client that integrates with the Allura Cathlab system. This integration and configuration is performed by a Field Service Engineer. This feature requires a license.

Once the iXR Plugin is configured, ISP listens to the Philips iXR Cathlab System for patient context changes. There are two modes of integration, Automatic (default) and Manual, which are described below.

Interventional Bookmark (iBookmark)

The current ISP bookmark feature has been extended to tag a bookmark as an Interventional Bookmark. This tagging is used to automatically launch the bookmark in the intervention room. Once a bookmark is saved as an Interventional Bookmark, all subsequent saving of bookmarks under the same “state” are marked as Interventional Bookmarks.

Workflow

Once the iXR Plugin is installed and configured, integration between IntelliSpace Portal and Philips iXR Cathlab System is complete.

To display Interventional Bookmarks in the Save Bookmark dialog:

- Go to **Preferences** and open the **Viewing Applications** page.
- Under **Interventional X-Ray**, place a check mark in the **Show Interventional Bookmark** checkbox.

Once enabled, it is possible to open any Review or Analysis application (except for NM applications) and save the Bookmark as an Interventional Bookmark by placing a check mark in the **Interventional Bookmark** checkbox, while saving the Bookmark.

Once the Bookmark is saved as Interventional Bookmark, it appears in the Patient Directory and is visible under the Bookmark pane. Interventional Bookmarks are tagged with an icon  on the Bookmark thumbnail.

It is possible to create an Interventional Bookmark from a normal bookmark that is already saved. This is done by placing a check mark in the **Interventional bookmark** check box in the **Save Bookmark** window. This creates a new Interventional Bookmark under a new collection. Once changed to an Interventional Bookmark, the bookmark cannot be converted to a normal bookmark.

Automatic Mode

Once a patient is selected for acquisition on the Philips iXR Cathlab System, the ISP client launches the latest Interventional Bookmark (iBookmark), if available. If there are multiple Interventional Bookmarks, either under the same study or across multiple studies of the same patient, the latest Interventional Bookmark is selected and launched automatically to the corresponding application.

NOTICE

An option in the setup dialog can be enabled to ignore Interventional Bookmarks that are older than a specified number of days. The default value is 90 days. If there are Interventional Bookmarks older than 90 days, the system will not launch the bookmark.

Use the **Studies** button on the Patient Bar to select and launch a study.

If the system does not find an Interventional Bookmark or insufficient details are available from PACS, the study selector is launched and the user can select the required study or bookmark. The Interventional Bookmark can be identified by looking for a check mark in the Interventional Bookmark column.

It is possible to query the PACS (which is configured as PACS node) to retrieve prior patient studies and launch the required applications from the study selector using the **Priors** button.

If a new patient is selected in the table, a message inquiring whether to continue with the existing study or to change to a new patient. Select **Yes** to proceed to a new patient scheduled in the Philips iXR Cathlab System or select **No** to continue with the current patient.

Manual Mode

In this mode, when there is a change in patient context, ISP will not launch the study automatically. However, the iXR Plugin updates patient context with the latest patient on the iXR System. To launch the study manually:

- Click on the iXR Plugin icon  on the taskbar.
- Select **Launch** from the context menu.

Once the option is launched, if the patient has any Interventional Bookmark, it is loaded. Otherwise, the study selector is launched.

Using ISP in Standalone Mode

It is also possible to invoke ISP in standalone mode if the user wants to review studies of any other patient and not the patient on the table. This is possible by exiting the ISP application selecting the ISP icon on the taskbar and selecting the **Exit** option. Once **Exit** is selected, the user can open ISP via the Desktop icon or from the Programs menu.

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Diagnostic X-Ray Review

Diagnostic X-ray images (RF, DX, and CR) can be displayed in MultiModality Viewer for basic 2D viewing. MultiModality Viewer provides tools for basic viewing and image manipulation of RF, DX, and CR images (for example: zoom, pan, rotate, and replay movie).

NOTICE

Mammo series cannot be loaded in MultiModality Viewer.

Images labeled either "For presentation" or " For processing" can be loaded.

NOTICE

Processing functions for native RF, DX, or CF images are not available.

For RF images, MultiModality Viewer equates one run with one series.

You can load RF, DX, and CR images with other multimodality studies for side-by-side review.

NOTICE

RF, DX, and CR images can be viewed, sent to reports, and exported. Printing is also available, but images are sent to the print application in Secondary Capture (SC) format only.

When you open an RF, DX, or CR study in MultiModality Viewer, all series and images in the study are loaded in the Series panel. The first run is loaded in the viewing area in a 1x1 layout.

Predefined layouts are available to support preferred viewing modes:

- DX or CR images can be viewed side-by-side: AP/PA view on the left and lateral view on the right.
- Linked DX and CR images can be arranged manually, according to your workflow needs.
- RF images can be viewed in a "matrix" layout: all images under one run in different tiled formats.

Viewing Tools

The following viewing tools are available when viewing RF, DX, or CR images:

- Flip
- Rotate
- Zoom

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- Pan
- Windowing
- Shutters

When you use these viewing tools on RF images, the changes are automatically propagated to all frames in the run.

Annotations

Annotations can also be added to RF, DX, or CR images. When you add an annotation, it is visible on the selected image only.

Pixel Size Calibration

You can apply manual calibration to images to display calibrated values for measurement annotations.

1. Right-click an image, point to **Pixel Size Calibration**, then do one of the following:
   - To create a calibration line and apply the calibration value manually, click **User-defined**.
   - To create a calibration line with a specific value, click one of the available options. You can select a value based on inches or millimeters.
2. Draw a calibration line along a known length in the image.

⇨ For example, you can draw a line along a ruler that may be included in the image.

⇨ If you selected a calibration line with a specific value, ensure that the line represents that value in the image.

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WARNING

If you use a small distance on the screen for the calibration line, the calibration may be inaccurate.

3. Enter a value for the length of the calibration line.

⇨ The calibration factor is calculated and applied to all images in the series.

⇨ While the calibration line is displayed, all measurement annotations, including existing measurements, display a calibrated value.

⇨ While the calibration line is displayed, a message is also displayed in the image as a reminder that manual calibration is in effect.

4. You can adjust the calibration by modifying the length of the calibration line and changing the calibration value of the line.
5. To delete the calibration line, right-click the line and click **Delete**.

⇨ When you delete the calibration line, existing measurements no longer display calibrated values.

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Run Replay

Run replay is available for RF runs only.

You can use the **Movie** panel to replay the run with standard cine viewing functions, including variable frame rate.

Electronic Shutters

You can overlay the following types of electronic shutters on RF, DX, or CR images:

- Polygonal
- Rectangular
- Circular

Rectangular shutters can be rotated.

Spatial Downscaling

When you open a high resolution XA study that has a matrix size greater than 512x512, it is automatically downscaled to 512x512 (or an equivalent scale for non-square data). This allows the study to be loaded faster and provides better performance when cine viewing. When a study has been automatically downscaled, an annotation is displayed in the viewport to inform you.

You can turn off automatic downscaling by clicking **Spatial Downscaling** in the common tools panel to deselect the function.

NOTICE

If you save or print a high resolution study, high resolution images are sent even if **Spatial Downscaling** is turned on.

Multi-Vendor Support

Multi-vendor support is included for basic viewing functions with RF, DX, and CR images, but only for specific releases of third-party scanners. For details, please contact your Philips representative.

Measurements and graphics

Accuracy of measurements

The accuracy of measurements depends on multiple factors that determine image quality:

- The accuracy of patient positioning and fixation
- Patient motion and organ motion

- The modality type and acquisition protocol, acquisition and reconstruction distortions
- Image resolution: both spatial and contrast resolution
- Other factors

In addition to these external factors, the image viewing settings in MultiModality Viewer influence the measurement accuracy. Settings such as grey level, window width, zoom and others may affect how the users perceive the dimensions of the anatomy displayed on the screen. These settings also influence the accuracy of positioning the measurement control points through mouse clicks.

