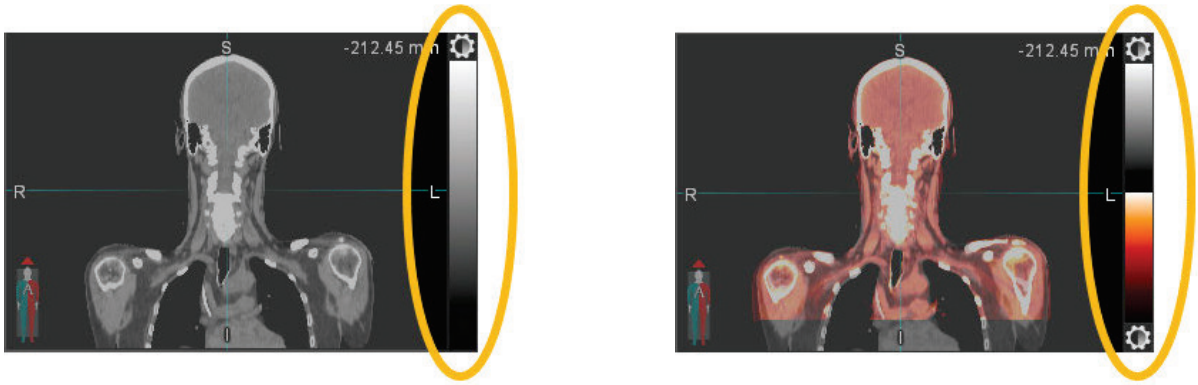
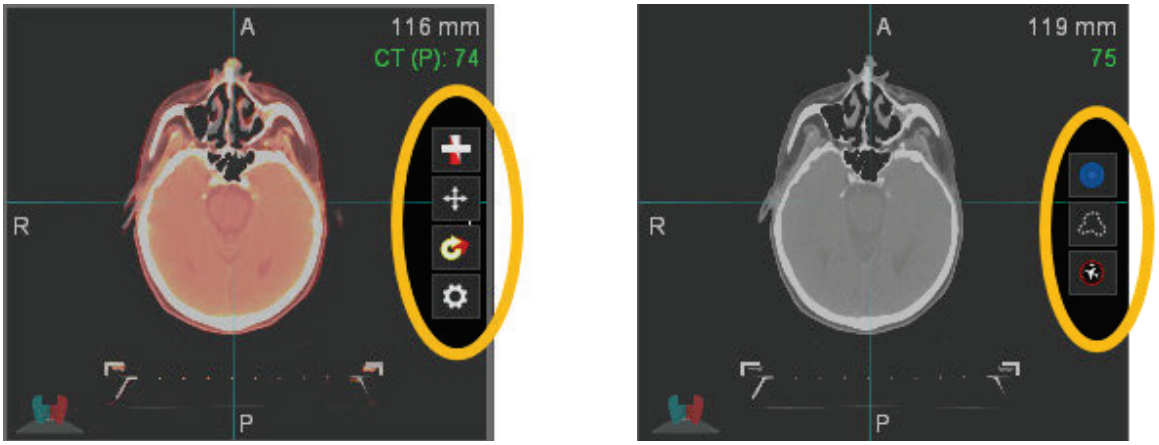
and Adjust Image Contrast.



Contrast and color table bars. The image on the left is for a single series. The image on the right is a fusion. Note that in the right image, there are two separate color and contrast bars—one for the primary image and one for the secondary image.

Tool Menus in Viewports

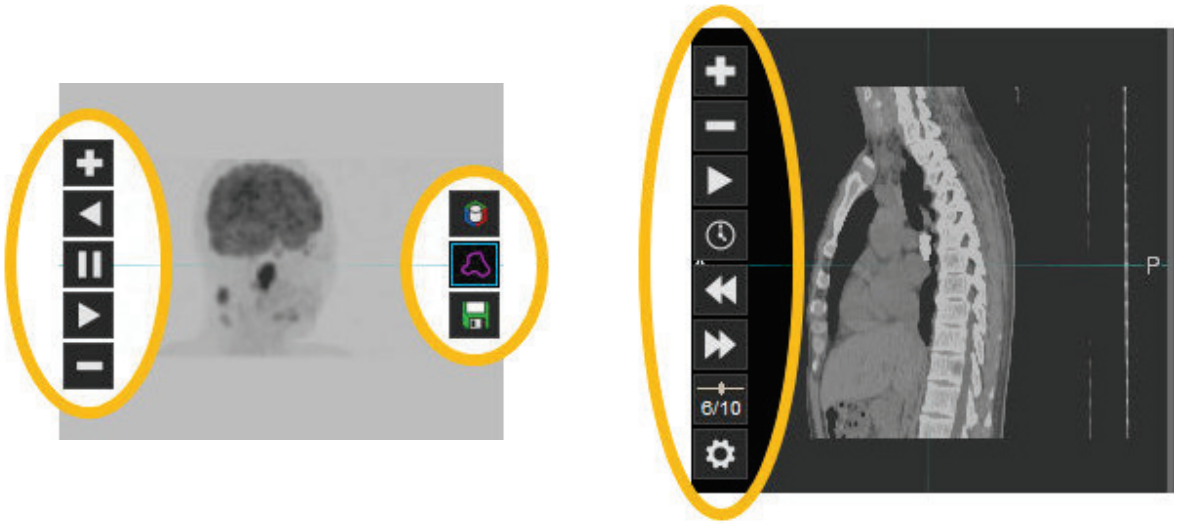
Many MIM tools have a menu of companion tools and options that appear along the right side of the active viewport. Hover over any tool in the menu for a brief description of what it does. Detailed information about specific tool menus is available in the user guide topics pertaining to each tool.



The companion tool menus for the Fusion tool (left) and the 2D Brush tool (right).

Dynamic Series Controls in Viewports

When your display includes a dynamic series, such as a 4D CT or MIP movie, controls for playing these series appear in the viewport.



The playback tool menus for a MIP movie (left image) and a 4D CT (right image).

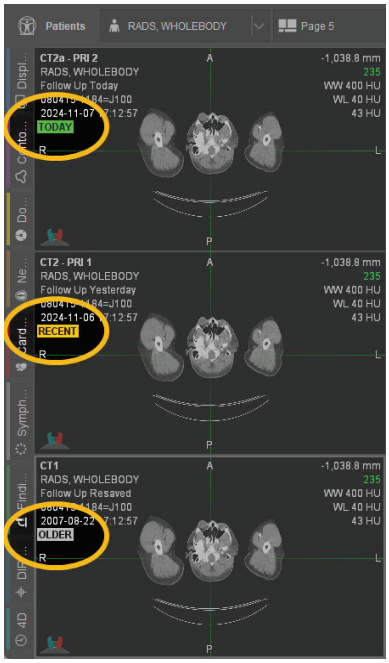
Use Time-Based Badges to Identify Recent Series

MIMTD-2026 • 24 Apr 2025

This feature is available in the following versions: MIM 7.3.8 and later; MIM 7.4.3 and later.
This feature is not available in the following versions: MIM prior to MIM 7.3.8; MIM 7.4.0 to MIM 7.4.2; MIM 7.4.70.

Overview

You can choose to display acquisition time badges below the series information in the viewport. Use these badges to quickly confirm that you are reading the correct series.



There are three different badges:

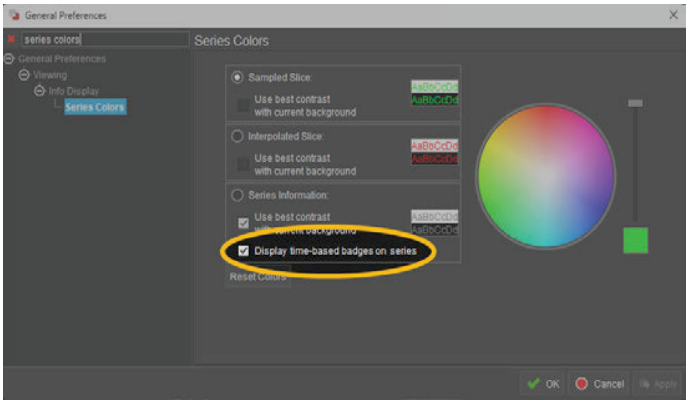
- **Today** — Identifies series acquired today
- **Recent** — Identifies studies that were not acquired today, but were acquired within the past 48 hours
- **Older** — Identifies studies older than 48 hours

Tip: Badges are applied to series based on the values of the Acquisition Date and Acquisition Time DICOM tags. If no values exist for these tags, the Series Date and Series Time tags are used instead.

Important: Badges are only shown when series information is displayed in the viewport. If this information is hidden, the badges are also hidden.

Display Time-Based Badges

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**series colors**". Select **Series Colors** on the left side.
3. In the Series Information section, select **Display time-based badges on series**.
4. Click **OK** to save the preference and close the window.



Localize and Scroll

MIMTD-606 • 25 Jul 2023

Overview

MIM's many settings let you configure localizing and scrolling behaviors to suit your individual preferences.

Contents

Localize

- Click within an image to localize on an area of interest in all planes.
- Left-click drag to gradually move the point of localization.
- Double-click in any plane to maximize the viewport. Double-click again to restore the viewport's original size.
- For information on series view links and disabling localization links between series, see Adjust Links between Series Using the Link Manager.

Change the Appearance of the Crosshairs and Cursor

Use the following default keyboard shortcuts to quickly change the appearance of the crosshairs:

Crosshair Change	Keyboard Shortcut
Change Crosshair Style	=

Change Crosshair Color	Shift+=
Toggle Crosshair Visibility	Ctrl+=

To change the style, color, and other crosshair settings, go to Settings ⚙ >> **General Preferences** and search for "**crosshairs**".

To change the style and color of the cursor, go to Settings ⚙ >> **General Preferences** and search for "**cursors**".

Scroll

To manually scroll through an image slice by slice, use any of the following methods:

- Right-click drag up or down.
- Scroll your mouse wheel up or down, or use two fingers on your trackpad.
- Press the up and down keys on your keyboard.

Tip: If you prefer to scroll through an image by left-click dragging, adjust the mouse behavior via Settings ⚙ >> **General Preferences** and searching for "**mouse behaviors**". See Configure Mouse Behaviors for more information.

Fast Scroll (MIM 7.2 and Later)

If scrolling seems too fast or too slow, you can adjust your fast scroll preference to control whether MIM skips slices when scrolling. Slices will not be skipped when you scroll the mouse wheel at a steady pace, or when you right-click drag.

Follow these steps to enable fast scrolling:

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**fast scroll**".
3. Select **Enable skipping of slices with fast scroll**.

Toggle Fast Scrolling in a Session with a Keyboard Shortcut (MIM 7.2 and Later)

Use a keyboard shortcut command to toggle fast scrolling on and off during a session. This command enables or disables fast scrolling in your current MIM session. The preference toggled in this command does not carry over after session is closed, and it does not change your fast scrolling preference (see Fast Scroll (MIM 7.2 and Later) above).

Follow these steps to assign a keyboard shortcut to toggle fast scrolling:

1. Click the Settings button in the upper-right corner of MIM, and go to **Keyboard Shortcuts...**.
2. Search for "Toggle fast scrolling" in the empty field below the Category dropdown menu.
3. Double-click **Toggle Fast Scrolling (Current Session)** and assign the desired key binding.

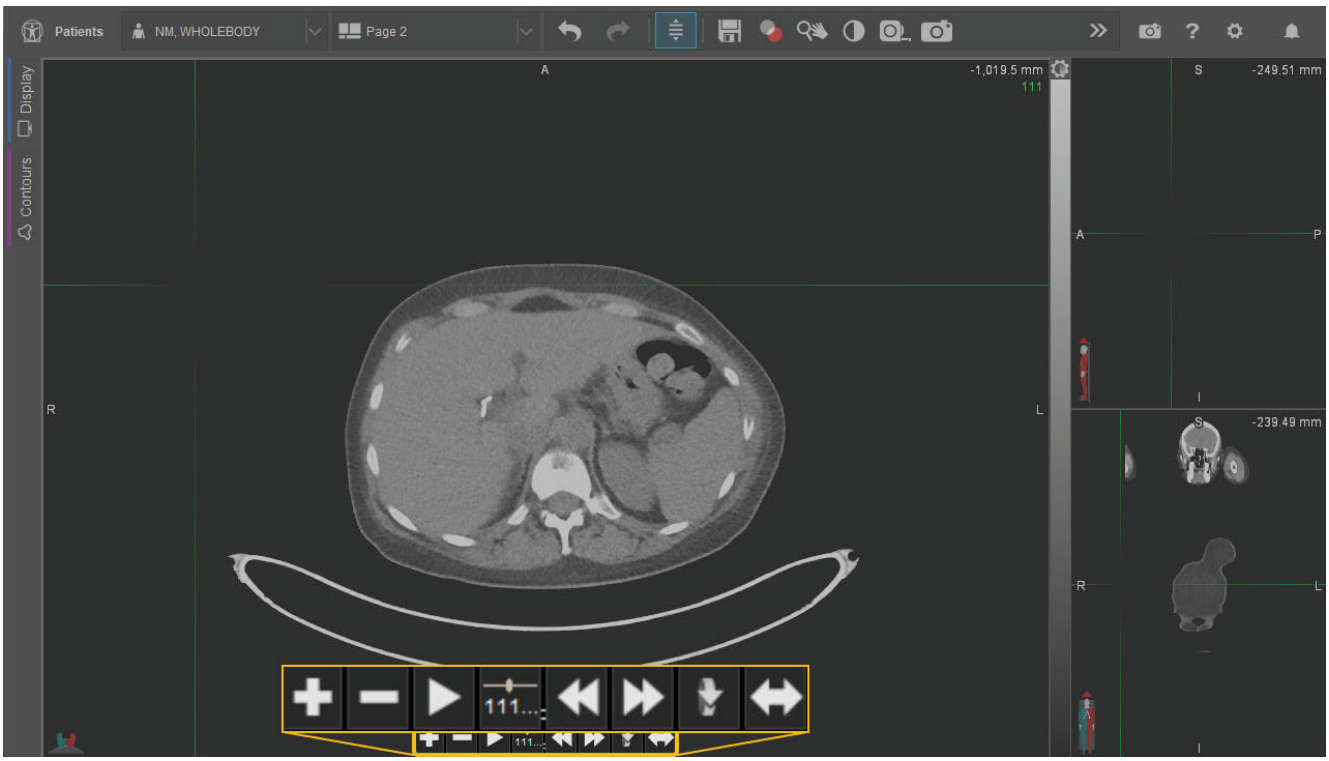
Related: For detailed instructions on using keyboard shortcuts, see Set Keyboard Shortcuts.

Autoscroll (MIM 7.2 and Later)

Use the Autoscroll tool to scroll automatically through an image in any plane. The tool lets you click a button, or press a key, to start playing through the axial, sagittal, or coronal plane slice by slice. Controls are available to adjust the speed, play/pause, step forward, step backward, play from the top, and reverse direction.

Activate Autoscroll

1. Activate the **Autoscroll** tool from the MIM toolbar or radial menu. You may need to click the button at the top of MIM to search for this tool.
2. Hover in any viewport. The autoscroll control buttons appear at the bottom of the viewport.
3. Use the buttons to control autoscrolling. Hover over each button for a short description of the functionality.



Tip: When you move the cursor to a different viewport, autoscrolling pauses.

Use Autoscroll with Keyboard Shortcuts

You can assign keyboard shortcuts for the following commands:

- Activate Autoscroll
- Play or pause Autoscroll
- Reverse direction
- Scroll from the top

Follow these steps to assign Autoscroll keyboard shortcuts:

1. Click the Settings button in the upper-right corner of MIM, and go to **Keyboard Shortcuts...**.
2. Search for "Autoscroll" in the empty field below the Category dropdown menu to see the relevant keyboard shortcuts.
3. Double-click each shortcut name and assign the desired key binding.

Related: For detailed instructions on using keyboard shortcuts, see Set Keyboard Shortcuts.

Autoscroll General Preferences

To adjust autoscroll general preferences, click the Settings button in the upper-right corner of MIM. Go to **General Preferences** >> **Viewing**.

The following preferences can be adjusted:

- **Start Autoscroll from the current localization** — Enable this preference to start autoscrolling from the slice that you are currently localized on. Disable this preference to start autoscrolling from the first slice in the series.
- **Autoscroll Delay (ms)** — Change the length of the delay between each slice. When you click the plus or minus button in the Autoscroll controls, the delay that is set in the general preferences decreases or increases by 50 ms with each click.

Access Tools: The Toolbar and the Radial Menu

MIMTD-1683 • 01 Nov 2023

Overview

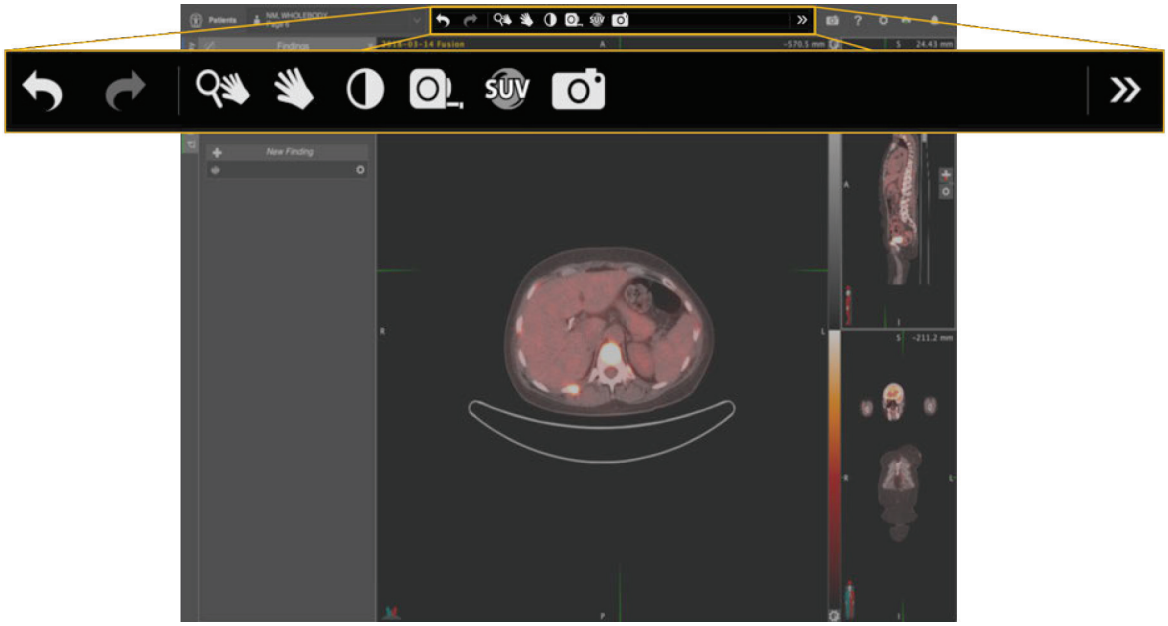
Access frequently used MIM® tools through the toolbar and the radial menu. You can add or remove tools so that your favorites are easy to find.

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

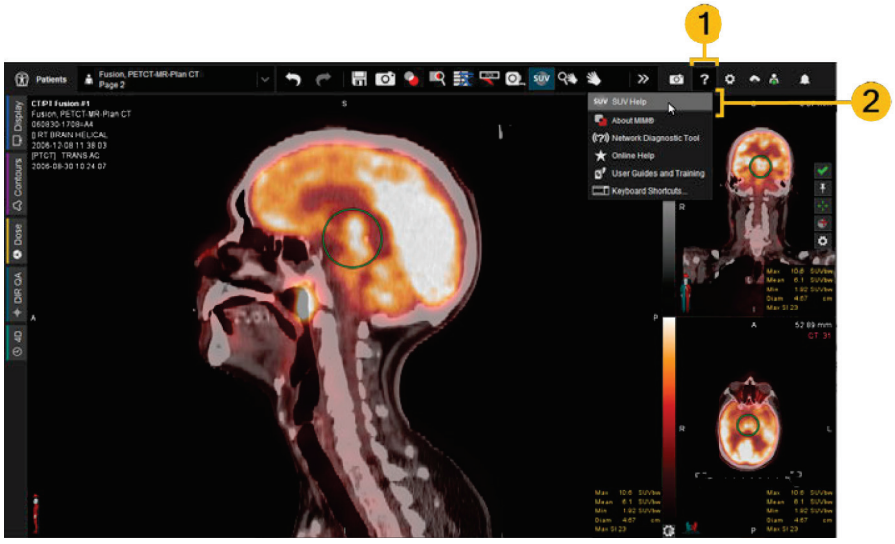
Contents

The Toolbar

The toolbar at the top of MIM contains many of the tools you use to view and process data. The toolbar begins with the Undo and Redo tools and ends with the double arrow button. Use the double arrow button to find tools that aren't currently shown in the toolbar.



- The active tool is highlighted in blue. Click the tool again to deactivate it.
- To view help information for the active tool:
    1. Click the question mark button in the upper-right corner.
    2. Select the first menu item.

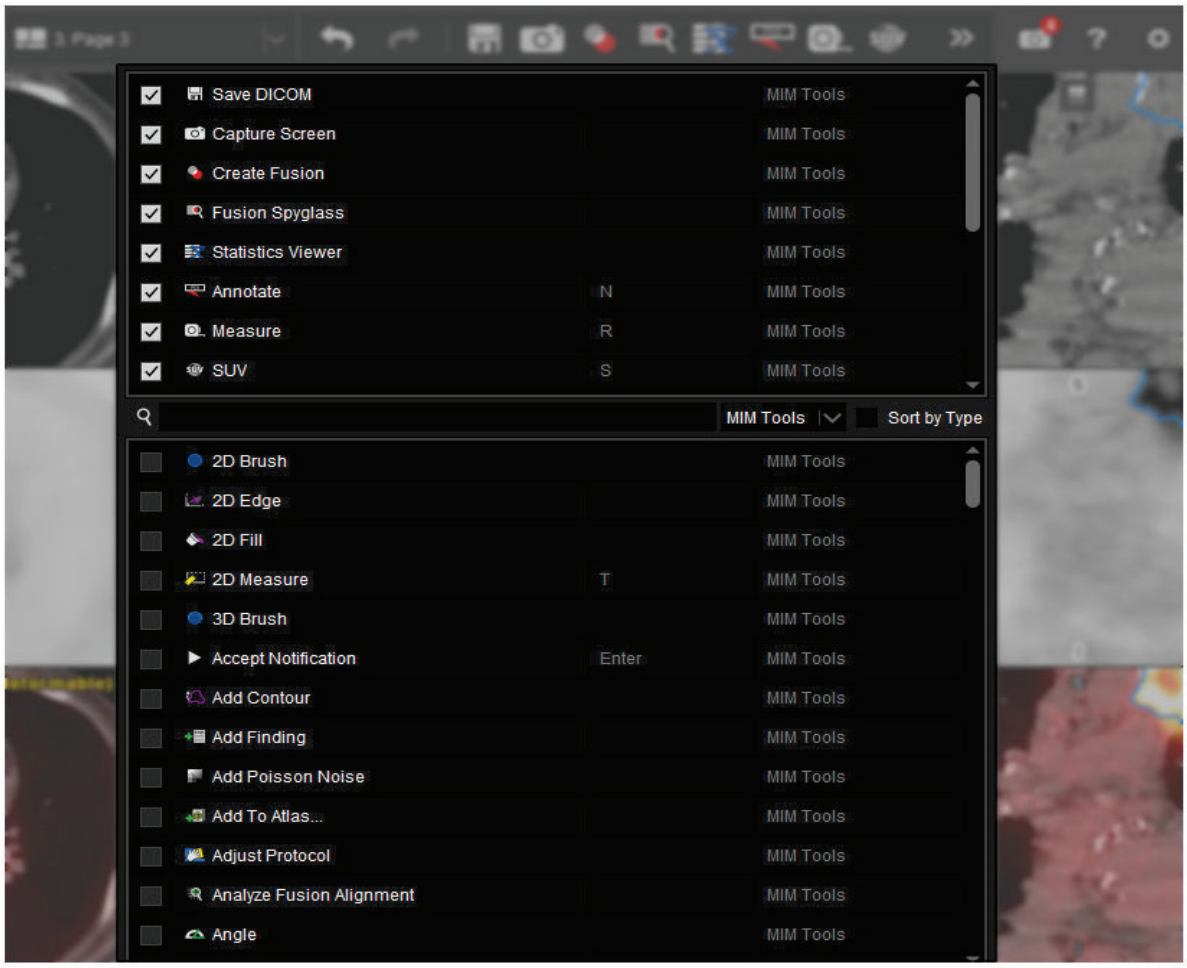


Customize the Toolbar

You can edit the toolbar to add tools you use frequently or remove tools you do not use:

1. Click the double arrow » button on the far right side of the toolbar.
2. Select the **Configure Toolbar** button at the top of the menu.
3. *MIM 7.3 and later:* Select tools in the bottom half of the list to add them to your toolbar. Deselect tools in the top half of the list to remove them from your toolbar.

   MIM 7.2 and earlier: There are no checkboxes. Click tools in the bottom half of the window to add them to the toolbar. Click tools in the top half of the window to remove them from the toolbar.



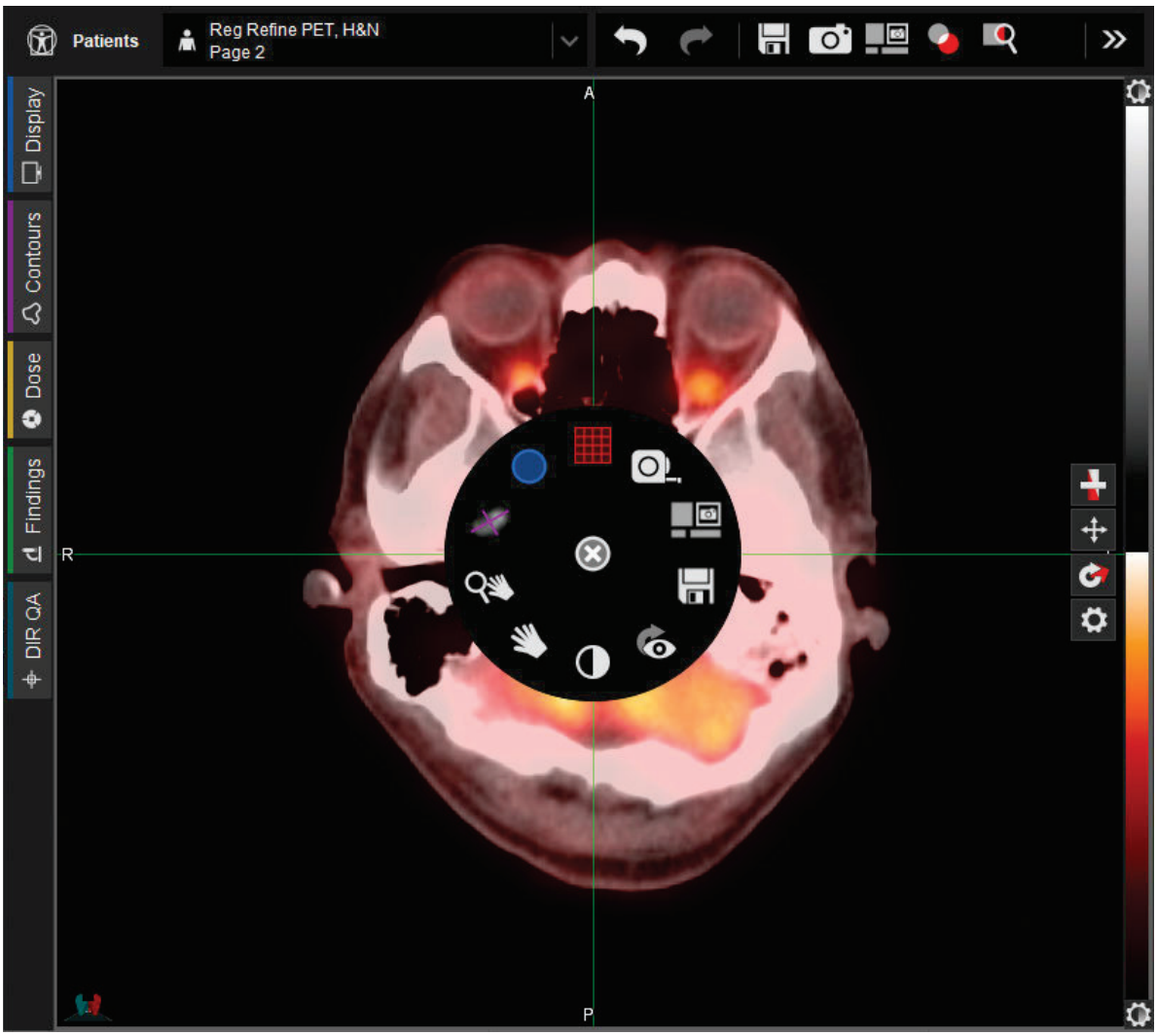
4. *MIM 7.3 and later:* Click **OK** at the bottom of the menu.

   MIM 7.2 and earlier: Click the double arrow » button to close the menu.

Tip: To see a list of MIM Workflows™ that can be added to your toolbar switch the dropdown menu (*MIM 7.3 and later*) or tab (*MIM 7.2 and earlier*) in the middle of the list from **MIM Tools** to **Workflow**. If you use MIM Extensions™, you can also switch the dropdown or tab to Extensions.

The Radial Menu

The radial menu lets you quickly access a set of frequently used tools with a right-click in any viewport. This reduces back-and-forth movement across your screen and lets you work more quickly.



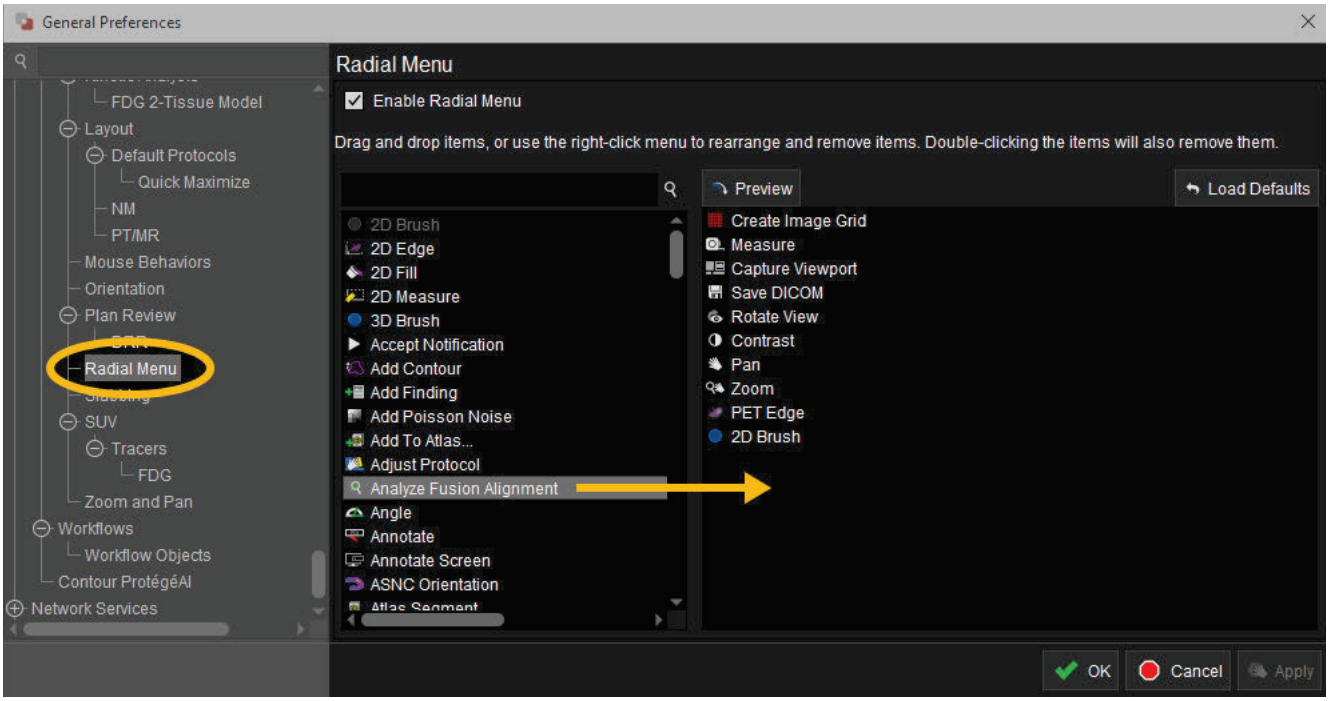
1. Access the radial menu by right-clicking on an image in an open session.
2. Click on a tool in the radial menu to activate it.

3. When you are finished using the tool, right-click again to access the radial menu. Select a new tool, or deactivate the current tool by clicking the X button in the center.
4. Move the cursor away from the radial menu to hide it.

Customize the Radial Menu

You can edit the radial menu to add tools you use frequently or remove tools you do not use:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**radial menu**".
3. Click **Radial Menu** on the left side.
4. Add items to your radial menu by dragging items from the left column to the right column.



5. Click **OK** to save the changes and close the window.

Zoom and Pan

MIMTD-607 • 05 Oct 2023

Overview

Interactively zoom and pan to inspect specific areas of an image.

Contents

Zoom

Access the **Zoom** tool from the toolbar or radial menu.

Related: For more information, see Access Tools: The Toolbar and the Radial Menu.

- Left-click drag up and down to zoom.
- Right-click drag to pan the image while in the zoom mode.

You can also use keyboard shortcuts for zooming. By default, the following shortcuts are set in MIM®:

1: Reset Zoom

2: Zoom In

3: Zoom In More

4: Zoom Out

Related: *MIM 7.3 and later*: You can configure MIM to zoom when you click or drag with a set mouse button. For more information, refer to Configure Mouse Behaviors. *MIM 7.2 and earlier*: This functionality is not available.

Pan

Access the **Pan** tool from the toolbar or radial menu.

Related: For more information, see Access Tools: The Toolbar and the Radial Menu.

- Left-click drag to pan the image.
- Right-click drag up and down to move through slices in the current plane (this behavior is the same when no tool is selected.)

Tip: You can also pan via right-click using the Zoom tool. Refer to Zoom above. If you prefer to pan via left-click, use the Pan tool.

Related: *MIM 7.3 and later*: You can configure MIM to pan when you click or drag with a set mouse button. For more information, refer to Configure Mouse Behaviors. *MIM 7.2 and earlier*: This functionality is not available.

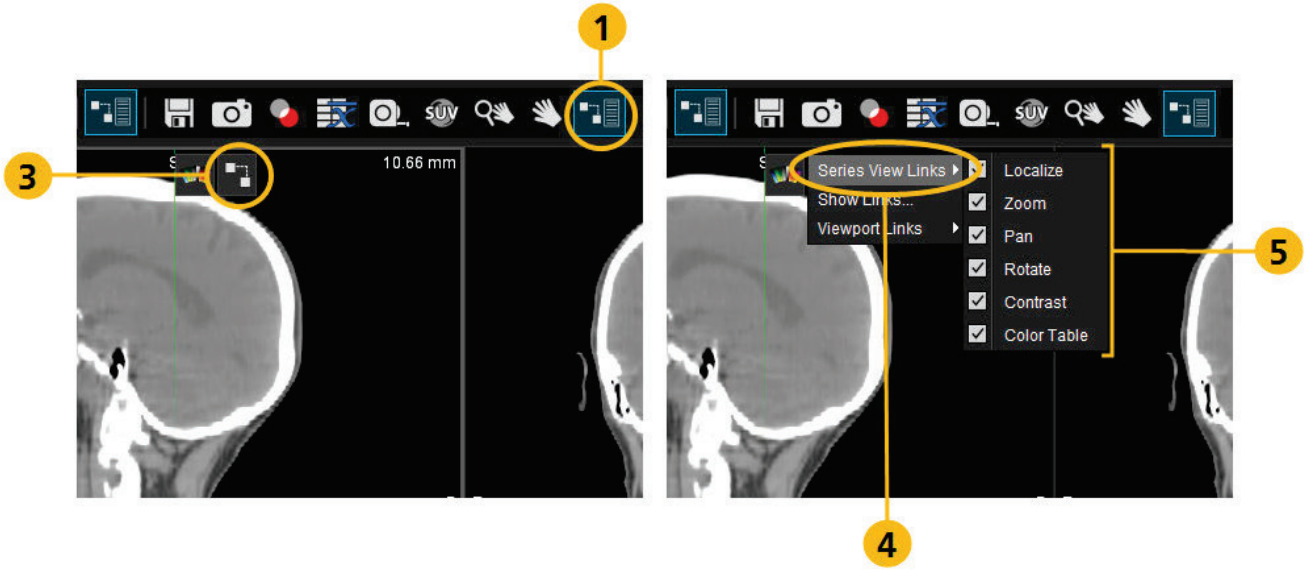
Scroll, Zoom, Pan, or Rotate a Series Independently

To scroll, zoom, pan, or rotate a series independently from all of the other series in the session, follow these steps:

1. Activate the **Link Manager** tool.

Related: If you use this tool regularly, you can add it to your toolbar for easy access. For more information, see Access Tools: The Toolbar and the Radial Menu.

2. Hover over the series that you want to scroll, zoom, pan, or rotate independently. The Link Manager button appears in the center at the top of the viewport.
3. Click the **Link Manager** button in the viewport.
4. Hover over **Series View Links**.



5. Toggle any of the settings to enable or disable the links:
   - To scroll the series separately, deselect **Localize**.
   - To zoom the series separately, deselect **Zoom**.
   - To pan the series separately, deselect **Pan**.
   - To rotate the series separately, deselect **Rotate**.

Important: If the series is part of a fusion, the fusion continues to localize, zoom, pan, or rotate with the primary image.

Related: For more information, see Adjust Links between Series Using the Link Manager.

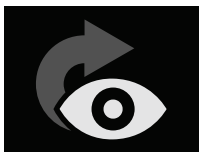
Rotate the View of a Volume

MIMTD-1027 • 16 Jan 2024

Overview

Rotate the view of a volume within the current plane.

Contents



Rotate View

Access the **Rotate View** tool from the toolbar or radial menu.

Related: For more information, see Access Tools: The Toolbar and the Radial Menu.

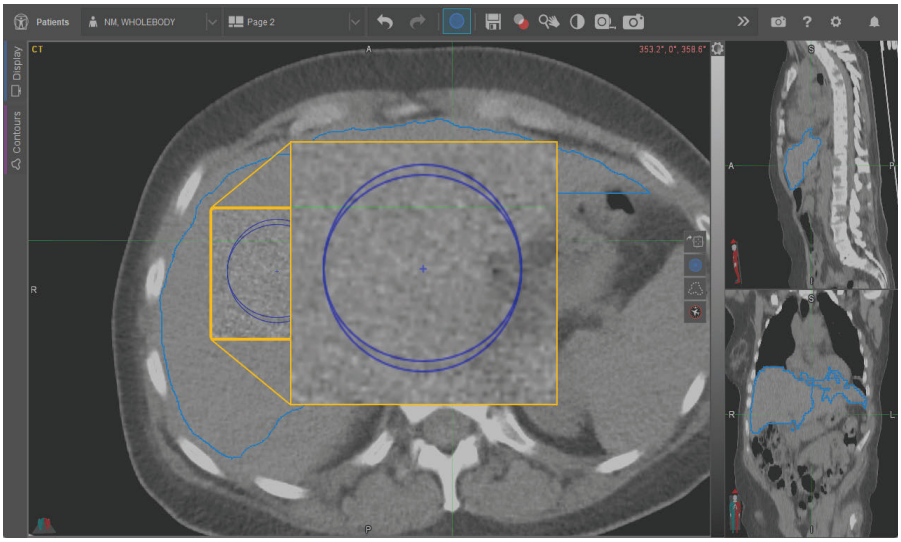
- Left-click drag up/down or left/right to rotate the volume in the current plane.
- Right-click drag up and down to move through slices in the current plane.

Tip: The right-click behavior is the same when no tool is selected.

Related: *MIM 7.3 and later*: You can configure MIM to rotate a view when you click or drag with a set mouse button. For more information, refer to Configure Mouse Behaviors. *MIM 7.2 and earlier*: The ability to configure mouse behaviors is not available.

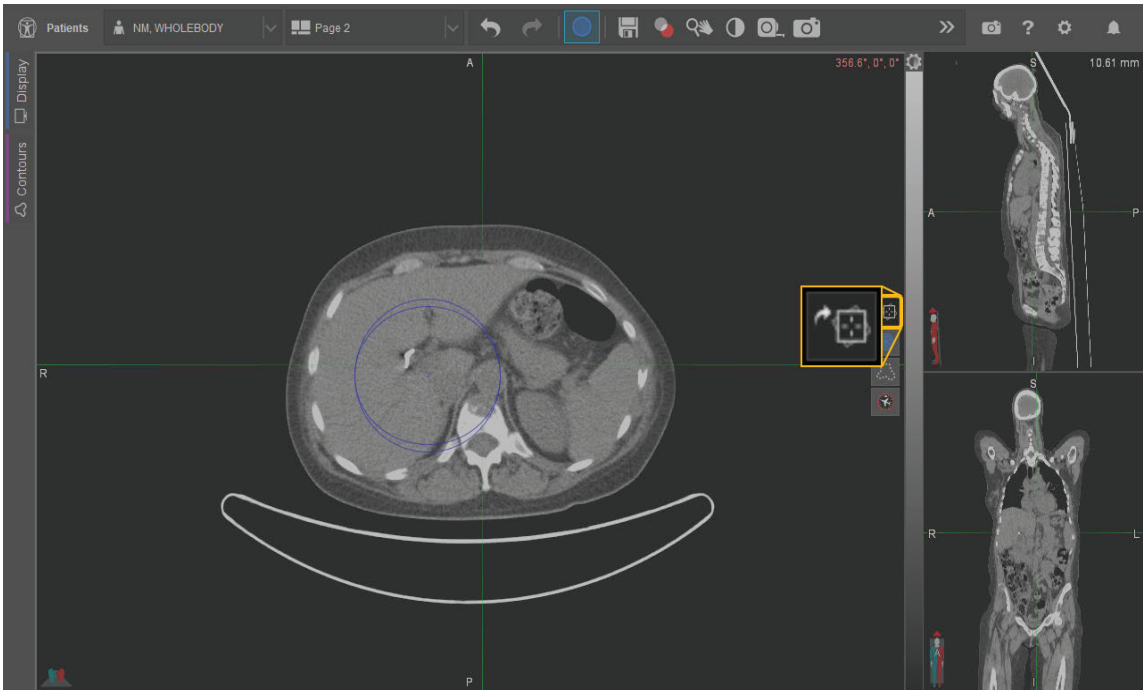
Reset Viewing Rotation and Correct Double 2D Brush

Use these steps to return a rotated volume to its native orientation. Resetting viewing rotation is also the most common way to fix the double 2D Brush shown below.



MIM 7.3 and later:

Click the reset viewing rotation button on the right side of the viewport to reset the viewing rotation and return to the normal 2D Brush.



Tip: If desired, click this button again to return to the rotated view.

MIM 7.2 and earlier:

1. Right-click the rotated image to open the radial menu.
2. Right-click the **Rotate View** tool to open an additional menu.
3. Click **Reset Viewing Rotation** to return to the normal 2D Brush.

Correct Patient Orientation

MIMTD-1393 • 24 Jan 2023

Overview

If the series you are viewing is rotated in an unexpected way (e.g., upside down) or is labeled with the incorrect patient orientation, follow these steps to correct the orientation, then save new DICOM files.

Important: There are two DICOM tags that commonly affect image display and orientation labels. Orientation problems result from an incorrect value in one or both of these tags. Unless you are certain of which DICOM tag is incorrect, it is important that you proceed through all of the following steps in order. This process ensures that the image is displayed appropriately and that both relevant DICOM tags are updated to correct values.

Important: This process does not change existing DICOM files. This process creates new DICOM files for the corrected series. As a result, you may need to send the corrected files to your PACS, TPS, or other systems in order to maintain compatibility.

Steps in the Reorientation Process

Prepare to Reorient the Series

1. Close the series you plan to reorient.
2. Click the Settings button in the upper-right corner of MIM.
3. Go to **General Preferences** and search for **"loading"**. Select **Loading** on the left side.
4. Record the value of the **Reorient Non-HFS Axial Non-MR Scans to Standard Orientation** preference. Keep this information for later use.

Tip: If you do not have access to this preference, it may be overridden by an administrator. Contact your MIM application administrator.

5. Verify that the **Reorient Non-HFS Axial Non-MR Scans to Standard Orientation** preference is set to **Never Reorient** (necessary when correcting patient orientation).
6. Click **OK** to save the changes and close the window.

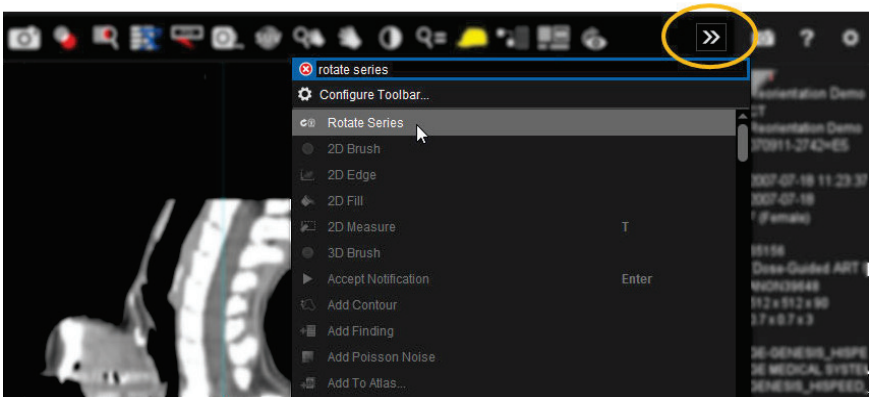
Ensure That the Series Displays as Desired

Open the series that needs to be reoriented.

If the image is facing the desired direction, but the onscreen orientation labels or the orientation man icon are incorrect, proceed to Correct the Image Orientation Patient DICOM Tag, below.

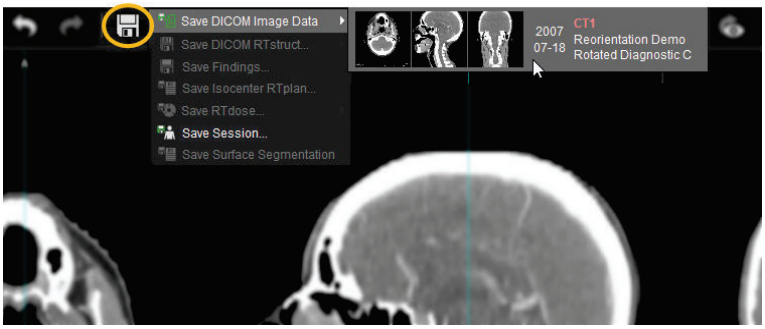
If the image is not facing the desired direction, complete the following steps:

1. Click the » button on the right side of the top toolbar.
2. Search for and select the **Rotate Series** tool.



3. Use the Rotate Series dialog to select the appropriate orientation for the image.

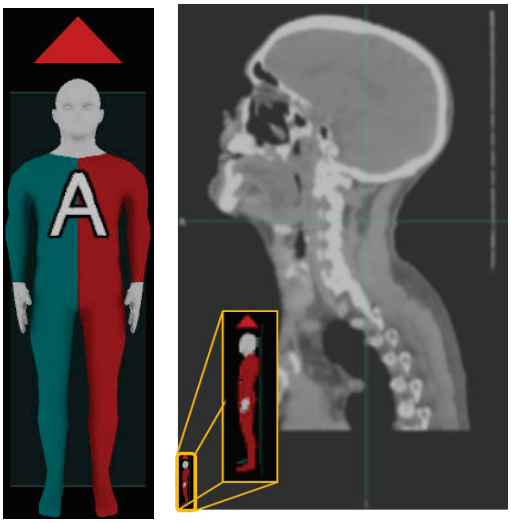
4. Click the save button and hover over **Save DICOM Image Data**, then click the thumbnail of the rotated series.



5. In the DICOM Save window, make any desired changes to the series information, then click **OK**. A new DICOM series is saved. The text **(rotated).** is prepended to the Series Description of the new series.
6. Close the session.
7. Open the new rotated series. This series has **(rotated).** prepended to its Series Description.
8. Proceed to Correct the Image Orientation Patient DICOM Tag.

Correct the Image Orientation Patient DICOM Tag

Compare the images in the series to the orientation man in the lower-left corner of each viewport. Determine whether the orientation man is facing the same direction as the image.

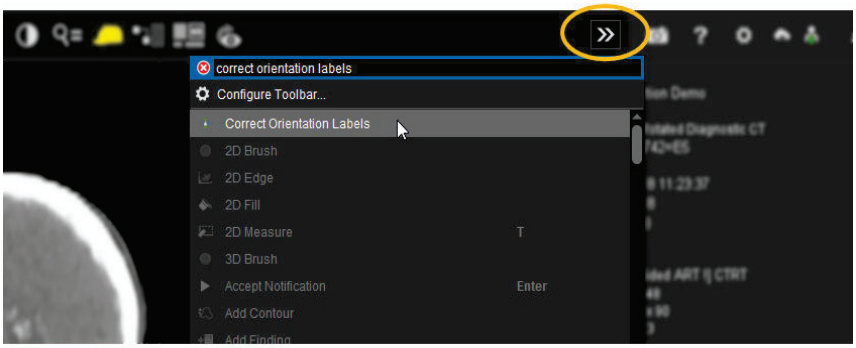


At this point, it is only important that the orientation man is facing the same direction as your patient. It is not necessary for the table or the arrow on the orientation man to be in the correct position. These items will be corrected in a later step.

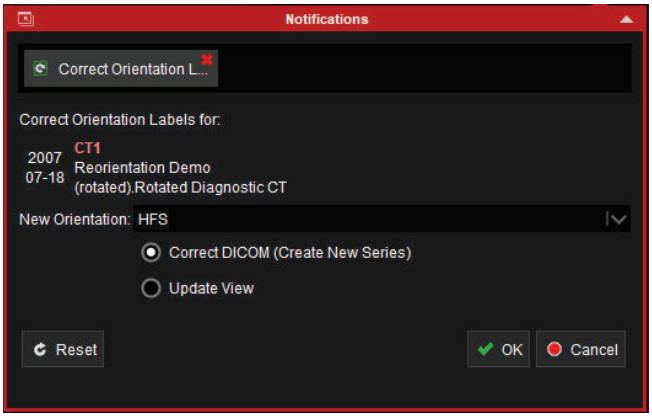
If the orientation man is facing the same direction as the series, proceed to Correct the Patient Position DICOM Tag, below.

If the orientation man is not facing the same direction as the series, follow the steps below:

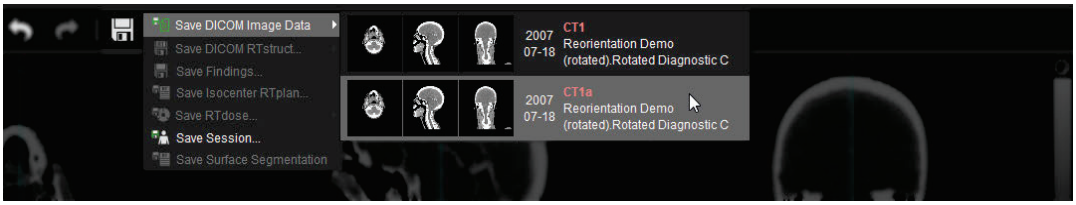
1. Click the ⏩ button on the right side of the top toolbar.
2. Search for the **Correct Orientation Labels** tool and select it.



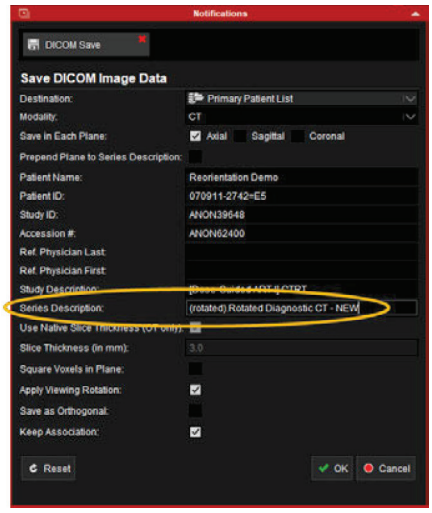
3. Use the dropdown in the **Correct Orientation Labels** window to select the correct orientation for the image.
4. Change the radio button in this window to **Correct DICOM (Create New Series)**.
5. Click **OK**. The orientation man updates to face the same direction as the image.



6. Click the save 💾 button and hover over **Save DICOM Image Data**, then click the thumbnail of the newly created series. This series is ordinarily labeled with the modality followed by "1a" as shown below.



7. In the DICOM Save window, edit the series description so that you will be able to identify this new series in your patient list. Click **OK**. A new DICOM series is saved.



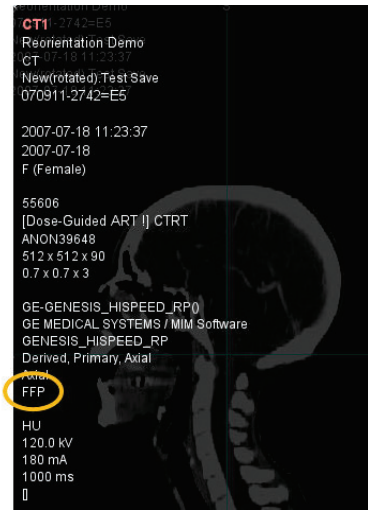
8. Close the session.
9. Open the newly saved series. Proceed to Correct the Patient Position DICOM Tag.

Correct the Patient Position DICOM Tag

Determine whether the patient position is listed correctly in the information panel on the right side of the screen.

Tip: If you do not have an information panel on the right side of the screen, hover over any viewport and press the spacebar to see the series information.

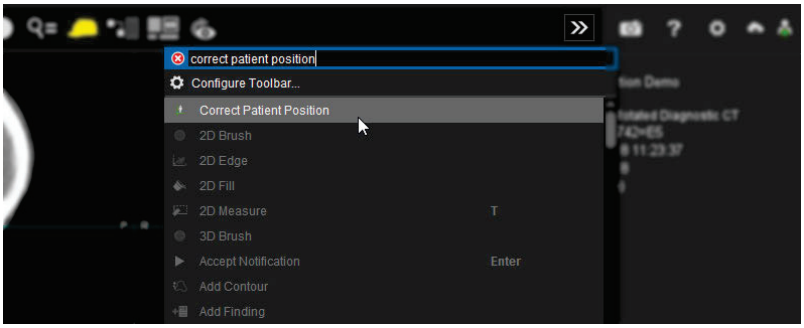
The image below shows an example of an *incorrect* patient position. The patient position is shown as FFP (feet first prone), but the image was actually acquired head first supine.



If the patient position is correct, proceed to Confirm the Corrected Orientation and Save.

If the patient position is incorrect, follow the steps below:

1. Click the ⏩ button on the right side of the top toolbar.
2. Search for the **Correct Patient Position** tool and select it.



3. Use the dropdown in the **Correct Patient Position** window to indicate the correct patient position for the image, then click **OK**. The patient position and the orientation man are updated. The Correct Patient Position tool does not create a new series on your screen.
4. Proceed to Confirm the Corrected Orientation and Save.

Confirm the Corrected Orientation and Save

Confirm the following before proceeding:

- The image is displaying as intended.
- The orientation man in the lower-left corner of each viewport matches the patient orientation.

