Draw and View Contours on Linked Series (Ghost Contours)

MIMTD-1323 • 15 Sep 2023

Overview

When you draw a contour, it is associated with a single series. However, when two series are aligned (e.g., through a frame of reference link or a fusion), contours drawn on one series can be displayed on the other.

In MIM, when a contour is displayed on a series that it is not directly associated with, it is known as a **ghost contour**. Ghost contours are indicated by a "ghost" icon in the contours sidebar:

Ghost contours are advantageous because they let you draw on whichever series provides the best visual information—even if the contours will ultimately be used on a different series.

Example: It is often easier to see and draw tumor volumes on a PET, even though the contours need to exist on a CT for treatment planning. If the PET and CT are linked, it is possible to have the contours associated with the CT, even if you draw them on the PET. See Draw Contours in a Session with Multiple Linked Series below for more information.

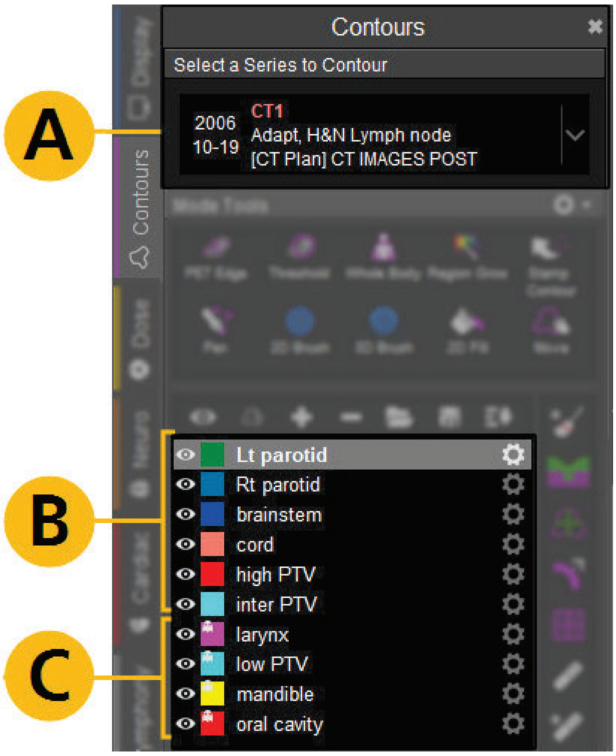
Contents

- Draw Contours in a Session with Multiple Linked Series
- Find Out Which Series a Ghost Contour Is Associated With
- Save Contours to a Different Series
- Hide or Display Ghost Contours

Draw Contours in a Session with Multiple Linked Series

It is common to work with multiple spatially linked (i.e., fused) series in a single MIM session. MIM's default behavior is to display contours on all series that are spatially linked. However, the contours are only truly associated with one series.

Follow the best practices below when you contour in a session with multiple linked series:



In the Contours sidebar, the **Select a Series to Contour** dropdown (**A**) determines which series you are directly interacting with.

- Contours you draw are associated with the series that is selected in the dropdown. Using the image on the left as an example, CT1 is the series to contour. You can draw on CT1 or on any series that is spatially linked to CT1. In either case, the contours are associated with CT1.
- The contour list in the sidebar shows the contours as they relate to the series that is selected in the dropdown:
    - Contours *without* a ghost icon (**B**) are associated with the series that is selected in the dropdown. In the image to the left, the first six contours in the list are associated with CT1.
    - Contours *with* a ghost icon (**C**) are not associated with the series that is selected in the dropdown. In the image to the left, the last four contours are not associated with CT1. However, the contours are displayed on CT1 and appear in the list because they are associated with a series that is spatially linked to CT1.

Find Out Which Series a Ghost Contour Is Associated With

- To find the series a ghost contour is associated with, change the series in the Set Series to Contour dropdown until the ghost icon disappears. When the contours no longer have a ghost icon, this indicates that the contours are associated with the selected series.
- If you have contours on many different series, or if you have multiple sets of contours with the same name, use the eye ◉ button to hide some of them while you look for the associated series for one or more ghost contours.

Save Contours to a Different Series

If you've already drawn contours but want them to be associated with a different series than the one that was originally selected, you have two options:

- Use the Transfer Contours tool to create copies of the contours on the desired series. See Transfer Contours for more information.
- Save an RTstruct file and choose the appropriate series to associate the contours to. During the saving process, you are asked whether you would like to transfer ghost contours to the series. Click **Yes** to transfer the contours to the chosen series automatically. See Save Patient Data for more information.

Note: In either of the above cases, the contours are not removed from the series they were originally associated with. If desired, you can delete the contours from the original series after transferring.

Hide or Display Ghost Contours

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for **"ghost"**. Select **Contouring** on the left side.
3. Select the desired option from the **Display Ghost (Remote) Contours** preference.
    - **Always** — Ghost contours are displayed any time you contour on a series that is spatially linked to another series.
    - **Sometimes** — Choose when ghost contours appear:
        - To use the DICOM Frame of Reference tag to determine whether ghost contours appear, select **Display ghost contours on series with the same frame of reference**.
        - To make the appearance of ghost contours dependent upon the series date, select **Display ghost contours on series acquired around the same date** and set the **Maximum number of days between acquisitions**. The series must still be linked in some way (e.g., through a fusion) for this option to take effect.
    - **Never** — Ghost contours are never displayed. You are only able to see contours on the series they are associated with.

    Note: If you select Sometimes or Always, you have the additional option to choose whether ghost contours are displayed as solid lines (default) or as dashed lines (when **Display ghost contours with dashed lines** is selected).

Work with Overlapping and Adjacent Contours

MIMTD-1738 • 01 Nov 2023

Overview

You might have situations where two contours should be flush against each other. For example, you might contour two structures that are adjacent but should not overlap. Or, you can make sure that the PTV does not extend beyond the skin or external contour.

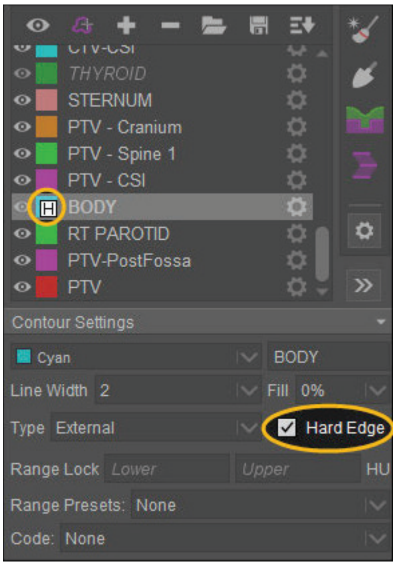
Use the following tools to help with contours that are close together.

Contents

- Use Hard Edges to Avoid Overlaps
  - Remove Overlap
  - Prevent Overlap
- Crop Contours So They Do Not Overlap
- Use a Boolean Operation to Remove Overlap

Use Hard Edges to Avoid Overlaps

You can set a contour as having a hard edge if other contours should not overlap with it.



Cyan BODY

Line Width 2 Fill 0%

Type External ☑ Hard Edge

Range Lock Lower Upper HU

Range Presets: None

Code: None

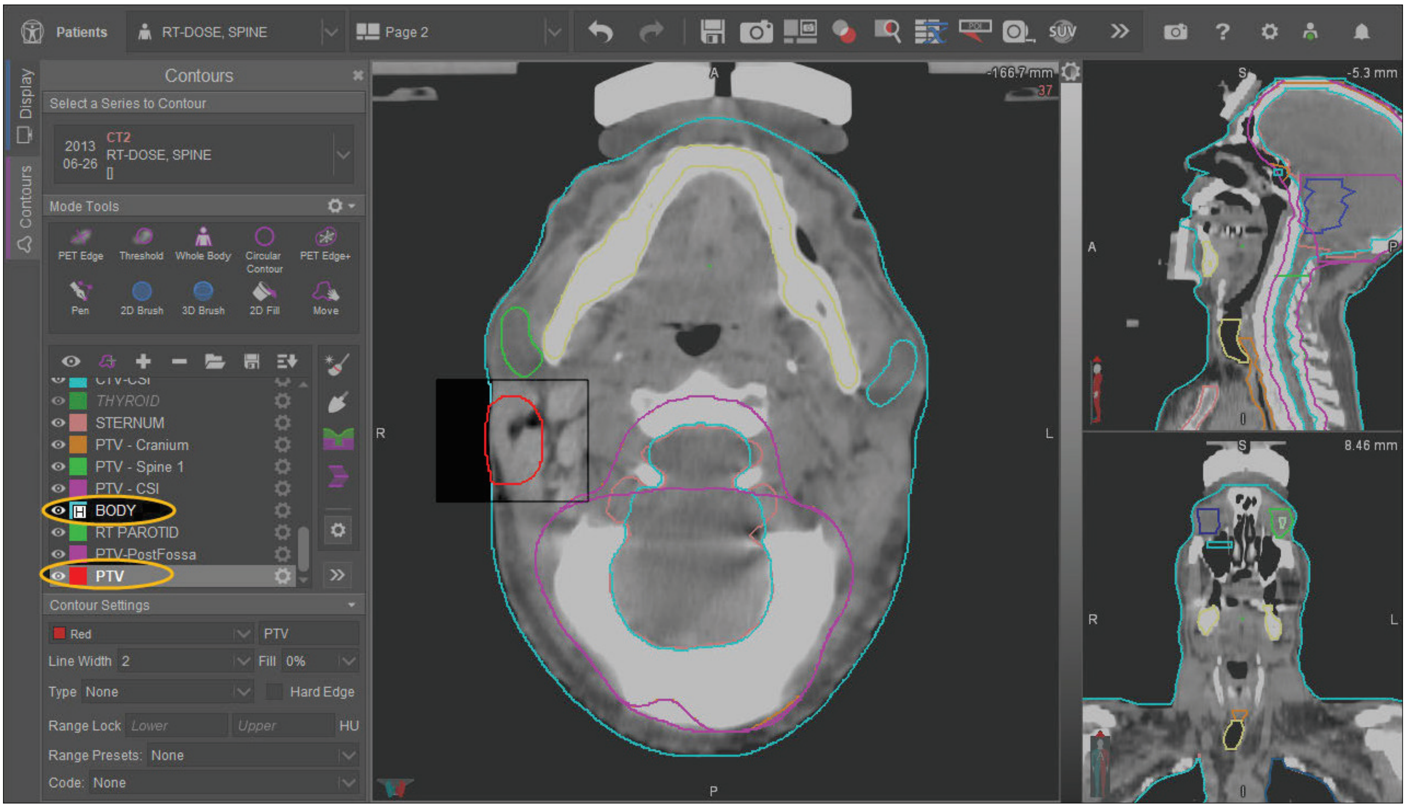
To do so:

1. On the Contours sidebar, select the contour that should have a hard edge. This contour will remain "whole" while other contours are cropped around it.
2. Right-click on the colored box next to the contour. Or, in the Contours Settings section, select **Hard Edge**. An H appears on the contour name.

You can then either remove overlap from existing contours that already overlap with the hard edge contour, or prevent contours from being created that overlap with the hard edge contour.

Remove Overlap

1. Select an existing contour that overlaps with a hard edge contour.
2. From the post-processing menu, click the **Remove Overlaps** tool. The contour is trimmed so that it no longer overlaps with the hard edge contour.



Red PTV
Line Width 2 Fill 0%
Type None ☐ Hard Edge
Range Lock Lower Upper HU
Range Presets: None
Code: None

In this example, the external Body contour has a hard edge. The PTV was selected and the Remove Overlaps tool used so that the PTV does not extend beyond the body.

Prevent Overlap

You can enable a setting so that new contours cannot be created that overlap with a hard edge contour when using certain contouring tools.

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for **"overlap"**. Select **Contouring** on the left side.
3. Select **Avoid overlapping hard contours with paintbrush, Region Grow, and Contour CoPilot tools**.
4. Click **OK** to save the changes and close the window.

Crop Contours So They Do Not Overlap

You can use the **Crop to Avoid Contours** tool for more control when adding space between contours. This tool does not use hard edges.

After you have drawn contours, complete the following steps:

1. On the Contours sidebar, select the contour that should not be overlapped. This contour will remain "whole" while other contours are cropped around it.
2. From the post-processing menu on the right side of the Contours sidebar, select the **Crop to Avoid Contours** tool.
3. In the Notifications window:
   - A. On the **To Crop** side (left), select which contours should be cropped. Use the plus to add a contour or the minus to remove a listed contour.
   - B. On the **To Avoid** side (right), confirm which contour should not be overlapped or cropped. Use the plus to add a contour or the minus to remove a listed contour.
   - C. In the **Crop Margin** field, set how much space should be around the non-overlapped contour.
   - D. Click **OK**.

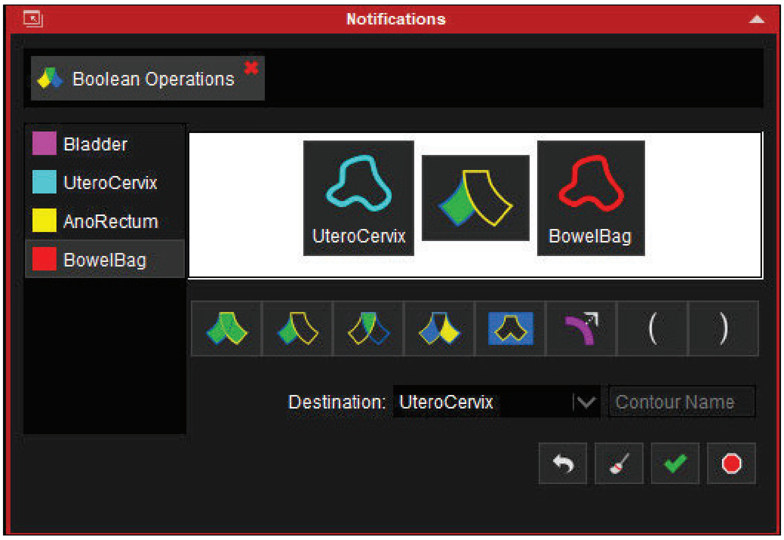
Crop Margin (cm): 0.2

Use a Boolean Operation to Remove Overlap

For further options or more complex scenario, you can use the **Boolean Operations** tool. Refer to Create and Adjust Contours Using Boolean Operations for more information about working with Boolean Operations.

To remove overlap:

1. Select the contour that is overlapping the "whole" contour and should not be.
2. Select the subtraction operation.
3. Select the "whole" contour.
4. Change the **Destination** to the first contour that you had selected to update that contour.



Destination: UteroCervix

Tip: Set the **Destination** to **New Contour** if you want to create a new contour of only the overlapping area.

Standardize Contour Names with ROI Templates

MIMTD-657 • 24 Aug 2023

Overview

Use ROI templates to standardize the contour names and colors used by different people across your organization. Once ROI templates are created, users can load them before contouring, and then select pre-formatted contour names and colors from the contour list. You can also configure contour settings for each item in an ROI template.

Contents

- Create ROI Templates
- Load ROI Templates for Use

Create ROI Templates

> **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.

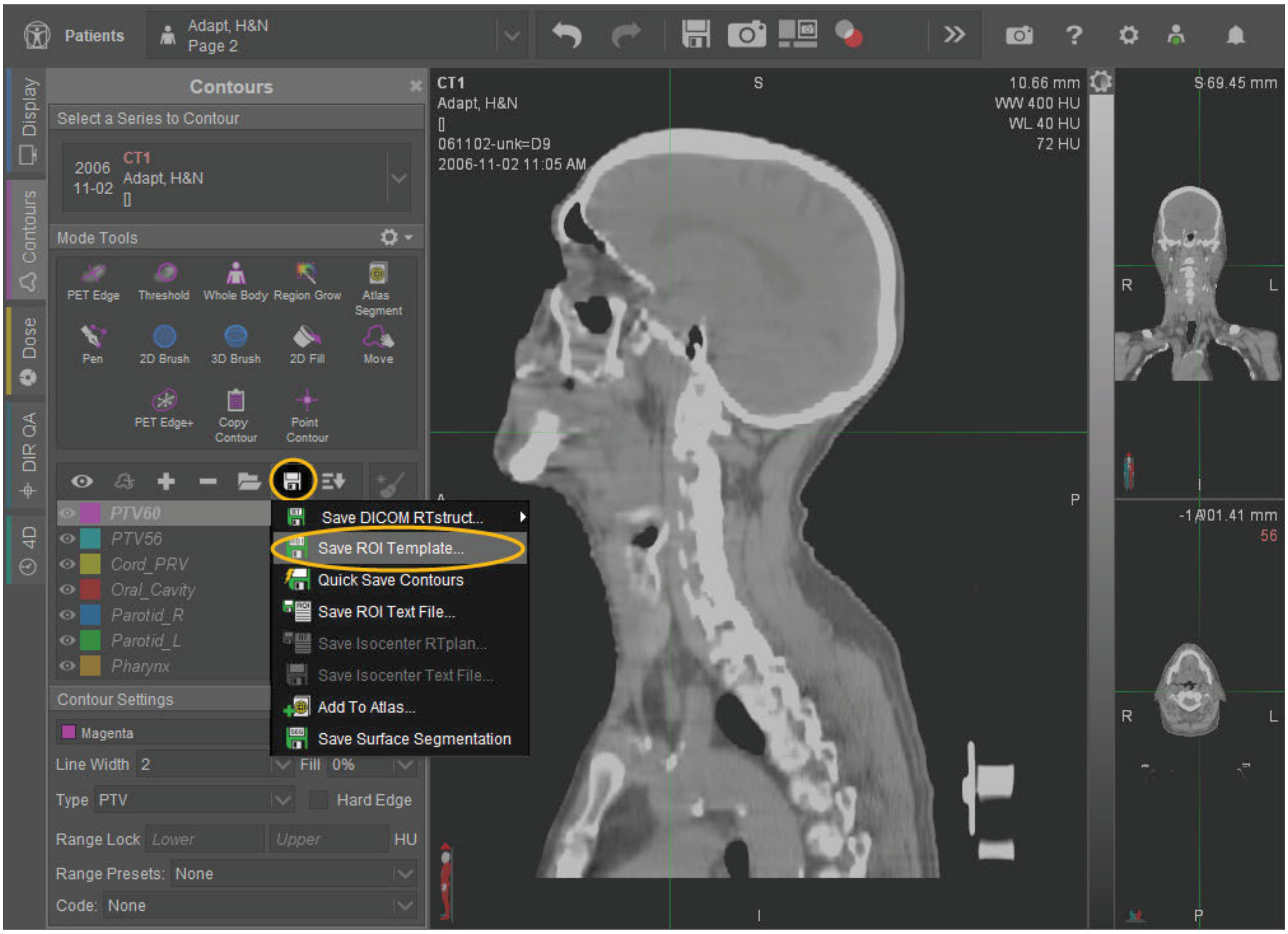
1. Open any series into a session.

   > **Tip**: If you have a series with contours that match or are nearly a match for the template you want to create, open that series and the RTstruct set. Then, you can simply modify the contours and settings as needed. The original RTstruct set is not altered.

2. Click on the **Contours** sidebar on the left side of MIM.
3. Use the ✚ button to add contours as necessary. You can:
   - Rename a contour by right-clicking on its name in the sidebar and selecting **Rename Contour**.
   - Change the contour color by scrolling over the colored box next to the contour name. Or, use the color dropdown options in the **Contour Settings** section at the bottom of the sidebar.

- Adjust additional individual contour settings as necessary from the **Contour Settings** section.See Create Contours Overview for more information.

4. Once all contours have been added and all settings are correct, click the save 🖫 button above the list of contour names.
5. Select **Save ROI Template...**.



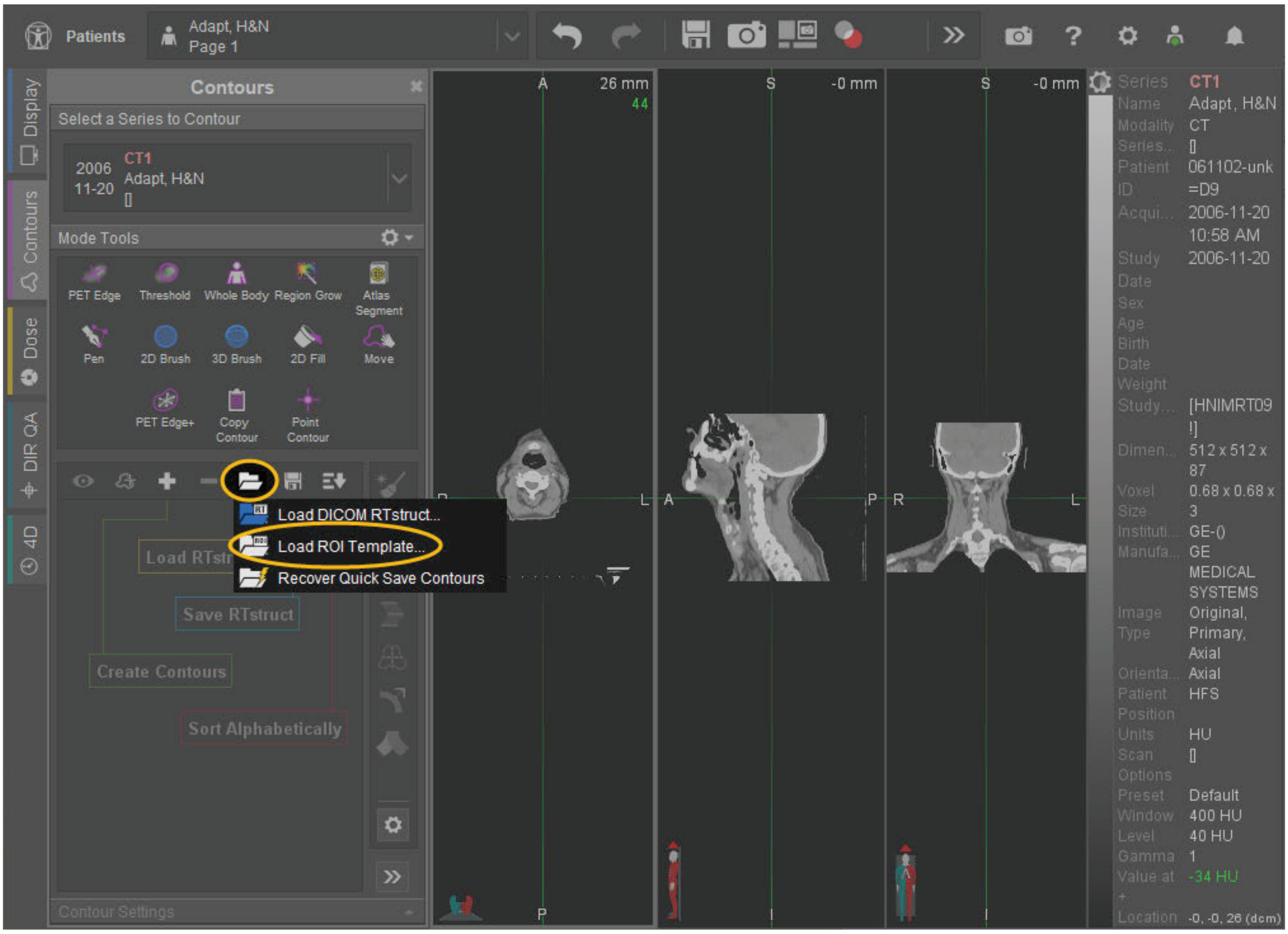
6. Follow the instructions in the Notifications window, and then click **Save**.

Load ROI Templates for Use

To use the template that you created:

1. Open a series into a session.
2. Click on the **Contours** sidebar on the left side of MIM.
3. Click the 🗁 button.
4. Select **Load ROI Template...**.

5. Follow the instructions in the Notifications window.



Tip: If you made this change as an administrator, communicate to users that the template is now available for use. Show them how to load it.

If you did not make the changes as an administrator but you want to share your templates with other users, you can do so from the Import Manager. See How Do I Share a Workflow with My Colleague? and use the same steps for ROI templates.

Save and Reuse Contour Shapes

MIMTD-925 • 26 Sep 2023

Overview

The Contour Shape Library lets you save contours in a library and load them onto any patient data set using the Stamp Contour tool. This reduces time spent contouring manually and is helpful for several actions:

- Loading pre-sized contours
- Loading contours for uniform shapes (e.g., ellipses, cylinders, cubes, spheres)
- Loading contours for equipment that does not change shape (e.g., treatment couch, catheters)
- Loading organ-shaped templates
- Using templated shapes and sizes to simplify QC tasks
- Contouring axial, inguinal, or mediastinal regions for lesion identification and cutoff threshold using PERCIST criteria

Contents

- Save a Contour as a Shape Template in the Contour Shape Library
- Remove Shape Templates from the Contour Shape Library
- Load a Shape Template from the Contour Library

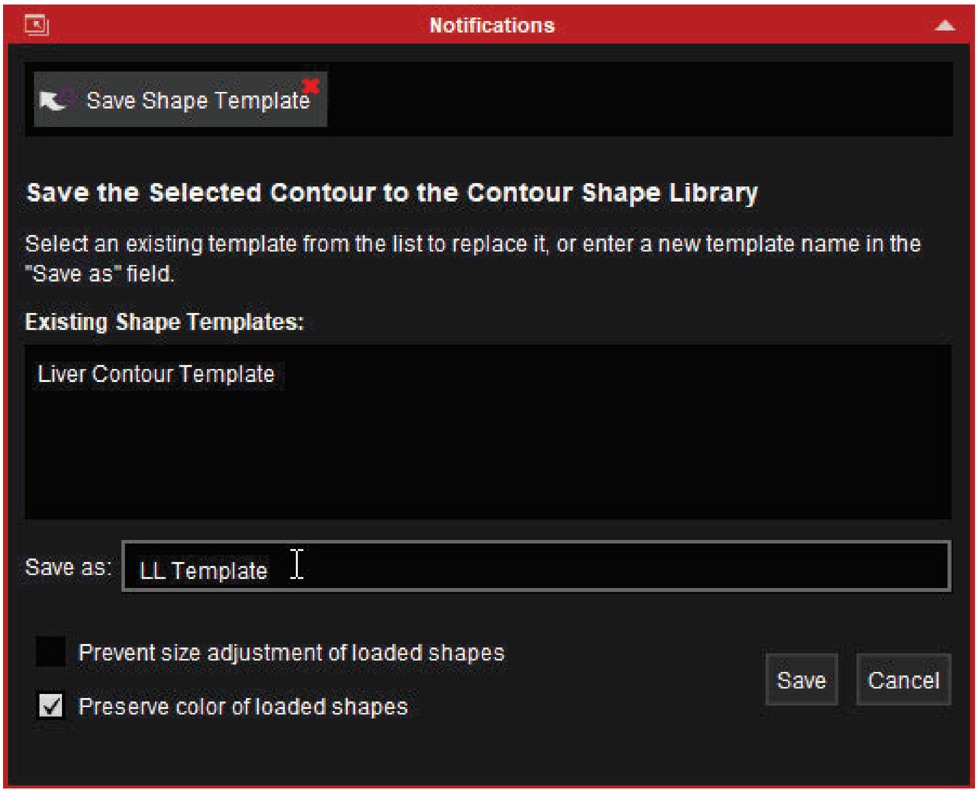
Save a Contour as a Shape Template in the Contour Shape Library

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. In the Contours sidebar, create or select a contour to add to the library.

> **Tip:** Ensure that the contour is named appropriately before saving the template to the Contour Shape Library. The template name and the contour name that appears in the Contours sidebar when the contour is placed are distinct.

2. Click the save button above the list of contours.
3. Select **Save to Contour Shape Library...**.
4. Enter information in the **Save Shape Template** dialog:



Save the Selected Contour to the Contour Shape Library

Select an existing template from the list to replace it, or enter a new template name in the "Save as" field.

Existing Shape Templates:

Liver Contour Template

Save as: LL Template

☐ Prevent size adjustment of loaded shapes

☑ Preserve color of loaded shapes

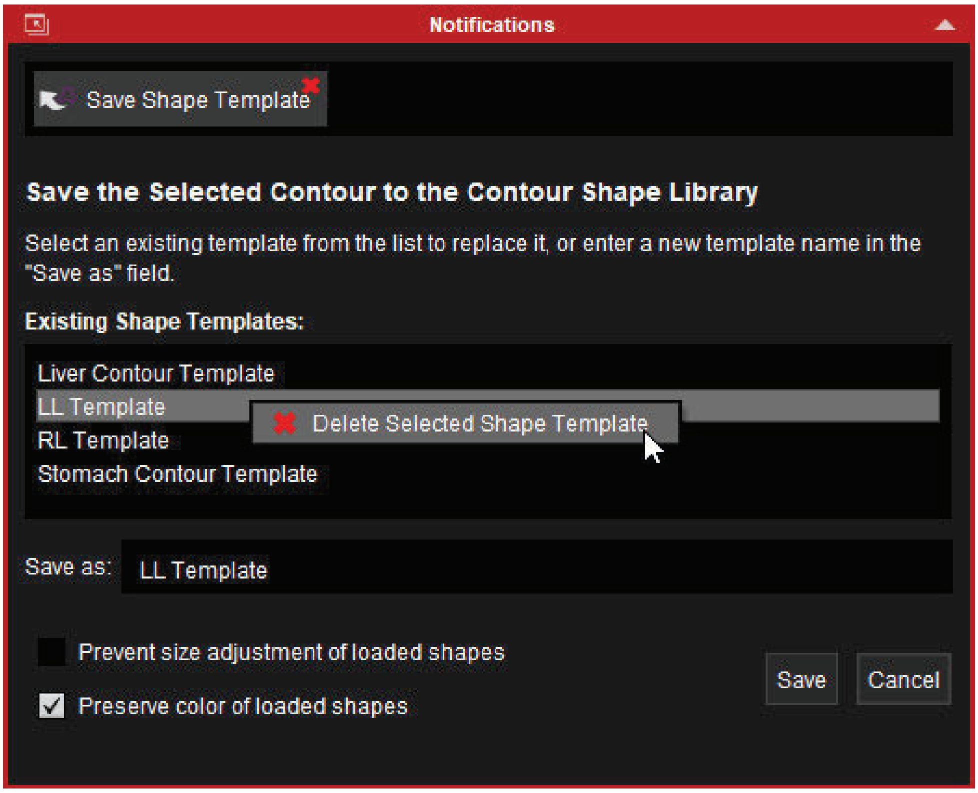
- To save the contour as a new shape template, enter a new template name in the **Save as** field.
- To replace an existing shape template, select an existing template from the list.
- If desired, use the checkboxes to prevent size adjustment and preserve the color of loaded templates.

5. Click **Save**.

Remove Shape Templates from the Contour Shape Library

1. Create or select any contour from the list in the Contours sidebar.
2. Click the save button above the list of contours.
3. Select **Save to Contour Shape Library...**.
4. In the **Save Shape Template** dialog, right-click the existing shape template you wish to remove and select **Delete Selected Shape Template**.

Important: Removing a shape template is permanent and cannot be undone.



Save the Selected Contour to the Contour Shape Library

Select an existing template from the list to replace it, or enter a new template name in the "Save as" field.

Existing Shape Templates:

- Liver Contour Template
- LL Template
- RL Template
- Stomach Contour Template

Save as: LL Template

☐ Prevent size adjustment of loaded shapes

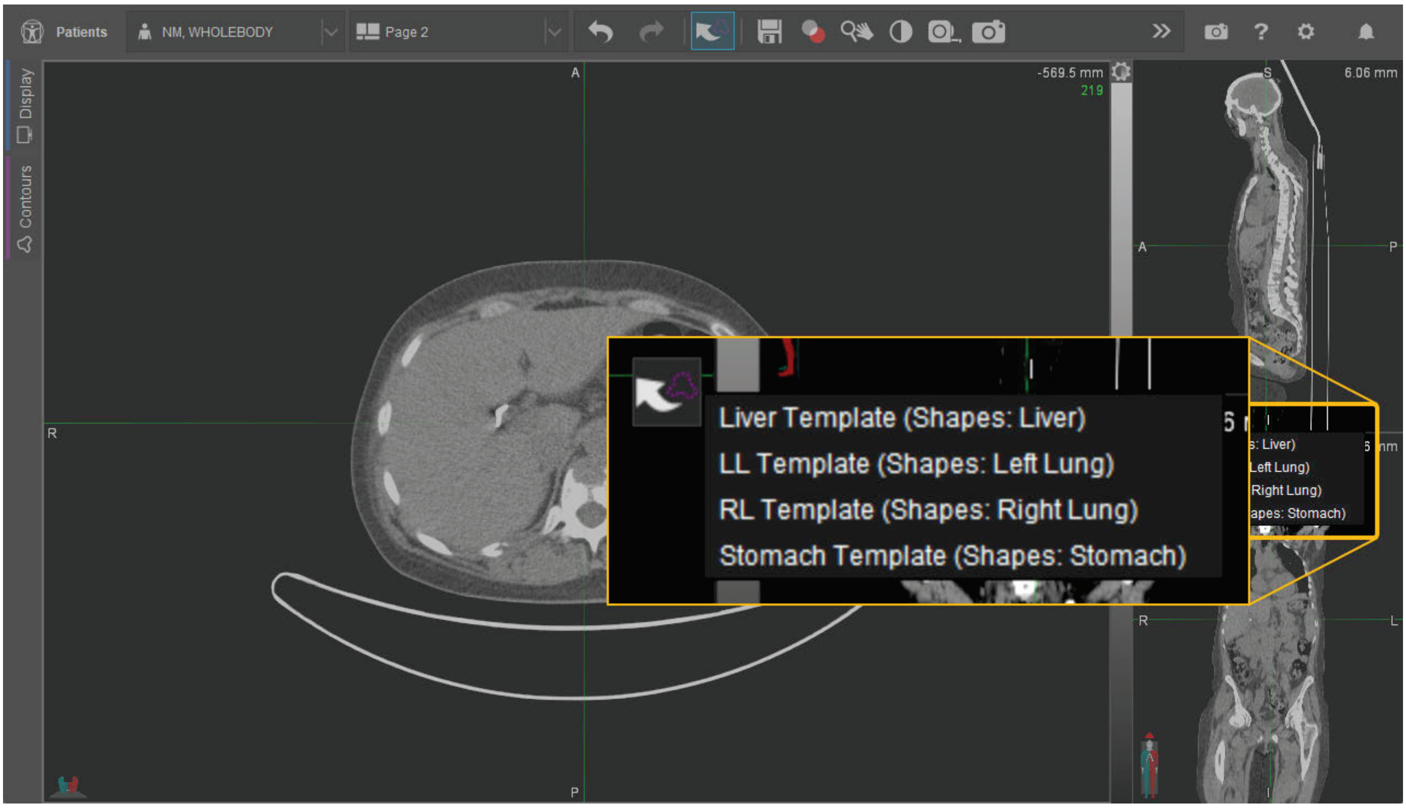
☑ Preserve color of loaded shapes

Load a Shape Template from the Contour Library

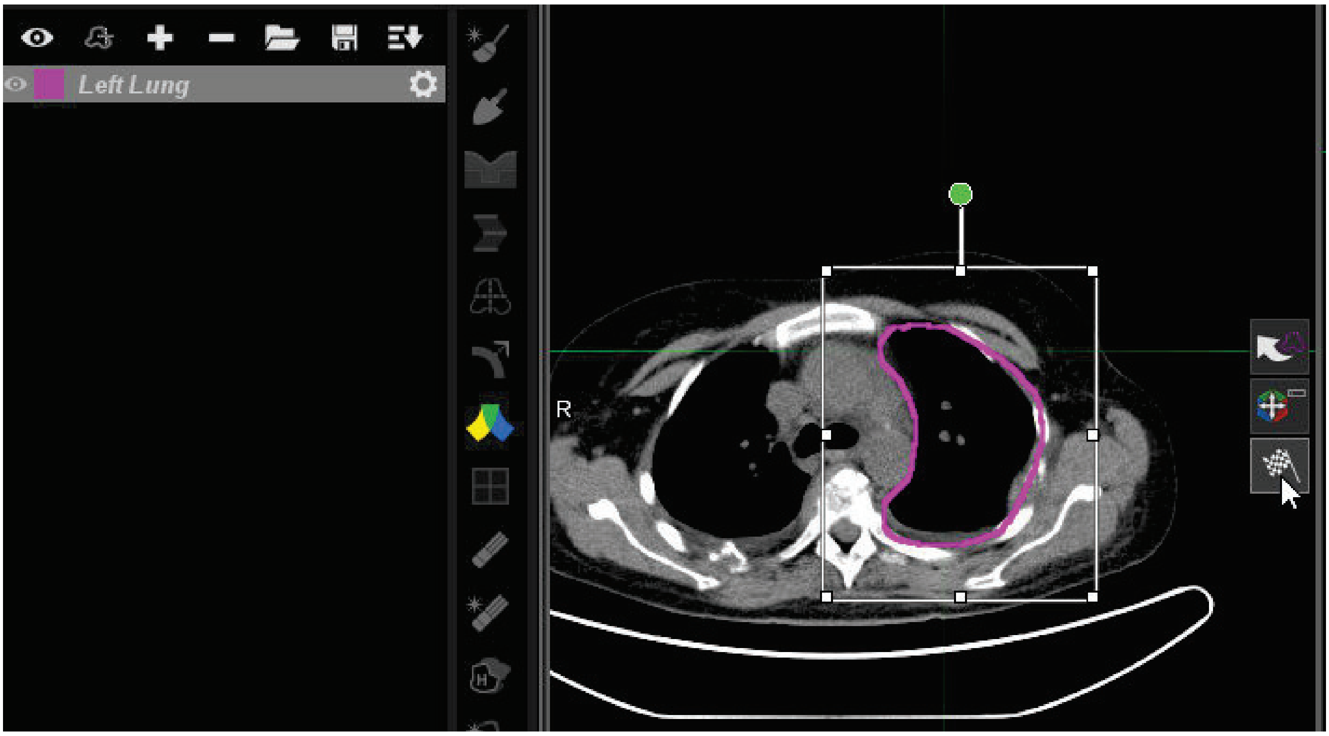
1. Activate the **Stamp Contour** tool from the top toolbar or radial menu.

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

2. Hover in any viewport and click the **Stamp Contour** button on the right side.
3. Select the shape template to use from the Contour Shape Library. The name of the placed contour is displayed next to the template name.



4. Hover over the shape in any viewport to show a bounding box and adjust the contour shape.



- To move the shape, left-click drag with the cursor inside of the box.
- To rotate the shape, left-click drag the green dot.
- To adjust the shape size:
    - Left-click drag on the edges of the box to scale and stretch the shape.
    - Right-click drag with the cursor inside of the box to scale the shape while maintaining its proportions.
    - Click the adjust contour shape button to adjust the contour by entering numerical values for translation and scaling amounts.

Tip: Size adjustment is not available if restrictions were placed when the shape was saved, as described in Save a Contour as a Shape Template in the Contour Shape Library.

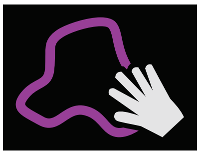
5. Click the checkered flag button to finalize the placement of the contour shape. If the Stamp Contour tool is deactivated before finalizing placement, no contour is placed.

Tip: If an empty contour has the same name of the contour to be placed, the template shape takes the place of that contour.

Move Contours

MIMTD-1641 • 24 Oct 2023

Overview



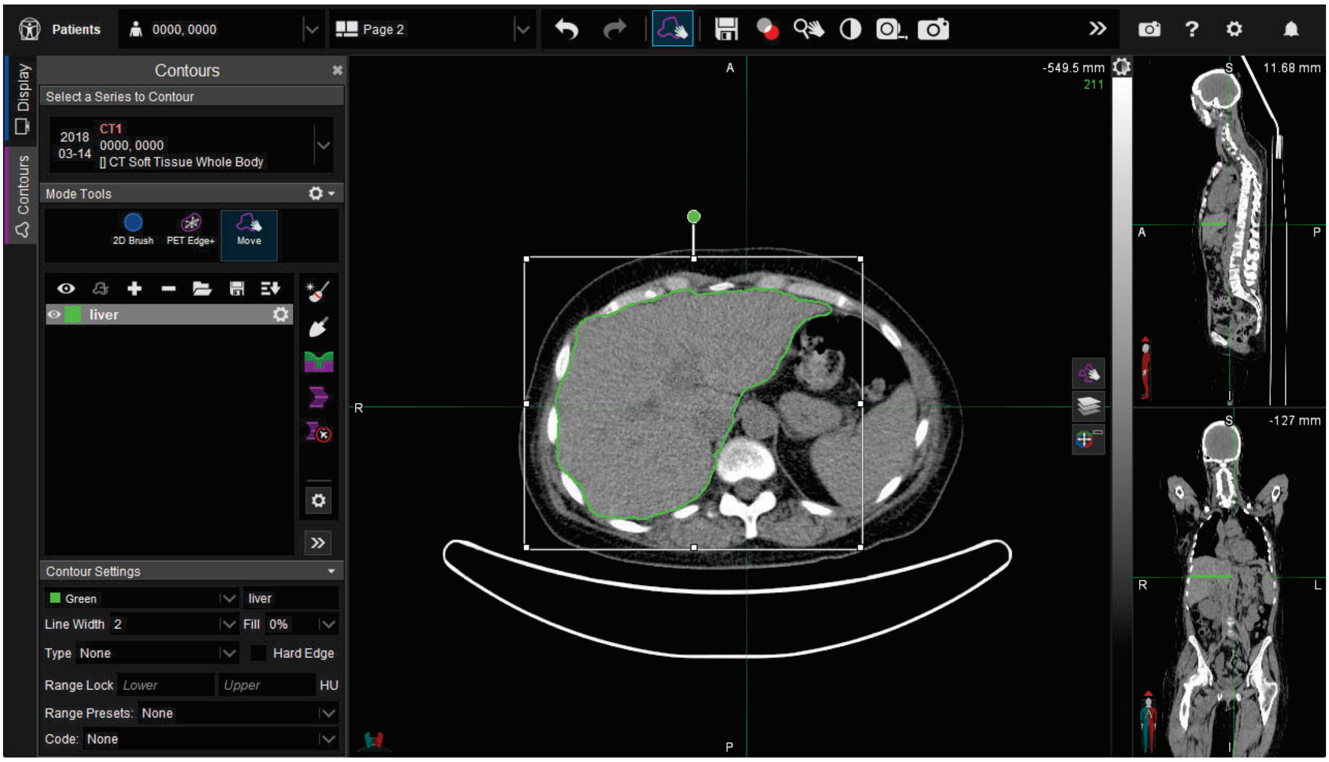
The Move tool lets you move one or more contours in a variety of ways. You can use the tool to reposition, rotate, or stretch the entire contour in any plane. It also features companion tools that can be used to assist with specific contouring tasks.

Contents

- Move a Contour
- Use Move Companion Tools

Move a Contour

1. Select the contour you want to move from the Contours sidebar.
2. Activate the **Move** tool.



Contour Settings

Green liver

Line Width 2 Fill 0%

Type None ☐ Hard Edge

Range Lock Lower Upper HU

Range Presets: None

Code: None

- Left-click drag the center of the box to reposition the contour.
- Left-click drag any of the box nodes to stretch the contour.
- Left-click drag the green circle left and right to rotate the contour.

Tip: The Move tool can also move a contour for all frames or per frame in a 2D dynamic series. For more information, see Work with Dynamic Series.

Use Move Companion Tools

Companion tools offer additional or enhanced functionality to the primary tool.

The Move tool has three companion tools that are displayed along the right side of the active viewport. These companion tools change the Move tool's functionality as described below:

Move All Visible Contours

When this option is active, the Move tool acts on all visible contours, not just the one selected in the Contours sidebar.

Move Contours on a Single Axial Slice

When this option is active, the Move tool acts only on the visible axial slice. You can use this option in combination with the **Move All Visible Contours** companion tool to modify all visible contours on the visible axial slice.

Specify a Contour's Translation, Rotation, and Scale in an Individual Plane

This option lets you enter numerical values to modify the contour. You can use it in combination with the other two companion tools to adjust all visible contours and/or to modify only the visible axial slice of the contour.

Expand or Contract Contours

MIMTD-1575 • 06 Jun 2023

Overview

Use the **Expand/Contract** tool to expand or contract a contour in various ways. For detailed information on how MIM applies the requested expansion or contraction, see Expand/Contract Contours Tool: Technical Details in the appendix.

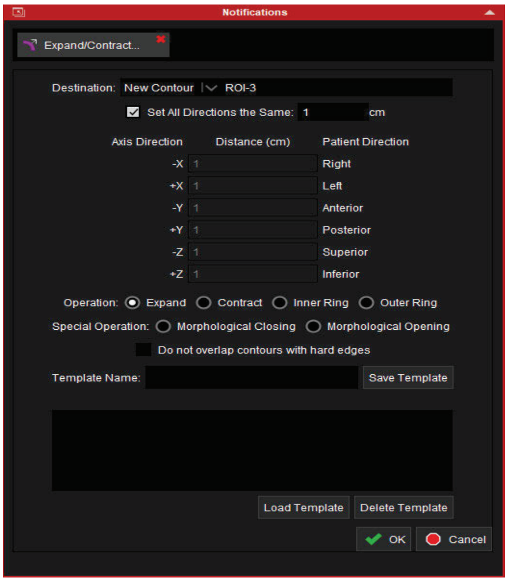
Contents

- Basic Use
- Set Expansion or Contraction Parameters in the Expand/Contract... Dialog

Basic Use

1. Click the **Expand/Contract...** button.
2. Use the Expand/Contract... dialog to set parameters for the expansion or contraction. Optionally, load a template to automatically set parameters for a routine expansion or contraction.

   See the following sections of this document for detailed information about the options in the Expand/Contract... dialog.
3. Click **OK** to apply the expansion or contraction.



Destination: New Contour ROI-3

☑ Set All Directions the Same: 1 cm

Axis Direction	Distance (cm)	Patient Direction
-X	1	Right
+X	1	Left
-Y	1	Anterior
+Y	1	Posterior
-Z	1	Superior
+Z	1	Inferior

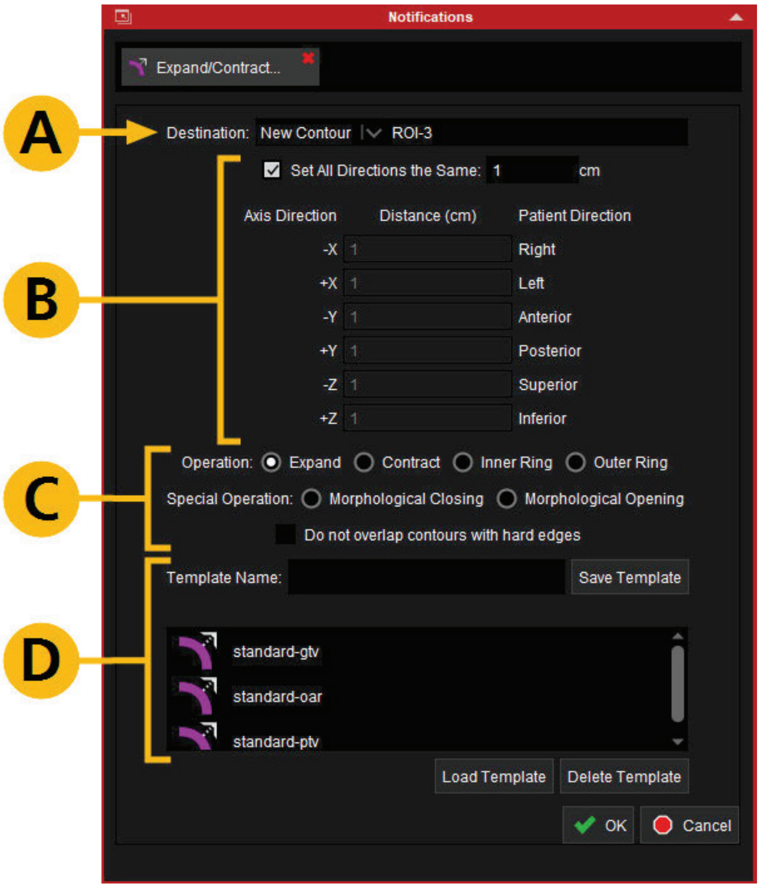
Operation: ● Expand ○ Contract ○ Inner Ring ○ Outer Ring

Special Operation: ○ Morphological Closing ○ Morphological Opening

☐ Do not overlap contours with hard edges

Template Name:

Set Expansion or Contraction Parameters in the Expand/Contract... Dialog



Destination: New Contour ROI-3

☑ Set All Directions the Same: 1 cm

Axis Direction	Distance (cm)	Patient Direction
-X	1	Right
+X	1	Left
-Y	1	Anterior
+Y	1	Posterior
-Z	1	Superior
+Z	1	Inferior

Operation: ● Expand ○ Contract ○ Inner Ring ○ Outer Ring

Special Operation: ○ Morphological Closing ○ Morphological Opening

☐ Do not overlap contours with hard edges

Template Name:

A. Select a Destination

The **Destination** dropdown lets you choose whether to create a new contour or apply the expansion or contraction to an existing contour.

If you choose to create a new contour, it will be created from the contour selected in the Contours sidebar, but the original contour will remain unchanged. The new contour will be named using a generic "ROI-#" label (*ROI-3* in the image above) unless you replace this name.

Examples:

- You select a contour named "GTV" in the Contours sidebar. You set the Destination dropdown to "New Contour" and replace the generic name with "GTV-Expanded." You set the parameters to expand the contour 1 cm in all directions. When you click OK, MIM creates a new contour named "GTV-Expanded"that is a 1 cm expansion of "GTV." The original "GTV" contour remains unchanged.

- You select a contour named "GTV" in the Contours sidebar. You set the Destination dropdown to "GTV." You set the parameters to expand the contour 1 cm in all directions. When you click OK, MIM expands the existing "GTV" contour by 1 cm in all directions. No new contour is created.

B. Set Expand or Contract Values

To create a uniform expansion or contraction in all directions:

i. Leave the **Set All Directions the Same** checkbox selected.
ii. Enter an expansion distance in the field that follows the checkbox.

To specify expansion or contraction parameters:

i. Deselect the **Set All Directions the Same** checkbox.
ii. Use the fields dialog to specify the amount to expand or contract the contour in each direction. All measurements are in cm, and only positive numbers are allowed.

C. Set Expand or Contract Options

Use the radio buttons in this section to specify the operation to perform on the contours.

Expand—Expands the selected contour as specified.

Contract—Contracts the selected contour as specified.

Inner Ring—Creates a contraction and subtracts the contracted volume from the original contour. The result is a hollow "shell" whose outside surface corresponds to the original contour.

Outer Ring—Creates an expansion, then removes the original contour volume from the expanded volume. The result is a hollow "shell" that surrounds the originally drawn contour volume.

Morphological Opening—First contracts, then expands the contour. Morphological opening may expand holes. Morphological Opening may also eliminate small segments of contour, and may reduce the contour's volume.

Morphological Closing—First expands, then contracts the contour. Morphological closing may shrink or completely fills holes in the contour. Morphological closing may also join contour segments, and may increase the contour's volume.

If you select **Do not overlap contours with hard edges** the expanded or contracted contour will be prevented from overlapping with any contour that has the Hard Edge option checked in the Contour Settings menu.

D. Create Expand or Contract Templates

An expand or contract template is a saved set of parameters that can be quickly applied. To create an expand or contract template, do the following:

1. Set all of the parameters for the expansion or contraction as described in sections A through C of this document.
2. Enter a name for the template in the **Template Name** field.
3. Click **Save Template**.

Use Expand or Contract Templates

In the contours sidebar, select the contour that you want to expand or contract.

1. Click the **Expand/Contract...** button.
2. Near the bottom of the Expand/Contract... dialog, double-click the template that you want to apply. The parameters in the dialog will update to the template parameters.
3. Click **OK** to apply the expansion or contraction.

Create and Adjust Contours Using Boolean Operations

MIMTD-1540 • 19 May 2023

Overview

MIM's Boolean Operations feature is a contour post-processing tool designed for flexibility. After contouring an image, you can use Boolean Operations to adjust existing contours and generate new contours.

The sections below describe how to use the tool and a few common examples. If there are particular operations that you find yourself using frequently or that you are having trouble accomplishing with the Boolean Operations tool, please contact MIM Software Support at support.mimsoftware.com. A different tool or a workflow might be a better fit for your situation.

Contents

- Create a Boolean Operation
- Common Operations:
    - Combine Contours
    - Subtract a Contour
    - Find Where Contours Intersect
- More Complex Scenarios:
    - Remove Overlapping Areas
    - Use Expand/Contract to Make a Skin Contour
    - Use Parentheses to Combine Operations

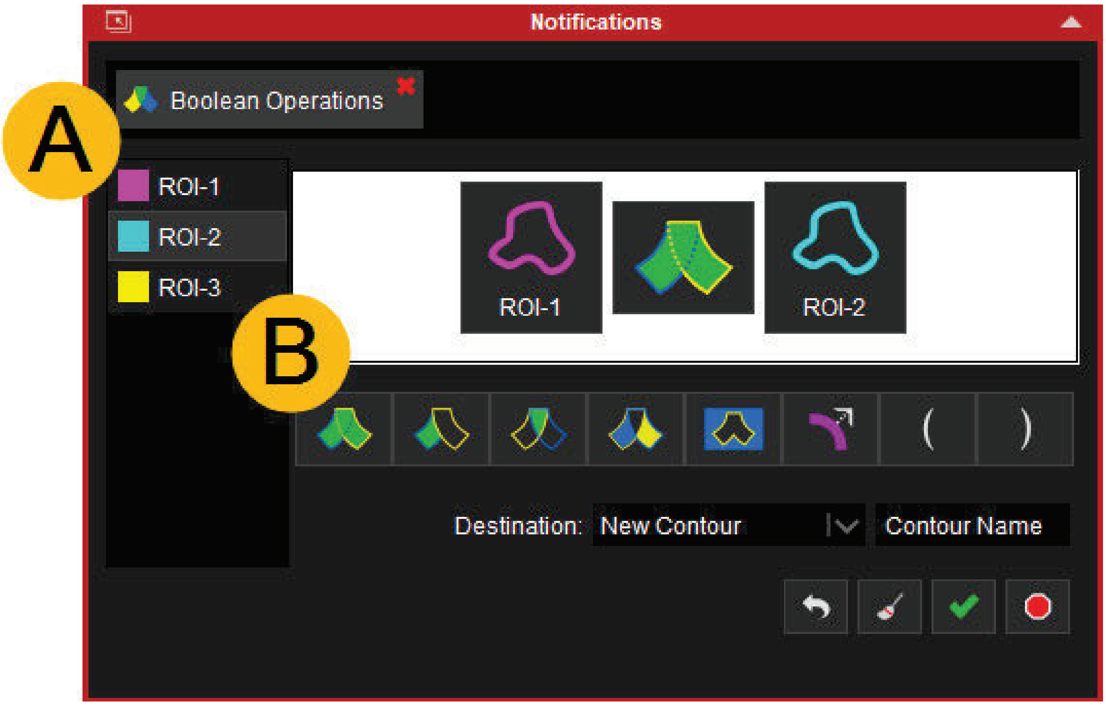
Create a Boolean Operation

To start, open a session and draw at least one ROI using 2D Brush, PET Edge®+, or any contouring tool of your choice.

Then, use the Boolean Operations tool:

1. In the top toolbar, click » to see additional tools.
2. Search for and select the Boolean Operations tool.

3. In the Notifications window, write your operation:
    i. Select a contour from the left pane. It is added to the operation box.
    ii. Select an operator from the bottom row. It is added to the operation box. Hover over an operator button to see what the operator does.
    iii. Continue adding contours (A) and operators (B) as needed.

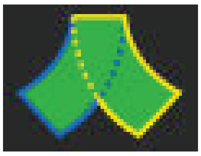


Destination: New Contour

    iv. Use the **Destination** dropdown to create a new contour or to select an existing contour to overwrite.

4. Click the green checkmark ✓ to run the operation. To clear the operation box and start over, click the broom 🧹.

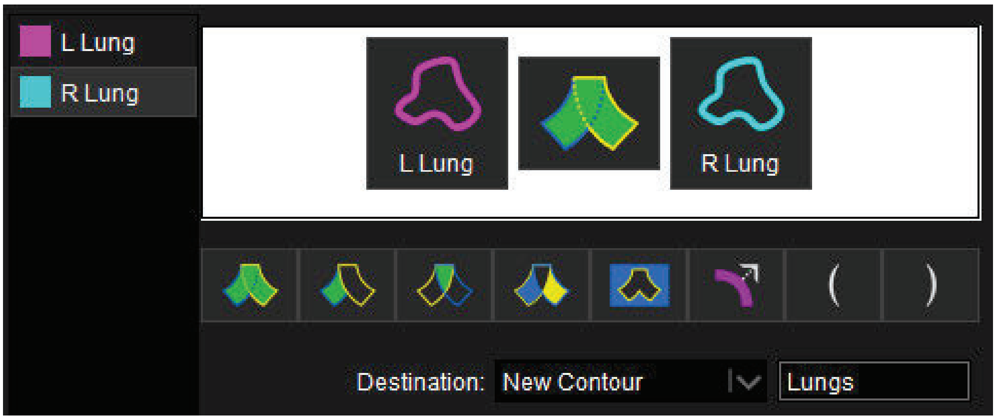
Combine Contours



You can use the union (OR) operator to combine multiple contours. For example, you might want to combine left and right lung contours to be a single structure or combine GTV contours for total calculations.

1. Select the first contour that you want to combine.
2. Select the union (OR) operator.
3. Select the second contour that you want to combine.

4. Choose to save the output as a new contour and enter a name. Alternatively, choose an existing contour to overwrite.



Destination: New Contour — Lungs

5. Click the checkmark ✓. The contour is created with both of the contours that you selected.

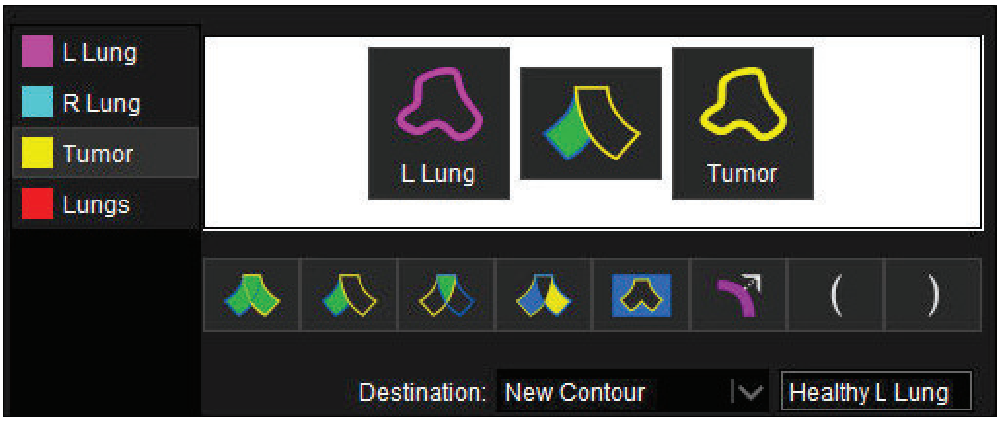
You can add the union (OR) operator multiple times to the same operation to combine more than two contours. If you select two contours in a row without specifying an operator, the union (OR) operator is automatically added.

Subtract a Contour

You can use the subtraction operator to remove one contour from another contour. For example, you might want to subtract a tumor to get normal organ counts, such as Lung minus GTV to get the healthy lung.

1. Select the contour that you want to remove from.
2. Select the subtraction operator.
3. Select the contour that you want to remove.

4. Choose to save the output as a new contour and enter a name. Alternatively, choose an existing contour to overwrite.



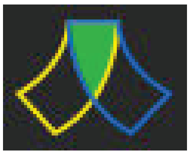
New Contour

Healthy L Lung

5. Click the checkmark ✓. The contour is created and does not include the area of the contour that you chose to subtract.

See Combine Contours below for examples of combing subtraction with other operators in more advanced operations.

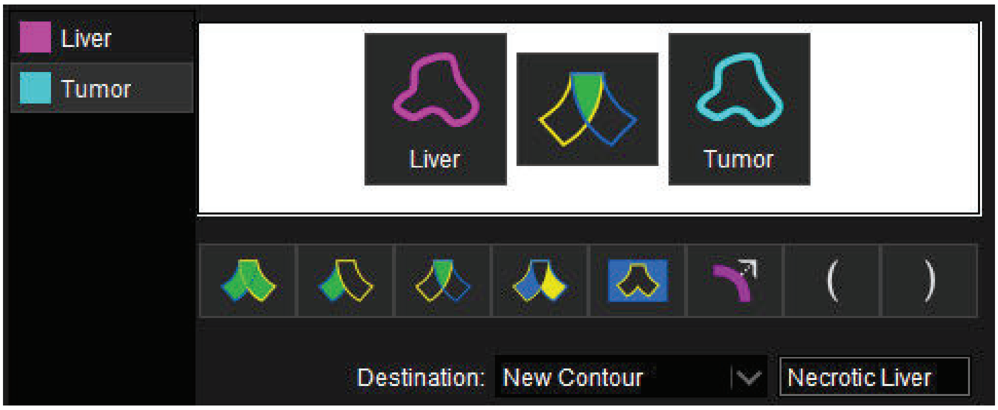
Find Where Contours Intersect



You can use the intersection (AND) operator to create a contour where two contours intersect. For example, you might want to see where the liver overlaps the tumor to get the necrotic liver.

1. Select the first contour.
2. Select the intersection (AND) operator.
3. Select the second contour.

4. Choose to save the output as a new contour and enter a name. Alternatively, choose an existing contour to overwrite.



Destination: New Contour
Necrotic Liver

5. Click the checkmark ✓. The contour is created and includes only the area where the contours that you selected overlap.

You could use intersection to make a more precise contour. For example, if draw an ROI on the lung while looking at different images, it may appear to go outside of the lung. You can use intersect to redraw the ROI only where it intersects with the R Lung contour.

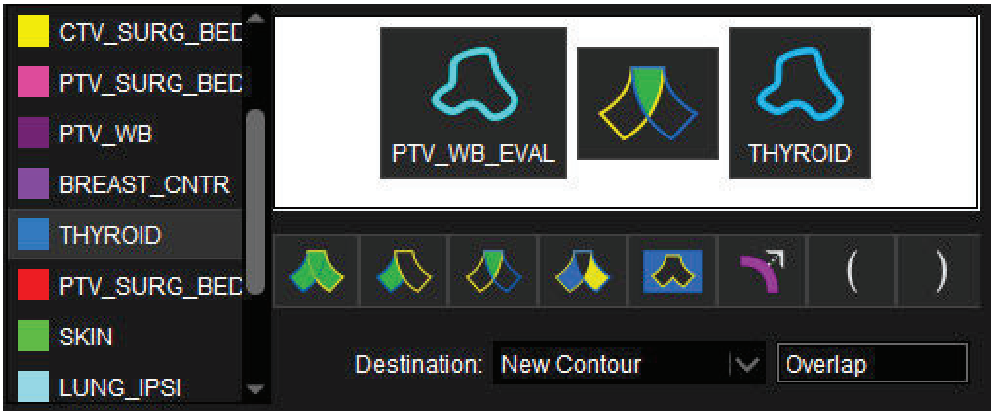
Remove Overlapping Areas

You can use the Boolean Operations tool if you have multiple ROIs next to each other that you want to be flush and not overlap. In this example, the PTV should not touch the thyroid.

Notice also how this example demonstrates running two operations sequentially. Part of the power of the Boolean Operations tool is the ability to run multiple operations, as this example and the following more complex examples in this document demonstrate.

1. Find where the contours overlap:
    i. Select the PTV contour.
    ii. Select the intersection (AND) operator.

iii. Select the thyroid contour.



Destination: New Contour
Overlap

iv. Set the **Destination** as **New Contour** and name it as desired, such as Overlap.

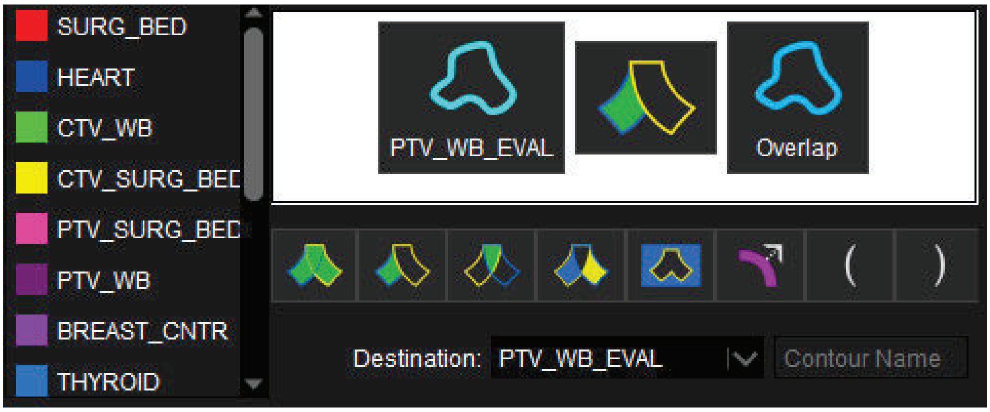
v. Click the green checkmark ✓ to run the operation. The system makes a new contour where the PTV overlaps with the thyroid.

2. Subtract the overlap contour from the PTV:

   i. Select the PTV contour.

   ii. Select the subtraction operator.

   iii. Select the overlap contour that you created in the previous step.



Destination: PTV_WB_EVAL
Contour Name

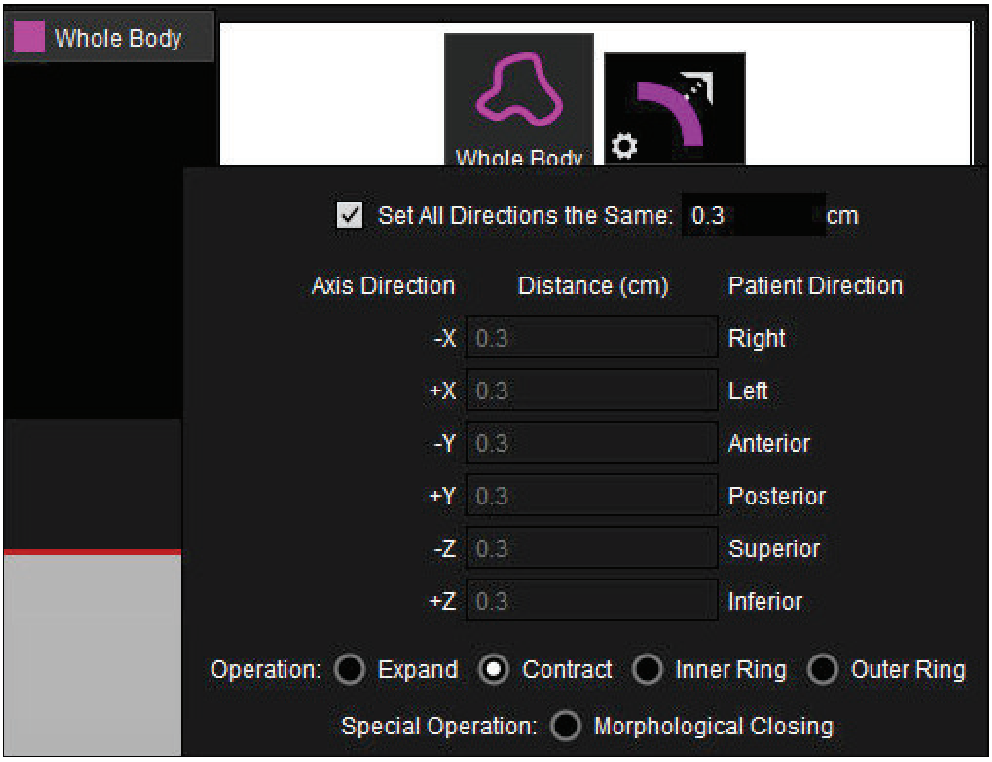
   iv. Set the **Destination** as the PTV contour to overwrite it.

   v. Click the green checkmark ✓ to run the operation. The system adjusts the PTV contour so that it no longer includes the area that overlapped with the thyroid.