The clinical user is responsible to judge the accuracy of the measurements based on the image quality and based on the accuracy of placing the measurement control points.

Selecting a measurement tool

Where multiple measurement tools are contained in a menu, the tool last used remains available. To use the tool again, just click the appropriate button. To select a different tool, click the arrow to open the tool's menu.

When making measurements, the selected measurement tool remains active until a measurement has been made. You can apply the measurement to any view, not only the selected view.

NOTICE

Some measurements are not available in MIP/MPR views.

If the selected measurement type is not available for the view at the pointer position, an alternative measurement type is used if you choose to make a measurement in that view.

Measuring a distance

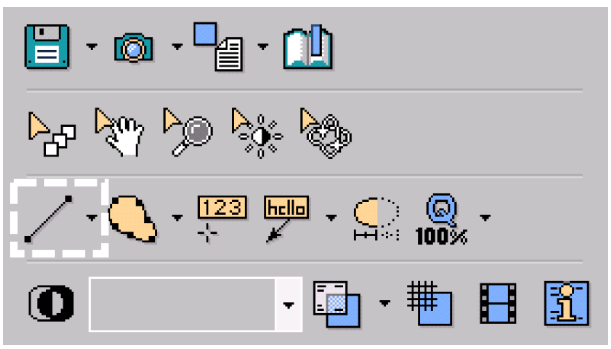

Fig. 32: Line and angle tools selector

▷ To measure a distance, use the line and angle tools selector in the Common tools panel. You can activate the line measurement tool by pressing D. After measuring a distance, the value of the measurement is displayed with the line.

1. To measure a distance along a straight line, click **Line** in the Common tools panel, and then do the following:

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- Move the pointer over the view in which you want to create the measurement.
- Click at the start point of the line, then move the pointer and click at the end point of the line.

2. To measure a distance along a line with multiple sections, click **Polyline** in the Common tools panel, and then do the following:
   - Move the pointer over the view in which you want to create the measurement.
   - Click at the start point of the line.
   - Move the pointer and click at the next point in the line.
   - Continue making points along the line, and then double-click at the end point of the line.

3. To measure a distance along a line with smoothed curves, click **Smoothed Polyline** in the Common tools panel, and then do the following:
   - Move the pointer over the view in which you want to create the measurement.
   - Click at the start point of the line.
   - Move the pointer and click at the next point in the line.
   - Continue making points along the line, and then double-click at the end point of the line.

Measuring an angle

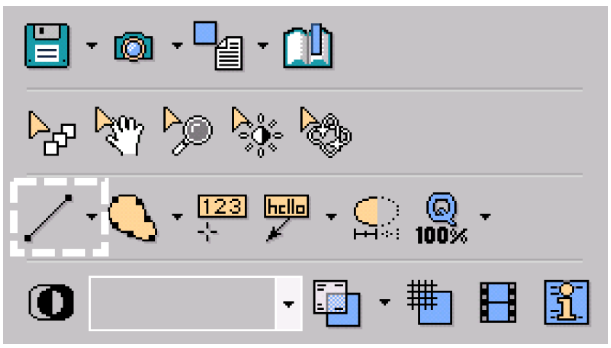

Fig. 33: Line and angle tools selector

▷ To measure an angle, use the line and angle tools selector in the Common tools panel. After measuring an angle, the value of the angle is displayed next to it.

1. To measure a closed angle, click **Angle** in the Common tools panel, and then do the following:
   - Move the pointer over the view in which you want to create the measurement.
   - Click at the start of the first leg.
   - Click at the apex.
   - Click at the end of the second leg.

2. To measure an open angle, click **Open Angle** in the Common tools panel, and then do the following:

- Move the pointer over the view in which you want to create the measurement.
- Click at the start of the first leg.
- Click at the end of the first leg.
- Click at the start of the second leg.
- Click at the end of the second leg.

Measuring a region of interest

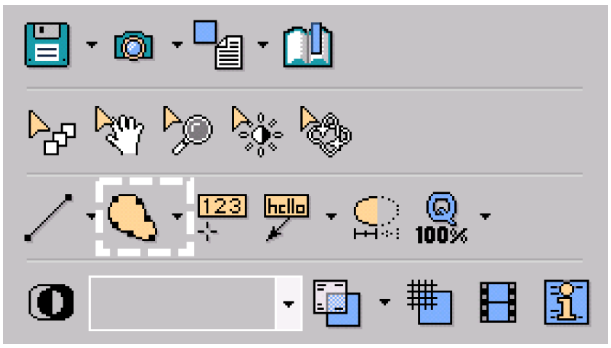

Fig. 34: ROI tools selector

▷ To measure a region of interest (ROI), use the ROI tools selector in the Common tools panel. After measuring a region of interest, the measurement details are displayed next to it.

1. To create a boxed region, click **Box** in the Common tools panel, and then drag to create an ROI.

2. To create a circular region, click **Circle** in the Common tools panel, and then drag to create an ROI.

3. To create an elliptical region, click **Ellipse** in the Common tools panel, and then do the following:
   - Drag across the first dimension of the ellipse, and the release the mouse button.
   - Move the pointer to set the perpendicular dimension, and then click the mouse button to create the ROI.

4. To create a closed region with a varying contour, click **Closed Contour** in the Common tools panel, and then do the following:
   - Click at the start point of the contour.
   - Trace the edge of the contour with the pointer, and then click to create the ROI.

5. To create a closed region with a smoothed contour, click **Smoothed Polygon** in the Common tools panel, and then do the following:
   - Click at the start point of the polygon.
   - Move the pointer, and then click at the next boundary point of the polygon.
   - Create as many boundary points as desired, and then double-click to create the ROI.

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Measuring a 3D region of interest

▷ To measure a 3-dimensional region of interest (3D ROI), use the **Volume Measurement** panel in the Task panel. The **Volume Measurement** panel provides the following methods for creating a 3D ROI:

- An Auto SUV threshold. This method is only available for PET series with predefined SUV calibrations (SUVbw only).
- A threshold specified as a percentage of a calculated local maximum. This method is only available for PET and SPECT 3D series.

▷ In a fusion view, a 3D ROI measurement applies to the overlay series. Turning fusion off or on switches measurements between the overlay and the underlay series automatically.

1. Select the series in which you want to make a volume measurement.

2. Click the task selector in the Task panel, and then click **Volume Measurement**.
3. To create a 3D ROI using an Auto SUV threshold, do the following:
   - If desired, change the **Threshold [SUV]** value (the default value is 2.5).
   -  Click **Seed Point** and then click on a region of interest to set a seed point.

⇨ Parts of the image that are connected to the seed point and that are equal to or greater than the threshold are identified with a border overlay.

WARNING

When placing a seed on a 3D image, verify its location on the reference images.

4. To create a 3D ROI using a threshold percentage, do the following:
   - If desired, change the **% of maximum** value (the default value is 40).
   - If desired, change the **Number of points to average** (the default value is 5).
   - 

Click **Seed Point** and then click on a region of interest to set a seed point.

⇨ Parts of the image that are connected to the seed point and that are equal to or greater than the threshold percentage are identified with a border overlay.

5. To hide the quantitative information displayed with the 3D ROI, rightclick the 3D ROI, and then click **ROI measurements** to cancel the selection in the shortcut menu.

   You can display the information again by selecting **ROI measurements** in the shortcut menu.
6. To change the settings used to create a 3D ROI, you must create a new 3D ROI.

⇨ After a 3D ROI is created, it cannot be edited, but you can create multiple 3D ROIs.

7. To delete a single 3D ROI, right-click it, and then click **Delete ROI**.

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8. To delete all 3D ROIs in the view, click **Delete all volume ROIs** in the **Volume Measurement** panel.

NOTICE

After you have created a 3D ROI, you should verify that it does not leak into neighboring organs.