- The arrow and the table shown in the orientation man icon accurately reflect the position the patient was scanned in.
- The patient position is listed correctly in the series data.

If any of these conditions are not met, please contact MIM Software Support at support.mimsoftware.com. Further investigation is needed.

If all of the above conditions are met, follow the steps below to complete the reorientaton process:

1. Click the save button and hover over **Save DICOM Image Data**, then click the thumbnail of the series.
2. In the DICOM Save window, edit the Series Description to indicate that this is the final reoriented series. Click **OK** to save the series.
3. Return to your patient list and delete the series that were created during the intermediate steps of this process.

> **Important:** Do not delete the original (incorrectly oriented) series until you have confirmed that the reoriented series is compatible with any planning that has already been done in your treatment planning system. For more information on deleting data, see Manage Patient Data.

If you changed the value of the Reorient Non-HFS Axial Non-MR Scans to Standard Orientation preference at the beginning of the reorientation process, reset it now:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for **"loading"**. Select **Loading** on the left side.
3. Reset **Reorient Non-HFS Axial Non-MR Scans to Standard Orientation** to its original value.
4. Click **OK**.

Supplemental Information

The DICOM tags that most commonly affect image orientation in MIM are Patient Position (0018,5100) and Image Orientation Patient (0020,0037). When followed completely, the steps above ensure that both of these tags have correct values.

Additional Information about the Orientation Man

The orientation man is labeled with an A on his anterior side and a P on his posterior side. When the Image Orientation Patient (0020,0037) DICOM tag is correct, the arrow at the orientation man's head or feet corresponds to the direction that the patient entered the scanner. Similarly, when the Image Orientation Patient (0020,0037) DICOM tag is correct, the table is correctly shown on the orientation man's anterior or posterior. In the image below, the orientation man is correctly matched to the HFS orientation of the scan.

Adjust Image Contrast

MIMTD-612 • 24 Aug 2023

Overview

MIM® has a variety of automatic and manual contrast adjustment methods for different modalities and tissue types. You can also create your own contrast presets, which is helpful when matching contrast to other systems.

Contents

Adjust Contrast with the Mouse (MIM 7.3 and Later)

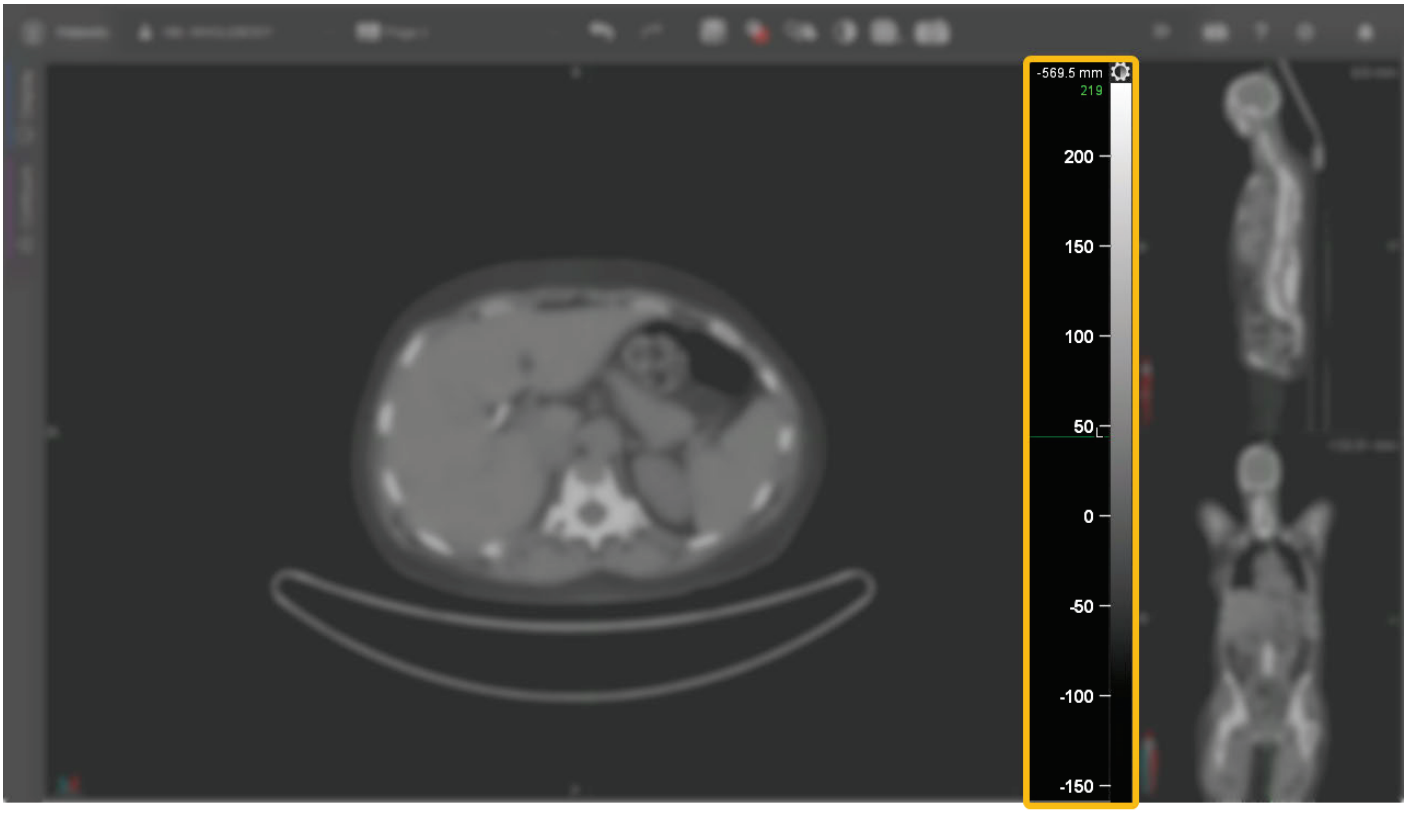
To adjust the contrast with the mouse, middle-click drag in any viewport. In MIM 7.2 and earlier, this functionality is not available.

- Drag up and down to change the window width.
- Drag left and right to change the window level.

Tip: You can configure any of your mouse buttons to adjust contrast. For more information, see Configure Mouse Behaviors.

Adjust Contrast with the Contrast Bar

The contrast bar appears on the right side of an image. Hover over the contrast bar to see the values.

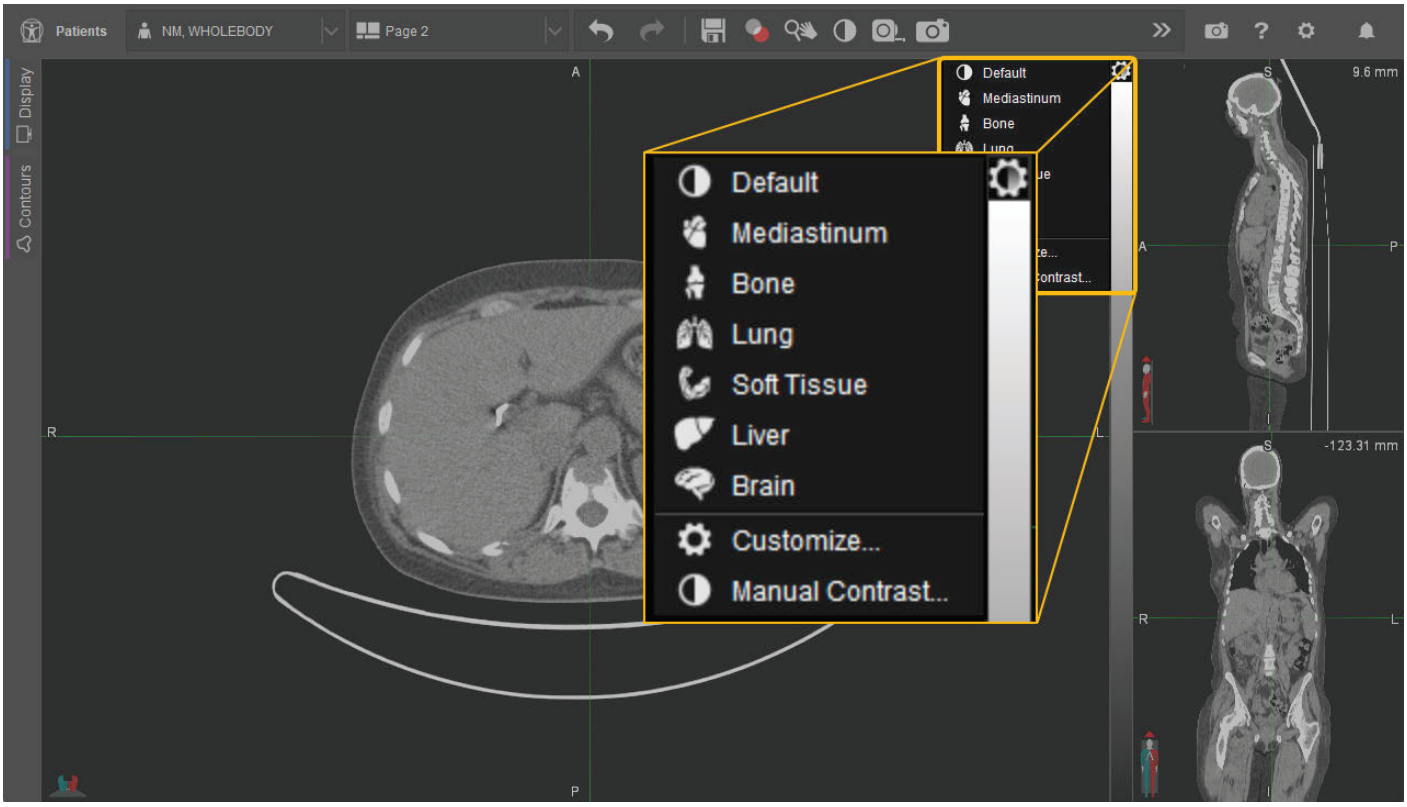


See the table below for possible contrast adjustments with the contrast bar:

Contrast Adjustment	Action
Adjust the window level	Left-click drag left/right on the contrast bar
Adjust the window width	Left-click drag up/down on the contrast bar
Reset the contrast	Right-click the contrast bar

Apply a Contrast Preset

Click the contrast preset button above the contrast bar to access the contrast preset menu.



Choose a default contrast preset from the menu. The modality of the image determines which options are available.

- CT: Mediastinum, Bone, Lung, Soft Tissue, Liver, and Brain.
- MR: Brain, T1, T2, and FLAIR.
- PET: Default and Autonormalize.

Related: For more information on PET autonormalization, see Autonormalize PET Series in MIM®.

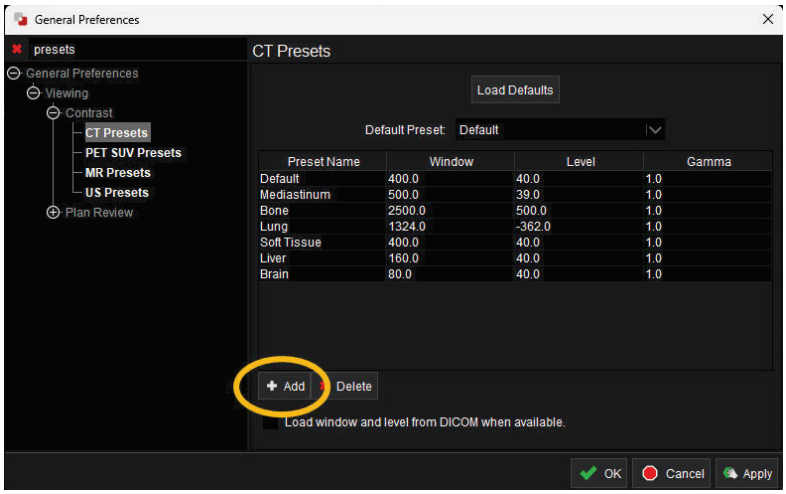
- US: No presets are offered.

Tip: Common presets are mapped to keyboard shortcuts by default. For more information, see Default Keyboard Shortcuts.

Create Your Own Contrast Presets

Adjust MIM-provided presets or create your own presets. This is helpful when matching contrast to other systems.

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**presets**". Select the desired preset modality from the left side.
    - To adjust an existing preset, double-click any value to change it.
    - To create a new preset, click **Add**, then adjust the values as desired.



Tip: If you use a preset often, map it to a keyboard shortcut. For more information, see Set Keyboard Shortcuts.

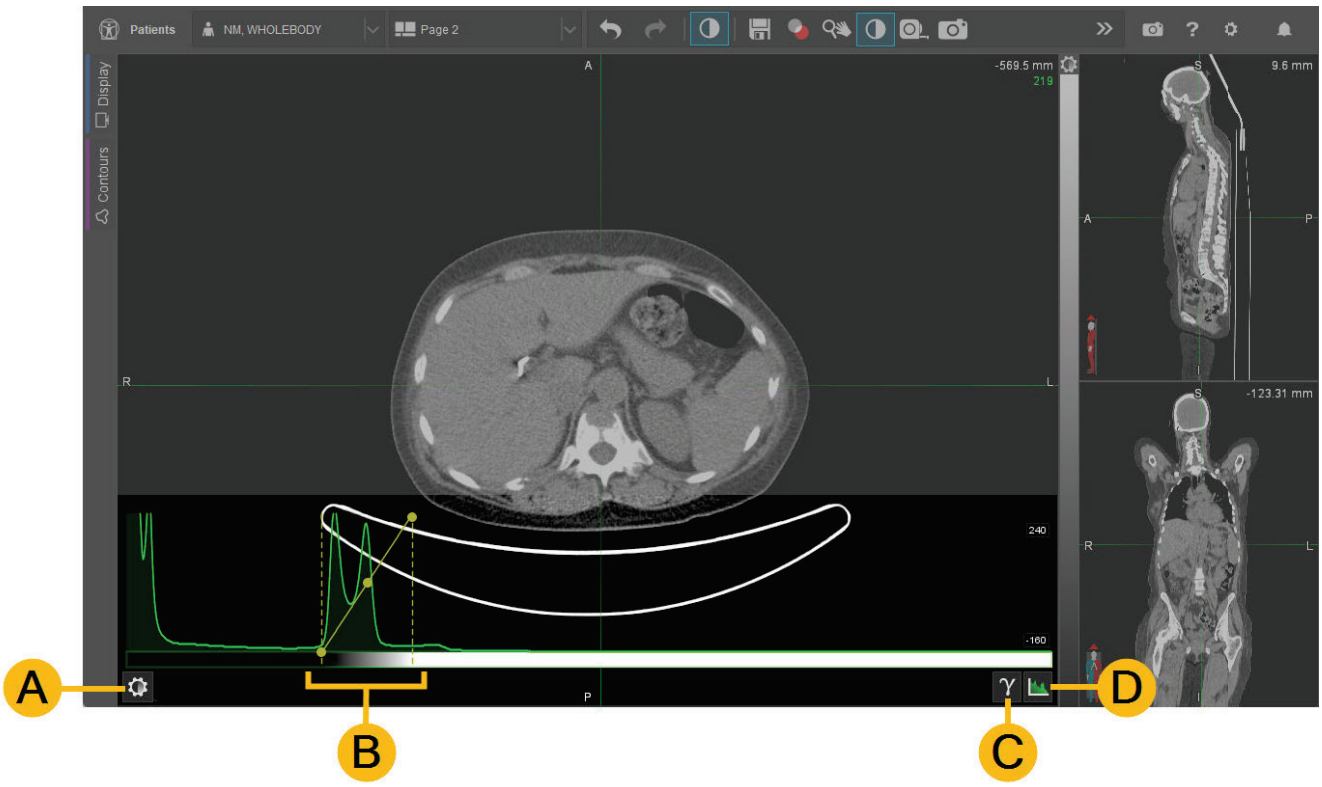
Tip: Image contrast, including presets, can also be applied in MIM Workflows™.

Adjust Contrast with the Contrast Tool

Activate the **Contrast** tool from the toolbar, radial menu, or with the W keyboard shortcut.

- To define the contrast window based on a region of interest, right-click drag on the image to define the region of interest.

- To access additional functions of the Contrast tool, hover in any viewport:



A. Contrast Preset Menu
B. Contrast Histogram
C. Gamma Correction Adjustment
D. Toggle the Contrast Histogram

Read the Contrast Histogram

The green line shows the values present in the image.

- In the screenshot above, the green line corresponds to the HU values of the CT.
- On a PT image, the green line corresponds to the SUV values of the PT.

The yellow dashed lines and dots form the contrast window. See the table below for possible contrast adjustments with the contrast histogram:

Contrast Adjustment	Action
Adjust the upper and lower contrast values	Left-click drag the yellow dots on each side

Contrast Adjustment	Action
Adjust the window center	Left-click drag left/right on the center point or anywhere inside the yellow lines
Adjust the window width	Left-click drag up/down anywhere inside the yellow lines

Adjust Contrast Bounds (MIM 7.3 and Later)

The color of the dots on the contrast histogram indicates whether the contrast bounds are locked.

Dot Color	Indication
Red	The bound is locked and cannot be adjusted
Yellow	The bound can be adjusted, but not beyond the minimum or maximum value for the series
Blue	The bound can be adjusted beyond the minimum or maximum value for the series

You can adjust the bound locks. In MIM 7.2 and earlier, this functionality is not available.

- To lock an upper or lower contrast value, click the corresponding yellow dot. It will turn red, indicating that it is locked and cannot be edited.
- To expand the upper or lower bound beyond the minimum or maximum value for the series, follow these steps:
    i. Lock the other bound, turning the dot red.
    ii. Click the dot for the bound you want to adjust. It will turn blue, indicating that it can be adjusted beyond the defined range of data.
    iii. Left-click drag to adjust the bound.

Tip: For PET images, the lower contrast bound is locked to zero by default. See the steps below to change this behavior.

Various preferences control these bounds and the lock behavior. To adjust these settings, follow the steps below:

1. Click the Settings button in the upper-right corner of MIM. .
2. Go to General Preferences and search for "**contrast**". Select **Contrast** on the left side.

3. If desired, deselect **Load PT or NM with lower contrast level locked**.
    - With this preference disabled, the lower contrast level is unlocked and can be adjusted (yellow), but not below the series minimum.
    - To adjust the lower contrast bound beyond the series minimum, either:
        - Lock the upper bound (click to make it red) and then click the lower bound (to make it blue). The lower bound can then be adjusted.
        - Deselect **For functional modalities, limit the contrast lower bound to the series minimum**. With this preference disabled, the lower bound will always be fully adjustable (a blue dot).

4. If desired, deselect one or more of the preferences that limit the contrast bound to the series maximum/minimum.

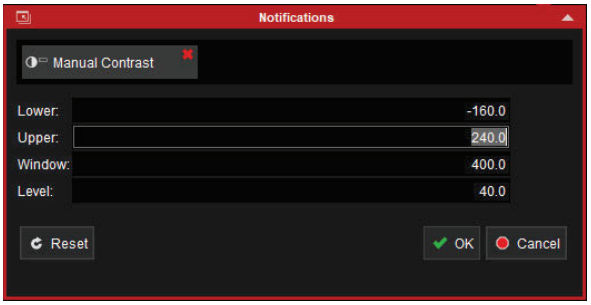
    For example, deselect **For functional modalities, limit the contrast upper bound to the series maximum**. The upper bound will be unlocked and you will be able to extend the bound above the series maximum.

Specify Manual Contrast Values

1. Activate the **Manual Contrast** tool from the toolbar or by clicking on the contrast preset menu and selecting **Manual Contrast...**.
2. *If multiple series are visible on the page,* use the **Select this series** button to choose the image you want to adjust.
3. Enter values for the **Lower**, **Upper**, **Window** (width), and **Level** (window center).

> **Tip:** The parameters automatically update as needed as you make changes (e.g., so that the window center always remains equidistant from the lower and upper values).

4. Click **OK** to save the changes and close the window.



Tip: If you regularly set the contrast manually, the Manual Contrast tool can be set to a keyboard shortcut. For more information, see Set Keyboard Shortcuts.

Autonormalize PET Series in MIM®

MIMTD-1640 • 20 Jun 2023

Overview

In PET series, autonormalization determines the contrast window by considering the distribution of image intensities within the series.

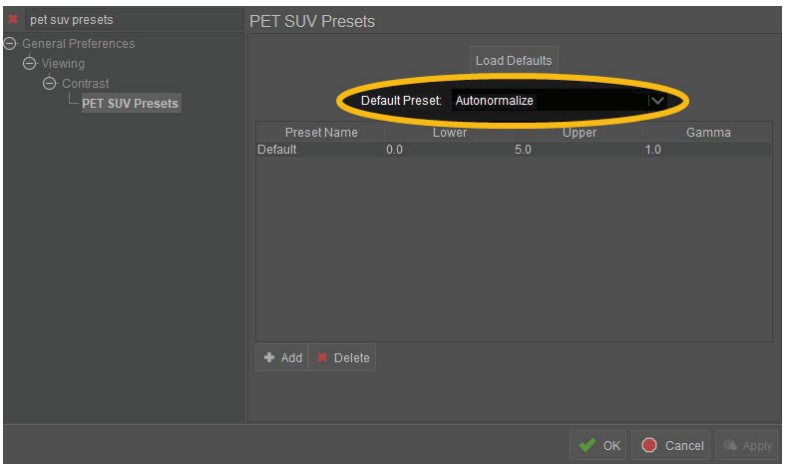
MIM identifies the lowest and highest intensity values in an image, which only account for a small percentage of the total voxels. These extreme values are excluded when determining the upper and lower bounds of the autonormalized contrast window. The lower bound is automatically set to zero unless a large number of values are negative.

Related: To set your own upper and lower contrast bounds, see Adjust Image Contrast.

Contents

Autonormalize Contrast by Default

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**pet suv presets**".
3. Click **PET SUV Presets** on the left side, and select **Autonormalize** from the **Default Preset** dropdown.



Autonormalize Contrast Within a Session

To autonormalize the contrast of an open series, click the **Contrast Preset** button in the upper-right of the viewport and select **Autonormalize**.

Adjust Image Color Tables

MIMTD-611 • 27 Jun 2023

You can change Color Tables (Look Up Tables) in MIM® by adjusting the default settings, or make changes individually in an open session.

Set Default Color Tables

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

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**color tables**".
3. Click **Color Tables** on the left side and set color tables for various modalities. This setting applies starting with the next session.

Fusion Color Tables

By default, the secondary image in a fusion is set to the Hot Metal color table.

If desired, you can assign different default colors to different pairs of fused images:

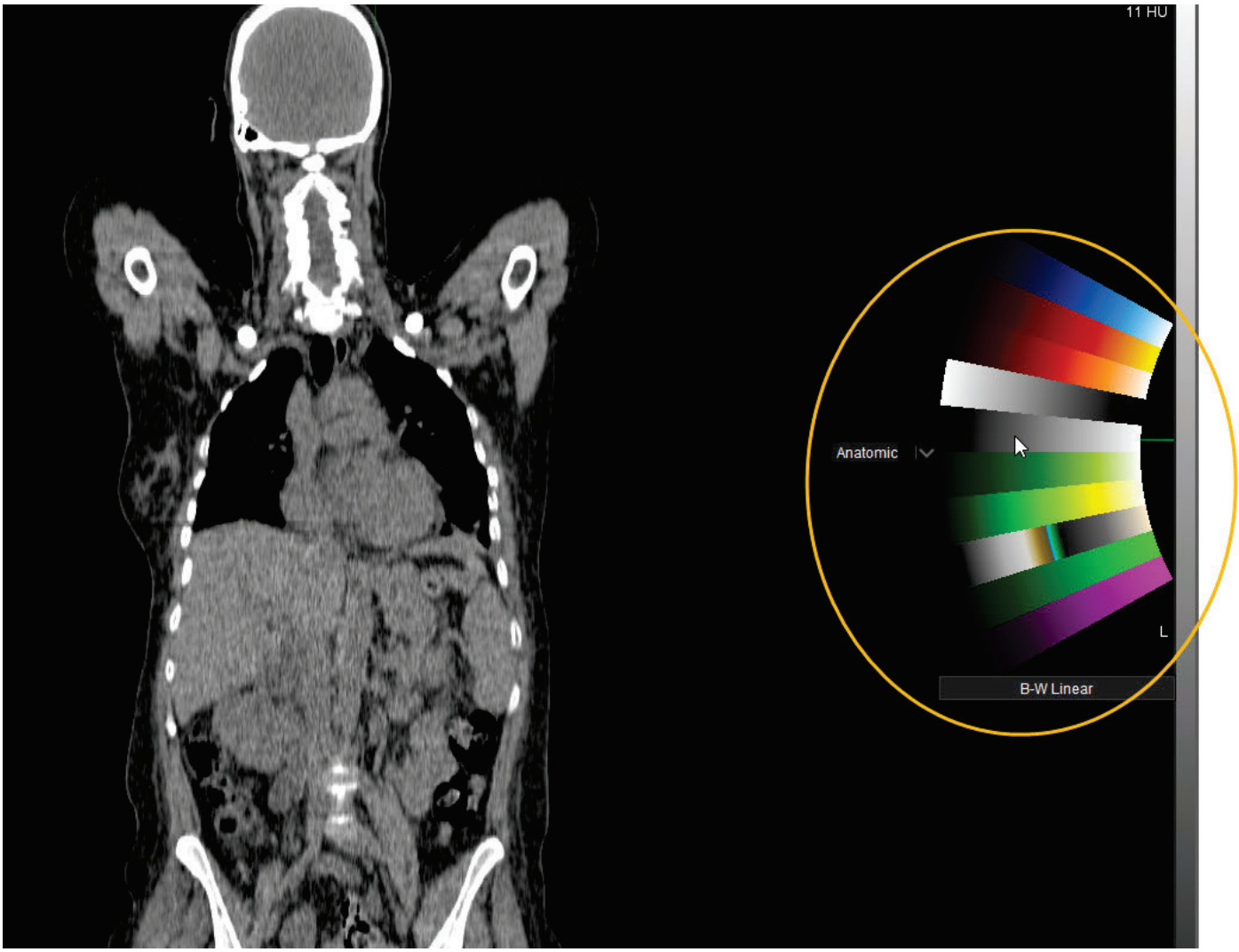
1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**color tables**".
3. Click **Fusion Color Tables** on the left side.
4. Click the **Add** button to create new pairs. This setting applies starting with the next session.

Adjust Color Tables in a Session

You can change the color table for an image in an open session:

1. Click on the contrast bar.
2. Hover over each color table to preview it on the image. Use the dropdown menu to the left of the color tables to reveal different options.
3. Click on a color table to apply it to the image.

Note: Fusion images contain two contrast bars, one that controls the primary image's color and one that controls the secondary image's color.



View Maximum Intensity Projections (MIP)

MIMTD-681 • 25 Jul 2023

Overview

MIM® can generate a MIP for single series (PT, CT, or SPECT) as well as PET/CT and SPECT/CT fusions.

Contents

6.1.1

Create a MIP

There are several ways to create a MIP:

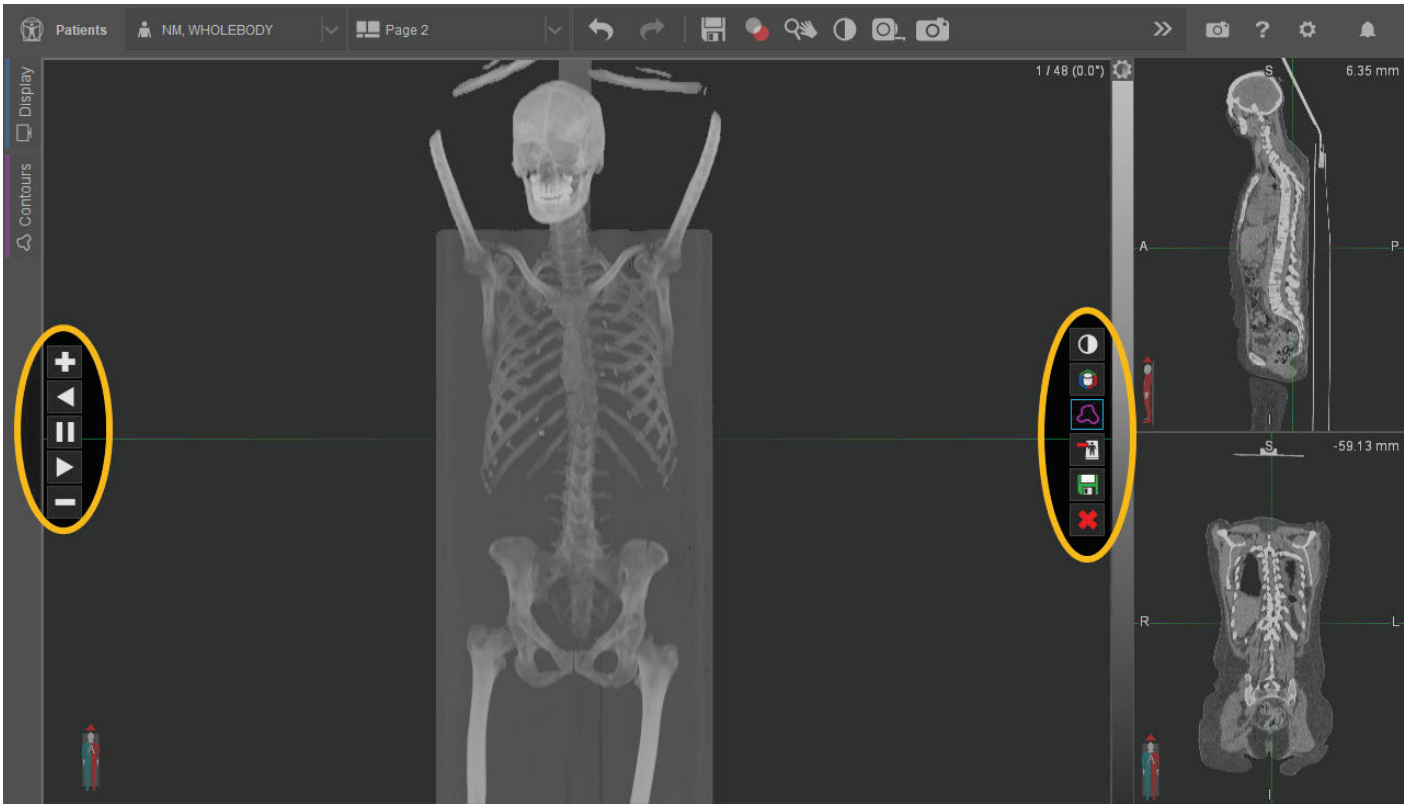
- Hover over a viewport and press the M key on your keyboard.
- Click Create MIP Movie from your top toolbar or radial menu, then select the desired viewport to generate the MIP.
- *In MIM 7.3 and later:* Configure a "Quick MIP" mouse behavior. In MIM 7.2 and earlier, this behavior is not available.

Related: For more information about accessing tools, see Access Tools: The Toolbar and the Radial Menu.

Related: For more information about configuring mouse behaviors, see Configure Mouse Behaviors.

Adjust a MIP

Use the playback controls on the left side of the viewport to play the MIP:



Increase the frame rate
Reverse
Pause
Play
Decrease the frame rate

- To rotate the MIP, right-click drag left/right or up/down.
- Set a keyboard shortcut to play/pause the MIP.

Tip: You can set the initial MIP direction and initial frame rate by clicking the Settings button in the upper-right corner of MIM and searching for "**mip movie preferences**".

Related: For more information on setting keyboard shortcuts, see Set Keyboard Shortcuts .

Use the companion tools on the right side of the viewport to make additional adjustments to the MIP:
Select the contrast for the image

 Set the view direction
 Toggle contour visibility
 Remove the couch (CT and fusion MIPs only)
 Save a MIP movie. A fusion MIP cannot be saved as a DICOM Cine.
 Close the MIP and return to the original view

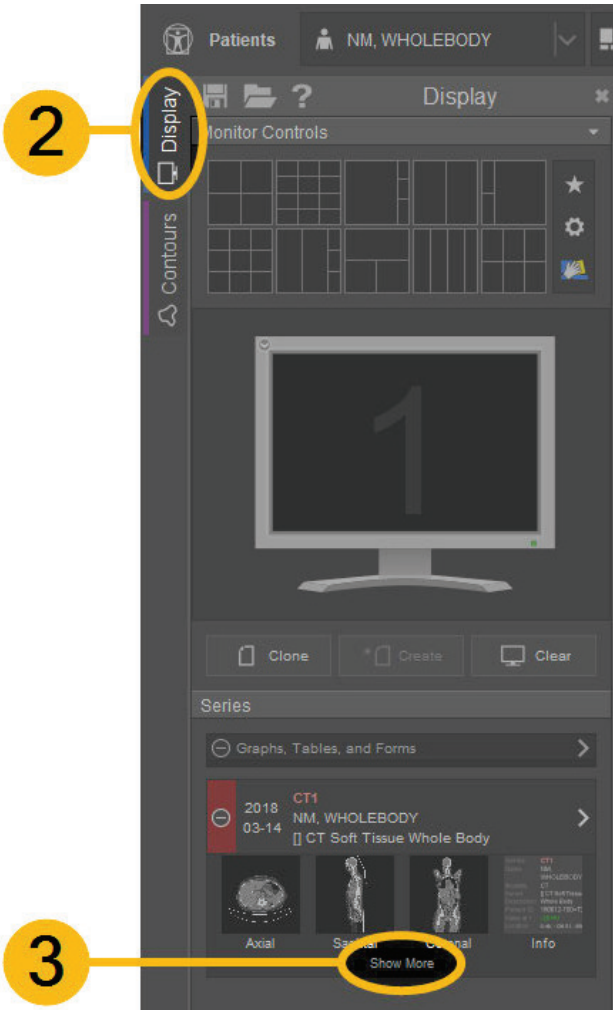
Hover over any of the tools for a title or description of their functionality.

Tip: The companion tools you see depend on the modality of the scan.

Tip: A MIP movie saved as an AVI is a movie file playable by common media applications such as Windows Media® Player and QuickTime® Player.

Create a MIP Hanging Protocol

To assign a MIP to its own viewport on a display page:



1. Open a PT, CT, SPECT, PET/CT fusion, or SPECT/CT fusion.
2. Open the **Display** sidebar on the left side of the screen.
3. Click **Show More** under the desired series.
4. *If you want to open the MIP on a separate page by itself*, click the MIP icon and then click **Create** below the monitor illustration.

   If you want to open a page that displays the MIP alongside other planes, click the MIP icon and other desired planes, then click **Create** below the monitor illustration.

Tip: You can also drag and drop the MIP icon directly onto the current hanging protocol.

Fusion MIPs

Fusion MIPs can be especially helpful for SPECT/CT images, bone studies, and complex anatomy that is not ideal to view in the standard three imaging planes.

Fusion Alignment

If you adjust the fusion alignment, the MIP will automatically regenerate to reflect the new alignment. This may take a few seconds. Adjust fusion alignment in a non-MIP (e.g., axial) viewport. You cannot adjust the fusion alignment within the MIP viewport.

Fusion Blend

Use the Blend tool to adjust the blending between the primary and secondary images. MIP and non-MIP viewports for the series will blend in sync. Similarly, adjusting the color table for a series will affect both the standard views and the MIP.

Fusion Contrast

For a MIP of a fusion, the contrast option adjusts the contrast of the primary image.

- By default, **Bone** contrast is selected for the primary (usually a CT) of a fusion.
- The **Linked Contrast** option links the MIP contrast to the original view. Thus, any adjustment to the image contrast will affect the MIP.

> **Related:** For more information on adjusting image contrast, see Adjust Image Contrast.

To adjust the secondary image's contrast, change the contrast on an original, non-MIP view of the image. The secondary image is typically the functional image in the fusion.

> **Tip:** You can also use the color bars on the right side of a non-MIP fusion viewport to adjust both primary and secondary image contrast.

> **Tip:** The contrast gear at the top of the fusion MIP color bar only adjusts the contrast of the secondary image.

Configure MIP Zoom Behavior

You can choose to zoom MIPs separately from their original images and any other linked series:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**zoom and pan**".
3. Click **Zoom and Pan** on the left and select **Zoom MIPs separately**.
4. Click **OK** to save the changes and close the window.

Create Projection Images

MIMTD-1644 • 20 Jun 2023

Overview

MIM can create projection images from a reconstructed SPECT image, which reduces scan time since acquisition of the planar images is not necessary.

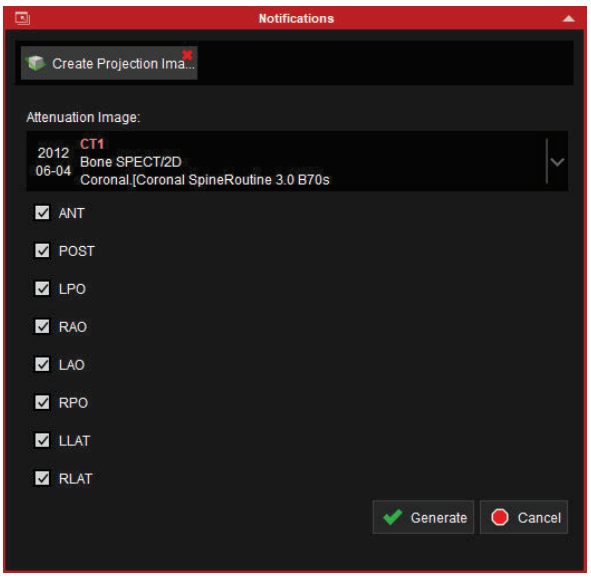
Projection images can also be created with a MIM Workflow™ or via MIM Assistant®. For more information, please contact MIM Software Support at support.mimsoftware.com.

Prerequisites

You must scan a CT density phantom to calculate the attenuation formulas, bilinear fit curves, and scatter windows specific to your camera. This process requires assistance from a MIM representative. For more information,please contact MIM Software Support at support.mimsoftware.com.

Create Projection Images

1. Activate the **Create Projection Images...** tool. You may need to click the ⏩ button at the top of MIM to search all tools.
2. If desired, select an attenuation image to add the effects of attenuation to your projection images.
3. Select which planar images to generate.
4. Click **Generate**.



i. *If you chose an attenuation image*, click the plus button in the new window to add the desired attenuation formula. If there are no attenuation formulas, please see Prerequisites.

ii. Adjust the attenuation formula as desired, then click **OK** to generate the projection images.

Combine Anatomical Images Using the Stitcher Workflow

MIMTD-1651 • 16 Nov 2023

Overview

The Stitcher workflow combines two anatomical series with different fields of view to create a single composite series. It is most often used for exceptionally large or tall patients, whose bodies cannot be easily or accurately scanned all at once.

MIM 7.3 and later: This workflow is included with MIM and can be imported like any other workflow. See Import MIM Workflows™ and Other Content for instructions.

MIM 7.2 and earlier: This workflow is available, but is not built into the software. Please contact MIM Software Support at support.mimsoftware.com to obtain a Stitcher workflow for MIM 7.2 or earlier.

Contents

Workflow Inputs

Two anatomical series of the same modality. The series should have different fields of view.

Before Running the Workflow: Expand the Field of View

Expanding the FOV of one series makes it easier to align the images. You only need to expand the field of view for one of the series.

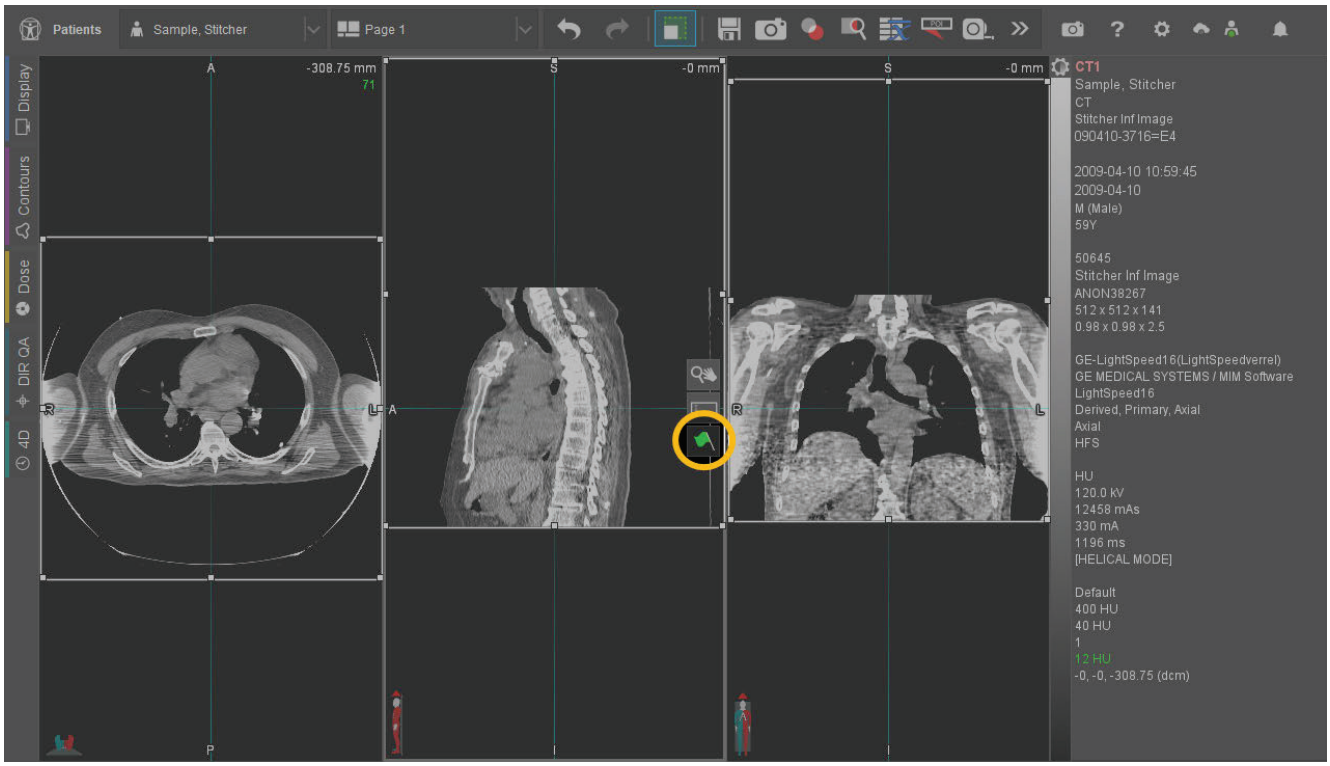
Tip: Adjusting the FOV creates a copy of the series. The original DICOM data remains unchanged.

To expand the FOV of the image, follow these steps:

1. Open the image whose FOV you want to adjust.
2. Click the double arrow ⏭ button on the right side of the top toolbar.

3. In the search box at the top of the tools menu, type "FOV Adjuster". Select the **FOV Adjuster** from the list of tools.
4. The FOV Adjuster places a box around the image's original FOV. Drag one or more edges of the box to expand the image's FOV as appropriate.

   Example: If you are working with an image of a patient's left side and you intend to combine it with an image of the patient's right side, drag the box to expand the field of view on the patient's right. Likewise, if you are working with an image of a patient's torso that will be fused to an image of the patient's legs, expand the field of view in the inferior direction.



Extending the image's field of view (FOV). Since this image will be combined with another image that shows the patient's head and neck, the FOV was extended in the superior direction. The circled button finalizes the extension.

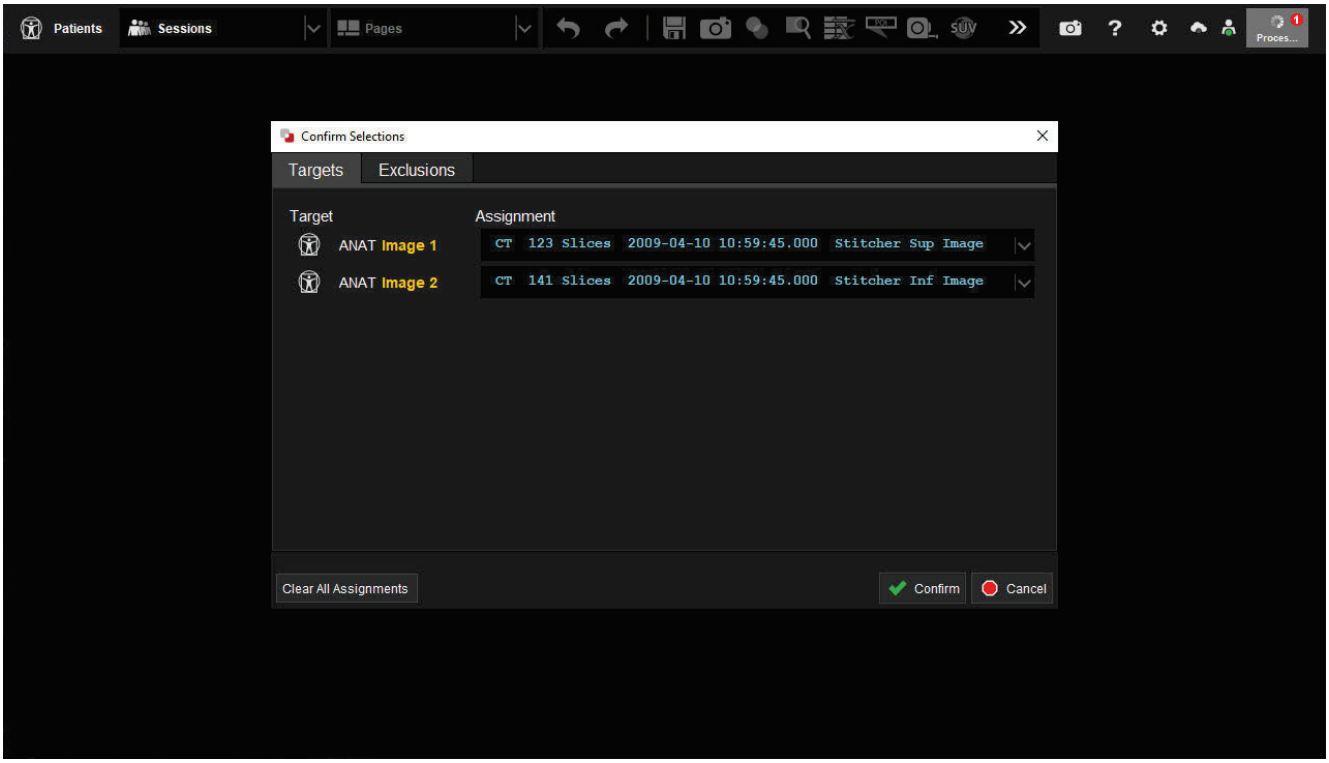
5. Click the green flag button to create a new series with an expanded FOV.
6. Save the new Expanded FOV image. For more information on saving images, see Save Patient Data.

Tip: Give the expanded FOV image a Series Description that will help you find it easily.

Run the Workflow

1. From the patient list, select the images you want to combine.
2. In your workflows list, double-click the **Stitcher** workflow.

3. When prompted, assign one image to each of the workflow targets. For this workflow, It does not matter which image is assigned to each target. Click the **Confrim** button. The workflow creates a rigid fusion between the images.



4. When prompted, check the fusion. Because you are aligning images with differing fields of view, there is a greater than normal likelihood that the initial fusion will require correction. Make adjustments as necessary to ensure that the series are properly aligned.

> **Tip:** After making initial adjustments to the fusion, use the Box-Based Assisted Alignment tool to rerun the fusion based on anatomy that is visible in both series.

5. When the images are properly aligned, click **Resume Workflow**. The workflow creates a combined series from the two input series and displays it onscreen. The combined series is also saved to your patient list.

Create and Save Secondary Captures

MIMTD-617 • 16 Aug 2023

Overview

You can create secondary captures, which are similar to screenshots. Consider the following examples of when to use secondary captures:

- Save data to a PACS that does not support DICOM image processing. Secondary captures are saved as OT files that can be opened by basic DICOM viewers. They do not include voxel data.
- Capture a static view. A screencapture saves exactly what you are currently looking at, which can be helpful to refer back to later.
- Send an image to another provider. Instead of sending the entire series, you can send only the screencapture of what you want them to see.
- Add the image to a structured report. See Create and Modify Structured Reports for more information about adding secondary captures to reports.

Important: If further processing is needed, save the session or DICOM image data instead of a secondary capture. For more information, see Save Patient Data.

Related: Refer to Configure Default Settings for Faster Captures for information about automating captures and configuring default capture settings.

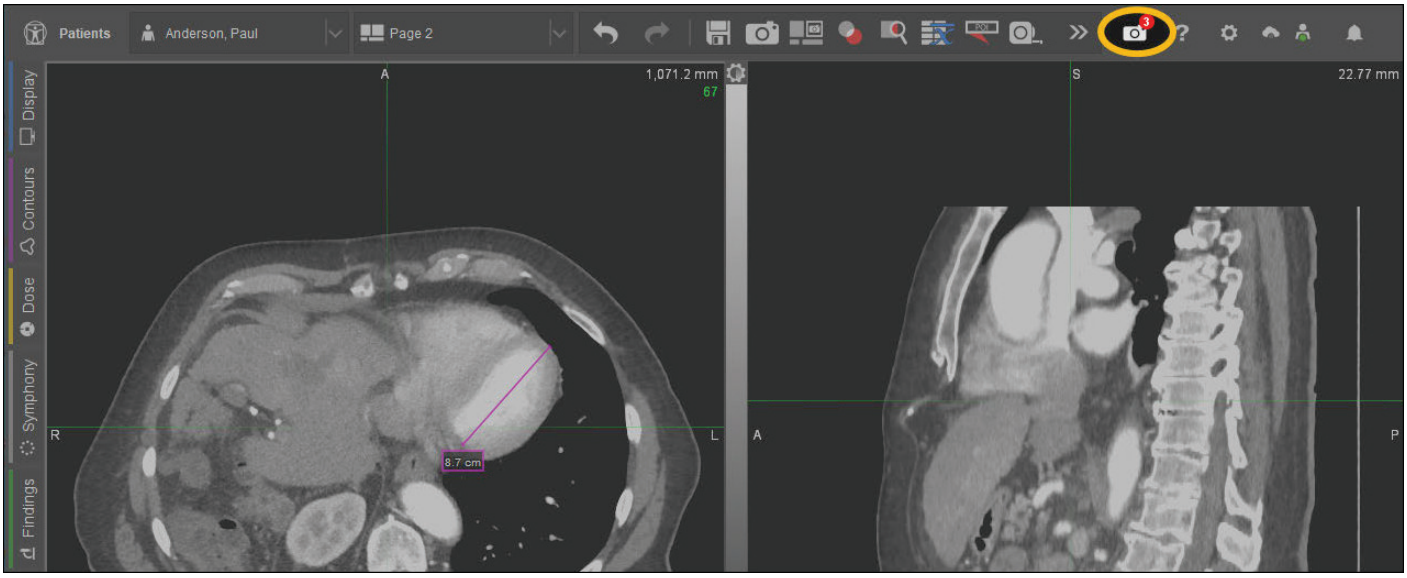
Contents

Create a Capture

You create a capture after opening a patient session and identifying what in the session that you want to capture. Then, you can use the **Capture Screen** tool on the top toolbar. Or, click the button on the right side of the toolbar to find any of the additional Capture Tools listed below.

Tip: Add the capture tools that you use most to your top toolbar or radial menu for easy access. See Access Tools: The Toolbar and the Radial Menu for details.

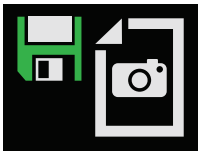
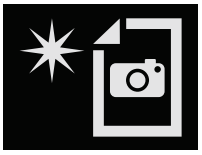
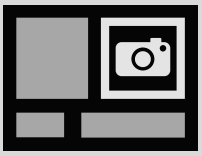
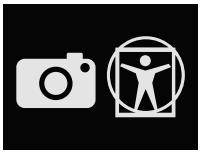
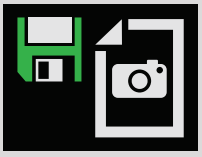
After creating the capture, click the **Capture Gallery** button on the right side of the screen to view captures from that session.

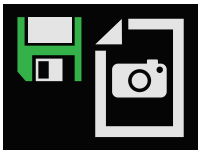


Tip: The number in red indicates how many captures have been taken and are in the gallery for the session.

Capture Tools

Capture Tool	What It Does	Scenario
	Capture Screen Takes a screenshot of the page you currently see. View the screenshot in the Capture Gallery.	Default tool. Save the image for your own future reference or to send to another system.

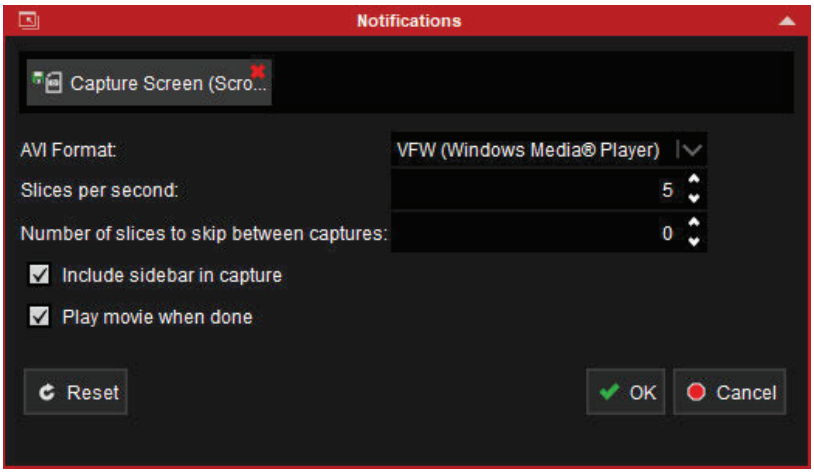
Capture Tool	What It Does	Scenario
	**Capture and Save Current Page** Takes a screenshot of the page you currently see. This tool skips the Capture Gallery and immediately saves the capture to the same patient list as the original data.	Consider making a keyboard shortcut for this tool so you can quickly take and save screenshots with a single key.
	**Capture Screen 1/2/3/4** Takes a screenshot of the specified page (e.g., page 1). View the screenshot in the Capture Gallery.	Quickly get a screenshot of a specific page, even if it is not the page you are currently looking at.
	**Capture All Pages** Takes a screenshot of each page in the session. View all of the screenshots in the Capture Gallery.	Quickly get a screenshot of every page.
	**Capture Viewport** Captures a single viewport that you select. View the capture in the Capture Gallery.	Get a screenshot of a single image on a page, instead of the entire page.
	**Capture Series** Captures all planes of the series that you select. View the capture in the Capture Gallery.	For example: The page shows PT and CT axial images. You select the PT series to capture. MIM creates a secondary capture that shows the PT axial, coronal, and sagittal planes.
	**Capture Screen (Scrolling)** Creates a movie file that captures the entire screen and shows auto-scrolling through a selected viewport. The file is saved outside of MIM. See Scrollable Captures below for more information.	Send this movie file to a third party so they can watch scrolling through multiple slices in the viewport.

Capture Tool	What It Does	Scenario
	**Save Page Captures for All Time Points** Capture a dynamic image including any statistics shown on screen. See Page Captures for All Time Points below for more information.	Capture a NM study and play or scroll through the frames.
	**Save DICOM Image Data: Fusion** *Fusions only; Secondary capture option* Saves a secondary capture of a fusion image. Users can scroll through slices in the saved image.	Save a fusion to a PACS as a secondary capture and be able to scroll through the fusion slices.

