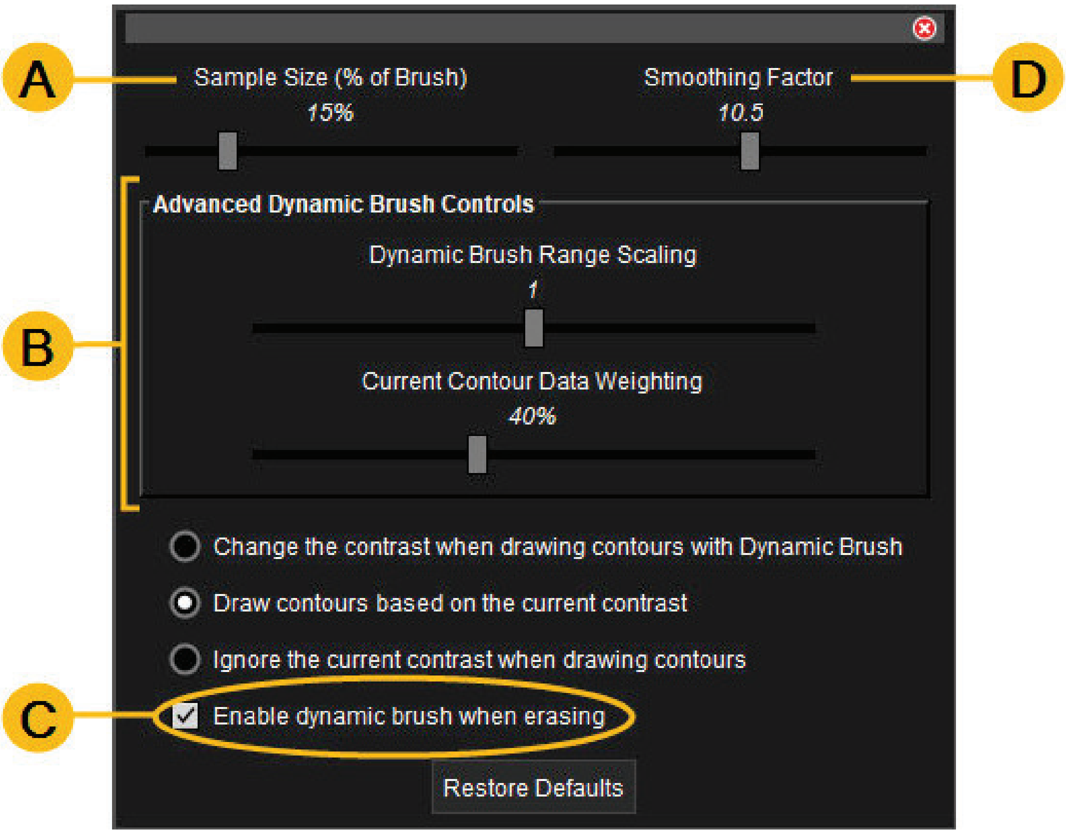


Sample Size (% of Brush)
15%

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** — Adjust the amount that the Dynamic Brush prediction includes the area covered by the existing contour versus just the area within the sampling circle.

C. **Enable dynamic brush when erasing** — Sample what to erase within the inner circle when the brush is in erase mode.

D. **Smoothing Factor** — Adjust the smoothness of the potential contour. 0 creates 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.

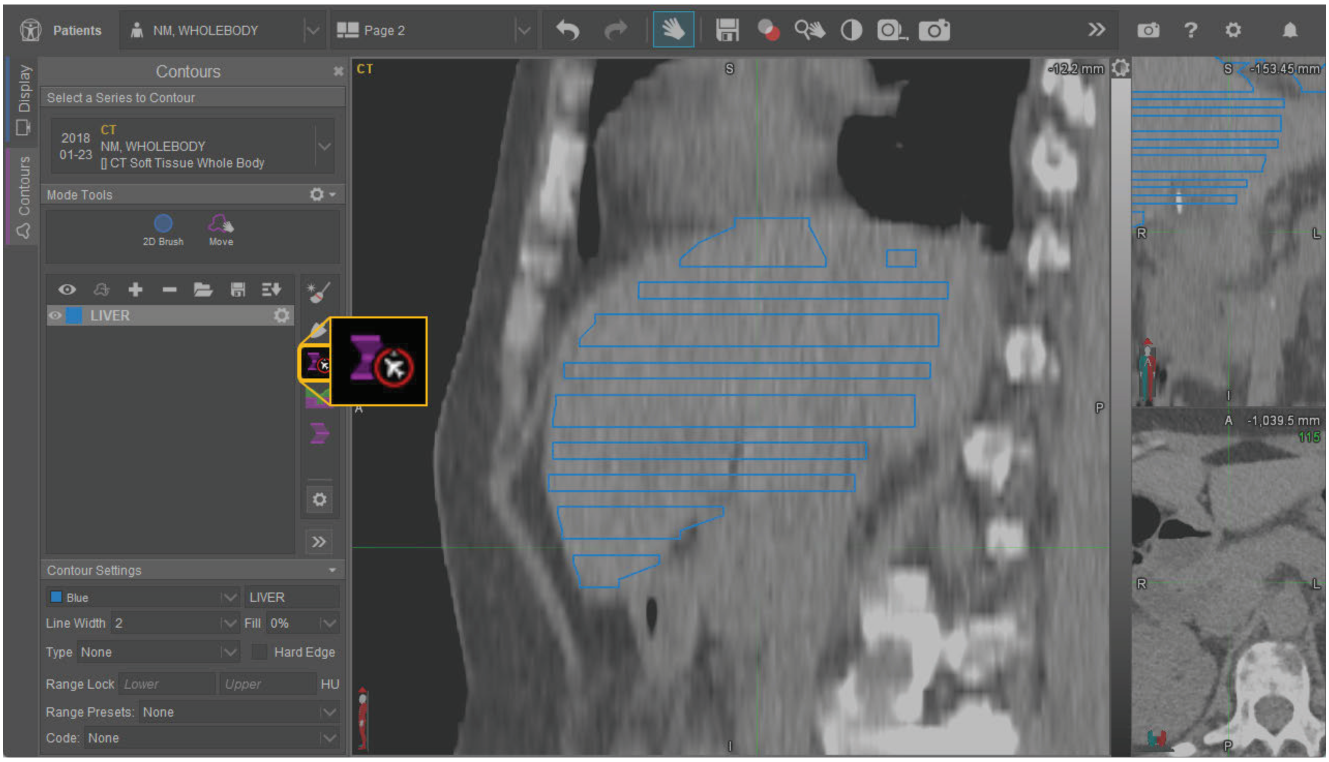
Additional Contouring Tools

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

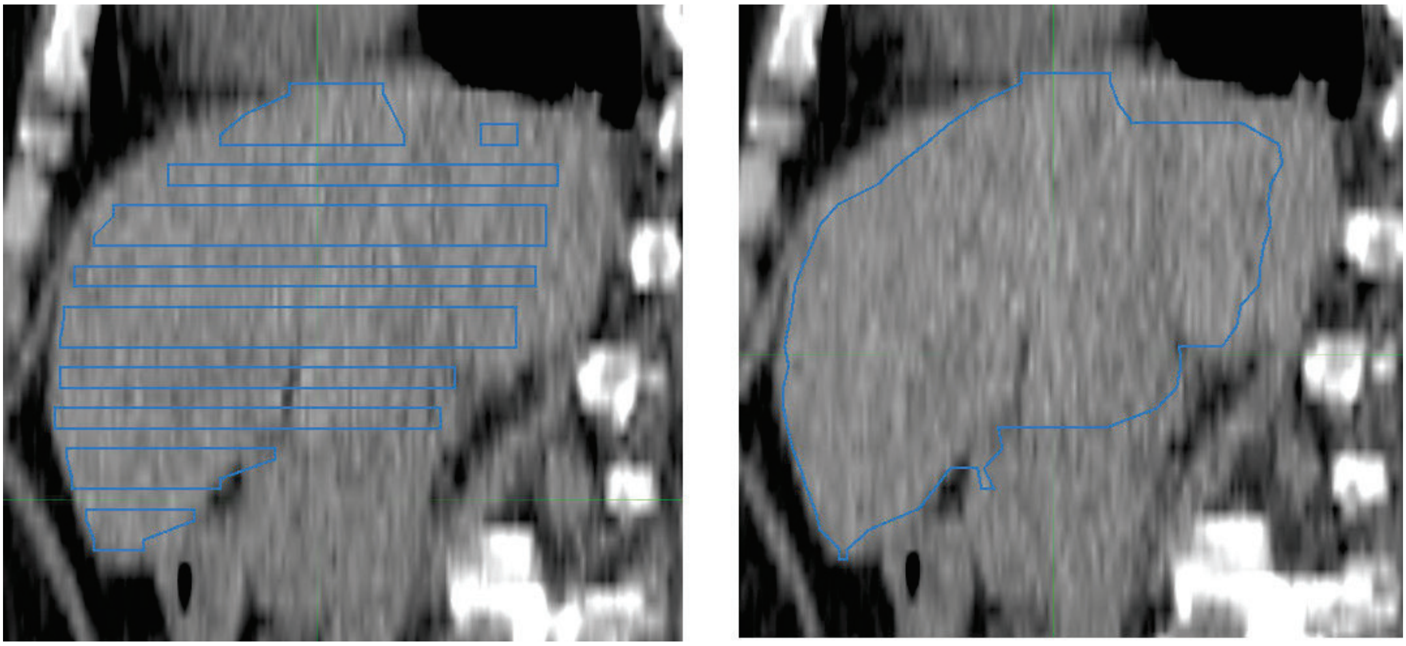
Code: None

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.

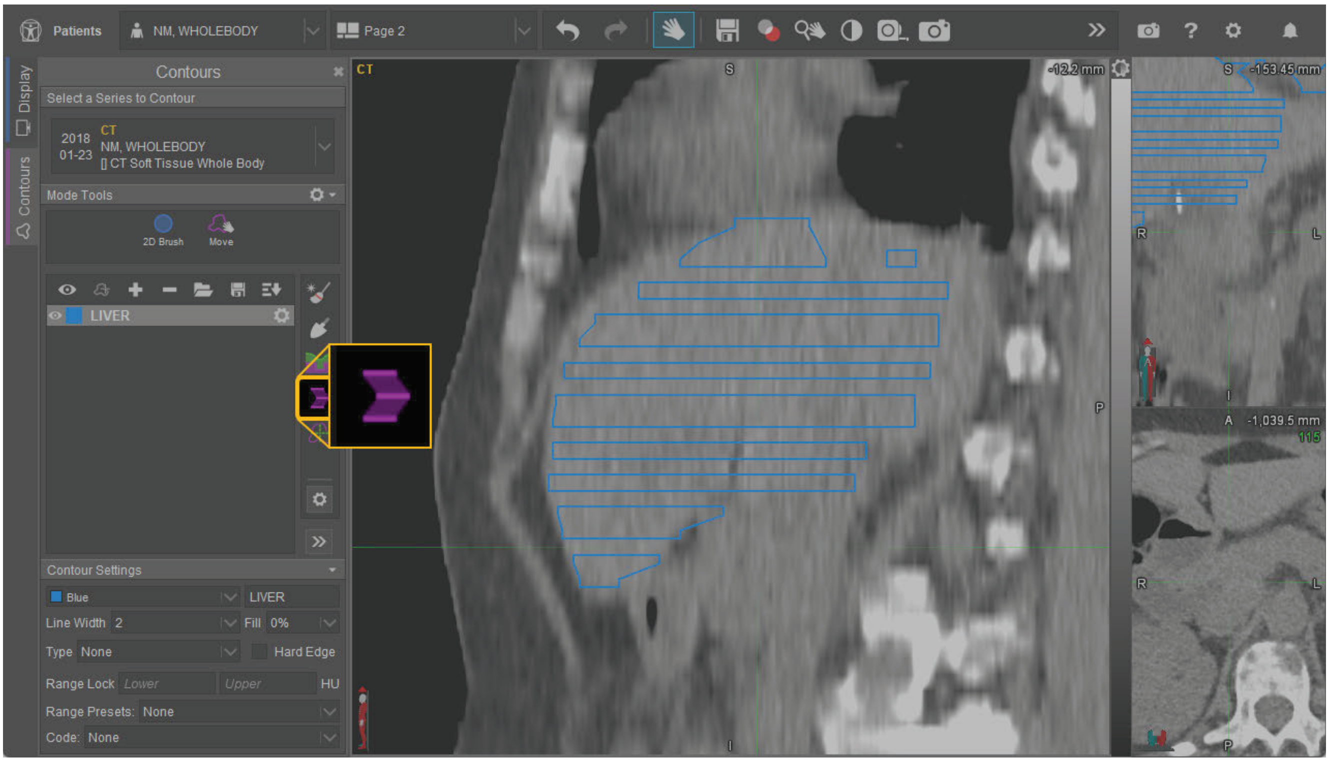
Tip: The Interpolate tool only works on contours created in an image's default acquisition plane. For example, using the tool in the axial plane of a sagittally acquired CT has no effect.



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

Create Contours with the 3D Brush

MIMTD-702 • 30 Nov 2023

Overview

The 3D Brush provides freehand contour editing using a 3D sphere. The contour extends into neighboring slices.

Contents

Draw and Erase with the 3D Brush

Activate and use the 3D Brush to draw contours freely on any image:

- To draw contours, left-click drag with the 3D 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.

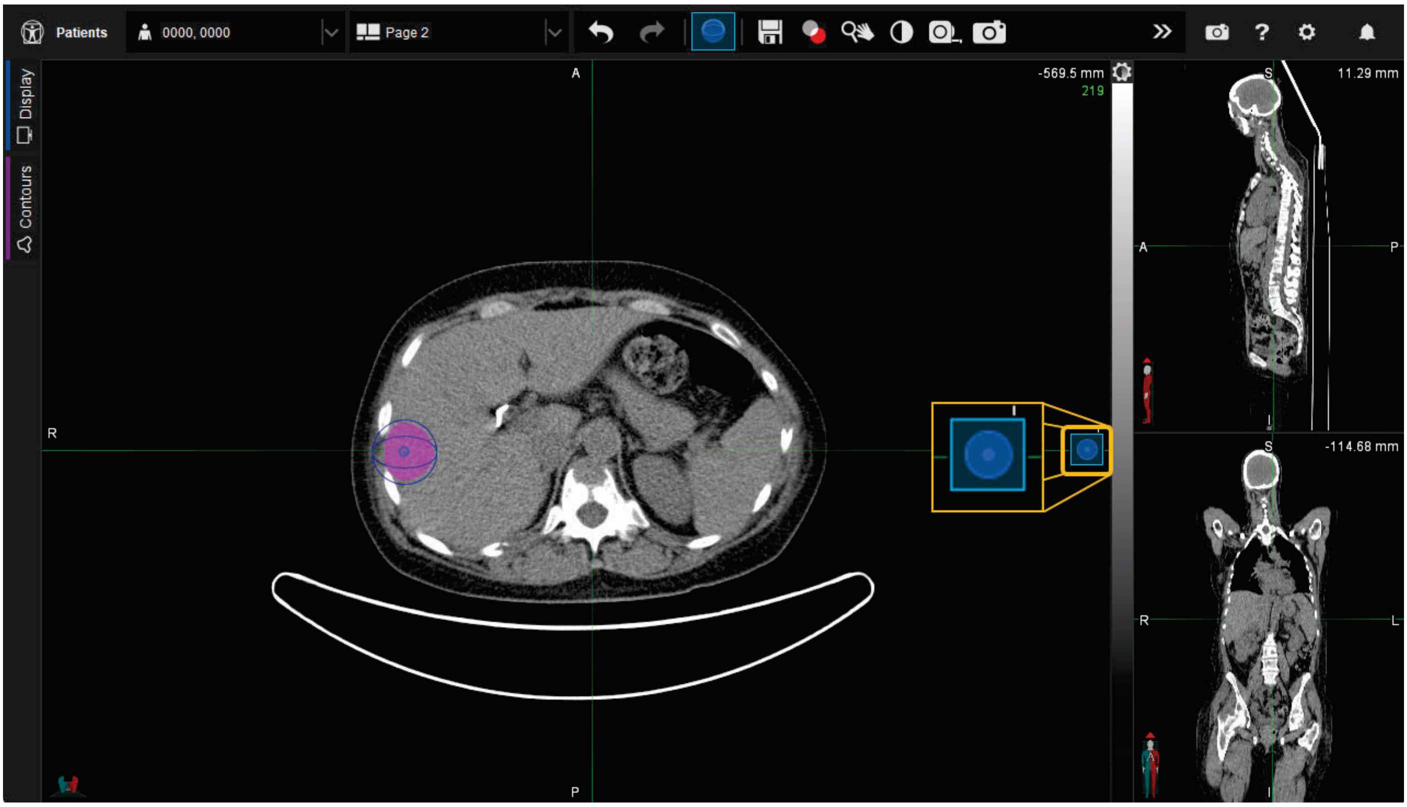
- To switch between draw and erase modes, press and hold the Alt (Windows®) or Option (macOS®) key. Holding the Alt/Option key allows you to draw non-contiguous regions. This is helpful for areas such as pelvic nodes.

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**.

3D Brush Companion Tool: Dynamic Brush™

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

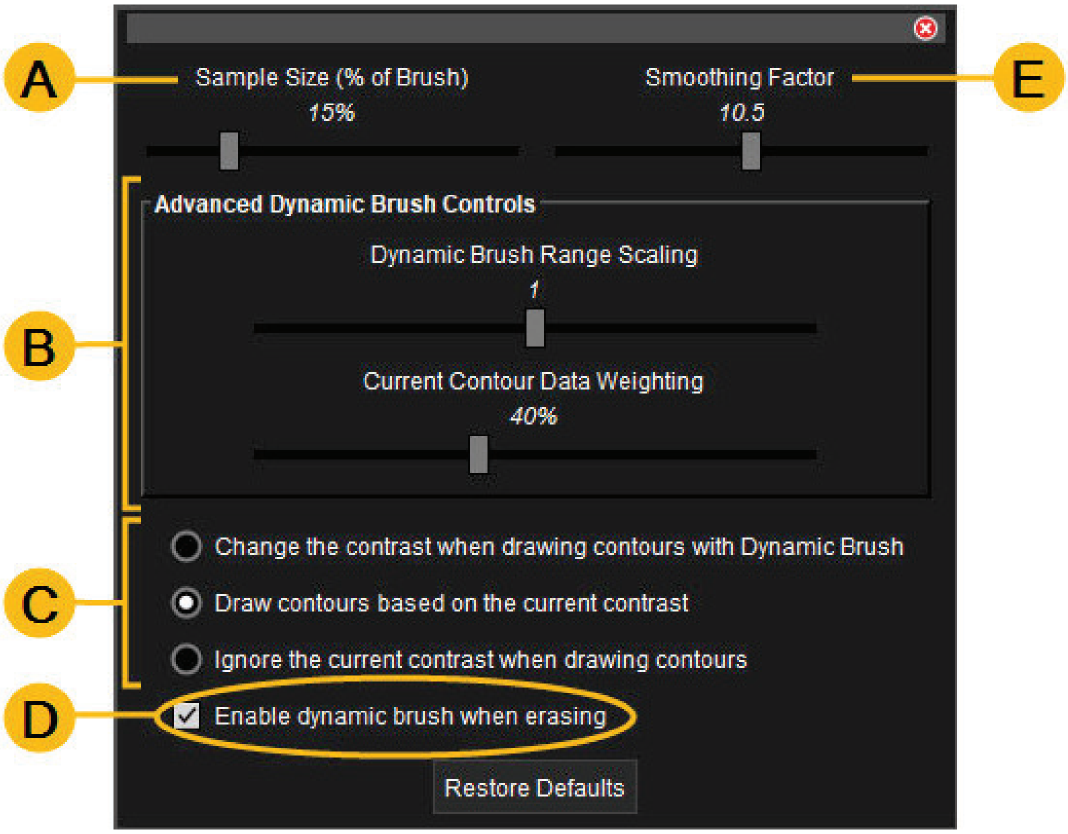
Use the Dynamic Brush to contour more quickly. When the Dynamic Brush is activated, the brush samples intensities within the inner circle in order to restrict the brush to areas of similar intensity.



- Activate the **3D 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 region of interest. The brush dynamically selects only regions 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** tool to open an advanced settings window as described below.

Advanced Dynamic Brush Settings

Adjust advanced settings for the Dynamic Brush by activating the **3D Brush** and right-clicking the **Dynamic Brush** button on the right side of the 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** — Adjust the amount that the Dynamic Brush prediction includes the area covered by the existing contour versus just the area within the sampling circle.

C. **Contrast options** — Adjust how the brush affects and is affected by the contrast of the image while drawing.

Tip: The options available depend on your version of MIM.

D. **Enable dynamic brush when erasing** — Sample what to erase within the inner circle when the brush is in erase mode.

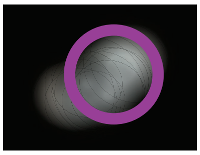
E. **Smoothing Factor** — Adjust the smoothness of the potential contour. 0 creates the roughest potential contour and 20 gives you the smoothest potential contour.

Tip: For best results with liver tissue, set the Sample Size to 15% and the Smoothing Factor to 2.5.

Create Contours with the Threshold Tool

MIMTD-703 • 07 Sep 2023

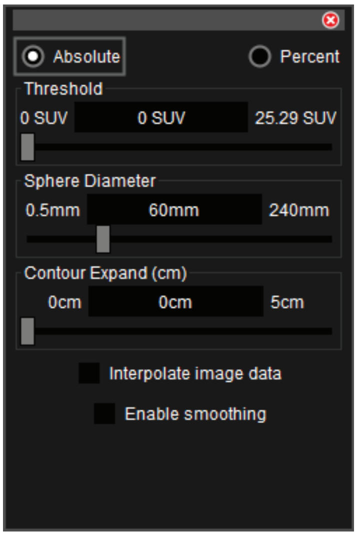
Overview



The Threshold tool contours voxels on anatomic (i.e., CT and MR) and functional (i.e., PET and NM) images above a specified threshold value within a spherical region.

Create a Contour

1. Activate the **Threshold** tool from the top toolbar, radial menu, or Contours sidebar.
2. Position the sphere by left-clicking or left-click dragging.
3. Click the button along the right edge of any viewport to configure threshold settings.



● Absolute ○ Percent

Threshold: 0 SUV, 0 SUV, 25.29 SUV

Sphere Diameter: 0.5mm, 60mm, 240mm

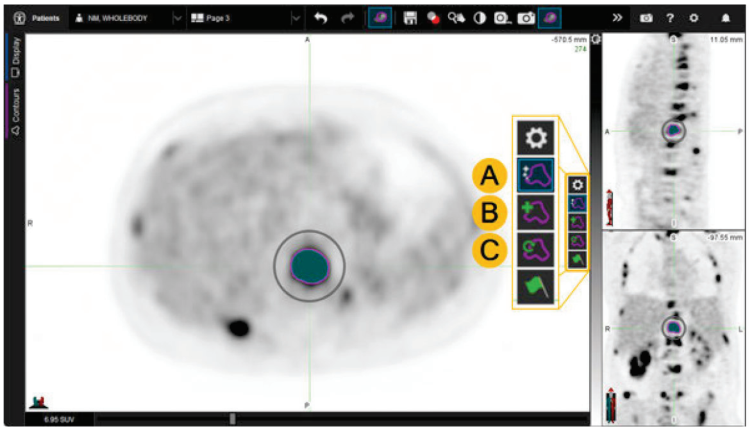
Contour Expand (cm): 0cm, 0cm, 5cm

☐ Interpolate image data

☐ Enable smoothing

   i. Select an absolute or percent-based threshold.
   ii. Adjust the threshold, sphere diameter, and contour expansion by dragging the sliders or manually specifying values.
   iii. Choose whether to interpolate image data.
   iv. Choose whether enable contour smoothing.

4. Click the green flag button to create the contour.
5. If you need to append to or replace the contour, click the appropriate button on the right side of the viewport, then click the green flag button again.

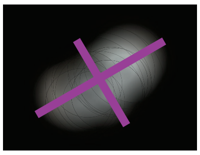


A. Create a new contour.
B. Append to the current contour.
C. Replace the existing contour.

Define Lesions with PET Edge®

MIMTD-654 • 05 Sep 2023

Overview



The PET Edge tool is used to segment PET and SPECT lesions based on changes in edge intensity, regardless of contrast settings. It defines an edge based on the change in count levels at the lesion border. This spatial derivative technique does not use thresholds or absolute SUV levels.

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

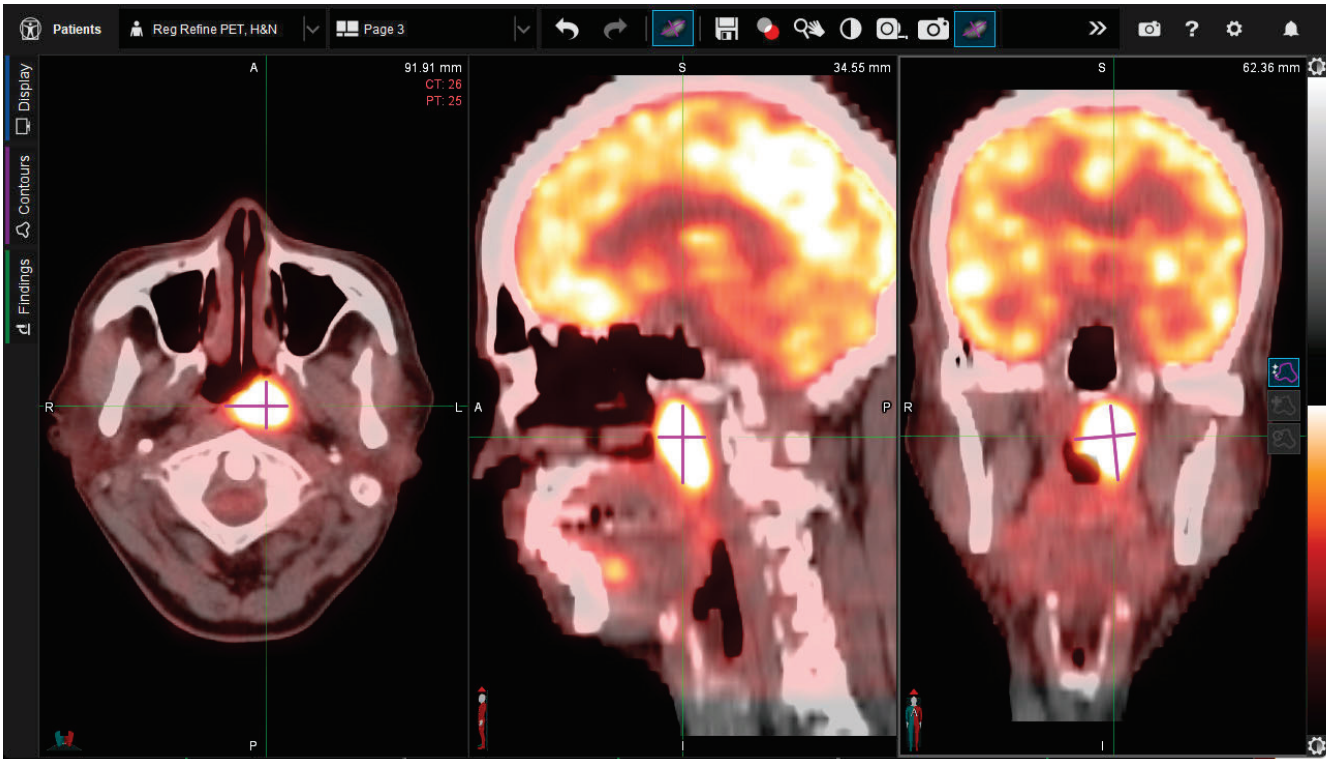
Important: A second tool, PET Edge®+ , is also available, which uses an active contour algorithm. This algorithm looks for areas of elevated voxel intensity, and then uses spatial derivatives to refine lesion boundaries. For more information, see Define Lesions with PET Edge®+ and The Advantages of PET Edge®+.

Contents

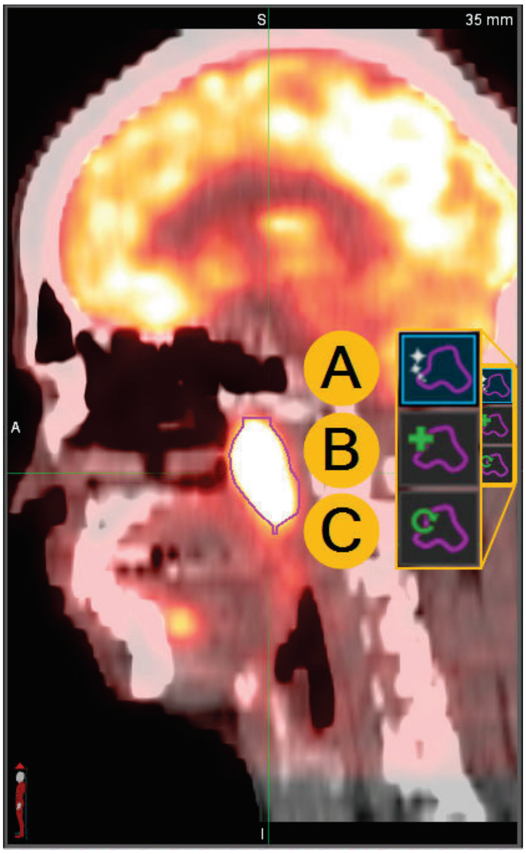
Segment Lesions with PET Edge

1. In the Contours sidebar, set the **Select a Series to Contour** dropdown to the series that you want the contours to be associated with. The series you choose determines the units of the statistics displayed for the contour, as well as the image that the contours will be associated with when they are saved.
2. In the **Contours** sidebar, click the **PET Edge** tool to activate it.
3. With all three planes displayed, localize to the center of the lesion in all planes.

4. On either the PET or the fusion image, left-click drag from the center of the lesion until the axes reach the edge of the lesion in all three planes. The axes provide approximate limits from which the contour will be calculated.



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



A. Create a new contour.
B. Append to the current contour.
C. Replace the existing contour.

Related: For technical details about PET Edge, see PET Edge® & PET Edge®+ Tools: Technical Details.

PET Edge Settings

If you do not have a User Profile applied in MIM, adjust the PET Edge and Fusion Settings described below.

Tip: Alternatively, apply a User Profile. Go to Settings ⚙ >> **General Preferences** >> **Application** and choose **Interventional Radiologist (SurePlan)** from the dropdown menu at the top. Note that applying a User Profile changes other settings as well.

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.

Apply Measurements to Functional Images Within Fusions

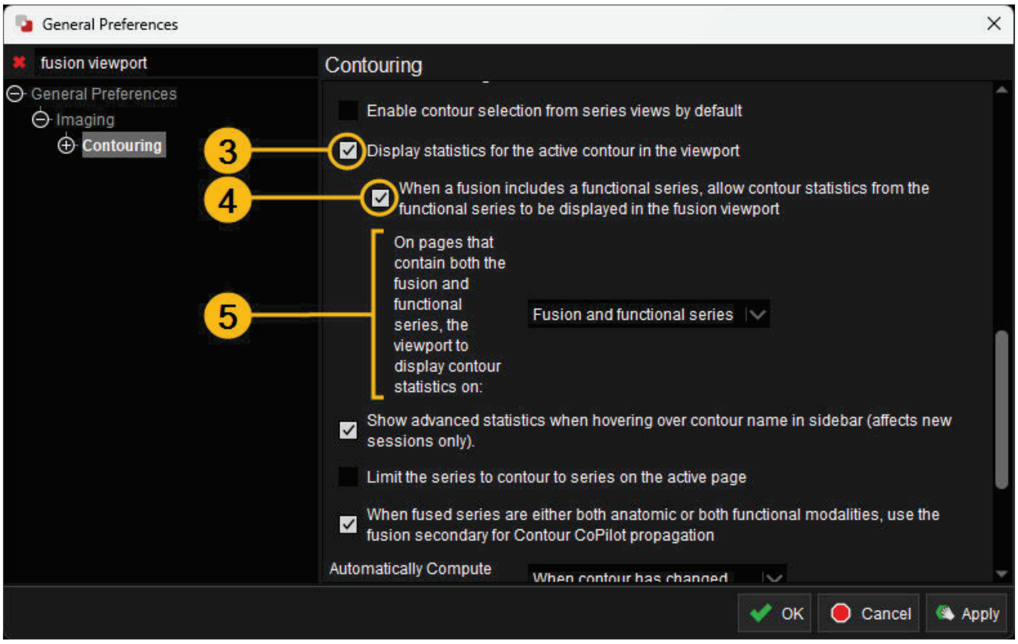
1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**pet edge**". Click **Contouring** on the left side.
3. Select **Create PET Edge or PET Edge+ contours on the functional series when used on a fusion with a single functional series**.
4. Click **OK** to apply and save the changes.

Display Statistics on Fusion Images (MIM 7.3 and Later)

Save time by viewing statistics in fusion viewports. This functionality is not available in MIM 7.2 and earlier.

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**fusion viewport**". Select **Contouring** on the left side.
3. Select **Display statistics for the active contour in the viewport**.
4. Select **When a fusion includes a functional series, allow contour statistics from the functional series to be displayed in the fusion viewport**.

5. Use the dropdown to choose which viewports to display contour statistics in.



☐ Enable contour selection from series views by default

☑ Display statistics for the active contour in the viewport

☑ When a fusion includes a functional series, allow contour statistics from the functional series to be displayed in the fusion viewport

On pages that contain both the fusion and functional series, the viewport to display contour statistics on: Fusion and functional series

☑ Show advanced statistics when hovering over contour name in sidebar (affects new sessions only).

☐ Limit the series to contour to series on the active page

☑ When fused series are either both anatomic or both functional modalities, use the fusion secondary for Contour CoPilot propagation

Automatically Compute: When contour has changed

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

Define Lesions with PET Edge®+

MIMTD-655 • 24 Aug 2023

Overview

Use the PET Edge+ tool to segment PET and SPECT lesions based on an active contour algorithm. This algorithm looks for areas of elevated voxel intensity, and then uses spatial derivatives to refine lesion boundaries. This technique does not use thresholds or absolute SUV levels, and is more consistent in its reproducibility than the PET Edge® tool. It has been shown to work better with lower uptake, smaller lesions, and lesions with necrotic sections. For more information comparing PET Edge to PET Edge+, see The Advantages of PET Edge®+.

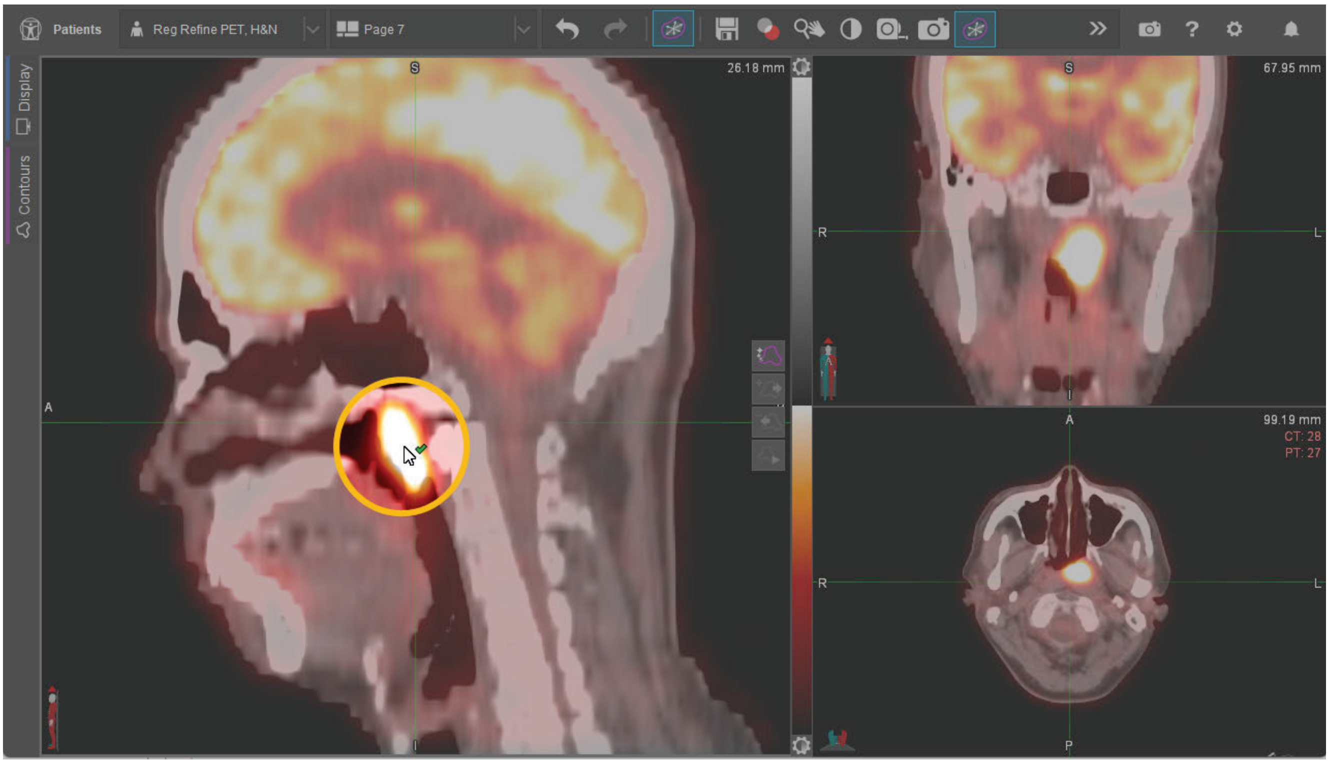
Caution: A qualified person must review all auto-generated contours for accuracy, and make adjustments if needed, before the contours are used clinically.

Contents

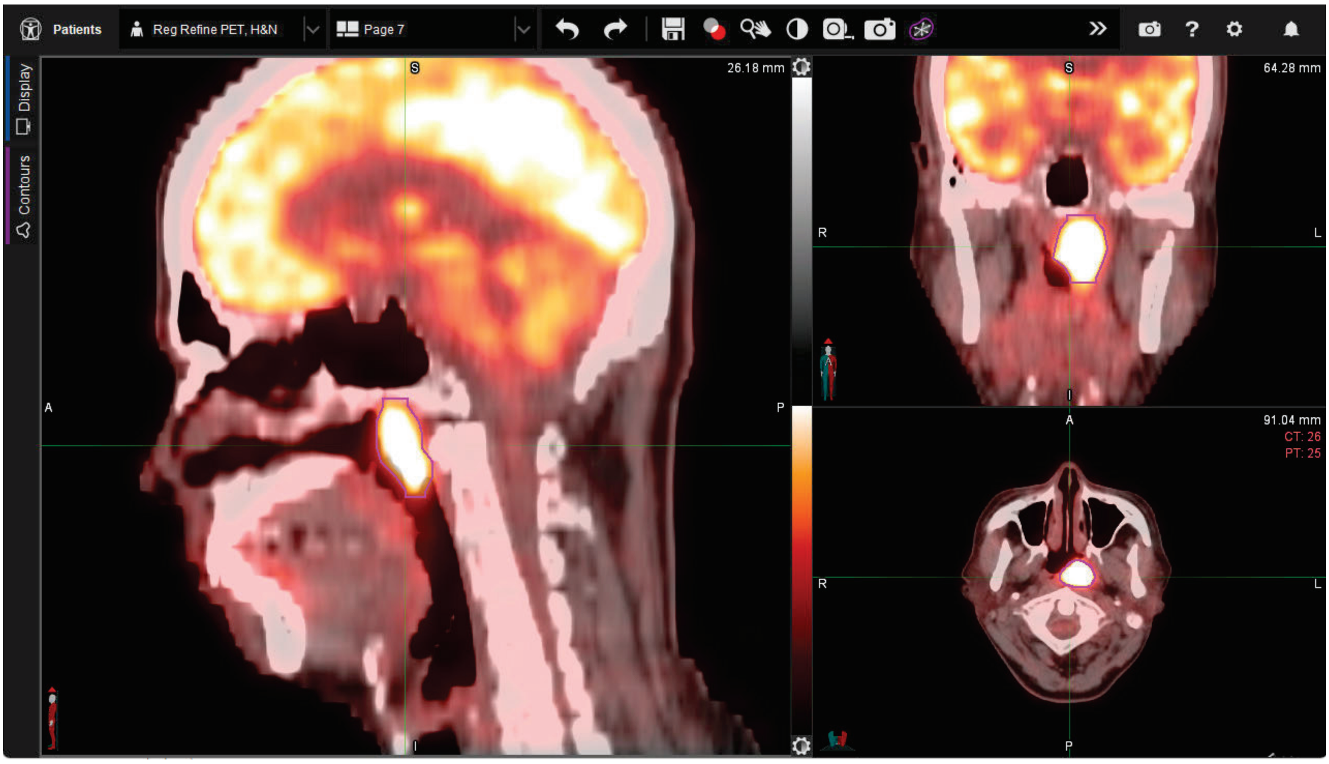
Segment Lesions with PET Edge+

1. In the Contours sidebar, set the **Select a Series to Contour** dropdown to the series that you want the contours to be associated with. The series you choose determines the units of the statistics displayed for the contour, as well as the image that the contours will be associated with when they are saved.
2. In the Contours sidebar, click the **PET Edge+** tool to activate it.
3. On either the PET or the fusion image, hover over the lesion (roughly in the center of the lesion) and pause.

4. Wait for MIM to show a green check mark ✅ next to the cursor.



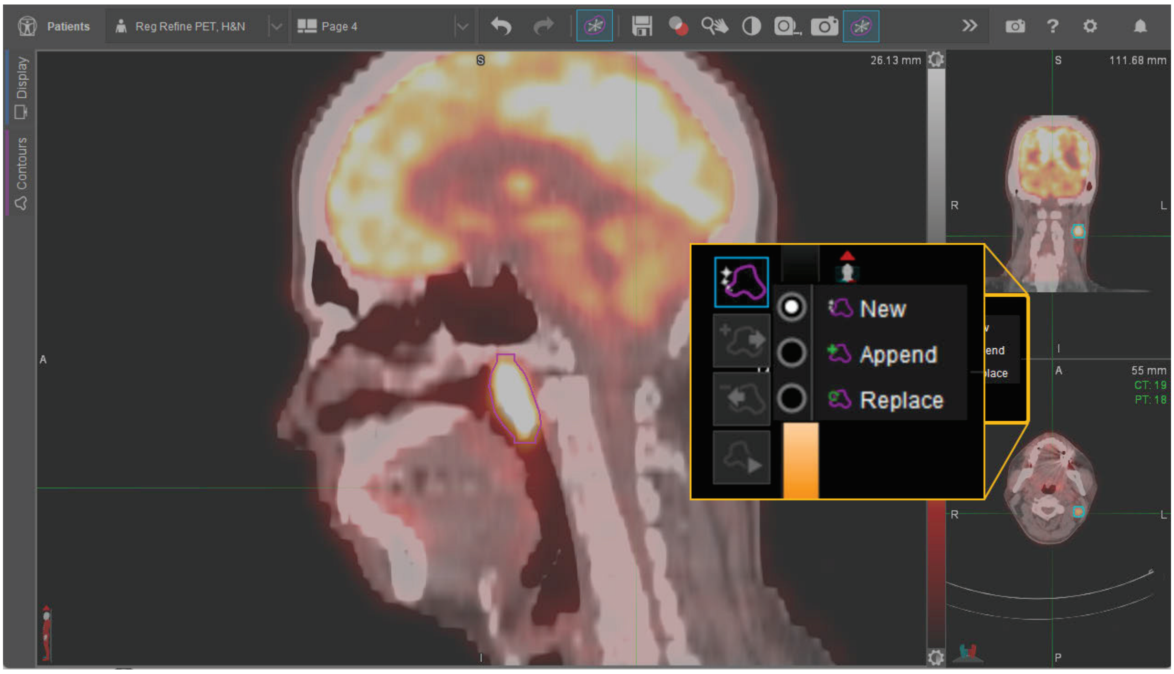
5. After the green check mark appears, click the lesion. MIM creates a contour that encompasses the lesion.



- For some lesions, (e.g., semi-connected lesions), MIM displays the auto-generated contour and also offers other contour options for the region of interest. To view contour options, click the **Next Contour Option** and **Previous Contour Option** buttons. Find these buttons on the right side of the viewport.

> **Tip:** If these buttons are grayed out, it means that there are no other contour options for the region of interest.

- For some large lesions, you may need to prompt MIM to generate larger candidate contours.
  i. Click the **Rerun to Find Larger Candidate Contours** button on the right side of the viewport.
  ii. Click the **Next Contour Option** button to view the new, larger contours.
- For some lesions, you may need to append to or replace the existing contour.
  i. Click the **Contour Creation Mode** button on the right side of the viewport.
  ii. Select **Append** or **Replace**. Append is used to add to the currently-selected contour if the entire lesion was not completely included in the initial contour. This can occur with multi-lobed lesions or lesions with finger-like projections.
  iii. Hover the cursor over the lesion or lesion segment, then click after the green check mark appears.



Related: For technical details about PET Edge+, see [PET Edge® & PET Edge®+ Tools: Technical Details](#).

PET Edge+ Settings

If you do not have a User Profile applied in MIM, adjust the PET Edge+ and Fusion Settings described below.

Tip: Alternatively, apply a User Profile. Go to Settings ⚙ >> **General Preferences** >> **Application** and choose **Interventional Radiologist (SurePlan)** from the dropdown menu at the top. Note that applying a User Profile changes other settings as well.

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.

Apply Measurements to Functional Images Within Fusions

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**pet edge**". Click **Contouring** on the left side.
3. Select **Create PET Edge or PET Edge+ contours on the functional series when used on a fusion with a single functional series**.
4. Click **OK** to apply and save the changes.

Fill Holes Setting

MIM is configured to automatically fill holes for contours created using the PET Edge+ tool. This works, for example, on lesions with necrotic centers. If desired, you can disable this behavior.

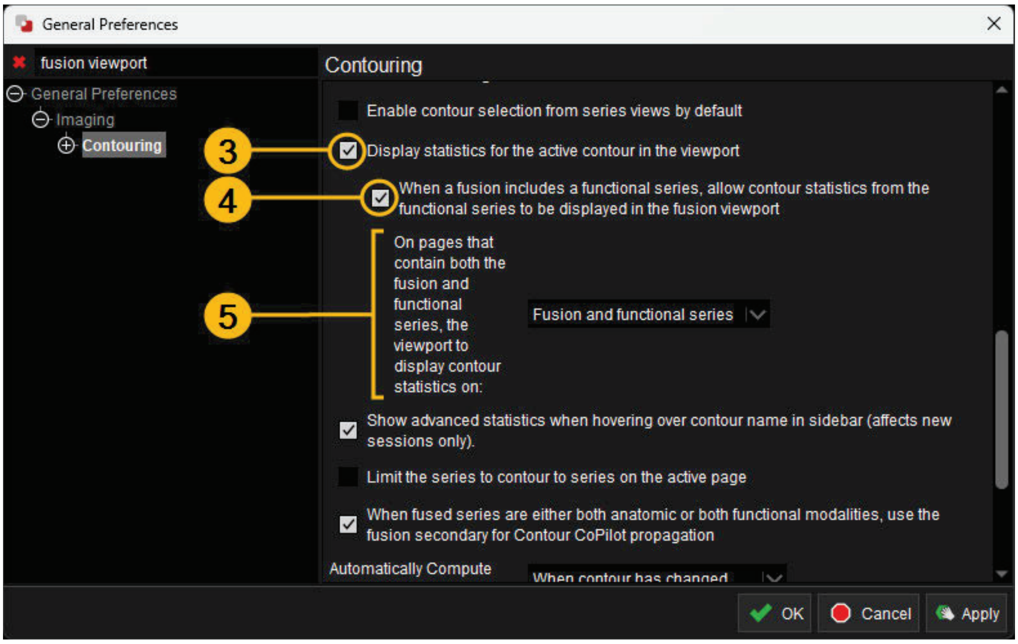
1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for " **fill holes**". Select **Advanced** on the left side.
3. Deselect **Automatically fill holes for contours from PET Edge+**.
4. Click **OK** to save the changes and close the window.

Display Statistics on Fusion Images (MIM 7.3 and Later)

Save time by viewing statistics in fusion viewports. This functionality is not available in MIM 7.2 and earlier.