Using the ROI Measurements panel

Details of ROIs and VOIs are available in the ROI Measurements panel in the main viewport.

▷ The ROI Measurements panel is available for MR volumes only.

1. To open the ROI Measurements panel, do one of the following:
   - Click **Restore**  in the lower-right corner of the main viewport.
   - Double-click **ROI Measurements** in the lower-left corner of the main viewport.

⇨ The ROI Measurements panel is displayed, providing details of ROI or VOI objects that are present in the series.

2. To display the location of an object in the main viewport, right-click the object and click **Show**.
3. To rename an object, do the following:
   - Click the name of the object.
   - When the text appears in a white box, type a new name.
   - Press ENTER.

4. To change the color of an object, right-click the object, point to **Color**, and then select a color from the submenu.

⇨ You can also open the Window color chooser from the submenu, and select a custom color in the color chooser.

5. To delete an object, right-click the object and click **Delete**.
6. To close the ROI Measurements panel, do one of the following:
   - Click **Minimize**  in the title bar of the ROI Measurements panel.
   - Double-click the title bar of the ROI Measurements panel.

Using the Object Manager

The Object Manager is a catalog of ROIs, VOIs, and fibers available in the currently viewed series.

▷ The Object Manager is available for MR volumes only.

1. To open the Object Manager, click the task selector in the Task panel and then click **Object Manager**.

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⇨ The **Object Manager** panel is displayed.

⇨ The Object Manager indicates the state of each object for each view.

2. To display the location of an object in the main viewport, right-click the object and click **Show**.
3. To show or hide an object in the main viewport, select or clear the check box next to the object in the Object Manager.

⇨ This setting applies only to the current view.

4. To rename an object, do the following:
   - Click the name of the object.
   - When the text appears in a white box, type a new name.
   - Press ENTER.

5. To change the color of an object, right-click the object, point to **Color**, and then select a color from the submenu.

⇨ You can also open the Window color chooser from the submenu, and select a custom color in the color chooser.

6. To delete an object, right-click the object and click **Delete**.

Measuring a point value

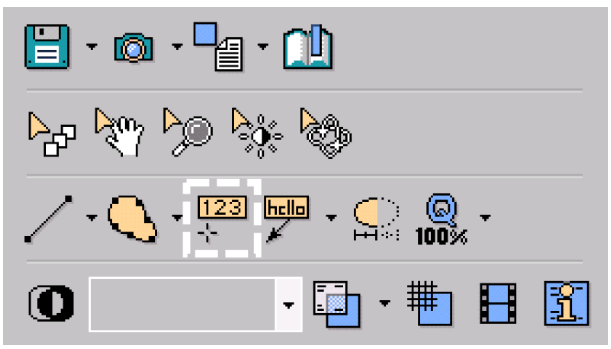

Fig. 35: Point value tool

▷ To measure a point value, use the point value tool in the Common tools panel.

1. To measure the value of a point in a 3D image, click **Voxel Value** in the Common tools panel, and then click on a point in a view.

⇨ The value of the point is displayed at the point marker.

2. To measure the location of a point in a 2D image, right-click the point marker and then click **3D Location**.

⇨ The point location is displayed at the point marker, using the right-handed DICOM patient coordinate system:

- L - Left

- P - Posterior
- S - Superior (head)

Creating an annotation

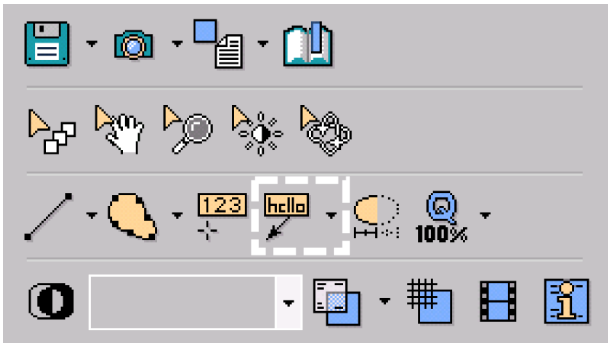

Fig. 36: Annotation tools selector

▷ To create an annotation, use the annotation tools selector in the Common tools panel.

1. To create an annotation with an arrow, click **Arrow With Text Box** in the Common tools panel, and then do the following:
   - Move the pointer over the view in which you want to place the annotation.
   - Click at the point of the arrow and then drag to create the arrow.
   - Release the mouse button and type the annotation.
   - Click outside the annotation to finish.

2. To create an annotation without an arrow, click **Text Box** in the Common tools panel, and then do the following:
   - Move the pointer over the view in which you want to place the annotation.
   - Click at the start of the annotation and type the annotation text.
   - Click outside the annotation to finish.

Modifying measurements and graphics

You can modify a measurement or graphic by moving it to a new position, by moving the points of a graphic to adjust its shape, or by changing its color, font, or size. Options are available from the shortcut menu to change the appearance of a graphic, including a properties panel for detailed modifications.

You can select multiple graphics in a view by clicking each graphic while pressing SHIFT. You can then apply changes to the appearance of all selected graphics in one step using the shortcut menu. Changes to the appearance of a graphic are applied immediately.

To move a graphic, drag it to a new position. You can move the measurement value of a measurement graphic independently of the graphic.

To move a point, drag it to a new position.

To modify the shape of a smoothed polygon, do one of the following:

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- Select a point and drag it to a new position.
- Click the border of the polygon and then drag to create a new point.

To delete a graphic, do one of the following:

- Select the graphic and press DELETE on the keyboard.
- Right-click the graphic and click **Delete**.

To copy a graphic, do one of the following:

- Select the graphic and press CTRL+C on the keyboard.
- Right-click the graphic and click **Copy**.
- You can then paste the graphic in a new position or in a new view: rightclick at the new position and then click **Paste**.

To paste a graphic that you have previously copied, do one of the following:

- Select the graphic and press CTRL+V on the keyboard.
- Right-click the graphic and click **Paste**.

To remove a graphic and store it on the clipboard, do one of the following:

- Select the graphic and press CTRL+X on the keyboard.
- Right-click the graphic and click **Cut**.
- You can then paste the graphic in a new position or in a new view.

 To hide all graphic objects in the selected view, click **Hide/ Show All Graphics Objects** in the Common tools panel.

To hide an individual graphic, right-click the graphic and click **Hide Selection**.

To change the color of a graphic, right-click the graphic, point to **Color**, and click a color. If you select **Custom**, the standard Windows **Color** dialog box is displayed, allowing you to select a custom color.

Graphics and Text Properties

You can change the appearance of graphic items and change the properties of text using the Graphics and Text Properties dialog box from the shortcut menu.

Changing graphics properties

▷ You change graphics properties using the **Graphics** tab of the **Graphics and Text Properties** dialog box.

▷ Your changes are applied immediately, but the **Graphics and Text Properties** dialog box provides controls for resetting your changes if desired.

1. Right click a measurement or graphic and then click **Properties**.
2. Click the **Graphics** tab to display graphics properties.
3. To change the line color properties, do the following:

- Click the **Line Color** arrow and select a color. The color is also applied to text labels.
- Select a line type (**Solid** or **Dashed**).

4. To fill the graphic with color, select **Fill**.

   Clear the **Fill** check box to display the graphic as an outline.

5. If you chose to fill the graphic, do the following to change the fill properties:
   - Click the **Fill Color** arrow and select a color.
   - Move the **Fill Transparency** slider to adjust the transparency of the graphic. The default transparency is 70%.
6. Select a **Marker Type** to mark the end of the line.

   Select the blank marker type option to suppress the display of line markers (this is the default option).

7. To reset your changes to the default graphics properties, click **Set to Initial**.
8. To define your current changes as the default graphics properties, click **Set as Default**.
9. To reset your change to the properties displayed when you opened the **Graphics and Text Properties** dialog box, click **Undo Changes**.
10. To accept your changes to the graphics properties click **Close** or click the **Text** tab to modify the text properties.