Scrollable Captures

Scrollable captures allow you to share and present dynamic views generated in MIM. Scrollable captures are saved as movie files playable by common media applications such as Windows Media® Player and QuickTime® Player.

1. In an active session, select the **Capture Screen (Scrolling)** tool from the top toolbar.
2. Select the viewport you wish to auto-scroll in the video. Only one view can auto-scroll in the saved video.
3. Select the **AVI Format**, **Slices per second**, and **Number of slices to skip between captures**. You can also choose whether to include the sidebar in the capture.

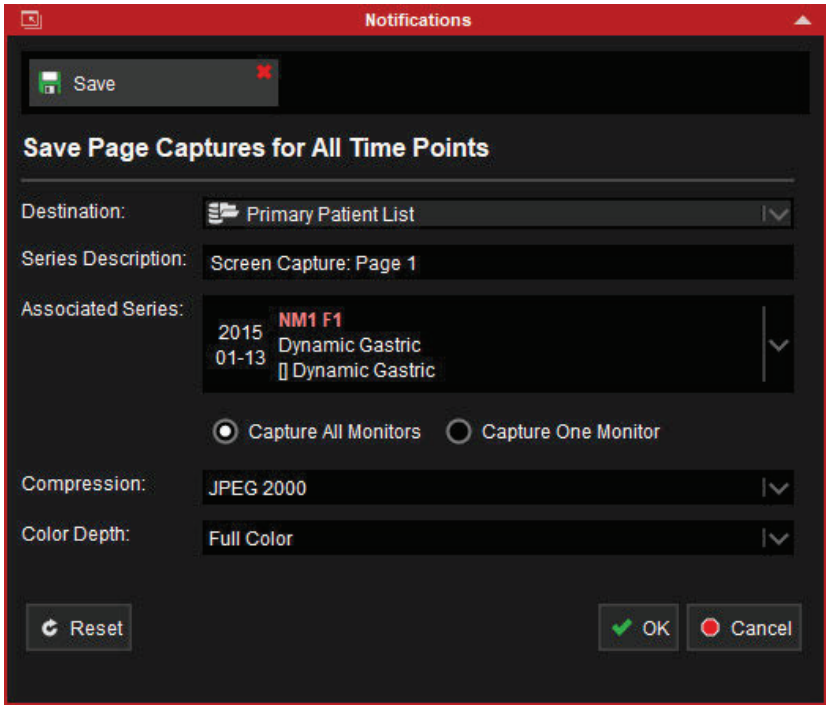


4. Click **OK**.
5. Choose the location on your workstation for the movie to save.
6. Click **Save**.

Page Captures for All Time Points

Use this tool to capture dynamic series with statistics. You can scroll through the image in a third-party system while seeing any graphs, tables, or other statistics alongside it.

1. In an active session with a dynamic series, select the **Save Page Captures for All Time Points** tool from the top toolbar.
2. Adjust the fields in the Notifications window as desired, and click **OK**.



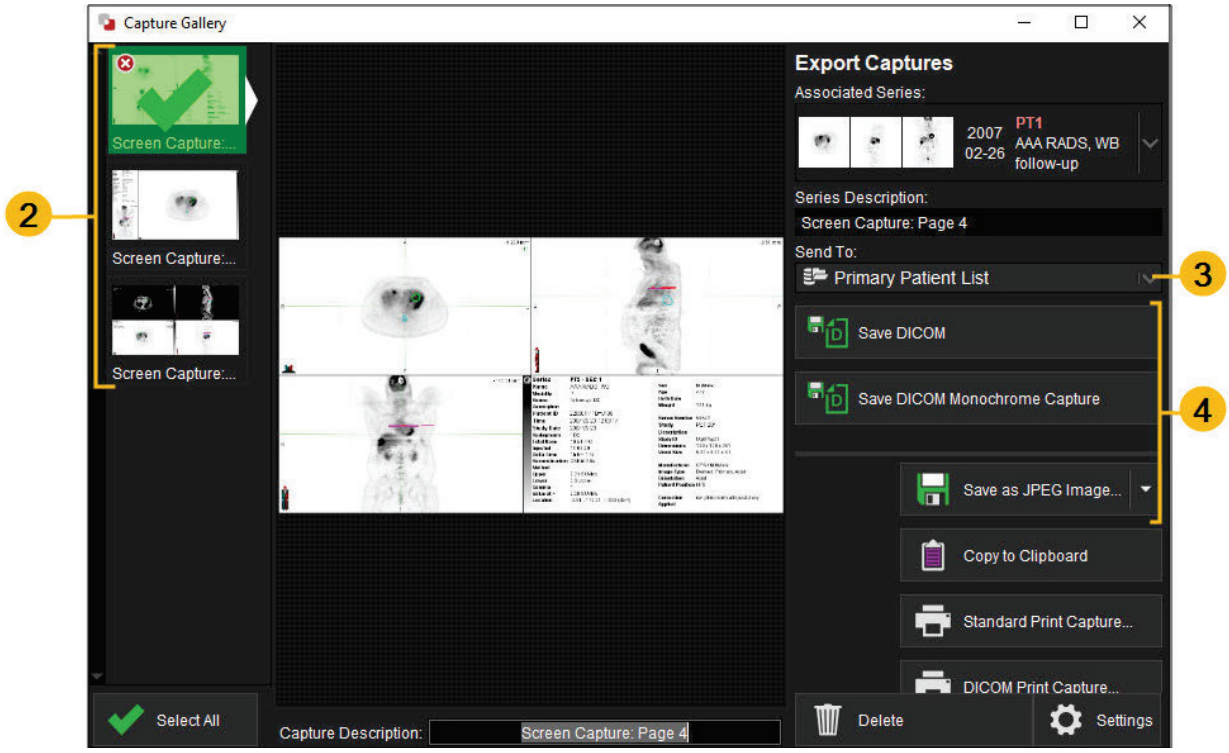
Save Secondary Captures

You can save secondary captures from the Capture Gallery.

1. Open the **Capture Gallery** from the upper-right corner of MIM.
2. On the left side of the Capture Gallery, select the captures that you want to save or click **Select All**.
3. On the right side of the Capture Gallery, select the Send To destination where you want to save the capture. You can select a MIM patient list, third-party DICOM location, CD, or folder.
4. Select the file type based on where you are saving:
    - **Save DICOM** — Save to MIM or to a third-party system that accepts DICOM.
    - **Save DICOM Monchrome Capture —** Save to a third-party system that accepts DICOM and allow the window/level to be adjusted after being sent to the other system.

- **Save as JPEG Image —** Save an image file to a folder or a location that does not support DICOM. Use the dropdown arrow to choose between file formats.

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



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

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

Configure Default Settings for Faster Captures

MIMTD-1672 • 10 Aug 2023

Overview

For fewer clicks and more efficient captures, you can configure the defaults below.

You might use secondary captures for a variety of reasons, such as to include in reports or send images to a third party. See Create and Save Secondary Captures for more information.

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

Contents

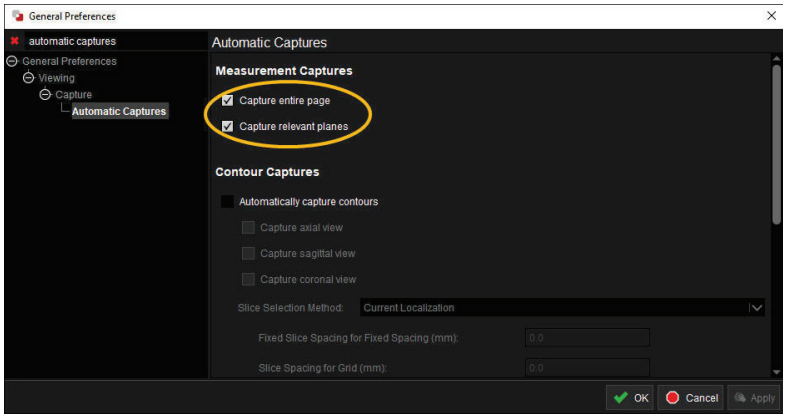
Enable Automatic Captures for Measurements and Contours

With automatic captures enabled, MIM creates and adds a capture to your Capture Gallery each time you make a measurement and/or contour.

1. Click the Settings button in the upper-right corner of MIM.
2. Select **General Preferences** and search for **"automatic captures"**. Select **Automatic Captures** on the left side.
3. Under **Measurement Captures**, choose what to capture:
   - **Capture entire page** — Capture the entire page with all viewports and info sidebars that are shown.

- **Capture relevant planes** — Capture only the plane that the measurement was taken in.

> **Tip:** Select both options for MIM to generate two captures for each measurement.

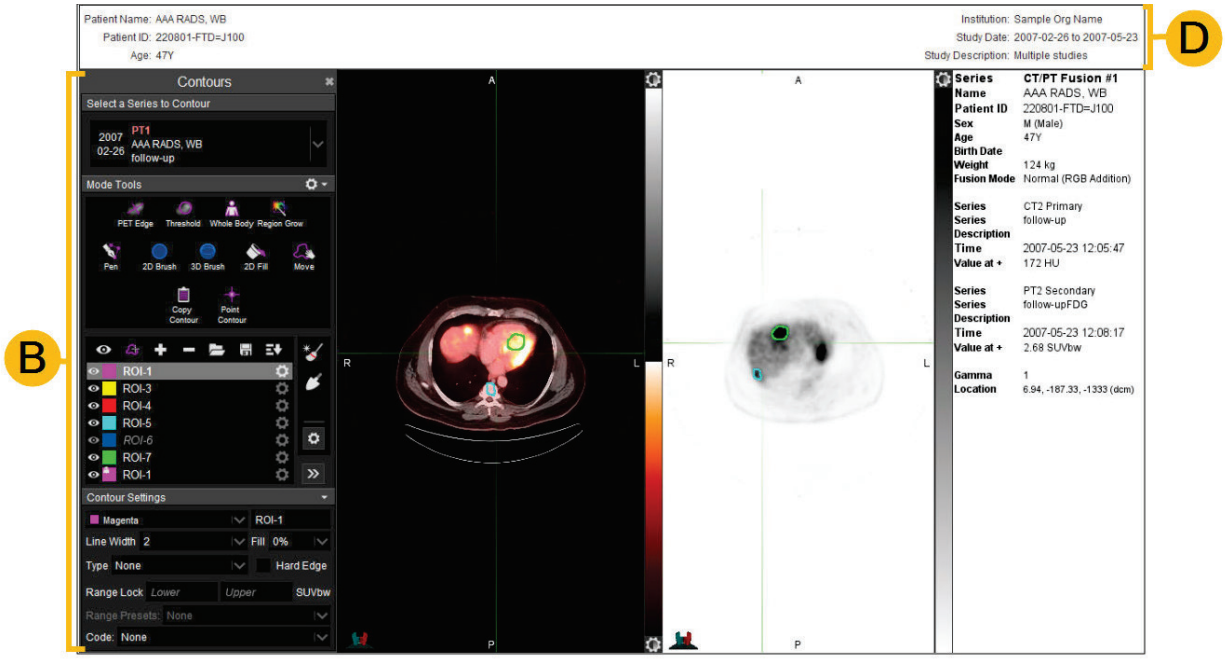


4. Under **Contour Captures**, select **Automatically capture contours**.
5. Select **Capture axial view**, **Capture sagittal view**, and/or **Capture coronal view** depending on which planes you would like captured.
6. Use the **Slice Selection Method** dropdown to select how contours are captured:
   - **Current Localization** — Capture the current localization point. With this method, users must remember to localize on the series before drawing.
   - **Fixed Spacing** — Create multiple, individual captures of the contour, at a fixed spacing, as configured in the **Fixed Slice Spacing for Fixed Spacing (mm)** preference.
   - **Grid View** — Create a single capture, containing a gridded view of the contour. The grid is determined by the **Slice Spacing for Grid (mm)** preference.
   - **Specific Fractions of the Contour** — Create multiple, individual captures of the contour based on the **Slices (List of Fractions)** preference. A capture is generated for each fraction. For example, if you enter .25, .50, and .75, three captures are created.
7. If desired, update the **Zoom Option**.
8. If desired, select **Hide other contours** if you want only the active contour visible in the capture.
9. Click **OK** to save the changes and close the window.

Configure Information Included in Captures

You can update the settings if you want to exclude patient information or change how patient information appears in captures.

1. Click the Settings button in the upper-right corner of MIM.
2. Go to General Preferences and search for "**capture**". Select **Capture** on the left side.
3. Evaluate the following options and update as desired:
   A. **Invert information colors** — Applies if the capture includes patient information or if a study information banner is included. Select this setting to for the text to appear black on a white background, as in the example below.
   B. **Include sidebar in capture** — Select this setting to include the sidebar in the capture.
   C. **Include patient information panel when capturing a viewport** — Applies only when using the Capture Viewport tool. Select this setting for the patient information to appear in the capture alongside the viewport. See far right column in the example below.
   D. **Include study information banner in page captures** — Select this setting to automatically append identifying information to the top of the capture. Your organization may want to use the **Institution Name Used for Study Information Banner** field to update what name appears.



4. Click **OK** to save the changes and close the window.

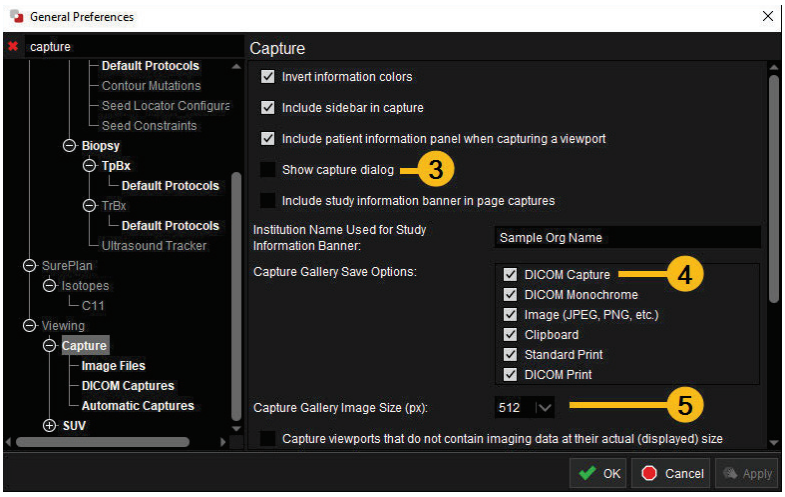
Determine Default Save Settings

Your organization can make it easier and faster for users to save secondary captures by configuring default save options.

Update the Capture Gallery

With most Capture Tools, the capture is sent to the Capture Gallery. Users open the Capture Gallery to see all of the captures from the session. They can choose which images to save, the format to use, and where to save them. Evaluate the following settings:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for **"capture"**. Select **Capture** on the left side.
3. Select **Show capture dialog** if you want the Capture Gallery window to always open as soon as a user takes a capture. If you do not select this option, users can open the Capture Gallery at any time by clicking the camera in the upper-right corner of the session.
4. Determine which **Capture Gallery Save Options** to show. You might want to deselect options that are not applicable for your organization.
5. Use the **Capture Gallery Image Size (px)** setting to determine how large the capture previews should appear in the Capture Gallery.

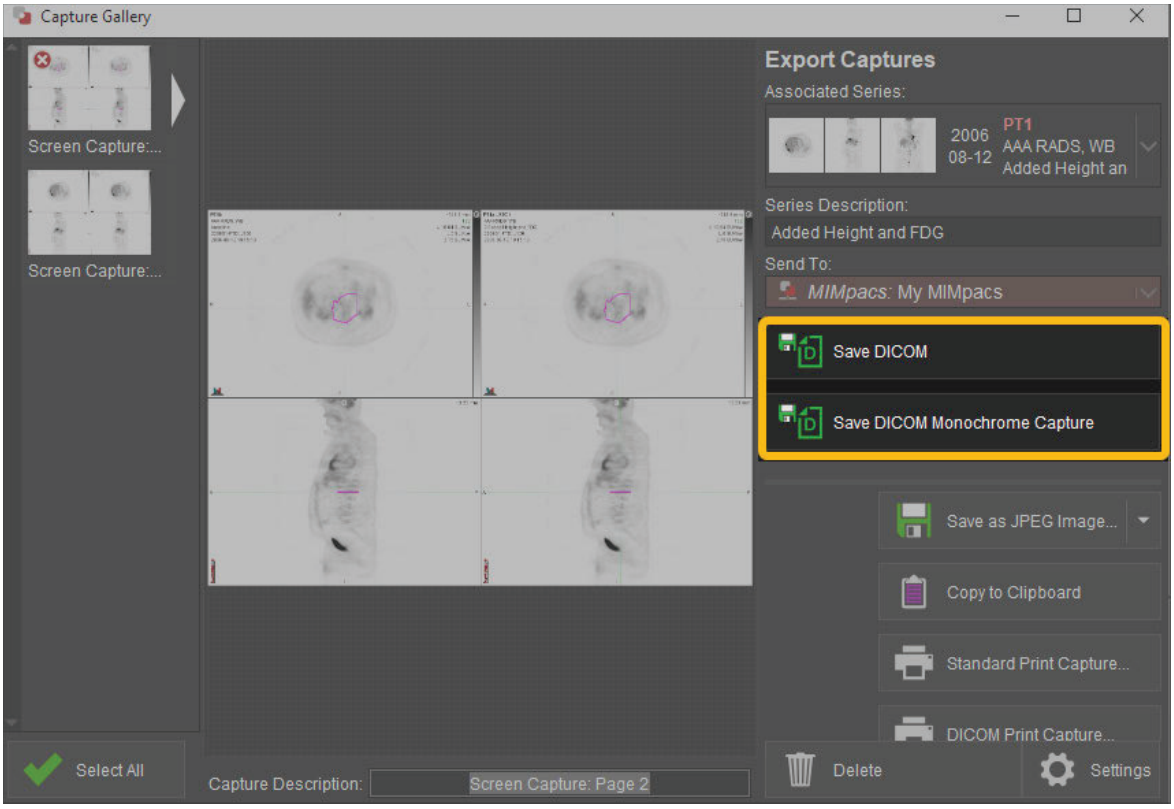


> **Tip:** If desired, you can also adjust the size of the actual capture image using the settings lower on this screen. These settings apply to all secondary capture images, including both captures saved as DICOM and as image files.

6. Click **OK** to save the changes and close the window.

Save As DICOM Captures

In most cases, users save secondary captures as DICOM (OT) files that they can send to PACS or other external systems.



Important: The options below apply only to saving DICOM captures. Other image files, such as JPEG or PNG files, are not affected.

To modify the default saving behavior for DICOM:

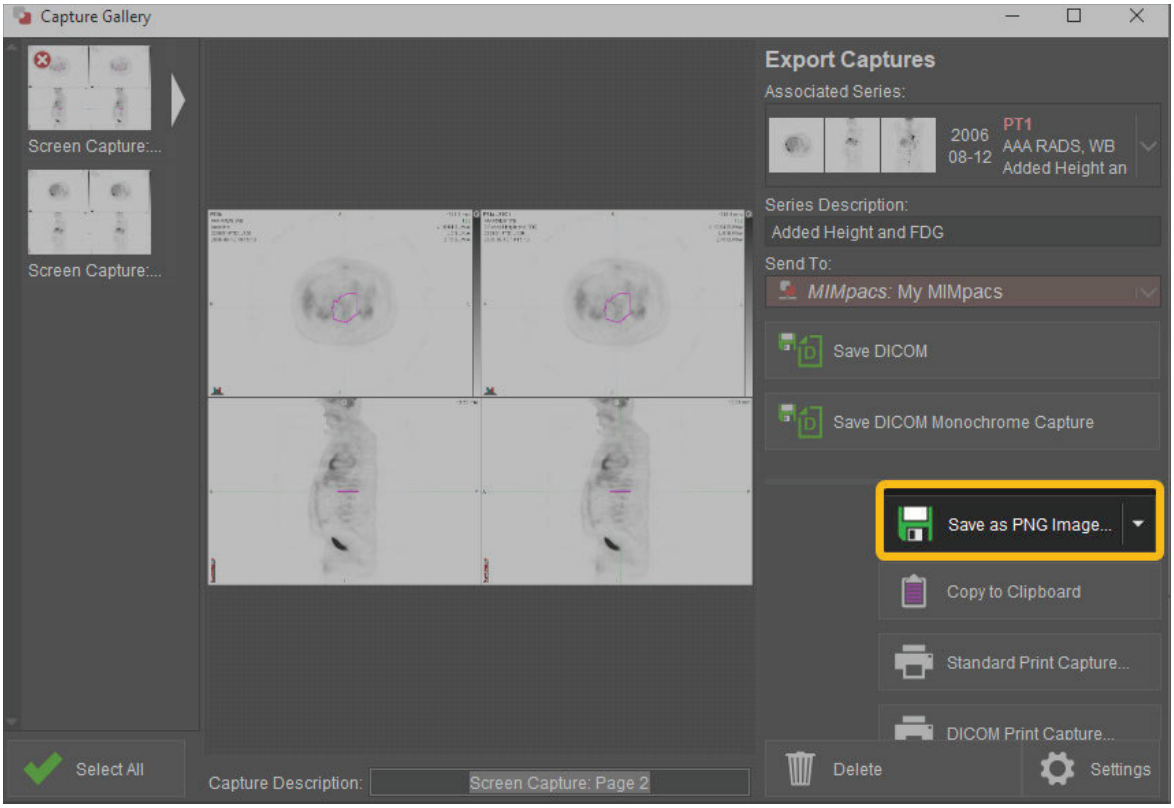
1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for **"DICOM captures"**. Select **DICOM Captures** on the left side.
3. Use the **Default Capture Destination** setting to determine where images should be saved to. Captures are typically saved to the patient list and later moved to a PACS or to MIMcloud as needed, but you could also configure captures to save to other destinations directly.

   Tip: The other settings on this screen are less common to update but are available when troubleshooting or for special situations.

4. Click **OK** to save the changes and close the window.

Save As Image Files

Secondary captures can be saved to a folder or drive outside of MIM. For example, you might want secondary captures to save as PNG files in a network storage folder.



Important: The options below apply only to saving image files, such as PNG or JPEG files. Saving DICOM captures is not affected.

To modify the default saving behavior for image files:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for **"image files"**. Select **Image Files** on the left side.
3. To always save files to a default location, select **Always use default location** and choose a **Default save location**. If you do not select this option, users are prompted to pick a save location when they click the Save as Image button.
4. Use the **DICOM secondary capture to Filetype** setting to determine which file type images should be saved as. The Save as Image button in the Capture Gallery updates accordingly with the file type that you choose.

5. Use the remaining settings on this screen to determine whether the capture files should be saved in subfolders and how the files should be named.
6. Click **OK** to save the changes and close the window.

Create and Modify Display Layouts

MIMTD-610 • 09 Nov 2023

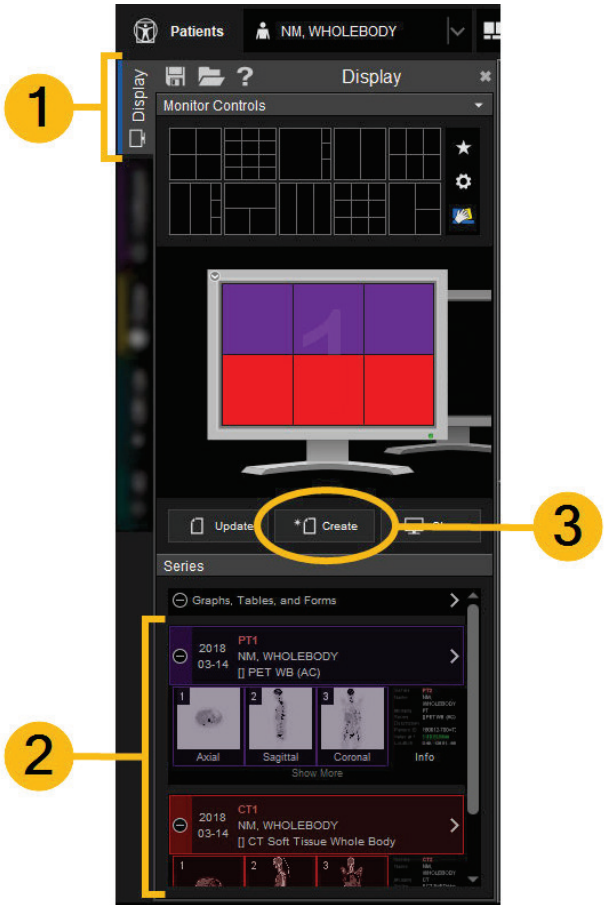
Overview

MIM® has numerous premade display layouts, also known as hanging protocols. You can also create, modify, and save your own display layouts. You can specify default display layouts to use with certain image types.

Tip: Saved display layouts can also be mapped into MIM Workflows™ so that the results are displayed exactly as you like. Please contact MIM Software Support at support.mimsoftware.com for assistance with this process.

Contents

Create a New Display Layout



Basic Steps

1. With images open in a session, click the **Display** tab to expand the Display sidebar.
2. Click the thumbnail of the series you want to add to your display, or drag and drop the thumbnail onto the preview monitor:
   - To add an entire row to the layout, click the title bar of the series.
   - To add only a single view to the layout (e.g., the axial view), click the thumbnail of that view.
   - You can add any number of series to the display layout.

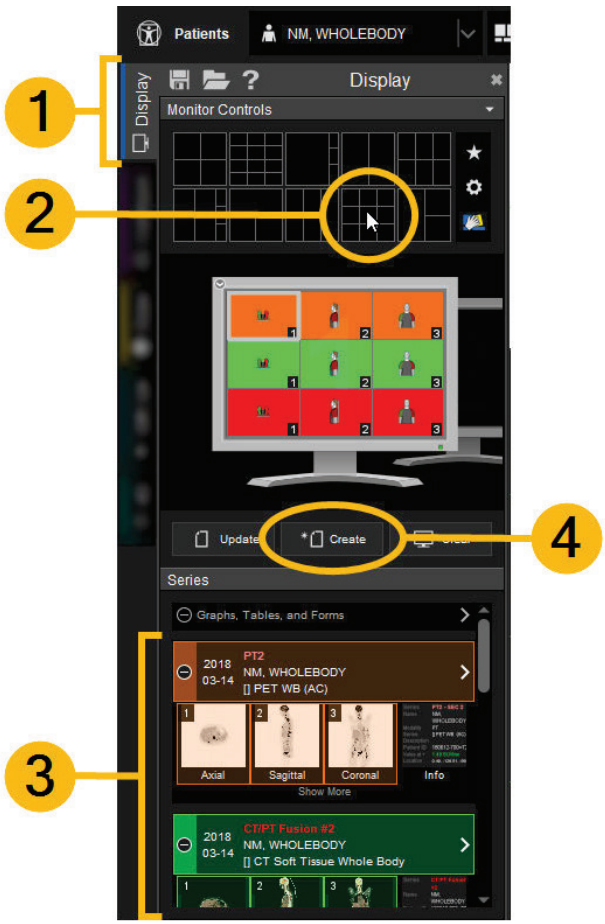
   The thumbnail is highlighted, and the corresponding color appears on the preview monitor to show where the series will be dispalyed.
3. Click the **Create** button below the preview monitor. A new page is created with the selected series.

Tip: If you don't see display layouts or the preview monitors, click **Monitor Controls** to expand the menu.

Additional Display Layout Options

- To see more data that can be added to your display, click **Show More** under the series thumbnails. Examples of available data include MIPs, DVHs, and dose constraint tables.
- If you use MIM on multiple monitors, multiple preview monitors appear in the Display sidebar. To add series to a display on a specific monitor, first click the corresponding preview monitor.
- To adjust the relative size of a particular series or view in your layout, hover over its thumbnail and use the scroll wheel of your mouse. The preview monitor updates accordingly.
- To replace your current display, rather than create a new display page, click **Update** instead of Create.

Use a Premade Display Layout



Basic Steps

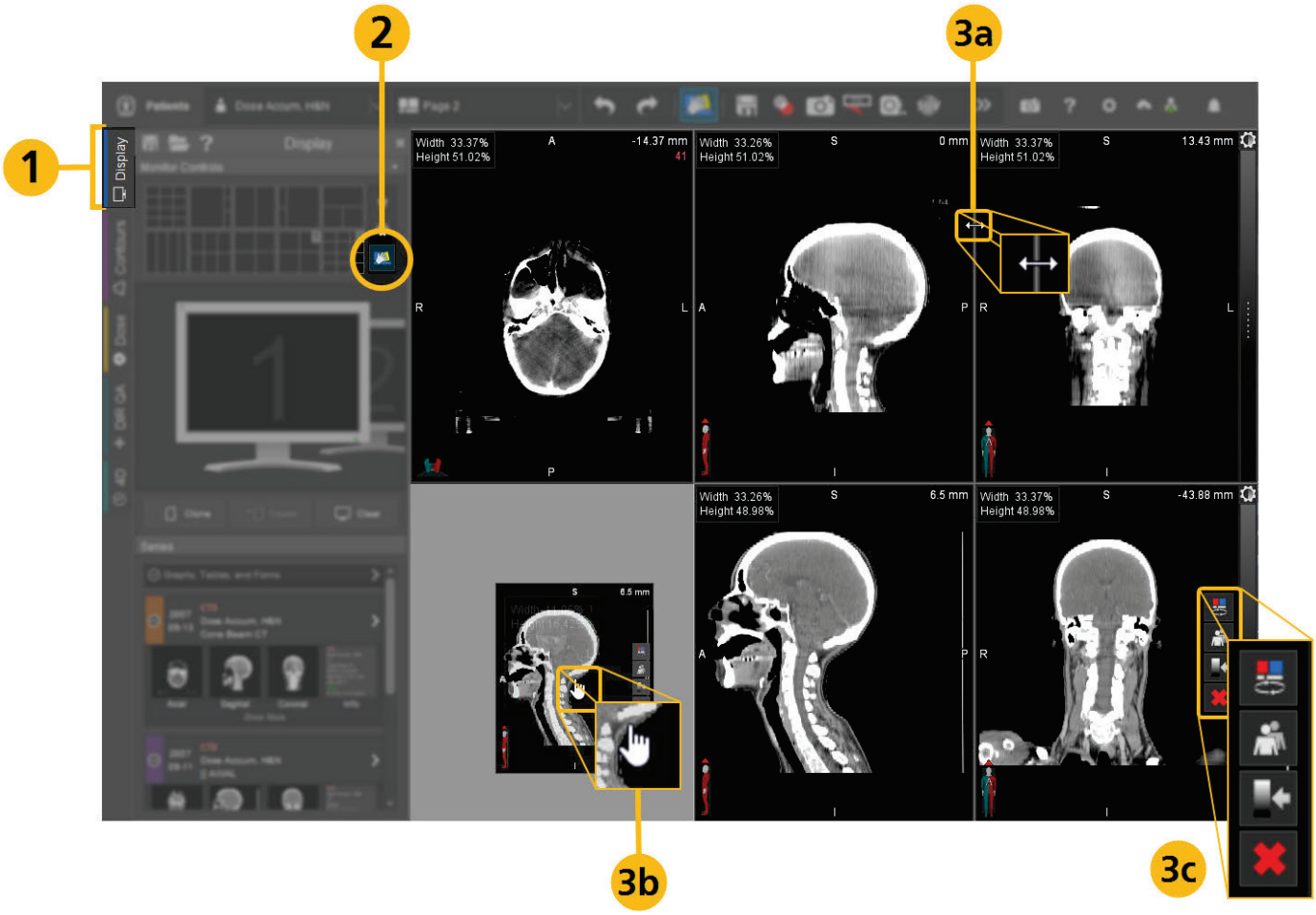
1. With images open in a session, click the **Display** tab to expand the Display sidebar.
2. Click a premade display layout at the top of the Display sidebar. The display layout appears on the preview monitor.
3. Click the thumbnail of the series you want to add to your display:
   - The display layout is filled from left to right beginning with the top row.
   - To add a series to the layout automatically, click the title bar of the series.
   - To add only a single view to the layout (e.g., the axial view), click the thumbnail of that view.

   The thumbnail is highlighted, and the corresponding color appears on the preview monitor to show where the series will be dispalyed.
4. Click the **Create** button below the preview monitor. A new page is created with the selected series and display layout.

Additional Tips for Working with Premade Display Layouts

- Multi-monitor display layouts are indicated by a small "1" in the upper-right corner. To add a multi-monitor display layout to all monitors at once, double-click the display layout.
- To view premade display layouts for a specific specialty (e.g., Radiation Oncology or Radiology), click the star ★ button near the top of the Display sidebar.
- To view all premade display layouts, click the gear icon ⚙ near the top of the Display sidebar. Use the plus ⊕ buttons and the minus ⊖ buttons to add and remove display layouts from the top of the Display sidebar.
- To replace your current display, rather than create a new display page, click **Update** instead of Create.

Adjust Your Current Display



1. With images open in a session, click the **Display** tab to expand the Display sidebar.
2. Click the **Adjust Protocol** tool near the top of the Display sidebar to activate the tool.
3. Use the following options to adjust the layout as desired:
    a. Left-click drag the borders of a viewport to resize the viewport.
    b. Left-click drag inside a viewport to rearrange or reposition the image.
    c. Hover in a viewport to see companion tools with more adjustment options. Hover over each button for more information.
4. Click the **Adjust Protocol** tool at the top of the Display sidebar to deactivate the tool.

Tip: If you don't see the **Adjust Protocol** tool, click **Monitor Controls** to expand the menu.

Save a Display Layout

1. Click the save button in the upper-left corner of the Display sidebar.
2. In the **Save Hanging Protocol** window, enter a Protocol Name and click **Save**. The rest of the information in the window is filled automatically.

To find all saved display layouts, click the gear button near the upper-right corner of the Display sidebar. For more information, see Use a Premade Display Layout.

Set Default Display Layouts

1. Click the Settings button in the upper-right corner of MIM.
2. Select **General Preferences**.
3. In the General Preferences window, search for "**Default Protocols**" and select **Default Protocols** from the left-side menu.
4. In the Default Protocols window, select a default 2D protocol and a default 3D protocol from the available options.

Swap Series in Display Layouts

MIMTD-1756 • 06 Nov 2023

Overview

Use the following tools to replace a series in your display layout with a different series from the current session. This is useful, for example, if you want to quickly view a prior exam without changing your display layout.

PT/CT

MIM 7.3 and later: Use the **Switch PT/CT Series** tool as described below.

MIM 7.2 and earlier: Use the tools in the All Modalities section.

Switch PT/CT Series — Replace a PT/CT from one time point with a PT/CT from a different time point. This tool is also known as "PET Swapping."

Tip: This tool appears only if you are viewing a display that doesn't include all of the available PT/CT time points from your session.

Follow these steps to use the tool:

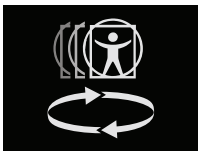
1. Hover in a viewport.
2. Click the **Switch PT/CT Series** button that appears at the top of the viewport.

3. Click the time point that you want to switch to. Your display updates to show the selected time point.

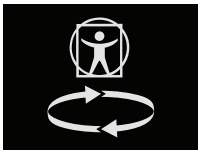
If you do not see the Switch PT/CT Series button at the top of your viewports, check the following:

- Ensure that you are viewing a display that does not include all of the available PT/CT time points from your session. If your display includes series from every time point, the Switch PT/CT Series button will not appear.
- Go to Settings >> **General Preferences** >> **Viewing** and ensure that **Show Switch PT/CT Series controls** is selected.

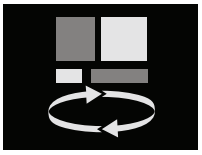
All Modalities



Swap Series — Replace a series or fusion group (i.e., the primary series of a fusion, the secondary series of a fusion, and the fusion itself) with another series or fusion group from the current session.



Swap Single Series — Replace a single series (i.e., an individual PT, CT, or fusion) with another single series from the current session.



Swap Viewports — Replace one view of one series with another view from the current session. For example, replace the axial view of one series with the axial view of another series.

Follow these steps to use **Swap Series**, **Swap Single Series**, or **Swap Viewports**:

1. Activate the desired tool from the toolbar, from the radial menu, or via keyboard shortcut:
   - To add the tools to your toolbar, click the double arrow button at the top of MIM, go to **Configure Toolbar...**, and click the checkbox next to the desired tools. For more information, see Access Tools: The Toolbar and the Radial Menu.
   - To add the tools to your radial menu, click the Settings button in the upper-right corner of MIM, go to **General Preferences** >> **Viewing** >> **Radial Menu**, and follow the instructions in the settings menu. For more information, see Access Tools: The Toolbar and the Radial Menu.
   - To add keyboard shortcuts for the tools, click the Settings button in the upper-right corner of MIM, go to **Keyboard Shortcuts**, and add a key binding next to the desired tools. For more information, see Set Keyboard Shortcuts.
2. If you activate the tool from the toolbar, follow the prompts to select the series, fusion group, or viewport that you want to replace.

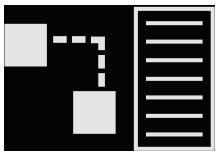
   Tip: If you activate the tool from the radial menu or via keyboard shortcut, the viewport that you are hovering in determines which series, fusion group, or viewport will be replaced.
3. In the Swap Series or Swap Viewport window that appears, click the series, fusion group, or viewport that you want to replace the selected item with. Your display layout now includes the selected series.

Adjust Links between Series Using the Link Manager

MIMTD-1277 • 12 Jan 2024

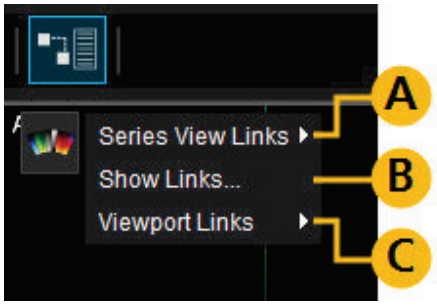
Overview

In MIM®, multiple series, or different views in the same series, can be linked.



Using the **Link Manager** tool, you can synchronize or desynchronize various display properties (e.g., localization, contrast) or behaviors (e.g., zooming, panning). Links can also be removed (or "broken") to separate series.

The Link Manager tool contains three options:



A. **Series View Links** — Adjust display properties (e.g., localization, contrast) for the series that you are hovered over.

B. **Show Links...** — Show spatial links for all series in the session.

C. **Viewport Links** — Adjust the zoom links for different views of the series that you are hovered over.

There is a distinction between "series" and "series views" in MIM.

- A "series" refers to a DICOM image series (e.g., CT, MR).
- A "series view" is a single, specific display of a series on screen. A series view includes display properties, such as the color table and contrast levels that are applied to a series for viewing.
- A single series can be displayed in multiple series views at the same time. The underlying DICOM data is the same, but display properties such as the color table may be different.
- When a new series view of an image is created, most display properties (e.g., localization) and behaviors (e.g., zooming, panning) are linked with other series views for that image.
- Some display properties can be linked between different series. For example, by default, fusions link localization between different series.
- When you remove a series view link for a particular series view, you are removing all links from that series view to every other series view in the session.

- MIM Workflows™ offer more advanced linking options, especially across groups of series.

  For assistance with your own workflows and linking, or if a default workflow is not providing the behavior you expect, please contact MIM Software Support at support.mimsoftware.com.

Contents

Link Manager Basics

Linking Use Cases

Series View Links: Scroll, Zoom, Pan, or Rotate a Series Independently

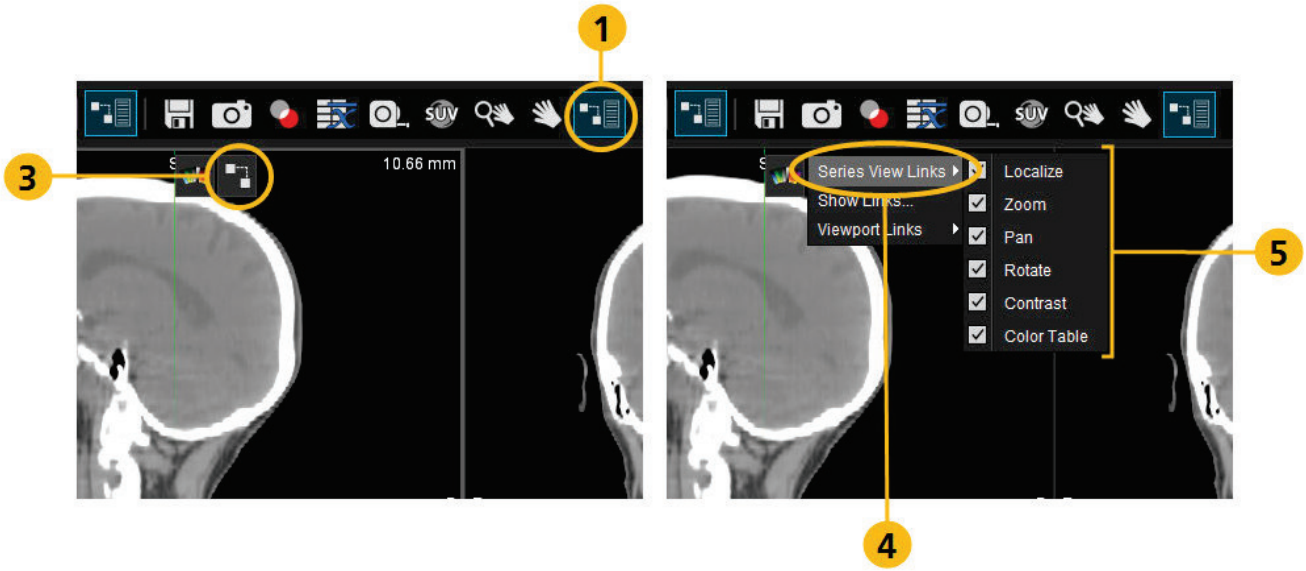
To scroll, zoom, pan, or rotate a series independently from all of the other series in the session, follow these steps:

1. Activate the **Link Manager** tool.

   Related: If you use this tool regularly, you can add it to your toolbar for easy access. For more information, see Access Tools: The Toolbar and the Radial Menu.

2. Hover over the series that you want to scroll, zoom, pan, or rotate independently. The Link Manager button appears in the center at the top of the viewport.
3. Click the **Link Manager** button in the viewport.

4. Hover over **Series View Links**.



5. Toggle any of the settings to enable or disable the links:
    - To scroll the series separately, deselect **Localize**.
    - To zoom the series separately, deselect **Zoom**.
    - To pan the series separately, deselect **Pan**.
    - To rotate the series separately, deselect **Rotate**.

Important: If the series is part of a fusion, the fusion continues to localize, zoom, pan, or rotate with the primary image.

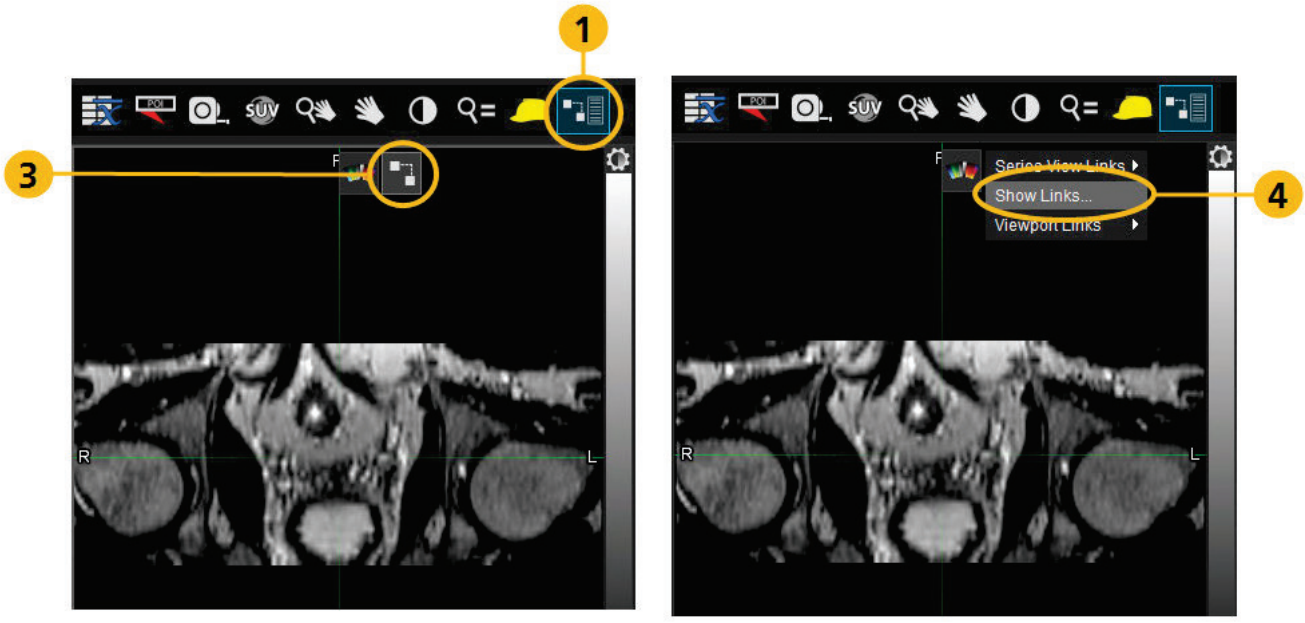
Show Links: Show the Spatial Links between Series

To see the links between all of the series in a session, follow these steps:

1. Activate the **Link Manager** tool.

Related: If you use this tool regularly, you can add it to your toolbar for easy access. For more information, see Access Tools: The Toolbar and the Radial Menu.

2. Hover over the series that you want to scroll, zoom, pan, or rotate independently. The Link Manager button appears in the center at the top of the viewport.
3. Click the **Link Manager** button in the viewport.

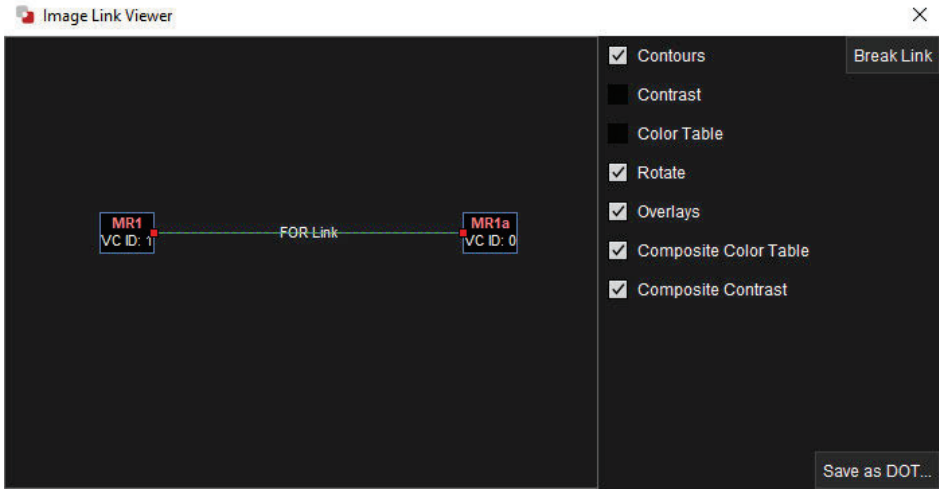


4. Click **Show Links...**. The Image Link Viewer window opens.

> **Tip:** You may need to reposition the series in the Image Link Viewer window to more easily visualize the links.

- The left side shows a graphic of the links between series.
- The right side shows features that can be toggled for each link.

- As desired, select a link from the left, and then toggle viewing parameters or features for that link on the right.



5. When finished, click the X to close the Image Link Viewer window.

Viewport Links: Adjust the Zoom for Different Views of a Single Series

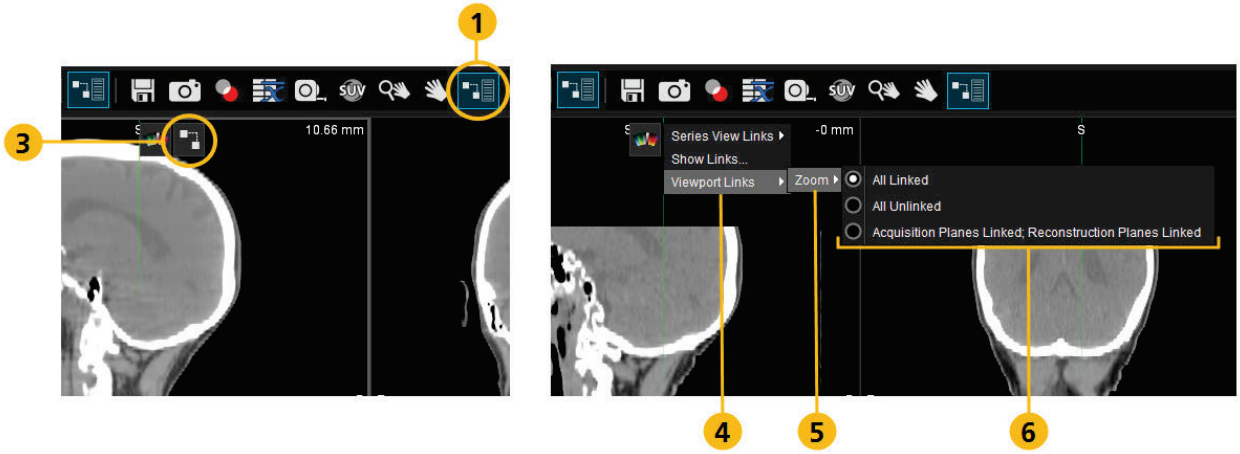
To adjust the zoom linking across series views (e.g., axial, sagittal, and coronal) for a single series, follow these steps:

1. Activate the **Link Manager** tool.

> **Related:** If you use this tool regularly, you can add it to your toolbar for easy access. For more information, see Access Tools: The Toolbar and the Radial Menu.

2. Hover over the series that you want to adjust the viewport zoom links for. The Link Manager button appears in the center at the top of the viewport.
3. Click the **Link Manager** button in the viewport.

4. Hover over **Viewport Links**.



5. Hover over **Zoom**.
6. Select the link behavior that you want:
    - **All Linked** — All viewports with the linked series zoom together.
    - **All Unlinked** — All viewports zoom independently.
    - **Acquisition Planes Linked; Reconstruction Planes Linked** — The acquisition plane zooms separately from any reconstruction planes. Reconstruction planes zoom together, but independently of the acquisition plane.

      For example: For an axially acquired CT, the axial plane zooms independently of the sagittal and coronal planes. The sagittal and coronal planes zoom together.

Quickly Unlink and Link Series across Time Points with the L Key

If you notice that the link between series across time points is not accurate, you can use the L key to quickly adjust the link. An example scenario is if the localization point between series are a few slices off.

To quickly unlink and link a series with the L key, follow these steps:

1. Hover over one of the linked series.
2. Press the L key to disable the links.
3. Scroll to localize to the correct point (i.e., scroll to the slice that matches the slice shown for the other time point).
4. Press the L key again to relink the series. This updates the link between time points, and the series now scroll together accurately.

Break Spatial Links between Series

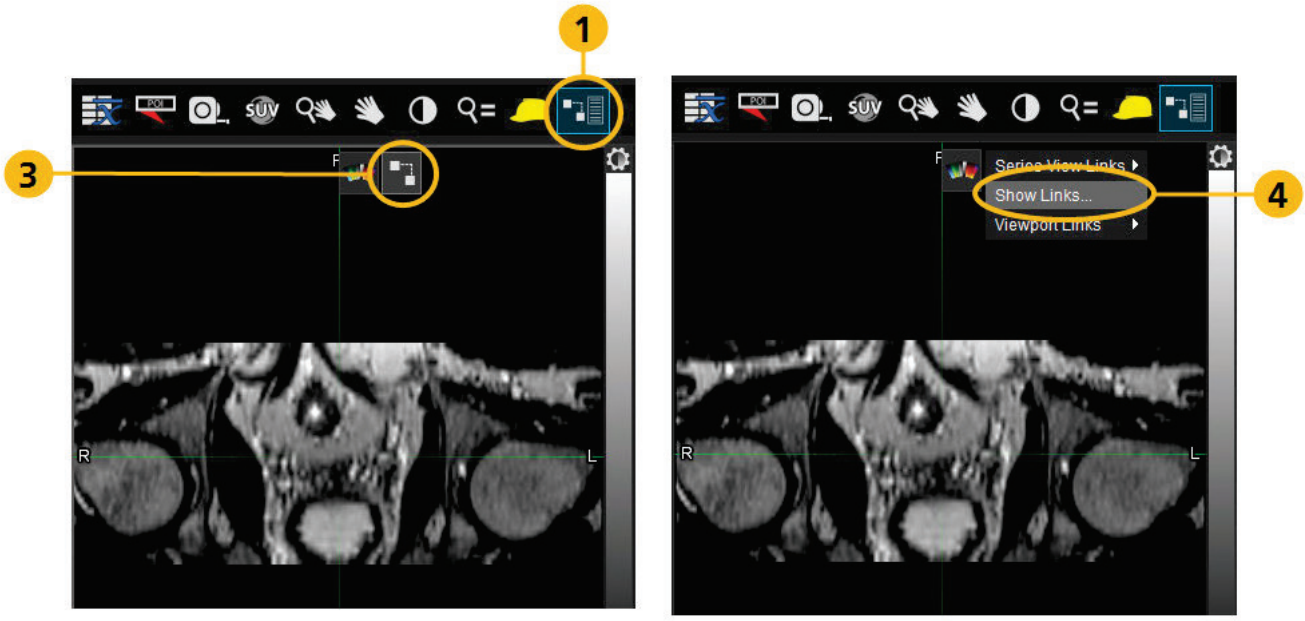
To break a spatial link between two series, follow these steps:

Tip: A spatial link refers to completely separate series (e.g., a PET and a CT) with a FOR or fusion link.

1. Activate the **Link Manager** tool.

Related: If you use this tool regularly, you can add it to your toolbar for easy access. For more information, see Access Tools: The Toolbar and the Radial Menu.

2. Hover over any series. The Link Manager button appears in the center at the top of the viewport.
3. Click the **Link Manager** button in the viewport.

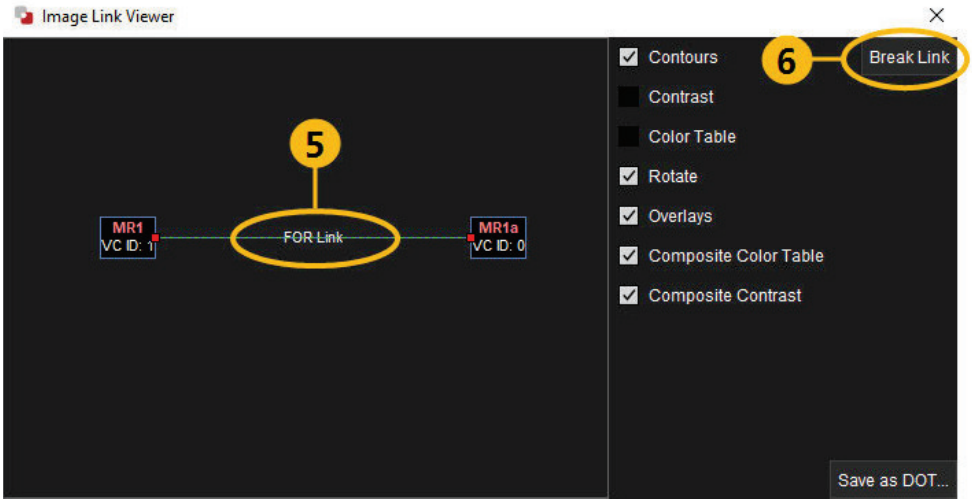


4. Click **Show Links...**. The Image Link Viewer window opens.

Tip: You may need to drag the series around in the window to more easily visualize the links.