Use Expand/Contract to Make a Skin Contour

You can use the Expand/Contract operator in your Boolean operation, which works the same way as the Expand/Contract tool. The example below demonstrates creating a skin contour by starting with a whole body contour, contracting it, and removing nonoverlapping space.

1. Select the Whole Body tool and draw a whole body contour on a CT sagittal or coronal image.
2. Rename the contour **Whole Body** to make it easier to identify.
3. Make a skin contour:
    i. Open the Boolean Operations tool.
    ii. Select the expand/contract operator.
    iii. Click the gear ⚙ on the operator to open the settings and configure the following:
        - Select the **Set All Directions the Same** checkbox.
        - Enter **0.3cm**.
        - Select **Contract**.



☑ Set All Directions the Same: 0.3 cm

Axis Direction	Distance (cm)	Patient Direction
-X	0.3	Right
+X	0.3	Left
-Y	0.3	Anterior
+Y	0.3	Posterior
-Z	0.3	Superior
+Z	0.3	Inferior

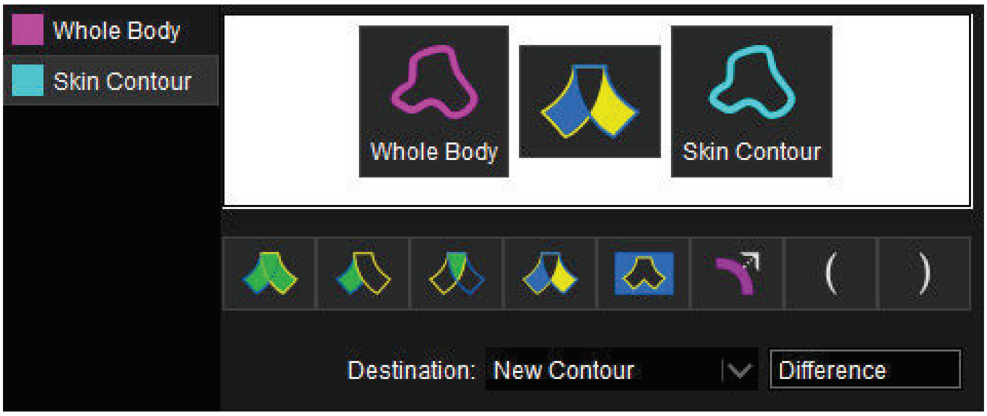
Operation: ○ Expand ● Contract ○ Inner Ring ○ Outer Ring

Special Operation: ○ Morphological Closing

    iv. Set the **Destination** as **New Contour** and name it as desired (e.g. Skin Contour).
    v. Click the green checkmark ✓ to run the operation. The system creates the contour.

> **Related:** See Expand or Contract Contours for more information abut the Expand/Contract tool, used either separately or within a Boolean operation.

4. Use the Boolean Operations tool again to find the difference:
    i. Open the Boolean Operations tool.
    ii. Select the **Whole Body** contour.
    iii. Select the nonoverlapping (XOR) operator.
    iv. Select the contour you created, such as Skin Contour.



Destination: New Contour
Difference

    v. Set the **Destination** to overwrite the contour you made earlier (e.g. Skin Contour) or create a new contour.
    vi. Click the green checkmark ✓ to run the operation. The system creates the new contour as a 0.3cm outline around the whole body.

Use Parentheses to Combine Operations

The previous examples showed using two operations sequentially. You can also use parentheses in a single operation to group together and order multiple operators. The example below demonstrates combining the lung contours and removing the tumor contour to get Lungs minus GTV.

1. Make the first part of the operation in parentheses:
    i. Select the left parenthesis (.
    ii. Select the L Lung contour.
    iii. Select the union (OR) operator.
    iv. Select the R Lung contour.
    v. Select the right parenthesis).

2. Add the second part of the operation after the parentheses:
   i. Select the subtraction operator.
   ii. Select the tumor contour.

Destination: New Contour

Lungs - GTV

3. Set the **Destination** as **New Contour** and name it as desired.
4. Click the green checkmark ✓ to run the operation. The system creates a new contour that includes both lung contours, minus the GTV contour.

Tips for Efficient Contouring

MIMTD-1737 • 02 Nov 2023

Overview

MIM® offers a variety of tools for generating and editing contours.

Take advantage of the following options to more efficiently work with contours in MIM.

Related: Go to Create Contours Overview for an introduction to contouring in MIM.

Contents

- Customize the Mode Tools Section of the Contours Sidebar
- Organize the Contour List
- Take Action on Multiple Contours at Once (MIM 7.3 and Later)
- Use Keyboard Shortcuts with Contouring
- See Statistics and Select Contours from the Viewport
- Use Contour Templates
- Save and Stamp Contour Shapes
- Use Ranges for Threshold-Based Contouring

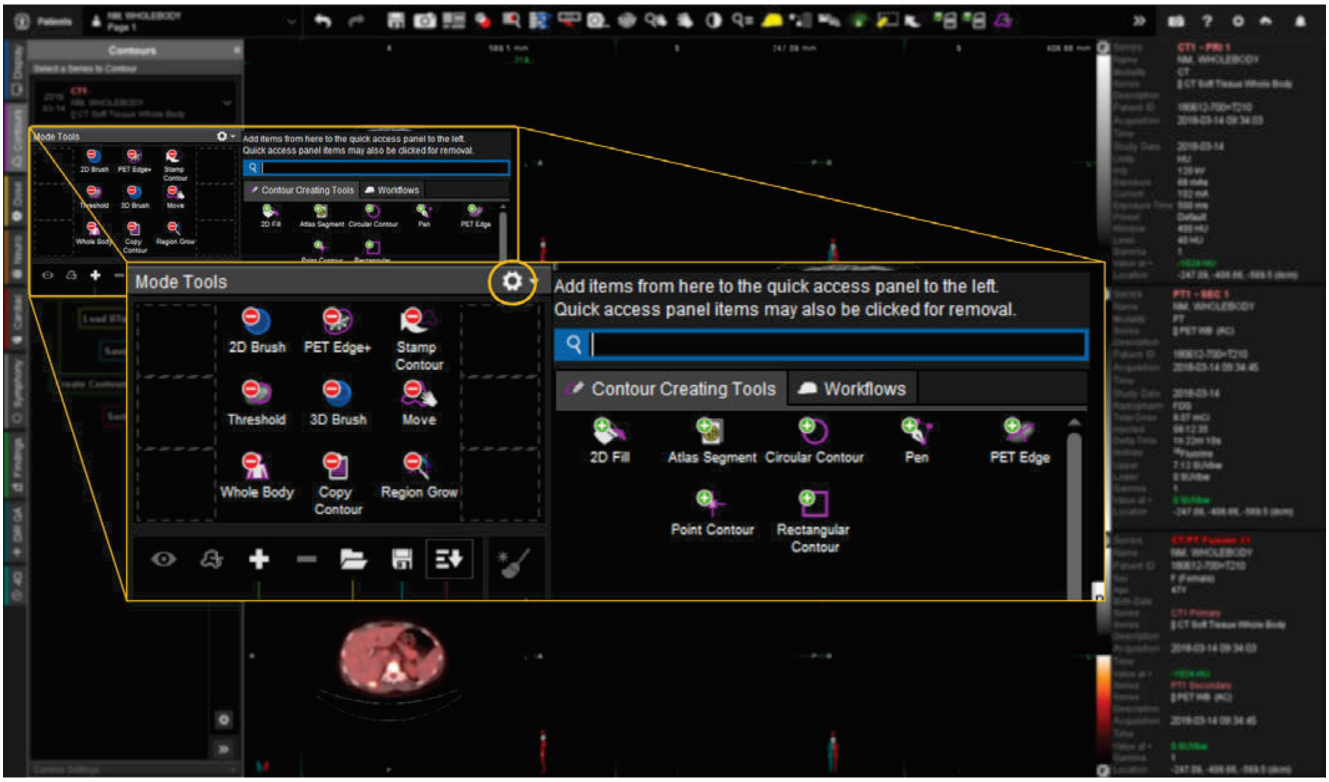
Customize the Mode Tools Section of the Contours Sidebar

You can customize the Mode Tools section to include the contouring tools you use the most.

Click on the gear button in the upper-right corner of the Mode Tools section. Then:

- Select tools in the Mode Tools section to remove them.
- Select tools in the gear menu list to add them to the Mode Tools section.

- When the gear menu is open, drag the icons to rearrange them in the Mode Tools section.



Add items from here to the quick access panel to the left.
Quick access panel items may also be clicked for removal.

Organize the Contour List

The contour list shows all contours that are currently drawn or loaded. By default, contours appear in the order in which they were created.

To keep your contours organized, you can:

- Rearrange the order of the contours by left-click dragging a contour in the list.
- Sort the contours alphabetically by clicking the sort button.

A contour name that is grayed out and italicized signifies that the contour does not have any data, meaning the contour is not yet drawn or was erased. You might have many empty contours that were created by a workflow or loaded with an ROI template. If you do not need them, you can clean up your contour list using the Remove Empty Contours tool:

1. From the toolbar at the top of the screen, click the double arrow » to expand additional options.
2. Search for and select the **Remove Empty Contours** tool.

> **Tip:** If you use this option frequently, consider adding it to your toolbar so that you don't have to search for it. Or, you can make a keyboard shortcut for the tool. Refer to Set Keyboard Shortcuts for more information.

Take Action on Multiple Contours at Once (MIM 7.3 and Later)

You can select multiple contours in the Contours sidebar at the same time. This functionality is not available in MIM 7.2 and earlier.

- Use Shift+click to select consecutive contours.
- Use Ctrl/Cmd+click to select nonconsecutive contours.

Use this functionality to perform an action (e.g., Delete or Smooth) on multiple contours at the same time.

When multiple contours are selected, tools that cannot operate on multiple contours are disabled. These tools become available again when a single contour is selected.

Use Keyboard Shortcuts with Contouring

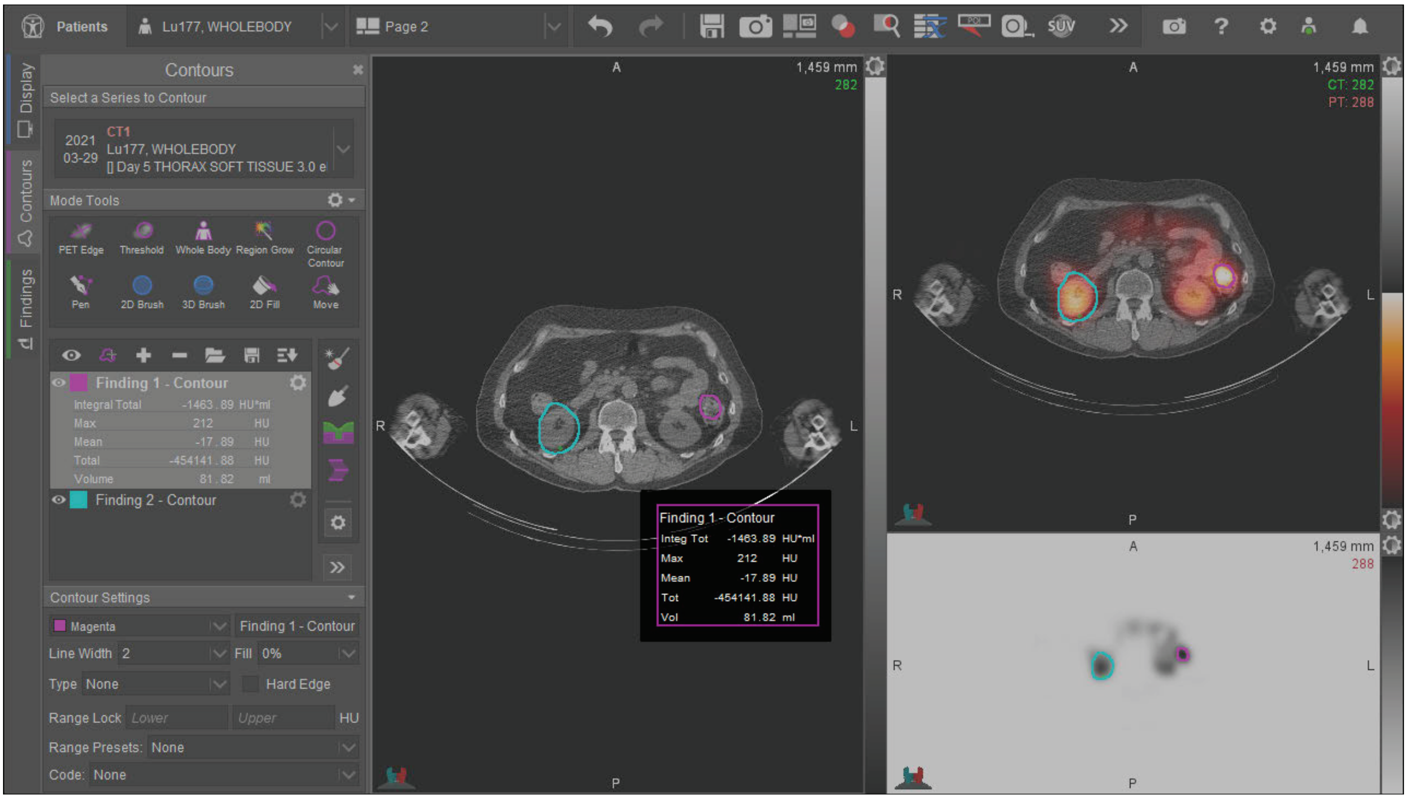
You can set up keyboard shortcuts to assist with quicker contouring. Refer to Set Keyboard Shortcuts for more information about changing the default shortcut key or adding your own shortcut key if there is no default.

Here are a few common options:

Command	Description
Cycle Active Contour (default: A)	Go to the next contour listed in the Contours sidebar.
Add Contour	Create a contour.
Delete Contour	Remove a contour from the series and the Contours sidebar. You might find this helpful if you have a lot of automatically generated contours that are not relevant for you.
Erase Contour	Erase the contour that is drawn so that you can redraw it.
Quick Save Contours (default: Ctrl+R)	Saves a DICOM RTstruct file with the contours.

See Statistics and Select Contours from the Viewport

In addition to seeing statistics for a contour in the Contours sidebar, you can enable statistics to appear in the viewport itself for the selected contour.



Finding 1 - Contour		
Integral Total	-1463.89	HU*ml
Max	212	HU
Mean	-17.89	HU
Total	-454141.88	HU
Volume	81.82	ml

Finding 2 - Contour

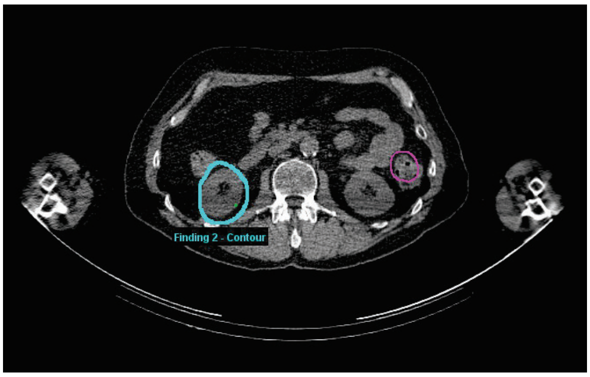
Finding 1 - Contour		
Integ Tot	-1463.89	HU*ml
Max	212	HU
Mean	-17.89	HU
Tot	-454141.88	HU
Vol	81.82	ml

Contour Settings
Magenta | Finding 1 - Contour
Line Width: 2 | Fill: 0%
Type: None | ☐ Hard Edge
Range Lock: Lower | Upper | HU
Range Presets: None
Code: None

To do so:

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for **"display statistics"**. Select **Contouring** on the left slide.
3. Select **Display statistics for the active contour in the viewport**.
4. *MIM 7.3 and later*: Select whether contour statistics for functional series should also appear on fusions. *MIM 7.2 and earlier*: This functionality is not available.

You can also enable selecting contours on the image by clicking the contour selection button above the contour list. With this option, MIM displays the contour name and shows a thicker line in the viewport when you hover over the contour. Click the contour in the viewport, and MIM selects the contour name in the sidebar.



Tip: This preference can be enabled by default by going to Settings ⚙ >> **General Preferences** >> **Imaging** >> **Contouring** and selecting **Enable contour selection from series views by default**.

Use Contour Templates

You can use ROI templates to standardize contour names and colors. ROI templates also save you time by pre-filling contour names and settings so you don't need to add and configure them with every study.

Refer to Standardize Contour Names with ROI Templates for more information about using ROI templates.

Save and Stamp Contour Shapes

You can save common contour shapes in the Contour Shape Library. Then, you can use the Stamp Contour tool to apply the shape to series and reduce time spent manually contouring. For example, you could create a shape for a wedge or other immobilization device so you can easily apply it to many series.

Refer to Save and Reuse Contour Shapes for more information about setting up and using contour shapes.

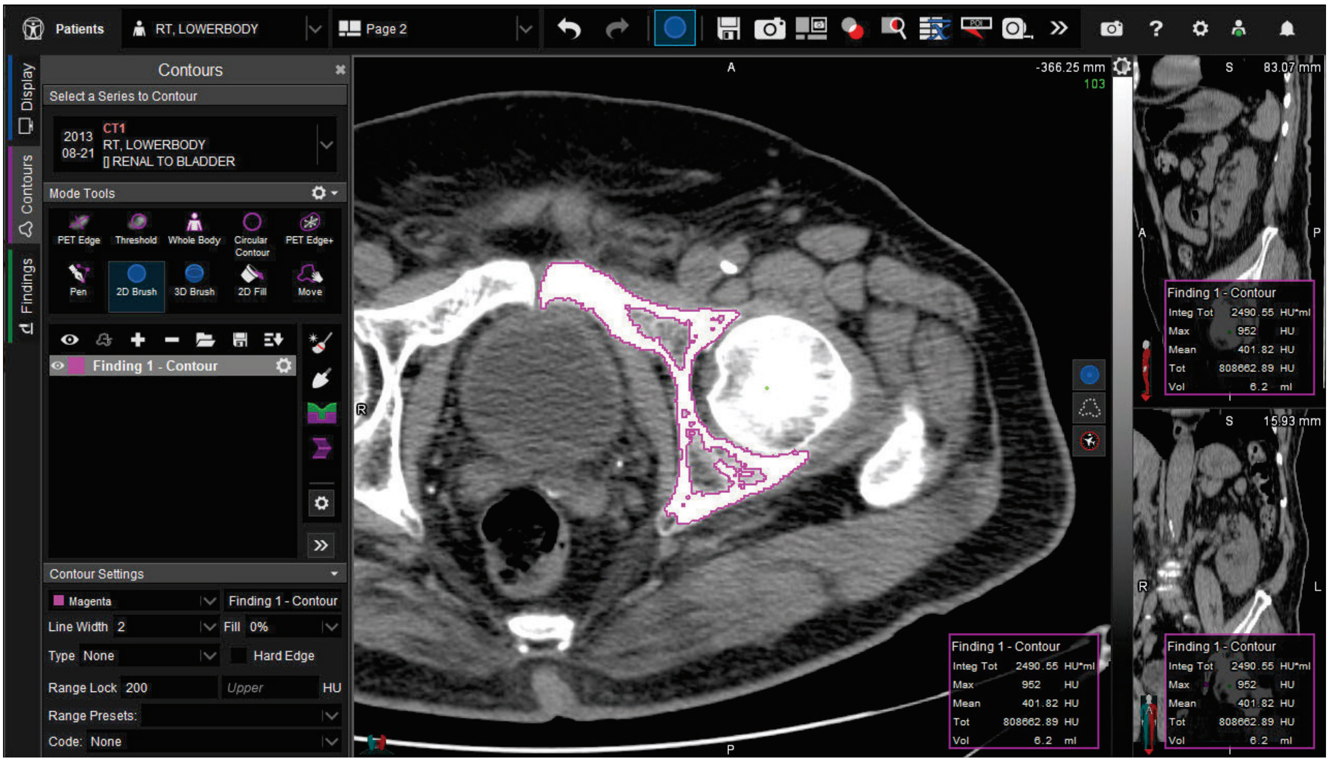
Use Ranges for Threshold-Based Contouring

When using a freehand contouring tool (2D Brush, 3D Brush, or Pen), you can set a range lock to help guide your contouring.

1. In the Contours sidebar, click the plus to create a new contour.
2. In the Contour Settings section at the bottom of the sidebar, enter a **Range Lock** value. Or, select a **Range Preset**.

Tip: You can enter a minimum range lock value, a maximum range lock value, or both.

3. Use your desired freehand contouring tool, such as 2D Brush, to draw the contour. The range lock prevents the contour from including regions that are above or below the range locks that you set.



2013 08-21 CT1 RT, LOWERBODY [] RENAL TO BLADDER

Finding 1 - Contour

Magenta

Finding 1 - Contour

Line Width 2

Fill 0%

Type None

Hard Edge

Range Lock 200 Upper HU

Range Presets:

Code: None

Finding 1 - Contour

Integ Tot	2490.55	HU*ml
Max	952	HU
Mean	401.82	HU
Tot	808662.89	HU
Vol	6.2	ml

For example, setting a minimum range lock of 200 HU allows you to contour only bone without also including tissue.

Reconstruct 3D Images

SPECTRA Recon® Overview

MIMTD-1752 • 10 Jun 2024

Overview

MIM Encore® includes SPECTRA Recon so that you can reconstruct 2D SPECT images.

Reconstruction includes attenuation correction, motion correction, scatter correction, and resolution recovery to produce a high-quality result.

Reconstruction requires additional setup to customize acquisition and reconstruction parameters based on your camera specifications. Talk to your MIM Implementation Specialist if you are not sure whether your organization has completed clinical commissioning to perform reconstruction with MIM®.

Reconstruction Process

Reconstruction in MIM uses the following process:

1. Your organization gathers data specific to your scanners and the isotopes that you are using. Refer to the *SPECTRA Recon and SPECTRA Quant Welcome Packet* provided by your MIM representative for details about the information to collect and send to MIM.
2. MIM creates reconstruction workflows that are specific to your parameters and helps you implement them. Your organization is responsible for clinical commissioning.
3. When the reconstruction workflows are ready, they can be run in two ways:
    - Automatically with MIM Assistant®. Your MIM Implementation Specialist likely set up MIM Assistant rules to run reconstruction workflows as part of your implementation. Please contact MIM Software Support at support.mimsoftware.com if you need further help with MIM Assistant rules.
    - Manually by users. Refer to Manually Run a Reconstruction Workflow for steps.
4. The workflow creates a reconstructed 3D image.
    - Depending on your scope of practice, you might then use this series as an input for a SurePlan™ LiverY90 or SurePlan™ MRT workflow.
    - If your organization has extended SPECTRA Recon capabilities with SPECTRA Quant®, MIM can produce quantitative images in units of Bq/ml and SUV. Refer to Use SPECTRA Quant for Bq/ml Conversion for more information about this feature. If you are interested in purchasing SPECTRA Quant, contact your MIM Site Development Manager.

Refer to Advanced Settings for SPECT Reconstruction for more information about the parameters used in reconstruction workflows.

Related: Refer to the white paper *SPECT/CT Reconstruction with SPECTRA Recon®* for technical details about how reconstruction works and the algorithms behind it.

Requirements

- MIM can reconstruct data from parallel hole collimators. Pin hole collimators are not supported. Contact MIM Support if your organization is using scanners with fan beam collimators instead.
- Data from certain cameras cannot be reconstructed. Refer to the information provided by your MIM representative during your implementation process about supported cameras.
- Refer to the *SPECTRA Recon and SPECTRA Quant Welcome Packet* provided by your MIM representative for more information about commissioning for MIM reconstruction.

Manually Run a Reconstruction Workflow

MIMTD-1753 • 04 Nov 2024

Overview

Caution: It is recommended that you complete clinical commissioning before using reconstruction in a clinical setting. Clinical commissioning can help you determine scatter window parameters, as well as which iterations and subsets are appropriate matches for your current data output. For assistance with this, please contact MIM Software Support at support.mimsoftware.com.

As part of your organization's implementation, MIM® configures a reconstruction workflow that accounts for your site's specific cameras. Because of this customization, the SPECTRA Recon® workflow typically runs with default settings and requires minimal user configuration.

The workflow may run automatically through MIM Assistant®. If you need to run the workflow manually, complete the following steps.

Important: This workflow changes significantly between versions. Make sure to refer to the relevant section based on which MIM version you are using.

Contents

- Run Reconstruction (MIM 7.3.4 and Later)
  - Launch the Workflow
  - Work with the Reconstruction
- Run Reconstruction (MIM 7.3.3 and Earlier)

Run Reconstruction (MIM 7.3.4 and Later)

The workflow automatically creates the initial reconstruction. Then, you can further adjust it as needed or take your next steps using the reconstruction side panel.

Launch the Workflow

1. From the patient list, select the Raw Projection NM series. Optionally, select a CT.

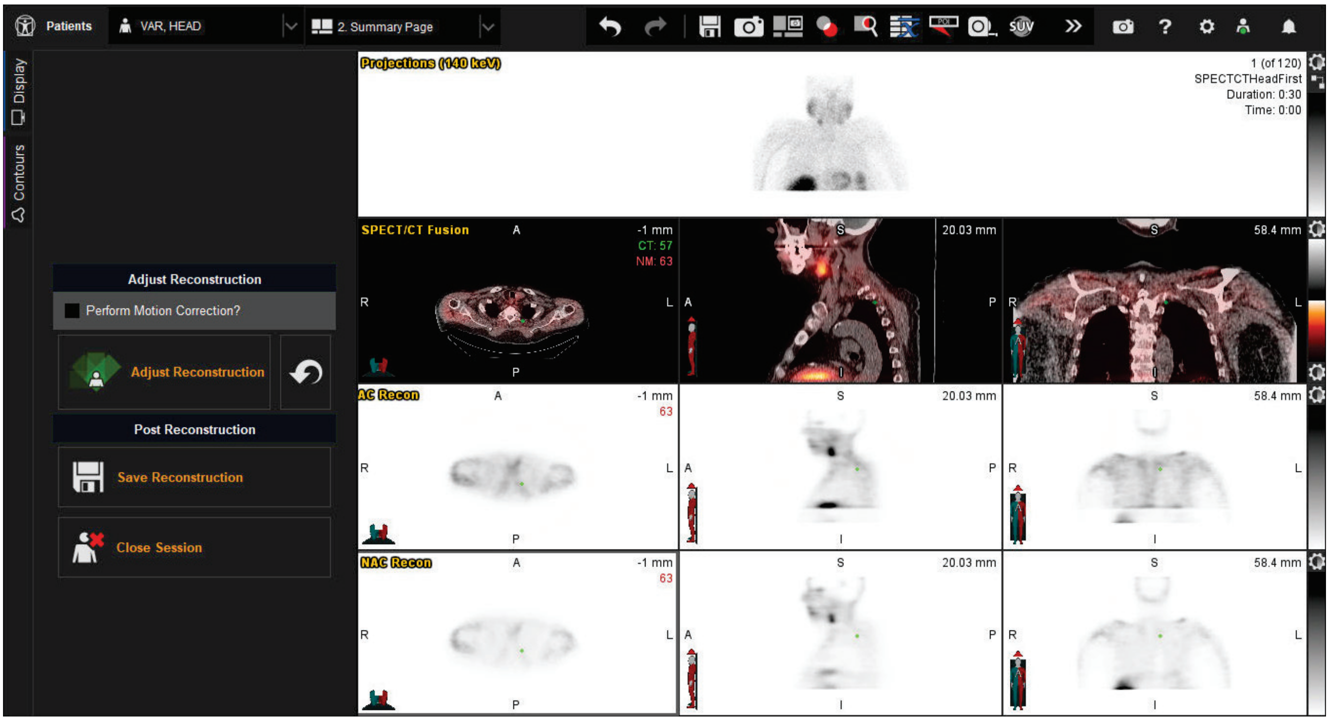
> ☆ **Important**: If the scatter projections are not included with the main window as a single NM series in the patient list, select the scatter projection files as well.

2. On the Workflows sidebar on the right side, find and launch your organization's reconstruction workflow.
3. In the Confirm Selections window, ensure the series assigned to the targets are correct. If not, click the dropdown under **Assignment** to choose the correct series for each **Target**. Click the **Confirm** button.

> ⚠ **Caution:** Before selecting raw data for processing, always make sure the correct data and reconstruction parameters are used. Verify that the patient and acquisition information is complete and accurate. Inaccurate data may lead to incorrect processing or misinterpretation of the image data.

4. Watch the Notifications window in the upper-right corner while the workflow runs:
    i. At the first prompt, select the **Exam Type**.
    ii. Respond to any additional prompts that appear.

5. When the workflow finishes running, review the reconstructed images on the summary page.



6. If you ran the workflow with a CT, review the SPECT/CT fusion. If necessary, adjust the alignment using the tools described in Adjust Fusions Manually.

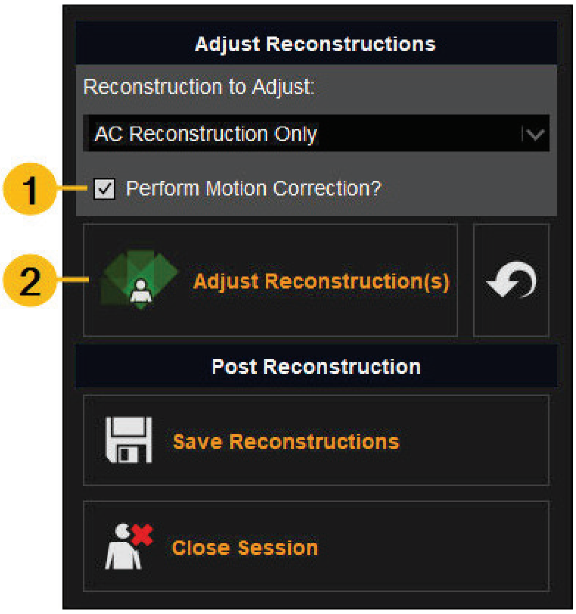
6.1.4

Caution: Attenuation correction is applied to the SPECT based on the CT. When reconstructing a SPECT using a separately acquired CT, ensure that the CT image has a similar patient position and body size as the SPECT image. It is always recommended to carefully review the results and compare results with the non-corrected images.

Work with the Reconstruction

After the workflow finishes running, you can take further action using the reconstruction side panel.

Related: Refer to Review the Reconstruction Output if you want to adjust your display to show other images or graphs.



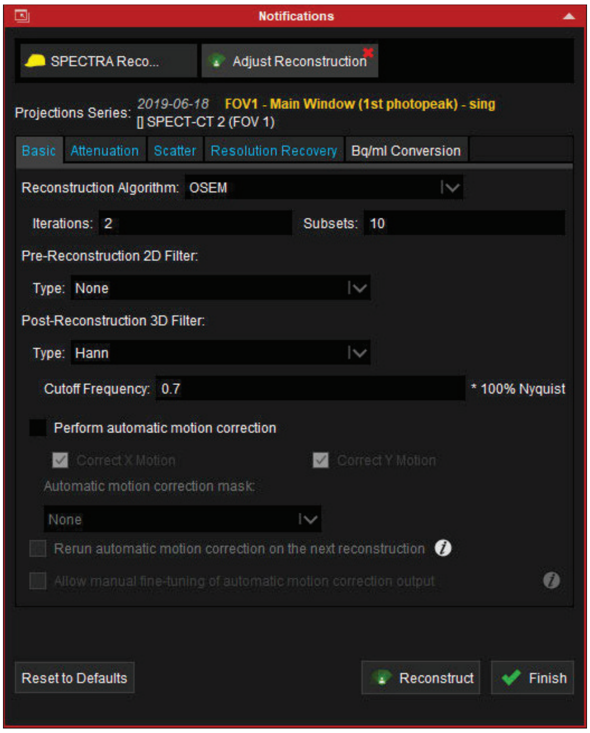
To apply motion correction:

1. Select **Perform Motion Correction?**. If you ran the workflow with a CT, you can select whether to apply adjustments to the AC reconstruction or NAC reconstruction.
2. Click the **Adjust Reconstruction(s)** button. The Adjust Reconstruction options open in the Notifications window, and motion correction automatically runs. Click the **Finish** button in the Notifications window to accept the reconstruction and return to the summary page.

Related: Refer to Apply and Adjust Motion Correction for more information about motion correction and additional manual options.

To adjust reconstruction parameters:

1. Click the **Adjust Reconstruction(s)** button in the reconstruction side panel. The Adjust Reconstruction options open in the Notifications window.



Projections Series: 2019-06-18 FOV1 - Main Window (1st photopeak) - sing
[] SPECT-CT 2 (FOV 1)

Reconstruction Algorithm: OSEM

Iterations: 2 Subsets: 10

Pre-Reconstruction 2D Filter:

Type: None

Post-Reconstruction 3D Filter:

Type: Hann

Cutoff Frequency: 0.7 * 100% Nyquist

☐ Perform automatic motion correction

☑ Correct X Motion ☑ Correct Y Motion

Automatic motion correction mask:

None

☐ Rerun automatic motion correction on the next reconstruction

☐ Allow manual fine-tuning of automatic motion correction output

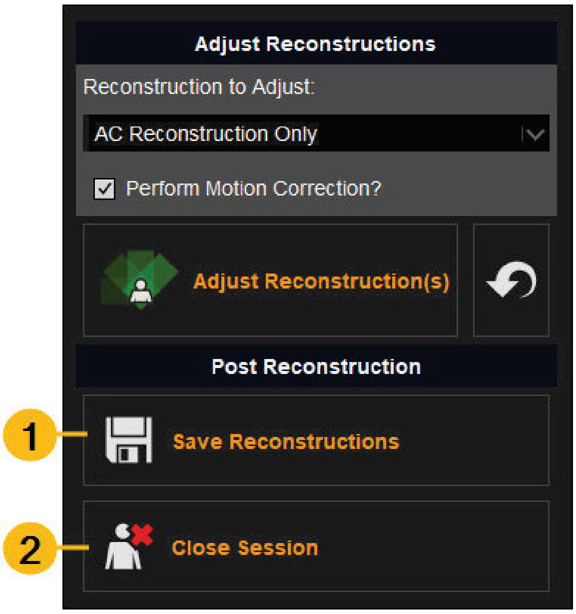
2. Review the settings and, if necessary, adjust them.

> **Important:** Because reconstruction workflows are clinically commissioned per camera and isotope, reconstruction should typically use the default settings. Parameters should generally not be changed on a per-patient basis.

> **Related:** Refer to Advanced Settings for SPECT Reconstruction if you need more information about the settings in the Adjust Reconstruction window.

3. Click the **Reconstruct** button to reconstruct the image with the updated parameters.
4. When you are satisfied with the reconstruction, click the **Finish** button to accept the reconstruction and return to the summary page.

To save and finish:



1. Click the **Save Reconstructions** button. An AC Recon series (if you ran reconstruction with a CT) and an NAC Recon series are saved to your patient list.
2. Click the **Close Session** button. If you did not save reconstructions or the session before closing the session, the reconstruction is not saved. You may need to run reconstruction again.

> ☆ **Important:** The Save Reconstructions button saves the DICOM image data. If you updated your display pages, added annotations, or made other changes, make sure to save the session as well. From the top toolbar, select save 🖫 >> **Save Session...**.

Run Reconstruction (MIM 7.3.3 and Earlier)

1. From the patient list, select the Raw Projection NM series. Optionally, select a CT.

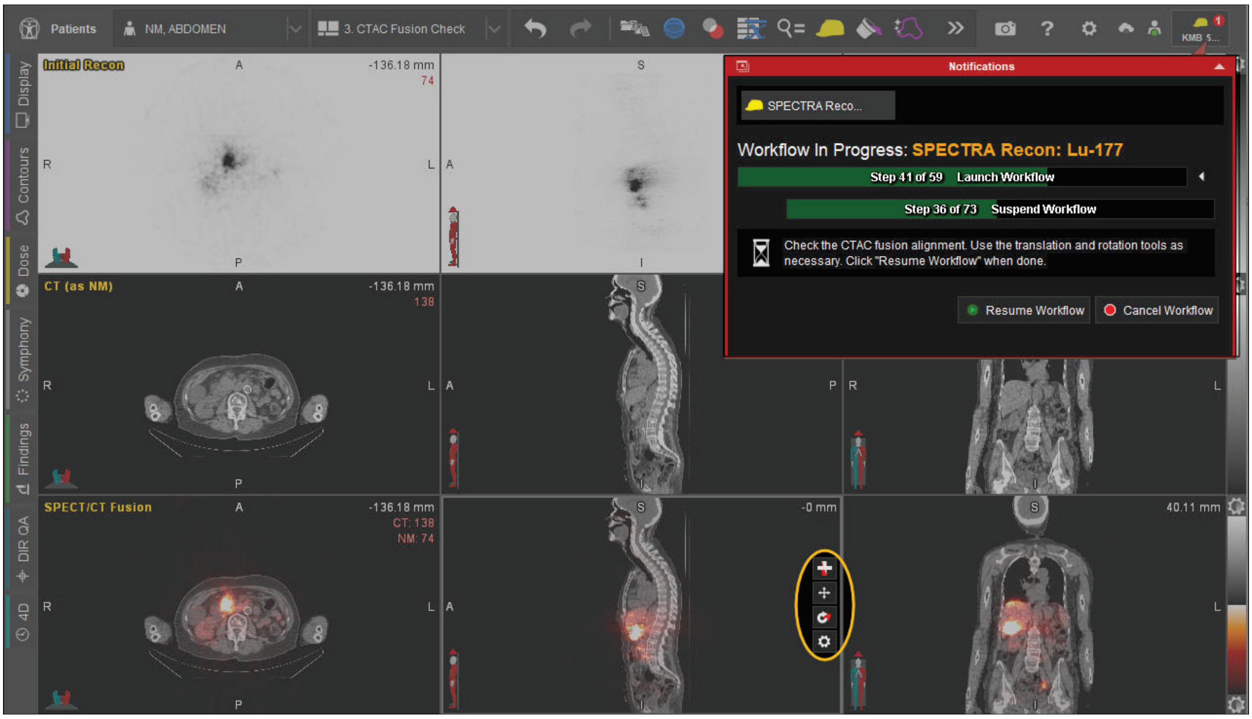
   > ☆ **Important**: If the scatter projections are not included with the main window as a single NM series in the patient list, select the scatter projection files as well.

2. On the Workflows sidebar on the right side, find and launch your organization's reconstruction workflow.

   > 💡 **Tip:** You might have multiple reconstruction workflows for different radioisotopes. Make sure to select the workflow for the relevant isotope.

3. In the Confirm Selections window, ensure the series assigned to the targets are correct. If not, click the dropdown under **Assignment** to choose the correct series for each **Target**. Click the **Confirm** button.

4. Watch the Notifications window in the upper-right corner and respond to prompts as needed while the workflow runs. If you are running the workflow with a CT, you may be prompted to review the CTAC alignment. To do so:
   i. Use the fusion tools on the right side of each viewport to align the activity of the SPECT with the CT. See Adjust Fusions Manually for more information on these tools.



Workflow In Progress: SPECTRA Recon: Lu-177

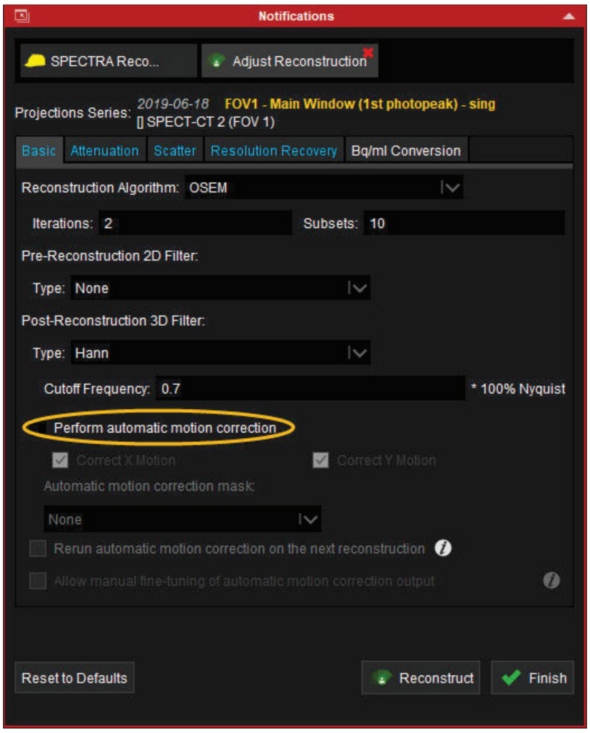
Step 41 of 59 Launch Workflow

Step 36 of 73 Suspend Workflow

Check the CTAC fusion alignment. Use the translation and rotation tools as necessary. Click "Resume Workflow" when done.

   ii. Click **Resume Workflow** once the series are aligned.

5. At the Adjust Reconstruction prompt, stay on the **Basic** tab. If you want to apply motion correction, select **Perform automatic motion correction**. Refer to Apply and Adjust Motion Correction for more information about motion correction options.



Projections Series: *2019-06-18* **FOV1 - Main Window (1st photopeak) - sing**
[] SPECT-CT 2 (FOV 1)

Reconstruction Algorithm: OSEM

Iterations: 2 Subsets: 10

Pre-Reconstruction 2D Filter:

Type: None

Post-Reconstruction 3D Filter:

Type: Hann

Cutoff Frequency: 0.7 * 100% Nyquist

☐ Perform automatic motion correction

☑ Correct X Motion ☑ Correct Y Motion

Automatic motion correction mask:

None

☐ Rerun automatic motion correction on the next reconstruction

☐ Allow manual fine-tuning of automatic motion correction output

Important: Because reconstruction workflows are clinically commissioned per camera and isotope, reconstruction should typically use the default settings. Parameters should generally not be changed on a per-patient basis.

Related: Refer to Advanced Settings for SPECT Reconstruction if you need more information about the settings in the Adjust Reconstruction window.

6. When you have reviewed the reconstruction settings, you can either:
   - Click the **Finish** button to reconstruct the image, close the Adjust Reconstruction window, and complete the workflow.
   - Click the **Reconstruct** button to reconstruct the image and stay on the reconstruction step:
     - After the image is reconstructed, you can further adjust the parameters as needed and then click **Reconstruct** again to rerun reconstruction with the updated parameters.
     - When you are satisfied with the reconstruction, click the **Finish** button to close the Adjust Reconstruction window, and complete the workflow.

7. Review the image display when the workflow is finished running. Go to Review the Reconstruction Output for more information about display options.

Apply and Adjust Motion Correction

MIMTD-1470 • 02 Nov 2024

Overview

You can choose whether to apply a motion correction algorithm to the reconstruction. You can optionally use a mask to determine where to focus the motion correction and/or manually fine-tune the motion correction output.

Related: Refer to Manually Run a Reconstruction Workflow for more information about reconstructing an image. You can use the output described to review motion correction adjustments.

Contents

- Focus Motion Correction (MIM 7.2.11 and Later)
- Run Reconstruction with Motion Correction
- Manually Adjust Motion Correction

Focus Motion Correction (MIM 7.2.11 and Later)

You can optionally use a motion correction mask to focus correction on a region of the image, such as the heart in a cardiac scan. *MIM 7.2.10 and earlier:* This functionality is not available.

To use this option, create a contour on the area that you want to focus on. For example, you can use the 2D Brush or Rectangular Contour tool. Then, proceed to the next section to run reconstruction with motion correction.

Related: Refer to Create Contours Overview for more information about creating contours.

Run Reconstruction with Motion Correction

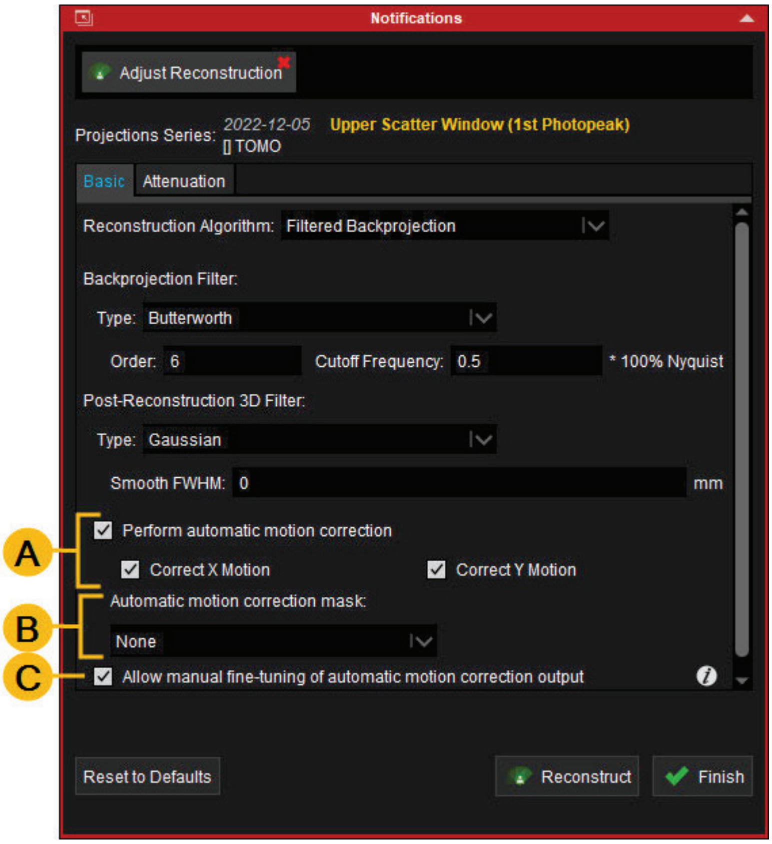
In the Adjust Reconstruction notification window:

1. Go to the **Basic** tab and select **Perform automatic motion correction**.
2. Configure the following options:
    A. **Correct X Motion, Correct Y Motion** — Apply motion correction to the x-direction, y-direction, or both directions.

    B. *MIM 7.2.11 and later:* **Automatic motion correction mask** — If you created a contour in the previous section to focus motion correction, select this option and use the dropdown to select the contour.
    MIM 7.2.10 and earlier: This functionality is not available.

    C. **Allow manual fine-tuning of automatic motion correction output** — Enable tools for manually adjusting motion correction.

    - Hover over the information ⓘ icon next to this option to see instructions on using the tools. Refer to below for more information.
    - When you run reconstruction after selecting this option, the **Rerun automatic motion correction on the next reconstruction** appears. If you select this option, your manual fine-tuning can be overridden by automatic motion correction the next time you rerun reconstruction.



Projections Series: 2022-12-05 [] TOMO Upper Scatter Window (1st Photopeak)

Reconstruction Algorithm: Filtered Backprojection

Backprojection Filter:
Type: Butterworth
Order: 6 Cutoff Frequency: 0.5 * 100% Nyquist

Post-Reconstruction 3D Filter:
Type: Gaussian
Smooth FWHM: 0 mm

☑ Perform automatic motion correction
☑ Correct X Motion ☑ Correct Y Motion
Automatic motion correction mask:
None
☑ Allow manual fine-tuning of automatic motion correction output

Related: Refer to the Motion Correction: Technical Details document for technical details on how motion correction is calculated.

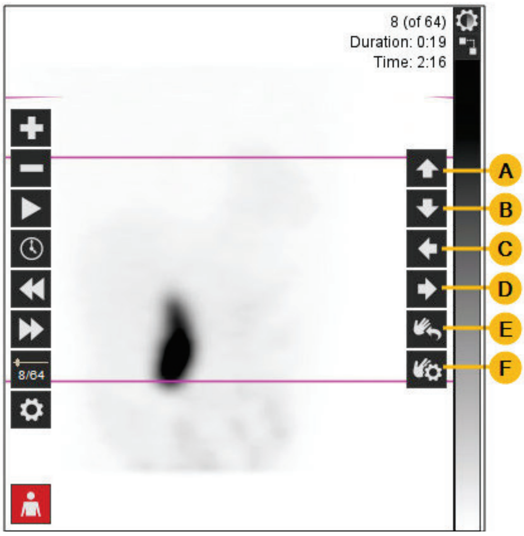
3. Click the **Reconstruct** button to reconstruct the image with automatic motion correction. If needed, after the image is reconstructed, you can:
    - Manually fine-tune the motion correction output using the tools described in Manually Adjust Motion Correction below.
    - Further adjust the parameters as needed, and then click **Reconstruct** again to rerun reconstruction with the updated parameters.

Important: Motion correction affects frame location. Carefully review all frames after motion correction is applied.

4. When you are satisfied with the reconstruction, click the **Finish** button to close the Adjust Reconstruction window, and complete the workflow.

Manually Adjust Motion Correction

Hover the cursor in the motion-corrected projection viewport to view the manual adjustment companion tools. Use the tools as needed until you are satisfied with the motion construction.



A. Move the current projection up.
B. Move the current projection down.
C. Move the current projection left.
D. Move the current projection right.
E. Reset manual motion correction for the current or all projections.
F. Customize adjustment amounts and specify frames affected by correction.

Tip: To make it easier to see, you can collapse the Notifications window by clicking the arrow in the upper-right corner or using the keyboard shortcut \. When you are finished making your changes, expand the Notifications window to continue the workflow.

Review the Reconstruction Output

MIMTD-1764 • 29 Oct 2024

Overview

When the SPECTRA Recon® workflow runs, it produces page displays with the reconstructed series. Depending on your organization's workflow, the output can also include additional information.

Below are a few images you may see. If these images are not in your default display, you can go to the Display sidebar and add them to a hanging protocol. Refer to Create and Modify Display Layouts for more information about working with hanging protocols.

Related: Refer to Manually Run a Reconstruction Workflow for more information about reconstructing an image.

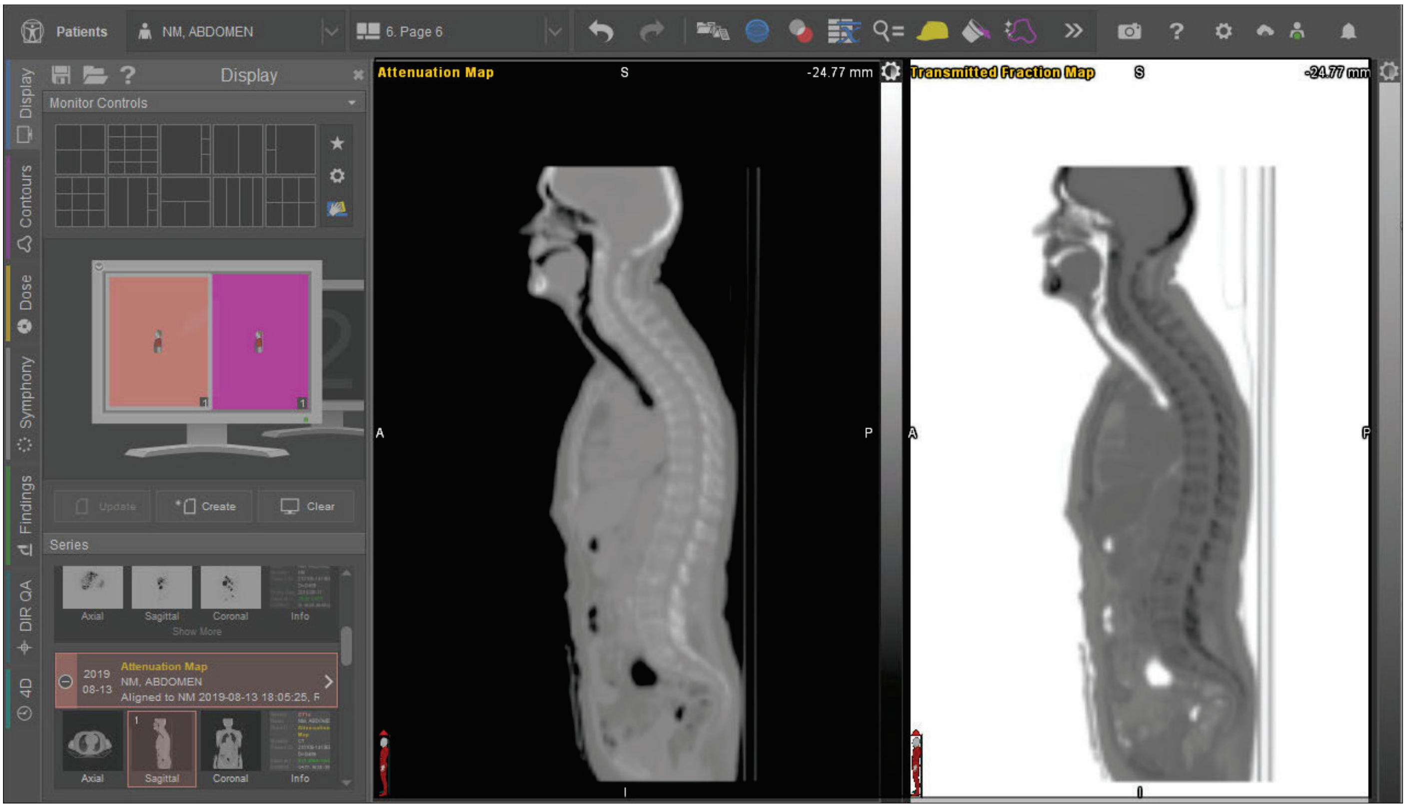
Tip: Use the arrows keys to cycle through pages that were created in your session. Or, use the page selector in the top toolbar.

Contents

- Attenuation Correction Information
- Motion Correction Information
- Linogram (MIM 7.4 and Later) and Sinogram
- Save with a PT DICOM Header (MIM 7.4 and Later)

Attenuation Correction Information

MIM® creates an attenuation map and transmitted fraction map. For example, you can use these images to ensure no artifacts are present that could affect the counts.



Left: Attenuation map image. Right: Transmitted fraction map image.

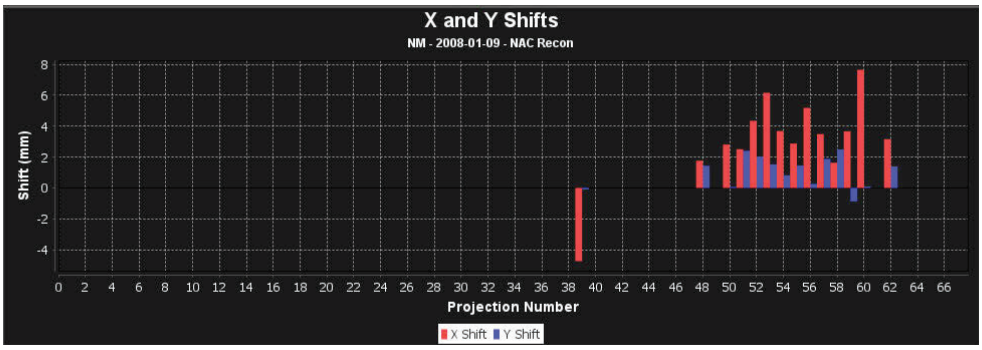
Tip: If you do not see the attenuation map and transmitted fraction map images listed in the Display sidebar, rerun or adjust reconstruction and ensure that the **Include aligned series in session** option on the Attenuation tab is selected.

Motion Correction Information

Reconstructing an image with motion correction applied generates the reconstructed image, a motion-corrected projection, and a graph showing how much shift was applied on each projection.

- X shifts are shown in red.
- Y shifts are shown in blue.
- The horizontal axis represents each projection.

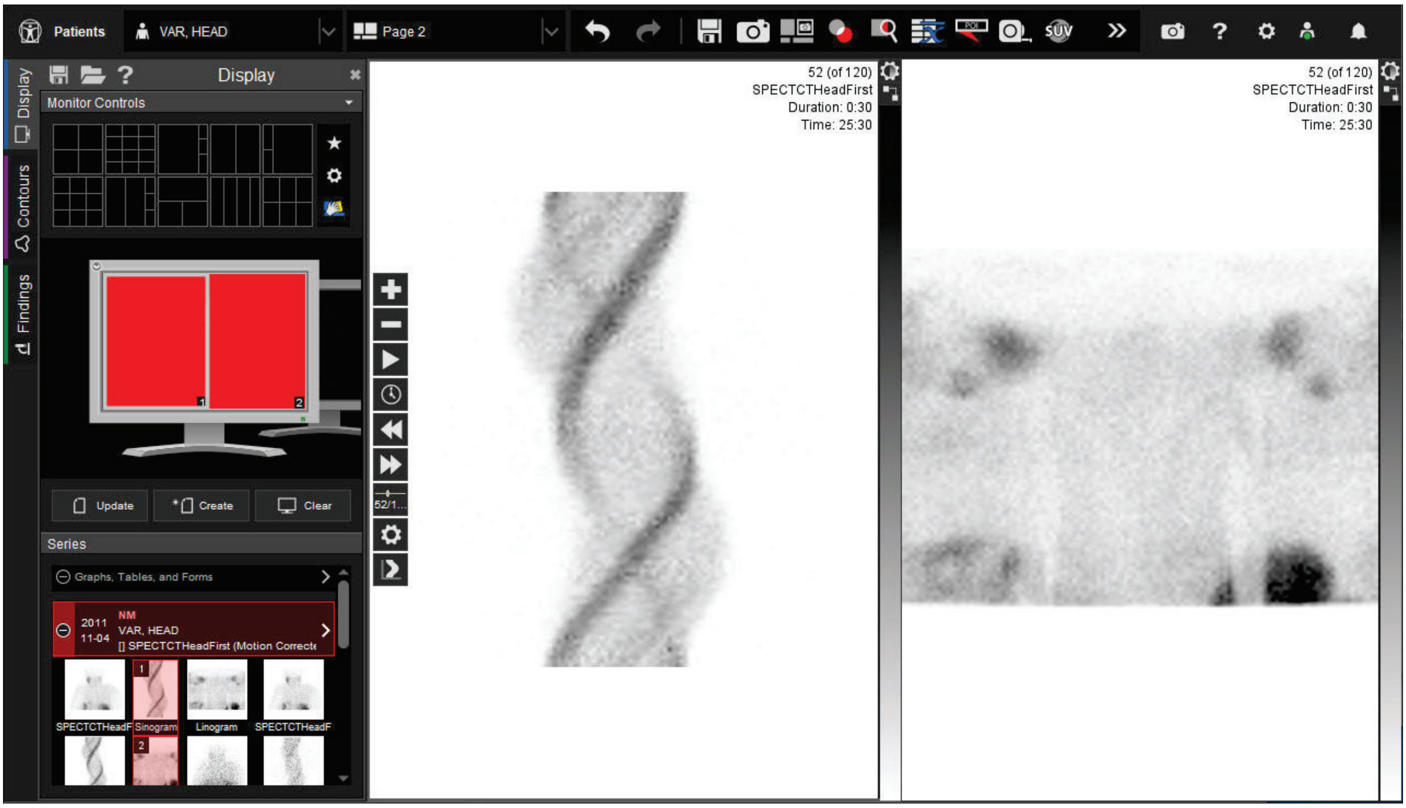
- The vertical axis represents the amount of shift that was applied.



Linogram (MIM 7.4 and Later) and Sinogram

After performing motion correction, you can view the following renderings to ensure no projection artifacts are present.

- Sinogram — Each Y coordinate represents a different image in the series.
- *MIM 7.4 and later:* Linogram — Each X coordinate represents a different image in the series. *MIM 7.3 and earlier*: This functionality is not available.



Left: Sinogram image. Right: Linogram image.

Save with a PT DICOM Header (MIM 7.4 and Later)

You might want to save the reconstructed NM image with a PT DICOM header for compatibility with other vendor systems. This functionality is not available in MIM 7.3 and earlier.

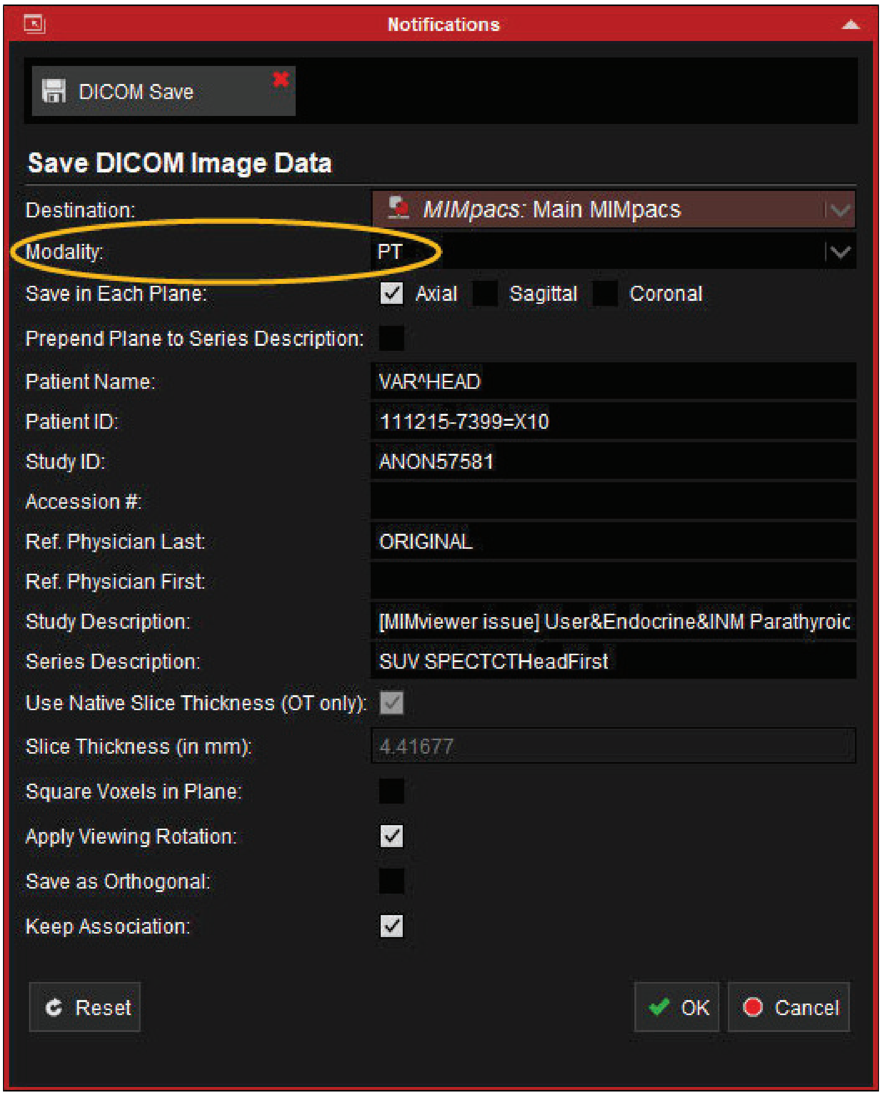
If you have quantitatively reconstructed the image, as described in Use SPECTRA Quant for Bq/ml Conversion, Bq/ml conversion and SUV units are preserved when saving with a PT header.

Tip: If your organization is using a MIM Assistant® rule to automate running the image reconstruction workflow, it can also save the output as a PT series. Please contact MIM Software Support at support.mimsoftware.com if you would like assistance implementing this option.

To manually save a reconstructed image with a PT DICOM header, complete the following steps:

1. Use the steps described in Manually Run a Reconstruction Workflow to reconstruct the image.
2. Click the save 🖫 button in the top toolbar and select **Save DICOM Image Data...**.
3. Select the AC Recon series.

4. In the Notifications window, change the **Modality** to **PT**.



Save DICOM Image Data

Destination: *MIMpacs:* Main MIMpacs
Modality: PT
Save in Each Plane: ☑ Axial ☐ Sagittal ☐ Coronal
Prepend Plane to Series Description: ☐
Patient Name: VAR^HEAD
Patient ID: 111215-7399=X10
Study ID: ANON57581
Accession #:
Ref. Physician Last: ORIGINAL
Ref. Physician First:
Study Description: [MIMviewer issue] User&Endocrine&INM Parathyroic
Series Description: SUV SPECTCTHeadFirst
Use Native Slice Thickness (OT only): ☑
Slice Thickness (in mm): 4.41677
Square Voxels in Plane: ☐
Apply Viewing Rotation: ☑
Save as Orthogonal: ☐
Keep Association: ☑

5. Update any other save information as desired and click **OK**.

Advanced Settings for SPECT Reconstruction

MIMTD-962 • 17 Nov 2023

Overview

> ⚠ **Caution:** It is recommended that you complete clinical commissioning before using reconstruction in a clinical setting. Clinical commissioning can help you determine scatter window parameters, as well as which iterations and subsets are appropriate matches for your current data output. For assistance with this, please contact MIM Software Support at support.mimsoftware.com.

As part of your implementation, MIM® works with you on configuring reconstruction parameters that are specific to your cameras. Although you are able to change settings in the Notification window if needed when running reconstruction, it is generally recommended to use the pre-configured settings.

Review the following information if you have a particular use case where the default settings need to be adjusted. Please contact MIM Software Support at support.mimsoftware.com if your default configuration needs to be updated.

Contents

- Reconstruction Algorithms
    - Filtered Backprojection
    - OSEM
- Motion Correction
- Attenuation Correction
    - CT Method
    - Chang Method
    - SPECT/CT Alignment
- Scatter Correction
- Resolution Recovery

Reconstruction Algorithms

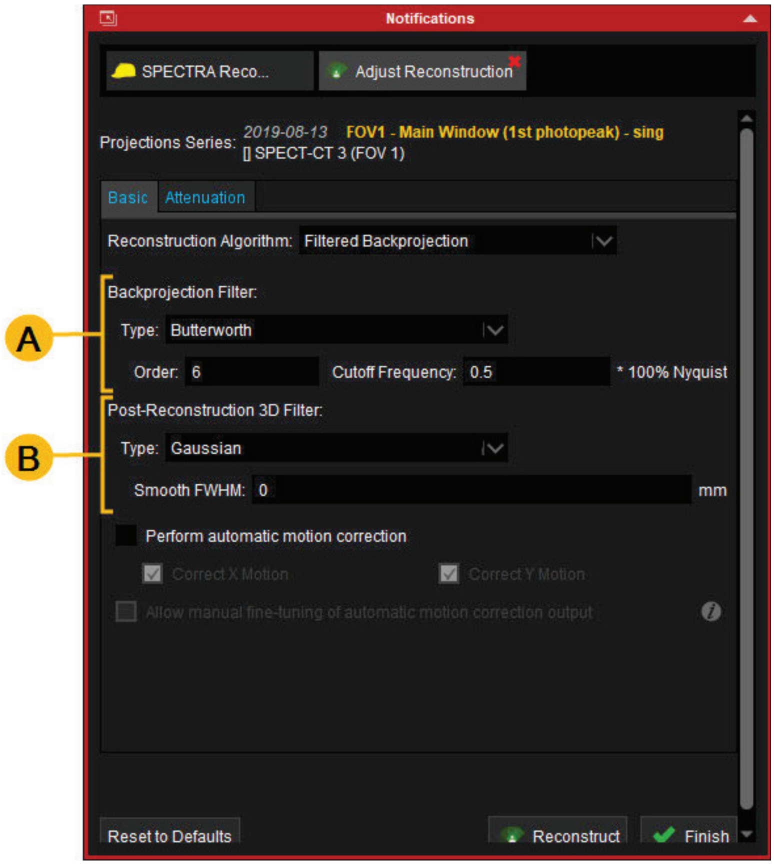
MIM supports two reconstruction algorithms: Filtered backprojection[1] and OSEM (ordered subset expectation maximization) [2].

Filtered Backprojection

To use this algorithm, go to the **Basic** tab and select **Filtered Backprojection**. Adjust the following as needed:

A. The **Backprojection Filter**. Select Butterworth, Hamming, or Hann and determine the cutoff frequency of the filter. If you select the Butterworth filter, specify the filter order.

