

Example: A registration between an image and an identical image, rotated 10 degrees along the z-axis can have a Pearson correlation coefficient above 0.7, but is clearly a poor registration.

- A Pearson correlation coefficient score above 0.95 or below -0.95 usually indicates a good fusion, but results can differ depending on image quality and modality.


Root Mean Square Difference

- Measures the average difference in intensity between two images.
- Is usually used to compare two images of the same modality. The root mean square difference has the same units as the image intensities. If the two images are not in the same modality, the root mean square difference may not have a clear meaning.
- Lower root mean square differences are better.

Analyze Fusion Alignment


The Analyze Fusion Alignment tool provides detailed information about the fusion alignment.

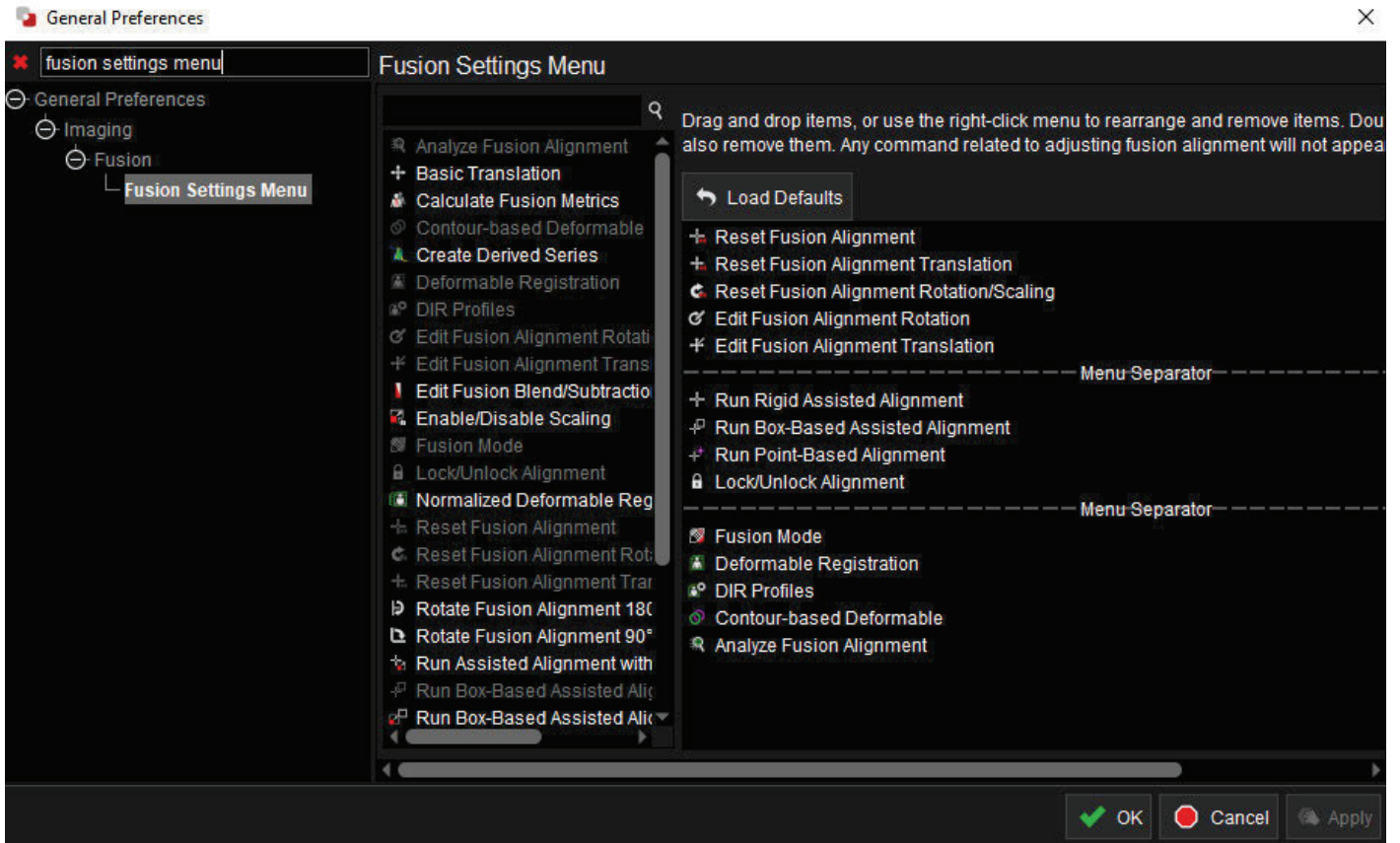
To view a fusion alignment analysis follow these steps:

1. Click the  button at the top of MIM to search all tools.
2. Type "**analyze fusion alignment**" in the search bar.
3. Select **Analyze Fusion Alignment** from the list of tools.
4. If desired, use the dropdown menus at the top of the Fusion Alignment Analysis window to change the coordinate system for the analysis or the direction the parameters are reported in (primary to secondary or secondary to primary).

Add Quantitative Analysis Tools to Your Fusion Settings Menu

If you use the Calculate Fusion Metrics tool or the Analyze Fusion Alignment tool regularly, you can add them to your fusion settings menu for easy access.

1. Click the Settings  button in the upper-right corner of MIM.
2. Select **General Preferences**.
3. In the General Preferences search bar, type "**fusion settings menu**". Click **Fusion Settings Menu** on the left side.
4. On the Fusion Settings Menu page, drag tools from the list on the left to the menu preview on the right.
5. Click **Apply** to save changes.



Configure Fusion Settings

MIMTD-1725 • 05 Oct 2023

Overview

Adjust fusion settings to increase the usability of fusion tools, access different fusion modes, and create seamless integration between MIM® and other systems.




Related: For information about adjusting image alignment, see [Adjust Fusions Manually](#) and [Optimize Fusions Automatically](#).

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- [Update the Fusion Settings Menu](#)
- [Adjust the Default Fusion Transparency](#)
- [Adjust the Fusion Blend Scale](#)
- [Show/Hide the Fusion Companion Tools](#)

Update the Fusion Settings Menu




Click the gear  button on the right side of a fusion viewport to open the **Fusion Settings Menu**, where you have a variety of automatic and manual alignment methods. Use an automatic method to optimize your fusion, then use the manual tools for additional refinement if desired.

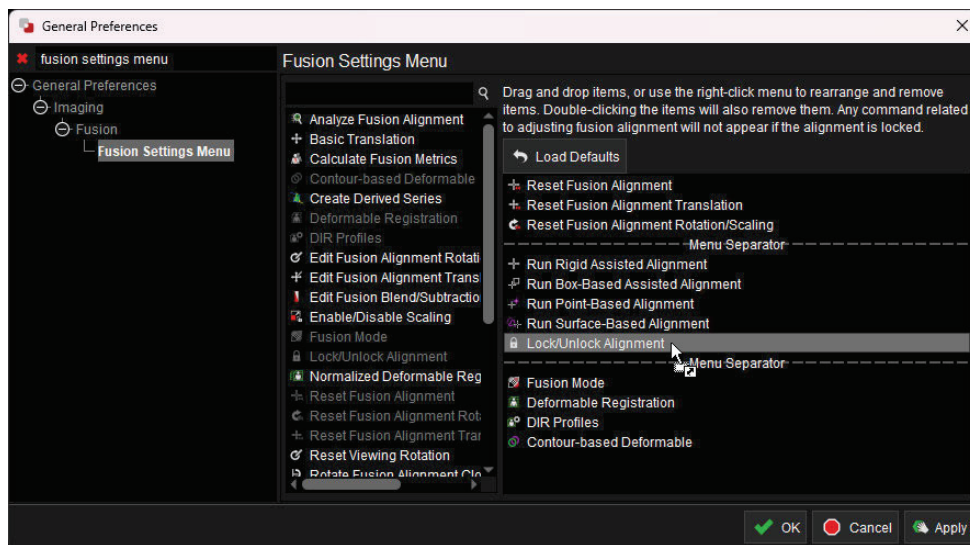


Related: For more information about manual adjustment tools, see [Adjust Fusions Manually](#).

Add to and organize the list of fusion optimization tools in the **Fusion Settings** menu:


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


3. Drag tools from the left menu to the right menu.

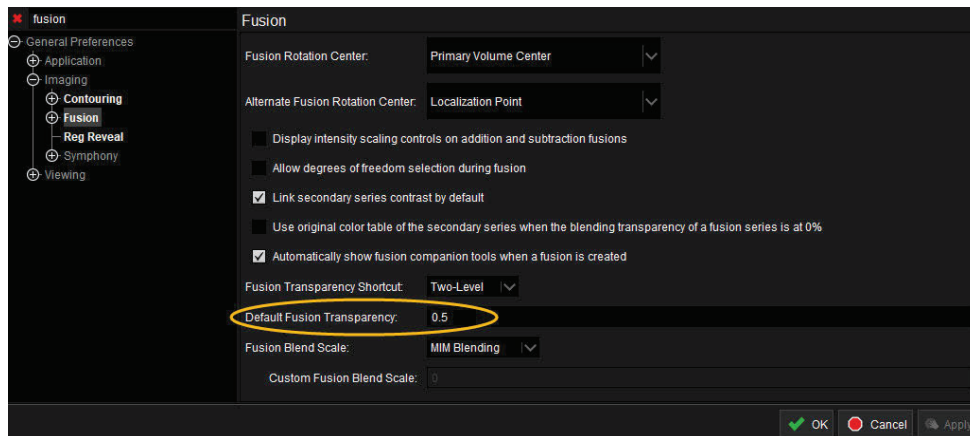


4. Click **OK** to save the changes and close the window.

Adjust the Default Fusion Transparency

When fusions are created, the default fusion transparency provides an equal display of both primary and secondary images. Make manual adjustment using the **Blend**  tool (see [Adjust Fusions Manually](#) for more information). To adjust the default transparency, follow these steps:

1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**fusion transparency**". Select **Fusion** on the left side.
3. Adjust the **Default Fusion Transparency** field to a value between 0 and 1.
 - 0 indicates 0% transparency, which means the secondary series is fully opaque. The primary series is not visible.
 - 1 indicates 100% transparency, which means the secondary series is fully transparent. Only the primary series is visible.




4. Click **OK**.



Tip: When changed, this setting will take effect beginning with the next-created fusion.

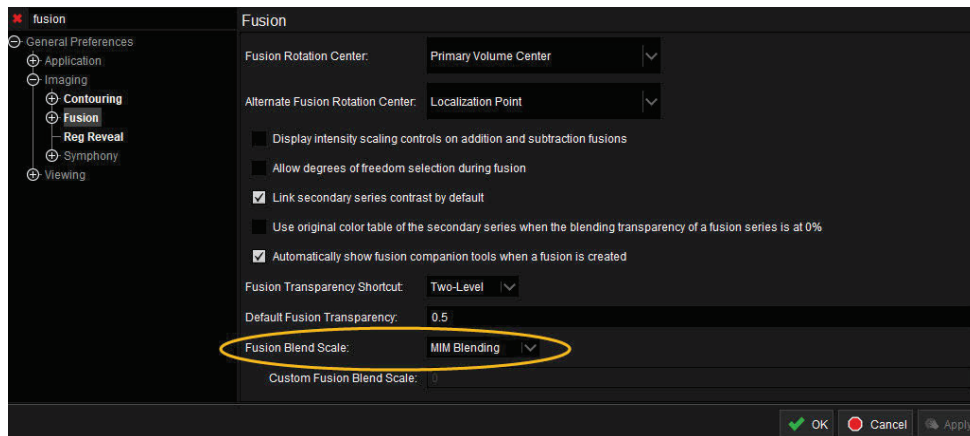
Adjust the Fusion Blend Scale

MIM uses a scaled blending algorithm in its fusions that affects the brightness of the image display. The scale is determined by the **Fusion Blend Scale** preference. This preference can be adjusted to let you to see more detail in lower values on the fusion and to more closely match the output of a third-party system.

1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**fusion blend**". Select **Fusion** on the left side.
3. Adjust the **Fusion Blend Scale** dropdown:
 - **MIM Blending** works well in fusions where the secondary color table goes from dark to bright. A good example is the Hot Metal color table option.
 - **Linear Blending** tends to more closely match the output of third-party systems.
 - **Custom** can be a value between 0 (linear blending) and 1 (MIM blending) to find a value that suits you.

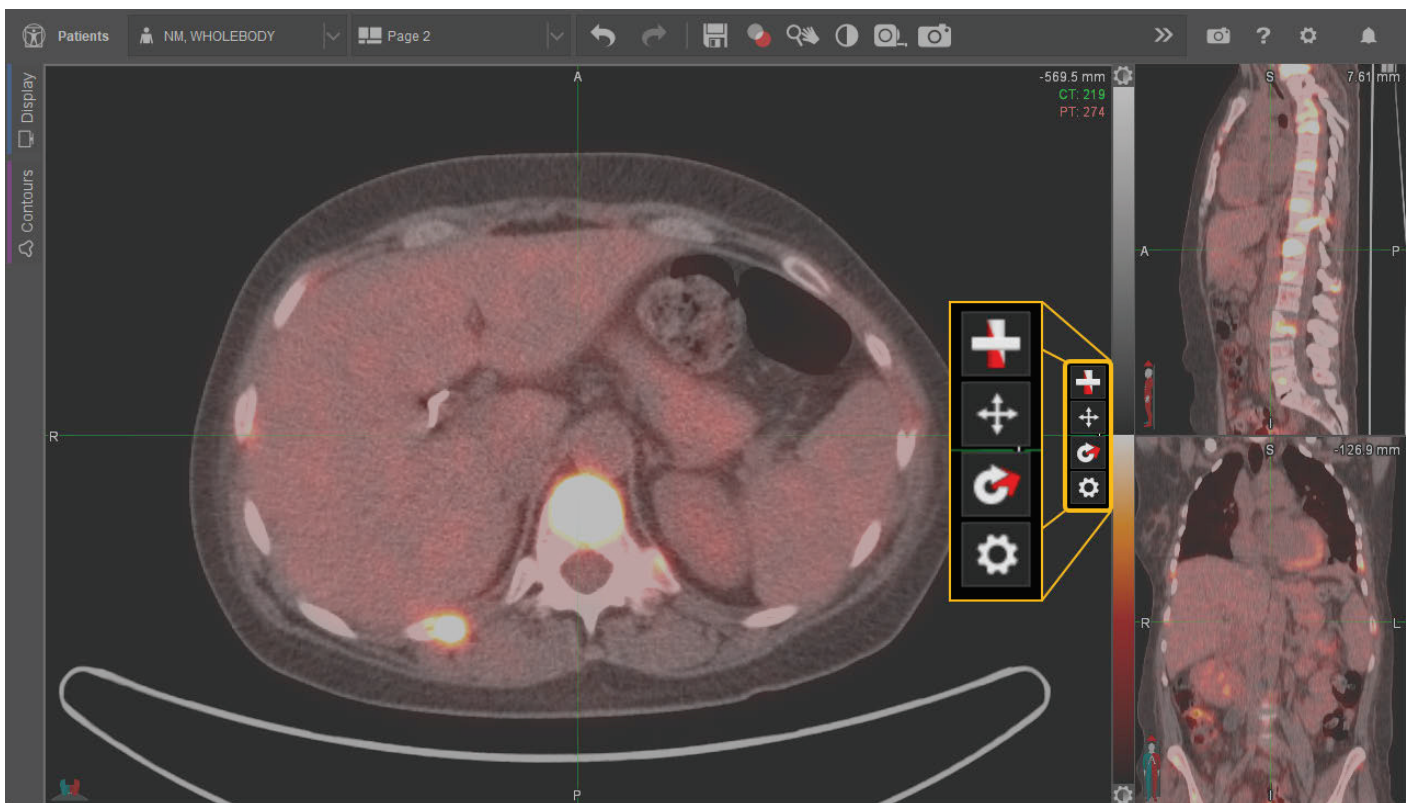


Tip: When changed, this setting takes effect in any open sessions that include a fusion.



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

Show/Hide the Fusion Companion Tools




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

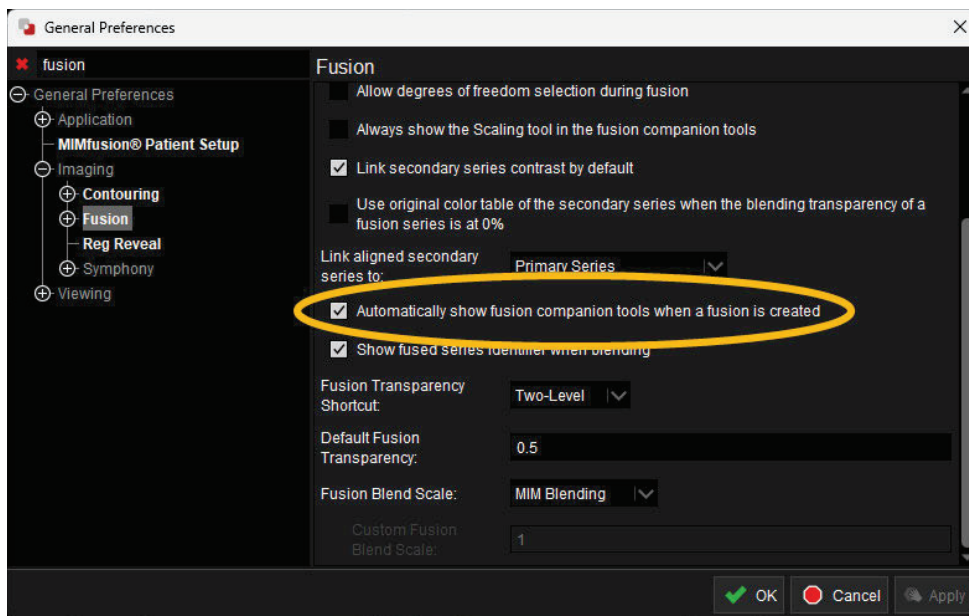


Related: For instructions on configuring keyboard shortcuts, see [Set Keyboard Shortcuts](#).

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

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

1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**fusion**". Select **Fusion** on the left side.
3. Deselect **Automatically show fusion companion tools when a fusion is created**.



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



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



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

Make Measurements

Use Measurement Tools

MIMTD-698 • 24 Oct 2023

Overview

MIM® has tools to create linear and bi-axial measurements. You can also create statistics and measurements simultaneously. Activate measurement tools via the toolbar or radial menu.



Related: For more information about the toolbar and radial menu, see [Access Tools: The Toolbar and the Radial Menu](#).

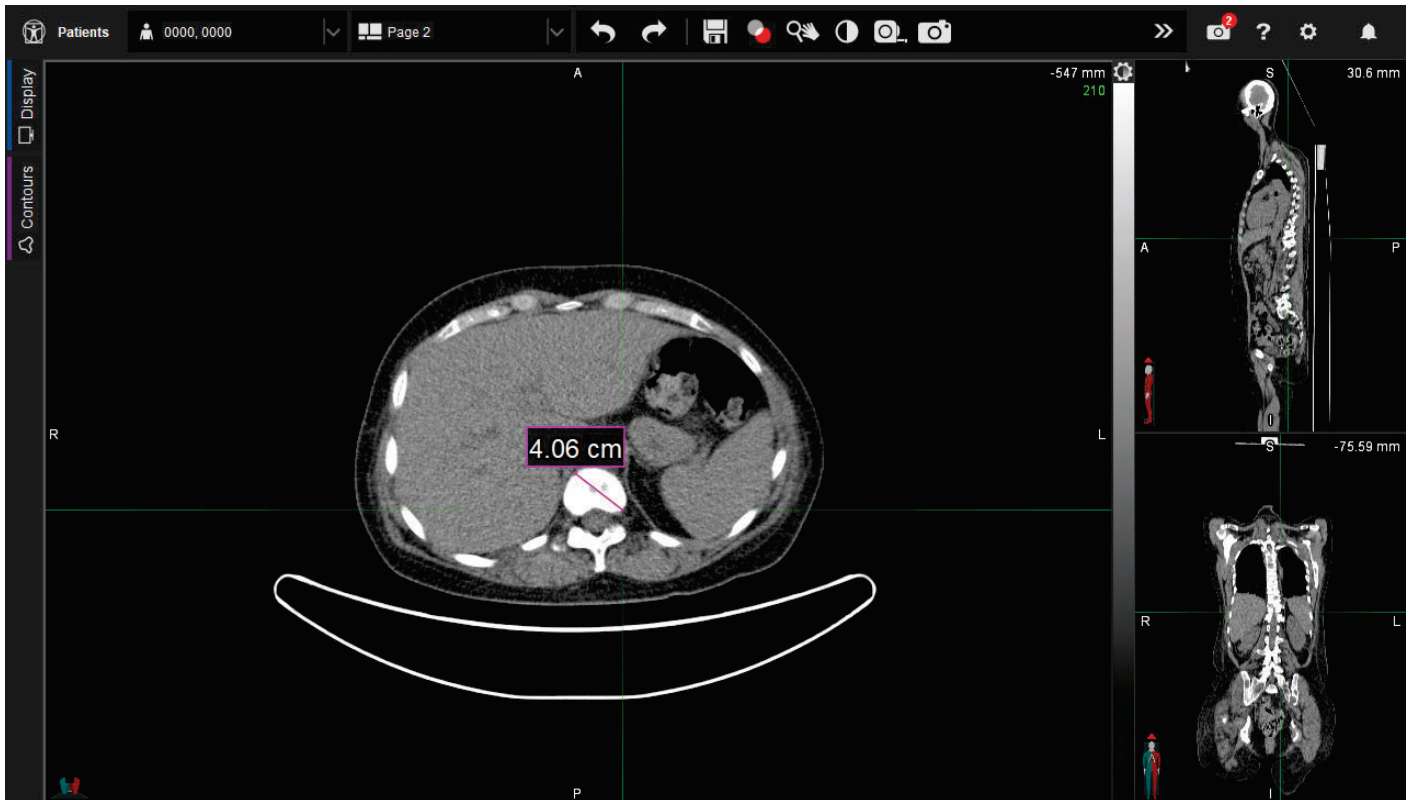
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- [Create Measurements, Contours, and SUV Statistics Simultaneously](#)
- [Show/Hide Measurements](#)

Measure Tool



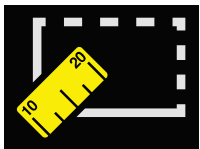
The Measure tool lets you create a linear measurement.



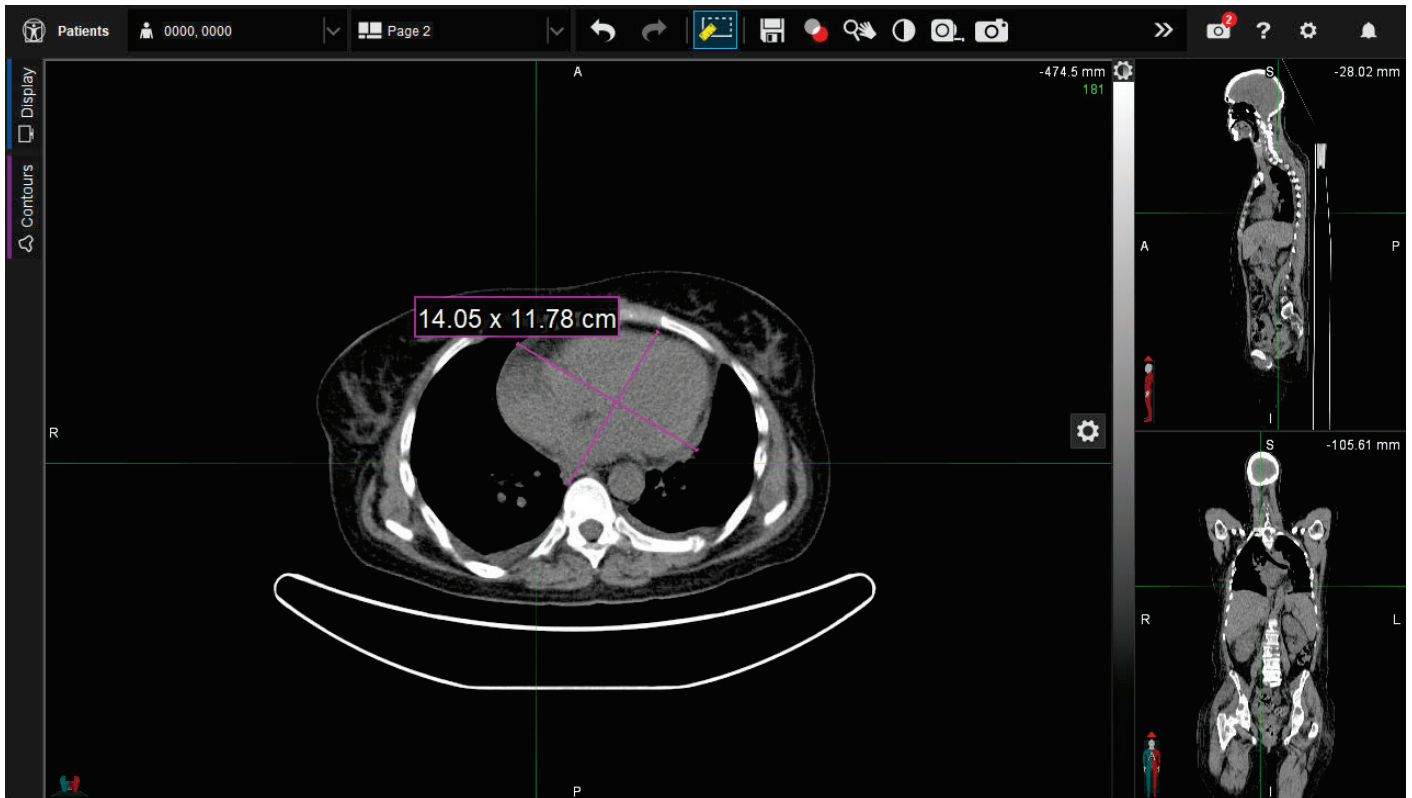
Left-click drag to create a line segment. An annotation label displays the value of the measurement.

- To extend or shorten your measurement, hover over the endpoint of a line. Left-click drag the square that appears to make changes.
- To move a measurement line, right-click drag on the corresponding annotation label.
- To move an annotation, left-click drag on the label.
- To delete a measurement, right-click on the annotation and choose **Delete**.

2D Measure Tool



The 2D Measure tool lets you create bi-axial measurements.



1. Left-click drag to create the first axis.
2. Without clicking, move the mouse to form half of the second axis.
3. Left click to place the first half of the second axis.
4. Without clicking, move the mouse to form the other half of the axis.
5. Finalize the second axis with a single left click.

You can perform the following actions after you create a bi-axial measurement:




- To extend or shorten an axis, hover over the endpoint of a line. Left-click drag the square that appears to make changes.
- To move a measurement, right-click drag on the corresponding annotation label.
- To move an annotation, left-click drag on the label.
- To delete a measurement, right-click on the annotation and choose **Delete**.

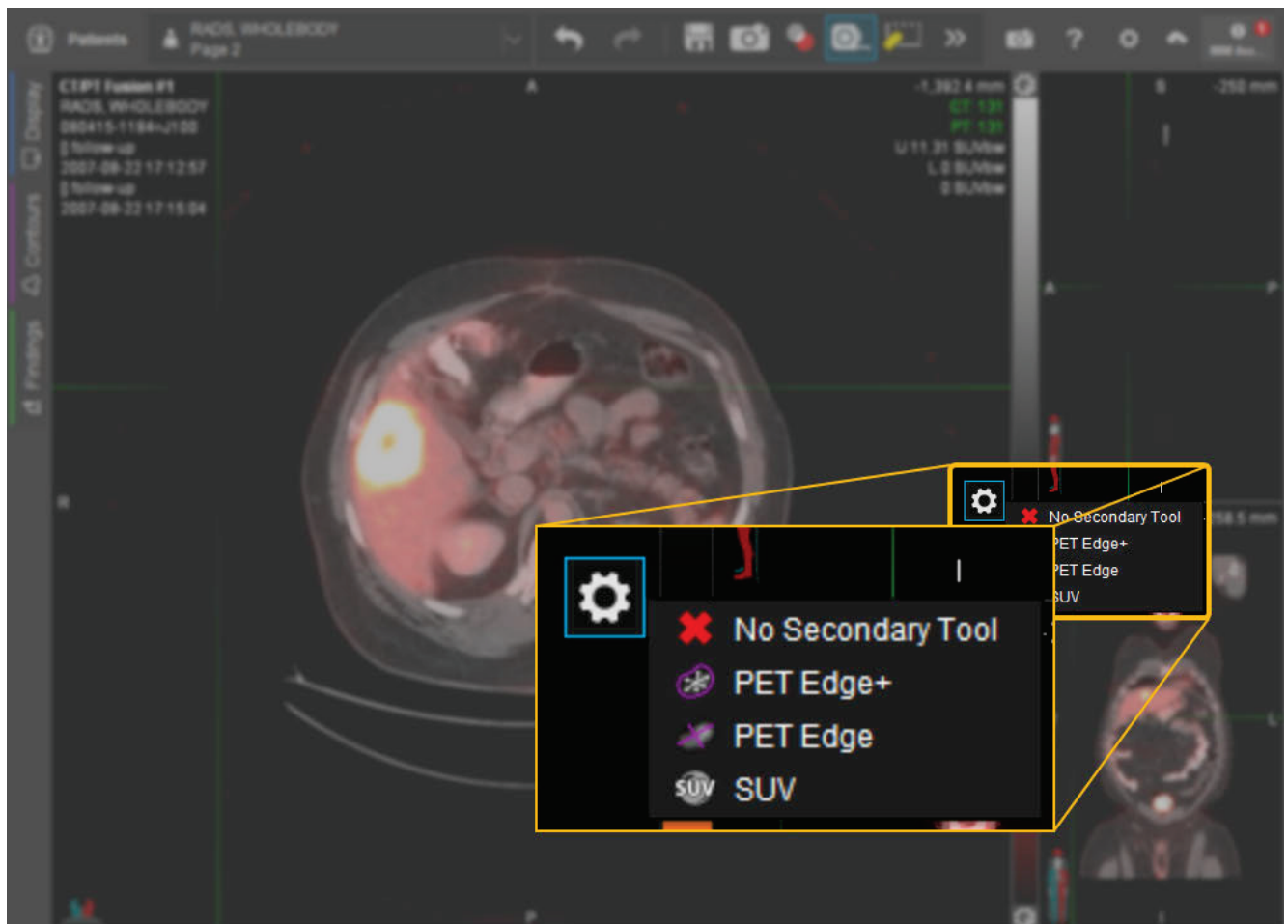
Create Measurements, Contours, and SUV Statistics Simultaneously




You can combine the Measure and 2D Measure tools with the PET Edge®+ (MIM 7.2 and later), PET Edge®, and SUV tools, saving clicks and time. The secondary tool you select is remembered for subsequent measurements, even in new sessions.



Important: If you adjust measure lines after the secondary tool has run, the corresponding secondary tool measurement is *not* updated.

1. Select the **Measure**  or **2D Measure**  tool from the toolbar or radial menu.
2. Click the gear  button on the right side of any viewport to access the secondary tool menu.



3. In the secondary tool menu, select **PET Edge+**  (MIM 7.2 and later), **PET Edge** , or **SUV**  as the secondary tool.

4. On the CT or fusion image, left-click drag to create the measurement. The selected secondary measurement is automatically created along with the initial measurement.



Tip: For the secondary tool to complete the SUV measurement on a PET image, a fusion or other link between the PET and CT must exist in the session.

If desired, you can adjust the SUV measurement in the PET image without exiting the measurement tool.


- *MIM 7.2 and later:* For a PET Edge+ measurement, use the tools on the right side of the viewport to view other candidate contours. For more information, see [Define Lesions with PET Edge®+](#). *MIM 7.1 and earlier:* This functionality is not available.
- For a PET Edge measurement, use the tools on the right side of the viewport to append to or replace the current contour. For more information, see [Define Lesions with PET Edge®](#).
- For an SUV measurement, right-click drag to resize the sphere and left-click drag to move the sphere. Confirm the SUV measurement with the green check mark. For more information, see [Measure SUV](#).



Tip: Once measurements are created, go to the Findings sidebar to view them.

Show/Hide Measurements

You can set a keyboard shortcut to show/hide all measurements displayed in viewports.

1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **Keyboard Shortcuts**.
3. In the search bar, type "**measurements**".
4. Select **Toggle All Measurements**.
5. Double-click the **Key Binding** field and input the desired keyboard shortcut.
6. Click **OK** to save the changes and close the window.

Measure SUV

MIMTD-690 • 30 Nov 2023

Overview

6.1.6




The SUV tool lets you calculate the Standardized Uptake Value (SUV) for a specified region. You can view statistics in viewports and in the Findings sidebar, change SUV calculation type, and adjust parameters, such as patient weight and radionuclide total dose.

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- [Configure SUV Measurement Calculations](#)
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Create and View SUV Measurements

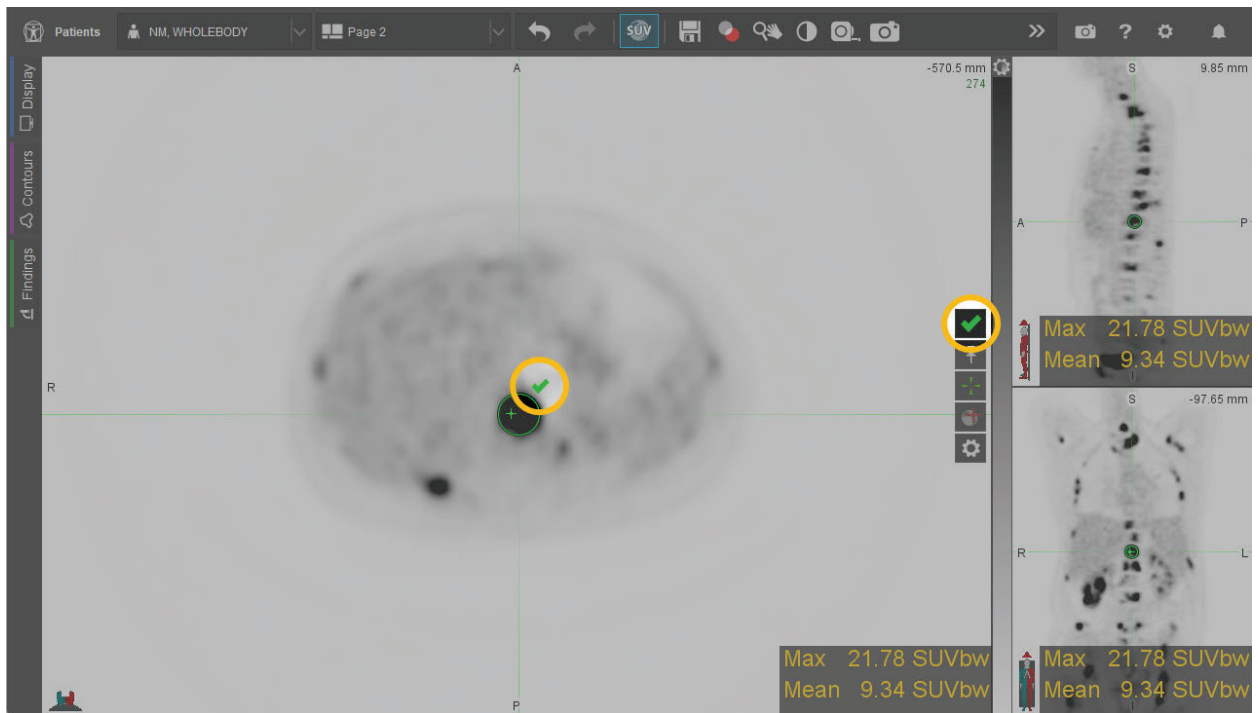
Create SUV Measurements

1. Click the **SUV**  tool in the MIM toolbar or radial menu, or press the S key on your keyboard.
2. On a PET or fusion series, adjust the SUV sphere:
 - Left-click drag the sphere to move it to the location you want to measure.
 - Right-click drag up and down to change the diameter of the sphere.



MIM Encore® User Guide


3. Click the green check mark  button to place an SUV sphere with a point contour at the maximum value. The sphere changes color and displays statistics for the area it covers.
 - *MIM 7.3 and later*: This button is located both immediately next to the sphere and on the right side of the viewport
 - *MIM 7.2 and earlier*: This button is located on the right side of the viewport.




Tip: You can also set a keyboard shortcut for placing SUV spheres. See [Set Keyboard Shortcuts](#) for more information.



Tip: Left-click drag the findings box containing the statistics to move it. To have the box automatically placed so it does not cover the series, see [Adjust SUV Findings Display](#).

4. Place additional spheres as desired by moving the sphere and clicking the green check mark  button. The color of each sphere corresponds with its findings box.

5. If desired, hide or delete a sphere:

- Right-click on the findings box and select **Hide** or **Delete**.
- Click the gear  button for the measurement in the Findings sidebar and select **Hide** or **Delete**.

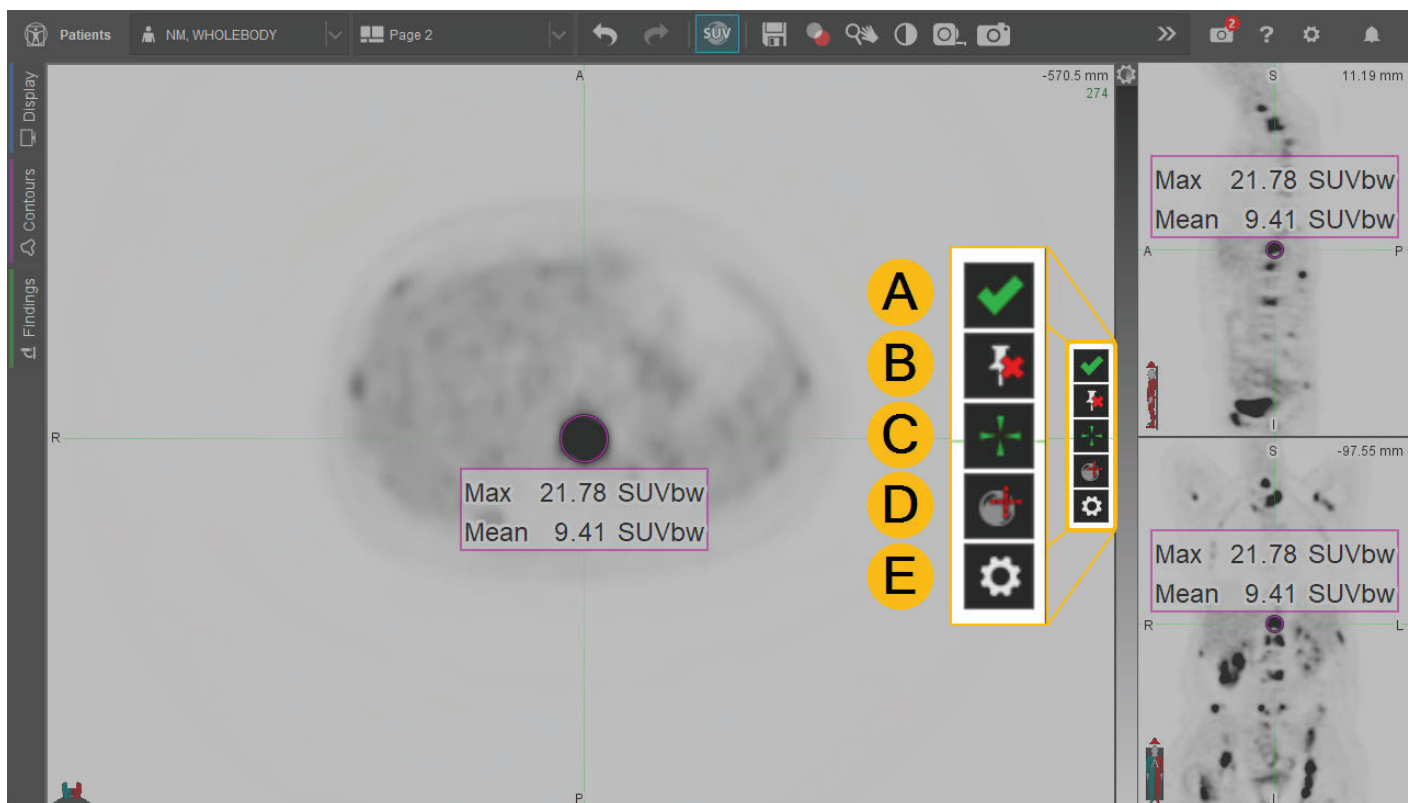


Tip: Change the color of the SUV sphere and findings box by right-clicking the box and selecting **Set Color**.

Use SUV Companion Tools

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

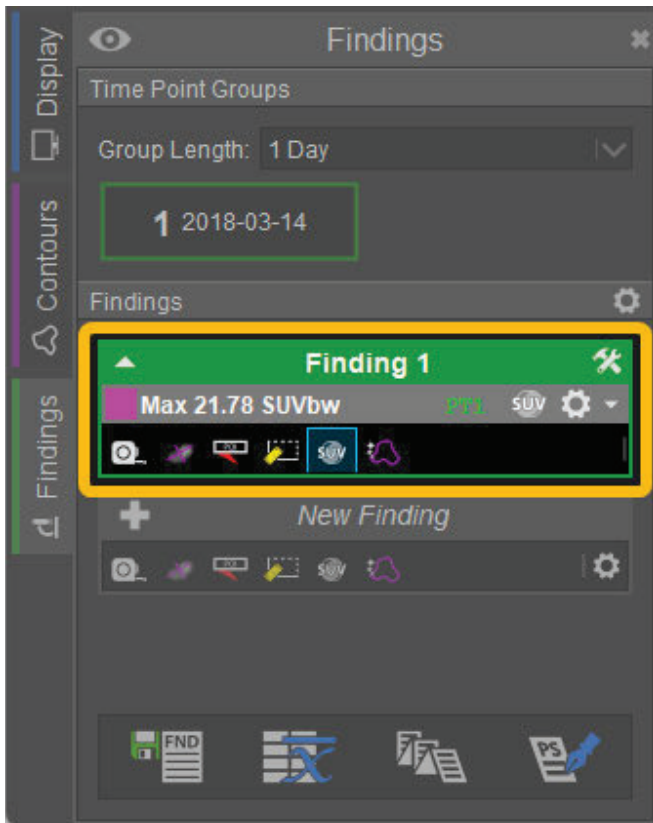
Companion tools for the SUV tool are located on the right side of a viewport when the mouse cursor is inside the viewport.



- A. Place SUV sphere
- B. Pin or unpin SUV sphere to a fixed location
- C. Localize to SUV sphere

- D. Localize to the sphere's maximum value
- E. Edit SUV Parameters

View SUV Measurements in the Findings Sidebar



Go to the **Findings** sidebar to see a list of all your measurements, including SUV measurements. If the sidebar doesn't contain any data, select **Click to Enable Findings** to populate the data.



Related: For more information about creating and viewing measurements in the Findings sidebar, see [Record Measurements Using the Findings Sidebar](#).



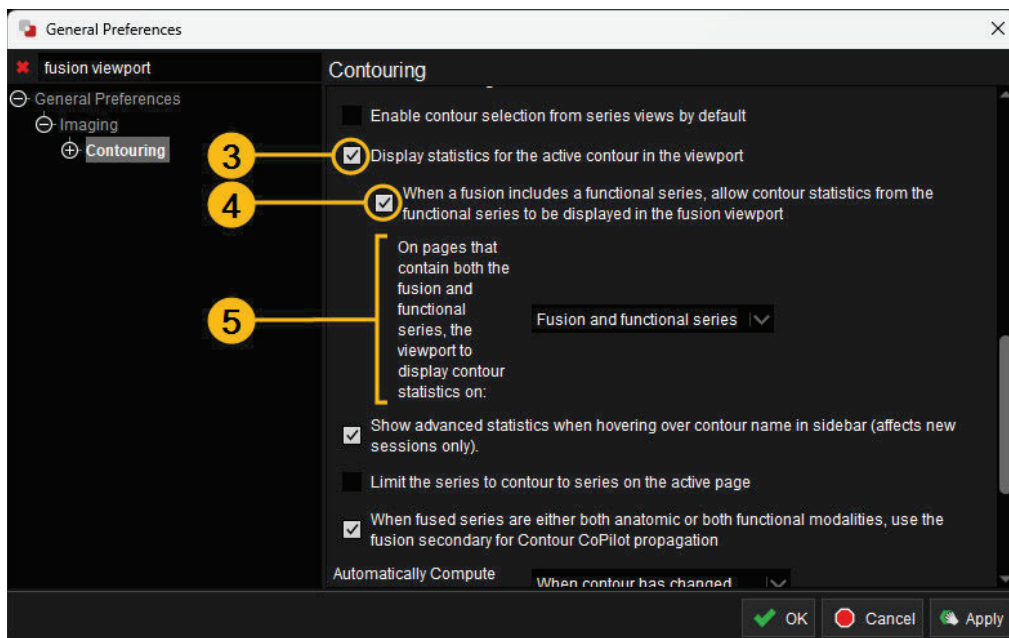
Related: For more information about SUV calculations, see [SUV: Technical Details](#).

Configure SUV Measurement Display Behavior

View SUV 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.