Changing text properties

▷ You change text properties using the **Text** tab of the **Graphics and Text Properties** dialog box.

▷ Your changes are applied immediately, but the **Graphics and Text Properties** dialog box provides controls for resetting your changes if desired.

1. Right click a measurement or graphic and then click **Properties**.
2. Click the **Text** tab to display text properties.
3. To change the font properties, do the following:
   - Click the **Type** arrow and select a font.
   - Click the **Style** arrow and select a font style.
   - In the **Size** box, type a value or click the up or down buttons.
4. To change the text color properties, do the following:
   - Click the **Foreground** arrow and select a color. The color is applied to the text.
   - Click the **Background** arrow and select a color. The color is applied to the background behind the text.
   - Click the **Shadow** arrow and select a color. The color is applied to the shadow under the text.
   - Move the **Background Transparency** slider to adjust the transparency of the background color. The default transparency is 70%.
5. Select an **Alignment** setting.

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6. To reset your changes to the default text properties, click **Set to Initial**.
7. To define your current changes as the default text properties, click **Set as Default**.
8. To reset your change to the properties displayed when you opened the **Graphics and Text Properties** dialog box, click **Undo Changes**.
9. To accept your changes to the text properties click **Close** or click the **Graphics** tab to modify the graphics properties.

Saving

WARNING

Images, snapshots, or movies that are saved to a file format using lossy compression should not be used for diagnosis.

Lossy compression creates images that are of lower quality than original DICOM images.

Saving images and copying images to film

Tools for saving images and copying images to film are located in the Common tools panel.

Save

The **Save** tool provides the following save options:

- Save selected images in Original DICOM, SC (DICOM), JPEG, TIFF, BMP, or AVI (Movie) format.
- Save a snapshot of the display in Original DICOM, SC (DICOM), JPEG, TIFF, or BMP format.

NOTICE

Images in JPEG, TIFF, or BMP format are of lower quality than original DICOM images and must not be used for diagnosis.

Film

The **Film** tool provides the following options to copy images to the film application:

- Copy selected images to the film sheet
- Copy a snapshot of the display to the film sheet
- Copy selected series to the film sheet

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NOTICE

When you send XA, RF, DX, CR, and US images to film, only secondary capture (SC) images are sent and the image quality may not be optimal.

The **Save** and **Film** tools display the last tool that you used. Click the tool button to use that tool again, or click the arrow to select another tool.

When you copy images or the display to film, the images are sent to the Film application. Images are sent with their current window settings, containing visible annotations and measurements. Zoom and pan settings are mapped to the current film layout, and can be changed in the film application, if desired. For details of using the Film application, please refer to the documentation provided with the Film application package.

Selecting multiple images

You can either save or copy to film one image at a time, or you can select multiple images and save them as a set of images, or copy them to film as one film section.

1. To select a range of adjacent images, hold CTRL and click the first image in the range, then hold SHIFT and click the last image in the range.
2. To select multiple images that are not adjacent, click the first image in the selection, and then do any of the following:
   - To select an additional image, hold CTRL and click the image to add it to the selection. You can repeat this action as many times as you want.
   - To add a range of images to the existing selection, hold CTRL and click the first image in the range, then hold CTRL and SHIFT and click the last image in the range.

⇨ Selected images in a series are marked:

-  One image selected
-  Multiple images selected

Saving images

1. In the viewing area, select the images that you want to save.

2. Click **Save Selected Images As** in the Common tools panel to display the **Save Selected Images As** dialog box.
3. If desired, change the description in the **Description** box.
4. To save the images as a new series in original DICOM format, select **Original (DICOM)** in the **Format** box.
5. To save the images as a set of snapshots in a new series, select **Secondary Capture (DICOM)** in the **Format** box.
6. To save the images as compressed image files (that can be opened on a standard computer), select **JPEG** in the **Format** box.

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7. To save the images as standard image files (that can be opened on a standard computer, not compressed), select **BMP** or **TIFF** in the **Format** box.
8. To save the images as a movie in AVI format, select **Movie** in the **Format** box.
9. When saving images as a movie you can also adjust the quality of the saved movie; drag the **Quality** slider between **Low** or **High**. The higher the quality, the larger the size of the saved movie file.
10. To de-identify the images, select **De-identify** (this function removes patient information before saving the images).
11. Select the location where you want to save the images in the **Destination** box.
12. Click **OK**.

Saving the display

1. Arrange the viewing area to display the views and information that you want to capture.

2. Click **Save Display As** in the Common tools panel to display the **Save Display As** dialog box.
3. If desired, change the description in the **Description** box.
4. To save the display as a snapshot, select **Secondary Capture** in the **Format** box.

⇨ When you save the display in this format, it is saved as a new series with the study.

5. To save the display as a compressed image file (that can be opened on a standard computer), select **JPEG** in the **Format** box.
6. To save the images as standard image files (that can be opened on a standard computer, not compressed), select **BMP** or **TIFF** in the **Format** box.
7. To de-identify the image, select **De-identify** (this function removes patient information before saving the image).
8. Select the location where you want to save the image in the **Destination** box.
9. Click **OK**.

Copying images to film

1. In the viewing area, select the images that you want to copy to film.

2. Click **Film Selected Images** in the Common tools panel.

⇨ The selected images are sent to the Film application.

Copying the display to film

1. Arrange the viewing area to display the views and information that you want to send to film as an image.

2. Click **Film Display** in the Common tools panel.

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⇨ A copy of the viewing area is sent to the Film application.

Copying series to film

1. In the **Series** panel, select the series that you want to copy to film.
2. Click **Film Selected Series** in the Common tools panel.

⇨ The selected series are sent to the Film application.

Filming Multi-Dimension MR Series

You can send multi-dimension MR series to film and define several properties such as order and range of images.

1. In the **Series** panel, select the multiphase dynamic MR series that you want to send to film.
2. Click **Film Selected Series** in the Common tools panel.

⇨ The **Film Selected Series** dialog box is displayed, providing options for configuring the series before sending it to film.

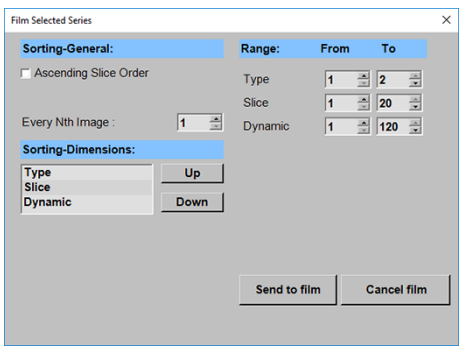

Fig. 37: Film Selected Series dialog box

3. To send the images to film in ascending order, select **Ascending Slice Order**. (The default order is descending slice order.)
4. To send a subset of images to film from the selected range and order, enter a number in the **Every Nth Image** box. (The default setting of **1** sends all images to film.)
5. Set the sort order of dimensions in the **Sorting-Dimensions** list using the **Up** and **Down** buttons.
6. For each dimension, set the **Range** of images using the **From** and **To** boxes.
7. Click **Send to film** when all options are configured as desired.

⇨ The selected series are sent to the Film application. You can preview the images in the Film application and make further adjustments, if desired.

Sending images and results to the Report application

At any point during your workflow with MultiModality Viewer, you can send images and ROI information to the Report application.

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You can send the following items to the Report application:

- A single image or a selection of images.
- The current display layout (viewing area).
- The results of an analysis package (for example, graphs or results summary tables) displayed in MultiModality Viewer.

The reporting tools in MultiModality Viewer are located in the Common tools panel. You may need to click the down arrow next to the tool to select a reporting option.