B. The **Post-Reconstruction 3D Filter**. Select a filter and set the cutoff frequency.
  - If you select the Butterworth filter, specify the filter order.
  - If you select the Gaussian filter, specify the **Full Width at Half Maximum (FWHM)** distance. (No cutoff frequency needed.)



Projections Series: 2019-08-13 FOV1 - Main Window (1st photopeak) - sing
[] SPECT-CT 3 (FOV 1)

Reconstruction Algorithm: Filtered Backprojection

Backprojection Filter:

Type: Butterworth

Order: 6 Cutoff Frequency: 0.5 * 100% Nyquist

Post-Reconstruction 3D Filter:

Type: Gaussian

Smooth FWHM: 0 mm

☐ Perform automatic motion correction

☑ Correct X Motion ☑ Correct Y Motion

☐ Allow manual fine-tuning of automatic motion correction output

---

[1] G.L. Zeng. Image reconstruction - a tutorial. Computerized Medical Imaging and Graphics. 2001; 25: 97-103.

[2] Hudson, HM, Larkin RS. Accelerated image reconstruction using ordered subsets of projection data. IEEE Trans Med Imaging 1994; 13: 601-609

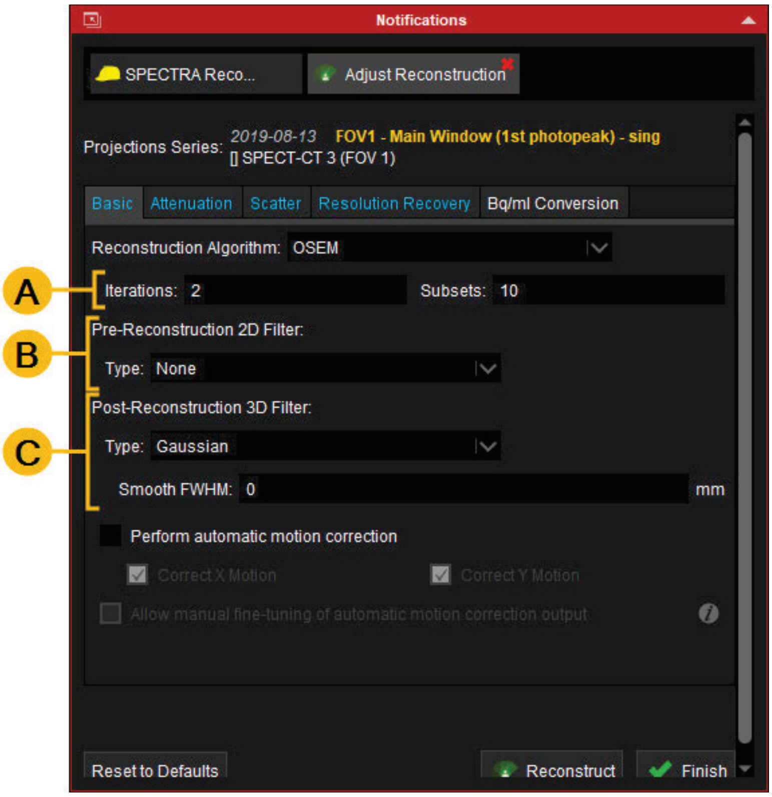
OSEM

To use this algorithm, go to the **Basic** tab and select **OSEM**. Adjust the following as needed:

A. The **Iterations** and **Subsets**.

B. The **Pre-Reconstruction 2D Filter**. Select a filter and set the cutoff frequency.
  - If you select the Butterworth filter, specify the filter order.
  - If you select the Gaussian filter, specify the **Full Width at Half Maximum (FWHM)** distance. (No cutoff frequency needed.)

C. The **Post-Reconstruction 3D Filter**. Select between the same options as the pre-reconstruction 3D filter.



Projections Series: 2019-08-13 FOV1 - Main Window (1st photopeak) - sing
[] SPECT-CT 3 (FOV 1)

Reconstruction Algorithm: OSEM

Iterations: 2 Subsets: 10

Pre-Reconstruction 2D Filter:
Type: None

Post-Reconstruction 3D Filter:
Type: Gaussian
Smooth FWHM: 0 mm

☐ Perform automatic motion correction
☑ Correct X Motion ☑ Correct Y Motion
☐ Allow manual fine-tuning of automatic motion correction output

Motion Correction

SPECTRA Recon can apply a motion correction algorithm[1] to the reconstruction. To use the motion correction, go to the **Basic** tab and select **Perform automatic motion correction**. Refer to Apply and Adjust Motion Correction for more information about motion correction.

---

[1] Bai C, Maddahi J, Kindem J. et al. Development and evaluation of a new fully automatic motion detection and correction technique in cardiac SPECT imaging. J Nucl Cardiol 2009; 16:580-589. doi:10.1007/s12350-009-9096-7.

Attenuation Correction

If you want to apply attenuation correction, you can use either the CT Method or the Chang Method. For more information on attenuation correction, see Motion Correction: Technical Details.

> **Important**: Attenuation correction typically requires scatter correction to also be applied during reconstruction.

CT Method

The CT method requires a CT image. To use this method, go to the **Attenuation** tab and select **CT Method** for Attenuation Correction. Adjust the following as needed:

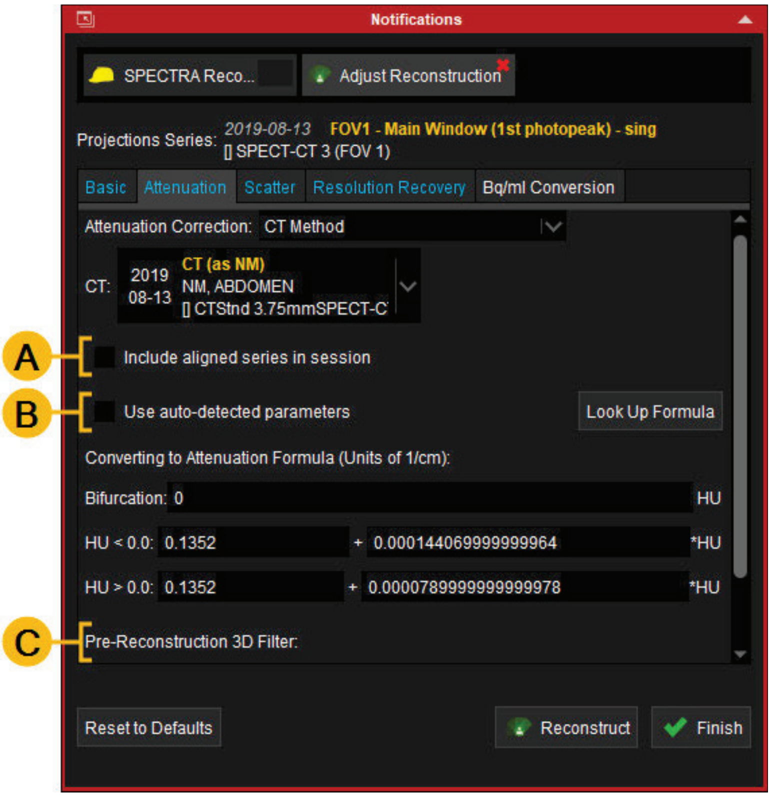
A. Select **Include aligned series in session** if you want to view the CT-based attenuation map and transmission fraction map. See Review the Reconstruction Output for more information.

B. By default, camera-specific attenuation formula values are automatically selected from a lookup table based on the CT being used for attenuation correction. These automatically selected values are not typically adjusted for standard reconstructions. If necessary, you can deselect **Use auto-detected parameters** to manually change the attenuation formula.

C. (Optional) Choose a **Pre-Reconstruction 3D Filter**. Select a filter and set the cutoff frequency.

  - If you select the Butterworth filter, specify the filter order.

- If you select the Gaussian filter, specify the **Full Width at Half Maximum (FWHM)** distance. (No cutoff frequency needed.)



Projections Series: 2019-08-13 FOV1 - Main Window (1st photopeak) - sing
[] SPECT-CT 3 (FOV 1)

Attenuation Correction: CT Method

CT: 2019 08-13 CT (as NM) NM, ABDOMEN [] CTStnd 3.75mmSPECT-C

☐ Include aligned series in session

☐ Use auto-detected parameters

Converting to Attenuation Formula (Units of 1/cm):

Bifurcation: 0 HU

HU < 0.0: 0.1352 + 0.000144069999999964 *HU

HU > 0.0: 0.1352 + 0.0000789999999999978 *HU

Pre-Reconstruction 3D Filter:

Chang Method

To apply the Chang Method[1], you must run an initial reconstruction and then create a contour on the reconstructed image to use as the attenuation mask. Once the contour is created, you can use the Chang Method for attenuation correction.

> ☆ **Important:** The Chang Method is not meant to be used on scans of the lungs because it assumes constant attenuation; this is not accurate in the thoracic region.

After the initial reconstruction, complete the following steps:

1. Use contour tools to draw a contour on the reconstructed image (bottom row) that encompasses the volume in which to apply attenuation correction.
2. Return to the Notifications window and, in the **Attenuation** tab, change the **Attenuation Correction** dropdown to **Chang Method**.

---

[1] Chang LT, A method for attenuation correction in radionuclide computed tomography, IEEE Trans Nucl Sci Vol NS-25 No. 1, pp 638-643, Feb 1978.

3. Select the attenuation mask contour that you drew from the dropdown.
4. If desired, deselect **Use auto-detected parameters** and adjust the **Attenuation Coefficient** as needed.
5. Click the **Reconstruct** button to create a reconstruction using the Chang Method.

SPECT/CT Alignment

Always check SPECT to CT alignment during or after reconstructions that apply attenuation correction. If the alignment is unsatisfactory, use the fusion adjustment tools to better align the images, and then generate a new reconstruction by clicking the **Reconstruct** button.

Scatter Correction

SPECTRA Recon uses an energy window-based scatter correction method, including dual energy window and triple energy window methods depending on the number of scatter windows present.

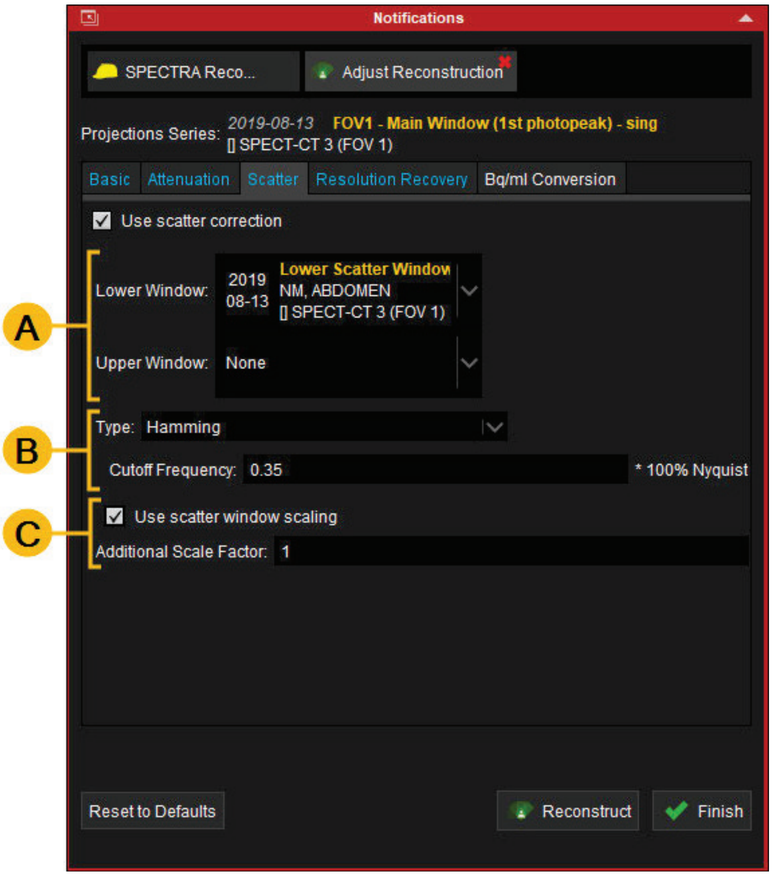
To use scatter correction, go to the **Scatter** tab and select **Use scatter correction**. Adjust the following as needed:

A. The **Lower Window** and/or **Upper Window** are automatically matched by the appropriate scatter image and assigned to the correct window based on the images' scatter windows. You can override if necessary.

B. (Optional) Use the **Type** to apply a filter to the scatter window. Select a filter and set the cutoff frequency.
   - If you select the Butterworth filter, specify the filter order.
   - If you select the Gaussian filter, specify the **Full Width at Half Maximum (FWHM)** distance. (No cutoff frequency needed.)

> **Tip:** Filters are helpful when working with narrow or noisy scatter windows.

C. Keep the default **Use scatter window scaling** option to scale based on ratios of the primary energy window widths to the scatter energy window widths. If you have a non-standard reconstruction, you can optionally enter an additional scale factor.



Projections Series: *2019-08-13* FOV1 - Main Window (1st photopeak) - sing
[] SPECT-CT 3 (FOV 1)

☑ Use scatter correction

Lower Window: 2019 08-13 Lower Scatter Window
NM, ABDOMEN
[] SPECT-CT 3 (FOV 1)

Upper Window: None

Type: Hamming

Cutoff Frequency: 0.35 * 100% Nyquist

☑ Use scatter window scaling

Additional Scale Factor: 1

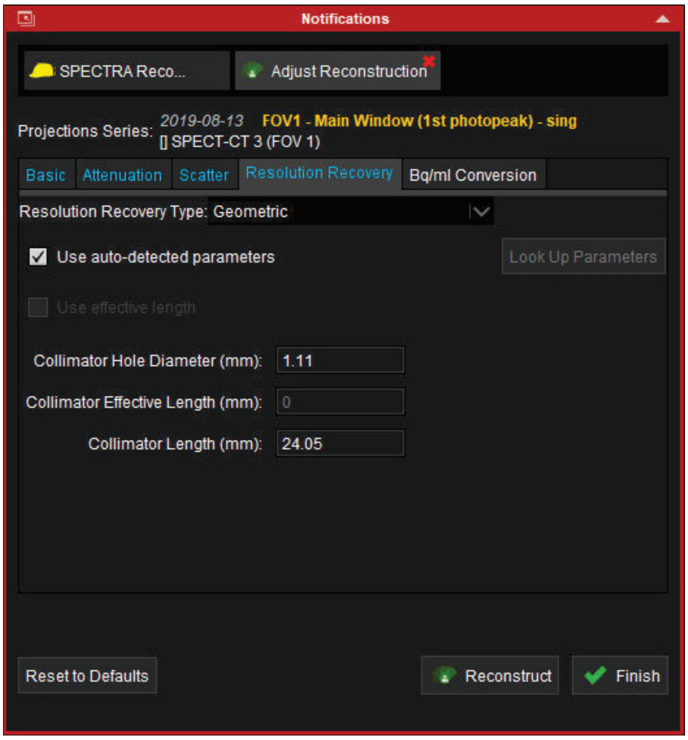
Resolution Recovery

You can use resolution recovery to compensate for depth-dependent resolution effects. For more information on resolution recovery, see the white paper *SPECT/CT Reconstruction with SPECTRA Recon*.

> ☆ **Important:** A SPECT series must have a radial position DICOM tag to use resolution recovery.

To perform resolution recovery, go to the **Resolution Recovery** tab. You have the following Resolution Recovery Type options:

Type	Required Information	How It Works
Geometric	The collimator hole diameter and length are needed. These are typically auto-detected in a lookup table or workflow and not adjusted for standard reconstructions. If necessary, you can deselect **Use auto-detected parameters** to manually change the parameters.	Corrects for the range of source locations based on a Gaussian curve.
Measured *MIM 7.4 and later*: Available with a SPECTRA Quant® license. *MIM 7.3 and earlier*: This functionality is not available.	As part of your initial setup and commissioning, specific phantom scans, calibrations, and preference files are needed to use this option. Contact MIM Support if you are not sure whether you are ready to use this option or if you want to implement it.	Corrects based on the specific source-to-detector distances configured for the camera, accounting for the point spread function. Note that this reconstruction method takes longer to run.



Projections Series: *2019-08-13* FOV1 - Main Window (1st photopeak) - sing
[] SPECT-CT 3 (FOV 1)

Resolution Recovery Type: Geometric

☑ Use auto-detected parameters

☐ Use effective length

Collimator Hole Diameter (mm): 1.11
Collimator Effective Length (mm): 0
Collimator Length (mm): 24.05

Use SPECTRA Quant for Bq/ml Conversion

6.1

MIMTD-968 • 02 Nov 2024

Overview

Important: This feature requires the SPECTRA Quant® license. If your organization would like to purchase SPECTRA Quant, contact your MIM Site Development Manager.

SPECTRA Quant extends SPECTRA Recon® by converting data in the reconstructed 3D image to quantitative units. Use Bq/ml conversion to convert your image from units of counts or counts per second to Bq/ml. Then, your images can be converted to SUV.

Contents

- Run Bq/ml Conversion
- Run SUV Conversion

Run Bq/ml Conversion

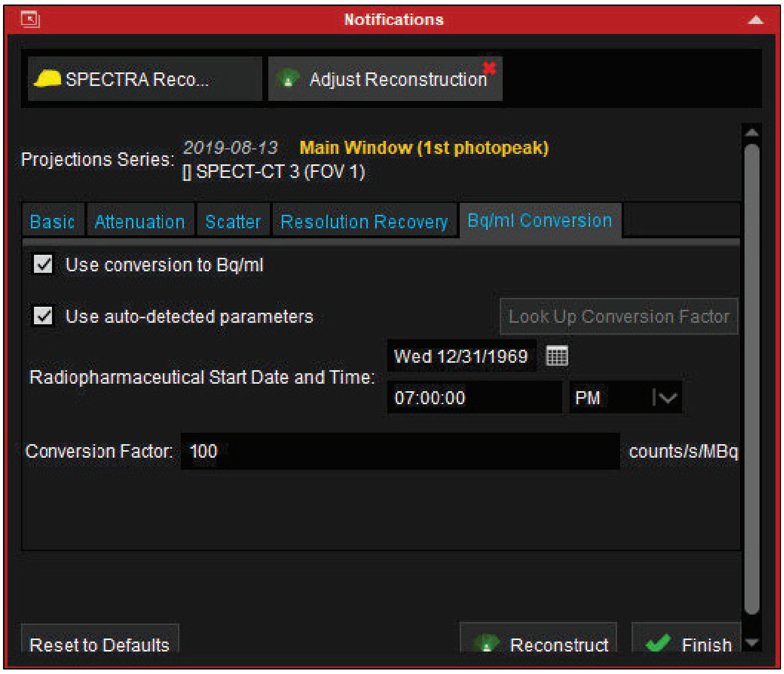
As described in Manually Run a Reconstruction Workflow, launch a SPECTRA reconstruction workflow.

- *MIM 7.3 and later:* After the workflow runs, click the **Adjust Reconstruction(s)** button in the side panel to open the Notifications window. Then, continue with the steps below.
- *MIM 7.2 and earlier:* When the workflow pauses, update the settings in the Notifications window as described below.

In the Notifications window:

1. Ensure that the following Adjust Reconstruction options are selected so that conversion is possible:
    - On the **Attenuation** tab, attenuation correction must be enabled.
    - On the **Scatter** tab, scatter correction must be enabled.
2. On the **Bq/ml Conversion** tab:
    - Select **Use conversion to Bq/ml**.
    - By default, **Use auto-detected parameters** is selected. The isotope- and camera- specific conversion factor is auto-detected in a lookup table or workflow. If needed, deselect this option and enter a **Conversion Factor** instead.

- Enter the **Radiopharmaceutical Start Date and Time**. This input is used for SUV conversion and as a reference point for future decay correction processing. It does not otherwise affect the reconstruction.
- By default, the isotope- and camera- specific conversion factor is auto-detected in a lookup table or workflow. If needed, the **Conversion Factor** can be adjusted.



Projections Series: 2019-08-13 Main Window (1st photopeak)
[] SPECT-CT 3 (FOV 1)

☑ Use conversion to Bq/ml

☑ Use auto-detected parameters

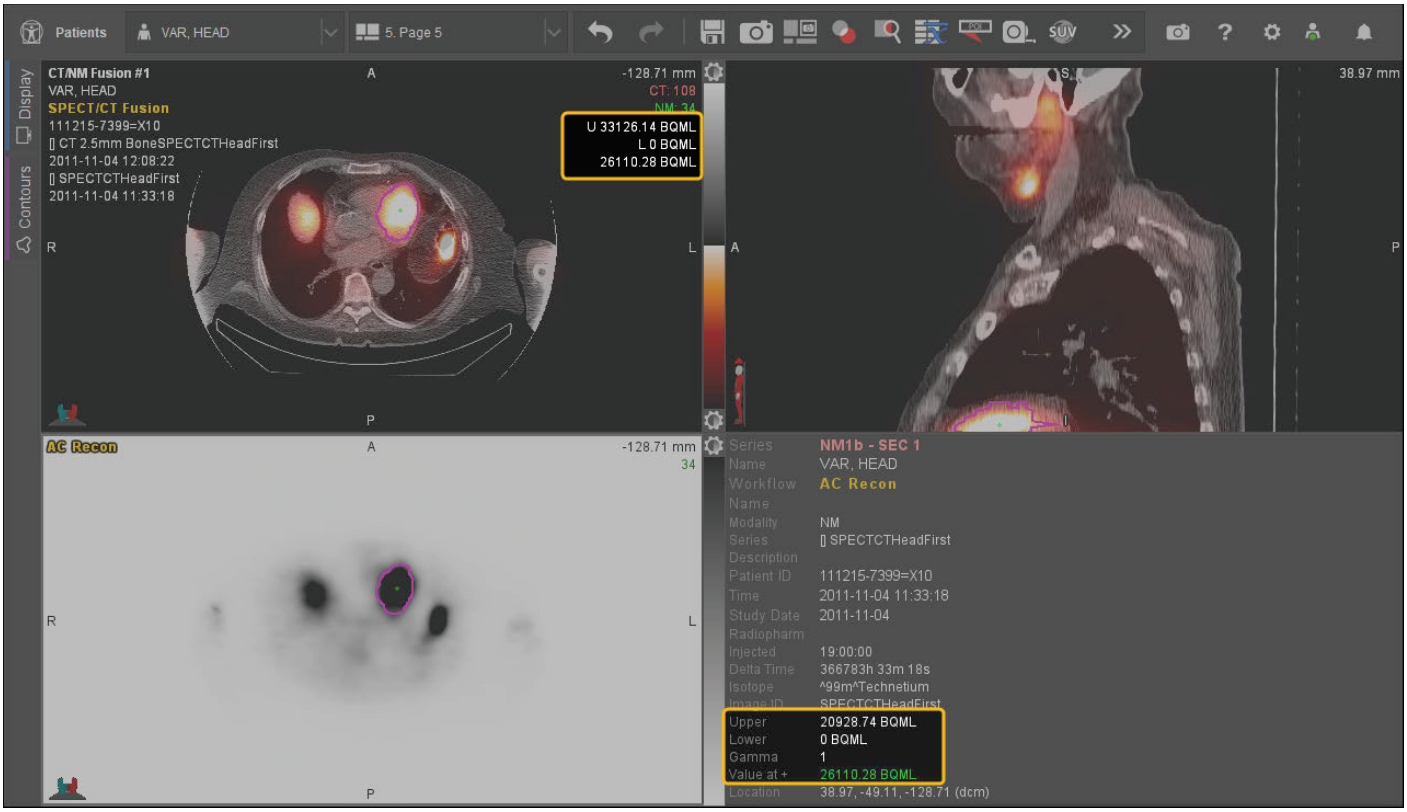
Radiopharmaceutical Start Date and Time: Wed 12/31/1969 07:00:00 PM

Conversion Factor: 100 counts/s/MBq

Caution: When performing quantitative reconstruction, applying a post-reconstruction filter may affect quantitative results. Always be cautious when applying appropriate filtering to the exam.

3. Click **Finish** to complete reconstruction and conversion.

You can now see BQML values for the series.



CT/NM Fusion #1
VAR, HEAD
SPECT/CT Fusion
111215-7399=X10
[] CT 2.5mm BoneSPECTCTHeadFirst
2011-11-04 12:08:22
[] SPECTCTHeadFirst
2011-11-04 11:33:18

U 33126.14 BQML
L 0 BQML
26110.28 BQML

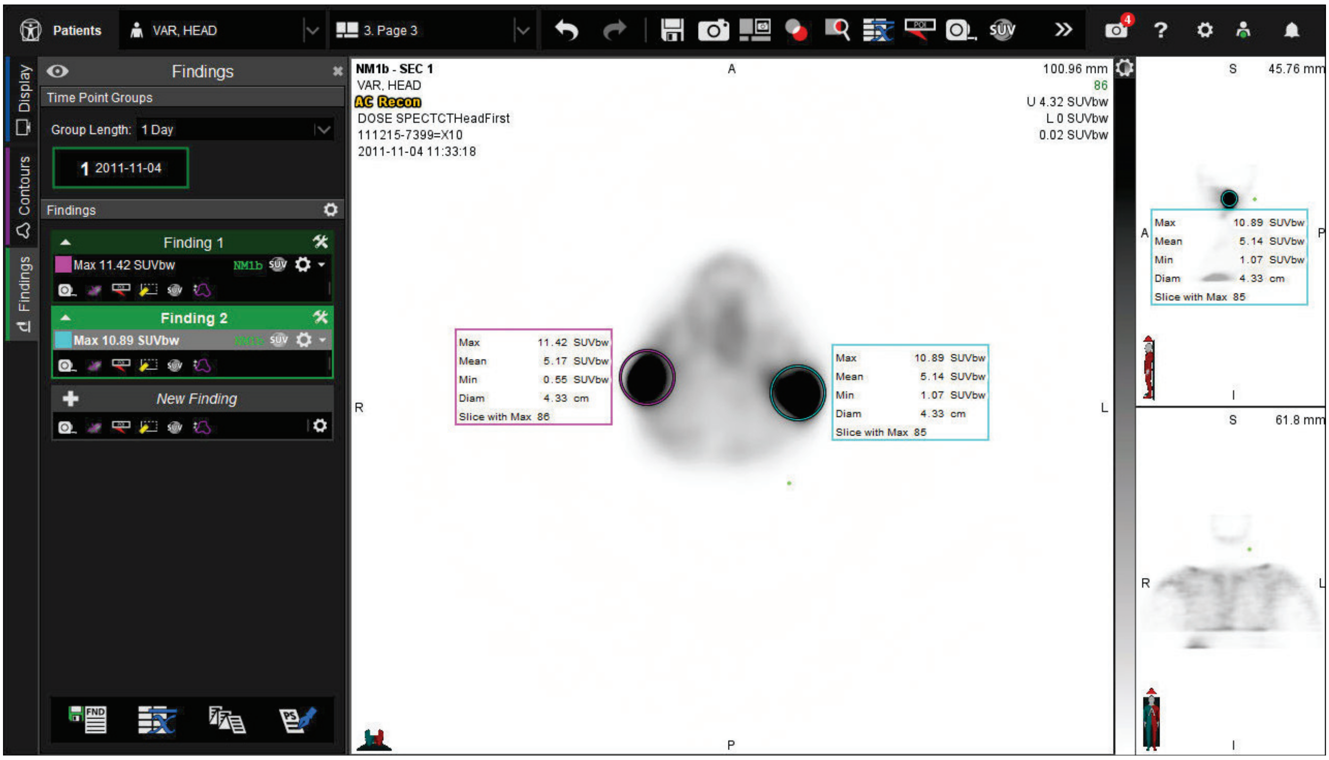
Series	NM1b - SEC 1
Name	VAR, HEAD
Workflow Name	AC Recon
Modality	NM
Series Description	[] SPECTCTHeadFirst
Patient ID	111215-7399=X10
Time	2011-11-04 11:33:18
Study Date	2011-11-04
Radiopharm	
Injected	19:00:00
Delta Time	366783h 33m 18s
Isotope	^99m^Technetium
Image ID	SPECTCTHeadFirst
Upper	20928.74 BQML
Lower	0 BQML
Gamma	1
Value at +	26110.28 BQML
Location	38.97, -49.11, -128.71 (dcm)

Run SUV Conversion

After Bq/ml conversion and pre-reconstruction decay correction have been applied, you can convert the reconstructed image to units of SUV:

1. From the top toolbar, select the **SUV** tool.
2. Hover over the reconstructed image and click the gear button on the right side of the viewport.
3. Set the **SUV Calculation Type** to **Body Weight (bw)**, **Lean Body Mass (lbm)**, or **Body Surface Area (bsa)**.

4. View results as SUV values.



Max 11.42 SUVbw
Mean 5.17 SUVbw
Min 0.55 SUVbw
Diam 4.33 cm
Slice with Max 86

Max 10.89 SUVbw
Mean 5.14 SUVbw
Min 1.07 SUVbw
Diam 4.33 cm
Slice with Max 85

Tip: Decay correction must be applied to each energy window prior to image reconstruction. It is automatically applied when you run reconstruction through MIM Workflows™. Decay correction can be applied to either the acquisition time or the radiopharmaceutical injection time.

Create Structured Reports

Create and Modify Structured Reports

MIMTD-618 • 01 Sep 2023

Overview

Structured reports let you turn information from a MIM® session into a document. MIM includes several default structured report templates. Your MIM Implementation Specialist might have also helped build custom templates for your organization as part of your MIM implementation.

A structured report is often automatically generated by a MIM Workflow™ using one of these templates. Alternatively, you can create a report from a template yourself. The report templates do the majority of the work for you, and typically only minimal edits are then needed for the report.

> **Tip:** For more information about MIM Workflows or for assistance with a workflow, contact MIM Software Support at support.mimsoftware.com.

Contents

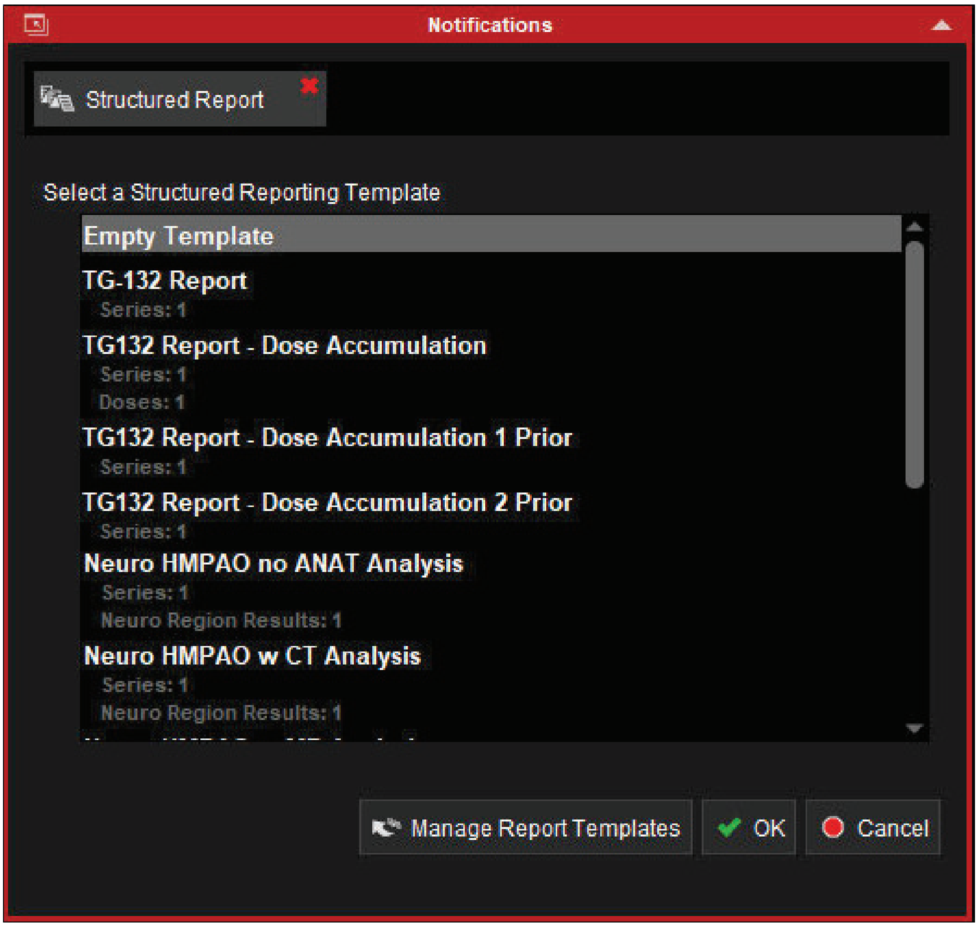
- Create a Structured Report
- Modify Structured Report Content
  - Make Common Updates
  - Add, Edit, and Delete Content
- Save Structured Reports

Create a Structured Report

If you are using a workflow that automatically generates a structured report, skip to Modify Structured Report Content. Otherwise, complete the following steps to create a report yourself:

1. In an open MIM session, click the **Create Structured Report** tool in the toolbar, in the radial menu, or via keyboard shortcut. For more information, see Access Tools: The Toolbar and the Radial Menu or Set Keyboard Shortcuts.

2. In the Notifications window, select the structured report template to use and click **OK**.



Notifications

Structured Report

Select a Structured Reporting Template

Empty Template

TG-132 Report
  Series: 1

TG132 Report - Dose Accumulation
  Series: 1
  Doses: 1

TG132 Report - Dose Accumulation 1 Prior
  Series: 1

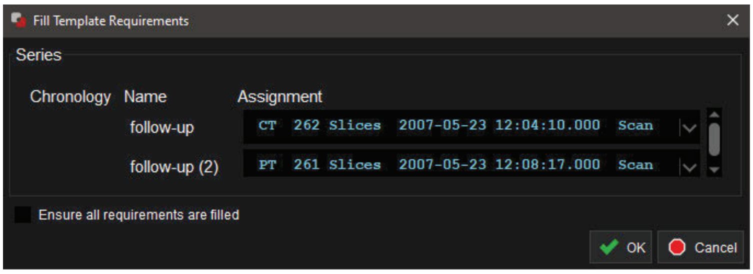
TG132 Report - Dose Accumulation 2 Prior
  Series: 1

Neuro HMPAO no ANAT Analysis
  Series: 1
  Neuro Region Results: 1

Neuro HMPAO w CT Analysis
  Series: 1
  Neuro Region Results: 1

Tip: If the Structured Report Builder opens immediately and displays a blank page, you do not have any structured report templates. Go to Create Structured Report Templates for more information about creating a report template from an empty template.

3. In the Fill Template Requirements window, ensure that the series and other requirements are correctly assigned in the **Assignment** fields. If any items are not correctly assigned, click the dropdown under **Assignment** to choose the correct series.



Fill Template Requirements

Series

Chronology	Name	Assignment
	follow-up	CT 262 Slices 2007-05-23 12:04:10.000 Scan
	follow-up (2)	PT 261 Slices 2007-05-23 12:08:17.000 Scan

☐ Ensure all requirements are filled

4. Click **OK**. The structured report is created and appears in the Structured Report Builder.

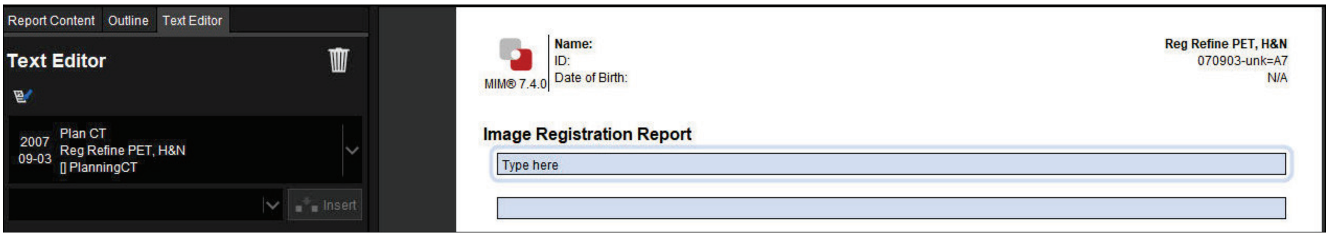
Modify Structured Report Content

After generating a report using a report template, you can further edit the report within the Structured Report Builder.

Make Common Updates

Review the report preview:

- Type in any blue text fields. Alternatively, use a macro to quickly add text or add dynamic DICOM information. Refer to Use Macros to Insert Frequently Used Text into Structured Reports for more information.

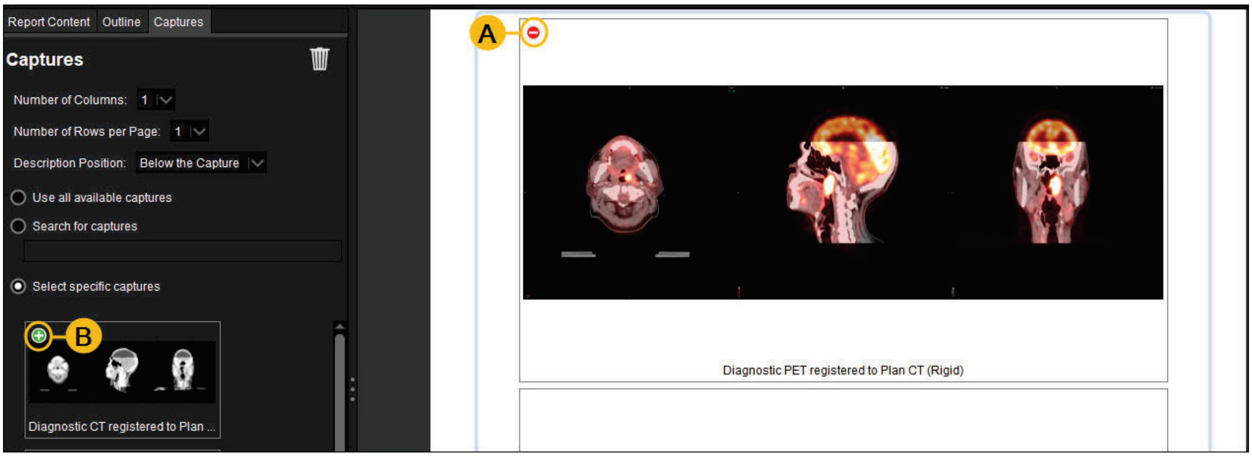


2007 09-03 Plan CT Reg Refine PET, H&N [] PlanningCT

Name: Reg Refine PET, H&N
ID: 070903-unk=A7
Date of Birth: N/A

Type here

- Check the screen captures included.
    A. Hover over an image and click the remove ⊖ button in the left corner to remove it.
    B. Add an image from the **Captures** sidebar by clicking the add ⊕ button.



Number of Columns: 1
Number of Rows per Page: 1
Description Position: Below the Capture
○ Use all available captures
○ Search for captures
● Select specific captures

Diagnostic CT registered to Plan ...

Diagnostic PET registered to Plan CT (Rigid)

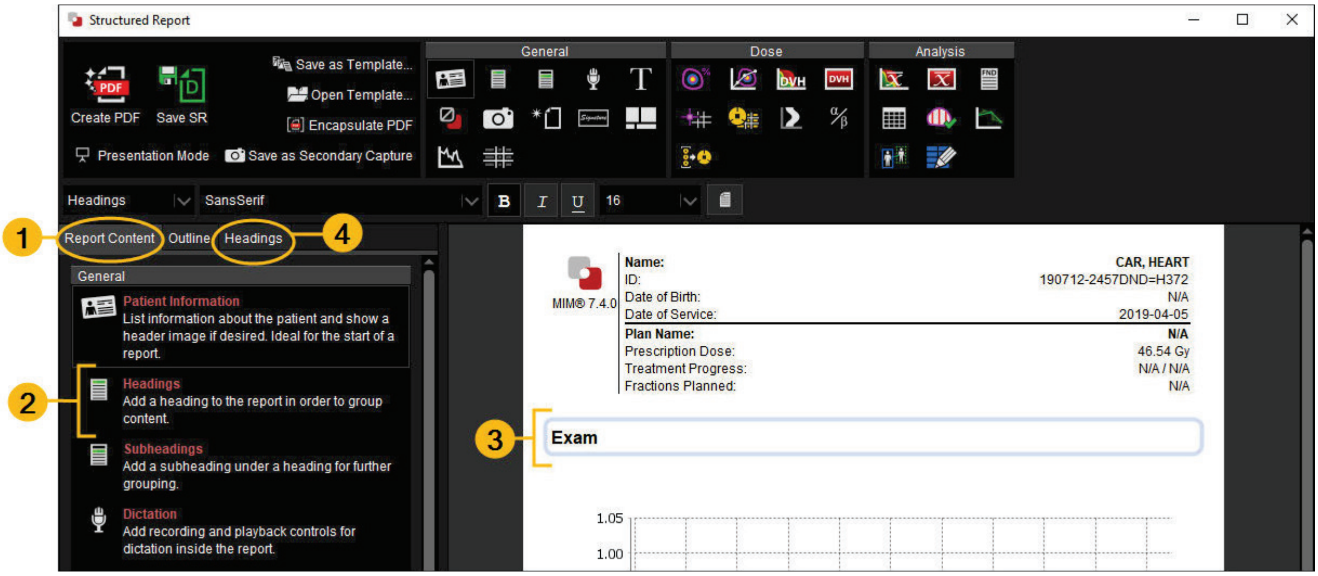
Add, Edit, and Delete Content

If needed, you can further add content to the report or rearrange the content automatically included from the report template.

1. Go to the **Report Content** tab.
2. Click the content type that you want to add to the structured report, such as Headings. The content is added to the report preview and a new tab appears with options for editing that content.

> **Tip:** You can also add content from the top toolbar of the Structured Report Builder.

3. View the selected content type that appears in the report preview.
4. Go to the new tab for that content to edit it.



Patient Information
List information about the patient and show a header image if desired. Ideal for the start of a report.

Headings
Add a heading to the report in order to group content.

Subheadings
Add a subheading under a heading for further grouping.

Dictation
Add recording and playback controls for dictation inside the report.

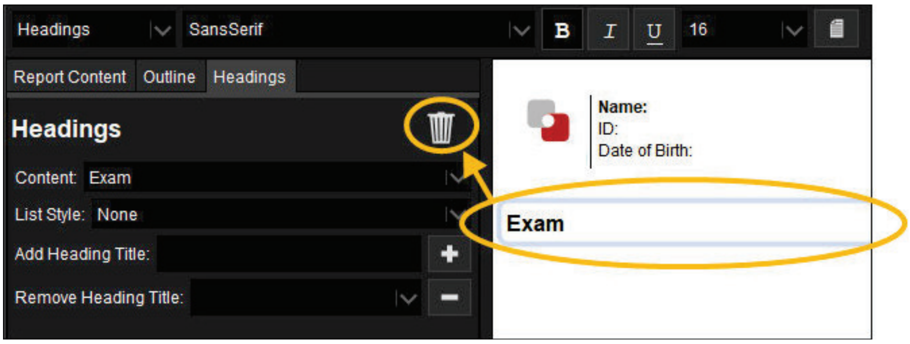
Name: CAR, HEART
ID: 190712-2457DND=H372
Date of Birth: N/A
Date of Service: 2019-04-05
Plan Name: N/A
Prescription Dose: 46.54 Gy
Treatment Progress: N/A / N/A
Fractions Planned: N/A

Exam

Refer to the following for more information about each type of content:

- Use Headings, Layouts, and Page Breaks to Organize Structured Report Content
- Add Secondary Captures to Structured Reports
- Add Statistics to Structured Reports

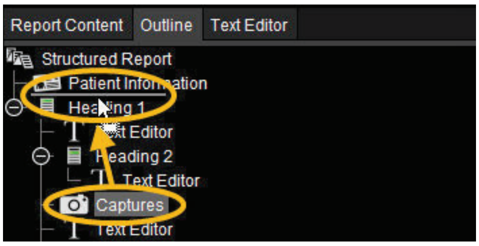
5. To delete content, click the trashcan 🗑 button in the upper-right corner of the same tab that you use to edit content.



Content: Exam
List Style: None

Important: If you delete a heading, subheading, or layout, all content that is grouped under it is also deleted. To see which items are grouped under a heading, subheading, or layout, go to the **Outline** tab.

6. To rearrange content, go to the **Outline** tab:
   - To move an item to a different position, left-click drag the item up or down. A line shows where the item will be moved.



   - To group an item under a heading or subheading, left-click drag the item onto the desired heading or subheading. The heading or subheading that the item will be added under is highlighted.

Tip: If you make a lot of edits, consider saving your work as a report template. Then, your edited structure and layout will be used for future reports so you don't have to make the changes again. Refer to Create Structured Report Templates for more information about working with report templates.

Save Structured Reports

To save a structured report, click the desired option in the upper-left corner of the Structured Report Builder:

Option	Description	Common Use
Create PDF	Create a PDF of the structured report.	View, print, or share a structured report from your computer.
Save SR	Save a structured report as an SR DICOM object.	Access and modify structured reports in future MIM sessions.
Save as Template...	Preserve a structured report outline that you can reuse.	See Create Structured Report Templates.
Encapsulate PDF	Save the structured report as a DICOM object with the modality of DOC.	Export structured reports to other systems via DICOM transfer.
Save as Secondary Capture	Save each page of the structured report as a DICOM object with the modality of OT.	View structured reports in systems that do not support SR or DOC DICOM modalities.

Create Structured Report Templates

MIMTD-1435 • 01 Sep 2023

Overview

When a structured report is generated, either from a MIM Workflow™ or manually, it uses a report template.

MIM includes several default structured report templates. Your MIM Implementation Specialist might have also helped build custom templates for your organization as part of your MIM implementation.

Use the following information if you want to further customize or create your own structured report templates.

Related: For more information about using report templates to create reports, see Create and Modify Structured Reports.

Contents

- Design a Structured Report
    - Change the Font, Font Style, and Font Size
    - Change the Page Orientation
    - Add Content to the Report
- Save the Report As a Report Template
- Distribute the Report Template

Design a Structured Report

Start by creating a report in the Structured Report Builder, which you will then save as a report template to use going forward.

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.

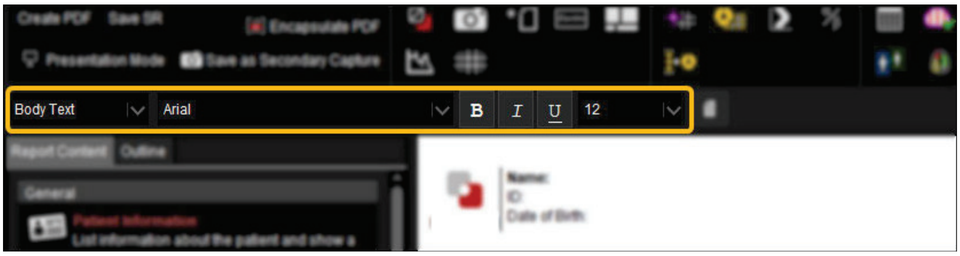
1. In an open MIM session, click the **Create Structured Report** tool in the toolbar, in the radial menu, or via keyboard shortcut. For more information, see Access Tools: The Toolbar and the Radial Menu or Set Keyboard Shortcuts.
2. In the Notifications window, either select the structured report template that you want to modify or select **Empty Template** to begin from a blank page. Click **OK**.

In the Structured Report Builder, determine the report layout and add content as needed.

> **Important**: Although patient-specific data is used to create structured report templates, only the structure and layout persist in saved templates. Saved templates do not contain any patient-specific data.

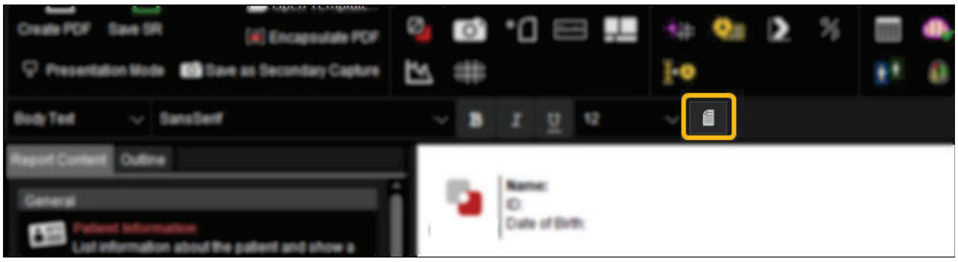
Change the Font, Font Style, and Font Size

Use the dropdowns and buttons above the structured report preview to change the font, font style (e.g., bold), and font size. In the first dropdown, select whether to adjust the font of headings, subheadings, or body text.In the first dropdown, select whether to adjust the font of headings, subheadings, body text, or findings tables. Changes to font settings apply to that content type throughout the structured report.



Change the Page Orientation

Click the page button above the structured report preview, and select **Portrait** or **Landscape**.



Add Content to the Report

You can add content from either the Report Content tab on the left side or from the top toolbar. When you select a content type, a new tab opens on the left side where you can edit the content.

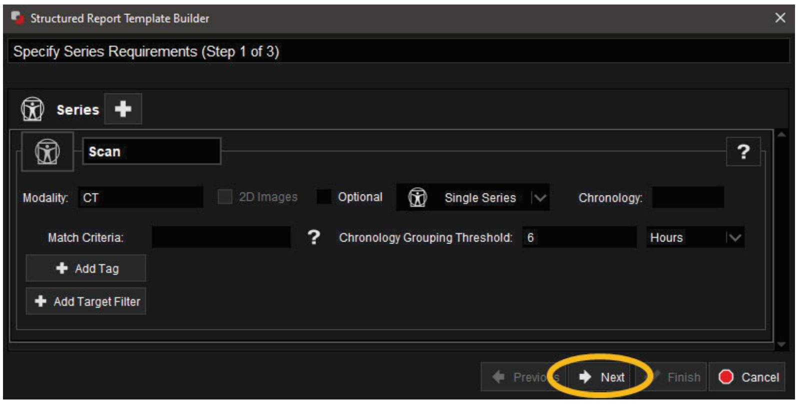
Review the following for more information about specific types of content that you can add:

- Use Headings, Layouts, and Page Breaks to Organize Structured Report Content
- Add Secondary Captures to Structured Reports
- Add Statistics to Structured Reports
- Use Macros to Insert Frequently Used Text into Structured Reports

Save the Report As a Report Template

When you are finished creating the report, save it as a template:

1. Click the **Save as Template...** button in the upper-left corner of the Structured Report Builder. The Structured Report Template Builder opens.
2. If desired, adjust the information in the **Specify Series Requirements** step. The information in this step is autofilled based on the study in your MIM session. In most cases, you do not need to adjust the information in this step. For advanced assistance, contact MIM Software Support at support.mimsoftware.com.
3. Click **Next**.



Scan

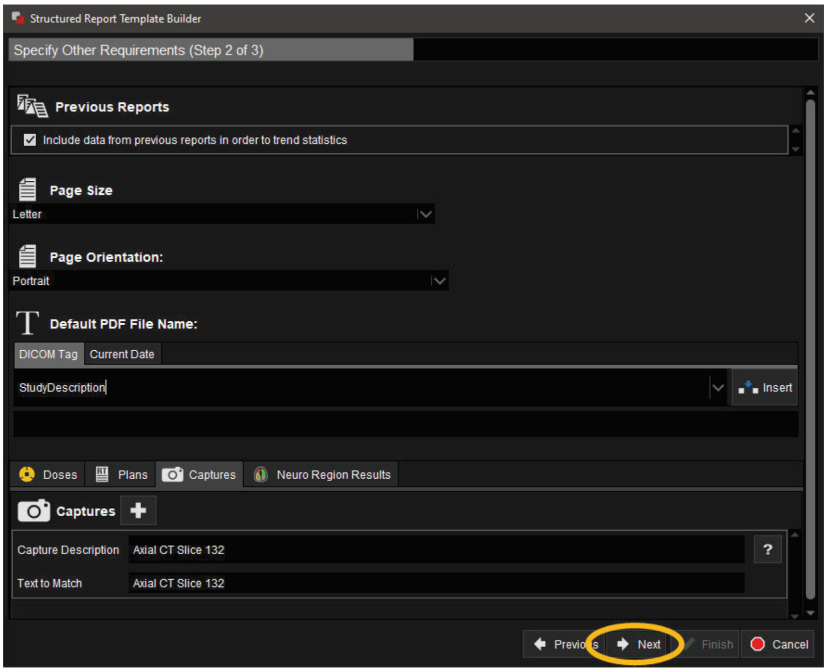
Modality: CT ☐ 2D Images ☐ Optional Single Series Chronology:

Match Criteria: ? Chronology Grouping Threshold: 6 Hours

4. If desired, adjust the information in the **Specify Other Requirements** step:
   - To compare data across structured reports from multiple time points, select **Include data from previous reports in order to trend statistics**. MIM trends data using any existing DICOM structured reports (i.e., structured reports that were saved with the **Save SR** option) from previous time points.
   - Adjust the default page size and orientation for the structured report. These selections take precedence over the settings configured under Settings ⚙ >> **General Preferences** >> **Application** >> **Structured Reporting**.
   - Add a default PDF filename. This filename takes precedence over any default PDF filename entered under Settings ⚙ >> **General Preferences** >> **Application** >> **Structured Reporting**.
   - Adjust requirements for any doses, plans, captures, or region results in the template. The information in this area is autofilled based on the data in your MIM session. In many cases, you

do not need to adjust the information in this area. For advanced assistance, contact MIM Software Support at support.mimsoftware.com.

5. Click **Next**.



☑ Include data from previous reports in order to trend statistics

Page Size: Letter

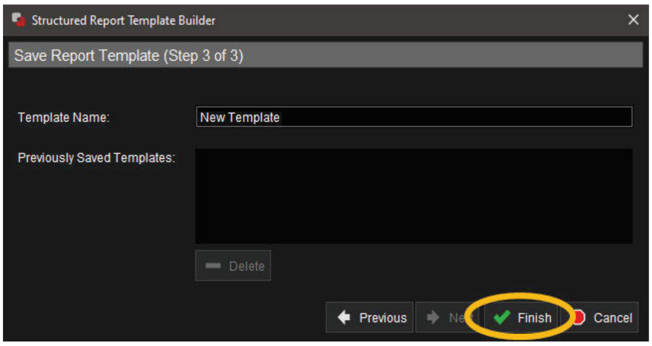
Page Orientation: Portrait

Default PDF File Name: StudyDescription

Capture Description: Axial CT Slice 132

Text to Match: Axial CT Slice 132

6. Enter a new name for the template, or select an existing template to overwrite.
7. Click **Finish**.



Template Name: New Template

The structured report template is now available for use. You can create a report using your template by using the **Create Structured Report** tool and selecting your template in the Notifications window.

Distribute the Report Template

If you created the report template while logged in as an administrator in the Edit Site Defaults mode, it is now available for anyone at your site to use.

Otherwise, you can share the report template with other users at your site using the Import Manager:

- *If you are an administrator*, right-click on the structured report template in the Import Manager and select **Move to the Site Default Level**.
- *If you are not an administrator*, select the structured report template in the Import Manager and export it. Save it to a shared file location and have others users import it.

Related: Refer to Import Content for Users for more information about using the Import Manager.

A workflow can automatically generate a structured report using your updated template. Please contact MIM Software Support at support.mimsoftware.com if you would like a workflow to use your template.

Use Headings, Layouts, and Page Breaks to Organize Structured Report Content

MIMTD-1436 • 14 Sep 2023

Overview

You can design how you want a structured report to appear by adding headings, layouts, and page breaks. For example, you might want to create a report template with an exam heading and a two-column layout on the first page.

Related: For more information about designing structured report templates, see Create Structured Report Templates.

Contents

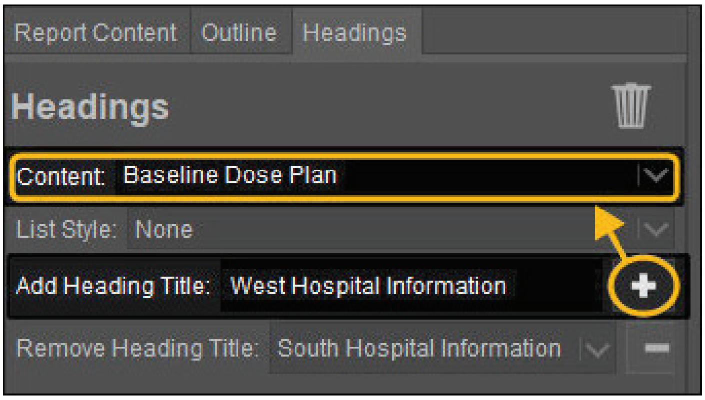
- Use Headings and Subheadings
- Arrange Content in Layouts
- Insert Page Breaks

Use Headings and Subheadings

Add headings and subheadings to your report:

1. Click **Headings** ▤ in the **Report Content** tab or the top toolbar of the Structured Report Builder.
2. On the **Headings** tab, you can either:
    - Select a pre-made heading from the **Content** dropdown.

- Enter your own heading in the **Add Heading Title** field. Then, click the plus ➕ to add it to the content options, and select it from the **Content** dropdown.



Report Content | Outline | Headings

Headings

Content: Baseline Dose Plan

List Style: None

Add Heading Title: West Hospital Information

Remove Heading Title: South Hospital Information

3. Return to the **Report Content** tab and select the content that you want to insert below the heading:
   - To add a **Subheading** ▤, first click the heading in the structured report preview that you want to add the subheading under. You can only add a subheading when a heading is selected in the structured report preview.
   - To group existing content under a heading or subheading, left-click drag the content in the **Outline** tab onto the desired heading or subheading. The heading or subheading that the content will be added under is highlighted.
   - If you want the content under the heading to appear as bullet points or a numbered list, return to the **Headings** or **Subheadings** tab and configure the **List Style** field.

☆ **Important:** If you delete a heading or subheading, all content that is grouped under the heading or subheading is also deleted. To see which items are grouped under a heading or subheading, go to the **Outline** tab.

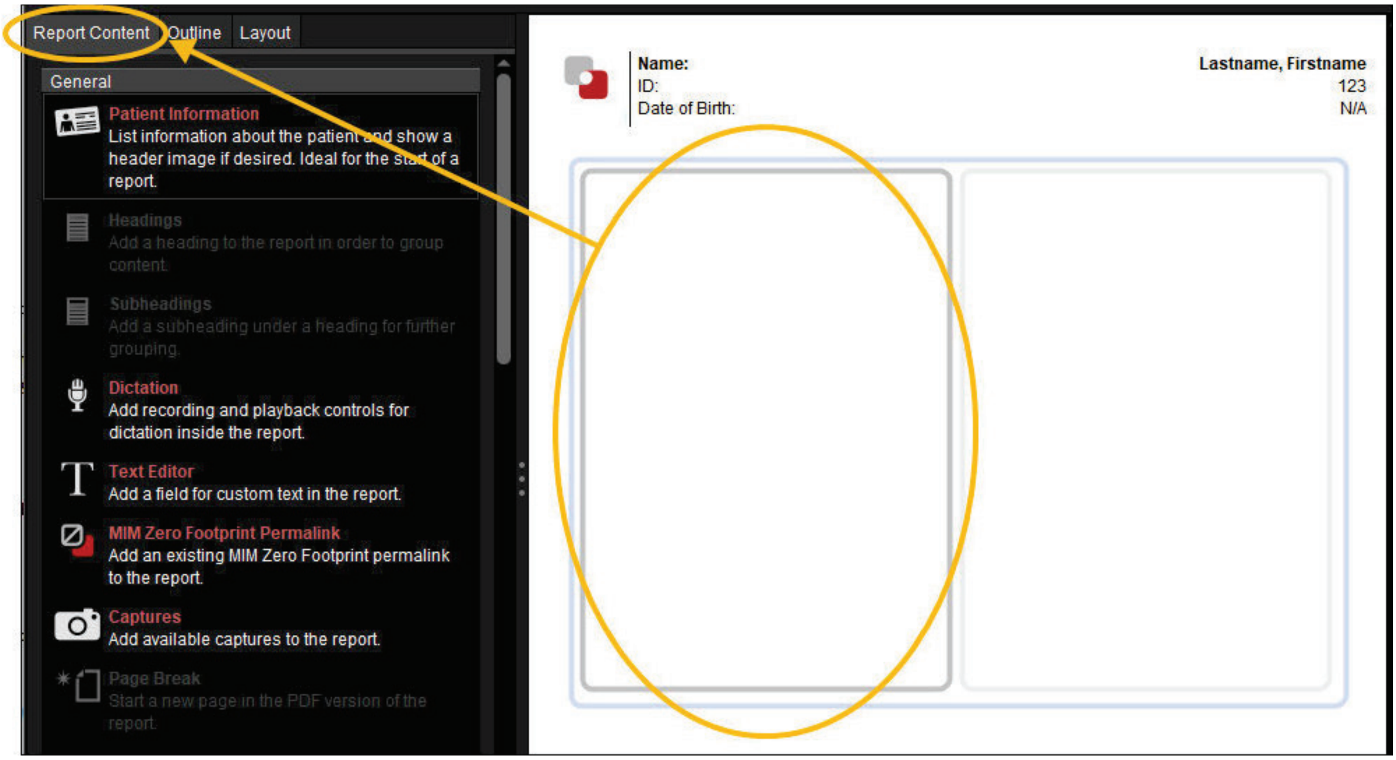
Arrange Content in Layouts

To arrange certain types of content, add a **Layout** ⊞ from the **Report Content** tab or the top toolbar of the Structured Report Builder.

On the **Layout** tab, you can determine:

- The type of layout, such as four cells or two columns.
- Whether to show a border.

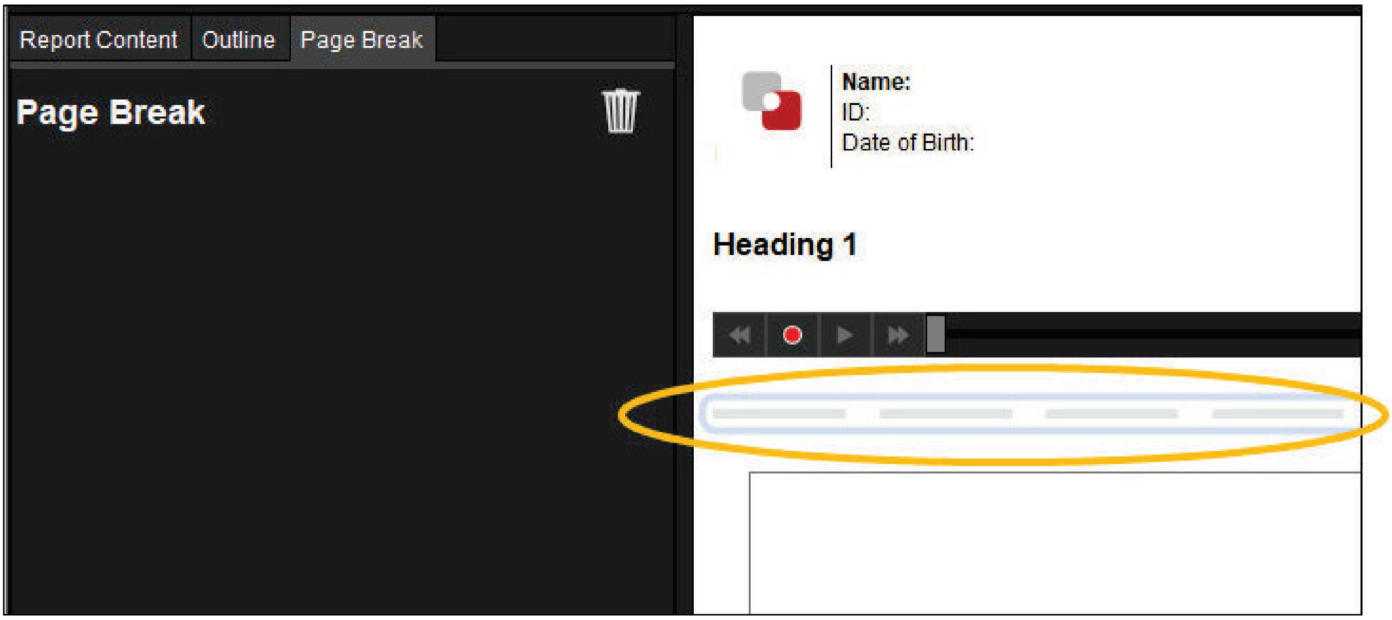
To add content to the layout, select a cell in the layout, then click the desired content in the **Report Content** tab.



☆ **Important:** If you delete a layout, all content within that layout is also deleted. You can see which items are within the layout on the **Outline** tab.

Insert Page Breaks

Add a **Page Break** from the **Report Content** tab of the Structured Report Builder. The page break appears as a dashed line on the structured report preview. This indicates where a new page starts in the saved PDF version of the structured report.



To remove the page break, click the dashed line in the structured report preview. Then, click the trashcan button in the upper-right corner of the **Page Break** tab.

Add Secondary Captures to Structured Reports

MIMTD-1437 • 13 Sep 2023

Overview

You can add screen captures to structured reports. Use the steps below if you are building a report template or if you want to add a Captures section to an existing report.

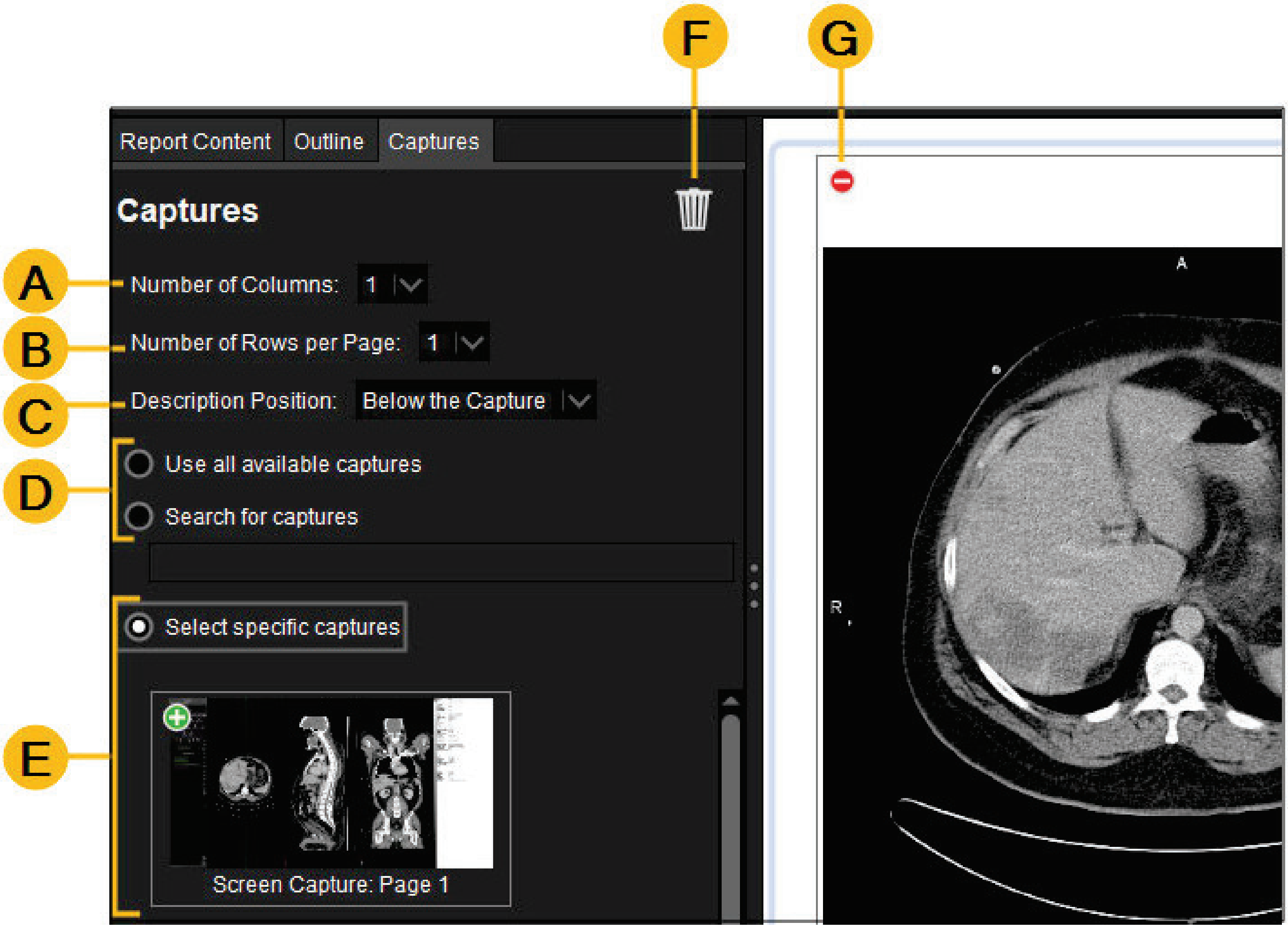
> **Related:** For more information about designing structured report templates, see Create Structured Report Templates.