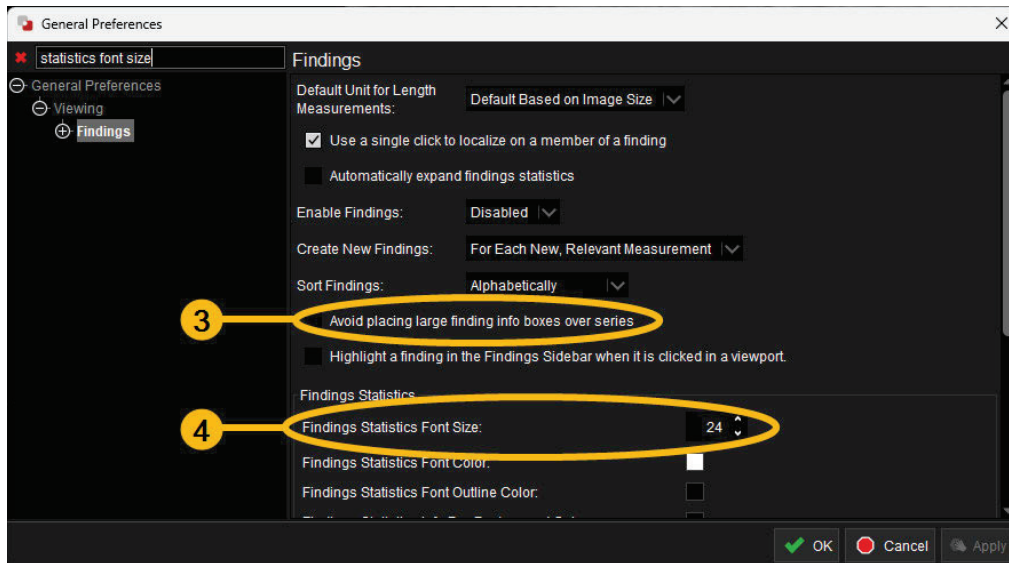
6. Click **OK** to save the changes and close the window.

Adjust SUV Findings Display

To automatically prevent findings boxes from covering a series, as well as change the font size of the statistics in the findings annotation, follow these steps:

1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**statistics font size**". Select **Findings** on the left side.
3. Select **Avoid placing large finding info boxes over series**.

- Adjust **Findings Statistics Font Size**. This setting applies when the next measurement is taken.



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

To edit which statistics are displayed by default, continue to Configure SUV Measurement Calculations below.

Configure SUV Measurement Calculations

Edit SUV Parameters

The options for editing SUV parameters change depending on whether the viewport shows a PET or a fusion.

In a PET viewport, click the gear  companion tool to perform the following actions:

- Correct the SUV calculation by adjusting options such as patient weight, radionuclide total dose, and others.
- Switch the SUV calculation type. The available options are **Body Weight (bw)**, **Lean Body Mass (lbm)**, **Body Surface Area (bsa)**, and **Bq/ml**.



Tip: If your SUV values appear in a different unit (e.g., PROPCPS, HU, Counts), ensure that you are using the tool with an attenuation-corrected PET series.



Tip: You can set a keyboard shortcut to quickly switch SUV calculation types. See [Set Keyboard Shortcuts](#) for more information.

In a PET or fusion viewport, click the gear  companion tool to perform the following actions:


- Edit the displayed statistics. The options are **Mean**, **Max**, **Longest Diameter**, **Min**, and **Max Slice**.
- Show or hide the hovering **SUV tooltip** that displays the SUV before placing a sphere.
- Manually enter a value for the sphere diameter.
- Toggle the point contour at max value.
- *MIM 7.3 and later:* Show or hide the green check mark next to the SUV sphere. *MIM 7.2 and earlier:* This functionality is not available.

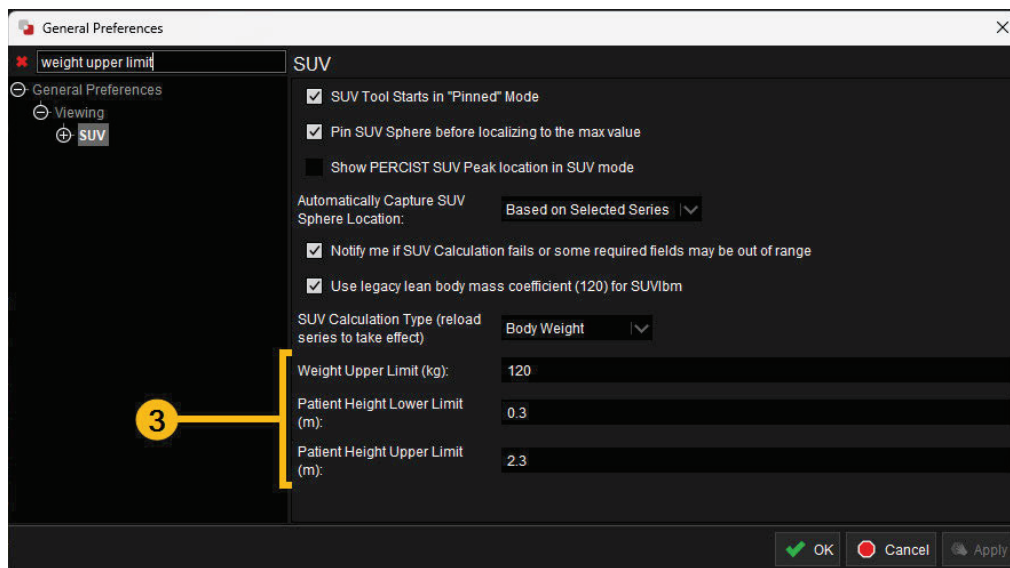


Tip: MIM remembers these companion tool settings for subsequent measurements.

Adjust Weight and Height Limits

If you regularly read scans for heavier, taller, or shorter patients, you may wish to adjust the default weight and/or height limits. This prevents notifications that a scan is outside of the existing default limits.

1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**weight upper limit**". Select **SUV** on the left side.
3. Adjust **Weight Upper Limit (kg)**, **Patient Height Lower Limit (m)**, and **Patient Height Upper Limit (m)** as desired.



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

Calculate SUV Peak for PERCIST


6.1.6

In addition to SUV, you can also calculate SUV Peak for a contour using the method defined in the PERCIST (PET Response Criteria in Solid Tumors) 1.0 guidelines. Peak value is displayed in the Findings sidebar.




Tip: SUV Peak is the mean value of the voxels in an SUV sphere.

Display SUV Peak Location

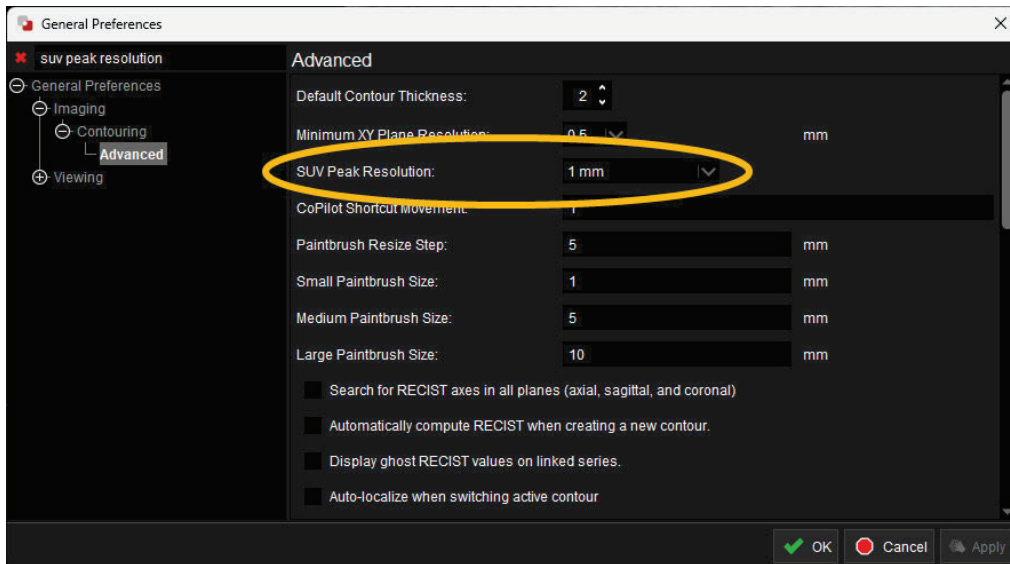
- Click the Settings  button in the upper-right corner of MIM.
- Go to **General Preferences** and search for "**percist**". Select **SUV** on the left side.
- Select **Show PERCIST SUV Peak location in SUV mode**.
- Click **OK** to save the changes and close the window.

Set SUV Peak Resolution

- Click the Settings  button in the upper-right corner of MIM.
- Go to **General Preferences** and search for "**suv peak resolution**". Select **Advanced** on the left side.
- Adjust the **SUV Peak Resolution** dropdown as desired.
 - 1 mm** — MIM samples the volume around the contour at 1 mm intervals in all planes. This method minimizes the number of samples that have an interpolated value, and it is more likely

to return values for small contours.

- **Volume Resolution** — MIM searches for the SUV Peak using the volume's resolution and does not use any interpolation.



Tip: Allow SUV Peak to be created for small structures by also selecting **Allow SUV Peak to include data outside the contour for small structures**.

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

Configure Tracers

MIMTD-1203 • 07 Nov 2023

Overview

MIM® lets you set SUV tracer limits for both minutes from dose to scan and the delivered dose limit.

If a user opens a scan where the timing or dose amount is outside of the range configured for that tracer, a Notifications window prompts the user to confirm that the scan information is correct.

Similarly, if the scan includes a tracer that is not configured, a Notifications window asks the user to manually verify that all scan information is correct.




Related: Refer to [Measure SUV](#) for more information about how the system calculates and displays SUV based on tracer configuration.

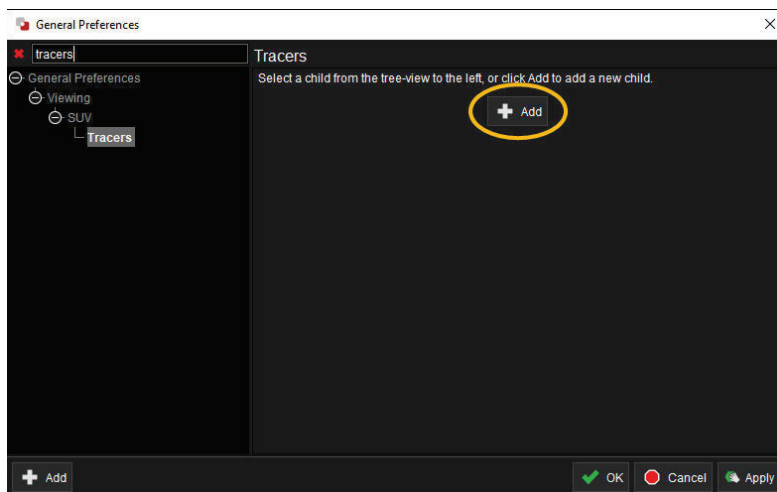
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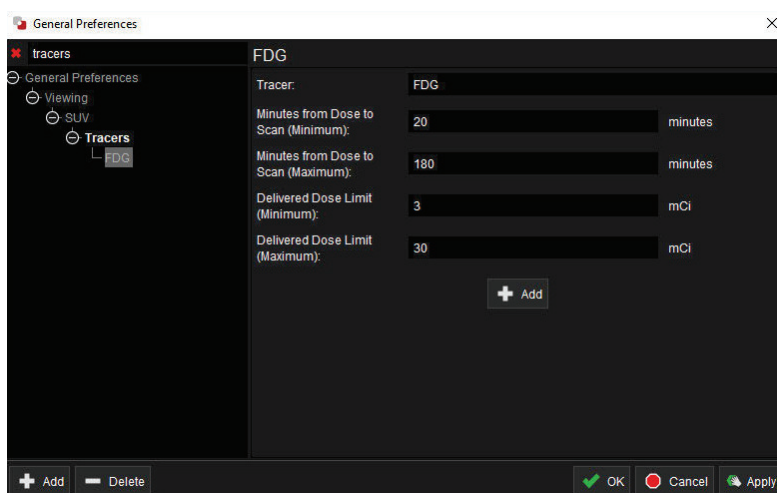
Add a Tracer

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

3. Click **Add**.



4. Enter a tracer name.
5. Enter values for **Minutes from Dose to Scan** and **Delivered Dose Limits** based on your organization's imaging protocols.



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

How MIM Identifies a Tracer

For MIM to identify a tracer, the tracer name that you configure must match the series DICOM.

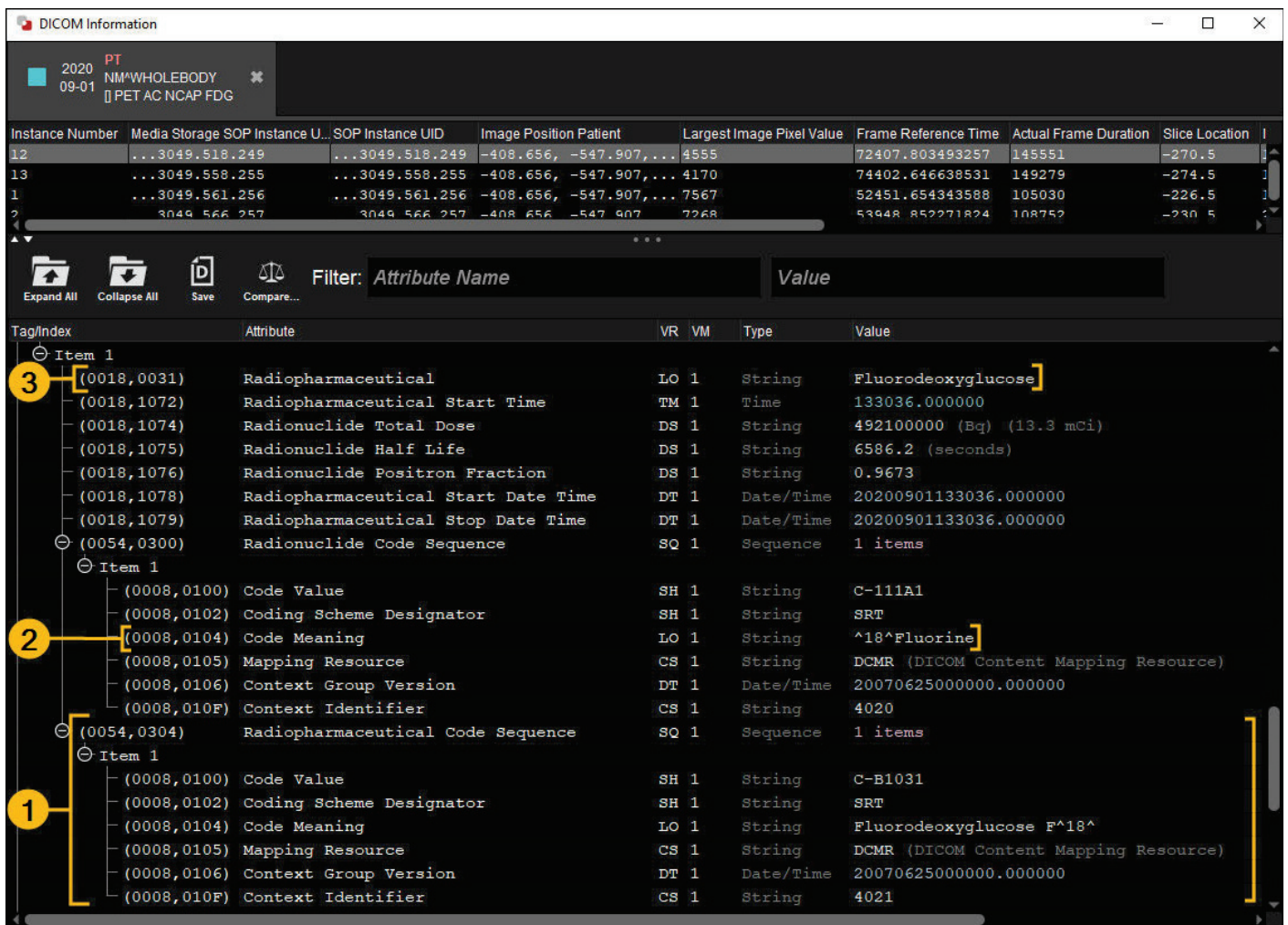
DICOM Values Checked

1. MIM first checks the code meaning associated with the value of the DICOM tag **RadiopharmaceuticalCodeSequence.CodeValue (0054, 0304)** per DICOM PS 3.16-2011 (Content Mapping Resource):

- CID 25: Radiopharmaceuticals
- CID 3107: PET Cardiology Radiopharmaceuticals
- CID 3111: Nuclear Cardiology Radiopharmaceuticals
- CID 4021: PET Radiopharmaceuticals

2. If that value is empty or is not present in the CID, MIM then checks the value of the DICOM tag **RadiopharmaceuticalCodeSequence.CodeMeaning (0008, 0104)**.
3. If that value is also empty, MIM then checks the value of the DICOM tag **RadiopharmaceuticalInformationSequence.Radiopharmaceutical (0018, 0031)**.

To view these DICOM values for a series, right-click on the series in the patient list and selecting **Show DICOM Information...** The DICOM Information window that opens show the value for each present DICOM tag.



Tag/Index	Attribute	VR	VM	Type	Value
Item 1					
(0018,0031)	Radiopharmaceutical	LO	1	String	Fluorodeoxyglucose
(0018,1072)	Radiopharmaceutical Start Time	TM	1	Time	133036.000000
(0018,1074)	Radionuclide Total Dose	DS	1	String	492100000 (Bq) (13.3 mCi)
(0018,1075)	Radionuclide Half Life	DS	1	String	6586.2 (seconds)
(0018,1076)	Radionuclide Positron Fraction	DS	1	String	0.9673
(0018,1078)	Radiopharmaceutical Start Date Time	DT	1	Date/Time	20200901133036.000000
(0018,1079)	Radiopharmaceutical Stop Date Time	DT	1	Date/Time	20200901133036.000000
(0054,0300)	Radionuclide Code Sequence	SQ	1	Sequence	1 items
Item 1					
(0008,0100)	Code Value	SH	1	String	C-111A1
(0008,0102)	Coding Scheme Designator	SH	1	String	SRT
(0008,0104)	Code Meaning	LO	1	String	^18^Fluorine
(0008,0105)	Mapping Resource	CS	1	String	DCMR (DICOM Content Mapping Resource)
(0008,0106)	Context Group Version	DT	1	Date/Time	20070625000000.000000
(0008,010F)	Context Identifier	CS	1	String	4020
(0054,0304)	Radiopharmaceutical Code Sequence	SQ	1	Sequence	1 items
Item 1					
(0008,0100)	Code Value	SH	1	String	C-B1031
(0008,0102)	Coding Scheme Designator	SH	1	String	SRT
(0008,0104)	Code Meaning	LO	1	String	Fluorodeoxyglucose F^18^
(0008,0105)	Mapping Resource	CS	1	String	DCMR (DICOM Content Mapping Resource)
(0008,0106)	Context Group Version	DT	1	Date/Time	20070625000000.000000
(0008,010F)	Context Identifier	CS	1	String	4021

MIM checks the DICOM tags listed above sequentially until the tracer is identified.

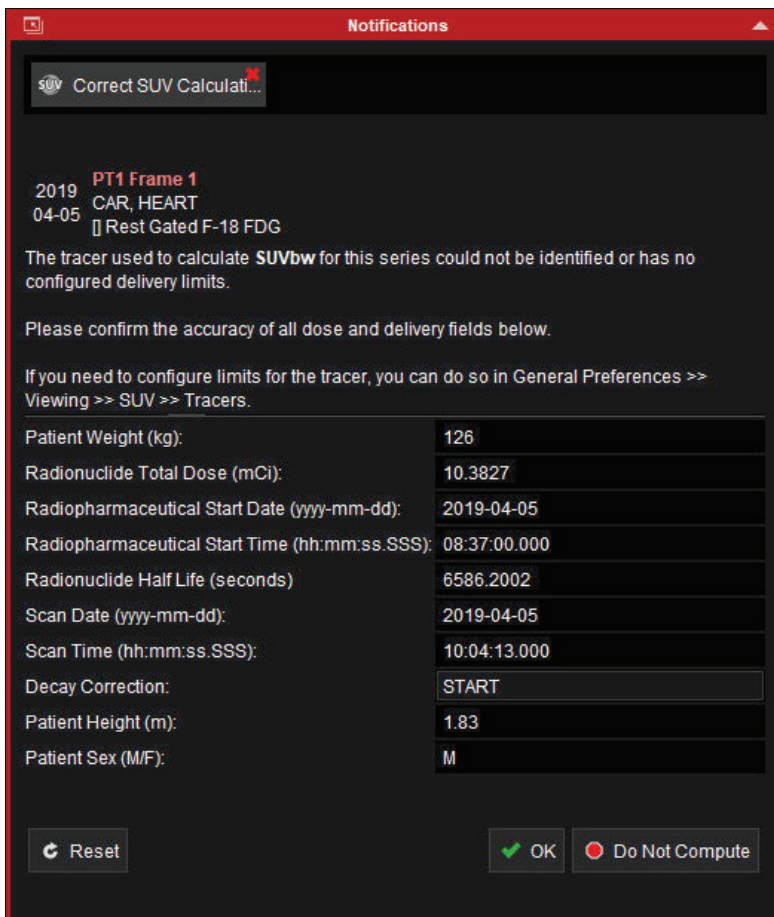
Add a Tracer Alias

There are circumstances where a tracer won't be detected by MIM due to the DICOM not matching your existing tracer naming protocols. For example, your organization may receive patient data from another organization that uses a different naming scheme.


You can address tracers with multiple naming protocols within the DICOM by creating separate tracer entries. Alternatively, you can create a tracer alias. If you are interested in adding a tracer alias, please contact MIM Software Support at support.mimsoftware.com.

Notification When a Tracer Is Not Recognized

When you open a series where the tracer has not been configured, the following notification appears: **The tracer used to calculate SUVbw for this series could not be identified or has no configured delivery limits.**



Notifications

 Correct SUV Calculati...




2019 **PT1 Frame 1**
04-05 CAR, HEART
[] Rest Gated F-18 FDG

The tracer used to calculate **SUVbw** for this series could not be identified or has no configured delivery limits.

Please confirm the accuracy of all dose and delivery fields below.

If you need to configure limits for the tracer, you can do so in General Preferences >> Viewing >> SUV >> Tracers.

Patient Weight (kg):	126
Radionuclide Total Dose (mCi):	10.3827
Radiopharmaceutical Start Date (yyyy-mm-dd):	2019-04-05
Radiopharmaceutical Start Time (hh:mm:ss.SSS):	08:37:00.000
Radionuclide Half Life (seconds)	6586.2002
Scan Date (yyyy-mm-dd):	2019-04-05
Scan Time (hh:mm:ss.SSS):	10:04:13.000
Decay Correction:	START
Patient Height (m):	1.83
Patient Sex (M/F):	M

 Reset  OK  Do Not Compute

You can manually review the information in the Notifications window and update it as necessary. Then, click **OK** to proceed with SUV calculation.



To automate this review and prevent this notification from appearing in the future, configure the tracer in MIM, using the steps in the [Add a Tracer](#) section above. Then, for future studies, MIM can recognize the tracer and not prompt for manual review.

Record Measurements Using the Findings Sidebar

MIMTD-692 • 11 Aug 2023

Overview

Record and group measurements from the same anatomical region of interest using the Findings sidebar. For example, create and automatically group an SUV measurement, a measure line, and an annotation for the same tumor.

Analyze findings for a single series, or for multiple series over time to assess treatment and progress. View measurements instantly from the Findings sidebar or in a report. Save findings and review them at a later time, or share them with other users.



Related: For more information about configuring how the Findings sidebar appears and how Findings are displayed in viewports, refer to [Customize Findings Settings](#).



Related: For more information about using Findings when working with multiple time points, refer to [Compare Findings Across Time Points](#).

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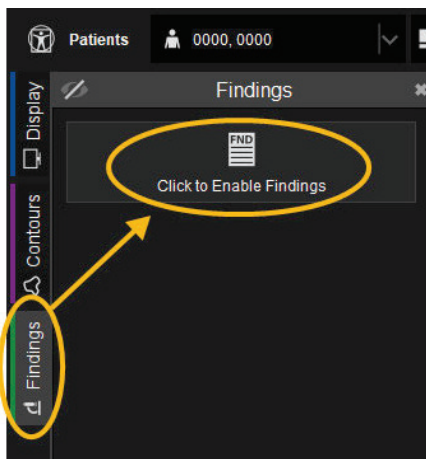
Prerequisites

Enable the Findings sidebar by going to Settings  >> **General Preferences** >> **Viewing** >> **Findings** and changing the **Enable Findings** dropdown to **Enabled**.



Tip: To enable the Findings sidebar for all users, a MIM administrative user should make this change while logged in to the **Edit Site Defaults** login mode. See [Update Default Settings for Users](#) for prerequisites and instructions.

If Findings have not been enabled as described above, you can enable Findings for an individual session. Select the Findings sidebar and click the **Click to Enable Findings** button.



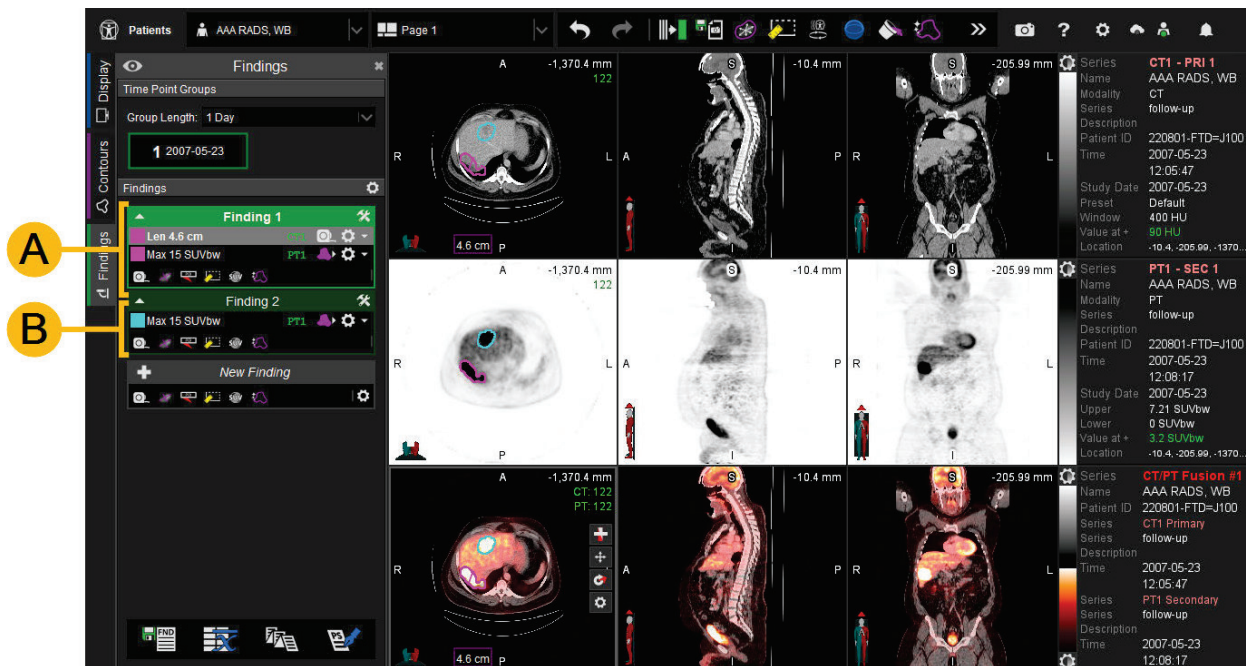
Create and View Findings

Findings group together the measurements, contours, or annotations that you make.

Create a Finding










1. From the patient list, open a session.
2. Use a measurement, contouring, or annotation tool. See [Tools That Create Findings](#) below for a list of tools.
 - A. The measurement's value or other information is recorded in the **Finding 1** box. By default, any additional measurements, contours, or annotations in the same region are added to the same Findings box. These findings are the same color.





- B. Measurements, contours, or annotations created in a different region are automatically recorded in the **Finding 2** box. These findings are a different color.




- Continue creating additional findings as necessary.
- Continue to [Review Findings in the Findings Sidebar](#) below for more information about the Findings sidebar.

Tools That Create Findings

Tool Type	Tool	More Information
Contour Tools	 2D Brush	<ul style="list-style-type: none"> Create Contours with the 2D Brush Create Contours with the 3D Brush Define Lesions with PET Edge® Define Lesions with PET Edge®+
	 3D Brush	
	 PET Edge®	
	 PET Edge®+	
	 2D Edge	
	 Threshold	
Measurement Tools	 Measure	Use Measurement Tools
	 2D Measure	
	 RECIST	

Tool Type	Tool	More Information
Annotation Tools	 Annotate	Annotate Images
	 Annotate Screen	
SUV Tools	 SUV Sphere	Measure SUV
	 PERCIST SUV Peak	

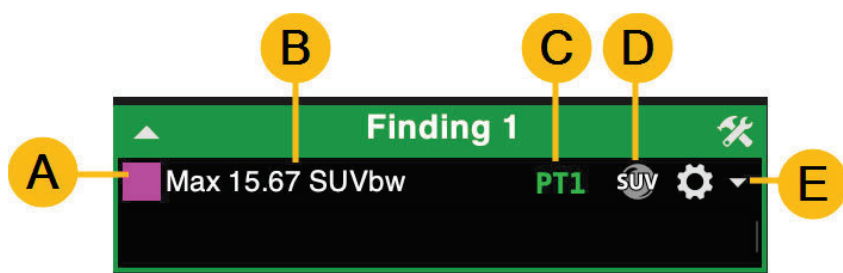
To see tips for using these tools, activate a tool, then click the  button in the upper-right corner of MIM. The first option displays the active tool and opens a help window.

Review Findings in the Findings Sidebar

You can see the findings that you created in the Findings sidebar.





Related: Refer to [Customize Findings Settings](#) for more information about configuring default display options.



- Click on the color of the finding to hide the finding in the image. Hover over the box and scroll to change the color.
- Click on the measurement name to localize to the measurement on the image.
- See which image the finding was created on. The numbers indicate the time point, with the oldest time point as 1. Refer to [Compare Findings Across Time Points](#) for more information about working with multiple time points.
- See which tool was used to make the finding.
- Click the arrow to expand the statistics for the finding.



Tip: For additional options for an individual measurement, click the gear  next to the measurement name. For additional options for a Findings group, click the  by the Findings group name.

Report and Save Findings

There are a few ways to save and export Findings information, depending on your scenario and how you would like to view the information later.

Save Findings to View or Edit in MIM

You can save a Findings object in MIM, which includes any findings you have created. Findings are also included when you save the session.




Important: Findings can be opened in MIM only. See [View Findings in Other Systems](#) below if you need to save the findings to PACS or send to another third-party system.

To save a Findings object:



1. Click the save findings  button at the bottom of the Findings sidebar.



Tip: If you want findings to save automatically, go to Settings  >> **General Preferences >> Application >> Shutdown** and select **Autosave findings on close**. For more information, see [Customize Findings Settings](#).

2. In the Notifications window, enter a **Series Description** and enter other information as desired.
3. Click the **OK** button to finish saving.



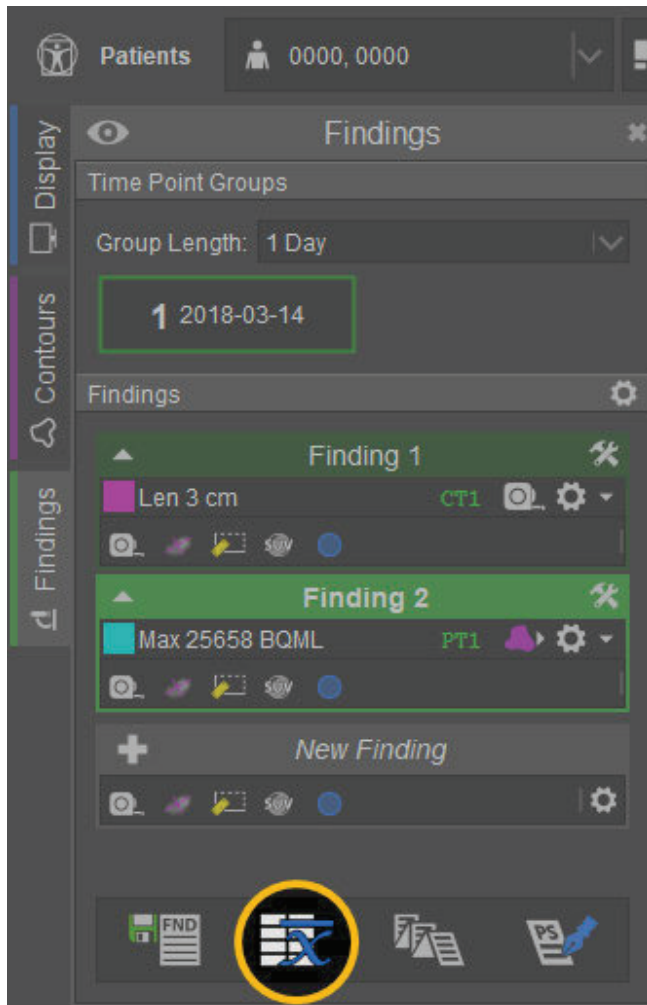
Tip: If desired, you can save Findings as a template (Findings gear  >> **Save Findings as Template**). In future sessions, you can load the template so that the finding names and associated tools are pre-created (Findings gear  >> **Load Findings Template**).



Report on Findings Statistics

View detailed statistics for each Finding and optionally create a report that you can refer back to.

To view Findings statistics:

1. Click the Statistics Viewer  button at the bottom of the Findings sidebar.



2. On the **Statistics** tab, use the **Toggle**  to select which findings you want to view statistics for.
3. If desired, use **Save As**  to save the statistics, such as a DICOM RTstruct, spreadsheet, or capture.



Related: For more information about working with statistics, refer to [View Statistics](#).


Include Findings in a Structured Report


If you are sharing information with another provider or a patient, you can include Findings in your structured report.

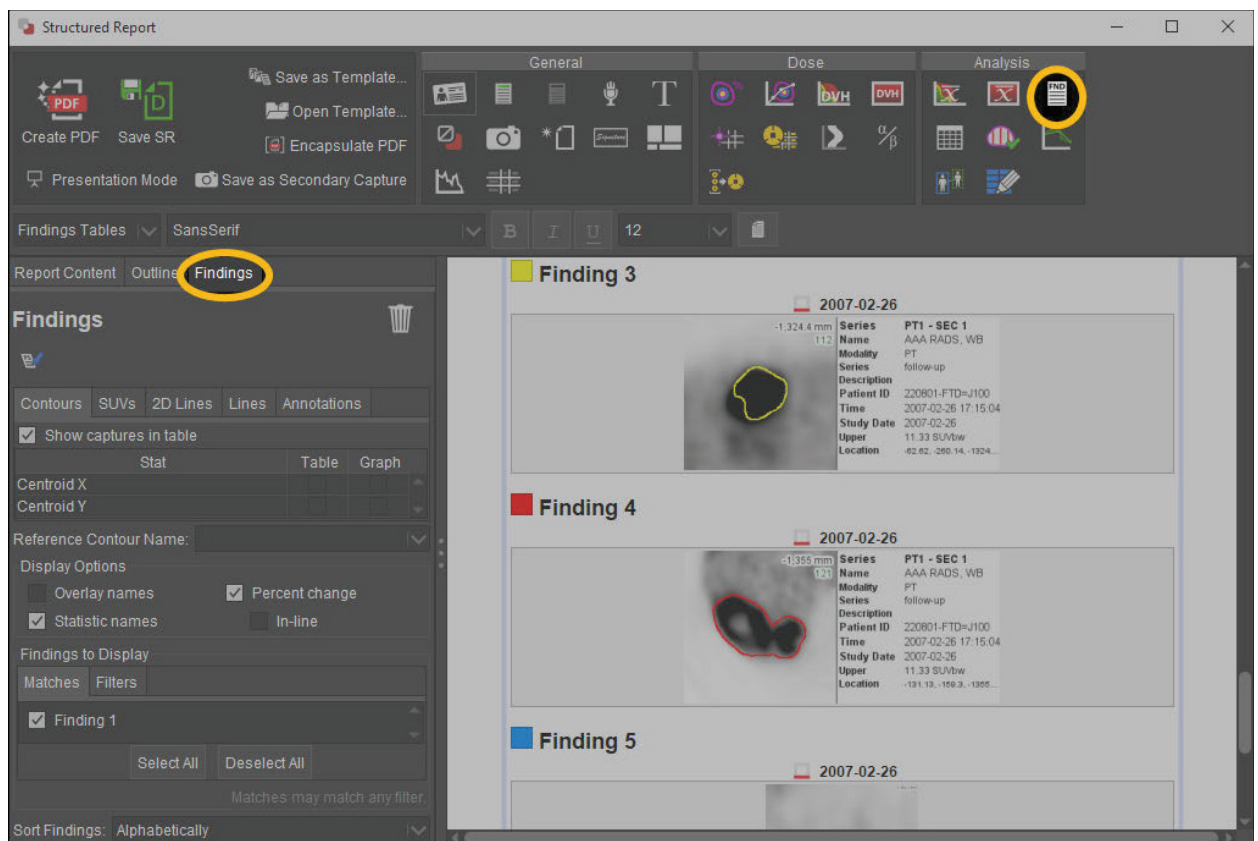
To add Findings to a structured report:

1. Click the structured report  button at the bottom of the Findings sidebar.



Tip: Alternatively, if your organization uses PowerScribe, you can use the external report  button to open a PowerScribe report. Please contact MIM Software Support at support.mimsoftware.com if you need help integrating with PowerScribe.

2. In the Notifications window, either select an existing report template or create a new report from an empty template.
3. If you are using an empty template or a template that does not include Findings by default, add Findings:
 - i. From the Analysis menu, select findings .
 - ii. In the **Findings** sidebar that opens, update the Findings display as desired.



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

View Findings in Other Systems

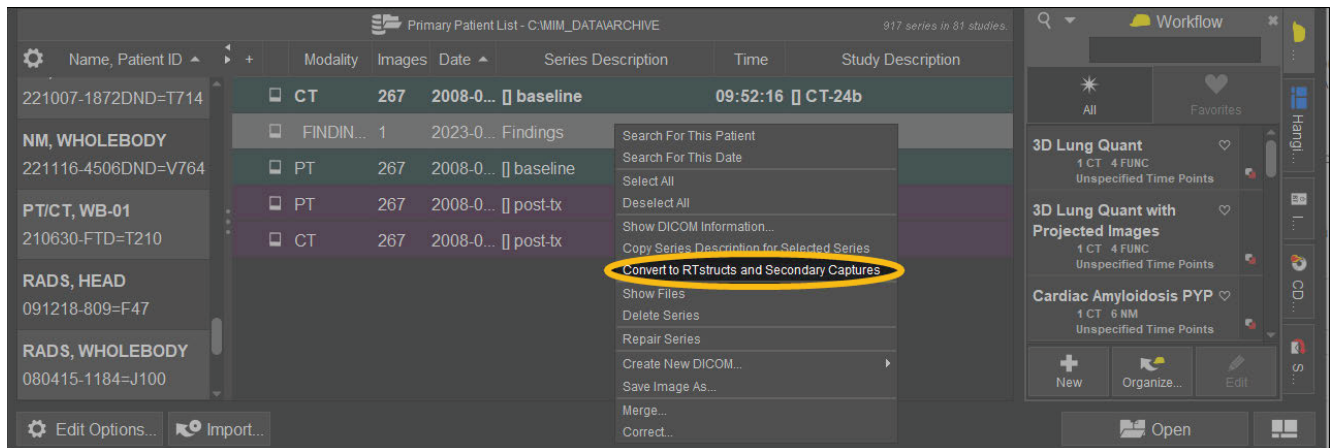
Because Findings objects can only be read MIM workstations, you need to convert the object into a RTstruct or OT modality if you want to save it to another DICOM-compliant system.



Important: The measurements used in MIM are not universal and may not display correctly (or at all) when loaded by other software.

To convert Findings into RTstruct and OT modalities:



1. Search for a study in the patient list.
2. Right-click on a saved **Findings** object.
3. Select **Convert to RTstructs and Secondary Captures**.



4. Export these converted modalities to the other system.

Copy Findings to Your Clipboard

If you want to copy the Findings information to paste into a note or other system, use MIM's clipboard tool:

1. Within the session with your findings created, click the  button on the right side of the top toolbar.
2. Search for and select the **Copy Findings Text to Clipboard**  tool. The Findings text is automatically copied.
3. In your desired application, paste the copied results.



Related: See [Customize Findings Settings](#) for information about settings to determine which findings and which findings statistics are copied.

Compare Findings Across Time Points

MIMTD-1675 • 10 Aug 2023

Overview

Findings are especially useful when comparing images from different time points. The Findings sidebar can automatically recognize and group findings from the same anatomical region.



Related: For more information about working with Findings, refer to [Record Measurements Using the Findings Sidebar](#).

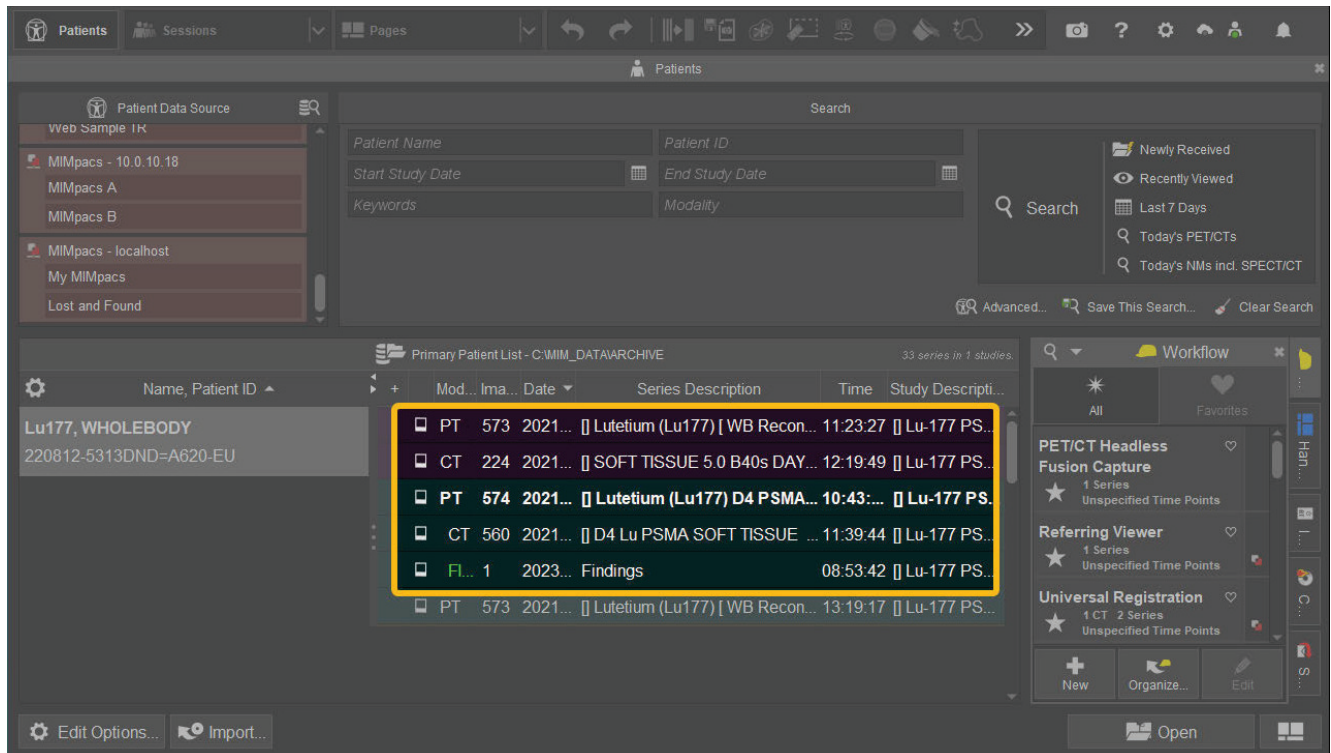
Contents

- [Run a Comparison Workflow](#)
- [View Findings for Multiple Time Points](#)

Run a Comparison Workflow

For MIM® to automatically recognize and group findings from different time points, you must use a comparison workflow. A comparison workflow links the series from different time points so that the same anatomical regions are identified.

1. From the patient list, select the original **PT**, **CT**, and **Findings** as well as the follow-up **PT** and **CT**.



2. Launch a MIM workflow that compares time points. You may have a site-defined workflow for viewing and reading, or you can use one of these default workflows:
 - PET/CT or SPECT/CT - Compare
 - Universal PET/CT Review
 - Universal PET/CT Review DM
 - Universal SPECT/CT Review
3. Respond to any prompts that appear in the Notifications window. When the workflow is finished running, continue to the next section below.



Related: For more information about default workflows, see [MIM Encore Default Workflows](#).