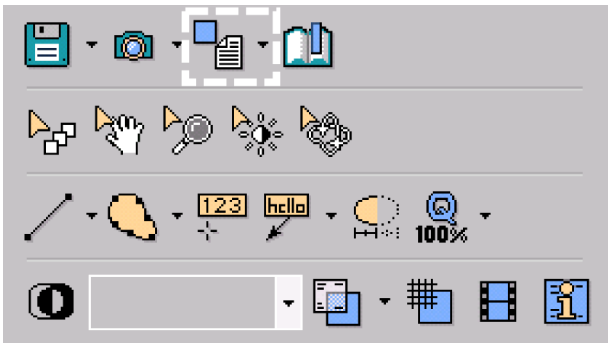

Fig. 38: Reporting tools in the Common tools panel

1. To send images to the Report application, do the following:
   - Select the images that you want to send by pressing CTRL and clicking the images. Selected images are displayed with a blue marker when they are selected.
   - In the Common tools panel, click **Send Selected Images to Report**  .

⇨ The images are saved with the study in the **Report Images** series. They are also available in the **Summary Images** panel in the Report application.

2. To send the current layout of the viewing area to the Report application, do the following:
   - Arrange the viewing area to display the views and information that you want to capture.
   - In the Common tools panel, click **Send Display to Report**  .

⇨ An image of the viewing area is available in the **Summary Images** panel in the Report application.

3. To send ROI information to the Report application, click **Send Results to Report**  in the Common tools panel.

⇨ The ROI Measurements panel is opened, and a copy is sent to the Report application. The ROI measurements table is available as an image in the **Summary Images** panel in the Report application.

Creating and saving batches

You can create a batch of images from a volume using the **Batch** panel settings in the Task panel. You can create the following types of batch:

Parallel

Creates a set of parallel slabs, in the current orientation of the slab displayed in the main image.

Radial (around the horizontal axis)

Creates a batch that rotates around the horizontal axes, around the position and orientation of the slab or volume currently in the main image.

Radial (around the vertical axis)

Creates a batch that rotates around the vertical axes, around the position and orientation of the slab or volume currently in the main image.

Freestyle

Creates a batch that around user-defined keyframes in the volume in the main image.

NOTICE

Newly created batches are not automatically displayed in the Series panel.

To view a newly created batch, you should close MultiModality Viewer, select the corresponding study in the Directory, and then open MultiModality Viewer again.

Creating a parallel batch

1. Select a slab or volume in the viewing area, click the task selector in the Task panel, and then click **Batch** to display the **Batch** panel.

2. Click **Parallel**.

3. Navigate to the start point in the view and click **Start**.

4. Navigate to the end point in the view and click **End**.
5. If desired, modify the batch properties:
   - **Nr Images**: Number of images to be generated.
   - **Increment**: The incremental step size in terms of the distance between the centers of the slabs. Initially this is equal to the current slab thickness of the image in the viewport.
   - **Thickness**: The slab thickness of the images to be generated. This is always equal to the current slab thickness of the image in the view. This helps in previewing the quality of the final result.

⇨ The effect of the selected range is visible by means of reference lines in the reference images indicating the positions of the images that are to be generated.

⇨ The number of images and the incremental step size are linked; for example, increasing the number of images decreases the incremental step size, keeping the distance between the center of the first slab and the last slab constant.

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6. To preview the batch, do one of the following:
   -  Click **Play/Stop** to preview the batch automatically.
   -  Click **Batch scroll interactor** to scroll through the batch manually.
   - **Clear batch** is used for resetting the parameters for all kinds of batches, including parallel, radial and freestyle.

Creating a radial batch

▷ When creating a radial batch, the current position and orientation of the main image is defined as the center of the batch to be generated.

1. Select a slab or volume in the viewing area, click the task selector in the Task panel, and then click **Batch** to display the **Batch** panel.
2. Select a radial batch option:
   -  **Radial** (around the horizontal axis)
   -  **Radial** (around the vertical axis)
3. If desired, modify the batch properties:
   - **Degrees**: Number of degrees for the total rotation.
   - **Nr Images**: Number of images to be generated.
   - **Increment**: The incremental step size in terms of the distance between the centers of the slabs. Initially this is equal to the current slab thickness of the image in the viewport.
   - **Thickness**: The slab thickness of the images to be generated. This is always equal to the current slab thickness of the image in the view. This helps in previewing the quality of the final result.

⇨ The batch is created around the current position and orientation of the image in the view; this image becomes the middle image in the batch that is created.

⇨ The effect of the selected range is visible by means of reference lines in the reference images indicating the positions of the images that are to be generated.

⇨ The number of images and increment are dependent upon each other: increasing the number of images decreases the angle increment, and vice versa, keeping the total angle between the first slab and the last slab constant, as far as possible.

4. To preview the batch, do one of the following:
   -  Click **Play/Stop** to preview the batch automatically.
   -  Click **Batch scroll interactor** to scroll through the batch manually.

Creating a freestyle batch

1. Select a slab or volume in the viewing area, click the task selector in the Task panel, and then click **Batch** to display the **Batch** panel.

2. Click **Freestyle**.

3. Navigate to the start point in the view and click **Add Keyframe**.

4. Manipulate the view to display the next point that you want to capture in the batch and click **Add Keyframe** again.

5. Optional step: To remove the last keyframe that you added, click **Remove last Keyframe**.
6. Continue to add keyframes as desired.

7. To remove all keyframes and start over, click **Remove all Keyframes**.

NOTICE

When creating a freestyle batch, reference lines of batch image positions are not displayed.

8. To preview the batch, do one of the following:
   -  Click **Play/Stop** to preview the batch automatically.
   -  Click **Batch scroll interactor** to scroll through the batch manually.
9. To adjust the speed of the move, drag the slider between **Slow** and **Fast**.
10. Enter a number in the **Playing time** box (measured in seconds) to set the duration of the movie.
11. Choose between setting a number of frames per second, or setting a total number of frames for the movie.

NOTICE

The speed and duration of the movie, and the number of images used are linked, and as you change one parameter, the other parameters are adjusted to achieve the requested result. Select one parameter that you wish to define and allow MultiModality Viewer to configure the other parameters.

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Saving a batch

1. To save the batch, click **Save Batch As** in the Common tools panel.

⇨ The **Save Batch As** dialog box is displayed.

2. If desired, change the batch description in the **Description** box.
3. To save the batch in original DICOM format, select **Derived Image** in the **Format** box.

⇨ When you save the batch in this format, the batch is saved as a new series with the study.

4. To save the batch as a movie (that can be played on a standard computer), select **AVI** in the **Format** box.
5. When saving the batch in AVI format, the following settings are also available:
   - **Quality**: drag the slider between **Low** or **High**. The higher the quality, the larger the size of the saved movie file.
   - **De-identify**: select this check box to de-identify the movie file (this function removes patient information before saving the movie).
6. Select the location where you want to save the batch in the **Destination** box.
7. Click **OK**.

⇨ The batch is automatically previewed once in the main display area before it is saved.

Bookmarks

A bookmark is a view on a set of data, including ROIs, VOIs, other measurements, and annotations, that can be recalled and opened in the original application.

Bookmarks can be created by, for example, Radiologists or Technologists, and then sent to a report or to a Physician for reference at a later stage.

NOTICE

Bookmarks cannot be created when viewing solely Ultrasound images. However, when viewing Ultrasound images with another study from a different modality, bookmarks can be created.

Saving a bookmark

1. Arrange the dataset in the way that you want to present it in the bookmark.

NOTICE

Before saving a bookmark, you should save any key images that you have created.

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2. In the Common tools panel, click **Save Bookmark**.

⇨ The **Save Bookmark** dialog box is displayed.

⇨ For a simple workflow, the **Name** and **Bookmark** boxes of the **Save Bookmark** dialog box are already filled in with default values.

3. If desired, enter new values for the name and description of the bookmark in the **Name** and **Bookmark** boxes.

⇨ The **Name** box is intended as a session name, and will be applied to subsequent bookmarks that you save during the same session (before closing MultiModality Viewer).