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**fusion viewport**". Select **Contouring** on the left side.
3. Select **Display statistics for the active contour in the viewport**.
4. Select **When a fusion includes a functional series, allow contour statistics from the functional series to be displayed in the fusion viewport**.

5. Use the dropdown to choose which viewports to display contour statistics in.



Contouring

☐ Enable contour selection from series views by default

☑ Display statistics for the active contour in the viewport

☑ When a fusion includes a functional series, allow contour statistics from the functional series to be displayed in the fusion viewport

On pages that contain both the fusion and functional series, the viewport to display contour statistics on: Fusion and functional series

☑ Show advanced statistics when hovering over contour name in sidebar (affects new sessions only).

☐ Limit the series to contour to series on the active page

☑ When fused series are either both anatomic or both functional modalities, use the fusion secondary for Contour CoPilot propagation

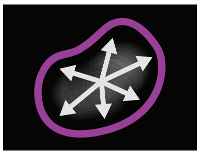
Automatically Compute: When contour has changed

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

The Advantages of PET Edge®+

MIMTD-1684 • 28 Nov 2023

Overview



MIM® has two similar gradient-based contouring tools available, PET Edge® and PET Edge+. PET Edge+ is an updated version that offers several advantages over the original PET Edge tool, as well as over the SUV tool when calculating statistics. The following example scenarios show these advantages.

Contents

Scenario #1: Tumor Clusters

A tumor is evident in the coronal and sagittal view. However, when scrolling through slices in the axial view, the single tumor may appear as multiple tumors.

PET Edge+

When contouring in the axial view, PET Edge+ does not encompass the entire tumor. However, the **Rerun to Find Larger Candidate Contours** button automatically identifies a larger candidate contour. You can also use the **Next Contour Option** and **Previous Contour Option** buttons to cycle through all potential contours before determining which one is most appropriate.

PET Edge

When contouring in the axial view, PET Edge does not encompass the entire tumor. To contour the remainder of the tumor, the view must be switched to the coronal plane before clicking the **Append** button and left-click dragging on the additional tumor section.

Scenario #2: Tumors Near the Bladder or Other Areas of Normal Activity

There are tumors near the bladder or other areas of normal activity. When contouring a tumor, the bladder may also be captured as part of the contour in addition to the tumor.

PET Edge+

When contouring with PET Edge+, selecting the **Replace** option prevents the need to delete the existing contour when scrolling to a slice better suited for contouring the tumor without including the bladder, then using the tool again.

PET Edge

When contouring with PET Edge, the contour must be deleted from the Contours sidebar before scrolling and attempting to find a more desirable slice to contour with the tool again.

Scenario #3: Tumors with Necrotic Centers

A tumor contains a necrotic center.

PET Edge+

PET Edge+ automatically fill holes when creating contours. This behavior can be disabled if desired. Using the **Next Contour Option** and **Previous Contour Option** buttons is also helpful for reviewing all candidate contours before determining which one is most appropriate.

PET Edge

PET Edge does not have any settings or adjustments for tumors with necrotic centers.

Scenario #4: Calculate Statistics with PET Edge+

PET Edge+

PET Edge+ calculates SUVmax, SUVmean, volume, and TLG/TLA, which may be more desirable when contouring tumors near the bladder or kidneys. Also, the amount of clicks between the SUV tool and PET Edge+ is the same.

SUV Tool

The SUV tool calculates only SUVmax and SUVmean. This may not be ideal when approaching tumors near the bladder or other areas of normal activity.

Create and Save Secondary Captures

MIMTD-617 • 16 Aug 2023

Overview

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

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

Contents

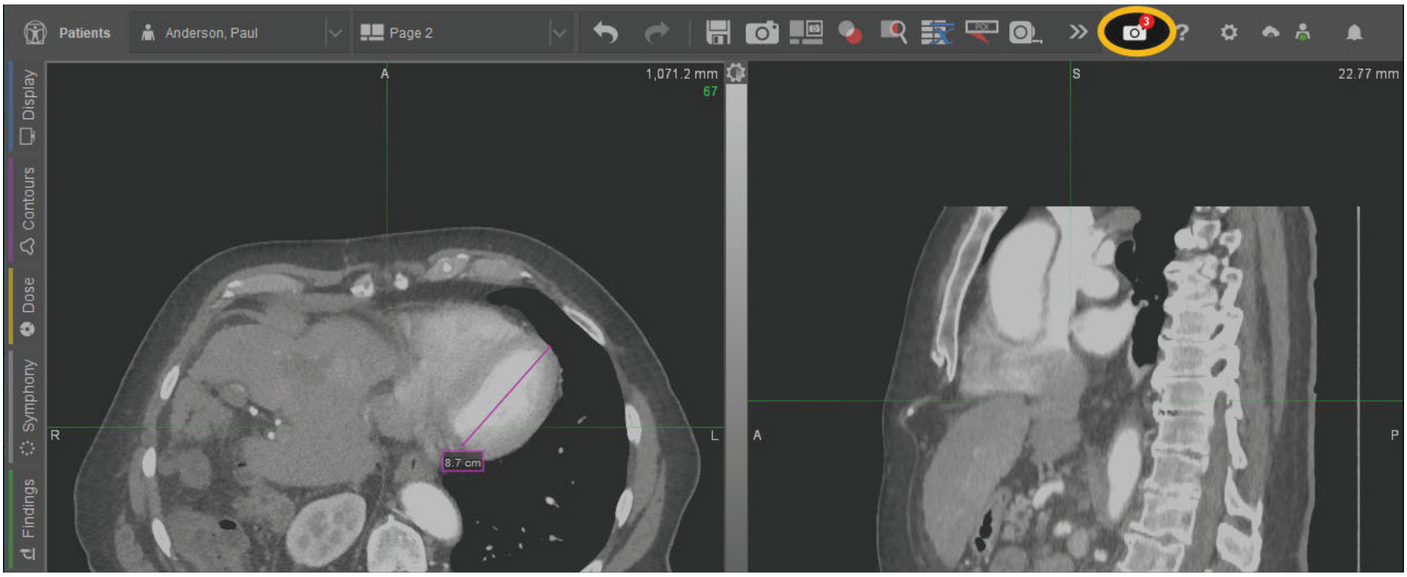
- Create a Capture
- Capture Tools
- Save Secondary Captures

Create a Capture

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

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

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



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

Capture Tools

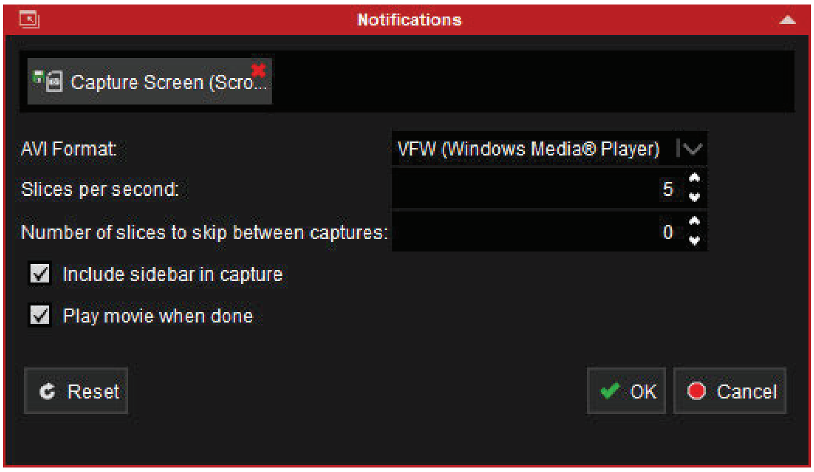
Capture Tool	What It Does	Scenario
📷	**Capture Screen** Takes a screenshot of the page you currently see. View the screenshot in the Capture Gallery.	Default tool. Save the image for your own future reference or to send to another system.
💾📷	**Capture and Save Current Page** Takes a screenshot of the page you currently see. This tool skips the Capture Gallery and immediately saves the capture to the same patient list as the original data.	Consider making a keyboard shortcut for this tool so you can quickly take and save screenshots with a single key.
🖥	**Capture Screen 1/2/3/4** Takes a screenshot of the specified page (e.g., page 1). View the screenshot in the Capture Gallery.	Quickly get a screenshot of a specific page, even if it is not the page you are currently looking at.

Capture Tool	What It Does	Scenario
	Capture All Pages Takes a screenshot of each page in the session. View all of the screenshots in the Capture Gallery.	Quickly get a screenshot of every page.
	Capture Viewport Captures a single viewport that you select. View the capture in the Capture Gallery.	Get a screenshot of a single image on a page, instead of the entire page.
	Capture Series Captures all planes of the series that you select. View the capture in the Capture Gallery.	For example: The page shows PT and CT axial images. You select the PT series to capture. MIM creates a secondary capture that shows the PT axial, coronal, and sagittal planes.
	Capture Screen (Scrolling) Creates a movie file that captures the entire screen and shows auto-scrolling through a selected viewport. The file is saved outside of MIM. See Scrollable Captures below for more information.	Send this movie file to a third party so they can watch scrolling through multiple slices in the viewport.
	Save DICOM Image Data: Fusion *Fusions only; Secondary capture option* Saves a secondary capture of a fusion image. Users can scroll through slices in the saved image.	Save a fusion to a PACS as a secondary capture and be able to scroll through the fusion slices.

Scrollable Captures

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

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



AVI Format: VFW (Windows Media® Player)

Slices per second: 5

Number of slices to skip between captures: 0

☑ Include sidebar in capture

☑ Play movie when done

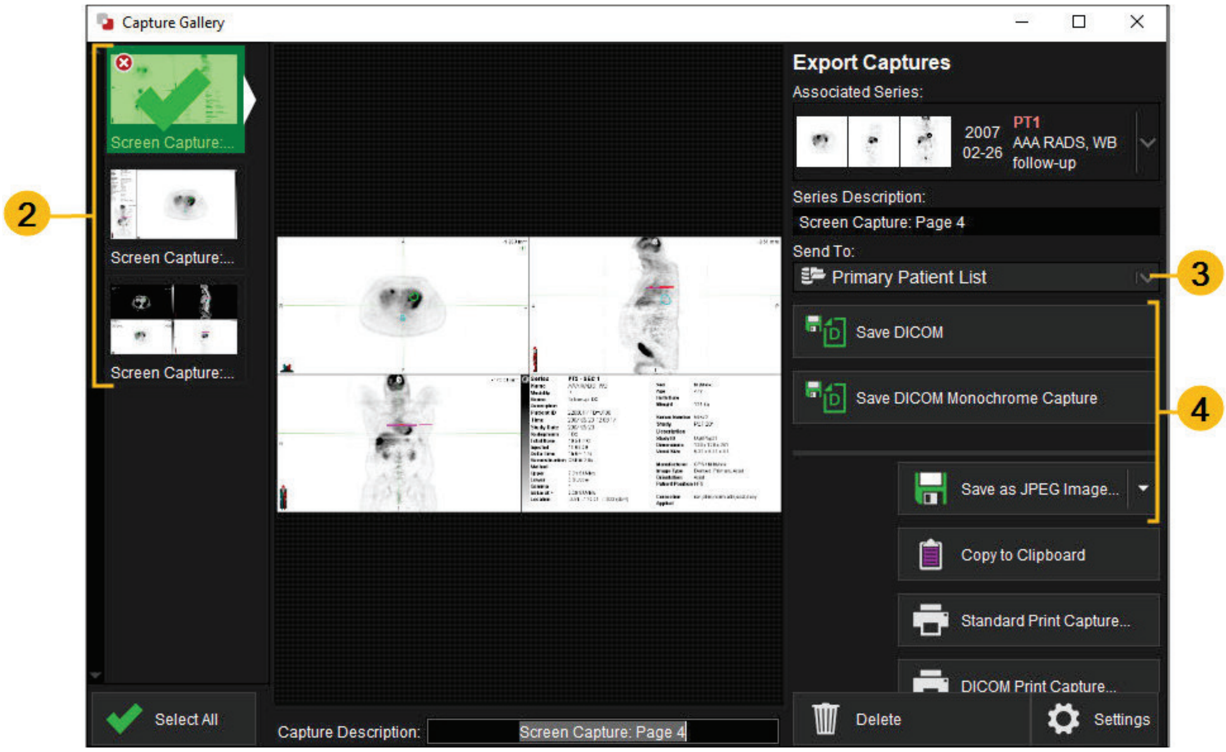
4. Click **OK**.
5. Choose the location on your workstation for the movie to save.
6. Click **Save**.

Save Secondary Captures

You can save secondary captures from the Capture Gallery.

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

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



Series Description: Screen Capture: Page 4

Send To: Primary Patient List

Capture Description: Screen Capture: Page 4

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

Save Contours

MIMTD-653 • 14 Aug 2023

Overview

After you create a contour, you will typically save it as a DICOM RTstruct. Alternatively, you can use other save options if needed for certain scenarios.

> **Tip:** Saving a session also saves the contours created in that session.

Contents

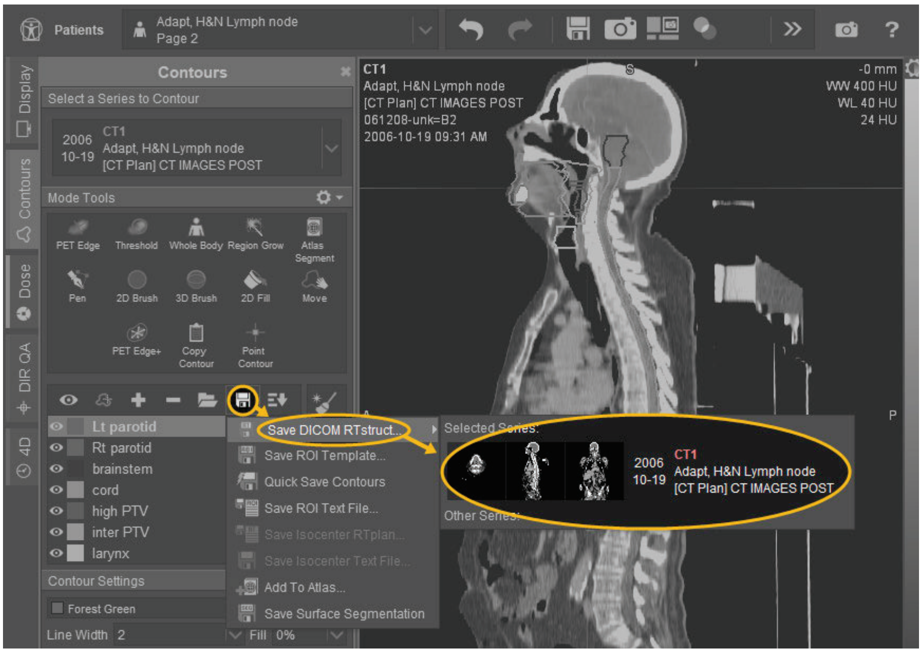
- Save As DICOM RTstruct
- Alternative Save Options
- Auto-Save Contour Backups

Save As DICOM RTstruct

RTstructs (RTst) are the DICOM for contours. You can see RTstructs on the patient list and modify an RTstruct that was previously saved. When sending the data to PACS or another third-party DICOM system, they are able to show contours that were saved as RTstructs.

Save contours as RTstructs:

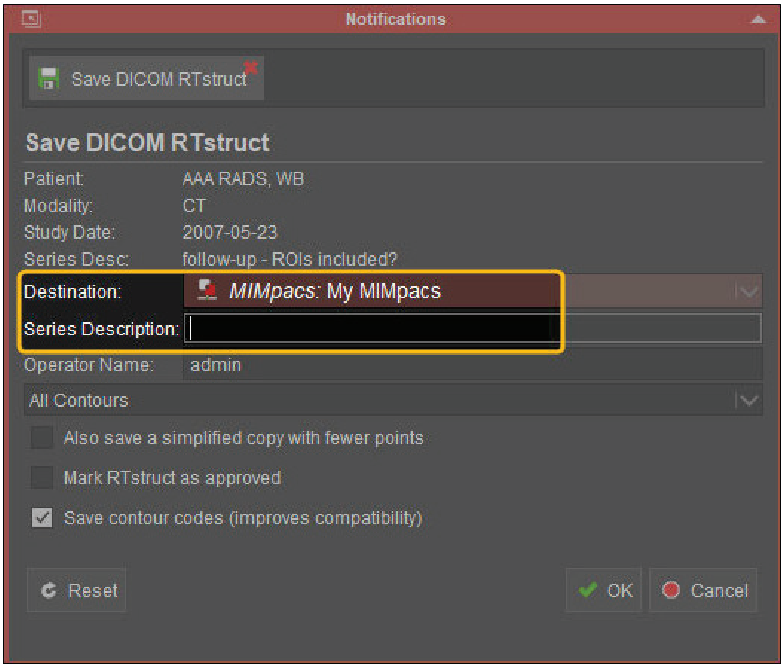
1. Click the save 💾 button above the list of contour names in the Contours sidebar. Or, you can click the save 💾 button in the top toolbar.
2. Hover over **Save DICOM RTstruct...** in the menu.
3. In the list of series that appear, click to select the series that you want the contours to be associated with.



Tip: You can associate the contours with series that have a registration or frame of reference (FOR) link with the series that the contours were created on.

4. In the Save DICOM RTstruct notification, ensure that the **Destination** is correct or update it to save the file to another location.

5. Enter a **Series Description** for the RTstruct set.



Save DICOM RTstruct

Patient: AAA RADS, WB
Modality: CT
Study Date: 2007-05-23
Series Desc: follow-up - ROIs included?
Destination: *MIMpacs:* My MIMpacs
Series Description:
Operator Name: admin
All Contours

☐ Also save a simplified copy with fewer points
☐ Mark RTstruct as approved
☑ Save contour codes (improves compatibility)

6. If needed, you can adjust other save options in the Notification window:
    - Use the dropdown to choose whether to save **All Contours**, **Visible Contours**, or **Specified Contours**.
    - Depending on the capabilities of the PACS or the system where you are sending the data, select **Also save a simplified copy with fewer points** if needed.
    - Based on your organization's policies, select **Mark RTstruct as approved**, if appropriate.

7. Click **OK**.

Alternative Save Options

Consider the following options to save contours for other scenarios. These options are available in the Save menu when you click the save 🖫 button above the list of contour names in the **Contours** sidebar.

Option	Description	Use Case
Save ROI Template...	Save an RTstruct template that can be loaded into other sessions.	Use when setting up standard ROIs and names for use across studies. This is typically done during MIM implementation, but you can add templates later as needed.

Option	Description	Use Case
Quick Save Contours	Save contours for the selected series. This option does not generate an RTstruct file on the patient list.	For unreliable workstations, use this option to save contours mid-session so you don't lose your work. If your session terminates unexpectedly, you can recover your contours by reopening the series and using the **Recover Quick Save Contours** option.
Save to Contour Shape Library...	Add a contour to the Contour Shape Library.	Use to consistently place the same shape on future studies, such as a contour of a certain size and shape for research, for a couch, or for a phantom.
Add to Atlas...	Add a contour to an atlas.	Use when setting up atlases for use across studies. This is typically done during custom atlas creation.

Auto-Save Contour Backups

MIM can automatically back up contours so that your work is not lost if your MIM session terminates unexpectedly. By default, contours are auto-saved every 10 minutes.

To adjust this setting:

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for **"contour autosave"**. Select **Contouring** on the left side.
3. Scroll down and update the auto-save settings as needed:
    - *If you want to turn off autosave*, deselect **Automatically save backups of contours**.
    - *If you want to change how frequently contours are saved*, update the **Contour autosave interval (in minutes)** field.
4. Click **OK** to save the changes and close the window.

Tip: Users can manually save backups for the contours that they are working on whenever they like by using the **Save** >> **Quick Save Contours** option.

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

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

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.

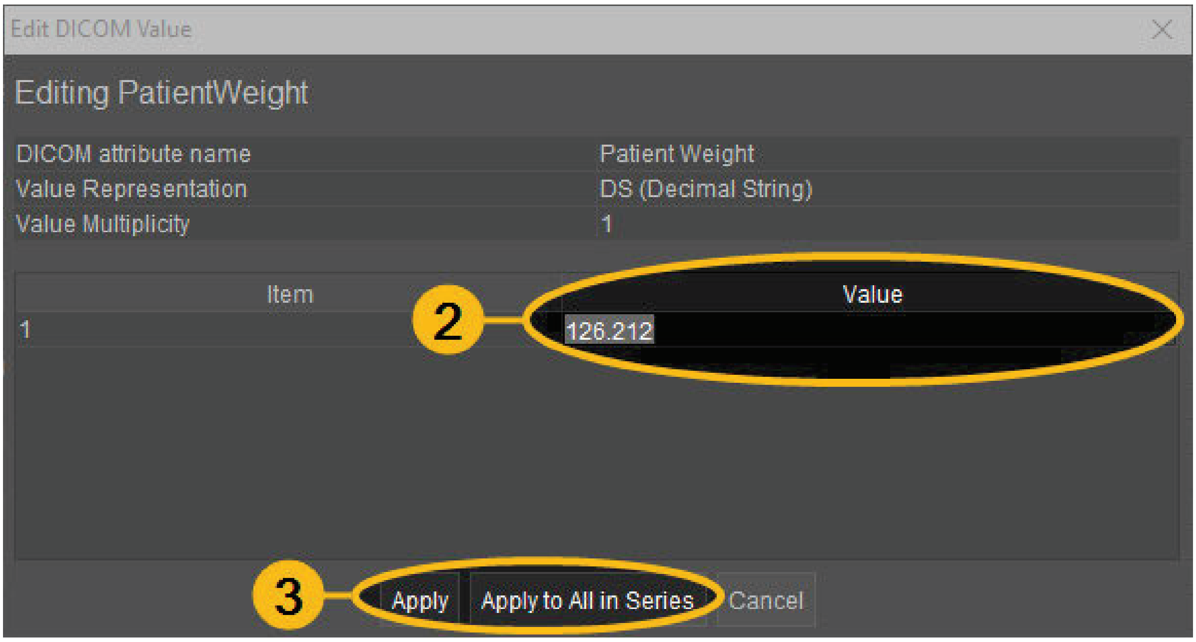
- *In MIM 7.3 and earlier*: A split pane view shows information for each series, but scrolling, searching, and expanding/collapsing are not synced between the panes. Differences are not highlighted.

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.



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.

Set Keyboard Shortcuts

MIMTD-616 • 30 Aug 2023

Overview

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

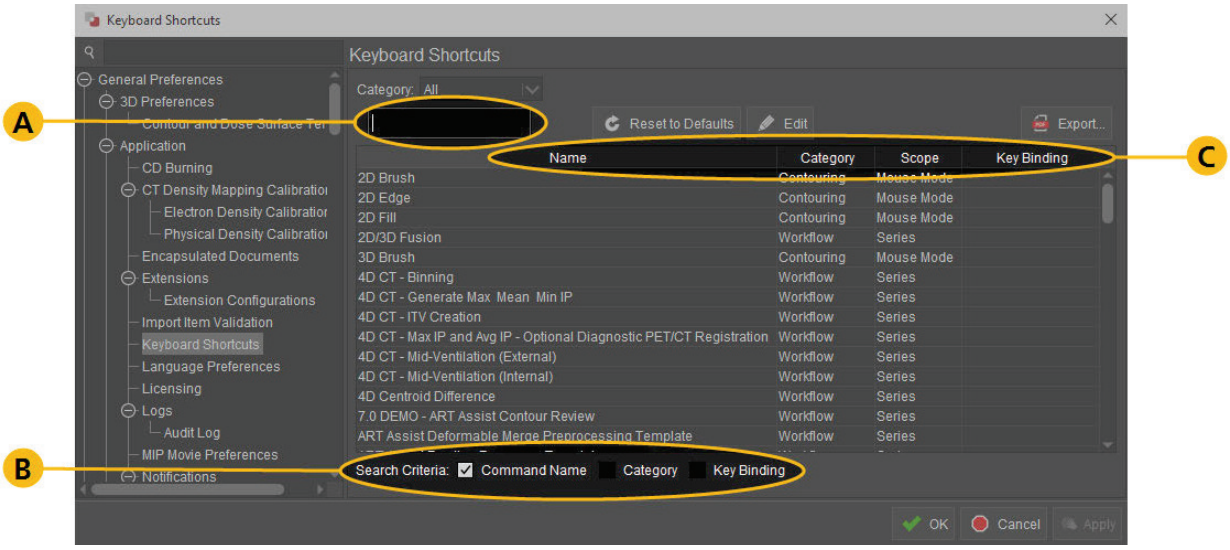
Related: By default, many commands are already assigned to keyboard shortcuts. For a list of default keyboard shortcuts, see Default Keyboard Shortcuts.

Contents

Assign or Reassign Keyboard Shortcuts

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

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

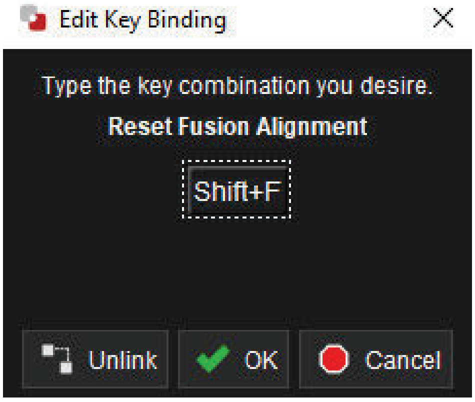


Name	Category	Scope	Key Binding
2D Brush	Contouring	Mouse Mode	
2D Edge	Contouring	Mouse Mode	
2D Fill	Contouring	Mouse Mode	
2D/3D Fusion	Workflow	Series	
3D Brush	Contouring	Mouse Mode	
4D CT - Binning	Workflow	Series	
4D CT - Generate Max Mean Min IP	Workflow	Series	
4D CT - ITV Creation	Workflow	Series	
4D CT - Max IP and Avg IP - Optional Diagnostic PET/CT Registration	Workflow	Series	
4D CT - Mid-Ventilation (External)	Workflow	Series	
4D CT - Mid-Ventilation (Internal)	Workflow	Series	
4D Centroid Difference	Workflow	Series	
7.0 DEMO - ART Assist Contour Review	Workflow	Series	
ART Assist Deformable Merge Preprocessing Template	Workflow	Series	

Search Criteria: ☑ Command Name ☐ Category ☐ Key Binding

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

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



Type the key combination you desire.

Reset Fusion Alignment

Shift+F

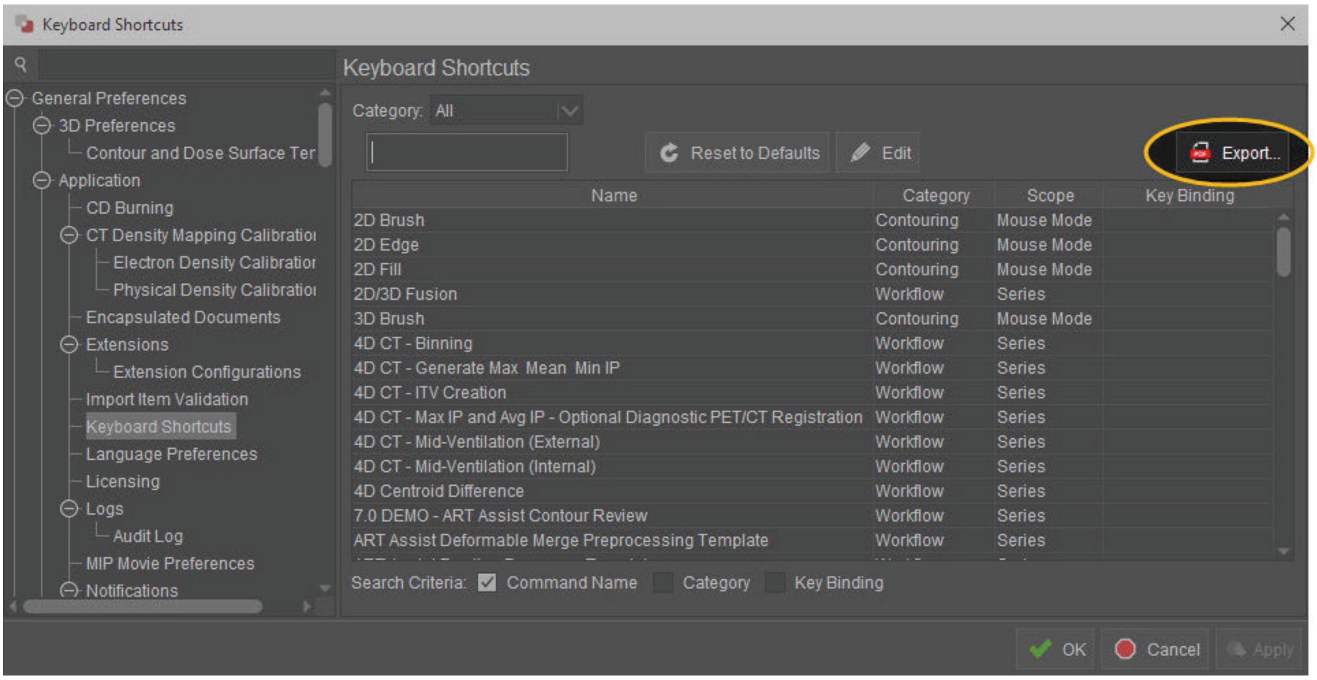
> ☆ **Important**: If the key binding is already in use, MIM warns you and shows the command that the key binding is assigned to. Type a different key binding, or click **OK** to use the key binding that you entered and unassign the key binding from the other command.

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

Export a PDF of Keyboard Shortcuts for Reference

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

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



Category: All

Name	Category	Scope	Key Binding
2D Brush	Contouring	Mouse Mode	
2D Edge	Contouring	Mouse Mode	
2D Fill	Contouring	Mouse Mode	
2D/3D Fusion	Workflow	Series	
3D Brush	Contouring	Mouse Mode	
4D CT - Binning	Workflow	Series	
4D CT - Generate Max Mean Min IP	Workflow	Series	
4D CT - ITV Creation	Workflow	Series	
4D CT - Max IP and Avg IP - Optional Diagnostic PET/CT Registration	Workflow	Series	
4D CT - Mid-Ventilation (External)	Workflow	Series	
4D CT - Mid-Ventilation (Internal)	Workflow	Series	
4D Centroid Difference	Workflow	Series	
7.0 DEMO - ART Assist Contour Review	Workflow	Series	
ART Assist Deformable Merge Preprocessing Template	Workflow	Series	

Search Criteria: ☑ Command Name ☐ Category ☐ Key Binding

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

Configure Mouse Behaviors

MIMTD-1282 • 07 Aug 2023

Overview

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

For example, you may want to scroll quickly through a series with a left-click drag instead of the default right-click drag (see Examples below for instructions).

Contents

Default Mouse Behaviors

MIM includes the following default mouse behaviors:

Action	Mouse Behavior	More Information
Localize	Left-click and left-click drag	Localize and Scroll
Adjust Contrast*	Middle-click drag	Adjust Image Contrast
Radial Menu	Right-click	Access Tools: The Toolbar and the Radial Menu
Scroll Slices	Right-click drag	Localize and Scroll

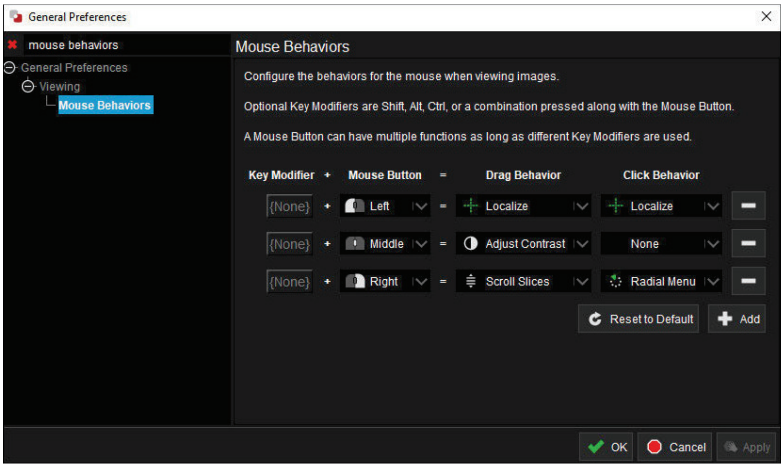
*The adjust contrast default is new in MIM 7.3 and later. In MIM 7.2 and earlier, there is no mouse behavior for this action.

Adjust Mouse Behaviors

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

To adjust the mouse behaviors, follow these steps:

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



Mouse Behaviors

Configure the behaviors for the mouse when viewing images.

Optional Key Modifiers are Shift, Alt, Ctrl, or a combination pressed along with the Mouse Button.

A Mouse Button can have multiple functions as long as different Key Modifiers are used.

Key Modifier	+	Mouse Button	=	Drag Behavior	Click Behavior
{None}	+	Left	=	Localize	Localize
{None}	+	Middle	=	Adjust Contrast	None
{None}	+	Right	=	Scroll Slices	Radial Menu

The following options can be combined:

Key Modifiers*	Mouse Button	Behaviors

- Windows®
  - Shift
  - Alt
  - Ctrl
- Mac®
  - shift
  - option
  - control
	- Left
	- Middle**
	- Right
		- Scroll Slices
		- Adjust Contrast
		- Localize
		- Rotate View
		- Pan
		- Zoom
		- Quick MIP

*Neither the Command key (for Macs) nor the Windows key are allowed with mouse behaviors.

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

Examples

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

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

Key Modifier +	Mouse Button =	Drag Behavior	Click Behavior
{None} +	Left =	Scroll Slices	Localize

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

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

Key Modifier +	Mouse Button =	Drag Behavior	Click Behavior
{None} +	Middle =	Pan	None

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

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

Key Modifier + Mouse Button = Drag Behavior Click Behavior

Ctrl + Left = Pan None

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

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

Key Modifier + Mouse Button = Drag Behavior Click Behavior

{None} + Right = Zoom Radial Menu

Automate Reconstruction and Segmentation

SPECTRA Quant® Overview

MIMTD-1752 • 10 Jun 2024

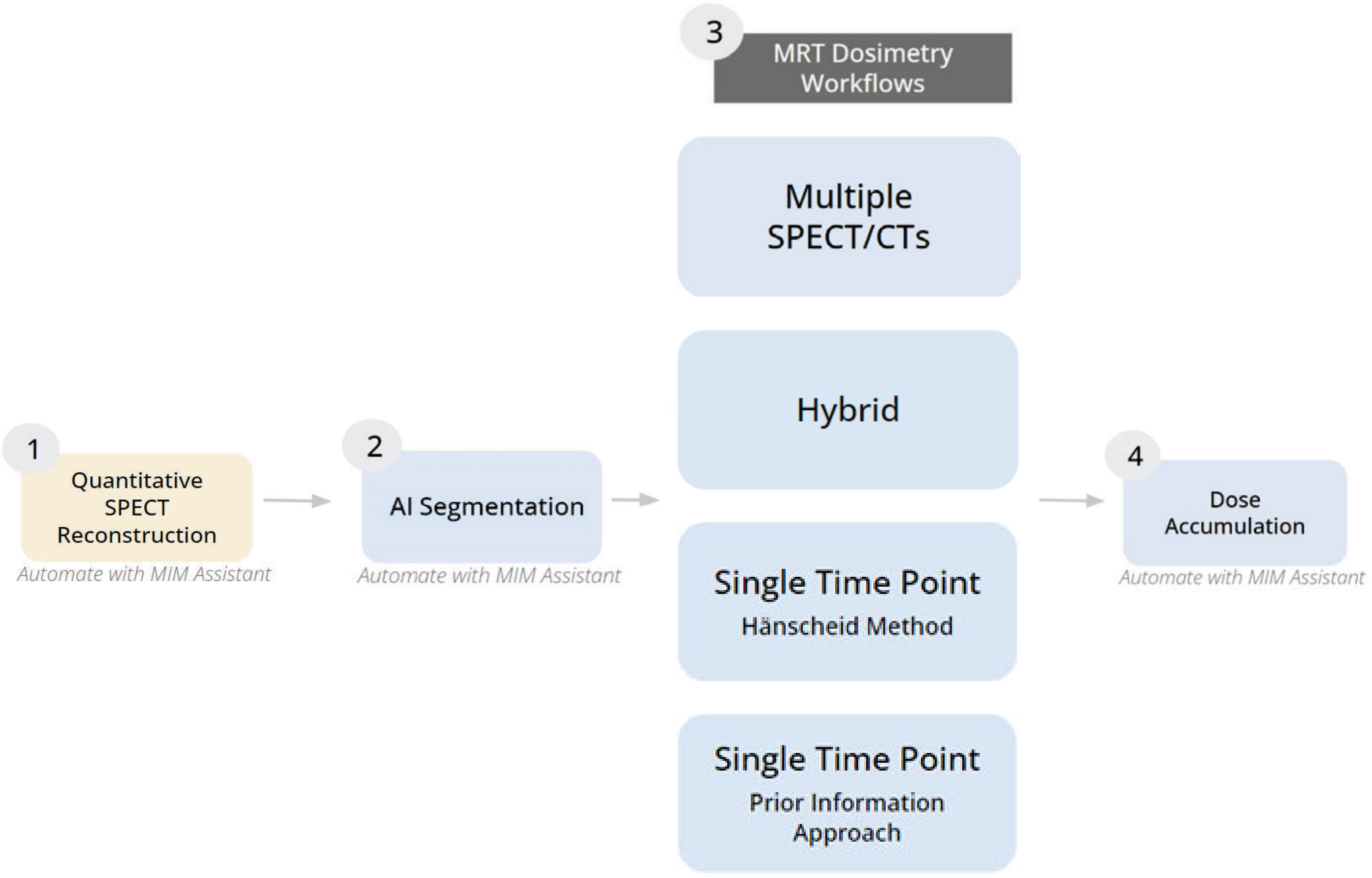
Overview

SurePlan™ MRT includes SPECTRA Quant® so that you can quantitatively 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®.

After the series is reconstructed, auto-contouring runs. You will use the reconstructed series for your MRT dosimetry workflows.



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 MRT for steps.
4. The workflow creates a reconstructed 3D image. This series is used as an input for your dosimetry 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 for MRT

MIMTD-1927 • 06 May 2024

Overview

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 Quant® 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.

Run Reconstruction

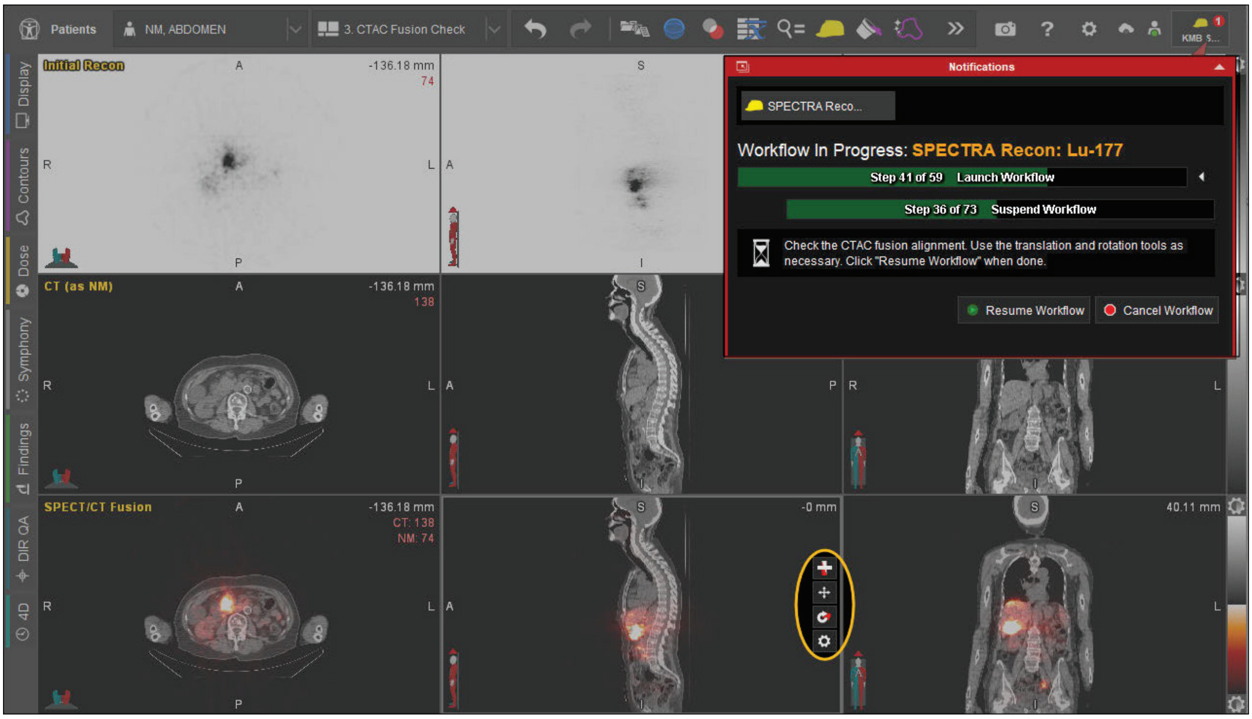
1. From the patient list, select the Raw Projection NM series and the CT.

   ☆ **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. When prompted, 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, check the following parameters:

   i. On the **Attenuation** tab, verify that **Attenuation Correction** is set to **CT Method**.

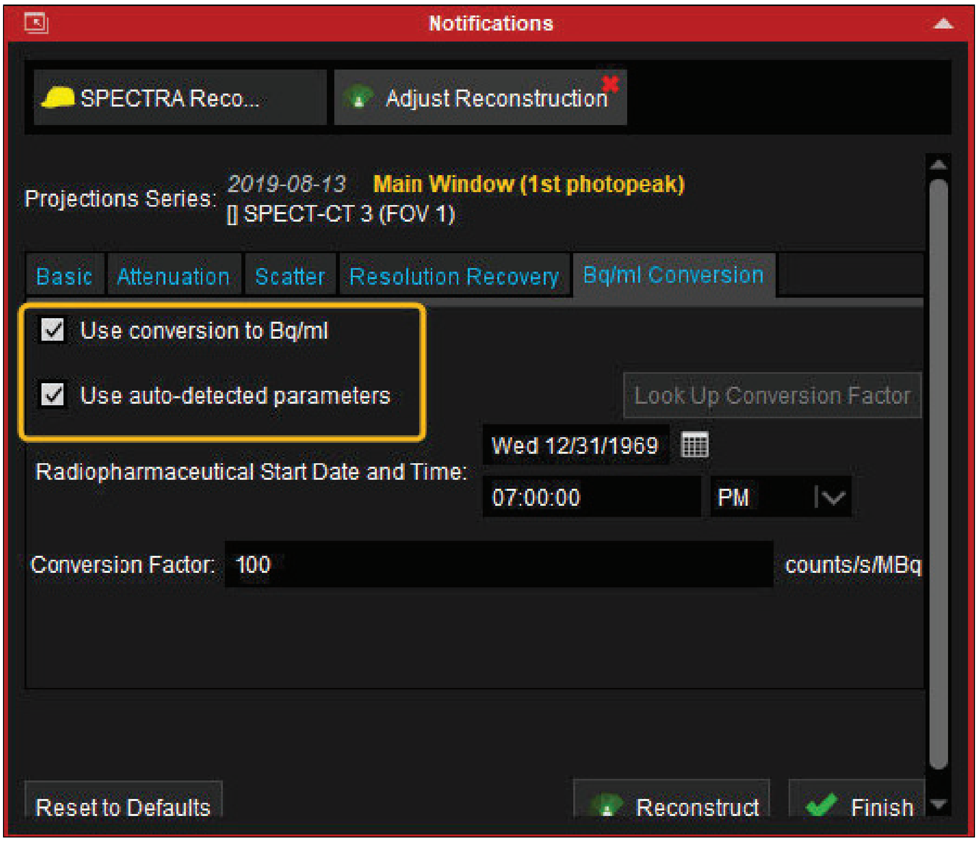
   ii. On the **Scatter** tab, verify that **Use scatter correction** is selected.

> ☆ **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.

   iii. On the **Bq/ml Conversion** tab, verify that both of the following options are selected:

   - **Use conversion to Bq/ml**

- **Use auto-detected parameters**



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

☑ Use conversion to Bq/ml

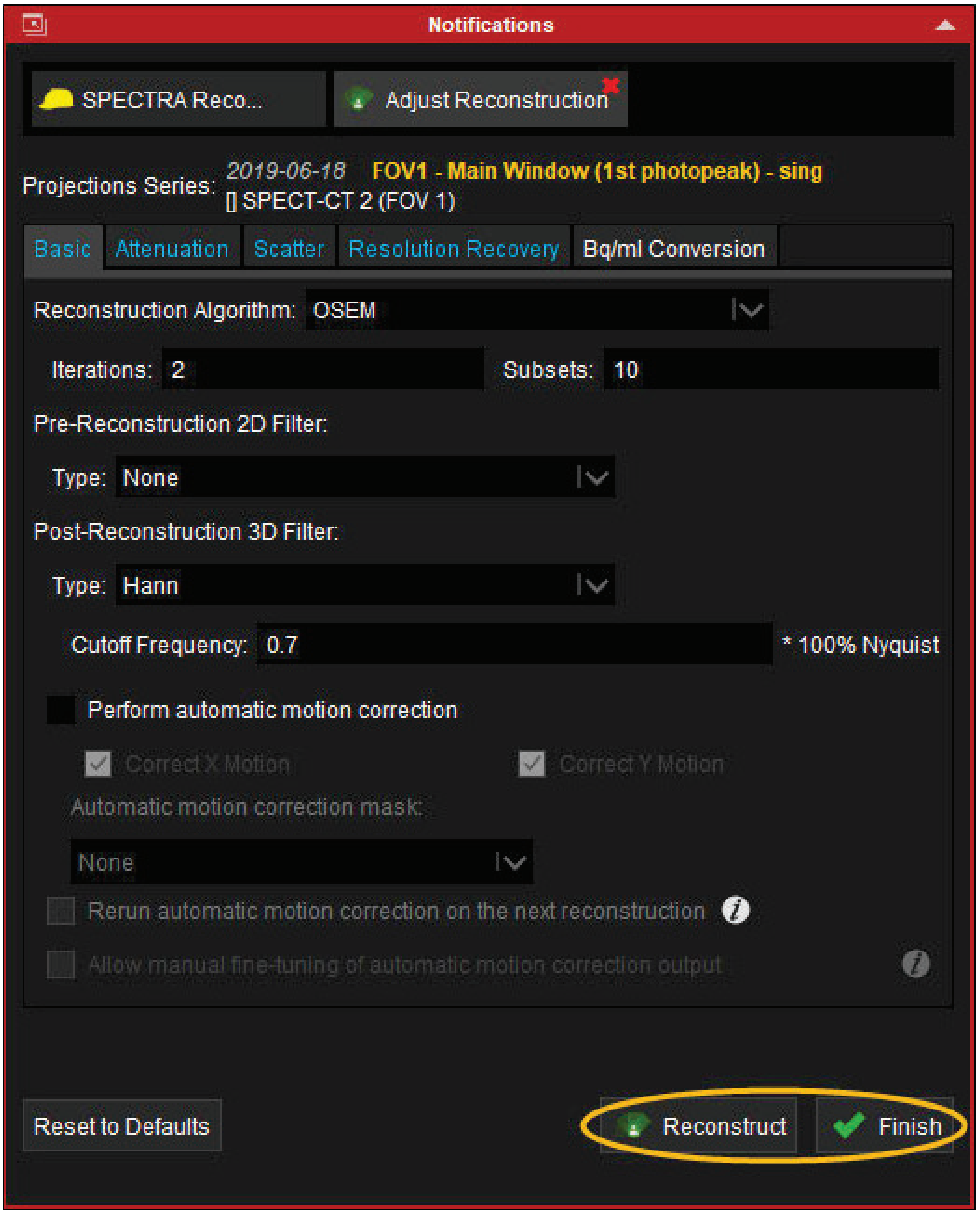
☑ Use auto-detected parameters

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

Conversion Factor: 100 counts/s/MBq

6. 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.



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

7. Save the reconstructed series to the patient list.

Contour ProtégéAI+™ for MRT Overview

MIMTD-1925 • 03 Jul 2024

Overview

Your organization can use Contour ProtégéAI+ to automate series segmentation using specially trained neural networks.

Contents

Get Started with Contour ProtégéAI+

Your MIM® representative helps you configure Contour ProtégéAI+ as part of your MIM SurePlan™ MRT implementation. This includes:

- Downloading and importing the SurePlan MRT model.
- Setting up a Contour ProtégéAI+ protocol that determines when and how auto-segmentation runs.
- (If applicable) Creating a MIM Assistant® rule that automatically triggers Contour ProtégéAI+ to run.