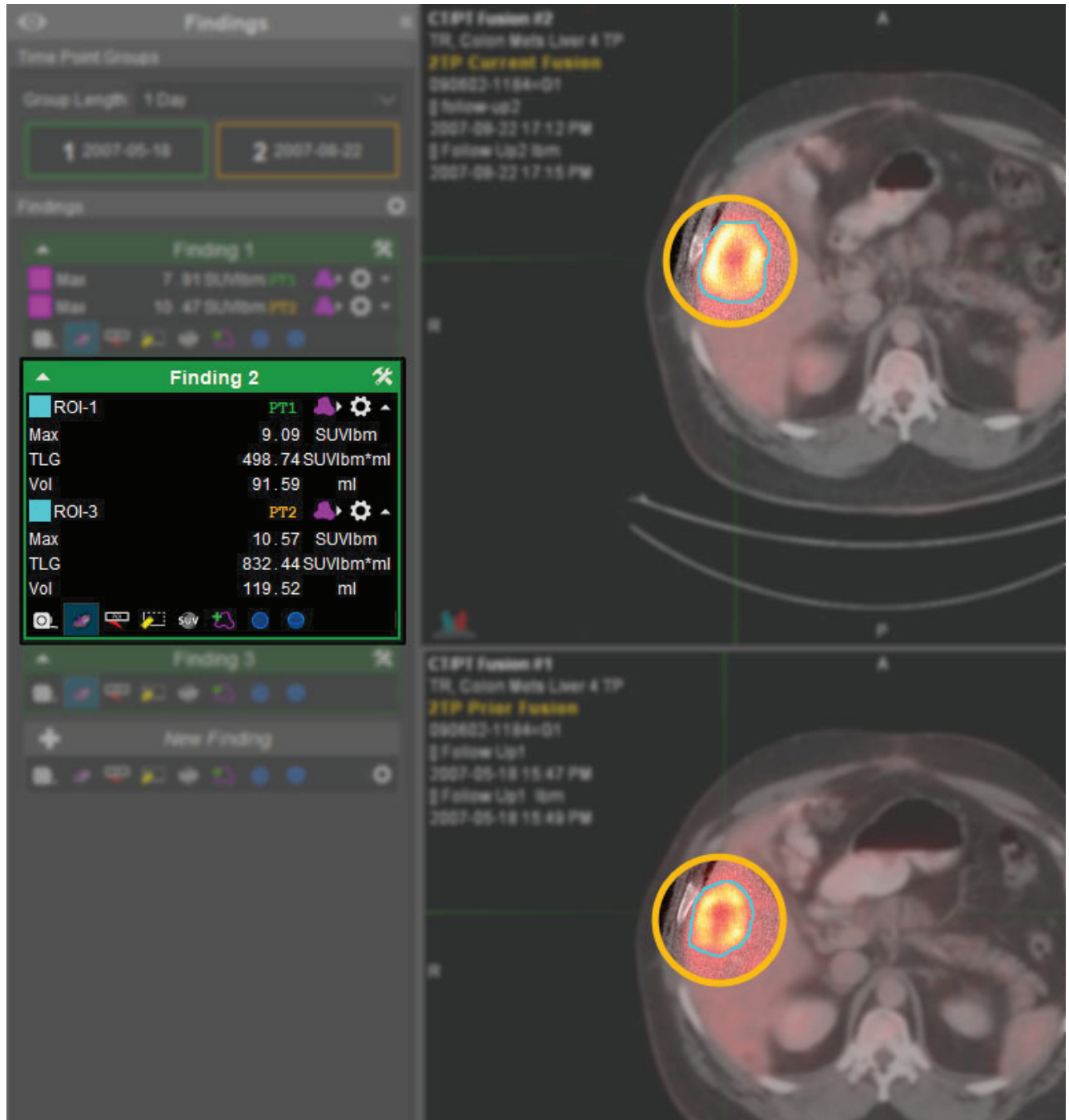
View Findings for Multiple Time Points

When the comparison workflow has finished running, complete the following steps:

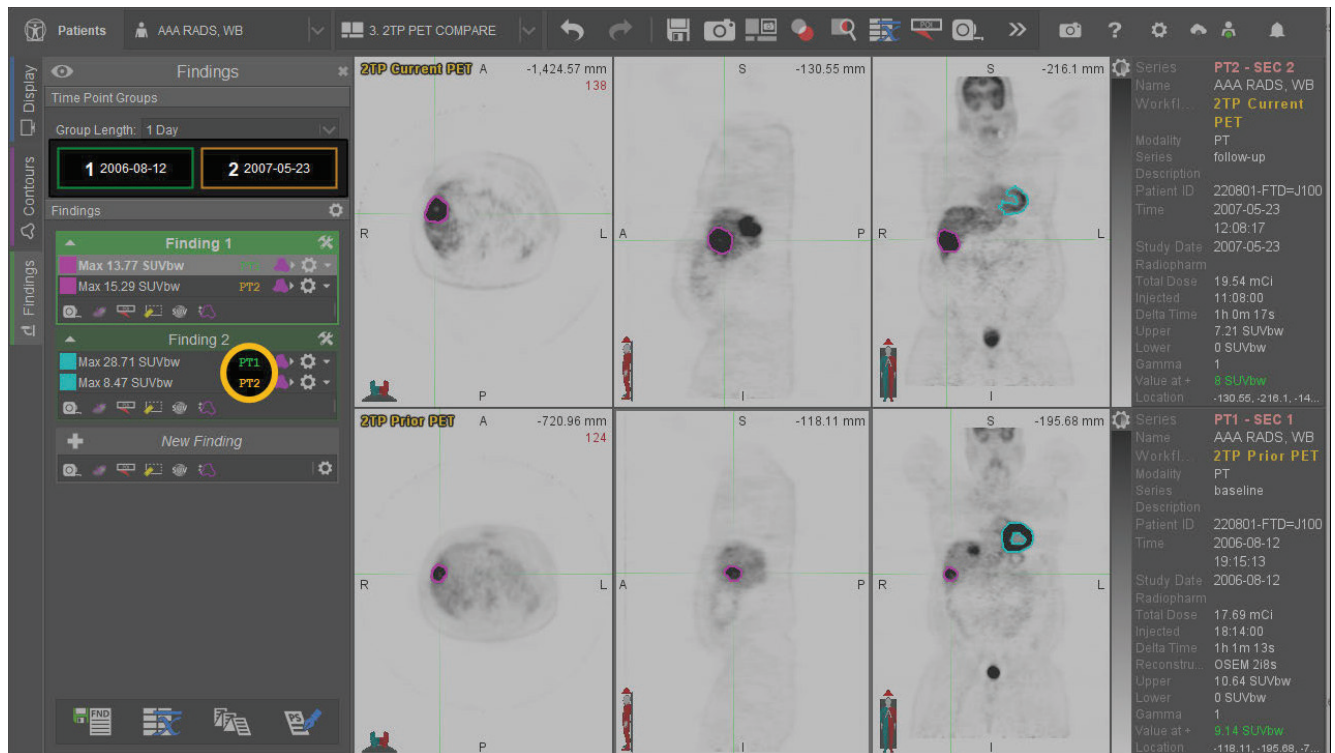


MIM Encore® User Guide

1. On the follow-up series, record a measurement of the existing region of interest. If you create a new region of interest in a location where a previously measured region of interest exists, MIM recognizes the regions of interest as the same finding and groups them together.



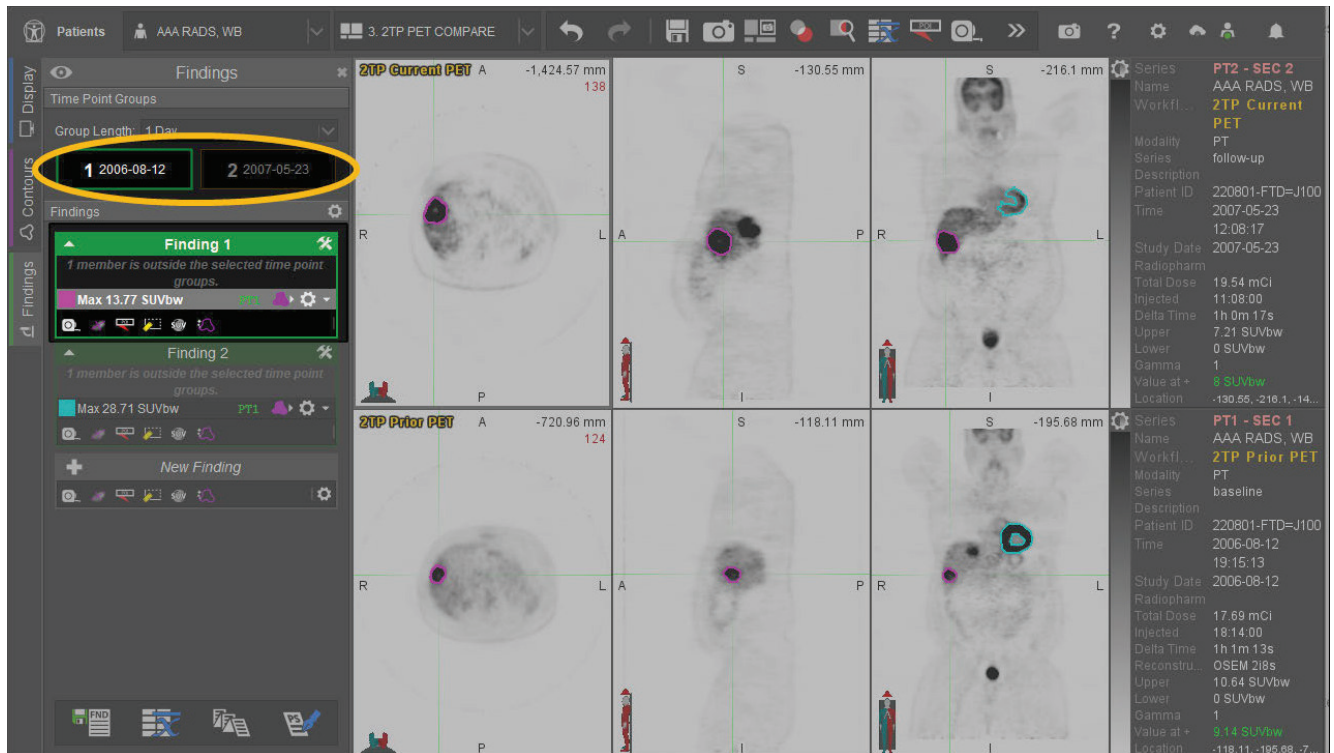
2. Look at the Findings sidebar. You can distinguish between two measurements in the same finding by looking at which series the measurements correspond to (in the example below, *PT1* or *PT2*).




Tip: The color of the text matches the corresponding time point in the **Time Point Groups** section.

3. Continue creating measurements as necessary.

- If desired, you can hide a time point by deselecting the **Time Point Group** button.



- Once you are finished creating measurements, click the save  button at the bottom of the sidebar to save the findings. Refer to [Record Measurements Using the Findings Sidebar](#) for more information about saving findings.



Tip: If desired, you can use the Statistics Viewer  to see stats for the findings across viewpoints. Refer to [View Statistics](#) for more information about working with the Statistics Viewer.

Customize Findings Settings

MIMTD-694 • 15 Aug 2023

Overview

You can configure how findings appear in the Findings sidebar and in the information box in the viewport. Depending on your scenario, you may also want to adjust how findings are saved or copied.



Related: See [Record Measurements Using the Findings Sidebar](#) for more information on creating and reviewing Findings.




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.

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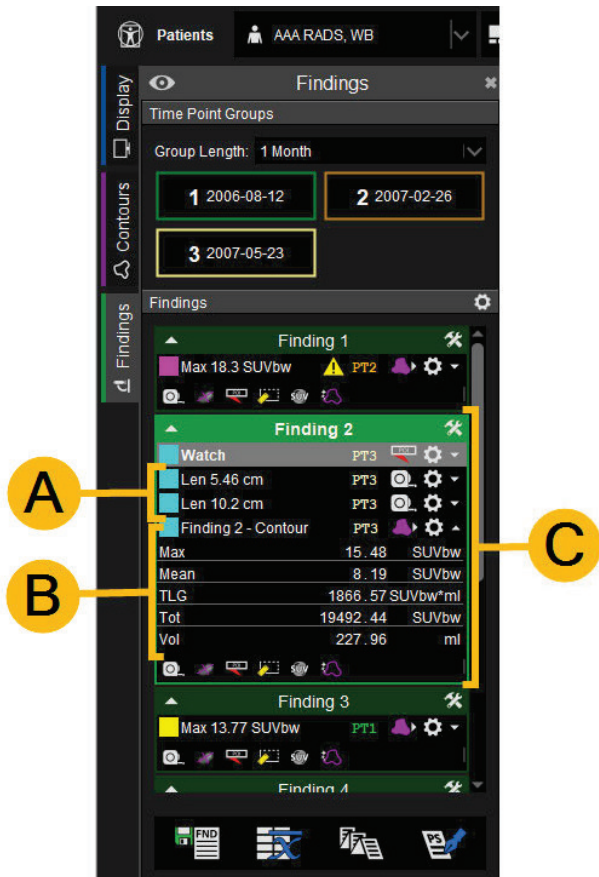
- [Determine Findings Sidebar Display](#)
- [Determine How Findings Appear in a Viewport](#)
- [Enable Automatic Saving](#)
- [Update Copy Settings](#)

Determine Findings Sidebar Display

You can adjust the following settings to update the display in the Findings sidebar based on your needs.

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

3. Review the following settings:

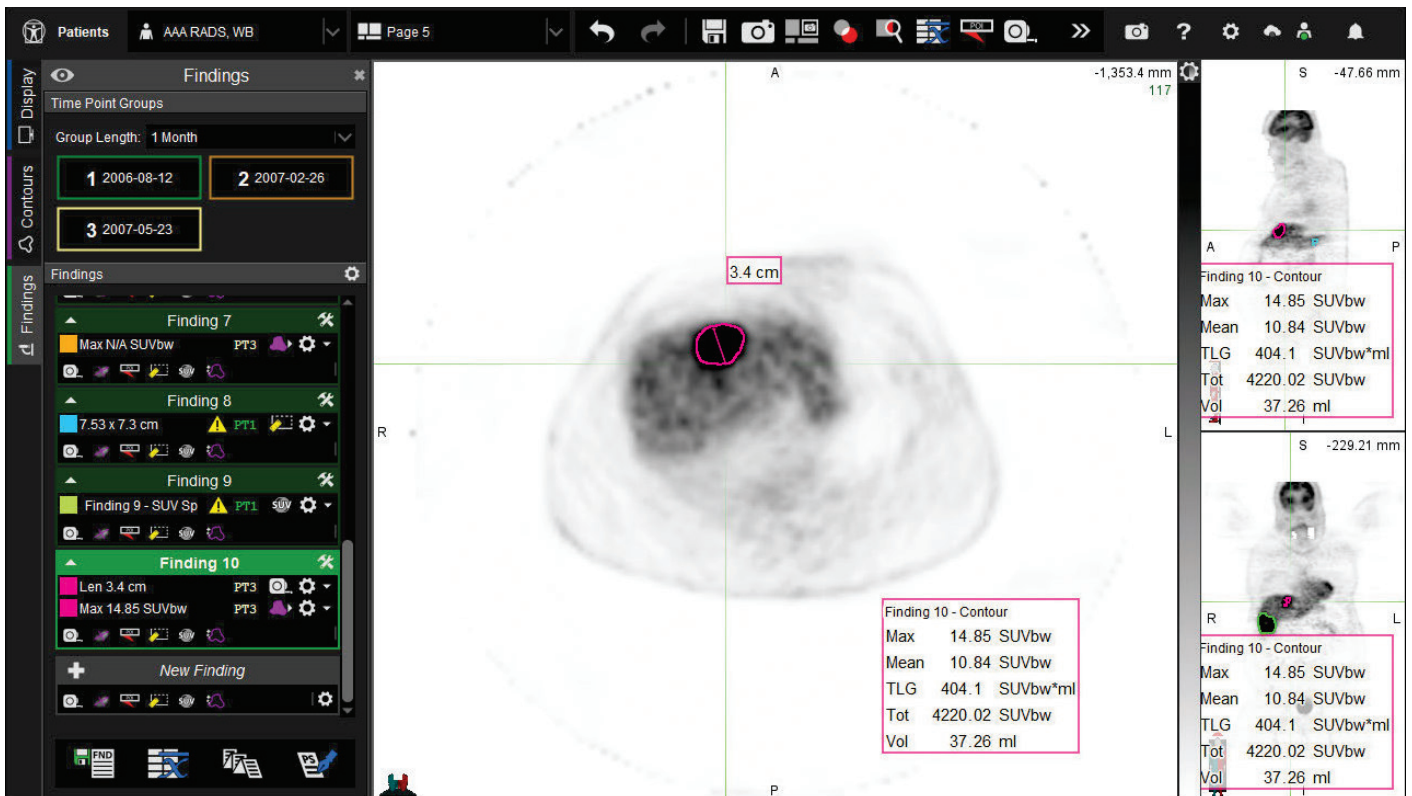



- A. **Default Unit for Length Measurements:**
By default, MIM displays the measurement based on the image DICOM. If desired, update to show always as millimeters or centimeters. *This image shows centimeters.*
- B. **Automatically expand finding statistics:**
This setting determines the default behavior. You can always expand or collapse statistics by clicking the arrow next to the measurement. *This image shows expanded statistics.*
- C. **Create New Findings:** By default, findings are grouped together based on region. Change this setting to **For Each Measurement** if you want a new Finding to always be created, regardless of a measurement's proximity to other measurements. *This image shows the default behavior of grouped findings.*
- D. **Sort Findings:** By default, findings are listed chronologically in the order of creation. If you often click on the finding names and rename them, you may want to change this setting to list Findings alphabetically instead. *This image shows the default behavior of listing Findings in the order of creation.*
- E. **Highlight a finding in the Findings Sidebar when it is clicked in a viewport:**
Enable this setting if you want Findings to be highlighted when selected. *This image shows Finding 2 highlighted.*

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


Determine How Findings Appear in a Viewport

If desired, you can update how findings information box appears within the viewport.



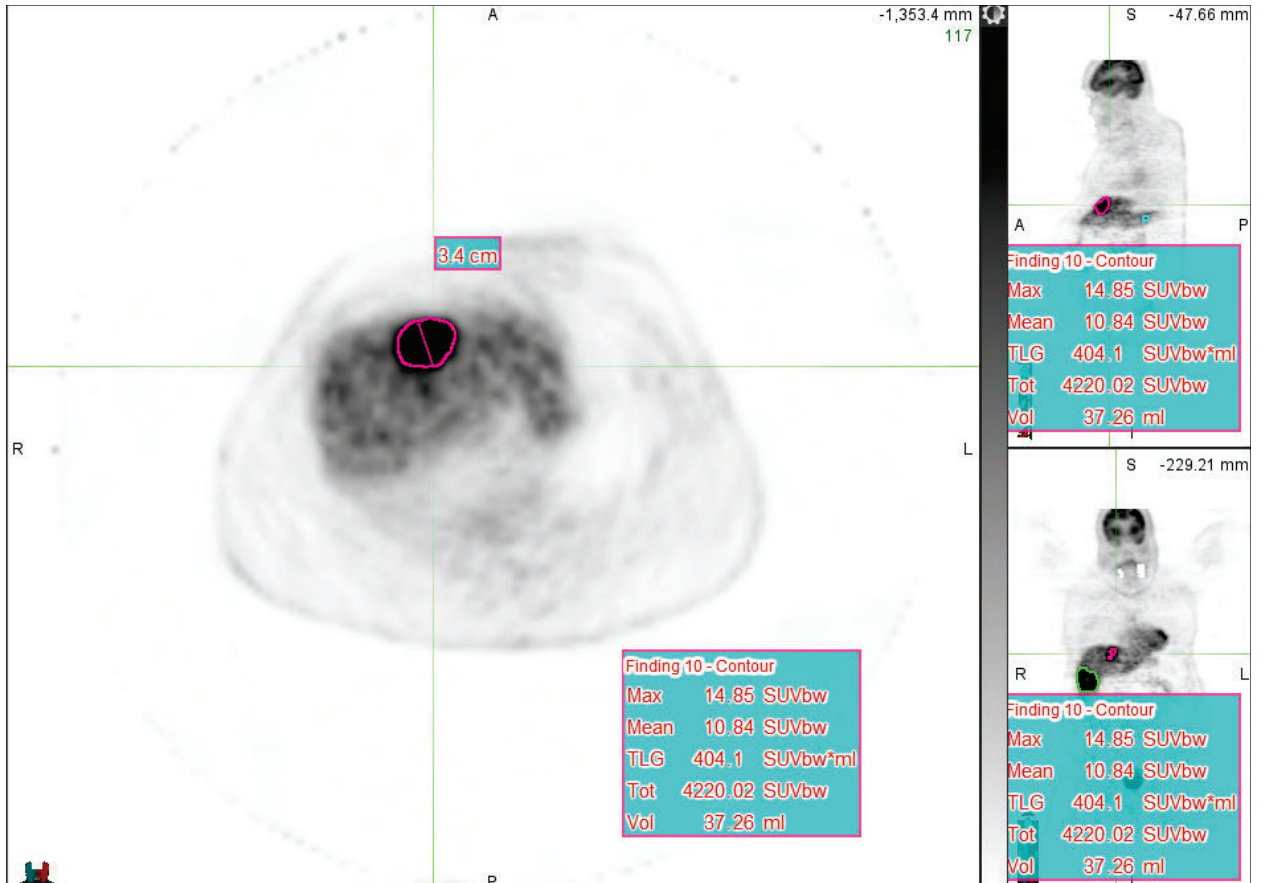
Tip: Measurements and annotations always appear in the viewport, unless hidden. To show information for contours, such as contours you create with the 2D Brush or PET Edge[®]+, go to Settings  >> **General Preferences** >> **Contouring** and select **Display statistics for the active contour in the viewport**.

Update the Information Box Display (MIM 7.2 and Later)

1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "findings". Select **Findings** on the left side.
3. Review the following settings, which are the most commonly updated:
 - **Avoid placing large finding info boxes over series** — Select this option so that information boxes appear on the side of the viewport, rather than over the image. Regardless of this setting, you can click and drag any information box to move it.
 - **Findings Statistic Font Size** — Adjust the font size for the statistics in the information box.

4. If needed, further adjust the information box display using the following settings:


- **Findings Statistic Font Color**
- **Findings Statistics Font Outline Color**
- **Findings Statistics Info Box Background Color**
- **Findings Statistics Info Box Background Opacity**



For the purposes of demonstration, this is how the information box appears when Font Color is red, Font Outline Color is white, Info Box Background Color is turquoise, and Info Box Background Opacity is increased (so the box appears darker).

5. Deselect **Invert Findings Statistics colors for low contrast background** if you want the information box to always appear as the same color, regardless of the image background.
6. Click **OK** to save the changes and close the window.

Update the Information Box Display (MIM 7.1 and Earlier)


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

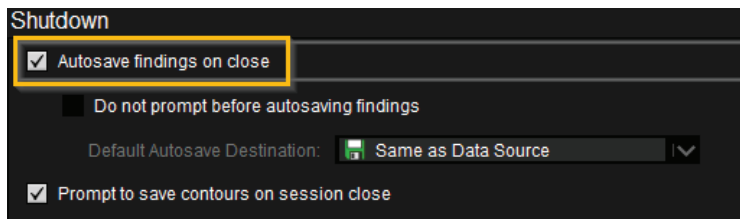
3. Review the following settings, which are the most commonly updated:
 - **Avoid placing large finding info boxes over series** — Select this option so that information boxes appear on the side of the viewport, rather than over the image. Regardless of this setting, you can click and drag any information box to move it.
 - **Findings Statistic Font Size** — Adjust the font size for the statistics in the information box.
4. **Findings Statistics Opacity** — Determine how dark or transparent the information box should appear.
5. Click **OK** to save the changes and close the window.

Enable Automatic Saving

Enable automatic saving so users don't have to remember to save findings for each patient.

To enable automatic saving of findings:

1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**autosave**". Select **Shutdown** on the left side.
3. Select **Autosave findings on close**.



4. If desired, select **Do not prompt before autosaving findings** and then select a **Default Autosave Destination** from the dropdown menu.
 - *If you enable this option, MIM saves findings automatically without prompting the user for any information, such as a save destination.*
 - *If you do not enable this option, when MIM or a session is closed, users are prompted to enter information for saving.*
5. If desired, select **Prompt to save contours on session close** so that users are prompted to save contours (an RTstruct set) anytime a session is closed.




Tip: This option is primarily used by researchers who want to save RTstruct files.

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

Update Copy Settings

The **Copy Findings Text to Clipboard**  tool copies findings to your computer clipboard so that you can paste them into a spreadsheet or third-party system as needed.

Use the following settings to determine what information is copied:

1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**findings**". Select **Findings** on the left side.
3. For **Findings to Copy when Copying Findings to Clipboard**, choose between the following:
 - **Expanded Findings** — Only copies Findings that are currently expanded in the sidebar.
 - **All Findings** — Copies all Findings in the sidebar.
4. For **Stats to Copy when Copying Findings to Clipboard**, choose between the following:
 - **Visible Stats** — Only copies statistics that are currently visible in the sidebar.
 - **Default Stats** — Copies the default statistics in the sidebar.
 - **All Stats** — Copies all statistics in the sidebar.
5. Click **OK** to save the changes and close the window.

View Statistics

MIMTD-1130 • 07 Sep 2023

Overview

Use the Statistics Viewer in MIM® to review all statistics for contours and measurements. You can compare statistics across time points and against a reference contour. MIM also calculates and displays ratio statistics.

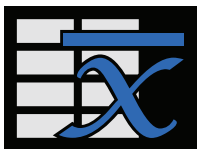
See [Statistics Definitions](#) for definitions of each statistic found in MIM.


Note: Statistics can also be reported from MIM Workflows™ via the Find Contour Statistic and Create Dynamic Stat workflow commands. You can also use MIM Workflows and MIM Extensions™ to calculate statistics not included by default in MIM. For assistance, please contact MIM Software Support at support@mimsoftware.com.

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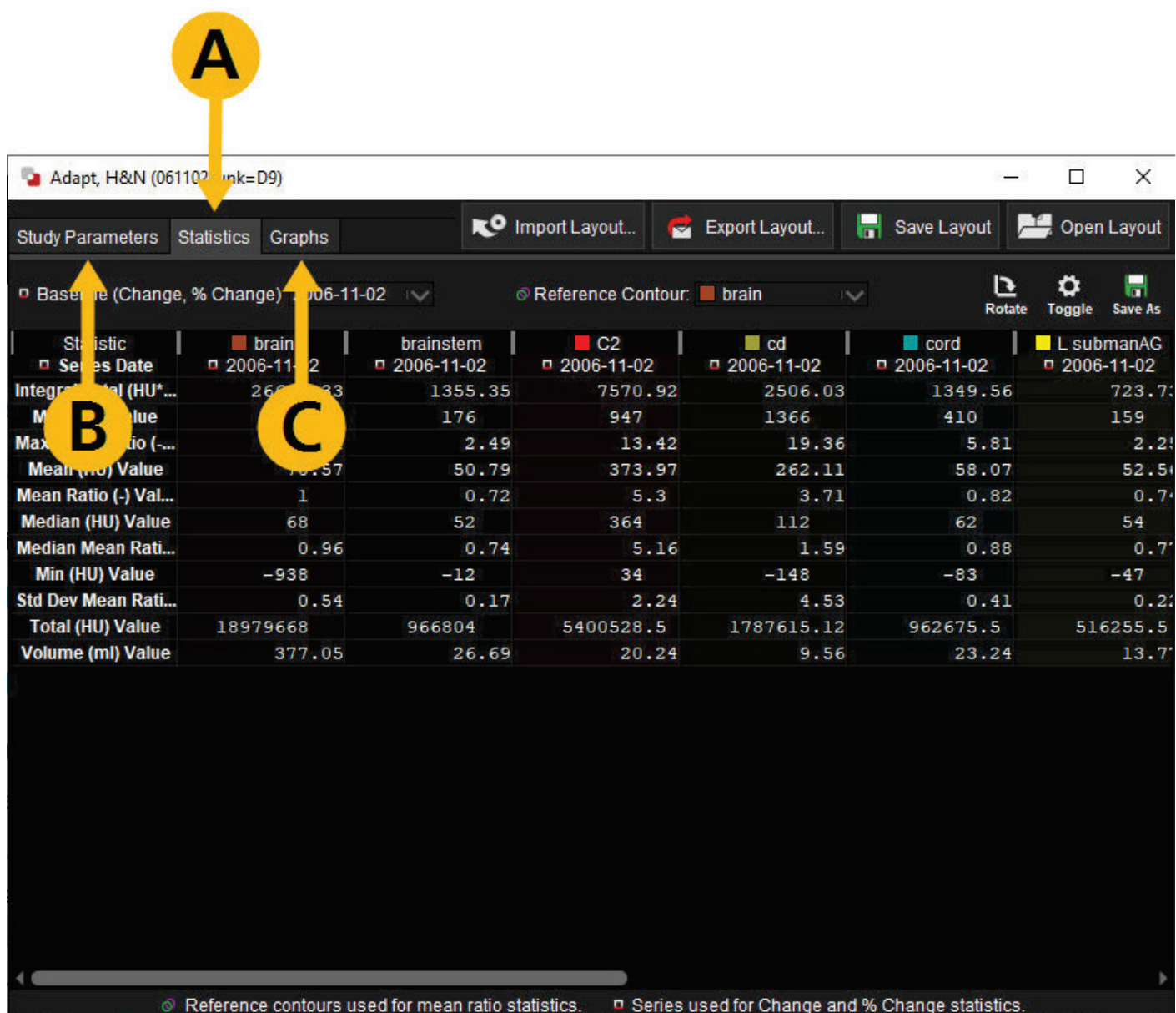
- [Statistics Viewer](#)
- [Statistics Tab](#)
- [Change Statistics](#)
- [Ratio Statistics](#)

Statistics Viewer



Click the  button from the toolbar, radial menu, or bottom of the Findings sidebar. The Statistics Viewer opens in a new window. For more information, see [Access Tools: The Toolbar and the Radial Menu](#) or [Record Measurements Using the Findings Sidebar](#).

- The Statistics Viewer includes contours from all series on the current page.
 - Look at the Series Date below each contour to disambiguate between contours from different series.
 - See [Change Statistics](#) below for more information on comparing statistics across time points.
- If desired, create a new page with a single series to view statistics for that series only.

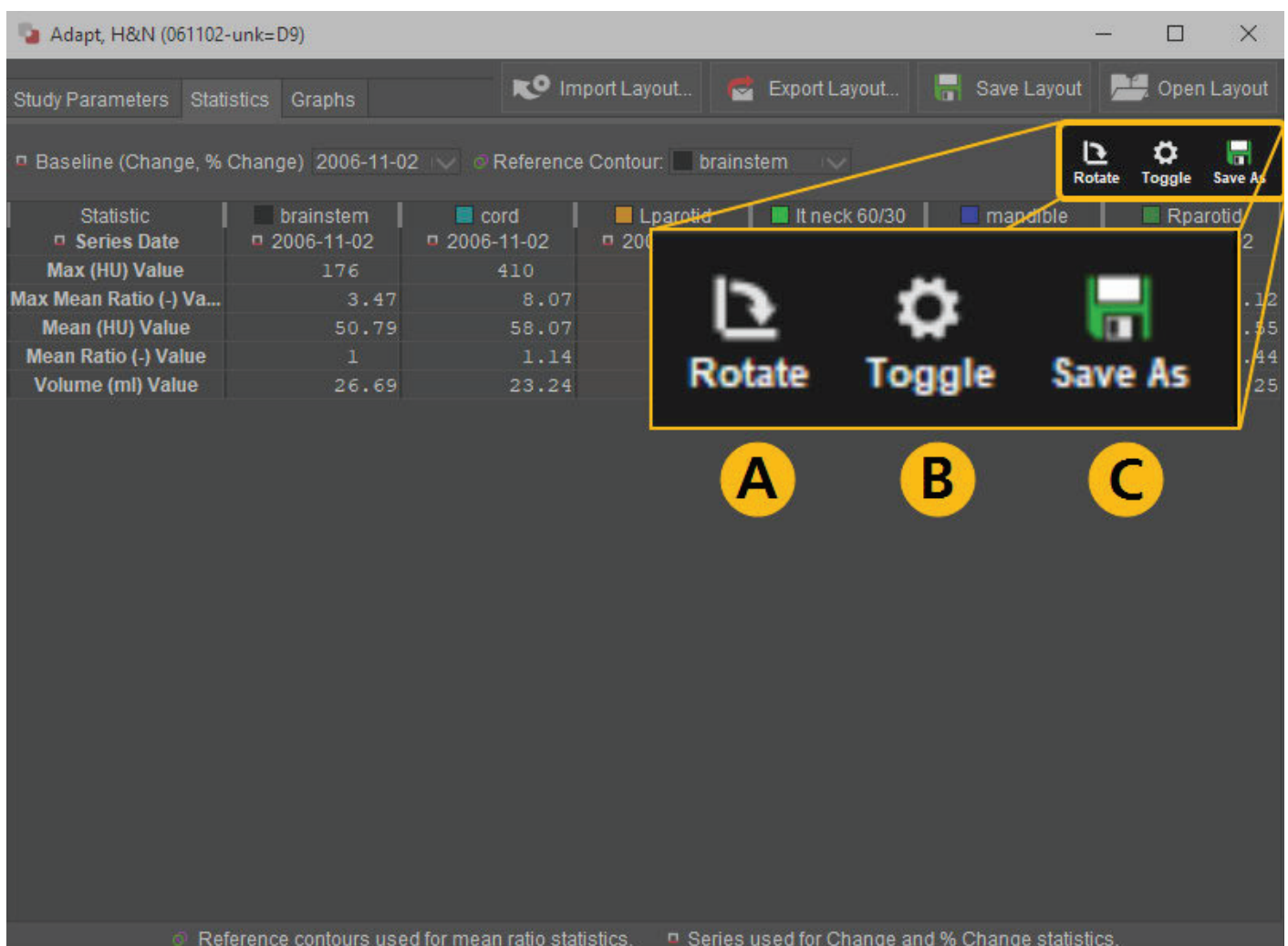


- A. The **Statistics** tab is shown by default when the Statistics Viewer opens.
- MIM displays contour names along the top, and the statistics on the left side.
 - Click a contour name in the Statistics Viewer to localize to the contour on the series.
 - See [Statistics Tab](#) below for more information.

- B. Go to the **Study Parameters** tab to view information about each series.
- You can change the **Series Identifier** from the Study Parameters tab.
 - The selected Series Identifier displays below the contour names in the Statistics tab and lets you disambiguate between contours from different series.
- C. Go to the **Graphs** tab to create graphs for any statistic.

Statistics Tab

The Statistics tab displays statistics in a table. Make adjustments or save the statistics using the buttons in the upper-right corner.



Statistic	brainstem	cord	Lparotid	It neck 60/30	mandible	Rparotid
Series Date	2006-11-02	2006-11-02	2006-11-02	2006-11-02	2006-11-02	2006-11-02
Max (HU) Value	176	410				
Max Mean Ratio (-) Value	3.47	8.07				
Mean (HU) Value	50.79	58.07				
Mean Ratio (-) Value	1	1.14				
Volume (ml) Value	26.69	23.24				

Reference contours used for mean ratio statistics. Series used for Change and % Change statistics.

- A. Use the **Rotate** button to switch the view so that statistics are listed at the top and contours are listed along the left side.

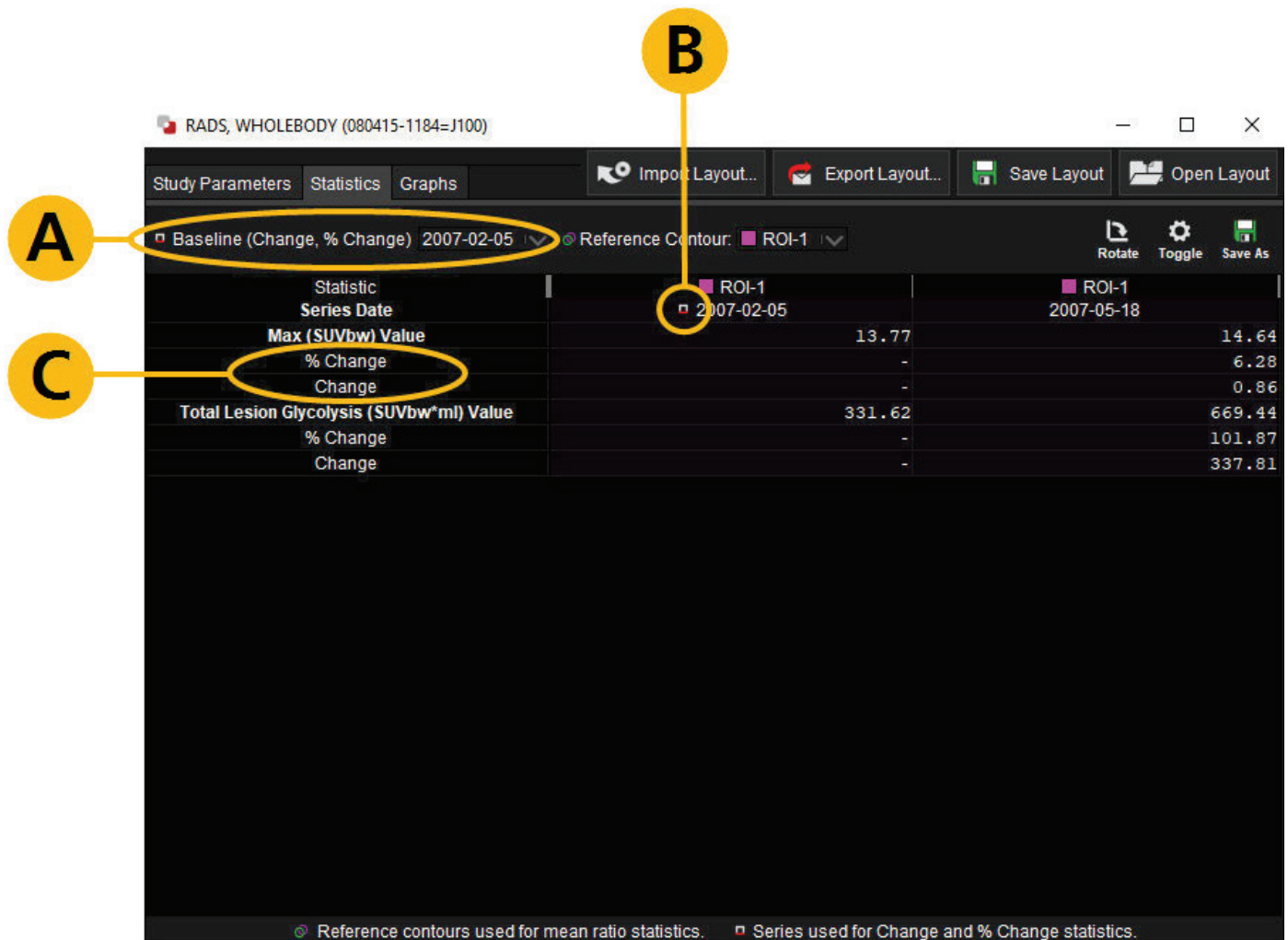


- B. Click the **Toggle** button to adjust which statistics are shown. When you click the **Toggle** button, a new menu opens with three tabs:
- **Matches** — Adjust the contours included in the viewer. Select or deselect individual contours as desired, or use the **Select All** and **Deselect All** buttons.
 - **Filters** — Adjust the contours included in the viewer via filters, including optional regex filters.
 - **Statistics** — Adjust the statistics included in the viewer. Select or deselect individual statistics as desired, or use the **Select All** and **Deselect All** buttons.
- C. Save the statistics in various formats using the **Save As** button. To save a CSV, select **Save As >> Spreadsheet**.

Change Statistics

Change statistics are calculated across time points based on a series which has been set as the baseline. By default, the baseline is the series with the earliest date.

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



- A. The baseline series is displayed in the upper-left corner.
- B. A small white and red indicator is displayed next to the baseline series.
- C. The change and percent change statistics can be viewed underneath each statistic value.

Ratio Statistics

Ratio statistics are calculated using a reference contour. The reference contour is set alphabetically by default.



Adapt, H&N (061102-unk=D9)

Study Parameters | Statistics | Graphs | Import Layout... | Export Layout... | Save Layout | Open Layout

Baseline (Change, % Change) 2006-11-02 | Reference Contour: brain

Statistic	brain	brainstem	C2	cd	cord	L submanAG
Series Date	2006-11-02	2006-11-02	2006-11-02	2006-11-02	2006-11-02	2006-11-02
Integral Total (HU*...)	26607.33	1355.35	7570.92	2506.03	1349.56	723.7
Max (HU) Value	920	176	947	1366	410	159
Max Mean Ratio (-...)	13.04	2.49	13.42	19.36	5.81	2.2
Mean (HU) Value	70.57	50.79	373.97	262.11	58.07	52.5
Mean Ratio (-) Val...	1	0.72	5.3	3.71	0.82	0.7
Median (HU) value	68	52	364	112	62	54
Median Mean Rati...	0.96	0.74	5.16	1.59	0.88	0.7
Min (HU) Value	-938	-12	34	-148	-83	-47
Std Dev Mean Rati...	0.54	0.17	2.24	4.53	0.41	0.2
Total (HU) Value	18979668	966804	5400528.5	1787615.12	962675.5	516255.5
Volume (ml) Value	377.05	26.69	20.24	9.56	23.24	13.7

Reference contours used for mean ratio statistics. Series used for Change and % Change statistics.

- Reference Contour** — The contour from which ratio statistics are calculated. Use the dropdown to change the reference contour.
- [statistic] Ratio** — The ratio of the given statistic value in that contour to the same statistic value in the reference contour. For example, the *Mean Ratio* of a contour is the contour mean divided by the mean of the reference contour.
- [statistic] [statistic] Ratio** — The ratio of the first statistic value in the contour to the second statistic in the reference contour. For example, the *Std Dev Mean Ratio* of a contour is the standard deviation of the contour divided by the mean of the reference contour.

Quantify Total Tumor Burden with LesionID®

MIMTD-1443 • 11 Oct 2023

Overview

Use the LesionID MIM Workflow™ to quantify areas of increased uptake. This workflow uses thresholds that you determine to automatically contour lesions. You can then calculate total tumor burden and other statistics.



Related: After reviewing the basics here about how to run the workflow, refer to [LesionID® Scenarios](#) for more information on using the workflow for scenarios such as multiple time points, PSMA studies, and to find DMAX.



Related: If your organization is licensed for LesionID Pro, go to [Quantify PSMA with LesionID® Pro](#) instead for more information about that feature.

Contents

- [Prerequisites](#)
- [Launch the LesionID Workflow](#)
- [Use LesionID to Process the Study](#)
 - [Segment Hotspots](#)
 - [Edit Lesions](#)
 - [Further Redefine or Edit Lesions](#)
 - [Create Total Tumor Burden](#)
 - [Save Contours](#)
- [Define Segmentation Settings](#)
- [Redefine Contours Based on Percent Threshold](#)
- [Optional Preferences for Higher Efficiency](#)

Prerequisites

MIM 7.3 and later: LesionID is a default workflow that is included with MIM Encore®. To import LesionID, follow the steps in [Import MIM Workflows™ and Other Content](#).

MIM 7.2 and earlier: Please contact MIM Software Support at support.mimsoftware.com if you would like to use the LesionID workflow.

Launch the LesionID Workflow

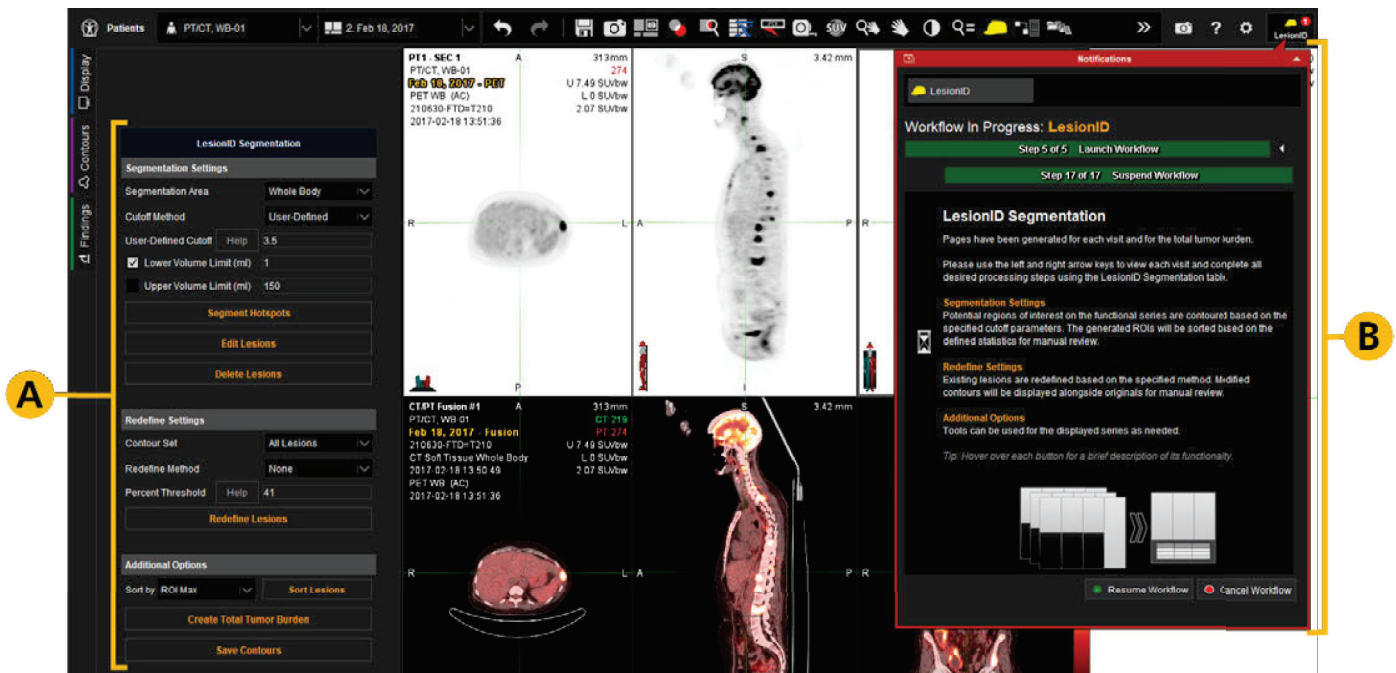
1. From the patient list, select a PET/CT or SPECT/CT series.



Tip: You can optionally select an RTstruct file as well, such as if you've already used LesionID to create contours and now you want to adjust them.

2. Launch the LesionID workflow.
3. If the **Confirm Selections** window appears, ensure that the series are correctly assigned to the targets. If the series are not correctly assigned, click the dropdown under **Assignment** to choose the correct series for each target, and click the **Confirm** button.

A page is generated for each time point, and a Notifications window appears:



- A. Access all LesionID settings and functions from the LesionID Segmentation sidebar.
- B. View quick instructions on using the functions in the sidebar.



Tip: To hide the Notifications window, click the arrow in the upper-right corner of the window or press the \ key on your keyboard. To expand the Notifications window again, click the flashing notification symbol in the upper-right corner of MIM or press the \ key.

Use LesionID to Process the Study

When the session opens with the LesionID workflow, work your way down the LesionID Segmentation sidebar.

Segment Hotspots

In the LesionID Segmentation sidebar, click **Segment Hotspots**. Contours are automatically drawn based on the Segmentation Settings. You can use the default settings or edit them as needed. See [Define Segmentation Settings](#) below for more information about editing these settings.