4. To copy a link to the bookmark while saving it, select **Copy Bookmark Link to Clipboard**.

⇨ The copied link is a URL link that will open a browser page when pasted into the address bar of a browser application. The browser page provides a link to open the bookmark using IntelliSpace Portal. You can also paste the link into any application that recognizes URLs: clicking the link opens the browser page.

5. To prevent the **Save Bookmark** dialog box from being displayed the next time that you save a bookmark during the same session, select **Do not show this dialog box again**.

⇨ Bookmarks are saved automatically using the configured application name and an incremental bookmark description (for example, "Bookmark1", "Bookmark2").

⇨ The next time that you open MultiModality Viewer, this setting is reset and the dialog box is displayed again when you save a bookmark.

6. To save the bookmark, click **Save Bookmark**.

⇨ The bookmark is saved with the series and is available from the **Bookmarks** panel.

7. To save the bookmark and email the bookmark link at the same time, click **Send Bookmark**.

⇨ The bookmark is saved and your configured email editor opens an email message containing a link to the bookmark.

NOTICE

You can send bookmark links using email at any time using the shortcut menu in the **Bookmarks** panel.

Opening a bookmark

Bookmarks can be opened in a number of ways:

- Select a study in the Directory and open a bookmark from the **Bookmarks** panel.
- Select the **Bookmarks** task panel in MultiModality Viewer (or another viewing / analysis application) and open a bookmark.
- Click a link to a bookmark, for example, received in a email message. The link opens a browser page that allows you to launch IntelliSpace Portal and display the bookmark.

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Opening a bookmark launches the application in which the bookmark was saved, opens the series, and displays contours, ROIs, VOIs, or other measurements available when the bookmark was saved, allowing you to resume a workflow immediately from a specific point.

For details of opening a bookmark from the Directory, please refer to the section describing the Directory in the Instructions for Use included with your IntelliSpace Portal system.

1. To open a bookmark in MultiModality Viewer, click the task selector in the Task panel and then click **Bookmarks**.

⇨ The **Bookmarks** panel is displayed.

⇨ To view details of a bookmark in a tooltip, pause the pointer over the bookmark.

2. Choose the bookmark that you want to open and do one of the following:
   - Double-click the bookmark
   - Right-click the bookmark and select **Open Bookmark**  .

⇨ Series that are currently open are closed and the data set that the bookmark represents is loaded.

NOTICE

After opening a bookmark, changes that you make are not saved automatically with the original bookmark. To save these changes, save a new bookmark.

Further actions with bookmarks in MultiModality Viewer

1. To copy a link to a bookmark, right-click the bookmark in the **Bookmarks** panel and click **Copy to Clipboard**.

2. To send a link to a bookmark in an email message, right-click the bookmark in the **Bookmarks** panel and click **Email Link**.

NOTICE

A bookmark can be deleted only in the Bookmarks panel in the Directory.

Key Images

You can save key images at relevant points during your workflow. Key images can be saved with a description as key image notes for use when reporting or documenting a study.

Creating Key Images

1. To create a key image of the currently selected viewport, do one of the following:

- Press Space.
- Right-click the viewport and click **Capture Viewer**.

2. To create a key image of the whole display, do one of the following:
   - Press Shift+Space.
   - Right-click a viewport and click **Capture Viewing Area**.

Managing Key Images

1. To view key images that you have created for the current study, click the task selector in the Task panel and then click **Key Images**.

2. To store all current key images, right-click a key image and click **Store all key images**.

⇨ The **Save Key Image Notes** dialog box is displayed.

3. Enter notes for the key images, define a context, and select a storage location, and then click **OK**.

NOTICE

Key image are not saved automatically. If you close the study without saving key images, they will be lost.

4. To clear the Key Images panel, right-click a key image and click **Remove all key images**.

Saving to Surgical Nav. Format for MR Data

You can save 3D anatomical volumes from MultiModality Viewer in surgical nav. format for export to surgery systems for review, preparation, and navigation during surgical interventions.

The following MR data types can be saved to surgical nav. format:

- Routine MR anatomical data (DICOM data)
- fMRI results (activation areas) as generated by the iViewBOLD package in IntelliSpace Portal
- White matter tracts (also called "fibers") as generated by the Diffusion Package in IntelliSpace Portal
- Segmented tumor

NOTICE

MR data that is combined with CT or PET data cannot be saved to surgical nav. format.

1. Select the data that you want to save to surgical nav. format.

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⇨ If a user-defined batch is not available, a parallel batch covering the entire volume is automatically generated. The geometry parameters are preserved: the number of slices, the slice thickness, and the orientation of the batch are the same as the anatomical data.

⇨ Alternatively, you can create a batch and define the parameters according to your needs. However, if you perform a bounding box or cut operation, this operation is not saved.

2. Click to **Save to Surgical Nav. Format** in the Common tools panel to display the **Save to Surgical Nav. Format** dialog box.
3. Enter a **Description** for the saved data, if desired (to a maximum of 64 characters).

⇨ A description is provided by default based on the type of data being saved.

4. Select the Options to apply to the saved data:
   - **Combine Data**: Results are combined (for example, underlay, overlay, maps, and fibers). This option is useful if the surgery system that you are exporting to does not support fusion. (Fused images can be saved if they meet the export requirements, for example: an MR series overlaid with another MR series.)
     - **Apply Transparency**: Selecting this option saves fibers, tumor segmentations, and fMRI activation areas with transparency, so that they can be used as overlays on corresponding (co-registered) anatomical images on the surgery system. If this option is not selected, overlay data is opaque.
   - **Separate Data**: Results are saved as separate series. Gray values for fMRI are preserved (but they are converted to standard MR data). For fibers and segmentations, the maximum grey value is used. This option is useful if the surgery system that you are exporting to supports fusion. Each object is stored with a different gray value, which maps to a specific color during fusion. Additionally, positive and negative activation (if available) in the SPM map are saved as separate objects, so that they can be easily distinguished on the surgery system.

⇨ The saved data can be exported to the following surgery systems:

- Stealth Navigation (Medtronic)
- iNtellect Cranial (Stryker)
- VectorVision (BrainLAB)

Glossary

Definitions

Definition	Explanation
1D All	A display sorting mode which displays all images of the series in one linear sequence.
1D Stacked	A display sorting mode available for multi-dimensional series, where one dimension is displayed in the viewports of the view (the “running dimension”), whereas the other dimensions are stacked behind each of the displayed images.
3D	A display mode, allowing three dimensional display and interactions, like rolling (swivelling) and clipping. Within a 3D view the shape of the volume can be a full volume, a slab or a thin intersection (slice).
3D-CA	Allura 3D-CA is an external software application that allows cardiologists to create a 3D view of the coronary arteries. The software constructs a 3D surface model of a coronary segment from two 2D projection images. These images are taken from the same phase within the cardiac cycle and have a difference in view angle of at least 30 degrees. Surface models and snapshots created using Allura 3D-CA can be viewed in MultiModality Viewer.
3D-RA	Allura 3D-RA is an external software application that enables the clinical user to visualize a 3D view of vessel or bone anatomy. A high-performance workstation is used to reconstruct a 3D volume from a rotational angio run created by the X-ray modality, and to visualize the vessels in the 3D data set. Volumes and snapshots created using Allura 3D-RA can be viewed in MultiModality Viewer.
AIP	Average Intensity Projection: See Projection. The average voxel value encountered along each ray is displayed on the projection plane (plane of the monitor).
Arrangement	Term used for the layout of views in the viewing area. This can be a regular arrangement or a custom arrangement with arbitrarily sized views. See also view and layout.
Bookmark	While using a viewer or another application, you can save a bookmark at any time to save the current status of your work. For example, you can save a bookmark at an intermediate point before trying a different procedure, and then return to the saved point later. Or you can save a bookmark and close the current work session, and then return at a later time to continue where you left off.