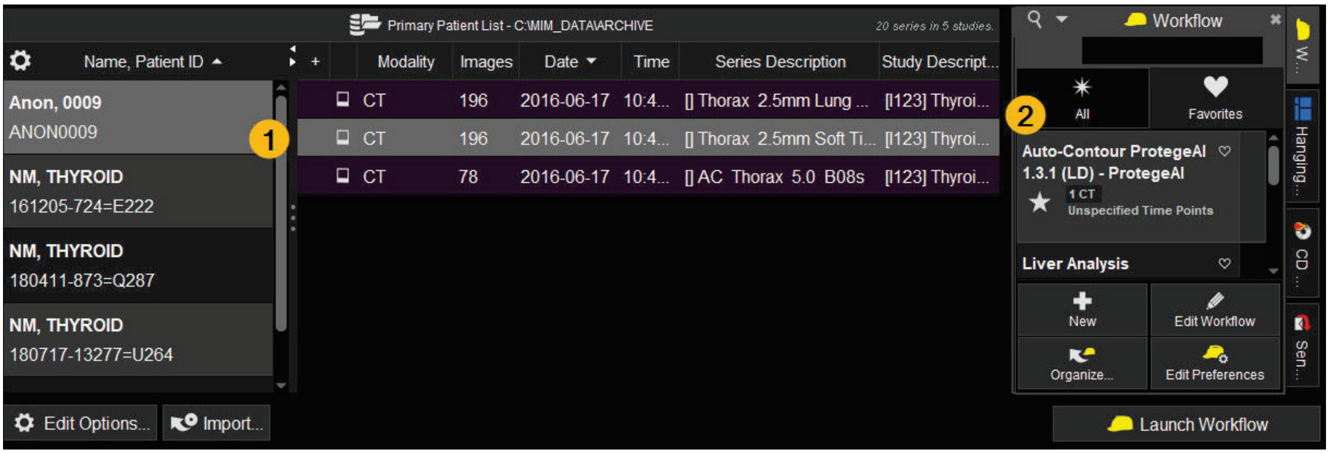
How to Use Auto-Contouring

If you are using MIM Assistant, auto-contouring automatically begins when data is sent to the designated location.

Tip: If auto-contouring does not automatically begin as expected, please contact MIM Software Support at support.mimsoftware.com. The data filters for your MIM Assistant rule may need to be adjusted.

If you are not using MIM Assistant or if you need to manually start auto-contouring, launch the Contour ProtégéAI+ workflow:

1. On the patient list, select the CT.
2. Go to the **Workflows** tab on the right side of the screen and select the Contour ProtégéAI+ workflow for MRT auto-contouring.



Name, Patient ID
Anon, 0009 ANON0009
NM, THYROID 161205-724=E222
NM, THYROID 180411-873=Q287
NM, THYROID 180717-13277=U264

Modality	Images	Date	Time	Series Description	Study Descript...
CT	196	2016-06-17	10:4...	[] Thorax 2.5mm Lung ...	[I123] Thyroi...
CT	196	2016-06-17	10:4...	[] Thorax 2.5mm Soft Ti...	[I123] Thyroi...
CT	78	2016-06-17	10:4...	[] AC Thorax 5.0 B08s	[I123] Thyroi...

Auto-Contour ProtegeAI 1.3.1 (LD) - ProtegeAI
1 CT
Unspecified Time Points

Liver Analysis

3. Watch as the workflow launches and auto-contouring runs.

When auto-contouring is complete, the system saves an RTstruct file to the patient list. You will include this RTstruct file when you launch an MRT dosimetry workflow. The workflow will prompt you to review the automatically generated contours and update as needed.

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

Contour ProtégéAI+ Version Support

Your Contour ProtégéAI+ version depends on which version of MIM you are running. Contour ProtégéAI+ is installed as part of your SurePlan MRT installation.

Contour ProtégéAI+ runs various models that can be updated in conjunction with or separately from a system upgrade. Contour ProtégéAI+ via cloud deployment uses the same model versions as local deployments. MIM performs the model upgrades for cloud deployments.

For local deployments, download the most recent SurePlan MRT model, depending on your version and location:

MIM Version	Contour ProtégéAI+ Version
MIM 7.3.5 and later	Version 1.3.0 Model 4.0.0: U.S., CE

MIM Version	Contour ProtégéAI+ Version
MIM 7.3.0-7.3.4	Version 1.2.0 Model 4.0.0: U.S., CE
MIM 7.2.12 and later	Version 1.3.0 Model 4.0.0: U.S., CE
MIM 7.2.0-7.2.11	Version 1.2.0 Model 4.0.0: U.S., CE

Additional Resources

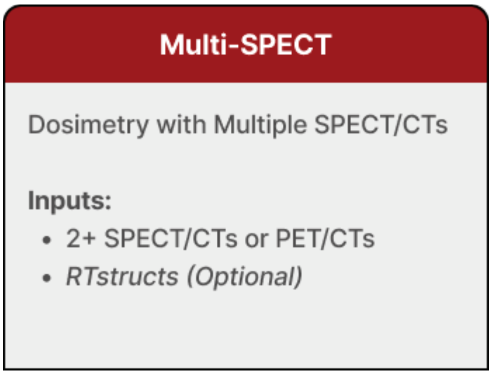
- For more information about implementing Contour ProtégéAI+, refer to Introduction to Contour ProtégéAI+.
- For a list of contours included in the SurePlan MRT model, refer to Contour ProtégéAI+™ Models and Contours.
- To see a demo of Contour ProtégéAI+ and learn more about best practices for efficient contouring, check out the Contour ProtégéAI+ Training Videos.

MIM SurePlan™ MRT Workflows

MRT: Dosimetry with Multiple SPECT/CTs

MIMTD-705 • 22 Nov 2024

Overview



Multi-SPECT

Dosimetry with Multiple SPECT/CTs

Inputs:
- 2+ SPECT/CTs or PET/CTs
- *RTstructs (Optional)*

After pre-processing steps have been performed, such as reconstruction or segmentation, run the **MRT: Dosimetry with Multiple SPECT/CTs** workflow. This workflow is for two or more SPECT/CTs or PET/CTs following one radiopharmaceutical administration.

Tip: Alternatively, you can use the **MRT: Dosimetry with Multiple SPECT/CTs (for Prior Information Approach)** workflow if you expect to run single-time-point dosimetry in future cycles of therapy. The output can then be used with the MRT: Dosimetry with 1 SPECT/CT (Prior Information Approach) workflow. The steps for both multiple SPECT/CTs workflows are the same, and the information below applies to both workflows.

The multiple SPECT/CT workflow guides you through reviewing contours and other steps as needed. It defines a Reference SPECT/CT (or PET/CT) as the time point for segmentation and as the time point that other series will be registered to.

The workflow produces a voxelized absorbed dose map and mean absorbed dose values, which can then be used for absorbed dose accumulation.

Tip: Use the steps below to run the workflow and to adjust study information and contours as needed. Use the My MIM SurePlan™ MRT Quick Sheet page to make your own notes about running the workflow.

Contents

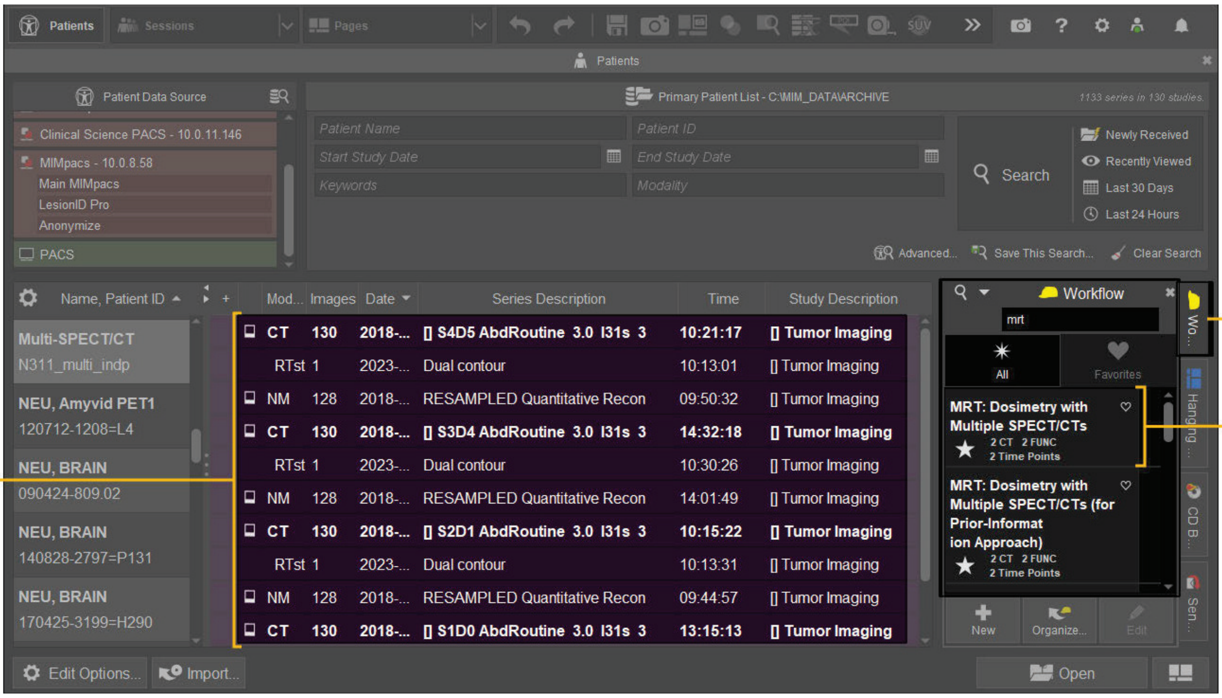
- Review Results
- Save Results
- Tips and Common Options
- Troubleshooting

Launch the Workflow

1. From the patient list, select two or more SPECT/CTs or PET/CTs following one radiopharmaceutical administration:
    - One CT for each time point and, if available, associated RTstructs
    - One PET or quantitative SPECT for each time point
    - (Optional) Prior CT to allow transferring contours from a previous radiopharmaceutical administration

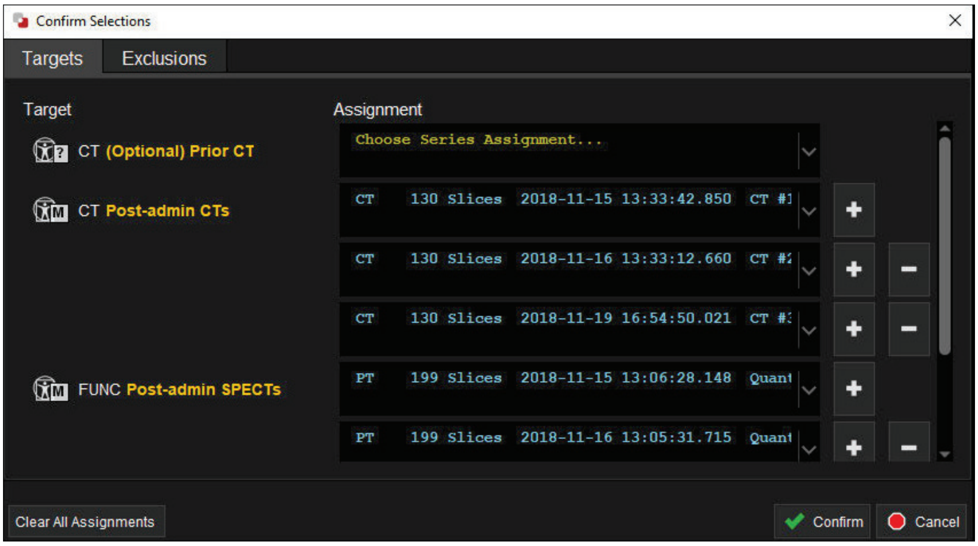
> **Tip:** To select multiple series, press and hold the Ctrl key. Or, click and drag down to select the list of series.

2. Select the **Workflow** tab in the patient list to expand it.
3. Double-click the **MRT: Dosimetry with Multiple SPECT/CTs** or the **MRT: Dosimetry with Multiple SPECT/CTs (for Prior-Information Approach)** workflow from the list to launch it.



Mod...	Images	Date	Series Description	Time	Study Description
CT	**130**	**2018-...**	**[] S4D5 AbdRoutine 3.0 I31s 3**	**10:21:17**	**[] Tumor Imaging**
RTst	1	2023-...	Dual contour	10:13:01	[] Tumor Imaging
NM	128	2018-...	RESAMPLED Quantitative Recon	09:50:32	[] Tumor Imaging
CT	**130**	**2018-...**	**[] S3D4 AbdRoutine 3.0 I31s 3**	**14:32:18**	**[] Tumor Imaging**
RTst	1	2023-...	Dual contour	10:30:26	[] Tumor Imaging
NM	128	2018-...	RESAMPLED Quantitative Recon	14:01:49	[] Tumor Imaging
CT	**130**	**2018-...**	**[] S2D1 AbdRoutine 3.0 I31s 3**	**10:15:22**	**[] Tumor Imaging**
RTst	1	2023-...	Dual contour	10:13:31	[] Tumor Imaging
NM	128	2018-...	RESAMPLED Quantitative Recon	09:44:57	[] Tumor Imaging
CT	**130**	**2018-...**	**[] S1D0 AbdRoutine 3.0 I31s 3**	**13:15:13**	**[] Tumor Imaging**

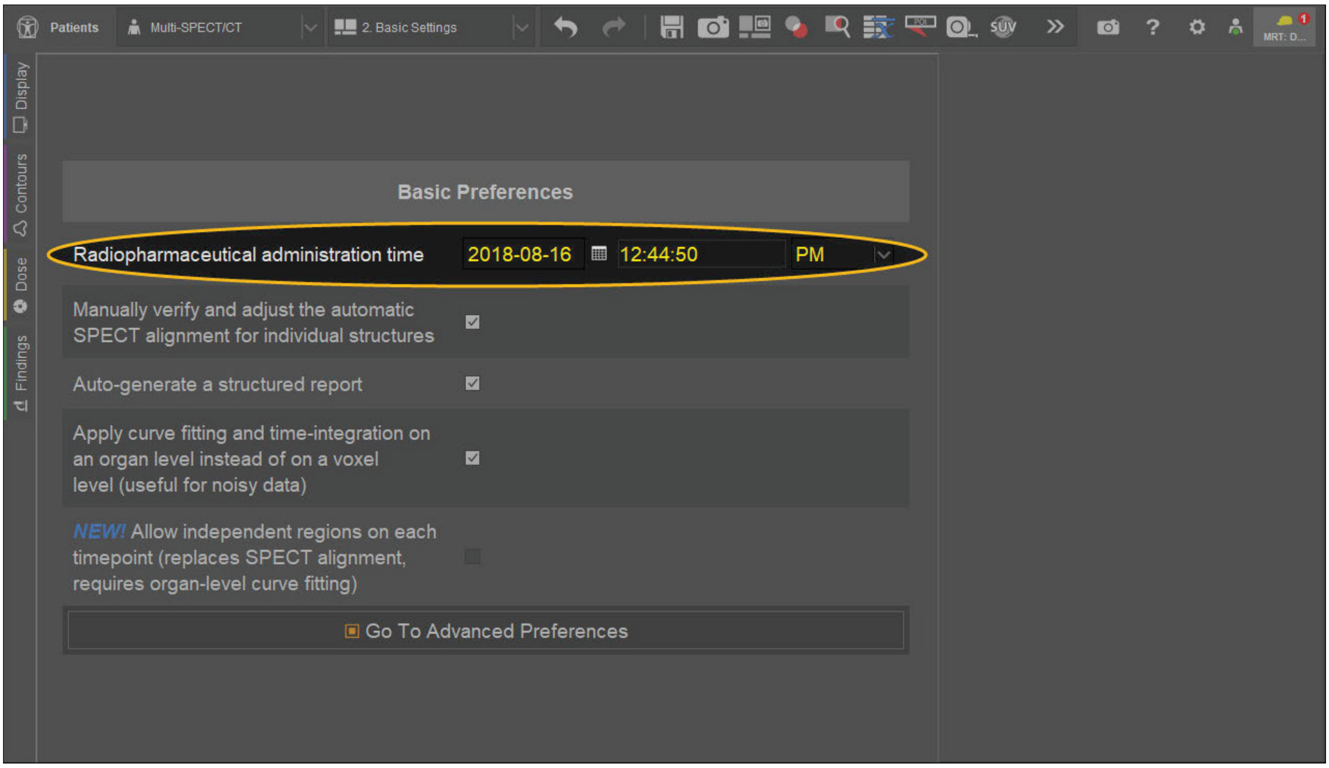
4. In the target confirmation window, verify the CTs and PETs or SPECTs you selected are listed for the Post-admin CT and Post-admin SPECT targets. If needed, click the plus ➕ to add a series or the minus ➖ to remove a series. Click **Confirm**.



Target	Assignment
CT (Optional) Prior CT	Choose Series Assignment...
CT Post-admin CTs	CT 130 Slices 2018-11-15 13:33:42.850 CT #1
	CT 130 Slices 2018-11-16 13:33:12.660 CT #2
	CT 130 Slices 2018-11-19 16:54:50.021 CT #3
FUNC Post-admin SPECTs	PT 199 Slices 2018-11-15 13:06:28.148 Quant
	PT 199 Slices 2018-11-16 13:05:31.715 Quant

Run Workflow Processing

1. On the Basic Preferences page, check the **Radiopharmaceutical administration time** and update it if needed. Click **Resume Workflow**.



Basic Preferences

Radiopharmaceutical administration time: 2018-08-16 12:44:50 PM

Manually verify and adjust the automatic SPECT alignment for individual structures ☑

Auto-generate a structured report ☑

Apply curve fitting and time-integration on an organ level instead of on a voxel level (useful for noisy data) ☑

NEW! Allow independent regions on each timepoint (replaces SPECT alignment, requires organ-level curve fitting) ☐

> **Tip:** If needed, you can go to the Advanced Preferences to modify additional workflow preferences. Refer to the tips below for common preferences or refer to Settings for Dosimetry with Multiple SPECT/CTs for more information about each advanced preference.

2. *If you included a Prior CT*, the workflow creates a rigid fusion between the Prior CT and the Reference CT and prompts you to review. If necessary, use the tools on the right side of the viewport to adjust the fusion.

> **Related**: See Adjust Fusions for more information.

> **Tip:** The Reference time point is designated as the primary time point for segmentation and registration between series. This rigid fusion is the starting point for the deformable registration, which is used to transfer contours from the Prior CT. If needed, you can update the Advanced Preferences to determine which time point is automatically selected as the Reference time point.

3. The workflow pauses and prompts you to contour ROIs on the Reference SPECT/CT or PET/CT image to include in the dosimetry analysis:
   - *If you loaded an RTstruct when launching the workflow*, the contours are listed in the Contours sidebar. *If you did not load an RTstruct*, click the plus ✚ button to create a contour.
   - Use the **2D Brush** or another contouring tool of your choice to draw or edit organ contours as needed. See Update Contours below for more contouring tips.
   - Use **PET Edge+**, the **Threshold** tool, or another contouring tool of your choice to draw or edit tumor contours as needed.
   - Ensure that each tumor contour created contains the word Tumor or Lesion.

   > **Tip:** Press the \ keyboard shortcut or click the arrow in the upper-right corner of the Notifications window to minimize the window. When you are finished with your adjustments, press \ again or click the flashing workflow button in the upper-right corner to re-expand the Notifications window.

Red
FOV Body
Line Width 2
Fill 0%
Type External
Hard Edge
Range Lock Lower Upper HU
Range Presets: None
Code: None

4. Click **Resume Workflow**.

> **Caution:** The workflow ordinarily locates the appropriate entry in the Physical Density Calibration table for the CT you are processing. If a matching calibration is not found and the workflow prompts you to select or add a calibration, please contact MIM Software Support for assistance.

5. At the prompt, click **OK** to save the RTdose file. The workflow also saves the output files needed for dose accumulation. See Save Results below for more information.

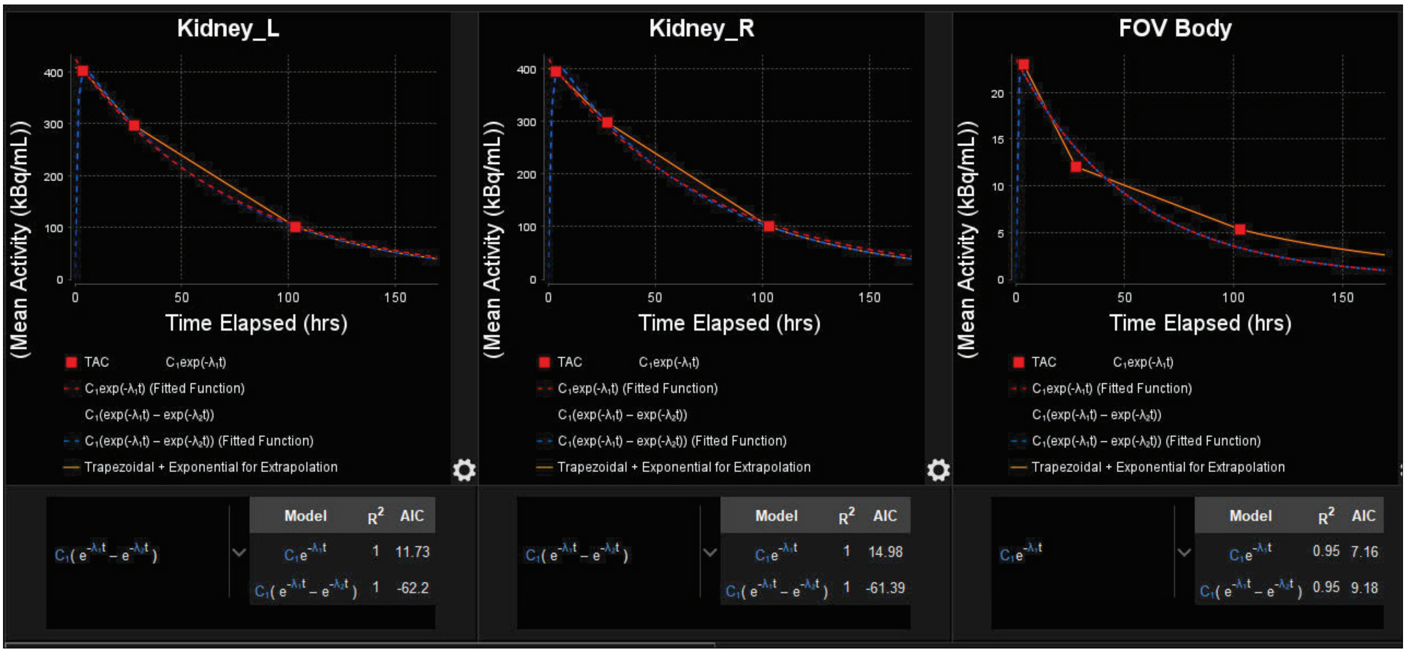
Review Results

The workflow completes and generates several results pages. Use the left and right arrow keys or page dropdown in the top toolbar to move between pages and review results.

Time Activity Curves

By default, the workflow aligns the images using a specialized alignment algorithm so that time-activity curves (TACs) and a time-integrated activity (TIA) image can be generated. After alignment, the workflow displays the aligned SPECT or PET time points as a dynamic series along with the resultant TACs.

You can cycle through the pages to see TACs for different contours. The Results Table includes the applied curve fit parameters.



Kidney_L

Model	R^2	AIC
$C_1 e^{-\lambda_1 t}$	1	11.73
$C_1(e^{-\lambda_1 t} - e^{-\lambda_2 t})$	1	-62.2

Kidney_R

Model	R^2	AIC
$C_1 e^{-\lambda_1 t}$	1	14.98
$C_1(e^{-\lambda_1 t} - e^{-\lambda_2 t})$	1	-61.39

FOV Body

Model	R^2	AIC
$C_1 e^{-\lambda_1 t}$	0.95	7.16
$C_1(e^{-\lambda_1 t} - e^{-\lambda_2 t})$	0.95	9.18

Example of time activity curve results page.

Dose Volume Histogram (DVH)

The DVH shows the distribution of absorbed dose across each segmented volume.

☐ Enforce same line styles for each dose

Name		Volume	Max Dose	Min Dose	Mean Dose	SD
Kidney_L	—	84.805	32.63	0.42	12.96	5.32
Kidney_R	—	187.373	35.07	0.37	17.98	7.50
Liver	—	1709.904	150.51	0.16	4.64	6.10
Lung_L	—	145.418	12.45	0.07	0.59	0.64
Lung_R	—	374.499	5.18	0.07	0.48	0.38

☐ Show dose constraint contours only None

☑ Show grid

Dose Value Type: Absolute Dose

☑ Normalize Volume

☐ Maximum Dose to Display (Gy) 30.00

☐ Show differential DVH

Number of DVH Bins to Combine: 1

- Review absorbed dose statistics for each region, including the mean, maximum, and minimum dose.
- Use the search field to see results only for certain regions. For example, search for "tumor" to see only results for tumor contours included in the DVH and table.
- Click the eye 👁 button to show/hide the region in the DVH. Click the line to change the color and format of the region in the DVH.

Tip: If information under the graph does not appear by default, click the **Show Options Panel** button in the lower-right corner of the DVH display to see additional information.

Absorbed Dose Map

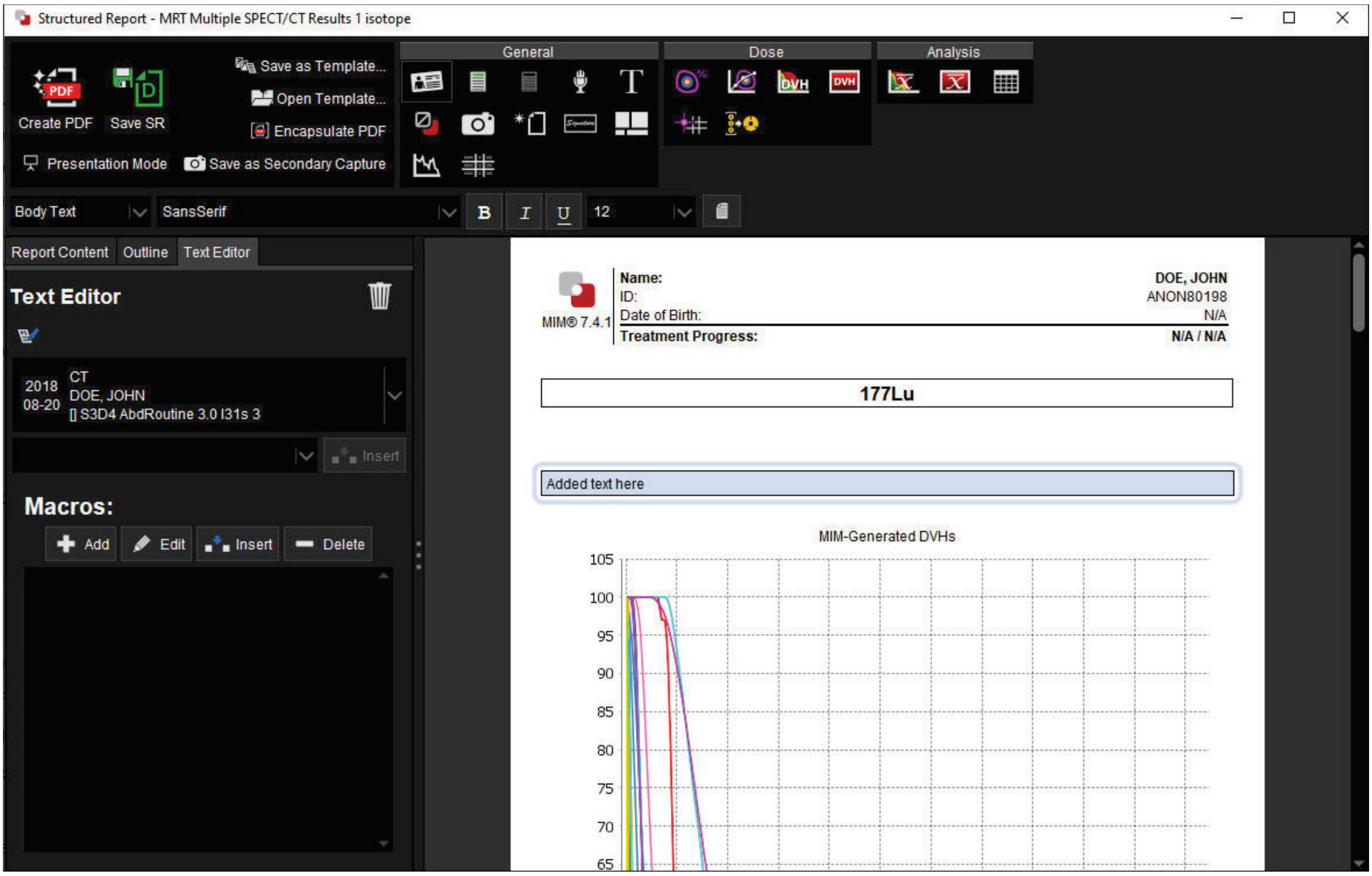
The results include a colored dose map overlaid on the Reference CT and the final SPECT/CT or PET/CT fusion.

Related: You can optionally use the **Dose** sidebar on the left side of the screen for more display options for dose. Refer to View Dose in MIM®: Fundamentals for more information.

Structured Report

The workflow automatically generates a structured report. As needed, update the report information. For example, on the Report Content tab, add a Text Editor field and type additional notes in the report.

Related: Refer to Create and Modify Structured Reports for more information about working with structured reports.



2018 08-20 CT DOE, JOHN [] S3D4 AbdRoutine 3.0 I31s 3

Name: DOE, JOHN
ID: ANON80198
Date of Birth: N/A
Treatment Progress: N/A / N/A

177Lu

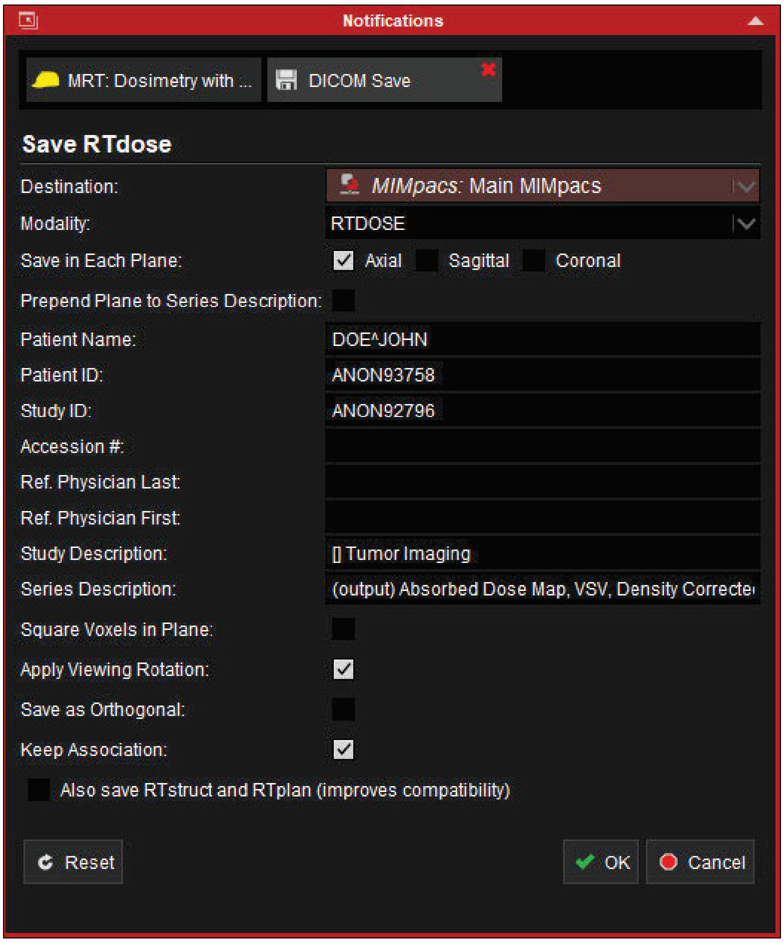
Added text here

When you are finished, save the structured report as a PDF or as a DICOM object (SR).

Tip: If you do not want a structured report, deselect the **Auto-generate a structured report** option on the Basic Preferences screen when running the workflow.

Save Results

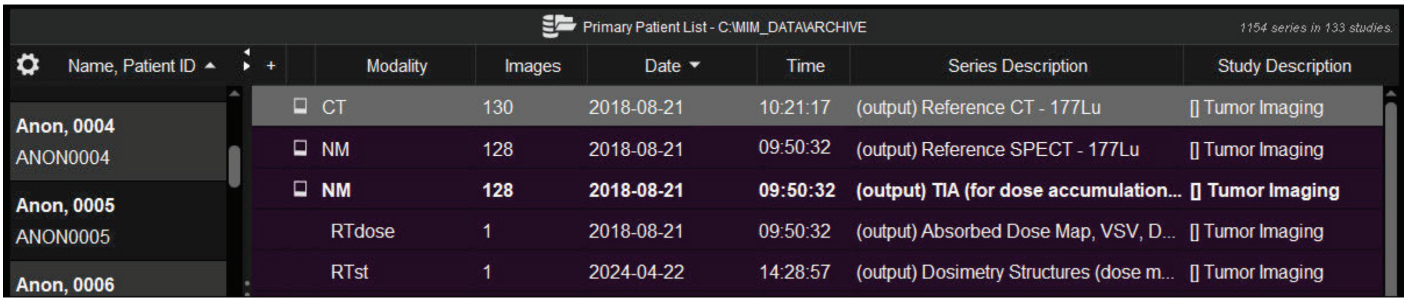
When processing is finished, the workflow prompts you to save the RTdose file. Click **OK**.



Save RTdose

Destination: *MIMpacs:* Main MIMpacs
Modality: RTDOSE
Save in Each Plane: ☑ Axial ☐ Sagittal ☐ Coronal
Prepend Plane to Series Description: ☐
Patient Name: DOE^JOHN
Patient ID: ANON93758
Study ID: ANON92796
Accession #:
Ref. Physician Last:
Ref. Physician First:
Study Description: [] Tumor Imaging
Series Description: (output) Absorbed Dose Map, VSV, Density Correcte
Square Voxels in Plane: ☐
Apply Viewing Rotation: ☑
Save as Orthogonal: ☐
Keep Association: ☑
☐ Also save RTstruct and RTplan (improves compatibility)

The workflow automatically saves five output files to your patient list. These series have "(output)" prepended to the series description. These output series are the inputs for the absorbed dose accumulation workflow to accumulate absorbed dose results from multiple radiopharmaceutical administrations. See Calculate Absorbed Dose Accumulation for more information.



Modality	Images	Date	Time	Series Description	Study Description
CT	130	2018-08-21	10:21:17	(output) Reference CT - 177Lu	[] Tumor Imaging
NM	128	2018-08-21	09:50:32	(output) Reference SPECT - 177Lu	[] Tumor Imaging
NM	**128**	**2018-08-21**	**09:50:32**	**(output) TIA (for dose accumulation...**	**[] Tumor Imaging**
RTdose	1	2018-08-21	09:50:32	(output) Absorbed Dose Map, VSV, D...	[] Tumor Imaging
RTst	1	2024-04-22	14:28:57	(output) Dosimetry Structures (dose m...	[] Tumor Imaging

You can also save the session so that you are able to resume where you left off with processing. Click the save 🖫 button in the top toolbar and select **Save Session...**.

Tip: To automatically save the session, select the Advanced Preference to **Save a session of the dosimetry results**. With this option enabled, you are also prompted to save the RTstruct and RTplan. Refer to Settings for Dosimetry with Multiple SPECT/CTs for more information about Advanced Preferences.

To re-open the session, double-click the saved session file from the patient list.

Tips and Common Options

Related: For more information about Advanced Preferences available when running these workflows, refer to Settings for Dosimetry with Multiple SPECT/CTs.

Update Contours

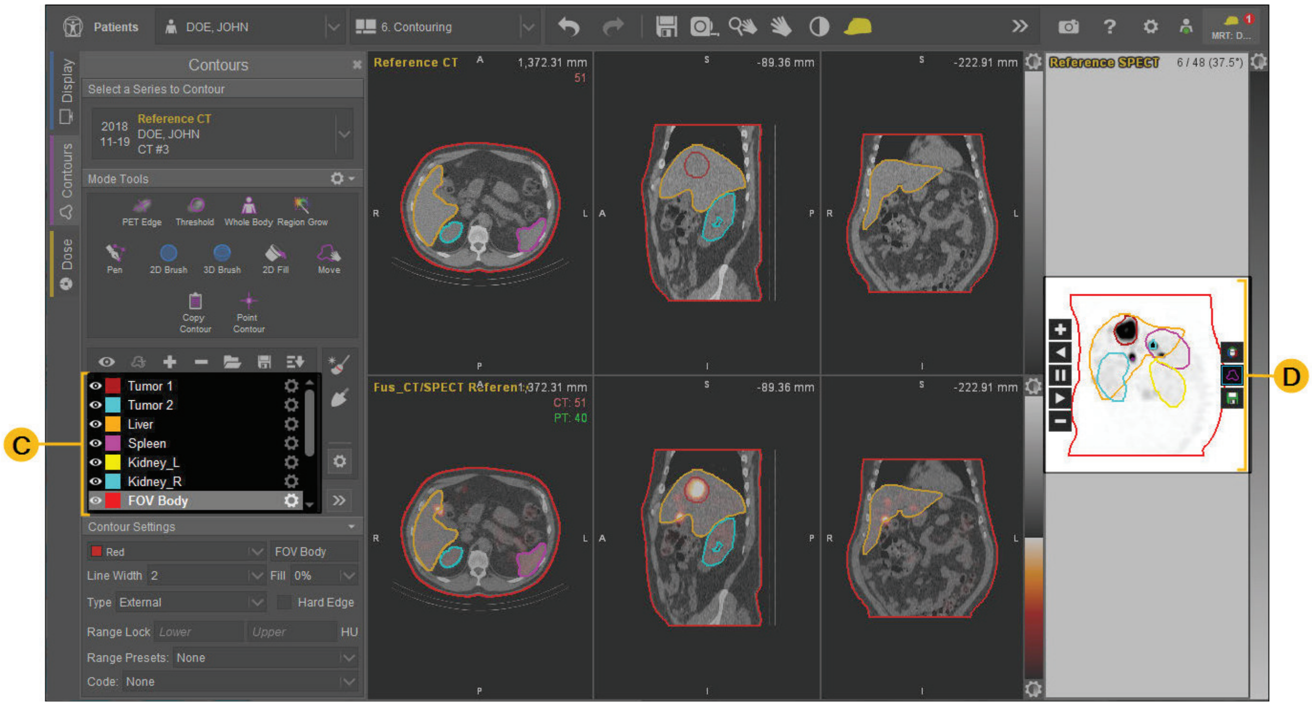
The workflow prompts you to review and/or add contours on the Reference CT. Keep the following tips in mind for efficient contouring:

A. Double-click on a viewport to make it larger. Use the 2 and 3 keys on your keyboard to zoom in.

B. Scroll to move between slices.

C. As needed, update the contour names and colors in the Contours sidebar.

D. Use the MIP to quickly and easily triangulate to tumors. Click a spot on the MIP, and MIM localizes to the highest intensity 3D location along that projection.



Tip: Use the play controls on the left side of the MIP to rotate the MIP.

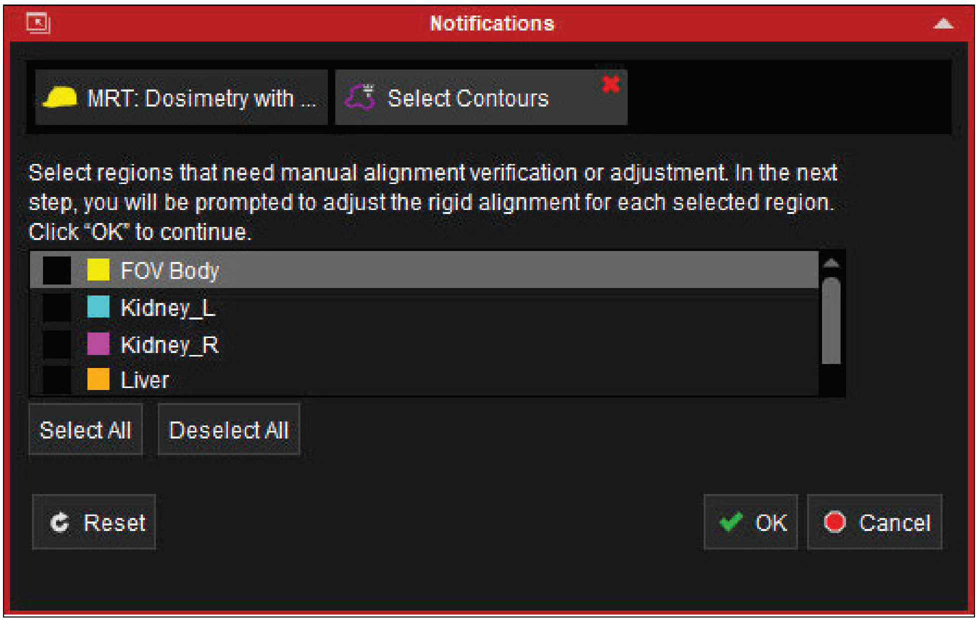
Update SPECT or PET Alignment

The system automatically registers SPECT or PET images to each other based on a specialized contour-based alignment technique. Alignments are combined to create a final series for each time point, which is registered to the Reference time point.

If desired, you can manually review and refine the SPECT or PET alignment:

1. On the Basics Preferences screen, select **Manually verify and adjust the automatic SPECT alignment for individual structures**.

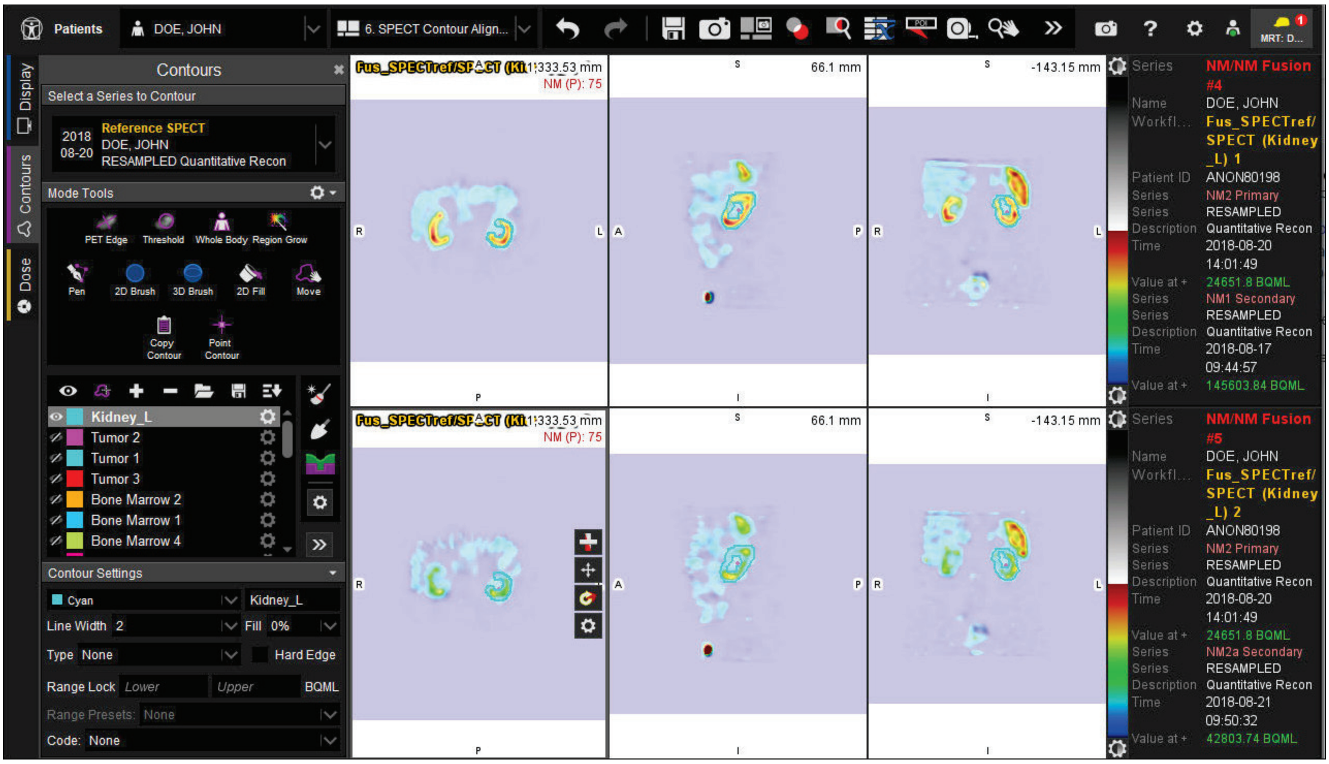
2. When prompted, select contours for manual verification or adjustment. Click **OK**.



Select regions that need manual alignment verification or adjustment. In the next step, you will be prompted to adjust the rigid alignment for each selected region. Click "OK" to continue.

3. Use the fusion tools on the right side of the viewport to adjust the fusion as needed.

Related: For more information on adjusting fusion alignments, see Adjust Fusions.



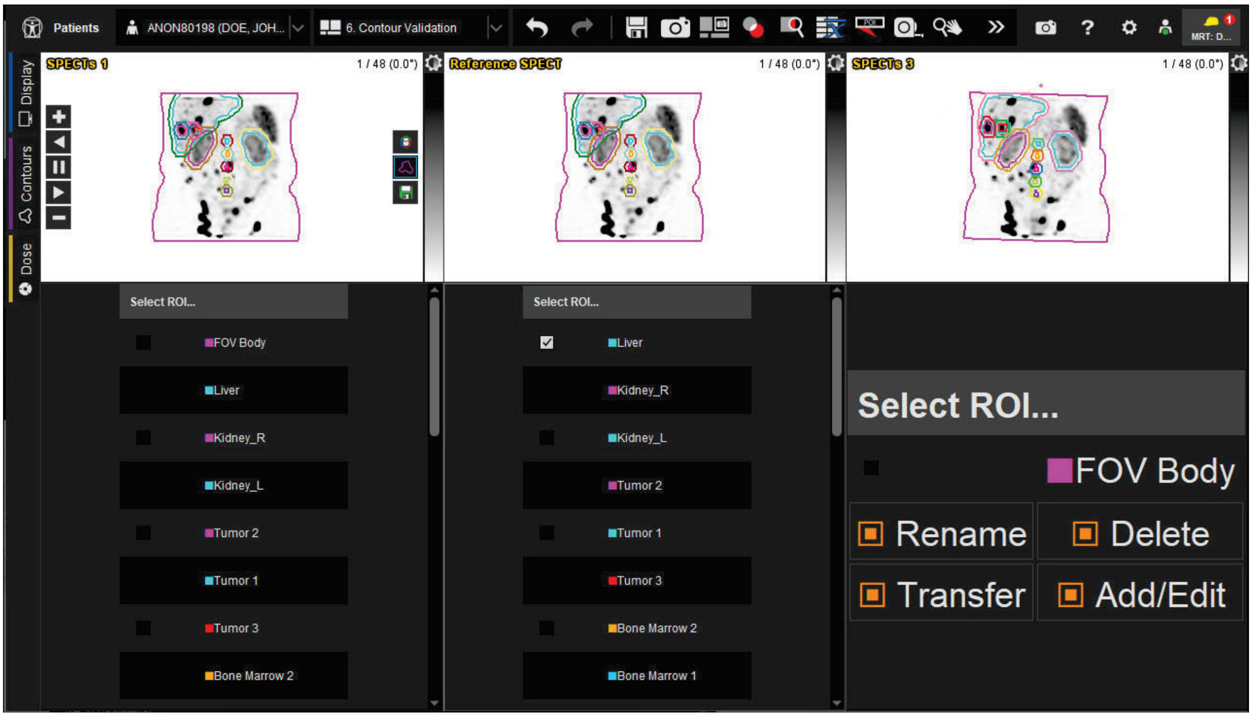
4. Repeat this step to align the registration for each contour that you selected.