Edit Lesions

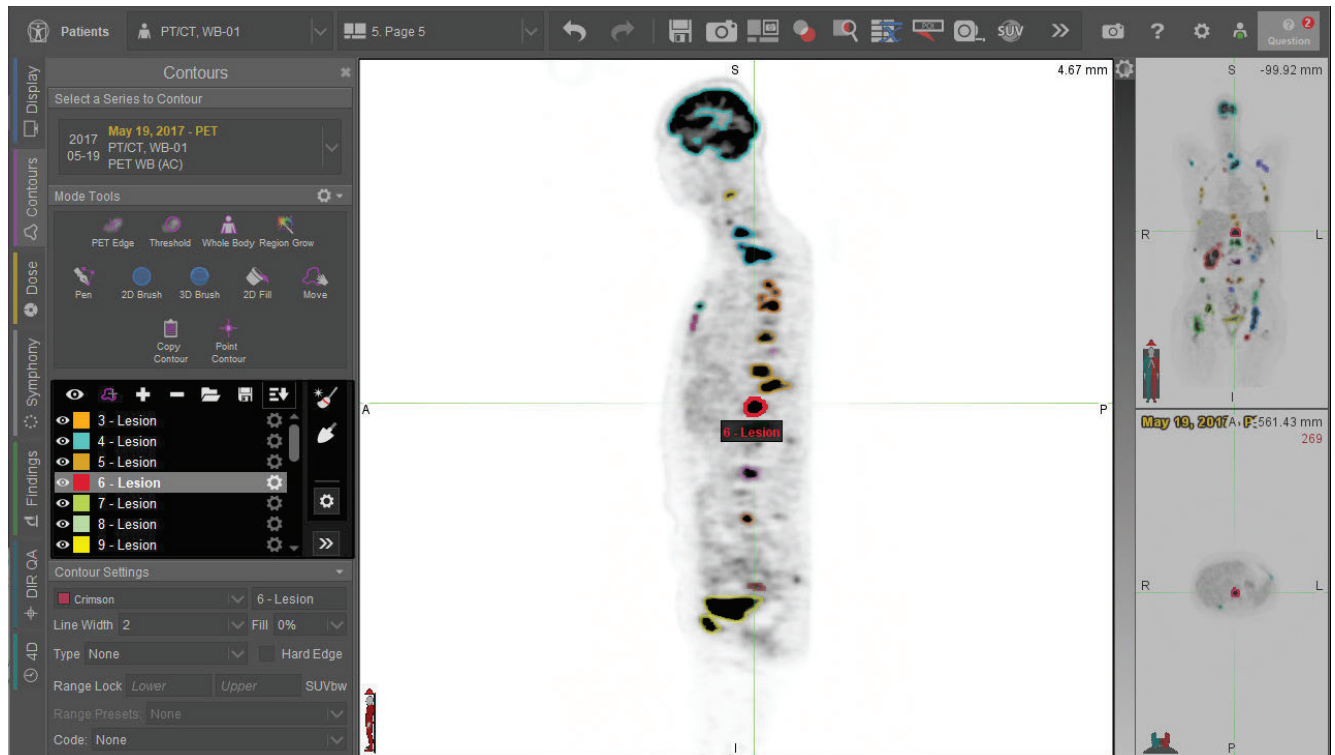
After segmenting hotspots, you are taken to a new Contour Review page. Review the automatically drawn contours. For efficiency, you can:

- Double-click on one of the viewports to see it larger.
- Press A to cycle to the next contour.
- Press D to delete the contour. (You may need to configure this shortcut, as described in [Set Keyboard Shortcuts](#).)
- Select a contour either from the Contours sidebar or from the image itself.



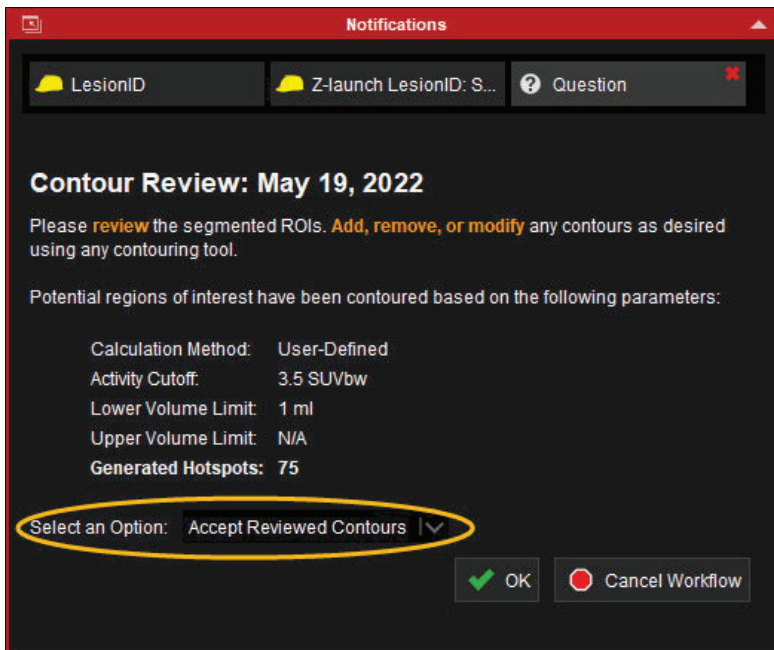
MIM Encore® User Guide

- Activate the **2D Brush**  and use it to manually edit a contour as needed.



Tip: See [Optional Preferences for Higher Efficiency](#) below for other options that you might find useful for reviewing contours quickly.

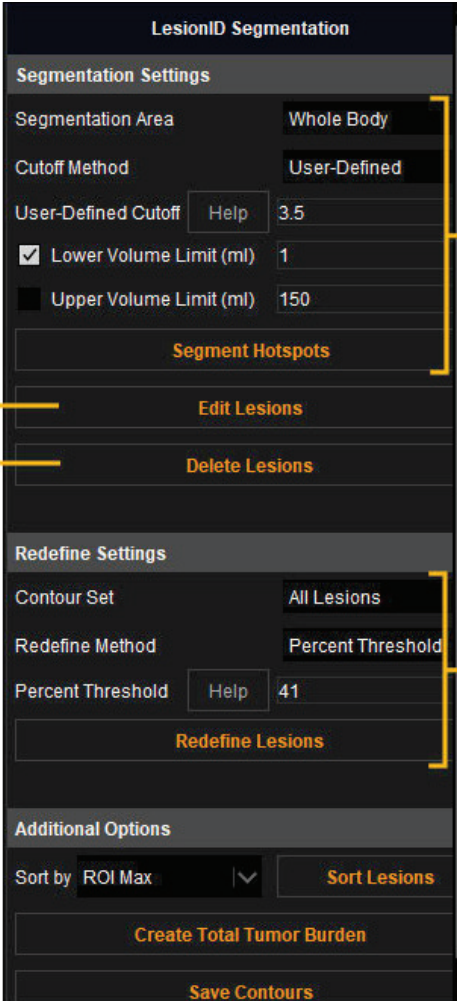
When you are finished, expand the Notifications window and select the **Accept Reviewed Contours** option. Click **OK**. The workflow closes the Contour Review page.



Tip: If you want to start over, select **Reject and Re-Segment** instead.

Further Redefine or Edit Lesions

You are back on the page with the LesionID Segmentation sidebar, and you have a few options:



The screenshot shows the 'LesionID Segmentation' sidebar. Callout A points to the 'Edit Lesions' button. Callout B points to the 'Delete Lesions' button. Callout C points to the 'Segmentation Settings' section, which includes 'Segmentation Area' (Whole Body), 'Cutoff Method' (User-Defined), 'User-Defined Cutoff' (3.5), 'Lower Volume Limit (ml)' (1), and 'Upper Volume Limit (ml)' (150). Callout D points to the 'Redefine Settings' section, which includes 'Contour Set' (All Lesions), 'Redefine Method' (Percent Threshold), and 'Percent Threshold' (41). Below these are buttons for 'Segment Hotspots', 'Redefine Lesions', 'Additional Options', 'Sort by ROI Max', 'Sort Lesions', 'Create Total Tumor Burden', and 'Save Contours'.

- To go back and make further edits, click **Edit Lesions**. The Contour Review page reopens. You can further edit as needed and then choose **Accept Reviewed Contours** when you are finished.
- To remove all contours and start over, click **Delete Lesions**.
- To rerun auto-contouring with a different cutoff, update the Segmentation Settings and select **Segment Hotspots**. See [Define Segmentation Settings](#) below for details.
- To rerun auto-contouring so that lesions are defined based on the percentage of their maximum value (%SUVmax), specify a **Percent Threshold** in the Redefine Settings and click **Redefine Lesions**. See [Redefine Contours Based on Percent Threshold](#) below for details.

When you are done defining and editing lesions, continue to see Total Tumor Burden.

Create Total Tumor Burden

6.1.3

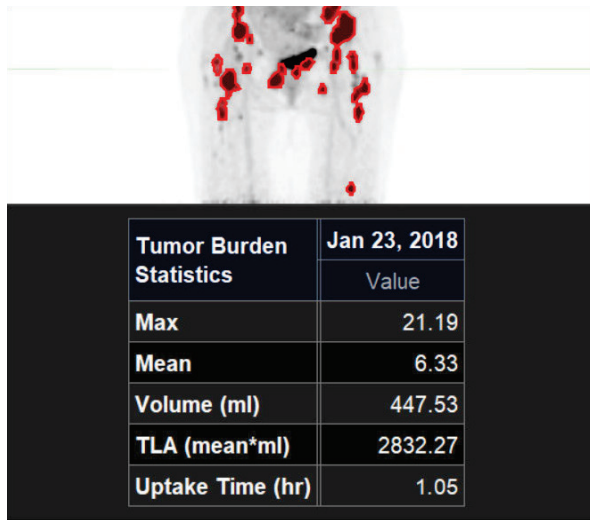
After you accept the reviewed lesions, as described above, use the Create Total Tumor Burden option to see statistics. With this feature, the workflow combines all lesion contours into one contour.



Tip: This step is optional. If you do not need the Total Tumor Burden, skip this section and continue to the next section to save the contours.

- On the LesionID Segmentation sidebar, click the **Create Total Tumor Burden** button. The workflow combines the contours so they appear as a single contour in a single color.
- Press the left and right arrow keys on your keyboard to switch to the Tumor Burden page.

3. Review the Tumor Burden Statistics table.



Related: For definitions of statistics in MIM, see [Statistics Definitions](#).

Save Contours

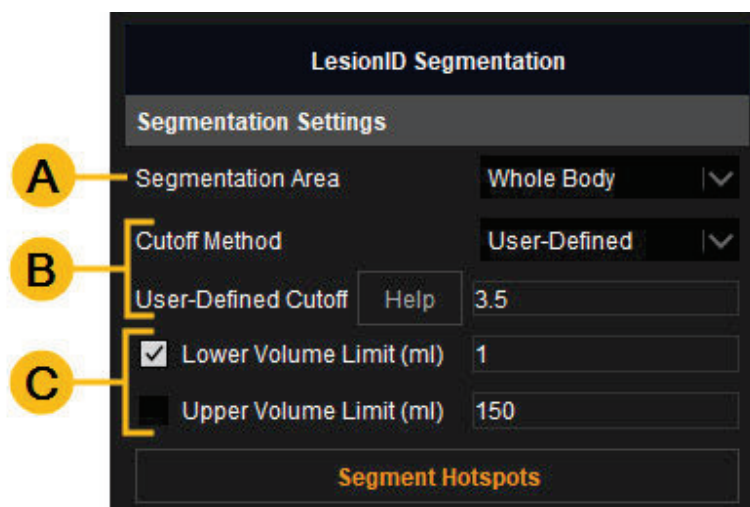
When you are finished, click the Save Contours button. Complete the information in the Notifications window to save an RTstruct set with the contours that were created.



Related: You can also save use Save in the top toolbar. For more information about saving options, refer to [Save Patient Data](#).

Define Segmentation Settings

You can update the segmentation settings based on your situation to determine how the workflow auto-contours lesions.



- A. Choose whether to segment regions of uptake in the whole body or in a specific area. If you choose **User-Defined**, the workflow prompts you to define the area.
- B. Choose whether to define your own activity-cutoff value or use PERCIST criteria to calculate an activity-cutoff value:

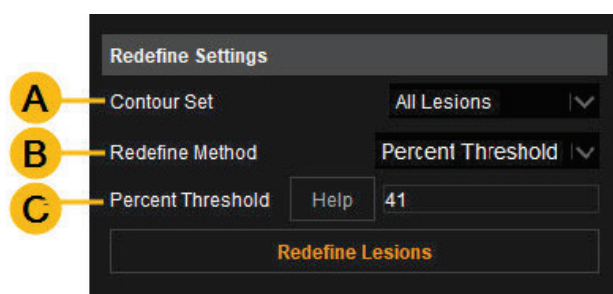
Cutoff Method	Reference Region	Activity Cutoff Value Calculation
User-Defined	N/A	Activity cutoff = The User-Defined Cutoff value using the unit of the current series Creates contours for any voxels in the defined segmentation area that are equal to or higher than the entered value.
PERCIST: Liver	Healthy region of the liver with representative uptake 3 cm diameter sphere	Activity cutoff = (1.5 * Reference Mean) + (2 * Reference Standard Deviation)
PERCIST: MBP	Mediastinal blood pool 2 cm diameter sphere	Activity cutoff = (2 * Reference Mean) + (2 * Reference Standard Deviation)

- C. If desired, define lower and upper volume limits to prevent unwanted regions from being contoured. When creating contours, the workflow automatically removes any contours that are above or below the limits. Applying a lower volume limit helps avoid creating contours for one- to two-voxel regions.

After adjusting the Segmentation Settings, click the **Segment Hotspots** button to run auto-contouring.

Redefine Contours Based on Percent Threshold

You can redefine each contour based on a percentage of its maximum value (%SUVmax).



- Choose whether to redefine all contours or selected contours. If you choose **User-Defined**, the workflow prompts you to select the contours to redefine.
- Choose **Percent Threshold** in the Redefine Method field.
- Enter the percent threshold to use. Each contour is redefined based on this percentage of its maximum value.




Important: The percent threshold method sometimes creates a new activity-cutoff value that is lower than the original activity-cutoff value defined in the segmentation settings. This is most common in low-uptake lesions. You may see a notification to review the affected contours with the new cutoff value.

After adjusting the Redefine Settings, click the **Redefine Lesions** button. Follow the workflow prompts to further review as needed.

Optional Preferences for Higher Efficiency

You might find the following preferences and shortcuts helpful to speed up your review of automatically drawn contours.

To update these preferences:

- Click the Settings  button in the upper-right corner of MIM.
- Go to the location that is noted in the below table.
- Enable the desired preference.
- Click **OK** to save the changes and close the window.

Preference	Note	Location
Auto-localize when switching active contour	Useful if you cycle through contours and delete them via keyboard shortcut.	General Preferences >> Imaging >> Contouring >> Advanced

Preference	Note	Location
Display contour list alphabetically	Displays the LesionID contour list by the selected statistic (descending).	General Preferences >> Imaging >> Contouring
Dim all contours except for the active one	Useful for high-burden patients with many contours to review.	General Preferences >> Imaging >> Contouring

LesionID® Scenarios

MIMTD-1726 • 11 Oct 2023

Overview

You can use the LesionID MIM Workflow™ to address specific scenarios. You might want to use this workflow for one of the use cases described below.



Related: Refer to [Quantify Total Tumor Burden with LesionID®](#) to get started with the basics of how to run the LesionID workflow.



Related: If your organization is licensed for LesionID Pro, go to [Quantify PSMA with LesionID® Pro](#) instead for more information about that feature.

Contents

- [Run LesionID for Multiple Time Points](#)
- [Calculate Statistics for Low Tumor Burden](#)
- [Calculate Additional Statistics](#)
- [Compare Cutoff Values](#)
- [Apply Contour Labels for Regional Tumor Burden](#)

Run LesionID for Multiple Time Points

You can run the LesionID workflow for more than one time point. For example, you might want to compare two or more studies to see the change in Total Tumor Burden over time and help evaluate therapy response.

Running the LesionID workflow for multiple time points works the same way as described in [Quantify Total Tumor Burden with LesionID®](#). Keep in mind the following:

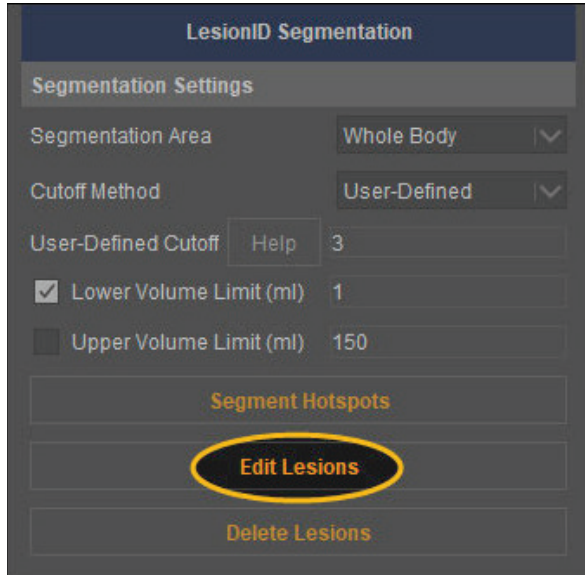
- From the patient list, select all of the PET/CT or SPECT/CT series for which you want to launch the workflow.
- The workflow creates a page for each time point. Press the left and right arrow keys on your keyboard to switch between time points.

- When you click a button on the LesionID Segmentation sidebar, the action only affects the time point that you are currently viewing. You need to repeat the action for each time point. This includes the following actions:
 - Segment Hotspots
 - Edit Lesions
 - Delete Lesions
 - Redefine Lesions
 - Sort Lesions
 - Create Total Tumor Burden

Calculate Statistics for Low Tumor Burden

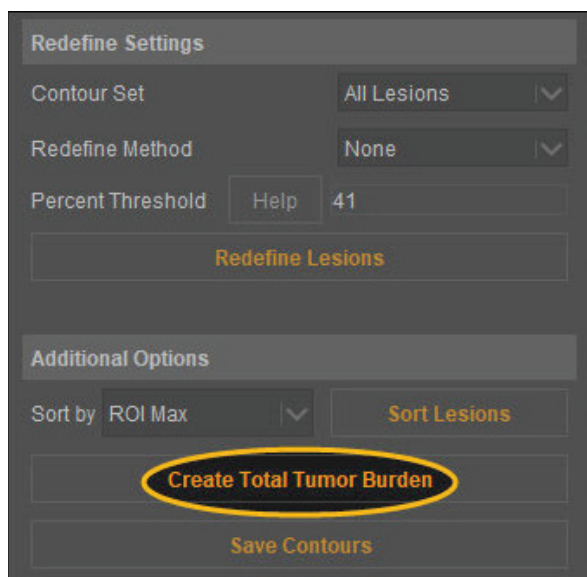
For low-burden cases, it might be challenging to review and delete unnecessary contours that are auto-created due to high physiological uptake. Instead, you can manually contour the lesions and use the Create Total Tumor Burden feature to add together the contours and report statistics.

1. Select the series and launch the LesionID workflow.
2. In the LesionID Segmentation sidebar, do not click the Segment Hotspots button. Instead, click the **Edit Lesions** button.



3. Manually draw regions of interest using the contouring tool of your choice, such as PET Edge®+.
4. When you are finished, select the **Accept Reviewed Contours** option in the Notifications window. Click **OK**.

- In the LesionID Segmentation sidebar, click the **Create Total Tumor Burden** button.



- Press the left and right arrow keys on your keyboard to switch to the Tumor Burden page and review the Tumor Burden Statistics table.

Calculate Additional Statistics

If your organization is doing research or has a scenario where you need to see additional data with the LesionID workflow, you may find one of the following variations of the LesionID workflow helpful:

- Lesion Dissemination — See a results table with Dmax, Dmax Bulk, Spread, and Spread Bulk statistics.
- Deauville Score — After you create liver and blood pool reference regions, the workflow predicts a Deauville score. It adds the score that you confirm as a screen annotation for the active PET. **6.1.7**

Please contact MIM Software Support at support.mimsoftware.com if you are interested in using one of these variations of the LesionID workflow.



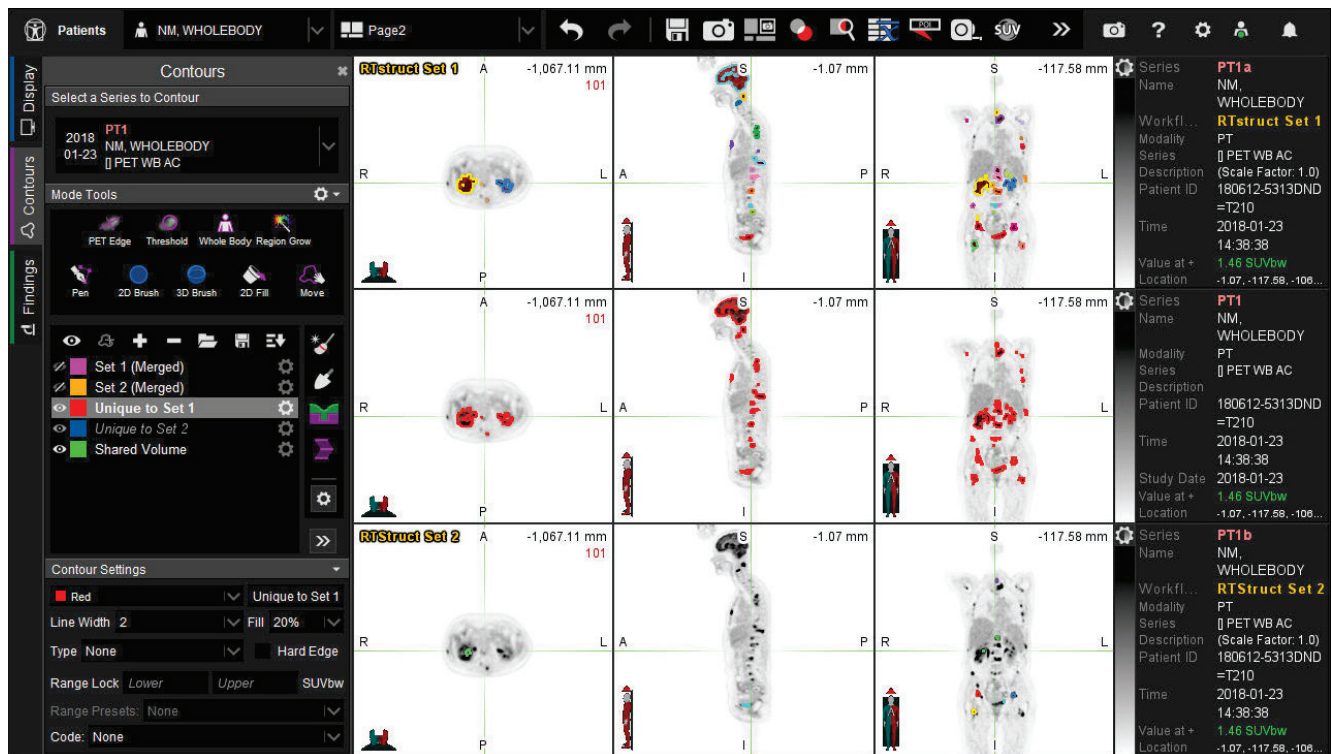
Tip: To calculate PSMA Total Tumor Burden segmentation, talk to your MIM representative about LesionID Pro (license required).

Compare Cutoff Values

In some research scenarios, it may be helpful to run LesionID multiple times with different thresholds to see differences in segmentation. Please contact MIM Software Support at support.mimsoftware.com if you would like to use the Compare RTstruct workflow.

With the comparison workflow, you do the following:

1. Run the LesionID workflow with a selected cutoff values. Review the contours and, when you are finished, save a DICOM RTstruct.
2. Change the selected cutoff value and run Segment Hotspots again. At the prompt, choose **Delete contours and re-segment the series**. Save the second set of contours as a DICOM RTstruct. Close the session.
3. From the patient list, select both of the RTsts you created and launch the **Compare RTstruct** workflow. The workflow shows the original series, both sets of contours, the shared volume where the contour sets overlap, and the regions that are unique to each set of contours.



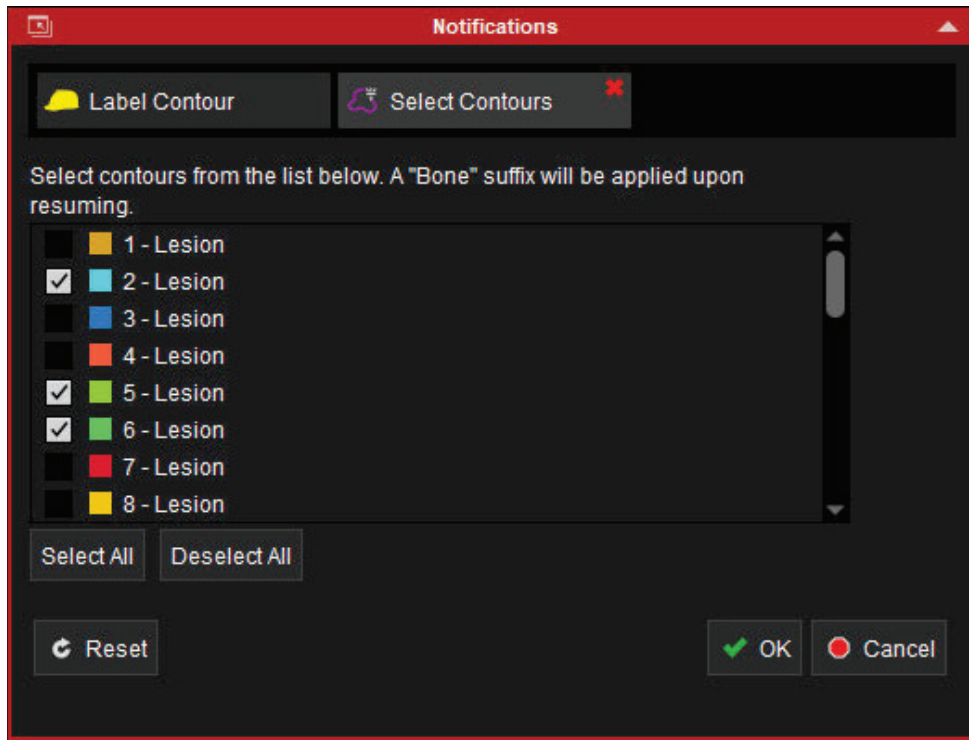
Apply Contour Labels for Regional Tumor Burden

After running the LesionID workflow, you can optionally run a supplemental workflow to update the contour names. For example, you can append an anatomical name to all contours in a given region. If desired, you can then run a second supplementary workflow to group Total Tumor Burden statistics by region.

Consider the following example:

1. Run the LesionID workflow, as described in [Quantify Total Tumor Burden with LesionID®](#).
2. Launch the **Label Contour** workflow and select a label to apply, such as Bone.

3. Select bone lesions identified by LesionID to add "Bone" to the lesion name.



4. Run the **Label Contour** workflow a second time to update the names of lesions in another region, such as to label lesions in lymph nodes.
5. Launch the **Regional Tumor Burden** workflow. The workflow generates Total Tumor Burden statistics tables for the identified Bone lesions and for the Lymph Node lesions.

Please contact MIM Software Support at support.mimsoftware.com if you are interested in using the Contour Labels and/or Regional Tumor Burden workflows.

Quantify PSMA with LesionID® Pro

MIMTD-1720 • 08 Nov 2023

Overview

LesionID Pro helps you visualize and report on PSMA studies for prostate cancer by automatically contouring regions of high uptake.

What LesionID Pro Shows

LesionID Pro:

- Automatically creates anatomical contours and identifies regions of high uptake.
- Identifies organs where physiological uptake is expected, such as the bladder.
- Calculates the Total Tumor Burden for all lesions to help with patient selection and evaluating therapy response.

How LesionID Pro Works

You can run LesionID Pro with a PET/CT or SPECT/CT. All automated contouring occurs on the CT.



Important: LesionID Pro should be used in a clinical setting for PSMA studies only. With other tracers, LesionID Pro must be used for research purposes only.

With LesionID Pro, you select which data to process and then can do other work as processing runs in the background (about 20 minutes per patient time point). When processing is finished, a prepared session is saved to your patient list.

Contents

- [Prerequisites](#)
- [Start Processing with LesionID Pro](#)
- [Evaluate Contours Created by LesionID Pro](#)
- [Review LesionID Pro Results](#)

Prerequisites

- MIM 7.3 or a later version
- LesionID Pro license



Related: If you do not have a LesionID Pro license, you might be interested in running the LesionID workflow that is included with MIM Encore®. Refer to [Quantify Total Tumor Burden with LesionID®](#) for more information about this workflow. It similarly segments hotspots based on uptake thresholds but requires more manual intervention to review and refine the contours identified.

- Contour ProtégéAI+™: Whole Body - Physiological Uptake Organs model
- MIM Assistant® installed

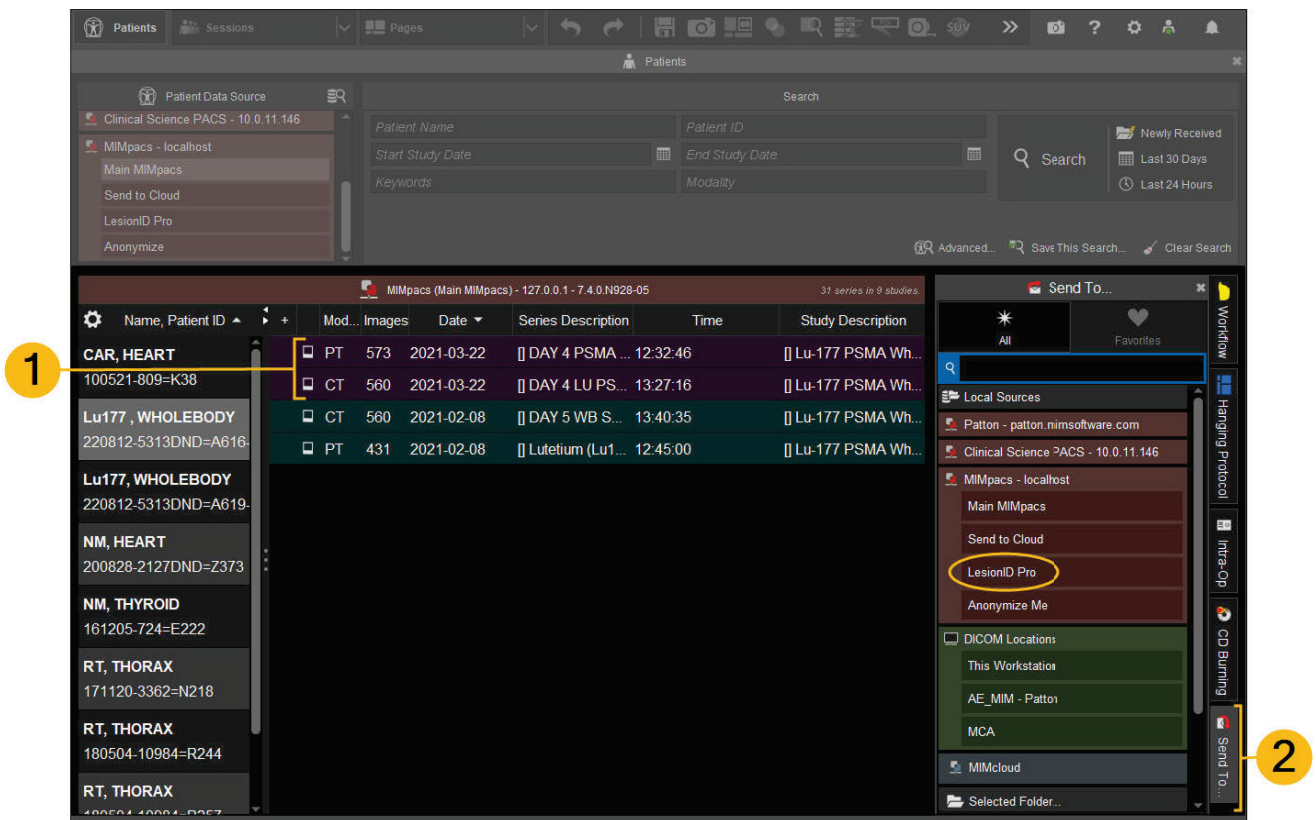
LesionID Pro is implemented for you by your MIM Implementation Specialist or Site Development Manager, as described in [Set Up LesionID® Pro](#).

Start Processing with LesionID Pro

As part of your implementation, your MIM representative sets up a designated patient list for LesionID Pro. To run LesionID Pro for a patient, use your normal steps to send the patient data to the LesionID Pro list:

1. On your patient list, select a PET/CT or SPECT/CT for a patient. As you select studies, note that:
 - You can optionally select multiple time points.
 - LesionID Pro looks for all PET/CT or SPECT/CT pairs in your list for a given patient to facilitate serial exam review. For example, if you have an existing baseline PET/CT with a finalized RTstruct in your list, sending the follow-up PET/CT automatically imports your results from the baseline scan.
 - The automated contouring part of LesionID Pro does not need to run again on series where the RTstruct is finalized, but it imports the results for comparison.

- Go to the **Send To...** tab and select the designated patient list for LesionID Pro.



- Confirm in the Notifications window that the transfer is successful.

LesionID Pro automatically begins running in the background. The automated processing takes about 20 minutes per patient time point and runs one at a time. For example, you might start processing for a patient with three time points, and then continue with different work. When you come back to your patient list about an hour later, the processing has finished and a session is ready for you.

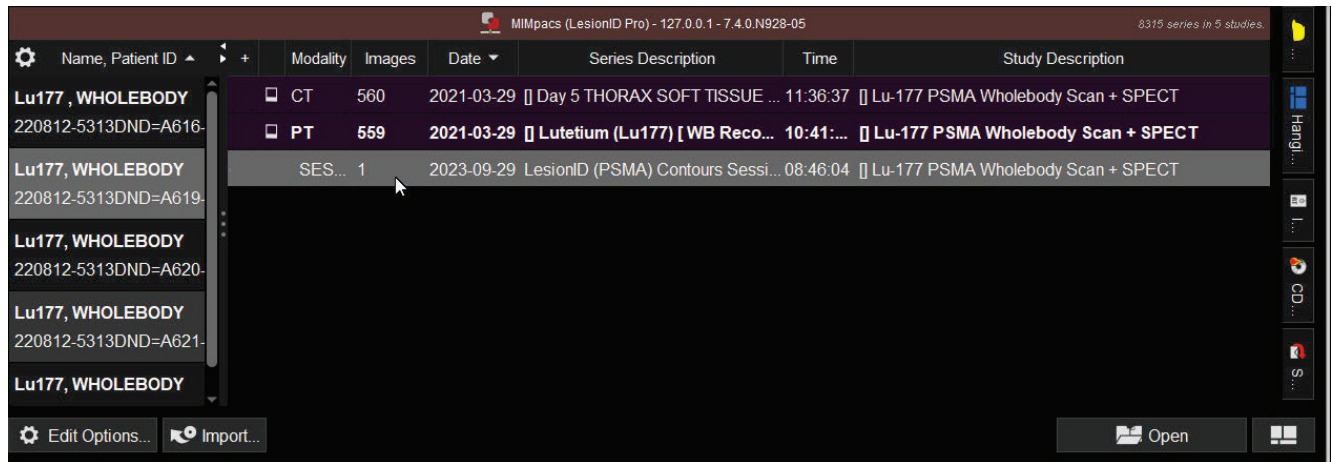
Evaluate Contours Created by LesionID Pro

Return to your LesionID Pro patient list when processing has finished and look for the session made by LesionID Pro:



MIM Encore® User Guide

1. Find the session that was created for the patient and double-click on the session to open it.

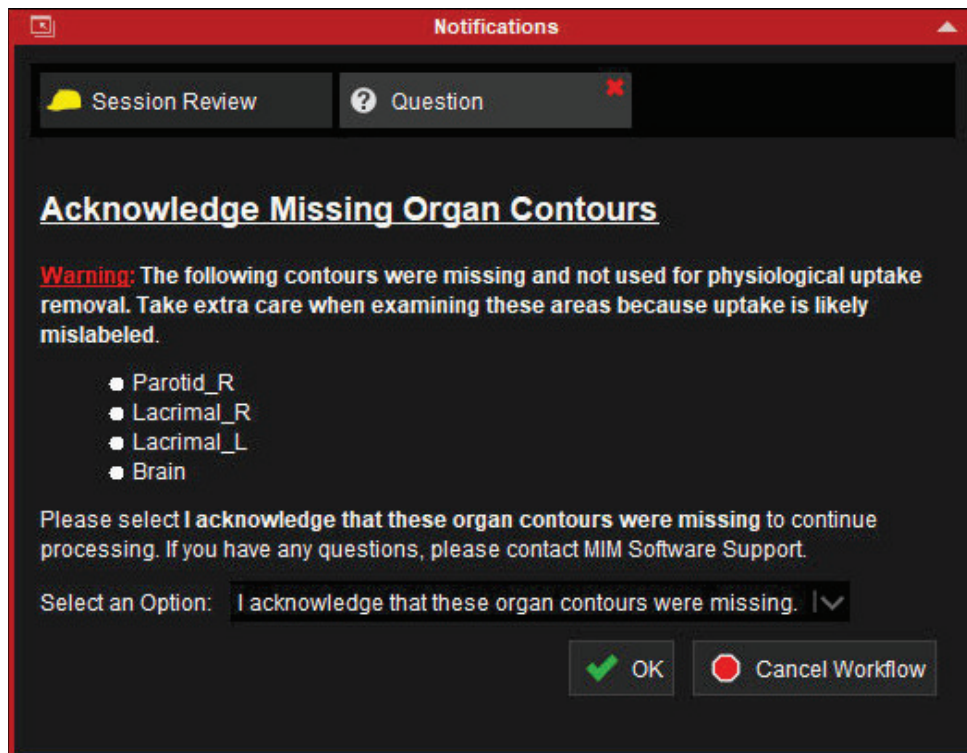


A workflow automatically launches when the session is opened. Prompts in the Notification window guide you through your next steps.

2. If you see the prompt to **Acknowledge Missing Organ Contours**, make note of the contours listed. Acknowledge that you have reviewed the notification and click **OK** to continue the workflow.

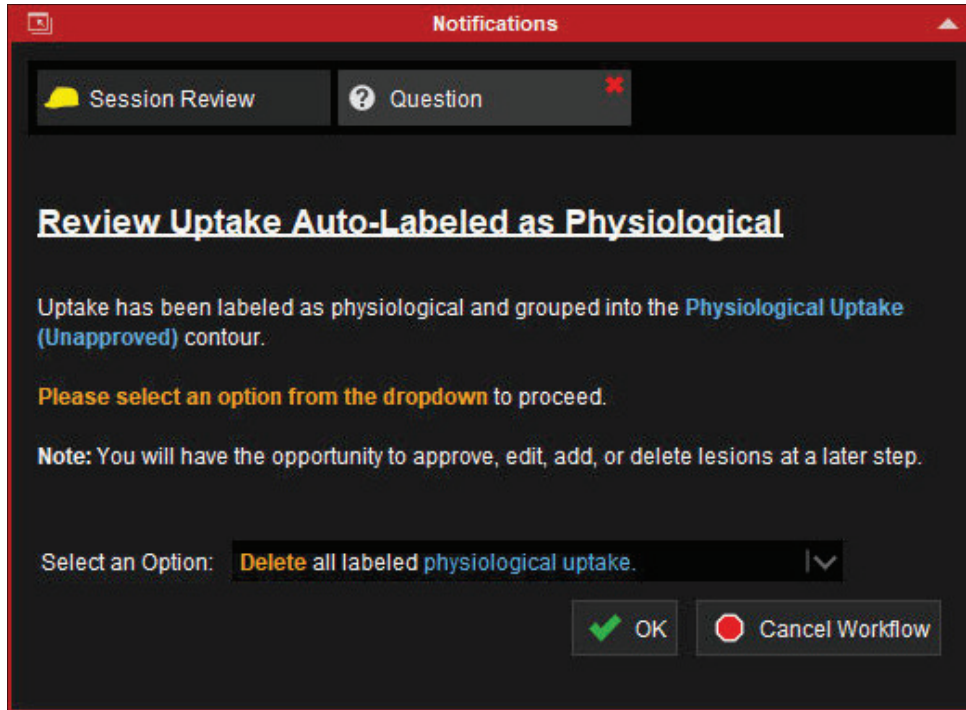


Important: Because the uptake in these regions could not be automatically subtracted, you will need to review them carefully later in the workflow so that they are not included in the total tumor burden.





3. At the prompt to **Review Uptake Auto-Labeled as Physiological**, select **Delete all labeled physiological uptake** to remove the physiological contours (blue) from the total tumor burden. If needed, you can manually add back regions as hotspots in the next step.



Tip: The other options are not typically used.



- **Keep labeled physiological uptake for manual editing** turns all the regions identified as physiological into hotspots instead.
- **Delete all labeled uptake** removes all of the contours that were automatically drawn from the total tumor burden, so you have to manually draw all contours.

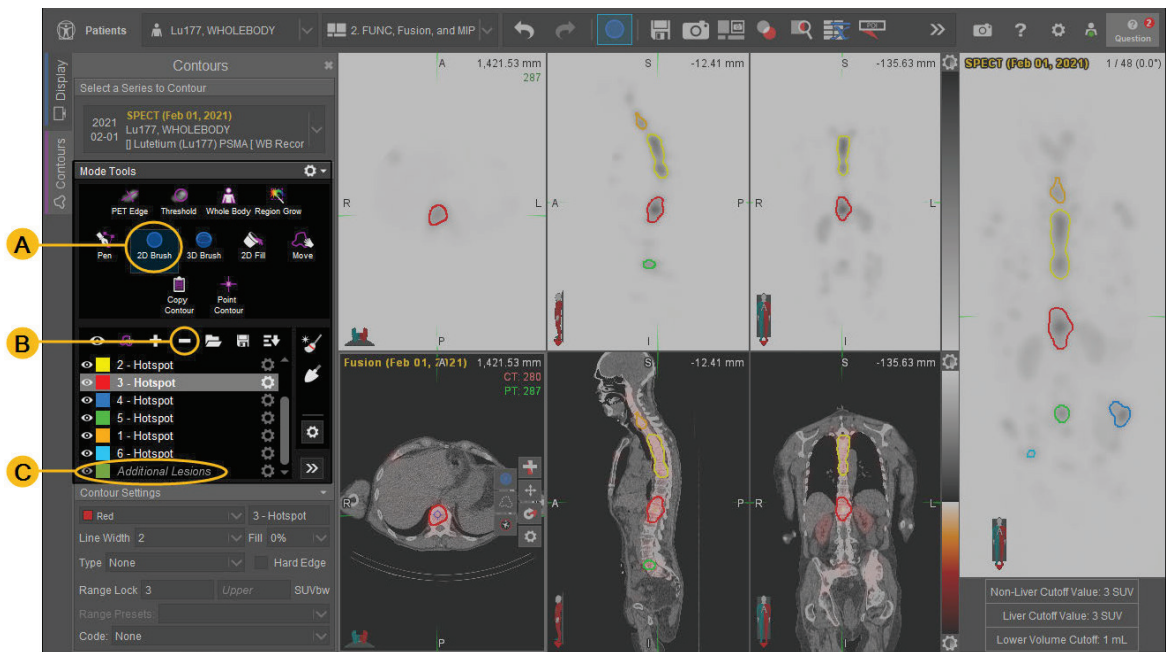
4. At the prompt to **Review Auto-Segmented Hotspots**:
 - i. Collapse the Notifications window by using the keyboard shortcut \ or clicking the arrow in the upper-right corner of the Notifications window.
 - ii. Use the Contours sidebar to review the hotspots created by the workflow and adjust as needed:

- A. Use the **2D Brush**  or another contouring tool to edit a contour.




Tip: Use the keyboard shortcut A to cycle quickly through the created contours. Double-click on a viewport to maximize it.

- B. Select an automatically drawn contour and click minus  to delete it or use the keyboard shortcut D.
- C. To add lesions, select the **Additional Lesions** contour.



When adding lesions:

- You can add multiple regions to the same Additional Lesions contour. The workflow automatically separates them in the next step.
- If you are using the **2D Brush** , press Alt (Windows®) or Option (Mac®) to draw non-contiguous regions.
- The Additional Lesions contour has the range lock set to 3, so areas where SUVbw is less than three are not included in the contour.