5. Click the link (shown as a line) that you want to break.

6. Click **Break Link** in the upper-right corner of the window. If there are any fusions open that rely on the link, MIM prompts you to confirm that you want to close the fusions before proceeding.



7. When finished, click the X to close the Image Link Viewer window.

Break Spatial Links to Create Independent Fusions

If you have series that were acquired together (e.g., two MR sequences) and you fuse each MR to your plan CT, adjustments to one fusion (MR1/CT) affect the other fusion (MR2/CT). This is because the MR2/CT fusion preserves the pre-existing acquisition link between MR1 and MR2. You can break the pre-existing link so that adjustments to the MR1/CT fusion do not affect the MR2/CT fusion.

If you want to adjust the two fusions separately, follow these steps:

1. Break the link between the two MR series.

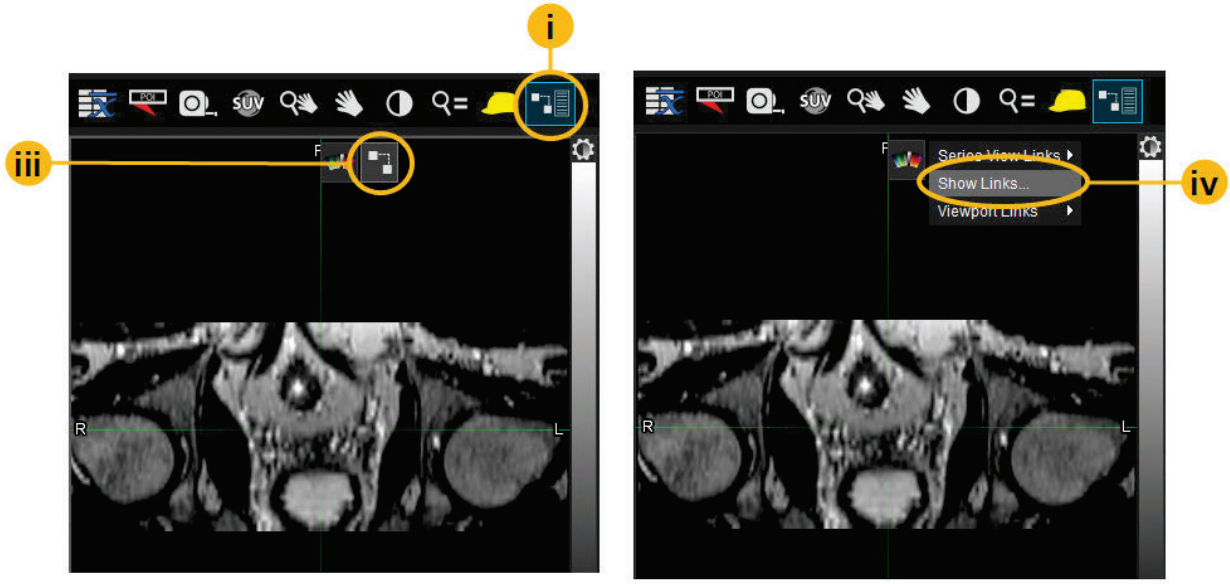
> **Tip:** Ensure you break the links between the MR series before fusing to the CT.

i. Activate the **Link Manager** tool.

> **Related:** If you use this tool regularly, you can add it to your toolbar for easy access. For more information, see Access Tools: The Toolbar and the Radial Menu.

ii. Hover over any series. The Link Manager button appears in the center at the top of the viewport.

iii. Click the **Link Manager** button in the viewport.

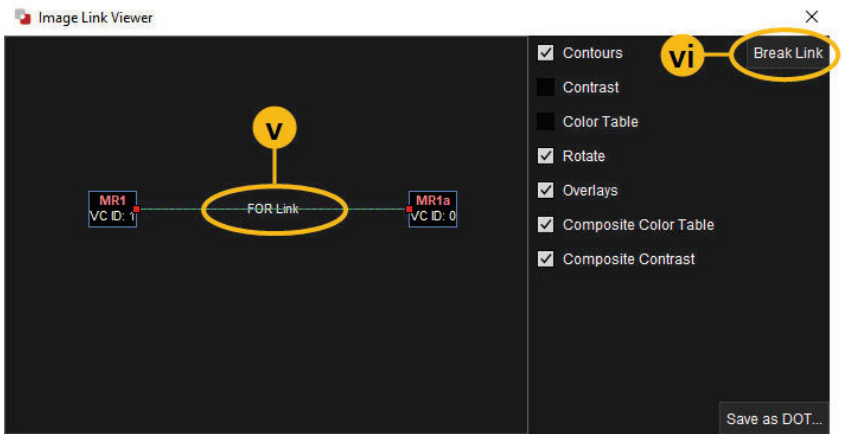


iv. Select **Show Links...**. The Image Link Viewer window opens.

> **Tip:** You may need to reposition the series in the Image Link Viewer window to more easily visualize the links.

v. Click the link (shown as a line) between the two MR series.

vi. Click **Break Link** in the upper-right corner of the window.



vii. When finished, click the X to close the Image Link Viewer window.

2. Fuse MR1 to the CT.
3. Fuse MR2 to the CT.

Related: For more information, see Create a Fusion Manually.

Create Multiple Fusions with the Same Series

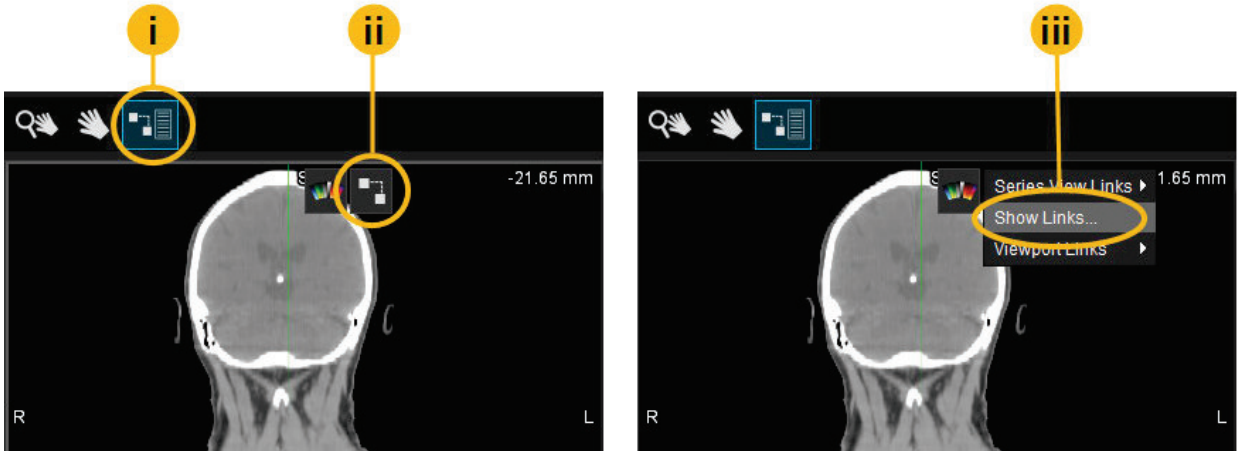
You can create multiple, but separate fusions. For example, you may want to visualize different fusions as part of the pre-planning process.

To create multiple separate fusions between the same two series, follow these steps:

1. Open the two series in a session (e.g., CT1 and CT2).
2. Return to the patient list, and double-click on the second series (the series that will be the secondary series in the fusion). A second copy of the series (CT2a) opens in the session.
   Alternatively, you can generate a second copy of the series using the Scale Image Intensity tool:
   i. Activate the **Scale Image Intensity** tool. (To find the tool, click the button at the top of MIM to search all tools.)
   ii. Select series CT2.
   iii. Enter 1 for the **Scale Factor** to create a copy of the series (CT2a).
3. Break the link between CT2 and CT2a.
   i. Activate the **Link Manager** tool.

Related: If you use this tool regularly, you can add it to your toolbar for easy access. For more information, see Access Tools: The Toolbar and the Radial Menu.

   ii. Click the **Link Manager** button in the viewport.

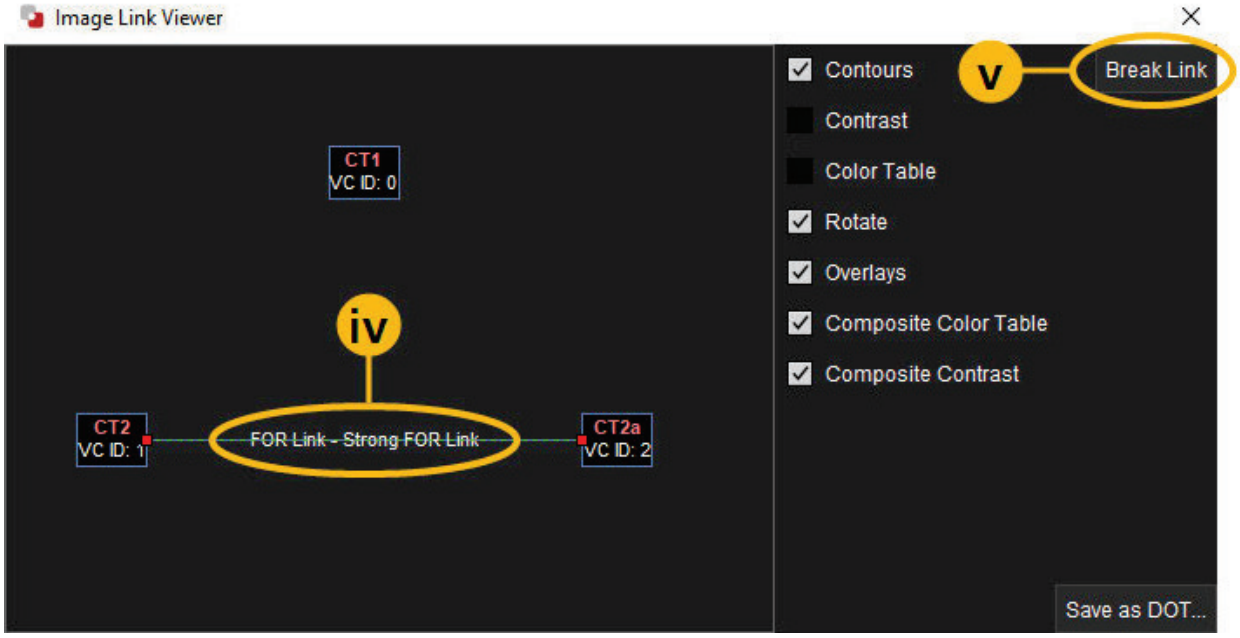


iii. Click **Show Links...**. The Image Link Viewer window opens.

> **Tip:** You may need to reposition the series in the Image Link Viewer window to more easily visualize the links.

iv. Click the **FOR Link - Strong FOR Link** between CT2 and CT2a in the Image Link Viewer window.

v. Click **Break Link** in the upper-right corner of the window.



vi. When finished, click the X to close the Image Link Viewer window.

4. Create and adjust the fusions.
   i. Fuse the primary and the secondary series (CT1 and CT2).
   ii. Create a second fusion between the primary and the copy of the secondary series (CT1 and CT2a).
   iii. Adjust the fusions as desired.

> **Related:** For more information see Create a Fusion Manually.

> **Related:** For more information, see Adjust Fusions.

Unlink Contrast between a PET Series and Fusion

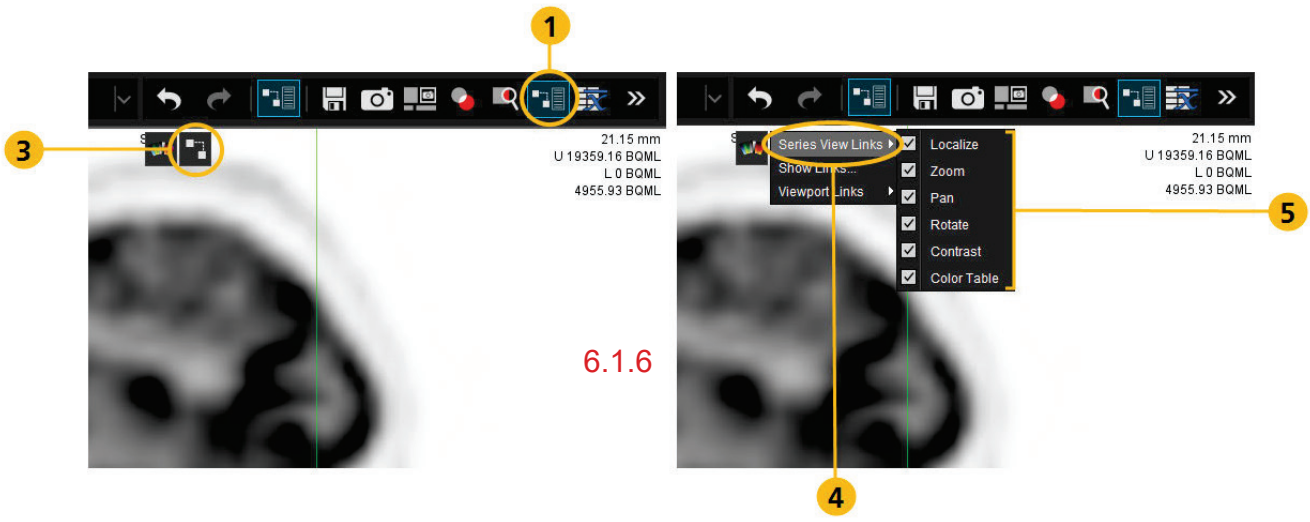
You can unlink the contrast between a PET series and the fusion formed from that PET series. This allows each view's contrast to update independently.

To unlink contrast between a PET series and the fusion, follow these steps:

1. Activate the **Link Manager** tool.

> **Related:** If you use this tool regularly, you can add it to your toolbar for easy access. For more information, see Access Tools: The Toolbar and the Radial Menu.

2. Hover over the PET series. The Link Manager button appears in the center at the top of the viewport.
3. Click the **Link Manager** button in the viewport.
4. Hover over **Series View Links**.



5. Deselect **Contrast**.

If you want to unlink contrast across time points, see Unlink Contrast between Two Time Points below.

> **Tip:** If you want the contrast between a secondary series (usually a PET) and its fusion to be disabled by default, go to Settings >> **General Preferences** >> **Imaging** >> **Fusion** and deselect **Link secondary series contrast by default**.

Tip: By default, contrast between different PET series is unlinked. If you want to link contrast between all series of the same modality in a session, go to Settings >> **General Preferences** >> **Viewing** >> **Contrast** and select **Link contrast across the same modality**.

Unlink Contrast between Two Time Points

You may have MIM sessions that contain multiple series and multiple links between those series (e.g., two separate time points, each with a PT/CT fusion, and a CT/CT fusion linking all the images). You may wish to adjust those links.

For example, you may want to adjust the CT/CT link that connects the two time points for the purpose of unlinking contrast across the time points.

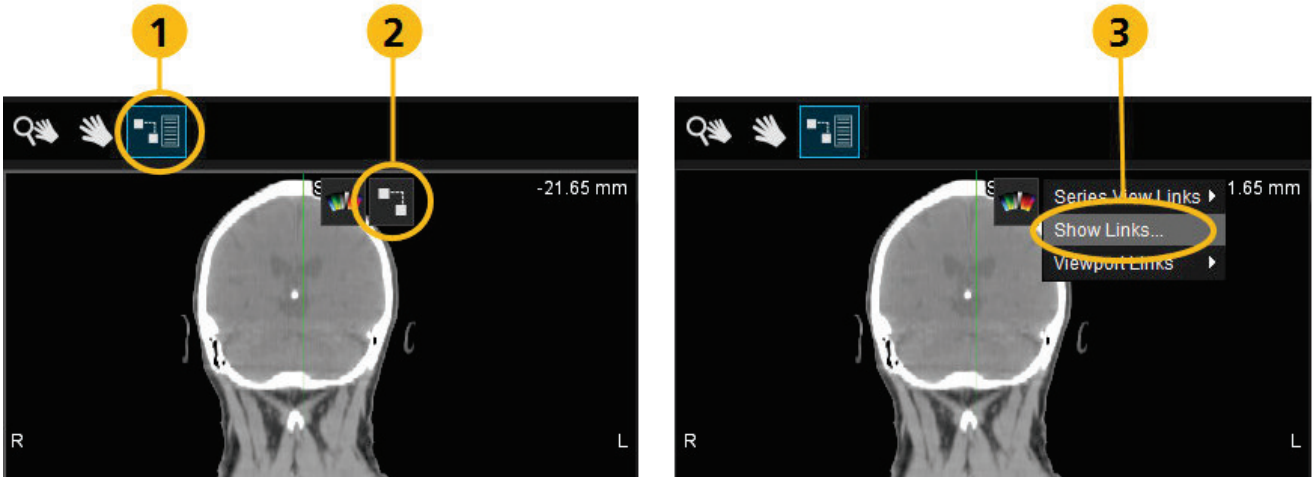
Tip: MIM Workflows can be used for this situation or to provide other advanced linking behavior between series and groups of series. For more information, please contact MIM Software Support at support.mimsoftware.com.

To disable the contrast link for the CT/CT fusion, follow these steps:

1. Activate the **Link Manager** tool.

Related: If you use this tool regularly, you can add it to your toolbar for easy access. For more information, see Access Tools: The Toolbar and the Radial Menu.

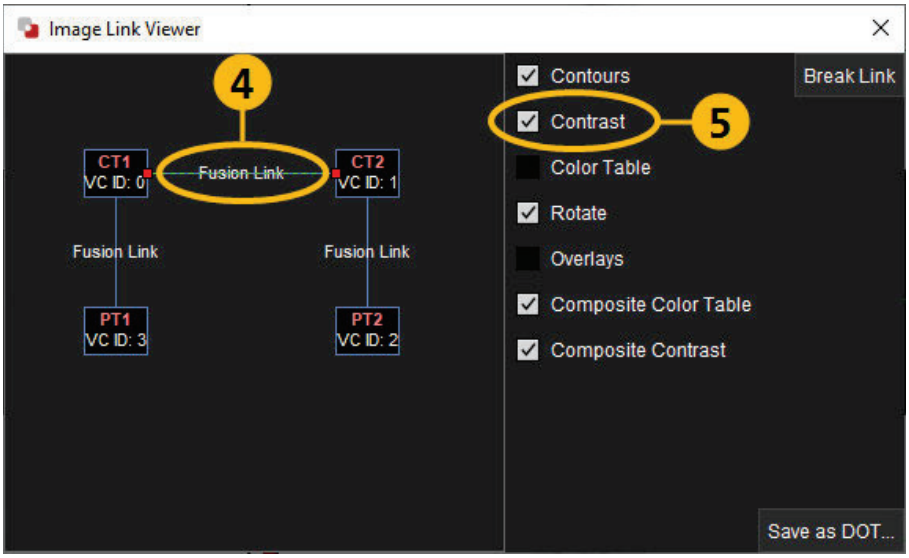
2. Click the **Link Manager** button in the viewport.



3. Click the **Show Links…** button. The Image Link Viewer window opens.

> **Tip:** You may need to reposition the series in the Image Link Viewer window to more easily visualize the links.

4. Click the **Fusion Link** between the two CTs.
5. Deselect **Contrast**.



6. When finished, click the X to close the Image Link Viewer window.

View and Adjust Slice Thickness

MIMTD-1285 • 28 Sep 2023

Overview

You can view the slice thickness for a series. If needed, you can update the slice thickness using one of the following options:

- Resampling — Save a new series with the specified resolution. This option changes the voxel size. For example, to make slices twice as thick, double the size of the Z voxels.
- Slabbing — View slices grouped together as slabs that you can scroll through more quickly. This option does not change the underlying DICOM data. It is a viewing mode that shows by default the maximum intensity projection from each of the slices. For example, slab four slices so that you can scroll through a 400-slice study in only 100 slices.

With either option, or with the original series, you can use the Grid tool to view multiple slices or slabs at a time.

Important: Downsampling (making slices thicker) and slabbing multiple slices together result in less detail because you are no longer viewing each acquired slice.

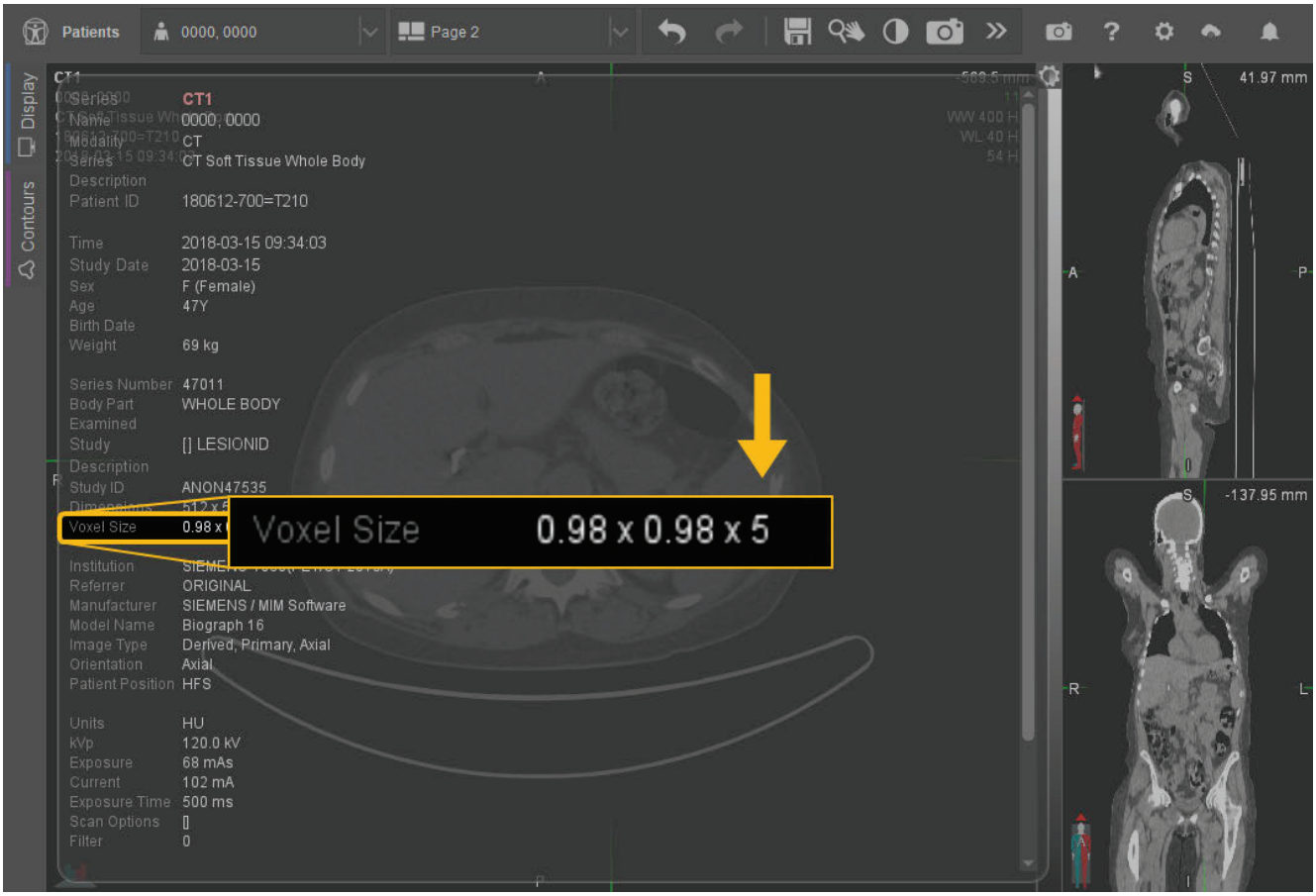
Related: Refer to Adjust Image Grids and Frames for Dynamic Series for similar options to adjust the frame duration for dynamic series.

Contents

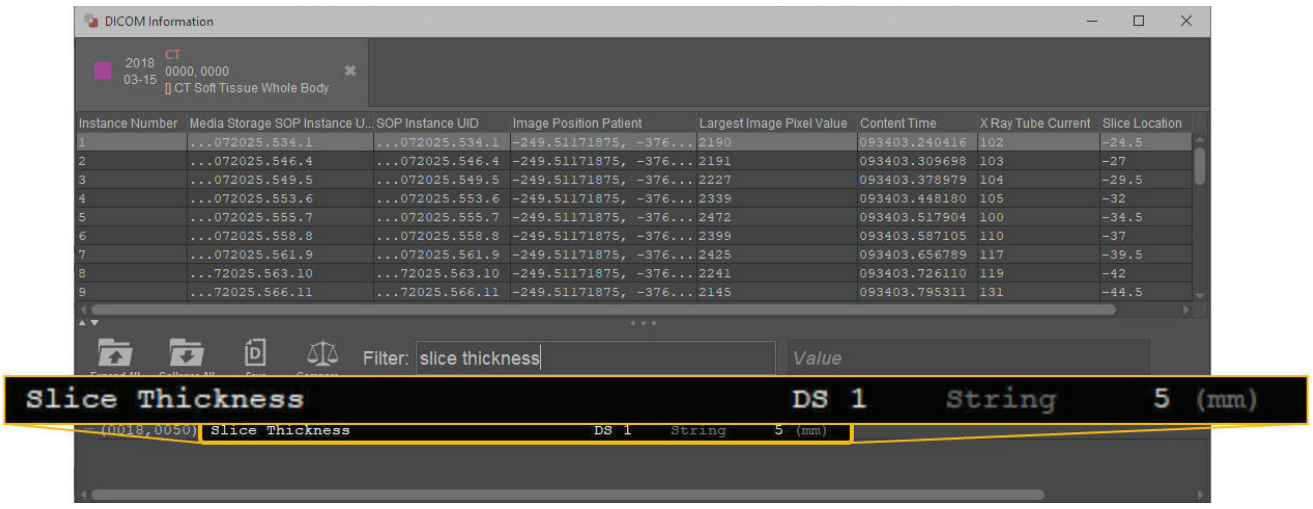
View Current Slice Thickness

You can view what the slice thickness is in two ways:

- Press the spacebar while hovering in any viewport. The Voxel Size Z dimension determines the slice thickness.



- View the series DICOM information from the patient list. Right-click on the series to select **Show DICOM Information...** and then search for the Slice Thickness DICOM tag.



If you see different dimensions when looking in both places for the same series, it is because the Voxel Size Z value indicated in the viewport is the actual distance when moving from slice to slice as measured by the Image Patient Position DICOM tag. The Slice Thickness DICOM tag is for a single slice in isolation and is not relevant for how MIM® assembles the data.

Adjust Slice Thickness by Resampling

Change slice thickness by updating the resolution of the Z voxel value.

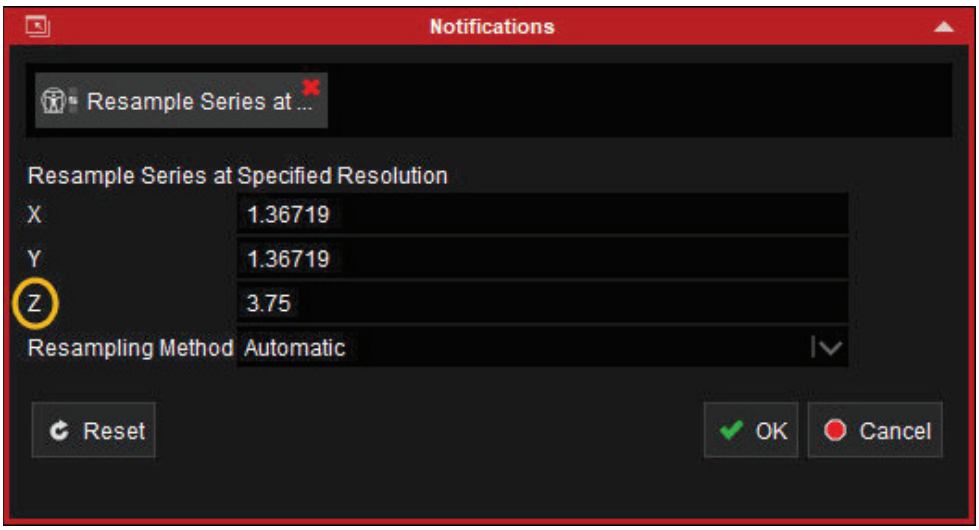
- Increasing slice thickness reduces image detail and standardizes the size of each voxel.
- Decreasing slice thickness interpolates between existing voxels to create additional voxels. It also standardizes the size of each voxel.

To use the resampling tool:

1. In an open session, activate the **Resample Series at Specified Resolution** tool from the top toolbar.

> **Tip:** If you don't see this tool, click the double arrow on the right side of the toolbar to search for it.

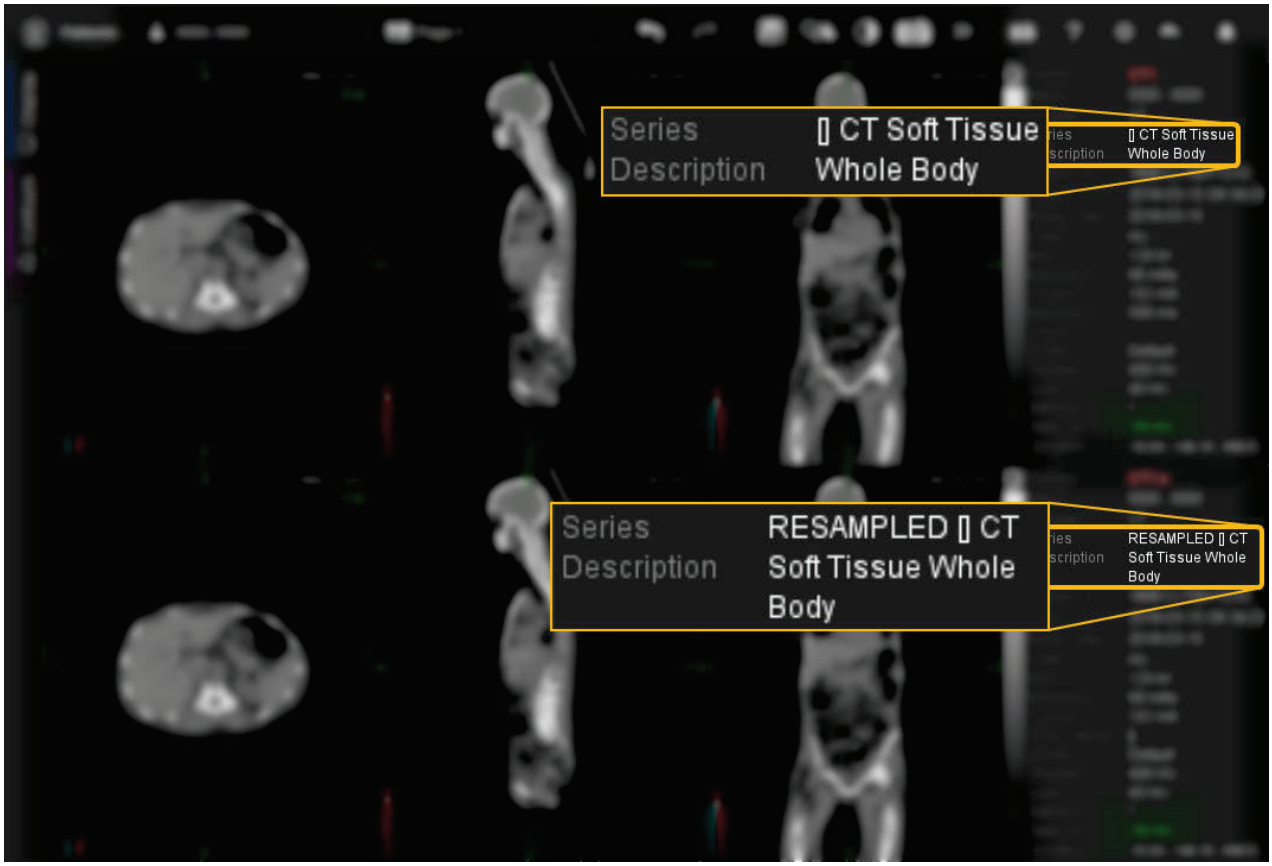
2. In the Notifications window, adjust the **Z** value to the desired slice thickness.



3. *MIM 7.3 and later*: Select the **Resampling Method**:
   - **Automatic** — If the data is non-volume normalized, the rebin data method is used. Otherwise, hierarchical is used.
   - **Linear** — Use linear interpolation to resample on a new voxel grid.
   - **Hierarchical** — Use multiple linear iterations for decreasing dimensions.
   - **Rebin Data** — Distribute the value of input voxels proportionally to overlap output voxels.

   MIM 7.2 and earlier: The linear method is used. The dropdown option is not available.
4. Click **OK**.

To prevent the loss of the original image, MIM creates a new resampled series, indicated by the text **RESAMPLED** in the series description.



The original series is on the top. The resampled series is on the bottom, indicated by RESAMPLED in the series description.

View Composite Slices by Slabbing

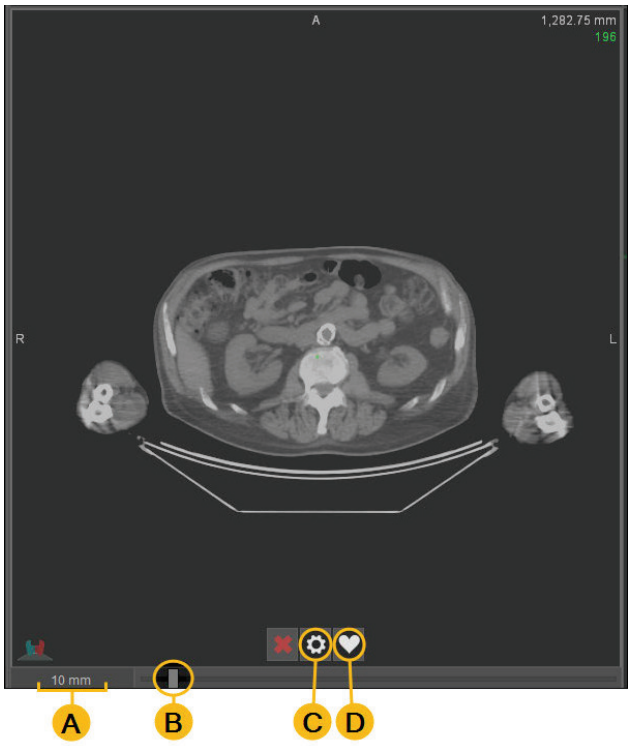
You can view multiple slices collapsed into a single slab. Keep in mind that this tool presents a viewing mode only and does not change the DICOM data.

1. In an open session, activate the **Show Planes/Frames as Slabs** tool from the top toolbar.

   Tip: If you don't see this tool, click the double arrow on the right side of the toolbar to search for it.

2. Select the desired viewport.

3. Use the slabbing options at the bottom of the viewport:



A. Type the exact thickness value to use.
B. Drag the slider left or right to adjust the slick thickness.
C. Select whether slices should be slabbed using the maximum, mean, or minimum intensity projection (IP).
D. Choose from your favorite slice thickness measurements. See below for more information about setting and deleting favorites.

6.1.1

4. Scroll through the series and make additional adjustments as needed.

> **Tip:** If you frequently use the same slabbing settings, you can set them as defaults. Go to Settings >> **General Preferences** and search for **"slab"**. Select **Slabbing** on the left side and update the settings.

5. When you are finished viewing the series slabs, click the close button to exit the slabbing tool and return to the original slice view.

> **Tip:** If you want to view the slabs in a grid, keep the slab view open. Then continue to the next section to use the Grid tool.

You can set favorites for the slab widths that you use the most:

- Click the heart button to view favorite slab thicknesses to choose from.
- To add a favorite, first set the slab using the slider bar or text field. Then, click the heart button and click **Add** at the bottom of the favorites list. The slab that you're adding is shown in parentheses.
- To delete a favorite, click the heart button and right-click on the slab thickness you wish to delete.

View Slices or Slabs on a Grid

You can view multiple slices or slabs on the same page using the Grid tool. Keep in mind that this tool presents a viewing mode only and does not change the DICOM data.

1. Activate the **Create Image Grid** tool from the top toolbar.

> **Tip:** If you don't see this tool, click the double arrow on the right side of the toolbar to search for it.

> **Related:** See Access Tools: The Toolbar and the Radial Menu if you want to add the Grid tool to the top toolbar or radial menu for easier access.

2. In the Notifications window, specify how many **Rows** and **Columns** to show in the layout.
3. Use the **Grid Spacing** slider or enter a value to determine the spacing between each slice or slab shown. For example, if you choose a spacing of 4, every fourth slice is shown in the grid.

Tip: The slice number is shown in the upper-right corner of the viewport. In the example above, you can see the slice numbers increasing by 4 because the grid shows every fourth slice.

4. Click **OK**.
5. When you are finished using the grid view, click the close button in the leftmost viewport to exit the grid view and return to the original slice or slab view.

Annotate Images

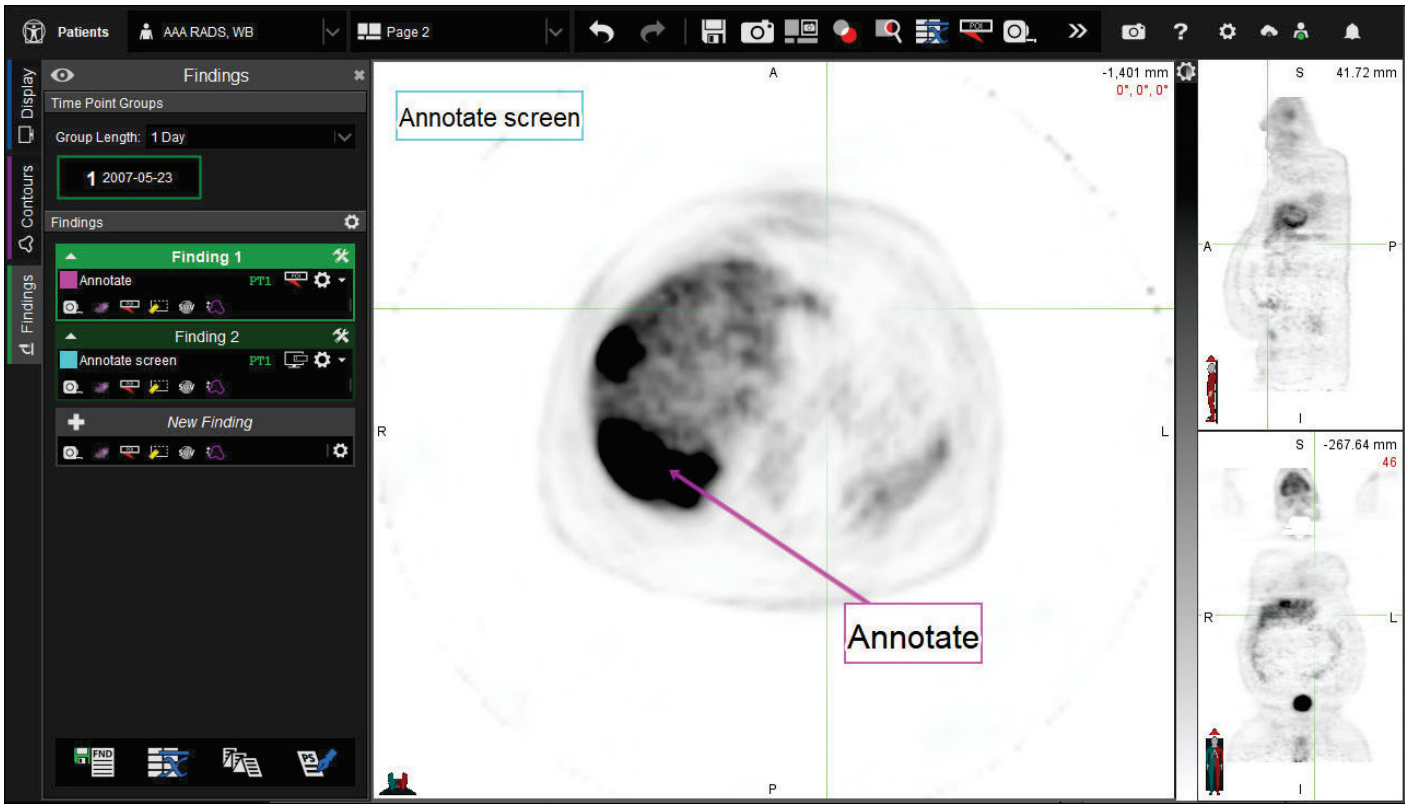
MIMTD-1674 • 18 Aug 2023

Overview

You can label or annotate an image to mark your findings and return to them later. MIM® has two annotation tools:

- **Annotate** — Mark a point of interest on a series. This annotation can be applied to a single slice or all slices in the series.
- **Annotate Screen** — Add an annotation text box to an area on screen. This annotation is like an on-screen sticky note and is not tied to the series slices.

With both tools, annotations that you create are shown in the Findings sidebar. Refer to Record Measurements Using the Findings Sidebar for more information about working with Findings.



The annotation made with the Annotate tool appears with an arrow in the pink box. The annotation made with the Annotate Screen tool appears in the blue box. Both annotations are in the Findings sidebar.

Contents

Create an Annotation

To create an annotation:

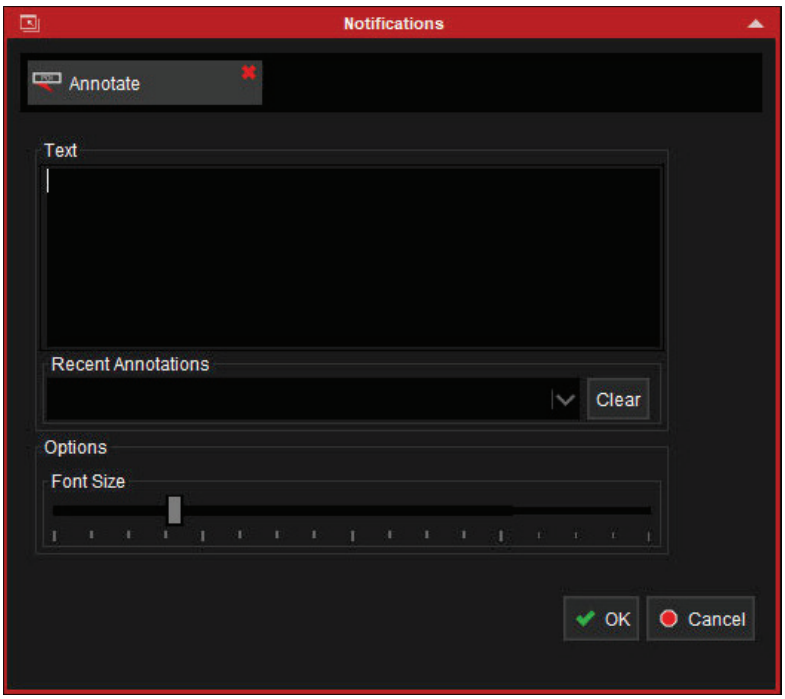
1. From the top toolbar, select the **Annotate** or **Annotate Screen** tool. Click the button on the right side of the toolbar to find the tool if you don't see it.

   Tip: Use the default keyboard shortcut N to quickly activate the Annotate tool.

   Tip: Add the annotation tool that you use most to your top toolbar or radial menu for easy access. See Access Tools: The Toolbar and the Radial Menu for details.

2. Click the area that you want to annotate.

3. In the Notifications window that opens, enter your text.



Tip: Click the question mark in the upper-right corner of MIM to view the tool help text with more information on how to use the tool.

4. Click **OK**.

Save Annotations

When you click save, the following options save annotations:

- **Save Findings...** and **Save Session...** — Use if you want to reopen and potentially edit the annotations in MIM.
- **Save DICOM RTstruct...** — Use if you want to include the annotations in the data sent to PACS or another third party.

Annotations are not included when saving DICOM image data. For more information on saving options, refer to Save Patient Data.

Configure Annotation Settings

Evaluate whether you want to update the following settings.

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

Copy Annotations to the Clipboard

By default, annotation text is not automatically copied to your clipboard. You might want to enable this setting so that, for example, you can more quickly paste the annotation text into a note in another system.

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for **"copy annotation"**. Select **Application** on the left side.
3. Select **Automatically copy annotation text to the clipboard** to enable this option.
4. Click **OK** to save the changes and close the window.

Show Annotations on Linked Series

By default, annotation text is not shown on linked series. If, for example, you have a PET/CT and want the annotation to appear on the PET, the CT, and the fusion, you can enable this setting.

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for **"suppress annotations"**. Select **Info Display** on the left side.
3. Deselect **Suppress annotations on linked series** to enable showing annotations on series that are linked to the series where the annotation was created.
4. Click **OK** to save the changes and close the window.

Create Volumetric Renderings

MIMTD-1161 • 04 Oct 2023

Overview

You can view a 3D rendering of a series in MIM®. 6.1.1

> **Related:** Go to Create Contour and Dose Surface Views for more information about 3D renderings of contours and doses.

Contents

Prerequisites

3D rendering uses the graphics card installed on your physical client workstation (thick client). By default, MIM enables 3D rendering. In most cases, you can view 3D series with no additional setup. If you are using MIM via Citrix® (thin client), ask your IT department to add GPU.

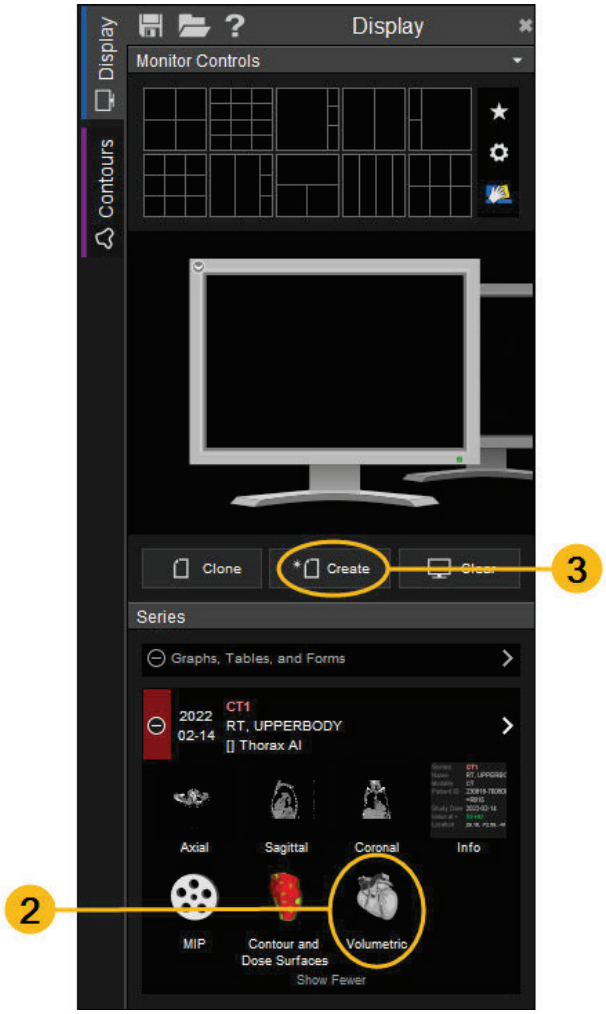
To check your GPU in MIM, go to Settings >> **General Preferences** >> **3D Preferences** and click **Check Hardware Compatibility...**.

> **Important**: Even if the test is successful, the speed and smoothness of render cannot be guaranteed.

See Troubleshoot the Rendering below for more information about working with your GPU.

Create a Volumetric Rendering

To create a volumetric rendering, open the series and adjust the display:



1. On the Display sidebar, click **Show More** below the series.
2. Select the **Volumetric** option and, if desired, additional planes that you want to show on the same page.
3. Click **Create**.

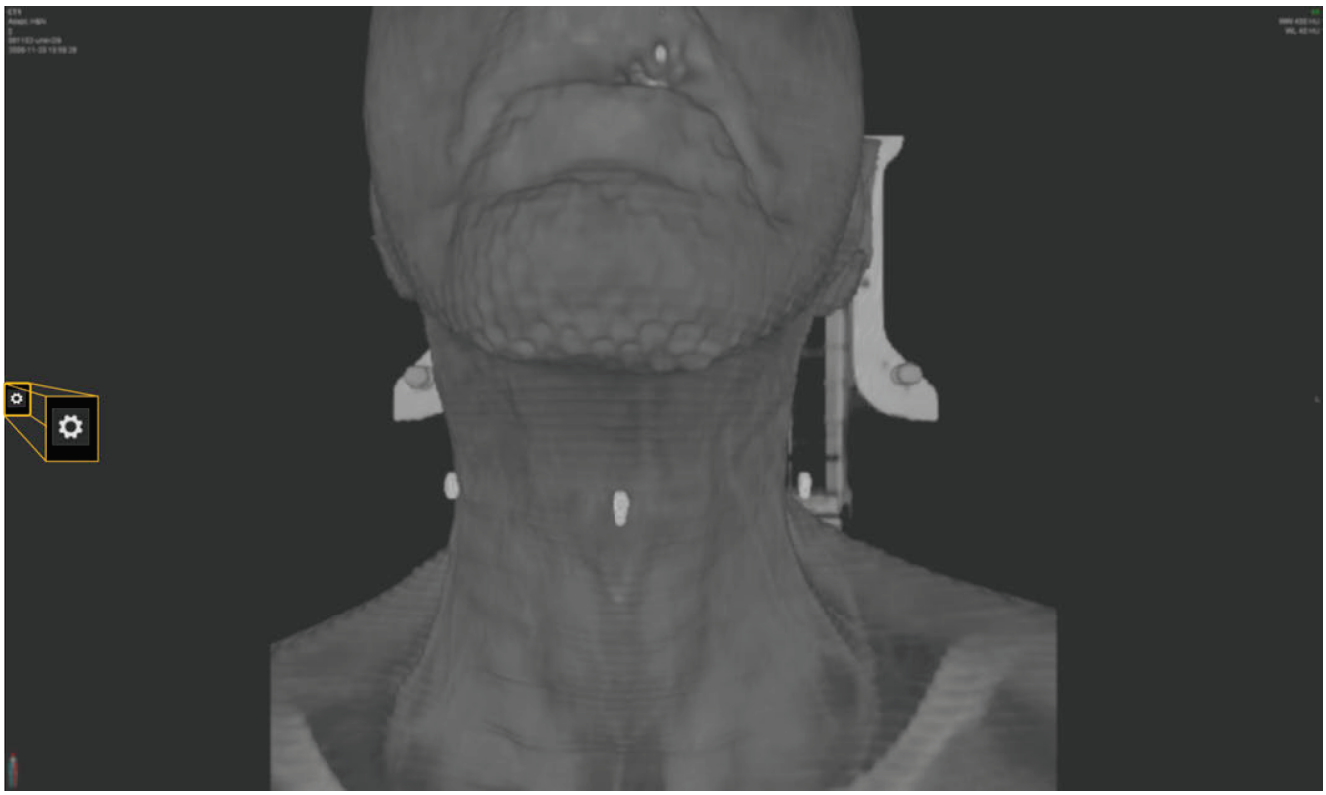
   A new page opens with the volumetric display.

Adjust a Volumetric Rendering

Left-click drag within the volumetric display to rotate and change the angle of the image.

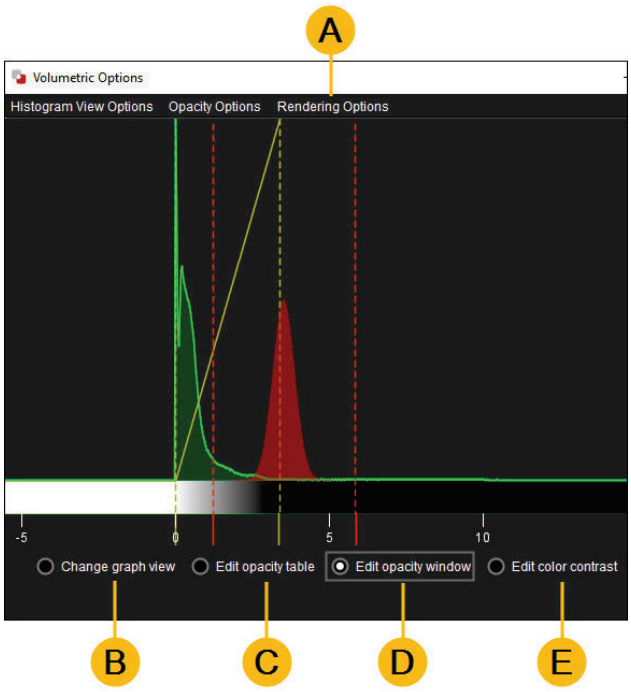
To further adjust a volumetric rendering:

1. Hover over the volumetric rendering and click the gear on the left side of the viewport.



6.1.1

2. In the Volumetric Options window that opens, adjust the rendering as needed:



A. **Rendering Options** — Change the angle of the display and use the Slice Plane to show a cross-slice in the 3D rendering.

B. **Change graph view** — Adjust the viewing range by left-click dragging the entire graph left or right. The Histogram View Options menu has similar functions.

C. **Edit opacity table** — Manually edit the opacity of the rendering. To add visible voxels, left-click drag the red region of the histogram. To remove visible voxels, right-click drag. Additionally, you can use presets from the Opacity Options menu.

D. **Edit opacity window** — (Red dotted line) Change which opacities are mapped to the voxels. 0% makes the voxels invisible, and 100% makes the voxels fully opaque. The red determines which voxels are going to be visible. To adjust the opacity window:

   - Left-click drag left or right to adjust the placement of the opacity window on the histogram.
   - Left-click drag up or down to increase or decrease the size of the opacity window.

E. **Edit color contrast** — (Yellow dotted line) Adjust the image contrast and change the colors of the voxels in the image. Any adjustments are linked to the Contrast tool. To adjust the contrast, left-click drag in any direction.

3. Click the x in upper-right corner to close the Volumetric Options window.

Troubleshoot the Rendering

To check your GPU in MIM, go to Settings >> **General Preferences** >> **3D Preferences**.

- If you are using MIM via Citrix (thin client), IT needs to add GPU. Virtual machines may require licensing for a virtual Nvidia GPU.
- A Nvidia Quadro® or GeForce® Series GPU is recommended for Windows machines.

- If there are no appropriate hardware devices available on the machine, or if MIM's OpenCL probe has failed, the **Hardware Rendering Device** preference shows "No Devices Found."
- If you want to use multiple devices:
  - Select **Use multiple devices when possible**.
  - Select the **Rendering Devices** to use.
- If you would like surface renderings to appear smoother, decrease the **Z Resolution** value.

Important: More interpolated 3D renderings are smoother, but less accurate to the contouring data.

If 3D rendering is not working, please contact MIM Software Support at support.mimsoftware.com for assistance adjusting advanced preferences.

Create Contour and Dose Surface Views

MIMTD-1715 • 29 Sep 2023

Overview

You can create 3D renderings of contours and dose surfaces in MIM.

You can also color the contour surface by dose to help you see the contour and dose information at the same time.

Related: Go to Create Volumetric Renderings for more information about 3D renderings of series (images).

Contents

Prerequisites

3D rendering uses the graphics card installed on your physical client workstation (thick client). By default, MIM enables 3D rendering. In most cases, you can view 3D series with no additional setup. If you are using MIM via Citrix® (thin client), ask your IT department to add GPU.

To check your GPU in MIM, go to Settings >> **General Preferences** >> **3D Preferences** and click **Check Hardware Compatibility...**.

Important: Even if the test is successful, the speed and smoothness of render cannot be guaranteed.