For instructions on creating secondary captures in your MIM session, see Create and Save Secondary Captures.

Add Capture Content

Click **Captures** 📷 in the **Report Content** tab or top toolbar of the Structured Report Builder.

Use these tips to make adjustments in the **Captures** tab:



Captures

Number of Columns: 1

Number of Rows per Page: 1

Description Position: Below the Capture

○ Use all available captures

○ Search for captures

● Select specific captures

A. Choose the number of columns that captures appear in.

B. Choose the number of rows per page that captures appear in.

C. Choose whether the description appears above or below captures.

D. Add all available captures from your MIM session, or search for captures.

E. Select from a list of captures that are available in your MIM session. Click the add ⊕ button to add a capture.

F. Delete the captures from the structured report.

G. Click the remove ⊖ button to remove a specific capture from the structured report preview.

Add Statistics to Structured Reports

MIMTD-1438 • 13 Sep 2023

Overview

You can add statistics from a session to a structured report. Use the steps below if you are building a report template or if you want to add a statistics graph or table to an existing report.

Tip: The **Statistics Graph** and **Statistics Table** items described here create a graph/table in the report based on contours in the session. If you instead want to include in the report a graph/table that was created by a workflow and is displayed in the session, use the **Graph** or **Table** items.

Related: For more information about designing structured report templates, see Create Structured Report Templates.

For instructions on viewing statistics in your MIM session, see View Statistics.

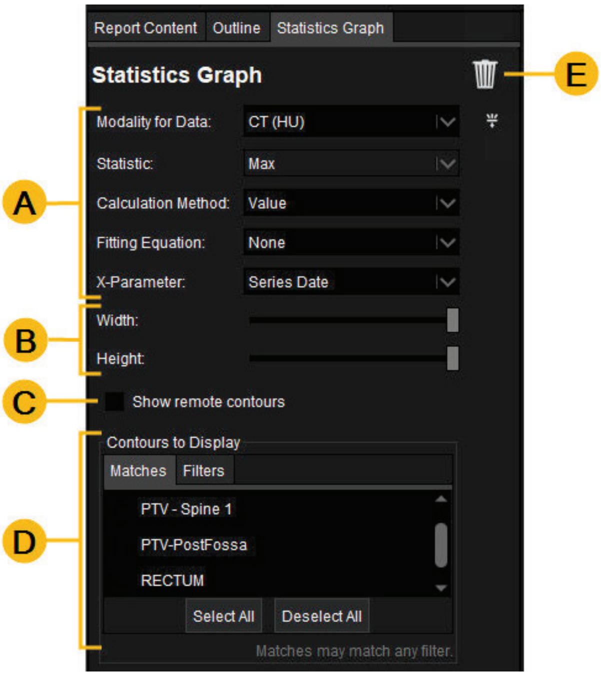
Contents

- Add a Statistics Graph
- Add a Statistics Table

Add a Statistics Graph

Click **Statistics Graph** in the **Report Content** tab or top toolbar of the Structured Report Builder.

Use these tips to make adjustments in the **Statistics Graph** tab of the Structured Report Builder:



Statistics Graph

Modality for Data: CT (HU)

Statistic: Max

Calculation Method: Value

Fitting Equation: None

X-Parameter: Series Date

Width:

Height:

☐ Show remote contours

Contours to Display

PTV - Spine 1

PTV-PostFossa

RECTUM

Matches may match any filter.

A. Select which statistic to display in the graph, and adjust various parameters. To add a search filter for a list of series, click the filter button next to the **Modality for Data** dropdown.

B. Drag the sliders to adjust the width and height of the graph.

C. Select whether to show contours that appear on the active series but belong to a different series. In a MIM session, remote contours are indicated by a ghost icon in the Contours sidebar.

D. Select the contours that you want to display statistics for.

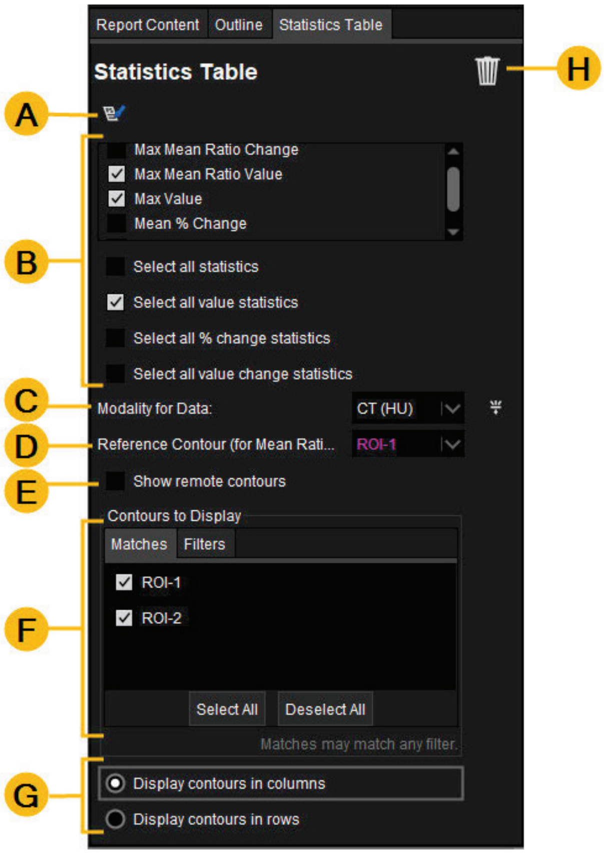
E. Delete the statistics graph from the structured report.

Tip: If you are using a Mac, expand the sidebar by dragging it to the right to access the filter options.

Add a Statistics Table

Click **Statistics Table** in the **Report Content** tab or top toolbar of the Structured Report Builder. The table can include multiple statistics for multiple contours and can show the change in values over time.

Use these tips to make adjustments in the **Statistics Table** tab of the Structured Report Builder:



☐ Max Mean Ratio Change
☑ Max Mean Ratio Value
☑ Max Value
☐ Mean % Change

☐ Select all statistics
☑ Select all value statistics
☐ Select all % change statistics
☐ Select all value change statistics

Modality for Data: CT (HU)
Reference Contour (for Mean Rati... ROI-1
☐ Show remote contours

☑ ROI-1
☑ ROI-2

● Display contours in columns
○ Display contours in rows

A. Set a field name that matches a PowerScribe® 360 custom field. For help with PowerScribe integration, please contact MIM Software Support at support.mimsoftware.com.

B. Add statistics to the table individually, or add all similar statistics to the table as a group.

C. If multiple image modalities are open in your MIM session, choose which modality to use. To add a search filter for a list of series, click the filter button next to the **Modality for Data** dropdown.

D. Select the reference contour to use when applying mean ratio statistics.

E. Select whether to show contours that appear on the active series but belong to a different series. In a MIM session, remote contours are indicated by a ghost icon in the Contours sidebar.

F. Choose which contours to display in the table.

G. Choose to display contours in columns or in rows.

H. Delete the table from the structured report.

Tip: If you are using a Mac, expand the sidebar by dragging it to the right to access the filter options.

Use Macros to Insert Frequently Used Text into Structured Reports

MIMTD-1440 • 21 Feb 2023

Overview

Macros let you quickly insert a standard word, phrase, or paragraph into a Text Editor in structured reports. Macros can include pieces of dynamic DICOM information that update depending on the active series. You can also insert dynamic DICOM information directly into Text Editor fields without creating macros.

Related: For more information about using report templates to create reports, see Create and Modify Structured Reports.

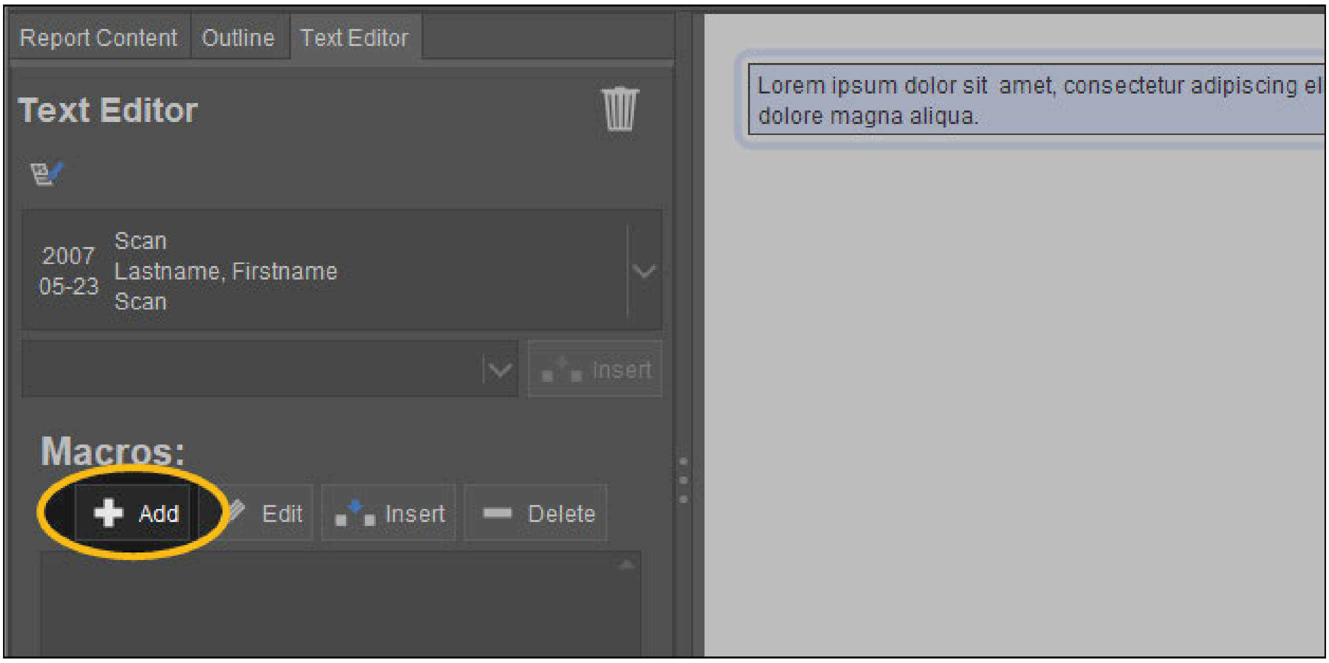
Contents

- Create and Insert Macros
- Add Dynamic DICOM Information Directly into Text Editor Fields

Create and Insert Macros

1. Add a **Text Editor** 🅃 field to your structured Report from the **Report Content** tab or top toolbar of the Structured Report Builder. Or click an existing Text Editor field in the structured report preview. The Text Editor field is highlighted in the structured report preview, and a **Text Editor** tab opens.

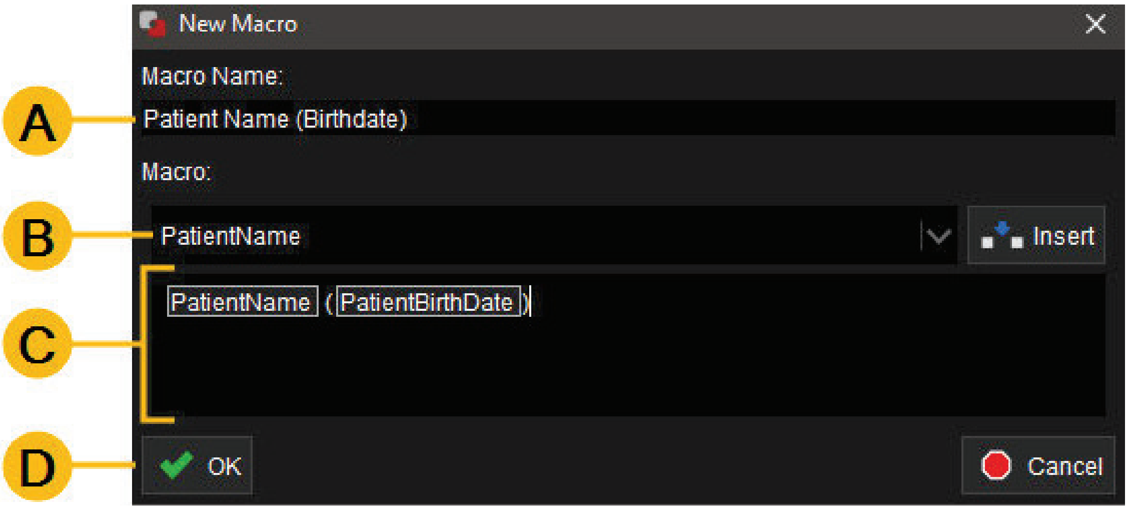
2. Click the **Add** button in the Macros section of the **Text Editor** tab. The New Macro window appears.



2007
05-23
Scan
Lastname, Firstname
Scan

Lorem ipsum dolor sit amet, consectetur adipiscing el
dolore magna aliqua.

3. Create a new macro:



Macro Name:
Patient Name (Birthdate)

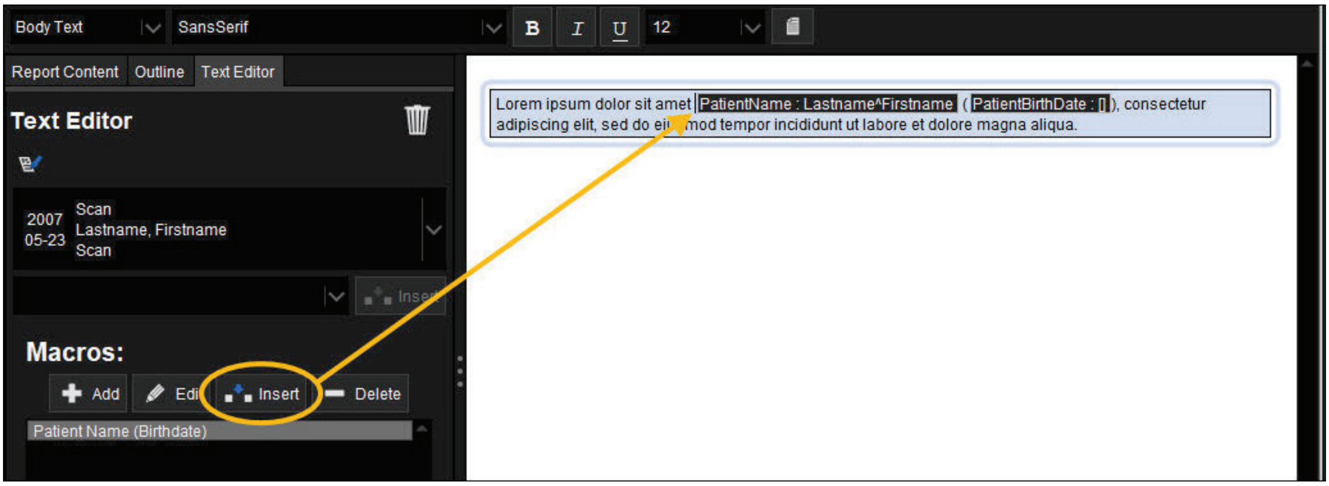
Macro:
PatientName

PatientName (PatientBirthDate)

   A. Assign the macro a name.
   B. To add dynamic DICOM information to the macro, start typing the name of a DICOM tag. Then, click the desired DICOM tag from the dropdown of search results that appears. Click the **Insert** button on the right side of the search box to add the DICOM information to the macro. The DICOM information appears below in the macro text field at the position of the cursor.
   C. If desired, type text around DICOM information that was added in step **B**.
   D. Click **OK** to save the macro and close the window.

4. Place the cursor in the Text Editor field where you want the macro to appear.

5. In the **Text Editor** tab, highlight the name of the macro that you created.
6. Click the **Insert** button. The macro appears in the Text Editor field.



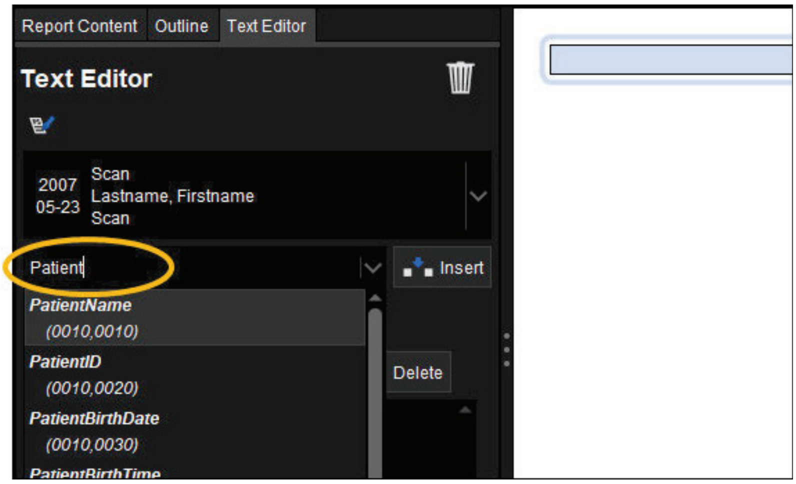
Lorem ipsum dolor sit amet PatientName : Lastname^Firstname (PatientBirthDate : []), consectetur adipiscing elit, sed do eiusmod tempor incididunt ut labore et dolore magna aliqua.

Tip: You can share structured reporting macros with other MIM users at your organization. For instructions, see Import MIM Workflows™ and Other Content.

Add Dynamic DICOM Information Directly into Text Editor Fields

1. Add a **Text Editor** T field to your structured Report from the **Report Content** tab or top toolbar of the Structured Report Builder. Or click an existing Text Editor field in the structured report preview. The Text Editor field is highlighted in the structured report preview, and a **Text Editor** tab opens.
2. In the Text Editor field in the report preview, place your cursor where you want the DICOM tag to appear.

3. In the **Text Editor** tab, start typing a DICOM tag in the search box below the series information.



Tip: The series dropdown above the search field determines from which series the DICOM tags are populated.

4. Click the desired DICOM tag from the dropdown of search results that appears.
5. Click the **Insert** button on the right side of the search box to add the DICOM information to the Text Editor field.

Manage Data

Manage Patient Data

MIMTD-626 • 07 Sep 2023

Overview

The patient list lets you view patient information, search, anonymize, correct, merge, delete, and more.

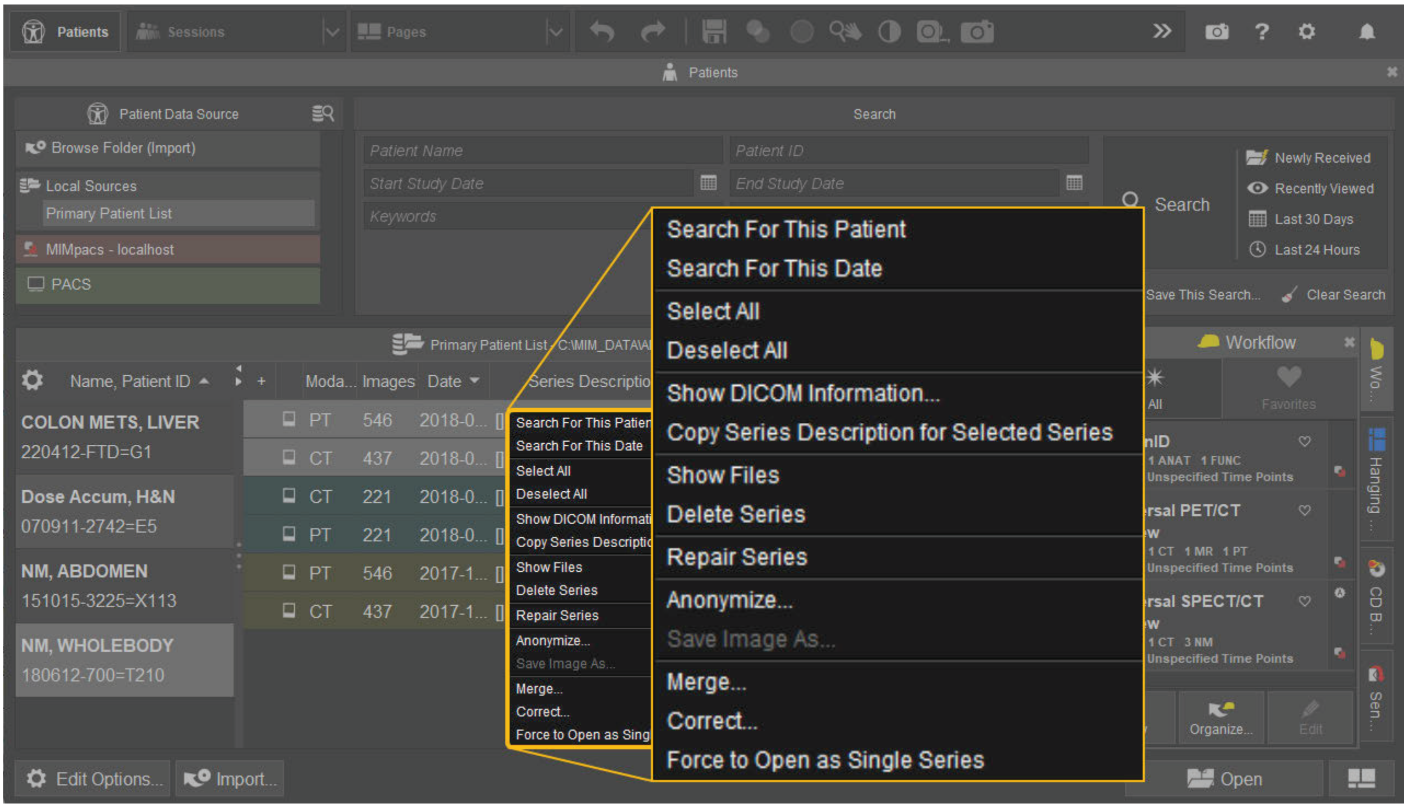
Contents

- Data Management Options
- Delete Old Data to Manage Drive Space

Data Management Options

Right-click on one or more series to access options for managing patient data.

> ☆ **Important:** Depending on the patient list and your user permissions, some options may be grayed out and unavailable. For example, when searching a remote patient list (a list of patient data stored on another MIM workstation), you cannot select **Show Files...** for a series because the files reside on another workstation.



- **Search for This Patient** — Search the patient list by name and patient ID.
- **Search for This Date** — Search the patient list by the series date.
- **Show DICOM Information...** — Open the DICOM information viewer.

Related: For more information about the DICOM information viewer, see View and Edit DICOM Information.

- **Show Files** — Open Windows File Explorer or Finder and view the DICOM files on disk.
- **Repair Series** — Repair the metabase information for the selected series. Try this tool if you are having problems opening data. The tool does not alter the DICOM file, so there are no negative side effects to using it.
- **Create New DICOM...** — There are multiple selections under this option.

Tip: Which of the below options appear depends on whether a single series or multiple series are selected.

  - **Anonymize...** — Create a copy of patient data and alter DICOM fields, including the Patient Name and ID, to anonymize the data. This is helpful if you need to send patient data to another organization without compromising sensitive information. The original data is retained in the MIM patient list.
  - **Encapsulate Document...** — Choose a document to encapsulate with the selected series. After selecting this option, click the **Add** button in the Notifications window to browse to and select the document.

Tip: Encapsulating a document saves the document as a DICOM object with the modality `DOC`. This is helpful when you wish to export a document, such as a structured report, to another system via DICOM transfer.

  - **Secondary Capture from Image...** — Select an image to save as a DICOM OT file with the patient. After selecting this option, click the **Browse** button in the Notifications window to browse to and select the image.
  - **Bin Series** — Bin a 4D CT (an RPM (.vxp) file is required).

- **Save Image As...** — Save an OT file to a folder on your workstation or network.
- **Delete Series** — Delete the selected series.

Important: Series deleted in MIM cannot be recovered.

- **Merge...** — Merge patient data that is "split" across two patient names or IDs. For more information, see Merge Patients.
- **Correct...** — Correct patient data by altering certain DICOM values, including patient name, patient ID, birth date, series description, and more.

Tip: This action creates a corrected copy of the patient data. The original data is retained in the MIM patient list. For more information, see Correct Patient Data.

- **Force to Open as a Single Series** — This option can be used to open dynamic series together when they do not open together automatically.

Tip: This option can also be used to open MR acquisitions that you would like to view together.

- **Status Actions** — Lock or unlock a series.

Tip: Status actions require network user logins. For more information, see Manage User Logins.

- **Owner Actions** — Set an owner for the series. See Set Owners on Series or Sessions for more information.

Delete Old Data to Manage Drive Space

Caution: Deleting patient data from MIM removes it permanently from disk. Deletion through any means, including but not limited to deletion through the MIM interface, manual deletion from MIM's underlying archive folder, deletion via an extension, or deletion via a MIM Assistant rule, all result in the data being permanently removed from disk.

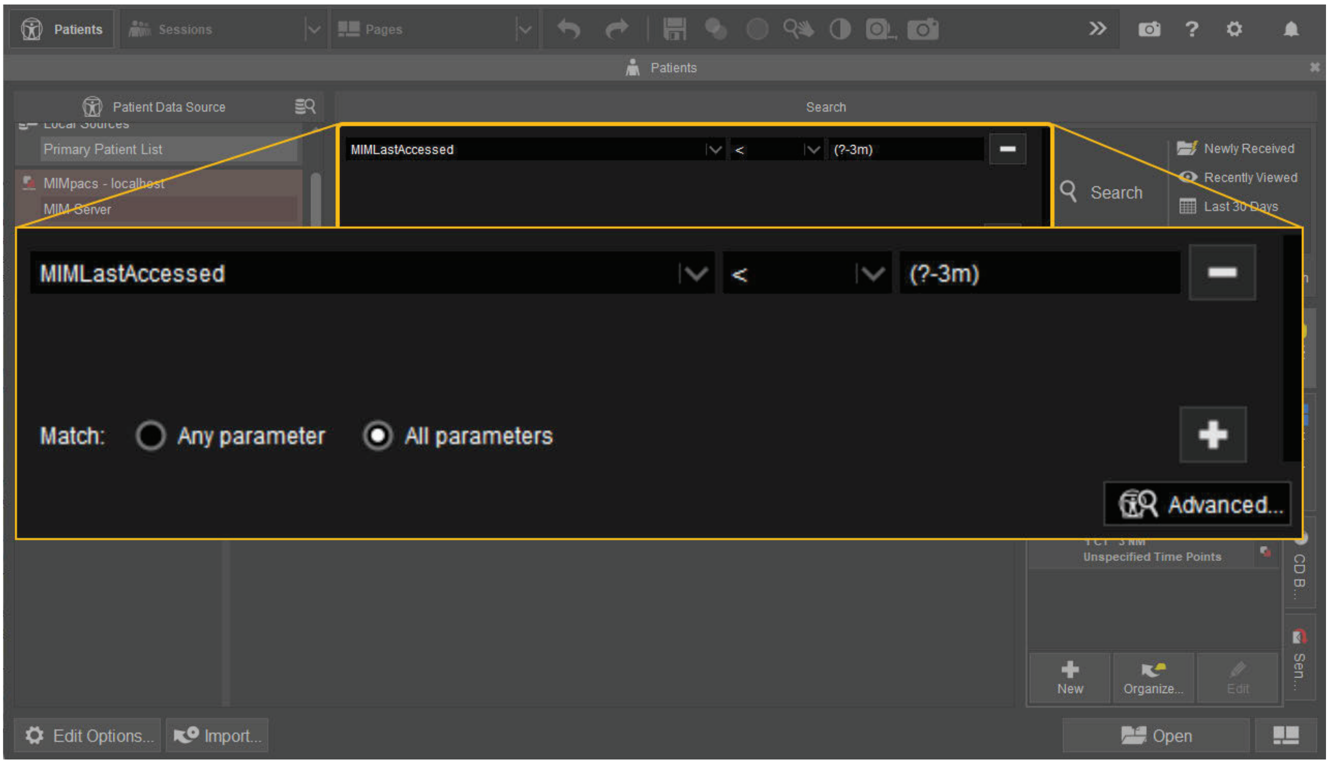
Before deleting patient data, verify with your IT department that patient data backups exist and have been tested for proper restoration. Failure to maintain data backups can result in permanent data loss for systems which are not backed up in accordance with long-term storage and recovery procedures. MIM Software is not responsible for permanent data loss resulting from improper or non-existent backups.

To regain space on your hard drive by deleting old patient data from MIM, perform an advanced search on the patient list that contains the data using the **MIMLastAccessed** DICOM tag. This tag records the last time MIM opened or moved a file, so it is the best way to identify data that has been unused for a long period of time.

1. Choose an appropriate patient list for your search. If you are on a client machine, this is most likely the Primary Patient List. If you are on the MIMpacs™ server, you may have many lists of locally stored data to choose from.
2. Click **Advanced...** in the MIM search area.

3. Enter search parameters as shown below, ensuring that the second dropdown contains the < symbol:

6.1.



MIMLastAccessed < (?-3m)

Match: ○ Any parameter ● All parameters

4. In the rightmost field, specify the date range you would like to search for, using the format `(?-3m)`. In this example, the < indicates that the search contains results that occur before the entered value, the `?` signifies the current day, and `-3m` means "three months before." So all together, this equation searches for studies that have not been accessed by MIM within the past 3 months.

Tip: You can use `y` (year), `m` (month), or `d` (day) to determine an appropriate range.

5. Perform the search to find series whose MIMLastAccessed tag meets your parameters. In the example above, the search would return any series whose MIMLastAccessed tag had a date that was more than 3 months ago. This indicates that the series has not been accessed in at least 3 months.
6. Delete the old data as needed to free space on your hard drive.

Tip: If your hard drive is near capacity, performing this search may be taxing to the system. Begin searching for series whose MIMLastAccessed date is very old. Then, as you delete older data, update your search to include more recent dates. This will prevent your machine from being overburdened by too many search results at once.

Tip: If you have a MIM Assistant® license, you can configure a rule to search for and delete old data automatically. For more information, see Archive and Clean Up Data with MIM Assistant.

View and Edit DICOM Information

MIMTD-627 • 27 Jul 2023

Overview

View and edit DICOM information for any series in MIM®. You can also compare DICOM files from the same series, or compare different series.

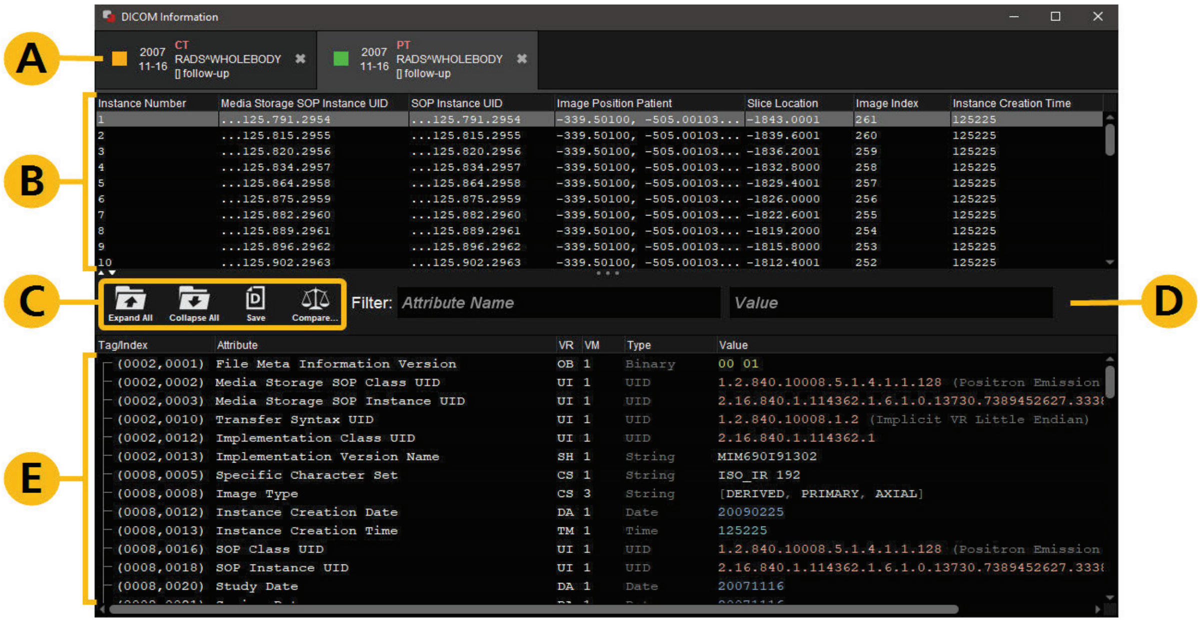
Contents

- Open the DICOM Information Viewer
- Navigate the DICOM Information Viewer
- Compare DICOM
- Edit DICOM

Open the DICOM Information Viewer

1. Search for a patient in MIM. (See Find and Open Patient Data.)
2. Select one or more series.
3. Right-click the series and choose **Show DICOM Information...** to open the DICOM Information viewer.

Navigate the DICOM Information Viewer



Instance Number	Media Storage SOP Instance UID	SOP Instance UID	Image Position Patient	Slice Location	Image Index	Instance Creation Time
1	...125.791.2954	...125.791.2954	-339.50100, -505.00103...	-1843.0001	261	125225
2	...125.815.2955	...125.815.2955	-339.50100, -505.00103...	-1839.6001	260	125225
3	...125.820.2956	...125.820.2956	-339.50100, -505.00103...	-1836.2001	259	125225
4	...125.834.2957	...125.834.2957	-339.50100, -505.00103...	-1832.8000	258	125225
5	...125.864.2958	...125.864.2958	-339.50100, -505.00103...	-1829.4001	257	125225
6	...125.875.2959	...125.875.2959	-339.50100, -505.00103...	-1826.0000	256	125225
7	...125.882.2960	...125.882.2960	-339.50100, -505.00103...	-1822.6001	255	125225
8	...125.889.2961	...125.889.2961	-339.50100, -505.00103...	-1819.2000	254	125225
9	...125.896.2962	...125.896.2962	-339.50100, -505.00103...	-1815.8000	253	125225
10	...125.902.2963	...125.902.2963	-339.50100, -505.00103...	-1812.4001	252	125225

Tag/Index	Attribute	VR	VM	Type	Value
(0002,0001)	File Meta Information Version	OB	1	Binary	00 01
(0002,0002)	Media Storage SOP Class UID	UI	1	UID	1.2.840.10008.5.1.4.1.1.128 (Positron Emission
(0002,0003)	Media Storage SOP Instance UID	UI	1	UID	2.16.840.1.114362.1.6.1.0.13730.7389452627.333
(0002,0010)	Transfer Syntax UID	UI	1	UID	1.2.840.10008.1.2 (Implicit VR Little Endian)
(0002,0012)	Implementation Class UID	UI	1	UID	2.16.840.1.114362.1
(0002,0013)	Implementation Version Name	SH	1	String	MIM690I91302
(0008,0005)	Specific Character Set	CS	1	String	ISO_IR 192
(0008,0008)	Image Type	CS	3	String	[DERIVED, PRIMARY, AXIAL]
(0008,0012)	Instance Creation Date	DA	1	Date	20090225
(0008,0013)	Instance Creation Time	TM	1	Time	125225
(0008,0016)	SOP Class UID	UI	1	UID	1.2.840.10008.5.1.4.1.1.128 (Positron Emission
(0008,0018)	SOP Instance UID	UI	1	UID	2.16.840.1.114362.1.6.1.0.13730.7389452627.333
(0008,0020)	Study Date	DA	1	Date	20071116

A. *Series Tabs*

- If you opened DICOM information for more than one series, use the tabs at the top to toggle between the series.
- Right-click a tab to view the following options:
    - Close
    - Close all other tabs
    - Split to new pane

B. *File List*

- Each column in this section displays an attribute whose values differ across the individual DICOM files (i.e., slices) for a series.
- Any DICOM attributes that are not displayed here are the same for all files in the series.
- The full DICOM information for the highlighted file is shown in the lower half of the window (section **E**). Highlight a different file in section **B** to update the DICOM information shown in section **E**.

C. *Expand, Collapse, Save, and Compare Functions*

- Click **Expand All** to expand all sequences in the DICOM information and view every attribute.

> **Tip**: To expand just one sequence and view its children, go to section **E** and click the + button for the individual sequence.
>
> *MIM 7.4 and later*: To fully expand an individual sequence and see all of its children, plus their children attributes, press the Ctrl or Cmd key and click the + button. This Ctrl/Cmd functionality is not available in MIM 7.3 and earlier.

- Click **Collapse All** to collapse all sequences in the DICOM information.
- Use the **Save** button after you make edits to generate a new copy of the series. For further instructions, see Edit DICOM below.
- Click **Compare...** and choose either **This Series** or another series. For further instructions, see Compare DICOM below.

D. *Filters* — Filter DICOM information by the DICOM *Attribute Name* (e.g., Modality) or *Value* (e.g., CT).

E. *Full DICOM Information* — View the full DICOM information for the file highlighted in section **B**.

Compare DICOM

Click the **Compare...** button in the middle of the DICOM Information viewer and choose either **This Series** or another series.

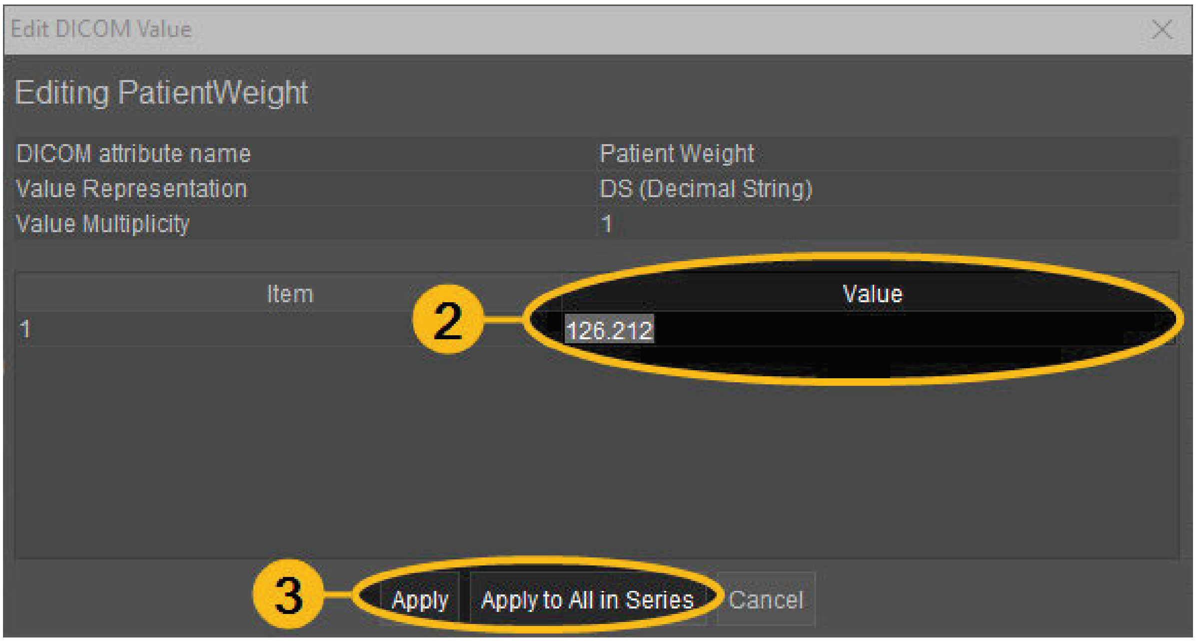
- Select **This Series** to highlight two files (from section **A**; see Navigate the DICOM Information Viewer above) — the already-highlighted file, plus the file that is immediately below it.
  - The full DICOM information in the lower-half of the window (section **E**; see Navigate the DICOM Information Viewer above) updates to highlight the differences between the two files in green.
  - Shift+click or Cmd+click to select a different pair of files to compare.
- Select another series to split the DICOM viewer into two panes, one for each series.
  - *In MIM 7.4 and later*: Scrolling, searching, and expanding/collapsing are synced between the panes. Differences between series are higlighted in green, yellow, and red.
  - *In MIM 7.3 and earlier*: A split pane view shows information for each series, but scrolling, searching, and expanding/collapsing are not synced between the panes. Differences are not highlighted.

Edit DICOM

Tip: Only existing DICOM tags can be altered. If a tag is not present for a particular series, the editor cannot be used to add it.

To edit DICOM values:

1. Double-click any value in the DICOM Information viewer. The Edit DICOM Value window opens.
2. Change the value.
3. Select **Apply** to change the value for the individual file (i.e., slice) or **Apply to All in Series** to change the value for all files of the series.



Edit DICOM Value

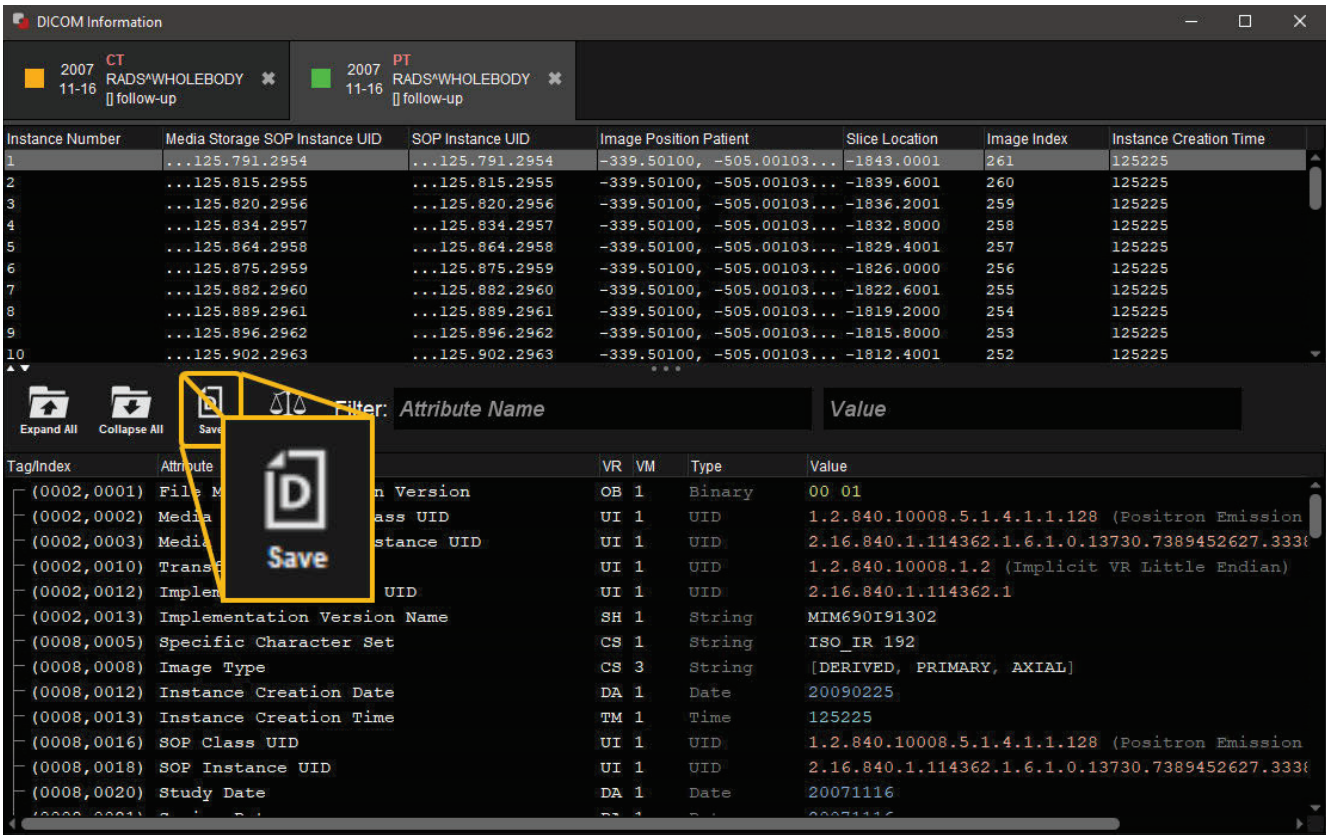
Editing PatientWeight

DICOM attribute name	Patient Weight
Value Representation	DS (Decimal String)
Value Multiplicity	1

Item	Value
1	126.212

4. Click the **Save** button in the DICOM Information viewer to generate a new series.

Tip: Editing DICOM does not overwrite existing data. MIM always creates new files and keeps the original data intact. When MIM creates new files, the SOP Instance UID and Series Instance UID are replaced because these are unique identifiers.



Instance Number	Media Storage SOP Instance UID	SOP Instance UID	Image Position Patient	Slice Location	Image Index	Instance Creation Time
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7	...125.882.2960	...125.882.2960	-339.50100, -505.00103...	-1822.6001	255	125225
8	...125.889.2961	...125.889.2961	-339.50100, -505.00103...	-1819.2000	254	125225
9	...125.896.2962	...125.896.2962	-339.50100, -505.00103...	-1815.8000	253	125225
10	...125.902.2963	...125.902.2963	-339.50100, -505.00103...	-1812.4001	252	125225

Tag/Index	Attribute	VR	VM	Type	Value
(0002,0001)	File M n Version	OB	1	Binary	00 01
(0002,0002)	Media ass UID	UI	1	UID	1.2.840.10008.5.1.4.1.1.128 (Positron Emission
(0002,0003)	Medi stance UID	UI	1	UID	2.16.840.1.114362.1.6.1.0.13730.7389452627.333
(0002,0010)	Trans	UI	1	UID	1.2.840.10008.1.2 (Implicit VR Little Endian)
(0002,0012)	Implem UID	UI	1	UID	2.16.840.1.114362.1
(0002,0013)	Implementation Version Name	SH	1	String	MIM690I91302
(0008,0005)	Specific Character Set	CS	1	String	ISO_IR 192
(0008,0008)	Image Type	CS	3	String	[DERIVED, PRIMARY, AXIAL]
(0008,0012)	Instance Creation Date	DA	1	Date	20090225
(0008,0013)	Instance Creation Time	TM	1	Time	125225
(0008,0016)	SOP Class UID	UI	1	UID	1.2.840.10008.5.1.4.1.1.128 (Positron Emission
(0008,0018)	SOP Instance UID	UI	1	UID	2.16.840.1.114362.1.6.1.0.13730.7389452627.333
(0008,0020)	Study Date	DA	1	Date	20071116

Anonymize Data

MIMTD-624 • 27 Jul 2023

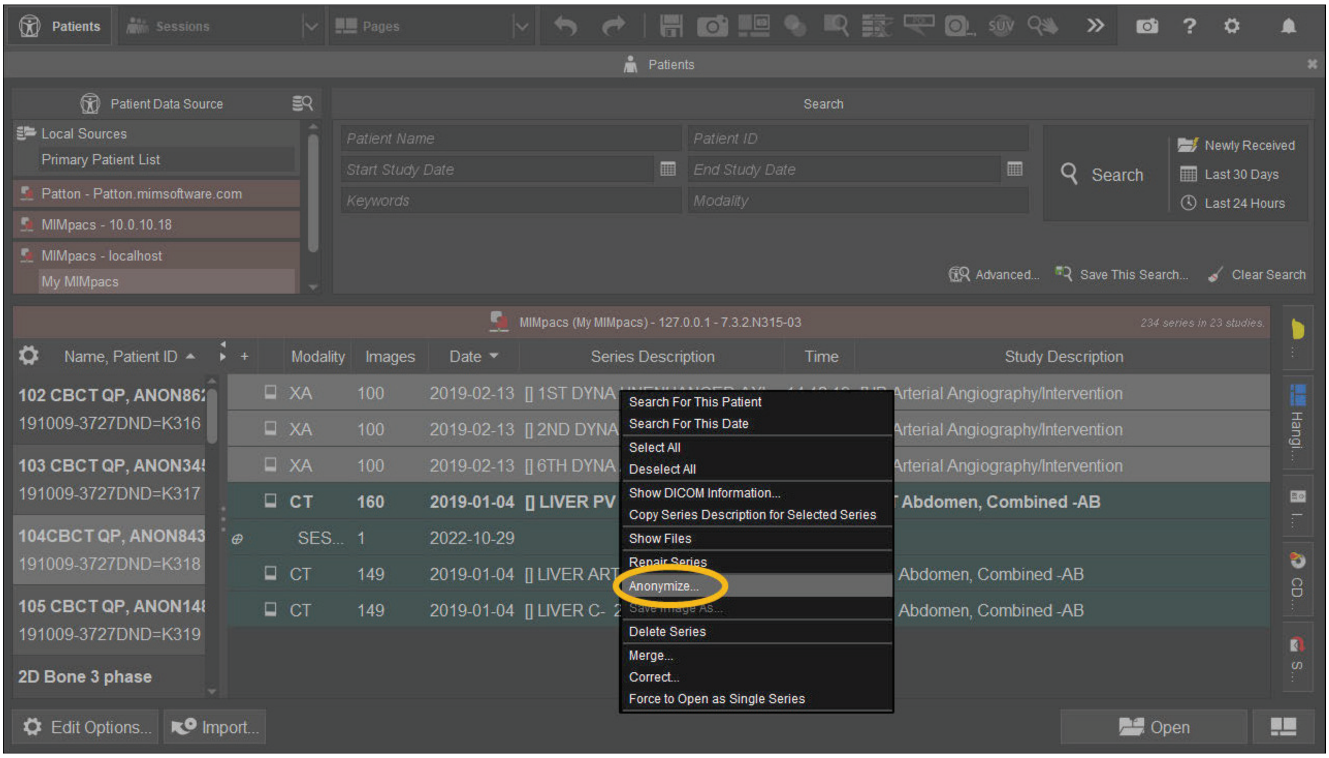
Overview

Anonymizing data in MIM® replaces the patient's name and ID with randomized, generic names and IDs and strips the birth date, referring physician name, and any private DICOM tags that exist.

> ☆ **Important:** Anonymizing data does not overwrite existing data. New DICOM files are created, keeping the original data intact.

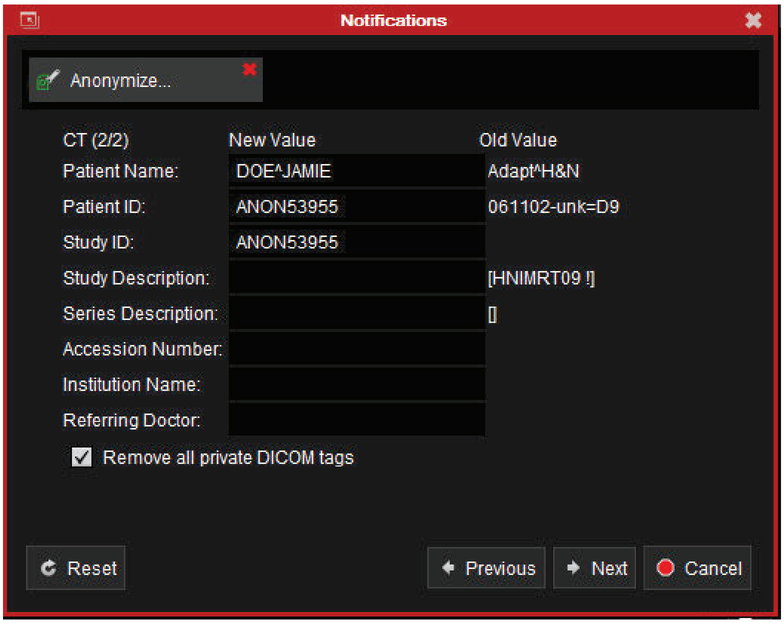
Anonymize Data

1. Select the study or individual series of a study in the MIM patient list that you want to anonymize. Do not open the study or series, only select them.
2. Right-click on the patient study in the left column or a set of selected series and choose **Anonymize...** in the right-click menu.



To anonymize a single series, highlight the series in the list, right-click and select **Create New DICOM** >> **Anonymize**.

3. In the Notifications window, a randomized Patient ID and Study ID are automatically assigned. Change these or any other fields if desired. If you had selected multiple series, click **Next** to review anonymized information for each series.



CT (2/2)	New Value	Old Value
Patient Name:	DOE^JAMIE	Adapt^H&N
Patient ID:	ANON53955	061102-unk=D9
Study ID:	ANON53955	
Study Description:		[HNIMRT09 !]
Series Description:		[]
Accession Number:		
Institution Name:		
Referring Doctor:		

☑ Remove all private DICOM tags

4. At the final step, choose the destination to store the anonymized data. Click **Finish** to produce the anonymized data and send it to the selected destination.

Correct Patient Data

MIMTD-625 • 07 Aug 2023

Overview

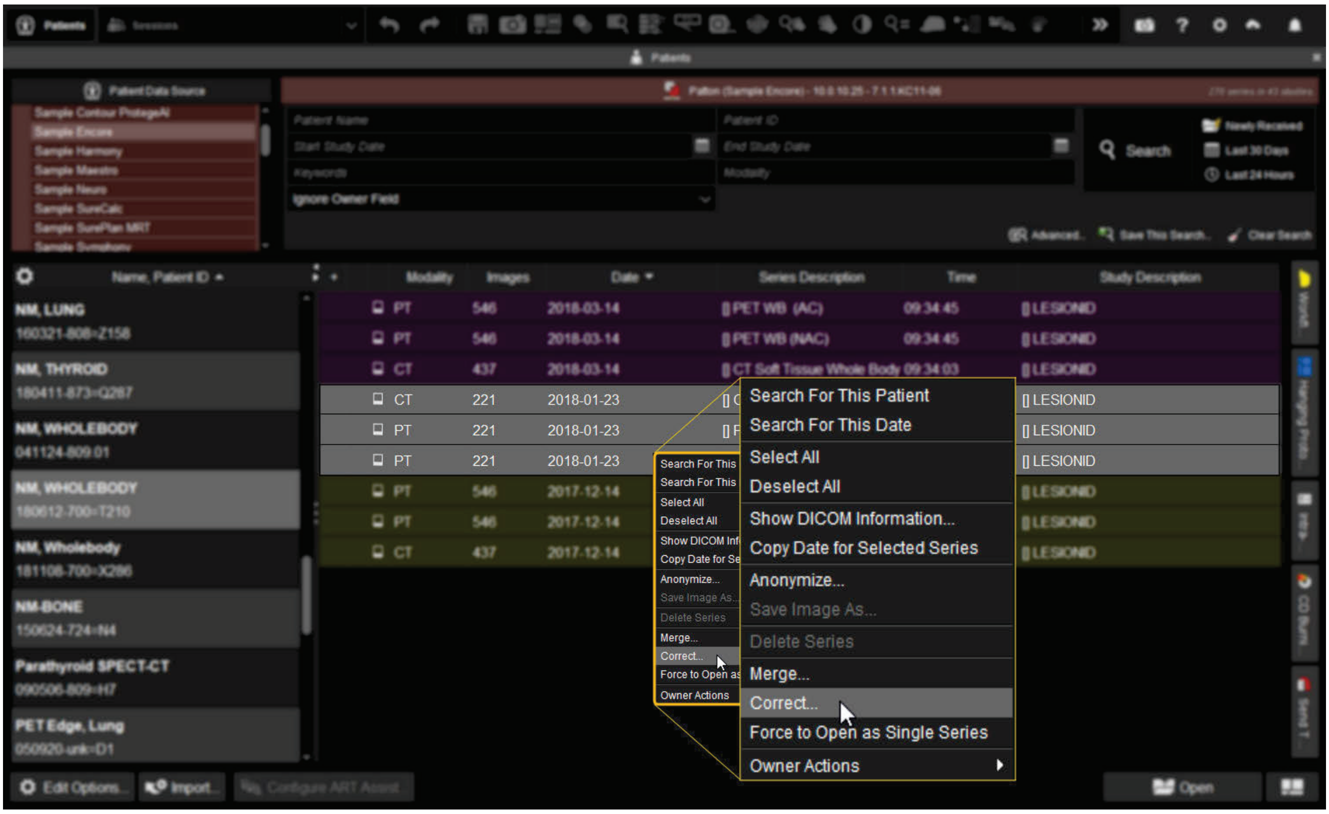
If the patient ID, patient name, or other data has been incorrectly or inconsistently entered, you can correct it in MIM®.

> **Important:** Correcting patient data creates new DICOM files, keeping the original data intact. It does not overwrite existing data or delete data.

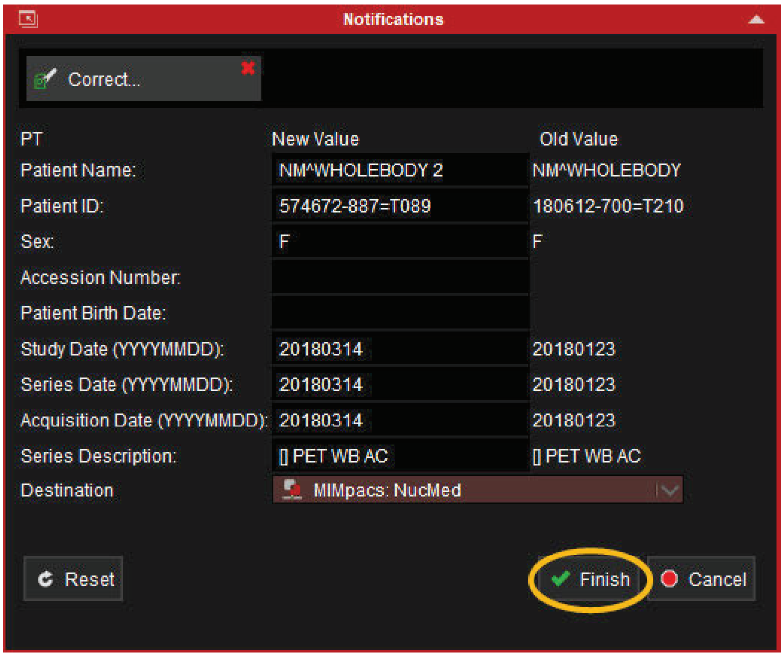
> **Important:** If a patient is listed multiple times in MIM due to different names, spellings, patient IDs, or other issues, see Merge Patients instead to align the data for all images.

Correct Data

1. With a patient selected, select the series that you want to correct.
2. Right-click on the selected series and select **Correct...**.



3. Edit the necessary fields in the **Correct...** notification window.
    - *If you are correcting one series,* select a save destination for the corrected file.
    - *If you are correcting multiple series,* continue clicking **Next** to review the data for each series. On the final screen, select a save destination for the corrected files.



PT	New Value	Old Value
Patient Name:	NM^WHOLEBODY 2	NM^WHOLEBODY
Patient ID:	574672-887=T089	180612-700=T210
Sex:	F	F
Accession Number:		
Patient Birth Date:		
Study Date (YYYYMMDD):	20180314	20180123
Series Date (YYYYMMDD):	20180314	20180123
Acquisition Date (YYYYMMDD):	20180314	20180123
Series Description:	[] PET WB AC	[] PET WB AC
Destination	MIMpacs: NucMed	

4. Click **Finish** to create new, corrected DICOM files in the selected destination.
5. If desired, delete the original, incorrect data after confirming that the correction was successful.

Merge Patients

MIMTD-628 • 07 Aug 2023

Overview

If patient IDs or patient names are incorrectly or inconsistently entered, the data is separated in MIM as if it were two different patients. For example, if you receive data from different institutions for the same patient with different patient IDs, the patient appears as two patients in MIM.

You can merge the data in MIM so that all of the series are grouped together for the same patient.

☆ **Important:** Merging patient data does not overwrite existing data or delete data. New files are created, keeping the original data intact.

☆ **Important:** Before merging patient data, ensure that one of the series has the desired DICOM information. If needed, first correct the DICOM data for one of the series, and then proceed with the merge. For more information on updating DICOM data, refer to Correct Patient Data or View and Edit DICOM Information.

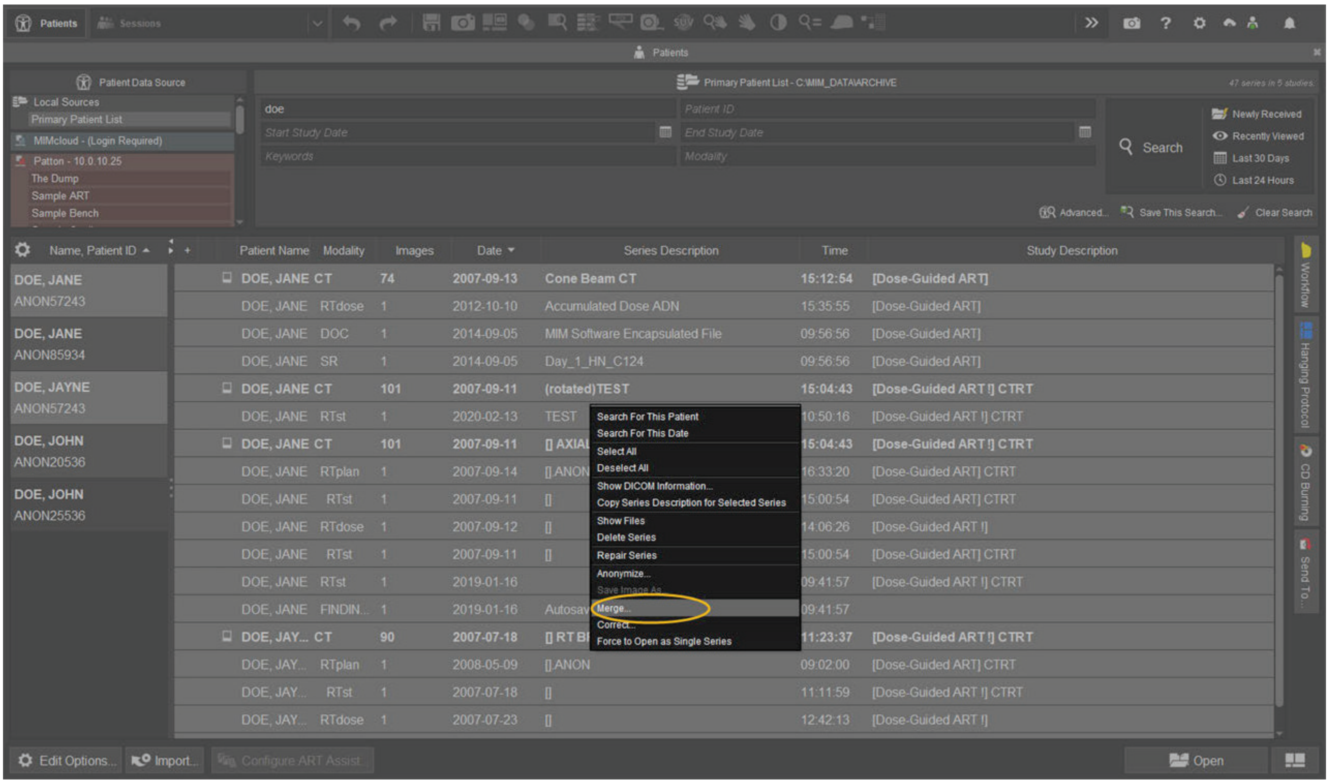
Combine Patient Records

To merge data:

1. Select the patients you would like to merge.
2. Select all of the records for the patient with the incorrect data and one record from the patient with the correct data.

   Tip: Left-click drag, or use Ctrl+Click (Windows®) or Command+Click (macOS®), to select multiple records.

3. Right-click on the series and select **Merge...** from the menu.



Patient Name	Modality	Images	Date	Series Description	Time	Study Description
DOE, JANE	**CT**	**74**	**2007-09-13**	**Cone Beam CT**	**15:12:54**	**[Dose-Guided ART]**
DOE, JANE	RTdose	1	2012-10-10	Accumulated Dose ADN	15:35:55	[Dose-Guided ART]
DOE, JANE	DOC	1	2014-09-05	MIM Software Encapsulated File	09:56:56	[Dose-Guided ART]
DOE, JANE	SR	1	2014-09-05	Day_1_HN_C124	09:56:56	[Dose-Guided ART]
DOE, JANE	**CT**	**101**	**2007-09-11**	**(rotated)TEST**	**15:04:43**	**[Dose-Guided ART !] CTRT**
DOE, JANE	RTst	1	2020-02-13	TEST	10:50:16	[Dose-Guided ART !] CTRT
DOE, JANE	**CT**	**101**	**2007-09-11**	**[] AXIAL**	**15:04:43**	**[Dose-Guided ART !] CTRT**
DOE, JANE	RTplan	1	2007-09-14	[].ANON	16:33:20	[Dose-Guided ART] CTRT
DOE, JANE	RTst	1	2007-09-11	[]	15:00:54	[Dose-Guided ART] CTRT
DOE, JANE	RTdose	1	2007-09-12	[]	14:06:26	[Dose-Guided ART !]
DOE, JANE	RTst	1	2007-09-11	[]	15:00:54	[Dose-Guided ART] CTRT
DOE, JANE	RTst	1	2019-01-16		09:41:57	[Dose-Guided ART !] CTRT
DOE, JANE	FINDIN...	1	2019-01-16	Autosav	09:41:57	
DOE, JAY...	**CT**	**90**	**2007-07-18**	**[] RT B**	**11:23:37**	**[Dose-Guided ART !] CTRT**
DOE, JAY...	RTplan	1	2008-05-09	[].ANON	09:02:00	[Dose-Guided ART] CTRT
DOE, JAY...	RTst	1	2007-07-18	[]	11:11:59	[Dose-Guided ART !] CTRT
DOE, JAY...	RTdose	1	2007-07-23	[]	12:42:13	[Dose-Guided ART !]

If you cannot select all of the patient data to merge at once (e.g., if you must use different search parameters to find it), you can perform the merge in two steps:

i. Select one set of data and select **Merge...** Make sure to leave the Notifications window open (although you can hide it).

ii. Search for and select the other set of data. Select **Merge...** again and the new data will be added to the original "merge" process, as seen in the Notifications window. You can repeat this step multiple times, searching for new data each time.

4. Select the desired information and options in the Notifications window.

   A. **Select the information to merge** — Choose **Merge patient information** for DICOM-standard, patient-level information or **Merge patient and study information** to also include study-level information. To see the differences, toggle between the options and review the changes in the next field.

   B. **Select a series with the correct DICOM information** — Use the dropdown menu to select the series with the correct DICOM. All other series will be edited to match this series.