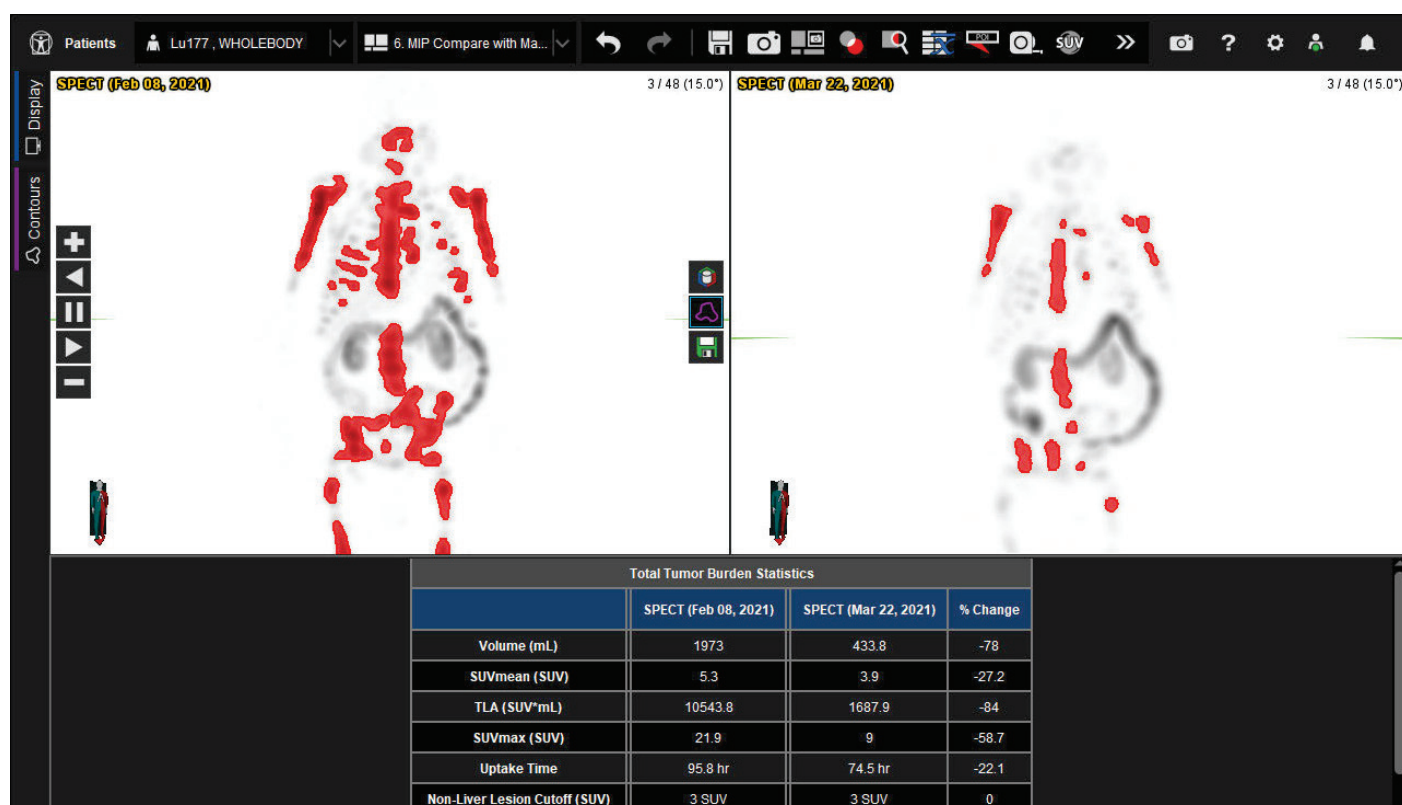
- iii. When you are ready to continue, expand the Notifications window and select the option **Proceed. Lesion segmentation is complete**. Click **OK**.

LesionID Pro finishes running and saves an RTstruct with the created contours. Continue to review the output.

Review LesionID Pro Results

LesionID Pro has created several display pages. Use the left and right arrows keys or the page dropdown from the top toolbar to navigate through the pages.

- All lesions are combined as a single Total Tumor Burden contour, shown in red.
- The Total Tumor Burden Statistics table shows the calculated results for all lesions.
- If you ran processing for multiple time points, the MIP Compare page shows the MIP and Total Tumor Burden Statistics for each time point for easy comparison.



Related: For definitions of statistics in MIM, see [Statistics Definitions](#).

LesionID Pro has also saved RTstructs to the patient list. You can use this structure set to re-review the same contours or have them available to present to a tumor board. The RTstructs could also be used to help identify target lesions for dosimetry calculations with MIM SurePlan™ MRT.

Set Up LesionID® Pro

MIMTD-1721 • 07 Jun 2024

Overview

LesionID Pro helps you visualize and report on PSMA studies for prostate cancer by automatically contouring regions of high uptake.

Your organization should work with your MIM® Implementation Specialist or Site Development Manager to implement this feature. You do not typically need to complete these steps on your own. To learn how to use the feature after setup is complete, go to [Quantify PSMA with LesionID® Pro](#).



Important: LesionID Pro should be used in a clinical setting for PSMA studies only. With other tracers, LesionID Pro must be used for research purposes only.

Contents

- [Prerequisites](#)
- [Configure System Settings for LesionID Pro Processing](#)
- [Set Up Automatic Processing](#)
 - [Create a Patient List](#)
 - [Import the LesionID Pro Workflow](#)
 - [Import the MIM Assistant Rule](#)
- [Set Up Client Workstations](#)

Prerequisites

- MIM 7.3.5 or later
- LesionID Pro license



Related: If you do not have a LesionID Pro license, you might be interested in running the LesionID workflow that is included with MIM Encore®. Refer to [Quantify Total Tumor Burden with LesionID®](#) for more information about this workflow. It similarly segments hotspots based on uptake thresholds but requires more manual intervention to review and refine the contours identified.

- Contour ProtégéAI+™: Whole Body - Physiological Uptake Organs model
- MIM Assistant® installed


Use a separate physical server or a new virtual machine (VM) for LesionID Pro. It requires the same resources as Contour ProtégéAI+.

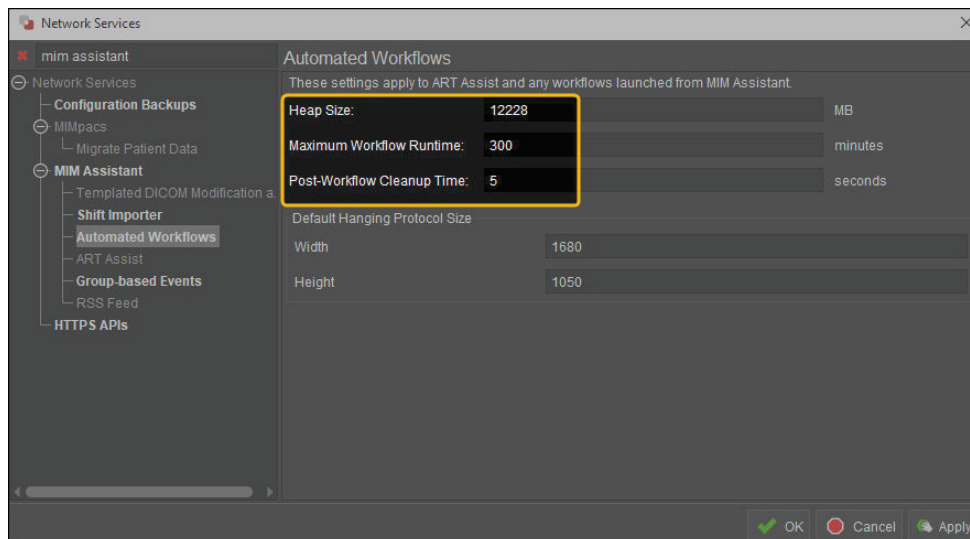


Important: Do not install LesionID Pro on a server that is also running other MIM Assistant rules because a single rule can be processed at a time and can result in other rules waiting a long time to run.

Configure System Settings for LesionID Pro Processing

Complete the following steps on the MIM Assistant server:

1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **Network Services** and search for "**MIM Assistant**". Select **MIM Assistant** on the left side.
3. Ensure that the MIM Assistant service is installed and increase the **Heap Size** to 4096 MB.
4. Select **Automated Workflows** on the left side:
 - Increase the **Heap Size** to 12228 MB.
 - Increase the **Maximum Workflow Runtime** to 300 minutes.
 - Increase the **Post-Workflow Cleanup Time** to 5 minutes.



5. Select **Group-based Events** on the left side. Change the **Group DICOM Tag Identifier** to **PatientID**.
6. Search for "**contour pro**". Select **Contour ProtégéAI** on the left side.

7. Change the **Contour ProtégéAI Local Deployment Thread Limit** to two less than the maximum. For example, if the server maximum is 16, set this field to 14.
8. Click **OK**. At the prompt, restart the MIM Assistant service for your changes to take effect.

Set Up Automatic Processing


A few components work together to automate LesionID Pro processing:

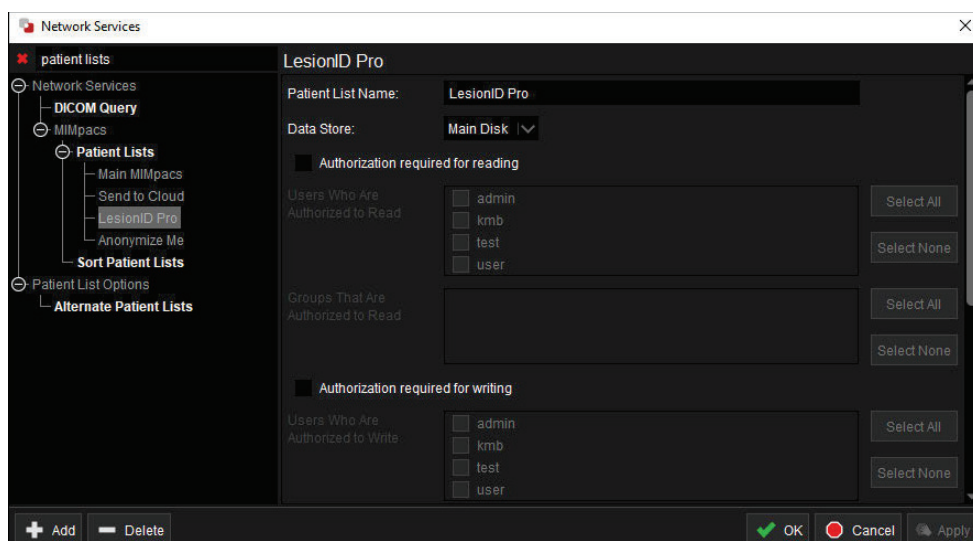
1. When patient data is sent to a particular patient list, a MIM Assistant rule runs for the patient.
2. The rule launches a workflow that uses a Contour ProtégéAI+ model to perform automatic contouring on the series.
3. When the rule finishes running, it saves a session that is ready for the user to launch.

Complete the following tasks to configure each component.

Create a Patient List

Make a patient list specifically for triggering LesionID Pro.

1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **Network Services** and search for "**patient lists**". Select **Patient Lists** (under MIMpacs) on the left side.
3. Click **Add** and create a new list:
 - i. Enter a **Patient List Name**.
 - ii. Select the **Data Store** for the patient list.




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



Tip: Users interact with this patient list. Name it intuitively and communicate to users that this is the patient list to use for LesionID Pro processing.

Import the LesionID Pro Workflow

Import the LesionID Pro workflow on the MIM Assistant server that will run LesionID Pro.


1. Log in to the server as an administrator in MIM Assistant configuration mode.
2. Go to Settings  >> **Import Manager...** to open the Import Manager.
3. Import the LesionID_Pro - Assistant zip file that was provided to you by your MIM representative.
4. Click **OK** to save the changes and close the window.



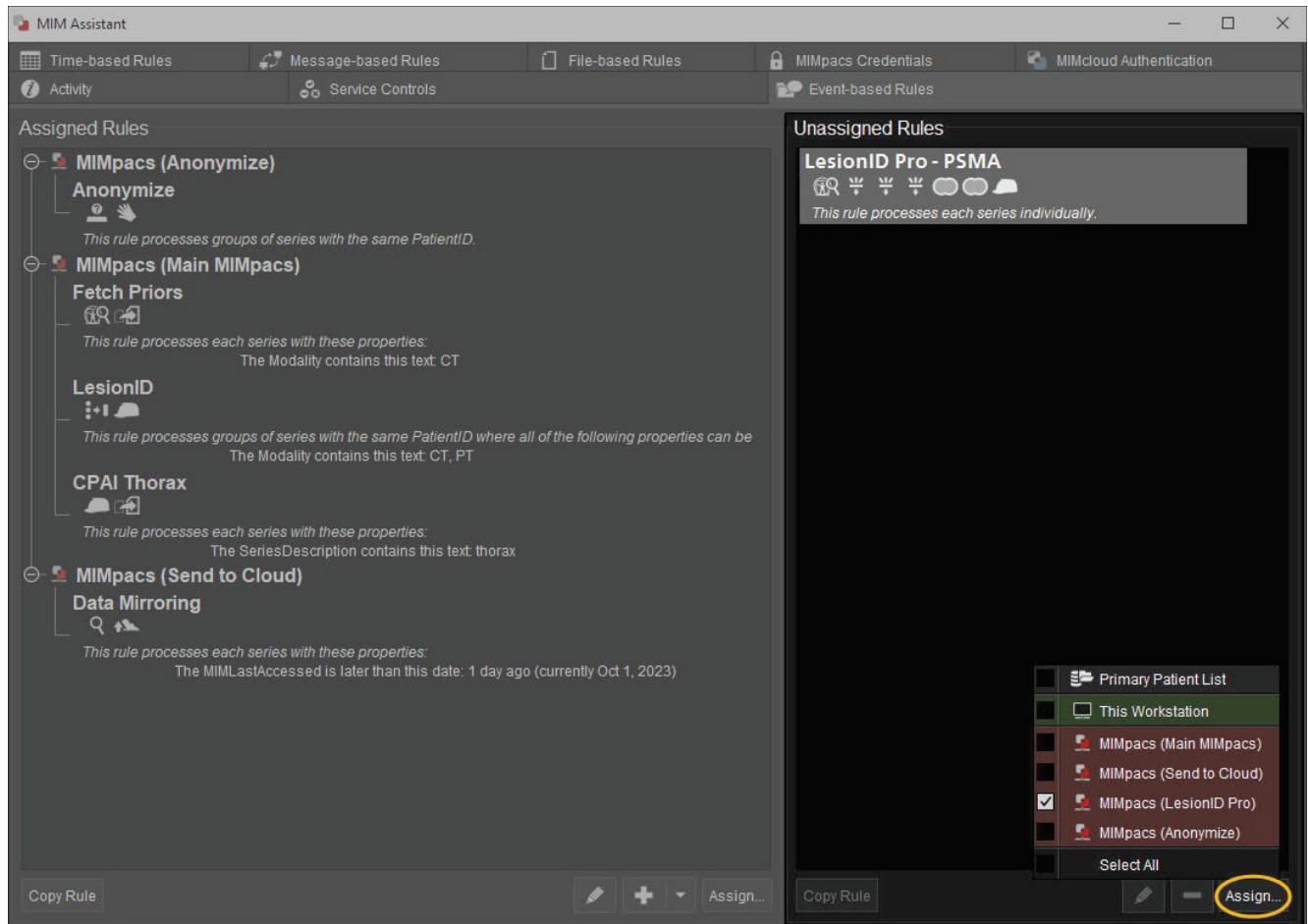
Related: For more information about importing workflows, refer to [Import MIM Workflows™ and Other Content](#).

Import the MIM Assistant Rule

The MIM Assistant rule for LesionID Pro needs to be imported on the MIM Assistant server.

1. Log in to the server as an administrator in MIM Assistant configuration mode.
2. Click the Settings  button in the upper-right corner of MIM.
3. Go to **MIM Assistant Manager...**
4. On the **Activity** tab (*MIM 7.4 and later*) or **About** tab (*MIM 7.3 and earlier*), click the **Import Rules** button.
5. In the file selection window that opens, select the file that was provided to you by your MIM representative.
6. When the import has completed, go to the **Event-based Rules** tab.
7. Verify that the rule does not appear red, which indicates an error. If the rule is red, please contact MIM Software Support at support.mimsoftware.com for assistance.

8. Select the **LesionID Pro - PSMA** rule and click the **Assign...** button to assign it to the LesionID Pro patient list that you created.




9. Close MIM Assistant.

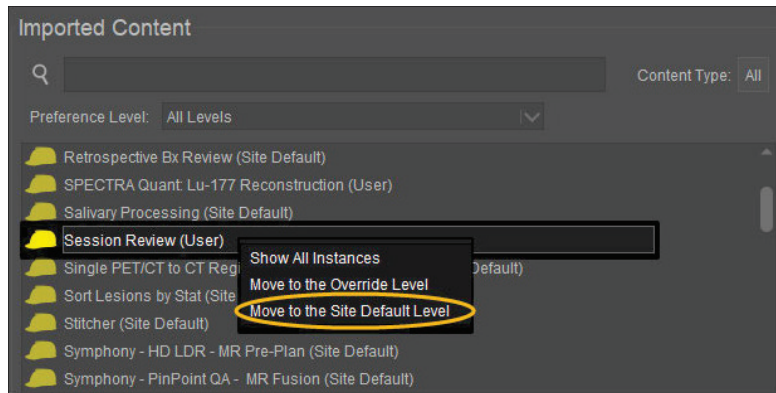
Set Up Client Workstations

For LesionID Pro sessions to be reviewed on a client workstation, the workstation needs to have the Session Review workflow imported.

If your organization has MIM user logins, log in to the MIM server and import the workflow at the site default level so it is available on all client workstations. If your organization does not have user logins, repeat these steps on each client workstation where LesionID Pro sessions will be reviewed.

1. Log in to the MIM server as an administrator.
2. Go to Settings  >> **Import Manager...** to open the Import Manager.
3. Import the Session Review workflow zip file that was provided to you by your MIM representative.

4. *If using user logins:* In the Imported Content pane, find the **Session Review** workflow. Right-click on the workflow and select **Move to the Site Default Level**.



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



Tip: The Session Review workflow is included within the LesionID Pro workflow that is imported on the MIM Assistant server, as described in [Import the LesionID Pro Workflow](#). You can review sessions on the MIM Assistant server, such as for testing, without separately importing the Session Review workflow.



Related: For more information about importing workflows, refer to [Import MIM Workflows™ and Other Content](#).

Create Contours

Create Contours Overview

MIMTD-1739 • 02 Nov 2023

Overview

You can use a variety of MIM® tools for quick and precise contouring. The Contours sidebar shows all contours in the session and provides many options for further processing.

This topic provides an overview of creating and editing contours for Nuclear Medicine.



Tip: Jump to [Explore More Contour Resources](#) below if you know the basics and are looking for more details on a certain contouring topic.

Contents

- [Contouring in MIM](#)
 - [Create PET/CT Contours](#)
 - [Create or Edit Contours During a Workflow](#)
- [Primary Contouring Tools](#)
- [Primary Contour Post-Processing Tools](#)
- [Explore More Contour Resources](#)

Contouring in MIM

In Nuclear Medicine departments, users typically contour in the following scenarios:

- Physicians who are doing PET/CT reads may want to contour.



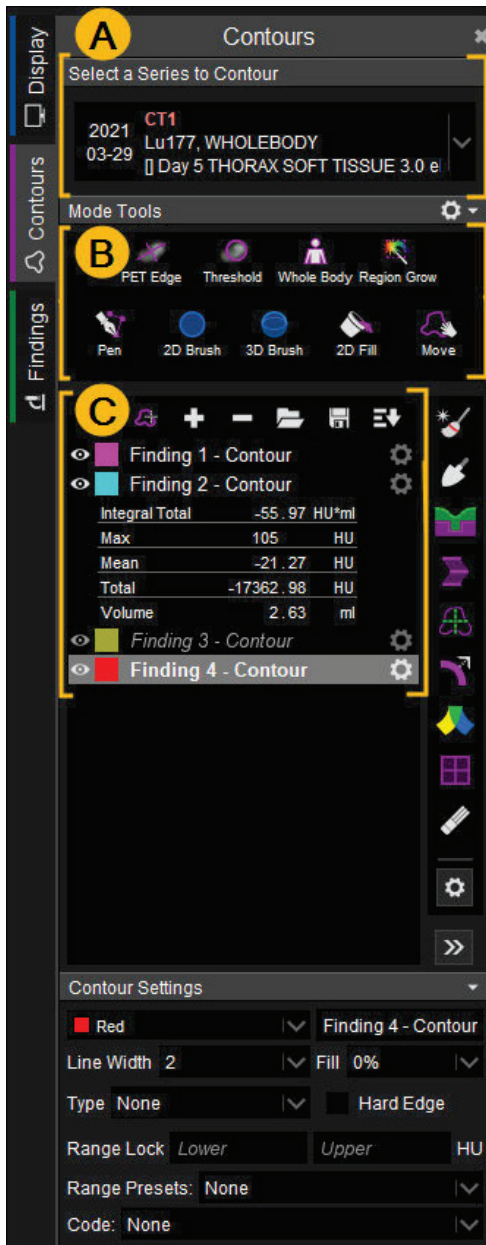
Related: Alternatively, physicians can use measurement tools and review results on the Findings sidebar. Refer to [Record Measurements Using the Findings Sidebar](#) for more information.

- Technologists run MIM Workflows™ to process exams. A workflow may prompt the user to contour a region or to review and edit an automatically generated contour.

While these scenarios are the most common, contouring tools are very flexible and can be used in a wide range of situations, depending on your use case.

Create PET/CT Contours

If you are contouring outside of a workflow, start at the top of the Contours sidebar and work your way down.



Select a Series (A)

In the Contours sidebar, check the **Select a Series to Contour** dropdown and change it if needed. You can draw on the selected series or any series that is linked to the selected series, but the contours will be associated with the series selected here.

Choose a Tool and Contour (B)

Select a common tool from the Mode Tools section of the Contours sidebar. You can update this section with your favorite tools, as described in [Tips for Efficient Contouring](#), or select a contouring tool from your right-click radial menu instead.

See [Primary Contouring Tools](#) below for a quick summary of the most commonly used tools.

When you've chosen your tool, create a contour on the image.

Manage Contours (C)

Contours appear in the Contours sidebar. You can:

- Create another new contour. Click the plus **+** in the sidebar.
- Edit a contour. Click on the contour you want to edit.
- Rename a contour. Right-click on the contour and select **Rename Contour**.
- Delete a contour. Click the minus **-** in the sidebar.
- See statistics for a contour. Double-click on the contour or hover over it for expanded statistics.
- Toggle which contours appear on the series by clicking the eye **👁**.

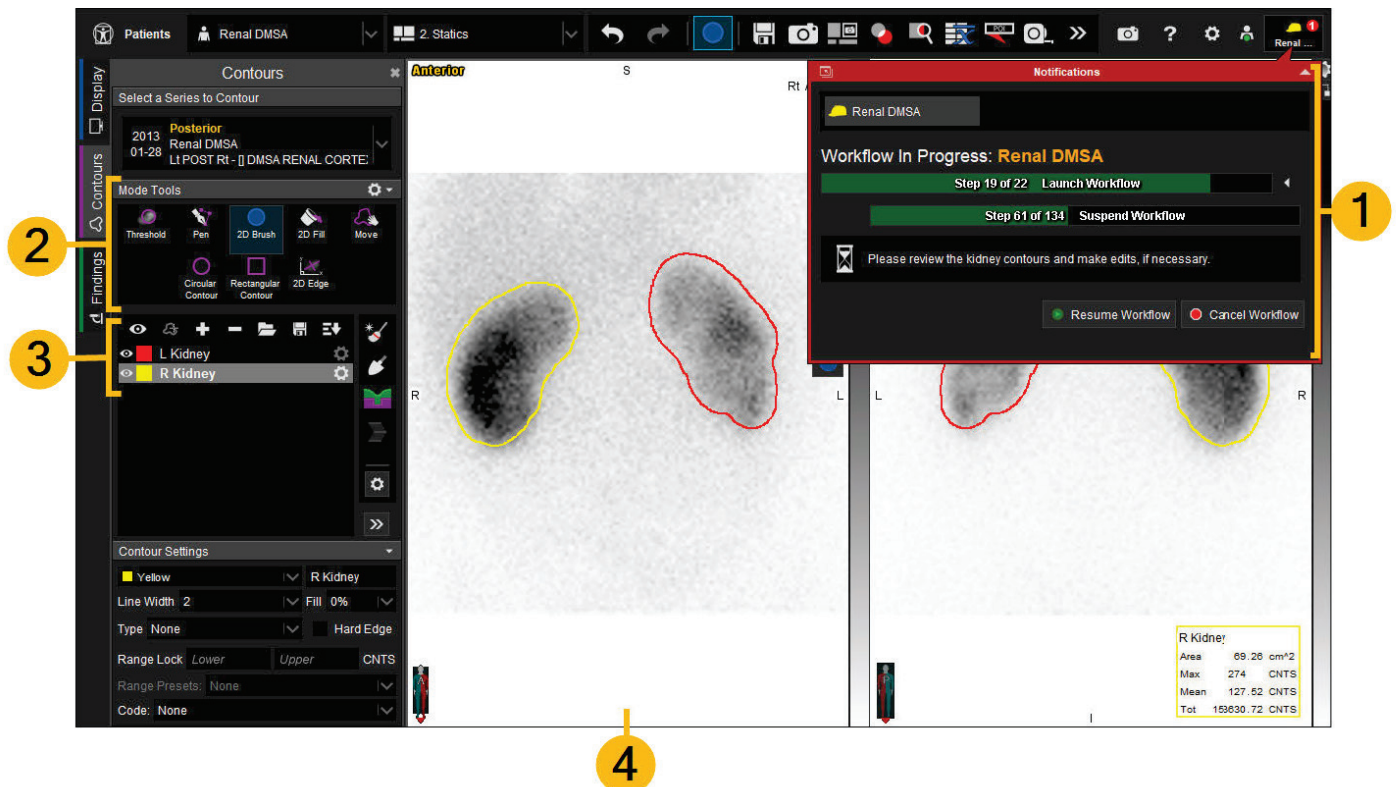
Finish and Save Contours

After you've created contours, you can optionally use post-processing tools to further adjust the contours. See [Primary Contour Post-Processing Tools](#) below for a quick summary of commonly used post-processing tools.

When you are finished, save your session or save the contours as a DICOM RTstruct file. Refer to [Save Contours](#) for more information about saving options.

Create or Edit Contours During a Workflow

When you are running a workflow to process an exam, the workflow may pause so that you can contour or review automated contours.



1. Review the Notifications prompt in the upper-right corner for instructions.
2. Select a contouring tool from the Mode Tools section of the Contours sidebar or from your right-click radial menu. See [Primary Contouring Tools](#) below for a quick summary of the most commonly used tools.






Tip: Some workflows may automatically activate a contouring tool for you, such as the 2D Brush. If desired, you can choose a different tool to use instead.



3. Select a contour in the Contours sidebar.
 - *If the contour was automatically drawn, select it to make edits.*
 - *If the contour has not been drawn, the contour name appears grayed out and italicized. Click on the contour name to draw it.*
4. Draw or edit the contour in the image viewport using your contouring tool of choice.
5. If you have multiple contours to draw or edit, select the next contour name from the Contours sidebar.
6. When you are finished drawing or editing all of the contours, return to the Notifications prompt and click **Resume Workflow**.

Primary Contouring Tools

Of the many contouring tool options in MIM, you will likely find two or three that you use the most. You may use other tools in only specific situations or for a particular kind of exam. Refer to [Contouring Structures](#) for information and tips on how to contour different structures.

MIM users typically rely on the following for their day-to-day work:

Tool	Description	Additional Information
 2D Brush	Draw or erase freehand with a resizable brush. Use with the Dynamic Brush™ and Contour CoPilot® companion tools to quickly contour on multiple slices.	Create Contours with the 2D Brush
 PET Edge® or PET Edge®+	Use with PET and NM to contour regions based on changes in intensity. Use PET Edge to place crosshairs yourself or use PET Edge+ to let the system do it for you.	Define Lesions with PET Edge® Define Lesions with PET Edge®+
 Pen	Place points that are automatically connected with straight lines, or left-click drag to draw freehand.	Create Contours with the Pen Tool

Tool	Description	Additional Information
 <p>Circular Contour or Rectangular Contour</p>	Draw a circular, elliptic, or rectangular contour.	N/A
 <p>Move</p>	Use with an existing contour to adjust the position of the contour, resize the contour, or rotate it.	Move Contours



Tip: You can add the contouring tools that you use most to your right-click radial menu or your top toolbar for easier access. Refer to [Access Tools: The Toolbar and the Radial Menu](#) for more information. Or, set a keyboard shortcut to activate a tool, as described in [Set Keyboard Shortcuts](#).

Primary Contour Post-Processing Tools

After you create a contour, MIM provides many ways to further adjust or manipulate the contour based on your situation.

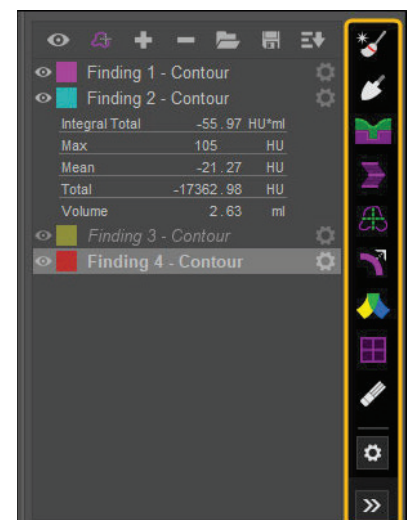



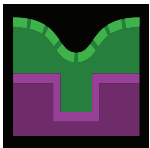
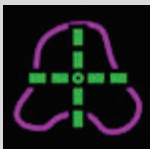
Tip: If you are contouring as part of a workflow, these tools are typically built in to the workflow and do not need to be used separately.



Refer to [Contouring Structures](#) for information and tips on contour post-processing for different structures.

These tools are available in the post-processing menu on the Contours sidebar.

The following tools are used most frequently:



Tool	Description
 <p>Fill Hole or Clean</p>	<p>Fill holes within the contour or clean parts that are disconnected from the main region of the contour. For the selected contour, use the options in the Notifications window to:</p> <ul style="list-style-type: none"> • Single Slice — Fill or clean the current slice. • Each Slice — Fill or clean every axial slice. • Volumetrically — Restrict the tool to filling only holes that are fully within the contour volume or removing parts of the contour that are a certain volume.
 <p>Smooth</p>	<p>Click Smooth to fill in tiny holes and smooth the edges of the contour. You can use Smooth as many times as needed on a contour. Be careful not to over-smooth so the contour is no longer accurate.</p>
 <p>Localize to Contour Centroid</p>	<p>Localize to the center of the contour in the viewport. This option is also available when you right-click on the contour name in the Contours sidebar.</p>

Click the double arrow  at the bottom of the post-processing menu to see additional tools. You can use the gear  to rearrange which tools appear in your menu.

Explore More Contour Resources

You might also be interested in the following contouring topics:

- [Tips for Efficient Contouring](#) — If you do a lot of manual contouring and are looking for ways to go faster, take a look at these tips.
- [Work with Overlapping and Adjacent Contours](#) — See best practices when working with contours that are close together.
- [Draw and View Contours on Linked Series \(Ghost Contours\)](#) — Learn more about the "ghost" contours that appear when two series are linked. For example, when you fuse a prior PET/CT to the current PET/CT, the contours from the prior appear as ghost contours on the current series.

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.



Related: Refer to [Create Contours Overview](#) for more information about how to create contours.



Contents

- [Save As DICOM RTstruct](#)
- [Alternative Save Options](#)
- [Auto-Save Contour Backups](#)

Save As DICOM RTstruct

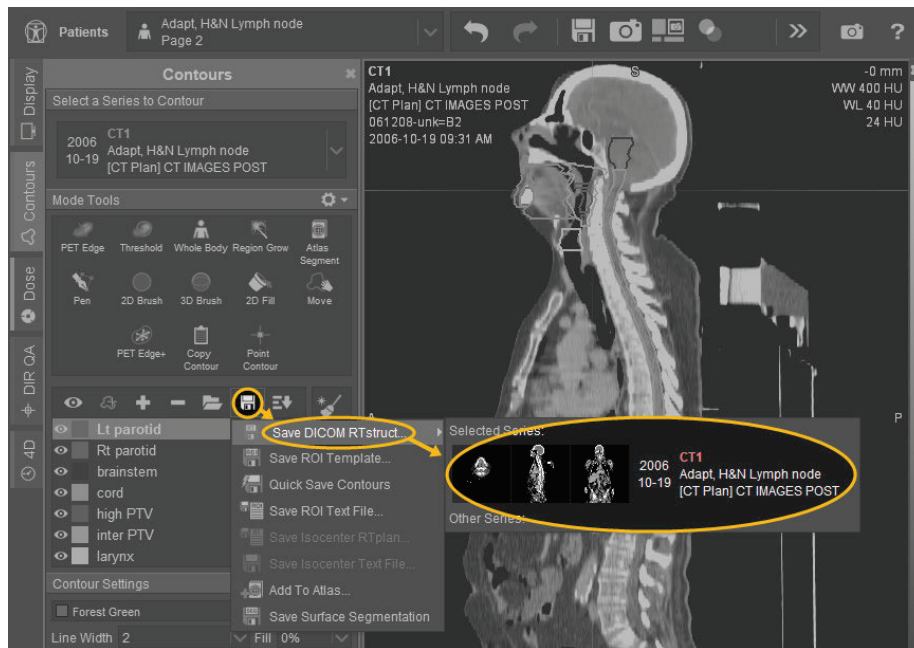
RTstructs (RTst) are the DICOM for contours. You can see RTstructs on the patient list and modify an RTstruct that was previously saved. When sending the data to PACS or another third-party DICOM system, they are able to show contours that were saved as RTstructs.

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.



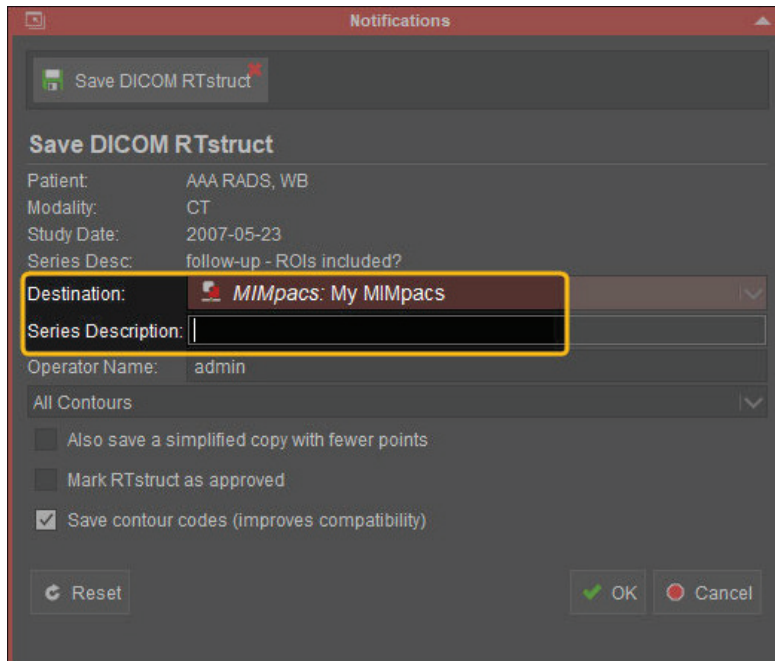
MIM Encore® User Guide



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.



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. See Standardize Contour Names with ROI Templates for more information.	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. See Save and Reuse Contour Shapes for more information.	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.
Save Surface Segmentation	Save a DICOM SEG file.	Export and send contours to third-party systems that support SEG files instead of RTstructs.

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.

Transfer Contours

MIMTD-1284 • 25 Oct 2023

Overview

You can transfer one or more contours from one series to another.



Important: When transferring contours to another series, MIM® does not remove the contour from the original series. The contour is copied to the destination series and the original contour is preserved.

Contents

- [Prepare to Transfer](#)
- [Transfer a Single Contour](#)
- [Transfer Multiple Contours](#)
- [Remove Contours from the Original Series](#)

Prepare to Transfer

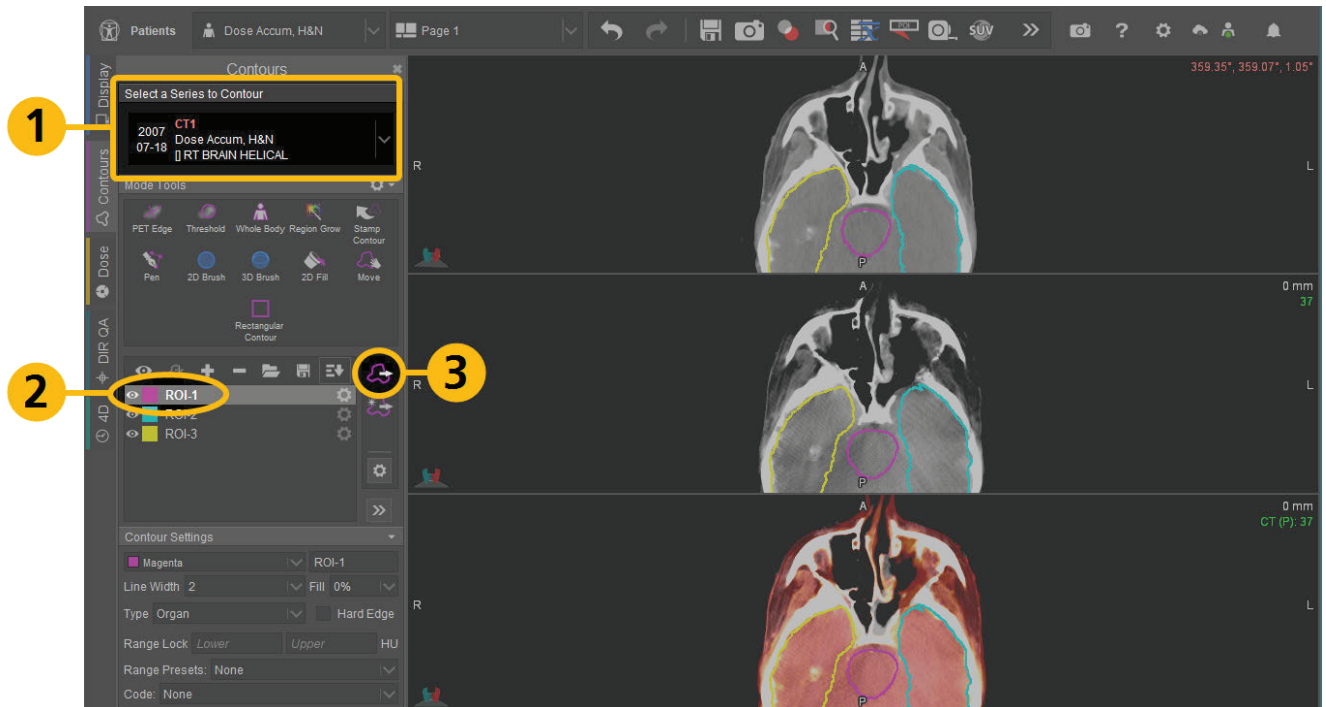
1. Ensure that a spatial link exists between the series you are transferring contours to and the series you are transferring contours from:
 - *If the series were acquired together (a PET/CT, for example), they are already linked.*
 - If the series were not acquired together, create a fusion to link them. See Create a [Create a Fusion Manually](#) for more information.
2. Ensure that the series you are transferring contours to and the series you are transferring contours from are displayed on the same page. See [Create and Modify Display Layouts](#) for more information.


Transfer a Single Contour

1. In the **Select a Series to Contour** dropdown at the top of the Contours sidebar, ensure that you have selected the series that the contour is currently associated with.
2. Select the contour you want to transfer.


3. Click the **Transfer Contour**  button.

- If a link only exists with one other series, the contour is automatically transferred to that series.
- If links exist to more than one series, you are prompted to select which series the contour will be transferred to.



Tip: If the Transfer Contour button is not in your menu of contour post-processing tools, click the double arrow  button at the bottom of the menu to see the list of all tools.



Tip: If you use this tool often, add it to your contour post-processing tools menu. Click the gear  menu at the bottom of the contour post-processing tools menu and select the tool to add it to the list.

Transfer Multiple Contours

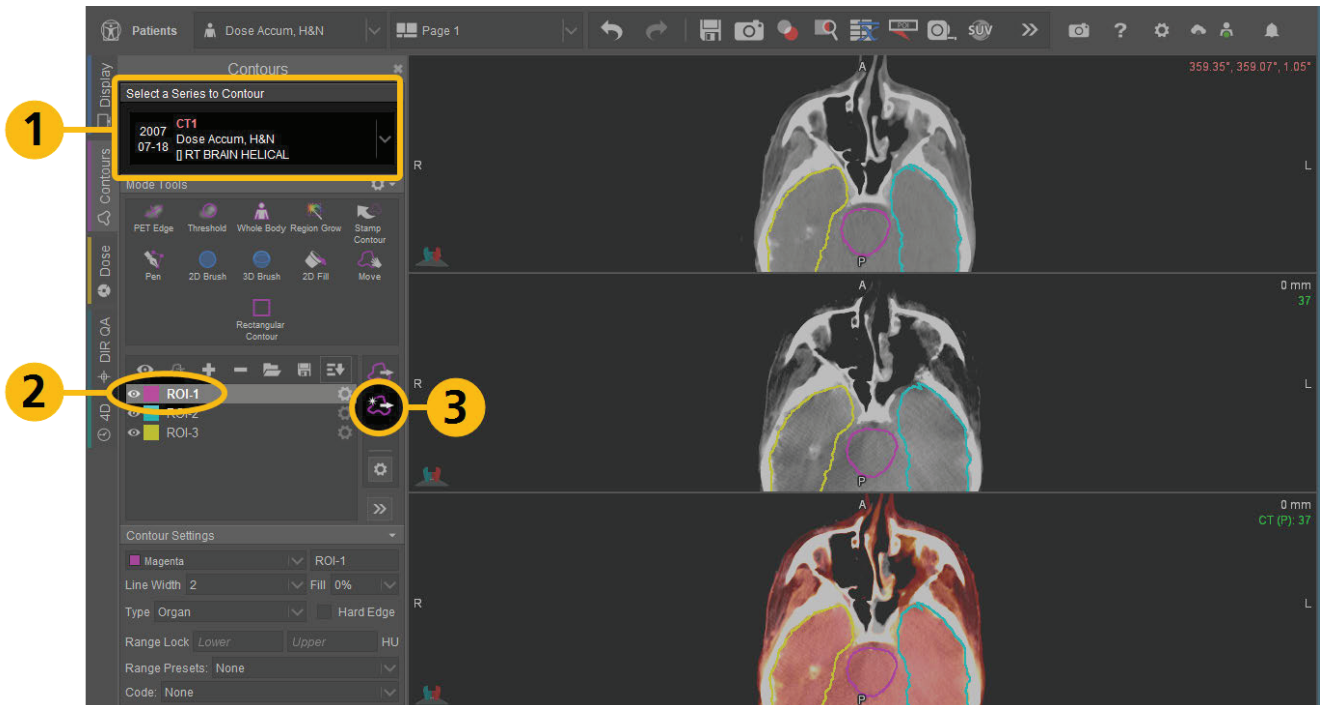
1. In the **Select a Series to Contour** dropdown at the top of the Contours sidebar, ensure you've selected the series that the contours are currently associated with.


2. Select any contour from the **Contours** sidebar.




Tip: It does not matter which contour you select in this step. A contour must be selected to enable the Transfer All Contours tool in the following step.

3. Click the **Transfer All Contours**  button.



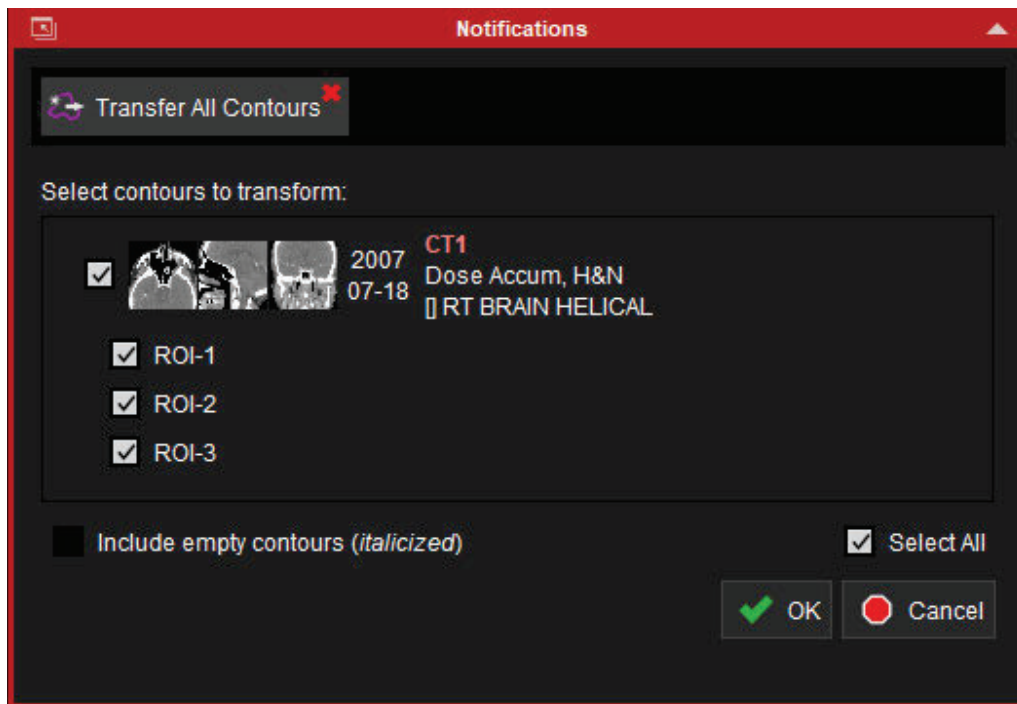
Tip: If the Transfer All Contours tool is not in your menu of contour post-processing tools, click the double arrow  button at the bottom of the menu to see the list of all tools.



Tip: If you use this tool often, add it to your contour post-processing tools menu. Click the gear  menu at the bottom of the contour post-processing tools menu and select the tool to add it to the list.



4. If links exist to more than one series, you are prompted to select which series the contours will be transferred to. If a link exists to only one other series, you will not be prompted.


5. In the Notifications window, select the contours you want to transfer.




6. Click **OK**.

Remove Contours from the Original Series

Both the Transfer Contour  tool and Transfer All Contours  tool create copies of existing contours on the new series. Contours are not removed from the original series. If you no longer want contours on the original series, follow these steps:

1. Ensure that the series you want to delete contours from is selected in the **Select a Series to Contour** dropdown.
2. Select the contour to remove.
3. Click the minus  button to delete the contour.



Tip: If you are not certain which series a contour is associated with, look at the **Select a Series to Contour** dropdown. Any contours that are *not* associated with the selected series display a ghost  icon next to the contour name. For more information, see [Draw and View Contours on Linked Series \(Ghost Contours\)](#).

Create Contours with the 2D Brush

MIMTD-701 • 29 Aug 2023

Overview



The 2D Brush lets you draw regions of interest on individual slices of a series. It also features companion tools that you can use to save time and increase contouring efficiency.