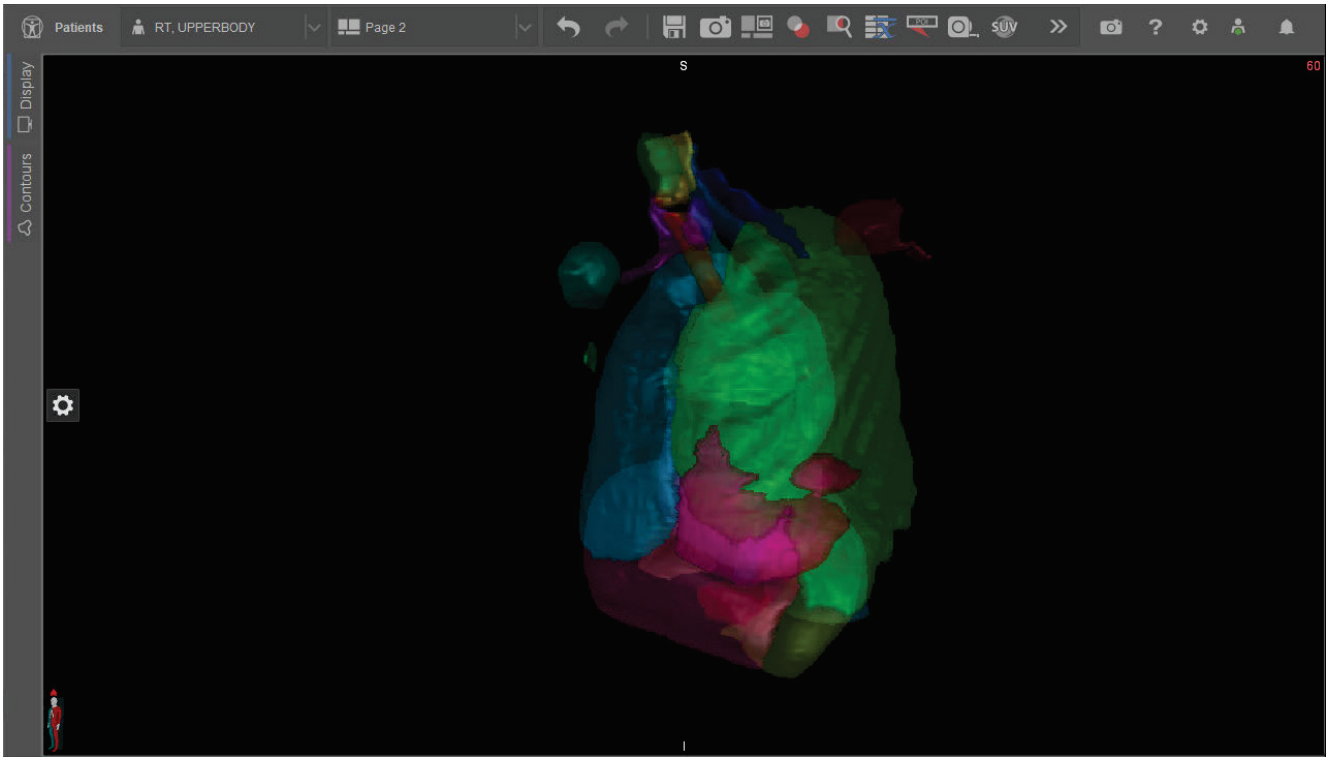
See Troubleshoot the Rendering below for more information about working with your GPU.

Create a Contour or Dose Surface View

1. Open a series in MIM:
   - Select a RTstruct set with the series if you want to make contour surface views. Optionally select an RTdose set as well if you want to color the contours by isodose line colors.
   - Select a RTdose set with the series if you want to make dose surface views.
2. To view a contour surface, go to the Contours sidebar and select a contour. You can add more contours to the view later if needed.

   Tip: *MIM 7.3 and later:* Press and hold Ctrl (Windows®) or Command (macOS®) to select multiple contours. *MIM 7.2 and earlier:* Select a single contour.
3. Hover over the viewport for which you want to make a 3D rendering and press the keyboard shortcut O. Alternatively, select the **Contour and Dose Surface View**  tool in the top toolbar.

   Tip: You can also make a display with the 3D rendering from the Display sidebar by selecting **Show More** for the series and selecting the **Contour and Dose Surfaces** option. Refer to Create and Modify Display Layouts for more information about working with displays.



- If you selected a contour, a 3D rendering of the contour surface is shown.
- If you did not select a contour and want to see a dose surface, the view appears blank. Continue to adjust the settings and add doses to the display.

Adjust the Contour and Dose Surface Views

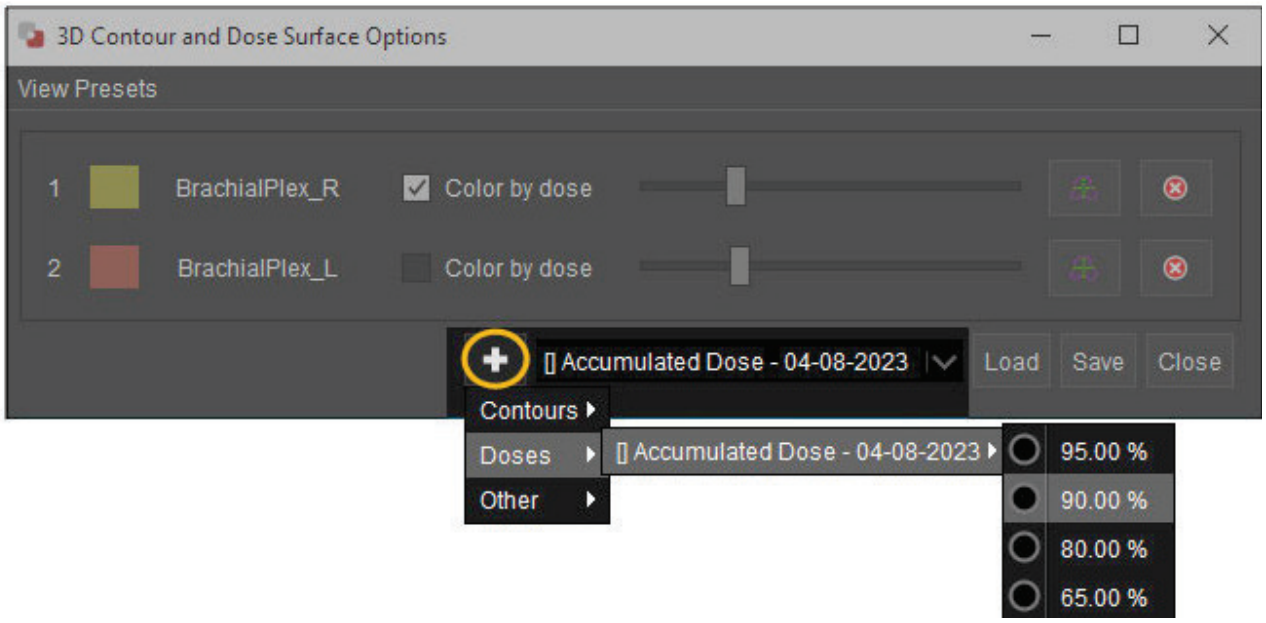
Click and drag within the volumetric display to rotate and change the angle of the image. You can also use the **Zoom** and **Pan** tools with a contour surface view.

To update the view options, click the gear on the left side of the viewport. The 3D Contour and Dose Surface Options window opens.

Add Doses to the Display

If you loaded the series with an RTdose set, you can select the doses to include in the surface view.

1. In the 3D Contour and Dose Surface Options window, click the plus ✚ >> **Doses**.
2. Select the percent isodose line to render.



Tip: The color rendered for the 3D view matches the color for the isodose line found in the Dose Settings section at the top of the Dose sidebar.

3. Click **Close** when you are finished in the 3D Contour and Dose Surface Options window.

Add Contours to the Display

If you loaded the series with an RTstruct set, you can select the contours to include in the surface view.

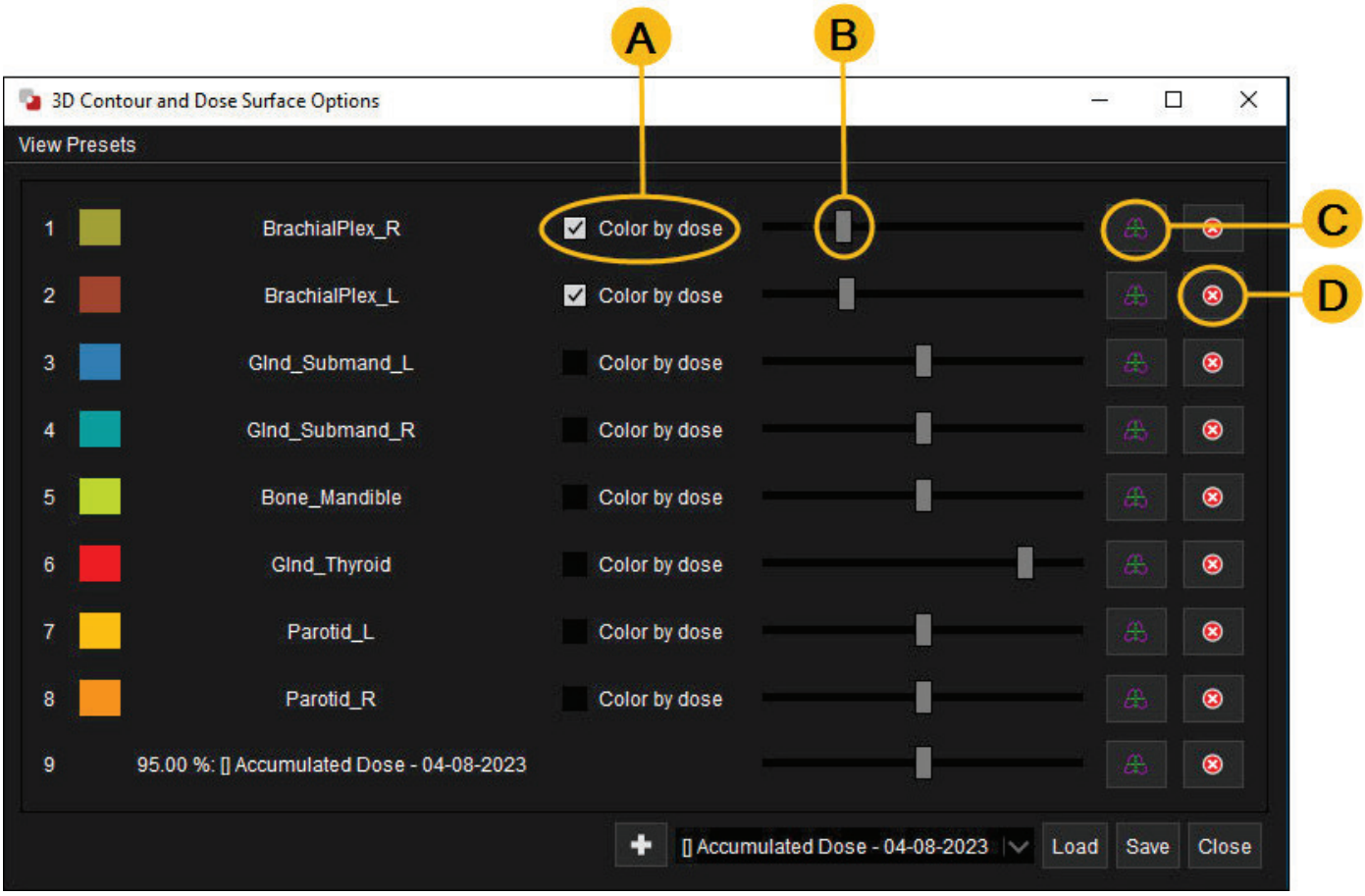
1. In the 3D Contour and Dose Surface Options window, click the plus ✚ >> **Contours**.
2. Select the contour to include.

Tip: To add all contours quickly, click the **Load** button and select **All Contours**.

3. Click **Close** when you are finished in the 3D Contour and Dose Surface Options window.

Update the Appearance of Doses and Contours

Along with adding doses and contours to the display, you can also adjust how the surface view appears.



A. Select **Color by dose** for contours to replace the contour color with the isodose line colors. The colors match the isodose line colors selected in the Dose Settings section at the top of the Dose sidebar.

B. Use the slider bar to adjust the opacity of the contour or isodose percentage.

C. Localize to the volumetric center of the contour or dose.

D. Remove the contour or isodose line from the rendering.

Use 3D Templates

You can optionally use templates to more quickly load structures into your 3D rendering. Templates allow you to add all contours with predefined names at once with the opacity already configured, instead of having to add and configure contours individually.

The Default Biopsy Template and Default Brachy Template are available by default.

Tip: To see available templates, go to Settings >> **General Preferences** >> **3D Preferences** >> **Contour and Dose Surface Templates**.

Load a Template

After you make a viewport show the Contour and Dose Surfaces view (even if it is blank), click the gear on the left side of the viewport:

1. In the 3D Contour and Dose Surface Options window, click the **Load** button.
2. Select the template that you want to load. The contours and doses in the session that match the contour names and doses built into the template are added to the rendering.
3. Click **Close** when you are finished in the 3D Contour and Dose Surface Options window.

Create a New Template

When you have added and adjusted the contours that you want included in a rendering, you can save it as a template so that you can quickly load the same settings in future sessions.

1. In the 3D Contour and Dose Surface Options window, click the **Save** button.
2. In the Notifications window, enter a name for the template and click **OK**. The template is saved with the contour names and doses that you had configured.
3. Click **Close** when you are finished in the 3D Contour and Dose Surface Options window.

Troubleshoot the Rendering

To check your GPU in MIM, go to Settings >> **General Preferences** >> **3D Preferences**.

- If you are using MIM via Citrix (thin client), IT needs to add GPU. Virtual machines may require licensing for a virtual Nvidia GPU.
- A Nvidia Quadro® or GeForce® Series GPU is recommended for Windows machines.
- If there are no appropriate hardware devices available on the machine, or if MIM's OpenCL probe has failed, the **Hardware Rendering Device** preference shows "No Devices Found."
- If you want to use multiple devices:
    - Select **Use multiple devices when possible**.
    - Select the **Rendering Devices** to use.

- If you would like surface renderings to appear smoother, decrease the **Z Resolution** value.

Important: More interpolated 3D renderings are smoother, but less accurate to the contouring data.

If 3D rendering is not working, please contact MIM Software Support at support.mimsoftware.com for assistance adjusting advanced preferences.

Reorient Images to Short Axis

MIMTD-921 • 21 Feb 2024

Overview

The American Society of Nuclear Cardiology (ASNC) recommends reviewing the short axis, horizontal long axis, and vertical long axis views of the heart. MIM® includes a short axis reorientation tool. You can use the tool when reconstructing a cardiac series in MIM or if you get a reconstruction from your camera manufacturer that is not correctly oriented.

Short axis orientation is necessary to auto-segment cardiac images. When you run MIM Workflows™ that perform auto-segmentation, you are prompted to reorient images that are not in short axis orientation.

Caution: Using an image that is not in short axis orientation could result in an inaccurate segmentation.

You might also need to reorient cardiac images before opening the series with third-party cardiac software. For more information about cardiac software integration, refer to Integrate with Third-Party Cardiac Software.

Tip: Alternatively, you might use the ASNC Orientation tool. This tool is designed for CT scans that are already in short axis orientation. The tool updates the series display based on ASNC guidance.

Contents

Use the Short Axis Reorientation Tool

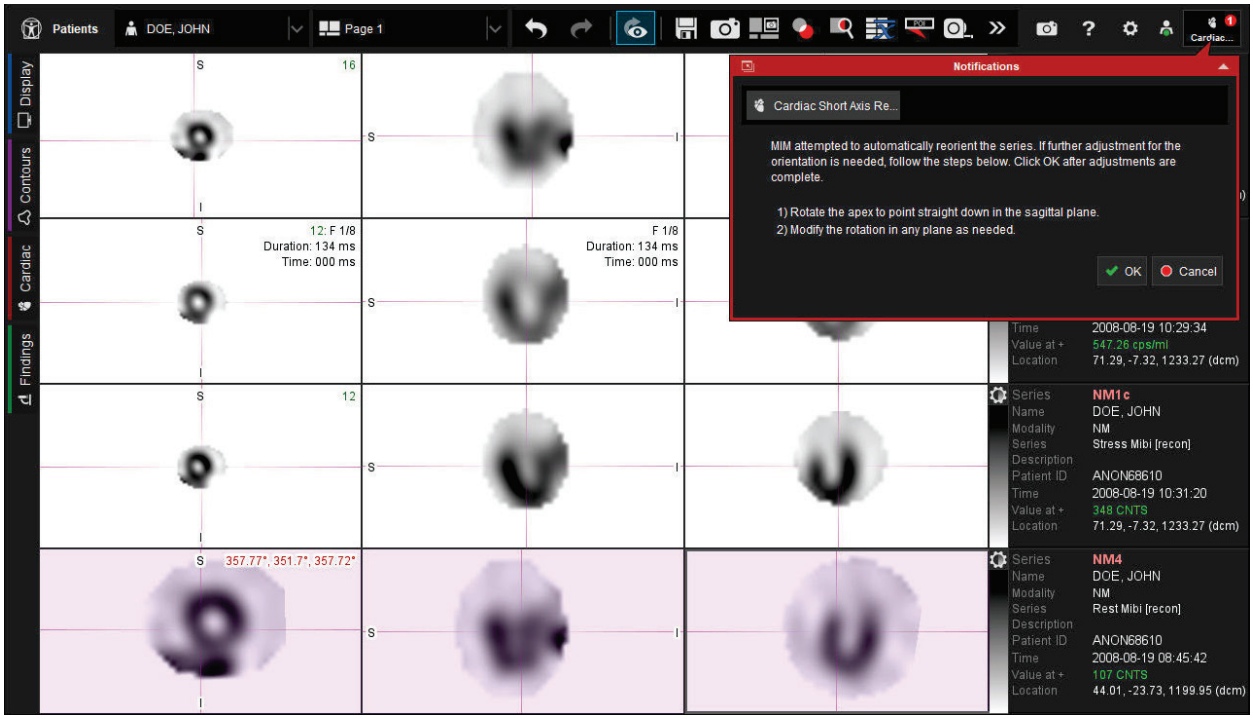
When you run the Cardiac Reconstruction workflow in MIM to reconstruct images, it automatically includes short axis reorientation.

If you have a reconstructed image that is not in short axis orientation, you can use the reorientation tool separately from the workflow. Follow these steps:

1. Open a cardiac series that is not in short axis orientation.
2. Click the **Short Axis Reorientation** button in the MIM toolbar to display a menu of open series.

> **Tip:** If you do not see this tool, click the double arrows on the right side of the toolbar and search for the Short Axis Reorientation tool.

3. Select the series to reorient from the menu.
4. Localize to the middle of the left ventricle.
5. Click **OK** in the Notifications window to continue. MIM reorients the image to short axis orientation and displays the reoriented image in a new row.
6. Follow the directions in the Notifications window to fine-tune the reoriented image as needed. The **Rotate View** tool is automatically activated for you.
    - Focus your adjustments in the sagittal plane. By default, the sagittal plane appears on the left.
    - Left-click drag left/right or up/down to use the rotation tool and adjust the rotation as needed.
    - Click **OK** in the Notifications window when you are finished.



7. If you have multiple series, such as a rest and a stress series, repeat these steps as needed to reorient the additional series as well.

Tip: MIM automatically adds (Short Axis) to the end of the series description to help you identify which series was reoriented.

Work with Reoriented Series

After using the Short Axis Reorientation tool, you might want to do the following.

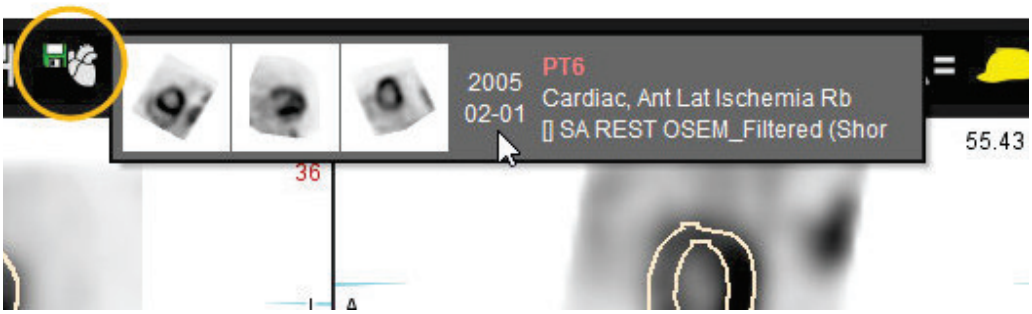
Save the Reoriented Series

You can save the reoriented series in all three planes using Cardiac DICOM Save. Follow these steps:

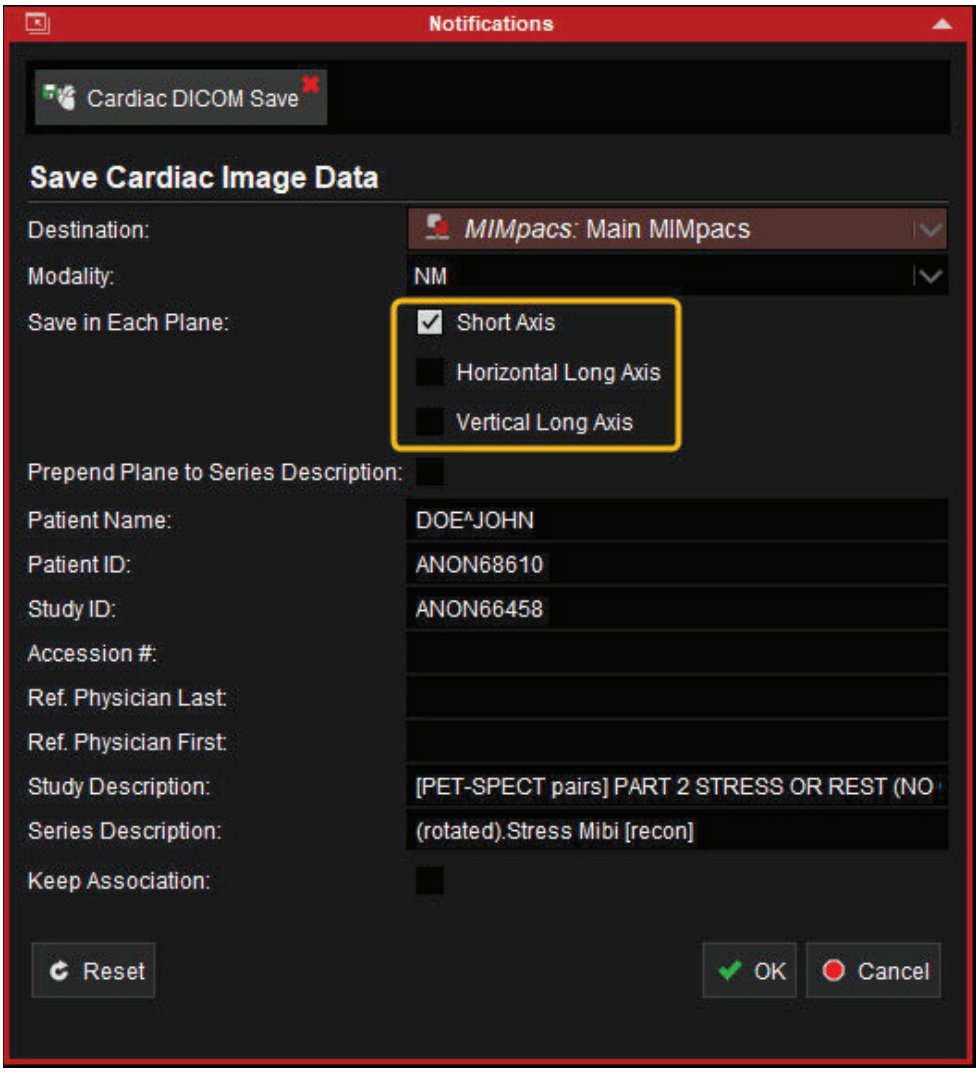
1. Click the **Cardiac DICOM Save** button in the MIM toolbar to display a list of all reoriented series in your current session.

   Tip: If you do not see this tool, click the double arrows on the right side of the toolbar and search for Cardiac DICOM Save.

2. Click the series you want to save.



3. Enter or edit information as desired in the **Cardiac DICOM Save** notification. You can select which planes you want to save (short axis, horizontal long axis, and vertical long axis).



4. Click **OK** to save the series to the selected patient list.
5. Repeat these steps as needed to save additional series that you reoriented. You can now process the series or use it with third-party cardiac software as needed.

Tip: The Image Orientation Patient (0020,0037) DICOM tag is now different in the reoriented series DICOM.

See Slices in a Grid

You can use the Grid tool to view multiple slices at once.

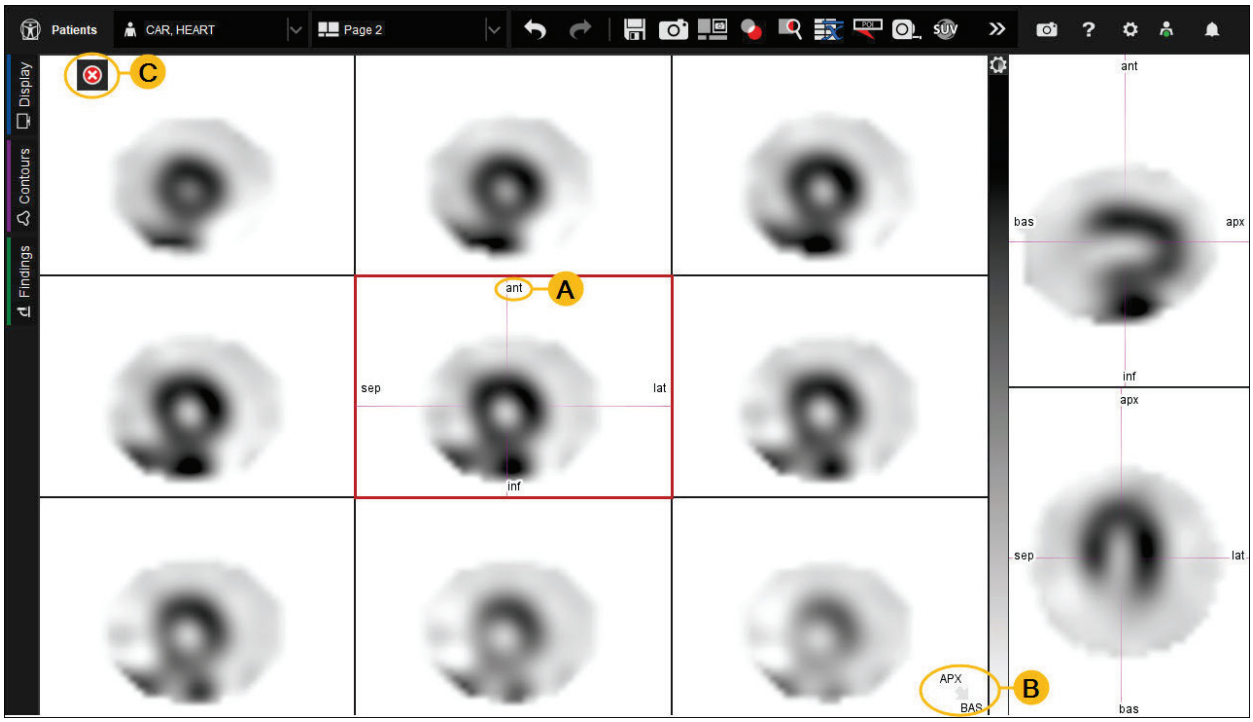
1. Activate the **Create Image Grid** tool from the top toolbar.

> **Tip:** If you do not see this tool, click the double arrows on the right side of the toolbar and search for Create Image Grid.

2. Select which plane you want to grid.
3. In the Notifications window, specify how many **Rows** and **Columns** to show in the layout. Click **OK**.

> **Tip**: Double-click on the viewport or create a display to view the grid at a larger size.

4. Review the grid:
   A. Click on a slice to see the cardiac orientation labels.
   B. Look in the lower-right corner for an indicator of the direction in which slices are being displayed. In the example below, the gridded slices of the short axis plane move from apex to base, as recommended by ASNC guidance.
   C. When you are finished, click the x in the upper-left corner to exit the grid view.



Related: Refer to View and Adjust Slice Thickness for more information about working with grids.

Use MIM Workflows™

MIM Encore® Default Workflows

MIMTD-689 • 06 Jun 2024

Overview

MIM® comes with default workflows built to handle common processing requests. MIM Workflows™ let you automate image display, Nuclear Medicine processing, and more.

You can begin using most workflows with your patient data immediately. When you launch a workflow, MIM attempts to correctly map all of your patient data to targets in the workflow. If this is not happening, please contact MIM Software Support at support.mimsoftware.com for assistance.

For information on finding and importing workflows, see Import MIM Workflows™ and Other Content. For information on launching workflows, see Launch MIM Workflows™.

Contents

General Default Workflows

2D/3D Fusion — Fuse a 2D NM image, CT, and PET or SPECT.

3D Lung Quant — Calculate user-selected lung quant statistics.

3D Lung Quant with Projected Images — Calculate user-selected lung quant statistics and display projected planar images (attenuated correction based on reconstruction setup).

Brain Autocontouring — Contour the brain on CT images using a threshold-based approach with advanced post processing. *MIM 7.3 and later.*

Cardiac Amyloidosis PYP — Calculate PYP analysis statistics (including heart to contralateral ratio). *MIM 7.2 and later.*

Combine Lumbar MR — Combine a set of lumbar MR slices into a single series. *MIM 7.3 and later.*

Important: The combined series is intended **only** for treatment planning and **not** diagnostic applications.

Create Total Tumor Burden Stat Table — Sum all VOIs on the functional series within a session into a Total Tumor Burden VOI and produce a Total Tumor Burden statistics table.

CT Bone Contouring — Create a single contour for all bone structures. *MIM 7.2 and later.*

Dual Intensity Whole Body Bone with Masking — Display dual intensity images for whole body and/or spot images with optional masking.

LesionID® — Quantify areas of increased uptake across any number of time points. For more information, see Quantify Total Tumor Burden with LesionID®.

Lung Autocontouring — Contour the lungs on CT images using a threshold-based approach with advanced post processing. *MIM 7.3 and later.*

Lung Processing — Display hanging protocols for planar and/or SPECT/CT VQ studies with optional quantitation.

Lung Ratio — Detect where ventilation is higher than perfusion and optionally fuse the series to a CT if present. *MIM 7.2 and later.*

NM Viewing — Display any number of planar images or SPECT/CT images.

Parathyroid Viewing and Subtraction — Display parathyroid planar images plus SPECT/CT images. Create subtractions between early and late ^{99m}Tc images or ^{99m}Tc and ^{123}I images. Create and display SPECT/CT fusions.

Planar Lung VQ with Fusion — Fuse and display planar perfusion and ventilation images in a single or dual monitor display.

Planar Lung VQ with Optional Quant — Display planar ventilation and perfusion images and optionally include quantitation on only the perfusion image, or on both the ventilation and perfusion images.

Stitcher — Combine two anatomical series with differing fields of view.

WB Bone and Planar Viewing — Display whole-body bone, flow, immediate, delay, blood pool, and static bone images for 1 or 2 time points. Whole-body images can be masked if desired.

Radiology-Specific Default Workflows

Hybrid PET/MR - Standard — Display PET/MR fusions.

Lung SPECT/CT Viewing — Display corrected or non-corrected SPECT/CT perfusion and/or ventilation and planar images. *MIM 7.2 and later.*

PET/CT or SPECT/CT - Compare — Display PET/CT or SPECT/CT series from 2 time points for comparison. Prior and current images are linked together based on CT anatomy. Both current and prior image sets will display as they were originally acquired, including accurate point-by-point linking. Slice numbers are displayed on both image sets.

PET/CT or SPECT/CT Quad — Display a PET/CT or SPECT/CT series from a single time point in various quad layouts.

Universal PET/CT Review — Display whole-body PET/CTs for up to 6 time points. Additional displays for further bed positions (up to 4 time points), diagnostic images (the 2 most recent time points), and a single PET/MR series will be included if those images are available. NAC series are optional and can also be included if available.

Universal PET/CT Review DM — For dual-monitor viewing. Display whole-body PET/CTs for up to 6 time points. Additional displays for further bed positions (up to 4 time points), diagnostic images (the 2 most recent time points), and a single PET/MR series will be included if those images are available. NAC series are optional and can also be included if available.

Universal SPECT/CT Review — View SPECT AC, NAC, and additional bed positions. Fuse SPECT AC and additional bed positions with the corresponding CT (if present). Display planar images. This workflow can be used for up to 2 time points and can handle up to 2 SPECTs of each type (AC, NAC, additional bed position) per time point.

Nuclear Medicine-Specific Default Workflows

Dynamic Flow Processing — Compare counts between contours for a specified time period. *MIM 7.3 and later.*

Gallbladder EF — Display flow and CCK images and calculate the ejection fraction on the CCK image.

Gastric Emptying - Dynamic — Process a dynamic gastric emptying exam and calculate retention emptying statistics based on the user's General Preferences.

Gastric Emptying - Static — Process a static gastric emptying exam and calculate retention statistics.

HIDA SOD — Generate time activity curves for liver and biliary ROIs, along with the percent of biliary duct emptying and the duct-to-bowel transit time.

Liver Functional Analysis — Process a dynamic liver exam and calculate the Liver Clearance Rate, and display a graph of uptake over time.

MUGA — Process a MUGA exam (EKG gated blood pool of the left ventricle). LLAT and ANT images are optional and can be included when running the workflow. The workflow generates a beat histogram based on the Curve Data DICOM tag when processing images from Siemens cameras.

R-L Shunt — Calculate the percentage of counts outside of the lungs.

Renal DMSA — Automatically generate ROIs for kidneys and backgrounds and process a renal exam.

Renal MAG3 (Single and Dual Acquisitions) — Process a single or two-part renal acquisition exam. Lasix injection is optional.

Salivary Processing — Process a dynamic planar acquisition and calculate time activity curves.

Sort Lesions by Stat — Choose a statistic by which the current list of contours is re-sorted. *MIM 7.3 and later.*

Thyroid Uptake — Calculate thyroid uptake for planar ^{123}I or ^{99m}Tc images. Inputs can be pre- and post-syringe images or pre-administration capsule images. If desired, a SPECT or CT may be included for viewing.

Y90 Default Workflows

Y90 - Couinaud Liver Segmentation — Generate liver, lobes, and segmental contours.

Y90 - Liver Subdivision — Segment a liver ROI by the Whole Liver, Uni-Lobar, Bi-Lobar (Sequential), Couinaud 8 Segment, or Perfused Target method.

Y90 - Lung Shunt 2D — Generate liver and lung ROIs and calculate the liver lung shunt on a 2D NM image.

Important: Additional Y90 workflows require a MIM SurePlan™ LiverY90 license. For more information, please contact MIM Software Support at support.mimsoftware.com.

Site-Defined Workflows

You can also create workflows that are specific to your organization's needs. Access self-guided courses here and use the following codes:

Course	Code
Workflow Builder - Basics	WORKBASICS
Workflow Builder - Advanced	WORKADV

Import MIM Workflows™ and Other Content

MIMTD-614 • 26 Apr 2021

Overview

Use the Import Manager to import default and content from other users at your organization, including workflows, into MIM®. For information about available default workflows, see MIM Encore® Default Workflows.

Content that you can import includes:

- Workflows
- Hanging protocols
- Structured report templates
- External report templates
- Extensions
- Custom viewport info layouts
- Findings templates
- Images
- Dose constraint sets
- Isodose settings
- ROI templates
- Contour shape templates
- BED profiles
- Color tables
- Statistics viewer layouts
- Target filters
- Sector assist segmentation models
- Anonymization templates
- Voxel S value kernels
- Public keys
- Private keys
- Structured reporting macros

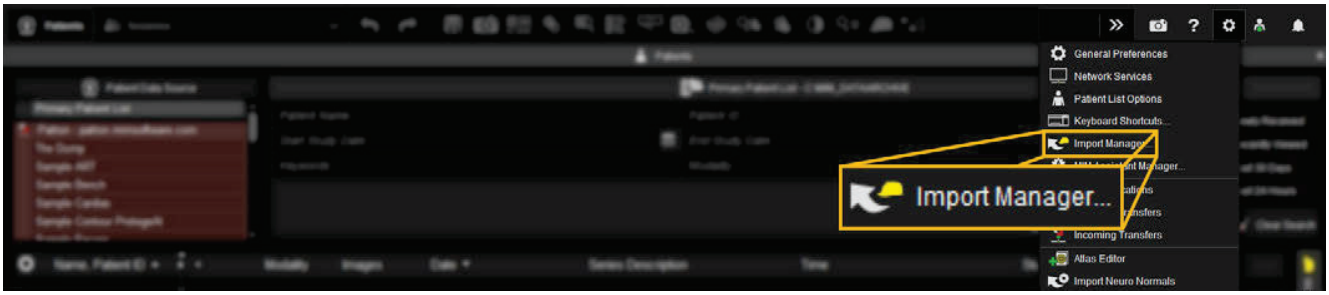
Notes:

- Some of the content types above may not apply to the MIM product or functionality that you use.
- If you are interested in developing your own site-defined content, please contact MIM Software Support at support.mimsoftware.com.

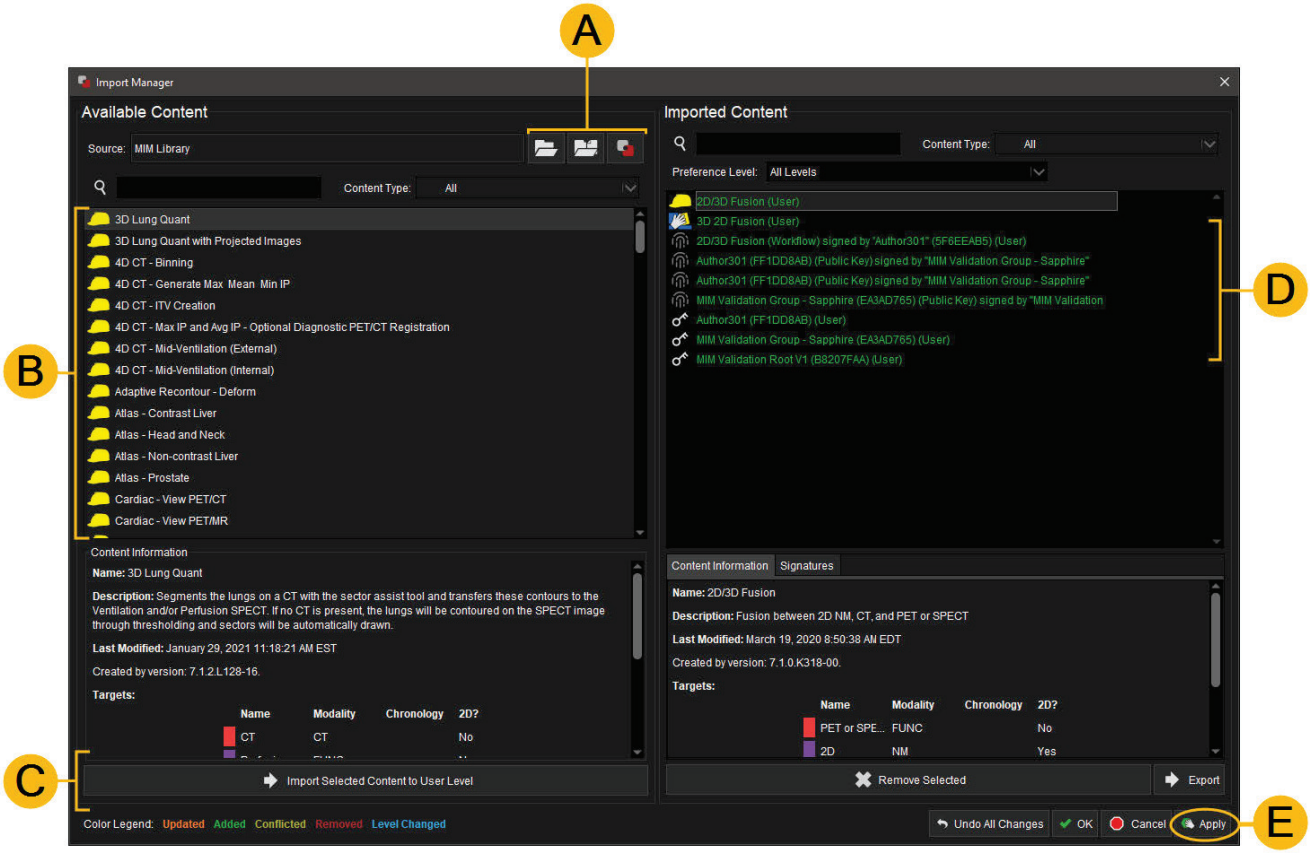
If your site has a MIMpacs™ license and MIM Network User logins are enabled, administrative users can import content for all users. For more information, see the *MIMpacs User Guide*.

To import content for one user or workstation:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **Import Manager...**.



3. View and import content:



A. Choose a content source:

- The MIM Library is automatically selected. You should keep this source selected if you want to import default workflows, for example. To change the content source back to the MIM Library anytime, click the MIM logo button.

- To import site-defined content that is stored in a local or network directory or file, click the open directory or open file buttons and go to the desired location. You should select one of these sources if you want to import a workflow that was built specifically for your site, for example.

B. Select one or more items. To select multiple items at a time, hold the Ctrl key or the Shift key while clicking.

C. Click **Import Selected Content to User Level**. After clicking the button, the selected content appears in the Imported Content column on the right side of the Import Manager.

D. Review the items in the Imported Content column.

Tip: The text color of the items being imported indicates their status. Check the Color Legend in the lower-left corner of the Import Manager to see what each color means.

E. Click **Apply**. The text color of the items being imported changes to white. The imported content is now available in MIM.

Launch MIM Workflows™

MIMTD-615 • 25 Jul 2023

Overview

MIM Workflows automate tasks to increase efficiency and standardization across your organization.

Contents

Prerequisites

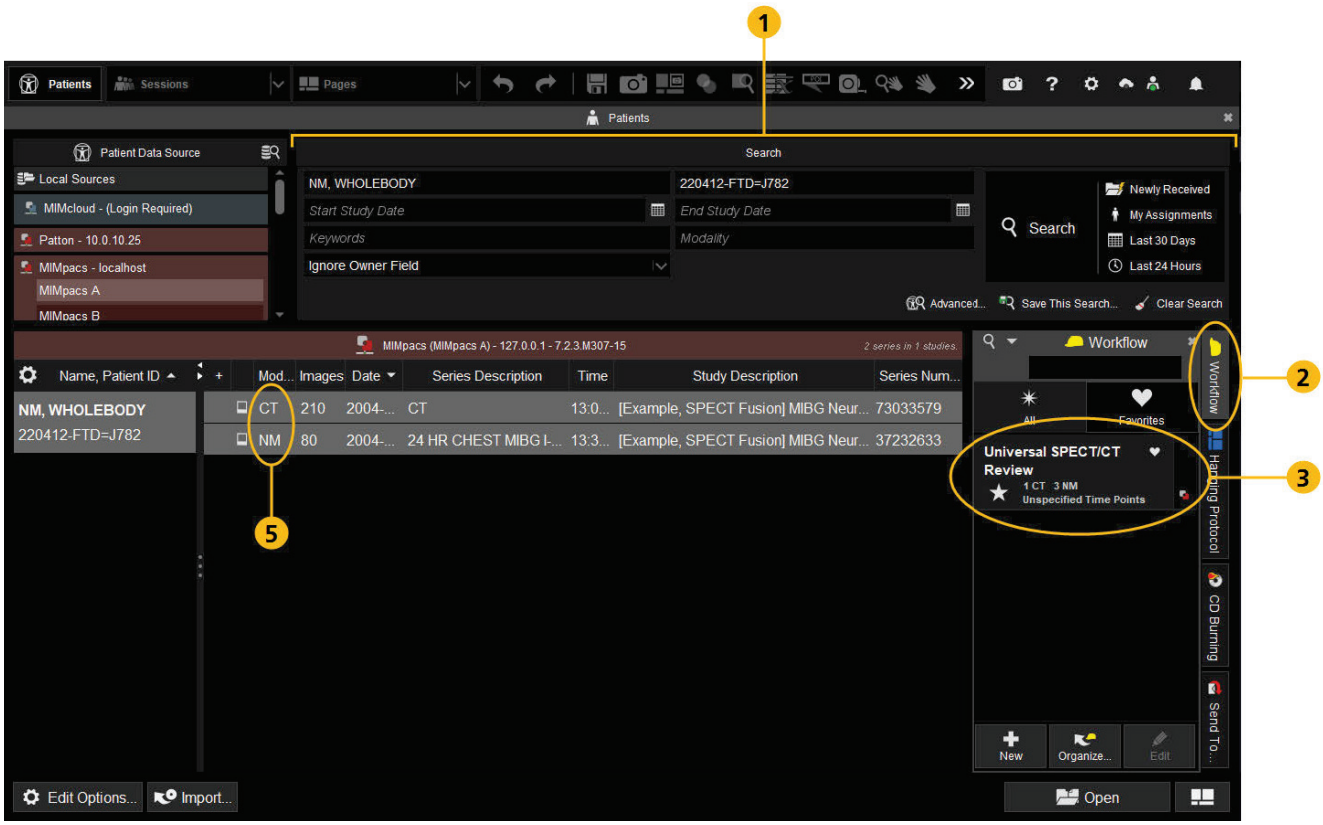
You must have workflows available to use. Available workflows can be viewed in the Workflows tab on the right side of MIM®.

Related: See Import MIM Workflows™ and Other Content to learn how to import MIM's default workflows. For assistance creating your own workflows, please contact MIM Software Support at support.mimsoftware.com.

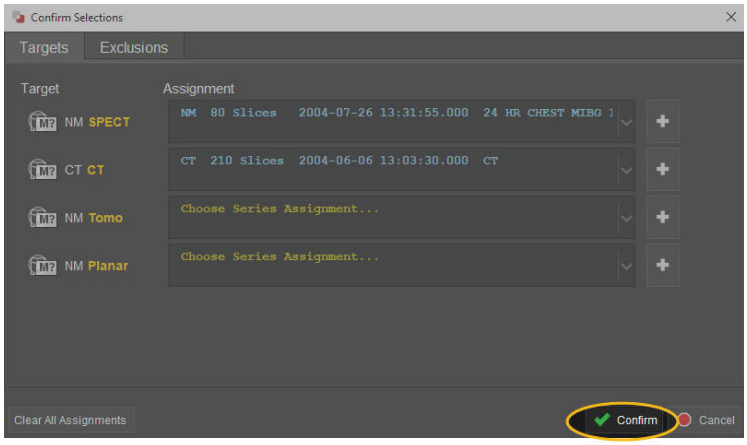
Launch MIM Workflows

1. Search for the patient whose data you want to run a workflow on.
2. Open the **Workflows** tab on the right side of MIM.
3. Find the workflow you want to launch.
4. Hover over the workflow to display the series requirements and ensure you have the correct series.
5. Select a patient or series from the patient list. The workflow lights up in white. A star indicates that MIM can use the DICOM information to map the selected series to the workflow inputs without

manual intervention.



6. Double-click the workflow name to launch it.
7. If the Confirm Selections window appears, review and confirm which series should be mapped to each workflow target. Click **Confirm** once you have confirmed the assignments for each target are correct.



8. Follow the workflow prompts in the Notifications window to complete the workflow.

You can designate a workflow as a "favorite" by clicking the ♡ next to the workflow name.

- Favorite workflows are listed first when they can be run using the selected patient data.
- If other workflows are a closer match, based on the workflow's targeting parameters, they may still be listed first.
- To only display favorite workflows, select the **Favorites** tab.

Related: For information about other icons you may see on workflows, see Manage Workflow Signatures.

Sign Workflows You Have Reviewed

MIMTD-1666 • 07 Aug 2023

Overview

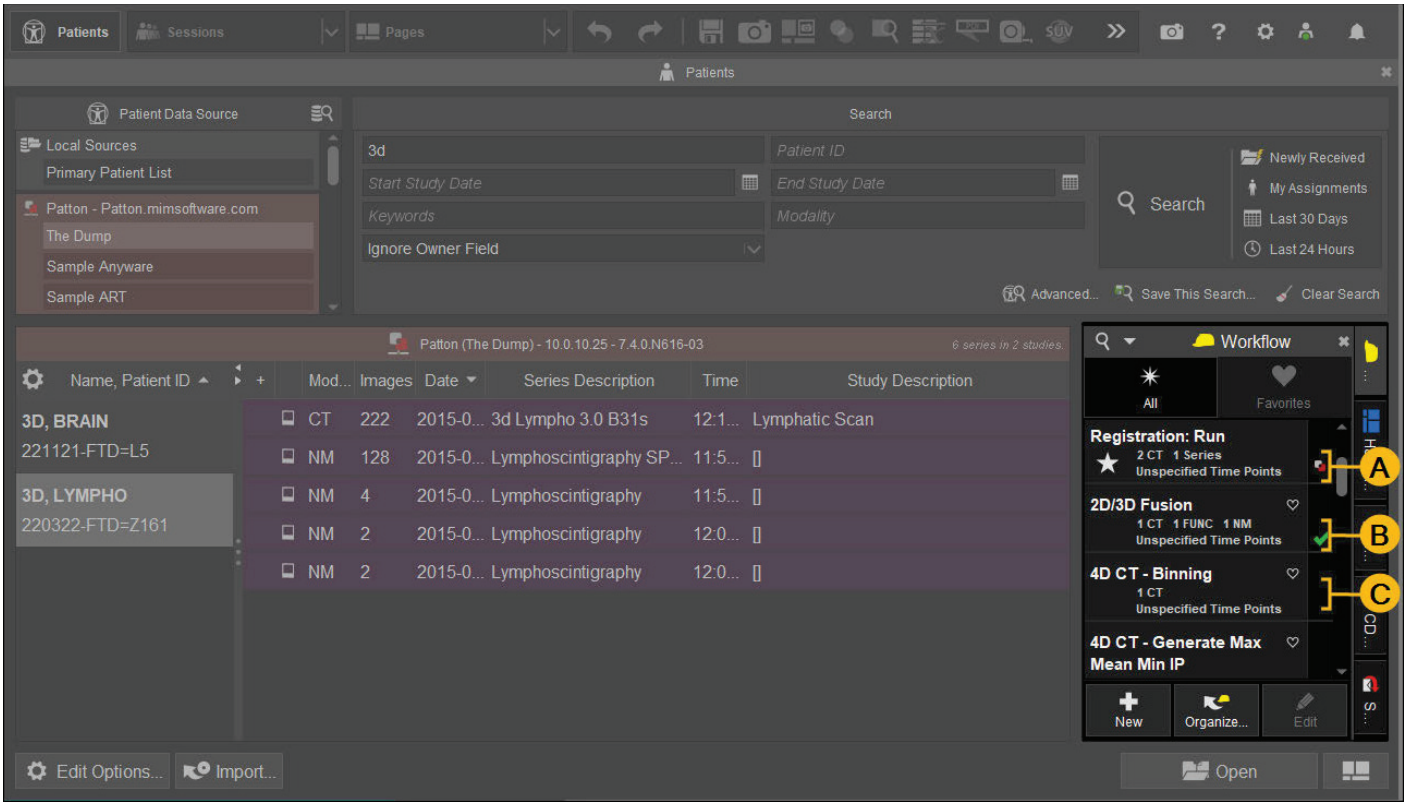
When a reviewer at your organization finalizes a workflow, the reviewer can add an electronic signature to the workflow in MIM®. Signatures serve as validation that the workflow is ready for use. Signatures also help ensure that all users are using the same approved workflow for consistent processing.

Reviewers apply a signature to a workflow using a key pair. Follow the instructions below to create a key pair. Or, skip to Sign a Workflow if you have a key pair and are ready to sign a workflow.

Contents

How Signatures Appear

Icons appear in the Workflow list for signed workflows:

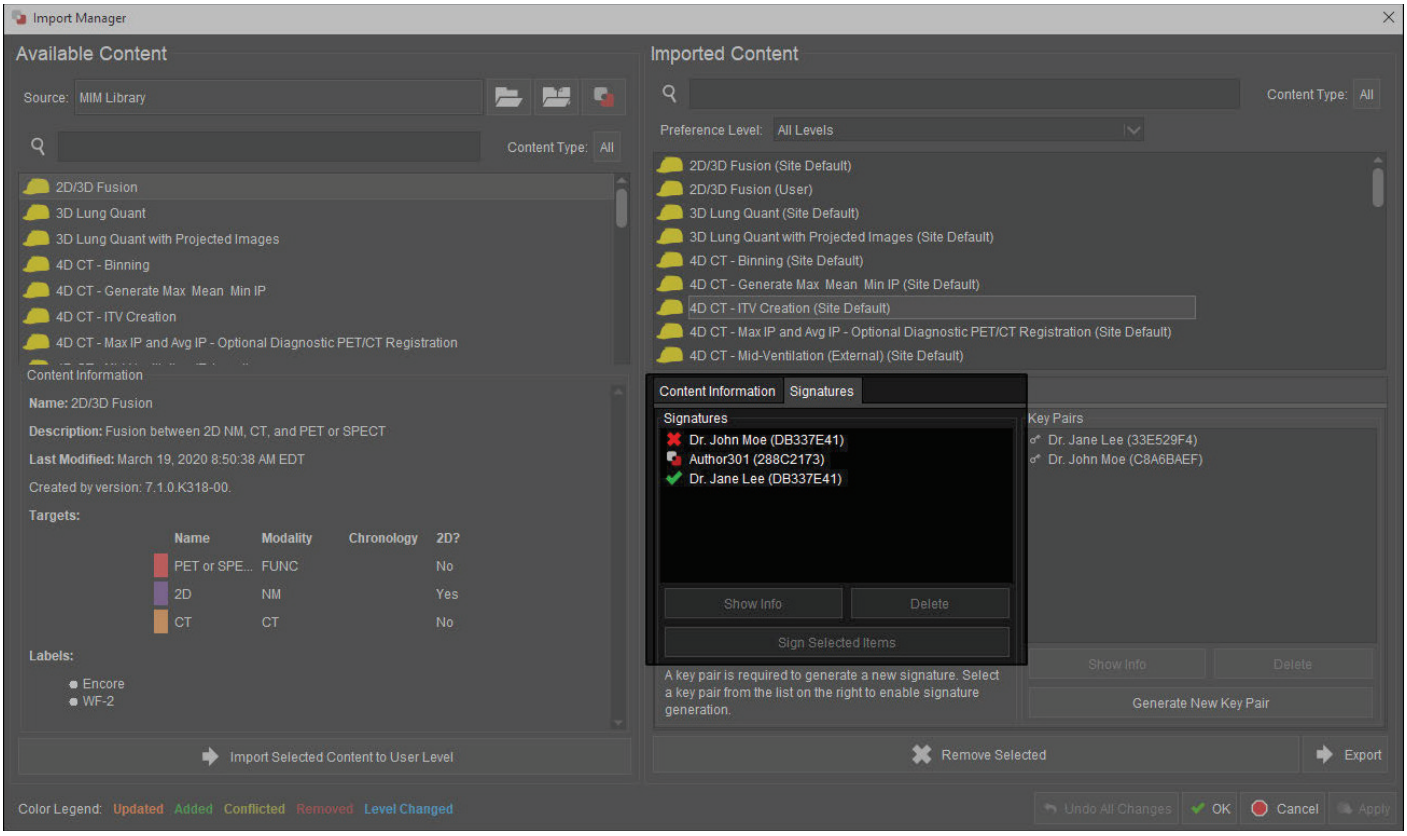


A. Default MIM workflows are internally validated and signed by MIM Software®. This signature is indicated by a MIM icon.