Define Contours per Time Point

If desired, you can define tumors independently on each time point. With this approach, the workflow does not do automatic SPECT alignment. Follow these steps:

1. On the Basics Preferences screen, select both of the following:
   - **Apply curve fitting and time-integration on an organ level instead of on a voxel level (useful for noisy data)**.
   - **Allow independent regions on each timepoint (replaces SPECT alignment, requires organ-level curve fitting)**.
2. When prompted, evaluate the contours per time point. Each contour must be present on each time point before proceeding.
   i. Select one or more contours for a time point.
   ii. Use the buttons on the bottom of the contour list to **Delete** the selected contours, **Transfer** the contours to another time point, or **Rename** the contours. Click **Add/Edit** to open a

segmentation screen for the selected time point.



3. When you are finished, click **Resume Workflow**.

See Gy/GBq Results (MIM 7.3 and Later)

You can include Gy/GBq results to consider dose constraints and project the cumulative absorbed dose for multiple cycles of therapy. This feature is not available in MIM 7.2 and earlier.

The results are calculated using the administered activity (either from the DICOM or that was entered when running the workflow) and the mean absorbed dose. You can review the limiting organs based on absorbed dose results and scale the results based on desired target doses to tumors or administered activity.

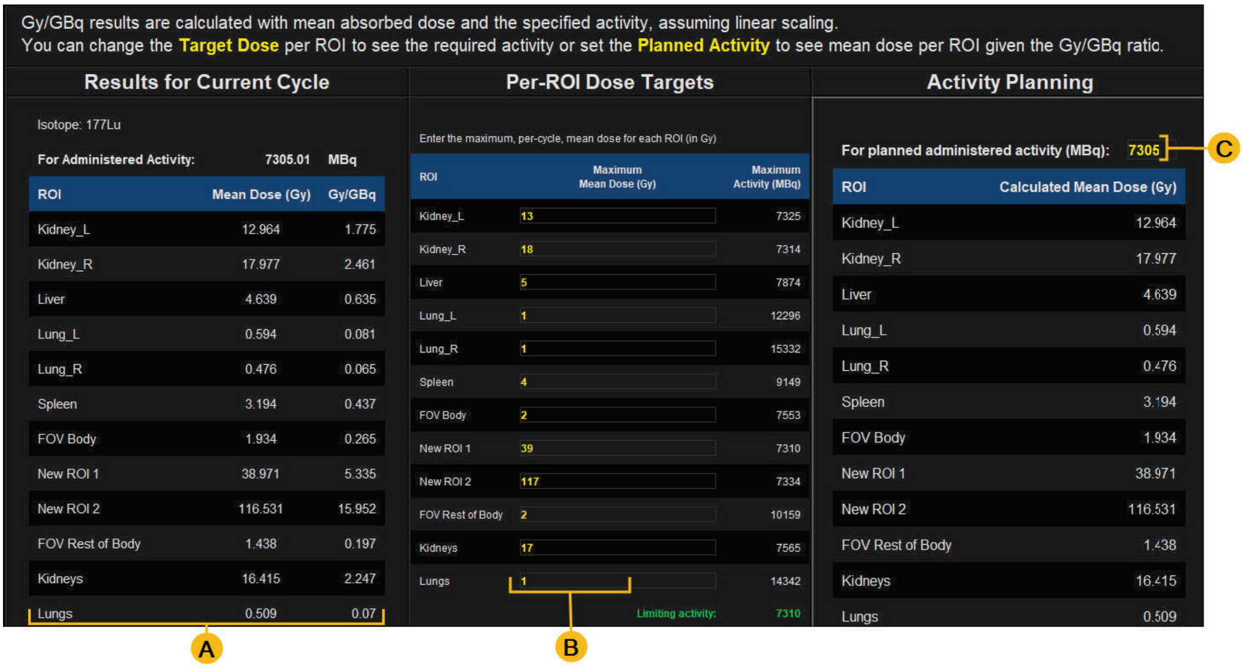
To view this page, you must run the workflow with the Advanced Preference for **Display Gy/GBq results review page** selected. Refer to Settings for Dosimetry with Multiple SPECT/CTs for more information about Advanced Preferences.

Then, when the workflow completes, follow these steps:

1. On the results page with the DVH, click the **Go to Gy/GBq Results** button in the lower-right corner.
2. Review the results:
    A. The **Results for Current Cycle** section is view-only and shows absorbed dose based on the provided treatment.

B. In the **Per-ROI Dose Targets** section, enter the maximum mean absorbed dose for a region. The system updates the projected maximum activity based on the absorbed dose you enter. At the bottom of the section, you can see calculations based on the target mean absorbed dose to tumors instead.

C. In the **Activity Planning** section, enter any planned activity, such as the activity from multiple administrations of the radiopharmaceutical. This section shows the projected mean dose per region, which is the inverse of the Per-ROI Dose Targets section.



Gy/GBq results are calculated with mean absorbed dose and the specified activity, assuming linear scaling.
You can change the **Target Dose** per ROI to see the required activity or set the **Planned Activity** to see mean dose per ROI given the Gy/GBq ratio.

Results for Current Cycle

Isotope: 177Lu

For Administered Activity: 7305.01 MBq

ROI	Mean Dose (Gy)	Gy/GBq
Kidney_L	12.964	1.775
Kidney_R	17.977	2.461
Liver	4.639	0.635
Lung_L	0.594	0.081
Lung_R	0.476	0.065
Spleen	3.194	0.437
FOV Body	1.934	0.265
New ROI 1	38.971	5.335
New ROI 2	116.531	15.952
FOV Rest of Body	1.438	0.197
Kidneys	16.415	2.247
Lungs	0.509	0.07

Per-ROI Dose Targets

Enter the maximum, per-cycle, mean dose for each ROI (in Gy)

ROI	Maximum Mean Dose (Gy)	Maximum Activity (MBq)
Kidney_L	13	7325
Kidney_R	18	7314
Liver	5	7874
Lung_L	1	12296
Lung_R	1	15332
Spleen	4	9149
FOV Body	2	7553
New ROI 1	39	7310
New ROI 2	117	7334
FOV Rest of Body	2	10159
Kidneys	17	7565
Lungs	1	14342

Limiting activity: 7310

Activity Planning

For planned administered activity (MBq): 7305

ROI	Calculated Mean Dose (Gy)
Kidney_L	12.964
Kidney_R	17.977
Liver	4.639
Lung_L	0.594
Lung_R	0.476
Spleen	3.194
FOV Body	1.934
New ROI 1	38.971
New ROI 2	116.531
FOV Rest of Body	1.438
Kidneys	16.415
Lungs	0.509

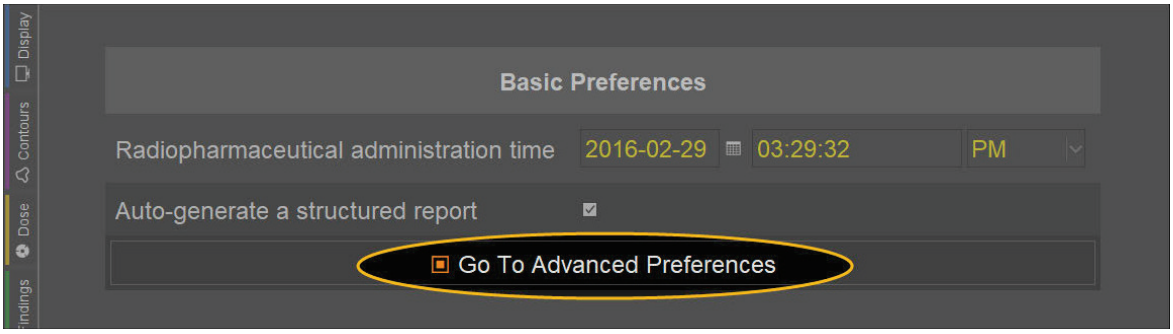
Tip: Click the screen capture 📷 button in the top toolbar to take a screen capture of this page. Go to the **Capture Gallery** to save the image so it is available for later reference.

Use Advanced Preferences

You can optionally use Advanced Preferences to further configure the workflow as needed. For example, you may adjust the workflow to support research.

To access additional settings when running the workflow, follow these steps:

1. When the workflow pauses on the Basic Preferences page, click the **Go To Advanced Preferences** button.



Basic Preferences

Radiopharmaceutical administration time 2016-02-29 03:29:32 PM

Auto-generate a structured report ☑

2. Update the settings as needed. Refer to Settings for Dosimetry with Multiple SPECT/CTs for more information about each setting.
3. Click **Resume Workflow**.

Tip: When the workflow completes, the Advanced Settings page is visible for your reference. Any updates made at this time are not reflected in the workflow results. You need to re-launch the workflow to run processing again with different settings.

A few common advanced settings include:

- Updating the **Default curve fitting method**.
- Displaying the **Output R^2 values** for more insight into the quality of the curve fitting.
- Including **Add residence times to results table** to support running model-based dosimetry in an external application.
- Including **Create a calendar of SPECT/CT acquisitions** for a visual representation of acquisition time points.

Related: Go to Settings for Dosimetry with Multiple SPECT/CTs for more information about every available setting.

Troubleshooting

The alignment between SPECTs or PETs needs to be improved.

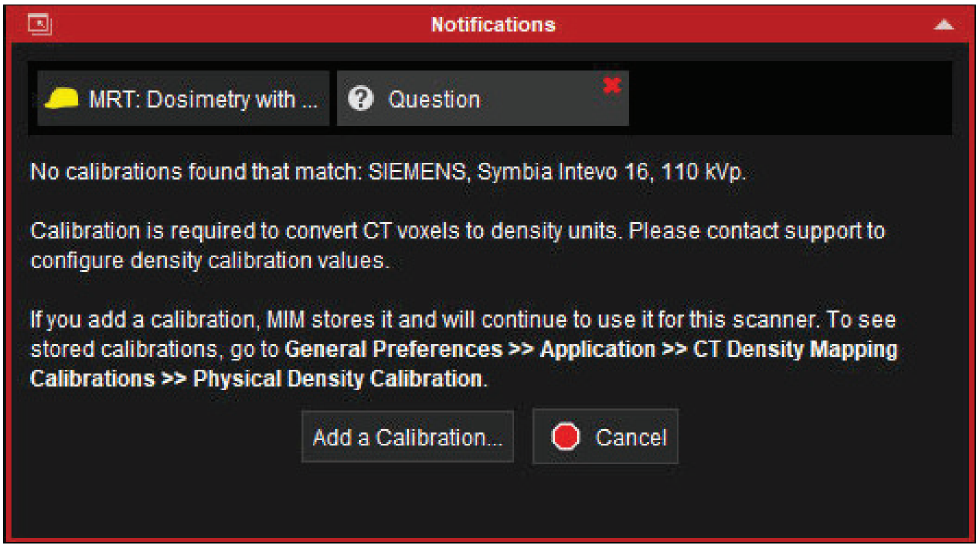
After the MRT workflow runs, you may notice contours where the alignment is not acceptable. You can reprocess the case and enable the **Manually verify and adjust the automatic SPECT alignment for individual structures** preference. Refer to Update SPECT or PET Alignment above for more information about using this option to correct alignment for selected contours.

The workflow takes a long time to run.

This workflow is resource intensive due to the amount of processing that it automates. Check the following to improve performance:

- Review the Advanced Preferences and look for options that require additional processing. Deselect options where "(Disabling improves speed)" is noted.
- Ensure that other processing is not running on the workstation at the same time as MIM. Close other applications or other patient sessions within MIM that could be using system resources.
- Verify that your workstation meets MIM's system requirements. Contact your MIM Site Development Manager or MIM Implementation Specialist if you need help evaluating your system specifications.

I see a notification that no calibrations were found.



No calibrations found that match: SIEMENS, Symbia Intevo 16, 110 kVp.

Calibration is required to convert CT voxels to density units. Please contact support to configure density calibration values.

If you add a calibration, MIM stores it and will continue to use it for this scanner. To see stored calibrations, go to **General Preferences >> Application >> CT Density Mapping Calibrations >> Physical Density Calibration**.

As part of your SurePlan™ MRT install, your MIM representative works with you to configure a density calibration file for each scanner. These calibration files are saved in the Physical Density Calibration table in MIM.

Do not proceed without a valid calibration file for the current CT. Please contact MIM Software Support for assistance.

I see a notification about the time of the images.

When you run the workflow for the radioisotope ^{177}Lu, the most accurate results can be achieved if the images are acquired during the following ranges:

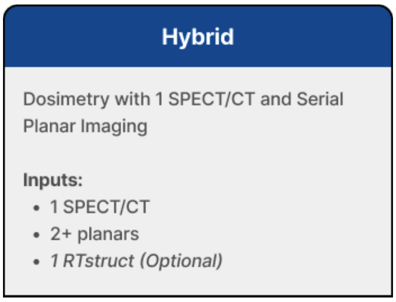
- Within 30 hours of injection; and
- More than 3 days after injection.

A notification appears if there are no time points within these two time ranges. Images from other time ranges can affect the accuracy of curve fitting.

MRT: Dosimetry with 1 SPECT/CT and Serial Planar Imaging

MIMTD-706 • 22 Nov 2024

Overview



Hybrid

Dosimetry with 1 SPECT/CT and Serial Planar Imaging

Inputs:

- 1 SPECT/CT
- 2+ planars
- *1 RTstruct (Optional)*

After pre-processing steps have been performed, such as reconstruction or segmentation, run the **MRT: Dosimetry with 1 SPECT/CT and Serial Planar Imaging** workflow. This workflow is for one SPECT/CT and up to six planar images.

The workflow guides you through reviewing contours and fusions. It produces a voxelized absorbed dose map and mean absorbed dose values, which can be used for absorbed dose accumulation.

> **Tip:** Use the steps below to run the workflow and to adjust study information and contours as needed. Use the My MIM SurePlan™ MRT Quick Sheet page to make your own notes about running the workflow.

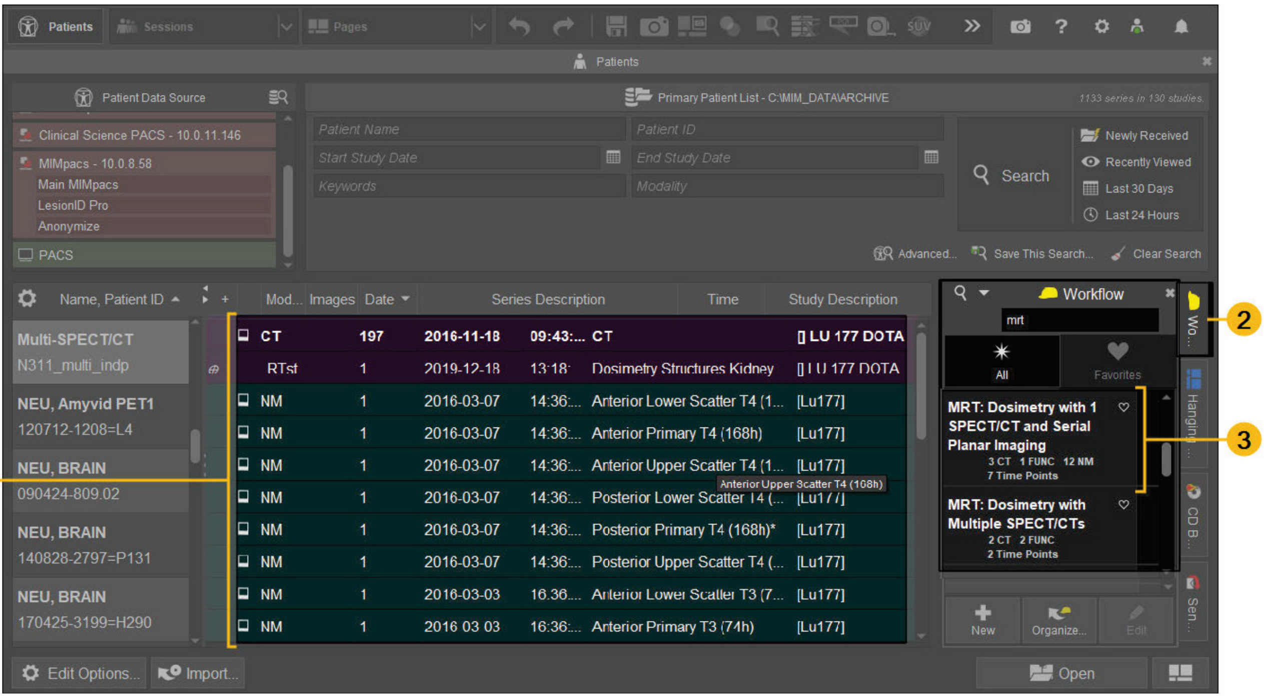
Contents

Launch the Workflow

1. From the patient list, select the following:
    - A CT and, if available, associated RTstruct
    - A quantitative SPECT with corresponding anterior and posterior planar images acquired within two hours of the SPECT
    - At least one additional anterior and posterior planar image pair obtained after the same treatment cycle
    - (Optional) A prior CT to allow transferring contours from a previous radiopharmaceutical administration

> **Tip:** To select multiple series, press and hold the Ctrl key. Or, click and drag down to select the list of series.

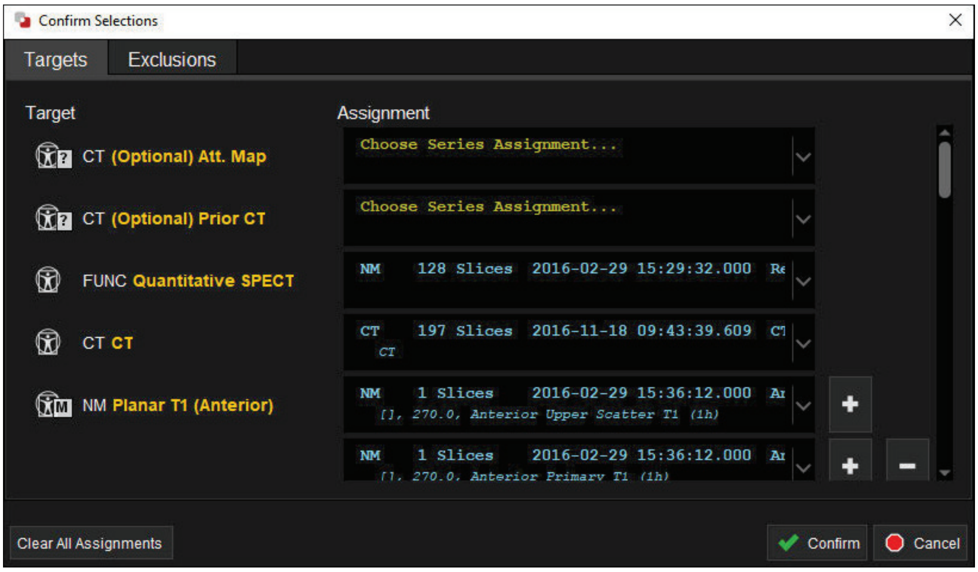
2. Select the **Workflow** tab in the patient list to expand it.
3. Double-click the **MRT: Dosimetry with 1 SPECT/CT and Serial Planar Imaging** workflow from the list to launch it.



Mod...	Images	Date	Time	Series Description	Study Description
CT	197	2016-11-18	09:43:...	CT	▯ LU 177 DOTA
RTst	1	2019-12-18	13:18:	Dosimetry Structures Kidney	▯ LU 177 DOTA
NM	1	2016-03-07	14:36:...	Anterior Lower Scatter T4 (1...	[Lu177]
NM	1	2016-03-07	14:36:...	Anterior Primary T4 (168h)	[Lu177]
NM	1	2016-03-07	14:36:...	Anterior Upper Scatter T4 (1...	[Lu177]
NM	1	2016-03-07	14:36:...	Posterior Lower Scatter T4 (...	[Lu177]
NM	1	2016-03-07	14:36:...	Posterior Primary T4 (168h)*	[Lu177]
NM	1	2016-03-07	14:36:...	Posterior Upper Scatter T4 (...	[Lu177]
NM	1	2016-03-03	16:36:...	Anterior Lower Scatter T3 (7...	[Lu177]
NM	1	2016-03-03	16:36:...	Anterior Primary T3 (74h)	[Lu177]

4. In the target confirmation window, verify the CT and SPECTs you selected are listed for the appropriate targets. If needed, click the plus ✚ button to add a planar image or the minus ▬ button

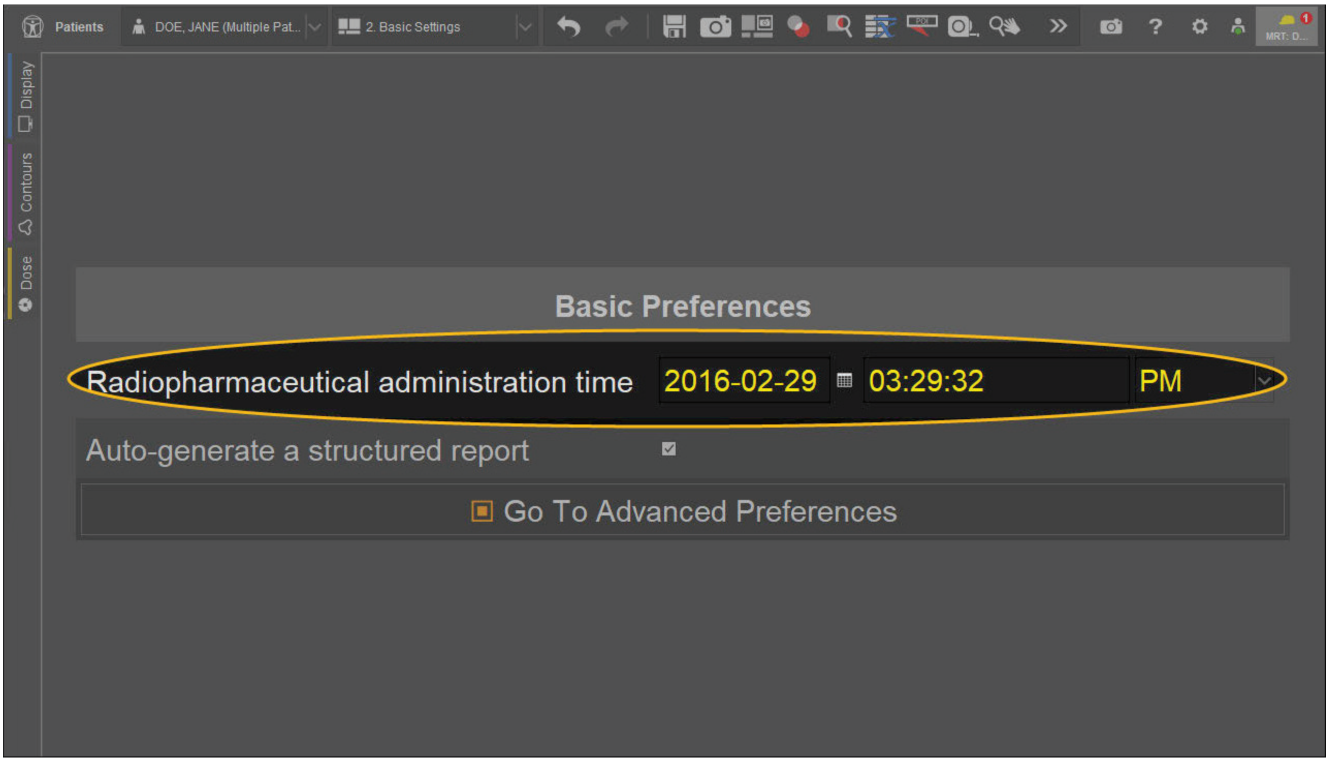
to remove a planar image. Click **Confirm**.



Target	Assignment
CT **(Optional) Att. Map**	Choose Series Assignment...
CT **(Optional) Prior CT**	Choose Series Assignment...
FUNC **Quantitative SPECT**	NM 128 Slices 2016-02-29 15:29:32.000 Re
CT **CT**	CT 197 Slices 2016-11-18 09:43:39.609 CT CT
NM **Planar T1 (Anterior)**	NM 1 Slices 2016-02-29 15:36:12.000 Ar [], 270.0, Anterior Upper Scatter T1 (1h)
	NM 1 Slices 2016-02-29 15:36:12.000 Ar [], 270.0, Anterior Primary T1 (1h)

Run Workflow Processing

1. On the Basic Preferences page, check the **Radiopharmaceutical administration time** and update it if needed. Click **Resume Workflow**.



Basic Preferences

Radiopharmaceutical administration time 2016-02-29 03:29:32 PM

Auto-generate a structured report ☑

Tip: If needed, you can go to the Advanced Preferences to modify additional workflow preferences. Refer to the tips below for common preferences or refer to Settings for Dosimetry with 1 SPECT/CT and Serial Planar Imaging for more information about each advanced preference.

2. *If you included a Prior CT*, the workflow creates a rigid fusion between the Prior CT and the current CT and prompts you to review. If necessary, use the tools on the right side of the viewport to adjust the fusion.

Related: See Adjust Fusions for more information.

Tip: This rigid fusion is the starting point for the deformable registration, which is used to transfer contours from the Prior CT.

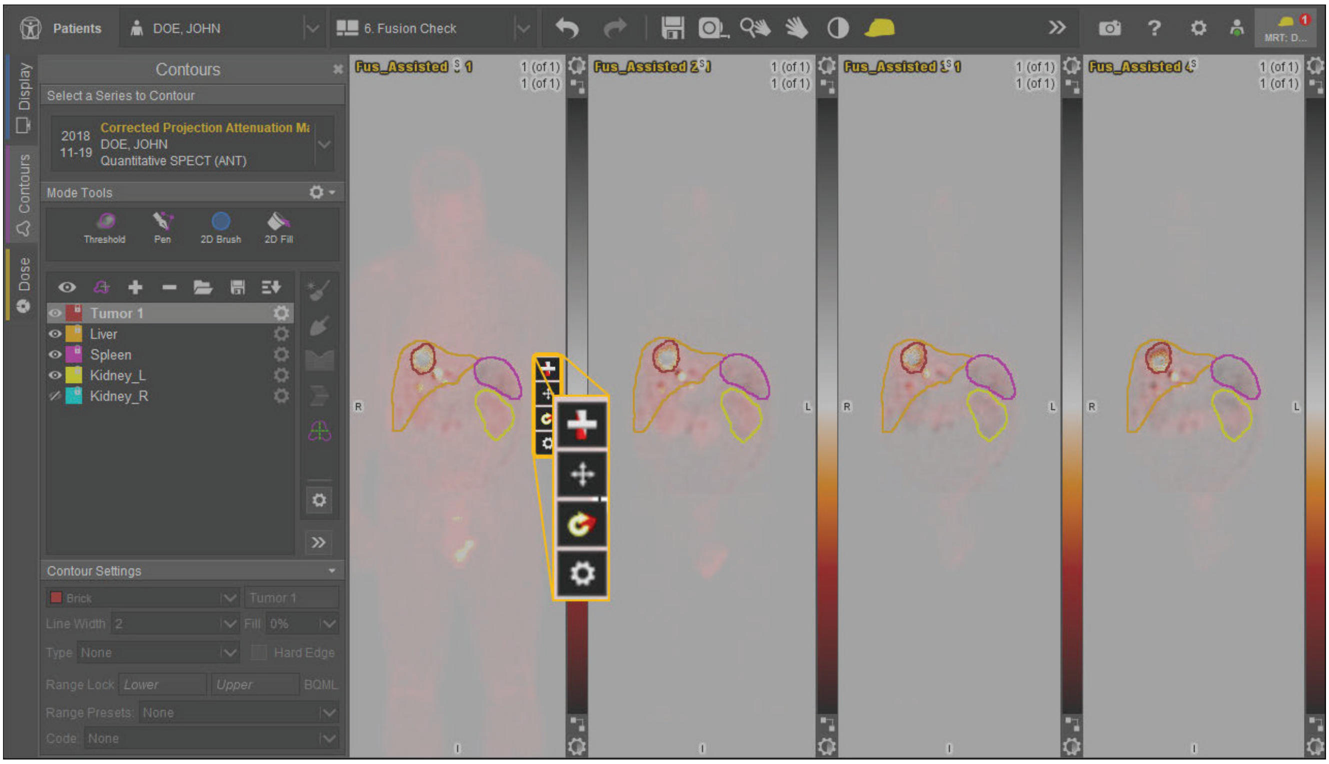
3. The workflow pauses and prompts you to contour ROIs on the fusion image to include in the dosimetry analysis:
    - *If you loaded an RTstruct when launching the workflow*, the contours are listed in the Contours sidebar. *If you did not load an RTstruct*, click the plus + button to create a contour.
    - Use the **2D Brush** or another contouring tool of your choice to draw or edit organ contours as needed. See Update Contours below for more contouring tips.
    - Use **PET Edge+**, the **Threshold** tool, or another contouring tool of your choice to draw or edit tumor contours as needed.
    - Ensure that each tumor contour created contains the word Tumor or Lesion.

Tip: Press the \ keyboard shortcut or click the arrow in the upper-right corner of the Notifications window to minimize the window. When you are finished with your adjustments, press \ again or click the flashing workflow button in the upper-right corner to re-expand the Notifications window.

Red
FOV Body
Line Width 2
Fill 0%
Type External
Hard Edge
Range Lock Lower Upper HU
Range Presets: None
Code: None

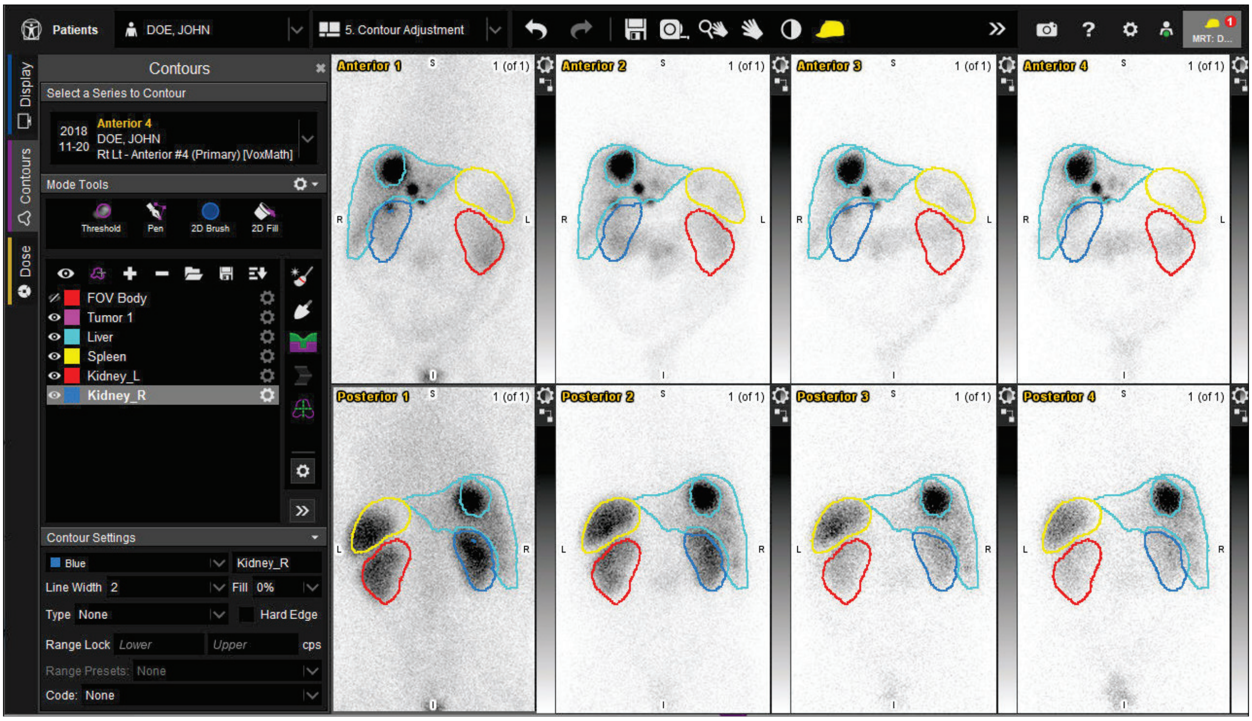
4. Click **Resume Workflow**.
5. Review the alignment generated between each planar time point and a projection derived from the SPECT. If necessary, use the tools on the right side of the viewport to adjust the fusion. See Update

Planar Alignment below for more tips.



6. Click **Resume Workflow**. The workflow transfers the contours from the 3D SPECT to the 2D planar images. Note the following behavior for overlapping contours:
   - If two non-tumor structures overlap, the overlap region is removed from both structures.
   - If a tumor contour overlaps a non-tumor structure, the tumor contour is removed from that structure.
   - If two tumor contours overlap, the overlap is not automatically removed and must be removed manually.
7. When prompted, review the contours on the 2D planar images. Carefully review and edit as needed:
   - Use the **Move** tool (activated by default) to make sure that the tumor contours are in the right location at each time point.

- Use the **2D Brush** ● to manually remove overlap.



Contours

Select a Series to Contour

2018 11-20 Anterior 4 DOE, JOHN Rt Lt - Anterior #4 (Primary) [VoxMath]

FOV Body
Tumor 1
Liver
Spleen
Kidney_L
Kidney_R

Contour Settings

Blue Kidney_R
Line Width 2 Fill 0%
Type None Hard Edge
Range Lock Lower Upper cps
Range Presets: None
Code: None

8. Click **Resume Workflow**. The workflow combines the shape of the planar time-activity curve and the magnitude of the quantitative SPECT image to derive time-integrated activity (TIA). It then calculates the absorbed dose results.

> ⚠ **Caution:** The workflow ordinarily locates the appropriate entry in the Physical Density Calibration table for the CT you are processing. If a matching calibration is not found and the workflow prompts you to select or add a calibration, please contact MIM Software Support for assistance.

9. At the prompt, click **OK** to save the RTdose file. The workflow also saves the output files needed for absorbed dose accumulation. See Save Results below for more information.

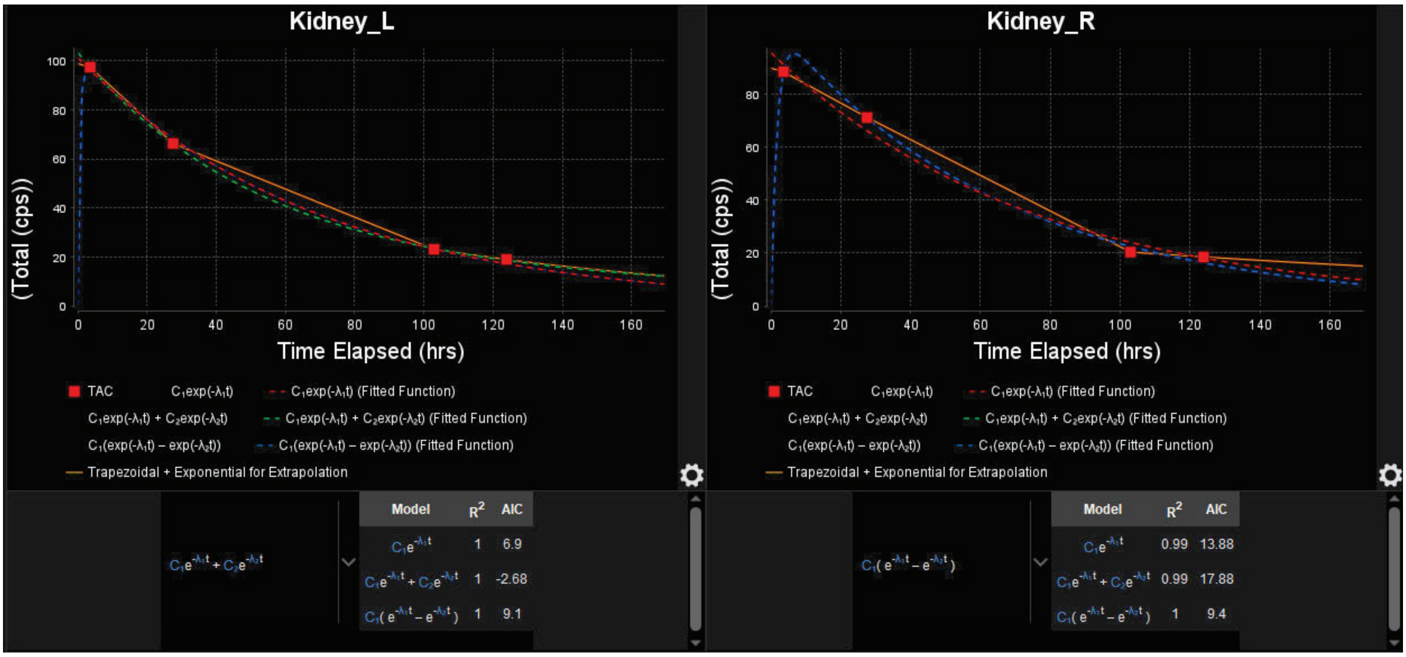
Review Results

The workflow completes and generates several results pages. Use the left and right arrow keys or page dropdown in the top toolbar to move between pages and review results.

Time Activity Curves

The workflow generates time-activity curves (TACs) and a TIA image that is normalized to the SPECT.

You can cycle through the pages to see TACs for different contours. The Results Table includes the applied curve fit parameters.



$C_1e^{-\lambda_1 t}+C_2e^{-\lambda_2 t}$

Model	R^2	AIC
$C_1e^{-\lambda_1 t}$	1	6.9
$C_1e^{-\lambda_1 t}+C_2e^{-\lambda_2 t}$	1	-2.68
$C_1(e^{-\lambda_1 t}-e^{-\lambda_2 t})$	1	9.1

$C_1(e^{-\lambda_1 t}-e^{-\lambda_2 t})$

Model	R^2	AIC
$C_1e^{-\lambda_1 t}$	0.99	13.88
$C_1e^{-\lambda_1 t}+C_2e^{-\lambda_2 t}$	0.99	17.88
$C_1(e^{-\lambda_1 t}-e^{-\lambda_2 t})$	1	9.4

Example of time activity curve results page.

Dose Volume Histogram (DVH)

The DVH shows the distribution of absorbed dose across each segmented volume.

Output Dose 2019-05-16

☐ Enforce same line styles for each dose

Name		Volume	Max Dose	Min Dose	Mean Dose	SD
Kidney_L	—	84.805	32.63	0.42	12.96	5.32
Kidney_R	—	187.373	35.07	0.37	17.98	7.50
Liver	—	1709.904	150.51	0.16	4.64	6.10
Lung_L	—	145.418	12.45	0.07	0.59	0.64
Lung_R	—	374.499	5.18	0.07	0.48	0.38

☐ Show dose constraint contours only None

☑ Show grid

Dose Value Type: Absolute Dose

☑ Normalize Volume

☐ Maximum Dose to Display (Gy) 30.00

☐ Show differential DVH

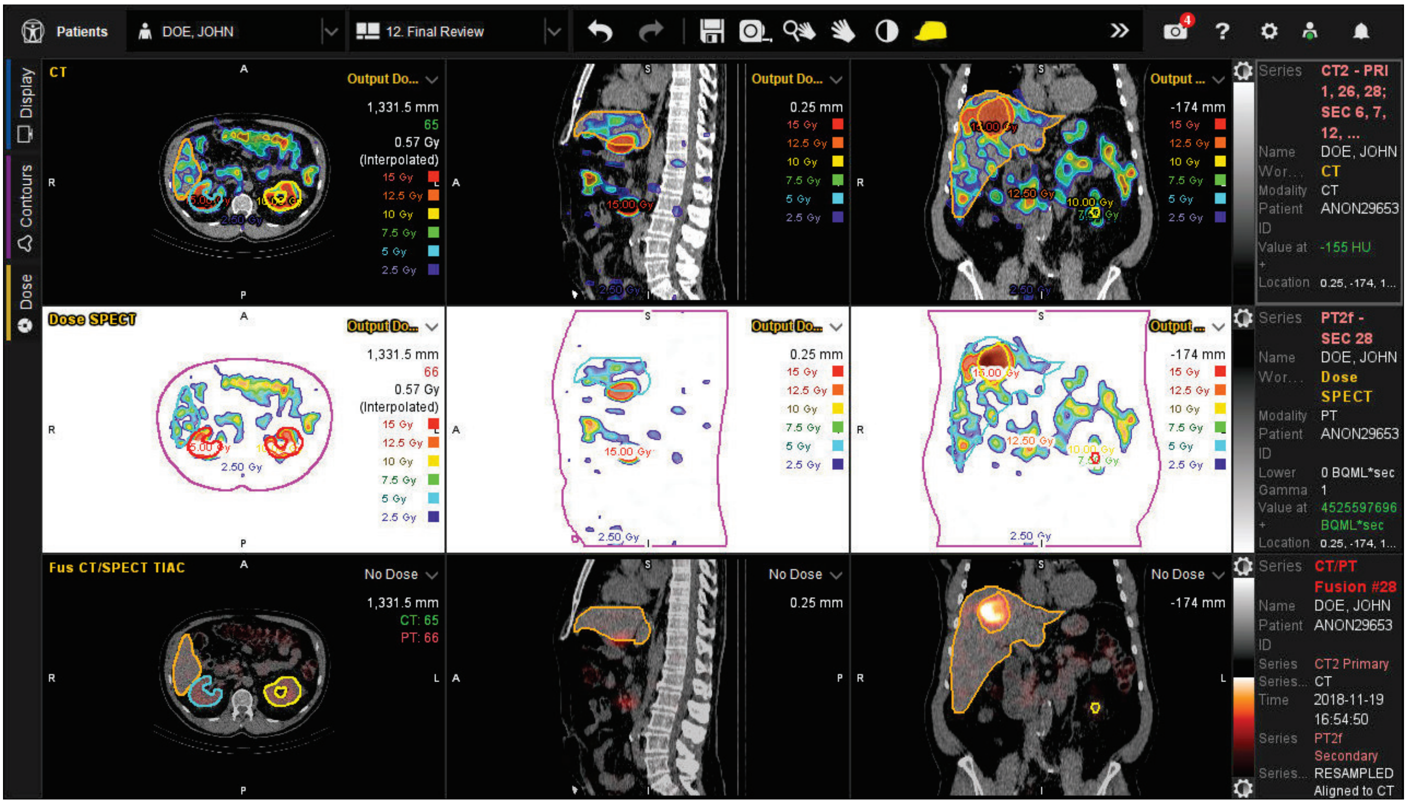
Number of DVH Bins to Combine: 1

- Review absorbed dose statistics for each region, including the mean, maximum, and minimum dose.
- Use the search field to see results only for certain regions. For example, search for "tumor" to see only results for tumor contours included in the DVH and table.
- Click the eye 👁 button to show/hide the region in the DVH. Click the line to change the color and format of the region in the DVH.

Tip: If information under the graph does not appear by default, click the **Show Options Panel** button in the lower-right corner of the DVH display to see additional information.

Dose Map

The results include a colored dose map overlaid on the CT, the derived SPECT projection, and the final fusion.



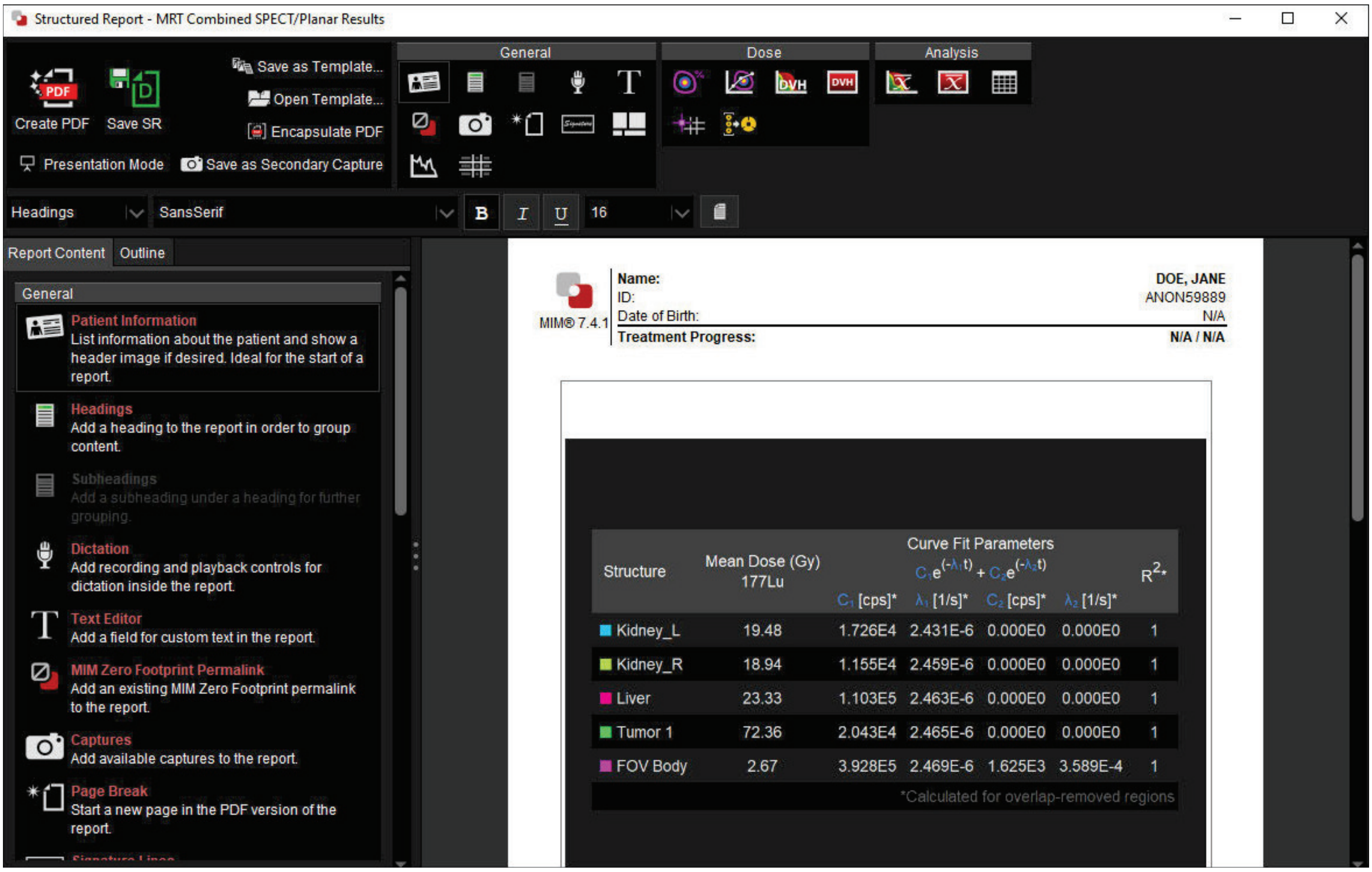
Related: You can optionally expand the **Dose** sidebar on the left side of the screen for more display options for dose. Refer to View Dose in MIM®: Fundamentals for more information.

Tip: By default, the dose map page is generated. If you do not need this page, go to **Advanced Preferences** and deselect **Output voxel-level dose map** to disable it. Refer to Settings for Dosimetry with 1 SPECT/CT and Serial Planar Imaging for more information about Advanced Preferences.

Structured Report

The workflow automatically generates a structured report. As needed, update the report information. For example, on the Report Content tab, add a Text Editor field and type additional notes in the report.

Related: Refer to [Create and Modify Structured Reports](#) for more information about working with structured reports.



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.

Text Editor
Add a field for custom text in the report.

MIM Zero Footprint Permalink
Add an existing MIM Zero Footprint permalink to the report.

Captures
Add available captures to the report.

Page Break
Start a new page in the PDF version of the report.