Contents

- [Draw and Erase with the 2D Brush](#)
- [Correct a Double 2D Brush](#)
- [2D Brush Companion Tools](#)
 - [Companion Tool: Contour CoPilot®](#)
 - [Companion Tool: Dynamic Brush™](#)
- [Additional Contouring Tools](#)
 - [Interpolate with Contour CoPilot](#)
 - [Interpolate](#)

Draw and Erase with the 2D Brush

Activate and use the 2D Brush to draw contours freely on any image:

- To draw contours, left-click drag with the 2D Brush.
- To adjust the diameter of the brush, right-click drag up or down.
- To erase, move the brush outside of the contour and then left-click drag.




Tip: When the brush is blue, it is in draw mode. When the brush is red, it is in erase mode.

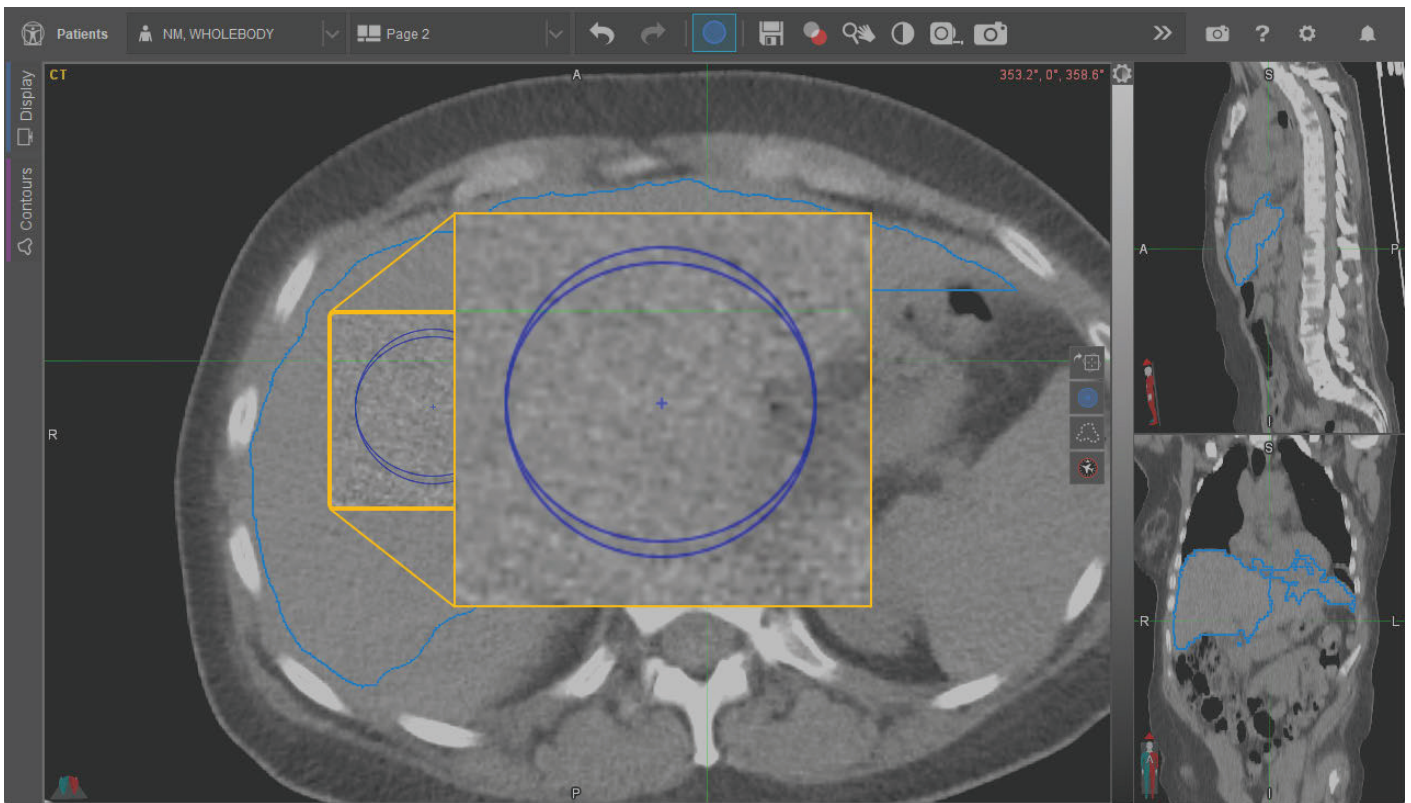


- To switch between draw and erase modes, press and hold the Alt (Windows®) or Option (macOS®) key. Holding the Alt/Option key allows you to draw non-contiguous regions. This is helpful for areas such as pelvic nodes.



Tip: Enable this behavior without a key modifier by going to Settings  >> **General Preferences** >> **Contouring** and selecting **Paintbrush** will add to existing contour when used a distance outside it.

Correct a Double 2D Brush



A double 2D Brush (two offset circles instead of one circle) appears when the viewport is showing multiple interpolated slices because a viewing rotation is applied to the series. Contours created with a double 2D Brush are typically not desirable because the contours are drawn on multiple slices at a time.


If you see the double 2D Brush, first rule out other issues by confirming the following:

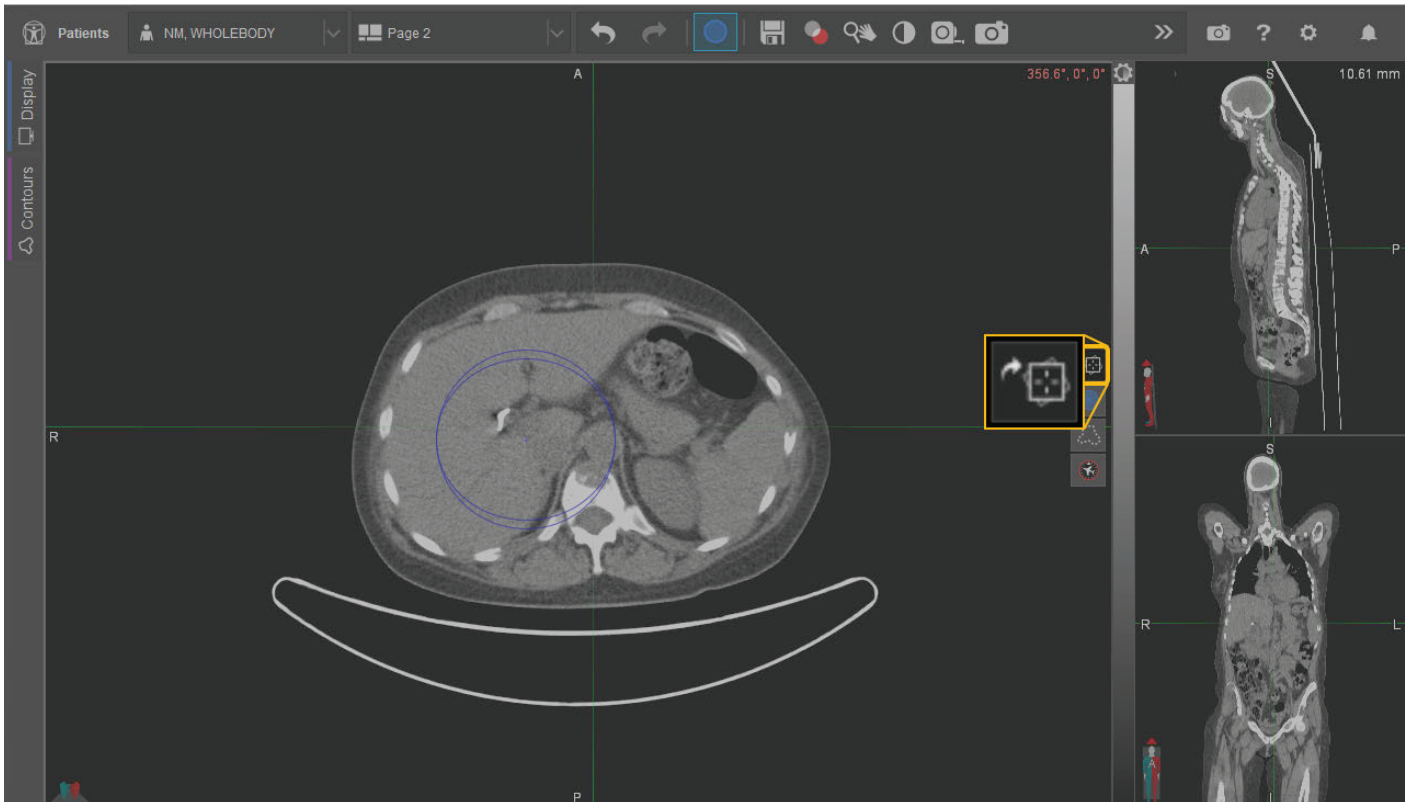
- Ensure that the correct series is selected from the **Select a Series to Contour** dropdown at the top of the Contours sidebar.

- Ensure that the correct contour is selected in the Contours sidebar.

If both of the above settings are correct, follow these steps:


MIM 7.3 and later:

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

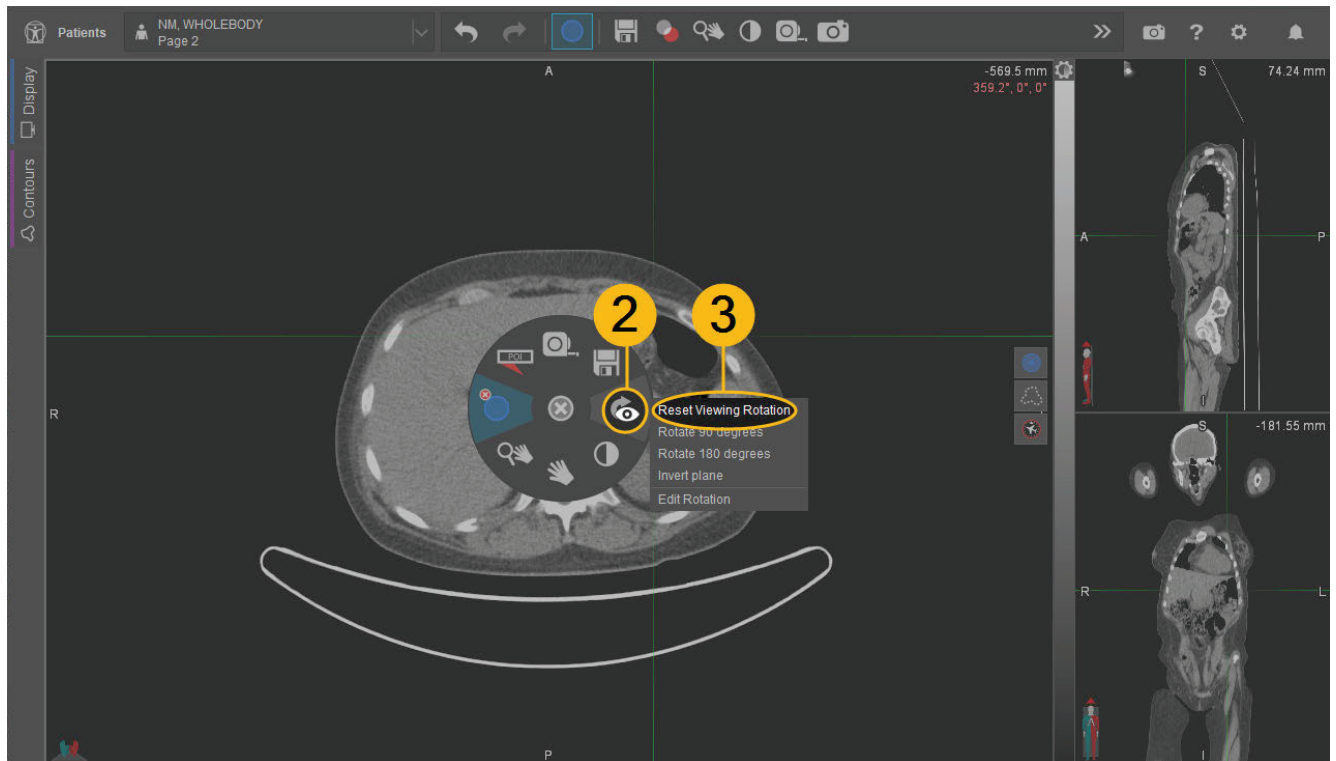


Tip: If desired, click this button again after contouring to return to the rotated view.

MIM 7.2 and earlier:

1. Right-click the rotated image to open the radial menu.
2. Right-click the **Rotate View**  tool to open an additional menu.

3. Click **Reset Viewing Rotation** to return to the normal 2D Brush.





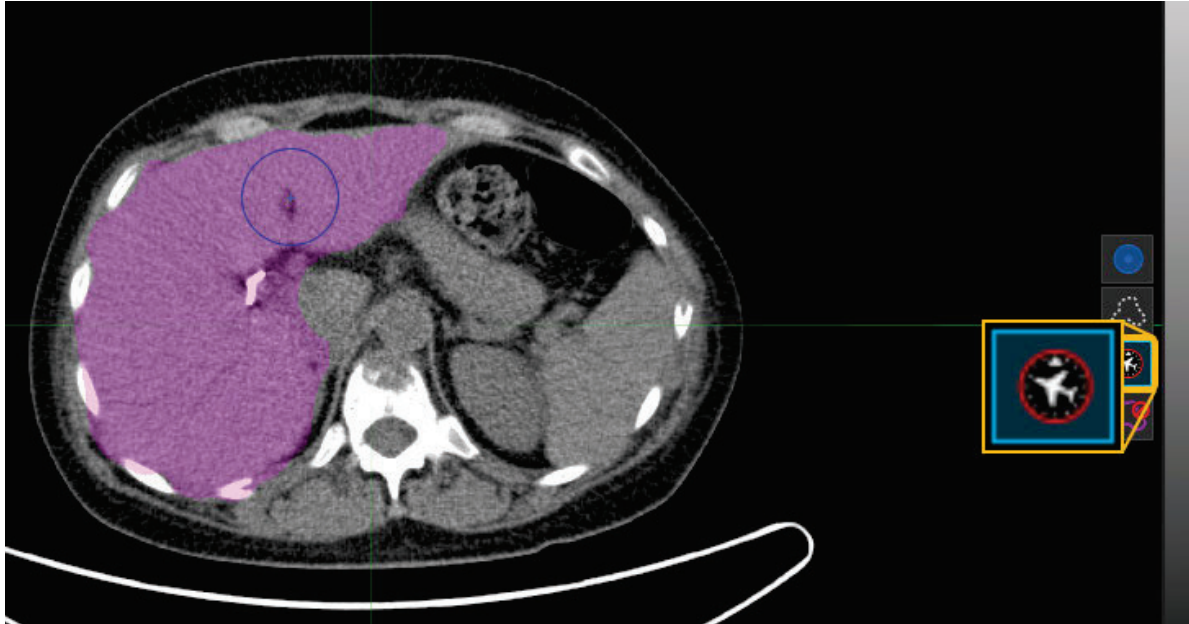
2D Brush Companion Tools

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


Companion Tool: Contour CoPilot®

Use Contour CoPilot in conjunction with the 2D Brush to quickly and semi-automatically contour an entire structure by assessing candidate contours. Candidate contours are automatically generated using the information from slices that are already drawn. Using these candidate contours reduces the need to manually draw each slice. MIM displays candidate contours as a color wash over the region being contoured.

1. Activate the **2D Brush**  and draw a contour on any slice of any plane.
2. Activate the **Contour CoPilot**  tool, found on the right edge of any viewport.



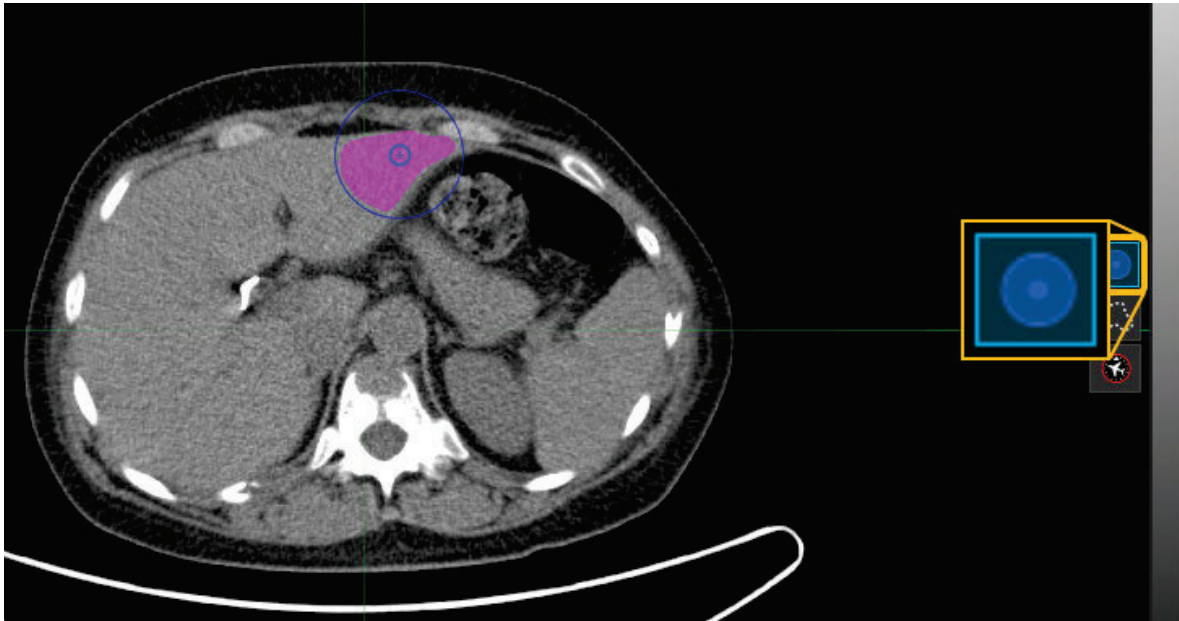
3. Scroll to another slice. A candidate contour automatically appears as a color wash on the visible slice.
4. To accept the contour, click within the viewport. If desired, continue to make edits manually with the 2D Brush.




To reject a candidate contour, click the  button on the right side of the viewport. After rejecting the candidate contour, use the 2D Brush to contour the slice manually.

5. Continue viewing additional slices, accepting candidates, editing, or redrawing contours as desired.



Companion Tool: Dynamic Brush[™]

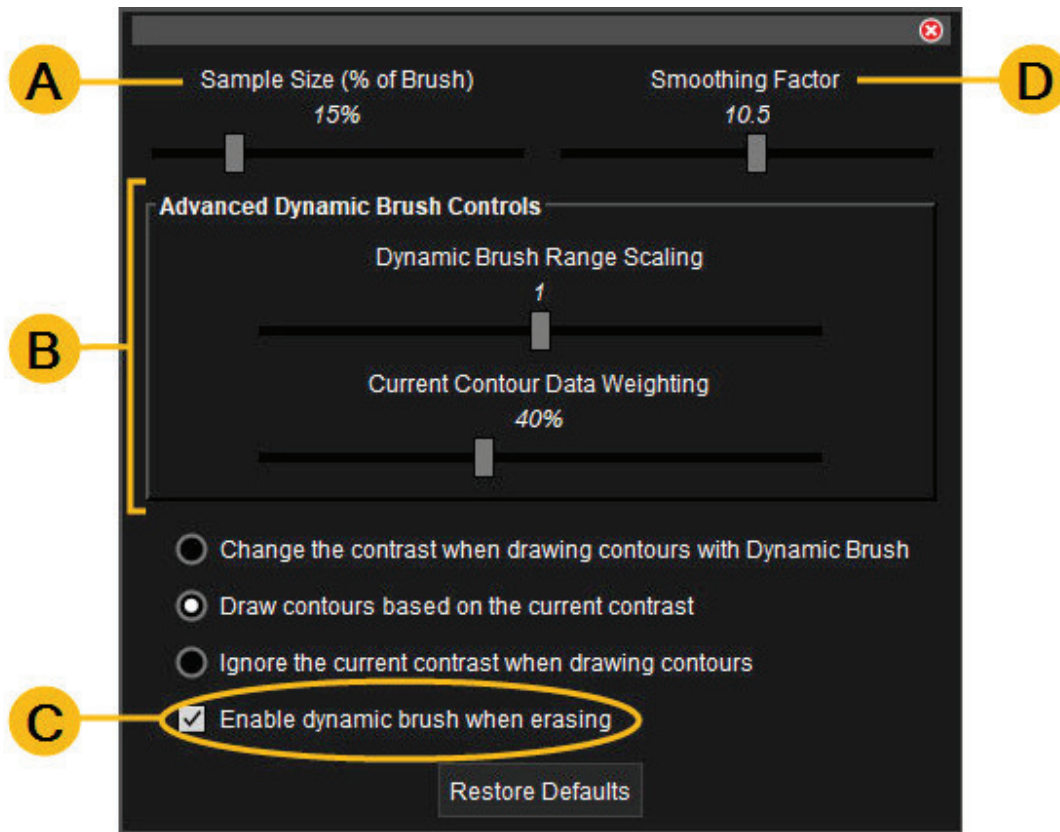
Use the Dynamic Brush to contour more quickly. When the Dynamic Brush is activated, the brush samples intensities within the inner circle in order to restrict the brush to areas of similar intensity.



- Activate the **2D Brush** , then activate the **Dynamic Brush**  tool, found on the right side of any viewport.
- Left-click drag to draw contours. Keep the inner circle of the brush inside the 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 **2D Brush**  and right-clicking the **Dynamic Brush**  button on the right side of the viewport.



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

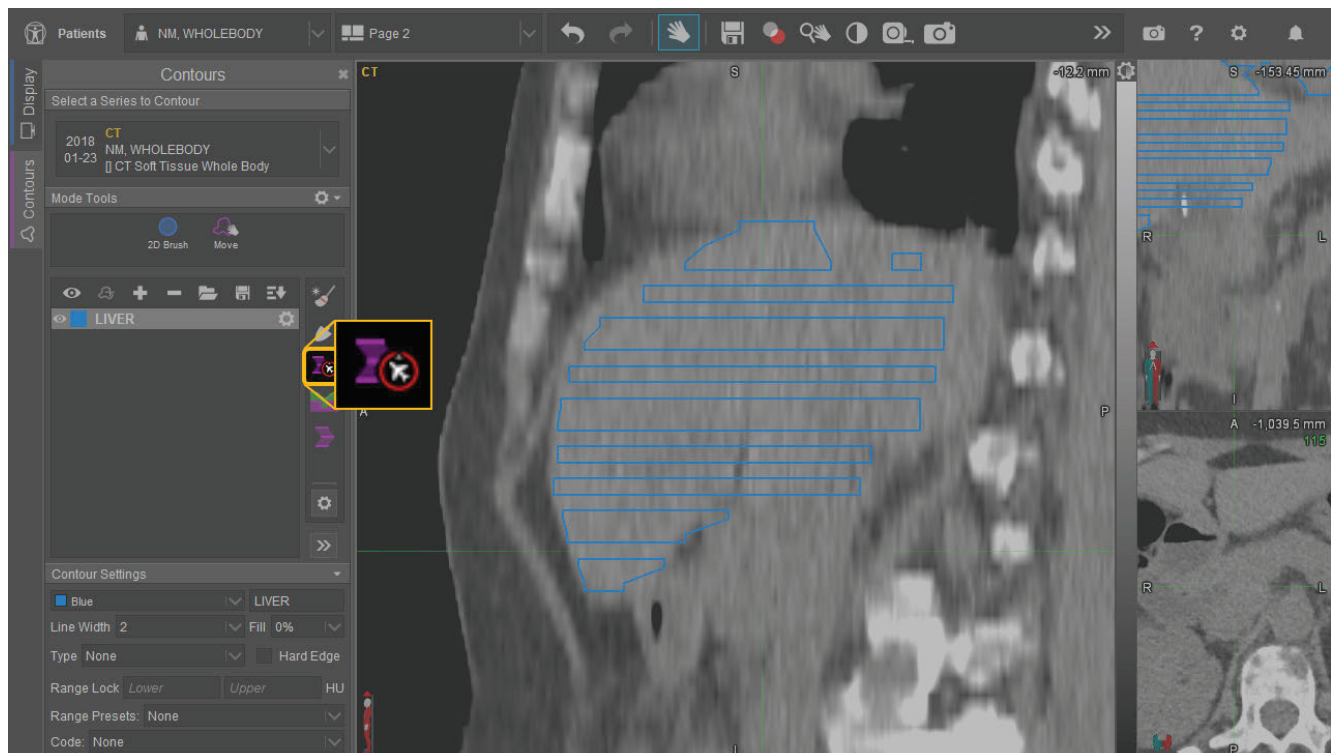


Interpolate with Contour CoPilot



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.





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.

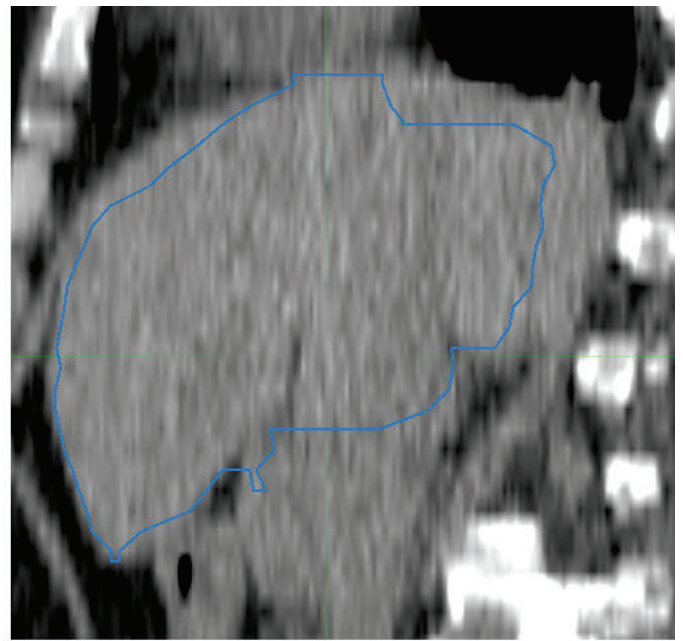
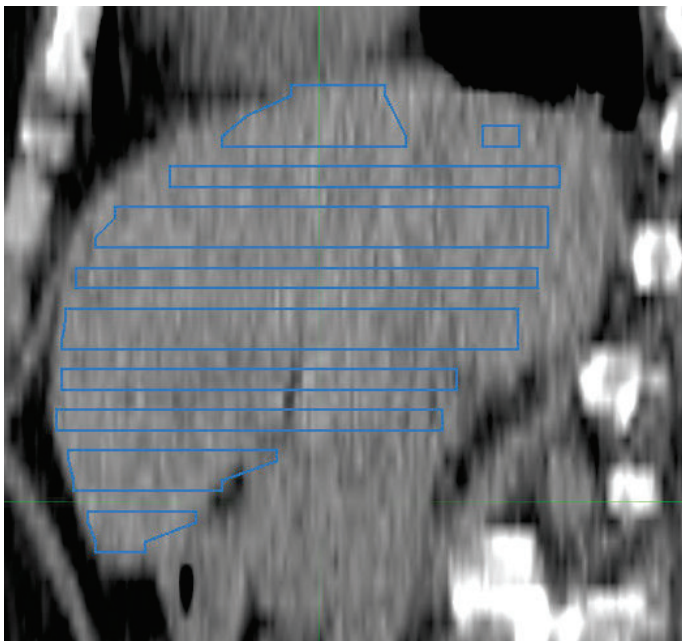


Interpolate

Use the Interpolate tool to save time by skipping slices when contouring. The Interpolate tool fills in the remaining slices using linear interpolation.




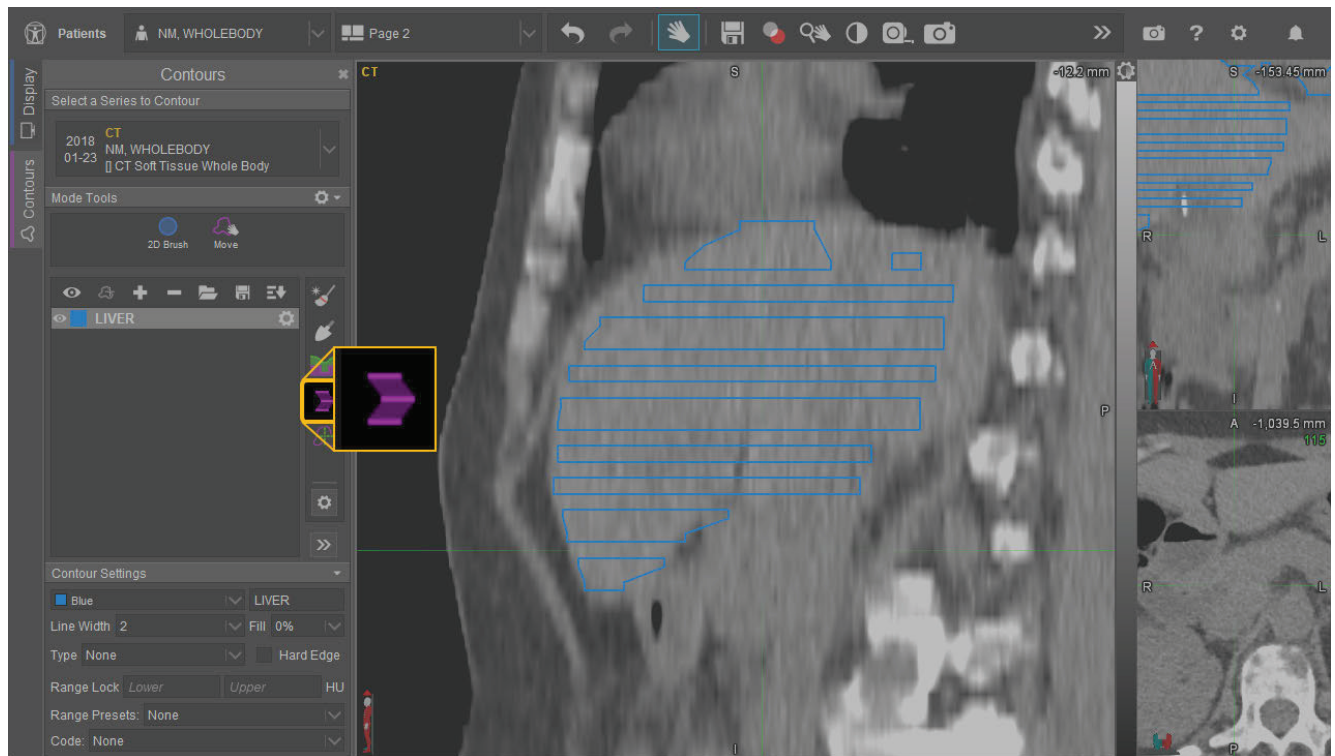
Tip: The Interpolate tool only works on contours created in an image's default acquisition plane. For example, using the tool in the axial plane of a sagittally acquired CT has no effect.



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.



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](#)
- [3D Brush Companion Tool: Dynamic Brush™](#)

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.

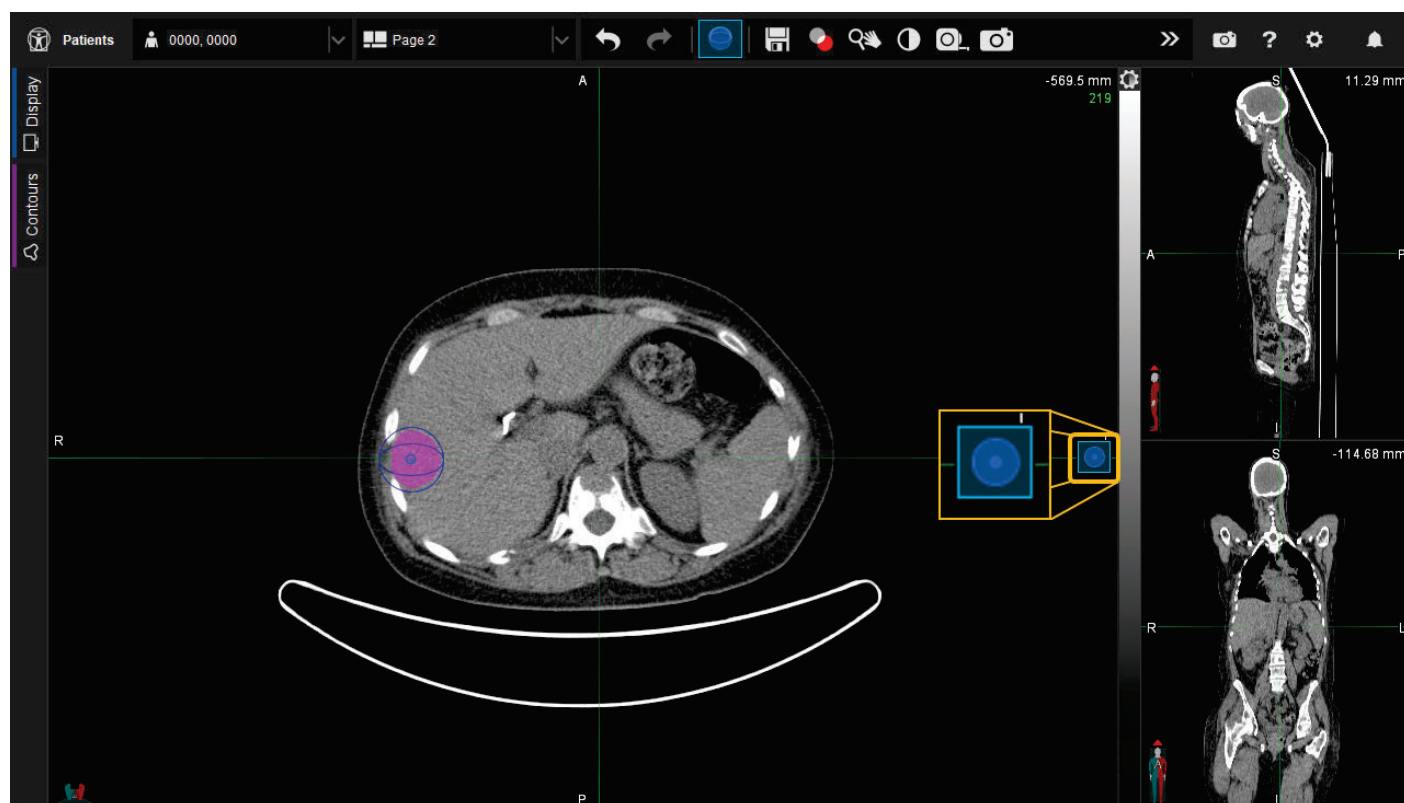





Tip: Enable this behavior without a key modifier by going to Settings  >> **General Preferences** >> **Contouring** and selecting **Paintbrush will add to existing contour when used a distance outside it.**

3D Brush Companion Tool: Dynamic Brush™



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

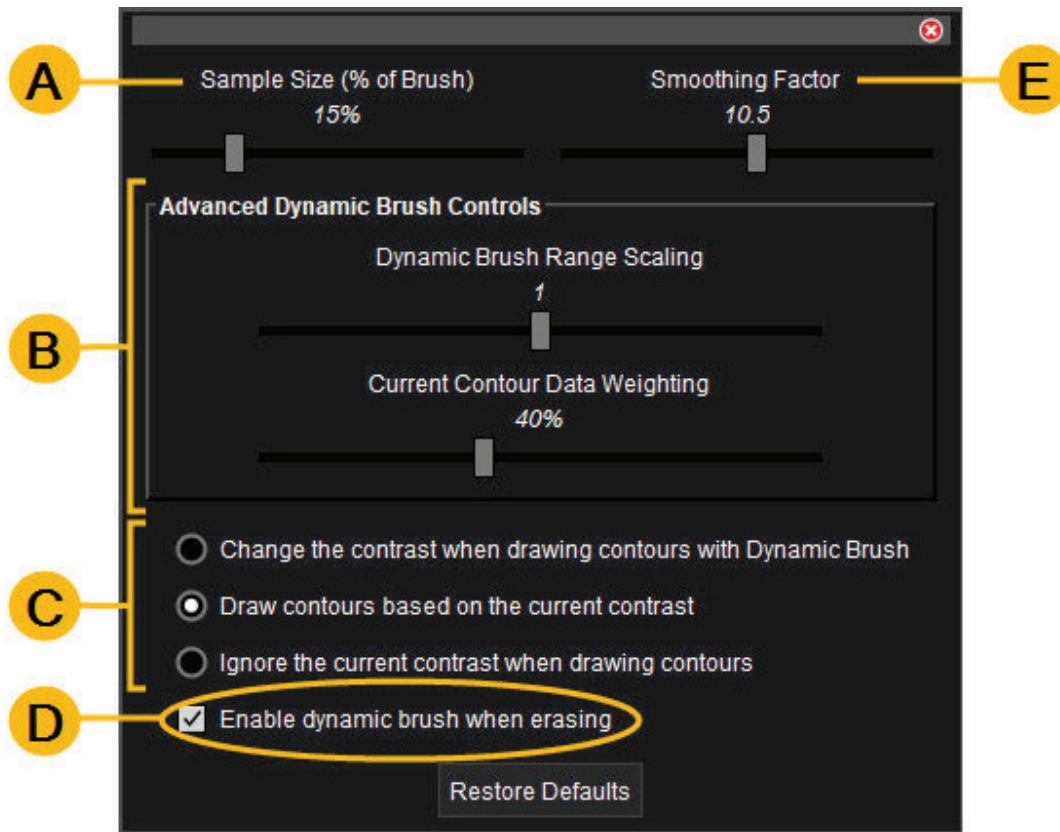
Use the Dynamic Brush to contour more quickly. When the Dynamic Brush is activated, the brush samples intensities within the inner circle in order to restrict the brush to areas of similar intensity.



- 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.



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.

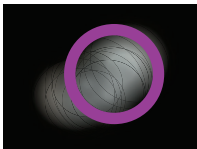


Tip: For best results with liver tissue, set the Sample Size to 15% and the Smoothing Factor to 2.5.

Create Contours with the Threshold Tool



MIMTD-703 • 07 Sep 2023

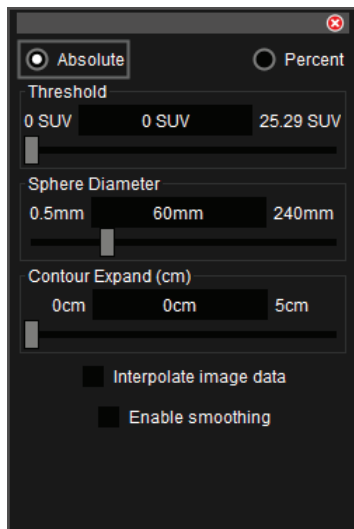
Overview







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.

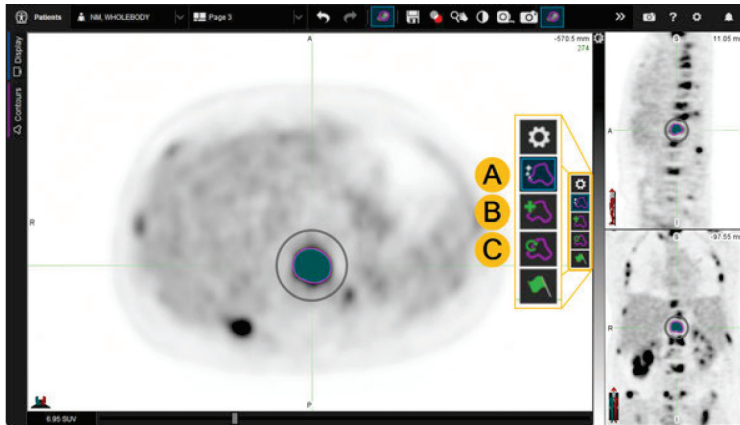
Create a Contour

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.



- 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.



Create Contours with the Pen Tool

MIMTD-1694 • 30 Oct 2023

Overview

Use the Pen tool to draw contours by placing points or by drawing freehand lines. Enable Contour CoPilot® with the Pen tool to contour faster.



Related: The 2D Brush is similar to the Pen tool. For more information, see [Create Contours with the 2D Brush](#).

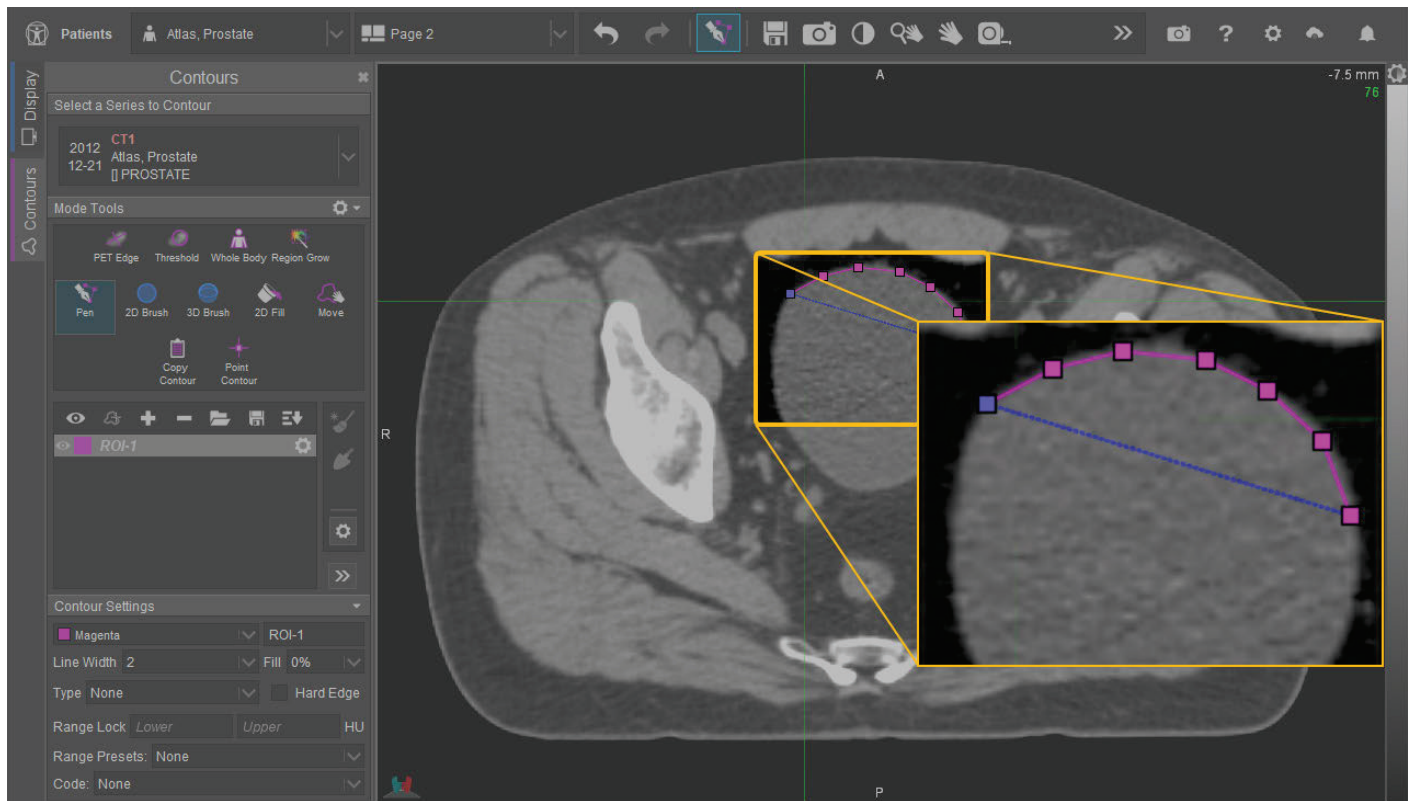



Related: If you use the Pen tool often, you can add it to your toolbar or radial menu. See [Access Tools: The Toolbar and the Radial Menu](#) for more information.

Contents

- [Create Contours Point-by-Point](#)
- [Create Contours Freehand](#)
- [Adjust Pen Tool Options](#)
- [Quickly Contour 3D Volumes with Contour CoPilot](#)

Create Contours Point-by-Point



Activate the **Pen**  tool from the toolbar, radial menu, or the Mode Tools section of the Contours sidebar.

- To place a point, click the desired location.
- To make adjustments as you draw, do any of the following:
 - To move an existing point, left-click drag the point.
 - To add a new point, click a line segment.
 - To delete a point, right-click the point.

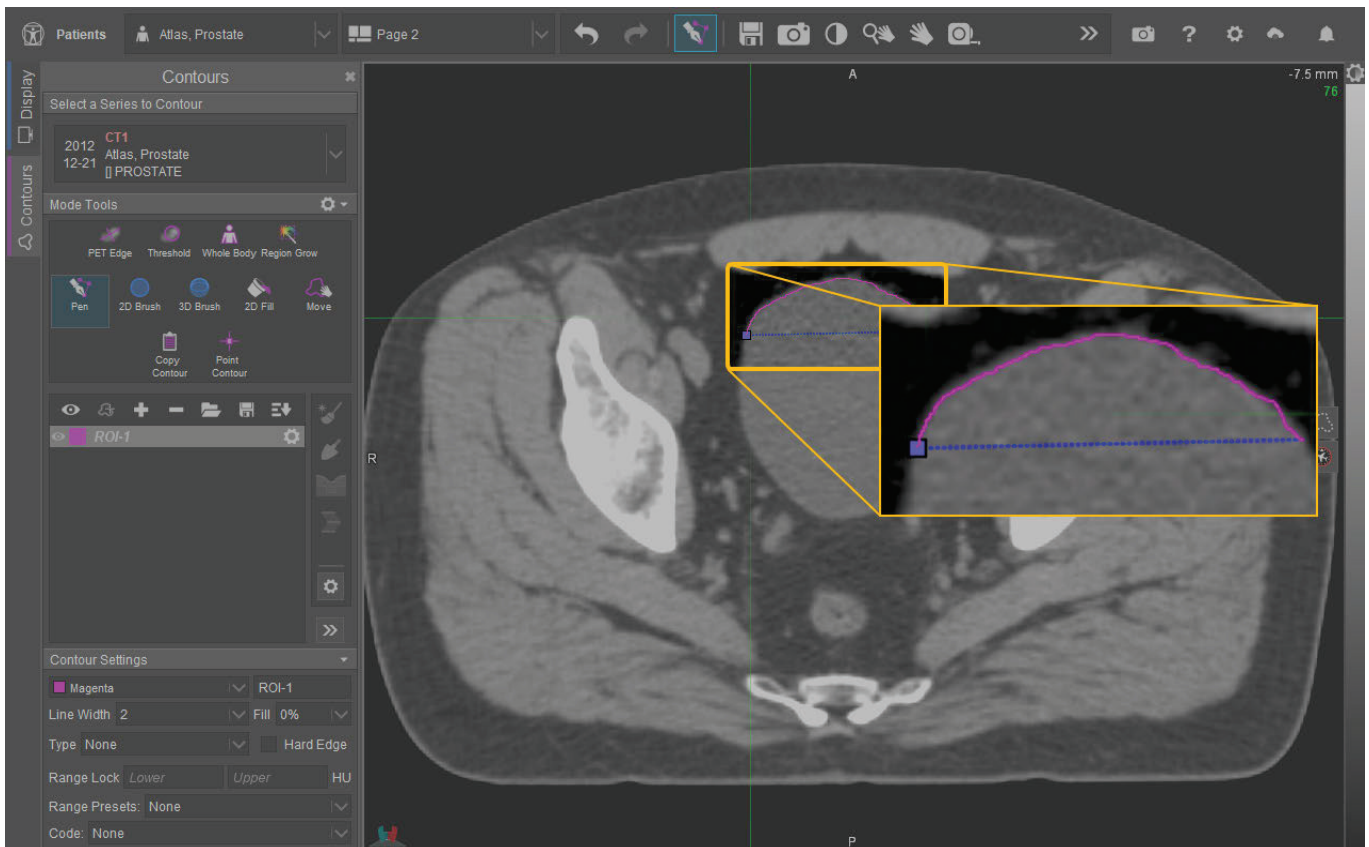


Tip: The above options are only available while you are creating the contour. Once the contour is completed, you can no longer add, delete, or edit points.