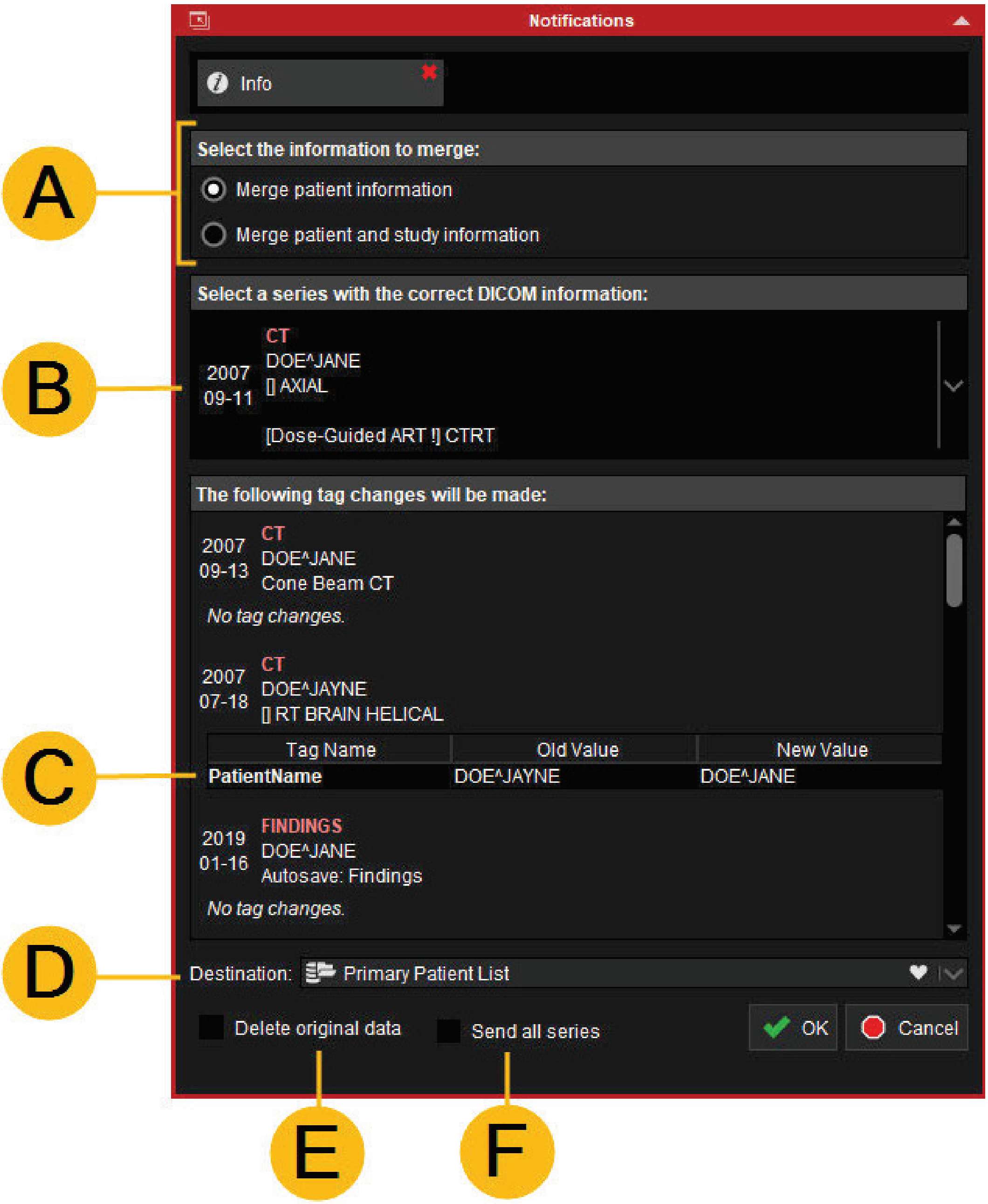
   C. **The following tag changes will be made** — Review the changes that will be made (you might need to scroll down). For each series that will be updated, review the **Tag Name**, **Old Value**, and **New Value**.

   D. **Destination —** Choose the location where you want the new series to be sent.

E. **Delete original data** — Select this option if you want the original data, with the "old" values, to be deleted. This option is disabled if you are merging patient sessions because the original data is necessary for the session to be reopened.

> **Important:** If deleted, the original data with its original values is no longer accessible in MIM unless the data is reimported.

F. *MIM 7.4 and later:* **Send all series** — Select this option if you want to send the series that were not updated in addition to the new series with the updated values to the selected destination. *MIM 7.3 and earlier:* This functionality is not available. Only the new series is sent. You can separately send the series that were not changed from the patient list.



Notifications

Info

Select the information to merge:

● Merge patient information

○ Merge patient and study information

Select a series with the correct DICOM information:

2007 09-11
CT
DOE^JANE
[] AXIAL
[Dose-Guided ART !] CTRT

The following tag changes will be made:

2007 09-13
CT
DOE^JANE
Cone Beam CT

No tag changes.

2007 07-18
CT
DOE^JAYNE
[] RT BRAIN HELICAL

Tag Name	Old Value	New Value
PatientName	DOE^JAYNE	DOE^JANE

2019 01-16
FINDINGS
DOE^JANE
Autosave: Findings

No tag changes.

Destination: Primary Patient List

☐ Delete original data ☐ Send all series

✓ OK ● Cancel

5. Click **OK** to merge the data and send it to the selected destination.

Set Owners on Series or Sessions

MIMTD-1107 • 24 Jul 2023

Overview

This feature is available for organizations that are using MIMpacs™ in Storage Server Mode, as described in Use a MIMpacs Server: Fundamentals.

You can optionally assign series or sessions to individual users or groups. The owner of a series or session is displayed in the patient list. You can also search for data by owner.

Contents

- Assign an Owner from the Patient List
- Assign an Owner when Saving a Session
- Search from the Patient List

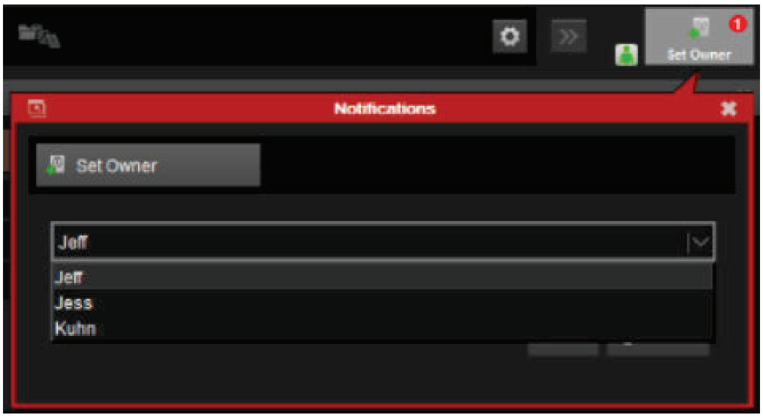
Prerequisites

- User logins enabled on the MIMpacs server. Refer to Support Network User Logins: Fundamentals for more information.
- Owners for series and sessions enabled on the MIMpacs server. Refer to Configure How Owners and Statuses Work for more information.

Assign an Owner from the Patient List

1. Right-click on a series or saved session in your patient list.
2. Select **Owner Actions** >> **Set Owner**. The Notifications window opens.

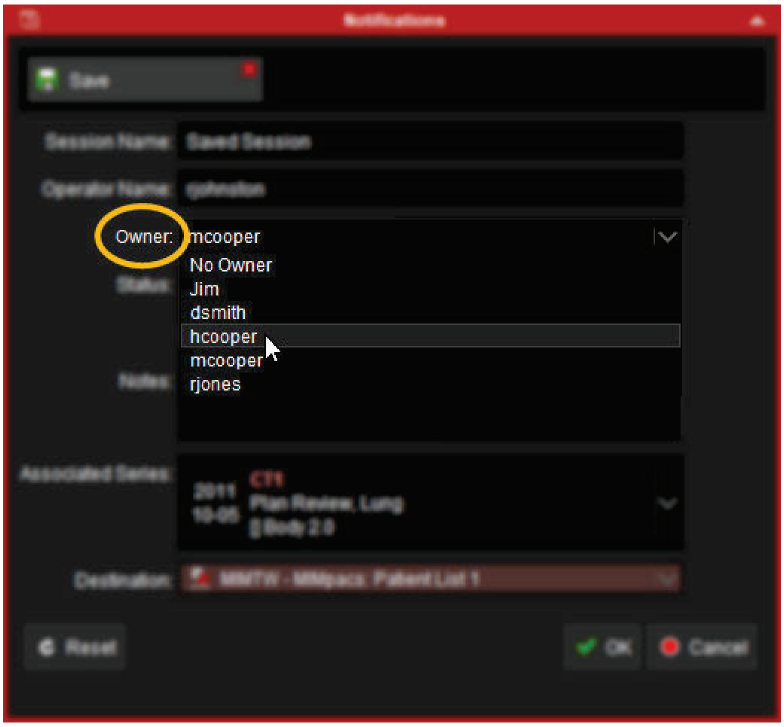
3. In the **Set Owner** field, select the person or group to own the series.



4. Click **OK**.

Assign an Owner when Saving a Session

When you save a session, the Save notification appears. Select the appropriate person or group in the **Owner** field.

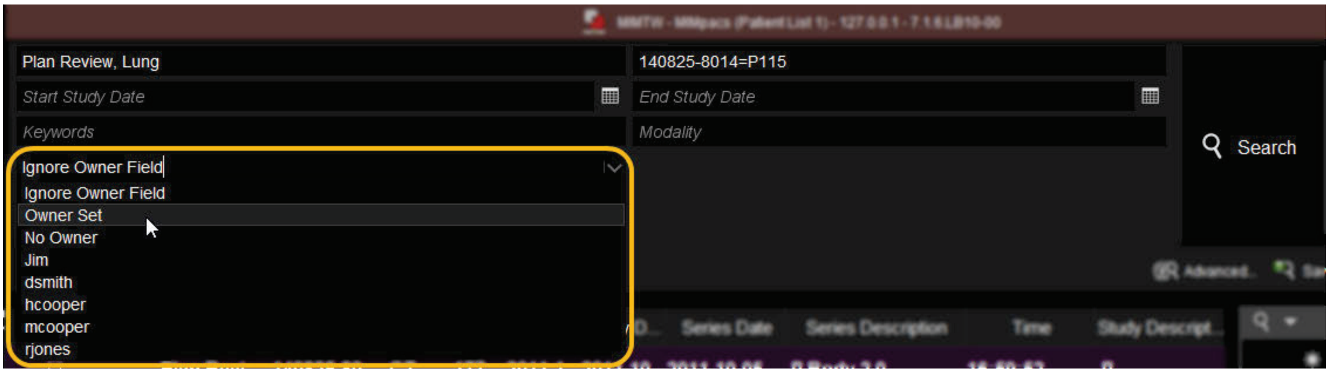

Owner: mcooper

Search from the Patient List

You can search the patient list for series or sessions based on owner.

Choose one of the following search options:

- **Ignore Owner Field** — The search returns all series regardless of owner.
- **Owner Set** — The search returns any series that has an owner assigned.
- **No Owner** — The search returns any series that does not have an owner assigned.
- Select a specific user or group — The search returns only the studies that the selected user or group is assigned.



Plan Review, Lung

140825-8014=P115

Ignore Owner Field

Tip: Users can save the search for an easily accessible worklist of sessions that they own.

Integrate with Third-Party Cardiac Software

MIMTD-866 • 09 May 2025

Overview

MIM Software® can integrate with the following third-party software packages to support cardiac studies:

- Cedars-Sinai Cardiac Suite
- Corridor4DM
- *MIM 7.4.70 and later:* Emory Cardiac Toolbox™.
  MIM 7.4 and earlier: This integration is not available.

At a high level, configuration involves the steps outlined below. Your MIM Implementation Specialist or MIM Site Development Manager will work closely with you on setting up this integration.

If you have additional questions or need further assistance, please contact MIM Software Support at support.mimsoftware.com.

Contents

- Set Up Integration with Cedars-Sinai Cardiac Suite
  - Install and License
  - Set Up in MIM
- Set Up Integration with INVIA Corridor4DM
  - Install and License
  - Set Up in MIM
- Set Up Integration with the Emory Cardiac Toolbox (MIM 7.4.70 and Later)
  - Install and License
  - Set Up in MIM
- Send a Study to the Third-Party Application
  - (Optional) Prepare Data by Masking
  - Open Cardiac Data with the Third-Party Application
- Send Back and Save an Image

Set Up Integration with Cedars-Sinai Cardiac Suite

Work with your MIM Implementation Specialist or MIM Site Development Manager to set up this integration.

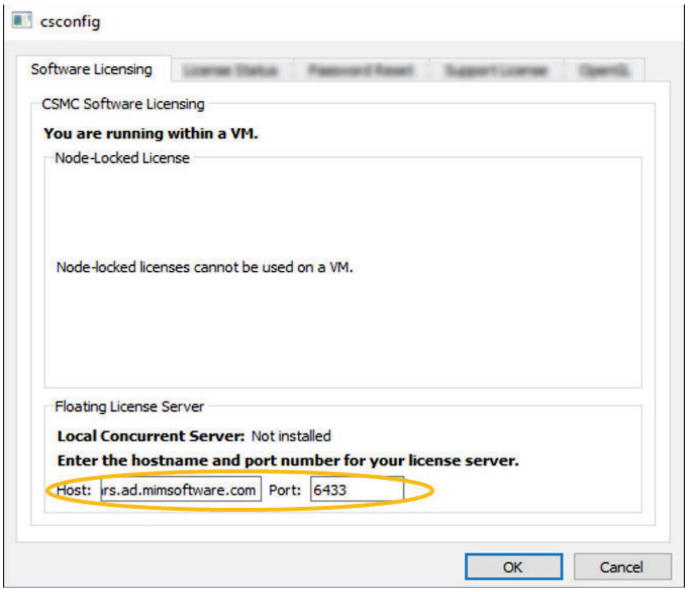
Go to https://www.thecardiacsuite.com/ifu/ and download the CSMC Cardiac Suite User Manual for the Cardiac Suite 2017.25 package for information about the Cedars application.

Install and License

If your organization is using a central MIMpacs™ server in Storage Server Mode, install and license the Cedars application on that machine, and then install the application on the client workstations and point them to your server machine. If your organization does not have a central MIMpacs server, install and license the application on each client workstation.

Work with your MIM representative to complete the following:

1. Download the Cedars installer ZIP file to the MIMpacs server and/or client workstation. The Cedars 2017 package is used for MIM 6.9 and later versions.
2. Extract the install files and run CSMC_Setup.exe on the MIMpacs server and/or client workstation.
3. Work with MIM Software Support to request and obtain a license file.
4. If you are using a central MIMpacs server:
   i. On client workstations, open the csconfig window for licensing.
   ii. In the **Host** and **Port** fields, enter the IP address of the MIMpacs server and the port (typically 6433).



You are running within a VM.

Node-locked licenses cannot be used on a VM.

Local Concurrent Server: Not installed

Enter the hostname and port number for your license server.

Host: rs.ad.mimsoftware.com Port: 6433

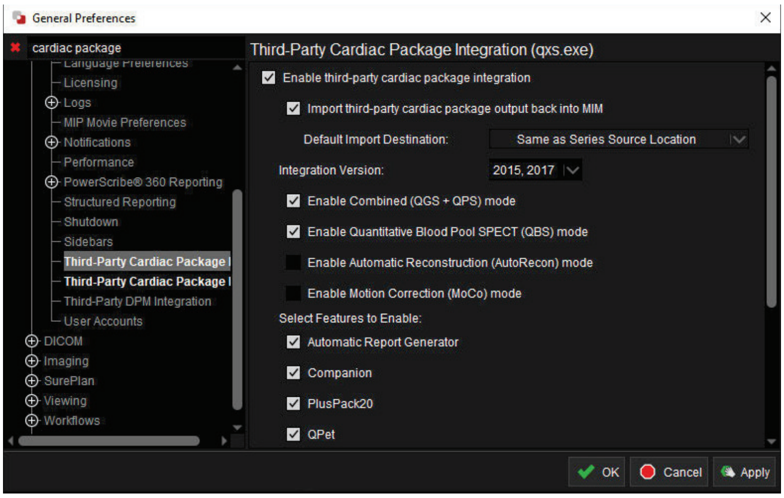
   iii. Click **OK** to save the changes and close the window.

Set Up in MIM

If you have user logins enabled, log in as an administrator to edit site defaults for all workstations at once. If you do not have user logins enabled, complete this configuration on each client workstation where you installed the Cedars application.

Work with your MIM representative to complete the following:

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Select **General Preferences** and search for **"cardiac package"**. Select **Third-Party Cardiac Package Integration (qxs.exe)** on the left side.
3. Select **Enable third-party cardiac package integration**.
4. Select **Import third-party cardiac package output back into MIM**.
5. Under **Integration Version**, select the modes that Cedars is licensed for.



Third-Party Cardiac Package Integration (qxs.exe)

☑ Enable third-party cardiac package integration

☑ Import third-party cardiac package output back into MIM

Default Import Destination: Same as Series Source Location

Integration Version: 2015, 2017

☑ Enable Combined (QGS + QPS) mode

☑ Enable Quantitative Blood Pool SPECT (QBS) mode

☐ Enable Automatic Reconstruction (AutoRecon) mode

☐ Enable Motion Correction (MoCo) mode

Select Features to Enable:

☑ Automatic Report Generator

☑ Companion

☑ PlusPack20

☑ QPet

6. Enable **Use shared configuration directory** and select a shared folder on the server or a shared network drive that all users can access. Make sure that:
   - The folder name ends in **Conf**.
   - Read/write access is enabled for the folder.
7. Click **OK** to save the changes and close the window.

Set Up Integration with INVIA Corridor4DM

Work with your MIM Implementation Specialist or MIM Software Support to set up this integration.

Go to https://inviasolutions.com/user-reference-guides/ and download the 2024 Corridor4DM User's Guide for information about the 4DM application.

Install and License

If your organization is using a central MIMpacs server in Storage Server Mode, install and license the 4DM application on that machine, and then install the application on the client workstations and point them to your server machine. If your organization does not have a central MIMpacs server, you need to install and license the application on each client workstation.

Work with your MIM representative to complete the following:

1. Download the 4DM installer ZIP file to the MIMpacs server and/or client workstation.
2. Extract the install files and run Corridor4DM_Installer.exe on the MIMpacs server and/or client workstation.
3. Work with MIM Software Support to request and obtain a license file.
4. If you are using a central MIMpacs server:
    1. On client workstations, run C:/Program Files (x86)/Invia/Corridor4DM/Licensing Manager.exe.
    2. Enter the IP address of the MIMpacs server and the port.

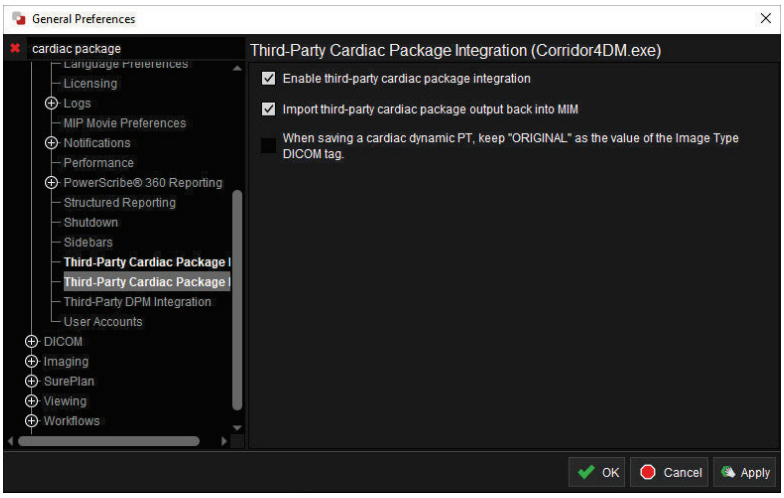
Set Up in MIM

If you have user logins enabled, log in as an administrator to edit site defaults for all workstations at once. If you do not have user logins enabled, complete these steps on each client workstation where you installed the 4DM application.

Work with your MIM representative to complete the following:

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Select **General Preferences** and search for **"cardiac package"**. Select **Third-Party Cardiac Package Integration (Corridor4DM.exe)** on the left side.
3. Select **Enable third-party cardiac package integration**.

4. Select **Import third-party cardiac package output back into MIM**.



Third-Party Cardiac Package Integration (Corridor4DM.exe)

☑ Enable third-party cardiac package integration

☑ Import third-party cardiac package output back into MIM

☐ When saving a cardiac dynamic PT, keep "ORIGINAL" as the value of the Image Type DICOM tag.

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

Set Up Integration with the Emory Cardiac Toolbox (MIM 7.4.70 and Later)

Work with your MIM Implementation Specialist or MIM Software Support to set up this integration.

Go to https://www.syntermed.com/client and download the Emory Toolbox User Manual for information about the Emory application.

Install and License

The Emory Cardiac Toolbox application must be installed and licensed on each client workstation where you plan to use the integration with MIM. If you have not yet installed the Emory Cardiac Toolbox or if you need to install and license the application on additional client workstations, contact Syntermed support for assistance.

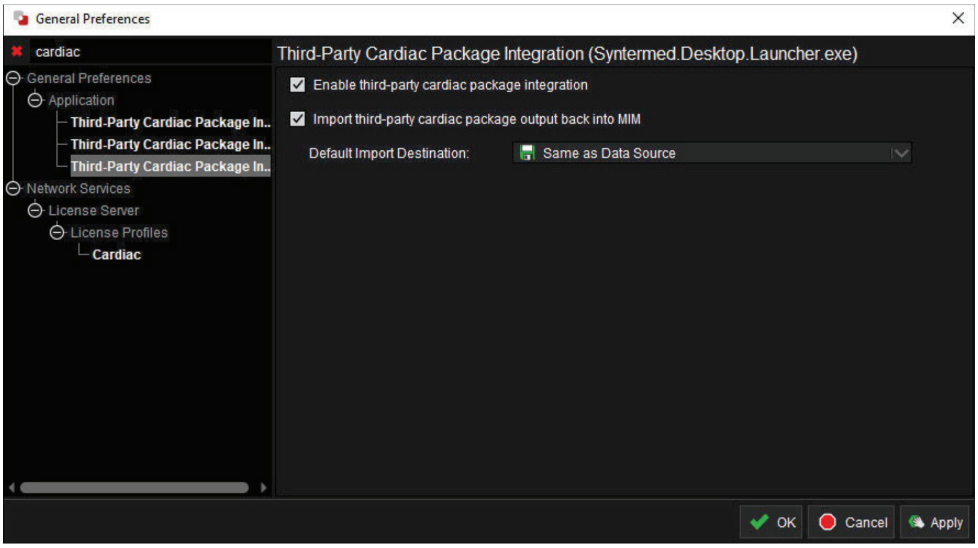
Set Up in MIM

Set up the MIM integration on each client workstation where the Emory Cardiac Toolbox (version 4.2) is installed.

Work with your MIM representative to complete the following:

1. Click the Settings ⚙ button in the upper-right corner of MIM. Select **General Preferences** and search for **"cardiac package"**.
2. Select **Third-Party Cardiac Package Integration (Syntermed.Desktop.Launcher.exe)** on the left side.
3. Select **Enable third-party cardiac package integration**.

4. Select **Import third-party cardiac package output back into MIM**.
5. Keep the **Default Import Destination** set to **Same as Data Source** so that the output that is sent to MIM is saved to the same patient list from which it was originally sent. Alternatively, use the dropdown to select a different save location.



Third-Party Cardiac Package Integration (Syntermed.Desktop.Launcher.exe)

☑ Enable third-party cardiac package integration

☑ Import third-party cardiac package output back into MIM

Default Import Destination: Same as Data Source

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

Send a Study to the Third-Party Application

From MIM, users can open data in the cardiac software.

(Optional) Prepare Data by Masking

Tip: If masking was performed during the GEHC Cardiac Reconstruction workflow, masking does not need to be performed again.

Because the third-party cardiac packages perform image registration based on the hottest values in the image, you might want to remove any extra data so that non-cardiac values do not interfere.

1. In MIM, open the series from the patient list.
2. Use the **2D Brush** to manually contour areas of high activity outside of the heart.
3. Scroll a few slices and draw the contour again. Continue scrolling and contouring every few slices.
4. Click **Interpolate** to fill in the contour on the slices that you skipped.

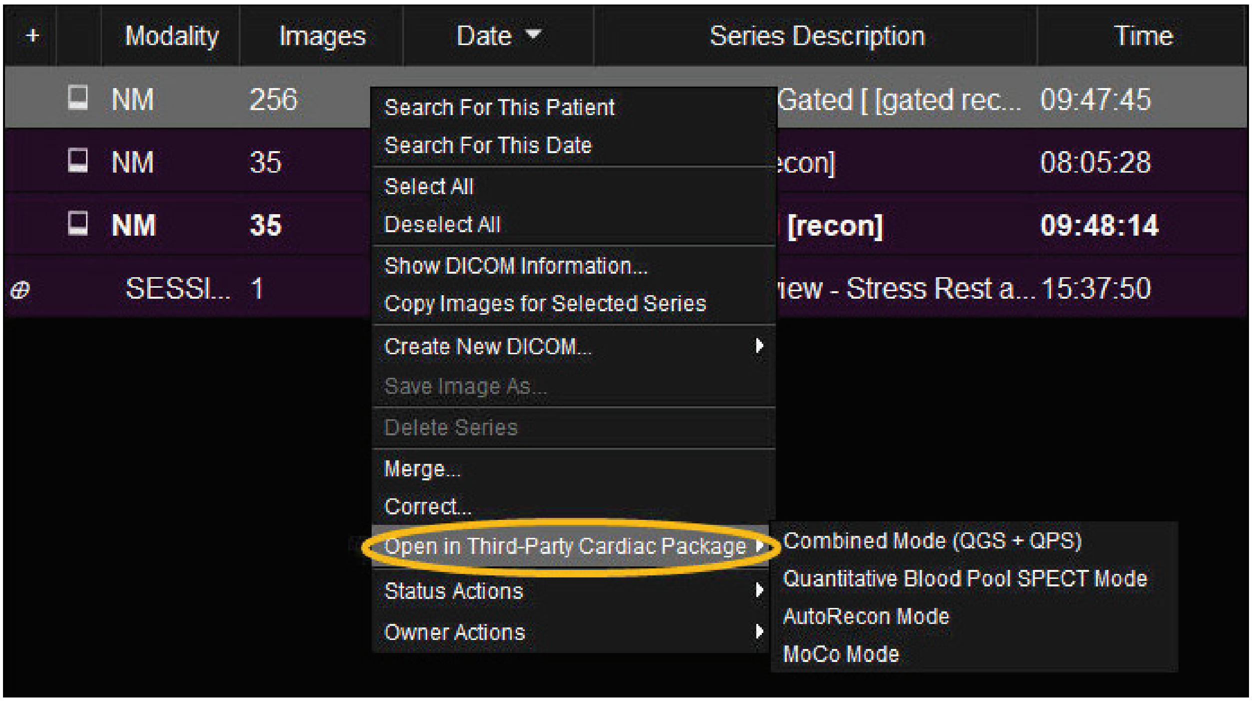
5. Select the **Mask** tool. In the Mask Volume notification, make sure that:
    - **Mask this contour** is selected.
    - **Mask to value** is set to **0.0**.
    - **Mask all dynamic frames** is selected.
6. Click **OK** to mask the ROI you drew.
7. As needed, repeat these steps to contour and mask other areas of high activity.

Tip: MIMcardiac® uses registration templates instead of registering based on the hottest values, so this step is not necessary.

Open Cardiac Data with the Third-Party Application

Tip: In addition to the steps below, you can open cardiac data with a third-party application in the GEHC Cardiac Reconstruction workflow.

1. Search the patient list for a cardiac study.
2. Right-click a series to open additional menu options:
    - *If you are using Cedars*, hover over **Open in Third-Party Cardiac Package** to expand the integration options menu and select the mode with which you want to open the series.



+	Modality	Images	Date	Series Description	Time
	NM	256		Gated [[gated rec...	09:47:45
	NM	35		econ]	08:05:28
	NM	**35**		**[recon]**	**09:48:14**
	SESSI...	1		iew - Stress Rest a...	15:37:50

- *If you are using 4DM*, select **Open in Third-Party Cardiac Package**.
- *If you are using Emory*, select **Open in Third-Party Cardiac Package Emory**.

3. Watch the Notifications window as MIM sends the selected series to the appropriate location and verify that the application launches.

Tip: Alternatively, you can launch an integration by selecting a series in the MIM patient list and opening the **Send To...** tab. Select the **Third Party Cardiac** package destination and then (if using Cedars) select the desired mode to run.

Send Back and Save an Image

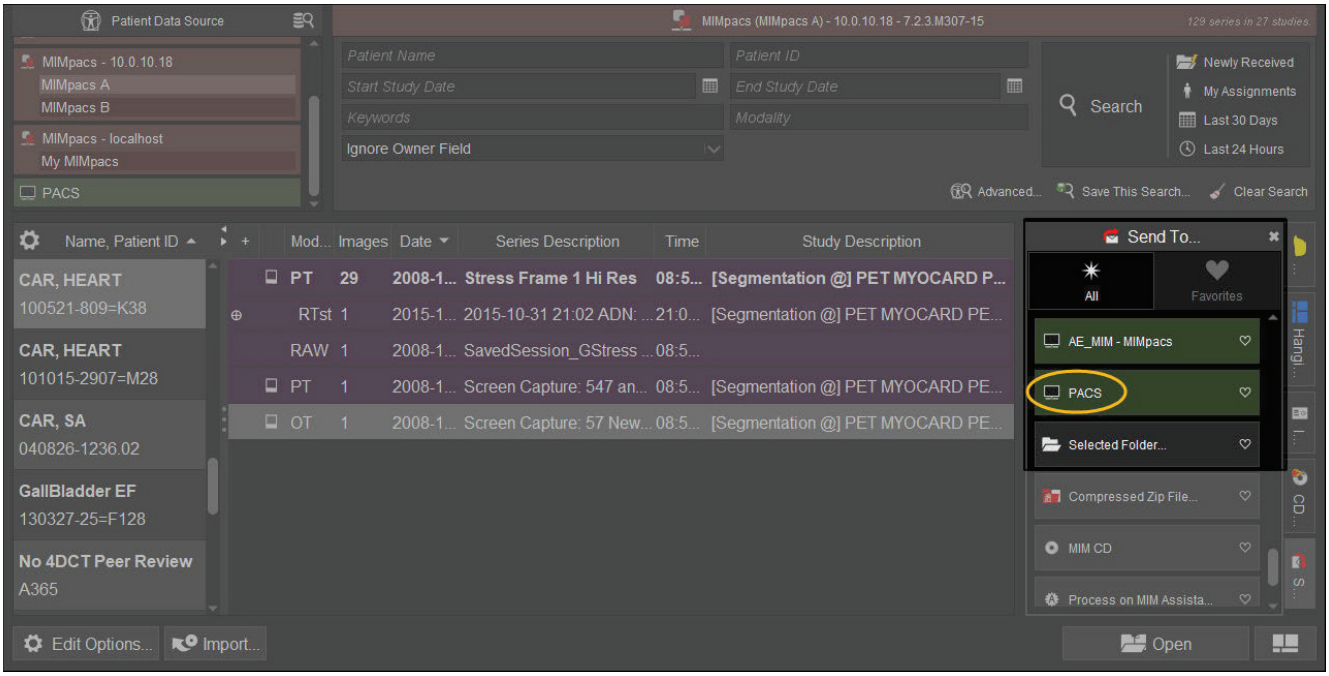
After processing the study in Cedars or 4DM, send the image back to MIM. The image appears alongside the raw study data in MIM as a screen capture (modality OT) on the patient list.

To send the data to MIM:

- *In Cedars*, click **Print** to save the image to MIM.
- *In 4DM*, click **Screen Capture** and click **Save**.
- *In Emory*, click the **Save** button to save the image to MIM.

After the data is back in MIM, you can save it to your PACS:

1. Select the images in the patient list.
2. On the **Send To...** tab, select your PACS destination (green).



Mod...	Images	Date	Series Description	Time	Study Description
PT	29	2008-1...	Stress Frame 1 Hi Res	08:5...	[Segmentation @] PET MYOCARD P...
RTst	1	2015-1...	2015-10-31 21:02 ADN: ...	21:0...	[Segmentation @] PET MYOCARD PE...
RAW	1	2008-1...	SavedSession_GStress ...	08:5...	
PT	1	2008-1...	Screen Capture: 547 an...	08:5...	[Segmentation @] PET MYOCARD PE...
OT	1	2008-1...	Screen Capture: 57 New...	08:5...	[Segmentation @] PET MYOCARD PE...

Appendix

Read PET/CTs and SPECT/CTs Quick Reference

MIMTD-1147 • 03 Jun 2024

Search for Patient Data

- Select the desired MIMpacs™ list (red data source) and search for your patient data.
- If you don't see the desired data, search from your PACS list (green data source) instead and move it to the MIMpacs list. See Query and Retrieve from PACS .

Load Patient Data

1. Select your desired series.
2. Find the workflow you wish to launch (e.g., PET/SPECT Review).
3. Double-click the workflow name.

Related: For information on opening patient data without using a workflow, see Find and Open Patient Data

Read Fusions

- Use the left and right arrow keys on your keyboard to switch between pages.
- Double-click a viewport to enlarge it. Double-click the viewport again to return to the previous view.
- Right-click in a viewport to display the radial menu containing tools such as **Zoom**, **Pan**, **Contrast**, **SUV**, linear measurement, and bi-axial measurement. You can also access these tools in the top toolbar.

Related: For information on adding and removing tools from the radial menu, see Access Tools: The Toolbar and the Radial Menu.

- If needed, use the fusion adjustment tools (**Blend**, **Translate**, **Rotate**, and **Scale**). In-depth information about these tools can be found in Adjust Fusions Manually.

Make Measurements

- To make a linear measurement, left-click drag.
- To make a bi-axial measurement, left-click drag to create the first line, then click on both sides of the new line to create the perpendicular measurement.

> **Tip:** To save time, use the **SUV**, **PET Edge**, and **PET Edge+** tools simultaneously with the measurement tools. See Use Measurement Tools for more information.

Measure SUV

1. Click the **SUV** button or use the S keyboard shortcut.
2. Left-click drag to move the sphere.
3. Right-click drag up/down to resize the sphere.
4. Click the green checkmark ✓ (either next to the sphere or on the right side of the viewport) to accept the sphere placement and create a finding. A "finding" is a measurement and its statistics.

Use PET Edge® +

1. Click the **PET Edge+** button.
2. Hover the cursor over the center of a lesion.
3. Left-click when the green checkmark appears to define the lesion's edges.

Use the Findings Sidebar

- View measurements and their statistics as they are created in the **Findings** sidebar.
- Save findings by clicking the **Save Findings** button at the bottom of the sidebar.

Work with Two Time Points

The L keyboard shortcut links/unlinks time points.

Save a Session

Click the **Save** button in the top toolbar, then select **Save Session...**.

Keyboard Shortcuts

General

S = SUV tool

R = Linear measurement tool

V = Cycle views (axial, sagittal, coronal)

Tab = Switch between a fusion and CT (fusion viewport only)

L = Link/unlink time points

Zoom

1 = Reset zoom

2 = Zoom in

3 = Zoom in more

4 = Zoom out

Contrast Presets

F1 = Soft Tissue (CT)

F2 = Lung (CT)

F3 = Bone (CT)

F4 = Brain (CT)

Default Keyboard Shortcuts

MIMTD-1363 • 26 Jul 2023

Overview

MIM® has many keyboard shortcuts that can help you save time and effort during viewing, contouring, creating measurements, and more.

Tip: Some keyboard shortcut commands may not be available in the MIM product that you use.

Related: To see more available keyboard shortcut commands, and to assign new keyboard shortcuts, click the Settings ⚙ button in the upper-right corner of MIM and go to **Keyboard Shortcuts...**. For detailed instructions, see Set Keyboard Shortcuts.

Related: If you want a personalized list of keyboard shortcuts, see Export a PDF of Keyboard Shortcuts for Reference.

Contents

- General
- Viewing, Localizing, and Scrolling
- Zoom
- Contrast
- Annotations, Measurements, and SUV
- Contouring
- Fusions
- Nuclear Medicine Processing
- Screen Captures
- Series Resolution

General

Command	Windows® Keyboard Shortcut	Mac® Keyboard Shortcut
Accept Notification	Enter	Return
Close Pages	Ctrl+W	Cmd+W
Find Tools	Ctrl+Shift+Space	Cmd+Shift+Space
Jump to Previous Page	J	J
New Session	Ctrl+N	Cmd+N
Next Page	Right	Right
Next Time Point	Alt+Right	Opt+Right
Previous Page	Left	Left
Previous Time Point	Alt+Left	Opt+Right
Redo	Ctrl+Y	Cmd+Y
Save Session	Ctrl+S	Cmd+S
Toggle Display Sidebar	D	D
Toggle Notifications	Back Slash	Back Slash
Undo	Ctrl+Z	Cmd+Z

Viewing, Localizing, and Scrolling

Command	Windows Keyboard Shortcut	Mac Keyboard Shortcut
Convert Ultrasound to 3D	Ctrl+U	Cmd+U
Create MIP Movie	M	M
Cycle Views	V	V
Image Grid Page Down	Page Down	Page Down
Image Grid Page Up	Page Up	Page Up
Jump to Localize	E	E
Link Manager	Ctrl+L	Cmd+L

Command	Windows Keyboard Shortcut	Mac Keyboard Shortcut
Link/Unlink	L	L
Localize	Escape	Escape
Localize to First	Ctrl+Page Up	Cmd+Page Up
Localize to Last	Ctrl+Page Down	Cmd+Page Down
Localize to Volume Center	Home	Home
Next Crosshair Color	Shift+Equals	Shift+Equals
Next Crosshair Style	Equals	Equals
Scroll Down	Down	Down
Scroll Up	Up	Up
Show Overlaid Info	Space	Space
Show Planes/Frames as Slabs	Alt+S	Opt+S
Toggle Anonymized Display	Shift+Slash	Shift+Slash
Toggle Crosshairs	Ctrl+Equals	Cmd+Equals
Toggle Dark/Light Background	Ctrl+I	Cmd+I
Toggle Viewport Patient Info	I	I

Zoom

Command	Windows Keyboard Shortcut	Mac Keyboard Shortcut
Reset Zoom	1	1
Zoom	Z	Z
Zoom Equalization	Ctrl+Alt+Shift+Z	Cmd+Opt+Shift+Z
Zoom In	2	2
Zoom In More	3	3
Zoom Out	4	4

Contrast

Command	Windows Keyboard Shortcut	Mac Keyboard Shortcut
Contrast	W	W
Contrast Preset: Bone (CT)	F3	F3
Contrast Preset: Brain (CT)	F4	F4
Contrast Preset: Lung (CT)	F2	F2
Contrast Preset: Soft Tissue (CT)	F1	F1
Manual Contrast	Alt+C	Opt+C
Quick Gamma	G	G

Annotations, Measurements, and SUV

Command	Windows Keyboard Shortcut	Mac Keyboard Shortcut
Annotate	N	N
Measure	R	R
SUV	S	S

Contouring

Command	Windows Keyboard Shortcut	Mac Keyboard Shortcut
Clean Single Slice	C	C
Contour and Dose Surface View	O	O
Contour CoPilot: Nearest Slice	Shift+0	Shift+0
Contour CoPilot: Next Slice	Shift+Down	Shift+Down
Contour CoPilot: Previous Slice	Shift+Up	Shift+Up
Cycle Active Contour	A	A
Discard CoPilot Suggestions	Backspace	Delete

Command	Windows Keyboard Shortcut	Mac Keyboard Shortcut
Erase Single Slice	X	X
Fill Single Slice	F	F
Next PET Edge+ Candidate Contour	Shift+Right	Shift+Right
Previous PET Edge+ Candidate Contour	Shift+Left	Shift+Left
PET Edge	P	P
Quick Save Contours	Ctrl+R	Cmd+R
Transfer All Contours	Ctrl+Shift+B	Cmd+Shift+B
Transfer Contour	Ctrl+Shift+T	Cmd+Shift+T

Fusions

Command	Windows Keyboard Shortcut	Mac Keyboard Shortcut
Calculate Fusion Metrics	Shift+M	Shift+M
Toggle Fusion Transparency	Tab	Tab

Nuclear Medicine Processing

Command	Windows Keyboard Shortcut	Mac Keyboard Shortcut
NM Processing	Ctrl+Shift+N	Cmd+Shift+N

Screen Captures

Command	Windows Keyboard Shortcut	Mac Keyboard Shortcut
Capture Screen 1	Shift+F1	Shift+F1
Capture Screen 2	Shift+F2	Shift+F2
Capture Screen 3	Shift+F3	Shift+F3
Capture Screen 4	Shift+F4	Shift+F4
Copy Screen Image to Clipboard	Shift+C	Shift+C

Command	Windows Keyboard Shortcut	Mac Keyboard Shortcut
Copy Viewport Image to Clipboard	Ctrl+C	Cmd+C

Series Resolution

Command	Windows Keyboard Shortcut	Mac Keyboard Shortcut
Change Series Resolution	Shift+R	Shift+R
Resample Series at Specified Resolution	Ctrl+Shift+R	Cmd+Shift+R

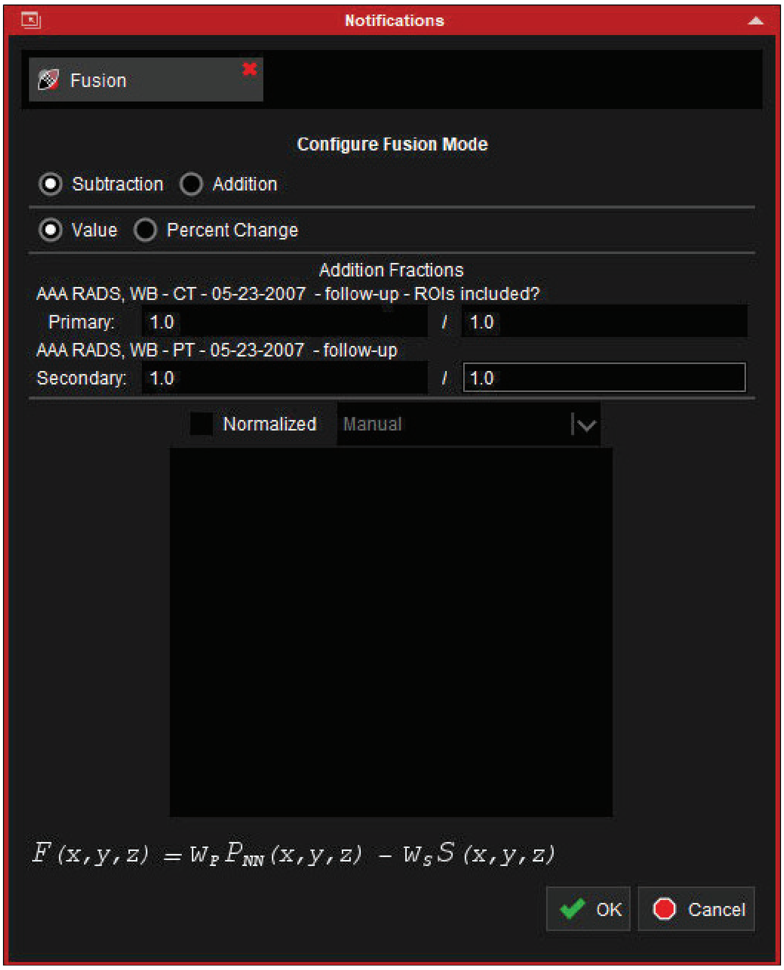
Fusion Image Subtraction Formulas: Technical Details

MIMTD-623 • 30 Aug 2023

Overview

The Subtraction fusion mode subtracts the secondary image from the primary image. To use it:

1. Open a fusion series and click the gear ⚙ on the right side of the viewport.
2. Select **Fusion Mode** >> **Subtraction or Addition...**.
3. Review the settings in the Notifications window that opens.



Configure Fusion Mode

● Subtraction ○ Addition

● Value ○ Percent Change

Addition Fractions

AAA RADS, WB - CT - 05-23-2007 - follow-up - ROIs included?

Primary: 1.0 / 1.0

AAA RADS, WB - PT - 05-23-2007 - follow-up

Secondary: 1.0 / 1.0

☐ Normalized Manual

$$F(x,y,z) = W_P P_{NN}(x,y,z) - W_S S(x,y,z)$$

You can choose:

- Whether to use **Value** or **Percent Change** subtraction
- Whether to use simple subtraction or **Normalized**

Related: Refer to View Images with Various Fusion Modes for more information about working with fusions.

Formulas Used for Subtraction

In the equations below:

- *F* is the voxel value of the output image
- *(x, y, z)* are the image coordinates
- *P(x, y, z)* is a sampling function of the primary image (uses nearest neighbor interpolation)
- *S(x, y, z)* is a sampling function of the secondary image (uses linear interpolation)
- W_P and W_S are values based on the intensity scaling controls (see Addition Fractions)
- U_P and U_S are normalization factors (see Contrast)

Value Subtraction

$$F(x, y, z) = W_p P(x, y, z) - W_s S(x, y, z)$$

Value Subtraction - Normalized

(see Apply Normalization)

$$F(x, y, z) = \frac{W_p}{U_p} P(x, y, z) - \frac{W_s}{U_s} S(x, y, z)$$

Percent-Change Subtraction

$$F(x, y, z) = \frac{P(x,y,z) - S(x,y,z)}{|S(x,y,z)|}$$

Percent-Change Subtraction - Normalized

(see Apply Normalization)

$$F(x, y, z) = \frac{(\frac{|U_S|}{U_P}) P(x,y,z) - S(x,y,z)}{|S(x,y,z)|}$$

Addition Fractions

Use the Addition Fractions section in the Fusion Notifications window to define the weights of W_P and W_S for intensity scaling. For example, if you decrease the weight of the primary image, the secondary image weighs heavier and more regions are subtracted (appear blue/negative).

Contrast

U_P and U_S are normalization factors based on the upper and lower bounds of the contrast window on the primary and secondary images. For example, the primary image has a contrast range of [0,100], and the secondary image has a contrast range of [0,300]. The value of U_P would be 1 (100/100 = 1) and the value of U_S would be 3 (300/100 = 3).

Apply Normalization

You can optionally select the Normalized setting to change the secondary image contrast window. The primary image is always normalized using the current contrast window of the primary image, regardless of whether you select the Normalized setting.

There are three options for normalization:

- **Manual** — The current contrast windows of the two images are used.
- **Auto** — MIM automatically determines the window to use for the secondary image.
- **Contour** — The values contained in a specified contour on the secondary image are used to determine the window to use for the secondary image.

The scaling factor for the secondary image is determined by applying a linear curve fit (iteratively reweighted least squares algorithm[1]). MIM uses the image's contrast to scale its intensity data. All intensity data that is lower than or equal to the image contrast lower bound is set to 0. All intensity data that is greater than or equal to the image contrast upper bound is set to 100. This scaling minimizes the mismatch between the series.

For example, the primary image has a contrast range of [0,100], and the secondary image has a contrast range of [0,300]. The secondary image contains twice as many counts as the primary, so the scaling factor is 2. With auto-normalization, the contrast range for the secondary image is normalized based on the scaling factor and is [0,150] ([0,300/2 = [0,150]). The value of U_S would then be updated based on this new contrast range to 1.5 (150/100 = 1.5).

Interpolation Levels

For the RGB fusion images displayed on screen, interpolation for both primary and secondary images is controlled by the interpolation level settings (Settings ⚙ >> **General Preferences** >> **Viewing** >> **Interpolation Levels**). The color corresponding to each voxel in the fusion and the calculated **Fusion Value** may not be the same because the color of each displayed voxel is based on the inerpolation applied.

Tip: Find the **Fusion Value** in the info viewport, or by hovering over a viewport and pressing the space bar.

[1] Reuter M, Rosas HD, Fischl B. Highly accurate inverse consistent registration: a robust approach. Neuroimage 2010; 53(4):1181-1196. doi:10.1016/j.neuroimage.2010.07.020

Assisted Alignment Fusion Method: Technical Details

MIMTD-622 • 9 Sep 2019

MIM Software provides Assisted Alignment which aligns images by maximization of mutual information. An optimization routine adjusts translation and rotation between the two series in order to maximize a mutual information metric. The mutual information metric is based on the intensities of overlapping voxels between the two objects that are being aligned and is partially based on joint entropy calculations between the volumes. The theory is that the ratio of intensity levels should vary little in regions of similar structures contained in the series. Therefore, the variability of this ratio should be minimized, and mutual information maximized, when the objects are aligned correctly. The advantage of this technique is that it is general in nature and can be used to align series of the same modality or different modalities.

It is possible for the optimization procedure to find a local and not a global maximum. In this instance, you can manually define an alignment that is close to an optimal alignment and initiate a new optimization by clicking the gear ⚙ button in the viewport and selecting **Run Rigid Assisted Alignment**.

PET Edge® & PET Edge®+ Tools: Technical Details

MIMTD-656 • 24 Oct 2023

6.1.3

MIM Software's PET Edge tool is based on finding object edges with spatial derivatives.[1] A point inside the object of interest and six points near the edge of the object are defined by the user by left-clicking near the center of the object and dragging to a point near the edge of the object. Five additional edge points are automatically determined at equal angular increments from the user-defined edge point. The software uses this initial edge definition to define a contiguous 3D set of edge points.

MIM Software's PET Edge+ tool requires a single, user-generated point inside of the lesion. An active contour algorithm is used to find the region of elevated activity corresponding to the lesion. Then, spatial derivatives are used to refine the boundaries and find the edges. PET Edge+ produces better and more consistent results than PET Edge. The active contour algorithm allows it to better segment lesions with complex shapes, such as non-ellipsoid lesions and lesions with a necrotic center. Additionally, this tool requires only a single user-generated point, instead of an ellipsoid, which reduces inter-user variability.

Both PET Edge and PET Edge+ are provided with MIM Encore®, MIM Maestro®, and MIM SurePlan™ licenses.

[1] Spatial derivatives are the change in image count levels as a function of location in the image. Assuming the object has different intensity than the background, there is a change in count level at the edge of the object.

SUV: Technical Details

MIMTD-696 • 18 Sep 2023

Overview

This topic contains technical details about SUV calculation in MIM®. For instructions on using the SUV tool, see Measure SUV.

Contents

- SUV Formulas
    - SUVbw
    - SUVlbm and SUVbsa
    - Additional Information
- SUV Peak
- SUV Total
- Total Glycolytic Activity (TGA), Total Lesion Glycolysis (TLG), Total Metabolic Index (TMI)
- Relevant DICOM Attributes

SUV Formulas

SUVbw

Standardized uptake value (SUV) is the ratio of the actual µCi/cc in a voxel to the expected µCi/cc in a voxel at that time, assuming that the radioactivity is uniformly distributed in the body and that the total radioactivity in the body decays only due to the physical half-life of the isotope. The density of body tissues is assumed to be equal to that of water so that expected µCi/cc equals (mCi of isotope injected * physical isotope decay at that time) / (kg weight of patient). Therefore,

$$SUV_{bw} = \frac{\mu Ci}{cc} \div \frac{mCi \times PD}{kg}$$

where µCi/cc is the measured µCi/cc, mCi is the amount of isotope injected, PD is the physical radioisotope decay from injection to scanning time, and kg is the patient weight in kilograms.

SUVlbm and SUVbsa

In addition to body-weight SUV (SUVbw), MIM can calculate lean-body-mass SUV (SUVlbm) and body-surface-area SUV (SUVbsa). The below formulas for calculating LBM and BSA are from Sugawara et al.[1] To Calculate SUVlbm or SUVbsa, MIM replaces the patient weight in kilograms in the SUVbw formula above with the LBM or BSA value:

$$LBM(female) = 1.07kg - 148(kg/cm)^2$$

$$LBM(male) = 1.1kg - coefficient(kg/cm)^2$$

$$BSA = 0.007184 \times kg^{.425} \times cm^{.725}$$

In these formulas, kg is the patient weight in kilograms, cm is the patient height in centimeters, and the coefficient is either 120 or 128. See LBM(male) Coefficient of 120 vs. 128 for more information.

Note: If the sex of the patient is "O," MIM uses the formula for LBM(male).

Additional Information

LBM(male) Coefficient of 120 vs. 128

By default, MIM uses a coefficient of 120 in calculations of SUVlbm for males. In MIM 6.8 and later, you can switch the SUVlbm coefficient for males to 128 instead of 120. To switch the coefficient, go to Settings ⚙ >> **General Preferences** and search for "lean body". Select **SUV** on the left side, and deselect **Use legacy lean body mass coefficient (120) for SUVlbm**.

The formula that uses a coefficient of 120 can be traced to an article by Morgan and Bray, in which the original LBM(male) formula is misquoted as using a coefficient of 120 instead of 128. Sugawara et al first incorporated LBM into SUV and cited the Morgan and Bray paper that contains the misquote. The version of the formula with 120 as the coefficient has been subsequently quoted in the PET literature. For more details, see *QIBA PET Profile Appendix H*.[2]

Note on SUV Activity Calculation

PET calculates the activity in a voxel as Bq/ml, which is emissions/sec/ml. To calculate SUV, MIM adjusts decay correction to be relative to the injection time. The uniform distribution of activity is calculated as Bq injected divided by the weight of the patient in g (Bq/g). Therefore, the ratio of SUV activity in a voxel relative to activity with uniform distribution is g/ml.

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[1] Y. Sugawara, K. R. Zasadny, A. W. Neuhoff, and R. L. Wahl. Reevaluation of the Standardized Uptake Value for FDG: Variations with Body Weight and Methods for Correction. Radiology. 1999 Nov;213(2):521-5.

[2] FDG-PET/CT Technical Committee. FDG-PET/CT as an Imaging Biomarker Measuring Response to Cancer Therapy, Quantitative Imaging Biomarkers Alliance, Version 1.05, Publicly Reviewed Version. QIBA, December 11, 2013. Available from: RSNA.ORG/QIBA.

SUV Peak

6.1.6

SUVpeak is calculated using the method defined in the PERCIST 1.0 guidelines.[3] The value of the spherical region is found by convolving a spherical kernel with the image data at the user's preferred resolution (either the volume's native resolution or 1x1x1 mm resolution). The value of each element in the kernel represents what percentage of the kernel's element is inside the sphere to account for partial voxels along the edge of the sphere. We consider the sphere to be outside of the contour if one of the kernel's elements is both partially in the sphere and its corresponding sample location on the volume is outside of the contour.

Note: To set SUV Peak resolution, go to Settings ⚙ >> **General Preferences** and search for **"peak"**. Select **Advanced** on the left side to access this setting.

SUV Total

SUVtotal is the sum of all activity over all voxels in an image:

$$SUV_{total} = SUV_{mean} \times number\ of\ voxels$$

6.1.6

Total Glycolytic Activity (TGA), Total Lesion Glycolysis (TLG), Total Metabolic Index (TMI)

The Total Glycolytic Activity (also known as the Total Lesion Glycolysis or Total Metabolic Index) of a region is calculated as the product of the region's volume and mean SUV.

Relevant DICOM Attributes

MIM uses the following DICOM tags for SUV calculation:

- Series Time or Acquisition Time
- Series Date or Acquisition Date
- Units
- Decay Correction
- Patient Weight
- Radionuclide Total Dose
- Acquisition Date/Time
- Radiopharmaceutical Start Date/Time
- Radionuclide Half Life

MIM uses these additional DICOM tags for SUVlbm and SUVbsa calculation:

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[3] Wahl RL, Jacene H, Kasamon Y, Lodge MA. From RECIST to PERCIST: evolving considerations for PET response criteria in solid tumors. J Nucl Med. 2009;50:122S–150S.

- Patient Sex
- Patient Size (height)

Note: If the above DICOM tags are not set or are incorrect, you can edit the DICOM tags. For more information, see Measure SUV.

Technical Details: ROI Interpreted Types in MIM®

MIMTD-1638 • 18 Dec 2023

Overview

MIM offers a variety of ROI types, as defined in the DICOM Standard section C.8.8.8.1[1]. The DICOM Standard section C.8.8.8.1 defines that the RT ROI Interpreted Type shall be used to describe the class of ROI.

Contents

- ROI Interpreted Types Used for Processing in MIM
- ROI Interpreted Types Not Used for Processing in MIM
- ROI Interpreted Type Usage in MIM
    - MIM Processing Procedures
    - MIM Workflow™ Commands

ROI Interpreted Types Used for Processing in MIM

MIM provides a number of ROI Interpreted Type attributes that are used for processing.

ROI Type in MIM	RT ROI Interpreted Type Attribute (3006,00A4)	Defined Term
PTV	PTV	Planning Target Volume (as defined in [ICRU Report 50])
CTV	CTV	Clinical Target Volume (as defined in [ICRU Report 50])
GTV	GTV	Gross Tumor Volume (as defined in [ICRU Report 50])
Organ	ORGAN	Patient organ
Marker	MARKER	Patient marker or marker on a localizer
Registration	REGISTRATION	Registration ROI

---

[1] NEMA PS3 / ISO 12052, Digital Imaging and Communications in Medicine (DICOM) Standard, National Electrical Manufacturers Association, Rosslyn, VA, USA (available free at http://www.dicomstandard.org/)

ROI Type in MIM	RT ROI Interpreted Type Attribute (3006,00A4)	Defined Term
External	EXTERNAL	External patient contour
Isocenter	ISOCENTER	Treatment isocenter to be used for external beam therapy

MIM provides three additional ROI Interpreted Types that do not come from the DICOM Standard section C.8.8.8.1.

ROI Type in MIM	RT ROI Interpreted Type Attribute (3006,00A4)	Defined Term
Epicardium	N/A	Exterior surface of the heart
Endocardium	N/A	Interior surfaces of the heart
None	N/A	No ROI Interpreted Type has been set

ROI Interpreted Types Not Used for Processing in MIM

There are a number of ROI Interpreted Type attributes included in MIM that are not used for processing. They can still be set for reference or for compatibility with other systems.

ROI Type in MIM	RT ROI Interpreted Type Attribute (3006,00A4)	Defined Term
Treated Volume	TREATED_VOLUME	Treated Volume (as defined in [ICRU Report 50])
Irrad. Volume	IRRAD_VOLUME	Irradiated Volume (as defined in [ICRU Report 50])
Bolus	BOLUS	Patient bolus to be used for external beam therapy
Avoidance	AVOIDANCE	Region in which dose is to be minimized
Contrast Agent	CONTRAST_AGENT	Volume into which a contrast agent has been injected
Cavity	CAVITY	Patient anatomical cavity
Dose Region	DOSE_REGION	ROI to be used as dose reference
Control	CONTROL	ROI to be used in control of dose optimization and calculation
Fixation	FIXATION	External patient fixation or immobilization device
Support	SUPPORT	External patient support device
Brachy Channel	BRACHY_CHANNEL	Brachytherapy channel
Brachy Accessory	BRACHY_ACCESSORY	Brachytherapy accessory device

ROI Type in MIM	RT ROI Interpreted Type Attribute (3006,00A4)	Defined Term
Brachy Src. App.	BRACHY_SRC_APP	Brachytherapy source applicator
Brachy Chnl. Shld.	BRACHY_CHNL_SHLD	Brachytherapy channel shield

ROI Interpreted Type Usage in MIM

There are a number of processes and workflow commands in MIM that utilize and require ROI Interpreted Type information to be set.

MIM Processing Procedures

Beam's Eye View (MIM Maestro®) — MIM utilizes contours with an "Isocenter" ROI Interpreted Type to match beam colors to isocenter point colors.

BED Contour Matching — MIM treats any contour with the "GTV", "CTV", or "PTV" ROI Interpreted Type as a tumor volume.

Brachytherapy Planning — MIM identifies the isocenter using the "Isocenter" ROI Interpreted Type. The skin contour is identified using the "External" ROI Interpreted Type. Depending on the brachy context (e.g., pre-op, post-op, breast, prostate, brain, or other), MIM looks to identify contours with the "Isocenter", "PTV", "CTV", "GTV", or "External" ROI Interpreted Type.

Cardiac Auto-Normalization (MIMcardiac®) — MIM auto-normalizes based on the myocardium. MIM determines the myocardium by identifying and subtracting the "Epicardium" and "Endocardium" ROI Interpreted Type contours.

Dose Constraints — MIM uses the ROI Interpreted Type as a fallback for the contour name. A contour can still match the dose constraint based on the set ROI Interpreted Type, even if the contour name doesn't match.

Fusion Point-Based Alignment — MIM aligns the images based on point contours with the "Registration" ROI Interpreted Type.

Load RTst — MIM loads any Elekta XiO® contours that have an "Organ" ROI Interpreted Type with the ROI Interpreted Type set to "None" instead. This is due to Elekta XiO inappropriately applying the "Organ" ROI Interpreted Type to tumor volume contours.

Plan Review (MIM Maestro) — MIM identifies the whole body contour by finding the "External" ROI Interpreted Type. If MIM is unable to identify the "External" ROI Interpreted Type, MIM defaults to searching for contour names containing "skin", "body", and "external".

Resetting Contrast — If the cardiac volume has the "Epicardium" ROI Interpreted Type, contrast is based on the contents of the epicardium contour, rather than being based on the color table.

Save RTst — *MIM 7.4 and later:* The setting **For compatibility with some treatment planning systems, write "patient" for the "ROI Observation Description" DICOM tag for structures of**

type External in saved RTstructs applies to "External" ROI Interpreted Type contours. *MIM 7.3 and earlier:* The setting **For planning system compatibility, save DICOM RTstructs with "patient" as the ROI Observation Description for structures of type External** applies to "External" ROI Interpreted Type contours.

Seed Constraint — MIM uses the ROI Interpreted Type as a fallback for the contour name. A contour can still match the seed constraint based on the set ROI Interpreted Type, even if the contour name doesn't match.

Surface Projection (Symphony LDR™ for Breast) — MIM identifies the contour with the "External" ROI Interpreted Type and creates a 3D rendering. Any contour set to the "PTV" or "CTV" ROI Interpreted Type is projected onto the 3D rendering.

Tile Overlay (MIM Symphony® for GammaTile®) — When MIM identifies a planning contour with the "PTV", "CTV", or "GTV" ROI Interpreted Type, a tile overlay is displayed.

MIM Workflow™ Commands

Capture Beam (MIM Maestro) — The "Show Targets Only" mode considers any contour with the "Isocenter" ROI Interpreted Type as a target. Additionally, any contour with the "PTV", "CTV", or "GTV" ROI Interpreted Type is considered a target.

Clip Dose Display to Contour — MIM generates a warning if the selected contour is not set to the "External" ROI Interpreted Type.

Contours From Seeds — MIM creates point contours with the "Marker"ROI Interpreted Type.

Crop to Avoid Contours — MIM defaults "Keep Inside" to true for contours with the "External" ROI Interpreted Type.

Contour Propagation — MIM sets contrast based on the contents of the Epicardium contour when propagating a contour that is set to the "Epicardium" ROI Interpreted Type.

Couch Removal — The command generates a warning if part of the body is removed. MIM identifies body contours by finding the "External" ROI Interpreted Type contour. If MIM is unable to identify the "External" ROI Interpreted Type contour, MIM defaults to searching for contour names containing "skin", "body", and "external".

Remove Overlap — If the hard-edge contour is not set to the "External" ROI Interpreted Type, removing the overlap removes parts within the contour. If the hard-edge contour is set to the "External" ROI Interpreted Type, removing the overlap removes parts outside the contour.

Save Isocenter RTPlan (MIM Maestro) — MIM treats point contours with the "Isocenter" ROI Interpreted Type as isocenters.

Expand/Contract Contours Tool: Technical Details

MIMTD-1587 • 16 Jan 2024

Overview

The Expand/Contract tool makes it easy to perform a variety of expansions or contractions on contours. This document explains how MIM® translates user input into a 3-dimensional contour adjustment.

Contents

- Background
- Expansion and Contraction Operations
- Error Analysis

Background

Voxel Grid

MIM models contours on an invisible 3-dimensional "contour voxel grid." The contour voxel grid covers the entire image volume. The spacing of the contour voxel grid is based on the voxel grid of the associated image series, but may vary from the image voxel grid in the xy-plane:

- Along the x- and y-axes, the contour voxel grid is created by subdividing the image voxels such that the resulting size of the contour voxels in those dimensions is less than or equal to the setting for **Minimum XY Plane Resolution**.
    - If the voxel size of a scan is already at or smaller than the Minimum XY Plane Resolution (e.g., a very high resolution CT), the image voxels are not subdivided. In this case, the contour voxels are the same size as the image voxels.
    - To change the Minimum XY Plane Resolution, go to **General Preferences** and search for "**Advanced**." The Minimum XY Plane Resolution is configurable in the **Advanced** window.
- Along the z-axis, the contour spacing matches the slice thickness of the associated image series.

Contour Delineation

When a contour is created, each voxel in the contour voxel grid is identified as either included in the contour volume or not included in the contour volume.

Conclusion

As a result of this modeling method, contours have a voxel size that may be smaller than the voxel size of their associated images. Contour voxel size determines how precisely MIM is able to delineate regions of the image series as being either inside or outside the contour.

Expansion and Contraction Operations

Summary

The expansion or contraction of contours in MIM is a morphological operation that takes two inputs:

- The first input is the binary-valued voxel data (i.e., included or not included, as described in Contour Delineation above) that defines the contour.
- The second input is a structuring element, also consisting of binary-valued voxels, which encodes the desired expansion or contraction.

Expansion is equivalent to a morphological dilation. Contraction is equivalent to a morphological erosion. Both operations are implemented in MIM as special cases of convolution. In keeping with the terminology associated with convolution, the structuring element is referred to as a kernel.

Kernel Generation

The basis for the kernel is an ellipsoid shape with radii equal in length to the distances specified for expansion or contraction in each axis of the image data. In order to execute the expansion or contraction algorithm the shape is voxelized as follows:

1. A voxel grid with spacing equal to the contour voxel size is created. This grid is approximately the same dimensions as the contour voxel grid, except that its dimensions are odd-numbered so that it always has a single central voxel.
2. The grid is positioned so that the middle of its central voxel is aligned with the center of the ellipsoid.
3. Each voxel of the grid is evaluated to determine the position of the center of the voxel relative to the ellipsoid’s surface.
    - If the voxel center is on the surface of, or inside the ellipsoid, the voxel is enabled (i.e., it is considered to be "in" the voxelized ellipsoid).
    - If the voxel center is outside the ellipsoid, the voxel is disabled (i.e., it is considered to be outside the voxelized ellipsoid).

This process results in a kernel that approximates the shape of the ellipsoid as closely as possible within the limits of the voxel resolution. Operations are performed by convolving the kernel with the contour voxel grid. The center of the kernel is positioned over each voxel in the contour voxel grid and the kernel is evaluated to determine whether that voxel should be included in the expanded or contracted contour:

To Perform an Expansion

The center of the kernel is positioned over each voxel of the original contour. In each position, any voxel in the contour voxel grid that corresponds to an enabled voxel in the kernel becomes part of the expanded contour. Portions of the kernel that fall outside the extents of the image are ignored.

To Perform a Contraction

The center of the kernel is positioned over each voxel of the original contour. In each position, if any enabled voxel in the kernel overlaps with a voxel in the contour voxel grid that is not included in the original contour, then the contour voxel at the center of the kernel is excluded from the contracted contour. Portions of the kernel that fall outside the extents of the image also cause the contour voxel at the center of the kernel to be excluded from the contracted contour.

Error Analysis

The precision with which expansion and contraction operations can be applied is constrained by the voxelized nature of contours in MIM. Due to the way it is generated, the surface of the kernel may be offset from the true ellipsoid surface by up to plus or minus one half the length of the contour voxel in each dimension.

Example: Consider the case where 5mm of expansion is requested on the z-axis of a series of images with 3mm slice spacing. The only options available to the expansion algorithm are to expand by 3mm or to expand by 6mm. Rounding to the nearest voxel boundary results in 6mm of expansion being applied.

When extended to three dimensions, the maximum amount of error resulting from an expansion or contraction is the result of taking the square root of the sum of the squared half-voxel length in each dimension.

$$MaxError = \sqrt{(\tfrac{1}{2}VoxelSizeX)^2 + (\tfrac{1}{2}VoxelSizeY)^2 + (\tfrac{1}{2}VoxelSizeZ)^2}$$

This corresponds to the worst-case scenario of the requested expansion or contraction distance placing the surface of the ellipsoid in the center of a voxel, with the voxelized approximation extending to the corner of the voxel.

Technical Details: Smooth Tool Calculations

MIMTD-1952 • 12 Jun 2024

The Smooth tool in MIM® uses a Gaussian smoothing algorithm. Starting from a large kernal size, the full width at half max (FWHM) parameter is determined iteratively. The iterative process repeats until one of the following occurs:

- The number of voxels in the smoothed contour is at least 95% of the original number of voxels.
- The percentage between two adjacent iterations is low enough that it is determined to be an insignificant change.
- The maximum number of iterations is reached.