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Definition	Explanation
Clinical application	A special kind of comprehensive application that is focused on a specific clinical end-result, like a conclusion to the clinical question for which this exam was performed. Such an application in general consists of several steps in which certain tools play a role, for instance to define the image rendering, or to produce an additional image series, or to perform an analysis leading to measurement data, graphs, findings, etc.
Co-registration	This term applies to any method for aligning images with the purpose of, for example, correcting for motion. Co-registration usually refers to the alignment of images from different modalities or from modalities with different characteristics. For example, an MRI low resolution T2* fMRI scan (EPI image) may be co-registered with a high resolution T1 structural image from the same individual.
CPR	Curved Planar reformatting. A technique similar to MPR to visualize structures that cannot be displayed in a flat cross section plane.
Layout	Term reserved for the internal layout of a view. This can be a regular layout for images in a 2D view, or a layout with a source image and reference images in a volume viewer. To avoid confusion the term used for the layout of views in the viewing area is arrangement.
Matrix	A display sorting mode, which sorts the multi-dimensional image set over rows and columns.
MinIP	Minimum Intensity Projection: see Projection. The minimum voxel value encountered along each ray is displayed on the projection plane (plane of the monitor). MinIP is commonly used to inspect objects of lowest density, such as air-filled structures.
MIP	Maximum Intensity Projection: see Projection. The maximum voxel value encountered along each ray is displayed on the projection plane (plane of the monitor). MIP is commonly used for vascular studies and 3D rotational angiography.
MPR	Multi-planar reformatting is a post-processing technique, which produces new slices from a stack of images. The original images are stacked one on top of the other. MPR then produces a reconstructed cross section plane of the anatomy in any desired orientation.
Original	The DICOM format for images and series, as acquired by a modality and stored in an image database or DICOM folder.
Projection	Projection is a post-processing technique, which uses raycasting. The original images are stacked one on top of the other. Virtual rays are directed from the viewpoint through the volume of stacked images, detecting certain voxel values (depending on the projection method: MIP, MinIP, AIP, VIP, and so on).
Render mode	A specific method to project a volume on a screen or film. In the Viewing environment, we distinguish the following render modes: MPR, MIP and MinIP.

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Definition	Explanation
Review mode	An image series can be reviewed in several alternative review modes, which show the same image set in different ways. Currently the review modes are “2D” (viewing the original slices), slab (thicker slice in any orientation with variable position and thickness), volume (the total stack of slices seen as a whole volume or projection), and endo (viewing the volume from the inside).
Running dimension	In 1D Stacked display sorting mode this is the sorting attribute that is different for the displayed images in the view. For example if the running attribute is ‘slices’ the viewports are filled with the slices of a certain single echo, phase, and so on, and these slices are displayed in linear order, from left to right and wrapped over the available viewport rows.
Secondary Capture	A snapshot of the image as displayed at the moment of capture, including all graphics, text (labels) image info (burned in).
Slab	When an MPR slice is widened, it becomes a slab. The result is then identical to an average intensity projection (AIP). But a slab can also be rendered as a volume or as a MIP/MinIP, etc.
Tool	A single function or set of functions and means to obtain one result. This can be measurement tools, or tools that create a 3D rendering, or tools for segmentation, for example.
View	Component in a viewer or in an application for viewing a specific image set, with its necessary tools. A viewer or application can have one or more views (to compare image sets).
Viewer	An application for viewing images, or reports. Examples are CT Viewer, CT Cardiac Viewer, MultiModality Viewer, DICOM viewer.
VIP	Volumetric Intensity Projection, also known as MIP-Fade, a technique in which the image data is multiplied by a “ramp” before MIP is calculated. The result is a MIP image in which anatomies closer to the eye have a “priority” and will be seen brighter.
Volume	The scanned set of slices seen as a whole volume, using various different rendering techniques and projections, like MIP.
XperCT	XperCT is an external software application that extends the functionality of X-ray equipment with soft tissue imaging. XperCT volumes are viewed as a slab, displaying soft tissue with very high image quality, approaching the image quality of CT scans. An XperCT volume can also be viewed as an overlay on a matching 3D contrast volume. Volumes and snapshots created using XperCT can be viewed in MultiModality Viewer.

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Abbreviations

Abbreviation	Explanation
3D-CA	3-Dimensional Coronary Angiography
3D-RA	3-Dimensional Rotational Angiography
CT	Computed Tomography
DICOM	Digital Imaging and Communications in Medicine
DXR	Diagnostic X-ray
IAC	Internal Auditory Canal
MIP	Maximum Intensity Projection
MPR	Multi-planar Reformatting
MR	Magnetic Resonance
NM	Nuclear Medicine
PET	Positron Emission Tomography
P.F.	Posterior Fossa
ROI	Region of Interest
SPECT	Single Photon Emission Computed Tomography
SUV	Standard Uptake Value
VOI	Volume of Interest
XA	X-ray Angiography

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Appendix

Direct Mouse Manipulation

You can switch between the following interaction tools using the Common tools panel. Alternatively, you can use direct mouse manipulation shortcuts to enable a tool using the mouse button combination described here.

Tool		Mouse button
	Scroll	This is the default tool when viewing a 2D view (left mouse button)
	Pan	Direct mouse manipulation shortcut: Left + Middle

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Tool		Mouse button
	Zoom	• This is the default tool when viewing a single 2D image (left mouse button) • Direct mouse manipulation shortcut: Right + Middle
	Roll / Rotate	• This is the default tool when viewing a 3D view (left mouse button) • Direct mouse manipulation shortcut: Left + Right
	Windowing	• Direct mouse manipulation shortcut: Middle • If the image is a PET or SPECT image, then the upper level / lower level windowing model is used instead of window width and level

When you enable a direct mouse manipulation shortcut, it is active for the duration that you press the mouse buttons.

When you switch between these interaction tools explicitly using the Common tools panel, the interaction mode is changed for all views that support that interaction. The interaction mode does not change for other views. The active interaction mode for any view is indicated by the pointer when it is moved over a view.

Shortcut menus

Series panel shortcut menu

Item	
	**Open / Replace** Opens a new view in an empty tile or replaces the active view.
	**Add As Tabbed View** Opens the selected series in a new tabbed view in the tile of the current active view.
	**Add 2D Slice View** Opens or adds the series as a 2D slice view. If the corresponding series is already displayed in any review mode, then add as a tab in the same container, or else in an empty tile (if available), or else as a tab in the current tab container.
	**Add Thin Slab / MPR View** Open/add as a slab. If the corresponding series is already displayed in any review mode, then add as a tab in the same container, or else in an empty tile (if any), or else as a tab in the current tab container.

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Item	
	**Add Volume / MIP View** Open/add as an entire volume MIP. If the corresponding series is already displayed in any review mode, then add as a tab in the same container, or else in an empty tile (if any), or else as a tab in the current tab container.
	**Add 3D / Ortho View** (MR viewing only) Open/add as a 3D view composed of three perpendicular planes. If the corresponding series is already displayed in any review mode, then add as a tab in the same container, or else in an empty tile (if available), or else as a tab in the current tab container
	**Layout protocols** (Fusion viewing only) Opens the Protocol Selection panel so that you select a layout protocol and add the selected series as a multi-series view. It is not necessary to indicate a floating series or reference series; the configuration of the view is determined according to typical fusion viewing settings for the selected series. For example, if NM and CT series are present, the NM series is defined as the floating series.
	**Add As Reference Series (underlay)** (Fusion viewing only) This is option is available if the floating series / reference series configuration cannot be determined automatically. Creates a fused view in the active view, or replaces the reference series if it is already open. The default layout protocol related to the new combination of fused series is applied. You can change the layout protocol using the Protocol Selection panel.
	**Add As Floating Series (overlay)** (Fusion viewing only) This is option is available if the floating series / reference series configuration cannot be determined automatically. Creates a fused view in the active view, or replaces the floating series if it is already open. The default layout protocol related to the new combination of fused series is applied. You can change the layout protocol using the Protocol Selection panel.
	**MobiView MPR** (Option for multistation MR data only) If the MobiView option is installed, this option creates a MobiView slab as a new view, or as a tabbed view if the series is already open.
	**MobiView MIP** (Option for multistation MR data only) If the MobiView option is installed, this option creates a MobiView volume as a new view, or as a tabbed view if the series is already open.
	**Analysis Application** Available applications are displayed in a submenu, depending on your installation.