- To complete the contour:
 - Click the starting point. A straight line is drawn from the most-recently placed point to the starting point.

- Double-click to place a final point and complete the contour. This option draws two line segments—one from the most-recently placed point to the location of your double-click, and one from the location of the double-click to the starting point.

Create Contours Freehand



Activate the **Pen**  tool from the toolbar, radial menu, or the Mode Tools section of the Contours sidebar.


- To draw a contour freehand, left-click drag.
- To complete the contour, release the mouse button. A straight line is drawn from the tool's current location to the starting point.
- To add to a contour, start drawing within the existing contour and continue outward. The shape you draw is added to the existing contour.
- To remove from a contour, start drawing outside the existing contour and continue inward. The shape you draw is erased from the existing contour.

Adjust Pen Tool Options

There are two options in MIM's General Preferences that directly affect how the Pen tool works:

- **Show completion line with the Pen tool** — Always displays a line from your most-recently placed point to the starting point.
- **Show cursor while contouring freehand using the Pen tool** — Shows a cursor while drawing to help you better track the movement of the tool.

To change either of these options:



1. Click the Settings  button in the upper-right corner of MIM.
2. Select **General Preferences**
3. In the search bar in the General Preferences window, search for "**Pen Tool.**"
4. Click **Advanced** in the left side menu. Both of the above options are available in this window.

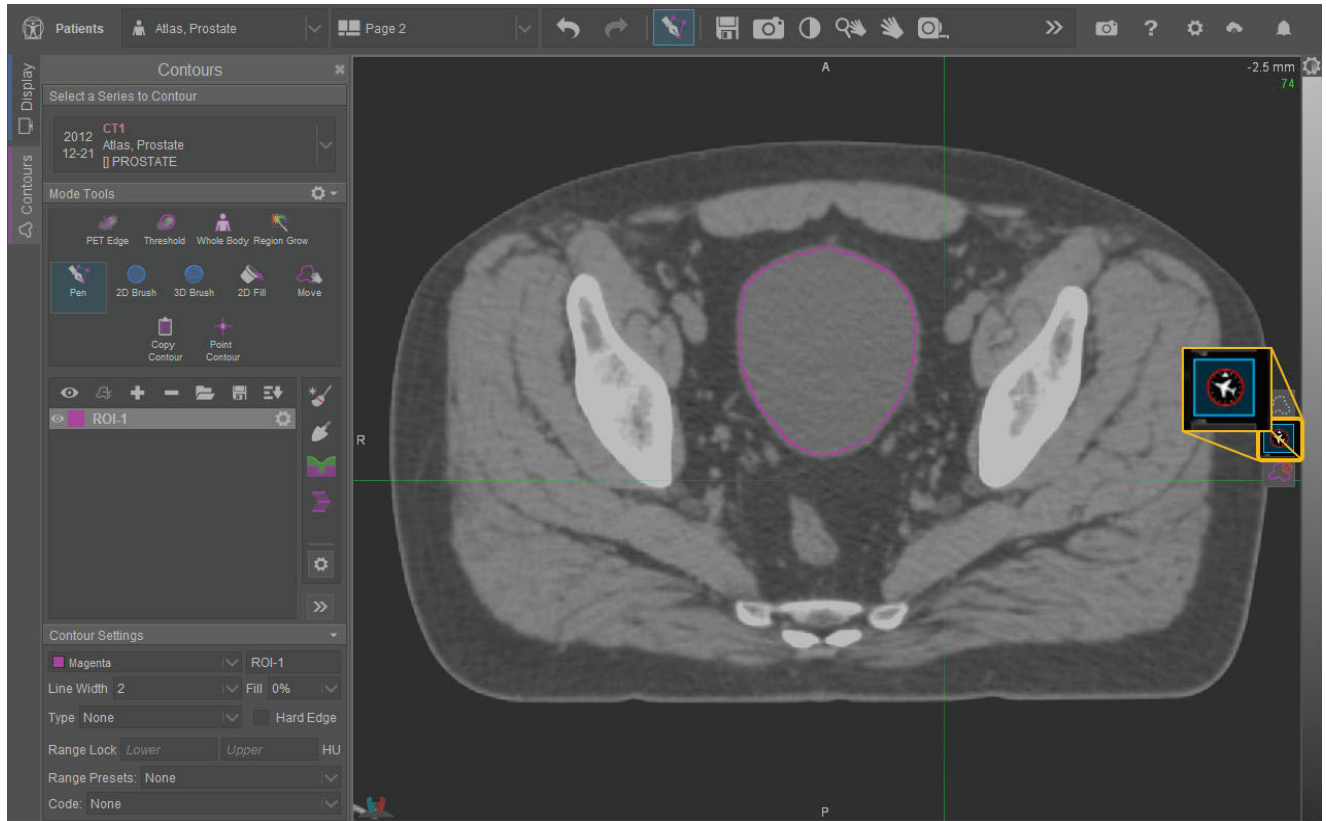


Tip: Choose **Advanced** under Contouring, not under Patient List Options.

Quickly Contour 3D Volumes with Contour CoPilot

Use Contour CoPilot with the Pen tool to quickly contour an entire structure by assessing candidate contours slice by slice. This reduces the need to manually draw on each slice.

1. Activate the **Pen**  tool and create a contour on any slice of any plane.
2. Activate the **Contour CoPilot**  tool from the right edge of any viewport.



3. Scroll to another slice. A candidate contour automatically appears as a color wash on the visible slice.

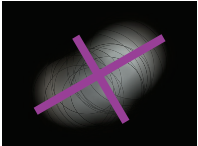


- To accept a candidate contour, click anywhere in the viewport. If necessary, continue to make edits with the Pen or another contouring tool.
 - To reject a candidate contour, right-click anywhere in the viewport. After rejecting the candidate contour, you may use the Pen tool to contour the slice manually.
4. Continue viewing additional slices. Accept the candidate contours where appropriate, and edit or redraw contours as necessary. Proceed in this way until you have contoured the entire volume of interest.

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](#)
- [Compute Long and Short Measurements](#)
 - [Automatic Long and Short Measurements](#)
 - [Manual Long and Short Measurements](#)
- [PET Edge Settings](#)
 - [Apply Measurements to Functional Images Within Fusions](#)
 - [Display Statistics on Fusion Images \(MIM 7.3 and Later\)](#)

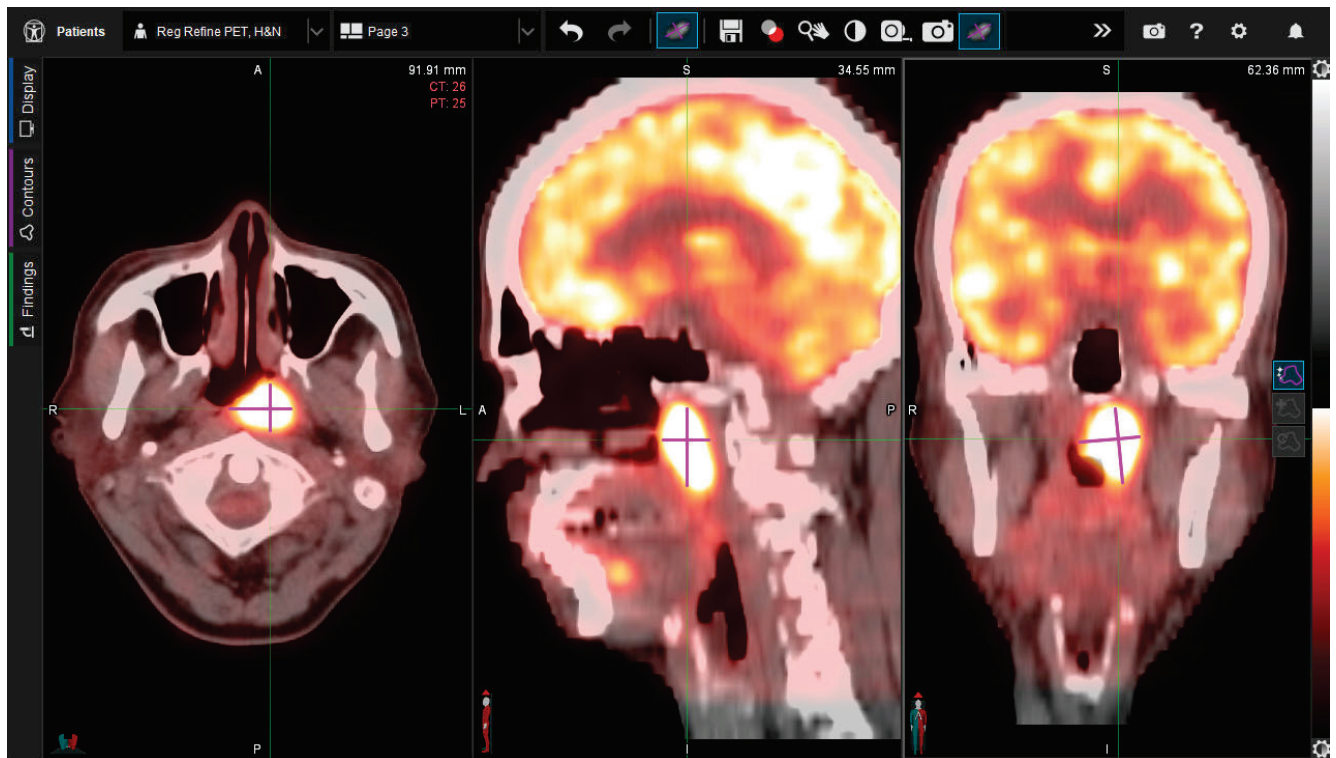
Segment Lesions with PET Edge




1. Select a PET or PET/CT study from the patient list and open the study in a new session.
2. Select the **PET Edge**  tool from the radial menu or MIM toolbar.



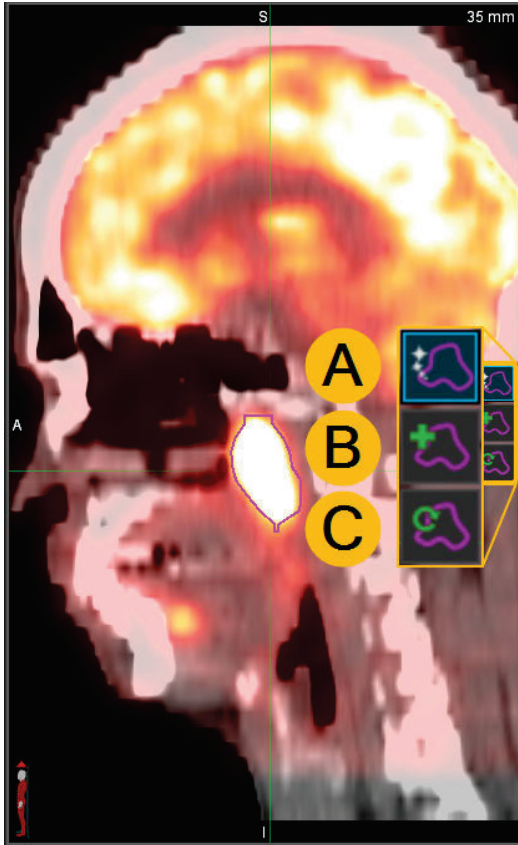
Related: For more information about adding tools to the toolbar or radial menu, see [Access Tools: The Toolbar and the Radial Menu](#).

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](#).

Compute Long and Short Measurements

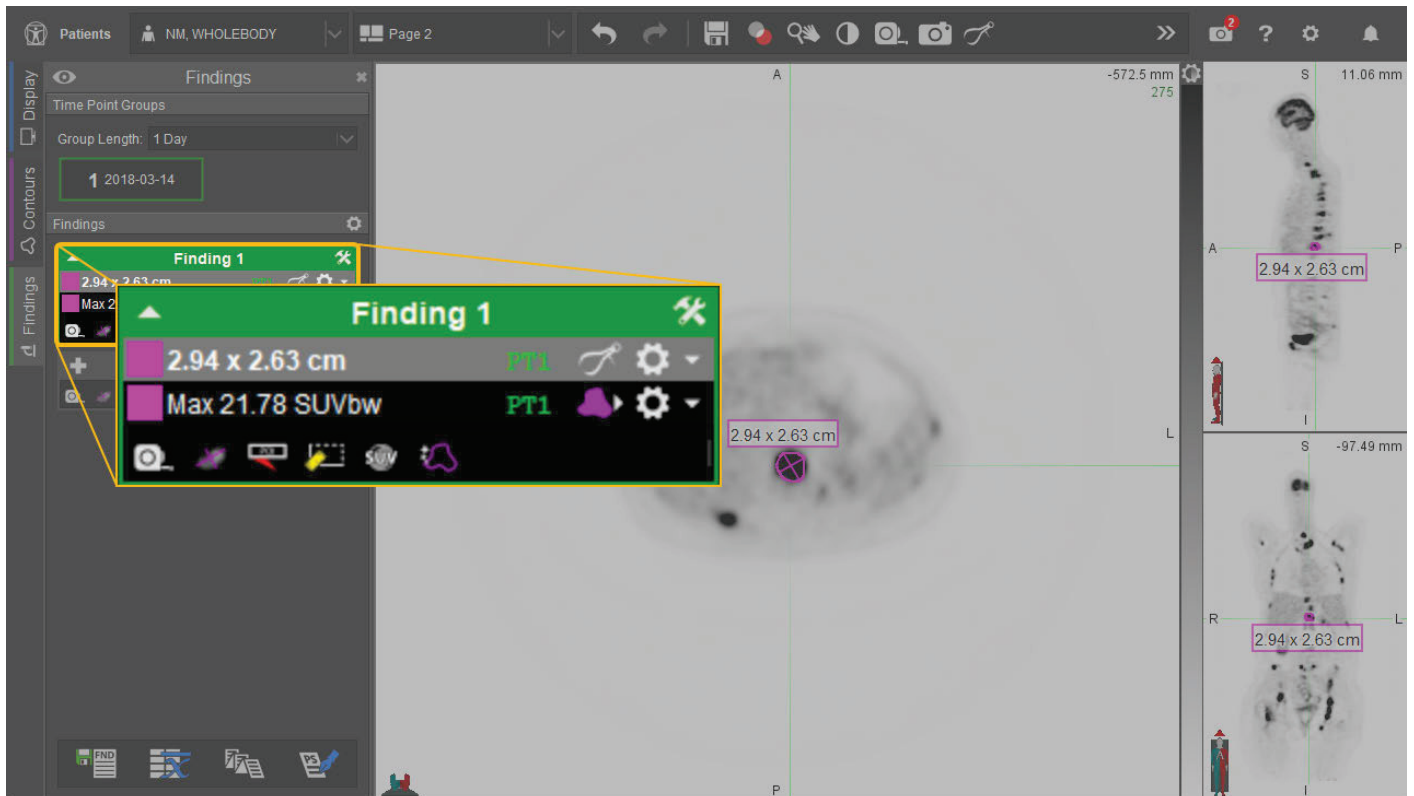
6.1.5

MIM can calculate long and short axes measurements from an ROI, including ROIs created by PET Edge on a functional image. This is useful when performing a tumor assessment, such as RECIST.

After creating a contour with PET Edge, use the **RECIST**  tool to create long and short measurements based on the bounds of the contour. If that contour is representative of the area of interest on the anatomic image, the long and short measurements may be appropriate for RECIST criteria.



Important: If the contour is **not** representative of the area of interest on the anatomic image, the long and short measurements may not be appropriate for RECIST criteria. Use the **2D Measure** tool on the anatomic image with PET Edge set as the secondary tool instead to report more appropriate measurements for RECIST criteria.




You can find the long and short measurements in the Findings sidebar.


Automatic Long and Short Measurements

6.1.5

You can set up MIM to automatically compute long and short measurements when creating a new contour:

1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**recist**". Select **Advanced** on the left side.
3. Select **Automatically compute RECIST when creating a new contour**.
4. Select **Display ghost RECIST values on linked series**.
5. Click **OK** to save the changes and close the window. The next time a contour is drawn, the long and short axes measurements appear along with the PET EdgePET Edge+ measurement in the Findings sidebar.

Manual Long and Short Measurements

1. Draw a contour with any tool such as PET EdgePET Edge+.
2. Click the **RECIST**  tool to display long and short measurements in the Findings sidebar and within the viewport.

PET Edge Settings

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




Related: For more information about applying a User Profile, see [Use Default Preferences with Radiology and Nuclear Medicine User Profiles](#). 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

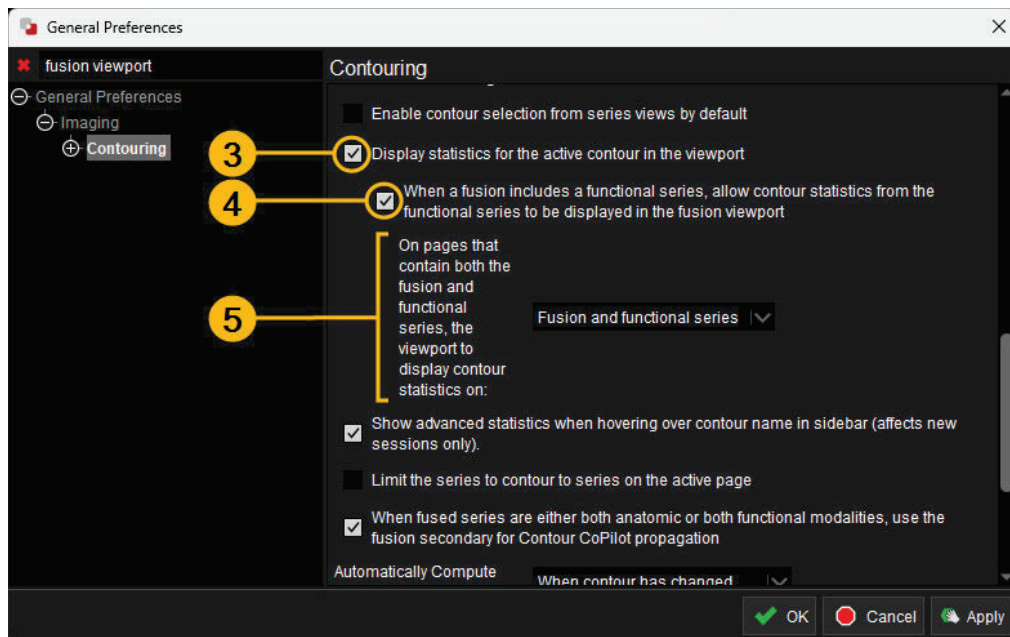
1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**pet edge**". Click **Contouring** on the left side.
3. Select **Create PET Edge or PET Edge+ contours on the functional series when used on a fusion with a single functional series**.
4. Click **Advanced** on the left side.
5. Select **Default the Series to Contour to be the secondary series if a single fusion is present**.
6. 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.



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

Define Lesions with PET Edge® +

MIMTD-655 • 24 Aug 2023

Overview

6.1.3



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.

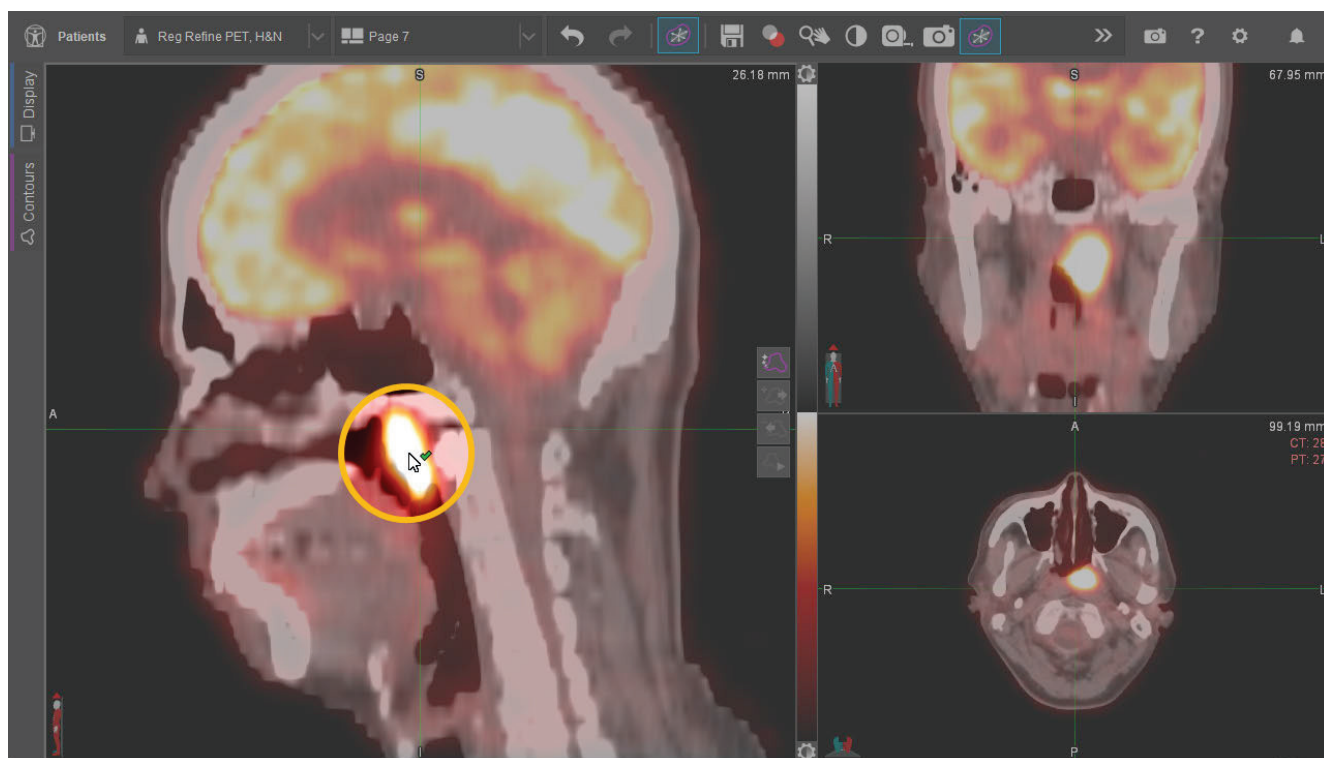
Contents

- [Segment Lesions with PET Edge+](#)
- [Compute Long and Short Measurements](#)
- [PET Edge+ Settings](#)
 - [Apply Measurements to Functional Images Within Fusions](#)
 - [Fill Holes Setting](#)
 - [Display Statistics on Fusion Images \(MIM 7.3 and Later\)](#)

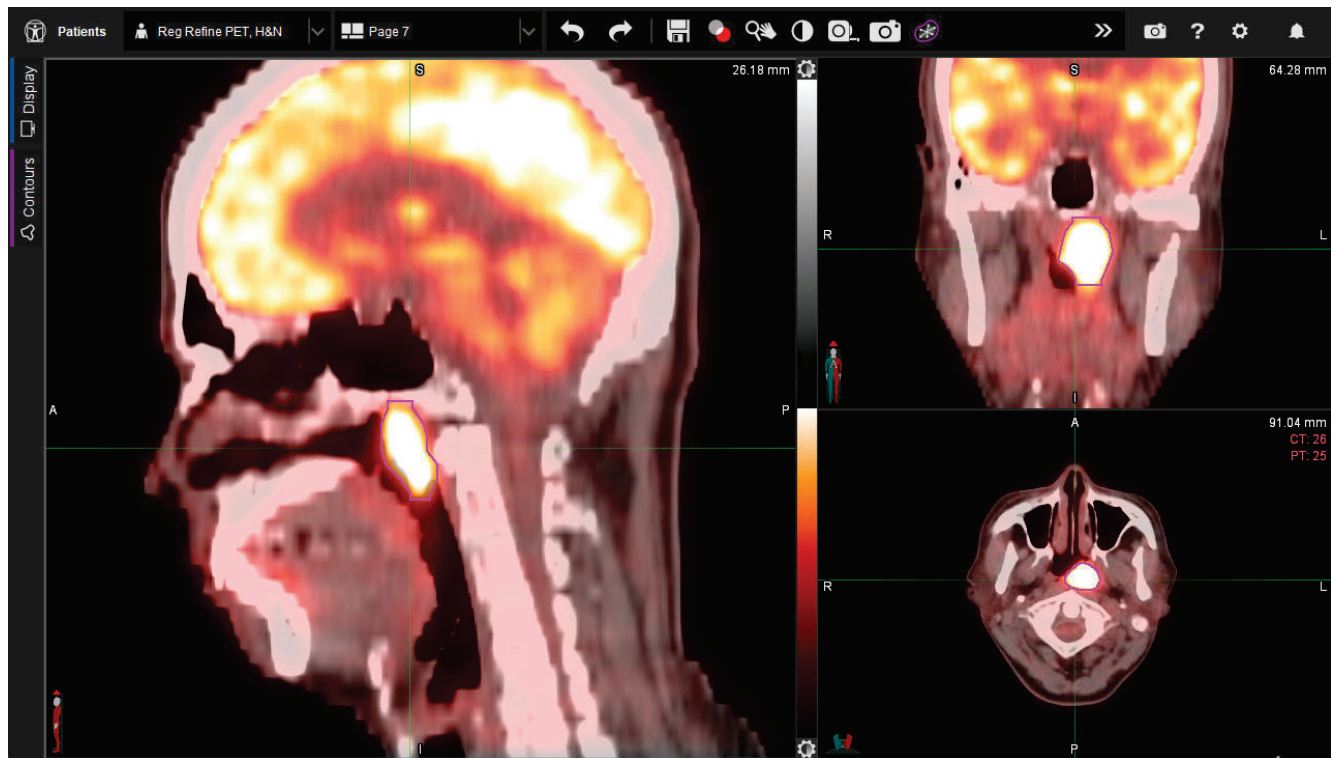
Segment Lesions with PET Edge+



1. Select a PET study from the patient list and open the study in a new session.
2. Select the **PET Edge+**  tool from the Findings sidebar or radial menu.
3. On either the PET or the fusion image, hover over the lesion (roughly in the center of the lesion) and pause.

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






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

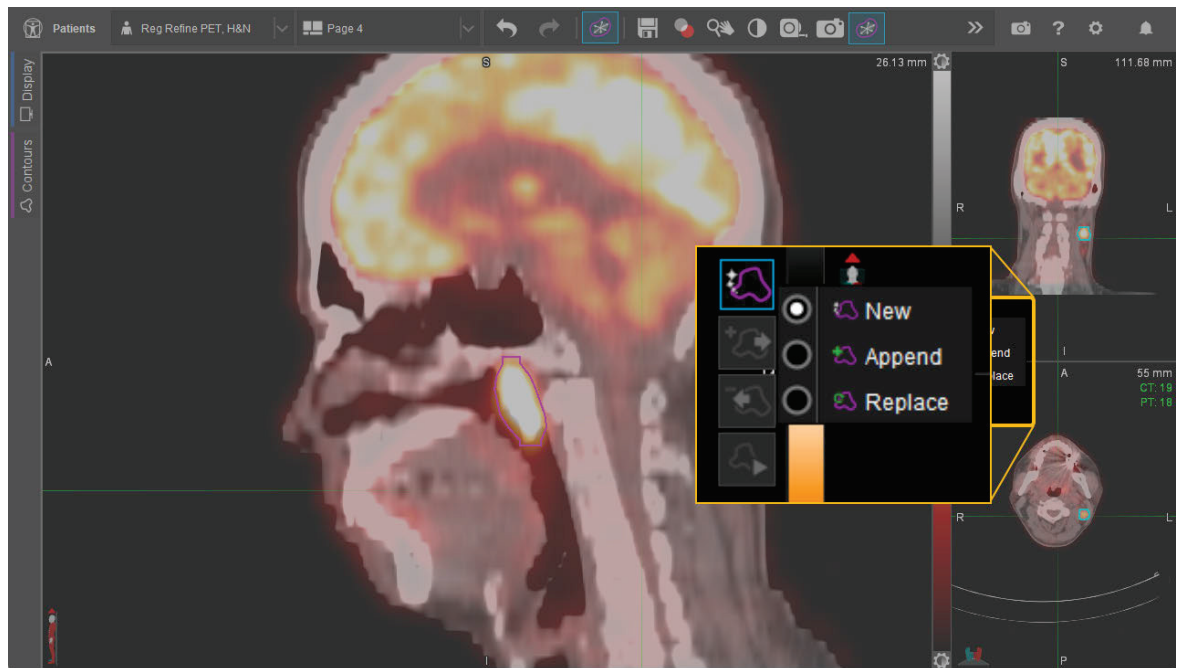


- For some lesions, (e.g., semi-connected lesions), MIM displays the auto-generated contour and also offers other contour options for the region of interest. To view contour options, click the **Next Contour Option**  and **Previous Contour Option**  buttons. Find these buttons on the right side of the 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.
 - Click the **Rerun to Find Larger Candidate Contours**  button on the right side of the viewport.
 - 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.
 - Click the **Contour Creation Mode**  button on the right side of the viewport.
 - 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.
 - Hover the cursor over the lesion or lesion segment, then click after the green check mark appears.




Tip: In MIM 7.3 and later, you can use PET Edge+ simultaneously with other measurement tools to save time. For more information, see [Use Measurement Tools](#). In MIM 7.2 and earlier, this functionality is not available.



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

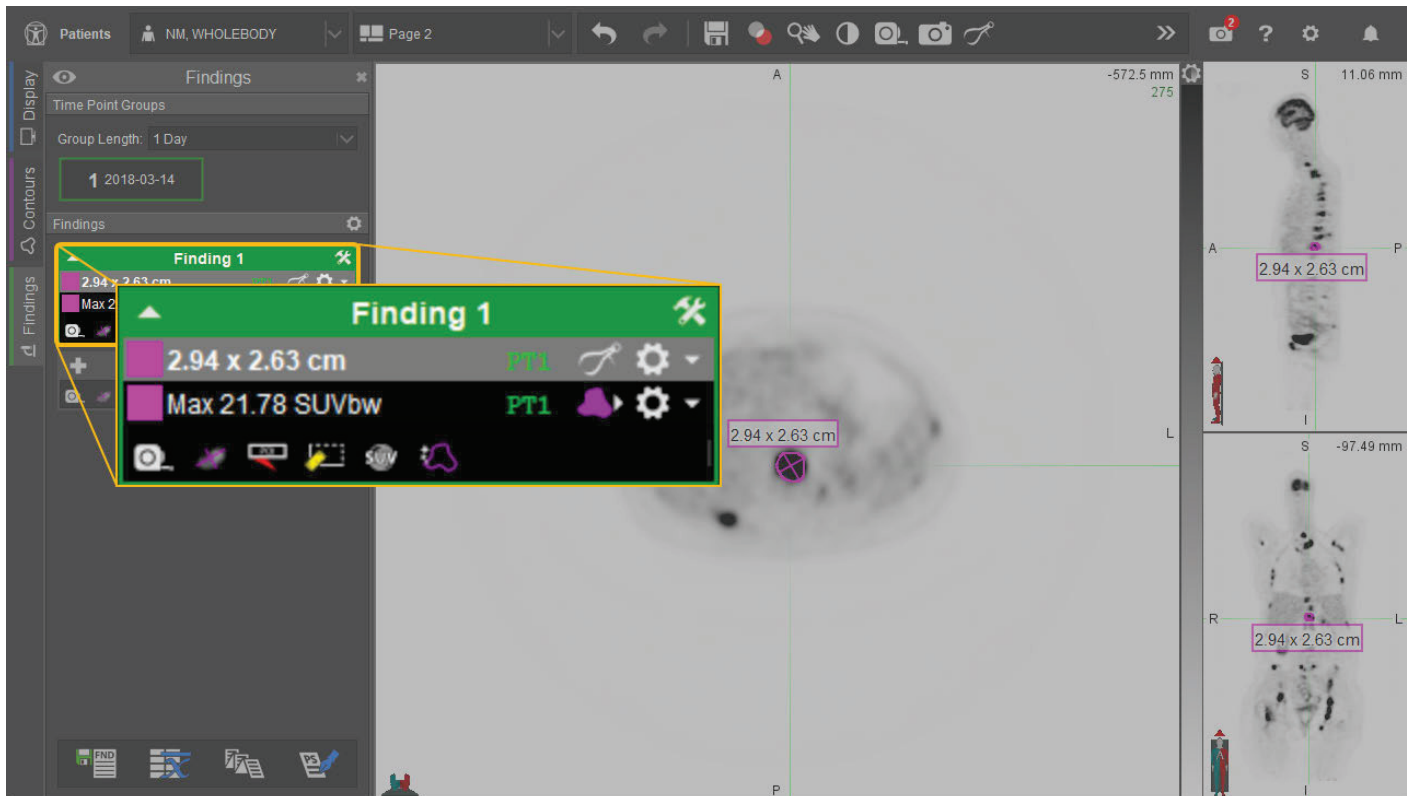
Compute Long and Short Measurements

MIM can calculate long and short axes measurements from an ROI, including ROIs created by PET Edge+ on a functional image. This is useful when performing a tumor assessment, such as RECIST.

After creating a contour with PET Edge+, use the **RECIST**  tool to create long and short measurements based on the bounds of the contour. If that contour is representative of the area of interest on the anatomic image, the long and short measurements may be appropriate for RECIST criteria.




Important: If the contour is **not** representative of the area of interest on the anatomic image, the long and short measurements may not be appropriate for RECIST criteria. Use the **2D Measure** tool on the anatomic image with PET Edge+ set as the secondary tool instead to report more appropriate measurements for RECIST criteria.




You can find the long and short measurements in the Findings sidebar.

Automatic Long and Short Measurements

You can set up MIM to automatically compute long and short measurements when creating a new contour:

1. Click the Settings  button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**recist**". Select **Advanced** on the left side.
3. Select **Automatically compute RECIST when creating a new contour**.
4. Select **Display ghost RECIST values on linked series**.
5. Click **OK** to save the changes and close the window. The next time a contour is drawn, the long and short axes measurements appear along with the PET EdgePET Edge+ measurement in the Findings sidebar.

Manual Long and Short Measurements

Draw a contour with any tool such as PET EdgePET Edge+. Click the **RECIST**  tool to display long and short measurements in the Findings sidebar and within the viewport.

PET Edge+ Settings

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




Related: For more information about applying a User Profile, see [Use Default Preferences with Radiology and Nuclear Medicine User Profiles](#). 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 **Advanced** on the left side.
5. Select **Default the Series to Contour to be the secondary series if a single fusion is present**.
6. Click **OK** to apply and save the changes.

Fill Holes Setting

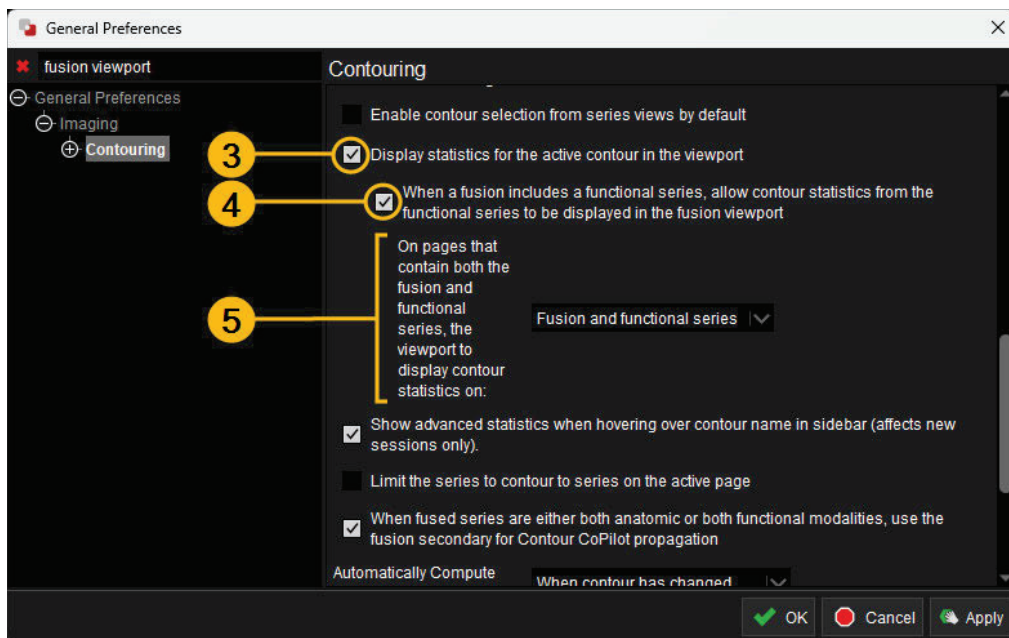
MIM is configured to automatically fill holes for contours created using the PET Edge+ tool. This works, for example, on lesions with necrotic centers. If desired, you can disable this behavior.

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.



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](#)
- [Scenario #2: Tumors Near the Bladder or Other Areas of Normal Activity](#)
- [Scenario #3: Tumors with Necrotic Centers](#)
- [Scenario #4: Calculate Statistics with PET Edge+](#)


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+

6.1.6

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.

Segment ROIs with Sector Assist

MIMTD-1009 • 24 Aug 2023




Overview



Use the Sector Assist tool to divide complex regions of interest (ROI) into precise, anatomically correct sectors. For example, divide a liver or lung contour into a separate sector for each lobe. Or, divide an ROI that includes numerous tumors throughout the body into a separate sector for each organ.

Sector Assist is typically used as part of a MIM Workflow™ that guides you through using the tool. Launch one of the default workflows below, and follow the prompts.



Tip: If you only need straight-line segmentation, use the Simple Sectors  or Complex Sectors  tools. Click the  button at the top of MIM to access these tools.



Related: Refer to [Use Your Own Segmentation Model](#) if you want to create your own segmentation model for Sector Assist or import and use a model separately from a workflow.

Use Sector Assist in a Workflow

1. Launch a workflow that uses Sector Assist. The MIM default workflows are:

- 3D Lung Quant
- 3D Lung Quant with Projected Images



Important: Although a CT is optional when running the 3D Lung Quant workflows, you must include a CT to see the processing described below.

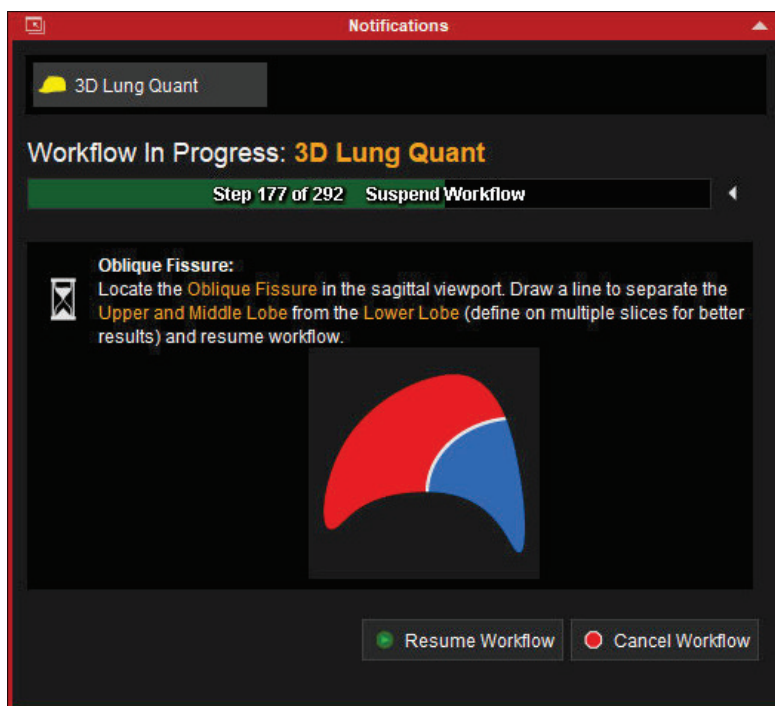


Related: Refer to [Import MIM Workflows™ and Other Content](#) and [Launch MIM Workflows™](#) for more information about working with workflows.

2. At the workflow prompt, left-click drag to draw a line and divide an ROI into sectors.



Tip: Depending on the workflow, you might complete several steps (e.g., contouring the lungs or liver) before you draw lines.

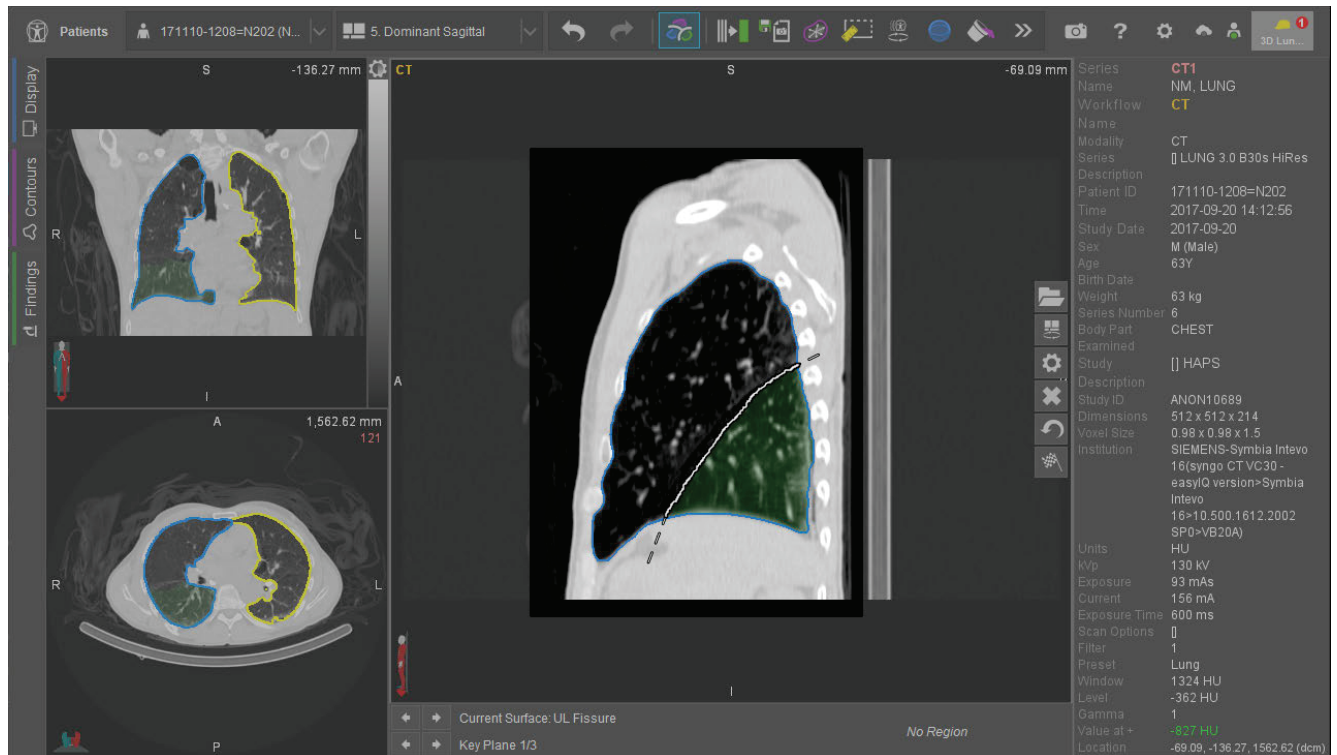


After you draw a line, the sector or sectors that you are creating are shaded with a color, and MIM automatically projects the line onto all slices within the ROI.