After one of these criteria is reached, MIM runs Gaussian smoothing using the determined FWHM.

Statistics Definitions

MIMTD-1131 • 12 Jan 2023

Overview

Some statistics are available with specific MIM® licenses or via MIM Workflows™. For more information, please contact MIM Software Support at support.mimsoftware.com.

Related: For instructions on viewing and reporting statistics, see View Statistics.

Contents

- 2D Contour Statistics
- 3D Contour Statistics
- 2D & 3D Contour Statistics
- Other Statistics
- Contour Comparison Statistics
- Change Statistics
- Ratio Statistics
- Contour Subvoxels and Contour Subpixels

2D Contour Statistics

- **Area** — The area of a contour on a 2D series.
- **Pixel Count** — The total quantity of image pixels that a contour covers on a 2D series. This number can be fractional due to contour subpixels. For more information about contour subpixels, see Contour Subvoxels and Contour Subpixels below.

3D Contour Statistics

- **Integral Total** — The product of the contour's volume and the contour's mean value; for example, the product of a region's volume and mean SUV.

Tip: Integral total is equal to the **Total Glycolytic Activity** (TGA), also known as the **Total Lesion Glycolysis** (TLG) or **Total Metabolic Index** (TMI).

- **SUV Peak** — The mean value of the voxels in an SUV sphere.
- **Slice with Maximum Value** — The slice number (image number) of a series on which the max value within the contour is found. If multiple slices share the max value, the slice with the largest slice number is used.
- **Volume** — The number of voxels in a contour multiplied by the volume per voxel.
- **Voxel Count** — The total quantity of image voxels that a contour covers on a 3D series. This number can be fractional due to contour subvoxels. For more information about contour subvoxels, see Contour Subvoxels and Contour Subpixels below.

2D & 3D Contour Statistics

- **Centroid X** — The DICOM coordinate for the centroid of a contour on the x-axis.
- **Centroid Y** — The DICOM coordinate for the centroid of a contour on the y-axis.
- **Centroid Z** — The DICOM coordinate for the centroid of a contour on the z-axis.
- **DICOM Position X** — The X-position in the DICOM coordinate system of a point contour.
- **DICOM Position Y** — The Y-position in the DICOM coordinate system of a point contour.
- **DICOM Position Z** — The Z-position in the DICOM coordinate system of a point contour.
- **Max** — The maximum value contained within a contour. This uses the current data unit for a series. For example, the max SUV value within a contour for a PT, or the max HU value within a contour for a CT.
- **Mean** — The average value contained within a contour. For example, the average SUV value of a contour on a PT series.
- **Median** — The median value contained within a contour. If the number of contour subvoxels is even, then the average of the two middle values is used. For more information about contour subvoxels, see Contour Subvoxels and Contour Subpixels below.
- **Min** — The minimum value contained within a contour. This uses the current data unit for a series. For example, the min SUV value within a contour for a PT, or the min HU value within a contour for a CT.
- **Kurtosis** — A number that describes whether the data distribution within a contour has more outliers or fewer outliers relative to a normal distribution. Kurtosis is calculated based on contour histogram data. Each contour subvoxel is a sample. A normal distribution has a kurtosis of 3. Kurtosis values that are higher than 3 indicate fewer outliers than a normal distribution. Kurtosis values that are lower than 3 indicate more outliers than a normal distribution. For more information about contour subvoxels, see Contour Subvoxels and Contour Subpixels below.

- **Longest Diameter** — The farthest distance between two points on the surface of a contour. This statistic creates a line overlay that shows the diameter.
- **RECIST Long** — The length of the long axis of the region, as defined by RECIST criteria.
- **RECIST Short** — The length of the short axis of the region, as defined by RECIST criteria.
- **Regions** — The number of disjoint regions that a contour has.
- **Skewness** — A number that describes how symmetric the data is. Skewness is calculated based on contour histogram data. Each contour subvoxel is a sample. The number indicates whether the distribution of data is skewed left or right of mean. 0 means that the distribution of data is centered. For more information about contour subvoxels, see Contour Subvoxels and Contour Subpixels below.
- **Sphere Diameter** — The diameter of a sphere that has the same volume as the contour.
- **Standard Deviation** — The standard deviation, where each contour subvoxel is a sample. This uses the current data unit for a series. For more information about contour subvoxels, see Contour Subvoxels and Contour Subpixels below.
- **Std Dev Mean Ratio** — The ratio of the standard deviation to the reference contour's mean value.

Tip: This is also known as the **Coefficient of Variation**.

- **Total** — The sum of all values in all contour subvoxels, scaled by subvoxel volume / image voxel volume. For more information about contour subvoxels, see Contour Subvoxels and Contour Subpixels below.

Other Statistics

- **Angle** — A measure of the angle created with the Angle tool.
- **Frame Duration** — The time elapsed during data acquisition for the contour's frame. The value is read from the DICOM, not calculated.
- **Length** — The length of a line created with the Measure tool.
- **PI-RADS® Score** — PI-RADS is a system for classifying the malignancy of prostate cancer. To display this information, a PI-RADS value must already be assigned to the contour.

Contour Comparison Statistics

- **Dice Coefficient** — A measure of similarity between two contours:
  $2 \times \frac{volume\ of\ intersection\ of\ A\ and\ B}{volume\ of\ A + volume\ of\ B}$
- **Jaccard Coefficient** — A measure of similarity between two contours:
  $\frac{volume\ of\ intersection\ of\ A\ and\ B}{volume\ of\ union\ of\ A\ and\ B}$
- **Max Hausdorff Distance (HD)** — The maximum distance across all points on a surface and their closest point on another surface. Max Hausdorff distance in MIM corresponds to what is commonly

labeled "Hausdorff distance" in the medical literature. MIM also offers the following supplementary statistics that are calculated over the same point distances as max Hausdorff distance:

- **Min Hausdorff Distance**
- **Mean Hausdorff Distance** (also known as **Mean Distance to Agreement** or MDA)
- **Median Hausdorff Distance**
- **Standard Deviation Hausdorff Distance**.

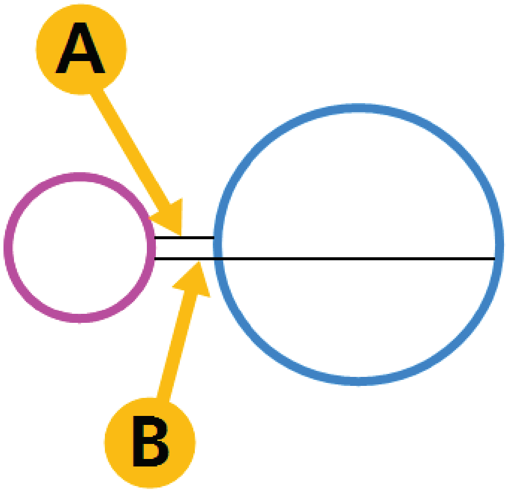
  To see an illustration of Hausdorff distance calculation at the slice level, see Hausdorff Distance Illustrations below.

> ☆ **Important:** Hausdorff distance calculations in MIM incorporate both the distances from points on surface A to surface B and the distances from points on surface B to surface A. This is commonly known as symmetric Hausdorff distance.

Hausdorff Distance Illustrations

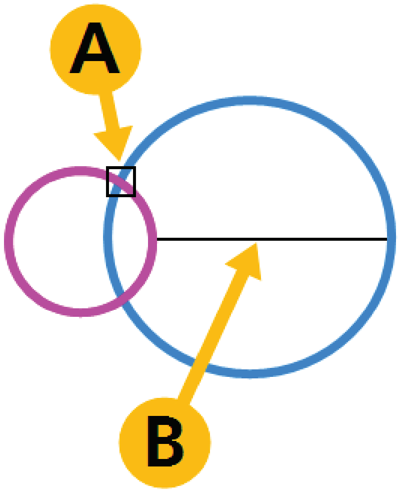
The following illustrations show how Hausdorff distance is calculated at the slice level.

No Overlap Between Contours



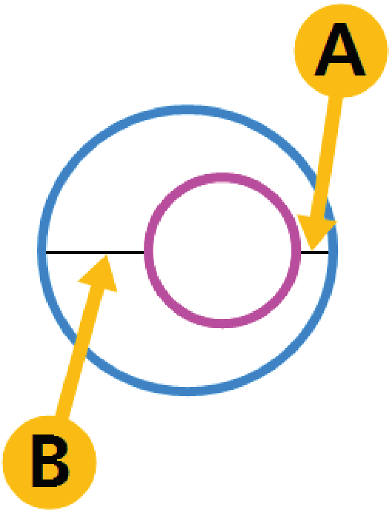
A. Min Hausdorff Distance
B. Max Hausdorff Distance

Partial Overlap Between Contours



A. Min Hausdorff Distance
B. Max Hausdorff Distance

Full Overlap Between Contours



A. Min Hausdorff Distance

B. Max Hausdorff Distance

Change Statistics

- **Baseline** — The time point from which other values are compared. By default, the baseline is the earliest time point.
- **[statistic] % Change** — The change in value from the baseline series as a percent of the baseline value:
  $\frac{(x-b)\times 100}{b}$, where x is the comparison value and b is the baseline value.
- **[statistic] Change** — The value minus the baseline series value:
  $x - b$, where x is the comparison value and b is the baseline value.

Ratio Statistics

- **Reference Contour** — The contour from which ratio statistics are calculated.
- **[statistic] Ratio** — The ratio of the given statistic value in that contour to the same statistic value in the reference contour.
- **[statistic] [statistic] Ratio** — The ratio of the first statistic value in the contour to the second statistic in the reference contour.

Contour Subvoxels and Contour Subpixels

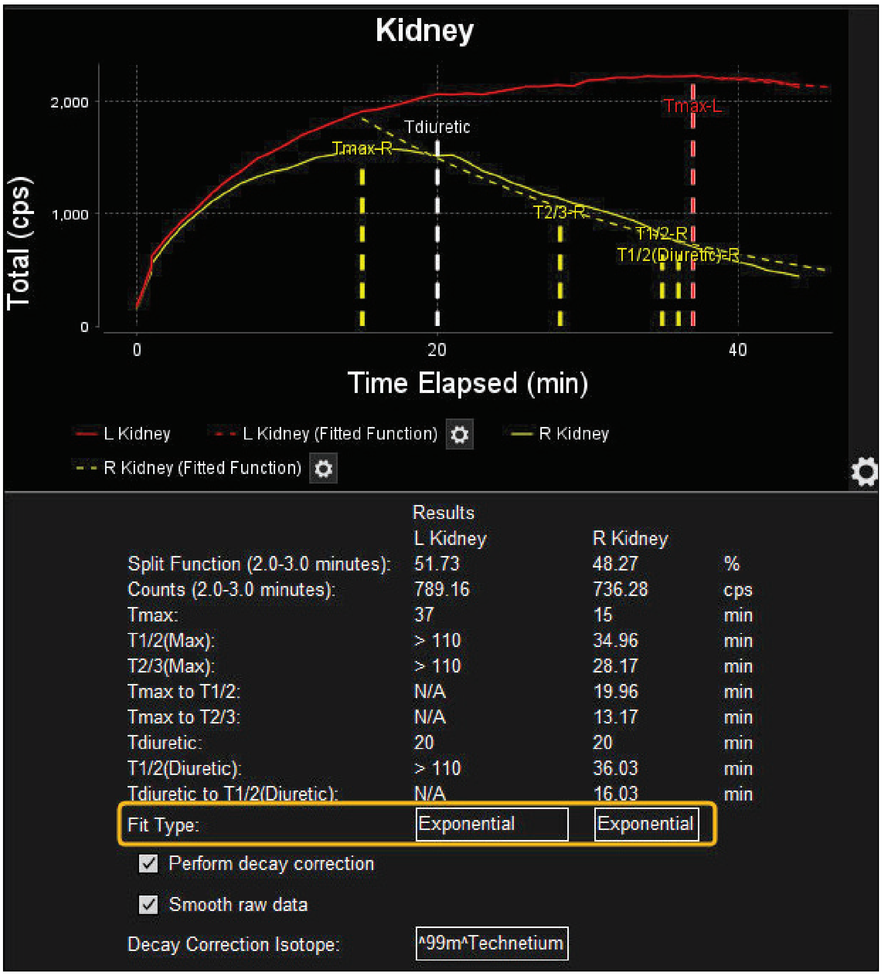
MIM uses contour subpixels or subvoxels to represent contours. Subpixels or Subvoxels are subdivisions of the image's pixels or voxels. The number of subdivisions varies depending on the image's pixel size or voxel size and the minimum resolution value. To check the minimum resolution value, go to Settings ⚙ >> **General Preferences** >> **Imaging** >> **Contouring** >> **Advanced** >> **Minimum XY Plane Resolution**.

Fit Type Calculations: Technical Details

MIMTD-1794 • 10 Jan 2024

Overview

Some workflows produce a graph display and apply a fit curve to the graph. For applicable workflows, you can use the **Fit Type** field below the graph to change the fit type.



	Results L Kidney	R Kidney	
Split Function (2.0-3.0 minutes):	51.73	48.27	%
Counts (2.0-3.0 minutes):	789.16	736.28	cps
Tmax:	37	15	min
T1/2(Max):	> 110	34.96	min
T2/3(Max):	> 110	28.17	min
Tmax to T1/2:	N/A	19.96	min
Tmax to T2/3:	N/A	13.17	min
Tdiuretic:	20	20	min
T1/2(Diuretic):	> 110	36.03	min
Tdiuretic to T1/2(Diuretic):	N/A	16.03	min
Fit Type:	Exponential	Exponential	

☑ Perform decay correction

☑ Smooth raw data

Decay Correction Isotope: ^99m^Technetium

In this example, the Renal MAG3 workflow shows a graph using an exponential fit type.

Tip: Click the gear ⚙ in the lower-right corner of the image and select **Emphasize Fit Curves** to dim the other lines on the graph. Or, select **Hide Fit Curves** if you don't want to see the fit curves.

Available Fit Types

Exponential

Extends the rate of change proportional to the initial amount of the quantity.

Hexic

A least-squares fit of a sextic polynomial to six points.

Linear

Provides a connect-the-dots fit between the data points provided. For values outside the domain of the points, it returns the Y value of the closest datapoint.

Quadratic

A least-squares fit of a cubic polynomial to four points.

Cubic

A least-squares fit of a cubic polynomial to three points.

Polynomial Spline

Fits spline functions between the points and interpolates between them.

Gaussian

Fits a peak (bell curve) to the data.

Harmonic

Fits a cosine function to the given data points. This fit type is unlikely to be useful for processed data.

Power

Custom function. This fit type is unlikely to be useful for processed data.

Motion Correction: Technical Details

MIMTD-966 • 25 Mar 2021

MIM uses a projection/reprojection fitting approach iteratively to correct motion during SPECT reconstruction.

In the first iteration, MIM reconstructs a 3D volume from the raw projection data using the user-specified reconstruction algorithm and parameters. MIM then reprojects the volume to generate reprojection data. During the reconstruction and reprojection procedure, most of the motion in the raw projection data should be averaged over all the projection views, so the reprojection data can be treated as motion-free data. MIM then aligns the raw projection data to the reprojection data to extract the motion in the raw data view-by-view. The raw projection data is then motion corrected.

In the second iteration, MIM uses the motion-corrected raw data from the first iteration to run reconstruction again. The reconstructed 3D volume from this iteration should eliminate most — if not all — of the motion in the original raw data.

SPECT/CT Reconstruction with SPECTRA Recon®

Aaron S. Nelson, MD Chief Medical Officer,
Benjamin P. Horstman Software Engineer Team Lead
MIM Software Inc.

Introduction

SPECTRA Recon® provides a vendor-neutral SPECT reconstruction suite that includes Ordered Subset Expectation Maximization (OSEM) reconstruction, CT-based attenuation correction, energy window-based scatter correction, and depth-dependent resolution recovery.

Ordered Subset Expectation Maximization (OSEM)

Ordered Subset Expectation Maximization (OSEM) is an iterative approach which is popular because it can be easily extended to model and account for imaging defects. OSEM is itself an optimization of Maximum Likelihood Expectation Maximization (MLEM).[1] The 3D OSEM method implemented in SPECTRA Recon was first described by Hudson et al. in 1994.[2] The pre-reconstruction and post-reconstruction filters provided for OSEM are Butterworth, Hamming, Hann, and Gaussian. The time saving method described by Wallis et al.[3] is also implemented whereby slices are rotated to be axis aligned during the projection steps.

Attenuation Correction

Attenuation is an effect that decreases the number of photons that are detected by the SPECT camera due to photon interactions with electrons. The amount of attenuation experienced by photons traveling through a material is dependent on the energy of the photons as well as the material composition and density. CT Hounsfield Units can be converted into a measure of the average attenuation per unit distance travelled by photons of a given energy. The SPECT reconstruction algorithm used in MIM corrects for the effects of attenuation with these CT-based attenuation estimates.

The CT scan is converted into a map of linear attenuation coefficients using the bi-linear fit conversion method.[4] The appropriate bi-linear fit curve is chosen based on the combination of CT camera, the energy of the CT scan in kVp, and the SPECT isotope energy in keV. If applicable, bi-linear fit curves can be input by the user.

The image used for attenuation correction can either be a CT scan in HU or the attenuation map (mu-map) output from the SPECT/CT camera. The CT scan used for attenuation correction can either be from a hybrid SPECT/CT scanner or from a separately acquired CT. It is important for the CT scan to rigidly align to the SPECT scan as well as possible. Otherwise, artifacts from attenuation correction could occur. After alignment of the SPECT and CT (internally, the CT is always aligned to the SPECT scan), the CT scan is interpolated to the SPECT scan resolution. Additional smoothing can optionally be applied to the CT scan. The bi-linear formula is then applied to convert the CT HU values to linear attenuation coefficients in units of 1/cm.

Scatter Correction

With SPECT imaging, a primary energy window is set to detect primary (non-scattered) photons of a known decay energy. A window must be used because of the finite energy resolution of the detector crystal. Because the window contains a range of energies, it's possible for photons scattered by the Compton effect to change direction but retain enough energy to be detected as primary photons. These scattered photons reduce image contrast.

Similarly, for multiple photopeak or multiple isotope imaging, it is possible for photons from higher energy emissions to "downscatter" into the primary energy window.

Scatter correction is a technique to estimate the fraction of scattered photons in the primary energy window and correct for it. SPECTRA Recon uses an energy window-based scatter correction method as originally described by Jaszczak et al in 1984.[5] However, to reduce bias, narrower energy windows can be used such as proposed by Ogawa et al.[6] SPECTRA Recon provides the ability to filter the scatter windows to reduce the noise inherent in narrow windows, as suggested by Ichihara[7] and Hashimoto.[8] The scatter contribution based on energy windows is automatically scaled using the trapezoidal estimation method as described by Ogawa,[6] where each pixel is scaled by the ratio of the main window to the scatter window. An additional experimentally determined scaling factor can also be applied to the scatter window.[9]

The scatter correction is not accomplished by subtraction of the scatter window as originally proposed,[5] rather, the scatter window is added to the denominator of the OSEM step.[10]

Both the Dual Energy Window (DEW)[9] and the Triple Energy Window (TEW)[7] methods are supported.

Resolution Recovery — Collimator Geometric Response

SPECT imaging cannot ascertain the direction of a detected photon. Therefore, absorbative collimators are used to create images. A parallel hole collimator consists of long thin holes in a dense material. This geometry causes photons to be blocked unless they are parallel to the hole. Because an infinite length collimator would acquire infinitely few counts, the collimated photons can only be approximately parallel. This limitation causes the acquired data to be blurred as distance from the detector increases.[11]

Three-dimensional depth-dependent resolution recovery is accomplished in both the forward and back projector[11] using the Gaussian Diffusion technique as proposed by McCarthy/Miller.[12] The collimator point-spread function is modelled as a Gaussian distribution but applied repeatedly in smaller increments as counts are diffused to and from the detector. The diffusion process is corrected for aliasing when the blur is small.[12,13] In this method, the hexagonal SPECT holes are treated as circles.[14,15] Collimator hole depth and width are included in a lookup table for various camera manufacturers. The "effective length" is calculated based on hole depth and SPECT isotope energy.[11] Additional collimators can be added to the lookup table if they are not included by default.

Motion Correction

The motion correction algorithm included in SPECTRA Recon is an iterative projection/reprojection fitting approach.[16] This iterative process is separate from the OSEM iterative process used for reconstructing the image. In the first iteration of motion correction, a 3D volume is reconstructed from the raw projection data using the user-specified reconstruction algorithm and parameters. The image volume is then reprojected to generate a reprojection dataset. During the reconstruction and reprojection procedure, most of the motion in the raw projection data should be averaged over all the projection views, allowing the reprojection data to be treated as motion-free data. The raw projection data is then aligned to the reprojection data to extract the motion in the raw data projection-by-projection. The raw projection data is then motion corrected. In the following iteration, the motion corrected raw data is used for the reconstruction. After running this for a few iterations, the reconstructed 3D volume should now be free from most, if not all, of the motion in the original raw data. In MIM, the default number of iterations for motion correction is 3, and this number is configurable if needed.

Decay Correction

As part of the reconstruction process, the data in each projection is decay corrected back to the earliest acquisition time listed in the DICOM. Optionally, the data can be decay corrected back to the time of injection if the time of injection is provided in the DICOM or input by the user.

SPECT Quantitation

Bq/ml conversion and SUV calculation are provided with MIM Software's SPECTRA Quant® product and detailed in a separate white paper, "Quantitative SPECT/CT Reconstruction with SPECTRA Quant."

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Quantitative SPECT/CT Reconstruction with SPECTRA Quant®

Aaron S. Nelson, MD Chief Medical Officer,
Benjamin P. Horstman Software Engineer Team Lead
MIM Software Inc.

Introduction

SPECTRA Quant® provides a vendor-neutral SPECT reconstruction suite that includes Ordered Subset Expectation Maximization (OSEM) reconstruction, CT-based attenuation correction, energy window-based scatter correction, depth-dependent resolution recovery, and Bq/ml conversion. SUVs can also be calculated from the activity concentration maps when the injected dose and time of injection and acquisition have been provided.

SPECTRA Quant must be added on to a MIM Encore® license, which includes SPECTRA Recon®. SPECTRA Quant thus extends SPECTRA Recon with the addition of Bq/ml conversion and SUV calculation.

SPECTRA Quant Applications: SPECTRA Quant can be used to generate quantified SPECT images to evaluate changes in bone and thyroid imaging. In addition, the quantitative imaging can be used as a key metric for dosimetry in therapeutic applications in Nuclear Medicine. This metric can be used for planning and reporting the molecular radiotherapy uptake distribution across the body (available in MIM SurePlan™ MRT).

SPECTRA Recon Applications: SPECTRA Recon's new technology enables users to make the most out of their current cameras today. The new reconstruction may improve image quality for cardiac imaging to help delineate the left ventricle as well as reduce the need for longer acquisitions. More precise activity will be present in exams to aide diagnosis for bone imaging, thyroid imaging, and pulmonary imaging. Quantitation in brain imaging may improve through more precise definition of normal activity such as the Striatum in DaTscan™ images.

Ordered Subset Expectation Maximization (OSEM)

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Resolution recovery is optional for SPECTRA Quant.

Motion Correction

The motion correction algorithm included in SPECTRA Recon is an iterative projection/reprojection fitting approach.[16] This iterative process is separate from the OSEM iterative process used for reconstructing the image. In the first iteration of motion correction, a 3D volume is reconstructed from the raw projection data using the user-specified reconstruction algorithm and parameters. The image volume is then reprojected to generate a reprojection dataset. During the reconstruction and reprojection procedure, most of the motion in the raw projection data should be averaged over all the projection views, allowing the reprojection data to be treated as motion-free data. The raw projection data is then aligned to the reprojection data to extract the motion in the raw data projection-by-projection. The raw projection data is then motion corrected. In the following iteration, the motion corrected raw data is used for the reconstruction. After running this for a few iterations, the reconstructed 3D volume should now be free from most, if not all, of the motion in the original raw data. In MIM, the default number of iterations for motion correction is 3, and this number is configurable if needed.

Decay Correction

As part of the reconstruction process, the data in each projection is decay corrected back to the earliest acquisition time listed in the DICOM. Optionally, the data can be decay corrected back to the time of injection if the time of injection is provided in the DICOM or input by the user.

Bq/ml Conversion

After a reconstruction is performed including the corrections described previously (attenuation, scatter, collimator geometric response, motion, decay), conversion into units of Bq/mL is the final step needed to produce absolute quantitative activity distributions. [17] The Bq/mL conversion factor (also known as a sensitivity factor) of the SPECT imaging system is determined in units of counts per second per megabecquerel (cps/MBq) and applied to a reconstruction to generate an output image in units of Bq/ml. This conversion factor is determined experimentally using the same corrections.

The procedure for calculating the conversion factor can be found in the NEMA protocols.[18] A cylindrical phantom large enough to avoid partial volume effects with a known activity concentration (in Bq/ml) is imaged. Attenuation and scatter effects are corrected for by using the same methods that will be used in clinical reconstructions. A large volume of interest (VOI) is placed in the reconstructed image. The start time of the acquisition, the duration of the acquisition, the half-life of the radionuclide, and the time of the activity calibration should be recorded and are used with the measured count rate from the VOI (in cps) to determine the SPECT imaging system conversion factor.

Standard Uptake Value (SUV) Calculation

After conversion of counts per second to Bq/ml using the Bq/ml conversion, SUV can then be calculated using the injected activity, time of injection, and patient's weight in kilograms (kg).

SUV is the ratio of the actual Bq/ml in a voxel to the expected Bq/ml in a voxel at that time assuming the radioactivity is uniformly distributed in the body and the total radioactivity in the body decays only due to the physical half-life of the isotope. The density of body tissues is assumed to be equal to that of water, so this "expected" Bq/ml used for normalization equals (Bq of isotope injected * physical isotope decay at that time) / (kg weight of patient). Therefore:

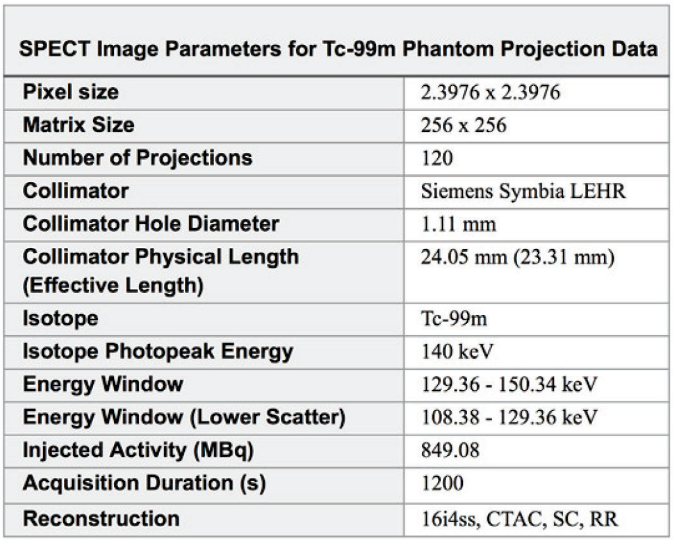
$$SUV = (Bq/ml) / (Bq*PD / kg),$$

where Bq/ml is the measured Bq/ml, Bq is the amount of isotope injected, PD is the physical radioisotope decay from injection to scanning time, and kg is the patient weight in kilograms.

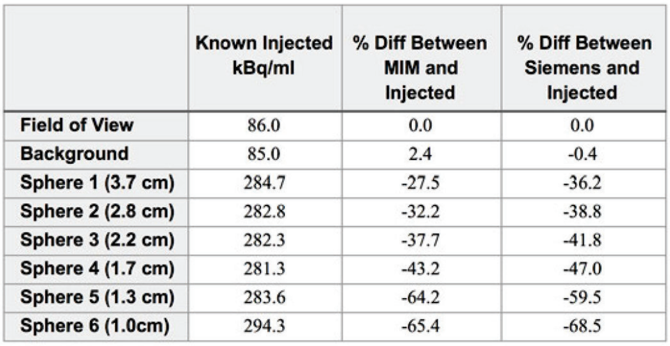
Quantitative Accuracy Testing Summary of SPECTRA Quant

^{99m}Tc Quantitative SPECT — Comparison to Known Injected Activity and Siemens OSEM Reconstruction (Test #1 - Accuracy)

A physical NEMA IEC Body Phantom was used to evaluate the quantitative accuracy of ^{99m}Tc reconstruction. A Bq/ml conversion factor is derived from the dataset that was acquired first, and then applied to each SPECT reconstruction. Applying this conversion factor to the scan from which it was derived is referred to in this document as self-calibration. Results are made in comparison to Siemens OSEM with similar reconstruction parameters. The error between the known and measured activities was calculated.



SPECT Image Parameters for Tc-99m Phantom Projection Data	
Pixel size	2.3976 x 2.3976
Matrix Size	256 x 256
Number of Projections	120
Collimator	Siemens Symbia LEHR
Collimator Hole Diameter	1.11 mm
Collimator Physical Length (Effective Length)	24.05 mm (23.31 mm)
Isotope	Tc-99m
Isotope Photopeak Energy	140 keV
Energy Window	129.36 - 150.34 keV
Energy Window (Lower Scatter)	108.38 - 129.36 keV
Injected Activity (MBq)	849.08
Acquisition Duration (s)	1200
Reconstruction	16i4ss, CTAC, SC, RR

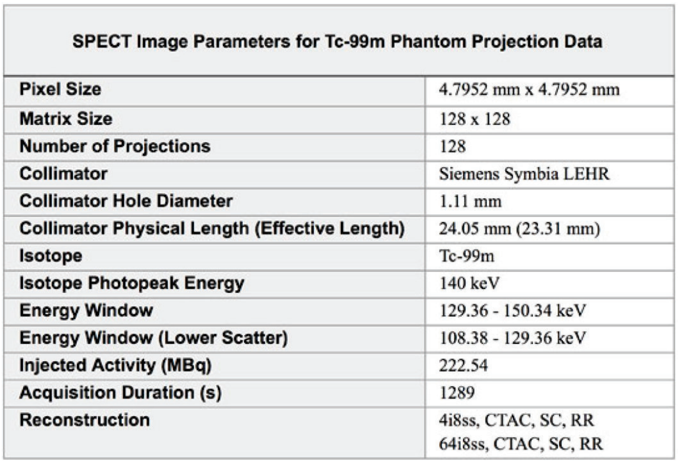


	Known Injected kBq/ml	% Diff Between MIM and Injected	% Diff Between Siemens and Injected
Field of View	86.0	0.0	0.0
Background	85.0	2.4	-0.4
Sphere 1 (3.7 cm)	284.7	-27.5	-36.2
Sphere 2 (2.8 cm)	282.8	-32.2	-38.8
Sphere 3 (2.2 cm)	282.3	-37.7	-41.8
Sphere 4 (1.7 cm)	281.3	-43.2	-47.0
Sphere 5 (1.3 cm)	283.6	-64.2	-59.5
Sphere 6 (1.0cm)	294.3	-65.4	-68.5

^{99m}Tc Quantitative SPECT — Comparison to Known Injected Activity and Siemens OSEM Reconstruction (Test #2 - Accuracy and Repeatability)

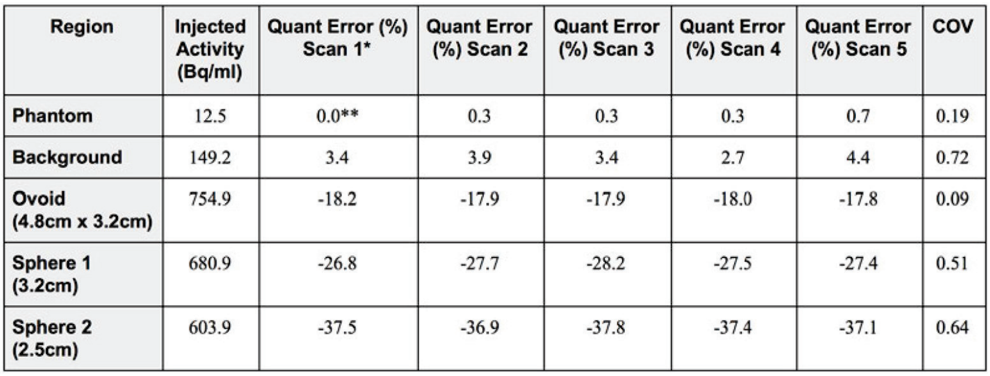
The purpose of this test is to validate ^{99m}Tc quantitative accuracy and consistency across multiple scans. This simultaneously validates the accuracy of MIM's decay correction tool. The 5 anthropomorphic torso phantom projection datasets used in this test were acquired over a period of 5 hours, acquired with the same camera, protocol, and phantom. In this test, a Bq/ml conversion factor is derived from the dataset that was acquired first, and then applied to each SPECT reconstruction. Applying this self-calibrated conversion factor to new scans allows us to evaluate the repeatability of results using a single Bq/ml conversion factor for the same camera, acquisition protocol, and reconstruction protocol. The activity concentration results in each scan should closely match the activity concentration injected into various structures of the phantom.

The first scan's self-calibration results are also compared to the self-calibration results achieved through a Siemens OSEM reconstruction with identical reconstruction parameters to ensure the quality of the reconstructions is equivalent. To match the Siemens OSEM reconstruction parameters, a Gaussian post-reconstruction filter is applied to MIM's reconstruction. Two additional reconstructions were performed; one with the same reconstruction parameters but no post-reconstruction smoothing to evaluate the effect of smoothing and the second with a higher number of iterations (64) to see how reconstructing closer to convergence affected the accuracy.



SPECT Image Parameters for Tc-99m Phantom Projection Data	
Pixel Size	4.7952 mm x 4.7952 mm
Matrix Size	128 x 128
Number of Projections	128
Collimator	Siemens Symbia LEHR
Collimator Hole Diameter	1.11 mm
Collimator Physical Length (Effective Length)	24.05 mm (23.31 mm)
Isotope	Tc-99m
Isotope Photopeak Energy	140 keV
Energy Window	129.36 - 150.34 keV
Energy Window (Lower Scatter)	108.38 - 129.36 keV
Injected Activity (MBq)	222.54
Acquisition Duration (s)	1289
Reconstruction	4i8ss, CTAC, SC, RR 64i8ss, CTAC, SC, RR

Quantitative Accuracy and Repeatability of ^{99m}Tc SPECT reconstruction using a Liver Phantom

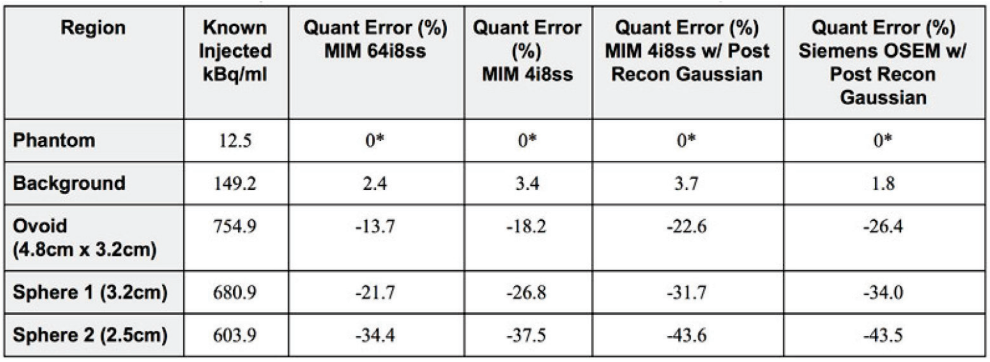


Region	Injected Activity (Bq/ml)	Quant Error (%) Scan 1*	Quant Error (%) Scan 2	Quant Error (%) Scan 3	Quant Error (%) Scan 4	Quant Error (%) Scan 5	COV
Phantom	12.5	0.0**	0.3	0.3	0.3	0.7	0.19
Background	149.2	3.4	3.9	3.4	2.7	4.4	0.72
Ovoid (4.8cm x 3.2cm)	754.9	-18.2	-17.9	-17.9	-18.0	-17.8	0.09
Sphere 1 (3.2cm)	680.9	-26.8	-27.7	-28.2	-27.5	-27.4	0.51
Sphere 2 (2.5cm)	603.9	-37.5	-36.9	-37.8	-37.4	-37.1	0.64

*Scan 1 was acquired at 2h 48min 1sec, Scan 2 was acquired at 3h 13min 26sec, Scan 3 was acquired at 3h 36min 15sec, Scan 4 was acquired at 3h 58min 55sec, and Scan 5 was acquired at 4h 21min 38sec.

**Scan 1 was used to derive the conversion factor for each of the imaging time points.

Quantitative Accuracy Comparison of ^{99m}Tc SPECT Reconstruction using a Liver Phantom

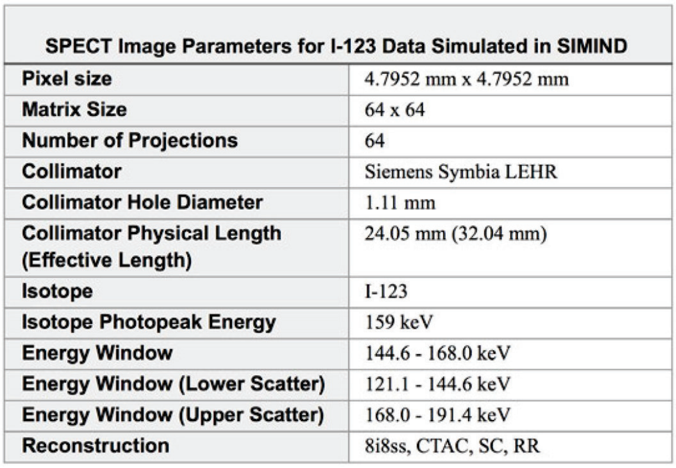


Region	Known Injected kBq/ml	Quant Error (%) MIM 64i8ss	Quant Error (%) MIM 4i8ss	Quant Error (%) MIM 4i8ss w/ Post Recon Gaussian	Quant Error (%) Siemens OSEM w/ Post Recon Gaussian
Phantom	12.5	0*	0*	0*	0*
Background	149.2	2.4	3.4	3.7	1.8
Ovoid (4.8cm x 3.2cm)	754.9	-13.7	-18.2	-22.6	-26.4
Sphere 1 (3.2cm)	680.9	-21.7	-26.8	-31.7	-34.0
Sphere 2 (2.5cm)	603.9	-34.4	-37.5	-43.6	-43.5

*Calibration was performed using self-calibration from the known injected activity in the entire phantom

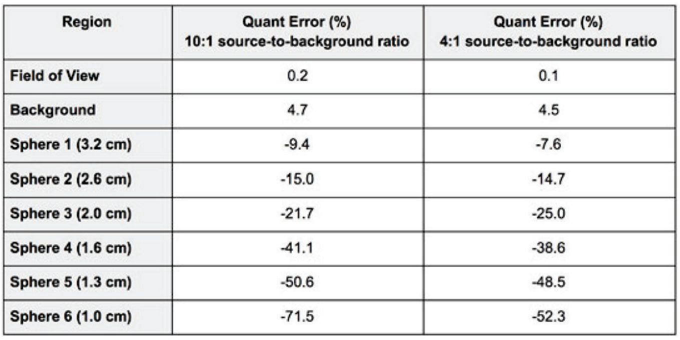
^{123}I Quantitative SPECT — Comparison to Known Injected Activity

The Monte Carlo SPECT simulation program SIMIND[19] was used to simulate ^{123}I projection datasets with clinical levels of Poisson noise from a NEMA IEC Body phantom with hot spheres. A simulated SPECT dataset without hot spheres was used as the calibration phantom to determine a Bq/ml conversion factor to use in this testing. Applying this conversion factor to new scans allows us to evaluate the repeatability of results using a single Bq/ml conversion factor for the same camera, acquisition protocol, and reconstruction protocol. The error between the known and measured activities was calculated.



SPECT Image Parameters for I-123 Data Simulated in SIMIND	
Pixel size	4.7952 mm x 4.7952 mm
Matrix Size	64 x 64
Number of Projections	64
Collimator	Siemens Symbia LEHR
Collimator Hole Diameter	1.11 mm
Collimator Physical Length (Effective Length)	24.05 mm (32.04 mm)
Isotope	I-123
Isotope Photopeak Energy	159 keV
Energy Window	144.6 - 168.0 keV
Energy Window (Lower Scatter)	121.1 - 144.6 keV
Energy Window (Upper Scatter)	168.0 - 191.4 keV
Reconstruction	8i8ss, CTAC, SC, RR

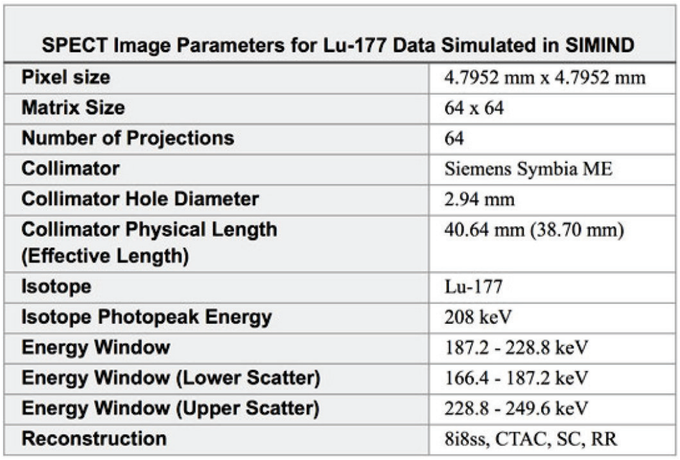
Quantitative Accuracy of ^{123}I SPECT reconstruction



Region	Quant Error (%) 10:1 source-to-background ratio	Quant Error (%) 4:1 source-to-background ratio
Field of View	0.2	0.1
Background	4.7	4.5
Sphere 1 (3.2 cm)	-9.4	-7.6
Sphere 2 (2.6 cm)	-15.0	-14.7
Sphere 3 (2.0 cm)	-21.7	-25.0
Sphere 4 (1.6 cm)	-41.1	-38.6
Sphere 5 (1.3 cm)	-50.6	-48.5
Sphere 6 (1.0 cm)	-71.5	-52.3

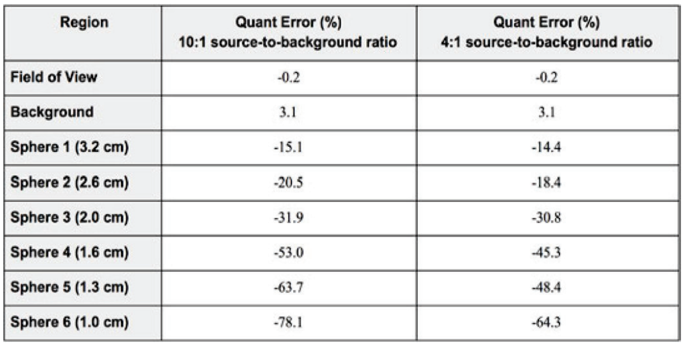
^{177}Lu Quantitative SPECT — Comparison to Known Injected Activity

SIMIND was used to simulate ^{177}Lu projection datasets with clinical levels of Poisson noise from a NEMA IEC Body phantom with hot spheres. A simulated SPECT dataset without hot spheres was used as the calibration phantom to determine a Bq/ml conversion factor to use in this testing. Applying this conversion factor to new scans allows us to evaluate the repeatability of results using a single Bq/ml conversion factor for the same camera, acquisition protocol, and reconstruction protocol. The error between the known and measured activities was calculated.



SPECT Image Parameters for Lu-177 Data Simulated in SIMIND	
Pixel size	4.7952 mm x 4.7952 mm
Matrix Size	64 x 64
Number of Projections	64
Collimator	Siemens Symbia ME
Collimator Hole Diameter	2.94 mm
Collimator Physical Length (Effective Length)	40.64 mm (38.70 mm)
Isotope	Lu-177
Isotope Photopeak Energy	208 keV
Energy Window	187.2 - 228.8 keV
Energy Window (Lower Scatter)	166.4 - 187.2 keV
Energy Window (Upper Scatter)	228.8 - 249.6 keV
Reconstruction	8i8ss, CTAC, SC, RR

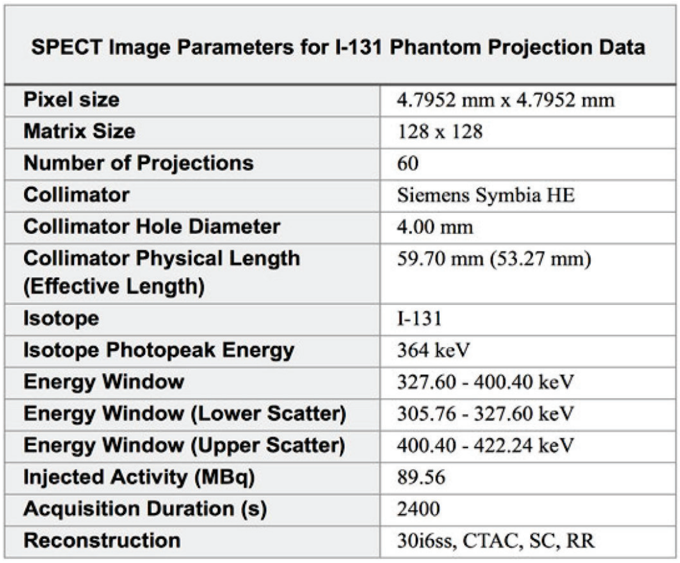
Quantitative Accuracy of ^{177}Lu SPECT reconstruction



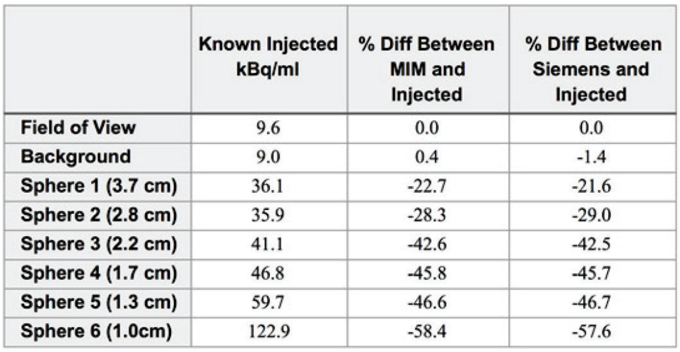
Region	Quant Error (%) 10:1 source-to-background ratio	Quant Error (%) 4:1 source-to-background ratio
Field of View	-0.2	-0.2
Background	3.1	3.1
Sphere 1 (3.2 cm)	-15.1	-14.4
Sphere 2 (2.6 cm)	-20.5	-18.4
Sphere 3 (2.0 cm)	-31.9	-30.8
Sphere 4 (1.6 cm)	-53.0	-45.3
Sphere 5 (1.3 cm)	-63.7	-48.4
Sphere 6 (1.0 cm)	-78.1	-64.3

I-131 Quantitative SPECT — Comparison to Known Injected Activity and Siemens OSEM Reconstruction

A physical NEMA IEC Body Phantom was used to evaluate the quantitative accuracy of ^{131}I reconstruction. The conversion factor from counts to Bq/ml was calculated by self-calibration. Results are made in comparison to Siemens OSEM with similar reconstruction parameters. The error between the known and measured activities was calculated.



SPECT Image Parameters for I-131 Phantom Projection Data	
Pixel size	4.7952 mm x 4.7952 mm
Matrix Size	128 x 128
Number of Projections	60
Collimator	Siemens Symbia HE
Collimator Hole Diameter	4.00 mm
Collimator Physical Length (Effective Length)	59.70 mm (53.27 mm)
Isotope	I-131
Isotope Photopeak Energy	364 keV
Energy Window	327.60 - 400.40 keV
Energy Window (Lower Scatter)	305.76 - 327.60 keV
Energy Window (Upper Scatter)	400.40 - 422.24 keV
Injected Activity (MBq)	89.56
Acquisition Duration (s)	2400
Reconstruction	30i6ss, CTAC, SC, RR



	Known Injected kBq/ml	% Diff Between MIM and Injected	% Diff Between Siemens and Injected
Field of View	9.6	0.0	0.0
Background	9.0	0.4	-1.4
Sphere 1 (3.7 cm)	36.1	-22.7	-21.6
Sphere 2 (2.8 cm)	35.9	-28.3	-29.0
Sphere 3 (2.2 cm)	41.1	-42.6	-42.5
Sphere 4 (1.7 cm)	46.8	-45.8	-45.7
Sphere 5 (1.3 cm)	59.7	-46.6	-46.7
Sphere 6 (1.0cm)	122.9	-58.4	-57.6

Quantitative Testing Summary:

SPECTRA Quant was found to have quantitative errors less than 5% in regions that are large enough not to be affected by partial volume effect for all of the isotopes tested (^{99m}Tc, ^{123}I, ^{131}I, ^{177}Lu).

In small targets, the partial volume effect lowers the accuracy as expected and was similar to the accuracy of the predicate device for these regions. Additional factors to consider when evaluating accuracy of quantitative SPECT reconstructions are the presence of motion during the SPECT acquisition and segmentation accuracy.

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Version 7.1 - 7.4

Have questions about MIM Software?
Contact MIM Software Support for technical assistance:
support.mimsoftware.com

Contour ProtégéAI+™

User Guide

Platform Version 1.3.2

View the most up-to-date versions of MIM user guides at www.mimsoftware.com/training.

Symbols Used in Documentation

Caution: Indicates potential hazards or restrictions on use that are critical for safe use of the product.

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

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

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

Regulatory Information

MIMTD-760 • 03 Sep 2024

Caution: US federal law and other national laws restrict this medical device to sale to, or use by, or on the order of a physician.

Important: The Contour ProtégéAI® models described in this guide may not yet be commercially available in some countries. Please contact your local MIM Software representative for further details.

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Indications For Use

Trained medical professionals use Contour ProtégéAI as a tool to assist in the automated processing of digital medical images of modalities CT and MR, as supported by ACR/NEMA DICOM 3.0. In addition, Contour ProtégéAI supports the following indications:

- Creation of contours using machine-learning algorithms for applications including, but not limited to, quantitative analysis, aiding adaptive therapy, transferring contours to radiation therapy treatment planning systems, and archiving contours for patient follow-up and management.
- Segmenting anatomical structures across a variety of CT anatomical locations. 6.1.3
- And segmenting the prostate, the seminal vesicles, and the urethra within T2-weighted MR images.

Appropriate image visualization software must be used to review and, if necessary, edit results automatically generated by Contour ProtégéAI.

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

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

Caution: Contour ProtégéAI can produce incorrect or implausible segmentations when the underlying anatomy is in the field of view of the scan but not clearly discernible due to image quality, noise, or the generally low contrast of some structures. This can occur in any situation where the organ at risk is not clearly discernible in the image, but has been observed for submandibular glands, optic nerves, and optic chiasms, in particular.

Caution: For head and neck models, while both images with and without IV contrast are represented in the training set, the effect of iodinated contrast can vary due to patient weight, contrast dosage, and time since injection. In cases where there is unusually intense brain enhancement, the posterior boundary of the brain can be incorrectly segmented.

⚠ **Caution:** In patients with spinal implants, artifact in the image may cause Contour ProtégéAI to miss a portion of the spinal cord or cauda equina, causing a gap between these adjacent structures.

⚠ **Caution:** In patients with very bright areas of contrast uptake, the posterior portion of the kidneys may not be fully contoured.

Intended Use

Contour ProtégéAI is an accessory to MIM software. It includes processing components to allow the contouring of anatomical structures using machine-learning-based algorithms automatically.

Appropriate image visualization software must be used to review and, if necessary, edit results automatically generated by Contour ProtégéAI.

Contour ProtégéAI is not intended to detect or contour lesions.

Device Description

Contour ProtégéAI is an accessory to MIM software that automatically creates contours on medical images through the use of machine-learning algorithms. It is designed for use in the processing of medical images and operates on Windows®, Mac®, and Linux computer systems. Contour ProtégéAI is deployed on a remote server using the MIMcloud® service for data management and transfer; or locally on the workstation or server running MIM software.

Note: Contour ProtégéAI+ is a trademarked name of Contour ProtégéAI.

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Introduction to Contour ProtégéAI+™

Contour ProtégéAI+™ Basics

MIMTD-897 • 14 Aug 2023

Overview

6.1.3

Contour ProtégéAI+ harnesses the power of specially trained neural networks to assist you with contouring various regions of the body.

In most organizations, Contour ProtégéAI+ is integrated with MIM Assistant® to partially or fully automate the auto-contouring process. When a series is sent to the appropriate patient list, the auto-contouring process runs, and the contours are returned. You then review and edit the contours as necessary, and proceed with your normal processing.

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

Important: All Contour ProtégéAI+ models have been trained exclusively on head first supine (HFS) oriented scans. If a non-HFS scan is processed by Contour ProtégéAI+, the resulting contours may be of a lower quality and extra review and correction may be needed.

Deployment Types

Contour ProtégéAI+ can be run in MIMcloud® as a cloud-hosted service, or on a locally hosted server. While the end results are the same, each of these implementations functions somewhat differently. It is important to know what type of implementation is in use in your organization. This information is important for instances where a case must be processed manually. It is also necessary for troubleshooting any issues that may arise.

MIM Workflows™ for Contour ProtégéAI+

- Workflows for Contour ProtégéAI+ segmentation are provided by MIM Software® during the initial setup and configuration of the system.
- Any processing that is normally done by a workflow can be added to a Contour ProtégéAI+ segmentation workflow.
- You can request additional workflows at support.mimsoftware.com.

Product Security Recommendations

MIMTD-631 • 15 Jan 2024

As part of our commitment to product security, MIM Software® recommends the following precautions be considered as part of your security policies. Please contact MIM Software Support at support.mimsoftware.com for additional information or questions about how MIM Software can support your efforts.

Organizational Responsibility

MIM® product security depends in large part on the security measures in place at your organization.

- Products developed by MIM Software are designed to be used by medical professionals and therefore should be located in a secured facility (i.e., facilities with encrypted, password-protected computers) that is not accessible to outsiders.
- To maintain security, MIM Software recommends the use of a local, secured network as well as the requirement of operating system credentials for workstations that are running our products.
- Because most vendors do not support encrypted DICOM, MIM Software strongly recommends that all third-party DICOM connectivity (e.g., modalities, PACS, TPS) be maintained over a segregated and secure internal network.
- Organizations are responsible for system maintenance and protection, including installing and maintaining antivirus software, firewalls, threat detection software, and other security measures as deemed necessary.
- MIM Software recommends enabling read/write permission controls for MIMpacs patient lists so that users have access to the minimum necessary information.
- Your site's incident response plan should include MIM data backups and disaster recovery planning.

Secure Product Design

MIM Software is committed to the safety, security, privacy, and protection of patients, organizations, and partners. To that end, all software manufactured by MIM Software is scanned, analyzed, and tested for potential cybersecurity issues.

- MIM products are designed to support the security policies our users employ by providing features such as compatibility with operating system encryption.
- To further support the security efforts of our users, MIM products do not require and should not have any inbound public internet network ports.
- MIM products do not require subnets or physical connectivity. This allows users to organize groups and support network components per their own defined policies.
- MIM-to-MIM traffic is encrypted.

- Any risks, vulnerabilities, or potential weaknesses are classified and handled according to their security risk level. Issues requiring mitigation receive patches as needed, and organizations are notified and updated.

Install a Contour ProtégéAI+™ Local Deployment

MIMTD-1766 • 14 Dec 2023

Overview

If you are using the cloud-based version of Contour ProtégéAI+, a MIM® representative will assist you with setup. If you are using the locally deployed version of Contour ProtégéAI+, follow these steps. If you need assistance, please contact MIM Software Support at support.mimsoftware.com.

☆ **Important:** Contour ProtégéAI+ should ordinarily be installed on the same server that runs MIM Assistant®. If you do not have MIM Assistant or prefer an alternative setup, please contact MIM Software Support at support.mimsoftware.com.

☆ **Important:** This process uses the Contour ProtégéAI+ Protocol Manager. The Contour ProtégéAI+ Protocol Manager is available in MIM 7.1.12, MIM 7.2.12, and MIM 7.3.5 or later. If you are not running one of these versions, you will need to upgrade before installing Contour ProtégéAI+. Please contact MIM Software Support at support.mimsoftware.com for assistance.

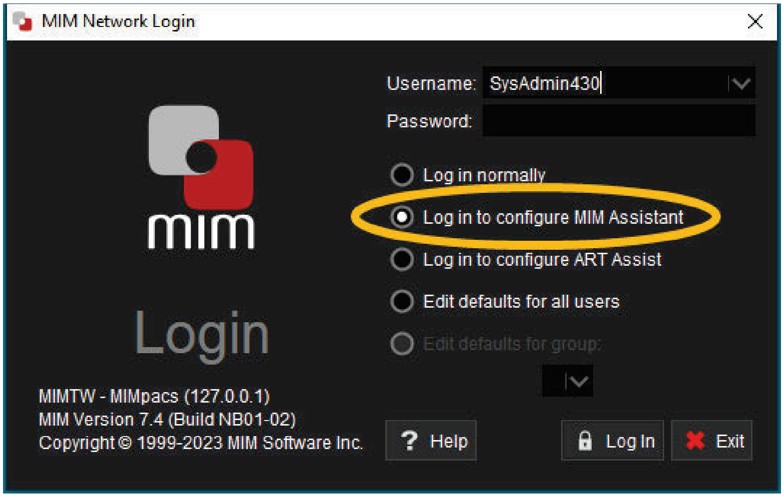
Contents

- Initial Configuration
- Use the Contour ProtégéAI+ Protocol Manager to Download and Import Contour ProtégéAI+ Models
- Create Contour ProtégéAI+ Protocols for Local Deployments
- Test Contour ProtégéAI+ Protocols for Local Deployments

Initial Configuration

1. On your MIM Assistant server, log in to MIM Assistant mode:
    i. Double-click the MIM icon on your desktop.
    ii. On the MIM Network Login screen, click **Advanced...**.

iii. Select **Log in to configure MIM Assistant**.



iv. Enter your password, then click **Log In**.

2. Click the Settings ⚙ button in the upper-right corner of MIM.

3. Go to **General Preferences** and search for "**Protege**". Select **Contour ProtégéAI** on the left side.

4. Set the **Contour ProtégéAI Local Deployment Thread Limit** to two less than the total number of processors available. For example, if you have 12 processors, set this preference to 10.

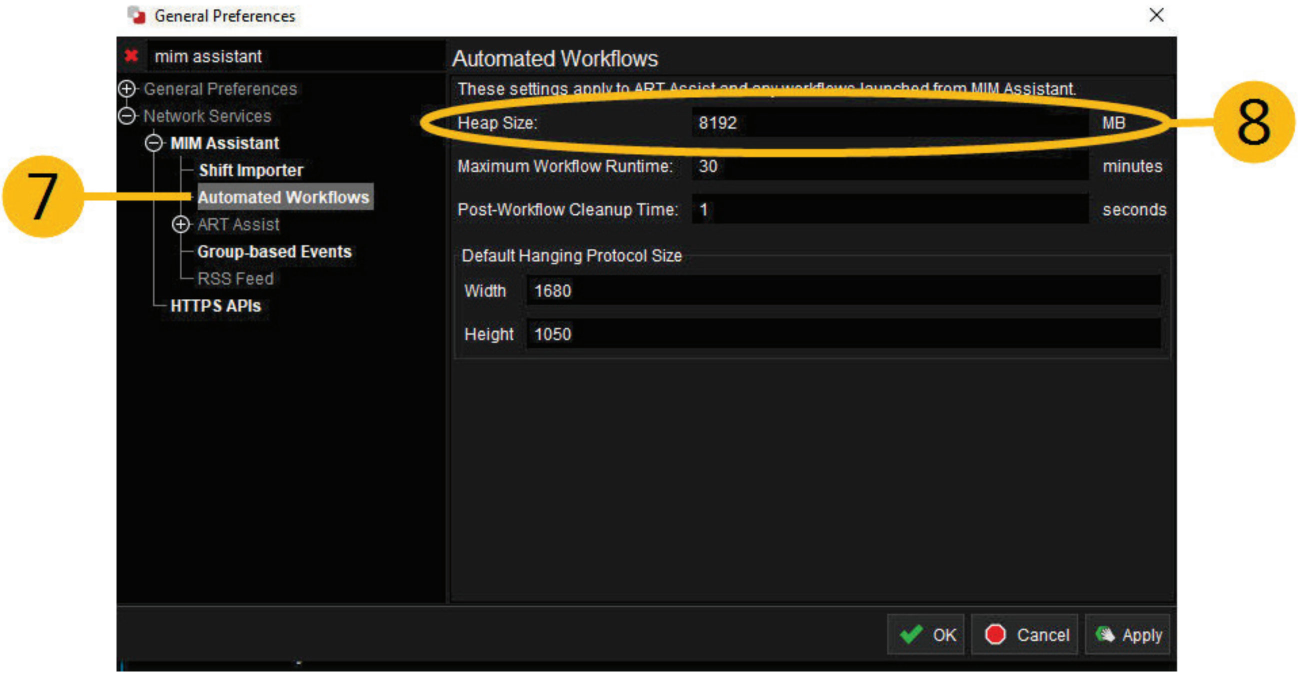
> **Tip:** To find the number of processors you have, open the Windows® Task Manager. Select the **Performance** tab and look for **Logical Processors**.

5. In the General Preferences window, search for "**MIM Assistant**" and select **MIM Assistant** from the menu on the left side of the screen.

6. On the MIM Assistant page, ensure that **Heap Size** is set to 4096 MB.

7. In the menu on the left side of the screen, select **Automated Workflows** (this option is nested under the MIM Assistant option you selected previously).

8. On the Automated Workflows page, ensure that the **Heap Size** is set to 8192 on machines with 16GB of RAM or 12288 on machines with 32GB of RAM or more.



Automated Workflows

These settings apply to ART Assist and any workflows launched from MIM Assistant.

Heap Size: 8192 MB

Maximum Workflow Runtime: 30 minutes

Post-Workflow Cleanup Time: 1 seconds

Default Hanging Protocol Size

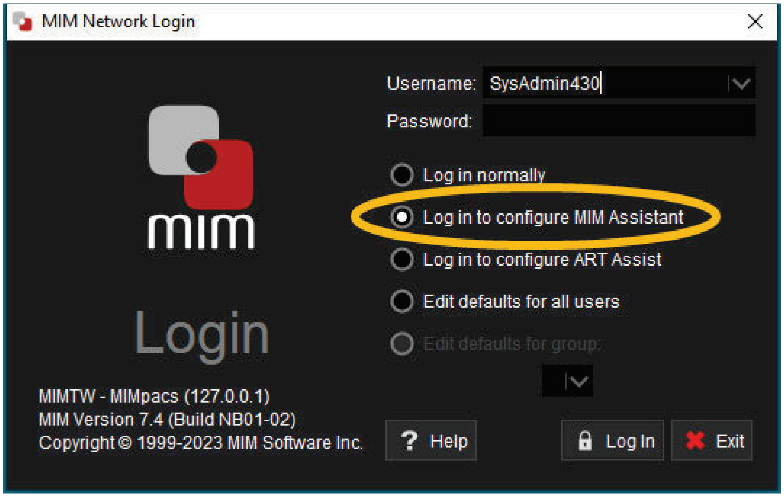
Width 1680

Height 1050

Use the Contour ProtégéAI+ Protocol Manager to Download and Import Contour ProtégéAI+ Models

1. On your MIM Assistant server, log in to MIM Assistant mode:
   i. Double-click the MIM icon on your desktop.
   ii. On the MIM Network Login screen, click **Advanced...**.

iii. Select **Log in to configure MIM Assistant**.



Username: SysAdmin430

Password:

○ Log in normally
● Log in to configure MIM Assistant
○ Log in to configure ART Assist
○ Edit defaults for all users
○ Edit defaults for group:

MIMTW - MIMpacs (127.0.0.1)
MIM Version 7.4 (Build NB01-02)
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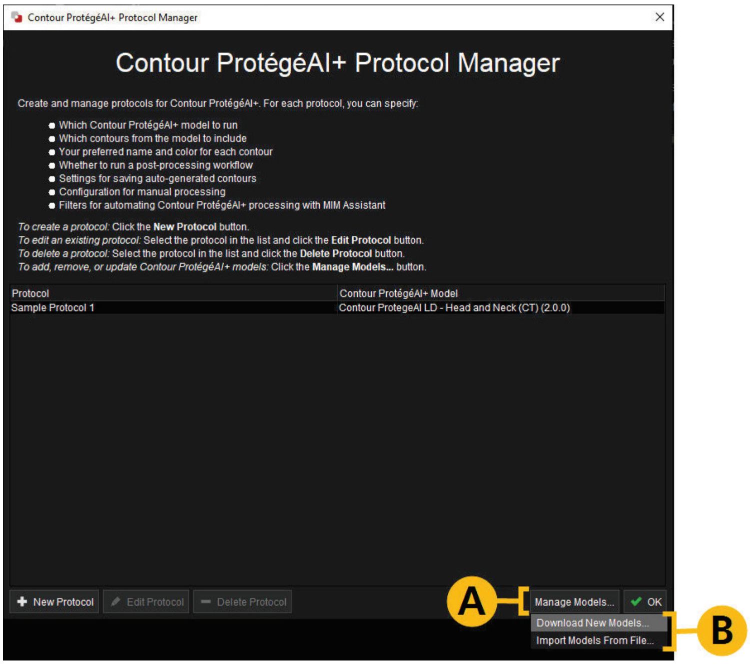
iv. Enter your password, then click **Log In**.

2. Click the Settings ⚙ button in the upper-right corner of MIM.
3. In the Settings menu, select **Manage Contour ProtégéAI+ Protocols...**. The Contour ProtégéAI+ Protocol Manager opens.
4. In the Contour ProtégéAI+ Protocol Manager, click the **Manage Models...** button (A). A menu of two additional options opens (B).



Contour ProtégéAI+ Protocol Manager

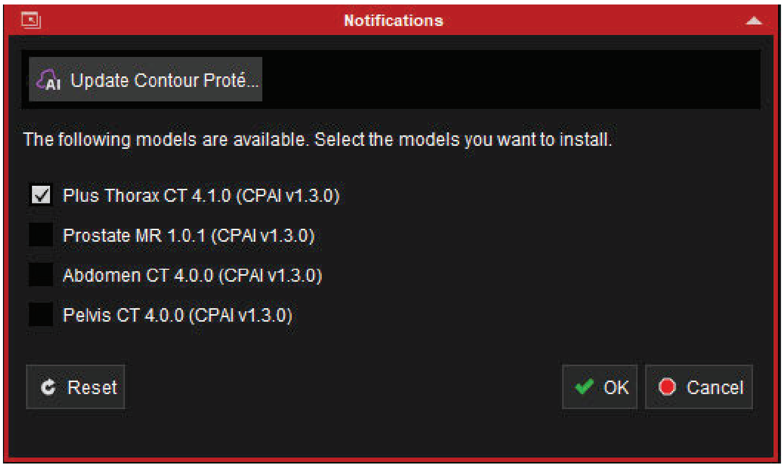
Create and manage protocols for Contour ProtégéAI+. For each protocol, you can specify:

- Which Contour ProtégéAI+ model to run
- Which contours from the model to include
- Your preferred name and color for each contour
- Whether to run a post-processing workflow
- Settings for saving auto-generated contours
- Configuration for manual processing
- Filters for automating Contour ProtégéAI+ processing with MIM Assistant

To create a protocol: Click the **New Protocol** button.
To edit an existing protocol: Select the protocol in the list and click the **Edit Protocol** button.
To delete a protocol: Select the protocol in the list and click the **Delete Protocol** button.
To add, remove, or update Contour ProtégéAI+ models: Click the **Manage Models...** button.