B. Workflows signed by a user at your organization have a green checkmark icon. If a workflow has been signed both by a user at your organization and by MIM Software, only the MIM icon appears.

C. Workflows that have not been signed do not have an icon.

Signatures also appear in the Import Manager. Select a workflow and click the **Signatures** tab to see who has signed it.



If a workflow or a dependency is edited after the workflow has been signed, the signature becomes invalid. Dependencies are standalone items that the workflow depends on (e.g., hanging protocols).

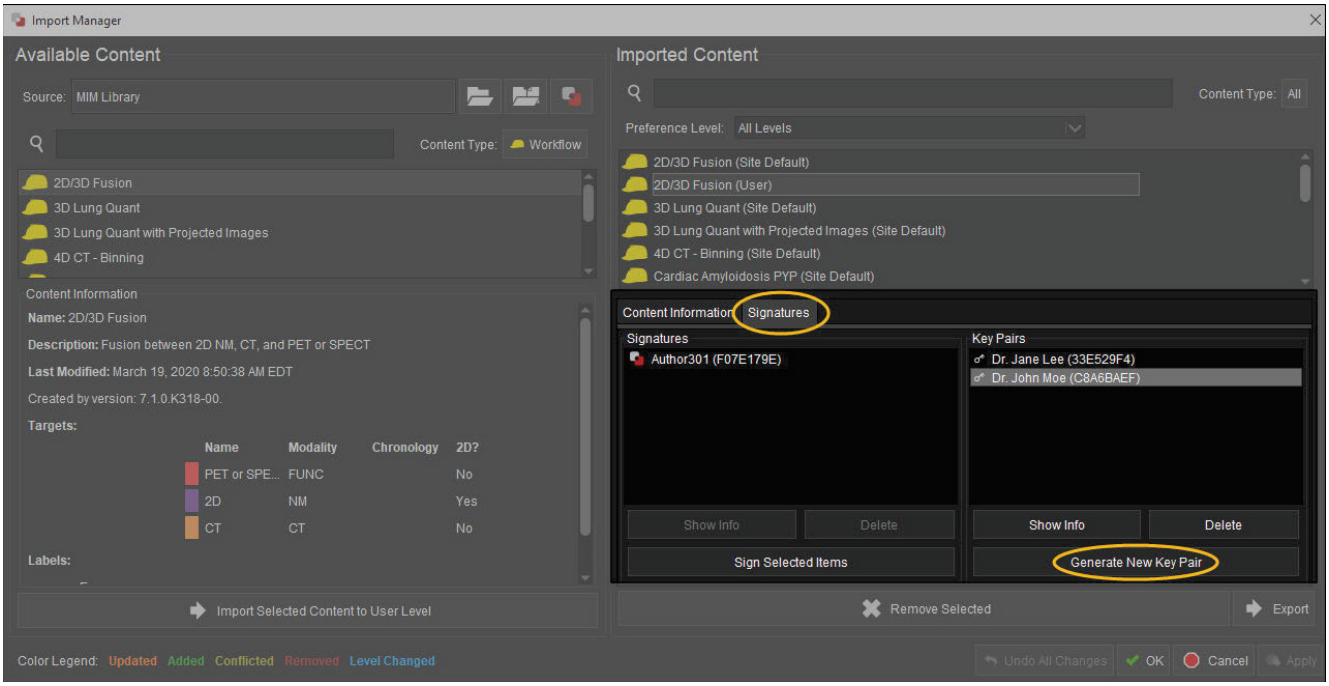
When the signature is invalid, the signature icon no longer appears in the workflow list. In the Import Manager, the icon next to the signature changes from a checkmark (✔) to an x (✖). This does not prevent the workflow from being launched. It only indicates that the workflow or a dependency has been edited since being signed.

Related: For information about removing or invalidating signatures, refer to Manage Workflow Signatures.

Generate a Key Pair

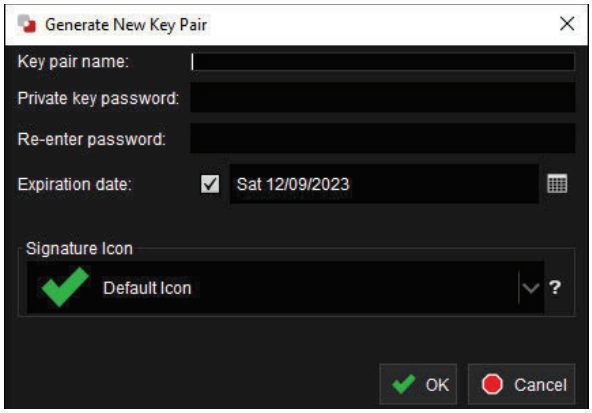
You must have a key pair before you can sign a workflow. Complete the following steps to generate a key pair. If you already have a key pair, go to Sign a Workflow below.

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Click **Import Manager...**.
3. Click the **Signatures** tab below the Imported Content list on the right side.
4. Click **Generate New Key Pair**.



5. In the window that opens, complete the following fields:
   i. Enter a name in the **Key pair name** field. This is the name of your signature.
   ii. Create a **Private key password** and re-enter it.
   iii. *MIM 7.2 and later*: If desired, select an expiration date for the key pair. Note that signatures generated by a key pair before the key pair's expiration date are valid even after the key pair expires. *MIM 7.1 and earlier*: This functionality is not available.
   iv. *MIM 7.2 and later*: If desired, select a signature icon. *MIM 7.1 and earlier*: This functionality is not available.

Tip: If you would like to use your own icon instead of the default green checkmark, please contact MIM Software Support at support.mimsoftware.com.



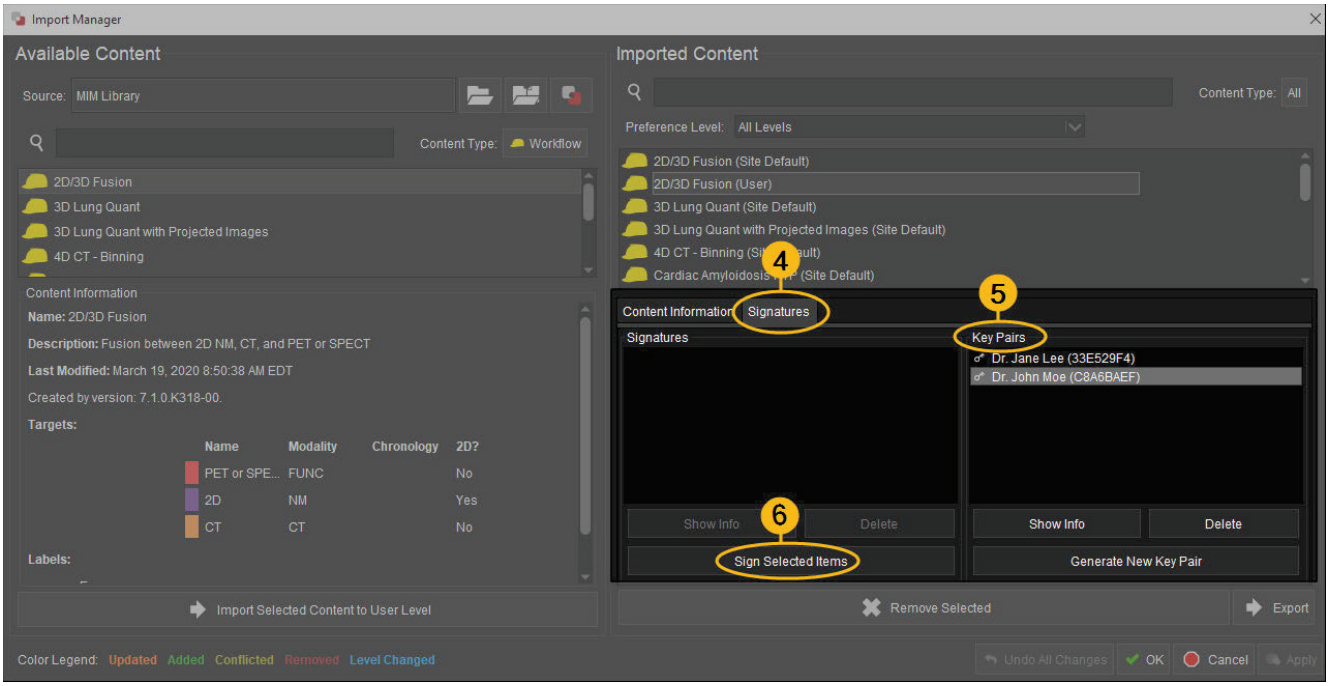
6. Click **OK**.

Sign a Workflow

Signing a workflow requires a key pair. See Generate a Key Pair above for more information.

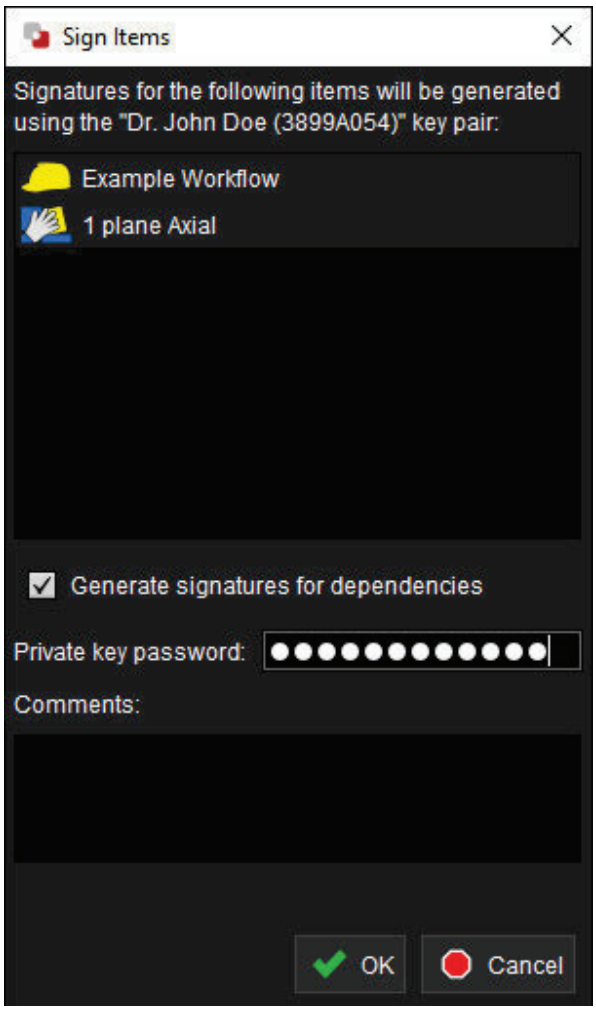
Tip: Multiple signatures can be added to a workflow, if desired.

1. Click the Settings button in the upper-right corner of MIM.
2. Click **Import Manager...**.
3. Select the workflow you wish to sign from the list of Imported Content on the right side.
4. Click the **Signatures** tab below the list.
5. Select your key pair from the **Key Pairs** section.
6. Click **Sign Selected Item**.



7. In the window that opens, complete the following fields:
    i. If desired, select **Generate signatures for dependencies**. Dependencies, such as hanging protocols, are listed along with the workflow if you select this option.

ii. In the **Private key password** field, enter your key pair password.



8. Click **OK**.

Manage Workflow Signatures

MIMTD-926 • 26 Jul 2023

Overview

Organizations can use workflow signatures to indicate when a workflow has been validated. If a workflow is signed, then edited at a later time, all signatures associated with that workflow become invalid (indicated by a ✖).

To ensure that signatures are a reliable indicator of workflow validity, your organization can remove or invalidate signatures. You can also control when a signature should no longer be used. Consider the following scenarios:

Example Scenarios	Task
A user accidentally signed the wrong workflow.	Remove a Signature from a Workflow
A user who previously signed workflows has changed roles. The user should no longer be able to sign workflows.	Delete a Key Pair
You want to see all of the workflows that were signed by a particular user.	View or Remove a Signature from All Workflows
A key pair was compromised. The affected signature should appear invalid on all previously signed workflows.	Revoke a Signature
Your organization wants all workflows to be reviewed annually. You want signatures to appear invalid after one year.	Revoke a Signature
You are doing maintenance and want to remove all invalid signatures.	Bulk Remove Invalid Signatures

Related: Go to Sign Workflows You Have Reviewed for more information about generating key pairs and signing workflows.

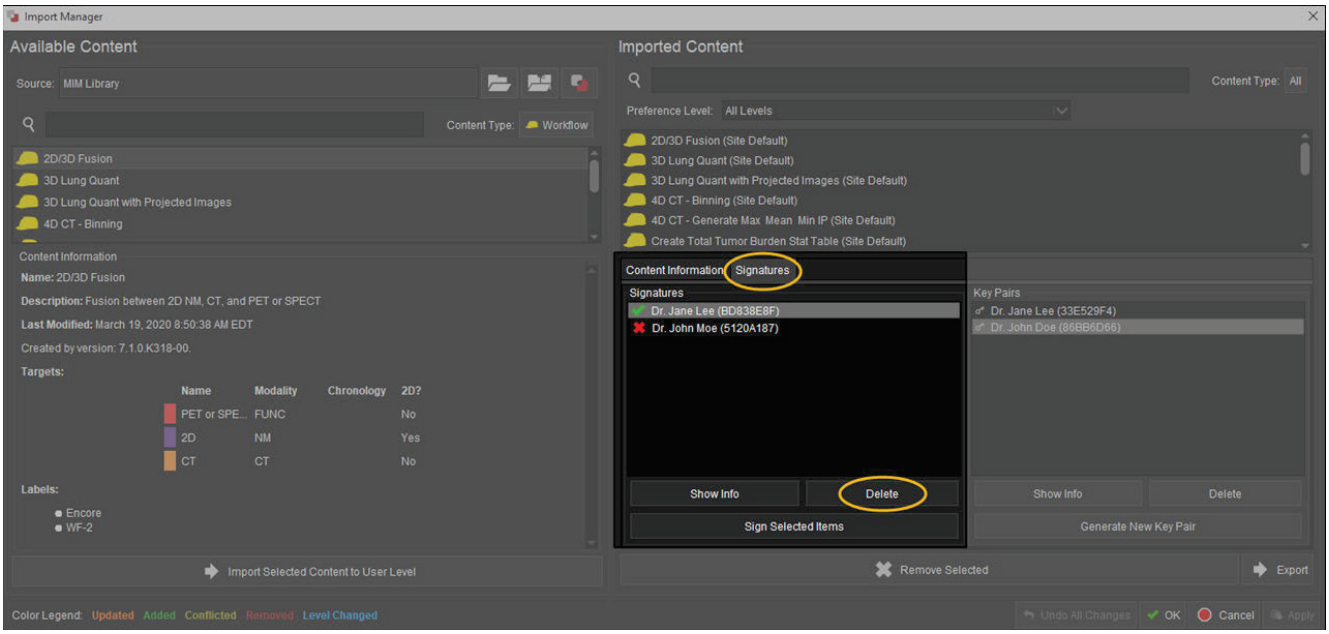
Remove a Signature from a Workflow

Complete the following steps to manually remove a signature from a workflow. For example, you can remove a signature that was added in error. Or, you can remove a signature that is invalid (indicated by a ✖).

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Click **Import Manager...**.
3. In the Imported Content list on the right side, select the workflow from which you want to remove a signature.

> **Tip:** Press and hold Shift to select multiple consecutive workflows or press and hold Ctrl to select multiple workflows that not in a row.

4. Click the **Signatures** tab.
5. Select the signature you wish to remove in the **Signatures** section.
6. Click **Delete**. At the prompt, confirm the deletion.

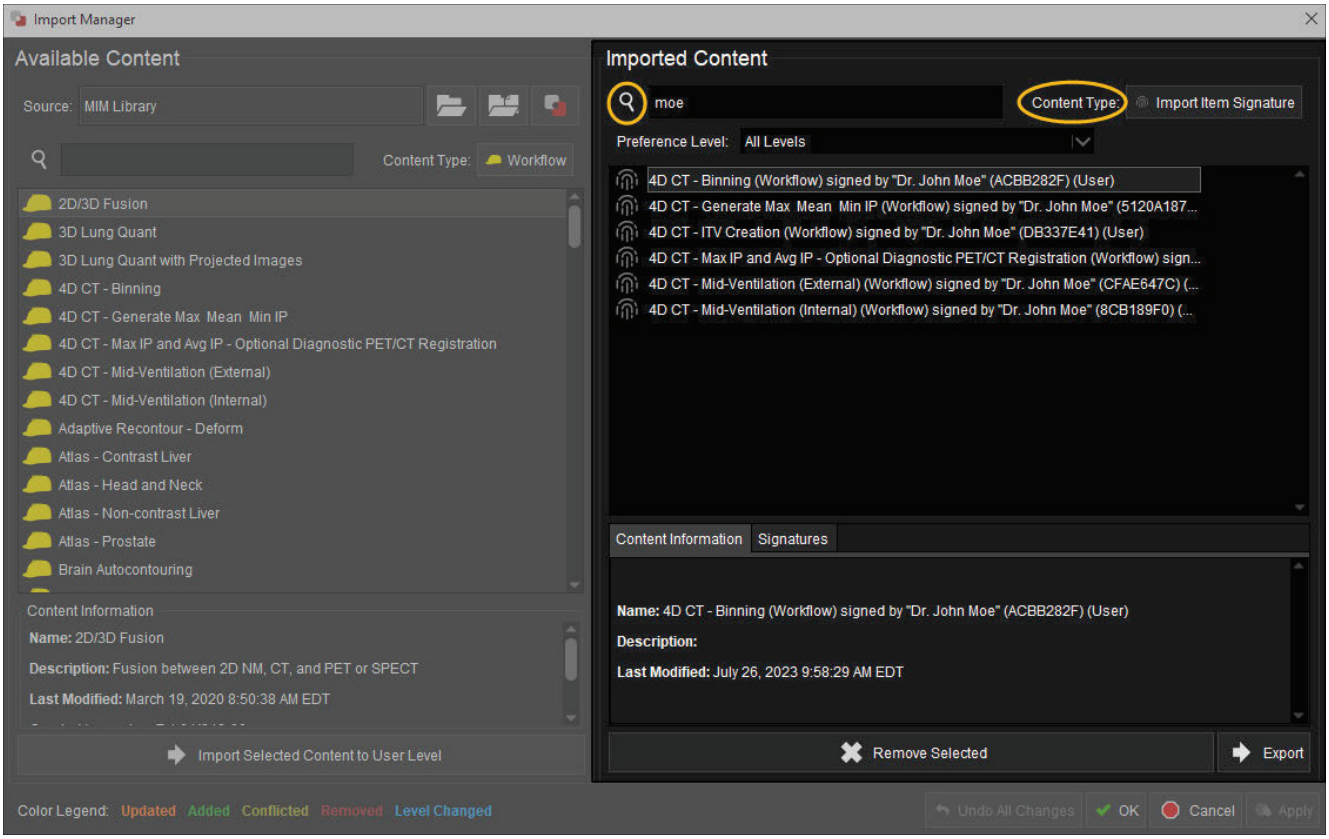


7. Click **Apply**.

View or Remove a Signature from All Workflows

Complete the following steps if you want to see all of the workflows with a particular signature. For example, you might want to see which workflows a certain user validated. Optionally, you can also remove the signature from the workflows identified.

1. Click the Settings button in the upper-right corner of MIM.
2. Click **Import Manager...**.
3. Click the **Content Type** dropdown menu in the top right of the window.
4. *In MIM 7.2 and later*: Select **Show Signatures**. *In MIM 7.1 and earlier*: Select **Import Item Signature**.
5. Use the search field to search for a signature if you want to review only items with that signature.



6. If desired, press and hold Shift to select all signatures found. Click **Remove Selected** to delete the signatures from the workflows.

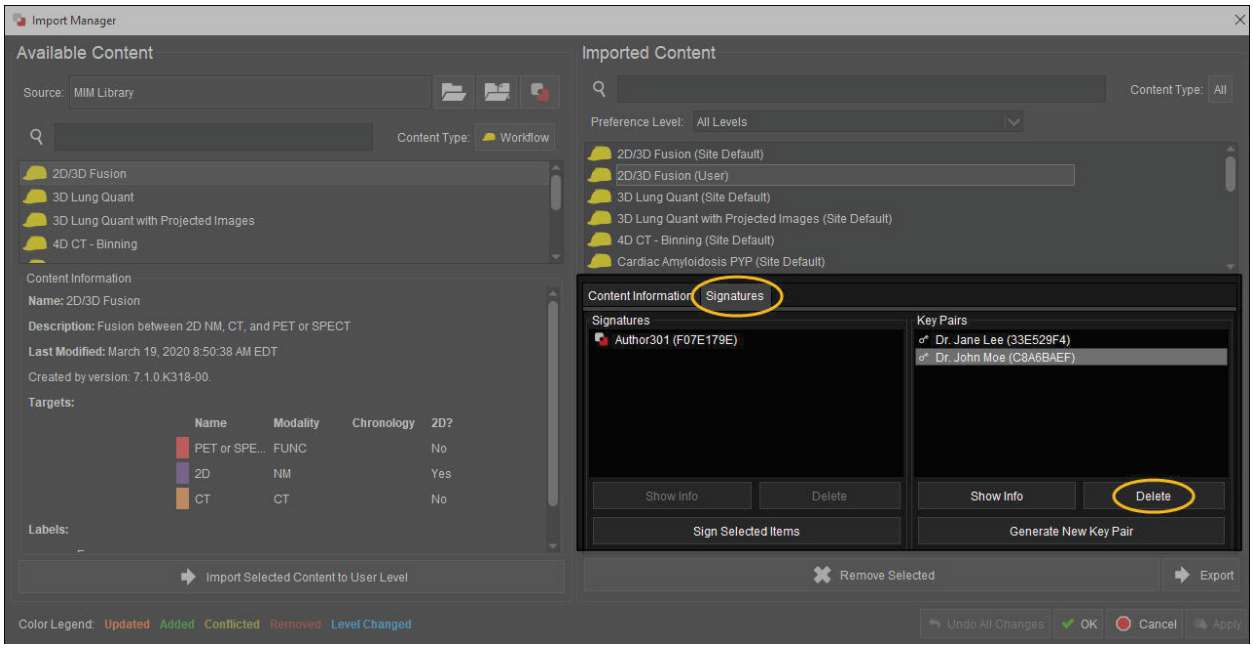
Delete a Key Pair

You can remove a key pair so that workflows can no longer be signed using that signature. For example, you might delete a key pair after a user leaves your organization or changes responsibilities.

Tip: To see all key pairs that have been used to sign items, go to the Import Manager and click the **Content Type** filter for the Imported Content list. Select **Public Key** to see keys that have been used to sign an item. Select **Private Key** to see all key pairs that can be used for signing.

Complete the following steps to remove a key pair:

1. Click the Settings button in the upper-right corner of MIM.
2. Click **Import Manager...**.
3. Below the Imported Content list on the right side, click the **Signatures** tab.
4. Select the key pair and click **Delete**.
5. Review the prompt:
   - *If there are no items currently signed using that key pair*, click **OK** to delete both the public and private keys. The key pair can no longer be used to sign items.
   - *If there are items currently signed using that key pair*, click **OK** to delete the private key. The key pair can no longer be used to sign items. Items already signed by the key pair retain their signature.

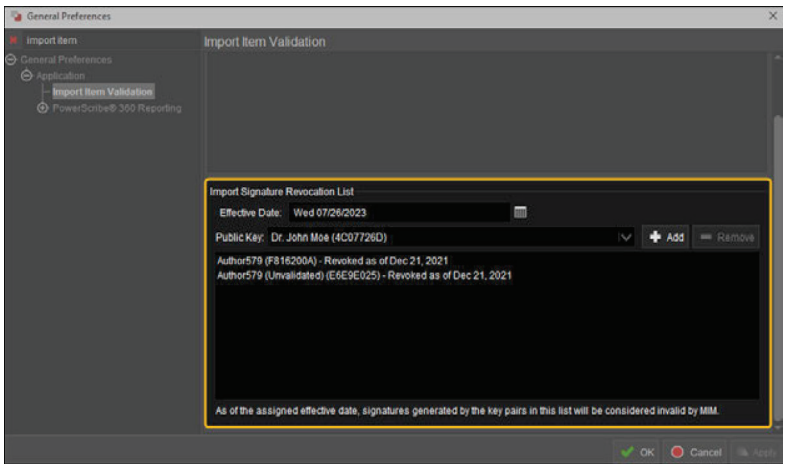


6. Click **OK**.
7. Consider whether you also want to:
   - Review which workflows were previously signed using that key pair. See View or Remove a Signature from All Workflows above for details.
   - Revoke the signature so the signature becomes invalid on all the workflows where it was used. See Revoke a Signature below for details.

Revoke a Signature

Complete the following steps to invalidate a signature on items where it was previously used. You can also use this feature to set an expiration date for when you want a signature to appear invalid.

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for **"import item"**. Select **Import Item Validation** on the left side.
3. Scroll down to the Import Signature Revocation List section and configure the following:
    i. In the **Effective Date** field, enter when the signature should appear invalid on all items where it was previously used.
    ii. In the **Public Key** field, select the key pair.
    iii. Click **Add**.



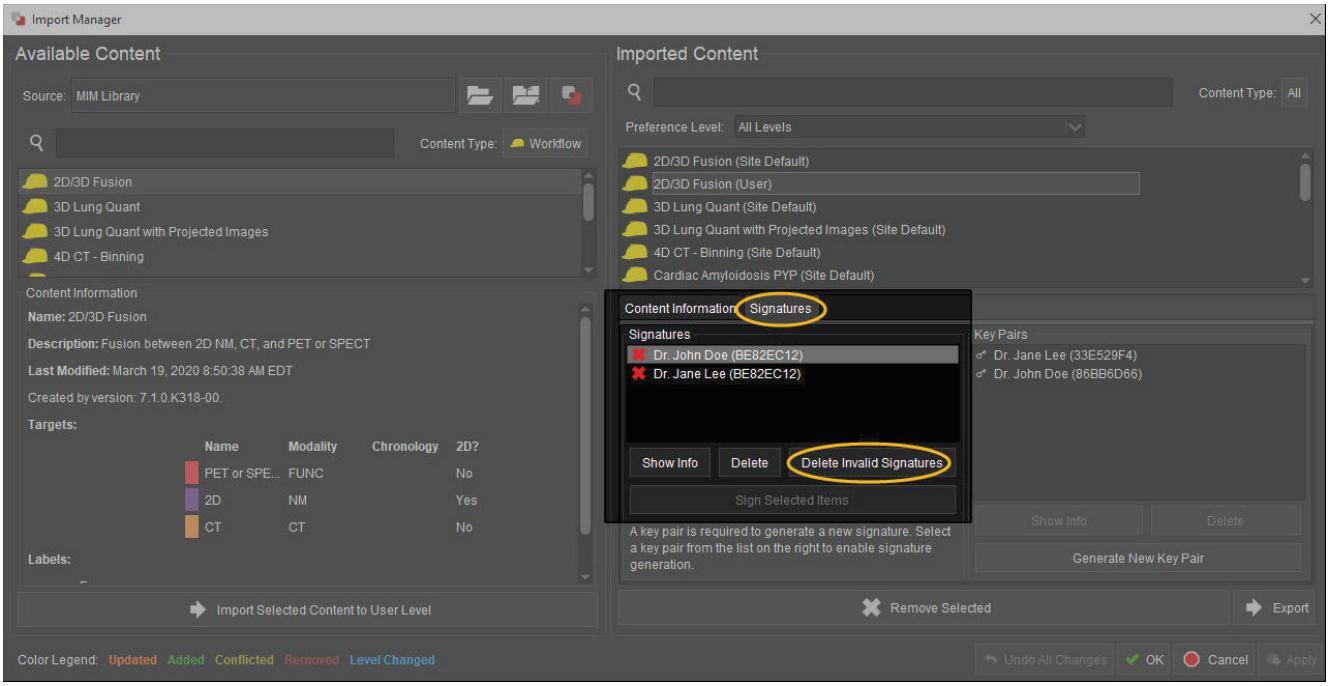
4. Click **OK** to save the changes and close the window.
5. Consider whether you also want to:
    - Delete the key pair so that the signature cannot be used again. See Delete a Key Pair above for details.
    - Remove that signature, which is now invalid, from all the items where it had been added. See View or Remove a Signature from All Workflows above for details.
    - Remove all signatures that now appear as invalid. See Bulk Remove Invalid Signatures below for details.

Bulk Remove Invalid Signatures

Complete the following steps to remove all invalid signatures from all items:

1. Click the Settings button in the upper-right corner of MIM.
2. Click **Import Manager...**.
3. In the Imported Content list on the right side, select the workflow from which you want to remove invalid signatures.
4. Click the **Signatures** tab.
5. Select an invalid signature.
6. Click **Delete Invalid Signatures**. At the prompt, confirm that you want to bulk delete all of the invalid signatures on the workflow.

> **Important:** Invalid signatures from all items are removed, not only the invalid signatures on the selected workflow.



7. Click **Apply**.

Work with 2D Images

Adjust 2D Zoom

MIMTD-1389 • 26 Oct 2023

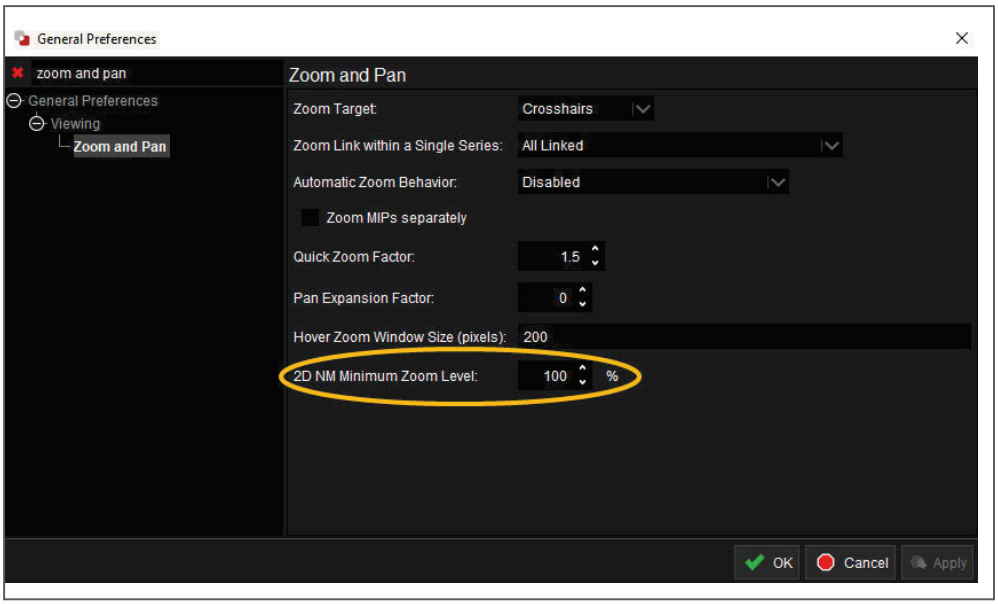
Overview

You can adjust settings in MIM® to let you zoom out further on 2D images. This is helpful if images are loaded beyond their intended resolution and are difficult to read.

Adjust 2D Zoom

To adjust 2D zoom, follow these steps:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**zoom and pan**". Select **Zoom and Pan** on the left side.
3. Enter a value less than 100% for the **2D NM Minimum Zoom Level**.



4. Click **OK** to save the changes and close the window.

Mask an ROI

MIMTD-1390 • 01 Dec 2023

Overview

You can use the Mask tool to apply a specified value to the voxels within a contour. For example, you might want to mask the injection site and bladder on a PT scan so they don't appear as areas of higher uptake. Or, you might want to mask an artifact so that it doesn't appear on an anatomical scan.

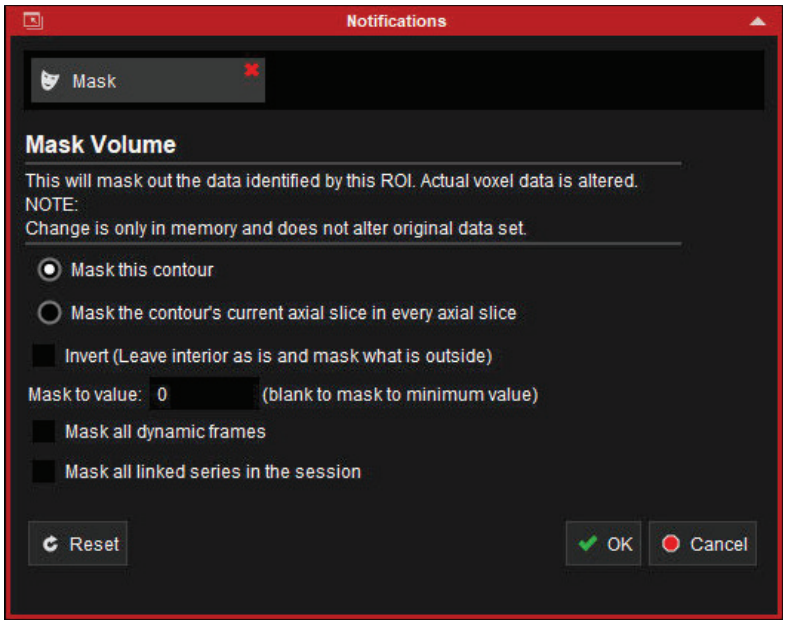
Contents

Create a Mask

Complete the following steps to mask an area in an image:

1. In a session, draw a contour around the area that you want to mask. Refer to Create Contours Overview for more information about contouring.
2. In the Contours sidebar, select the contour that you created.
3. In the top toolbar, select the **Mask** tool. If the tool does not appear in your toolbar, click the button to search all tools.
4. In the Notifications window, adjust the mask settings as needed.
   - Select **Mask the contour's current axial slice in every axial slice** if you want to apply the mask as if the contour was drawn on every slice. This option is helpful if what you are masking is relatively static between slices.
   - Select **Invert** if you want to apply the mask to everything that is outside of the contour instead of to the voxels that are inside of the contour.
   - Set the **Mask to value**. This field autopopulates with a low value that essentially erases the voxels. On a functional image, this defaults to 0. On a CT, this defaults to -1000 or lower.
   - Select **Mask all dynamic frames** if you are working with a dynamic series and want to apply the mask to each frame in the series.

- Select **Mask all linked series in the session** if desired. For example, this can be helpful when you are working with an anterior and posterior image and want to mask both views.



5. Click **OK** to apply the mask.

Masking Tips and Tricks

You might find the following helpful depending on your scenario.

Tip: Masks can also be automatically applied as part of a workflow. Please contact MIM Software Support at support.mimsoftware.com if you are interested in updating a workflow to automate masking.

Apply a Mask to Multiple Series

You can use the **Mask all linked series in the session** option in the Notification window for the Mask tool to apply a mask to multiple series. If the series have different modalities or units (for example, a PET and a CT), you first need to copy the contour to the second series.

Follow these steps:

1. Draw the contour on the first series.
2. Use the **Transfer Contour** tool to copy the contour to the second series.

> **Tip:** The Contours sidebar shows the contour drawn on the selected series and a second ghost contour for the series that is not selected. For more information, refer to Transfer Contours.

3. Select the **Mask** tool.
4. In the Mask notifications window, select **Mask all linked series in the session**.
5. Click **OK** to mask the contour.

> **Tip:** For 2D series with the same modality and unit, such as a posterior and anterior image, you can also use this masking option. Refer to Mask Linked Images for more information.

Remove Background

You can use the **Invert** option in the Notification window for the Mask tool to focus on a particular place in an image and remove the background. For example, you might want to remove part of an image for better registration.

Complete the following steps:

1. Draw the contour around the part of the image that you want to keep (not what you want to remove).
2. Select the **Mask** tool.
3. In the Mask notifications window, select **Invert (Leave interior as is and mask what is outside)**.
4. Click **OK** to run the tool.

Remove a Couch

In most cases, remove the couch from an image using the Couch Removal tool. If you are unable to remove the couch with that tool, try the following:

1. Use the **Couch Contour** tool or manually draw a contour around the couch.
2. Select the contour and select the **Mask** tool.
3. In the Mask notifications window, set the **Mask to value** to 0. Click **OK** to mask the contour.

Mask Linked Images

MIMTD-1741 • 02 Jan 2024

Overview

When masking an ROI, you can also mask all linked series in the session. This can be helpful when you are working with an anterior and posterior image and want to mask both views.

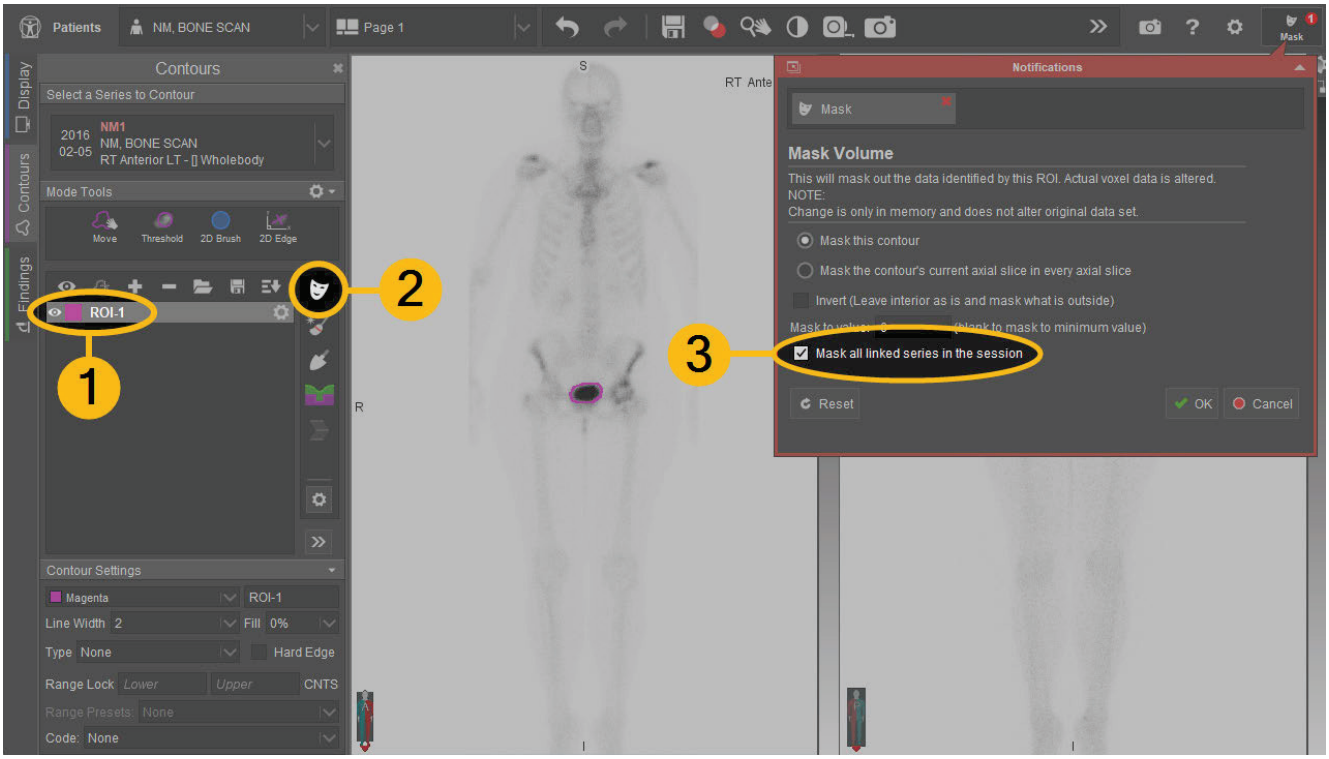
Tip: For basic information about using the Mask tool, see Mask an ROI.

Contents

Mask Linked Images

1. Select a contour.
2. Click the **Mask** tool.
3. In the Notifications window, enable **Mask all linked series in the session**.

Tip: If the tool does not appear in your toolbar, add it to your contouring tools via the gear button at the bottom of the post processing tools in the Contours sidebar.

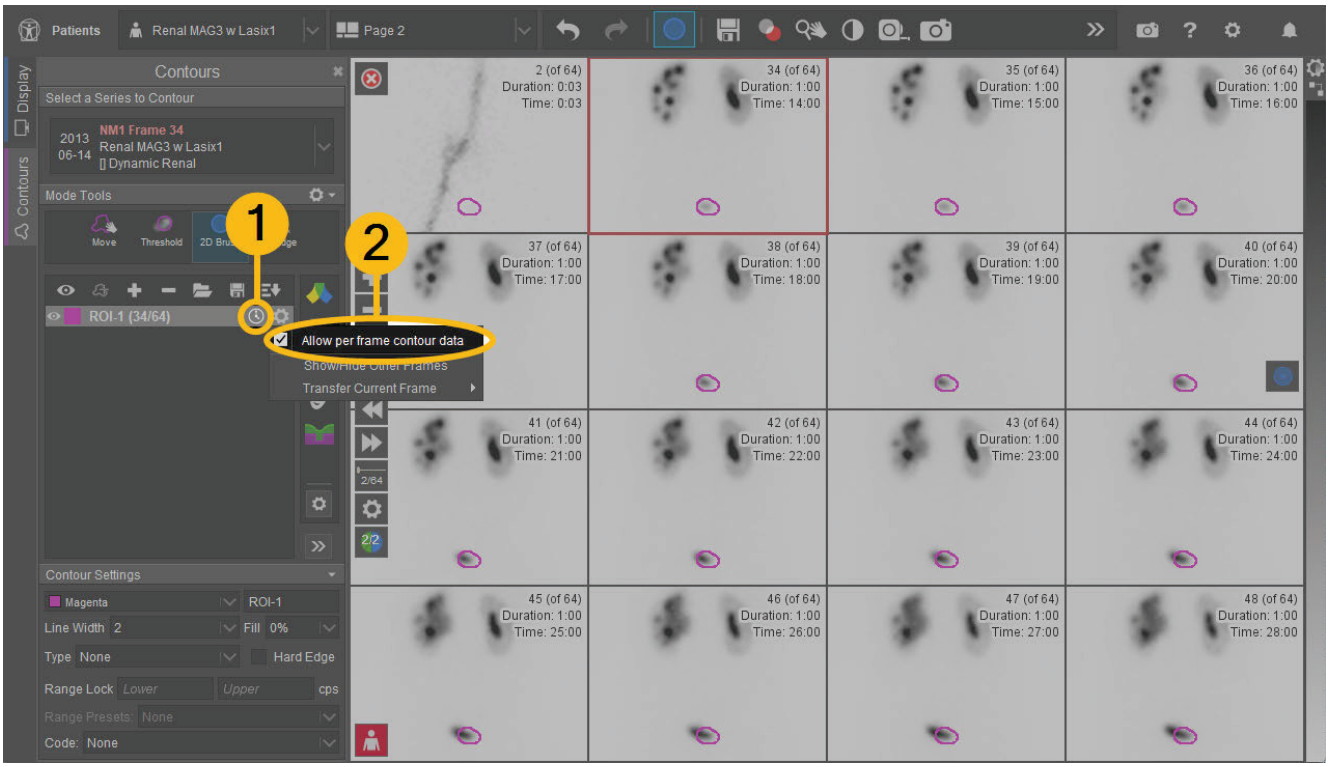


4. Click **OK** to save the changes and close the window.

Use Different Masks on a Dynamic Series

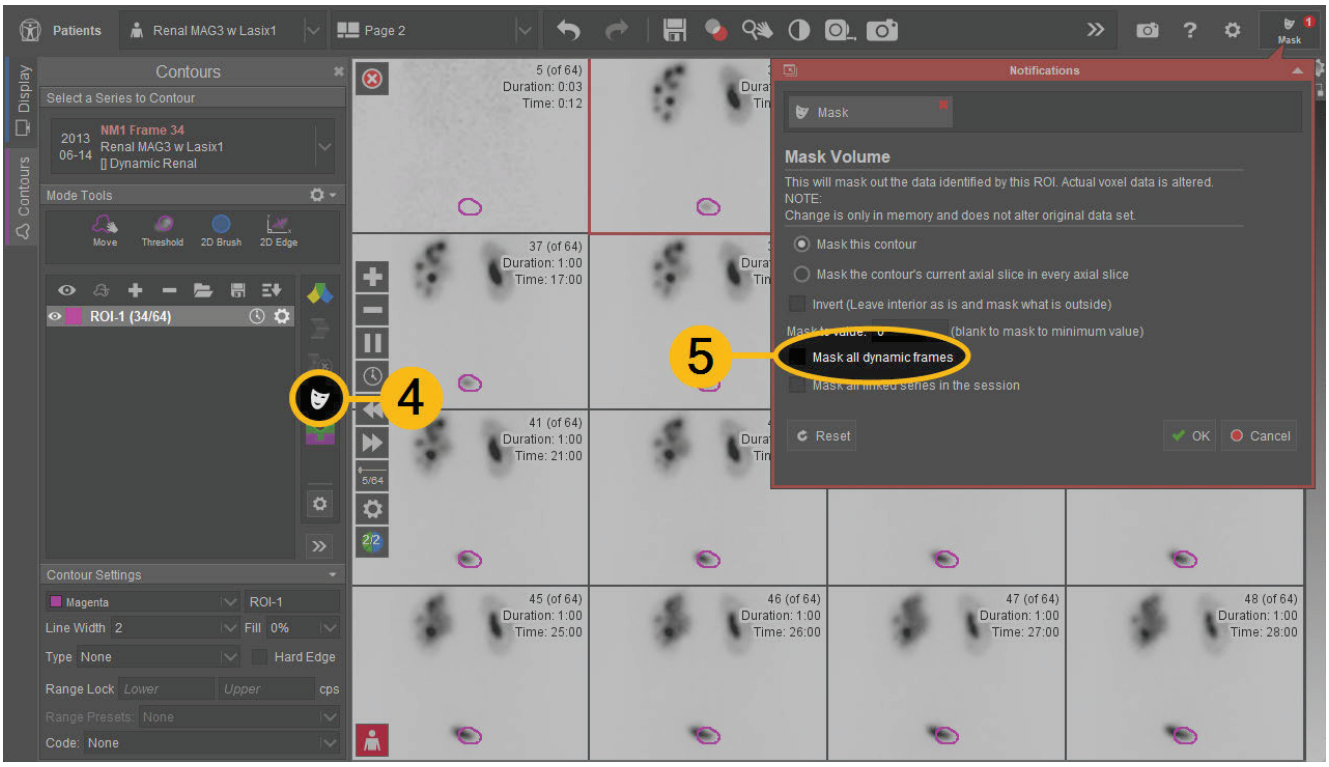
You can use contours on dynamic series to correspond to different areas across frames. This allows for masking different regions on each frame. For example, you may want to remove a hot injection site on a tomographic SPECT image.

1. Click the clock icon next to a contour name in the Contours sidebar.
2. Select **Allow per frame contour data**.



3. Make per frame modifications to the contour as necessary.
4. Click the **Mask** tool.

5. In the Notifications window, select **Mask all dynamic frames**.

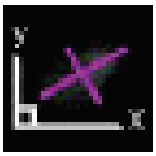


6. Click **OK** to save the changes and close the window.

Create Contours with the 2D Edge Tool

MIMTD-1742 • 24 Oct 2023

Overview

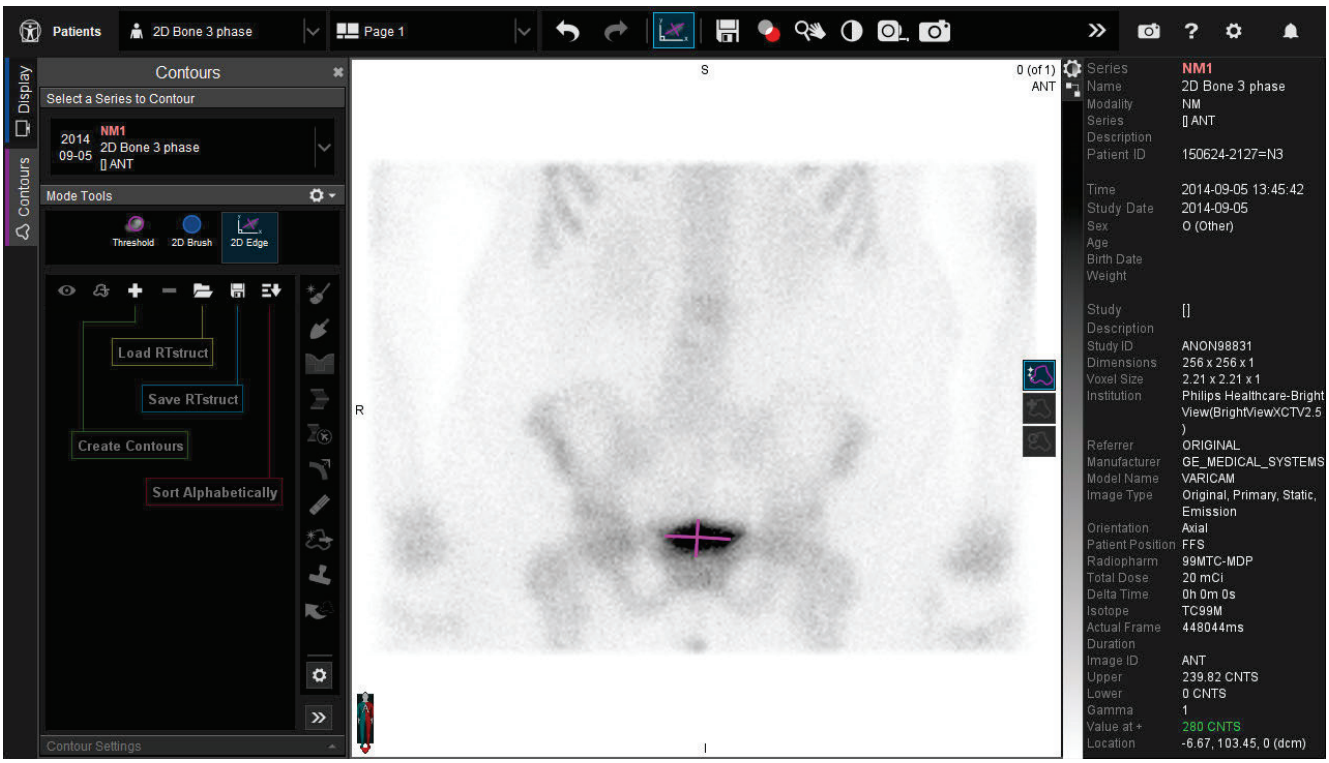


The 2D Edge tool is used to define normal structures or lesions based on changes in the image gradient, regardless of contrast settings. It defines an edge based on the change in count levels at the structure's border.

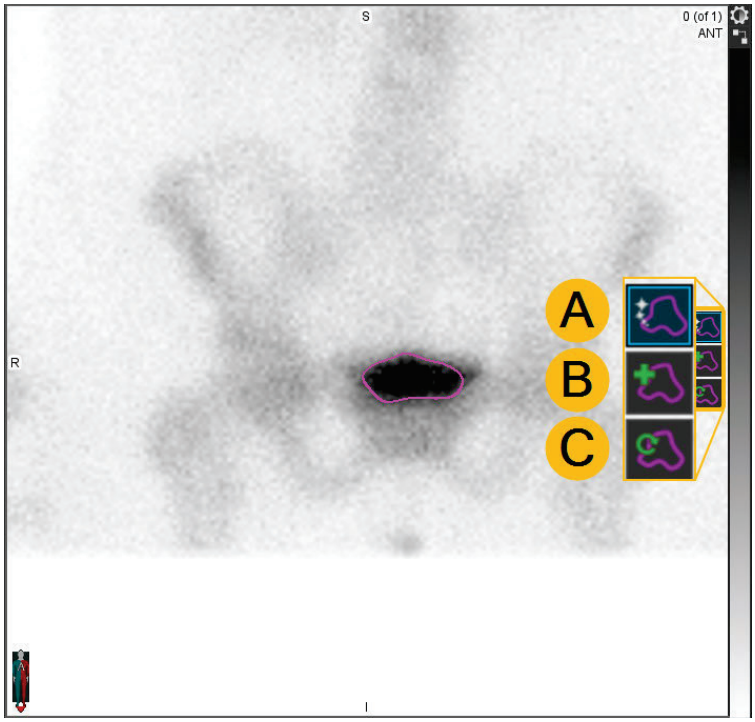
Caution: A qualified person must review all auto-generated contours for accuracy, and make adjustments if needed, before the contours are used clinically.

Create Contours

1. Open a 2D image from the patient list.
2. Select the **2D Edge** tool from the Contours sidebar.
3. Left-click drag from the center of the structure until the axes reach the edge of the structure. The axes provide approximate limits from which the contour will be calculated.



4. Release the mouse to create the contour.
    - By default, each subsequent left-click drag generates a new contour because the create button is selected on the right side of the viewport.
    - If you need to append to or replace an existing contour instead, select the contour from the Contours sidebar and choose the appropriate button on the right of the viewport. Continue left-click dragging and releasing to append to or replace the existing contour.
    - The append option is used to add to the currently-selected contour if the entire structure was not completely included in the initial contour. This can sometimes occur with multi-lobed lesions or lesions with finger-like projections.



A. Create a new contour.

B. Append to the current contour.

C. Replace the existing contour.

Adjust Image Grids and Frames for Dynamic Series

MIMTD-1391 • 04 Oct 2023

Overview

When working with 2D dynamic images, you can adjust the frame duration or how many frames are displayed.

Related: Refer to View and Adjust Slice Thickness for similar options to adjust the slice thickness for 3D static series.