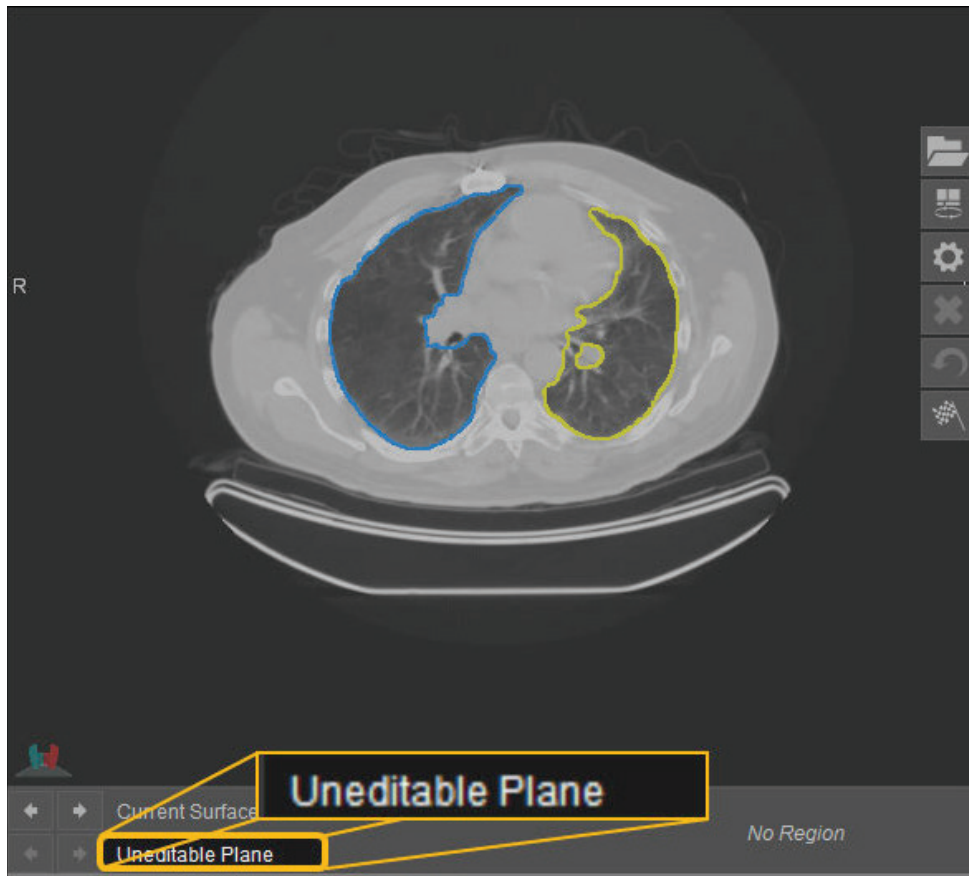
Tip: Press Tab if you want to toggle the color shading on/off.

Lines that you draw appear as solid lines. Automatically generated lines appear as dashed lines.









If you see **Uneditable Plane** in the lower-left corner of the viewport and you cannot draw lines, you are not in the correct viewport. Move your cursor to a different viewport (or press the V key).






3. If you are not satisfied with the line, redraw it on the same slice. You can redraw as many times as needed, which automatically replaces the previous line with your newly drawn line.

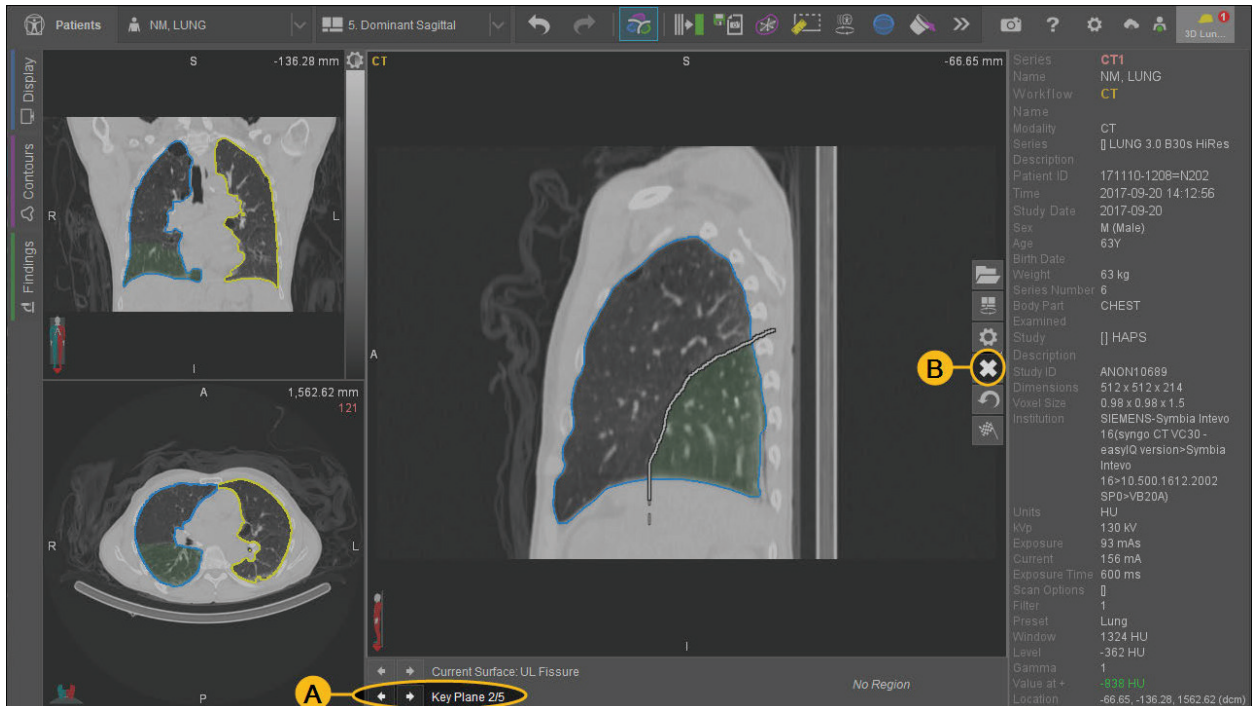




Tip: To revert to a line that you drew previously or compare multiple line attempts, click the undo  button (Ctrl+Z) and the redo  button (Ctrl+Y) as needed.



4. To improve sector accuracy, scroll through the ROI and draw additional lines on several slices. The slices that you draw on are marked as key planes. MIM uses linear interpolation based on the key planes to automatically generate lines onto every slice throughout the ROI.
5. Review your work and adjust the lines or draw more lines as necessary:
 - A. Click the left arrow  and right arrow  buttons in the lower-left corner of the viewport (next to Key Plane) to move between the slices where you manually drew lines.

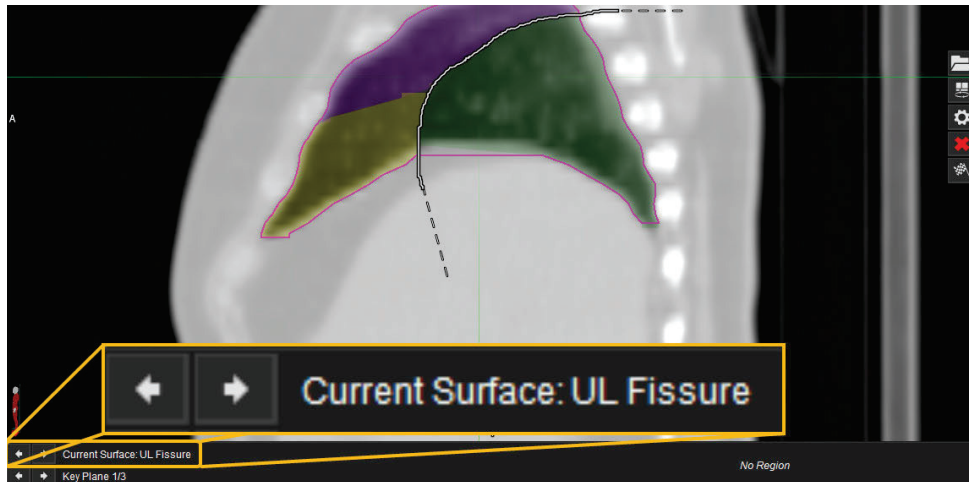
B. To remove the key plane:

- *MIM 7.4 and later:* Click the  button on the right side of the viewport to remove the key plane you are viewing. Click the  button to remove all key planes and start over with segmentation.
- *MIM 7.3 and earlier:* Click the  button on the right side of the viewport to remove the key plane you are viewing.



C. If you see **Normal Plane** instead of **Key Plane** in the lower-left corner of the viewport, you are viewing a plane that does not have a manually drawn line. Click the left arrow  or right arrow  button to jump to a key plane.

6. Click the **Resume Workflow** button in the Notifications window. If the workflow creates multiple sectors, follow the prompts to create the next sectors by repeating steps 2 through 5 above as many times as needed.
7. If the workflow creates more than two sectors and you'd like to review the lines that you drew for previous sectors, click the left arrow  and right arrow  buttons in the lower-left corner of the viewport, next to **Current Surface**. As needed, add or adjust key planes for any of the sectors.



Tip: *MIM 7.4 and later:* If the workflow segments two contours, such as the right and left lung, you can select the contour from the Contours sidebar to return to using Sector Assist on that contour.

MIM 7.3 and earlier: You are not able to go back to a contour that has already been segmented.

8. After you have created all of the sectors that are needed for the workflow, follow the remaining prompts to complete the workflow and review the results.

Use Your Own Segmentation Model

MIMTD-1685 • 05 Sep 2023

Overview

You can create your own Sector Assist model. You can manually apply this model to help quickly segment surfaces.



Related: Refer to [Segment ROIs with Sector Assist](#) for more information about using Sector Assist within MIM Workflows™.

Contents

- [How Segmentation Models Work](#)
- [Create Segmentation Models](#)
- [Import Segmentation Models](#)
- [Use Sector Assist to Segment ROIs](#)

How Segmentation Models Work

Sector Assist uses segmentation models to determine how many sectors to create, where to create sectors, and which order to create sectors in. Segmentation models consist of:

- **Segmentation surfaces** —The area that is divided by a user-drawn line. A segmentation surface is the parent of two segmentation regions or additional segmentation surfaces that have their own children.
- **Segmentation regions** — The sectors that are created by a user-drawn line. Segmentation regions are children of a segmentation surface. Segmentation regions cannot have children.

Example Segmentation Model 1: Liver Lobes (Two Sectors)



- Mid Hepatic Vein (Segmentation Surface)
 - Right Lobe (Segmentation Region)
 - Left Lobe (Segmentation Region)

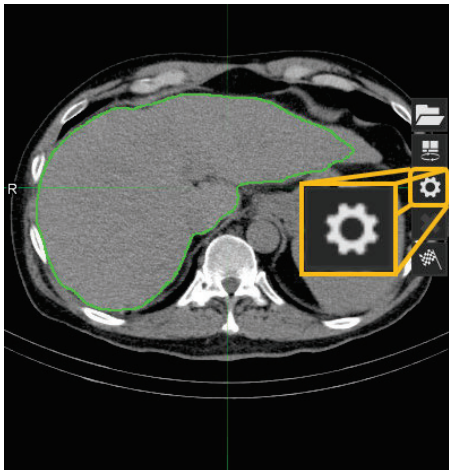
Example Segmentation Model 2: Right Lung Lobes (Three Sectors)

- UL Fissure (Segmentation Surface)
 - MU Fissure (Segmentation Surface)
 - Right Upper Lung (Segmentation Region)
 - Right Middle Lung (Segmentation Region)
 - Right Lower Lung (Segmentation Region)

Create Segmentation Models

If you have a segmentation model, such as one created by a colleague, go to [Import Segmentation Models](#). Otherwise, complete the following steps to create a model.

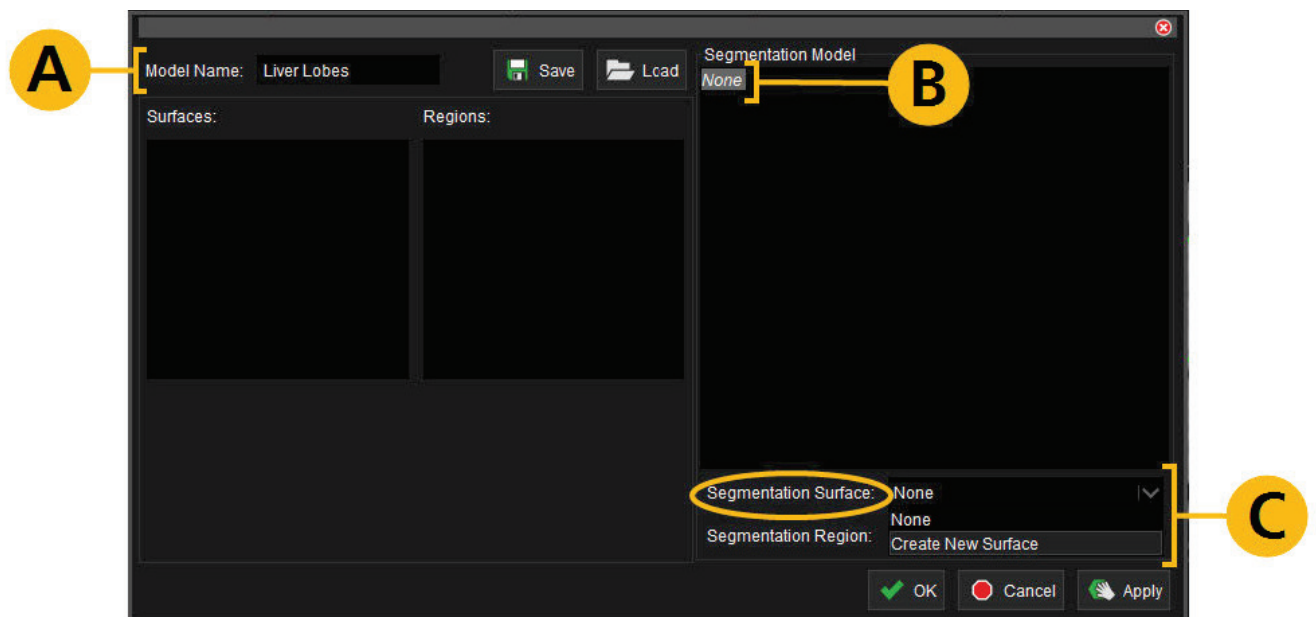
1. Activate the **Sector Assist**  tool from the MIM toolbar.
2. Click the gear  button on the right side of any viewport. The segmentation model window opens.



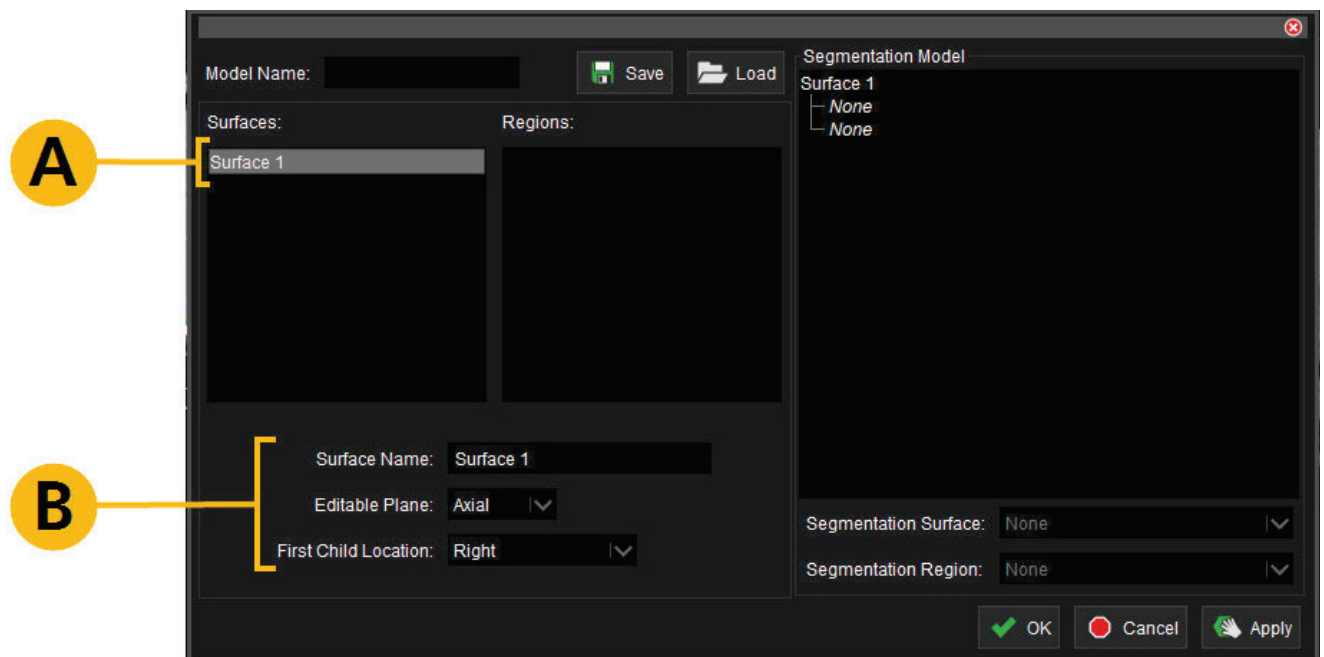
3. Set up the segmentation model:



Tip: If you'd like to base your segmentation model on an existing model, click the **Load** button at the top of the menu and choose the desired model. Enter a new name, make the desired changes, and click the **Save** button.



- A. Enter a name. Choose a name that relates to the sectors that will be created. For example, name the model **Liver Lobes**.
 - B. Click **None** in the **Segmentation Model** column to highlight it.
 - C. From the **Segmentation Surface** dropdown, select **Create New Surface**. The **Surface 1** segmentation surface is created with two empty children.
4. Set up the segmentation surface:



A. Click **Surface 1** in the **Surfaces** column.

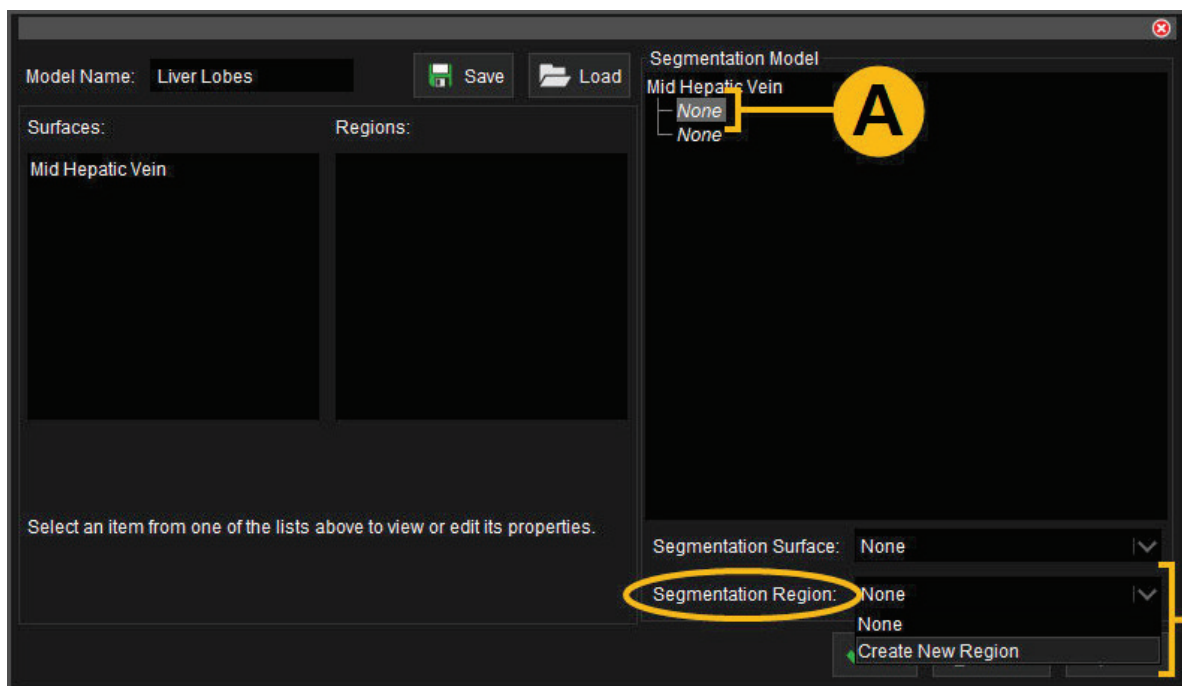
B. Edit the surface properties:

- Enter a **Surface Name** — In most cases, the name should describe a division that you will make when using Sector Assist. For example, if you are segmenting the liver lobes along the middle hepatic vein, call the surface **Mid Hepatic Vein**.
- Choose the **Editable Plane** — This is the plane (i.e., axial, sagittal, or coronal) where users will draw lines to create sectors.
- Choose a **First Child Location** — This is the location that Sector Assist will assign to the first child in your segmentation model hierarchy. For example, if the first child in your segmentation model hierarchy is the **Right Lobe** region, you want the right lobe to be created on the right side of the liver. Choose **Right** from the First Child Location dropdown.



Tip: To delete a segmentation surface, right-click the surface in the **Surfaces** column and select **Delete Surface**.

5. Create segmentation regions:

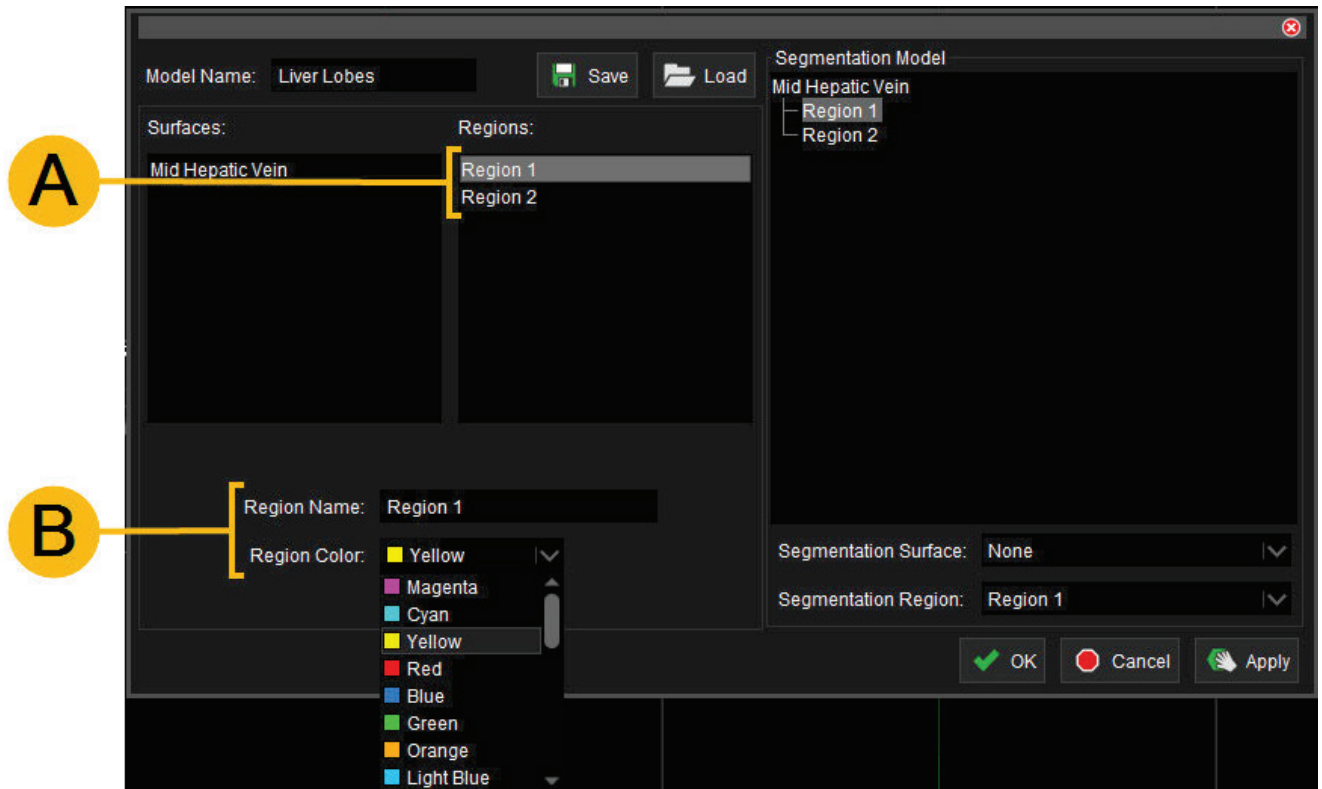


A. Click the first instance of **None** in the **Segmentation Model** column under the segmentation surface.

B. Select **Create New Region** from the **Segmentation Region** dropdown. The **Region 1** region is created.

Follow the same steps for the second instance of **None** in the **Segmentation Model** column.

6. Edit region properties:



A. Click a region in the **Regions** column.

B. Name the region and assign a color. This will be the name and color of the contour that is created for the sector. For example, name the first region **Right Lobe** and the second region **Left Lobe**.

Follow the same steps for all regions in the **Regions** column.



Tip: To delete a segmentation region, right-click the region in the **Regions** column and select **Delete Region**.

7. If you're creating more than two sectors, set up the hierarchy accordingly. For example, set up a segmentation surface, then add another segmentation surface as one of its children. For more information, see [How Segmentation Models Work](#) above.



Tip: Multiple regions or surfaces can be linked together. Use the **Segmentation Surface** dropdown and **Segmentation Region** dropdown to set up part of the hierarchy to be a previously created surface or region.

8. Click the **Save** button at the top of the segmentation model window. Your segmentation model is now available for use.



Important: Clicking the **OK** or **Apply** buttons at the bottom of the segmentation model menu does not save changes. Click the **Save** button to save your model.

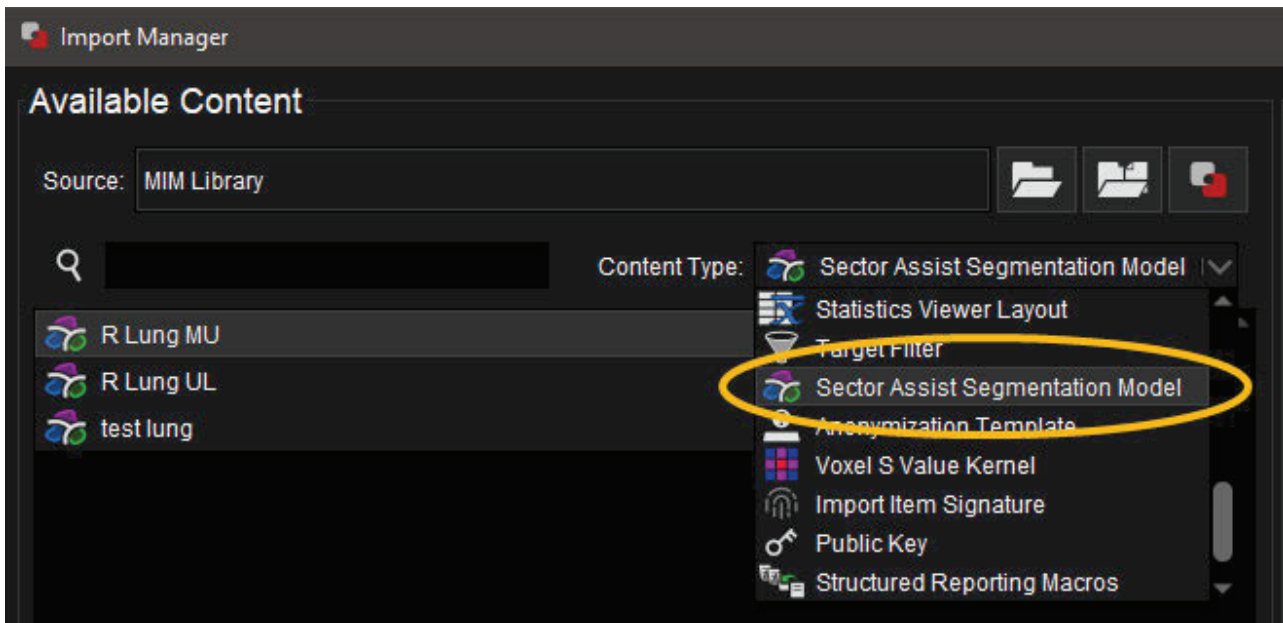
Import Segmentation Models

Use the MIM Import Manager to import and export segmentation models. This is useful, for example, if you'd like to use a segmentation model that was made by a colleague at your site. For instructions, see [Import MIM Workflows™ and Other Content](#).

Once you have imported the segmentation model that you need, see [Use Sector Assist to Segment ROIs](#) below.





Tip: Use the **Content Type** filter in the Import Manager to see only Sector Assist segmentation models.

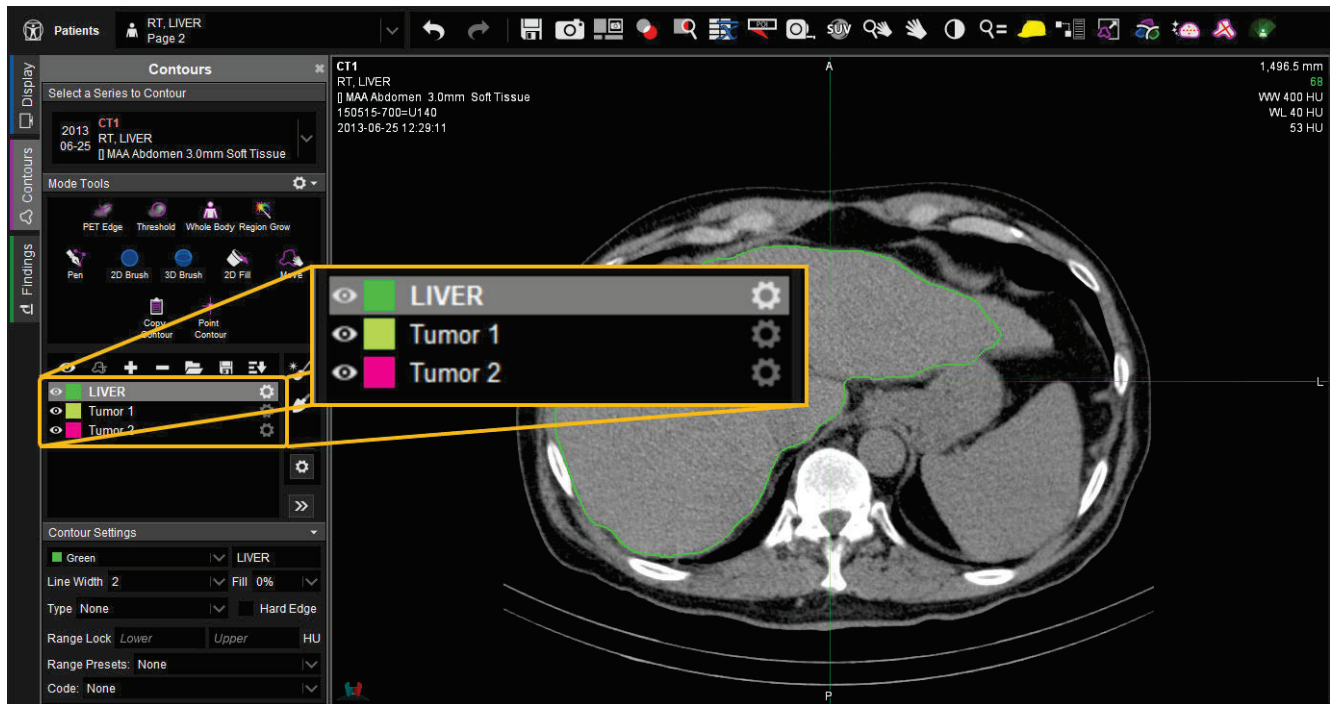


Use Sector Assist to Segment ROIs

Complete the following steps to use the model that you created or imported.

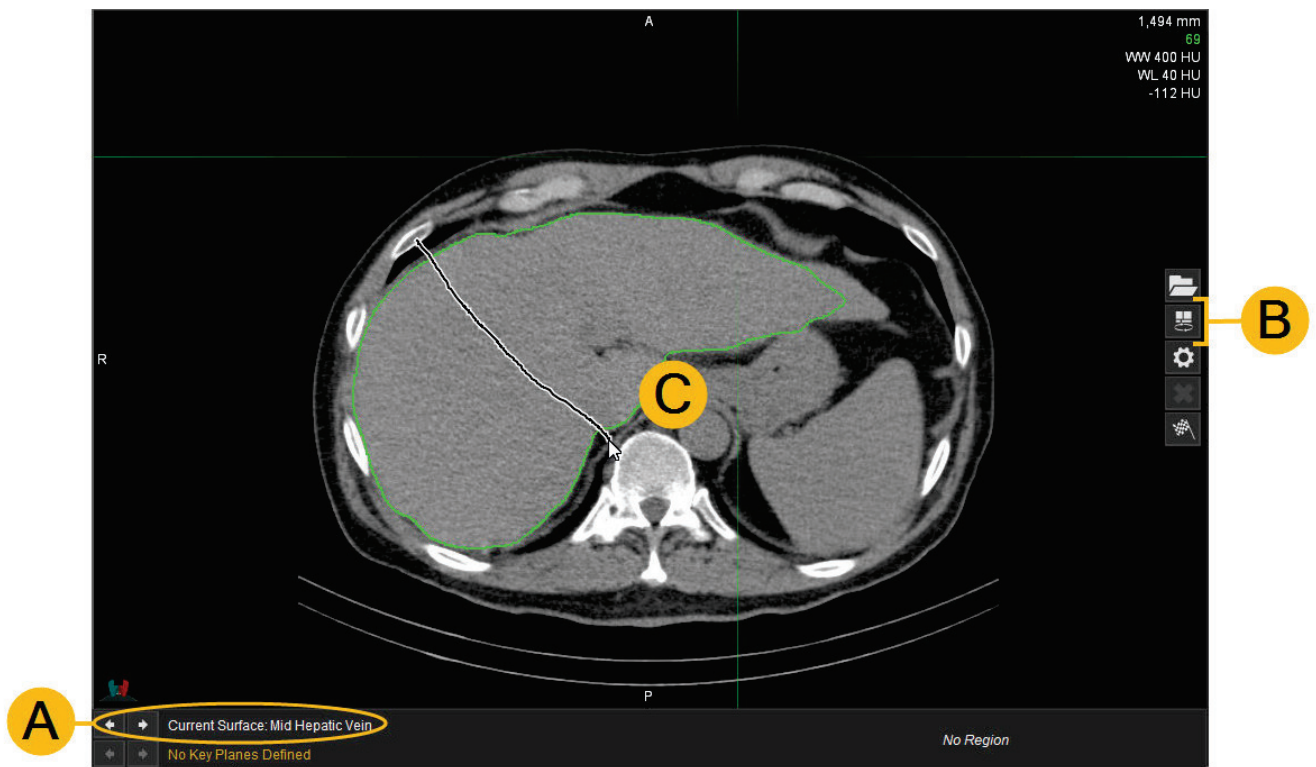
1. Open or create the ROI that you want to divide into sectors (e.g., the liver or the lungs).
2. Activate the **Sector Assist**  tool from the MIM toolbar. If Sector Assist is not on your toolbar, click the  button at the top of MIM to search for the tool.




3. In the Contours sidebar, highlight the ROI that you want to segment.



4. Click the folder  button that appears on the right side of any viewport and select the desired segmentation model.

5. Draw a line to begin creating sectors:



- View the current segmentation surface at the bottom of the viewport. Depending on how the segmentation model is set up, the name of the current surface should indicate where the ROI is being divided. If the segmentation model has multiple segmentation surfaces, click the left arrow  and right arrow  buttons to switch between the surfaces as needed.
- Click the  button on the right side of the viewport to see all available segmentation surfaces in the model and select the desired surface.
- Left-click drag and release to draw a line in the appropriate viewport (i.e., axial, sagittal, or coronal) based on the current surface. For example, draw a line along the middle hepatic vein in the axial viewport.




Tip: If you see **Uneditable Plane** in the lower-left corner of the viewport and you cannot draw lines, you are not in the correct viewport. Move your cursor to a different viewport (or press the V key), or adjust the segmentation model.

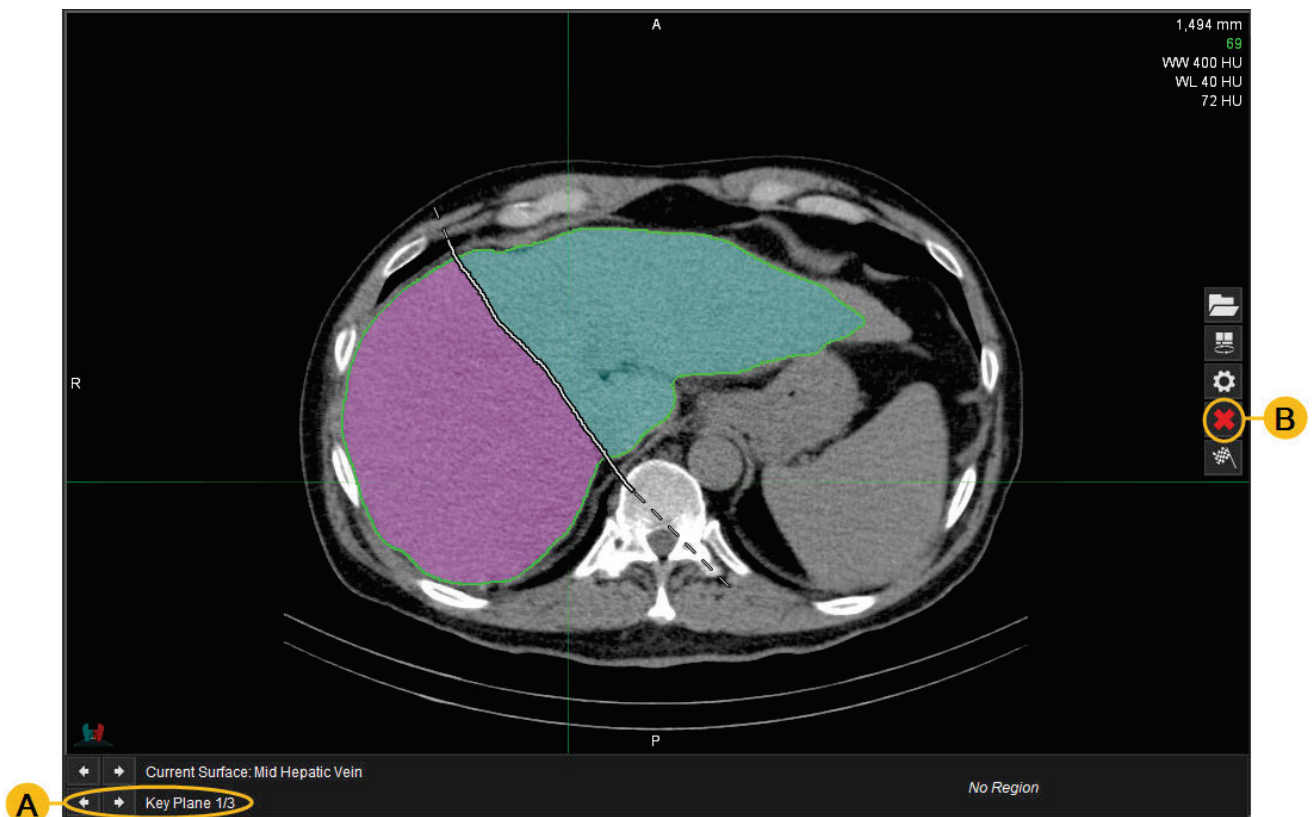
After you draw a line, the sector or sectors that you are creating are shaded with colors, and MIM automatically projects the line that you drew onto all slices within the ROI.





6. If you are not satisfied with the line, redraw it on the same slice. You can redraw as many times as needed.






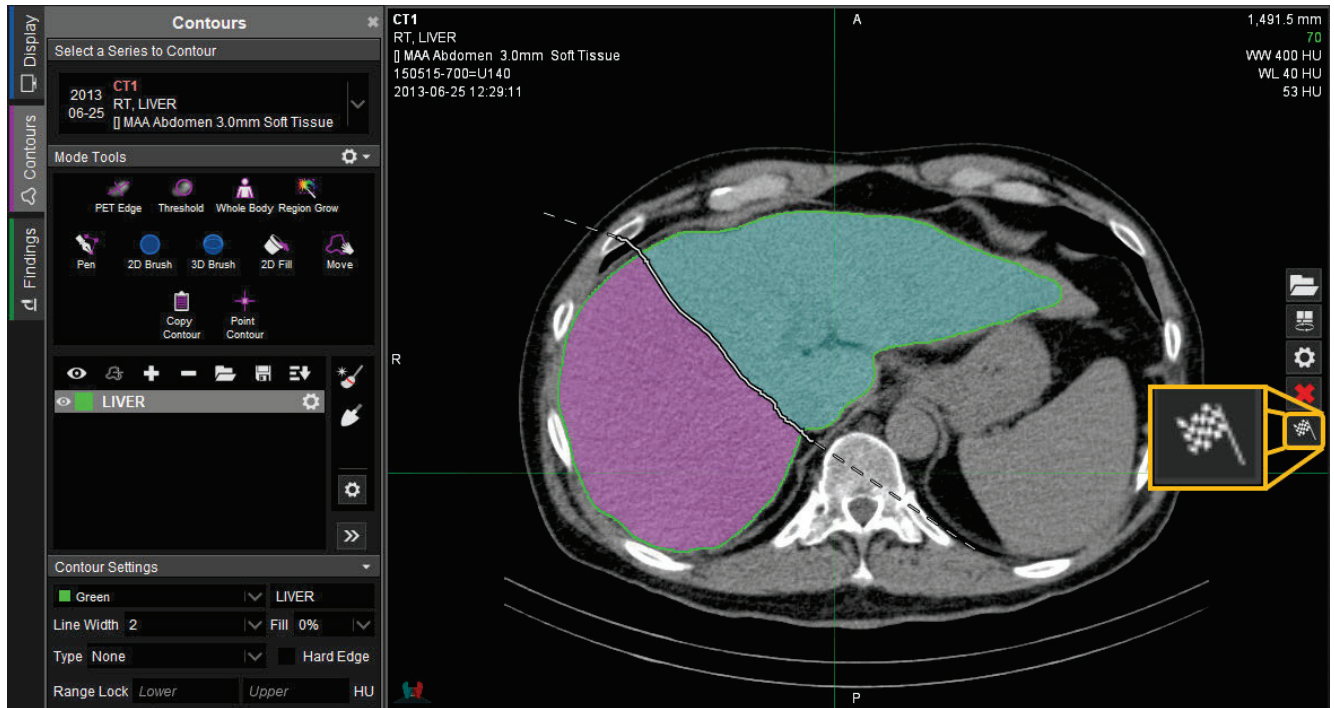
Tip: To revert to a line that you drew previously or compare multiple line attempts, click the undo  button (Ctrl+Z) and the redo  button (Ctrl+Y) as needed.

7. To improve sector accuracy, scroll through the ROI and draw additional lines on several slices. The slices that you draw on are marked as key planes. MIM uses linear interpolation based on the key planes to automatically generate lines onto every slice throughout the ROI. Review your work and adjust the lines or draw more lines as necessary:



- A. Click the left arrow  and right arrow  buttons in the lower-left corner of the viewport (next to Key Plane) to move between the slices where you manually drew lines.
- B. To remove the key plane:
 - *MIM 7.4 and later:* Click the  button on the right side of the viewport to remove the key plane you are viewing. Click the  button to remove all key planes and start over with segmentation.
 - *MIM 7.3 and earlier:* Click the  button on the right side of the viewport to remove the key plane you are viewing.

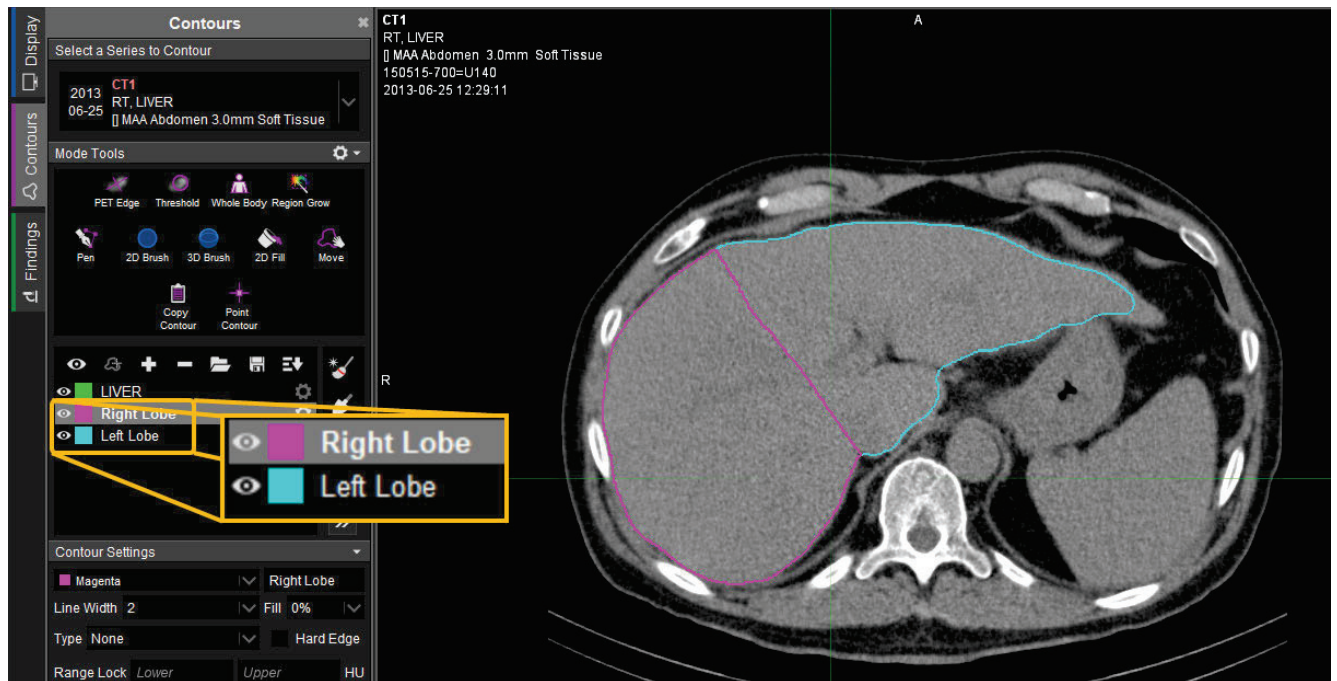
- C. If you see **Normal Plane** instead of **Key Plane** in the lower-left corner of the viewport, you are viewing a plane that does not have a manually drawn line. Click the left arrow  or right arrow  button to jump to a key plane.
8. Follow the steps above as many times as needed until you have created all of the sectors in your segmentation model.
9. Click the flag  button on the right side of the viewport.





A contour is created for each sector.



MIM Encore® User Guide



Tip: After you complete segmentation, clicking the undo  button does not reactivate Sector Assist or restore your segmentation progress. Instead, clicking the undo  button removes the contours that were created for your sectors.