MIM® 7.4.1

Name: DOE, JANE
ID: ANON59889
Date of Birth: N/A
Treatment Progress: N/A / N/A

Structure	Mean Dose (Gy) 177Lu	Curve Fit Parameters $C_1e^{(-\lambda_1 t)} + C_2e^{(-\lambda_2 t)}$				R^2*
		C_1 [cps]*	λ_1 [1/s]*	C_2 [cps]*	λ_2 [1/s]*	
Kidney_L	19.48	1.726E4	2.431E-6	0.000E0	0.000E0	1
Kidney_R	18.94	1.155E4	2.459E-6	0.000E0	0.000E0	1
Liver	23.33	1.103E5	2.463E-6	0.000E0	0.000E0	1
Tumor 1	72.36	2.043E4	2.465E-6	0.000E0	0.000E0	1
FOV Body	2.67	3.928E5	2.469E-6	1.625E3	3.589E-4	1

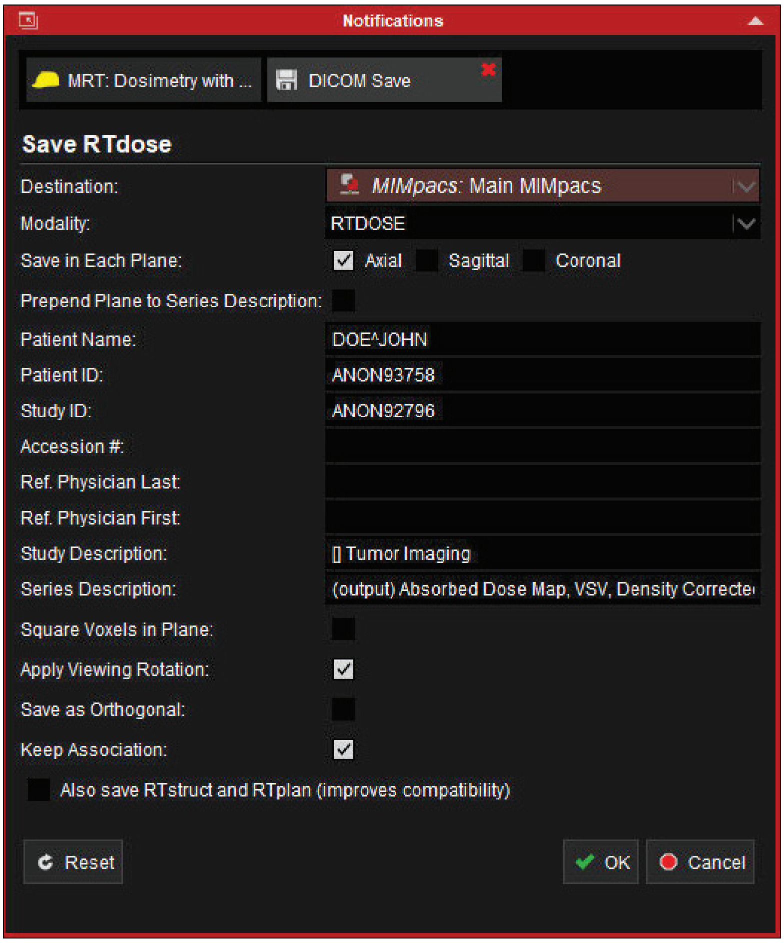
*Calculated for overlap-removed regions

When you are finished, save the structured report as a PDF or as a DICOM object (SR).

Tip: If you do not want a structured report, deselect the **Auto-generate a structured report** option on the Basic Preferences screen when running the workflow.

Save Results

When processing is finished, the workflow prompts you to save the RTdose file. Click **OK**.

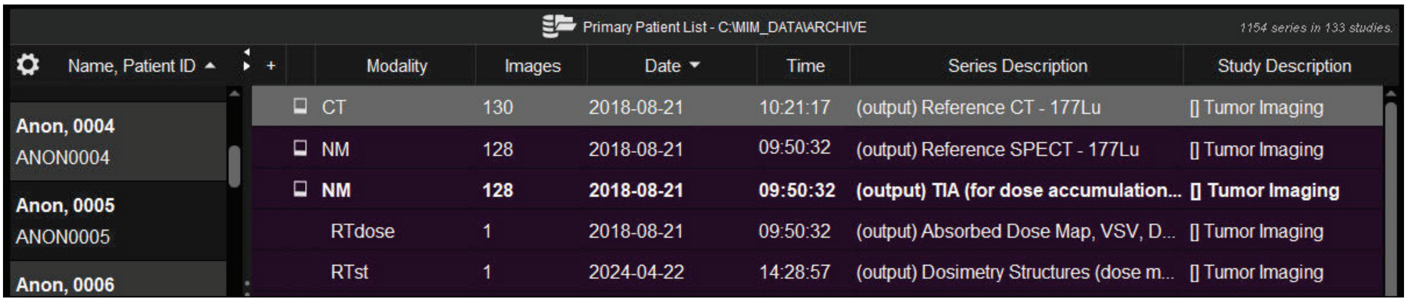


Save RTdose

Destination:	*MIMpacs:* Main MIMpacs
Modality:	RTDOSE
Save in Each Plane:	☑ Axial ☐ Sagittal ☐ Coronal
Prepend Plane to Series Description:	☐
Patient Name:	DOE^JOHN
Patient ID:	ANON93758
Study ID:	ANON92796
Accession #:	
Ref. Physician Last:	
Ref. Physician First:	
Study Description:	[] Tumor Imaging
Series Description:	(output) Absorbed Dose Map, VSV, Density Correcte
Square Voxels in Plane:	☐
Apply Viewing Rotation:	☑
Save as Orthogonal:	☐
Keep Association:	☑

☐ Also save RTstruct and RTplan (improves compatibility)

The workflow automatically saves five output series to your patient list. These series have "(output)" prepended to the series description. These output series are the inputs for the absorbed dose accumulation workflow to accumulate absorbed dose results from multiple radiopharmaceutical administrations. See Calculate Absorbed Dose Accumulation for more information.



Modality	Images	Date	Time	Series Description	Study Description
CT	130	2018-08-21	10:21:17	(output) Reference CT - 177Lu	[] Tumor Imaging
NM	128	2018-08-21	09:50:32	(output) Reference SPECT - 177Lu	[] Tumor Imaging
NM	**128**	**2018-08-21**	**09:50:32**	**(output) TIA (for dose accumulation...**	**[] Tumor Imaging**
RTdose	1	2018-08-21	09:50:32	(output) Absorbed Dose Map, VSV, D...	[] Tumor Imaging
RTst	1	2024-04-22	14:28:57	(output) Dosimetry Structures (dose m...	[] Tumor Imaging

You can also save the session so that you are able to resume where you left off with processing. Click the save 🖫 button in the top toolbar and select **Save Session...**.

Tip: To automatically save the session, select the Advanced Preference to **Save a session of the dosimetry results**. With this option enabled, you are also prompted to save the RTstruct and RTplan. Refer to Settings for Dosimetry with 1 SPECT/CT and Serial Planar Imaging for more information about Advanced Preferences.

To re-open the session, double-click the saved session file from the patient list.

Tips and Common Options

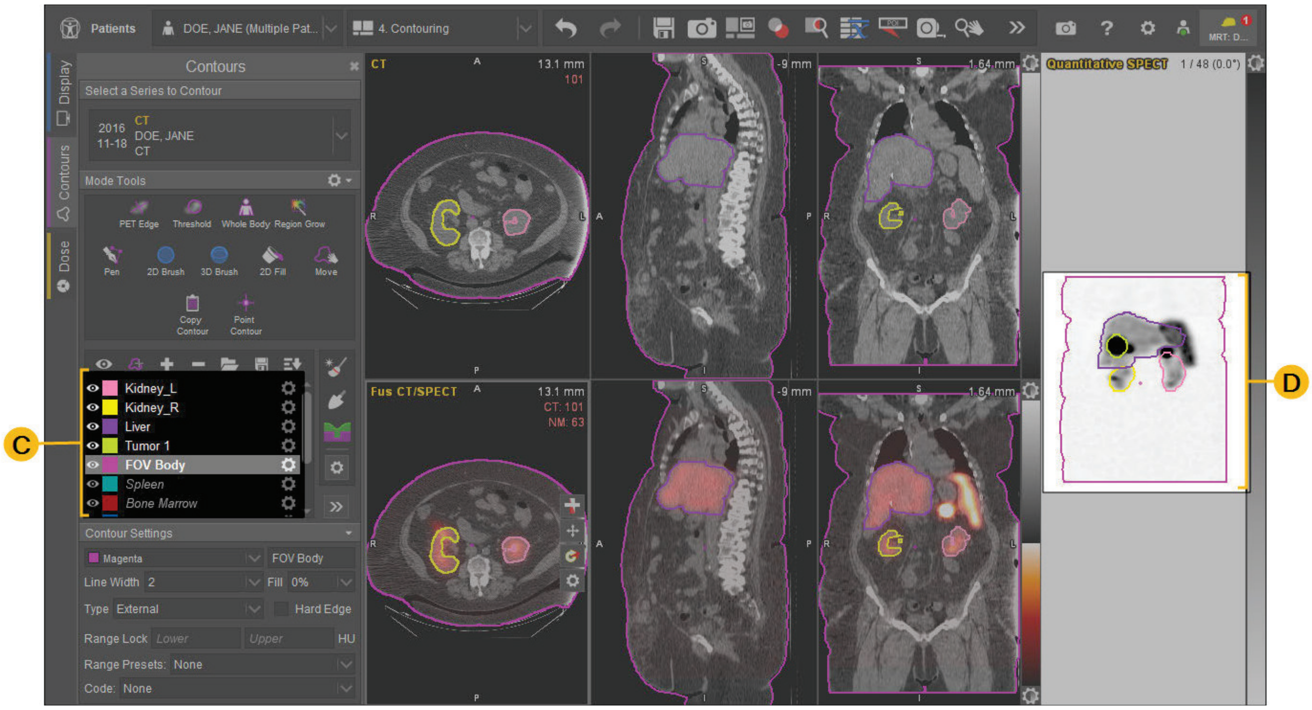
Related: For more information about the Advanced Preferences available when running this workflows, refer to Settings for Dosimetry with 1 SPECT/CT and Serial Planar Imaging.

Update Contours

The workflow prompts you to review and/or add contours on the Reference CT. Keep the following tips in mind for efficient contouring:

A. Double-click on a viewport to make it larger. Use the 2 and 3 keys on your keyboard to zoom in.
B. Scroll to move between slices.
C. As needed, update the contour names and colors in the Contours sidebar.

D. Use the MIP to quickly and easily triangulate to tumors. Click a spot on the MIP, and MIM localizes to the highest intensity 3D location along that projection.



Update Planar Alignment

The 3D SPECT image must be aligned with the 2D planar images to accurately transfer contours from the SPECT to the planar images.

Tip: You are able to further adjust contours as needed after they are transferred to the planar images.

When you are prompted by the workflow to review the fusion, try the following tips:

- Adjust the contrast of both images so that the key anatomical landmarks are visible in both.
- Double-click on the **Translate** button to perform a rigid registration using the current alignment as a starting point.
- Left-click drag the **Blend** tool up and down to check the alignment. Right-click on the blend tool to return to a 50/50 blend.

Related: For more information about working with image alignment, refer to Adjust Fusions.

Correct Planar Quality

The workflow optionally applies corrections to the planar images to prepare them for curve fitting and integration. The planar corrections are described in the *Hybrid SPECT/Planar Dosimetry for Targeted Molecular Radiotherapy* white paper in the Appendix.

To further correct planar quality, the workflow can apply an attenuation formula, as well as scatter correction and advanced background correction.

Prerequisite

Work with your MIM representative to set up an attenuation formula. If you are performing clinical SPECT reconstruction in MIM, this formula was already set up as part of your implementation.

You must run the workflow with scatter windows and an attenuation profile/attenuation map input.

Run the Workflow

Follow the steps in Run Workflow Processing above to run the workflow, noting the following:

1. In Advanced Preferences, update the following settings:
    - Deselect **Allow independent regions on each planar time point**.
    - Select **Apply planar image correction for attenuation, scatter, and background**.
2. Background contours are automatically generated when contours are transferred from the 3D SPECT to the 2D planar images. When you are prompted to review the contours on the 2D planar images, review the information in the Notifications window and use the **Move** tool or **2D Brush** to update the background contours as needed.

    Important: Contours are updated on all planar images and cannot be edited separately on each image. The 2D contours must overlap with their original position because attenuation and background corrections rely on preserving the link between the 2D and 3D contours.

3. When the workflow completes, review the results. The result calculations are adjusted based on the planar image corrections applied.

See Gy/GBq Results (MIM 7.3 and Later)

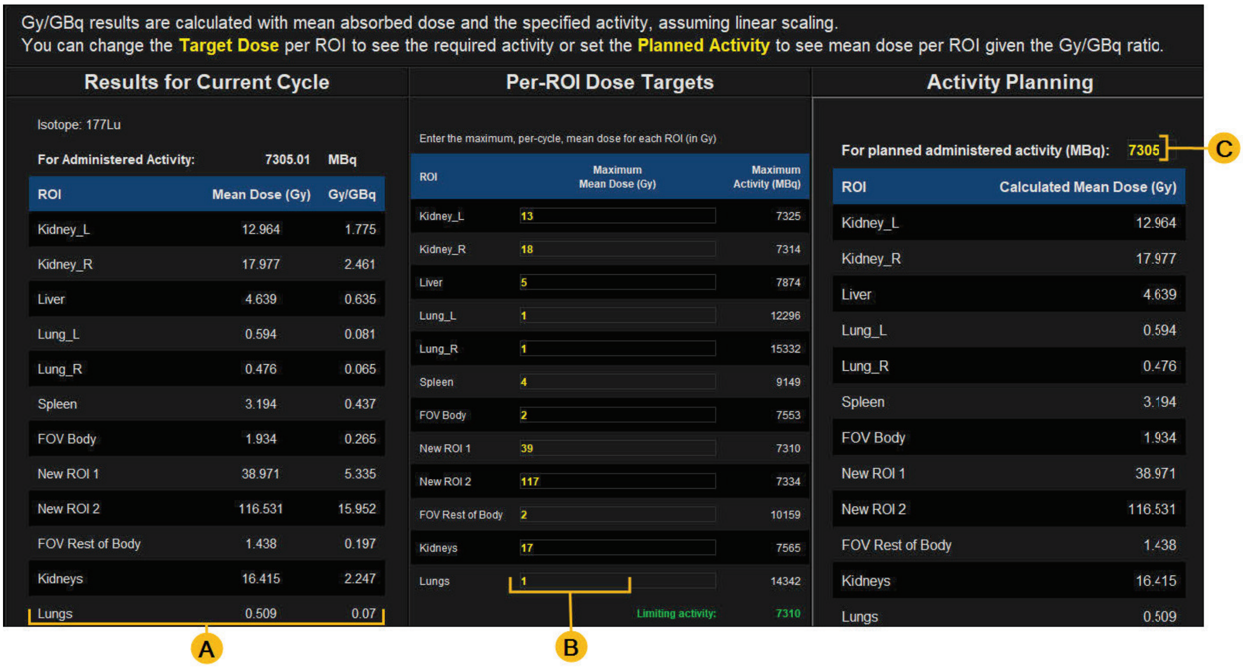
You can include Gy/GBq results to consider dose constraints and project the cumulative absorbed dose for multiple cycles of therapy. This feature is not available in MIM 7.2 and earlier.

The results are calculated using the administered activity (either from the DICOM or that was entered when running the workflow) and the mean absorbed dose. You can review the limiting organs based on absorbed dose results and scale the results based on desired target doses to tumors or administered activity.

To view this page, you must run the workflow with the Advanced Preference for **Display Gy/GBq results review page** selected. Refer to Settings for Dosimetry with 1 SPECT/CT and Serial Planar Imaging for more information about Advanced Preferences.

Then, when the workflow completes, follow these steps:

1. On the results page with the DVH, click the **Go to Gy/GBq Results** button in the lower-right corner.
2. Review the results:
   A. The **Results for Current Cycle** section is view-only and shows absorbed dose based on the provided treatment.
   B. In the **Per-ROI Dose Targets** section, enter the maximum mean absorbed dose for a region. The system updates the projected maximum activity based on the absorbed dose you enter. At the bottom of the section, you can see calculations based on the target mean absorbed dose to tumors instead.
   C. In the **Activity Planning** section, enter any planned activity, such as the activity from multiple administrations of the radiopharmaceutical. This section shows the projected mean dose per region, which is the inverse of the Per-ROI Dose Targets section.


Gy/GBq results are calculated with mean absorbed dose and the specified activity, assuming linear scaling.
You can change the Target Dose per ROI to see the required activity or set the Planned Activity to see mean dose per ROI given the Gy/GBq ratio.

Results for Current Cycle

Isotope: 177Lu

For Administered Activity: 7305.01 MBq

ROI	Mean Dose (Gy)	Gy/GBq
Kidney_L	12.964	1.775
Kidney_R	17.977	2.461
Liver	4.639	0.635
Lung_L	0.594	0.081
Lung_R	0.476	0.065
Spleen	3.194	0.437
FOV Body	1.934	0.265
New ROI 1	38.971	5.335
New ROI 2	116.531	15.952
FOV Rest of Body	1.438	0.197
Kidneys	16.415	2.247
Lungs	0.509	0.07

Per-ROI Dose Targets

Enter the maximum, per-cycle, mean dose for each ROI (in Gy)

ROI	Maximum Mean Dose (Gy)	Maximum Activity (MBq)
Kidney_L	13	7325
Kidney_R	18	7314
Liver	5	7874
Lung_L	1	12296
Lung_R	1	15332
Spleen	4	9149
FOV Body	2	7553
New ROI 1	39	7310
New ROI 2	117	7334
FOV Rest of Body	2	10159
Kidneys	17	7565
Lungs	1	14342
	Limiting activity:	7310

Activity Planning

For planned administered activity (MBq): 7305

ROI	Calculated Mean Dose (Gy)
Kidney_L	12.964
Kidney_R	17.977
Liver	4.639
Lung_L	0.594
Lung_R	0.476
Spleen	3.194
FOV Body	1.934
New ROI 1	38.971
New ROI 2	116.531
FOV Rest of Body	1.438
Kidneys	16.415
Lungs	0.509

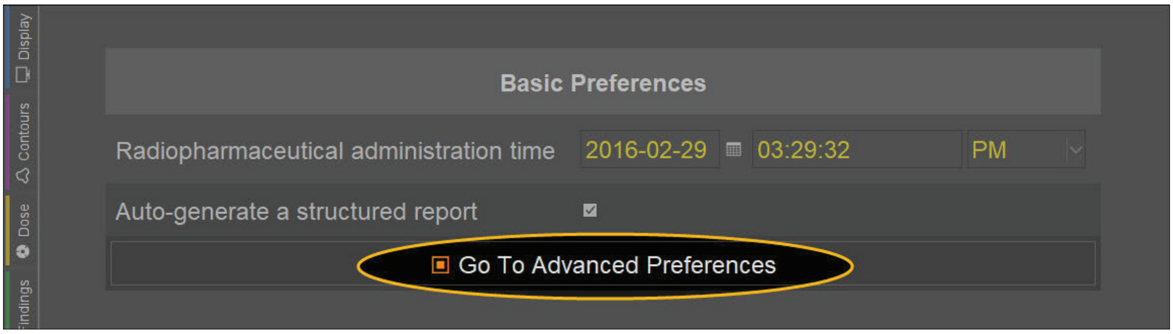
Tip: Click the screen capture 📷 button in the top toolbar to take a screen capture of this page. Go to the **Capture Gallery** to save the image so it is available for later reference.

Use Advanced Preferences

You can optionally use Advanced Preferences to further configure the workflow as needed. For example, you may adjust the workflow to support research.

To access additional settings when running the workflow, follow these steps:

1. When the workflow pauses on the Basic Preferences page, click the **Go To Advanced Preferences** button.



Basic Preferences

Radiopharmaceutical administration time: 2016-02-29 03:29:32 PM

Auto-generate a structured report ☑

Go To Advanced Preferences

2. Update the settings as needed. Refer to [Settings for Dosimetry with 1 SPECT/CT and Serial Planar Imaging]() for more information about each setting.
3. Click **Resume Workflow**.

Tip: When the workflow completes, the Advanced Settings page is visible for your reference. Any updates made at this time are not reflected in the workflow results. You need to re-launch the workflow to run processing again with different settings.

A few common settings include:

- Updating the **Default curve fitting method**.
- Displaying the **Output R2 values** for more insight into the quality of the curve fitting.
- Including **Add residence times to results table** to support running model-based dosimetry in an external application.

Related: Go to Settings for Dosimetry with 1 SPECT/CT and Serial Planar Imaging for more information about every available setting.

Troubleshooting

The workflow fails after reviewing contours for overlap removal.

This issue occurs when there is a non-tumor contour that is completely overlapped by another contour when projected into 2D space. This causes the contour to disappear at the overlap removal step and the workflow to fail.

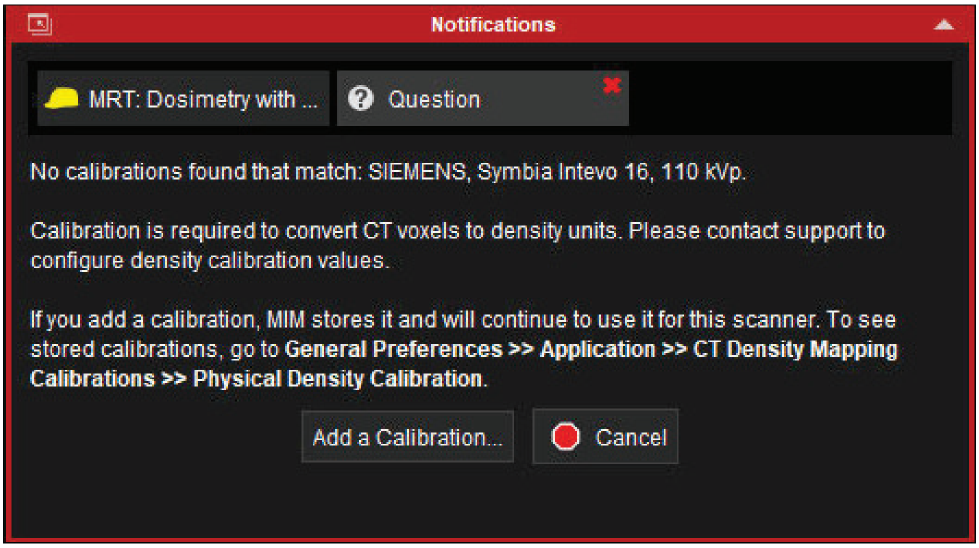
1. Re-launch the workflow.
2. At the step to review contours on the 3D image, ensure that no non-tumor contours are completely overlapping or could be overlapping after projection into 2D space. Use the **Move** tool or **2D Brush** to update the contours as needed.
3. Resume the workflow and verify that it runs as expected.

The workflow doesn't run and has an error about "Get List Item".

This issue may occur when the workflow is run with 2D anterior images without corresponding posterior images, or vice versa.

1. Ensure that you have selected the correct images and launch the workflow again.
2. In the Confirm Selections window, verify that the series listed for each target is correct. If needed, click the plus button to add a planar image or the minus button to remove a planar image.
3. Click **Confirm** and verify that the workflow runs as expected.

I see a notification that no calibrations were found.



No calibrations found that match: SIEMENS, Symbia Intevo 16, 110 kVp.

Calibration is required to convert CT voxels to density units. Please contact support to configure density calibration values.

If you add a calibration, MIM stores it and will continue to use it for this scanner. To see stored calibrations, go to **General Preferences >> Application >> CT Density Mapping Calibrations >> Physical Density Calibration**.

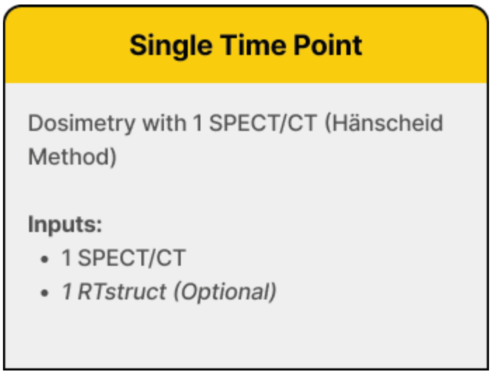
As part of your SurePlan™ MRT install, your MIM representative works with you to configure a density calibration file for each scanner. These calibration files are saved in the Physical Density Calibration table in MIM.

Do not proceed without a valid calibration file for the current CT. Please contact MIM Software Support for assistance.

MRT: Dosimetry with 1 SPECT/CT (Hänscheid Method)

MIMTD-1115 • 22 Nov 2024

Overview



Single Time Point

Dosimetry with 1 SPECT/CT (Hänscheid Method)

Inputs:

- 1 SPECT/CT
- *1 RTstruct (Optional)*

After pre-processing steps have been performed, such as reconstruction or segmentation, run the **MRT: Dosimetry with 1 SPECT/CT (Hänscheid Method)** workflow. This workflow is for a single SPECT/CT.

This workflow supports ^{177}Lu-DOTATATE and ^{177}Lu-PSMA.

Related: If you have a time-integrated activity (TIA) map from a previous treatment cycle with multiple time points, use the MRT: Dosimetry with 1 SPECT/CT (Prior Information Approach) workflow instead.

The workflow guides you through reviewing contours. The workflow produces a voxelized absorbed dose map and mean absorbed dose values, which can then be used for absorbed dose accumulation.

Tip: Use the steps below to run the workflow and to adjust study information and contours as needed. Use the My MIM SurePlan™ MRT Quick Sheet page to make your own notes about running the workflow.

Contents

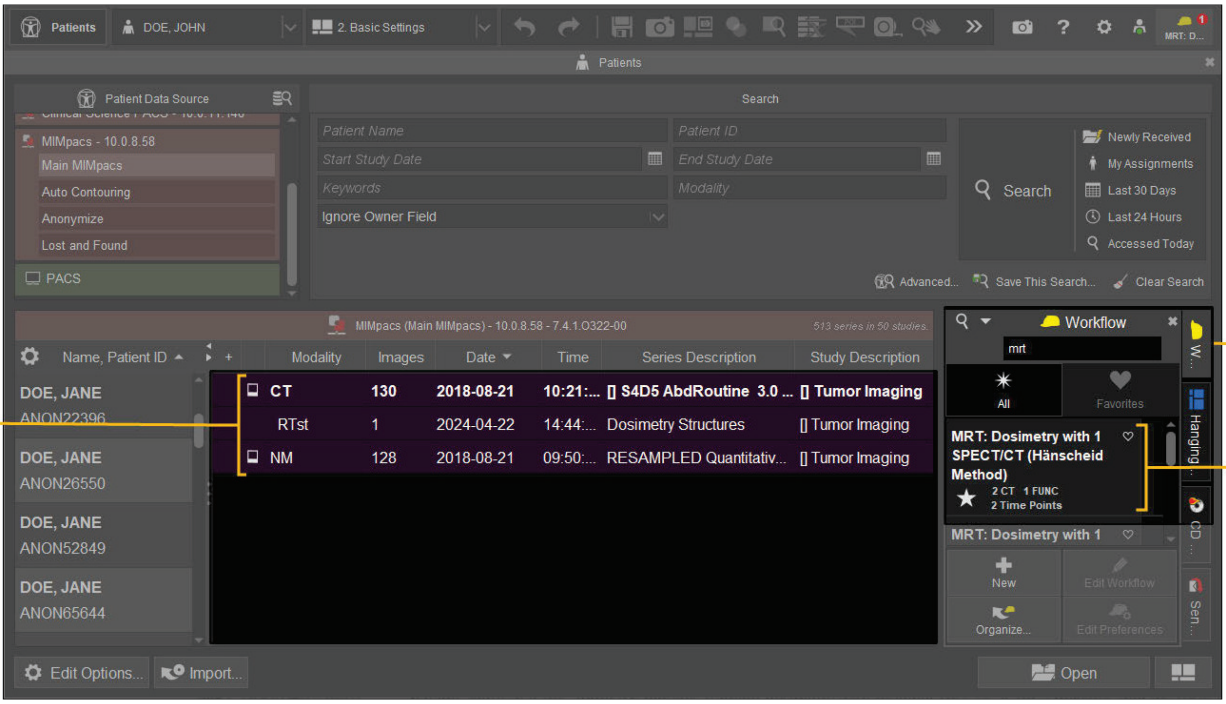
- Troubleshooting
- Clinical Details

Launch the Workflow

1. From the patient list, select a SPECT/CT:
    - A CT and, if available, associated RTstruct
    - A quantitative SPECT
    - (Optional) A prior CT to allow transferring contours from a previous radiopharmaceutical administration

> **Tip:** To select multiple series, press and hold the Ctrl key. Or, click and drag down to select the list of series.

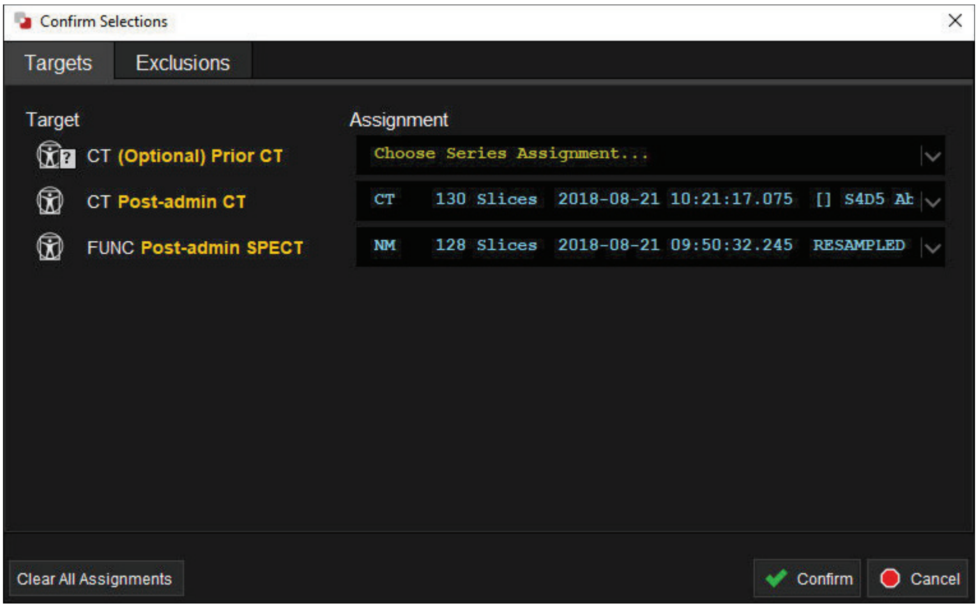
2. Select the **Workflow** tab in the patient list to expand it.
3. Double-click the **MRT: Dosimetry with 1 SPECT/CT (Hänscheid Method)** workflow from the list to launch it.



Modality	Images	Date	Time	Series Description	Study Description
CT	130	2018-08-21	10:21:...	[] S4D5 AbdRoutine 3.0 ...	[] Tumor Imaging
RTst	1	2024-04-22	14:44:...	Dosimetry Structures	[] Tumor Imaging
NM	128	2018-08-21	09:50:...	RESAMPLED Quantitativ...	[] Tumor Imaging

MRT: Dosimetry with 1 SPECT/CT (Hänscheid Method)
2 CT 1 FUNC
2 Time Points

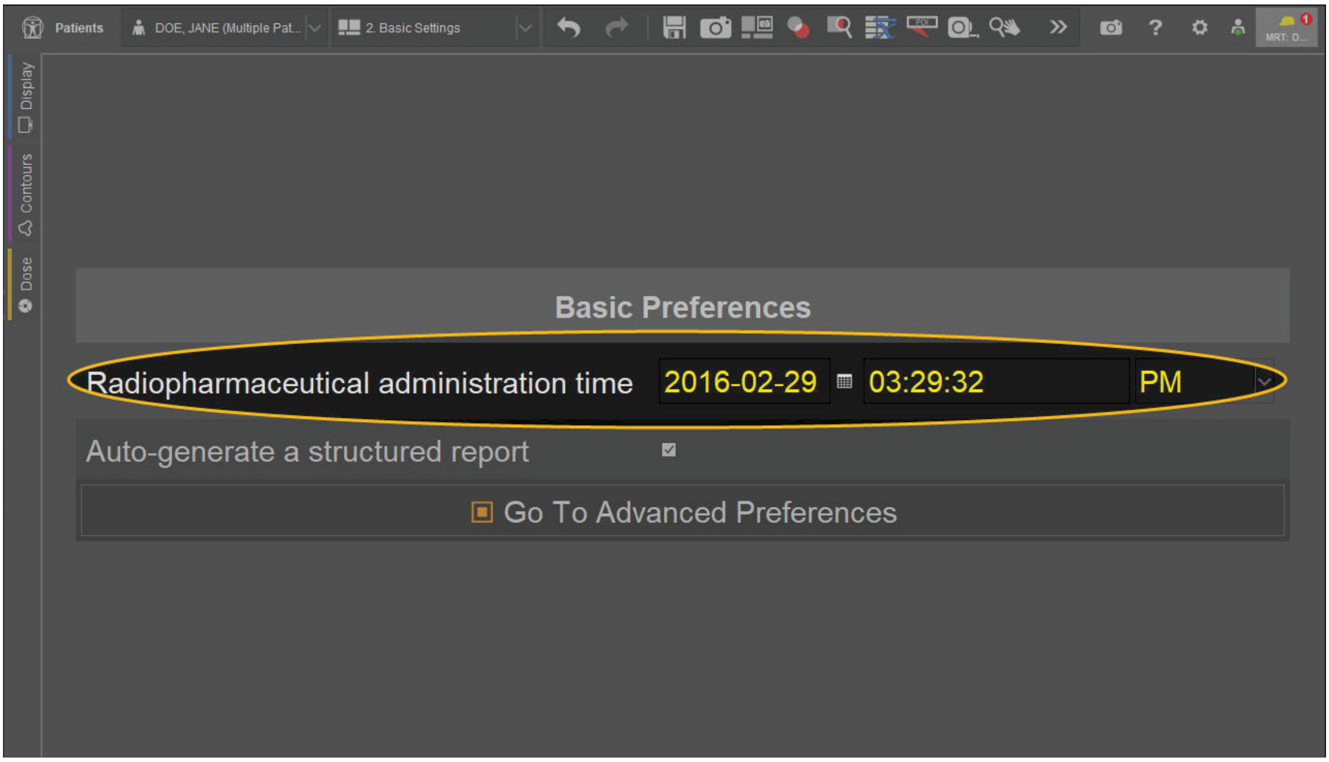
4. In the target confirmation window, verify the CT and SPECT you selected are listed for the Post-admin CT and Post-admin SPECT targets. Click **Confirm**.



Target	Assignment
CT (Optional) Prior CT	Choose Series Assignment...
CT Post-admin CT	CT 130 Slices 2018-08-21 10:21:17.075 [] S4D5 Ab
FUNC Post-admin SPECT	NM 128 Slices 2018-08-21 09:50:32.245 RESAMPLED

Run Workflow Processing

1. On the Basic Preferences page, check the **Radiopharmaceutical administration time** and update it if needed. Click **Resume Workflow**.



Basic Preferences

Radiopharmaceutical administration time 2016-02-29 03:29:32 PM

Auto-generate a structured report ☑

> **Tip:** If needed, you can go to the Advanced Preferences to modify additional workflow preferences. Refer to the tips below for common preferences or refer to Settings for Dosimetry with 1 SPECT/CT for more information about each advanced preference.

2. *If you included a Prior CT*, the workflow creates a rigid fusion between the Prior CT and the current CT and prompts you to review. If necessary, use the tools on the right side of the viewport to adjust the fusion.

> **Related**: See Adjust Fusions for more information.

> **Tip:** This rigid fusion is the starting point for the deformable registration, which is used to transfer contours from the Prior CT.

3. The workflow pauses and prompts you to contour ROIs on the fusion image to include in the dosimetry analysis:
   - *If you loaded an RTstruct when launching the workflow*, the contours are listed in the Contours sidebar. *If you did not load an RTstruct*, click the plus + button to create a contour.
   - Use the **2D Brush** or another contouring tool of your choice to draw or edit organ contours as needed. See Update Contours below for more contouring tips.
   - Use **PET Edge+**, the **Threshold** tool, or another contouring tool of your choice to draw or edit tumor contours as needed.
   - Ensure that each tumor contour created contains the word Tumor or Lesion.

> **Tip:** Press the \ keyboard shortcut or click the arrow in the upper-right corner of the Notifications window to minimize the window. When you are finished with your adjustments, press \ again or click the flashing workflow button in the upper-right corner to re-expand the Notifications window.

2019 05-16 Post-admin CT DOE, JANE CT #2

Glnd_Lacrimal_L
Glnd_Lacrimal_R
Glnd_Submand_L
Glnd_Submand_R
Glnd_Thyroid
Kidney_L
Kidney_R

Contour Settings
Cyan Glnd_Lacrimal_L
Line Width 2 Fill 0%
Type None Hard Edge
Range Lock Lower Upper HU
Range Presets: None
Code: None

4. Click **Resume Workflow**.

> **Caution:** The workflow ordinarily locates the appropriate entry in the Physical Density Calibration table for the CT you are processing. If a matching calibration is not found and the workflow prompts you to select or add a calibration, please contact MIM Software Support for assistance.

5. At the prompt, click **OK** to save the RTdose file. The workflow also saves the output files needed for absorbed dose accumulation. See Save Results below for more information.

Review Results

The workflow completes and generates several results pages. Use the left and right arrow keys or page dropdown in the top toolbar to move between pages and review results.

Dose Volume Histogram (DVH)

The DVH shows the distribution of absorbed dose across each segmented volume.

☐ Enforce same line styles for each dose

	Name		Volume	Max Dose	Min Dose	Mean Dose	SD
👁	Kidney_L	—	84.805	32.63	0.42	12.96	5.32
👁	Kidney_R	—	187.373	35.07	0.37	17.98	7.50
👁	Liver	—	1709.904	150.51	0.16	4.64	6.10
👁	Lung_L	—	145.418	12.45	0.07	0.59	0.64
👁	Lung_R	—	374.499	5.18	0.07	0.48	0.38

☐ Show dose constraint contours only None

☑ Show grid

Dose Value Type: Absolute Dose

☑ Normalize Volume

☐ Maximum Dose to Display (Gy) 30.00

☐ Show differential DVH

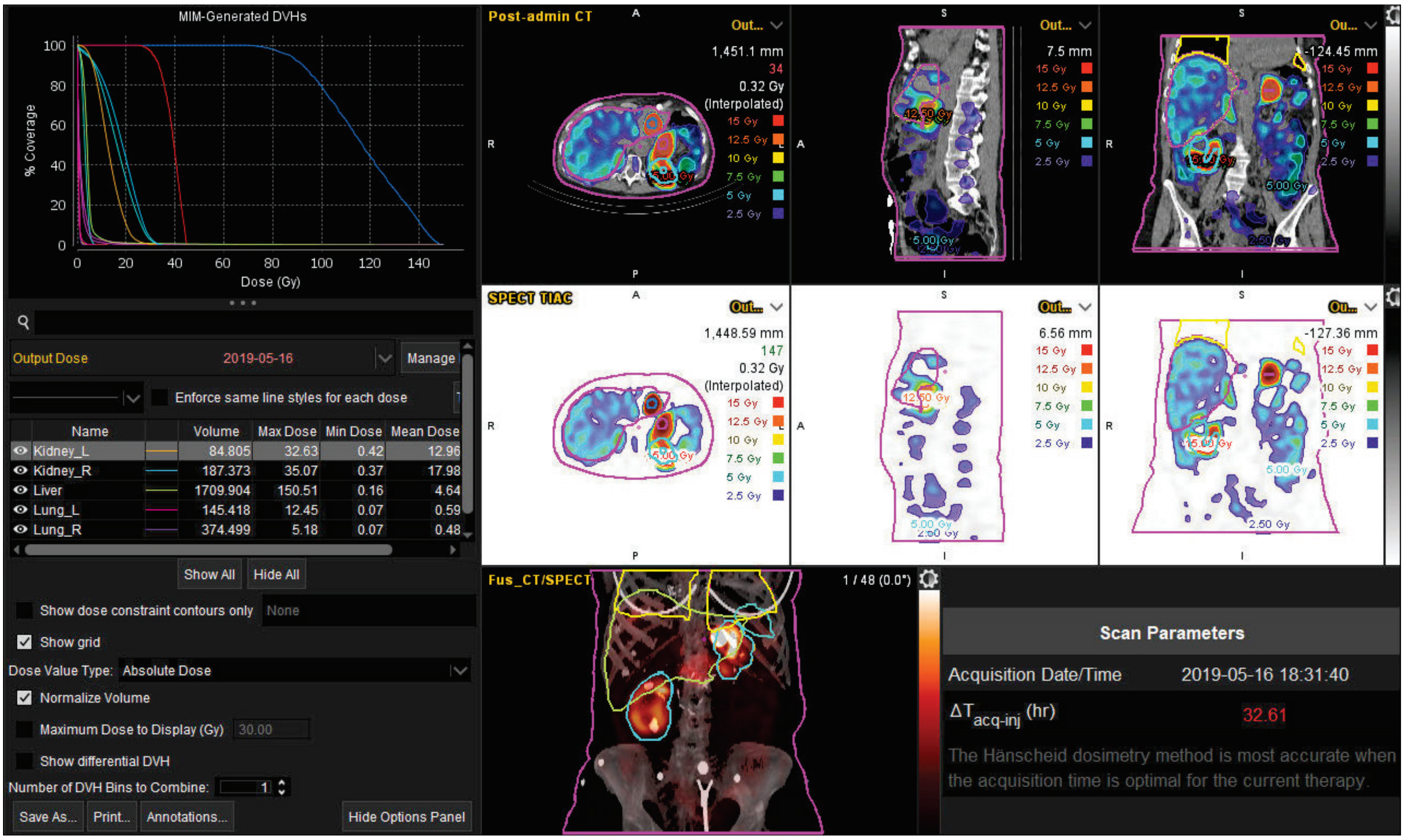
Number of DVH Bins to Combine: 1

- Review absorbed dose statistics for each region, including the mean, maximum, and minimum dose.
- Use the search field to see results only for certain regions. For example, search for "tumor" to see only results for tumor contours included in the DVH and table.
- Click the eye 👁 button to show/hide the region in the DVH. Click the line to change the color and format of the region in the DVH.

Tip: If information under the graph does not appear by default, click the **Show Options Panel** button in the lower-right corner of the DVH display to see additional information.

Dose Map

The results include a colored dose map overlaid on the CT and the final fusion.



Output Dose 2019-05-16 Manage

☐ Enforce same line styles for each dose

Name		Volume	Max Dose	Min Dose	Mean Dose
Kidney_L		84.805	32.63	0.42	12.96
Kidney_R		187.373	35.07	0.37	17.98
Liver		1709.904	150.51	0.16	4.64
Lung_L		145.418	12.45	0.07	0.59
Lung_R		374.499	5.18	0.07	0.48

Show All   Hide All

☐ Show dose constraint contours only: None

☑ Show grid

Dose Value Type: Absolute Dose

☑ Normalize Volume

☐ Maximum Dose to Display (Gy): 30.00

☐ Show differential DVH

Number of DVH Bins to Combine: 1

Save As...   Print...   Annotations...   Hide Options Panel

Scan Parameters

Acquisition Date/Time	2019-05-16 18:31:40
$\Delta T_{acq\text{-}inj}$ (hr)	32.61

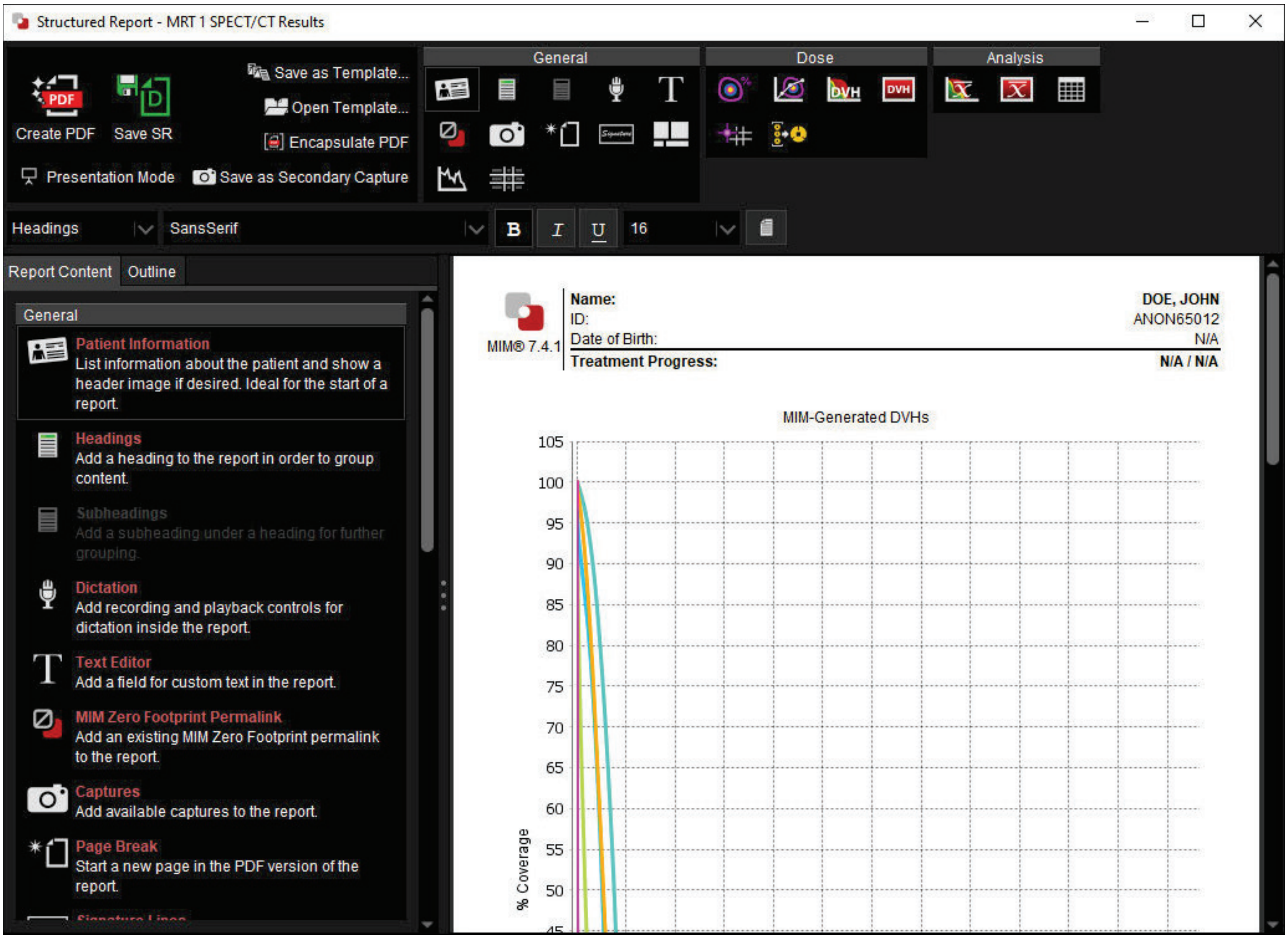
The Hänscheid dosimetry method is most accurate when the acquisition time is optimal for the current therapy.

Related: You can optionally use the **Dose** sidebar on the left side of the screen for more display options for dose. Refer to View Dose in MIM®: Fundamentals for more information.

Structured Report

The workflow automatically generates a structured report. As needed, update the report information. For example, on the Report Content tab, add a Text Editor field and type additional notes in the report.

Related: Refer to Create and Modify Structured Reports for more information about working with structured reports.



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.

Text Editor
Add a field for custom text in the report.

MIM Zero Footprint Permalink
Add an existing MIM Zero Footprint permalink to the report.

Captures
Add available captures to the report.

Page Break
Start a new page in the PDF version of the report.

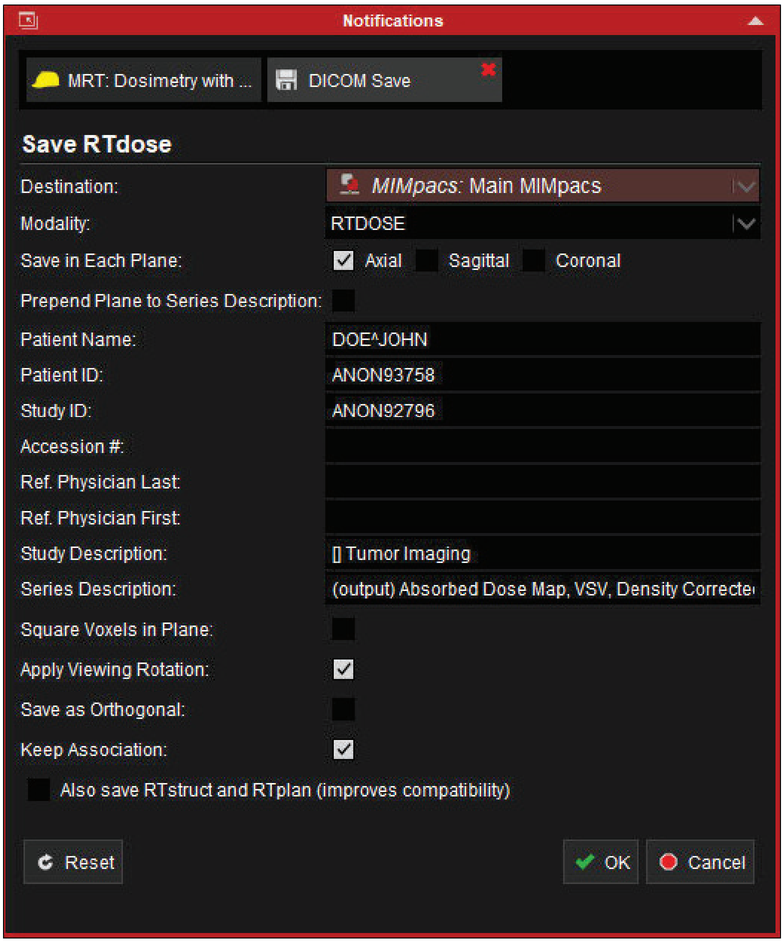
Name:	**DOE, JOHN**
ID:	ANON65012
Date of Birth:	N/A
Treatment Progress:	**N/A / N/A**

When you are finished, save the structured report as a PDF or as a DICOM object (SR).