Contents

Change Frames Shown in a Grid

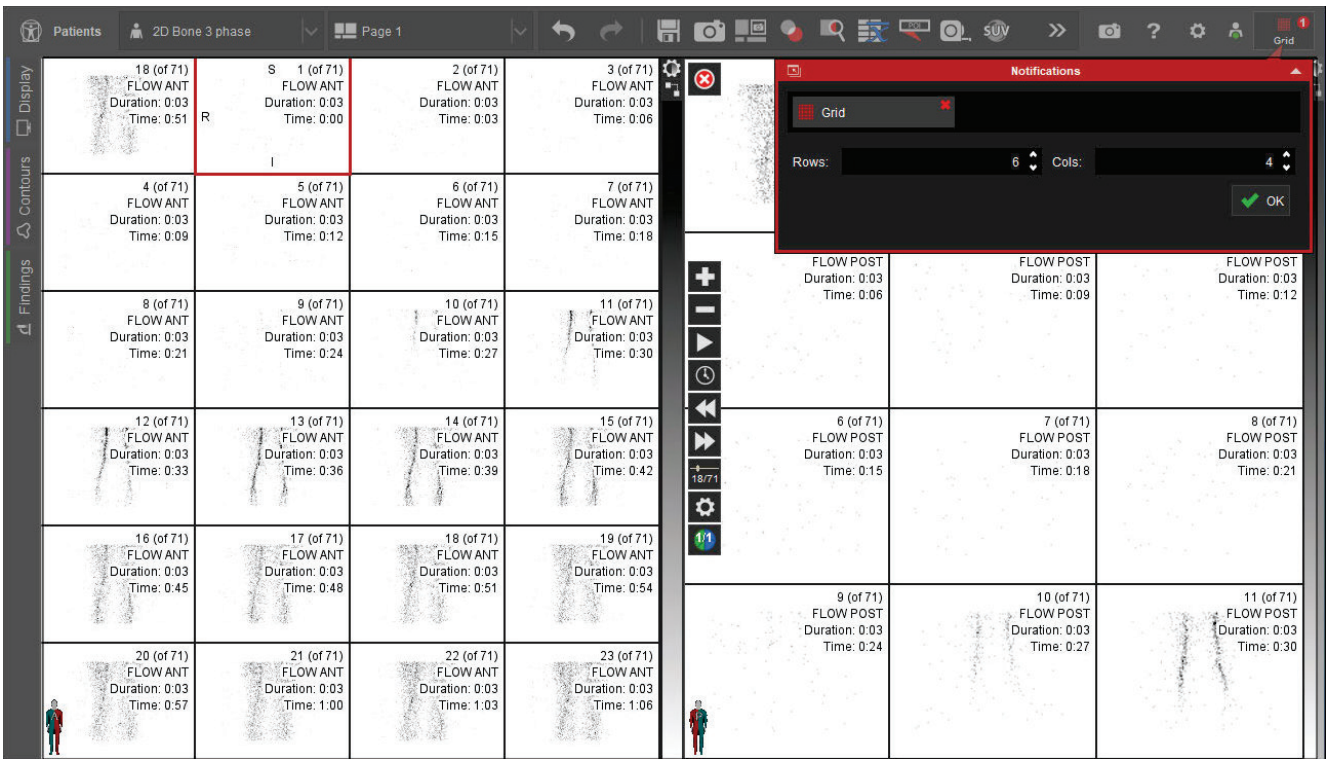
You can change the number of frames shown on a page using the Grid tool. For example, you might want more frames shown so they all fit in a single screen capture.

1. Activate the **Create Image Grid** tool from the top toolbar.

Tip: If you don't see this tool, click the double arrow on the right side of the toolbar to search for it.

Related: See Access Tools: The Toolbar and the Radial Menu if you want to add the Grid tool to the top toolbar or radial menu for easier access.

2. In the Notifications window, specify how many **Rows** and **Columns** to show in the layout.



> **Tip:** The frame number is shown in the upper-right corner of the viewport.

3. Click **OK**.

> **Tip**: By default, NM scans open in a grid view, and the cine in the upper-left corner displays the image playing. If you want to change this default behavior, go to Settings >> **General Preferences** and search for **"grids"**. Select **NM** on the left side to access these NM settings.

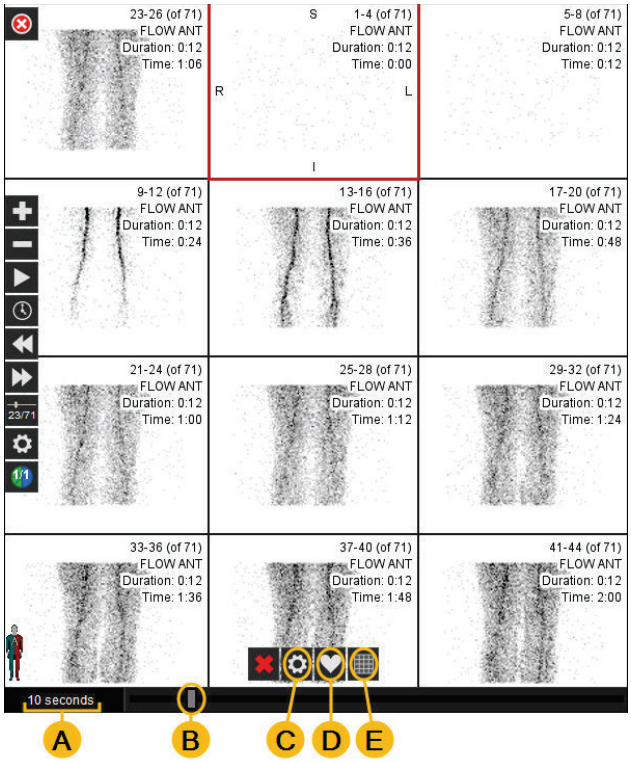
View Dynamic Frames by Slabbing

You can view multiple frames collapsed into a single slab. By default, the maximum intensity projection from each frame is shown in the slabbed frame.

1. In an open session, activate the **Show Planes/Frames as Slabs** tool from the top toolbar.

> **Tip:** If you don't see this tool, click the double arrow on the right side of the toolbar to search for it.

2. Select the desired viewport.
3. Use the slabbing options at the bottom of the viewport:



A. Type the duration of each frame you want to see.

B. Drag the slider left or right to adjust the frame duration.

C. Select whether frames should be slabbed using the maximum, mean, or minimum intensity projection (IP).

D. Choose from your favorite frame lengths. See below for more information about setting and deleting favorites.

E. If you previously used the Grid tool, as described above, adjust the duration so the series fits within the grid you created.

You can see the duration, time stamp, and which of the original frames are included in a frame in the upper-right corner of each frame.

4. Scroll through the series and make additional adjustments as needed.

> **Tip:** If you frequently use the same slabbing settings, you can set them as defaults. Go to Settings >> **General Preferences** and search for **"slab"**. Select **Slabbing** on the left side and update the settings. Or, add favorites as described below.

5. When you are finished viewing the series slabs, click the close button to exit the slabbing tool and return to the original frame view.

You can set favorites for the frame durations that you use the most:

- With the Show Planes/Frames as Slabs tool active, click the heart button from the options at the bottom of the viewport. A list opens of favorite frame duration options so you can quickly select what you need.
- To add a favorite, first set the frame duration using the slider bar or text field. Then, click the heart button and click **Add** at the bottom of the favorites list. The frame duration that you're adding is shown in parentheses.
- To delete a favorite, click the heart button and right-click on the frame duration you wish to delete.

Work with Dynamic Series

MIMTD-1392 • 04 Jan 2024

Overview

MIM® has various playback options for dynamic series. You can adjust frame settings such as duration and motion correction, as well as create derived static series or a gated movie.

Related: For information about creating image grids and summing dynamic frames, see Adjust Image Grids and Frames for Dynamic Series.

Contents

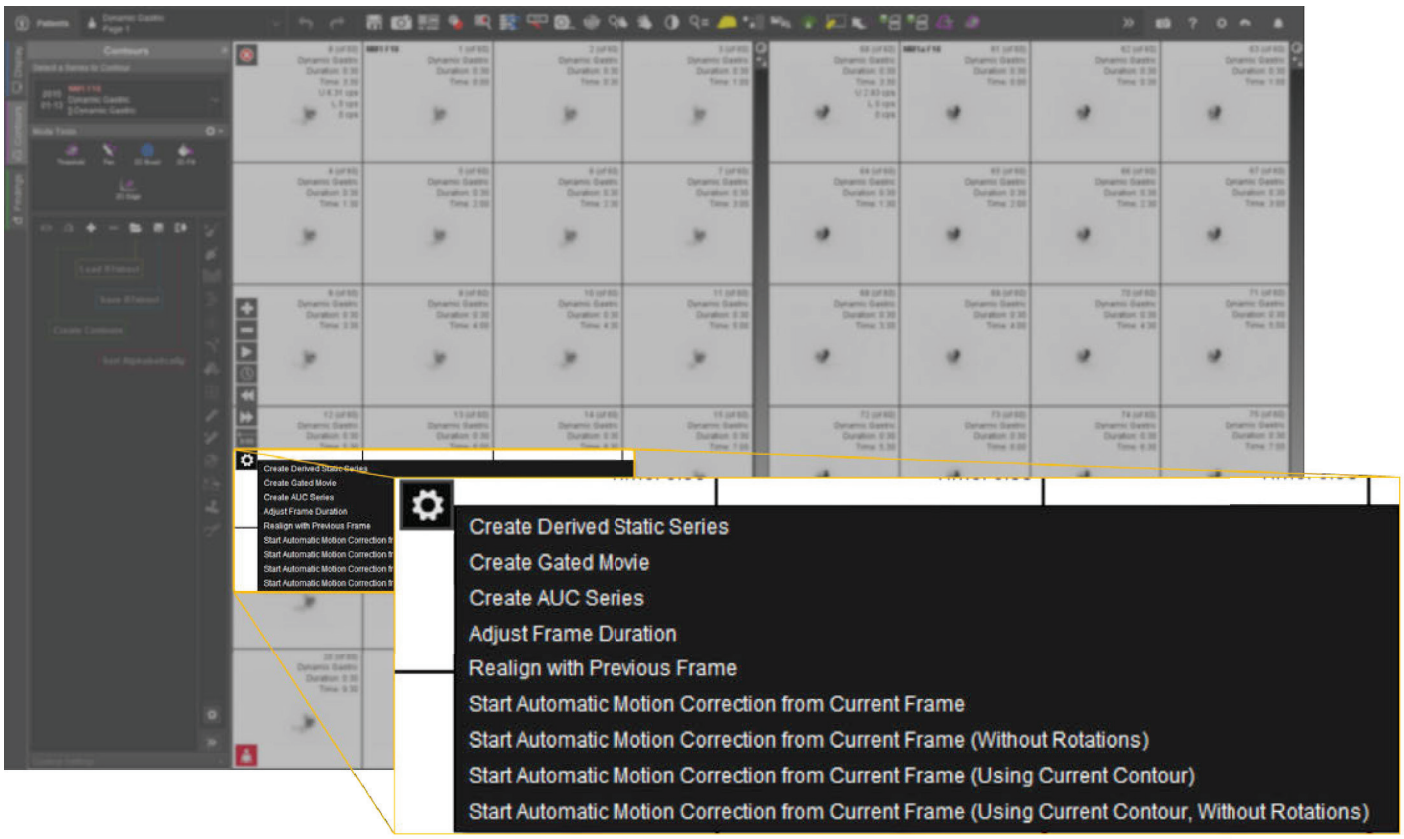
Control 2D Dynamic Playback

On the left side of a 2D dynamic series viewport, use the dynamic series controls to adjust playback as desired:

A. Increase speed
B. Decrease speed
C. Pause/Play
D. Show/Hide dynamic series controls
E. Previous frame
F. Next frame
G. Current frame (use slider bar to adjust)
H. Additional options
I. Choose the phases to display

Additional 2D Dynamic Options

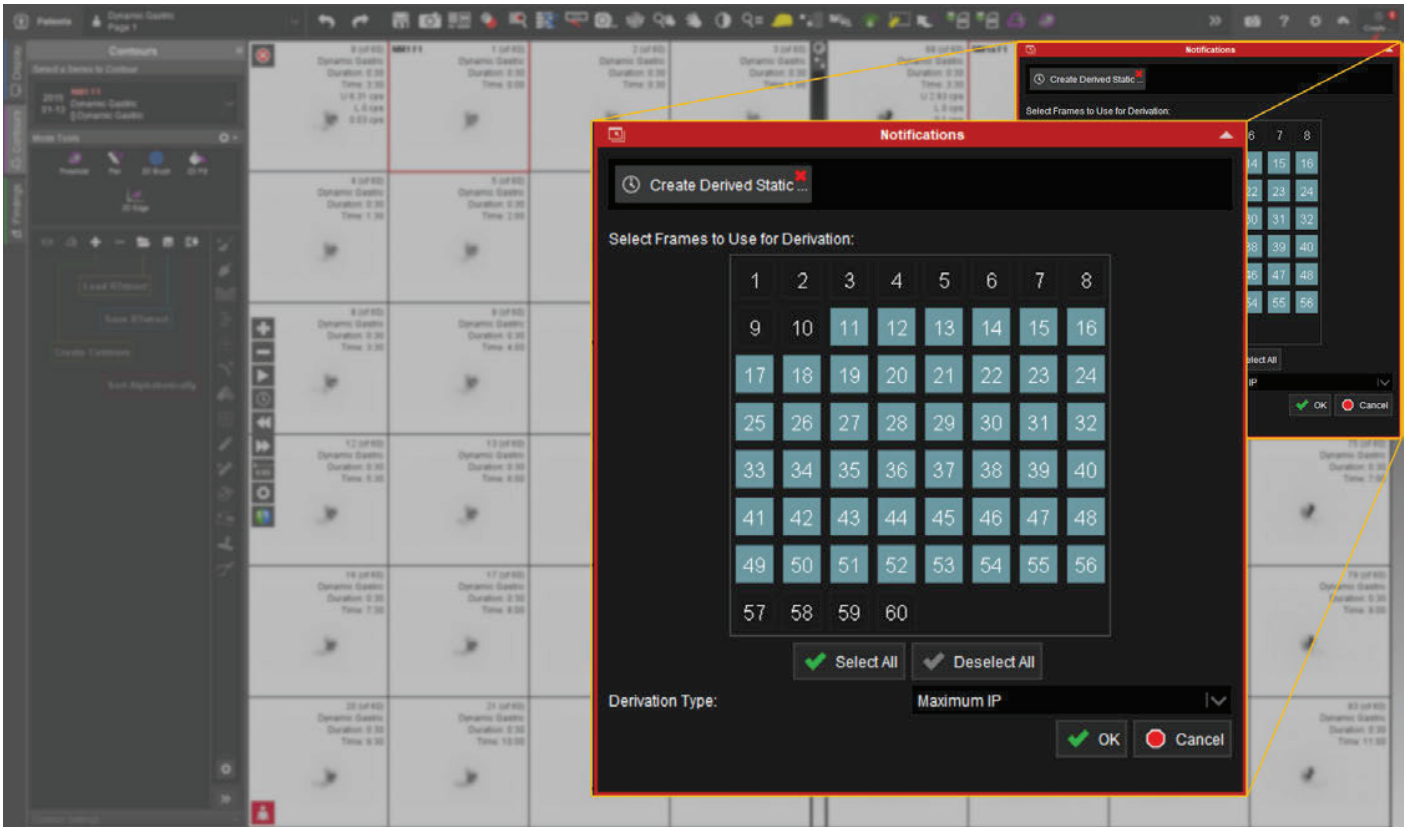
On the left side of a 2D dynamic series viewport, click the gear button to access a menu with additional options.



Create Derived Static Series

1. Select **Create Derived Static Series** from the menu.
2. Select the desired frames:
    - Left-click drag over the desired number of frames.
    - Shift+click to select a range of frames.
    - Ctrl+click to select frames individually.

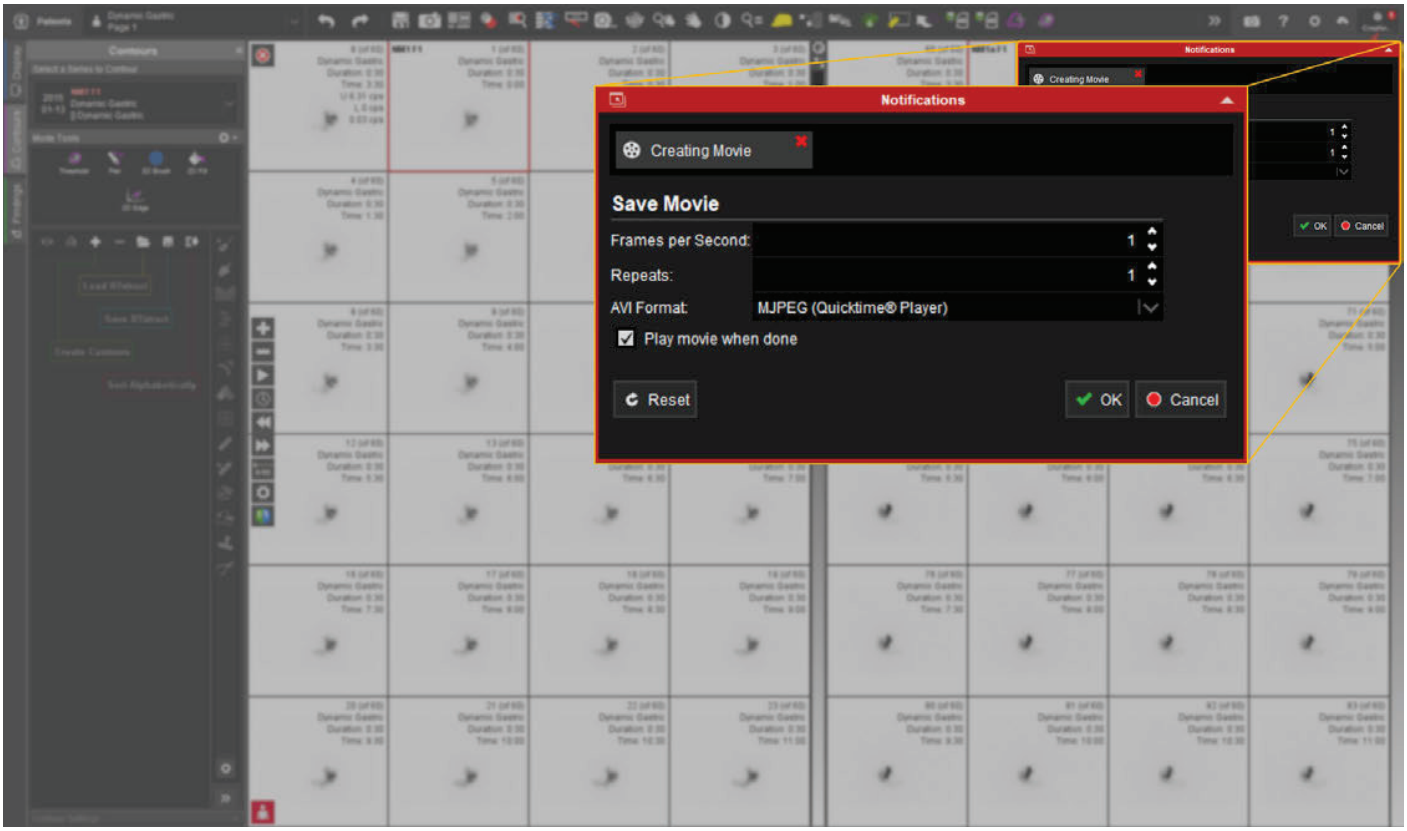
    The selected frames highlight in blue.
3. Choose the **Derivation Type** from the dropdown at the bottom of the window. These include **Maximum IP**, **Mean IP**, **Minimum IP**, and **Sum IP**.
4. Click **OK** to generate the derived static series and display it in a new row.



Create Gated Movie

Save a dynamic image as an AVI movie clip. Select **Create Gated Movie** from the menu and adjust the **Frames per Second** and **Repeats** fields in the Notifications window as desired.

Tip: You can save this movie in a QuickTime® Player or Windows Media® Player format.



Create AUC Series

Calculate and display the AUC (area under the curve) for every voxel across a dynamic series.

Tip: This option only performs mathematical AUC calculation on the dynamic series. It does not calculate total dose or activity administered.

Adjust Frame Duration

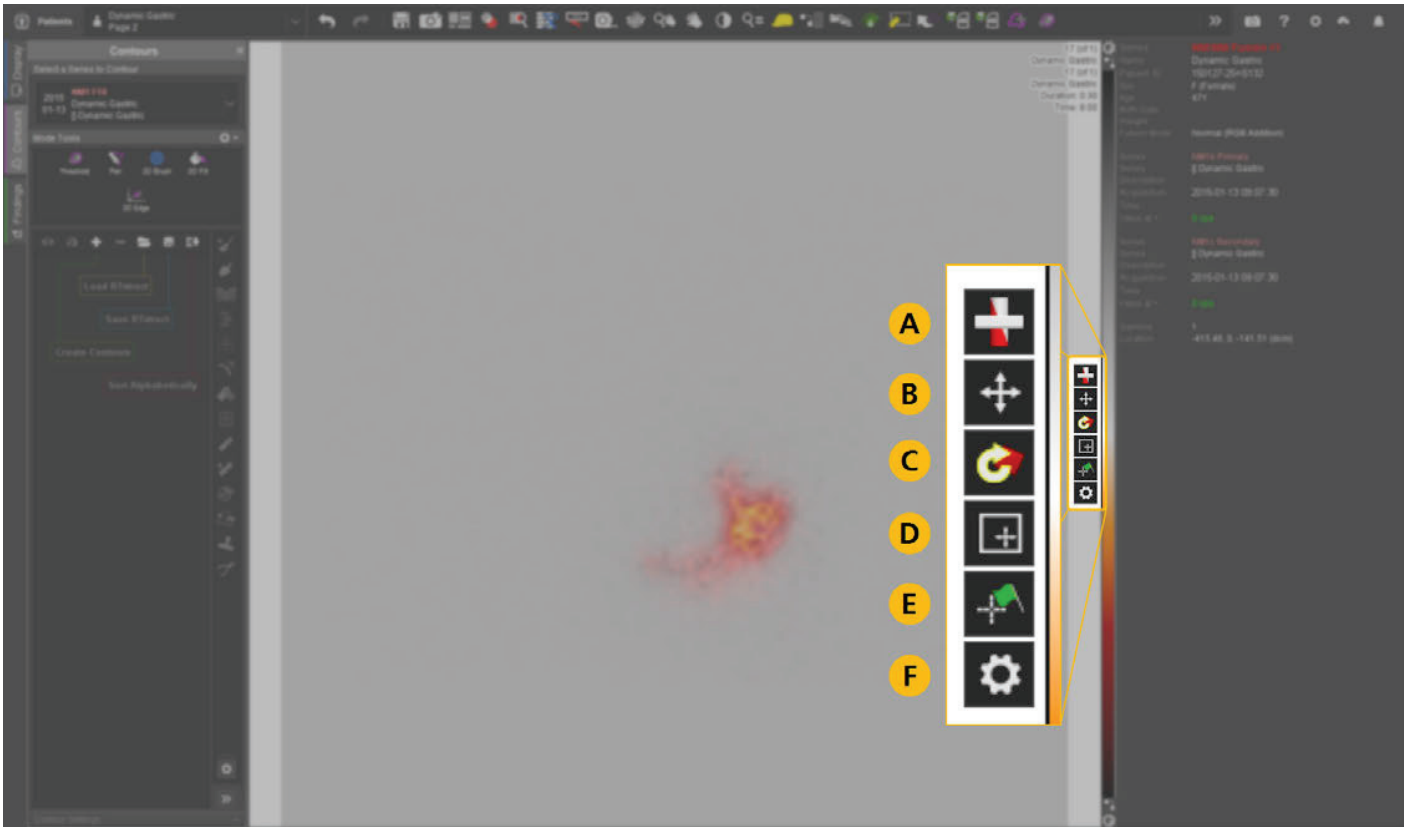
Select **Adjust Frame Duration** from the menu and choose a new frame duration from the dropdown in the Notifications window.

Realign with Previous Frame

Manually realign the current frame with the previous frame for single-frame motion correction.

Tip: If you choose the first frame for realignment, you're prompted to advance to a subsequent frame, as there is no frame prior to the first.

1. Click the frame that you would like to realign. The frame appears outlined in red.
2. Select **Realign with Previous Frame** from the settings menu. A new page appears showing the selected frame (as the secondary image) fused to the previous frame (the primary image).
3. Adjust the alignment between the two frames using the manual fusion tools on the right side of the viewport.
4. Once the alignment is accurate, click the green flag button to accept the newly adjusted alignment. The adjustment is applied to all subsequent frames in the dynamic series.



A. Adjust blending of the primary and secondary images
B. Adjust fusion translation
C. Adjust fusion rotation
D. Run again from the current alignment

E. Accept adjusted alignment
F. Fusion settings

Start Automatic Motion Correction from Current Frame

The **Start Automatic Motion Correction from Current Frame** options automatically correct for motion in a dynamic series based on the current frame. The correction made to the current frame is then applied to the entire series.

There are multiple automatic motion correction options:

- Choose one of the **Using Current Contour** options to use the contour currently selected in the Contours sidebar when applying motion correction.

  Tip: These are typically the preferred methods for motion correction because MIM focuses on a structure (e.g., the kidney) without other movement affecting the correction (e.g., in the bladder).

- Choose one of the **Without Rotations** options to apply motion correction using translation only.

Move Contours on Dynamic Series

You can move contours on a select frame or on all frames simultaneously.

1. Select the **Move** tool in the Contours sidebar.
2. *If you want to move contours on select frames*, click the clock icon next to the contour name in the Contours sidebar and select **Allow per frame contour data**.

   Tip: Disabling per frame contour data merges all contours from all frames into a single contour that propagates to all frames.

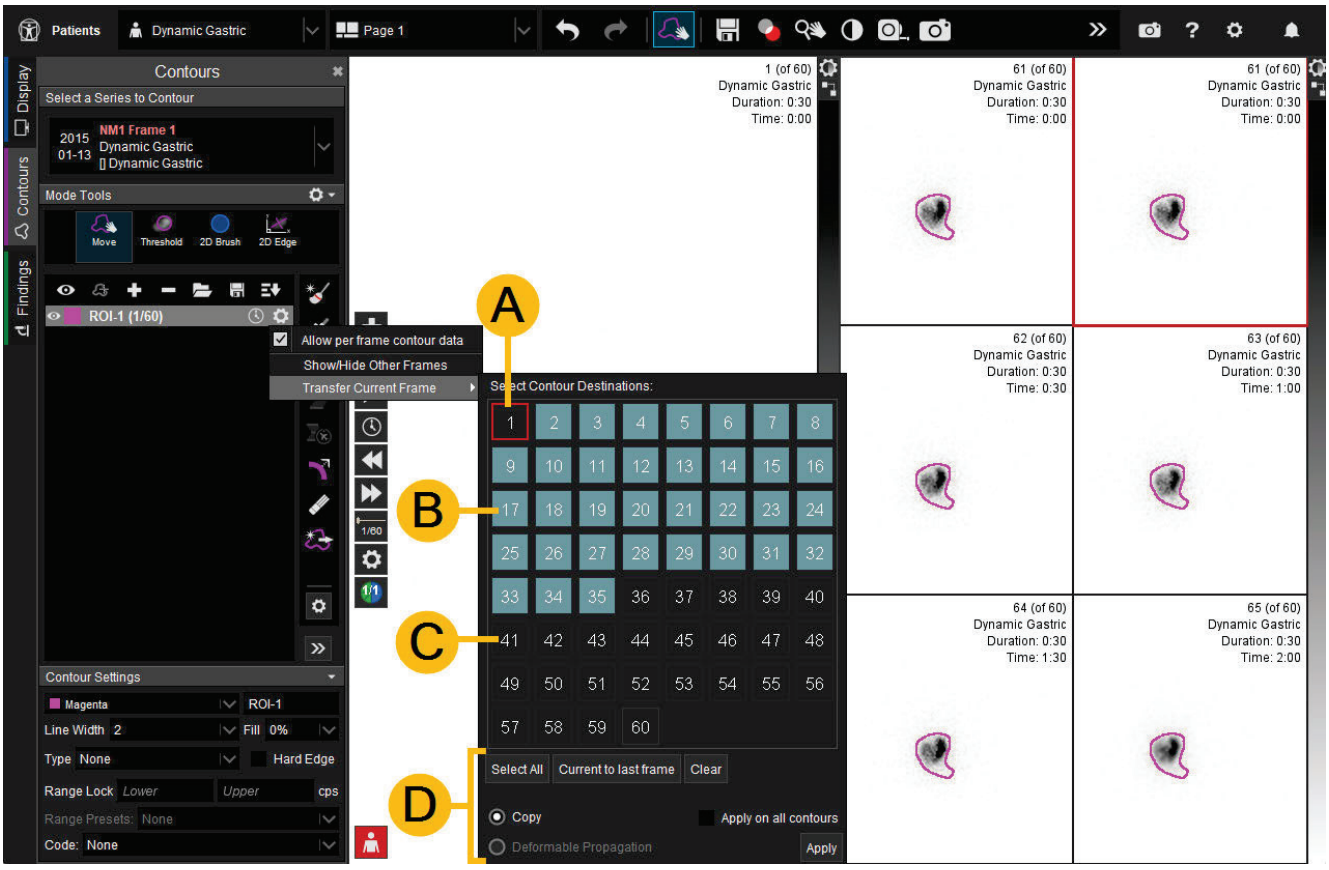
Transfer Contours to Other Frames

1. Click the clock icon next to a contour name in the Contours sidebar and select **Allow per frame contour data**.

   Tip: Disabling per frame contour data merges all contours from all frames into a single contour that propagates to all frames.

2. Hover over **Transfer Current Frame**.

3. Select which frames to transfer the contour to.
4. Click **Apply**.



A. The currently selected frame.
B. The frames that the contour will be transferred to (highlighted in blue).
C. The frames that the contour will not be transferred to.
D. Additional transfer options.

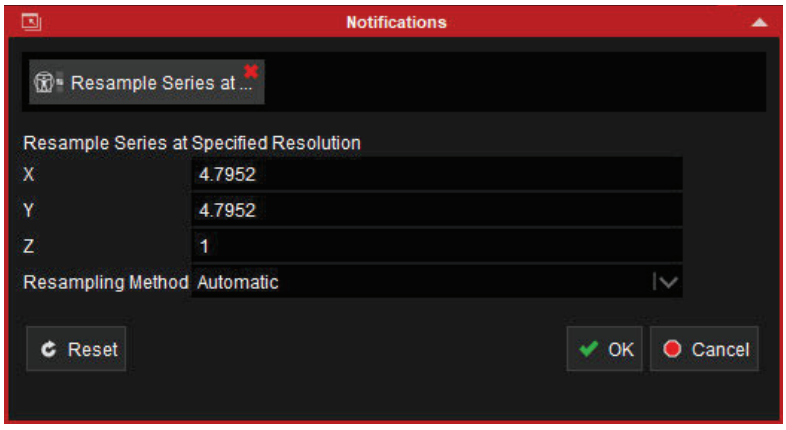
Resample Dynamic Series

To resample all frames of a dynamic series, follow these steps:

1. In an open session with a dynamic series, activate the **Resample Series at Specified Resolution** tool.

Tip: You may need to manually locate this tool by clicking the double arrow ⏩ button on the far right side of the top toolbar.

2. Select the desired series, if prompted.
3. Adjust X, Y, and Z values in millimeters as desired.
4. Specify the resampling method as desired:
    - **Automatic** — Automatically select a method based on the image data.
    - **Linear** — Use linear interpolation to calculate each output voxel value.
    - **Hierarchical** — Perform multiple iterations of linear interpolation. This method only applies for images with decreasing dimensions.
    - **Rebin Data** — Distribute the value of each input voxel proportionally to the overlapping output voxels.



5. Click **OK** to create the resampled series. You can identify the resampled series by the text **RESAMPLED** in the series description.

Create and Adjust Fusions

Create a Fusion Manually

MIMTD-620 • 21 Dec 2023

Overview

A fusion produces a link between two series that lets you localize and scroll on both series simultaneously, transfer contours, and more.

Contents

Create a Fusion

To manually create a fusion, follow these steps:

Tip: When opening a series (e.g., a PET/CT series) it is possible a fusion is created automatically by MIM®.

1. Open or create a session with multiple series displayed on the same page.
2. Activate the **Create Fusion** tool from the top toolbar.

Related: For more information, see Access Tools: The Toolbar and the Radial Menu.

3. Click the **Select this series** button for the series that you want to be the primary series (see Primary vs. Secondary Series for more information).
4. *If only one other series exists on the page*, MIM automatically selects it as the secondary series.

   If multiple other series exist on the page, click the **Select this series** button for the series that you want to be the secondary series (see Primary vs. Secondary Series for more information).

A fusion is created and appears in a new row at the bottom of the current page.

5. If necessary, make adjustments to the fusion.

Related: See Adjusting Fusions for more information.

Primary vs. Secondary Series

The primary series in a fusion is the series that remains unaltered when a fusion is performed. Typically, this series is:

- The most current time point out of the two series
- The CT in a PET/CT study

The secondary series in a fusion is the series that is adjusted via rotation and translation to align with the primary series.

Break Spatial Links To Create Independent Fusions

If you have series that were acquired together (e.g., two MR sequences) and you fuse each MR to your plan CT, adjustments to one fusion (MR1/CT) affect the other fusion (MR2/CT). This is because the MR2/CT fusion preserves the pre-existing acquisition link between MR1 and MR2. You can break the pre-existing link so that adjustments to the MR1/CT fusion do not affect the MR2/CT fusion.

If you want to adjust the two fusions separately, follow these steps:

1. Break the link between the two MR series.

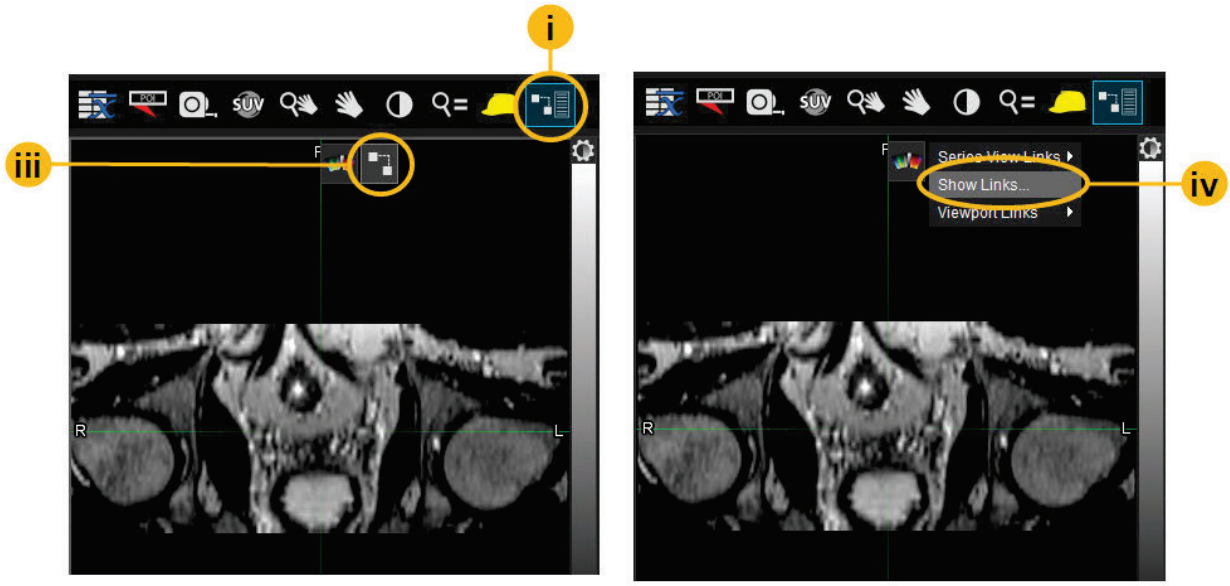
> **Tip:** Ensure you break the links between the MR series before fusing to the CT.

i. Activate the **Link Manager** tool.

> **Related:** If you use this tool regularly, you can add it to your toolbar for easy access. For more information, see Access Tools: The Toolbar and the Radial Menu.

ii. Hover over any series. The Link Manager button appears in the center at the top of the viewport.

iii. Click the **Link Manager** button in the viewport.

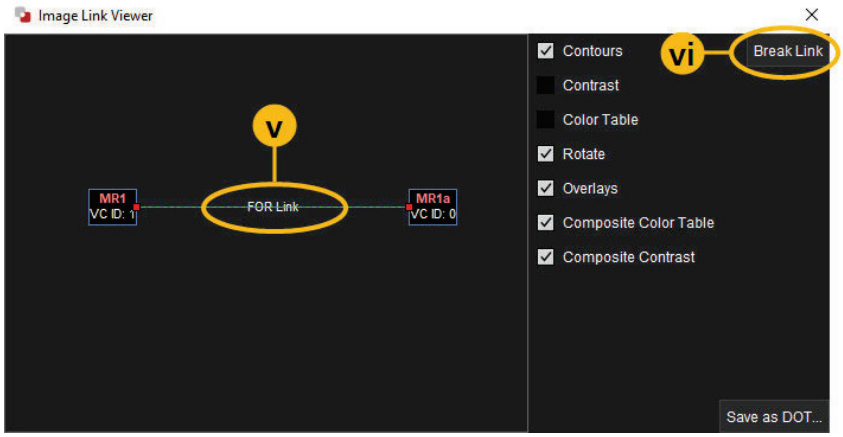


iv. Select **Show Links...**. The Image Link Viewer window opens.

> **Tip:** You may need to reposition the series in the Image Link Viewer window to more easily visualize the links.

v. Click the link (shown as a line) between the two MR series.

vi. Click **Break Link** in the upper-right corner of the window.



vii. When finished, click the X to close the Image Link Viewer window.

2. Fuse MR1 to the CT.
3. Fuse MR2 to the CT.

> **Related:** See Adjust Links between Series Using the Link Manager for more information on links between series.

Create Multiple Fusions with the Same Series

> **Tip:** If you would like to automate this process using a MIM Workflow™, please speak with your MIM Site Development Manager or contact MIM Software Support at support.mimsoftware.com.

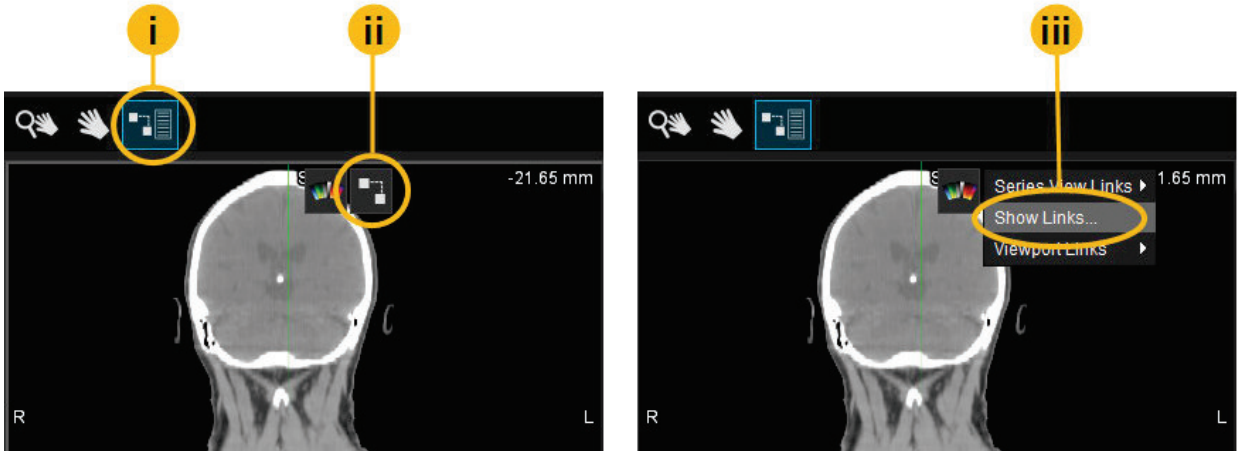
You can create multiple, but separate fusions. For example, you may want to visualize different fusions as part of the pre-planning process.

To create multiple separate fusions between the same two series, follow these steps:

1. Open the two series in a session (e.g., CT1 and CT2).
2. Return to the patient list, and double-click on the second series (the series that will be the secondary series in the fusion). A second copy of the series (CT2a) opens in the session.
   Alternatively, you can generate a second copy of the series using the Scale Image Intensity tool:
   i. Activate the **Scale Image Intensity** tool. (To find the tool, click the button at the top of MIM to search all tools.)
   ii. Select series CT2.
   iii. Enter 1 for the **Scale Factor** to create a copy of the series (CT2a).
3. Break the link between CT2 and CT2a.
   i. Activate the **Link Manager** tool.

> **Related:** If you use this tool regularly, you can add it to your toolbar for easy access. For more information, see Access Tools: The Toolbar and the Radial Menu.

   ii. Click the **Link Manager** button in the viewport.

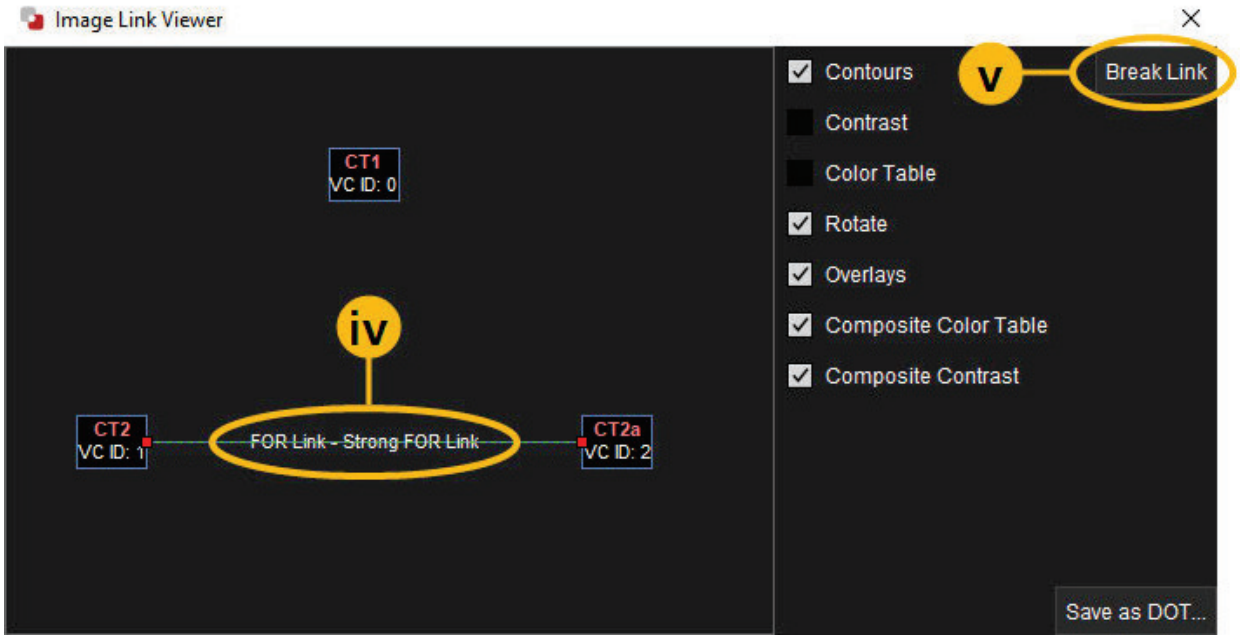


   iii. Click **Show Links…**. The Image Link Viewer window opens.

> **Tip:** You may need to reposition the series in the Image Link Viewer window to more easily visualize the links.

   iv. Click the **FOR Link - Strong FOR Link** between CT2 and CT2a in the Image Link Viewer window.

v. Click **Break Link** in the upper-right corner of the window.

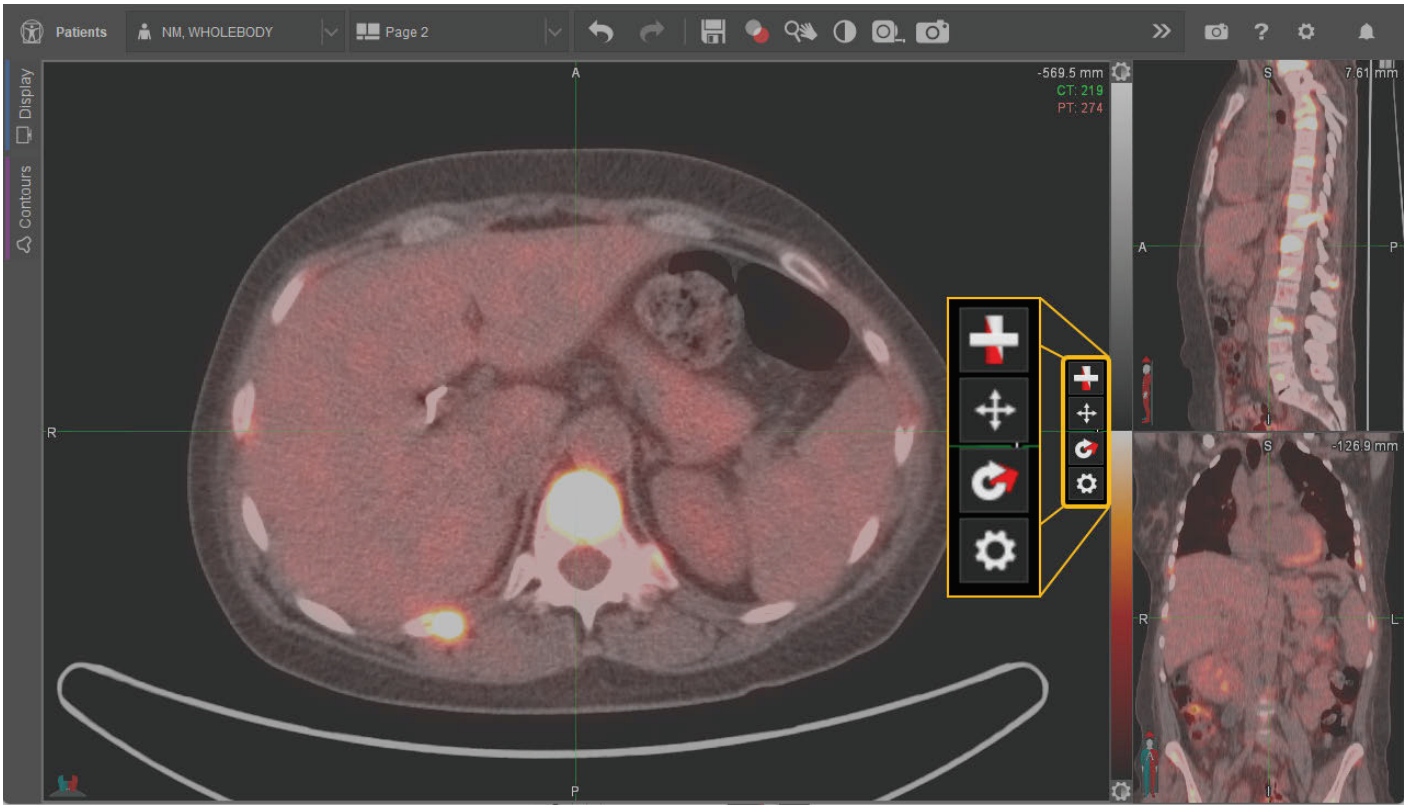


vi. When finished, click the X to close the Image Link Viewer window.

4. Create and adjust the fusions.
   i. Fuse the primary and the secondary series (CT1 and CT2).
   ii. Create a second fusion between the primary and the copy of the secondary series (CT1 and CT2a).
   iii. Adjust the fusions as desired.

Related: See Adjusting Links between Series Using the Link Manager for more information on links between series.

Show/Hide the Fusion Companion Tools



By default, the fusion companion tools always appear when hovering in a fusion viewport. To toggle the fusion companion tools on and off within a session, you can create a keyboard shortcut.

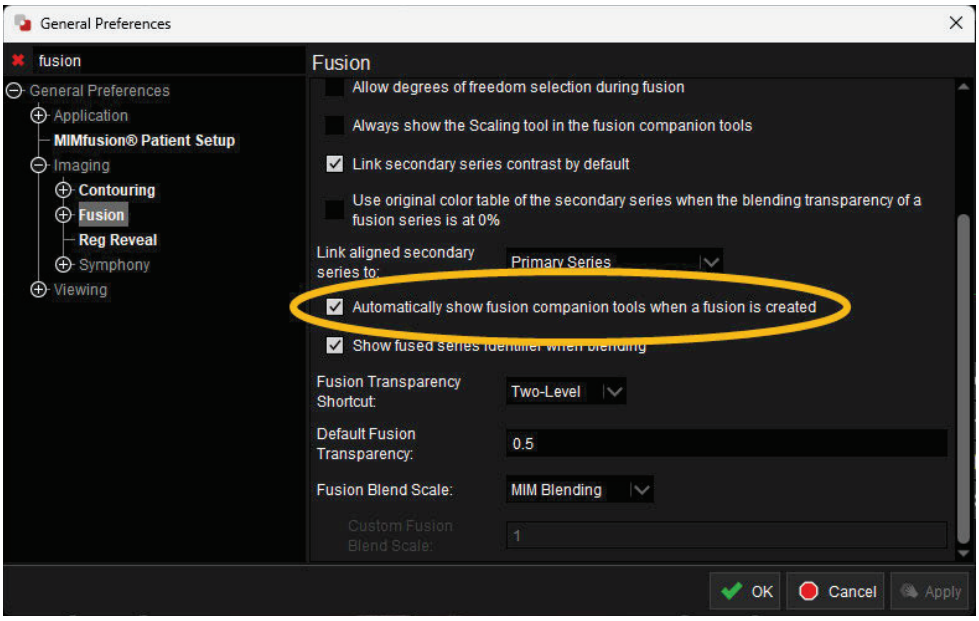
Related: For instructions on configuring keyboard shortcuts, see Set Keyboard Shortcuts.

The default behavior can also be changed. This is helpful if a viewport size is very small or zoomed in and the fusion companion tools are obstructing the image.

To hide the fusion companion tools by default, follow the steps below:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**fusion**". Select **Fusion** on the left side.

3. Deselect **Automatically show fusion companion tools when a fusion is created**.



4. Click **OK** to save the changes and close the window.

Tip: When changed, this setting takes effect in any open sessions that include a fusion.

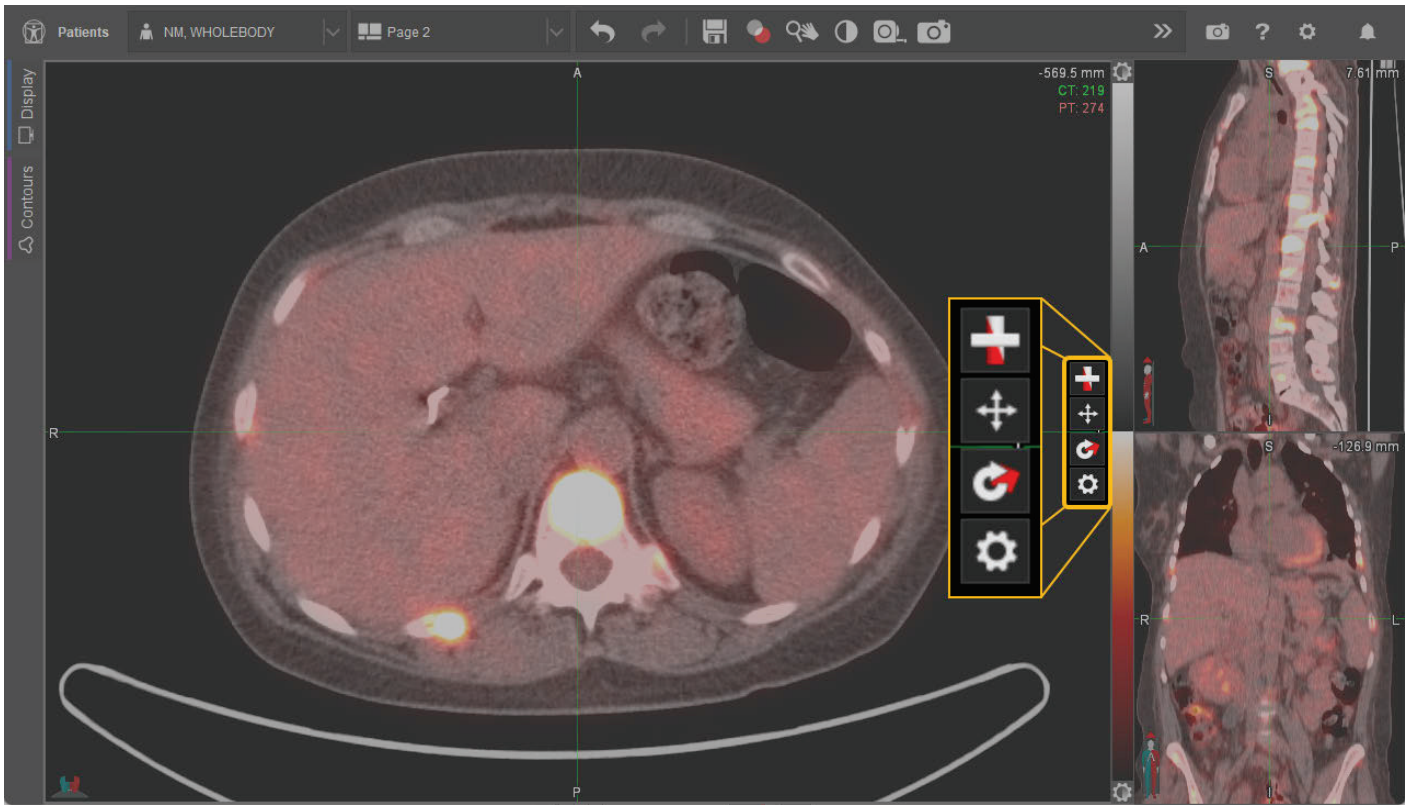
Tip: Your preference to show/hide fusion companion tools is not included when you save a session. If a saved session is opened by another user, the fusion companion tools are shown or hidden according to that user's preference.

Adjust Fusions Manually

MIMTD-621 • 02 Jan 2024

Overview

When you hover over a fusion viewport in any plane, MIM® displays companion tools on the right side. Use these tools to adjust the alignment of the two images. Fusions are typically done automatically when using a workflow, and you're prompted to review and make adjustments as desired.

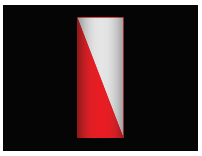


You can automatically show or hide these companion tools. For more information, see Configure Fusion Settings.

Related: For information about optimizing fusions automatically, see Optimize Fusions Automatically.

Tip: *MIM 7.2 and later*: The Scale (MIM 7.2 and Later) tool can also be enabled. *MIM 7.1 and earlier*: This functionality is not available.

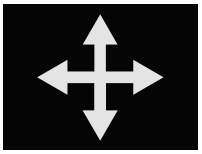
Contents



Blend

- Left-click drag up/down to blend between the primary series and secondary series.
- Right-click the Blend tool to reset the blend.

Tip: Press the Tab key on your keyboard to toggle between the primary series and blend.



Translate

- Left-click drag to move the secondary series up/down or left/right to better align with the primary.
- Double-click on the tool to automatically rerun rigid assisted alignment.
- Right-click the Translate tool to reset the original position of the series.
- Use keyboard shortcuts to fine-tune the adjustment. Ensure the Translate tool is still activated:

	Large Adjustments	Small Adjustments	Very Small Adjustments
Windows®	Ctrl+arrow keys	Shift+arrow keys	Alt+arrow keys
macOS®	Command+arrow keys	Shift+arrow keys	Option+arrow keys

Tip: To view and manually specify the exact translation in millimeters in the X, Y, and Z directions, use the **Edit Fusion Alignment Translation** tool. To access the tool, add it to your fusion settings menu. For more information, see Configure Fusion Settings.

Rotate

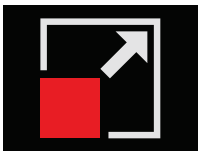
- Left-click drag to rotate the secondary series around the center of the primary series.

Tip: Drag straight up/down or left/right for best performance. Moving the mouse in a circular fashion results in erratic movements.

Tip: If desired, you can change the rotation center to the secondary series center, isocenter, DICOM origin, or localization point via **Settings** ⚙ **>> General Preferences >> Imaging >> Fusion**.

- Right-click the Rotate tool to reset the original position of the series.

Tip: To view and manually specify the exact rotation in degrees in each plane, use the **Edit Fusion Alignment Rotation** tool. To access the tool, add it to your fusion settings menu. For more information, see Configure Fusion Settings.



Scale (MIM 7.2 and Later)

To use the Scale tool, follow the steps below. In MIM 7.1 and earlier, this functionality is not available.