Protocol	Contour ProtégéAI+ Model
Sample Protocol 1	Contour ProtegeAI LD - Head and Neck (CT) (2.0.0)

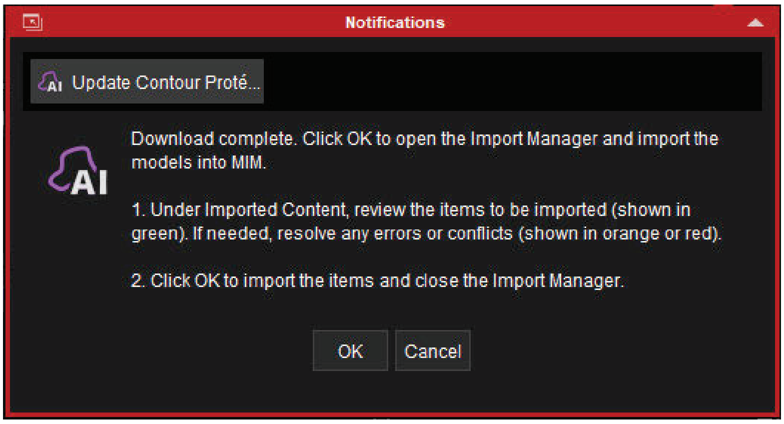
5. Select **Download New Models...**. The Notifications window presents a list of available Contour ProtégéAI+ models.
6. Select the models you want to install and click **OK**. The models begin to download.



The following models are available. Select the models you want to install.

☑ Plus Thorax CT 4.1.0 (CPAI v1.3.0)
☐ Prostate MR 1.0.1 (CPAI v1.3.0)
☐ Abdomen CT 4.0.0 (CPAI v1.3.0)
☐ Pelvis CT 4.0.0 (CPAI v1.3.0)

7. When the Notifications window confirms that the download is complete, review the instructions, then click **OK** to proceed to the Import Manager.

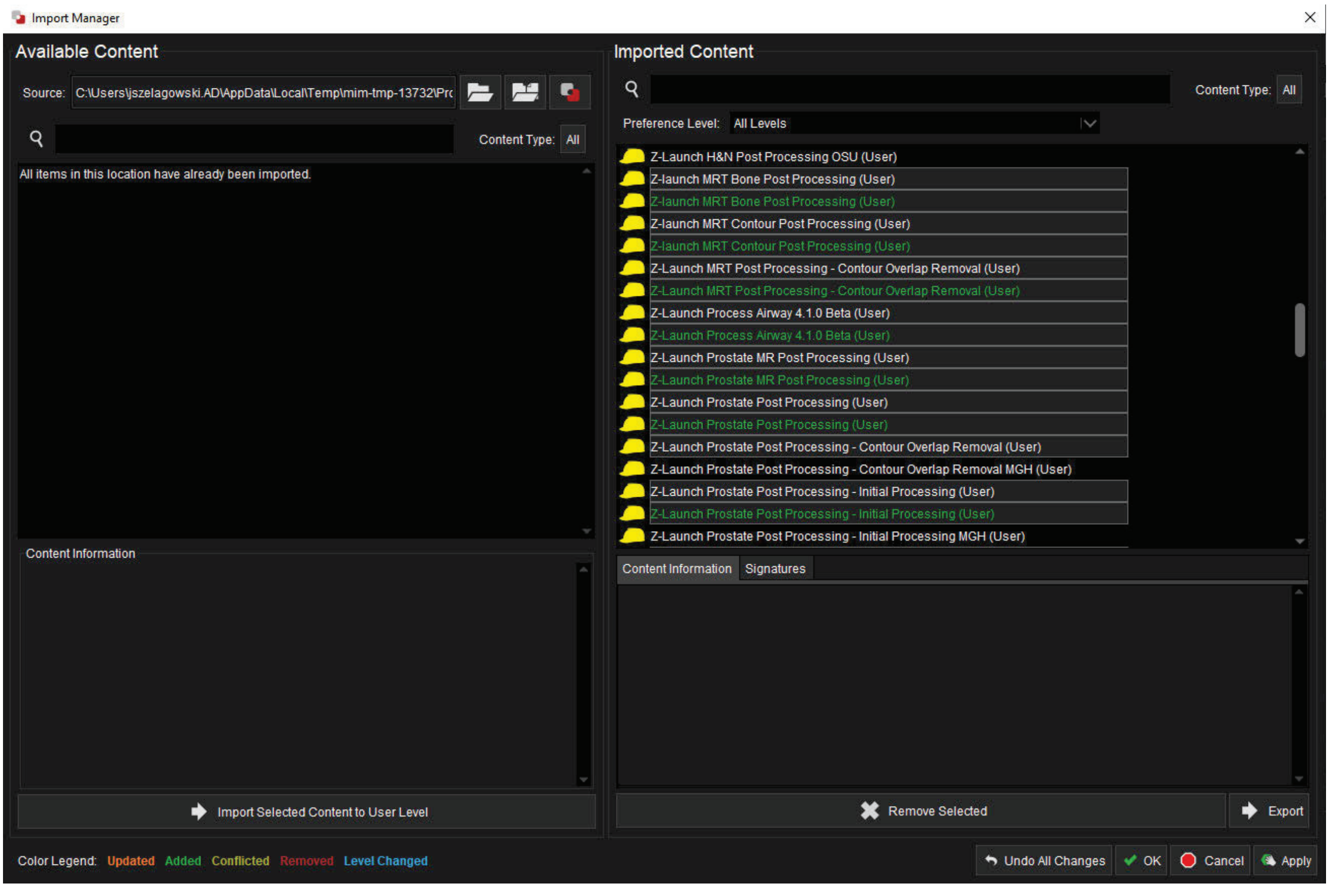


Download complete. Click OK to open the Import Manager and import the models into MIM.

1. Under Imported Content, review the items to be imported (shown in green). If needed, resolve any errors or conflicts (shown in orange or red).

2. Click OK to import the items and close the Import Manager.

8. Review the items selected for import in the Import Manager (they are shown in green on the right side). Click **OK** to complete the import and close the Import Manager.



Source: C:\Users\jszelagowski.AD\AppData\Local\Temp\mim-tmp-13732\Prc

Content Type: All

All items in this location have already been imported.

Content Type: All

Preference Level: All Levels

Z-Launch H&N Post Processing OSU (User)
Z-launch MRT Bone Post Processing (User)
Z-launch MRT Bone Post Processing (User)
Z-launch MRT Contour Post Processing (User)
Z-launch MRT Contour Post Processing (User)
Z-Launch MRT Post Processing - Contour Overlap Removal (User)
Z-Launch MRT Post Processing - Contour Overlap Removal (User)
Z-Launch Process Airway 4.1.0 Beta (User)
Z-Launch Process Airway 4.1.0 Beta (User)
Z-Launch Prostate MR Post Processing (User)
Z-Launch Prostate MR Post Processing (User)
Z-Launch Prostate Post Processing (User)
Z-Launch Prostate Post Processing (User)
Z-Launch Prostate Post Processing - Contour Overlap Removal (User)
Z-Launch Prostate Post Processing - Contour Overlap Removal MGH (User)
Z-Launch Prostate Post Processing - Initial Processing (User)
Z-Launch Prostate Post Processing - Initial Processing (User)
Z-Launch Prostate Post Processing - Initial Processing MGH (User)

9. A final message in the Notifications window confirms that the import was successful and provides additional options for working with the new models. Click **Create New Contour ProtégéAI+ Protocol** to configure your first Contour ProtégéAI+ protocol.

Create Contour ProtégéAI+ Protocols for Local Deployments

Once models have been downloaded and imported, the Contour ProtégéAI+ Protocol Wizard guides you through the process of creating Contour ProtégéAI+ protocols. Protocols are templated instructions for how Contour ProtégéAI+ processes various case types.

- Follow the instructions in each step of the Contour ProtégéAI+ Protocol Wizard to create your first protocol.
- If you are configuring MIM Assistant® automation as part of a protocol, see Configure MIM Assistant® Filters for Locally Deployed Contour ProtégéAI+™ Processing for more information.
- When you are finished creating the protocol, click the **New Protocol** button in the bottom left corner of the Contour ProtégéAI+ Protocol Manager to add another.
- After creating all required protocols, click **OK** in the bottom right corner of the Contour ProtégéAI+ Protocol Manager.

Test Contour ProtégéAI+ Protocols for Local Deployments

Contour ProtégéAI+ is now ready for use, according to the configurations you established in the Contour ProtégéAI+ Protocol Manager. To test your setup, follow these steps:

If you configured an AE Title for manual submission:

1. Send a CT to the newly configured destination.
2. Wait several minutes for Contour ProtégéAI+ to run, then check the patient that you configured to receive the contours.

If you configured MIM Assistant automation:

1. Locate a series that matches the filters you configured to trigger Contour ProtégéAI+ processing.
2. Send this series to the destination you configured for MIM Assistant automation.
3. Wait several minutes for Contour ProtégéAI+ to run, then check the patient that you configured to receive the contours.

If more than 15 minutes have passed and you still do not see the expected Contour ProtégéAI+ contour sets, please contact MIM Software Support at support.mimsoftware.com.

Upgrade Contour ProtégéAI+™ Local Deployment Models

MIMTD-1768 • 13 Dec 2023

Overview

The Contour ProtégéAI+ Protocol Manager guides you through the process of downloading and installing updates to locally deployed Contour ProtégéAI+ models. It then lets you decide whether to update your existing protocols to use the new models. Optionally, the Contour ProtégéAI+ Protocol Manager can also delete previous versions of the models.

Important: The following procedure is for Contour ProtégéAI+ environments that were previously installed or upgraded using the Contour ProtégéAI+ Protocol Manager. If your Contour ProtégéAI+ environment was configured manually, it must first be converted to work with the Contour ProtégéAI+ Protocol Manager. Please contact MIM Software Support at support.mimsoftware.com for assistance with the conversion.

Contents

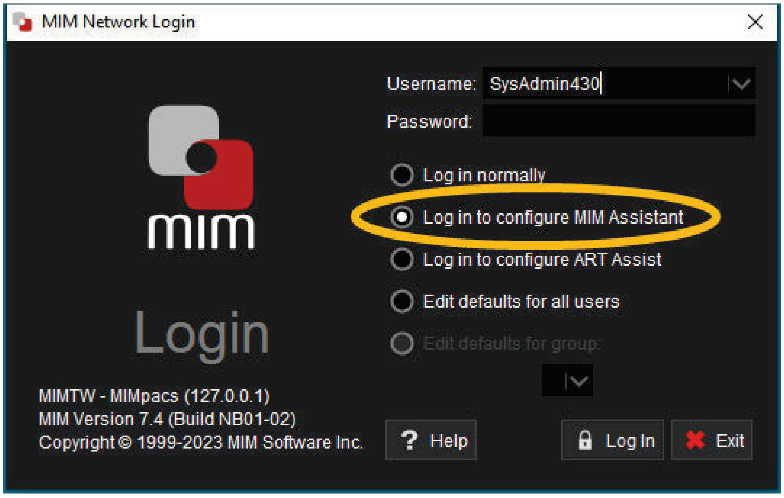
- Download and Import the New Models (Online)
- Download and Import the New Models (Offline)
- Upgrade Existing Contour ProtégéAI+ Protocols to Use the New Models
- Optional: Create New Contour ProtégéAI+ Protocols
- Test Contour ProtégéAI+ Protocols

Download and Import the New Models (Online)

Tip: If your Contour ProtégéAI+ server is connected to the internet, you will be notified upon opening MIM® when new Contour ProtégéAI+ models are available. If your Contour ProtégéAI+ server is not connected to the internet, you will need to download updated models on an internet-connected machine and transfer them to the Contour ProtégéAI+ server. See Download and Import the New Models (Offline) below.

Important: These instructions assume that Contour ProtégéAI+ is installed on the same server that runs MIM Assistant®. If you have a separate Contour ProtégéAI+ server, or do not have MIM Assistant, please contact MIM Software Support at support.mimsoftware.com for assistance.

1. On your MIM Assistant server, log in to MIM Assistant mode:
   i. Double-click the MIM icon on your desktop.
   ii. On the MIM Network Login screen, click **Advanced...**.
   iii. Select **Log in to configure MIM Assistant**.



MIM Network Login

Username: SysAdmin430

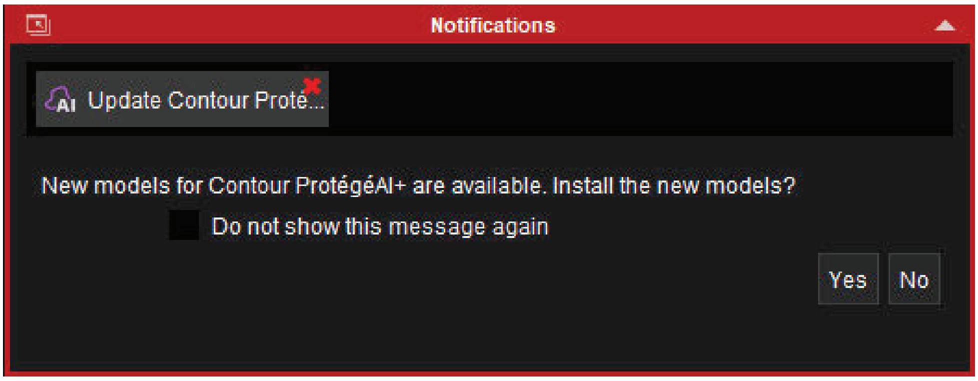
Password:

○ Log in normally
● Log in to configure MIM Assistant
○ Log in to configure ART Assist
○ Edit defaults for all users
○ Edit defaults for group:

MIMTW - MIMpacs (127.0.0.1)
MIM Version 7.4 (Build NB01-02)
Copyright © 1999-2023 MIM Software Inc.

   iv. Enter your password, then click **Log In**.

2. Click **Yes** in the Notifications window to begin the update process.



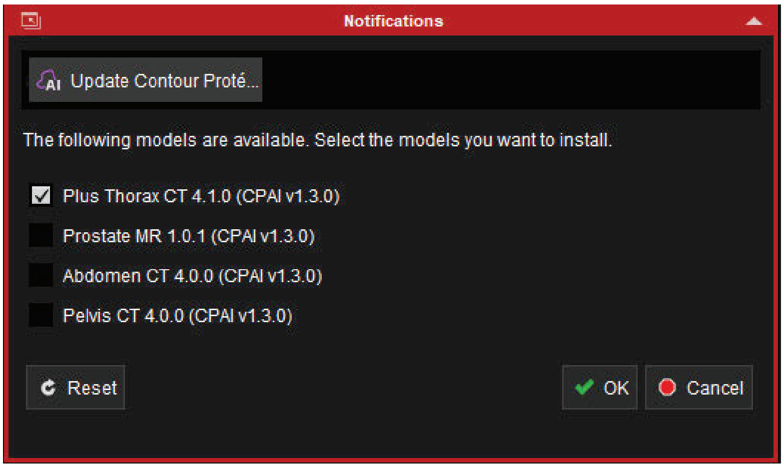
Notifications

New models for Contour ProtégéAI+ are available. Install the new models?

☐ Do not show this message again

Tip: If you accidentally close the message, you can open the Contour ProtégéAI+ Protocol Manager from the Settings ⚙ menu in the upper-right corner of MIM instead. Then, click **Manage Models** in the lower-right corner of the Contour ProtégéAI+ Protocol Manager.

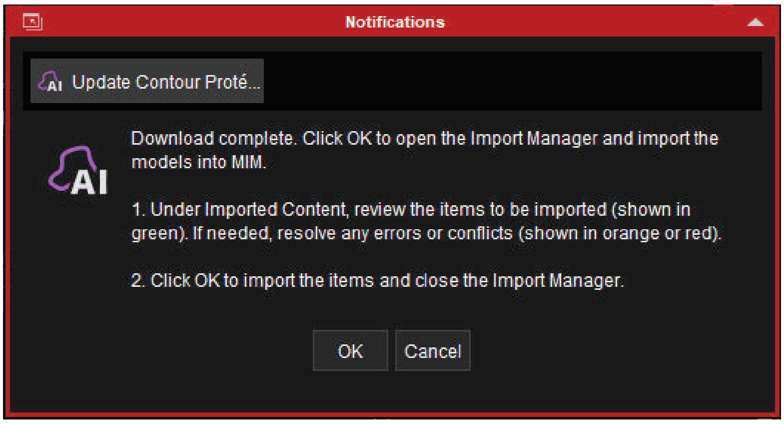
3. Select the models you want to install or update, then click **OK**. The models begin to download.



The following models are available. Select the models you want to install.

☑ Plus Thorax CT 4.1.0 (CPAI v1.3.0)
☐ Prostate MR 1.0.1 (CPAI v1.3.0)
☐ Abdomen CT 4.0.0 (CPAI v1.3.0)
☐ Pelvis CT 4.0.0 (CPAI v1.3.0)

4. When the Notifications window confirms that the download is complete, review the instructions, then click **OK** to proceed to the Import Manager.

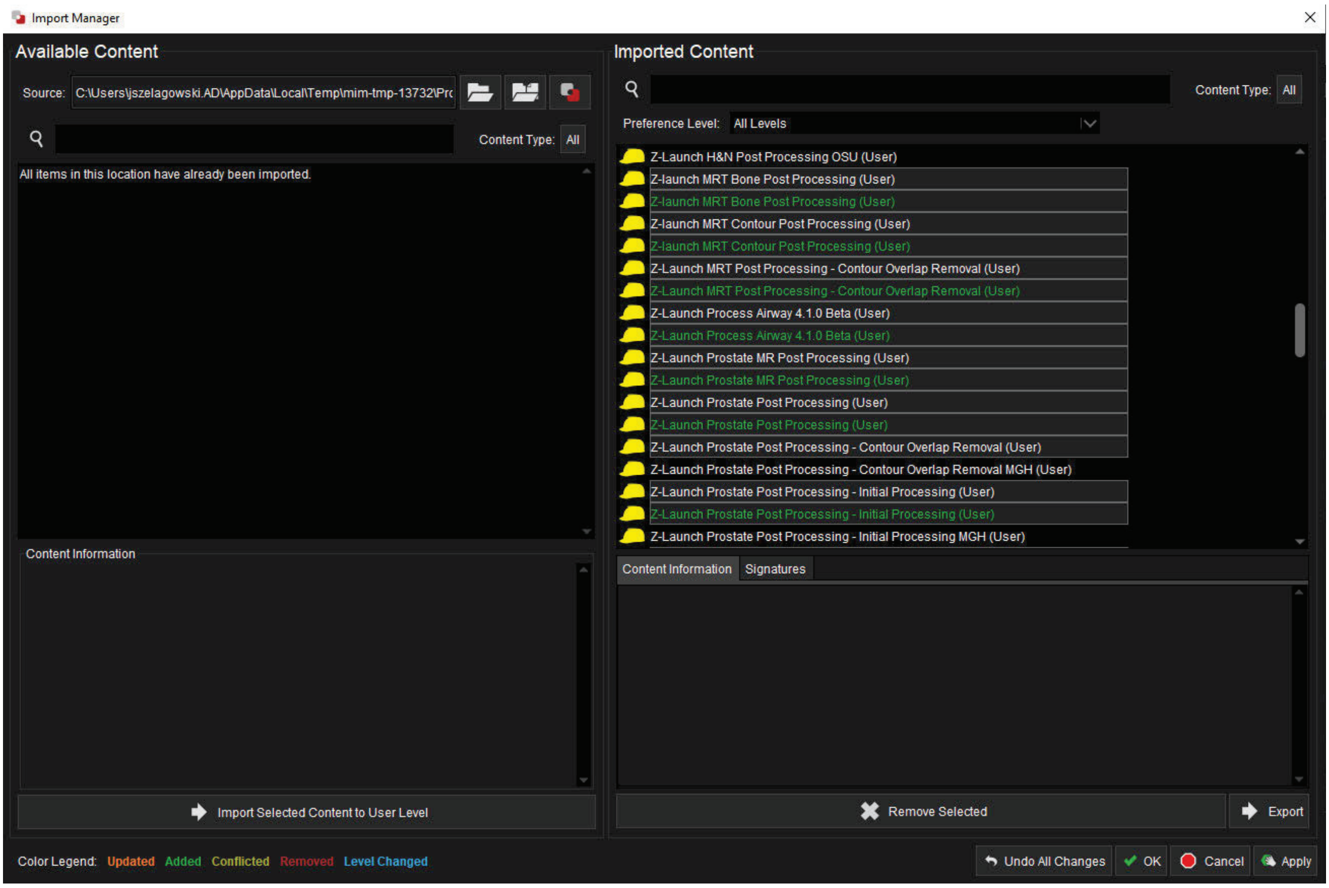


Download complete. Click OK to open the Import Manager and import the models into MIM.

1. Under Imported Content, review the items to be imported (shown in green). If needed, resolve any errors or conflicts (shown in orange or red).

2. Click OK to import the items and close the Import Manager.

5. Review the items selected for import in the Import Manager. New items are shown in green. Updated items are shown in orange. Click **OK** to complete the import and close the Import Manager.



Source: C:\Users\jszelagowski.AD\AppData\Local\Temp\mim-tmp-13732\Prc

Content Type: All

All items in this location have already been imported.

Content Type: All

Preference Level: All Levels

Z-Launch H&N Post Processing OSU (User)
Z-launch MRT Bone Post Processing (User)
Z-launch MRT Bone Post Processing (User)
Z-launch MRT Contour Post Processing (User)
Z-launch MRT Contour Post Processing (User)
Z-Launch MRT Post Processing - Contour Overlap Removal (User)
Z-Launch MRT Post Processing - Contour Overlap Removal (User)
Z-Launch Process Airway 4.1.0 Beta (User)
Z-Launch Process Airway 4.1.0 Beta (User)
Z-Launch Prostate MR Post Processing (User)
Z-Launch Prostate MR Post Processing (User)
Z-Launch Prostate Post Processing (User)
Z-Launch Prostate Post Processing (User)
Z-Launch Prostate Post Processing - Contour Overlap Removal (User)
Z-Launch Prostate Post Processing - Contour Overlap Removal MGH (User)
Z-Launch Prostate Post Processing - Initial Processing (User)
Z-Launch Prostate Post Processing - Initial Processing (User)
Z-Launch Prostate Post Processing - Initial Processing MGH (User)

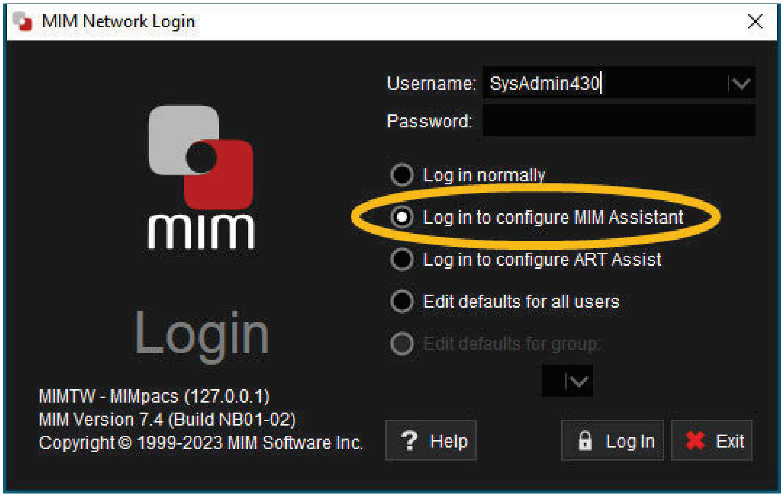
6. Proceed to Upgrade Existing Contour ProtégéAI+ Protocols to Use the New Models below to continue the upgrade process.

Download and Import the New Models (Offline)

If your MIM Assistant server is not connected to the internet, you need to download updated Contour ProtégéAI+ local deployment models manually and transfer them to the server through a shared network drive or USB. To upgrade Contour ProtégéAI+ on a server without internet access, follow these steps:

1. On a computer with Internet access, go to mimsoftware.com/download and download the desired Contour ProtégéAI+ models. Save the models to a shared network drive that your MIM Assistant server can access, or to a USB drive.
2. On your MIM Assistant server, log in to MIM Assistant mode:
    i. Double-click the MIM icon on your desktop.
    ii. On the MIM Network Login screen, click **Advanced...**.

iii. Select **Log in to configure MIM Assistant**.



Username: SysAdmin430
Password:

○ Log in normally
● Log in to configure MIM Assistant
○ Log in to configure ART Assist
○ Edit defaults for all users
○ Edit defaults for group:

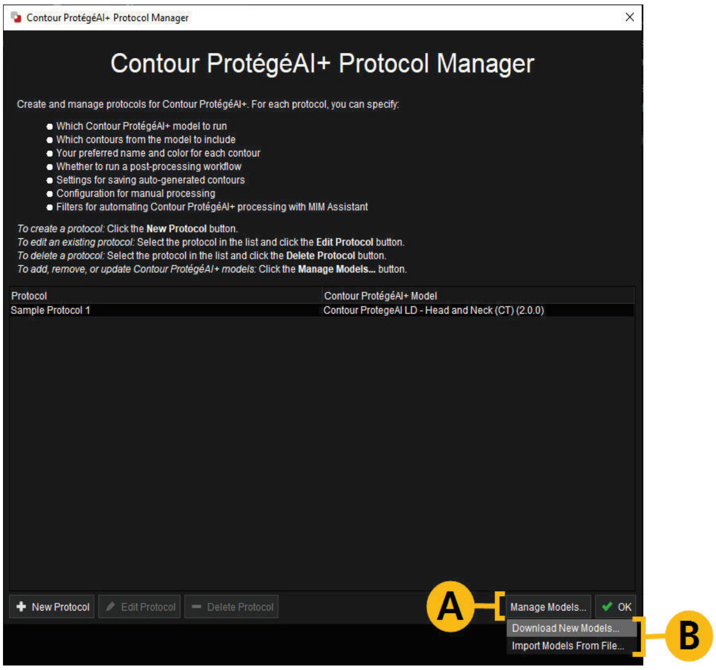
MIMTW - MIMpacs (127.0.0.1)
MIM Version 7.4 (Build NB01-02)
Copyright © 1999-2023 MIM Software Inc.

iv. Enter your password, then click **Log In**.

3. Click the Settings ⚙ button in the upper-right corner of MIM.

4. In the Settings menu, select **Manage Contour ProtégéAI+ Protocols...**. The Contour ProtégéAI+ Protocol Manager opens.

5. In the Contour ProtégéAI+ Protocol Manager, click the **Manage Models...** button (A). A menu of two additional options opens (B).



Contour ProtégéAI+ Protocol Manager

Create and manage protocols for Contour ProtégéAI+. For each protocol, you can specify:

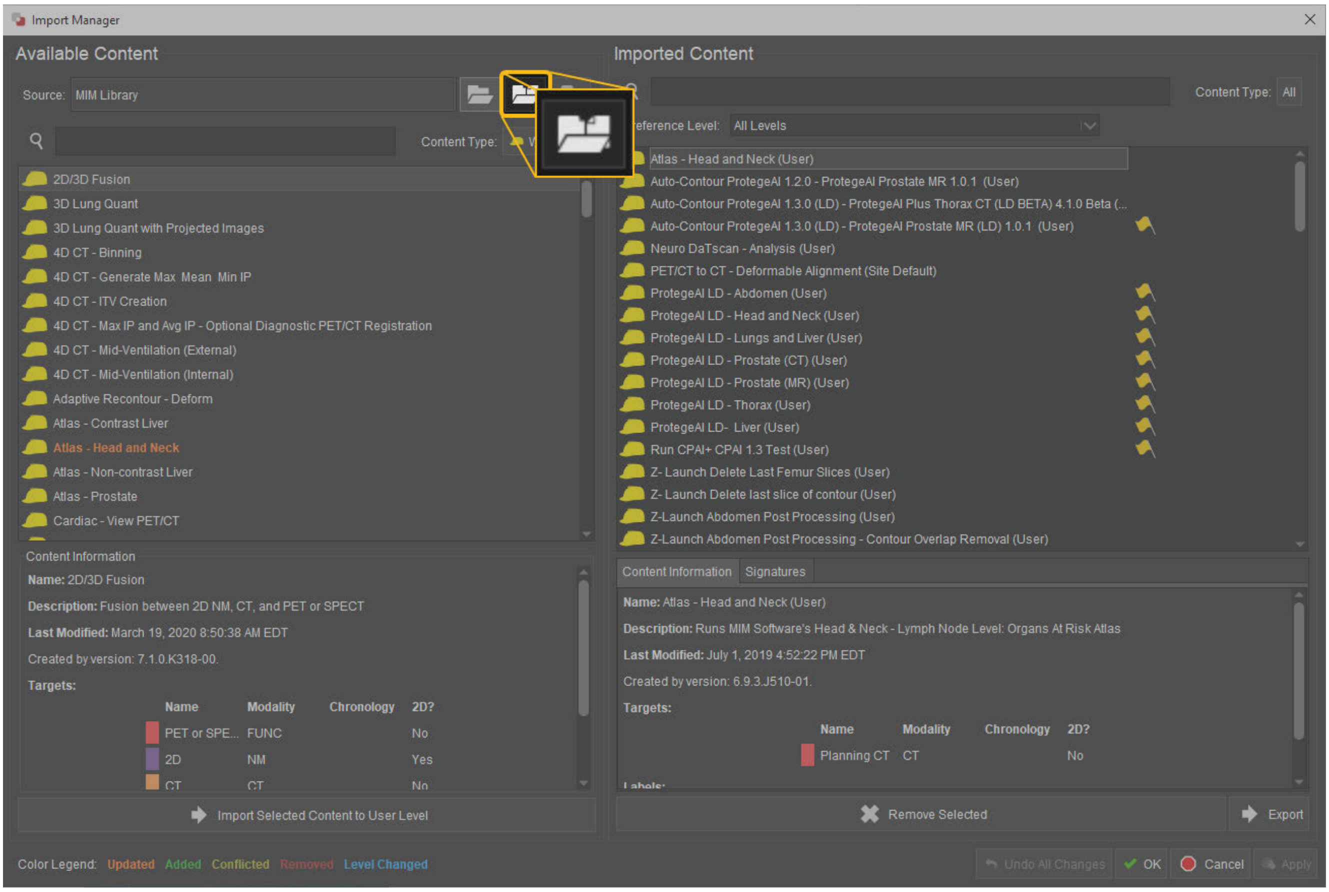
- Which Contour ProtégéAI+ model to run
- Which contours from the model to include
- Your preferred name and color for each contour
- Whether to run a post-processing workflow
- Settings for saving auto-generated contours
- Configuration for manual processing
- Filters for automating Contour ProtégéAI+ processing with MIM Assistant

To create a protocol: Click the **New Protocol** button.
To edit an existing protocol: Select the protocol in the list and click the **Edit Protocol** button.
To delete a protocol: Select the protocol in the list and click the **Delete Protocol** button.
To add, remove, or update Contour ProtégéAI+ models: Click the **Manage Models...** button.

Protocol	Contour ProtégéAI+ Model
Sample Protocol 1	Contour ProtegeAI LD - Head and Neck (CT) (2.0.0)

6. Select **Import Models From File...**. The Import Manager opens.

7. In the Import Manager, click the open file 🗁 button.



- 2D/3D Fusion
- 3D Lung Quant
- 3D Lung Quant with Projected Images
- 4D CT - Binning
- 4D CT - Generate Max Mean Min IP
- 4D CT - ITV Creation
- 4D CT - Max IP and Avg IP - Optional Diagnostic PET/CT Registration
- 4D CT - Mid-Ventilation (External)
- 4D CT - Mid-Ventilation (Internal)
- Adaptive Recontour - Deform
- Atlas - Contrast Liver
- Atlas - Head and Neck
- Atlas - Non-contrast Liver
- Atlas - Prostate
- Cardiac - View PET/CT

Name: 2D/3D Fusion

Description: Fusion between 2D NM, CT, and PET or SPECT

Last Modified: March 19, 2020 8:50:38 AM EDT

Created by version: 7.1.0.K318-00.

Targets:

Name	Modality	Chronology	2D?
🟥 PET or SPE...	FUNC		No
🟪 2D	NM		Yes
🟫 CT	CT		No

- Atlas - Head and Neck (User)
- Auto-Contour ProtegeAI 1.2.0 - ProtegeAI Prostate MR 1.0.1 (User)
- Auto-Contour ProtegeAI 1.3.0 (LD) - ProtegeAI Plus Thorax CT (LD BETA) 4.1.0 Beta (...
- Auto-Contour ProtegeAI 1.3.0 (LD) - ProtegeAI Prostate MR (LD) 1.0.1 (User)
- Neuro DaTscan - Analysis (User)
- PET/CT to CT - Deformable Alignment (Site Default)
- ProtegeAI LD - Abdomen (User)
- ProtegeAI LD - Head and Neck (User)
- ProtegeAI LD - Lungs and Liver (User)
- ProtegeAI LD - Prostate (CT) (User)
- ProtegeAI LD - Prostate (MR) (User)
- ProtegeAI LD - Thorax (User)
- ProtegeAI LD- Liver (User)
- Run CPAI+ CPAI 1.3 Test (User)
- Z- Launch Delete Last Femur Slices (User)
- Z- Launch Delete last slice of contour (User)
- Z-Launch Abdomen Post Processing (User)
- Z-Launch Abdomen Post Processing - Contour Overlap Removal (User)

Name: Atlas - Head and Neck (User)

Description: Runs MIM Software's Head & Neck - Lymph Node Level: Organs At Risk Atlas

Last Modified: July 1, 2019 4:52:22 PM EDT

Created by version: 6.9.3.J510-01.

Targets:

Name	Modality	Chronology	2D?
🟥 Planning CT	CT		No

Labels:

8. Browse to the location of the Contour ProtégéAI+ model you want to upgrade, select it, and click **Open**. The Contour ProtégéAI+ model and all its dependencies appear on the left side of the Import Manager.

> ☆ **Important:** Do not unzip the file before importing it.

9. Select all items on the left side of the Import Manager and click **Import Selected Content to User Level** at the bottom of the window. The content moves to the right side of the Import Manager.
10. Repeat steps 7 through 9 for any additional Contour ProtégéAI+ models you want to import or update.
11. Click **OK** to complete the import and close the Import Manager.
12. Proceed to [Upgrade Existing Contour ProtégéAI+ Protocols to Use the New Models]() below to continue the upgrade process.

Upgrade Existing Contour ProtégéAI+ Protocols to Use the New Models

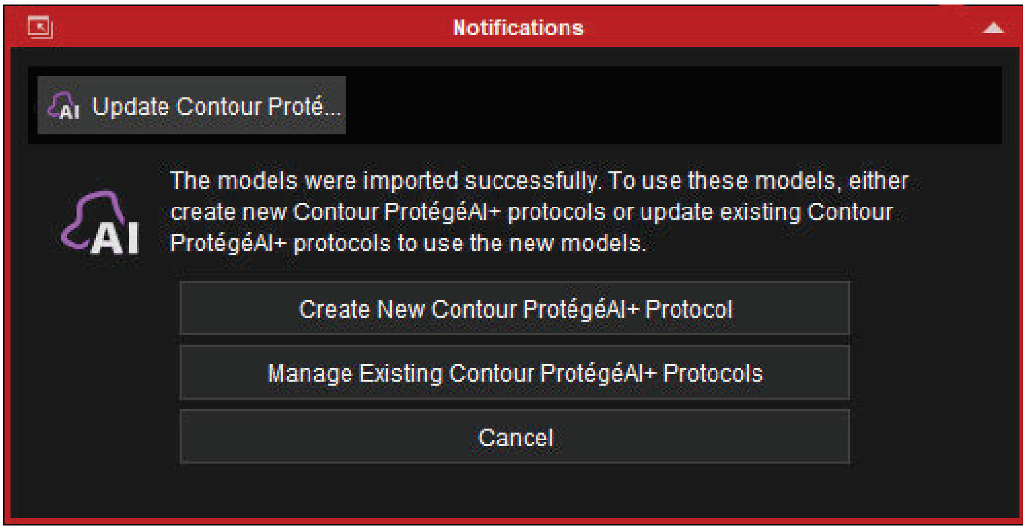
1. The Notifications window asks whether you would like to upgrade your existing Contour ProtégéAI+ protocols.
    - *If you choose **Upgrade protocols**:* Existing Contour ProtégéAI+ protocols that use an older version of the model are upgraded to use the new model.
    - *If you choose **Do not upgrade**:* Existing Contour ProtégéAI+ protocols remain unchanged. Create new protocols to use the new models.

    Click the option that you prefer.

2. *If you chose to upgrade existing protocols:* You are prompted to choose whether to delete older versions of the newly installed models. Click the option that you prefer.

    If you chose not to upgrade existing protocols: Proceed to the next step.

3. The final notification in the update process confirms that your Contour ProtégéAI+ models were installed or updated successfully. You are presented with three options:



The models were imported successfully. To use these models, either create new Contour ProtégéAI+ protocols or update existing Contour ProtégéAI+ protocols to use the new models.

- *If you choose **Create New Contour ProtégéAI+ Protocol**:* The Contour ProtégéAI+ Protocol Wizard opens. See Optional: Create New Contour ProtégéAI+ Protocols for more information.
- *If you choose **Manage Existing Contour ProtégéAI+ Protocols**:* The Contour ProtégéAI+ Protocol Manager opens. Select any existing protocol to edit it.
- *If you choose **Cancel**:* The Notifications window closes.

Optional: Create New Contour ProtégéAI+ Protocols

Once models have been downloaded and imported, you can use them in new Contour ProtégéAI+ protocols:

- Follow the instructions in each step of the Contour ProtégéAI+ Protocol Wizard to create a new protocol.
- If you are configuring MIM Assistant® automation as part of a protocol, see Configure MIM Assistant® Filters for Locally Deployed Contour ProtégéAI+™ Processing for more information.
- When you are finished creating the protocol, click the **New Protocol** button in the bottom left corner of the Contour ProtégéAI+ Protocol Manager to add another.
- After creating all required protocols, click **OK** in the bottom right corner of the Contour ProtégéAI+ Protocol Manager.

Test Contour ProtégéAI+ Protocols

Contour ProtégéAI+ is now ready for use, according to the configurations you established in the Contour ProtégéAI+ Protocol Manager. To test your setup, follow these steps:

If you configured an AE Title for manual submission:

1. Send a CT to the newly configured destination.
2. Wait several minutes for Contour ProtégéAI+ to run, then check the patient that you configured to receive the contours.

If you configured MIM Assistant automation:

1. Locate a series that matches the filters you configured to trigger Contour ProtégéAI+ processing.
2. Send this series to the destination you configured for MIM Assistant automation.
3. Wait several minutes for Contour ProtégéAI+ to run, then check the patient that you configured to receive the contours.

If more than 15 minutes have passed and you still do not see the expected Contour ProtégéAI+ contour sets, please contact MIM Software Support at support.mimsoftware.com.

Configure MIM Assistant® Filters for Locally Deployed Contour ProtégéAI+™ Processing

MIMTD-1770 • 05 Dec 2023

Overview

Step 6 of the Contour ProtégéAI+ Protocol Wizard lets you configure MIM Assistant Automation. With automation enabled, MIM Assistant examines every series sent to a specified patient list. Series that meet the configured filtering criteria are automatically processed by Contour ProtégéAI+, while other series are ignored.

> **Tip:** Configuring automated processing is optional. If you do not want to configure automated processing, deselect **Enable automation** on this screen, then click **Finish**. With automation disabled, Contour ProtégéAI+ processing will only occur when it is manually initiated.

Use the information below to help you configure the filters in this step correctly. If you need assistance, please contact MIM Software Support at support.mimsoftware.com.

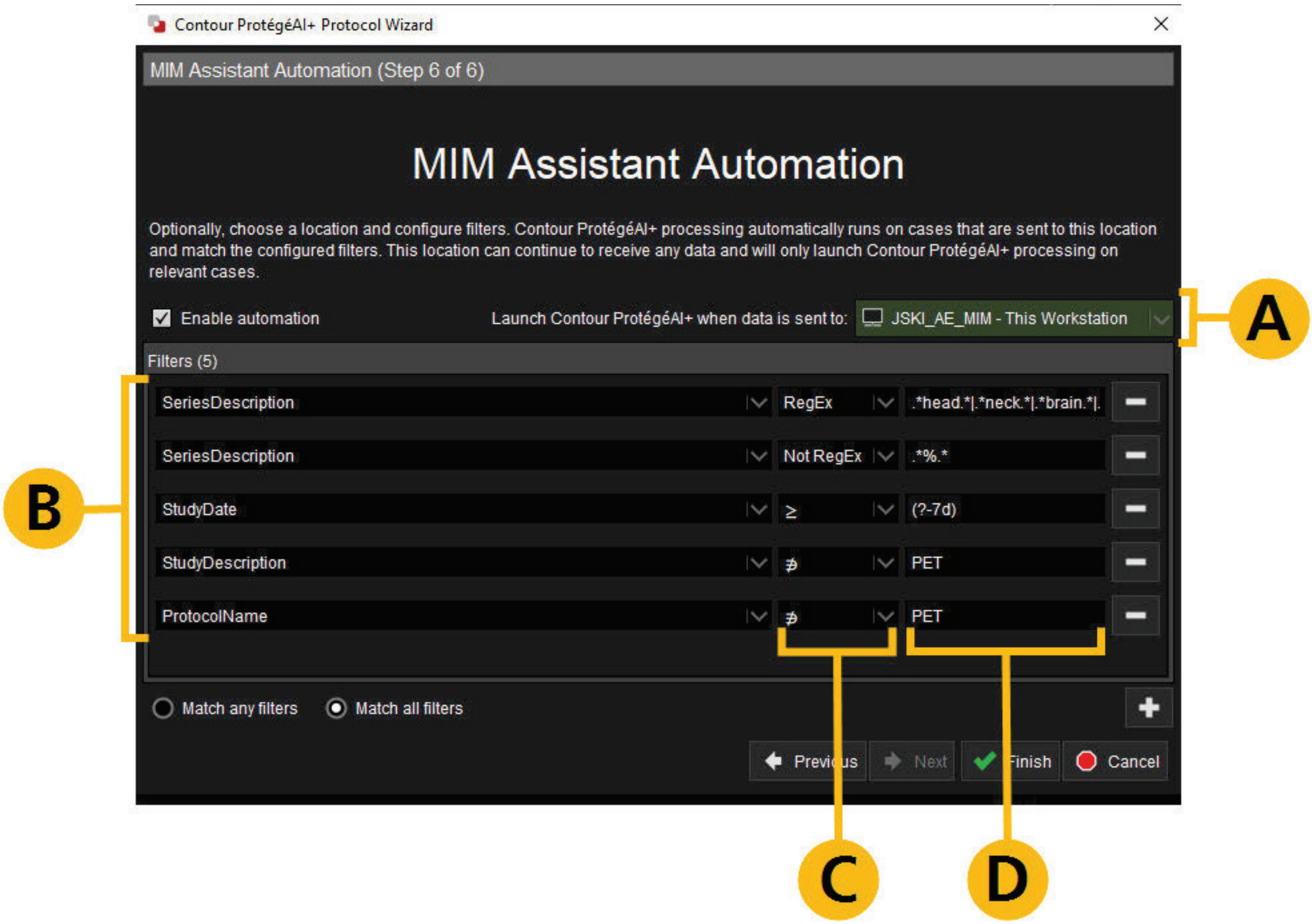
> **Caution:** Building MIM Assistant rules with incorrect operators or without understanding the operators used can lead to unintended system behavior.

Contents

- Basic Functionality
- Compare Text
- Compare Numbers
- Compare Dates
  - Absolute Dates and Times
  - Relative Dates
- Check for a Value Using Exists (∃) and Not Exist (∄)
- Compare Strings Using Contains (∋) and Does Not Contain (∌)
- Match Patterns Using RegEx and Not RegEx

Basic Functionality

If you use MIM Assistant, the Contour ProtégéAI Protocol Wizard provides you with an interface for configuring automated processing:



Contour ProtégéAI+ Protocol Wizard

MIM Assistant Automation (Step 6 of 6)

MIM Assistant Automation

Optionally, choose a location and configure filters. Contour ProtégéAI+ processing automatically runs on cases that are sent to this location and match the configured filters. This location can continue to receive any data and will only launch Contour ProtégéAI+ processing on relevant cases.

☑ Enable automation

Launch Contour ProtégéAI+ when data is sent to: JSKI_AE_MIM - This Workstation

Filters (5)

SeriesDescription	RegEx	.*head.*|.*neck.*|.*brain.*|.
SeriesDescription	Not RegEx	.*%.*
StudyDate	≥	(?-7d)
StudyDescription	∌	PET
ProtocolName	∌	PET

○ Match any filters ● Match all filters

A. The DICOM location that the filters will be applied to. Series sent to this location that meet the filtering criteria will be processed by Contour ProtégéAI+.

B. The DICOM tags to evaluate. Add a tag by clicking the add ✚ button in the lower-right corner of the window. Remove a tag by clicking the corresponding remove ▬ button on the far right of the window.

C. The operator to use when evaluating the value of the DICOM tag. See additional information below.

D. The values to compare to the DICOM tag value. See additional information below.

Compare Text

For tags that contain text, the values are compared alphabetically and are case-insensitive.

- Less than (<): Left value is alphabetically before the right value
- Greater than (>): Left value is alphabetically after the right value
- Equals (=): Left value and right value are exactly the same

Examples:

- apple < banana (The letter a comes before the letter b.)
- HEAD&NECK = head&neck (The comparison is case-insensitive.)

Compare Numbers

Tags that contain numbers are compared mathematically.

Examples:

- 100 > 20 (100 is greater than 20.)
- 1 = 1 (The numbers are the same.)
- 4 ≥ -1 (Four is greater than or equal to -1.)

Compare Dates

Dates and times are compared chronologically.

Absolute Dates and Times

For absolute dates, the date format is yyyyMMdd where yyyy is the year, MM is the month, and dd is the day.

- Less than (<): Left value is earlier than the right value
- Greater than (>): Left value is later than the right value

The format for comparing absolute times is HHmmss where HH is the hour (00-23), mm is the minutes (00-59), and ss is the seconds (00-59). To compare absolute date times, use the format yyyyMMddHHmmss.

Examples:

- StudyDate < 20180831 (The study date DICOM tag’s value is earlier than August 31, 2018.)
- StudyDate = 20180101 (The study date is exactly January 1, 2018.)
- StudyDate > 20181113010000 (The study datetime is later than November 13, 2018 at 1:00 a.m.)

Relative Dates

Most commonly, organizations use relative dates that calculate based on today. Configure relative dates in parentheses by using:

- A question mark (?), which indicates today
- Earlier (- or <) or later (+ or >)
- A number
- A unit of day (d), month (m), or year (y)

Examples:

- (?-5d) 5 days before today
- (?+7d) 1 week from today (Note that "w" cannot be used.)
- (?-6m) 6 months ago
- StudyDate < (?-1d) The study date is earlier than yesterday’s date

Check for a Value Using Exists (∃) and Not Exist (∄)

A DICOM tag is evaluated as not existing if any of the following conditions are true:

- The DICOM tag does not exist in the DICOM file at all.
- The DICOM tag exists but has no value.
- The DICOM tag exists but is explicitly set to null or an empty string.

If all of these conditions are false, the DICOM tag exists.

Compare Strings Using Contains (∋) and Does Not Contain (∌)

For tags with string values, you can use the "contains" and "does not contain" operators to match exact text.

- Contains (∋): The right value is within the left value
- Does not contain (∌): The right value is not within the left value

Examples:

- cat ∋ a (The text "cat" contains the letter "a".)
- MIM ∌ 0 (The text “MIM” does not contain "0".)
- dog ∌ go (The text “dog” does not contain the text “go.”)

Match Patterns Using RegEx and Not RegEx

Use a regular expression (RegEx) for the most flexible way to match patterns instead of exact text.

- RegEx evaluates to "true" when Operand_1 matches the pattern defined in Operand_2. Otherwise, it is false.
- Not RegEx evaluates to "true" when Operand_1 does not match the pattern defined in Operand_2.

Examples:

Modality PT | CT - RegEx evaluates to true when the modality of the series is either PT or CT.

Work with Contour ProtégéAI+™ Contours

Optimize Auto-Generated Contours

MIMTD-1068 • 14 Feb 2024

Overview

After reviewing your auto-generated contours, use any MIM® contouring tool to refine the contours as needed. Many MIM users prefer the 2D Brush for this purpose because it is flexible and easy to use. To learn more about the 2D Brush, see Create Contours with the 2D Brush.

Many auto-generated contours require minimal editing. If you find that a contour needs extensive editing, try the following process. It has worked well in MIM testing.

Important: The tools described below are features of MIM software, and are not included with a stand-alone Contour ProtégéAI+™ subscription.

If you do not have MIM, you can use the contouring tools in your treatment planning system to refine Contour ProtégéAI+ contours.

Contents

- Step 1: Erase Contour Slices
    - How the Erase Contour Slices Tool Works
    - Suggestions for Using the Erase Contour Slices Tool
- Step 2: Refine Remaining Slices and Confirm Contour Extents
- Step 3: Interpolate with Contour CoPilot™ and Review Optimized Contour

Step 1: Erase Contour Slices

Erasing contour slices reduces the number of edits you need to make. The resulting gaps in the contour are filled in later using an interpolation tool.

1. With the contour selected in the Contours sidebar, click the double arrow » button at the top of MIM to search all tools.
2. Type "**erase contour slices**" into the tools menu search bar, and press the **Enter** key to activate the tool.

Tip: If you use this tool regularly, you can add it to your toolbar for easy access. Click **Configure Toolbar** at the top of the tools menu and follow the instructions in the window to customize your options.

3. Enter the number of slices to erase, as instructed by the tool dialog, then click **OK**.

How the Erase Contour Slices Tool Works

Caution: Because this tool removes slices at regular, user-specified intervals, it may remove slices from the inferior portion of the contour. It is your responsibility to ensure that the most superior and inferior slices of the volume of interest are contoured appropriately prior to using any interpolation tool to fill in missing slices.

- The Erase Contour Slices tool keeps the most superior slice of the contour, then erases a certain number of slices in the inferior direction, based on your input.
- The tool keeps another single slice, then again deletes the specified number of slices.
- Processing continues in this manner, moving from superior to inferior, until the tool has moved through the entire volume of the contour.

Suggestions for Using the Erase Contour Slices Tool

- There is no specific recommendation for how many slices to erase. Consider the size and shape of the structure to guide your decision.
- For large structures where the shape does not change significantly from slice to slice (e.g., a lung) you may find it helpful to erase as many as 7 or 8 slices.
- For small structures, or those that change significantly from slice to slice, erasing only 2-3 slices in between each kept slice gives you more control over how the contour is recreated.
- In all cases, you must ensure that the most superior and inferior slices of the volume of interest are properly contoured prior to using any interpolation tool to fill in missing slices.

Step 2: Refine Remaining Slices and Confirm Contour Extents

In this step, you refine the remaining contour slices to ensure they are accurate.

1. After erasing slices, use your preferred contouring tool (e.g., the 2D Brush ●) to refine the remaining slices of the contour.

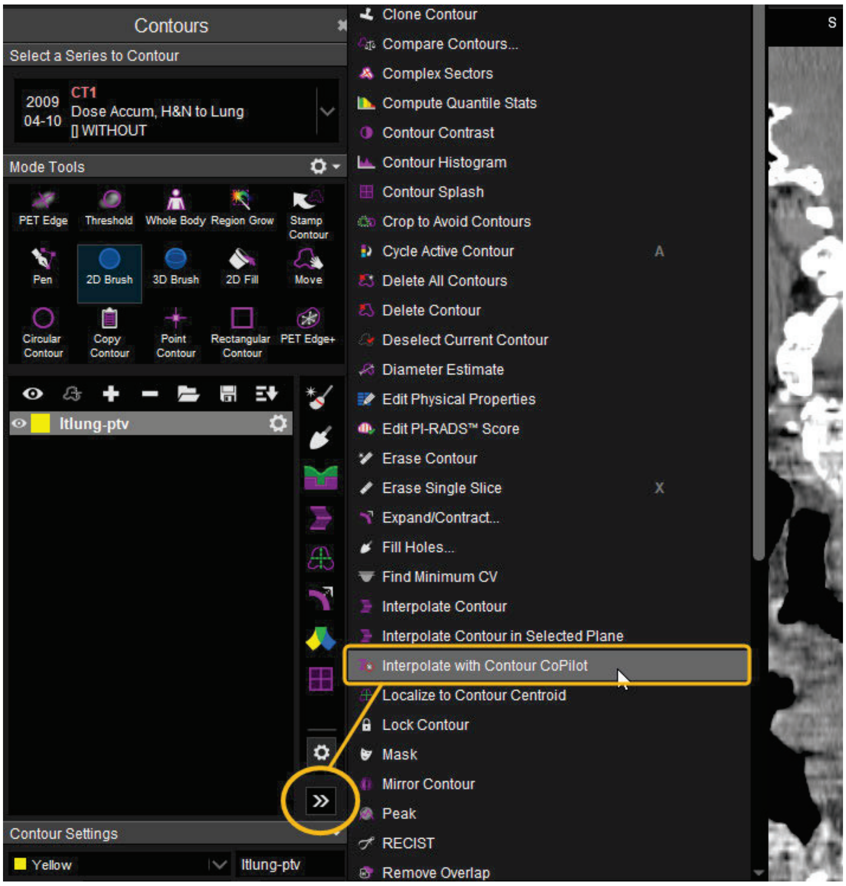
2. If needed, draw new superior or inferior slices to expand the area covered by the contour. You do not need to fill in any of the gaps that were created by erasing slices.

Step 3: Interpolate with Contour CoPilot™ and Review Optimized Contour

You complete the process by using Interpolate with Contour CoPilot to fill in the gaps in the contour. Always review the final contour for accuracy before using it clinically.

1. After making all necessary adjustments, activate the **Interpolate with Contour CoPilot** tool. To find this tool, click the double arrow button in the Contours sidebar.

   Interpolate with Contour CoPilot uses MIM's Contour CoPilot algorithm to deformably interpolate between slices.



Tip: If you use this tool regularly, use the gear ⚙ button near the bottom of the Contours sidebar to add it to your menu.

2. Review the resulting contour and make any necessary adjustments using your preferred contouring tool (e.g., the 2D Brush ●).

Create Contours with the 2D Brush

MIMTD-701 • 29 Aug 2023

Overview

The 2D Brush lets you draw regions of interest on individual slices of a series. It also features companion tools that you can use to save time and increase contouring efficiency.

Contents

- Draw and Erase with the 2D Brush
- Correct a Double 2D Brush
- 2D Brush Companion Tools
  - Companion Tool: Contour CoPilot®
  - Companion Tool: Dynamic Brush™
- Additional Contouring Tools
  - Interpolate with Contour CoPilot
  - Interpolate

Draw and Erase with the 2D Brush

Activate and use the 2D Brush to draw contours freely on any image:

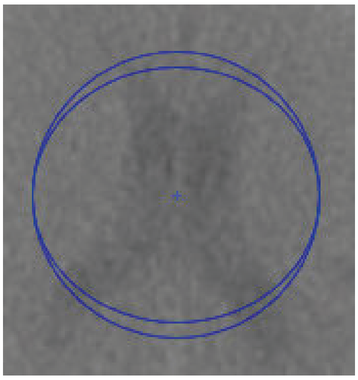
- To draw contours, left-click drag with the 2D Brush.
- To adjust the diameter of the brush, right-click drag up or down.
- To erase, move the brush outside of the contour and then left-click drag.

> **Tip:** When the brush is blue, it is in draw mode. When the brush is red, it is in erase mode.

- To switch between draw and erase modes, press and hold the Alt (Windows®) or Option (macOS®) key. Holding the Alt/Option key allows you to draw non-contiguous regions. This is helpful for areas such as pelvic nodes.

Tip: Enable this behavior without a key modifier by going to Settings ⚙ >> **General Preferences** >> **Contouring** and selecting **Paintbrush will add to existing contour when used a distance outside it**.

Correct a Double 2D Brush



A double 2D Brush (two offset circles instead of one circle) appears when the viewport is showing multiple interpolated slices because a viewing rotation is applied to the series. Contours created with a double 2D Brush are typically not desirable because the contours are drawn on multiple slices at a time.

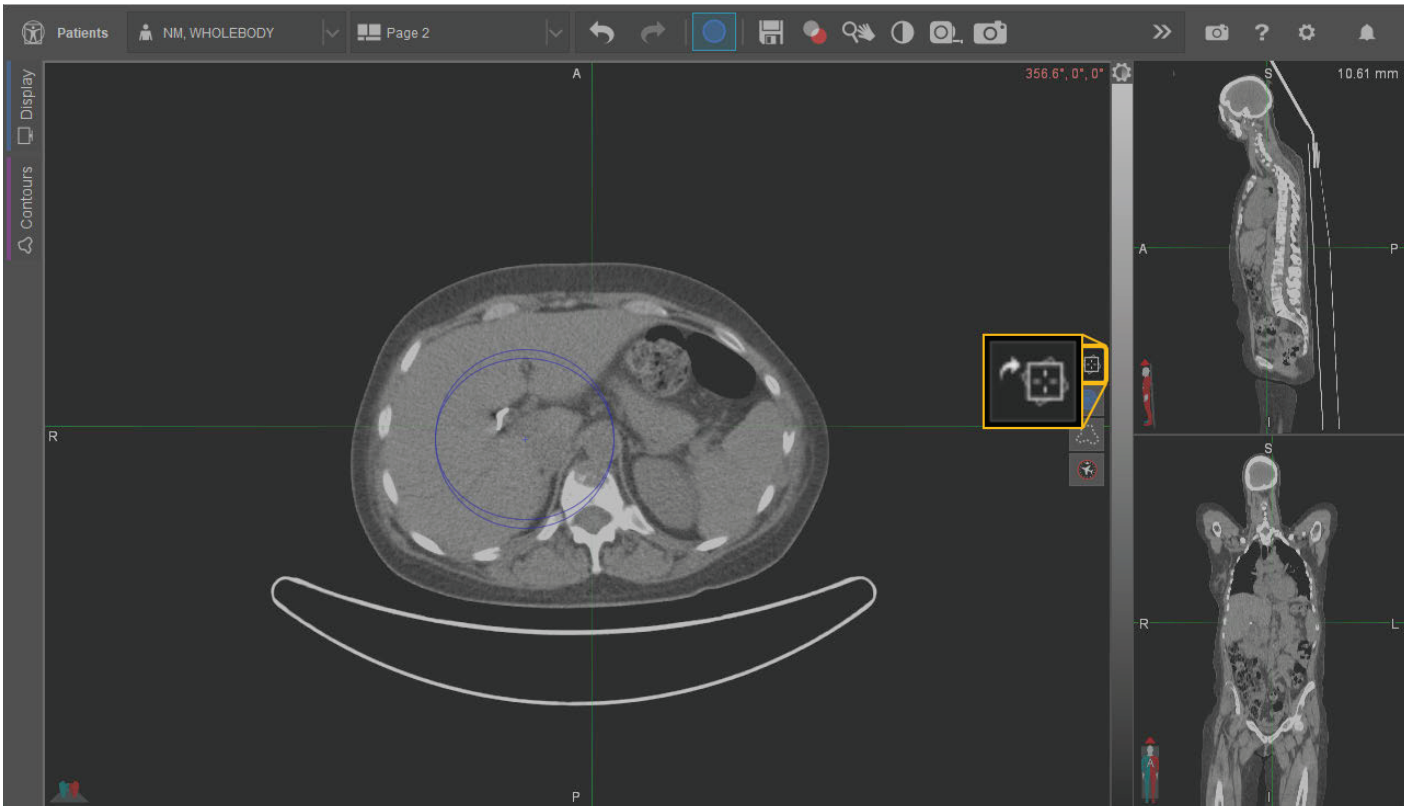
If you see the double 2D Brush, first rule out other issues by confirming the following:

- Ensure that the correct series is selected from the **Select a Series to Contour** dropdown at the top of the Contours sidebar.
- Ensure that the correct contour is selected in the Contours sidebar.

If both of the above settings are correct, follow these steps:

MIM 7.3 and later:

Click the ⟲ 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 after contouring 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.

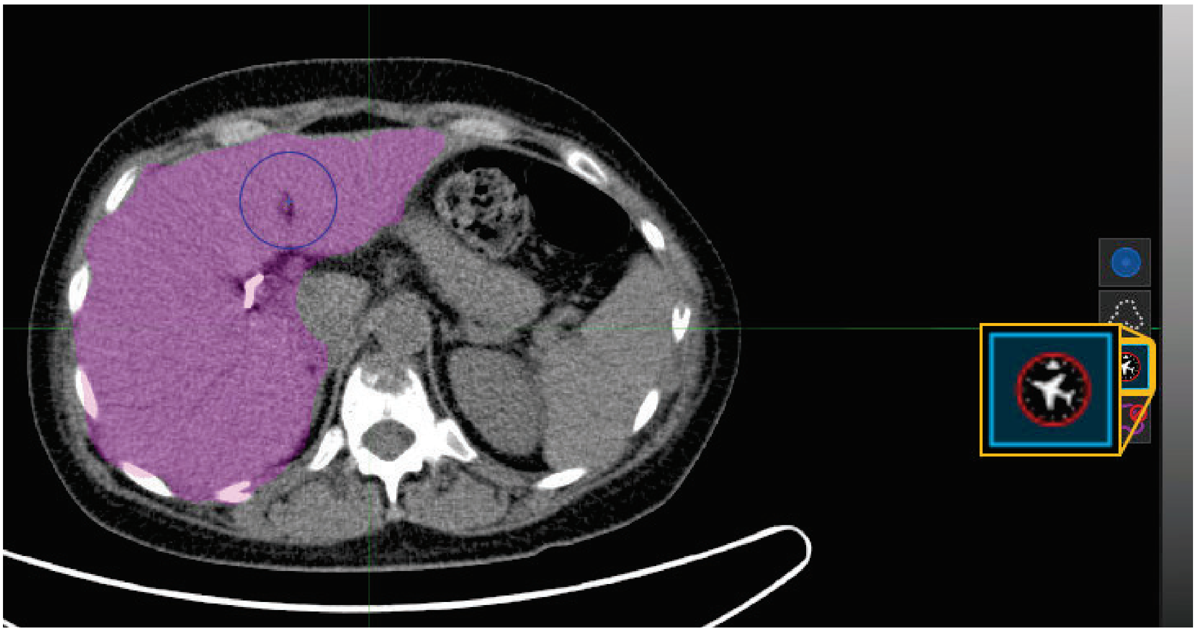
2D Brush Companion Tools

Companion tools offer additional or enhanced functionality to the primary tool.

Companion Tool: Contour CoPilot®

Use Contour CoPilot in conjunction with the 2D Brush to quickly and semi-automatically contour an entire structure by assessing candidate contours. Candidate contours are automatically generated using the information from slices that are already drawn. Using these candidate contours reduces the need to manually draw each slice. MIM displays candidate contours as a color wash over the region being contoured.

1. Activate the **2D Brush** and draw a contour on any slice of any plane.
2. Activate the **Contour CoPilot** tool, found on the right edge of any viewport.

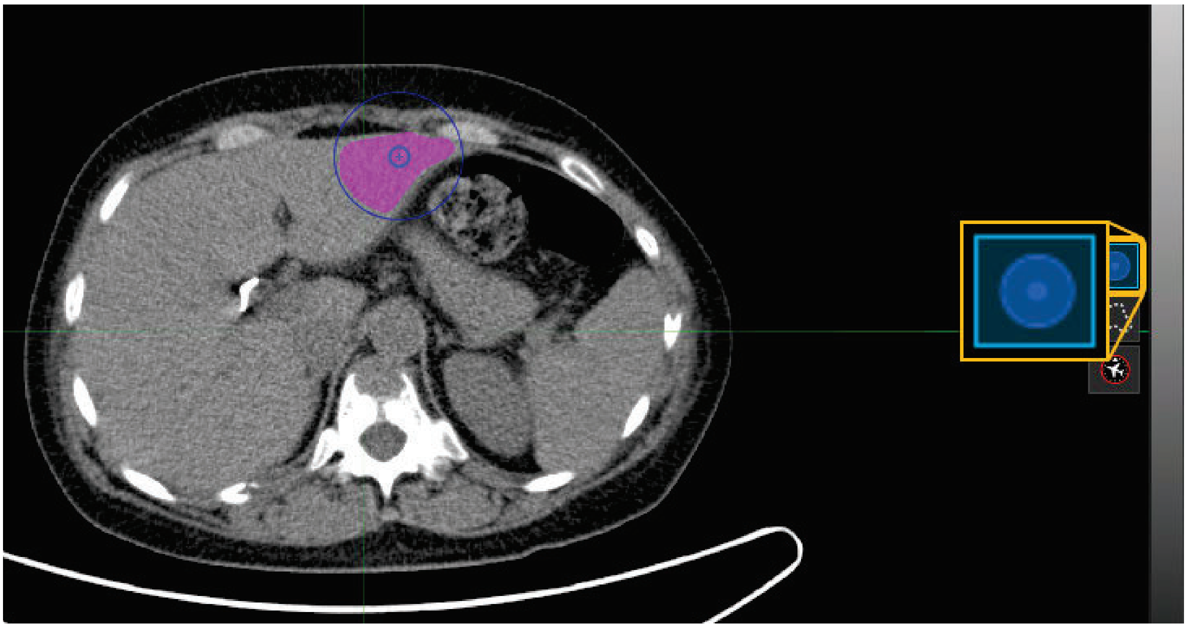


3. Scroll to another slice. A candidate contour automatically appears as a color wash on the visible slice.
4. To accept the contour, click within the viewport. If desired, continue to make edits manually with the 2D Brush.

   To reject a candidate contour, click the button on the right side of the viewport. After rejecting the candidate contour, use the 2D Brush to contour the slice manually.
5. Continue viewing additional slices, accepting candidates, editing, or redrawing contours as desired.

Companion Tool: Dynamic Brush™

Use the Dynamic Brush to contour more quickly. When the Dynamic Brush is activated, the brush samples intensities within the inner circle in order to restrict the brush to areas of similar intensity.

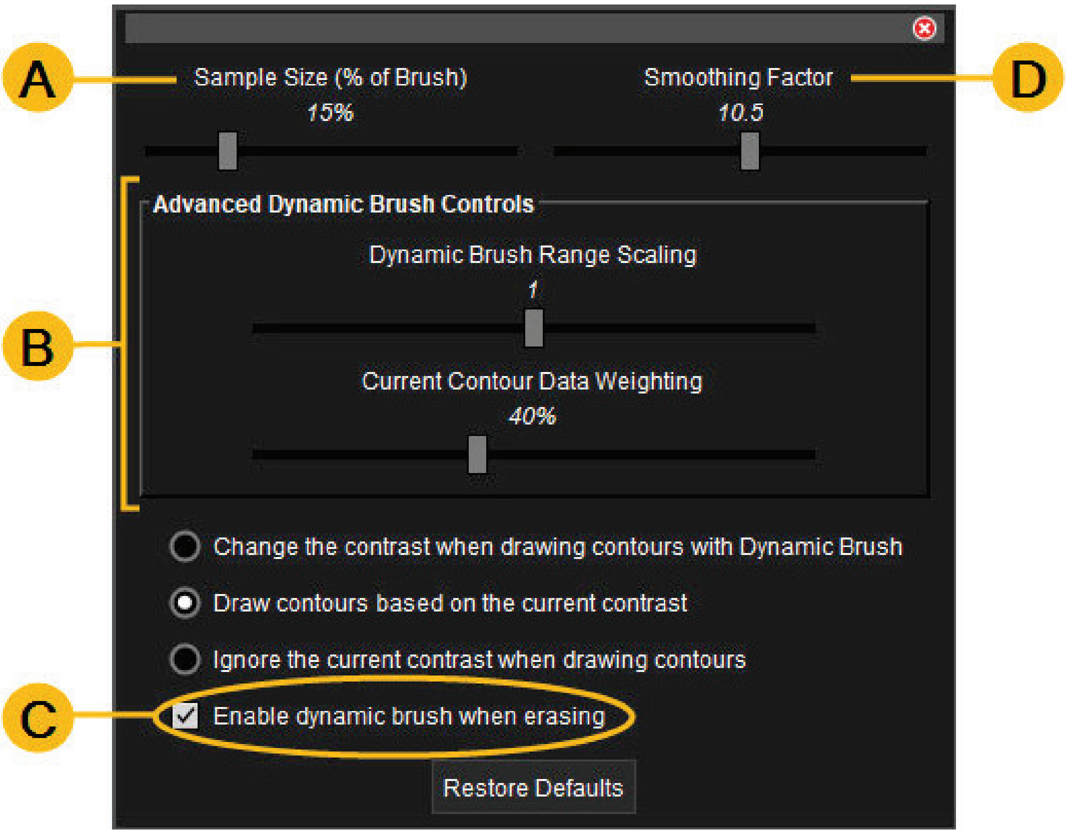


- Activate the 2D Brush, then activate the Dynamic Brush tool, found on the right side of any viewport.
- Left-click drag to draw contours. Keep the inner circle of the brush inside the tissue of interest. The brush dynamically selects only tissue within a range generated from the inner circle.
- Right-click drag up or down to adjust the diameter of the brush.
- Right-click the **Dynamic Brush** ◉ button to open an advanced settings window.