Tip: If you do not want a structured report, deselect the **Auto-generate a structured report** option on the Basic Preferences screen when running the workflow.

Save Results

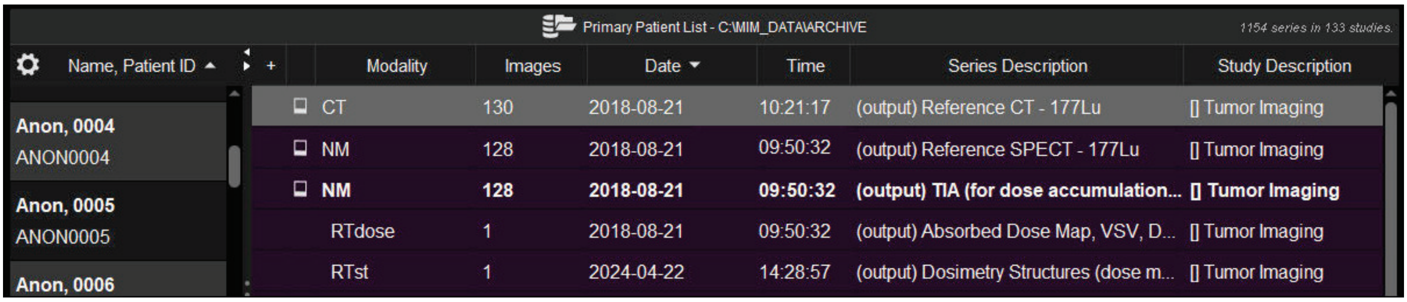
When processing is finished, the workflow prompts you to save the RTdose file. Click **OK**.



Save RTdose

Destination: *MIMpacs:* Main MIMpacs
Modality: RTDOSE
Save in Each Plane: ☑ Axial ☐ Sagittal ☐ Coronal
Prepend Plane to Series Description: ☐
Patient Name: DOE^JOHN
Patient ID: ANON93758
Study ID: ANON92796
Accession #:
Ref. Physician Last:
Ref. Physician First:
Study Description: [] Tumor Imaging
Series Description: (output) Absorbed Dose Map, VSV, Density Correcte
Square Voxels in Plane: ☐
Apply Viewing Rotation: ☑
Save as Orthogonal: ☐
Keep Association: ☑
☐ Also save RTstruct and RTplan (improves compatibility)

The workflow automatically saves five output files to your patient list. These series have "(output)" prepended to the series description. These output series are the inputs for the absorbed dose accumulation workflow to accumulate absorbed dose results from multiple radiopharmaceutical administrations. See Calculate Absorbed Dose Accumulation for more information.



Modality	Images	Date	Time	Series Description	Study Description
CT	130	2018-08-21	10:21:17	(output) Reference CT - 177Lu	[] Tumor Imaging
NM	128	2018-08-21	09:50:32	(output) Reference SPECT - 177Lu	[] Tumor Imaging
NM	**128**	**2018-08-21**	**09:50:32**	**(output) TIA (for dose accumulation...**	**[] Tumor Imaging**
RTdose	1	2018-08-21	09:50:32	(output) Absorbed Dose Map, VSV, D...	[] Tumor Imaging
RTst	1	2024-04-22	14:28:57	(output) Dosimetry Structures (dose m...	[] Tumor Imaging

You can also save the session so that you are able to resume where you left off with processing. Click the save 💾 button in the top toolbar and select **Save Session...**.

Tip: To automatically save the session, select the Advanced Preference to **Save a session of the dosimetry results**. With this option enabled, you are also prompted to save the RTstruct and RTplan. Refer to Settings for Dosimetry with 1 SPECT/CT for more information about Advanced Preferences.

To re-open the session, double-click the saved session file from the patient list.

Tips and Common Options

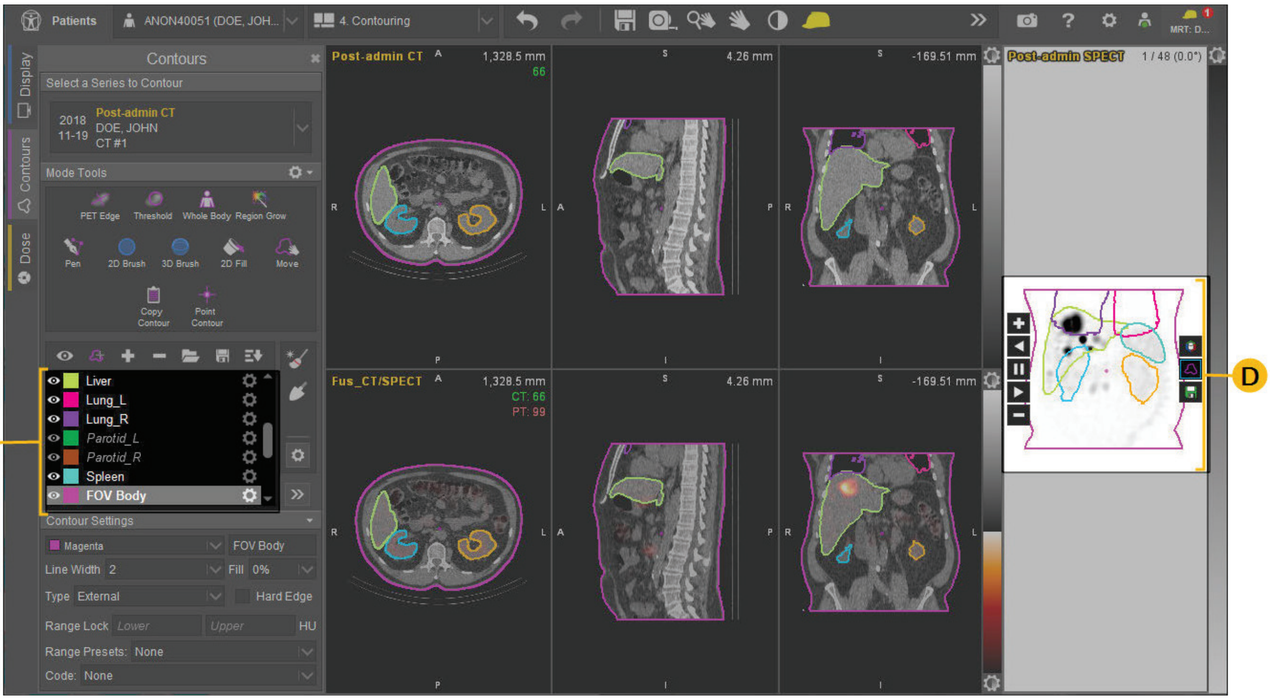
Related: For more information about Advanced Preferences available when running this workflows, refer to Settings for Dosimetry with 1 SPECT/CT.

Update Contours

The workflow prompts you to review and/or add contours on the CT. Keep the following tips in mind for efficient contouring:

A. Double-click on a viewport to make it larger. Use the 2 and 3 keys on your keyboard to zoom in.
B. Scroll to move between slices.
C. As needed, update the contour names and colors in the Contours sidebar.

D. Use the MIP to quickly and easily triangulate to tumors. Click a spot on the MIP, and MIM localizes to the highest intensity 3D location along that projection.



Magenta
FOV Body
Line Width 2
Fill 0%
Type External
Hard Edge
Range Lock Lower Upper HU
Range Presets: None
Code: None

See Gy/GBq Results (MIM 7.3 and Later)

You can include Gy/GBq results to consider dose constraints and project the cumulative absorbed dose for multiple cycles of therapy. This feature is not available in MIM 7.2 and earlier.

The results are calculated using the administered activity (either from the DICOM or that was entered when running the workflow) and the mean absorbed dose. You can review the limiting organs based on absorbed dose results and scale the results based on desired target doses to tumors or administered activity.

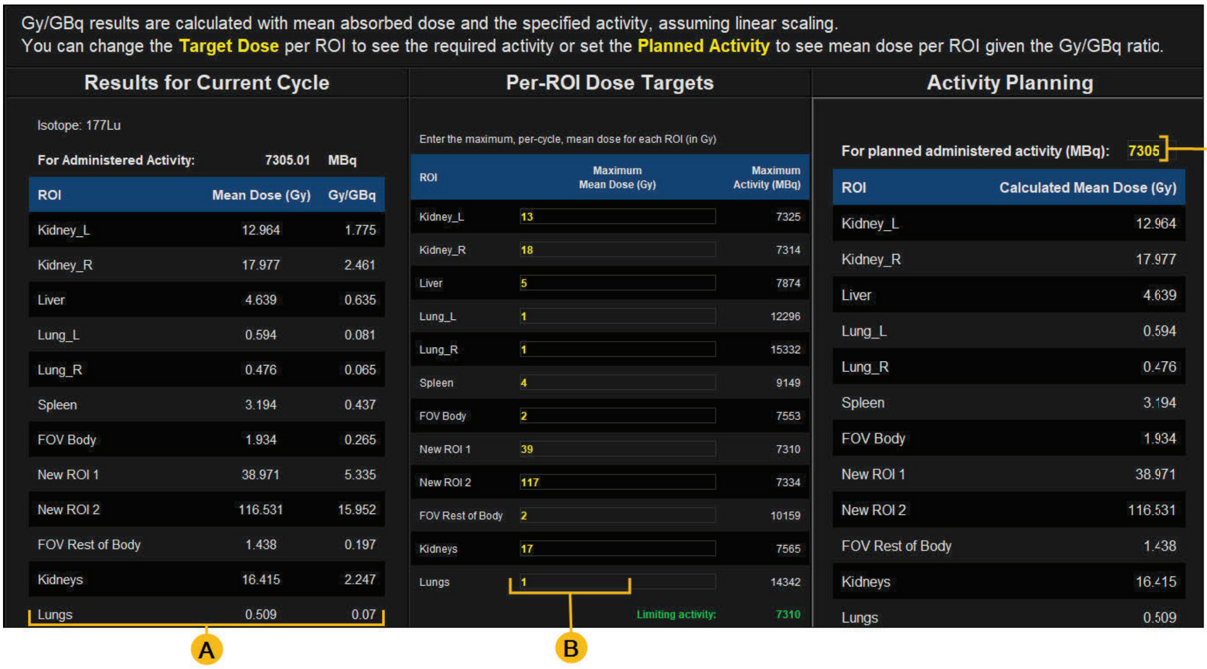
To view this page, you must run the workflow with the Advanced Preference for **Display Gy/GBq results review page** selected. Refer to Settings for Dosimetry with 1 SPECT/CT for more information about Advanced Preferences.

Then, when the workflow completes, follow these steps:

1. On the results page with the DVH, click the **Go to Gy/GBq Results** button in the lower-right corner.
2. Review the results:
    A. The **Results for Current Cycle** section is view-only and shows absorbed dose based on the provided treatment.
    B. In the **Per-ROI Dose Targets** section, enter the maximum mean absorbed dose for a region. The system updates the projected maximum activity based on the absorbed dose you enter. At

the bottom of the section, you can see calculations based on the target mean absorbed dose to tumors instead.

C. In the **Activity Planning** section, enter any planned activity, such as the activity from multiple administrations of the radiopharmaceutical. This section shows the projected mean dose per region, which is the inverse of the Per-ROI Dose Targets section.



Gy/GBq results are calculated with mean absorbed dose and the specified activity, assuming linear scaling.
You can change the **Target Dose** per ROI to see the required activity or set the **Planned Activity** to see mean dose per ROI given the Gy/GBq ratio.

Results for Current Cycle

Isotope: 177Lu

For Administered Activity: **7305.01** **MBq**

ROI	Mean Dose (Gy)	Gy/GBq
Kidney_L	12.964	1.775
Kidney_R	17.977	2.461
Liver	4.639	0.635
Lung_L	0.594	0.081
Lung_R	0.476	0.065
Spleen	3.194	0.437
FOV Body	1.934	0.265
New ROI 1	38.971	5.335
New ROI 2	116.531	15.952
FOV Rest of Body	1.438	0.197
Kidneys	16.415	2.247
Lungs	0.509	0.07

Per-ROI Dose Targets

Enter the maximum, per-cycle, mean dose for each ROI (in Gy)

ROI	Maximum Mean Dose (Gy)	Maximum Activity (MBq)
Kidney_L	13	7325
Kidney_R	18	7314
Liver	5	7874
Lung_L	1	12296
Lung_R	1	15332
Spleen	4	9149
FOV Body	2	7553
New ROI 1	39	7310
New ROI 2	117	7334
FOV Rest of Body	2	10159
Kidneys	17	7565
Lungs	1	14342

Limiting activity: 7310

Activity Planning

For planned administered activity (MBq): 7305

ROI	Calculated Mean Dose (Gy)
Kidney_L	12.964
Kidney_R	17.977
Liver	4.639
Lung_L	0.594
Lung_R	0.476
Spleen	3.194
FOV Body	1.934
New ROI 1	38.971
New ROI 2	116.531
FOV Rest of Body	1.438
Kidneys	16.415
Lungs	0.509

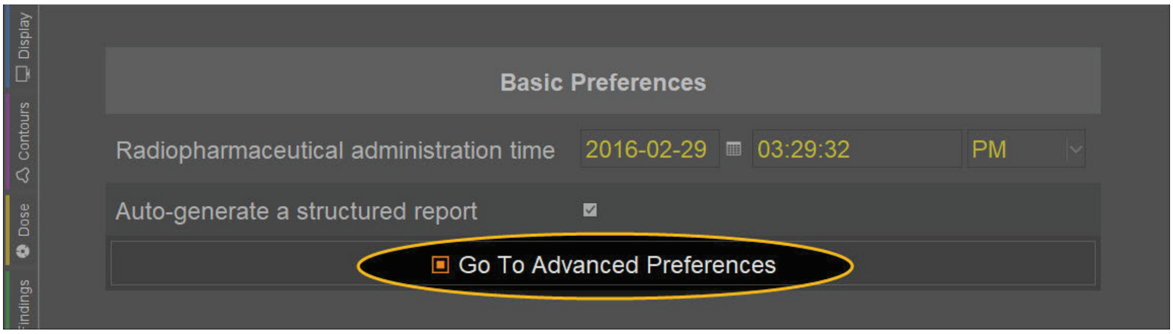
Tip: Click the screen capture 📷 button in the top toolbar to take a screen capture of this page. Go to the **Capture Gallery** to save the image so it is available for later reference.

Use Advanced Preferences

You can optionally use Advanced Preferences to further configure the workflow as needed. For example, you may adjust the workflow to support research.

To access additional settings when running the workflow, follow these steps:

1. When the workflow pauses on the Basic Preferences page, click the **Go To Advanced Preferences** button.



Basic Preferences

Radiopharmaceutical administration time 2016-02-29 03:29:32 PM

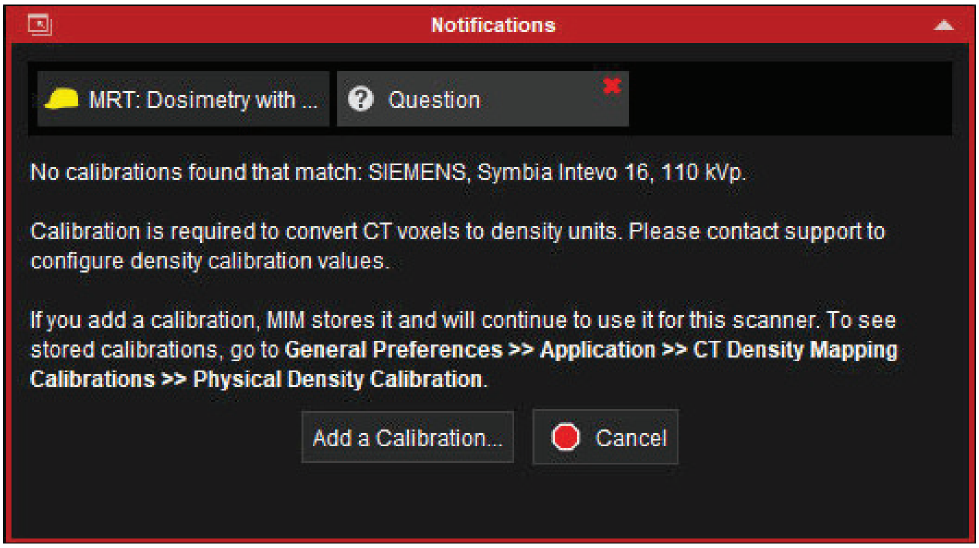
Auto-generate a structured report ☑

2. Update the settings as needed. Refer to Settings for Dosimetry with 1 SPECT/CT for more information about each setting.
3. Click **Resume Workflow**.

> **Tip:** When the workflow completes, the Advanced Settings page is visible for your reference. Any updates made at this time are not reflected in the workflow results. You need to re-launch the workflow to run processing again with different settings.

Troubleshooting

I see a notification that no calibrations were found.



No calibrations found that match: SIEMENS, Symbia Intevo 16, 110 kVp.

Calibration is required to convert CT voxels to density units. Please contact support to configure density calibration values.

If you add a calibration, MIM stores it and will continue to use it for this scanner. To see stored calibrations, go to **General Preferences >> Application >> CT Density Mapping Calibrations >> Physical Density Calibration**.

As part of your SurePlan™ MRT install, your MIM representative works with you to configure a density calibration file for each scanner. These calibration files are saved in the Physical Density Calibration table in MIM.

Do not proceed without a valid calibration file for the current CT. Please contact MIM Software Support for assistance.

Clinical Details

The Hänscheid Method starts with the assumption that the time-activity curve can be approximated with mono-exponential decay determined by the patient-specific effective half-life. This accounts for physiological decay and biological decay.

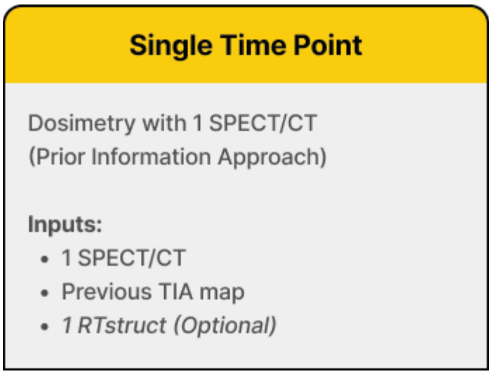
The time-integral of the exponential equation can be simplified to eliminate the effective half-life term for activity measured at a time point that is optimally 75-250% of the effective half-life.

Time-integrated activity is calculated on a voxel level based on the activity measured at an optimally timed 3D SPECT acquisition.

MRT: Dosimetry with 1 SPECT/CT (Prior Information Approach)

MIMTD-1116 • 22 Nov 2024

Overview



Single Time Point

Dosimetry with 1 SPECT/CT (Prior Information Approach)

Inputs:

- 1 SPECT/CT
- Previous TIA map
- *1 RTstruct (Optional)*

After pre-processing steps have been performed, such as reconstruction or segmentation, run the **MRT: Dosimetry with 1 SPECT/CT (Prior Information Approach)** workflow.

Use this workflow with a single SPECT/CT after you have processed dosimetry from a previous therapy cycle with the MRT: Dosimetry with Multiple SPECT/CTs workflow.

Related: Use the MRT: Dosimetry with 1 SPECT/CT (Hänscheid Method) workflow instead if you have not processed a previous therapy cycle with the MRT: Dosimetry with Multiple SPECT/CTs (for Prior Information Approach) workflow.

The workflow guides you through reviewing contours. It produces a voxelized absorbed dose map and mean absorbed dose values, which can be used for absorbed dose accumulation.

Tip: Use the steps below to run the workflow and to adjust study information and contours as needed. Use the My MIM SurePlan™ MRT Quick Sheet page to make your own notes about running the workflow.

Contents

- Troubleshooting
- Clinical Details

Launch the Workflow

1. From the patient list, select your images:
    - A current cycle CT and, if available, associated RTstruct
    - A quantitative SPECT
    - A time-integrated activity (TIA) map from a previous treatment cycle

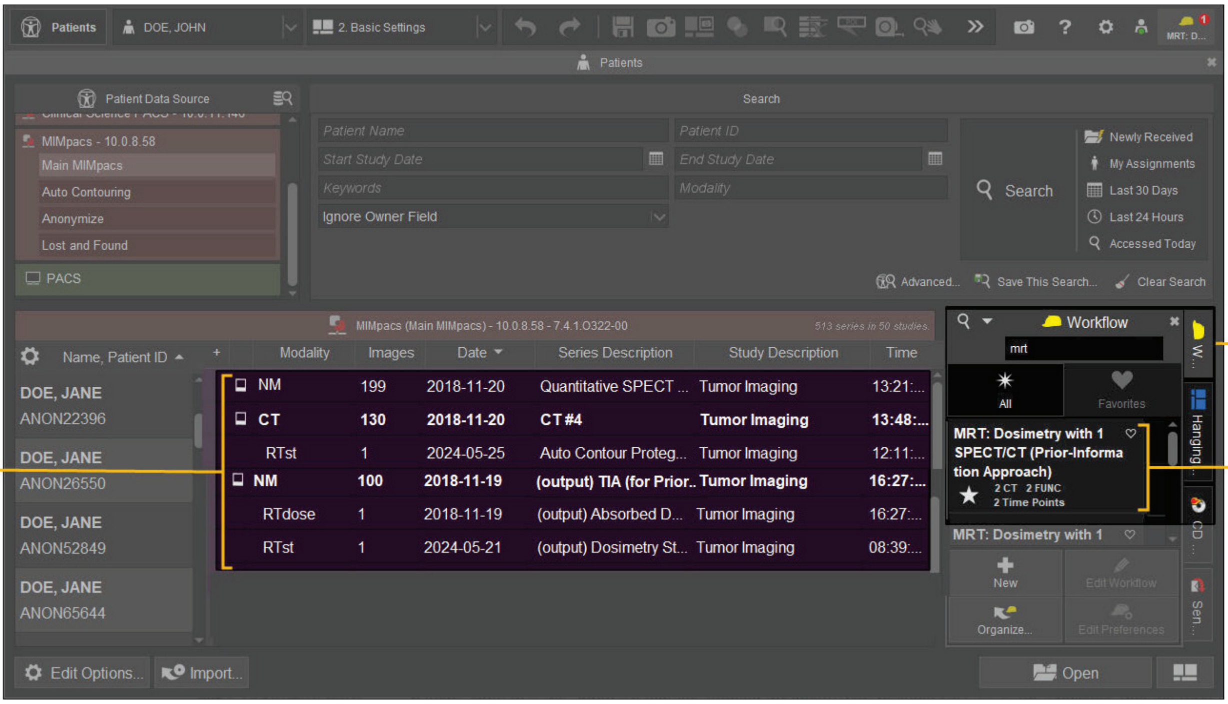
    > **Tip:** *MIM 7.3 and later*: If you don't select the TIA map, the workflow will automatically find and include the TIA map if it is available in the patient list. *MIM 7.2 and earlier*: You must select the TIA map and ensure that it is assigned in the target confirmation window (see step 4 below).

    - (Optional) A prior CT to allow transferring contours from a previous radiopharmaceutical administration

    > **Tip:** To select multiple series, press and hold the Ctrl key. Or, click and drag down to select the list of series.

2. Select the **Workflow** tab in the patient list to expand it.

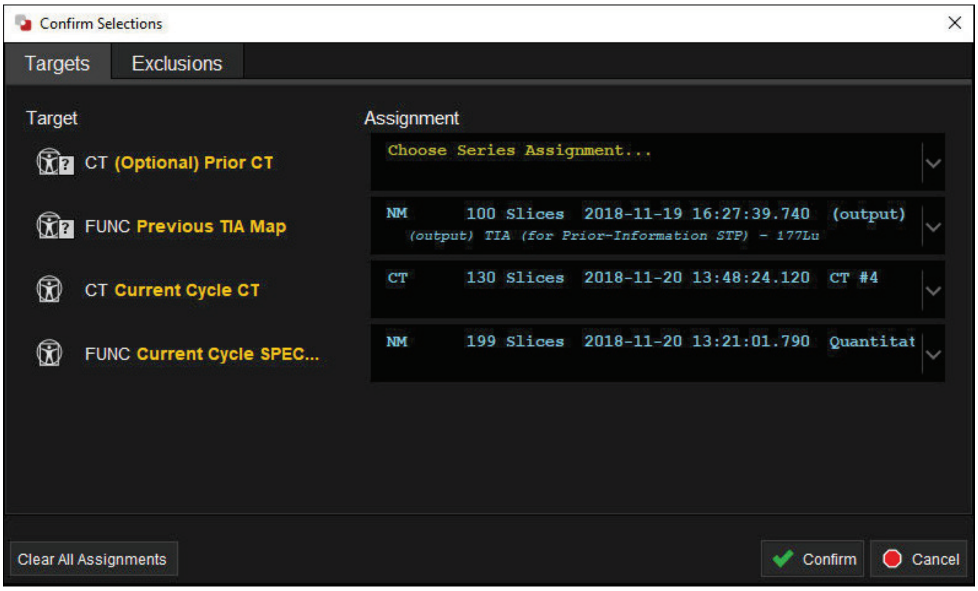
3. Double-click the **MRT: Dosimetry with 1 SPECT/CT (Prior Information Approach)** workflow from the list to launch it.



MIMpacs (Main MIMpacs) - 10.0.8.58 - 7.4.1.O322-00 513 series in 50 studies.

Modality	Images	Date	Series Description	Study Description	Time
NM	199	2018-11-20	Quantitative SPECT ...	Tumor Imaging	13:21:...
CT	**130**	**2018-11-20**	**CT #4**	**Tumor Imaging**	**13:48:...**
RTst	1	2024-05-25	Auto Contour Proteg...	Tumor Imaging	12:11:...
NM	**100**	**2018-11-19**	**(output) TIA (for Prior..**	**Tumor Imaging**	**16:27:...**
RTdose	1	2018-11-19	(output) Absorbed D...	Tumor Imaging	16:27:...
RTst	1	2024-05-21	(output) Dosimetry St...	Tumor Imaging	08:39:...

4. In the target confirmation window, verify the series are listed as expected. Click **Confirm**.

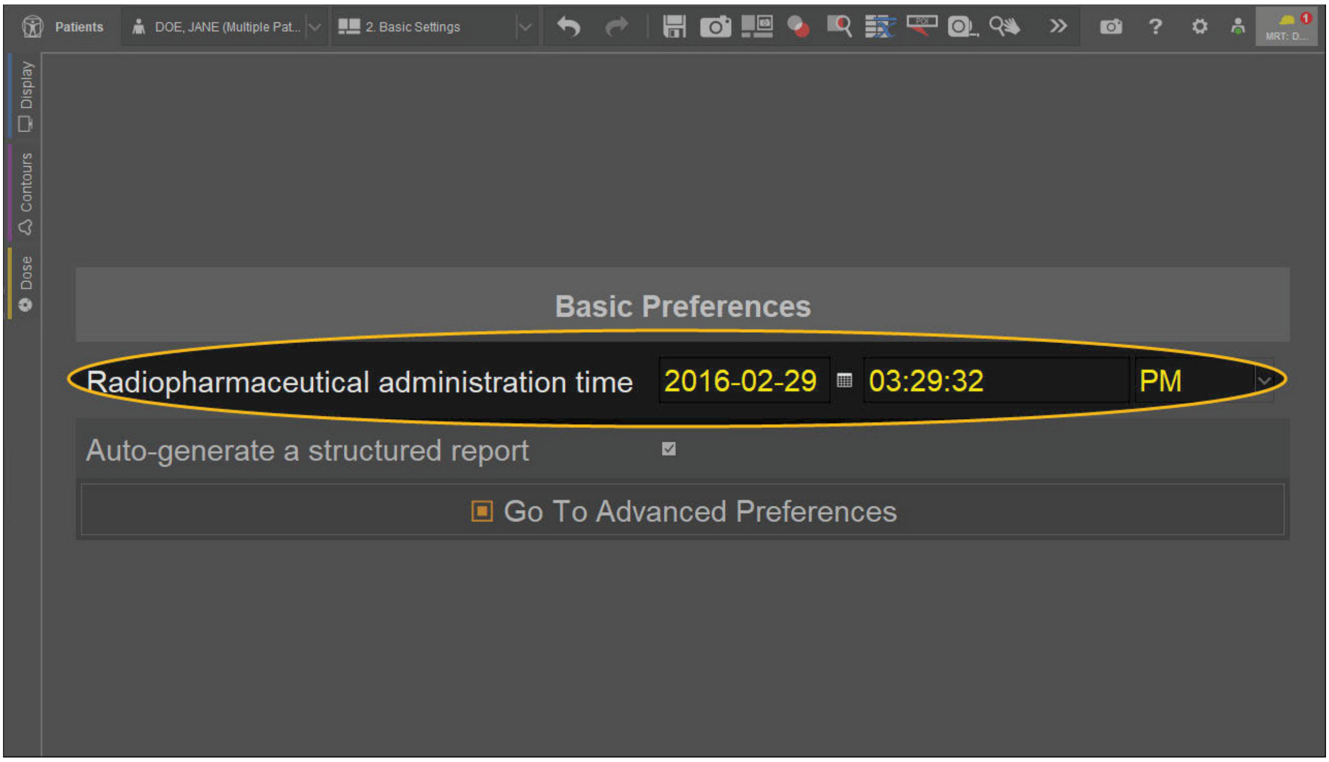


Confirm Selections

Target	Assignment
CT **(Optional) Prior CT**	Choose Series Assignment...
FUNC **Previous TIA Map**	NM 100 Slices 2018-11-19 16:27:39.740 (output) (output) TIA (for Prior-Information STP) - 177Lu
CT **Current Cycle CT**	CT 130 Slices 2018-11-20 13:48:24.120 CT #4
FUNC **Current Cycle SPEC...**	NM 199 Slices 2018-11-20 13:21:01.790 Quantitat

Run Workflow Processing

1. On the Basic Preferences page, check the **Radiopharmaceutical administration time** and update it if needed. Click **Resume Workflow**.



Basic Preferences

Radiopharmaceutical administration time 2016-02-29 03:29:32 PM

Auto-generate a structured report ☑

Go To Advanced Preferences

Tip: If needed, you can go to Advanced Preferences to modify additional workflow preferences. Refer to the tips below for common preferences or refer to Settings for Dosimetry with 1 SPECT/CT for more information about each advanced preference.

2. *If you included a Prior CT*, the workflow creates a rigid fusion between the Prior CT and the Post-admin CT and prompts you to review. If necessary, use the tools on the right side of the viewport to adjust the fusion.

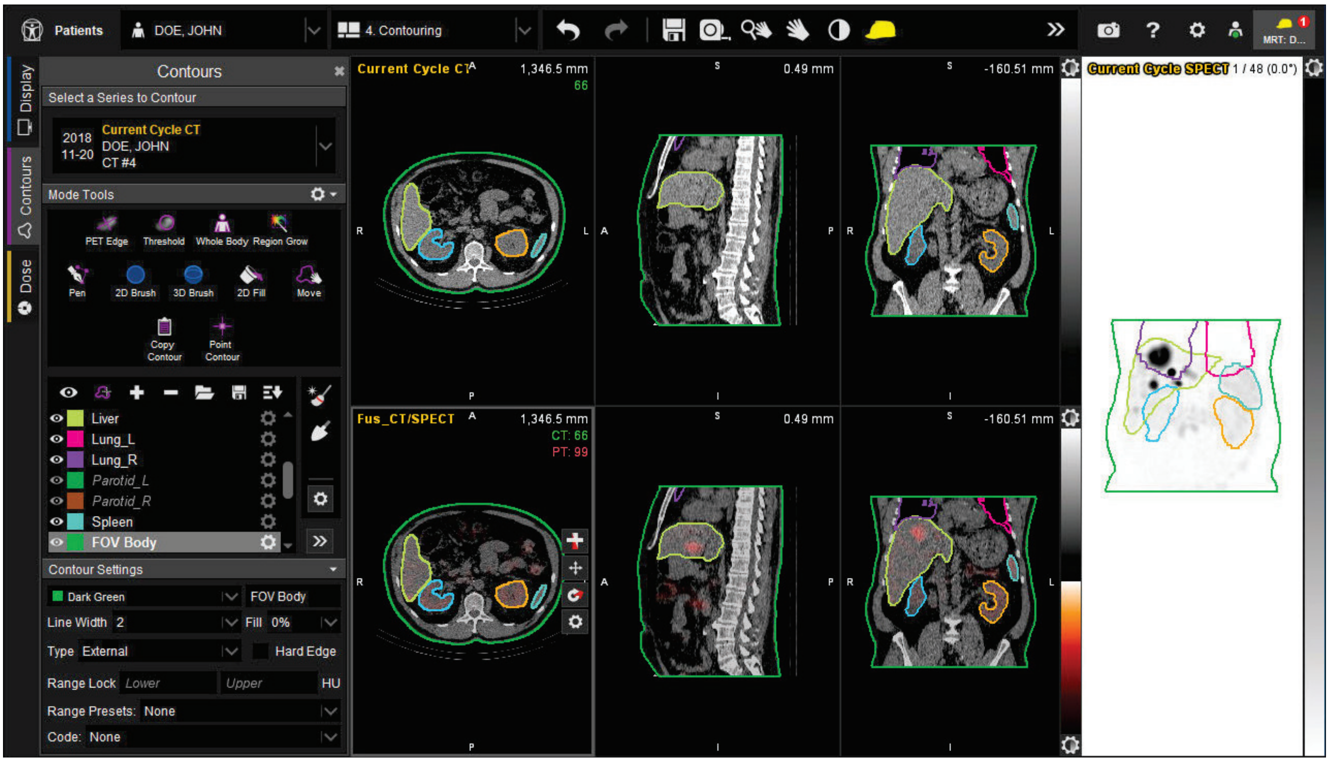
Related: See Adjust Fusions for more information.

Tip: This rigid fusion is the starting point for the deformable registration, which is used to transfer contours from the prior CT.

3. The workflow pauses and prompts you to contour ROIs on the fusion image to include in the dosimetry analysis:

- *If you loaded an RTstruct when launching the workflow*, the contours are listed in the Contours sidebar. *If you did not load an RTstruct*, click the plus ✚ button to create a contour.
- Use the **2D Brush** or another contouring tool of your choice to draw or edit organ contours as needed. See Update Contours below for more contouring tips.
- Use **PET Edge+**, the **Threshold** tool, or another contouring tool of your choice to draw or edit tumor contours as needed.
- Ensure that each tumor contour created contains the word Tumor or Lesion.

> **Tip:** Press the \ keyboard shortcut or click the arrow in the upper-right corner of the Notifications window to minimize the window. When you are finished with your adjustments, press \ again or click the flashing workflow button in the upper-right corner to re-expand the Notifications window.



Dark Green — FOV Body
Line Width 2 — Fill 0%
Type External — Hard Edge
Range Lock Lower Upper HU
Range Presets: None
Code: None

4. Click **Resume Workflow**.

> ⚠ **Caution:** The workflow ordinarily locates the appropriate entry in the Physical Density Calibration table for the CT you are processing. If a matching calibration is not found and the workflow prompts you to select or add a calibration, please contact MIM Software Support for assistance.

5. At the prompt, click **OK** to save the RTdose file. The workflow also saves the output files needed for dose accumulation. See Save Results below for more information.

Review Results

The workflow completes and generates several results pages. Use the left and right arrow keys or page dropdown in the top toolbar to move between pages and review results.

Dose Volume Histogram (DVH)

The DVH shows the distribution of absorbed dose across each segmented volume.

Output Dose 2019-05-16

☐ Enforce same line styles for each dose

	Name		Volume	Max Dose	Min Dose	Mean Dose	SD
👁	Kidney_L	—	84.805	32.63	0.42	12.96	5.32
👁	Kidney_R	—	187.373	35.07	0.37	17.98	7.50
👁	Liver	—	1709.904	150.51	0.16	4.64	6.10
👁	Lung_L	—	145.418	12.45	0.07	0.59	0.64
👁	Lung_R	—	374.499	5.18	0.07	0.48	0.38

☐ Show dose constraint contours only None

☑ Show grid

Dose Value Type: Absolute Dose

☑ Normalize Volume

☐ Maximum Dose to Display (Gy) 30.00

☐ Show differential DVH

Number of DVH Bins to Combine: 1

- Review absorbed dose statistics for each region, including the mean, maximum, and minimum dose.
- Use the search field to see results only for certain regions. For example, search for "tumor" to see only results for tumor contours included in the DVH and table.
- Click the eye 👁 button to show/hide the region in the DVH. Click the line to change the color and format of the region in the DVH.

Tip: If information under the graph does not appear by default, click the **Show Options Panel** button in the lower-right corner of the DVH display to see additional information.

Dose Map

The results include a colored dose map overlaid on the CT and the final fusion.

☐ Show dose constraint contours only None

☑ Show grid

Dose Value Type: Absolute Dose

☑ Normalize Volume

☐ Maximum Dose to Display (Gy) 30.00

☐ Show differential DVH

Number of DVH Bins to Combine: 1

Save As... Print... Annotations... Hide Options Panel

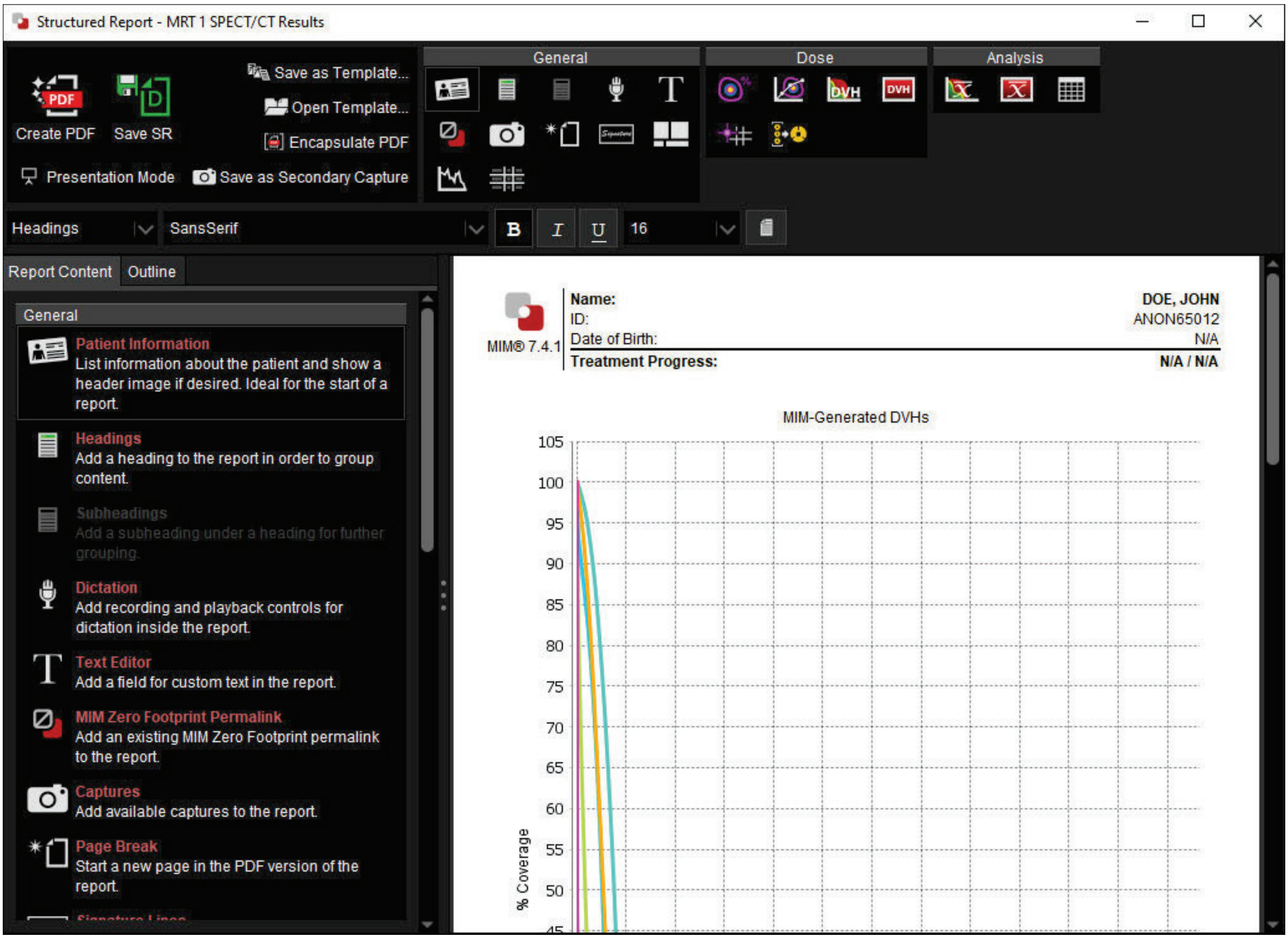
Note: This dosimetry approach assumes that there are no dramatic changes in the uptake and decay rates within each evaluated ROI from the previous cycle of therapy.

Related: You can optionally expand the **Dose** sidebar on the left side of the screen for more display options for dose. Refer to View Dose in MIM®: Fundamentals for more information.

Structured Report

The workflow automatically generates a structured report. As needed, update the report information. For example, on the Report Content tab, add a Text Editor field and type additional notes in the report.

Related: Refer to Create and Modify Structured Reports for more information about working with structured reports.



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.

Text Editor
Add a field for custom text in the report.

MIM Zero Footprint Permalink
Add an existing MIM Zero Footprint permalink to the report.

Captures
Add available captures to the report.

Page Break
Start a new page in the PDF version of the report.

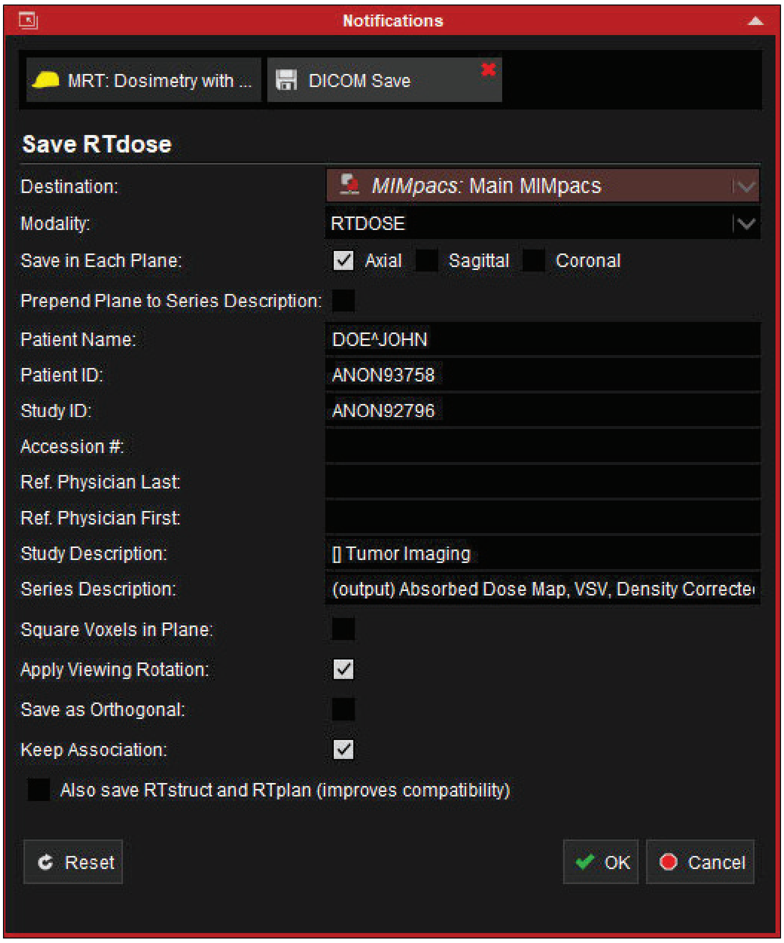
Name: DOE, JOHN
ID: ANON65012
Date of Birth: N/A
Treatment Progress: N/A / N/A

When you are finished, save the structured report as a PDF or as a DICOM object (SR).

Tip: If you do not want a structured report, deselect the **Auto-generate a structured report** option on the Basic Preferences screen when running the workflow.

Save Results

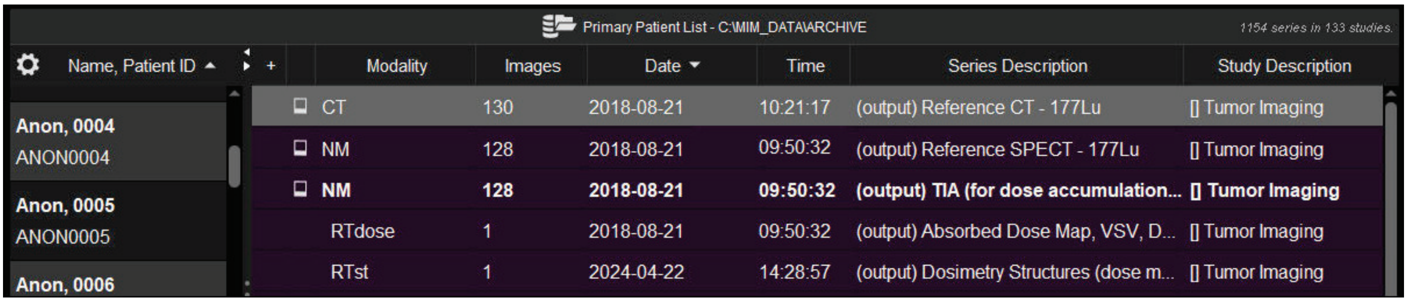
When processing is finished, the workflow prompts you to save the RTdose file. Click **OK**.



Save RTdose

Destination: *MIMpacs:* Main MIMpacs
Modality: RTDOSE
Save in Each Plane: ☑ Axial ☐ Sagittal ☐ Coronal
Prepend Plane to Series Description: ☐
Patient Name: DOE^JOHN
Patient ID: ANON93758
Study ID: ANON92796
Accession #:
Ref. Physician Last:
Ref. Physician First:
Study Description: [] Tumor Imaging
Series Description: (output) Absorbed Dose Map, VSV, Density Correcte
Square Voxels in Plane: ☐
Apply Viewing Rotation: ☑
Save as Orthogonal: ☐
Keep Association: ☑
☐ Also save RTstruct and RTplan (improves compatibility)

The workflow automatically saves five output series to your patient list. These series have "(output)" prepended to the series description. These output series are the inputs for the absorbed dose accumulation workflow to accumulate absorbed dose results from multiple radiopharmaceutical administrations. See Calculate Absorbed Dose Accumulation for more information.



Modality	Images	Date	Time	Series Description	Study Description
CT	130	2018-08-21	10:21:17	(output) Reference CT - 177Lu	[] Tumor Imaging
NM	128	2018-08-21	09:50:32	(output) Reference SPECT - 177Lu	[] Tumor Imaging
NM	**128**	**2018-08-21**	**09:50:32**	**(output) TIA (for dose accumulation...**	**[] Tumor Imaging**
RTdose	1	2018-08-21	09:50:32	(output) Absorbed Dose Map, VSV, D...	[] Tumor Imaging
RTst	1	2024-04-22	14:28:57	(output) Dosimetry Structures (dose m...	[] Tumor Imaging

You can also save the session so that you are able to resume where you left off with processing. Click the save 🖫 button in the top toolbar and select **Save Session...**.

Tip: To automatically save the session, select the Advanced Preference to **Save a session of the dosimetry results**. With this option enabled, you are also prompted to save the RTstruct and RTplan. Refer to Settings for Dosimetry with 1 SPECT/CT for more information about Advanced Preferences.