MIM 7.3 and later:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**fusion**". Select **Fusion** on the left side.
3. Select **Always show the Scaling tool in the fusion companion tools**.
4. Click **OK** to save the changes and close the window.
5. In the viewport, select the Scale tool.
6. Left-click drag up/down or left/right to adjust the scale of the secondary series.
7. Right-click the Scale tool to reset the secondary series to its original size and position.

Tip: If you activate the Scale tool on a fusion that does not have scaling enabled, you are prompted to enable scaling for that fusion.

In MIM 7.2:

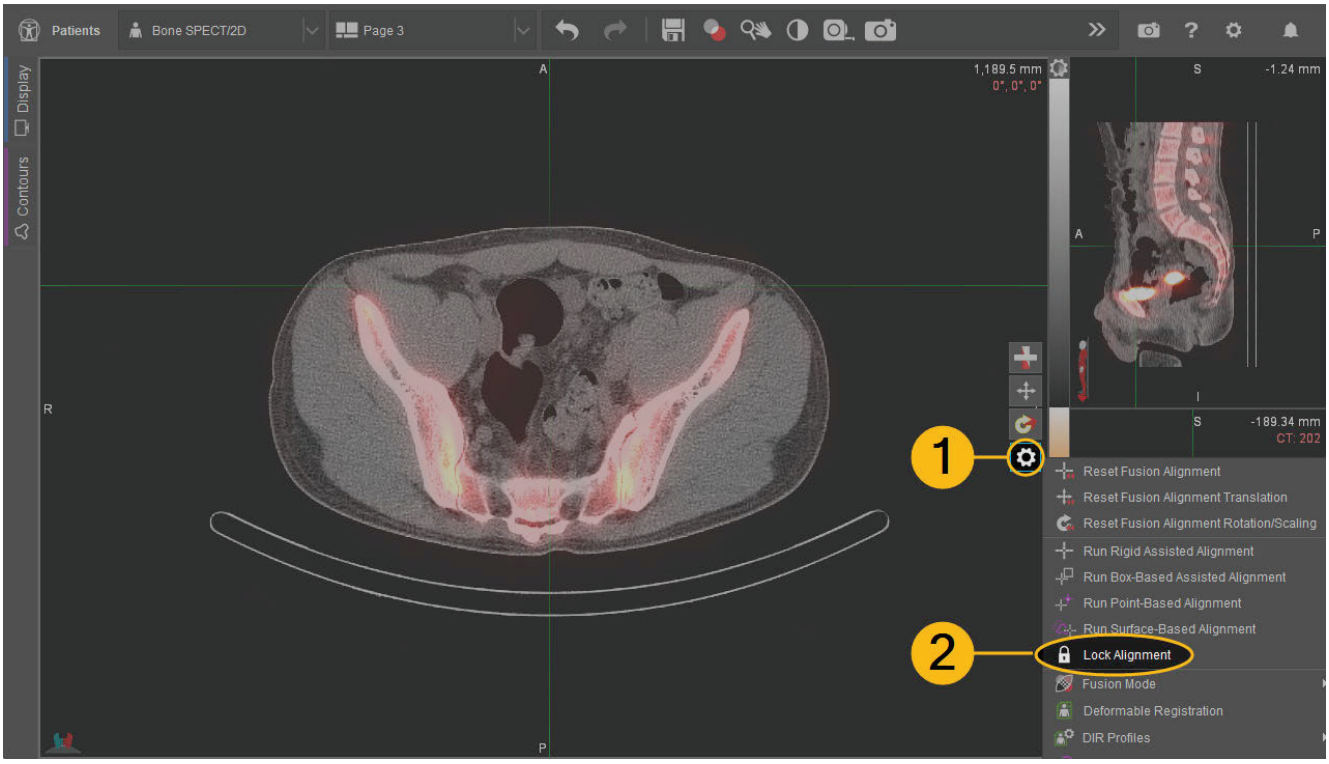
1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**fusion settings menu**". Select **Fusion Settings Menu** on the left side.
3. Drag **Enable/Disable Scaling** from the left menu to the right menu.
4. Click **OK** to save the changes and close the window.
5. In the viewport, open the Fusion Settings Menu and select the Scale tool.
6. Left-click drag up/down or left/right to adjust the scale of the secondary series.
7. Right-click the Scale tool to reset the secondary series to its original size and position.

Tip: If you activate the Scale tool on a fusion that does not have scaling enabled, you are prompted to enable scaling for that fusion.

Lock/Unlock Alignment

Lock a fusion alignment to prevent changes from being made:

1. Click the Settings button on the right side of a fusion viewport.
2. Select **Lock Alignment**.



Tip: To unlock an alignment, click the Fusion Settings menu and select **Unlock Alignment**.

Optimize Fusions Automatically

MIMTD-1724 • 17 Oct 2023

Overview

6.1.5

MIM® has many automatic tools and methods that let you adjust the alignment of two images. Images can be aligned by a specific region of interest, by contour intensity, by contour borders, by landmark points, and with or without a pre-existing link.

Related: For information about adjusting fusions manually, see Adjust Fusions Manually.

6.1.5

Tip: Fusions are typically done automatically when using a workflow, and you're prompted to review and make adjustments as desired.

Contents

Run Rigid Assisted Alignment vs. Reset Fusion Alignment

Rigid Assisted Alignment is run when you use the **Create Fusion** tool to register two images.

If there is a pre-existing link between two series, MIM uses that link to generate a fusion. A pre-existing link results from:

- A shared Frame of Reference (FOR) between two series (e.g., when images are acquired together on the same scanner).
- A REG file that links the two images. REG files contain information that dictates how two images are aligned, and do not contain any image data.

- A link to another series. For example, if Series A and Series B share a FOR, and Series A is fused to Series C (which has a different FOR), Rigid Assisted Alignment runs. Then, if Series B is fused to Series C, the existing link between Series A and Series C is used for the new fusion.

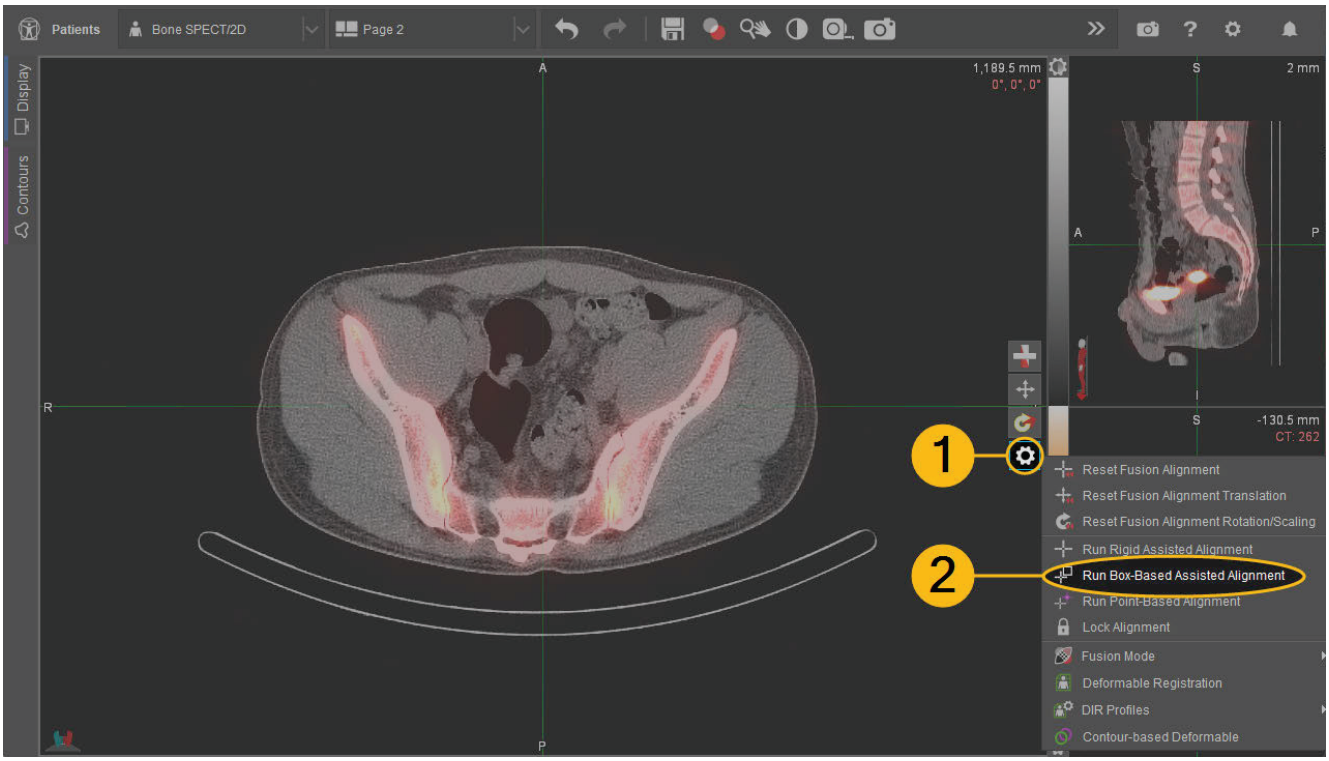
Reset Fusion Alignment resets the fusion using the DICOM orientation to attempt to orient the patient images in the same direction.

- If the scans share a Frame of Reference (FOR), the tool sets the translation based on the image's DICOM coordinates.
- If the images do not share a FOR, the tool aligns the scans center-to-center.

Box-Based Assisted Alignment

Box-Based Assisted Alignment works like Rigid Assisted Alignment by maximizing mutual information, but it restricts the data considered to what is contained within the user-specified box.

1. Click the **Fusion Settings** menu.
2. Select the **Box-Based Assisted Alignment**. A white box displays on the fusion image.



3. Adjust the size of the box to fit around the area of interest in all three planes:
    - To move the box, left-click drag with the cursor inside the box.
    - To resize the box, left-click drag any points on the box, or right-click drag up/down within the box.
4. With the box adjusted to the correct dimensions around the area of interest, click the box-based assisted alignment button located below the **Fusion Settings** menu. This reruns the Rigid Assisted Alignment algorithm with the emphasis placed on the area within the box.

> **Tip:** You can run the Box-Based Assisted Alignment tool as many times as needed.

Contour-Based Alignment

Contour-Based Alignment works like Rigid Assisted Alignment by maximizing mutual information, but it restricts the data considered to what is contained within the user-specified contour.

> **Important:** Contour-Based Alignment does *not* register images by matching contours on the primary and secondary image. It restricts the area considered for rigid alignment to the area of the selected contour on the primary image. If you would like to align images based on contour borders, see Surface-Based Alignment.

1. Use an existing contour or draw a contour of an area of interest on the primary series of the fusion you want to use for alignment.
2. Click the **Fusion Settings** menu.
3. Select **Run Contour-Based Alignment**.
    - If only one contour exists on the primary series, the algorithm automatically uses this contour.
    - If multiple contours exist on the primary series, select which contour to use from the Notifications window and click **OK**.

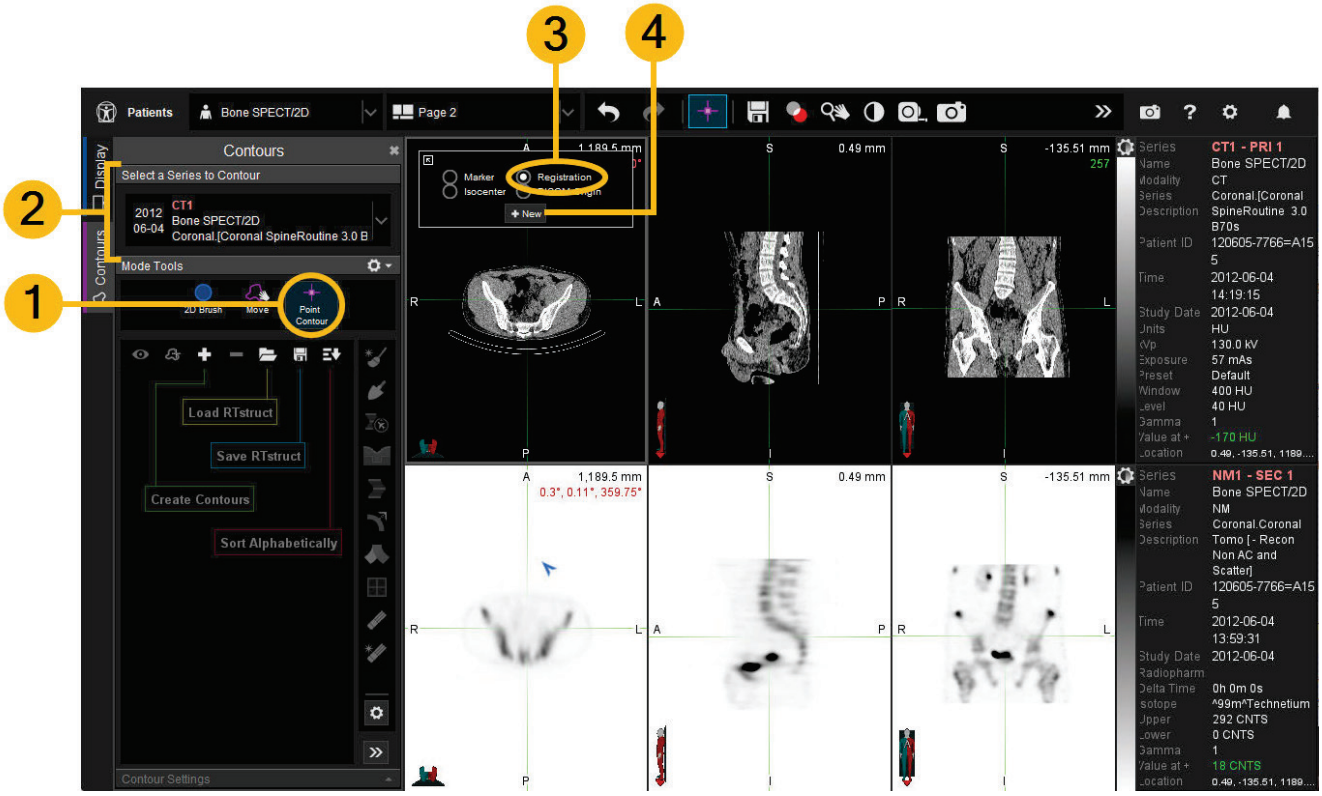
Point-Based Alignment

Point-Based Alignment works by minimizing distances between selected landmark points. Create registration points before manually fusing series.

Create at least one pair of corresponding registration point contours on the series being aligned. Points can be placed at fiducial and/or internal markers or in corresponding anatomic structures in both series. Registration point contours are matched based on the order in which they were created. For example, if a

point contour was created on the primary series, and then the secondary series, MIM recognizes these as a pair.

1. Activate the **Point Contour** contouring tool.
2. Set the primary series as the active series to contour.
3. Ensure the **Registration** radio button is selected in the box at the top of the viewport.
4. Localize where you would like to create a point contour on the primary series. Click the **New** button at the top of the viewport to create the contour.

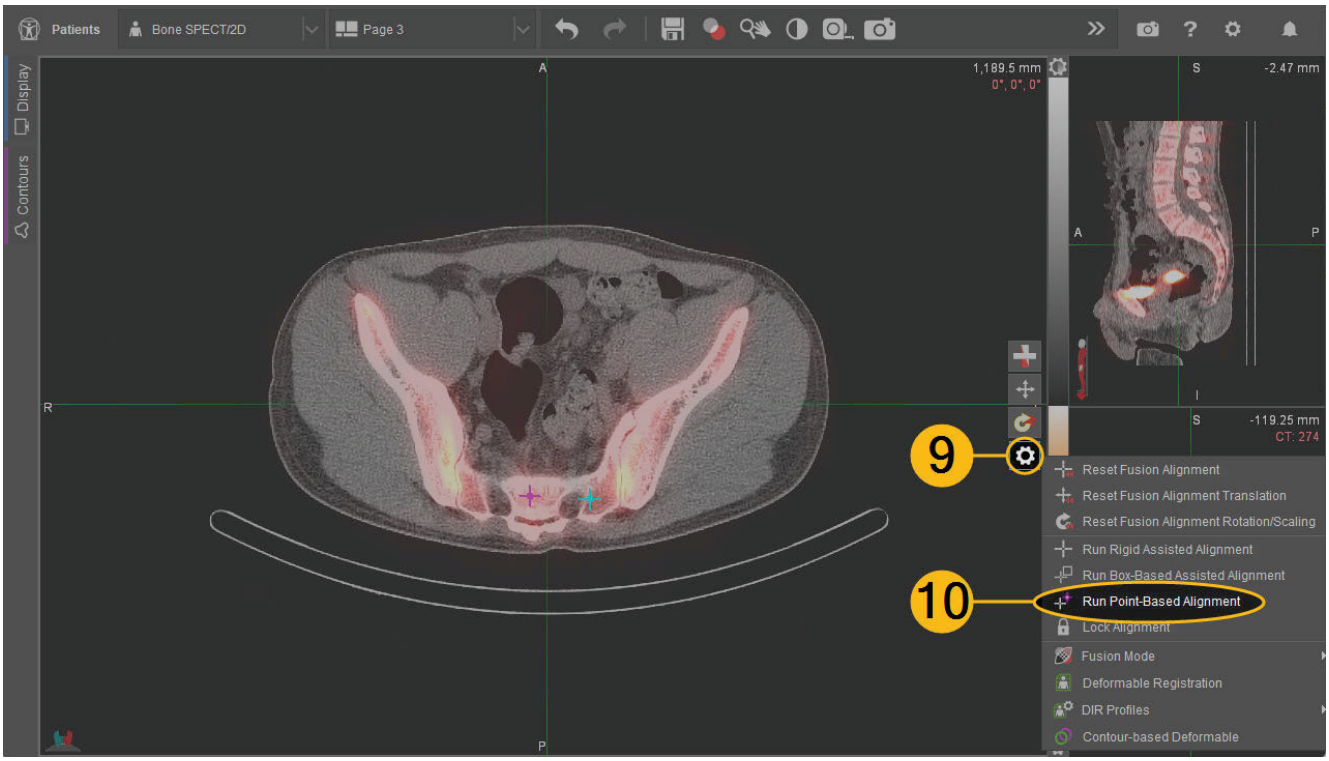


5. Set the secondary series as the active series to contour.
6. Localize where you would like to create a point contour on the secondary series and click **New** to create the corresponding contour.
7. Repeat steps 2 through 6 to create all corresponding contours as necessary.

> **Tip:** Point-Based Alignment performs translation (no rotation) if only one pair of landmark points is created.

8. Once all registration point contours are created, manually fuse series with the **Create Fusion** tool.
9. Click the **Fusion Settings** menu.

10. Select **Run Point-Based Alignment** to run the alignment based on the registration point contours. If additional alignment is necessary, use the manual adjustment tools.



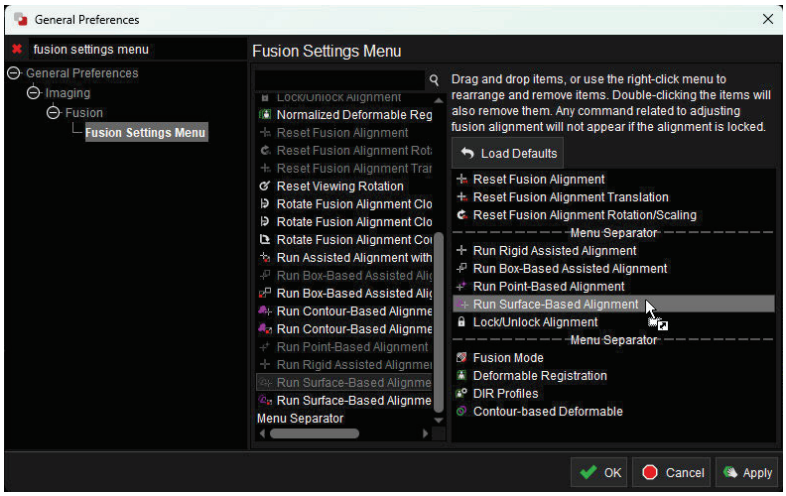
Related: For information about using the manual adjustment tools, see Adjust Fusions Manually.

Surface-Based Alignment

Surface-Based Alignment works by aligning images based on contour borders, not intensity.

1. Add Surface-Based Alignment to the Fusion Settings Menu.
   i. Click the Settings button in the upper-right corner of MIM.
   ii. Go to **General Preferences** and search for "**fusion settings menu**". Select **Fusion Settings Menu** on the left side.

iii. Drag **Run Surface-Based Alignment** from the left menu to the right menu.



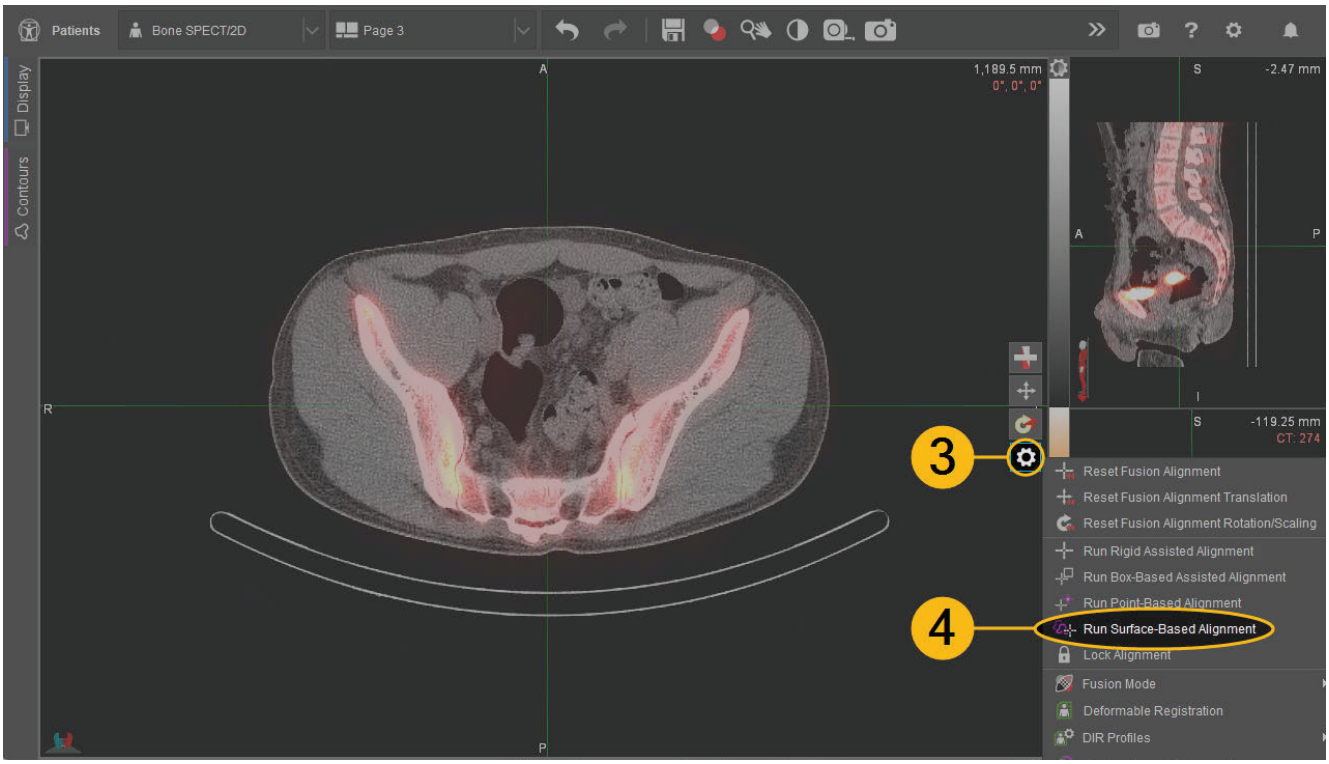
iv. Click **OK** to save the changes and close the window.

2. Use existing contours or draw contours of an area of interest on both the primary and secondary series you want to align.

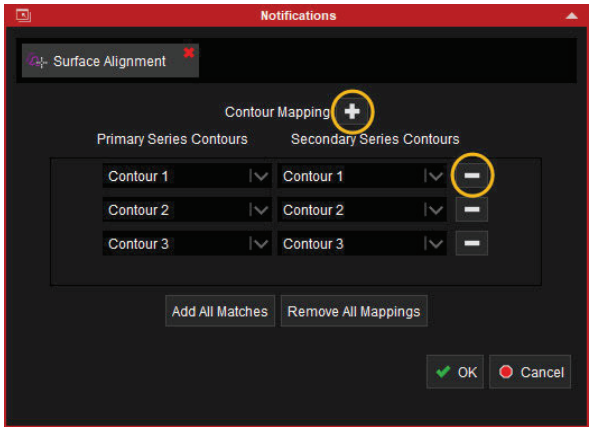
> **Tip:** If drawing contours, ensure the correct series is selected from the **Select a Series to Contour** dropdown.

3. Click the **Fusion Settings** menu.

4. Select **Run Surface-Based Alignment**.



5. In the Notifications window that appears, MIM automatically matches all contours that have identical names.
   - To add another match, click the plus ✚ button and select the desired contours.
   - To remove a match, click the minus ▬ button.

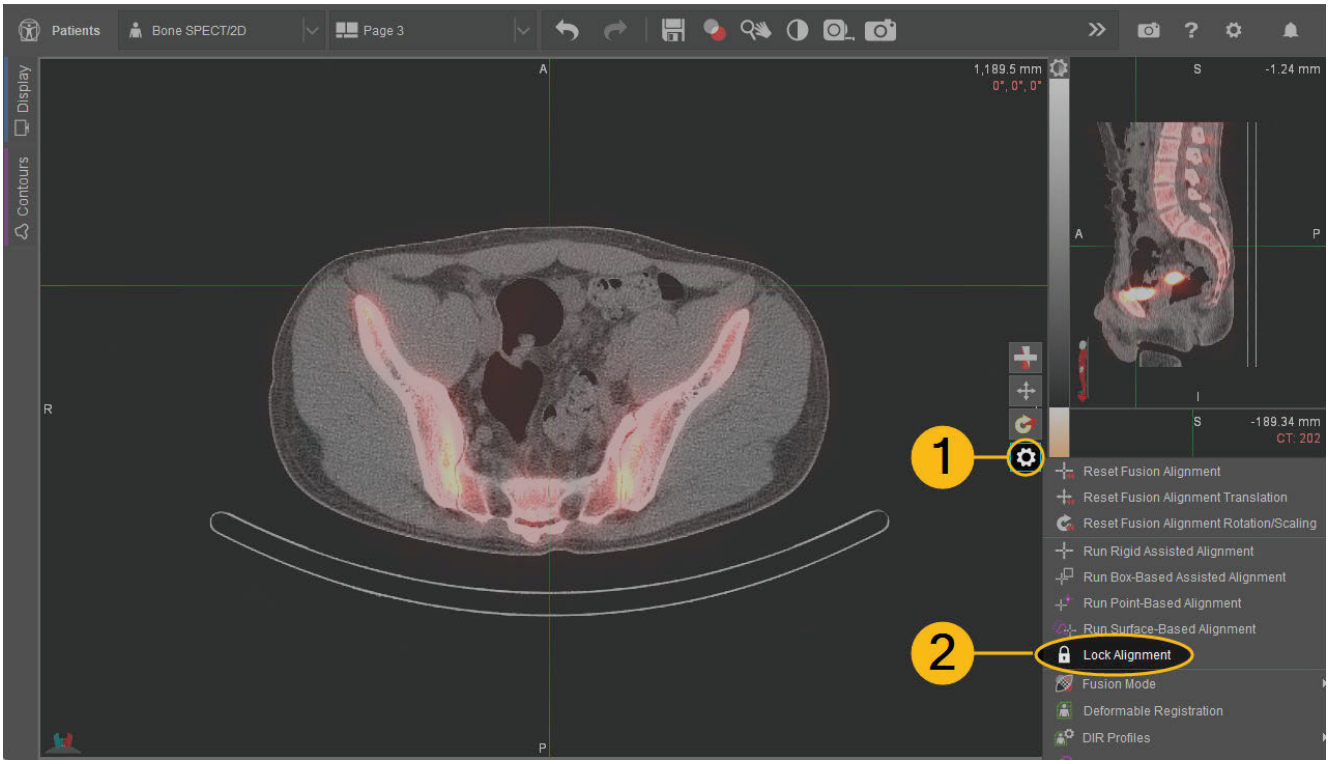


6. Click **OK** to run the alignment based on the contour pairs selected.

Lock/Unlock Alignment

Lock a fusion alignment to prevent changes from being made:

1. Click the Settings ⚙ button on the right side of a fusion viewport.
2. Select **Lock Alignment**.



Tip: To unlock an alignment, click the Fusion Settings ⚙ menu and select **Unlock Alignment**.

View Images with Various Fusion Modes

MIMTD-1298 • 09 Jan 2024

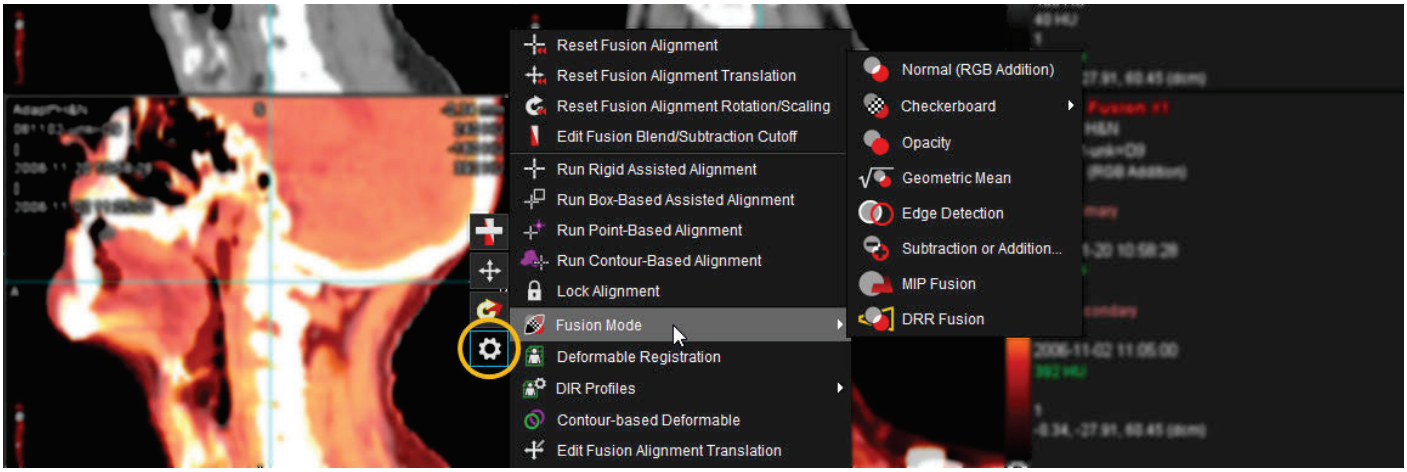
Overview

MIM® provides a number of different ways to visualize image fusions. These different fusion modes allow for the variability of personal preference and can provide specialized viewing conditions for particular types of studies.

Contents

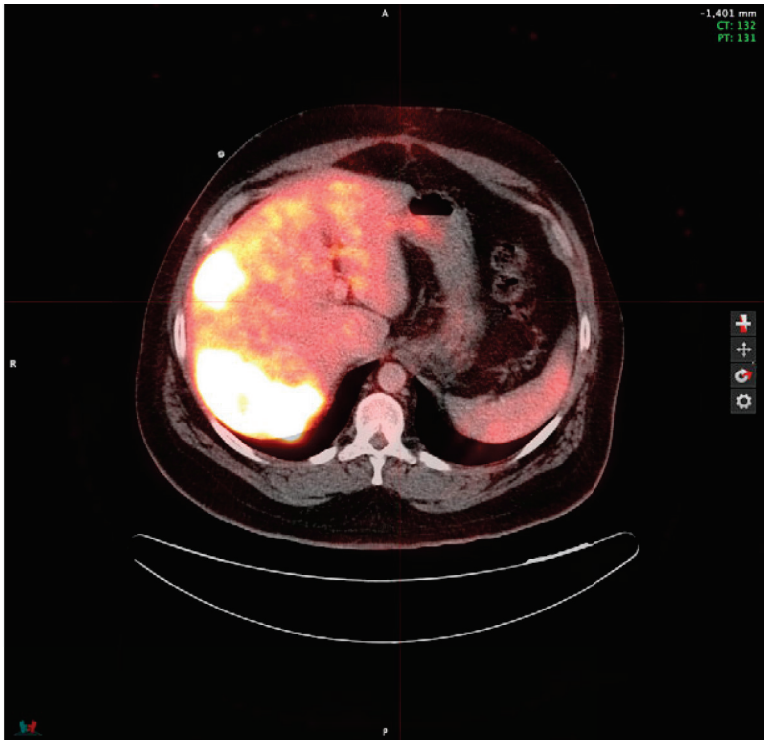
Change Fusion Modes in a Session

1. Click the gear button on the right side of any fusion viewport.
2. In the menu that opens, hover over **Fusion Mode** to see available options.



Fusion Modes

Normal (RGB Addition)



This is the default fusion mode in MIM. In this mode, MIM adds color to color (red to red, green to green, blue to blue) at each voxel location to create the fusion you see.

MIM uses a scaled blending algorithm that, at the middle point of "50%" displays 80% of the primary and 80% of the secondary. This works well in fusions where the secondary color table goes from dark to bright,

like Hot Metal (MIM's default for PT/CT fusions). However, it may not be ideal for a secondary color table, like Rainbow, that has equivalent brightness throughout. With this color table, the default blending algorithm can result in a washed-out image.

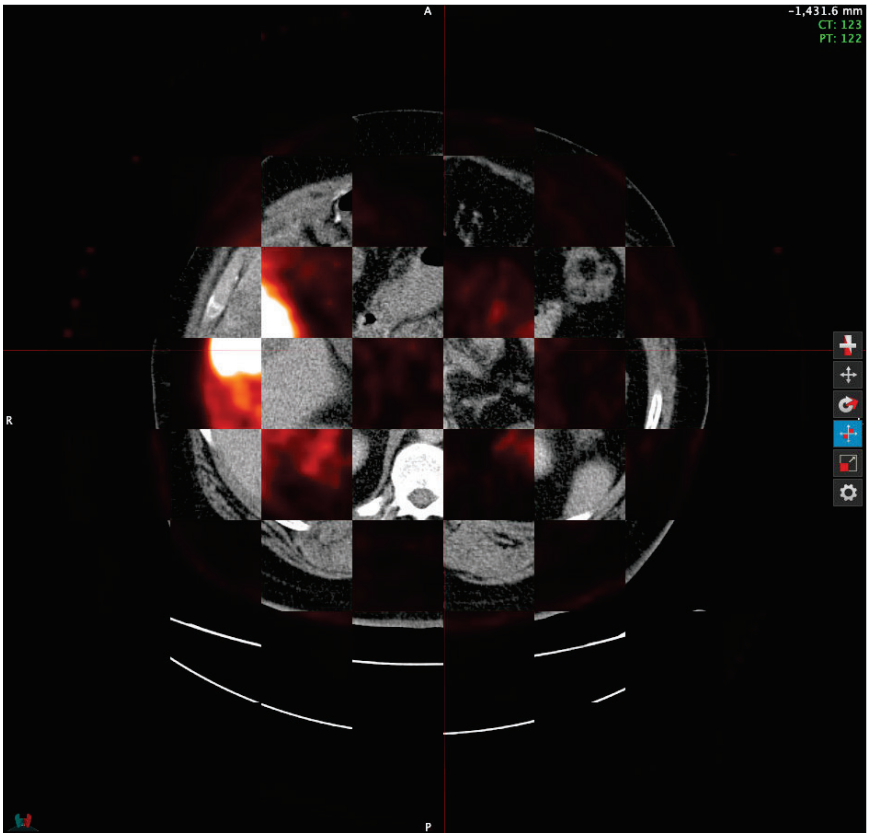
Configure Linear Fusion Blending

MIM's fusion blending algorithm is configurable. If you would like to configure MIM to use linear fusion blending, which is common in other imaging systems, follow these steps:

Tip: Linear blending matches the output produced from some other systems.

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search "**fusion**". Select **Fusion** on the left side.
3. Use the **Fusion Blend Scale** dropdown to select your preferred blending option:
    - **MIM Blending** — MIM's default blending algorithm as described above.
    - **Linear Blending** — More commonly used by other systems, such as Siemens, for fusion display.
    - **Custom** — Lets you set your own blending scale using the Custom Fusion Blend Scale field below the dropdown.

Checkerboard



Checkerboard mode lets you see both the primary and secondary series at the same time in a checkerboard pattern. It can be useful for visualizing whether the edges of specific anatomical structures line up well between the primary and secondary images.

There are three options for viewing in Checkerboard mode:

- **Fusion Checkerboard** — A standard checkerboard display of the primary and secondary images
- **MIP Checkerboard** — Overlays the MIP of the secondary onto the primary image
- **DRR Checkerboard** — Overlays a DRR of the secondary onto the primary

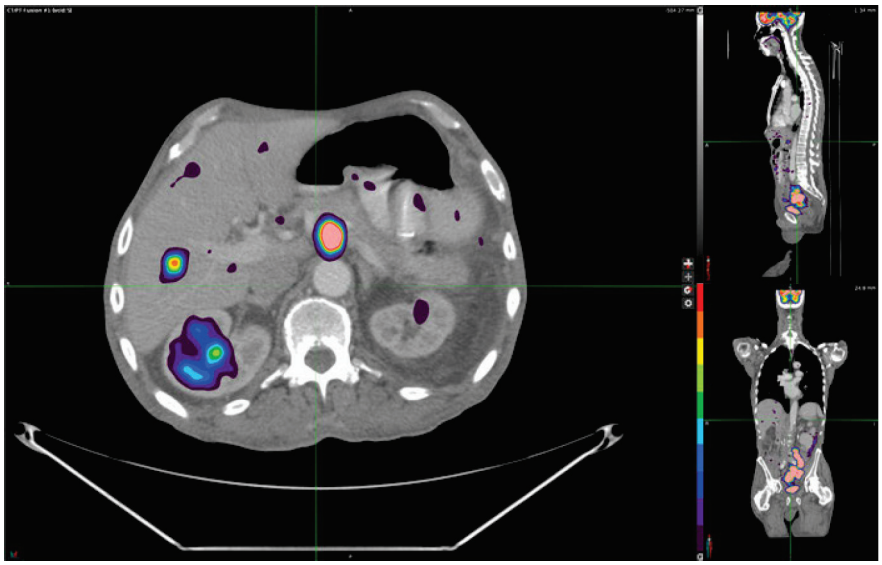
When you view a fusion in Checkerboard mode, two tools are added to the Fusion Companion Tools:

Change the position of the checkerboard grid on the images.

Change the scale of the checkerboard grid on the images.

Related: For more information on the basic Fusion Companion Tools, see Adjust Fusions Manually.

Opacity



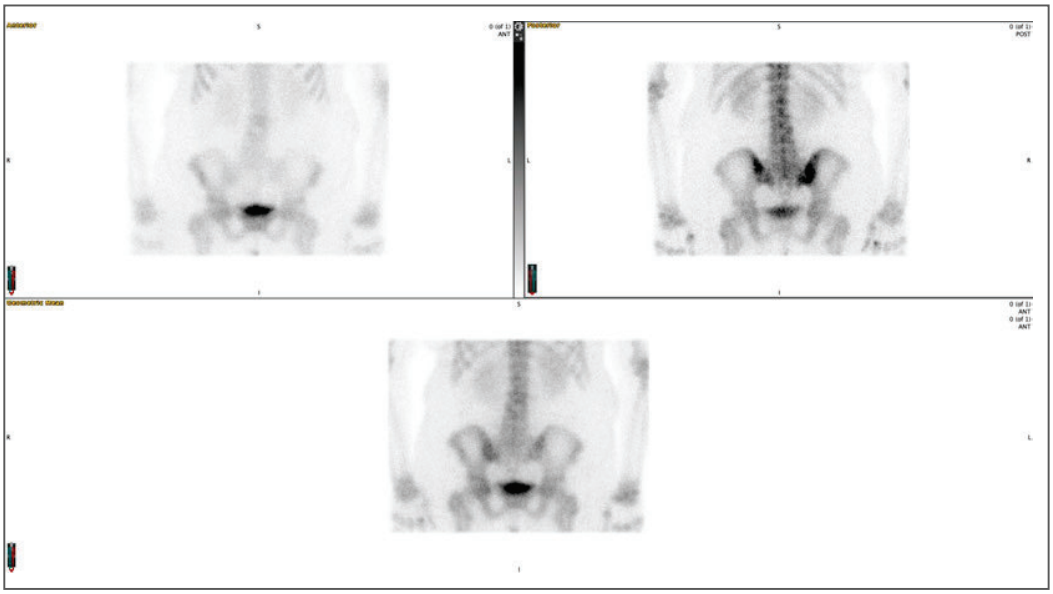
Opacity mode is similar to Normal fusion mode, except that it has special handling for low values and for blending.

In Opacity mode, the color that represents the lowest values in the image becomes transparent. Any image pixels that map to this color, including those below the contrast window, are treated as transparent.

Tip: When used with a color table like Rainbow 10, this mode lets you ignore low pixel values that are irrelevant to the analysis.

At 50/50 blend (half primary/half secondary), MIM shows the visible voxels in the secondary image according to the color table. In areas where the voxels are treated as transparent, as described above, only the primary image is shown.

Geometric Mean



This mode creates a geometric mean image comprised of the primary and secondary images. This is typically used in Nuclear Medicine when anterior and posterior images are available and a geometric mean image is needed for additional statistical calculations.

Edge Detection

This mode is typically used in MR/CT fusion cases. It shows the edges of the primary and secondary images in order to better visualize the fusion and align anatomical structures.

When you view a fusion in Edge Detection mode, three tools are added to the Fusion Companion Tools:

Choose colors for the edge indicators. Colors can be specified for both the primary and the secondary image.

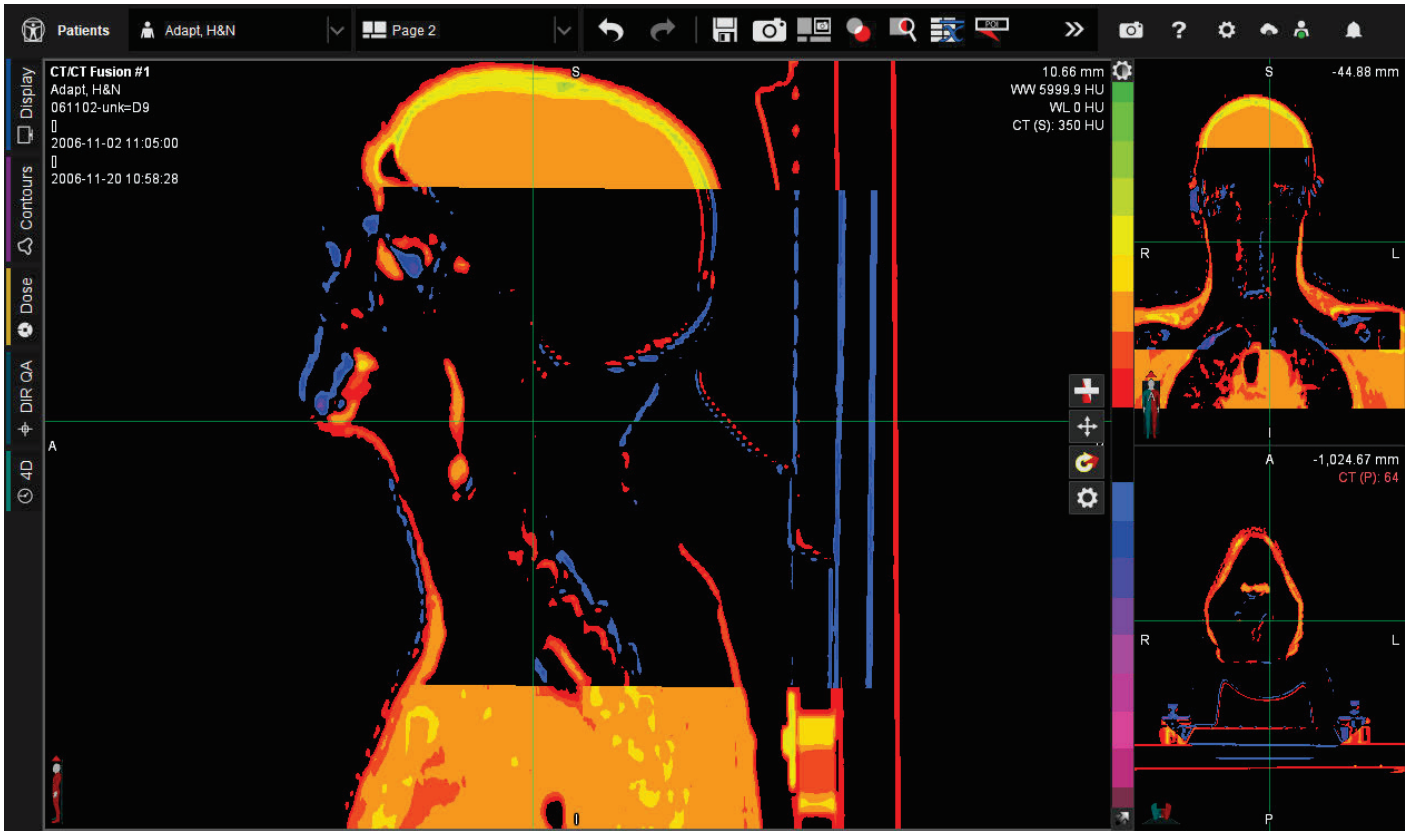
Left-click drag up or down on this button to adjust the upper threshold for detecting edges.

Left-click drag up or down on this button to adjust the lower threshold for detecting edges.

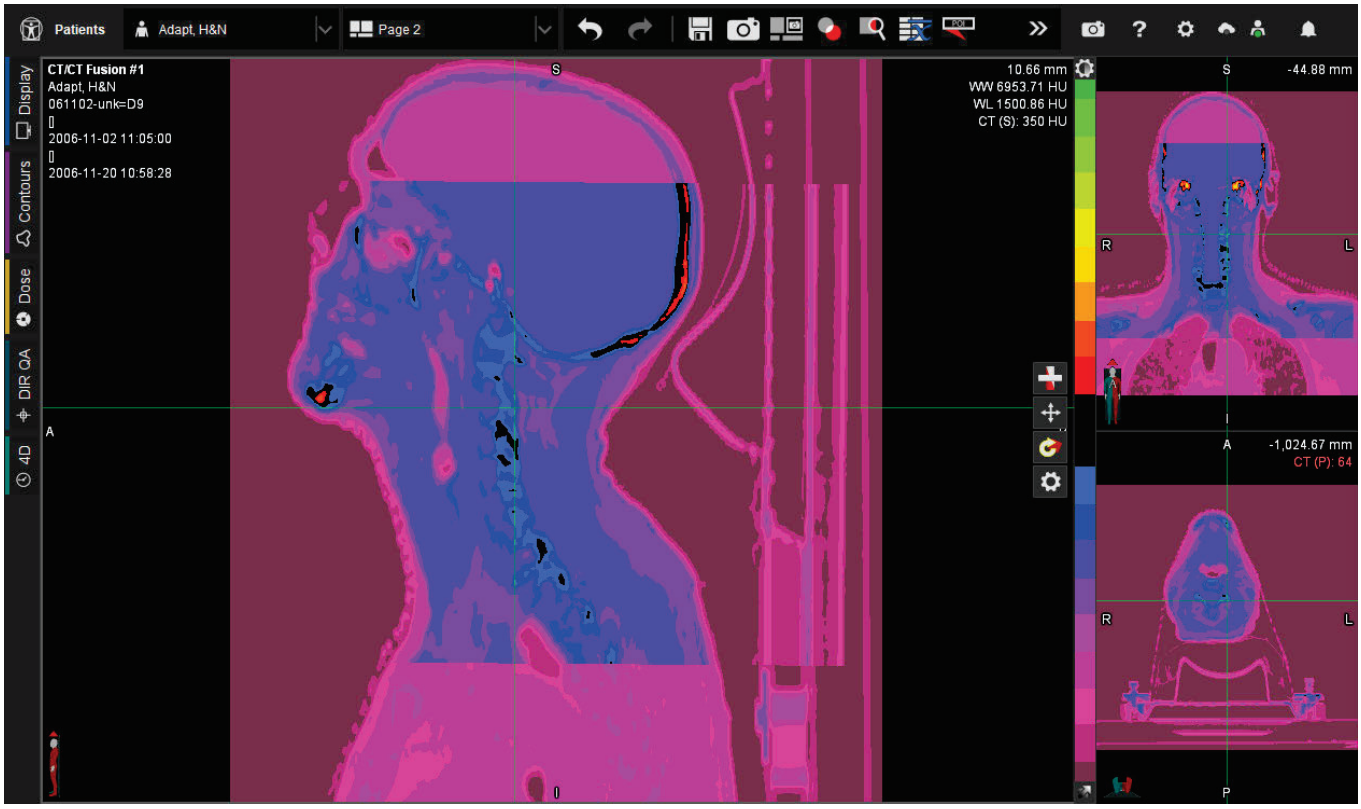
Related: For more information on the basic Fusion Companion Tools, see Adjust Fusions Manually.

Subtraction or Addition

This mode lets you create a single image by either subtracting the secondary from the primary or adding the secondary to the primary. Use subtractions when you want to see the difference between two images. Use additions to look at the summation of two images.



An example of a subtraction in MIM.



An example of an addition in MIM.

When this fusion mode is selected, the Configure Fusion Mode dialog opens. Use this dialog to define the parameters of the addition or subtraction, then click **OK** to create the new image.

Related: When you select **Normalized** in the Configure Fusion Mode window, MIM uses the image's contrast to scale its intensity data. For detailed information, see Fusion Image Subtraction Formulas: Technical Details.

MIP Fusion

This mode creates a maximum intensity projection (2D image) of the secondary to be overlaid on the primary image. This can be utilized when it is difficult to see the anatomy in the secondary due to tracer uptake.

DRR Fusion

This is designed for a special case when you have a current x-ray and want to see what an x-ray from this angle would have looked like on a different CT. This could be used to assist with patient setup for EBRT.

Create User-Defined Fusion Blending Rules (MIM 7.3 and Later)

MIM 7.3 and later: It is possible to create user-defined blending rules in MIM. These rules are automatically applied to fusions based on the modalities of the images involved and the fusion mode selected. *MIM 7.2 and earlier:* This functionality is not available.

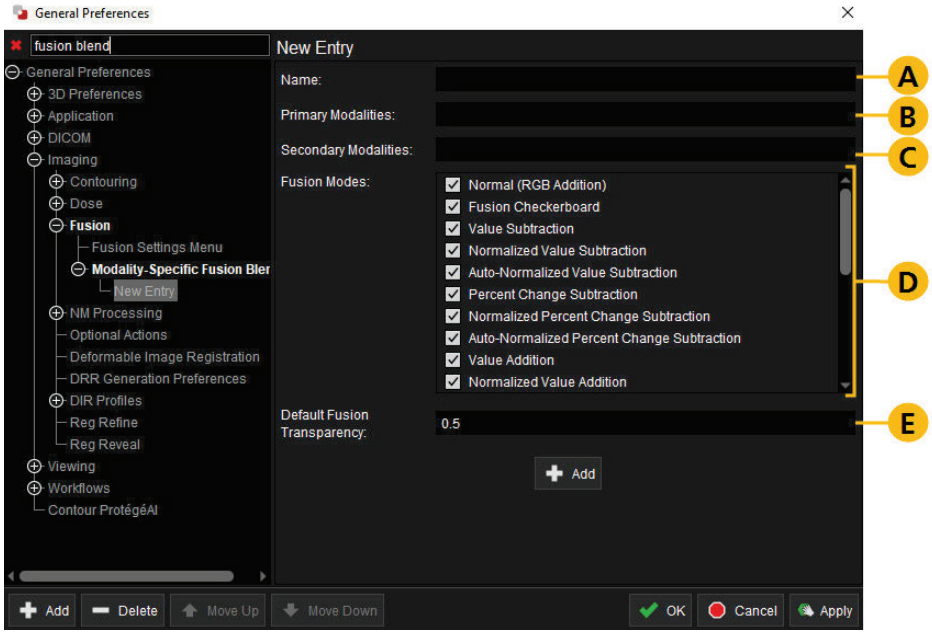
To create a Modality-Specific Fusion Blend Rule:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search "**fusion blend**". Select **Modality-Specific Fusion Blend Rules** on the left side.
3. Click **Add** to create a new entry.
4. Configure the rule by filling the fields as desired:
    A. The name of the rule.
    B. The primary image modalities that will be considered as part of the rule.
    C. The secondary image modalities that will be considered as part of the rule.

> **Important:** You are not required to define either the primary or the secondary modalities. A rule with no modalities defined will apply to all future fusions. If modalities are defined for primary modalities, secondary modalities, or both, the rule will only be applied to fusions that meet the rule criteria.

    D. The fusion modes that the rule applies to.
    E. The fusion transparency that will be automatically applied to fusions that meet the rule

parameters.



5. Click **OK** to save the rule and close the window. The rule will be applied to all future fusions that meet its parameters.

Evaluate Fusions Quantitatively

MIMTD-1629 • 04 Jan 2024

Overview

There are two primary ways to view quantitative data about fusions in MIM®: **Calculate Fusion Metrics** and **Analyze Fusion Alignment**.

Contents

Calculate Fusion Metrics

Tip: MIM has a default keyboard shortcut (Shift+M) for the Calculate Fusion Metrics tool. Ensure that your cursor is hovering over a fusion before pressing the shortcut keys.

The Calculate Fusion Metrics tool provides 3 statistical analyses of a fusion:

- Normalized mutual information
- Pearson correlation coefficient
- Root mean square difference

For detailed information about each option, see Fusion Metrics Information, below.

To view fusion metrics, follow these steps:

1. Click the ⏩ button at the top of MIM to search all tools.
2. Type "**calculate fusion metrics**" in the search bar.
3. Select **Calculate Fusion Metrics** from the list of tools. You will be prompted to select a series for the calculation.
4. Click the **Select this series** button on the fusion you want to see metrics for. The metrics will be displayed in the Notifications window.

Fusion Metrics Information

Normalized Mutual Information

- Answers the question: "Does a particular range of values in one image correspond to a particular range of values in the other image?"
- Is reported as a unitless value between 0 and 1. A higher number indicates higher association.
- Can be used even if the two images have differing data ranges (e.g., on images of different modalities).

Example: On CT, bone typically appears bright. On MR, bone typically appears dark. Adipose tissue has the opposite relationship—it appears dark on CT, but bright on MR. Normalized mutual information can account for these different value relationships. The Pearson correlation coefficient would not provide valuable infromation in this instance.

Pearson Correlation Coefficient

- Answers the question: "Are the values in one image associated with similar values in the other image?"
- Reported as a unitless value between -1 and 1. Typically, results that are closer to -1 or 1 are better.
    - A positive coefficient means that large values in the first image are associated with large values in the second image.
    - A negative coefficient means that large values in the first image are associated with small values in the second image.
- Works best when images are of the same modality.

Limitations of Pearson Correlation Coefficient

- If the relationship between the two image modalities is nonlinear, the Pearson correlation coefficient can return poor scores for good fusions.
- The Pearson correlation coefficient has low sensitivity to misalignments in many cases.