> **Related:** For more information about advanced settings, see Advanced Dynamic Brush Settings.

Advanced Dynamic Brush Settings

Adjust advanced settings for the Dynamic Brush by activating the 2D Brush and right-clicking the **Dynamic Brush** ◉ button on the right side of any viewport.



Sample Size (% of Brush)
15%

Smoothing Factor
10.5

Advanced Dynamic Brush Controls

Dynamic Brush Range Scaling
1

Current Contour Data Weighting
40%

○ Change the contrast when drawing contours with Dynamic Brush

● Draw contours based on the current contrast

○ Ignore the current contrast when drawing contours

☑ Enable dynamic brush when erasing

A. **Sample Size** — Adjust the inner circle of the brush.

B. **Advanced Dynamic Brush Controls:**

  - **Dynamic Brush Range Scaling** — Adjust the range of included voxels to compare to the interior of the sampling ring. 0 is the narrowest range of values, while 2 is the widest range of values.
  - **Current Contour Data Weighting** — Choose whether the Dynamic Brush prediction includes the area covered by the existing contour or just the area within the sampling circle.

C. **Enable dynamic brush when erasing** — When in erase mode, the inner circle samples what to erase instead of what to draw.

D. **Smoothing Factor** — Adjust the smoothness of the potential contour. 0 gives you the roughest potential contour and 20 gives you the smoothest potential contour.

Tip: For best results with liver tissue, set the Sample Size to 15% and the Smoothing Factor to 2.5.

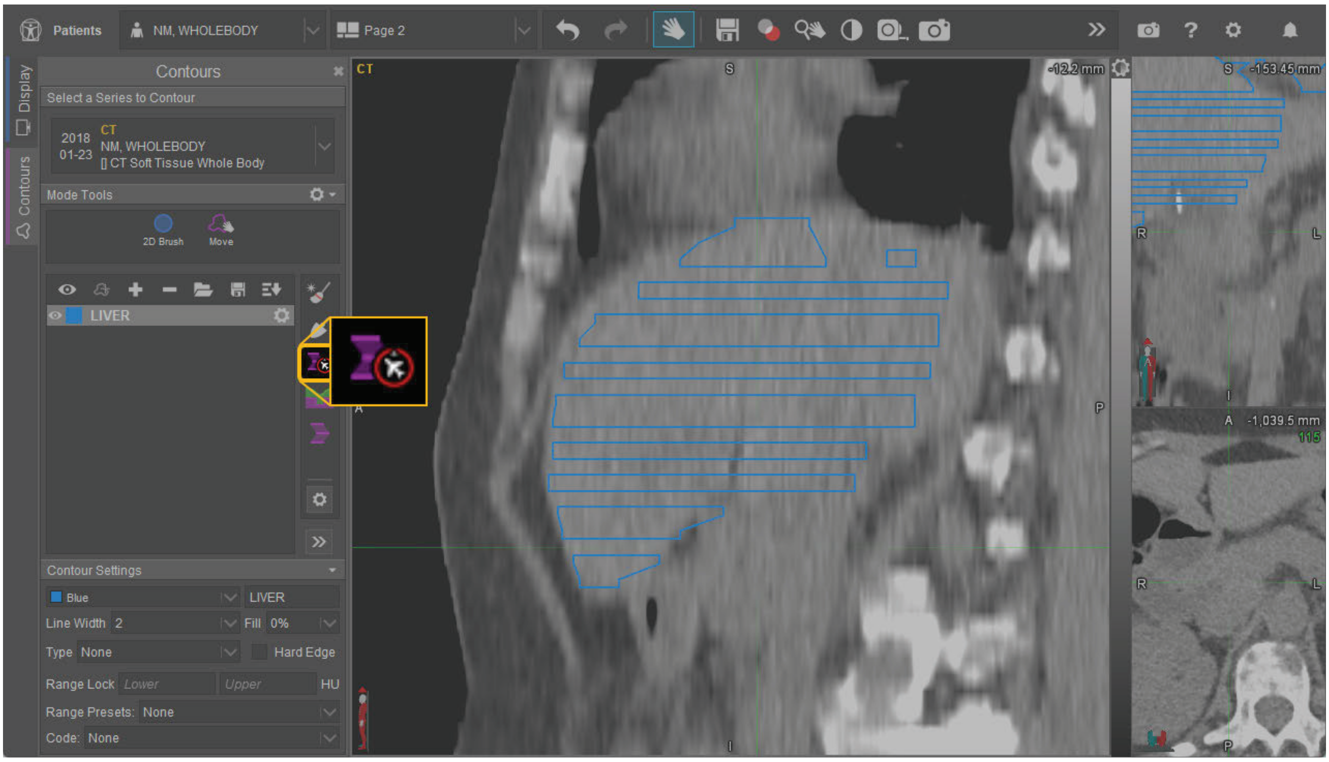
Additional Contouring Tools

Interpolate with Contour CoPilot

Use the Interpolate with Contour CoPilot tool to save time by skipping slices when contouring. Interpolate with Contour CoPilot utilizes the Contour CoPilot algorithm to dynamically interpolate between slices, as opposed to the traditional Interpolate tool, which performs linear interpolation.

To use the Interpolate with Contour CoPilot tool, follow the steps below:

1. Contour a slice.
2. Scroll to skip one or more slices, then contour another slice.
3. Repeat the previous steps until there are contours covering the entire structure.
4. Click the **Interpolate with Contour CoPilot** tool in the Contour Editing Tools menu to fill in the remaining slices.



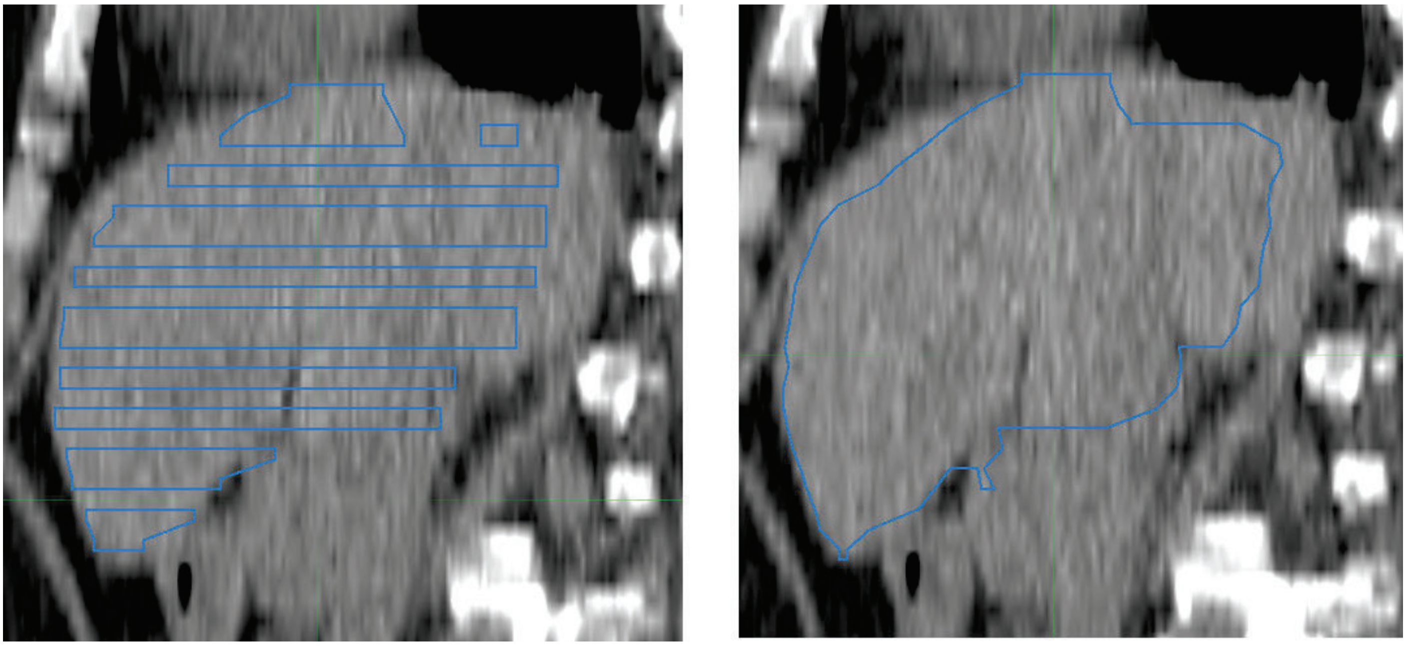
Blue
LIVER
Line Width 2
Fill 0%
Type None
Hard Edge
Range Lock Lower Upper HU
Range Presets: None
Code: None

Tip: Interpolate with Contour CoPilot may not appear in the Contour Editing Tools menu by default. You can locate the tool by clicking on the » button. Or, click the ⚙ button at the bottom of the Contour Editing Tools menu to choose which tools are always shown in the menu.

Interpolate

Use the Interpolate tool to save time by skipping slices when contouring. The Interpolate tool fills in the remaining slices using linear interpolation.

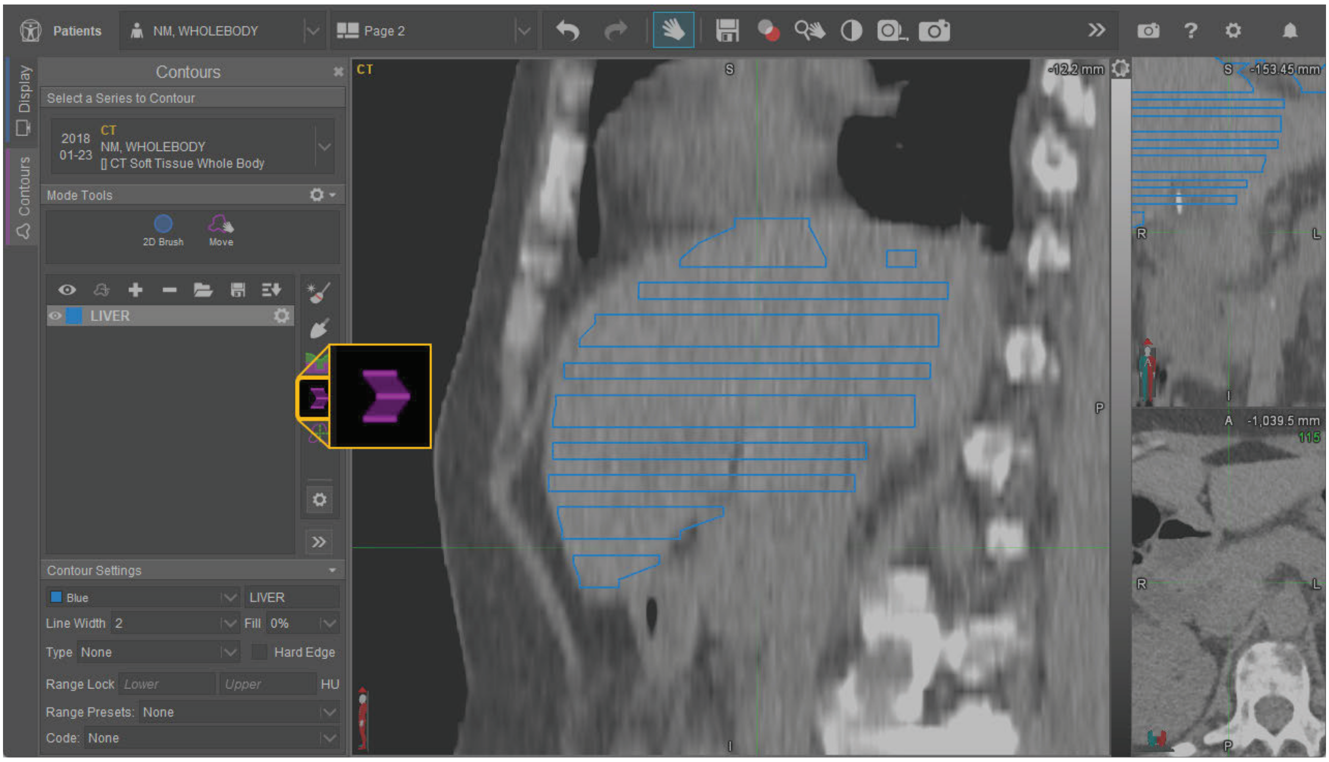
Tip: The Interpolate tool only works on contours created in an image's default acquisition plane. For example, using the tool in the axial plane of a sagittally acquired CT has no effect.



The image on the left shows the manually contoured slices. The image on the right shows the remaining slices filled after interpolation.

To use the Interpolate tool, follow the steps below:

1. Contour a slice.
2. Scroll to skip one or more slices, then contour another slice.
3. Repeat the previous steps until there are contours covering the entire structure.
4. Click the **Interpolate** button in the Contour Editing Tools menu to fill in the remaining slices.



2018
01-23
CT
NM, WHOLEBODY
[] CT Soft Tissue Whole Body

Blue LIVER
Line Width 2
Fill 0%
Type None
☐ Hard Edge
Range Lock Lower Upper HU
Range Presets: None
Code: None

-12.2 mm
-153.45 mm
-1,039.5 mm

Check Progress or Manually Launch Processing

Check the Progress of a Contour ProtégéAI+™ Case

MIMTD-1668 • 19 Sep 2023

Overview

There are many factors that may affect the speed of Contour ProtégéAI+ processing, including:

- Configuration type
- Local network traffic
- Specifications of local hardware

If a case is taking longer than expected, follow the steps below to check its progress.

Procedure

Check the Status of the Job in the MIMapp Catalyst Manager (Cloud-hosted deployments only)

> **Important:** If any of the icons or menu options in these directions are not available to you, they may be restricted by your organization. Please contact your organization's MIMcloud administrator for assistance.

1. Click the ☁ icon in the upper-right corner of MIM.
2. If you are not already logged in, log in to MIMcloud. Then, click the ☁ icon again to reopen the MIMcloud menu.
3. Click **Open MIMapp Catalyst Manager...**.
4. Open the **Patient Data Source** dropdown in the upper-left corner of the MIMapp Catalyst Manager.
5. Select the group that is configured for your organization's Contour ProtégéAI+ processing. This group is usually called **[organization name] Protege Processing**.
6. Look for the patient in the **Waiting** or **Running** tables of the MIMapp Catalyst Manager. If you see the patient in either of these tables, processing is functioning as expected. Please wait for the case to finish processing.
7. If the patient is not listed in the Waiting or Running tables of the MIMapp Catalyst Manager, look for the patient in the **Completed** table:

   If the patient is listed in the Completed table: Proceed to the next step.

If the patient is not listed in the Completed table: The issue is likely related to networking or MIM Assistant filtering. Please skip to the section titled Check the Status of the Job in the MIM Assistant Manager, below.

8. Check the **Status** column of the Completed table to confirm the status of the case:
    - *If the status is **Finished***:
        i. Please ask an administrative user to contact MIM Software Support. The administrative user must have access to the MIM Assistant server.
        ii. The administrative user should inform a MIM Clinical Support Engineer that the case has processed successfully, but the results are not available in the patient list. The Clinical Support Engineer will assist with further troubleshooting.
    - *If the status is **Failed***:
        i. Please make a note of the **Task ID** in the MIMapp Catalyst Manager.
        ii. Provide the Task ID to a MIM administrative user, and ask them to contact MIM Software Support for assistance with additional troubleshooting.

Check the Status of the Job in the MIM Assistant Manager

Important: This troubleshooting must be done on the MIM Assistant server.

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Select **MIM Assistant Manager...**.
3. Look for the patient's name in the tables on the **Activity** tab of the MIM Assistant Manager.
    - *If you see the patient in the **Waiting for Study**, **Waiting Workflow Jobs**, or **Running Jobs** tables:* MIM Assistant is processing the job as expected. Please wait for the job to complete.
    - *If you see the patient in the **Completed Jobs** table, but you still do not see the contours in your patient list:*
        i. Please make a note of any information in the "Status" and "Message" columns of the **Completed Jobs** table.
        ii. Contact MIM Software Support at support.mimsoftware.com.

Manually Launch Contour ProtégéAI+™ Processing

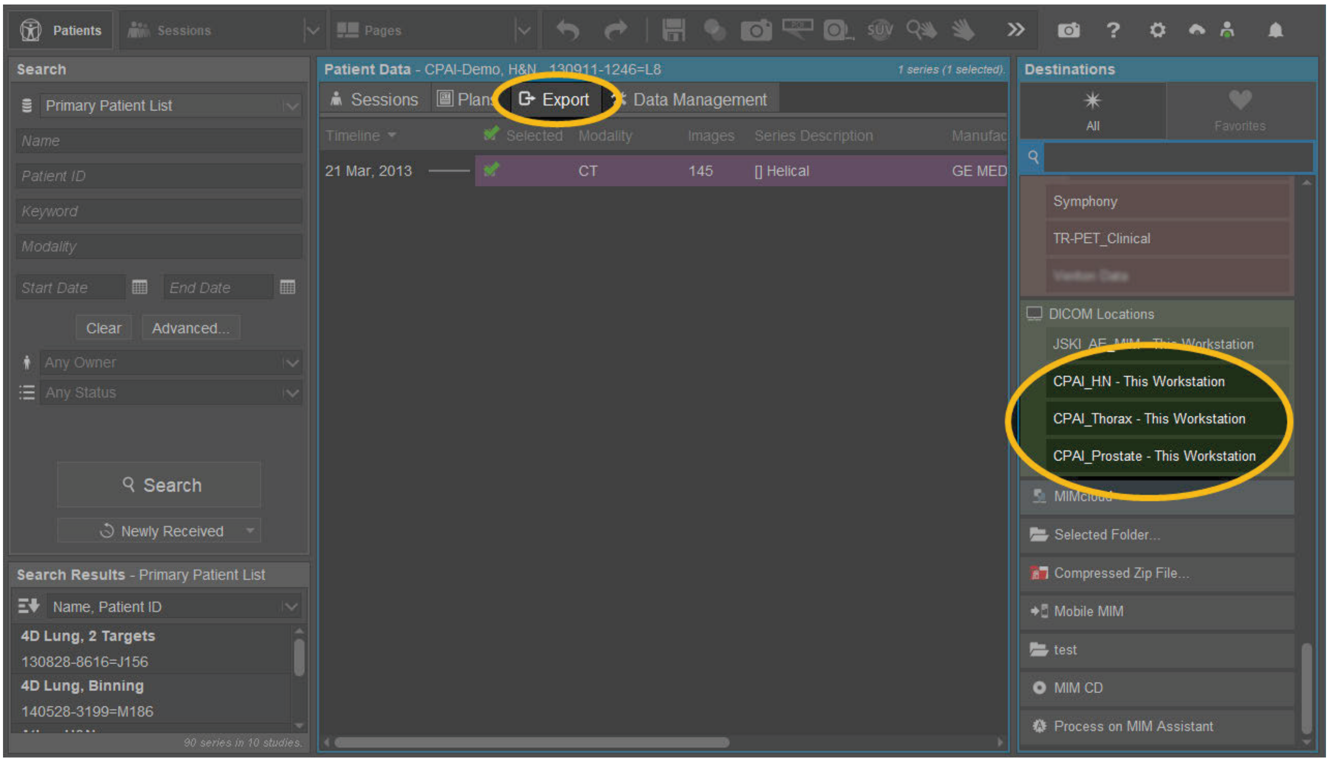
MIMTD-1096 • 12 Feb 2024

Overview

Contour ProtégéAI+ processing is normally initiated automatically, and the results of this processing are returned to a designated patient list. However, there will likely be occasional cases that do not follow your normal workflow, or do not meet the criteria to trigger automatic processing. For these cases, you can initiate Contour ProtégéAI+ processing manually.

Radiation Oncology Patient List

1. Search for the patient in MIM as you normally would.
2. Click the **Export** tab near the top of the screen.

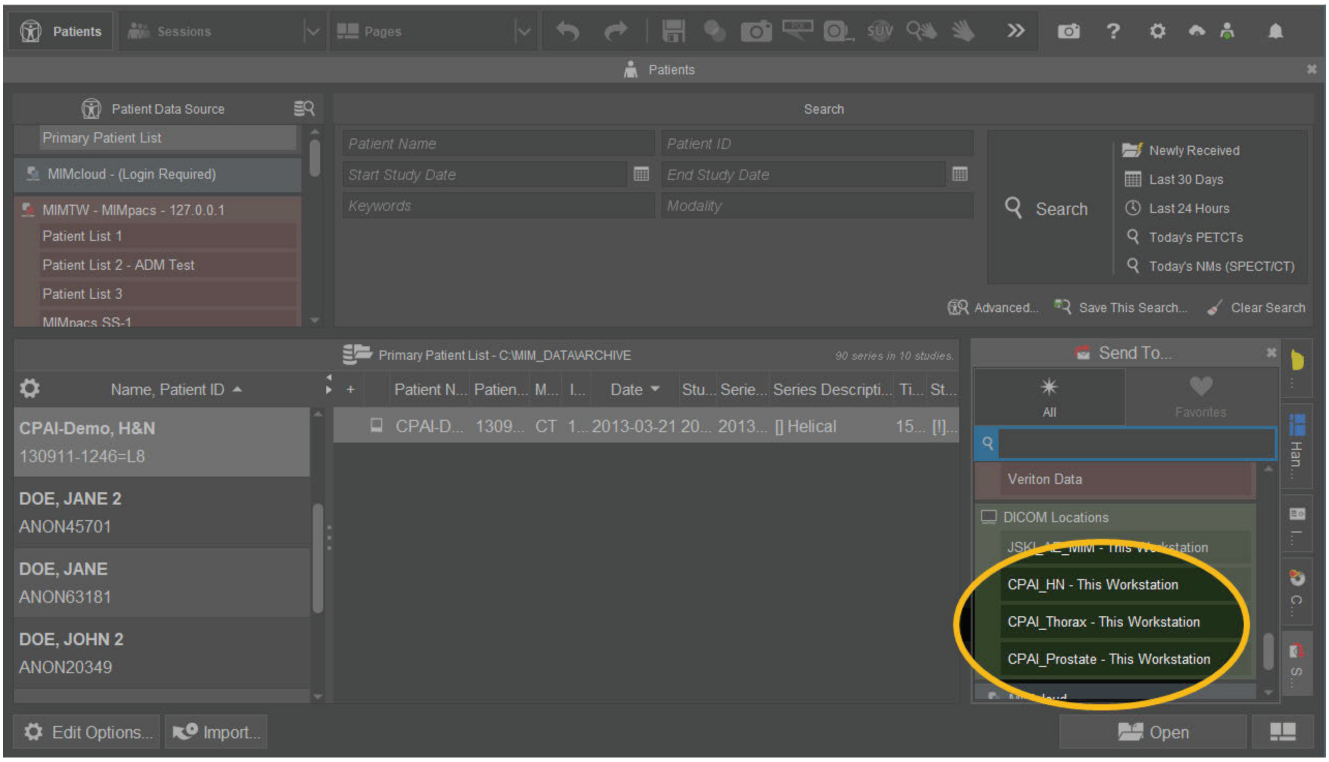


3. Select the CT or MR that you want to process using Contour ProtégéAI+.
4. In the **Destinations** panel along the right side of the screen, click the appropriate destination for manual Contour ProtégéAI+ processing, based on the case type. These destinations typically start with **CPAI_** followed by an abbreviation of the anatomical region they segment (e.g., **CPAI_HN**, for head and neck processing).

Tip: Contour ProtégéAI+ processing normally takes several minutes. The RTstruct will be returned to the same patient list that RTstructs are sent to after automated processing.

Classic Patient List

1. Search for the patient in MIM as you normally would.



2. Select the CT or MR that you want to process using Contour ProtégéAI+.
3. Open the **Send To...** tab along the right side of the screen.
4. Click the appropriate Send To... destination for manual Contour ProtégéAI+ processing, based on the case type. These destinations typically start with **CPAI_** followed by an abbreviation of the anatomical region they segment (e.g., **CPAI_HN**, for head and neck processing).

Tip: Contour ProtégéAI+ processing normally takes several minutes. The RTstruct will be returned to the same patient list that RTstructs are sent to after automated processing.

Appendix

Contour ProtégéAI+™ Models and Contours (September 2024)

MIMTD-1480 • 29 Aug 2024

Contours shown in **bold** are new to this model version.

Abdomen 4.0.0

This model is intended to be used alongside MIM’s suite of tools in radiation therapy treatment planning.

Bladder	Cauda Equina	Liver
Bowel	Kidney L	Spinal Cord
Bowel Bag	Kidney R	Stomach

Head & Neck 4.1.1

This model is intended to be used alongside MIM®’s suite of tools in radiation therapy treatment planning.

Brachial Plexus L	Lacrimal Gland R	LN Neck III L	Optic Chiasm
Brachial Plexus R	**Larynx**	LN Neck III R	Optic Nerve L
Brain	Lens L	LN Neck IV L	Optic Nerve R
Brainstem	Lens R	LN Neck IV R	Oral Cavity
Cochlea L	Lips	LN Neck V L	Parotid L
Cochlea R	LN Neck IA	LN Neck V R	Parotid R
Constrictor Muscles	LN Neck IB L	LN Neck VIA	Pituitary
Cricoid	LN Neck IB R	LN Retropharynx L	Spinal Cord
Esophagus	LN Neck IIA L	LN Retropharynx R	Submandibular Gland L
Eye L	LN Neck IIA R	LN Retrostyloid L	Submandibular Gland R
Eye R	LN Neck IIB L	LN Retrostyloid R	Thyroid
Lacrimal Gland L	LN Neck IIB R	Mandible	**Trachea**

Pelvis 4.1.1

This model is intended to be used alongside MIM's suite of tools in radiation therapy treatment planning.

Bladder	Femur Head R	Prostate	Seminal Vesicle
Bowel	LN Iliac	Rectum	Sigmoid Colon
Femur Head L	Penile Bulb	Sacrum	

SurePlan™ MRT 4.0.0

This model is intended to be used alongside MIM's suite of tools in the planning of Molecular Radiotherapy treatments.

Bone	Lacrimal Gland R	Parotid L	Submandibular Gland R
Kidney L	Liver	Parotid R	Thyroid
Kidney R	Lung L	Spleen	
Lacrimal Gland L	Lung R	Submandibular Gland L	

Thorax 4.1.1

This model is intended to be used alongside MIM's suite of tools in radiation therapy treatment planning.

Brachial Plexus L	Constrictor Muscles	Liver	LN Sclav L
Brachial Plexus R	Esophagus	LN Ax L1 L	LN Sclav R
Breast L	Great Vessels	LN Ax L1 R	Lung L
Breast L RTOG	Heart	LN Ax L2 L	Lung R
Breast R	Humerus Head L	LN Ax L2 R	Pancreas
Breast R RTOG	Humerus Head R	LN Ax L3 L	Spinal Cord
Bronchus	Kidney L	LN Ax L3 R	Stomach
Carina	Kidney R	LN IMN L	Thyroid
Cricoid	Larynx	LN IMN R	Trachea

Whole Body - Physiological Uptake Organs 4.1.0

This model is intended to be used alongside MIM's suite of tools in the analysis of PET/CT and SPECT/CT images.

Bladder	Oral Cavity	Heart	Parotid L
Bone	Lacrimal Gland L	Kidney L	Parotid R
Bowel	Lacrimal Gland R	Kidney R	Prostate
Bowel Bag	Submandibular Gland L	Liver	Spleen
Brain	Submandibular Gland R	LN Iliac	

Prostate 1.0.1 (MR)

This model is intended to be used alongside MIM's suite of tools in radiation therapy treatment planning.

Prostate	Urethra	Seminal Vesicle

Contour ProtégéAI+™ 4.1.1 Model Training Data Demographics

MIMTD-1702 • 04 Mar 2024

Overview

The 257 training data images for the three 4.1.1 CT neural network models included the following available demographics: age, sex, contrast/non-contrast, and CT scanner make/model. The training data was anonymized to remove PHI, and these demographics are the only ones available after anonymization. The N/A category for each demographic means that the DICOM information for that tag was missing, corrupt, or lost during anonymization.

Table 1: Training Data Breakdown by Sex for 4.1.1 Models

Sex	Head & Neck	Thorax	Pelvis
Male	63	18	67
Female	42	84	0
N/A*	29	16	3
Total:	134	118	70

Table 2: Training Data Breakdown by Age for 4.1.1 Models

Age	Head & Neck	Thorax	Pelvis
1-20	0	0	0
20-40	2	4	1
40-60	9	23	7
60+	18	24	32
N/A*	105	67	30
Total:	134	118	70

Table 3: Training Data Contrast vs. Non-Contrast for 4.1.1 Models

Age	Head & Neck	Thorax	Pelvis
Contrast	32	5	12
Non-Contrast	102	113	58
Total:	134	118	70

Table 4: Training Data Breakdown by Manufacturer and Scanner Model for 4.1.1 Models

Manufacturer	Scanner Model	% of Head & Neck Data	% of Thorax Data	% of Pelvis Data
GE Medical Systems	Brightspeed	1.49%	1.69%	0.00%
	Discovery CT590 RT	5.22%	0.85%	0.00%
	Discovery RT	2.24%	0.85%	1.43%
	Discovery ST	0.00%	0.00%	1.43%
	LightSpeed Plus	0.00%	0.00%	2.86%
	LightSpeed QX/i	0.00%	0.00%	4.29%
	LightSpeed RT	0.00%	0.00%	11.43%
	LightSpeed RT16	5.22%	0.00%	5.71%
	Optima 560	11.19%	8.47%	2.86%
	Optima CT580	0.75%	0.85%	0.00%
	Revolution EVO	2.24%	1.69%	0.00%
Phillips	Brilliance Big Bore	26.87%	22.88%	21.43%
	GEMINI TF Big Bore	2.99%	3.39%	0.00%
Siemens	Biograph 16	0.00%	1.69%	1.43%
	Biograph 6	1.49%	9.32%	1.43%
	Biograph64	0.00%	3.39%	0.00%
	Emotion 16	0.00%	2.54%	0.00%
	Emotion 16 (2007)	0.00%	0.85%	0.00%
	Emotion 6	0.00%	0.85%	1.43%
	Emotion 6 (2007)	0.00%	0.85%	4.29%
	Sensation Open	0.75%	0.85%	0.00%
	SOMATOMConfidence	0.00%	8.47%	5.71%
	SOMATOM Definition AS	0.00%	4.24%	5.71%
Toshiba	Aquilion/LB	5.97%	6.78%	1.43%
N/A*	N/A	33.58%	19.49%	27.14%

*The N/A category for each demographic means that the DICOM information for that tag was removed during the anonymization process.

Contour ProtégéAI+™ 4.1.0 Whole Body - Physiological Uptake Organs Model Training Data Demographics

Overview

The 485 training data images for the 4.1.0 *Whole Body - Physiological Uptake Organs* CT neural network model included the following demographics: age, sex, contrast/non-contrast, and CT scanner make/model. The training data was anonymized to remove PHI, and these demographics are the only ones available after anonymization. The N/A category for each demographic means that the DICOM information for that tag was missing, corrupt, or lost during anonymization.

Table 5: Breakdown by Sex

Sex	# of Images
Male	310
Female	84
N/A*	91
Total:	485

Table 6: Breakdown by Age

Age	# of Images
1-20	1
20-40	6
40-60	33
60+	109
N/A*	336
Total:	485

Table 7: Breakdown by Contrast vs. Non-Contrast

Image Type	# of Images
Contrast	211
Non-Contrast	274
Total:	485

Table 8: Breakdown by Manufacturer and Scanner Model

Manufacturer	Scanner Model	% of Data
GE Medical Systems	Brightspeed	0.62%
	Discovery CT590 RT	2.27%
	Discovery IQ	0.62%
	Discovery MI	0.21%
	Discovery RT	1.65%
	Discovery ST	0.21%
	HiSpeed QX/i	0.21%
	LightSpeed Plus	0.41%
	LightSpeed QX/i	1.03%
	LightSpeed RT	2.27%
	LightSpeed RT16	2.47%
	LightSpeed16	0.21%
	Optima 560	3.71%
	Optima CT580	0.82%
	Optima CT660	1.24%
	Revolution EVO	0.62%
	SafeCT	0.21%
Philips	Big Bore	0.62%
	Brilliance 64	0.41%
	Brilliance Big Bore	31.96%
	GEMINI TF Big Bore	0.82%
	Ingenuity TF PET/CT	6.60%
	Vereos PET/CT	0.21%

Manufacturer	Scanner Model	% of Data
Siemens	Biograph 16	0.41%
	Biograph 6	1.03%
	Biograph 64	0.41%
	Biograph64_mCT 3R	0.21%
	Emotion 16	0.21%
	Emotion 16 (2007)	0.21%
	Emotion 6	0.21%
	Emotion 6 (2007)	2.89%
	Sensation Open	0.41%
	SOMATOM Confidence	2.89%
	SOMATOM Definition AS	1.24%
	SOMATOM Definition AS+	0.41%
	SOMATOM Definition Edge	0.41%
	SOMATOM Definition Flash	0.62%
Toshiba	Aquilion/LB	2.68%
	Aquilion ONE	0.41%
N/A*	N/A	25.98%

*The N/A category for each demographic means that the DICOM information for that tag was removed during the anonymization process.

Contour ProtégéAI+™ 4.1.1 Model Testing Data Demographics

MIMTD-1703 • 04 Mar 2024

Overview

The 888 testing images for the three 4.1.1 CT neural network models included the following demographics: age, sex, and CT scanner make/model. The testing data was anonymized to remove PHI, and these demographics are the only ones available after anonymization. The N/A category for each demographic means that the DICOM information for that tag was missing, corrupt, or lost during anonymization.

Table 1: Testing Data Breakdown by Sex for 4.1.1 Models

Sex	Head & Neck	Thorax	Pelvis
Male	147	151	235
Female	101	274	39
N/A*	0	80	51
Total:	248	505	325

Table 2: Testing Data Breakdown by Age for 4.1.1 Models

Age	Head & Neck	Thorax	Pelvis
1-20	2	2	0
20-40	12	26	8
40-60	50	117	29
60+	98	278	239
N/A*	86	82	49
Total:	248	505	325

Table 3: Testing Data Breakdown by Manufacturer and Scanner Model for 4.1.1 Models

Manfacturer	Scanner Model	% of Head & Neck Data	% of Thorax Data	% of Pelvis Data
GE Medical Systems	Discovery 710	0.40%	0.20%	0.00%
	Discovery RT	2.02%	1.58%	0.00%
	Discovery ST	3.63%	0.00%	0.00%
	LightSpeed QX/i	0.00%	0.00%	10.77%
	LightSpeed RT16	5.24%	2.97%	3.38%
	LightSpeed Xtra	0.00%	11.68%	1.54%
	LightSpeed16	0.40%	0.20%	0.00%
	Optima 560	0.00%	1.98%	0.00%
	Optima CT580	16.53%	24.16%	8.00%
	Revolution EVO	0.00%	0.79%	0.62%
Marconi Medical Systems	PQ5000	2.02%	0.00%	0.00%
Phillips	Brilliance 40	0.40%	0.00%	0.00%
	Brilliance Big Bore	25.0%	20.59%	1.54%
	Gemini	0.40%	0.00%	0.00%
Siemens	Biograph20	0.00%	0.20%	0.00%
	Emotion	0.00%	0.40%	0.00%
	Sensation 64	0.00%	0.59%	0.00%
	Sensation Open	0.00%	0.00%	10.77%
	SOMATOM Confidence	12.50%	14.46%	5.23%
	SOMATOM Definition AS	0.00%	1.78%	0.00%
	SOMATOM go.Sim	0.00%	0.59%	0.00%
Toshiba	Aquilion	0.00%	0.59%	0.00%
N/A*	N/A	31.45%	17.23%	58.15%

*The N/A category for each demographic means that the DICOM information for that tag was removed during the anonymization process.

Contour ProtégéAI+™ 4.1.0 Whole Body - Physiological Uptake Organs Model Testing Data Demographics

Overview

The 361 testing data images for the 4.1.0 *Whole Body - Physiological Uptake Organs* CT neural network model included the following demographics: age, sex, and CT scanner make/model. The testing data was anonymized to remove PHI, and these demographics are the only ones available after anonymization. The N/A category for each demographic means that the DICOM information for that tag was missing, corrupt, or lost during anonymization.

Table 4: Breakdown by Sex

Sex	# of Images
Male	167
Female	151
N/A*	43
Total:	361

Table 5: Breakdown by Age

Age	# of Images
1-20	2
20-40	19
40-60	70
60+	153
N/A*	117
Total:	361

Table 6: Breakdown by Manufacturer and Scanner Model

Manufacturer	Scanner Model	% of Data
GE Medical Systems	Discovery RT	1.39%
	LightSpeed QX/i	9.70%
	LightSpeed RT16	6.93%
	LightSpeed16	0.28%
	Optima CT580	18.01%

Manufacturer	Scanner Model	% of Data
Siemens	Biograph 16	0.28%
	Biograph 20	0.55%
	Biograph 64	1.94%
	Emotion	0.55%
	Sensation 64	0.83%
	Sensation Open	9.70%
	SOMATOM Confidence	17.45%
	SOMATOM Definition AS	0.55%
	Symbia Intevo 16	3.88%
	SOMATOM go.Sim	0.55%
Toshiba	Aquilion	0.28%
N/A	N/A	27.15%

*The N/A category for each demographic means that the DICOM information for that tag was removed during the anonymization process.

Contour ProtégéAI+

WHITE PAPER

Automated Contouring Using Neural Networks

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Introduction

Automated segmentation of structures on medical images has always been challenging. In clinical practice, much of the segmentation is performed manually, which is highly time-consuming. Many semi- and fully-automated algorithms have been developed to aid physicians in contouring, such as thresholding[1], edge detection based methods[2], deformable models[3], and atlas-based registration[4].

However, many structures have various textural and intensity patterns, making it almost impossible for any single computer vision-based algorithm to work effectively in a universal fashion. In recent years, research on the use of neural networks has grown rapidly. The performance of these networks on many computer vision tasks has often surpassed that of a human, such as in image classification tasks like ImageNet[5].

Contour ProtégéAI+™ provides a neural network framework for automated contouring of normal structures on CT and MR images.

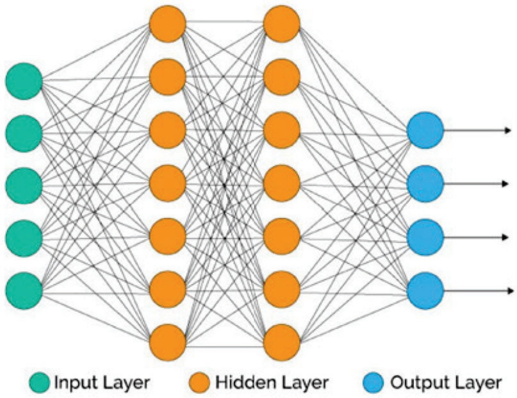

FIGURE 1 *Schematic of a basic neural network*

Neural networks attempt to mimic how the human brain works. The brain consists of billions of neurons. Each neuron receives multiple signals from other neurons and sends out a signal based on those inputs. These neurons are often organized into layers, allowing the brain to use simple building blocks to process complicated input signals. Figure 1 shows an example of a basic neural network. Each line has a weight and an associated bias.

Therefore, each node calculates a weighted sum of its inputs and then applies some activation function. The output is then sent to the next node until the final output layer is reached. When training a neural network, pairs of inputs and desired outputs are shown. The network learns to adjust the network parameters to minimize the difference between its outputs and the desired outputs. Essentially, neural networks learn to recognize patterns much in the same way the human brain does. This pattern learning is what makes neural networks so powerful, allowing them to exceed the performance of traditional methods.

Contour ProtégéAI+'s neural network model is based on the U-Net architecture, which has been used for segmentation in numerous different applications. The model consists of many layers of weights and biases as mentioned above to transform the input image to a segmentation mask for each structure at the final output layer. This output is then post-processed to keep the single, largest connected component. Appropriate image visualization software must be used to review and, if necessary, edit results automatically generated by Contour ProtégéAI+.

Training and Validation

A large, multi-institution dataset was assembled for training, along with a separate, large multi-institution dataset for validation. None of the validation data came from any of the institutions from the training pool. The mean and standard deviation of the model performance on this validation set was then calculated.

Results

Five different sets of metrics were used to assess the performance of the neural network segmentations:

1. Dice coefficient - a measure of the spatial overlap between the ground truth contours and the neural network segmentations.
2. Mean distance to agreement (MDA) - the mean symmetric surface distance between the ground truth contours and the neural network segmentations.
3. Qualitative user feedback score - assessment of contour quality by experienced users on a scale of 1-3 (none, moderate, significant time savings compared to contouring from scratch).
4. Localization success - percentage of images where the structure was correctly localized by the neural network segmentation.
5. Added path length (APL) - a measure of the cumulative amount of editing in mm needed to match the ground truth contour.

Tables 1-3 tabulate the Dice, MDA, user feedback score, and localization success for each of the models, and Table 4 shows the APL per model. Figures 2-7 compare the mean Dice and mean MDA of the neural network and MIM Software's atlas using majority vote 5. In all cases, Contour ProtégéAI+'s neural network segmentations were proportionate or superior to atlas-based segmentation.

Structure	Mean ± Std Dice	MDA (Mean ± Std mm)	Beta User Feedback Score	Localization Success on Relavant FOV CTs	Localization Success on Whole Body CTs
Bone_Mandible	0.86 ± 0.07	0.64 ± 0.31	2.86	100	100
BrachialPlex_L	0.22 ± 0.10	2.82 ± 2.61	2.60	100	91
BrachialPlex_R	0.19 ± 0.09	2.73 ± 2.38	2.60	100	95
Brain	0.98 ± 0.01	0.52 ± 0.36	2.71	100	100
Brainstem	0.82 ± 0.08	1.20 ± 0.65	2.71	100	100
Cavity_Oral	0.76 ± 0.13	3.20 ± 1.93	2.71	100	100
Cochlea_L	0.30 ± 0.18	1.17 ± 0.87	2.29	95	95
Cochlea_R	0.32 ± 0.20	1.05 ± 0.68	2.29	96	95
Eye_L	0.87 ± 0.06	0.65 ± 0.51	2.57	100	100
Eye_R	0.86 ± 0.07	0.66 ± 0.48	2.57	100	100
Glnd_Lacrimal_L	0.40 ± 0.16	0.68 ± 0.35	2.71	98	100
Glnd_Lacrimal_R	0.45 ± 0.14	0.71 ± 0.52	2.71	100	100
Glnd_Submand_L	0.77 ± 0.11	0.76 ± 0.32	3.00	100	100
Glnd_Submand_R	0.75 ± 0.11	0.81 ± 0.34	3.00	100	100
Glnd_Thyroid	0.71 ± 0.19	1.38 ± 3.18	2.71	98	95
Lens_L	0.61 ± 0.17	0.56 ± 0.47	2.29	97	100
Lens_R	0.63 ± 0.16	0.55 ± 0.33	2.29	97	95
Lips	0.37 ± 0.15	5.26 ± 3.41	2.83	100	95
OpticChiasm	0.13 ± 0.13	2.46 ± 1.99	2.00	80	91
OpticNrv_L	0.53 ± 0.14	0.77 ± 0.85	2.57	99	100
OpticNrv_R	0.52 ± 0.13	0.80 ± 0.83	2.57	99	100
Parotid_L	0.79 ± 0.09	1.30 ± 0.62	3.00	99	100
Parotid_R	0.80 ± 0.06	1.26 ± 0.43	3.00	100	100
Pituitary	0.54 ± 0.15	0.87 ± 0.54	3.00	100	86
SpinalCord	0.65 ± 0.16	0.73 ± 0.41	2.86	99	100
LN_Neck_IA	0.60 ± 0.14	0.47 ± 0.45	2.75	100	100
LN_Neck_IB_L	0.79 ± 0.04	0.73 ± 0.24	2.75	100	100
LN_Neck_IB_R	0.79 ± 0.05	0.73 ± 0.20	2.75	100	100
LN_Neck_IIA_L	0.75 ± 0.05	1.54 ± 0.44	2.25	100	100
LN_Neck_IIA_R	0.76 ± 0.04	1.41 ± 0.49	2.25	100	95
LN_Neck_IIB_L	0.80 ± 0.06	0.63 ± 0.31	3.00	100	100
LN_Neck_IIB_R	0.80 ± 0.06	0.58 ± 0.15	3.00	100	95
LN_Neck_III_L	0.75 ± 0.07	0.92 ± 0.44	3.00	100	100
LN_Neck_III_R	0.75 ± 0.07	0.99 ± 0.37	3.00	100	100
LN_Neck_IV_L	0.69 ± 0.08	1.13 ± 0.37	2.75	100	100
LN_Neck_IV_R	0.71 ± 0.09	1.06 ± 0.33	2.75	100	95
LN_Neck_V_L	0.58 ± 0.09	1.13 ± 0.59	3.00	100	100
LN_Neck_V_R	0.58 ± 0.11	1.43 ± 0.98	3.00	100	91
LN_Neck_VIA	0.36 ± 0.11	0.80 ± 0.35	2.75	100	100

6.1.5

Continued on next page.

6.1.5

Structure	Mean ± Std Dice	MDA (Mean ± Std mm)	Beta User Feedback Score	Localization Success on Relavant FOV CTs	Localization Success on Whole Body CTs
LN_Retropharynx_L	0.28 ± 0.10	1.54 ± 1.47	2.75	100	100
LN_Retropharynx_R	0.28 ± 0.09	1.49 ± 1.36	2.75	95	100
LN_Retrostyloid_L	0.64 ± 0.09	1.23 ± 0.48	2.75	100	100
LN_Retrostyloid_R	0.66 ± 0.11	1.13 ± 0.66	2.75	100	100

TABLE 1 *Performance statistics for the* CT Head & Neck *model*

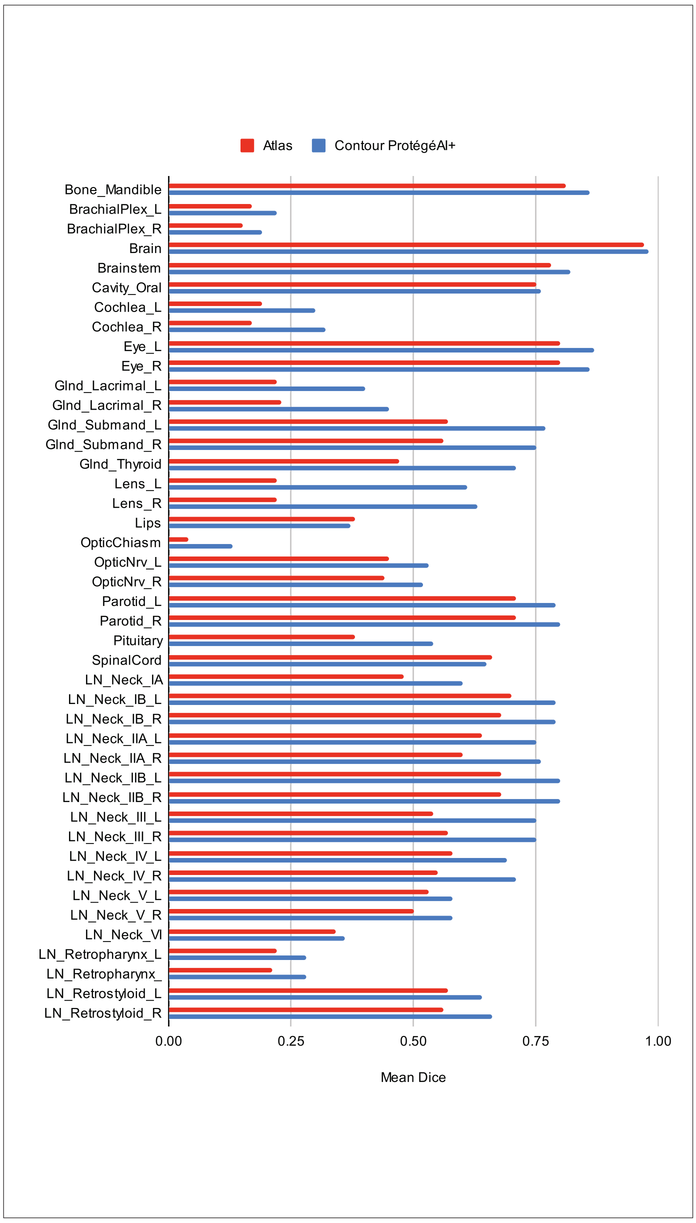

FIGURE 2 *Comparison of atlas and Contour ProtégéAI+ Dice on the* CT Head & Neck *model*

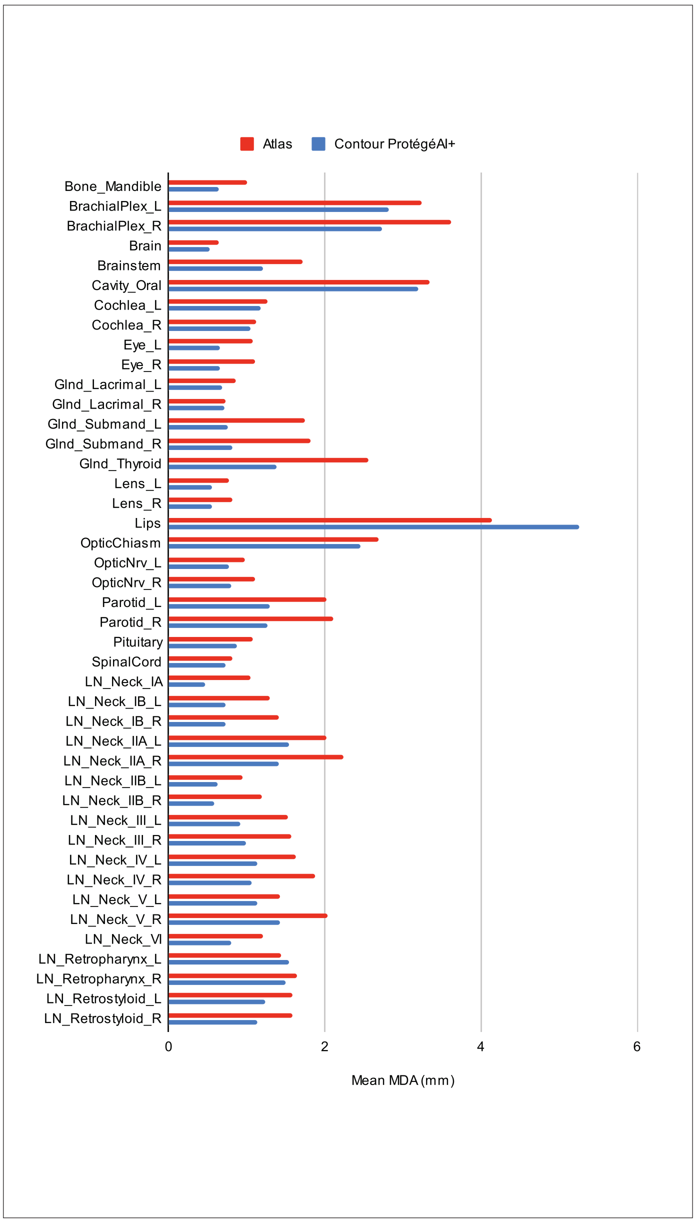

FIGURE 3 *Comparison of atlas and Contour ProtégéAI+ Mean MDA on the* CT Head & Neck *model*

Structure	Mean ± Std Dice	MDA (Mean ± Std mm)	Beta User Feedback Score	Localization Success on Relavant FOV CTs	Localization Success on Whole Body CTs
BrachialPlex_L	0.38 ± 0.14	2.94 ± 1.84	3.00	100	100
BrachialPlex_R	0.37 ± 0.16	3.28 ± 2.60	3.00	100	100
Breast_L	0.76 ± 0.15	3.64 ± 1.85	2.80	100	100
Breast_R	0.78 ± 0.15	3.45 ± 1.51	2.60	96	91
Bronchus	0.66 ± 0.13	1.90 ± 1.22	2.60	100	100
Carina	0.49 ± 0.12	1.03 ± 0.47	2.40	98	100
Cricoid	0.04 ± 0.05	5.71 ± 1.24	2.40	67	100
Esophagus	0.70 ± 0.15	0.97 ± 0.54	2.80	100	100
Glnd_Thyroid	0.65 ± 0.17	1.75 ± 1.78	2.75	100	100
GreatVes	0.74 ± 0.10	2.67 ± 1.73	3.00	100	100
Heart	0.90 ± 0.09	2.55 ± 1.40	3.00	100	100
Humerus_Head_L	0.95 ± 0.02	0.40 ± 0.31	2.80	100	95
Humerus_Head_R	0.96 ± 0.02	0.31 ± 0.26	2.80	100	100
Kidney_L	0.92 ± 0.05	0.94 ± 0.80	3.00	97	91
Kidney_R	0.91 ± 0.07	0.98 ± 0.66	3.00	97	95
Larynx	0.52 ± 0.14	3.06 ± 1.08	2.40	99	95
Liver	0.93 ± 0.06	2.00 ± 1.79	3.00	100	100
Lung_L	0.96 ± 0.02	0.77 ± 0.37	3.00	100	100
Lung_R	0.96 ± 0.02	0.89 ± 0.43	3.00	100	100
Musc_Constrict	0.45 ± 0.16	2.07 ± 1.52	2.00	100	91
Pancreas	0.41 ± 0.24	8.68 ± 11.12	2.25	54	91
SpinalCord	0.66 ± 0.16	1.41 ± 0.63	2.75	100	100
Stomach	0.79 ± 0.19	2.33 ± 2.12	3.00	100	100
Trachea	0.74 ± 0.16	0.88 ± 0.54	3.00	99	100
LN_Ax_L1_L	0.65 ± 0.10	2.58 ± 1.17	3.00	100	100
LN_Ax_L1_R	0.60 ± 0.14	3.19 ± 1.61	3.00	100	100
LN_Ax_L2_L	0.55 ± 0.15	2.10 ± 0.96	2.67	100	100
LN_Ax_L2_R	0.51 ± 0.16	2.70 ± 1.77	2.67	100	100
LN_Ax_L3_L	0.52 ± 0.17	2.15 ± 1.52	3.00	100	100
LN_Ax_L3_R	0.51 ± 0.17	2.53 ± 1.41	3.00	100	100
LN_IMN_L	0.44 ± 0.17	1.63 ± 0.96	2.67	100	100
LN_IMN_R	0.40 ± 0.16	1.55 ± 1.60	2.67	100	100
LN_Sclav_L	0.58 ± 0.13	1.87 ± 0.89	2.67	100	100
LN_Sclav_R	0.54 ± 0.11	2.60 ± 0.85	2.67	100	100

6.1.5

TABLE 2 *Performance statistics for the* CT Thorax *model*

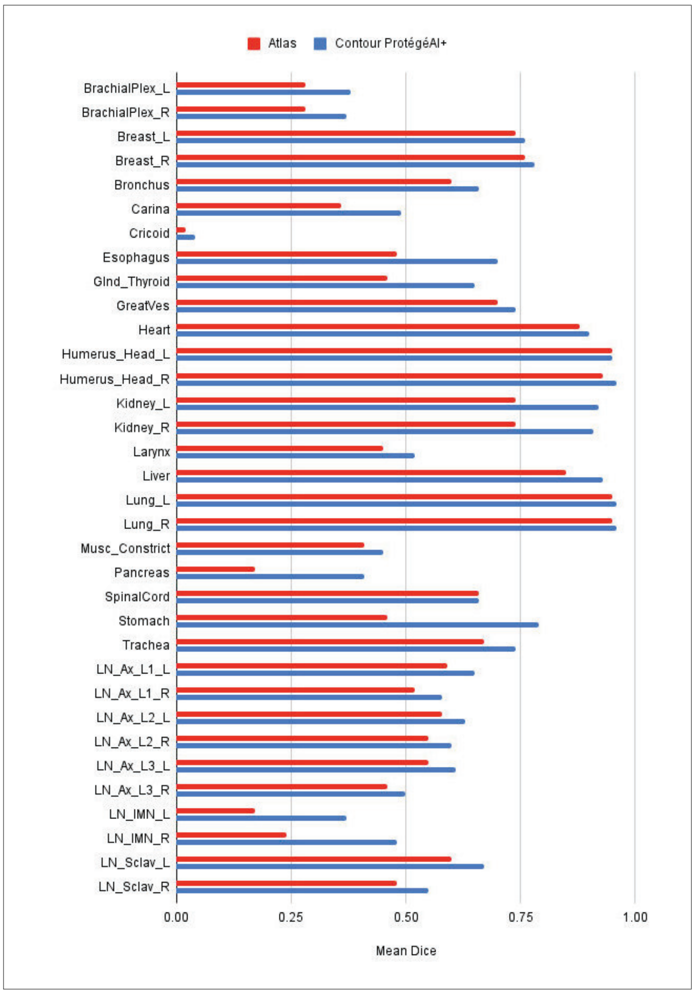

FIGURE 4 *Comparison of atlas and Contour ProtégéAI+ Dice on the CT Thorax model*

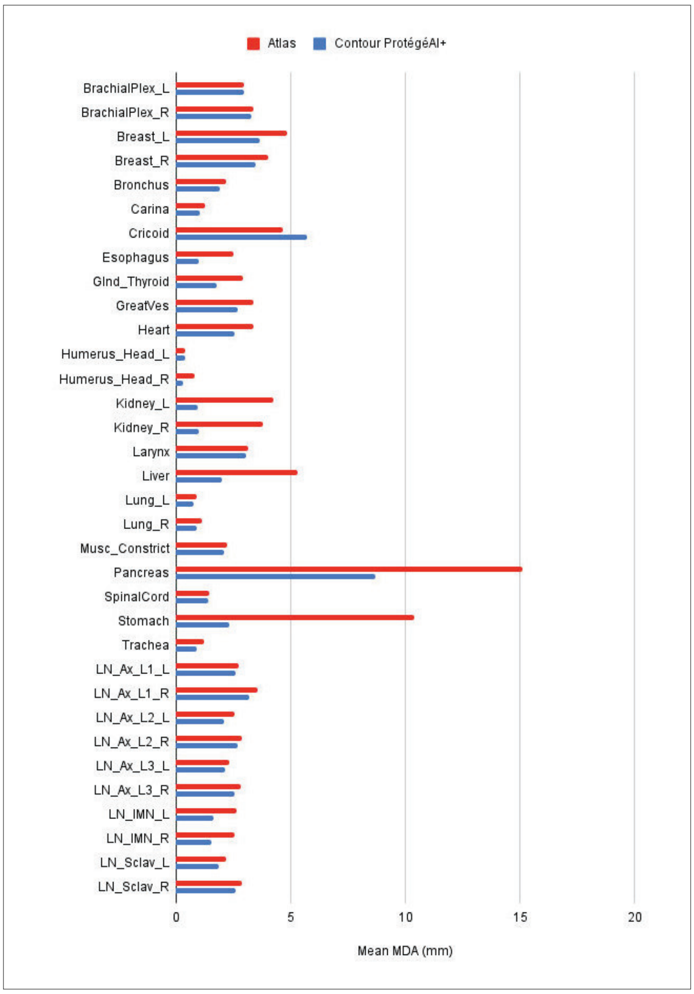

FIGURE 5 *Comparison of atlas and Contour ProtégéAI+ Mean MDA on the CT Thorax model*

Structure	Mean ± Std Dice	MDA (Mean ± Std mm)	Beta User Feedback Score	Localization Success on Whole Body CTs
Bladder	0.92 ± 0.16	0.91 ± 1.02	3.00	95
Bone	0.87 ± 0.05	0.48 ± 0.13	3.00	100
Bowel	0.74 ± 0.10	7.69 ± 5.07	3.00	100
BowelBag	0.75 ± 0.15	17.18 ± 5.24	3.00	100
Brain	0.97 ± 0.03	0.91 ± 1.17	3.00	100
Cavity_Oral	0.78 ± 0.12	3.19 ± 1.66	3.00	100
Glnd_Lacrimal_L	0.37 ± 0.16	0.72 ± 0.43	3.00	100
Glnd_Lacrimal_R	0.46 ± 0.14	0.81 ± 0.79	3.00	100
Glnd_Submand_L	0.79 ± 0.06	0.81 ± 0.35	3.00	100
Glnd_Submand_R	0.77 ± 0.06	0.81 ± 0.38	3.00	100
Heart	0.91 ± 0.04	2.65 ± 0.93	3.00	100
Kidney_L	0.93 ± 0.04	0.90 ± 0.51	3.00	95
Kidney_R	0.92 ± 0.07	0.85 ± 0.44	3.00	100
Liver	0.93 ± 0.07	2.26 ± 3.82	3.00	100
LN_Iliac	0.71 ± 0.03	1.59 ± 0.33	3.00	64
Parotid_L	0.81 ± 0.05	1.30 ± 0.47	3.00	100
Parotid_R	0.82 ± 0.05	1.34 ± 0.56	3.00	100
Prostate	0.85 ± 0.05	1.55 ± 0.61	3.00	100
Spleen	0.95 ± 0.01	0.61 ± 0.38	3.00	100

TABLE 3 *Performance statistics for the* Whole Body - Physiological Uptake Organs *model*

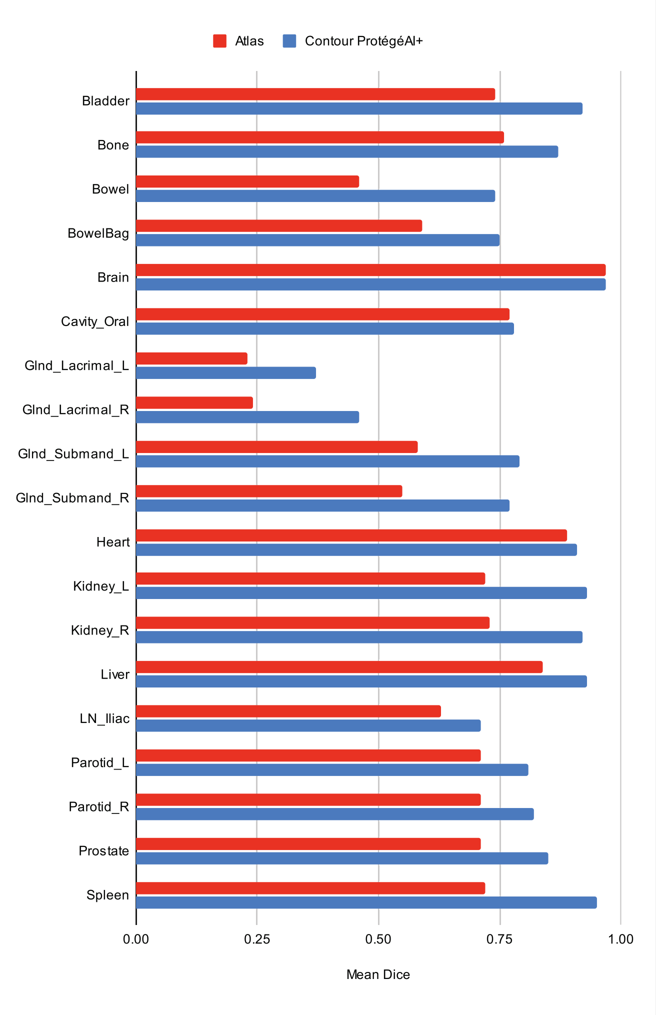

FIGURE 6 *Comparison of atlas and Contour ProtégéAI+ Dice on the* Whole Body - Physiological Uptake Organs *model*

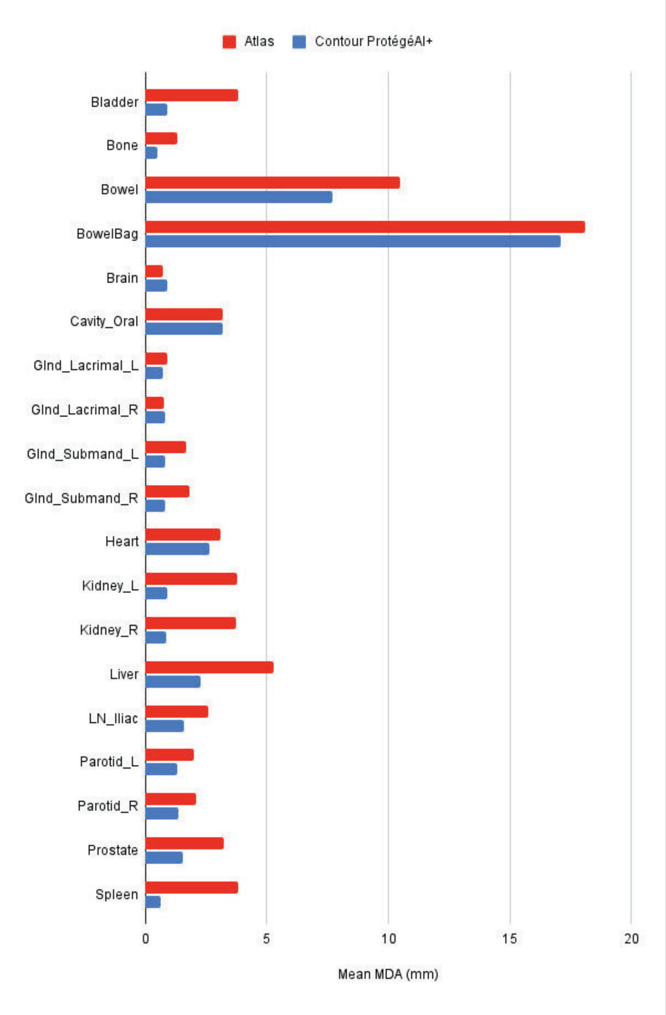

FIGURE 7 *Comparison of atlas and Contour ProtégéAI+ Mean MDA on the* Whole Body - Physiological Uptake Organs *model*

Model	Atlas	Contour ProtégéAI+
Head & Neck	38.69 ± 33.36	28.61 ± 29.59
Thorax	89.24 ± 82.73	65.44 ± 68.85
Whole Body - Physiological Uptake Organs	138.06 ± 142.42	98.20 ± 127.11

TABLE 4 *Mean added path length, atlas vs. Contour ProtégéAI+*

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Contour ProtégéAI+™

Version 1.3.2

Have questions about MIM Software?
Contact MIM Software Support for technical assistance.

866-421-2536
support@mimsoftware.com

MIM Encore Workflows and Nuclear Medicine Processing

User Guide

Version 7.4

☆ **Important:** View the most up-to-date versions of MIM documentation at www.mimsoftware.com/training. Downloaded or printed content may be supplanted or superseded by updated versions. You may obtain the most current documentation from the MIM Software Knowledge Center.

Symbols Used in This Guide

⚠ **Caution**: Indicates potential hazards or restrictions on use that are critical for safe use of the product.

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

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

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