To re-open the session, double-click the saved session file from the patient list.

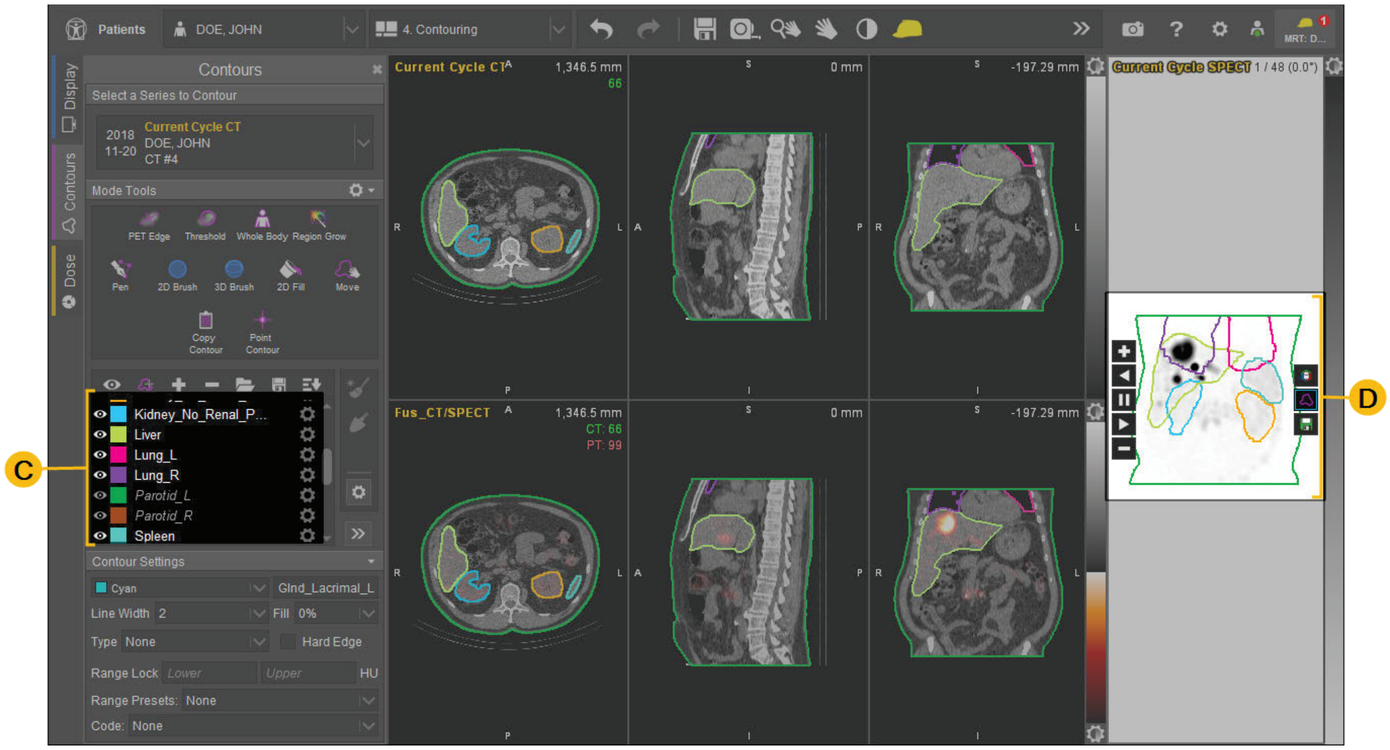
Tips and Common Options

Related: For more information about the Advanced Preferences available when running this workflow, refer to Settings for Dosimetry with 1 SPECT/CT.

Update Contours

The workflow prompts you to review and/or add contours on the current cycle CT. Keep the following tips in mind for efficient contouring:

A. Double-click on a viewport to make it larger. Use the 2 and 3 keys on your keyboard to zoom in.
B. Scroll to move between slices.
C. As needed, update the contour names and colors in the Contours sidebar.
D. Use the MIP to quickly and easily triangulate to tumors. Click a spot on the MIP, and MIM localizes to the highest intensity 3D location along that projection.



See Gy/GBq Results (MIM 7.3 and Later)

You can include Gy/GBq results to consider dose constraints and project the cumulative absorbed dose for multiple cycles of therapy. This feature is not available in MIM 7.2 and earlier.

The results are calculated using the administered activity (either from the DICOM or that was entered when running the workflow) and the mean absorbed dose. You can review the limiting organs based on absorbed dose results and scale the results based on desired target doses to tumors or administered activity.

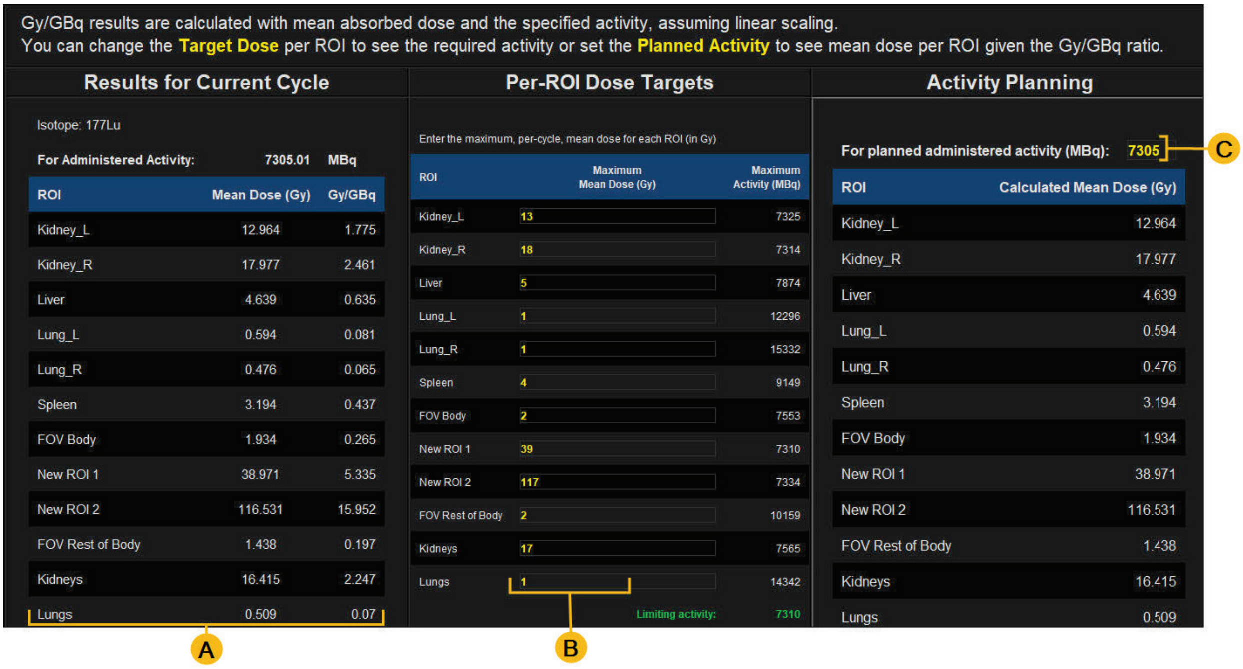
To view this page, you must run the workflow with the Advanced Preference for **Display Gy/GBq results review page** selected. Refer to Settings for Dosimetry with 1 SPECT/CT for more information about Advanced Preferences.

Then, when the workflow completes, follow these steps:

1. On the results page with the DVH, click the **Go to Gy/GBq Results** button in the lower-right corner.
2. Review the results:
    A. The **Results for Current Cycle** section is view-only and shows absorbed dose based on the provided treatment.
    B. In the **Per-ROI Dose Targets** section, enter the maximum mean absorbed dose for a region. The system updates the projected maximum activity based on the absorbed dose you enter. At

the bottom of the section, you can see calculations based on the target mean absorbed dose to tumors instead.

C. In the **Activity Planning** section, enter any planned activity, such as the activity from multiple administrations of the radiopharmaceutical. This section shows the projected mean dose per region, which is the inverse of the Per-ROI Dose Targets section.



Gy/GBq results are calculated with mean absorbed dose and the specified activity, assuming linear scaling.
You can change the **Target Dose** per ROI to see the required activity or set the **Planned Activity** to see mean dose per ROI given the Gy/GBq ratio.

Results for Current Cycle

Isotope: 177Lu

For Administered Activity: 7305.01 MBq

ROI	Mean Dose (Gy)	Gy/GBq
Kidney_L	12.964	1.775
Kidney_R	17.977	2.461
Liver	4.639	0.635
Lung_L	0.594	0.081
Lung_R	0.476	0.065
Spleen	3.194	0.437
FOV Body	1.934	0.265
New ROI 1	38.971	5.335
New ROI 2	116.531	15.952
FOV Rest of Body	1.438	0.197
Kidneys	16.415	2.247
Lungs	0.509	0.07

Per-ROI Dose Targets

Enter the maximum, per-cycle, mean dose for each ROI (in Gy)

ROI	Maximum Mean Dose (Gy)	Maximum Activity (MBq)
Kidney_L	13	7325
Kidney_R	18	7314
Liver	5	7874
Lung_L	1	12296
Lung_R	1	15332
Spleen	4	9149
FOV Body	2	7553
New ROI 1	39	7310
New ROI 2	117	7334
FOV Rest of Body	2	10159
Kidneys	17	7565
Lungs	1	14342
	Limiting activity:	7310

Activity Planning

For planned administered activity (MBq): 7305

ROI	Calculated Mean Dose (Gy)
Kidney_L	12.964
Kidney_R	17.977
Liver	4.639
Lung_L	0.594
Lung_R	0.476
Spleen	3.194
FOV Body	1.934
New ROI 1	38.971
New ROI 2	116.531
FOV Rest of Body	1.438
Kidneys	16.415
Lungs	0.509

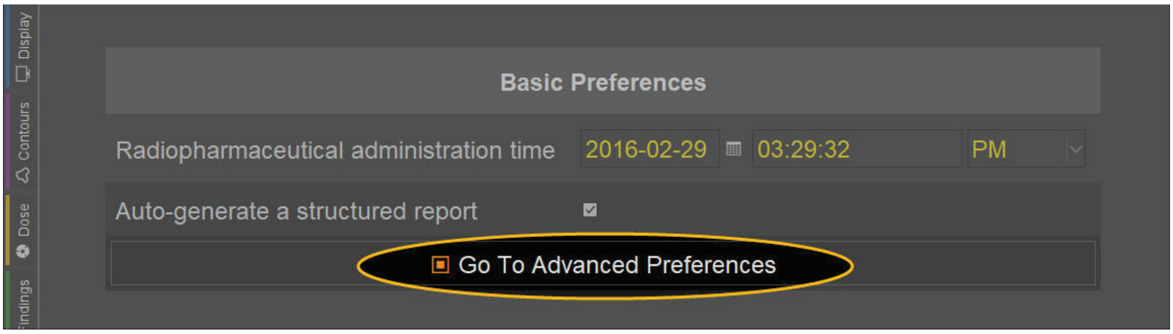
Tip: Click the screen capture 📷 button in the top toolbar to take a screen capture of this page. Go to the **Capture Gallery** to save the image so it is available for later reference.

Use Advanced Preferences

You can optionally use Advanced Preferences to further configure the workflow as needed. For example, you may adjust the workflow to support research.

To access additional settings when running the workflow, follow these steps:

1. When the workflow pauses on the Basic Preferences page, click the **Go To Advanced Preferences** button.



Basic Preferences

Radiopharmaceutical administration time: 2016-02-29 03:29:32 PM

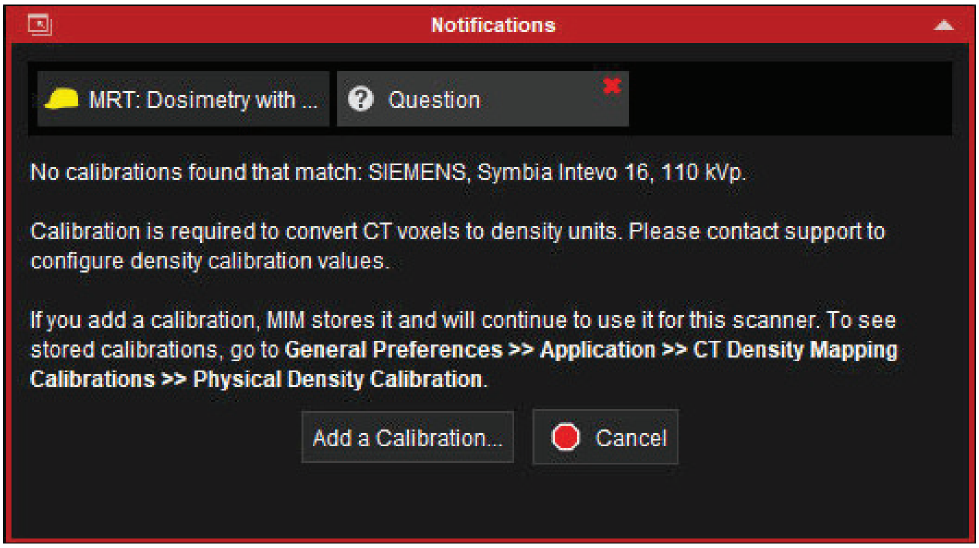
Auto-generate a structured report ☑

2. Update the settings as needed. Refer to Settings for Dosimetry with 1 SPECT/CT for more information about each setting.
3. Click **Resume Workflow**.

> **Tip:** When the workflow completes, the Advanced Settings page is visible for your reference. Any updates made at this time are not reflected in the workflow results. You need to re-launch the workflow to run processing again with different settings.

Troubleshooting

I see a notification that no calibrations were found.



No calibrations found that match: SIEMENS, Symbia Intevo 16, 110 kVp.

Calibration is required to convert CT voxels to density units. Please contact support to configure density calibration values.

If you add a calibration, MIM stores it and will continue to use it for this scanner. To see stored calibrations, go to **General Preferences >> Application >> CT Density Mapping Calibrations >> Physical Density Calibration**.

As part of your SurePlan™ MRT install, your MIM representative works with you to configure a density calibration file for each scanner. These calibration files are saved in the Physical Density Calibration table in MIM.

Do not proceed without a valid calibration file for the current CT. Please contact MIM Software Support for assistance.

Clinical Details

The Prior Information Approach assumes that the shapes of the time activity curves are relatively consistent across multiple treatment cycles for a given patient. Note that this approach requires running dosimetry with multiple SPECT/CTs for a previous therapy cycle to generate curve fit parameters for each contour. Refer to MRT: Dosimetry with Multiple SPECT/CTs for more information.

Time-integrated activity is calculated on a voxel level based on the activity measured with a single 3D SPECT acquisition using previously determined models per contour.

Settings for Dosimetry with Multiple SPECT/CTs

MIMTD-1117 • 05 Jun 2024

Overview

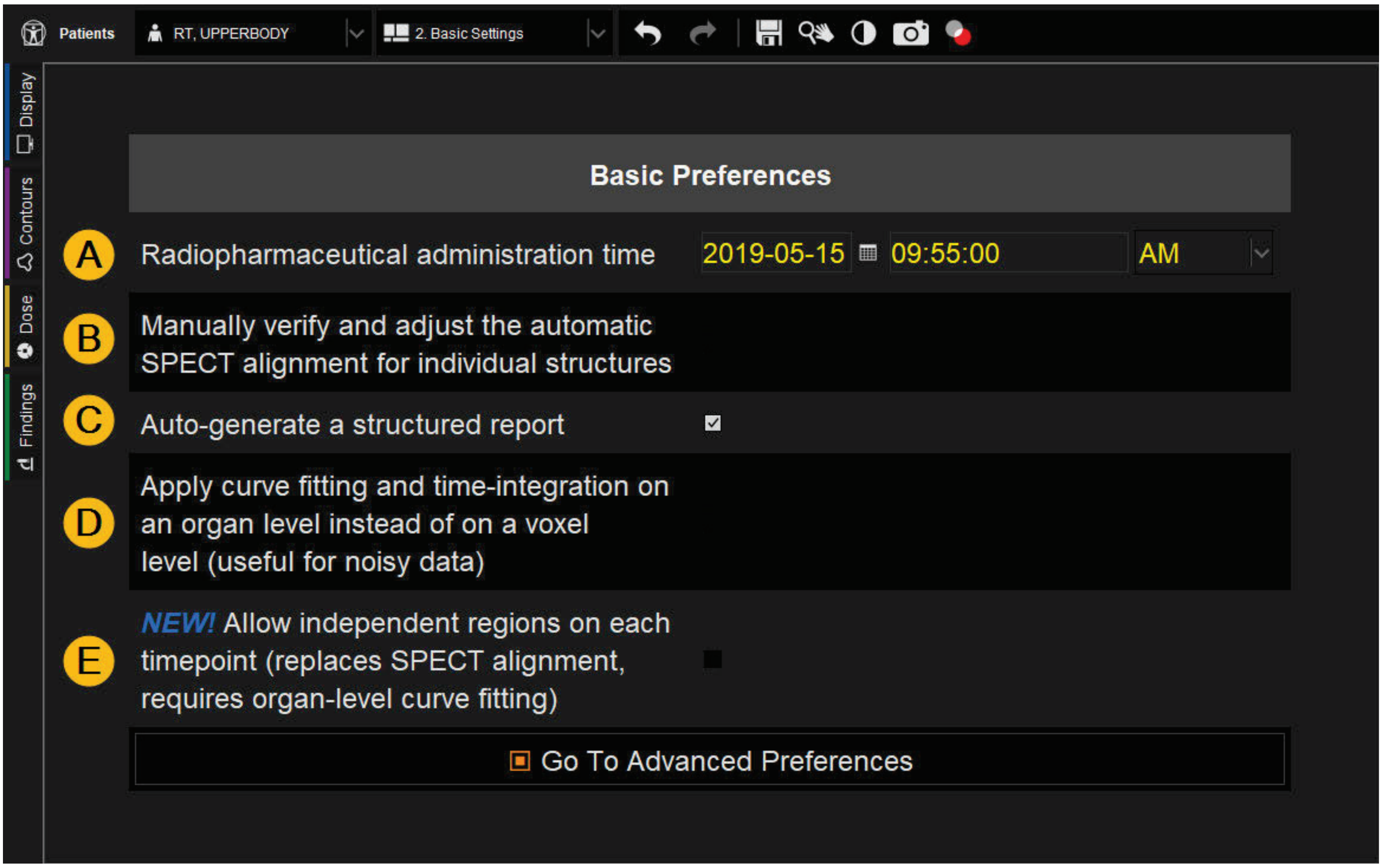
The settings described below apply to both the **MRT: Dosimetry with Multiple SPECT/CTs** and the **MRT: Dosimetry with Multiple SPECT/CTs (for Prior-Information Approach)** workflows. For more information about these workflows, refer to MRT: Dosimetry with Multiple SPECT/CTs.

You are prompted to review the **Basic Preferences** while running the workflow. You can optionally click **Go To Advanced Preferences** to configure additional options.

☆ **Important:** Settings are not saved across sessions. Adjust these settings as needed each time that you run the workflow. If there are some settings that you want always to be used by default, contact MIM Software Support at support.mimsoftware.com for help modifying your workflow.

Contents

Basic Preferences



Basic Preferences

A Radiopharmaceutical administration time 2019-05-15 09:55:00 AM

B Manually verify and adjust the automatic SPECT alignment for individual structures

C Auto-generate a structured report ☑

D Apply curve fitting and time-integration on an organ level instead of on a voxel level (useful for noisy data)

E *NEW!* Allow independent regions on each timepoint (replaces SPECT alignment, requires organ-level curve fitting) ■

Go To Advanced Preferences

A. Adjust the radiopharmaceutical administration date and time. This is essential for dosimetry. The date and time are pulled from the DICOM data, if available.

> **Tip:** The pre-populated date or time may be incorrect with retrospective data that may have been anonymized, or where only the time is stored without a date.

B. Choose whether to manually verify and adjust functional series alignment for individual structures. When this setting is enabled, the workflow prompts the user to select which ROIs to review. Each contour can be reviewed separately for contour-based alignment for each functional time point.

C. Choose whether to auto-generate a structured report. A structured report contains important session information and screenshots.

Related: For more information about working with structured reports, see Create and Modify Structured Reports.

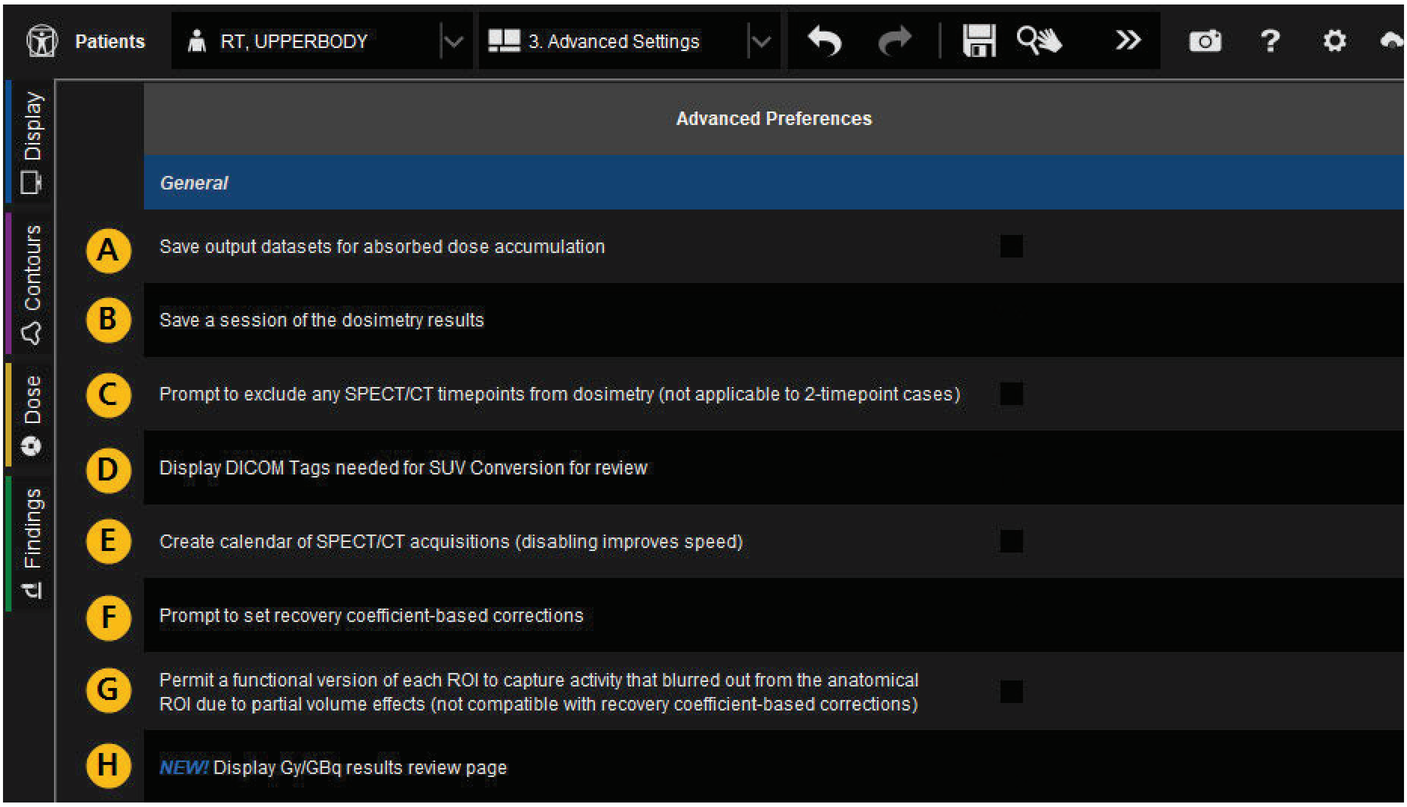
D. Choose whether to apply curve fitting and time-integration on an organ level.

   - This setting optimizes the curve fit model per ROI rather than per voxel. Subsequent dosimetry is still performed on the voxel level.
   - This setting is useful for noisy SPECT or PET data that leads to falsely heterogeneous activity within the ROIs.

E. *MIM 7.3 and later:* Choose whether to allow independent regions on each time point. When this option is enabled, the user can define ROIs on each time point instead of having the same ROIs aligned on all functional time points.
MIM 7.2 and earlier: This functionality is not available.

Advanced Preferences

General



Advanced Preferences

General

A Save output datasets for absorbed dose accumulation ■

B Save a session of the dosimetry results

C Prompt to exclude any SPECT/CT timepoints from dosimetry (not applicable to 2-timepoint cases) ■

D Display DICOM Tags needed for SUV Conversion for review

E Create calendar of SPECT/CT acquisitions (disabling improves speed) ■

F Prompt to set recovery coefficient-based corrections

G Permit a functional version of each ROI to capture activity that blurred out from the anatomical ROI due to partial volume effects (not compatible with recovery coefficient-based corrections) ■

H *NEW!* Display Gy/GBq results review page

A. Choose whether to save results needed for the Dose Accumulation workflow. Five outputs are saved:

  - Reference CT
  - Reference SPECT or PET
  - TIA map
  - Dosimetry structures
  - Absorbed dose

B. Choose whether to save a session of the dosimetry results.

C. Choose whether to prompt the user to select time points to remove. The user can review and remove unwanted time points without needing to restart the workflow. For example, there may be SPECT time points loaded that are unsuitable for dosimetry.

D. Choose whether to display DICOM tags needed for SUV conversion for review, such as radiopharmaceutical total dose.

E. Choose whether to create a calendar of SPECT/CT or PET/CT acquisitions. This calendar appears on the final results page and shows injection and acquisition times. Disabling this setting improves processing speed.

F. Choose whether to prompt the user to set recovery coefficient-based corrections.

> **Tip:** Partial volume effects can cause activity within an ROI to be blurred outside of the anatomical volume. You can use this option or the next option to help correct for partial volume effects.

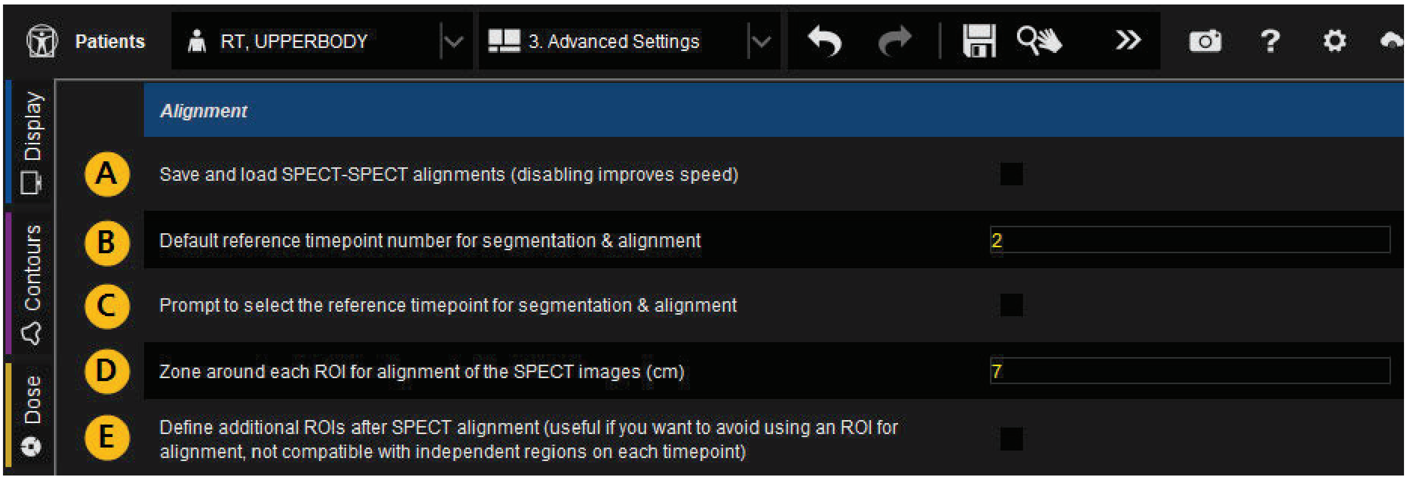
  - This prompt allows the user to make changes to the recovery coefficient method during the workflow.
  - When this option is enabled, an additional settings table appears to adjust recovery coefficient parameters after the SPECT or PET alignment.

G. Choose whether to permit a functional version of each ROI.

  - This setting allows the user to define activity regions for each ROI to capture that activity and map it back to the anatomical volume.
  - This setting cannot be enabled if the recovery coefficient prompt (see above) is enabled.

H. *MIM 7.3 and later:* Choose whether to display an interactive Gy/GBq results page. For more information about this page, refer to See Gy/GBq Results (MIM 7.3 and Later).
MIM 7.2 and earlier: This functionality is not available.

Alignment



Alignment

A	Save and load SPECT-SPECT alignments (disabling improves speed)	☐
B	Default reference timepoint number for segmentation & alignment	2
C	Prompt to select the reference timepoint for segmentation & alignment	☐
D	Zone around each ROI for alignment of the SPECT images (cm)	7
E	Define additional ROIs after SPECT alignment (useful if you want to avoid using an ROI for alignment, not compatible with independent regions on each timepoint)	☐

A. Choose whether to save and load SPECT-to-SPECT or PET-to-PET alignments. For example, a user can enable this setting if they expect to run the dosimetry workflow multiple times for the same data set.

   - This setting saves registrations for each ROI alignment for each aligned time point.
   - Saved registrations are loaded upon subsequent runs of the workflow.

B. Set the reference time point. The reference time point is used for segmentation and time point registration.

> **Tip:** If you consistently use a time point other than the second time point as the reference time point, contact MIM Software Support at support.mimsoftware.com for assistance updating the workflow to use your preferred time point by default.

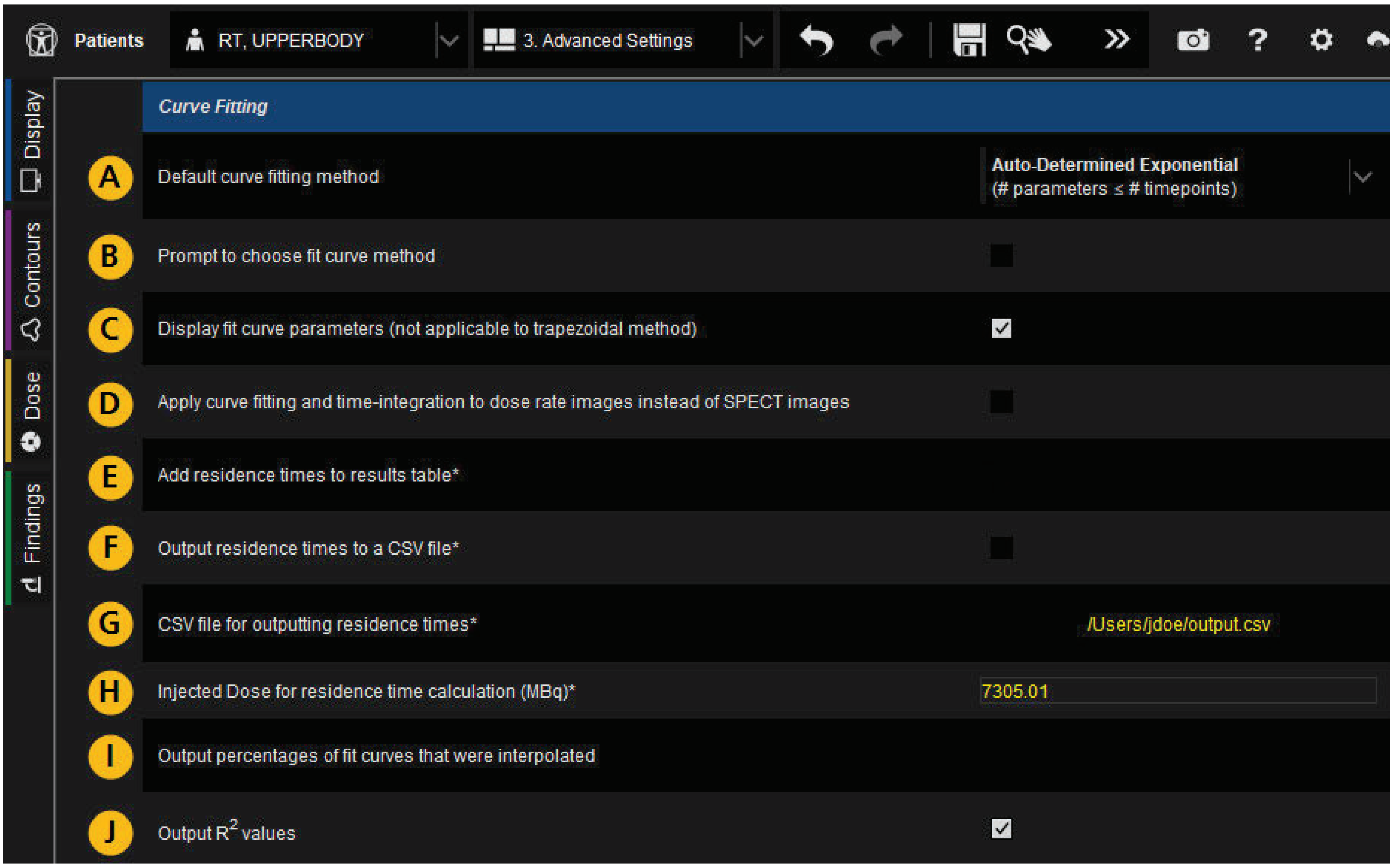
C. Choose whether to prompt the user to select the reference time point. This prompt allows the user to choose which time point to use for contouring and SPECT or PET alignment instead of using the default time point.

D. Set the expanded region around each ROI to use for alignment of the SPECT or PET images. The default expansion zone was optimized based on internal testing with human data, but the value is adjustable if needed.

E. Choose whether to prompt the user to define additional ROIs after SPECT or PET alignment. This is useful for defining ROIs to obtain dosimetry without affecting the SPECT or PET alignment (e.g., if the ROIs are small or there is low activity).

Tip: Use the **Define additional ROIs on dose map** setting below if you want to see absorbed dose results before choosing whether to draw additional ROIs.

Curve Fitting



Curve Fitting

A Default curve fitting method: Auto-Determined Exponential (# parameters ≤ # timepoints)

B Prompt to choose fit curve method ☐

C Display fit curve parameters (not applicable to trapezoidal method) ☑

D Apply curve fitting and time-integration to dose rate images instead of SPECT images ☐

E Add residence times to results table*

F Output residence times to a CSV file* ☐

G CSV file for outputting residence times*: /Users/jdoe/output.csv

H Injected Dose for residence time calculation (MBq)*: 7305.01

I Output percentages of fit curves that were interpolated

J Output R^2 values ☑

A. Set the default curve fitting method.

Related: For more information, see the *Dosimetry for Targeted Molecular Radiotherapy* white paper in the Appendix.

- Trapezoidal + Exponential for Extrapolation — Integration with exponential extrapolation
- Mono-exponential
- Bi-Exponential A — 4-parameter Bi-exponential

- Bi-Exponential B — 3-parameter Bi-exponential assuming 0 activity at t = 0
- Auto-Determined Exponential (# parameters ≤ # timepoints) — Fit model is optimized per voxel or ROI, selected from the available exponential models. The number of parameters is limited to the number of time points.
- Auto-Determined Exponential (# parameters ≤ # timepoints - 1) — Fit model is optimized per voxel or ROI, selected from the available exponential models. The number of parameters is limited to 1 less than the number of time points

B. Choose whether the user is prompted to select the curve fit method.

C. Choose whether to display fit curve parameters to the user.
  - For organ-level curve fitting, these parameters are added to a results table.
  - For voxel-level curve fitting, parameter maps are generated and displayed on an additional results page.

D. Choose whether to fit absorbed dose rate maps instead of the SPECT or PET images. When this option is enabled, the order of operations changes to:
  1. SPECT or PET activity is converted to absorbed dose rate in units of Gy/s.
  2. The absorbed dose rate is used for curve fitting and time integration.
  3. The result of time-integration is the absorbed dose.

E. Choose whether to output residence times to the results table.

F. Choose whether to output residence times to a CSV. This exports residence times, administered activity, mass, and volume for all ROIs, which is what might be needed to run model-based dosimetry in a different system.

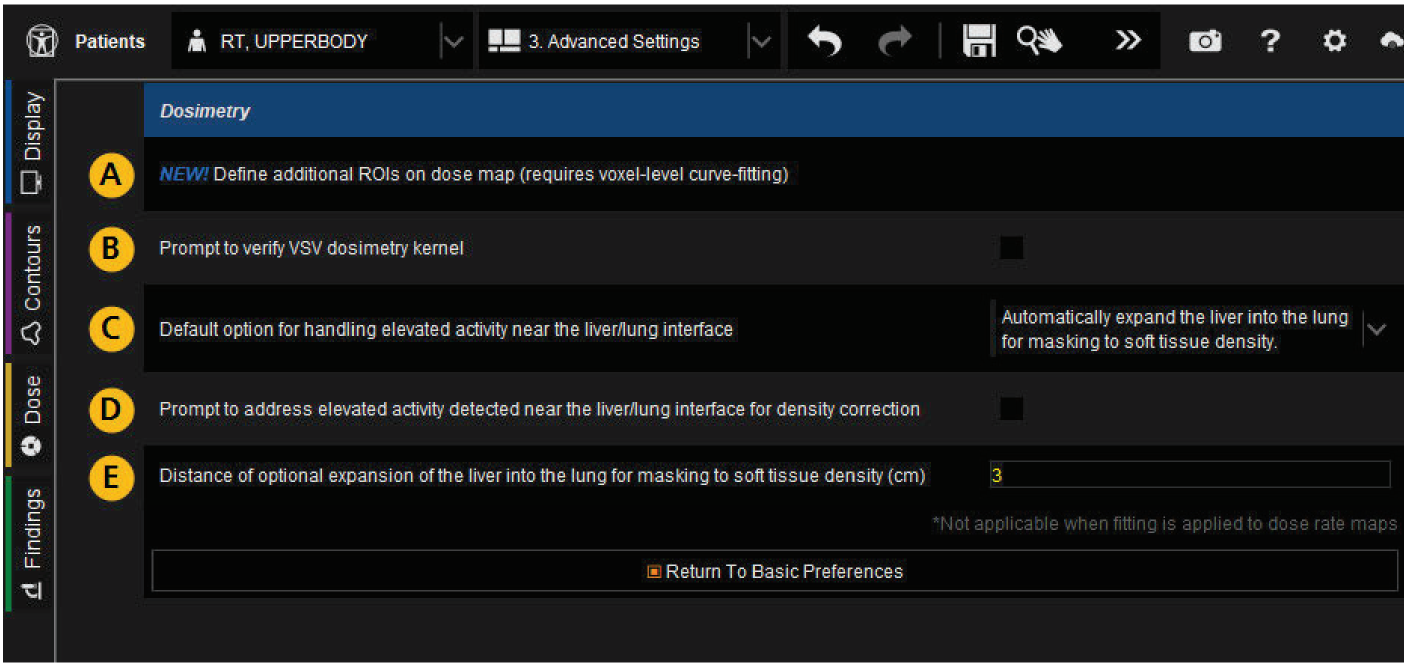
G. Set the file path for saving the CSV output times. If not configured, the user is prompted for a file name for the CSV.

H. Set the administered activity for calculating residence times.

I. Choose whether to calculate and output the percentages of interpolated activity for each organ or voxel. This informs the user about the percentage of the activity that comes from beyond the imaging time points (from injection time to the first time point and from the last time point to infinity). If this number is low, it could indicate that dosimetry results are unreliable.

J. Choose whether to output R^2. For organ-level curve fitting, the accuracy of the curve fit, R^2, is added to the results table for each ROI. A low or negative R^2 indicates an inaccurate curve fit, which may indicate that results are unreliable.

Dosimetry



Dosimetry

A NEW! Define additional ROIs on dose map (requires voxel-level curve-fitting)

B Prompt to verify VSV dosimetry kernel ☐

C Default option for handling elevated activity near the liver/lung interface: Automatically expand the liver into the lung for masking to soft tissue density.

D Prompt to address elevated activity detected near the liver/lung interface for density correction ☐

E Distance of optional expansion of the liver into the lung for masking to soft tissue density (cm): 3

*Not applicable when fitting is applied to dose rate maps

Return To Basic Preferences

A. *MIM 7.3 and later:* Choose whether to define additional structures on the dose map. Review takes place before final results are generated.
   - This setting requires voxel-level curve fitting.
   - Similar to the **Define additional ROIs after SPECT alignment** setting above, this setting can be used to bypass alignment for structures with low uptake. In addition, this setting allows the user to see absorbed dose results before choosing whether to draw additional ROIs.

   MIM 7.2 and earlier: This functionality is not available.
B. Choose whether to show the VSV dialog. When multiple dose kernels are installed for a single isotope, this setting can be enabled to allow the user to select which kernel to use.
C. Set the default option for handling elevated activity near the lung/liver interface. If elevated activity is detected (such as a tumor in the superior portion of the liver), the workflow can:
   - (Default) Apply a soft tissue density mask to a zone in the lung along the lung/liver interface for a more accurate absorbed dose value after density correction. Use the **Distance of optional expansion** setting (E) below to determine the size.
   - Make no adjustments.
   - Create a manual region for soft tissue masking.
   - Perform no density correction.
D. Choose whether to prompt the user to select how to handle elevated activity at the lung/liver interface. When this option is enabled, the workflow pauses for the user to review the flagged

activity before determining how it should be handled. When this option is disabled, the default behavior configured in the previous setting is always used.

E. Set the expansion (in cm) of the liver into the lung in order to mask for soft tissue density. This option applies when the default behavior configured in setting C above is to automatically expand the liver to apply a soft tissue density mask.

Settings for Dosimetry with 1 SPECT/CT and Serial Planar Imaging

MIMTD-1118 • 05 Jun 2024

Overview

These settings apply to the MRT: Dosimetry with 1 SPECT/CT and Serial Planar Imaging workflow.

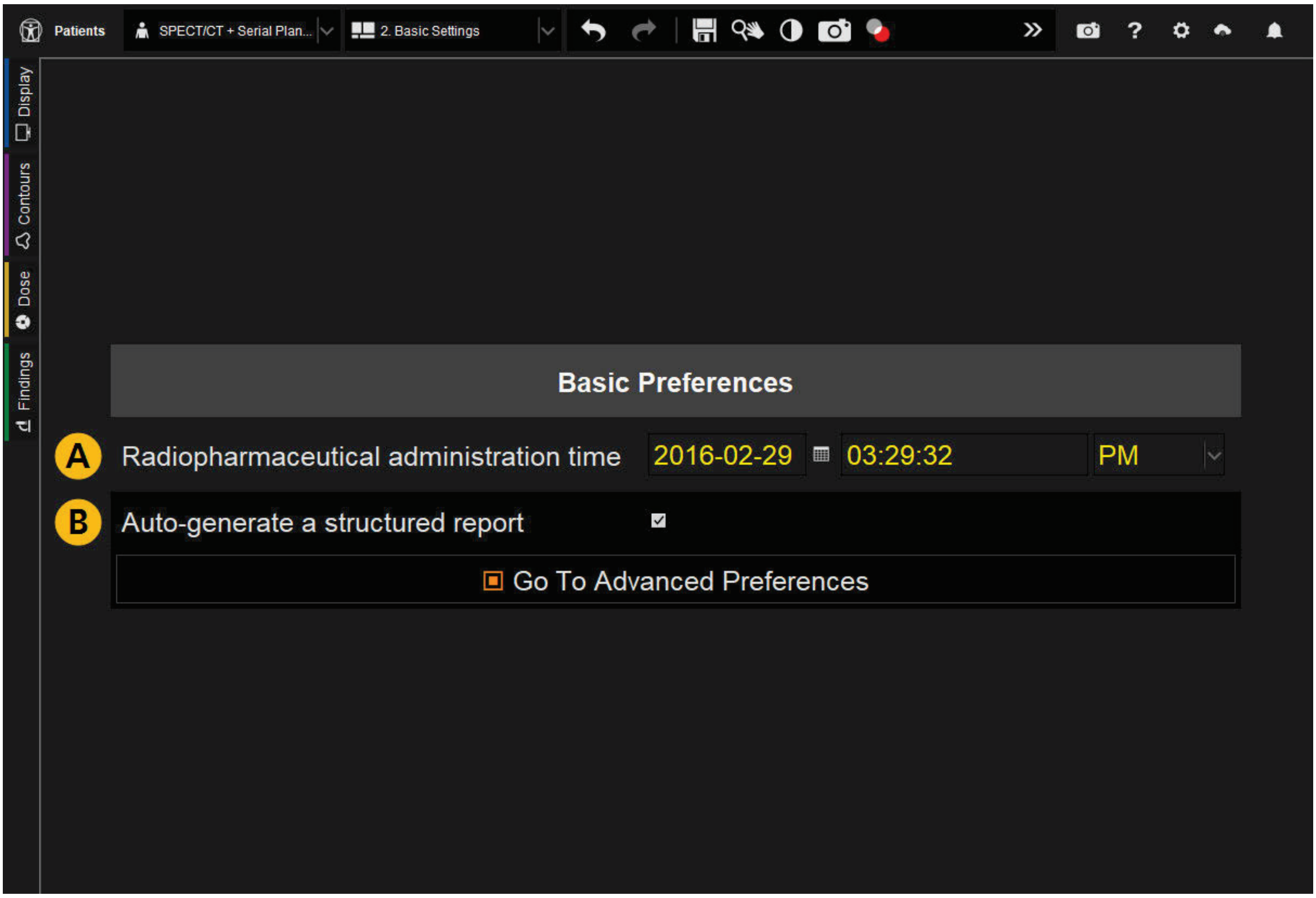
The user is prompted to review the **Basic Preferences** while running the workflow. Users can optionally click **Go To Advanced Preferences** to configure additional options.

> ☆ **Important:** Settings are not saved across sessions. Adjust these settings as needed each time that you run the workflow. If there are some settings that you want always to be used by default, contact MIM Software Support at support.mimsoftware.com for help modifying your workflow.

Contents

- Basic Preferences
- Advanced Preferences
  - General
  - Planar Corrections
  - Curve Fitting
  - Dosimetry

Basic Preferences



Basic Preferences

Radiopharmaceutical administration time 2016-02-29 03:29:32 PM

Auto-generate a structured report ☑

A. Adjust the radiopharmaceutical administration date and time. This is essential for dosimetry. The date and time are pulled from the DICOM data, if available.

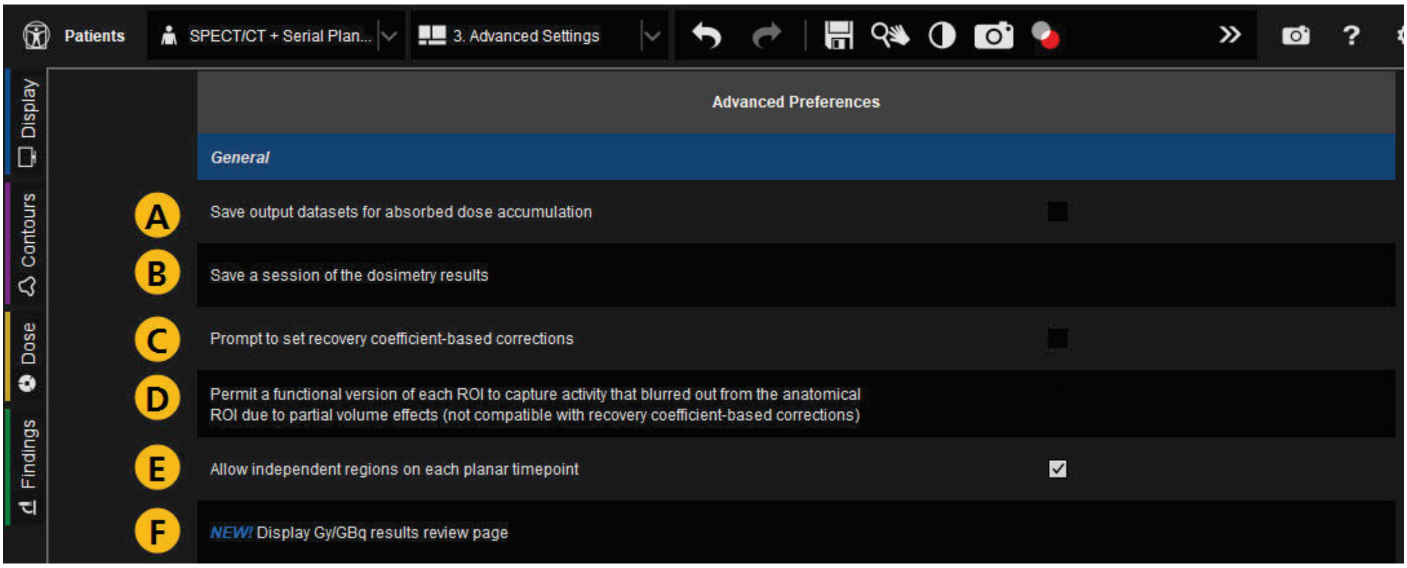
> **Tip:** The pre-populated date or time may be incorrect with retrospective data that may have been anonymized, or where only the time is stored without a date.