Image shortcut menu

Item (with keyboard shortcut and submenu, if available)	
	**Scroll** For 3D viewing, you can also use this tool to change the slab thickness
	**Pan**
	**Zoom**
	**Roll/Rotate** 3D viewing only
	**Gray Level**
	**Alpha Blend** Fusion viewing only
	**Add 2D Slice View** Adds a new tabbed view in the tab container
	**Add Thin Slab / MPR View** Adds a new tabbed view in the tab container
	**Add Volume / MIP View** Adds a new tabbed view in the tab container
	**Add 3D / Ortho View** (MR viewing only) Adds a new tabbed view in the tab container
	**MobiView MPR** (Option for multistation MR data only) If the MobiView option is installed, this option creates a MobiView slab as a new view, or as a tabbed view if the series is already open
	**MobiView MIP** (Option for multistation MR data only) If the MobiView option is installed, this option creates a MobiView volume as a new view, or as a tabbed view if the series is already open
	**Fusion** Turns Fusion on or off
	**Select Underlay**
	**Axial Feet** A

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Item (with keyboard shortcut and submenu, if available)				
	**Coronal Front**	C		
	**Sagittal Left**	S		
	**Play** 2D viewing only	PAUSE		
	**Layout** For 2D views			Layout 1 x 1
				Layout 1 x 2
				Layout 2 x 1
				Layout 2 x 2
				Layout 3 x 3
				Layout 4 x 4
				Layout 2 + 1 + 1
				Layout 1 + 1 + 1 + 2
				Add row CTRL +DOWN
				Remove row CTRL +UP
				Add column CTRL +RIGHT
				Remove column CTRL +LEFT
				Automatic
	**Layout** For 3D views			References at Right

Item (with keyboard shortcut and submenu, if available)		
		 References at Bottom
		 1x1 No reference images
		 1x2 Main with original
		 2x2 Main with 3 references
	Apply Window To You can use this menu item to control how windowing is propagated to dimensions	All Echoes All Slices
	**Fit To View**	
	**Remove Graphics**	
	**Select Color Map** MR (original images), PET, or NM series only For MR series, this function is also available for derived images that contain windowing and quantitative information.	Available color maps are displayed in a submenu
	**Color Scale** PET or NM series only	
	**Save Image Viewing Settings**	CTRL+S
	**Reset All**	CTRL+R
	**Align Other Views**	Aligns other views to the selected view (source view)
	Center Rotation Point 3D viewing only, right-click the rotation point to display this shortcut option	
	Reset Rotation Point 3D viewing only, right-click the rotation point to display this shortcut option	

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Item (with keyboard shortcut and submenu, if available)	
	**Create SUV ROI** Creates a volume measurement at the mouse pointer position using the SUV Threshold method
	**Create Percent of Max ROI** Creates a volume measurement at the mouse pointer position using the Percentage of Maximum Value method
	Hide/Show Bitmap Overlays Hides or shows graphics overlays that have been created on a different system
	Align View To Grid (Spectroscopy)
	Show Quality Indicator (Spectroscopy) Right-click the grid to display this shortcut option
	Show Mini Spectra (Spectroscopy) Right-click the grid to display this shortcut option
	Swap Main and Chart (Spectroscopy) Swaps the results analysis graph between a reference view and the main viewport, right-click the main viewport or the reference view to display this option
	Show Actual Spectrum (Spectroscopy) Displays the line representing raw data (yellow line)
	Show Fitted Spectrum (Spectroscopy) Displays the smoothed line representing processed data for the selected metabolites (light blue line)
	Show Fixed Baseline (Spectroscopy) Displays the baseline of the fitted spectrum (orange line)

Graphics shortcut menu

Item (with keyboard shortcut, if available)		Description
	**Align View To Measurement**	Rotates the view so that the measurement is parallel with the viewing plane.
	**Text Label**	Hides or shows the text label of the selected measurement.

Item (with keyboard shortcut, if available)			Description
	**Color**		Opens a submenu of standard colors. You can select a color from the standard Windows color picker by selecting **Custom**
	**Properties**		Opens the Graphics and Text Properties panel. You can use this panel to change the appearance of graphics and to change the font settings.
	**Cut**	CTRL+X	Cuts the selected graphics, to be pasted to another image
	**Copy**	CTRL+C	Copies the selected graphics, to be pasted to another image via the image shortcut menu or with Ctrl+V
	**Delete**	DELETE	Deletes the selected graphics
	**Hide Selection**		Hides the selected graphics, to be restored via the show/hide graphics function in the side-panel.
	**Voxel Value** Right-click a point marker to display this shortcut option		Hides or shows the value of the point.
	**3D Location** Right-click a point marker to display this shortcut option		Hides or shows the coordinates of the point using the DICOM patient coordinate system.
	**VOI Measurements** Right-click a volume measurement to display this shortcut option		Hides or shows the volume measurement information of the selected measurement.
	**Remove ROI** Right-click a volume measurement to display this shortcut option		Deletes the selected volume measurement.

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Item (with keyboard shortcut, if available)		Description
	**Longest Diameter** Right-Click an MR segmentation to display this shortcut option	Displays lines representing the longest horizontal and vertical diameters, with measurement values.
	Show Right-Click an object in the Object Manager or the ROI Measurements panel to display this shortcut option	Displays the location of the selected object in the main viewport.

Keyboard Shortcuts

Group	Shortcut	Action
Orientation	A	Axial view (in MIP/MPR)
	C	Coronal view (in MIP/MPR)
	S	Sagittal view (in MIP/MPR)
Annotation	D	Activate the line measurement tool
Save	<Shift>+D	Save Display As ...
	<Shift>+S	Save Selected Image(s) As ...
Viewing Tools	CTRL+I	Image information level
	CTRL+R	Reset to last presentation state
	CTRL+DOWN ARROW	Add row to layout
	CTRL+UP ARROW	Remove last row
	CTRL+RIGHT ARROW	Add column to layout
	CTRL+LEFT ARROW	Remove last column
	DOWN ARROW	Scroll one row down
	UP ARROW	Scroll one row up
	RIGHT ARROW	Scroll one column right / next image
	LEFT ARROW	Scroll one column left / previous image
	CTRL+SHIFT+DOWN ARROW	Scroll down in the third dimension
	CTRL+SHIFT+UP ARROW	Scroll up in the third dimension
	PAGE UP	Page up
	PAGE DOWN	Page down
	CTRL+PAGE UP	Page to the right
	CTRL+PAGE DOWN	Page to the left

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Group	Shortcut	Action
	HOME	Go to the first image
	END	Go to the last image
	CTRL+HOME	Go to the first image in all dimensions
	CTRL+END	Go to the last image in all dimensions
	PAUSE	Pause / resume movie
Standard	CTRL+A	Select all graphics in view (if any)
	CTRL+C	Copy selected graphics
	CTRL+V	Paste copied graphics
	CTRL+X	Cut selected graphic
	DELETE	Delete selected graphic
	CTRL+SHIFT+A	Deselect all graphics and tags in view
Key Image	SPACE	Add the current image as a Key Image
	SHIFT+SPACE	Add the whole display as a Key Image
Windowing	0	Preset window: Colon
	1	Preset window: P.F.
	2	Preset window: Brain
	3	Preset window: IAC
	4	Preset window: Spine
	5	Preset window: Bone
	6	Preset window: Lung
	7	Preset window: Abdomen
	8	Preset window: Liver
	9	Preset window: Cardiac
Film	F	Add selected image(s) to film sheet

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