B. Choose whether to auto-generate a structured report. A structured report contains important session information and screenshots.

> **Related:** For more information about working with structured reports, see Create and Modify Structured Reports.

Advanced Preferences

General



Advanced Preferences

General

- A Save output datasets for absorbed dose accumulation ☐
- B Save a session of the dosimetry results
- C Prompt to set recovery coefficient-based corrections ☐
- D Permit a functional version of each ROI to capture activity that blurred out from the anatomical ROI due to partial volume effects (not compatible with recovery coefficient-based corrections)
- E Allow independent regions on each planar timepoint ☑
- F *NEW!* Display Gy/GBq results review page

A. Choose whether to save results needed for the Dose Accumulation workflow. Five outputs are saved:
   - Reference CT
   - Reference SPECT
   - TIA map
   - Dosimetry structures
   - Absorbed dose

B. Choose whether to save a session of the dosimetry results.

C. Choose whether to prompt the user to set recovery coefficient-based corrections.

Tip: Partial volume effects can cause activity within an ROI to be blurred outside of the anatomical volume. You can use this option or the next option to help correct for partial volume effects.

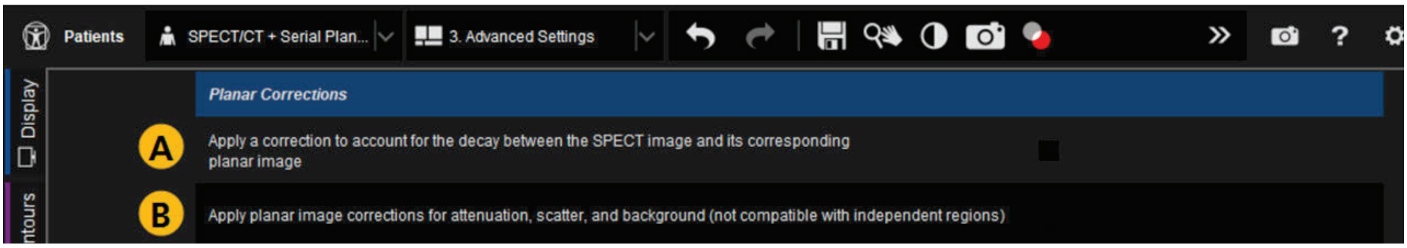
- This prompt allows the user to make changes to the recovery coefficient method during the workflow.
- When this option is enabled, an additional settings table appears to adjust recovery coefficient parameters after the SPECT alignment.

D. Choose whether to permit a functional version of each ROI.
   - This setting allows the user to define activity regions for each ROI to capture that activity and map it back to the anatomical volume.
   - This setting cannot be enabled if the recovery coefficient prompt (see above) is enabled.

E. Choose whether to allow independent regions on each time point. When planar corrections are disabled, the ROIs can be adjusted independently on each time point.

F. *MIM 7.3 and later:* Choose whether to display an interactive Gy/GBq results page. For more information about this page, refer to See Gy/GBq Results (MIM 7.3 and Later).
MIM 7.2 and earlier: This functionality is not available.

Planar Corrections



Planar Corrections

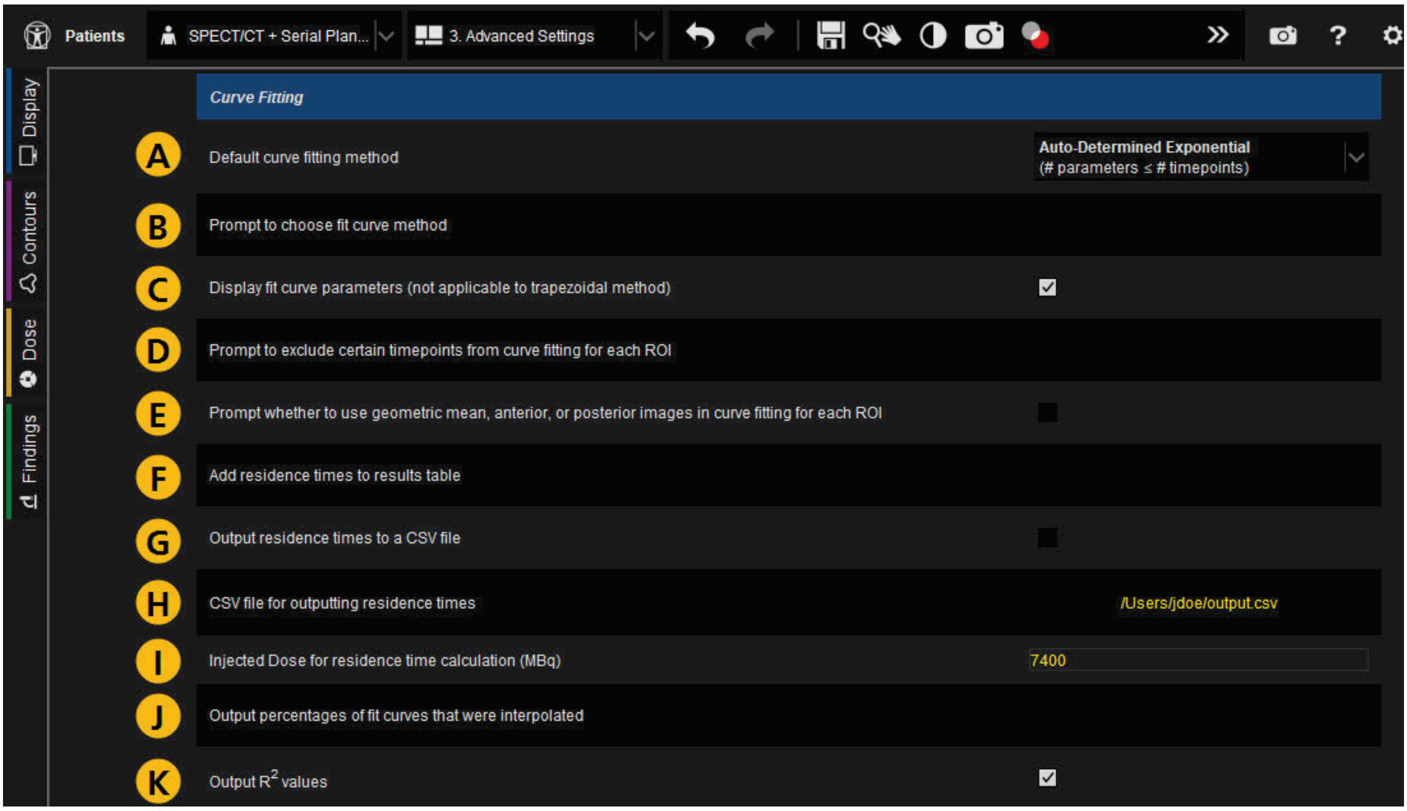
Apply a correction to account for the decay between the SPECT image and its corresponding planar image ☐

Apply planar image corrections for attenuation, scatter, and background (not compatible with independent regions)

A. Choose whether to correct for decay between the SPECT and reference planar series. Enable this preference if the reference planar is acquired more than 1 hour from the SPECT.

B. Choose whether to apply planar corrections.
   - This option applies corrections for attenuation, background, and scatter.
   - Using corrections requires scatter windows and an attenuation profile/attenuation map input.
   - Users are not able to edit independent contours per time point when this option is enabled.

Curve Fitting



Curve Fitting

A Default curve fitting method: Auto-Determined Exponential (# parameters ≤ # timepoints)

B Prompt to choose fit curve method

C Display fit curve parameters (not applicable to trapezoidal method) ☑

D Prompt to exclude certain timepoints from curve fitting for each ROI

E Prompt whether to use geometric mean, anterior, or posterior images in curve fitting for each ROI ☐

F Add residence times to results table

G Output residence times to a CSV file ☐

H CSV file for outputting residence times: /Users/jdoe/output.csv

I Injected Dose for residence time calculation (MBq): 7400

J Output percentages of fit curves that were interpolated

K Output R^2 values ☑

A. Set the default curve fitting method.

> **Related:** For more information, see the *Hybrid SPECT/Planar Dosimetry for Targeted Molecular Radiotherapy* white paper in the Appendix.

- Trapezoidal + Exponential for Extrapolation — Integration with exponential extrapolation
- Mono-exponential
- Bi-Exponential A — 4-parameter Bi-exponential
- Bi-Exponential B — 3-parameter Bi-exponential assuming 0 activity at t = 0
- Auto-Determined Exponential (# parameters ≤ # timepoints) — Fit model is optimized per voxel or ROI, selected from the available exponential models. The number of parameters is limited to the number of time points.
- Auto-Determined Exponential (# parameters ≤ # timepoints - 1) — Fit model is optimized per voxel or ROI, selected from the available exponential models. The number of parameters is limited to 1 less than the number of time points

B. Choose whether the user is prompted to select the curve fit method.

C. Choose whether to display fit curve parameters in the results table.

D. Choose whether to prompt the user to select time points to remove from curve fitting per ROI.

  - This prompt allows users to review and remove unwanted time points for specific ROIs. For example, a user could remove a time point if there is significant activity from nearby structures overlapping with the ROI on that particular time point.
  - The workflow ensures that each ROI has at least two time points.

E. Choose whether to prompt the user to select which image to use for curve fitting per ROI. This can be useful if some structures have better imaging qualities or less overlapping activity from nearby structures on the anterior or posterior image. For each ROI, users are prompted to select from the following images:

  - Geometric mean
  - Anterior
  - Posterior

F. Choose whether to output residence times to the results table. This setting is not applicable when fitting is applied to dose rate maps.

G. Choose whether to output residence times to a CSV. This exports residence times, administered activity, mass, and volume for all ROIs, which is what might be needed to run model-based dosimetry in a different system.

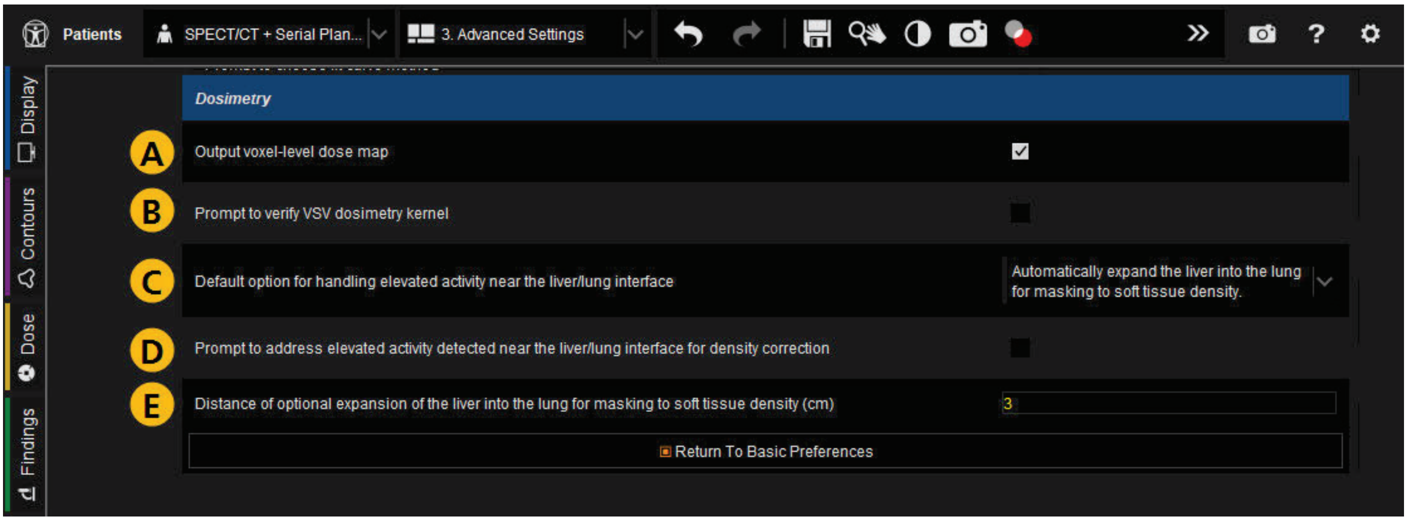
H. Set the file path for saving the CSV output times. If not configured, the user is prompted for a file name for the CSV.

I. Set the administered activity for calculating residence times.

J. Choose whether to calculate and output the percentages of interpolated activity for each organ or voxel. This informs the user about the percentage of the activity that comes from beyond the imaging time points (from injection time to the first time point and from the last time point to infinity). If this number is low, it could indicate that dosimetry results are unreliable.

K. Choose whether to output R^2. For organ-level curve fitting, the accuracy of the curve fit, R^2, is added to the results table for each ROI. A low or negative R^2 indicates an inaccurate curve fit, which may indicate that results are unreliable.

Dosimetry



Dosimetry

Output voxel-level dose map ☑

Prompt to verify VSV dosimetry kernel ☐

Default option for handling elevated activity near the liver/lung interface: Automatically expand the liver into the lung for masking to soft tissue density.

Prompt to address elevated activity detected near the liver/lung interface for density correction ☐

Distance of optional expansion of the liver into the lung for masking to soft tissue density (cm): 3

A. Choose whether to output a voxel-level dose map.
   - SPECT activity distribution is preserved and used to calculate voxel-level dose results.
   - Final outputs include a DVH and dose map in addition to mean doses per ROI.

B. Choose whether to show the VSV dialog. When multiple dose kernels are installed for a single isotope, this setting can be enabled to allow the user to select which kernel to use.

C. Set the default option for handling elevated activity near the lung/liver interface. If elevated activity is detected (such as a tumor in the superior portion of the liver), the workflow can:
   - (Default) Apply a soft tissue density mask to a zone in the lung along the lung/liver interface for a more accurate absorbed dose value after density correction. Use the **Distance of optional expansion** setting (E) below to determine the size.
   - Make no adjustments.
   - Create a manual region for soft tissue masking.
   - Perform no density correction.

D. Choose whether to prompt the user to select how to handle elevated activity at the lung/liver interface. When this option is enabled, the workflow pauses for the user to review the flagged activity before determining how it should be handled. When this option is disabled, the default behavior configured in the previous setting is always used.

E. Set the expansion (in cm) of the liver into the lung in order to mask for soft tissue density. This option applies when the default behavior configured in setting C above is to automatically expand the liver to apply a soft tissue density mask.

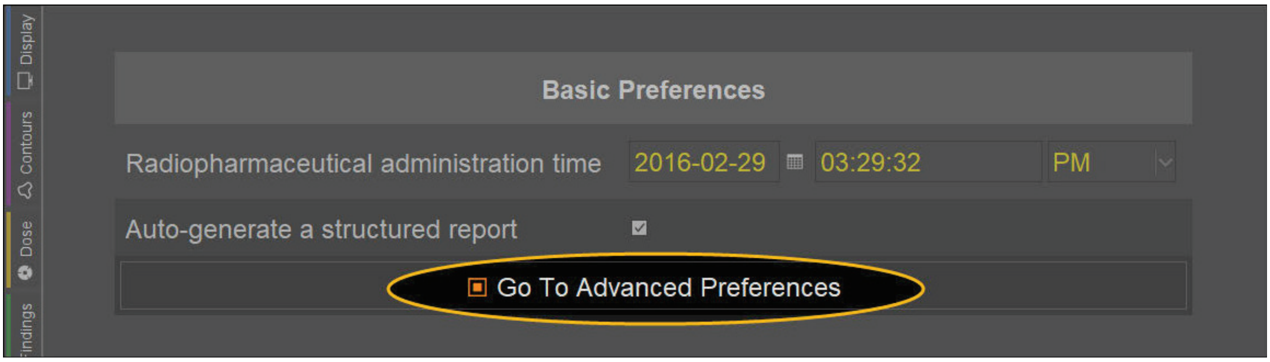
Settings for Dosimetry with 1 SPECT/CT

MIMTD-1119 • 05 Jun 2024

Overview

These settings apply to both MRT: Dosimetry with 1 SPECT/CT (Hänscheid Method) and MRT: Dosimetry with 1 SPECT/CT (Prior Information Approach).

The user is prompted to review the **Basic Preferences** while running the workflow. Users can optionally click **Go To Advanced Preferences** to configure additional options.



Basic Preferences

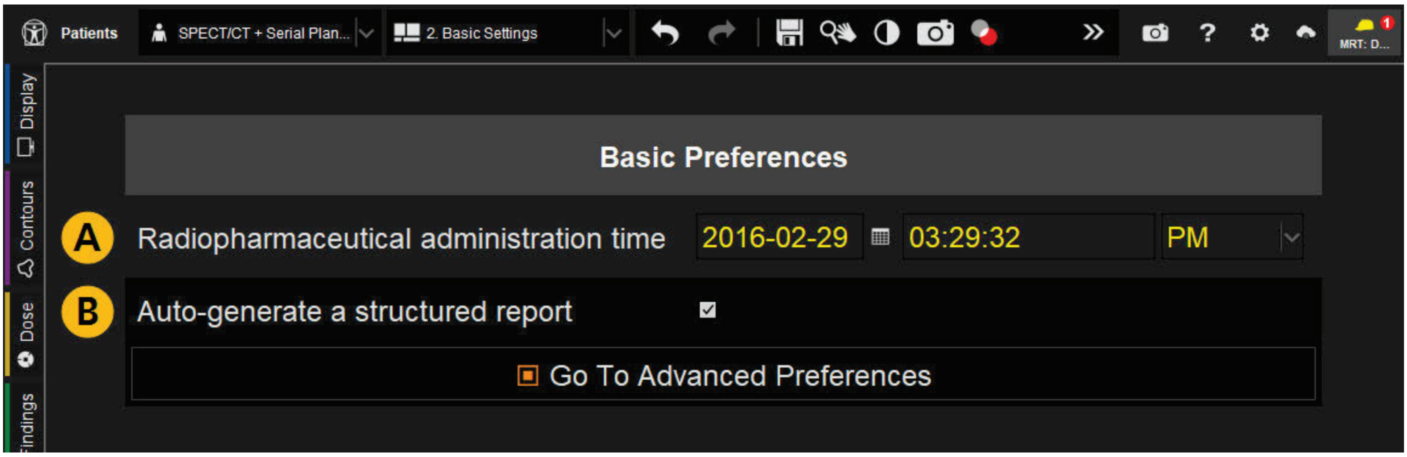
Radiopharmaceutical administration time: 2016-02-29 03:29:32 PM

Auto-generate a structured report ☑

Important: Settings are not saved across sessions. Adjust these settings as needed each time that you run the workflow. If there are some settings that you want always to be used by default, contact MIM Software Support at support.mimsoftware.com for help modifying your workflow.

Contents

Basic Preferences



Basic Preferences

A Radiopharmaceutical administration time 2016-02-29 03:29:32 PM

B Auto-generate a structured report ☑

Go To Advanced Preferences

A. Adjust the radiopharmaceutical administration date and time. This is essential for dosimetry. The date and time are pulled from the DICOM data, if available.

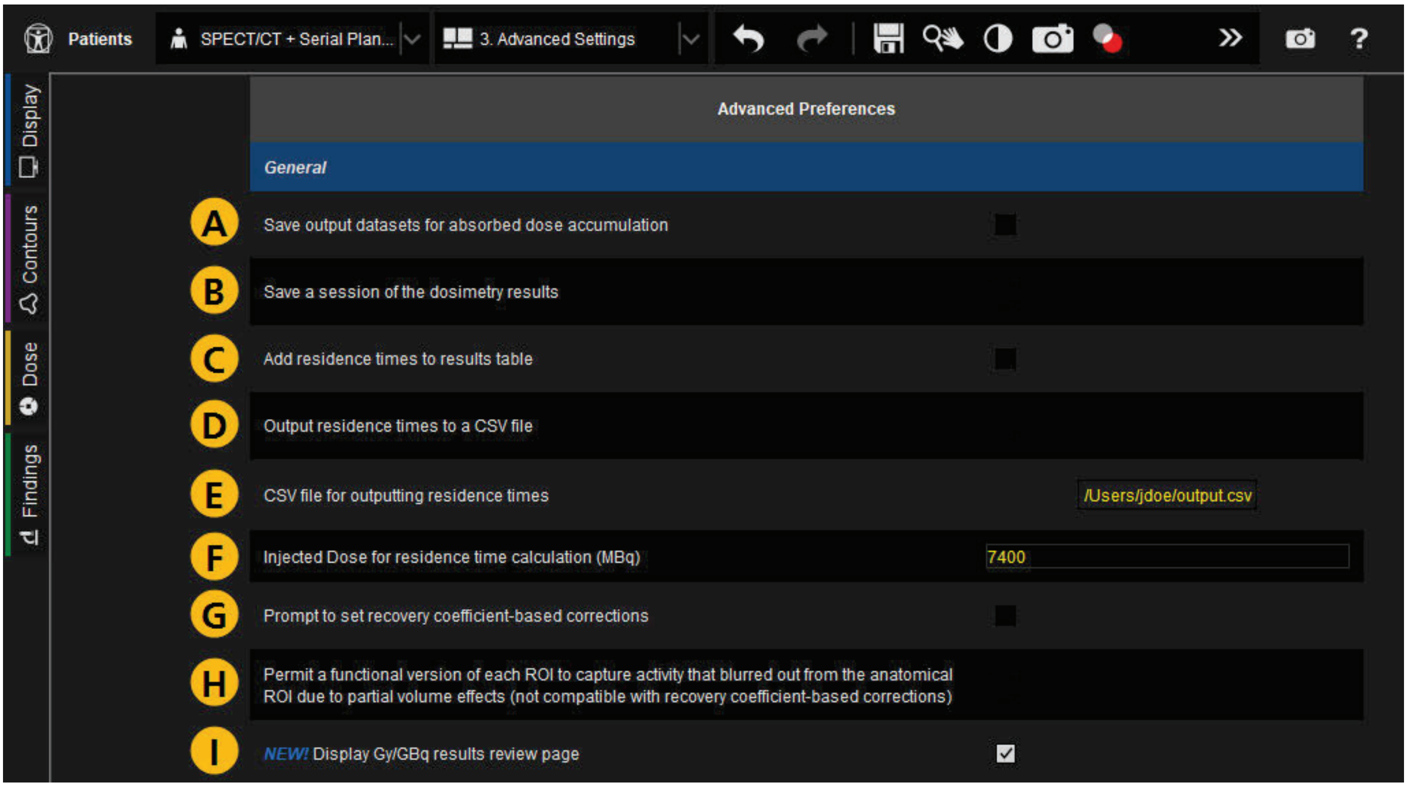
> **Tip:** The pre-populated date or time may be incorrect with retrospective data that may have been anonymized, or where only the time is stored without a date.

B. Choose whether to auto-generate a structured report. A structured report contains important session information and screenshots.

> **Related:** For more information about working with structured reports, see Create and Modify Structured Reports.

Advanced Preferences

General



Advanced Preferences

General

A Save output datasets for absorbed dose accumulation ☐

B Save a session of the dosimetry results

C Add residence times to results table ☐

D Output residence times to a CSV file

E CSV file for outputting residence times /Users/jdoe/output.csv

F Injected Dose for residence time calculation (MBq) 7400

G Prompt to set recovery coefficient-based corrections ☐

H Permit a functional version of each ROI to capture activity that blurred out from the anatomical ROI due to partial volume effects (not compatible with recovery coefficient-based corrections)

I *NEW!* Display Gy/GBq results review page ☑

A. Choose whether to save results needed for the Dose Accumulation workflow. Five outputs are saved:
   - Reference CT
   - Reference SPECT
   - TIA map
   - Dosimetry structures
   - Absorbed dose
B. Choose whether to save a session of the dosimetry results.
C. Choose whether to output residence times to the results table. This setting is not applicable when fitting is applied to dose rate maps.
D. Choose whether to output residence times to a CSV file. This exports residence times, administered activity, mass, and volume for all ROIs, which is what might be needed to run model-based dosimetry in a different system.
E. Set the file path for saving the CSV output times. If not configured, the user is prompted for a file name for the CSV.

F. Set the administered activity for calculating residence times. This setting is not applicable when fitting is applied to dose rate maps.

G. Choose whether to prompt the user to set recovery coefficient-based corrections.

> **Tip:** Partial volume effects can cause activity within an ROI to be blurred outside of the anatomical volume. You can use this option or the next option to help correct for partial volume effects.

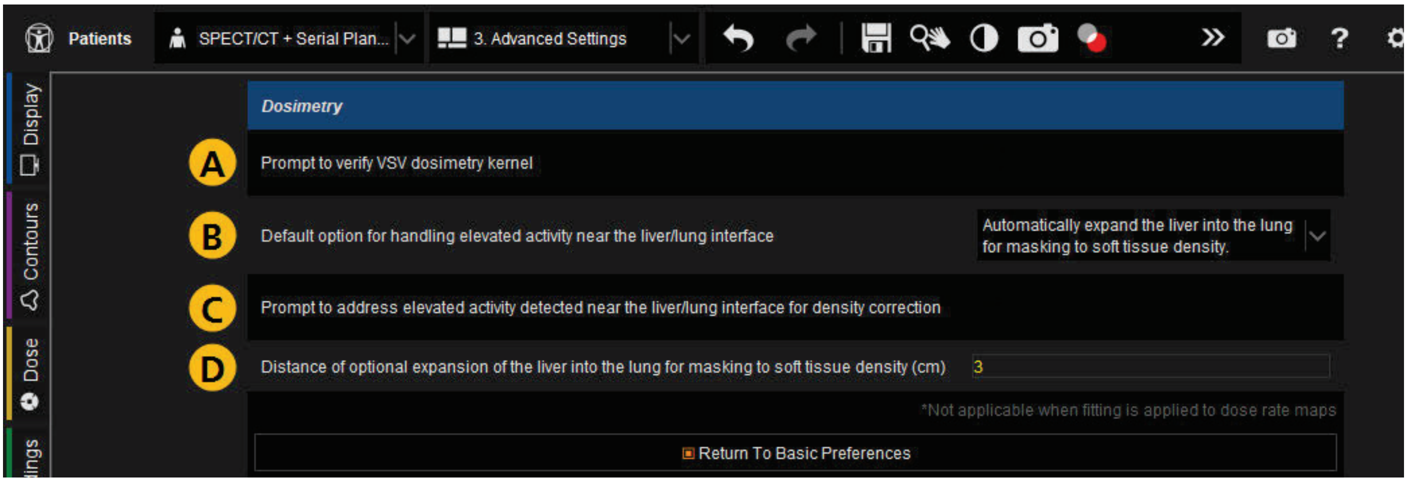
- This prompt allows the user to make changes to the recovery coefficient method during the workflow.
- When this option is enabled, an additional settings table appears to adjust recovery coefficient parameters after the SPECT alignment.

H. Choose whether to permit a functional version of each ROI.

- This setting allows the user to define activity regions for each ROI to capture that activity and map it back to the anatomical volume.
- This setting cannot be enabled if the recovery coefficient prompt (see above) is enabled.

I. *MIM 7.3 and later:* Choose whether to display an interactive Gy/GBq results page. For more information about this page, refer to the workflow information.
MIM 7.2 and earlier: This functionality is not available

Dosimetry



Dosimetry

Prompt to verify VSV dosimetry kernel

Default option for handling elevated activity near the liver/lung interface: Automatically expand the liver into the lung for masking to soft tissue density.

Prompt to address elevated activity detected near the liver/lung interface for density correction

Distance of optional expansion of the liver into the lung for masking to soft tissue density (cm): 3

*Not applicable when fitting is applied to dose rate maps

A. Choose whether to show the VSV dialog. When multiple dose kernels are installed for a single isotope, this setting can be enabled to allow the user to select which kernel to use.

B. Set the default option for handling elevated activity near the lung/liver interface. If elevated activity is detected (such as a tumor in the superior portion of the liver), the workflow can:

- (Default) Apply a soft tissue density mask to a zone in the lung along the lung/liver interface for a more accurate absorbed dose value after density correction. Use the **Distance of optional expansion** setting (D) below to determine the size.
- Make no adjustments.
- Create a manual region for soft tissue masking.
- Perform no density correction.

C. Choose whether to prompt the user to select how to handle elevated activity at the lung/liver interface. When this option is enabled, the workflow pauses for the user to review the flagged activity before determining how it should be handled. When this option is disabled, the default behavior configured in the previous setting is always used.

D. Set the expansion (in cm) of the liver into the lung in order to mask for soft tissue density. This option applies when the default behavior configured in setting C above is to automatically expand the liver to apply a soft tissue density mask.

Work with Dose in MIM

Calculate Absorbed Dose Accumulation

MIMTD-1926 • 04 Jun 2024

Overview

After completing a dosimetry workflow, use the **MRT: Absorbed Dose Accumulation** workflow to calculate absorbed dose across treatment cycles.

This workflow can run automatically with MIM Assistant®. Contact your MIM® representative if you would like to automate this workflow. Skip to Review Results below for more information about the workflow output.

If you need to run the workflow manually, follow the Run the Workflow steps below.

Contents

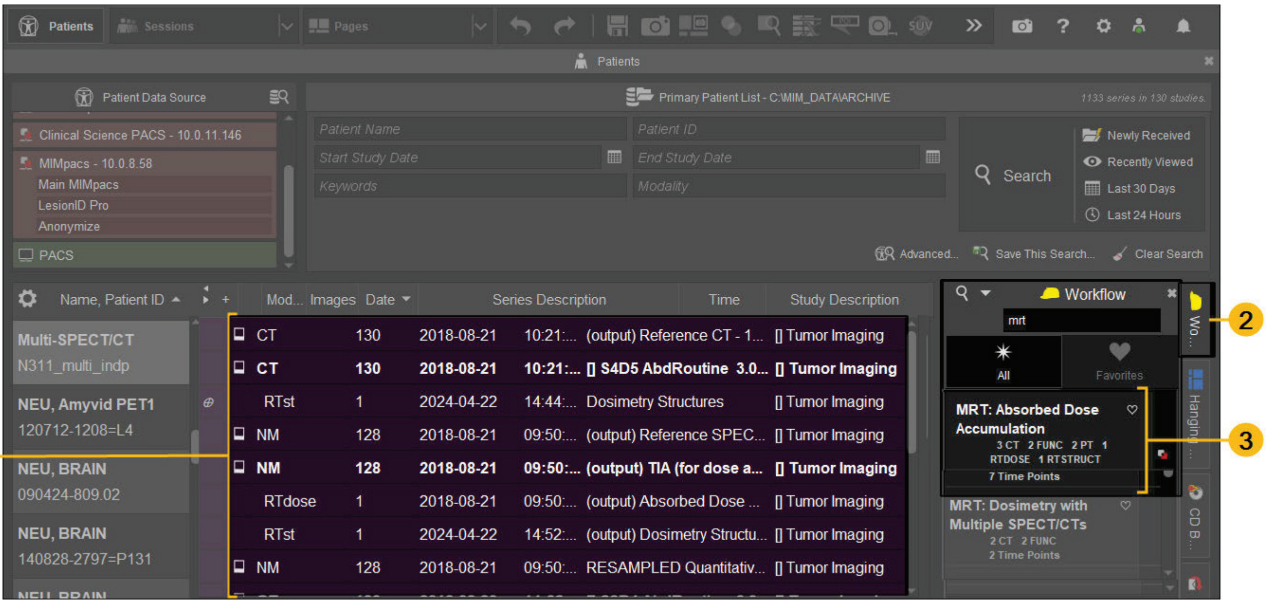
Run the Workflow

1. From the patient list, select the output series created by the dosimetry workflow for each treatment cycle. Depending on your organization's setup, these output series may be saved to a different patient list. Select the following:
    - (output) Reference CT
    - (output) Reference SPECT
    - (output) TIA
    - (output) Absorbed Dose Map
    - (output) Dosimetry Structures (dose map)
    - *Optional:* Pre-therapy PET/CT
    - *Optional:* Post-therapy PET/CT

    Tip: To select multiple series, press and hold the Ctrl key. Or, click and drag down to select the list of series.

Tip: If needed, you can search for the series using the keyword "**output**", which the dosimetry workflows automatically prepend to the series description.

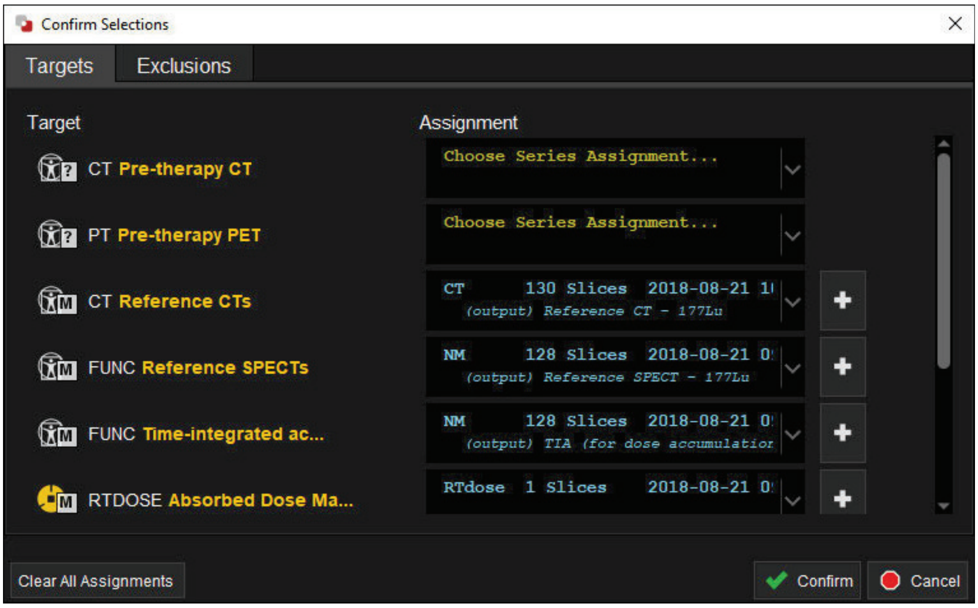
2. Select the **Workflow** tab in the patient list to expand it.
3. Double-click the **MRT: Absorbed Dose Accumulation** workflow from the list to launch it.



Mod...	Images	Date	Series Description	Time	Study Description
CT	130	2018-08-21	(output) Reference CT - 1...	10:21:...	[] Tumor Imaging
CT	**130**	**2018-08-21**	**[] S4D5 AbdRoutine 3.0...**	**10:21:...**	**[] Tumor Imaging**
RTst	1	2024-04-22	Dosimetry Structures	14:44:...	[] Tumor Imaging
NM	128	2018-08-21	(output) Reference SPEC...	09:50:...	[] Tumor Imaging
NM	**128**	**2018-08-21**	**(output) TIA (for dose a...**	**09:50:...**	**[] Tumor Imaging**
RTdose	1	2018-08-21	(output) Absorbed Dose ...	09:50:...	[] Tumor Imaging
RTst	1	2024-04-22	(output) Dosimetry Structu...	14:52:...	[] Tumor Imaging
NM	128	2018-08-21	RESAMPLED Quantitativ...	09:50:...	[] Tumor Imaging

4. In the target confirmation window, verify that the series you selected are listed for the appropriate targets. If needed, click the plus ➕ button to add a series or the minus ➖ button to remove a series.

Click **Confirm**.


Confirm Selections

Target	Assignment
CT **Pre-therapy CT**	Choose Series Assignment...
PT **Pre-therapy PET**	Choose Series Assignment...
CT **Reference CTs**	CT 130 Slices 2018-08-21 1 (output) Reference CT - 177Lu
FUNC **Reference SPECTs**	NM 128 Slices 2018-08-21 0 (output) Reference SPECT - 177Lu
FUNC **Time-integrated ac...**	NM 128 Slices 2018-08-21 0 (output) TIA (for dose accumulatior
RTDOSE **Absorbed Dose Ma...**	RTdose 1 Slices 2018-08-21 0

5. The workflow runs automatically and produces the results. The session is automatically saved to your patient list.

Review Results

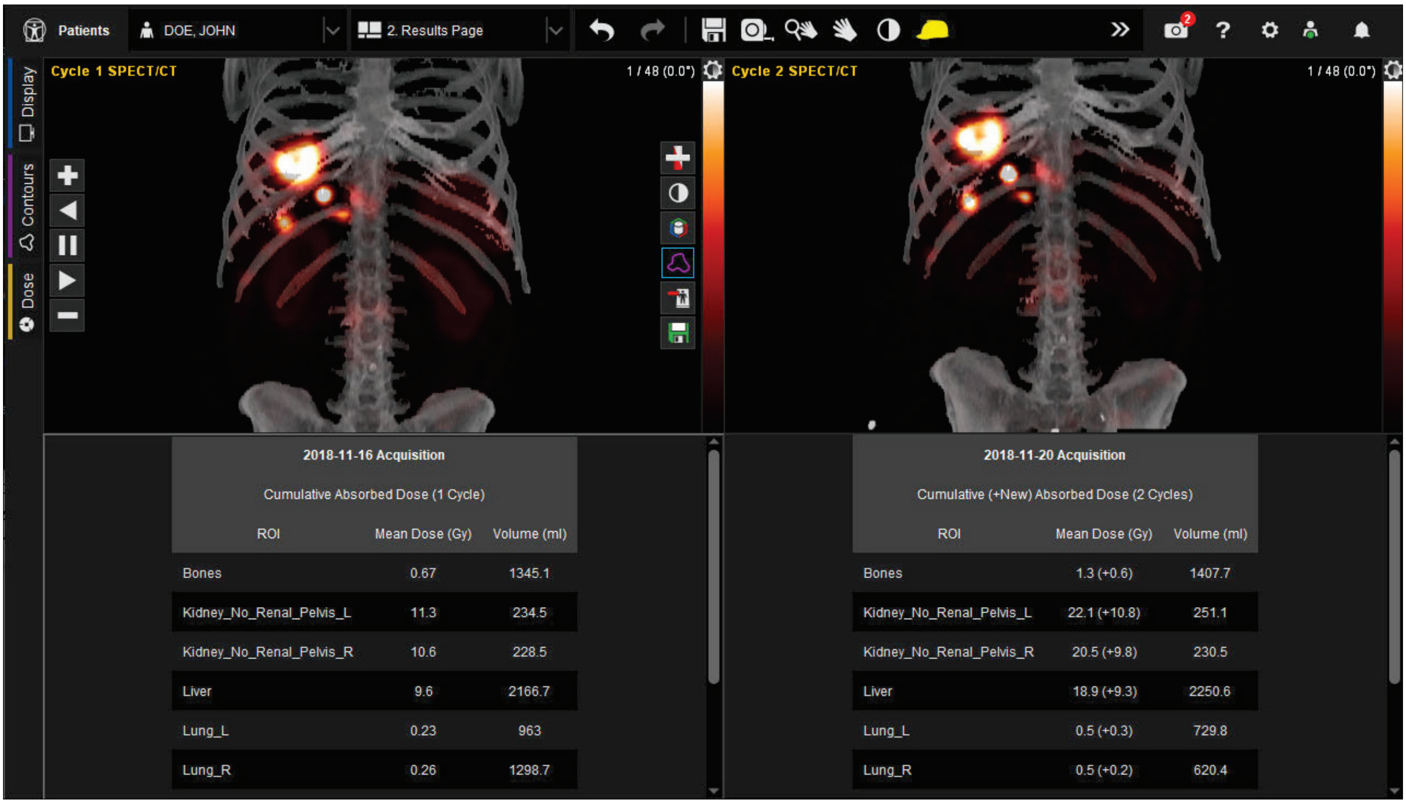
The workflow completes and generates several results pages. Use the left and right arrow keys or page dropdown in the top toolbar to move between pages and review results.

Dose Results

The results page shows the cumulative absorbed dose for each contour for each treatment cycle.

Subsequent treatment cycles show the cumulative absorbed dose as well as the additional dose for that treatment cycle (shown in parentheses).

> **Tip:** Use the play controls on the left side of the viewport to rotate the MIP.



2018-11-16 Acquisition

Cumulative Absorbed Dose (1 Cycle)

ROI	Mean Dose (Gy)	Volume (ml)
Bones	0.67	1345.1
Kidney_No_Renal_Pelvis_L	11.3	234.5
Kidney_No_Renal_Pelvis_R	10.6	228.5
Liver	9.6	2166.7
Lung_L	0.23	963
Lung_R	0.26	1298.7

2018-11-20 Acquisition

Cumulative (+New) Absorbed Dose (2 Cycles)

ROI	Mean Dose (Gy)	Volume (ml)
Bones	1.3 (+0.6)	1407.7
Kidney_No_Renal_Pelvis_L	22.1 (+10.8)	251.1
Kidney_No_Renal_Pelvis_R	20.5 (+9.8)	230.5
Liver	18.9 (+9.3)	2250.6
Lung_L	0.5 (+0.3)	729.8
Lung_R	0.5 (+0.2)	620.4

Example of absorbed dose accumulation results for two treatment cycles.

Dose Map Results

The dose maps page shows the same cumulative absorbed dose per contour as the results page, alongside the time-integrated activity (TIA) maps.

2018-11-20 Acquisition

Cumulative (+New) Absorbed Dose (2 Cycles)

ROI	Mean Dose (Gy)	Volume (ml)
Bones	1.3 (+0.6)	1407.7
Kidney_No_Renal_Pelvis_L	22.1 (+10.8)	251.1
Kidney_No_Renal_Pelvis_R	20.5 (+9.8)	230.5
Liver	18.9 (+9.3)	2250.6
Lung_L	0.5 (+0.3)	729.8
Lung_R	0.5 (+0.2)	620.4
Spleen	27.6 (+14.3)	235.7
FOV Body	2.9 (+1.5)	32452.7
FOV Rest of Body	1.3 (+0.6)	26726.8
Lungs	0.5 (+0.2)	1350.2

Example of absorbed dose accumulation results with TIA maps.

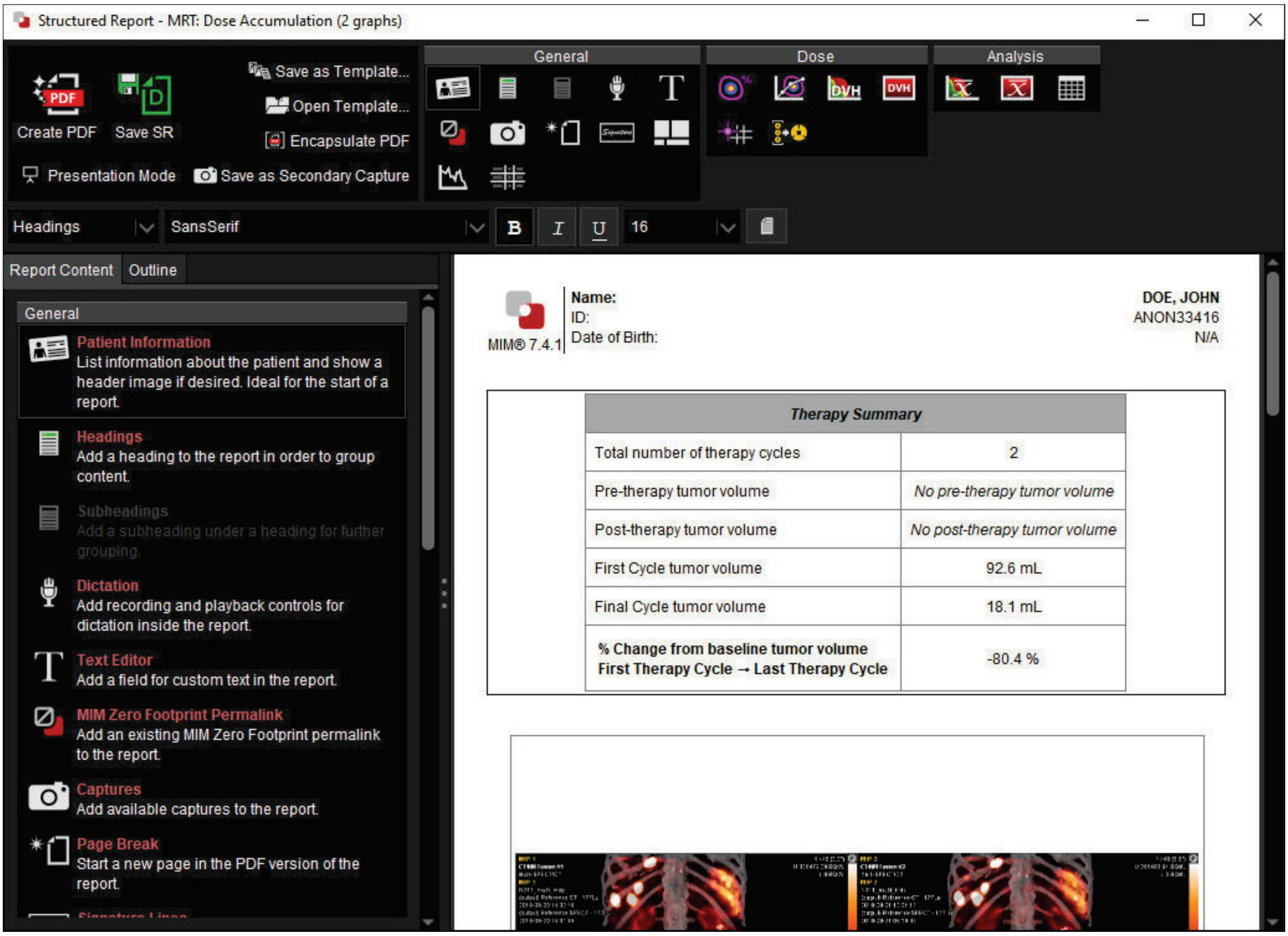
Tip: Right-click on the results table to copy it to your clipboard or save the results as a CSV file.

Tip: If tumor segmentation is included, there is also a Volume Progression page that shows the tumor volume for each treatment cycle.

Structured Report

The workflow automatically generates a structured report. As needed, update the report information. For example, on the Report Content tab, add a Text Editor field and type additional notes in the report.

Related: Refer to Create and Modify Structured Reportsfor more information about working with structured reports.



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.

Text Editor
Add a field for custom text in the report.

MIM Zero Footprint Permalink
Add an existing MIM Zero Footprint permalink to the report.

Captures
Add available captures to the report.

Page Break
Start a new page in the PDF version of the report.

Signature Lines

Name: DOE, JOHN
ID: ANON33416
Date of Birth: N/A

Therapy Summary	
Total number of therapy cycles	2
Pre-therapy tumor volume	*No pre-therapy tumor volume*
Post-therapy tumor volume	*No post-therapy tumor volume*
First Cycle tumor volume	92.6 mL
Final Cycle tumor volume	18.1 mL
% Change from baseline tumor volume **First Therapy Cycle → Last Therapy Cycle**	-80.4 %

When you are finished, save the structured report as a PDF or as a DICOM object (SR).

View Dose in MIM®: Fundamentals

MIMTD-662 • 16 Jan 2024

Overview

MIM is a vendor-neutral solution. You can load, display, and sum dose files from any other system or TPS. This topic covers the basics of how MIM displays dose. For more detailed information on working with multiple doses, please see Work with Multiple Doses.

Contents

Set Up Dose and Isodose Preferences

Change Dose Units

By default, MIM displays dose values in Gy. If desired, you can adjust MIM to display doses in cGy.

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

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. In the Settings menu, select **General Preferences**.
3. In the General Preferences window, search for "**dose**" and select **Dose** from the menu on the left side of the window.
4. On the dose page, change the **Default Dose Unit** to **cGy**.
5. Click **Apply**.
6. Restart MIM for the change to take effect.

Create, Edit, and Save Isodose Settings

You can create and save both percentage-based and absolute-value-based isodose settings in MIM. To create, edit, or save isodose settings, follow these steps:

1. Open an RTdose in a session. You can use any dose; it does not matter what the dose value or type is.
2. Open the **Dose** sidebar on the left side of the screen.
3. Make adjustments to the isodose lines at the top of the sidebar.

Tip: After making adjustments to isodose settings, the setting name is displayed with an * to indicate that it has been changed.